

Supplementary Information

Supplemental Table 1

Primers for PCR-genotyping, QRT-PCR, and Sanger sequencing

Primer	Sequence (5'→3')	Locus	Usage	Product (bp)
<i>Ciz1_int1_F1</i>	catccaggggtcatggatt	NC_000068 32363397 - 416	Genotyping	
<i>Ciz1_int1_R1</i>	gaagggggtatggtggtag	NC_000068 32363802 - 783	Genotyping	406 (with <i>Ciz1_int1_F1</i>)
<i>V76_F</i>	cttgcaaaatggcgttacttaagc	Gene trap vector	Genotyping	292 (with <i>Ciz1_int1_R1</i>)
<i>Ciz1_Q18F</i>	aggcacagacacagacctctc	NM_028412 1080 - 1100	QRT-PCR	
<i>Ciz1_Q18R</i>	atgggggctgtgatgta	NM_028412 1160 - 1143	QRT-PCR	81 (with <i>Ciz1_Q18F</i>)
<i>Ciz1_Q31F</i>	cccagaaacaggccagaac	NM_028412 648 - 666	QRT-PCR	
<i>Ciz1_Q31R</i>	agaggcacctctgagaaga	NM_028412 720 - 701	QRT-PCR	73 (with <i>Ciz1_Q31F</i>)
<i>Ciz1_Q40F</i>	cttggggaaatacaacactcg	NM_028412 1799 - 1819	QRT-PCR	
<i>Ciz1_Q40R</i>	gtgttcaccagcgtttg	NM_028412 1911 - 1894	QRT-PCR	113 (with <i>Ciz1_Q40F</i>)
<i>Nup35_Q18F</i>	ggcctccactagtactacca	NM_027091 960 - 980	QRT-PCR	
<i>Nup35_Q18R</i>	agcatagcggctcagctcc	NM_027091 1090 - 1073	QRT-PCR	131 (with <i>Nup35_Q18F</i>)
<i>Zbtb16_Q72F</i>	agcacagggagaaccctagat	NM_001033324 3412 - 3432	QRT-PCR	
<i>Zbtb16_Q72R</i>	agctcctcccctctgctc	NM_001033324 3507 - 3490	QRT-PCR	96 (with <i>Zbtb16_Q72F</i>)
<i>Entpd4_Q64F</i>	cgacctccatcgactgaagat	NM_026174 1682 - 1703	QRT-PCR	
<i>Entpd4_Q64R</i>	ggagaagcctttgtgaaca	NM_026174 1754 - 1735	QRT-PCR	73 (with <i>Entpd4_Q64F</i>)
<i>Npy_Q9F</i>	ccgctctgcgacactacat	NM_023456 241 - 259	QRT-PCR	
<i>Npy_Q9R</i>	tgtctcagggtggatctct	NM_023456 308 - 289	QRT-PCR	68 (with <i>Npy_Q9F</i>)
<i>Mpp4_Q41F</i>	gcctctgtcgcaggaagt	NM_001164682 1904 - 1921	QRT-PCR	
<i>Mpp4_Q41R</i>	ccgctgttacctcaccac	NM_001164682 2016 - 1999	QRT-PCR	113 (with <i>Mpp4_Q41F</i>)
<i>Creld2_Q6F</i>	gcagacagcagaaggcaaa	NM_029720 1053 - 1071	QRT-PCR	
<i>Creld2_Q6R</i>	tgcccgtcacaatcctc	NM_029720 1125 - 1108	QRT-PCR	73 (with <i>Creld2_Q6F</i>)
<i>Psat1_Q21F</i>	ccggtggatgttccaagt	NM_177420 689 - 707	QRT-PCR	
<i>Psat1_Q21R</i>	ggatcctccggacaatca	NM_177420 782 - 765	QRT-PCR	94 (with <i>Psat1_Q21F</i>)
<i>Nkain2_Q58F</i>	aggctggagatctctcaaagg	NM_001013411 473 - 493	QRT-PCR	
<i>Nkain2_Q58R</i>	gggtgcacagacgtcaccat	NM_001013411 584 - 565	QRT-PCR	112 (with <i>Nkain2_Q58F</i>)
<i>Zfhx4_Q22F</i>	tcgaccttgagatccacat	NM_030708 5149 - 5168	QRT-PCR	
<i>Zfhx4_Q22R</i>	acttggtccagctttgcag	NM_030708 5220 - 5201	QRT-PCR	72 (with <i>Zfhx4_Q22F</i>)
<i>Nr4a1_Q76F</i>	agttctgccgctccaga	NM_010444 1096 - 1113	QRT-PCR	
<i>Nr4a1_Q76R</i>	ggctgtctgtccgtacaact	NM_010444 1161 - 1141	QRT-PCR	66 (with <i>Nr4a1_Q76F</i>)
<i>Opalin_Q55F</i>	tgaactttactgccatcgaa	NM_153520 91 - 112	QRT-PCR	
<i>Opalin_Q55R</i>	cagtccaatagaggaccaca	NM_153520 176 - 156	QRT-PCR	86 (with <i>Opalin_Q55F</i>)
<i>Nr4a2_Q64F</i>	tcagagcccacgtcgatt	NM_013613 1551 - 1568	QRT-PCR	
<i>Nr4a2_Q64R</i>	tagtcagggtttgctggaa	NM_013613 1623 - 1604	QRT-PCR	73 (with <i>Nr4a2_Q64F</i>)

Supplemental Table 2Hematology and serum chemistry values for *Ciz1*^{-/-} (KO) mice and *Ciz1*^{+/+} (WT) littermates (10 mo)

