

## INVENTORY OF SUPPLEMENTAL INFORMATION

### Loss of TMEM106B Ameliorates Lysosomal and Frontotemporal Dementia-Related Phenotypes in Progranulin-Deficient Mice

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#### Supplemental figures

Figure S1. PGRN deficiency induces transcriptional up-regulation of TYROBP network genes (Related to Figure 1)

Figure S2. Autofluorescence in *Grn*<sup>-/-</sup> brain (Related to Figure 2)

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Figure S4. TMEM106B deficiency does not revert transcriptional changes of lysosomal genes and complement C1q in *Grn*<sup>-/-</sup> mice (Related to Figure 5 and Figure 7)

Figure S5. PGRN deficiency has no significant effects on levels of V-ATPase V0 and V1 subunits (Related to Figure 5)

Figure S6. TMEM106B deficiency causes impairment in lysosomal acidification (Related to Figure 5).

Figure S7. Chronic Bafilomycin A1 treatment decreases lysosomal proteolysis in *Grn*<sup>-/-</sup> neurons (Related to Figure 5)

Figure S8. *Tmem106b* deletion does not revert lipofuscin and CD68-positive microglial accumulation in *Grn*<sup>-/-</sup> retina (Related to Figure 7).

#### Supplemental tables

Table S1. Lysosomal DE genes (WT vs. *Grn*<sup>-/-</sup>) identified by RNASeq (Related to Figure 1)

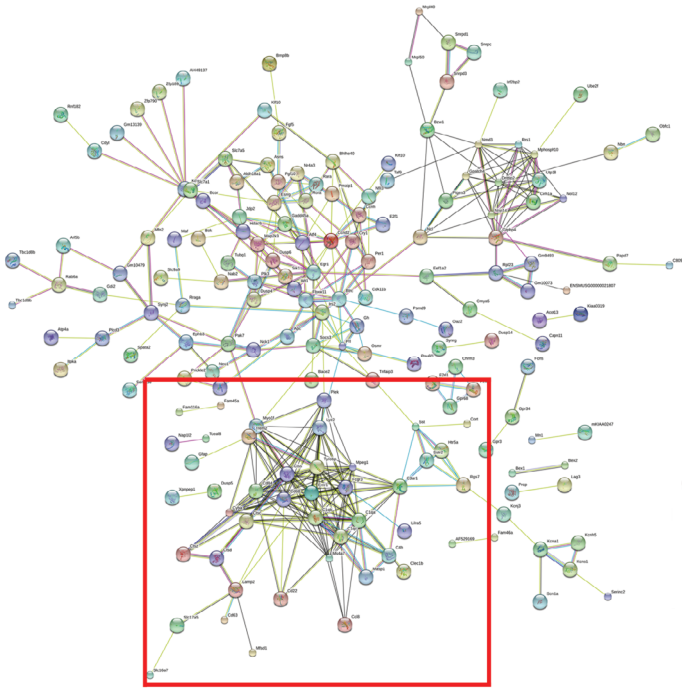
Table S2. Lysosomal DE genes (WT vs. *Grn*<sup>-/-</sup>) identified by LFQ-LCMS (Related to Figure 1)

Table S3. Transcriptional changes of typical microglial inflammatory genes and markers in *Grn*<sup>-/-</sup> by RNASeq (Related to Figure 1)

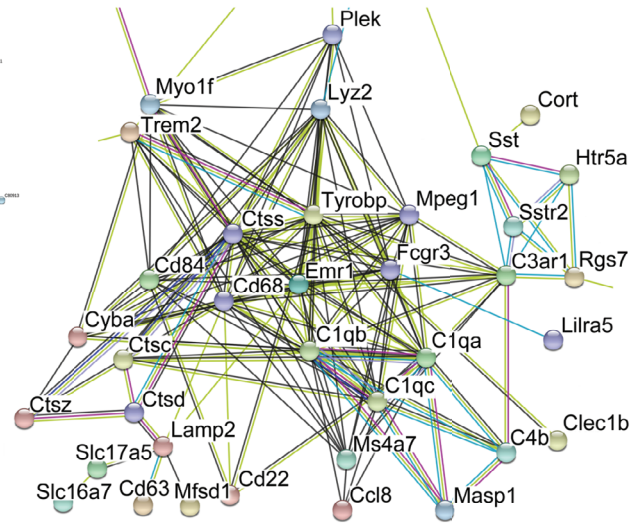
Table S4. DE genes (WT vs. *Tmem106b*<sup>-/-</sup>) identified by RNASeq (Related to Figure 3)

Table S5. Transcriptional changes of typical microglial inflammatory genes and markers and TNG in *Tmem106b*<sup>-/-</sup> by RNASeq (Related to Figure 3)

