

SUPPLEMENTAL MATERIAL 1. Differences between PS1PS2KO and CNT mice regardless of age or brain region (>50%, p<0.05)

Probe Set	Gene Title	Symbol	Unigene	NCBI ID	allWT	allKO	ALR all	ALR HC	ALR FC	pVal ALL	PrPval HC	PrPval FC
1417851_at	chemokine (C-X-C motif) ligand 13	Cxcl13	Mm.10116.1	AF030636	5.13	7.43	2.31	2.02	2.59	0.00452	0.13134	0.02250
1419202_at	cystatin F (leukocystatin)	Cstf	Mm.12965.1	NM_009977	4.75	6.72	1.97	1.41	2.53	0.00143	0.08791	0.00992
1417266_at	chemokine (C-C motif) ligand 6	Ccl6	Mm.137.1	BC002073	5.26	6.84	1.58	1.23	1.92	0.00025	0.04007	0.00373
1446181_at	expressed sequence C85699	C85699	Mm.172989.1	BG067253	4.13	5.62	1.49	1.96	1.01	0.01975	0.13849	0.06535
1420699_at	C-type lectin domain family 7, member a	Clec7a	Mm.132943.1	NM_020008	5.08	6.56	1.47	1.20	1.75	0.00100	0.06092	0.01402
1426509_s_at	glial fibrillary acidic protein	Gfap	Mm.1239.1	BB183081	8.93	10.36	1.43	1.13	1.73	0.00124	0.04247	0.02356
1418021_at	complement component 4B	C4b	Mm.16106.1	NM_009780	8.13	9.47	1.34	1.07	1.61	0.00507	0.11087	0.03941
1450792_at	TYRO protein tyrosine kinase binding protein	Tyrbp	Mm.46301.1	NM_011662	7.77	9.11	1.34	1.13	1.56	0.00088	0.06521	0.01056
1426508_at	glial fibrillary acidic protein	Gfap	Mm.1239.1	BB183081	9.28	10.60	1.32	0.98	1.67	0.00260	0.05941	0.03135
1448859_at	chemokine (C-X-C motif) ligand 13	Cxcl13	Mm.10116.1	AF030636	6.10	7.41	1.32	1.07	1.56	0.00426	0.13192	0.02315
1436996_x_at	lysozyme	Lyz	Mm.45436.2	AV066625	6.72	7.88	1.16	0.79	1.54	0.00803	0.15150	0.03980
1423547_at	lysozyme	Lyzs	Mm.45436.1	AW208566	7.05	8.16	1.11	0.71	1.51	0.00851	0.12182	0.04666
1417381_at	complement component 1, q subcomponent, alpha	C1qa	Mm.370.1	NM_007572	8.73	9.84	1.11	0.94	1.28	0.00180	0.09314	0.01369
1439426_x_at	lysozyme	Lyz	Mm.45436.3	AV058500	4.69	5.75	1.06	0.74	1.37	0.00311	0.07813	0.02788
1449164_at	CD68 antigen	Cd68	Mm.15819.1	BC021637	6.28	7.31	1.03	0.85	1.22	0.00342	0.09923	0.02970
1419128_at	integrin alpha X	Itgax	Mm.22378.1	NM_021334	5.02	6.02	1.00	0.57	1.43	0.00244	0.12644	0.00716
1460218_at	CD52 antigen	Cd52	Mm.24130.1	NM_013706	5.62	6.61	0.99	0.81	1.16	0.00108	0.07929	0.00912
1417063_at	complement component 1, q subcomponent, beta	C1qb	Mm.2570.1	NM_009777	8.45	9.41	0.97	0.84	1.10	0.00297	0.10032	0.02402
1437726_x_at	complement component 1, q subcomponent, beta	C1qb	Mm.2570.3	BB111335	5.79	6.75	0.96	0.94	0.98	0.00025	0.02432	0.01219
1452968_at	collagen triple helix repeat containing 1	Cthrc1	Mm.41556.1	AK003674	5.37	6.33	0.96	1.00	0.92	0.00030	0.02034	0.04006
1425519_a_at	CD74 antigen (invariant polypeptide of MHC class II)	Cd74	Mm.7043.1	BC003476	6.49	7.44	0.95	0.69	1.21	0.00850	0.16952	0.03817
1421792_s_at	triggering receptor expressed on myeloid cells 2	Trem2	Mm.195828.1	NM_031254	6.61	7.54	0.93	0.66	1.20	0.00288	0.12005	0.01573
