





Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
152 40S ribosomal protein S6	P62753	0.0521	0.1479	0.11	0.3417	0.6999	0.14	0.0025	0.0273
153 40S ribosomal protein S7	P62081	0.0047	0.0436	0.26	0.2885	0.6598	0.25	0.0023	0.0266
154 40S ribosomal protein S8	P62241	0.0109	0.0602	0.23	0.2954	0.6714	0.20	0.0055	0.0359
155 40S ribosomal protein S9	P46781	0.0307	0.1081	0.25	0.4552	0.7878	0.15	0.0163	0.0604
156 40S ribosomal protein SA	P08865	0.0041	0.0408	0.19	0.5178	0.8395	0.09	0.0105	0.0477
157 45 kDa calcium-binding protein	Q9BRK5	0.0008	0.0218	-0.28	0.5098	0.8320	0.11	0.5387	0.5555
158 4-aminobutyrate aminotransferase mitochondrial	P08404	0.0070	0.0499	0.17	0.7109	0.6308	0.16	0.0055	0.0361
159 4f2 cell-surface antigen heavy chain	P08195	0.0003	0.0173	0.69	0.1600	0.6641	0.35	0.0002	0.0182
160 4-trimethylaminobutylaldehyde dehydrogenase	P49189	0.0000	0.0000	0.28	0.4154	0.4498	0.15	0.0107	0.0483
161 5'-3' exoribonuclease 1	Q81ZH2	0.2544	0.4421	-0.06	0.7656	0.8304	0.05	0.3238	0.5115
162 5'-3' exoribonuclease 2	Q9H0D6	0.0946	0.2168	-0.10	0.6066	0.7088	0.09	0.0019	0.0240
163 5'-AMP-activated protein kinase catalytic subunit alpha-1	Q13131	0.4108	0.6303	-3.31	0.5752	0.8820	-1.75	0.5661	0.7870
164 5'-AMP-activated protein kinase subunit beta-1	Q9Y478	0.0637	0.1672	-0.13	0.3574	0.7088	0.13	0.0064	0.0385
165 5'-AMP-activated protein kinase subunit beta-2	Q43741	0.4108	0.6301	-3.31	0.5752	0.8818	-1.75	0.5661	0.7868
166 5'-AMP-activated protein kinase subunit gamma-1	P54619	0.4108	0.6299	-3.31	0.5752	0.8815	-1.75	0.5661	0.7866
167 5-methylcytosine rRNA methyltransferase NSUN4	Q96CB9	0.1760	0.3382	0.07	0.5401	0.8556	0.07	0.8106	0.8466
168 5-nucleotidase domain-containing protein 1	Q5TFE4	0.1086	0.2381	-0.15	0.5854	0.6915	-0.05	0.0157	0.0590
169 5-nucleotidase domain-containing protein 3	Q86UY8	0.1578	0.3120	-0.25	0.6676	0.8308	-0.05	0.1233	0.2416
170 60 kDa heat shock protein mitochondrial	P10809	0.0001	0.0167	0.38	0.1033	0.6340	0.33	0.0001	0.0179
171 60 kDa SS-A/Ro ribonucleoprotein	P10155	0.0398	0.1259	0.26	0.2729	0.6652	0.09	0.8840	0.9078
172 60S acidic ribosomal protein P0	P05388	0.0003	0.0171	0.39	0.2470	0.6588	0.21	0.0034	0.0310
173 60S acidic ribosomal protein P0-like	Q8NHWS	0.1295	0.2706	-0.26	0.3547	0.7064	-0.21	0.3085	0.4926
174 60S acidic ribosomal protein P1	P05386	0.3330	0.5399	-3.31	0.3843	0.7303	0.06	0.0074	0.0406
175 60S acidic ribosomal protein P2	P05387	0.0153	0.0717	0.28	0.2581	0.6628	0.20	0.0037	0.0316
176 60S ribosomal export protein NMD3	Q96D46	0.0671	0.1718	-0.07	0.5574	0.8713	-0.09	0.0005	0.0184
177 60S ribosomal protein L10	P27635	0.0328	0.1130	0.12	0.0225	0.4757	0.15	0.0009	0.0221
178 60S ribosomal protein L10a	P29006	0.0460	0.1371	0.19	0.6471	0.7390	0.09	0.0371	0.1010
179 60S ribosomal protein L10-like	Q96L21	0.1820	0.3457	-0.57	0.1404	0.6528	-0.52	0.1255	0.2449
180 60S ribosomal protein L11	P29213	0.0920	0.2130	0.19	0.2570	0.6640	0.19	0.0047	0.0334
181 60S ribosomal protein L12	P30050	0.0011	0.0234	0.36	0.0194	0.4652	-0.15	0.8532	0.8829
182 60S ribosomal protein L13	P26373	0.2089	0.3817	0.10	0.3808	0.7273	0.17	0.0208	0.0697
183 60S ribosomal protein L13a	P40429	0.0652	0.1690	0.13	0.3986	0.7427	0.19	0.0196	0.0674
184 60S ribosomal protein L14	P50914	0.0086	0.0551	0.25	0.4098	0.7506	0.15	0.0078	0.0415
185 60S ribosomal protein L15	P61313	0.0787	0.1922	0.14	0.3164	0.6803	0.21	0.0096	0.0456
186 60S ribosomal protein L17	P18621	0.0350	0.1170	0.14	0.3626	0.7107	0.18	0.0062	0.0381
187 60S ribosomal protein L18	Q70720	0.0371	0.1212	0.21	0.5461	0.8614	0.11	0.0202	0.0683
188 60S ribosomal protein L18a	Q02543	0.0148	0.0708	0.33	0.1890	0.6696	0.26	0.0122	0.0516
189 60S ribosomal protein L19	P04808	0.0546	0.1529	0.15	0.2164	0.6602	0.26	0.0063	0.0384
190 60S ribosomal protein L21	P46778	0.5610	0.6298	0.03	0.4056	0.7485	0.13	0.0398	0.1062
191 60S ribosomal protein L22	P35268	0.0267	0.0990	0.18	0.2687	0.6634	0.20	0.0005	0.0188
192 60S ribosomal protein L22-like 1	Q6P5R6	0.0071	0.0498	0.22	0.3304	0.6893	0.14	0.0109	0.0483
193 60S ribosomal protein L23	P62829	0.0325	0.1123	0.22	0.2645	0.6641	0.19	0.0107	0.0482
194 60S ribosomal protein L23a	P62750	0.0163	0.0745	0.31	0.2469	0.6599	0.24	0.0054	0.0358
195 60S ribosomal protein L24	P83731	0.0130	0.0667	0.16	0.6864	0.7708	-0.07	0.4464	0.6595
196 60S ribosomal protein L26	P61254	0.0217	0.0878	0.22	0.3217	0.6838	0.22	0.0075	0.0410
197 60S ribosomal protein L27	P61353	0.0226	0.0896	0.15	0.4695	0.7992	0.12	0.0144	0.0564
198 60S ribosomal protein L27a	P46776	0.0353	0.1174	0.21	0.4714	0.8006	0.12	0.0273	0.0829
199 60S ribosomal protein L28	P46779	0.0256	0.0969	0.26	0.2107	0.6623	0.31	0.0045	0.0331
200 60S ribosomal protein L29	P47914	0.5218	0.5935	-0.03	0.6177	0.7171	0.09	0.0120	0.0512
201 60S ribosomal protein L3	P39023	0.0071	0.0498	0.21	0.3257	0.6855	0.22	0.0006	0.0190
202 60S ribosomal protein L30	P62888	0.0047	0.0435	0.42	0.1467	0.6562	0.25	0.0097	0.0460
203 60S ribosomal protein L31	P62899	0.0119	0.0630	0.19	0.2428	0.6595	0.26	0.0107	0.0483
204 60S ribosomal protein L32	P62910	0.9371	0.9524	0.00	0.8314	0.8785	0.02	0.0005	0.0182
205 60S ribosomal protein L34	P49207	0.0089	0.0562	-1.28	0.2124	0.6628	-0.63	0.3404	0.5329
206 60S ribosomal protein L35	P42766	0.3806	0.5965	-0.05	0.8110	0.8642	0.02	0.0219	0.0721
207 60S ribosomal protein L35a	P18077	0.0435	0.1324	0.23	0.2613	0.6645	0.22	0.0132	0.0537
208 60S ribosomal protein L36	Q9Y3U8	0.0004	0.0180	0.46	0.6559	0.7464	0.07	0.0820	0.1760
209 60S ribosomal protein L36a-like	Q969Q0	0.0103	0.0592	0.21	0.2782	0.6650	0.28	0.0020	0.0249
210 60S ribosomal protein L37	P61927	0.4288	0.5063	0.08	0.2502	0.6602	0.16	0.0017	0.0234
211 60S ribosomal protein L37a	P61513	0.0454	0.1361	0.20	0.2911	0.6693	0.12	0.0651	0.1490
212 60S ribosomal protein L38	P63173	0.0206	0.0848	0.18	0.2669	0.6426	-0.18	0.3057	0.4889
213 60S ribosomal protein L39	P62891	0.0030	0.0371	-0.17	0.0423	0.5677	-0.40	0.4255	0.6352
214 60S ribosomal protein L3-like	Q92901	0.0041	0.0407	-0.24	0.1272	0.6428	0.33	0.0070	0.0401
215 60S ribosomal protein L4	P36578	0.1110	0.2421	0.12	0.5645	0.8781	0.09	0.0188	0.0655
216 60S ribosomal protein L5	P46777	0.0601	0.1621	0.18	0.2204	0.6595	0.21	0.0056	0.0363
217 60S ribosomal protein L6	Q02878	0.0315	0.1100	0.18	0.4753	0.8025	0.18	0.0039	0.0315
218 60S ribosomal protein L7	P18124	0.0463	0.1376	0.21	0.2919	0.6693	0.25	0.0072	0.0401
219 60S ribosomal protein L7a	P62424	0.0299	0.1061	0.17	0.3696	0.7179	0.21	0.0055	0.0358
220 60S ribosomal protein L8	P62917	0.2593	0.4482	0.09	0.2577	0.6715	0.25	0.0354	0.0981
221 60S ribosomal protein L9	P32969	0.0009	0.0225	0.20	0.4963	0.8187	0.05	0.5494	0.7235
222 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 1	P16118	0.4108	0.6298	-3.31	0.5752	0.8813	-1.75	0.5661	0.7864
223 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2	P06825	0.0166	0.0754	0.69	0.0604	0.5926	0.38	0.0649	0.1488
224 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 3	Q16875	0.3850	0.6018	0.04	0.7571	0.8239	0.04	0.5805	0.6377
225 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 4	Q16877	0.1038	0.2305	0.45	0.8339	0.8805	0.11	0.0524	0.1294
226 6-phosphogluconate dehydrogenase decarboxylating	P52209	0.0056	0.0455	0.55	0.2096	0.6616	0.28	0.0059	0.0373
227 6-phosphogluconolactonase	P09536	0.0051	0.0440	0.05	0.6929	0.7240	0.02	0.0896	0.1877
228 7, 8-dihydro-8-oxoguanine triphosphatase	P36639	0.8853	0.9099	0.00	0.4553	0.7877	0.10	0.0167	0.0612
229 7-dehydrocholesterol reductase	Q9UBM7	0.0283	0.1023	0.16	0.5689	0.8828	0.09	0.0624	0.1453
230 7SK snRNA methylphosphate capping enzyme	Q7L210	0.1009	0.2265	0.09	0.4399	0.7759	0.07	0.0100	0.0466

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control	
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
231	A disintegrin and metalloproteinase with thrombospondin motifs 12	P58397	0.4108	0.6296	-3.31	0.5752	0.8810	-1.75	0.5661	0.7862
232	A disintegrin and metalloproteinase with thrombospondin motifs 17	Q8TE56	0.0260	0.0976	-0.11	0.5746	0.8861	-0.06	0.0431	0.1128
233	A disintegrin and metalloproteinase with thrombospondin motifs 19	Q8TE59	0.0039	0.0398	0.41	0.1872	0.6665	0.26	0.0031	0.0302
234	ABI gene family member 3	Q9P2A4	0.6937	0.7483	-0.07	0.3086	0.6782	-0.36	0.9219	0.9388
235	Abi interactor 1	Q8IZP0	0.7642	0.8080	0.03	0.7133	0.7900	0.06	0.5727	0.6304
236	Abi interactor 2	Q9NYB9	0.4108	0.6294	-3.31	0.5752	0.8807	-1.75	0.5661	0.7860
237	Abnormal spindle-like microcephaly-associated protein	Q8IZT6	0.0310	0.1088	0.17	0.0490	0.5743	0.35	0.0055	0.0362
238	Acetoacetyl-CoA synthetase	Q86V21	0.4011	0.6209	-0.04	0.4489	0.7837	0.14	0.1321	0.2540
239	Acetolactate synthase-like protein	A1L0T0	0.1073	0.2359	-0.22	0.9365	0.9570	0.01	0.0273	0.0828
240	Acetyl-CoA acetyltransferase cytosolic	Q9BWD1	0.3851	0.6016	-0.17	0.4866	0.8100	-0.26	0.0265	0.0815
241	Acetyl-CoA acetyltransferase mitochondrial	P24752	0.4465	0.5239	0.02	0.9156	0.9416	-0.01	0.0003	0.0192
242	Acetyl-CoA carboxylase 1	I13085	0.0253	0.0962	0.07	0.0856	0.6210	0.21	0.0059	0.0374
243	Acetyl-CoA carboxylase 2	O00763	0.2165	0.3916	-0.19	0.2014	0.6603	-0.27	0.9372	0.9517
244	Acidic fibroblast growth factor intracellular-binding protein	O43427	0.7436	0.7917	-0.01	0.8279	0.8761	0.02	0.8382	0.8694
245	Acidic leucine-rich nuclear phosphoprotein 32 family member A	P39687	0.0038	0.0396	0.33	0.1105	0.6332	0.30	0.0038	0.0319
246	Acidic leucine-rich nuclear phosphoprotein 32 family member B	Q92688	0.0990	0.2237	0.24	0.6598	0.7490	-0.15	0.0042	0.0320
247	Acidic leucine-rich nuclear phosphoprotein 32 family member C	O43423	0.1633	0.3201	0.50	0.1048	0.6320	0.64	0.1370	0.2606
248	Acidic leucine-rich nuclear phosphoprotein 32 family member D	O95626	0.5163	0.5887	-0.17	0.6526	0.7436	-0.19	0.2709	0.4441
249	Acidic leucine-rich nuclear phosphoprotein 32 family member E	Q9BT10	0.0061	0.0471	-0.22	0.0142	0.4540	-0.34	0.0063	0.0387
250	Acid-sensing ion channel 1	P78348	0.9800	0.9861	0.00	0.4641	0.7958	-0.43	0.6335	0.6867
251	Aconitate hydratase mitochondrial	Q99798	0.0756	0.1874	0.12	0.2950	0.6717	0.20	0.0160	0.0598
252	Aconitase-binding protein	Q8NEB7	0.5829	0.6503	-0.03	0.2151	0.6613	-0.09	0.3776	0.5768
253	Actin alpha skeletal muscle	P68133	0.0063	0.0480	0.15	0.6255	0.7229	-0.04	0.0004	0.0180
254	Actin aortic smooth muscle	P62736	0.0721	0.1806	-0.59	0.8488	0.8913	0.03	0.0059	0.0370
255	Actin cytoplasmic 1	P60709	0.0095	0.0576	0.34	0.2653	0.6633	0.24	0.0013	0.0224
256	Actin cytoplasmic 2	P63261	0.0050	0.0438	0.25	0.3748	0.7223	-0.18	0.4417	0.6535
257	Actin gamma-enteric smooth muscle	P63267	0.1594	0.3143	-0.32	0.4824	0.8071	0.13	0.0325	0.0927
258	Actin-binding LIM protein 3	O94929	0.4108	0.6292	-3.31	0.5752	0.8805	-1.75	0.5661	0.7857
259	Actin-histidine N-methyltransferase	Q86T17	0.0740	0.1845	0.15	0.0578	0.5871	0.27	0.0089	0.0442
260	Actin-like protein 6A	O96019	0.9839	0.9885	0.00	0.0105	0.4422	-0.31	0.0315	0.0908
261	Actin-like protein 7A	Q9Y615	0.7483	0.7950	0.10	0.5931	0.6976	0.14	0.6145	0.6690
262	Actin-like protein 7B	Q9Y614	0.0096	0.0577	0.36	0.0395	0.5637	0.42	0.5661	0.7906
263	Actin-related protein 2	P61160	0.0001	0.0162	0.18	0.6929	0.7745	0.03	0.4831	0.7029
264	Actin-related protein 2/3 complex subunit 1A	Q92747	0.4108	0.6290	-3.31	0.5752	0.8802	-1.75	0.5661	0.7855
265	Actin-related protein 2/3 complex subunit 1B	O15143	0.1941	0.3618	-0.07	0.7620	0.8278	0.05	0.2329	0.3934
266	Actin-related protein 2/3 complex subunit 2	O15144	0.0205	0.3737	0.05	0.2047	0.6590	0.28	0.0063	0.0385
267	Actin-related protein 2/3 complex subunit 3	O15145	0.1016	0.2276	-0.11	0.9508	0.9672	0.00	0.0235	0.0753
268	Actin-related protein 2/3 complex subunit 4	P59998	0.2703	0.4627	0.08	0.4888	0.8121	-0.10	0.0340	0.0956
269	Actin-related protein 2/3 complex subunit 5	O15511	0.0166	0.0754	0.27	0.8265	0.8752	-0.01	0.0300	0.0879
270	Actin-related protein 2/3 complex subunit 5-like protein	Q9BXP5	0.0021	0.0320	-0.16	0.7927	0.8082	0.01	0.1838	0.3285
271	Actin-related protein 3	P61158	0.2427	0.4281	0.04	0.0082	0.4084	0.15	0.0023	0.0271
272	Actin-related protein 3B	Q9P1U1	0.0984	0.2227	-0.12	0.0861	0.6186	-0.33	0.0013	0.0234
273	Actin-related protein 8	Q9H981	0.4108	0.6288	-3.31	0.5752	0.8800	-1.75	0.5661	0.7853
274	Activated RNA polymerase II transcriptional coactivator p15	P53999	0.3764	0.5917	0.03	0.5975	0.7012	0.08	0.0294	0.0870
275	Activating signal cointegrator 1	Q15650	0.4108	0.6286	-3.31	0.5752	0.8797	-1.75	0.5661	0.7851
276	Activating signal cointegrator 1 complex subunit 3	Q8N3C0	0.4108	0.6285	-3.31	0.5752	0.8794	-1.75	0.5661	0.7849
277	Activator of 90 kDa heat shock protein ATPase homolog 1	O95433	0.0086	0.0551	0.18	0.1454	0.6566	0.26	0.0030	0.0301
278	Active breakpoint cluster region-related protein	Q12979	0.4108	0.6283	-3.31	0.5752	0.8792	-1.75	0.5661	0.7847
279	Actin receptor type-2B	O13795	0.4108	0.6281	-3.31	0.5752	0.8799	-1.75	0.5661	0.7845
280	Activity-dependent neuroprotector homeobox protein 2	Q6Q332	0.5770	0.6446	0.10	0.0949	0.6310	-0.38	0.5097	0.7312
281	Acyl carrier protein mitochondrial	O14561	0.2328	0.4147	-0.09	0.4074	0.7502	-0.06	0.0471	0.1203
282	Acyl carnitine-coA-releasing enzyme	P13798	0.0081	0.0534	0.23	0.0517	0.5759	0.21	0.0033	0.0310
283	Acyl-CoA dehydrogenase family member 9 mitochondrial	Q9H845	0.1852	0.3500	0.09	0.4037	0.7476	-0.15	0.5140	0.7347
284	Acyl-CoA desaturase	O00767	0.0002	0.0170	0.30	0.2170	0.6597	0.08	0.0035	0.0313
285	Acyl-CoA synthetase family member 2 mitochondrial	Q96CM8	0.4882	0.5625	0.02	0.3377	0.6696	0.14	0.0018	0.0188
286	Acyl-CoA-binding protein	P07108	0.0640	0.1676	0.17	0.4666	0.7979	0.11	0.0428	0.1123
287	Acyl-coenzyme A synthetase ACSM5 mitochondrial	Q6NUN0	0.0726	0.1816	0.14	0.0943	0.6303	0.17	0.1147	0.2155
288	Acyl-coenzyme A thioesterase 2 mitochondrial	P49753	0.4108	0.6279	-3.31	0.5752	0.8787	-1.75	0.5661	0.7843
289	Acyl-coenzyme A thioesterase 8	O14734	0.0720	0.1806	-0.13	0.2469	0.6996	0.13	0.0473	0.1205
290	Acyl-coenzyme A thioesterase 9 mitochondrial	Q9Y305	0.4108	0.6277	-3.31	0.5752	0.8784	-1.75	0.5661	0.7841
291	Acyglycerol kinase mitochondrial	Q53H12	0.8562	0.8860	0.01	0.0877	0.6215	0.20	0.1780	0.3212
292	Acyphosphatase-1	P07311	0.4108	0.6275	-3.31	0.5752	0.8781	-1.75	0.5661	0.7839
293	Acyphosphatase-1	Q75608	0.3786	0.5945	0.03	0.5534	0.6869	0.08	0.0283	0.0851
294	Acyl-protein thioesterase 2	O95372	0.0598	0.1619	-0.30	0.7309	0.8040	-0.04	0.0206	0.0692



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7			MDA-MB-231		
		p value	BH q value	log2FC	p value	BH q value	log2FC
376 Alpha-2-macroglobulin receptor-associated protein	P30533	0.0315	0.1099	-0.15	0.1312	0.6454	0.19
377 Alpha-actinin-1	P12814	0.0060	0.0471	0.19	0.2000	0.6637	0.27
378 Alpha-actinin-2	P35609	0.1308	0.2727	0.08	0.2743	0.6646	0.19
379 Alpha-actinin-3	Q08043	0.0872	0.2053	0.18	0.1361	0.6510	0.28
380 Alpha-actinin-4	Q43707	0.0680	0.1733	0.11	0.5314	0.8506	0.10
381 Alpha-aminoadipyl semialdehyde dehydrogenase	P49419	0.1728	0.3341	0.05	0.3477	0.7030	0.14
382 Alpha-actinin-5	P61163	0.1488	0.2977	0.09	0.1085	0.6315	0.23
383 Alpha-actinin-6	Q43768	0.1863	0.3516	0.09	0.6325	0.7289	0.09
384 Alpha-actinin-7	P06733	0.0002	0.0167	0.43	0.0020	0.6174	0.44
385 Alpha-galactosidase A	Q06801	0.9401	0.9548	0.00	0.2801	0.6646	-0.33
386 Alpha-internexin	P16352	0.4108	0.6257	-3.31	0.5782	0.8756	-1.75
387 Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3	Q96083	0.1047	0.2318	0.14	0.9575	0.9714	0.00
388 Alpha-ketoglutarate-dependent dioxygenase alkB homolog 4	Q9NXW9	0.0032	0.0372	-2.64	0.3076	0.6777	-2.15
389 Alpha-ketoglutarate-dependent dioxygenase FTO	Q9C0B1	0.4108	0.6255	-3.31	0.5752	0.8753	-1.75
390 Alpha-N-acetylgalactosaminidase	P17050	0.0067	0.0493	0.27	0.0702	0.4098	0.27
391 Alpha-N-acetylglucosaminidase	P54802	0.0283	0.1022	0.29	0.5913	0.6960	-0.05
392 Alpha-parvin	Q9NVD7	0.9431	0.9573	0.00	0.1103	0.6327	0.13
393 Alpha-protein kinase 2	Q861B3	0.4108	0.6253	-3.31	0.5752	0.8750	-1.75
394 Alpha-S1-asein	P47710	0.5135	0.5961	0.04	0.4777	0.8037	-0.51
395 Alpha-soluble NSF attachment protein	P54920	0.0892	0.2085	-0.12	0.8068	0.8608	0.01
396 Alpha-tubulin	P40222	0.5840	0.6511	0.04	0.0109	0.4343	0.32
397 Aridolipid phosphatase	Q06203	0.1231	0.2605	0.06	0.8978	0.9275	0.01
398 Arine oxidase [flavin-containing] A	P21397	0.9862	0.9896	0.00	0.9790	0.9857	0.00
399 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	Q12904	0.0091	0.0568	0.16	0.2996	0.6736	0.14
400 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	Q13155	0.0010	0.0229	0.28	0.1253	0.6420	0.14
401 Aminopeptidase B	Q9H4A4	0.3504	0.5600	-0.04	0.3152	0.6809	0.12
402 Amyloid-beta A4 precursor protein-binding family B member 2	P15514	0.0010	0.0228	0.85	0.3790	0.7258	-0.18
403 Amyloid-beta A4 precursor protein-binding family B member 3	Q92870	0.4108	0.6251	-3.31	0.5752	0.8748	-1.75
404 Amyloid-beta A4 precursor protein-binding family B member 3	Q95704	0.4108	0.6249	-3.31	0.5752	0.8745	-1.75
405 Amyloid-beta precursor protein	P05067	0.6059	0.6709	-0.03	0.0528	0.5819	-0.38
406 Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 12 protein	Q96Q35	0.4108	0.6248	-3.31	0.5752	0.8743	-1.75
407 AN1-type zinc finger protein 1	Q8TCF1	0.0163	0.0744	-0.37	0.6954	0.7755	-0.07
408 AN1-type zinc finger protein 6	Q6FIF0	0.2190	0.3950	-0.09	0.8433	0.8875	0.06
409 Anaromins	Q6F81R	0.1206	0.2563	0.06	0.5352	0.8512	0.09
410 Anarobins	Q8N7X0	0.4108	0.6246	-3.31	0.5752	0.8740	-1.75
411 Anarobins-associated migratory cell protein	Q13685	0.1370	0.2818	-0.25	0.0803	0.6318	-0.70
412 Angiotensin-1	Q15389	0.0255	0.0966	-0.29	0.7795	0.8412	0.04
413 Angiotensin-2	Q15123	0.4108	0.6244	-3.31	0.5752	0.8738	-1.75
414 Anillin	Q9N0W6	0.0019	0.0305	-0.86	0.1015	0.6319	-0.61
415 Anion exchange protein 3	P48751	0.1886	0.3544	-0.25	0.1980	0.6690	-0.26
416 Ankocorin	Q9P0K7	0.4108	0.6242	-3.31	0.5752	0.8735	-1.75
417 Ankocorin and armadillo repeat-containing protein	Q7Z3J8	0.8031	0.8411	0.06	0.6419	0.7360	-0.18
418 Ankocorin repeat and KH domain-containing protein 1	Q8WZ23	0.6383	0.7002	0.02	0.3806	0.7275	0.07
419 Ankocorin repeat and LIM domain-containing protein 1	Q8NAC6	0.0101	0.0387	-1.28	0.2795	0.6654	-1.23
420 Ankocorin repeat and MYND domain-containing protein 2	Q8V3R8	0.4108	0.6240	-3.31	0.5752	0.8733	-1.75
421 Ankocorin repeat domain-containing protein 11	Q6UB99	0.4108	0.6238	-3.31	0.5752	0.8730	-1.75
422 Ankocorin repeat domain-containing protein 12	Q6UB98	0.4108	0.6237	-3.31	0.5752	0.8727	-1.75
423 Ankocorin repeat domain-containing protein 16	Q6P6B7	0.0480	0.1410	-0.50	0.1743	0.6610	-0.20
424 Ankocorin repeat domain-containing protein 17	Q75179	0.4108	0.6235	-3.31	0.5752	0.8725	-1.75
425 Ankocorin repeat domain-containing protein 18A	Q8V4F6	0.1538	0.3052	-0.30	0.3237	0.6855	-0.19
426 Ankocorin repeat domain-containing protein 20A3	Q5VUR7	0.1483	0.2969	0.03	0.6454	0.7382	0.03
427 Ankocorin repeat domain-containing protein 20A4	Q4UJ75	0.4108	0.6233	-3.31	0.5752	0.8722	-1.75
428 Ankocorin repeat domain-containing protein 20B	Q5CZ79	0.0187	0.0804	0.17	0.0657	0.5950	0.30
429 Ankocorin repeat domain-containing protein 26	Q9UP88	0.3879	0.6047	-0.05	0.7666	0.8306	0.04
430 Ankocorin repeat domain-containing protein 35	Q8N283	0.8871	0.9108	0.01	0.3357	0.6950	0.05
431 Ankocorin repeat domain-containing protein 36C	Q5JPF3	0.1764	0.3387	0.25	0.3024	0.6755	-0.74
432 Ankocorin repeat domain-containing protein 50	Q5ULJ7	0.6440	0.7057	0.02	0.1676	0.6607	0.45
433 Ankocorin repeat domain-containing protein 54	Q6NXT1	0.0003	0.0167	0.42	0.0019	0.2289	0.36
434 Ankocorin repeat domain-containing protein 62	Q6N5T7	0.5168	0.5891	0.03	0.0927	0.2498	0.45
435 Ankocorin-2	Q01484	0.0672	0.1718	0.12	0.0998	0.6351	0.26
436 Ankocorin A1	P04083	0.4108	0.6231	-3.31	0.5752	0.8720	-1.75
437 Ankocorin A11	P05995	0.8816	0.9068	0.01	0.8178	0.8700	0.03
438 Ankocorin A13	P27216	0.1106	0.2414	-0.16	0.1077	0.7123	-0.06
439 Ankocorin A2	P07355	0.0020	0.0311	0.22	0.1905	0.6690	0.26
440 Ankocorin A3	P12429	0.4108	0.6229	-3.31	0.5752	0.8717	-1.75
441 Ankocorin A4	P09525	0.0842	0.2005	-0.06	0.1503	0.6598	0.17
442 Ankocorin A5	P08758	0.0042	0.0408	0.14	0.2020	0.6096	0.18
443 Ankocorin A6	P08133	0.1108	0.2418	0.07	0.1568	0.6620	0.25
444 Ankocorin A7	P20073	0.0276	0.1007	0.25	0.1022	0.6623	0.22
445 Ankocorin A8	P13928	0.0000	0.0000	5.34	0.1346	0.6492	2.90
446 Ankocorin A9	Q76027	0.0084	0.0545	-0.52	0.0600	0.4933	-0.41
447 Anosmin-1	P23352	0.4108	0.6228	-3.31	0.5752	0.8715	-1.75
448 Anosmin gradient protein 2 homolog	Q95994	0.0723	0.1810	0.10	0.1503	0.6604	0.27
449 AP-1 complex subunit beta-1	Q10567	0.5998	0.6659	0.05	0.1925	0.6679	0.17







Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
602 Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase	Q02742	0.0709	0.1785	-0.19	0.8414	0.8862	0.02	0.0210	0.0701
603 Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 4	Q9P109	0.0004	0.0176	0.30	0.2797	0.6652	0.21	0.0022	0.0263
604 Beta-1,3-galactosyltransferase 2	O43825	0.0639	0.1674	-0.12	0.6767	0.6858	-0.08	0.3231	0.5107
605 Beta-actin-like protein 2	Q562R1	0.0069	0.0498	0.14	0.1089	0.6303	-0.15	0.0006	0.0202
606 Beta-adenosine receptor kinase 2	P15626	0.4108	0.6186	-3.31	0.5752	0.8656	-1.75	0.5661	0.7737
607 Beta-arrestin-1	P49407	0.0046	0.0431	-0.63	0.6575	0.7476	-0.07	0.0064	0.0385
608 Beta-catenin-like protein 1	Q8WY46	0.4108	0.6184	-3.31	0.5752	0.8654	-1.75	0.5661	0.7737
609 Beta-contractin	P42025	0.0314	0.1098	0.11	0.1060	0.6311	0.19	0.0183	0.0648
610 Beta-crystallin A3	P05813	0.1871	0.3528	-1.48	0.1683	0.6605	-2.26	0.1399	0.2647
611 Beta-defensin 116	Q30KQ4	0.1474	0.2957	0.30	0.1163	0.6361	0.33	0.0559	0.1351
612 Beta-defensin 119	Q8N690	0.5438	0.6141	-0.04	0.5558	0.8701	-0.08	0.2663	0.4374
613 Beta-defensin 132	Q7Z7B7	0.4108	0.6182	-3.31	0.5752	0.8651	-1.75	0.5661	0.7733
614 Beta-enolase	P13929	0.0114	0.0613	0.25	0.0445	0.5678	0.26	0.0199	0.0680
615 Beta-hexosaminidase subunit alpha	P06865	0.6609	0.7209	0.01	0.3327	0.6916	-0.03	0.1327	0.2548
616 Beta-hexosaminidase subunit beta	P07686	0.0291	0.1042	-0.17	0.6337	0.7070	-0.02	0.2277	0.3867
617 Beta-klotho	Q86214	0.1684	0.3271	-0.10	0.0580	0.5879	-0.31	0.2108	0.3652
618 Beta-parvin	Q9HIB1	0.0056	0.0453	-0.28	0.1164	0.6360	-0.19	0.0299	0.0878
619 Beta-soluble NSF attachment protein	Q9H115	0.2100	0.3826	-0.15	0.0337	0.5290	0.33	0.0196	0.0675
620 Beta-tetradopropionase	Q9UIR1	0.5731	0.6405	1.27	0.1244	0.6412	1.62	0.6062	0.6618
621 BH3-interacting domain death agonist	P55957	0.4456	0.5230	-0.08	0.3158	0.6805	0.11	0.7279	0.7717
622 Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	O43252	0.0024	0.0338	-0.20	0.9971	0.9981	0.00	0.0530	0.1303
623 Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	O95340	0.0150	0.0711	-0.29	0.9879	0.9913	0.00	0.0042	0.0320
624 Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	Q6NYC1	0.2378	0.4221	0.17	0.0122	0.4358	0.37	0.0133	0.0539
625 Bifunctional coenzyme A synthase	Q13057	0.7365	0.7858	-0.02	0.1750	0.6617	0.12	0.5850	0.6412
626 Bifunctional glutamate/proline-tRNA ligase	P07814	0.0261	0.0979	0.12	0.0638	0.7985	0.10	0.0038	0.0314
627 Bifunctional methyltetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	P13995	0.0085	0.0547	0.40	0.3327	0.6921	0.19	0.0369	0.1008
628 Bifunctional purine biosynthesis protein PURH	P31939	0.0653	0.1691	0.08	0.1364	0.6512	0.21	0.0051	0.0350
629 Biliverdin reductase A	P53004	0.0424	0.1303	0.21	0.2008	0.6621	0.23	0.0139	0.0553
630 Biogenesis of lysosome-related organelles complex 1 subunit 1	P78537	0.0148	0.0707	-4.36	0.0495	0.5749	-9.86	0.0125	0.0526
631 Biogenesis of lysosome-related organelles complex 1 subunit 2	Q6QNY1	0.8111	0.8479	0.05	0.6385	0.7335	-0.08	0.1693	0.3089
632 Biorientation of chromosomes in cell division protein 1-like 1	Q8NFC6	0.0001	0.0148	-0.21	0.9107	0.9379	0.02	0.3991	0.6022
633 Bleomycin hydrolase	Q13867	0.0667	0.1711	-2.56	0.0669	0.5934	-9.23	0.0992	0.2028
634 Blood vessel epicardial substance	Q8NE79	0.0601	0.1621	-0.11	0.5007	0.8231	-0.27	0.0008	0.0202
635 Bloom syndrome protein	P54132	0.1634	0.3201	-0.14	0.3762	0.7242	0.08	0.1743	0.3161
636 BMP-binding endothelial regulator protein	Q8NRU9	0.0280	0.1017	0.16	0.4160	0.7548	0.11	0.3642	0.5615
637 BoLA-like protein 1	Q9Y3E2	0.0423	0.1303	-0.40	0.1424	0.6545	-0.33	0.6689	0.7193
638 BoLA-like protein 2	Q9H3K6	0.0446	0.1345	0.12	0.0578	0.5882	0.18	0.0013	0.0235
639 Bone marrow proteoglycan	P13727	0.8767	0.9028	0.15	0.4547	0.7875	0.50	0.0015	0.0225
640 Bone morphogenetic protein 5	P22003	0.4108	0.6180	-3.31	0.5752	0.8649	-1.75	0.5661	0.7731
641 Bone morphogenetic protein receptor type-1A	P36894	0.0049	0.0435	1.22	0.2169	0.6601	0.41	0.0137	0.0549
642 Box C/D snRNA protein 1	Q8NWK9	0.4108	0.6179	-3.31	0.5752	0.8646	-1.75	0.5661	0.7729
643 Brain acid soluble protein 1	P80723	0.0068	0.0494	-0.49	0.3130	0.6807	0.25	0.0664	0.1512
644 Brain-specific angiogenesis inhibitor 1-associated protein 2	Q9UQB8	0.0486	0.1418	0.12	0.4508	0.7849	0.04	0.0041	0.0320
645 Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	Q9UIH4	0.0263	0.0983	0.15	0.1315	0.6457	0.12	0.0033	0.0310
646 Branched-chain-amino-acid aminotransferase, mitochondrial	O15382	0.0843	0.2005	0.19	0.4093	0.7508	-0.17	0.6132	0.6680
647 BRCA1-A complex subunit RAP80	Q96R1L	0.8381	0.8707	-0.02	0.3247	0.6857	0.15	0.3889	0.5902
648 BRCA1-associated ATM activator 1	Q6PJG6	0.2202	0.3963	-0.19	0.2003	0.4715	0.35	0.4504	0.6641
649 BRCA1-associated protein	Q7Z569	0.4108	0.6177	-3.31	0.5752	0.8644	-1.75	0.5661	0.7727
650 BRCA2 and CDKN1A-interacting protein	Q9P287	0.7473	0.7944	0.05	0.6060	0.7086	-0.20	0.6218	0.6760
651 Breast cancer anti-estrogen resistance protein 1	P56945	0.6678	0.7272	0.02	0.5932	0.6976	0.04	0.0232	0.0750
652 Breast cancer anti-estrogen resistance protein 3	Q75815	0.5469	0.6161	-0.02	0.7382	0.8096	0.05	0.0118	0.0508
653 Breast carcinoma-amplified sequence 1	Q75363	0.0379	0.1223	-0.14	0.1176	0.6319	0.31	0.8132	0.8486
654 Brefeldin A-inhibited guanine nucleotide-exchange protein 1	Q9Y6D6	0.0000	0.0000	-0.97	0.0671	0.5911	-0.21	0.9691	0.9740
655 Brefeldin A-inhibited guanine nucleotide-exchange protein 2	Q9Y6D5	0.0023	0.0331	-1.29	0.4994	0.8220	-0.91	0.0438	0.1140
656 BR13-binding protein	Q8WY22	0.0186	0.0802	-0.11	0.0860	0.6196	-0.11	0.1760	0.3184
657 BRIS1 and BRCA1-A complex member 2	Q9NXX7	0.0135	0.0680	0.70	0.1035	0.6337	0.29	0.5102	0.7313
658 BRIS1 complex subunit Abraxas 2	Q15018	0.5694	0.6373	-0.01	0.0597	0.5924	0.18	0.0023	0.0269
659 BRO1 domain-containing protein BROX	P5VW32	0.1374	0.2822	0.16	0.1252	0.5959	0.19	0.0175	0.0630
660 Bromodomain adjacent to zinc finger domain protein 2B	Q9UIF8	0.4108	0.6175	-3.31	0.5752	0.8641	-1.75	0.5661	0.7725
661 Bromodomain-containing protein 2	P25440	0.4108	0.6173	-3.31	0.5752	0.8639	-1.75	0.5661	0.7723
662 Bromodomain-containing protein 3	P15059	0.4108	0.6172	-3.31	0.5752	0.8636	-1.75	0.5661	0.7721
663 Bromodomain-containing protein 4	O60885	0.4108	0.6170	-3.31	0.5752	0.8634	-1.75	0.5661	0.7719
664 Bromodomain-containing protein 7	Q9NPI1	0.4108	0.6168	-3.31	0.5752	0.8631	-1.75	0.5661	0.7717
665 BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 1	Q8WZ19	0.4108	0.6166	-3.31	0.5752	0.8629	-1.75	0.5661	0.7715
666 BTB/POZ domain-containing protein 9	Q96Q07	0.4108	0.6164	-3.31	0.5752	0.8626	-1.75	0.5661	0.7713





Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
819	Cell cycle and apoptosis regulator protein 2	Q8N163	0.2064	0.3790	-0.05	0.7343	0.8065	-0.04	0.6977	0.7453
820	Cell cycle checkpoint control protein RAD9A	Q9638	0.1710	0.3313	-0.13	0.8709	0.9066	0.01	0.1416	0.2674
821	Cell cycle progression protein 1	Q9UL66	0.8607	0.8897	-0.02	0.4117	0.7520	0.12	0.7579	0.7991
822	Cell death activator CIDE-B	Q9U1UD4	0.0063	0.0479	0.50	0.0014	0.2198	0.75	0.0017	0.0241
823	Cell division control protein 42 homolog	P60953	0.0002	0.0162	0.62	0.2386	0.6624	0.13	0.5334	0.7541
824	Cell division cycle 5-like protein	Q94959	0.8376	0.8705	-0.01	0.7508	0.8193	0.00	0.4788	0.6981
825	Cell division cycle and apoptosis regulator protein 1	QRX12	0.0665	0.1710	0.21	0.3477	0.7033	-0.48	0.0069	0.0397
826	Cell division cycle protein 123 homolog	Q75794	0.1176	0.2523	0.03	0.3402	0.6990	0.12	0.0159	0.0595
827	Cell division cycle protein 20 homolog B	Q86Y33	0.2946	0.4926	-0.06	0.5575	0.8711	0.10	0.7051	0.7518
828	Cell division cycle protein 23 homolog	Q9UJX2	0.4108	0.6092	-3.31	0.5752	0.8525	-1.75	0.5661	0.7630
829	Cell division cycle protein 27 homolog	P30260	0.4108	0.6090	-3.31	0.5752	0.8523	-1.75	0.5661	0.7629
830	Cell division cycle-associated 7-like protein	Q96GN5	0.4108	0.6089	-3.31	0.5752	0.8520	-1.75	0.5661	0.7627
831	Cell division cycle-associated protein 2	Q6GYH5	0.2590	0.4480	-0.04	0.3145	0.6799	0.06	0.0635	0.1468
832	Cell division cycle-associated protein 7	Q9BWT1	0.0118	0.0628	0.44	0.2012	0.6605	0.21	0.0207	0.0695
833	Cell growth regulator with EF hand domain protein 1	Q9674	0.0302	0.1069	-0.58	0.2234	0.6579	-0.31	0.0303	0.0885
834	Cell growth-regulating nuclear protein	Q9NXS8	0.4108	0.6087	-3.31	0.5752	0.8518	-1.75	0.5661	0.7625
835	Cell surface glycoprotein MUC18	P43121	0.4108	0.6085	-3.31	0.5752	0.8515	-1.75	0.5661	0.7623
836	Cellular nucleic acid-binding protein	P26233	0.3976	0.6131	-0.04	0.5911	0.6959	0.03	0.0167	0.0611
837	Cellular retinoic acid-binding protein 1	P29762	0.3121	0.5133	-0.08	0.5965	0.9977	0.00	0.7439	0.7864
838	Cellular retinoic acid-binding protein 2	P29773	0.7733	0.8157	0.02	0.4676	0.7976	0.15	0.7185	0.7636
839	Centrin-1	Q12798	0.0324	0.1121	-2.45	0.3866	0.7973	-2.24	0.2682	0.4402
840	Centrin-2	P41208	0.4108	0.6083	-3.31	0.5752	0.8513	-1.75	0.5661	0.7621
841	Centriolin	Q727A1	0.0053	0.0446	0.21	0.0942	0.6304	0.28	0.0018	0.0242
842	Centromere protein F	P49454	0.4108	0.6082	-3.31	0.5752	0.8511	-1.75	0.5661	0.7619
843	Centromere protein J	Q9HC77	0.4108	0.6080	-3.31	0.5752	0.8508	-1.75	0.5661	0.7617
844	Centromere protein R	Q13352	0.0025	0.0340	0.35	0.0457	0.5623	0.26	0.0005	0.0214
845	Centromere protein V	Q7Z7K6	0.4108	0.6078	-3.31	0.5752	0.8506	-1.75	0.5661	0.7615
846	Centromere protein X	ARMT69	0.0994	0.2241	0.15	0.0113	0.4304	0.36	0.0258	0.0800
847	Centromere/kinetochore protein zw10 homolog	Q43264	0.0263	0.0982	-0.21	0.2305	0.6615	-0.28	0.0295	0.0872
848	Centromere-associated protein E	Q02224	0.0031	0.0370	0.26	0.0104	0.6621	0.17	0.0031	0.0301
849	Centrosomal protein of 128 kDa	Q6ZU80	0.4108	0.6076	-3.31	0.5752	0.8503	-1.75	0.5661	0.7613
850	Centrosomal protein of 135 kDa	Q66C89	0.0648	0.1684	0.10	0.0845	0.6200	0.21	0.1832	0.3280
851	Centrosomal protein of 152 kDa	Q94986	0.4108	0.6075	-3.31	0.5752	0.8501	-1.75	0.5661	0.7611
852	Centrosomal protein of 162 kDa	STBT80	0.1544	0.3062	-0.13	0.3459	0.7027	-0.12	0.3986	0.6020
853	Centrosomal protein of 170 kDa	Q5SW79	0.0002	0.0159	0.25	0.0663	0.5942	0.31	0.1197	0.2361
854	Centrosomal protein of 192 kDa	Q8TEP8	0.2676	0.4593	0.12	0.4652	0.7963	0.10	0.0896	0.1878
855	Centrosomal protein of 290 kDa	Q15078	0.0129	0.0665	0.31	0.2009	0.6620	0.20	0.0036	0.0316
856	Centrosomal protein of 295 kDa	Q15079	0.0129	0.0665	0.31	0.2009	0.6620	0.20	0.0036	0.0316
857	Centrosomal protein of 41 kDa	Q9BYV8	0.1807	0.3405	0.08	0.3902	0.7242	0.15	0.0915	0.1904
858	Centrosomal protein of 83 kDa	Q9Y592	0.1249	0.2631	0.08	0.0834	0.6189	0.22	0.0018	0.0242
859	Centrosomal protein of 85 kDa-like	Q4S2L2	0.4108	0.6073	-3.31	0.5752	0.8498	-1.75	0.5661	0.7609
860	Centrosomal protein of 95 kDa	Q96GE4	0.5623	0.6305	-0.25	0.7671	0.8309	-0.14	0.6882	0.7372
861	Centrosome and spindle pole-associated protein 1	Q1MSI5	0.0610	0.1636	-0.83	0.3712	0.7183	-0.71	0.0655	0.1001
862	Centrosome-associated protein 350	Q5VT06	0.2554	0.4432	0.09	0.8555	0.8963	-0.03	0.0060	0.0375
863	Centrosome-associated protein CP250	Q9BY73	0.4108	0.6071	-3.31	0.5752	0.8496	-1.75	0.5661	0.7607
864	Ceramide synthase 2	Q96G23	0.1938	0.3615	-0.04	0.4660	0.7974	-0.08	0.0031	0.0298
865	cGMP-gated cation channel alpha-1	P29973	0.4108	0.6069	-3.31	0.5752	0.8494	-1.75	0.5661	0.7605
866	Charged multivesicular body protein 1a	Q9HD42	0.2064	0.3789	-0.04	0.2386	0.6620	0.12	0.0019	0.0241
867	Charged multivesicular body protein 2b	Q9UQN3	0.2605	0.4498	-0.10	0.2264	0.6385	0.20	0.4306	0.6408
868	Charged multivesicular body protein 3	Q9Y3E7	0.0571	0.1568	-0.36	0.0849	0.6203	-0.20	0.0002	0.0203
869	Charged multivesicular body protein 4a	Q9BY43	0.0058	0.0461	0.13	0.1738	0.6610	0.11	0.0016	0.0235
870	Charged multivesicular body protein 4b	Q9H444	0.0086	0.0550	0.17	0.1982	0.6671	0.26	0.0101	0.0468
871	Charged multivesicular body protein 4c	Q96CF2	0.0041	0.0405	0.61	0.0086	0.4203	0.46	0.0046	0.0337
872	Charged multivesicular body protein 5	Q9NZ23	0.3507	0.5602	-0.04	0.1772	0.6632	0.21	0.0403	0.1072
873	Charged multivesicular body protein 6	Q96FZ7	0.3397	0.5476	0.16	0.1420	0.6544	0.27	0.0496	0.0904
874	Chitinase domain-containing protein 1	Q9BWS9	0.5303	0.5602	0.14	0.0194	0.4631	0.56	0.2057	0.3589
875	Chloride channel CLIC-like protein 1	Q96S66	0.0511	0.1465	0.22	0.0507	0.5734	0.18	0.0514	0.1274
876	Chloride intracellular channel protein 1	Q00299	0.2522	0.4391	0.05	0.2604	0.6645	0.26	0.0176	0.0632
877	Chloride intracellular channel protein 2	Q15247	0.4108	0.6068	-3.31	0.5752	0.8491	-1.75	0.5661	0.7603
878	Chloride intracellular channel protein 3	Q95833	0.0000	0.0000	-0.04	0.0046	0.3556	0.25	0.0004	0.0244
879	Chloride intracellular channel protein 4	Q9Y696	0.1163	0.2503	0.10	0.1216	0.6388	0.38	0.0047	0.0335
880	Chloride intracellular channel protein 5	Q9NZA1	0.6836	0.7402	-0.44	0.2734	0.6628	-1.55	0.3174	0.5043
881	Choline O-acetyltransferase	P28329	0.4108	0.6066	-3.31	0.5752	0.8489	-1.75	0.5661	0.7601
882	Choline transporter-like protein 1	QRW015	0.4108	0.6064	-3.31	0.5752	0.8486	-1.75	0.5661	0.7599
883	Choline-phosphate cytidylyltransferase A	P49585	0.0021	0.0318	-0.09	0.9118	0.9384	-0.01	0.0070	0.0395
884	Choline-phosphate cytidylyltransferase B	Q9Y5K3	0.1261	0.2650	-0.08	0.5319	0.8501	0.10	0.0068	0.0394
885	Chondrolectin	Q9H9P2	0.9225	0.9407	-0.01	0.0860	0.6187	0.16	0.0063	0.0386
886	Chromatin accessibility complex protein 1	Q9NRG0	0.4108	0.6063	-3.31	0.5752	0.8484	-1.75	0.5661	0.7597
887	Chromatin complex subunit BAP18	Q8IXM2	0.4108	0.6061	-3.31	0.5752	0.8481	-1.75	0.5661	0.7595
888	Chromatin target of PRMT1 protein	Q9Y3Y2	0.4108	0.6059	-3.31	0.5752	0.8479	-1.75	0.5661	0.7593
889	Chromobox protein homolog 1	P83916	0.0624	0.1657	-0.13	0.0264	0.4955	-0.33	0.0993	0.9994
890	Chromobox protein homolog 3	Q13185	0.0409	0.1279	0.10	0.3400	0.6909	0.17	0.0630	0.2004
891	Chromobox protein homolog 5	P45973	0.1307	0.2726	0.04	0.3787	0.7260	0.05	0.2065	0.3596
892	Chromodomain-helicase-DNA-binding protein 1	Q14646	0.0113	0.0612	-0.21	0.0858	0.6199	-0.25	0.0716	0.1596
893	Chromodomain-helicase-DNA-binding protein 1-like	QR6W11	0.3763	0.5918	-0.02	0.3510	0.7039	-0.10	0.0973	0.1999
894	Chromodomain-helicase-DNA-binding protein 3	Q12873	0.4108	0.6057	-3.31	0.5752	0.8477	-1.75	0.5661	0.7591
895	Chromodomain-helicase-DNA-binding protein 4	Q14839	0.1426	0.2892	0.09	0.3639	0.7127	0.12	0.0505	0.0477
896	Chromosome-associated kinesin KIF4A	Q95239	0.4108	0.6056	-3.31	0.5752	0.8474	-1.75	0.5661	0.7589
897	Chromosome-associated kinesin KIF4B	Q2VIQ3	0.0008	0.0217	0.18	0.0939	0.6309	0.24	0.0466	0.1194
898	Chymotrypsin-C	Q98995	0.4108	0.6054	-3.31	0.5752	0.8472	-1.75	0.5661	0.7587
899	Chymotrypsin-like elastase family member 2A	P08217	0.2172	0.3924	-0.06	0.0116	0.4323	-0.29	0.0097	0.0460
900	Cilia- and flagella-associated protein 161	Q6P656	0.4108	0.6052	-3.31	0.5752	0.8469	-1.75	0.5661	0.7585
901	Cilia- and flagella-associated protein 20	Q9Y6A4	0.4108	0.6050	-3.31	0.5752	0.8467	-1.75	0.5661	0.7583
902	Cilia- and flagella-associated protein 298	P57076	0.3525	0.5625	-0.15	0.3726	0.7204	-0.18	0.6487	0.7009



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
984 Coiled-coil domain-containing protein 66	A2RUB6	0.0126	0.0655	-0.10	0.0143	0.4517	-0.30	0.0781	0.1693
985 QH2F9	Q9H2F9	0.4108	0.6025	-3.31	0.5752	0.8431	-1.75	0.5661	0.7556
986 Coiled-coil domain-containing protein 7	Q96M83	0.0425	0.1306	-0.19	0.5509	0.8663	-0.08	0.4398	0.5440
987 Coiled-coil domain-containing protein 83	Q8W8F9	0.0375	0.1217	0.21	0.2934	0.6698	-0.27	0.0229	0.0745
988 Coiled-coil domain-containing protein 85B	Q15834	0.2391	0.4236	0.13	0.1159	0.6367	0.21	0.3174	0.5045
989 Coiled-coil domain-containing protein 91	Q7Z6B0	0.4108	0.6023	-3.31	0.5752	0.8431	-1.75	0.5661	0.7556
990 Coiled-coil domain-containing protein 93	Q567V6	0.4108	0.6021	-3.31	0.5752	0.8429	-1.75	0.5661	0.7552
991 Coiled-coil domain-containing protein 97	Q9BF63	0.3220	0.5260	0.13	0.7050	0.7828	0.07	0.2012	0.3529
992 Coiled-coil-helix-coiled-coil-helix domain-containing protein 5	Q9BSY4	0.0217	0.0877	0.38	0.1314	0.4421	0.62	0.0028	0.0294
993 Cold shock domain-containing protein E1	Q75534	0.0131	0.0669	0.35	0.8931	0.9241	0.01	0.0093	0.0448
994 Cold-inducible RNA-binding protein	Q14011	0.0141	0.0695	-0.27	0.2771	0.6642	-0.12	0.0602	0.1419
995 Collagen alpha-1(V) chain	P20908	0.0450	0.1353	0.21	0.1457	0.6546	0.20	0.0011	0.0217
996 Collagen alpha-1(XVIII) chain	P39060	0.0268	0.0992	-0.18	0.9442	0.9632	0.00	0.3454	0.5394
997 Collagen alpha-1(XIII) chain	Q86Y22	0.4328	0.5101	-0.04	0.2829	0.6640	0.17	0.0849	0.1808
998 Collagen alpha-1(XVIII) chain	Q2UY09	0.1980	0.3675	0.16	0.0184	0.4627	0.33	0.1244	0.2432
999 Collagen alpha-2(XI) chain	P13942	0.0319	0.1110	5.48	0.0278	0.5053	5.44	0.0220	0.0646
1000 Collagen alpha-3(VI) chain	P12111	0.6725	0.7306	-0.15	0.7550	0.8221	0.07	0.6277	0.6809
1001 Collagen alpha-5(VI) chain	AXTX70	0.4108	0.6020	-3.31	0.5752	0.8426	-1.75	0.5661	0.7550
1002 Collagen alpha-6(VI) chain	A6NMZ7	0.4108	0.6018	-3.31	0.5752	0.8424	-1.75	0.5661	0.7548
1003 Collagen triple helix repeat-containing protein 1	Q96C08	0.0031	0.0369	0.60	0.0100	0.4466	0.38	0.5044	0.7264
1004 Collagen type IV alpha-3-binding protein	Q9Y5P4	0.0635	0.1669	-1.56	0.0521	0.5791	-10.00	0.0158	0.0594
1005 Collectrin	Q9HBJ8	0.0330	0.1135	0.07	0.3340	0.6932	0.15	0.0187	0.0654
1006 COMM domain-containing protein 1	Q8NG68	0.4108	0.6016	-3.31	0.5752	0.8422	-1.75	0.5661	0.7546
1007 COMM domain-containing protein 3	Q9UB1L	0.9583	0.9690	0.01	0.5317	0.8501	-0.17	0.0612	0.1436
1008 Complement C1q tumor necrosis factor-related protein 6	Q9BX19	0.0000	0.0000	3.75	0.0046	0.3504	1.71	0.0343	0.0963
1009 Complement C2	P06681	0.2451	0.4307	-0.02	0.6029	0.7064	0.09	0.0263	0.0809
1010 Complement C3	P01024	0.4108	0.6015	-3.31	0.5752	0.8419	-1.75	0.5661	0.7544
1011 Complement C5	P01031	0.4108	0.6013	-3.31	0.5752	0.8417	-1.75	0.5661	0.7542
1012 Complement component 1 Q subcomponent-binding protein_mitochondrial	Q07021	0.0305	0.1076	0.10	0.0079	0.4052	0.20	0.0002	0.0247
1013 Complement component C7	P10643	0.4108	0.6011	-3.31	0.5752	0.8414	-1.75	0.5661	0.7540
1014 Complement component receptor 1-like protein	Q2VPA4	0.3252	0.5307	0.05	0.6198	0.7178	0.08	0.0061	0.0377
1015 Complement factor H	P08603	0.0924	0.2137	0.28	0.5427	0.8576	-0.08	0.5450	0.7678
1016 Complex I assembly factor TIMMDC1_mitochondrial	Q9NPL8	0.0047	0.0434	-0.17	0.3947	0.7384	-0.08	0.3163	0.5590
1017 Complex I intermediate-associated protein 30_mitochondrial	Q9Y3Y5	0.0644	0.1681	0.17	0.6613	0.9000	-0.01	0.7827	0.8217
1018 Complex III assembly factor LYRM7	Q5USX0	0.9608	0.9711	0.00	0.8667	0.7326	0.05	0.1351	0.2580
1019 Complex-4	Q14810	0.4108	0.6009	-3.31	0.5752	0.8412	-1.75	0.5661	0.7538
1020 Complex-4	Q772G2	0.0003	0.0164	0.32	0.3753	0.7230	0.11	0.0004	0.0183
1021 Condensin complex subunit 1	Q15021	0.1888	0.3546	0.06	0.5741	0.8859	-0.03	0.4851	0.7053
1022 Condensin complex subunit 2	Q15003	0.4108	0.6008	-3.31	0.5752	0.8410	-1.75	0.5661	0.7536
1023 Condensin complex subunit 3	Q9BFX3	0.0165	0.0750	-0.15	0.2038	0.6598	-0.17	0.8788	0.9041
1024 Condensin-2 complex subunit H2	G6IBW4	0.4108	0.6006	-3.31	0.5752	0.8407	-1.75	0.5661	0.7534
1025 Connector enhancer of kinase suppressor of ras 1	Q969H4	0.1426	0.2891	0.06	0.1289	0.6433	0.33	0.2116	0.3663
1026 Connector enhancer of kinase suppressor of ras 2	Q8WX12	0.0246	0.0947	0.44	0.0107	0.4470	0.63	0.3436	0.5285
1027 Conserved oligomeric Golgi complex subunit 1	Q8WWT3	0.2460	0.4315	-0.12	0.2524	0.6620	-0.15	0.0827	0.1771
1028 Conserved oligomeric Golgi complex subunit 2	Q14746	0.3907	0.6076	-0.05	0.0277	0.5088	0.33	0.1517	0.0591
1029 Conserved oligomeric Golgi complex subunit 4	Q9H9E3	0.9927	0.9942	0.00	0.6613	0.7504	0.05	0.5277	0.7487
1030 Conserved oligomeric Golgi complex subunit 5	Q9UP83	0.0142	0.0697	-0.25	0.0129	0.4425	-0.24	0.0477	0.1212
1031 Constitutive coactivator of peroxisome proliferator-activated receptor gamma	Q96EK7	0.1536	0.3052	0.08	0.1384	0.6511	0.21	0.0233	0.0753
1032 Constitutive coactivator of PPAR-gamma-like protein 1	Q9NZB2	0.1200	0.2556	0.12	0.1839	0.6634	0.27	0.0090	0.0443
1033 Contactin-associated protein-like 2	Q9UHC6	0.4108	0.6004	-3.31	0.5752	0.8405	-1.75	0.5661	0.7532
1034 Contactin-associated protein-like 3	Q9BZ76	0.0007	0.0212	-0.79	0.8733	0.9084	0.03	0.0035	0.0310
1035 Contactin-associated protein-like 4	Q9CDA0	0.0120	0.0632	0.31	0.1660	0.6599	0.27	0.0642	0.1478
1036 COP9 signalosome complex subunit 1	Q13098	0.0374	0.1216	0.15	0.2162	0.6607	0.14	0.0695	0.1564
1037 COP9 signalosome complex subunit 2	P61201	0.1133	0.2454	0.09	0.4045	0.7475	0.09	0.0739	0.1627
1038 COP9 signalosome complex subunit 3	Q9UN52	0.1914	0.3579	0.13	0.4122	0.7524	0.09	0.1341	0.2565
1039 COP9 signalosome complex subunit 4	Q9BT78	0.8667	0.8947	0.01	0.9557	0.9897	0.00	0.1650	0.3019
1040 COP9 signalosome complex subunit 5	Q9Z905	0.1785	0.3414	-0.06	0.0385	0.5571	0.12	0.8121	0.8478
1041 COP9 signalosome complex subunit 6	Q7LSN1	0.0295	0.1052	-0.15	0.0108	0.4371	-0.25	0.0032	0.0305
1042 COP9 signalosome complex subunit 7a	Q9UBW8	0.6692	0.7281	-0.03	0.7457	0.8158	0.03	0.4090	0.6150
1043 COP9 signalosome complex subunit 8	Q9P627	0.7604	0.8053	0.00	0.6781	0.7641	-0.04	0.6677	0.7183
1044 Copme-1	Q98299	0.4108	0.6003	-3.31	0.5752	0.8403	-1.75	0.5661	0.7531
1045 Copme-2	Q96FN4	0.4108	0.6001	-3.31	0.5752	0.8400	-1.75	0.5661	0.7529
1046 Copme-3	Q75131	0.0069	0.0497	0.25	0.4288	0.7641	0.10	0.4000	0.6030
1047 Copme-5	Q9HHC1	0.7031	0.7559	0.12	0.1937	0.6600	-0.80	0.0027	0.0285
1048 Copme-8	Q86YQ8	0.4108	0.5999	-3.31	0.5752	0.8398	-1.75	0.5661	0.7527
1049 Copper transport protein ATOX1	Q00244	0.0079	0.0527	0.08	0.6455	0.7381	0.03	0.0400	0.1065
1050 Cordan-blue protein-like 1	Q53SF7	0.9990	0.9992	0.00	0.9646	0.9757	-0.01	0.1256	0.2450
1051 Coronin-1A	P11146	0.0275	0.1005	0.25	0.7211	0.7959	-0.05	0.0305	0.0888
1052 Coronin-1B	Q9BR76	0.0045	0.0425	-0.26	0.4745	0.8019	-0.06	0.2525	0.4199
1053 Coronin-1C	Q9ULV4	0.4108	0.5998	-3.31	0.5752	0.8395	-1.75	0.5661	0.7525
1054 Coronin-2A	Q9Z828	0.4108	0.5996	-3.31	0.5752	0.8393	-1.75	0.5661	0.7523
1055 Coronin-7	P57737	0.0436	0.1325	0.08	0.0818	0.6168	0.14	0.1183	0.2340
1056 Corrinoid adenosyltransferase	Q96EY8	0.6646	0.7242	-0.08	0.5687	0.8831	-0.08	0.3958	0.5984
1057 Costars family protein ABRA1	Q9P1F3	0.3005	0.4997	0.10	0.9562	0.9710	-0.01	0.9064	0.9262
1058 COX assembly mitochondrial protein 2 homolog	Q9NRD2	0.0454	0.1360	-2.32	0.2425	0.6601	-0.57	0.1677	0.3269
1059 Coxsaekavirus and adenovirus receptor	P78310	0.4108	0.5994	-3.31	0.5752	0.8391	-1.75	0.5661	0.7521
1060 Craniofacial development protein 1	Q9UEE9	0.0070	0.0499	-0.21	0.0354	0.5409	-0.32	0.0195	0.0672
1061 Creatine kinase B-type	P12277	0.4108	0.5993	-3.31	0.5752	0.8388	-1.75	0.5661	0.7519

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
1062	Creatine kinase U-type mitochondrial	P12532	0.5304	0.6016	0.04	0.9321	0.9544	0.01	0.0321	0.0918
1063	Crk-like protein	P46109	0.1374	0.2821	-0.10	0.3288	0.6882	-0.05	0.0895	0.1878
1064	Crooked-neck-like protein 1	Q9BZ00	0.4108	0.5991	-3.31	0.5752	0.8386	-1.75	0.5661	0.7517
1065	Cytochrome-c	Q949A0	0.4108	0.5989	-3.31	0.5752	0.8384	-1.75	0.5661	0.7515
1066	CTST complex subunit STN1	Q9H668	0.3965	0.6151	-0.06	0.2452	0.6591	-0.08	0.3054	0.4886
1067	CTACF family member 2	Q96R16	0.2325	0.4143	-1.00	0.3713	0.7182	-0.92	0.8406	0.8716
1068	C-terminal-binding protein 1	L13363	0.1900	0.3562	-0.36	0.3793	0.7258	-0.37	0.0598	0.1415
1069	C-terminal-binding protein 2	P56545	0.7069	0.7591	-0.09	0.8334	0.8801	0.02	0.1304	0.2514
1070	CTP synthase 1	P17812	0.0895	0.2091	0.19	0.3229	0.6852	0.21	0.1106	0.2215
1071	CTP synthase 2	Q9NRF8	0.2046	0.3768	-0.07	0.2815	0.6643	-0.08	0.0344	0.0965
1072	CTTNBP2 N-terminal-like protein	Q9P2B4	0.4108	0.5987	-3.31	0.5752	0.8381	-1.75	0.5661	0.7513
1073	C-type lectin domain family 12 member A	Q5QGZ9	0.4108	0.5986	-3.31	0.5752	0.8379	-1.75	0.5661	0.7511
1074	C-type lectin domain family 2 member B	Q92478	0.4108	0.5984	-3.31	0.5752	0.8377	-1.75	0.5661	0.7509
1075	C-type lectin domain family 4 member A	Q9UHP7	0.0317	0.1105	-0.29	0.1506	0.6594	-0.98	0.0165	0.0609
1076	C-type lectin domain family 4 member A	Q9UMR7	0.0945	0.2167	0.11	0.4078	0.7496	0.07	0.0164	0.0606
1077	C-type lectin domain family 4 member D	Q8WXI8	0.6220	0.6852	0.02	0.8507	0.6209	-0.16	0.4675	0.6849
1078	C-type lectin domain family 4 member G	Q6UXB4	0.2871	0.4835	-0.21	0.4300	0.7660	-0.50	0.1615	0.2966
1079	C-type mannose receptor 2	Q9UBG0	0.4108	0.5982	-3.31	0.5752	0.8374	-1.75	0.5661	0.7507
1080	CUB domain-containing protein 1	Q9H5V8	0.4108	0.5981	-3.31	0.5752	0.8372	-1.75	0.5661	0.7505
1081	CUE domain-containing protein 1	Q9NWM3	0.2881	0.4845	0.15	0.1211	0.6388	-0.45	0.0712	0.1591
1082	CUGBP Elav-like family member 1	Q92879	0.0021	0.0317	1.15	0.0708	0.6002	0.23	0.3729	0.5711
1083	Cullin-1	L13616	0.0766	0.1889	-0.10	0.1148	0.6533	0.25	0.0013	0.0233
1084	Cullin-2	L13617	0.0153	0.0717	0.15	0.7703	0.8334	-0.03	0.7276	0.7709
1085	Cullin-3	L13618	0.0345	0.1166	0.14	0.3341	0.6931	0.08	0.0201	0.0682
1086	Cullin-4A	L13619	0.0036	0.0387	1.36	0.0562	0.7078	0.13	0.9770	0.9808
1087	Cullin-4B	L13620	0.7008	0.7547	0.03	0.8781	0.6120	0.19	0.0513	0.1273
1088	Cullin-5	Q93034	0.4108	0.5979	-3.31	0.5752	0.8369	-1.75	0.5661	0.7504
1089	Cullin-associated NEDD8-dissociated protein 1	Q86VP6	0.0196	0.0823	0.20	0.2930	0.6698	0.20	0.0092	0.0448
1090	Cullin-associated NEDD8-dissociated protein 2	Q75155	0.5203	0.5921	0.07	0.0376	0.5549	-0.46	0.0477	0.1211
1091	CWF19-like protein 2	Q2TBE0	0.0320	0.1111	0.36	0.0736	0.3139	-0.36	0.9986	0.9990
1092	XXXX motif containing zinc binding protein	Q9NWW4	0.2249	0.4035	-0.05	0.1240	0.6417	-0.08	0.9504	0.9608
1093	XXXX-type zinc finger protein 1	Q9PU04	0.8934	0.9166	-0.01	0.3671	0.7157	0.15	0.6370	0.6899
1094	Cyclic AMP-responsive element-binding protein 3-like protein 4	Q8TEY5	0.4108	0.5977	-3.31	0.5752	0.8367	-1.75	0.5661	0.7502
1095	Cyclic nucleotide-gated cation channel alpha-3	Q16281	0.0351	0.1170	0.24	0.0551	0.5861	0.18	0.6919	0.7400
1096	Cyclic nucleotide-gated cation channel alpha-4	Q8V777	0.0206	0.0848	0.73	0.3295	0.6888	-0.38	0.3348	0.2568
1097	Cyclin-dependent kinase 1	P06493	0.1070	0.2356	0.10	0.4832	0.8072	-0.08	0.0281	0.0847
1098	Cyclin-dependent kinase 12	Q9NYY4	0.4108	0.5986	-3.31	0.5752	0.8365	-1.75	0.5661	0.7500
1099	Cyclin-dependent kinase 13	Q14004	0.0000	0.0000	0.42	0.1683	0.6610	0.24	0.0025	0.0276
1100	Cyclin-dependent kinase 15	Q96A00	0.0054	0.0447	0.28	0.6567	0.7470	0.02	0.6038	0.6596
1101	Cyclin-dependent kinase 16	Q00536	0.4194	0.4970	0.09	0.2189	0.6600	-0.20	0.6991	0.7464
1102	Cyclin-dependent kinase 17	Q00537	0.4108	0.5974	-3.31	0.5752	0.8362	-1.75	0.5661	0.7498
1103	Cyclin-dependent kinase 18	Q07002	0.1597	0.3148	-0.94	0.3458	0.7030	0.49	0.2047	0.3576
1104	Cyclin-dependent kinase 21	P24941	0.8417	0.8736	-0.02	0.4143	0.6540	0.21	0.4727	0.6901
1105	Cyclin-dependent kinase 3	Q00526	0.3788	0.5946	0.03	0.6444	0.7375	0.04	0.2943	0.4748
1106	Cyclin-dependent kinase 4	P11802	0.0104	0.0591	-0.77	0.0241	0.4876	-0.69	0.0061	0.0380
1107	Cyclin-dependent kinase 6	Q00534	0.0186	0.0801	-1.41	0.7114	0.7884	0.11	0.0363	0.0998
1108	Cyclin-dependent kinase 9	P50750	0.0475	0.1480	-0.20	0.6228	0.5893	-0.20	0.8823	0.9072
1109	Cyclin-dependent kinase inhibitor 1	P38936	0.0008	0.0214	-1.21	0.1171	0.6332	-0.38	0.4863	0.7064
1110	Cyclin-dependent kinase inhibitor 3	Q16667	0.8249	0.8598	-0.01	0.7070	0.6011	0.35	0.0967	0.1992
1111	Cyclin-dependent kinase-5	Q76039	0.0173	0.0770	-0.25	0.2071	0.6637	0.07	0.4170	0.6243
1112	Cyclin-dependent kinases regulatory subunit 1	P61024	0.1536	0.3051	0.23	0.1611	0.6649	0.36	0.0341	0.0958
1113	Cyclin-dependent kinase 5	Q00535	0.2664	0.4582	0.07	0.2811	0.6655	-0.12	0.2760	0.4503
1114	Cyclin-K	Q75909	0.0008	0.0213	-0.36	0.0202	0.4735	-0.34	0.0646	0.1483
1115	Cystathionine beta-synthase	P35520	0.4108	0.5972	-3.31	0.5752	0.8360	-1.75	0.5661	0.7496
1116	Cystathionine beta-synthase-like protein	P0DN79	0.0149	0.0709	0.35	0.0881	0.6201	0.23	0.0594	0.1410
1117	Cytosin-B	P04080	0.4050	0.6253	0.02	0.4666	0.8034	-0.10	0.8208	0.8550
1118	Cytosin-C	P01034	0.0129	0.0664	-0.40	0.1662	0.4586	0.32	0.0127	0.0529
1119	Cysteine and glycine-rich protein 1	P21291	0.5006	0.5742	-0.40	0.4189	0.7576	0.08	0.7902	0.8279
1120	Cysteine and glycine-rich protein 2	Q16527	0.3552	0.5658	0.06	0.4114	0.7517	0.10	0.4320	0.6425
1121	Cysteine and histidine-rich domain-containing protein 1	Q9UHD1	0.1561	0.3091	0.06	0.2735	0.6648	-0.04	0.1920	0.3393
1122	Cysteine and histidine-rich protein 1	Q6ZMK1	0.9976	0.9980	0.00	0.1571	0.6616	-0.37	0.2634	0.4336
1123	Cysteine dioxygenase type 1	Q16878	0.4108	0.5971	-3.31	0.5752	0.8358	-1.75	0.5661	0.7494
1124	Cysteine protease ATG4B	Q9Y4P1	0.0345	0.1165	0.07	0.0222	0.4812	0.19	0.3712	0.5694
1125	Cysteine protease ATG4C	Q96D76	0.4108	0.5969	-3.31	0.5752	0.8355	-1.75	0.5661	0.7492
1126	Cysteine protease ATG4D	Q86T10	0.9785	0.9857	0.00	0.9490	0.9660	0.02	0.5464	0.7693
1127	Cysteine/serine-rich nuclear protein 3	Q8WYX3	0.4108	0.5967	-3.31	0.5752	0.8353	-1.75	0.5661	0.7490
1128	Cysteine-rich protein 1	P50238	0.4108	0.5966	-3.31	0.5752	0.8351	-1.75	0.5661	0.7488
1129	Cysteine-rich protein 2	P52943	0.6844	0.7404	-0.03	0.2396	0.6612	0.27	0.1302	0.2512
1130	Cysteine-rich with EGF-like domain protein 2	Q6U390	0.0330	0.1134	0.15	0.1302	0.6448	0.16	0.0071	0.0440
1131	Cysteine-RNA ligase, cytoplasmic	P49589	0.0828	0.1981	0.25	0.1353	0.6501	0.22	0.0004	0.0199
1132	Cytochrome b-245 light chain	P13498	0.1529	0.3409	0.09	0.0976	0.6335	-0.19	0.0038	0.0320
1133	Cytochrome b5	P00167	0.2813	0.4746	0.11	0.1170	0.6333	0.30	0.3417	0.5347
1134	Cytochrome b5 type B	Q43169	0.2907	0.4878	-0.05	0.6542	0.7448	0.05	0.2726	0.4663
1135	Cytochrome b561	P49447	0.0011	0.0232	-0.46	0.9505	0.9671	0.00	0.0407	0.0333
1136	Cytochrome b-c1 complex subunit 1 mitochondrial	P31930	0.0402	0.1264	0.14	0.3109	0.6792	0.15	0.0050	0.0344
1137	Cytochrome b-c1 complex subunit 2 mitochondrial	P22695	0.0350	0.1168	0.13	0.4314	0.7677	0.12	0.0201	0.0681
1138	Cytochrome b-c1 complex subunit 6 mitochondrial	P07919	0.0008	0.0211	-0.26	0.3456	0.7029	-0.39	0.0001	0.0144
1139	Cytochrome b-c1 complex subunit 7-like mitochondrial	AD0961P55	0.1143	0.2472	0.09	0.3046	0.6775	0.17	0.0043	0.0323
1140	Cytochrome b-c1 complex subunit 7	P14927	0.0643	0.1680	0.07	0.0553	0.7485	0.10	0.0029	0.0293
1141	Cytochrome b-c1 complex subunit 9	Q9UDW1	0.4580	0.5349	0.02	0.6298	0.7266	0.06	0.0065	0.0388
1142	Cytochrome b-c1 complex subunit Rieske mitochondrial	P47985	0.8435	0.8751	0.01	0.8022	0.8571	-0.02	0.8338	0.1791
1143	Cytochrome c	P99999	0.0075	0.0511	0.26	0.3221	0.6841	0.04	0.0016	0.0231





Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7						MDA-MB-231					
		Dai SC20 vs control			Gen SC20 vs control			Dai IC20 vs control			Gen IC20 vs control		
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC
1223 Dehydrogenase/reductase SDR family member 7B	Q6IAN0	0.6020	0.6677	0.02	0.1948	0.6691	0.19	0.0332	0.0942	0.12	0.0038	0.0249	0.24
1224 Delphin	A4D2P6	0.4375	0.5152	-0.07	0.2471	0.6581	-0.52	0.0018	0.0238	0.72	0.0170	0.0545	0.36
1225 Delta(14)-sterol reductase	Q14739	0.4108	0.5946	-3.31	0.5752	0.8323	-1.75	0.5661	0.7465	-1.19	0.5388	0.7057	0.89
1226 Delta(24)-sterol reductase	Q15392	0.7753	0.8169	0.27	0.0970	0.6336	-1.41	0.0026	0.0282	-1.36	0.7434	0.7789	0.31
1227 Delta(3, 5)-Delta(2, 4)-dienoyl-CoA isomerase_mitochondrial	P13011	0.1139	0.2465	0.04	0.3993	0.7430	0.09	0.1424	0.2684	-0.05	0.0415	0.1010	0.06
1228 Delta-1-pyrroline-5-carboxylate dehydrogenase_mitochondrial	P30038	0.0010	0.0225	-0.47	0.0077	0.4029	-0.26	0.0025	0.0280	-0.60	0.0006	0.0130	-0.52
1229 Delta-1-pyrroline-5-carboxylate synthase	P54886	0.1143	0.2471	-0.14	0.4756	0.8025	0.05	0.0336	0.0949	-0.22	0.7301	0.7671	0.02
1230 Delta-aminolevulinic acid dehydratase	P13716	0.1217	0.2583	-0.11	0.3318	0.6911	0.09	0.1845	0.3293	-0.09	0.5627	0.6127	-0.03
1231 DENN domain-containing protein 2A	Q9ULE3	0.0796	0.1935	0.68	0.2066	0.6598	0.14	0.0085	0.0436	0.19	0.0000	0.0000	0.40
1232 DENN domain-containing protein 2C	Q68D51	0.1413	0.2870	-0.30	0.2994	0.6737	0.17	0.0654	0.1495	0.40	0.6079	0.6552	0.08
1233 DENN domain-containing protein 2D	Q9H6A0	0.0014	0.0258	-0.41	0.0434	0.5720	0.28	0.1458	0.2730	-0.21	0.0109	0.0419	-0.22
1234 DENN domain-containing protein 4C	Q5VZ89	0.1483	0.2968	0.10	0.2181	0.6607	0.08	0.4573	0.6724	0.07	0.0181	0.0567	-0.23
1235 Density-regulated protein	O43583	0.2545	0.4421	0.20	0.5169	0.8386	-0.32	0.0646	0.1483	-0.74	0.1850	0.3124	-0.66
1236 Deoxycytidine kinase	P27707	0.0103	0.0591	-0.56	0.0154	0.4585	-0.23	0.0211	0.0704	-0.19	0.0030	0.0224	-0.58
1237 Deoxycytidine deaminase	P32321	0.0035	0.0384	-0.46	0.0179	0.4707	-0.40	0.0069	0.0399	-0.52	0.0138	0.0477	-0.54
1238 Deoxycytidine synthase	P49366	0.0068	0.0493	-0.35	0.5428	0.8575	-0.07	0.0040	0.0318	-0.45	0.0476	0.1112	-0.17
1239 Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	Q9Y323	0.0436	0.1324	-0.05	0.1919	0.6671	-0.06	0.1859	0.3311	0.02	0.0040	0.0255	-0.12
1240 Deoxyribonuclease-2-alpha	O00115	0.9952	0.9958	0.00	0.0003	0.1943	0.24	0.0148	0.0573	0.30	0.0046	0.0275	0.20
1241 Deoxyribose-phosphate aldolase	Q9Y315	0.4108	0.5944	-3.31	0.5752	0.8320	-1.75	0.5661	0.7463	-1.19	0.5388	0.7055	0.89
1242 Deoxycytidine 5'-triphosphate nucleotidohydrolase_mitochondrial	P33316	0.1150	0.2484	0.10	0.4737	0.8014	0.07	0.0171	0.0621	0.21	0.0574	0.1274	0.14
1243 Dertin-1	Q9BLN8	0.3008	0.4999	-0.02	0.6381	0.7335	0.04	0.0896	0.1878	-0.08	0.7673	0.7997	-0.01
1244 Desmin	P17661	0.5019	0.5754	-0.03	0.2438	0.6584	0.14	0.5812	0.6381	0.05	0.8731	0.8910	-0.01
1245 Desmoglein-1	Q02413	0.0750	0.1862	0.14	0.4575	0.7897	-0.03	0.0476	0.1210	0.18	0.0028	0.0216	0.22
1246 Desmoglein-2	Q14126	0.1801	0.3436	-1.02	0.3131	0.6806	-0.35	0.2348	0.3957	0.24	0.0616	0.1344	-0.92
1247 Desmoplakin	P15924	0.0029	0.0364	0.20	0.0299	0.5062	0.13	0.0189	0.0658	0.34	0.0006	0.0124	0.30
1248 Destrin	P60981	0.0337	0.1147	0.21	0.4472	0.7823	0.12	0.2584	0.4270	0.10	0.0530	0.1201	0.15
1249 Deuterosome assembly protein 1	Q0SD60	0.1682	0.3269	-0.05	0.0620	0.5904	0.33	0.0724	0.1608	0.04	0.6762	0.7169	0.01
1250 Developmentally-regulated GTP-binding protein 1	Q9Y295	0.6253	0.6887	-0.06	0.2650	0.6628	-0.19	0.0539	0.1318	-0.38	0.0456	0.1078	-0.44
1251 Developmentally-regulated GTP-binding protein 2	P55039	0.4108	0.5942	-3.31	0.5752	0.8318	-1.75	0.5661	0.7462	-1.19	0.5388	0.7053	0.89
1252 Diabolo homolog_mitochondrial	Q9NR28	0.2759	0.4693	0.05	0.4196	0.7579	0.09	0.0490	0.1233	-0.12	0.0216	0.0638	0.07
1253 Diacylglycerol kinase theta	P52824	0.4108	0.5941	-3.31	0.5752	0.8316	-1.75	0.5661	0.7460	-1.19	0.5388	0.7052	0.89
1254 Diacylglycerol O-acyltransferase 2	Q96PD7	0.0081	0.0533	1.46	0.9951	0.9970	0.01	0.0236	0.0754	0.88	0.0053	0.0292	1.45
1255 Diacylglycerol acetyltransferase 1	P21673	0.1638	0.3305	-0.65	0.3558	0.7078	-1.26	0.0797	0.1721	-1.01	0.0421	0.1021	-1.18
1256 Differentially expressed in FDCP 6 homolog	Q9H4E7	0.1378	0.2826	0.08	0.2329	0.6629	0.22	0.0071	0.0399	0.32	0.0035	0.0238	0.33
1257 Digestive organ expansion factor homolog	Q68CQ4	0.4108	0.5939	-3.31	0.5752	0.8313	-1.75	0.5661	0.7458	-1.19	0.5388	0.7050	0.89
1258 Dihydrofolate reductase	P00374	0.4758	0.5513	-0.20	0.7022	0.7848	-0.12	0.2458	0.4114	0.13	0.8836	0.9005	0.01
1259 Dihydrofoloyl dehydrogenase_mitochondrial	P09622	0.0864	0.2044	0.19	0.1027	0.6311	0.32	0.0290	0.0865	0.29	0.0179	0.0564	0.37
1260 Dihydrofoloyl-synase-residue acetyltransferase component of pyruvate dehydrogenase complex_mitochondrial	P10515	0.4108	0.5937	-3.31	0.5752	0.8311	-1.75	0.5661	0.7456	-1.19	0.5388	0.7048	0.89
1261 Dihydrofoloyl-synase-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex_mitochondrial	P36957	0.1993	0.3696	0.06	0.3248	0.6856	0.08	0.0155	0.0586	0.17	0.0656	0.1412	0.11
1262 Dihydroorotate dehydrogenase (quinone)_mitochondrial	Q02127	0.3997	0.6192	-0.06	0.2287	0.6600	-0.10	0.0087	0.0438	-0.33	0.6615	0.7042	0.03
1263 Dihydroteridine reductase	P09417	0.4108	0.5936	-3.31	0.5752	0.8309	-1.75	0.5661	0.7454	-1.19	0.5388	0.7046	0.89
1264 Dihydroxymethylase-related protein 1	Q14194	0.0507	0.1457	-0.73	0.4133	0.7522	-1.57	0.0289	0.0863	-0.43	0.0499	0.1149	-1.11
1265 Dihydroxymethylase-related protein 2	P16555	0.1889	0.3547	0.14	0.4442	0.9630	-0.01	0.0568	0.1362	0.25	0.1200	0.2230	0.18
1266 Dihydroxymethylase-related protein 3	Q14195	0.4108	0.5944	-3.31	0.5752	0.8306	-1.75	0.5661	0.7452	-1.19	0.5388	0.7044	0.89
1267 Dihydroxymethylase-related protein 4	Q14531	0.9360	0.9516	-0.01	0.0763	0.6156	0.43	0.1987	0.3495	0.17	0.0237	0.1213	0.32
1268 Dihydroxymethylase-related protein 5	Q9BP06	0.1651	0.3224	-0.07	0.4041	0.7375	-0.07	0.1287	0.2494	-0.10	0.0307	0.0815	-0.17
1269 Dipetidase 2	Q9H4A9	0.4860	0.5604	-0.17	0.5684	0.8302	-0.40	0.1496	0.6275	0.23	0.6752	0.7161	-0.11
1270 Dipetidyl peptidase 1	P53634	0.6346	0.6964	-0.04	0.4277	0.7629	0.08	0.3363	0.5285	0.09	0.3399	0.5139	0.07
1271 Dipetidyl peptidase 2	Q9UHL4	0.0347	0.1166	0.20	0.0043	0.3480	0.23	0.2546	0.4227	0.10	0.1027	0.1978	0.12
1272 Dipetidyl peptidase 3	Q9NY33	0.0196	0.0822	0.14	0.1948	0.6696	0.22	0.0048	0.0337	0.24	0.0013	0.0167	0.31
1273 Diposphomevalonate decarboxylase	P53602	0.4319	0.5094	0.06	0.8288	0.8769	-0.03	0.5629	0.7872	0.03	0.3077	0.4747	-0.06
1274 DIS3-like exonuclease 1	Q8TF46	0.0194	0.0818	0.20	0.5014	0.8230	-0.05	0.1791	0.3225	0.12	0.0626	0.1363	-0.14
1275 DIS3-like exonuclease 2	Q7HBY7	0.4124	0.4904	-0.09	0.1693	0.6619	0.11	0.2082	0.3618	0.27	0.1012	0.1957	0.13
1276 Discoidin CUB and LCC domain-containing protein 2	Q96PD2	0.4108	0.5932	-3.31	0.5752	0.8304	-1.75	0.5661	0.7450	-1.19	0.5388	0.7043	0.89
1277 Disco-interacting protein 2 homolog B	Q9P265	0.2712	0.4639	-0.04	0.4992	0.8220	-0.07	0.9747	0.9789	0.00	0.0143	0.0486	-0.19
1278 Dishevelled-associated activator of morphogenesis 1	Q9Y4D1	0.0820	0.1973	0.12	0.1293	0.6434	-0.51	0.0004	0.0201	-0.17	0.0014	0.0174	-0.78
1279 Dishevelled-associated activator of morphogenesis 2	Q86T65	0.0022	0.0324	0.36	0.0422	0.5722	0.52	0.0014	0.0231	0.55	0.0319	0.0839	0.39
1280 Disintegrin and metalloproteinase domain-containing protein 10	O14672	0.4108	0.5931	-3.31	0.5752	0.8302	-1.75	0.5661	0.7448	-1.19	0.5388	0.7041	0.89
1281 Disintegrin and metalloproteinase domain-containing protein 17	P78536	0.0959	0.2185	-9.28	0.9593	0.9724	0.08	0.0318	0.0913	-7.16	0.0861	0.1736	1.74
1282 Disintegrin and metalloproteinase domain-containing protein 22	Q9P0K1	0.5040	0.5771	0.05	0.2877	0.6683	-0.45	0.0110	0.0486	0.32	0.0018	0.0186	0.46
1283 Disintegrin and metalloproteinase domain-containing protein 7	Q9H2U9	0.0334	0.1143	-1.19	0.7651	0.8300	0.17	0.0299	0.0877	-0.85	0.3019	0.4671	-0.24
1284 Disintegrin and metalloproteinase domain-containing protein 9	Q13443	0.4108	0.5929	-3.31	0.5752	0.8300	-1.75	0.5661	0.7446	-1.19	0.5388	0.7039	0.89
1285 Disks large homolog 1	Q12959	0.1527	0.3038	0.12	0.1899	0.6696	0.19	0.8363	0.8681	0.02	0.3546	0.5323	0.06
1286 Disks large homolog 2	Q15700	0.3103	0.5114	0.30	0.4835	0.8084	0.29	0.3939	0.5961	-0.23	0.2786	0.4365	0.31
1287 Disks large homolog 5	Q8TDM6	0.0149	0.0709	0.25	0.0072	0.4054	0.19	0.0007	0.0213	0.32	0.8751	0.8929	0.00