**A** STRING analysis using 347 up-regulated genes (logFC > 0.2, FDR < 0.05) in *Grn*<sup>-/-</sup> by RNASeq



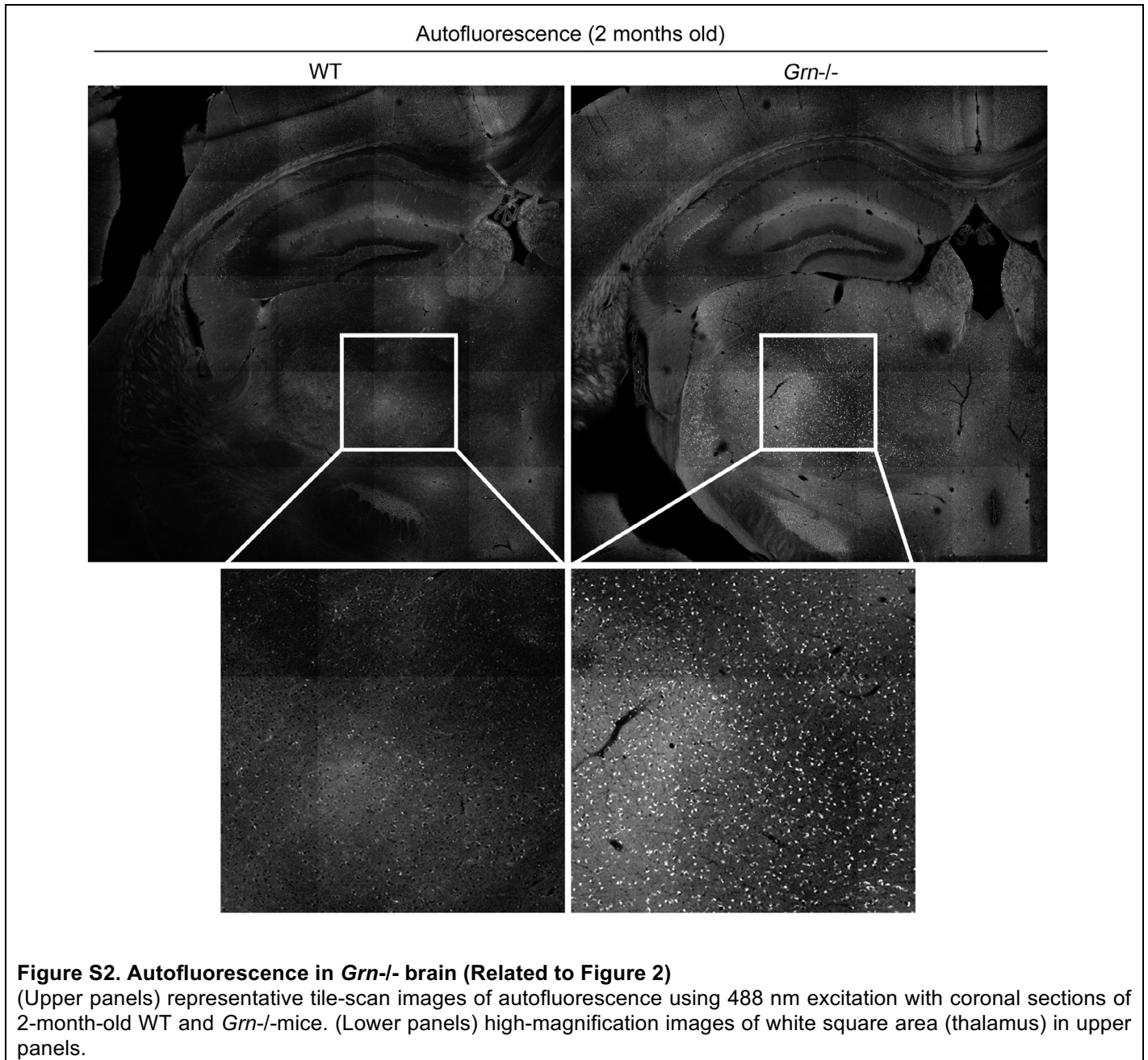
**B** TYROBP network genes (TNG)

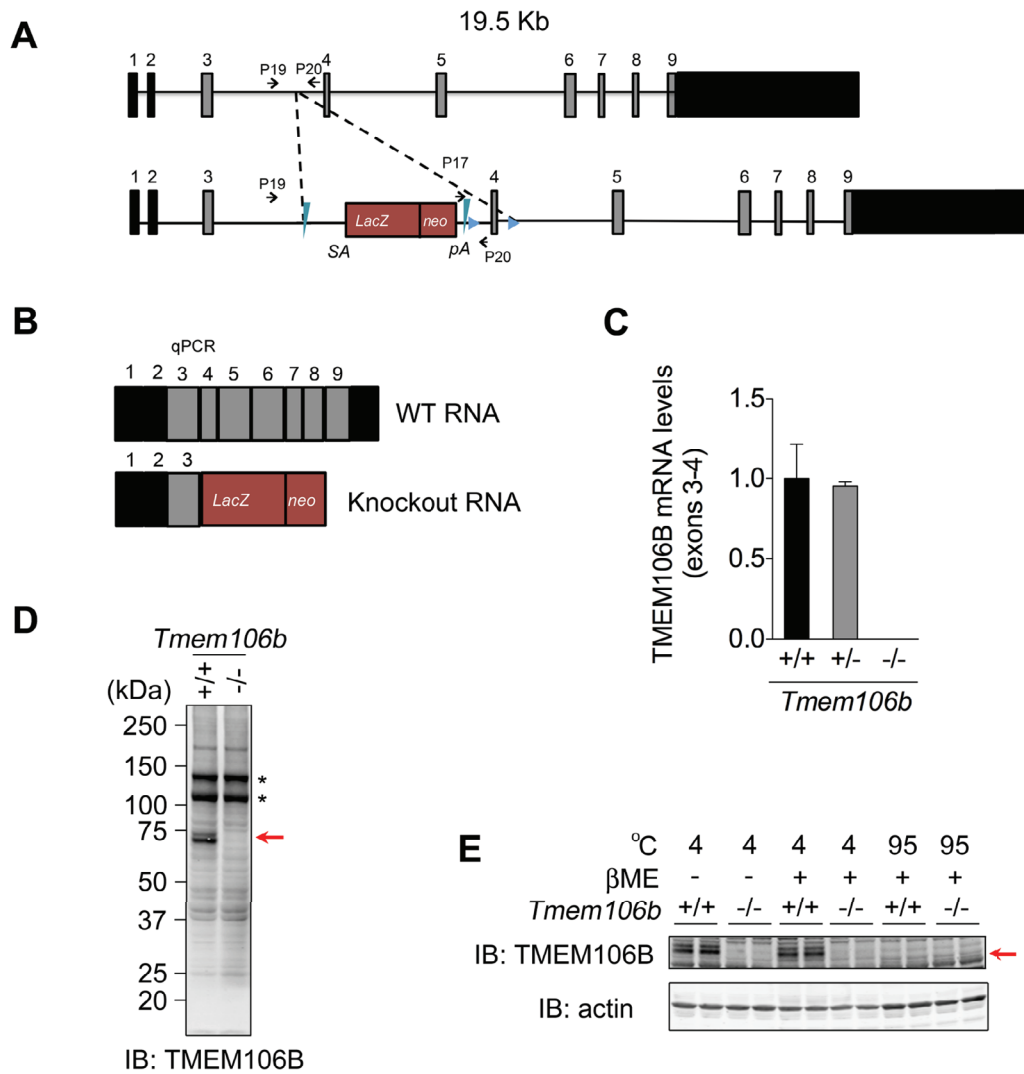


**Figure S1. PGRN deficiency induces transcriptional up-regulation of TYROBP network genes (Related to Figure 1)**

(A) Protein-protein interaction network by STRING analysis using 347 upregulated genes (logFC > 0.2, FDR < 0.05) in *Grn*<sup>-/-</sup> mice in RNASeq. A red square shows a gene cluster that consists of microglial genes.

(B) High magnification of a red square in (A) showing TYROBP network genes (TNG).

