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Supplementary Online Material
for

"Knockout of G protein β5 impairs brain development and causes multiple neurologic abnormalities in mice"
by Zhang *et al*

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1. Supplementary Materials and Methods

Mouse genotyping

Mouse genotyping was performed by QPCR analysis of genomic DNA extracted from mouse tails using the DirectPCR (tail) solution (Viagen, Cat# 102-T) according to manufacturer's instructions. The Gβ5 knock-out allele was identified employing the primer pair, Fwd: 5'-GCC ACC AGA AGT CAG CAG AAG AGG-3', and Rev: 5'-GCA GCG CAT CGC CTT CTA TC-3'. The wild type Gβ5 allele was identified employing the same forward primer as above with the reverse primer 5'-GTA ACT TTG AGG TCA CTC ACA GCA T-3'. PCR conditions used were 95°C for 10 min followed by 40 cycles of 95°C 30 sec, 57°C for 1 min and 72°C for 1 min. The specificity of the PCR products was evaluated by one cycle of dissociation curve analysis (95°C for 1 min, 55°C for 30 sec and 95°C for 30 sec).

Mice hemizygous for a transgene expressing Enhanced Green Fluorescent Protein (EGFP) under the direction of the mouse Purkinje cell protein 2 promoter (strain B6; FVB-Tg(Pcp2-EGFP)2Yuza/J; stock no. 004690) were obtained from The Jackson Laboratory (Bar Harbor, ME). The Pcp2-EGFP allele was identified by PCR genotyping employing the primers: Fwd: 5'-AAG TTC ATC TGC ACC ACC G-3', and Rev: 5'-TCC TTG AAG AAG ATG GTG CG-3'.

Motor coordination and activity testing

Testing on the accelerating rotarod (Model No 7650; Ugo Basile, Varese, Italy) was according to the protocol of Le Marec and Lalonde (Le Marec & Lalonde 1997). Briefly, after habituation in the test room for an hour, mice were acclimatized to balance on the rotarod for 10 min. During each session mice were placed on the rotarod accelerating from 4 to 40 rpm over 5 minutes. Time spent by mice on the rotarod was observed until the mice dropped slowly from the rod to the platform. Mice received 3 trials per day for five consecutive days at 20 minute intervals. During trials, some of the mice clung to the rod without moving and were thus passively rotated. The time spent on rotarod, and the time spent in passive rotation were noted. Passive rotation was tabulated only on those trials where the mice used this strategy until the end of the trial. Locomotor activity was measured by the open field test following the protocol of Crawley (Crawley 2007). The mouse was placed in the center of the open field apparatus (2.5 L chambers with wire-mesh floors; Accuscan Instruments Inc. Ohio, USA) and allowed to acclimatize for 10 min, and then data were collected for 60 min. The maze was cleaned with 70% ethanol after each trial. Each mouse was tested once daily for three consecutive days. Data for various motor activities was analyzed using the accompanying Fusion Software (Accuscan Instruments Inc.). After rotarod testing, mice from the same cohort were tested for locomotor activity by the open field test and then again, when 3 months old, for footprint/ gait analysis. The one month-old mice used for footprint/ gait analysis were a separate cohort.

Immunofluorescence methodology

For immunostaining, sections were washed in PBS 3 X 10 minutes each and permeabilized in 0.2% Triton X-100 in PBS for 30 min. Sections were blocked with 8% BSA for 1h and then incubated with primary antibodies goat anti-calbindin-1 (1:250 dilution, Cat No sc-7691, Santa Cruz) or rabbit polyclonal anti-Pcp2 N-terminal antibody (1:200 dilution; Cat No AP6365a, Abgent, San Diego, CA) overnight at 4° C. Sections were washed in PBS containing 1% BSA and incubated with secondary antibodies (Alexa Fluor 594 (Molecular Probes, Invitrogen) anti-goat (1:250 dilution; Cat. No. A11080) or anti-rabbit IgG (1:250 dilution; A21207)) for one hour. After washing sections three times in PBS, mounting medium containing 4’, 6-diamidino-2-phenylindole (DAPI) (Vectashield with DAPI, Vector Labs, Burlingame, CA, USA; Cat. H-1200) was added and the slides were incubated for 5 min to provide nuclear counterstaining. Cover slips were then added and the sections visualized under an inverted epifluorescence microscope (Leica DFC500, Leica Microsystems). For visualizing the GFP fluorescence in Pcp2-GFP hemizygous mice, brain sections were put on slides, mounted and visualized use either epifluorescence or laser confocal microscopy. Cerebellar slices (300 μm) from these mice were obtained using the Microtome VF-300 (Crystalgen Inc.) according to manufacturer's instructions, maintained in serum-free neuron culture medium (Neurobasal A medium containing B27 and N2 supplements, Invitrogen Inc.) and visualized in a stereo fluorescence microscope (Nikon, C-DSD115).

Cresyl violet staining

Mice from different age populations were anesthetized with avertin and transcardially perfused with cold PBS followed by 4% (w/v) paraformaldehyde in PBS. Brains were carefully removed from the calvarium and kept overnight at 4° C in the same fixative. Brains were allowed to settle down in sucrose (30%) at 4° C and then were sectioned sagittally using a freezing cryotome. Ten-micron thick sections were cut serially and collected on silanated slides. Sections were stained with cresyl violet stain, cleared in xylene and mounted using DPX Mountant (Sigma-Aldrich). Sections were observed using an inverted microscope (Leica DM4000 B) and photographed.

Hippocampal histomorphometry

One week and 3 week-old wild-type and *Gnb5* KO littermates were anesthetized, transcardially perfused with 4% paraformaldehyde and kept in sucrose at 4°C until the brains settled down. Comparable, twenty microns thick, free-floating sagittal sections were stained for calbindin-1 immunoreactivity as described above. The thickness (in pixels) of the calbindin-1 immunostain positive granule and molecular layers were measured using the ImageJ software (Rasband, W.S., ImageJ, U. S. National Institutes of

Health, Bethesda, Maryland, USA, http://imagej.nih.gov/ij/, 1997-2011) with the "Measure and Label" plug-in. For each section, 15 or more measurements were taken for each layer at different locations as shown in the corresponding images (see Fig. 5, K, L). The ratio of the thickness of the molecular layer to the granule layer was used in comparisons between *Gnb5* KO and wt mice.

To quantify the number of ectopic dentate gyrus granule cells in the molecular layer, the number of calbindin 1-positive granule cells in the molecular layer, at least one cell body length from the molecular-granule layer interface per section of dentate gyrus were counted.

Laser confocal scanning and intensity analysis

Images were acquired on a Leica TCS-SP5 confocal microscope (Leica Microsystems) using a 40x/NA1.25 oil immersion objective. GFP was excited with an argon laser at 488 nm. A stack of images was acquired using a step size of 0.17 μm. Huygens Essential (version 3.6; Scientific Imaging BV, Hilversum, The Netherlands) and Imaris (version 7.1; Bitplane AG, Zurich, Switzerland) software were used for deconvolution and image processing.

Additional primary and secondary antibodies employed

Primary antibodies employed included anti-Gβ5 N-terminal rabbit polyclonal antibody ATDG (Zhang & Simonds 2000), mouse anti-β-actin monoclonal (A5316; Sigma, St. Louis, MO, USA), goat anti-calbindin-1 (C-20), (sc-7691; Santa Cruz Biotechnology, Santa Cruz, CA, USA), rabbit anti-calbindin-2 (HPA007305; Sigma), rabbit anticerebellin (ab64184, Abcam), goat anti-parvalbumin (C-19) (sc-7449; Santa Cruz), goat anti-tropomodulin 3 (Tmod3) (C-13) (sc-19206; Santa Cruz), goat anti-synaptopodin (Synpo) (P-19) (sc-21537; Santa Cruz), mouse anti-Pcp2 (N-terminal) (AP6356a, Abgent) antibodies, rabbit anti-Trim37 polyclonal (13037-1-AP; Proteintech, Chicago, IL, USA), and rabbit anti-GRID2 polyclonal (ab74866; Abcam). Secondary antibody utilized for immunofluorescence was Cy3-conjugated donkey anti-mouse IgG (715-165-150; Jackson ImmunoResearch Labs, West Grove, PA, USA) and for immunoblots was IR secondary antibody (anti-rabbit IR 800 and anti-mouse Red and Green) from LI-COR Bioscience (Lincoln, NE, USA).

Microarray analysis

Microarray analysis was performed with mRNA isolated from the cerebella and non-cerebellar regions of the 2 week old *Gnb5* KO mice and their wild type littermates using RNeasy® mini kit (QIAGEN). The RNA quality was checked by an Agilent Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA). Three pairs of mice from different litters were used for each region of the brain. Target labeling and hybridization to GeneChips were carried out in the NIDDK Microarray Core facility using the GeneChip Mouse 430 2.0 Array (Affymetrix, Santa Clara, CA, USA). Each microarray experiment employed triplicate biological repeats. The microarray signals were normalized using the RMA algorithm. The genes with significantly altered expression were selected based on ANOVA analysis by Partek Pro software (Partek, St. Charles, MO, USA). The genes with ANOVA P values of ≤ 0.05 and absolute values of fold-change of ≥ 1.5 were used in the gene ontology analysis by the commercial gene pathway analysis web tool (http://trials.genego.com/cgi/index.cgi). The microarray data presented in this publication have been deposited in NCBI's Gene Expression Omnibus (Edgar *et al*. 2002, Barrett *et al*. 2011) and are accessible through GEO Reference Series accession number GSE29083 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE29083).

2. References for Supplementary Methods

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Le Marec, N. and Lalonde, R. (1997) Sensorimotor learning and retention during equilibrium tests in Purkinje cell degeneration mutant mice. *Brain Res,* 768, 310-316.

