

SUPPLEMENTARY DATA

Table S1. Results table of an example of CCD1 protein detection by LCMS, *Petunia x hybrida* PhCCD1 with MW 61.3 kDa, line 6731

1	Checked	Master	Accession	Description	Cove#	Peq#	PSI#	Uni#	AA	MW	calc.	Score#	Peq	Biological	Cellular	Cl	Molecular	Pfam	IDs	Entrez	Gen	Ensembl	Gene	Sym	Chro	KEGG	Path	WikiPath	Reactome	#	Pro	Four	#	Pro		
6470	FALSE	Master	Pn Q03558	NADPH dehydrogenase 2 OS=Saccharomyces cerevisiae (stra	34	11	17	11	400	45	6.57	476	11	cell death, cytoplasm	catalytic	a	Pf00724	856584	YHR179W	OYE2	VIII									0	High	1				
6491	FALSE	Master	Pn P38693	Acid phosphatase PHO12 OS=Saccharomyces cerevisiae (stra	20	10	20	8	467	52.7	5.16	476	10	metabolic vacuole	catalytic	a	Pf00328	856625	YHR215W	PHO12	VIII	Metabolic								2	High	1				
6515	FALSE	Master	Pn P07262	NADP-specific glutamate dehydrogenase 1 OS=Saccharomyc	32	11	15	7	454	49.5	5.69	457	11	metabolic cytoplasm	catalytic	a	Pf00208	854557	YOR375C	GDH1	XV	Arginine b Superpath	Amino aci							12	High	1				
6534	FALSE	Master	Pn P14126	60S ribosomal protein L3 OS=Saccharomyces cerevisiae (stra	40	15	17	15	387	43.7	10.3	456	15	cell organi cytoplasm	nucleotidi		Pf00297	854229	YOR063W	RPL3	XV	Ribosome	Cytoplasm	Formatior					14	High	1					
6555	FALSE	Master	Pn C7GV29	40S ribosomal protein S1-B OS=Saccharomyces cerevisiae (st	42	12	14	2	255	28.8	10.1	456	12	metabolic cytoplasm	structural		Pf01015																			
6573	FALSE	Master	Pn P46955	Beta-glucosidase-like protein NCA3, mitochondrial OS=Sacch	21	7	14	6	337	35.4	4.46	456	7	cell organi cell surfac			Pf03856	853326	YIL116C	NCA3	X															
6591	FALSE	Master	Pn P41939	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Saccharon	25	9	14	8	412	46.5	6.19	454	9	metabolic cytoplasm	catalytic	a	Pf00180	850871	YLR174W	IDP2	XII	Carbon m	Principle F	Citric acid					26	High	1					
6609	FALSE	Master	Pn P31539	Heat shock protein 104 OS=Saccharomyces cerevisiae (strain	18	13	14	13	908	102	5.45	448	13	cell organi cytoplasm	catalytic	a	Pf00004	850633	YLL026W	HSP104	XII	Longevity									1	High	1			
6627	FALSE	Master	Pn B3RHV0	40S ribosomal protein S1-A OS=Saccharomyces cerevisiae (st	42	12	14	2	255	28.7	9.99	445	12	metabolic cytoplasm	structural		Pf01015		SCRG_043																	
6645	FALSE	Master	Pn P19097	Fatty acid synthase subunit alpha OS=Saccharomyces cerevis	11	18	18	18	1887	207	5.44	442	18	metabolic cytoplasm	catalytic	a	Pf00106	855845	YPL231W	FAS2	XVI	Fatty acid	Fatty Acid							6	High	1				
6667	FALSE	Master	Pn P0CX82	60S ribosomal protein L19-A OS=Saccharomyces cerevisiae (	26	7	11	7	189	21.7	11.4	430	7	cell organi cytoplasm	RNA bindi		Pf01280	852254	8 YBL027W	RPL19B	R II	Ribosome	Cytoplasm	Formatior					14	High	1					
6682	FALSE	Master	Pn P60010	Actin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2	30	9	15	3	375	41.7	5.68	425	9	cell organi cytoplasm	catalytic	a	Pf00022	850504	YFL039C	ACT1	VI	Phagosome		RHO GTPa					10	High	1					
