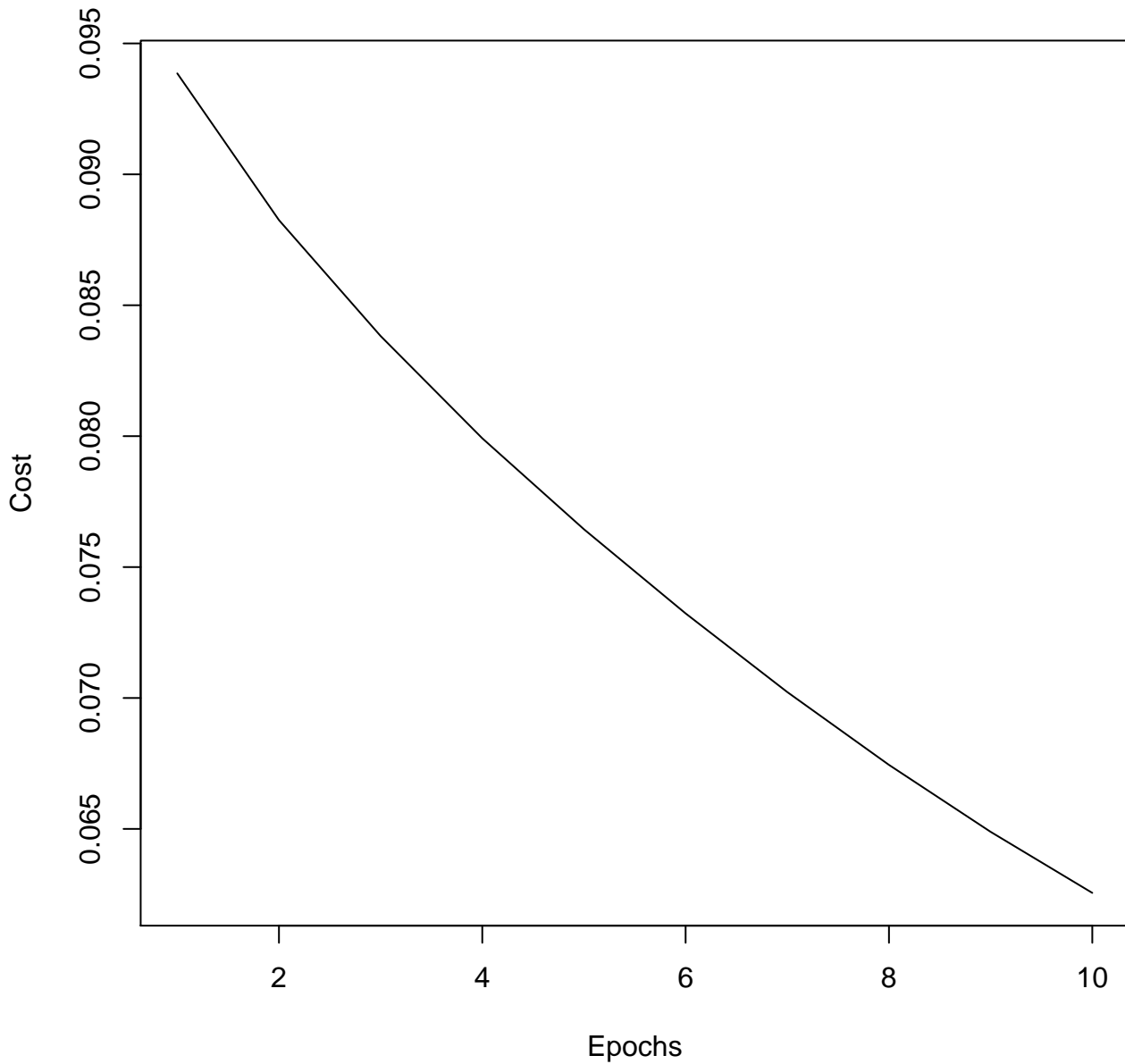