Dataset 3. Common transcripts significantly altered in P301S mice relative to WT mice

		P301S vs WT		P301S;*Ssh1-/-* vs P301S	
Gene name	**Gene description**	**Log2(FC)**	**p value**	**Log2(FC)**	**p value**
Ovol3	ovo like zinc finger 3 [Source:MGI Symbol;	4.683668	0.001387	-4.6556148	0.005185207
Gm6750	predicted gene 6750 [Source:MGI Symbol;	4.238597	9.73E-05	-1.0049742	0.0141161
Gm12089	predicted gene 12089 [Source:MGI Symbo	4.149957	0.013183	-3.8136282	0.035907032
4930512J16Rik	RIKEN cDNA 4930512J16 gene [Source:M	4.127679	0.022154	-4.0874273	0.031292633
Gm15976	predicted gene 15976 [Source:MGI Symbo	4.037428	0.000394	-2.8465385	0.025141482
Gm21057	predicted gene, 21057 [Source:MGI Symbc	3.837739	0.002977	-2.3821103	0.021021391
Gm17040	predicted gene 17040 [Source:MGI Symbo	3.787428	0.003857	-3.7593742	0.011969306
Fcrla	Fc receptor-like A [Source:MGI Symbol;Acc	3.585198	0.019178	-4.4056148	0.023828243
Gm10723	predicted gene 10723 [Source:MGI Symbo	3.537428	0.002434	-3.5093742	0.008453828
Gm13039	predicted gene 13039 [Source:MGI Symbo	3.537428	0.003667	-3.5093742	0.011827571
Igfals	insulin-like growth factor binding protein, ac	3.488597	0.017535	-4.5518554	0.001050019
Mir6929	microRNA 6929 [Source:MGI Symbol;Acc:I	3.385233	0.01068	-2.9927791	0.043306031
AC154486.1	ribosomal protein L7A (Rpl7a) pseudogene	3.335198	0.011332	-4.1556148	0.009162413
Vwde	von Willebrand factor D and EGF domains	3.335198	0.011332	-4.1556148	0.009162413
Gm20149	predicted gene, 20149 [Source:MGI Symbc	3.281474	0.037525	-3.1390197	0.034253606
Rpl10a-ps2	ribosomal protein L10A, pseudogene 2 [So	3.231438	0.03552	-4.0518554	0.035753138
C8b	complement component 8, beta polypeptid	2.786762	0.018869	-3.4927791	0.012324461
Gm43612	predicted gene 43612 [Source:MGI Symbo	2.784036	0.004786	-1.8281471	0.017130564
A930041C12Rik	RIKEN cDNA A930041C12 gene [Source:N	2.696116	0.045513	-3.5093742	0.016564384
Gm47062	predicted gene, 47062 [Source:MGI Symbc	2.691498	0.047039	1.26081535	0.009521946
Gm42488	predicted gene 42488 [Source:MGI Symbo	2.690833	0.015065	-2.6666968	0.048836863
Gm15801	predicted gene 15801 [Source:MGI Symbo	2.640522	0.001579	-2.0419954	0.005032777
Kcnmb4os1	potassium large conductance calcium-activ	2.539304	0.025356	-3.294946	0.005560425
Stx19	syntaxin 19 [Source:MGI Symbol;Acc:MGI:	2.489268	0.047833	-3.294946	0.008173507
Gm15614	predicted gene 15614 [Source:MGI Symbo	2.140522	0.04762	-3.7593742	0.007449763
4930527J03Rik	RIKEN cDNA 4930527J03 gene [Source:M	1.84952	9.78E-05	-1.2470794	0.030634494
Gm15690	predicted gene 15690 [Source:MGI Symbo	1.760484	0.001517	-1.4080435	0.042162481
Fabp4	fatty acid binding protein 4, adipocyte [Sour	1.647956	0.047395	-3.2989048	0.004188998
Gm8860	predicted gene 8860 [Source:MGI Symbol;	1.528082	0.047986	-3.5646304	0.026113021
Gm40603	predicted gene, 40603 [Source:MGI Symbc	1.444726	0.004766	-3.76203	0.019769773
Gm29156	predicted gene 29156 [Source:MGI Symbo	1.299514	0.007099	-1.1643554	0.007435106
