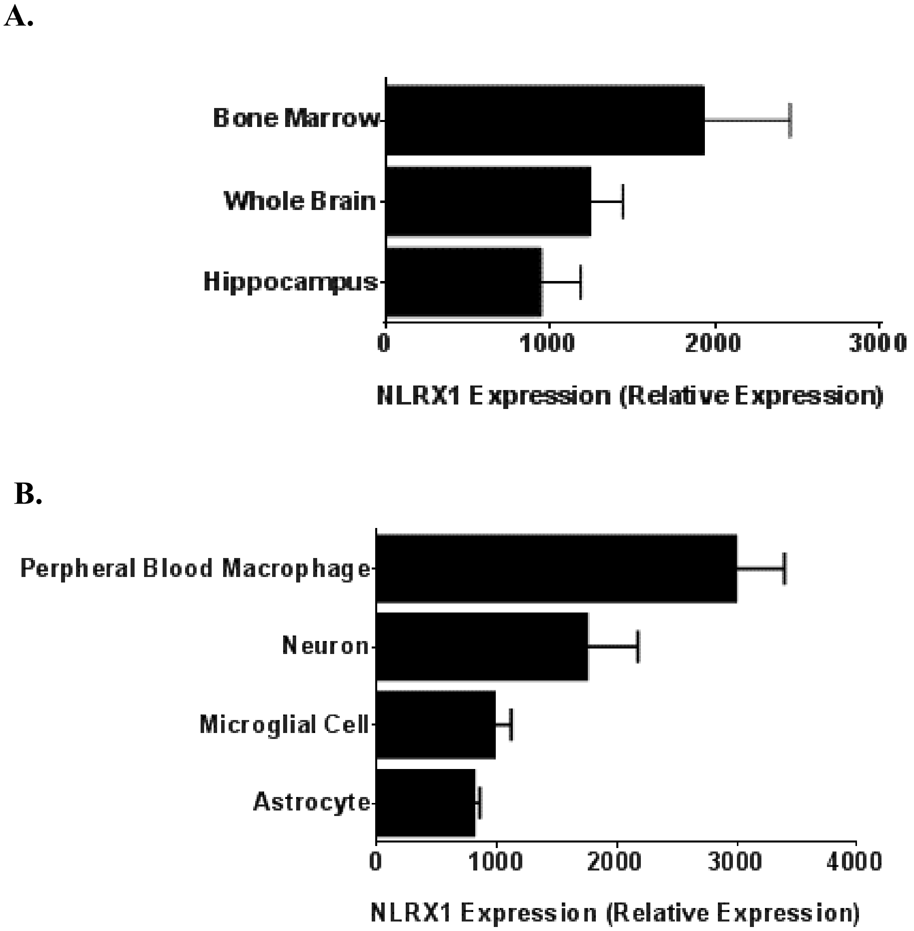
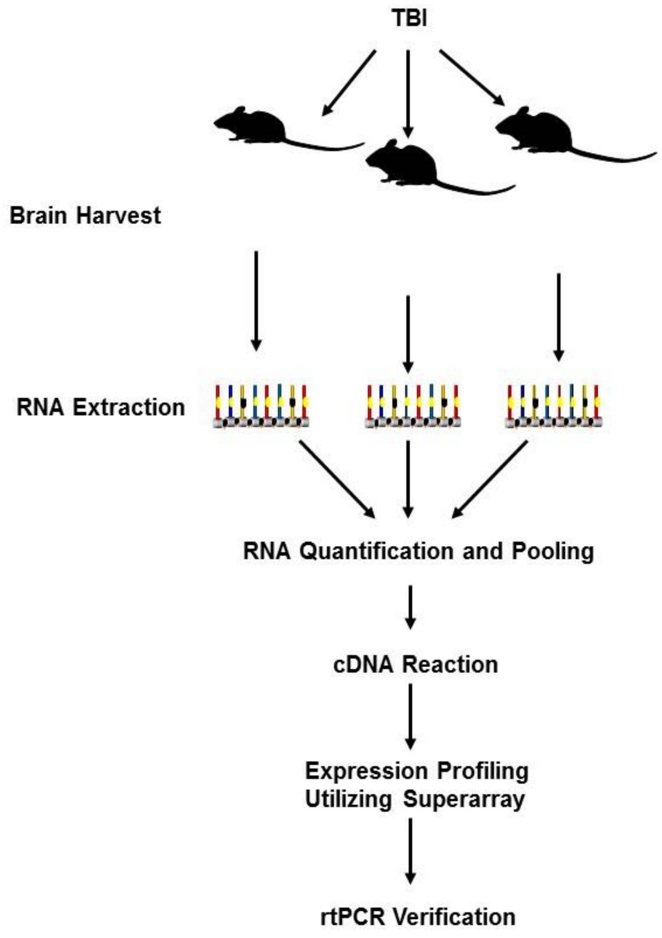
Supplemental Figure 1.



