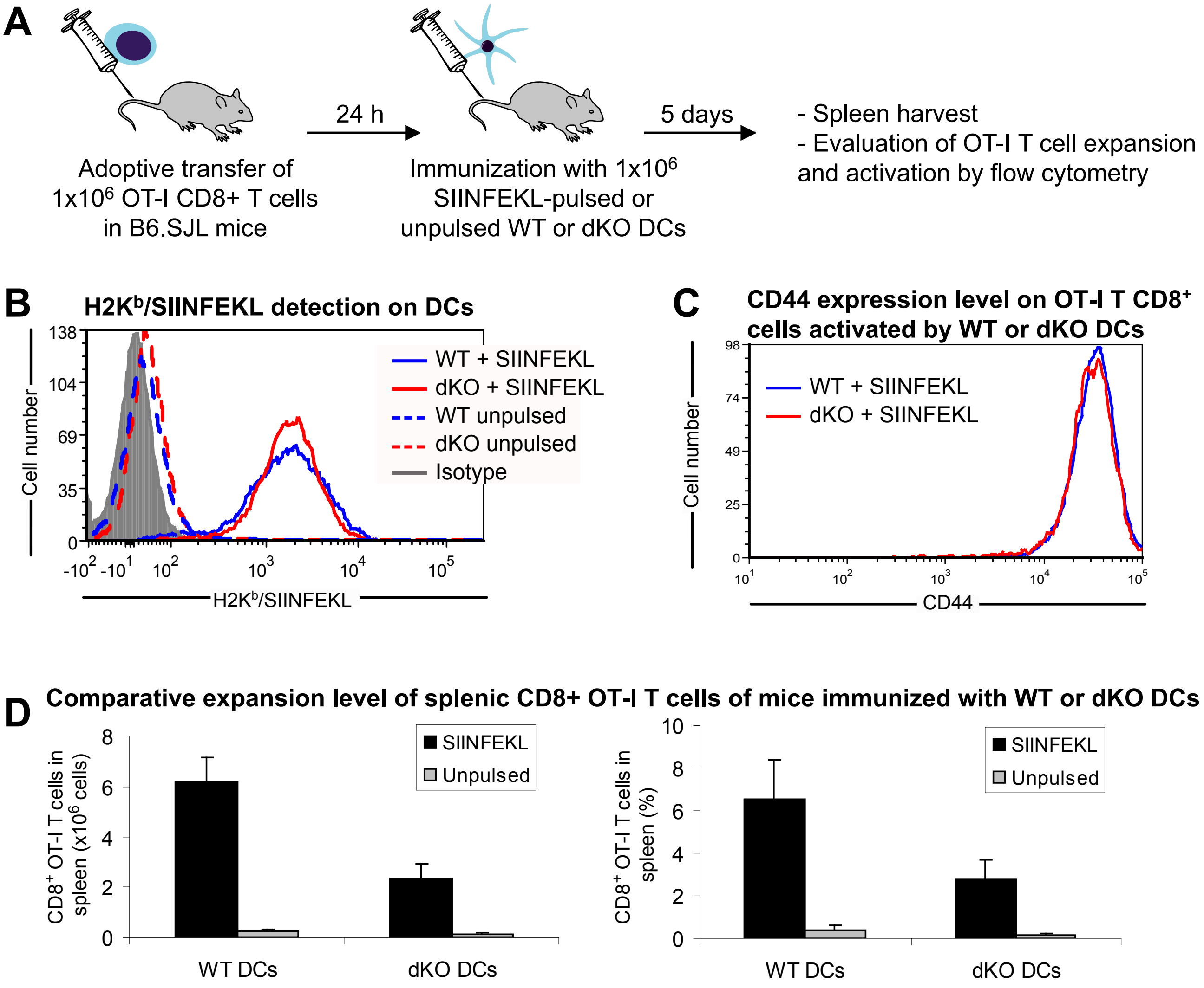

Figure S1. dKO DCs are able to activate T cells but are less efficient than WT DCs. (*A*) Experimental model. (*B*) WT and dKO DCs pulsed with SIINFEKL express similar levels of H2K^b/SIINFEKL at cell surface. Mature WT and dKO DCs were either left untouched or stripped with mild acid buffer, pulsed with 2 μM of SIINFEKL peptide for 1h at 26°C followed by a 3h incubation at 37°C. SIINFEKL cell-surface level was compared by flow cytometry using the 25-D1.16 antibody (Porgador A et al, Immunity 1997, 6:715-26). Showing one representative experiment. (*C*) dKO DCs are able to activate CD8$^+$ OT-I T cells. CD8$^+$ OT-I T cells from mice primed with SIINFEKL-pulsed WT or dKO DCs express similar levels of CD44. Showing one representative experiment. (*D*) dKO DCs activate OT-I T cells less efficiently than WT DCs. Mice primed with SIINFEKL-pulsed WT or dKO DCs were evaluated for their abundance of splenic CD8$^+$ OT-I T cells (mean +/- SD of triplicate experiments).

Supplemental Table S1. Total list of MHC I-peptides detected on DCs

Peptide			Mascot	Average intensity		Fold change		MHC I					
number	*m/z*	Charge	score	WT	dKO	WT / dKO	P value	allele	Peptide sequence	IPI accession	Gene ID	Gene symbol	Description
1	520,22	2	66	17719197	15000	≥ 1181,3	0,0121	H2Db	GGVVNMYHM	IPI00116712	16913	Psmb8	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)
2	460,25	2	40	5711531	15000	≥ 380,8	0,0289	H2Kb	ATRSFPQL	IPI00114017	11750	Anxa7	annexin A7
3	624,83	2	44	3109929	15000	≥ 207,3	0,0521	H2Db	HAIRNSFQYL	IPI00129408	170749	Mtmr4	myotubularin related protein 4
4	472,28	2	55	17359812	108141	160,5	n/a	H2Kb	TIIIFHSL	IPI00409303	14049	Eya2	eyes absent 2 homolog (Drosophila)
4	472,28	2	55	17359812	108141	160,5	n/a	H2Kb	TIIIFHSL	IPI00409303	14050	Eya3	eyes absent 3 homolog (Drosophila)
5	497,27	2	43	2389015	15000	≥ 159,3	0,0166	H2Kb	VVYIYHSL	IPI00131778	67014	Mina	myc induced nuclear antigen
6	467,28	2	47	6002847	49705	120,8	0,0416	H2Kb	SALRFLNL	IPI00467059	71728	Stk11ip	serine/threonine kinase 11 interacting protein
7	479,28	2	39	1646903	15000	≥ 109,8	0,0062	H2Kb	KNVLFSHL	IPI00119575	19085	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta
7	479,28	2	39	1646903	15000	≥ 109,8	0,0062	H2Kb	KNVLFSHL	IPI00119575	19084	Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha
8	524,27	2	65	1452443	15000	≥ 96,8	0,0113	H2Db	RQILNADAM	IPI00348445	66185	1110037F02Rik	RIKEN cDNA 1110037F02 gene
9	496,78	2	42	1408070	15000	≥ 93,9	0,0069	H2Db	SGLLNMTKI	IPI00336411	216445	Arhgap9	Rho GTPase activating protein 9
10	525,26	2	29	1400447	15000	≥ 93,4	0,0036	H2Kb	HVYYFAHL	IPI00458896	74558	Gvin1	GTPase, very large interferon inducible 1
11	510,80	2	56	1249205	15000	≥ 83,3	0,0097	H2Kb	VITNFSARI	IPI00652882	68505	1110014N23Rik	RIKEN cDNA 1110014N23 gene
12	507,26	2	49	1232097	15000	≥ 82,1	0,0232	H2Kb	STLIYRNM	IPI00111739	75660	Lin37	lin-37 homolog (C. elegans)
13	597,28	2	27	1207015	15000	≥ 80,5	0,0030	H2Db	SAIHNFYDNI	IPI00115639	68652	Map3k7ip2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2
14	523,75	2	34	1154077	15000	≥ 76,9	0,0141	H2Db	SQVYNDAHI	IPI00669369	66923	Pbrm1	polybromo 1
15	537,27	2	40	1142903	15000	≥ 76,2	0,0366	H2Kb	LVYQFKEM	IPI00120304	13709	Elf1	E74-like factor 1
15	537,27	2	40	1142903	15000	≥ 76,2	0,0366	H2Kb	LVYQFKEM	IPI00120304	56501	Elf4	E74-like factor 4 (ets domain transcription factor)
16	461,76	2	62	12933107	188768	68,5	n/a	H2Db	GAVQNIAHL	IPI00187396	74125	Armc8	armadillo repeat containing 8
17	496,28	2	32	4515404	66333	68,1	0,0047	H2Kb	ISLEFRNL	IPI00134836	14137	Fdft1	farnesyl diphosphate farnesyl transferase 1
18	506,30	2	43	996092	15000	≥ 66,4	0,0619	H2Kb	KSYLFQLL	IPI00124240	12566	Cdk2	cyclin-dependent kinase 2
19	447,74	2	53	35875678	654361	54,8	0,0034	H2Db	GGIQNVGHI	IPI00624746	23918	Impdh2	inosine 5'-phosphate dehydrogenase 2
20	493,24	2	41	695711	15000	≥ 46,4	0,0534	H2Kb	SNYRFEGL	IPI00606873	319955	Ercc6	excision repair cross-complementing rodent repair deficiency, complementation group 6
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100039840	LOC100039840	glyceraldehyde-3-phosphate dehydrogenase pseudogene
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100041342	LOC100041342	glyceraldehyde-3-phosphate dehydrogenase pseudogene
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	215974	EG215974	predicted gene, EG215974
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	638833	EG638833	predicted gene, EG638833
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100040109	LOC100040109	similar to Glyceraldehyde-3-phosphate dehydrogenase
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100041831	LOC100041831	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)

21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	676923	LOC676923	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100040634	LOC100040634	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100048117	LOC100048117	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100047352	LOC100047352	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100044981	LOC100044981	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100039258	LOC100039258	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	640374	LOC640374	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100041236	LOC100041236	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
21	479,75	2	37	628058	15000	≥ 42,0	0,0783	Qa2	GLMTTVHAI	IPI00271869	100039875	LOC100039875	similar to LOC654472 protein
22	645,34	2	33	604411	15000	≥ 40,3	0,0041	H2Db	AQYGNILKHVM	IPI00469331	69482	Nup35	nucleoporin 35
23	486,78	2	48	3552727	89347	39,8	0,0043	H2Db	KAPLNIAVM	IPI00515476	432555	EG432555	predicted gene, EG432555
23	486,78	2	48	3552727	89347	39,8	0,0043	H2Db	KAPLNIAVM	IPI00515476	245240	9930111J21Rik	RIKEN cDNA 9930111J21 gene
23	486,78	2	48	3552727	89347	39,8	0,0043	H2Db	KAPLNIAVM	IPI00515476	667214	RP23-269N23.3	interferon-inducible GTPase family member
24	510,81	2	54	563705	15000	≥ 37,6	0,0368	H2Db	YGLLNVTKI	IPI00223751	75415	Arhgap12	Rho GTPase activating protein 12
25	501,27	2	42	561646	15000	≥ 37,4	0,0298	H2Db	SALANYIHL	IPI00331026	58245	Gpr180	G protein-coupled receptor 180
26	488,76	2	41	491858	15000	32,8	0,0201	H2Kb	VNQKFNNL	IPI00310862	218977	Dlg7	discs, large homolog 7 (Drosophila)
27	524,81	2	41	5781657	178129	32,5	0,0022	H2Db	YGIRNSLLI	IPI00331302	20133	Rrm1	ribonucleotide reductase M1
28	470,24	2	44	443727	15000	≥ 29,6	0,0531	H2Kb	SALRFQAM	IPI00462761	74015	Fcho1	FCH domain only 1
29	472,25	2	48	3934188	140122	28,1	0,0228	H2Kb	VNFVHTNL	IPI00111412	67891	Rpl4	ribosomal protein L4
30	529,79	2	50	410092	15000	≥ 27,3	0,0934	H2Db	SSLLNIQHF	IPI00762371	75089	Uhrf1bp1l	UHRF1 (ICBP90) binding protein 1-like
31	456,22	2	53	402561	15000	≥ 26,8	0,0126	H2Kb	SGYSFTHI	IPI00110922	67019	Actr6	ARP6 actin-related protein 6 homolog (yeast)
32	515,78	2	48	401402	15000	≥ 26,8	0,0955	H2Kb	SALEFLTHL	IPI00225210	231841	AA881470	EST AA881470
33	459,79	2	29	1152330	45333	25,4	0,0030	H2Kb	IALRYVAL	IPI00120503	70349	Copb1	coatomer protein complex, subunit beta 1
34	543,29	2	44	1760804	69450	25,4	0,0257	H2Db	FAVVNHQGTL	IPI00228479	216825	Usp22	ubiquitin specific peptidase 22
35	496,28	2	49	380271	15000	≥ 25,4	0,0014	H2Db	VAVKNSGGFL	IPI00266942	52635	D12Ertd551e	DNA segment, Chr 12, ERATO Doi 551, expressed
36	561,27	2	31	377387	15000	≥ 25,2	0,0832	H2Db	WAVSNREML	IPI00330873	68477	Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)
37	552,30	2	49	337581	15000	≥ 22,5	n/a	H2Db	SSLVNKEDVL	IPI00222429	211548	Nomo1	nodal modulator 1
38	591,32	2	38	337381	15000	≥ 22,5	0,0023	H2Db	NAPVNPTRAEL	IPI00124757	58801	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1
39	525,78	2	55	5520689	247575	22,3	0,1098	H2Kb	RVAEFTTNL	IPI00123181	17886	Myh9	myosin, heavy polypeptide 9, non-muscle
40	713,83	2	92	4177474	188411	22,2	n/a	H2Db	SVMENSKVLGEAM	IPI00465786	21894	Tln1	talin 1
41	507,29	2	36	796850	36000	22,1	0,0009	H2Kb	ISYLYNKL	IPI00121293	57259	Tob2	transducer of ERBB2, 2
41	507,29	2	36	796850	36000	22,1	0,0009	H2Kb	ISYLYNKL	IPI00121293	22057	Tob1	transducer of ErbB-2.1