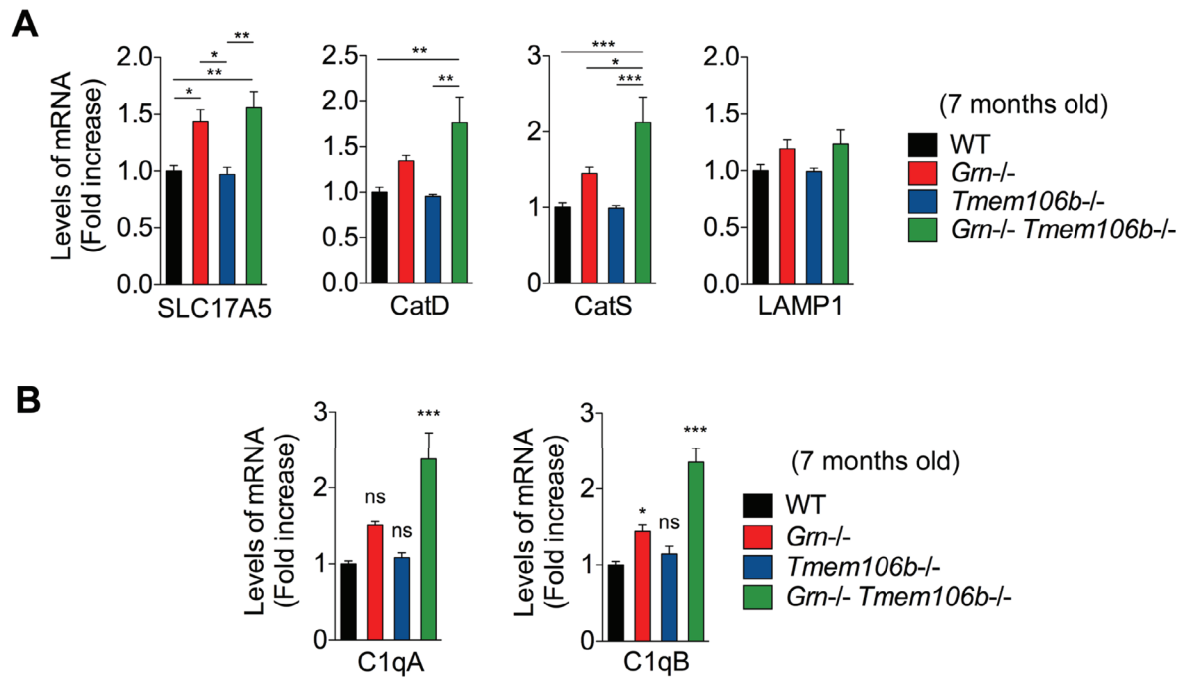




### Figure S3. Generation of *Tmem106b*<sup>-/-</sup> mice (Related to Figure 3)

- (A) Schematic drawing of the targeting strategy for the *Tmem106b* locus. Coding exons are represented in grey and non-coding exons are represented in black. LacZ and neomycin cassette is represented in red. P19 and P20 are the PCR primer pairs that amplify the WT allele and P19 and P17 are the primer pairs that amplify the knockout allele. Green triangles represent the FRT insertion. Blue arrowheads represent Lox-P sites.
- (B) RNA product from WT vs. Knockout.
- (C) Quantitative real-time PCR on total brain lysates of *Tmem106b*<sup>+/-</sup> and *Tmem106b*<sup>-/-</sup> mice with primers spanning the exon 3-4 junction showing total *Tmem106b* mRNA expression relative to WT. Mean ± sem.
- (D) Western blot analysis of WT and *Tmem106b*<sup>-/-</sup> brain lysates using anti-TMEM106B antibody. A red arrow shows bands that are knocked out in *Tmem106b*<sup>-/-</sup> brain. Asterisks show nonspecific bands.
- (E) Western blot analysis of WT and *Tmem106b*<sup>-/-</sup> brain lysates treated with 2× sample buffer with or without βME and with or without boiling for 5 min.





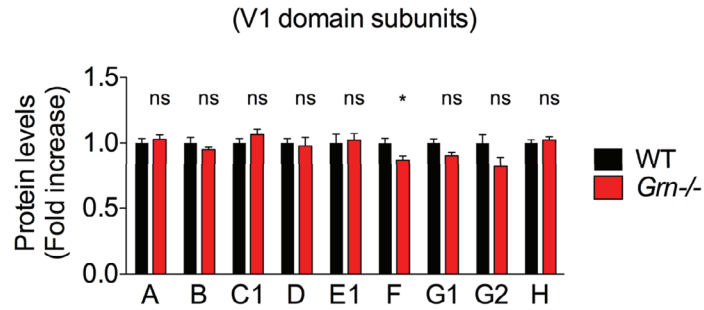
**Figure S4. TMEM106B deficiency does not revert transcriptional changes of lysosomal genes and complement C1q in *Grn*<sup>-/-</sup> mice (Related to Figure 5 and Figure 7)**

- (A) Quantitative real-time PCR analysis of transcription of SLC17A5, CatD, CatS, and LAMP1 in 7-month-old WT, *Grn*<sup>-/-</sup>, *Tmem106b*<sup>-/-</sup>, and *Grn*<sup>-/-</sup> *Tmem106b*<sup>-/-</sup> mice. Mean  $\pm$  sem, n = 3-4/genotype. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001; One-way ANOVA with Tukey's multiple comparisons *post hoc* test.
- (B) Quantitative real-time PCR analysis of transcription of C1qA and C1qB in 7-month-old WT, *Grn*<sup>-/-</sup>, *Tmem106b*<sup>-/-</sup>, and *Grn*<sup>-/-</sup> *Tmem106b*<sup>-/-</sup> mice. Mean  $\pm$  sem, n = 3-4/genotype. \*p < 0.05, \*\*\*p < 0.001; One-way ANOVA with Dunnett's *post hoc* test.

