

# Integrative clinical transcriptome analysis reveals *TMPRSS2-ERG* dependency of prognostic biomarkers in prostate adenocarcinoma

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## SUPPLEMENTARY DATA

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## SUPPLEMENTARY TABLES

**Supplementary Table 1. Patients' characteristics of both discovery cohorts and the first validation cohort.**

Parameter	TCGA		GSE46691		GSE16560	
	T2E-negative	T2E-positive	T2E-negative	T2E-positive	T2E-negative	T2E-positive
<b>Number of patients</b>	190	109	242	242	226	46
<b>Age</b> (years, median & range)	63 (44-78)	61 (46-75)	-	-	74 (51-91)	74 (60-91)
<b>PSA</b> (ng/ml) Median (range)	0.1 (0-37.36)	0.1 (0-19.8)	-	-	-	-
<b>ISUP Grade group (Gleason Score):</b>						
1 (3+3)	8	4	26	26	75	2
2 (3+4)	47	38	104	143	90	24
3 (4+3)	41	17				
4 (4+4, 3+5, 5+3)	31	22	38	22	23	4
5 (>4+5)	63	28	72	50	38	16
<b>pN-stage</b>						
pN0	154	89	147	152	-	-
pN1	36	20	95	90	-	-
<b>R-status</b>						
R0	119	73	-	-	-	-
R1	66	30	-	-	-	-
<b>pT-stage</b>						
pT2	62	36	-	-	-	-
pT3	118	71	-	-	-	-
pT4	7	2	-	-	-	-
<b>EFS</b>						
no	128	82	-	-	71	3
yes	44	24	-	-	155	43
<b>Median follow-up, month (range)</b>						
	24 (1-114)	26 (2-140)	-	-	110 (7-259)	66 (6-170)

**Supplementary Table 2. Patients' characteristics of the second validation cohort used for IHC stratified by T2E-status.**

Parameter	ERG-negative sub-cohort	ERG-positive sub-cohort
<b>Number of patients</b>	88	47
<b>Age</b> (years, median & range)	65 (48-75)	65 (45-75)
<b>PSA</b> (ng/ml) Median (range)	7.5 (1.0-163)	6.6 (1.5-58.4)
<b>ISUP Grade group (Gleason Score):</b>		
1 (3+3)	37	23
2 (3+4)	19	12
3 (4+3)	7	4
4 (4+4, 3+5, 5+3)	17	4
5 (>4+5)	7	2
<b>pN-stage</b>		
pN0	79	42
pN1	8	5
<b>R-status</b>		
R0	51	23
R1	37	23
<b>pT-stage</b>		
pT2	49	26
pT3	37	20
pT4	2	1
<b>BCR</b>		
no	64	38
yes	24	9
<b>Median follow-up,</b> Months (range)	62 (1-134)	60 (10-136)

**Supplementary Table 3. Top 20 functional gene-signatures from ranked GSEA of rGL.**NES, normalized enrichment score; NOM, nominal *P* value; FDR, false discovery rate.