42	567,77	2	75	42373792	2076049	20,4	0,0092	H2Db	YAGSNFPEHI	IPI00177038	66713	Actr2	ARP2 actin-related protein 2 homolog (yeast)
43	527,81	2	39	12264388	657047	18,7	0,0003	H2Kb	RQYIFSKL	IPI00227871	74558	Gvin1	GTPase, very large interferon inducible 1
44	485,31	2	34	1089937	59766	18,2	0,0238	H2Db	AALQNLVKI	IPI00323881	16211	Kpnb1	karyopherin (importin) beta 1
45	480,26	2	40	1386867	77854	17,8	0,0889	H2Db	AANINKESI	IPI00122743	226414	Dars	aspartyl-tRNA synthetase
46	481,81	2	39	261937	15000	≥ 17,5	0,0734	H2Kb	SILRFITI	IPI00127375	17874	Myd88	myeloid differentiation primary response gene 88
47	468,27	2	52	8225059	478984	17,2	0,0973	H2Kb	VNVRFSTI	IPI00122070	19252	Dusp1	dual specificity phosphatase 1
48	532,75	2	34	249036	15000	≥ 16,6	0,0681	H2Kb	TTYKYEMI	IPI00463573	223691	Eif3eip	eukaryotic translation initiation factor 3, subunit E interacting protein
49	579,30	2	50	3495990	226647	15,4	0,0263	Qa2	DLLDIRHEF	IPI00132722	11745	Anxa3	annexin A3
50	456,76	2	44	229185	15000	≥ 15,3	0,0064	H2Kb	KSFLFSAL	IPI00461438	170439	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)
51	521,28	2	55	2901091	194952	14,9	0,1049	H2Kb	LQYEFTKL	IPI00474689	71409	Fmnl2	formin-like 2
51	521,28	2	55	2901091	194952	14,9	0,1049	H2Kb	LQYEFTKL	IPI00474689	22379	Fmnl3	formin-like 3
52	482,28	2	49	6161253	418613	14,7	0,0398	H2Kb	TSLRFLNL	IPI00458889	434215	Lrrc32	leucine rich repeat containing 32
53	525,77	2	53	11387673	782044	14,6	0,0020	H2Kb	LQYEFTHL	IPI00131441	57778	Fmnl1	formin-like 1
54	490,81	2	33	200879	15000	≥ 13,4	n/a	Qa2	SVISVIHLI	IPI00162949	52858	Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
55	495,74	2	30	200826	15000	≥ 13,4	0,0391	H2Kb	IAMEFNHL	IPI00128389	19224	Ptgs1	prostaglandin-endoperoxide synthase 1
56	484,77	2	72	916462	68817	13,3	n/a	Qa2	ASIDILHSI	IPI00222515	69077	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
57	503,78	2	41	1761490	132445	13,3	0,1818	H2Kb	EIVTFERL	IPI00122521	14359	Fxr1h	fragile X mental retardation gene 1, autosomal homolog
58	495,27	2	42	26808072	2027338	13,2	0,0162	H2Db	STIRNAQSI	IPI00652172	17969	Ncf1	neutrophil cytosolic factor 1
59	666,31	2	42	196682	15000	≥ 13,1	0,0032	H2Db	SAPRNQTFTYM	IPI00129741	13654	Egr2	early growth response 2
60	509,26	2	44	2288829	176919	12,9	0,0184	H2Kb	FAYRFSNL	IPI00469755	110816	Pwp2	PWP2 periodic tryptophan protein homolog (yeast)
61	503,33	2	39	204874	16000	12,8	n/a	Qa2	AILQVLHVL	IPI00115875	224020	Pi4ka	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
62	465,75	2	39	931036	73850	12,6	n/a	H2Kb	VGITYQHI	IPI00120322	73830	Eif3k	eukaryotic translation initiation factor 3, subunit K
63	555,29	2	48	8021880	637848	12,6	0,0043	H2Db	SMVQNRVFL	IPI00475204	94176	Dock2	dedicator of cyto-kinesis 2
64	469,79	2	54	1430854	116793	12,3	0,2439	H2Kb	VFYAVKVL	IPI00125834	20393	Sgk1	serum/glucocorticoid regulated kinase 1
65	505,28	2	36	879332	72617	12,1	0,0894	H2Kb	SAPRFLTAF	IPI00652892	233575	Frag1	FGF receptor activating protein 1
66	469,26	2	66	25200554	2124039	11,9	0,0186	H2Kb	VNVDYSKL	IPI00125929	17992	Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4
67	624,30	2	55	276431	23993	11,5	n/a	H2Kb	VSYWFDQRF	IPI00108849	20442	St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
68	553,76	2	50	172275	15000	≥ 11,5	0,0118	H2Db	RANQNFDEI	IPI00624420	77480	Kidins220	kinase D-interacting substrate 220
69	477,27	2	30	171521	15000	≥ 11,4	0,0002	H2Db	VSLINAHSL	IPI00461570	268749	Rnf31	ring finger protein 31
70	583,31	2	30	573279	50668	11,3	n/a	H2Db	YTVENAKDII	IPI00113738	22375	Wars	tryptophanyl-tRNA synthetase
71	547,75	2	45	1470764	131072	11,2	0,1288	H2Db	YVLHNSNTM	IPI00123494	21762	Psmd2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
72	562,80	2	72	565347	50628	11,2	n/a	H2Db	SAVENILEHL	IPI00269020	121022	Mrps6	mitochondrial ribosomal protein S6

73	525,30	2	54	4426653	398013	11,1	0,0039	H2Db	KTVVNKDVF	IPI00749639	19942	Rpl27	ribosomal protein L27
74	546,28	2	46	161509	15000	≥ 10,8	0,0015	H2Db	YMLANLTHL	IPI00133107	66689	Klhl28	kelch-like 28 (Drosophila)
75	480,78	2	43	1038860	97779	10,6	0,0050	H2Db	KAIVNVIGM	IPI00623284	81898	Sf3b1	splicing factor 3b, subunit 1
76	511,78	2	36	3037235	296617	10,2	0,1106	H2Db	KSVENFVSL	IPI00117274	94176	Dock2	dedicator of cyto-kinesis 2
77	563,34	2	73	6073794	602404	10,1	0,0096	H2Db	FALANHLIKV	IPI00126083	13660	Ehd1	EH-domain containing 1
77	563,34	2	73	6073794	602404	10,1	0,0096	H2Db	FALANHLIKV	IPI00126083	57440	Ehd3	EH-domain containing 3
78	521,32	2	48	14031756	1420380	9,9	0,0030	H2Db	VSILNRQVL	IPI00263048	101706	Numa1	nuclear mitotic apparatus protein 1
79	545,80	2	49	591593	59989	9,9	0,0550	H2Db	VSNLNRQFL	IPI00130173	22200	Ube1c	ubiquitin-activating enzyme E1C
79	545,80	2	49	591593	59989	9,9	0,0550	H2Db	VSNLNRQFL	IPI00130173	50995	Uba2	ubiquitin-like modifier activating enzyme 2
80	555,29	2	44	1776196	180375	9,8	0,0214	Qa2	QQQQQLHSL	IPI00462992	192191	Med9	mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)
81	508,77	2	43	1590254	162926	9,8	0,0098	H2Db	SAVENKQQI	IPI00314845	20620	Plk2	polo-like kinase 2 (Drosophila)
82	510,79	2	63	6653949	684846	9,7	0,0067	H2Db	SLITNKVVM	IPI00607023	18950	Pnp	purine-nucleoside phosphorylase
83	457,76	2	47	112535617	11603225	9,7	0,0023	H2Kb	ATLVFHNL	IPI00228955	20848	Stat3	signal transducer and activator of transcription 3
84	440,76	2	63	142975	15000	≥ 9,5	0,0444	H2Kb	VSISFKSL	IPI00663048	14727	Gp49a	glycoprotein 49 A
84	440,76	2	63	142975	15000	≥ 9,5	0,0444	H2Kb	VSISFKSL	IPI00663048	22201	Uba1	ubiquitin-like modifier activating enzyme 1
85	490,26	2	54	10089368	1103707	9,1	0,0174	H2Kb	QSIEFSRL	IPI00129276	13669	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)
86	577,83	2	45	751757	85255	8,8	n/a	H2Kb	KIFEFKETL	IPI00226188	227541	Camk1d	calcium/calmodulin-dependent protein kinase ID
87	523,77	2	40	131832	15000	≥ 8,8	0,0507	Qa2	YSIQGQHTI	IPI00128904	23983	Pcbp1	poly(rC) binding protein 1
88	479,26	2	39	129686	15000	≥ 8,6	0,0092	H2Kb	KVYTFNSV	IPI00127713	67972	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1
88	479,26	2	39	129686	15000	≥ 8,6	0,0092	H2Kb	KVYTFNSV	IPI00127713	11941	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2
88	479,26	2	39	129686	15000	≥ 8,6	0,0092	H2Kb	KVYTFNSV	IPI00127713	320707	Atp2b3	ATPase, Ca++ transporting, plasma membrane 3
88	479,26	2	39	129686	15000	≥ 8,6	0,0092	H2Kb	KVYTFNSV	IPI00127713	381290	Atp2b4	ATPase, Ca++ transporting, plasma membrane 4
89	569,28	2	42	128395	15000	≥ 8,6	0,1660	H2Kb	TNFEYLTHL	IPI00399954	17101	Lyst	lysosomal trafficking regulator
90	480,74	2	40	2142444	258053	8,3	0,0472	H2Kb	TSFRYSSL	IPI00356888	319448	Fndc3a	fibronectin type III domain containing 3a
91	465,75	2	49	447882	57333	7,8	0,0073	H2Db	TGPSNVDKL	IPI00387390	12649	Chek1	checkpoint kinase 1 homolog (S. pombe)
92	485,27	2	27	116831	15000	≥ 7,8	0,1169	H2Kb	KAFTYINL	IPI00124700	22042	Tfrc	transferrin receptor
93	497,27	2	66	12776823	1654672	7,7	0,0770	H2Kb	INFDFPKL	IPI00109932	13209	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
94	499,77	2	32	1900935	246770	7,7	0,0948	H2Kb	ISFEFRSL	IPI00113049	210582	Coq10a	coenzyme Q10 homolog A (yeast)
94	499,77	2	32	1900935	246770	7,7	0,0948	H2Kb	ISFEFRSL	IPI00113049	67876	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)
95	467,79	2	31	289484	37667	7,7	0,0258	H2Kb	VILSFRSL	IPI00319320	50884	Nckap1	NCK-associated protein 1
96	494,25	2	26	115047	15000	≥ 7,7	n/a	H2Kb	SSYNYRVV	IPI00117630	16438	Itpr1	inositol 1,4,5-triphosphate receptor 1
97	558,79	2	41	6105677	800126	7,6	0,0482	H2Db	YVHVNRDTL	IPI00124762	59047	Pnkp	polynucleotide kinase 3'- phosphatase
98	490,76	2	36	5675159	749774	7,6	0,0075	H2Kb	SGYIYHKL	IPI00420949	19704	Upf1	UPF1 regulator of nonsense transcripts homolog (yeast)
99	665,33	2	60	112840	15000	≥ 7,5	0,0045	H2Db	SQMTNLQELHL	IPI00350794	231549	Lrrc8d	leucine rich repeat containing 8D