A

Gene ID	Gene name	FC	LogCPM	LR	PValue	FDR
ENSMUSG00000019302	Atp6v0a1	1.009966282	8.910329551	0.095096815	0.757794937	0.928086097
ENSMUSG00000024121	Atp6v0c	1.023190038	8.830102874	0.421199177	0.516339284	0.817472158
ENSMUSG00000013160	Atp6v0d1	1.065034459	7.812810601	5.64328608	0.017522336	0.169477331
ENSMUSG00000019087	Atp6ap1	1.045697869	8.273236365	2.024879549	0.154741192	0.509942566

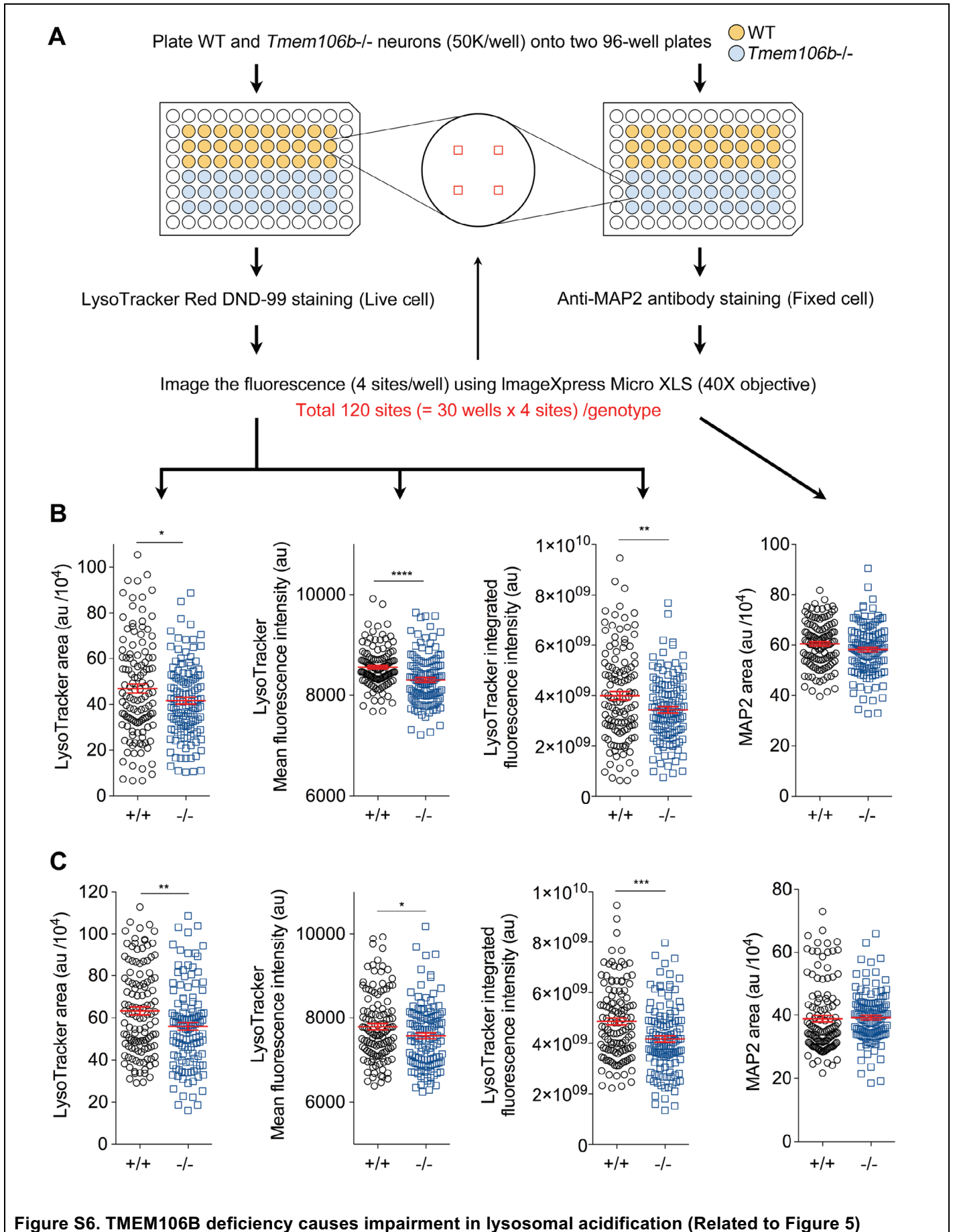
B



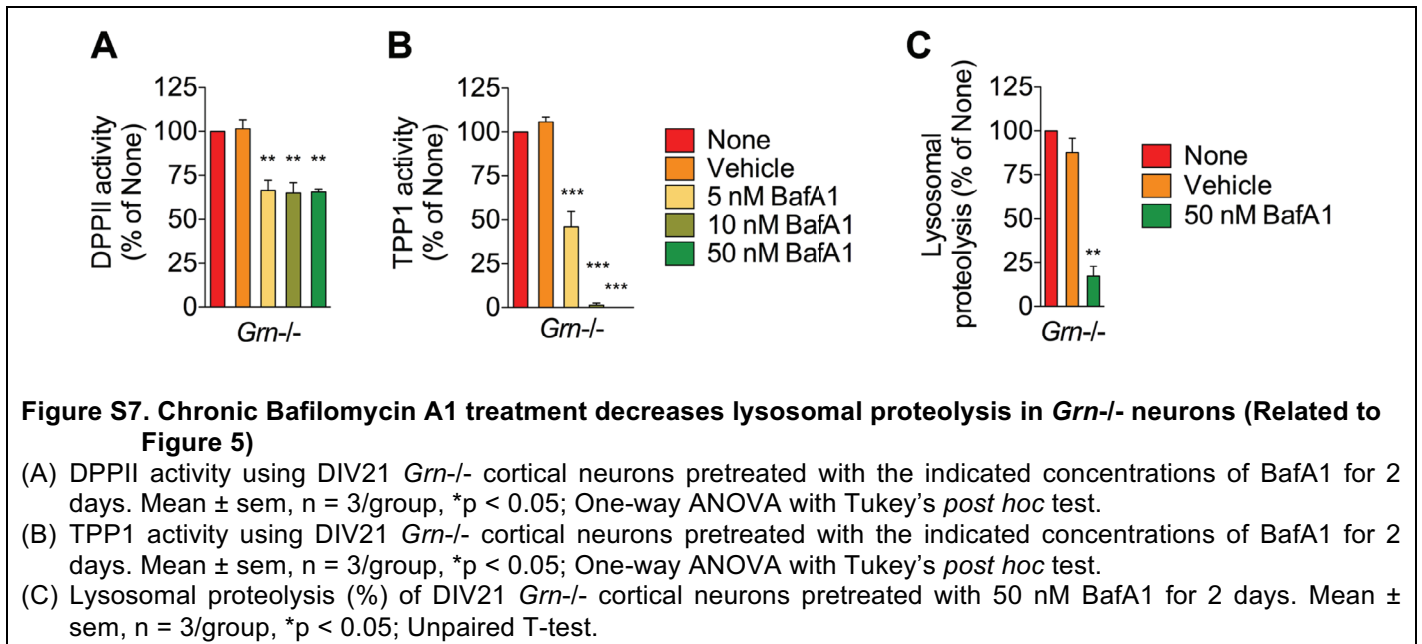
**Figure S5. PGRN deficiency has no significant effects on levels of V-ATPase V0 and V1 subunits (Related to Figure 5)**