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3. Legends to Supplemental Figures

Figure S1. Open field locomotor analysis of wild-type, Gβ5 heterozygous, and Gβ5

homozygous KO littermates. Mice of the indicated genotypes were subjected to open field locomotor analysis as described in Materials and Methods, with the results of various parameters shown. (n=6 wild-type, n=4 *Gnb5* heterozygotes and n=11 *Gnb5* KO,*$P < 0.05$; **$P < 0.02$; ***$P < 0.0001$; versus wt, two-tailed unpaired t-test).

Figure S2. Delayed Purkinje cell maturation in the cerebellar cortex of seven-day old Gβ5-homozygous knockout mice (low power images). Upper panels: DAPI (blue) and calbindin-1-immunostaining (red) (left), DAPI (blue) and Pcp2-GFP reporter fluorescence (green) (center), and merged (right) images of frozen sections of cerebella of Gβ5 wild-type and KO mouse littermates. Lower panels: DAPI (blue) and Pcp2-immunostaining (red) (left), DAPI (blue) and Pcp2-GFP reporter fluorescence (green) (center), and merged (right) images of frozen sections of cerebella of Gβ5 wild-type and KO mouse littermates.

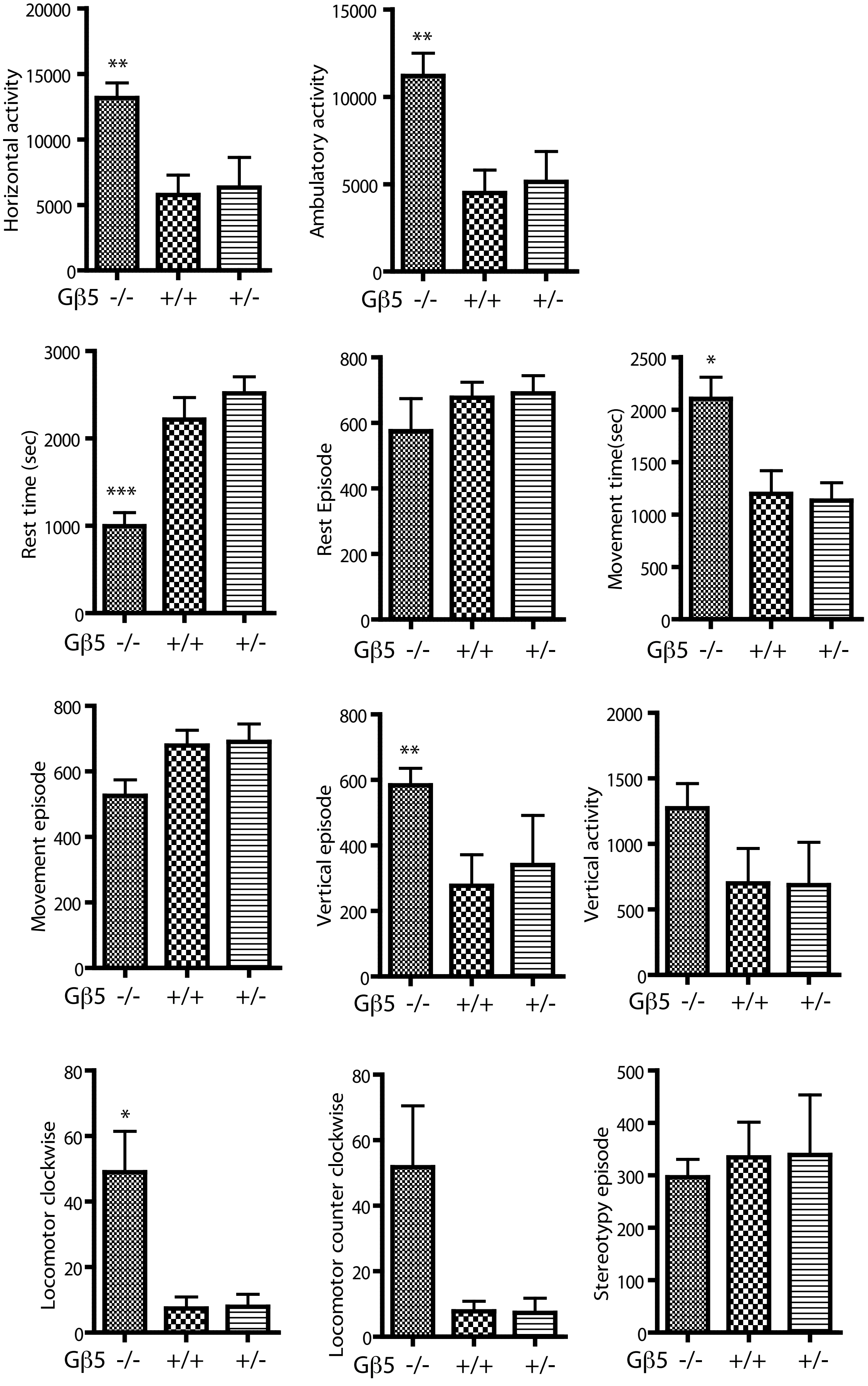
Figure S3. Delayed cerebellar development in *Gnb5* knockout mice. Analysis of Pcp2-GFP hemizygous *Gnb5* KO (A, C, E) and Pcp2-GFP hemizygous *Gnb5* wild-type (B, D, F) littermate mice. (A, B) Epifluorescence of vibratome sections of 4-6 day old littermates showing faint green Pcp2-GFP signal in periphery of wild-type sections. (C, D) Whole brains dissected from seven to 10 day old mice showing faint, limited cerebellar fluorescence in Gβ5 homozygous KO mice compared to bright, extensive signal in wild-type littermates. (E, F) Whole brains dissected from 14-15 day old mice showing comparable cerebellar fluorescence in Gβ5 KO and wild-type mice.

Figure S4. Wild-type mouse brain para-sagittal sections stained with cresyl violet

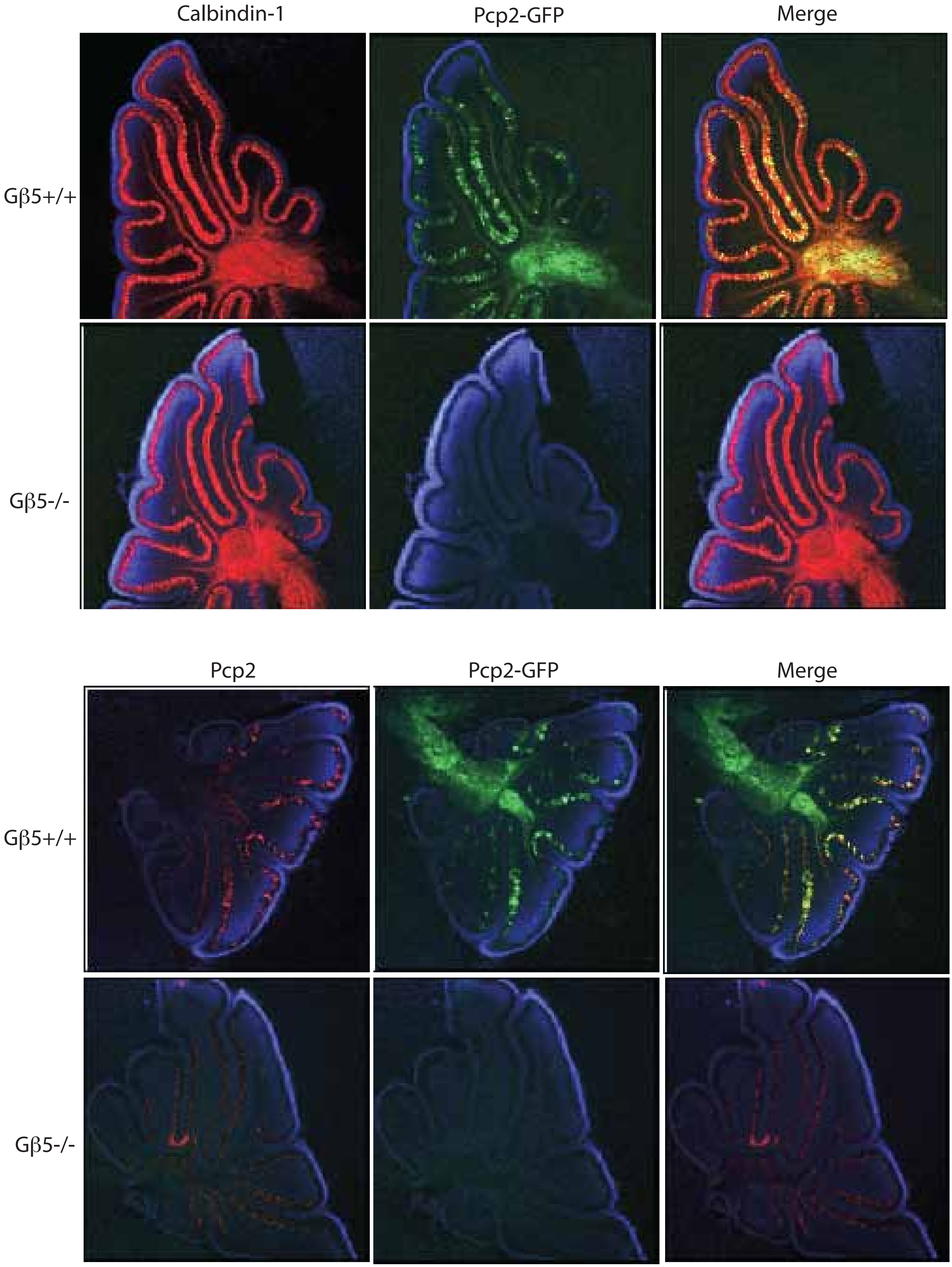
Morphological changes of the angular zone (AZ) of dentate gyrus during mouse brain development. Wild type mouse brains at indicated postnatal developmental stages were para-sagittally sectioned and Nissl stained with cresyl violet (left). The corresponding mediolateral positions of para-sagittal planes A and B in the displayed sections of the mouse brains are indicated (right). Section images were captured at 50 X magnification.