Index	WT-M1	WT-M2	WT-F1	WT-F2	WT (mean±SEM)	KO-M1	KO-M2	KO-F1	KO-F2	KO (mean±SEM)	Reference (M/F)
WBC (10 ³ /μl)	8.08	5.03	5.18	6.70	6.25 ± 0.72	12.49	9.42	8.46	5.03	8.85 ± 1.53	4.45-13.96 3.90-13.94
LYM (10 ³ /μl)	7.50	4.43	4.53	6.04	5.62 ± 0.73	9.72	8.44	6.5	3.6	7.05 ± 1.34	3.24-11.15 2.88-10.92
MON (10 ³ /μl)	0.07	0.04	0.26	0.05	0.10 ± 0.05	0.91	0.34	0.84	0.03	0.53 ± 0.21	0.15-0.94 0.17-0.69
NEU (10 ³ /μl)	0.51	0.56	0.39	0.61	0.52 ± 0.05	1.87	0.64	1.11	1.44	1.26 ± 0.26	0.53-3.09 0.42-2.55
LYM%	92.9	88.2	87.5	90.1	89.7 ± 1.2	78.0	89.7	76.9	70.8	78.8 ± 3.9	61.26-87.18 70.19-87.82
MON%	0.8	0.8	5.1	0.7	1.85 ± 1.08	7.2	3.5	9.9	0.6	5.30 ± 2.04	2.18-11.02 2.19-7.06
NEU%	6.4	11.0	7.5	9.1	8.49 ± 1.01	14.8	6.8	13.2	18.5	13.33 ± 2.44	7.36-28.59 7.44-22.67
RBC (10 ⁶ /μl)	9.3	9.3	9.9	9.0	9.39 ± 0.20	10.4	9.4	9.0	8.6	9.35 ± 0.38	7.14-12.20 7.37-11.50
HGB g/dl	13.0	13.1	14.5	13.3	13.46 ± 0.35	14.7	14.4	13.5	12.4	13.75 ± 0.52	10.8-19.2 10.9-18.1
HCT %	37.1	37.5	40.2	37.5	38.07 ± 0.72	42.8	39.5	37.7	36.2	39.06 ± 1.42	37.3-62.0 37.2-58.0
MCV fl	40	40	41	42	40.75 ± 0.48	41	42	42	42	41.75 ± 0.25	42.7-56.0 42.6-55.6
MCH pg	14.0	14.0	14.7	14.9	14.4 ± 0.23	14.2	15.3	15.0	14.4	14.7 ± 0.26	11.7-16.3 13.0-16.8
MCHC g/dl	35.1	34.9	36.1	35.5	35.39 ± 0.27	34.5	36.4	35.7	34.3	35.21 ± 0.51	24.6-34.9 26.0-35.9
RDWc %	18.3	18.3	18.6	17.9	18.28 ± 0.0.14	18.7	18.2	18.2	19.9	18.74 ± 0.40	15.9-20.3 16.1-21.1
PLT (10 ³ /μl)	499	675	599	471	561 ± 47	486	658	573	644	590 ± 39	841-2159 565-1849
MPV fl	6.8	7.1	7.6	6.7	7.04 ± 0.21	7.2	6.9	7.2	8.0	7.32 ± 0.24	4.3-6.1 4.3-5.6
Alkaline phosphatase	43	56	81	67	61.75 ± 8.08	50	41	82	116	72.25 ± 17.03	111-275 105-228
SGPT (ALT)	24	20	18	22	21.00 ± 1.29	20	27	31	33	27.75 ± 2.88	28-129 27-195
SGOT (AST)	55	33	48	29	41.25 ± 6.14	41	33	46	45	41.25 ± 2.95	46-392 43-397
CPK	130	154	221	23	132 ± 41	173	84	224	77	140 ± 36	NA
Albumin	2.6	2.7	2.7	2.8	2.70 ± 0.04	2.6	2.7	2.8	2.5	2.65 ± 0.06	2.8-3.8 2.4-4.3
Total protein	4.5	4.5	4.5	4.5	4.5 ± 0.0	5.0	4.8	4.9	4.5	4.8 ± 0.1	4.8-7.0 4.8-7.2
Globulin	1.9	1.8	1.8	1.7	1.80 ± 0.04	2.4	2.1	2.1	2.0	2.15 ± 0.09	NA
Total bilirubin	0.1	0.1	0.1	0.1	0.1 ± 0.0	0.1	0.1	0.1	0.1	0.1 ± 0.0	0.2-0.6 0.2-0.6
BUN	27	30	22	28	26.75 ± 1.70	26	28	28	24	26.5 ± 0.96	7-28 5-26
Creatinine	0.1	0.1	0.1	0.1	0.1 ± 0.0	0.1	0.1	0.1	0.1	0.1 ± 0.0	0.2-0.5 0.2-0.5
Cholesterol	99	78	80	96	88.25 ± 5.39	108	114	76	71	92.25 ± 10.94	69-169 55-164
Glucose	237	237	279	210	240.8 ± 14.3	218	215	191	156	195.0 ± 14.3	172-372 177-348
Calcium	9.1	8.9	9.1	9.0	9.03 ± 0.05	9.3	9.2	9.3	9.6	9.35 ± 0.09	9.7-12.5 9.7-12.3
Phosphorus	5.6	5.5	7.2	6.6	6.23 ± 0.41	6.4	6.6	6.5	6.4	6.48 ± 0.05	5.9-14.5 5.3-13.5
Bicarbonate	20	19	15	22	19.00 ± 1.47	23	23	19	21	21.50 ± 0.96	NA
Chloride	106	108	108	109	107.8 ± 0.6	106	107	110	112	108.8 ± 1.4	96.7-129.8 96.9-134.0
Potassium	4.3	3.9	3.9	3.2	3.83 ± 0.23	4.0	3.9	3.5	4.6	4.00 ± 0.23	5.3-11.2 5.3-10.8
Sodium	147	150	146	147	147.5 ± 0.9	152	150	147	149	149.5 ± 1.0	145.2-176.2 147.5-181.2

NA, reference ranges not available. SEM, standard error of the mean.

Supplemental Table 3Genes significantly up- and down-regulated in *Ciz1*^{-/-} mice

Affymetrix Cluster ID	Gene Symbol	Gene Description	Fold Change (FC≥1.25; p<0.05)
17478817	<i>Gm22228</i>	Predicted gene 22228	1.250
17223509	<i>Mpp4</i>	Membrane protein, palmitoylated 4	1.251
17219758	<i>Olfir248</i>	Olfactory receptor 248	1.254
17294402	<i>Zfp72</i>	Zinc finger protein 72	1.257
17407240	<i>Rps27</i>	Ribosomal protein S27	1.257
17254166	<i>Slfn2</i>	Schlafen2	1.257
17346069	<i>Zfp119b</i>	Zinc finger protein 119b	1.258
17543639	<i>Gm25828</i>	Predicted gene 25828	1.259
17494254	<i>Olfir66</i>	Olfactory receptor 66	1.260
17459341	<i>Igkv2-109</i>	Immunoglobulin kappa variable 2-109	1.262
17291337	<i>Gm11346</i>	X-linked lymphocyte-regulated 5 pseudogene	1.265
17216721	<i>Gm24547</i>	Predicted gene 24547	1.266
17344953	<i>Crisp1</i>	Cysteine-rich secretory protein 1	1.267
17548213	<i>Wdr83os</i>	WD repeat domain 83 opposite strand	1.268
17548454	<i>Tomm5</i>	Translocase of outer mitochondrial membrane 5 homolog (yeast)	1.268
17341392	<i>Zfp947</i>	Zinc finger protein 947	1.269
17476698	<i>Gm12766</i>	Predicted gene 12766	1.270
17236150	<i>Ascl4</i>	Achaete-Scute complex homolog 4 (Drosophila)	1.271
17477369	<i>Klk1b3</i>	kallikrein1-relatedpeptidaseb3	1.272
17508984	<i>Gm23531</i>	Predicted gene 23531	1.275
17417821	<i>Olfir1331</i>	Olfactory receptor 1331	1.276
17372810	<i>Olfir1076</i>	Olfactory receptor 1076	1.277
17340548	<i>Tmem181b-ps</i>	Transmembrane protein 181B, pseudogene	1.278
17212872	<i>Gm24053</i>	Predicted gene 24053	1.278
17351321	<i>Mir122a</i>	MicroRNA 122a	1.280
17547859	<i>Wdr83os</i>	WD repeat domain 83 opposite strand	1.281
17550304	<i>Gm10999</i>	Predicted gene 10999	1.285
17458514	<i>Npy</i>	Neuropeptide Y	1.285
17490274	<i>Spib</i>	Spi-B transcription factor (Spi-1/PU.1 related)	1.296
17542727	<i>LOC100503280</i>	L antigen family member 3-like	1.297
17477331	<i>Klk1b27</i>	kallikrein1-related peptidase b27	1.303
17262241	<i>9930111J21Rik2</i>	RIKEN cDNA 9930111J21gene 2	1.304
17424928	<i>Gm8069</i>	Predicted pseudogene 8069	1.306
17520156	<i>Gm26611</i>	Predicted gene 26611	1.306
17462738	<i>Clec4a3</i>	C-type lectin domain family 4, member A3	1.306
17477002	<i>Vmn2r60</i>	Vomer nasal 2, receptor 60	1.310
17412717	<i>Gm22732</i>	Predicted gene 22732	1.315
17353356	<i>Gm22814</i>	Predicted gene 22814	1.316
17467466	<i>Igkv4-55</i>	Immunoglobulin kappa variable 4-55	1.317