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7			MDA-MB-231		
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC
1288	Disks large-associated protein 3	Q95886	0.0009	0.0222	-0.46	0.0430	0.5697	-0.50
1289	Disks large-associated protein 5	Q15398	0.4108	0.5927	-3.31	0.5752	0.8297	-1.75
1290	Dixin	Q155Q3	0.0158	0.0731	0.23	0.4242	0.7609	0.04
1291	DNA (cytosine-5)-methyltransferase 1	P26358	0.0005	0.0190	0.19	0.1257	0.6428	0.15
1292	DNA (cytosine-5)-methyltransferase 3-like	Q9U1W3	0.4108	0.5926	-3.31	0.5752	0.8295	-1.75
1293	DNA damage-binding protein 1	Q16531	0.1104	0.2413	0.07	0.1705	0.6606	0.21
1294	DNA damage-induced apoptosis suppressor protein	Q8IXT1	0.0010	0.0234	-0.62	0.0506	0.5735	-0.20
1295	DNA dC→dU-editing enzyme APOBEC-3B	Q9UHI7	0.4108	0.5924	-3.31	0.5752	0.8293	-1.75
1296	DNA dC→dU-editing enzyme APOBEC-3C	Q9NRW3	0.0005	0.0189	0.22	0.4148	0.6998	0.89
1297	DNA dC→dU-editing enzyme APOBEC-3G	Q9HC16	0.4108	0.5922	-3.31	0.5752	0.8290	-1.75
1298	DNA endonuclease RBBP8	Q99708	0.1049	0.2321	0.97	0.0316	0.5099	1.11
1299	DNA excision repair protein ERCC-6	Q03468	0.0528	0.1491	0.16	0.2901	0.6685	0.21
1300	DNA excision repair protein ERCC-6-like	Q2NKC8	0.4108	0.5921	-3.31	0.5752	0.8288	-1.75
1301	DNA fragmentation factor subunit alpha	Q00273	0.0753	0.1867	0.09	0.6027	0.7063	0.07
1302	DNA helicase MCM8	Q9U1A3	0.1236	0.2611	0.10	0.2346	0.6612	-0.10
1303	DNA ligase 1	P18858	0.4108	0.5919	-3.31	0.5752	0.8286	-1.75
1304	DNA polymerase delta 1-associated protein 1	Q9NPFS	0.3612	0.5739	0.08	0.1016	0.6310	0.29
1305	DNA mismatch repair protein Msh2	P43246	0.0422	0.1303	0.21	0.0464	0.5629	0.24
1306	DNA mismatch repair protein Msh3	P20585	0.4108	0.5918	-3.31	0.5752	0.8283	-1.75
1307	DNA mismatch repair protein Msh6	P52701	0.0566	0.1558	0.08	0.2812	0.6648	0.18
1308	DNA polymerase alpha catalytic subunit	P09884	0.9325	0.9486	-0.01	0.8427	0.8872	0.03
1309	DNA polymerase beta	P06746	0.4108	0.5916	-3.31	0.5752	0.8281	-1.75
1310	DNA polymerase delta catalytic subunit	P28400	0.4108	0.5914	-3.31	0.5752	0.8279	-1.75
1311	DNA polymerase delta subunit 2	P99905	0.0825	0.1979	-0.10	0.8498	0.8922	0.02
1312	DNA polymerase delta subunit 3	Q15054	0.4108	0.5913	-3.31	0.5752	0.8276	-1.75
1313	DNA polymerase epsilon catalytic subunit A	Q07864	0.0150	0.0710	0.15	0.0355	0.5393	0.17
1314	DNA polymerase epsilon subunit 3	Q9NRF9	0.0006	0.0202	0.56	0.0914	0.6288	0.32
1315	DNA polymerase epsilon subunit 4	Q9NR33	0.0249	0.0953	-0.57	0.2076	0.6585	-0.60
1316	DNA polymerase kappa	Q9UBT6	0.2107	0.3836	-0.04	0.0010	0.2252	0.38
1317	DNA polymerase zeta catalytic subunit	Q06073	0.4108	0.5911	-3.31	0.5752	0.8274	-1.75
1318	DNA primase small subunit	P49642	0.1557	0.3084	-0.14	0.6181	0.7172	0.06
1319	DNA repair and recombination protein RAD54-like	Q92698	0.2621	0.4521	-0.12	0.3584	0.7083	-0.13
1320	DNA repair protein complementing XP-G cells	P28715	0.0608	0.1634	-0.18	0.0059	0.3869	-0.24
1321	DNA repair protein RAD50	Q92878	0.9632	0.9730	-0.01	0.5183	0.8393	-0.25
1322	DNA repair protein RAD51 homolog 1	Q06609	0.0590	0.1607	0.60	0.4366	0.7727	-0.16
1323	DNA repair protein REV1	Q9UBZ9	0.0028	0.0357	0.24	0.0707	0.6004	0.31
1324	DNA repair protein XRCC1	P18887	0.0004	0.0173	-0.28	0.5570	0.8714	-0.02
1325	DNA repair protein XRCC2	Q43543	0.4108	0.5908	-3.31	0.5752	0.8272	-1.75
1326	DNA repair protein XRCC4	Q13426	0.4108	0.5908	-3.31	0.5752	0.8270	-1.75
1327	DNA replication ATP-dependent helicase/nuclease DNA2	P51530	0.0063	0.0478	0.15	0.0642	0.5928	0.56
1328	DNA replication complex GINS protein PSF1	Q14691	0.0259	0.0974	0.37	0.0271	0.5031	0.36
1329	DNA replication complex GINS protein PSF2	Q9Y248	0.4217	0.4991	-0.09	0.0623	0.5901	-0.28
1330	DNA replication complex GINS protein PSF3	Q9BRX5	0.0684	0.1738	-0.25	0.2541	0.6624	-2.98
1331	DNA replication complex GINS protein SLD5	Q9BRT9	0.4108	0.5906	-3.31	0.5752	0.8267	-1.75
1332	DNA replication licensing factor MCM2	P49736	0.0742	0.1848	0.07	0.2141	0.6625	0.12
1333	DNA replication licensing factor MCM3	P25205	0.1173	0.2519	-0.09	0.0974	0.7175	0.00
1334	DNA replication licensing factor MCM4	P33991	0.8318	0.8656	0.01	0.2551	0.6620	0.15
1335	DNA replication licensing factor MCM5	P33992	0.4254	0.5029	0.01	0.2151	0.6616	0.15
1336	DNA replication licensing factor MCM6	Q14566	0.1117	0.2428	0.08	0.1179	0.6309	0.29
1337	DNA replication licensing factor MCM7	P33993	0.1308	0.2725	0.09	0.3858	0.7310	0.12
1338	DNA topoisomerase 1	P11387	0.4803	0.5550	0.03	0.4778	0.8033	-0.11
1339	DNA topoisomerase 2-alpha	P11388	0.4108	0.5904	-3.31	0.5752	0.8265	-1.75
1340	DNA topoisomerase 2-beta	Q02880	0.4108	0.5903	-3.31	0.5752	0.8263	-1.75
1341	DNA topoisomerase 2-alpha	Q13472	0.3646	0.5777	0.12	0.8716	0.9072	0.02
1342	DNA topoisomerase 1 mitochondrial	Q06906	0.1455	0.2932	0.08	0.5578	0.8711	0.09
1343	DNA-(apurinic or apyrimidinic site) lyase	P27695	0.0009	0.0021	0.28	0.1866	0.6666	0.32
1344	DNA-3-methyladenine glycosylase	P9372	0.0236	0.0924	-0.30	0.2024	0.2438	0.43
1345	DNA-binding protein SATB2	Q9UPW6	0.0041	0.0405	0.97	0.8986	0.9282	0.03
1346	DNA-dependent protein kinase catalytic subunit	P78527	0.0030	0.0368	0.16	0.1623	0.6615	0.20
1347	DNA-directed RNA polymerase II subunit RPB2	P30876	0.0040	0.0401	0.59	0.2730	0.6652	0.01
1348	DNA-directed RNA polymerase II subunit RPC5	Q9NVU0	0.4108	0.5901	-3.31	0.5752	0.8260	-1.75
1349	DNA-directed RNA polymerase III subunit RPC9	Q75575	0.0007	0.0211	-0.40	0.3575	0.7084	-0.16
1350	DNA-directed RNA polymerases I and III subunit RPAC1	Q15160	0.3511	0.5606	-0.21	0.6778	0.7641	-0.08
1351	DNA-directed RNA polymerases I, II, and III subunit RPABC1	P19388	0.0568	0.1563	-12.68	0.0473	0.5685	-11.12
1352	DNA-directed RNA polymerases I, II, and III subunit RPABC3	P52434	0.0039	0.0397	0.15	0.2929	0.6704	0.25
1353	DnaI homolog subfamily A member 1	P31689	0.1343	0.2777	0.09	0.5484	0.8642	0.06
1354	DnaI homolog subfamily A member 2	Q60884	0.9300	0.9472	0.00	0.6998	0.7787	0.02
1355	DnaI homolog subfamily A member 3 mitochondrial	Q96Y11	0.4108	0.5899	-3.31	0.5752	0.8258	-1.75
1356	DnaI homolog subfamily A member 4	Q8WW22	0.2244	0.4030	-0.24	0.2187	0.6606	-2.34
1357	DnaI homolog subfamily B member 1	P25685	0.5034	0.5768	0.01	0.6936	0.7745	0.02
1358	DnaI homolog subfamily B member 11	Q9UBS4	0.0232	0.0911	0.20	0.0790	0.6126	0.28
1359	DnaI homolog subfamily B member 12	Q9NXW2	0.2553	0.4432	-0.09	0.3518	0.7041	-0.11
1360	DnaI homolog subfamily B member 3	Q8WWF6	0.4108	0.5898	-3.31	0.5752	0.8256	-1.75
1361	DnaI homolog subfamily B member 4	Q9UDY4	0.3552	0.5656	0.11	0.6516	0.7431	-0.22
1362	DnaI homolog subfamily B member 6	Q75190	0.4108	0.5896	-3.31	0.5752	0.8254	-1.75
1363	DnaI homolog subfamily B member 9	Q9UBS3	0.4108	0.5895	-3.31	0.5752	0.8251	-1.75
1364	DnaI homolog subfamily C member 10	Q8IXB1	0.2223	0.3989	-0.09	0.4282	0.7633	-0.06
1365	DnaI homolog subfamily C member 13	Q75165	0.1809	0.3446	0.12	0.4478	0.7826	0.11
1366	DnaI homolog subfamily C member 2	Q99543	0.0033	0.0379	0.26	0.1070	0.6306	0.24
1367	DnaI homolog subfamily C member 21	Q5F1R6	0.9519	0.9646	0.00	0.3196	0.6824	0.17

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
1368 DnaI homolog subfamily C member 3	Q13217	0.4108	0.5893	-3.31	0.5752	0.8249	-1.75	0.5661	0.7405
1369 DnaI homolog subfamily C member 7	Q9615	0.0389	0.1240	0.07	0.1046	0.6330	0.25	0.0015	0.0231
1370 DnaI homolog subfamily C member 8	Q75937	0.0720	0.1805	0.15	0.1944	0.6687	0.18	0.1529	0.2839
1371 DnaI homolog subfamily C member 9	Q8WXX5	0.0005	0.0188	0.43	0.2432	0.6603	0.28	0.0070	0.0398
1372 DnaI-type zinc finger protein	Q5SXM8	0.0050	0.2015	0.05	0.2960	0.6719	0.11	0.0721	0.1603
1373 Docking protein 5	Q9P104	0.4108	0.5891	-3.31	0.5752	0.8247	-1.75	0.5661	0.7403
1374 Dolichol-phosphate mannosyltransferase subunit 1	O60762	0.0023	0.0329	0.21	0.3978	0.7420	0.15	0.3657	0.5629
1375 Dolichol-phosphate mannosyltransferase subunit 3	Q9P2X0	0.6144	0.6789	0.05	0.1641	0.6636	0.23	0.0380	0.1027
1376 Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit	P39656	0.0149	0.0708	0.20	0.3702	0.7185	-0.07	0.0262	0.0808
1377 Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1	P04843	0.0047	0.0433	0.22	0.2295	0.6612	0.26	0.0013	0.0227
1378 Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2	P04844	0.0016	0.0274	0.14	0.0975	0.6337	0.11	0.0001	0.0192
1379 Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit DAD1	P61803	0.7990	0.8371	0.02	0.0447	0.5675	-0.23	0.3867	0.5879
1380 Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit STT3A	P46977	0.0093	0.0572	0.21	0.2163	0.6602	0.21	0.0034	0.0311
1381 Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit STT3B	Q8TCJ2	0.4108	0.5890	-3.31	0.5752	0.8244	-1.75	0.5661	0.7401
1382 Dol-P-Man:Man5GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase	Q9Y673	0.1657	0.3232	-0.15	0.6466	0.7386	0.07	0.0455	0.1174
1383 Double-strand break repair protein MRE11A	Q92685	0.4236	0.5010	0.11	0.2689	0.6630	0.13	0.0201	0.0682
1384 Doublecortin domain-containing protein 1	MOR2J8	0.4108	0.5888	-3.31	0.5752	0.8242	-1.75	0.5661	0.7399
1385 Doublecortin domain-containing protein 2B	A2VCK2	0.4108	0.5886	-3.31	0.5752	0.8240	-1.75	0.5661	0.7398
1386 Doublecortin domain-containing protein 2C	ARMY07	0.4108	0.5885	-3.31	0.5752	0.8238	-1.75	0.5661	0.7396
1387 Double-strand break repair protein MRE11A	P49959	0.4108	0.5883	-3.31	0.5752	0.8235	-1.75	0.5661	0.7394
1388 Double-stranded RNA-binding protein Staufen homolog 1	O95793	0.2389	0.4237	-0.04	0.2574	0.6624	0.04	0.1236	0.2419
1389 Double-stranded RNA-binding protein Staufen homolog 2	Q9NUL3	0.8040	0.8417	0.01	0.9324	0.9543	0.00	0.8896	0.9120
1390 Double-stranded RNA-specific adenosine deaminase	P55265	0.9201	0.9391	-0.01	0.1460	0.6548	0.14	0.9677	0.9735
1391 Drebrin-like protein	Q16643	0.5328	0.6035	0.04	0.4582	0.7901	0.12	0.0990	0.2025
1392 DTF domain-containing protein 2	Q9U1U6	0.0157	0.0729	0.17	0.1116	0.6304	0.21	0.0247	0.0780
1393 Dual oxidase 2	Q9N1A8	0.0210	0.0858	-0.19	0.3520	0.7040	-0.15	0.3083	0.4924
1394 Dual oxidase 2	Q9NRD8	0.4108	0.5882	-3.31	0.5752	0.8233	-1.75	0.5661	0.7392
1395 Dual serine/threonine and tyrosine protein kinase	Q6LUX3	0.5273	0.5987	-0.06	0.2731	0.6651	0.16	0.0352	0.0977
1396 Dual specificity mitogen-activated protein kinase kinase 1	Q02750	0.1893	0.3553	-0.09	0.9087	0.9365	0.01	0.5735	0.6311
1397 Dual specificity mitogen-activated protein kinase kinase 2	P36507	0.0036	0.0386	-0.38	0.6685	0.7561	-0.03	0.2428	0.4074
1398 Dual specificity mitogen-activated protein kinase kinase 3	P46734	0.0132	0.0670	-0.12	0.0412	0.5676	0.29	0.0739	0.1628
1399 Dual specificity mitogen-activated protein kinase kinase 4	P45985	0.1113	0.2424	0.05	0.9525	0.9686	0.01	0.4753	0.6933
1400 Dual specificity protein kinase TTK	P33981	0.4108	0.5880	-3.31	0.5752	0.8231	-1.75	0.5661	0.7390
1401 Dual specificity protein phosphatase 3	P51452	0.0132	0.0670	3.16	0.0799	0.6123	-8.09	0.0078	0.0418
1402 Dynactin subunit 1	Q14203	0.0070	0.0498	0.21	0.1258	0.6426	0.33	0.0068	0.0398
1403 Dynactin subunit 2	Q13561	0.0181	0.0790	0.19	0.1018	0.4305	0.19	0.0179	0.0639
1404 Dynactin subunit 4	Q9U1U0	0.0349	0.1168	-0.13	0.4495	0.7840	-0.08	0.0751	0.1646
1405 Dynactin subunit 5	Q9BTE1	0.1198	0.2556	0.21	0.5321	0.8499	0.05	0.0141	0.0556
1406 Dynamin-1	Q05193	0.0098	0.0582	0.32	0.6089	0.7110	0.08	0.1684	0.3075
1407 Dynamin-1-like protein	Q00429	0.0053	0.0445	0.29	0.0476	0.7500	0.13	0.0075	0.0409
1408 Dynamin-2	P50570	0.3096	0.5106	0.04	0.1838	0.6644	0.21	0.0213	0.0707
1409 Dynamin-3	Q9ULQ16	0.0071	0.0497	9.51	0.5792	0.8862	-1.75	0.5661	0.7900
1410 Dynamin-like 120 kDa protein mitochondrial	O60313	0.0086	0.0549	0.16	0.1899	0.6705	0.24	0.0015	0.0227
1411 Dynein assembly factor 1 axonemal	Q8NEP3	0.1349	0.2785	-0.27	0.2258	0.6590	-0.77	0.4357	0.6465
1412 Dynein assembly factor 5 axonemal	Q86Y56	0.0030	0.0367	0.44	0.1786	0.6646	0.36	0.0055	0.0360
1413 Dynein heavy chain 1 axonemal	Q9P2D7	0.4108	0.5878	-3.31	0.5752	0.8228	-1.75	0.5661	0.7388
1414 Dynein heavy chain 10 axonemal	Q8IVF4	0.1101	0.2408	0.12	0.2787	0.6647	0.13	0.0061	0.0378
1415 Dynein heavy chain 12 axonemal	Q6ZK08	0.0824	0.1978	0.08	0.1417	0.6576	-0.09	0.0119	0.0511
1416 Dynein heavy chain 14 axonemal	Q0VDD8	0.0433	0.1321	0.19	0.1472	0.6539	0.10	0.0025	0.0277
1417 Dynein heavy chain 17 axonemal	Q9UFH2	0.0180	0.0788	-0.50	0.2573	0.6631	-0.35	0.0186	0.0654
1418 Dynein heavy chain 2 axonemal	Q9P225	0.0089	0.0561	0.21	0.2745	0.6644	0.13	0.0339	0.0954
1419 Dynein heavy chain 3 axonemal	Q8TE57	0.4108	0.5877	-3.31	0.5752	0.8226	-1.75	0.5661	0.7386
1420 Dynein heavy chain 5 axonemal	Q8TD73	0.1883	0.3543	0.12	0.0637	0.5924	0.12	0.0762	0.1664
1421 Dynein heavy chain 7 axonemal	Q9UC66	0.5448	0.6144	-0.03	0.6063	0.7086	0.05	0.0713	0.1592
1422 Dynein heavy chain 8 axonemal	Q8WXX0	0.1814	0.3450	-1.46	0.2304	0.6616	-0.71	0.1813	0.0648
1423 Dynein heavy chain 9 axonemal	Q6YB1	0.0004	0.0017	-0.33	0.0001	0.2590	-0.42	0.0730	0.5711
1424 Dynein heavy chain domain-containing protein 1	Q9NYC9	0.4108	0.5875	-3.31	0.5752	0.8224	-1.75	0.5661	0.7385
1425 Dynein heavy chain 12 axonemal	Q96M86	0.3639	0.5768	0.10	0.1985	0.6647	0.17	0.0560	0.7799
1426 Dynein light chain 1 cytoplasmic	P63167	0.0052	0.0442	0.18	0.0408	0.5681	0.40	0.0013	0.0236
1427 Dynein light chain 2 cytoplasmic	Q96FJ2	0.0555	0.1541	0.07	0.0038	0.3281	-0.33	0.0005	0.0221
1428 Dynein light chain roadblock-type 1	Q9NP97	0.4108	0.5873	-3.31	0.5752	0.8222	-1.75	0.5661	0.7383
1429 Dynein light chain roadblock-type 2	Q8TF09	0.0057	0.0456	0.37	0.0368	0.5999	0.13	0.0320	0.0917
1430 Dynein light chain Tctex-type 1	P63172	0.0610	0.1635	-0.56	0.7611	0.8272	0.05	0.1910	0.3380
1431 Dynein light chain Tctex-type 3	P51808	0.4108	0.5872	-3.31	0.5752	0.8219	-1.75	0.5661	0.7381
1432 Dynein regulatory complex protein 8	Q5VUJ9	0.3025	0.5021	0.06	0.7577	0.8244	-0.02	0.0016	0.0228
1433 Dynein regulatory complex protein 9	Q9H095	0.0185	0.0801	-0.25	0.5780	0.6869	0.09	0.2215	0.3787
1434 Dyx1in	Q03001	0.4108	0.5870	-3.31	0.5752	0.8217	-1.75	0.5661	0.7379
1435 Dyx1robrein alpha	Q9Y4J8	0.0613	0.1638	-1.52	0.1789	0.6676	-1.32	0.1971	0.3469
1436 Dyx1robrein beta	O60941	0.4108	0.5869	-3.31	0.5752	0.8215	-1.75	0.5661	0.7377
1437 Dyx1robrin	Q14118	0.5868	0.6535	-0.04	0.2420	0.6598	-0.22	0.0145	0.0566
1438 Dyx1robrin	P11532	0.9445	0.9582	0.00	0.3865	0.7294	0.11	0.0081	0.0423

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	SSE IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
1439 E1A-binding protein p400	Q96L91	0.3134	0.5149	-0.11	0.2900	0.6685	0.17	0.0329	0.0935	0.28	0.2982	0.4622	0.13	0.1019	0.2559	0.19	0.5410	0.7729	0.09	0.3736	0.4575	-2.55	0.8708	0.9549	-0.33	0.0651	0.1225	2.06
1440 EF2-associated phosphoprotein	Q56P03	0.0164	0.0748	0.34	0.1310	0.6680	0.34	0.0267	0.0818	0.38	0.0161	0.0527	0.31	0.7182	0.7786	0.002	0.0463	0.1429	0.23	0.3736	0.5642	-2.55	0.8708	1.1495	-0.33	0.0651	0.1727	2.06
1441 E3 SUMO-protein ligase PIA3	Q9Y6X2	0.0045	0.0425	0.39	0.0217	0.4783	0.34	0.8821	0.9071	-0.01	0.0045	0.0271	0.45	0.0261	0.1168	0.24	0.0251	0.1007	0.28	0.3736	0.5859	-2.55	0.8708	1.1880	-0.33	0.0651	0.1847	2.06
1442 E3 SUMO-protein ligase RanBP2	P49792	0.2505	0.4368	0.03	0.3178	0.6808	0.13	0.0046	0.0333	0.27	0.0084	0.0371	0.17	0.1356	0.3054	0.05	0.0056	0.0616	0.23	0.3736	0.1793	0.37	0.9861	0.9899	0.00	0.2923	0.3541	0.04
1443 E3 ubiquitin-ITG15 ligase TRIM25	Q14258	0.00189	0.0010	0.20	0.3924	0.7362	0.12	0.0393	0.1053	0.14	0.0103	0.0408	0.24	0.5753	0.4548	-0.02	0.0130	0.0764	0.23	0.0992	0.2544	0.24	0.217	0.5202	-0.13	0.6698	0.7234	-0.04
1444 E3 ubiquitin-protein ligase ARIH1	Q9Y4X3	0.5926	0.6992	-0.07	0.0296	0.5077	-0.37	0.0742	0.1631	-0.28	0.5726	0.6222	-0.06	0.2799	0.5061	-0.13	0.3217	0.5349	0.21	0.3736	0.4783	-2.55	0.8708	0.9936	-0.33	0.0651	0.1313	2.06
1445 E3 ubiquitin-protein ligase ARIH2	Q95376	0.0242	0.0935	-0.21	0.1279	0.6414	-0.26	0.0133	0.0232	-0.50	0.1003	0.1946	-0.24	0.5564	0.6398	-0.13	0.1126	0.2539	-0.37	0.3736	0.5305	-2.55	0.8708	1.0890	-0.33	0.0651	0.1553	2.06
1446 E3 ubiquitin-protein ligase BRE1A	Q5VTR2	0.0025	0.0339	0.21	0.2161	0.6616	0.19	0.0002	0.0170	0.51	0.0020	0.0200	0.29	0.0008	0.0220	0.28	0.0009	0.0476	0.59	0.1610	0.3543	0.22	0.2288	0.5419	0.12	0.3348	0.4059	-0.08
1447 E3 ubiquitin-protein ligase BRE1B	Q75150	0.0304	0.1075	0.16	0.0561	0.5847	0.20	0.0108	0.0486	0.28	0.0051	0.0288	0.36	0.0004	0.0170	0.59	0.5333	0.1562	0.14	0.1011	0.2573	0.35	0.4792	0.8900	-0.08	0.3560	0.6019	-0.09
1448 E3 ubiquitin-protein ligase CBL	P22681	0.4108	0.5867	-3.31	0.5752	0.8213	-1.75	0.5661	0.7375	-1.19	0.5388	0.6972	0.89	0.2938	0.4812	-1.88	0.9510	1.1165	0.09	0.0446	0.1697	0.31	0.0032	0.0467	0.82	0.9119	0.9295	-0.01
1449 E3 ubiquitin-protein ligase CHIP	Q9UNE7	0.1042	0.2310	0.06	0.4397	0.7758	-0.03	0.0038	0.0314	-0.18	0.0521	0.1185	0.15	0.0174	0.0948	-0.12	0.0373	0.1249	0.24	0.0586	0.1925	0.31	0.0136	0.0604	1.85	0.4012	0.7159	3.99
1450 E3 ubiquitin-protein ligase DCST1	Q5T197	0.9551	0.9665	0.00	0.4714	0.8003	0.13	0.0918	0.1910	0.11	0.0945	0.1860	0.11	0.3313	0.4285	-0.05	0.0921	0.0931	0.00	0.3736	0.4295	-2.55	0.8708	0.9021	-0.33	0.0651	0.1114	2.06
1451 E3 ubiquitin-protein ligase HECTD1	Q9ULT8	0.3624	0.5753	-0.05	0.1991	0.6645	-0.21	0.0039	0.0318	-0.32	0.0076	0.0353	-0.26	0.0097	0.0707	-0.28	0.0276	0.1066	-0.23	0.3736	0.5831	-2.55	0.8708	1.1830	-0.33	0.0651	0.1831	2.06
1452 E3 ubiquitin-protein ligase HECTD3	Q5T447	0.2494	0.4359	0.40	0.5570	0.8712	0.85	0.0053	0.0355	1.88	0.8282	0.8515	0.29	0.1263	0.2932	-0.56	0.5596	0.7950	-0.43	0.3736	0.4561	-2.55	0.8708	0.9522	-0.33	0.0651	0.1220	2.06
1453 E3 ubiquitin-protein ligase Mdm2	Q95714	0.0001	0.0133	0.49	0.6372	0.7328	-0.06	0.0065	0.0388	0.22	0.0001	0.0081	0.62	0.0001	0.0126	0.53	0.0396	0.1300	0.43	0.0166	0.1201	0.27	0.0725	0.2610	0.13	0.0144	0.1032	0.25
1454 E3 ubiquitin-protein ligase HUWE1	Q7Z6Z7	0.0554	0.1540	0.14	0.1543	0.6606	0.25	0.0082	0.0427	0.27	0.0051	0.0288	0.29	0.0435	0.1540	0.16	0.0159	0.0839	0.26	0.0332	0.1523	0.32	0.0633	0.2416	0.20	0.0103	0.0895	0.45
1455 E3 ubiquitin-protein ligase Itchy homolog	Q96J02	0.4108	0.5865	-3.31	0.5752	0.8210	-1.75	0.5661	0.7373	-1.19	0.5388	0.6970	0.89	0.2938	0.4810	-1.88	0.9510	1.1163	0.09	0.0231	0.1361	-0.25	0.0141	0.0992	-0.30	0.0467	0.1891	-0.23
1456 E3 ubiquitin-protein ligase LRSAM1	Q6UWE0	0.0784	0.1920	0.18	0.3093	0.6783	0.08	0.0427	0.1221	0.22	0.0115	0.0430	0.35	0.0706	0.2025	0.19	0.0750	0.1948	0.19	0.0075	0.0891	0.48	0.2631	0.5918	0.11	0.0849	0.1370	0.22
1457 E3 ubiquitin-protein ligase MARCH1	A6NN9E9	0.0033	0.0378	0.19	0.1327	0.6479	0.19	0.1299	0.2507	0.11	0.0074	0.0349	0.18	0.0004	0.0166	0.29	0.0626	0.1740	0.17	0.3736	0.5542	-2.55	0.8708	1.1316	-0.33	0.0651	0.1674	2.06
1458 E3 ubiquitin-protein ligase MARCH5	Q9NX47	0.6315	0.6938	0.02	0.1307	0.6448	0.19	0.4281	0.6376	0.04	0.0428	0.1030	0.10	0.0371	0.1401	0.12	0.0767	0.1975	0.08	0.3736	0.5456	-2.55	0.8708	1.1162	-0.33	0.0651	0.1629	2.06
1459 E3 ubiquitin-protein ligase MARCH7	Q9H992	0.0905	0.2108	0.14	0.0941	0.6306	0.30	0.0019	0.0247	0.33	0.0021	0.0202	0.29	0.0041	0.0476	0.33	0.0699	0.1859	0.11	0.3736	0.5493	-2.55	0.8708	1.1229	-0.33	0.0651	0.1648	2.06
1460 E3 ubiquitin-protein ligase Mdm1	Q90887	0.2227	0.4003	0.07	0.5491	0.8648	0.08	0.1058	0.2133	0.25	0.9577	0.9635	0.00	0.0991	0.2516	-0.12	0.3553	0.5609	0.06	0.3736	0.4737	-2.55	0.8708	0.9851	-0.33	0.0651	0.1794	2.06
1461 E3 ubiquitin-protein ligase MGN1	Q60291	0.4108	0.5864	-3.31	0.5752	0.8208	-1.75	0.5661	0.7372	-1.19	0.5388	0.6969	0.89	0.2938	0.4808	-1.88	0.9510	1.1160	0.09	0.0025	0.0558	-1.61	0.0012	0.0296	0.95	0.0758	0.1259	-0.39
1462 E3 ubiquitin-protein ligase MIB1	Q86Y76	0.1772	0.3395	0.19	0.8240	0.8738	0.03	0.8192	0.8536	0.02	0.8191	0.8439	-0.03	0.7817	0.8289	-0.03	0.6447	0.8814	-0.05	0.3736	0.4479	-2.55	0.8708	0.9368	-0.33	0.0651	0.1186	2.06
1463 E3 ubiquitin-protein ligase NEDD4	P46934	0.0152	0.0717	-0.51	0.0010	0.2355	-0.27	0.0031	0.0307	-0.31	0.0170	0.0545	-0.64	0.0240	0.1121	-0.53	0.0722	0.1898	-0.13	0.3736	0.5482	-2.55	0.8708	1.1210	-0.33	0.0651	0.1643	2.06
1464 E3 ubiquitin-protein ligase NEDD4-like	Q96PU5	0.4108	0.5862	-3.31	0.5752	0.8206	-1.75	0.5661	0.7370	-1.19	0.5388	0.6967	0.89	0.2938	0.4807	-1.88	0.9510	1.1158	0.09	0.0358	0.1564	0.28	0.1701	0.5421	0.12	0.0201	0.6782	0.02
1465 E3 ubiquitin-protein ligase NDR3	Q9UPQ7	0.4108	0.5860	-3.31	0.5752	0.8204	-1.75	0.5661	0.7368	-1.19	0.5388	0.6965	0.89	0.2938	0.4805	-1.88	0.9510	1.1155	0.09	0.7466	0.7841	0.06	0.7399	1.1822	-0.06	0.0138	0.1017	0.73
1466 E3 ubiquitin-protein ligase pellino homolog 3	Q8NZH9	0.4108	0.5859	-3.31	0.5752	0.8201	-1.75	0.5661	0.7366	-1.19	0.5388	0.6964	0.89	0.2938	0.4804	-1.88	0.9510	1.1153	0.09	0.4372	0.4930	0.11	0.0748	0.2656	0.26	0.7030	0.7544	0.05
1467 E3 ubiquitin-protein ligase PPP1R11	Q60927	0.0072	0.0502	0.49	0.4342	0.7708	-0.42	0.0086	0.0437	-0.47	0.1169	0.2184	0.44	0.2189	0.4245	-0.12	0.3279	0.5305	0.38	0.3736	0.4769	-2.55	0.8708	0.9909	-0.33	0.0651	0.1307	2.06
1468 E3 ubiquitin-protein ligase RAD18	Q9NS91	0.4108	0.5857	-3.31	0.5752	0.8199	-1.75	0.5661	0.7364	-1.19	0.5388	0.6962	0.89	0.2938	0.4802	-1.88	0.9510	1.1150	0.09	0.0128	0.1073	0.38	0.0057	0.0609	0.22	0.0013	0.0449	0.44
1469 E3 ubiquitin-protein ligase RBBP6	Q7Z6F9	0.0175	0.0775	0.12	0.4546	0.7876	0.18	0.0191	0.0663	0.35	0.0021	0.0199	0.34	0.8443	0.8800	0.01	0.0030	0.0547	0.27	0.3736	0.6381	-2.55	0.8708	1.2789	-0.33	0.0651	0.2167	2.06
1470 E3 ubiquitin-protein ligase RBX1	P62877	0.0144	0.0700	-0.97	0.6375	0.7330	-0.06	0.1173	0.2323	-0.25	0.5405	0.5920	-0.09	0.2040	0.4053	-0.17	0.0347	0.1200	-0.45	0.3736	0.5749	-2.55	0.8708	1.1686	-0.33	0.0651	0.1785	2.06
1471 E3 ubiquitin-protein ligase RNF113A	Q15541	0.3975	0.6163	-0.08	0.4995	0.8124	0.07	0.4470	0.6602	-0.12	0.4949	0.6981	0.06	0.1125	0.2736	-0.18	0.3423	0.5466	-0.09	0.0073	0.0875	-0.47	0.0137	0.0975	-0.75	0.1730	0.2390	-1.29
1472 E3 ubiquitin-protein ligase RNF114	Q9Y508	0.0389	0.1239	0.16	0.2767	0.6651	0.19	0.0026	0.0278	0.36	0.0038	0.0251	0.32	0.4719	0.5627	0.04	0.0242	0.0993	0.24	0.0117	0.1041	0.40	0.1469	0.4109	0.11	0.1474	0.2098	0.10
1473 E3 ubiquitin-protein ligase RNF123	Q5XP14	0.1234	0.2699	1.80	0.5248	0.8440	-0.88	0.4852	0.7052	-0.60	0.2144	0.3515	2.22	0.2863	0.5160	-0.93	0.2148	0.3962	2.68	0.3736	0.4995	-2.55	0.8708	1.0327	-0.33	0.0651	0.1407	2.06
1474 E3 ubiquitin-protein ligase RNF126	Q9VBH8	0.5717	0.6393	-0.06	0.6949	0.7743	0.07	0.0553	0.1342	0.34	0.3568	0.5351	0.11	0.2574	0.4774	0.15	0.0856	0.1233	0.01	0.0607	0.1943	0.23	0.1604	0.4341	0.15	0.0026	0.0545	0.81
1475 E3 ubiquitin-protein ligase RNF14	Q9UBS8	0.4108	0.5856	-3.31	0.5752	0.8197	-1.75	0.5661	0.7362	-1.19	0.5388	0.6960	0.89	0.2938	0.4801	-1.88	0.9510	1.1148	0.09	0.0012	0.0447	1.05	0.0000	0.0000	0.76	0.0000	0.0000	1.26
1476 E3 ubiquitin-protein ligase RNF187	Q7A331	0.2314	0.4130	0.12	0.4059	0.7488	0.15	0.0894	0.1876	0.20	0.0897	0.1787	0.20	0.7119	0.7724	-0.03	0.0256	0.0896	-0.02	0.3736	0.4365	-2.55	0.8708	0.9153	-0.33	0.0651	0.1141	2.06

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control	
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
1523	ELAV-like protein 1	Q15717	0.0484	0.1414	0.10	0.6132	0.7146	0.01	0.0311	0.0901
1524	Electrogenic sodium bicarbonate cotransporter 1	O9YG61	0.4108	0.5838	-3.31	0.5752	0.8172	-1.75	0.5661	0.7342
1525	Electron transfer flavoprotein subunit alpha _mitochondrial	P13804	0.5648	0.6327	0.03	0.1672	0.6606	0.15	0.1659	0.3033
1526	Electron transfer flavoprotein subunit beta	P38117	0.5580	0.6267	-0.04	0.6657	0.7537	0.03	0.1781	0.3027
1527	ELKS/Rab6-interacting CAST family member 1	Q8IU02	0.4108	0.5836	-3.31	0.5752	0.8170	-1.75	0.5661	0.7340
1528	Ellis-van Creveld syndrome protein	P57679	0.0131	0.0668	-0.19	0.5662	0.8704	-0.15	0.0015	0.0224
1529	Elongation factor 1-alpha 1	P68104	0.4108	0.5835	-3.31	0.5752	0.8168	-1.75	0.5661	0.7338
1530	Elongation factor 1-alpha 2	Q05639	0.1523	0.3033	0.08	0.1598	0.6690	0.15	0.0357	0.0987
1531	Elongation factor 1-beta	P24534	0.0014	0.0257	0.11	0.5464	0.8613	0.05	0.0022	0.0261
1532	Elongation factor 1-delta	P29692	0.0422	0.1302	0.20	0.3866	0.7290	0.17	0.0097	0.0458
1533	Elongation factor 1-gamma	P26641	0.0095	0.0575	0.24	0.2500	0.6600	0.25	0.0013	0.0225
1534	Elongation factor 2	P13639	0.0086	0.0549	0.31	0.2781	0.6654	0.24	0.0014	0.0223
1535	Elongation factor G _mitochondrial	Q96R99	0.4032	0.6231	-0.08	0.7882	0.8476	0.03	0.8761	0.9019
1536	Elongation factor Ts _mitochondrial	P43897	0.2980	0.4968	0.04	0.0489	0.5744	0.19	0.0290	0.0865
1537	Elongation factor Tu _mitochondrial	P49411	0.0086	0.0548	0.26	0.2035	0.6609	0.26	0.0080	0.0421
1538	Elongation of very long chain fatty acids protein 1	Q9BW60	0.4108	0.5833	-3.31	0.5752	0.8165	-1.75	0.5661	0.7336
1539	Elongator complex protein 1	O95163	0.6923	0.7474	-0.13	0.8344	0.8803	-0.11	0.2098	0.3638
1540	Elongator complex protein 5	Q8TE02	0.4108	0.5832	-3.31	0.5752	0.8163	-1.75	0.5661	0.7335
1541	Elongin-B	Q15370	0.8818	0.9067	-0.01	0.4466	0.7821	0.15	0.5711	0.6289
1542	Elongin-C	Q15369	0.0121	0.0636	0.21	0.0450	0.5672	0.23	0.0002	0.0230
1543	Embryonic stem cell-specific 5-hydroxymethylcytosine-binding protein	Q96F22	0.3391	0.5472	0.08	0.6522	0.7435	0.03	0.6807	0.7303
1544	Embryonic testis differentiation protein homolog B	P0DDP9	0.4108	0.5830	-3.31	0.5752	0.8161	-1.75	0.5661	0.7333
1545	Emerin	P50402	0.0491	0.1422	-0.46	0.0438	0.5686	-1.16	0.3836	0.5844
1546	Ena/VASP-like protein	Q9UI08	0.0257	0.0970	-0.44	0.3242	0.6855	-0.16	0.2139	0.3685
1547	Endogenous Bornavirus-like nucleoprotein 2	Q6P217	0.4108	0.5828	-3.31	0.5752	0.8159	-1.75	0.5661	0.7331
1548	Endogenous retrovirus group 3 member 1 Env polyprotein	Q14264	0.4108	0.5827	-3.31	0.5752	0.8156	-1.75	0.5661	0.7329
1549	Endogenous retrovirus group K member 104 Rec protein	P61576	0.0545	0.1528	-0.53	0.2624	0.6634	-0.43	0.0125	0.0524
1550	Endonuclease 8-like 2	O96952	0.5232	0.5947	0.08	0.0703	0.7789	-0.12	0.9840	0.9870
1551	Endonuclease 8-like 3	Q8TAT5	0.2850	0.4806	-0.24	0.1864	0.6668	-0.89	0.0476	0.1211
1552	Endonuclease/exonuclease/phosphatase family domain-containing protein 1	Q7L9B9	0.4108	0.5825	-3.31	0.5752	0.8154	-1.75	0.5661	0.7327
1553	Endophilin-A1	Q99862	0.4108	0.5824	-3.31	0.5752	0.8152	-1.75	0.5661	0.7326
1554	Endophilin-A2	Q99861	0.0582	0.1590	-0.25	0.1759	0.6627	-0.08	0.2553	0.0790
1555	Endophilin-B2	Q0NR46	0.1469	0.2952	0.12	0.1992	0.6644	0.28	0.0064	0.0388
1556	Endoplasmic reticulum aminopeptidase 1	Q9NZ08	0.4108	0.5822	-3.31	0.5752	0.8150	-1.75	0.5661	0.7324
1557	Endoplasmic reticulum chaperone BiP	P11021	0.0032	0.0372	0.42	0.2011	0.6610	0.29	0.0009	0.0210
1558	Endoplasmic reticulum junction formation protein lunapark	Q9COE8	0.0991	0.2239	-0.17	0.0629	0.7368	-0.08	0.1606	0.2954
1559	Endoplasmic reticulum metalloproteinase 1	Q722K6	0.0312	0.1093	-0.22	0.7397	0.8108	0.05	0.0930	0.1931
1560	Endoplasmic reticulum protein SC65	Q92791	0.0745	0.1850	-2.58	0.3092	0.6787	-2.13	0.0333	0.0943
1561	Endoplasmic reticulum resident protein 29	P30040	0.0106	0.0596	0.23	0.3092	0.6790	0.13	0.0052	0.0352
1562	Endoplasmic reticulum resident protein 44	Q9BS26	0.0028	0.0356	0.34	0.1662	0.6602	0.38	0.0105	0.0479
1563	Endoplasmic reticulum-Golgi intermediate compartment protein 1	Q969X5	0.0632	0.1665	-0.10	0.2002	0.6635	0.08	0.0566	0.1361
1564	Endoplasmic reticulum-Golgi intermediate compartment protein 2	Q96RQ1	0.4108	0.5820	-3.31	0.5752	0.8147	-1.75	0.5661	0.7322
1565	Endoplasmic reticulum-Golgi intermediate compartment protein 3	Q9Y282	0.0216	0.0875	-0.16	0.2839	0.6642	0.14	0.0039	0.0317
1566	Endoplasmic reticulum protein	P14625	0.0049	0.0434	0.38	0.1982	0.6675	0.31	0.0014	0.0227
1567	Endonuclease LACTB2	Q33H82	0.1194	0.2549	-0.33	0.7552	0.8222	0.05	0.0414	0.6655
1568	Endothelial differentiation-related factor 1	O60869	0.2489	0.4354	0.07	0.3303	0.6893	0.17	0.0359	0.0991
1569	Endothelin-converting enzyme 1	P42892	0.4108	0.5819	-3.31	0.5752	0.8145	-1.75	0.5661	0.7320
1570	Enhancer of filamentation 1	Q14511	0.4108	0.5817	-3.31	0.5752	0.8143	-1.75	0.5661	0.7318
1571	Enhancer of mRNA-decapping protein 4	Q6P2E9	0.3183	0.5211	0.02	0.3699	0.7182	-0.07	0.0088	0.0439
1572	Enhancer of rudimentary homolog	P84099	0.0184	0.0798	-0.38	0.9895	0.9924	0.00	0.8454	0.8757
1573	Enolase-phosphatase E1	Q9UHY7	0.1466	0.2948	-0.26	0.0871	0.6189	-0.37	0.0628	0.1457
1574	Enoyl-CoA delta isomerase 1 _mitochondrial	P42126	0.0309	0.1086	0.28	0.6255	0.7228	0.05	0.2185	0.3749
1575	Enoyl-CoA delta isomerase 2 _mitochondrial	O75521	0.1037	0.2303	0.12	0.3682	0.7289	0.06	0.1249	0.2439
1576	Enoyl-CoA hydratase domain-containing protein 2 _mitochondrial	Q86YB7	0.0613	0.1637	0.14	0.3119	0.6800	0.22	0.0122	0.0518
1577	Enoyl-CoA hydratase _mitochondrial	P30084	0.0035	0.0383	0.16	0.5000	0.5743	0.24	0.8569	0.8862
1578	Enscosin	Q14244	0.0144	0.0700	0.31	0.1918	0.6686	0.31	0.0010	0.0212
1579	Envoplakin	Q92817	0.6023	0.6679	-0.02	0.2491	0.6593	0.17	0.3359	0.5284
1580	Envoplakin-like protein	AKM236	0.4108	0.5816	-3.31	0.5752	0.8141	-1.75	0.5661	0.7316
1581	Ephrin type-A receptor 2	P29317	0.4108	0.5814	-3.31	0.5752	0.8139	-1.75	0.5661	0.7315
1582	Ephrin type-A receptor 4	P47654	0.0135	0.0679	1.41	0.0135	0.4436	1.24	0.0118	0.0509
1583	Ephrin type-A receptor 6	Q9UF33	0.4108	0.5812	-3.31	0.5752	0.8136	-1.75	0.5661	0.7313
1584	Ephrin type-A receptor 7	Q15375	0.4108	0.5811	-3.31	0.5752	0.8134	-1.75	0.5661	0.7311
1585	Ephrin type-B receptor 3	P54753	0.2978	0.4967	0.07	0.2476	0.6581	0.20	0.0291	0.0867
1586	Ephrin type-B receptor 4	P54760	0.0930	0.2147	0.35	0.1066	0.6304	0.31	0.6183	0.6726
1587	Epidermal growth factor receptor	P00533	0.4108	0.5809	-3.31	0.5752	0.8132	-1.75	0.5661	0.7309
1588	Epidermal growth factor receptor kinase substrate 8	Q12929	0.4108	0.5808	-3.31	0.5752	0.8130	-1.75	0.5661	0.7307
1589	Epidermal growth factor receptor kinase substrate 8-like protein 1	Q8TE68	0.1490	0.2980	-7.40	0.1842	0.6635	-5.85	0.1746	0.3163
1590	Epidermal growth factor receptor kinase substrate 8-like protein 2	Q9H6S3	0.1205	0.2562	0.07	0.0661	0.5934	-0.08	0.0088	0.0440
1591	Epidermal growth factor receptor substrate 15	P42566	0.5998	0.6657	0.08	0.0325	0.5180	0.37	0.4325	0.6429
1592	Epidermal growth factor receptor substrate 15-like 1	O9UBC2	0.0119	0.0629	-0.42	0.1724	0.6610	-0.22	0.3516	0.5458
1593	Epidermal growth factor receptor substrate 15-like 1	O9UBH3	0.0250	0.0955	-3.91	0.2742	0.6646	-3.81	0.2302	0.3896
1594	Epilakin	P58107	0.4445	0.5221	0.04	0.1731	0.6598	0.21	0.0185	0.0653

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
1595 Epithelial cell adhesion molecule	P16422	0.0151	0.0713	0.18	0.4832	0.8082	0.09	0.0010	0.2027	0.37	0.0014	0.0172	0.31	0.0118	0.0783	0.27	0.0058	0.0622	0.38	0.3736	0.6267	-2.55	87808	1.2593	-0.33	0.0651	0.2093	2.06
1596 Epithelial splicing regulatory protein 1	Q6NXG1	0.4108	0.5806	-3.31	0.5752	0.8127	-1.75	0.5661	0.7305	-0.19	0.5388	0.6907	0.89	0.2938	0.4754	-1.88	0.9510	1.1070	0.09	0.0128	0.1071	-0.51	0.0040	0.0512	0.68	0.9517	0.9623	0.01
1597 Epithelial splicing regulatory protein 2	Q9H6T0	0.0003	0.0162	-1.55	0.0001	0.5180	-1.59	0.0065	0.0391	-0.19	0.0003	0.0109	-3.74	0.0006	0.0206	-0.66	0.1815	0.3512	0.18	0.3736	0.5066	-2.55	87808	1.0456	-0.33	0.0651	0.1439	2.06
1598 Epithelial-stromal interaction protein 1	Q96J88	0.7097	0.7614	-0.03	0.6862	0.7709	0.04	0.0247	0.0779	-0.29	0.0137	0.0475	-0.36	0.0209	0.1039	-0.37	0.5263	0.7558	0.04	0.3736	0.4385	-2.55	87808	0.9567	-0.33	0.0651	0.1229	2.06
1599 Epoxide hydrolase 1	P07099	0.0674	0.1721	0.23	0.4434	0.7794	-0.07	0.1358	0.2588	0.16	0.2902	0.4522	0.19	0.0119	0.0782	-0.43	0.0970	0.0648	0.61	0.0261	0.1407	0.30	0.0314	0.1508	0.24	0.1904	0.2582	0.11
1600 Epsin	O95925	0.0532	0.1499	0.36	0.0222	0.4792	0.24	0.0178	0.0638	0.43	0.0028	0.0218	0.24	0.0100	0.0720	-0.18	0.0040	0.0602	0.51	0.3736	0.6347	-2.55	87808	1.2731	-0.33	0.0651	0.2145	2.06
1601 Epsin-sarcoglycan	O43556	0.0624	0.1656	4.69	0.5772	0.6862	0.94	0.0741	0.1629	1.61	0.4183	0.6102	1.02	0.5373	0.6219	-0.60	0.1599	0.3207	1.04	0.3736	0.5122	-2.55	87808	1.0559	-0.33	0.0651	0.1466	2.06
1602 Epsin-1	Q9Y643	0.4108	0.5805	-3.31	0.5752	0.8125	-1.75	0.5661	0.7304	-0.19	0.5388	0.6905	0.89	0.2938	0.4753	-1.88	0.9510	1.1068	0.09	0.2261	0.4510	-0.19	0.3235	0.6762	-0.12	0.0716	0.1200	-0.24
1603 Epsin-2	O95208	0.4108	0.5803	-3.31	0.5752	0.8123	-1.75	0.5661	0.7302	-0.19	0.5388	0.6903	0.89	0.2938	0.4751	-1.88	0.9510	1.1065	0.09	0.0140	0.1107	-0.52	0.0191	0.1185	-0.55	0.0912	0.1449	-0.58
1604 Equilibrative nucleoside transporter 1	Q99808	0.0864	0.2043	0.10	0.3293	0.6886	0.19	0.0310	0.0900	0.21	0.0030	0.0223	0.28	0.1387	0.3102	0.07	0.0497	0.1495	0.13	0.0789	0.2232	0.47	0.0258	0.1439	0.13	0.0305	0.1475	0.22
1605 ER lumen protein-retaining receptor 1	P24390	0.0039	0.0396	-0.42	0.1024	0.6337	-0.25	0.0071	0.0400	-0.35	0.0063	0.0318	-0.33	0.0126	0.0802	-0.40	0.0902	0.2191	-0.32	0.3736	0.5377	-2.55	87808	1.1021	-0.33	0.0651	0.1589	2.06
1606 ER membrane protein complex subunit 1	Q8N766	0.8315	0.8654	0.01	0.5947	0.6990	-0.04	0.5058	0.7278	-0.04	0.4206	0.6122	0.08	0.5205	0.6083	-0.05	0.8468	1.0820	-0.01	0.0099	0.0996	-0.16	0.0143	0.1001	-0.13	0.3568	0.4284	-0.03
1607 ER membrane protein complex subunit 2	Q15006	0.5296	0.6009	0.05	0.8330	0.8799	-0.03	0.0234	0.0751	0.29	0.2548	0.4051	0.14	0.2290	0.4387	0.12	0.6376	0.8747	0.06	0.9073	0.9241	0.02	0.9059	0.9298	-0.02	0.1929	0.2608	0.23
1608 ER membrane protein complex subunit 3	Q9P0I2	0.0197	0.0824	0.27	0.0105	0.4458	-0.25	0.5179	0.7384	-0.03	0.2193	0.3579	-0.18	0.0598	0.1843	-0.17	0.2148	0.3964	0.14	0.0577	0.1915	-0.54	0.0598	0.2338	0.14	0.6280	0.6857	0.04
1609 ER membrane protein complex subunit 4	Q5J8M3	0.0484	0.1413	-0.08	0.1462	0.6551	0.13	0.1462	0.2737	0.05	0.1940	0.3241	-0.05	0.0345	0.1354	-0.11	0.0850	0.2120	0.06	0.0087	0.0933	-0.48	0.0002	0.0164	-0.72	0.0005	0.0328	-0.09
1610 ER membrane protein complex subunit 7	Q9NPA0	0.0089	0.0560	-0.70	0.0607	0.5933	-0.27	0.0101	0.0469	-0.23	0.0131	0.0464	-0.21	0.0033	0.0429	-0.31	0.0091	0.0690	-0.33	0.3736	0.6163	-2.55	87808	1.2413	-0.33	0.0651	0.2028	2.06
1611 ER membrane protein complex subunit 8	O43402	0.2858	0.4814	0.05	0.9111	0.9381	0.01	0.6149	0.6692	-0.02	0.2116	0.3479	0.06	0.0253	0.1143	-0.15	0.7361	0.9759	0.03	0.3736	0.4429	-2.55	87808	0.9276	-0.33	0.0651	0.1166	2.06
1612 Erbin	Q96RT1	0.4108	0.5801	-3.31	0.5752	0.8121	-1.75	0.5661	0.7300	-0.19	0.5388	0.6902	0.89	0.2938	0.4750	-1.88	0.9510	1.1063	0.09	0.0939	0.0667	0.71	0.0005	0.0229	0.67	0.0026	0.0554	0.52
1613 ERC protein 2	O15083	0.4108	0.5800	-3.31	0.5752	0.8119	-1.75	0.5661	0.7298	-0.19	0.5388	0.6900	0.89	0.2938	0.4748	-1.88	0.9510	1.1060	0.09	0.5450	0.5960	-0.02	0.2106	0.5129	-0.12	0.0071	0.1564	0.07
1614 Erln-1	O75477	0.0295	0.1052	0.17	0.2816	0.6642	0.15	0.0210	0.0471	0.26	0.0224	0.0654	0.22	0.0442	0.1552	0.15	0.0211	0.0941	0.21	0.0424	0.1675	-1.56	0.0008	0.0247	-2.08	0.1037	0.1597	-0.58
1615 Erln-2	Q94905	0.0270	0.0996	0.17	0.2627	0.6655	0.15	0.0177	0.0635	0.13	0.8457	0.8676	0.01	0.1666	0.5527	0.06	0.2028	0.3806	0.06	0.0323	0.1511	0.17	0.4039	0.7898	0.04	0.7557	0.7987	-0.02
1616 ERα-like protein alpha	Q96H17	0.1025	0.2290	0.12	0.1616	0.6628	0.15	0.0166	0.0610	0.24	0.0358	0.0908	0.23	0.1294	0.2972	0.11	0.0467	0.1436	0.20	0.2293	0.4561	0.08	0.3317	0.6884	-0.04	0.5169	0.5832	-0.03
1617 ERα-like protein beta	Q86YB8	0.0580	0.1586	0.15	0.2109	0.6625	0.15	0.0082	0.0426	0.19	0.0539	0.1215	0.15	0.7031	0.7642	-0.01	0.3865	0.5975	0.07	0.0205	0.1324	0.40	0.0759	0.2687	0.15	0.0351	0.1606	0.19
1618 Erythrocyte band 7 integral membrane protein	P27105	0.0000	0.0000	3.07	0.9453	0.9637	-0.01	0.6535	0.7049	-0.02	0.0061	0.0064	1.05	0.0049	0.0529	-0.47	0.0042	0.0606	0.25	0.0728	0.2135	0.31	0.0043	0.0524	0.19	0.0007	0.0333	0.62
1619 Erythroid differentiation-related factor 1	Q3BT11	0.4108	0.5798	-3.31	0.5752	0.8116	-1.75	0.5661	0.7296	-0.19	0.5388	0.6898	0.89	0.2938	0.4747	-1.88	0.9510	1.1058	0.09	0.0867	0.2360	0.36	0.0097	0.0813	0.38	0.2230	0.2929	-0.03
1620 ESF1 homolog	Q9H501	0.0332	0.1137	0.42	0.0800	0.6112	0.32	0.0004	0.0223	0.51	0.0189	0.0582	0.21	0.0769	0.2131	0.10	0.0032	0.0572	0.34	0.3736	0.6374	-2.55	87808	1.2778	-0.33	0.0651	0.2163	2.06
1621 Ester hydrolase C1orf54	Q9H0W9	0.4108	0.5797	-3.31	0.5752	0.8114	-1.75	0.5661	0.7295	-0.19	0.5388	0.6896	0.89	0.2938	0.4746	-1.88	0.9510	1.1055	0.09	0.2994	0.5563	-0.18	0.0026	0.0420	-0.69	0.0288	0.1450	-0.71
1622 Esterase CVCA2	Q8WZ82	0.0935	0.2151	0.38	0.1080	0.4685	0.68	0.4932	0.7142	0.13	0.5871	0.6361	0.12	0.1475	0.3233	0.33	0.3782	0.5867	-0.17	0.3736	0.4707	-2.55	87808	0.9795	-0.33	0.0651	0.1281	2.06
1623 Estrogen receptor beta	Q92731	0.3415	0.5492	0.09	0.1646	0.6604	0.28	0.0083	0.0430	0.46	0.0005	0.0124	0.47	0.0054	0.0548	-0.20	0.0937	0.2250	0.37	0.3736	0.5364	-2.55	87808	1.0996	-0.33	0.0651	0.1582	2.06
1624 Ethanolamine-phosphate cytidylyltransferase	Q99447	0.1350	0.2786	-0.13	0.2028	0.6599	-0.13	0.1047	0.2116	0.10	0.4686	0.6680	-0.09	0.0223	0.1074	-0.19	0.2193	0.4007	-0.07	0.9562	0.9644	-0.03	0.8497	1.2911	0.17	0.3206	0.3920	0.56
1625 Ethylmalonyl-CoA decarboxylase	Q9NTX5	0.4108	0.5795	-3.31	0.5752	0.8112	-1.75	0.5661	0.7293	-0.19	0.5388	0.6895	0.89	0.2938	0.4744	-1.88	0.9510	1.1053	0.09	0.0015	0.0505	7.24	0.0016	0.0329	7.97	0.0017	0.0495	8.70
1626 ETS domain-containing protein Elk-4	P28324	0.1770	0.3393	-0.26	0.4439	0.7795	-0.13	0.2767	0.4510	0.32	0.6797	0.7200	-0.07	0.2804	0.5068	-0.19	0.8616	1.0974	-0.03	0.3736	0.4354	-2.55	87808	0.9133	-0.33	0.0651	0.1137	2.06
1627 ETS translocation variant 3	P41162	0.2015	0.3722	-0.26	0.0052	0.3741	-0.24	0.3391	0.5316	-0.11	0.0005	0.0117	-0.44	0.0050	0.0532	-0.35	0.0663	0.1805	-0.19	0.3736	0.5510	-2.55	87808	1.1260	-0.33	0.0651	0.1657	2.06
1628 ETS translocation variant 5	P41161	0.2674	0.4593	0.06	0.3515	0.7046	0.10	0.0788	0.1705	0.12	0.5184	0.7234	0.04	0.2048	0.4065	0.07	0.8277	1.0615	-0.01	0.7805	0.8145	0.04	0.6070	1.0387	0.09	0.9142	0.9311	0.01
1629 ETS-related transcription factor E1f-4	Q96067	0.0269	0.0994	-0.25	0.1006	0.6332	0.38	0.7255	0.7695	0.03	0.1159	0.2170	0.27	0.2178	0.4235	0.16	0.1323	0.2833	-0.13	0.1352	0.3133	-0.81	0.5123	0.9315	-0.15	0.7621	0.8038	-0.03
1630 Eukaryotic initiation factor 4A-I	P60842	0.0197	0.0823	0.21	0.2934	0.6701	0.22	0.0042	0.0321	0.33	0.0097	0.0397	0.27	0.5493	0.6331	-0.01	0.0161	0.0842	0.27	0.0558	0.1873	0.35	0.0657	0.2472	0.25	0.4785	0.5487	0.06
1631 Eukaryotic initiation factor 4A-II	Q14240	0.7008	0.7546	-0.04	0.1813	0.6646	-0.19	0.0937	0.1941	-0.26	0.1301	0.2366	-0.23	0.2523	0.4706	-0.15	0.6393	0.8765	-0.05	0.8739	0.8953	0.01	0.0533	0.2191	0.15	0.2301	0.3003	0.06
1632 Eukaryotic initiation factor 4A-III	P38919	0.0698	0.1764	0.12	0.3450	0.7028	0.16	0.2455	0.0774	0.22	0.0074	0.0349	0.24	0.2143	0.4191	-0.06	0.0563	0.1622	0.13	0.0080	0.0427	0.35	0.0080	0.0449	0.0009	0.0382	0.49	
1633 Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	P15170	0.4719	0.5480	0.04	0.4847	0.8091	0.12	0.0691	0.1557	0.15	0.0928</																	

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
1672 Eukaryotic translation initiation factor 6	P56537	0.0027	0.0351	0.22	0.1880	0.6675	0.25	0.0039	0.0318	0.20	0.0015	0.0176	0.29	0.0457	0.1575	0.09	0.0081	0.0669	0.19	0.4160	0.4718	-0.09	0.0163	0.1082	-0.26	0.0140	0.1024	-0.29
1673 EVI5-like protein	Q96CNA	0.0198	0.0826	0.28	0.0534	0.5848	0.37	0.0025	0.0279	0.44	0.0034	0.0236	0.41	0.0058	0.0563	0.30	0.0326	0.0132	0.22	0.3736	0.5782	-2.55	0.8708	1.1744	-0.33	0.0651	0.1803	-2.06
1674 Exocyst complex component 1	Q9NV70	0.2793	0.4726	-0.07	0.3135	0.6803	-0.17	0.9395	0.9529	-0.01	0.4314	0.6240	-0.02	0.8533	0.8870	0.01	0.1280	0.2774	0.02	0.3736	0.5250	-2.55	0.8708	1.0791	-0.33	0.0651	0.1527	2.06
1675 Exocyst complex component 4	Q96A65	0.0031	0.0368	0.15	0.2666	0.6633	0.22	0.0004	0.0190	0.36	0.0062	0.0316	0.18	0.5789	0.6576	0.01	0.0249	0.1005	0.28	0.3736	0.1527	0.34	0.9969	0.9975	-0.00	0.5366	0.6923	0.05
1676 Exocyst complex component 5	Q90471	0.1470	0.2951	0.06	0.4865	0.8106	0.04	0.1466	0.2741	-0.16	0.4409	0.6351	0.03	0.2143	0.4189	-0.06	0.1506	0.3082	-0.06	0.3736	0.5165	-2.55	0.8708	1.0636	-0.33	0.0651	0.1486	2.06
1677 Exocyst complex component 6B	Q9Y2D4	0.4108	0.5789	-3.31	0.5752	0.8103	-1.75	0.5661	0.7285	-1.19	0.5388	0.6888	0.89	0.2938	0.4738	-1.88	0.9510	1.1043	0.09	0.3034	0.1476	0.49	0.0067	0.0667	0.91	0.0996	0.0872	0.35
1678 Exocyst complex component 7	Q9UPT5	0.9528	0.9647	-0.00	0.8342	0.8804	-0.02	0.4990	0.7212	-0.06	0.1502	0.2655	0.12	0.0130	0.0812	-0.22	0.0265	0.1044	0.18	0.3736	0.5847	-2.55	0.8708	1.1858	-0.33	0.0651	0.1840	2.06
1679 Exocyst complex component 8	Q8YVJ6	0.0108	0.0599	-0.19	0.3500	0.7049	-0.19	0.0038	0.0315	0.22	0.0051	0.0289	-0.29	0.0113	0.0761	-0.14	0.0479	0.1459	0.43	0.0241	0.1373	0.56	0.2339	0.5335	0.16	0.0107	0.0907	0.27
1680 Exonuclease 3'-5' domain-containing protein 2	Q9NVH0	0.0355	0.1177	-0.26	0.0372	0.5506	-0.27	0.1466	0.2742	-0.15	0.5272	0.7335	-0.05	0.0748	0.2101	-0.19	0.5441	0.7766	-0.05	0.3736	0.4572	-2.55	0.8708	0.9543	-0.33	0.0651	0.1224	2.06
1681 Exosome complex component CSL4	Q9Y3B2	0.0236	0.0923	0.43	0.6138	0.7145	0.06	0.0040	0.0317	0.23	0.3366	0.5107	0.03	0.0026	0.0392	-0.38	0.2074	0.3870	-0.16	0.1769	0.3763	-0.17	0.6772	1.1165	-0.05	0.0579	0.2142	-0.34
1682 Exosome complex component MTR3	Q5RKY6	0.4108	0.5787	-3.31	0.5752	0.8101	-1.75	0.5661	0.7284	-1.19	0.5388	0.6886	0.89	0.2938	0.4737	-1.88	0.9510	1.1040	0.09	0.0417	0.1674	0.25	0.5773	0.4293	-0.23	0.4895	0.5578	0.09
1683 Exosome complex component RRP42	Q15024	0.0527	0.1489	0.14	0.6638	0.7524	-0.06	0.0177	0.0635	0.21	0.4485	0.6437	0.05	0.9812	0.9860	0.00	0.4380	0.6597	0.09	0.5748	0.6243	0.23	0.2764	0.6121	0.49	0.1835	0.2509	0.66
1684 Exosome complex component RRP45	Q06265	0.4108	0.5786	-3.31	0.5752	0.8099	-1.75	0.5661	0.7282	-1.19	0.5388	0.6885	0.89	0.2938	0.4735	-1.88	0.9510	1.1038	0.09	0.9586	0.9659	0.00	0.4180	0.8100	0.12	0.9422	0.9536	-0.01
1685 Exosome complex exonuclease RRP44	Q9Y2L1	0.0777	0.1908	-0.08	0.0016	0.2072	0.21	0.0013	0.0240	0.32	0.0076	0.0354	0.15	0.0109	0.0746	0.28	0.0104	0.0702	0.14	0.2224	0.4457	0.04	0.1494	0.4165	0.09	0.0223	0.1268	0.02
1686 Exosome component 10	Q01780	0.0050	0.0436	0.24	0.5607	0.8748	-0.07	0.0276	0.0836	0.15	0.2326	0.3765	0.11	0.0602	0.1846	0.12	0.0226	0.0963	0.24	0.4092	0.4649	0.03	0.0711	0.2581	-0.08	0.0441	0.1838	-0.36
1687 Exosome RNA helicase MTR4	P42285	0.1760	0.3380	-0.06	0.7642	0.8295	-0.03	0.2301	0.3895	0.07	0.2940	0.4572	0.04	0.0279	0.1213	-0.10	0.7854	1.0237	-0.02	0.0316	0.1503	0.58	0.2032	0.5024	0.15	0.0095	0.0869	0.39
1688 Exostosin-like 3	O43909	0.0053	0.0444	-0.15	0.1140	0.6325	0.28	0.1440	0.2704	0.19	0.5026	0.7063	-0.02	0.8347	0.8717	-0.01	0.0026	0.0545	-0.23	0.3736	0.6412	-2.55	0.8708	1.2844	-0.33	0.0651	0.2188	2.06
1689 Exportin-1	I14980	0.0593	0.1610	0.06	0.1834	0.6643	0.18	0.0086	0.0438	0.13	0.0072	0.0344	0.13	0.0380	0.1423	-0.07	0.1677	0.3322	0.04	0.0256	0.1397	0.25	0.0523	0.2169	0.17	0.5414	0.6070	0.03
1690 Exportin-2	P55060	0.0098	0.0581	0.14	0.2475	0.6585	0.21	0.0086	0.0438	0.22	0.0031	0.0228	0.31	0.2216	0.4285	0.04	0.0714	0.1885	0.20	0.0640	0.1992	0.39	0.4581	0.8632	0.09	0.6877	0.7408	-0.03
1691 Exportin-5	Q9HVA9	0.0068	0.0492	0.22	0.1990	0.6650	0.27	0.0006	0.0193	0.38	0.0023	0.0208	0.27	0.6539	0.7207	0.02	0.0335	0.0979	0.15	0.9062	0.9237	-0.01	0.6986	1.1419	0.02	0.0038	0.0600	0.40
1692 Exportin-7	Q9U1U9	0.1130	0.2448	0.12	0.0920	0.6304	0.15	0.2911	0.3757	0.06	0.0446	0.1059	0.09	0.6507	0.7184	0.02	0.7136	0.9539	-0.01	0.3736	0.4446	-2.55	0.8708	0.9306	-0.33	0.0651	0.1173	2.06
1693 Exportin-T	Q43592	0.0111	0.0606	0.14	0.1807	0.6638	0.13	0.0153	0.0582	0.12	0.0124	0.0450	0.15	0.0391	0.1446	-0.09	0.3440	0.5597	0.03	0.0008	0.0410	-1.73	0.0038	0.0503	-0.58	0.0749	0.1247	-1.21
1694 Extended synaptotagmin-1	Q9BSJ8	0.0098	0.0586	0.18	0.2319	0.6632	0.19	0.0074	0.0407	0.19	0.0397	0.0980	0.12	0.1088	0.2679	-0.07	0.0803	0.2037	0.21	0.1290	0.3029	0.12	0.4187	0.8111	0.05	0.3252	0.3965	0.06
1695 Extended synaptotagmin-2	ADFR83	0.1458	0.2936	-0.08	0.5338	0.8990	-0.02	0.2721	0.4456	-0.06	0.5314	0.7390	-0.03	0.2687	0.4906	-0.06	0.9906	0.9925	0.00	0.1012	0.2572	-0.18	0.0862	0.2909	0.15	0.0819	0.1332	0.18
1696 Ezrin	P15311	0.2490	0.4355	-0.07	0.2910	0.6640	0.16	0.0878	0.1855	0.13	0.1535	0.2701	0.09	0.1277	0.2953	-0.11	0.1921	0.3662	0.09	0.0398	0.1641	0.53	0.1869	0.4769	0.17	0.6200	0.6783	0.04
1697 FACT complex subunit SPT16	Q9Y5B9	0.0010	0.0223	0.31	0.1438	0.6594	0.27	0.0062	0.0382	0.30	0.0011	0.0157	0.30	0.0430	0.1532	0.10	0.0040	0.0597	0.25	0.0246	0.1388	0.40	0.0623	0.2389	0.20	0.8406	0.8729	0.01
1698 FACT complex subunit SSRP1	Q08945	0.0277	0.1008	0.07	0.1658	0.6606	0.16	0.0010	0.0213	0.18	0.0084	0.0372	0.10	0.0450	0.1562	-0.05	0.0352	0.1210	0.07	0.1258	0.2985	0.19	0.9220	0.9427	0.01	0.0389	0.1702	-0.26
1699 F-actin-capping protein subunit alpha-1	P52907	0.8353	0.8687	-0.01	0.5636	0.8770	0.05	0.3627	0.5602	0.05	0.3899	0.5766	-0.04	0.1397	0.3114	-0.08	0.1616	0.3231	0.08	0.0638	0.1988	0.20	0.2369	0.5530	-0.08	0.8465	0.8761	-0.01
1700 F-actin-capping protein subunit alpha-2	P47755	0.8277	0.8620	0.22	0.9554	0.9704	-0.06	0.5547	0.7791	-0.62	0.7855	0.8156	-0.27	0.1729	0.3617	1.82	0.7483	0.9866	-0.32	0.0142	0.1116	-0.32	0.0076	0.0720	-0.42	0.0220	0.1265	-0.39
1701 F-actin-capping protein subunit beta	P47756	0.0997	0.2244	-0.05	0.2120	0.6263	0.20	0.0076	0.0414	-0.14	0.0031	0.0228	0.17	0.1091	0.2682	0.05	0.0283	0.1076	0.13	0.0784	0.2224	0.31	0.0836	0.2847	0.17	0.0277	0.1428	0.24
1702 FAD synthase	Q8NFF5	0.0162	0.0743	0.21	0.2656	0.6627	0.18	0.0293	0.0870	0.14	0.0008	0.0142	0.43	0.0083	0.0657	0.22	0.0011	0.0471	0.49	0.3736	0.6485	-2.55	0.8708	1.2969	-0.33	0.0651	0.2238	2.06
1703 FAD-linked sulphydryl oxidase ALR	P55789	0.0098	0.0580	-0.24	0.1555	0.6619	0.31	0.0315	0.0907	0.32	0.0052	0.0290	0.43	0.0997	0.2528	0.12	0.9300	1.1673	0.01	0.3736	0.4327	-2.55	0.8708	0.9081	-0.33	0.0651	0.1126	2.06
1704 Fanconi anemia group A protein	O15360	0.4108	0.5784	-3.31	0.5752	0.8097	-1.75	0.5661	0.7280	-1.19	0.5388	0.6883	0.89	0.2938	0.4734	-1.88	0.9510	1.1035	0.09	0.1697	0.3658	-0.27	0.1863	0.4766	0.36	0.0157	0.1071	0.50
1705 Fanconi anemia group C protein	Q00597	0.8870	0.9109	0.00	0.0668	0.5935	-0.07	0.4830	0.7032	-0.02	0.2328	0.3767	0.04	0.3572	0.4550	-0.05	0.0167	0.0848	0.28	0.0148	0.1121	0.48	0.2533	0.5778	0.23	0.1713	0.2371	0.82
1706 Fanconi anemia group I protein	Q9NVJ7	0.0391	0.1244	0.07	0.1307	0.6460	0.35	0.0102	0.0471	0.34	0.0021	0.0200	0.46	0.0004	0.0176	0.28	0.1094	0.2489	0.34	0.0664	0.2027	0.40	0.2986	0.6418	0.17	0.2270	0.2973	-0.21
1707 Fanconi anemia group M protein	Q8YD88	0.3826	0.5988	0.02	0.5849	0.6914	0.07	0.0013	0.0220	0.20	0.0010	0.0156	0.15	0.3575	0.4550	0.01	0.0020	0.0518	0.14	0.0023	0.0576	-0.36	0.8650	1.3075	-0.03	0.4511	0.5197	-0.03
1708 Far upstream element-binding protein 1	Q96A64	0.0646	0.1682	0.11	0.3731	0.7209	0.17	0.0089	0.0441	0.28	0.0111	0.0240	0.20	0.6249	0.6961	-0.02	0.0413	0.1336	0.15	0.0953	0.2487	0.36	0.8313	1.2740	-0.02	0.4654	0.5318	-0.06
1709 Far upstream element-binding protein 2	Q92945	0.3246	0.5301	0.05	0.3319	0.6910	0.19	0.0141	0.0556	0.21	0.0140	0.0482	0.21	0.6359	0.7058	-0.02	0.0662	0.1806	0.14	0.1587	0.3102	0.21	0.0257	0.1438	0.22	0.1910	0.1771	0.14
1710 Far upstream element-binding protein 3	Q06Z24	0.1208	0.2567	0.06	0.1846	0.6645	0.23	0.0079	0.0419	0.19	0.0025	0.0212	0.22	0.8885	0.9146</													

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
1752 Filamin A-interacting protein 1-like	Q4L180	0.4108	0.5764	-3.31	0.5752	0.8068	-1.75	0.5661	0.7257	-1.19	0.5388	0.6861	0.89	0.2938	0.4715	-1.88	0.9510	1.1003	0.09	0.3230	0.5885	-0.09	0.0014	0.0297	-0.49	0.0047	0.0676	-0.62
1753 Filamin-A	P21333	0.0014	0.0256	0.41	0.1575	0.8617	0.36	0.0008	0.0216	-0.12	0.0002	0.0115	0.62	0.0030	0.0418	0.39	0.0037	0.0595	0.59	0.0804	0.0257	0.38	0.5964	1.0298	0.06	0.9860	0.9891	0.00
1754 Filamin-A-interacting protein 1	Q7Z7B0	0.2593	0.4480	-0.19	0.4044	0.7476	-0.44	0.0298	0.0876	-0.53	0.0585	0.1291	-0.41	0.8304	0.8683	0.03	0.6481	0.8851	0.09	0.0229	0.1363	0.30	0.0106	0.0845	0.24	0.3262	0.3976	0.05
1755 Filamin-B	Q75369	0.0144	0.0699	0.26	0.1790	0.6477	0.27	0.0036	0.0317	0.36	0.0034	0.0235	-0.36	0.0225	0.1081	0.24	0.0114	0.0733	0.37	0.0431	0.1682	0.47	0.2809	0.6184	0.13	0.6135	0.6730	0.04
1756 Filamin-binding LIM protein 1	Q8W1P2	0.4108	0.5762	-3.31	0.5752	0.8066	-1.75	0.5661	0.7255	-1.19	0.5388	0.6859	0.89	0.2938	0.4713	-1.88	0.9510	1.1001	0.09	0.0493	0.1770	0.42	0.2854	0.6238	0.12	0.2738	0.3458	0.10
1757 Filamin-C	Q14315	0.4108	0.5761	-3.31	0.5752	0.8064	-1.75	0.5661	0.7253	-1.19	0.5388	0.6857	0.89	0.2938	0.4712	-1.88	0.9510	1.0998	0.09	0.0010	0.0411	0.40	0.0046	0.0550	0.31	0.0053	0.0704	0.24
1758 FK506-binding protein 15	Q1T1M5	0.2533	0.4406	0.12	0.0747	0.6123	0.24	0.0526	0.1297	0.24	0.1469	0.2608	0.15	0.5568	0.6398	0.05	0.4061	0.6224	0.07	0.3736	0.4688	-2.55	0.8708	0.9759	-0.33	0.0651	0.1273	2.06
1759 Flap endonuclease 1	P39748	0.4423	0.5199	0.03	0.2279	0.6602	0.10	0.0057	0.0365	0.22	0.0303	0.0809	0.15	0.0123	0.0794	-0.18	0.5121	0.7389	0.02	0.0396	0.1640	0.18	0.8775	0.9071	-0.01	0.0661	0.1126	0.14
1760 Flavin reductase (NADPH)	P30043	0.0001	0.0126	0.39	0.1168	0.6355	0.29	0.1898	0.3364	0.10	0.0152	0.0508	0.27	0.8487	0.8837	0.00	0.0334	0.1177	0.33	0.1400	0.3206	-0.18	0.0058	0.0612	-0.46	0.0048	0.0676	-0.65
1761 Flotillin-1	Q75955	0.4108	0.5759	-3.31	0.5752	0.8062	-1.75	0.5661	0.7251	-1.19	0.5388	0.6856	0.89	0.2938	0.4710	-1.88	0.9510	1.0996	0.09	0.0004	0.0357	-1.12	0.0011	0.0285	-1.42	0.0010	0.0395	-1.51
1762 FLYWCH family member 2	Q96CP2	0.0240	0.0931	-0.16	0.1993	0.8398	0.11	0.3420	0.5351	-0.05	0.6759	0.7167	-0.02	0.0041	0.0469	-0.02	0.2998	0.1108	-0.12	0.0777	0.2218	0.23	0.0688	0.2533	0.12	0.1488	0.2113	0.09
1763 FLYWCH-type zinc finger-containing protein 1	Q4VC44	0.0029	0.0363	-0.55	0.0111	0.4291	0.28	0.0047	0.0338	0.32	0.0101	0.0404	0.40	0.2496	0.4668	0.07	0.1314	0.2823	-0.18	0.3736	0.5237	-2.55	0.8708	1.0768	-0.33	0.0651	0.1520	2.06
1764 Folate receptor beta	P14207	0.0950	0.2172	0.25	0.0279	0.5036	0.51	0.0360	0.0994	0.39	0.8506	0.8711	0.03	0.2036	0.4049	0.37	0.1511	0.3086	-0.19	0.3736	0.5159	-2.55	0.8708	1.0626	-0.33	0.0651	0.1483	2.06
1765 Foliculin-interacting protein 1	Q8TF40	0.0592	0.1610	0.15	0.0658	0.5938	0.23	0.0251	0.0787	0.18	0.1037	0.1992	0.12	0.0860	0.2290	0.12	0.4733	0.6969	0.04	0.3736	0.4624	-2.55	0.8708	0.9640	-0.33	0.0651	0.1246	2.06
1766 Foliculin-interacting protein 2	Q9P278	0.3672	0.5808	0.28	0.2042	0.6594	0.45	0.1029	0.2090	0.65	0.5055	0.7092	0.23	0.0496	0.1642	0.87	0.6359	0.8733	0.14	0.3736	0.4490	-2.55	0.8708	0.9390	-0.33	0.0651	0.1191	2.06
1767 Follistatin	P19883	0.0031	0.0367	-0.17	0.4227	0.7600	-0.14	0.0700	0.1572	-0.16	0.3256	0.4975	0.06	0.0008	0.0211	-0.14	0.3823	0.5920	-0.07	0.1113	0.2747	-0.19	0.0364	0.1786	-0.30	0.0001	0.0199	-6.56
1768 Follistatin-related protein 1	Q12841	0.4108	0.5757	-3.31	0.5752	0.8059	-1.75	0.5661	0.7249	-1.19	0.5388	0.6854	0.89	0.2938	0.4709	-1.88	0.9510	1.0993	0.09	0.0104	0.1018	-0.51	0.0165	0.1092	-0.56	0.0003	0.0239	-0.78
1769 Follitropin subunit beta	P01225	0.3832	0.5995	0.07	0.2659	0.6625	0.20	0.9089	0.9281	-0.01	0.1216	0.2252	0.12	0.3140	0.4113	-0.09	0.5609	0.7958	0.03	0.0200	0.1311	-7.28	0.0908	0.3002	-4.10	0.1002	0.1558	-4.68
1770 Poly(hydroxybutyrate) synthase mitochondrial	O05932	0.4108	0.5756	-3.31	0.5752	0.8057	-1.75	0.5661	0.7248	-1.19	0.5388	0.6852	0.89	0.2938	0.4707	-1.88	0.9510	1.0991	0.09	0.3873	0.4433	0.11	0.0601	0.2344	0.15	0.5310	0.5972	-0.03
1771 Forkhead box protein D4-like 1	Q9NU39	0.0297	0.1057	0.24	0.8444	0.8883	0.02	0.0008	0.0199	0.46	0.4247	0.6169	0.13	0.0794	0.2174	-0.20	0.3967	0.6101	0.09	0.3736	0.4695	-2.55	0.8708	0.9772	-0.33	0.0651	0.1275	2.06
1772 Forkhead box protein M1	Q08050	0.4108	0.5754	-3.31	0.5752	0.8055	-1.75	0.5661	0.7246	-1.19	0.5388	0.6851	0.89	0.2938	0.4706	-1.88	0.9510	1.0989	0.09	0.2074	0.4230	-0.19	0.0046	0.0544	-0.62	0.0065	0.0757	-0.92
1773 Formin-1	Q68DA7	0.0345	0.1163	0.16	0.8584	0.8977	-0.01	0.0023	0.0263	0.58	0.0002	0.0108	0.38	0.0033	0.0435	0.36	0.0213	0.0944	0.23	0.0526	0.1815	-0.24	0.0012	0.0285	-0.21	0.0081	0.0805	0.13
1774 Formin-2	Q9NZ66	0.0767	0.1891	-10.53	0.0661	0.5944	-8.98	0.0230	0.0746	-8.42	0.0014	0.0169	-6.34	0.0058	0.0564	-9.11	0.0075	0.0653	-7.14	0.0000	0.0612	8.72	0.0029	0.0454	9.17	0.0030	0.0551	9.67
1775 Four and a half LIM domains protein 1	Q13642	0.4108	0.5753	-3.31	0.5752	0.8053	-1.75	0.5661	0.7244	-1.19	0.5388	0.6849	0.89	0.2938	0.4704	-1.88	0.9510	1.0986	0.09	0.0781	0.2222	0.20	0.8157	1.2605	-0.01	0.1230	0.1821	-0.08
1776 Four and a half LIM domains protein 2	Q14192	0.4108	0.5751	-3.31	0.5752	0.8051	-1.75	0.5661	0.7242	-1.19	0.5388	0.6847	0.89	0.2938	0.4703	-1.88	0.9510	1.0984	0.09	0.0128	0.1069	0.50	0.0807	0.2794	0.21	0.0051	0.0686	0.69
1777 Four and a half LIM domains protein 5	Q3TD97	0.0671	0.1716	0.12	0.0875	0.6209	0.36	0.0103	0.0473	0.44	0.0005	0.0123	0.44	0.0027	0.0401	0.40	0.0069	0.0645	0.26	0.3736	0.6225	-2.55	0.8708	1.2519	-0.33	0.0651	0.2066	2.06
1778 Fragile X mental retardation syndrome-related protein 1	P51114	0.0058	0.0460	0.17	0.1622	0.6616	0.20	0.0008	0.0215	0.34	0.0047	0.0279	0.17	0.3677	0.4647	0.02	0.0186	0.0881	0.25	0.0239	0.1373	0.34	0.6312	1.0678	0.03	0.5380	0.6037	0.03
1779 Fragile X mental retardation syndrome-related protein 2	P51116	0.2745	0.4674	-0.07	0.3996	0.7432	0.15	0.0158	0.0592	0.18	0.8493	0.8700	-0.01	0.0022	0.0362	0.26	0.0509	0.1519	-0.05	0.1853	0.3866	0.17	0.0737	0.2635	0.25	0.0557	0.2091	0.33
1780 Free fatty acid receptor 2	O15552	0.2850	0.4804	-0.06	0.7380	0.8096	-0.05	0.0752	0.1647	0.17	0.2098	0.3456	0.08	0.0660	0.1955	-0.14	0.1506	0.3083	0.09	0.3736	0.5166	-2.55	0.8708	1.0639	-0.33	0.0651	0.1486	2.06
1781 Fructose-1,6-bisphosphatase 1	P09467	0.7514	0.7976	-0.01	0.2333	0.6588	0.25	0.4875	0.7076	-0.04	0.2689	0.4247	-0.06	0.0330	0.1327	-0.19	0.2117	0.3932	-0.07	0.3736	0.5003	-2.55	0.8708	1.0341	-0.33	0.0651	0.1410	2.06
1782 Fructose-1,6-bisphosphatase isozyme 2	O00757	0.3094	0.5104	-0.40	0.2510	0.6607	0.22	0.5057	0.7281	0.05	0.4435	0.6380	0.03	0.0235	0.1107	-0.17	0.2254	0.4085	-0.10	0.3736	0.4966	-2.55	0.8708	1.0273	-0.33	0.0651	0.1393	2.06
1783 Fructose-2,6-bisphosphatase TIGAR	Q9NQ88	0.0025	0.0337	0.33	0.1665	0.6431	0.45	0.0011	0.0217	0.67	0.0002	0.0113	0.54	0.0568	0.1784	0.11	0.0043	0.0604	0.47	0.0657	0.2017	0.40	0.8026	1.2459	0.02	0.1862	0.2536	0.10
1784 Fructose-bisphosphate aldolase A	P04075	0.0098	0.0579	0.36	0.1565	0.6623	0.28	0.0039	0.0319	0.43	0.0016	0.0177	0.56	0.0404	0.1479	0.21	0.0044	0.0605	0.72	0.0541	0.1847	0.47	0.9423	0.9584	0.01	0.9163	0.9318	-0.01
1785 Fructose-bisphosphate aldolase B	P05062	0.4605	0.5374	-0.02	0.9300	0.9562	-0.01	0.0199	0.0679	0.25	0.1794	0.3044	0.13	0.1912	0.3872	0.09	0.2837	0.4799	0.10	0.3909	0.4466	0.11	0.5808	0.9496	-0.12	0.0955	0.1502	-0.38
1786 Fructose-bisphosphate aldolase C	P09972	0.0087	0.0551	0.23	0.1956	0.6688	0.30	0.0013	0.0230	0.39	0.0002	0.0111	0.62	0.0126	0.0803	0.21	0.0007	0.0432	0.67	0.0049	0.0740	0.36	0.2215	0.5292	0.11	0.0227	0.1274	0.29
1787 Fumarate hydratase mitochondrial	P07954	0.0044	0.0420	-0.38	0.2395	0.6617	-0.19	0.0046	0.0334	-0.45	0.0084	0.0372	-0.39	0.0984	0.2505	-0.16	0.0061	0.0620	-0.42	0.0343	0.1542	0.27	0.2834	0.6210	0.10	0.2235	0.2935	0.12
1788 Fumarylacetoacetate hydrolase domain-containing protein 2A	Q96GK7	0.3406	0.5486	0.18	0.1976	0.6699	-0.32	0.0731	0.1618	0.36	0.2035	0.3371	0.30	0.0419	0.1512	0.48	0.1883	0.3613	0.67	0.3736	0.5052	-2.55	0.8708	1.0429	-0.33	0.0651	0.1433	2.06
1789 Fumarylacetoacetate hydrolase domain-containing protein 2B	Q6P213	0.4108	0.5750	-3.31	0.5752	0.8048	-1.75	0.5661	0.7240	-1.19	0.5388	0.6846	0.89	0.2938	0.4702	-1.88	0.9510	1.0981	0.09	0.3457	0.6188	0.24	0.8607	1.3025	0.04	0.2113	0.2800	0.35
1790 FYXD domain-containing ion transport regulator 3	Q14802	0.0238	0.0926	-0.17	0.1767	0.6																						



