SUPPLEMENTARY FIGURES FOR THE PUBLICATION:

Spatiotemporal proteomics reveals the molecular consequences of hormone treatment in a mouse model of lower urinary tract dysfunction

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Supplemental material

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Figure S-2. Temporal urinary proteomics of hormone treatment in mice: significantly modulated urine proteins related to immunologic processes
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Figure S-5. Full gene ontology network of mouse prostate proteomics (from Fig. 4B)
Figure S-6. Significantly enriched biological processes in a prior analysis of human patients with lower urinary tract symptoms (*n*=25 patients vs *n*=15 controls)

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Figure S-4. Three-dimensional animation of microcomputed tomography experiment in A: one untreated mouse and B: one hormone-treated mouse at 4 weeks
Table S-1. Full list of urine proteins across time (with iBAQ intensity and RM-ANOVA/ Tukey's results)
Table S-2. Full list of prostate tissue proteins at 8 weeks (with iBAQ intensity)
Table S-3. Significantly modulated prostate proteins (Perseus volcano results)

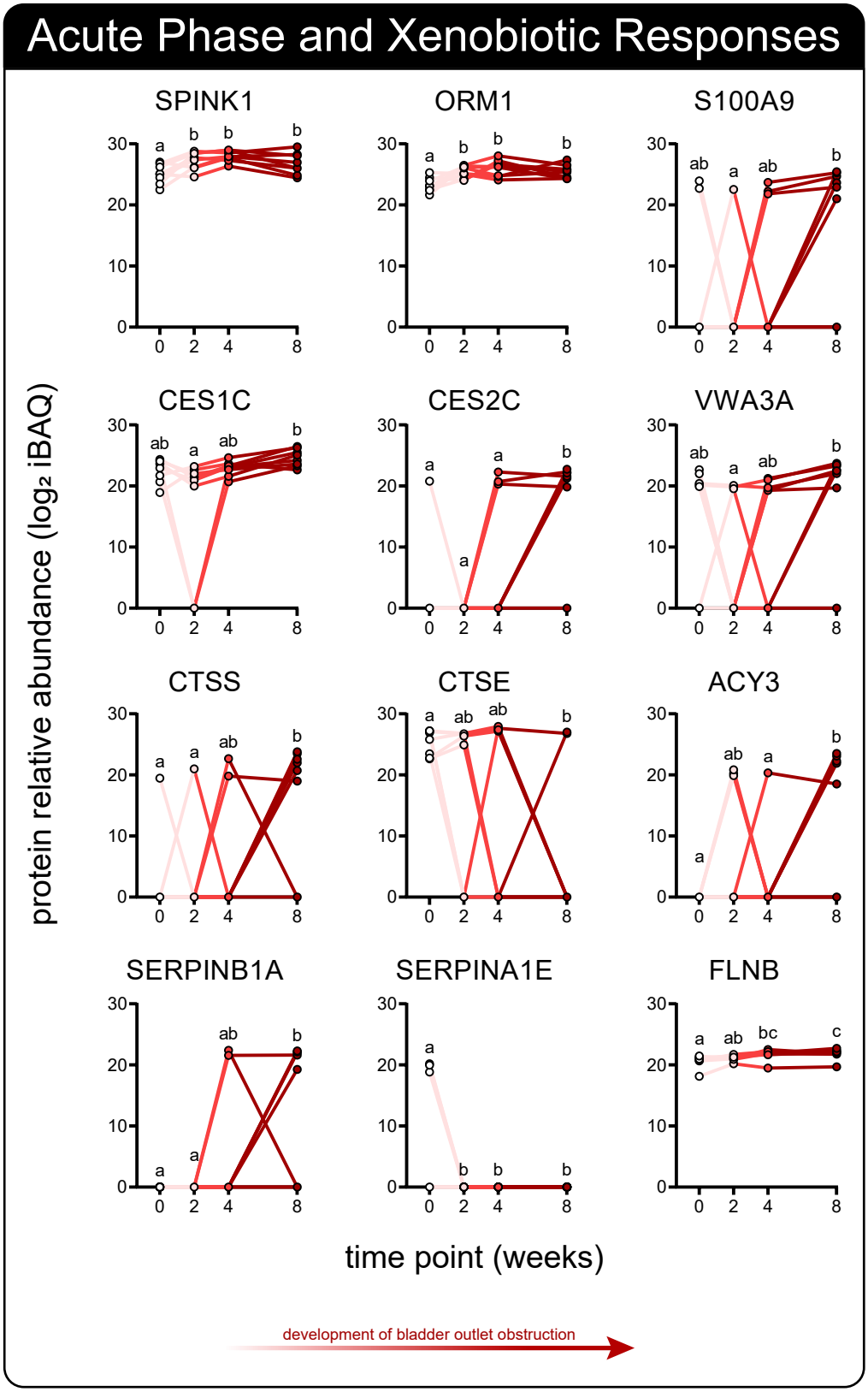

Figure S-1. A subset of significantly modulated urine proteins are related to the acute phase and xenobiotic responses; protein relative abundance (LFQ iBAQ) across 4 time points of disease progression. Distinct letters denote groups with significant differences (n = 8; RM-ANOVA, Tukey's post-hoc test, α = 0.05).

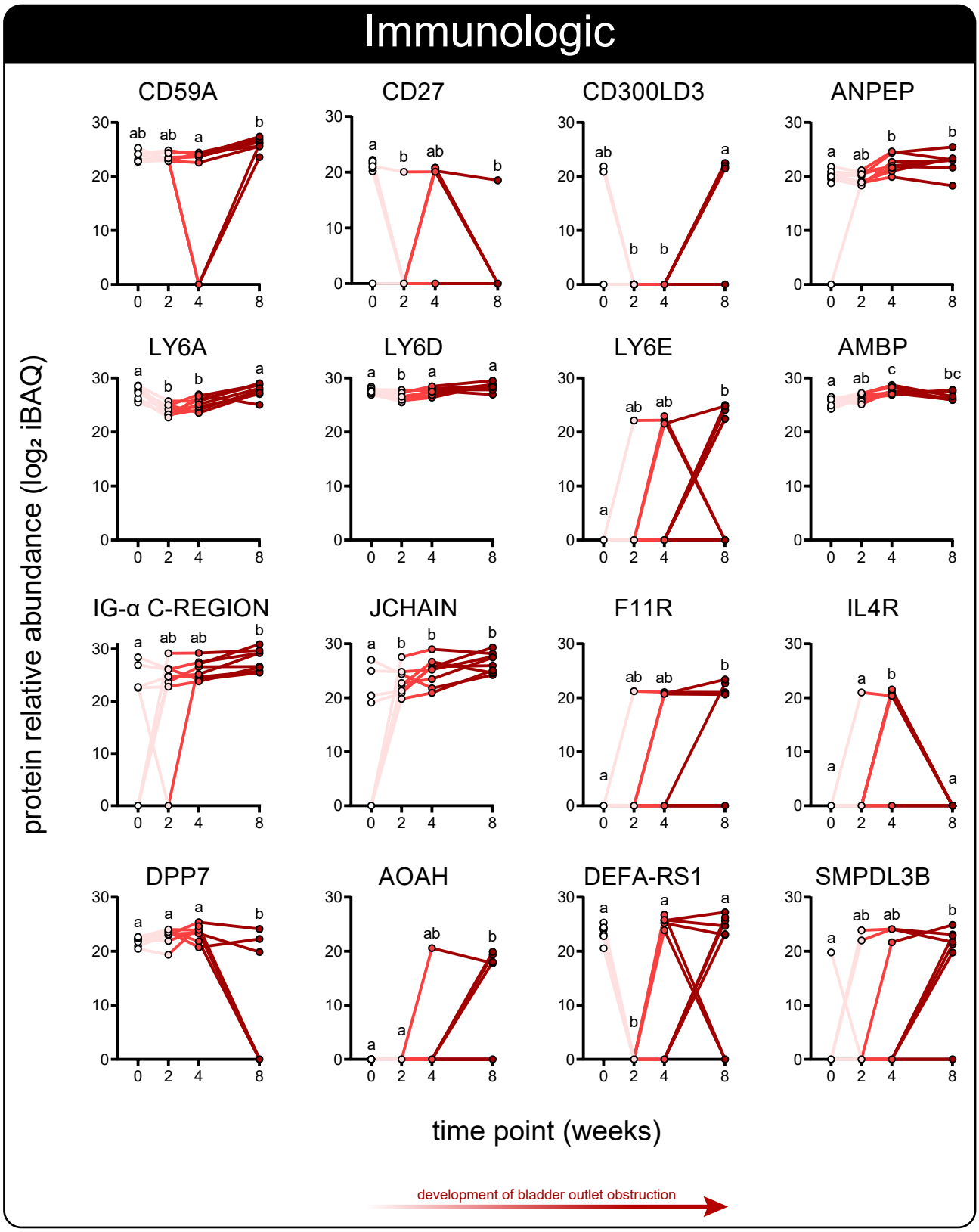

Figure S-2. A subset of significantly modulated urine proteins are related to immunologic processes; protein relative abundance (LFQ iBAQ) across 4 time points of disease progression. Distinct letters denote groups with significant differences (n = 8; RM-ANOVA, Tukey's post-hoc test, α = 0.05).

