## **Supplementary Figures**



Supplementary Figure S1. SHIP-1+/+ and SHIP-1+/- had comparable immunological responses to brain injury and behavioral changes at 1-week post-injury. SHIP-1+/+ and SHIP-1+/- mice underwent experimental TBI surgeries at p21. Behavior and brains were collected at 1-week post-injury. (a-d) Relative expression of the indicated genes in the ipsilateral cortex compared to sham SHIP-1+/+ control animals. (e) Percentage time spent in the open arm and (f) total distance traveled during Elevated Plus Maze. (g) Percentage time spent in the center zone and (h) total distance traveled during open-field. (i) Seconds to fall during rotarod. (j) Discrimination index calculated from time spent in novel arm against familiar arm during y-maze. n=4-5/group. Solid = female, open = male. \*p < 0.05, \*\*p < 0.005, \*\*\*\*p < 0.0001. Two-way ANOVA and three-way ANOVA;

Supplementary Table S1. Statistical analysis of the expression of various genes in SHIP-1+/+ and SHIP-1+/- mice at 1-week post-injury, as well as percentage time spent in the open arm and total distance traveled during Elevated Plus Maze; time spent in the center zone and total distance traveled during open-field; seconds to fall during rotarod and discrimination index calculated from time spent in novel arm against familiar arm during y-maze (presented graphically in Supplementary Figure S1).

Gene	Injury (F, p)	Genotype (F, p)	Time (F, p)	Interactions
Fcgr3	F <sub>1, 14</sub> = 30.72,	$F_{1, 14} = 0.78,$	N/A	None
	p < 0.0001****	p = 0.3913		
Chil3	$F_{1, 14} = 6.40,$	$F_{1, 14} = 0.04,$	N/A	None
	p = 0.0251*	p = 0.8484		
Gfap	$F_{1, 14} = 10.10,$	$F_{1, 14} = 0.07,$	N/A	None
	p = 0.0067**	p = 0.7895		
Ccl2	F <sub>1,14</sub> = 6.70,	F <sub>1,14</sub> = 0.12,	N/A	None
	p = 0.0214*	p = 0.7361		
Measurement	Injury (F, p)	Genotype (F, p)		Interactions
Time in open arm	$F_{1, 14} = 4.81,$	$F_{1, 14} = 0.01,$	N/A	None
<ul> <li>Elevated Plus</li> </ul>	p = 0.0456*	p = 0.9394		
Maze				
Distance traveled	$F_{1, 14} = 3.71,$	$F_{1, 14} = 1.66,$	N/A	None
<ul> <li>Elevated Plus</li> </ul>	p = 0.0746	p = 0.2191		
Maze				
Time in center	$F_{1, 14} = 0.84,$	$F_{1, 14} = 0.01,$	N/A	None
zone – open-field	p = 0.3750	p = 0.9217		
test				
Total distance	$F_{1,14} = 1.22,$	$F_{1,14} = 0.022,$	N/A	None
traveled - open-	p = 0.2874	p = 0.8844		
field test				
Seconds to fall –	$F_{1, 28} = 0.09,$	$F_{1, 28} = 0.02,$	$F_{1, 28} = 9.55,$	None
Rotarod test	p = 0.7649	p = 0.8746	p = 0.0045**	
Discrimination	$F_{1, 14} = 0.12,$	$F_{1, 14} = 0.20,$	N/A	None
index – Y-maze	p = 0.2028	p = 0.6594		
test				

Supplementary Table S2. The number of pediatric SHIP-1+/- and SHIP-1-/- mice allocated to each procedure and their respective sex distribution within each cohort (F = female; M = male).

