

Table S1. Association results of the VRK2 SNPs with depression in Europeans (PGC2 [1], UK Biobank [2] and 23andMe [3]) and Han Chinese (CONVERGE [4]) GWAS.

CHR	POS	SNP	A1	A2	Frequency of A1		PGC2+UKB			23andMe			PGC2+UKB+23andMe meta-analysis			CONVERGE			
					European	Chinese	OR	SE	P	OR	SE	P	P	OR	Q	I	OR	SE	P
2	57956088	rs13025126	A	G	0.385	0.411	1.017	0.0044	1.16E-04	1.027	0.0062	1.55E-05	1.34E-08	1.021	0.197	39.82	1.081	0.028	6.02E-03
2	57987593	rs11682175	T	C	0.528	0.558	0.981	0.0043	6.91E-06	0.968	0.0060	9.10E-08	1.10E-11	0.977	0.083	66.74	0.935	0.028	1.57E-02
2	57988194	rs11688767	A	T	0.514	0.540	0.981	0.0043	8.84E-06	0.969	0.0060	1.39E-07	1.86E-11	0.977	0.088	65.68	0.939	0.028	2.29E-02
2	57995348	rs13016665	A	C	0.429	0.580	1.016	0.0044	4.27E-04	1.029	0.0062	4.54E-06	3.32E-08	1.020	0.090	65.27	1.077	0.029	2.04E-02
2	57998040	rs11695135	A	C	0.610	0.582	0.981	0.0044	2.24E-05	0.972	0.0062	3.59E-06	7.55E-10	0.978	0.197	39.82	0.920	0.028	2.95E-03
2	58012833	rs1568452	T	C	0.381	0.413	1.022	0.0044	1.51E-06	1.032	0.0062	3.19E-07	5.65E-12	1.025	0.180	44.44	1.087	0.028	2.93E-03
2	58029645	rs2717066	A	C	0.371	0.414	1.019	0.0045	2.58E-05	1.030	0.0062	1.77E-06	5.83E-10	1.023	0.155	50.6	1.085	0.028	3.33E-03
2	58041936	rs2717046	T	C	0.378	0.409	1.020	0.0044	7.95E-06	1.030	0.0062	1.43E-06	1.11E-10	1.023	0.188	42.2	1.092	0.028	1.70E-03
2	58065936	rs2717079	A	T	0.390	0.453	1.019	0.0044	1.96E-05	1.028	0.0061	9.39E-06	1.11E-09	1.022	0.270	17.88	1.082	0.028	4.73E-03
2	58095252	rs2717067	C	G	0.393	0.430	1.019	0.0044	2.79E-05	1.028	0.0061	9.11E-06	1.66E-09	1.022	0.242	26.95	1.089	0.028	2.20E-03
2	58111064	rs6720288	A	G	0.617	0.573	0.981	0.0044	9.99E-06	0.973	0.0062	6.56E-06	4.73E-10	0.978	0.281	14.04	0.920	0.028	2.68E-03
2	58111922	rs1533725	T	G	0.617	0.577	0.981	0.0044	1.01E-05	0.973	0.0062	7.65E-06	6.00E-10	0.978	0.287	11.9	0.917	0.028	2.06E-03
2	58115072	rs2678911	C	G	0.383	0.458	1.020	0.0044	1.02E-05	1.028	0.0062	8.36E-06	6.75E-10	1.022	0.299	7.39	1.081	0.028	4.18E-03
2	58116640	rs2683632	T	C	0.615	0.540	0.981	0.0044	1.65E-05	0.973	0.0062	8.19E-06	1.14E-09	0.978	0.264	20	0.929	0.028	5.93E-03
2	58117095	rs2678913	T	C	0.615	0.542	0.981	0.0044	2.03E-05	0.973	0.0062	8.21E-06	1.44E-09	0.979	0.253	23.64	0.928	0.028	5.64E-03
