

Table S1 Primer sequences for RT-qPCR

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
<i>β-actin</i>	GGAGATTACTGCCCTGGCTCCTA	GACTCATCGTACTCCTGCTTGCTG
<i>TLR2</i>	GCCCTCAGTTCTGGAGTGTG	GCGCCCTAAGAGCAGGATCAA
<i>S100A8</i>	GGGATGACTTCAGGAAAATGGTC	CTGTCTTTATGAGCTGCCACG

Table S2 Molecular docking parameters for simvastatin with *TLR2* and *S100A8*

Parameter	<i>TLR2</i> (PDB: 2Z7X)	<i>S100A8</i>
Software	AutoDock Vina 1.2.7	AutoDock Vina 1.2.7
Grid box center (x, y, z)	-16.6, -21.6, 10.7	16, -46, -21
Grid box size (x, y, z)	16.9, 28.6, 17.8	30, 35, 35
Exhaustiveness	10	10

Table S3 Effect sizes, confidence intervals, and post-hoc statistical power for molecular validation endpoints

Assay	Comparison	n (Control)	n (IC)	Cohen's d	95% CI	Mean ± SD (Control)	Mean ± SD (IC)	Actual Power
WB	S100A8 protein	3	3	2.382	0.29 - 4.475	0.7599±0.2703	1.274±0.1417	0.5704331
WB	TLR2 protein	3	3	2.306	0.241 - 4.37	0.8240±0.1321	1.199±0.1883	0.5704331
RT-qPCR	S100A8 mRNA	3	3	4.436	1.858 - 7.013	1.113±0.6443	34.64±10.67	0.9764591
RT-qPCR	TLR2 mRNA	3	3	3.375	1.217 - 5.533	1.018±0.2301	23.01±9.212	0.8644749

Power analysis conducted using G*Power 3.1 for two-tailed independent *t*-test, $\alpha=0.05$.

Table S4 Spearman correlation coefficients and adjusted p-values for the associations between S100A8/TLR2 expression and 22 immune cell subsets

immune_cell	gene	cor	p.value	p.adj	pstar
B cells naive	S100A8	0.316137	0.077949	0.125917	
B cells memory	S100A8	0.030803	0.86709	0.954545	
Plasma cells	S100A8	-0.15837	0.38664	0.477614	
T cells CD8	S100A8	-0.44738	0.010249	0.032972	*
T cells CD4 naive	S100A8	0.346287	0.052197	0.091345	
T cells CD4 memory resting	S100A8	-0.44359	0.010991	0.032972	*
T cells CD4 memory activated	S100A8	0.690049	1.24E-05	0.000261	***
T cells follicular helper	S100A8	0.500772	0.003509	0.018424	*
T cells regulatory (Tregs)	S100A8	NA	NA	NA	NA
T cells gamma delta	S100A8	0.008431	0.963472	0.963472	
NK cells resting	S100A8	0.276106	0.126102	0.189152	
NK cells activated	S100A8	-0.38639	0.028931	0.067507	
Monocytes	S100A8	0.482283	0.005184	0.021775	*
Macrophages M0	S100A8	0.615982	0.000175	0.001833	**
Macrophages M1	S100A8	0.261937	0.147557	0.193668	
Macrophages M2	S100A8	-0.56509	0.000752	0.005265	**
Dendritic cells resting	S100A8	-0.03331	0.856378	0.954545	
Dendritic cells activated	S100A8	0.355295	0.045984	0.087984	
Mast cells resting	S100A8	-0.42265	0.015956	0.041884	*
Mast cells activated	S100A8	-0.02102	0.90909	0.954545	
Eosinophils	S100A8	0.26596	0.141214	0.193668	
Neutrophils	S100A8	0.355139	0.046087	0.087984	
B cells naive	TLR2	0.530592	0.001784	0.006244	**
B cells memory	TLR2	0.317198	0.076901	0.17114	
Plasma cells	TLR2	-0.25534	0.158406	0.237609	
T cells CD8	TLR2	-0.47525	0.005981	0.017944	*
T cells CD4 naive	TLR2	0.304977	0.089645	0.17114	
T cells CD4 memory resting	TLR2	-0.53304	0.001683	0.006244	**
T cells CD4 memory activated	TLR2	0.741463	1.20E-06	2.53E-05	***
T cells follicular helper	TLR2	0.18556	0.309253	0.382019	
T cells regulatory (Tregs)	TLR2	NA	NA	NA	NA
T cells gamma delta	TLR2	0.23717	0.191213	0.267698	
NK cells resting	TLR2	0.31089	0.083291	0.17114	
NK cells activated	TLR2	-0.709	5.57E-06	5.85E-05	***
Monocytes	TLR2	-0.04174	0.820542	0.861569	
Macrophages M0	TLR2	0.611017	0.000204	0.001069	**
Macrophages M1	TLR2	0.419943	0.016718	0.043884	*
Macrophages M2	TLR2	-0.25999	0.150697	0.237609	
Dendritic cells resting	TLR2	0.101081	0.582002	0.643266	
Dendritic cells activated	TLR2	0.267554	0.138756	0.237609	
Mast cells resting	TLR2	-0.63673	8.93E-05	0.000625	***
Mast cells activated	TLR2	0.007006	0.969641	0.969641	
Eosinophils	TLR2	-0.10291	0.575171	0.643266	
Neutrophils	TLR2	0.216245	0.234548	0.307844	