<b>Top 20 functional gene-signatures pathways from ranked GSEA of rGL-pos</b>	<b>NES</b>	<b>NOM <i>P</i></b>	<b>FDR <i>q</i></b>
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	2.06	0.000	0.095
BIDUS_METASTASIS_UP	2.00	0.000	0.104
CROONQUIST_IL6_DEPRIVATION_DN	1.95	0.000	0.106
CHANG_CYCLING_GENES	1.91	0.000	0.118
ODONNELL_TFRC_TARGETS_DN	1.91	0.009	0.094
WINNEPENNINGCKX_MELANOMA_METASTASIS_UP	1.89	0.006	0.095
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	1.84	0.003	0.129
WHITFIELD_CELL_CYCLE_G1_S	1.82	0.000	0.138
FISCHER_DREAM_TARGETS	1.81	0.000	0.134
WEST_ADRENOCORTICAL_TUMOR_UP	1.77	0.000	0.170
NIKOLSKY_BREAST_CANCER_8Q23_Q24_AMPLICON	1.75	0.007	0.187
SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP	1.74	0.003	0.190
FISCHER_G2_M_CELL_CYCLE	1.71	0.014	0.220
ROY_WOUND_BLOOD_VESSEL_UP	1.68	0.013	0.253
ZHAN_MULTIPLE_MYELOMA_CD1_AND_CD2_UP	1.67	0.030	0.247
JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_DN	1.65	0.020	0.275
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	1.65	0.005	0.260
NIKOLSKY_MUTATED_AND_AMPLIFIED_IN_BREAST_CANCER	1.65	0.023	0.249
JIANG_TIP30_TARGETS_UP	1.62	0.029	0.277
HORIUCHI_WTAP_TARGETS_DN	1.62	0.000	0.270
<b>Top 20 functional gene-signatures pathways from ranked GSEA of rGL-neg</b>	<b>NES</b>	<b>NOM <i>P</i></b>	<b>FDR <i>q</i></b>
POOLA_INVASIVE_BREAST_CANCER_UP	3.11	0.000	0.000
WIELAND_UP_BY_HBV_INFECTION	2.66	0.000	0.000
SANA_RESPONSE_TO_IFNG_UP	2.47	0.000	0.000
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP	2.43	0.000	0.000
THUM_SYSTOLIC_HEART_FAILURE_UP	2.42	0.000	0.000
FULCHER_INFLAMMATORY_RESPONSE_LLECTIN_VS_LPS_DN	2.41	0.000	0.000
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	2.40	0.000	0.000
HELLER_SILENCED_BY_METHYLATION_UP	2.39	0.000	0.000
LINDSTEDT_DENDRITIC_CELL_MATURATION_A	2.38	0.000	0.000
BROWNE_INTERFERON_RESPONSIVE_GENES	2.43	0.000	0.000
LEE_DIFFERENTIATING_T_LYMPHOCYTE	2.33	0.000	0.000
RODWELL_AGING_KIDNEY_UP	2.32	0.000	0.000

GAURNIER_PSMD4_TARGETS	2.32	0.000	0.000
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP	2.32	0.000	0.000
BOSCO_TH1_CYTOTOXIC_MODULE	2.31	0.000	0.000
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	2.31	0.000	0.000
MCLACHLAN_DENTAL_CARIES_UP	2.30	0.000	0.000
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	2.29	0.000	0.000
KIM_GLIS2_TARGETS_UP	2.29	0.000	0.000
GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP	2.29	0.000	0.000

**Supplementary Table 4. Result summary of all statistical tests of topGL-pos.**

topGL-pos						
Dataset	GSE46691	TCGA			GSE16560	
Gene	P value (metastasis)	P value (metastasis)	P value (EFS)	Expression level associated with long EFS	P value (EFS)	Expression level associated with long EFS
<i>ANP32E</i>	3.74E-01	2.80E-01	8.58E-01	low	8.50E-02	low
<i>ASF1B</i>	4.97E-01	2.64E-01	5.89E-01	low	-	-
<i>CDC20</i>	2.36E-01	5.62E-02	4.43E-01	low	7.20E-02	high
<i>CKS2</i>	6.27E-01	1.06E-01	2.51E-01	low	9.84E-01	low
<i>DEPDC1</i>	1.19E-01	1.41E-01	1.63E-01	low	-	-
<i>FAM83D</i>	4.28E-01	1.57E-02	3.06E-01	low	-	-
<i>GMNN</i>	4.08E-05	5.61E-03	1.39E-01	low	6.40E-01	high
<i>KIF4A</i>	8.53E-01	6.14E-02	3.92E-01	low	-	-
<i>PTTG1</i>	7.00E-01	1.50E-01	1.70E-01	low	8.37E-01	low
<i>RRM2</i>	5.06E-03	1.90E-01	4.19E-01	high	2.15E-01	low
<i>SPC25</i>	3.91E-01	4.45E-02	5.38E-01	low	-	-
<i>TROAP</i>	2.11E-02	3.24E-02	6.70E-02	low	1.17E-01	high
<i>TYMS</i>	2.86E-05	3.12E-01	6.68E-01	high	6.87E-01	low
<i>UBE2C</i>	4.41E-01	7.40E-02	2.37E-01	low	1.66E-01	high
<i>UHRF1</i>	7.87E-02	1.78E-01	3.52E-01	low	-	-
<i>WEE1</i>	1.07E-04	1.65E-03	1.98E-01	low	2.11E-01	high