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	p value	BH q value	log2FC	p value
1832 General transcription factor IIF subunit 2	P13984	0.4998	0.5735	-0.04	0.4936	0.07	0.0776	0.1685	-0.14
1833 General transcription factor II-I	P78347	0.9213	0.9400	0.01	0.9531	0.9688	-0.01	0.1288	0.2494
1834 General transcription factor II-I repeat domain-containing protein 2B	Q6EKJO	0.0038	0.0394	0.29	0.1499	0.6603	0.13	0.3661	0.0995
1835 General vesicular transport factor p115	O60763	0.0050	0.0453	0.27	0.1562	0.6627	0.24	0.0099	0.0211
1836 Genuylipyl transferase type-2 subunit alpha	Q92696	0.1102	0.2410	0.09	0.6183	0.7172	0.08	0.0446	0.1155
1837 Genuylipyl transferase type-2 subunit beta	P33611	0.1331	0.2740	-0.11	0.4703	0.7998	0.10	0.0238	0.0756
1838 Germ cell-less protein-like-2	Q8NEA9	0.4108	0.5739	-3.31	0.5752	0.8033	-1.75	0.5661	0.7228
1839 Germinal-center associated nuclear protein	O60318	0.0763	0.1883	-1.32	0.4881	0.8117	-0.43	0.0814	0.1751
1840 Gigaxonin	Q9H2C0	0.0001	0.0123	-5.53	0.2189	0.6604	-4.12	0.0087	0.0439
1841 Girdin	Q3V6T2	0.0417	0.1294	0.14	0.1055	0.6318	0.18	0.0073	0.0405
1842 Glia maturation factor beta	P60983	0.6390	0.7008	0.02	0.1938	0.6679	0.08	0.0046	0.0334
1843 Glial fibrillary acidic protein	P14136	0.0223	0.0891	0.38	0.9428	0.9621	-0.01	0.1289	0.2494
1844 GLIPR1-like protein 2	Q4G1C9	0.1737	0.3351	0.99	0.3164	0.6801	0.68	0.1721	0.3130
1845 Glucocorticoid modulatory element-binding protein 2	Q9UKD1	0.7433	0.7918	-0.13	0.9866	0.9904	0.01	0.5115	0.7325
1846 Glucosamine 6-phosphate N-acetyltransferase	Q96EK6	0.0267	0.0989	0.14	0.1511	0.6594	0.08	0.6389	0.6918
1847 Glucosamine-6-phosphate isomerase 1	P46926	0.0142	0.0697	0.25	0.0073	0.4023	-0.25	0.0088	0.0440
1848 Glucose-6-phosphate 1-dehydrogenase	P11413	0.0032	0.0371	0.39	0.2549	0.6625	0.24	0.0017	0.0234
1849 Glucose-6-phosphate isomerase	P06744	0.0428	0.1312	0.18	0.1753	0.6608	0.29	0.0105	0.0478
1850 Glucose-fructose oxidoreductase domain-containing protein 3	Q3B7J2	0.4108	0.5737	-3.31	0.5752	0.8031	-1.75	0.5661	0.7226
1851 Glucose-induced degradation protein 8 homolog	Q9NWU2	0.1588	0.3135	-0.03	0.9730	0.9573	0.02	0.4477	0.6927
1852 Glucosidase 2 subunit beta	P14314	0.0144	0.0698	0.26	0.2812	0.6651	0.24	0.0286	0.0857
1853 Glutamate dehydrogenase 1 mitochondrial	P00367	0.2304	0.4115	0.06	0.2944	0.6715	0.17	0.0444	0.1152
1854 Glutamate dehydrogenase 2 mitochondrial	P49448	0.4829	0.5575	0.03	0.3221	0.7041	0.10	0.0066	0.0392
1855 Glutamate receptor ionotropic NMDA 2A	Q12879	0.3084	0.5092	0.08	0.3577	0.6860	-0.08	0.0347	0.0969
1856 Glutamate-cysteine ligase regulatory subunit	P48507	0.4108	0.5736	-3.31	0.5752	0.8030	-1.75	0.5661	0.7224
1857 Glutamate-rich protein 4	A6NGS2	0.4261	0.5036	-0.02	0.9992	0.6369	-0.23	0.0078	0.0417
1858 Glutamate-rich protein 6B	Q5W0A0	0.4843	0.5588	-0.28	0.4584	0.8095	-0.52	0.3680	0.5655
1859 Glutamate-rich WD repeat-containing protein 1	Q9BQ67	0.1702	0.3298	0.14	0.1068	0.6308	-0.23	0.0258	0.0800
1860 Glutamine kinase isoform mitochondrial	Q94925	0.5286	0.5999	0.04	0.7233	0.7978	-0.03	0.9606	0.9681
1861 Glutamine amidotransferase-like class 1 domain-containing protein 3B mitochondrial	A0A0B4J2D5	0.0836	0.1994	-0.16	0.6169	0.4583	-0.27	0.3258	0.5142
1862 Glutamine-fructose-6-phosphate aminotransferase [isomerizing] 1	Q06210	0.0217	0.0876	0.16	0.2066	0.6602	0.21	0.0064	0.0387
1863 Glutamine-fructose-6-phosphate aminotransferase [isomerizing] 2	Q94808	0.3676	0.5811	0.03	0.2749	0.6651	0.19	0.0644	0.1481
1864 Glutamine-rich protein 1	Q2TAL8	0.4108	0.5734	-3.31	0.5752	0.8027	-1.75	0.5661	0.7223
1865 Glutamine-tRNA ligase	P47897	0.2538	0.4413	0.05	0.4652	0.7966	0.10	0.1403	0.2653
1866 Glutathyl-RNA(Gln) amidotransferase subunit A mitochondrial	Q9H0R6	0.4108	0.5733	-3.31	0.5752	0.8025	-1.75	0.5661	0.7221
1867 Glutathyl-RNA(Gln) amidotransferase subunit C mitochondrial	Q43716	0.4108	0.5731	-3.31	0.5752	0.8022	-1.75	0.5661	0.7219
1868 Glutaredoxin-3	O76003	0.0001	0.0120	0.17	0.3413	0.6999	0.09	0.0074	0.0406
1869 Glutaredoxin-related protein 5 mitochondrial	Q86S56	0.9794	0.9863	0.00	0.6676	0.7556	-0.07	0.0877	0.1853
1870 Glutathione peroxidase 2	P18283	0.2837	0.4785	0.12	0.2848	0.9368	0.13	0.9148	0.9321
1871 Glutathione peroxidase 6	P59796	0.0007	0.0208	0.70	0.8641	0.9017	-0.12	0.0770	0.1676
1872 Glutathione reductase mitochondrial	P00390	0.0199	0.0829	0.20	0.2432	0.6596	0.20	0.0249	0.0783
1873 Glutathione S-transferase kappa 1	Q9Y2Q3	0.2742	0.4675	-0.06	0.9380	0.9580	0.01	0.5631	0.7873
1874 Glutathione S-transferase LANCE1	O43813	0.0971	0.2205	0.14	0.0964	0.6345	0.20	0.3643	0.5615
1875 Glutathione S-transferase Mu 1	P09488	0.0345	0.1163	0.44	0.2528	0.6624	-0.16	0.2886	0.4675
1876 Glutathione S-transferase Mu 2	P28161	0.0466	0.1383	-0.18	0.1342	0.6497	0.23	0.9179	0.9350
1877 Glutathione S-transferase Mu 3	P21266	0.0001	0.0118	0.60	0.2470	0.6592	0.24	0.1631	0.2991
1878 Glutathione S-transferase Mu 4	P46439	0.0322	0.1116	0.36	0.4687	0.7963	0.13	0.3876	0.5890
1879 Glutathione S-transferase omega-1	P78417	0.0207	0.0850	0.21	0.1788	0.6644	0.25	0.0045	0.0332
1880 Glutathione S-transferase P	P09211	0.4108	0.5730	-3.31	0.5752	0.8020	-1.75	0.5661	0.7217
1881 Glutathione S-transferase theta-4	A0A1W2PR19	0.2728	0.4658	-0.32	0.6280	0.7098	-0.26	0.0850	0.1810
1882 Glutathione synthetase	P48637	0.0775	0.1905	0.16	0.4259	0.7618	0.14	0.4671	0.6845
1883 Glyceraldehyde-3-phosphate dehydrogenase	P04406	0.0000	0.0000	0.53	0.1523	0.6607	0.16	0.0010	0.0215
1884 Glyceraldehyde-3-phosphate dehydrogenase testis-specific	O14556	0.1003	0.2255	-8.96	0.0912	0.6290	-7.40	0.0313	0.0905
1885 Glycero-3-phosphate dehydrogenase [NAD(+) ] cytoplasmic	P21695	0.4108	0.5728	-3.31	0.5752	0.8018	-1.75	0.5661	0.7216
1886 Glycero-3-phosphate dehydrogenase mitochondrial	P43304	0.4990	0.5727	-0.04	0.7213	0.7960	-0.05	0.6905	0.7389
1887 Glycero-3-phosphate phosphatase	A6NDG6	0.0461	0.1372	0.09	0.2588	0.7999	0.06	0.0152	0.0579
1888 Glycine cleavage system H protein mitochondrial	P23434	0.0382	0.1228	0.13	0.9450	0.9636	-0.02	0.0244	0.0772
1889 Glycine receptor subunit alpha-2	P23416	0.4108	0.5726	-3.31	0.5752	0.8016	-1.75	0.5661	0.7214
1890 Glycine receptor subunit alpha-3	Q75311	0.0063	0.0477	0.12	0.9118	0.9382	0.01	0.0094	0.0179
1891 Glycine-tRNA ligase	P41250	0.0061	0.0470	0.27	0.2282	0.6600	0.17	0.0014	0.0225
1892 Glycogen [starch] synthase muscle	P13807	0.1018	0.2278	0.09	0.1916	0.6692	0.24	0.0186	0.0655
1893 Glycogen debranching enzyme	P35573	0.4108	0.5725	-3.31	0.5752	0.8014	-1.75	0.5661	0.7212
1894 Glycogen phosphorylase brain form	P11216	0.0229	0.0905	0.20	0.2605	0.6644	0.17	0.0426	0.1121
1895 Glycogen phosphorylase liver form	P06737	0.0284	0.1024	0.22	0.2800	0.6650	0.22	0.0109	0.0484
1896 Glycogen phosphorylase muscle form	P11217	0.8089	0.8460	0.02	0.9337	0.9885	0.00	0.1149	0.2280
1897 Glycogen synthase kinase-3 alpha	P49840	0.0002	0.0152	0.60	0.2584	0.6630	0.21	0.0002	0.0167
1898 Glycogen synthase kinase-3 beta	P49841	0.0119	0.0628	0.14	0.7948	0.8512	0.03	0.4615	0.6778
1899 Glycophorin-1	P46976	0.0004	0.0168	-0.68	0.0242	0.4859	-0.20	0.0005	0.0216
1900 Glycophorin-A	P02724	0.4108	0.5723	-3.31	0.5752	0.8012	-1.75	0.5661	0.7210
1901 Glycosylmethyltransferase	Q75063	0.7433	0.7916	0.04	0.2943	0.6718	0.16	0.0719	0.8125
1902 Glycosylmethyltransferase 1	P30419	0.5174	0.5897	-0.09	0.1853	0.6666	0.30	0.1232	0.2416
1903 Glycylpeptide N-tetradecanoyltransferase 2	O60551	0.1851	0.3499	0.11	0.0466	0.5240	0.22	0.8738	0.9002
1904 Glyoxalase domain-containing protein 4	Q9HC38	0.0080	0.0529	0.21	0.3739	0.7616	0.08	0.0561	0.1353
1905 Glyoxylate reductase/hydroxypruvate reductase	Q9UBQ7	0.4108	0.5722	-3.31	0.5752	0.8010	-1.75	0.5661	0.7208

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
1906 GMP reductase 2	Q9P2T1	0.4108	0.5720	-3.31	0.5752	0.8007	-1.75	0.5661	0.7207
1907 GMP synthase [glutamine-hydrolyzing]	P49915	0.0373	0.1214	0.12	0.1215	0.6396	0.22	0.0007	0.2077
1908 Golgi apparatus protein 1	P29896	0.0661	0.1704	0.14	0.2284	0.6599	0.44	0.0136	0.0546
1909 Golgi membrane protein 1	Q8N8B4	0.0261	0.0978	-1.48	0.2641	0.6638	-2.25	0.0014	0.0224
1910 Golgi phosphoprotein 3	Q9H4A6	0.3449	0.6018	-0.54	0.8574	0.8971	-0.11	0.5033	0.7254
1911 Golgi assembly-stacking protein 2	Q9H3Y8	0.7636	0.8077	0.02	0.7314	0.8042	0.05	0.5042	0.7263
1912 Golgi resident protein GCp60	Q7H3P7	0.0382	0.1227	0.17	0.1443	0.6545	0.23	0.0034	0.0313
1913 Golgi SNAP receptor complex member 2	Q14653	0.2589	0.4479	0.71	0.9832	0.9882	0.03	0.2133	0.3681
1914 Golgi to ER traffic protein 4 homolog	Q7LSD6	0.1388	0.2834	0.06	0.2416	0.6594	-0.09	0.0012	0.0226
1915 Golgin subfamily A member 1	Q92805	0.7216	0.7723	-0.02	0.5251	0.8439	0.11	0.1213	0.2388
1916 Golgin subfamily A member 2	Q08379	0.0019	0.0303	0.23	0.0582	0.6593	0.15	0.0153	0.0581
1917 Golgin subfamily A member 3	Q08378	0.0486	0.1417	0.08	0.3619	0.7104	-0.06	0.0093	0.0449
1918 Golgin subfamily A member 4	Q13439	0.0207	0.0850	0.05	0.2281	0.6601	0.16	0.0445	0.1154
1919 Golgin subfamily A member 5	Q8TB66	0.2011	0.3718	0.04	0.1089	0.6296	0.22	0.0125	0.0525
1920 Golgin subfamily A member 8C	A6NN73	0.4108	0.5719	-3.31	0.5752	0.8005	-1.75	0.5661	0.7205
1921 Golgin subfamily A member 8R	J61899	0.4108	0.5717	-3.31	0.5752	0.8003	-1.75	0.5661	0.7203
1922 Golgin subfamily B member 1	Q14789	0.0013	0.0252	0.22	0.0801	0.6111	0.25	0.0001	0.0216
1923 Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	Q92538	0.0106	0.0596	-0.13	0.3389	0.6986	-0.07	0.7456	0.7880
1924 GON-4-like protein	Q23819	0.0647	0.1683	0.23	0.3788	0.7203	0.08	0.1549	0.2868
1925 G-patch domain and KOW motifs-containing protein	Q92877	0.0041	0.0044	-0.39	0.0837	0.6203	-0.43	0.0623	0.1451
1926 GPI transamidase component PG1-T	Q696N2	0.2914	0.4888	-0.13	0.2645	0.6638	0.14	0.3834	0.5843
1927 GPN-loop GTPase 1	Q9HCN4	0.2964	0.4948	-2.20	0.2754	0.6638	-1.99	0.3883	0.5899
1928 GPN-loop GTPase 3	Q9UHW5	0.4948	0.5692	-0.44	0.2359	0.6629	-1.48	0.1793	0.3226
1929 G-protein-signaling modulator 1	Q86YR5	0.4108	0.5716	-3.31	0.5752	0.8001	-1.75	0.5661	0.7201
1930 G-protein-signaling modulator 2	R81274	0.0629	0.1660	-0.39	0.2649	0.6602	-0.62	0.0224	0.0733
1931 Grancalcin	P28676	0.0060	0.0468	-0.25	0.7683	0.8319	-0.04	0.0044	0.0326
1932 GRB10-interacting GYF protein 2	Q6Y7W6	0.6269	0.6899	0.03	0.3984	0.7426	0.11	0.8691	0.8966
1933 GRB2-related adapter protein	Q13588	0.0067	0.0492	-3.31	0.1965	0.6692	-2.24	0.0456	0.1176
1934 G-rich sequence factor 1	Q12849	0.0000	0.0000	1.00	0.0294	0.5093	0.20	0.0052	0.0354
1935 GRIP1-associated protein 1	Q4V328	0.2078	0.3804	-0.06	0.7477	0.8171	0.02	0.3025	0.4854
1936 Growth arrest and DNA damage-inducible protein-interacting protein 1	Q8TAE8	0.3021	0.5016	0.06	0.9771	0.9715	0.00	0.0597	0.1413
1937 Growth factor receptor-bound protein 2	P62993	0.0558	0.1545	0.14	0.1909	0.6691	0.20	0.0043	0.0325
1938 Growth hormone-inducible transmembrane protein	Q9H3K2	0.4108	0.5714	-3.31	0.5752	0.7999	-1.75	0.5661	0.7200
1939 Growth/differentiation factor 5	P43026	0.4279	0.5054	-0.08	0.4859	0.8101	-0.10	0.2616	0.4311
1940 Grp1 protein homolog 1 mitochondrial	Q55040	0.8384	0.8708	0.01	0.5525	0.8680	-0.07	0.0047	0.0334
1941 GTP-AMP phosphotransferase AK3 mitochondrial	Q9UJ07	0.1907	0.3570	-0.07	0.8020	0.8571	0.06	0.6239	0.7677
1942 GTPase HRas	P01112	0.0490	0.1420	0.17	0.4683	0.7982	0.05	0.3491	0.5432
1943 GTPase IMAP family member 4	Q9N1V9	0.2096	0.3823	-0.39	0.6739	0.7609	-0.09	0.0347	0.0968
1944 GTPase IMAP family member 5	Q96F15	0.4108	0.5713	-3.31	0.5752	0.7997	-1.75	0.5661	0.7198
1945 GTPase KRas	P01116	0.6811	0.7379	0.03	0.5388	0.8546	-0.09	0.2550	0.4230
1946 GTPase NRas	P01111	0.0409	0.1277	0.12	0.7380	0.8098	0.04	0.3200	0.5071
1947 GTPase-activating protein and VPS9 domain-containing protein 1	Q14C86	0.0113	0.0610	0.20	0.2200	0.6599	0.26	0.0009	0.0209
1948 GTP-binding nuclear protein Ran	P62826	0.0083	0.0540	0.34	0.2744	0.6645	0.28	0.0096	0.0457
1949 GTP-binding protein Rheb	Q15382	0.0339	0.1151	0.17	0.3238	0.6854	0.09	0.0162	0.0602
1950 GTP-binding protein Rhes	Q96D21	0.4108	0.5711	-3.31	0.5752	0.7994	-1.75	0.5661	0.7196
1951 GTP-binding protein Ral1	Q92963	0.4108	0.5710	-3.31	0.5752	0.7992	-1.75	0.5661	0.7194
1952 GTP-binding protein SAR1a	Q9NR31	0.2805	0.4739	-0.04	0.3658	0.7140	-0.13	0.2746	0.4484
1953 GTP-binding protein SAR1b	Q9Y6B6	0.0547	0.1531	0.07	0.0169	0.4607	0.12	0.0212	0.0706
1954 Guanine dinucleotide N-methyltransferase	Q14353	0.4108	0.5708	-3.31	0.5752	0.7990	-1.75	0.5661	0.7193
1955 Guanine nucleotide exchange factor DBS	Q15068	0.1685	0.3271	-0.08	0.8854	0.9184	0.01	0.0705	0.1580
1956 Guanine nucleotide exchange factor VAV2	P52735	0.1412	0.2871	0.23	0.0378	0.5547	0.42	0.0001	0.0247
1957 Guanine nucleotide-binding protein G(i) subunit alpha-1	P63096	0.0159	0.0734	-0.60	0.1112	0.6323	-0.56	0.0106	0.0480
1958 Guanine nucleotide-binding protein G(i) subunit alpha-2	P04899	0.0711	0.1789	0.16	0.5799	0.6617	0.12	0.0101	0.0468
1959 Guanine nucleotide-binding protein G(i)(G(s))/G(o) subunit gamma-12	Q9UBI6	0.4108	0.5706	-3.31	0.5752	0.7988	-1.75	0.5661	0.7191
1960 Guanine nucleotide-binding protein G(i)(G(s)/G(t) subunit beta-1	P62873	0.0359	0.1184	0.10	0.2915	0.6693	0.18	0.1649	0.3018
1961 Guanine nucleotide-binding protein G(i)(G(s)/G(t) subunit beta-2	P62879	0.0127	0.0659	0.15	0.3439	0.7011	0.17	0.1518	0.2822
1962 Guanine nucleotide-binding protein G(i)(G(s)/G(t) subunit beta-3	P16520	0.6980	0.7523	-0.05	0.0859	0.6197	0.30	0.3031	0.4861
1963 Guanine nucleotide-binding protein G(k) subunit alpha	P08754	0.0809	0.1960	-0.22	0.0107	0.4434	-0.14	0.2313	0.3999
1964 Guanine nucleotide-binding protein G(o) subunit alpha	P09471	0.0376	0.1219	0.19	0.8615	0.9001	0.02	0.0408	0.1080
1965 Guanine nucleotide-binding protein G(o) subunit alpha	P38405	0.0157	0.0729	0.24	0.0116	0.4354	0.18	0.0647	0.1484
1966 Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	Q5JWF2	0.1757	0.3378	0.06	0.3256	0.6856	0.21	0.0220	0.0724
1967 Guanine nucleotide-binding protein G(i) subunit alpha-1	P11488	0.1629	0.3196	-0.03	0.1822	0.6661	0.20	0.0406	0.1077
1968 Guanine nucleotide-binding protein G(i) subunit alpha-2	P19087	0.4381	0.5158	-0.18	0.4108	0.7514	-0.47	0.3302	0.5200
1969 Guanine nucleotide-binding protein G(i) subunit alpha-3	ASMTJ3	0.0003	0.0160	0.65	0.0225	0.4777	0.47	0.1254	0.3703
1970 Guanine nucleotide-binding protein G(s) subunit alpha-1	P29992	0.0659	0.1702	0.33	0.0189	0.4662	0.59	0.0131	0.0536
1971 Guanine nucleotide-binding protein subunit alpha-12	Q03113	0.4108	0.5705	-3.31	0.5752	0.7986	-1.75	0.5661	0.7189
1972 Guanine nucleotide-binding protein subunit alpha-13	Q14344	0.0476	0.1401	0.14	0.3045	0.6775	0.15	0.0466	0.0333
1973 Guanine nucleotide-binding protein subunit alpha-14	Q95837	0.4108	0.5703	-3.31	0.5752	0.7984	-1.75	0.5661	0.7187
1974 Guanine nucleotide-binding protein subunit beta-4	Q9HIAV	0.1045	0.2314	-0.24	0.7538	0.8508	-0.04	0.1006	0.2049
1975 Guanine nucleotide-binding protein subunit beta-5	O14775	0.1586	0.3132	-0.09	0.1232	0.6401	0.13	0.5698	0.6276

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control	
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
1976	Guanine nucleotide-binding protein-like 1	P36915	0.0079	0.0526	0.23	0.1870	0.6671	0.28	0.0008	0.0210
1977	Guanylate kinase	P16774	0.0642	0.1679	0.16	0.7042	0.7823	0.06	0.0233	0.0481
1978	Guanylate-binding protein 2	P32456	0.0336	0.1145	0.26	0.9807	0.9868	-0.01	0.0140	0.0554
1979	GUANR22	Q2090	0.3817	-0.18	0.4149	0.7536	-0.10	0.0266	0.0817	-0.46
1980	Guanthyl cyclase-activating protein 2	Q9UMX6	0.5257	0.5972	-0.12	0.3132	0.6800	-0.15	0.0213	0.0705
1981	Halicoid dehalogenase-like hydrolase domain-containing 5	Q9BXW7	0.0026	0.0342	0.33	0.2601	0.6644	0.14	0.0233	0.0265
1982	Hamartin	Q92574	0.9682	0.9765	0.01	0.9763	0.9845	0.01	0.5504	0.7735
1983	HAIUS augmin-like complex subunit 5	O94927	0.5284	0.5998	-0.10	0.5316	0.8507	-0.17	0.0086	0.0436
1984	HBS1-like protein	Q9Y450	0.1027	0.2293	0.13	0.4915	0.8144	0.08	0.5018	0.7244
1985	HCLS1-associated protein X-1	O00165	0.6582	0.7188	0.03	0.1043	0.6334	0.23	0.0937	0.1942
1986	HD domain-containing protein 2	Q7Z4H3	0.2698	0.4622	0.07	0.2722	0.6654	0.17	0.1151	0.2283
1987	HEAT repeat-containing protein 3	Q7Z4Q2	0.4108	0.5702	-3.31	0.5752	0.7982	-1.75	0.5661	0.7185
1988	HEAT repeat-containing protein 6	Q6A108	0.1745	0.3363	-0.03	0.1553	0.6621	0.11	0.0012	0.0227
1989	Heat shock 70 kDa protein 14	Q0VD99	0.0879	0.2062	-0.16	0.0342	0.5304	-0.24	0.0975	0.1904
1990	Heat shock 70 kDa protein 1A	P0DMV8	0.0111	0.0605	0.37	0.1209	0.6606	0.34	0.0069	0.0397
1991	Heat shock 70 kDa protein 1-like	P34931	0.0025	0.0336	0.77	0.1704	0.6413	0.88	0.0006	0.0199
1992	Heat shock 70 kDa protein 4	P34932	0.0031	0.0367	0.28	0.1099	0.6325	0.36	0.0002	0.0192
1993	Heat shock 70 kDa protein 4L	O95757	0.0228	0.0902	0.17	0.1613	0.6636	0.25	0.0081	0.0424
1994	Heat shock 70 kDa protein 6	P17066	0.5613	0.6297	-0.04	0.0096	0.4480	-0.33	0.1241	0.4238
1995	Heat shock cognate 71 kDa protein	P11142	0.0142	0.0696	0.32	0.3066	0.6784	0.24	0.0038	0.0317
1996	Heat shock protein 105 kDa	Q92598	0.0242	0.0935	0.23	0.2159	0.6624	0.21	0.0029	0.0294
1997	Heat shock protein 75 kDa mitochondrial	Q12931	0.0067	0.0492	0.20	0.3032	0.6761	0.16	0.0014	0.0222
1998	Heat shock protein beta-1	P04792	0.0249	0.0993	0.17	0.0923	0.6308	0.28	0.0031	0.0304
1999	Heat shock protein HSP 90-alpha	P07900	0.0106	0.0595	0.34	0.2111	0.6623	0.29	0.0026	0.0279
2000	Heat shock protein HSP 90-alpha A2	Q14568	0.6032	0.6686	0.04	0.4838	0.8084	0.06	0.1431	0.2694
2001	Heat shock protein HSP 90-beta	P08238	0.0070	0.0497	0.34	0.1933	0.6684	0.36	0.0023	0.0267
2002	Heat shock-related 70 kDa protein 2	P54652	0.9884	0.9915	0.00	0.2538	0.6630	0.11	0.0672	0.1525
2003	Helicase MOV-10	Q9HCE1	0.5325	0.6034	-0.03	0.1794	0.6647	0.19	0.3189	0.5064
2004	Helicase SKI2W	Q15477	0.1768	0.3392	-0.09	0.2355	0.6578	-0.10	0.5555	0.7796
2005	Helicase SRCAP	Q6ZRS2	0.4108	0.5700	-3.31	0.5752	0.7979	-1.75	0.5661	0.7184
2006	Helicase with zinc finger domain 2	Q9BYK8	0.0401	0.1262	0.32	0.0811	0.6142	0.28	0.0064	0.0389
2007	Helicase-like transcription factor	Q14527	0.5494	0.6185	0.05	0.0386	0.5570	-0.25	0.1522	0.2829
2008	Helix-loop-helix protein 2	Q02577	0.4108	0.5699	-3.31	0.5752	0.7977	-1.75	0.5661	0.7182
2009	Hematopoietically-expressed homeobox protein HHEX	Q30314	0.0000	0.0000	0.64	0.1477	0.6573	0.30	0.0144	0.0565
2010	Heme oxygenase 1	P09601	0.4108	0.5697	-3.31	0.5752	0.7975	-1.75	0.5661	0.7180
2011	Heme oxygenase 2	P30519	0.0506	0.1455	0.15	0.2180	0.6611	0.30	0.0223	0.0731
2012	Heme-binding protein 1	Q0N1V9	0.0516	0.1471	-0.26	0.1991	0.6650	-0.33	0.0615	0.1441
2013	Heme-binding protein 2	Q9Y5Z4	0.0556	0.1540	0.13	0.0073	0.3980	0.26	0.0725	0.1609
2014	Hemectin-2	Q8NDA2	0.0402	0.1264	0.13	0.4243	0.7608	0.05	0.0194	0.0670
2015	Hemogen	Q9BXL5	0.8150	0.8513	0.02	0.8141	0.8670	0.02	0.2560	0.4241
2016	Hemoglobin subunit alpha	P69905	0.0070	0.0496	0.56	0.0830	0.6204	0.62	0.1835	0.3282
2017	Hemoglobin subunit delta	P20242	0.1601	0.3150	0.17	0.0639	0.7097	0.65	0.9297	0.9456
2018	Heparan-sulfate 6-O-sulfotransferase 1	O60243	0.4108	0.5696	-3.31	0.5752	0.7973	-1.75	0.5661	0.7178
2019	Heparan-sulfate 6-O-sulfotransferase 2	Q96MM7	0.1629	0.3195	0.14	0.082	0.6782	0.11	0.7525	0.7944
2020	Hepatocyte growth factor-regulated tyrosine kinase substrate	O14964	0.0002	0.0150	0.84	0.0097	0.4486	0.27	0.0004	0.0238
2021	Hepatocyte nuclear factor 4-gamma	Q14541	0.4108	0.5694	-3.31	0.5752	0.7971	-1.75	0.5661	0.7177
2022	Hepatoma-derived growth factor	P51858	0.3074	0.5079	0.05	0.2636	0.6644	0.16	0.0260	0.0804
2023	Hepatoma-derived growth factor-like protein 1	Q5TGJ6	0.9394	0.9543	0.00	0.1113	0.6294	-0.26	0.6117	0.6665
2024	Hepatoma-derived growth factor-related protein 2	Q7Z4V5	0.4053	0.6256	-0.31	0.9810	0.9869	0.01	0.9991	0.9281
2025	Hermansky-Pudlak syndrome 3 protein	Q969F9	0.2447	0.4303	-0.22	0.1709	0.6602	-0.12	0.0715	0.1595
2026	Heterogeneous nuclear ribonucleoprotein A/B	Q99729	0.1036	0.2302	-0.17	0.2217	0.6585	-0.12	0.6859	0.7350
2027	Heterogeneous nuclear ribonucleoprotein A1	Q13151	0.0555	0.1540	-0.13	0.6477	0.7393	0.07	0.1010	0.2056
2028	Heterogeneous nuclear ribonucleoprotein A1-like 2	P09651	0.0190	0.0811	0.09	0.3195	0.6825	0.10	0.0010	0.0211
2029	Heterogeneous nuclear ribonucleoprotein C-like 2	Q32P51	0.6274	0.6902	0.09	0.2614	0.6638	0.23	0.1367	0.2603
2030	Heterogeneous nuclear ribonucleoprotein C3	P51991	0.3215	0.5257	-0.05	0.6587	0.7481	0.05	0.0522	0.1289
2031	Heterogeneous nuclear ribonucleoprotein C-like 2	B2RXH8	0.0046	0.0429	-0.35	0.0898	0.6244	-0.21	0.1412	0.6172
2032	Heterogeneous nuclear ribonucleoprotein C-like 3	B7WZ38	0.4108	0.5693	-3.31	0.5752	0.7969	-1.75	0.5661	0.7175
2033	Heterogeneous nuclear ribonucleoprotein D	Q14103	0.2382	0.4226	-0.05	0.9191	0.8104	0.04	0.0435	0.1134
2034	Heterogeneous nuclear ribonucleoprotein D-like	O14979	0.6406	0.7024	0.04	0.5332	0.8496	0.07	0.1854	0.3306
2035	Heterogeneous nuclear ribonucleoprotein F	P52597	0.0176	0.0776	-0.15	0.4732	0.8018	-0.06	0.0291	0.0866
2036	Heterogeneous nuclear ribonucleoprotein H	P31943	0.0346	0.1164	0.09	0.7804	0.8417	0.03	0.0033	0.0306
2037	Heterogeneous nuclear ribonucleoprotein H2	P55795	0.7693	0.8128	0.01	0.1601	0.6310	-0.09	0.3151	0.5021
2038	Heterogeneous nuclear ribonucleoprotein H3	P31942	0.0009	0.0220	-0.16	0.1437	0.6547	-0.16	0.0042	0.0323
2039	Heterogeneous nuclear ribonucleoprotein K	P61978	0.0141	0.0694	0.14	0.3740	0.7215	0.15	0.0075	0.0409
2040	Heterogeneous nuclear ribonucleoprotein L	P14866	0.7549	0.8007	0.02	0.9942	0.9963	0.00	0.0135	0.0543
2041	Heterogeneous nuclear ribonucleoprotein L-like	Q8WVV9	0.3103	0.5112	-0.08	0.8310	0.8783	0.02	0.1597	0.2941
2042	Heterogeneous nuclear ribonucleoprotein M	P52772	0.0007	0.0207	0.25	0.1825	0.6657	0.25	0.0128	0.0532
2043	Heterogeneous nuclear ribonucleoprotein Q	Q60506	0.0220	0.0883	0.04	0.3765	0.7242	0.05	0.0000	0.0000
2044	Heterogeneous nuclear ribonucleoprotein R	Q43390	0.0596	0.1616	0.15	0.2407	0.6607	0.25	0.0129	0.0532
2045	Heterogeneous nuclear ribonucleoprotein U	Q00839	0.0205	0.0847	-0.09	0.1137	0.6340	-0.08	0.0063	0.0386
2046	Heterogeneous nuclear ribonucleoprotein U-like protein 1	Q9BUJ2	0.2323	0.4141	0.07	0.2439	0.6580	0.17	0.0015	0.0226
2047	Heterogeneous nuclear ribonucleoprotein U-like protein 2	Q1KMD3	0.6693	0.7280	-0.08	0.0185	0.4629	-0.32	0.5203	0.7412
2048	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	0.4679	0.5442	-0.04	0.9352	0.9562	-0.01	0.0038	0.0313
2049	Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	0.6157	0.6800	-0.02	0.5907	0.6957	-0.04	0.0829	0.1773
2050	Hexokinase-1	P19367	0.0007	0.0206	0.36	0.3398	0.6990	0.13	0.0119	0.0510
2051	Hexokinase-2	P52789	0.3973	0.6162	0.12	0.7078	0.7853	-0.12	0.2801	0.4553
2052	Hexokinase-3	P52790	0.0079	0.0525	-0.31	0.0002	0.0357	-0.61	0.0003	0.0099
2053	HHIP-like protein 1	Q96JK4	0.0003	0.0159	-2.00	0.5556	0.8703	-0.36	0.1631	0.2990
2054	High affinity cAMP-specific 3', 5'-cyclic phosphodiesterase 7A	P13946	0.0247	0.0949	-0.34	0.051	0.5643	0.10	0.1540	0.2855

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

			MCF-7				SSE				MDA-MB-231				SSE				SSE										
			Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control		Gen IC20 vs control		SSE IC20 vs control		Dai IC20 vs control		Gen IC20 vs control		SSE IC20 vs control										
Protein name	UniProt		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC									
2055 High affinity cAMP-specific and IBMX-insensitive 3', 5'-cyclic phosphodiesterase 8A	P06058		0.1064	0.2347	-0.57	0.8436	0.8876	-0.04	0.3468	0.5409	-0.27	0.5210	0.7261	-0.14	0.7905	0.8357	0.05	0.7329	0.9719	-0.10	0.3736	0.4431	-2.55	0.8708	0.9278	-0.33	0.0651	0.1167	2.06
2056 High mobility group nucleosome-binding domain-containing protein 5	P82970		0.0013	0.0251	0.46	0.0071	0.4132	0.85	0.0001	0.0324	0.96	0.0003	0.0123	0.67	0.0007	0.0218	1.19	0.0034	0.0589	0.50	0.0109	0.1025	0.40	0.0944	0.3068	0.17	0.2067	0.2755	-0.12
2057 High mobility group protein B1	P09429		0.8800	0.9055	0.00	0.6305	0.7269	0.11	0.1064	0.2144	0.15	0.8883	0.9047	0.00	0.0003	0.0138	-0.38	0.0675	0.1823	-0.05	0.1969	0.4064	0.22	0.6861	1.1279	0.04	0.4615	0.5297	-0.05
2058 High mobility group protein B2	P26583		0.0253	0.0961	0.16	0.2496	0.6600	0.28	0.0116	0.0504	0.31	0.0034	0.0235	0.29	0.0703	0.2021	-0.11	0.0221	0.0953	0.18	0.0544	0.1853	0.47	0.0470	0.2019	0.19	0.1284	0.1879	0.11
2059 High mobility group protein B3	O15347		0.0633	0.1666	0.15	0.2859	0.6665	0.27	0.0117	0.0506	0.28	0.0537	0.1213	0.18	0.0587	0.1821	-0.17	0.1478	0.3041	0.10	0.3984	0.4545	0.11	0.4650	0.8730	-0.08	0.3355	0.1938	-0.12
2060 High mobility group protein HMG/HMG-Y	P17096		0.4108	0.5691	-3.31	0.5752	0.7967	-1.75	0.5661	0.7173	-1.19	0.5388	0.6782	0.89	0.2938	0.4647	-1.88	0.9510	1.0889	0.09	0.1134	0.2779	0.39	0.5104	0.9293	-0.08	0.3210	0.3922	-0.07
2061 Hippocalcin-like protein 1	P37235		0.0049	0.0433	0.40	0.2372	0.6620	0.05	0.0138	0.0551	0.08	0.0092	0.0386	0.12	0.8780	0.9069	-0.01	0.4010	0.6158	0.40	0.3173	0.5798	-0.37	0.1297	0.3766	0.44	0.0116	0.0936	0.51
2062 Hippocalcin-like protein 4	Q9UM19		0.5777	0.6451	-0.33	0.8855	0.9183	-0.11	0.0091	0.0446	-3.16	0.7900	0.8194	0.29	0.3325	0.4296	0.47	0.6632	0.9014	-0.20	0.3736	0.4470	-2.55	0.8708	0.9353	-0.33	0.0651	0.1183	2.06
2063 Histidine triad nucleotide-binding protein 1	P49773		0.0092	0.0571	0.11	0.3367	0.6954	0.21	0.0158	0.0593	0.26	0.0025	0.0211	0.30	0.4334	0.5275	0.02	0.0069	0.0641	0.22	0.0551	0.1865	0.37	0.0339	0.1664	0.31	0.1146	0.1722	0.13
2064 Histidine triad nucleotide-binding protein 2 mitochondrial	Q9BX68		0.0442	0.1337	-0.09	0.1037	0.6335	-0.18	0.4638	0.6806	-0.04	0.0299	0.0802	-0.12	0.5810	0.6593	-0.02	0.7042	0.9462	0.01	0.2626	0.5034	0.11	0.0142	0.0995	0.31	0.4610	0.5293	-0.11
2065 Histidine-tRNA ligase cytoplasmic	P12081		0.0559	0.1546	0.14	0.2257	0.6609	0.16	0.0162	0.0602	0.24	0.0276	0.0756	0.22	0.3219	0.4190	0.06	0.0758	0.1957	0.13	0.0948	0.2478	0.24	0.7470	1.1880	-0.02	0.0576	0.2137	-0.15
2066 Histone acetyltransferase KAT8	Q9H726		0.3703	0.5848	-0.05	0.3175	0.6810	-0.08	0.0031	0.0300	0.32	0.5174	0.7226	-0.04	0.0155	0.0886	-0.21	0.3571	0.5633	0.07	0.0586	0.1922	0.23	0.2053	0.5057	-0.09	0.1912	0.2590	-0.07
2067 Histone acetyltransferase p300	O09472		0.4108	0.5690	-3.31	0.5752	0.7965	-1.75	0.5661	0.7171	-1.19	0.5388	0.6781	0.89	0.2938	0.4646	-1.88	0.9510	1.0887	0.09	0.0932	0.2451	0.33	0.6897	1.1320	-0.03	0.0410	0.1758	-0.16
2068 Histone acetyltransferase type B catalytic subunit	O14929		0.0248	0.0951	0.59	0.8466	0.8895	-0.09	0.2669	0.3600	-0.25	0.0565	0.1259	0.86	0.4875	0.5775	-0.13	0.0311	0.0767	0.82	0.1406	0.3214	0.08	0.0611	0.2364	-0.10	0.7225	0.7709	-0.02
2069 Histone chaperone ASF1A	Q9Y294		0.9426	0.9570	-0.01	0.1983	0.6661	-0.57	0.1839	0.3286	-0.22	0.0410	0.1002	-0.47	0.1188	0.2828	-0.23	0.7408	0.9802	-0.03	0.3736	0.4423	-2.55	0.8708	0.9264	-0.33	0.0651	0.1164	2.06
2070 Histone chaperone ASF1B	Q9N1P2		0.0245	0.0946	-0.59	0.0536	0.5822	-0.56	0.0000	0.0000	-0.51	0.0152	0.0509	-0.71	0.0017	0.0320	-1.11	0.0426	0.1363	-1.24	0.3736	0.5682	-2.55	0.8708	1.1566	-0.33	0.0651	0.1748	2.06
2071 Histone deacetylase 1	O13547		0.0008	0.0210	-0.15	0.8397	0.8850	-0.02	0.4207	0.6287	-0.02	0.0412	0.1005	-0.09	0.0008	0.0024	-0.19	0.3065	0.5050	0.03	0.0719	0.1038	0.68	0.0039	0.0505	0.42	0.0047	0.0673	0.39
2072 Histone deacetylase 11	Q96DB2		0.0152	0.0716	-0.09	0.4594	0.7914	-0.07	0.5004	0.7230	0.05	0.5473	0.5981	-0.02	0.1478	0.3239	0.09	0.4301	0.6511	-0.12	0.3736	0.4664	-2.55	0.8708	0.9715	-0.33	0.0651	0.1263	2.06
2073 Histone deacetylase 2	Q92769		0.1571	0.3108	-0.09	0.4041	0.5645	-0.17	0.8872	0.9106	-0.01	0.0118	0.0435	-0.26	0.0031	0.0416	-0.35	0.1072	0.2453	-0.16	0.2586	0.4974	0.12	0.1532	0.4230	-0.09	0.9750	0.9797	0.00
2074 Histone deacetylase 7	Q8WU4		0.0374	0.1215	-0.56	0.0024	0.2391	-0.74	0.0083	0.0431	-0.65	0.0040	0.0257	-2.05	0.0913	0.2387	-0.30	0.0775	0.1986	0.40	0.3736	0.5450	-2.55	0.8708	1.1151	-0.33	0.0651	0.1626	2.06
2075 Histone H1.0	P07305		0.0313	0.5004	0.21	0.3092	0.6784	-0.39	0.0085	0.0435	-0.48	0.1006	0.1950	0.19	0.2314	0.4417	-0.15	0.9540	0.9620	0.01	0.0013	0.0468	1.08	0.5176	0.9391	0.14	0.4755	0.5442	0.41
2076 Histone H1.2	P16403		0.0233	0.0914	-0.46	0.0980	0.6346	-0.22	0.0193	0.0668	-0.39	0.0055	0.0297	-0.66	0.0032	0.0425	-0.48	0.0674	0.1821	-0.91	0.0278	0.1444	0.60	0.9203	0.9416	-0.01	0.0173	0.1120	0.37
2077 Histone H1.4	P10412		0.3216	0.5257	-0.07	0.0511	0.8122	0.07	0.0511	0.1270	0.19	0.7371	0.7732	0.02	0.0030	0.0405	-0.58	0.2867	0.4830	-0.07	0.3736	0.4841	-2.55	0.8708	1.0042	-0.33	0.0651	0.1338	2.06
2078 Histone H1.5	P16401		0.1052	0.2327	0.15	0.4963	0.8185	0.14	0.0212	0.0704	0.31	0.0270	0.0744	0.25	0.0348	0.1354	-0.25	0.1743	0.3421	0.11	0.0514	0.1795	0.51	0.8367	1.2804	0.02	0.0025	0.0535	0.49
2079 Histone H1t	P22492		0.3812	0.5969	-0.07	0.8188	0.8704	0.03	0.7219	0.7668	0.03	0.8114	0.8374	0.02	0.1509	0.3286	-0.12	0.9185	1.1557	-0.01	0.3736	0.4332	-2.55	0.8708	0.9092	-0.33	0.0651	0.1128	2.06
2080 Histone H1x	Q92522		0.0060	0.0467	-0.14	0.0934	0.6291	-0.17	0.0348	0.0970	-0.11	0.0003	0.0105	-0.29	0.0000	0.0000	-0.67	0.0695	0.1853	-0.27	0.1599	0.3529	0.11	0.1798	0.4673	0.07	0.0994	0.2679	0.06
2081 Histone H2A type 1	PC0C58		0.6261	0.6895	-0.03	0.3850	0.7302	-0.14	0.6485	0.7009	-0.03	0.0416	0.1012	0.17	0.0035	0.0438	-0.56	0.0632	0.1753	0.16	0.0048	0.0736	0.66	0.0130	0.0951	0.49	0.0002	0.0235	1.89
2082 Histone H2A.Z	PC0C55		0.4108	0.5688	-3.31	0.5752	0.7962	-1.75	0.5661	0.7170	-1.19	0.5388	0.6779	0.89	0.2938	0.4644	-1.88	0.9510	1.0884	0.09	0.2770	0.5237	-0.14	0.2374	0.5534	-0.14	0.3778	0.4491	0.06
2083 Histone H2B type 1-K	O60814		0.3657	0.5791	-0.14	0.2091	0.6613	-0.51	0.1196	0.2360	-0.27	0.1159	0.2172	0.29	0.3857	0.4832	-0.12	0.2574	0.4482	0.17	0.3736	0.4887	-2.55	0.8708	1.0127	-0.33	0.0651	0.1358	2.06
2084 Histone H2B type 1-L	Q9N880		0.4108	0.5687	-3.31	0.5752	0.7960	-1.75	0.5661	0.7168	-1.19	0.5388	0.6778	0.89	0.2938	0.4643	-1.88	0.9510	1.0882	0.09	0.0217	0.1343	0.56	0.2534	0.5775	0.15	0.0005	0.0282	1.48
2085 Histone H3.1	P68431		0.1751	0.3369	0.08	0.4473	0.7822	0.12	0.9397	0.9529	-0.01	0.0273	0.0749	0.20	0.0357	0.1370	-0.19	0.6652	0.9037	-0.02	0.0207	0.1324	0.53	0.8993	0.9246	0.02	0.0040	0.0615	1.28
2086 Histone H4	PC2805		0.9822	0.9877	0.00	0.6348	0.7312	0.09	0.5982	0.6543	-																		

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control	
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
2122	HLA class II histocompatibility antigen, DRB1-10 beta chain	Q30167	0.4108	0.5665	-3.31	0.5752	0.7931	-1.75	0.5661	0.7143
2123	Holliday junction recognition protein	Q8NCD3	0.4108	0.5664	-3.31	0.5752	0.7929	-1.75	0.5661	0.7142
2124	Q9H161	0.0590	0.1442	0.15	0.4192	0.7574	-0.34	0.0008	0.0205	-0.19
2125	Homeobox protein cut-like 1	P39890	0.6927	0.7475	-0.03	0.7772	0.8392	0.03	0.0304	0.0887
2126	Homeobox protein cut-like 2	O14529	0.1264	0.2653	0.21	0.1431	0.6542	0.18	0.2012	0.3531
2127	Homeobox protein engrailed-2	P19622	0.0626	0.1656	0.12	0.0762	0.6177	0.21	0.6358	0.6890
2128	Homeobox protein Hox-A13	P13271	0.0384	0.1231	-1.40	0.3611	0.7099	-1.91	0.1763	0.3188
2129	Homeobox protein Hox-B5	P09067	0.2585	0.4474	0.10	0.4597	0.7911	-0.06	0.7102	0.7559
2130	Homeobox protein Hox-C11	O43248	0.7623	0.8067	-0.07	0.7815	0.8427	0.07	0.9668	0.9728
2131	Homeobox protein Hox-C5	Q00444	0.0033	0.0377	-0.22	0.4737	0.8016	0.10	0.5907	0.6469
2132	Homeobox protein Hox-C6	P09630	0.0115	0.0617	-0.34	0.7584	0.8250	0.06	0.0078	0.0415
2133	Homeobox protein Nkx-2.8	O15522	0.9188	0.9380	0.00	0.0187	0.4657	0.17	0.8284	0.8615
2134	Homeobox protein Nkx-6.1	P78426	0.2664	0.4580	0.51	0.1657	0.6618	0.42	0.0826	0.1770
2135	Homeobox protein SIX1	Q15475	0.0182	0.0791	1.37	0.1775	0.6629	0.69	0.0557	0.1348
2136	Host cell factor 1	P51610	0.4108	0.5662	-3.31	0.5752	0.7926	-1.75	0.5661	0.7140
2137	Hsc70-interacting protein	P50502	0.0061	0.0469	0.19	0.1413	0.6529	0.24	0.0010	0.0216
2138	Hsp70-binding protein 1	Q9NZL4	0.0102	0.0590	0.50	0.6712	0.7586	0.07	0.2267	0.3857
2139	Hsp90 co-chaperone Cdc37	P16543	0.5372	0.6078	0.02	0.6436	0.5703	0.12	0.0029	0.0297
2140	Huntingtin-associated protein 1	P54257	0.4108	0.5661	-3.31	0.5752	0.7924	-1.75	0.5661	0.7138
2141	Huntingtin-interacting protein 1-related protein	O75146	0.3876	0.6046	0.03	0.5177	0.8396	-0.04	0.0097	0.0457
2142	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Q16836	0.1775	0.3398	-0.08	0.5556	0.8700	-0.05	0.9024	0.9227
2143	Hydroxyacylglutathione hydrolase, mitochondrial	Q16775	0.7839	0.8247	0.05	0.2615	0.6637	0.22	0.1331	0.2554
2144	Hydroxymethylglutaryl-CoA lyase, mitochondrial	P35914	0.3179	0.5206	-0.18	0.2072	0.8611	0.04	0.5150	0.7355
2145	Hydroxymethylglutaryl-CoA synthase cytoplasmic	Q01581	0.0258	0.0972	0.08	0.2574	0.6627	0.18	0.0072	0.0401
2146	Hydroxyproline dehydrogenase	Q9UF12	0.8490	0.8796	0.02	0.9775	0.9853	0.00	0.0046	0.0331
2147	Hydroxystyroid dehydrogenase-like protein 2	Q6YN16	0.0495	0.1431	0.08	0.3667	0.7152	0.07	0.0535	0.1310
2148	Hypoxanthine-guanine phosphoribosyltransferase	P00492	0.0000	0.0000	0.46	0.1025	0.6336	0.20	0.0001	0.0185
2149	Hypoxia up-regulated protein 1	Q9Y4L1	0.0006	0.0199	0.33	0.1191	0.6684	0.26	0.0002	0.0179
2150	Hypoxia-inducible factor 1-alpha inhibitor	Q9NWT6	0.0292	0.1045	1.24	0.0396	0.5635	1.28	0.0533	0.1307
2151	Iduronate 2-sulfatase	P22304	0.3858	0.6023	0.03	0.2830	0.6639	0.10	0.0066	0.0393
2152	Immunity-related GTPase family O protein	Q8WZ49	0.4108	0.5659	-3.31	0.5752	0.7922	-1.75	0.5661	0.7137
2153	Immunoglobulin heavy variable alpha 1	P01876	0.3191	0.5221	0.34	0.8213	0.8725	-0.07	0.2246	0.3825
2154	Immunoglobulin heavy variable 1-6D9	AA0A0B4J2H0	0.0680	0.1733	2.26	0.0549	0.5851	2.18	0.1387	0.2629
2155	Immunoglobulin heavy variable 3-43	AA0A0B4J1X8	0.1166	0.2507	-2.70	0.0476	0.5694	-10.93	0.1216	0.2390
2156	Immunoglobulin superfamily member 3	O70054	0.0041	0.0403	-0.24	0.0207	0.4745	0.20	0.0659	0.1504
2157	Importin subunit alpha-1	P22292	0.0250	0.0954	-0.15	0.0965	0.6206	-0.22	0.5605	0.1424
2158	Importin subunit alpha-3	Q00629	0.1032	0.2298	0.17	0.2485	0.6584	-1.09	0.1255	0.2494
2159	Importin subunit alpha-5	P52294	0.6265	0.6896	0.04	0.5123	0.8348	0.06	0.1228	0.2410
2160	Importin subunit alpha-6	O15131	0.0847	0.2010	-0.10	0.2124	0.6624	0.10	0.0567	0.1363
2161	Importin subunit alpha-7	O60684	0.9061	0.9269	0.01	0.1484	0.6587	0.21	0.0176	0.0633
2162	Importin subunit beta-1	Q14974	0.0587	0.1600	0.17	0.1288	0.6654	0.27	0.0068	0.0397
2163	Importin-4	Q8TEX9	0.0002	0.0148	0.38	0.5942	0.6986	0.06	0.3774	0.5767
2164	Importin-5	O00410	0.2810	0.4744	-0.05	0.3728	0.7206	0.04	0.0740	0.1628
2165	Importin-7	Q95373	0.3559	0.5666	0.04	0.0249	0.4831	0.16	0.0082	0.0428
2166	Importin-9	Q96P70	0.0146	0.0701	-0.14	0.0480	0.8055	-0.03	0.0009	0.0204
2167	Inactive C-alpha-formylglycine-generating enzyme 2	Q8NB37	0.0030	0.0367	0.44	0.1167	0.6363	0.27	0.0154	0.0584
2168	Inactive peptidyl-prolyl cis-trans isomerase FKBP6	O75344	0.5233	0.5947	-0.07	0.8665	0.8968	0.05	0.1245	0.2433
2169	Inactive polypeptide N-acetylglucosaminyltransferase-like protein 5	Q7Z4T8	0.2934	0.4914	-0.46	0.1815	0.6644	-0.79	0.1141	0.2268
2170	Inactive rhomboid protein 2	Q6PIF5	0.4108	0.5658	-3.31	0.5752	0.7920	-1.75	0.5661	0.7135
2171	Inactive tyrosine-protein kinase 7	Q13308	0.4108	0.5656	-3.31	0.5752	0.7918	-1.75	0.5661	0.7133
2172	Inactive tyrosine-protein kinase PEA3	Q0H792	0.4108	0.5655	-3.31	0.5752	0.7916	-1.75	0.5661	0.7131
2173	Inactive ubiquitin thioesterase OTULINL	Q9NUU6	0.0016	0.0274	0.38	0.0017	0.2148	0.38	0.0031	0.0306
2174	Influenza virus NS1A-binding protein	Q9Y6Y0	0.0026	0.0341	0.37	0.0298	0.5078	0.34	0.0227	0.0741
2175	Inhibitor of Bruton tyrosine kinase	Q9P2D0	0.1076	0.2361	-0.13	0.4445	0.7802	-0.05	0.6635	0.7148
2176	Inhibitor of nuclear factor kappa-B kinase subunit beta	O14920	0.8067	0.8442	0.01	0.3657	0.7140	0.77	0.0073	0.0404
2177	Inhibitor of nuclear factor kappa-B kinase subunit epsilon	Q14164	0.7843	0.8247	0.01	0.8099	0.8634	0.02	0.7073	0.7536
2178	Inhibitor of nuclear factor kappa-B kinase-interacting protein	Q70UQ0	0.4108	0.5653	-3.31	0.5752	0.7914	-1.75	0.5661	0.7130
2179	Inner nuclear membrane protein Man1	Q9Y2U8	0.4385	0.5159	0.06	0.5808	0.6886	0.05	0.0162	0.0601
2180	Inorganic pyrophosphatase	Q15181	0.0010	0.0222	0.21	0.1307	0.6466	0.19	0.0898	0.1879
2181	Inorganic pyrophosphatase 2, mitochondrial	Q9H2U2	0.2477	0.4338	0.04	0.6441	0.7373	0.07	0.0019	0.0239
2182	Inosine triphosphatase pyrophosphatase	Q9BY32	0.4108	0.5652	-3.31	0.5752	0.7912	-1.75	0.5661	0.7128
2183	Inosine-3-monophosphate dehydrogenase 1	P20839	0.0815	0.1967	-0.91	0.4942	0.8171	-0.25	0.1851	0.3202
2184	Inosine-5-monophosphate dehydrogenase 2	P12268	0.0169	0.0761	0.15	0.3841	0.7301	0.17	0.0009	0.0205
2185	Inositol 1, 4, 5-trisphosphate receptor type 1	Q14643	0.6686	0.7276	0.10	0.1291	0.6430	0.48	0.8424	0.8733
2186	Inositol 1, 4, 5-trisphosphate receptor type 2	Q14571	0.4108	0.5650	-3.31	0.5752	0.7910	-1.75	0.5661	0.7126
2187	Inositol monophosphatase 1	P29218	0.4108	0.5649	-3.31	0.5752	0.7907	-1.75	0.5661	0.7124
2188	Inositol monophosphatase 3	Q9NX62	0.7410	0.7901	-0.04	0.2181	0.6603	-0.12	0.0806	0.1737
2189	Inositol polyphosphate 1-phosphatase	P49441	0.3107	0.5117	-0.08	0.7005	0.7788	-0.08	0.0068	0.0394
2190	Inositol polyphosphate 5-phosphatase OCRL-1	Q01968	0.8392	0.8713	0.01	0.5617	0.8756	0.07	0.2272	0.3862
2191	Inositol-3-phosphate synthase 1	Q9NPH2	0.6136	0.6781	-0.03	0.9208	0.9456	-0.01	0.0871	0.1845
2192	Inositol-tetrakisphosphate 1-kinase	Q13572	0.0477	0.1402	0.53	0.7870	0.8467	-0.11	0.1949	0.3436
2193	Insulin	P01308	0.4108	0.5647	-3.31	0.5752	0.7905	-1.75	0.5661	0.7123
2194	Insulin receptor substrate 1	P35568	0.0145	0.0700	0.44	0.1930	0.6683	0.18	0.0787	0.1726
2195	Insulin-degrading enzyme	P14735	0.2196	0.3958	0.07	0.5252	0.8438	0.08	0.0486	0.1226
2196	Insulin-like growth factor 1 receptor	R08069	0.0015	0.0266	-0.31	0.1488	0.6599	-0.29	0.8336	0.8659
2197	Insulin-like growth factor 2 mRNA-binding protein 1	Q9NZT8	0.4108	0.5646	-3.31	0.5752	0.7903	-1.75	0.5661	0.7121
2198	Insulin-like growth factor 2 mRNA-binding protein 2	Q9YGM1	0.4108	0.5644	-3.31	0.5752	0.7901	-1.75	0.5661	0.7119
2199	Insulin-like growth factor 2 mRNA-binding protein 3	O00425	0.1900	0.3559	0.19	0.1009	0.6328	0.08	0.1866	0.3318

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
2200	Insulin-like growth factor-binding protein 7	Q16270	0.4108	0.5643	-3.31	0.5752	0.7899	-1.75	0.5661	0.7117
2201	Integrator complex subunit 1	Q8N201	0.0014	0.0255	0.19	0.5752	0.5858	0.47	0.0029	0.0296
2202	Integrator complex subunit 13	Q9NVM9	0.1335	0.2767	-0.10	0.2443	0.6567	0.11	0.0487	0.1228
2203	Integrator complex subunit 3	Q68E01	0.8839	0.9086	0.01	0.5718	0.8849	0.03	0.0011	0.0214
2204	Integrator complex subunit 5	Q6P9B9	0.4108	0.5641	-3.31	0.5752	0.7897	-1.75	0.5661	0.7116
2205	Integrin alpha-2	P17301	0.0070	0.0495	0.33	0.1005	0.6341	0.22	0.0004	0.0214
2206	Integrin alpha-3	P26006	0.7083	0.7063	-0.02	0.2998	0.6732	0.10	0.0270	0.0823
2207	Integrin alpha-E	P38570	0.0094	0.0574	-0.66	0.2432	0.6599	-0.44	0.0039	0.0317
2208	Integrin alpha-V	P06756	0.4108	0.5640	-3.31	0.5752	0.7895	-1.75	0.5661	0.7114
2209	Integrin alpha-X	P20702	0.4108	0.5638	-3.31	0.5752	0.7893	-1.75	0.5661	0.7112
2210	Integrin beta-1	P05556	0.5920	0.6586	-0.03	0.5065	0.8282	0.17	0.0616	0.1442
2211	Integrin beta-5	P18084	0.9351	0.9509	0.00	0.2884	0.6687	-0.07	0.2143	0.3689
2212	Integrin beta-like protein 1	O95965	0.1588	0.3134	0.04	0.3569	0.7083	0.18	0.0221	0.0725
2213	Integrin-linked kinase-associated serine/threonine phosphatase 2C	Q9H0C8	0.4108	0.5637	-3.31	0.5752	0.7891	-1.75	0.5661	0.7111
2214	Integrin-linked protein kinase	Q13418	0.0020	0.0310	0.48	0.0647	0.5890	0.77	0.0004	0.0225
2215	Integrin alpha-5	P01569	0.4108	0.5635	-3.31	0.5752	0.7889	-1.75	0.5661	0.7109
2216	Interferon regulatory factor 2-binding protein 2	Q7Z519	0.2895	0.4864	0.09	0.2184	0.6608	0.16	0.0742	0.1630
2217	Interferon regulatory factor 2-binding protein-like	Q9H1B7	0.3174	0.5200	-0.21	0.8510	0.8952	0.04	0.7964	0.8336
2218	Interferon regulatory factor 4	Q15306	0.0768	0.1893	0.28	0.9594	0.9724	-0.01	0.4913	0.7119
2219	Interferon-induced helicase C domain-containing protein 1	Q9BYX4	0.0517	0.1472	0.16	0.0662	0.6597	0.21	0.0201	0.0683
2220	Interferon-induced protein with tetratricopeptide repeats 3	O14879	0.6264	0.6896	0.05	0.6625	0.7514	0.07	0.1195	0.2359
2221	Interferon-induced protein with tetratricopeptide repeats 5	Q13325	0.4108	0.5634	-3.31	0.5752	0.7887	-1.75	0.5661	0.7107
2222	Interferon-induced transmembrane protein 3	Q01628	0.5905	0.6571	-0.30	0.5320	0.8500	-0.38	0.4418	0.6535
2223	Interferon-induced double-stranded RNA-activated protein kinase	P19525	0.0024	0.0335	0.09	0.0990	0.6363	-0.06	0.0473	0.1206
2224	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	O75569	0.0003	0.0157	0.85	0.0102	0.4440	0.30	0.5231	0.7442
2225	Interferon-stimulated gene 20 kDa protein	Q96AZ6	0.0106	0.0594	0.50	0.8448	0.8882	-0.02	0.3456	0.5394
2226	Interleukin enhancer-binding factor 2	Q12905	0.0011	0.0229	0.27	0.0809	0.6154	0.21	0.0007	0.0211
2227	Interleukin enhancer-binding factor 3	Q12906	0.1663	0.3242	0.08	0.3771	0.7245	0.16	0.0262	0.0807
2228	Interleukin-1 receptor accessory protein-like 1	Q9NZN1	0.5632	0.6313	-0.28	0.3962	0.7398	-0.24	0.5067	0.7283
2229	Interleukin-1 receptor accessory protein-like 3	Q9Y616	0.2505	0.4366	-0.03	0.2980	0.6723	0.17	0.0489	0.1231
2230	Interleukin-1 receptor-like 2	Q9HB29	0.4108	0.5632	-3.31	0.5752	0.7884	-1.75	0.5661	0.7105
2231	Interleukin-12 receptor subunit beta-1	P42701	0.4108	0.5631	-3.31	0.5752	0.7882	-1.75	0.5661	0.7104
2232	Interleukin-13 receptor subunit alpha-1	P78552	0.4108	0.5629	-3.31	0.5752	0.7880	-1.75	0.5661	0.7104
2233	Interleukin-17 receptor B	Q9NRM6	0.4268	0.5043	-0.12	0.0882	0.6191	0.27	0.8993	0.9201
2234	Interleukin-17B	Q9UIH5	0.4108	0.5628	-3.31	0.5752	0.7878	-1.75	0.5661	0.7102
2235	Interleukin-6 receptor subunit beta	P40189	0.4108	0.5627	-3.31	0.5752	0.7876	-1.75	0.5661	0.7100
2236	Intermediate filament family orphan 1	Q0D215	0.4108	0.5625	-3.31	0.5752	0.7874	-1.75	0.5661	0.7099
2237	Intersectin-1	Q15811	0.0819	0.1971	0.11	0.1731	0.6603	0.22	0.0465	0.1193
2238	Intracellular hyaluronan-binding protein 4	Q5JVS0	0.2714	0.4641	0.38	0.4784	0.8041	0.25	0.0785	0.1699
2239	Intracellular transport protein 122 homolog	Q9HBB6	0.0005	0.0186	0.15	0.4465	0.7822	0.04	0.4320	0.6423
2240	Intracellular transport protein 172 homolog	Q9UG01	0.0140	0.0693	-2.82	0.4086	0.7498	-1.02	0.0149	0.0575
2241	Intracellular transport protein 74 homolog	Q96LB3	0.1164	0.2504	-0.08	0.2728	0.6653	-0.14	0.0031	0.0300
2242	Inverted formin-2	Q27181	0.0026	0.0340	-0.15	0.1414	0.6528	0.27	0.0032	0.0305
2243	Ispirin	Q8N2Y8	0.7655	0.8091	0.02	0.6506	0.7423	0.02	0.0139	0.0553
2244	IQ domain-containing protein E	Q6IPM2	0.4108	0.5624	-3.31	0.5752	0.7872	-1.75	0.5661	0.7097
2245	IQ motif and SEC7 domain-containing protein 1	Q6DN90	0.3583	0.5698	0.06	0.0158	0.4547	0.29	0.8991	0.9201
2246	Iron-sulfur cluster assembly enzyme ISC1, mitochondrial	Q9H1K1	0.9901	0.9922	0.00	0.5610	0.8748	-0.25	0.4102	0.6164
2247	Iset cell autoantigen 1	Q05084	0.0185	0.0800	-0.17	0.1134	0.6344	-0.16	0.1034	0.2098
2248	Isochrysin-CoA dehydrogenase, mitochondrial	Q9UKU7	0.4108	0.5622	-3.31	0.5752	0.7870	-1.75	0.5661	0.7095
2249	Isochorismatase domain-containing protein 1	Q96CN7	0.0637	0.1671	-0.22	0.2020	0.6597	0.12	0.1288	0.2495
2250	Isochorismatase domain-containing protein 2	Q96AB3	0.1920	0.3587	-0.06	0.1538	0.6601	-0.09	0.0027	0.0286
2251	Isochorismatase [NAD] subunit alpha, mitochondrial	P50213	0.0705	0.1778	0.10	0.2765	0.6649	0.14	0.0285	0.0856
2252	Isochorismatase [NAD] subunit beta, mitochondrial	O43837	0.0268	0.0992	0.09	0.4944	0.8169	0.08	0.8357	0.8677
2253	Isochorismatase [NADP] cytoplasmic	O75874	0.0162	0.0743	0.24	0.6855	0.7708	0.02	0.0027	0.0284
2254	Isochorismatase [NADP] mitochondrial	P48735	0.0055	0.0449	-0.19	0.9644	0.9759	0.00	0.0194	0.0670
2255	Isochorismatase [NADP] cytoplasmic	P41252	0.0090	0.0576	0.15	0.1983	0.6670	0.18	0.0004	0.0194
2256	Isochorismatase [NADP] mitochondrial	Q9NS54	0.6686	0.6725	0.05	0.2951	0.6713	0.13	0.3099	0.4944
2257	Isochorismatase [NADP] cytoplasmic	Q13907	0.0265	0.0987	0.31	0.0182	0.4644	0.13	0.0087	0.0440
2258	Isochorismatase [NADP] cytoplasmic	Q9BXS1	0.0694	0.1755	0.11	0.6541	0.7448	0.04	0.2974	0.4786
2259	IST1 homolog	P53990	0.1618	0.6302	0.04	0.6258	0.7229	0.05	0.0165	0.0608
2260	Izumo sperm-egg fusion protein 2	Q6UXV1	0.1114	0.2425	-0.10	0.7437	0.8146	0.03	0.8029	0.8392
2261	Izumo sperm-egg fusion protein 3	Q5V272	0.4108	0.5621	-3.31	0.5752	0.7868	-1.75	0.5661	0.7093
2262	Jerk protein homolog	O75564	0.2778	0.4718	0.10	0.6523	0.7434	0.04	0.9067	0.9264
2263	Junction plakoglobin	P14923	0.0791	0.1929	-0.08	0.8735	0.9084	0.02	0.2977	0.4551
2264	Junctional protein associated with coronary artery disease	Q9P266	0.0870	0.2050	0.06	0.0002	0.2590	0.31	0.0090	0.0444
2265	Junctophilin-3	Q8WXH2	0.0037	0.0389	3.45	0.1688	0.6609	1.89	0.0607	0.1428
2266	Junctophilin microtubule associated homolog 1	Q9UK76	0.3349	0.5414	0.01	0.2636	0.6632	0.16	0.0009	0.0207
2267	Junctophilin microtubule associated homolog 2	Q9H910	0.0771	0.1898	-0.12	0.4803	0.8054	0.12	0.5357	0.7569
2268	Kalirin	O60229	0.4108	0.5619	-3.31	0.5752	0.7866	-1.75	0.5661	0.7092
2269	Kalikrein-14	Q9PQ03	0.0000	0.0000	2.37	0.0040	0.3397	0.48	0.3480	0.5418
2270	Kanadapin	Q9BWU0	0.0133	0.0673	-0.14	0.9299	0.9527	-0.01	0.0321	0.0919
2271	Katanin p60 ATPase-containing subunit A1	O75449	0.4108	0.5618	-3.31	0.5752	0.7864	-1.75	0.5661	0.7090

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	MCF-7						MDA-MB-231					
	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC
2272 Katanin p60 ATPase-containing subunit A-like 1	Q9BW62	0.4108	0.5616	-3.31	0.5752	0.7862	-1.75	0.5661	0.7088	-1.19	0.5388	0.6703
2273 Katanin p60 ATPase-containing subunit A-like 2	Q8IY74	0.0031	0.0364	-0.41	0.2382	0.6627	-0.15	0.0674	0.1666	-0.10	0.0057	0.0302
2274 Kazrin	Q6T478	0.4108	0.5615	-3.31	0.5752	0.7859	-1.75	0.5661	0.7087	-1.19	0.5388	0.6701
2275 Kelch domain-containing protein 4	Q8TBB5	0.0727	0.1818	-0.47	0.5422	0.8573	-0.11	0.3641	0.5615	-0.21	0.6723	0.7135
2276 Kelch domain-containing protein 8A	Q8IYD2	0.4108	0.5613	-3.31	0.5752	0.7857	-1.75	0.5661	0.7085	-1.19	0.5388	0.6699
2277 Kelch domain-containing protein 9	Q8NIEP	0.0265	0.0986	-0.44	0.0639	0.5921	-0.30	0.0323	0.0923	-0.43	0.0309	0.0819
2278 Kelch repeat and BTH domain-containing protein 11	Q94819	0.4108	0.5612	-3.31	0.5752	0.7855	-1.75	0.5661	0.7083	-1.19	0.5388	0.6698
2279 Kelch-like protein 13	Q9P2N7	0.8421	0.8738	-0.08	0.3412	0.7000	-1.50	0.8692	0.8965	-0.06	0.6936	0.7332
2280 Kelch-like protein 15	Q96M94	0.4107	0.6320	-0.53	0.6655	0.6628	1.01	0.5008	0.7232	0.39	0.3577	0.5358
2281 Kelch-like protein 20	Q9Y2M5	0.0001	0.0115	0.48	0.2930	0.6704	0.08	0.0028	0.0291	0.16	0.0140	0.0482
2282 Kelch-like protein 24	Q6TFL4	0.1056	0.2333	-0.19	0.2571	0.6636	-0.27	0.0971	0.1997	-0.19	0.0088	0.0379
2283 Kelch-like protein 25	Q9H0H3	0.1286	0.2692	0.19	0.1676	0.6612	0.22	0.0887	0.1869	0.25	0.0745	0.1552
2284 Kelch-like protein 26	Q53HCS	0.4108	0.5610	-3.31	0.5752	0.7853	-1.75	0.5661	0.7081	-1.19	0.5388	0.6696
2285 Kelch-like protein 31	Q9H511	0.4108	0.5609	-3.31	0.5752	0.7851	-1.75	0.5661	0.7080	-1.19	0.5388	0.6695
2286 Kelch-like protein 5	Q96P07	0.2441	0.4296	-0.08	0.0951	0.6299	0.16	0.2806	0.4559	-0.11	0.0891	0.1779
2287 Keratin type I cuticular Ha1	Q15323	0.0022	0.0321	-0.83	0.0614	0.5934	-1.85	0.0013	0.0235	-1.09	0.0284	0.0772
2288 Keratin type I cuticular Ha2	Q14532	0.1235	0.2610	0.11	0.0975	0.6146	0.21	0.2961	0.4768	0.06	0.0339	0.0874
2289 Keratin type I cuticular Ha3-II	Q14525	0.0466	0.1382	0.24	0.2686	0.6635	0.10	0.3373	0.5298	-0.15	0.3375	0.5113
2290 Keratin type I cuticular Ha5	Q92764	0.7285	0.7787	0.02	0.4730	0.8017	0.15	0.1053	0.2125	0.12	0.0214	0.0634
2291 Keratin type I cuticular Ha6	Q76013	0.0022	0.0320	0.40	0.0147	0.4506	0.25	0.2206	0.3775	0.05	0.0654	0.1409
2292 Keratin type I cuticular Ha7	Q76014	0.0006	0.0198	-0.27	0.1834	0.6648	-0.40	0.2892	0.4683	0.44	0.0340	0.0876
2293 Keratin type I cuticular Ha8	Q76015	0.0047	0.0432	-0.52	0.2996	0.6739	-0.40	0.1551	0.2870	-0.15	0.3324	0.5057
2294 Keratin type I cuticular Ha9	Q94956	0.0008	0.0209	-0.36	0.9637	0.9754	0.01	0.0796	0.1719	0.15	0.3752	0.5585
2295 Keratin type I cytoskeletal 13	P13646	0.6887	0.7443	-0.03	0.1430	0.8365	0.09	0.7492	0.7915	-0.03	0.8896	0.9059
2296 Keratin type I cytoskeletal 14	P02533	0.0250	0.0954	0.20	0.2695	0.6629	0.13	0.0013	0.0224	0.50	0.1561	0.2737
2297 Keratin type I cytoskeletal 15	P19012	0.0361	0.1190	0.15	0.1634	0.6633	0.15	0.0032	0.0304	0.28	0.0104	0.0410
2298 Keratin type I cytoskeletal 16	P08779	0.0796	0.1934	0.14	0.2136	0.6621	0.25	0.0302	0.0883	0.28	0.0098	0.0397
2299 Keratin type I cytoskeletal 17	Q04695	0.0000	0.0000	1.03	0.0108	0.4405	0.20	0.0059	0.0309	0.33	0.0020	0.0352
2300 Keratin type I cytoskeletal 18	P05783	0.0039	0.0395	0.31	0.1190	0.6348	0.30	0.0084	0.0432	0.27	0.0000	0.0000
2301 Keratin type I cytoskeletal 19	P08727	0.0065	0.0482	0.38	0.1960	0.6693	0.31	0.0545	0.1328	0.18	0.0014	0.0168
2302 Keratin type I cytoskeletal 20	P35900	0.5547	0.6240	-0.08	0.1906	0.6685	0.14	0.5738	0.6313	-0.07	0.1616	0.2809
2303 Keratin type I cytoskeletal 24	Q2M215	0.3633	0.5760	0.03	0.3328	0.6915	0.13	0.0907	0.1896	0.12	0.0068	0.0333
2304 Keratin type I cytoskeletal 25	Q72320	0.0284	0.1024	-0.66	0.2621	0.6636	-0.92	0.0525	0.1295	-0.91	0.0167	0.0538
2305 Keratin type I cytoskeletal 26	Q723Y9	0.7728	0.8153	0.02	0.1931	0.6682	0.17	0.6906	0.7388	0.04	0.1227	0.2263
2306 Keratin type I cytoskeletal 28	Q723Y7	0.0673	0.1719	0.11	0.3782	0.7256	0.05	0.0920	0.1913	0.07	0.0015	0.0171
2307 Keratin type I cytoskeletal 39	Q6A163	0.4108	0.5607	-3.31	0.5752	0.7849	-1.75	0.5661	0.7078	-1.19	0.5388	0.6693
2308 Keratin type II cuticular Hb2	Q9NSB4	0.0003	0.0155	0.22	0.1730	0.6604	0.26	0.0001	0.0162	0.33	0.0000	0.0000
2309 Keratin type II cuticular Hb4	P35900	0.4108	0.5613	-3.31	0.5752	0.7851	-1.75	0.5661	0.7080	-1.19	0.5388	0.6695
2310 Keratin type II cuticular Hb5	P78386	0.5970	0.6630	-0.03	0.2421	0.6597	0.10	0.0649	0.1487	-0.07	0.0169	0.0542
2311 Keratin type II cuticular Hb6	Q43790	0.3392	0.5472	-0.07	0.3391	0.6987	0.21	0.8399	0.8710	0.02	0.0186	0.0576
2312 Keratin type II cytoskeletal 3	P12035	0.0818	0.1970	0.23	0.6889	0.7721	0.05	0.0481	0.1217	0.08	0.1419	0.2536
2313 Keratin type II cytoskeletal 4	P19013	0.0473	0.1397	0.10	0.7369	0.8089	-0.01	0.0349	0.0970	0.10	0.0353	0.0900
2314 Keratin type II cytoskeletal 5	P13647	0.0004	0.0167	0.18	0.1639	0.6638	0.18	0.3821	0.5828	0.02	0.0000	0.0000
2315 Keratin type II cytoskeletal 6A	P02538	0.0215	0.0873	0.21	0.1842	0.6640	0.25	0.0001	0.0157	0.27	0.0119	0.0438
2316 Keratin type II cytoskeletal 6B	P04259	0.2389	0.4235	0.05	0.9377	0.9579	-0.01	0.0129	0.0531	0.27	0.0274	0.0751
2317 Keratin type II cytoskeletal 7	P08729	0.4399	0.5174	-0.02	0.5886	0.6942	0.05	0.0204	0.0687	0.08	0.0154	0.0513
2318 Keratin type II cytoskeletal 71	Q3SY84	0.0271	0.0999	0.28	0.2477	0.6649	0.23	0.0128	0.0530	0.36	0.0277	0.0758
2319 Keratin type II cytoskeletal 72	Q14CN4	0.0272	0.1000	0.15	0.3687	0.7175	0.05	0.0056	0.0362	0.25	0.0136	0.0472
2320 Keratin type II cytoskeletal 73	Q86Y46	0.0026	0.0339	0.26	0.1839	0.6643	0.23	0.0046	0.0335	0.20	0.0014	0.0171
2321 Keratin type II cytoskeletal 74	Q7RTS7	0.0007	0.0205	0.45	0.0317	0.5100	0.28	0.0061	0.0379	0.59	0.0009	0.0150
2322 Keratin type II cytoskeletal 75	Q95678	0.0095	0.0574	0.34	0.1339	0.6638	0.22	0.3920	0.5937	0.06	0.0027	0.0216
2323 Keratin type II cytoskeletal 78	Q8N1N4	0.7564	0.8017	0.01	0.1397	0.6531	0.17	0.0669	0.1521	0.21	0.9868	0.9887
2324 Keratin type II cytoskeletal 79	Q5XKES	0.0056	0.0453	0.06	0.0437	0.5702	0.20	0.0031	0.0505	0.10	0.0004	0.0120
2325 Keratin type II cytoskeletal 80	P05787	0.0058	0.0459	0.47	0.1548	0.6616	0.39	0.0054	0.0360	0.43	0.0008	0.0146
2326 Keratin type II cytoskeletal 8	Q6KB66	0.0050	0.0435	0.13	0.2482	0.6583	0.17	0.1266	0.2463	0.12	0.0032	0.0229
2327 Keratin-like protein KRT222	KRNLAD	0.0398	0.1258	0.18	0.1000	0.8321	0.07	0.0498	0.1247	0.41	0.0563	0.1258
2328 Keratinocyte-associated protein 2	Q8N6L1	0.1646	0.3219	-0.11	0.0428	0.5685	-0.47	0.0091	0.0446	-0.37	0.0085	0.0373
2329 KH domain-containing RNA-binding signal transduction-associated protein 1	Q07666	0.5845	0.6515	-0.05	0.2005	0.6628	-0.23	0.0013	0.0228	-0.22	0.5912	0.6396
2330 KH domain-containing RNA-binding signal transduction-associated protein 2	Q5VWX1	0.4108	0.5606	-3.31	0.5752	0.7847	-1.75	0.5661	0.7076	-1.19	0.5388	0.6691
2331 KICSTOR complex protein SZT2	Q5T011	0.4108	0.5604	-3.31	0.5752	0.7845	-1.75	0.5661	0.7075	-1.19	0.5388	0.6690
2332 KIF1-binding protein	Q96KE5	0.1685	0.3270	0.13	0.1898	0.6706	0.27	0.0104	0.0476	0.41	0.0097	0.0395
2333 Killer cell immunoglobulin-like receptor 2DL3	P43628	0.0530	0.1495	-0.43	0.0130	0.4430	-0.46	0.0601	0.1418	-0.23	0.0009	0.0146
2334 Killer cell lectin-like receptor subfamily B member 1	Q12918	0.2433	0.4287	0.51	0.4699	0.7996	0.44	0.0404	0.1073	0.32	0.0225	0.0655
2335 Kinase D-interacting substrate of 220 kDa	Q5ULH0	0.2196	0.3957	-0.20	0.1965	0.7176	-0.03	0.5967	0.6449	-0.08	0.3280	0.4250
2336 Kinecin	Q86U92	0.0218	0.0878	0.10	0.2770	0.6646	0.14	0.1020	0.0512	0.22	0.0023	0.0204
2337 Kinesin heavy chain isoform 5A	Q12840	0.3526	0.5625	0.05	0.1909	0.6686	0.11	0.0597	0.1414	0.15	0.0338	0.0873
2338 Kinesin heavy chain isoform 5C	Q60232	0.0001	0.0113	0.34	0.0968	0.6347	0.39	0.0095	0.0209	0.37	0.0009	0.0401
2339 Kinesin light chain 1	Q07866	0.0393	0.1248	-0.04	0.3366	0.6955	0.19	0.0201	0.0681	0.24	0.0004	0.0113
2340 Kinesin light chain 2	Q9H0B6	0.0204	0.0845	-0.17	0.9584	0.9717	-0.01	0.3840	0.5845	-0.12	0.9796	0.9823
2341 Kinesin light chain 4	Q9NSK0	0.1602	0.3150	0.07	0.0865	0.6197	0.20	0.0039	0.0320	0.26	0.0021	0.0201
2342 Kinesin-1 heavy chain	P31716	0.2581	0.4468	0.09	0.2005	0.6632	0.20	0.0652	0.1492	0.21	0.1075	0.2051
2343 Kinesin-like protein KIF11	P52732	0.4108	0.5603	-3.31	0.5752	0.7843	-1.75	0.5661	0.7073	-1.19	0.5388	0.6688
2344 Kinesin-like protein KIF13B	Q9NQ78	0.4108	0.5601	-3.31	0.5752	0.7841	-1.75	0.5661	0.7071	-1.19	0.5388	0.6687
2345 Kinesin-like protein KIF15	Q9NS87	0.4108	0.5600	-3.31	0.5752	0.7839	-1.75	0.5661	0.7069	-1.19	0.5388	0.6685
2346 Kinesin-like protein KIF16B	Q96L93	0.9138	0.9336	0.01	0.3909	0.7350	0.16	0.1000	0.2040	0.20	0.3456	0.5212
2347 Kinesin-like protein KIF18A	Q8N177	0.4139	0.4919	-0.06	0.4348	0.7708	-0.07	0.3830	0.5839	0.07	0.0782	0.1612
2348 Kinesin-like protein KIF1A	Q12756	0.4108	0.5598	-3.31	0.5752	0.7837	-1.75	0.5661	0.7068	-1.19	0.5388	0.6683
2349 Kinesin-like protein KIF1B	Q60333	0.2563	0.4442	0.08	0.1648	0.6607	0.17	0.1483	0.2767	0.21	0.0028	0.0216
2350 Kinesin-like protein KIF27	Q86VH2	0.0005	0.0185	0.34	0.0628	0.5915	0.26	0.0054	0.0360	0.42	0.0012	0.0161
2351 Kinesin-like protein KIF28P	BTZC32	0.0871	0.2052	0.07	0.1020	0.6320	0.16	0.0004	0.0211	0.17	0.0125	0.0453

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
2352 Kinesin-like protein KIF2A	O00139	0.0889	0.2079	0.13	0.3041	0.6769	0.10	0.0089	0.0441	0.29	0.0863	0.1739	0.14	0.7714	0.8215	-0.01	0.3656	0.5723	0.05	0.0309	0.1488	0.45	0.3178	0.6676	0.12	0.2893	0.3613	-0.11
2353 Kinesin-like protein KIF2C	Q99661	0.1260	0.2650	0.11	0.0819	0.9874	0.00	0.0012	0.0223	0.55	0.0015	0.0179	0.34	0.4665	0.5577	-0.00	0.0005	0.0365	0.58	0.0421	0.3238	0.15	0.8927	0.9199	-0.01	0.6831	0.7363	-0.02
2354 Kinesin-like protein KIF3B	I15066	0.4108	0.5597	-3.31	0.5752	0.7835	-1.75	0.5661	0.7066	-1.19	0.5388	0.6682	0.89	0.2938	0.4561	-1.88	0.9510	1.0742	0.09	0.0449	0.1701	0.42	0.6269	1.0623	0.05	0.1251	0.1846	0.16
2355 Kinesin-like protein KIF3C	I14782	0.0012	0.0241	1.10	0.1774	0.6630	0.66	0.0037	0.0318	0.96	0.0002	0.0104	1.32	0.3021	0.4002	-0.12	0.0029	0.0354	1.10	0.2451	0.4791	0.21	0.6364	1.0738	-0.35	0.0170	0.1115	-0.66
2356 Kinesin-like protein KIF7	Q2M1P5	0.4108	0.5595	-3.31	0.5752	0.7833	-1.75	0.5661	0.7064	-1.19	0.5388	0.6680	0.89	0.2938	0.4559	-1.88	0.9510	1.0739	0.09	0.2642	0.5057	-0.14	0.0323	0.1630	-0.45	0.0186	0.1175	-0.40
2357 Kinesin-like protein KIF9	Q9HAA2	0.0487	0.1416	0.16	0.3518	0.7044	0.06	0.0056	0.0362	0.33	0.0092	0.0386	0.28	0.0018	0.0334	-0.30	0.0083	0.0671	0.25	0.3736	0.6179	-2.55	0.8708	1.2440	-0.33	0.0651	0.2038	-2.06
2358 Kinesin-like protein KIFC1	QBW19	0.1040	0.1040	0.19	0.1050	0.6317	0.22	0.0099	0.0214	0.51	0.0887	0.1774	0.14	0.5260	0.6124	-0.03	0.0167	0.0847	0.32	0.6907	0.7323	0.03	0.0121	0.0918	-0.20	0.2428	0.3132	-0.05
2359 Kinetochore protein NDC80 homolog	I14777	0.4108	0.5594	-3.31	0.5752	0.7831	-1.75	0.5661	0.7063	-1.19	0.5388	0.6679	0.89	0.2938	0.4558	-1.88	0.9510	1.0737	0.09	0.0364	0.1583	0.13	0.0005	0.0212	-0.26	0.0456	0.1869	0.10
2360 Kinetochore protein Spc24	Q8NBT2	0.0007	0.0204	1.85	0.0419	0.5727	0.38	0.1222	0.3669	-0.10	0.0168	0.0541	0.30	0.0148	0.0869	-0.28	0.0019	0.0521	0.73	0.3736	0.6449	-2.55	0.8708	1.2906	-0.33	0.0651	0.2213	2.06
2361 Kinetochore protein Spc25	Q9HBM1	0.8692	0.8964	0.05	0.6982	0.7778	-0.41	0.4358	0.6465	-0.31	0.4749	0.6749	-0.30	0.7376	0.7945	-0.11	0.2735	0.4677	-0.38	0.3736	0.4865	-2.55	0.8708	1.0087	-0.33	0.0651	0.1348	2.06
2362 Klotho	Q9UEF7	0.0820	0.1972	0.50	0.1959	0.4633	0.85	0.0195	0.0673	0.87	0.0386	0.0960	0.81	0.0101	0.0724	1.25	0.0700	0.1860	0.59	0.3736	0.5492	-2.55	0.8708	1.1226	-0.33	0.0651	0.1647	2.06
2363 Kruppel-like factor 11	I14901	0.0191	0.0812	0.18	0.1871	0.6670	0.22	0.0235	0.0754	0.25	0.0237	0.0681	0.17	0.4187	0.5131	0.03	0.0431	0.1368	0.13	0.3736	0.5672	-2.55	0.8708	1.1548	-0.33	0.0651	0.1743	2.06
2364 Kunitz-type protease inhibitor 1	O43278	0.3196	0.5227	0.07	0.2153	0.6603	0.17	0.2429	0.4075	0.09	0.0326	0.0852	0.22	0.6695	0.7338	-0.03	0.0643	0.1769	0.19	0.3736	0.5520	-2.55	0.8708	1.1277	-0.33	0.0651	0.1662	2.06
2365 Kunitz-type protease inhibitor 2	O43291	0.0916	0.2122	0.10	0.0569	0.5860	-0.13	0.0038	0.0321	-0.30	0.0684	0.1454	-0.12	0.2029	0.4041	-0.06	0.7999	1.0366	-0.05	0.3736	0.4385	-2.55	0.8708	0.9192	-0.33	0.0651	0.1149	2.06
2366 Kunitz-type protease inhibitor 4	O6UDR6	0.4108	0.5592	-3.31	0.5752	0.7829	-1.75	0.5661	0.7061	-1.19	0.5388	0.6677	0.89	0.2938	0.4557	-1.88	0.9510	1.0735	0.09	0.3375	0.6079	0.07	0.2542	0.5785	0.07	0.0119	0.0938	-0.28
2367 Kv channel-interacting protein 1	Q9NZ12	0.2290	0.4097	0.05	0.1793	0.6648	0.08	0.0004	0.0195	0.36	0.0062	0.0317	0.24	0.5708	0.6511	0.02	0.0137	0.0776	0.26	0.3736	0.6057	-2.55	0.8708	1.2228	-0.33	0.0651	0.1963	2.06
2368 Kv channel-interacting protein 2	Q9NS61	0.6902	0.7458	-0.03	0.2025	0.6754	-0.12	0.0532	0.1307	-0.23	0.0133	0.0468	-0.42	0.0778	0.2144	-0.22	0.1119	0.2528	-0.28	0.0186	0.1263	0.34	0.1956	0.4904	0.11	0.2253	0.2955	-0.09
2369 Kynreninase	I16719	0.0042	0.0406	-0.53	0.0548	0.5877	-0.24	0.0000	-0.51	0.0025	0.0215	-0.61	0.0161	0.0908	-0.58	0.1299	0.2806	-0.56	0.3736	0.5243	-2.55	0.8708	1.0778	-0.33	0.0651	0.1523	2.06	
2370 L-2-hydroxyglutarate dehydrogenase mitochondrial	Q9H9P8	0.0458	0.1367	-0.15	0.4777	0.8039	0.04	0.0716	0.6889	0.04	0.0189	0.0851	-0.23	0.0638	0.1913	-0.16	0.2661	0.4590	-0.10	0.3736	0.4876	-2.55	0.8708	1.0107	-0.33	0.0651	0.1353	2.06
2371 Lactacystin-binding protein 1	Q8V120	0.3067	0.5077	-0.36	0.8787	0.9127	-0.05	0.6840	0.7333	0.13	0.6110	0.6581	-0.16	0.9965	0.9980	0.00	0.8707	1.0648	-0.07	0.3736	0.4362	-2.55	0.8708	0.9148	-0.33	0.0651	0.1140	2.06
2372 Lactoferrin	P02788	0.1713	0.3317	0.31	0.5027	0.8235	-0.19	0.2602	0.4294	0.16	0.7359	0.7723	-0.04	0.5755	0.6549	-0.04	0.7527	0.9016	0.15	0.0000	0.0000	0.0000	0.0000	1.09	0.0011	0.0419	0.71	
2373 Lactylglutathione lyase	Q04760	0.0415	0.1290	0.21	0.6760	0.7627	0.05	0.2214	0.3786	0.08	0.6888	0.7286	0.03	0.1342	0.3036	-0.11	0.0691	0.1848	0.16	0.8873	0.9069	-0.02	0.1089	0.3360	-0.21	0.0210	0.1238	-0.43
2374 Ladinin-1	O00515	0.0003	0.0154	-0.62	0.0155	0.4588	-0.26	0.0068	0.0399	-0.18	0.0069	0.0336	-0.19	0.0002	0.0140	-0.38	0.1456	0.3013	-0.19	0.3736	0.5180	-2.55	0.8708	1.0664	-0.33	0.0651	0.1493	2.06
2375 Lambda-crystallin homolog	Q9Y2S2	0.0007	0.0203	-1.17	0.0933	0.6309	-0.27	0.1048	0.2117	-0.25	0.0044	0.0992	-0.35	0.0553	0.1755	-0.36	0.0712	0.0855	-0.54	0.3736	0.5980	-2.55	0.8708	1.2093	-0.33	0.0651	0.1917	2.06
2376 Lamina-associated polypeptide 2 isoform alpha	P42166	0.0389	0.1238	0.09	0.3127	0.6806	0.16	0.0193	0.0667	0.15	0.0356	0.0905	0.09	0.0020	0.0349	-0.29	0.0435	0.6311	0.03	0.5223	0.5754	0.04	0.0822	0.2818	0.18	0.2488	0.3197	0.15
2377 Lamina-associated polypeptide 2 isoforms beta/gamma	P42167	0.0959	0.2185	-0.16	0.0927	0.5077	-0.28	0.0480	0.1216	-0.22	0.0140	0.0481	-0.39	0.0248	0.1139	-0.35	0.0209	0.0935	-0.38	0.1207	0.2907	0.18	0.9330	0.9514	0.01	0.2805	0.3523	0.09
2378 Lamin-B1	P20700	0.2073	0.3800	0.09	0.3291	0.6885	0.16	0.0140	0.0555	0.26	0.0283	0.0772	0.21	0.6816	0.7450	-0.02	0.0588	0.1671	0.18	0.0121	0.1039	0.37	0.4870	0.8977	0.06	0.0148	0.1046	0.47
2379 Lamin-B2	Q03252	0.4108	0.5591	-3.31	0.5752	0.7826	-1.75	0.5661	0.7059	-1.19	0.5388	0.6675	0.89	0.2938	0.4555	-1.88	0.9510	1.0735	0.09	0.0139	0.1109	0.37	0.1086	0.3354	0.02	0.1453	0.2074	0.29
2380 Laminin subunit alpha-5	I15230	0.2112	0.3841	0.05	0.1994	0.6638	0.15	0.0079	0.0419	0.19	0.0025	0.0212	0.24	0.4928	0.5824	0.02	0.0104	0.0699	0.17	0.0014	0.0497	-1.67	0.0093	0.0791	-1.16	0.0552	0.2077	-1.09
2381 Laminin subunit beta-1	P07942	0.0028	0.0355	0.16	0.0900	0.4357	0.26	0.2990	0.4809	0.05	0.8157	0.8407	-0.01	0.0002	0.0120	0.27	0.2319	0.4158	-0.16	0.1773	0.3769	0.59	0.0065	0.0656	0.83	0.135	0.1009	0.94
2382 L-aminooxidase-semialdehyde dehydrogenase-phosphopantetheinyl transferase	Q9NRN7	0.0015	0.0265	-0.45	0.1516	0.6605	-0.10	0.0723	0.1606	0.13	0.9276	0.9366	-0.01	0.4694	0.5603	0.04	0.1894	0.3627	-0.08	0.0578	0.1914	0.52	0.0171	0.1107	0.32	0.1097	0.1668	0.16
2383 LanC-like protein 2	Q9NS86	0.4108	0.5590	-3.31	0.5752	0.7824	-1.75	0.5661	0.7058	-1.19	0.5388	0.6674	0.89	0.2938	0.4554	-1.88	0.9510	1.0730	0.09	0.4081	0.4638	-0.05	0.7175	1.1622	-0.02	0.7398	0.7856	0.02
2384 L16850	I16850	0.0073	0.0504	-0.12	0.2557	0.6613	-0.12	0.0076	0.0413	-0.17	0.1569	0.7221	-0.01	0.0081	0.0649	-0.12	0.3914	0.6032	0.02	0.0086	0.0934	0.32	0.0246	0.1399	0.23	0.0062	0.0743	0.35
2385 Lanosterol synthase	P48449	0.4108	0.5588	-3.31	0.5752	0.7822	-1.75	0.5661	0.7056	-1.19	0.5388	0.6672	0.89	0.2938	0.4552	-1.88	0.9510	1.0728	0.09	0.0273	0.1431	0.39	0.0632	0.2414	0.26	0.0964	0.1514	0.10
2386 La-related protein 1	O6PKG0	0.0063	0.0476	0.13	0.0496	0.5735	0.20	0.0023	0.0270	0.31	0.0205	0.0615	0.20	0.0262	0.1171	0.08	0.0040	0.0601	0.21	0.2303	0.4576	0.12	0.0486	0.7951	0.06	0.0156	0.1732	-0.16
2387 La-related protein 1B	Q65934	0.0375	0.1216	0.26	0.0450	0.5658	0.36	0.0028	0.0293	0.58	0.0035	0.0239	0.52	0.0733	0.2069	0.19	0.0074	0.0650	0.54	0.3736	0.6205	-2.55	0.8708	1.2485	-0.33	0.0651	0.2054	2.06
2388 La-related protein 4	Q7JBC2	0.2400	0.4246	0.11	0.2177	0.7930	0.14	0.3399	0.5244	0.08	0.3165	0.2035	0.18	0.5566	0.6307	-0.05	0.3923	0.5917	0.08	0.3096	0.5609	0.79	0.5766	1.0070	0.49	0.4022	0.4737	0.62
2389 La-related protein 4B	Q9G215	0.4381	0.5156	-0.13	0.2737	0.6616	-0.48	0.2599	0.4178	0.22	0.4226	0.6146	0.29	0.1441	0.3184	-0.31	0.2602	0.4517	-0.23	0.1075	0.2677	0.22	0.0562	0.2265	0.30	0.1425	0.2039	0.20
2390 La-related protein 7	Q4G033	0.0593	0.1609	-1.50	0.1787	0.6645	-1.62	0.0599	0.1417	0.22	0.0171	0.0545	0.54	0.0157	0.0893													