Pediatric TBI Animal Numbers				
		Acute		
Procedure	Injury Type	Genotype		
		Control (SHIP-1+/-)	Knockout (SHIP-1-/-)	
Behavior	Sham	n=15 (F=6; M=9)	n=11 (F=2; M=9)	
	Severe TBI	n=17 (F=5; M=12)	n=12 (F=6; M=6)	
Histology	Sham	n=6 (F=5; M=1)	n=5 (F=2; M=3)	
	Severe TBI	n=7 (F=5; M=2)	n= 6 (F=2; M=4)	
Gene Expression (6 Hours Post-injury)	Sham	n=5 (F=2; M=3)	n=5 (F=4; M=1)	
	Severe TBI	n=6 (F=4; M=2)	n=6 (F=2; M=4)	
Gene Expression	Sham	n=5 (F=2; M=3)	n=6 (F=2; M=4)	
	Severe TBI	n=6 (F=2; M=4)	n=5 (F=3; M=2)	
		Chronic	1	
Procedure	Injury Type	Gen	otype	
		Control (SHIP-1+/-)	Knockout (SHIP-1-/-)	
Behavior	Sham	n=15 (F=6; M=9)	n=9 (F=1; M=8)	
	Severe TBI	n=17 (F=5; M=12)	n=10 (F=6; M=4)	
Histology	Sham	n=6 (F=3; M=3)	n=5 (F=1; M=4)	
	Severe TBI	n=6 (F=3; M=3)	n= 6 (F=3; M=3)	
Gene Expression	Sham	n=5 (F=2; M=3)	n=4 (F=2; M=2)	
	Severe TBI	n=4 (F=1; M=3)	n= 5 (F=3; M=2)	
Serum Cytokines	Sham	n=6 (F=3; M=3)	n=6 (F=1; M=5)	
	Severe TBI	n=6 (F=3; M=3)	n= 6 (F=3; M=3)	

Supplementary Table S3. Gene names and assay ID used for quantitative

polymerase chain reaction experiments.

Marker	Gene Name	Gene Assay ID
		(Thermo Fisher)
Chemokine (C-C Motif) Ligand 2 (CCL2)	Ccl2	Mm00441242_m1
CD16	Fcgr3	Mm00438882_m1
CD68	Cd68	Mm03047343_m1
CD86	Cd86	Mm00444540_m1
CD206	Mrc1	Mm01329362_m1
Corticotrophin-releasing Hormone	Crh	Mm01293920_s1
C-X3-C Motif Chemokine Receptor 1 (CX3CR1)	Cx3cr1	Mm00438354_m1
Excitatory Amino Acid Transporter 2 (SLC1A2)	Slc1a2	Mm01275814_m1
Interleukin 1 beta (IL-1β)	ll1b	Mm00434228_m1
Ionized Calcium-binding Adapter Molecule 1 (IBA-1)	Aif1	Mm00479862_g1
Insulin Growth Factor Binding Protein 7 (IGFBP7)	lgfbp7	Mm03807886_m1
Glial Fibrillary Acidic Protein (GFAP)	Gfap	Mm01253033_m1
Multiple EGF Like Domains 10	Megf10	Mm01257625_m1
MHC Class II	H2-ab1	Mm00439216_m1
Matrix Metallopeptidase 12	Mmp12	Mm00500554_m1
Reduced Nicotinamide Adenine Dinucleotide Phosphate (NADPH)	Nox2	Mm01287743_m1
Spalt Like Transcription Factor 1 (SALL1)	Sall1	Mm00491266_m1
Src Homology 2 Domain Containing Inositol Polyphosphate 5-phosphate 1 (SHIP-1)	Inpp5d	Mm00494963_m1
Transforming Growth Factor $\beta$ (TGF- $\beta$ )	Tgfb	Mm01178820_m1
Translocator Protein (TSPO)	Tspo	Mm00437828_m1
TMEM119	Tmem119	Mm00525305_m1
TREM2	Trem2	Mm04209424_g1

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Ym1	Chil3	Mm00657889_mH
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Supplementary Table S4. Statistical analysis of the expression of various genes in SHIP-1+/- and SHIP-1-/- mice at 6 hours post-injury (presented graphically in Figure 1).

Gene	Injury (F, p)	Genotype (F, p)	Interactions
Tnf	$F_{1, 15} = 7.37,$	$F_{1, 15} = 0.76,$	None
	p = 0.0160*	p = 0.3973	
Ccl-2	F <sub>1, 18</sub> = 8.98,	F <sub>1, 18</sub> = 0.46,	None
	p = 0.0077**	p = 0.5065	
ll1b	$F_{1, 16} = 3.54,$	$F_{1, 16} = 1.26,$	None
	p = 0.0780*	p = 0.2781	
Chil3	$F_{1,18} = 9.64,$	$F_{1,18} = 8.05,$	None
	p = 0.0061**	p = 0.0109*	
H2-ab1	F <sub>1,18</sub> = 5.83,	$F_{1,18} = 0.01,$	None
	p = 0.0266*	p = 0.9064	
Gfap	F <sub>1, 17</sub> = 6.15,	$F_{1, 17} = 0.59,$	None
	p = 0.0239*	p = 0.4519	



Supplementary Figure S2. Changes in body weight and spleen weight at 1-week post-injury. (a) Body weight and (b) spleen weight of SHIP-1+/- and SHIP-1-/- mice at 1-week post-injury. \*\*\*\*p < 0.0001. Two-way ANOVA. n=10-17/group. Solid = female, open = male. Complete statistical analysis is presented in supplementary table S4.