**Supplementary Table 5. Result summary of all statistical tests of topGL-neg.**

topGL-neg						
Dataset	GSE46691	TCGA			GSE16560	
Gene	<i>P</i> value (metastasis)	<i>P</i> value (metastasis)	<i>P</i> value (EFS)	Expression level associated with long EFS	<i>P</i> value (EFS)	Expression level associated with long EFS
<i>AIF1</i>	7.65E-01	3.95E-04	2.40E-02	low	1.10E-01	low
<i>APOC1</i>	1.28E-01	1.69E-03	5.00E-02	low	8.60E-01	low
<i>APOE</i>	1.10E-01	1.20E-02	2.10E-02	low	5.00E-03	low
<i>ARHGDI1B</i>	1.79E-02	6.77E-05	1.37E-01	low	8.24E-01	low
<i>ASPN</i>	7.37E-05	8.92E-06	1.00E-03	low	3.05E-04	low
<i>BGN</i>	2.53E-03	3.52E-04	1.50E-02	low	4.84E-04	low
<i>BST2</i>	2.08E-01	9.49E-03	1.22E-01	low	5.69E-01	high
<i>C1QB</i>	1.60E-01	9.89E-05	4.40E-02	low	7.39E-01	low
<i>CCL2</i>	1.21E-01	1.47E-01	8.88E-01	low	8.50E-01	low
<i>CCL8</i>	5.42E-02	6.22E-05	1.78E-01	low	7.45E-01	low
<i>CCR1</i>	9.57E-01	6.10E-06	1.62E-01	low	3.85E-01	low
<i>CD14</i>	7.62E-02	7.30E-02	7.30E-02	low	3.17E-01	low
<i>CD52</i>	1.71E-02	1.55E-04	5.80E-02	low	6.18E-01	high
<i>CD53</i>	1.55E-01	5.29E-06	1.21E-01	low	5.59E-01	high
<i>CD74</i>	5.39E-02	3.81E-04	2.53E-01	low	6.29E-01	high
<i>CDH11</i>	9.99E-04	4.55E-04	4.34E-01	low	8.06E-01	high
<i>CFB</i>	1.79E-01	2.07E-01	1.88E-01	high	3.50E-02	high
<i>COL1A1</i>	1.57E-04	9.64E-06	2.50E-02	low	7.00E-03	low
<i>COL1A2</i>	2.45E-03	2.75E-03	3.50E-01	low	2.32E-01	low
<i>COL3A1</i>	3.19E-04	2.34E-05	1.26E-01	low	8.00E-03	low
<i>COMP</i>	3.25E-01	5.55E-06	3.00E-03	low	9.60E-02	low
<i>CTSS</i>	6.21E-02	5.31E-05	3.77E-01	low	7.97E-01	low
<i>CXCL11</i>	2.93E-01	3.65E-06	5.30E-02	low	4.07E-01	high
<i>CXCL13</i>	2.33E-03	1.21E-02	5.19E-01	low	9.00E-03	high
<i>CXCL9</i>	9.40E-01	2.09E-06	3.10E-02	low	2.20E-01	high
<i>CXCR4</i>	9.25E-03	1.00E-03	1.66E-01	low	3.50E-01	low
<i>EVI2B</i>	9.61E-03	1.84E-05	4.35E-01	low	1.82E-01	high
<i>F13A1</i>	5.15E-01	7.11E-03	4.28E-01	low	2.68E-01	low
<i>FCGR2A</i>	3.71E-01	1.98E-05	5.70E-02	low	3.70E-02	low
<i>FN1</i>	9.92E-04	4.01E-04	6.90E-02	low	2.90E-02	low
<i>FYB</i>	1.32E-01	4.65E-06	2.75E-01	low	7.99E-01	high
<i>GBP1</i>	1.69E-01	3.35E-04	4.36E-01	low	8.44E-01	low
<i>GPNMB</i>	2.45E-03	6.78E-04	9.10E-02	low	9.70E-02	low
<i>GZMB</i>	1.24E-01	6.68E-02	9.00E-01	low	7.70E-01	high
<i>GZMK</i>	8.94E-01	1.36E-03	5.30E-01	low	6.00E-03	high
<i>HCLS1</i>	9.99E-02	6.22E-05	1.80E-02	low	8.12E-01	high