Gm7367	predicted pseudogene 7367 [Source:MGI S	1.260484	0.000245	-1.853031	0.001028783
Ltb4r1	leukotriene B4 receptor 1 [Source:MGI Syn	1.245761	0.047572	-1.8354563	0.02946965
Gm33366	predicted gene, 33366 [Source:MGI Symbc	1.20776	0.014797	-1.328492	0.024370852
Rad21l	RAD21-like (S. pombe) [Source:MGI Symb	1.200766	0.047127	-0.9911016	0.048910196
Cd300e	CD300E molecule [Source:MGI Symbol;Ac	1.057039	0.005243	-2.9898284	0.000106694
9530059O14Rik	RIKEN cDNA 9530059O14 gene [Source:N	1.04617	0.004183	-0.7932012	0.019648432
Gm10167	predicted pseudogene 10167 [Source:MGI	1.008094	0.020019	-0.8429042	0.042667612
Cnga2	cyclic nucleotide gated channel alpha 2 [Sc	0.901494	0.042571	-2.66087	0.034111423
Iqgap3	IQ motif containing GTPase activating prot	0.740254	0.04434	0.83969211	0.044107317
Gm42047	predicted gene, 42047 [Source:MGI Symbc	0.736194	0.032699	-0.8505333	0.017295278
Rpl29	ribosomal protein L29 [Source:MGI Symbol	0.706871	0.041628	-0.828619	0.016889261
Gm14176	predicted gene 14176 [Source:MGI Symbo	0.616299	0.036197	-0.6275913	0.02617353
Gm10250	predicted pseudogene 10250 [Source:MGI	0.542642	0.034175	-0.7005342	0.0468569
1810010H24Rik	RIKEN cDNA 1810010H24 gene [Source:N	0.492291	0.008813	-0.5586193	0.049924998
Dmrtc1a	DMRT-like family C1a [Source:MGI Symbo	0.490646	0.02843	-0.6227733	0.030110868
Mrnip	MRN complex interacting protein [Source:N	0.45343	0.018501	-0.5287196	0.025624472
Gm20735	predicted gene, 20735 [Source:MGI Symbc	0.425444	0.019047	-0.6073278	0.015509364
Gm23935	predicted gene, 23935 [Source:MGI Symbc	0.423261	0.004848	-0.3297819	0.036272467
Lars2	leucyl-tRNA synthetase, mitochondrial [Sou	0.383722	0.018112	-0.3089443	0.027088529

Vgf	VGF nerve growth factor inducible [Source:	0.379565	0.014366	-0.3893928	0.033488905
Mad2l1bp	MAD2L1 binding protein [Source:MGI Syml	0.365967	0.018229	-0.3603763	0.021137648
Fkbpl	FK506 binding protein-like [Source:MGI Sy	0.363148	0.042243	-0.424111	0.006026827
Hdhd3	haloacid dehalogenase-like hydrolase dom	0.35711	0.006615	-0.2348154	0.032208652
Mttp	microsomal triglyceride transfer protein [So	0.339517	0.012595	-0.278117	0.02881365
Fdx1	ferredoxin 1 [Source:MGI Symbol;Acc:MGI	0.312537	0.049365	-0.495483	0.025138244
Lrif1	ligand dependent nuclear receptor interacti	0.310736	0.018425	-0.4202633	0.028300423
Cluap1	clusterin associated protein 1 [Source:MGI	0.298018	0.010213	-0.2450457	0.046527273
Nppc	natriuretic peptide type C [Source:MGI Sym	0.294581	0.037406	-0.6094606	0.008391772
Timm10	translocase of inner mitochondrial membra	0.279155	0.039584	-0.423956	0.043111169
Orc6	origin recognition complex, subunit 6 [Sour	0.278412	0.019092	-0.2903881	0.017517887
Alg5	asparagine-linked glycosylation 5 (dolichyl-	0.254815	0.042822	-0.3494157	0.030577486
Bud31	BUD31 homolog [Source:MGI Symbol;Acc:	0.244768	0.000696	-0.280127	0.0021594
Mettl13	methyltransferase like 13 [Source:MGI Sym	0.236875	0.024261	-0.1828156	0.023872731