Supplementary Table S5. Statistical analysis of body weight, spleen weight relative to body weight, IBA-1 fluorescence, number of IBA-1+ microglia and microglial morphology analysis at 1-week post-injury (presented graphically in figure 2).

Measurements	Injury (F, p)	Genotype (F, p)	Interactions
Body weight	$F_{1,41} = 0.40,$	$F_{1,41} = 3.24,$	None
	p = 0.5293	p = 0.0793	
Spleen weight	F <sub>1,42</sub> = 1.92,	F <sub>1,42</sub> = 65.0,	None
	p = 0.1731	p < 0.0001****	
IBA-1 fluorescence – ipsilateral	F <sub>1,20</sub> = 32.58,	$F_{1,20} = 0.02,$	None
cortex	p < 0.0001****	p = 0.9031	
IBA-1 fluorescence – ipsilateral	$F_{1, 20} = 40.48,$	$F_{1,20} = 0.46,$	None
peri-lesional cortex	p < 0.0001****	p = 0.5057	
IBA-1 fluorescence – ipsilateral	$F_{1,20} = 20.29,$	$F_{1,20} = 0.29,$	None
dentate gyrus	p = 0.0002***	p = 0.5972	
IBA-1 fluorescence – ipsilateral	F <sub>1,20</sub> = 21.57,	$F_{1,20} = 0.19,$	None
dorsolateral thalamus	p = 0.0002***	p = 0.5650	
Number of IBA-1+ microglia -	F <sub>1,20</sub> = 54.87,	$F_{1,20} = 0.36,$	None
ipsilateral cortex	p < 0.0001****	p = 0.5570	
Number of IBA-1+ microglia –	$F_{1,20} = 66.79,$	$F_{1,20} = 0.21,$	None
ipsilateral peri-lesional cortex	p < 0.0001****	p = 0.6533	
Number of IBA-1+ microglia –	$F_{1,20} = 43.60,$	$F_{1,20} = 0.54,$	None
ipsilateral dentate gyrus	p < 0.0001****	p = 0.4727	
Number of IBA-1+ microglia –	$F_{1,20} = 54.81,$	$F_{1,20} = 0.22,$	None
ipsilateral dorsolateral thalamus	p < 0.0001****	p = 0.6433	
Microglial morphology - average	F <sub>1,21</sub> = 11.07,	$F_{1,21} = 0.02,$	None
branch length	p = 0.0032**	p = 0.9019	
Microglial morphology - number	$F_{1,21} = 9.14,$	F <sub>1,21</sub> = 2.23,	None
of branches	p = 0.0065**	p = 0.1498	
Microglial morphology - soma	F <sub>1,21</sub> = 15.43,	F <sub>1,21</sub> = 0.92,	None
area	p = 0.0008***	p = 0.3492	

Supplementary Table S6. Statistical analysis of the expression of various genes in SHIP-1+/- and SHIP-1-/- mice at 1-week post-injury (presented graphically in figure 3).

Gene	Injury (F, p)	Genotype (F, p)	Interactions
Cd86	$F_{1,17} = 1.47,$	$F_{1,17} = 0.34,$	None
	p = 0.2421	p = 0.5685	
Fcgr3	$F_{1,16} = 3.79,$	F <sub>1,16</sub> = 7.83,	None
	p = 0.0694	p = 0.0129*	
Mrc1	$F_{1,15} = 1.08,$	$F_{1,15} = 7.93,$	None
	p = 0.05769	p = 0.0130*	
Tmem119	$F_{1,19} = 0.75,$	$F_{1,19} = 2.30,$	None
	p = 0.3969	p = 0.1455	
Trem2	F <sub>1,20</sub> = 1.96,	F <sub>1,20</sub> = 1.52,	None
	p = 0.1765	p = 0.2312	
Sall1	$F_{1,20} = 0.41,$	$F_{1,20} = 5.26,$	None
	p = 0.5278	p = 0.03280*	

Supplementary Table S7. Statistical analysis of CD68 and GFAP fluorescence, and *Ccl2* gene expression at 1-week post-injury (presented graphically in figure 4 and supplementary figure S3).