1427076_at	macrophage expressed gene 1	Mpeg1	Mm.3999.1	L20315	7.17	8.10	0.93	0.85	1.01	0.00038	0.03121	0.01347
1449401_at	complement component 1, q subcomponent, C	C1qc	Mm.3453.1	NM_007574	8.45	9.38	0.93	0.79	1.07	0.00185	0.07523	0.02206
1449911_at	lymphocyte-activation gene 3	Lag3	Mm.4528.1	NM_008479	5.71	6.62	0.91	0.59	1.24	0.00267	0.12388	0.01152
1433935_at	expressed sequence AU020206	AU020206	Mm.200422.1	B1151331	5.24	6.14	0.90	0.74	1.05	0.00219	0.06900	0.02895
1429846_at	RIKEN cDNA 9030411K21 gene	9030411K21R	Mm.100469.1	BM250766	4.19	5.08	0.89	1.03	0.76	0.00464	0.02851	0.15935
1422903_at	lymphocyte antigen 86	Ly86	Mm.2639.1	NM_010745	7.44	8.31	0.87	0.60	1.13	0.00215	0.09559	0.01465
1417868_a_at	cathepsin Z	Ctsz	Mm.156919.1	NM_022325	7.44	8.30	0.86	0.81	0.90	0.00256	0.08309	0.02592
1440807_at	Membrane associated guanylate kinase 2	Magi2	Mm.132480.1	BB337886	4.17	5.03	0.86	1.05	0.66	0.03780	0.02008	0.40748
1451780_at	B-cell linker	Blink	Mm.9749.1	AF068182	6.66	7.50	0.85	0.81	0.89	0.00379	0.08357	0.04229
1419483_at	complement component 3a receptor 1	C3ar1	Mm.2408.1	NM_009779	5.32	6.14	0.82	0.66	0.98	0.00251	0.05516	0.03805
1417870_x_at	cathepsin Z	Ctsz	Mm.156919.1	NM_022325	7.84	8.65	0.81	0.70	0.92	0.00369	0.11343	0.02486
1434819_at	beta galactoside alpha 2,6 sialyltransferase 2	St6gal2	Mm.83662.1	BB709312	6.17	6.98	0.81	1.17	0.45	0.03765	0.15352	0.06530
1457797_at	expressed sequence AI605517	AI605517	Mm.37805.1	AV340788	6.70	7.51	0.81	0.79	0.82	0.04990	0.24921	0.24132
1445111_at	---	AW548720	Mm.215518.1	AW548720	4.69	5.49	0.80	0.92	0.68	0.01468	0.12396	0.15998
1427351_s_at	immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6	Mm.218842.1	BB226392	7.32	8.12	0.80	0.85	0.74	0.01885	0.14780	0.10140
1435290_x_at	histocompatibility 2, class II antigen A, alpha	H2-Aa	Mm.175310.2	BE688749	5.98	6.75	0.78	0.54	1.01	0.02613	0.33849	0.03616
1430096_at	RIKEN cDNA 2900017F05 gene	2900017F05R	Mm.17681.1	AK013544	5.28	6.05	0.78	1.23	0.32	0.03778	0.06260	0.34964
1416066_at	CD9 antigen	Cd9	Mm.2956.1	NM_007657	8.45	9.22	0.77	0.67	0.87	0.00160	0.06631	0.02275
1438200_at	sulfatase 1	Sulf1	Mm.45563.1	BB065799	6.33	7.08	0.75	1.24	0.26	0.02865	0.01863	0.28295
1416382_at	cathepsin C	Ctsc	Mm.684.1	NM_009982	6.44	7.17	0.73	0.56	0.90	0.00157	0.05315	0.02338
1442241_at	Serine/arginine-rich protein specific kinase 2	Srpk2	Mm.82655.1	BE979921	6.19	6.90	0.71	0.82	0.61	0.01075	0.11007	0.13599
1436905_x_at	lysosomal-associated protein transmembrane 5	Laptm5	Mm.4554.2	BB218107	5.76	6.48	0.71	0.69	0.73	0.00014	0.01123	0.01530
1428114_at	solute carrier family 14 (urea transporter), member 1	Slc14a1	Mm.33832.1	AW556396	6.06	6.76	0.71	0.44	0.98	0.00222	0.08049	0.01390
