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Supplementary Material

New insight into the castrated mouse epididymis based on comparative proteomics

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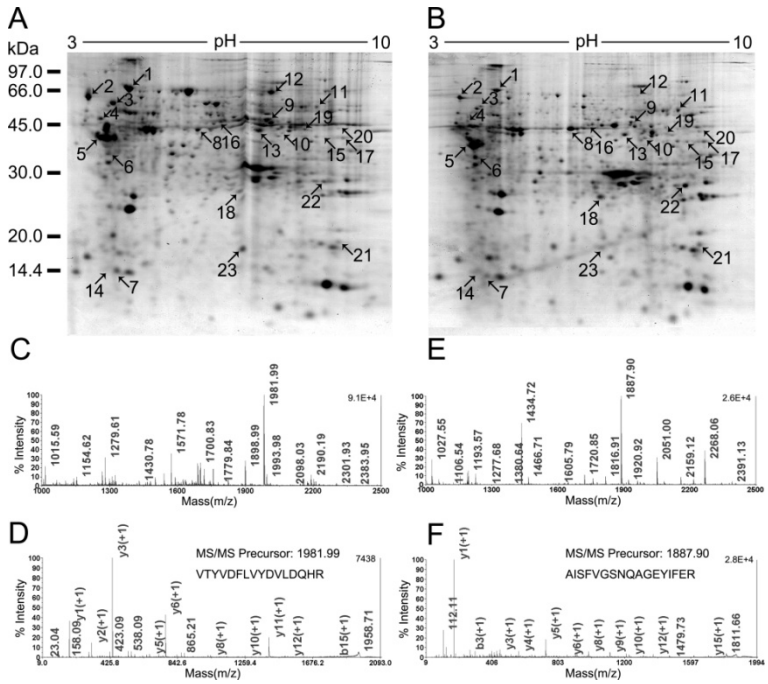

Fig. S1. Separation and identification of sham-operated control mice and castrated mice epididymal tissue proteins by 2D-PAGE and MALDI-MS Spectra. Reference map of (A) sham-operated control mice epididymal tissue and (B) castrated mice epididymal tissue; example spectra of (C, D) glutathione S-transferase Mu2 (spot 22), (E, F) methylmalonate-semialdehyde dehydrogenase (spot 19). The MS map (C) and MS/MS map (D) marked with b ions and y ions for glutathione S-transferase Mu2 identification. The sequence of precursor at m/z 1981.99 was analyzed by MS/MS to be VTYVDFLVYDVLDQHR and the protein identified as glutathione S-transferase Mu2. The MS map (E) and MS/MS map (F) marked with b ions and y ions for methylmalonate-semialdehyde dehydrogenase identification. The sequence of precursor at *m*/*z* 1887.90 was analyzed by MS/MS to be AISFVGSNQAGEYIFER and identified as methylmalonate-semialdehyde dehydrogenase.

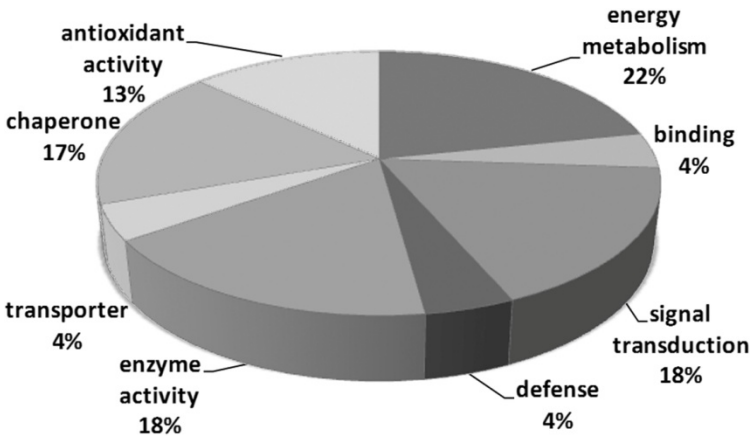

Fig. S2. Pie diagrams of the proportion of differential proteins found in sham-operated control mice and castrated mice epididymal tissues categorized by function. Function classification of 23 differential epididymal tissue proteins between sham-operated control mice and castrated mice.