Measurement	Injury (F, p)	Genotype (F, p)	Interactions
CD68 fluorescence	$F_{1,20} = 11.84,$	F <sub>1,20</sub> < 0.00,	None
<ul> <li>injury site</li> </ul>	p = 0.0026**	p = 0.9681	
CD68 fluorescence	$F_{1,20} = 30.93,$	$F_{1,20} = 0.020,$	None
<ul> <li>ipsilateral corpus</li> </ul>	p < 0.0001****	p = 0.8900	
callosum/external			
capsule			
GFAP fluorescence	$F_{1,21} = 54.90,$	F <sub>1,21</sub> = 1.51,	None
<ul> <li>injury site</li> </ul>	p < 0.0001****	p = 0.2328	
Ccl2 gene	$F_{1,18} = 4.97$ ,	$F_{1,18} = 0.31$ ,	None
expression	p = 0.0388	p = 0.5844	



Supplementary Figure S3. *Ccl2* gene expression relative to sham SHIP-1+/- control mice at the cortex at of SHIP-1+/- and SHIP-1-/- mice at 1-week post-injury. \*p < 0.05. Two-way ANOVA; n=4-6/group. Solid = female, open = male. Complete statistical analysis is presented in supplementary table S6.

Supplementary Table S8. Statistical analysis of remaining healthy tissue at the cortex and hippocampus, measurements of anxiety-like behavior, explorative tendency, motor skills and working memory at 1-week post-injury (presented graphically in figure 5).

Measurement	Injury (F, p)	Genotype (F, p)	Time (F,p)	Interactions
Healthy remaining	F <sub>1,21</sub> = 50.79,	F <sub>1,21</sub> = 2.10,	N/A	None
tissue - cortex	p < 0.0001****	p < 0.1619		
Healthy reaming	F <sub>1,21</sub> = 1.73,	F <sub>1,21</sub> = 1.32,	N/A	None
tissue –	p = 0.2025	p = 0.2628		
hippocampus				
Time in open arm	$F_{1,54} = 0.10,$	F <sub>1,54</sub> = 1.87,	N/A	None
<ul> <li>Elevated Plus</li> </ul>	p = 0.8822	p = 0.9127		
Maze				
Distance travelled	$F_{1,54} = 1.30,$	$F_{1,54} = 5.97,$	N/A	None
<ul> <li>Elevated Plus</li> </ul>	p = 0.2585	p = 0.0178*		
Maze				
Time in center	$F_{1,55} = 13.44,$	$F_{1,55} = 4.49,$	N/A	lnjury x
zone – open-field	p = 0.0006***	p = 0.0387*		genotype
test				$F_{1,55} = 5.68$ ,
				p = 0.0206*
Total distance	$F_{1,55} = 0.05$ ,	$F_{1,55} = 8.11,$	N/A	lnjury x
traveled – open-	p = 0.8269	p = 0.0062**		genotype
field test				$F_{1,55} = 5.52,$
				p = 0.0224*
Seconds to fall –	$F_{1,54} = 1.04$ ,	$F_{1,54} = 1.25$ ,	$F_{1,54} = 19.39,$	None
Rotarod test	p = 0.3134	p = 0.2680	p < 0.0001****	
Discrimination	$F_{1,54} = 4.02,$	$F_{1,54} = 0.05$ ,	N/A	None
index – Y-maze	p = 0.0501	p = 0.8309		
test				

Supplementary Table S9. Statistical analysis of body weight, spleen weight and serum cytokine concentration of SHIP-1+/- and SHIP-1-/- mice at 12-weeks post-injury (presented graphically in figure 6).

Measurement	Injury (F, p)	Genotype (F, p)	Interactions
Body weight	F <sub>1,49</sub> = 2.20,	F <sub>1,49</sub> = 19.40,	None
	p = 0.1443	p < 0.0001****	
Spleen weight	F <sub>1, 49</sub> = 1.04,	F <sub>1, 49</sub> = 65.38,	None
	p = 0.3131	p < 0.0001****	
Serum Cytokine	Injury (F, p)	Genotype (F, p)	Interactions
G-CSF	$F_{1,20} = 0.04,$	$F_{1,20} = 5.22,$	None
	p = 0.8379	p = 0.0334*	
IL-4	$F_{1,20} = 0.57,$	F <sub>1,20</sub> = 15.83,	None
	p = 0.4592	p = 0.0007***	
IL-6	$F_{1,20} = 0.28,$	$F_{1,20} = 7.02,$	None
	p = 0.6021	p = 0.0154*	
IFN-γ	F <sub>1,20</sub> = 7.39,	$F_{1,20} = 2.22,$	None
	p = 0.0132*	p = 0.1520	
IL-12(p40)	F <sub>1,20</sub> < 0.00,	$F_{1,20} = 25.24,$	None
	p = 0.9889	p < 0.0001****	
IL-10	F <sub>1,20</sub> = 7.20,	$(F_{1,20} = 50.83,$	None
	p = 0.0142*	p < 0.0001****	
MIP-1α	F <sub>1,20</sub> = 6.13,	$F_{1,20} = 40.40,$	None
	p = 0.0224*	p < 0.0001****	
MIP-1β	$F_{1,20} = 3.141,$	$F_{1,20} = 8.81,$	None
	p = 0.0916	p = 0.0076*	