1422124_a_at	protein tyrosine phosphatase, receptor type, C	Ptprc	Mm.143846.1	NM_011210	4.94	5.65	0.71	0.61	0.81	0.00493	0.04972	0.07405
1448591_at	cathepsin S	Ctss	Mm.3619.1	NM_021281	9.00	9.70	0.70	0.50	0.90	0.00214	0.12149	0.00945
1454268_a_at	cytochrome b-245, alpha polypeptide	Cyba	Mm.448.2	AK018713	6.32	7.02	0.70	0.43	0.96	0.00208	0.06983	0.01453
1417869_s_at	cathepsin Z	Ctsz	Mm.156919.1	NM_022325	5.76	6.46	0.70	0.64	0.76	0.00157	0.04719	0.03422

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1453620_at	cortactin binding protein 2	Cttnbp2	Mm.133159.1	AW488544	7.67	8.36	0.69	0.81	0.57	0.02683	0.14380	0.23360
1416714_at	interferon regulatory factor 8	Irf8	Mm.3182.1	BG069095	5.45	6.14	0.69	0.44	0.94	0.00365	0.10040	0.02244
1434366_x_at	complement component 1, q subcomponent, beta	C1qb	Mm.2570.2	AW227993	6.71	7.40	0.69	0.60	0.78	0.00113	0.03548	0.03044
1429135_at	RIKEN cDNA 1110059M19 gene	1110059M19R	Mm.23496.1	AV015858	5.41	6.09	0.69	1.03	0.34	0.02029	0.03778	0.25963
1436107_at	LSM8 homolog, U6 small nuclear RNA associated	Lsm8	Mm.133137.1	AV167707	5.03	5.71	0.68	0.79	0.57	0.04282	0.21509	0.23001
1420697_at	solute carrier family 15, member 3	Slc15a3	Mm.218870.1	NM_023044	4.39	5.07	0.68	0.49	0.87	0.00648	0.04774	0.06500
1446772_at	---	BB453864	Mm.215970.1	BB453864	4.12	4.79	0.67	0.87	0.47	0.00352	0.01143	0.12967
1437874_s_at	hexosaminidase B	Hexb	Mm.219675.2	AV225808	8.62	9.29	0.67	0.58	0.75	0.00171	0.07442	0.02038
1426808_at	lectin, galactose binding, soluble 3	Lgals3	Mm.2970.1	X16834	4.99	5.65	0.66	0.48	0.83	0.00605	0.00033	0.08579
1419004_s_at	B-cell leukemia/lymphoma 2 related protein A1	Bcl2a1	Mm.196731.1	L16462	5.69	6.34	0.65	0.45	0.86	0.00561	0.08845	0.04303
1419132_at	toll-like receptor 2	Tlr2	Mm.87596.1	NM_011905	5.11	5.76	0.65	0.42	0.89	0.00867	0.11926	0.04823
1418340_at	Fc receptor, IgE, high affinity I, gamma polypeptide	Fcer1g	Mm.22673.1	NM_010185	6.88	7.52	0.65	0.47	0.82	0.00215	0.07978	0.02018
1448118_a_at	cathepsin D	Ctsd	Mm.2147.1	NM_009883	10.56	11.20	0.64	0.60	0.69	0.00147	0.05952	0.02417
1427329_a_at	immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6	Mm.28362.2	A1326478	5.94	6.58	0.64	0.65	0.62	0.01051	0.12194	0.07176
1440637_at	Intersectin 1 (SH3 domain protein 1A)	Itns1	Mm.103075.1	BG074656	6.12	6.76	0.63	0.75	0.52	0.01805	0.11570	0.20112
1450678_at	integrin beta 2	Itgb2	Mm.1137.1	NM_008404	5.90	6.53	0.63	0.44	0.82	0.00512	0.13998	0.02652
1456440_s_at	ST8 a-N-acetyl-neuraminide alpha-2,8-sialyltransf 6	St8sia6	Mm.24267.2	AV375081	5.33	5.96	0.63	0.72	0.53	0.02041	0.00816	0.31737
1456655_at	16 days neonate cerebellum cDNA	BM231698	Mm.69077.1	BM231698	6.96	7.57	0.62	0.68	0.56	0.01113	0.06220	0.20169
1448748_at	pleckstrin	Plek	Mm.98232.1	AF181829	6.29	6.90	0.61	0.54	0.69	0.00499	0.08747	0.05320