2	58117926	rs2678914	C	G	0.615	0.542	0.981	0.0044	1.91E-05	0.973	0.0062	8.04E-06	1.28E-09	0.979	0.258	21.85	0.928	0.028	5.64E-03
2	58119122	rs2717060	A	G	0.617	0.542	0.982	0.0044	4.46E-05	0.973	0.0062	8.36E-06	3.37E-09	0.979	0.221	33.17	0.928	0.028	5.59E-03
2	58119582	rs2678916	T	G	0.384	0.456	1.019	0.0044	1.64E-05	1.028	0.0062	9.80E-06	1.21E-09	1.022	0.287	11.9	1.076	0.028	7.32E-03
2	58119657	rs2717059	C	G	0.618	0.544	0.982	0.0044	6.21E-05	0.973	0.0062	8.29E-06	5.28E-09	0.979	0.202	38.57	0.929	0.028	7.31E-03
2	58120553	rs2678917	A	T	0.385	0.456	1.019	0.0044	1.94E-05	1.028	0.0062	8.61E-06	1.36E-09	1.022	0.264	20	1.076	0.028	7.32E-03
2	58121391	rs2678918	T	C	0.384	0.456	1.019	0.0044	1.82E-05	1.028	0.0062	9.15E-06	1.28E-09	1.022	0.275	16.1	1.075	0.028	7.59E-03
2	58127907	rs2717057	T	C	0.382	0.456	1.019	0.0044	1.50E-05	1.029	0.0062	4.92E-06	5.98E-10	1.023	0.237	28.64	1.079	0.028	4.99E-03
2	58133522	rs2678907	A	G	0.618	0.542	0.981	0.0044	1.83E-05	0.972	0.0062	4.64E-06	7.56E-10	0.978	0.226	31.71	0.927	0.028	4.70E-03
2	58135023	rs867740	T	C	0.617	0.544	0.981	0.0044	1.36E-05	0.972	0.0062	4.88E-06	5.01E-10	0.978	0.237	28.64	0.932	0.028	9.00E-03
2	58136220	rs2717000	C	G	0.617	0.540	0.981	0.0044	1.36E-05	0.972	0.0062	5.05E-06	5.64E-10	0.978	0.247	25.36	0.933	0.028	9.91E-03
2	58138581	rs2678902	A	G	0.383	0.460	1.019	0.0044	1.92E-05	1.028	0.0062	5.90E-06	1.01E-09	1.022	0.237	28.64	1.071	0.028	1.06E-02
2	58139906	rs2678895	A	T	0.618	0.544	0.981	0.0044	1.22E-05	0.973	0.0062	6.61E-06	5.99E-10	0.978	0.269	18.08	0.930	0.028	7.12E-03
2	58144542	rs951965	A	C	0.383	0.456	1.020	0.0044	1.14E-05	1.028	0.0062	6.00E-06	5.65E-10	1.023	0.264	20	1.074	0.028	7.61E-03
2	58145060	rs2717005	A	G	0.619	0.540	0.981	0.0044	1.30E-05	0.973	0.0062	7.03E-06	7.15E-10	0.978	0.269	18.08	0.934	0.028	1.08E-02
2	58148349	rs2465805	T	C	0.382	0.460	1.019	0.0044	1.31E-05	1.028	0.0062	5.73E-06	5.99E-10	1.023	0.253	23.64	1.071	0.028	1.03E-02
2	58149158	rs2717008	T	C	0.618	0.540	0.981	0.0044	1.17E-05	0.972	0.0062	5.81E-06	5.32E-10	0.978	0.258	21.85	0.934	0.028	1.06E-02
2	58152280	rs2717012	A	C	0.382	0.460	1.019	0.0044	1.49E-05	1.028	0.0062	8.76E-06	9.58E-10	1.022	0.281	14.04	1.070	0.028	1.14E-02
