

PrognosiT: Pathway/gene set-based tumour volume
prediction using multiple kernel learning
— Supplementary figures —

Ayyüce Begüm Bektaş¹ and Mehmet Gönen^{2,3}

¹Graduate School of Science and Engineering, Koç University, İstanbul 34450, Turkey

²Department of Industrial Engineering, College of Engineering, Koç University, İstanbul 34450, Turkey

³School of Medicine, Koç University, İstanbul 34450, Turkey

HALLMARK_HYPOXIA	99	PID_CONE_PATHWAY	98
HALLMARK_KRAS_SIGNALING_DN	99	PID_HIF1_TFPATHWAY	98
HALLMARK_SPERMATOGENESIS	96	PID_NFAT_TFPATHWAY	88
HALLMARK_PANCREAS_BETA_CELLS	95	PID_ARF6_PATHWAY	85
HALLMARK_INFLAMMATORY_RESPONSE	86	PID_HNF3A_PATHWAY	85
HALLMARK_XENOBIOTIC_METABOLISM	85	PID_FRA_PATHWAY	84
HALLMARK_FATTY_ACID_METABOLISM	75	PID_ERBB_NETWORK_PATHWAY	82
HALLMARK_NOTCH_SIGNALING	73	PID_HNF3B_PATHWAY	81
HALLMARK_KRAS_SIGNALING_UP	62	PID_WNT_SIGNALING_PATHWAY	77
HALLMARK_ANGIOGENESIS	54	PID_RHODOPSIN_PATHWAY	77
HALLMARK_P53_PATHWAY	41	PID_UPA_UPAR_PATHWAY	74
HALLMARK_MYOGENESIS	39	PID_TCR_CALCIIUM_PATHWAY	66
HALLMARK_GLYCOLYSIS	37	PID_FANCONI_PATHWAY	63
HALLMARK_BILE_ACID_METABOLISM	34	PID_LIS1_PATHWAY	63
HALLMARK_HEDGEHOG_SIGNALING	33	PID_HES_HEY_PATHWAY	60
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	33	PID_IL23_PATHWAY	57
HALLMARK_COAGULATION	32	PID_ERB_GENOMIC_PATHWAY	53
HALLMARK_CHOLESTEROL_HOMEOSTASIS	30	PID_VEGF_VEGFR_PATHWAY	49
HALLMARK_G2M_CHECKPOINT	30	PID_ATR_PATHWAY	46
HALLMARK_E2F_TARGETS	30	PID_ALPHA_SYNUCLEIN_PATHWAY	46
HALLMARK_APICAL_JUNCTION	26	PID_SYNDECAN_4_PATHWAY	44
HALLMARK_APOPTOSIS	23	PID_FOXM1_PATHWAY	43
HALLMARK_ESTROGEN_RESPONSE_LATE	22	PID_BETA_CATENIN_NUC_PATHWAY	43
HALLMARK_MYC_TARGETS_V2	19	PID_EPHB_FWD_PATHWAY	39
HALLMARK_TNFA_SIGNALING_VIA_NFKB	18	PID_CMYB_PATHWAY	39
HALLMARK_ADIPOGENESIS	18	PID_REG_GR_PATHWAY	37
HALLMARK_PEROXISOME	18	PID_PLK1_PATHWAY	37
HALLMARK_WNT_BETA_CATENIN_SIGNALING	13	PID_CD8_TCR_DOWNSTREAM_PATHWAY	37
HALLMARK_DNA_REPAIR	12	PID_TRAIL_PATHWAY	34
HALLMARK_COMPLEMENT	12	PID_CDC42_PATHWAY	33
HALLMARK_MYC_TARGETS_V1	12	PID_LKB1_PATHWAY	32
HALLMARK_INTERFERON_GAMMA_RESPONSE	10	PID_P53_DOWNSTREAM_PATHWAY	30
HALLMARK_IL2_STAT5_SIGNALING	10	PID_GLYPICAN_1PATHWAY	29
HALLMARK_ANDROGEN_RESPONSE	9	PID_SYNDECAN_3_PATHWAY	28
HALLMARK_HEME_METABOLISM	7	PID_FGF_PATHWAY	28
HALLMARK_TGF_BETA_SIGNALING	6	PID_SYNDECAN_1_PATHWAY	26
HALLMARK_INTERFERON_ALPHA_RESPONSE	6	PID_IL3_PATHWAY	25
HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY	6	PID_NEPHRIN_NEPH1_PATHWAY	24
HALLMARK_ESTROGEN_RESPONSE_EARLY	5	PID_DELTA_NP63_PATHWAY	24
HALLMARK_APICAL_SURFACE	3	PID_RAS_PATHWAY	24
HALLMARK_UV_RESPONSE_UP	3	PID_AP1_PATHWAY	22
HALLMARK_IL6_JAK_STAT3_SIGNALING	2	PID_MYC_REPRESS_PATHWAY	22
HALLMARK_PI3K_AKT_MTOR_SIGNALING	2	PID_REELIN_PATHWAY	21
HALLMARK_UV_RESPONSE_DN	2	PID_PRL_SIGNALING_EVENTS_PATHWAY	20
HALLMARK_MITOTIC_SPINDLE	0	PID_AURORA_B_PATHWAY	20
HALLMARK_PROTEIN_SECRETION	0	PID_ARF_3PATHWAY	20
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0	PID_INSULIN_GLUCCOSE_PATHWAY	20
HALLMARK_MTORC1_SIGNALING	0	PID_PS1_PATHWAY	19
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0	PID_P38_MK2_PATHWAY	17
HALLMARK_ALLOGRAFT_REJECTION	0	PID_AVB3_OPN_PATHWAY	16