100	546,79	2	49	1289095	172374	7,5	0,0489	H2Db	YKNVNQEVV	IPI00320165	53415	Htatip2	HIV-1 tat interactive protein 2, homolog (human)
101	579,28	2	38	518070	69364	7,5	0,0239	H2Db	YTLRNQDTF	IPI00554857	18626	Per1	period homolog 1 (Drosophila)
102	483,77	2	62	36755744	4936084	7,4	0,0056	H2Db	ASVLNVNHI	IPI00465535	81702	Ankrd17	ankyrin repeat domain 17
103	530,76	2	36	1615730	219039	7,4	0,0056	H2Db	SSPSNKFFF	IPI00462466	235626	Setd2	SET domain containing 2
104	464,75	2	47	2401123	332807	7,2	0,2597	H2Kb	SAFSFRTL	IPI00341601	107035	Fbxo38	F-box protein 38
105	456,25	2	63	6686479	930627	7,2	0,0024	H2Db	ASVINGHTL	IPI00473543	329154	Ankrd44	ankyrin repeat domain 44
106	491,29	2	52	2959450	417161	7,1	0,1239	Qa2	SVLNVLHSL	IPI00463573	223691	Eif3eip	eukaryotic translation initiation factor 3, subunit E interacting protein
107	516,29	2	56	7004022	1000822	7	0,0001	H2Db	ISLKNSQEI	IPI00227871	74558	Gvin1	GTPase, very large interferon inducible 1
108	495,74	2	56	14695737	2149127	6,8	0,0274	H2Db	SAPENAVRM	IPI00127501	14790	Grcc10	gene rich cluster, C10 gene
109	478,79	2	51	1591992	233484	6,8	0,0184	H2Db	VAVVNKVDI	IPI00742278	18145	Npc1	Niemann Pick type C1
110	581,79	2	40	100369	15000	≥ 6,7	0,1202	Qa2	EFIEVFHEL	IPI00322431	224860	Plcl2	phospholipase C-like 2
111	523,29	2	70	53986773	8193413	6,6	0,0277	H2Db	NSIRNLDTI	IPI00123202	54138	Atxn10	ataxin 10
112	511,29	2	28	4424290	679547	6,5	0,0048	H2Db	AAITNKYQL	IPI00127454	106298	Rrn3	RRN3 RNA polymerase I transcription factor homolog (yeast)
113	555,80	2	60	4478468	694556	6,4	0,0006	H2Kb	IGPTYYQRL	IPI00320034	231329	Polr2b	polymerase (RNA) II (DNA directed) polypeptide B
114	450,78	2	48	6328638	985316	6,4	0,0316	H2Db	GAVTNVKVI	IPI00108271	15568	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)
114	450,78	2	48	6328638	985316	6,4	0,0316	H2Db	GAVTNVKVI	IPI00108271	15569	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)
114	450,78	2	48	6328638	985316	6,4	0,0316	H2Db	GAVTNVKVI	IPI00108271	15571	Elavl3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)
115	494,76	2	34	95634	15000	≥ 6,4	0,1584	H2Kb	ISLDYQHL	IPI00224519	72503	2610507B11Rik	RIKEN cDNA 2610507B11 gene
116	536,30	2	50	17404078	2734634	6,4	0,0037	H2Db	IGIENIHYL	IPI00626860	68995	Mcts1	malignant T cell amplified sequence 1
116	536,30	2	50	17404078	2734634	6,4	0,0037	H2Db	IGIENIHYL	IPI00626860	66405	Mcts2	malignant T cell amplified sequence 2
117	514,27	2	38	95155	15000	≥ 6,3	0,1171	H2Kb	AVVAFVMKM	IPI00674528	14972	H2-K1	histocompatibility 2, K1, K region
118	503,77	2	38	2346888	370301	6,3	0,0012	H2Kb	TTYKYFAL	IPI00262966	214290	Zcchc6	zinc finger, CCHC domain containing 6
119	435,74	2	54	7201463	1150790	6,3	0,0756	H2Kb	SGYKFGVL	IPI00653716	68153	Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)
120	503,78	2	33	217329	35500	6,1	n/a	H2Kb	VTYIFNHL	IPI00123216	107769	Tm6sf1	transmembrane 6 superfamily member 1
121	555,80	2	53	8017302	1311707	6,1	0,0147	Qa2	SQLDREHIL	IPI00458546	22029	Traf1	Tnf receptor-associated factor 1
122	438,78	2	43	91590	15000	≥ 6,1	0,0396	H2Kb	AIIAFKTL	IPI00170221	73341	Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
123	539,29	2	43	3454044	574091	6	0,0397	Qa2	TLLNVYHAF	IPI00128818	13204	Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
124	532,28	2	38	88234	15000	≥ 5,9	0,1412	H2Kb	SNLYYKYL	IPI00135233	56697	Akap10	A kinase (PRKA) anchor protein 10
125	681,37	2	64	87789	15000	≥ 5,9	n/a	H2Db	YQLVNSIFQHL	IPI00751623	74558	Gvin1	GTPase, very large interferon inducible 1
126	560,31	2	42	11805196	2026677	5,8	0,0018	H2Db	AAIRNYGIEL	IPI00123775	17769	Mthfr	5,10-methylenetetrahydrofolate reductase
127	422,24	2	39	86037	15000	≥ 5,7	n/a	H2Kb	AIVSFAHV	IPI00118158	17685	Msh2	mutS homolog 2 (E. coli)

128	465,77	2	31	85884	15000	≥ 5,7	0,0623	H2Db	LSVRNGATL	IPI00128366	170826	Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta
129	496,32	2	64	1828535	322130	5,7	0,1475	Qa2	IVIGVLHQL	IPI00114852	21428	Mlx	MAX-like protein X
130	563,77	2	35	84476	15000	≥ 5,6	0,0181	H2Db	SQVRNNVYM	IPI00330961	14411	Slc6a12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12
131	465,77	2	47	4102305	728523	5,6	0,0218	H2Db	ASLVNADKL	IPI00321497	233405	Vps33b	vacuolar protein sorting 33B (yeast)
132	490,76	2	47	2084226	380550	5,5	0,0194	H2Kb	SNIQYRSL	IPI00229599	215690	Nav1	neuron navigator 1
133	526,79	2	27	3167245	583437	5,4	0,0018	H2Db	FAPKNIYSI	IPI00108003	12978	Csf1r	colony stimulating factor 1 receptor
134	558,80	2	50	680742	126667	5,4	0,0225	H2Db	SQLKNADVEL	IPI00753468	11772	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit
135	461,27	2	53	9480546	1767412	5,4	0,0634	H2Kb	QSIVFKSL	IPI00652317	11630	Aim1	absent in melanoma 1
136	503,77	2	40	14069564	2637800	5,3	n/a	H2Kb	ISFKFDHL	IPI00330063	12340	Capza1	capping protein (actin filament) muscle Z-line, alpha 1
137	569,27	2	49	77526	15000	≥ 5,2	0,0983	H2Kb	NTYNYKSTF	IPI00116309	97112	Nmd3	NMD3 homolog (S. cerevisiae)
138	530,27	2	33	76976	15000	≥ 5,1	n/a	H2Kb	MSYLFRNI	IPI00153950	212627	Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2
139	543,78	2	27	454923	88859	5,1	0,0100	H2Db	YTVANKEYV	IPI00321744	67458	Ergic1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1
140	534,77	2	47	2293267	448006	5,1	n/a	H2Db	QTVENVEHL	IPI00269223	75425	2610036D13Rik	RIKEN cDNA 2610036D13 gene
141	510,80	2	36	818888	161119	5,1	0,2405	H2Kb	IVYKWVNV	IPI00119320	27060	Tcirg1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3
142	466,77	2	33	3217624	633719	5,1	0,0593	H2Db	GSLKNVTTL	IPI00454039	59079	Erbb2ip	Erbb2 interacting protein
143	549,28	2	49	902930	178935	5	0,0459	H2Db	NAPQNPESKL	IPI00420697	76022	5830417I10Rik	RIKEN cDNA 5830417I10 gene
144	631,37	2	43	1717417	345408	5	0,0761	H2Db	TAVVNRVFDKL	IPI00309379	16912	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)
145	551,77	2	52	1618769	326593	5	0,0438	H2Kb	RNYQFDFL	IPI00457731	67465	Sf3a1	splicing factor 3a, subunit 1
146	505,29	2	52	350771	70981	4,9	n/a	H2Db	VTVLNVDHL	IPI00124590	26885	Casp8ap2	caspase 8 associated protein 2
147	458,76	2	73	985900	199991	4,9	0,0169	H2Db	ASIVNKDGL	IPI00271799	19015	Ppard	peroxisome proliferator activator receptor delta
148	526,80	2	39	266011	55782	4,8	n/a	Qa2	EILEVLHSL	IPI00319965	66413	Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6
149	473,81	2	40	1740629	365196	4,8	0,1401	H2Kb	VIVRFLTV	IPI00230660	267019	Rps15a	ribosomal protein S15a
150	571,30	2	66	664090	140496	4,7	0,0632	H2Kb	KTYQFLNDI	IPI00128482	224823	BC011248	cDNA sequence BC011248
151	487,73	2	58	7498251	1600516	4,7	0,2220	H2Kb	STLTYSRM	IPI00125834	20393	Sgk1	serum/glucocorticoid regulated kinase 1
152	496,79	2	60	40343097	8640481	4,7	0,0043	H2Db	YGLKNLTAL	IPI00798457	83490	Pik3ap1	phosphoinositide-3-kinase adaptor protein 1
153	593,81	2	47	176635	38145	4,6	0,0621	H2Db	RALENPDTASL	IPI00464166	104831	Ptpn23	protein tyrosine phosphatase, non-receptor type 23
154	496,76	2	62	29473934	6416519	4,6	0,0043	H2Db	AAMKNVTEL	IPI00230707	22628	Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
155	524,78	2	52	4770048	1039064	4,6	0,0153	H2Kb	VSFTYRYL	IPI00120923	80743	Vps16	vacuolar protein sorting 16 (yeast)
156	546,79	2	54	255074	57078	4,5	0,1658	H2Kb	TIVEFLHSF	IPI00130157	116848	Baz2a	bromodomain adjacent to zinc finger domain, 2A
157	635,79	2	66	32121773	7188670	4,5	0,0082	H2Db	SMGKNPTDEYL	IPI00758006	67268	2900073G15Rik	RIKEN cDNA 2900073G15 gene
158	466,79	2	29	66993	15000	≥ 4,5	n/a	H2Kb	AVIKFLEL	IPI00118158	17685	Msh2	mutS homolog 2 (E. coli)

159	469,27	2	49	330632	75423	4,4	0,0002	H2Kb	SNLKYSLL	IPI00120860	70028	Dopey2	dopey family member 2
160	555,79	2	36	6323471	1444711	4,4	0,0044	H2Db	SSIQNGKYTL	IPI00551078	338523	Jhdm1d	jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)
161	590,79	2	51	36044628	8307834	4,3	0,0041	H2Db	SAPRNFVENF	IPI00461189	58523	Elp2	elongation protein 2 homolog (S. cerevisiae)
162	487,76	2	27	2330731	540269	4,3	0,0938	H2Db	AALENDKTI	IPI00110312	140858	Wdr5	WD repeat domain 5
162	487,76	2	27	2330731	540269	4,3	0,0938	H2Db	AALENDKTI	IPI00110312	69544	Wdr5b	WD repeat domain 5B
163	543,78	2	44	33624179	7820120	4,3	0,0206	H2Db	FGIHNGVETL	IPI00223864	74182	Prei4	preimplantation protein 4
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	12648	Chd1	chromodomain helicase DNA binding protein 1
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	244059	Chd2	chromodomain helicase DNA binding protein 2
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	216848	Chd3	chromodomain helicase DNA binding protein 3
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	107932	Chd4	chromodomain helicase DNA binding protein 4
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	269610	Chd5	chromodomain helicase DNA binding protein 5
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	320790	Chd7	chromodomain helicase DNA binding protein 7
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	93761	Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
164	505,28	2	26	810986	191114	4,2	0,3220	H2Kb	RVLIFSQM	IPI00396802	93762	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
165	449,24	2	64	3375703	816049	4,1	0,0045	H2Db	ISGVNGTHI	IPI00387234	20815	Srpk1	serine/arginine-rich protein specific kinase 1
166	490,30	2	43	61464	15000	≥ 4,1	n/a	H2Kb	KVLVFNFL	IPI00308184	102566	Tmem16k	transmembrane protein 16K
167	634,84	2	53	470712	115333	4,1	0,0844	H2Db	FVISNYREQL	IPI00317217	67392	4833420G17Rik	RIKEN cDNA 4833420G17 gene
168	462,26	2	40	3276975	809774	4	0,0364	H2Kb	KSLTFTNL	IPI00756323	65969	Cubn	cubilin (intrinsic factor-cobalamin receptor)
169	578,82	2	33	353890	90003	3,9	0,0443	H2Db	NSVVNPNKATI	IPI00331301	54644	Otud5	OTU domain containing 5
170	526,32	2	34	58131	15000	≥ 3,9	n/a	H2Kb	IIVQFRYI	IPI00221884	233280	Nipa1	non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)
171	532,81	2	41	2657114	688524	3,9	0,0179	Qa2	EQVALVHRL	IPI00387354	12181	Bop1	block of proliferation 1
172	562,79	2	62	1082263	280875	3,9	0,0723	H2Db	FQKQNVTIM	IPI00125726	18126	Nos2	nitric oxide synthase 2, inducible, macrophage
173	535,75	2	66	1360798	357528	3,8	0,0037	H2Db	LSMRNTSVM	IPI00677484	12176	Bnip3	BCL2/adenovirus E1B interacting protein 1, NIP3
174	479,78	2	43	1537438	407561	3,8	0,0461	H2Db	SAVENVVKL	IPI00314451	85031	Pla1a	phospholipase A1 member A
175	512,29	2	42	349941	93362	3,7	n/a	Qa2	ALLDQLHTL	IPI00113730	17979	Ncoa3	nuclear receptor coactivator 3
176	547,29	2	45	1528582	413711	3,7	0,0338	Qa2	DVINVFHHL	IPI00123092	56706	Ccnl1	cyclin L1
177	474,75	2	41	1825910	497712	3,7	0,1073	H2Kb	SGYKFFSL	IPI00131321	74781	Wipi2	WD repeat domain, phosphoinositide interacting 2
178	522,79	2	47	10783479	3064662	3,5	0,0220	H2Db	RAIENIDTL	IPI00129319	66385	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7