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

			MCF-7				Gen SC20 vs control				SSE SC20 vs control				Dai IC20 vs control				Gen IC20 vs control				SSE IC20 vs control				MDA-MB-231				Dai IC20 vs control				Gen IC20 vs control				SSE IC20 vs control			
Protein name			UniProt	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC						
2429	LIM and senescent cell antigen-like-containing domain protein 2	Q7Z4I7	0.4108	0.5569	-3.31	0.5752	0.7796	-1.75	0.5661	0.7034	-1.19	0.5388	0.6652	0.89	0.2938	0.4535	-1.88	0.9510	1.0697	0.09	0.7976	0.8291	0.07	0.4461	0.8474	0.20	0.3468	0.4180	0.30													
2430	LIM and SH3 domain protein 1	Q14847	0.0061	0.0468	0.36	0.0778	0.6125	0.31	0.0011	0.0223	0.57	0.0013	0.0168	0.51	0.0146	0.0861	0.31	0.0045	0.0604	0.64	0.0652	0.2013	0.35	0.8244	1.2702	0.02	0.4553	0.5735	0.05													
2431	LIM domain and actin-binding protein 1	Q9U1H6	0.0005	0.0184	-0.29	0.2199	0.6607	-0.16	0.0034	0.0311	-0.30	0.2213	0.7591	0.02	0.0914	0.7541	0.01	0.0097	0.0701	0.17	0.3736	0.6150	-2.55	0.8708	1.2389	-0.33	0.0651	0.2019	2.06													
2432	LIM domain kinase 1	P53667	0.4108	0.5568	-3.31	0.5752	0.7794	-1.75	0.5661	0.7032	-1.19	0.5388	0.6650	0.89	0.2938	0.4533	-1.88	0.9510	1.0695	0.09	0.0226	0.1363	-0.20	0.2620	0.5808	0.06	0.6031	0.6634	0.02													
2433	LIM domain kinase 2	P53671	0.0128	0.0663	-0.33	0.5164	0.8391	-0.14	0.1345	0.2571	-0.15	0.5414	0.5929	-0.03	0.0552	0.1754	-0.09	0.2484	0.4369	-0.25	0.3736	0.4904	-2.55	0.8708	1.0159	-0.33	0.0651	0.1366	2.06													
2434	LIM domain only protein 7	Q8RWI1	0.4315	0.5090	-0.01	0.2440	0.6576	0.13	0.0001	0.0152	0.16	0.0044	0.0270	0.15	0.0455	0.1573	-0.12	0.0610	0.1714	0.23	0.5247	0.5777	-0.09	0.0057	0.0605	-0.28	0.1151	0.1728	-0.06													
2435	LIM/homeobox protein Lhx4	Q969G2	0.0486	0.1415	-0.24	0.3485	0.7041	-0.06	0.0236	0.0755	0.27	0.7713	0.8032	-0.02	0.4119	0.5069	-0.05	0.2079	0.3878	-0.09	0.3736	0.5010	-2.55	0.8708	1.0353	-0.33	0.0651	0.1413	2.06													
2436	Limbin	Q86UK5	0.4108	0.5566	-3.31	0.5752	0.7792	-1.75	0.5661	0.7030	-1.19	0.5388	0.6648	0.89	0.2938	0.4532	-1.88	0.9510	1.0693	0.09	0.0004	0.0351	0.84	0.0007	0.0261	0.87	0.0060	0.0738	0.97													
2437	LINE-1 retrotransposon element ORF1 protein	Q9UN81	0.7812	0.8221	-0.01	0.3531	0.7051	0.17	0.0220	0.0723	0.19	0.1041	0.1996	0.10	0.5392	0.6236	-0.02	0.8708	1.1064	-0.01	0.6526	0.6971	-0.06	0.8468	1.2890	0.02	0.9584	0.9666	-0.01													
2438	LINE-1 type transposase domain-containing protein 1	Q5T7N2	0.0417	0.1293	0.13	0.3101	0.6795	0.08	0.0079	0.0418	0.30	0.0125	0.0452	0.21	0.0389	0.1442	0.15	0.0064	0.0624	0.27	0.4079	0.4638	0.09	0.0871	0.2928	-0.14	0.4342	0.5051	-0.05													
2439	Lipid droplet-associated hydrolase	Q9H6V9	0.7306	0.7808	0.01	0.3574	0.7085	0.17	0.1082	0.2173	0.18	0.5907	0.6393	0.07	0.1406	0.3130	0.09	0.0468	0.1438	-0.13	0.3736	0.5634	-2.55	0.8708	1.1481	-0.33	0.0651	0.1722	2.06													
2440	Lipocalin-15	Q6UWW0	0.4108	0.5565	-3.31	0.5752	0.7790	-1.75	0.5661	0.7029	-1.19	0.5388	0.6647	0.89	0.2938	0.4531	-1.88	0.9510	1.0690	0.09	0.3585	0.6362	-0.26	0.3315	0.6882	-0.10	0.0841	0.1359	0.22													
2441	Lipocalin-2	Q86X29	0.1685	0.3269	0.12	0.4770	0.8035	0.11	0.0249	0.0783	0.26	0.0069	0.0335	0.39	0.6128	0.6869	0.03	0.0279	0.1068	0.33	0.3151	0.5770	0.08	0.1155	0.3489	-0.06	0.5175	0.5838	-0.02													
2442	Lipoma-preferred partner	Q93052	0.0010	0.0221	-0.31	0.6863	0.7708	0.06	0.0471	0.1202	-0.08	0.0003	0.0104	0.10	0.0005	0.0195	0.13	0.1070	0.2451	0.06	0.0118	0.1038	-0.18	0.0503	0.2111	-0.14	0.0488	0.1931	-0.10													
2443	Lipopolysaccharide-responsive and beige-like anchor protein	P50851	0.0648	0.1683	0.10	0.1113	0.6308	0.23	0.0272	0.0827	0.17	0.0023	0.0204	0.30	0.0070	0.0608	0.27	0.1003	0.0704	0.21	0.3736	0.6120	-2.55	0.8708	1.2338	-0.33	0.0651	0.2001	2.06													
2444	Liprin-alpha-1	Q13136	0.0049	0.0432	0.22	0.0774	0.6121	0.23	0.0583	0.1388	0.22	0.0001	0.0069	0.28	0.0112	0.0757	0.13	0.0003	0.0379	0.24	0.0050	0.0749	0.71	0.0142	0.0997	0.58	0.0161	0.1087	0.85													
2445	Liprin-alpha-3	Q75145	0.0784	0.1919	0.12	0.2276	0.6605	0.23	0.0043	0.0323	0.33	0.0050	0.0285	0.35	0.0926	0.2401	0.13	0.0081	0.0666	0.40	0.0086	0.0938	0.35	0.0025	0.0414	0.23	0.0281	0.1433	0.35													
2446	Liprin-beta-1	Q86W92	0.0000	0.0000	-0.33	0.1953	0.6682	-0.21	0.0054	0.0359	-0.12	0.0054	0.0295	-0.27	0.0066	0.0815	-0.02	0.0009	0.0436	-0.20	0.0454	0.1710	-0.22	0.0070	0.0687	-0.39	0.2481	0.3190	-0.18													
2447	L-lactate dehydrogenase A chain	P00338	0.0035	0.0382	0.46	0.1143	0.6326	0.49	0.0020	0.0251	0.56	0.0016	0.0179	0.58	0.0418	0.1512	0.23	0.0127	0.0759	0.48	0.0670	0.2034	0.39	0.1945	0.4893	0.17	0.9881	0.9906	0.00													
2448	L-lactate dehydrogenase B chain	P07195	0.0068	0.0491	-0.22	0.1780	0.6633	-0.18	0.0639	0.1473	-0.26	0.0266	0.0735	-0.16	0.0000	0.0000	-0.35	0.0020	0.0537	-0.15	0.0857	0.2341	0.41	0.5562	0.9820	0.07	0.2489	0.3198	-0.12													
2449	L-lactate dehydrogenase C chain	P07864	0.1453	0.2930	-0.22	0.0820	0.6156	-0.27	0.1410	0.2665	-0.21	0.1499	0.2651	-0.21	0.5123	0.6015	-0.08	0.0601	0.8975	-0.08	0.3406	0.6111	-0.11	0.0666	0.2489	0.16	0.7549	0.7980	0.03													
2450	LON peptidase N-terminal domain and RING finger protein 2	Q1L5Z9	0.2574	0.4458	0.04	0.2063	0.6601	-0.06	0.0213	0.0706	0.14	0.1656	0.2857	-0.07	0.0332	0.1329	-0.12	0.0188	0.0887	0.18	0.3736	0.5955	-2.55	0.8708	1.2048	-0.33	0.0651	0.1902	2.06													
2451	Lon protease homolog mitochondrial	P36776	0.0052	0.0442	0.29	0.1411	0.6532	0.38	0.0025	0.0277	0.46	0.0061	0.0314	0.40	0.1812	0.3737	0.08	0.0065	0.0622	0.36	0.3736	0.6231	-2.55	0.8708	1.2530	-0.33	0.0651	0.2070	2.06													
2452	Long-chain fatty acid transport protein 4	Q6P1M0	0.0006	0.0195	-2.09	0.1829	0.6649	-1.08	0.0130	0.0534	-1.15	0.0060	0.0311	-1.74	0.6523	0.7195	-0.05	0.0006	0.0393	-0.27	0.3736	0.6514	-2.55	0.8708	1.3018	-0.33	0.0651	0.2257	2.06													
2453	Long-chain-fatty-acid-CoA ligase 3	Q95Y73	0.3292	0.5359	0.05	0.2522	0.6621	0.16	0.0038	0.0249	0.36	0.0038	0.0249	0.36	0.0251	0.1143	0.24	0.0029	0.0548	0.74	0.0305	0.1478	0.38	0.0426	0.1904	0.12	0.1223	0.0957	0.12													
2454	Long-chain-fatty-acid-CoA ligase 4	Q60488	0.0454	0.1359	0.19	0.6641	0.7524	0.62	0.2297	0.3892	0.14	0.4176	0.6097	-0.04	0.0221	0.1073	-0.21	0.1369	0.2896	0.09	0.0207	0.1325	0.26	0.5768	1.0070	-0.03	0.0988	0.1542	0.16													
2455	Low affinity immunoglobulin epsilon Fc receptor	P06734	0.8672	0.8948	0.02	0.2086	0.6601	-0.18	0.6657	0.7169	0.05	0.0884	0.1770	-0.28	0.2122	0.4159	-0.20	0.5961	0.8323	-0.08	0.3736	0.4528	-2.55	0.8708	0.9460	-0.33	0.0651	0.1206	2.06													
2456	Low molecular weight phosphotyrosine protein phosphatase	P24666	0.4490	0.5267	-0.06	0.5313	0.8507	-0.08	0.0755	0.1652	-0.19	0.1540	0.2705	-0.14	0.1154	0.2782	-0.16	0.0419	0.8785	0.03	0.3736	0.4483	-2.55	0.8708	0.9376	-0.33	0.0651	0.1188	2.06													
2457	Low-density lipoprotein receptor-related protein 1B	Q9NZR2	0.4108	0.5563	-3.31	0.5752	0.7788	-1.75	0.5661	0.7027	-1.19	0.5388	0.6645	0.89	0.2938	0.4529	-1.88	0.9510	1.0688																							

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
2504 Malate dehydrogenase_mitochondrial	P40926	0.0015	0.0263	0.53	0.1724	0.6615	0.25	0.0223	0.0731
2505 Malactin	Q14165	0.7477	0.7946	0.01	0.2140	0.6626	0.11	0.0470	0.1202
2506 Malignant T-cell-amplified sequence 1	Q9ULC4	0.5097	0.5825	-0.06	0.8166	0.8689	0.03	0.2739	0.4476
2507 Malonyl-CoA decarboxylase_mitochondrial	P59322	0.5309	0.6018	0.09	0.0369	0.5493	0.33	0.5642	0.7884
2508 Malase-glucosylase_intestinal	Q42451	0.4108	0.5550	-3.31	0.5752	0.7769	-1.75	0.5661	0.7012
2509 Mannan-binding lectin serine protease 1	P48740	0.2605	0.4496	-0.10	0.3836	0.7305	-0.23	0.5925	0.6487
2510 Mannan-1-phosphate guanyltransferase beta	Q9Y5P6	0.0988	0.2234	0.12	0.8766	0.9113	0.02	0.0863	0.1831
2511 Mannose-6-phosphate isomerase	P34949	0.0055	0.0449	-0.13	0.6040	0.7072	0.02	0.1259	0.2454
2512 Mannosyl-oligosaccharide 1-2-alpha-mannosidase IB	O60476	0.2568	0.4449	0.06	0.1529	0.6584	0.27	0.0078	0.0417
2513 Mannosyl-oligosaccharide glucosidase	Q13724	0.4795	0.5543	-0.17	0.6876	0.7716	0.06	0.8267	0.8602
2514 MAP kinase-activated protein kinase 2	P49137	0.9898	0.9921	0.00	0.5587	0.8720	0.04	0.2107	0.3651
2515 MAP/microtubule affinity-regulating kinase 3	P27448	0.0965	0.2192	0.22	0.1985	0.6651	0.24	0.0621	0.1448
2516 MAP7 domain-containing protein 1	Q3KQU3	0.0326	0.1125	-1.06	0.0216	0.4782	-0.62	0.1561	0.2885
2517 MARCKS-related protein	P49006	0.6069	0.6716	-0.02	0.1242	0.6408	0.20	0.1518	0.2823
2518 Matrin-3	P43243	0.1011	0.2268	0.14	0.7910	0.8497	0.03	0.9389	0.9529
2519 Matrix metalloproteinase-15	P51511	0.0440	0.1333	0.21	0.0346	0.5318	0.24	0.7003	0.7475
2520 Matrix metalloproteinase-21	Q8N119	0.4108	0.5549	-3.31	0.5752	0.7767	-1.75	0.5661	0.7010
2521 Matrix-remodeling-associated protein 5	Q9NR89	0.0351	0.1169	0.23	0.2985	0.6729	0.12	0.0571	0.1367
2522 MBT domain-containing protein 1	O05BQ5	0.0551	0.1536	-12.77	0.0452	0.5642	-11.21	0.3827	0.5836
2523 Mdm2-binding protein	Q96DY7	0.0359	0.1184	-3.37	0.0340	0.5289	-0.62	0.0082	0.0427
2524 Mediator of DNA damage checkpoint protein 1	Q14676	0.0122	0.0640	-0.17	0.1098	0.6327	-0.09	0.4433	0.1131
2525 Mediator of RNA polymerase II transcription subunit 20	Q9J944	0.4108	0.5547	-3.31	0.5752	0.7765	-1.75	0.5661	0.7009
2526 Mediator of RNA polymerase II transcription subunit 23	Q9ULK4	0.0128	0.0662	-0.23	0.0205	0.4720	-0.54	0.0731	0.1619
2527 Mediator of RNA polymerase II transcription subunit 24	Q75448	0.9054	0.9263	0.01	0.9787	0.9855	0.00	0.0128	0.0129
2528 Medium-chain specific acyl-CoA dehydrogenase_mitochondrial	P11310	0.4108	0.5546	-3.31	0.5752	0.7763	-1.75	0.5661	0.7007
2529 Mesakarovoc-associated tyrosine-protein kinase	P42679	0.4108	0.5544	-3.31	0.5752	0.7761	-1.75	0.5661	0.7005
2530 Meskine-specific coiled-coil domain-containing protein MEIOC	AZURB1	0.0647	0.1682	-1.22	0.5846	0.6965	-0.54	0.2466	0.4163
2531 Meiosis-specific nuclear structural protein 1	Q8NEH6	0.5567	0.6255	0.05	0.2045	0.6596	0.24	0.0499	0.1249
2532 Melanoma inhibitory activity protein 2	Q96PC5	0.5563	0.6252	0.03	0.6888	0.7321	-0.04	0.0427	0.1120
2533 Melanoma-associated antigen B18	Q96M61	0.1104	0.2412	0.21	0.0045	0.5522	0.44	0.5986	0.6546
2534 Melanoma-associated antigen D1	Q9Y5V3	0.8173	0.8529	-0.01	0.1761	0.6615	0.27	0.5157	0.7361
2535 Melanoma-associated antigen D2	Q9UNF1	0.3727	0.5875	0.02	0.0663	0.6300	0.17	0.0036	0.0318
2536 Melanophilin	Q9BV36	0.5194	0.5913	0.10	0.2555	0.6627	0.21	0.4041	0.6087
2537 Melanoregulin	Q8NS65	0.0649	0.1685	-0.24	0.0667	0.5937	-0.27	0.0349	0.0971
2538 Membrane magnesium transporter 1	Q8N4V1	0.0034	0.0382	-0.24	0.0181	0.4688	-0.29	0.0042	0.0326
2539 Membrane-associated progesterone receptor component 1	O00264	0.1602	0.3149	-0.08	0.0738	0.6117	0.27	0.0009	0.0217
2540 Membrane-associated progesterone receptor component 2	O15173	0.3470	0.5560	0.05	0.1452	0.6569	0.16	0.1807	0.3244
2541 Merlin	P35240	0.0907	0.2108	-1.21	0.4319	0.7680	-0.61	0.4045	0.6091
2542 Mesencephalic astrocyte-derived neurotrophic factor	P55145	0.1732	0.3345	0.08	0.2085	0.6066	0.17	0.2943	0.4749
2543 Metabotropic glutamate receptor 1	Q13255	0.4108	0.5543	-3.31	0.5752	0.7759	-1.75	0.5661	0.7004
2544 Metallothionein-1E	P04732	0.4108	0.5542	-3.31	0.5752	0.7757	-1.75	0.5661	0.7002
2545 Metallothionein-1F	P04733	0.4108	0.5540	-3.31	0.5752	0.7755	-1.75	0.5661	0.7000
2546 Metallothionein-1M	Q8N139	0.0337	0.1146	0.18	0.5308	0.8248	-1.91	0.7232	0.7675
2547 Metallothionein-1X	P08297	0.4108	0.5539	-3.31	0.5752	0.7753	-1.75	0.5661	0.6999
2548 Metallothionein-2	P02795	0.4108	0.5537	-3.31	0.5752	0.7751	-1.75	0.5661	0.6997
2549 Metal-response element-binding transcription factor 2	Q9Y483	0.0943	0.2164	0.08	0.3766	0.7239	0.06	0.8368	0.8685
2550 Metastasis-associated protein MTA1	Q13330	0.0528	0.1490	-1.85	0.1516	0.6599	-1.39	0.3615	0.5591
2551 Metastasis-associated protein MTA2	Q94776	0.0013	0.0248	0.19	0.0673	0.5909	0.33	0.0231	0.0749
2552 Metastasis-associated protein MTA3	Q9BTC8	0.0001	0.0110	-0.95	0.1411	0.6538	0.26	0.0004	0.0197
2553 Metaxin-1	Q13505	0.0612	0.1637	0.25	0.4755	0.8026	0.15	0.7227	0.8130
2554 Metaxin-2	Q75431	0.4108	0.5536	-3.31	0.5752	0.7749	-1.75	0.5661	0.6995
2555 Methanethiol oxidase	Q13228	0.0044	0.0418	0.25	0.2017	0.6600	0.15	0.3961	0.5987
2556 Methionine adenosyltransferase 2 subunit beta	Q9NZL9	0.0036	0.0384	0.22	0.0409	0.7509	0.11	0.0043	0.0322
2557 Methionine aminopeptidase 1	P35382	0.5462	0.6157	-0.06	0.4435	0.7793	-0.05	0.0600	0.1417
2558 Methionine aminopeptidase 2	P50579	0.4975	0.5715	0.06	0.0495	0.5736	0.36	0.0369	0.1008
2559 Methionine synthase reductase	Q9UBK8	0.0480	0.1409	-0.20	0.2524	0.6623	0.21	0.6893	0.7380
2560 Methionine-tRNA ligase_cytoplasmic	P56192	0.0016	0.0273	0.33	0.2120	0.6627	0.19	0.0016	0.0233
2561 Methionyl-tRNA formyltransferase_mitochondrial	Q96DP5	0.4108	0.5534	-3.31	0.5752	0.7747	-1.75	0.5661	0.6994
2562 Methylated-DNA-protein-cysteine methyltransferase	P16455	0.5088	0.5818	-0.06	0.8362	0.8818	0.02	0.3223	0.5098
2563 Methyl-CpG-binding domain protein 4	Q9Y5243	0.4108	0.5533	-3.31	0.5752	0.7745	-1.75	0.5661	0.6992
2564 Methyl-CpG-binding domain protein 5	Q9P267	0.0665	0.1709	-0.07	0.2371	0.6624	-0.10	0.0488	0.1229
2565 Methylcrotonyl-CoA carboxylase beta chain_mitochondrial	Q9HCC0	0.1732	0.3344	-0.09	0.4318	0.7526	0.14	0.1617	0.2968
2566 Methylcrotonyl-CoA carboxylase subunit alpha_mitochondrial	Q96RQ3	0.0168	0.0759	0.12	0.1397	0.6537	0.21	0.0948	0.1959
2567 Methylcrotonyl-CoA carboxylase subunit beta_mitochondrial	Q6N021	0.0265	0.0985	-0.13	0.3317	0.6912	-0.12	0.4398	0.6513
2568 Methylmalonate-semialdehyde dehydrogenase [acylating]_mitochondrial	Q02252	0.2055	0.3780	-0.05	0.3411	0.7000	0.16	0.3021	0.4849
2569 Methylmalonyl-CoA mutase_mitochondrial	P22033	0.0466	0.1381	0.10	0.0916	0.6293	0.20	0.0333	0.0944
2570 Methylmalonate protein 50	Q9BQA1	0.2800	0.4735	0.23	0.8806	0.9143	-0.10	0.5326	0.7536
2571 Methylmalonate protein pLcn	P54105	0.9569	0.9677	0.00	0.5051	0.5742	-0.23	0.0557	0.1349
2572 Methylsterol monooxygenase 1	Q15800	0.0054	0.0445	0.25	0.0093	0.4420	0.33	0.0003	0.0232
2573 Methylthioribose-1-phosphate isomerase	Q9BV20	0.1647	0.3218	0.09	0.9720	0.9811	0.00	0.0985	0.2018
2574 Methylthioribose-1-phosphate dehydratase	Q96GX9	0.0426	0.1307	0.19	0.0339	0.5305	0.28	0.0325	0.0928
2575 Methyltransferase-like protein 2A	Q96Z16	0.4108	0.5531	-3.31	0.5752	0.7743	-1.75	0.5661	0.6990
2576 Methyltransferase-like protein 2B	Q6P1Q9	0.4567	0.5338	-0.03	0.0546	0.5668	-0.10	0.0669	0.1522
2577 MHC class I polypeptide-related sequence B	Q29980	0.4108	0.5530	-3.31	0.5752	0.7741	-1.75	0.5661	0.6989
2578 MICOS complex subunit MIC19	Q9NX63	0.3102	0.5114	0.05	0.9659	0.9766	-0.01	0.0702	0.1575
2579 MICOS complex subunit MIC60	Q16891	0.0221	0.0886	0.24	0.4040	0.7479	0.19	0.0078	0.0416

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7			MDA-MB-231		
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control
		p value BH q value log2FC	p value BH q value log2FC	p value BH q value log2FC	p value BH q value log2FC	p value BH q value log2FC	p value BH q value log2FC
2580 Microtubule-associated protein 1	P55081	0.0082	0.0537	0.43	0.0014	0.2133	0.45
2581 Microtubule-associated protein 3-like	U7121	0.0129	0.0664	-0.26	0.0015	0.4784	0.33
2582 Microprocessor complex subunit DCCR8	Q8WYQ5	0.0084	0.0543	-0.47	0.2086	0.6605	-0.16
2583 Microsomal glutathione S-transferase 3	I14880	0.1963	0.3651	-0.21	0.0056	0.3817	-1.05
2584 Microtubule cross-linking factor 1	Q9Y4B5	0.4108	0.5529	-3.31	0.5752	0.7739	-1.75
2585 Microtubule-actin cross-linking factor 1 isoforms 1/2/3/5	Q9UPN3	0.1721	0.3331	-0.10	0.7443	0.8146	0.06
2586 Microtubule-associated protein 1A	P78559	0.0273	0.1002	-0.75	0.0620	0.5915	-0.83
2587 Microtubule-associated protein 1B	P46821	0.0016	0.0272	-0.89	0.4692	0.7990	-0.08
2588 Microtubule-associated protein 2	P11137	0.4108	0.5527	-3.31	0.5752	0.7737	-1.75
2589 Microtubule-associated protein 4	P27816	0.1854	0.3500	0.10	0.3537	0.7055	0.11
2590 Microtubule-associated protein 9	Q49MG5	0.4108	0.5526	-3.31	0.5752	0.7735	-1.75
2591 Microtubule-associated protein RP/EB family member 1	Q15691	0.4790	0.5538	0.05	0.4215	0.7592	0.14
2592 Microtubule-associated protein RP/EB family member 3	Q9UPY8	0.0181	0.0789	0.39	0.4537	0.7871	0.12
2593 Microtubule-associated protein tau	P10636	0.2355	0.4186	-0.07	0.1374	0.6512	0.41
2594 Microtubule-associated proteins 1A/1B light chain 3A	Q9H492	0.5658	0.6337	0.03	0.1531	0.6504	0.30
2595 Microtubule-associated serine/threonine-protein kinase 4	O15021	0.5341	0.6046	-0.01	0.0793	0.6140	0.11
2596 Microtubule-associated tumor suppressor candidate 2	Q5JR59	0.1963	0.3650	0.03	0.7442	0.8148	0.04
2597 Midline	P21741	0.7082	0.7603	-0.02	0.4595	0.7910	0.07
2598 MIF4G domain-containing protein	A0U1W6	0.7852	0.8255	-0.02	0.5749	0.8860	-0.03
2599 Mini-chromosome maintenance complex-binding protein	Q9BTB3	0.4582	0.5350	0.03	0.0796	0.6118	0.08
2600 Minor histocompatibility antigen H13	Q8TC79	0.0166	0.0752	0.39	0.0243	0.4841	0.54
2601 Mirror-image polydactyl gene 1 protein	Q8TD10	0.6078	0.6724	0.02	0.2169	0.6597	-0.24
2602 Misl 8-binding protein 1	Q6P0N0	0.4108	0.5524	-3.31	0.5752	0.7733	-1.75
2603 Mitochondrial repair endonuclease PMS2	P54278	0.0300	0.1064	-0.22	0.4760	0.8026	-0.05
2604 Missapen-like kinase 1	Q8N4C8	0.4108	0.5523	-3.31	0.5752	0.7731	-1.75
2605 Mitochondrial 2-oxoglutarate/malate carrier protein	Q02978	0.4540	0.5315	-0.04	0.2662	0.6626	0.21
2606 Mitochondrial antiviral-signaling protein	Q7Z434	0.0118	0.0628	-0.39	0.1044	0.6332	-0.31
2607 Mitochondrial cardiolipin hydrolase	Q8N2A8	0.0372	0.1213	0.43	0.0936	0.7615	-0.21
2608 Mitochondrial carrier homolog 2	Q9Y6C9	0.0545	0.1527	0.16	0.2404	0.6606	0.22
2609 Mitochondrial chaperone BC51	Q9Y276	0.4108	0.5521	-3.31	0.5752	0.7729	-1.75
2610 Mitochondrial dicarboxylate carrier	Q9UBX3	0.9674	0.9761	0.00	0.5008	0.8228	0.11
2611 Mitochondrial fission 1 protein	Q9Y3D6	0.7371	0.7863	-0.01	0.2189	0.6596	0.24
2612 Mitochondrial fission factor	Q9GZY8	0.5393	0.6097	-0.06	0.0615	0.5921	-0.31
2613 Mitochondrial genome maintenance exonuclease 1	Q9BOP7	0.8185	0.8538	0.01	0.0439	0.5685	0.17
2614 Mitochondrial glutamate carrier 1	Q9H936	0.0652	0.1690	-0.10	0.1806	0.6616	-0.09
2615 Mitochondrial import inner membrane translocase subunit Tim10	P62072	0.4524	0.5299	-0.07	0.0589	0.8633	-0.02
2616 Mitochondrial import inner membrane translocase subunit Tim13	Q9Y5L4	0.0054	0.0445	0.29	0.5627	0.8766	0.06
2617 Mitochondrial import inner membrane translocase subunit TIM14	Q96DA6	0.7442	0.7919	0.02	0.1713	0.6612	-0.13
2618 Mitochondrial import inner membrane translocase subunit Tim23	O14925	0.4108	0.5520	-3.31	0.5752	0.7727	-1.75
2619 Mitochondrial import inner membrane translocase subunit TIM44	O43615	0.0281	0.1019	0.17	0.3424	0.7002	0.23
2620 Mitochondrial import inner membrane translocase subunit TIM50	Q3ZCQ8	0.0153	0.0716	0.14	0.3016	0.6751	0.04
2621 Mitochondrial import inner membrane translocase subunit Tim8 A	O60220	0.6462	0.7078	0.04	0.5984	0.7019	-0.06
2622 Mitochondrial import inner membrane translocase subunit Tim9	Q9Y517	0.1470	0.2950	0.07	0.4418	0.7776	0.14
2623 Mitochondrial import receptor subunit TOM22 homolog	Q9NS69	0.0051	0.0437	-0.12	0.8447	0.8884	-0.03
2624 Mitochondrial import receptor subunit TOM34	Q15785	0.0248	0.0950	0.16	0.0745	0.6116	0.29
2625 Mitochondrial import receptor subunit TOM40 homolog	Q96008	0.0266	0.0988	0.14	0.0842	0.4124	-0.29
2626 Mitochondrial import receptor subunit TOM7 homolog	Q9P0U1	0.0074	0.0507	-0.26	0.0032	0.2858	-0.45
2627 Mitochondrial import receptor subunit TOM70	Q94826	0.0038	0.0393	0.18	0.2100	0.6621	0.12
2628 Mitochondrial inner membrane protein OXA1L	Q15070	0.0358	0.1184	0.13	0.1219	0.6385	0.17
2629 Mitochondrial ornithine transporter 1	Q9Y419	0.3746	0.5898	-0.11	0.1455	0.6554	-0.22
2630 Mitochondrial proton/calcium exchanger protein	Q95202	0.0013	0.0218	0.19	0.0460	0.5607	0.14
2631 Mitochondrial Rho GTPase 2	Q8X1I1	0.0041	0.0402	-0.28	0.9959	0.9974	0.00
2632 Mitochondrial ribonuclease P catalytic subunit	O15091	0.4101	0.6317	-0.08	0.4716	0.8004	0.07
2633 Mitochondrial tRNA-specific 2-thiouridylase 1	Q75648	0.4975	0.5714	0.03	0.2979	0.6724	-0.12
2634 Mitochondrial-processing-peptidase subunit alpha	Q10713	0.0052	0.0441	0.37	0.2480	0.6585	0.27
2635 Mitochondrial-processing-peptidase subunit beta	Q75439	0.8213	0.8563	-0.01	0.5784	0.6872	0.07
2636 Mitogen-activated protein kinase 1	P28482	0.3478	0.5567	0.13	0.3516	0.7043	-0.21
2637 Mitogen-activated protein kinase 14	Q16539	0.0898	0.2096	-0.09	0.2437	0.6592	0.17
2638 Mitogen-activated protein kinase 3	P27361	0.2647	0.4563	0.04	0.2570	0.7775	0.04
2639 Mitogen-activated protein kinase 9	P45984	0.0337	0.1145	-0.30	0.3071	0.6775	-0.24
2640 Mitogen-activated protein kinase kinase 1	Q13233	0.4968	0.5710	-0.10	0.9473	0.9652	0.01
2641 Mitogen-activated protein kinase kinase kinase 12	Q12852	0.0035	0.0381	0.68	0.1441	0.6548	0.10
2642 Mitogen-activated protein kinase kinase kinase 13	O43283	0.0067	0.0491	1.06	0.7960	0.8519	0.17
2643 Mitogen-activated protein kinase kinase kinase 15	Q6ZN16	0.0612	0.1637	0.10	0.1590	0.6637	0.07
2644 Mitogen-activated protein kinase kinase kinase 2	Q9Y2U5	0.0009	0.0219	-0.47	0.6161	0.7162	-0.06
2645 Mitogen-activated protein kinase kinase kinase 20	Q9NYL2	0.4108	0.5519	-3.31	0.5752	0.7725	-1.75

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
2646 Mitogen-activated protein kinase kinase kinase 3	Q9Y979	0.2360	0.4192	-0.05	0.3707	0.7189	-0.07	0.3474	0.5412	-0.05	0.2224	0.3623	-0.05	0.1867	0.3823	-0.08	0.1189	0.2633	0.14	0.0605	0.1948	0.35	0.0423	0.1899	0.22	0.1732	0.2391	0.10
2647 Mitogen-activated protein kinase kinase kinase 4	Q9Y6R4	0.0625	0.1656	0.22	0.4244	0.7607	0.02	0.0052	0.0351	-0.15	0.5975	0.6456	-0.01	0.0026	0.0390	-0.11	0.8935	1.1302	0.02	0.1767	0.3761	0.20	0.8820	0.9110	0.02	0.4248	0.4963	-0.10
2648 Mitogen-activated protein kinase kinase kinase 7	Q43318	0.7344	0.7840	-0.01	0.9482	0.9653	0.00	0.4631	0.6799	0.03	0.2827	0.4417	-0.06	0.9703	0.9771	0.00	0.3080	0.5070	-0.12	0.3736	0.4803	-2.55	0.8708	0.9973	-0.33	0.0651	0.1321	2.06
2649 Mitotic checkpoint protein BUB3	Q43684	0.0742	0.1847	0.13	0.3414	0.6998	0.18	0.0675	0.1530	0.14	0.0499	0.1149	-0.16	0.2780	0.5032	-0.06	0.1352	0.2871	0.10	0.1274	0.3008	0.21	0.5032	0.9198	0.06	0.2392	0.3096	-0.11
2650 Mitotic spindle assembly checkpoint protein MAD1	Q9Y6D9	0.0655	0.1694	0.21	0.2432	0.6591	0.19	0.0077	0.0416	0.27	0.0127	0.0456	0.15	0.0177	0.0954	0.13	0.0375	0.1253	0.12	0.0020	0.0537	-0.32	0.4293	0.8258	0.04	0.0920	0.0496	-0.54
2651 Mitotic spindle assembly checkpoint protein MAD2A	Q13257	0.4108	0.5517	-3.31	0.5752	0.7723	-1.75	0.5661	0.6974	-1.19	0.5388	0.6595	0.89	0.2938	0.4487	-1.88	0.9510	1.0614	0.09	0.1383	0.3181	0.18	0.7219	1.1668	0.04	0.6594	0.7144	-0.03
2652 Mixed lineage kinase domain-like protein	Q8N816	0.4108	0.5516	-3.31	0.5752	0.7721	-1.75	0.5661	0.6972	-1.19	0.5388	0.6593	0.89	0.2938	0.4485	-1.88	0.9510	1.0612	0.09	0.3784	0.4341	0.09	0.4610	0.8068	-0.08	0.2895	0.3164	-0.09
2653 MMS19 nucleotide excision repair protein homolog	Q96T76	0.4533	0.5308	-0.04	0.6684	0.7561	0.06	0.8248	0.8584	-0.02	0.1438	0.2562	0.09	0.2242	0.4329	-0.07	0.7931	1.0307	-0.02	0.3736	0.4390	-2.55	0.8708	0.9202	-0.33	0.0651	0.1151	2.06
2654 MOB kinase activator 1B	Q7L9L4	0.3688	0.5828	-0.05	0.5441	0.8692	0.10	0.9303	0.9458	0.00	0.0730	0.1525	0.13	0.1170	0.2802	-0.11	0.1399	0.2934	-0.11	0.5320	0.5843	0.03	0.9772	0.9838	0.00	0.1059	0.1622	-0.11
2655 MOB-like protein p130cas	Q9Y3A3	0.1320	0.2739	0.18	0.7857	0.8456	-0.03	0.6673	0.7180	-0.05	0.1851	0.3122	0.23	0.1307	0.2986	-0.20	0.9120	1.1489	-0.01	0.0000	0.0000	1.13	0.0001	0.0192	1.05	0.0201	0.1219	1.04
2656 Moesin	P26038	0.0140	0.0693	0.25	0.1705	0.6611	0.18	0.0514	0.1273	0.17	0.0464	0.1094	0.18	0.1333	0.3022	0.10	0.0289	0.1090	0.25	0.0224	0.1360	-2.55	0.8708	0.9333	-0.33	0.0651	0.1294	0.19
2657 Molybdopter synthase catalytic subunit	Q96007	0.0971	0.2204	0.16	0.3486	0.7037	0.06	0.0576	0.1374	0.17	0.0978	0.1909	0.14	0.7998	0.8438	0.02	0.2015	0.3787	0.09	0.3736	0.5020	-2.55	0.8708	1.0372	-0.33	0.0651	0.1418	2.06
2658 Monoacylglycerol lipase ABHD12	Q8N2K0	0.0457	0.1368	-0.20	0.6992	0.7784	0.05	0.2584	0.4268	-0.11	0.2769	0.4348	0.08	0.0465	0.1584	-0.21	0.6801	0.9193	-0.05	0.3736	0.4460	-2.55	0.8708	0.9333	-0.33	0.0651	0.1179	2.06
2659 Monocarboxylate transporter 1	P53985	0.4108	0.5514	-3.31	0.5752	0.7719	-1.75	0.5661	0.6970	-1.19	0.5388	0.6592	0.89	0.2938	0.4484	-1.88	0.9510	1.0610	0.09	0.0007	0.0398	0.80	0.0204	0.0417	0.59	0.0178	0.1144	0.33
2660 Monocarboxylate transporter 4	O15427	0.4108	0.5513	-3.31	0.5752	0.7717	-1.75	0.5661	0.6969	-1.19	0.5388	0.6590	0.89	0.2938	0.4483	-1.88	0.9510	1.0608	0.09	0.0928	0.2446	0.27	0.2038	0.5032	0.15	0.2263	0.2967	0.14
2661 Monofunctional C1-tetrahydrofolate synthase, mitochondrial	Q6UB35	0.0018	0.0292	0.24	0.0972	0.6341	0.22	0.0004	0.0216	0.32	0.0012	0.0166	0.23	0.0384	0.1429	0.08	0.0033	0.0576	0.18	0.3058	0.5653	0.12	0.2046	0.5042	0.19	0.2646	0.3364	-0.13
2662 MORC family CW-type zinc finger protein 4	Q8TE76	0.4108	0.5511	-3.31	0.5752	0.7715	-1.75	0.5661	0.6967	-1.19	0.5388	0.6589	0.89	0.2938	0.4481	-1.88	0.9510	1.0605	0.09	0.0275	0.1435	-0.30	0.0527	0.2177	-0.18	0.1205	0.1790	-0.13
2663 MORN repeat-containing protein 2	Q502X0	0.0487	0.1415	0.17	0.2032	0.6603	0.12	0.0128	0.0531	-0.29	0.1229	0.2266	0.11	0.0343	0.1354	-0.21	0.7105	0.9513	0.03	0.3736	0.4449	-2.55	0.8708	0.9312	-0.33	0.0651	0.1174	2.06
2664 Mortalin family class 1 protein 2	Q15014	0.0264	0.0985	0.29	0.6050	0.7076	-0.04	0.0774	0.1682	-0.15	0.6263	0.6727	-0.03	0.0089	0.0673	-0.35	0.5613	0.7961	-0.04	0.3736	0.4558	-2.55	0.8708	0.9516	-0.33	0.0651	0.1218	2.06
2665 Motilin receptor	Q43193	0.0229	0.0904	0.49	0.0237	0.4852	0.86	0.0273	0.0829	-0.99	0.0288	0.0781	6.49	0.0298	0.1257	-5.83	0.0323	0.1160	5.30	0.3736	0.5791	-2.55	0.8708	1.1759	-0.33	0.0651	0.1808	2.06
2666 M-phase inducer phosphatase 1	P30304	0.4108	0.5510	-3.31	0.5752	0.7713	-1.75	0.5661	0.6965	-1.19	0.5388	0.6587	0.89	0.2938	0.4480	-1.88	0.9510	1.0603	0.09	0.0028	0.0587	1.20	0.0003	0.0199	1.17	0.0013	0.0458	0.56
2667 M-phase inducer phosphatase 3	P30307	0.0027	0.0350	-0.74	0.0515	0.8229	-0.21	0.0480	0.1216	-0.43	0.0249	0.0704	-0.64	0.0919	0.2390	0.22	0.0077	0.0659	-0.79	0.3736	0.6197	-2.55	0.8708	1.2471	-0.33	0.0651	0.2049	2.06
2668 M-phase phosphoprotein 9	Q9Y550	0.4608	0.5376	0.05	0.8663	0.9031	0.03	0.0094	0.0451	0.29	0.3070	0.4739	0.07	0.0058	0.0558	-0.47	0.3288	0.5316	-0.06	0.0065	0.0844	0.36	0.0224	0.1304	0.27	0.0058	0.0724	0.62
2669 MRG/MORF4L-binding protein	Q9NV56	0.0740	0.1844	-0.19	0.5299	0.8488	0.05	0.3624	0.5602	0.02	0.0126	0.0454	-0.24	0.1168	0.2801	-0.10	0.0043	0.0602	-0.27	0.3736	0.6331	-2.55	0.8708	1.2703	-0.33	0.0651	0.2134	2.06
2670 mRNA (2'-O-methyladenosine-N(6)-1-methyltransferase	Q9H4Z3	0.0610	0.1634	0.25	0.1974	0.6705	0.15	0.0102	0.0210	0.25	0.9097	0.9216	-0.02	0.4719	0.5626	-0.10	0.9236	1.1604	-0.01	0.0818	0.2282	0.26	0.6917	1.1339	-0.04	0.8269	0.8599	-0.01
2671 mRNA cap guanine-N7 methyltransferase	Q43148	0.7949	0.8339	0.02	0.3154	0.6810	0.07	0.2979	0.4792	0.08	0.0422	0.1022	0.09	0.2546	0.4742	0.04	0.3025	0.5005	0.14	0.0778	0.2218	0.19	0.0508	0.2127	-0.22	0.0148	0.1049	-0.26
2672 mRNA export factor	P78406	0.2459	0.4315	-0.03	0.8988	0.9280	-0.02	0.5935	0.6497	-0.02	0.8635	0.8826	0.00	0.0156	0.0888	-0.10	0.5899	0.8265	-0.03	0.0115	0.1038	-0.35	0.0130	0.0950	-0.34	0.0420	0.1780	-0.27
2673 mRNA turnover protein 4 homolog	Q9UKD2	0.4506	0.5282	-0.11	0.6903	0.7733	0.07	0.7207	0.7656	-0.05	0.6308	0.6768	0.07	0.4225	0.5171	0.12	0.4703	0.6929	-0.10	0.0824	0.2295	0.29	0.4310	0.8278	0.07	0.0337	0.1568	0.28
2674 mRNA-capping enzyme	O60942	0.0010	0.0220	1.24	0.1135	0.6335	0.71	0.0937	0.1941	0.65	0.0193	0.0590	0.76	0.1350	0.3047	0.10	0.0311	0.1133	0.91	0.2866	0.5379	-0.42	0.1414	0.4005	-0.35	0.1079	0.1643	0.12
2675 Mx2-interacting protein	Q96T58	0.0379	0.1222	-0.11	0.1352	0.6503	-0.32	0.5104	0.7314	-0.05	0.0728	0.1523	-0.26	0.0673	0.1974	-0.26	0.7879	1.0255	-0.01	0.3736	0.4395	-2.55	0.8708	0.9211	-0.33	0.0651	0.1153	2.06
2676 Myt9/38 domain-containing protein	Q9H7C9	0.4108	0.5509	-3.31	0.5752	0.7711	-1.75	0.5661	0.6964	-1.19	0.5388	0.6586	0.89	0.2938	0.4479	-1.88	0.9510	1.0601	0.09	0.2708	0.5138	0.18	0.2948	0.6363	-0.16	0.1223	0.1813	-0.30
2677 Mucin-1	P15941	0.7495	0.7959	0.01	0.6157	0.7161	-0.02	0.0095	0.0454	0.27	0.5736	0.6230	0.03	0.0036	0.0444	-0.26	0.6399	0.8769	-0.40	0.3736	0.4485	-2.55	0.8708	0.9380	-0.33	0.0651	0.1189	2.06
2678 Mucopolip-2	Q8IZK6	0.0018	0.0291	1.58	0.0567	0.9713	-0.02	0.3050	0.4882	-0.74	0.8368	0.8595	-0.07	0.5751	0.6547	0.13	0.0325	0.1160	0.72	0.3736	0.5784	-2.55	0.8708	1.1747	-0.33	0.0651	0.1804	2.06
2679 Multidrug resistance protein 1	P08183	0.7357	0.7851	-0.02	0.2299	0.6609	0.15	0.8769	0.9025	-0.01	0.0919	0.1820	0.06	0.1088	0.2677	0.13	0.2168	0.3982	0.02	0.3736	0.4989	-2.55	0.8708	1.0315	-0.33	0.0651	0.1404	2.06
2680 Multifunctional methyltransferase subunit TRM112-like protein	Q9UI30	0.9168	0.9365	0.01	0.7192	0.7942	-0.03	0.3155	0.5022	-0.07	0.9939	0.9945	0.00	0.5643	0.6461	0.04	0.7697	1.0073	-0.02	0.1718	0.3691	0.06	0.1715	0.4537	0.08	0.7993	0.8363	0.02
2681 Multifunctional procollagen lysine hydroxylase and aldosyltransferase LH3	O60568	0.0073	0.0503	0.16	0.0852	0.6207	0.24	0.0060	0.0376	0.24	0.0213	0.0631	0.14	0.0805	0.2188	0.07	0.0065	0.0625	0.19	0.0586	0.1929	0.37	0.1808	0.4680	0.09	0.0464	0.1884	0.10
2682 Multifunctional protein ADE2	P22234	0.0145	0.0699	0.25	0.0616	0.5920	0.18	0.0068	0.0398	0.30	0.0102	0.0405	0.26	0.1052	0.2609	0.11	0.0384	0.1274	0.19	0.2668	0.5092	0.17	0.6158	1.0500	-0.05	0.1236	0.1829	-0.14
2683 Multivesicular body subunit 12A	Q96EY5	0.0177	0.0780	-0.27	0.2787	0.6650	-0.48	0.0008	0.0206	-0.77	0.0004	0.0126	-1.39	0.0593	0.1836	-0.33	0.0521	0.1541	-1.25	0.3736	0.5593	-2.55	0.8708	1.1408	-0.33	0.0651	0.1701	2.06
2684 Musklennin	Q9UL63	0.8384	0.8707	-0.02	0.4328	0.7688	-0.31	0.7164	0.7617</																			

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
2721 Myotrophin	P58546	0.0037	0.0388	0.21	0.1056	0.6309	0.27	0.0370	0.1009
2724 Myotubularin-related protein 14	QNCCE2	0.4108	0.5491	-3.31	0.5752	0.7687	-1.75	0.5661	0.6944
2725 Myotubularin-related protein 4	Q9NYA4	0.0070	0.0495	-0.29	0.3361	0.6950	-0.06	0.6368	0.6898
2726 Myotubularin-related protein 5	Q95248	0.3341	0.5407	0.06	0.1384	0.6506	-0.15	0.5225	0.7438
2727 Myotubularin-related protein 7	Q9V216	0.1911	0.3449	-0.24	0.0643	0.5916	-0.44	0.0235	0.0754
2728 Myotubularin-related protein 8	Q96F00	0.0003	0.0152	4.14	0.7974	0.8529	0.19	0.0326	0.0928
2729 Myristoylated alanine-rich C-kinase substrate	T29966	0.4108	0.5490	-3.31	0.5752	0.7687	-1.75	0.5661	0.6944
2730 N(G)-N(G)-dimethylarginine dimethylaminohydrolase 1	Q94760	0.4108	0.5489	-3.31	0.5752	0.7683	-1.75	0.5661	0.6941
2731 N(G)-N(G)-dimethylarginine dimethylaminohydrolase 2	O95865	0.0196	0.0821	-0.18	0.1697	0.6624	0.19	0.0336	0.0950
2732 N6-adenosine-methyltransferase catalytic subunit	Q86U44	0.5072	0.5802	0.06	0.9780	0.9856	0.00	0.0914	0.1904
2733 N6-adenosine-methyltransferase non-catalytic subunit	Q9HCES	0.0138	0.0689	9.31	0.5732	0.8852	-1.75	0.2310	0.3905
2734 Na(+)/H(+) exchange regulatory cofactor NHE-RF1	I14745	0.0274	0.1002	0.23	0.2977	0.6725	0.25	0.0109	0.0483
2735 NAC-alpha domain-containing protein 1	I15069	0.0064	0.0480	-0.31	0.1548	0.6611	-0.31	0.0701	0.1574
2736 N-acetyl-D-glucosamine kinase	Q9UJ70	0.4848	0.5593	0.04	0.3019	0.6749	0.07	0.9651	0.9717
2737 N-acetylglucosamine-6-sulfatase	P15586	0.0877	0.2063	0.12	0.0076	0.4017	0.29	0.4594	0.6753
2738 NACHT domain- and WD repeat-containing protein 1	I149M9	0.6836	0.7400	0.01	0.1326	0.6480	0.09	0.0339	0.0955
2739 NACHT_LRR and PYD domains-containing protein 13	Q86W25	0.4108	0.5487	-3.31	0.5752	0.7681	-1.75	0.5661	0.6939
2740 NACHT_LRR and PYD domains-containing protein 2	Q9NX02	0.1785	0.3413	0.10	0.1167	0.6357	0.24	0.0272	0.0827
2741 NACHT_LRR and PYD domains-containing protein 3	Q96P20	0.4108	0.5486	-3.31	0.5752	0.7679	-1.75	0.5661	0.6937
2742 NACHT_LRR and PYD domains-containing protein 5	P59047	0.2225	0.4001	-0.06	0.1624	0.6613	0.28	0.0010	0.0214
2743 NACHT_LRR and PYD domains-containing protein 7	Q8W394	0.0564	0.1554	0.14	0.0027	0.2543	0.40	0.0294	0.0872
2744 NACHT_LRR and PYD domains-containing protein 9	Q7BTU0	0.0143	0.0696	0.16	0.2682	0.6635	0.09	0.0704	0.1576
2745 N-acetylneuraminate cytidyltransferase	Q8NFW8	0.1758	0.3379	-0.08	0.0262	0.4935	0.15	0.0267	0.0819
2746 N-acetylneuraminate-9-ethylsulfatase	Q8TBE9	0.2555	0.4431	-0.08	0.8771	0.9196	0.01	0.0069	0.0396
2747 NAD kinase 2_mitochondrial	Q4GQ04	0.0565	0.1556	0.17	0.0181	0.4665	0.23	0.0543	0.1325
2748 NAD(P) transhydrogenase_mitochondrial	Q13423	0.4108	0.5484	-3.31	0.5752	0.7677	-1.75	0.5661	0.6936
2749 NAD(P)H dehydrogenase [quinone] 1	P15559	0.0705	0.1777	0.12	0.7640	0.8295	-0.05	0.0331	0.0940
2750 NAD(P)H-hydrate epimerase	Q8NCW5	0.0399	0.1259	-0.21	0.3660	0.7241	-0.28	0.0034	0.0308
2751 NAD-dependent malic enzyme_mitochondrial	T23368	0.6871	0.7429	0.03	0.5725	0.8847	0.05	0.3431	0.5364
2752 NAD-dependent protein deacetylase sirtuin-2	Q8IXJ6	0.4108	0.5483	-3.31	0.5752	0.7675	-1.75	0.5661	0.6934
2753 NAD-dependent protein deacetylase sirtuin-5_mitochondrial	Q9NXA8	0.3071	0.5077	-0.06	0.0553	0.5834	-0.18	0.0891	0.1875
2754 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 2	Q8N183	0.1852	0.3499	0.04	0.2014	0.6607	0.17	0.0119	0.0510
2755 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	Q9P032	0.2454	0.4311	0.09	0.2935	0.6697	0.17	0.0565	0.1359
2756 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_mitochondrial	O95299	0.7913	0.8308	0.01	0.1215	0.6390	0.19	0.0332	0.0942
2757 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	Q86Y39	0.5341	0.6045	-0.05	0.1036	0.6336	-0.21	0.1047	0.2117
2758 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	Q9U109	0.0942	0.2163	-0.09	0.5964	0.7005	0.07	0.9291	0.9452
2759 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Q9P0J0	0.0884	0.2072	0.10	0.6267	0.7237	0.06	0.1741	0.3159
2760 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Q16718	0.0002	0.0142	0.57	0.2932	0.6699	0.14	0.1685	0.3076
2761 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	P56556	0.0952	0.2175	0.07	0.8770	0.9113	0.02	0.0547	0.1330
2762 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	O95182	0.9461	0.9594	-0.04	0.8429	0.8873	0.09	0.4555	0.6703
2763 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	P51970	0.3990	0.6183	-0.04	0.0069	0.4156	-0.46	0.0300	0.0879
2764 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_mitochondrial	Q16795	0.2756	0.4691	0.06	0.9231	0.9469	0.01	0.3280	0.5171
2765 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	O96000	0.3739	0.5889	-0.01	0.3123	0.6806	0.12	0.0214	0.0707
2766 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11_mitochondrial	Q9NX14	0.0387	0.1237	0.21	0.0378	0.5563	0.22	0.2135	0.3682
2767 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	O43676	0.7683	0.8119	-0.06	0.3315	0.6910	-0.55	0.3244	0.5123
2768 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	O95168	0.2988	0.4977	0.05	0.7467	0.8165	0.04	0.2474	0.4134
2769 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5_mitochondrial	O43674	0.1807	0.3444	-0.24	0.2591	0.6641	-0.54	0.0881	0.1858
2770 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	O95139	0.8968	0.9188	0.01	0.1796	0.6636	-0.16	0.0210	0.0702
2771 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	P17568	0.0253	0.0960	-0.22	0.5384	0.8544	0.25	0.0260	0.0803
2772 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8_mitochondrial	O95169	0.9213	0.9398	0.01	0.5974	0.7012	-0.17	0.7013	0.7484
2773 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	Q9Y6M9	0.2423	0.4276	-0.07	0.5660	0.8389	-0.07	0.3189	0.5061
2774 NADH dehydrogenase [ubiquinone] 1 subunit C2	O95298	0.8991	0.9208	0.01	0.5182	0.8399	-0.13	0.2710	0.4441
2775 NADH dehydrogenase [ubiquinone] flavoprotein 1_mitochondrial	P49821	0.1261	0.2649	0.07	0.3704	0.7186	-0.08	0.0075	0.0410
2776 NADH dehydrogenase [ubiquinone] flavoprotein 2_mitochondrial	P19404	0.2085	0.3812	-0.11	0.6163	0.7161	-0.08	0.0073	0.0403
2777 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2_mitochondrial	O75306	0.0319	0.1109	-0.04	0.2621	0.6633	0.06	0.0008	0.0207
2778 NADH dehydrogenase [ubiquinone] iron-sulfur protein 3_mitochondrial	O75489	0.0175	0.0774	-0.31	0.0529	0.5806	-0.34	0.0018	0.0244

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
2779 NADH dehydrogenase [ubiquinone] iron-sulfur protein 4_mitochondrial	O43181	0.1568	0.3104	-0.15	0.5553	0.8508	-0.07	0.9534	0.9633
2780 NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	O43920	0.0635	0.1668	0.08	0.8572	0.8970	-0.01	0.4263	0.6362
2781 NADH dehydrogenase [ubiquinone] iron-sulfur protein 6_mitochondrial	O75380	0.0224	0.0891	0.19	0.6162	0.7162	0.06	0.9529	0.9631
2782 NADH dehydrogenase [ubiquinone] iron-sulfur protein 8_mitochondrial	O00217	0.0618	0.1647	-0.22	0.6430	0.7367	-0.11	0.0055	0.0357
2783 NADH-cytochrome b5 reductase 3	P00387	0.0110	0.0602	0.17	0.3066	0.6787	0.14	0.1465	0.2742
2784 NADH-ubiquinone oxidoreductase 75 kDa subunit_mitochondrial	P28331	0.0141	0.0694	0.19	0.2866	0.6672	0.22	0.0125	0.0523
2785 NADH-ubiquinone oxidoreductase chain 4	P03905	0.5248	0.5963	-0.05	0.3548	0.7063	-0.09	0.1338	0.2561
2786 NADP-dependent malic enzyme	P48163	0.0214	0.0871	0.13	0.7612	0.8271	-0.02	0.0028	0.0288
2787 NADP-dependent malic enzyme_mitochondrial	P16798	0.4557	0.5329	-1.46	0.3311	0.6905	-2.64	0.0001	0.0148
2788 NADPH:cytochrome P450 reductase	P22570	0.0099	0.0581	0.13	0.1637	0.6640	0.15	0.0468	0.1198
2789 NADPH-cytochrome P450 reductase	P16435	0.0105	0.0592	0.32	0.2151	0.6620	0.24	0.0176	0.0589
2790 N-alpha-acetyltransferase 10	P41227	0.2723	0.4651	0.13	0.2135	0.6626	0.21	0.0652	0.1491
2791 N-alpha-acetyltransferase 11	Q9BSU3	0.0377	0.1218	-0.16	0.0245	0.4835	0.21	0.0429	0.1125
2792 N-alpha-acetyltransferase 15_NatA auxiliary subunit	Q9BXJ9	0.0074	0.0494	0.33	0.3501	0.7043	0.20	0.0149	0.0576
2793 N-alpha-acetyltransferase 16_NatA auxiliary subunit	Q6N069	0.4780	0.5533	0.07	0.1918	0.6672	0.14	0.0157	0.0591
2794 N-alpha-acetyltransferase 20	P61599	0.6697	0.7282	0.03	0.6547	0.7452	-0.03	0.0439	0.1142
2795 N-alpha-acetyltransferase 35_NatC auxiliary subunit	Q5VZE5	0.0752	0.1866	-0.22	0.2442	0.6568	0.13	0.0419	0.6270
2796 N-alpha-acetyltransferase 40	Q86UY6	0.0004	0.0166	2.43	0.6362	0.7322	0.33	0.2759	0.4503
2797 N-alpha-acetyltransferase 50	Q9GZZ1	0.1584	0.3129	0.09	0.6666	0.7765	0.04	0.0277	0.0837
2798 Nascent polypeptide-associated complex subunit alpha_muscle-specific form	E9PAV3	0.1242	0.2621	0.10	0.2969	0.6603	0.17	0.0117	0.0507
2799 Natural cytotoxicity triggering receptor 2	O95944	0.4311	0.5087	0.06	0.4170	0.7550	0.15	0.1614	0.2966
2800 Nck-associated protein 1	Q9Y2A7	0.0101	0.0586	0.90	0.5081	0.8300	0.10	0.0393	0.1052
2801 Nck-associated protein 5-like	Q9CHC0	0.0238	0.0926	-0.19	0.0810	0.6152	-0.36	0.4723	0.6897
2802 Nebulette	T60401	0.4215	0.4989	0.09	0.0741	0.6112	0.20	0.1182	0.2339
2803 Nebulin	P20929	0.4108	0.5482	-3.31	0.5752	0.7673	-1.75	0.5661	0.6932
2804 Nebulin-related-anchoring protein	Q86V77	0.1282	0.2684	0.09	0.0236	0.4851	0.34	0.0571	0.1367
2805 NEDD4-binding protein 1	Q75113	0.4108	0.5480	-3.31	0.5752	0.7673	-1.75	0.5661	0.6931
2806 NEDD4-binding protein 2	Q68LW6	0.4682	0.5441	0.11	0.7693	0.8351	0.06	0.5471	0.7001
2807 NEDD8	P15843	0.0405	0.1269	-0.40	0.1054	0.6326	0.30	0.0866	0.1835
2808 NEDD8-activating enzyme E1 catalytic subunit	Q8TBC4	0.4108	0.5479	-3.31	0.5752	0.7669	-1.75	0.5661	0.6929
2809 NEDD8-activating enzyme E1 regulatory subunit	P13564	0.9813	0.9872	0.40	0.0564	0.5831	-10.13	0.0238	0.0757
2810 NEDD8-conjugating enzyme Ubc12	P61081	0.0653	0.1690	0.12	0.0824	0.5055	0.18	0.0126	0.0526
2811 NEDD8-conjugating enzyme UBE2F	Q969M7	0.0009	0.0218	0.47	0.0559	0.5838	0.30	0.0002	0.0225
2812 Negative elongation factor 1	Q9H3P2	0.7749	0.8167	0.01	0.3107	0.5912	0.31	0.0068	0.0398
2813 Negative elongation factor 2	Q8W9X2	0.0096	0.0574	-0.31	0.8955	0.9263	0.02	0.0001	0.0133
2814 Negative elongation factor C/D	Q8IXH7	0.0875	0.2059	-0.12	0.4077	0.7500	0.09	0.0513	0.1272
2815 Negative elongation factor E	P18615	0.1404	0.2858	0.17	0.1910	0.6685	0.20	0.1899	0.3364
2816 Nephrocystin-3	Q7Z494	0.0330	0.1134	-0.22	0.2557	0.6623	-0.08	0.0512	0.1271
2817 Nesprin-1	Q8NFP1	0.0172	0.0767	0.15	0.1355	0.6505	0.18	0.0037	0.0319
2818 Nesprin-2	Q8W9X0	0.1345	0.2780	0.10	0.1866	0.6544	0.23	0.0654	0.1209
2819 Nestin	P48681	0.0116	0.0620	0.16	0.2393	0.6615	0.17	0.0042	0.0322
2820 Netrin receptor UNC5D	Q6UXZ4	0.3032	0.5029	-0.06	0.4040	0.7477	-0.08	0.0559	0.1351
2821 Neudeuin	Q9UMX5	0.4108	0.5477	-3.31	0.5752	0.7667	-1.75	0.5661	0.6927
2822 Netrin-specific leucine zipper protein	P54845	0.8935	0.9165	0.00	0.5395	0.8549	0.08	0.1745	0.3163
2823 Neuraligin-like protein 4	Q961N8	0.5385	0.6090	-0.09	0.4745	0.7807	0.07	0.8880	0.9112
2824 Neuroblast differentiation-associated protein AHNK	Q96666	0.0098	0.0579	0.16	0.1266	0.6429	0.31	0.0012	0.0229
2825 Neuroblastoma breakpoint family member 12	Q5TGA4	0.4567	0.5337	0.05	0.2923	0.6694	0.10	0.5157	0.7359
2826 Neuroblastoma breakpoint family member 6	Q5VWK0	0.3940	0.6120	0.40	0.2681	0.6638	0.18	0.0464	0.1193
2827 Neuroblastoma-amplified sequence	A2RRP1	0.0803	0.1949	-0.13	0.4624	0.7947	0.12	0.1537	0.2851
2828 Neurokinin-delta	P61601	0.0034	0.0381	0.22	0.5866	0.6923	-0.08	0.2132	0.3681
2829 Neurokinin-B receptor 1	P29120	0.0169	0.0760	0.28	0.1262	0.6434	0.30	0.5618	0.7863
2830 Neuroendocrine convertase 2	P16519	0.4675	0.5438	0.03	0.0453	0.5614	-0.12	0.0970	0.1966
2831 Neurofilament	O94856	0.8414	0.8734	0.01	0.2634	0.6432	0.35	0.0572	0.1368
2832 Neurofilament	P21359	0.0014	0.0254	-0.22	0.7869	0.8467	0.04	0.0049	0.0340
2833 Neurofilament light polypeptide	P07196	0.4108	0.5476	-3.31	0.5752	0.7665	-1.75	0.5661	0.6926
2834 Neurofilament medium polypeptide	P07197	0.4108	0.5475	-3.31	0.5752	0.7663	-1.75	0.5661	0.6924
2835 Neurogenic differentiation factor 4	Q9HD90	0.4108	0.5473	-3.31	0.5752	0.7661	-1.75	0.5661	0.6923
2836 Neurogenic differentiation factor 6	Q96NK8	0.4108	0.5472	-3.31	0.5752	0.7659	-1.75	0.5661	0.6921
2837 Neurogenic locus notch homolog protein 1	P46531	0.4108	0.5470	-3.31	0.5752	0.7658	-1.75	0.5661	0.6919
2838 Neurogenic locus notch homolog protein 2	Q04721	0.0154	0.0719	0.30	0.1436	0.6548	0.34	0.0019	0.0245
2839 Neurokinin B receptor	Q9BYT9	0.0011	0.0226	0.16	0.1781	0.6632	0.10	0.0000	0.0000
2840 Neuronal acetylcholine receptor subunit alpha-7	P36544	0.0075	0.0510	0.17	0.1596	0.6640	-0.15	0.0093	0.0451
2841 Neuronal calcium sensor 1	P62166	0.4108	0.5469	-3.31	0.5752	0.7656	-1.75	0.5661	0.6918
2842 Neuronal migration protein doublecortin	Q43602	0.4108	0.5467	-3.31	0.5752	0.7654	-1.75	0.5661	0.6916
2843 Neuronal pentraxin-2	P47972	0.4108	0.5466	-3.31	0.5752	0.7652	-1.75	0.5661	0.6914
2844 Neuron-specific calcium-binding protein hippocampal	P84074	0.0419	0.1299	0.14	0.0483	0.5738	-0.24	0.6250	0.6783
2845 Neurexin and toll-like protein 2	Q8NC67	0.4108	0.5465	-3.31	0.5752	0.7650	-1.75	0.5661	0.6913
2846 Neuronal alpha-glucosidase AB	P14697	0.0073	0.0502	0.19	0.3505	0.7043	0.17	0.0038	0.0315
2847 Neuronal amino acid transporter A	P43007	0.0021	0.0316	0.93	0.2204	0.6599	0.20	0.0048	0.0337
2848 Neuronal amino acid transporter B(O)	P15758	0.0099	0.0580	0.27	0.2204	0.6579	0.26	0.0009	0.0208
2849 Neuronal and basic amino acid transport protein rBAT	Q07837	0.4108	0.5463	-3.31	0.5752	0.7648	-1.75	0.5661	0.6911
2850 Neuronal ceramidase	Q9NR71	0.4108	0.5462	-3.31	0.5752	0.7646	-1.75	0.5661	0.6910
2851 Neuronal cholesterol ester hydrolase 1	Q6PIU2	0.4108	0.5460	-3.31	0.5752	0.7644	-1.75	0.5661	0.6908
2852 NFATC2-interacting protein	Q8NCF5	0.0205	0.0847	-2.00	0.0964	0.6353	-1.98	0.0203	0.0686
2853 NF-kappa-B essential modulator	Q9Y6K9	0.0004	0.0164	-0.97	0.0016	0.2181	-0.57	0.2050	0.3580

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control																				
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC															
2854 NF-kappa-B inhibitor-like protein 1	Q9UBC1	0.4108	0.5459	-3.31	0.5752	0.7642	-1.75	0.5661	0.6906	-1.19	0.5388	0.6532	0.89	0.2938	-1.88	0.9510	1.0522	0.09	0.0015	0.0501	0.74	0.0078	0.0725	0.51	0.5024	0.5695	0.17	
2855 NF-kappa-B-activating protein	Q8NSV7	0.6476	0.7091	-0.07	0.0343	0.5288	-0.69	0.4130	0.6192	0.21	0.0625	0.1361	-0.31	0.1129	0.2740	-0.27	0.4888	0.7142	0.08	0.7376	0.4612	-2.55	0.8708	0.9618	-0.33	0.0651	0.1241	2.06
2856 NF-X1-type zinc finger protein NFXL1	Q6GNB6	0.2007	0.3716	-0.06	0.2364	0.6634	-0.06	0.2333	0.3938	-0.03	0.0065	0.0323	-0.11	0.4129	0.5077	0.05	0.2146	0.3962	0.08	0.7376	0.4997	-2.55	0.8708	1.0329	-0.33	0.0651	0.1407	2.06
2857 NF-X1-type zinc finger-containing protein 1	Q9P2E3	0.8936	0.9164	-0.02	0.0759	0.6172	0.46	0.0294	0.0872	0.39	0.1027	0.1979	0.25	0.0668	0.1966	0.31	0.0601	0.1697	0.34	0.0207	0.1329	0.46	0.4487	0.8514	-0.11	0.2863	0.5382	0.06
2858 NGF1-A-binding protein 1	Q13506	0.0606	0.1630	-0.07	0.3395	0.6977	-0.12	0.042	0.2108	0.07	0.0161	0.0526	-0.03	0.0205	0.1028	-0.10	0.0645	0.1772	0.18	0.0093	0.0633	-0.98	0.0001	0.0120	-2.09	0.0001	0.0273	-1.81
2859 NGF1-A-binding protein 2	Q15742	0.6236	0.6912	-0.02	0.2798	0.6648	0.18	0.0349	0.0970	0.17	0.0220	0.0645	-0.20	0.1145	0.2766	-0.09	0.7314	0.9712	0.01	0.7376	0.4435	-2.55	0.8708	0.9285	-0.33	0.0651	0.1168	2.06
2860 NHP2-like protein 1	Q55739	0.0025	0.0025	-0.07	0.3734	0.9823	0.08	0.0286	0.0838	0.07	0.0264	0.0366	-0.03	0.3178	0.4949	-0.02	0.4888	0.7314	0.08	0.7376	0.4612	-2.55	0.8708	0.9618	-0.33	0.0651	0.1241	2.06
2861 NHP2-like protein 1	Q6P7A1	0.0138	0.2792	-0.02	0.2469	0.6502	0.08	0.0286	0.0838	0.07	0.0264	0.0366	-0.03	0.3178	0.4949	-0.02	0.4888	0.7314	0.08	0.7376	0.4612	-2.55	0.8708	0.9618	-0.33	0.0651	0.1241	2.06
2862 Nibrin	Q6O934	0.4108	0.5458	-3.31	0.5752	0.7642	-1.75	0.5661	0.6905	-1.19	0.5388	0.6530	0.89	0.2938	0.4432	-1.88	0.9510	1.0519	0.09	0.0916	0.2430	0.22	0.1025	0.5131	-0.11	0.5715	0.6346	-0.07
2863 Nicotin	Q69V93	0.0103	0.0590	0.24	0.0958	0.6322	-0.17	0.0050	0.0346	0.34	0.0019	0.0194	0.39	0.0306	0.1277	0.18	0.0078	0.0662	0.30	0.7363	0.4321	0.05	0.1379	0.3933	0.10	0.1059	0.1623	0.11
2864 Nicotin-1	Q9BSH3	0.6558	0.7167	-0.21	0.4253	0.7618	-1.20	0.0580	0.1382	-1.81	0.1691	0.2905	-0.74	0.5034	0.5926	-0.31	0.3519	0.5573	-0.58	0.7376	0.4742	-2.55	0.8708	0.9860	-0.33	0.0651	0.1295	2.06
2865 Nicotinamide N-methyltransferase	Q6A021	0.4108	0.5456	-3.31	0.5752	0.7638	-1.75	0.5661	0.6903	-1.19	0.5388	0.6529	0.89	0.2938	0.4431	-1.88	0.9510	1.0517	0.09	0.0696	0.2077	0.36	0.3324	0.6893	0.10	0.1133	0.0926	0.51
2866 Nicotinamide phosphoribosyltransferase	P43490	0.0531	0.1497	0.11	0.2689	0.6633	0.10	0.0031	0.0301	0.19	0.0090	0.0383	0.20	0.5434	0.6279	0.02	0.0090	0.0687	0.22	0.1749	0.7376	-0.09	0.0375	0.1763	0.11	0.0372	0.1657	-0.12
2867 Nicotinate phosphoribosyltransferase	Q6XQ06	0.4108	0.5455	-3.31	0.5752	0.7636	-1.75	0.5661	0.6901	-1.19	0.5388	0.6527	0.89	0.2938	0.4429	-1.88	0.9510	1.0515	0.09	0.1049	0.2640	0.28	0.4038	0.7899	0.13	0.1020	0.0940	0.58
2868 NIK-related protein kinase	Q722Y5	0.5438	0.6140	-0.04	0.6408	0.7352	-0.01	0.6905	0.7390	0.01	0.2928	0.0800	0.11	0.4317	0.5259	-0.03	0.2326	0.4166	-0.06	0.7376	0.4944	-2.55	0.8708	1.0233	-0.33	0.0651	0.1384	2.06
2869 NIN	Q8N4C6	0.2682	0.4600	0.07	0.4024	0.7460	0.13	0.0305	0.0889	0.19	0.2352	0.3799	0.07	0.0989	0.2513	0.13	0.0108	0.0871	0.29	0.0175	0.1228	0.16	0.0023	0.0407	0.90	0.134	0.1009	0.33
2870 NIPA-like protein 2	Q9H8A1	0.0007	0.0200	-0.16	0.0189	0.4654	-0.21	0.0047	0.0338	-0.12	0.0503	0.1154	-0.19	0.0102	0.0721	-0.41	0.0149	0.0812	-0.26	0.7376	0.6029	-2.55	0.8708	1.2178	-0.33	0.0651	0.1946	2.06
2871 Nipped-B-like protein	Q6CK79	0.0014	0.0254	-0.48	0.0481	0.9686	-0.01	0.0047	0.0333	-0.43	0.0097	0.0397	-0.30	0.0095	0.0695	-0.37	0.0093	0.0691	-0.40	0.7376	0.6155	-2.55	0.8708	1.2399	-0.33	0.0651	0.2023	2.06
2872 Nitric oxide synthase-interacting protein	Q9Y314	0.9892	0.9921	0.00	0.3224	0.6844	-0.07	0.0214	0.0707	-0.17	0.4191	0.6108	-0.18	0.0600	0.1845	-0.13	0.7318	0.9712	-0.01	0.6519	0.6965	-0.05	0.0035	0.0486	-0.20	0.1105	0.1675	0.06
2873 NLR family member X1	Q8MT76	0.1576	0.3117	-0.11	0.0869	0.6200	-0.54	0.0346	0.0968	-0.33	0.8941	0.9099	0.02	0.0870	0.2310	-0.13	0.1624	0.3242	0.29	0.0374	0.1605	-0.20	0.7944	1.2372	-0.01	0.9090	0.9274	-0.01
2874 NmrA-like family domain-containing protein 1	Q9HBL8	0.0684	0.1736	0.13	0.1249	0.7523	0.11	0.0408	0.1080	0.16	0.0857	0.1731	0.12	0.0293	0.1246	0.19	0.0624	0.1738	0.14	0.7376	0.5545	-2.55	0.8708	1.1322	-0.33	0.0651	0.1675	2.06
2875 Nodal modulator 1	Q15155	0.2487	0.4352	-0.05	0.1570	0.6623	0.08	0.0092	0.0450	0.16	0.0063	0.0317	0.18	0.0185	0.0971	0.13	0.0665	0.1808	0.08	0.7376	0.5509	-2.55	0.8708	1.1257	-0.33	0.0651	0.1656	2.06
2876 Nodal modulator 3	Q69849	0.6815	0.7382	-0.04	0.2004	0.6653	0.10	0.0731	0.1617	-0.11	0.1144	0.2152	0.47	0.0444	0.1355	0.13	0.0337	0.1183	0.60	0.7376	0.5765	-2.55	0.8708	1.1713	-0.33	0.0651	0.1794	2.06
2877 Noelin-3	Q69P87	0.4108	0.5453	-3.31	0.5752	0.7634	-1.75	0.5661	0.6900	-1.19	0.5388	0.6526	0.89	0.2938	0.4428	-1.88	0.9510	1.0513	0.09	0.1341	0.5676	-0.15	0.7591	1.2010	-0.02	0.8269	0.4499	0.62
2878 Non-histone chromosomal protein HMG-14	Q05114	0.4021	-0.4021	-1.12	0.0272	0.9804	0.06	0.0501	0.1251	-1.26	0.1848	0.3121	-0.51	0.1826	0.3758	-0.42	0.1153	0.2557	-3.15	0.0095	0.0997	0.47	0.1198	0.3579	0.78	0.2833	0.1475	3.47
2879 Non-histone chromosomal protein HMG-17	Q05210	0.4108	0.5452	-3.31	0.5752	0.7632	-1.75	0.5661	0.6899	-1.19	0.5388	0.6524	0.89	0.2938	0.4427	-1.88	0.9510	1.0510	0.09	0.0528	0.1817	0.07	0.0851	0.2809	0.44	0.4573	0.1905	0.07
2880 Non-POU domain-containing octamer-binding protein 1	Q15233	0.0245	0.0945	0.14	0.2616	0.6636	0.21	0.0123	0.0520	0.32	0.0102	0.0164	0.41	0.0195	0.1000	0.15	0.0076	0.0656	0.30	0.0272	0.1456	0.59	0.2211	0.5285	0.13	0.0588	0.2168	0.21
2881 Non-receptor tyrosine-protein kinase TYK2	P25997	0.8264	0.8608	0.06	0.0402	0.8851	-0.12	0.7312	0.7244	-0.07	0.3832	0.5681	-0.26	0.7679	0.8195	0.06	0.9400	1.1761	-0.05	0.7376	0.4320	-2.55	0.8708	0.9069	-0.33	0.0651	0.1123	2.06
2882 Non-specific lipid-transfer protein	P22307	0.1780	0.3406	0.11	0.2674	0.6653	0.13	0.9144	0.9722	0.00	0.3260	0.4978	0.02	0.2727	0.4965	-0.04	0.2596	0.4509	0.03	0.2449	0.7879	0.11	0.2459	0.5669	-0.05	0.2072	0.2760	-0.03
2883 Non-structural maintenance of chromosomes element 3 homolog	Q96MG7	0.0053	0.0444	0.31	0.4616	0.7941	-0.07	0.9129	0.9314	-0.01	0.1977	0.3289	-0.08	0.0285	0.1226	-0.20	0.1460	0.3017	-0.10	0.0321	0.1512	-0.18	0.0003	0.0179	-0.84	0.0293	0.1465	-1.24
2884 Nostriin	Q8IV19	0.0905	0.2106	0.08	0.3270	0.6861	0.03	0.0290	0.0864	0.28	0.3055	0.4718	-0.10	0.0537	0.1718	0.10	0.3719	0.5799	0.03	0.7376	0.4716	-2.55	0.8708	0.9810	-0.33	0.0651	0.1184	2.06
2885 Notch homolog 2 N-terminal-like protein C	P0DPK4	0.3531	0.5631	0.21	0.4340	0.7707	0.17	0.9143	0.9323	-0.02	0.8474	0.8687	-0.04	0.5362	0.6216	-0.14	0.6272	0.8631	0.10	0.7376	0.4496	-2.55	0.8708	0.9401	-0.33	0.0651	0.1293	2.06
2886 Notchless protein homolog 1	Q9NVY2	0.4108	0.5451	-3.31	0.5752	0.7630	-1.75	0.5661	0.6897	-1.19	0.5388	0.6523	0.89	0.2938	0.4425	-1.88	0.9510	1.0508	0.09	0.2027	0.4155	-0.10	0.6582	1.0991	-0.19	0.0221	0.1264	0.77
2887 NPC intracellular cholesterol transporter 2	P61916	0.4108	0.5449	-3.31	0.5752	0.7628	-1.75	0.5661	0.6895	-1.19	0.5388	0.6521	0.89	0.2938	0.4424	-1.88	0.9510	1.0506	0.09	0.0006	0.0374	-5.61	0.0009	0.0071	-4.59	0.0000	0.0000	-5.18
2888 NSF1 cofactor p47	Q9UNZ2	0.0660	0.1703	0.16	0.1995	0.6637	0.18	0.0150	0.0576	0.27	0.0121	0.0442	0.40	0.0924	0.2398	0.14	0.0114	0.0731	0.40	0.0371	0.1600	0.38	0.4850	0.8957	0.08	0.3246	0.3960	0.10
2889 N-terminal Kinase-like protein	Q96K69	0.0376	0.1218	-0.09	0.4458	0.7817	0.07	0.0456	0.1175	-0.13	0.0000	0.0000	-0.22	0.0039	0.0468	-0.15	0.0009	0.0453	-0.15	0.2143	0.4336	0.24	0.2826	0.6208	0.18	0.2246	0.1265	0.66
2890 N-terminal Xaa-Pro-Lys-N-methyltransferase 1	Q9BV86	0.9897	0.9922	0.00	0.5279	0.8463	0.08	0.0168	0.0613	0.33	0.0667	0.1475	0.19	0.2183	0.4242	0.11	0.1022	0.2370	0.19	0.5570	0.6076	0.11	0.8794	0.9089	0.03	0.9926	0.9939	0.00
2891 Nuclear apoptosis-inducing factor 1	Q69Y17	0.0640	0.1675	-1.17	0.0535	0.5847	-10.14	0.0189	0.0658	-9.58	0.0009	0.0149	-7.50	0.0353	0.1361	-1.77	0.0084	0.0476	-8.31	0.7376	0.6173	-2.55	0.8708	1.2430	-0.33	0.0651	0.2034	2.06
2892 Nuclear autoantigen Sp-100	P23497	0.0098	0.0578	0.24	0.2112	0.6620	0.27	0.0018	0.0240	0.51	0.0166	0.0537	0.21	0.0207	0.1030	-0.14	0.0109	0.0716	0.27	0.0081	0.0914	0.64	0.0316	0.0977	0.43	0.0074	0.0784	0.02
2893 Nuclear autoantigenic sperm protein	P09378	0.0626	0.2626	0.00	0.2660	0.6620	0																					

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
2936 Nucleolar protein 58	Q9Y2X3	0.0938	0.2156	-0.10	0.9063	0.9348	-0.01	0.8576	0.8865
2937 Nucleolar protein 8	Q76FK4	0.0104	0.0591	-0.42	0.4840	0.8085	-0.10	0.1225	0.2407
2938 Nucleolar protein 9	Q86U38	0.4108	0.5438	-3.31	0.5752	0.7613	-1.75	0.5661	0.6882
2939 Nucleolar RNA helicase 2	Q9NR30	0.9362	0.9516	0.01	0.7502	0.8188	-0.04	0.0567	0.1360
2940 Nucleolar transcription factor 1	P17480	0.0830	0.1984	0.14	0.2754	0.6641	0.17	0.1070	0.2154
2941 Nucleolin	P19338	0.0018	0.0290	0.21	0.0820	0.6165	0.21	0.0001	0.0207
2942 Nucleosyn TIA-1 isoform p40	P11483	0.6720	0.7304	-0.03	0.1527	0.6586	0.13	0.0641	0.1477
2943 Nucleosyn TIAR	Q10185	0.4326	0.5100	-0.45	0.2343	0.6607	-2.82	0.0706	0.1581
2944 Nucleosom	P06748	0.0993	0.2240	0.17	0.0312	0.4411	0.16	0.0014	0.0232
2945 Nucleoplasmin-3	Q75607	0.2091	0.3817	0.15	0.0698	0.6016	0.29	0.8616	0.8898
2946 Nucleoporin NUP188 homolog	Q5SR5E	0.5093	0.5821	-0.04	0.2814	0.6650	-0.15	0.6473	0.7000
2947 Nucleoporin NUP35	Q8NFH5	0.4108	0.5437	-3.31	0.5752	0.7611	-1.75	0.5661	0.6880
2948 Nucleoporin Nup37	Q8NFH4	0.5395	0.6096	-0.06	0.2784	0.6649	0.17	0.9489	0.9598
2949 Nucleoporin p54	Q723B4	0.0000	0.0000	0.37	0.0509	0.5719	-0.27	0.0000	0.0000
2950 Nucleoporin SEH1	Q96E3E	0.9313	0.9480	0.01	0.3139	0.6806	0.36	0.3681	0.5655
2951 Nucleoporin-like protein 2	U15504	0.0825	0.1978	-0.86	0.1103	0.6334	-0.48	0.2540	0.4220
2952 Nucleoprotein TPR	P12270	0.8674	0.8949	0.01	0.3475	0.7037	0.15	0.0151	0.0577
2953 Nucleoredoxin	Q6DKJ4	0.4108	0.5435	-3.31	0.5752	0.7609	-1.75	0.5661	0.6879
2954 Nucleoredoxin-like protein 1	Q96CM4	0.5036	0.5768	0.79	0.2609	0.7184	-0.18	0.6222	0.7662
2955 Nucleoredoxin-like protein 2	Q5V203	0.4108	0.5434	-3.31	0.5752	0.7607	-1.75	0.5661	0.6877
2956 Nucleoside diphosphate kinase 3	Q13232	0.1459	0.2936	0.29	0.6586	0.7481	0.06	0.0555	0.1346
2957 Nucleoside diphosphate kinase 7	Q9Y3B8	0.4108	0.5433	-3.31	0.5752	0.7605	-1.75	0.5661	0.6875
2958 Nucleoside diphosphate kinase A	P15531	0.0024	0.0333	0.15	0.5027	0.8238	0.13	0.0190	0.0660
2959 Nucleoside diphosphate kinase B	P23292	0.0046	0.0429	0.30	0.3934	0.7373	0.18	0.0040	0.0321
2960 Nucleoside diphosphate-linked moiety X motif 19	ARMXV4	0.3714	0.5858	0.06	0.7496	0.8187	0.02	0.0947	0.1957
2961 Nucleosome assembly protein 1-like 1	P55209	0.0006	0.0194	0.21	0.0315	0.5115	0.23	0.0002	0.0235
2962 Nucleosome assembly protein 1-like 2	Q99457	0.4108	0.5431	-3.31	0.5752	0.7603	-1.75	0.5661	0.6874
2963 Nucleosome assembly protein 1-like 4	Q99733	0.3532	0.5631	0.03	0.1141	0.6342	0.10	0.0062	0.0382
2964 Nucleosome-remodeling factor subunit BPTF	Q12830	0.0297	0.1056	-0.27	0.1370	0.6517	-0.30	0.0113	0.0493
2965 Nucleosome-associated protein 1	Q96RE7	0.0038	0.0392	0.17	0.6178	0.5913	0.12	0.0108	0.0485
2966 Nucleosome-associated protein 2	Q96RF6	0.7203	0.7715	-0.06	0.6109	0.7124	-0.04	0.9051	0.9251
2967 Nucleosome-associated protein 3	Q96RF6	0.4663	0.5426	0.03	0.4560	0.7879	0.06	0.4927	0.7137
2968 Nucleosome-associated protein 4	Q8WVJ2	0.0008	0.0207	0.59	0.4002	0.7441	0.10	0.0149	0.0576
2969 Nucleosome-associated protein 5	Q8WVJ2	0.0008	0.0207	0.59	0.4002	0.7441	0.10	0.0149	0.0576
2970 NXPE family member 1	Q8N323	0.3756	0.5908	-0.06	0.0668	0.4193	-0.33	0.0045	0.0333
2971 Obg-like ATPase 1	Q9NTK5	0.0382	0.1226	0.18	0.2828	0.6644	0.21	0.0135	0.0544
2972 Obscurin	Q5V579	0.0812	0.1965	0.21	0.1526	0.6593	0.24	0.0024	0.0271
2973 Occludin	P11625	0.0079	0.0525	-0.06	0.3946	0.7384	0.10	0.0212	0.0704
2974 OCIA domain-containing protein 1	Q9N400	0.0446	0.1344	-0.15	0.9299	0.9525	-0.01	0.6264	0.4321
2975 OCIA domain-containing protein 2	Q56V13	0.0778	0.1908	-0.23	0.2703	0.6632	-0.13	0.5401	0.7621
2976 Oligomycin resistance factor	Q9Y3B8	0.4108	0.5430	-3.31	0.5752	0.7601	-1.75	0.5661	0.6872
2977 Oligomycin resistance factor complex subunit OSTC	Q9NRP0	0.0008	0.0206	0.41	0.0114	0.4310	-0.26	0.2035	0.3559
2978 Omega-3 fatty acid desaturase	Q9NOR4	0.0381	0.1227	-0.56	0.5629	0.8764	-0.11	0.0681	0.1540
2979 Oncoferritin	P0CE72	0.6002	0.6659	-0.13	0.5808	0.6885	-0.51	0.2795	0.4546
2980 Oncoferritin-like protein	Q9NZT2	0.0936	0.2152	-0.10	0.0007	0.2266	0.14	0.5345	0.7554
2981 Oncoferritin-like protein	Q14982	0.1900	0.3558	-0.64	0.2570	0.6636	-1.51	0.5776	0.6351
2982 Oral-facial-digital syndrome 1 protein	Q75665	0.4108	0.5428	-3.31	0.5752	0.7609	-1.75	0.5661	0.6871
2983 Ornithine aminotransferase mitochondrial	P04181	0.0033	0.0376	0.09	0.4358	0.7718	0.08	0.0049	0.0341
2984 Orotidine	Q9HC10	0.0972	0.2205	0.05	0.7994	0.8548	-0.01	0.1698	0.3094
2985 Orotidine	Q9NRC9	0.9848	0.9888	0.00	0.2822	0.6642	-0.08	0.9148	0.9323
2986 OTU domain-containing protein 7B	Q6GQO9	0.0078	0.0523	0.23	0.0435	0.5705	0.29	0.0020	0.0195
2987 Outer dense fiber protein 2	Q5BJF6	0.0259	0.0974	0.15	0.0076	0.4059	0.22	0.0147	0.0573
2988 Overexpressed in colon carcinoma 1 protein	Q8TAD7	0.4745	0.5501	-0.68	0.1614	0.6635	-1.88	0.0537	0.1314
2989 Oxidation resistance protein 1	Q8N573	0.0029	0.0362	-0.42	0.0850	0.6201	-0.30	0.7934	0.8309
2990 Oxidative stress-induced growth inhibitor 1	Q9UJX0	0.0792	0.1930	-0.64	0.3177	0.6809	-1.02	0.6932	0.7411
2991 Oxidoreductase HTATIP2	Q9BUP3	0.0179	0.0676	0.21	0.0645	0.5903	0.30	0.0175	0.0631
2992 Oxygen-dependent coproporphyrinogen-III oxidase mitochondrial	P36551	0.0010	0.0219	-1.26	0.1207	0.6380	-0.93	0.0026	0.0281
2993 Oxyester-binding protein 1	P22059	0.2730	0.4659	0.10	0.1989	0.6651	0.09	0.0000	0.0000
2994 Oxyester-binding protein-related protein 2	Q9H1P3	0.4108	0.5427	-3.31	0.5752	0.7597	-1.75	0.5661	0.6869
2995 Oxyester-binding protein-related protein 3	Q9H4L5	0.0181	0.0789	0.21	0.2319	0.6626	0.18	0.0126	0.0526
2996 Oxyester-binding protein-related protein 9	Q96SU4	0.4108	0.5426	-3.31	0.5752	0.7595	-1.75	0.5661	0.6867
2997 Oxytocin receptor	P30559	0.5004	0.5741	-0.05	0.0232	0.4807	-0.31	0.2767	0.4512
2998 Oxytocin-neurophysin 1	P01178	0.6342	0.6962	0.12	0.2414	0.6617	0.32	0.9477	0.9590
2999 P antigen family member 2	Q722X7	0.0088	0.0557	0.43	0.0913	0.6300	0.26	0.0248	0.0782
3000 P antigen family member 5	Q96GU1	0.0334	0.1142	5.50	0.0162	0.4536	6.00	0.0304	0.0887
3001 P2X purinoceptor 4	Q95771	0.0114	0.0613	0.22	0.4836	0.8083	0.17	0.0131	0.0535
3002 Patchy domain protein 2 homolog	Q15645	0.0785	0.1920	0.28	0.5169	0.8088	-0.11	0.2435	0.4082
3003 PAK4-inhibitor INKA2	Q5N717	0.5553	0.6245	-0.07	0.4165	0.7549	-0.19	0.1147	0.2278
3004 Palmitoyl-protein thioesterase 1	P08977	0.0003	0.0149	-0.38	0.0010	0.2647	-0.27	0.0170	0.0619
3005 Pancreatic alpha-amylase	P04746	0.9751	0.9833	0.00	0.2971	0.6715	-0.08	0.1476	0.2757
3006 Pancreatic progenitor cell differentiation and proliferation factor	Q9H3Y8	0.0039	0.0394	-0.48	0.0410	0.5694	-12.05	0.0009	0.0220
3007 Pancreatic prohomone	P01298	0.1600	0.3150	0.26	0.2631	0.6638	0.22	0.1483	0.2766
3008 Pantothate kinase 2 mitochondrial	Q9BZ23	0.4108	0.5424	-3.31	0.5752	0.7593	-1.75	0.5661	0.6866
3009 Pantothate kinase 4	Q9NVE7	0.1391	0.2837	0.09	0.5556	0.5830	0.34	0.0179	0.0639
3010 Paraneoplastic antigen Ma1	Q8ND90	0.0154	0.0719	0.12	0.0405	0.5685	0.13	0.0473	0.1206
3011 Parascle component 1	Q8WXP1	0.4103	0.6316	-0.06	0.3381	0.6972	0.08	0.6818	0.7312
3012 Parathyroidin	P20962	0.0812	0.1964	-0.21	0.6678	0.7556	-0.21	0.0096	0.0456
3013 Partitioning defective 3 homolog	Q8TEW0	0.2132	0.3872	-0.08	0.1777	0.6993	0.16	0.4499	0.6636
3014 Partitioning defective 6 homolog beta	Q9BYG5	0.9614	0.9715	0.00	0.3793	0.7255	0.05	0.4912	0.7119
3015 Partner of Y14 and maso	Q9BRP8	0.0995	0.2242	-0.11	0.4138	0.7529	0.11	0.4708	0.6879
3016 Paxillin	P49023	0.0035	0.0380	0.15	0.2097	0.6615	0.20	0.1117	0.6178