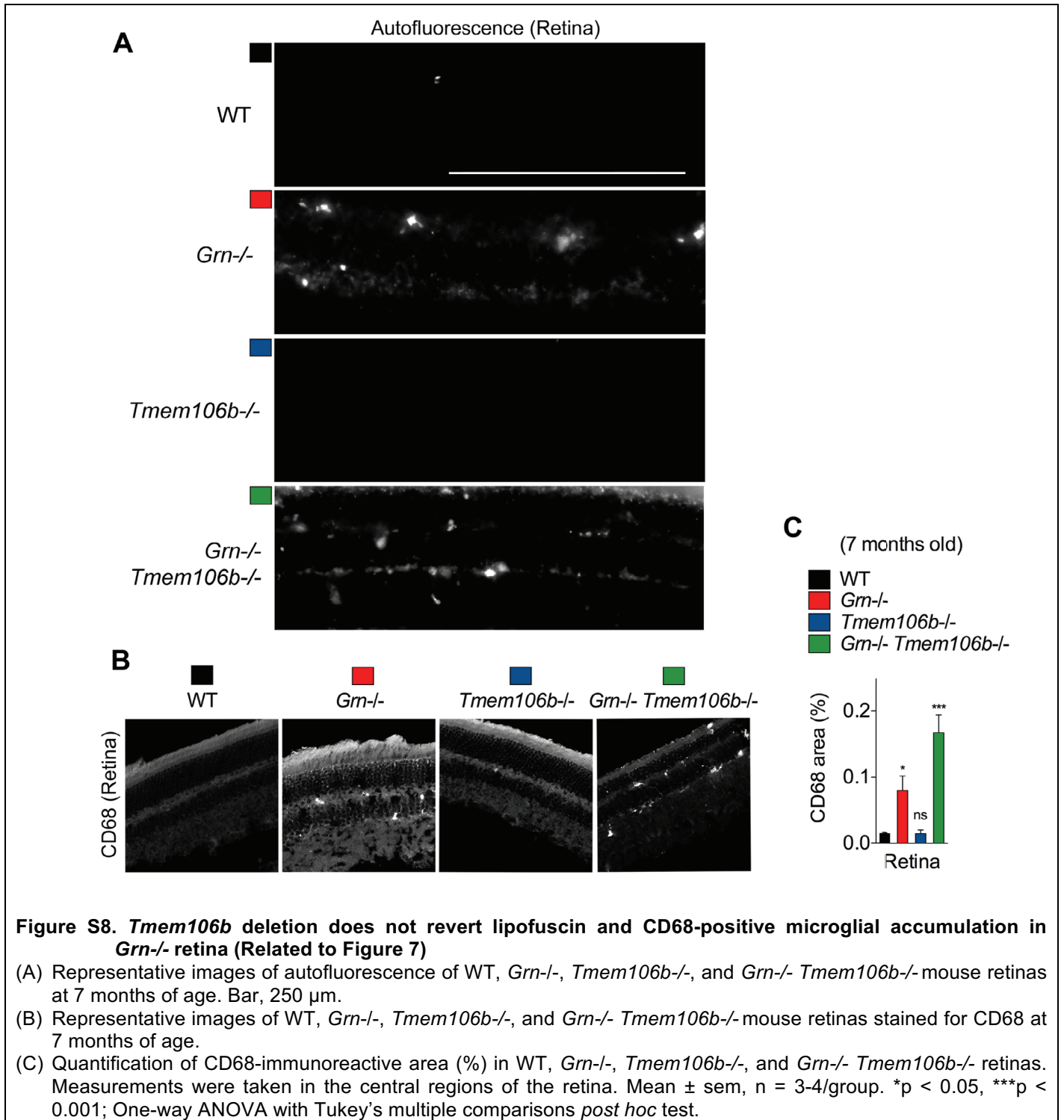
(A) Transcriptional changes in V-ATPase V0 subunits in *Grn*<sup>-/-</sup> brain by RNASeq.

(B) Protein levels of V-ATPase V1 subunits in *Grn*<sup>-/-</sup> brain detected by LFQ-LCMS analysis. Mean  $\pm$  sem, n= 6 (WT), 4 (KO), \*p < 0.05.



- (A) Diagram showing the experimental procedures of LysoTracker Red DND-99 and anti-MAP2 staining using WT and *Tmem106b*<sup>-/-</sup> primary cultured neurons.
- (B) A result from an independent experiment showing LysoTracker-positive area, LysoTracker mean fluorescence intensity, LysoTracker integrated fluorescence intensity, and MAP2-positive area in WT and *Tmem106b*<sup>-/-</sup> primary cultured neurons. Mean  $\pm$  sem, \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\*\* $p < 0.0001$ ; Unpaired T-test.
- (C) A result from another independent experiment showing LysoTracker-positive area, LysoTracker mean fluorescence intensity, LysoTracker integrated fluorescence intensity, and MAP2-positive area in WT and *Tmem106b*<sup>-/-</sup> primary cultured neurons. Mean  $\pm$  sem, \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ; Unpaired T-test.





