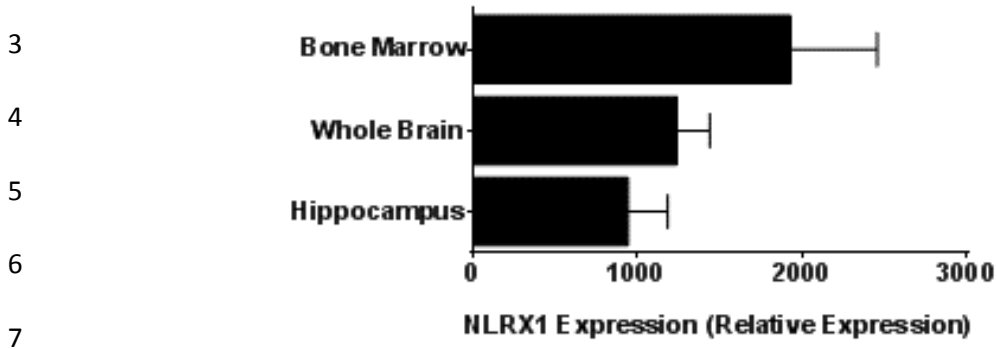
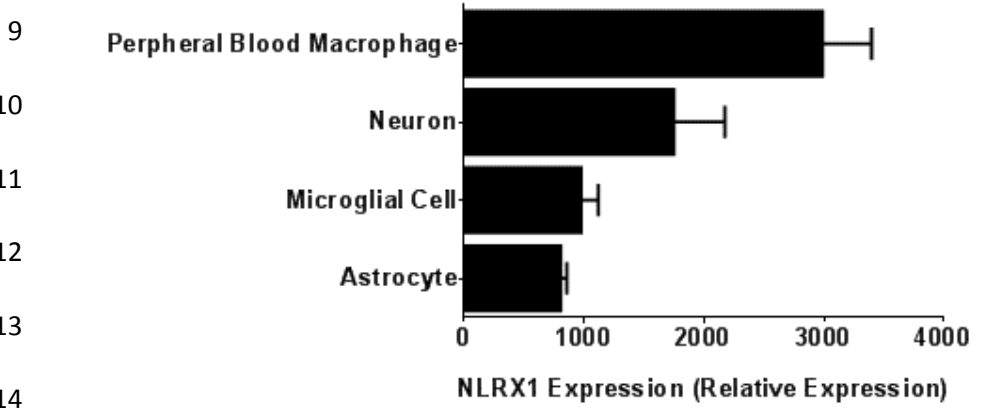


1 **Supplemental Figure 1.**

2 **A.**



8 **B.**



15

16 **Supplemental Figure 1. *NLRX1* is highly expressed in the brain and cells relevant to injury.**

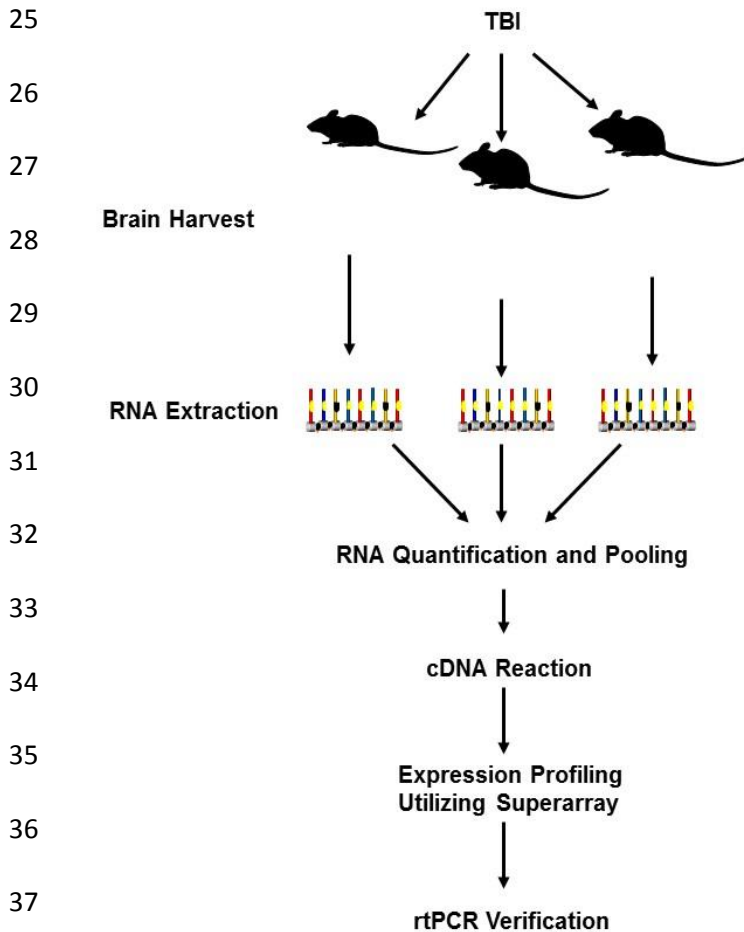
17 Expression of human *NLRX1* was evaluated in the brain and select cell types using a publicly
18 accessible microarray metadata analysis search engine (Nextbio:
19 <http://www.nextbio.com/b/search/ba.nb>. Accessed 2015 Dec. 10). Expression was compared
20 with bone marrow and macrophages, which highly express *NLRX1*.