Figure S5. Venn diagram of *Gnb5*-regulated genes identified by microarray analysis

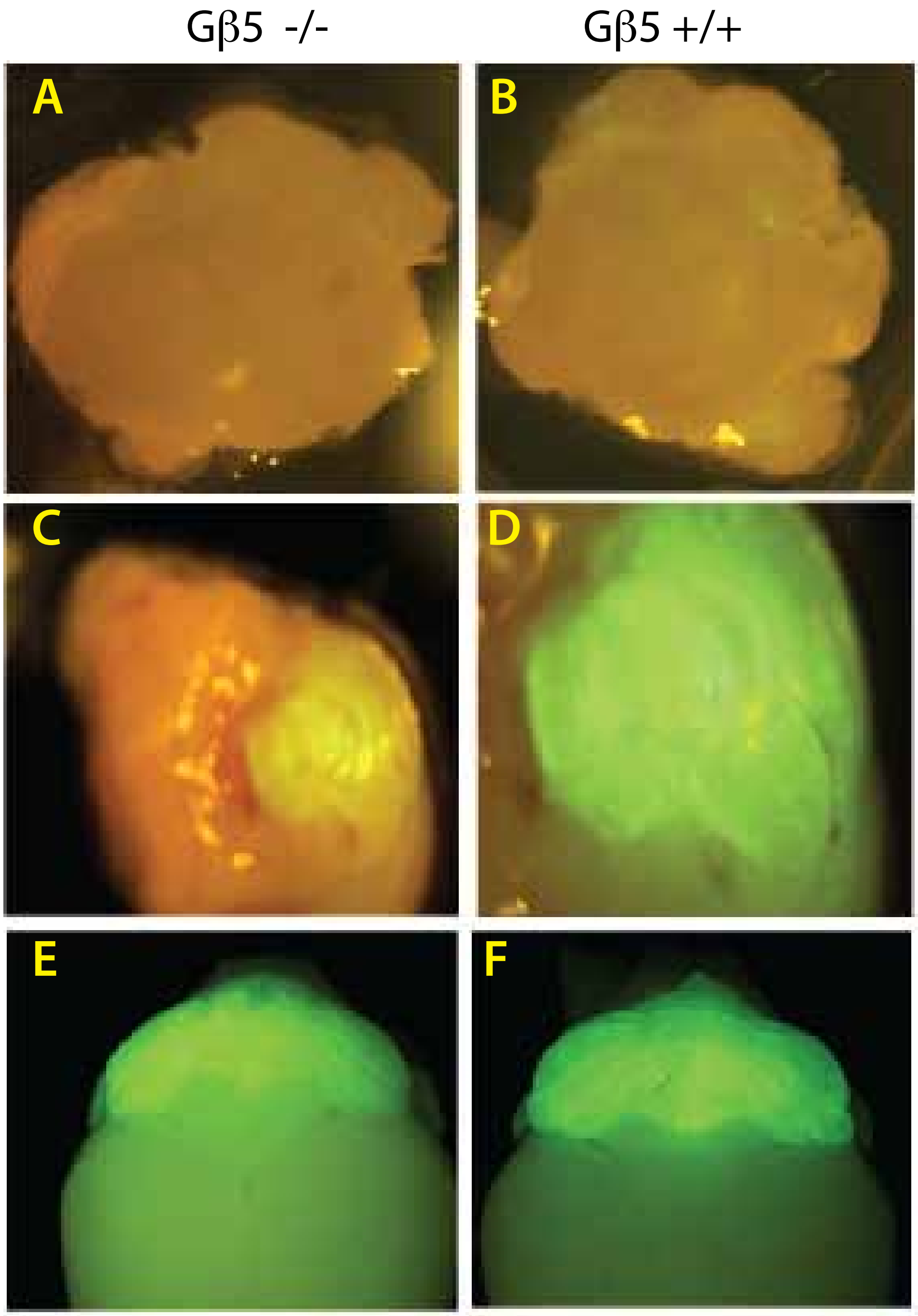
Identification of *Gnb5* target genes in cerebellar and non-cerebellar regions of mouse brain using whole genome oligo microarray. Bioinformatic analysis of gene expression, comparing transcripts from wild type and *Gnb5* KO mouse brain regions, identified 150 genes (256 probe sets; see corresponding probe set IDs in Supplemental Table 1) in cerebellar regions and 228 genes (346 probe sets; see corresponding probe set IDs in Supplemental Table 2) in non-cerebellar brain regions as well as 39 genes common to both regions (69 probe sets; see corresponding probe set IDs in Supplemental Table 3) that are regulated by *Gnb5* gene.