179	489,27	2	65	35462555	10090507	3,5	0,0417	H2Kb	VNIEFKDL	IPI00133416	11307	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1
180	482,30	2	41	1957937	569292	3,4	0,2928	H2Kb	TTLIFQKL	IPI00129426	19696	Rel	reticuloendotheliosis oncogene
181	543,77	2	38	318474	93007	3,4	n/a	Qa2	AQNDIEHLF	IPI00226564	224171	C330027C09Rik	RIKEN cDNA C330027C09 gene
182	553,76	2	53	249701	73233	3,4	n/a	H2Db	FSLDNSSSHL	IPI00357440	100125587	OTTMUSG00000007002	predicted gene, OTTMUSG00000007002
183	480,76	2	57	500647	146960	3,4	0,3410	H2Kb	SALGYLHSI	IPI00228378	170755	Sgk3	serum/glucocorticoid regulated kinase 3
184	460,71	2	46	1082666	322317	3,4	0,0719	H2Kb	SGYKYVGM	IPI00128941	68090	Yif1a	Yip1 interacting factor homolog A (S. cerevisiae)
185	579,28	2	36	7068279	2108268	3,4	0,0408	H2Db	RSLDNGGYYI	IPI00230138	12143	Blk	B lymphoid kinase
185	579,28	2	36	7068279	2108268	3,4	0,0408	H2Db	RSLDNGGYYI	IPI00230138	17096	Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog
186	553,78	2	58	6254494	1876623	3,3	0,0387	H2Kb	KNHEFIATF	IPI00760055	18753	Prkcd	protein kinase C, delta
187	529,29	2	38	49813	15000	≥ 3,3	0,0644	Qa2	NIAETLHFL	IPI00623570	14897	Trip12	thyroid hormone receptor interactor 12
188	506,78	2	40	616667	186428	3,3	0,0029	H2Db	GAVKNLTYF	IPI00314673	20443	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
189	476,78	2	59	457456	141204	3,2	0,1080	Qa2	GLLEIAHSL	IPI00464115	320938	Tnpo3	transportin 3
190	523,77	2	47	6574724	2052330	3,2	0,0260	H2Kb	HIYEFPQL	IPI00225371	106840	Unc119b	unc-119 homolog B (C. elegans)
191	472,78	2	51	829317	261967	3,2	0,0255	H2Db	VGLINKDSV	IPI00553465	192195	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)
192	546,26	2	29	288516	91752	3,1	n/a	H2Db	DAIHNFDFL	IPI00665580	224088	Atp13a3	ATPase type 13A3
193	510,76	2	44	2817509	904068	3,1	0,3795	H2Kb	STYKFFEV	IPI00762267	66480	Rpl15	ribosomal protein L15
194	540,79	2	54	5483080	1784688	3,1	0,1839	Qa2	NVIEVEHQL	IPI00676977	16950	Loxl3	lysyl oxidase-like 3
195	475,27	2	45	14863382	4848856	3,1	0,0162	H2Kb	SVIKFENL	IPI00132057	66980	Zdhhc6	zinc finger, DHHC domain containing 6
196	556,76	2	34	6219583	2057745	3	0,2028	H2Kb	EIYEFHKM	IPI00652172	17969	Ncf1	neutrophil cytosolic factor 1
197	459,29	2	28	213151	70686	3	0,0656	H2Kb	VIVKFAQL	IPI00551454	18572	Pdcd11	programmed cell death protein 11
198	464,77	2	33	45108	15000	≥ 3,0	0,1436	H2Kb	TALNFLHL	IPI00117183	12452	Ccng2	cyclin G2
199	551,25	2	48	1837938	635734	2,9	0,0602	H2Db	FSEENHEPL	IPI00111181	65114	Vps35	vacuolar protein sorting 35
200	639,87	2	31	316374	110254	2,9	n/a	H2Db	FSPLNPVRVHI	IPI00133916	98758	Hnrpf	heterogeneous nuclear ribonucleoprotein F
200	639,87	2	31	316374	110254	2,9	n/a	H2Db	FSPLNPVRVHI	IPI00133916	59013	Hnrph1	heterogeneous nuclear ribonucleoprotein H1
201	528,79	2	56	1234899	432774	2,9	n/a	Qa2	AMLTILHEI	IPI00762278	77987	Ascc3	activating signal cointegrator 1 complex subunit 3
202	436,24	2	28	2433837	856225	2,8	0,1314	H2Kb	ASPIFTHV	IPI00467423	80744	Cwc22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)
203	472,73	2	65	764360	277941	2,8	0,0504	H2Kb	SGYDFSRL	IPI00415905	235623	Scap	SREBF chaperone
204	446,76	2	48	168522	61417	2,7	n/a	H2Kb	AVVSFKEL	IPI00322431	224860	Plcl2	phospholipase C-like 2
205	433,74	2	36	968823	355130	2,7	n/a	Qa2	AAPTGTHVL	IPI00345025	223672	Apol9a	apolipoprotein L 9a
206	475,29	2	27	697402	255688	2,7	0,1199	H2Kb	SNLKYILV	IPI00135072	29808	Mga	MAX gene associated
207	470,26	2	47	3013939	1114045	2,7	0,0929	H2Kb	VAYGFRNI	IPI00309907	67563	Narfl	nuclear prelamin A recognition factor-like
208	516,28	2	59	4395068	1640585	2,7	0,0779	H2Db	RQLENGTTL	IPI00266942	52635	D12Ertd551e	DNA segment, Chr 12, ERATO Doi 551, expressed
209	453,77	2	51	3701041	1387241	2,7	0,0126	H2Kb	SAVIFRTL	IPI00474393	326622	Upf2	UPF2 regulator of nonsense transcripts homolog (yeast)
210	477,28	2	42	402906	152143	2,6	0,1438	H2Kb	AQFKFTVL	IPI00119305	18813	Pa2g4	proliferation-associated 2G4

211	457,76	2	42	384270	145208	2,6	0,0531	H2Kb	VINSFVHV	IPI00387216	71745	Cul2	cullin 2
212	659,81	2	39	490480	186537	2,6	0,0487	H2Db	TSPINPYKDHM	IPI00420464	24136	Zeb2	zinc finger E-box binding homeobox 2
213	486,76	2	33	1017833	388574	2,6	n/a	H2Kb	EIVSFQHL	IPI00404595	100604	Lrrc8c	leucine rich repeat containing 8 family, member C
214	571,30	2	30	238504	91538	2,6	0,0354	H2Kb	SNIQYITRF	IPI00124636	56715	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1
215	536,77	2	31	32582739	12531740	2,6	n/a	H2Kb	RNYSYEKL	IPI00229475	16480	Jup	junction plakoglobin
216	460,79	2	41	38367	15000	≥ 2,6	0,1045	H2Kb	SSLKFLLL	IPI00460651	320209	Ddx11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)
217	435,77	2	51	518782	204616	2,5	0,0587	H2Db	GAIVNGKVL	IPI00454161	56784	Garnl1	GTPase activating RANGAP domain-like 1
218	516,26	2	43	9869988	3919416	2,5	0,0514	H2Db	FAHTNIESL	IPI00230108	14827	Pdia3	protein disulfide isomerase associated 3
219	450,23	2	42	724865	288269	2,5	0,1575	H2Db	GSLANHTSI	IPI00135048	77573	Vps33a	vacuolar protein sorting 33A (yeast)
220	548,28	2	31	450043	180589	2,5	0,2803	Qa2	QQLDVEHNL	IPI00132454	66366	Ergic3	ERGIC and golgi 3
221	541,30	2	57	897701	365214	2,5	n/a	Qa2	DLIQTIHEL	IPI00752114	319565	Syne2	synaptic nuclear envelope 2
222	576,28	2	32	1409341	574981	2,5	0,0138	H2Db	YSVANHNSFL	IPI00135993	74734	Rhoh	ras homolog gene family, member H
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	56774	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	103098	Slc6a15	solute carrier family 6 (neurotransmitter transporter), member 15
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	74338	Slc6a19	solute carrier family 6 (neurotransmitter transporter), member 19
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	102680	Slc6a20a	solute carrier family 6 (neurotransmitter transporter), member 20A
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	22599	Slc6a20b	solute carrier family 6 (neurotransmitter transporter), member 20B
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	14411	Slc6a12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	102857	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	13162	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	232333	Slc6a1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	243616	Slc6a11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	14412	Slc6a13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	104245	Slc6a5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	14664	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	20538	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2
223	547,79	2	43	192523	78606	2,4	0,4565	H2Kb	NVWRFPYL	IPI00108676	21366	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6

224	559,25	2	44	7814219	3191640	2,4	0,3250	H2Kb	SNYHFYSSI	IPI00120388	18024	Nfe2l2	nuclear factor, erythroid derived 2, like 2
225	516,28	2	45	18639536	7633235	2,4	0,2136	H2Kb	AQYKFIYV	IPI00225419	15170	Ptpn6	protein tyrosine phosphatase, non-receptor type 6
226	541,29	2	60	2028967	835767	2,4	0,5685	H2Db	RQIFNGTFV	IPI00458337	19989	Rpl7	ribosomal protein L7
227	506,29	2	28	84893	23333	2,4	0,2217	H2Kb	VIAAFTSRF	IPI00380785	20544	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	665596	RP23-38E20.1	H2b histone family, member A
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319178	Hist1h2bb	histone cluster 1, H2bb
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319181	Hist1h2bg	histone cluster 1, H2bg
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319182	Hist1h2bh	histone cluster 1, H2bh
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319183	Hist1h2bj	histone cluster 1, H2bj
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319184	Hist1h2bk	histone cluster 1, H2bk
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319186	Hist1h2bm	histone cluster 1, H2bm
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319188	Hist1h2bp	histone cluster 1, H2bp
228	485,78	2	52	7459515	3091435	2,4	0,3152	H2Kb	SVYVYKVL	IPI00752556	319189	Hist2h2bb	histone cluster 2, H2bb
229	572,80	2	54	452104	188408	2,4	0,3320	H2Db	SQLRNADVEL	IPI00622911	11771	Ap2a1	adaptor protein complex AP-2, alpha 1 subunit
230	576,29	2	44	2340458	984319	2,4	0,0462	H2Db	SALENGRYEL	IPI00461396	217578	Baz1a	bromodomain adjacent to zinc finger domain 1A
231	491,27	2	54	2483751	1051135	2,4	0,1066	H2Db	AALENTHLL	IPI00133355	68523	Fam96b	family with sequence similarity 96, member B
232	512,31	2	61	1538833	651275	2,4	0,1018	Qa2	KVLDVLHSL	IPI00339747	77877	6030458C11Rik	RIKEN cDNA 6030458C11 gene
233	509,78	2	25	324243	139764	2,3	0,0958	H2Db	NQLKNTSTI	IPI00109932	13209	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
234	505,31	2	33	2117376	917189	2,3	0,5385	H2Kb	LIYKFLNV	IPI00395038	103573	Xpo1	exportin 1, CRM1 homolog (yeast)
235	502,29	2	47	372658	161852	2,3	n/a	H2Kb	KVLHFFNV	IPI00284595	69608	Sec24d	SEC24 related gene family, member D (S. cerevisiae)
236	500,79	2	38	8134170	3554466	2,3	0,0224	H2Db	SAVKNLQQL	IPI00466915	17168	Mare	alpha globin regulatory element containing gene
237	478,26	2	48	1125926	494490	2,3	0,0656	H2Db	GSLTNLHTL	IPI00129289	110521	Hivep1	human immunodeficiency virus type I enhancer binding protein 1
238	463,75	2	53	9212375	4052009	2,3	0,2521	H2Kb	VAFDFTKV	IPI00404438	233489	Picalm	phosphatidylinositol binding clathrin assembly protein
239	544,28	2	50	6970036	3101600	2,2	n/a	H2Db	YVVDNIDHL	IPI00753518	26374	Rfwd2	ring finger and WD repeat domain 2
240	517,80	2	65	6444588	2870549	2,2	0,1252	H2Kb	QSIAFISRL	IPI00607961	67878	Tmem33	transmembrane protein 33
241	484,28	2	46	468586	213451	2,2	0,1093	H2Db	LGLSNLTHL	IPI00318748	81897	Tlr9	toll-like receptor 9
242	538,80	2	59	8886586	4053684	2,2	0,0697	H2Db	RSIQNAQFL	IPI00154056	11432	Acp2	acid phosphatase 2, lysosomal
243	528,78	2	51	2552874	1168351	2,2	0,1033	H2Db	IQLMNTAHL	IPI00120165	74114	Crot	carnitine O-octanoyltransferase
244	507,30	2	40	916220	422699	2,2	0,1014	H2Db	AKLVNQEVL	IPI00308882	227197	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1
245	498,28	2	49	2368489	1098655	2,2	n/a	Qa2	DLLGTLHNL	IPI00229328	66185	1110037F02Rik	RIKEN cDNA 1110037F02 gene
246	556,79	2	50	20099606	9414809	2,1	0,3398	H2Kb	ASYEFVQRL	IPI00119876	13424	Dync1h1	dynein cytoplasmic 1 heavy chain 1
247	477,23	2	57	919146	431577	2,1	0,0322	H2Kb	RGPTYVNM	IPI00420171	15463	Hrb	HIV-1 Rev binding protein
248	522,30	2	40	1395323	657500	2,1	0,2494	H2Kb	TLNSFIHVL	IPI00308278	68801	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	408067	9630025I21Rik	RIKEN cDNA 9630025I21 gene
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	67911	Zfp169	zinc finger protein 169

249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	22693	Zfp30	zinc finger protein 30
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	245368	Zfp300	zinc finger protein 300
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	328274	Zfp459	zinc finger protein 459
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	235907	Zfp71-rs1	zinc finger protein 71, releated sequence
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	78251	Zfp712	zinc finger protein 712
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	212276	Zfp748	zinc finger protein 748
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	233056	Zfp790	zinc finger protein 790
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	238693	Zfp817	zinc finger protein 817
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	170763	Zfp87	zinc finger protein 87
249	561,27	2	35	280407	132434	2,1	n/a	H2Db	VMLENYSHL	IPI00113254	22754	Zfp92	zinc finger protein 92
250	537,29	2	40	61761574	29505364	2,1	n/a	H2Kb	RTYTYEKL	IPI00125899	12387	Ctnnb1	catenin (cadherin associated protein), beta 1
251	498,76	2	30	7922606	3805752	2,1	0,1783	Qa2	NQVDSIHAL	IPI00464181	277360	Prex1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1
252	527,27	2	52	5710784	2766557	2,1	0,0571	H2Db	SQHVNLDQL	IPI00228832	218978	D14Ertd436e	DNA segment, Chr 14, ERATO Doi 436, expressed
253	443,77	2	36	450358	220351	2	0,2587	H2Db	KALANVATV	IPI00118674	59287	Ncstn	nicastrin
254	499,27	2	27	412380	202179	2	0,2865	H2Kb	VSQYYPKL	IPI00342766	15441	Hp1bp3	heterochromatin protein 1, binding protein 3
255	540,81	2	60	33477408	16424022	2	0,0932	H2Db	FQIVNPHLL	IPI00331302	20133	Rrm1	ribonucleotide reductase M1
256	498,75	2	29	911867	447469	2	0,0836	H2Kb	SSYSFRHL	IPI00130764	54397	Ppt2	palmitoyl-protein thioesterase 2
257	440,25	2	36	7720015	3818328	2	0,0777	H2Kb	SGLKYVNV	IPI00122412	108143	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor
258	527,29	2	45	786018	389248	2	0,2679	Qa2	ELSDIAHRI	IPI00221402	11674	Aldoa	aldolase 1, A isoform
259	514,76	2	37	8373104	4163315	2	0,1065	H2Db	GALKNTDYF	IPI00187512	107569	Nt5c3	5'-nucleotidase, cytosolic III
260	509,31	2	39	410809	204923	2	0,2306	Qa2	LQIPIPHSL	IPI00606087	70208	Med23	mediator complex subunit 23
261	533,82	2	34	446940	223981	2	0,0844	Qa2	KQLEVVHTL	IPI00317684	67490	1810074P20Rik	RIKEN cDNA 1810074P20 gene
262	495,28	2	37	75273	38000	2	0,0148	H2Db	NTVTNKVTL	IPI00225578	230700	Foxj3	forkhead box J3
263	537,79	2	28	316149	160471	2	0,1145	H2Db	RLITNSEEI	IPI00135646	19299	Abcd3	ATP-binding cassette, sub-family D (ALD), member 3
264	547,28	2	36	246559	126485	1,9	0,0059	H2Db	FSNKNLEEL	IPI00223964	213550	Dis3l	DIS3 mitotic control homolog (S. cerevisiae)-like
265	498,75	2	32	191145	98333	1,9	0,1975	H2Db	YTVKNGDSL	IPI00380108	216131	Tmem1	transmembrane protein 1
266	476,27	2	26	306384	157820	1,9	n/a	H2Kb	SNYRVSLL	IPI00119157	110078	Pygb	brain glycogen phosphorylase
266	476,27	2	26	306384	157820	1,9	n/a	H2Kb	SNYRVSLL	IPI00119157	110095	Pygl	liver glycogen phosphorylase
266	476,27	2	26	306384	157820	1,9	n/a	H2Kb	SNYRVSLL	IPI00119157	19309	Pygm	muscle glycogen phosphorylase
267	438,78	2	55	131176	68129	1,9	n/a	H2Kb	VIASFKVL	IPI00118899	60595	Actn4	actinin alpha 4
268	447,26	2	41	273556	143175	1,9	0,1322	H2Kb	TSIAFKNI	IPI00128363	226778	Mark1	MAP/microtubule affinity-regulating kinase 1
268	447,26	2	41	273556	143175	1,9	0,1322	H2Kb	TSIAFKNI	IPI00128363	17169	Mark3	MAP/microtubule affinity-regulating kinase 3
269	560,30	2	32	819903	429818	1,9	0,1083	H2Db	AAYRNLGQNL	IPI00222509	108911	Rcc2	regulator of chromosome condensation 2
270	493,78	2	72	49437184	26187050	1,9	0,0446	H2Db	KALINADEL	IPI00753815	20740	Spna2	spectrin alpha 2
271	470,78	2	36	119650	63549	1,9	0,3671	H2Kb	VKYLFTGL	IPI00270877	59025	Usp14	ubiquitin specific peptidase 14
272	456,24	2	33	980218	526800	1,9	0,3346	H2Kb	AAYGFRNI	IPI00111842	67608	Narf	nuclear prelamin A recognition factor