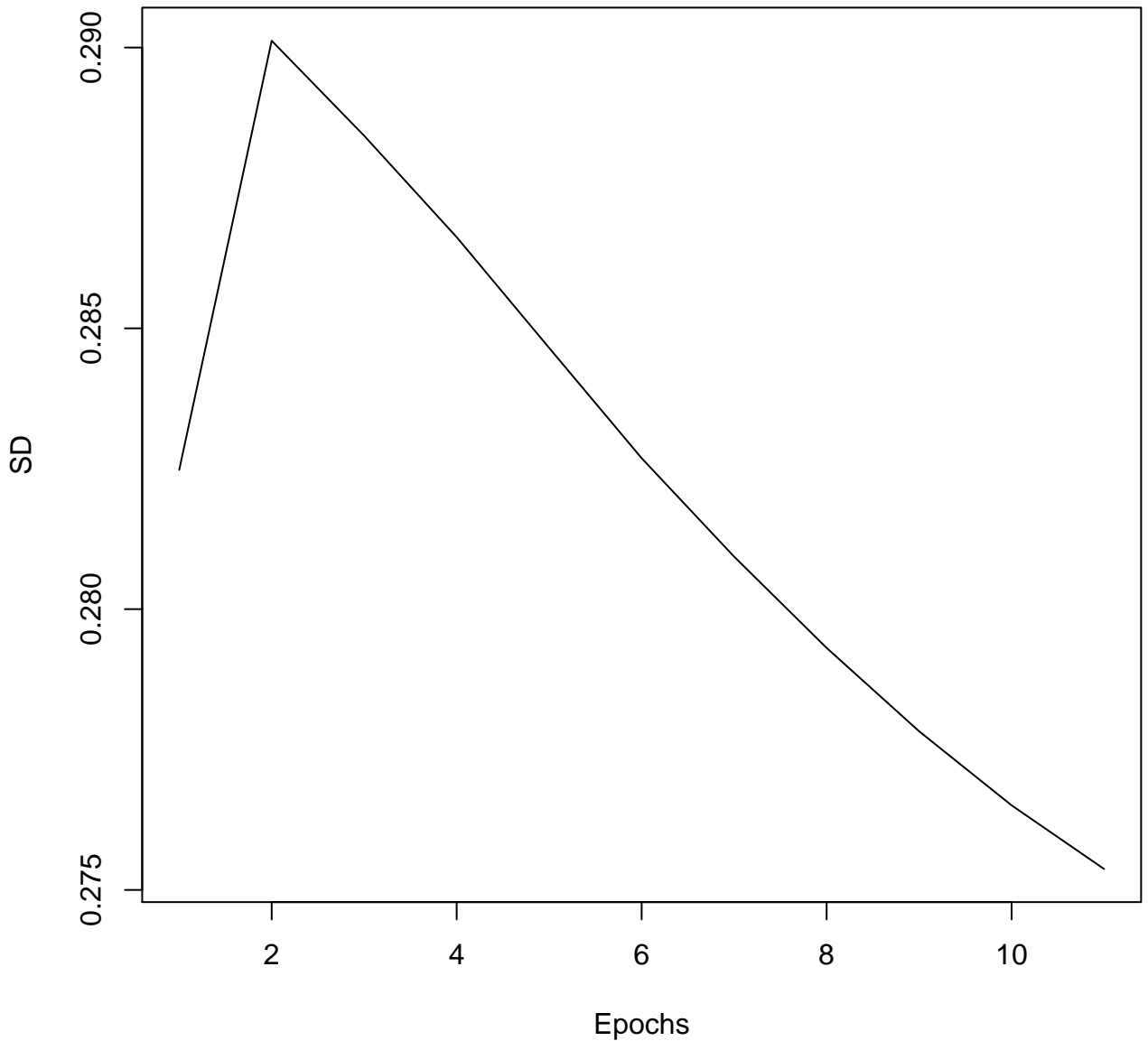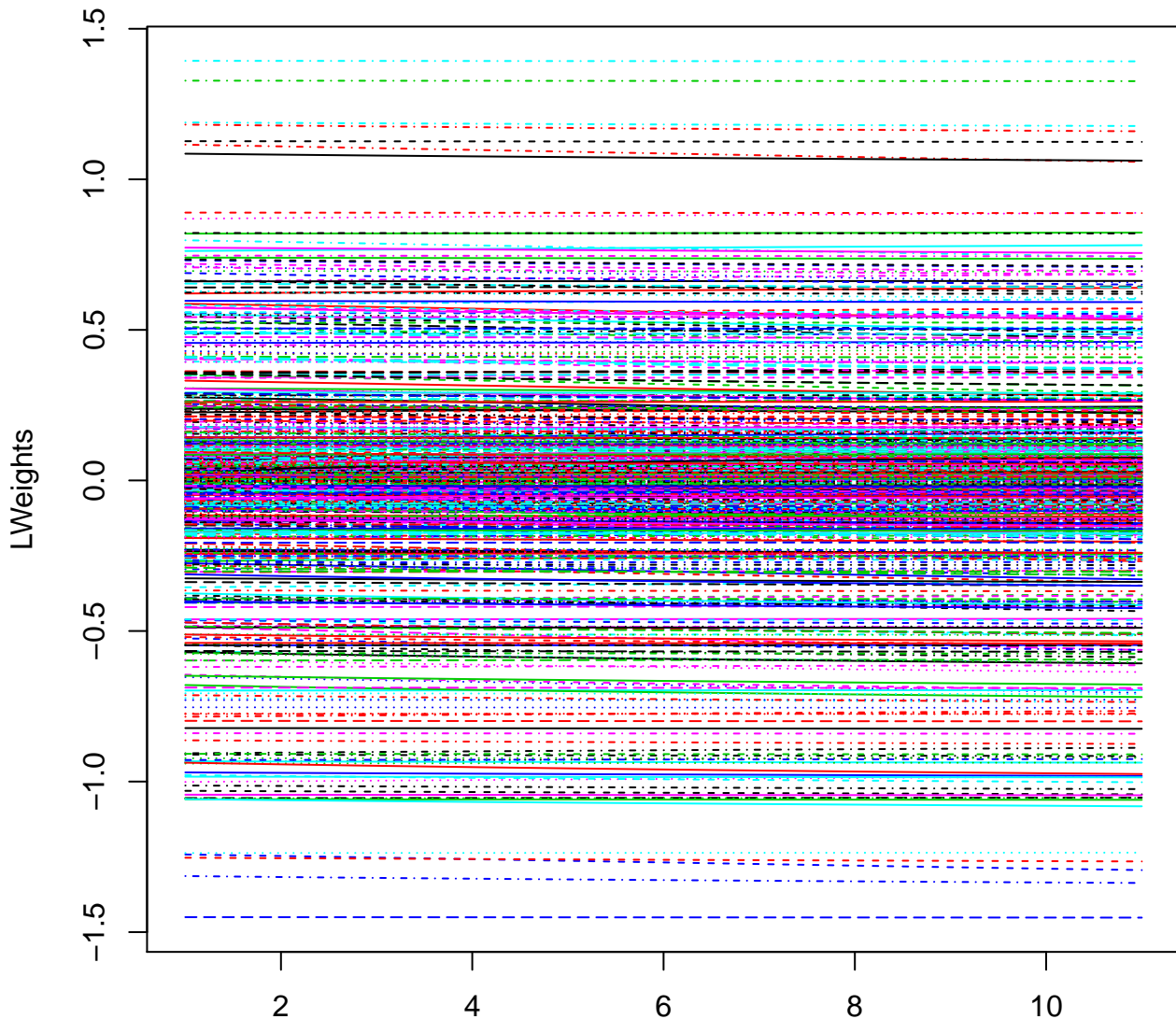