Figure S1: The selection frequencies of gene sets in the Hallmark collection over 100 replications resulted from PrognosiT algorithm and the selection frequencies of top 50 pathways in the PID collection over 100 replications resulted from PrognosiT algorithm.

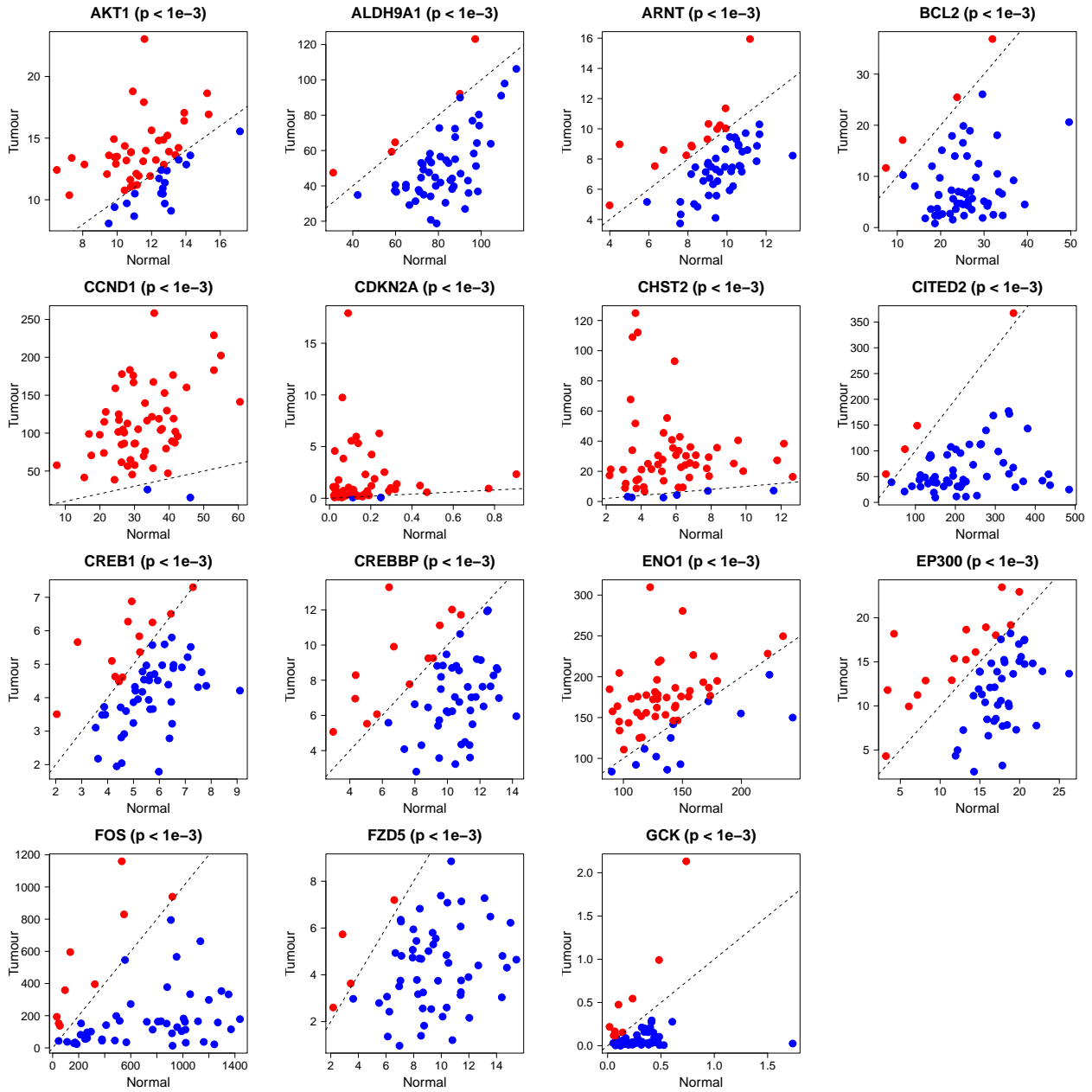


Figure S2: Statistically significantly up- or down-regulated genes during tumor progression selected by PrognosiT algorithm on thyroid carcinoma (i.e., THCA) data set over 100 replications. We performed paired Wilcoxon test to determine whether there is a significant difference (i.e., p -value < 0.05) between the gene expressions coming from tumor and normal tissues.