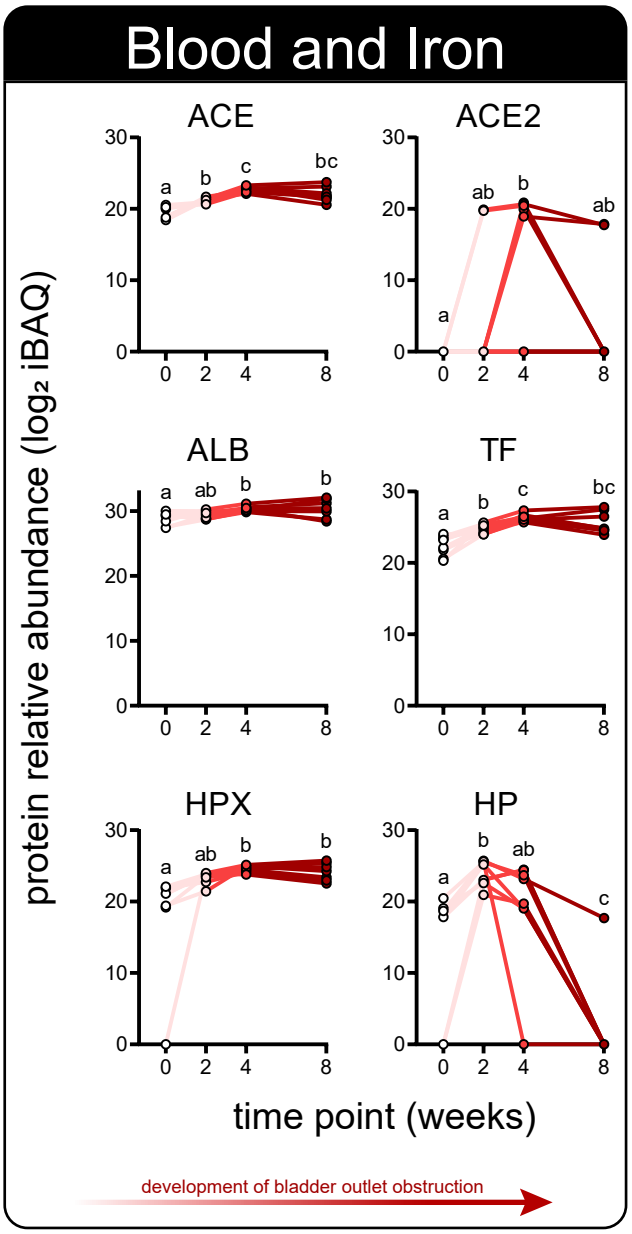

Figure S-3. A subset of significantly modulated urine proteins are related to blood and iron homeostasis; protein relative abundance (LFQ iBAQ) across 4 time points of disease progression. Distinct letters denote groups with significant differences (n = 8; RM-ANOVA, Tukey's post-hoc test, α = 0.05).