21

22

23

24 **Supplemental Figure 2.**



39 **Supplemental Figure 2. Schematic Illustrating the Experimental Design for Expression**

40 **Profiling. A.** Multiple mice from each genotype and condition were subjected to either TBI or

41 sham. Brains were harvested 3 days following the initial injury. The total brain RNA from each

42 brain hemisphere (TBI or contralateral) was quantified for each mouse and pooled in equal

43 amounts in separate reactions for each genotype. The pooled RNA was converted into cDNA and

44 expression profiling was conducted using a panel of Superarrays (Qiagen). Expression data was

45 verified by evaluation of gene expression changes of a subset of individual genes using rtPCR

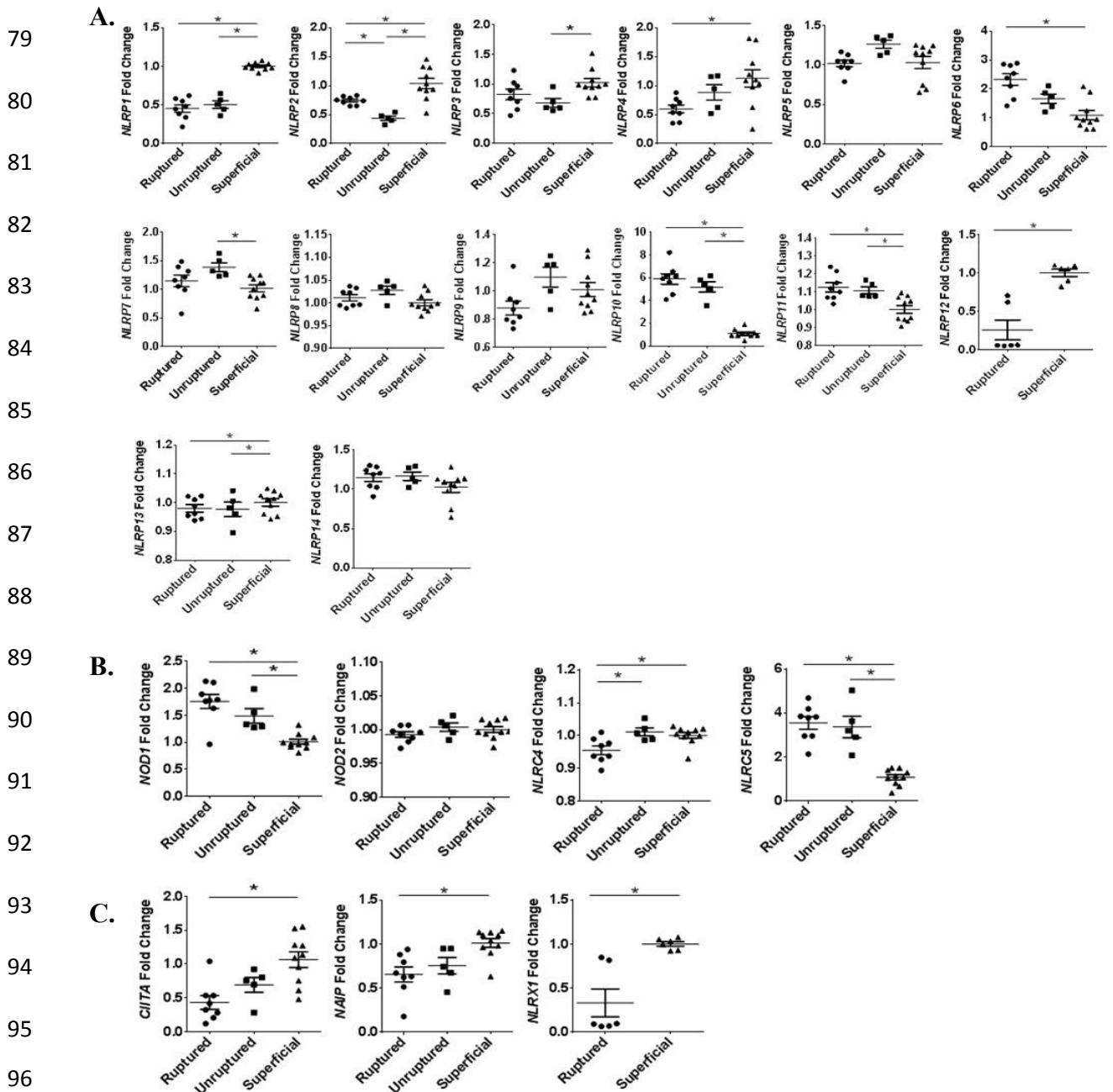
46 from both pooled and un-pooled samples.