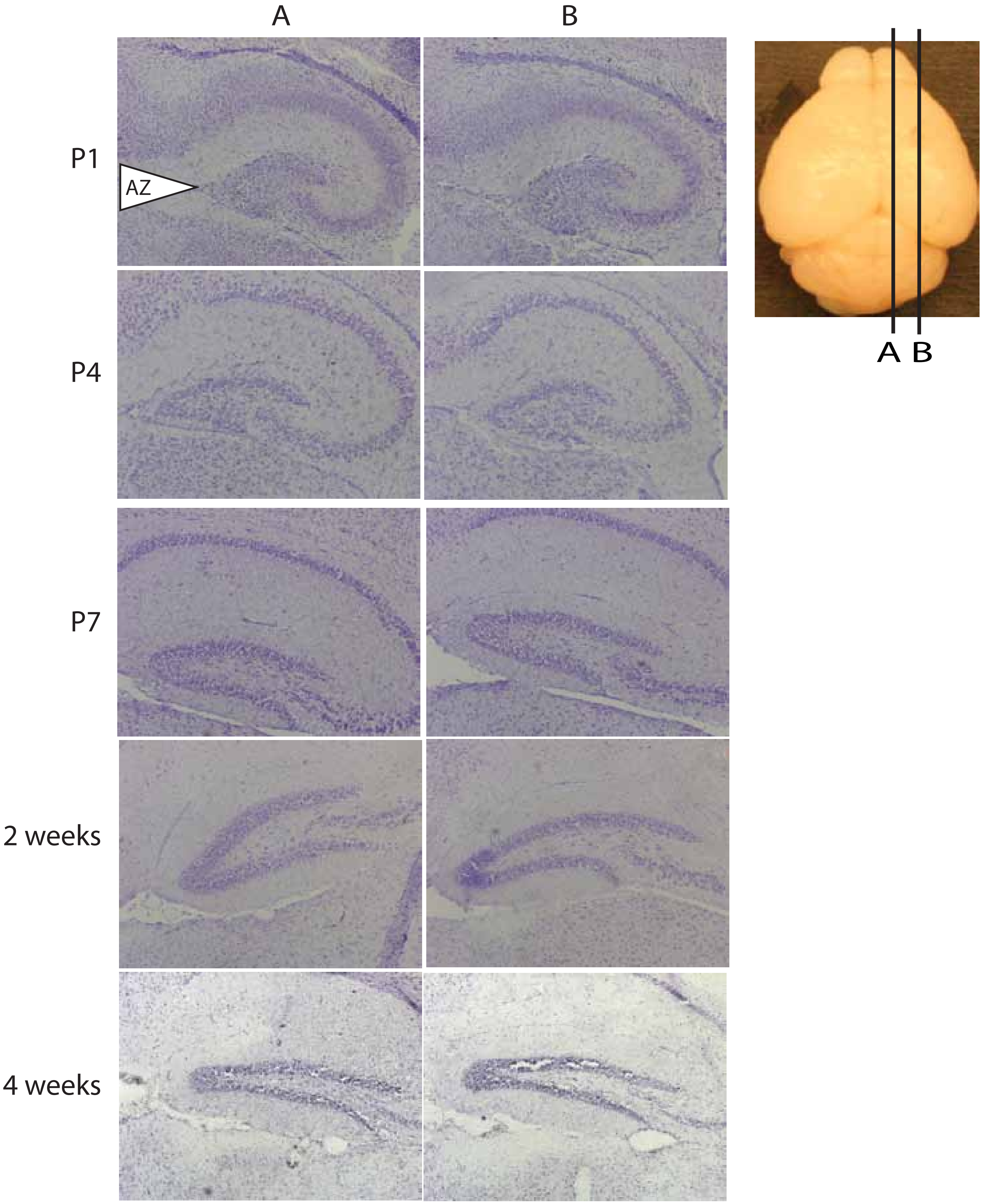
Suppl. Fig. 1 Zhang *et al*



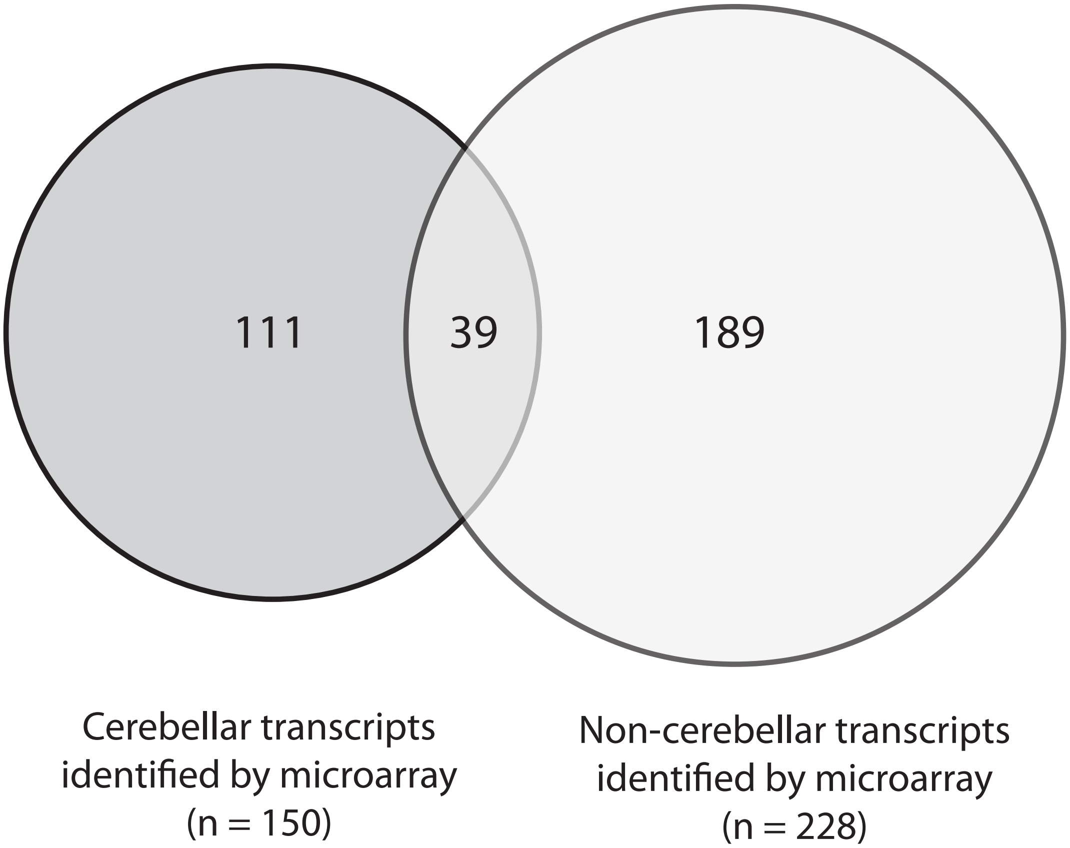
Suppl. Fig. 2 Zhang *et al*



Suppl. Fig. 3 Zhang *et al*



Suppl. Fig. 4 Zhang *et al*



Suppl. Fig. 5 Zhang *et al*

Supplemental Table 1.
Comparison of cerebellar gene expression differences between wild type and Gnb5 KO mice.

Affymetrix Gene Chip Probe set ID	**Gene Symbol**	**Gene Title**	**RefSeq Transcript ID**	**p-value (KO vs. WT)**	**Fold-Change (KO vs. WT)**
1446433_at	Acbd5	acyl-Coenzyme A binding domain containing 5	NM_001102436 /// NM_0011024	0.020	-1.59
1436742_a_at	Accsl	1-aminocyclopropane-1-carboxylate synthase ho	NM_001033452	0.020	1.59
1449895_at	Acr	acrosin prepropeptide	NM_013455	0.014	1.78
1434068_s_at	AI662270	expressed sequence AI662270	NR_015519 /// XM_001474264	0.043	-1.53
1434730_at	AI854517	expressed sequence AI854517	XM_979851 /// XM_982358	0.033	1.53
1451675_a_at	Alas2	aminolevulinic acid synthase 2, erythroid	NM_001102446 /// NM_009653	0.019	-4.23
1457307_at	Apol11b	apolipoprotein L 11b	NM_001143686 /// XR_001572	0.004	-4.75
1458613_at	Arrdc1	arrestin domain containing 1	NM_001162485 /// NM_178408	0.020	1.53
1424759_at	Arrdc4	arrestin domain containing 4	NM_001042592 /// NM_025549	0.005	2.21
1455851_at	Bmp5	bone morphogenetic protein 5	NM_007555	0.010	-1.66
1417325_at	Btrc	beta-transducin repeat containing protein	NM_001037758 /// NM_009771	0.043	1.54
1417461_at	Cap1	CAP, adenylate cyclase-associated protein 1 (yea	NM_007598	0.002	-5.39
1452218_at	Ccdc117	coiled-coil domain containing 117	NM_134033	0.004	-1.56
1451799_at	Ccdc25	coiled-coil domain containing 25	NM_145944	0.013	-1.59
1430190_at	Ccdc30	coiled-coil domain containing 30	NM_029286	0.005	1.63
1456168_at	Ccnjl	cyclin J-like	NM_001045530	0.016	-1.66
1424727_at	Ccr5	chemokine (C-C motif) receptor 5	NM_009917	0.026	-1.52
1460538_at	Cdh10	cadherin 10	NM_009865	0.003	-1.97
1453482_at	Cflar	CASP8 and FADD-like apoptosis regulator	NM_009805 /// NM_207653	0.008	2.35
1450427_at	Chrna6	cholinergic receptor, nicotinic, alpha polypeptide	NM_021369	0.021	-1.67
1437271_at	Clcf1	cardiotrophin-like cytokine factor 1	NM_019952	0.014	1.75
1426684_at	Cnot6	CCR4-NOT transcription complex, subunit 6	NM_212484	0.026	-1.59
1434411_at	Col12a1	collagen, type XII, alpha 1	NM_007730	0.001	-4.27
1449847_a_at	Col4a3bp	collagen, type IV, alpha 3 (Goodpasture antigen)	NM_001164222 /// NM_023420	0.046	1.58
1441558_at	D230044B12Rik	RIKEN cDNA D230044B12 gene	---	0.011	-1.57
1457668_x_at	D4Ertd617e	DNA segment, Chr 4, ERATO Doi 617, expresse	NR_029469 /// XM_001473428	0.003	1.97
1455474_at	D6Wsu116e	DNA segment, Chr 6, Wayne State University 11	NM_026585	0.009	1.65
1438962_s_at	Ddx31	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	NM_001033294	0.022	-1.57
1435132_at	Disp1	dispatched homolog 1 (Drosophila)	NM_026866	0.027	1.84
1458220_at	Dlc1	deleted in liver cancer 1	NM_015802	0.046	-3.53
1427410_at	Dleu2	deleted in lymphocytic leukemia, 2	NR_028264 /// XM_001000367	0.025	-2.10
1429573_at	Dmrtc1a	DMRT-like family C1a	NM_001038616 /// NM_027591	0.011	1.54
1430291_at	Dock5	dedicator of cytokinesis 5	NM_177780	0.014	-1.61
1460372_at	Duoxa1	dual oxidase maturation factor 1	NM_145395	0.031	1.53
1418276_at	Elf2	E74-like factor 2	NM_023502	0.047	-1.50
1440354_at	Elovl7	ELOVL family member 7, elongation of long chai	NM_029001	0.026	-1.58

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1418294_at	Epb4.1l4b	erythrocyte protein band 4.1-like 4b	NM_019427 /// XM_001476161	0.006	2.00
1429914_at	Epc1	enhancer of polycomb homolog 1 (Drosophila)	NM_007935 /// NM_027497	0.024	1.64
1435663_at	Esr1	estrogen receptor 1 (alpha)	NM_007956	0.016	1.93
1438427_at	Fam120b	family with sequence similarity 120, member B	NM_024203 /// NR_033586	0.009	1.89
1448021_at	Fam46c	family with sequence similarity 46, member C	NM_001142952 /// XR_001536	0.005	-4.15
1436550_at	Fbxo30	F-box protein 30	NM_001168297 /// NM_027968	0.014	-1.88
1418243_at	Fcna	ficolin A	NM_007995	0.001	1.50
1418323_at	Fem1b	feminization 1 homolog b (C. elegans)	NM_010193	0.012	2.02
1419322_at	Fgd6	FYVE, RhoGEF and PH domain containing 6	NM_053072	0.015	1.54
1436650_at	Filip1	filamin A interacting protein 1	NM_001081243	0.008	2.12
1416693_at	Foxc2	forkhead box C2	NM_013519	0.001	-1.58
1444066_at	Gapvd1	GTPase activating protein and VPS9 domains 1	NM_025709	0.010	-1.69
1460431_at	Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	NM_001136484 /// NM_010265	0.010	-1.77
1438648_x_at	Gkn3	gastrokine 3	NM_026860	0.022	-1.57
1427455_x_at	Gm10883 /// Gm14	predicted gene 10883 /// predicted gene 1420 ///	XM_001476664 /// XM_001476	0.010	-1.79
1421683_at	Gm3417 /// Gm344	predicted gene 3417 /// predicted gene 3448 /// t-	NM_001123367 /// NM_001123	0.025	1.54
1437418_at	Gm3515	predicted gene 3515	XM_001477025	0.025	-1.78
1430295_at	Gna13	guanine nucleotide binding protein, alpha 13	NM_010303	0.003	1.51
1422208_a_at	Gnb5	guanine nucleotide binding protein (G protein), b	NM_010313 /// NM_138719	0.000	-40.76
1425138_at	Guca1b	guanylate cyclase activator 1B	NM_146079	0.000	27.94
1430357_at	H3f3b	H3 histone, family 3B	NM_008211	0.024	1.52
1452757_s_at	Hba-a1 /// Hba-a2	hemoglobin alpha, adult chain 1 /// hemoglobin a	NM_001083955 /// NM_008218	0.033	-2.13
1417184_s_at	Hbb-b1 /// Hbb-b2	hemoglobin, beta adult major chain /// hemoglobi	NM_008220 /// NM_016956	0.008	-1.70
1427865_at	Hbb-b2	hemoglobin, beta adult minor chain	NM_016956	0.010	-1.51
1438328_at	Hcfc2	host cell factor C2	NM_001081218	0.014	-1.60
1425378_at	Herc1	hect (homologous to the E6-AP (UBE3A) carbox	NM_145617 /// XM_001477062	0.035	1.58
1420573_at	Hoxd1	homeobox D1	NM_010467	0.002	-2.40
1431182_at	Hspa8 /// LOC6248	heat shock protein 8 /// hypothetical LOC624853	NM_031165 /// NR_015570 ///	0.004	-1.73
1425201_a_at	Hyi	hydroxypyruvate isomerase homolog (E. coli)	NM_026601 /// NR_003946	0.004	1.81
1415931_at	Igf2	insulin-like growth factor 2	NM_001122736 /// NM_001122	0.012	-1.60
1419569_a_at	Isg20	interferon-stimulated protein	NM_001113527 /// NM_020583	0.017	-4.07
1433902_at	Kbtbd8	kelch repeat and BTB (POZ) domain containing	NM_001008785 /// NM_00110	0.017	-1.67
1455182_at	Kif1b	kinesin family member 1B	NM_008441 /// NM_207682	0.015	-1.56
1438247_at	Klhl15	kelch-like 15 (Drosophila)	NM_001039059 /// NM_001039	0.035	1.59
1430340_at	Lca5	Leber congenital amaurosis 5 (human)	NM_027448 /// NM_029434	0.007	1.52
1431792_a_at	LOC100047492 ///	similar to serine/threonine kinase 11 interacting p	NM_027886 /// XM_001478275	0.007	1.58
1416632_at	LOC677317 /// Me1	similar to NADP-dependent malic enzyme (NAD	NM_008615 /// XM_001004685	0.016	1.54
1431056_a_at	Lpl	lipoprotein lipase	NM_008509	0.028	1.52
1447954_at	Lrrc49	leucine rich repeat containing 49	NM_001146046 /// NM_00114	0.037	1.63
1428626_at	Lysmd2	LysM, putative peptidoglycan-binding, domain co	NM_027309	0.005	1.69