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
3017 PDZ and LIM domain protein 1	O00151	0.7021	0.7555	-0.05	0.6631	0.7519	0.06	0.8276	0.8608	-0.02	0.2974	0.4612	-0.13	0.3172	0.4144	0.11	0.5120	0.7390	0.07	0.6417	0.6865	-0.06	0.6641	1.0119	-0.03	0.0452	0.1857	-0.16
3018 PDZ and LIM domain protein 2	Q96YV6	0.4108	0.5423	-3.31	0.5752	0.7591	-1.75	0.5661	0.6864	-0.19	0.5388	0.6492	0.89	0.2938	0.4400	-1.88	0.9510	1.0463	0.09	0.6273	0.1430	0.38	0.3781	0.7547	0.09	0.2311	0.3012	-0.17
3019 PDZ and LIM domain protein 5	Q96HIC4	0.3476	0.5566	-0.07	0.6189	0.7175	0.03	0.7076	0.1580	0.14	0.0401	0.0986	0.19	0.1039	0.2591	0.11	0.0611	0.1716	0.16	0.2958	0.5516	0.12	0.5763	1.0068	0.04	0.8492	0.8784	-0.01
3020 PDZ and LIM domain protein 7	Q9NR12	0.0030	0.0366	1.74	0.2210	0.6598	-0.39	0.0539	0.1318	0.53	0.0229	0.0664	0.35	0.0877	0.2318	0.23	0.0096	0.0700	0.50	0.3031	0.5615	0.24	0.0122	0.24	0.0064	0.0752	0.33	
3021 PDZ domain-containing protein 2	Q15018	0.1620	0.3181	0.18	0.3450	0.7025	-0.12	0.0626	0.1454	-0.28	0.1169	0.2184	-0.21	0.2050	0.4067	-0.16	0.9522	0.9805	0.01	0.3736	0.4308	-2.55	0.8708	0.9047	-0.33	0.0651	0.1119	2.06
3022 PDZ domain-containing protein 4	Q76C19	0.9842	0.9886	0.00	0.9120	0.9383	0.01	0.7382	0.7812	0.03	0.2699	0.4257	0.11	0.2594	0.4801	-0.12	0.9115	1.1485	0.01	0.7178	0.7582	-0.15	0.2246	0.5344	0.37	0.0427	0.1798	0.74
3023 PDZ domain-containing protein 8	Q9NEN9	0.8625	0.8912	0.01	0.8220	0.8936	0.03	0.0668	0.1520	0.22	0.2042	0.3378	0.13	0.7597	0.8122	-0.03	0.3206	0.5234	0.09	0.3736	0.4785	-2.55	0.8708	0.9940	-0.33	0.0651	0.1314	2.06
3024 PDZ domain-containing protein GIPC1	Q14908	0.7875	0.8276	-0.01	0.8181	0.8702	0.03	0.4704	0.6879	0.04	0.2012	0.3338	0.09	0.1785	0.3694	-0.08	0.2197	0.4010	-0.07	0.3736	0.4980	-2.55	0.8708	1.0299	-0.33	0.0651	0.1400	2.06
3025 Pecanex-like protein 4	Q63HM2	0.1850	0.3499	-0.18	0.6338	0.7447	0.11	0.3596	0.5565	-0.11	0.8822	0.8992	0.02	0.0249	0.1136	-0.55	0.2096	0.3907	0.17	0.3736	0.5007	-2.55	0.8708	1.0348	-0.33	0.0651	0.1412	2.06
3026 Peflin	Q9UBV8	0.2891	0.4859	-0.72	0.4733	0.8017	-0.58	0.2947	0.4753	-0.19	0.4458	0.6402	0.25	0.2154	0.4201	0.26	0.1957	0.3709	0.44	0.3736	0.5032	-2.55	0.8708	1.0393	-0.33	0.0651	0.1423	2.06
3027 Peptidocopeptide repeat domain-containing protein 3_mitochondrial	Q96EY7	0.1189	0.2541	-0.16	0.7512	0.8195	0.08	0.6113	0.6664	-0.07	0.2910	0.4531	-0.27	0.0765	0.2125	0.20	0.1372	0.2901	-0.23	0.9720	0.9773	0.00	0.2037	0.5032	-0.16	0.9640	0.9713	0.00
3028 Peptidase M20 domain-containing protein 2	Q8IYS1	0.4108	0.5422	-3.31	0.5752	0.7589	-1.75	0.5661	0.6863	-1.19	0.5388	0.6491	0.89	0.2938	0.4399	-1.88	0.9510	1.0461	0.09	0.1986	0.4090	0.11	0.1742	0.4576	0.13	0.8016	0.8380	-0.02
3029 Peptide chain release factor 1_mitochondrial	O75570	0.4108	0.5420	-3.31	0.5752	0.7587	-1.75	0.5661	0.6861	-1.19	0.5388	0.6489	0.89	0.2938	0.4397	-1.88	0.9510	1.0459	0.09	0.2271	0.4526	0.81	0.0737	0.2631	-1.67	0.5344	0.6003	-1.08
3030 Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	Q96IV0	0.0002	0.0140	0.40	0.9463	0.9645	-0.01	0.0268	0.0820	0.31	0.0249	0.0704	0.11	0.3520	0.4498	0.03	0.3393	0.5435	0.09	0.3736	0.4753	-2.55	0.8708	0.9879	-0.33	0.0651	0.1299	2.06
3031 Peptidyl-prolyl cis-trans isomerase A	P62937	0.0005	0.0182	0.49	0.1980	0.6695	0.24	0.0036	0.0316	0.35	0.0045	0.0274	0.26	0.4589	0.5510	0.03	0.0029	0.0542	0.40	0.1909	0.3970	0.22	0.0575	0.2293	-0.21	0.0264	0.1387	-0.31
3032 Peptidyl-prolyl cis-trans isomerase A-like 4A	Q9Y536	0.1580	0.3123	-0.14	0.1291	0.6436	-0.08	0.3582	0.5550	0.08	0.0765	0.1584	-0.18	0.8480	0.8833	-0.01	0.2278	0.4104	-0.06	0.9955	0.9963	0.00	0.0955	0.3084	0.28	0.0055	0.0714	0.71
3033 Peptidyl-prolyl cis-trans isomerase A-like 4G	P0DN37	0.0046	0.0428	0.32	0.0924	0.6298	0.15	0.0163	0.0604	0.26	0.3656	0.5464	-0.05	0.0448	0.1559	0.16	0.0572	0.1645	0.13	0.6649	0.7090	0.09	0.1570	0.4287	-0.22	0.0455	0.1822	-0.41
3034 Peptidyl-prolyl cis-trans isomerase A-like 4H	A0AF75B767	0.0025	0.0335	-0.84	0.0494	0.5776	-1.01	0.0099	0.0219	-1.11	0.0032	0.0233	-1.31	0.0015	0.0305	-1.28	0.0060	0.0623	-0.92	0.3736	0.6255	-2.55	0.8708	1.2572	-0.33	0.0651	0.2085	2.06
3035 Peptidyl-prolyl cis-trans isomerase B	P23284	0.0107	0.0998	0.37	0.3380	0.6807	0.20	0.0079	0.0416	0.34	0.0047	0.0278	0.38	0.0383	0.1426	0.23	0.0074	0.0651	0.50	0.2516	0.4878	0.14	0.3490	0.7112	-0.10	0.0478	0.1989	-0.25
3036 Peptidyl-prolyl cis-trans isomerase C	P45877	0.4686	0.5445	-0.04	0.4721	0.8010	-0.05	0.0321	0.0919	-0.13	0.0101	0.0403	-0.18	0.0568	0.1783	-0.10	0.4498	0.6726	0.04	0.3736	0.4643	-2.55	0.8708	0.9673	-0.33	0.0651	0.1254	2.06
3037 Peptidyl-prolyl cis-trans isomerase D	Q80752	0.0009	0.0217	0.36	0.3834	0.7307	-0.07	0.3220	0.5095	-0.05	0.2166	0.3545	-0.08	0.1443	0.3188	-0.12	0.1171	0.2526	0.08	0.2106	0.4280	0.12	0.5470	0.9724	0.04	0.1043	0.1605	-0.24
3038 Peptidyl-prolyl cis-trans isomerase F_mitochondrial	P30405	0.7159	0.7675	0.02	0.1917	0.6687	0.13	0.0254	0.0792	0.29	0.0028	0.0217	0.39	0.1183	0.2821	0.11	0.0090	0.0693	0.34	0.0075	0.0893	-0.36	0.0309	0.0506	-0.48	0.0143	0.1033	-0.36
3039 Peptidyl-prolyl cis-trans isomerase FKBP10	Q96AY3	0.0049	0.0432	0.15	0.0293	0.5128	0.12	0.0034	0.0315	0.20	0.0132	0.0467	0.11	0.0441	0.1555	0.07	0.0995	0.2332	0.16	0.0916	0.2431	0.30	0.7027	1.1446	0.05	0.2435	0.3136	-0.15
3040 Peptidyl-prolyl cis-trans isomerase FKBP14	Q9NWM8	0.5870	0.6536	-0.08	0.8626	0.9009	-0.02	0.2952	0.4758	-0.10	0.4191	0.6107	0.07	0.0367	0.1394	0.68	0.8671	1.1033	-0.02	0.0278	0.1365	-0.25	0.3249	0.6789	0.09	0.0797	0.9027	0.01
3041 Peptidyl-prolyl cis-trans isomerase FKBP1A	P62942	0.0560	0.1548	0.17	0.2387	0.6609	0.21	0.0233	0.0752	0.22	0.0366	0.0920	0.20	0.0631	0.1903	0.17	0.0230	0.0969	0.25	0.1842	0.3854	0.23	0.6290	1.0651	-0.04	0.0687	0.1161	-0.11
3042 Peptidyl-prolyl cis-trans isomerase FKBP2	P26885	0.0452	0.1356	0.09	0.2873	0.8935	-0.01	0.0093	0.0448	-0.20	0.0046	0.0275	-0.19	0.1594	0.3422	-0.05	0.4667	0.6891	0.05	0.0030	0.0600	-0.38	0.0199	0.1224	-0.31	0.0008	0.0345	-0.71
3043 Peptidyl-prolyl cis-trans isomerase FKBP3	Q00688	0.0273	0.1001	0.23	0.1918	0.6681	0.26	0.0151	0.0578	0.28	0.0117	0.0434	0.32	0.4888	0.5785	0.04	0.0122	0.0743	0.36	0.1079	0.2682	0.19	0.0088	0.0771	0.39	0.3636	0.4351	0.07
3044 Peptidyl-prolyl cis-trans isomerase FKBP4	Q02790	0.0092	0.0569	0.28	0.1603	0.6643	0.27	0.0015	0.0229	0.45	0.0104	0.0410	0.32	0.0492	0.1634	0.17	0.0230	0.0970	0.26	0.0668	0.2033	0.34	0.7295	1.1746	-0.03	0.0766	0.8161	-0.02
3045 Peptidyl-prolyl cis-trans isomerase FKBP5	P13451	0.0211	0.0861	0.11	0.2817	0.6642	0.19	0.0345	0.0966	0.14	0.0012	0.0158	0.25	0.5332	0.6187	0.02	0.0074	0.0646	0.18	0.0135	0.1101	0.56	0.8396	1.2837	-0.02	0.6778	0.7312	0.08
3046 Peptidyl-prolyl cis-trans isomerase FKBP7	Q9Y680	0.2193	0.3954	0.15	0.9186	0.9439	0.01	0.0376	0.1020	-0.39	0.7571	0.7907	-0.06	0.2247	0.4333	-0.14	0.7061	0.9478	0.15	0.3736	0.4453	-2.55	0.8708	0.9320	-0.33	0.0651	0.1176	2.06
3047 Peptidyl-prolyl cis-trans isomerase FKBP8	Q14318	0.2414	0.4269	0.08	0.1383	0.6513	0.23	0.0070	0.0400	0.24	0.1866	0.3140	0.10	0.1850	0.3794	0.06	0.0101	0.0700	0.24	0.0105	0.1024	-0.30	0.0017	0.0339	-0.43	0.0033	0.0578	-0.41
3048 Peptidyl-prolyl cis-trans isomerase FKBP9	Q95302	0.0030	0.0365	-0.08	0.1215	0.6503	-0.15	0.0004	0.0203	-0.21	0.0008	0.0150	-0.25	0.0004	0.0177	-0.20	0.1683	0.3333	-0.11	0.3736	0.5101	-2.55	0.8708	1.0519	-0.33	0.0651	0.1455	2.06
3049 Peptidyl-prolyl cis-trans isomerase H	Q43447	0.4108	0.5419	-3.31	0.5752	0.7585	-1.75	0.5661	0.6859	-1.19	0.5388	0.6488	0.89	0.2938	0.4396	-1.88	0.9510	1.0457	0.09	0.7632	0.7987	0.06	0.3142	0.6624	-0.18	0.1940	0.2620	-0.27
3050 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	P13526	0.3503	0.5600	0.03	0.1031	0.6449	0.14	0.0633	0.0611	0.11	0.0633	0.1373	0.05	0.0118	0.0781	0.08	0.1009	0.2349	0.11	0.0689	0.2068	0.33	0.0182	0.2800	0.35	0.0171	0.0934	0.79
3051 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	Q9Y237	0.0114	0.0612	0.05	0.1604	0.6642	0.36	0.0449	0.1161	0.22	0.0015	0.0172	0.21	0.0008	0.0223	0.11	0.1298	0.2806	0.10	0.3736	0.5245	-2.55	0.8708	1.0781	-0.33	0.0651	0.1524	2.06
3052 Peptidyl-prolyl cis-trans isomerase-like 1	Q9Y3C6	0.2163	0.3915	-0.10	0.5705	0.8837	0.08	0.1272	0.2471	0.13	0.0761	0.1579	0.17	0.5598	0.6424	-0.04	0.2266	0.4096	0.09	0.0397	0.1640	0.42	0.2651	0.5950	0.07	0.0412	0.1032	0.25
3053 Peptidyl-prolyl isomerase domain and WD repeat-containing protein 1	Q96BP3	0.1822	0.3460	0.16	0.6182	0.7172	-0.07	0.5612	0.7857	-0.07	0.3354	0.5092	-0.11	0.4814	0.5713	-0.08	0.7722	1.0096	-0.03	0.4882	0.5421	0.07	0.8456	1.2883	0.02	0.1865	0.2539	0.16
3054 Peptidyl-rRNA hydrolase 2_mitochondrial	Q9Y3E5	0.0213	0.0869	-0.17	0.0315	0.5099	-0.34	0.0333	0.0944	-0.10	0.0009	0.0147	-0.32	0.0056	0.0558	-0.18	0.0784	0.2003	-0.11	0.3736	0.5445	-2.55	0.8708	1				

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

			MCF-7				Gen SC20 vs control				SSE SC20 vs control				Dai IC20 vs control				Gen IC20 vs control				SSE IC20 vs control				MDA-MB-231				Gen IC20 vs control				SSE IC20 vs control			
	Protein name	UniProt	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC			
3095	Phosphatidylinositol 3_4_5-trisphosphate-dependent Rac exchanger 1 protein	Q8TCU6	0.0004	0.0162	0.37	0.1310	0.6457	0.18	0.0128	0.0532	0.23	0.0001	0.0076	0.22	0.0000	0.0000	0.27	0.0359	0.1224	0.27	0.3736	0.5736	-2.55	0.8708	1.1662	-0.33	0.0651	0.1778	2.06									
3096	Phosphatidylinositol 3_4_5-trisphosphate-dependent Rac exchanger 2 protein	Q70Z35	0.2792	0.4728	-0.04	0.4113	0.7518	0.08	0.0431	0.1129	0.12	0.2174	0.3554	0.05	0.0682	0.1988	-0.11	0.1344	0.2866	0.10	0.0070	0.0865	0.36	0.8035	1.2469	-0.01	0.0366	0.1643	0.42									
3097	Phosphatidylinositol 3-kinase catalytic subunit type 3	Q8NEB9	0.7401	0.7893	0.06	0.4103	0.7507	-0.41	0.0863	0.1831	-0.52	0.2293	0.3725	-0.34	0.0422	0.1518	-0.60	0.0717	0.1890	-0.80	0.3736	0.5489	-2.55	0.8708	1.1221	-0.33	0.0651	0.1646	2.06									
3098	Phosphatidylinositol 3-kinase regulatory subunit beta	Q00459	0.4799	0.5546	0.15	0.3102	0.6794	-0.52	0.3650	0.5622	-0.20	0.1774	0.3017	-0.34	0.6480	0.7160	0.09	0.9358	1.1717	-0.02	0.3736	0.4322	-2.55	0.8708	0.9072	-0.33	0.0651	0.1124	2.06									
3099	Phosphatidylinositol 4_5-bisphosphate 3-kinase catalytic subunit beta isoform	P42338	0.0002	0.0136	0.34	0.1664	0.6600	0.15	0.5974	0.6537	-0.03	0.1576	0.2754	0.04	0.0183	0.0963	0.11	0.2331	0.4171	0.12	0.3736	0.4942	-2.55	0.8708	1.0228	-0.33	0.0651	0.1383	2.06									
3100	Phosphatidylinositol 4-kinase alpha	P42356	0.0171	0.0764	0.16	0.2919	0.6696	0.11	0.0032	0.0302	0.32	0.0498	0.1148	0.11	0.2746	0.4991	0.05	0.0115	0.0732	0.22	0.3726	0.6545	0.07	0.4066	0.7924	-0.06	0.4779	0.5464	-0.05									
3101	Phosphatidylinositol 4-kinase type 2-alpha	Q9BTU6	0.4108	0.5404	-3.31	0.5752	0.7566	-1.75	0.5661	0.6843	-1.19	0.5388	0.6473	0.89	0.2938	0.4383	-1.88	0.9510	1.0435	0.09	0.0089	0.0935	-0.83	0.0042	0.0526	-0.94	0.0163	0.1095	-0.73									
3102	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	O00443	0.4108	0.5402	-3.31	0.5752	0.7564	-1.75	0.5661	0.6842	-1.19	0.5388	0.6471	0.89	0.2938	0.4382	-1.88	0.9510	1.0432	0.09	0.1478	0.3329	0.36	0.0925	0.3023	0.48	0.8138	0.8492	0.04									
3103	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	Q99755	0.4108	0.5401	-3.31	0.5752	0.7562	-1.75	0.5661	0.6840	-1.19	0.5388	0.6470	0.89	0.2938	0.4381	-1.88	0.9510	1.0430	0.09	0.0019	0.0526	0.87	0.0060	0.0622	0.81	0.0129	0.0990	0.56									
3104	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta	P78356	0.4108	0.5400	-3.31	0.5752	0.7560	-1.75	0.5661	0.6839	-1.19	0.5388	0.6468	0.89	0.2938	0.4380	-1.88	0.9510	1.0428	0.09	0.0258	0.1401	-0.59	0.0363	0.1738	-0.85	0.1867	0.2540	-0.73									
3105	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	Q8TBX8	0.0058	0.0459	0.27	0.1010	0.4350	0.23	0.0014	0.0233	0.39	0.0030	0.0227	0.36	0.0159	0.0900	0.30	0.0029	0.0550	0.39	0.3736	0.6387	-2.55	0.8708	1.2800	-0.33	0.0651	0.2171	2.06									
3106	Phosphatidylinositol transfer protein alpha isoform	Q00169	0.0031	0.0363	0.60	0.0099	0.4459	0.46	0.4005	0.6036	0.03	0.0874	0.1753	-0.12	0.1217	0.2872	0.09	0.2030	0.3809	-0.09	0.2190	0.4407	0.08	0.1506	0.4185	0.13	0.2431	0.3134	0.07									
3107	Phosphatidylinositol transfer protein beta isoform	P48739	0.3297	0.5359	0.09	0.2795	0.6650	0.13	0.0746	0.1637	0.21	0.1151	0.2160	0.16	0.4048	0.5010	0.07	0.4328	0.6538	0.10	0.1035	0.2614	0.28	0.2678	0.5979	0.14	0.2645	0.3364	0.14									
3108	Phosphatidylinositol-binding clathrin assembly protein	Q13492	0.0059	0.0464	0.19	0.0618	0.5917	0.39	0.0112	0.0492	0.40	0.0007	0.0136	0.33	0.0011	0.0265	0.30	0.0081	0.0672	0.23	0.6064	0.6541	0.05	0.4607	0.8672	-0.04	0.0355	0.1612	-0.26									
3109	Phosphoenolpyruvate carboxykinase	Q95394	0.2792	0.4726	0.06	0.1701	0.6610	0.19	0.0035	0.0314	0.29	0.0013	0.0167	0.39	0.0239	0.1119	0.22	0.0072	0.0650	0.30	0.0065	0.0850	0.55	0.0352	0.1707	0.24	0.0009	0.0367	0.54									
3110	Phosphoenolpyruvate carboxykinase [GTP]_mitochondrial	Q11682	0.0019	0.0302	0.29	0.4580	0.7903	0.06	0.0002	0.0159	0.34	0.0000	0.0000	0.54	0.1304	0.2987	-0.05	0.0001	0.0247	0.57	0.0286	0.1458	0.51	0.0669	0.2490	0.17	0.0214	0.1248	0.34									
3111	Phosphoenolpyruvate carboxykinase cytosolic [GTP]	P35558	0.3613	0.5739	0.11	0.7442	0.8147	0.04	0.0996	0.2033	0.25	0.0914	0.1812	0.25	0.4020	0.4982	0.10	0.0909	0.2201	0.26	0.3736	0.5373	-2.55	0.8708	1.1013	-0.33	0.0651	0.1587	2.06									
3112	Phosphoglucosyltransferase	P36871	0.0009	0.0216	0.93	0.0312	0.5098	0.41	0.0095	0.0456	0.47	0.0894	0.1782	0.37	0.0069	0.0602	0.64	0.0071	0.0649	0.65	0.1601	0.3532	0.12	0.5851	1.0171	-0.04	0.0563	0.2107	-0.18									
3113	Phosphoglucomutase-2	Q96G03	0.5119	0.5846	0.04	0.8116	0.8647	0.02	0.5138	0.7346	0.03	0.8688	0.8875	0.01	0.1261	0.2929	-0.10	0.3014	0.4994	0.06	0.0071	0.0867	0.28	0.0333	0.1651	0.18	0.0241	0.1324	0.21									
3114	Phosphoglycerate kinase 1	P00558	0.0002	0.0135	0.45	0.0517	0.5772	0.24	0.0005	0.0212	0.38	0.0022	0.0205	0.28	0.1741	0.3631	0.05	0.0045	0.0598	0.34	0.9739	0.9790	0.00	0.0136	0.0973	-0.39	0.0165	0.1101	-0.48									
3115	Phosphoglycerate kinase 2	P07205	0.5998	0.6656	-0.04	0.1693	0.6614	-0.13	0.6982	0.7457	-0.03	0.5163	0.7215	0.06	0.8876	0.9139	-0.01	0.0607	0.1709	0.34	0.6442	0.6889	-0.03	0.6738	1.1130	0.03	0.8602	0.8867	0.01									
3116	Phosphoglycerate mutase 1	P18669	0.0051	0.0437	0.18	0.2280	0.6602	0.24	0.0017	0.0235	0.26	0.0019	0.0195	0.17	0.1908	0.3871	-0.03	0.0250	0.1005	0.19	0.2701	0.5131	0.14	0.2431	0.5614	-0.10	0.4813	0.5496	-0.04									
3117	Phosphoglycerate mutase 2	P15259	0.1501	0.2995	-0.45	0.2863	0.6671	-1.21	0.3189	0.5063	-0.29	0.5589	0.6098	-0.15	0.1989	0.6070	-0.18	0.2770	0.4723	-0.33	0.0007	0.0417	-1.05	0.0003	0.0213	-0.71	0.4476	0.5173	-0.09									
3118	Phosphoinositide 3-kinase adapter protein 1	Q6ZUJ8	0.4108	0.5398	-3.31	0.5752	0.7558	-1.75	0.5661	0.6837	-1.19	0.5388	0.6467	0.89	0.2938	0.4378	-1.88	0.9510	1.0426	0.09	0.0003	0.0338	10.14	0.8708	1.3120	-0.33	0.0027	0.0542	9.75									
3119	Phosphoinositide 3-kinase regulatory subunit 6	Q5UJ93	0.4108	0.5397	-3.31	0.5752	0.7557	-1.75	0.5661	0.6835	-1.19	0.5388	0.6465	0.89	0.2938	0.4377	-1.88	0.9510	1.0423	0.09	0.0475	0.1745	0.49	0.2548	0.5794	0.06	0.1849	0.2523	0.06									
3120	Phospholipase A2-activating protein	Q9Y263	0.3116	0.5127	0.04	0.3707	0.7186	0.11	0.0199	0.0680	0.13	0.5367	0.7443	0.03	0.0651	0.1944	-0.09	0.2192	0.4007	0.05	0.1119	0.2754	0.33	0.3340	0.6912	-0.09	0.2428	0.3131	-0.09									
3121	Phospholipase D1	Q13393	0.0996	0.2243	0.24	0.6805	0.7665	0.03	0.9619	0.9690	0.00	0.3203	0.4913	-0.16	0.1079	0.2662	0.17	0.7150	0.9551	-0.04	0.2358	0.4653	0.08	0.7467	1.1879	-0.03	0.1834	0.2509	0.16									
3122	Phospholipase D2	Q14939	0.7329	0.7828	-0.03	0.2437	0.6585	0.16	0.9428	0.9553	0.00	0.6429	0.6872	-0.04	0.3432	0.4400	0.09	0.7405	0.9803	0.03	0.3736	0.4425	-2.55	0.8708	0.9268	-0.33	0.0651	0.1165	2.06									
3123	Phospholipase DDHD2	Q94K30	0.2688	0.4607	0.09	0.0121	0.4353	0.43	0.0123	0.0521	0.34	0.0006	0.0126	0.76	0.0013	0.0284	0.80	0.0027	0.0562	0.63	0.1115	0.2749	0.22	0.3828	0.7612	-0.14	0.2600											

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
3163 Platelet-activating factor acetylhydrolase IB subunit alpha	P43034	0.0142	0.0694	0.19	0.2136	0.6625	0.19	0.0088	0.0439
3164 Platelet-activating factor acetylhydrolase IB subunit gamma	Q15102	0.6184	0.6820	0.04	0.1963	0.6690	0.28	0.1332	0.2554
3165 Platelet-derived growth factor receptor alpha	P16234	0.9943	0.9951	0.00	0.9433	0.9624	0.03	0.1013	0.2061
3166 Pleckstrin homology domain-containing family A member 1	Q9HB21	0.3885	0.6052	0.09	0.9644	0.9757	-0.01	0.1420	0.2679
3167 Pleckstrin homology domain-containing family B member 1	Q9UF11	0.0028	0.0355	-0.94	0.5963	0.7006	-0.11	0.0087	0.0437
3168 Pleckstrin homology domain-containing family G member 3	A1L390	0.2469	0.4327	0.07	0.2720	0.6652	0.19	0.0528	0.1300
3169 Pleckstrin homology domain-containing family G member 4B	Q96PX9	0.4108	0.5382	-3.31	0.5752	0.7535	-1.75	0.5661	0.6818
3170 Pleckstrin homology domain-containing family H member 1	Q9ULM0	0.4108	0.5380	-3.31	0.5752	0.7534	-1.75	0.5661	0.6816
3171 Pleckstrin homology domain-containing family H member 2	Q8IVE3	0.3869	0.6037	0.20	0.3948	0.7383	-0.07	0.8241	0.8581
3172 Pleckstrin homology domain-containing family H member 3	Q7Z736	0.0128	0.0662	-0.21	0.1737	0.6611	0.25	0.6114	0.6663
3173 Pleckstrin homology domain-containing family M member 1	Q9Y4G2	0.6430	0.7048	-0.02	0.0656	0.5951	0.09	0.1376	0.2614
3174 Pleckstrin homology-like domain family B member 2	Q86S00	0.0128	0.0661	0.22	0.2898	0.6687	0.21	0.0931	0.1932
3175 Pleckstrin-2	Q9NYT0	0.4108	0.5379	-3.31	0.5752	0.7532	-1.75	0.5661	0.6815
3176 Plectin	Q15149	0.0358	0.1183	0.20	0.1912	0.6683	0.28	0.0043	0.0324
3177 Plexin-A1	Q9UIW2	0.4108	0.5378	-3.31	0.5752	0.7530	-1.75	0.5661	0.6813
3178 Plexin-A3	P51805	0.4108	0.5376	-3.31	0.5752	0.7528	-1.75	0.5661	0.6812
3179 PMS1 protein homolog 1	P54277	0.0015	0.0263	-0.42	0.5211	0.8412	-0.05	0.0432	0.1129
3180 Poly [ADP-ribose] polymerase 1	P09874	0.0517	0.1471	0.16	0.2209	0.6599	0.19	0.0034	0.0310
3181 Poly [ADP-ribose] polymerase 2	Q9UGN5	0.1885	0.3544	0.04	0.2205	0.7590	-0.04	0.1120	0.2235
3182 Poly(A) polymerase alpha	P51003	0.1335	0.2766	0.08	0.1702	0.6609	0.14	0.0325	0.0927
3183 Poly(A) polymerase beta	Q9NRJ5	0.6273	0.6902	-0.04	0.5537	0.8691	-0.15	0.0039	0.0314
3184 Poly(A) RNA polymerase mitochondrial	Q9NVV4	0.5611	0.6297	0.01	0.2110	0.6624	0.20	0.0557	0.1348
3185 Poly(A)-specific ribonuclease PARN	O95453	0.4108	0.5375	-3.31	0.5752	0.7526	-1.75	0.5661	0.6810
3186 Poly(C)-binding protein 1	Q15365	0.0048	0.0435	0.19	0.3007	0.6737	0.22	0.0053	0.0311
3187 Poly(C)-binding protein 2	Q15366	0.0008	0.0205	0.43	0.2999	0.6731	-0.15	0.0234	0.0753
3188 Poly(C)-binding protein 4	P57723	0.0142	0.0693	-0.59	0.2659	0.6628	-0.30	0.0492	0.1236
3189 Poly(U)-binding splicing factor PUF60	Q9UIHX1	0.8118	0.8485	0.01	0.2575	0.6623	-0.09	0.0755	0.1653
3190 Polyadenylate-binding protein 1	P11940	0.0102	0.0589	0.32	0.4251	0.7617	0.13	0.0360	0.0992
3191 Polyadenylate-binding protein 1-like	Q4VXU2	0.3026	0.5021	0.08	0.3287	0.6882	0.10	0.7953	0.8326
3192 Polyadenylate-binding protein 1-like 2	Q5JQF8	0.0584	0.1593	0.08	0.0949	0.6319	0.32	0.0065	0.0390
3193 Polyadenylate-binding protein 3	Q9H361	0.9421	0.9567	0.04	0.9472	0.9653	-0.02	0.0249	0.0782
3194 Polyadenylate-binding protein 4	Q13310	0.0019	0.0301	-0.68	0.1974	0.6710	-0.38	0.0013	0.0229
3195 Polyadenylate-binding protein 4-like	POCB38	0.0005	0.0180	0.34	0.1017	0.6309	0.25	0.8705	0.8975
3196 Polyadenylate-binding protein 5	Q96DU9	0.7969	0.8356	-0.02	0.2960	0.6716	0.11	0.4980	0.7202
3197 Polyadenylate-binding protein-interacting protein 1	Q9H074	0.5491	0.6183	0.04	0.5630	0.9301	0.16	0.8537	0.8832
3198 Polyamine-modulated factor 1-binding protein 1	Q8TBY8	0.4172	0.4949	0.04	0.0548	0.5853	0.31	0.0159	0.0596
3199 Polycomb protein SCMH1	Q96GD3	0.4108	0.5374	-3.31	0.5752	0.7524	-1.75	0.5661	0.6808
3200 Polyclin-2	Q13563	0.0887	0.2077	0.19	0.3541	0.7057	-0.13	0.1610	0.2959
3201 Polyubiquitin-binding protein 1	Q60828	0.4108	0.5372	-3.31	0.5752	0.7522	-1.75	0.5661	0.6807
3202 Polyubiquitin-interacting protein 2	Q9Y257	0.0266	0.0987	-0.05	0.2442	0.6571	0.16	0.0929	0.1930
3203 Polymeric immunoglobulin receptor	P01833	0.1493	0.2984	0.04	0.4983	0.8207	0.04	0.0367	0.1005
3204 Polypeptide N-acetylgalactosaminyltransferase 11	Q8NCW6	0.0246	0.0947	0.13	0.5060	0.8279	0.12	0.0028	0.0289
3205 Polypeptide N-acetylgalactosaminyltransferase 2	Q10471	0.1749	0.3367	0.08	0.4068	0.8279	0.07	0.2277	0.3868
3206 Polypeptide N-acetylgalactosaminyltransferase 3	Q14435	0.0622	0.1654	-1.37	0.2309	0.6841	-0.99	0.0841	0.1795
3207 Polypeptide N-acetylgalactosaminyltransferase 4	Q8N4A0	0.4108	0.5371	-3.31	0.5752	0.7520	-1.75	0.5661	0.6805
3208 Polypeptide N-acetylgalactosaminyltransferase 6	Q8NCL4	0.3486	0.5578	-0.10	0.4789	0.8046	0.06	0.4983	0.7204
3209 Polypyrimidine tract-binding protein 1	P26599	0.1666	0.3246	-0.03	0.0771	0.6116	-0.09	0.2113	0.3659
3210 Polypyrimidine tract-binding protein 2	Q9UKA9	0.5089	0.5818	-0.02	0.1795	0.6637	-0.21	0.0007	0.0205
3211 Polypyrimidine tract-binding protein 3	Q95758	0.1443	0.2913	-0.07	0.1063	0.6307	-0.24	0.0007	0.0208
3212 Polyrhombic nucleotide nucleotidyltransferase 1, mitochondrial	Q8TCS8	0.0347	0.1166	0.23	0.2826	0.6645	0.17	0.0070	0.0397
3213 Porphobilinogen deaminase	P08397	0.0012	0.0240	0.14	0.4475	0.7823	0.13	0.0267	0.0817
3214 Potassium voltage-gated channel subfamily A member 2	P16389	0.0050	0.0434	0.98	0.9215	0.9458	-0.04	0.0491	0.6271
3215 Potassium voltage-gated channel subfamily A member 5	P22460	0.0009	0.0245	-1.02	0.0219	0.4455	-0.52	0.0042	0.0264
3216 Potassium voltage-gated channel subfamily G member 3	Q8TAE7	0.0791	0.1928	-0.68	0.2339	0.6614	-0.71	0.0305	0.0889
3217 Potassium-transporting ATPase alpha chain 1	P20648	0.0555	0.1539	0.10	0.7870	0.8465	-0.04	0.3218	0.5093
3218 Potassium-transporting ATPase alpha chain 2	P54707	0.0073	0.0502	0.18	0.2633	0.6637	0.26	0.0162	0.0602
3219 POTE ankyrin domain family member A	Q6S8U7	0.0225	0.0894	0.17	0.8987	0.9281	-0.01	0.0179	0.0636
3220 POTE ankyrin domain family member E	Q6S8U3	0.5263	0.5977	0.06	0.1772	0.6707	0.10	0.6036	0.6595
3221 POTE ankyrin domain family member F	ASA3E0	0.0024	0.0232	0.20	0.0581	0.5878	0.20	0.0004	0.0230
3222 POTE ankyrin domain family member I	POCC38	0.0015	0.0362	0.29	0.2855	0.6652	0.22	0.0285	0.0855
3223 POTE ankyrin domain family member J	POCC39	0.4108	0.5370	-3.31	0.5752	0.7518	-1.75	0.5661	0.6804
3224 PR domain zinc finger protein 4	Q9UKN5	0.6974	0.7518	-0.05	0.0312	0.0882	0.26	0.5070	0.7285
3225 PRAI family protein 2	O60831	0.3293	0.5359	-0.13	0.0295	0.5077	-0.44	0.0236	0.0755
3226 PRAI family protein 3	O75915	0.0166	0.0752	-0.25	0.3346	0.6933	-0.17	0.0064	0.0386
3227 PRAME family member 17	Q5VTA0	0.0511	0.1463	-0.21	0.3927	0.7365	-0.27	0.9967	0.9973
3228 PRAME family member 18	Q5VWM3	0.0052	0.0440	0.50	0.0041	0.3371	0.47	0.0059	0.0374
3229 PRAME family member 19	Q5WSL8	0.4108	0.5368	-3.31	0.5752	0.7516	-1.75	0.5661	0.6802
3230 PRAME family member 2	O60811	0.4108	0.5367	-3.31	0.5752	0.7515	-1.75	0.5661	0.6801
3231 PRAME family member 33	AOA0G2JMD5	0.0776	0.1907	0.53	0.0776	0.6118	0.30	0.0022	0.0267
3232 Pre-B-cell leukemia transcription factor 1	P40424	0.7417	0.7905	0.03	0.9854	0.9896	0.00	0.0102	0.0470
3233 Pre-B-cell leukemia transcription factor 4	Q9BYU1	0.4108	0.5365	-3.31	0.5752	0.7513	-1.75	0.5661	0.6799
3234 Prefoldin subunit 1	O60925	0.2616	0.4514	-0.04	0.5739	0.8858	0.05	0.4159	0.6228
3235 Prefoldin subunit 2	Q9UHV9	0.0317	0.1104	0.18	0.4778	0.8036	0.16	0.0088	0.0438

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
3236 Prefoldin subunit 3	P61758	0.1671	0.3252	0.04	0.2549	0.6618	0.17	0.0567	0.1362	0.13	0.0336	0.0870	0.16	0.0004	0.0161	0.10	0.0006	0.0420	0.12	0.9134	0.9294	0.01	0.0146	0.1012	-0.30	0.0108	0.0908	-0.38
3237 Prefoldin subunit 4	Q9NQP4	0.0826	0.1979	0.08	0.5494	0.7087	0.04	0.0020	0.0248	0.33	0.0013	0.0168	0.29	0.2421	0.4559	0.04	0.0144	0.0799	0.17	0.2079	0.4233	0.16	0.0548	0.2240	-0.23	0.2662	0.3377	-0.09
3238 Prefoldin subunit 5	Q9Y471	0.0157	0.0728	0.21	0.2103	0.6622	0.26	0.0035	0.0313	0.35	0.0024	0.0210	0.33	0.3277	0.4249	0.03	0.0052	0.0568	0.23	0.2568	0.4956	0.09	0.8080	1.2513	-0.01	0.0976	0.1528	-0.01
3239 Prefoldin subunit 6	Q15212	0.8135	0.8501	0.01	0.2735	0.6642	0.13	0.0126	0.0525	0.18	0.0557	0.1248	0.11	0.3894	0.4865	0.03	0.0891	0.2177	0.09	0.0276	0.1438	0.18	0.0233	0.1346	0.17	0.2509	0.1342	0.21
3240 Pregnancy-specific beta-1-glycoprotein 5	Q15238	0.0974	0.2708	0.17	0.0018	0.2230	-0.62	0.0301	0.0881	-0.26	0.0485	0.1127	-0.34	0.0128	0.0807	-0.38	0.5428	0.7746	-0.05	0.3736	0.4573	-2.55	0.8708	0.9545	-0.33	0.0651	0.1224	0.06
3241 Pregnancy-specific beta-1-glycoprotein 9	Q00887	0.0229	0.0903	0.17	0.0389	0.5582	0.14	0.0042	0.0252	0.30	0.1333	0.2410	0.17	0.2303	0.4402	0.07	0.2727	0.4668	0.14	0.3102	0.5706	0.12	0.1398	0.3970	-0.25	0.0278	0.1430	-0.43
3242 Prelamin-A/C	P02545	0.9035	0.9252	0.01	0.6599	0.7490	0.09	0.1007	0.0350	0.17	0.9741	0.9777	0.00	1.903	3.864	-0.12	0.0615	0.1724	0.24	0.0114	0.1040	0.77	0.0501	0.2105	0.29	0.0054	0.0706	0.06
3243 Pre-mRNA 3' end processing protein WDR33	Q9C0U8	0.4108	0.5364	-3.31	0.5752	0.7511	-1.75	0.5661	0.6797	-1.19	0.5388	0.6429	0.89	0.2938	0.4347	-1.88	0.9510	1.0371	0.09	0.0956	0.2490	0.53	0.7367	1.1804	-0.05	0.3292	0.4004	0.16
3244 Pre-mRNA-processing factor 17	O60508	0.4108	0.5363	-3.31	0.5752	0.7509	-1.75	0.5661	0.6796	-1.19	0.5388	0.6428	0.89	0.2938	0.4346	-1.88	0.9510	1.0369	0.09	0.0011	0.0422	1.25	0.0002	0.0185	1.13	0.0030	0.0557	1.06
3245 Pre-mRNA-processing factor 19	Q9UM54	0.1166	0.2506	0.08	0.5391	0.8548	0.11	0.0228	0.0743	0.15	0.0062	0.0315	0.22	0.0223	0.1077	-0.19	0.0547	0.1589	0.13	0.0695	0.2075	0.20	0.6880	1.1299	0.03	0.2922	0.3640	0.09
3246 Pre-mRNA-processing factor 40 homolog A	O75400	0.9070	0.9276	0.01	0.3968	0.7407	-0.08	0.0393	0.1052	0.21	0.4714	0.6710	0.05	0.4884	0.5781	-0.05	0.5398	0.7718	0.07	0.0502	0.1784	0.17	0.0005	0.0211	-0.15	0.0271	0.1407	-0.07
3247 Pre-mRNA-processing factor 40 homolog B	Q6NWY9	0.0137	0.0685	-0.14	0.5203	0.8409	-0.08	0.0206	0.0692	0.20	0.3456	0.5213	-0.03	0.0187	0.0975	0.17	0.0021	0.0536	0.45	0.0031	0.0615	0.18	0.8838	1.334	0.18	0.8838	1.334	0.18
3248 Pre-mRNA-processing factor 6	O94906	0.0084	0.0543	-0.51	0.0553	0.5846	-0.28	0.7613	0.8022	0.03	0.0074	0.0348	-0.53	0.0022	0.0366	-0.86	0.0093	0.0692	-0.58	0.1334	0.3106	0.18	0.8838	1.334	0.18	0.8838	1.334	0.18
3249 Pre-mRNA-processing-splicing factor 8	Q6P2Q9	0.4108	0.5361	-3.31	0.5752	0.7507	-1.75	0.5661	0.6794	-1.19	0.5388	0.6426	0.89	0.2938	0.4345	-1.88	0.9510	1.0367	0.09	0.0561	0.1875	0.33	0.0011	0.0278	0.33	0.0095	0.0874	0.19
3250 Pre-mRNA-splicing factor 38B	Q5VTL8	0.0844	0.2005	-0.12	0.1984	0.6656	-0.75	0.0982	0.2013	0.11	0.1857	0.3129	0.08	0.0245	0.1132	-0.24	0.0071	0.0646	-0.52	0.0935	0.2454	-0.30	0.0501	0.0569	-0.23	0.0293	0.1464	-0.24
3251 Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	O43143	0.7996	0.8376	0.02	0.8575	0.8970	0.01	0.8886	0.9115	-0.01	0.1275	0.2330	-0.11	0.0370	0.1399	-0.20	0.6867	1.1048	-0.01	0.0006	0.0398	0.65	0.0056	0.0607	0.42	0.0022	0.0520	0.46
3252 Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	Q9V620	0.4108	0.5360	-3.31	0.5752	0.7505	-1.75	0.5661	0.6793	-1.19	0.5388	0.6425	0.89	0.2938	0.4343	-1.88	0.9510	1.0364	0.09	0.3091	0.5696	-0.77	0.3650	0.7345	-0.66	0.4307	0.5021	-0.56
3253 Pre-mRNA-splicing factor SLU7	O95391	0.4108	0.5359	-3.31	0.5752	0.7503	-1.75	0.5661	0.6791	-1.19	0.5388	0.6423	0.89	0.2938	0.4342	-1.88	0.9510	1.0362	0.09	0.0195	0.1290	0.91	0.0030	0.0453	0.81	0.1620	0.2264	-0.09
3254 Pre-mRNA-splicing factor SPF27	O75934	0.3393	0.5472	-0.08	0.1423	0.6546	-0.19	0.2287	0.3882	-0.11	0.1232	0.2261	-0.16	0.0359	0.1374	-0.31	0.3764	0.5853	-0.07	0.3736	0.4712	-2.55	0.8708	0.9804	-0.33	0.0651	0.1283	0.06
3255 Pre-mRNA-splicing factor 1	Q0U1G3	0.9483	0.9613	0.01	0.4081	0.7494	0.12	0.3627	0.5603	0.12	0.1833	0.3099	0.21	0.0780	0.2100	0.34	0.1259	0.2744	0.26	0.0006	0.0414	0.68	0.0005	0.0242	1.01	0.0077	0.0498	0.90
3256 Pre-mRNA-splicing factor TSR1 homolog	Q2NL82	0.2876	0.4840	-0.07	0.5846	0.6914	0.06	0.1963	0.3457	0.10	0.2035	0.3370	0.10	0.1615	0.3444	-0.11	0.1523	0.3097	-0.11	0.0958	0.2490	0.19	0.0326	0.1627	-0.15	0.5061	0.5728	-0.04
3257 Pre-mRNA-splicing factor TSR2 homolog	Q9P6E8	0.4108	0.5357	-3.31	0.5752	0.7501	-1.75	0.5661	0.6790	-1.19	0.5388	0.6422	0.89	0.2938	0.4341	-1.88	0.9510	1.0360	0.09	0.0489	0.1770	-0.54	0.0121	0.0920	-0.56	0.4009	0.4923	-0.10
3258 Pre-mRNA-splicing factor 1	Q5JRX3	0.0663	0.1705	0.08	0.6008	0.7044	0.06	0.0007	0.0199	0.60	0.0094	0.0395	0.16	0.3559	0.4536	0.03	0.0060	0.0618	0.26	0.3448	0.6176	0.10	0.7171	1.1626	-0.03	0.0835	0.1352	-0.12
3259 Prior-like protein doppel	Q9UKY0	0.1346	0.2781	0.40	0.5004	0.8229	-0.14	0.1578	0.2912	0.36	0.1699	0.2915	0.34	0.0173	0.0944	0.88	0.0227	0.0965	0.90	0.3736	0.5895	-2.55	0.8708	1.1943	-0.33	0.0651	0.1867	0.06
3260 PRK2 apoptosis WT1 regulator protein	Q961Z0	0.3419	0.5495	0.05	0.0548	0.5865	0.30	0.0015	0.0232	0.34	0.0150	0.0503	0.25	0.0046	0.0504	0.25	0.0234	0.0982	0.21	0.1610	0.3541	0.13	0.1026	0.3229	0.06	0.0007	0.0318	0.22
3261 PRK2-interacting protein 1	Q9H875	0.0013	0.0246	-0.34	0.0474	0.6656	-0.75	0.0982	0.2013	0.11	0.1857	0.3129	0.08	0.0245	0.1132	-0.24	0.0071	0.0646	-0.52	0.0935	0.2454	-0.30	0.0501	0.0569	-0.23	0.0293	0.1464	-0.24
3262 Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	P46087	0.4108	0.5356	-3.31	0.5752	0.7499	-1.75	0.5661	0.6788	-1.19	0.5388	0.6420	0.89	0.2938	0.4340	-1.88	0.9510	1.0358	0.09	0.0225	0.1362	0.43	0.8200	1.2642	-0.03	0.2100	0.2786	0.09
3263 Probable 28S rRNA (cytosine-C(5))-methyltransferase	Q96P11	0.2052	0.3776	-0.07	0.3972	0.7412	-0.04	0.0516	0.1276	-0.15	0.0884	0.1771	-0.11	0.0286	0.1227	-0.21	0.2260	0.4090	-0.14	0.3736	0.4962	-2.55	0.8708	1.0266	-0.33	0.0651	0.1392	0.06
3264 Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 mitochondrial	Q96H77	0.0644	0.1681	0.14	0.2472	0.6607	0.19	0.0178	0.0636	0.19	0.0043	0.0266	0.24	0.1714	0.2779	-0.01	0.0045	0.0592	0.35	0.3736	0.6316	-2.55	0.8708	1.2678	-0.33	0.0651	0.2125	0.06
3265 Probable aminopeptidase NPEPL1	Q8NDH3	0.3414	0.5494	-0.06	0.0610	0.5939	0.24	0.0038	0.0321	0.19	0.5339	0.7412	0.02	0.0280	0.1214	0.10	0.0430	0.1367	-0.16	0.3736	0.5675	-2.55	0.8708	1.1554	-0.33	0.0651	0.1745	0.06
3266 Probable ATP-dependent RNA helicase DDX17	Q9Y281	0.6526	0.7135	-0.01	0.3614	0.7099	0.14	0.0097	0.0458	0.18	0.0037	0.0246	0.15	0.0234	0.1108	-0.11	0.0110	0.0719	0.12	0.0112	0.1032	0.44	0.0310	0.1595	0.19	0.2005	0.1229	0.28
3267 Probable ATP-dependent RNA helicase DDX20	Q9U1H6	0.1461	0.2939	0.11	0.1474	0.6565	0.20	0.0381	0.1030	0.20	0.0428	0.1030	0.19	0.2030	0.4040	0.09	0.1031	0.2382	0.13	0.0716	0.2238	0.17	0.9193	0.9409	0.01	0.0527	0.2022	0.22
3268 Probable ATP-dependent RNA helicase DDX4	Q9N0P0	0.0431	0.1319	-0.10	0.0950	0.6309	-0.21	0.0565	0.1360	0.08	0.0956	0.1876	-0.05	0.0361	0.1381	-0.06	0.1856	0.3573	-0.06	0.0032	0.0621	0.41	0.0156	0.1055	0.19	0.0018	0.0491	0.49
3269 Probable ATP-dependent RNA helicase DDX46	Q7L014	0.1386	0.2832	0.07	0.3100	0.6796	0.16	0.0602	0.1419	0.12	0.1451	0.2581	0.07	0.0742	0.2090	-0.10	0.1600	0.3207	0.07	0.0018	0.0527	-1.04	0.0005	0.0240	-1.16	0.0013	0.0455	-0.59
3270 Probable ATP-dependent RNA helicase DDX5	P17844	0.0217	0.0875	0.16	0.3652	0.7136	0.14	0.0079	0.0418	0.28	0.0084	0.0371	0.21	0.1259	0.2931	-0.08	0.1699	0.3855	0.24	0.0325	0.1511	0.36	0.6546	1.0945	-0.04	0.2690	0.3408	-0.09
3271 Probable ATP-dependent RNA helicase DDX53	Q86TM3	0.4108	0.5355	-3.31	0.5752	0.7499	-1.75	0.5661	0.6786	-1.19	0.5388	0.6419	0.89	0.2938	0.4338	-1.88	0.9510	1.0356	0.09	0.8393	0.8647	-0.02	0.0975	0.3120	0.22	0.3254	0.7817	-0.02
3272 Probable ATP-dependent RNA helicase DDX6	P26196	0.0482	0.1412	0.15	0.2270	0.6598	0.24	0.0207	0.0694	0.23	0.0112	0.0426	0.24	0.1980	0.3978	-0.07	0.0352	0.1209	0.16	0.2325	0.4602	-0.10	0.4193	0.8116	-0.05	0.3764	0.1539	-0.24
3273 Probable bifunctional dTTP/UTP pyrophosphatase/methyltransferase protein	Q95671	0.0562	0.1552	0.20	0.1437	0.6541	0.23	0.0046	0.0335	0.19	0.0045	0.0273	0.41	0.0075	0.0629	0.12	0.0137	0.0780	0.05	0.0671	0.2035	0.44	0.0096	0.0810	0.89	0.2001	0.2686	0.25
3274 Probable C-mannosyltransferase DPY19L4	Q7Z388	0.																										

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
3312 Programmed cell death protein 4	Q53EL6	0.5641	0.6322	-0.05	0.0136	0.4431	-0.52	0.0769	0.1675	-0.25	0.0328	0.0856	-0.32	0.0412	0.1498	-0.34	0.0694	0.9082	-0.04	0.6314	0.6770	-0.10	0.0065	0.0654	0.18	0.0056	0.0716	-0.29
3313 Programmed cell death protein 5	I14737	0.1770	0.3392	-0.10	0.1320	0.6475	-0.17	0.5267	0.7477	0.04	0.1118	0.2116	-0.13	0.0410	0.1496	-0.21	0.1694	0.3343	-0.10	0.8313	0.8325	0.03	0.9332	0.9514	0.01	0.4776	0.5461	-0.06
3314 Programmed cell death protein 6	O75340	0.0610	0.1633	0.13	0.5841	0.6913	0.07	0.6668	0.7179	-0.02	0.6228	0.6692	-0.02	0.1336	0.3027	-0.09	0.4640	0.6867	0.04	0.0041	0.0690	-0.46	0.0033	0.0476	-0.33	0.0004	0.0276	-0.68
3315 Prohibitin	P35232	0.0308	0.1083	0.18	0.2760	0.6650	0.21	0.0117	0.7506	0.24	0.0072	0.0344	0.27	0.6626	0.7279	-0.02	0.0031	0.0972	0.23	0.0791	0.2233	0.33	0.6200	1.0551	0.04	0.0792	0.1300	-0.13
3316 Prohibitin-2	Q96K23	0.0314	0.1097	0.17	0.4410	0.7770	0.14	0.0209	0.6609	0.27	0.0275	0.0754	0.19	0.0985	0.2506	-0.11	0.0139	0.0886	0.24	0.0349	0.1546	0.39	0.2332	0.5483	0.16	0.8497	0.8787	0.02
3317 Prolactin regulatory element-binding protein	Q9HCU5	0.2255	0.4043	0.32	0.0398	0.5633	0.73	0.0286	0.0858	0.82	0.1484	0.2629	0.41	0.0215	0.1057	0.93	0.3588	0.5649	0.22	0.3736	0.4734	-2.55	0.8708	0.9844	-0.33	0.0651	0.1292	-0.06
3318 Proliferating cell nuclear antigen	P12004	0.0055	0.0448	0.29	0.1795	0.6642	0.29	0.0384	0.1035	0.24	0.0031	0.0227	0.31	0.0883	0.2328	-0.10	0.0469	0.1439	0.15	0.1165	0.2839	0.30	0.2069	0.5079	-0.15	0.0810	0.1321	-0.24
3319 Proliferation-associated protein 2G4	Q9UCQ8	0.0387	0.1236	0.17	0.2541	0.6631	0.25	0.0034	0.0309	0.38	0.0048	0.0281	0.33	0.6323	0.7024	0.02	0.0224	0.0958	0.26	0.0423	0.1676	0.51	0.2414	0.5595	0.15	0.2087	0.2776	0.13
3320 Proline-rich protein 18	Q8N4B5	0.2253	0.4041	-0.05	0.1307	0.6454	-0.38	0.0132	0.0538	-0.36	0.0086	0.0375	-0.52	0.0002	0.0136	-0.78	0.0276	0.1067	-0.83	0.3736	0.5833	-2.55	0.8708	1.1833	-0.33	0.0651	0.1832	-0.06
3321 Proline-serine-threonine phosphatase-interacting protein 1	O43586	0.7458	0.7931	0.02	0.5317	0.8503	0.08	0.6223	0.6762	0.03	0.2298	0.3729	0.10	0.5129	0.6019	-0.05	0.1842	0.3551	0.11	0.3736	0.5058	-2.55	0.8708	1.0442	-0.33	0.0651	0.1436	-0.06
3322 Proline-serine-threonine phosphatase-interacting protein 2	Q9H939	0.4108	0.5339	-3.31	0.5752	0.7475	-1.75	0.5661	0.6768	-1.19	0.5388	0.6401	0.89	0.2938	0.4324	-1.88	0.9510	1.0330	0.09	0.0088	0.0932	-0.95	0.0021	0.0380	-0.73	0.6449	0.7014	-0.20
3323 Prolyl 3-hydroxylase 1	Q32P28	0.4108	0.5337	-3.31	0.5752	0.7473	-1.75	0.5661	0.6766	-1.19	0.5388	0.6400	0.89	0.2938	0.4322	-1.88	0.9510	1.0327	0.09	0.1815	0.3823	0.15	0.3945	0.7782	-0.03	0.3551	0.4268	-0.08
3324 Prolyl 3-hydroxylase 2	Q8IVL5	0.0205	0.0846	0.80	0.0603	0.5938	-0.81	0.0051	0.0350	1.43	0.0017	0.0183	1.57	0.0020	0.0355	1.16	0.0321	0.1157	2.38	0.0885	0.2395	1.12	0.1170	0.3522	-0.87	0.1945	0.2625	1.27
3325 Prolyl 3-hydroxylase OGFOD1	Q8N543	0.4108	0.5336	-3.31	0.5752	0.7471	-1.75	0.5661	0.6764	-1.19	0.5388	0.6398	0.89	0.2938	0.4321	-1.88	0.9510	1.0325	0.09	0.5347	0.5867	0.05	0.7867	1.2304	-0.02	0.6020	0.6628	0.03
3326 Prolyl 4-hydroxylase subunit alpha-1	P13674	0.2517	0.4384	-0.08	0.1010	0.6326	0.33	0.3379	0.5304	0.07	0.6983	0.7376	-0.03	0.0693	0.2003	-0.18	0.5909	0.8277	-0.03	0.1314	0.5718	0.11	0.9034	0.9278	0.01	0.0162	0.1090	-0.28
3327 Prolyl 4-hydroxylase subunit alpha-2	I15460	0.4108	0.5335	-3.31	0.5752	0.7469	-1.75	0.5661	0.6763	-1.19	0.5388	0.6397	0.89	0.2938	0.4320	-1.88	0.9510	1.0323	0.09	0.3685	0.6501	-0.13	0.1973	0.4930	0.21	0.0458	0.1871	0.42
3328 Prolyl endopeptidase	P48147	0.3058	0.5067	0.08	0.2340	0.6609	0.13	0.0030	0.0299	0.25	0.0093	0.0388	0.18	0.2436	0.4577	0.05	0.0196	0.0902	0.26	0.0704	0.2095	0.23	0.0549	0.2241	-0.26	0.6501	0.7061	-0.15
3329 Prolyl endopeptidase FAP	U12884	0.0321	0.1114	0.45	0.1981	0.6681	0.53	0.0021	0.0258	0.27	0.0043	0.0268	0.55	0.0335	0.1339	-0.20	0.7700	0.3353	0.27	0.1584	0.3506	-3.54	0.4404	0.8421	-1.35	0.9327	0.9460	0.12
3330 Pro-opiomelanocortin	P01189	0.1992	0.3696	-0.27	0.3592	0.7086	-0.37	0.4898	0.7384	0.10	0.2098	0.3454	0.26	0.9898	0.9931	0.00	0.5603	0.7956	-0.10	0.3736	0.4560	-2.55	0.8708	0.9820	-0.33	0.0651	0.1219	-0.06
3331 Proprotein convertase subtilisin/kexin type 4	Q6UW60	0.1649	0.3221	-0.17	0.8656	0.9029	0.02	0.0396	0.1058	-0.20	0.1663	0.2865	0.17	0.9057	0.9288	0.01	0.2305	0.4137	-0.15	0.9176	0.9329	-0.01	0.8744	0.9050	0.01	0.3331	0.1554	0.20
3332 Proserpine homeobox protein 1	Q92786	0.7316	0.7815	0.01	0.2313	0.6627	0.22	0.0002	0.0093	0.27	0.0054	0.0550	0.12	0.0070	0.0649	-0.18	0.0407	0.1657	-0.34	0.1906	0.4830	-0.10	0.0026	0.0543	-0.28			
3333 Prostaglandin E synthase 2	Q9H727	0.7523	0.7982	-0.01	0.1284	0.6426	-0.09	0.0260	0.0805	-0.24	0.0170	0.0545	-0.18	0.0102	0.0723	-0.20	0.2274	0.4104	-0.11	0.3736	0.4957	-2.55	0.8708	1.0256	-0.33	0.0651	0.1389	-0.06
3334 Prostaglandin H synthase 3	Q15185	0.0052	0.0439	0.20	0.8399	0.8850	-0.01	0.0066	0.0392	0.23	0.4148	0.6070	0.03	0.0344	0.1353	-0.11	0.2556	0.4458	0.09	0.6640	0.7082	0.04	0.0104	0.0837	-0.26	0.0304	0.1479	-0.19
3335 Prostaglandin F2 receptor negative regulator	Q9P2B2	0.5305	0.6016	0.04	0.3011	0.6743	0.17	0.5280	0.7489	0.05	0.1535	0.2699	0.11	0.6664	0.7310	-0.03	0.1731	0.3403	0.10	0.3736	0.5090	-2.55	0.8708	1.0500	-0.33	0.0651	0.1450	-0.06
3336 Prostaglandin reductase 1	Q14914	0.0623	0.1655	0.09	0.2546	0.6627	0.18	0.0106	0.0479	0.27	0.0001	0.0077	0.42	0.0025	0.0392	0.37	0.0290	0.1092	0.31	0.0618	0.1960	0.52	0.0935	0.3042	0.24	0.0245	0.1329	0.31
3337 Prostate and testis expressed protein 2	Q6UY27	0.5928	0.6592	0.08	0.2895	0.6686	0.14	0.3273	0.5161	0.27	0.2016	0.3343	0.18	0.5778	0.6565	-0.02	0.1446	0.2997	-0.42	0.0435	0.1683	0.37	0.3481	0.7105	0.12	0.0955	0.1208	0.64
3338 Prostate tumor-overexpressed gene 1 protein	Q86YD1	0.2737	0.4668	-0.43	0.3437	0.7009	-0.66	0.3773	0.7953	0.08	0.3288	0.5006	0.24	0.5052	0.5942	-0.16	0.5727	0.8079	-0.24	0.3736	0.4545	-2.55	0.8708	0.9492	-0.33	0.0651	0.1213	-0.06
3339 Proteasomal ubiquitin receptor ADRM1	U16186	0.0071	0.0496	0.23	0.0171	0.4613	0.31	0.0006	0.0210	0.41	0.0002	0.0116	0.55	0.0180	0.0959	-0.17	0.0021	0.0539	0.39	0.0965	0.2496	0.43	0.1444	0.4061	-0.19	0.2154	0.2841	-0.19
3340 Proteasome activator complex subunit 1	Q06323	0.4014	0.6212	-0.06	0.5909	0.6968	0.10	0.9533	0.9633	0.00	0.3154	0.4852	0.08	0.1015	0.2555	-0.14	0.1222	0.3934	0.09	0.1070	0.2670	0.17	0.8147	1.2594	0.02	0.0799	0.1309	-0.14
3341 Proteasome activator complex subunit 2	Q9UL46	0.0713	0.1792	0.10	0.2324	0.6622	0.27	0.0040	0.0321	0.25	0.0022	0.0203	0.29	0.3654	0.4622	0.04	0.0105	0.0704	0.29	0.0845	0.2322	0.21	0.4587	0.8637	0.02	0.1014	0.1572	-0.03
3342 Proteasome activator complex subunit 3	P61289	0.1685	0.3268	-0.09	0.2820	0.8938	0.01	0.0821	0.1761	0.13	0.0663	0.7087	-0.02	0.0917	0.2389	0.12	0.0428	0.1365	-0.19	0.0016	0.0528	0.18	0.0743	0.2643	0.06	0.0100	0.0384	-0.26
3343 Proteasome activator complex subunit 4	I14997	0.0947	0.2167	0.07	0.4912	0.8145	0.04	0.0023	0.0264	0.11	0.0020	0.0198	0.11	0.5252	0.6120	0.02	0.0092	0.0688	0.15	0.3736	0.6157	-2.55	0.8708	1.2402	-0.33	0.0651	0.2024	-0.06
3344 Proteasome adapter and scaffold protein ECM29	Q5VYK3	0.0141	0.0693	0.18	0.2192	0.6601	0.20	0.0037	0.0317	0.23	0.0042	0.0265	0.23	0.4604	0.5524	0.03	0.0171	0.0851	0.16	0.0505	0.1789	0.27	0.9731	0.9807	0.00	0.1913	0.2590	0.05
3345 Proteasome assembly chaperone 1	Q95456	0.0022	0.0318	0.24	0.4131	0.7524	0.12	0.0029	0.0293	0.31	0.0083	0.0370	0.15	0.1764	0.3670	0.05	0.0016	0.0508	0.27	0.0212	0.1344	-0.26	0.2940	0.6533	-0.15	0.0952	0.1498	0.39
3346 Proteasome assembly chaperone 2	Q969U7	0.2065	0.3789	-0.28	0.5988	0.7098	-0.41	0.8335	0.9497	0.04	0.2540	0.7878	0.07	0.2210	0.4967	0.24	0.2545	0.8004	-0.12	0.0269	0.1420	-0.68	0.0332	0.9951	1.28	0.4783	0.5467	-0.13
3347 Proteasome assembly chaperone 3	Q9T173	0.0071	0.0496	-0.19	0.0671	0.5901	-0.18	0.0218	0.0718	-0.50	0.0003	0.0106	-0.78	0.0056	0.0560	-0.60	0.5212	0.7493	-0.16	0.3736	0.4587	-2.55	0.8708	0.9571	-0.33	0.0651	0.1230	-0.06
3348 Proteasome assembly chaperone 4	Q3J554	0.0400	0.1260	0.21	0.8971	0.9272	0.02	0.0032	0.0301	-0.18	0.0840	0.1702	0.20	0.8079	0.8506	0.02	0.0119	0.0739	0.18	0.6133	0.6608	-0.98	0.8396	1.2833	0.36	0.7216	0.7702	0.63
3349 Proteasome inhibitor P131 subunit	Q92530	0.0596	0.1615	-0.35	0.0283	0.5072	-0.47	0.1989	0.3496	-0.68	0.0091	0.0382	-0.65	0.0296	0.1256	-0.47	0.0614	0.1723	-0.36	0.1947	0.4031	0.22	0.1623	0.4381	0.14	0.0567	0.2118	0.19
3350 Proteasome subunit alpha type-1	P25786	0.7794	0.8206	0.02	0																							

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	SSE IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
3394 Protein CYR61	O00622	0.0335	0.1144	-0.84	0.1747	0.6610	-2.85	0.7556	0.7970	-0.11	0.5589	0.6096	-0.14	0.2289	0.4387	-0.38	0.2501	0.4395	-0.44	0.0114	0.1036	0.45	0.0910	0.3002	0.18	0.0352	0.1609	0.42
3395 Q9P219	0.4108	0.5320	-3.81	0.5752	0.7449	-1.75	0.5661	0.6746	-0.19	0.5388	0.6381	0.89	0.2938	0.4306	-1.88	0.9510	1.0299	0.09	0.4850	0.5397	0.09	0.0189	0.4741	-0.13	0.0101	0.1982	-0.23	
3396 Protein DDH1 homolog 2	Q5TDH0	0.0094	0.2159	-0.08	0.1529	0.6589	-0.15	0.0177	0.0635	-0.21	0.0218	0.0642	-0.31	0.0011	0.0260	-0.33	0.1295	0.2803	-0.23	0.3736	0.5247	-2.55	0.8708	1.0786	-0.33	0.0651	0.1525	2.06
3397 P35659	0.0940	0.0573	0.26	0.7650	0.8301	-0.02	0.9538	0.9635	0.00	0.4999	0.7033	-0.02	0.0763	0.3125	-0.09	0.3414	0.5457	-0.03	0.6286	0.6746	0.11	0.1476	0.4126	-0.18	0.9964	0.9974	0.00	
3398 Protein diaphanous homolog 1	Q60610	0.0524	0.1482	0.12	0.2671	0.6630	0.18	0.0106	0.0483	0.20	0.0345	0.0886	0.14	0.1248	0.2917	-0.09	0.1303	0.2649	0.09	0.0147	0.1120	0.34	0.2084	0.5099	0.07	0.1401	0.2014	0.08
3399 Protein disulfide-isomerase	P07373	0.0024	0.0332	0.37	0.2144	0.6615	0.27	0.0005	0.0192	0.53	0.0002	0.0118	0.66	0.0038	0.0461	0.38	0.0017	0.0521	0.68	0.0278	0.1446	0.48	0.3737	0.7468	0.09	0.5286	0.5950	0.05
3400 Protein disulfide-isomerase A3	P10101	0.0017	0.0282	0.24	0.2552	0.6612	0.27	0.0022	0.0264	0.38	0.0005	0.0126	0.41	0.0171	0.0939	0.17	0.0015	0.0511	0.46	0.0817	0.2281	0.31	0.9446	0.9602	0.01	0.6846	0.7377	-0.02
3401 Protein disulfide-isomerase A4	P13667	0.0054	0.0444	0.32	0.1474	0.6571	0.31	0.0009	0.0212	0.54	0.0007	0.0140	0.55	0.0152	0.0880	0.30	0.0058	0.0621	0.56	0.0587	0.1923	0.39	0.8816	0.9108	-0.02	0.6931	0.7452	-0.04
3402 Protein disulfide-isomerase A5	I14554	0.0057	0.0454	-1.82	0.2838	0.6643	-1.74	0.2004	0.3520	-0.71	0.0023	0.0203	-1.52	0.4565	0.5490	-0.19	0.0325	0.1161	-0.84	0.3736	0.5785	-2.55	0.8708	1.1750	-0.33	0.0651	0.1805	2.06
3403 Protein disulfide-isomerase A6	I15084	0.0157	0.0727	0.20	0.1573	0.6619	0.17	0.0033	0.0309	0.27	0.0060	0.0312	0.22	0.0252	0.1141	0.16	0.0103	0.0700	0.28	0.0704	0.2096	0.26	0.3029	0.6478	-0.09	0.2873	0.3592	0.07
3404 Protein doxey-1	Q5JWR5	0.8135	0.8499	0.04	0.5102	0.8319	-0.09	0.0546	0.1329	-0.38	0.2122	0.3487	0.22	0.3752	0.4724	-0.12	0.9476	1.1839	0.01	0.5070	0.1790	-0.74	0.0352	0.1704	-0.27	0.0064	0.0748	-0.26
3405 Protein Dr1	Q01658	0.4108	0.5319	-3.31	0.5752	0.7447	-1.75	0.5661	0.6744	-1.19	0.5388	0.6379	0.89	0.2938	0.4305	-1.88	0.9510	1.0297	0.09	0.4705	0.5253	0.05	0.0173	0.1110	-0.26	0.0255	0.1359	-0.28
3406 Protein ECT2	Q9H8V3	0.9206	0.9395	0.01	0.4189	0.7574	0.08	0.0772	0.1679	0.12	0.4205	0.6122	-0.04	0.9281	0.9462	-0.01	0.0590	0.1676	0.15	0.3294	0.5974	-0.26	0.6040	1.0374	-0.09	0.9147	0.9311	-0.02
3407 Protein EFR3 homolog B	Q9Y2G0	0.0440	0.1332	-0.24	0.0944	0.6301	0.17	0.4482	0.6616	0.05	0.1177	0.2195	-0.15	0.5005	0.5900	0.06	0.2278	0.4106	0.17	0.3736	0.4956	-2.55	0.8708	1.0254	-0.33	0.0651	0.1389	2.06
3408 Protein enabled homolog	Q8N8S7	0.0592	0.1609	-0.17	0.6167	0.7164	0.07	0.0448	0.1159	0.18	0.4257	0.6177	-0.05	0.0381	0.1422	-0.23	0.3177	0.5200	-0.06	0.0483	0.1758	0.38	0.0018	0.0348	0.08	0.0233	0.1299	0.65
3409 Protein ERGIC-53	P49257	0.0193	0.0815	0.18	0.1102	0.6336	0.21	0.0043	0.0327	0.28	0.0055	0.0298	0.30	0.0399	0.1467	0.15	0.0047	0.0601	0.32	0.0462	0.1725	0.39	0.0027	0.0432	0.31	0.0041	0.0628	0.31
3410 Protein eyes shut homolog	Q5T1H1	0.7694	0.8127	0.01	0.3073	0.6774	0.14	0.5286	0.7496	-0.02	0.0463	0.1092	0.14	0.1481	0.3241	-0.06	0.2791	0.4753	0.04	0.3736	0.4858	-2.55	0.8708	1.0073	-0.33	0.0651	0.1345	2.06
3411 Protein FAM102B	Q5TR83	0.4027	0.6227	-0.12	0.7085	0.7859	0.07	0.0532	0.1307	-0.28	0.0100	0.0401	-0.50	0.0088	0.0671	-0.57	0.0054	0.0622	-0.72	0.3736	0.6285	-2.55	0.8708	1.2625	-0.33	0.0651	0.2105	2.06
3412 Protein FAM104B	Q5XKR9	0.1017	0.2277	0.35	0.8872	0.9195	-0.06	0.0910	0.1899	0.36	0.0314	0.0828	0.54	0.1372	0.3077	0.31	0.0559	0.1615	0.53	0.0226	0.1364	0.55	0.0103	0.0838	0.51	0.0090	0.0849	0.80
3413 Protein FAM114A2	Q9NRY5	0.0084	0.0542	0.22	0.7139	0.7905	-0.04	0.9136	0.9320	0.00	0.0409	0.1001	0.13	0.0818	0.2208	0.09	0.0284	0.1078	0.16	0.3736	0.5819	-2.55	0.8708	1.1808	-0.33	0.0651	0.1824	2.06
3414 Protein FAM112B	Q7Z309	0.4630	0.5399	0.13	0.9101	0.9374	-0.03	0.5848	0.6412	0.10	0.5098	0.7145	0.12	0.7885	0.8339	0.05	0.6788	0.9178	0.08	0.1276	0.1065	0.21	0.3565	0.7231	-0.05	0.0084	0.0818	0.34
3415 Protein FAM124B	Q9H5Z6	0.0737	0.1940	0.06	0.0125	0.4405	0.14	0.0001	0.0273	0.40	0.0004	0.0134	0.29	0.0001	0.0120	0.46	0.0007	0.0453	0.34	0.3736	0.6512	-2.55	0.8708	1.3014	-0.33	0.0651	0.2256	2.06
3416 Protein FAM135B	Q9A4J0	0.7724	0.8132	-0.05	0.0666	0.5938	-0.25	0.0470	0.1203	0.23	0.0281	0.0766	-0.27	0.9713	0.9775	0.00	0.0188	0.0882	0.36	0.3736	0.5951	-2.55	0.8708	1.2041	-0.33	0.0651	0.1900	2.06
3417 Protein FAM136A	Q96C01	0.4691	0.5450	0.04	0.3517	0.6811	0.13	0.1783	0.3214	0.09	0.0194	0.0591	0.12	0.7940	0.8390	0.01	0.0538	0.1573	0.13	0.8791	0.8994	-0.01	0.1064	0.3306	-0.10	0.1613	0.1092	-0.22
3418 Protein FAM160A1	Q0SDH4	0.4108	0.5317	-3.31	0.5752	0.7445	-1.75	0.5661	0.6743	-1.19	0.5388	0.6378	0.89	0.2938	0.4304	-1.88	0.9510	1.0295	0.09	0.0316	0.1502	-0.22	0.0230	0.1333	0.24	0.1392	0.2005	0.13
3419 Protein FAM162A	Q96A26	0.0002	0.0133	0.72	0.6137	0.7149	-0.15	0.0378	0.1023	-0.17	0.0362	0.0914	-0.35	0.0740	0.2086	-0.37	0.2661	0.4589	0.06	0.3736	0.4875	-2.55	0.8708	1.0105	-0.33	0.0651	0.1353	2.06
3420 Protein FAM167B	Q9BTA0	0.4108	0.5316	-3.31	0.5752	0.7443	-1.75	0.5661	0.6741	-1.19	0.5388	0.6376	0.89	0.2938	0.4303	-1.88	0.9510	1.0293	0.09	0.1059	0.2660	-0.22	0.0084	0.0752	-0.28	0.0212	0.1246	-0.36
3421 Protein FAM170A	AIAS19	0.2068	0.3793	0.68	0.7893	0.8484	0.12	0.7189	0.7639	0.16	0.7415	0.7772	-0.14	0.5716	0.6517	-0.25	0.3442	0.5483	0.46	0.0079	0.0909	-1.42	0.0610	0.2363	-6.69	0.0006	0.0293	-4.30
3422 Protein FAM177A1	Q8N128	0.0174	0.0772	0.22	0.5276	0.8461	0.09	0.0867	0.1837	0.12	0.1981	0.3294	0.08	0.2075	0.4101	0.07	0.1023	0.2371	0.12	0.3736	0.5331	-2.55	0.8708	1.0938	-0.33	0.0651	0.1566	2.06
3423 Protein FAM183BP	Q6ZV57	0.4108	0.5315	-3.31	0.5752	0.7441	-1.75	0.5661	0.6740	-1.19	0.5388	0.6375	0.89	0.2938	0.4302	-1.88	0.9510	1.0291	0.09	0.0002	0.0296	-1.08	0.0127	0.0940	-1.63	0.0209	0.1239	-2.23
3424 Protein FAM186A	AGNE01	0.4108	0.5313	-3.31	0.5752	0.7440	-1.75	0.5661	0.6738	-1.19	0.5388	0.6374	0.89	0.2938	0.4300	-1.88	0.9510	1.0289	0.09	0.3070	0.5667	0.08	0.0271	0.1484	0.18	0.0251	0.1346	0.30
3425 Protein FAM193A	P78312	0.4108	0.5312	-3.31	0.5752	0.7438	-1.75	0.5661	0.6736	-1.19	0.5388	0.6372	0.89	0.2938	0.4299	-1.88	0.9510	1.0286	0.09	0.0333	0.1521	0.06	0.0975	0.9546	0.00	0.8222	0.8566	-0.02
3426 Protein FAM204A	Q9HRW3	0.5223	0.5940	-0.28	0.9708	0.9803	-0.03	0.6557	0.7070	0.19	0.8046	0.8322	0.12	0.6447	0.7131	0.21	0.6566	0.8936	-0.20	0.3736	0.4474	-2.55	0.8708	0.9358	-0.33	0.0651	0.1184	2.06
3427 Protein FAM217A	Q8IXS0	0.0108	0.0598	-0.24	0.0021	0.2266	-0.30	0.0018	0.0245	-0.40	0.0026	0.0217	-0.31	0.0114	0.0766	0.18	0.2143	0.3959	-0.06	0.3736	0.4998	-2.55	0.8708	1.0332	-0.33	0.0651	0.1408	2.06
3428 Protein FAM236D	AOA1B0G7K5	0.1975	0.3667	2.63	0.0699	0.6015	-8.94	0.1383	0.2624	0.72	0.0949	0.1863	0.69	0.0202	0.1020	1.12	0.0114	0.0734	1.62	0.3736	0.6101	-2.55	0.8708	1.2304	-0.33	0.0651	0.1989	2.06
3429 Protein FAM3C	Q92520	0.2013	0.3720	0.27	0.7080	0.8416	-0.13	0.0766	0.1670	0.50	0.3164	0.4866	0.21	0.0803	0.2185	0.44	0.0886	0.2170	0.43	0.0461	0.1725	-0.22	0.0251	0.1415	-0.80	0.0029	0.0548	-1.17
3430 Protein FAM49A	Q9HQ00	0.4108	0.5311	-3.31	0.5752	0.7436	-1.75	0.5661	0.6735	-1.19	0.5388	0.6371	0.89	0.2938	0.4298	-1.88	0.9510	1.0284	0.09	0.4700	0.5248	0.12	0.0575	0.2291	-0.33	0.0480	0.1911	-0.40
3431 Protein FAM49B	Q8N1Q9	0.5445	0.6144	-0.03	0.5713	0.8847	0.09	0.9314	0.9644	0.01	0.0244	0.0604	0.16	0.1214	0.1054	-0.19	0.0646	0.1774	0.16	0.0145	0.3588	0.28	0.8263	1.2705	-0.02	0.8756	0.8984	0.02
3432 Protein FAM50A	Q14320	0.0034	0.0380	0.19	0.0284	0.5073	0.11	0.0078	0.0419	0.21	0.2515	0.4010	0.06	0.1767	0.3672	0.05	0.0052	0.0614	0.23	0.0584	0.							