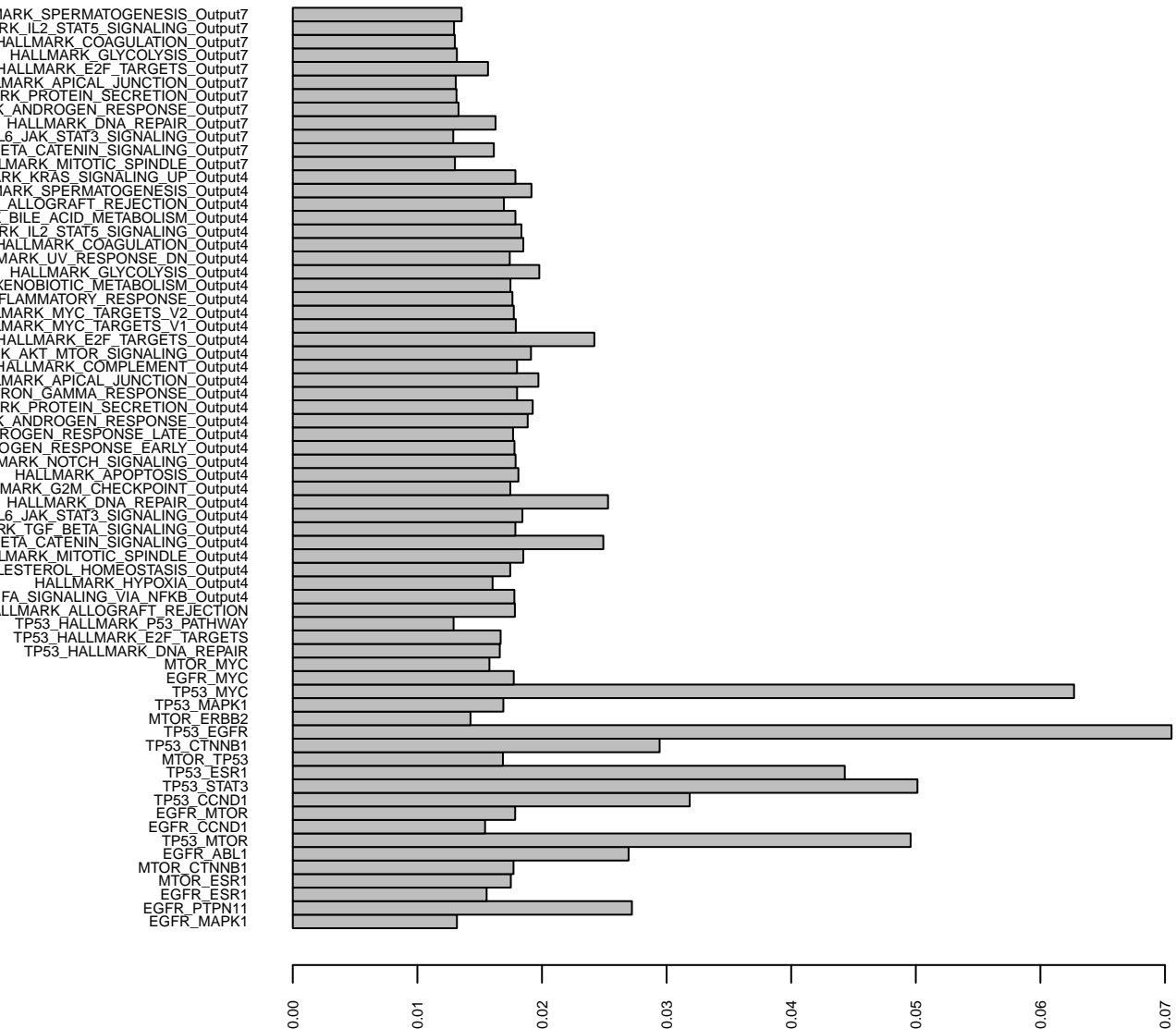**Evolution of std deviations
in outputs through learning**