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1438352_at	Mapre2	Microtubule-associated protein, RP/EB family, me	NM_001162941 /// NM_0011629	0.040	-1.52
1436415_at	Med29	mediator complex subunit 29	NM_026042	0.025	1.56
1457836_at	Mfsd11	major facilitator superfamily domain containing 1	NM_178620	0.034	1.60
1434322_at	Micall2	MICAL-like 2	NM_174850	0.024	1.70
1430798_x_at	Mrpl15	mitochondrial ribosomal protein L15	NM_001177658 /// NM_025300	0.016	2.22
1443021_at	Mthfs	5, 10-methenyltetrahydrofolate synthetase	NM_026829	0.017	1.74
1455645_at	Mybpc1	myosin binding protein C, slow-type	NM_175418	0.047	1.54
1426851_a_at	Nov	nephroblastoma overexpressed gene	NM_010930	0.005	-1.89
1419662_at	Ogn	osteoglycin	NM_008760	0.030	-1.51
1444029_at	Parp11	poly (ADP-ribose) polymerase family, member 11	NM_181402	0.019	2.23
1438946_at	Pdgfra	platelet derived growth factor receptor, alpha poly	NM_001083316 /// NM_011058	0.045	1.91
1449374_at	Pipox	pipecolic acid oxidase	NM_008952	0.020	1.59
1436712_at	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-	NM_001004762 /// NM_001168	0.001	-1.52
1429862_at	Pla2g4e	phospholipase A2, group IVE	NM_177845	0.006	1.55
1439840_at	Polb	polymerase (DNA directed), beta	NM_011130	0.006	-1.69
1426839_at	Pold3	polymerase (DNA-directed), delta 3, accessory s	NM_133692	0.029	1.65
1418480_at	Ppbp	pro-platelet basic protein	NM_023785	0.001	-2.24
1431505_at	Ppih	peptidyl prolyl isomerase H	NM_001110129 /// NM_001110	0.002	-2.75
1456805_a_at	Ppp4r1l	protein phosphatase 4, regulatory subunit 1-like	NR_027957 /// XM_001481221	0.012	1.54
1452473_at	Prr15	proline rich 15	NM_030024	0.004	1.54
1450680_at	Rag1	recombination activating gene 1	NM_009019	0.002	-1.56
1444441_at	Rapgefl1	Rap guanine nucleotide exchange factor (GEF)-li	NM_001080925	0.009	1.81
1431749_a_at	Rasgrp1	RAS guanyl releasing protein 1	NM_011246	0.025	1.72
1425166_at	Rbl1	retinoblastoma-like 1 (p107)	NM_001139516 /// NM_011249	0.018	1.51
1435158_at	Rbm12b	RNA binding motif protein 12B	NM_028226	0.050	-1.63
1429169_at	Rbm3	RNA binding motif protein 3	NM_001166409 /// NM_00116	0.017	-4.77
1416355_at	Rbmx	RNA binding motif protein, X chromosome	NM_001166623 /// NM_011252	0.009	-1.64
1443215_at	Rims2	regulating synaptic membrane exocytosis 2	NM_053271	0.025	2.29
1459573_at	Rpf1	ribosome production factor 1 homolog (S. cerevis	NM_027332 /// NM_027371	0.039	1.50
1434817_s_at	Rprd2	regulation of nuclear pre-mRNA domain containi	NM_001081293	0.002	1.92
1453466_at	Rps6	ribosomal protein S6	NM_009096	0.012	2.00
1436058_at	Rsad2	radical S-adenosyl methionine domain containin	NM_021384	0.002	-4.51
1421009_at	Rsad2	radical S-adenosyl methionine domain containin	NM_021384	0.003	-4.60
1458882_at	Serpinb8	serine (or cysteine) peptidase inhibitor, clade B, r	NM_001159748 /// NM_011459	0.043	-1.53
1436871_at	Sfrs7	splicing factor, arginine/serine-rich 7	NM_146083	0.006	1.79
1417750_a_at	Slc25a37	solute carrier family 25, member 37	NM_026331	0.015	-1.93
1415958_at	Slc2a4	solute carrier family 2 (facilitated glucose transpo	NM_009204	0.005	1.52
1421249_at	Slc39a9	solute carrier family 39 (zinc transporter), membe	NM_026244 /// XM_001472453	0.001	1.69
1418395_at	Slc47a1	solute carrier family 47, member 1	NM_026183	0.045	-1.51
1416464_at	Slc4a1	solute carrier family 4 (anion exchanger), membe	NM_011403	0.021	-3.17

Supplemental Table 1.
Comparison of cerebellar gene expression differences between wild type and Gnb5 KO mice.

1434502_x_at	Slc4a1	solute carrier family 4 (anion exchanger), membe	NM_011403	0.021	-3.72
1417415_at	Slc6a3	solute carrier family 6 (neurotransmitter transport	NM_010020	0.014	-2.51
1426690_a_at	Srebf1	sterol regulatory element binding transcription fac	NM_011480	0.028	1.63
1436257_at	Ss18	synovial sarcoma translocation, Chromosome 18	NM_001161369 /// NM_001161	0.044	-1.55
1444053_at	Ssbp1	single-stranded DNA binding protein 1	NM_028358 /// NM_212468	0.018	1.53
1436561_at	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosop	NM_022724 /// NR_027509	0.000	-1.55
1455171_at	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosc	NM_001167884 /// NM_001167	0.009	1.52
1427045_at	Synpo	synaptopodin	NM_001109975 /// NM_177340	0.025	1.54
1450281_a_at	Tbata	thymus, brain and testes associated	NM_001017407 /// NM_001017	0.040	-1.62
1455336_at	Thap2	THAP domain containing, apoptosis associated p	NM_025780	0.012	-1.53
1448529_at	Thbd	thrombomodulin	NM_009378	0.003	-1.65
1454018_at	Tlk2	tousled-like kinase 2 (Arabidopsis)	NM_001112705 /// NM_011903	0.008	1.88
1425079_at	Tm6sf2	transmembrane 6 superfamily member 2	NM_181540	0.004	-1.77
1443619_at	Tmem30a	transmembrane protein 30A	NM_133718	0.001	-8.96
1438556_a_at	Tmod3	tropomodulin 3	NM_016963	0.001	-6.31
1430579_at	Tnik	TRAF2 and NCK interacting kinase	NM_001163007 /// NM_001163	0.027	1.53
1436394_at	Trim37	tripartite motif-containing 37	NM_197987	0.014	1.54
1438542_at	Trp53	Transformation related protein 53	NM_001127233 /// NM_011640	0.028	1.83
1439989_at	Tsc1	tuberous sclerosis 1	NM_022887	0.031	1.50
1420587_at	Tsga13	testis specific gene A13	NM_054073	0.036	2.02
1424649_a_at	Tspan8	tetraspanin 8	NM_001168679 /// NM_001168	0.008	-1.86
1444214_at	Tubb1	tubulin, beta 1	NM_001080971	0.035	-1.76
1415996_at	Txnip	thioredoxin interacting protein	NM_001009935 /// NM_023719	0.004	1.65
1429363_at	Vps37a	vacuolar protein sorting 37A (yeast)	NM_033560	0.011	-1.80
1435386_at	Vwf	Von Willebrand factor homolog	NM_011708	0.007	1.55
1416084_at	Zfand5	zinc finger, AN1-type domain 5	NM_009551	0.046	1.72
1425098_at	Zfp106	zinc finger protein 106	NM_011743	0.032	1.50
1425010_at	Zfp119	zinc finger protein 119	NM_144546	0.032	-1.64
1459690_at	Zfp426	zinc finger protein 426	NM_001110309 /// NM_146221	0.023	1.54
1439475_at	Zfp429	zinc finger protein 429	NM_001080941	0.020	-1.67
1439869_at	Zfp493	zinc finger protein 493	NM_028402 /// XM_619117 /// X	0.001	-1.53
1451902_at	Zfp758	zinc finger protein 758	NM_145484	0.043	-1.53
1427499_at	Zfp81	zinc finger protein 81	NM_207541	0.008	1.64
1452610_at	Zkscan14	zinc finger with KRAB and SCAN domains 14	NM_023322	0.013	1.67

Supplemental Table 2.
Comparison of non-cerebellar gene expression differences between wild type and Gnb5 KO mice.

