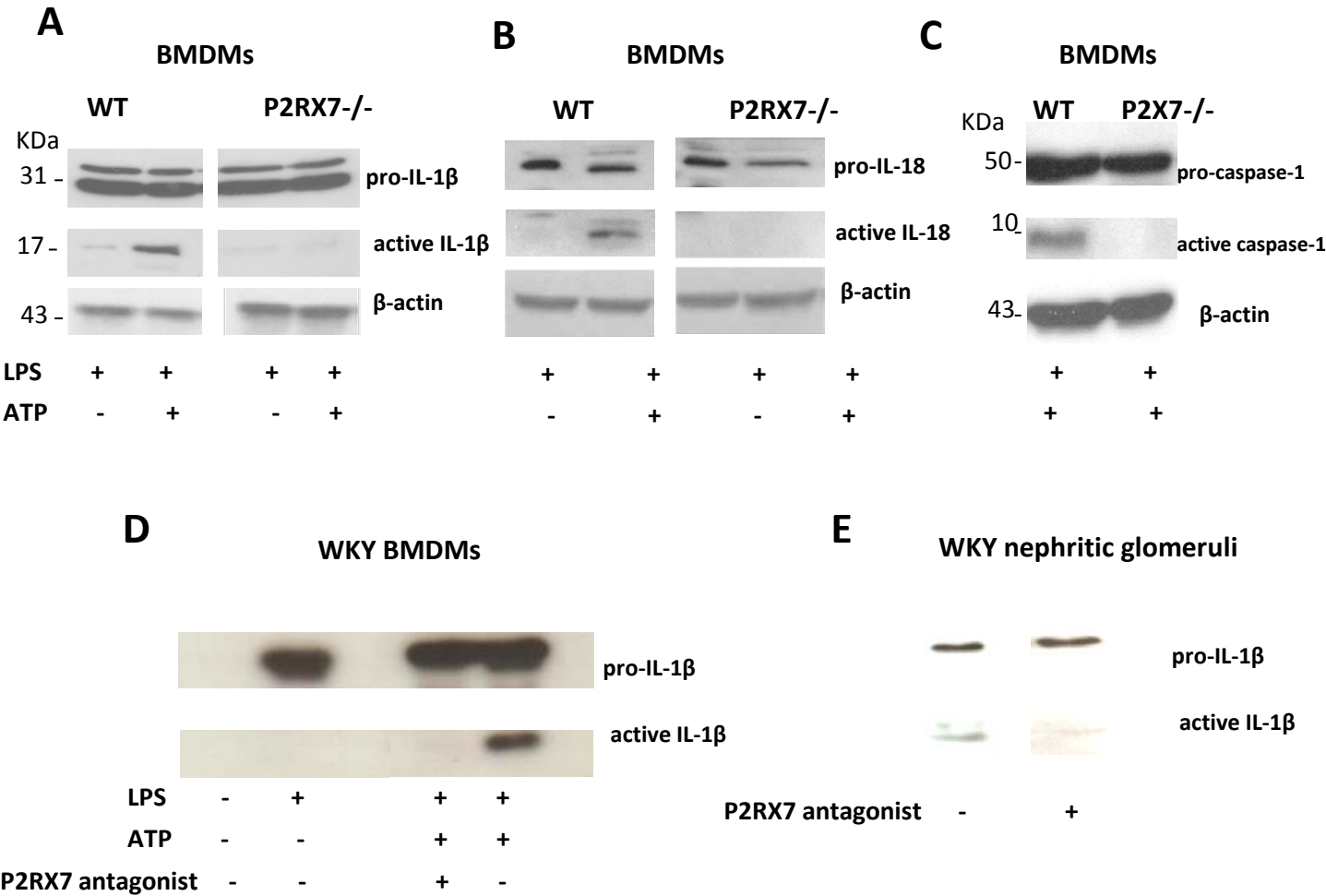


INDEL								
Gene ID	Chr	Position	Reference sequence	Alternative sequence	LEW	WKY	Indel size	Variant type
P2rx7	12	35072083	-	T	0	2	-1	DOWNSTREAM
P2rx7	12	35073540	A	-	0	2	1	DOWNSTREAM
P2rx7	12	35074234	CCCCA	-	2	0	5	3PRIME_UTR
P2rx7	12	35074346	T	-	0	2	1	3PRIME_UTR
P2rx7	12	35074525	GACCC	-	2	0	5	3PRIME_UTR
P2rx7	12	35119052	-	A	0	1	-1	UPSTREAM
P2rx7	12	35119065	-	AAG	2	0	-3	UPSTREAM
P2rx7	12	35119850	GTGT	-	2	0	4	UPSTREAM
P2rx7	12	35119924	-	GT	2	0	-2	UPSTREAM
P2rx7	12	35119960	TGTC	-	1	0	4	UPSTREAM
P2rx7	12	35121772	-	T	2	0	-1	UPSTREAM
P2rx7	12	35121773	AAATAAAA	-	2	0	8	UPSTREAM
P2rx7	12	35121817	AAAT	-	2	0	4	UPSTREAM
SNP								
Gene ID	Chr	Position	Reference sequence	Alternative sequence	LEW	WKY	Variant type	
P2rx7	12	35072383	T	C	0	2	DOWNSTREAM	
P2rx7	12	35072670	T	C	0	2	DOWNSTREAM	
P2rx7	12	35072741	C	T	0	2	DOWNSTREAM	
