

SUPPLEMENTARY MATERIAL

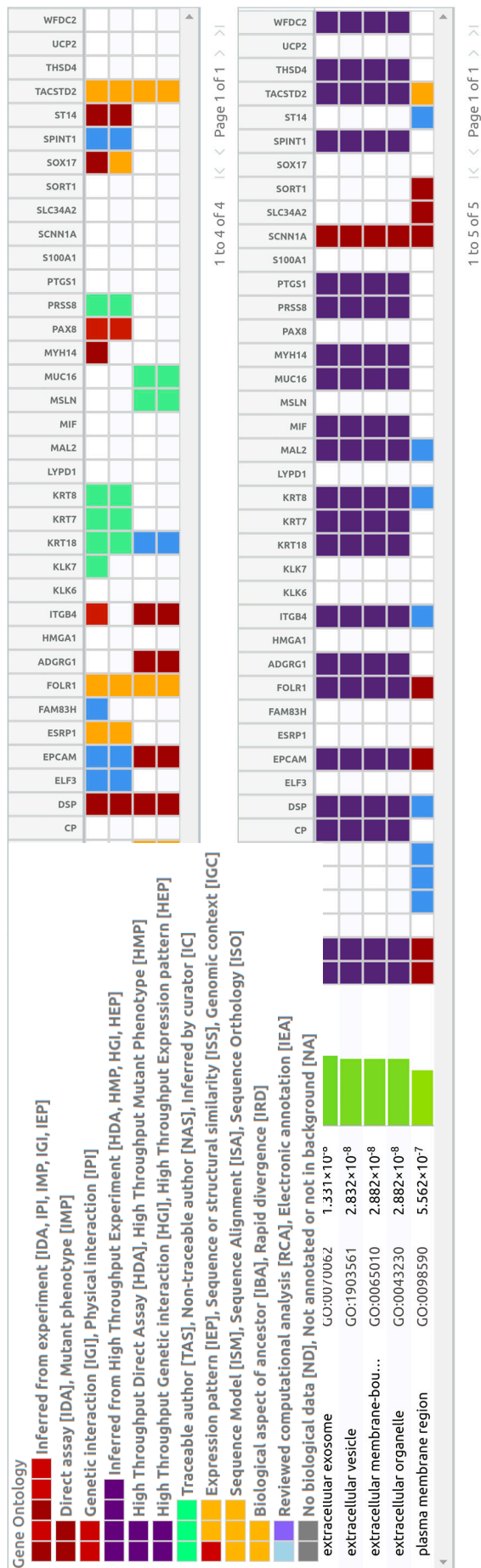
Supplementary Table S1. Ranks of the 41 OSCA biomarkers from TCGA and GTEx

GENE	OSCA Av. Exp. (Rank)	Control Av. Exp. (Rank)		GENE	OSCA Av. Exp. (Rank)	Control Av. Exp. (Rank)		GENE	OSCA Av. Exp. (Rank)	Control Av. Exp. (Rank)
KRT8	14.41 (55)	3.50 (9367)		DSP	13.03 (218)	1.41 (10898)		ITGB4	12.10 (593)	2.56 (9600)
WFDC2	14.21 (70)	2.48 (9667)		PAX8	12.87 (262)	0.82 (11765)		KLK7	12.06 (612)	0.07 (14788)
MIF	14.04 (80)	1.92 (10293)		ELF3	12.81 (285)	0.22 (13519)		FOLR1	11.93 (708)	0.18 (13729)
KRT18	13.95 (90)	6.00 (6855)		EPCAM	12.77 (297)	0.66 (12091)		SOX17	11.91 (720)	2.37 (9791)
SLC34A2	13.67 (123)	0.21 (13568)		SPINT1	12.62 (350)	1.42 (10878)		LYPD1	11.87 (759)	0.26 (13313)
MSLN	13.60 (128)	1.55 (10722)		ST14	12.50 (395)	0.42 (12703)		PRSS8	11.84 (783)	0.26 (13300)
CLDN3	13.54 (138)	0.27 (13262)		CP	12.50 (402)	0.60 (12234)		S100A1	11.79 (817)	0.21 (13587)
MUC16	13.53 (140)	0.06 (14977)		PTGS1	12.47 (412)	1.08 (11335)		CLDN7	11.74 (855)	0.47 (12561)
HMGAI	13.41 (159)	2.39 (9775)		ADGRG1	12.34 (461)	1.57 (10696)		THSD4	11.73 (873)	1.17 (11191)
CLDN4	13.29 (172)	0.29 (13194)		TACSTD2	12.33 (466)	0.93 (11580)		ESRP1	11.73 (875)	0.12 (14215)
KRT7	13.22 (186)	0.44 (12643)		CDH1	12.26 (498)	1.20 (11147)		MYH14	11.71 (883)	0.17 (13832)
UCP2	13.21 (187)	1.81 (10438)		SORT1	12.22 (524)	3.35 (8853)		KLK6	11.62 (957)	0.40 (12780)
SCNN1A	13.06 (210)	1.75 (10497)		FAM83H	12.17 (542)	0.28 (13225)		ATP6V1B1	11.59 (993)	0.97 (11504)
MAL2	13.06 (213)	0.20 (13663)		CELSR2	12.14 (566)	0.73 (11936)				

Average gene expression values (Av. Exp.) are indicated using the measure units originally reported in TCGA, i.e. TPM for OSCA samples, and in GTEx, i.e. RPKM for control healthy ovarian tissues. The rank indicates the position that the gene occupies in the lists of 18734 genes ordered from the highest to the lowest average gene expression value for OSCA samples and control samples separately.

Supplementary Table S2. Information on patients affected by the OSCA samples analyzed by the NanoString nCounter technology.

Median age		year (range)
		60.6 (40-87)
FIGO stage		number (%)
	I	5 (11.9)
	II	8 (19.1)
	III	25 (59.5)
	IV	4 (9.5)
pN		number (%)
	0	35 (83.3)
	1	7 (16.7)
pM		number (%)
	0	38 (90.5)
	1	4 (9.5)
Grade		number (%)
	1	0 (0)
	2	10 (23.8)
	3	32 (76.2)



Supplementary Figure S1. Gene Ontology enrichment analysis of 41 OSCA biomarkers.

Output of the g:Profiler tool reporting statistically significant Gene Ontology terms that were over-represented in the 41 OSCA gene-expression biomarkers.