273	453,77	2	47	321393	173949	1,8	n/a	H2Kb	SALVFTRL	IPI00459432	56700	0610031J06Rik	RIKEN cDNA 0610031J06 gene
274	571,32	2	64	2186905	1208981	1,8	0,2393	Qa2	KFLEQVHQL	IPI00467004	20846	Stat1	signal transducer and activator of transcription 1
275	483,79	2	38	295786	164809	1,8	n/a	H2Kb	IILKYIGM	IPI00123519	54208	Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1
276	463,76	2	53	483782	269911	1,8	0,1796	H2Kb	ASYLFRGL	IPI00648936	217353	Tmc6	transmembrane channel-like gene family 6
277	504,79	2	29	298185	168373	1,8	n/a	Qa2	AVLEVVHEL	IPI00353935	214616	Spata5l1	spermatogenesis associated 5-like 1
278	476,25	2	49	1199932	683510	1,8	0,2821	H2Kb	VSYLFSHV	IPI00653091	19139	Prps1	phosphoribosyl pyrophosphate synthetase 1
278	476,25	2	49	1199932	683510	1,8	0,2821	H2Kb	VSYLFSHV	IPI00653091	75456	Prps1l1	phosphoribosyl pyrophosphate synthetase 1-like 1
278	476,25	2	49	1199932	683510	1,8	0,2821	H2Kb	VSYLFSHV	IPI00653091	110639	Prps2	phosphoribosyl pyrophosphate synthetase 2
279	516,79	2	35	929774	533088	1,7	0,5801	H2Db	TSIKNQTQL	IPI00127274	78697	Pus7	pseudouridylate synthase 7 homolog (S. cerevisiae)
280	507,29	2	35	192232	110839	1,7	0,3593	H2Db	AGILNHYLI	IPI00129296	11690	Alox5ap	arachidonate 5-lipoxygenase activating protein
281	451,72	2	40	202981	117299	1,7	n/a	H2Kb	ANVDFSHL	IPI00453859	54711	Plagl2	pleiomorphic adenoma gene-like 2
282	456,25	2	46	2058438	1191798	1,7	0,3558	H2Kb	VAFAYKNV	IPI00120826	67437	Ssr3	signal sequence receptor, gamma
283	542,78	2	37	802513	470139	1,7	0,5881	H2Db	LSLENGTHTL	IPI00469323	13433	Dnmt1	DNA methyltransferase (cytosine-5) 1
284	479,78	2	49	2968193	1741834	1,7	0,1381	H2Kb	RAPQFINL	IPI00377615	213109	Phf3	PHD finger protein 3
285	512,80	2	55	1196326	704515	1,7	0,4972	H2Db	RAIPNNQVL	IPI00754785	59022	Edf1	endothelial differentiation-related factor 1
286	561,27	2	37	264906	156909	1,7	0,0642	Qa2	EQQPQQHNL	IPI00223001	23856	Dido1	death inducer-obliterator 1
287	514,79	2	47	2871484	1742138	1,6	0,3451	H2Db	GQIQNKEVL	IPI00676717	107182	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)
288	466,28	2	48	1296754	792417	1,6	0,1544	H2Kb	VSPLFQKL	IPI00461469	216443	Mars	methionine-tRNA synthetase
289	476,27	2	41	16928769	10354966	1,6	0,3536	H2Kb	TSVRFTQL	IPI00109529	66394	Nosip	nitric oxide synthase interacting protein
290	512,77	2	65	4832399	3016361	1,6	0,5028	H2Db	HLVTNQEAL	IPI00229277	229898	Gbp5	guanylate nucleotide binding protein 5
291	538,78	2	34	67229	42590	1,6	0,5854	H2Db	RQATNQIVM	IPI00130000	19155	Npepps	aminopeptidase puromycin sensitive
292	511,79	2	30	1192941	757087	1,6	0,5657	H2Db	AQLDNIHVL	IPI00267405	235527	Plscr4	phospholipid scramblase 4
293	512,79	2	49	3371118	2150166	1,6	0,2514	Qa2	KAIETVHNL	IPI00758301	57314	Th1l	TH1-like homolog (Drosophila)
294	610,85	2	51	960100	614097	1,6	n/a	H2Db	KSLLNKEEFL	IPI00230372	432555	EG432555	predicted gene, EG432555
294	610,85	2	51	960100	614097	1,6	n/a	H2Db	KSLLNKEEFL	IPI00230372	620913	OTTMUSG00000005523	predicted gene, OTTMUSG00000005523
294	610,85	2	51	960100	614097	1,6	n/a	H2Db	KSLLNKEEFL	IPI00230372	667214	RP23-269N23.3	interferon-inducible GTPase family member
295	467,26	2	29	8430679	5394616	1,6	0,2598	H2Kb	VGPRYTQL	IPI00230277	26417	Mapk3	mitogen-activated protein kinase 3
296	534,25	2	45	196605	127524	1,5	0,5415	H2Db	SQFPNAEKM	IPI00117274	94176	Dock2	dedicator of cyto-kinesis 2
297	509,81	2	62	1176270	770332	1,5	n/a	H2Kb	SIAAFIQRL	IPI00130381	224727	Bat3	HLA-B-associated transcript 3
298	550,75	2	53	15362601	10089844	1,5	0,2784	H2Kb	SGYDFENRL	IPI00112093	72747	Ttc39c	tetratricopeptide repeat domain 39C
299	541,78	2	34	152442	100390	1,5	0,4078	Qa2	SQEEIIHNI	IPI00308086	12122	Bid	BH3 interacting domain death agonist
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100041342	LOC100041342	glyceraldehyde-3-phosphate dehydrogenase pseudogene
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100039840	LOC100039840	glyceraldehyde-3-phosphate dehydrogenase pseudogene

300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	215974	EG215974	predicted gene, EG215974
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100040109	LOC100040109	similar to Glyceraldehyde-3-phosphate dehydrogenase
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100041831	LOC100041831	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100048253	LOC100048253	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100040634	LOC100040634	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100048117	LOC100048117	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100041399	LOC100041399	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100047352	LOC100047352	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100044981	LOC100044981	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100039258	LOC100039258	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	640374	LOC640374	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100047129	LOC100047129	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
300	666,82	2	49	1608203	1059124	1,5	0,2353	H2Db	YGYSNRVVDLM	IPI00465584	100041236	LOC100041236	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
301	479,23	2	51	124127	82750	1,5	0,2863	H2Kb	RSISFSNM	IPI00265718	18201	Nsmaf	neutral sphingomyelinase (N-SMase) activation associated factor
302	602,30	2	62	708205	472468	1,5	0,5419	H2Db	SALQNAESDRL	IPI00399663	229841	Cenpe	centromere protein E
303	517,26	2	59	430140	287072	1,5	n/a	H2Db	LGVTNFVHM	IPI00132825	239554	Foxred2	FAD-dependent oxidoreductase domain containing 2
304	489,77	2	40	1900764	1276634	1,5	0,4981	H2Kb	RSYQQALL	IPI00112201	170742	Sertad3	SERTA domain containing 3
305	485,26	2	39	463437	312424	1,5	0,5919	H2Kb	RAYLFNSV	IPI00110127	106369	Ypel1	yippee-like 1 (Drosophila)
305	485,26	2	39	463437	312424	1,5	0,5919	H2Kb	RAYLFNSV	IPI00110127	77864	Ypel2	yippee-like 2 (Drosophila)
305	485,26	2	39	463437	312424	1,5	0,5919	H2Kb	RAYLFNSV	IPI00110127	66090	Ypel3	yippee-like 3 (Drosophila)
305	485,26	2	39	463437	312424	1,5	0,5919	H2Kb	RAYLFNSV	IPI00110127	241525	Ypel4	yippee-like 4 (Drosophila)
306	557,30	2	78	825380	559698	1,5	0,3869	H2Db	KSISNPPGSNL	IPI00621852	232341	Wnk1	WNK lysine deficient protein kinase 1
307	497,75	2	33	435000	295094	1,5	n/a	H2Kb	AQQSYERL	IPI00761177	214459	Fnbp1l	formin binding protein 1-like
308	454,74	2	34	292977	199424	1,5	n/a	H2Kb	VADKFSEL	IPI00222306	73699	Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
309	460,25	2	33	106463193	74360193	1,4	0,1671	H2Kb	VGPRYTNL	IPI00119663	26413	Mapk1	mitogen-activated protein kinase 1
310	547,80	2	38	4537850	3200674	1,4	0,1945	Qa2	RLLQEAHDL	IPI00119142	66884	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2
311	535,79	2	39	9104485	6439826	1,4	0,4949	H2Db	ISGVNRYYV	IPI00132940	54405	Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1
312	589,81	2	54	10009783	7150610	1,4	0,3903	H2Db	SLGKNPTDAYL	IPI00132705	67938	Mylc2b	myosin light chain, regulatory B
313	560,31	2	34	2931802	2107869	1,4	0,5534	H2Db	AGVRNPQQHL	IPI00124287	18458	Pabpc1	poly A binding protein, cytoplasmic 1
314	534,27	2	34	232466	168102	1,4	0,1221	H2Db	SSVQNKEYL	IPI00135122	100515	Zfp518b	zinc finger protein 518B