<i>HLA-DMB</i>	2.32E-01	4.06E-04	1.90E-02	low	4.95E-01	high
<i>HLA-DPA1</i>	2.90E-02	1.64E-04	7.20E-02	low	9.38E-01	high
<i>HLA-DPB1</i>	5.98E-02	2.06E-03	4.60E-02	low	6.42E-01	high
<i>HLA-DRA</i>	2.91E-03	2.20E-05	1.60E-01	low	8.65E-01	high
<i>HLA-DRB1</i>	4.64E-01	8.05E-04	2.60E-02	low	9.74E-01	high
<i>HLA-E</i>	1.65E-01	4.97E-04	9.48E-01	high	1.65E-01	high
<i>HLA-F</i>	3.82E-01	5.63E-04	2.90E-02	low	9.97E-01	high
<i>IFI27</i>	2.35E-02	4.78E-04	1.04E-01	low	1.98E-01	low
<i>IFI30</i>	2.45E-03	9.36E-05	1.40E-02	low	2.75E-01	low
<i>IFI44</i>	6.44E-01	8.36E-07	1.10E-02	low	5.00E-02	high
<i>IFIT3</i>	4.59E-01	1.54E-08	2.20E-02	low	5.45E-01	high
<i>INHBA</i>	8.47E-03	4.50E-06	9.10E-02	low	5.07E-04	low
<i>ISG15</i>	9.18E-01	1.55E-04	8.64E-01	high	7.36E-01	high
<i>LAPTM5</i>	7.16E-02	4.74E-05	3.90E-02	low	2.49E-01	low
<i>LRRC15</i>	1.76E-01	3.27E-03	2.05E-01	low	-	-
<i>LST1</i>	1.62E-01	1.46E-03	4.70E-02	low	3.26E-01	high
<i>LTB</i>	5.51E-01	1.94E-04	8.70E-01	low	5.12E-01	low
<i>LUM</i>	2.25E-02	3.80E-02	6.96E-01	high	2.66E-01	low
<i>LY96</i>	8.76E-01	4.34E-05	1.00E-03	low	4.30E-02	low
<i>LYZ</i>	4.25E-02	2.86E-04	2.01E-01	low	2.45E-01	high
<i>MS4A4A</i>	8.83E-01	1.22E-03	8.10E-02	low	9.59E-01	low
<i>MS4A6A</i>	9.10E-03	8.37E-06	1.70E-02	low	9.24E-01	low
<i>PLA2G7</i>	2.68E-05	3.95E-02	5.20E-02	low	4.31E-06	low
<i>PLEK</i>	9.60E-01	5.82E-06	5.76E-01	low	5.31E-01	high
<i>POSTN</i>	2.78E-04	3.06E-04	6.60E-02	low	7.00E-03	low
<i>PSMB9</i>	5.86E-01	1.01E-05	1.41E-01	low	1.93E-01	high
<i>PTPRC</i>	2.55E-01	2.45E-05	1.11E-01	low	9.28E-01	low
<i>RARRES3</i>	1.60E-01	1.00E-03	3.42E-01	low	2.93E-01	high
<i>RGS1</i>	4.94E-02	2.48E-05	1.98E-01	low	6.01E-01	high
<i>RRM2</i>	4.36E-02	8.02E-05	4.35E-05	low	2.00E-03	low
<i>SAMHD1</i>	1.50E-01	1.25E-03	8.06E-01	high	5.45E-01	low
<i>SPARC</i>	1.38E-04	6.53E-04	5.08E-01	low	1.82E-01	low
<i>STAT1</i>	1.32E-01	2.04E-05	5.39E-01	high	1.36E-01	high
<i>SULF1</i>	4.44E-04	1.55E-03	6.12E-01	low	7.58E-01	high
<i>TRIM22</i>	2.34E-01	1.44E-03	6.88E-01	high	8.55E-01	high
<i>TYMS</i>	8.81E-03	1.77E-02	1.00E-03	low	3.29E-06	low
<i>TYROBP</i>	1.81E-02	6.78E-04	8.10E-02	low	5.20E-01	low
<i>UBE2L6</i>	1.60E-01	3.87E-05	9.80E-01	high	9.16E-01	high