17400220	<i>Gm22301</i>	Predicted gene 22301	1.317
17543102	<i>Gm24812</i>	Predicted gene 24812	1.318
17494418	<i>Trim30e-ps1</i>	Tripartite motif-containing 30E, pseudogene 1	1.318
17285834	<i>Hist1h2bg</i>	Histone cluster 1, H2bg	1.322
17385363	<i>Gm23315</i>	Predicted gene 23315	1.322
17301615	<i>Entpd4</i>	Ectonucleoside triphosphate diphosphohydrolase 4	1.339
17301647	<i>Entpd4</i>	Ectonucleoside triphosphate diphosphohydrolase 4	1.348
17349902	<i>Pcdhb11</i>	Proto cadherin beta 11	1.356
17284498	<i>Ighv10-1</i>	Immunoglobulin heavy variable 10-1	1.365
17487533	<i>Vmn1r103</i>	Vomer nasal 1 receptor 103	1.372
17299135	<i>Gm21991</i>	Predicted gene 21991	1.384
17346001	<i>Mrps36-ps1</i>	Mitochondrial ribosomal protein S36, pseudogene 1	1.388
17330649	<i>Gm17783</i>	Predicted gene 17783	1.398
17387758	<i>Olf1128</i>	olfactoryreceptor1128	1.402
17231617	<i>Gm23601</i>	Predicted gene 23601	1.403
17352345	<i>Gm25418</i>	Predicted gene 25418	1.405
17526707	<i>Zbtb16</i>	Zinc finger and BTB domain containing 16	1.409
17547846	<i>Gm21464</i>	Predicted gene 21464	1.414
17424217	<i>Gm26084</i>	Predicted gene 26084	1.417
17536233	<i>Gm5941</i>	Predicted gene5941	1.417
17547837	<i>Gm21464</i>	Predicted gene 21464	1.420
17550582	<i>mt-Tp</i>	Mitochondrially encoded tRNA proline	1.422
17337570	<i>Olf1108</i>	Olfactory receptor 108	1.434
17397555	<i>Gm24851</i>	Predicted gene 24851	1.436
17537906	<i>Kir3dl1</i>	Killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	1.449
17337595	<i>Olf1122</i>	Olfactory receptor 122	1.463
17258642	<i>Snord1b</i>	Small nucleolar RNA,C/Dbox1B	1.466
17355133	<i>Gm24679</i>	Predicted gene 24679	1.475
17266967	<i>Ccl3</i>	Chemokine (C-Cmotif) ligand 3	1.476
17532653	<i>mt-Tp</i>	Mitochondrially encoded tRNA proline	1.478
17495368	<i>Nup35</i>	nucleoporin35	1.481
17291019	<i>Hist1h4m</i>	histonecluster1,H4m	1.486
17532643	<i>mt-Tc</i>	Mitochondrially encoded tRNA cysteine	1.494
17550558	<i>mt-Tc</i>	Mitochondrially encoded tRNA cysteine	1.494
17510624	<i>Gm22544</i>	Predicted gene 22544	1.495
17532645	<i>mt-Ty</i>	Mitochondrially encoded tRNA tyrosine	1.495
17285780	<i>Gm11314</i>	predictedgene11314	1.542
17467537	<i>LOC637260</i>	IgkappachainV-IVregionB17precursor-like	1.560
17550560	<i>mt-Ty</i>	Mitochondrially encoded tRNA tyrosine	1.563
17547840	<i>Gm10325</i>	Predicted gene 10325	1.576
17549910	<i>Tomm5</i>	Translocase of outer mitochondrial membrane 5 homolog (yeast)	1.593
17532641	<i>mt-Tn</i>	Mitochondrially encoded tRNA asparagine	1.596

