Figure S1

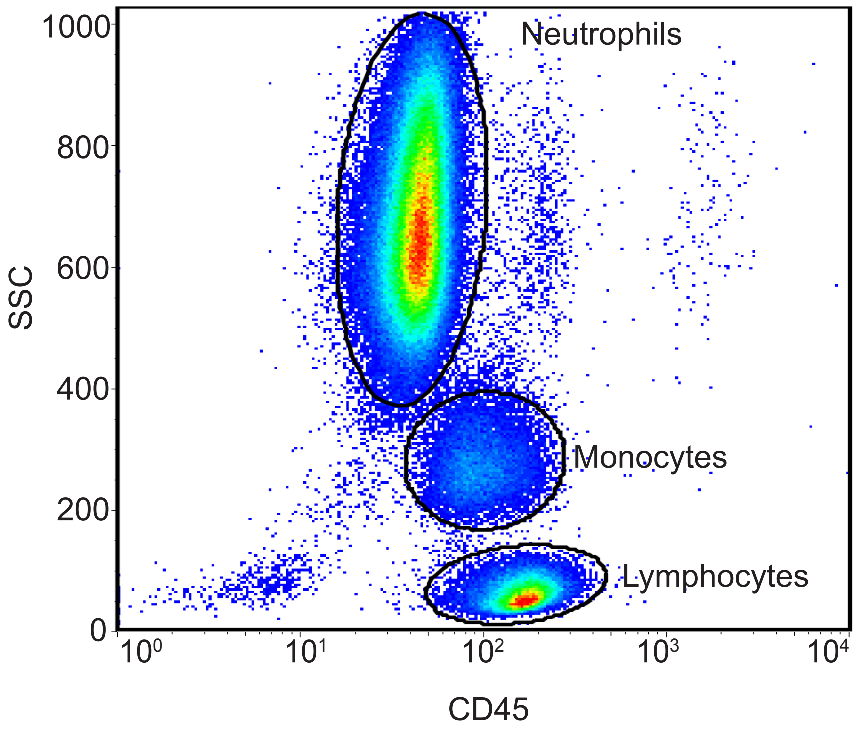

Figure S1: Gating strategy for clarifying monocyte, lymphocyte, and neutrophil populations in peripheral blood samples via flow cytometry. Neutrophil population was identified by forward and side scatter profile, CD45+, CD11b+, CD32+, CD177+, reduced positive correlation for CD14 (compared to monocytes), CD3-, CD19-, and CD20-. Monocyte population was identified by forward and side scatter profile, CD45+, CD3-, CD19-, and CD20-.

Table S1: Differences in expression of specific inflammatory markers in Brain Death and Sham compared to naive kidney tissue