2	58152537	rs2717013	A	G	0.382	0.460	1.019	0.0044	1.59E-05	1.028	0.0062	6.21E-06	8.03E-10	1.022	0.247	25.36	1.070	0.028	1.17E-02
2	58154915	rs2678874	A	T	0.378	0.462	1.020	0.0044	7.69E-06	1.028	0.0062	6.07E-06	3.31E-10	1.023	0.281	14.04	1.069	0.028	1.26E-02
2	58155829	rs2312143	A	G	0.378	0.463	1.020	0.0044	9.18E-06	1.028	0.0062	6.32E-06	3.96E-10	1.023	0.281	14.04	1.069	0.028	1.31E-02
2	58159852	rs2717020	T	C	0.622	0.540	0.980	0.0044	7.75E-06	0.972	0.0062	6.05E-06	3.31E-10	0.978	0.281	14.04	0.936	0.028	1.32E-02
2	58160138	rs2678885	T	G	0.622	0.535	0.981	0.0044	1.01E-05	0.973	0.0062	7.11E-06	4.73E-10	0.978	0.281	14.04	0.932	0.028	8.49E-03
2	58160605	rs2717021	A	G	0.378	0.456	1.020	0.0044	9.84E-06	1.028	0.0062	6.00E-06	4.20E-10	1.023	0.269	18.08	1.073	0.028	8.72E-03
2	58163146	rs2717025	T	G	0.378	0.463	1.020	0.0044	8.53E-06	1.028	0.0062	6.13E-06	3.52E-10	1.023	0.287	11.9	1.073	0.028	8.31E-03
2	58163178	rs2717026	A	G	0.623	0.537	0.980	0.0044	8.52E-06	0.972	0.0062	6.09E-06	3.52E-10	0.978	0.287	11.9	0.932	0.028	8.31E-03

2	58165595	rs2717029	T	G	0.378	0.465	1.020	0.0044	9.41E-06	1.028	0.0062	7.53E-06	4.46E-10	1.023	0.293	9.69	1.076	0.028	5.98E-03
2	58165694	rs2717030	T	C	0.622	0.542	0.981	0.0044	9.47E-06	0.972	0.0062	6.15E-06	4.20E-10	0.978	0.269	18.08	0.929	0.028	5.76E-03
2	58168831	rs2717038	A	G	0.623	0.538	0.980	0.0044	4.34E-06	0.972	0.0062	6.22E-06	1.61E-10	0.977	0.318	0	0.929	0.028	5.80E-03
2	58169166	rs2717039	T	G	0.377	0.460	1.021	0.0044	3.59E-06	1.028	0.0062	8.59E-06	1.61E-10	1.023	0.357	0	1.076	0.028	5.83E-03
2	58171964	rs2678898	T	C	0.620	0.537	0.981	0.0045	1.44E-05	0.973	0.0062	7.86E-06	1.09E-09	0.978	0.273	16.82	0.931	0.028	7.96E-03
2	58237405	rs4672228	T	C	0.612	0.502	0.982	0.0044	4.55E-05	0.974	0.0062	2.15E-05	6.62E-09	0.979	0.287	11.9	0.942	0.028	2.61E-02
2	58253423	rs13033536	A	G	0.373	0.503	1.019	0.0045	2.50E-05	1.026	0.0062	4.91E-05	8.00E-09	1.021	0.404	0	1.060	0.028	3.42E-02

Abbreviation

CHR, chromosome; POS, position; SNP, single nucleotide polymorphism; A1, allele 1; A2, allele 2; OR, odds ratio; SE, standard error.

Table S2. Overview of the differentially phosphorylated proteins between *Vrk2*^{-/-} and *Vrk2*^{+/+} mice.