6701	FALSE	Master	Pn P47143	Adenosine kinase OS=Saccharomyces cerevisiae (strain ATCC	40	9	13	9	340	36.4	5.16	425	9	metabolic cytoplasm	catalytic	a	Pf00294	853569	YIR105W	ADO1	X	Metabolic		Purine sal						6	High	1				
6718	FALSE	Master	Pn P36110	Protein PRY2 OS=Saccharomyces cerevisiae (strain ATCC 204	13	3	9	3	329	33.8	4.6	420	3	transport endoplasr			Pf00188	853882	YKR013W	PRY2	XI															
6731	FALSE	Master	Pn JT_Ph_CCD1	<i>Petunia x hybrida</i> carotenoid cleavage dioxygenase 1 (CCD1)	24	10	12	10	546	61.3	6.27	420	10																							
6747	FALSE	Master	Pn P54070	Mannosyltransferase KTR6 OS=Saccharomyces cerevisiae (st	28	11	13	11	446	52.1	5.5	417	11	cell organi Golgi;men	catalytic	a	Pf01793	856054	YPL053C	KTR6	XVI	Metabolic									2	High	1			
6764	FALSE	Master	Pn P23254	Transketolase 1 OS=Saccharomyces cerevisiae (strain ATCC 2	22	13	17	13	680	73.8	7.01	413	13	metabolic cytoplasm	catalytic	a	Pf00456	856188	YPR074C	TKL1	XVI	Pentose p	Principle F	Pentose p						18	High	1				
6785	FALSE	Master	Pn P00729	Carboxypeptidase Y OS=Saccharomyces cerevisiae (strain AT	20	10	15	10	532	59.8	4.73	412	10	metabolic cytoplasm	catalytic	a	Pf00450	855343	YMR297W	PRC1	XIII			Neutroph					3	High	1					
6804	FALSE	Master	Pn P37291	Serine hydroxymethyltransferase, cytosolic OS=Saccharomyc	32	14	14	13	469	52.2	7.43	386	14	metabolic cytoplasm	catalytic	a	Pf00155	850747	YLR058C	SHM2	XII	Cyanoami	Pathways	Carnitine					22	High	1					
6822	FALSE	Master	Pn P13130	Sporulation-specific wall maturation protein OS=Saccharomyc	14	3	6	3	326	34.2	5.41	385	3	cell differe	catalytic	a	Pf00710	856541	YHR139C	SPS100	VIII															
6832	FALSE	Master	Pn P38887	Uncharacterized protein YHR202W OS=Saccharomyces cerev	22	13	18	13	602	69	6.23	381	13	metabolic cytosol;va	catalytic	a	Pf00149	856609	YHR202W	YHR202W	VIII															
6854	FALSE	Master	Pn P15992	Heat shock protein 26 OS=Saccharomyces cerevisiae (strain	58	9	13	9	214	23.9	5.53	378	9	metabolic cytoplasm	protein bi		Pf00011	852364	YBR072W	HSP26	II	Protein pr									1	High	1			
6871	FALSE	Master	Pn P38109	Putative serine carboxypeptidase YBR139W OS=Saccharomyc	20	9	15	9	508	57.6	5.31	376	9	metabolic vacuole	catalytic	a	Pf00450	852436	YBR139W	YBR139W	II			Neutroph						3	High	1				
6890	FALSE	Master	Pn P53090	Aromatic/aminoadipate aminotransferase 1 OS=Saccharomyc	24	11	12	11	500	56.1	6.01	373	11	metabolic cytoplasm	catalytic	a	Pf00155	852672	YGL202W	ARO8	VII	Lysine bio	Phenylalal	Lysine cat						23	High	1				
6906	FALSE	Master	Pn P00817	Inorganic pyrophosphatase OS=Saccharomyces cerevisiae (st	48	9	13	9	287	32.3	5.58	372	9	metabolic cytoplasm	catalytic	a	Pf00719	852296	YBR011C	IPP1	II	Oxidative	UDP-Glucc	Cytosolic t						9	High	1				
6923	FALSE	Master	Pn Q08271	1,3-beta-glucanoyltransferase GAS4 OS=Saccharomyces cer	18	7	12	7	471	53.8	4.89	370	7	cell organi membran	catalytic	a	Pf00150	853988	YOL132W	GAS4	XV															
