

Table S3. Differential expression for 11 of the selected 14 marker genes present in the TCGA data set for prostate cancer, comparing low (Gleason score $\leq 3+4$) against high grade cancer (Gleason score $\geq 4+3$). The symbol * indicates the fold change having opposite direction compared to the periprostatic fat cohort.

Genes	logFC	logCPM	LR	p-Value	FDR
SAA2*	-0.51	2.70	2.10	0.14	0.30
MYH11	-0.57	12.00	28.00	1.40E-07	5.80E-06
RERGL	-0.04	0.75	0.09	0.77	0.86
SOCS3	-0.28	6.50	3.00	0.08	0.20
PLA2G2A	0.32	11.00	2.00	0.16	0.32
SLC2A1	-0.03	5.80	0.29	0.59	0.74
GPR34	0.37	2.10	16.00	5.50E-05	8.10E-04
CLDN1*	0.14	5.30	1.10	0.30	0.48
PCDH10	-0.04	4.60	0.20	0.65	0.79
SELE	-0.24	4.40	1.50	0.22	0.39
OLFM4*	0.13	7.40	0.32	0.57	0.73