315	460,27	2	59	2020302	1471629	1,4	0,2125	H2Kb	ATQVYPKL	IPI00170162	107976	Bre	brain and reproductive organ-expressed protein
316	492,28	2	34	1670008	1241635	1,3	0,4099	H2Kb	KGYVFKEL	IPI00122181	170743	Tlr7	toll-like receptor 7
317	521,25	2	49	28236959	21224480	1,3	0,3215	H2Db	FGPVNHEEL	IPI00133537	12576	Cdkn1b	cyclin-dependent kinase inhibitor 1B
318	494,78	2	37	685144	521588	1,3	0,4014	H2Db	TGVTNRDLI	IPI00330139	71435	Arhgap21	Rho GTPase activating protein 21
319	447,77	2	55	315750	240409	1,3	0,6733	H2Kb	SGLTYIKI	IPI00134095	12211	Birc6	baculoviral IAP repeat-containing 6
320	567,84	2	37	434082	335287	1,3	n/a	Qa2	QQLQIIHRV	IPI00154076	116748	Lsm10	U7 snRNP-specific Sm-like protein LSM10
321	544,79	2	39	6525067	5209696	1,3	0,6023	Qa2	GQIKEYHTL	IPI00756252	672511	LOC672511	hypothetical LOC672511
322	552,25	2	56	197324	160201	1,2	n/a	H2Kb	DQIEYHEGL	IPI00462949	75974	Dock11	dedicator of cytokinesis 11
323	548,30	2	38	398108	324088	1,2	0,6699	H2Db	AGLLNNPHFI	IPI00116331	52551	Sgta	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha
324	523,25	2	49	193728	158392	1,2	0,7516	H2Db	VSVTNEHLM	IPI00119330	22035	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10
325	549,26	2	60	1329501	1092659	1,2	0,7615	H2Db	RQAENGMYI	IPI00380280	69719	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
326	458,75	2	29	540203	447434	1,2	0,7882	H2Db	AAGINRDSL	IPI00127227	234309	Cbr4	carbonyl reductase 4
327	462,27	2	28	321274	266998	1,2	0,7001	Qa2	NISGVIHAL	IPI00111558	80909	Gats	opposite strand transcription unit to Stag3
328	527,28	2	49	114523	97283	1,2	n/a	Qa2	SELQVLHDI	IPI00459331	70495	Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2
329	505,27	2	49	5182114	4504961	1,2	0,6861	H2Db	ISPENHISL	IPI00471256	23992	Prkra	protein kinase, interferon inducible double stranded RNA dependent activator
330	548,79	2	34	418168	363730	1,1	0,6973	Qa2	EQSDLVHRI	IPI00133066	66997	Psmd12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
331	462,29	2	29	833120	728358	1,1	n/a	H2Kb	VAFAFKKL	IPI00420934	108960	Irak2	interleukin-1 receptor-associated kinase 2
332	526,81	2	38	489790	429800	1,1	0,8531	Qa2	TQLIQTHVL	IPI00153791	68979	Nol11	nucleolar protein 11
333	506,78	2	42	5175757	4572904	1,1	0,8405	H2Kb	KSYLMNKL	IPI00474587	14468	Gbp1	guanylate nucleotide binding protein 1
333	506,78	2	42	5175757	4572904	1,1	0,8405	H2Kb	KSYLMNKL	IPI00474587	14469	Gbp2	guanylate nucleotide binding protein 2
333	506,78	2	42	5175757	4572904	1,1	0,8405	H2Kb	KSYLMNKL	IPI00474587	229898	Gbp5	guanylate nucleotide binding protein 5
334	532,79	2	42	4862683	4321543	1,1	0,8004	H2Db	RTVENVTVF	IPI00126072	26949	Vat1	vesicle amine transport protein 1 homolog (T californica)
335	501,29	2	53	86350920	77431050	1,1	0,8643	Qa1	AMAPRTLLL	IPI00110805	14964	H2-D1	histocompatibility 2, D region locus 1
335	501,29	2	53	86350920	77431050	1,1	0,8643	Qa1	AMAPRTLLL	IPI00110805	15007	H2-Q10	histocompatibility 2, Q region locus 10
335	501,29	2	53	86350920	77431050	1,1	0,8643	Qa1	AMAPRTLLL	IPI00110805	15016	H2-Q5	histocompatibility 2, Q region locus 5
336	555,28	2	46	9384195	8416125	1,1	0,6561	Qa2	TQDHVMHLL	IPI00762266	16149	Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
337	540,31	2	38	346728	315296	1,1	0,8370	H2Kb	VAYKFPELL	IPI00405095	224826	Ubr2	ubiquitin protein ligase E3 component n-recognin 2
338	446,26	2	49	449548	409452	1,1	0,7588	H2Kb	VNVRFTGV	IPI00222705	75007	Fam63a	family with sequence similarity 63, member A
338	446,26	2	49	449548	409452	1,1	0,7588	H2Kb	VNVRFTGV	IPI00222705	235461	B230380D07Rik	RIKEN cDNA B230380D07 gene
339	621,79	2	43	110264	100628	1,1	n/a	H2Db	YAMENTRQTI	IPI00274795	20185	Ncor1	nuclear receptor co-repressor 1
340	557,32	2	37	791113	727483	1,1	0,7724	H2Db	VSPRNSLEVL	IPI00170055	242418	Wdr32	WD repeat domain 32

341	467,28	2	47	90600	84764	1,1	n/a	H2Kb	SQIRFGLL	IPI00129529	16834	Cog1	component of oligomeric golgi complex 1
342	468,77	2	37	823404	783679	1,1	0,8891	H2Db	AAIANHQVL	IPI00311140	69192	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16
343	601,78	2	35	298372	285000	1	n/a	Qa2	QQQQEYHEL	IPI00453673	70661	BC033915	cDNA sequence BC033915
344	466,27	2	27	1330473	1272280	1	0,9622	H2Kb	VGYRQPLV	IPI00124221	11933	Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide
345	479,26	2	52	1908441	1868196	1	0,9775	H2Kb	VNSIFQHL	IPI00227871	74558	Gvin1	GTPase, very large interferon inducible 1
346	506,76	2	37	268350	263181	1	0,9738	H2Kb	ENFTFQKV	IPI00760055	18753	Prkcd	protein kinase C, delta
347	484,79	2	45	194608	191005	1	n/a	H2Kb	ITFIFKSL	IPI00268673	56717	Frap1	FK506 binding protein 12-rapamycin associated protein 1
348	439,75	2	44	891734	887694	1	0,9761	H2Kb	SGPTYIKL	IPI00221830	57869	Adck2	aarF domain containing kinase 2
349	488,24	2	31	182110	182465	-1	n/a	H2Kb	NGYKYMAL	IPI00123814	11605	Gla	galactosidase, alpha
350	508,77	2	47	372122	376201	-1	n/a	H2Db	RVVANSEEI	IPI00112111	11666	Abcd1	ATP-binding cassette, sub-family D (ALD), member 1
351	578,76	2	33	85715	87287	-1	n/a	H2Kb	VNYHYMSQV	IPI00134095	12211	Birc6	baculoviral IAP repeat-containing 6
352	472,75	2	34	175824	180665	-1	0,9208	H2Kb	SSVYFRSV	IPI00109805	72368	2310045N01Rik	RIKEN cDNA 2310045N01 gene
353	498,78	2	38	5192335	5352892	-1	0,9218	H2Kb	QALKYFNL	IPI00131143	20338	Sel1l	sel-1 suppressor of lin-12-like (C. elegans)
354	554,23	2	34	278758	288778	-1	n/a	Qa2	SMMDVDHQI	IPI00116279	12465	Cct5	chaperonin subunit 5 (epsilon)
355	479,26	2	32	195881	202966	-1	0,9599	H2Kb	TNVLFNHL	IPI00109401	71919	Rpap3	RNA polymerase II associated protein 3
356	447,76	2	34	275794	286050	-1	n/a	H2Kb	ATLRYASL	IPI00187397	11787	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2
357	497,79	2	39	207878	215910	-1	n/a	Qa2	ALNNLLHSL	IPI00403352	233789	Smg1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
358	515,77	2	41	172650	181755	-1,1	n/a	Qa2	SMTLAIHEI	IPI00113731	13244	Degs1	degenerative spermatocyte homolog 1 (Drosophila)
359	488,75	2	37	137107	150456	-1,1	0,8838	H2Kb	AGPWYRNL	IPI00475210	50771	Atp9b	ATPase, class II, type 9B
360	523,26	2	54	220907	245984	-1,1	n/a	H2Kb	ATYSYKEAL	IPI00221621	69957	Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)
361	555,73	2	45	1014439	1136004	-1,1	0,8799	H2Kb	RSYDFEFM	IPI00329942	30930	Vps26a	vacuolar protein sorting 26 homolog A (yeast)
362	564,28	2	41	323562	362795	-1,1	0,8254	Qa2	EQLNINHMI	IPI00311914	140630	Ube4a	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)
363	526,79	2	43	1249816	1402497	-1,1	0,8618	Qa2	TLNDLIHNI	IPI00470092	80986	Ckap2	cytoskeleton associated protein 2
364	553,30	2	49	1817100	2049057	-1,1	0,8815	H2Kb	INQIYEARV	IPI00169911	216859	Centb1	centaurin, beta 1
365	568,32	2	32	3782659	4290597	-1,1	0,7006	Qa2	QQLQQQHLL	IPI00120267	108655	Foxp1	forkhead box P1
365	568,32	2	32	3782659	4290597	-1,1	0,7006	Qa2	QQLQQQHLL	IPI00120267	74123	Foxp4	forkhead box P4
366	517,27	2	44	171784	195779	-1,1	0,7523	H2Db	SAIMNPASKV	IPI00169916	67300	Cltc	clathrin, heavy polypeptide (Hc)
367	495,75	2	43	1272812	1456029	-1,1	0,8333	H2Kb	SNPEFRQL	IPI00551078	338523	Jhdm1d	jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)
368	462,76	2	59	4670137	5916607	-1,3	0,7179	Qa2	ALIGVDHSL	IPI00316214	12455	Ccnt1	cyclin T1
369	511,78	2	39	213316	272675	-1,3	0,6472	Qa2	NQLDGIHLL	IPI00319214	56335	Mettl3	methyltransferase-like 3
370	513,29	2	74	12392586	16025178	-1,3	0,6720	Qa2	GQVVIIHML	IPI00130444	11774	Ap3b1	adaptor-related protein complex 3, beta 1 subunit
371	526,25	2	32	279780	374435	-1,3	0,0794	H2Db	YMGTNIHSL	IPI00114801	16329	Inpp1	inositol polyphosphate-1-phosphatase

372	579,78	2	42	3112524	4177217	-1,3	0,1882	Qa2	YQNQEIHNL	IPI00453860	213895	Bms1	BMS1 homolog, ribosome assembly protein (yeast)
373	456,74	2	49	1296793	1763452	-1,4	0,5517	Qa2	VSPTGTHTL	IPI00124640	14824	Grn	granulin
374	489,29	2	62	363333	501767	-1,4	0,7761	H2Kb	KILTFDQL	IPI00665953	19899	Rpl18	ribosomal protein L18
375	479,30	2	39	772652	1074468	-1,4	0,6677	H2Kb	VNIPFVRL	IPI00653556	98999	Znfx1	zinc finger, NFX1-type containing 1
376	514,27	2	70	8160127	11634092	-1,4	n/a	H2Db	VGIENIHVM	IPI00123689	219135	Mtmr6	myotubularin related protein 6
377	485,74	2	29	205704	300494	-1,5	n/a	H2Kb	NSFRYNGL	IPI00222547	19943	Rpl28	ribosomal protein L28
378	539,77	2	41	166202	246358	-1,5	n/a	Qa2	VLSEIMHSF	IPI00409936	70572	Ranbp5	RAN binding protein 5
379	516,81	2	37	2195800	3291330	-1,5	0,2194	H2Db	IGTFNVIRL	IPI00320847	15108	Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10
380	458,75	2	35	937515	1490554	-1,6	0,6068	H2Kb	STFSFTKV	IPI00266942	52635	D12Ertd551e	DNA segment, Chr 12, ERATO Doi 551, expressed
381	548,23	2	42	67349	107237	-1,6	0,3036	H2Db	MSMTNTHEL	IPI00227508	215900	Fam26f	family with sequence similarity 26, member F
382	493,79	2	41	352711	565643	-1,6	n/a	H2Kb	ISILYHQL	IPI00316471	68295	0610011L14Rik	RIKEN cDNA 0610011L14 gene
383	489,77	2	44	1725116	2776831	-1,6	0,4276	H2Db	SAALNKDFL	IPI00118304	74081	Cep350	centrosomal protein 350
384	524,28	2	69	664396	1073572	-1,6	0,3246	H2Kb	GQVTFLHVF	IPI00124382	54325	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
385	605,81	2	48	80283	132268	-1,6	n/a	H2Db	EVVQNFAKEF	IPI00132575	72042	Cotl1	coactosin-like 1 (Dictyostelium)
386	517,76	2	43	293737	485137	-1,7	n/a	Qa2	AQSFIAHNF	IPI00461710	211255	Kbtbd7	kelch repeat and BTB (POZ) domain containing 7
387	513,76	2	47	771335	1304081	-1,7	0,1762	Qa2	ESQSVIHNL	IPI00284595	69608	Sec24d	SEC24 related gene family, member D (S. cerevisiae)
388	547,81	2	45	1377620	2333397	-1,7	0,1686	Qa2	EIIKDIHNL	IPI00400016	226519	Lamc1	laminin, gamma 1
389	424,75	2	46	231364	405760	-1,8	0,4015	H2Kb	SAARFALL	IPI00125829	107723	Slc12a6	solute carrier family 12, member 6
390	514,80	2	39	974863	1752182	-1,8	0,5166	H2Db	FSPLNPVRV	IPI00133916	98758	Hnrpf	heterogeneous nuclear ribonucleoprotein F
390	514,80	2	39	974863	1752182	-1,8	0,5166	H2Db	FSPLNPVRV	IPI00133916	59013	Hnrph1	heterogeneous nuclear ribonucleoprotein H1
391	470,76	2	56	921496	1675857	-1,8	0,2595	Qa2	ALSEISHAL	IPI00756605	432555	EG432555	predicted gene, EG432555
391	470,76	2	56	921496	1675857	-1,8	0,2595	Qa2	ALSEISHAL	IPI00756605	667214	RP23-269N23.3	interferon-inducible GTPase family member
392	564,30	2	33	226945	420841	-1,9	0,0041	Qa2	RLLEEIHAM	IPI00395196	67222	Srfbp1	serum response factor binding protein 1
393	491,28	2	39	90527	176972	-2	n/a	H2Kb	YGVLFRNL	IPI00221911	12508	Cd53	CD53 antigen
394	509,25	2	35	87754	175834	-2	0,4580	H2Db	SSPRNSQEL	IPI00348883	332579	Card9	caspase recruitment domain family, member 9
395	511,29	2	49	2517357	5070687	-2	0,3249	Qa2	SQLPVDHIL	IPI00404856	12847	Copa	coatomer protein complex subunit alpha
396	537,80	2	47	1846975	3952174	-2,1	0,3536	H2Kb	ISPRFDVQL	IPI00230660	267019	Rps15a	ribosomal protein S15a
397	508,25	2	37	174667	379566	-2,2	0,2138	Qa2	AQQNTGHFL	IPI00132299	16364	Irf4	interferon regulatory factor 4
398	483,75	2	28	219556	482480	-2,2	0,1062	H2Db	AGIKNSTEF	IPI00660746	100702	Mpa2l	macrophage activation 2 like
399	544,28	2	37	1284529	2931852	-2,3	0,3326	Qa2	FISDVEHQL	IPI00229742	76681	Trim12	tripartite motif protein 12
400	575,78	2	47	323333	739488	-2,3	0,0738	H2Db	YVHVNQYDI	IPI00120503	70349	Copb1	coatomer protein complex, subunit beta 1
401	505,77	2	26	73269	170801	-2,3	n/a	H2Kb	SNIRFQFV	IPI00123689	219135	Mtmr6	myotubularin related protein 6
402	487,73	2	36	193460	462680	-2,4	n/a	H2Kb	KSYSFDEV	IPI00320188	59027	Pbef1	pre-B-cell colony-enhancing factor 1
403	594,34	2	34	23500	57092	-2,4	n/a	H2Db	KALINPANVTF	IPI00130018	18777	Lypla1	lysophospholipase 1