Gene Name	Mol weight [kDa]	Sequence length	Position	AA	Sequence window	Vrk2 ^{-/-} Intensity			Vrk2 ^{+/+} Intensity			GroupB/ GroupA	P value
						GroupB-4	GroupB-5	GroupB-6	GroupA-1	GroupA-2	GroupA-3		
Ubr4	572.3	5180	226	S	ISPQALVEGENDEQSSPDQVSAAKTKSVFIA	245123.6		321869.2		35769.0	44943.4	7.02	0.024
Mical3	223.7	1993	1452	T	TLGQSQFNSTSDSTMLTPPSSPPPPPPNEEP	1897069.2	2149835.3	3375999.8	434864.9		343224.7	6.36	0.039
Mical3	223.7	1993	1456	S	QSFNTSDSTMLTPPSSPPPPPPNEEPATLR	1897069.2	2149835.3	3375999.8	434864.9		343224.7	6.36	0.039
Psm2	100.2	908	20	T	GRDKTPVQSQQPSATTSPSGADEKSSGKERRD	582612.0		366467.8	186195.3	35688.2	38519.2	5.47	0.033
Smim13	10.0	88	70	S	NEQPSGSETEEDPSASQKIRARQRRPPVD	344611.8	384056.0	607126.4	59893.9	108826.4		5.28	0.043
Cdk14	53.0	469	134	S	SSPSSTSPKFGKADSYEKLEKLGESYATV	1650301.3	1224611.6	1502772.7		512840.6	46691.9	5.22	0.016
Smim13	10.0	88	63	T	TGSQEGDNEQPSGSETEEDPSASQKIRAR	2014821.6	5607686.4	4571735.6	1331622.7	359781.5	649708.8	5.21	0.041
H1-4	22.0	219	2	S	_____MSETAAPAAPAPAEK	1804220.9	3021450.7	3334752.2	336845.3	737596.1		5.06	0.039
Prnt2	35.9	346	208	S	LQAGDGEEGPAPQPHSPSTKTPPANGAPPR	2888253.9	3225053.8	3940701.9	1612988.9	367630.2	279290.2	4.45	0.0081
Cys1	15.5	145	116	S	KGNPEDSCASEAPGNSPKRPEQSAISYDYS	206978.4	233562.6	300297.0	17080.0		118930.6	3.63	0.042
Jph1	71.9	660	461	T	PPSPKESPHFYRKGTTPRSPESPQKSHSP	344123.5	322684.3		79754.3	100679.7	110676.7	3.44	0.00047
Alad	36.0	330	215	S	FASCFYGFPRDAAQSSPAFGDRRCYQLPPGA	414454.5		312369.1	120107.1	167918.4	31777.6	3.41	0.028
Fgd1	106.4	960	98	S	PQHHRALRFSYHLEGSQPRPLGHQGNRILVK	11061955.4	13628403.7	10805647.1	653681.2	5306820.9	4578582.8	3.37	0.0081
Fgd1	106.4	960	92	S	LPCGSPQHHRALRFSYHLEGSQPRPLGHQG	11061955.4	13628403.7	10805647.1	653681.2	3024990.1	7088324.9	3.30	0.017
Basp1	22.1	226	192	S	APSSKETPAASEAPSSAAKAPAAAPAAEP	844441.9	905234.7	1092598.0	98933.3	108039.3	665401.8	3.26	0.031
Zbtb20	81.0	741	432	S	AESSAQNPQLEPAGSSPERSNESEMDNTVIT	1128340.8	1770693.3	1354292.1	279178.6	294124.0	746435.4	3.22	0.016
Uso1	107.0	959	940	S	SKLKDGHVPEEEDESGDQEDDDDEIDGDGK	828678.6	1518852.4	1999312.9	250717.4	567449.2	541630.1	3.20	0.048
Pclo	550.8	5068	3506	S	GGSLGCQTETDPDQTSPPYMGATSPPKDKKR	2814740.2	3414376.8	3709463.4	2107181.1	666644.7	444630.1	3.09	0.019