Psma4	proteasome (prosome, macropain) subunit	0.232586	0.01233	-0.3518851	0.026252108
Ntmt1	N-terminal Xaa-Pro-Lys N-methyltransferas	0.232065	0.018441	-0.2381795	0.040042235
Rpusd2	RNA pseudouridylate synthase domain con	0.22692	0.024307	-0.279537	0.008903955
Hsf2	heat shock factor 2 [Source:MGI Symbol;A	0.217225	0.040972	-0.1981349	0.025773593
Imp3	IMP3, U3 small nucleolar ribonucleoprotein	0.214698	0.021862	-0.2324785	0.047037171
Gucd1	guanylyl cyclase domain containing 1 [Sour	0.210149	0.013176	-0.2154271	0.001605514
Clp1	CLP1, cleavage and polyadenylation factor	0.208247	0.030468	-0.3853391	0.01888076
Farsa	phenylalanyl-tRNA synthetase, alpha subur	0.205818	0.022955	-0.2040077	0.047715831
Ube2f	ubiquitin-conjugating enzyme E2F (putative	0.20309	0.010943	-0.195776	0.029229091
Nt5c3	5'-nucleotidase, cytosolic III [Source:MGI S	0.196685	0.036537	-0.3582722	0.013284684
Rnps1	ribonucleic acid binding protein S1 [Source	0.183429	0.002725	-0.152014	0.021125419
Cstf1	cleavage stimulation factor, 3' pre-RNA, su	0.172386	0.011139	-0.1678077	0.004599089
Rheb	Ras homolog enriched in brain [Source:MG	0.172152	0.004846	-0.2776453	0.044094188
Unc50	unc-50 homolog [Source:MGI Symbol;Acc:	0.171671	0.038143	-0.2970858	0.045483868
4930453N24Rik	RIKEN cDNA 4930453N24 gene [Source:M	0.168431	0.049047	-0.321802	0.04096068
Ip6k2	inositol hexaphosphate kinase 2 [Source:M	0.153049	0.036602	-0.2586188	0.030061394
Reep6	receptor accessory protein 6 [Source:MGI	0.152555	0.025334	0.12007067	0.023313132
Rab24	RAB24, member RAS oncogene family [So	0.148298	0.000249	-0.1485293	0.009568983
Smarcb1	SWI/SNF related, matrix associated, actin	0.133293	0.027238	-0.1824141	0.001066882
Atp5d	ATP synthase, H+ transporting, mitochond	0.120196	0.039129	-0.1945205	0.022410354
Tkfc	triokinase, FMN cyclase [Source:MGI Sym	0.118669	0.032495	-0.1605788	0.030857951
Kat5	K(lysine) acetyltransferase 5 [Source:MGI	0.117739	0.048202	-0.1767459	0.040154762
Gtf2f1	general transcription factor IIF, polypeptide	0.117595	0.023323	-0.2030841	0.026960994
Zdhhc24	zinc finger, DHHC domain containing 24 [S	0.112662	0.011844	0.09025868	0.037613319
Mepce	methylphosphate capping enzyme [Source:	0.10016	0.030073	-0.1695207	0.010731614
Ing3	inhibitor of growth family, member 3 [Sourc	0.083921	0.04086	-0.0785008	0.036942941
Mrs2	MRS2 magnesium transporter [Source:MG	-0.0683	0.018391	0.08850367	0.022378741
Anapc1	anaphase promoting complex subunit 1 [So	-0.1042	0.03468	0.21080668	0.009668496
Arid4b	AT rich interactive domain 4B (RBP1-like) [	-0.11168	0.020379	0.1717186	0.02810778
Slc25a35	solute carrier family 25, member 35 [Sourc	-0.1274	0.015579	0.51066271	0.000598716
Eif2ak4	eukaryotic translation initiation factor 2 alph	-0.1508	0.020132	0.23366104	0.01356601
Tcf12	transcription factor 12 [Source:MGI Symbol	-0.15313	0.03142	0.17978157	0.047251376
Dtna	dystrobrevin alpha [Source:MGI Symbol;Ac	-0.16892	0.048438	0.25485236	0.011375596
Gid4	GID complex subunit 4, VID24 homolog [So	-0.18476	0.016358	0.27783129	0.017583743