**Table S1. Lysosomal DE genes (WT vs. *Grn*<sup>-/-</sup>) identified by RNASeq (Related to Figure 1)**

Gene ID	Gene name	FC (KO/WT)	LogCPM	LR	PValue	FDR
ENSMUSG00000007891	Ctsd	1.229009835	8.357909378	43.99259471	3.30E-11	8.53E-09
ENSMUSG00000003948	Mmd	1.195215619	8.221937819	43.4093542	4.44E-11	1.12E-08
ENSMUSG00000018774	Cd68	1.513754854	3.146479311	38.81841472	4.65E-10	9.78E-08
ENSMUSG00000038642	Ctss	1.26217449	5.806007008	35.52816403	2.51E-09	4.72E-07
ENSMUSG00000070934	Rraga	1.149545311	6.735359396	23.41010913	1.31E-06	0.000132551
ENSMUSG00000049624	Slc17a5	1.279810468	4.548337259	23.23106104	1.44E-06	0.000143209
ENSMUSG00000031447	Lamp1	1.119088723	8.249854963	22.08191094	2.61E-06	0.000243928
ENSMUSG00000021939	Ctsb	1.132302328	9.010809054	18.61453816	1.60E-05	0.001070741
ENSMUSG00000005142	Man2b1	1.173484496	5.397363067	18.19128763	2.00E-05	0.001263745
ENSMUSG00000021680	Crhbp	1.258045378	4.281552584	16.33276309	5.31E-05	0.002825131
ENSMUSG00000016256	Ctsz	1.207275796	4.89159043	15.83033036	6.93E-05	0.003385808
ENSMUSG00000016534	Lamp2	1.16764638	6.462705847	15.11460237	0.000101178	0.004613568
ENSMUSG000000021242	Npc2	1.140552318	5.629407519	14.02434175	0.000180459	0.007173942
ENSMUSG00000030560	Ctsc	1.246713745	3.511111916	13.87187737	0.000195705	0.007707398
ENSMUSG00000025351	Cd63	1.151256771	5.292495419	13.55074873	0.000232199	0.008714283
ENSMUSG00000029434	Vps33a	1.113674372	6.740525479	12.90627343	0.000327483	0.011355105
ENSMUSG00000073725	Lmbrd1	1.097141523	7.716785327	11.94358692	0.000548358	0.016674047
ENSMUSG00000021665	Hexb	1.14486092	6.151646185	11.68477682	0.000630135	0.018340108
ENSMUSG00000025393	Atp5b	1.076806322	9.828915744	11.00863116	0.000906886	0.02431064
ENSMUSG00000000594	Gm2a	1.120706565	6.220101697	10.57062914	0.001148986	0.028936309
ENSMUSG00000026878	Rab14	1.11520882	8.120076588	10.53509277	0.00117129	0.029317405
ENSMUSG00000079477	Rab7	1.099417306	8.188069594	10.23078462	0.001381159	0.033044229
ENSMUSG000000061119	Prcp	1.227041959	3.539198751	9.629539267	0.001914726	0.041410014
ENSMUSG00000019850	Tnfaip3	1.244037558	2.763438125	9.35588207	0.00222271	0.045892841
ENSMUSG00000034708	Grn	0.015229069	4.633446828	2662.524723	0	0
ENSMUSG00000040701	Ap1g2	0.696787362	1.735112606	13.58980604	0.000227417	0.008585333
ENSMUSG00000025241	Fyco1	0.874425599	5.537165699	13.20994262	0.000278468	0.009962384
ENSMUSG00000004626	Stxbp2	0.863178834	4.490285269	10.34068218	0.001301299	0.03172543
ENSMUSG00000026426	Arl8a	0.90576296	7.69079045	10.03241518	0.001538092	0.035773239

(Red) Up-regulated genes; (Blue) Down-regulated genes



**Table S2. Lysosomal DE genes (WT vs. *Grn*<sup>-/-</sup>) identified by LFQ-LCMS (Related to Figure 1)**

Accession	Description	FC (KO/WT)	Minus log anova	Anova (p)
SCRB2_MOUSE	Lysosome membrane protein 2 OS=Mus musculus GN=Scarb2 PE=1 SV=3	1.717460849	3.599625908	0.000251405
HEXB_MOUSE	Beta-hexosaminidase subunit beta OS=Mus musculus GN=Hexb PE=2 SV=2	1.419799297	3.37642307	0.000420317
PPGB_MOUSE	Lysosomal protective protein OS=Mus musculus GN=Ctsa PE=1 SV=1	1.606164408	2.959928356	0.001096659
TPP1_MOUSE	Tripeptidyl-peptidase 1 OS=Mus musculus GN=Tpp1 PE=1 SV=2	1.537969104	2.756333981	0.001752532
CATB_MOUSE	Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	1.433319645	2.734587799	0.00184252
LYAG_MOUSE	Lysosomal alpha-glucosidase OS=Mus musculus GN=Gaa PE=1 SV=2	1.36516915	2.305368949	0.004950295
CATL1_MOUSE	Cathepsin L1 OS=Mus musculus GN=Ctsl PE=1 SV=2	1.879201231	2.225050107	0.005955934
PAG15_MOUSE	Group XV phospholipase A2 OS=Mus musculus GN=Pla2g15 PE=1 SV=1	1.473324785	1.837822381	0.014527056
STX7_MOUSE	Syntaxin-7 OS=Mus musculus GN=Stx7 PE=1 SV=3	1.376776076	1.752895215	0.01766464
ANK3_MOUSE	Ankyrin-3 OS=Mus musculus GN=Ank3 PE=1 SV=1	1.139407233	1.467623802	0.034070319
PLD3_MOUSE	Phospholipase D3 OS=Mus musculus GN=Pld3 PE=2 SV=1	1.258318747	1.464831411	0.034290087
PLBL2_MOUSE	Putative phospholipase B-like 2 OS=Mus musculus GN=Plbd2 PE=1 SV=2	1.392080131	1.457473373	0.034875997
ASSY_MOUSE	Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1	1.246646865	1.415477407	0.038416924
SAP3_MOUSE	Ganglioside GM2 activator OS=Mus musculus GN=Gm2a PE=1 SV=2	2.410155811	1.413809738	0.038564727
NAGAB_MOUSE	Alpha-N-acetylgalactosaminidase OS=Mus musculus GN=Naga PE=2 SV=2	1.275311603	1.407688581	0.039112126
TM9S1_MOUSE	Transmembrane 9 superfamily member 1 OS=Mus musculus GN=Tm9sf1 PE=2 SV=2	1.249762294	1.405046227	0.039350819
DPP2_MOUSE	Dipeptidyl peptidase 2 OS=Mus musculus GN=Dpp7 PE=2 SV=2	1.504111976	1.393936744	0.040370419
FLOT2_MOUSE	Flotillin-2 OS=Mus musculus GN=Flot2 PE=1 SV=2	0.855796512	2.101575183	0.007914524
NOS1_MOUSE	Nitric oxide synthase, brain OS=Mus musculus GN=Nos1 PE=1 SV=1	0.790561842	1.919909798	0.012025142

(Red) Up-regulated proteins; (Blue) Down-regulated proteins

**Table S3. Transcriptional changes of typical microglial inflammatory genes and markers in *Grn<sup>-/-</sup>* by RNASeq (Related to Figure 1)**