17532635	<i>mt-Tt</i>	Mitochondrially encoded tRNA threonine	1.612
17526657	<i>Gm22805</i>	Predicted gene 22805	1.623
17547835	<i>Gm20236</i>	Predicted gene 20236	1.637
17547844	<i>Gm20236</i>	Predicted gene 20236	1.637
17550580	<i>mt-Tt</i>	Mitochondrially encoded tRNA threonine	1.730
17383886	<i>1110008P14Rik</i>	RIKEN cDNA 1110008P14 gene	1.762
17290666	<i>Prl2c3</i>	Prolactinfamily2, subfamily c, member 3	1.941
17290674	<i>Prl2c2</i>	Prolactinfamily2, subfamily c, member 2	1.972
17547842	<i>Gm10002</i>	Predicted gene 10002	2.536
17547849	<i>Gm10002</i>	Predicted gene 10002	2.536
17395969	<i>Gm23237</i>	Predicted gene 23237	2.652
17550158	<i>Gm23237</i>	Predicted gene 23237	2.652
17308165	<i>Gm21464</i>	Predicted gene 21464	3.143
17369789	<i>Ciz1</i>	CDKN1A interacting zinc finger protein 1	-3.111
17546762	<i>Mid1</i>	Midline1	-2.023
17478459	<i>Slc17a6</i>	Solute carrier family 17(sodium-dependent inorganic phosphate co-transporter), member 6	-1.938
17546215	<i>Gm15726</i>	Predicted gene 15726	-1.903
17237336	<i>Kcnc2</i>	Potassium voltage gated channel, Shaw-related subfamily, member 2	-1.604
17443801	<i>Gm22956</i>	Predicted gene 22956	-1.600
17385374	<i>Nr4a2</i>	Nuclear receptor subfamily 4, group A, member 2	-1.597
17381774	<i>C1q3</i>	C1q-like3	-1.531
17233022	<i>Cd24a</i>	CD24a antigen	-1.518
17486261	<i>Vmn2r41</i>	Vomer nasal 2, receptor 41	-1.463
17304512	<i>Gm24916</i>	Predicted gene 24916	-1.403
17492858	<i>Gm10160</i>	Predicted gene 10160	-1.392
17389608	<i>Meis2</i>	Meis homeobox 2	-1.378
17298654	<i>Gm25498</i>	Predicted gene 25498	-1.369
17529640	<i>Ankrd34c</i>	Ankyrin repeat domain 34C	-1.369
17364588	<i>Opalin</i>	Oligodendrocytic myelin paranodal and inner loop protein	-1.367
17315178	<i>Nr4a1</i>	Nuclear receptor subfamily 4, group A, member 1	-1.358
17299869	<i>Trav9d-4</i>	T-cell receptor alpha variable 9D-4	-1.350
17536420	<i>Gpr165</i>	G-protein-coupled receptor 165	-1.346
17525088	<i>Gm25346</i>	Predicted gene 25346	-1.341
17395985	<i>Zfx4</i>	Zinc finger homeodomain 4	-1.340
17282098	<i>Gm22696</i>	Predicted gene 22696	-1.327
17467418	<i>Igkv4-79</i>	Immunoglobulin kappa variable 4-79	-1.324
17236892	<i>Gad1-ps</i>	Glutamate decarboxylase 1, pseudogene	-1.321
17542062	<i>Mir743</i>	Micro RNA 743	-1.319
17472288	<i>Lmo3</i>	LIM domain only 3	-1.311
17471648	<i>Klra5</i>	Killer cell lectin-like receptor, subfamily A, member 5	-1.302
17502084	<i>Mir1969</i>	Micro RNA 1969	-1.300
17548294	<i>Gm10931</i>	Predicted gene 10931	-1.293

17548498	<i>Gm10931</i>	Predicted gene 10931	-1.293
17441524	<i>Hrk</i>	Harakiri, BCL2 interacting protein (contains only BH3 domain)	-1.289
17484266	<i>C030029H02Rik</i>	RIKEN Cdna C030029H02 gene	-1.288
17516410	<i>Mirlet7a-2</i>	Micro RNA let7a-2	-1.286
17550428	<i>Neat1</i>	Nuclear paraspeckle assembly transcript1 (non-proteinencoding)	-1.283
17358598	<i>Il33</i>	Interleukin 33	-1.281
17391332	<i>Mal</i>	Myelin and lymphocyte protein, T-cell differentiation protein	-1.281
17344822	<i>Mog</i>	Myelin oligodendrocyte glycoprotein	-1.278
17235352	<i>Gm22721</i>	Predicted gene 22721	-1.278
17418581	<i>Col8a2</i>	Collagen, type VIII, alpha 2	-1.278
17288946	<i>Mir9-2</i>	Micro RNA 9-2	-1.278
17524969	<i>Anln</i>	Anillin, actin binding protein	-1.273
17413945	<i>Nr4a3</i>	Nuclear receptor subfamily 4, group A, member 3	-1.272
17330152	<i>Gm25024</i>	Predicted gene 25024	-1.272
17550464	<i>Sox2ot</i>	SOX2 overlapping transcript (non-proteinencoding)	-1.271
17240109	<i>Nkain2</i>	Na ⁺ /K ⁺ transporting ATPase interacting 2	-1.268
17363204	<i>Psat1</i>	Phosphoserine aminotransferase 1	-1.268
17385398	<i>Ernm</i>	Ermin, ERM-like protein	-1.258
17487211	<i>Fosb</i>	FBJ osteosarcoma oncogene B	-1.255
17309366	<i>Gm23242</i>	Predicted gene 23242	-1.254
17299842	<i>Trav9n-4</i>	T-cell receptor alpha variable 9N-4	-1.254
17483190	<i>Kctd13</i>	Potassium channel tetramerisation domain containing 13	-1.254
17266627	<i>Gm24454</i>	Predicted gene 24454	-1.251
17342642	<i>Dusp1</i>	Dual specificity phosphatase 1	-1.251

Supplemental Table 4

Enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. ^aEnrichment relative to number of reference genes in the genome based on the hypergeometric test. ^bHypergeometric test based.

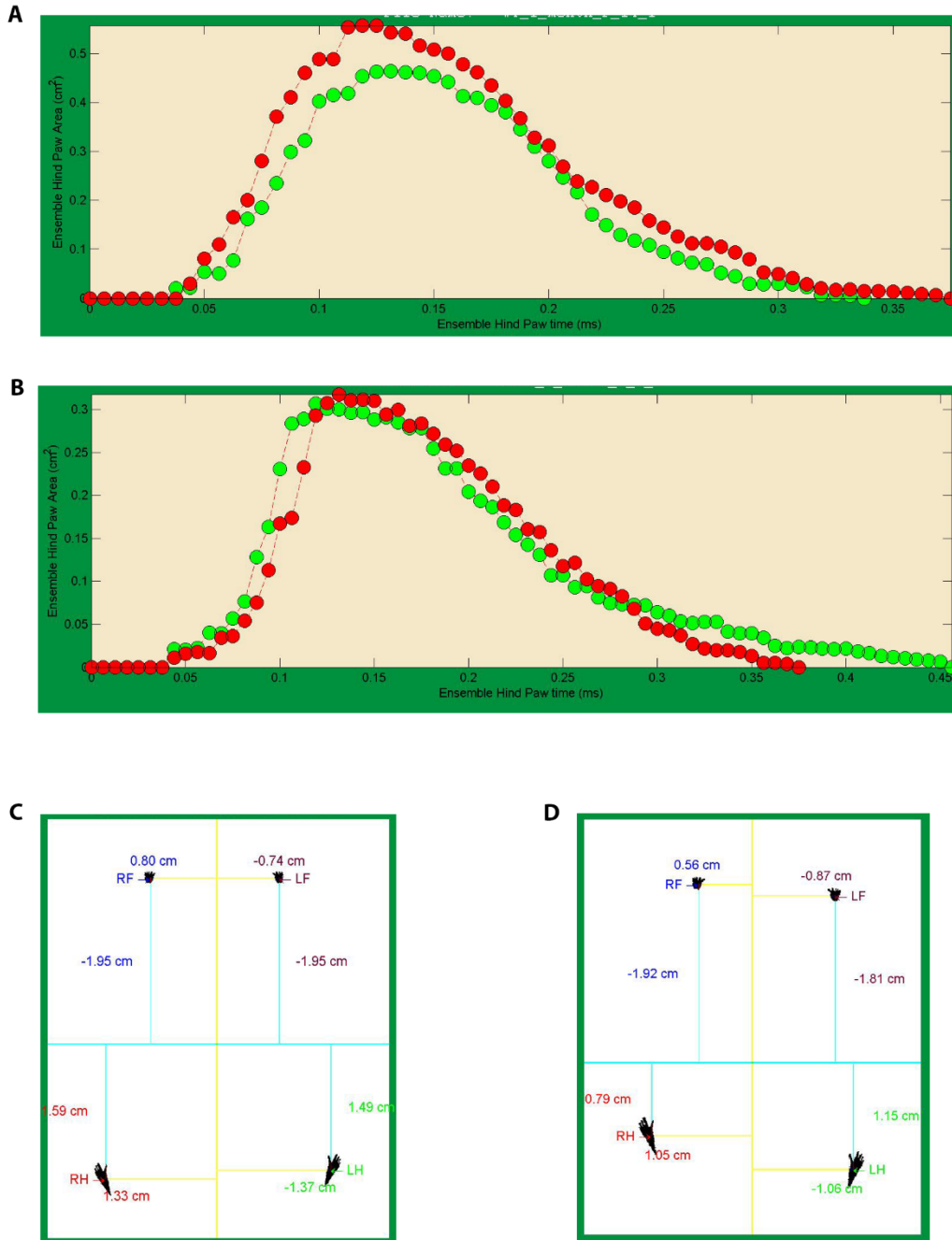
^cBenjamini & Hochberg multiple test correction.