6939	FALSE	Master	Pn P06168	Ketol-acid reductoisomerase, mitochondrial OS=Saccharomyc	30	9	12	9	395	44.3	9.04	368	9	cell organi mitochoni	catalytic	a	Pf01450	851069	YLR355C	ILV5	XII	Metabolic	Isoleucine							10	High	1				
6955	FALSE	Master	Pn P36105	60S ribosomal protein L14-A OS=Saccharomyces cerevisiae (	52	10	12	10	138	15.2	10.9	365	10	cell comm cytoplasm	nucleotidi		Pf01929	853864	YKL006W	RPL14A	XI	Ribosome	Cytoplasm							2	High	1				

Table S2. Results table indicating no detection by LCMS of any CCD1 protein secreted from the empty plasmid (p\_Empty) between the range of CCD1 sizes used: MW 61.1 kDa – 62.4 kDa

1	Checked	Master	Accession	Description	Cove#	Per#	PSI#	Un#	AA	MW	calc.	Score#	Per	Biological	Cellular C	Molecular	Pfam IDs	Entrez	Ge	Ensembl	Gene Sym	Chro	KEGG	Path	WikiPath	Reactome	#	Pro	Four	Pro	
12170	FALSE	Master Pri	P33734	Imidazole glycerol phosphate synthase hisH OS=Saccharo	9	5	6	5	552	61	5.49	126	5	metabolic	cytoplasm	catalytic	a PF00117, f852550	YBR248C	HIS7	II					Histidine r	Histidine t	5	High	1		
12176	FALSE	Master Pri	Q08224	Hydroxymethylpyrimidine/phosphomethylpyrimidine kina	3	2	2	2	551	61.2	6.16	59	2	metabolic	cytosol	catalytic	a PF05048, f854099	YOL055C	THI20	XV					Metabolic		2	High	1		
12181	FALSE	Master Pri	P12709	Glucose-6-phosphate isomerase OS=Saccharomyces cerev	57	26	61	26	554	61.3	6.46	1868	26	metabolic	cytoplasm	catalytic	a PF00342, 852495	YBR196C	PGI1	II	Gluconeo			Pentose p	Principle F	25	High	1			
12186	FALSE	Master Pri	P06169	Pyruvate decarboxylase isozyme 1 OS=Saccharomyces cer	54	24	77	21	563	61.5	6.19	2776	24	metabolic	cytoplasm	catalytic	a PF00205, f850733	YLR044C	PDC1	XII				Glycolysis	Principle F	9	High	1			
12193	FALSE	Master Pri	P26263	Pyruvate decarboxylase isozyme 3 OS=Saccharomyces cer	12	4	22	1	563	61.5	6.19	771	4	metabolic	cytoplasm	catalytic	a PF00205, f852978	YGR087C	PDC6	VII				Glycolysis	Principle F	9	High	1			
12199	FALSE	Master Pri	P47079	T-complex protein 1 subunit theta OS=Saccharomyces cer	7	4	4	4	568	61.6	5.72	70	4	metabolic	cytoplasm	nucleotid	PF00118, f853447	YJL008C	CCT8	X	Cooperati					8	High	1			
12204	FALSE	Master Pri	P43590	Uncharacterized peptidase YFR006W OS=Saccharomyces c	3	2	2	2	535	61.7	6.16	51	2	metabolic	cytoplasm	catalytic	a PF00557, f850556	YFR006W	YFR006W	VI						0	High	1			
12209	FALSE	Master Pri	P53966	Probable mannosyltransferase KTR5 OS=Saccharomyces ce	2	1	2	1	522	61.7	5.73	23	1	metabolic	endoplasm	catalytic	a PF01793, 855703	YNL029C	KTR5	XIV						0	High	1			
12214	FALSE	Master Pri	P40413	T-complex protein 1 subunit epsilon OS=Saccharomyces ce	4	2	2	2	562	61.9	5.53	58	2	metabolic	cytoplasm	nucleotid	PF00118, 853527	YJR064W	CCT5	X	Cooperati					5	High	1			
12221	FALSE	Master Pri	P23292	Casein kinase I homolog 2 OS=Saccharomyces cerevisiae (c	8	3	3	3	546	62	9.07	129	3	cell organi	cytoplasm	catalytic	a PF00069, f855568	YNL154C	YCK2	XIV				Hippo sign		2	High	1			
12227	FALSE	Master Pri	P38628	Phosphoacetylglucosamine mutase OS=Saccharomyces ce	2	1	1	1	557	62	5.91	38	1	cell organi	cytoplasm	catalytic	a PF00408, f856652	YEL058W	PCM1	V	Synthesis	Amino sug	UDP-N-Ac		10	High	1				