Gene ID	Gene name	Protein name	FC (KO/WT)	logCPM	LR	PValue	FDR
ENSMUSG00000020826	Nos2	iNOS	0.889401112	-0.461154605	0.322524931	0.57009419	0.844485938
ENSMUSG00000027398	Il1b	IL1 $\beta$	1.069998811	-1.617255988	0.043552335	0.834688715	0.952695327
ENSMUSG00000041736	Tspo	TSPO	0.977332782	1.404841348	0.044595355	0.832749842	0.951628872
	Il6	IL6	n.d.				
	Tnf	TNF $\alpha$	n.d.				
	Cxcl2	CXCL-2	n.d.				
	Ccl2	MCP-1	n.d.				
ENSMUSG00000002603	Tgfb1	TGF $\beta$	0.999540027	2.747534118	4.12E-05	0.994881142	0.998166643
ENSMUSG00000039239	Tgfb2	TGF $\beta$	1.113647335	4.203231776	3.792162081	0.051493094	0.306773286
ENSMUSG000000021253	Tgfb3	TGF $\beta$	0.972487863	3.711871767	0.24785678	0.618588244	0.870700029
ENSMUSG00000000869	Il4	IL4	0.897255216	2.748627265	2.273100556	0.131636313	0.474630815
ENSMUSG00000050335	Lgals3	Galectin3	1.312583603	-0.740947157	1.41660482	0.233963042	0.60292875
	Retnla	Fizz-1	n.d.				
	Arg1	ARG1	n.d.				
	Il10	IL-10	n.d.				
	Chil3	Ym1	n.d.				
ENSMUSG00000024397	Aif1	Iba1	1.016499831	2.139374281	0.032621876	0.856669568	0.960032176
ENSMUSG00000030786	Irgam	CD11b	0.955080319	4.575065915	0.948902327	0.329998858	0.69492553
ENSMUSG00000026395	Ptprc	CD45	1.161138943	2.285824799	3.290563131	0.069679121	0.354844595
ENSMUSG00000036353	P2ry12	P2ry12	0.975456495	5.601921255	0.284159349	0.593987902	0.85790284

(Red) Pro-inflammatory genes; (Blue) Anti-inflammatory genes; (Green) Microglial markers

Table S4. DE genes (WT vs. *Tmem106b*<sup>-/-</sup>) identified by RNASeq (Related to Figure 3)

Gene ID	Gene name	FC (KO/WT)	LogCPM	LR	PValue	FDR
ENSMUSG00000038801	Scgb1c1	4.581810493	-1.52946609	18.29516975	1.89E-05	0.010707942
ENSMUSG00000016942	Tmprss6	3.568384986	-1.255765602	17.10879045	3.53E-05	0.016567934
ENSMUSG00000027483	Bpifa1	3.055213926	-0.827585084	17.87488535	2.36E-05	0.012971223
ENSMUSG00000033383	Rtp1	2.232771461	-0.369645817	14.64504494	0.000129775	0.046332256
ENSMUSG00000004328	Hif3a	1.994962989	2.363708467	58.43874113	2.10E-14	1.35E-10
ENSMUSG000000025150	Cbr2	1.785837301	0.724160762	15.3858561	8.76E-05	0.035884679
ENSMUSG000000086189	Gm15462	1.551721516	1.416433007	15.58471453	7.89E-05	0.033364413
ENSMUSG000000037185	Krt80	1.504850176	1.84541335	17.37255922	3.07E-05	0.015205292
ENSMUSG000000024066	Xdh	1.437973425	2.315546844	17.36686679	3.08E-05	0.015205292
ENSMUSG00000004609	Cd33	1.404999411	2.64768083	18.36974546	1.82E-05	0.010707942
ENSMUSG00000015843	Rxrg	1.372247112	4.221827603	21.98104177	2.75E-06	0.002649485
ENSMUSG000000040010	Slc7a5	1.257930526	5.777217944	29.38109145	5.95E-08	8.80E-05
ENSMUSG000000020893	Per1	1.236178503	6.154401537	32.45176651	1.22E-08	2.61E-05
ENSMUSG000000042292	Mkl1	1.206249447	5.905653763	17.55376362	2.79E-05	0.014526485
ENSMUSG00000014361	Mertk	1.196978085	5.472001039	17.62206461	2.69E-05	0.014403279
ENSMUSG000000037887	Dusp8	1.146431828	7.543969856	15.56414297	7.98E-05	0.033364413
ENSMUSG000000062078	Qk	0.879867084	8.737482279	15.01685255	0.000106555	0.04045806
ENSMUSG000000027562	Car2	0.858902855	7.292901745	18.2982	1.89E-05	0.010707942
ENSMUSG000000033904	Ccp110	0.853790625	6.360223017	16.09533731	6.02E-05	0.026955989
ENSMUSG000000003746	Man1a	0.852889053	5.410225435	14.64161831	0.000130012	0.046332256
ENSMUSG000000020486	Sept4	0.848146958	6.811317046	15.07147377	0.000103516	0.04045806
ENSMUSG000000036634	Mag	0.836626942	6.990191718	18.89727009	1.38E-05	0.008849029
ENSMUSG000000041607	Mbp	0.822629094	10.84551907	24.80384754	6.35E-07	0.000814286
ENSMUSG000000031714	Gab1	0.820943375	4.753729654	15.3020811	9.16E-05	0.036730191
ENSMUSG000000039904	Gpr37	0.814315882	5.701275775	24.35189298	8.02E-07	0.000908406
ENSMUSG000000073680	Tmem88b	0.812578601	5.140095229	16.2435576	5.57E-05	0.025520599
ENSMUSG000000006782	Cnp	0.807396291	8.051800683	41.5226997	1.17E-10	2.80E-07
ENSMUSG000000056966	Gjc3	0.80012246	5.603041151	31.51212602	1.98E-08	3.81E-05
ENSMUSG000000076439	Mog	0.785455191	5.54962515	27.46300168	1.60E-07	0.000220108
ENSMUSG000000027858	Tspan2	0.784581728	6.885040504	31.2027023	2.32E-08	4.07E-05
ENSMUSG000000032517	Mobp	0.782059642	9.256554333	30.00550681	4.31E-08	6.91E-05
ENSMUSG000000031425	Plp1	0.774278047	10.37637202	56.40102634	5.91E-14	2.84E-10
ENSMUSG000000033579	Fa2h	0.770551359	4.930733883	20.19010732	7.01E-06	0.005622022
ENSMUSG000000020774	Aspa	0.77002112	3.869636142	21.30867383	3.91E-06	0.003419821
ENSMUSG000000037625	Cldn11	0.744323456	7.009526095	42.47986011	7.14E-11	1.96E-07
ENSMUSG000000033949	Trim36	0.734179748	2.815875169	15.00510018	0.000107221	0.04045806
ENSMUSG000000027375	Mal	0.72805254	7.410384462	45.16136418	1.81E-11	5.82E-08
ENSMUSG000000038173	Enpp6	0.720007476	2.375812709	15.65608714	7.60E-05	0.033225496
ENSMUSG000000036777	Anln	0.718032618	4.699217449	17.30808836	3.18E-05	0.015290856
ENSMUSG000000049892	Rasd1	0.711012541	2.715777023	14.68203156	0.000127254	0.046332256
ENSMUSG000000026830	Ernm	0.710748342	5.534621557	50.95604881	9.45E-13	3.64E-09
ENSMUSG000000034317	Trim59	0.707069571	4.130795602	24.58408526	7.11E-07	0.000855598
ENSMUSG000000032854	Ugt8a	0.698284041	5.690440856	70.14992318	5.50E-17	5.29E-13
ENSMUSG00000019232	Etnppl	0.674475679	3.955651969	19.71637898	8.98E-06	0.006648666
ENSMUSG000000021948	Prkcd	0.640770853	3.794817581	20.08940079	7.39E-06	0.005688921
ENSMUSG000000066652	Lefty2	0.407885519	-0.239512955	19.26079495	1.14E-05	0.008126943
ENSMUSG000000079466	Prdm12	0.325496566	-0.76301034	18.31148304	1.88E-05	0.010707942
ENSMUSG000000023964	Calcr	0.289863522	-0.601142145	22.64546193	1.95E-06	0.002015109
ENSMUSG000000029571	Tmem106b	0.261051544	7.078459598	1200.385629	5.03E-263	9.68E-259
ENSMUSG000000037727	Avp	0.157005208	2.055751823	21.71021918	3.17E-06	0.002905822
ENSMUSG000000094065	Gm21541	0.134757655	-0.159400539	18.99574136	1.31E-05	0.008693678
ENSMUSG000000027301	Oxt	0.128250892	0.867644729	22.60509903	1.99E-06	0.002015109
ENSMUSG000000073878	Gm13304	0.126741531	-0.29528205	19.00863381	1.30E-05	0.008693678
ENSMUSG000000021342	Prl	0.070698744	-0.757273767	20.75768052	5.21E-06	0.004361035