**Supplementary Table 6. Top 20 functional gene-signatures from ranked GSEA of T2E-negative PCa cases stratified by the median gene expression levels of either *ASPN*, *BGN*, *COL1A1*, *RRM2* or *TYMS*, respectively.**

<b>ASPN low</b>	<b>ASPN high</b>
POOLA_INVASIVE_BREAST_CANCER_UP	POOLA_INVASIVE_BREAST_CANCER_UP
BROWNE_INTERFERON_RESPONSIVE_GENES	WIELAND_UP_BY_HBV_INFECTION
DER_IFN_ALPHA_RESPONSE_UP	LEE_DIFFERENTIATING_T_LYMPHOCYTE
BOSCO_TH1_CYTOTOXIC_MODULE	BROWNE_INTERFERON_RESPONSIVE_GENES
KRASNOSELSKAYA_ILF3_TARGETS_UP	BOSCO_TH1_CYTOTOXIC_MODULE
RADAEVA_RESPONSE_TO_IFNA1_UP	SANA_RESPONSE_TO_IFNG_UP
WIELAND_UP_BY_HBV_INFECTION	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
LEE_DIFFERENTIATING_T_LYMPHOCYTE	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
SANA_RESPONSE_TO_IFNG_UP	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
DER_IFN_BETA_RESPONSE_UP	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
FARMER_BREAST_CANCER_CLUSTER_1	SMIRNOV_RESPONSE_TO_IR_6HR_DN
FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	FARMER_BREAST_CANCER_CLUSTER_1
BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
DER_IFN_GAMMA_RESPONSE_UP	VILIMAS_NOTCH1_TARGETS_UP
ZHAN_MULTIPLE_MYELOMA_LB_DN	LU_IL4_SIGNALING
GAURNIER_PSMD4_TARGETS	MCLACHLAN_DENTAL_CARIES_UP
GRAESSMANN_RESPONSE_TO_MC_AND_SEBUM_DEPRIVATION_UP	WALLACE_PROSTATE_CANCER_RACE_UP
MORI_MATURE_B_LYMPHOCYTE_UP	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
WORSCHER_TUMOR_REJECTION_UP	GAURNIER_PSMD4_TARGETS
SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
<b>BGN low</b>	<b>BGN high</b>
POOLA_INVASIVE_BREAST_CANCER_UP	POOLA_INVASIVE_BREAST_CANCER_UP
FISCHER_DREAM_TARGETS	WIELAND_UP_BY_HBV_INFECTION
WIELAND_UP_BY_HBV_INFECTION	LEE_DIFFERENTIATING_T_LYMPHOCYTE
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
BROWNE_INTERFERON_RESPONSIVE_GENES	BROWNE_INTERFERON_RESPONSIVE_GENES
PUJANA_BRCA2_PCC_NETWORK	SANA_RESPONSE_TO_IFNG_UP
RASHI_RESPONSE_TO_IONIZING_RADIATION_6	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP
FARMER_BREAST_CANCER_CLUSTER_1	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
LEE_DIFFERENTIATING_T_LYMPHOCYTE	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	RASHI_RESPONSE_TO_IONIZING_RADIATION_6