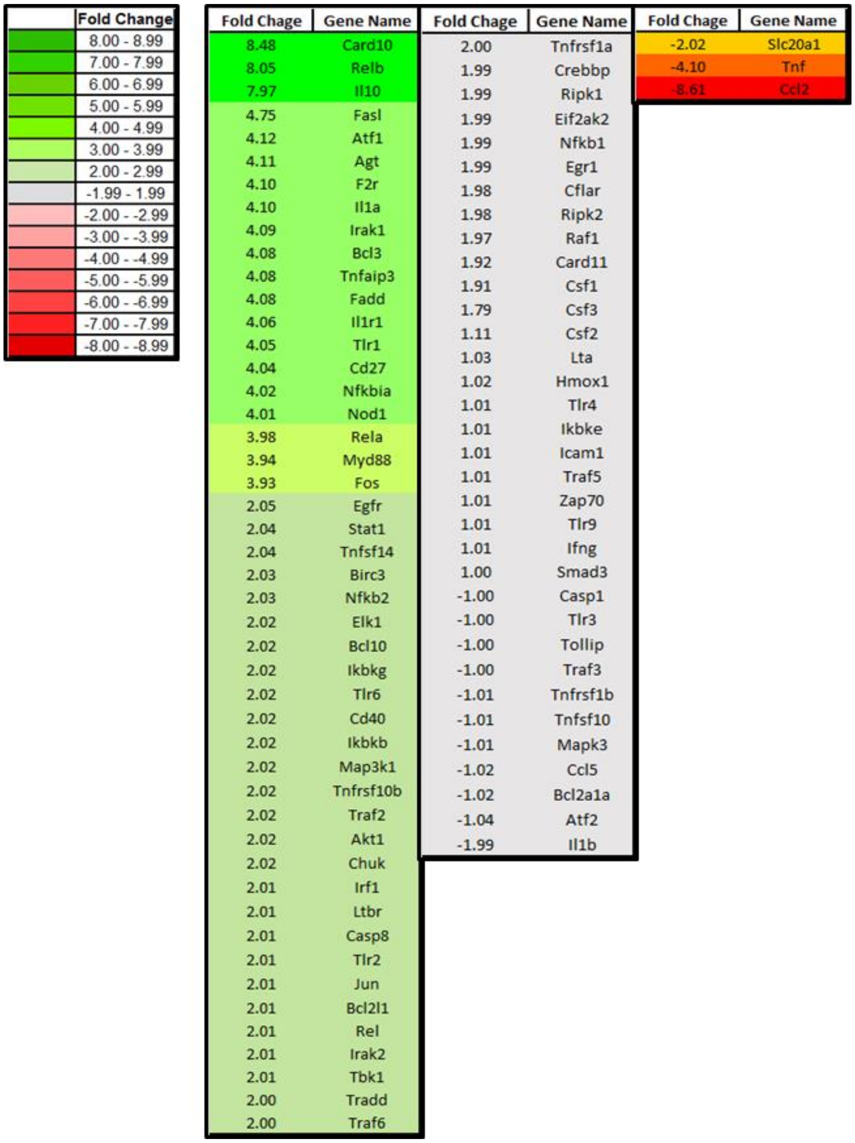
Supplemental Figure 1. ***NLRX1*** **is highly expressed in the brain and cells relevant to injury.** Expression of human *NLRX1* was evaluated in the brain and select cell types using a publicly accessible microarray metadata analysis search engine (Nextbio: http://www.nextbio.com/b/search/ba.nb. Accessed 2015 Dec. 10). Expression was compared with bone marrow and macrophages, which highly express *NLRX1*.