404	480,79	2	53	671080	1636329	-2,4	0,4843	H2Kb	ARIIFNQV	IPI00116671	12044	Bcl2a1a	B-cell leukemia/lymphoma 2 related protein A1a
404	480,79	2	53	671080	1636329	-2,4	0,4843	H2Kb	ARIIFNQV	IPI00116671	12045	Bcl2a1b	B-cell leukemia/lymphoma 2 related protein A1b
404	480,79	2	53	671080	1636329	-2,4	0,4843	H2Kb	ARIIFNQV	IPI00116671	12047	Bcl2a1d	B-cell leukemia/lymphoma 2 related protein A1d
405	524,78	2	55	300466	734032	-2,4	0,2364	H2Kb	INQRFEEL	IPI00114979	20850	Stat5a	signal transducer and activator of transcription 5A
406	512,27	2	44	5232840	12904443	-2,5	0,0682	Qa2	SQNPTNHLL	IPI00119320	27060	Tcirg1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3
407	534,28	2	56	6187615	15857424	-2,6	0,1286	Qa2	QLNEQVHSL	IPI00403682	212307	Mapre2	microtubule-associated protein, RP/EB family, member 2
408	476,24	2	26	103333	276277	-2,7	0,0917	H2Kb	RNPTFMGL	IPI00310131	11772	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit
409	600,33	2	62	126887	341797	-2,7	0,1693	H2Db	FALKNPFYSL	IPI00112785	60409	Trappc4	trafficking protein particle complex 4
410	455,26	2	61	424541	1219996	-2,9	0,1344	Qa2	GALGTLHQL	IPI00311809	20525	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1
410	455,26	2	61	424541	1219996	-2,9	0,1344	Qa2	GALGTLHQL	IPI00311809	20526	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2
411	560,32	2	48	114304	334647	-2,9	n/a	H2Db	KQILNIYDL	IPI00229777	71732	Vps11	vacuolar protein sorting 11 (yeast)
412	512,80	2	45	861220	2682909	-3,1	0,0340	Qa2	TLTNVIHNL	IPI00133384	66844	Ormdl2	ORM1-like 2 (S. cerevisiae)
413	539,30	2	51	4654285	15315480	-3,3	0,1335	H2Kb	TTPEFLTRI	IPI00462137	19225	Ptgs2	prostaglandin-endoperoxide synthase 2
414	502,29	2	33	1530000	5191317	-3,4	0,0122	H2Kb	QVVQFNRL	IPI00133047	56692	Map2k1ip1	mitogen-activated protein kinase kinase 1 interacting protein 1
415	544,79	2	34	39000	141003	-3,6	0,0750	H2Db	TALKNPNAML	IPI00467447	29875	Iqgap1	IQ motif containing GTPase activating protein 1
416	486,30	2	31	102794	416454	-4,1	n/a	H2Db	VALLNKTNV	IPI00125899	12387	Ctnnb1	catenin (cadherin associated protein), beta 1
417	575,80	2	39	457532	2035291	-4,4	0,0626	Qa2	QQQQQQHLI	IPI00125670	94112	Med15	mediator complex subunit 15

All possible MIP source proteins are shown. MIPs that were not detected on dKO cells were attributed the intensity value 15,000, which represents the threshold for limit of detection. Ratios with the symbol ≥ indicate peptides that were detected above threshold only in WT DCs, and thus, from which the exact fold change could not be measured. P values noted "n/a" correspond to peptides that were detected in 2 out of 3 replicates.

Supplemental Table S2. Pathways enriched in MIP source genes from DCs and thymocytes

	Pathway Name	**ID**	**Genes in sample**	**Genes in InnateDB**	**P value**	**Gene Symbols**
Pathways enriched in DC peptide source genes	Acute myeloid leukemia – Myeloid differentiation	671	7	57	0,0007	Frap1, Jup, Mapk1, Mapk3, Ppard, Stat3, Stat5a
	Proteasome	630	6	45	0,0011	Psmb8, Psmb9, Psmd11, Psmd12, Psmd2, Psmd6
	Adherens junction	741	6	74	0,0132	Actn4, Ctnnb1, Iqgap1, Mapk1, Mapk3, Ptpn6
	Long-term depression [a]	775	6	75	0,0141	Itpr1, Lyn, Mapk1, Mapk3, Nos2, Ppp2r1b
	Toll-like receptor signaling pathway	699	7	99	0,0156	Map3k7ip2, Mapk1, Mapk3, Myd88, Stat1, Tlr7, Tlr9
	Nicotinate and nicotinamide metabolism	615	3	24	0,0245	Nampt, Nt5c3, Pnp1
	Pentose phosphate pathway	611	3	24	0,0245	Aldoa, Prps1, Prps2
	Small cell lung cancer	747	6	86	0,0259	Cdk2, Cdkn1b, Lamc1, Nos2, Ptgs2, Traf1
	Fatty acid elongation in mitochondria	668	2	10	0,0273	Hsd17b10, Ppt2
	P53 signaling pathway [a]	666	5	65	0,0283	Bid, Ccng2, Cdk2, Chek1, Pmaip1
	Type II diabetes mellitus	641	4	45	0,0304	Frap1, Mapk1, Mapk3, Prkcd
	Prostate cancer	773	6	90	0,0315	Cdk2, Cdkn1b, Ctnnb1, Frap1, Mapk1, Mapk3
	Thyroid cancer	704	3	28	0,0368	Ctnnb1, Mapk1, Mapk3
	Pancreatic cancer	795	5	72	0,0414	Arhgef6, Mapk1, Mapk3, Stat1, Stat3
	Glycosphingolipid biosynthesis - globoseries	760	2	13	0,0449	Gla, St3gal1
	Prion disease	789	2	13	0,0449	Lamc1, Nfe2l2
	Ribosome [a]	756	5	74	0,0457	Rpl18, Rpl28, Rpl4, Rpl7, Rps15a
Pathways enriched in thymocyte peptide source genes	Tight junction	607	5	129	0,0127	Ash1l, Myh9, Mylc2b, Ppp2r1a, Ppp2r1b
	Purine metabolism	771	5	149	0,0223	Impdh2, Pde2a, Pnp1, Polr2b, Rrm1
	Cell cycle	717	4	110	0,0310	Ccnd3, Cdkn1b, Chek1, Pcna
	P53 signaling pathway [a]	666	3	65	0,0331	Ccnd3, Ccng1, Chek1
	Renal cell carcinoma	620	3	70	0,0399	Cul2, Epas1, Mapk1
	Pancreatic cancer	795	3	72	0,0428	Arhgef6, Mapk1, Stat3
	Ribosome [a]	756	3	74	0,0459	Rps15, Rps15a, Rps7
	Long-term depression [a]	775	3	75	0,0474	Mapk1, Ppp2r1a, Ppp2r1b

The InnateDB resource was used to identify enriched KEGG pathways associated to genes coding for MIPs eluted from DCs and thymocytes(1). Only significantly enriched pathways are shown ($P < 0.05$). [a] Enriched pathways shared between DC and thymocyte datasets.

Supplemental Table S3. DC- or immune-related function of genes differentially expressed in WT vs. dKO DCs

Classification	Gene ID	Gene Symbol	DC or immune related function	WT/dKO ratio	P value	References
Resistance to infection	140780	Bmp2k	Level inversely correlated with mouse susceptibility to T cruzi.	20,64	0,0000	(2)
	21672	Prdx2	Up-regulated in activated CD8$^+$ T cells during HIV infection.	11,11	0,0002	(3, 4)
	12774	Ccr5	Facilitated infection by HIV.	10,71	0,0003	(5, 6)
	80287	Apobec3	Level inversely correlated with susceptibility to HIV. Edits viral RNA, mutates DNA.	5,59	0,0001	(7, 8)
	12345	Capzb	CapG$^{-/-}$ mice are more susceptible to Listeria monocytogenes.	4,09	0,0100	(9)
	18406	Orm2	Binds antiretroviral protease inhibitors and was found increased in HIV patients.	-6,59	0,0045	(10)
	56066	Cxcl11	Inversely correlated with mouse susceptibility to T cruzi. T cell α chemoattractant.	-10,89	0,0683	(2, 11)
Antigen presentation	16913	Psmb8	Immunoproteasome catalytic subunit (LMP7).	594,77	0,0001	(12)
	12260	C1qb	Enhances antigen presentation to CD8$^+$ T cells and phagocytosis by DCs.	13,20	0,0087	(13-16)
	13032	Ctsc	Activates granzymes A and B, cathepsin family involved in MHC II presentation	10,66	0,0000	(17, 18)
	330812	Rnf150	Part of E3 ubiquitin ligases family, which was found to affect MHC II traffic in DCs.	9,15	0,0042	(19)
	258832	Olfr109	Part of a cluster of genes in the MHC I region; potential reciprocal influence.	5,82	0,0006	(20)
	258503	Olfr98	Part of a cluster of genes in the MHC I region; potential reciprocal influence.	3,66	0,0029	(20)
Phagocytosis	245049	Myrip	Interacts with myosin VIIA, which is involved in DC endocytosis.	8,44	0,0036	(21)
	11745	Anxa3	Ca^{2+} and phospholipid-binding protein involved in membrane fusion, aggregation and transport of different vesicles in DCs	7,56	0,0001	(22)
	20346	Sema3a	Suppressed T cell proliferation by inhibiting actin cytoskeleton reorganization.	4,80	0,0147	(23-25)
	18784	Pla2g5	Regulated phagocytosis and contributed to innate response against C albicans.	-2,60	0,0003	(26)
	21968	Tom1	Binds polyubiquitin chains and recruits clathrin to endosomes.	-2,68	0,0031	(27, 28)
	67733	Itgb3bp	Binds integrin β3, which is involved in apoptotic body engulfment and exosome endocytosis by DCs.	-3,57	0,0101	(29, 30)

	11828	Aqp3	Water channel; volume control mechanism during macropinocytosis in DCs.	-4,02	0,0181	(31)
	381823	Apold1	Link between programmed cell death of host cells (via apoptosis or autophagic death) and immunity to pathogens.	-13,24	0,0085	(32)
Immune signaling	320713	Mysm1	Histone 2H de-ubiquitinase that contains Myb-like domains.	10,31	0,0006	(33)
	27967	Cherp	Involved in Ca2+ mobilization, NFAT activation and cell proliferation (Jurkat Tcells)	6,72	0,0005	(34)
	231474	Paqr3	Adiponectin receptor inhibiting proinflammatory TNFα and inducing anti-inflammatory cytokines (IL-10 and IL-1Rα).	5,86	0,0016	(35, 36)
	17691	Snf1lk	Prevents persistent CREB/TORC1-dependent transcription and is involved in c-Jun activation via MEF2/HDAC4 attenuation.	5,14	0,0008	(37)
	22223	Uchl1	Attenuates TNFα-induced NF-κB activity and increases IκB-alpha (vascular cells).	4,69	0,0002	(38, 39)
	494504	Apcdd1	Target of the Wnt/β-catenin pathway.	4,55	0,0028	(40)
	211228	Lrrc25	Contains PI3K-interaction and ITAM motifs; possibly a novel type of pattern-recognition receptor involved in the activation of immune cells.	3,35	0,0163	(41)
	17268	Meis1	Up-regulated by NUP98-HOXA9, and c-Myb is one of its strong targets.	2,57	0,0003	(42, 43)
	17863	Myb	Activates transcription via CREB binding protein, and p38MAPK delta controls its degradation in response to stress.	-2,24	0,0000	(44, 45)
	11555	Adrb2	Binding to its agonists inhibits LPS-induced IL-18 and IL-12 production in monocytes.	-2,69	0,0005	(46)
	16163	Il13	Up-regulates FcγRII, a negative regulator of immune response, on DCs.	-3,04	0,0039	(47)
	19715	Rex2	Is a Rac GEF connecting GPCRs, through Gβγ and PI3k, to Rac activation.	-3,57	0,0018	(48)
	72049	Tnfrsf13c	B cell activating molecule produced by DCs and modulated by AIRE.	-3,76	0,0030	(49)
	21809	Tgfb3	Induces tolerance in DCs.	-4,44	0,0157	(50)
	20187	Ryk	Wnt receptor; Wnt modulates DC maturation.	-4,51	0,0014	(51)
	12326	Camk4	Ca^{2+}-dependent signaling cascade comprising CaMK4-CREB-Bcl-2 involved in a DC survival signal implicating TLR4.	-4,57	0,0027	(52)
	20347	Sema3b	Inhibits the PI3k/Akt pathway through neuropilin-1 (lung and breast cancer cells).	-5,02	0,0050	(53)
	14268	Fn1	Implicated in liver stroma-mediated activation of NK cells via TLR3 signaling.	-9,67	0,0005	(54)

DC Maturation	23792	Adam23	Family members up-regulated during DC maturation.	4,23	0,0012	(55, 56)
	107477	Guca1b	Family member YC-1 inhibits LPS-induced co-stimulatory molecular expression of DCs by inhibiting Akt activation, IκBα degradation and NFκB translocation.	3,48	0,0080	(57)
	16847	Lepr	Receptor of leptin, which activates DCs, induces functional and morphological changes and promotes their survival.	-4,11	0,0735	(58, 59)
	22359	Vldlr	Oxidized low-density lipoprotein that induces differention of monocytes into DCs.	-4,36	0,0656	(60, 61)
	16564	Kif21a	Kinesin family member; kinesin-2 was found up-regulated during DC maturation.	-6,03	0,0235	(62)
DC Migration	72054	Cyp4f18	Induced by LPS in DCs, and inactivates leukotriene B4 (LTB4), a receptor that promotes DC migration.	3,43	0,0046	(63, 64)
	20856	Stc2	Stc1 modulates leukocyte and macrophages migration.	-3,05	0,0016	(65)
	15199	Hebp1	FL2 (Hepb1-derived peptide) chemoattracts DCs, inhibits LPS-induced maturation.	-8,67	0,0028	(66)
	171167	Fut10	Fucosyltransferases mediates emigration of iDCs into inflammation sites.	-8,68	0,0390	(67)

WT/dKO ratio represents the relative intensity detected from WT hybridized samples compared to dKO samples. Negative values represent dKO/WT ratio.