CROONQUIST_IL6_DEPRIVATION_DN	THUM_SYSTOLIC_HEART_FAILURE_UP
BOSCO_TH1_CYTOTOXIC_MODULE	MORI_MATURE_B_LYMPHOCYTE_UP
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE
BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP	BOSCO_TH1_CYTOTOXIC_MODULE
MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	DER_IFN_ALPHA_RESPONSE_UP
FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
MCLACHLAN_DENTAL_CARIES_UP	LINDSTEDT_DENDRITIC_CELL_MATURATION_A
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	RODWELL_AGING_KIDNEY_UP
MORI_MATURE_B_LYMPHOCYTE_UP	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN
<b>COL1A1 low</b>	<b>COL1A1 high</b>
FISCHER_DREAM_TARGETS	POOLA_INVASIVE_BREAST_CANCER_UP
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	WIELAND_UP_BY_HBV_INFECTION
SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP	BASSO_CD40_SIGNALING_UP
POOLA_INVASIVE_BREAST_CANCER_UP	LEE_DIFFERENTIATING_T_LYMPHOCYTE
PUJANA_BRCA2_PCC_NETWORK	SANA_RESPONSE_TO_IFNG_UP
CROONQUIST_IL6_DEPRIVATION_DN	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
FARMER_BREAST_CANCER_CLUSTER_1	BROWNE_INTERFERON_RESPONSIVE_GENES
BROWNE_INTERFERON_RESPONSIVE_GENES	GAURNIER_PSMD4_TARGETS
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	DER_IFN_BETA_RESPONSE_UP
ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	WALLACE_PROSTATE_CANCER_RACE_UP
WHITEFORD_PEDIATRIC_CANCER_MARKERS	MCLACHLAN_DENTAL_CARIES_UP
RADAEVA_RESPONSE_TO_IFNA1_UP	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
BENPORATH_PROLIFERATION	DER_IFN_ALPHA_RESPONSE_UP
ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION
MORI_MATURE_B_LYMPHOCYTE_UP	THUM_SYSTOLIC_HEART_FAILURE_UP
FISCHER_G2_M_CELL_CYCLE	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE	BOSCO_TH1_CYTOTOXIC_MODULE
WIELAND_UP_BY_HBV_INFECTION	LINDSTEDT_DENDRITIC_CELL_MATURATION_A
MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
ZHAN_MULTIPLE_MYELOMA_LB_DN	FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP
<b>RRM2 low</b>	<b>RRM2 high</b>
POOLA_INVASIVE_BREAST_CANCER_UP	POOLA_INVASIVE_BREAST_CANCER_UP
RODWELL_AGING_KIDNEY_UP	WIELAND_UP_BY_HBV_INFECTION

SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
THUM_SYSTOLIC_HEART_FAILURE_UP	LEE_DIFFERENTIATING_T_LYMPHOCYTE
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	BOSCO_TH1_CYTOTOXIC_MODULE
WIELAND_UP_BY_HBV_INFECTION	BROWNE_INTERFERON_RESPONSIVE_GENES
RASHI_RESPONSE_TO_IONIZING_RADIATION_6	HELLER_SILENCED_BY_METHYLATION_UP
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP
LEE_DIFFERENTIATING_T_LYMPHOCYTE	SANA_RESPONSE_TO_IFNG_UP
MORI_MATURE_B_LYMPHOCYTE_UP	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP
GAURNIER_PSMD4_TARGETS	DER_IFN_BETA_RESPONSE_UP
FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	WALLACE_PROSTATE_CANCER_RACE_UP
RODWELL_AGING_KIDNEY_NO_BLOOD_UP	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
PUJANA_ATM_PCC_NETWORK	DER_IFN_ALPHA_RESPONSE_UP
KIM_GLIS2_TARGETS_UP	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP
MCLACHLAN_DENTAL_CARIES_UP	RODWELL_AGING_KIDNEY_UP
ANASTASSIOU_MULTICANCER_INVASIVENESS_SIGNATURE	KRASNOSELSKAYA_ILF3_TARGETS_UP
BROWNE_INTERFERON_RESPONSIVE_GENES	GAURNIER_PSMD4_TARGETS
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	QI_PLASMACYTOMA_UP
<b>TYMS low</b>	<b>TYMS high</b>
POOLA_INVASIVE_BREAST_CANCER_UP	POOLA_INVASIVE_BREAST_CANCER_UP
RASHI_RESPONSE_TO_IONIZING_RADIATION_6	WIELAND_UP_BY_HBV_INFECTION
LEE_DIFFERENTIATING_T_LYMPHOCYTE	BOSCO_TH1_CYTOTOXIC_MODULE
WIELAND_UP_BY_HBV_INFECTION	NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP
FARMER_BREAST_CANCER_CLUSTER_1	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_UP
ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN
THUM_SYSTOLIC_HEART_FAILURE_UP	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP
FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN	RASHI_RESPONSE_TO_IONIZING_RADIATION_6
GAURNIER_PSMD4_TARGETS	BROWNE_INTERFERON_RESPONSIVE_GENES
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	LEE_DIFFERENTIATING_T_LYMPHOCYTE
BROWNE_INTERFERON_RESPONSIVE_GENES	GARY_CD5_TARGETS_UP
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	DODD_NASOPHARYNGEAL_CARCINOMA_DN
MCLACHLAN_DENTAL_CARIES_UP	SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP	THUM_SYSTOLIC_HEART_FAILURE_UP

TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	WALLACE_PROSTATE_CANCER_RACE_UP
VILIMAS_NOTCH1_TARGETS_UP	QI_PLASMACYTOMA_UP
HADDAD_B_LYMPHOCYTE_PROGENITOR	HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN
BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE	FLORIO_NEOCORTEX_BASAL_RADIAL_GLIADN
RODWELL_AGING_KIDNEY_UP	ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER

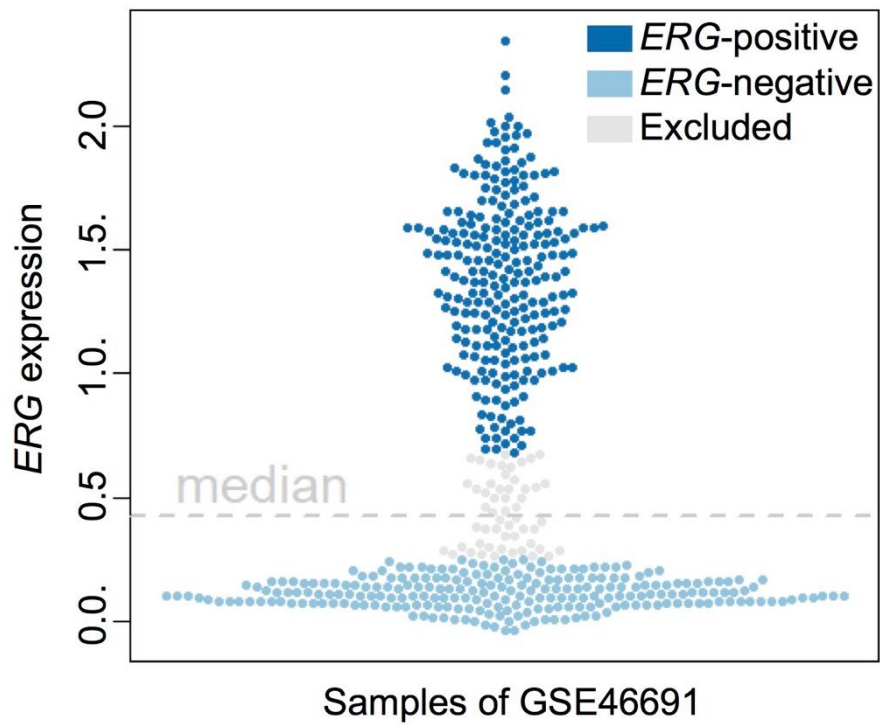
**Supplementary Table 7. Summary of *P* values of Kaplan-Meier analyses (Fig. 5B).**