Affymetrix Gene Chip Probe set ID	Gene Symbol	Gene Title	RefSeq Transcript ID	p-value (KO vs. WT)	Fold-Change (KO vs. WT)
1418043_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	NM_013790 /// NM_176839	0.026	1.55
1449895_at	Acr	acrosin prepropeptide	NM_013455	0.003	1.61
1460316_at	Acsl1	acyl-CoA synthetase long-chain family member 1	NM_007981	0.039	-1.52
1435825_at	Acvrl1	activin A receptor, type II-like 1	NM_009612	0.002	1.87
1448539_a_at	Acy3	aspartoacylase (aminoacylase) 3	NM_027857	0.020	1.58
1457042_at	AI256396	EST AI256396	---	0.007	-1.70
1437923_at	AI314760	expressed sequence AI314760	---	0.026	-1.53
1451634_at	Airn	antisense Igf2r RNA	NR_002853 /// NR_027772 ///	0.022	-1.63
1450455_s_at	Akr1c12 /// Akr1c13	aldo-keto reductase family 1, member C12 /// aldo-keto reduct	NM_013777 /// NM_013778	0.013	1.52
1447734_x_at	Aldoa	aldolase A, fructose-bisphosphate	NM_001177307 /// NM_00117	0.008	-1.57
1436071_at	Ankrd26	ankyrin repeat domain 26	NM_001081112	0.017	-1.54
1460449_at	Anks1b	ankyrin repeat and sterile alpha motif domain containing 1B	NM_001128086 /// NM_00117	0.034	-1.69
1457303_at	Anks3	ankyrin repeat and sterile alpha motif domain containing 3	NM_028301	0.015	1.53
1449396_at	Aoc3	amine oxidase, copper containing 3	NM_009675	0.035	-1.53
1428607_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	NM_001159645 /// NM_00970	0.005	-1.75
1436258_at	Arhgef9	CDC42 guanine nucleotide exchange factor (GEF) 9	NM_001033329	0.029	-1.67
1424020_at	Arl6ip6	ADP-ribosylation factor-like 6 interacting protein 6	NM_022989	0.008	-1.91
1437849_x_at	Armcx2	armadillo repeat containing, X-linked 2	NM_001166397 /// NM_00116	0.038	-1.52
1458613_at	Arrdc1	arrestin domain containing 1	NM_001162485 /// NM_17840	0.049	1.72
1424759_at	Arrdc4	arrestin domain containing 4	NM_001042592 /// NM_02554	0.004	2.22
1438921_at	Atr	Ataxia telangiectasia and Rad3 related	NM_019864	0.000	-1.72
1433599_at	Baz1a	bromodomain adjacent to zinc finger domain 1A	NM_013815 /// XM_885873 ///	0.015	-1.54
1435761_at	BC100530 /// Stfa1	cDNA sequence BC100530 /// stefin A1	NM_001082543 /// NM_00108	0.015	2.23
1443837_x_at	Bcl2	B-cell leukemia/lymphoma 2	NM_009741 /// NM_177410 ///	0.031	-1.56
1439431_x_at	Bicd1	bicaudal D homolog 1 (Drosophila)	NM_001112796 /// NM_00975	0.008	-1.58
1455851_at	Bmp5	bone morphogenetic protein 5	NM_007555	0.001	-1.86
1456141_x_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	NM_001166457 /// NM_00116	0.032	-1.66
1437455_a_at	Btg1 /// LOC100047353	B-cell translocation gene 1, anti-proliferative /// similar to myoc	NM_007569 /// XM_00147796	0.044	-1.50
1458879_at	C76798	expressed sequence C76798	---	0.002	-1.61
1459610_at	C87490	expressed sequence C87490	---	0.002	1.69
1435146_s_at	Cadm2	cell adhesion molecule 2	NM_001145977 /// NM_17872	0.038	-1.98
1453824_at	Ccdc76	coiled-coil domain containing 76	NM_030016	0.011	-1.81
1453330_at	Ccdc88c	coiled-coil domain containing 88C	NM_026681	0.007	1.62
1419413_at	Ccl17	chemokine (C-C motif) ligand 17	NM_011332	0.001	1.60
1418070_at	Cdyl	chromodomain protein, Y chromosome-like	NM_001123386 /// NM_00988	0.012	-1.83
1453482_at	Cflar	CASP8 and FADD-like apoptosis regulator	NM_009805 /// NM_207653	0.001	1.77
1446844_at	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	NM_181391	0.011	-1.53
1440158_x_at	Chchd7	Coiled-coil-helix-coiled-coil-helix domain containing 7	NM_181391	0.019	-1.95
1439342_at	Clpx	Caseinolytic peptidase X (E.coli)	NM_001044389 /// NM_01180	0.040	-1.61
1426684_at	Cnot6	CCR4-NOT transcription complex, subunit 6	NM_212484	0.019	-1.55
1438628_x_at	Cntn3	contactin 3	NM_008779	0.009	-1.73
1434411_at	Col12a1	collagen, type XII, alpha 1	NM_007730	0.000	-4.22

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1448734_at	Cp	ceruloplasmin	NM_001042611 /// NM_00775	0.026	-1.55
1435435_at	Cttnbp2	cortactin binding protein 2	NM_080285	0.016	-1.79
1447494_at	D7Bwg0826e	DNA segment, Chr 7, Brigham & Women's Genetics 0826 exp	---	0.047	1.51
1437256_at	Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (	NM_029775	0.006	-1.61
1456000_at	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	NM_025860	0.044	1.54
1435132_at	Disp1	dispatched homolog 1 (Drosophila)	NM_026866	0.039	1.59
1417787_at	Dkkl1	dickkopf-like 1	NM_015789	0.017	1.65
1439376_x_at	Dmtf1	cyclin D binding myb-like transcription factor 1	NM_001110327 /// NM_01180	0.029	-1.54
1420165_s_at	Dnajc17	DnaJ (Hsp40) homolog, subfamily C, member 17	NM_139139	0.023	1.51
1449373_at	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	NM_008929	0.000	-1.61
1419513_a_at	Ect2	ect2 oncogene	NM_001177625 /// NM_00117	0.039	-1.62
1443682_at	Eng	Endoglin	NM_001146348 /// NM_00114	0.012	1.55
1447900_x_at	Entpd4 /// LOC100048085	ectonucleoside triphosphate diphosphohydrolase 4 /// similar t	NM_026174 /// XR_034152	0.018	-1.68
1418294_at	Epb4.1l4b	erythrocyte protein band 4.1-like 4b	NM_019427 /// XM_00147616	0.008	1.54
1435631_x_at	Exoc6	exocyst complex component 6	NM_175353	0.004	1.50
1438427_at	Fam120b	family with sequence similarity 120, member B	NM_024203 /// NR_033586	0.002	1.71
1430685_at	Fam131b	family with sequence similarity 131, member B	NM_001113327 /// NM_02952	0.027	1.55
1436685_at	Fam181a	family with sequence similarity 181, member A	XM_619025 /// XM_909635	0.042	1.50
1448021_at	Fam46c	family with sequence similarity 46, member C	NM_001142952 /// XR_00153	0.008	-1.57
1436550_at	Fbxo30	F-box protein 30	NM_001168297 /// NM_02796	0.004	-1.57
1418323_at	Fem1b	feminization 1 homolog b (C. elegans)	NM_010193	0.000	1.69
1416693_at	Foxc2	forkhead box C2	NM_013519	0.015	-1.62
1437388_at	Fut10	fucosyltransferase 10	NM_001012517 /// NM_13416	0.010	1.67
1440788_at	Gas8	growth arrest specific 8	NM_018855	0.002	-1.71
1448397_at	Gjb6	gap junction protein, beta 6	NM_001010937 /// NM_00812	0.010	-1.50
1440945_at	Glcci1	Glucocorticoid induced transcript 1	NM_133236	0.020	1.63
1424825_a_at	Glycam1	glycosylation dependent cell adhesion molecule 1	NM_008134	0.001	1.61
1444616_x_at	Gm2380	predicted gene 2380	XM_001473723 /// XR_03311	0.024	-1.69
1428033_at	Gm4979	predicted gene 4979	NM_001142411 /// XM_00148	0.004	-1.53
1457365_at	Gm6860	Predicted gene 6860	XM_900516	0.002	-2.07
1435217_at	Gm7969	Predicted gene 7969	XM_001473218 /// XM_98217	0.032	-1.71
1422208_a_at	Gnb5	guanine nucleotide binding protein (G protein), beta 5	NM_010313 /// NM_138719	0.000	-49.11
1423142_a_at	Gtpbp4	GTP binding protein 4	NM_027000	0.048	-1.56
1425138_at	Guca1b	guanylate cyclase activator 1B	NM_146079	0.000	35.64
1425643_at	Gypa	glycophorin A	NM_010369	0.021	-1.53
1427865_at	Hbb-b2	hemoglobin, beta adult minor chain	NM_016956	0.031	-1.60
1439424_x_at	Herpud2	HERPUD family member 2	NM_020586	0.022	-1.65
1434150_a_at	Higd1c /// Mettl7a1 /// Mett	HIG1 domain family, member 1C /// methyltransferase like 7A1	NM_001002900 /// NM_02733	0.010	-1.64
1428242_at	Hmha1	histocompatibility (minor) HA-1	NM_001142701 /// NM_02752	0.002	1.51
1428224_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	NM_016690	0.039	-1.57
1430040_at	Hspa12a	heat shock protein 12A	NM_175199	0.007	1.53
1457666_s_at	Ifi202b	interferon activated gene 202B	NM_008327 /// NM_011940	0.045	1.73
1436831_at	Iqub	IQ motif and ubiquitin domain containing	NM_172535	0.011	-1.51
1438247_at	Klhl15	kelch-like 15 (Drosophila)	NM_001039059 /// NM_00103	0.018	1.68
1426978_at	Klhl2	kelch-like 2, Mayven (Drosophila)	NM_178633 /// XM_00147546	0.023	-1.52
1449378_at	Krt27	keratin 27	NM_010666	0.026	1.51