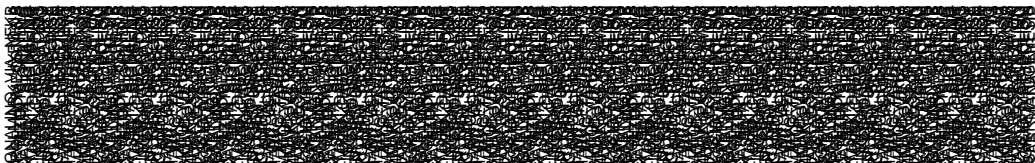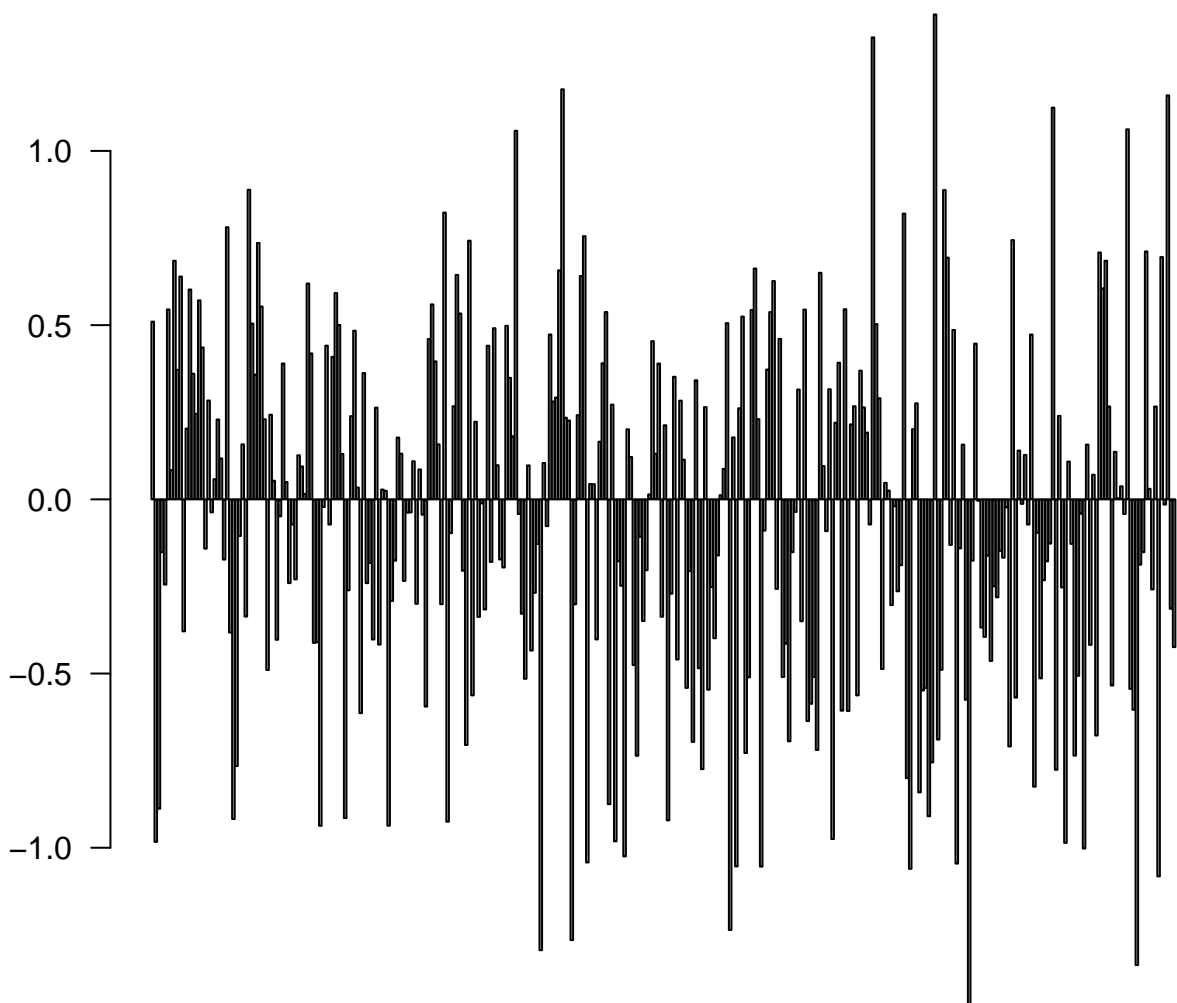**Evolution of weights through learning**

