Table S11. Comparision of gene expression in primitive prostate cell populations as determined by quantitive PCR

Category	Gene	UGE	Sca-1Hi	Sca-1Lo
Cell cycle/ Self-renewal	Wnt4	5.0 ± 0.4	8.4 ± 0.6	2.7 ± 0.1
	Wnt6	22.4 ± 4.6	1.2 ± 0.3	1.5 ± 0.6
	Fzd6	5.0 ± 0.4	3.4 ± 0.2	3.0 ± 0.1
	Shh	35.3 ± 5.9	6.3 ± 0.8	4.1 ± 1.4
	Gli3	3.7 ± 0.2	2.9 ± 0.9	2.5 ± 0.2
	E2f3	3.4 ± 0.2	1.3 ± 0.1	1.1 ± 0.1
	Cdc2a	12.1 ± 1.8	0.7 ± 0.1	1.0 ± 0.5
	Tead2	4.1 ± 0.8	0.4 ± 0.1	0.9 ± 0.3
TGF-β pathway	Clu	0.1 ± 0.1	3.4 ± 0.9	2.5 ± 0.2
Ahr pathway	Ahr	2.4 ± 0.1	3.5 ± 0.2	1.8 ± 0.2
RA pathway	Crabp2	46.6 ± 3.9	1.2 ± 0.2	2.3 ± 0.4
	Rxra	4.2 ± 0.4	3.3 ± 0.1	1.8 ± 0.4
	Rarb	2.8 ± 0.3	1.8 ± 0.1	1.3 ± 0.1
	Rarg	1.5 ± 0.4	3.0 ± 0.2	2.2 ± 0.1
Phospholipid	Pltp	1.7 ± 0.3	8.1 ± 2.2	5.9 ± 1.3
Calcium regulators	Itpr3	0.7 ± 0.1	1.7 ± 0.3	1.1 ± 0.3
	Thbd	1.5 ± 1.9	20.3 ± 6.0	10.3 ± 4.5
Chromatin modifiers	Ezh2	4.4 ± 0.4	1.7 ± 0.1	1.3 ± 0.1

qPCR analysis of selected genes from functional categories that were identified in primitive prostate cells. Transcript levels were normalized to the expression of HPRT (housekeeping gene). Data [mean ± SD, n=3] are presented as the fold change of the expression of each gene in UGE, Sca-1Hi or Sca-1Lo cells relative to its expression in Sca-1Neg cells.