12232	FALSE	Master Pri	P35527	SWISS-PROT:P35527 Tax_Id=9606 Gene_Symbol=KRT9 Ker	43	21	50	21	623	62.1	5.3	1826	21	cell death	cytosol;	structural	PF00038, f3857						17				0	High	1		
12237	FALSE	Master Pri	B3LJRO	Folypolyglutamate synthase OS=Saccharomyces cerevisiae	2	1	1	1	548	62.1	8.82	28	1	metabolic	cytoplasm	catalytic	a PF02875							SCRG_016			0	High	1		
12243	FALSE	Master Pri	P54838	Dihydroxyacetone kinase 1 OS=Saccharomyces cerevisiae (	20	11	12	11	584	62.2	5.41	367	11	metabolic	cytoplasm	catalytic	a PF02733, f854932	YML070W	DAK1	XIII	Fructose c	Carbon m	Xylulose-n		10	High	1				
12249	FALSE	Master Pri	P38707	Asparagine--tRNA ligase, cytoplasmic OS=Saccharomyces c	22	10	12	10	554	62.2	5.85	288	10	metabolic	cytoplasm	catalytic	a PF00152, f856412	YHR019C	DED81	VIII				Aminoacyl	Cytoplasm	2	High	1			
12254	FALSE	Master Pri	P13647	SWISS-PROT:P13647 Tax_Id=9606 Gene_Symbol=KRT5 Ker	23	15	23	7	590	62.3	7.74	729	15	cell death	cytoplasm	catalytic	a PF00038, f3852	ENSG0000	KRT5	12	Formation					6	High	1			
12259	FALSE	Master Pri	P21264	Phosphoribosylaminoimidazole carboxylase OS=Saccharo	15	8	10	8	571	62.3	7.33	215	8	metabolic	cytoplasm	catalytic	a PF00731, f854295	YOR128C	ADE2	XV				Metabolic	De Novo	5	High	1			
12264	FALSE	Master Pri	Q06336	ADP-ribosylation factor-binding protein GGA1 OS=Sacchar	10	4	4	4	557	62.3	5.62	77	4	transport	cytosol;	Gc protein bi	PF00790, f851960	YDR358W	GGA1	IV	TBC/RABC					4	High	1			
12270	FALSE	Master Pri	P28240	Isocitrate lyase OS=Saccharomyces cerevisiae (strain ATCC	58	28	66	28	557	62.4	6.42	2107	28	metabolic	cytoplasm	catalytic	a PF00463, f856794	YER065C	ICL1	V				Carbon m	Principle F	7	High	1			
12276	FALSE	Master Pri	Q08977	Cu(2+) suppressing and bleomycin sensitive protein 1 OS=	5	3	3	3	551	62.7	5.12	77	3		cytoplasm		PF10303, 855867	YPL260W	YPL260W	XVI					0	High	1				
12282	FALSE	Master Pri	P30952	Malate synthase 1 OS=Saccharomyces cerevisiae (strain AT	49	29	58	29	554	62.8	7.18	1337	29	metabolic	cytoplasm	catalytic	a PF01274, 855606	YNL117W	MLS1	XIV				Carbon m	Principle F	7	High	1			
12287	FALSE	Master Pri	P39522	Dihydroxy-acid dehydratase, mitochondrial OS=Saccharom	8	3	3	3	585	62.8	7.83	62	3	metabolic	mitochondri	catalytic	a PF00920, 853473	YJR016C	ILV3	X				Metabolic	Isoleucine	11	High	1			
12292	FALSE	Master Pri	P37012	Phosphoglucomutase 2 OS=Saccharomyces cerevisiae (str	31	16	32	14	569	63	6.62	1001	16	cellular hc	cytoplasm	catalytic	a PF00408, f855131	YMR105C	PGM2	XIII	Galactose	Pentose p	Starch anc		24	High	1				
12297	FALSE	Master Pri	Q04636	FACT complex subunit POB3 OS=Saccharomyces cerevisiae	3	3	3	3	552	63	4.86	63	3	cell organi	chromoso	DNA bindi	PF03531, f854933	YML069W	POB3	XIII	TP53 Regu					8	High	1			
12302	FALSE	Master Pri	P23287	Serine/threonine-protein phosphatase 2B catalytic subuni	2	1	1	1	553	63	6.67	31	1	cell divisio	cytoplasm	catalytic	a PF00149, 851153	YLR433C	CNA1	XII						0	High	1			