	BD (n=16) vs Naïve (n=12)			Sham (n=6) vs Naïve (n=12)		
Gene	**FC**	**p value**	**FDR**	**FC**	**p value**	**FDR**
Inflammation						
CASP1	2.15	4.30E-05	4.20E-03	1.57	3.30E-02	3.44E-01
CASP4	1.42	6.82E-01	8.96E-01	1.87	7.17E-01	9.43E-01
CASP5	1.33	1.86E-01	5.52E-01	1.25	2.07E-01	6.91E-01
CCL2	8.63	5.53E-11	3.44E-07	3.79	6.12E-05	1.51E-02
CXCL8	1.68	4.20E-05	4.20E-03	1.42	3.40E-02	3.47E-01
IFNG	1.08	2.28E-01	6.02E-01	1.08	6.49E-01	9.24E-01
IL10	-1.12	9.36E-01	9.83E-01	1.11	6.79E-01	9.30E-01
IL12A	-1.01	7.07E-01	9.06E-01	-1.02	8.70E-01	9.78E-01
IL12B	-1.1	9.76E-01	9.93E-01	-1.01	9.52E-01	9.93E-01
IL17A	-1.22	4.12E-01	7.56E-01	-1.11	4.34E-01	8.44E-01
IL1B	1.41	3.13E-02	2.29E-01	1.28	1.17E-01	5.63E-01
IL6	4.56	2.15E-05	2.70E-03	1.65	1.83E-01	6.63E-01
TNF	1.16	7.98E-02	3.70E-01	1.21	2.88E-02	3.27E-01
Macrophage expression						
CCL11	3.33	1.88E-07	1.00E-04	2.98	9.18E-05	1.93E-02
CCL17	-1.04	7.69E-01	9.32E-01	1.09	4.93E-01	8.70E-01
CD14	1.93	8.40E-01	9.55E-01	1.35	3.32E-01	7.85E-01
CD68	1.55	6.20E-03	9.49E-02	1.4	7.94E-02	4.90E-01
CD80	1.05	7.54E-01	9.27E-01	1.03	6.78E-01	9.30E-01
EGR1	2.38	1.80E-03	4.61E-02	1.67	1.43E-01	6.06E-01
IL12B	-1.1	9.76E-01	9.93E-01	-1.01	9.52E-01	9.93E-01
IL1R1	1.96	7.91E-01	9.39E-01	2.19	9.50E-01	9.93E-01
MRC1L1	1.13	5.17E-01	8.18E-01	1.71	4.94E-01	8.70E-01
NR4A1	1.41	3.70E-03	7.09E-02	1.48	3.78E-02	3.61E-01
SOCS3	1.57	8.00E-04	2.80E-02	1.22	1.95E-01	6.76E-01
TGM2	1.43	5.07E-02	2.94E-01	1.34	2.30E-01	7.13E-01
TLR1	1.18	7.90E-03	1.08E-01	-1.01	9.56E-01	9.94E-01
TLR2	1.43	8.83E-02	3.90E-01	-1.12	6.70E-01	9.29E-01
TLR8	-1.02	9.77E-01	9.94E-01	-1.08	2.38E-01	7.21E-01
MAMU-DQA1	-1.08	9.30E-02	3.99E-01	-1.31	3.60E-03	1.28E-01
MAMU-DMA	1.42	5.09E-02	2.95E-01	-1.01	6.03E-01	9.11E-01
MAMU-DOB	1.2	9.44E-02	4.03E-01	1.01	9.84E-01	9.98E-01
MAMU-DPB	1.39	2.40E-03	5.46E-02	1.24	1.35E-01	5.94E-01
MAMU-DQB1	1.53	2.14E-02	1.88E-01	1.17	7.67E-01	9.55E-01
MAMU-DRB1	1.31	2.44E-02	2.01E-01	1.03	8.03E-01	9.62E-01
MAMU-DMB	1.56	4.80E-03	8.28E-02	1.26	1.76E-01	6.54E-01
Neutrophil expression						
C3AR1	1.51	8.75E-02	3.89E-01	1.16	8.77E-01	9.80E-01
MME	-1.17	1.33E-01	4.71E-01	1.43	2.61E-01	7.37E-01
SELL	1.12	0.6125	0.8643	1.5	0.0317	0.3388
ITGAM	1.17	0.6685	0.8905	1.03	0.6773	0.93
CSF2RB	1.2	0.0665	0.3404	1.18	0.2107	0.6942
CSF3R	1.06	0.8703	0.963	1.16	0.6603	0.927
FCGR3	2.08	0.8862	0.9684	1.75	0.9112	0.9879
FCGRT	-1.45	0.0493	0.2897	-1.58	0.0103	0.215
FPR1	1.02	0.5514	0.8353	-1.09	0.6369	0.9208
IL1R2	-1.11	0.0059	0.0934	-1.09	0.0295	0.3281
IL1RN	1.42	0.046	0.2787	1.17	0.0497	0.4046
IL8RB	-1.33	0.0157	0.1592	1.19	0.9516	0.9932
MPO	-1.05	0.8082	0.9456	1.11	0.414	0.8329

Table S1: Transcription analysis shows that genes in renal tissue related to inflammation – including CXCL8, CCL2, and CASP1 – are significantly upregulated in BD and sham compared to naïve, with intensified expression in BD conditions. Macrophage and neutrophil gene markers present only minimal evidence of condition-related changes.