Pathway	No. of Genes	Enrichment^a	raw P-value^b	adj P-value^c
<i>Up-regulated</i>				
Metabolic pathways	23	2.5	6.73E-05	3.70E-03
Cytokine-cytokine receptor interaction	9	4.73	1.00E-04	3.70E-03
Rheumatoid arthritis	5	7.95	4.00E-04	9.70E-03
Olfactory transduction	18	2.30	1.10E-03	2.01E-02
Cysteine and methionine metabolism	3	9.91	3.40E-03	4.96E-02
Systemic lupus erythematosus	5	4.32	6.30E-03	5.04E-02
N-Glycan biosynthesis	3	7.73	6.90E-03	5.04E-02
Small cell lung cancer	4	5.92	4.80E-03	5.04E-02
Parkinson's disease	5	4.35	6.10E-03	5.04E-02
Dilated cardiomyopathy	4	5.79	5.20E-03	5.04E-02
<i>Down-regulated</i>				
Metabolic pathways	30	2.81	5.64E-07	5.36E-05
Focal adhesion	10	5.54	1.60E-05	8.00E-04
Glycosaminoglycan biosynthesis - chondroitin sulfate	4	20.15	4.21E-05	1.20E-03
Neuroactive ligand-receptor interaction	11	4.40	5.10E-05	1.20E-03
TGF-beta signaling pathway	6	7.82	1.00E-04	1.60E-03
ECM-receptor interaction	6	7.73	1.00E-04	1.60E-03
MAPK signaling pathway	10	4.14	2.00E-04	2.70E-03
Toll-like receptor signaling pathway	6	6.58	3.00E-04	3.60E-03
B cell receptor signaling pathway	5	7.29	6.00E-04	6.30E-03
Osteoclast differentiation	6	5.64	7.00E-04	6.60E-03

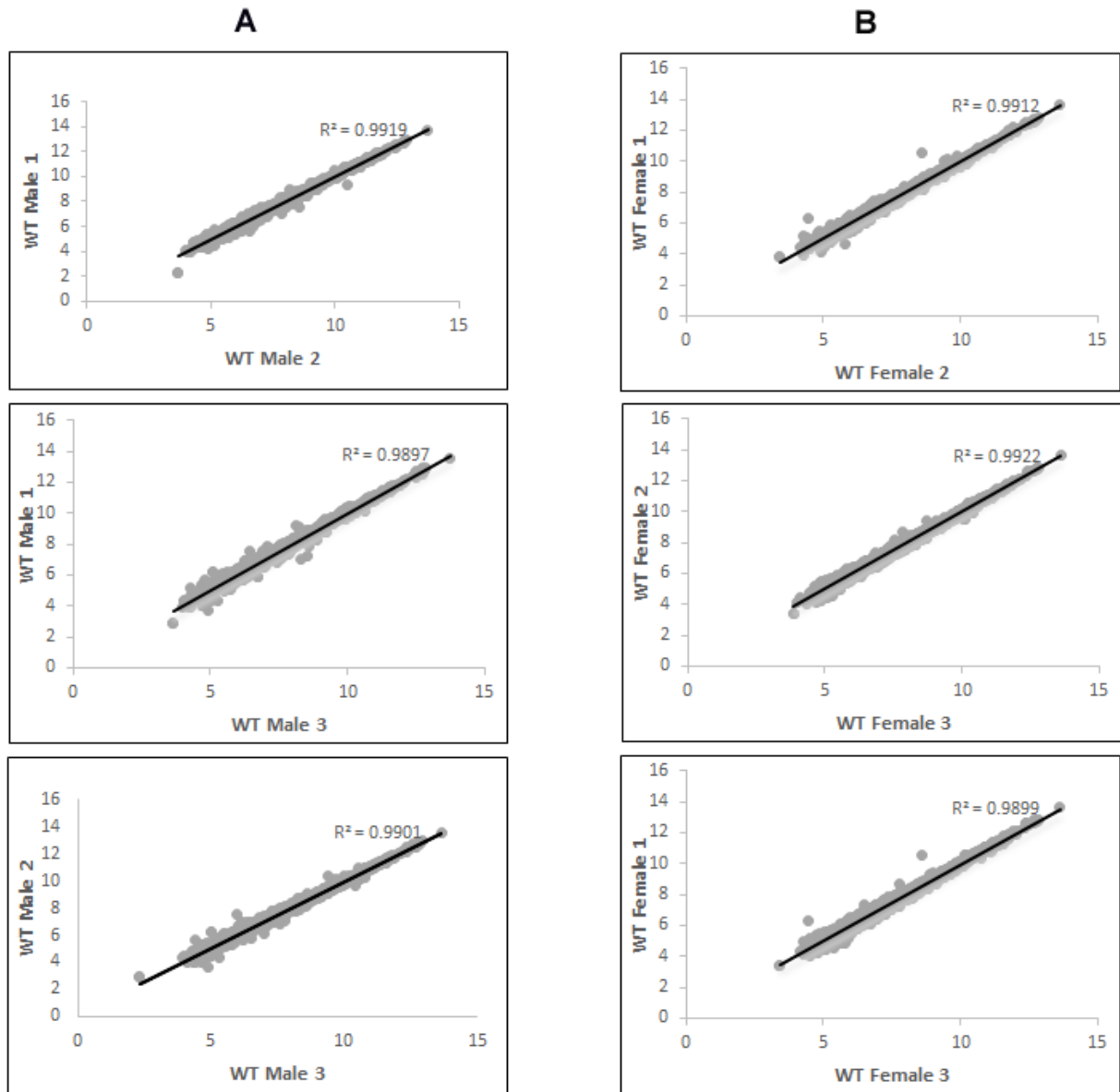
Supplemental Table 5

Ingenuity Pathway Analysis (IPA) top up- and down-regulated biological functions and canonical pathways. ^aFischer's exact test was used to calculate a p-value determining the probability that each biological function assigned to that data set is due to chance alone. ^bFischer's exact test was used to calculate a p-value determining the probability that each canonical pathway assigned to that data set is due to chance alone. ^cNumber of genes in a pathway that were found in our significant gene list compared to the total number of genes in that pathway. ^dNetwork score is the negative log of the p-value for the likelihood that network molecules would be found together by chance alone. A higher score indicates a greater statistical significance that molecules depicted in the network are interconnected.