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1435989_x_at	Krt8	keratin 8	NM_031170	0.009	1.76
1426040_a_at	LOC100047199 /// Odf2	similar to outer dense fiber of sperm tails 2 /// outer dense fibe	NM_001113213 /// NM_00111	0.025	1.70
1438931_s_at	LOC100047324 /// Sesn1	similar to Sesn1 protein /// sestrin 1	NM_001013370 /// NM_00116	0.031	-1.51
1416632_at	LOC677317 /// Me1	similar to NADP-dependent malic enzyme (NADP-ME) (Malic	NM_008615 /// XM_00100468	0.022	1.63
1416121_at	Lox	lysyl oxidase	NM_010728	0.024	-1.61
1440112_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	NM_178678	0.024	-1.51
1455926_at	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisi	NM_030145	0.016	1.59
1428626_at	Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	NM_027309	0.002	1.61
1453025_at	Macrod2	MACRO domain containing 2	NM_001013802 /// NM_02838	0.002	-1.52
1425252_a_at	Mad1l1	mitotic arrest deficient 1-like 1	NM_010752	0.006	1.59
1419677_at	Masp1	mannan-binding lectin serine peptidase 1	NM_008555	0.001	1.74
1437575_at	Mcm9	minichromosome maintenance complex component 9	NM_027830	0.020	-1.59
1458343_x_at	Med6	mediator of RNA polymerase II transcription, subunit 6 homolo	NM_027213	0.044	-1.63
1437058_at	Megf6	multiple EGF-like-domains 6	NM_001162977 /// XM_62014	0.007	1.57
1447861_x_at	Meis2	Meis homeobox 2	NM_001136072 /// NM_00115	0.039	-1.50
1454858_x_at	Mettl7a1	methyltransferase like 7A1	NM_027334	0.002	-1.53
1433853_at	Mib1	mindbomb homolog 1 (Drosophila)	NM_144860	0.001	-1.63
1416759_at	Mical1	microtubule associated monoxygenase, calponin and LIM dom	NM_001164433 /// NM_13831	0.016	1.56
1434322_at	Micall2	MICAL-like 2	NM_174850	0.044	1.74
1441546_at	Mpp6	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily me	NM_001164733 /// NM_00116	0.027	-1.71
1436274_at	Mrap2	melanocortin 2 receptor accessory protein 2	NM_001101482 /// NM_00117	0.002	1.53
1430798_x_at	Mrpl15	mitochondrial ribosomal protein L15	NM_001177658 /// NM_02530	0.002	2.06
1451536_at	Mtfr1	mitochondrial fission regulator 1	NM_026182	0.002	-1.87
1431739_at	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae	NM_026658	0.002	-1.50
1430729_at	Myg1	melanocyte proliferating gene 1	NM_021713	0.048	1.55
1427768_s_at	Myl3	myosin, light polypeptide 3	NM_010859	0.035	1.51
1421334_x_at	Mynn	myoneurin	NM_030557	0.002	-1.54
1424933_at	Myo5c	myosin VC	NM_001081322	0.018	-1.51
1439708_at	Myom3	myomesin family, member 3	NM_001085509 /// XM_14409	0.045	1.63
1446718_at	Nfkbib	nuclear factor of kappa light polypeptide gene enhancer in B-c	NM_010908	0.001	1.57
1436136_at	Noc2l	nucleolar complex associated 2 homolog (S. cerevisiae)	NM_021303	0.000	1.57
1431597_a_at	Nrip3	nuclear receptor interacting protein 3	NM_020610	0.048	-1.54
1458492_x_at	Ntm	neurotrimin	NM_172290	0.001	-1.57
1430341_at	Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	NM_016918	0.010	-1.58
1435216_a_at	Odf2	outer dense fiber of sperm tails 2	NM_001113213 /// NM_00111	0.030	1.66
1419663_at	Ogn	osteoglycin	NM_008760	0.004	-1.61
1418745_at	Omd	osteomodulin	NM_012050	0.005	-1.61
1444029_at	Parp11	poly (ADP-ribose) polymerase family, member 11	NM_181402	0.003	2.07
1440203_at	Pcgf3	polycomb group ring finger 3	NM_172716	0.028	1.59
1443869_at	Pde12	phosphodiesterase 12	NM_178668	0.018	-1.69
1427213_at	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	NM_008824	0.023	1.60
1437594_x_at	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	NM_133779	0.024	-1.57
1454838_s_at	Pkdcc	protein kinase domain containing, cytoplasmic	NM_134117 /// XM_00148048	0.041	-1.59
1436851_at	Pkn1 /// Ptger1	protein kinase N1 /// prostaglandin E receptor 1 (subtype EP1)	NM_013641 /// NM_177262	0.048	1.57
1439840_at	Polb	polymerase (DNA directed), beta	NM_011130	0.000	-1.73
1426839_at	Pold3	polymerase (DNA-directed), delta 3, accessory subunit	NM_133692	0.005	1.51

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1428923_at	Ppp1r3g	protein phosphatase 1, regulatory (inhibitor) subunit 3G	NM_029628 /// XM_127272 ///	0.014	-1.60
1443144_at	Prkcb	protein kinase C, beta	NM_008855	0.000	1.58
1437671_x_at	Prss23	protease, serine, 23	NM_029614	0.003	-1.96
1445445_s_at	Ptger1	prostaglandin E receptor 1 (subtype EP1)	NM_013641	0.041	1.59
1438562_a_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	NM_001127177 /// NM_00897	0.048	-1.66
1424456_at	Pvrl2	poliovirus receptor-related 2	NM_001159724 /// NM_00899	0.024	1.51
1457257_x_at	Pvrl3	poliovirus receptor-related 3	NM_021495 /// NM_021496 ///	0.003	-1.60
1417073_a_at	Qk	quaking	NM_001159516 /// NM_00115	0.001	-1.53
1429169_at	Rbm3	RNA binding motif protein 3	NM_001166409 /// NM_00116	0.000	-4.00
1438021_at	Rbm47	RNA binding motif protein 47	NM_001127382 /// NM_13906	0.043	-1.57
1416355_at	Rbmx	RNA binding motif protein, X chromosome	NM_001166623 /// NM_01125	0.004	-1.65
1433976_at	Reep3	Receptor accessory protein 3	NM_178606	0.007	-1.57
1430128_a_at	Reep6	receptor accessory protein 6	NM_139292	0.048	1.60
1455265_a_at	Rgs16	regulator of G-protein signaling 16	NM_011267	0.023	-1.81
1435284_at	Rtn4	reticulon 4	NM_024226 /// NM_194051 ///	0.002	-1.64
1440846_at	Scai	suppressor of cancer cell invasion	NM_178778	0.000	-1.51
1437307_at	Senp8	SUMO/sentrin specific peptidase 8	NM_001172068 /// NM_00117	0.024	-1.58
1417815_a_at	Serinc3	serine incorporator 3	NM_012032	0.009	-1.53
1436871_at	Sfrs7	splicing factor, arginine/serine-rich 7	NM_146083	0.003	1.83
1437033_a_at	Skp2	S-phase kinase-associated protein 2 (p45)	NM_013787 /// NM_145468	0.028	-1.55
1436989_s_at	Slc12a6	solute carrier family 12, member 6	NM_133648 /// NM_133649	0.001	-1.68
1434188_at	Slc16a12	solute carrier family 16 (monocarboxylic acid transporters), me	NM_172838	0.002	-1.91
1443749_x_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter)	NM_148938	0.019	-1.59
1455506_at	Slc25a34	solute carrier family 25, member 34	NM_001013780	0.034	1.71
1447783_x_at	Slc25a39	solute carrier family 25, member 39	NM_026542	0.024	-1.60
1447893_x_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	NM_139143	0.006	-1.59
1434502_x_at	Slc4a1	solute carrier family 4 (anion exchanger), member 1	NM_011403	0.015	-1.90
1447186_at	Slc6a16	solute carrier family 6, member 16	XM_355900 /// XM_914689	0.046	1.50
1443536_at	Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ syst	NM_011990	0.013	-1.71
1437870_at	Slco4c1	solute carrier organic anion transporter family, member 4C1	NM_172658	0.014	-1.68
1425977_a_at	Slk	STE20-like kinase (yeast)	NM_001164639 /// NM_00928	0.008	-1.52
1445720_at	Sltm	SAFB-like, transcription modulator	NM_025690 /// NM_026337	0.012	-1.54
1449254_at	Spp1	secreted phosphoprotein 1	NM_009263	0.000	-1.51
1437638_at	Srrm2	serine/arginine repetitive matrix 2	NM_175229	0.035	-1.58
1436257_at	Ss18	synovial sarcoma translocation, Chromosome 18	NM_001161369 /// NM_00116	0.041	-1.72
1452617_at	Ssbp1	single-stranded DNA binding protein 1	NM_028358 /// NM_212468	0.028	-1.53
1443554_at	Ssbp3	Single-stranded DNA binding protein 3	NM_023672 /// NM_198438	0.008	1.57
1442452_at	Stradb	STE20-related kinase adaptor beta	NM_172656	0.032	-1.52
1435058_x_at	Stxbp3a	syntaxin binding protein 3A	NM_011504	0.048	-1.69
1441906_x_at	Syap1	synapse associated protein 1	NM_025932	0.017	-1.71
1430133_at	Tbc1d8b	TBC1 domain family, member 8B	NM_001081499	0.007	-1.55
1456033_at	Tbx4	T-box 4	NM_011536 /// NM_172798	0.011	1.61
1439619_at	Tcf12	transcription factor 12	NM_011544	0.034	-1.60
1421909_at	Tcf20	transcription factor 20	NM_001114140 /// NM_01383	0.039	1.53
1426639_a_at	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	NM_001142918 /// NM_00114	0.025	1.58
1449640_at	Tlr7	toll-like receptor 7	NM_133211	0.011	1.68

Supplemental Table 2.
Comparison of non-cerebellar gene expression differences between wild type and Gnb5 KO mice.