Oxr1	95.9	866	346	S	TEESLSEDAFTESELSPIRELLSSEPRQEK	3214179.3	1817840.1	2622364.6	431046.3	846347.2	1236693.9	3.04	0.021
Sgip1	86.1	806	335	T	PEHVTPELTPREQVVTPPAASDIPADSPAPA	5026362.1	6409429.8	8240542.2	1611336.9	2657304.3	2570795.9	2.88	0.012
Slc38a3	55.6	505	53	S	TQHCGEGKGLQKSPKPEHFTDFEGKTSFG	172958.2	269147.8		82968.3	94915.6	56064.8	2.83	0.035
Lsm14a	50.5	462	183	S	QDTRSVPKQLAQGRSSQLDPLRKSPTMEQA		1219922.7	1189962.5	480459.4	402490.1	394896.5	2.83	0.00023
Clip4	75.8	704	580	S	SNKQNH5YPGFRRSFSTTSASSQKINRRNA	152114.6	126908.2	106525.8	60767.0	46449.3	32530.3	2.76	0.0061
Map1a	300.1	2776	895	S	EATQGLDYVPSAGTISPTSSLEEDKGFKSP	14802999.2	13587497.7	19453709.0	4397554.1	5489777.0	8101646.5	2.66	0.0090
Cd34	41.0	382	343	S	TENGGGQGYSSGPGASPETQGGKANVTRGAQE	142186.1	147633.6			65850.9	43419.4	2.65	0.016
Hsph1	96.4	858	558	S	PQVQTDGQQTSSQSPPELTSSESKTPDADK	3158099.3	4209161.7	4023592.3	1980523.0	1242459.7	1185503.7	2.58	0.0049
Arhgap35	170.4	1499	975	S	ACSTTEEVFNPRAGSPLCNSNLQDSEEDVE	1789377.0	1743053.5	2548831.9	987802.3	495382.4	931398.5	2.52	0.016
Syngap1	148.2	1340	892	S	LTAALGLRPAPAGRLSQSGSSITAAAGMRLS	695075.4	620605.8	1018452.2	327547.5	417261.8	199844.3	2.47	0.028
Wdr44	101.6	915	27	S	DAPEDVHLGTGYPVGGSPGKVGLLSFKEAENT	852692.3	636207.0	619934.1		285712.9	294617.2	2.42	0.024
Cntn20a1	74.2	681	269	S	VCPMRKRIEREVKSSPESPLMEKKSNLKE	1500363.2	1462555.2	1596742.2	659112.6	598235.9		2.42	0.00055
Nckip5d	78.6	714	260	S	HTTVSQPQSPSKAPSPPEPTTEVAETNST	4997677.8	4677095.4	5386550.5	1175585.3	3147538.8	2261738.3	2.29	0.0096
Ttyh3	57.7	524	437	S	DGEEETAPGPRQAHDSLRYHMPSLYSCGSS	162441.8	187179.3	219747.0	71433.3	91581.6	88088.6	2.27	0.0039
Rmdn3	52.0	470	212	S	EDEVSCETVRMGRKDSLDDVEAASSPAAAA	229016.5	262403.2		91185.4	104192.4	134893.7	2.23	0.0074
Camkv	54.8	512	436	S	ITPATDGSVTPATDRSATPATDGRATPATEE	988391.6	919456.6	1385483.3	338784.7	796762.9	360103.6	2.20	0.045
Ank2	426.3	3898	2206	S	EESYKHEGLAETPETSPELSFSPKKEEQI	232664.5	269324.2		110820.1	94274.0	145354.6	2.15	0.011
Jph3	81.2	744	420	S	AQEEARIARITAKEFSPSQFHRENGLEYQRP	1343248.2	1588710.6	2067568.5	683329.1	911273.1	790288.9	2.10	0.017
Rtn3	103.9	964	31	S	SSSGAEPALGGGGSPGACPALGAKSCGSS	13114235.0	15490494.0	18949774.3	11552339.3	3577244.7	8176381.2	2.04	0.048