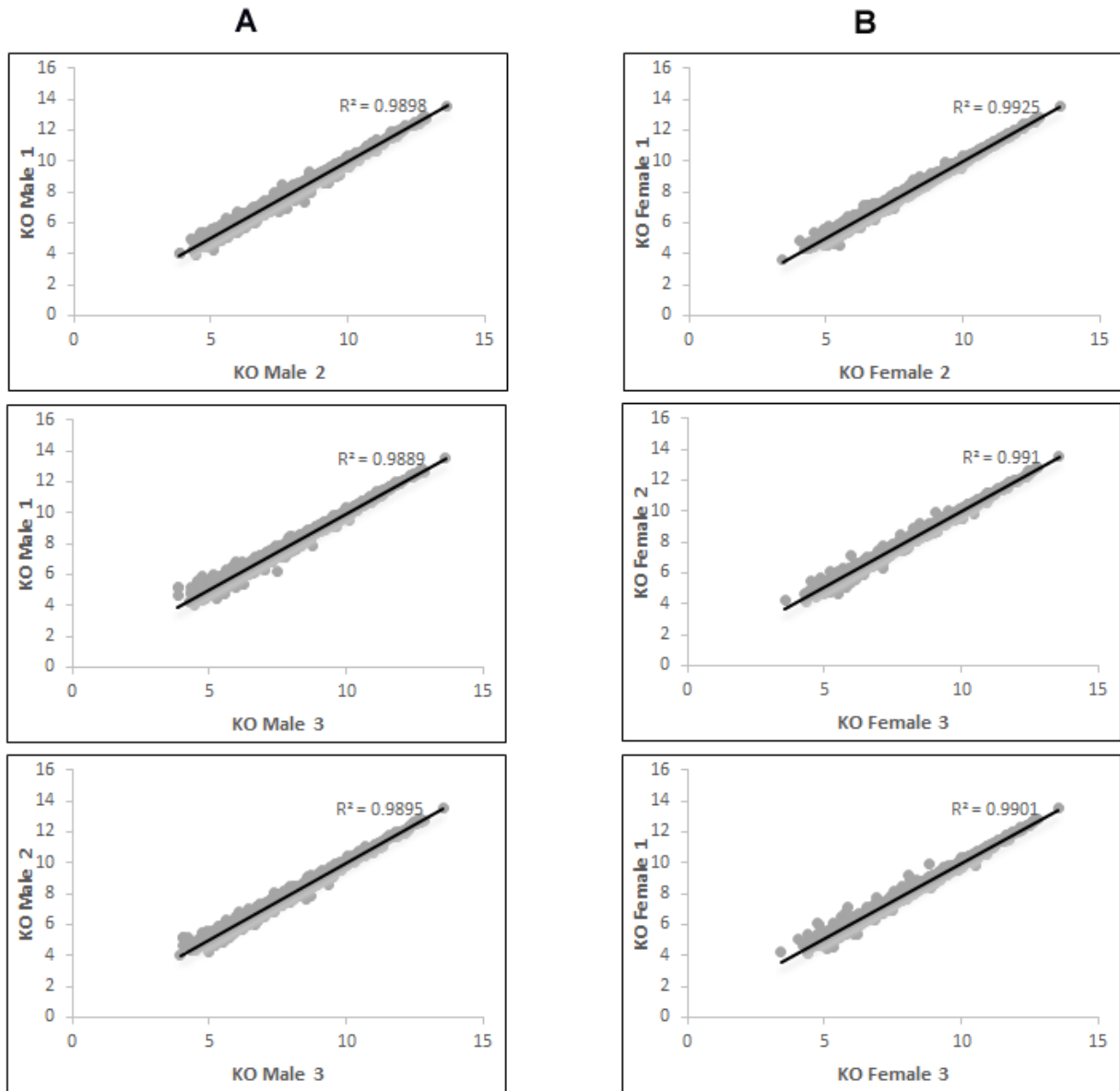
Top Up-Regulated Biological Functions		P value ^a	No. of Molecules
Molecular and Cellular Functions			
	Cellular Movement	4.74E-02 – 1.18E-05	4
	Cell Development	4.74E-02 – 2.36E-05	16
	Cellular Growth and Proliferation	4.74E-02 – 2.36E-05	17
	Cell Morphology	4.74E-02 – 1.38E-04	13
	Cell-To-Cell Signaling and Interaction	3.29E-02 – 3.34E-04	19
Physiological System Development and Function			
	Hair and Skin Development and Function	1.18E-05 – 1.18E-05	2
	Tissue Morphology	4.74E-02 – 1.18E-05	15
	Embryonic Development	4.30E-02 – 3.53E-05	7
	Lymphoid Tissue Structure and Development	4.74E-02 – 3.53E-05	9
	Organ Development	4.74E-02 – 3.53E-05	8
Top Up-Regulated Canonical Pathways		P value^b	Overlap^c
	Primary Immunodeficiency Signaling	6.16E-03	5.9%
	Crosstalk between Dendritic Cells and Natural Killer Cells	2.32E-02	2.9%
	Atherosclerosis Signaling	5.57E-02	1.8%
	B Cell Development	7.35E-02	4.5%
	Intrinsic Prothrombin Activation Pathway	8.94E-02	3.7%
ID	Associated Network Functions		Score^d
1	Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function		29
2	Protein Synthesis, Endocrine System Development and Function, Molecular Transport		19
3	Inflammatory Response, Cellular Movement, Hematological System Development and Function		13
4	DNA Replication, Recombination, and Repair, Nucleic Acid Metabolism, Small Molecule Biochemistry		2
5	Embryonic Development, Organ Development, Organismal Development		2
Top Down-Regulated Biological Functions		P value^a	No. of Molecules
Molecular and Cellular Functions			
	Cell Cycle	8.29E-03 – 6.87E-08	4
	Cellular Development	2.87E-02 – 6.87E-08	33
	Cell Death and Survival	2.58E-02 – 1.18E-06	22
	Gene Expression	2.54E-02 – 1.79E-05	12
	Cell Morphology	2.47E-02 – 1.02E-04	23
Physiological System Development and Function			
	Embryonic Development	2.87E-02 – 3.79E-06	23
	Nervous System Development and Function	2.87E-02 – 3.79E-06	22
	Organ Morphology	2.87E-02 – 3.79E-06	18
	Organismal Development	2.87E-02 – 3.79E-06	28
	Connective Tissue Development and Function	2.87E-02 – 4.42E-05	11
Top Down-Regulated Canonical Pathways		P value^b	Overlap^c
	Sulfate Activation for Sulfonation	8.29E-03	50.0%
	Neuroprotective Role of THOP1 in Alzheimer's Disease	9.27E-03	5.7%
	Serine Biosynthesis	1.65E-02	25.0%
	Superpathway of Serine and Glycine Biosynthesis I	2.47E-02	16.7%
	Acute Phase Response Signaling	2.76E-02	1.9%
ID	Associated Network Functions		Score^d
1	Cellular Development, Cellular Growth and Proliferation, Nervous System Development and Function		26
2	Cellular Development, Cellular Growth and Proliferation, Digestive System Development and Function		24
3	Cell Cycle, Cellular Development, Cell Death and Survival		17
4	Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function		8
5	Hematological System Development and Function, Hematopoiesis, Tissue Development		2