(Red) Up-regulated genes; (Blue) Down-regulated genes

**Table S5. Transcriptional changes of typical microglial inflammatory genes and markers and TNG in *Tmem106b*<sup>-/-</sup> by RNASeq (Related to Figure 3)**

Gene ID	Gene name	FC (KO/WT)	LogCPM	LR	PValue	FDR
ENSMUSG00000020826	Nos2	0.863620046	-0.43152845	0.486932825	0.4852987	0.901756677
ENSMUSG00000027398	Il1b	0.939569499	-1.675767135	0.034809371	0.851995675	0.983559521
ENSMUSG00000041736	Tspo	1.112652982	1.493664249	0.939838696	0.332319328	0.849184494
	Il6	n.d.				
	tnf	n.d.				
	cxcl2	n.d.				
	ccl2	n.d.				
ENSMUSG00000039239	Tgfb2	0.896992913	4.055378928	1.431572569	0.231507966	0.803611265
ENSMUSG00000021253	Tgfb3	0.969478596	3.707855494	0.257772458	0.611654653	0.935897843
ENSMUSG00000002603	Tgfb1	0.981204603	2.734025814	0.063906622	0.80042463	0.975262314
ENSMUSG00000000869	Il4	1.085303634	2.881495158	1.140144812	0.28562173	0.830601733
ENSMUSG000000050335	Lgals3	1.191810641	-0.806256756	0.554736978	0.456388601	0.896281242
	retnla	n.d.				
	arg1	n.d.				
	Il10	n.d.				
	chil3	n.d.				
ENSMUSG00000024397	Aif1	1.017419805	2.144017108	0.034615558	0.852403538	0.983673941
ENSMUSG00000030786	Iltgam	1.052216821	4.646835502	0.912525878	0.339445116	0.851122527
ENSMUSG00000026395	Ptpcr	1.051716022	2.210878754	0.334546252	0.562994274	0.923703784
ENSMUSG00000036353	P2ry12	0.992892233	5.616997279	0.021034877	0.884683984	0.98559328
ENSMUSG00000030579	Tyrobp	1.15538277	3.203228563	4.615380091	0.031686472	0.556469087
ENSMUSG00000023992	Trem2	1.18277939	3.421411877	5.632426	0.017631214	0.481238276
ENSMUSG00000018774	Cd68	1.21665417	2.968832656	6.970305085	0.008287337	0.35389059
ENSMUSG00000024672	Ms4a7	1.585950844	-0.558311216	4.52958319	0.033313731	0.564018739
ENSMUSG00000004730	Emr1	1.079450178	2.724934584	1.027034658	0.31085616	0.841130982
ENSMUSG00000036887	C1qa	1.194275767	5.366414516	7.969836166	0.004756324	0.295513111
ENSMUSG00000036905	C1qb	1.231966604	5.318484745	13.76648633	0.000206996	0.064248927
ENSMUSG000000069516	Lyz2	1.248362645	3.247704824	5.552452942	0.018454807	0.486543254
ENSMUSG00000038642	Ctss	1.022018806	5.644075364	0.268108328	0.604603554	0.934237256
ENSMUSG00000016256	Ctsz	1.116858995	4.829002523	3.745000474	0.052965712	0.615554375
ENSMUSG00000006519	Cyba	1.104979273	2.104215244	1.197469065	0.273828118	0.825254483
ENSMUSG00000016534	Lamp2	0.956335888	6.312532399	1.163414819	0.280758461	0.828076273
ENSMUSG00000073418	C4b	1.127717557	4.065320385	4.784308273	0.028720181	0.538340496
ENSMUSG00000020120	Plek	1.031625948	4.09203326	0.29980923	0.584002041	0.929776844
ENSMUSG00000025351	Cd63	1.016212858	5.196610041	0.123149104	0.725643815	0.962892201
ENSMUSG00000024300	Myo1f	1.175715534	1.596898951	2.360965614	0.124405163	0.730084855
ENSMUSG00000030577	Cd22	0.872899268	-1.21367473	0.237994729	0.625658193	0.939965362
	ccl8	n.d.				

(Red) Pro-inflammatory genes; (Blue) Anti-inflammatory genes; (Green) Microglial markers; (Purple) TNG