Supplemental Figure 2.



Supplemental Figure 2. Schematic Illustrating the Experimental Design for Expression Profiling. A. Multiple mice from each genotype and condition were subjected to either TBI or sham. Brains were harvested 3 days following the initial injury. The total brain RNA from each brain hemisphere (TBI or contralateral) was quantified for each mouse and pooled in equal amounts in separate reactions for each genotype. The pooled RNA was converted into cDNA and expression profiling was conducted using a panel of Superarrays (Qiagen). Expression data was verified by evaluation of gene expression changes of a subset of individual genes using rtPCR from both pooled and un-pooled samples.

Supplemental Figure 3.



	Fold Change
🟩	8.00 - 8.99
🟩	7.00 - 7.99
🟩	6.00 - 6.99
🟩	5.00 - 5.99
🟩	4.00 - 4.99
🟩	3.00 - 3.99
🟩	2.00 - 2.99
⬜	-1.99 - 1.99
🟥	-2.00 - -2.99
🟥	-3.00 - -3.99
🟥	-4.00 - -4.99
🟥	-5.00 - -5.99
🟥	-6.00 - -6.99
🟥	-7.00 - -7.99
🟥	-8.00 - -8.99

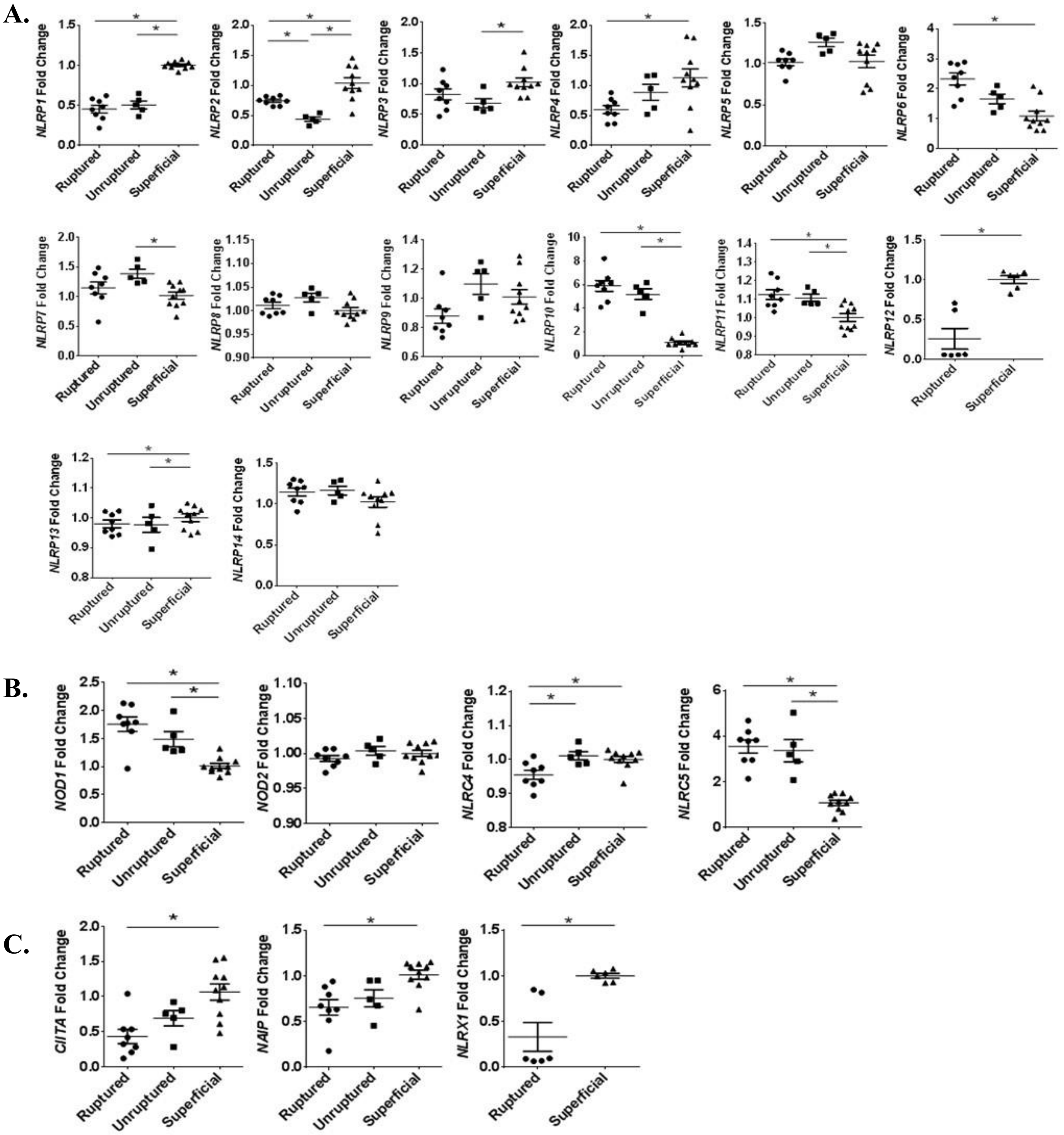
Fold Chage	Gene Name
8.48	Card10
8.05	Relb
7.97	Il10
4.75	Fasl
4.12	Atf1
4.11	Agt
4.10	F2r
4.10	Il1a
4.09	Irak1
4.08	Bcl3
4.08	Tnfaip3
4.08	Fadd
4.06	Il1r1
4.05	Tlr1
4.04	Cd27
4.02	Nfkbia
4.01	Nod1
3.98	Rela
3.94	Myd88
3.93	Fos
2.05	Egfr
2.04	Stat1
2.04	Tnfsf14
2.03	Birc3
2.03	Nfkb2
2.02	Elk1
2.02	Bcl10
2.02	Ikbkg
2.02	Tlr6
2.02	Cd40
2.02	Ikbkb
2.02	Map3k1
2.02	Tnfrsf10b
2.02	Traf2
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