Nipbl	NIPBL cohesin loading factor [Source:MGI	-0.18907	0.046032	0.28191321	0.007051302
Fktn	fukutin [Source:MGI Symbol;Acc:MGI:2179	-0.20719	0.022801	0.24879587	0.040454524
Wdr59	WD repeat domain 59 [Source:MGI Symbo	-0.20957	0.028461	0.16749982	0.033705897
Rab30	RAB30, member RAS oncogene family [So	-0.21277	0.002569	0.16137825	0.002734962
Zfp862-ps	zinc finger protein 862, pseudogene [Sourc	-0.2179	0.009067	0.35514743	0.014947883
Arid2	AT rich interactive domain 2 (ARID, RFX-lik	-0.22189	0.043685	0.28181967	0.036232496

Tbc1d9b	TBC1 domain family, member 9B [Source:M	-0.22296	0.024949	0.32565557	0.023649773
Bcl2	B cell leukemia/lymphoma 2 [Source:MGI S	-0.22466	0.002555	0.18914644	0.019778892
Cep85l	centrosomal protein 85-like [Source:MGI Sy	-0.23184	0.031003	0.2671589	0.023657183
Bicd2	BICD cargo adaptor 2 [Source:MGI Symbo	-0.23497	0.028851	0.2701729	0.029381921
Zfp800	zinc finger protein 800 [Source:MGI Symbo	-0.23951	0.035353	0.16811682	0.047963939
Lamc1	laminin, gamma 1 [Source:MGI Symbol;Acc	-0.24574	0.02704	0.29003121	0.030779796
AI464131	expressed sequence AI464131 [Source:MG	-0.24786	0.033096	0.19350714	0.016846024
Marf1	meiosis regulator and mRNA stability 1 [So	-0.25223	0.007537	0.2152207	0.030721012
Rbm41	RNA binding motif protein 41 [Source:MGI	-0.25577	0.04346	0.64861159	0.004426074
Epb41l1	erythrocyte membrane protein band 4.1 like	-0.25852	0.027322	0.3748448	0.006510943
Cpd	carboxypeptidase D [Source:MGI Symbol;A	-0.26509	0.020195	0.27069309	0.036895074
Gabpa	GA repeat binding protein, alpha [Source:M	-0.27069	0.005604	0.16391043	0.025205397
Tjp1	tight junction protein 1 [Source:MGI Symbo	-0.27823	0.026662	0.37702893	0.02339366
Zfp462	zinc finger protein 462 [Source:MGI Symbo	-0.28253	0.014307	0.20218598	0.013601029
Pag1	phosphoprotein associated with glycosphin	-0.28583	0.03579	0.2676123	0.011657104
Sptb	spectrin beta, erythrocytic [Source:MGI Sym	-0.30063	0.03618	0.49999174	0.008293645
Abcc4	ATP-binding cassette, sub-family C (CFTR	-0.30414	0.033599	0.59478658	0.003412594
Utrn	utrophin [Source:MGI Symbol;Acc:MGI:104	-0.30913	0.041956	0.36364163	0.016216248
Nwd1	NACHT and WD repeat domain containing	-0.31779	0.041572	0.52781871	0.044272686
Pogk	pogo transposable element with KRAB dom	-0.32647	0.014939	0.30128431	0.015349385
Nr6a1	nuclear receptor subfamily 6, group A, men	-0.33445	0.004746	0.29364024	0.012936818
S1pr3	sphingosine-1-phosphate receptor 3 [Sourc	-0.36406	0.040742	0.40333058	0.049554323
Clic5	chloride intracellular channel 5 [Source:MG	-0.36635	0.017426	0.39443218	0.006580328
Gpr157	G protein-coupled receptor 157 [Source:MG	-0.37018	0.016792	0.3339413	0.005319876
Slc7a2	solute carrier family 7 (cationic amino acid	-0.39789	0.01246	0.4899681	0.034828873
Flt1	FMS-like tyrosine kinase 1 [Source:MGI Sy	-0.40878	0.046694	0.51287398	0.025239051
Gm6483	predicted gene 6483 [Source:MGI Symbol;A	-0.4303	0.002854	0.44415727	0.001266379