*P* values were determined via Mantel-Haenszel test by comparing samples with high versus low expression of the indicated subtype-specific biomarkers separately in cases stratified by low (I-III) and high (IV/V) GGG. Significant genes are highlighted in bold font.

		TCGA-PRAD		GSE16560	
PCa subtype	Gene	GGG low (I-III)	GGG high (IV/V)	GGG low (I-III)	GGG high (IV/V)
T2E-positive	<i>ASPN</i>	0.249	0.357	0.275	0.471
	<i>BGN</i>	0.301	0.828	0.430	0.132
	<i>COL1A1</i>	0.520	0.857	0.211	0.978
	<i>RRM2</i>	0.622	0.800	0.467	0.704
	<i>TYMS</i>	0.506	0.722	0.685	0.758
T2E-negative	<b><i>ASPN</i></b>	0.919	0.151	<b>0.005</b>	0.104
	<i>BGN</i>	0.391	0.374	0.111	0.674
	<i>COL1A1</i>	0.958	0.090	0.064	0.077
	<b><i>RRM2</i></b>	0.262	<b>0.003</b>	<b>0.007</b>	<b>0.001</b>
	<b><i>TYMS</i></b>	0.391	<b>0.004</b>	<b>0.001</b>	<b>0.021</b>

**SUPPLEMENTARY FIGURES**

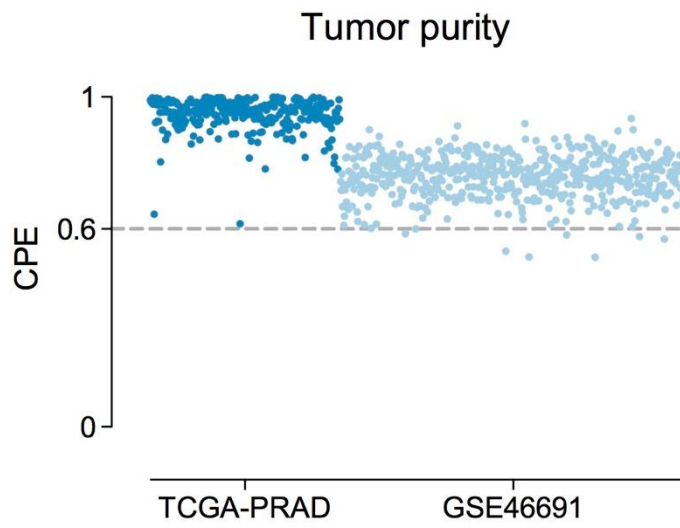
**Supplementary Figure 1** Gerke *et al.*



**Supplementary Fig. 1. T2E-fusion status in samples of the GSE46691-cohort.**

The T2E-fusion status was defined by median *ERG* expression (0.42). Samples ranging with their *ERG* expression between the 45<sup>th</sup> and 55<sup>th</sup> percentile (grey) were excluded.

**Supplementary Figure 2** Gerke *et al.*



**Supplementary Fig. 2. Tumor purity of TCGA-PRAD- and GSE46691-cohorts.**

Consensus Purity Estimation (CPE) calculated with the ESTIMATE algorithm for all samples of both discovery cohorts.