Table S2: Specific markers of Complement, Contact, and Coagulation related pathways genes in Brain Death and Sham kidneys vs naïve kidney expression

	BD (n=16) vs Naïve (n=12)			Sham (n=6) vs Naïve (n=12)		
Gene	**FC**	**p value**	**FDR**	**FC**	**p value**	**FDR**
Complement						
C1QA	1.07	6.12E-01	8.64E-01	-1.08	6.12E-01	8.64E-01
LOC718307; C1QC	1.41	9.21E-01	9.78E-01	1.24	9.21E-01	9.78E-01
C1QL2	-1.08	8.22E-01	9.51E-01	-1.1	8.22E-01	9.51E-01
C1QL3	-1.04	8.70E-01	9.63E-01	1.12	8.70E-01	9.63E-01
C1R	1.83	5.48E-01	8.33E-01	2.44	5.48E-01	8.33E-01
C1S	1.39	2.46E-01	6.19E-01	2.66	2.46E-01	6.19E-01
C1S	-1.13	2.01E-01	5.72E-01	1.6	2.01E-01	5.72E-01
C3	1.43	8.96E-02	3.92E-01	2.09	8.96E-02	3.92E-01
C3	1.34	1.08E-01	4.29E-01	2.43	1.08E-01	4.29E-01
C5	-1.99	1.83E-05	2.40E-03	-2.1	1.83E-05	2.40E-03
C5AR1	2.2	3.00E-04	1.61E-02	1.41	3.00E-04	1.61E-02
C6	1.13	1.94E-02	1.77E-01	1.34	1.94E-02	1.77E-01
C7	1.3	1.50E-01	4.99E-01	1.57	1.50E-01	4.99E-01
C8A	1.07	1.05E-02	1.27E-01	1.18	1.05E-02	1.27E-01
C8B	-1.05	5.10E-03	8.61E-02	-1.2	5.10E-03	8.61E-02
C9	-1.87	1.23E-02	1.38E-01	-1.75	1.23E-02	1.38E-01
CFB	3.37	8.68E-01	9.63E-01	5.15	8.68E-01	9.63E-01
MASP2; LOC722714	1.07	1.74E-02	1.67E-01	1.19	1.74E-02	1.67E-01
MBL2	1.17	1.46E-02	1.53E-01	1.15	1.46E-02	1.53E-01
Coagulation						
VWF; LOC723248	1.05	2.29E-01	6.02E-01	1.29	1.73E-01	6.49E-01
F10	-2.88	7.00E-04	2.71E-02	-2.08	4.54E-02	3.91E-01
F7	-1.5	1.00E-03	3.27E-02	-1.4	2.24E-02	2.95E-01
F8; LOC100424151	-1.32	5.00E-03	8.55E-02	1.07	2.62E-01	7.38E-01
F9	-1.01	7.10E-03	1.02E-01	-1.04	2.63E-02	3.15E-01
F11	1.12	1.21E-02	1.38E-01	1.08	3.85E-02	3.65E-01
FGA	-1.06	5.10E-03	8.61E-02	1.01	3.51E-02	3.51E-01
FGB	1.07	1.03E-02	1.25E-01	1.53	9.26E-02	5.16E-01
FGG	-1.11	6.10E-03	9.40E-02	-1.11	2.02E-02	2.83E-01
Fibrinolysis						
PLG	-4.82	5.90E-03	9.34E-02	-1.61	6.57E-01	9.26E-01
PLAU	1.93	1.34E-02	1.46E-01	1.36	2.00E-01	6.82E-01
PLAT	1.22	0.0609	0.3246	1.63	0.0121	0.2302
Contact						
F12	-1.05	3.70E-03	7.10E-02	-1.04	2.35E-02	2.99E-01
KLKB1	-4.86	2.00E-04	1.24E-02	-4.61	3.40E-03	1.23E-01
KNG1	-1.98	0.0003	0.0165	-1.69	0.0393	0.3683
SERPING1	1.43	2.77E-01	6.49E-01	1.81	3.54E-01	8.00E-01
BDKRB2	2.22	0.0463	0.2801	1.54	0.4023	0.8288

Table S2: Transcription analysis of genes in renal tissue related to complement, contact, or coagulation pathways demonstrate only minor changes in expression in BD and sham vs naïve samples. These pathways are regulated at the level of protein, which are mainly expressed in liver rather than kidney.