Top weights' correction

Labels (top to bottom):
- MARK_SPERMATOGENESIS_Output7
- RK_IL2_STAT5_SIGNALING_Output7
- HALLMARK_COAGULATION_Output7
- HALLMARK_GLYCOLYSIS_Output7
- HALLMARK_E2F_TARGETS_Output7
- MARK_APICAL_JUNCTION_Output7
- RK_PROTEIN_SECRETION_Output7
- K_ANDROGEN_RESPONSE_Output7
- HALLMARK_DNA_REPAIR_Output7
- 6_JAK_STAT3_SIGNALING_Output7
- ETA_CATENIN_SIGNALING_Output7
- LMARK_MITOTIC_SPINDLE_Output7
- RK_KRAS_SIGNALING_UP_Output4
- MARK_SPERMATOGENESIS_Output4
- _ALLOGRAFT_REJECTION_Output4
- _BILE_ACID_METABOLISM_Output4
- RK_IL2_STAT5_SIGNALING_Output4
- HALLMARK_COAGULATION_Output4
- MARK_UV_RESPONSE_DN_Output4
- HALLMARK_GLYCOLYSIS_Output4
- KENOBIOTIC_METABOLISM_Output4
- FLAMMATORY_RESPONSE_Output4
- MARK_MYC_TARGETS_V2_Output4
- MARK_MYC_TARGETS_V1_Output4
- HALLMARK_E2F_TARGETS_Output4
- K_AKT_MTOR_SIGNALING_Output4
- HALLMARK_COMPLEMENT_Output4
- MARK_APICAL_JUNCTION_Output4
- RON_GAMMA_RESPONSE_Output4
- RK_PROTEIN_SECRETION_Output4
- K_ANDROGEN_RESPONSE_Output4
- ROGEN_RESPONSE_LATE_Output4
- OGEN_RESPONSE_EARLY_Output4
- MARK_NOTCH_SIGNALING_Output4
- HALLMARK_APOPTOSIS_Output4
- MARK_G2M_CHECKPOINT_Output4
- HALLMARK_DNA_REPAIR_Output4
- 6_JAK_STAT3_SIGNALING_Output4
- RK_TGF_BETA_SIGNALING_Output4
- ETA_CATENIN_SIGNALING_Output4
- LMARK_MITOTIC_SPINDLE_Output4
- LESTEROL_HOMEOSTASIS_Output4
- HALLMARK_HYPOXIA_Output4
- FA_SIGNALING_VIA_NFKB_Output4
- HALLMARK_ALLOGRAFT_REJECTION
- TP53_HALLMARK_P53_PATHWAY
- TP53_HALLMARK_E2F_TARGETS
- TP53_HALLMARK_DNA_REPAIR
- MTOR_MYC
- EGFR_MYC
- TP53_MYC
- TP53_MAPK1
- MTOR_ERBB2
- TP53_EGFR
- TP53_CTNNB1
- MTOR_TP53
- TP53_ESR1
- TP53_STAT3
- TP53_CCND1
- EGFR_MTOR
- EGFR_CCND1
- TP53_MTOR
- EGFR_ABL1
- MTOR_CTNNB1
- MTOR_ESR1
- EGFR_ESR1
- EGFR_PTPN11
- EGFR_MAPK1

x-axis: 0.00, 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07

predictions

C−index = 0.576 ; std = 0.067
MSE = 0.058

True survival time intervals

Predicted mean survival probability

predictions

C−index = 0.534 ; std = 0.095
MSE = 0.078

True survival time intervals

Predicted mean survival probability