Fold Chage	Gene Name
2.00	Tnfrsf1a
1.99	Crebbp
1.99	Ripk1
1.99	Eif2ak2
1.99	Nfkb1
1.99	Egr1
1.98	Cflar
1.98	Ripk2
1.97	Raf1
1.92	Card11
1.91	Csf1
1.79	Csf3
1.11	Csf2
1.03	Lta
1.02	Hmox1
1.01	Tlr4
1.01	Ikbke
1.01	Icam1
1.01	Traf5
1.01	Zap70
1.01	Tlr9
1.01	Ifng
1.00	Smad3
-1.00	Casp1
-1.00	Tlr3
-1.00	Tollip
-1.00	Traf3
-1.01	Tnfrsf1b
-1.01	Tnfsf10
-1.01	Mapk3
-1.02	Ccl5
-1.02	Bcl2a1a
-1.04	Atf2
-1.99	Il1b

Fold Chage	Gene Name
-2.02	Slc20a1
-4.10	Tnf
-8.61	Ccl2

Supplemental Figure 3. Genes associated with NF-κB signaling are significantly up-regulated in *Nlrx1*$^{-/-}$ mice following TBI. Gene transcription was profiled from RNA collected from wild type and *Nlrx1*$^{-/-}$ brains 3 days following injury. Data reflects the fold change in expression for genes associated with NF-κB signaling that were identified as being significantly up- or down-regulated in the brain of *Nlrx1*$^{-/-}$ mice compared to the wild type animals. Greater than a 2-fold change in gene expression is considered significant. Three randomly selected brains from each genotype and treatment group were selected and pooled for profiling studies.

Supplemental Figure 4.



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