1425079_at	Tm6sf2	transmembrane 6 superfamily member 2	NM_181540	0.019	-1.65
1441890_x_at	Tmeff1	transmembrane protein with EGF-like and two follistatin-like d	NM_021436	0.024	-1.66
1443619_at	Tmem30a	transmembrane protein 30A	NM_133718	0.000	-5.72
1433735_a_at	Tmem64	transmembrane protein 64	NM_181401	0.029	-1.66
1423088_at	Tmod3	tropomodulin 3	NM_016963	0.000	-1.80
1436826_at	Tmtc3	transmembrane and tetratricopeptide repeat containing 3	NM_001033332 /// NM_00111	0.008	-1.52
1426095_a_at	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	NM_023680	0.025	1.57
1420351_at	Tnfrsf4	tumor necrosis factor receptor superfamily, member 4	NM_011659	0.037	1.76
1418726_a_at	Tnnt2	troponin T2, cardiac	NM_001130174 /// NM_00113	0.010	1.52
1423176_at	Tob1	transducer of ErbB-2.1	NM_009427	0.012	-1.69
1448667_x_at	Tob2	transducer of ERBB2, 2	NM_020507	0.012	-1.59
1423310_at	Tpbg	trophoblast glycoprotein	NM_001164792 /// NM_01162	0.040	1.89
1456089_at	Trim23	tripartite motif-containing 23	NM_030731	0.019	-1.68
1436393_a_at	Trim37	tripartite motif-containing 37	NM_197987	0.003	1.64
1440268_at	Trim41	tripartite motif-containing 41	NM_145377 /// XM_00147546	0.023	-1.60
1460375_at	Trmt112	tRNA methyltransferase 11-2 homolog (S. cerevisiae)	NM_001166370 /// NM_02630	0.000	1.77
1438542_at	Trp53	Transformation related protein 53	NM_001127233 /// NM_01164	0.001	1.56
1420772_a_at	Tsc22d3	TSC22 domain family, member 3	NM_001077364 /// NM_01028	0.026	-1.51
1455853_x_at	Tspan31	tetraspanin 31	NM_025982	0.022	1.53
1453392_at	Ttc39b	tetratricopeptide repeat domain 39B	NM_027238	0.008	1.53
1452054_at	Ube2w	ubiquitin-conjugating enzyme E2W (putative)	NM_025773	0.035	-1.51
1436882_at	Ubl5	ubiquitin-like 5	NM_025401	0.013	1.53
1436628_at	Ulk4	unc-51-like kinase 4 (C. elegans)	NM_177589 /// XM_00147956	0.005	1.63
1452613_at	Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	NM_025352	0.010	1.51
1437293_x_at	Ust	uronyl-2-sulfotransferase	NM_177387	0.013	-1.56
1453162_at	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	NM_026031	0.006	-1.54
1420909_at	Vegfa	vascular endothelial growth factor A	NM_001025250 /// NM_00102	0.044	-1.52
1455299_at	Vgll3	vestigial like 3 (Drosophila)	NM_028572 /// XM_00148040	0.005	-1.58
1428811_at	Wfikkn2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin doma	NM_181819	0.027	1.67
1421054_at	Xpo4	exportin 4	NM_020506	0.047	1.58
1434298_at	Zeb2	zinc finger E-box binding homeobox 2	NM_015753	0.028	-1.81
1425010_at	Zfp119	zinc finger protein 119	NM_144546	0.006	-1.50
1454885_at	Zfp141	zinc finger protein 141	XM_485924 /// XM_916641	0.009	-1.50
1460085_at	Zfp281	Zinc finger protein 281	NM_001160251 /// NM_17764	0.005	-1.52
1444352_at	Zfp287	zinc finger protein 287	NM_133208	0.007	-1.71
1444528_at	Zfp316	zinc finger protein 316	NM_017467	0.001	1.65
1455638_at	Zfp319	zinc finger protein 319	NM_024467	0.006	-1.74
1458003_at	Zfp398	zinc finger protein 398	NM_027477 /// NM_173034	0.020	1.72
1450929_at	Zfp57	zinc finger protein 57	NM_001013745 /// NM_00116	0.042	1.56
1419787_a_at	Zfp628	zinc finger protein 628	NM_170759	0.008	1.60
1438140_a_at	Zfp64	zinc finger protein 64	NM_009564	0.000	1.52
1435916_at	Zfp84	zinc finger protein 84	NM_023750 /// XM_00148014	0.005	-1.54
1443640_at	Zfp882	zinc finger protein 882	NM_001166645 /// XM_90423	0.033	-1.57
1438737_at	Zic3	zinc finger protein of the cerebellum 3	NM_009575	0.014	-1.59
1452610_at	Zkscan14	zinc finger with KRAB and SCAN domains 14	NM_023322	0.004	1.59
1437892_at	Zkscan3	zinc finger with KRAB and SCAN domains 3	NM_001145778 /// NM_02368	0.040	-1.66

1431259_at	Zscan29	zinc finger SCAN domains 29	NM_178889 /// XM_00148055	0.016	-1.70
1417240_at	Zyx	zyxin	NM_011777	0.010	1.63

Supplemental Table 3.
Gene expression differences in wild type and Gnb5 KO mice common to both cerebellar and non-cerebellar regions.

Affymetrix Gene Chip Probe set ID	Gene Symbol	Gene Title	RefSeq Transcript ID	p-value (KO vs. WT) Cerebellar	Fold-Change (KO vs. WT) Cerebellar	p-value (KO vs. WT) Non-cerebellar	Fold-Change (KO vs. WT) Non-cerebellar
1449895_at	Acr	acrosin prepropeptide	NM_013455	0.014	1.78	0.003	1.61
1458613_at	Arrdc1	arrestin domain containing 1	NM_001162485 /// NM_17840	0.020	1.53	0.049	1.72
1424759_at	Arrdc4	arrestin domain containing 4	NM_001042592 /// NM_02554	0.005	2.21	0.004	2.22
1455851_at	Bmp5	bone morphogenetic protein 5	NM_007555	0.010	-1.66	0.001	-1.86
1459610_at	C87490	expressed sequence C87490	---	0.021	1.59	0.002	1.69
1453482_at	Cflar	CASP8 and FADD-like apoptosis regulator	NM_009805 /// NM_207653	0.008	2.35	0.001	1.77
1426684_at	Cnot6	CCR4-NOT transcription complex, subunit 6	NM_212484	0.026	-1.59	0.019	-1.55
1434411_at	Col12a1	collagen, type XII, alpha 1	NM_007730	0.001	-4.27	0.000	-4.22
1435132_at	Disp1	dispatched homolog 1 (Drosophila)	NM_026866	0.027	1.84	0.039	1.59
1418294_at	Epb4.1l4b	erythrocyte protein band 4.1-like 4b	NM_019427 /// XM_00147616	0.006	2.00	0.008	1.54
1438427_at	Fam120b	family with sequence similarity 120, member B	NM_024203 /// NR_033586	0.009	1.89	0.002	1.71
1448021_at	Fam46c	family with sequence similarity 46, member C	NM_001142952 /// XR_00153	0.005	-4.15	0.008	-1.57
1436550_at	Fbxo30	F-box protein 30	NM_001168297 /// NM_02796	0.014	-1.88	0.004	-1.57
1418323_at	Fem1b	feminization 1 homolog b (C. elegans)	NM_010193	0.012	2.02	0.000	1.69
1416693_at	Foxc2	forkhead box C2	NM_013519	0.001	-1.58	0.015	-1.62
1422208_a_at	Gnb5	guanine nucleotide binding protein (G protein), beta 5	NM_010313 /// NM_138719	0.000	-40.76	0.000	-49.11
1425138_at	Guca1b	guanylate cyclase activator 1B	NM_146079	0.000	27.94	0.000	35.64
1427865_at	Hbb-b2	hemoglobin, beta adult minor chain	NM_016956	0.010	-1.51	0.031	-1.60
1438247_at	Klhl15	kelch-like 15 (Drosophila)	NM_001039059 /// NM_00103	0.035	1.59	0.018	1.68
1416632_at	LOC677317 /// Me1	similar to NADP-dependent malic enzyme (NADP-ME) (Ma	NM_008615 /// XM_00100468	0.016	1.54	0.022	1.63
1428626_at	Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	NM_027309	0.005	1.69	0.002	1.61
1434322_at	Micall2	MICAL-like 2	NM_174850	0.024	1.70	0.044	1.74
1430798_x_at	Mrpl15	mitochondrial ribosomal protein L15	NM_001177658 /// NM_02530	0.016	2.22	0.002	2.06
1419662_at	Ogn	osteoglycin	NM_008760	0.030	-1.51	0.017	-1.65
1444029_at	Parp11	poly (ADP-ribose) polymerase family, member 11	NM_181402	0.019	2.23	0.003	2.07
1439840_at	Polb	polymerase (DNA directed), beta	NM_011130	0.006	-1.69	0.000	-1.73
1426839_at	Pold3	polymerase (DNA-directed), delta 3, accessory subunit	NM_133692	0.029	1.65	0.005	1.51
1429169_at	Rbm3	RNA binding motif protein 3	NM_001166409 /// NM_00116	0.017	-4.77	0.000	-4.00
1416355_at	Rbmx	RNA binding motif protein, X chromosome	NM_001166623 /// NM_01125	0.009	-1.64	0.004	-1.65
1436871_at	Sfrs7	splicing factor, arginine/serine-rich 7	NM_146083	0.006	1.79	0.003	1.83
1434502_x_at	Slc4a1	solute carrier family 4 (anion exchanger), member 1	NM_011403	0.021	-3.72	0.015	-1.90
1436257_at	Ss18	synovial sarcoma translocation, Chromosome 18	NM_001161369 /// NM_00116	0.044	-1.55	0.041	-1.72
1452617_at	Ssbp1	single-stranded DNA binding protein 1	NM_028358 /// NM_212468	0.036	-1.65	0.028	-1.53
1425079_at	Tm6sf2	transmembrane 6 superfamily member 2	NM_181540	0.004	-1.77	0.019	-1.65
1443619_at	Tmem30a	transmembrane protein 30A	NM_133718	0.001	-8.96	0.000	-5.72
1423088_at	Tmod3	tropomodulin 3	NM_016963	0.002	-2.03	0.000	-1.80
1438542_at	Trp53	Transformation related protein 53	NM_001127233 /// NM_01164	0.028	1.83	0.001	1.56
1425010_at	Zfp119	zinc finger protein 119	NM_144546	0.032	-1.64	0.006	-1.50
1452610_at	Zkscan14	zinc finger with KRAB and SCAN domains 14	NM_023322	0.013	1.67	0.004	1.59