Numb1	64.1	604	263	S	AAPAVAPGPAQPGHVSPTPATTSPEKGEAG		2114145.5	2371076.0	1191822.7	711214.9	1394736.6	2.04	0.026
Sos1	150.9	1319	1120	S	FDSHSA5PFHRSASVSSISLSKGTDEVPV	50181.8	53106.7		29433.6	21276.2		2.04	0.026
Cntnap2	148.2	1332	1304	S	RHKGYHTNEAKGAESAESAADAAMNNDPNF	904017.3	1028639.7	884657.6	286081.0	628078.2	486043.1	2.01	0.012
Cntnap2	148.2	1332	1307	S	GTYHTNEAKGAESAESAADAAMNNDPNFTET	1183936.6	1340598.5	1231618.4	424899.3	824494.5	618678.3	2.01	0.0072
Rtn4	126.6	1162	953	S	VKPKVLTKEAEELKPSDTEKEDRSLTAVLSA	4171989.3	2696642.2	3148040.6	1085250.9	1760471.1	2145914.7	2.01	0.035
Ppp1r7	41.3	361	12	S	_____MAAERGAGQQSQEMMEVDRRVESEES	73112.1	66487.1	43578.7	102469.3	129740.6	135753.6	0.50	0.011
Tagln3	22.5	199	163	S	PSWFHRKAQQNRRGFSEEQLRQQQNVIGLQM	212729.6	260794.9	100513.2	328307.7	427544.7	400820.5	0.50	0.026
Snx2	58.5	519	185	S	LSMFSKSEFVSKRRFDFLGLHSLKASKYLH	33669.9	31624.6	17529.5	45172.1	61525.8	63272.6	0.49	0.019

Psd3	114.7	1037	719	S	EGGDFSKDLLKALYNSIKNEKLEWAVDDEEK	18991.1		37005.3	59205.5	57044.8	56422.6	0.49	0.022
Nostrin	57.7	506	479	S	IVTVHEKKEEGWVFGSLKGRGHFPAAYVEE		34678.5	51540.1		91961.4	85657.6	0.49	0.037
Pkp4	131.6	1190	280	S	LPAQRAASPYQRPASPTAVRRVGSVTSRQT	146512.4	632400.2	538352.4	829705.6	874223.8	1011746.0	0.49	0.042
Shank1	226.3	2167	615	S	VGWFPSCDLEEVANRSQEGRQESRDKAKRL	480547.2	610964.8	409141.4	787380.3	1292477.2	1022519.6	0.48	0.027
Slc4a3	135.4	1227	175	S	PPQKAKFSIGSDEDDSPGLPVKAPCAKALPS	123574.5	63573.3	59167.2		173444.4	166389.7	0.48	0.047
Ctnna1	81.5	731	373	S	QLLSVWMQTQSRKTKSAEEELTVLKISHS	24708.7	22760.7		37578.4	52394.9	57707.5	0.48	0.047
Pgm2	68.7	620	173	S	TVSHLKLKAGIMITASHNPKQDNGYKVVYWDN	88016.1	88006.0	71551.7	186478.2	141691.0	193165.1	0.47	0.0059
Nsfl1c	40.7	370	176	S	PEEESAYVAGERRRHSGQDVHVVLKWKTF	873427.6	984514.7	1599931.0	2613289.8	2202723.7	2479200.8	0.47	0.0075
Sgip1	86.1	806	528	S	LSAATPTVGSRRGSPSPLTMGAQDLPVAAA	29021.8		18074.2	50891.4		49553.2	0.47	0.040
Sgip1	86.1	806	484	S	LPPGKPGVGDVSRPFPPIHSSPPPIAPLA		894917.3	1031806.5	2289761.3	1862126.3		0.46	0.038
Pip4p1	30.0	284	169	S	CKRIINLGPVHPGPLSPPEQPMGVRVICGHC	175280.7	233417.3	99924.9	399433.1	254502.5	451932.0	0.46	0.048
Nrbp2	57.3	499	207	S	VVYRIFSNALPDDLRSPIRAEREELRNLHFF	150739.0	62212.1	196438.2	321485.1	284013.0	288937.8	0.46	0.017
