Supplementary Figure S5. Changes in the cellular and transcriptional regulatory networks of somatic cell types during human testicular aging; related to Fig. 4. (**A–C**) Immunostaining and quantification of CYP17A1 (A), SOX9 (B), and α-SMA (C) in young and old human testis sections. Left, representative image of CYP17A1 (A), SOX9 (B), and α-SMA (C) in human testis sections. Right, quantification of CYP17A1+ (A), SOX9+ (B), and α-SMA+ (C) cells per seminiferous tubule. Scale bars, 35 μm. Bars represent the mean with SEM of 60 independent tubules per group (Young, n = 10 samples; Old, n = 10 samples). Significance was determined by Student's t-test. ns = not significant. (**D**) Heatmap showing expression patterns of upregulated (red) and downregulated (blue) genes found in the GenAge database.