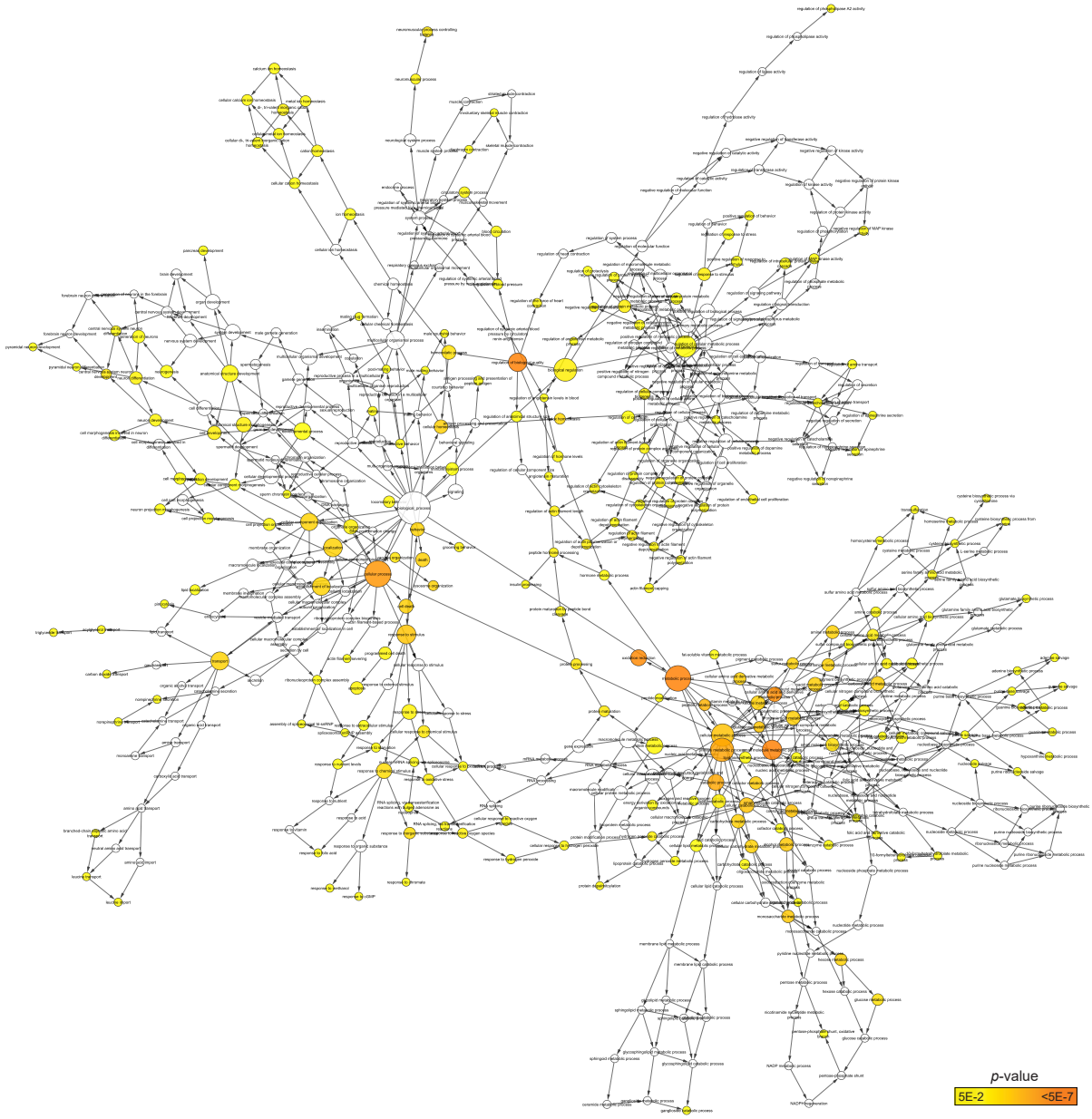

Figure S-5. Full gene ontology network of mouse prostate proteomics (from Fig. 5B): significantly enriched biological processes (Hypergeometric test with Benjamini & Hochberg FDR correction; Cytoscape BiNGO tool).

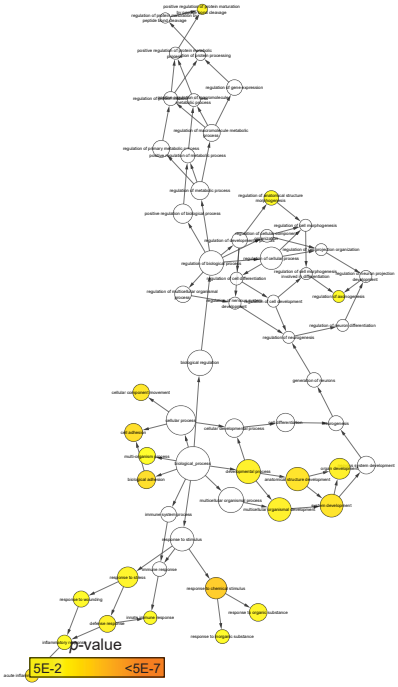

Figure S-6. Significantly enriched biological processes in a prior analysis of human patients with lower urinary tract symptoms (*n* = 25 patients *vs n* = 15 controls). Note similar processes: response to stress, etc. (from DOI: 10.1371/journal.pone.0135415.s004; Hypergeometric test with Benjamini & Hochberg FDR correction; Cytoscape BiNGO tool).