1418365_at	cathepsin H	Ctsh	Mm.2277.1	NM_007801	6.45	7.06	0.61	0.52	0.71	0.00174	0.02609	0.04492
1417268_at	CD14 antigen	Cd14	Mm.3460.1	NM_009841	5.83	6.43	0.61	0.40	0.81	0.00008	0.01818	0.00027
1419482_at	complement component 3a receptor 1	C3ar1	Mm.2408.1	NM_009779	5.31	5.91	0.60	0.28	0.91	0.02177	0.34027	0.03940
1418989_at	cathepsin E	Ctse	Mm.33671.1	NM_007799	4.96	5.55	0.59	0.30	0.89	0.04693	0.37190	0.09581
1450249_s_at	kinesin family member 5	Kif5	Mm.30355.1	NM_008447	9.84	9.26	-0.59	-0.74	-0.43	0.00679	0.07550	0.02867
1430144_at	RIKEN cDNA 5830411G16 gene	5830411G16R	Mm.105343.1	BB815600	5.84	5.25	-0.59	-0.73	-0.45	0.00053	0.01204	0.00490
1445061_at	Protocadherin 9	Pcdh9	Mm.155985.1	BM941356	5.38	4.78	-0.59	-0.74	-0.45	0.00315	0.02633	0.10991
1445631_at	---	BE865226	Mm.156043.1	BE865226	7.89	7.29	-0.60	-0.99	-0.22	0.02380	0.01433	0.20587
1445081_at	RIKEN cDNA A930041I02 gene	A930041I02R	Mm.204836.1	BB335888	4.92	4.31	-0.61	-0.82	-0.40	0.04799	0.09968	0.41230
1428484_at	oxysterol binding protein-like 3	Osbp13	Mm.31024.1	AK004768	7.69	7.08	-0.61	-0.75	-0.47	0.02787	0.11734	0.27315
1430597_at	janus kinase and microtubule interacting protein 1	Jakmp1	Mm.159667.1	BB206614	6.40	5.78	-0.61	-0.77	-0.45	0.01141	0.07705	0.16765
1457142_at	EF hand calcium binding protein 1	Efcbb1	Mm.131089.1	BB667731	6.88	6.26	-0.61	-0.99	-0.23	0.01915	0.01058	0.11194
1440318_at	WD repeat domain 35	Wdr35	Mm.131476.1	BB475816	6.73	6.12	-0.62	-0.96	-0.27	0.02358	0.04541	0.20028
1458314_at	Solute carrier family 1 (glial-glutamate transporter), 2	Slc1a2	Mm.101872.1	AW491006	5.17	4.55	-0.62	-0.31	-0.93	0.02922	0.20100	0.08620
1443597_at	cofactor required for Sp1 transcriptional activation 2	Crsp2	Mm.187323.1	BB463128	5.88	5.27	-0.62	-0.94	-0.30	0.01610	0.01351	0.25133
1447513_at	potassium voltage-gated channel, Shal, member 3	Kcnd3	Mm.54226.1	BE957136	5.42	4.80	-0.62	-0.98	-0.26	0.02069	0.02902	0.17797
1459826_at	Potassium voltage-gated channel, subfamily Q, 2	Kcng2	Mm.131914.1	BB264132	6.53	5.91	-0.62	-1.00	-0.24	0.02561	0.03962	0.11719
1457756_at	zinc finger protein 192	Zfp192	Mm.151515.1	BB483373	5.15	4.53	-0.62	-0.70	-0.54	0.00573	0.11085	0.05755
1429517_at	zinc finger, FYVE domain containing 20	Zfyve20	Mm.26129.1	BC017622	5.66	5.04	-0.63	-0.87	-0.38	0.00844	0.00014	0.23081
1431371_at	RIKEN cDNA 9030411M13 gene	9030411M13R	Mm.97440.1	BQ228391	5.19	4.56	-0.63	-0.75	-0.51	0.00613	0.08545	0.08782
1431196_at	ATPase, Ca++-sequestering	Atp2c1	Mm.153302.1	BG296252	7.44	6.80	-0.64	-1.11	-0.18	0.03415	0.01496	0.20644
1452418_at	RIKEN cDNA 1200016E24 gene	1200016E24R	Mm.171545.1	BF719154	8.44	7.79	-0.65	-0.70	-0.59	0.00925	0.07114	0.11799
1455960_at	multiple EGF-like-domains 9	Megf9	Mm.28686.3	BB483642	7.16	6.51	-0.66	-1.06	-0.26	0.02330	0.03328	0.10127