Nsfl1c	40.7	370	140	S	GAKEHGAVAVERVTKSPGETSKPRPFAGGGY	52740.3	24655.3		91600.6	85653.3	76888.5	0.46	0.030
Kcnab1	44.7	401	60	S	IIARSLGFTTPQHHSIKESTAKQTMKMYRN	35074.0	46221.5	9100.5	61232.4	62730.9	76977.5	0.45	0.038
Cldn11	22.1	207	198	S	QSFGENRFYSSGSSSPTHAKSAHV	5954299.3	6895677.2	8602328.4	12374248.9	17050066.5	18672669.8	0.45	0.012
Syn1	74.1	706	427	S	NKMTQALPRQPQRDASPRGRGSHSQSSSPGAL	1138603.1	703095.6	590521.2	1770978.9	1649494.6	2064983.5	0.44	0.0080
Ampd2	92.0	798	53	S	MDGKCKEIAEELFSRSLAESELSAPYEFPE	23915.8	29044.8	20177.9	44554.8	67047.0		0.44	0.040
Brsk2	81.7	735	424	S	QRSRSISGASSGLSTSPSSPRVTPHPSPRG	916512.1	829929.0	738549.6	1716278.2	2355112.2	1702148.6	0.43	0.0078
Syt3	63.3	587	382	S	FSVPLAELAQRKHLHFSVYDFDRFSRHDLIGQ	173047.9	99134.9	42841.7	242399.3	202545.9	293544.1	0.43	0.037
Mbp	27.2	250	206	S	DSHTRTHYGLSPKQSHGRTRQDENPVVHFF	86754.0	127560.6	53377.1	162454.1	273193.9	198032.8	0.42	0.035
Rbm12	102.8	992	424	S	PRSKSPSGKRSRSPHAGFCVYLKGLPF	72412.2	70752.5	103225.4	186888.0	207697.0	200562.8	0.41	0.00068
Nefl	61.5	543	13	S	MSSFGYDYPFSTSYKRRYVETPRVHISS	20764.4	31176.9	12030.0		48591.5	56177.0	0.41	0.027
Map1a	300.1	2776	1797	T	PSAPGQESPVPDTKSTPPTRNEPTPSWLAE	2892636.8	1890548.6	2029504.8	4759884.9	6055727.2	6150966.6	0.40	0.0035
Kcnj3	56.6	501	385	S	PLIAPAITSKERNHNSVECLDGLDDISTKLP	34738.9	52832.9	58960.7	108798.4	133350.5	124119.9	0.40	0.0020
Map1b	270.3	2464	1775	S	SLASEKVQSLGEKLSPKSDISPLTPRESSP	719329.3	849612.5	255646.3	1346592.6	1957697.2	1270247.4	0.40	0.032
Grin2b	166.0	1482	930	S	NGSPQASLDFIRRESSVYDISEHRRSFTHSD	111053.4	174429.9	251608.8	448180.8	588379.7	318024.1	0.40	0.036
Phyhipl	42.3	375	12	S	MEVPRLDHALSSPSPCEEIKNLSLEA	308333.7	187283.0	281176.9	684010.4	779128.3	521706.0	0.39	0.0086
Git1	85.3	770	419	S	EPLPSAGATRNRRARSMDSSDLSDGAVTLQE	158474.4	64470.4	94883.4	228911.6		325627.6	0.38	0.043
Mical3	223.7	1993	1406	S	KSAGDQPPLLTPKSPDKELRSSQEERRDLS	26995.4	59668.7		118066.2		118424.9	0.37	0.044
Mical3	223.7	1993	1404	S	LPKSAGDQPPLLTPKSPDKELRSSQEERRD	26995.4	59668.7		118066.2		118424.9	0.37	0.044
Nipbl	315.5	2798	2666	S	GSPKNNTAADTEDEESDGEDRGGGTSGLRR		54239.0	37652.6	126375.8	124694.5		0.37	0.011
Relch	134.6	1216	56	S	LGAGVGLDPGSAGSLSPQDPMALGSSARPG	243548.8	164864.3	160686.1		546635.6	530629.7	0.35	0.0022
