Table S8. Key transcription factors significantly associated with differentially expressed genes between *Klf5*-wildtype and *Klf5*-null mouse dorsal prostates, as defined by MetaCore's interactome analysis for transcription factors. Related biological processes are also shown. The ranking is based on *p*-Values. Total nodes refer to all nodes in a transcription factor network, while seed nodes refer to the genes differentially expressed between the experimental groups.

#	Network	GO processes	Total nodes	Seed nodes	Pathways	*p*-Value	zScore	gScore
1	CREB1	developmental process (55.5%; 3.015e-17), system development (47.6%; 4.248e-17), anatomical structure development (50.8%; 3.889e-16), multicellular organismal development (51.2%; 4.525e-16), single-multicellular organism process (63.4%; 5.535e-16)	276	275	0	0.00E+00	132.95	132.95
2	SP1	response to organic substance (51.5%; 1.965e-29), response to oxygen-containing compound (39.8%; 1.028e-28), response to endogenous stimulus (38.8%; 6.018e-27), response to chemical (59.7%; 1.498e-24), response to organic cyclic compound (30.6%; 1.905e-24)	202	201	0	0.00E+00	113.52	113.52
3	ESR1 (nuclear)	response to endogenous stimulus (40.6%; 2.493e-21), response to oxygen-containing compound (39.9%; 1.125e-20), response to organic substance (50.7%; 2.572e-20), response to hormone (32.6%; 1.386e-19), response to organic cyclic compound (31.2%; 3.213e-18)	144	143	0	3.28E-262	95.62	95.62
4	c-Myc	system development (61.8%; 2.323e-21), multicellular organismal development (66.2%; 3.031e-21), single-organism developmental process (61.0%; 6.762e-21), developmental process (69.1%; 7.525e-21), response to organic substance (51.5%; 8.814e-21)	142	141	0	1.81E-258	94.94	94.94
5	Androgen receptor	response to hormone (28.0%; 1.308e-12), response to endogenous stimulus (33.9%; 1.341e-12), response to organic substance (44.1%; 2.319e-12), developmental process (61.0%; 3.805e-12), response to steroid hormone (20.3%; 5.312e-12)	123	122	0	5.09E-223	88.25	88.25

6	GCR-alpha	response to organic cyclic compound (32.8%; 4.400e-17), response to hormone (31.0%; 3.520e-15), response to organic substance (47.4%; 1.212e-14), response to lipid (29.3%; 1.908e-14), response to oxygen-containing compound (36.2%; 2.171e-14)	120	119	0	1.94E-217	87.15	87.15
7	RelA (p65 NF-kB subunit)	response to wounding (48.2%; 7.088e-33), response to oxygen-containing compound (54.4%; 1.423e-32), response to organic substance (63.2%; 8.483e-29), response to endogenous stimulus (49.1%; 2.075e-26), response to organic cyclic compound (39.5%; 8.249e-24)	119	118	0	1.41E-215	86.78	86.78
8	Oct-3/4	response to organic substance (47.2%; 2.474e-13), anatomical structure development (60.4%; 4.601e-13), developmental process (64.2%; 4.951e-13), system development (55.7%; 1.253e-12), single-organism developmental process (54.7%; 3.473e-12)	117	116	0	7.34E-212	86.03	86.03
9	c-Jun	response to organic cyclic compound (41.7%; 5.487e-25), response to lipid (40.7%; 7.520e-25), response to oxygen-containing compound (48.1%; 3.072e-24), response to organic substance (59.3%; 1.535e-23), response to wounding (39.8%; 7.253e-22)	115	114	0	3.82E-208	85.28	85.28
10	HIF1A	response to hypoxia (20.4%; 6.416e-16), response to decreased oxygen levels (20.4%; 8.605e-16), response to oxygen levels (20.4%; 2.918e-14), response to oxygen-containing compound (37.0%; 3.747e-14), response to organic cyclic compound (30.6%; 4.952e-14)	115	114	0	3.82E-208	85.28	85.28
11	C/EBPbeta	response to lipid (38.3%; 4.889e-22), response to oxygen-containing compound (45.8%; 1.025e-21), response to organic cyclic compound (38.3%; 3.095e-21), response to organic substance (56.1%; 1.821e-20), response to stimulus (86.0%; 1.198e-17)	113	112	0	1.98E-204	84.52	84.52
12	p53	regulation of cell proliferation (38.2%; 1.017e-15), system development (60.8%; 1.165e-15), positive regulation of cellular process (57.8%; 4.410e-15), response to endogenous stimulus (39.2%; 4.934e-15), anatomical structure development (63.7%; 7.385e-15)	108	107	0	3.74E-195	82.59	82.59