P2rx7	12	35072774	C	T	0	2	DOWNSTREAM	
P2rx7	12	35072918	G	A	0	2	DOWNSTREAM	
P2rx7	12	35073362	C	T	0	2	DOWNSTREAM	
P2rx7	12	35073393	G	A	0	2	DOWNSTREAM	
P2rx7	12	35073765	G	A	0	2	DOWNSTREAM	
P2rx7	12	35073771	C	T	0	2	DOWNSTREAM	
P2rx7	12	35074991	C	T	2	0	3PRIME_UTR	
P2rx7	12	35075336	T	G	2	0	3PRIME_UTR	
P2rx7	12	35075338	G	A	2	0	3PRIME_UTR	
P2rx7	12	35089723	A	G	2	0	SPLICE_SITE	
P2rx7	12	35094464	G	T	2	0	SYNONYMOUS_CODING	
P2rx7	12	35117199	G	T	2	0	UPSTREAM	
P2rx7	12	35117606	G	C	2	0	UPSTREAM	
P2rx7	12	35117607	G	A	2	0	UPSTREAM	
P2rx7	12	35118188	A	G	2	0	UPSTREAM	
P2rx7	12	35118226	T	C	2	0	UPSTREAM	
P2rx7	12	35118252	C	T	2	0	UPSTREAM	
P2rx7	12	35118942	C	T	2	0	UPSTREAM	
P2rx7	12	35118970	A	G	2	0	UPSTREAM	
P2rx7	12	35119042	C	T	2	0	UPSTREAM	
P2rx7	12	35119179	T	C	2	0	UPSTREAM	
P2rx7	12	35119422	T	C	2	0	UPSTREAM	
P2rx7	12	35119830	A	G	2	0	UPSTREAM	
P2rx7	12	35121637	T	C	2	0	UPSTREAM	