Scn2a	227.9	2006	488	S	DFSGAGGIGVFSESSSVASKLSSKSEKELKN	80585.6	52010.6	143058.6		278441.4	244093.8	0.35	0.020
Hnrnpm	77.6	729	452	S	GLVMDRMGVSVERMGSSIERMGLPLGDHMASS	38537.2		15540.4	74684.1	84180.0	73869.3	0.35	0.013
Phyhipl	42.3	375	11	S	MEVPRLDHALSSPSPCEEIKNLSLE	308333.7	187283.0	192510.1	684010.4	779128.3	521706.0	0.35	0.0070
Ak5	63.3	562	181	S	LLRKKIHSASSNRKWSLIAKIITNGELAPQE	11449.8		9807.1	28060.0	33399.3		0.35	0.019
Rims1	163.2	1463	1448	S	SSLVDPTLPLTRRASQSSLESSSGPPCIRS	108700.7	577385.9		1091474.6	914079.2	1048769.9	0.34	0.037
Rab3c	25.9	227	211	S	SESLETDPAITAAKQSTRLKETPPPPQPNCG		24271.8	19814.8	65913.4		66408.7	0.33	0.0026
Syn1	74.1	706	438	S	QRDASPRGRGSHSQSSSPGALTGRQTSQPPA	2015020.8	467526.5	581879.6	4020810.1	3543062.8	2262549.7	0.31	0.036
Itpr2	307.5	2701	937	S	HGVGEMMTQMVLRSRGSIFPVSPDAQPIVHP	90452.7	16823.3	55776.5	158208.7	160769.6	205764.7	0.31	0.010
C2cd5	111.7	1016	659	S	PIPEPRQRSRLRSQSESSDEVTELDLSHGK	30863.7	24627.5			100404.2	91267.1	0.29	0.0065
Tmem63b	94.8	832	114	S	HGDSDHRYERLTSVSSSVDFDQRDNGFCSWL	26126.8	41402.8	20591.9	97248.2		119992.8	0.27	0.0065
Ptds1	55.6	473	442	S	EISWHHGKSGKSEDSPPKHSHHSHSSRR	32593.9	36182.0			139714.1	115076.7	0.27	0.017
Ncam1	119.4	1115	788	T	ESKEPIVEVTEERTPNHDGGKHTEPNETT	1445268.8	216252.4		3617220.8	3428369.0	2512572.3	0.26	0.034
Pclo	550.8	5068	1563	S	RKSSTSFDDDAGRHRSHWHDEDETFDESP	166528.7	168688.3	32631.9	443573.4	778470.8	332320.1	0.24	0.049
Dbn1	77.3	706	387	S	SHRRMAPTPIPTRSPSDSSTASTPIAEQIER		360926.6	378977.9	1524847.9	1704395.8		0.23	0.0052
Rims1	163.2	1463	1110	S	IHKDQYRSCDNASAKSSDSVSDVSAISRAS		54826.8	38622.0	232432.4	186766.9		0.22	0.021
Fip1l1	65.0	581	479	S	RERERTRERERERDHSPTPSVFNSSDEERYR	40743.9	52801.9	45797.7	273709.1	253559.0	170346.1	0.20	0.0043
Clec2l	23.7	211	29	S	PPPAARPAAPRPRSPAEAEARGPEGLLRR	42608.6	138683.7		378231.7	411084.1	584103.7	0.20	0.027
Cdkn2aip	59.7	563	169	S	KSAKTRDSAAQRQENSSPSRGSSTKSESGGTS		63750.0	13676.0	176135.5	168537.9	242636.3	0.20	0.022

Dlg2	94.9	852	574	S	GLSFKYGDILHVINASDDEWWQARRVTLGDG		4139.4	2644.1	15236.4		19462.1	0.20	0.025
Slc9a3r1	38.6	355	294	S	ALARSASDSTSEELNSQDSPKRQVSTEPST	29261.2	83065.7		337790.7	423822.5	368366.2	0.15	0.0035
Slc4a4	121.5	1079	68	S	EKKEKERISENYSKSDVENADESSSILKP	85626.4	57308.6			1196166.8	1452625.5	0.05	0.010

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