Table S3: Specific markers of acute kidney injury related genes in Brain Death and Sham kidneys vs naïve kidney expression

Gene	BD (n=16) vs Naïve (n=12)			Sham (n=6) vs Naïve (n=12)		
	FC	p value	FDR	FC	p value	FDR
Complement						
SPP1	27.99	4.09E-13	7.64E-09	28.19	7.35E-11	2.75E-06
HAVCR1	19.88	2.06E-09	5.14E-06	16.85	1.64E-07	3.00E-04
LGALS3	4.77	2.03E-07	1.00E-04	3.69	3.58E-05	1.04E-02
CYR61	3.61	1.45E-07	1.00E-04	2.12	3.36E-02	3.46E-01
TNC; LOC100427764	3.15	1.64E-02	1.63E-01	2.75	2.08E-01	6.91E-01
ANXA3	2.82	9.49E-07	3.00E-04	2.1	5.00E-03	1.51E-01
CXCL1	2.47	1.00E-04	8.90E-03	2.7	5.70E-03	1.62E-01
EGR1	2.38	1.80E-03	4.61E-02	1.67	1.43E-01	6.06E-01
ACTA2	2.24	1.30E-03	3.81E-02	2.22	1.31E-02	2.38E-01
PEA15	2.07	4.36E-06	1.00E-03	1.39	6.53E-02	4.53E-01
CLDN7	2.07	1.44E-05	2.00E-03	1.7	2.50E-03	1.07E-01
IER2; LOC100423359	1.92	2.03E-06	5.00E-04	1.31	2.09E-01	6.92E-01
TNFRSF1A	1.85	4.00E-04	1.80E-02	1.78	7.00E-04	5.51E-02
CLU	1.84	3.16E-02	2.30E-01	1.19	8.16E-01	9.66E-01
AKAP12	1.83	5.00E-04	2.02E-02	1.18	4.59E-01	8.55E-01
VCAM1	1.76	7.40E-03	1.04E-01	1.23	4.21E-01	8.38E-01
FOSL1	1.76	3.00E-04	1.51E-02	1.31	1.19E-01	5.67E-01
A2M	1.69	8.79E-01	9.67E-01	2.04	1.84E-01	6.64E-01
CDKN1A	1.57	2.96E-01	6.66E-01	1.99	1.16E-01	5.61E-01
ANXA2	1.52	9.83E-06	1.60E-03	1.21	3.43E-02	3.49E-01
HMOX1	1.33	2.36E-01	6.11E-01	3.19	1.00E-03	6.94E-02
FOS	1.3	8.60E-02	3.85E-01	1.36	2.37E-01	7.20E-01
SRXN1	1.3	1.19E-01	4.48E-01	2.23	3.40E-03	1.23E-01
SPHK1	1.28	9.50E-03	1.19E-01	1.14	6.44E-01	9.23E-01
MYO5A	1.27	5.49E-01	8.34E-01	1.34	6.75E-02	4.59E-01
TUBB	1.26	2.21E-01	5.93E-01	1.16	4.64E-01	8.58E-01
BCAT1	1.19	2.06E-02	1.83E-01	1.2	1.60E-01	6.32E-01
SLC16A7	1.07	2.34E-01	6.09E-01	-1.21	6.95E-01	9.35E-01
EGF	1.06	2.88E-01	6.58E-01	1.12	3.61E-01	8.05E-01
COL3A1	-1.06	5.87E-01	8.52E-01	-1.66	2.92E-02	3.27E-01
IL18	-1.07	9.40E-02	4.02E-01	-1.36	2.40E-02	3.02E-01
COL18A1	-1.1	8.93E-02	3.92E-01	-1.08	2.49E-01	7.28E-01
LIFR	-1.3	5.22E-02	2.99E-01	-1.56	5.85E-02	4.33E-01
AQP1	-1.52	1.81E-01	5.45E-01	-1.02	6.15E-02	4.41E-01
GAS2	-1.97	3.90E-03	7.32E-02	-2.69	4.70E-03	1.46E-01
AFM	-4.29	1.30E-03	3.77E-02	-1.54	6.01E-01	9.10E-01

Table S3: Transcription analysis of genes in renal tissue related to AKI, particularly SPP1 and HAVCR1 (KIM1) along with a variety of mitogens, show increased expression in both BD and sham conditions compared to naïve.