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
3473 Protein IIN homolog	Q5TKA1	0.2763	0.4699	0.17	0.3619	0.7098	-0.13	0.8833	0.9073	0.05	0.1547	0.2716	0.39	0.0085	0.0659	0.88	0.0751	0.1950	0.59	0.3736	0.5468	-2.55	0.8708	1.1185	-0.33	0.0651	0.1635	2.06
3474 Protein LLP homolog	Q9BRT6	0.1366	0.2812	-0.10	0.0405	0.7050	-0.15	0.1133	0.2255	-0.10	0.0073	0.0346	-0.28	0.0109	0.0747	-0.31	0.0358	0.1126	-0.20	0.3736	0.5805	-2.55	0.8708	1.1784	-0.33	0.0651	0.1816	2.06
3475 Protein LSM14A homolog A	Q8ND56	0.0124	0.0648	-0.20	0.9692	0.9790	0.00	0.0163	0.0603	0.16	0.9094	0.9215	0.00	0.1565	0.3378	0.06	0.1028	0.2380	-0.08	0.0903	0.2416	0.19	0.2165	0.5226	-0.17	0.3742	0.4460	-0.05
3476 Protein LTV1 homolog	Q96AG3	0.0102	0.0588	-0.25	0.2592	0.6637	-0.19	0.0269	0.0821	-0.21	0.5993	0.6649	0.03	0.0927	0.2400	-0.19	0.0386	0.1278	-0.38	0.0927	0.9389	0.00	0.0365	0.5480	-0.48	0.2545	0.3365	-0.04
3477 Protein LYRK	Q861E4	0.0011	0.0225	-0.14	0.1805	0.6650	0.22	0.0120	0.0513	0.35	0.0002	0.0091	0.26	0.0014	0.0292	0.27	0.0003	0.0420	0.28	0.0120	0.1041	1.00	0.05	0.1054	0.92	0.3121	0.3836	0.23
3478 Protein mago nashi homolog	P61326	0.0100	0.0583	0.20	0.0179	0.4683	0.17	0.0024	0.0274	0.49	0.0039	0.0254	0.29	0.2514	0.4694	0.05	0.1390	0.5218	0.13	0.0425	0.1670	0.31	0.6161	1.0501	0.02	0.0005	0.0278	0.40
3479 Protein NAK1A homolog	Q9BXY0	0.0142	0.0693	0.30	0.0005	0.2355	0.19	0.1118	0.2233	0.03	0.7943	0.8227	-0.01	0.8092	0.8516	0.00	0.2632	0.4555	0.14	0.2198	0.4411	-0.25	0.0458	1.1992	-0.24	0.1202	0.2152	-0.15
3480 Protein mas	P61244	0.4108	0.5307	-3.31	0.5752	0.7430	-1.75	0.5661	0.6730	-1.19	0.5388	0.6366	0.89	0.2938	0.4294	-1.88	0.9510	1.0278	0.09	0.1533	0.3420	-0.29	0.5405	0.9658	-0.06	0.0254	0.1355	0.37
3481 Protein NMD12D	Q8YB1	0.4108	0.5305	-3.31	0.5752	0.7428	-1.75	0.5661	0.6729	-1.19	0.5388	0.6365	0.89	0.2938	0.4293	-1.88	0.9510	1.0276	0.09	0.0028	0.0585	-0.38	0.0148	0.1025	-0.16	0.0677	0.1149	-0.19
3482 Protein Mdm4	O15151	0.0460	0.1370	0.47	0.1638	0.6639	0.43	0.2230	0.3804	0.23	0.0158	0.0520	0.78	0.0806	0.2189	0.40	0.0527	0.1552	0.44	0.2747	0.5197	-0.37	0.0776	0.2729	-0.81	0.2160	0.2848	-0.65
3483 Protein MEMO1	Q9Y316	0.4108	0.5304	-3.31	0.5752	0.7427	-1.75	0.5661	0.6727	-1.19	0.5388	0.6363	0.89	0.2938	0.4292	-1.88	0.9510	1.0274	0.09	0.0298	0.1470	1.32	0.0141	0.0991	1.40	0.0752	0.1250	0.84
3484 Protein misato homolog 1	Q9BUK6	0.0608	0.1634	-0.33	0.0484	0.5737	-0.41	0.0068	0.0399	-0.70	0.0212	0.0630	-0.55	0.0519	0.1689	-0.41	0.0119	0.0741	-0.63	0.3736	0.6086	-2.55	0.8708	1.2277	-0.33	0.0651	0.1980	2.06
3485 Protein mono-ADP-ribosyltransferase TIPARP	Q7Z3E1	0.4350	0.5123	0.26	0.3181	0.6806	0.33	0.3200	0.5072	0.33	0.1025	0.1977	0.72	0.8869	0.9133	0.05	0.6735	0.9114	0.15	0.3736	0.4463	-2.55	0.8708	0.9339	-0.33	0.0651	0.1180	2.06
3486 Protein moonraker	Q2KHM9	0.3411	0.5491	-0.40	0.8566	0.8968	0.02	0.0072	0.0400	0.25	0.6277	0.6739	0.03	0.0484	0.1616	-0.15	0.1717	0.3379	-0.07	0.3736	0.5094	-2.55	0.8708	1.0507	-0.33	0.0651	0.1452	2.06
3487 Protein NDRG1	Q92597	0.8457	0.8772	0.01	0.5347	0.8507	0.08	0.8990	0.9201	0.01	0.5199	0.7249	-0.02	0.0048	0.0519	-0.17	0.6493	0.8860	-0.01	0.7358	0.7745	0.06	0.1083	0.3351	-0.40	0.3185	0.3898	-0.19
3488 Protein NDRG3	Q9UGV2	0.0013	0.0245	-1.83	0.2632	0.6638	-1.23	0.1312	0.2526	-1.64	0.0005	0.0119	-3.29	0.1407	0.3131	0.37	0.0095	0.0694	-1.54	0.0571	0.1898	-0.29	0.0901	0.2984	-0.25	0.0593	0.2177	-0.34
3489 Protein Niban	Q9BZ08	0.4108	0.5303	-3.31	0.5752	0.7425	-1.75	0.5661	0.6726	-1.19	0.5388	0.6362	0.89	0.2938	0.4291	-1.88	0.9510	1.0271	0.09	0.0356	0.1559	0.31	0.0969	0.3108	0.24	0.2099	0.1474	0.42
3490 Protein NipSnap homolog 1	Q9BPW8	0.0230	0.0905	0.21	0.2258	0.6597	0.21	0.0187	0.0655	-0.23	0.0200	0.0604	0.18	0.6494	0.7172	0.02	0.0295	0.1100	0.17	0.4317	0.4876	0.07	0.0293	0.1544	-0.14	0.0076	0.0791	-0.23
3491 Protein NipSnap homolog 3A	O75323	0.4108	0.5301	-3.31	0.5752	0.7423	-1.75	0.5661	0.6724	-1.19	0.5388	0.6360	0.89	0.2938	0.4289	-1.88	0.9510	1.0269	0.09	0.0955	0.2490	0.42	0.2362	0.5526	-0.17	0.1412	0.2027	0.22
3492 Protein NipSnap homolog 3B	Q9UFN0	0.2005	0.3713	-0.20	0.0028	0.2545	-0.52	0.1883	0.3343	-0.11	0.0069	0.0335	-0.53	0.0199	0.1010	-0.42	0.5802	0.8147	-0.05	0.4207	0.4764	-0.16	0.1849	0.4744	-0.25	0.8015	0.8381	-0.07
3493 Protein NipSnap homolog 3B	Q9BS92	0.0061	0.0467	-0.21	0.9787	0.9857	0.00	0.0066	0.0391	-0.29	0.0497	0.1147	-0.12	0.0148	0.0867	-0.20	0.4947	0.7200	-0.06	0.3736	0.4607	-2.55	0.8708	0.9608	-0.33	0.0651	0.1238	2.06
3494 Protein Nima-R1	Q9LAS0	0.4108	0.5300	-3.31	0.5752	0.7421	-1.75	0.5661	0.6723	-1.19	0.5388	0.6359	0.89	0.2938	0.4288	-1.88	0.9510	1.0267	0.09	0.5345	0.5866	-0.06	0.1715	0.4535	-0.16	0.0967	0.9975	0.00
3495 Protein NOXPD1	Q8WTE2	0.0498	0.1929	-3.31	0.5752	0.7419	-1.75	0.5661	0.6721	-1.19	0.5388	0.6358	0.89	0.2938	0.4287	-1.88	0.9510	1.0265	0.09	0.7073	0.7485	-0.17	0.9387	0.9549	0.05	0.0147	0.1045	1.69
3496 Protein NRH2F2 homolog	Q9H7Z3	0.0933	0.2239	0.64	0.3161	0.6805	0.32	0.5022	0.7246	-0.22	0.1139	0.2144	0.62	0.0070	0.0606	1.81	0.8899	1.1265	-0.05	0.3736	0.4343	-2.55	0.8708	0.9113	-0.33	0.0651	0.1132	2.06
3497 Protein numb homolog	P49757	0.4987	0.5725	-0.05	0.2126	0.6626	0.22	0.0072	0.0401	-0.27	0.0103	0.0408	0.17	0.0217	0.1058	0.10	0.0063	0.0626	0.20	0.1241	0.2965	1.16	0.2153	0.5209	0.81	0.1199	0.1782	1.19
3498 Protein odr-4 homolog	Q5SWX8	0.5211	0.5929	0.12	0.0417	0.5714	0.56	0.9558	0.9646	-0.01	0.1405	0.2518	0.30	0.0368	0.1394	0.47	0.0861	0.2138	0.37	0.3736	0.5413	-2.55	0.8708	1.086	-0.33	0.0651	0.1607	2.06
3499 Protein O-GlcNAcase	O60502	0.0072	0.0501	0.40	0.1646	0.6615	3.62	0.0201	0.0683	4.30	0.1281	0.2338	3.60	0.6783	0.7419	-0.57	0.6103	0.8478	2.04	0.3736	0.4517	-2.55	0.8708	0.9441	-0.33	0.0651	0.1102	2.06
3500 Protein O-glucosyltransferase 2	Q6UW63	0.7352	0.7847	0.10	0.8054	0.8598	0.07	0.1863	0.3316	0.46	0.3391	0.5132	0.30	0.6569	0.7229	0.13	0.8958	1.1329	-0.06	0.3736	0.4341	-2.55	0.8708	0.9109	-0.33	0.0651	0.1232	2.06
3501 Protein O-glucosyltransferase 3	Q7Z4H8	0.4108	0.5297	-3.31	0.5752	0.7417	-1.75	0.5661	0.6720	-1.19	0.5388	0.6356	0.89	0.2938	0.4286	-1.88	0.9510	1.0263	0.09	0.0027	0.0580	-2.15	0.0001	0.0133	-2.90	0.0009	0.0379	-2.58
3502 Protein O-mannosyl-transferase TMT3	Q6ZXV5	0.4108	0.5296	-3.31	0.5752	0.7415	-1.75	0.5661	0.6718	-1.19	0.5388	0.6355	0.89	0.2938	0.4285	-1.88	0.9510	1.0261	0.09	0.5897	0.6386	0.06	0.0209	0.1249	-0.24	0.0024	0.0536	-0.32
3503 Protein OS-9	I13438	0.0273	0.1000	0.37	0.8159	0.8938	-0.01	0.8144	0.8495	0.02	0.5033	0.7069	0.06	0.3988	0.4952	-0.09	0.0231	0.0973	0.37	0.0058	0.0810	0.28	0.0218	0.1279	0.18	0.0106	0.0908	0.29
3504 Protein PAT1 homolog 1	Q86TB9	0.5142	0.5867	-0.07	0.1078	0.6310	0.21	0.3322	0.5230	0.08	0.0611	0.1336	0.17	0.2986	0.3967	-0.08	0.6182	0.8542	0.03	0.1364	0.3153	-0.22	0.0139	0.0982	-0.38	0.9120	0.9294	-0.01
3505 Protein PAXX	Q9BUH6	0.7916	0.8309	-0.06	0.2296	0.6611	-0.12	0.0684	0.1546	-0.44	0.0302	0.0806	-0.23	0.2055	0.4071	-0.10	0.3590	0.5651	-0.07	0.3736	0.4733	-2.55	0.8708	0.9842	-0.33	0.0651	0.1292	2.06
3506 Protein PBD1C1	Q9BVG4	0.0136	0.0681	0.30	0.2656	0.6634	0.21	0.1274	0.2474	0.09	0.0375	0.0937	0.16	0.7701	0.8211	0.01	0.1492	0.3062	0.20	0.1604	0.3534	0.21	0.7245	1.1699	0.03	0.0247	0.3365	-0.07
3507 Protein pelota homolog	Q9BRX2	0.1379	0.2826	0.17	0.6215	0.7189	-0.08	0.1241	0.2427	0.20	0.0447	0.1061	0.31	0.0362	0.1382	0.35	0.4694	0.6919	-0.09	0.1015	0.2579	0.39	0.0593	0.2325	0.49	0.0241	0.1322	0.76
3508 Protein phosphatase 1 regulatory subunit 12A	I14974	0.0552	0.1538	0.10	0.2831	0.6636	0.21	0.0451	0.1165	0.16	0.1006	0.0412	0.18	0.0480	0.1608	0.10	0.0901	0.2189	0.09	0.7807	0.8143	0.04	0.0413	0.2725	0.07	0.3639	0.4533	-0.07
3509 Protein phosphatase 1 regulatory subunit 14B	Q96C90	0.0020	0.0309	-0.26	0.4467	0.7820	0.10	0.0470	0.1202	-0.06	0.0009	0.0147	-0.21	0.2864	0.5160	-0.02	0.0652	0.1781	-0.29	0.0065	0.0846	-0.31	0.3136	0.6622	-0.03	0.2409	0.3111	-0.07
3510 Protein phosphatase 1 regulatory subunit 26	Q2T8A7	0.2184	0.3943	0.07	0.0681	0.5919	0.20	0.1922	0.3396	0.09	0.0095	0.0390	0.38	0.2051	0.4066	0.07	0.0312	0.1536	0.18	0.3736	0.5600	-2.55	0.8708	1.1420	-0.33	0.0651	0.1704	2.06
3511 Protein phosphatase 1 regulatory subunit 3C	Q9UOK1	0.0085	0.0546	-0.25	0.0182	0.4667	0.33	0.0048	0.0339	0.27	0.0598	0.1315	-0.12	0.4315	0.5858	0.04	0.0355	0.1216										

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
			p value	BH q value	log2FC	p value	p value	BH q value	log2FC	p value
3557	Protein SOGA3	Q5TF21	0.4108	0.5286	-3.31	0.5752	0.7401	-1.75	0.5661	0.6706
3558	Protein SOX-15	Q60248	0.7209	0.7719	-0.03	0.6752	0.6626	0.25	0.1135	0.2258
3559	Protein spore homolog 2	Q8WDL2	0.1001	0.2251	0.15	0.2218	0.6577	-1.19	0.3848	0.5856
3560	Protein SPT2 homolog	Q68D10	0.4108	0.5284	-3.31	0.5752	0.7399	-1.75	0.5661	0.6704
3561	Protein SSC4	Q60224	0.4108	0.5283	-3.31	0.5752	0.7397	-1.75	0.5661	0.6703
3562	Protein TALPID3	Q9BVV6	0.0092	0.0568	-0.50	0.1727	0.6612	-0.27	0.1653	0.3023
3563	Protein TM53	Q96M34	0.4108	0.5282	-3.31	0.5752	0.7395	-1.75	0.5661	0.6701
3564	Protein TESPA1	A2RU30	0.4108	0.5280	-3.31	0.5752	0.7393	-1.75	0.5661	0.6700
3565	Protein TFG	Q92734	0.0030	0.0363	0.29	0.1075	0.6306	0.30	0.0065	0.0389
3566	Protein TMED8	Q6PL24	0.4108	0.5279	-3.31	0.5752	0.7392	-1.75	0.5661	0.6698
3567	Protein TOPAZ1	Q8N9V7	0.0082	0.0536	-0.60	0.5341	0.8500	-0.16	0.1095	0.2196
3568	Protein transport protein Sec16A	I15027	0.0924	0.2136	-0.07	0.8227	0.8733	-0.02	0.3768	0.5761
3569	Protein transport protein Sec23A	Q15436	0.4967	0.5710	-0.11	0.1085	0.6301	-0.12	0.0509	0.1269
3570	Protein transport protein Sec23B	Q15437	0.1030	0.2296	0.03	0.1205	0.6376	0.06	0.0001	0.0167
3571	Protein transport protein Sec24B	O95487	0.0549	0.1533	-0.22	0.0420	0.5710	-0.20	0.0700	0.1574
3572	Protein transport protein Sec24C	P53992	0.0592	0.1608	0.10	0.2611	0.6646	0.19	0.0479	0.1214
3573	Protein transport protein Sec31A	O94979	0.1112	0.2423	-0.09	0.1889	0.8703	0.02	0.0720	0.1603
3574	Protein transport protein Sec61 subunit alpha isoform 1	P61619	0.0259	0.0973	0.12	0.1782	0.6119	0.24	0.0075	0.0411
3575	Protein transport protein Sec61 subunit beta	P04668	0.0048	0.0434	0.42	0.1513	0.6597	0.37	0.0043	0.0326
3576	Protein tyrosine phosphatase domain-containing protein 1	A2A3K4	0.0179	0.0785	0.29	0.9482	0.9655	0.01	0.0029	0.0292
3577	Protein unc-119 homolog A	Q13432	0.1836	0.3482	-0.08	0.2919	0.6690	-0.12	0.2653	0.4361
3578	Protein unc-13 homolog A	Q9UPW8	0.4897	0.5637	-0.13	0.6879	0.7716	0.11	0.2484	0.4148
3579	Protein unc-13 homolog C	Q8NB66	0.0885	0.2073	-0.23	0.2788	0.6682	-0.16	0.1803	0.3241
3580	Protein unc-13 homolog D	Q70J99	0.0399	0.1258	-0.43	0.5894	0.6948	-0.30	0.0515	0.1275
3581	Protein unc-45 homolog A	Q9H3U1	0.0030	0.0032	0.14	0.1198	0.6358	0.22	0.0040	0.0322
3582	Protein unc-79 homolog	Q9P2D8	0.4108	0.5278	-3.31	0.5752	0.7399	-1.75	0.5661	0.6697
3583	Protein unc-80 homolog	Q8N2C7	0.2423	0.4275	0.14	0.4022	0.7450	0.15	0.0067	0.0394
3584	Protein Wnt-1	O96014	0.0144	0.0697	0.18	0.0176	0.4699	0.53	0.0015	0.0233
3585	Protein Wnt-5b	Q9H1J7	0.4108	0.5276	-3.31	0.5752	0.7388	-1.75	0.5661	0.6695
3586	Protein XRP2	U75695	0.4108	0.5275	-3.31	0.5752	0.7386	-1.75	0.5661	0.6693
3587	Protein yippee-like 5	P62699	0.4108	0.5274	-3.31	0.5752	0.7384	-1.75	0.5661	0.6692
3588	Protein zer-1 homolog	Q7Z7L7	0.4108	0.5272	-3.31	0.5752	0.7382	-1.75	0.5661	0.6690
3589	Protein/nucleic acid dephycase DJ-1	Q99497	0.0014	0.0252	0.42	0.1806	0.6649	0.28	0.0024	0.0271
3590	Protein-arginine deiminase type-2	Q9Y2J8	0.4108	0.5271	-3.31	0.5752	0.7381	-1.75	0.5661	0.6689
3591	Protein-arginine deiminase type-4	Q9UM07	0.0088	0.0556	-0.28	0.1059	0.6339	-0.32	0.0100	0.0468
3592	Protein-activated receptor 1	P25116	0.4108	0.5270	-3.31	0.5752	0.7379	-1.75	0.5661	0.6687
3593	Protein-glutamate O-methyltransferase	Q80893	0.0002	0.0130	-0.48	0.8693	0.9051	-0.01	0.0095	0.0181
3594	Protein-glutamine gamma-glutamyltransferase 2	P21980	0.4108	0.5268	-3.31	0.5752	0.7377	-1.75	0.5661	0.6686
3595	Protein-glutamine gamma-glutamyltransferase 4	P49221	0.4108	0.5267	-3.31	0.5752	0.7375	-1.75	0.5661	0.6684
3596	Protein-L-isoaspartate O-methyltransferase domain-containing protein 2	Q9NV79	0.7203	0.7714	0.04	0.5610	0.8750	-0.43	0.0968	0.1993
3597	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	P22061	0.0035	0.0379	-0.08	0.1093	0.6305	-0.08	0.0006	0.0201
3598	Protein-tyrosine kinase 6	Q13882	0.0600	0.1620	0.20	0.0354	0.5393	0.32	0.0023	0.0270
3599	Proteolipid protein 2	Q04941	0.0022	0.0317	0.37	0.1131	0.6347	0.19	0.0364	0.1000
3600	Prothymosin alpha	P06454	0.1676	0.3259	0.11	0.0780	0.6122	0.59	0.0042	0.0324
3601	Protocadherin alpha-1	Q9Y5I3	0.4108	0.5266	-3.31	0.5752	0.7373	-1.75	0.5661	0.6683
3602	Protocadherin alpha-10	Q9Y5I2	0.4108	0.5265	-3.31	0.5752	0.7371	-1.75	0.5661	0.6681
3603	Protocadherin alpha-9	Q9Y5I5	0.4108	0.5263	-3.31	0.5752	0.7370	-1.75	0.5661	0.6680
3604	Protocadherin beta-1	Q9Y5F3	0.4108	0.5262	-3.31	0.5752	0.7368	-1.75	0.5661	0.6678
3605	Protocadherin beta-14	Q9Y5E9	0.9756	0.9834	0.00	0.3596	0.7083	-0.22	0.4964	0.7183
3606	Protocadherin beta-6	Q9Y5E3	0.1281	0.2683	-0.38	0.1836	0.6646	-0.32	0.9899	0.9910
3607	Protocadherin beta-8	Q9UN66	0.0173	0.0769	-0.37	0.6812	0.7668	-0.12	0.0016	0.0228
3608	Protocadherin Fat 2	Q9NYQ8	0.4598	0.5368	0.04	0.0193	0.4672	-0.17	0.1126	0.2245
3609	Protocadherin Fat 3	Q8TDW7	0.2321	0.4139	0.07	0.7313	0.8043	0.01	0.9883	0.9900
3610	Protocadherin gamma-C3	Q9UN70	0.4108	0.5261	-3.31	0.5752	0.7366	-1.75	0.5661	0.6677
3611	Proto-oncogene c-Rel	Q04864	0.0113	0.0609	-0.33	0.1747	0.6615	-2.72	0.0224	0.0733
3612	Proto-oncogene DBL	P10911	0.0025	0.0334	0.28	0.2667	0.6632	0.26	0.0087	0.0438
3613	Proto-oncogene tyrosine-protein kinase receptor Ret	P07949	0.4108	0.5259	-3.31	0.5752	0.7364	-1.75	0.5661	0.6675
3614	Proto-oncogene tyrosine-protein kinase Src	P12931	0.0004	0.0161	-0.34	0.3250	0.6855	0.11	0.0004	0.0185
3615	Pseudouridylate synthase 7 homolog	Q96PZ0	0.1066	0.2351	-0.05	0.9292	0.9252	0.01	0.3192	0.5064
3616	Pterin-4-alpha-carbinolamine dehydratase	P61457	0.0054	0.0443	0.08	0.2549	0.6622	0.14	0.0820	0.1760
3617	Pterin-4-alpha-carbinolamine dehydratase 2	Q9H0N5	0.4108	0.5258	-3.31	0.5752	0.7362	-1.75	0.5661	0.6674
3618	Pulmonary surfactant-associated protein A2	Q8RWL1	0.4108	0.5257	-3.31	0.5752	0.7361	-1.75	0.5661	0.6672
3619	Pumilio homolog 1	Q14671	0.0363	0.1195	0.34	0.0984	0.6348	0.23	0.0073	0.0405
3620	Purine nucleoside phosphorylase	P00491	0.1420	0.2883	0.08	0.4590	0.7910	-0.05	0.0014	0.0221
3621	Puromycin-sensitive aminopeptidase	P55786	0.1176	0.2521	0.09	0.3067	0.6784	0.17	0.0440	0.1144
3622	Puromycin-sensitive aminopeptidase-like protein	A6NEC2	0.1237	0.2611	0.20	0.5680	0.8822	0.07	0.6809	0.7304
3623	Putative 40S ribosomal protein S26-like 1	Q3JN25	0.6212	0.6848	-0.01	0.4213	0.7593	-0.26	0.0056	0.0361
3624	Putative 60S ribosomal protein L13a protein RPL13AP3	Q6NVV1	0.0363	0.1194	-0.25	0.2283	0.7399	-0.36	0.1478	0.2760
3625	Putative activator of 90 kDa heat shock protein ATPase homolog 2	Q71990	0.4108	0.5255	-3.31	0.5752	0.7359	-1.75	0.5661	0.6671
3626	Putative ankyrin repeat domain-containing protein 31	Q8NTZ5	0.4435	0.5212	-0.03	0.2761	0.6646	0.18	0.0097	0.0459
3627	Putative ATP-dependent RNA helicase DDX12	Q92771	0.4108	0.5254	-3.31	0.5752	0.7357	-1.75	0.5661	0.6669
3628	Putative beta-actin-like protein 3	Q9BYX7	0.2152	0.3900	-0.03	0.0239	0.4874	-0.19	0.0204	0.0688
3629	Putative chaperone multivesicular body protein 4B-like protein CHMP4BP1	P59074	0.4108	0.5253	-3.31	0.5752	0.7355	-1.75	0.5661	0.6668
3630	Putative ciliary rootlet coiled-coil protein 2	HTBZ55	0.7631	0.8074	0.03	0.4881	0.8114	-0.30	0.3362	0.5287
3631	Putative ciliary rootlet coiled-coil protein-like 2 protein	Q8IVF0	0.0052	0.0439	0.20	0.0212	0.6609	0.20	0.0054	0.0358
3632	Putative cleavage and polyadenylation specificity factor subunit 4-like protein	A6NMK7	0.4108	0.5252	-3.31	0.5752	0.7353	-1.75	0.5661	0.6666
3633	Putative CNGA1-overlapping antisense gene protein	Q8IZM0	0.3012	0.5004	-0.14	0.5091	0.8311	-0.09	0.3392	0.5315



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control	
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
3634	Putative coiled-coil domain-containing protein 144C	Q8Y1A2	0.3884	0.6053	-1.15	0.1751	0.6606	-2.00	0.1812	0.3251
3635	Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9_mitochondrial	Q5T1J5	0.4108	0.5250	-3.31	0.5752	0.7351	-1.75	0.5661	0.6665
3636	Putative cTAGE family member 3	Q8IX95	0.0037	0.0387	-0.79	0.4468	0.7819	-0.13	0.0028	0.0290
3637	Putative dehydrogenase/reductase SDR family member 4-like 1	P0CG22	0.2004	0.3713	0.26	0.4674	0.7975	0.13	0.0615	0.1441
3638	Putative deoxyribonuclease TATDN1	Q6P1N9	0.0150	0.0710	0.08	0.0913	0.6289	0.27	0.0186	0.0655
3639	Putative deoxyribonuclease TATDN2	Q93075	0.0001	0.0098	1.38	0.0020	0.2302	0.32	0.0008	0.0224
3640	Putative dimethylamine monoxygenase [N-oxide-forming] 6	O60774	0.0154	0.0718	-2.18	0.3297	0.6889	-1.30	0.1496	0.2788
3641	Putative E3 ubiquitin-protein ligase makorin-4	Q13434	0.3270	0.5330	-0.15	0.1165	0.6359	0.33	0.0751	0.1646
3642	Putative E3 ubiquitin-protein ligase UBR7	Q8N806	0.8996	0.9211	-0.01	0.1176	0.6306	-0.15	0.0561	0.1354
3643	Putative elongation factor 1-alpha-like 3	Q5VTE0	0.0134	0.0675	0.25	0.2621	0.6639	0.20	0.0020	0.0250
3644	Putative endoplasmic-like protein	Q58FF3	0.9656	0.9746	-0.01	0.0951	0.6291	0.32	0.1295	0.2504
3645	Putative fatty acid-binding protein 5-like protein 3	ARMU11	0.0382	0.1225	0.16	0.9932	0.9955	0.00	0.0663	0.1356
3646	Putative ferritin heavy polypeptide-like 19	POC7X4	0.0921	0.2131	0.13	0.1334	0.6482	0.25	0.1433	0.2695
3647	Putative GEF domain-containing protein DNM1P46	O6ZS02	0.4108	0.5249	-3.31	0.5752	0.7350	-1.75	0.5661	0.6665
3648	Putative golgin subfamily A member 8l	A6NC78	0.4108	0.5248	-3.31	0.5752	0.7348	-1.75	0.5661	0.6665
3649	Putative heat shock 70 kDa protein 7	P48741	0.4095	0.0573	-0.67	0.0183	0.4647	-0.57	0.0002	0.0241
3650	Putative heat shock protein HSP 90-alpha A4	Q58FG1	0.0111	0.0604	0.22	0.2643	0.6640	0.09	0.0050	0.0345
3651	Putative heat shock protein HSP 90-alpha A5	Q58FG0	0.2988	0.4975	0.12	0.8302	0.8790	0.04	0.0542	0.1323
3652	Putative heat shock protein HSP 90-beta 2	Q58FF8	0.0978	0.2215	0.12	0.3141	0.6799	0.22	0.0225	0.0735
3653	Putative heat shock protein HSP 90-beta 4	Q58FF6	0.8760	0.9023	0.00	0.7155	0.7914	0.01	0.9842	0.9871
3654	Putative heat shock protein HSP 90-beta 3	Q58FF7	0.0170	0.0762	0.30	0.2558	0.6622	0.15	0.0972	0.1998
3655	Putative hexokinase HKDC1	Q2TB90	0.0000	0.0000	0.52	0.1026	0.6327	0.33	0.0060	0.0375
3656	Putative high mobility group protein B1-like 1	B2RPK0	0.9622	0.9721	0.04	0.2690	0.6629	1.08	0.8722	0.8991
3657	Putative HLA class I histocompatibility antigen alpha chain H	P01893	0.0328	0.1129	0.31	0.0896	0.6238	0.33	0.1319	0.2538
3658	Putative homeodomain transcription factor 1	Q9UMS5	0.0650	0.1687	0.13	0.3835	0.7306	0.15	0.2711	0.4441
3659	Putative hydrolase RBBP9	OT5884	0.4108	0.5246	-3.31	0.5752	0.7346	-1.75	0.5661	0.6660
3660	Putative inactive cathepsin L-like protein CTSL3P	Q5NE16	0.9940	0.9950	0.00	0.1725	0.6609	-1.27	0.5305	0.7518
3661	Putative keratin-87 protein	A6NCN2	0.9661	0.9749	0.00	0.0916	0.6285	-0.47	0.2599	0.0802
3662	Putative lipocalin 1-like protein 1	Q5VSP4	0.0016	0.0271	1.54	0.0503	0.5759	1.41	0.0024	0.0273
3663	Putative methyltransferase-like protein 15P1	POC7V9	0.8260	0.8606	-0.03	0.5575	0.8709	0.10	0.0831	0.1777
3664	Putative monooxygenase p33MONOX	Q96A73	0.1363	0.2807	-0.14	0.4888	0.8123	-0.84	0.1407	0.2660
3665	Putative nascent polypeptide-associated complex subunit alpha-like protein	Q9BZK3	0.2559	0.4436	1.71	0.3681	0.7168	1.26	0.4109	0.6171
3666	Putative oncomodulin-2	P0CE71	0.2430	0.4284	-0.22	0.5250	0.8440	-0.37	0.5135	0.7344
3667	Putative peptidyl-RNA hydrolase PTRHD1	Q6GMV3	0.0010	0.0217	-0.34	0.7766	0.8390	-0.02	0.0367	0.1005
3668	Putative PIP5K1A and PSMΔ4-like protein	A2A3N6	0.0092	0.0567	-0.41	0.0101	0.4472	-0.35	0.0633	0.0999
3669	Putative postmeiotic segregation increased 2-like protein 1	A4D2B8	0.2320	0.4138	-1.99	0.1759	0.6622	-3.09	0.0430	0.1127
3670	Putative postmeiotic segregation increased 2-like protein 3	Q13401	0.0098	0.0578	-1.43	0.5253	0.8437	-0.09	0.0297	0.0874
3671	Putative PRAME family member 13	Q5VWM6	0.8243	0.8593	-0.03	0.5126	0.8350	0.08	0.0464	0.1192
3672	Putative protein FAM104A	Q8RIZP	0.4108	0.5245	-3.31	0.5752	0.7344	-1.75	0.5661	0.6658
3673	Putative protein FAM10A5	Q8NF61	0.0901	0.2101	-0.13	0.6047	0.7076	-0.09	0.1324	0.2545
3674	Putative protein FAM45B	O6NSW5	0.5338	0.6044	-0.09	0.7489	0.8451	-0.02	0.9126	0.9313
3675	Putative protein PLEKHA9	O95397	0.4108	0.5244	-3.31	0.5752	0.7342	-1.75	0.5661	0.6657
3676	Putative protein SSX6	Q7RTT6	0.4108	0.5243	-3.31	0.5752	0.7341	-1.75	0.5661	0.6655
3677	Putative protein SSX9	Q7RTT3	0.4108	0.5241	-3.31	0.5752	0.7339	-1.75	0.5661	0.6654
3678	Putative protein ZNF151	AKS554	0.4108	0.5240	-3.31	0.5752	0.7337	-1.75	0.5661	0.6652
3679	Putative pyridoxal-dependent decarboxylase domain-containing protein 2	Q6P474	0.0368	0.1207	0.21	0.7500	0.8188	-0.05	0.8109	0.8467
3680	Putative Ras-related protein Rab-1C	Q92928	0.0169	0.0759	0.47	0.0545	0.5869	0.43	0.0617	0.1444
3681	Putative RNA polymerase II subunit B1 CTD phosphatase RPA2	Q8IXW5	0.4108	0.5239	-3.31	0.5752	0.7335	-1.75	0.5661	0.6651
3682	Putative RNA-binding protein Luc7-like 1	Q9NQ29	0.1295	0.2705	0.14	0.4541	0.7872	0.10	0.0801	0.1728
3683	Putative RNA-binding protein Luc7-like 2	Q9Y383	0.1609	0.3162	0.08	0.2663	0.6783	0.20	0.0248	0.0781
3684	Putative small nuclear ribonucleoprotein G-like protein 15	AKMWD9	0.2281	0.4083	-0.40	0.2623	0.6634	-1.05	0.0423	0.1115
3685	Putative testis-expressed protein 13C	AA0A9YWL9	0.0345	0.1162	-0.24	0.3237	0.6858	-0.14	0.0182	0.0647
3686	Putative trace amine-associated receptor 3	Q9P1P4	0.1848	0.3497	-1.54	0.3619	0.7101	-2.04	0.0580	0.1426
3687	Putative tRNA pseudouridine synthase Pus-10	Q3MIT2	0.0105	0.0592	0.26	0.7598	0.8263	-0.03	0.0089	0.0439
3688	Putative tubulin-like protein alpha-4B	Q9H853	0.9799	0.9862	-0.01	0.7274	0.8012	-0.22	0.5827	0.6498
3689	Putative ubiquitin-conjugating enzyme E2-N-like	Q5XJB2	0.0481	0.1411	0.13	0.1178	0.6310	0.34	0.0900	0.0443
3690	Putative ubiquitin-conjugating enzyme E2Q2-like protein	HOY1L9	0.1290	0.2699	0.07	0.4640	0.7960	0.09	0.0771	0.1677
3691	Putative uncharacterized protein C22orf34	Q6ZV56	0.4108	0.5237	-3.31	0.5752	0.7333	-1.75	0.5661	0.6649
3692	Putative uncharacterized protein C9orf129	Q5T035	0.0048	0.0433	-0.30	0.9476	0.9653	0.00	0.0034	0.0307
3693	Putative uncharacterized protein encoded by LINC00114	Q6XXX2	0.2257	0.4044	-0.30	0.4271	0.7592	-0.57	0.5621	0.7865
3694	Putative uncharacterized protein encoded by LINC00471	Q8NS55	0.3917	0.6088	-0.06	0.3238	0.6852	-0.08	0.0659	0.1503
3695	Putative uncharacterized protein encoded by MIR7-3HG	Q8NGC7	0.0560	0.1547	-12.47	0.4473	0.0566	-10.36	0.0005	0.0121
3696	Putative uncharacterized protein FL45721	Q6ZS92	0.2742	0.4674	0.18	0.3261	0.6856	-0.34	0.3951	0.5976
3697	Putative uncharacterized protein FL45831	Q6ZS49	0.4108	0.5236	-3.31	0.5752	0.7332	-1.75	0.5661	0.6648
3698	Putative uncharacterized protein KTN1-AS1	Q6B5Y8	0.4108	0.5235	-3.31	0.5752	0.7330	-1.75	0.5661	0.6646
3699	Putative uncharacterized protein LOC10128429	Q6ZWV4	0.1397	0.2848	-2.72	0.1924	0.6680	-2.14	0.4073	0.6126
3700	Putative uncharacterized protein LOC10128554	QOVFX4	0.4108	0.5234	-3.31	0.5752	0.7328	-1.75	0.5661	0.6645
3701	Putative uncharacterized protein MGC13053	Q9BRP9	0.4108	0.5232	-3.31	0.5752	0.7326	-1.75	0.5661	0.1082
3702	Putative uncharacterized protein MYRPRG-AS1	Q2M3A8	0.0213	0.0868	0.29	0.1571	0.6621	0.18	0.1277	0.2477
3703	Putative uncharacterized protein MYH16	Q9H6N6	0.4108	0.5231	-3.31	0.5752	0.7324	-1.75	0.5661	0.6643
3704	Putative uncharacterized SMG1-like protein	Q6P435	0.5562	0.6252	-0.07	0.6418	0.7360	0.03	0.0677	0.1533

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
3705 Putative UPF0607 protein ENSP0000383783	AKRMU18	0.0101	0.0585	-0.41	0.0592	0.5909	-0.27	0.1382	0.2623
3706 Putative UPF0633 protein LOC554249	USXG85	0.7605	0.8051	-0.03	0.4084	0.7496	0.21	0.1234	0.2417
3707 Putative zinc finger and SCAN domain-containing protein 5C	A6NGD5	0.6845	0.7404	-0.01	0.2970	0.6718	0.03	0.1388	0.0593
3708 PWWP domain-containing DNA repair factor 3B	SH9PM0	0.0162	0.0742	0.28	0.0332	0.5275	0.19	0.3034	0.4861
3709 PX domain-containing protein kinase-like protein	Q7Z7A4	0.5694	0.6372	0.10	0.4773	0.8038	0.12	0.3737	0.5720
3710 Pygopus homolog 2	Q9BRQ0	0.0044	0.0417	-0.47	0.0278	0.5071	-0.29	0.0175	0.0631
3711 Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 1	Q8WU10	0.4108	0.5230	-3.31	0.5752	0.7323	-1.75	0.5661	0.6642
3712 Pyridoxal kinase	O00764	0.1593	0.3142	-0.07	0.2548	0.6629	0.08	0.5035	0.7255
3713 Pyridoxal phosphate homeostasis protein	O94903	0.0140	0.0691	-0.51	0.7374	0.8093	0.05	0.3127	0.4984
3714 Pyridoxal-dependent decarboxylase domain-containing protein 1	Q6P996	0.0236	0.0923	0.12	0.1722	0.6612	0.07	0.0254	0.0792
3715 Pyridoxase-5'-phosphate oxidase	Q9NV59	0.2444	0.4300	-0.02	0.0622	0.5901	-0.10	0.0858	0.1825
3716 Pyru domain-containing protein 5	W6CW81	0.2981	0.4968	0.07	0.2415	0.6598	0.08	0.0898	0.1879
3717 Pyroglutamate-peptidase 1	Q9NXJ5	0.4061	0.6264	-0.08	0.1433	0.6489	-0.57	0.6536	0.7049
3718 Pyruvate-5-carboxylate reductase 1 mitochondrial	P32322	0.1612	0.3167	0.08	0.7521	0.8204	0.06	0.0889	0.1872
3719 Pyruvate-5-carboxylate reductase 2	Q9C636	0.1186	0.2555	0.22	0.5924	0.6969	-0.06	0.7274	0.7713
3720 Pyruvate-5-carboxylate reductase 3	Q53H96	0.6445	0.7061	-0.01	0.7486	0.7177	0.02	0.0308	0.0896
3721 Pyruvate carboxylase mitochondrial	P11498	0.0003	0.0145	0.15	0.4536	0.7872	0.09	0.0258	0.0799
3722 Pyruvate dehydrogenase E1 component subunit alpha_testis-specific form_mitochondrial	P29803	0.4108	0.5228	-3.31	0.5752	0.7321	-1.75	0.5661	0.6640
3723 Pyruvate dehydrogenase E1 component subunit alpha_somatic form_mitochondrial	P08559	0.4823	0.5569	0.03	0.8689	0.9049	0.01	0.0197	0.0676
3724 Pyruvate dehydrogenase E1 component subunit beta_mitochondrial	P11177	0.0358	0.1183	0.15	0.0692	0.6004	0.08	0.0038	0.0320
3725 Pyruvate dehydrogenase phosphatase regulatory subunit_mitochondrial	Q8NCN5	0.4108	0.5227	-3.31	0.5752	0.7319	-1.75	0.5661	0.6639
3726 Pyruvate dehydrogenase protein X component_mitochondrial	O00330	0.4108	0.5226	-3.31	0.5752	0.7317	-1.75	0.5661	0.6637
3727 Pyruvate kinase PKLR	P30613	0.0083	0.0539	-0.22	0.0770	0.6127	-0.18	0.0011	0.0224
3728 Pyruvate kinase PKM	P14618	0.0006	0.0192	0.35	0.0631	0.5900	0.36	0.0002	0.0216
3729 Queuine tRNA-rNOSyltransferase accessory subunit 2	Q9H974	0.0048	0.0432	0.23	0.0205	0.4741	0.24	0.0005	0.0218
3730 Quercetin salvage protein	Q748V5	0.7438	0.7916	-0.06	0.2986	0.6725	-0.44	0.7325	0.7756
3731 Quinone oxidoreductase	Q08257	0.0196	0.0820	0.24	0.5394	0.8550	0.15	0.0217	0.0715
3732 Rab effector MyRIP	Q8NF9W	0.0172	0.0767	-0.76	0.5317	0.8506	-0.34	0.0935	0.1939
3733 Rab effector Nac2	Q9UNE2	0.4108	0.5225	-3.31	0.5752	0.7315	-1.75	0.5661	0.6636
3734 Rab GDP dissociation inhibitor alpha	P31150	0.0020	0.0308	0.24	0.1678	0.6610	0.23	0.0086	0.0439
3735 Rab GDP dissociation inhibitor beta	P50395	0.0015	0.0260	0.18	0.0606	0.6782	0.16	0.0038	0.0316
3736 Rab GTPase-activating protein 1	Q9Y3P9	0.3053	0.5061	0.10	0.4850	0.8094	-0.09	0.5490	0.7721
3737 Rab GTPase-activating protein 1-like isoform 10	B7ZAP0	0.0168	0.0758	0.27	0.0644	0.5904	0.21	0.0343	0.0962
3738 Rab GTP-binding effector protein 1	Q15276	0.0318	0.1107	0.64	0.3954	0.7391	0.13	0.2221	0.3793
3739 Rab11 family-interacting protein 2	Q7LR04	0.0013	0.0244	0.31	0.0278	0.5088	0.15	0.0021	0.0260
3740 Rab3 GTPase-activating protein catalytic subunit	Q15042	0.0069	0.0494	0.07	0.1994	0.6642	0.19	0.0002	0.0176
3741 Rab3 GTPase-activating protein non-catalytic subunit	Q9H2M9	0.0257	0.0970	0.28	0.2251	0.6603	-0.27	0.3971	0.6601
3742 Rab9 effector protein with kelch motifs	Q7Z6M1	0.0932	0.2149	0.43	0.6810	0.7669	0.07	0.5802	0.6376
3743 Rabunyk-5	Q9P2R3	0.4108	0.5223	-3.31	0.5752	0.7314	-1.75	0.5661	0.6634
3744 Rab-interacting lysosomal protein	Q96N2A	0.9836	0.9884	0.00	0.1080	0.6307	0.35	0.1368	0.2604
3745 Rab-like protein 3	Q5YH78	0.9222	0.9405	-0.01	0.0631	0.5879	0.17	0.0054	0.0360
3746 Rab-like protein 6	Q3Y1C7	0.0012	0.0239	-0.31	0.3361	0.6953	0.05	0.1264	0.2460
3747 RAC-alpha serine/threonine-protein kinase	P31749	0.0006	0.0191	-0.32	0.1892	0.6699	0.13	0.2660	0.4371
3748 RAC-beta serine/threonine-protein kinase	P31751	0.7604	0.8052	0.14	0.4499	0.7841	-0.58	0.1504	0.2799
3749 RAC-gamma serine/threonine-protein kinase	Q9Y243	0.0055	0.0447	-0.66	0.0308	0.5081	-0.74	0.0230	0.0746
3750 RAD51-associated protein 2	Q09MP3	0.0481	0.1410	0.08	0.7355	0.8077	0.06	0.0909	0.1899
3751 Radial spoke head 1 homolog	Q8WYR4	0.8335	0.8670	-0.02	0.5136	0.8361	-0.04	0.2138	0.3684
3752 Radial spoke head protein 3 homolog	Q86UC2	0.3301	0.5364	-0.12	0.8610	0.8999	-0.02	0.5818	0.6385
3753 Radixin	P35241	0.0010	0.0216	-0.21	0.6106	0.7124	0.08	0.4278	0.6373
3754 RAF proto-oncogene serine/threonine-protein kinase	P04049	0.1126	0.2442	-0.10	0.2398	0.6614	0.20	0.6479	0.7004
3755 Rafin1	Q14699	0.4108	0.5222	-3.31	0.5752	0.7312	-1.75	0.5661	0.6633
3756 Regulator complex protein LAMTOR1	Q6IAA8	0.3086	0.5094	-0.04	0.6370	0.7328	0.02	0.0660	0.1505
3757 Regulator complex protein LAMTOR5	Q43504	0.0152	0.0714	-0.43	0.0055	0.3850	-0.56	0.0002	0.0268
3758 Ras GTPase-activating protein subunit alpha-2	Q2PPJ7	0.0065	0.0482	-0.33	0.4866	0.8102	-0.16	0.2293	0.3887
3759 Ras GTPase-activating protein 1	P46060	0.0175	0.0773	0.09	0.3473	0.7038	0.14	0.0174	0.0629
3760 Ras-binding protein 3	Q9H6Z4	0.2367	0.4203	-0.15	0.5374	0.8531	-0.08	0.1161	0.2300
3761 Ras-specific GTPase-activating protein	P43487	0.0309	0.1085	0.18	0.1163	0.6368	0.29	0.0044	0.0205
3762 Rap guanine nucleotide exchange factor 2	Q9Y4G8	0.0486	0.1414	0.15	0.2725	0.6655	0.17	0.0446	0.1156
3763 Rap guanine nucleotide exchange factor 5	Q92565	0.1442	0.2912	-0.10	0.1268	0.6427	-0.19	0.0112	0.0492
3764 Rap guanine nucleotide exchange factor 6	Q8TEU7	0.4108	0.5221	-3.31	0.5752	0.7310	-1.75	0.5661	0.6631
3765 Rap1 GTPase-GDP dissociation stimulator 1	P52306	0.0402	0.1263	0.16	0.5862	0.6920	0.03	0.0661	0.0377
3766 Ras and EF-hand domain-containing protein	Q8IZ41	0.4108	0.5219	-3.31	0.5752	0.7308	-1.75	0.5661	0.6630
3767 Ras and Rab interactor-like protein	Q6ZS11	0.4108	0.5218	-3.31	0.5752	0.7306	-1.75	0.5661	0.6628
3768 Ras association domain-containing protein 2	P50749	0.1682	0.3268	-0.15	0.4687	0.7986	0.06	0.0390	0.1046
3769 Ras association domain-containing protein 8	Q8NHQ8	0.2667	0.4584	0.11	0.1699	0.6334	0.30	0.0609	0.0398
3770 Ras GTPase-activating protein 1	P20936	0.4108	0.5217	-3.31	0.5752	0.7305	-1.75	0.5661	0.6627
3771 Ras GTPase-activating protein 3	Q14644	0.0010	0.0215	0.15	0.2971	0.6717	0.19	0.0049	0.0342
3772 Ras GTPase-activating protein-binding protein 1	Q13283	0.7765	0.8180	0.02	0.6769	0.7632	-0.05	0.1412	0.2667
3773 Ras GTPase-activating protein-binding protein 2	Q9UN86	0.0297	0.1055	-0.41	0.2733	0.6650	-0.18	0.0093	0.0450
3774 Ras GTPase-activating-like protein IQGAP1	P46940	0.0558	0.1544	0.09	0.2158	0.6611	0.21	0.0224	0.0733
3775 Ras GTPase-activating-like protein IQGAP2	Q13576	0.0014	0.0251	0.33	0.5404	0.8555	0.08	0.0400	0.1319
3776 Ras GTPase-activating-like protein IQGAP3	Q86V13	0.4108	0.5216	-3.31	0.5752	0.7303	-1.75	0.5661	0.6625
3777 Ras suppressor protein 1	Q15404	0.4108	0.5214	-3.31	0.5752	0.7301	-1.75	0.5661	0.6626
3778 Ras/Rap GTPase-activating protein SvnGAP	Q96PV0	0.0041	0.0240	0.15	0.0036	0.3161	0.17	0.0017	0.0240

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name		MCF-7						MDA-MB-231																					
		Dai SC20 vs control			Gen SC20 vs control			Dai IC20 vs control			Gen IC20 vs control																		
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																
3779	Ras-GEF domain-containing family member 1B	QOVMAM2	0.0386	0.1234	0.10	0.1011	0.6325	0.25	0.0721	0.1604	0.15	0.0003	0.0102	0.47	0.0003	0.0169	0.30	0.0027	0.0564	0.49	0.3736	0.6410	-2.55	0.8708	1.2840	-0.33	0.0651	0.2187	2.06
3780	Ras-GEF domain-containing family member 1C	QKN431	0.3891	0.6058	0.18	0.7448	0.8150	-0.07	0.03161	0.5030	-0.22	0.09811	0.9836	0.00	0.7534	0.8072	-0.00	0.7286	0.9682	-0.07	0.3736	0.4477	-2.55	0.8708	0.9289	-0.33	0.0651	0.1169	2.06
3781	Ras-related C3 botulinum toxin substrate 1	P63000	0.0258	0.0971	0.24	0.661	0.7974	0.14	0.0493	0.1237	0.19	0.0128	0.0459	0.30	0.9374	0.9519	0.00	0.0185	0.0878	0.32	0.5449	0.5960	0.08	0.0284	0.1523	-0.35	0.042	0.0442	-0.46
3782	Ras-related GTP-binding protein B	Q5VJZM2	0.4108	0.5213	-3.31	0.5752	0.7299	-1.75	0.5661	0.6622	-1.19	0.5388	0.6265	0.89	0.2938	0.4210	-1.88	0.9510	0.1028	0.09	0.0189	0.1275	-1.31	0.2234	0.5325	0.09	0.0032	0.0562	-0.49
3783	Ras-related protein Rab-10	P61026	0.0058	0.0457	-0.18	0.0858	0.6207	-0.12	0.0048	0.0338	-0.22	0.0015	0.0175	-0.30	0.0077	0.0639	-0.19	0.2291	0.4123	-0.12	0.1247	0.2973	0.11	0.0944	0.3066	0.11	0.0603	0.6664	-0.03
3784	Ras-related protein Rab-11B	Q15907	0.3947	0.6129	0.04	0.3937	0.7373	0.17	0.1535	0.2849	0.09	0.0264	0.0732	0.15	0.2867	0.5164	-0.05	0.0891	0.2178	0.09	0.0851	0.2331	0.36	0.8397	1.2831	0.02	0.8344	0.8660	0.01
3785	Ras-related protein Rab-12	Q6Q022	0.0234	0.0890	0.16	0.2753	0.6645	0.15	0.1759	0.3184	0.09	0.0148	0.0498	0.19	0.2378	0.4249	0.04	0.0148	0.0519	0.15	0.1730	0.3694	0.05	0.0729	0.9322	0.07	0.0669	0.2353	0.32
3786	Ras-related protein Rab-13	P51153	0.0002	0.0128	0.53	0.2465	0.6595	0.20	0.0434	0.1033	0.13	0.0013	0.0162	0.25	0.0002	0.0148	0.35	0.1514	0.3009	0.17	0.1271	0.3004	0.13	0.0061	0.0627	0.47	0.0442	0.1840	0.02
3787	Ras-related protein Rab-14	P61106	0.8956	0.9181	0.01	0.8250	0.8745	0.02	0.0383	0.1033	0.15	0.0415	0.1011	0.14	0.6644	0.7295	-0.02	0.0137	0.0776	0.21	0.0636	0.1988	0.26	0.2315	0.5453	0.10	0.8509	0.8797	-0.41
3788	Ras-related protein Rab-15	P59190	0.4635	0.5403	0.23	0.7605	0.8267	-0.07	0.1097	0.2199	-0.15	0.0998	0.1939	0.33	0.3806	0.4777	0.07	0.0170	0.0854	0.41	0.3059	0.5953	0.07	0.0252	0.1720	-0.23	0.0418	0.0941	-0.43
3789	Ras-related protein Rab-17	Q9H077	0.1816	0.3451	0.17	0.5362	0.8517	0.07	0.0714	0.1594	-0.30	0.2695	0.4254	-0.14	0.7448	0.8001	0.03	0.4136	0.6311	-0.09	0.3736	0.4680	-2.55	0.8708	0.9745	-0.33	0.0651	0.1269	2.06
3790	Ras-related protein Rab-18	Q9NP72	0.6465	0.7080	0.02	0.9413	0.9610	-0.01	0.5514	0.7747	0.03	0.1797	0.3046	0.07	0.8428	0.8789	-0.01	0.0342	0.1193	-0.18	0.5173	0.5707	0.05	0.7461	1.1881	-0.02	0.0628	0.2239	-0.15
3791	Ras-related protein Rab-1A	P62820	0.0617	0.1645	0.14	0.2362	0.6635	0.21	0.0209	0.0700	0.20	0.0197	0.0598	0.21	0.2013	0.4020	0.07	0.0113	0.0729	0.29	0.0161	0.1185	0.56	0.5757	1.0061	-0.10	0.5443	0.2175	0.19
3792	Ras-related protein Rab-1B	Q9H0U4	0.1685	0.3267	-0.03	0.0715	0.6042	0.29	0.0228	0.0744	0.15	0.0509	0.1164	0.11	0.7497	0.8044	0.01	0.1049	0.2413	0.14	0.0364	0.1586	0.37	0.2764	0.6124	0.11	0.1642	0.7007	-0.02
3793	Ras-related protein Rab-20	Q9NX57	0.1358	0.2799	-0.14	0.1580	0.6611	0.13	0.0350	0.0972	0.28	0.2301	0.3732	0.11	0.5215	0.6088	-0.07	0.2178	0.3992	-0.14	0.3736	0.4985	-2.55	0.8708	1.0308	-0.33	0.0651	0.1402	2.06
3794	Ras-related protein Rab-21	Q9UL25	0.0019	0.0300	0.15	0.2930	0.6701	0.15	0.0014	0.0222	0.18	0.0003	0.0112	0.23	0.0060	0.0569	0.08	0.0786	0.2007	0.18	0.4941	0.5479	0.06	0.0612	0.2362	-0.09	0.2787	0.3506	-0.02
3795	Ras-related protein Rab-22A	Q9UL26	0.1294	0.2705	0.03	0.7318	0.8045	-0.02	0.0155	0.0585	0.13	0.8715	0.8895	-0.01	0.0381	0.1421	0.21	0.1861	0.3581	0.12	0.8823	0.9022	0.03	0.5390	0.9641	-0.15	0.3219	0.3931	-0.24
3796	Ras-related protein Rab-24	Q969Q5	0.3139	0.5155	0.17	0.2591	0.6638	0.19	0.7614	0.8021	-0.04	0.2613	0.4142	0.19	0.4323	0.5263	0.12	0.3645	0.5715	0.15	0.3736	0.4725	-2.55	0.8708	0.9827	-0.33	0.0651	0.1288	2.06
3797	Ras-related protein Rab-25	P57735	0.5896	0.6562	0.02	0.4012	0.7449	0.35	0.0295	0.0871	0.24	0.0082	0.0366	0.31	0.0526	0.1701	-0.06	0.0170	0.0857	0.18	0.1670	0.3616	0.28	0.7248	1.1700	-0.05	0.1370	0.1980	-0.31
3798	Ras-related protein Rab-2A	P61019	0.0190	0.0810	0.22	0.2212	0.6589	0.11	0.0312	0.0903	0.20	0.1177	0.2196	0.08	0.1684	0.3550	0.07	0.0083	0.0668	0.26	0.3538	0.5165	0.21	0.1141	0.3460	0.13	0.0445	0.1843	0.21
3799	Ras-related protein Rab-2B	Q8RWD1	0.9842	0.9884	0.00	0.3445	0.7020	-0.12	0.3259	0.7468	0.04	0.4798	0.6802	0.05	0.4642	0.5557	-0.06	0.1598	0.3206	-0.11	0.6089	0.6564	-0.09	0.0456	0.9220	0.04	0.0090	0.0846	0.23
3800	Ras-related protein Rab-30	Q15771	0.0021	0.0315	0.30	0.0920	0.2252	0.21	0.1272	0.2472	0.12	0.0239	0.0785	0.22	0.0025	0.0387	0.19	0.0217	0.0950	0.21	0.6627	0.7071	-0.10	0.5699	0.9920	0.11	0.2399	0.3901	0.25
3801	Ras-related protein Rab-32	Q13637	0.6633	0.7232	0.09	0.8680	0.9041	0.03	0.7601	0.8011	0.07	0.9082	0.9206	-0.03	0.6299	0.7003	0.12	0.3641	0.5714	0.21	0.0213	0.1337	0.13	0.3099	0.6582	0.07	0.2899	0.3618	0.05
3802	Ras-related protein Rab-33B	Q9H082	0.0170	0.0761	-0.13	0.4252	0.5689	-0.17	0.0038	0.0322	-0.15	0.0046	0.0276	-0.31	0.0011	0.0261	-0.28	0.0066	0.0631	-0.21	0.0239	0.1374	0.36	0.0303	0.0246	0.75	0.9535	0.6545	0.03
3803	Ras-related protein Rab-34	Q9BZG1	0.4108	0.5212	-3.31	0.5752	0.7297	-1.75	0.5661	0.6621	-1.19	0.5388	0.6263	0.89	0.2938	0.4208	-1.88	0.9510	0.1028	0.09	0.0189	0.1275	-1.31	0.2234	0.5325	0.09	0.0032	0.0562	-0.49
3804	Ras-related protein Rab-35	Q15286	0.7176	0.7691	-0.01	0.9620	0.9742	0.01	0.3215	0.5090	-0.06	0.0115	0.0429	-0.26	0.0056	0.0355	-0.36	0.1656	0.3290	-0.43	0.6951	0.7362	-0.03	0.0406	0.1848	-0.07	0.0128	0.0985	-0.15
3805	Ras-related protein Rab-37	Q96AX2	0.0036	0.0384	-0.50	0.0527	0.5821	0.22	0.0119	0.0511	-0.35	0.0243	0.0693	-0.29	0.1467	0.3220	0.09	0.2628	0.4553	-0.09	0.0418	0.1119	-0.41	0.0047	0.0548	-0.58	0.0113	0.0931	-0.51
3806	Ras-related protein Rab-38	P57729	0.2102	0.3829	-0.11	0.2870	0.6679	0.06	0.3837	0.5844	-0.09	0.0035	0.0237	-0.28	0.0212	0.1049	0.20	0.0099	0.0706	-0.29	0.3736	0.6142	-2.55	0.8708	1.2375	-0.33	0.0651	0.2014	2.06
3807	Ras-related protein Rab-39A	Q14964	0.0208	0.0852	0.18	0.4054	0.7484	0.06	0.4286	0.6380	0.03	0.1140	0.2145	0.08	0.1804	0.3724	0.06	0.0213	0.0941	-0.29	0.0993	0.2545	-0.25	0.7330	1.1759	-0.03	0.7082	0.7584	-0.04
3808	Ras-related protein Rab-39B	Q96DA2	0.4108	0.5210	-3.31	0.5752	0.7296	-1.75	0.5661	0.6619	-1.19	0.5388	0.6262	0.89	0.2938	0.4208	-1.88	0.9510	0.1024	0.09	0.0409	0.1662	0.42	0.6696	1.1074	0.06	0.0147	0.1046	0.69
3809	Ras-related protein Rab-3A	P20336	0.5707	0.6385	-0.02	0.7633	0.8289	0.02	0.0118	0.0507	0.32	0.0442	0.1055	0.24	0.0063	0.0580	0.25	0.0278	0.1068	0.09	0.0507	0.0807	0.57	0.0013	0.0302	0.51	0.0317	0.1512	0.57
3810	Ras-related protein Rab-3B	P20337	0.5488	0.6181																									

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
3859	Regulator of G-protein signaling 2	P41220	0.0203	0.0842	0.09	0.5444	0.8590	0.05	0.2069	0.3601
3860	Regulator of G-protein signaling 21	Q2M5E4	0.0407	0.1273	0.62	0.0665	0.6505	-0.50	0.0198	0.0679
3861	Regulator of G-protein signaling 4	P49798	0.4108	0.5198	-3.31	0.5752	0.7278	-1.75	0.5661	0.6605
3862	Regulator of G-protein signaling 7	P49802	0.1852	0.3497	0.09	0.6449	0.7359	0.03	0.4265	0.6363
3863	Regulator of microtubule dynamics protein 1	Q96D85	0.5084	0.5915	-0.12	0.2092	0.6612	-0.25	0.1075	0.2163
3864	Regulator of noncense transcripts 1	Q29200	0.1668	0.3247	-0.05	0.6019	0.7056	0.03	0.0553	0.1343
3865	Regulator of noncense transcripts 2	Q9HAU5	0.0256	0.0969	0.25	0.2277	0.6600	0.16	0.2884	0.4674
3866	RelA-associated inhibitor	Q8WUF5	0.0048	0.0431	-0.20	0.2181	0.6611	0.21	0.7805	0.8197
3867	Remodeling and spacing factor 1	Q96723	0.1829	0.3472	0.07	0.0844	0.6219	0.30	0.0016	0.0237
3868	Renin receptor	Q75787	0.0077	0.0519	0.30	0.5793	0.6876	-0.08	0.6745	0.7247
3869	Replication factor C subunit 2	P35250	0.1093	0.2393	0.07	0.1741	0.6607	0.18	0.0125	0.0525
3870	Replication factor C subunit 3	P40938	0.8663	0.8944	0.02	0.5844	0.6915	0.05	0.1587	0.2927
3871	Replication factor C subunit 4	P35249	0.6317	0.6939	0.05	0.6079	0.7102	-0.06	0.1949	0.3437
3872	Replication factor C subunit 5	P40937	0.8476	0.8785	0.01	0.5903	0.6956	0.02	0.0411	0.1087
3873	Replication protein A 14 kDa subunit	P35244	0.4108	0.5196	-3.31	0.5752	0.7276	-1.75	0.5661	0.6603
3874	Replication protein A 30 kDa subunit	Q13156	0.4108	0.5195	-3.31	0.5752	0.7274	-1.75	0.5661	0.6602
3875	Replication protein A 32 kDa subunit	P15927	0.5932	0.6593	0.31	0.6168	0.7549	0.49	0.1493	0.2783
3876	Replication protein A 70 kDa DNA-binding subunit	P27694	0.1200	0.2555	0.11	0.1382	0.6520	0.08	0.0294	0.0871
3877	Replication stress response regulator SDE2	Q6IO49	0.6669	0.7264	-0.02	0.0040	0.3342	0.28	0.4274	0.6373
3878	Required for meiotic nuclear division protein 1 homolog	Q9NWS8	0.0007	0.0199	-0.39	0.1618	0.6620	-0.15	0.1585	0.2924
3879	Resistin	Q9HDB9	0.2258	0.4044	-0.31	0.3421	0.7001	0.28	0.8732	0.9998
3880	REST corepressor 1	Q9UKL0	0.1502	0.2996	0.09	0.1620	0.6613	0.20	0.0197	0.0677
3881	Reticulocalbin-1	Q15293	0.1204	0.2561	0.07	0.2896	0.6685	0.17	0.0032	0.0303
3882	Reticulocalbin-2	Q14257	0.3271	0.5330	0.02	0.1100	0.4284	0.08	0.0088	0.0440
3883	Reticulocalbin-3	Q96D15	0.5021	0.5755	-0.11	0.3078	0.6779	0.17	0.9481	0.9592
3884	Reticulon-1	P16799	0.4108	0.5194	-3.31	0.5752	0.7272	-1.75	0.5661	0.6600
3885	Reticulon-3	Q95197	0.0051	0.0435	0.33	0.4211	0.7595	0.10	0.0459	0.1181
3886	Reticulon-4	Q9NOC3	0.0762	0.1881	-0.12	0.0762	0.6167	0.24	0.4476	0.6609
3887	Reticulon-4 receptor-like 2	Q86UN3	0.0000	0.0000	0.86	0.0598	0.6330	0.26	0.0617	0.1443
3888	Retinol dehydrogenase 2	Q94788	0.4108	0.5193	-3.31	0.5752	0.7271	-1.75	0.5661	0.6600
3889	Retinal rod rhodopsin-sensitive cGMP 3', 5'-cyclic phosphodiesterase subunit delta	Q43924	0.4108	0.5191	-3.31	0.5752	0.7269	-1.75	0.5661	0.6599
3890	Retinoid dehydrogenase 1	P12271	0.1086	0.2380	-0.95	0.8038	0.8783	0.03	0.0130	0.0533
3891	Retinoblastoma-associated protein	P06400	0.4108	0.5190	-3.31	0.5752	0.7267	-1.75	0.5661	0.6597
3892	Retinoic acid receptor alpha	P10276	0.0573	0.1572	-0.18	0.0612	0.5937	-0.21	0.3442	0.5380
3893	Retinoic acid receptor RXR-alpha	P19793	0.4108	0.5189	-3.31	0.5752	0.7265	-1.75	0.5661	0.6596
3894	Retinoic acid receptor RXR-gamma	P48443	0.4108	0.5188	-3.31	0.5752	0.7264	-1.75	0.5661	0.6594
3895	Retinoic acid-induced protein 3	Q90002	0.0002	0.0123	-0.72	0.0057	0.3835	-0.44	0.0002	0.0059
3896	Retinol dehydrogenase 11	Q8T1C2	0.8741	0.9009	0.01	0.5631	0.8788	0.07	0.1108	0.2218
3897	Retinol-binding protein 1	P09455	0.4108	0.5186	-3.31	0.5752	0.7262	-1.75	0.5661	0.6593
3898	Retinol-binding protein 2	P51020	0.4108	0.5185	-3.31	0.5752	0.7260	-1.75	0.5661	0.6591
3899	Retinoid demethylase factor 1	Q9HMC1	0.1535	0.3051	0.12	0.1679	0.6599	0.80	0.0015	0.0228
3900	RGM domain family member B	Q6NWC4	0.4108	0.5184	-3.31	0.5752	0.7258	-1.75	0.5661	0.6590
3901	Rho GDP-dissociation inhibitor 1	P52565	0.0629	0.1659	-0.11	0.4304	0.7664	0.13	0.2189	0.3755
3902	Rho GTPase-activating protein 1	Q07960	0.0066	0.0488	-0.13	0.2394	0.9475	-0.01	0.0851	0.1811
3903	Rho GTPase-activating protein 15	Q3Q0Z3	0.4108	0.5183	-3.31	0.5752	0.7257	-1.75	0.5661	0.6588
3904	Rho GTPase-activating protein 17	Q68M7Q	0.0245	0.0944	-0.15	0.0101	0.4434	-0.20	0.0698	0.1570
3905	Rho GTPase-activating protein 18	Q8N392	0.4108	0.5181	-3.31	0.5752	0.7255	-1.75	0.5661	0.6587
3906	Rho GTPase-activating protein 20	Q9P2F6	0.0669	0.1714	0.42	0.0662	0.6855	-0.36	0.8936	0.9153
3907	Rho GTPase-activating protein 21	Q5T5U3	0.2783	0.4723	0.08	0.4889	0.8120	0.09	0.0955	0.1969
3908	Rho GTPase-activating protein 26	Q9UNAI	0.1016	0.2275	0.11	0.5187	0.8396	0.06	0.0182	0.0646
3909	Rho GTPase-activating protein 28	Q9P2N2	0.0034	0.0379	-2.89	0.2251	0.6606	-1.87	0.0014	0.0225
3910	Rho GTPase-activating protein 29	Q52LW3	0.0109	0.0599	-0.07	0.1838	0.6649	-0.07	0.1525	0.2833
3911	Rho GTPase-activating protein 35	Q9NRY4	0.0062	0.0474	0.27	0.3200	0.6830	0.13	0.0511	0.1272
3912	Rho GTPase-activating protein 40	Q5T330	0.0256	0.0968	0.21	0.1077	0.6311	0.27	0.0380	0.1028
3913	Rho GTPase-activating protein 44	Q17B89	0.0064	0.0478	-0.88	0.0538	0.5855	-0.51	0.0103	0.0474
3914	Rho GTPase-activating protein 45	Q92619	0.2943	0.4924	0.08	0.2712	0.6642	0.14	0.7400	0.7828
3915	Rho GTPase-activating protein 5	Q13017	0.4108	0.5180	-3.31	0.5752	0.7253	-1.75	0.5661	0.6585
3916	Rho guanine nucleotide exchange factor 1	Q92888	0.0008	0.0203	0.11	0.4557	0.7879	0.05	0.0687	0.1551
3917	Rho guanine nucleotide exchange factor 11	Q15085	0.9558	0.9668	0.00	0.5915	0.6960	-0.04	0.2064	0.3595
3918	Rho guanine nucleotide exchange factor 16	Q5VV41	0.0555	0.1538	-0.39	0.7857	0.8458	-0.12	0.2880	0.4669
3919	Rho guanine nucleotide exchange factor 17	Q96PE2	0.3444	0.5528	-0.14	0.2334	0.6621	0.20	0.6684	0.7189
3920	Rho guanine nucleotide exchange factor 18	Q6ZS25	0.1248	0.2630	-0.78	0.8810	0.9144	-0.07	0.0320	0.0917
3921	Rho guanine nucleotide exchange factor 2	Q92974	0.4108	0.5179	-3.31	0.5752	0.7251	-1.75	0.5661	0.6584
3922	Rho guanine nucleotide exchange factor 28	Q8N1W1	0.1000	0.2250	0.23	0.2232	0.6584	0.14	0.0814	0.1752
3923	Rho guanine nucleotide exchange factor 4	Q9NR80	0.4108	0.5177	-3.31	0.5752	0.7249	-1.75	0.5661	0.6582
3924	Rho guanine nucleotide exchange factor 7	Q14155	0.4108	0.5176	-3.31	0.5752	0.7248	-1.75	0.5661	0.6581
3925	Rho guanine nucleotide exchange factor 9	Q43307	0.5336	0.6043	0.05	0.1088	0.6586	0.12	0.4404	0.6520
3926	Rho-associated protein kinase 1	Q13464	0.0031	0.0362	-2.34	0.0467	0.5639	-1.12	0.0029	0.0297
3927	Rho-associated protein kinase 2	Q75116	0.0221	0.0885	0.28	0.0771	0.5822	0.23	0.3380	0.5304
3928	Rhopiliin-2	Q8B1C4	0.0108	0.0598	0.25	0.0224	0.4775	0.20	0.0287	0.0859
3929	Rho-related GTP-binding protein RhoC	P62745	0.0633	0.1665	-0.63	0.0502	0.5740	-0.08	0.0132	0.0538
3930	Rho-related GTP-binding protein RhoG	P08134	0.2015	0.3721	0.06	0.7013	0.7794	0.05	0.2019	0.3537
3931	Rho-related GTP-binding protein RhoH	P84095	0.0761	0.1882	0.06	0.5102	0.8321	0.09	0.1609	0.2959
3932	Rho-related GTP-binding protein RhoI	Q9H4E5	0.4108	0.5175	-3.31	0.5752	0.7246	-1.75	0.5661	0.6579
3933	Rhotekin	Q9B5T9	0.7068	0.7591	0.01	0.4737	0.8011	-0.25	0.0009	0.0204
3934	Ribonuclease inhibitor	P13489	0.0078	0.0522	0.26	0.4640	0.7818	0.08	0.0829	0.1774
3935	Ribonuclease P protein subunit p20	Q75817	0.4728	0.5485	-0.07	0.1985	0.6642	-0.15	0.9426	0.9555
3936	Ribonuclease P protein subunit p40	Q75818	0.0028	0.0354	0.29	0.1855	0.6668	0.19	0.0508	0.1268
3937	Ribonuclease T2	Q00584	0.3770	0.5925	0.11	0.8568	0.8968	-0.03	0.0426	0.1119
3938	Ribonuclease P/MPR protein subunit POP1	Q95755	0.0412	0.1285	-0.20	0.3791	0.7257	0.11	0.3026	0.4854
3939	Ribonucleoprotein PTB-binding 1	Q8YI67	0.0034	0.0378	0.28	0.0995	0.6355	0.35	0.0018	0.0241
3940	Ribonucleoside-diphosphate reductase large subunit	P23921	0.1841	0.3487	0.04	0.0572	0.224	0.0303	0.0316	0.42
3941	Ribonucleoside-diphosphate reductase subunit M2	P31350	0.0017	0.0281	0.35	0.1479	0.6576	0.26	0.0244	0.0773

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

MCF-7												MDA-MB-231																
Protein name	UniProt	Dai SC20 vs control			Gen SC20 vs control			SSE SC20 vs control			Dai IC20 vs control			Gen IC20 vs control			SSE IC20 vs control											
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC									
3942 Ribonucleoside-diphosphate reductase subunit M2 B	Q7LG56	0.3693	0.5834	0.06	0.1594	0.6643	0.40	0.0658	0.1504	0.20	0.1449	0.2850	0.47	0.0000	0.0000	0.36	0.0501	0.1504	0.22	0.2989	0.5563	-0.26	0.2205	0.5276	0.31	0.5250	0.5916	0.14
3943 Ribose-5-phosphate isomerase	P49247	0.0944	0.2166	-3.22	0.2051	0.6595	-1.75	0.0233	0.0752	-3.47	0.0039	0.0253	-4.53	0.8887	0.9147	-0.01	0.1016	0.2361	-3.35	0.3736	0.5336	-2.55	0.8708	1.0946	-0.33	0.0651	0.1568	2.06
3944 Ribose-phosphate pyrophosphokinase 1	P60891	0.4491	0.5267	-0.04	0.0422	0.5678	-0.30	0.0057	0.0366	-0.28	0.4260	0.6178	-0.04	0.5145	0.6032	0.03	0.7710	1.0065	0.03	0.0555	0.0787	-0.55	0.0304	0.0456	-0.50	0.0468	0.0777	-0.49
3945 Ribose-phosphate pyrophosphokinase 2	P11908	0.0293	0.1047	0.10	0.4133	0.7525	0.09	0.3391	0.5315	0.04	0.2885	0.4499	0.02	0.0102	0.0719	-0.09	0.3502	0.5553	0.03	0.1019	0.2587	-0.19	0.0024	0.0406	2.84	0.0006	0.0317	2.91
3946 Ribosomal biogenesis protein SBDS	P21108	0.4462	0.5236	-0.04	0.3169	0.6806	0.12	0.0235	0.0753	-0.25	0.0038	0.0250	-0.39	0.0114	0.0765	-0.35	0.0167	0.0849	-0.28	0.2862	0.5521	-5.13	0.3373	0.6950	1.11	0.2523	0.3236	0.87
3947 Ribosomal biogenesis protein LAS1L	Q9Y4W2	0.0082	0.0535	0.21	0.7474	0.8170	-0.03	0.1883	0.3342	0.13	0.3277	0.4996	0.07	0.6429	0.7117	0.01	0.0054	0.0613	0.19	0.3736	0.6279	-2.55	0.8708	1.2614	-0.33	0.0651	0.2101	0.06
3948 Ribosomal oxygenase 1	Q9HWG3	0.0017	0.0280	-0.55	0.0310	0.5082	-0.30	0.0092	0.0450	-0.29	0.0012	0.0160	-0.93	0.8090	0.2343	-0.13	0.0856	0.2129	0.12	0.3736	0.5418	-2.55	0.8708	1.1094	-0.33	0.0651	0.1610	2.06
3949 Ribosomal protein S6 kinase alpha-1	Q15418	0.3629	0.5756	0.20	0.9071	0.9355	-0.08	0.9425	0.9556	-0.01	0.0808	0.1656	-0.41	0.1873	0.3827	-0.23	0.8071	1.0444	-0.05	0.0734	0.2148	0.14	0.7865	1.2305	0.02	0.0490	0.1936	0.18
3950 Ribosomal protein S6 kinase alpha-2	Q15349	0.7010	0.7546	-0.03	0.8999	0.9216	0.02	0.7901	0.8280	-0.02	0.5595	0.6100	0.09	0.2578	0.4780	-0.11	0.6241	0.8593	0.04	0.0005	0.0375	-0.42	0.0010	0.0278	-0.34	0.0038	0.0608	-0.56
3951 Ribosomal protein S6 kinase alpha-3	P51812	0.0001	0.0096	0.14	0.1633	0.6634	0.18	0.0067	0.0395	0.29	0.0013	0.0165	0.30	0.1808	0.4958	-0.11	0.0015	0.0508	0.28	0.7336	0.6464	-2.55	0.8708	1.2932	-0.33	0.0651	0.2223	2.06
3952 Ribosomal protein S6 kinase beta-1	P23443	0.0050	0.0433	0.15	0.9581	0.9716	0.01	0.0911	0.1899	0.09	0.5596	0.6099	0.02	0.0009	0.0224	-0.16	0.1289	0.2793	0.15	0.3736	0.5249	-2.55	0.8708	1.0789	-0.33	0.0651	0.1526	2.06
3953 Ribosomal protein S6 kinase delta-1	Q96S38	0.0154	0.0717	0.18	0.3860	0.7305	0.16	0.0097	0.0458	0.31	0.0080	0.0362	0.22	0.4243	0.1127	0.16	0.0111	0.0723	0.29	0.1656	0.3604	-0.25	0.2692	0.6005	-0.15	0.6288	0.6863	-0.04
3954 Ribosomal RNA processing protein 1 homolog A	P56182	0.5441	0.6140	-0.37	0.2907	0.6690	-2.19	0.6140	0.6687	-0.19	0.0581	0.1284	-0.40	0.6078	0.6822	0.16	0.9150	1.1518	-0.03	0.0061	0.0829	-0.88	0.1169	0.3521	0.42	0.0536	0.2039	-0.36
3955 Ribosomal RNA processing protein 36 homolog	Q96E06	0.5446	0.6143	0.19	0.9648	0.9757	0.01	0.5276	0.7488	-0.14	0.0089	0.0380	-0.26	0.0251	0.1142	0.38	0.2858	0.4822	-0.26	0.3736	0.4844	-2.55	0.8708	1.0048	-0.33	0.0651	0.1339	2.06
3956 Ribosome biogenesis protein BMS1 homolog	Q14692	0.5056	0.5785	-0.07	0.3451	0.7024	-0.23	0.1449	0.2716	-0.20	0.6276	0.6739	0.05	0.3967	0.4929	0.10	0.2405	0.4263	0.14	0.2705	0.5136	0.15	0.4553	0.8595	0.02	0.0025	0.0537	0.41
3957 Ribosome biogenesis protein BOP1	Q14137	0.0374	0.1215	-0.93	0.3060	0.6783	-0.68	0.0008	0.0204	-3.30	0.0168	0.0541	-2.20	0.7013	0.7627	-0.11	0.0275	0.1064	-1.22	0.2820	0.5314	0.88	0.0956	0.3085	1.63	0.0780	0.1286	1.98
3958 Ribosome biogenesis protein WDR12	Q9GZL7	0.1054	0.2329	0.08	0.5211	0.8406	0.08	0.3476	0.5414	-0.06	0.4781	0.6783	-0.03	0.0090	0.0671	-0.22	0.1173	0.2611	-0.05	0.0167	0.1201	-1.42	0.0124	0.0921	-1.62	0.0050	0.0683	-1.28
3959 Ribosome maturation protein SBDS	Q9Y3A5	0.4108	0.5174	-3.31	0.5752	0.7244	-1.75	0.5661	0.6578	-1.19	0.4744	0.6223	0.89	0.2938	0.4175	-1.88	0.9510	1.0066	0.36	0.0296	0.4099	-0.17	0.3136	0.5181	0.02	0.0051	0.1185	0.02
3960 Ribosome-binding protein 1	Q9P2F9	0.0023	0.0238	0.26	0.9353	0.9301	0.29	0.0004	0.0218	-0.42	0.0002	0.0120	-0.55	0.0200	0.0358	0.37	0.0020	0.0331	0.56	0.2909	0.1474	-0.47	0.8592	1.3010	0.02	0.1409	0.3023	0.13
3961 Ribosome-recycling factor mitochondrial	Q96E11	0.0056	0.0452	0.38	0.1225	0.6384	0.62	0.0066	0.1550	0.28	0.0298	0.0800	0.32	0.9718	0.9778	0.00	0.2336	0.4177	0.27	0.1174	0.2851	-0.31	0.0105	0.0842	-0.23	0.2003	0.2687	-0.11
3962 Ribosylhydrolase/oxalacetate dehydrogenase [quinone]	P16083	0.0904	0.2106	0.51	0.2658	0.6629	-0.28	0.0002	0.0164	1.05	0.0053	0.0295	0.99	0.0003	0.0147	0.77	0.0227	0.0965	1.19	0.3736	0.5897	-2.55	0.8708	1.1946	-0.33	0.0651	0.1868	2.06
3963 RILP-like protein 2	Q969X0	0.2504	0.4367	-0.40	0.1149	0.6332	-0.20	0.2037	0.3561	-0.14	0.1050	0.2011	-0.19	0.0365	0.1388	-0.29	0.1188	0.2633	-0.37	0.3736	0.5277	-2.55	0.8708	1.0841	-0.33	0.0651	0.1540	2.06
3964 RIMS-binding protein 3C	AGN1Z7	0.0173	0.0769	-1.06	0.2202	0.6601	-0.78	0.0703	0.1576	-0.51	0.0647	0.1396	-0.53	0.3527	0.0454	-0.21	0.0910	0.2202	-0.46	0.3736	0.5370	-2.55	0.8708	1.1007	-0.33	0.0651	0.1585	2.06
3965 RING finger and CHY zinc finger domain-containing protein 1	Q96PM5	0.6567	0.7174	-0.04	0.7524	0.8205	-0.04	0.6800	0.7299	-0.03	0.2045	0.3382	-0.10	0.6748	0.7385	0.04	0.7617	0.9996	-0.04	0.5561	0.6067	0.12	0.3879	0.7687	0.18	0.4680	0.5365	-0.30
3966 RING finger protein 122	Q9H9V4	0.6180	0.6818	0.04	0.4724	0.8013	0.06	0.0494	0.1239	-0.23	0.1306	0.2373	-0.14	0.0144	0.0852	0.32	0.0369	0.1245	-0.29	0.3736	0.5719	-2.55	0.8708	1.1632	-0.33	0.0651	0.1768	2.06
3967 RING finger protein 212B	ASMTL3	0.9265	0.9440	0.00	0.2761	0.6643	0.15	0.0504	0.1259	0.15	0.2540	0.4040	0.07	0.0304	0.1271	0.17	0.0692	0.1850	0.14	0.3736	0.5496	-2.55	0.8708	1.1235	-0.33	0.0651	0.1650	2.06
3968 RING-box protein 2	Q9UBF6	0.2494	0.4357	-0.21	0.8864	0.9190	-0.02	0.5209	0.7419	-0.10	0.1471	0.2610	-0.29	0.1968	0.3964	0.25	0.8591	1.0947	0.03	0.3736	0.4356	-2.55	0.8708	0.9137	-0.33	0.0651	0.1137	2.06
3969 RNA binding motif protein X-linked-like-1	Q96E39	0.4108	0.5172	-3.31	0.5752	0.7242	-1.75	0.5661	0.6576	-1.19	0.5388	0.6222	0.89	0.2938	0.4174	-1.88	0.9510	1.0064	0.09	0.1778	0.3770	-0.12	0.0503	0.2110	-0.25	0.0878	0.1405	-0.11
3970 RNA binding protein fox-1 homolog 1	Q9NWB1	0.1918	0.3584	-0.26	0.1176	0.6313	-0.72	0.2922	0.4724	-0.18	0.4974	0.7011	-0.15	0.0509	0.1669	0.46	0.1169	0.2606	0.34	0.3736	0.5286	-2.55	0.8708	1.0856	-0.33	0.0651	0.1544	2.06
3971 RNA polymerase II subunit A C-terminal domain phosphatase SSU72	Q9NP77	0.4108	0.5171	-3.31	0.5752	0.7241	-1.75	0.5661	0.6575	-1.19	0.5388	0.6222	0.89	0.2938	0.4173	-1.88	0.9510	1.0062	0.09	0.0009	0.0405	-0.80	0.0008	0.0259	-1.08	0.0124	0.0963	-1.17
3972 RNA polymerase II-associated factor 1 homolog	Q8N7H5	0.5228	0.5944	-0.18	0.7497	0.8186	0.16	0.7101	0.7559	-0.07	0.8204	0.8445	-0.11	0.1684	0.3549	-0.20	0.5992	0.8355	0.07	0.3736	0.4526	-2.55	0.8708	0.9456	-0.33	0.0651	0.1205	2.06
3973 RNA polymerase II-associated protein 3	Q9HG73	0.0233	0.0914	0.26	0.2704	0.6638	0.14	0.0083	0.0430	0.39	0.0126	0.0455	0.30	0.1181	0.2820	0.13	0.0277	0.1910	0.20	0.0470	0.1739	0.41	0.8297	1.2731	0.02	0.8452	0.8751	0.01
3974 RNA polymerase II-associated protein CTR9 homolog	O6PD62	0.0348	0.1167	-0.49	0.5809	0.8826	-0.23	0.0089	0.0439	0.69	0.2947	0.4579	0.16	0.0893	0.2347	0.23	0.0678	0.1418	0.26	0.0777	0.2216	0.39	0.9536	0.9669	0.01	0.0209	0.1234	0.28
3975 RNA polymerase-associated protein RTF1 homolog	Q92541	0.0661	0.1703	0.16	0.0617	0.5919	0.17	0.2615	0.4311	0.08	0.1059	0.2026	0.13	0.1429	0.2918	0.13	0.5693	0.8040	0.08	0.2820	0.5312	-0.30	0.1696	0.4501	0.21	0.0412	0.1761	0.31
3976 RNA transcription, translation and transport factor protein	Q9Y224	0.7975	0.8361	0.04	0.3476	0.7036	-0.15	0.0511	0.1271	0.19	0.0120	0.0439	0.34	0.0447	0.1561	0.17	0.0443	0.1388	0.40	0.1580	0.3499	0.07	0.0550	0.2240	-0.14	0.0117	0.0937	-0.22
3977 RNA-binding motif protein X chromosome	P38159	0.0129	0.0663	-0.25	0.3268	0.6862	-0.08	0.8515	0.8813	0.01	0.0451	0.0671	-0.03	0.1446	0.3190	0.08	0.1690	0.3339	-0.06	0.0539	0.1843	0.41	0.0219	0.1283	0.36	0.0403	0.1738	0.39
3978 RNA-binding motif protein X-linked-like-2	Q75526	0.0356	0.1179	-0.20	0.3126	0.6807	0.07	0.0003	0.0194	-0.67	0.0015	0.0179	-0.45	0.2502	0.1653	-0.27	0.0018	0.0527	-0.56	0.0543	0.1852	0.41	0.8834	0.9119	0.02	0.2843	0.3563	0.15
3979 RNA-binding motif protein X-linked-like-3	Q8N7X1	0.4108	0.5170	-3.31	0.5752	0.7239	-1.75	0.5661	0.6573	-1.19	0.5388	0.6219	0.89	0.2938	0.4172	-1.88	0.9510	1.0060	0.09	0.0002	0.0288	0.75	0.0009	0.0274	0.73	0.0018	0.0499	0.79
3980 RNA-binding protein 12	Q9NTZ6	0.2160	0.3911	-0.06	0.5765	0.6857	0.07	0.1760	0.3183	-0.07	0.2914	0.4524	-0.05	0.0434	0.1540	-0.13	0.0557	0.1										

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control	
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
4015	Sadenosylmethionine synthase isoform type-1	Q00266	0.3832	0.5993	0.71	0.3140	0.6800	-1.95	0.0229	0.0744
4016	Sadenosylmethionine synthase isoform type-2	P11153	0.0093	0.0571	-0.07	0.7802	0.8416	-0.04	0.7527	0.7944
4017	SAM domain-containing protein SAMSN-1	Q9NSI8	0.4108	0.5162	-3.31	0.5752	0.7228	-1.75	0.5661	0.6565
4018	SAM pointed domain-containing Ets transcription factor	O95238	0.3342	0.5406	-0.11	0.7096	0.7868	-0.06	0.6692	0.7195
4019	SAP domain-containing ribonucleoprotein	P82979	0.4108	0.5161	-3.31	0.5752	0.7227	-1.75	0.5661	0.6565
4020	SAP30-binding protein	Q9UIH5	0.1039	0.2306	-0.57	0.0470	0.6114	-0.74	0.1475	0.2756
4021	Sarcomal membrane-associated protein	Q14BNA	0.0368	0.1206	0.20	0.0780	0.6199	0.54	0.7322	0.5774
4022	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	O14983	0.3394	0.5472	-0.07	0.0994	0.6357	0.18	0.6240	0.6776
4023	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	P16615	0.0094	0.0572	0.16	0.1367	0.6520	0.26	0.0003	0.0213
4024	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	Q93084	0.0030	0.0361	-0.30	0.8811	0.9143	-0.01	0.0011	0.0213
4025	S-arrestin	P10523	0.4108	0.5160	-3.31	0.5752	0.7225	-1.75	0.5661	0.6562
4026	Scaffold attachment factor B1	Q15424	0.4108	0.5159	-3.31	0.5752	0.7223	-1.75	0.5661	0.6560
4027	Scaffold attachment factor B2	Q14151	0.7908	0.8307	0.06	0.2843	0.6646	-2.02	0.3176	0.5045
4028	Scavenger receptor class B member 1	Q8WTV0	0.7039	0.7566	-0.04	0.8956	0.9262	0.03	0.0352	0.0976
4029	Scavenger receptor cysteine-rich type 1 protein M160	Q9NR16	0.0223	0.0890	0.14	0.1140	0.6343	0.27	0.0136	0.0547
4030	Schlafen family member 11	Q7Z7L1	0.0237	0.0924	0.17	0.1806	0.6644	0.29	0.0376	0.1020
4031	Schwannomin-interacting protein 1	PD0PB3	0.4108	0.5157	-3.31	0.5752	0.7221	-1.75	0.5661	0.6559
4032	SCL-interacting locus protein	Q15468	0.6747	0.7324	-0.02	0.6434	0.7951	0.13	0.0816	0.1754
4033	SCY1-like protein 2	O6P3W7	0.0598	0.1618	-0.31	0.5974	0.7014	-0.11	0.2027	0.3547
4034	Sec1 family domain-containing protein 1	Q8WVM8	0.0036	0.0383	-0.31	0.2362	0.6639	0.17	0.0019	0.0242
4035	Sec1 family domain-containing protein 2	Q8WVU7	0.4108	0.5156	-3.31	0.5752	0.7220	-1.75	0.5661	0.6557
4036	SFIC23-interacting protein	Q9YYSX	0.0103	0.0589	0.14	0.2691	0.6628	0.11	0.3295	0.5191
4037	Secernin-1	Q12765	0.0213	0.0867	0.11	0.0806	0.6140	0.26	0.0271	0.0825
4038	Secernin-2	Q96FV2	0.0035	0.0378	-0.95	0.5858	0.6918	-0.23	0.5481	0.7711
4039	Secotransaminase	P05060	0.0915	0.2121	-0.28	0.6454	0.7383	-0.23	0.0105	0.0476
4040	Secotransaminase-1	P13521	0.4108	0.5155	-3.31	0.5752	0.7218	-1.75	0.5661	0.6556
4041	Secretory carrier-associated membrane protein 1	O15126	0.1475	0.2958	-0.07	0.6293	0.7262	0.06	0.0118	0.0508
4042	Secretory carrier-associated membrane protein 2	O15127	0.0147	0.0704	-0.65	0.5600	0.7079	-0.90	0.3872	0.5885
4043	Secretory carrier-associated membrane protein 3	O14828	0.0869	0.2050	0.06	0.3846	0.7303	0.08	0.0200	0.0682
4044	Secretory carrier-associated membrane protein 4	Q969E2	0.1438	0.2907	-0.07	0.2016	0.6601	0.17	0.2886	0.4676
4045	Sedohexulokinase	Q9UHH6	0.4108	0.5154	-3.31	0.5752	0.7216	-1.75	0.5661	0.6554
4046	Segment polarity protein dishevelled homolog DVL-2	O14641	0.0145	0.0699	0.43	0.0458	0.5595	0.57	0.0008	0.0222
4047	Segment polarity protein dishevelled homolog DVL-3	Q92997	0.4108	0.5152	-3.31	0.5752	0.7214	-1.75	0.5661	0.6553
4048	Selenide water dikinase 1	P49903	0.1435	0.2904	-0.09	0.9814	0.9871	0.00	0.3360	0.5316
4049	Separin	Q14674	0.0851	0.2017	-0.60	0.1185	0.6328	-0.51	0.1421	0.2680
4050	Serine peptidase	P35270	0.0608	0.1633	0.07	0.1830	0.6648	0.28	0.0212	0.0645
4051	Serpin-10	Q9P0V9	0.0000	0.0000	-1.23	0.1649	0.6655	-1.17	0.0017	0.0237
4052	Serpin-11	Q9N1A2	0.3754	0.5907	-0.91	0.1427	0.6547	0.23	0.0270	0.0824
4053	Serpin-14	Q9ZU15	0.0690	0.1748	-0.60	0.2899	0.6686	-1.02	0.3775	0.1018
4054	Serpin-1	Q15019	0.0538	0.1513	0.12	0.3108	0.6796	0.13	0.0124	0.0523
4055	Serpin-4	Q43236	0.1311	0.2729	-0.11	0.2276	0.6654	0.14	0.7059	0.7524
4056	Serpin-6	Q14141	0.8037	0.8416	0.01	0.1905	0.6686	0.27	0.3585	0.5553
4057	Serpin-7	P16181	0.0174	0.0772	0.12	0.0271	0.5050	0.12	0.0067	0.0396
4058	Serpin-8	Q92599	0.3467	0.5557	-0.10	0.6116	0.7129	0.06	0.7888	0.8270
4059	Serpin-9	Q9UHD8	0.0717	0.1799	0.12	0.2717	0.6651	0.20	0.0085	0.0435
4060	Sequestosome-1	Q13501	0.0225	0.0893	-0.20	0.0266	0.4974	-0.36	0.9433	0.9557
4061	Serine dehydratase-like	Q96GA7	0.0074	0.0506	0.10	0.5286	0.8472	0.07	0.0015	0.0225
4062	Serine hydroxymethyltransferase cytosolic	P34896	0.9235	0.9413	0.00	0.0611	0.5938	-0.16	0.1816	0.3257
4063	Serine hydroxymethyltransferase mitochondrial	P34897	0.0072	0.0501	0.25	0.8772	0.7293	0.14	0.0059	0.0440
4064	Serine palmitoyltransferase 1	O15269	0.0487	0.1414	-0.11	0.6927	0.7745	0.06	0.7788	0.8183
4065	Serine palmitoyltransferase 2	O15270	0.0024	0.0331	0.12	0.0448	0.5674	0.28	0.0178	0.0637
4066	Serine protease 33	Q8NF86	0.4108	0.5151	-3.31	0.5752	0.7213	-1.75	0.5661	0.6551
4067	Serine protease 38	A1L453	0.0877	0.2062	-0.38	0.1593	0.6644	-0.64	0.2421	0.4064
4068	Serine protease HTRA1	Q92743	0.2928	0.4907	-0.20	0.6839	0.7695	0.10	0.3905	0.6468
4069	Serine protease inhibitor Kazal-type 5	Q8NC38	0.9436	0.9577	0.01	0.1523	0.6596	0.21	0.4460	0.6591
4070	Serine protease inhibitor Kazal-type 8	POCT11	0.0056	0.0401	3.91	0.1129	0.6250	-0.65	0.0443	0.1150
4071	Serine racemase	Q9GZT4	0.4108	0.5150	-3.31	0.5752	0.7211	-1.75	0.5661	0.6550
4072	Serine/arginine repetitive matrix protein 1	Q8IYB3	0.0609	0.1635	-12.21	0.2164	0.6598	-1.34	0.7843	0.8229
4073	Serine/arginine repetitive matrix protein 2	Q9LUQ35	0.4074	0.6281	-0.04	0.4003	0.7437	0.14	0.0024	0.0270
4074	Serine/arginine-rich splicing factor 1	Q07955	0.3950	0.6132	0.05	0.4893	0.8124	0.07	0.0057	0.0365
4075	Serine/arginine-rich splicing factor 11	Q05519	0.4108	0.5149	-3.31	0.5752	0.7209	-1.75	0.5661	0.6548
4076	Serine/arginine-rich splicing factor 2	Q01130	0.0376	0.1217	0.16	0.1435	0.6549	0.12	0.0046	0.0336
4077	Serine/arginine-rich splicing factor 3	P84103	0.1885	0.3543	-0.40	0.5168	0.8389	-0.05	0.0018	0.0236
4078	Serine/arginine-rich splicing factor 4	Q08170	0.2784	0.4722	0.30	0.4048	0.7478	0.38	0.0594	0.1409
4079	Serine/arginine-rich splicing factor 5	Q13243	0.9735	0.9815	0.00	0.7689	0.8324	0.03	0.0319	0.0915
4080	Serine/arginine-rich splicing factor 6	Q13247	0.0679	0.1732	0.13	0.2400	0.6613	0.21	0.0139	0.0553
4081	Serine/arginine-rich splicing factor 7	O16629	0.0003	0.0144	-0.24	0.0006	0.2391	-0.22	0.0044	0.0329
4082	Serine/arginine-rich splicing factor 8	Q9BR16	0.1176	0.2520	0.26	0.1652	0.6608	1.03	0.1554	0.2873
4083	Serine/arginine-rich splicing factor 9	Q13242	0.4747	0.5502	-0.21	0.1697	0.6619	-1.21	0.0098	0.0461
4084	Serine/threonine-protein kinase	Q95747	0.1962	0.3652	0.05	0.5986	0.7020	0.03	0.8922	0.9141
4085	Serine/threonine-protein kinase 10	Q94804	0.0402	0.1261	-0.32	0.9537	0.9692	0.01	0.1392	0.2636
4086	Serine/threonine-protein kinase 17A	O4108	0.5147	0.5147	-3.31	0.5752	0.7207	-1.75	0.5661	0.6547
4087	Serine/threonine-protein kinase 19	P49842	0.7265	0.7771	-0.05	0.0645	0.5882	0.31	0.5058	0.7280
4088	Serine/threonine-protein kinase 24	Q9Y6E0	0.2967	0.4951	0.12	0.2331	0.6623	0.22	0.8906	0.9126
4089	Serine/threonine-protein kinase 25	O05056	0.0100	0.0583	-1.25	0.6386	0.7335	-0.29	0.0028	0.0288
4090	Serine/threonine-protein kinase 26	Q9P289	0.2683	0.4600	0.07	0.8663	0.9033	-0.02	0.1088	0.2184
4091	Serine/threonine-protein kinase 3	P13188	0.4108	0.5146	-3.31	0.5752	0.7206	-1.75	0.5661	0.6546
4092	Serine/threonine-protein kinase 31	Q9BXU1	0.4108	0.5145	-3.31	0.5752	0.7204	-1.75	0.5661	0.6544
4093	Serine/threonine-protein kinase 32A	Q8WU08	0.4108	0.5144	-3.31	0.5752	0.7202	-1.75	0.5661	0.6543
4094	Serine/threonine-protein kinase 38-like	Q9Y2H1	0.7739	0.8160	-0.03	0.2335	0.6617	0.13	0.2384	0.4007
4095	Serine/threonine-protein kinase 4	Q13043	0.0727	0.1817	-10.98	0.0626	0.5907	-9.42	0.0241	0.0764
4096	Serine/threonine-protein kinase ATR	Q13535	0.4578	0.5348	-0.02	0.5002	0.8231	-0.03	0.0136	0.0545
4097	Serine/threonine-protein kinase Chk1	O14757	0.4108	0.5142	-3.31	0.5752	0.7200	-1.75	0.5661	0.6541
4098	Serine/threonine-protein kinase greatwall	Q96GX5	0.6168	0.6810	0.07	0.1760	0.6616	-0.23	0.1082	0.2174

