

Supplementary file

Table S1. Landscape of camel transcriptional regulation 6, 12, and 24h after injection with ChAdOx2-MERS vaccine (All comparisons are done with respect to time 0). A gene is defined as differentially regulated in a statistically significant way when $\text{abs}(\log_2(\text{fold change})) \geq 1$ and $\text{FDR} \leq 0.05$. All the genes in the table have $\text{abs}(\log_2(\text{fold change})) \geq 1$; their FDR is typeset in bold whenever $\text{FDR} \leq 0.05$, i.e. whenever differential regulation for that gene at the time point considered is statistically significant. LFC: limit fold change; FDR: false discovery rate; T=6h: study point 6 hours post vaccination; T=12h: study point 12 hours post vaccination; T=24h: study point 24 hours post vaccination.

Gene name (CamDro3 names)	Gene name (mapped to ENSEMBL human)	Gene name (InterPro)	Gene name (human Readable)	Gene description	T=6h		T=12h		T=24h	
					LFC	FDR	LFC	FDR	LFC	FDR
Cadr_000009117	ENSG00000168209	Q9NX09	DDIT4	DNA damage-inducible transcript 4 protein	-2.57	0.0021	-2.84	0.00078	-2.94	0.00056
Cadr_000018634	ENSG00000179094	O15534	PER1	Period circadian protein homolog 1	-1.58	0.013	-1.76	0.015	-1.96	0.005
Cadr_000022112	ENSG00000204539	Q15517	CDSN	Corneodesmosin	7.49	0.0052	5.91	0.035	7.2	0.0053
Cadr_000028245	ENSG00000182541	P53671	LIMK2	LIM domain kinase 2	2.47	0.0072	1.31	0.063	0.228	0.99
Cadr_000005463					2.23	0.013	1.87	0.054	0.237	0.99
Cadr_000011526	ENSG00000089351	Q96CP6	GRAMD1A	Protein Aster-A	1.54	0.013	0.845	0.072	-0.0587	1
Cadr_000028656	ENSG00000128789	Q969U7	PSMG2	Proteasome assembly chaperone 2	1.06	0.013	0.689	0.059	0.0823	0.99
Cadr_000001885	ENSG00000169429	P10145	CXCL8	Interleukin-8	-1.8	0.023	-2.01	0.028	-2.08	0.015
Cadr_000011353					1.52	0.017	0.455	0.42	-0.181	0.98
Cadr_000002514	ENSG00000198883	Q96PV4	PNMA5	Paraneoplastic antigen-like protein 5	3.89	0.023	0.915	0.61	-0.0643	1

Cadr_000003390	ENSG00000102312	Q9H237	PORCN	Protein-serine O-palmitoleoyltransferase porcupine	2.24	0.023	0.358	0.79	-0.36	0.98
Cadr_000004852	ENSG00000133710	Q9NQ38	SPINK5	Serine protease inhibitor Kazal-type 5	5.88	0.023	5.44	0.054	5.76	0.061
Cadr_000010146	ENSG00000135587	O60906	SMPD2	Sphingomyelin phosphodiesterase 2	1.33	0.023	0.583	0.22	0.227	0.97
Cadr_000011846	ENSG00000069399	P20749	BCL3	B-cell lymphoma 3 protein	1.19	0.023	0.688	0.096	0.0744	1
Cadr_000021957	ENSG00000096060	Q13451	FKBP5	Peptidyl-prolyl cis-trans isomerase FKBP5	-2.45	0.023	-2.16	0.054	-2.25	0.078
Cadr_000023115	ENSG00000090104	Q08116	RGS1	Regulator of G-protein signaling 1	-2.85	0.023	-0.514	0.73	-0.943	0.68
Cadr_000023477	ENSG00000133055	Q13203	MYBPH	Myosin-binding protein H	2.07	0.023	1.59	0.056	0.541	0.85
Cadr_000023835					1.47	0.023	0.875	0.097	0.208	0.98
Cadr_000028639	ENSG00000156052	P50148	GNAQ	Guanine nucleotide-binding protein G subunit alpha	1.08	0.023	0.656	0.094	0.261	0.91
Cadr_000026275	ENSG00000179361	Q8IVW6	ARID3B	AT-rich interactive domain-containing protein 3B	1.13	0.027	0.315	0.56	0.166	0.98
Cadr_000007726				hypothetical protein	1.47	0.028	0.717	0.2	0.72	0.43
Cadr_000012219	ENSG00000186818	Q8NHJ6	LILRB4	Leukocyte immunoglobulin-like receptor subfamily B member 4	1.61	0.028	0.934	0.12	0.186	0.99
Cadr_000015194	ENSG00000110195	P15328	FOLR1	Folate receptor alpha	3.16	0.028	1.4	0.22	0.448	0.98
Cadr_000016822	ENSG00000167767	Q6KB66	KRT80	Keratin, type II cytoskeletal 80	3.9	0.034	2.63	0.086	3.84	0.078