Supplementary Table S10. Statistical analysis of gene expression analysis of the cortex and hippocampus of SHIP-1+/- and SHIP-1-/- mice at 12-weeks post-injury (presented graphically in figure 7).

Cortex				
Gene	Injury (F, p)	Genotype (F, p)	Interactions	
Inpp5d	$F_{1,16} = 0.74,$	$F_{1,16} = 71.37,$	None	
	p = 0.4022	p < 0.0001****		
Cd86	$F_{1,16} = 0.61,$	F <sub>1,16</sub> = 25.12,	F <sub>1,16</sub> = 7.24,	
	p = 0.4492	p < 0.0001****	p = 0.0161*	
Nadph	$F_{1,16} = 0.13,$	$F_{1,16} = 15.24,$	None	
	p = 0.7178	p = 0.0013**		
Mcr1	F <sub>1,16</sub> < 0.00,	$F_{1,16} = 3.940,$	Injury x genotype	
	p = 0.9795	p = 0.0646	$F_{1,16} = 4.76,$	
			p = 0.0444*	
Megf10	$F_{1,16} = 0.0345,$	$F_{1,16} = 5.918,$	None	
	p = 0.8550	p = 0.0271*		
	Ніррос	campus		
Gene	Injury (F, p)	Genotype (F, p)	Interactions	
Cd86	$F_{1,16} = 0.08,$	$F_{1,16} = 19.59,$	None	
	p = 0.7817	p = 0.0004***		
Nadph	$F_{1,16} = 12.73,$	F <sub>1,16</sub> = 15.72,	None	
	p = 0.0026***	p = 0.0011***		
Mcr1	$F_{1,16} = 8.003,$	F <sub>1,16</sub> < 0.00,	None	
	p = 0.0121*	p = 0.9731		
Megf10	$F_{1,16} = 3.73,$	$F_{1,16} = 4.21,$	None	
	p = 0.0714	p = 0.0568		
Cd68	$F_{1,16} = 28.04,$	$F_{1,16} = 12.45,$	Injury x genotype	
	p < 0.0001****	p = 0.0028***	$F_{1,16} = 7.28,$	
			p = 0.0158*	
Cx3cr1	$F_{1,16} = 4.67,$	F <sub>1,16</sub> = 11.85,	None	
	p = 0.0462*	p = 0.0033**		
Ccl2	$F_{1,16} = 4.64,$	$F_{1,16} = 21.67,$	None	
	p = 0.0468*	p = 0.0003***		
Mmp12	$F_{1,16} = 6.94,$	$F_{1,16} = 1.54,$	None	
	p = 0.0187*	p = 0.2334		
Crh	$F_{1,16} = 21.19,$	$F_{1,16} = 1.18,$	None	
	p = 0.0003***	p = 0.2930		
Tspo	$F_{1,16} = 7.64,$	F <sub>1,16</sub> = 6.52,	None	
	p = 0.0138*	p = 0.0213*		



Supplementary Figure S4. *Inpp5d* expression relative to sham SHIP-1+/- mice in the ipsilateral cortex of SHIP-1+/- and SHIP-1-/- mice at 12-weeks post-injury. \*\*\*\*p < 0.0001. Two-way ANOVA; n=3-6/group. Solid = female, open = male. Statistics presented in Supplementary Table S9.

Supplementary Table S11. Statistical analysis of IBA-1 fluorescence, number of IBA-1+ microglia, microglial morphology and GFAP fluorescence of SHIP-1+/- and SHIP-1-/- mice at 12-weeks post-injury (presented graphically in figures 8, 9 and 10).