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

MCF-7										MDA-MB-231																		
Protein name	UniProt	Dai SC20 vs control			Gen SC20 vs control			SSE SC20 vs control			Dai IC20 vs control			Gen IC20 vs control			SSE IC20 vs control			Dai IC20 vs control			Gen IC20 vs control			SSE IC20 vs control		
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC
4099 Serine/threonine-protein kinase ICK	Q9UPZ9	0.8646	0.8929	-0.01	0.1109	0.6327	0.11	0.0147	0.0572	0.24	0.9796	0.9824	0.00	0.0123	0.0790	0.25	0.8859	1.1234	-0.01	0.3736	0.4347	-2.55	0.8708	0.9120	-0.33	0.0651	0.1134	2.06
4100 Serine/threonine-protein kinase MAK	P20794	0.5883	0.6549	-0.12	0.3280	0.6876	-0.45	0.3169	0.5038	-0.25	0.3412	0.5156	-0.24	0.3957	0.4925	-0.22	0.4602	0.6827	-0.18	0.1072	0.2674	-0.38	0.7435	1.1861	-0.02	0.0304	0.1473	0.10
4101 Serine/threonine-protein kinase MARK1	Q9P0L2	0.0933	0.2150	-9.52	0.0844	0.6228	-7.96	0.0337	0.0951	-7.41	0.0033	0.0233	-5.32	0.5886	0.6657	0.26	0.0178	0.0871	-6.13	0.3736	0.5966	-2.55	0.8708	1.2067	-0.33	0.0651	0.1908	2.06
4102 Serine/threonine-protein kinase MARK2	Q7KZ17	0.0352	0.1171	-0.21	0.8875	0.9196	0.02	0.8823	0.9070	-0.01	0.9367	0.9445	-0.01	0.5310	0.6167	0.05	0.2834	0.4797	-0.15	0.3723	0.6542	0.09	0.9205	0.9416	-0.01	0.0297	0.1468	0.29
4103 Serine/threonine-protein kinase MRCK beta	Q9Y5S2	0.0381	0.1225	-0.27	0.2768	0.6650	0.11	0.0540	0.1319	-0.14	0.0026	0.0213	0.17	0.1660	0.3521	0.08	0.3322	0.5352	-0.11	0.3736	0.4762	-2.55	0.8708	0.9896	-0.33	0.0651	0.1304	2.06
4104 Serine/threonine-protein kinase N2	Q16513	0.4108	0.5141	-3.31	0.5752	0.7199	-1.75	0.5661	0.6540	-1.19	0.5388	0.6187	0.89	0.2938	0.4146	-1.88	0.9510	1.0013	0.09	0.3169	0.5792	0.32	0.0822	0.2820	0.70	0.0681	0.1155	0.86
4105 Serine/threonine-protein kinase Nek1	Q8NG66	0.0160	0.0737	0.23	0.2902	0.6684	0.23	0.0104	0.0475	0.27	0.0075	0.0351	0.34	0.0829	0.2230	0.11	0.3191	0.5218	0.08	0.3736	0.4788	-2.55	0.8708	0.9944	-0.33	0.0651	0.1315	2.06
4106 Serine/threonine-protein kinase Nek8	Q8SG66	0.1722	0.3331	-0.20	0.0128	0.4450	0.29	0.0625	0.1453	-0.22	0.9268	0.9360	0.01	0.0348	0.1353	0.22	0.2101	0.3909	-0.28	0.3736	0.5005	-2.55	0.8708	1.0343	-0.33	0.0651	0.1411	2.06
4107 Serine/threonine-protein kinase PAK 1	Q13153	0.1467	0.2949	-0.06	0.5737	0.8860	-0.05	0.0031	0.0297	0.38	0.6471	0.6911	-0.04	0.1182	0.2820	-0.16	0.8091	1.0460	-0.02	0.0036	0.0652	0.47	0.7317	1.1756	0.03	0.0093	0.0859	0.75
4108 Serine/threonine-protein kinase PAK 2	Q13177	0.2492	0.4357	0.05	0.4916	0.8141	0.11	0.6577	0.7090	0.02	0.9694	0.9737	0.00	0.0165	0.0914	-0.16	0.4435	0.6649	0.03	0.5378	0.5895	0.05	0.2897	0.6292	-0.08	0.0098	0.0872	-0.21
4109 Serine/threonine-protein kinase PAK 3	Q75914	0.0060	0.0466	0.13	0.3590	0.7087	0.13	0.0031	0.0299	-0.13	0.1285	0.2344	0.12	0.0124	0.0793	-0.11	0.2025	0.3803	-0.09	0.0016	0.0525	-0.61	0.0177	0.1131	-0.30	0.0090	0.0848	-0.61
4110 Serine/threonine-protein kinase PAK 4	Q96013	0.0012	0.0237	-0.29	0.2366	0.6632	-0.14	0.0996	0.2034	-0.17	0.0002	0.0086	-0.47	0.0034	0.0437	-0.23	0.0024	0.0560	-0.31	0.3736	0.6423	-2.55	0.8708	1.2862	-0.33	0.0651	0.2195	2.06
4111 Serine/threonine-protein kinase PAK 6	Q9NQUS	0.0019	0.0299	0.24	0.0412	0.5691	0.24	0.1217	0.2392	0.18	0.0233	0.0674	0.20	0.0050	0.0530	0.15	0.0178	0.0872	0.12	0.0674	0.2038	0.13	0.0165	0.1090	-0.30	0.0074	0.0781	-0.43
4112 Serine/threonine-protein kinase PLK1	P53350	0.2431	0.4285	0.09	0.0467	0.5626	0.24	0.0778	0.1688	0.17	0.0678	0.1443	0.18	0.0123	0.0791	0.33	0.2665	0.4594	0.08	0.3736	0.4873	-2.55	0.8708	1.0102	-0.33	0.0651	0.1352	2.06
4113 Serine/threonine-protein kinase PLK2	Q9NY93	0.6947	0.7491	0.03	0.0722	0.6062	-0.15	0.0560	0.1352	-0.17	0.1103	0.2091	-0.16	0.0427	0.1526	-0.19	0.1188	0.2632	-0.13	0.5997	0.6479	-0.03	0.1759	0.4606	0.09	0.2015	0.2697	-0.08
4114 Serine/threonine-protein kinase PLK3	Q9H4B4	0.0047	0.0431	-0.30	0.2557	0.6626	0.07	0.1507	0.2804	0.08	0.8650	0.8839	-0.01	0.9422	0.9557	0.00	0.8250	1.0591	0.01	0.1246	0.2972	-0.31	0.4494	0.8521	-0.12	0.3302	0.4013	-0.16
4115 Serine/threonine-protein kinase PRP4 homolog	Q13523	0.2080	0.3805	0.18	0.0144	0.4493	-0.47	0.0147	0.0573	-0.47	0.0062	0.0315	-0.67	0.3137	0.4113	-0.10	0.0855	0.2127	-0.57	0.0357	0.1562	1.82	0.0551	0.1052	1.87	0.0074	0.0782	2.80
4116 Serine/threonine-protein kinase RIO1	Q9BR52	0.0777	0.1907	-0.79	0.1812	0.6647	-1.22	0.5334	0.7543	-0.23	0.2723	0.4291	-0.36	0.5898	0.6668	0.16	0.3703	0.5781	-0.25	0.3736	0.4718	-2.55	0.8708	0.9814	-0.33	0.0651	0.1285	2.06
4117 Serine/threonine-protein kinase RIO2	Q9BV54	0.0887	0.2076	-0.31	0.7831	0.8437	-0.04	0.0883	0.1862	-0.34	0.1041	0.1996	-0.30	0.4101	0.5055	-0.12	0.0572	0.1643	-0.49	0.3736	0.5571	-2.55	0.8708	1.1368	-0.33	0.0651	0.1689	2.06
4118 Serine/threonine-protein kinase SIK3	Q9Y2K2	0.4108	0.5140	-3.31	0.5752	0.7197	-1.75	0.5661	0.6538	-1.19	0.5388	0.6186	0.89	0.2938	0.4145	-1.88	0.9510	1.0011	0.09	0.0268	0.1418	0.99	0.7102	1.1547	-0.13	0.0972	0.1523	0.59
4119 Serine/threonine-protein kinase SMG1	Q96015	0.0006	0.0190	0.44	0.0003	0.2590	0.23	0.0003	0.0235	0.25	0.0005	0.0136	0.23	0.0217	0.1060	0.17	0.0008	0.0436	0.27	0.0103	0.1022	0.39	0.1668	0.4456	0.11	0.0953	0.1499	-0.05
4120 Serine/threonine-protein kinase TA01	Q7L7X3	0.9081	0.9285	0.02	0.1252	0.6421	0.65	0.8154	0.8504	-0.05	0.0403	0.0990	0.18	0.1563	0.3375	0.15	0.0091	0.0687	-0.54	0.3736	0.6161	-2.55	0.8708	1.2409	-0.33	0.0651	0.2027	2.06
4121 Serine/threonine-protein kinase TBK1	Q9UHD2	0.4108	0.5139	-3.31	0.5752	0.7195	-1.75	0.5661	0.6537	-1.19	0.5388	0.6184	0.89	0.2938	0.4143	-1.88	0.9510	1.0008	0.09	0.0721	0.2127	0.35	0.0707	0.2572	0.14	0.2728	0.3447	0.04
4122 Serine/threonine-protein kinase tousel-like 1	Q9UKH8	0.4294	0.5068	-0.11	0.6756	0.7626	0.19	0.9661	0.9725	-0.01	0.0106	0.0411	0.70	0.2059	0.4077	0.21	0.5642	0.7989	-0.35	0.9002	0.9183	0.01	0.0149	0.1029	0.40	0.0810	0.1321	0.23
4123 Serine/threonine-protein kinase tousel-like 2	Q86UE8	0.0500	0.1440	-0.40	0.2413	0.6603	-0.46	0.2412	0.4051	-0.18	0.1027	0.1978	-0.29	0.1654	0.3510	-0.22	0.6313	0.8674	-0.06	0.0022	0.0556	-1.06	0.0013	0.0303	-0.76	0.0000	0.0000	-1.27
4124 Serine/threonine-protein kinase ULK3	Q6PHR2	0.0027	0.0349	1.44	0.2848	0.6648	0.67	0.0039	0.0316	2.17	0.0035	0.0239	1.45	0.5549	0.6383	-0.12	0.0026	0.0547	1.79	0.3736	0.6414	-2.55	0.8708	1.2847	-0.33	0.0651	0.2190	-0.26
4125 Serine/threonine-protein kinase WNK1	Q9H4A3	0.0226	0.0895	0.19	0.0332	0.5259	0.22	0.0123	0.0521	0.42	0.1235	0.2271	0.08	0.7681	0.8195	0.01	0.0063	0.0622	0.28	0.0113	0.1038	-0.40	0.0123	0.0925	-0.45	0.0015	0.0471	-0.59
4126 Serine/threonine-protein kinase WNK2	Q9Y3S1	0.9793	0.9863	-0.01	0.6137	0.7145	-0.25	0.3717	0.5696	0.22	0.2536	0.4035	0.30	0.2333	0.4441	0.32	0.3573	0.5632	0.23	0.5716	0.6215	-0.09	0.0383	0.1783	-0.19	0.1189	0.1771	0.16
4127 Serine/threonine-protein kinase WNK3	Q9BY77	0.2356	0.4187	0.07	0.2825	0.6646	-0.12	0.2248	0.3827	-0.08	0.0909	0.1803	-0.13	0.0329	0.1324	-0.19	0.0305	0.1120	0.25	0.3320	0.6011	0.18	0.3792	0.7555	0.13	0.8448	0.8749	-0.03
4128 Serine/threonine-protein kinase/endoribonuclease IRE2	Q76MU5	0.0149	0.0707	-0.12	0.0176	0.4675	-0.24	0.1694	0.3090	-0.12	0.0657	0.1413	-0.26	0.0017	0.0319	-0.33	0.0405	0.1323	-0.09	0.3736	0.5697	-2.55	0.8708	1.1593	-0.33	0.0651	0.1756	2.06
4129 Serine/threonine-protein phosphatase 1 regulatory subunit 10	Q96QC0	0.0150	0.0709	-0.11	0.3117	0.6798	-0.26	0.8306	0.8636	-0.02	0.0819	0.1668	-0.09	0.0012	0.0270	-0.19	0.0150	0.0816	0.30	0.2716	0.5148	-0.09	0.1265	0.3715	0.25	0.2299	0.3003	-0.12
4130 Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	P63151	0.0297	0.1054	0.14	0.5023	0.8239	0.06	0.0677	0.1533	0.16	0.0257	0.0719	0.16	0.0053	0.0541	0.28	td											

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
4150	Serine/threonine-protein phosphatase 5	P53041	0.0111	0.0603	-0.22	0.1728	0.6601	-0.23	0.1752	0.3172
4151	Serine/threonine-protein phosphatase 6 catalytic subunit	O00743	0.0074	0.0506	0.17	0.2324	0.6625	0.15	0.0285	0.0857
4152	Serine/threonine-protein phosphatase 6 regulatory subunit 2	O75170	0.1812	0.3450	-0.22	0.0789	0.6146	0.08	0.3839	0.5845
4153	Serine/threonine-protein phosphatase 6 regulatory subunit 3	Q5H9R7	0.0117	0.0624	0.10	0.1605	0.6640	0.13	0.0244	0.0772
4154	Serine/threonine-protein phosphatase PGAM5_mitochondrial	Q96HS1	0.0074	0.0505	0.18	0.4967	0.8189	0.09	0.0190	0.0660
4155	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	P62136	0.4923	0.5664	0.05	0.5484	0.8640	0.10	0.6889	0.7378
4156	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	P62140	0.0223	0.0889	-0.19	0.2790	0.6648	-0.15	0.0116	0.0503
4157	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	P36873	0.1634	0.3200	0.09	0.2611	0.6643	0.17	0.2193	0.3759
4158	Serine-protein kinase ATM	Q13315	0.4108	0.5135	-3.31	0.5752	0.7190	-1.75	0.5661	0.6532
4159	Serine-threonine kinase receptor-associated protein	Q9Y3F4	0.0021	0.0314	0.34	0.3595	0.7086	0.12	0.0031	0.0298
4160	Serine-IRNA ligase cytoplasmic	P40591	0.0016	0.0270	0.40	0.0849	0.6212	0.27	0.0008	0.0218
4161	Serine-IRNA ligase mitochondrial	Q9N181	0.1174	0.2520	-0.11	0.9028	0.9318	-0.02	0.2496	0.1615
4162	Serologically defined colon cancer antigen 8	Q86S07	0.0216	0.0875	0.51	0.0004	0.2302	0.28	0.5584	0.7824
4163	Serotransferrin	P02787	0.0078	0.0521	-0.24	0.4568	0.7887	-0.07	0.3019	0.4848
4164	Serin B4	P48594	0.4108	0.5134	-3.31	0.5752	0.7188	-1.75	0.5661	0.6531
4165	Serin B6	P35237	0.8918	0.9151	0.00	0.8353	0.8811	0.02	0.0242	0.0767
4166	Serin B7	O75635	0.4108	0.5133	-3.31	0.5752	0.7187	-1.75	0.5661	0.6529
4167	Serin B8	P50452	0.6086	0.6730	0.02	0.1740	0.6613	0.10	0.9865	0.9886
4168	Serin H1	P50454	0.0343	0.1161	0.09	0.2750	0.6650	0.18	0.0063	0.0383
4169	Serrate RNA effector molecule homolog	Q9BXPS	0.0194	0.0818	0.17	0.1762	0.6614	0.26	0.0138	0.0552
4170	Serum albumin	P02768	0.0992	0.2239	0.15	0.6912	0.7736	0.08	0.0147	0.0570
4171	S-formylglutathione hydrolase	P10768	0.0047	0.0430	0.15	0.0880	0.6210	0.21	0.0184	0.0650
4172	SH2 domain-containing protein 3C	Q8NSH7	0.4108	0.5131	-3.31	0.5752	0.7185	-1.75	0.5661	0.6528
4173	SH2 domain-containing protein 4A	Q9H788	0.0001	0.0094	-0.86	0.7929	0.8509	-0.02	0.0027	0.0284
4174	SH2 domain-containing protein 4B	Q5SQS7	0.7040	0.7566	-0.06	0.0301	0.5046	-0.83	0.0784	0.1699
4175	SH3 and cysteine-rich domain-containing protein	Q99469	0.7456	0.7931	0.03	0.8592	0.8982	-0.02	0.4862	0.7065
4176	SH3 and PX domain-containing protein 2B	A1X283	0.4108	0.5130	-3.31	0.5752	0.7183	-1.75	0.5661	0.6527
4177	SH3 domain-binding glutamic acid-rich-like protein	O75368	0.1600	0.3149	-0.06	0.7178	0.7930	0.04	0.3389	0.1044
4178	SH3 domain-binding glutamic acid-rich-like protein 3	Q9H289	0.0063	0.0476	0.08	0.0458	0.5609	0.34	0.0011	0.0227
4179	SH3 domain-binding kinase-binding protein 1	Q96B97	0.4108	0.5129	-3.31	0.5752	0.7181	-1.75	0.5661	0.6525
4180	SHC SH2 domain-binding protein 1	Q8NEM2	0.6290	0.6913	0.03	0.1441	0.6542	-0.20	0.1851	0.6726
4181	SHC-transforming protein 1	P29353	0.5771	0.6445	-0.40	0.1817	0.6647	-0.30	0.8746	0.9009
4182	Shoon-1	A0M266	0.4785	0.5534	0.03	0.1644	0.6617	0.24	0.0070	0.0399
4183	Short stature homeobox protein 2	O60902	0.4108	0.5128	-3.31	0.5752	0.7180	-1.75	0.5661	0.6524
4184	Short/branched chain specific acyl-CoA dehydrogenase_mitochondrial	P45954	0.4108	0.5126	-3.31	0.5752	0.7178	-1.75	0.5661	0.6522
4185	Short-wave-sensitive opsin 1	P03999	0.4108	0.5125	-3.31	0.5752	0.7176	-1.75	0.5661	0.6521
4186	Shuoshin 2	Q562F6	0.4108	0.5124	-3.31	0.5752	0.7174	-1.75	0.5661	0.6519
4187	Sialic acid synthase	Q9NR45	0.0229	0.0903	0.23	0.2068	0.6596	0.26	0.0008	0.0208
4188	Sialidase-1	Q99519	0.0021	0.0313	0.66	0.3298	0.6889	-0.10	0.3511	0.5452
4189	Sideroflexin-1	Q9H9B4	0.0627	0.1658	0.18	0.2340	0.6613	0.22	0.0533	0.1307
4190	Sideroflexin-2	Q96NB2	0.0038	0.0391	-0.18	0.2466	0.7625	-0.10	0.5388	0.7607
4191	Sideroflexin-3	Q9BWM7	0.0148	0.0707	-0.62	0.5070	0.8287	-0.33	0.0204	0.0687
4192	Signal peptidase complex catalytic subunit SEC11A	P67812	0.8961	0.9183	-0.01	0.2710	0.6644	-0.13	0.1036	0.2100
4193	Signal peptidase complex subunit 1	Q9Y6A9	0.0908	0.2108	0.11	0.4036	0.7477	0.15	0.0536	0.1312
4194	Signal peptidase complex subunit 2	P15005	0.0002	0.0120	0.22	0.1998	0.6639	0.06	0.0672	0.1525
4195	Signal peptidase complex subunit 3	P61009	0.0593	0.1608	-0.05	0.2950	0.6720	-0.11	0.0042	0.0321
4196	Signal peptidase complex-like 2A	Q8TCT8	0.0353	0.1172	-1.88	0.0975	0.6290	-7.47	0.3237	0.5115
4197	Signal recognition particle 14 kDa protein	P37108	0.0020	0.0307	0.22	0.0279	0.5053	0.19	0.0004	0.0233
4198	Signal recognition particle 19 kDa protein	P09132	0.2856	0.4813	-0.08	0.4275	0.7628	0.08	0.0168	0.0614
4199	Signal recognition particle 54 kDa protein	P61011	0.5724	0.6400	0.04	0.1824	0.6658	0.27	0.0645	0.1482
4200	Signal recognition particle 9 kDa protein	P49458	0.0102	0.0588	0.23	0.0830	0.6195	0.24	0.0006	0.0203
4201	Signal recognition particle receptor subunit alpha	P08240	0.0019	0.0298	-0.30	0.6113	0.7127	-0.10	0.2056	0.3394
4202	Signal recognition particle receptor subunit beta	Q9Y5M8	0.0369	0.1209	0.20	0.3031	0.6765	0.19	0.0371	0.1010
4203	Signal recognition particle subunit SRP68	Q9UHH9	0.6478	0.7091	0.02	0.2257	0.6602	0.19	0.0377	0.1021
4204	Signal recognition particle subunit SRP72	O76094	0.1972	0.3664	0.07	0.2691	0.6625	0.19	0.0334	0.0542
4205	Signal transducer and activator of transcription 1-alpha/beta	P42224	0.0005	0.0177	0.12	0.1701	0.6620	0.15	0.0008	0.0214
4206	Signal transducer and activator of transcription 3	P40763	0.0958	0.2185	0.10	0.0044	0.3506	0.29	0.0061	0.0381
4207	Signal transducing adapter molecule 1	Q92783	0.0430	0.1317	-0.53	0.5064	0.8283	-0.13	0.1380	0.2620
4208	Signal transducing adapter molecule 2	O75886	0.3123	0.5132	-0.31	0.0243	0.4804	-0.36	0.0971	0.1998
4209	Signal-induced proliferation-associated 1-like protein 2	Q9P287	0.5149	0.5874	-0.06	0.9163	0.9418	0.02	0.3155	0.5022
4210	Signal-induced proliferation-associated 1-like protein 3	O60292	0.4551	0.5323	-0.09	0.3461	0.7028	0.19	0.6672	0.7181
4211	Signaling lymphocytic activation molecule	Q13291	0.4108	0.5123	-3.31	0.5752	0.7173	-1.75	0.5661	0.6518
4212	Single-stranded DNA-binding protein 2	P81877	0.0040	0.0400	-1.31	0.8342	0.8806	-0.04	0.1540	0.2853
4213	Single-stranded DNA-binding protein mitochondrial	Q04837	0.0099	0.0579	0.26	0.1704	0.6612	0.25	0.0051	0.0349
4214	Sister chromatid cohesion protein PDS5 homolog A	Q29RF7	0.0660	0.1703	0.05	0.1328	0.6471	0.24	0.3549	0.5504
4215	Sjogrens syndrome/scleroderma autoantigen 1	O60232	0.0089	0.0559	0.29	0.2375	0.6614	-0.13	0.0762	0.0429
4216	SKI-like protein	P12757	0.0295	0.1051	0.09	0.8459	0.8892	0.03	0.0275	0.0834
4217	SLAN motif-containing protein 2	Q9P270	0.2655	0.4572	-0.12	0.2886	0.6616	0.14	0.2116	0.3662
4218	SLIT homolog 2 protein	O94813	0.4108	0.5121	-3.31	0.5752	0.7171	-1.75	0.5661	0.6516
4219	SLIT-ROBO Rho GTPase-activating protein 1	Q7Z6B7	0.4108	0.5120	-3.31	0.5752	0.7169	-1.75	0.5661	0.6515
4220	SLIT-ROBO Rho GTPase-activating protein 2	O75044	0.4108	0.5119	-3.31	0.5752	0.7168	-1.75	0.5661	0.6514
4221	Small acid protein	O00193	0.0392	0.1246	-0.06	0.0014	0.2014	-0.10	0.0015	0.0235
4222	Small EDRK-rich factor 2	P84101	0.1121	0.2435	-0.22	0.1743	0.6605	-0.62	0.1337	0.2560



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
4223	Small G-protein signaling modulator 3	Q96HU1	0.2999	0.4989	-0.06	0.7359	0.8080	0.03	0.0663	0.1510
4224	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	O43765	0.4108	0.5118	-3.31	0.5752	0.7166	-1.75	0.5661	0.6512
4225	Small glutamine-rich tetratricopeptide repeat-containing protein beta	Q96EQ0	0.4108	0.5116	-3.31	0.5752	0.7164	-1.75	0.5661	0.6511
4226	Small nuclear ribonucleoprotein F	P62306	0.8881	0.8887	-0.05	0.1992	0.6640	-0.41	0.2745	0.4484
4227	Small nuclear ribonucleoprotein Sm D1	P62314	0.8896	0.8880	0.01	0.1430	0.6544	-0.12	0.0237	0.0756
4228	Small nuclear ribonucleoprotein Sm D2	P62316	0.4616	0.5384	-0.03	0.4727	0.8015	-0.13	0.0044	0.0327
4229	Small nuclear ribonucleoprotein Sm D3	P62318	0.0449	0.1351	0.08	0.8214	0.8724	-0.02	0.0018	0.0235
4230	Small nuclear ribonucleoprotein-associated proteins B and B'	P14678	0.4108	0.5115	-3.31	0.5752	0.7162	-1.75	0.5661	0.6509
4231	Small proline-rich protein 2A	P35322	0.4108	0.5114	-3.31	0.5752	0.7161	-1.75	0.5661	0.6508
4232	Small subunit processome component 20 homolog	O75691	0.0430	0.1316	0.12	0.0110	0.4317	0.25	0.0111	0.0489
4233	Small ubiquitin-related modifier 1	P63165	0.4108	0.5113	-3.31	0.5752	0.7159	-1.75	0.5661	0.6506
4234	Small ubiquitin-related modifier 2	P61956	0.0140	0.0691	0.25	0.1985	0.6655	0.34	0.0061	0.0379
4235	Small ubiquitin-related modifier 3	P55854	0.4108	0.5112	-3.31	0.5752	0.7157	-1.75	0.5661	0.6505
4236	S-methyl-5'-thioadenosine phosphorylase	Q13126	0.4108	0.5110	-3.31	0.5752	0.7155	-1.75	0.5661	0.6503
4237	snRNA-activating protein complex subunit 3	O29266	0.4108	0.5109	-3.31	0.5752	0.7154	-1.75	0.5661	0.6502
4238	Snurportin-1	O95149	0.0100	0.0582	11.31	0.5752	0.8860	-1.75	0.5661	0.7898
4239	SNW domain-containing protein 1	Q13573	0.2058	0.3784	-0.04	0.1105	0.6325	0.07	0.7367	0.7798
4240	Sodium channel protein type 5 subunit alpha	Q14524	0.4108	0.5108	-3.31	0.5752	0.7152	-1.75	0.5661	0.6501
4241	Sodium/potassium-transporting ATPase subunit alpha-1	P05023	0.0447	0.1346	0.17	0.3459	0.7029	0.18	0.0136	0.0456
4242	Sodium/potassium-transporting ATPase subunit alpha-2	P50993	0.0015	0.0259	0.28	0.0881	0.6209	0.32	0.0035	0.0315
4243	Sodium/potassium-transporting ATPase subunit alpha-3	P13637	0.0049	0.0430	0.30	0.4709	0.8003	-0.13	0.3915	0.5933
4244	Sodium/potassium-transporting ATPase subunit alpha-4	Q13733	0.0934	0.2149	0.14	0.2434	0.6587	0.10	0.3345	0.5396
4245	Sodium/potassium-transporting ATPase subunit beta-1	P05026	0.4090	0.6302	-0.05	0.2276	0.6578	0.17	0.2230	0.3802
4246	Sodium/potassium-transporting ATPase subunit beta-3	P54709	0.2976	0.4965	0.04	0.8798	0.9137	0.02	0.5006	0.7231
4247	Sodium-coupled neutral amino acid transporter 2	Q96QD8	0.1787	0.3416	-0.13	0.2076	0.6639	-0.16	0.6148	0.6692
4248	Soluble calcium-activated nucleoside 1	Q8WVQ1	0.2499	0.4360	0.15	0.1904	0.6691	0.16	0.0295	0.0872
4249	Solute carrier family 12 member 1	Q13621	0.4108	0.5107	-3.31	0.5752	0.7150	-1.75	0.5661	0.6499
4250	Solute carrier family 12 member 7	Q9Y666	0.4108	0.5105	-3.31	0.5752	0.7149	-1.75	0.5661	0.6498
4251	Solute carrier family 12 member 8	AOAV02	0.4108	0.5104	-3.31	0.5752	0.7147	-1.75	0.5661	0.6496
4252	Solute carrier family 2, facilitated glucose transporter member 1	P11166	0.0017	0.0280	0.33	0.4560	0.7881	0.08	0.0007	0.0201
4253	Solute carrier family 2, facilitated glucose transporter member 3	P11169	0.0370	0.1210	-0.33	0.4939	0.8169	-0.08	0.9496	0.9602
4254	Solute carrier family 27 member 3	Q5K4L6	0.0023	0.0327	-0.30	0.1335	0.6481	-0.15	0.0093	0.0451
4255	Sorbin and SH3 domain-containing protein 2	O94875	0.0878	0.2063	0.09	0.0425	0.5674	0.12	0.0818	0.1757
4256	Sorbitol dehydrogenase	Q00796	0.0570	0.1566	0.07	0.2483	0.6582	0.11	0.0013	0.0226
4257	Sorcin	P30626	0.0161	0.0740	0.36	0.4865	0.8108	0.07	0.3757	0.5749
4258	Soritin	O99523	0.3170	0.5198	0.05	0.1033	0.4416	0.23	0.0525	0.1296
4259	Sorting and assembly machinery component 50 homolog	Q9Y512	0.4108	0.5103	-3.31	0.5752	0.7145	-1.75	0.5661	0.6495
4260	Sorting nexin-1	Q13596	0.4214	0.4989	0.05	0.2143	0.6615	0.22	0.0076	0.0414
4261	Sorting nexin-12	Q9UMY4	0.2319	0.4138	-0.11	0.1273	0.6415	-0.26	0.2570	0.4255
4262	Sorting nexin-13	Q9YSW8	0.0450	0.1352	0.21	0.1567	0.6621	0.27	0.0196	0.0674
4263	Sorting nexin-2	O60749	0.0187	0.0803	0.14	0.1721	0.6618	0.34	0.0098	0.0461
4264	Sorting nexin-27	Q96L92	0.0219	0.0880	0.18	0.3928	0.7372	0.17	0.0352	0.0977
4265	Sorting nexin-3	O60493	0.7096	0.7615	-0.01	0.0895	0.6248	-0.08	0.3015	0.4843
4266	Sorting nexin-32	Q86XE0	0.4108	0.5102	-3.31	0.5752	0.7143	-1.75	0.5661	0.6493
4267	Sorting nexin-4	O95219	0.2897	0.4864	-0.09	0.2613	0.6641	0.18	0.0529	0.1302
4268	Sorting nexin-5	Q9Y5X3	0.0025	0.0333	0.45	0.3578	0.7079	0.03	0.0446	0.1155
4269	Sorting nexin-6	Q9UNH7	0.1020	0.2281	0.07	0.4080	0.7494	0.13	0.0333	0.0943
4270	Sorting nexin-7	Q9UNH6	0.0096	0.0373	0.23	0.1886	0.6691	0.25	0.0540	0.1319
4271	Sorting nexin-8	Q9YSX2	0.5391	0.6096	-0.05	0.0441	0.5683	0.21	0.1116	0.2231
4272	Sorting nexin-9	Q9YSX1	0.4108	0.5101	-3.31	0.5752	0.7142	-1.75	0.5661	0.6492
4273	SPATS2-like protein	Q9NUQ6	0.4126	0.4905	0.03	0.0342	0.5288	0.34	0.0693	0.1561
4274	Speckle-type P	Q6Q16	0.0012	0.0236	0.52	0.2504	0.6604	0.24	0.0054	0.0357
4275	Spectrin alpha chain erythrocytic 1	P02549	0.1388	0.2832	-0.09	0.3036	0.6764	0.07	0.0068	0.0397
4276	Spectrin alpha chain non-erythrocytic 1	Q13813	0.0021	0.0313	0.26	0.1675	0.6613	0.24	0.0025	0.0276
4277	Spectrin beta chain non-erythrocytic 1	Q01082	0.0366	0.1203	0.10	0.1301	0.6455	0.11	0.0028	0.0292
4278	Spectrin beta chain non-erythrocytic 2	O15020	0.0050	0.0432	0.37	0.3807	0.7274	0.19	0.0193	0.0667
4279	Spectrin beta chain non-erythrocytic 4	Q9H254	0.0162	0.0741	-0.14	0.3560	0.7076	-0.08	0.0425	0.1119
4280	Spectrin beta chain non-erythrocytic 5	Q9NR65	0.3713	0.5858	0.05	0.0771	0.6107	0.39	0.0078	0.0418
4281	Speedy protein E1	Q8NFV5	0.1317	0.2735	-2.04	0.6906	0.7735	0.09	0.2170	0.3727
4282	Speedy protein E5	A6N1Y4	0.0347	0.1165	-1.80	0.3158	0.6808	-1.17	0.1013	0.0492
4283	Sperm flagellar protein 2	Q8C093	0.4108	0.5099	-3.31	0.5752	0.7140	-1.75	0.5661	0.6490
4284	Sperm-associated antigen 5	Q96R06	0.0991	0.2238	-0.30	0.0568	0.5861	-0.46	0.0674	0.1529
4285	Spermatid-perinuclear RNA-binding protein	Q96B39	0.0054	0.0443	0.17	0.7556	0.8224	0.02	0.0464	0.1192
4286	Spermatid-specific manchette-related protein 1	Q8NCRC	0.4108	0.5098	-3.31	0.5752	0.7138	-1.75	0.5661	0.6489
4287	Spermatogenesis-associated protein 13	Q96N96	0.0432	0.1319	-0.27	0.4759	0.8027	-0.82	0.1193	0.2356
4288	Spermatogenesis-associated protein 17	Q96L03	0.0053	0.0443	0.22	0.5340	0.8501	-0.31	0.0000	0.0000
4289	Spermatogenesis-associated protein 5-like protein 1	Q9BVD7	0.0030	0.0361	-0.82	0.1803	0.6652	-0.48	0.0117	0.0507
4290	Spermatogenesis-associated protein 8	Q6RV06	0.4108	0.5097	-3.31	0.5752	0.7137	-1.75	0.5661	0.6488
4291	Spermatogenesis-associated serine-rich protein 2	Q86XZ4	0.5463	0.6157	0.04	0.1250	0.6424	0.45	0.0063	0.0385
4292	Spermatogenesis-defective protein 39 homolog	Q9H9C1	0.0542	0.1522	-0.40	0.2050	0.4814	-0.35	0.0464	0.7064
4293	Spermatogenesis leucine zipper protein 1	Q9BXG8	0.4108	0.5096	-3.31	0.5752	0.7135	-1.75	0.5661	0.6486
4294	Spermidine synthase	P19623	0.5466	0.6159	0.04	0.8236	0.8737	0.02	0.0266	0.0816
4295	Spermine synthase	P52788	0.1812	0.3448	0.23	0.8662	0.9033	0.07	0.1230	0.2413
4296	S-phase kinase-associated protein 1	P63208	0.1972	0.3663	0.08	0.1466	0.6595	0.11	0.0601	0.1418
4297	Sphingomyelin phosphodiesterase	P17405	0.2924	0.4902	0.09	0.1615	0.6629	-0.07	0.4552	0.6701
4298	Sphingomyelin phosphodiesterase 3	Q9NY59	0.0103	0.0588	0.30	0.1481	0.6579	0.26	0.2533	0.4209
4299	Sphingomyelin phosphodiesterase 4	Q9NXE4	0.4108	0.5094	-3.31	0.5752	0.7133	-1.75	0.5661	0.6485

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
4300 Spliceosome-1-phosphate lyase 1	O95470	0.7446	0.7922	0.02	0.3234	0.6854	0.24	0.0347	0.0970	0.20	0.0309	0.0819	0.19	0.3347	0.4315	0.06	0.0522	0.1543	0.16	0.6397	0.6849	0.05	0.2274	0.5398	0.13	0.2937	0.3653	0.11
4301 Spindle assembly abnormal protein 6 homolog	Q6UJ00	0.4108	0.5093	-3.31	0.5752	0.7131	-1.75	0.5661	0.6483	-1.19	0.5388	0.6134	0.89	0.2938	0.4102	-1.88	0.9510	0.9934	0.09	0.0842	0.2316	0.49	0.2092	0.5112	0.26	0.8506	0.8791	0.06
4302 Spindlin-2A	Q99865	0.0980	0.2219	-0.93	0.4415	0.7774	-0.49	0.2955	0.4761	-0.23	0.0422	0.1023	-0.56	0.0322	0.1310	-0.24	0.0672	0.1820	-1.15	0.3736	0.5506	-2.55	0.8708	1.1252	-0.33	0.0651	0.1655	2.06
4303 Spliceosome RNA helicase DDX39B	Q13838	0.0036	0.0382	0.35	0.1130	0.6349	0.38	0.0169	0.0616	0.51	0.0007	0.0135	0.40	0.0150	0.0875	0.24	0.0007	0.0417	0.54	0.0376	0.1513	0.24	0.5553	0.9811	0.04	0.6977	0.7498	0.02
4304 Spliceosome-associated protein CWC27 homolog	Q1U304	0.0419	0.1397	-0.17	0.0161	0.4582	-0.36	0.0415	0.1096	0.20	0.0212	0.0629	-0.28	0.4068	0.5027	-0.05	0.0448	0.1398	0.32	0.2689	0.5115	0.84	0.3734	0.7468	0.65	0.2318	0.3020	0.95
4305 Splicing factor 1	Q15637	0.0089	0.0559	0.22	0.2276	0.6609	0.24	0.0081	0.0423	0.33	0.0068	0.0334	0.33	0.5968	0.6732	-0.02	0.0265	0.1042	0.20	0.0406	0.1657	0.04	0.6636	1.1017	0.04	0.4200	0.4914	0.06
4306 Splicing factor 3A subunit 1	Q15459	0.0202	0.0838	0.21	0.0674	0.6717	0.26	0.0086	0.0205	0.52	0.0674	0.1436	0.22	0.7876	0.8331	-0.01	0.0106	0.0701	0.29	0.1716	0.3688	0.15	0.1768	0.4616	0.12	0.0708	0.6340	0.04
4307 Splicing factor 3A subunit 2	Q15428	0.4108	0.5092	-3.31	0.5752	0.7130	-1.75	0.5661	0.6482	-1.19	0.5388	0.6133	0.89	0.2938	0.4101	-1.88	0.9510	0.9932	0.09	0.0610	0.1949	0.28	0.4870	0.8974	0.03	0.0889	0.1418	0.28
4308 Splicing factor 3A subunit 3	Q12874	0.0090	0.0563	0.32	0.1249	0.6425	0.29	0.0145	0.0567	0.25	0.0110	0.0421	0.29	0.3150	0.4123	0.06	0.0653	0.1782	0.28	0.1822	0.3833	0.14	0.0863	0.2910	-0.20	0.0074	0.0779	-0.33
4309 Splicing factor 3B subunit 1	O75533	0.0256	0.0967	-0.09	0.8241	0.8737	0.02	0.0210	0.0701	0.13	0.6414	0.6863	0.02	0.0018	0.0328	-0.26	0.3345	0.5378	-0.03	0.2815	0.5306	0.12	0.1061	0.3301	-0.19	0.3268	0.3979	-0.10
4310 Splicing factor 3B subunit 2	Q13435	0.1406	0.2861	0.06	0.845	0.7304	0.17	0.0279	0.0843	0.18	0.0153	0.0510	0.18	0.1452	0.3198	-0.15	0.3477	0.5528	0.06	0.0118	0.1036	0.29	0.4365	0.8371	0.06	0.0128	0.0984	0.30
4311 Splicing factor 3B subunit 3	Q15393	0.2111	0.3841	0.07	0.3069	0.6776	0.16	0.0097	0.0459	0.21	0.0109	0.0419	0.20	0.1702	0.3580	-0.07	0.0954	0.2277	0.10	0.0118	0.1040	0.40	0.0412	0.1867	0.18	0.0303	0.1475	0.21
4312 Splicing factor 3B subunit 4	Q15427	0.0587	0.1600	-0.12	0.6382	0.7335	-0.06	0.0044	0.0327	-0.18	0.0589	0.1299	-0.08	0.0115	0.0769	-0.13	0.0270	0.1052	-0.19	0.0077	0.0900	0.59	0.8708	1.3101	-0.33	0.0021	0.0506	7.39
4313 Splicing factor 3B subunit 5	Q9BWJ5	0.0094	0.0572	0.27	0.2326	0.6624	0.19	0.0310	0.0900	0.22	0.0107	0.0414	0.27	0.1577	0.3395	0.09	0.2700	0.4633	0.07	0.0437	0.1683	-0.23	0.0122	0.0923	-0.31	0.0130	0.0990	-0.44
4314 Splicing factor 3B subunit 6	Q9Y3B4	0.0396	0.1255	0.14	0.4951	0.8173	-0.03	0.0567	0.1361	0.08	0.8626	0.8818	-0.02	0.0001	0.0076	0.20	0.8439	1.0791	-0.02	0.0790	0.2231	-0.22	0.0209	0.1250	-0.29	0.0515	0.1989	-0.17
4315 Splicing factor 45	Q96125	0.0085	0.0546	-0.33	0.8102	0.8635	0.03	0.0291	0.0865	-0.37	0.0131	0.0464	-0.33	0.1500	0.3273	-0.10	0.3366	0.5405	-0.28	0.3736	0.4756	-2.55	0.8708	0.9885	-0.33	0.0651	0.1301	2.06
4316 Splicing factor U2AF 26 kDa subunit	Q8WU68	0.1431	0.2898	0.12	0.6939	0.7745	0.04	0.2938	0.4743	-0.06	0.5888	0.6375	0.03	0.5856	0.6632	-0.03	0.5770	0.8115	-0.03	0.0010	0.0421	0.43	0.0058	0.0613	0.17	0.0080	0.0800	0.29
4317 Splicing factor U2AF 35 kDa subunit-like protein	P0DN76	0.7896	0.8296	0.02	0.8126	0.8656	0.02	0.0174	0.0628	0.23	0.2912	0.4533	0.07	0.2997	0.3979	-0.06	0.3317	0.5351	0.05	0.1464	0.3304	0.20	0.1442	0.4057	-0.14	0.0686	0.1160	-0.22
4318 Splicing factor U2AF 65 kDa subunit	P26368	0.0155	0.0721	0.24	0.2233	0.6583	-0.08	0.7731	0.8133	0.02	0.2360	0.3808	0.12	0.2008	0.4014	-0.09	0.4062	0.6223	0.05	0.0099	0.0409	-0.83	0.0001	0.0148	-1.01	0.0004	0.0292	-1.54
4319 Splicing factor proline- and glutamine-rich	P23246	0.4239	0.5012	0.03	0.4521	0.7853	0.12	0.0036	0.0313	0.27	0.0144	0.0489	0.17	0.0535	0.1716	-0.11	0.0962	0.2289	0.09	0.0115	0.1040	0.61	0.1187	0.3558	0.20	0.0367	0.1643	0.34
4320 SPOC domain-containing protein 1	Q6ZMY3	0.0086	0.0547	0.26	0.4231	0.7599	0.09	0.0826	0.1770	0.11	0.4425	0.6469	0.04	0.2550	0.4746	-0.06	0.5521	0.7861	-0.03	0.3736	0.4567	-2.55	0.8708	0.9534	-0.33	0.0651	0.1222	2.06
4321 Spindin-2	Q9B1D6	0.0093	0.0570	0.22	0.1402	0.6543	0.27	0.0256	0.0795	0.30	0.0113	0.0428	0.22	0.3546	0.4522	0.05	0.1820	0.3519	0.08	0.3736	0.5065	-2.55	0.8708	1.0454	-0.33	0.0651	0.1439	2.06
4322 Sproy-related EVH1 domain-containing protein 1	Q7Z699	0.0434	0.1322	-0.18	0.2131	0.6626	-0.10	0.1890	0.3353	-0.09	0.4081	0.5994	-0.06	0.0325	0.1314	0.21	0.8114	1.0481	-0.02	0.3736	0.4379	-2.55	0.8708	0.9180	-0.33	0.0651	0.1147	2.06
4323 Sproy-related EVH1 domain-containing protein 2	Q7Z698	0.7988	0.8371	0.03	0.1554	0.6620	0.15	0.9023	0.9228	0.02	0.1840	0.3110	0.11	0.1700	0.3578	0.12	0.8007	1.0372	-0.04	0.3736	0.4384	-2.55	0.8708	0.9191	-0.33	0.0651	0.1149	2.06
4324 SPRY domain-containing protein 3	Q8NCJ5	0.1124	0.2440	0.07	0.9964	0.9977	0.00	0.2218	0.3789	0.13	0.1803	0.3051	0.07	0.0174	0.0947	-0.15	0.0437	0.1378	0.16	0.3736	0.5660	-2.55	0.8708	1.1528	-0.33	0.0651	0.1736	2.06
4325 SPRY domain-containing SOCS box protein 1	Q96BD6	0.0046	0.0427	-0.22	0.0098	0.4453	-0.21	0.0001	0.0305	-0.49	0.0001	0.0157	-0.65	0.0000	0.0000	-0.72	0.0112	0.0728	-0.30	0.0599	0.1939	-0.32	0.0229	0.1328	0.39	0.2127	0.2814	-0.15
4326 Squalene monooxygenase	Q14534	0.3805	0.5965	-0.05	0.5889	0.6944	-0.04	0.0138	0.0550	-0.19	0.1398	0.2509	-0.08	0.0076	0.0633	-0.22	0.1852	0.3566	0.11	0.3736	0.5054	-2.55	0.8708	1.0434	-0.33	0.0651	0.1434	2.06
4327 Squalene synthase	P73268	0.0832	0.1987	-0.29	0.0441	0.5697	-0.42	0.5555	0.7798	-0.10	0.0061	0.0312	-0.69	0.0811	0.2198	-0.28	0.1925	0.3665	0.18	0.3736	0.5041	-2.55	0.8708	1.0410	-0.33	0.0651	0.1428	2.06
4328 Squalene cell carcinoma antigen recognized by T-cells 3	Q15020	0.0334	0.1141	0.14	0.1386	0.6509	0.24	0.0006	0.0198	0.40	0.0014	0.0173	0.34	0.9431	0.9558	0.00	0.0370	0.1243	0.27	0.0744	0.2166	0.25	0.3642	0.7355	0.03	0.0207	0.1231	0.12
4329 SRA stem-loop-interacting RNA-binding protein_mitochondrial	Q9GZT3	0.2189	0.3950	0.12	0.4391	0.7758	0.11	0.0669	0.1431	0.23	0.0766	0.1585	0.21	0.7763	0.8245	-0.02	0.1016	0.3913	0.13	0.2486	0.4847	0.11	0.5441	0.9699	-0.05	0.1566	0.2203	-0.14
4330 Src substrate cortactin	Q14247	0.0838	0.1998	0.15	0.1217	0.6381	0.29	0.0053	0.0356	0.38	0.0055	0.0298	0.37	0.1017	0.2557	0.15	0.0316	0.1144	0.28	0.0567	0.1894	0.45	0.7928	1.2358	0.03	0.1805	0.2474	0.12
4331 SRSF protein kinase 1	Q96SB4	0.4108	0.5091	-3.31	0.5752	0.7128	-1.75	0.5661	0.6480	-1.19	0.5388	0.6131	0.89	0.2938	0.4100	-1.88	0.9510	0.9930	0.09	0.0378	0.1610	0.40	0.1532	0.4232	0.11	0.1436	0.2052	0.09
4332 SRFB protein kinase 2	P7362	0.0097	0.0578	-0.91	0.1659	0.6600	-0.81	0.0132	0.0537	-0.62	0.0105	0.0411	-0.88	0.9295	0.9467	-0.01	0.0266	0.1041	-0.62	0.3736	0.5840	-2.55	0.8708	1.1845	-0.33	0.0651	0.1836	2.06
4333 STAM-binding protein	Q95630	0.9117	0.9318	-0.02	0.0881	0.6192	-1.03	0.0025	0.0278	-1.03	0.0071	0.0342	-1.10	0.0150	0.0873	-1.21	0.2034	0.3815	-0.61	0.2259	0.4564	0.17	0.6972	1.1404	-0.03	0.1239	0.1832	0.19
4334 Staphylococcal nuclease domain-containing protein 1	Q7KZP4	0.0024	0.0330	0.33	0.1343	0.6496	0.29	0.0034	0.0314	0.45	0.0005	0.0126	0.51	0.0175	0.0951	0.25	0.0201	0.0563	0.46	0.2259	0.4505	0.40	0.9964	0.9976	0.00	0.9486	0.9955	0.00
4335 Starch-binding domain-containing protein 1	O95210	0.2632	0.4539	-0.19	0.0070	0.4120	0.94	0.1841	0.3288	0.20	0.0249	0.0704	0.49	0.0231	0.1102	0.53	0.2719	0.4661	0.15	0.3736	0.4867	-2.55	0.8708	1.0091	-0.33	0.0651	0.1349	2.06
4336 StAR-related lipid transfer protein 9	Q9P2P6	0.0048	0.0429	-0.11	0.1326	0.6486	-0.15	0.2076	0.3610	0.03	0.0008	0.0141	-0.19	0.0059	0.0566	-0.12	0.0019	0.0526	0.37	0.0081	0.0918	0.69	0.0005	0.0225	0.81	0.0079	0.0799	0.32
4337 START domain-containing protein 10	Q9Y365	0.1939	0.3616	0.07	0.3059	0.6786	0.17	0.0095	0.0454	0.23	0.2137	0.3506	0.07	0.4489	0.5424	-0.04	0.0903	0.2190	0.11	0.3736	0.5376	-2.55	0.8708	1.1018	-0.33	0.0651	0.1588	2.06
4338 Stathmin	P16949	0.0188	0.0806	0.																								

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
		p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
4372 Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	P55809	0.4108	0.5083	-3.31	0.5752	0.7118	-1.75	0.5661	0.6472
4373 Sulfhydryl oxidase 2	O6ZRP7	0.6603	0.7207	0.07	0.4217	0.7593	-0.18	0.0073	0.0403
4374 Sulfide:quinone oxidoreductase, mitochondrial	Q9Y6N5	0.0142	0.0692	-0.55	0.1407	0.6531	-0.75	0.0039	0.0319
4375 Sulfotransferase 1A1	P40225	0.0003	0.0143	0.36	0.2277	0.6604	0.12	0.0006	0.0191
4376 Sulfotransferase 1A2	P50226	0.9315	0.9478	0.02	0.1645	0.6616	0.44	0.2463	0.4120
4377 Sulfotransferase 1A3	P02MM9	0.8152	0.8514	-0.03	0.8147	0.8673	0.03	0.0619	0.1446
4378 Sulfotransferase 1C2	O00338	0.4108	0.5082	-3.31	0.5752	0.7116	-1.75	0.5661	0.6470
4379 Sulfotransferase family cytosolic 2B member 1	O00204	0.0107	0.0597	3.95	0.2593	0.6636	0.76	0.0326	0.0928
4380 SUMO-activating enzyme subunit 1	Q9UBE0	0.0021	0.0312	0.32	0.9782	0.9856	0.00	0.0314	0.0905
4381 SUMO-activating enzyme subunit 2	Q9UBT2	0.3473	0.5563	0.06	0.4041	0.7473	0.09	0.8380	0.8694
4382 SUMO-conjugating enzyme UBC9	P63279	0.1073	0.2358	0.07	0.4213	0.7596	0.14	0.4006	0.6036
4383 SUMO-specific isopeptidase USPL1	Q5W0Q7	0.4108	0.5081	-3.31	0.5752	0.7114	-1.75	0.5661	0.6469
4384 Superoxide dismutase [Cu-Zn]	P00441	0.0431	0.1317	0.25	0.3676	0.7164	0.07	0.5586	0.7825
4385 Superoxide dismutase [Mn], mitochondrial	P04179	0.4108	0.5080	-3.31	0.5752	0.7113	-1.75	0.5661	0.6468
4386 Suppression of tumorigenicity 5 protein	P78524	0.1067	0.2352	0.05	0.3091	0.6790	0.12	0.0013	0.0222
4387 Suppressor of IKBKE 1	Q9BRV8	0.1152	0.2486	-0.14	0.7275	0.8011	0.04	0.0891	0.1873
4388 Surfeit locus protein 2	Q15527	0.9854	0.9890	0.00	0.6881	0.7477	-0.03	0.7024	0.7493
4389 Surfeit locus protein 4	I15260	0.6181	0.6818	0.07	0.6516	0.7506	-0.14	0.0624	0.1452
4390 Surfeit locus protein 6	Q75683	0.0790	0.1928	-0.30	0.4197	0.7578	0.27	0.6216	0.6759
4391 SURP and G-patch domain-containing protein 1	Q8WJZ8	0.1008	0.2263	0.19	0.5739	0.8861	0.11	0.0312	0.0902
4392 Survival motor neuron protein	O16637	0.1337	0.2769	0.16	0.2045	0.6600	0.34	0.0322	0.0751
4393 Survival of motor neuron-related-apoptosis factor 30	O75940	0.0627	0.1656	-0.15	0.0081	0.4114	-0.44	0.0603	0.1420
4394 Sushi repeat-containing protein SRPX2	O60687	0.2789	0.4276	0.13	0.6846	0.7699	-0.10	0.2851	0.4627
4395 SUZ domain-containing protein 1	Q7Z422	0.4971	0.5712	0.06	0.1861	0.6667	0.22	0.1540	0.2854
4396 SWI/SNF complex subunit SMARCC1	Q92922	0.4108	0.5079	-3.31	0.5752	0.7111	-1.75	0.5661	0.6466
4397 SWI/SNF complex subunit SMARCC2	O8TAQ2	0.4108	0.5077	-3.31	0.5752	0.7109	-1.75	0.5661	0.6465
4398 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1	Q9H4L7	0.1375	0.2821	-0.05	0.0422	0.5693	0.12	0.5254	0.7467
4399 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	O60264	0.1182	0.2531	0.06	0.4947	0.8171	0.09	0.0016	0.0229
4400 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1	Q9NZC9	0.0654	0.1692	0.13	0.9423	0.9618	0.01	0.8867	0.9102
4401 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	Q96GM5	0.4646	0.5409	0.05	0.1523	0.6602	0.13	0.3472	0.5412
4402 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3	Q6STE5	0.4074	0.6279	-0.23	0.3059	0.6783	-0.26	0.2729	0.4465
4403 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	Q969G3	0.4108	0.5076	-3.31	0.5752	0.7108	-1.75	0.5661	0.6463
4404 Synapse differentiation-inducing gene protein 1	Q9H7V2	0.0009	0.0211	-0.22	0.1453	0.6568	0.20	0.1353	0.2582
4405 Synapse-associated protein 1	Q96A49	0.4884	0.5626	-0.04	0.0789	0.6127	0.20	0.0229	0.0746
4406 Synapsin-3	I14994	0.2201	0.3963	0.41	0.6227	0.7202	-0.41	0.2238	0.3813
4407 Synaptic functional regulator FMR1	Q06787	0.0037	0.0386	0.22	0.7070	0.6352	0.20	0.0348	0.0970
4408 Synaptic vesicle 2-related protein	Q8N4V2	0.0007	0.0197	1.06	0.8488	0.8915	-0.23	0.0009	0.0202
4409 Synaptic vesicle membrane protein VAT-1 homolog	Q9Y936	0.0094	0.0571	0.24	0.3053	0.6760	0.13	0.2290	0.3884
4410 Synaptic vesicle membrane protein VAT-1 homolog-like	Q9HCJ6	0.4108	0.5075	-3.31	0.5752	0.7106	-1.75	0.5661	0.6462
4411 Synaptobrevin homolog YKT6	I15498	0.0050	0.0432	0.28	0.0999	0.6287	0.36	0.0046	0.0337
4412 Synaptogyrin-1	Q43739	0.4108	0.5074	-3.31	0.5752	0.7104	-1.75	0.5661	0.6460
4413 Synaptogyrin-2	Q43760	0.3651	0.5784	0.04	0.3131	0.6803	0.09	0.0986	0.2019
4414 Synaptotagmin-2-binding protein	P57105	0.0017	0.0279	-0.25	0.9740	0.9825	0.00	0.0442	0.1148
4415 Synaptotagmin complex central element protein 1	Q8N0S2	0.0236	0.0922	-0.19	0.0896	0.6247	0.08	0.2732	0.4469
4416 Synaptotagmin complex central element protein 2	Q6PIF2	0.0575	0.1576	0.14	0.8464	0.8895	-0.03	0.8328	0.8654
4417 Synaptotagmin complex central element protein 3	A1L190	0.0832	0.1986	0.20	0.2257	0.6605	0.17	0.0263	0.0810
4418 Synaptotagmin complex protein 2-like	Q5T4T6	0.4108	0.5073	-3.31	0.5752	0.7103	-1.75	0.5661	0.6459
4419 Synaptophysin-like protein 1	Q16563	0.4679	0.5440	0.04	0.3139	0.6809	0.21	0.1449	0.2717
4420 Synaptosomal-associated protein 23	O00161	0.0047	0.0429	-0.15	0.4982	0.8208	-0.06	0.1331	0.2553
4421 Synaptosomal-associated protein 29	O95721	0.0000	0.0000	0.17	0.0151	0.4574	0.19	0.0003	0.0229
4422 Synaptotagmin-16	Q178D7	0.8510	0.8815	0.07	0.0413	0.5675	-0.78	0.2362	0.3975
4423 Synaptotagmin-like protein 2	Q9CHH5	0.0001	0.0093	-1.60	0.0144	0.4521	-0.38	0.0000	0.0000
4424 Synaptotagmin-like protein 4	Q96C24	0.0955	0.2180	0.16	0.5419	0.8571	0.09	0.5411	0.7631
4425 Synectin-1	P18827	0.1380	0.2825	-0.13	0.3108	0.6793	0.16	0.3474	0.5143
4426 Synexin	Q96JG6	0.4108	0.5071	-3.31	0.5752	0.7101	-1.75	0.5661	0.6458
4427 Synembyrin-A	Q9NPKQ	0.1458	0.2935	0.26	0.2337	0.6615	0.27	0.0485	0.1226
4428 Synemin	I15061	0.0003	0.0141	0.23	0.1404	0.6546	0.26	0.0785	0.1700
4429 Synenulin	Q9NX95	0.4108	0.5070	-3.31	0.5752	0.7099	-1.75	0.5661	0.6456
4430 Syntaxin-10	O60499	0.0072	0.0500	-4.77	0.2375	0.6618	-3.01	0.0018	0.0238
4431 Syntaxin-11	O75558	0.6372	0.6992	-0.04	0.4365	0.7228	-1.19	0.0013	0.0221
4432 Syntaxin-12	Q86Y82	0.2931	0.4910	-0.07	0.6829	0.7685	-0.03	0.0981	0.2012
4433 Syntaxin-16	I14662	0.3438	0.5522	-0.03	0.1929	0.6684	-0.19	0.0799	0.1725
4434 Syntaxin-17	P56962	0.0184	0.0797	0.16	0.2009	0.6616	0.25	0.0002	0.0173
4435 Syntaxin-19	Q8N4C7	0.0067	0.0490	0.88	0.0013	0.2494	1.02	0.1327	0.2549
4436 Syntaxin-1B	P61266	0.4108	0.5069	-3.31	0.5752	0.7098	-1.75	0.5661	0.6455
4437 Syntaxin-4	Q12846	0.1636	0.3203	-0.09	0.1404	0.6534	0.27	0.3989	0.6021
4438 Syntaxin-5	Q13190	0.0099	0.0579	0.36	0.0796	0.6136	0.54	0.0010	0.0220
4439 Syntaxin-6	O43752	0.5865	0.6535	0.04	0.1014	0.6321	0.24	0.1562	0.2886
4440 Syntaxin-7	I15400	0.0369	0.1208	0.13	0.1123	0.6337	0.24	0.3454	0.5396
4441 Syntaxin-binding protein 1	P61764	0.0714	0.1794	0.11	0.3567	0.7085	0.31	0.0069	0.0396
4442 Syntaxin-binding protein 2	Q15833	0.0028	0.0353	0.36	0.2269	0.6607	0.12	0.2091	0.3629

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
4443	Syntaxin-binding protein 3	O00186	0.0170	0.0760	0.39	0.7263	0.8001	-0.03	0.0036	0.0312
4444	Syntaxin-1	O00560	0.0025	0.0332	0.19	0.1435	0.6555	0.04	0.0003	0.0210
4445	T cell receptor alpha constant	P01848	0.1884	0.3544	0.13	0.7292	0.8028	0.04	0.0960	0.1979
4446	T cell receptor alpha variable 12-2	A0A075B6T6	0.4108	0.5068	-3.31	0.5752	0.7096	-1.75	0.5661	0.6453
4447	T cell receptor beta variable 12-4	A0A0B4J2E0	0.4108	0.5067	-3.31	0.5752	0.7094	-1.75	0.5661	0.6452
4448	T cell receptor beta variable 7-9	P04435	0.4108	0.5065	-3.31	0.5752	0.7092	-1.75	0.5661	0.6451
4449	T cell receptor gamma constant 2	P03986	0.4108	0.5064	-3.31	0.5752	0.7091	-1.75	0.5661	0.6449
4450	Tail-anchored protein insertion receptor WRB	O00258	0.4108	0.5063	-3.31	0.5752	0.7089	-1.75	0.5661	0.6448
4451	Talin-1	Q9Y490	0.0687	0.1742	0.07	0.3173	0.6811	0.13	0.0054	0.0557
4452	Talin-2	Q9Y4G6	0.4108	0.5062	-3.31	0.5752	0.7087	-1.75	0.5661	0.6446
4453	TAR DNA-binding protein 43	Q13148	0.1201	0.2556	-0.11	0.7952	0.8514	0.02	0.0363	0.0998
4454	Target of EGFR1 protein 1	Q96GM8	0.6725	0.7303	-0.03	0.3286	0.6883	0.08	0.0571	0.1366
4455	Target of Myb protein 1	O60784	0.0433	0.1319	-0.23	0.1223	0.6399	-0.15	0.0475	0.1209
4456	Target of rapamycin complex subunit LST8	Q9BYC4	0.0262	0.0980	-0.31	0.5813	0.6889	-0.07	0.8748	0.9009
4457	TATA element modulatory factor	P82094	0.0056	0.0450	0.27	0.6994	0.7784	-0.07	0.4707	0.6880
4458	TATA-binding protein-associated factor 2N	Q92804	0.0345	0.1161	-0.14	0.3070	0.6776	0.12	0.0313	0.0904
4459	Tau-tubulin kinase 1	Q5TCY1	0.4108	0.5061	-3.31	0.5752	0.7086	-1.75	0.5661	0.6445
4460	Tax1-binding protein 1	Q86VP1	0.9247	0.9423	-0.01	0.241	0.4858	-0.22	0.5801	0.6376
4461	TBC domain-containing protein kinase-like protein	Q8TEA7	0.4108	0.5059	-3.31	0.5752	0.7084	-1.75	0.5661	0.6443
4462	TBC1 domain family member 1	Q86T10	0.4139	0.4917	0.07	0.1062	0.6309	0.38	0.0187	0.0655
4463	TBC1 domain family member 10A	Q9BX36	0.1039	0.2305	-0.22	0.6885	0.7721	-0.07	0.2203	0.3771
4464	TBC1 domain family member 10B	Q4K4MP7	0.0054	0.0442	-0.12	0.7170	0.7928	0.04	0.2460	0.4116
4465	TBC1 domain family member 13	Q9NVGR	0.1815	0.3450	-0.19	0.4454	0.7813	0.20	0.2564	0.2446
4466	TBC1 domain family member 15	Q8TQ07	0.0024	0.0329	-1.34	0.0524	0.5812	-0.50	0.0183	0.0648
4467	TBC1 domain family member 16	Q8TBP0	0.0744	0.1850	-0.05	0.8882	0.9202	0.01	0.0309	0.0898
4468	TBC1 domain family member 23	Q8NLY8	0.0122	0.0639	-0.64	0.0586	0.5906	-0.43	0.0150	0.0577
4469	TBC1 domain family member 2A	Q9BYX2	0.1787	0.3414	-0.05	0.5386	0.8545	-0.08	0.0086	0.0435
4470	TBC1 domain family member 30	Q9Y219	0.0619	0.1648	-0.13	0.2432	0.6592	0.16	0.0340	0.0957
4471	TBC1 domain family member 3D	QA087WVF3	0.1481	0.2968	-0.38	0.1259	0.6425	-0.39	0.0336	0.0950
4472	TBC1 domain family member 4	O60343	0.8619	0.8908	-0.01	0.2072	0.6589	0.41	0.0145	0.0566
4473	TBC1 domain family member 5	Q92609	0.1667	0.3246	-0.59	0.0538	0.5842	-10.26	0.3784	0.5775
4474	TBC1 domain family member 8	Q95759	0.4031	0.6231	-0.04	0.7469	0.8166	0.06	0.0257	0.0798
4475	TBC1 domain family member 8B	Q0IMM8	0.4108	0.5058	-3.31	0.5752	0.7082	-1.75	0.5661	0.6442
4476	TBC1 domain family member 9B	Q66K14	0.4108	0.5057	-3.31	0.5752	0.7081	-1.75	0.5661	0.6441
4477	T-box transcription factor TBX15	Q96SF7	0.0962	0.2188	0.11	0.0552	0.4551	0.22	0.0323	0.0923
4478	T-cell activation Rho GTPase-activating protein	Q8N103	0.4108	0.5056	-3.31	0.5752	0.7079	-1.75	0.5661	0.6439
4479	T-complex protein 1 subunit alpha	P17987	0.0124	0.0647	0.20	0.1381	0.6533	0.26	0.0069	0.0398
4480	T-complex protein 1 subunit beta	P28171	0.0080	0.0528	0.21	0.0764	0.7055	0.26	0.0025	0.0278
4481	T-complex protein 1 subunit delta	P50991	0.0038	0.0391	0.27	0.0797	0.6116	0.33	0.0006	0.0204
4482	T-complex protein 1 subunit epsilon	P48643	0.0023	0.0326	0.29	0.1765	0.6620	0.26	0.0008	0.0213
4483	T-complex protein 1 subunit eta	Q9P332	0.0675	0.1722	0.18	0.2010	0.6611	0.15	0.0099	0.0463
4484	T-complex protein 1 subunit gamma	P49368	0.0105	0.0591	0.22	0.1228	0.6624	0.23	0.0010	0.0211
4485	T-complex protein 1 subunit theta	P50990	0.0079	0.0524	0.36	0.2020	0.6602	0.30	0.0043	0.0324
4486	T-complex protein 1 subunit zeta	P40227	0.0015	0.0258	0.26	0.1823	0.6659	0.15	0.0028	0.0292
4487	T-complex protein 1 subunit zeta-2	Q92526	0.0194	0.0817	-0.22	0.0591	0.5921	-0.40	0.0645	0.1482
4488	T-complex protein 11-like protein 2	Q8N4U5	0.4108	0.5054	-3.31	0.5752	0.7077	-1.75	0.5661	0.6438
4489	Tctex1 domain-containing protein 1	Q8N7M0	0.4108	0.5053	-3.31	0.5752	0.7076	-1.75	0.5661	0.6436
4490	Tesart homolog 3	Q63HK5	0.0036	0.0381	-0.24	0.8514	0.8935	-0.03	0.0894	0.1877
4491	Tectonin beta-propeller repeat-containing protein 1	Q7Z6L1	0.0111	0.0603	-0.15	0.2963	0.6720	0.10	0.0789	0.1855
4492	Tektin-1	Q96V94	0.4108	0.5052	-3.31	0.5752	0.7074	-1.75	0.5661	0.6435
4493	Tektin-5	Q96M29	0.0723	0.1809	-0.30	0.0011	0.2374	-0.34	0.0088	0.0441
4494	Telethonin	O15273	0.6151	0.6795	-0.10	0.0721	0.6063	0.22	0.0917	0.9319
4495	Telomerase RNA component interacting RNase	Q9BO61	0.0322	0.1116	0.21	0.0752	0.6144	0.37	0.0110	0.0486
4496	Telomerase length and silencing protein 1 homolog	Q9NZ63	0.2434	0.4286	-0.17	0.9842	0.9888	-0.01	0.1614	0.2365
4497	Telomerase-associated protein RIF1	Q5UIB0	0.4056	0.6359	-0.05	0.7391	0.8103	-0.05	0.2737	0.4475
4498	Telomeric repeat-binding factor 2-interacting protein 1	Q9NBY0	0.0133	0.0671	-0.24	0.0707	0.7789	-0.02	0.0130	0.0533
4499	Tenascin-X	P22105	0.4108	0.5051	-3.31	0.5752	0.7072	-1.75	0.5661	0.6434
4500	Tenascin-X	Q9P273	0.0862	0.2040	-0.22	0.0277	0.5106	-0.18	0.0337	0.0951
4501	Tensin-3	Q68C22	0.0205	0.0845	0.23	0.0542	0.5874	0.31	0.0360	0.0993
4502	Terminal nucleotidyltransferase 5C	Q5VWP2	0.0784	0.1918	0.20	0.0893	0.6251	0.17	0.0396	0.1059
4503	Terminal uridylyltransferase 4	Q5TAX3	0.4108	0.5050	-3.31	0.5752	0.7071	-1.75	0.5661	0.6432
4504	Testican-2	Q92563	0.0582	0.1588	-0.25	0.1976	0.6703	-0.58	0.4980	0.7204
4505	Testican-3	Q9BQ16	0.0241	0.0932	-0.14	0.5793	0.6875	0.07	0.5622	0.7864
4506	Testin	Q5054	0.0504	0.1450	-0.03	0.6395	0.7343	0.02	0.0001	0.0140
4507	Testis development-related protein	Q86YL5	0.9311	0.9479	0.01	0.6984	0.7778	-0.07	0.9032	0.9233
4508	Testis-expressed protein 10	Q9NXF1	0.0067	0.0489	-0.63	0.4272	0.7628	0.08	0.0021	0.0257
4509	Testis-expressed protein 101	Q9BY14	0.1316	0.2736	0.90	0.4342	0.7705	0.77	0.4693	0.6869
4510	Testis-expressed protein 15	Q9BXT5	0.2757	0.4692	0.07	0.7474	0.6112	0.13	0.7232	0.7677
4511	Testis-expressed protein 264	Q9Y619	0.0072	0.0499	-0.17	0.0494	0.5763	0.12	0.4879	0.7079
4512	Testis-expressed protein 48	AOA1B0GUV7	0.4108	0.5049	-3.31	0.5752	0.7069	-1.75	0.5661	0.6431
4513	Testis-expressed protein 52	A6GNC8	0.5113	0.5840	0.05	0.2533	0.6627	0.30	0.0715	0.1594
4514	Testis-expressed protein 54	Q9BZW7	0.4108	0.5047	-3.31	0.5752	0.7067	-1.75	0.5661	0.6430
4515	Testis-specific gene 10 protein	Q9BZW7	0.4108	0.5046	-3.31	0.5752	0.7067	-1.75	0.5661	0.6429
4516	Testis-specific serine/threonine-protein kinase 3	Q96N98	0.0499	0.1440	0.22	0.1010	0.6837	0.12	0.5362	0.7574
4517	Testis-specific serine/threonine-protein kinase 4	Q6SA08	0.0522	0.1479	0.14	0.3999	0.6349	0.29	0.0024	0.0273
4518	Testis-specific Y-encoded-like protein 5	Q86VY4	0.1253	0.2638	-0.06	0.3100	0.4401	0.19	0.0188	0.0657
4519	Tether containing UBX domain for GLUT4	Q9BZE9	0.7436	0.7916	-0.02	0.0307	0.7041	0.13	0.7544	0.7959
4520	Tetraspanin-13	Q95857	0.2123	0.3860	0.04	0.4124	0.7525	-0.10	0.0010	0.0208
4521	Tetraspanin-15	Q95858	0.0019	0.0297	-0.26	0.0232	0.4826	-0.30	0.1797	0.2322
4522	Tetraspanin-31	Q12999	0.0573	0.1571	-0.12	0.2728	0.6656	0.12	0.5575	0.7816
4523	Tetralipopeptide repeat protein 1	Q99614	0.4784	0.5534	0.04	0.6404	0.7350	0.05	0.8233	0.8574
4524	Tetralipopeptide repeat protein 13	Q8NBPO	0.1313	0.2733	-0.12	0.3890	0.7322	0.09	0.0037	0.0316
4525	Tetralipopeptide repeat protein 14	Q96N46	0.5185	0.5904	-0.04	0.2402	0.6604	0.14	0.0021	0.0258
4526	Tetralipopeptide repeat protein 21A	Q8NDW8	0.1182	0.2530	0.32	0.1642	0.6629	0.25	0.1261	0.2457

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control
			p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
4527	Tetralactide repeat protein 24	A2A3L6	0.2720	0.4647	0.20	0.7756	0.8380	0.05	0.5685	0.6263
4528	Tetralactide repeat protein 25	Q96NG3	0.4108	0.5045	-3.31	0.5752	0.7064	-1.75	0.5661	0.6426
4529	Tetralactide repeat protein 27	Q6P3X3	0.4547	0.5319	-0.16	0.7328	0.8054	-0.13	0.9678	0.9734
4530	Tetralactide repeat protein 28	Q96A94	0.4108	0.5044	-3.31	0.5752	0.7062	-1.75	0.5661	0.6425
4531	Tetralactide repeat protein 30A	Q6MWT1	0.0222	0.0889	-0.99	0.2221	0.6574	-1.09	0.0512	0.1271
4532	Tetralactide repeat protein 38	Q5R3I4	0.4108	0.5043	-3.31	0.5752	0.7061	-1.75	0.5661	0.6424
4533	Tetralactide repeat protein 4	Q95801	0.0928	0.2143	0.27	0.6767	0.7632	-0.08	0.0811	0.1747
4534	Tetralactide repeat protein 7A	Q9ULI0	0.2800	0.4734	0.11	0.6094	0.6002	-0.26	0.0139	0.0554
4535	Tetralactide repeat protein 7B	Q86TV6	0.0174	0.0771	0.17	0.3643	0.7132	0.18	0.0142	0.0559
4536	Tetralactide repeat protein 8	Q8TAM2	0.3730	0.5878	0.04	0.4548	0.7874	-0.08	0.0077	0.0415
4537	TGF-beta receptor type-1	P36897	0.4108	0.5041	-3.31	0.5752	0.7059	-1.75	0.5661	0.6422
4538	TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	Q8NSC8	0.0040	0.0399	0.38	0.1191	0.6347	0.31	0.0041	0.0323
4539	Thimet oligopeptidase	P52888	0.0020	0.0307	0.21	0.1444	0.6538	0.20	0.0423	0.1116
4540	Thioredoxin	P10599	0.0139	0.0691	0.19	0.1613	0.6642	0.11	0.0064	0.0388
4541	Thioredoxin domain-containing protein 12	Q95881	0.0160	0.0737	-0.62	0.2216	0.6593	-0.36	0.0131	0.0536
4542	Thioredoxin domain-containing protein 17	Q9BRA2	0.0118	0.0626	0.17	0.7441	0.8149	0.03	0.7051	0.7517
4543	Thioredoxin domain-containing protein 5	Q8NB89	0.0102	0.0587	0.20	0.3530	0.7052	0.17	0.0039	0.0316
4544	Thioredoxin domain-containing protein 6	Q86XW9	0.9825	0.9878	-0.02	0.1251	0.6422	-6.09	0.0347	0.0970
4545	Thioredoxin domain-containing protein 8	Q6A555	0.4108	0.5040	-3.31	0.5752	0.7057	-1.75	0.5661	0.6421
4546	Thioredoxin domain-containing protein 9	Q14530	0.4108	0.5039	-3.31	0.5752	0.7055	-1.75	0.5661	0.6419
4547	Thioredoxin reductase 1 cytoplasmic	P16881	0.5439	0.5139	0.05	0.1054	0.6319	-0.14	0.0825	0.9070
4548	Thioredoxin reductase 2 mitochondrial	Q9NNW7	0.4108	0.5038	-3.31	0.5752	0.7054	-1.75	0.5661	0.6418
4549	Thioredoxin-dependent peroxide reductase mitochondrial	P30048	0.0005	0.0176	0.26	0.3501	0.7046	0.15	0.0022	0.0261
4550	Thioredoxin-like protein 1	O43396	0.5308	0.6018	0.03	0.0824	0.6168	0.20	0.0138	0.0552
4551	Thioredoxin-related transmembrane protein 1	Q9H3N1	0.1027	0.2292	0.09	0.3072	0.6774	0.19	0.0187	0.0655
4552	Thioredoxin-related transmembrane protein 2	Q9Y320	0.0442	0.1336	-0.61	0.0012	0.2486	-0.41	0.0000	0.0000
4553	Thiosulfate sulfurtransferase	P16762	0.0007	0.0196	0.60	0.0211	0.4773	0.14	0.0215	0.0709
4554	Thiosulfate:glutathione sulfurtransferase	Q8NFU3	0.2874	0.4838	-0.06	0.0157	0.6308	-0.07	0.0067	0.0396
4555	THO complex subunit 4	Q86V81	0.0069	0.0494	-0.21	0.2162	0.6611	-0.22	0.6088	0.6642
4556	Threonine-tRNA ligase cytoplasmic	P26639	0.2348	0.4177	-0.04	0.9597	0.9225	0.00	0.0315	0.0905
4557	Threonylcarbamoyladenosine tRNA methyltransferase	Q5VV42	0.4108	0.5037	-3.31	0.5752	0.7052	-1.75	0.5661	0.6417
4558	Thrombospondin type-1 domain-containing protein 4	Q6ZMP0	0.0358	0.1182	0.20	0.4160	0.7545	0.05	0.2605	0.4297
4559	Thrombospondin-4	P97996	0.5034	0.5767	-0.21	0.0760	0.6013	-9.00	0.6516	0.7036
4560	Thrombospondin-4	P35443	0.5936	0.6598	0.05	0.6109	0.7174	0.08	0.2491	0.4156
4561	THUMP domain-containing protein 1	QXNGX2	0.7583	0.8034	-0.05	0.3840	0.7302	0.11	0.4687	0.8662
4562	THUMP domain-containing protein 3	Q9BV44	0.0834	0.1990	0.08	0.2323	0.8732	-0.01	0.5597	0.7838
4563	Thymidine kinase cytosolic	P04183	0.0655	0.1693	0.16	0.0513	0.5752	0.17	0.0078	0.0419
4564	Thymidine kinase	P23919	0.0020	0.0306	0.49	0.0118	0.4335	0.42	0.0061	0.0380
4565	Thymidine synthase	P04818	0.1092	0.2392	0.16	0.4145	0.7531	-0.07	0.3230	0.5107
4566	Thymocyte nuclear protein 1	Q9P016	0.4108	0.5035	-3.31	0.5752	0.7050	-1.75	0.5661	0.6415
4567	Thymosin beta-10	P63313	0.3578	0.5692	0.05	0.4438	0.7795	-0.05	0.1774	0.3204
4568	Thymosin beta-4	P62328	0.0010	0.0214	0.50	0.0159	0.4550	0.38	0.0004	0.0235
4569	Thyroid hormone receptor-associated protein 3	Q9Y2W1	0.2680	0.4598	0.08	0.0588	0.5903	0.34	0.0004	0.0228
4570	Thyroid peroxidase	P07202	0.0367	0.1205	-0.43	0.3760	0.7240	-0.28	0.4337	0.6441
4571	Thyroid receptor-interacting protein 11	Q15643	0.4949	0.5692	-0.09	0.3246	0.6857	-0.19	0.8097	0.8458
4572	Thyroid receptor-interacting protein 6	Q15654	0.4719	0.5478	-0.02	0.1277	0.6607	0.26	0.0616	0.1443
4573	Thyrotropin-releasing hormone-degrading ectonuclease	Q9UKU6	0.0271	0.0998	-0.18	0.5820	0.6894	-0.02	0.5144	0.7351
4574	Tigger transposable element-derived protein 5	Q53EQ6	0.9486	0.9614	0.00	0.2427	0.6596	-0.11	0.0005	0.0190
4575	TIPI4-like protein	Q75663	0.0144	0.0696	2.59	0.3211	0.6836	0.50	0.4151	0.6218
4576	Titin	Q8WZ42	0.0047	0.0429	0.29	0.2007	0.6626	0.28	0.0033	0.0307
4577	TNF receptor-associated factor 5	Q00463	0.2714	0.4640	-0.09	0.3732	0.7208	-0.25	0.2224	0.3796
4578	TNF receptor-associated factor 6	Q9Y4K3	0.1023	0.2286	0.92	0.3503	0.7044	0.45	0.1340	0.2564
4579	TNFAIP3-interacting protein 2	Q8NFZ5	0.5709	0.6386	-0.14	0.5713	0.8844	-0.16	0.7522	0.7942
4580	TOG array regulator of axonemal microtubules protein 2	Q6ZUX3	0.4108	0.5034	-3.31	0.5752	0.7049	-1.75	0.5661	0.6414
4581	Toll-interacting protein	Q9H0E2	0.2983	0.4970	0.71	0.2991	0.6733	0.93	0.4139	0.6202
4582	Toll-like receptor 5	Q60602	0.4108	0.5033	-3.31	0.5752	0.7047	-1.75	0.5661	0.6412
4583	Tonsin-like protein	Q96HA7	0.0000	0.0000	-2.62	0.2027	0.6608	-2.24	0.0005	0.0193
4584	Torsin-1A	Q14656	0.0019	0.0296	0.15	0.2052	0.6594	0.18	0.5227	0.7438
4585	Torsin-1A-interacting protein 1	Q5TJY8	0.1161	0.2500	0.13	0.4214	0.7593	0.09	0.0297	0.0875
4586	Torsin-1A-interacting protein 2	Q8NFQ8	0.0070	0.0493	-0.26	0.1684	0.6603	-0.15	0.0498	0.1247
4587	Torsin-3A	Q9H149	0.7949	0.8337	0.05	0.2382	0.6623	-0.44	0.8452	0.8756
4588	TP53-regulated inhibitor of apoptosis 1	O43715	0.0347	0.1164	-0.41	0.0940	0.6307	-0.49	0.0910	0.1901
4589	TPR and ankryrin repeat-containing protein 1	O15050	0.0131	0.0667	-0.31	0.0811	0.6151	-0.16	0.5320	0.7529
4590	TPST1-like protein	Q56UQ5	0.1499	0.2993	0.06	0.2053	0.6593	-0.05	0.1174	0.2324
4591	Tracking protein particle complex subunit 13	ASPLN9	0.4108	0.5032	-3.31	0.5752	0.7045	-1.75	0.5661	0.6411
4592	Tracking protein particle complex subunit 2-like protein	Q9UL33	0.0472	0.1395	-0.17	0.0504	0.5725	-10.57	0.0889	0.1873
4593	TRAF-type zinc finger domain-containing protein 1	O14545	0.0035	0.0378	-1.35	0.2211	0.6578	-0.48	0.5254	0.7465
4594	Trans-acting, T-cell-specific transcription factor GATA-3	P23771	0.1295	0.2704	0.00	0.0989	0.9996	0.00	0.0012	0.0173
4595	Transaldolase	P78377	0.0273	0.0999	0.24	0.1984	0.6660	0.35	0.0095	0.0455
4596	Transcalabrin-2	T20062	0.2498	0.4360	-0.25	0.4269	0.7625	-0.18	0.5121	0.7000
4597	Transcription and mRNA export factor ENY2	Q9NP88	0.0786	0.1921	-0.43	0.1833	0.6649	-0.62	0.4793	0.6986
4598	Transcription elongation factor A protein 1	P23193	0.0282	0.1020	0.15	0.3132	0.6802	0.16	0.0141	0.0557
4599	Transcription elongation factor A protein 2	O15560	0.9678	0.9763	0.02	0.3393	0.6988	-0.50	0.0511	0.1271
4600	Transcription elongation factor A protein 3	O75764	0.4108	0.5031	-3.31	0.5752	0.7044	-1.75	0.5661	0.6410
4601	Transcription elongation factor A protein-like 1	Q15170	0.1028	0.2293	0.33	0.1211	0.6619	0.24	0.0670	0.1522
4602	Transcription elongation factor A protein-like 2	Q9H3H9	0.0414	0.1288	0.25	0.1266	0.6598	0.17	0.4495	0.6632
4603	Transcription elongation factor A protein-like 4	Q96E15	0.7101	0.7617	-0.02	0.4382	0.7744	-0.03	0.0861	0.1829
4604	Transcription elongation factor A protein-like 5	Q5H9L2	0.0335	0.1142	-0.36	0.4454	0.7816	-0.08	0.1050	0.0575
4605	Transcription elongation factor SPT5	O00267	0.8629	0.8915	0.01	0.5621	0.8760	0.10	0.0161	0.0599
4606	Transcription elongation regulator 1	O14776	0.0372	0.1212	0.17	0.3606	0.6954	0.11	0.0268	0.0820
4607	Transcription factor 15	O12870	0.0017	0.0278	1.13	0.1132	0.6346	0.45	0.0368	0.1007

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																							
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																				
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																		
4608	Transcription factor 20	Q9UGU0	0.4108	0.5029	-3.31	0.5752	0.7042	-1.75	0.5661	0.6408	-1.19	0.5388	0.6063	0.89	0.2938	0.4044	-1.88	0.9510	0.9831	0.09	0.0559	0.1874	-0.22	0.9822	0.9873	0.00	0.1576	0.2214	0.21
4609	Transcription factor 25	Q9B070	0.0302	0.1069	0.16	0.2413	0.6606	0.22	0.0094	0.0452	-0.24	0.1135	0.2138	0.10	0.8013	0.8450	0.01	0.1642	0.3273	0.09	0.3736	0.5110	-2.55	0.8708	1.0537	-0.33	0.0651	0.1460	0.26
4610	Transcription factor 7	P36402	0.4108	0.5028	-3.31	0.5752	0.7040	-1.75	0.5661	0.6407	-0.19	0.5388	0.6062	0.89	0.2938	0.4043	-1.88	0.9510	0.9829	0.09	0.0132	0.1087	0.42	0.0001	0.0118	1.62	0.0691	0.1166	0.24
4611	Transcription factor 7-like 2	Q9NQB0	0.1075	0.2360	0.16	0.2204	0.6592	0.14	0.8451	0.8759	-0.01	0.0074	0.0348	0.30	0.0256	0.1153	0.12	0.0238	0.0989	0.15	0.3736	0.5886	-2.55	0.8708	1.1927	-0.33	0.0651	0.1862	0.26
4612	Transcription factor A mitochondrial	Q90059	0.7019	0.7554	0.03	0.2912	0.6602	0.17	0.8558	0.8852	-0.01	0.1710	0.2910	0.12	0.7504	0.8049	0.02	0.1403	0.2940	0.14	0.0425	0.1672	0.42	0.1078	0.3344	0.09	0.0198	0.1217	0.16
4613	Transcription factor BTF3	P20290	0.2467	0.4326	-0.15	0.5366	0.8521	-0.18	0.7914	0.8290	0.03	0.8140	0.8398	0.02	0.0560	0.1768	-0.33	0.9797	0.9839	0.00	0.7267	0.7660	0.09	0.7989	1.2431	0.05	0.5559	0.6205	0.12
4614	Transcription factor BTF3 homolog 4	Q9K617	0.4108	0.5027	-3.31	0.5752	0.7039	-1.75	0.5661	0.6405	-0.19	0.5388	0.6061	0.89	0.2938	0.4042	-1.88	0.9510	0.9827	0.09	0.0619	0.1958	-0.83	0.9859	0.9899	0.01	0.7571	0.7999	-0.09
4615	Transcription factor E2F8	ADAVK6	0.4108	0.5026	-3.31	0.5752	0.7037	-1.75	0.5661	0.6404	-0.19	0.5388	0.6059	0.89	0.2938	0.4041	-1.88	0.9510	0.9825	0.09	0.0392	0.1638	-0.86	0.0003	0.0175	-0.75	0.1475	0.2098	-0.37
4616	Transcription factor ETV7	Q9Y603	0.4633	0.5402	0.04	0.3762	0.7239	0.13	0.0133	0.0538	0.23	0.0443	0.1056	-0.15	0.0218	0.1062	0.24	0.1070	0.2450	0.11	0.3736	0.5315	-2.55	0.8708	1.0909	-0.33	0.0651	0.1558	0.26
4617	Transcription factor HIVEP2	P31629	0.3897	0.6064	-0.21	0.4094	0.7504	-0.21	0.9342	0.9490	0.02	0.1879	0.3156	-0.36	0.5996	0.6753	-0.12	0.6667	0.9048	0.10	0.3736	0.4467	-2.55	0.8708	0.9347	-0.33	0.0651	0.1182	0.26
4618	Transcription factor HIVEP3	Q5T1R4	0.0005	0.0175	-0.25	0.2298	0.6613	-0.31	0.0003	0.0199	-0.39	0.0011	0.0163	-2.26	0.6144	0.6883	-0.08	0.0028	0.0541	-2.17	0.3736	0.6395	-2.55	0.8708	1.2815	-0.33	0.0651	0.2177	0.26
4619	Transcription factor jun-D	P17535	0.0370	0.1209	-0.64	0.1962	0.6691	-0.89	0.1295	0.2503	-0.47	0.0374	0.0937	-0.45	0.5904	0.6673	-0.09	0.1655	0.3290	-0.22	0.3736	0.5104	-2.55	0.8708	1.0524	-0.33	0.0651	0.1457	0.26
4620	Transcription factor p65	Q04206	0.6518	0.7128	0.07	0.7674	0.8311	-0.09	0.1124	0.2242	0.33	0.8918	0.9077	0.03	0.0690	0.2001	0.45	0.7876	1.0256	0.06	0.0012	0.0454	1.17	0.0071	0.0694	0.59	0.0033	0.0576	0.94
4621	Transcription factor RelB	Q01201	0.7559	0.8014	-0.02	0.0852	0.6199	-0.12	0.0002	0.0199	0.71	0.0035	0.0240	0.44	0.0039	0.0465	-0.40	0.0029	0.0556	0.73	0.3736	0.6391	-2.55	0.8708	1.2807	-0.33	0.0651	0.2174	0.26
4622	Transcription factor Sp1	P08047	0.0877	0.2061	-0.32	0.4314	0.7674	-0.26	0.5571	0.7812	0.10	0.7583	0.7913	-0.05	0.9674	0.9744	-0.01	0.0821	0.2063	-0.33	0.3736	0.5425	-2.55	0.8708	1.1107	-0.33	0.0651	0.1613	0.26
4623	Transcription factor TFIIB component B' homolog	A6H8Y1	0.0000	0.0000	0.91	0.0014	0.2339	0.34	0.0031	0.0306	0.25	0.0011	0.0159	0.25	0.0000	0.0000	0.68	0.0192	0.0890	0.12	0.9378	0.9488	0.01	0.7682	1.2110	0.02	0.0021	0.0508	0.40
4624	Transcription initiation factor IIB	Q00403	0.4108	0.5025	-3.31	0.5752	0.7036	-1.75	0.5661	0.6403	-0.19	0.5388	0.6058	0.89	0.2938	0.4040	-1.88	0.9510	0.9823	0.09	0.2869	0.5381	0.17	0.0094	0.0796	-0.50	0.1178	0.1759	-0.34
4625	Transcription initiation factor TFIIH subunit 11	Q15544	0.4108	0.5023	-3.31	0.5752	0.7034	-1.75	0.5661	0.6401	-0.19	0.5388	0.6057	0.89	0.2938	0.4039	-1.88	0.9510	0.9821	0.09	0.3718	0.6540	0.88	0.1864	0.4766	1.49	0.1122	0.1695	1.92
4626	Transcription intermediary factor 1-alpha	O15164	0.1264	0.2652	-0.58	0.2761	0.6649	-0.41	0.1421	0.1866	0.13	0.3182	0.4885	-0.37	0.0386	0.1433	-0.22	0.1925	0.3666	-0.49	0.3736	0.5042	-2.55	0.8708	1.0413	-0.33	0.0651	0.1428	0.26
4627	Transcription intermediary factor 1-beta	I31263	0.0053	0.0442	0.18	0.5229	0.8420	0.10	0.0014	0.0220	0.33	0.0359	0.0910	0.12	0.1109	0.2715	-0.37	0.0053	0.0611	0.27	0.0591	0.1930	0.24	0.8272	1.2711	0.01	0.4270	0.4932	0.04
4628	Transcription termination factor 1 mitochondrial	Q9NS51	0.9901	0.9920	0.01	0.0189	0.4640	-0.40	0.0465	0.1194	-0.26	0.0017	0.0180	-0.72	0.0319	0.1306	-0.30	0.3405	0.5447	0.60	0.0166	0.0521	0.81	0.0015	0.0317	1.40	0.1522	0.2153	0.34
4629	Transcription termination factor 4 mitochondrial	Q7Z6M4	0.0222	0.0888	0.35	0.1541	0.6602	0.22	0.0862	0.1830	0.23	0.4073	0.5984	-0.11	0.2945	0.3925	-0.12	0.6871	0.9269	-0.04	0.3736	0.4457	-2.55	0.8708	0.9257	-0.33	0.0651	0.1177	0.26
4630	Transcriptional activator protein Pur-beta	Q960R8	0.1229	0.2603	-0.07	0.5958	0.7001	-0.07	0.3270	0.5159	0.03	0.0932	0.1838	-0.12	0.0014	0.0287	-0.18	0.0708	0.1873	0.05	0.0642	0.1994	0.21	0.0374	0.176	-0.29	0.3939	0.6121	-0.28
4631	Transcriptional adapter 2-alpha	Q75478	0.4108	0.5022	-3.31	0.5752	0.7032	-1.75	0.5661	0.6400	-0.19	0.5388	0.6056	0.89	0.2938	0.4038	-1.88	0.9510	0.9819	0.09	0.6629	0.7071	0.12	0.0414	0.1871	-0.61	0.0785	0.1738	-0.07
4632	Transcriptional coactivator YAP1	P46937	0.0009	0.0210	-1.22	0.3180	0.6810	-0.49	0.2505	0.4175	-0.63	0.0027	0.0216	-1.09	0.4659	0.5575	0.09	0.0035	0.0589	-1.18	0.0232	0.1364	-0.28	0.0102	0.0832	-0.51	0.0064	0.0753	-0.55
4633	Transcriptional regulator ERG	P11308	0.0003	0.0140	0.01	0.0063	0.5950	1.06	0.0000	0.0000	-1.22	0.0001	0.0167	-1.47	0.0381	0.1424	0.14	0.0001	0.0259	1.29	0.3736	0.6549	-2.55	0.8708	1.3078	-0.33	0.0651	0.2282	0.26
4634	Transcriptional repressor CTCFL	Q8N151	0.4108	0.5021	-3.31	0.5752	0.7031	-1.75	0.5661	0.6398	-0.19	0.5388	0.6054	0.89	0.2938	0.4037	-1.88	0.9510	0.9817	0.09	0.0297	0.1468	-0.34	0.0379	0.1773	-0.37	0.0360	0.1622	-0.23
4635	Transcriptional repressor p66-alpha	Q86YPA	0.0475	0.1400	-0.07	0.0450	0.5644	-0.07	0.0662	0.1509	0.07	0.4167	0.6089	-0.04	0.0012	0.0268	-0.27	0.1812	0.0874	-0.14	0.9496	0.9509	0.01	0.8904	0.9177	-0.02	0.1656	0.2308	0.29
4636	Transcriptional repressor p66-beta	Q8WX19	0.1371	0.2819	0.09	0.7818	0.8428	0.05	0.5025	0.7249	0.06	0.0374	0.0936	0.16	0.6542	0.7209	-0.02	0.0611	0.1715	0.12	0.0204	0.1323	0.45	0.6628	1.1015	0.04	0.1023	0.1582	0.20
4637	Transcriptional repressor protein YY1	P25490	0.1052	0.2326	0.25	0.2258	0.6593	0.19	0.0686	0.1549	0.30	0.1475	0.2616	0.21	0.9094	0.9319	0.01	0.3895	0.6012	0.11	0.7788	0.8130	-0.04	0.7047	1.1465	0.06	0.8499	0.8787	-0.03
4638	Transducin beta-like protein 2	Q9Y4P3	0.0072	0.0499	0.14	0.3847	0.7302	0.11	0.0007	0.0203	0.33	0.2115	0.3478	0.05	0.6589	0.7243	-0.02	0.0092	0.0687	0.18	0.1683	0.3634	-0.20	0.0727	0.2613	0.30	0.5339	0.5999	-0.09
4639	Transferrin receptor protein 1	P02786	0.0066	0.0487	0.39	0.6146	0.7151	0.08	0.0037	0.0315	0.34	0.0015	0.0177	0.50	0.9668	0.9739	0.00	0.0071	0.0643	0.46	0.0774	0.2216	0.25	0.7881	0.6154	0.11	0.5706	0.6341	0.05
4640	Transferrin receptor protein 2	Q9UP52	0.0026	0.0338	-0.35	0.7931	0.8507	0.03	0.1298	0.2506	-0.08	0.4275	0.6194	0.03	0.0320	0.1304	-0.25	0.0111	0.0722	-0.23	0.3736	0.6105	-2.55	0.8708	1.2311	-0.33	0.0651	0.1992	0.26
4641	Transformation/transcription domain-associated protein	Q9Y4A5	0.4108	0.5020	-3.31	0.5752	0.7029	-1.75	0.5661	0.6397	-0.19	0.5388	0.6053	0.89	0.2938	0.4036	-1.88	0.9510	0.9815	0.09	0.0998	0.2555	-0.12	0.0453	0.1977	0.16	0.2027	0.2711	0.15
4642	Transformer-2 protein homolog alpha	P13595	0.4108	0.5019	-3.31	0.5752	0.7027	-1.75	0.5661	0.6396	-0.19	0.5388	0.6052	0.89	0.2938	0.4035	-1.88	0.9510	0.9813	0.09	0.4692	0.5243	0.06	0.0033	0.1648	0.30	0.3324	0.4035	0.09
4643	Transformer-2 protein homolog beta	P62995	0.0034	0.0377	-0.19	0.2457	0.6584	-0.11	0.0104	0.2922	-0.01	0.0016	0.0176	-0.24	0.0005	0.0189	-0.32	0.0409	0.1331	-0.21	0.0039	0.0673	0.59	0.0002	0.0179	0.66	0.0022	0.0525	0.49
4644	Transforming acidic coiled-coil-containing protein 3	P1Y6A5	0.0421	0.1300	-0.35	0.0053	0.3761	-0.71	0.1309	0.2521	-0.25	0.0097	0.0395	-0.56	0.0072	0.0619	-0.74	0.0086	0.0681	-0.96	0.0662	0.2495	0.39	0.0911	0.3002	0.39	0.1669	0.2322	0.29
4645	Transforming growth factor beta 1 protein	Q91137	0.4108	0.5018	-3.31	0.5752	0.7026	-1.75	0.5661	0.6394	-0.19	0.5388	0.6049	0.89	0.2938	0.4034	-1.88	0.9510	0.9811	0.09	0.0027	0.1678	0.56	0.0132					