1417432_a_at	guanine nucleotide binding protein, beta 1	Gnb1	Mm.2344.1	NM_008142	9.30	8.64	-0.66	-0.63	-0.69	0.00689	0.09981	0.06402
1445473_at	DIRAS family, GTP-binding RAS-like 2	Diras2	Mm.123719.1	BB229114	8.68	8.01	-0.67	-0.91	-0.43	0.01493	0.04776	0.24360
1459317_at	ankyrin 2, brain	Ank2	Mm.208496.1	BB280924	6.36	5.68	-0.68	-0.81	-0.54	0.00157	0.03391	0.05471
1435770_at	thioredoxin domain containing 13	Txndc13	Mm.44400.1	BB215068	8.05	7.37	-0.68	-1.14	-0.22	0.03786	0.04575	0.26496
1444139_at	DNA-damage-inducible transcript 4-like	Ddit4l	Mm.205420.1	BG797099	7.15	6.47	-0.68	-0.60	-0.76	0.00392	0.03772	0.10333
1418610_at	solute carrier family 17, member 6	Slc17a6	Mm.70945.1	NM_080853	6.52	5.84	-0.68	-0.78	-0.59	0.00014	0.01017	0.01269
1447222_at	heat shock protein 12A	Hspa12a	Mm.86619.1	A1854582	7.00	6.31	-0.68	-1.11	-0.25	0.01935	0.01092	0.05581
1456827_at	expressed sequence AA987161	AA987161	Mm.138283.1	BB131790	5.13	4.45	-0.68	-0.95	-0.42	0.00508	0.02914	0.04150
1437257_at	WD repeat domain 47	Wdr47	Mm.125895.1	BB344753	7.67	6.97	-0.70	-1.15	-0.24	0.04503	0.08890	0.05026
1444141_at	sorting nexin 13	Snx13	Mm.213991.1	BB828008	5.53	4.83	-0.71	-1.11	-0.30	0.04571	0.11210	0.21738

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1439517_at	myb-like, SWIRM and MPN domains 1	Mysm1	Mm.202463.1	BB660695	6.16	5.42	-0.74	-1.05	-0.43	0.00762	0.03639	0.04338
1454696_at	guanine nucleotide binding protein, beta 1	Gnb1	Mm.200776.1	BG071068	11.05	10.31	-0.75	-0.52	-0.97	0.00583	0.06708	0.05214
1453787_at	thioredoxin domain containing 13	Txndc13	Mm.156901.1	AK015667	8.39	7.61	-0.78	-1.27	-0.28	0.02433	0.02602	0.07444
1431254_at	kelch repeat and BTB (POZ) domain containing 11	Kbtbd11	Mm.153428.1	BG807055	6.93	6.15	-0.78	-0.97	-0.59	0.01026	0.07136	0.16856
1446652_at	RALBP1 associated protein 2	Reps2	Mm.151793.1	BB547008	6.67	5.88	-0.79	-1.08	-0.50	0.00899	0.07116	0.02248
1444298_at	RIKEN cDNA A130090K04 gene	A130090K04R	Mm.122667.1	BB703415	6.60	5.81	-0.79	-1.06	-0.52	0.01443	0.07289	0.18248
1459430_at	G protein-coupled receptor 158	Gpr158	Mm.209128.1	BB429778	7.42	6.62	-0.81	-1.10	-0.51	0.00407	0.00783	0.10519
1444001_at	RIKEN cDNA C230082I21R gene	C230082I21R	Mm.39545.1	AW488249	8.99	8.05	-0.94	-1.48	-0.40	0.02240	0.04672	0.06925
1432646_a_at	predicted gene, EG667653	EG667653	Mm.15985.3	BE859789	8.89	7.91	-0.97	-1.48	-0.47	0.01130	0.05039	0.00798
1431214_at	hypothetical gene LOC433762	LOC433762	Mm.157900.1	BG297038	8.49	7.46	-1.03	-1.13	-0.93	0.00466	0.07314	0.05397
1456911_at	CLIP associating protein 2	Clasp2	Mm.214961.1	BB831639	7.42	6.30	-1.13	-1.25	-1.00	0.03548	0.15935	0.26848
1431213_a_at	hypothetical gene LOC433762	LOC433762	Mm.157900.1	BG297038	9.44	8.27	-1.17	-1.38	-0.96	0.00474	0.06365	0.05443