Measurements	Injury (F, p)	Genotype (F, p)	Interactions
IBA-1 fluorescence	$F_{1,19} = 0.08,$	$F_{1,19} = 1.66,$	None
<ul> <li>ipsilateral cortex</li> </ul>	p = 0.7812	p = 0.2134	
IBA-1 fluorescence	F <sub>1,19</sub> < 0.00,	$F_{1,19} = 1.83,$	None
<ul> <li>ipsilateral peri-</li> </ul>	p = 0.9730	p = 0.1925	
lesional cortex			
IBA-1 fluorescence	$F_{1,18} = 0.17,$	F <sub>1,18</sub> < 0.00,	None
<ul> <li>– ipsilateral dentate</li> </ul>	p = 0.6864	p = 0.9390	
gyrus			
IBA-1 fluorescence	$F_{1,19} = 0.04,$	$F_{1,19} = 0.36,$	None
<ul> <li>ipsilateral</li> </ul>	p = 0.8494	p = 0.5567	
dorsolateral			
thalamus			
Number of iba-1+	$F_{1,19} = 0.49,$	$F_{1,19} = 1.31,$	None
microglia - ipsilateral	p = 0.4943	p = 0.7216	
cortex			
Number of IBA-1+	$F_{1,19} = 0.37,$	$F_{1,19} = 1.23,$	None
microglia –	p = 0.5526	p = 0.2810	
ipsilateral peri-			
lesional cortex			
Number of IBA-1+	$F_{1,18} = 1.20,$	$F_{1,19} = 0.07,$	None
microglia –	p = 0.2881	p = 0.4118	
ipsilateral dentate			
gyrus			
Number of IBA-1+	$F_{1,18} = 1.49,$	$F_{1,19} = 1.08,$	None
microglia –	p = 0.2379	p = 0.3125	
ipsilateral			
dorsolateral			
thalamus			
Microglial	$F_{1,15} = 3.22,$	$F_{1,15} = 1.82,$	None
morphology –	p = 0.5791	p = 0.1971	
number of branches			
Microglial	$F_{1,15} = 0.49,$	$F_{1,15} = 2.17,$	None
morphology –	p = 0.4961	p = 0.1664	
number of endpoints			
Microglial	F <sub>1,15</sub> < 0.00,	$F_{1,15} = 3.61,$	None
morphology –	p = 0.9841	p = 0.0768	
branch length			
GFAP fluorescence	$F_{1,19} = 46.16,$	$F_{1,19} = 6.33,$	Injury x genotype
<ul> <li>ipsilateral cortex</li> </ul>	p < 0.0001****	p = 0.0210*	$F_{1,19} = 6.16,$
			p = 0.0225*

Supplementary Table S12. Statistical analysis of remaining healthy tissue at the cortex and hippocampus, measurements of anxiety-like behavior, explorative tendency, motor skills and working memory at 12-week post-injury (presented graphically in figure 11).

Measurement	Injury (F, p)	Genotype (F, p)	Time (F,p)	Interactions
Healthy remaining	$F_{1,19} = 441.10,$	F <sub>1,19</sub> = 3.12,	N/A	None
tissue - cortex	p < 0.001****	p = 0.0935		
Healthy reaming	F <sub>1,19</sub> = 31.65,	F <sub>1,19</sub> = 17.0,	N/A	None
tissue –	p < 0.001****	p = 0.6827		
hippocampus				
Time in open arm	$F_{1,49} = 0.018,$	$F_{1,49} = 2.54,$	N/A	None
<ul> <li>Elevated Plus</li> </ul>	p = 0.8937	p = 0.1176		
Maze				
Distance traveled	$F_{1,49} = 0.30,$	F <sub>1,49</sub> = 15.88,	N/A	None
<ul> <li>Elevated Plus</li> </ul>	p = 0.5858	p = 0.0002***		
Maze				
Time in center	$F_{1,49} = 0.18,$	$F_{1,49} = 0.72,$	N/A	Injury x genotype
zone – open-field	p = 0.6768	p = 0.3999		$F_{1,55} = 5.68,$
test				p = 0.0206*
Total distance	$F_{1,49} = 1.488,$	$F_{1,49} = 10.76,$	N/A	Injury x genotype
traveled – open-	p = 0.2284	p = 0.0019**		$F_{1,55} = 5.52,$
field test				p = 0.0224*
Seconds to fall –	$F_{1,43} = 0.89,$	F <sub>1,43</sub> = 1.20,	$F_{1,86} = 1.21$ ,	None
Rotarod test	p = 0.3498	p = 0.6637	p = 0.2735	
Discrimination	$F_{1,49} = 0.57,$	$F_{1,49} = 4.21,$	N/A	None
index – Y-maze	p = 0.4525	p = 0.0457*		
test				