Table S5 Urodynamic parameters measured by filling cystometry in the CYP-induced IC model and normal control groups

Group	MI_s	UV_mL	Pmax_cmH2O	RV_mL
Control1	317.25	0.20068	39.722	0.02394
Control2	294	0.1861	40.73	0.02092
Control3	334.75	0.20752	36.392	0.0222
Control4	291.75	0.18654	36.818	0.02266
Control5	293.5	0.18706	36.446	0.02432
Control6	277	0.179033	38.20167	0.01835
Control7	327.5	0.201	40.014	0.02184
Control8	287.4	0.179767	38.985	0.026617
CYP1	73.95833	0.03724	44.9264	0.060392
CYP2	90.70588	0.051211	43.66778	0.061111
CYP3	79.63636	0.0422	46.06773	0.060891
CYP4	78.8	0.045086	44.5219	0.060419
CYP5	77.45455	0.0416	44.63565	0.061991
CYP6	91.38889	0.053972	45.01722	0.060167
CYP7	64.62963	0.032271	43.81964	0.061414
CYP8	97.4375	0.054224	43.37294	0.059735

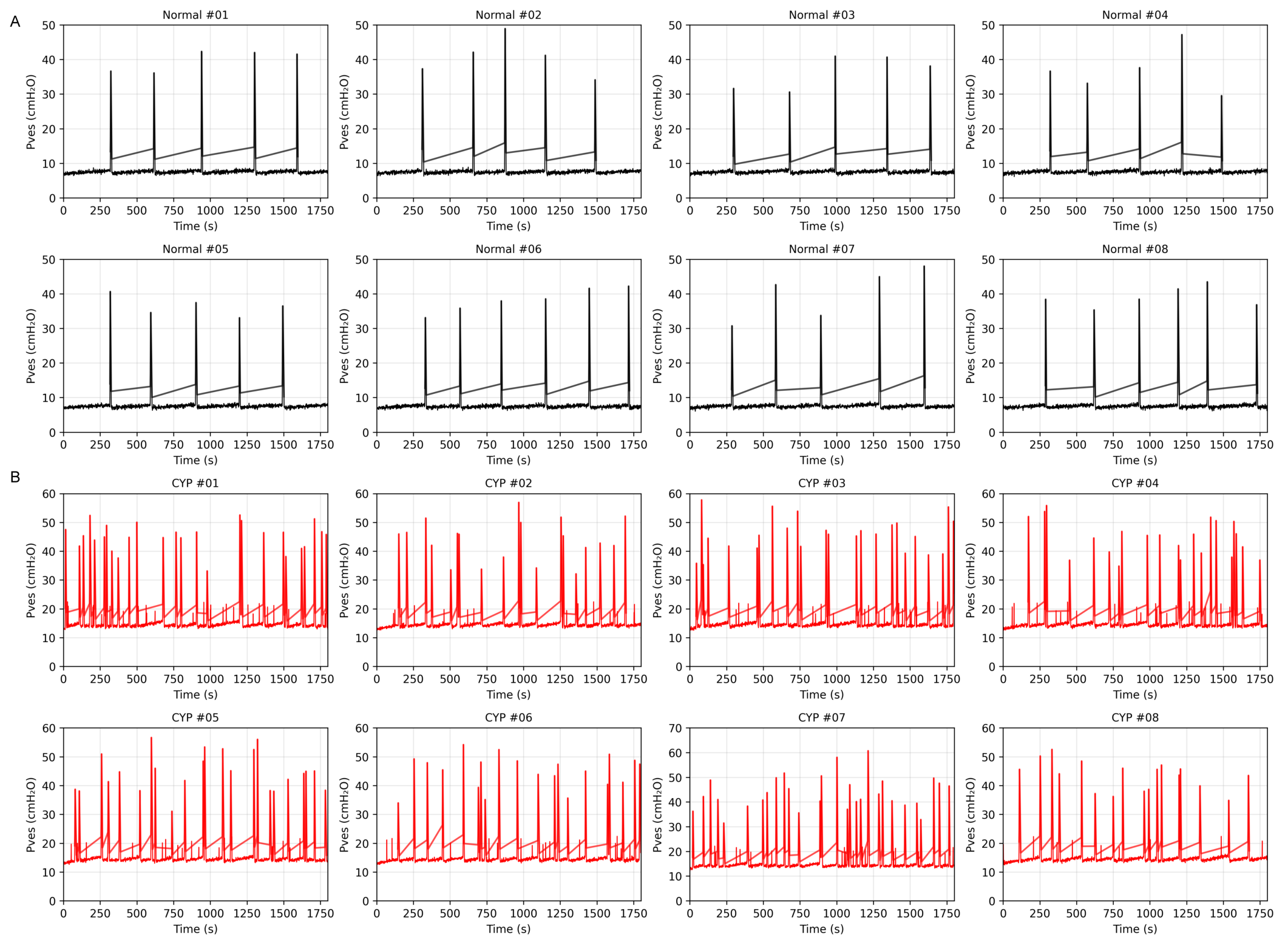


Figure S1 Complete urodynamic pressure-time tracings of all experimental animals. (A) Normal control group (n=8, black traces). (B) CYP-induced IC model group (n=8, red traces). CYP, cyclophosphamide; IC, interstitial cystitis.