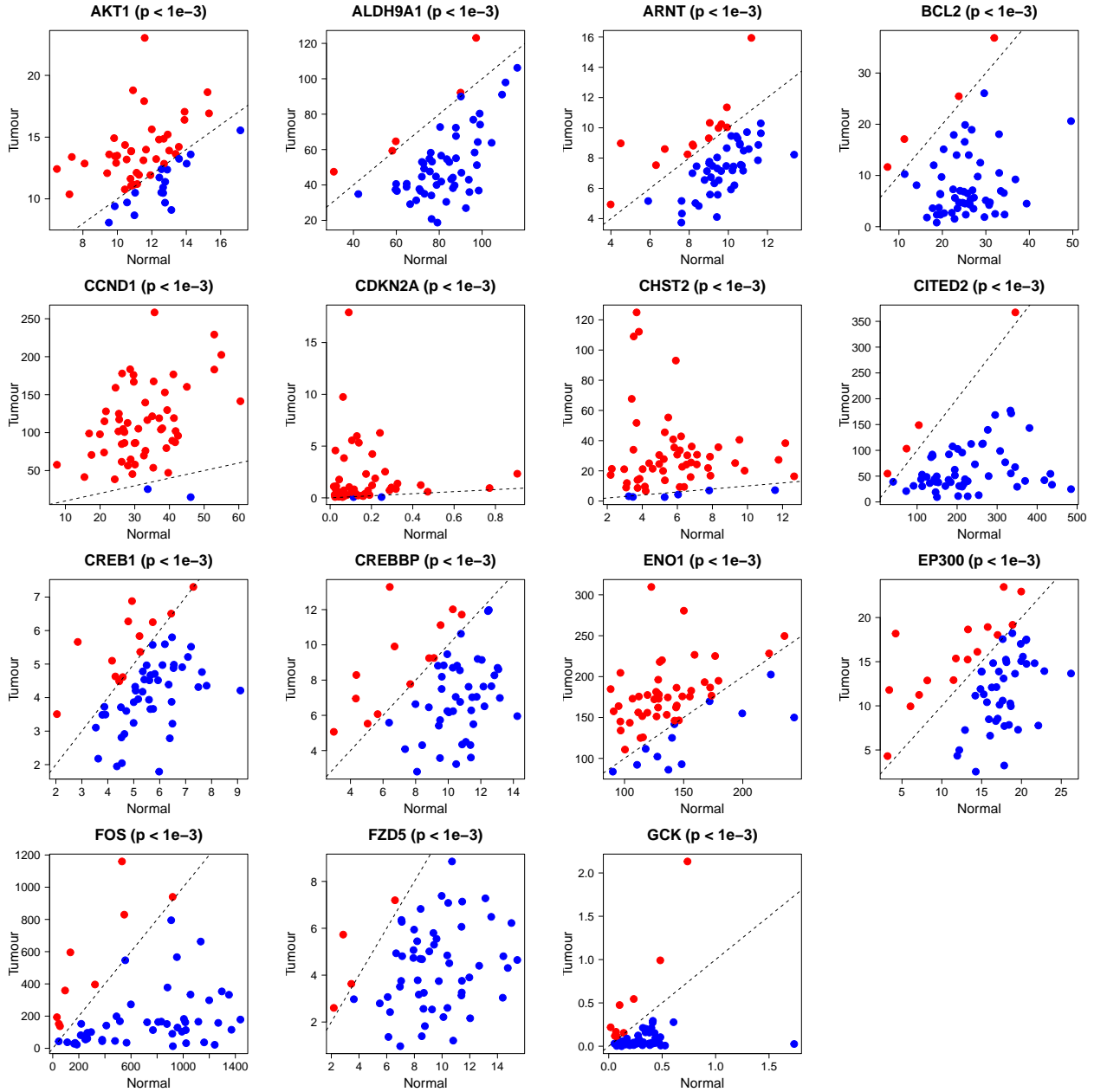


Figure S3: Statistically significantly up- or down-regulated genes during tumor progression selected by PrognosiT algorithm on thyroid carcinoma (i.e., THCA) data set over 100 replications. We performed paired Wilcoxon test to determine whether there is a significant difference (i.e., p -value < 0.05) between the gene expressions coming from tumor and normal tissues.