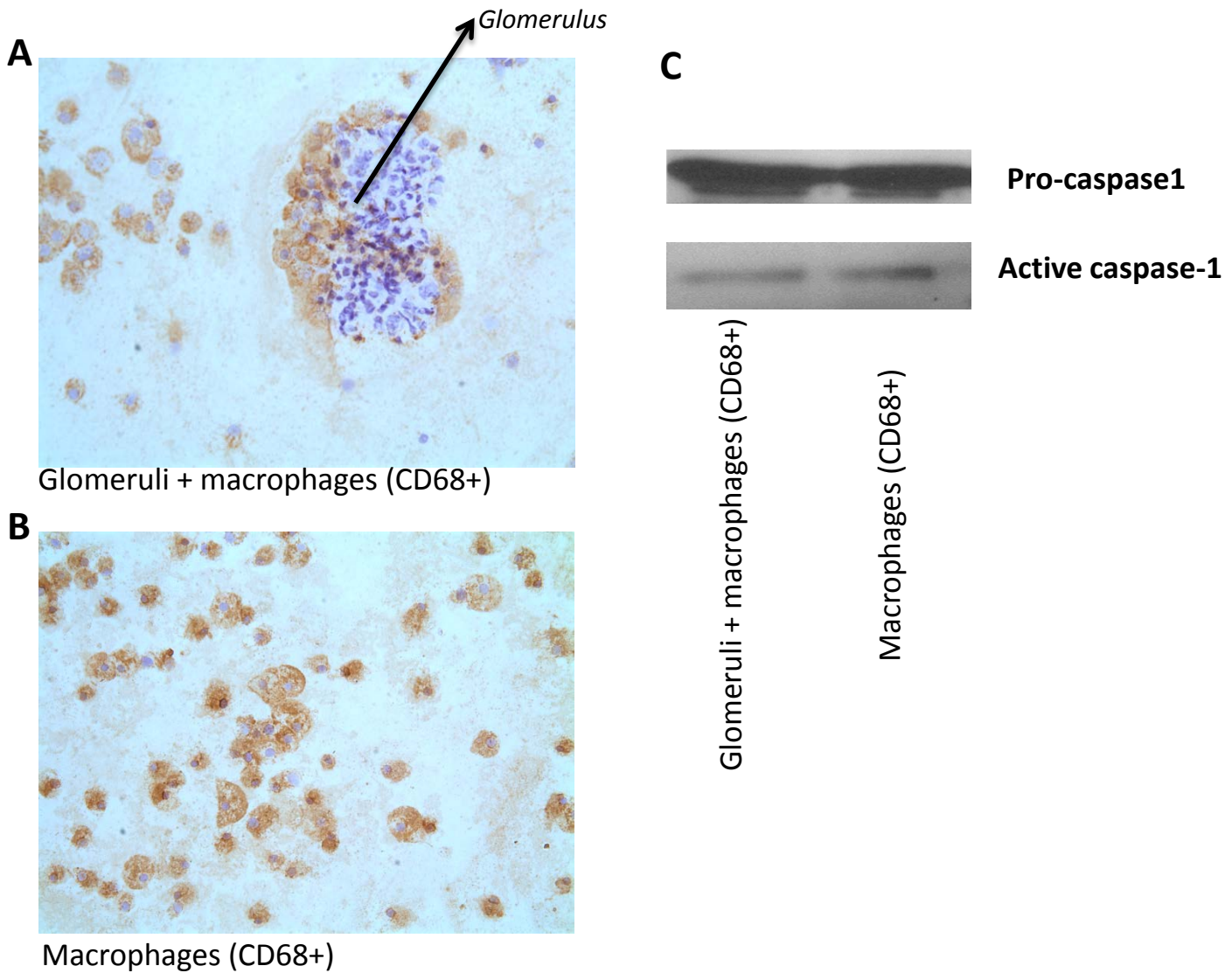
Supplemental Figure S1. P2RX7 gene sequence variants between WKY and LEW strains. The first panel shows insertion/deletions (indel) downstream, within the coding region, untranslated regions (UTR) and upstream P2RX7. The lower panel shows single nucleotide polymorphisms (SNPs) throughout the whole gene. “0” designates homozygous reference (Brown Norway RGSC_v3.4) allele; “1” designates heterozygous and “2” designates homozygous variant genotype (different to BN). The synonymous coding SNP is highlighted in yellow.

Supplemental Figure S2



Supplemental Figure S2. P2RX7 is essential for ATP-induced Nlrp3 inflammasome activation in rodent bone marrow derived macrophages. To confirm that caspase-1 dependent IL-1 β and IL-18 release was regulated by P2RX7, BMDMs from P2RX7 deficient (P2RX7^{-/-}) and wild-type (WT) mice were primed with LPS (1 μ g/ml, 5 hours) and incubated 30 min with ATP (5mM). Cell lysates and supernatants were subjected to Western Blotting for detection of pro- and active forms of IL-1 β (A), IL-18 (B) and caspase-1 (C). (D) WKY BMDMs were subjected to Western Blotting to detect IL-1 β with (+) or without (-) pre-incubation with P2RX7 antagonist (AZ10606120, 3 μ M, 1h) in LPS primed (+) and ATP-stimulated cells (+). (E) P2RX7 antagonist (AZ10606120, 3 μ M, 24h) was also used in ex vivo cultured WKY nephritic glomeruli 4 days following the induction of NTN. These results are representative of three independent experiments.

Supplemental Figure S3



Supplemental figure S3. (A) *Ex vivo* culture of the WKY nephritic glomeruli shows a glomerulus positively stained for CD68 as well as surrounding CD68+ macrophages. (B) after 24 hours of culture, glomeruli were washed and the remaining macrophages were cultured for an additional 24 hours. Cells and supernatants were collected from glomeruli+macrophages and macrophages only were subjected to Caspase-1 Western Blotting (C). N=3 WKY rats were used for NTN induction.