Supplemental Table S4. Complete list of genes differentially expressed in WT vs. dKO DCs

No.	Gene ID	Gene Symbol	Gene Name	WT/dKO ratio	P value
1	16913	Psmb8	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	594,77	0,0001
2	382045	Gpr114	G protein-coupled receptor 114	-62,43	0,0007
3	68616	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	-54,75	0,0012
4	112422	2610305D13Rik	RIKEN cDNA 2610305D13 gene	-45,12	0,0022
5	668581	EG668581	predicted gene, EG668581	38,96	0,0771
6	19944	Rpl29	ribosomal protein L29	33,92	0,0013
7	50768	Dlc1	deleted in liver cancer 1	23,74	0,0001
8	109361	D730005E14Rik	RIKEN cDNA D730005E14 gene	22,88	0,0002
9	140780	Bmp2k	BMP2 inducible kinase	20,64	0,0000
10	22351	Vill	villin-like	17,35	0,0033
11	67878	Tmem33	transmembrane protein 33	16,98	0,0000
12	232441	Rerg	RAS-like, estrogen-regulated, growth-inhibitor	-15,19	0,0003
13	546368	Gm5945	predicted gene 5945	14,08	0,0048
14	667597	BC023105	cDNA sequence BC023105	-13,88	0,0015
15	381823	Apold1	apolipoprotein L domain containing 1	-13,24	0,0085
16	12260	C1qb	complement component 1, q subcomponent, beta polypeptide	13,20	0,0087
17	57425	U90926	cDNA sequence U90926	12,92	0,0115
18	73061	3110007F17Rik	RIKEN cDNA 3110007F17 gene	12,12	0,0049

19	56043	Akr1e1	aldo-keto reductase family 1, member E1	11,89	0,0003
20	382265	Gm5167	predicted gene 5167	11,18	0,0048
21	21672	Prdx2	peroxiredoxin 2	11,11	0,0002
22	56066	Cxcl11	chemokine (C-X-C motif) ligand 11	-10,89	0,0683
23	12774	Ccr5	chemokine (C-C motif) receptor 5	10,71	0,0003
24	13032	Ctsc	cathepsin C	10,66	0,0000
25	320713	Mysm1	myb-like, SWIRM and MPN domains 1	10,31	0,0006
26	14768	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1	-9,90	0,0072
27	56219	Extl1	exostoses (multiple)-like 1	9,75	0,0008
28	14268	Fn1	fibronectin 1	-9,67	0,0005
29	236069	Gm13238	predicted gene 13238	9,60	0,0000
30	330812	Rnf150	ring finger protein 150	9,15	0,0042
31	171167	Fut10	fucosyltransferase 10	-8,68	0,0390
32	15199	Hebp1	heme binding protein 1	-8,67	0,0028
33	245049	Myrip	myosin VIIA and Rab interacting protein	8,44	0,0036
34	70359	Gtpbp3	GTP binding protein 3	-7,83	0,0025
35	230806	Aim1l	absent in melanoma 1-like	-7,78	0,0016
36	11745	Anxa3	annexin A3	7,56	0,0001
37	626665	LOC626665	similar to zinc finger protein 665	-7,51	0,0028
38	433762	LOC433762	hypothetical gene LOC433762	7,38	0,0012

39	74134	Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	-7,36	0,0121
40	668462	EG668462	predicted gene, EG668462	6,89	0,0153
41	433791	Gm13251	predicted gene 13251	6,75	0,0000
42	58238	A830059I20Rik	family with sequence similarity 181, member B	-6,72	0,0004
43	27967	Cherp	calcium homeostasis endoplasmic reticulum protein	6,72	0,0005
44	18406	Orm2	orosomucoid 2	-6,59	0,0045
45	668280	EG668280	predicted gene, EG668280	6,49	0,0100
46	83486	Rbm5	RNA binding motif protein 5	6,23	0,0004
47	20148	Dhrs3	dehydrogenase/reductase (SDR family) member 3	6,21	0,0021
48	230848	Zbtb40	zinc finger and BTB domain containing 40	6,05	0,0001
49	16564	Kif21a	kinesin family member 21A	-6,03	0,0235
50	231474	Paqr3	progestin and adipoQ receptor family member III	5,86	0,0016
51	258832	Olfr109	olfactory receptor 109	5,82	0,0006
52	433790	Gm13241	predicted gene 13241	5,63	0,0010
53	666026	EG666026	predicted gene, EG666026	5,59	0,0323
54	80287	Apobec3	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3	5,59	0,0001
55	70673	Prdm16	PR domain containing 16	5,58	0,0002
56	233115	Dpy19l3	dpy-19-like 3 (C. elegans)	-5,56	0,0043
57	226791	Lyplal1	lysophospholipase-like 1	-5,51	0,0076
58	72386	2610035D17Rik	RIKEN cDNA 2610035D17 gene	5,48	0,0018

59	231510	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase 9	-5,40	0,0002
60	269211	BC035947	cDNA sequence BC035947	-5,31	0,0479
61	71583	9130008F23Rik	RIKEN cDNA 9130008F23 gene	5,27	0,0005
62	545248	EG545248	predicted gene, EG545248	5,20	0,0110
63	13860	Eps8	epidermal growth factor receptor pathway substrate 8	5,17	0,0006
64	76508	2210015D19Rik	RIKEN cDNA 2210015D19 gene	-5,16	0,0000
65	17691	Sik1	salt inducible kinase 1	5,14	0,0008
66	381549	Zfp69	zinc finger protein 69	-5,13	0,0010
67	20347	Sema3b	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	-5,02	0,0050
68	67621	Bend5	BEN domain containing 5	-4,91	0,0503
69	20346	Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	4,80	0,0147
70	667337	LOC667337	hypothetical LOC667337	4,74	0,0004
71	22223	Uchl1	ubiquitin carboxy-terminal hydrolase L1	4,69	0,0002
72	276829	Smtnl2	smoothelin-like 2	-4,68	0,0046
73	69392	1700024P12Rik	RIKEN cDNA 1700024P12 gene	4,66	0,0013
74	668645	Gm9282	predicted gene 9282	-4,62	0,0013
75	68681	1110030E23Rik	RIKEN cDNA 1110030E23 gene	4,58	0,0006
76	12326	Camk4	calcium/calmodulin-dependent protein kinase IV	-4,57	0,0027

77	494504	Apcdd1	adenomatosis polyposis coli down-regulated 1	4,55	0,0028
78	638940	EG638940	predicted gene, EG638940	4,55	0,0017
79	382686	LOC382686	RIKEN cDNA 3110053B16 gene	-4,55	0,0397
80	97130	C77080	expressed sequence C77080	4,51	0,0037
81	20187	Ryk	receptor-like tyrosine kinase	-4,51	0,0014
82	14245	Lpin1	lipin 1	-4,45	0,0076
83	21809	Tgfb3	transforming growth factor, beta 3	-4,44	0,0157
84	78923	Chsy3	chondroitin sulfate synthase 3	-4,43	0,0377
85	22359	Vldlr	very low density lipoprotein receptor	-4,36	0,0656
86	104271	Tex15	testis expressed gene 15	-4,34	0,0005
87	244416	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	-4,33	0,0008
88	23792	Adam23	a disintegrin and metallopeptidase domain 23	4,23	0,0012
89	73656	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	4,21	0,0003
90	67276	Eri1	exoribonuclease 1	-4,17	0,0007
91	12331	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	-4,14	0,0000
92	16847	Lepr	leptin receptor	-4,11	0,0735
93	12345	Capzb	capping protein (actin filament) muscle Z-line, beta	4,09	0,0100
94	77634	Snapc3	small nuclear RNA activating complex, polypeptide 3	4,06	0,0002
95	26458	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	-4,05	0,0028
96	110877	Slc18a1	solute carrier family 18 (vesicular monoamine), member 1	4,03	0,0002

97	11828	Aqp3	aquaporin 3	-4,02	0,0181
98	195522	Zfp691	zinc finger protein 691	-4,02	0,0024
99	71665	Fuca1	fucosidase, alpha-L- 1, tissue	3,94	0,0002
100	666532	Gm13139	predicted gene 13139	3,93	0,0002
101	215772	9130014G24Rik	RIKEN cDNA 9130014G24 gene	3,90	0,0015
102	104383	Rcor2	REST corepressor 2	-3,85	0,0038
103	78816	Gmip	Gem-interacting protein	-3,84	0,0026
104	239559	A4galt	alpha 1,4-galactosyltransferase	-3,83	0,0001
105	26382	Fgd2	FYVE, RhoGEF and PH domain containing 2	3,81	0,0123
106	72049	Tnfrsf13c	tumor necrosis factor receptor superfamily, member 13c	-3,76	0,0030
107	665081	EG665081	predicted gene, EG665081	3,76	0,0046
108	625719	EG625719	predicted gene, EG625719	3,75	0,0026
109	228576	Mall	mal, T-cell differentiation protein-like	-3,72	0,0060
110	234353	Psd3	pleckstrin and Sec7 domain containing 3	3,68	0,0017
111	72701	Zfp618	zinc fingerprotein 618	-3,67	0,0024
112	258503	Olfr98	olfactory receptor 98	3,66	0,0029
113	15572	Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	-3,60	0,0228
114	17965	Nbl1	neuroblastoma, suppression of tumorigenicity 1	-3,59	0,0207
115	244556	Zfp791	zinc finger protein 791	-3,58	0,0010
116	19715	Rex2	reduced expression 2	-3,57	0,0018

117	67733	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	-3,57	0,0101
118	70713	Gpr137c	G protein-coupled receptor 137C	-3,52	0,1119
119	383940	LOC383940	similar to reduced expression 2	-3,50	0,0130
120	74374	Clec16a	C-type lectin domain family 16, member A	-3,49	0,0089
121	102093	Phkb	phosphorylase kinase beta	3,48	0,0002
122	107477	Guca1b	guanylate cyclase activator 1B	3,48	0,0080
123	72054	Cyp4f18	cytochrome P450, family 4, subfamily f, polypeptide 18	3,43	0,0046
124	231287	Atp10d	ATPase, class V, type 10D	-3,39	0,0034
125	259277	Klk8	kallikrein related-peptidase 8	-3,37	0,0162
126	230972	Arhgef16	Rho guanine nucleotide exchange factor (GEF) 16	-3,37	0,0745
127	211228	Lrrc25	leucine rich repeat containing 25	3,35	0,0163
128	13730	Emp1	epithelial membrane protein 1	-3,35	0,0024
129	381853	Gipr	gastric inhibitory polypeptide receptor	-3,34	0,0054
130	622205	EG622205	predicted gene, EG622205	3,34	0,0008
131	76499	Clasp2	CLIP associating protein 2	-3,33	0,0019
132	667103	Gm13570	predicted gene 13570	3,31	0,0030
133	21784	Tff1	trefoil factor 1	3,29	0,0001
134	19652	Rbm3	RNA binding motif protein 3	-3,28	0,0079
135	55948	Sfn	stratifin	3,21	0,0060
136	12286	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-3,21	0,0006

137	228576	Mall	mal, T-cell differentiation protein-like	-3,20	0,0121
138	71306	Mfap3l	microfibrillar-associated protein 3-like	3,20	0,0040
139	244579	Tox3	TOX high mobility group box family member 3	-3,18	0,0139
140	224796	Clic5	chloride intracellular channel 5	3,15	0,0037
141	67742	Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1	3,13	0,0001
142	67451	Pkp2	plakophilin 2	-3,13	0,0137
143	100038586	Gm10330	predicted gene 10330	3,10	0,0002
144	69590	Gpx8	glutathione peroxidase 8 (putative)	-3,09	0,0021
145	70005	1700029I01Rik	RIKEN cDNA 1700029I01 gene	3,06	0,0001
146	20856	Stc2	stanniocalcin 2	-3,05	0,0016
147	16163	Il13	interleukin 13	-3,04	0,0039
148	72297	B3gnt3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	3,04	0,0009
149	13640	Efna5	ephrin A5	-3,02	0,0069
150	19041	Ppl	periplakin	-2,99	0,0046
151	319701	Fbxo48	F-box protein 48	-2,99	0,0040
152	625355	EG625355	predicted gene, EG625355	2,98	0,0094
153	102060	Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	-2,92	0,0002
154	67405	Nts	neurotensin	-2,89	0,0033
155	13009	Csrp3	cysteine and glycine-rich protein 3	-2,89	0,0001
156	72309	Tmem158	transmembrane protein 158	-2,85	0,0095

157	21916	Tmod1	tropomodulin 1	-2,85	0,0012
158	106529	Tecr	trans-2,3-enoyl-CoA reductase	-2,84	0,0023
159	230767	Iqcc	IQ motif containing C	-2,84	0,0037
160	19651	Rbl2	retinoblastoma-like 2	-2,76	0,0005
161	72281	Sh2d4a	SH2 domain containing 4A	2,74	0,0007
162	11555	Adrb2	adrenergic receptor, beta 2	-2,69	0,0005
163	234366	Gatad2a	GATA zinc finger domain containing 2A	2,69	0,0004
164	21968	Tom1	target of myb1 homolog (chicken)	-2,68	0,0031
165	18784	Pla2g5	phospholipase A2, group V	-2,60	0,0003
166	666266	Gm8013	predicted gene 8013	2,59	0,0003
167	17268	Meis1	Meis homeobox 1	2,57	0,0003
168	59092	Pcbp4	poly(rC) binding protein 4	2,56	0,0045
169	72709	C1qtnf6	C1q and tumor necrosis factor related protein 6	-2,49	0,0000
170	65973	Asph	aspartate-beta-hydroxylase	-2,47	0,0004
171	17863	Myb	myeloblastosis oncogene	-2,24	0,0000

WT/dKO ratio represents the relative intensity detected from WT hybridized samples compared to dKO samples (mean of three replicates). Negative values represent dKO/WT ratio.

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