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

		MCF-7				MDA-MB-231			
		Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
Protein name	UniProt	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value
4688 Transmembrane protein 135	Q86B99	0.0089	0.0558	0.19	0.5223	0.8413	0.10	0.0040	0.0319
4689 Transmembrane protein 151A	Q8N4L1	0.4108	0.5010	-3.31	0.5752	0.7016	-1.75	0.5661	0.6386
4690 Transmembrane protein 165	Q9HC07	0.0152	0.0713	-0.24	0.3987	0.7426	-0.09	0.0121	0.0614
4691 Transmembrane protein 186	Q96B77	0.0059	0.0464	0.16	0.8240	0.8739	0.02	0.4110	0.6171
4692 Transmembrane protein 192	Q8H195	0.3626	0.5753	-0.11	0.8392	0.8846	-0.01	0.7890	0.8270
4693 Transmembrane protein 205	Q6UW68	0.2444	0.4299	-0.10	0.4925	0.8151	0.12	0.8750	0.9009
4694 Transmembrane protein 40	Q87008	0.0063	0.0255	0.31	0.9304	0.9145	0.11	0.0084	0.0345
4695 Transmembrane protein 43	Q8WVA1	0.4108	0.5009	-3.31	0.5752	0.7014	-1.75	0.5661	0.6384
4696 Transmembrane protein 43	Q9BTU4	0.0498	0.1438	0.21	0.4791	0.8047	0.04	0.0294	0.0871
4697 Transmembrane protein 87A	Q8NB33	0.4108	0.4951	-0.12	0.0737	0.6128	0.34	0.1214	0.2389
4698 Transmembrane protein KIAA1109	Q2LD37	0.4108	0.5008	-3.31	0.5752	0.7012	-1.75	0.5661	0.6383
4699 Transport and Golgi organization protein 1 homolog	Q5JRA6	0.7720	0.8150	-0.01	0.9701	0.9797	-0.00	0.0532	0.1305
4700 Transportin-1	Q92973	0.2494	0.4336	0.03	0.0615	0.5932	0.09	0.0110	0.0487
4701 Transportin-2	O14787	0.0076	0.0513	-1.74	0.1287	0.6429	-1.27	0.0037	0.0319
4702 Transportin-3	Q9YSL0	0.4108	0.5007	-3.31	0.5752	0.7011	-1.75	0.5661	0.6382
4703 Treacle protein	Q13428	0.0000	0.0000	-1.71	0.3019	0.6752	-1.07	0.1632	0.2990
4704 Trefol factor 2	Q03403	0.0060	0.0465	0.35	0.0190	0.4642	0.42	0.0183	0.0649
4705 Treslin	Q72221	0.0002	0.0119	0.59	0.1202	0.6366	0.37	0.0005	0.0201
4706 Trichoxylate transport protein mitochondrial	P53007	0.0048	0.0428	0.36	0.3434	0.7006	-0.17	0.0032	0.0302
4707 Trichostatin A	O07283	0.0001	0.0091	-0.88	0.0545	0.5881	-0.84	0.0066	0.0393
4708 Trifunctional enzyme subunit alpha mitochondrial	P40939	0.0060	0.0465	0.17	0.3364	0.6954	0.06	0.0048	0.0336
4709 Trifunctional enzyme subunit beta mitochondrial	P55084	0.1316	0.2734	0.08	0.3068	0.6783	0.14	0.0476	0.1210
4710 Trifunctional purine biosynthetic protein adenosine-3	P22102	0.0049	0.0854	0.22	0.1797	0.6649	0.20	0.0059	0.0339
4711 Trimucleotide repeat-containing gene 18 protein	G15417	0.0162	0.0741	0.18	0.0421	0.0465	0.30	0.0023	0.0206
4712 Trimucleotide repeat-containing gene 6A protein	Q8HNV7	0.0060	0.0421	0.52	0.7572	0.7009	-1.75	0.1499	0.1965
4713 TRIO E3 ubiquitin-binding protein	Q9H246	0.4108	0.5005	-3.31	0.5752	0.7007	-1.75	0.5661	0.6379
4714 Triokinase/TMN cyclase	Q13123	0.6590	0.7194	0.01	0.3687	0.7169	0.08	0.2768	0.4509
4715 Triosephosphate isomerase	P60174	0.0001	0.0089	0.52	0.1106	0.6323	0.35	0.0011	0.0218
4716 Tripartite motif-containing protein 10	Q1UDY6	0.7049	0.7572	0.07	0.6855	0.7706	-0.06	0.0458	0.1179
4717 Tripartite motif-containing protein 16-like protein	Q309B1	0.1032	0.2297	-0.56	0.2741	0.6647	-0.53	0.6644	0.7157
4718 Tripartite motif-containing protein 29	Q14134	0.0305	-3.31	0.5752	0.7006	-1.75	0.5661	0.6378	-1.19
4719 Tripartite motif-containing protein 34	Q9BYJ4	0.4108	0.5002	-3.31	0.5752	0.7004	-1.75	0.5661	0.6376
4720 Tripartite motif-containing protein 42	Q8IWZ5	0.2552	0.4432	0.05	0.2677	0.6635	-0.13	0.0733	0.1618
4721 Tripartite motif-containing protein 45	Q9H1W5	0.4108	0.5001	-3.31	0.5752	0.7002	-1.75	0.5661	0.6375
4722 Tripartite motif-containing protein 51	Q9BSJ1	0.3952	0.6133	0.13	0.2753	0.6645	0.15	0.0147	0.0572
4723 Tripartite motif-containing protein 52	Q96A61	0.1302	0.2717	0.11	0.0796	0.6127	0.16	0.0620	0.1447
4724 Tripartite motif-containing protein 55	Q9BYV6	0.1740	0.3354	0.07	0.0879	0.6212	-0.25	0.0670	0.1522
4725 Tripartite motif-containing protein 77	HYAP6	0.4108	0.5000	-3.31	0.5752	0.7001	-1.75	0.5661	0.6373
4726 tRNA (cytosine(34)-C)-methyltransferase	Q80K23	0.0030	0.0359	0.22	0.1224	0.6398	0.09	0.0017	0.0238
4727 tRNA (guanine(10-N2)-methyltransferase homolog	Q72Z44	0.0444	0.1340	1.18	0.6970	0.7768	0.21	0.9662	0.9724
4728 tRNA-methyltransferase 10 homolog	Q7U103	0.3251	0.5307	0.06	0.1578	0.6619	-0.13	0.0585	0.1391
4729 tRNA pseudouridine synthase A	Q9Y406	0.0062	0.0424	0.22	0.0562	0.0623	0.20	0.0066	0.0336
4730 tRNA-pseudouridine synthetase protein 1	A2RUC4	0.4108	0.4999	-3.31	0.5752	0.6999	-1.75	0.5619	0.6372
4731 tRNA-adenylsuccinylase(20) synthase [NAD(P)+]-like	Q9NXC4	0.0599	0.1619	-0.19	0.8026	0.8574	0.02	0.0311	0.0534
4732 tRNA-dihydroxydipicolinate(20) synthase [NAD(P)+]-like	Q95620	0.6275	0.6901	0.29	0.6759	0.7628	-0.85	0.8830	0.9072
4733 tRNA-specific adenosine decaminase 1	Q9UBU4	0.2997	0.4987	-0.06	0.3085	0.6783	-0.09	0.9546	0.9641
4734 tRNA-splicing endonuclease subunit Sen15	Q8WW01	0.0247	0.0948	-0.19	0.0184	0.6649	-0.19	0.0018	0.0245
4735 tRNA-splicing ligase RtcH homolog	Q9Y330	0.1348	0.2784	0.37	0.2143	0.6619	-0.11	0.1305	0.2515
4736 Trophoblast glycoprotein	Q13641	0.0217	0.0875	0.16	0.7390	0.8508	0.05	0.2350	0.3959
4737 Tropomodulin-2	Q9NZR1	0.0632	0.1664	0.30	0.2634	0.6633	0.59	0.0192	0.0665
4738 Tropomodulin-3	Q9NYL9	0.0063	0.0475	0.09	0.3158	0.6810	0.07	0.9253	0.9418
4739 Tropomyosin-4	Q9NZQ9	0.0264	0.6227	-0.29	0.2684	0.6713	-0.54	0.1734	0.3151
4740 Tropomyosin alpha-1 chain	P09493	0.6771	0.7342	0.28	0.5899	0.7088	0.85	0.3892	0.5905
4741 Tropomyosin alpha-3 chain	P06753	0.1962	0.3651	0.08	0.3241	0.6855	0.20	0.0174	0.0629
4742 Tropomyosin alpha-4 chain	P67936	0.5053	0.5784	0.02	0.4140	0.7527	0.12	0.0277	0.0838
4743 Tropomyosin beta chain	P07951	0.0095	0.0572	-0.26	0.2076	0.6589	0.07	0.3564	0.5526
4744 Tropom C skeletal-associated factor	P02585	0.0013	0.0243	0.30	0.0234	0.4829	0.18	0.0038	0.0323
4745 TRPM channel-associated factor 1	Q9Y452	0.0060	0.0466	0.09	0.2836	0.6641	-0.11	0.4305	0.4956
4746 Trypanothione S-hydroxylase 1	P17752	0.0813	0.1965	-0.08	0.0411	0.5692	-0.13	0.2317	0.4187
4747 Trypanothione S-hydroxylase 2	Q8IWIU	0.4108	0.4974	-0.02	0.8417	0.8067	0.04	0.1258	0.2453
4748 Trypanothione-5 lyase cytoplasmic	P23381	0.0004	0.0159	0.33	0.1656	0.6619	0.23	0.0007	0.0206
4749 Trypanothione-5 lyase mitochondrial	Q9UGM6	0.4108	0.4998	-3.31	0.5752	0.6998	-1.75	0.5661	0.6371
4750 Ubiquitin-related protein 1	O0D924	0.0001	0.0088	0.80	0.0511	0.6316	0.53	0.0007	0.0210
4751 Ube2A	P49815	0.0384	0.1230	0.31	0.1412	0.6531	0.29	0.0052	0.0353
4752 Ube2B	A6NHL2	0.0961	0.2188	0.18	0.0613	0.5935	-0.23	0.0009	0.0218
4753 Ube2C	Q7U136	0.4108	0.4996	-3.31	0.5752	0.6996	-1.75	0.5661	0.6369
4754 Ube2D	Q9BOE3	0.0008	0.0202	0.34	0.1754	0.6613	0.26	0.0006	0.0194
4755 Ube2E	P0DPH7	0.1217	0.2582	-3.15	0.8655	0.9030	-0.21	0.0307	0.0893
4756 Ube2F	P68366	0.0263	0.0627	0.37	0.5466	0.8220	-0.05	0.0325	0.0926
4757 Ube2G	Q9NY65	0.0554	0.1540	0.23	0.3084	0.6783	0.14	0.8451	0.8757
4758 Ube2H	P07437	0.0137	0.0684	0.22	0.1345	0.6493	0.10	0.0041	0.0323
4759 Ube2I	Q9I4B7	0.0645	0.1681	-0.10	0.3741	0.7215	-0.03	0.1567	0.2894
4760 Ube2J	Q13885	0.1182	0.2529	-0.12	0.6920	0.7744	-0.04	0.0150	0.0574
4761 Ube2K	Q13509	0.0005	0.0174	0.35	0.0209	0.4748	0.36	0.0013	0.0237
4762 Ube2L	P49430	0.2665	0.4571	0.36	0.4571	0.6553	-0.72	0.0332	0.0785
4763 Ube2M	P68371	0.0060	0.0466	0.29	0.0188	0.2451	0.6582	0.21	0.0038
4764 Ube2N	Q9BUP5	0.1725	0.0651	0.38	0.1741	0.6612	0.24	0.0006	0.0195
4765 Ube2O	Q32M27	0.0197	0.3430	0.06	0.2441	0.6575	0.18	0.0071	0.0398
4766 Ube2P	A6NNZ2	0.0271	0.0998	-0.05	0.0980	0.6338	-0.16	0.6332	0.6865
4767 Ube2Q	P23258	0.0496	0.1433	-13.41	0.0397	0.5634	-11.85	0.0133	0.0539
4768 Ube2R	Q9NRH3	0.0006	0.0187	-4.05	0.2372	0.6624	-2.53	0.1947	0.3435
4769 Ube2S	Q99426	0.0300	0.1063	0.10	0.4916	0.8144	0.13	0.0018	0.0237
4770 Ube2T	Q75347	0.0420	0.1300	0.15	0.2153	0.6607	0.30	0.0111	0.0489
4771 Ube2U	Q15814	0.0785	0.1719	-0.16	0.0463	0.5630	-0.19	0.7289	0.7724

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

		MCF-7				MDA-MB-231							
		Dai IC20 vs control		Gen IC20 vs control		SSE IC20 vs control		Dai IC20 vs control		Gen IC20 vs control		SSE IC20 vs control	
Protein name	UniProt	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC
4772	Tubulin-specific chaperone D	Q9BTW9	0.0933	0.2149	0.11	0.1970	0.6705	0.30	0.0023	0.0267	0.43	0.0024	0.0545
4773	Tubulin-specific chaperone E	Q15813	0.4108	0.4995	-3.31	0.5752	0.6994	-1.75	0.5661	0.6368	-1.49	0.9774	0.0821
4774	Tubulin-tyrosine ligase-like protein 12	Q14166	0.0098	0.0577	0.12	0.0769	0.6128	0.09	0.0018	0.0243	0.26	0.0504	0.0823
4775	Tubulin-tyr carboxypeptidase 1	Q7L8A9	0.0261	0.0978	0.26	0.4813	0.8063	-0.24	0.0021	0.0257	0.64	0.0952	0.2326
4776	Tubulin-tyrosine ligase-like protein 12	Q9Y2W6	0.0322	0.1115	-0.19	0.0906	0.2230	-0.55	0.0014	0.0235	-0.48	0.1501	0.0651
4777	Tadpole domain-containing protein 6	Q60522	0.0074	0.0504	0.16	0.3216	0.6839	0.10	0.0004	0.0187	0.29	0.0512	0.0936
4778	Tubulin-interacting protein 11	Q9UBB9	0.4108	0.4994	-3.31	0.5752	0.6993	-1.75	0.5661	0.6366	-1.49	0.9772	0.1622
4779	Tumor necrosis factor alpha-induced protein 8	Q95379	0.4108	0.4993	-3.31	0.5752	0.6991	-1.75	0.5661	0.6365	-1.49	0.9770	0.1839
4780	Tumor necrosis factor receptor superfamily member EDAR	Q9UNE0	0.3295	0.5361	1.61	0.2704	0.6635	-1.84	0.0083	0.0429	1.60	0.8576	0.0651
4781	Tumor protein D52	P55327	0.1548	0.3069	-0.07	0.7304	0.8036	0.04	0.1305	0.2514	0.08	0.5435	0.7165
4782	Tumor protein D53	Q16890	0.1848	0.3496	-0.08	0.3646	0.7132	-0.16	0.5440	0.7668	0.04	0.3736	0.291
4783	Tumor protein D54	Q43399	0.1129	0.2447	0.12	0.8447	0.8883	0.01	0.0403	0.1071	0.23	0.0652	0.6819
4784	Tumor protein p53-inducible protein 11	Q14683	0.0179	0.0784	0.18	0.0443	0.5694	0.46	0.0204	0.0688	0.31	0.0733	0.1984
4785	Tumor suppressor candidate gene 1 protein	Q2TAM9	0.0522	0.1478	-0.18	0.4127	0.7525	0.10	0.0710	0.1588	-0.03	0.4324	0.261
4786	Tumor susceptibility gene 101 protein	Q99816	0.0043	0.0412	0.33	0.3145	0.6802	0.08	0.8630	0.8907	-0.01	0.0764	0.1614
4787	Tumor-associated calcium signal transducer 2	P09758	0.0104	0.0589	0.28	0.1658	0.6612	0.26	0.0014	0.0229	0.45	0.0987	0.0851
4788	Twinfilin-1	T12792	0.0539	0.1515	0.13	0.3914	0.7354	0.09	0.3058	0.4889	0.08	0.0328	0.7208
4789	Twinfilin-2	Q6IIB80	0.0003	0.0139	1.24	0.6685	0.7705	-0.01	0.0147	0.0570	-0.20	0.9630	0.0305
4790	Twisted gastrulation protein homolog 1	Q9GZX9	0.4108	0.4992	-3.31	0.5752	0.6989	-1.75	0.5661	0.6364	-1.49	0.9768	0.1654
4791	Twist-related protein 1	Q15672	0.0034	0.0376	1.07	0.0504	0.5738	0.30	0.2692	0.4417	0.13	0.0874	0.1599
4792	Type II insulin 1 4-5-phosphatase 5-phosphatase	P12019	0.1366	0.2811	-0.06	0.0176	0.4651	-0.12	0.9554	0.9645	0.00	0.1528	0.1690
4793	Type II insulin 3 4-phosphatase 4-phosphatase	U15327	0.0192	0.0814	-0.50	0.8187	0.8705	0.02	0.0309	0.0898	-0.39	0.0219	0.1877
4794	Type-1 anaplastic T-cell receptor-associated protein	Q6RW13	0.4108	0.4990	-3.31	0.5752	0.6988	-1.75	0.5661	0.6362	-1.49	0.9766	0.1256
4795	Tyrosine aminotransferase	P17735	0.4108	0.4989	-3.31	0.5752	0.6986	-1.75	0.5661	0.6361	-1.49	0.9749	0.0389
4796	Tyrosine-protein kinase BTK	Q60187	0.4108	0.4988	-3.31	0.5752	0.6984	-1.75	0.5661	0.6360	-1.49	0.9763	0.1295
4797	Tyrosine-protein kinase CSK	P14240	0.5610	0.6297	0.03	0.5331	0.8499	0.04	0.0431	0.1128	0.06	0.0956	0.1737
4798	Tyrosine-protein kinase Fer	P16591	0.0003	0.0138	0.80	0.0431	0.5695	1.78	0.0708	0.1584	-5.29	0.0067	0.1355
4799	Tyrosine-protein kinase Fgr	P09769	0.0376	0.1216	-0.21	0.0973	0.6340	0.16	0.2639	0.4341	-0.07	0.9776	0.2019
4800	Tyrosine-protein kinase HCK	P08631	0.1105	0.2413	0.07	0.0487	0.5746	0.12	0.8310	0.8637	-0.01	0.9877	0.3841
4801	Tyrosine-protein kinase JAK1	P23458	0.4108	0.4987	-3.31	0.5752	0.6983	-1.75	0.5661	0.6358	-1.49	0.9761	0.4659
4802	Tyrosine-protein kinase Lyn	P07948	0.4108	0.4986	-3.31	0.5752	0.6981	-1.75	0.5661	0.6357	-1.49	0.9739	0.4840
4803	Tyrosine-protein kinase receptor Tie-1	P35590	0.4108	0.4985	-3.31	0.5752	0.6979	-1.75	0.5661	0.6355	-1.49	0.9757	0.4408
4804	Tyrosine-protein kinase receptor UFO	P30530	0.4108	0.4983	-3.31	0.5752	0.6978	-1.75	0.5661	0.6354	-1.49	0.9755	0.3752
4805	Tyrosine-protein kinase transmembrane receptor ROR2	Q01974	0.4108	0.4982	-3.31	0.5752	0.6976	-1.75	0.5661	0.6353	-1.49	0.9753	0.8243
4806	Tyrosine-protein kinase Yes	P07947	0.6517	0.7128	-0.09	0.4483	0.7829	0.20	0.5060	0.7279	-0.13	0.3094	0.4459
4807	Tyrosine-protein kinase ZAP-70	P43403	0.2648	0.4563	0.49	0.9804	0.9867	-0.01	0.3402	0.5327	0.40	0.9539	0.049
4808	Tyrosine-protein phosphatase non-receptor type 1	P18031	0.0072	0.0446	0.24	0.1651	0.6609	0.29	0.0005	0.0195	0.49	0.1526	0.7215
4809	Tyrosine-protein phosphatase non-receptor type 11	Q60124	0.0642	0.2004	0.10	0.0127	0.6318	0.16	0.0108	0.0485	0.28	0.0603	0.5576
4810	Tyrosine-protein phosphatase non-receptor type 12	Q05209	0.7910	0.8308	0.13	0.4379	0.7742	-0.39	0.6527	0.7044	-0.23	0.2976	0.4410
4811	Tyrosine-protein phosphatase non-receptor type 13	T12923	0.2074	0.3798	0.09	0.0290	0.9873	0.00	0.0599	0.1415	-0.17	0.0669	0.1655
4812	Tyrosine-protein phosphatase non-receptor type 2	P17706	0.4108	0.4981	-3.31	0.5752	0.6975	-1.75	0.5661	0.6351	-1.49	0.9769	0.0489
4813	Tyrosine-protein phosphatase non-receptor type 20	Q4JDL3	0.4451	0.5227	-0.04	0.8963	0.9267	-0.01	0.0859	0.1826	-0.09	0.0828	0.1582
4814	Tyrosine-protein phosphatase non-receptor type 23	Q9H387	0.1093	0.2392	0.06	0.9635	0.9754	0.00	0.4072	0.6126	0.03	0.0836	0.1448
4815	Tyrosine-protein phosphatase non-receptor type 26	P29350	0.0662	0.1704	-0.10	0.2655	0.6631	0.14	0.3917	0.5935	0.04	0.0462	0.1798
4816	Tyrosine-tRNA ligase cytoplasmic	P54577	0.0190	0.0809	0.18	0.2815	0.6649	0.20	0.0073	0.0404	0.23	0.0017	0.2579
4817	Tyrosine-tRNA ligase mitochondrial	Q9Y2Z4	0.0011	0.0223	0.25	0.2984	0.6692	-1.51	0.0580	0.1383	-5.92	0.0687	0.0589
4818	Tyrosyl-DNA phosphodiesterase 1	Q9NUW8	0.1730	0.3343	0.50	0.3599	0.7083	0.36	0.1536	0.2850	0.53	0.3812	0.1265
4819	Tyrosyl-DNA phosphodiesterase 2	O95551	0.4108	0.4980	-3.31	0.5752	0.6973	-1.75	0.5661	0.6350	-1.49	0.9749	0.1829
4820	U1 small nuclear ribonucleoprotein 70 kDa	P08621	0.0393	0.1247	0.15	0.5795	0.6874	0.09	0.0040	0.0318	0.34	0.3739	0.1511
4821	U1 small nuclear ribonucleoprotein A	P09012	0.0651	0.1689	-0.11	0.8254	0.8745	-0.03	0.2551	0.4230	0.07	0.0502	0.1035
4822	U1 small nuclear ribonucleoprotein C	P09234	0.2099	0.3826	-0.13	0.0002	0.2072	-0.46	0.4455	0.1174	-0.15	0.0129	0.5072
4823	U1/U12 small nuclear ribonucleoprotein 35 kDa protein	Q16560	0.4108	0.4979	-3.31	0.5752	0.6971	-1.75	0.5661	0.6349	-1.49	0.9739	0.1218
4824	U2 small nuclear ribonucleoprotein A'	P09661	0.0147	0.0704	0.30	0.0475	0.5696	0.21	0.0052	0.0353	0.16	0.0563	0.1802
4825	U2 small nuclear ribonucleoprotein B'	P08759	0.0190	0.0809	0.23	0.2134	0.6657	0.42	0.0128	0.0531	0.34	0.0617	0.0427
4826	U3 small nuclear ribonucleoprotein protein IMP3	Q9NU31	0.2059	0.3785	0.18	0.8628	0.9099	0.04	0.9851	0.1493	0.26	0.0134	0.1519
4827	U3 small nuclear ribonucleoprotein protein IMP4	P09621	0.2037	0.3754	-0.52	0.5435	0.8578	-0.29	0.1100	0.7560	-0.13	0.0526	0.0861
4828	U3 small nuclear RNA-associated protein 14 homolog A	Q9BV16	0.0878	0.2062	-0.24	0.1561	0.6628	-0.51	0.4730	0.6904	0.08	0.1734	0.5681
4829	U3 small nuclear RNA-associated protein 18 homolog	Q9Y5J1	0.2200	0.3962	-0.13	0.4093	0.7505	-0.07	0.0642	0.1477	-0.22	0.1263	0.1596
4830	U3 small nuclear RNA-associated protein 6 homolog	Q9NYH9	0.4108	0.4978	-3.31	0.5752	0.6970	-1.75	0.5661	0.6347	-1.49	0.9738	0.6856
4831	U4/U6 small nuclear ribonucleoprotein Prp3	Q43395	0.6923	0.7473	0.02	0.5443	0.6623	0.10	0.1078	0.2168	0.09	0.0375	0.1637
4832	U4/U6 small nuclear ribonucleoprotein Prp31	Q8WVY3	0.7798	0.8208	-0.02	0.5528	0.8683	0.05	0.4693	0.6867	0.07	0.6101	0.5131
4833	U4/U6 small nuclear ribonucleoprotein Prp3	Q43172	0.0640	0.1674	0.16	0.1429	0.6545	-0.12	0.0769	0.1674	0.18	0.6913	0.2917
4834	U4/U6/U5 tri-snRNP-associated protein 1	Q43290	0.1518	0.3025	-0.05	0.3257	0.6853	-0.03	0.5026	0.7248	-0.02	0.0514	0.1365
4835	U4/U6/U5 tri-snRNP-associated protein 2	Q53G59	0.0609	0.1634	0.14	0.2116	0.6589	0.17	0.0248	0.0781	0.07	0.0032	0.1967
4836	U5 small nuclear ribonucleoprotein 200 kDa helicase	Q75643	0.4108	0.4976	-3.31	0.5752	0.6968	-1.75	0.5661	0.6346	-1.49	0.9748	0.0427
4837	U6 snRNP-associated Sm-like protein LSm2	Q9Y333	0.0431	0.1316	-0.36	0.5587	0.8722	-0.10	0.8616	0.9653	-0.27	0.0317	0.0941
4838	U6 snRNP-associated Sm-like protein LSm4	Q9Y420	0.2001	0.3708	0.13	0.8017	0.8570	0.04	0.6863	0.7533	0.03	0.0282	0.2004
4839	U6 snRNP-associated Sm-like protein LSm8	Q9Y577	0.5156	0.5880	-0.16	0.0417	0.7453	-0.48	0.4485	0.6619	-0.18	0.4006	0.1334
4840	Ubiquitin-1	Q9UMX0	0.2809	0.4744	-0.02	0.2120	0.6619	-0.13	0.0093	0.0451	-0.12	0.0167	0.7538
4841	Ubiquitin-2	Q9UID9	0.0379	0.1222	0.15	0.1960	0.6688	0.18	0.0037	0.0317	0.33	0.0002	0.4910
4842	Ubiquitin-4	Q9NRR5	0.1628	0.3196	-0.05								



Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
4853 Ubiquitin carboxyl-terminal hydrolase 30	Q70CQ3	0.4108	0.4973	-3.31	0.5752	0.6963	-1.75	0.5661	0.6342	-1.19	0.5388	0.6001	0.89	0.2938	0.3993	-1.88	0.9510	0.9737	0.09	0.0204	0.1319	-7.72	0.4360	0.8365	0.10	0.0015	0.0468	1.42
4854 Ubiquitin carboxyl-terminal hydrolase 32	Q8NFA0	0.0257	0.0969	0.14	0.0399	0.5632	0.14	0.0199	0.0681	0.20	0.0968	0.1894	0.16	0.0929	0.2404	0.08	0.1437	0.2991	0.12	0.3736	0.5190	-2.55	0.8708	1.0681	-0.33	0.0651	0.1497	2.06
4855 Ubiquitin carboxyl-terminal hydrolase 34	Q70CQ2	0.0034	0.0376	0.11	0.2782	0.6653	0.19	0.0003	0.0197	0.34	0.0004	0.0130	0.21	0.5513	0.6346	0.01	0.0146	0.0804	0.15	0.1350	0.3130	0.08	0.4052	0.7903	0.04	0.0623	0.2232	0.12
4856 Ubiquitin carboxyl-terminal hydrolase 47	Q96K76	0.0049	0.0429	0.17	0.1427	0.6553	0.20	0.0166	0.0611	0.14	0.0557	0.1247	0.09	0.0019	0.0345	0.22	0.0258	0.1023	0.17	0.1303	0.3053	0.28	0.0323	0.1621	0.39	0.4334	0.5946	0.13
4857 Ubiquitin carboxyl-terminal hydrolase 48	Q96K75	0.4108	0.4972	-3.31	0.5752	0.6962	-1.75	0.5661	0.6340	-1.19	0.5388	0.6000	0.89	0.2938	0.3992	-1.88	0.9510	0.9736	0.09	0.0544	0.1851	0.37	0.5478	0.9734	-0.07	0.0883	0.1374	-0.21
4858 Ubiquitin carboxyl-terminal hydrolase 49	Q70CQ1	0.5123	0.5849	-0.04	0.3871	0.7294	0.10	0.9645	0.9714	0.00	0.6779	1.1444	0.19	0.1518	0.3298	0.12	0.9290	1.1663	-0.01	0.3736	0.4327	-2.55	0.8708	0.9083	-0.33	0.0651	0.1126	-2.06
4859 Ubiquitin carboxyl-terminal hydrolase 5	P45974	0.0223	0.0889	0.05	0.0970	0.6344	0.19	0.0045	0.0332	0.20	0.0004	0.0118	0.24	0.0026	0.0396	0.12	0.0030	0.0557	0.17	0.0346	0.1545	0.41	0.266	0.3713	0.15	0.3139	0.3851	0.08
4860 Ubiquitin carboxyl-terminal hydrolase 7	Q93009	0.0235	0.0921	0.18	0.3404	0.6992	0.07	0.0167	0.0612	0.23	0.0302	0.0807	0.15	0.0583	0.1813	-0.12	0.0284	0.1079	0.18	0.9918	0.9937	0.00	0.0923	0.3018	0.28	0.0479	0.1912	0.40
4861 Ubiquitin carboxyl-terminal hydrolase 8	P40818	0.0451	0.1354	-0.09	0.5011	0.8230	0.11	0.1157	0.2294	0.10	0.1010	0.0421	0.14	0.6970	0.7590	0.01	0.5516	0.7856	0.02	0.0255	0.1396	0.26	0.0626	0.2395	0.15	0.0860	0.1383	0.22
4862 Ubiquitin carboxyl-terminal hydrolase isozyme L3	P15374	0.1150	0.2483	0.25	0.0201	0.4733	0.41	0.0008	0.0223	0.46	0.0037	0.0247	0.38	0.0029	0.0412	0.33	0.0343	0.1196	0.56	0.1826	0.3839	-0.08	0.2037	0.5034	-0.07	0.2914	0.3633	-0.05
4863 Ubiquitin carboxyl-terminal hydrolase isozyme L5	Q9Y5K5	0.0195	0.0819	0.12	0.6999	0.7787	0.04	0.0154	0.0583	0.14	0.0671	0.1432	0.08	0.0553	0.1754	-0.09	0.0879	0.2159	0.07	0.0108	0.1021	-0.28	0.0167	0.1098	-0.17	0.0316	0.1510	-0.17
4864 Ubiquitin conjugation factor E4 A	Q14139	0.7841	0.8247	-0.01	0.0569	0.5848	0.35	0.0014	0.0230	0.24	0.0258	0.0722	0.23	0.0004	0.0162	0.22	0.1352	0.2873	0.07	0.3736	0.5221	-2.55	0.8708	1.0737	-0.33	0.0651	0.1512	-2.06
4865 Ubiquitin conjugation factor E4 B	O95155	0.4108	0.4971	-3.31	0.5752	0.6960	-1.75	0.5661	0.6339	-1.19	0.5388	0.5998	0.89	0.2938	0.3991	-1.88	0.9510	0.9734	0.09	0.0717	0.2120	0.29	0.747	1.1836	0.02	0.4018	0.4735	0.08
4866 Ubiquitin domain-containing protein UBFD1	U14562	0.2088	0.3816	-0.05	0.6250	0.7225	0.14	0.1131	0.2252	0.13	0.0162	0.0528	0.14	0.2401	0.4533	-0.05	0.6274	0.8632	-0.04	0.3736	0.4495	-2.55	0.8708	0.9399	-0.33	0.0651	0.1193	-2.06
4867 Ubiquitin recognition factor in ER-associated degradation protein 1	Q92890	0.0598	0.1818	-0.35	0.3050	0.6772	-0.08	0.0547	0.1330	-0.36	0.4716	0.6711	-0.05	0.0521	0.1691	-0.19	0.0138	0.0780	-0.34	0.1010	0.2572	-1.24	0.0416	0.1877	-0.66	0.0246	0.1329	-2.04
4868 Ubiquitin thioesterase	Q96FW1	0.1315	0.2735	0.09	0.2633	0.6634	0.25	0.0407	0.1078	0.16	0.0095	0.0391	0.25	0.1178	0.2816	0.09	0.0218	0.0951	0.25	0.8637	0.8868	0.02	0.0485	0.2059	-0.25	0.0397	0.1724	-0.28
4869 Ubiquitin thioesterase outlin	Q96BN8	0.0201	0.0835	-0.14	0.0070	0.4168	-0.19	0.0004	0.0241	-0.43	0.0036	0.0242	-0.25	0.0008	0.0218	-0.44	0.0370	0.1248	0.12	0.1030	0.2606	0.18	0.0253	0.1421	-0.22	0.0454	0.5268	-0.04
4870 Ubiquitin-40S ribosomal protein S27a	P62979	0.0006	0.0186	0.55	0.0601	0.5953	0.62	0.0002	0.0220	0.74	0.0001	0.0136	0.87	0.0028	0.0407	-1.48	0.0027	0.0559	0.74	0.0118	0.1045	0.60	0.5866	1.0190	0.06	0.0532	0.2034	0.21
4871 Ubiquitin-associated and SH3 domain-containing protein B	Q8T142	0.4108	0.4970	-3.31	0.5752	0.6958	-1.75	0.5661	0.6338	-1.19	0.5388	0.5997	0.89	0.2938	0.3990	-1.88	0.9510	0.9732	0.09	0.0223	0.1356	0.22	0.2856	0.6240	-0.07	0.0518	0.6258	0.05
4872 Ubiquitin-associated domain-containing protein 2	Q8NBM4	0.1768	0.3391	-0.14	0.4649	0.7964	0.06	0.0530	0.1304	-0.18	0.0813	0.1662	0.18	0.0039	0.0460	0.65	0.6884	0.9284	-0.06	0.3736	0.4456	-2.55	0.8708	0.9325	-0.33	0.0651	0.1177	-2.06
4873 Ubiquitin-associated domain-2-like	Q14157	0.0031	0.0362	0.39	0.1667	0.6597	0.31	0.0013	0.0231	0.36	0.0015	0.0178	0.32	0.0941	0.2429	0.09	0.0091	0.0689	0.28	0.0310	0.1488	0.37	0.6441	1.0822	0.04	0.6683	0.7226	0.03
4874 Ubiquitin-conjugating enzyme E2 C	U00762	0.5296	0.6008	-0.08	0.1174	0.6322	-1.10	0.5033	0.7256	-0.18	0.2747	0.4320	-0.26	0.1279	0.2955	-0.41	0.0967	0.2295	-0.18	0.3375	0.6081	-0.28	0.7387	1.1810	-0.11	0.3572	0.4285	-0.02
4875 Ubiquitin-conjugating enzyme E2 D3	P61077	0.0104	0.0588	-0.24	0.2426	0.6597	-0.16	0.3214	0.5090	0.10	0.0006	0.0123	-0.48	0.0015	0.0306	-0.31	0.5141	0.7414	-0.08	0.0004	0.0377	-1.33	0.0374	0.1766	-0.24	0.0007	0.0321	-1.08
4876 Ubiquitin-conjugating enzyme E2 E1	P51965	0.0004	0.0157	0.46	0.0998	0.6359	0.36	0.0002	0.0195	0.63	0.0000	0.0000	0.59	0.0083	0.0659	0.22	0.0001	0.0273	0.89	0.0066	0.0848	-1.32	0.0002	0.0173	-1.07	0.0513	0.1989	-0.92
4877 Ubiquitin-conjugating enzyme E2 G2	P60604	0.4769	0.5524	-0.08	0.9403	0.9601	-0.01	0.1002	0.2042	0.18	0.5715	0.6214	0.05	0.0505	0.1660	0.30	0.1143	0.2569	0.18	0.3736	0.5298	-2.55	0.8708	1.0877	-0.33	0.0651	0.1550	-2.06
4878 Ubiquitin-conjugating enzyme E2 J1	Q9Y385	0.2059	0.3783	0.80	0.7402	0.8411	-0.19	0.2605	0.4296	0.63	0.2731	0.4301	0.60	0.3644	0.4612	0.49	0.3224	0.5252	0.53	0.3736	0.4778	-2.55	0.8708	0.9927	-0.33	0.0651	0.1311	-2.06
4879 Ubiquitin-conjugating enzyme E2 K1	P61086	0.0435	0.1323	0.20	0.0145	0.4771	0.30	0.1857	0.3309	0.11	0.0025	0.0209	0.51	0.0586	0.1819	0.20	0.4518	0.6739	-0.05	0.0183	0.1256	-0.35	0.0050	0.0567	-0.23	0.0046	0.0666	-0.27
4880 Ubiquitin-conjugating enzyme E2 L3	P68036	0.0292	0.1044	0.15	0.2414	0.6602	0.19	0.1864	0.3317	0.09	0.0177	0.0561	0.17	0.1185	0.2824	-0.08	0.1519	0.3095	0.07	0.0661	0.2021	0.48	0.0614	0.2368	0.23	0.0855	0.1378	-0.20
4881 Ubiquitin-conjugating enzyme E2 N1	P61088	0.0219	0.0879	0.11	0.2577	0.6625	0.11	0.0728	0.1614	0.14	0.0004	0.0111	0.22	0.7598	0.8122	-0.01	0.0413	0.0796	0.21	0.3494	0.6243	-0.12	0.1110	0.3398	-0.19	0.2607	0.3328	-0.08
4882 Ubiquitin-conjugating enzyme E2 S	U16763	0.4108	0.4968	-3.31	0.5752	0.6957	-1.75	0.5661	0.6336	-1.19	0.5388	0.5996	0.89	0.2938	0.3989	-1.88	0.9510	0.9730	0.09	0.8425	0.8675	0.02	0.0464	0.2005	0.43	0.4827	0.5510	-0.09
4883 Ubiquitin-conjugating enzyme E2 T	Q9NPD8	0.0281	0.1018	-0.41	0.2046	0.6595	-0.19	0.0911	0.1900	-0.21	0.7801	0.8109	0.03	0.0759	0.2118	-0.24	0.0164	0.0850	-0.45	0.0169	0.1209	0.19	0.3323	0.6894	0.04	0.9576	0.9666	-0.01
4884 Ubiquitin-conjugating enzyme E2 variant 1	U13404	0.0185	0.0799	0.23	0.2662	0.6629	0.18	0.1037	0.2100	0.11	0.0229	0.0664	0.20	0.1045	0.2604	0.10	0.0298	0.1107	0.20	0.0809	0.2266	0.25	0.0459	0.1993	0.26	0.0542	0.2051	-0.20
4885 Ubiquitin-conjugating enzyme E2 variant 2	U15819	0.3113	0.5124	0.07	0.3267	0.6863	0.20	0.0417	0.1101	0.19	0.0165	0.0535	0.26	0.9358	0.9640	0.00	0.0576	0.1165	0.19	0.1020	0.1039	-0.24	0.3553	0.7209	-0.06	0.0201	0.1716	-0.21
4886 Ubiquitin-conjugating enzyme E2 Z	Q9H832	0.0070	0.0492	0.16	0.3498	0.7048	0.15	0.0036	0.0314	0.29	0.0195	0.0594	0.07	0.0045	0.0499	-0.11	0.0012	0.0486	0.24	0.0628	0.1974	0.32	0.4098	0.7968	-0.07	0.3966	0.4681	-0.05
4887 Ubiquitin-fold modifier 1	P61969	0.0038	0.0390	0.21	0.0212	0.4754	-0.50	0.0245	0.0734	-0.25	0.0008	0.0000	-0.54	0.0011	0.0066	-0.45	0.0060	0.0624	0.32	0.0313	0.1406	-0.84	0.0000	0.0000	-0.50	0.0000	0.0000	-1.16
4888 Ubiquitin-fold modifier-conjugating enzyme 1	Q9Y3C8	0.5339	0.5405	-0.07	0.2908	0.6717	0.17	0.5836	0.6401	-0.05	0.6526	0.6963	-0.03	0.7330	0.7909	-0.02	0.3899	0.4247	-0.10	0.3736	0.4927	-2.55	0.8708	1.0201	-0.33	0.0651	0.1376	-2.06
4889 Ubiquitin-like domain-containing CTD phosphatase 1	Q8WYV7	0.4152	0.4931	0.04	0.6299	0.7265	-0.05	0.1959	0.3452	-0.27	0.9175	0.9283	-0.01	0.0667	0.0593	-0.26	0.0917	0.2214	0.11	0.0760	0.2194	0.29	0.1108	0.3400	0.13	0.0968	0.0762	-0.18
4890 Ubiquitin-like modifier-activating enzyme 1	P22314	0.0869	0.2049	0.15	0.1003	0.6697	0.24	0.0317	0.0911	0.22	0.0471	0.1104	0.21	0.5727	0.6526	0.04	0.0282	0.1073	0.28	0.0195	0.1293	0.44	0.1366	0.3905	0.17	0.351		

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

		MCF-7				MDA-MB-231																						
		Dai SC20 vs control		Gen SC20 vs control		SSE SC20 vs control		Dai IC20 vs control		Gen IC20 vs control		SSE IC20 vs control																
Protein name	UniProt	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC															
4934 Uncharacterized protein KIAA1841	Q6NS18	0.4108	0.4954	-3.31	0.5752	0.6937	-1.75	0.5661	0.6320	-1.19	0.5388	0.5980	0.89	0.2938	0.3977	-1.88	0.9510	0.9707	0.09	0.0111	0.1029	-0.37	0.6602	1.1007	0.03	0.1097	0.1667	-0.16
4935 Uncharacterized protein KIAA1958	Q8HNK9	0.4108	0.4953	-3.31	0.5752	0.6936	-1.75	0.5661	0.6318	-1.19	0.5388	0.5979	0.89	0.2938	0.3976	-1.88	0.9510	0.9705	0.09	0.0244	0.8517	-0.03	0.0555	0.2246	0.36	0.1495	0.2122	0.41
4936 Uncharacterized protein KIAA2026	Q5HYC2	0.3415	0.5490	-0.07	0.2669	0.6628	0.13	0.1355	0.2584	0.13	0.0551	0.0895	0.26	0.7021	0.7634	-0.03	0.7992	1.0365	0.02	0.3736	0.4387	-2.55	0.8708	0.9196	-0.33	0.0651	0.1510	2.06
4937 Unconventional myosin-Ib	Q13795	0.4089	0.5359	-0.16	0.6306	0.7269	-0.06	0.3630	0.5605	-0.07	0.8336	0.5684	0.07	0.0297	0.1255	-0.26	0.4010	0.4269	0.10	0.3736	0.4918	-2.55	0.8708	1.0185	-0.33	0.0651	0.1372	2.06
4938 Unconventional myosin-Ib	Q9H179	0.0842	0.2003	-0.07	0.3467	0.6445	0.01	0.1393	0.2637	0.04	0.0426	0.32	0.2351	0.4467	0.07	0.2998	0.4129	0.10	0.3736	0.4248	-2.55	0.8708	0.9070	-0.01	0.2792	0.3510	-0.07	
4939 Unconventional myosin-Ib	Q9H432	0.7857	0.8259	0.01	0.9800	0.9913	0.00	0.1842	0.3289	0.08	0.9198	0.9297	-0.01	0.2294	0.3949	-0.08	0.2553	0.4454	0.07	0.3736	0.6271	0.06	0.0614	0.2366	-0.25	0.0202	0.1220	0.41
4940 Unconventional myosin-Ib	Q12965	0.6330	0.6950	-0.21	0.8157	0.8682	-0.11	0.5160	0.7361	-0.29	0.4064	0.5975	-0.39	0.4502	0.5435	-0.39	0.5321	0.7629	-0.28	0.0774	0.2215	-0.13	0.0065	0.0658	-0.29	0.2144	0.2832	-0.06
4941 Unconventional myosin-Ib	Q8N1T3	0.4108	0.4952	-3.31	0.5752	0.6934	-1.75	0.5661	0.6317	-1.19	0.5388	0.5978	0.89	0.2938	0.3975	-1.88	0.9510	0.9703	0.09	0.0834	0.2307	0.28	0.1567	0.4286	-0.17	0.1555	0.2189	0.27
4942 Unconventional myosin-Dxa	B2RTY4	0.6817	0.7383	-0.03	0.0765	0.6144	0.24	0.5397	0.7618	0.05	0.0499	0.1148	0.18	0.2488	0.4658	-0.08	0.5299	0.7604	0.04	0.3736	0.4584	-2.55	0.8708	0.9565	-0.33	0.0651	0.1229	2.06
4943 Unconventional myosin-Dxb	Q13459	0.4108	0.4951	-3.31	0.5752	0.6932	-1.75	0.5661	0.6316	-1.19	0.5388	0.5976	0.89	0.2938	0.3974	-1.88	0.9510	0.9701	0.09	0.0737	0.2153	0.20	0.0374	0.1760	0.17	0.0690	0.1165	0.14
4944 Unconventional myosin-Va	Q9Y411	0.2993	0.4982	-0.09	0.1372	0.6508	0.14	0.8144	0.8497	0.02	0.0316	0.0833	0.26	0.4013	0.4977	0.08	0.1613	0.3226	-0.13	0.3736	0.5117	-2.55	0.8708	1.0549	-0.33	0.0651	0.1463	2.06
4945 Unconventional myosin-Vb	Q9ULV0	0.0033	0.0375	0.32	0.0581	0.5867	0.33	0.0055	0.0361	0.33	0.0058	0.0306	0.25	0.0314	0.1299	0.13	0.0181	0.0372	0.22	0.7089	0.7500	-0.01	0.0983	0.3139	-0.11	0.0535	0.2039	-0.07
4946 Unconventional myosin-Vc	Q9NQX4	0.4108	0.4950	-3.31	0.5752	0.6931	-1.75	0.5661	0.6314	-1.19	0.5388	0.5975	0.89	0.2938	0.3973	-1.88	0.9510	0.9699	0.09	0.2522	0.5780	-0.07	0.5657	0.9933	-0.07	0.1102	0.1671	-0.16
4947 Unconventional myosin-VI	Q9ULM4	0.8687	0.8960	-0.01	0.4791	0.8045	-0.12	0.8886	0.9117	0.01	0.1239	0.2274	0.08	0.2247	0.3335	-0.06	0.0440	0.1381	0.16	0.2133	0.1341	0.30	0.0002	0.0162	0.23	0.0604	0.2196	0.31
4948 Unconventional myosin-VIb	Q6PIE6	0.4108	0.4949	-3.31	0.5752	0.6929	-1.75	0.5661	0.6313	-1.19	0.5388	0.5974	0.89	0.2938	0.3972	-1.88	0.9510	0.9697	0.09	0.0971	0.9975	0.00	0.1392	0.3957	0.10	0.0076	0.0784	0.28
4949 Unconventional myosin-VIIIb	Q18UIG5	0.3719	0.5864	-0.11	0.4875	0.8109	0.09	0.2139	0.3684	-0.17	0.0973	0.1903	-0.26	0.9289	0.9463	0.01	0.1409	0.2947	-0.22	0.3736	0.5195	-2.55	0.8708	1.0692	-0.33	0.0651	0.1500	2.06
4950 UPF0160 protein MYG1 mitochondrial	Q9H1B07	0.0473	0.5462	0.05	0.0219	0.6602	0.21	0.6806	0.7304	-0.07	0.7011	0.1480	0.13	0.3208	0.4178	-0.06	0.0671	0.1819	0.13	0.6421	0.6688	-0.05	0.2343	0.5339	0.14	0.0400	0.1731	-0.17
4951 UPF0487 protein C5orf33	Q9H1T9	0.0011	0.2604	0.11	0.1814	0.6445	0.01	0.1393	0.2637	0.04	0.0426	0.32	0.2351	0.4467	0.07	0.2998	0.4129	0.10	0.3736	0.4248	-2.55	0.8708	0.9070	-0.01	0.2792	0.3510	-0.07	
4952 UPF0487 protein C5orf33	Q9H1T9	0.0011	0.2604	0.11	0.1814	0.6445	0.01	0.1393	0.2637	0.04	0.0426	0.32	0.2351	0.4467	0.07	0.2998	0.4129	0.10	0.3736	0.4248	-2.55	0.8708	0.9070	-0.01	0.2792	0.3510	-0.07	
4953 UPF0487 protein C5orf33	Q9H1T9	0.0011	0.2604	0.11	0.1814	0.6445	0.01	0.1393	0.2637	0.04	0.0426	0.32	0.2351	0.4467	0.07	0.2998	0.4129	0.10	0.3736	0.4248	-2.55	0.8708	0.9070	-0.01	0.2792	0.3510	-0.07	
4954 UPF0600 protein C5orf51	Q6NDU8	0.5407	0.6109	0.05	0.0103	0.4446	0.29	0.0944	0.1954	-0.18	0.2188	0.3573	-0.09	0.1144	0.2765	0.17	0.7169	0.9569	-0.03	0.0490	0.1765	-0.41	0.0787	0.2751	-0.35	0.6314	0.6883	-0.05
4955 UPF0687 protein C20orf27	Q9GZN8	0.0568	0.1562	-0.14	0.0158	0.4572	-0.23	0.0109	0.0485	-0.26	0.0600	0.0311	-0.34	0.0319	0.0842	-0.28	0.0555	0.1608	-0.42	0.1155	0.2823	0.08	0.3609	0.7286	-0.04	0.1444	0.2062	-0.08
4956 UPF0711 protein C18orf21	Q32NCO	0.4108	0.4948	-3.31	0.5752	0.6928	-1.75	0.5661	0.6312	-1.19	0.5388	0.5973	0.89	0.2938	0.3970	-1.88	0.9510	0.9695	0.09	0.0004	0.0334	1.00	0.0000	0.0000	1.61	0.0216	0.1257	0.41
4957 Up-regulated during skeletal muscle growth protein 5	Q96IX5	0.0175	0.0772	0.14	0.2572	0.6632	0.17	0.0563	0.1357	0.10	0.0982	0.1273	0.11	0.0082	0.0652	0.18	0.0297	0.1106	0.15	0.0741	0.2161	0.17	0.2746	0.6102	0.13	0.0443	0.0840	-0.24
4957 Up-regulator of cell proliferation	Q8TCY9	0.0014	0.0250	-0.43	0.0570	0.5847	-0.46	0.1273	0.2472	-0.14	0.0003	0.0101	-0.87	0.0086	0.0666	-0.30	0.1140	0.2565	-0.46	0.3736	0.5299	-2.55	0.8708	1.0880	-0.33	0.0651	0.1550	2.06
4958 Upstream-binding factor 1-like protein 1	POCB47	0.2073	0.2737	0.27	0.5324	0.8499	-0.11	0.9613	0.9686	0.01	0.0789	0.1624	-0.06	0.0796	0.5057	-0.39	0.2313	0.4149	-0.24	0.3736	0.4947	-2.55	0.8708	1.0238	-0.33	0.0651	0.1385	2.06
4959 Uracil-DNA glycosylase	P13051	0.0014	0.0249	-0.25	0.0598	0.6634	-0.15	0.0034	0.0312	-0.17	0.0093	0.0388	-0.36	0.0001	0.0094	-0.35	0.1348	0.2871	-0.42	0.3736	0.5223	-2.55	0.8708	1.0742	-0.33	0.0651	0.1514	2.06
4960 Uracine-5-monophosphate synthase	P11172	0.8196	0.8547	-0.01	0.1230	0.6403	-0.17	0.0166	0.0612	-0.30	0.0106	0.0413	-0.32	0.0026	0.0393	-0.51	0.0209	0.0937	-0.28	0.1435	0.3260	-0.34	0.8701	1.3121	0.03	0.2205	0.2900	-0.20
4961 Uridine phosphorylase 1	Q16831	0.4108	0.4946	-3.31	0.5752	0.6926	-1.75	0.5661	0.6310	-1.19	0.5388	0.5971	0.89	0.2938	0.3969	-1.88	0.9510	0.9693	0.09	0.0829	0.2300	0.19	0.5826	1.0144	0.05	0.1466	0.2297	-0.11
4962 Uridine-cytidine kinase 2	Q9HBX22	0.3387	0.5467	-0.24	0.0356	0.5376	-0.10	0.2203	0.3772	-0.17	0.0426	0.1026	-0.42	0.0039	0.0461	-0.20	0.0035	0.0596	-0.24	0.0500	0.1785	-0.17	0.0107	0.0847	-0.19	0.0334	0.1566	-0.26
4963 Uridine-thymidine phosphorylase	Q9H132	0.0310	0.1087	0.08	0.0162	0.8785	-0.04	0.6760	0.7262	-0.03	0.1032	0.18	0.0603	0.1946	0.17	0.0787	0.0937	0.10	0.0475	0.1289	0.07	0.0554	0.1698	0.07	0.0354	0.1498	0.28	
4964 Uridine-thymidine phosphorylase	Q16831	0.0126	0.0655	-0.19	0.2400	0.6581	-0.08	0.9451	0.9571	0.00	0.4179	0.6100	-0.04	0.7872	0.8329	-0.01	0.8545	1.0897	0.01	0.0193	0.1287	-0.28	0.3707	0.7428	0.07	0.5913	0.6527	0.04
4965 Urothrin	P46939	0.4108	0.4945	-3.31	0.5752	0.6924	-1.75	0.5661	0.6309	-1.19	0.5388	0.5970	0.89	0.2938	0.3968	-1.88	0.9510	0.9691	0.09	0.2494	0.4851	0.18	0.1761	0.4609	-0.12	0.0599	0.2187	-0.23
4966 UV excision repair protein RAD23 homolog A	P54725	0.6765	0.7337	-0.12	0.5725	0.8850	-0.19	0.0575	0.1373	0.80	0.0170	0.0544	-1.25	0.0247	0.1137	-1.38	0.0279	0.1069	-1.11	0.3736	0.5824	-2.55	0.8708	1.1818	-0.33	0.0651	0.1827	2.06
4967 UV excision repair protein RAD23 homolog B	P54727	0.5138	0.5864	0.04	0.2455	0.6582	0.23	0.0221	0.0725	0.25	0.0472	0.1106	0.18	0.7398	0.7965	-0.02	0.0621	0.1733	0.19	0.1062	0.2665	0.35	0.5439	0.9698	-0.05	0.6566	0.7118	0.03
4968 Uveal autotransmembrane with coiled-coil domains and ankyrin repeats	Q9H2B9	0.0093	0.0569	0.10	0.1561	0.6633	0.15	0.0746	0.1637	0.13	0.0015	0.0171	0.17	0.0008	0.0222	0.15	0.1591	0.3193	0.05	0.3736	0.5124	-2.55	0.8708	1.0561	-0.33	0.0651	0.1466	2.06
4969 Vacuolar fusion protein CCZ1 homolog B	P86790	0.0064	0.0478	-0.17	0.9323	0.9544	-0.01	0.2276	0.3688	-0.17	0.0932	0.1838	-0.10	0.3029	0.4007	-0.15	0.0100	0.0702	-0.18	0.3736	0.6130	-2.55	0.8708	1.2355	-0.33	0.0651	0.2007	2.06
4970 Vacuolar fusion protein MON1 homolog A	Q86VX9	0.4108	0.4948	-3.31	0.5752	0.6923	-1.75	0.5661	0.6308	-1.19	0.5388	0.5969	0.89	0.2938	0.3967	-1.88	0.9510	0.9690	0.09	0.0019	0.0521	-0.92	0.0009	0.0266	0.85	0.0069	0.0772	0.71
4971 Vacuolar fusion protein MON1 homolog B	Q7L1V2	0.0133	0.0671	0.65	0.0800	0.6121	-0.33	0.3927	0.5944	-0.13	0.0650	0.1402	0.36	0.0710	0.2030	0.35	0.0746	0.1943	0.39	0.3736	0.5473	-2.55	0.8708	1.1193	-0.33	0.0651	0.1638	2.06
4972 Vacuolar protein sorting-associated protein 11 homolog																												

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

Protein name	UniProt	MCF-7				MDA-MB-231																						
		Dai SC20 vs control	Gen SC20 vs control	SSE SC20 vs control	Dai IC20 vs control	Gen IC20 vs control	SSE IC20 vs control	Dai IC20 vs control	Gen IC20 vs control																			
p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC																	
5011 Vesicle-trafficking protein SEC22a	Q96W7	0.0422	0.1301	-0.24	0.1275	0.6412	-0.19	0.5212	0.7421	0.08	0.1351	0.2437	-0.11	0.7517	0.8058	0.03	0.1632	0.3256	0.22	0.3736	0.5113	-2.55	0.8708	1.0542	-0.33	0.0651	0.1461	2.06
5012 Vesicle-trafficking protein SEC22b	Q75396	0.0261	0.0977	0.12	0.2176	0.6607	0.21	0.0018	0.0240	0.26	0.0018	0.0189	0.26	0.1121	0.2729	0.07	0.0057	0.0614	0.34	0.6461	0.6908	0.05	0.9089	0.9325	-0.01	0.3515	0.4229	-0.10
5013 Vesicular integral-membrane protein VIP36	Q12907	0.0005	0.0173	0.31	0.0994	0.6365	0.20	0.0011	0.0222	0.20	0.0001	0.0096	0.29	0.0054	0.0551	-0.11	0.0430	0.1368	0.28	0.4795	0.5340	-0.04	0.0851	0.2889	-0.13	0.0567	0.2119	-0.16
5014 Viginin	Q00341	0.9851	0.9889	0.00	0.2811	0.6652	0.21	0.0056	0.0365	0.27	0.0049	0.0082	0.29	0.1542	0.3336	0.08	0.0324	0.1160	0.20	0.0761	0.2194	0.39	0.8435	1.2870	-0.01	0.8982	0.9190	-0.01
5015 Vincristin	P08670	0.2734	0.4665	-0.14	0.4273	0.7637	-0.11	0.6529	0.7044	-0.06	0.1040	0.1995	0.25	0.2655	0.4872	-0.14	0.4694	0.6917	0.20	0.0046	0.0729	0.87	0.0074	0.0710	0.48	0.0008	0.0351	2.04
5016 Vinculin	P18206	0.0011	0.0223	0.16	0.3667	0.7154	0.17	0.0059	0.0371	0.35	0.0001	0.0084	0.36	0.0029	0.0415	0.12	0.0001	0.0324	0.43	0.1086	0.2695	0.28	0.6611	1.1011	0.05	0.2776	0.3495	-0.09
5017 Vitamin D-binding protein	Q02774	0.0354	0.1175	-0.26	0.0200	0.4731	0.14	0.2919	0.4722	0.12	0.0377	0.0941	0.11	0.0040	0.0469	0.35	0.2002	0.3768	-0.06	0.3736	0.5024	-2.55	0.8708	1.0379	-0.33	0.0651	0.1420	2.06
5018 Vitamin K epoxide reductase complex subunit 1	Q9BQB6	0.5798	0.6473	0.03	0.3155	0.6810	0.15	0.6821	0.7314	0.05	0.0504	0.1156	0.14	0.3082	0.4058	0.05	0.1996	0.3760	0.09	0.3506	0.6256	-0.09	0.2501	0.5730	-0.14	0.0231	0.1291	-0.31
5019 Vitronectin	P04004	0.4108	0.4938	-3.31	0.5752	0.6915	-1.75	0.5661	0.6301	-1.19	0.5388	0.5962	0.89	0.2938	0.3962	-1.88	0.9510	0.9680	0.09	0.3652	0.6456	-0.47	0.8428	1.2871	-0.09	0.6303	0.6875	-0.22
5020 Voltage-dependent anion-selective channel protein 1	P21796	0.0056	0.0450	0.38	0.2146	0.6609	0.19	0.0006	0.0192	0.51	0.0011	0.0163	0.21	0.0787	0.2164	0.08	0.0056	0.0617	0.47	0.0774	0.2218	0.08	0.0297	0.1556	0.15	0.0122	0.0950	-0.13
5021 Voltage-dependent anion-selective channel protein 2	P45880	0.0040	0.0398	0.18	0.7894	0.8484	-0.02	0.0092	0.0448	0.21	0.0054	0.0295	0.04	0.5143	0.6031	-0.01	0.0955	0.2277	0.23	0.3897	0.4456	0.10	0.3677	0.6943	0.09	0.0274	0.1416	-0.26
5022 Voltage-dependent anion-selective channel protein 3	Q9Y277	0.5644	0.6324	-0.03	0.1247	0.6421	-0.15	0.5118	0.7328	0.02	0.0332	0.0862	-0.12	0.0291	0.1242	-0.15	0.3965	0.6100	0.05	0.4023	0.4582	0.06	0.0580	0.2300	0.17	0.1125	0.3840	-0.14
5023 Voltage-dependent calcium channel subunit alpha-2/delta-3	Q8IZS8	0.0013	0.0242	0.19	0.3253	0.6858	0.18	0.0036	0.0314	0.24	0.0008	0.0147	0.25	0.0313	0.1297	0.09	0.0015	0.0505	0.25	0.4526	0.5075	-0.10	0.4449	0.1966	-0.35	0.0300	0.1476	-0.43
5024 Voltage-dependent L-type calcium channel subunit alpha-1C	Q13936	0.3291	0.5359	-0.06	0.5907	0.6959	0.05	0.8508	0.8809	0.01	0.3106	0.4788	-0.06	0.4969	0.5861	0.05	0.3484	0.5534	0.10	0.3736	0.4744	-2.55	0.8708	0.9864	-0.33	0.0651	0.1296	2.06
5025 Voltage-dependent L-type calcium channel subunit beta-1	Q02641	0.4108	0.4937	-3.31	0.5752	0.6913	-1.75	0.5661	0.6299	-1.19	0.5388	0.5961	0.89	0.2938	0.3961	-1.88	0.9510	0.9678	0.09	0.1629	0.3568	-0.20	0.0636	0.2421	-0.14	0.1772	0.2433	-0.05
5026 Voltage-dependent T-type calcium channel subunit alpha-11	Q9P0X4	0.0060	0.0464	0.29	0.0618	0.5906	0.22	0.0597	0.1415	0.48	0.0030	0.0222	0.50	0.0222	0.1077	0.26	0.0007	0.0412	0.62	0.3736	0.6507	-2.55	0.8708	1.3007	-0.33	0.0651	0.2253	2.06
5027 von Willebrand factor A domain-containing protein 3B	Q502W6	0.0231	0.0909	0.39	0.5078	0.8298	0.11	0.0132	0.0536	0.52	0.0174	0.0553	0.45	0.0077	0.0635	0.53	0.0162	0.0845	0.45	0.0390	0.1638	0.19	0.0485	0.2061	-0.20	0.5079	0.5743	0.02
5028 VPS9 domain-containing protein 1	Q9Y2B5	0.0577	0.1581	0.34	0.0168	0.4604	0.54	0.0154	0.0584	0.24	0.0510	0.1335	0.34	0.0397	0.1461	0.40	0.1150	0.2580	0.24	0.0741	0.2160	0.30	0.0477	0.2039	-0.26	0.0049	0.0675	-0.27
5029 V-set and transmembrane domain-containing protein 4	Q8RW00	0.2393	0.4238	-0.15	0.4580	0.7900	-0.23	0.0367	0.1006	0.35	0.0815	0.1663	0.27	0.0139	0.0840	0.48	0.1157	0.2588	0.27	0.3736	0.5290	-2.55	0.8708	1.0864	-0.33	0.0651	0.1546	2.06
5030 V-type proton ATPase 116 kDa subunit a isoform 1	Q93050	0.0926	0.2139	1.06	0.0201	0.6597	0.29	0.0777	0.1022	0.10	0.0030	0.0223	0.50	0.2005	0.4015	-0.05	0.0675	0.1820	0.68	0.3736	0.5503	-2.55	0.8708	1.1246	-0.33	0.0651	0.1653	2.06
5031 V-type proton ATPase 116 kDa subunit a isoform 3	Q13488	0.0630	0.1661	-0.15	0.0922	0.6309	-0.19	0.7176	0.7628	-0.03	0.5506	0.6016	-0.05	0.4077	0.5033	-0.05	0.1446	0.2999	-0.11	0.3736	0.5181	-2.55	0.8708	1.0666	-0.33	0.0651	0.1493	2.06
5032 V-type proton ATPase catalytic subunit A	P38606	0.7283	0.7287	-0.02	0.4768	0.8035	0.07	0.5110	0.7320	0.05	0.0429	0.1032	0.16	0.3057	0.4033	0.06	0.0171	0.0853	0.25	0.1800	0.3803	-0.03	0.0089	0.0774	0.10	0.0414	0.1033	0.10
5033 V-type proton ATPase subunit B brain isoform	P21281	0.6760	0.7336	0.02	0.1494	0.6603	0.17	0.4659	0.6831	0.40	0.0612	0.1337	0.16	0.2720	0.4956	0.06	0.7083	0.9500	-0.02	0.3927	0.4486	0.04	0.0718	0.2601	-0.14	0.2097	0.2785	-0.06
5034 V-type proton ATPase subunit E 1	P36543	0.7416	0.7906	0.04	0.4673	0.7976	-0.25	0.5556	0.7795	-0.09	0.5025	0.7064	0.09	0.9165	0.9375	0.01	0.6534	0.8905	0.07	0.3874	0.4433	-0.11	0.0098	0.0814	-0.39	0.0504	0.1969	-0.19
5035 V-type proton ATPase subunit E 2	Q96A05	0.1198	0.2554	-0.23	0.4003	0.7440	0.12	0.8029	0.8394	-0.03	0.9190	0.9290	0.01	0.2496	0.4666	0.15	0.2766	0.4718	0.14	0.3736	0.4860	-2.55	0.8708	1.0078	-0.33	0.0651	0.1346	2.06
5036 V-type proton ATPase subunit G 1	Q75348	0.0007	0.0193	-0.18	0.4397	0.7760	0.05	0.5637	0.7879	-0.01	0.0063	0.0317	0.11	0.0056	0.0556	0.14	0.0562	0.1621	0.10	0.2681	0.5109	0.14	0.0139	0.0981	-0.53	0.0401	0.1732	0.32
5037 V-type proton ATPase subunit H	Q9U112	0.1422	0.2886	-0.17	0.6798	0.7658	-0.04	0.7384	0.7812	0.03	0.6350	0.6803	-0.05	0.6513	0.7189	0.04	0.0782	0.2000	-0.23	0.0267	0.1421	0.49	0.0059	0.0616	0.23	0.0116	0.0939	0.20
5038 WAP four-disulfide core domain protein 8	Q8IUAO	0.4108	0.4936	-3.31	0.5752	0.6911	-1.75	0.5661	0.6298	-1.19	0.5388	0.5960	0.89	0.2938	0.3960	-1.88	0.9510	0.9676	0.09	0.0087	0.0929	0.73	0.0000	0.0000	1.97	0.0001	0.0305	1.65
5039 WAP_Kazal_ immunoglobulin_Kunitz and NTR domain-containing protein 2	Q8TEU8	0.8161	0.8518	-0.04	0.2882	0.6686	-0.47	0.3674	0.5647	0.16	0.2002	0.3327	-0.25	0.4341	0.5281	-0.15	0.5138	0.7412	-0.11	0.3285	0.5966	-0.18	0.5460	0.9713	0.07	0.0124	0.0960	0.35
5040 WASH complex subunit 1	AK8Q23	0.4108	0.4935	-3.31	0.5752	0.6910	-1.75	0.5661	0.6297	-1.19	0.5388	0.5959	0.89	0.2938	0.3959	-1.88	0.9510	0.9674	0.09	0.0280	0.2286	0.25	0.0498	0.2099	0.57	0.0157	0.1074	0.40
5041 WASH complex subunit 2A	Q641Q2	0.0189	0.0809	-0.18	0.4282	0.5707	-0.06	0.9188	0.9358	-0.01	0.8143	0.8398	-0.02	0.1644	0.3493	-0.03	0.1392	0.2928	-0.08	0.2868	0.4668	0.19	0.2507	0.5736	0.18	0.1162	0.1740	0.31
5042 WASH complex subunit 2C	Q9Y4E1	0.0223	0.0888	-0.53	0.3649	0.7153	-0.57	0.0880	0.1857	-0.33	0.0709	0.1491	-0.26	0.0601	0.1845	-0.38	0.0503	0.1506	-0.21	0.3736	0.5605	-2.55	0.8708	1.1428	-0.33	0.0651	0.1707	2.06
5043 WASH complex subunit 2D	SSRD80	0.4108	0.4934	-3.31	0.5752	0.6908	-1.75	0.5661	0.6295	-1.19	0.5388	0.5957	0.89	0.2938	0.3958	-1.88	0.9510	0.9672	0.09	0.4759	0.5304	-0.13	0.0887	0.2951	0.11	0.0085	0.0823	0.41
5044 WASH complex subunit 4	Q2M899	0.4108	0.4933	-3.31	0.5752	0.6907	-1.75	0.5661	0.6294	-1.19	0.5388	0.5956	0.89	0.2938	0.3957	-1.88	0.9510	0.9671	0.09	0.3767	0.6075	0.26	0.0002	0.0150	2.71	0.0172	0.1121	0.75
5045 WASH complex subunit 5	Q12768	0.8558	0.8857	-0.02	0.2338	0.6614	0.13	0.0125	0.0524	0.41	0.0242	0.0691	0.35	0.2264	0.4356	0.12	0.0806	0.2042	0.30	0.3736	0.5435	-2.55	0.8708	1.1124	-0.33	0.0651	0.1618	2.06
5046 WD repeat and FYVE domain-containing protein 2	Q96P53	0.0881	0.2066	-0.14	0.2038	0.6841	0.12	0.1139	0.2265	-0.15	0.0194	0.0592	0.23	0.0167	0.0923	0.28	0.0133	0.0767	0.25	0.3736	0.6063	-2.55	0.8708	1.2238	-0.33	0.0651	0.1966	2.06
5047 WD repeat and HMG-box DNA-binding protein 1	Q75717	0.4108	0.4932	-3.31	0.5752	0.6905	-1.75	0.5661	0.6293	-1.19	0.5388	0.5955	0.89	0.2938	0.3956	-1.88	0.9510	0.9669	0.09	0.2483	0.4843	0.08	0.5302	0.9533	0.05	0.7660	0.8075	-0.02
5048 WD repeat and SOCS domain-containing protein 2	Q9NYS7	0.2096	0.3822	0.10	0.1646	0.6610	0.20	0.1447	0.2714	0.22	0.0438	0.1047	0.21	0.6089	0.6831	-0.04	0.7858	1.0240	0.02	0.3736	0.4398	-2.55	0.8708	0.9217	-0.33	0.0651	0.1154	2.06
5049 WD repeat-containing protein 1	Q75083	0																										

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

	Protein name	UniProt	MCF-7				MDA-MB-231			
			Dai SC20 vs control		Gen SC20 vs control		Dai IC20 vs control		Gen IC20 vs control	
			p value	BH q value	log2FC	p value	p value	BH q value	log2FC	p value
5090	Zinc finger CCH domain-containing protein 4	Q9UPT8	0.0112	0.0607	-0.29	0.6911	0.7739	-0.04	0.2083	0.3618
5091	Zinc finger CCH domain-containing protein 6	P61129	0.0145	0.0697	-0.40	0.0951	0.6308	-0.57	0.1815	0.4880
5092	Zinc finger CCH domain-containing protein 7A	Q8W1R0	0.4652	0.5414	0.20	0.9983	0.9985	0.00	0.0014	0.0220
5093	Zinc finger CCH domain-containing protein 7B	Q9UGR2	0.0093	0.0568	-0.10	0.7046	0.7826	0.06	0.4950	0.7166
5094	Zinc finger CCH domain-containing protein 8	Q8NSP1	0.4108	0.4919	-3.31	0.5752	0.6888	-1.75	0.5661	0.6276
5095	Zinc finger CCH-type antiviral protein 1	Q727W4	0.0027	0.0347	-0.12	0.6440	0.7375	-0.01	0.1913	0.3383
5096	Zinc finger CCH-type antiviral protein 1-like	Q9UHT9	0.4108	0.4918	-3.31	0.5752	0.6886	-1.75	0.5661	0.6277
5097	Zinc finger CCH domain-containing protein 7	Q8N3Z6	0.4108	0.4917	-3.31	0.5752	0.6884	-1.75	0.5661	0.6275
5098	Zinc finger CCH domain-containing protein 8	Q6NZY4	0.1832	0.3476	0.10	0.5720	0.8850	-0.10	0.5413	0.6732
5099	Zinc finger FYVE domain-containing protein 16	Q7Z3T8	0.0041	0.0400	0.17	0.4349	0.7707	0.05	0.8195	0.8538
5100	Zinc finger FYVE domain-containing protein 21	Q9BG24	0.2139	0.3881	0.07	0.3002	0.6732	-0.04	0.0608	0.1430
5101	Zinc finger FYVE domain-containing protein 9	Q95405	0.0075	0.0509	0.31	0.0013	0.2322	0.37	0.9651	0.9719
5102	Zinc finger HIT domain-containing protein 2	Q9UHR6	0.4108	0.4916	-3.31	0.5752	0.6883	-1.75	0.5661	0.6274
5103	Zinc finger homeobox protein 3	Q15911	0.4108	0.4914	-3.31	0.5752	0.6881	-1.75	0.5661	0.6273
5104	Zinc finger imprinted 3	Q96PE6	0.4108	0.4913	-3.31	0.5752	0.6880	-1.75	0.5661	0.6271
5105	Zinc finger matrin-type protein 2	Q96NC0	0.4108	0.4912	-3.31	0.5752	0.6878	-1.75	0.5661	0.6270
5106	Zinc finger MYM-type protein 2	Q9UBW7	0.0867	0.2048	-0.30	0.1169	0.6341	-0.26	0.3311	0.3936
5107	Zinc finger MYND domain-containing protein 15	Q9H091	0.0169	0.0759	-1.14	0.0338	0.5391	-0.67	0.0103	0.0474
5108	Zinc finger protein 114	Q8NC26	0.0091	0.0567	-0.33	0.2218	0.6584	-0.20	0.0633	0.1466
5109	Zinc finger protein 121	P58117	0.1115	0.2425	0.17	0.4448	0.5664	0.31	0.1320	0.2539
5110	Zinc finger protein 136	P52737	0.0029	0.0360	0.66	0.0685	0.6614	0.29	0.0035	0.0314
5111	Zinc finger protein 174	Q15697	0.4108	0.4911	-3.31	0.5752	0.6876	-1.75	0.5661	0.6268
5112	Zinc finger protein 185	Q15231	0.0470	0.7318	0.01	0.0406	0.5669	0.12	0.0042	0.0325
5113	Zinc finger protein 2	Q9B5G1	0.4108	0.4910	-3.31	0.5752	0.6875	-1.75	0.5661	0.6267
5114	Zinc finger protein 243	Q8NDW4	0.4108	0.4909	-3.31	0.5752	0.6873	-1.75	0.5661	0.6266
5115	Zinc finger protein 268	Q14978	0.4108	0.4908	-3.31	0.5752	0.6872	-1.75	0.5661	0.6264
5116	Zinc finger protein 276	Q8NS54	0.8281	0.8620	-0.03	0.1111	0.6324	-0.40	0.6413	0.6941
5117	Zinc finger protein 318	Q5VUA4	0.0034	0.0375	-6.12	0.2891	0.6691	-2.27	0.1553	0.2873
5118	Zinc finger protein 324B	Q6AW86	0.4108	0.4906	-3.31	0.5752	0.6870	-1.75	0.5661	0.6265
5119	Zinc finger protein 330	Q9Y3S2	0.0238	0.0924	-0.21	0.5167	0.8390	-0.14	0.0070	0.0395
5120	Zinc finger protein 354C	Q86Y25	0.0109	0.0598	-0.54	0.4924	0.8152	-0.09	0.5316	0.7528
5121	Zinc finger protein 382	Q96SR6	0.0002	0.0118	0.27	0.0745	0.6126	0.12	0.1792	0.3225
5122	Zinc finger protein 383	Q8NA42	0.4108	0.4905	-3.31	0.5752	0.6868	-1.75	0.5661	0.6262
5123	Zinc finger protein 394	Q53G03	0.4108	0.4904	-3.31	0.5752	0.6867	-1.75	0.5661	0.6260
5124	Zinc finger protein 397	Q8NF99	0.0086	0.0547	-2.38	0.2348	0.6614	-1.29	0.0734	0.1620
5125	Zinc finger protein 40	P15822	0.0405	0.1268	-0.17	0.0240	0.4875	0.59	0.0348	0.0323
5126	Zinc finger protein 42 homolog	Q96MM3	0.4108	0.4903	-3.31	0.5752	0.6865	-1.75	0.5661	0.6259
5127	Zinc finger protein 428	Q9B6S4	0.0096	0.0354	-0.29	0.2236	0.6641	-0.14	0.4571	0.6723
5128	Zinc finger protein 454	Q8N6P8	0.9643	0.9737	0.01	0.5158	0.8869	-0.88	0.7470	0.7243
5129	Zinc finger protein 468	Q5VY5	0.4108	0.4902	-3.31	0.5752	0.6864	-1.75	0.5661	0.6258
5130	Zinc finger protein 469	Q96G99	0.1738	0.3352	0.07	0.2022	0.6596	0.26	0.0252	0.0789
5131	Zinc finger protein 484	Q5VU22	0.0461	0.1371	-0.48	0.2047	0.6594	-0.64	0.2510	0.4178
5132	Zinc finger protein 496	Q9JTG1	0.0474	0.1398	-0.24	0.7132	0.7901	0.06	0.5319	0.7530
5133	Zinc finger protein 511	Q8NB15	0.4108	0.4901	-3.31	0.5752	0.6862	-1.75	0.5661	0.6256
5134	Zinc finger protein 518A	Q6AHz1	0.0371	0.1211	-0.34	0.3099	0.5045	-0.35	0.1678	0.3066
5135	Zinc finger protein 541	Q9H0D2	0.5861	0.6532	0.07	0.1159	0.6360	-0.23	0.8173	0.8520
5136	Zinc finger protein 552	Q9H707	0.4108	0.4900	-3.31	0.5752	0.6861	-1.75	0.5661	0.6255
5137	Zinc finger protein 57	Q6E8A5	0.0131	0.0666	0.20	0.5721	0.8846	-0.07	0.0203	0.0685
5138	Zinc finger protein 57 homolog	Q9NU63	0.3073	0.5079	0.06	0.9797	0.9862	0.00	0.1440	0.2703
5139	Zinc finger protein 578	Q96N58	0.4108	0.4899	-3.31	0.5752	0.6859	-1.75	0.5661	0.6254
5140	Zinc finger protein 616	Q08AN1	0.0962	0.2188	0.08	0.4035	0.7478	0.13	0.0414	0.1094
5141	Zinc finger protein 620	Q6ZNG0	0.0107	0.0596	0.19	0.0056	0.3868	0.42	0.0314	0.0906
5142	Zinc finger protein 648	Q5T619	0.0467	0.1383	-0.63	0.5678	0.8822	-0.11	0.0712	0.1590
5143	Zinc finger protein 674	Q2M3X9	0.6328	0.6949	0.02	0.3078	0.6776	0.15	0.4137	0.6201
5144	Zinc finger protein 678	Q5XNM1	0.4775	0.5528	1.56	0.2202	0.6597	0.96	0.5082	0.7298
5145	Zinc finger protein 705A	Q9Z7N9	0.4108	0.4897	-3.31	0.5752	0.6857	-1.75	0.5661	0.6252
5146	Zinc finger protein 763	Q0ZJ25	0.0860	0.2036	0.14	0.9073	0.9355	-0.01	0.0913	0.1902
5147	Zinc finger protein 781	Q8NSC0	0.7001	0.7541	-0.09	0.1325	0.6487	0.51	0.3698	0.5676
5148	Zinc finger protein 789	Q5FWF6	0.4108	0.4896	-3.31	0.5752	0.6856	-1.75	0.5661	0.6251
5149	Zinc finger protein 791	Q3KP31	0.5421	0.6123	-0.09	0.2154	0.6602	0.21	0.9344	0.9491
5150	Zinc finger protein 8	P17098	0.4108	0.4895	-3.31	0.5752	0.6854	-1.75	0.5661	0.6250
5151	Zinc finger protein 816	Q0VGE8	0.0218	0.0877	-0.70	0.1327	0.6473	-1.07	0.5664	0.6242
5152	Zinc finger protein 830	Q96NB3	0.0117	0.0624	0.28	0.1630	0.6627	0.07	0.0144	0.0565
5153	Zinc finger protein 837	Q96EG3	0.1230	0.2604	-0.39	0.5422	0.8771	-0.08	0.0388	0.1043
5154	Zinc finger protein 891	AMT6T5	0.3170	0.5196	-0.83	0.1527	0.6592	3.61	0.0636	0.1469
5155	Zinc finger protein Aiolos	Q9UKT9	0.3069	0.5079	0.12	0.0668	0.6588	-0.52	0.0323	0.0922
5156	Zinc finger protein basophilin-2	Q6ZNG0	0.4108	0.4894	-3.31	0.5752	0.6853	-1.75	0.5661	0.6248
5157	Zinc finger protein casein homolog 1	Q86V15	0.0276	0.1005	0.15	0.0842	0.6222	0.19	0.1054	0.2126
5158	Zinc finger protein DZIP1	Q86YF9	0.4108	0.4893	-3.31	0.5752	0.6851	-1.75	0.5661	0.6247
5159	Zinc finger protein Eos	Q9H2S9	0.5726	0.6401	0.14	0.6282	0.7251	0.17	0.0471	0.1202
5160	Zinc finger protein GLI1	P08151	0.3372	0.5447	-0.06	0.0369	0.5508	0.23	0.2272	0.3864
5161	Zinc finger protein Helios	Q9GKS7	0.0002	0.0116	-4.03	0.1950	0.6604	-2.77	0.0630	0.0370
5162	Zinc finger protein neuro-d4	Q72782	0.6485	0.7096	0.03	0.4865	0.8103	-0.06	0.4527	0.6669
5163	Zinc finger protein RIF	Q13129	0.0016	0.0268	0.30	0.1563	0.6620	0.23	0.0016	0.0236
5164	Zinc finger protein ubi-d4	Q92785	0.4108	0.4892	-3.31	0.5752	0.6850	-1.75	0.5661	0.6246
5165	Zinc finger protein with KRAB and SCAN domains 1	P17029	0.2147	0.3894	-0.65	0.2951	0.6716	-2.09	0.0130	0.0534
5166	Zinc finger protein with KRAB and SCAN domains 3	Q9BRR0	0.5660	0.6338	0.05	0.5752	0.8712	-0.12	0.8492	0.8700
5167	Zinc finger protein with KRAB and SCAN domains 4	Q969J2	0.4108	0.4891	-3.31	0.5752	0.6848	-1.75	0.5661	0.6244
5168	Zinc finger protein ZPR1	Q75312	0.2255	0.4042	-0.09	0.7954	0.8515	0.06	0.7224	0.7671
5169	Zinc finger protein-like 1	Q95159	0.7224	0.7730	0.01	0.1371	0.6509	0.06	0.0121	0.0515
5170	Zinc finger Ran-binding domain-containing protein 2	Q95218	0.1371	0.2818	-0.11	0.9051	0.9338	0.01	0.3525	0.5469
5171	Zinc finger SWIM domain-containing protein 1	Q9BR11	0.3348	0.5414	-0.40	0.4850	0.8091	-0.35	0.2224	0.0732
5172	Zinc finger SWIM domain-containing protein 4	Q9H7M6	0.0007	0.0192	1.13	0.2480	0.6888	-0.28	0.1154	0.3702
5173	Zinc finger SWIM domain-containing protein 5	Q9P217	0.8488	0.8795	-0.01	0.1005	0.6333	-0.06	0.0003	0.0216

Supplementary Table S2. Overview on all relatively quantified 5180 proteins statistical analysis

		MCF-7												MDA-MB-231															
		Dai SC20 vs control			Gen SC20 vs control			SSE SC20 vs control			Dai IC20 vs control			Gen IC20 vs control			SSE IC20 vs control			Dai IC20 vs control			Gen IC20 vs control			SSE IC20 vs control			
Protein name		UniProt	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC	p value	BH q value	log2FC
5174	Zinc finger SWIM domain-containing protein 6	Q9HCJ5	0.0168	0.0757	0.40	0.0307	0.5097	0.35	0.0731	0.1618	-0.24	0.8410	0.8635	-0.02	0.0335	0.1334	0.39	0.7985	1.0359	0.02	0.3736	0.4388	-2.55	0.8708	0.9198	-0.33	0.0651	0.1150	2.06
5175	Zinc finger transcription factor Trps1	Q9UHF7	0.4108	0.4890	-3.31	0.5752	0.6846	-1.75	0.5661	0.6243	-1.19	0.5388	0.5908	0.89	0.2938	0.3918	-1.88	0.9510	0.9599	0.09	0.1596	0.3525	-0.16	0.1865	0.4766	0.20	0.8250	0.8585	-0.10
5176	Zinc finger-containing ubiquitin peptidase 1	Q96AP4	0.0115	0.0616	0.16	0.5325	0.8498	0.08	0.2652	0.4361	0.07	0.0049	0.0280	0.21	0.1632	0.3473	0.06	0.0155	0.0829	0.22	0.1476	0.3326	2.31	0.3235	0.6765	1.73	0.1084	0.1651	2.90
5177	Zinc phosphodiesterase ELAC protein 2	Q9BQ52	0.0683	0.1737	0.24	0.2648	0.6639	0.10	0.7355	0.7786	0.03	0.3201	0.4911	-0.11	0.2690	0.4906	0.11	0.1955	0.3707	-0.12	0.0560	0.1876	0.17	0.6944	1.1368	-0.02	0.1354	0.1961	-0.07
5178	Zona pellucida sperm-binding protein 1	P60852	0.4108	0.4888	-3.31	0.5752	0.6845	-1.75	0.5661	0.6242	-1.19	0.5388	0.5907	0.89	0.2938	0.3917	-1.88	0.9510	0.9597	0.09	0.0009	0.0398	0.97	0.1118	0.3417	0.22	0.0063	0.0747	0.66
5179	Zygote arrest protein 1	Q86SH2	0.0311	0.1090	0.40	0.2298	0.6609	0.13	0.1527	0.2836	0.17	0.4823	0.6832	0.07	0.5269	0.6133	-0.07	0.2252	0.4083	0.16	0.3736	0.4967	-2.55	0.8708	1.0275	-0.33	0.0651	0.1394	2.06
5180	Zyxin	Q15942	0.0914	0.2119	-0.07	0.8058	0.8599	0.03	0.8946	0.9162	-0.01	0.0919	0.1819	0.11	0.0121	0.0785	0.13	0.0411	0.1335	0.09	0.7409	0.7785	-0.04	0.3661	0.7356	-0.09	0.2423	0.3126	-0.10