13	LHX2	developmental process (68.5%; 9.158e-14), anatomical structure development (64.0%; 2.432e-13), system development (57.3%; 9.390e-12), multicellular organismal development (60.7%; 4.165e-11), single-multicellular organism process (71.9%; 1.455e-10)	101	100	0	3.48E-182	79.81	79.81
14	STAT3	positive regulation of biological process (69.2%; 4.788e-19), positive regulation of cellular process (64.8%; 2.008e-18), response to organic substance (56.0%; 1.355e-17), multicellular organismal development (70.3%; 1.451e-17), developmental process (73.6%; 1.483e-17)	96	95	0	6.18E-173	77.77	77.77
15	HNF4-alpha	developmental process (69.0%; 2.252e-13), response to endogenous stimulus (38.1%; 6.573e-12), response to organic substance (48.8%; 8.620e-12), response to organic cyclic compound (31.0%; 1.705e-11), anatomical structure development (61.9%; 1.827e-11)	91	90	0	1.07E-163	75.67	75.67
16	C/EBPalpha	organ development (61.5%; 2.722e-18), response to organic substance (59.0%; 3.377e-17), response to stimulus (89.7%; 6.611e-16), system development (66.7%; 8.570e-16), developmental process (74.4%; 1.032e-15)	85	84	0	1.25E-152	73.07	73.07
17	GATA-3	regulation of multicellular organismal process (49.3%; 4.817e-13), epithelium development (32.0%; 1.089e-12), positive regulation of cellular process (60.0%; 1.283e-12), positive regulation of macromolecule metabolic process (46.7%; 1.680e-12), positive regulation of metabolic process (48.0%; 2.844e-12)	84	83	0	8.71E-151	72.63	72.63
18	PU.1	response to wounding (38.2%; 1.277e-14), response to organic substance (55.3%; 1.894e-14), positive regulation of biological process (65.8%; 4.938e-14), defense response (40.8%; 6.809e-14), regulation of multicellular organismal process (50.0%; 1.351e-13)	84	83	0	8.71E-151	72.63	72.63
19	PPAR-gamma	response to oxygen-containing compound (47.3%; 1.847e-16), anatomical structure development (73.0%; 1.868e-16), developmental process (75.7%; 8.479e-16), response to lipid (37.8%; 2.556e-15), response to organic substance (56.8%; 5.292e-15)	81	81	0	5.22E-149	72.19	72.19

20	NANOG	negative regulation of macromolecule metabolic process (42.1%; 1.838e-13), positive regulation of cellular process (60.5%; 4.612e-13), response to organic substance (52.6%; 6.755e-13), response to stimulus (85.5%; 1.261e-12), negative regulation of metabolic process (42.1%; 1.459e-12)	83	82	0	6.06E-149	72.18	72.18
21	E2F1	negative regulation of cellular process (63.5%; 6.179e-16), positive regulation of developmental process (35.1%; 9.350e-15), regulation of signal transduction (51.4%; 1.713e-14), positive regulation of cellular process (63.5%; 1.874e-14), negative regulation of biological process (63.5%; 2.496e-14)	82	81	0	4.22E-147	71.73	71.73