47 **Supplemental Figure 3.**

	Fold Change	Fold Change	Gene Name	Fold Change	Gene Name	Fold Change	Gene Name
48	8.00 - 8.99	8.48	Card10	2.00	Tnfrsf1a	-2.02	Slc20a1
49	7.00 - 7.99	8.05	Relb	1.99	Crebbp	-4.10	Tnf
50	6.00 - 6.99	7.97	Il10	1.99	Ripk1	-8.61	Ccl2
51	5.00 - 5.99	4.75	Fas1	1.99	Eif2ak2		
52	4.00 - 4.99	4.12	Atf1	1.99	Nfkb1		
53	3.00 - 3.99	4.11	Agt	1.99	Egr1		
54	2.00 - 2.99	4.10	F2r	1.98	Cflar		
55	-1.99 - 1.99	4.10	Il1a	1.98	Ripk2		
56	-2.00 - -2.99	4.09	Irak1	1.97	Raf1		
57	-3.00 - -3.99	4.08	Bcl3	1.92	Card11		
58	-4.00 - -4.99	4.08	Tnfaip3	1.91	Csf1		
59	-5.00 - -5.99	4.08	Fadd	1.79	Csf3		
60	-6.00 - -6.99	4.06	Il1r1	1.11	Csf2		
61	-7.00 - -7.99	4.05	Tlr1	1.03	Lta		
62	-8.00 - -8.99	4.04	Cd27	1.02	Hmox1		
63		4.02	Nfkbia	1.01	Tlr4		
64		4.01	Nod1	1.01	Ikbke		
65		3.98	Rela	1.01	Icam1		
66		3.94	Myd88	1.01	Traf5		
67		3.93	Fos	1.01	Zap70		
68		2.05	Egfr	1.01	Tlr9		
69		2.04	Stat1	1.01	Ifng		
70		2.04	Tnfsf14	1.01	Smad3		
71		2.03	Birc3	1.00	Casp1		
72		2.03	Nfkb2	-1.00	Tlr3		
73		2.02	Elk1	-1.00	Tollip		
74		2.02	Bcl10	-1.00	Traf3		
75		2.02	Ikbkg	-1.01	Tnfrsf1b		
76		2.02	Tlr6	-1.01	Tnfsf10		
77		2.02	Cd40	-1.01	Mapk3		
		2.02	Ikbkb	-1.02	Ccl5		
		2.02	Map3k1	-1.02	Bcl2a1a		
		2.02	Tnfrsf10b	-1.04	Atf2		
		2.02	Traf2	-1.99	Il1b		
		2.02	Akt1				
		2.02	Chuk				
		2.01	Irf1				
		2.01	Ltbr				
		2.01	Casp8				
		2.01	Tlr2				
		2.01	Jun				
		2.01	Bcl2l1				
		2.01	Rel				
		2.01	Irak2				
		2.01	Tbk1				
		2.00	Tradd				
		2.00	Traf6				

71 **Supplemental Figure 3. Genes associated with NF-κB signaling are significantly up-**
 72 **regulated in *Nlr1*^{-/-} mice following TBI.** Gene transcription was profiled from RNA collected
 73 from wild type and *Nlr1*^{-/-} brains 3 days following injury. Data reflects the fold change in
 74 expression for genes associated with NF-κB signaling that were identified as being significantly
 75 up- or down-regulated in the brain of *Nlr1*^{-/-} mice compared to the wild type animals. Greater
 76 than a 2-fold change in gene expression is considered significant. Three randomly selected brains
 77 from each genotype and treatment group were selected and pooled for profiling studies.

78 Supplemental Figure 4.



97 **Supplemental Figure 4. NLR expression following non-traumatic brain injury in human**
 98 **subjects. A-C)** The fold change in gene expression was determined for the 22 human NLR family
 99 members using a retrospective analysis of gene expression metadata from studies evaluating either
 100 ruptured, unruptured, or superficial intracranial aneurysms in human subjects (GSE26969;
 101 GSE54083). (n=5-10 specimens/group; *p<0.05).