Gm15631	predicted gene 15631 [Source:MGI Symbo	-0.46049	0.007976	0.43210641	0.008259854
Lonrf3	LON peptidase N-terminal domain and ring	-0.50454	0.014875	0.70847261	0.008185687
Parp4	poly (ADP-ribose) polymerase family, mem	-0.5049	0.03495	0.58005329	0.026120095
C230034O21Rik	RIKEN cDNA C230034O21 gene [Source:M	-0.51794	0.021696	0.63704826	0.023778917
Klf12	Kruppel-like factor 12 [Source:MGI Symbol	-0.52258	0.030167	0.5061875	0.048439554
Gm27202	predicted gene 27202 [Source:MGI Symbo	-0.54651	0.027996	0.51024095	0.023901766
Gm9803	predicted gene 9803 [Source:MGI Symbol;A	-0.6256	0.001933	-1.3904688	0.008390767
Gm15672	predicted gene 15672 [Source:MGI Symbo	-0.67546	0.047803	1.05387799	0.045408471
Uprt	uracil phosphoribosyltransferase [Source:M	-0.69657	0.006623	0.70513808	0.028558348
Gm26894	predicted gene, 26894 [Source:MGI Symbo	-0.71898	0.034117	1.06115058	0.019093785
Gm9299	predicted gene 9299 [Source:MGI Symbol;A	-0.72528	0.001049	0.86022992	0.009222598
Ptar1	protein prenyltransferase alpha subunit rep	-0.77228	0.034365	0.77206199	0.017775253
Gm37824	predicted gene, 37824 [Source:MGI Symbo	-0.79037	0.038707	0.97049937	0.045067574
Gm10069	predicted gene 10069 [Source:MGI Symbo	-0.81054	0.015149	0.92444747	0.029276169
Pde11a	phosphodiesterase 11A [Source:MGI Symb	-0.93305	0.036169	0.9060893	0.002255583
Txlnb	taxilin beta [Source:MGI Symbol;Acc:MGI:2	-1.01227	0.005108	1.19330146	0.000428317
Eps8l1	EPS8-like 1 [Source:MGI Symbol;Acc:MGI:	-1.0221	0.015437	1.11729268	0.029431965
4930412L05Rik	RIKEN cDNA 4930412L05 gene [Source:M	-1.13008	0.012216	1.08003835	0.032597656
Alas2	aminolevulinic acid synthase 2, erythroid [S	-1.13303	0.042519	1.28988404	0.044368717
Fgf23	fibroblast growth factor 23 [Source:MGI Sym	-1.40429	0.021688	1.62929814	0.003813172
Cd27	CD27 antigen [Source:MGI Symbol;Acc:MG	-1.41968	0.027696	1.64481638	0.01680066
Gm17202	predicted gene 17202 [Source:MGI Symbo	-1.92821	0.024734	1.95160419	0.003375112
Gm13841	predicted gene 13841 [Source:MGI Symbo	-1.9492	0.044117	2.93443235	0.013172178
Gm15696	predicted gene 15696 [Source:MGI Symbo	-2.10415	0.042214	2.28865896	0.029935183
Inhbe	inhibin beta-E [Source:MGI Symbol;Acc:MG	-2.16055	0.038959	2.53124139	0.000119941
Gm47856	predicted gene, 47856 [Source:MGI Symbo	-2.41019	0.001258	2.79747634	0.000916535
Spata46	spermatogenesis associated 46 [Source:M	-2.42492	0.024978	2.30729196	0.028899955

Gm18774	predicted gene, 18774 [Source:MGI Symb	-2.73822	0.043386	4.2418687	0.009481804
Gm7368	predicted gene 7368 [Source:MGI Symbol;	-2.76316	0.020387	3.23189937	0.016926771
Gm8210	predicted pseudogene 8210 [Source:MGI	-3.3292	0.032041	5.23697795	0.000935212
Mir874	microRNA 874 [Source:MGI Symbol;Acc:M	-3.58415	0.005565	4.0468812	0.001251607
Tex13c2	TEX13 family member C2 [Source:MGI Sy	-3.58415	0.00464	3.90853536	0.030726172
Dhx58os	DEAH (Asp-Glu-Ala-His) box polypeptide 5	-3.82868	0.004193	4.41928757	0.005116318
Gm13410	predicted gene 13410 [Source:MGI Symbo	-4.67591	0.034207	4.62765897	0.002271713