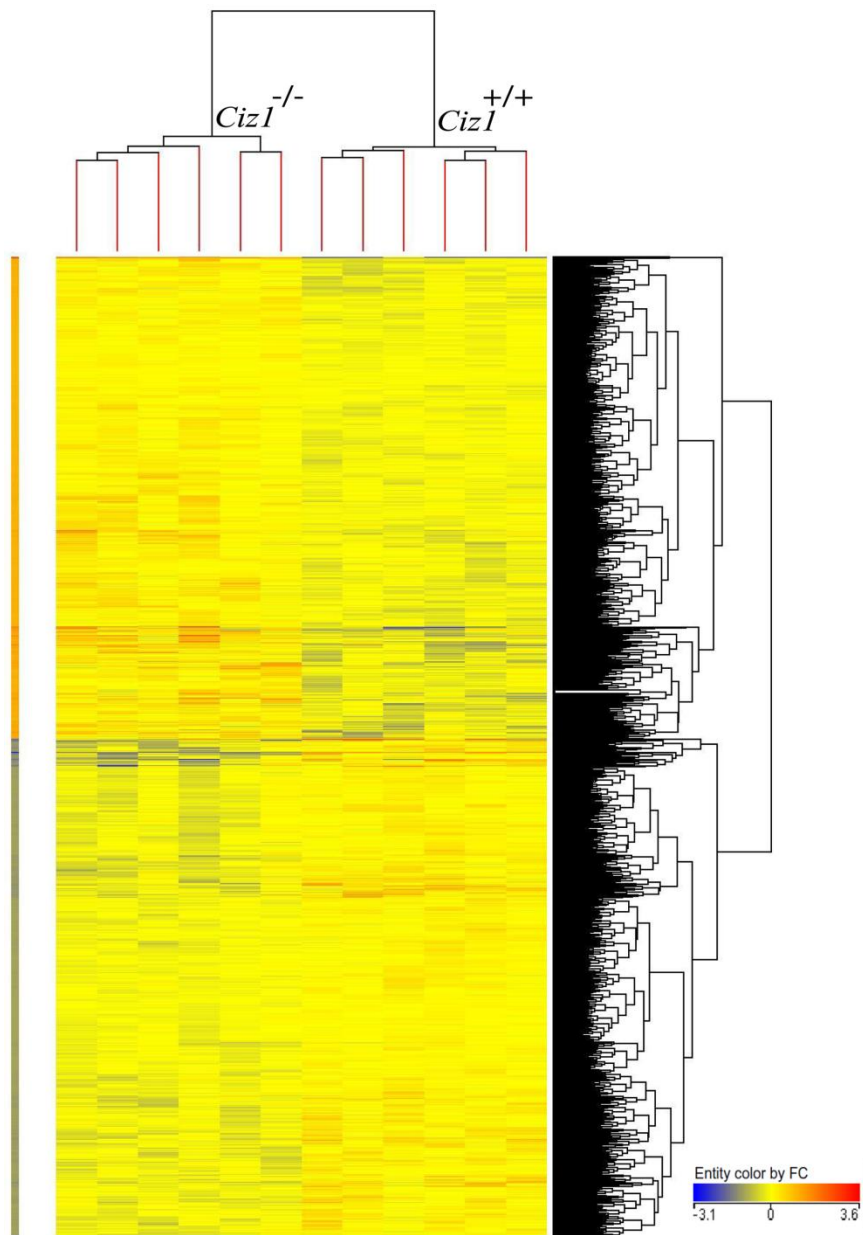
Supplemental Fig. 1. DigiGait™ data from WT (A and C) and *Ciz1*^{-/-} (B and D) mice. Left (green) and right (red). Panels C and D show automated measurements of gait parameters including paw areas, stance width and stride length. LF/RF, left/right forepaws. LH/RH, left/right hindpaws.



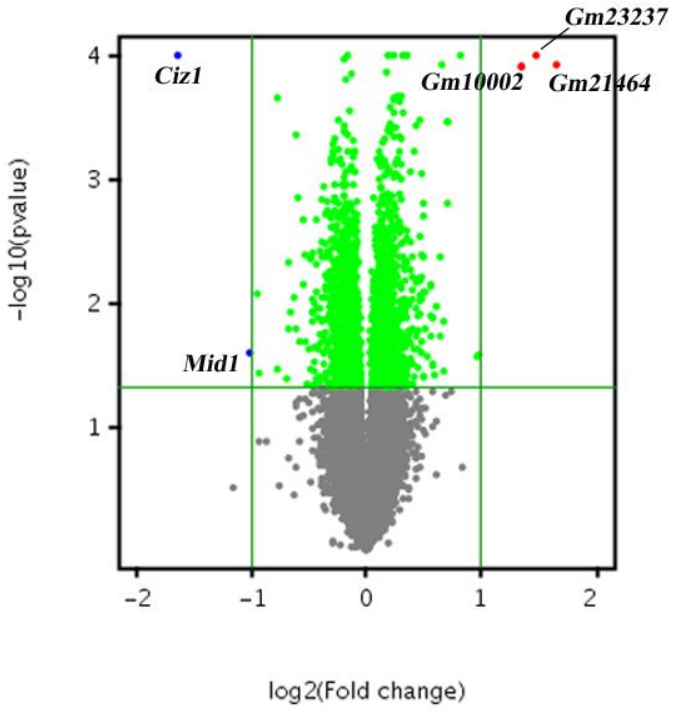
Supplemental Fig. 2. Scatter plots of filtered and normalized expression values for three male (A) and three female (B) WT mouse arrays.