Cadr_000030773	ENSG0000000851 6	Q9NPA2	MMP25	Matrix metalloproteinase-25	1.87	0.034	0.99	0.17	- 0.00766	1
Cadr_000019826	ENSG0000009292 9	Q70J99	UNC13D	Protein unc-13 homolog D	1.22	0.036	0.616	0.2	-0.0201	1
Cadr_000000564	ENSG0000011391 6	P41182	BCL6	B-cell lymphoma 6 protein	1.98	0.041	1.34	0.092	0.269	0.99
Cadr_000001890	ENSG0000016373 9	P09341	CXCL1	Growth-regulated alpha protein	- 3.21	0.07	-5.61	0.041	-5.17	0.05
Cadr_000002580				hypothetical protein	1.65	0.041	0.922	0.18	-0.104	1
Cadr_000004067	ENSG0000016868 5	P16871	IL7R	Interleukin-7 receptor subunit alpha	- 1.51	0.041	-1.16	0.073	-1.2	0.19
Cadr_000010587	ENSG0000014647 7	O75751	SLC22A3	Solute carrier family 22 member 3	2.2	0.041	0.538	0.68	0.182	1
Cadr_000012111	ENSG0000014251 2	Q96LC7	SIGLEC10	Sialic acid-binding Ig-like lectin 10	1.29	0.041	1.08	0.063	0.404	0.84
Cadr_000012112	ENSG0000012945 0	Q9Y336	SIGLEC9	Sialic acid-binding Ig-like lectin 9	1.76	0.041	1.33	0.073	0.564	0.81
Cadr_000016314	ENSG0000017528 7	Q5SRE7	PHYHD1	Phytanoyl-CoA dioxygenase domain-containing protein 1	1.88	0.041	1.06	0.16	-0.921	0.49
Cadr_000016800	ENSG0000020542 0	P02538	KRT6A	Keratin, type II cytoskeletal 6A	5.61	0.058	6.51	0.054	7.61	0.041
Cadr_000025545	ENSG0000018672 3	Q9Y4A9	OR10H1	Olfactory receptor 10H1	2.74	0.041	0.248	0.91	0.416	0.98
Cadr_000027936	ENSG0000013078 3	Q6P9F0	CCDC62	Coiled-coil domain-containing protein 62	1.31	0.041	0.899	0.096	0.734	0.41
Cadr_000028624	ENSG0000016845 4	Q86VQ3	TXNDC2	Thioredoxin domain-containing protein 2	2.18	0.041	1.9	0.057	1.29	0.36
Cadr_000029654	ENSG0000014745 4	Q9NYZ2	SLC25A37	Mitoferrin-1	1.87	0.041	1.8	0.054	0.816	0.58

Cadr_000012282	ENSG0000016768 5	Q8N0Y2	ZNF444	Zinc finger protein 444	1.71	0.042	0.93	0.19	0.0416	1
Cadr_000013472	ENSG0000017579 3	P31947	SFN	14-3-3 protein sigma	1.36	0.043	0.573	0.37	0.251	0.98
Cadr_000015197	ENSG0000016545 8	O15357	INPPL1	Phosphatidylinositol 3,4,5-trisphosphate 5- phosphatase 2	1.01	0.043	0.477	0.29	0.233	0.96
Cadr_000009001	ENSG0000027643 0	B3EWG5	FAM25C	Protein FAM25C	4.83	0.047	4.08	0.065	4.95	0.096
Cadr_000016797	ENSG0000020542 0	P02538	KRT6A	Keratin, type II cytoskeletal 6A	5.96	0.053	6.65	0.054	7.47	0.047
Cadr_000025199	ENSG0000021445 6	Q00G26	PLIN5	Perilipin-5	2.84	0.048	0.845	0.6	0.586	0.97
Cadr_000025074					1.12	0.05	0.453	0.42	0.0936	1