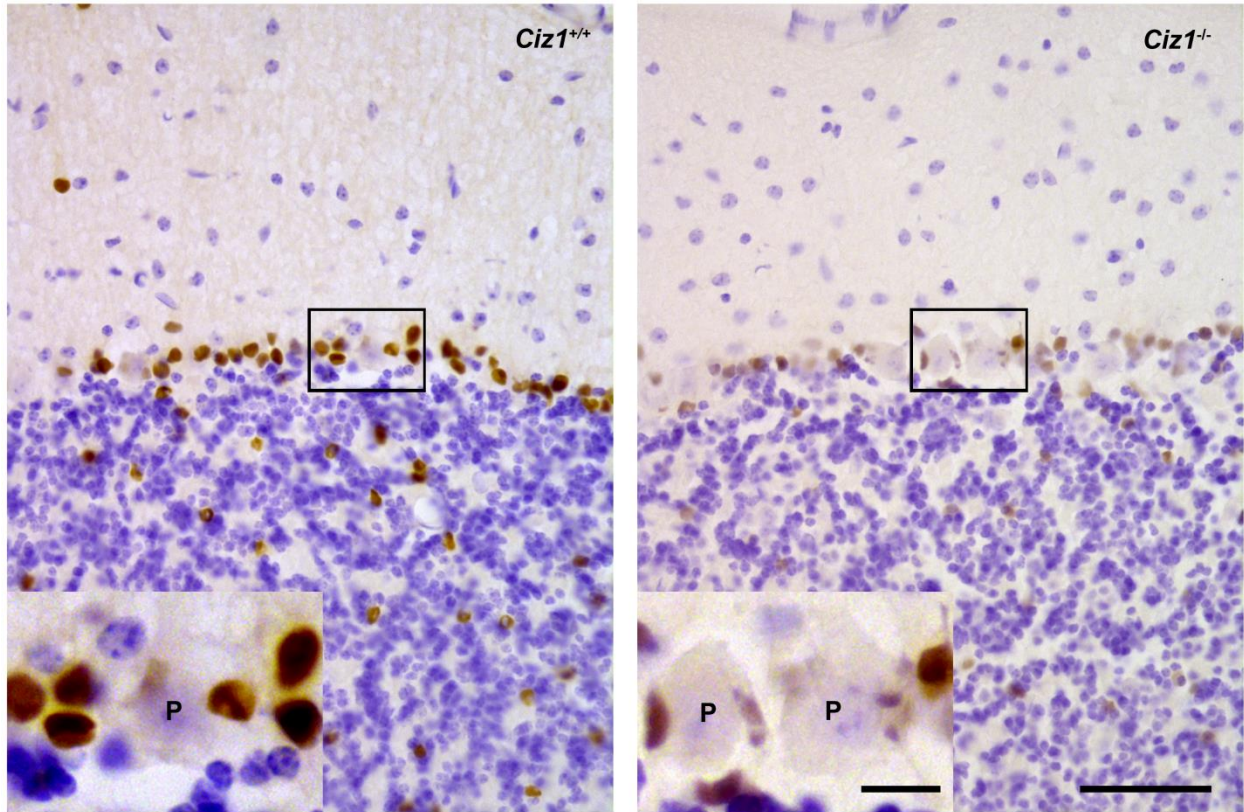
Supplemental Fig. 3. Scatter plots of filtered and normalized expression values for three male (A) and three female (B) *Ciz1*^{-/-} mouse arrays.



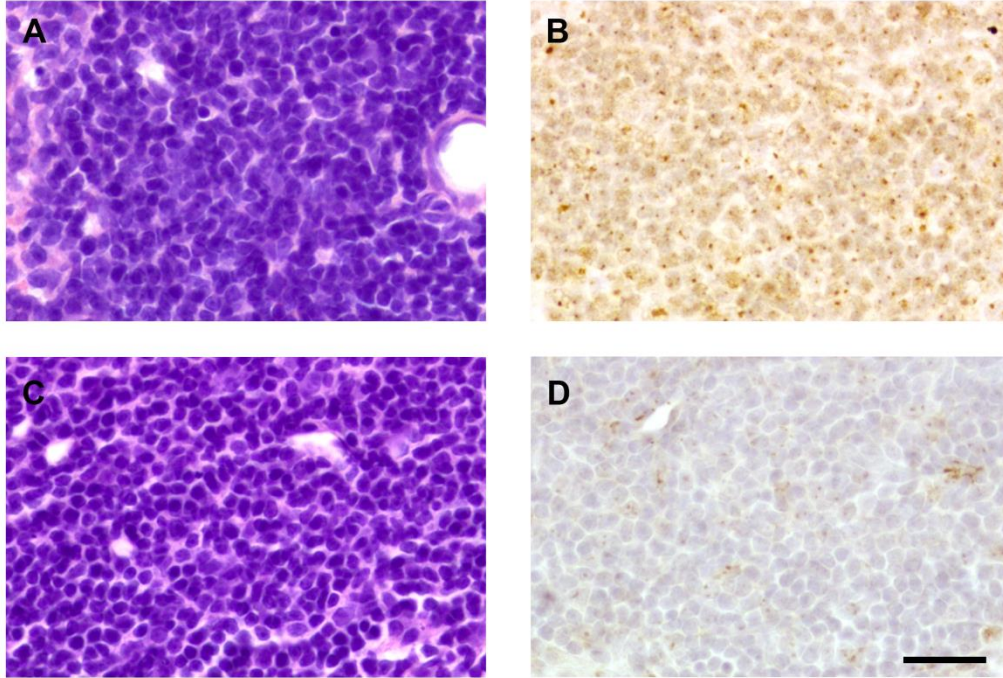
Supplemental Fig. 4. Heat map for whole-genome gene expression analysis of *Ciz1*^{-/-} mouse cerebellum (*Ciz1*^{-/-}, 3 male and 3 female mice; *Ciz1*^{+/+}, 3 male and 3 female littermates).



Supplemental Fig. 5. A volcano plot for whole-genome gene expression analysis of *Ciz1*^{-/-} mouse cerebellum (*Ciz1*^{-/-}, 3 male and 3 female mice; *Ciz1*^{+/+}, 3 male and 3 female littermates). The plot displays mean fold differences for each probe set in *Ciz1*^{+/+} and *Ciz1*^{-/-} samples as a function of *p* value. Genes showing differential expression with *p* values < 0.05 are depicted with green dots. Other genes are represented with gray dots. Red dots represent genes with > 2X up-regulation (*p* < 0.05) and blue dots represent genes with > 2X down-regulation (*p* < 0.05).



Supplemental Fig. 6. Immunohistochemistry of CIZ1 expression in cerebellum of *Ciz1*^{+/+} (WT) and *Ciz1*^{-/-} mice. P, Purkinje cell. Scale bar = 50 μ m.



Supplemental Fig. 7. Contiguous paraffin sections from *Ciz1*^{+/+} (A, B) and *Ciz1*^{-/-} (C, D) spleen stained with hematoxylin and eosin (A, C) or processed for immunohistochemical detection of CIZ1.