

Table S3. This library contains 229 colorectal cancer-related non-redundant position weight matrices (PWMs) based on the TRANSFAC database (release 2014.1) to minimize the rate of false predictions in promoter analyses. Using the F-MATCH program of the geneXplain platform, this library was used to predict enriched transcription factor binding sites in the promoter sequences (-1000 to 100 bp regions relative to transcription start sites) of the signature genes of the colorectal cell lines 1638N-T1 and CMT-93.

ID

V\$AHRARNT_01
V\$AHRARNT_02
V\$AHRHIF_Q6
V\$ALPHACP1_01
V\$ALX4_01
V\$AML1_01
V\$AML1_Q6
V\$AML_Q6
V\$AP1FJ_Q2
V\$AP1_01
V\$AP1_Q2_01
V\$AP1_Q6_01
V\$AP2ALPHA_01
V\$AP2ALPHA_02
V\$AP2_Q3
V\$AP2_Q6
V\$AP2_Q6_01
V\$AREB6_01
V\$AREB6_02
V\$AREB6_03
V\$AREB6_04
V\$ARNT_01
V\$ARNT_02
V\$AR_01
V\$AR_02
V\$AR_Q2
V\$AR_Q6_01
V\$ATF3_Q6
V\$ATF4_Q2
V\$BETACATENIN_Q6
V\$BRACH_01
V\$BRCA_01
V\$CACCCBINDINGFACTOR_Q6
V\$CDPCR1_01
V\$CDPCR3HD_01
V\$CDPCR3_01
V\$CDP_01
V\$CDP_02
V\$CDX2_Q5
V\$CDX_Q5
V\$CEBPB_01
V\$CEBPB_02
V\$CEBP_Q3
V\$CETS1P54_01
V\$CETS1P54_02
V\$CHOP_01
V\$CLOCKBMAL_Q6
V\$CMYB_01
V\$COUP_01
V\$CREBP1CJUN_01
V\$CREB_Q3
V\$CREL_01
V\$DEAF1_01
V\$DEAF1_02
V\$DEC_Q1
V\$DELTAEF1_01
V\$DR1_Q3
V\$DR3_Q4
V\$DR4_Q2
V\$E12_Q6
V\$E2F1DP1_01
V\$E2F1DP2_01
V\$E2F1_Q3
V\$E2F1_Q3_01

V\$E2F1_Q4
V\$E2F4DP1_01
V\$E2F_01
V\$E2F_02
V\$E2F_03
V\$E2F_Q2
V\$E2F_Q3_01
V\$E2F_Q4_01
V\$E47_01
V\$E47_02
V\$EBF_Q6
V\$EBOX_Q6_01
V\$EFC_Q6
V\$EGR1_01
V\$EGR_Q6
V\$EN1_01
V\$ER_Q6
V\$ETS1_B
V\$ETS_Q4
V\$FOX01_01
V\$FOX01_02
V\$FOX03_01
V\$FOXP3_Q4
V\$FOX_Q2
V\$FXR_Q3
V\$GATA4_Q3
V\$GATA6_01
V\$GLI_Q2
V\$HAND1E47_01
V\$HEB_Q6
V\$HES1_Q2
V\$HFBH8_01
V\$HIC1_02
V\$HIC1_03
V\$HIF1_Q5
V\$HMG1Y_Q3
V\$HMG1Y_Q6
V\$HNF1_01
V\$HNF1_C
V\$HNF1_Q6
V\$HNF3ALPHA_Q6
V\$HNF3B_01
V\$HNF3_Q6
V\$HNF4ALPHA_Q6
V\$HNF4_01
V\$HNF4_01_B
V\$HNF4_Q6_01
V\$HNF6_Q6
V\$HOX13_01
V\$HSF1_01
V\$HSF1_Q6
V\$HSF_Q6
V\$IK1_01
V\$IK2_01
V\$IK3_01
V\$IPF1_Q4
V\$IPF1_Q4_01
V\$IRF_Q6
V\$KAT5_01
V\$KROX_Q6
V\$LEF1_Q2
V\$LXR_Q3
V\$LYF1_01
V\$MAF_Q6_01
V\$MEIS1AHOXA9_01
V\$MEIS1BHOXA9_02
V\$MYB_Q3
V\$MYB_Q6
V\$MYC_MAX_01
V\$MYC_MAX_02
V\$MYC_MAX_B
V\$MYC_Q2

V\$MYOD_01
V\$MYOD_Q6
V\$MYOD_Q6_01
V\$MZF1_01
V\$MZF1_02
V\$NANO_01
V\$NFAT_Q6
V\$NFKAPPAB50_01
V\$NFKAPPAB65_01
V\$NFKAPPAB_01
V\$NFKB_C
V\$NFKB_Q6
V\$NFKB_Q6_01
V\$NFY_01
V\$NFY_C
V\$NFY_Q6
V\$NRF2_Q4
V\$NRSE_B
V\$NRSF_01
V\$NRSF_Q4
V\$OCT4_01
V\$OCT4_02
V\$OCT_Q6
V\$OSF2_Q6
V\$OTX_Q1
V\$P300_01
V\$P53_01
V\$P53_02
V\$PAX2_01
V\$PAX2_02
V\$PAX3_01
V\$PAX3_B
V\$PAX6_01
V\$PAX6_Q2
V\$PAX_Q6
V\$PBX_Q3
V\$PPARA_02
V\$PPARG_01
V\$PPARG_02
V\$PPARG_Q3
V\$RBPJK_01
V\$RBPJK_Q4
V\$RFX_Q6
V\$RORA1_01
V\$RORA2_01
V\$RUSH1A_02
V\$SMAD3_Q6
V\$SMAD4_Q6
V\$SMAD_Q6
V\$SMAD_Q6_01
V\$SOX9_B1
V\$SOX_Q6
V\$SP1_01
V\$SP1_Q4_01
V\$SP1_Q6
V\$SP1_Q6_01
V\$SP3_Q3
V\$SREBP1_01
V\$SREBP1_02
V\$SREBP1_Q6
V\$SREBP_Q3
V\$SRF_01
V\$SRF_C
V\$SRF_Q4
V\$SRF_Q5_01
V\$SRF_Q6
V\$STAT1_01
V\$STAT3_01
V\$STAT5A_01
V\$STAT5A_02
V\$STAT_01
V\$STAT_Q6

V\$TAL1BETAE47_01
V\$TATA_01
V\$TATA_C
V\$TBP_01
V\$TBP_Q6
V\$TBX5_01
V\$TBX5_02
V\$TBX5_Q5
V\$TCF4_Q5
V\$TEF1_Q6
V\$TFE_Q6
V\$USF2_Q6
V\$USF_01
V\$USF_02
V\$USF_C
V\$USF_Q6
V\$USF_Q6_01
V\$VDR_Q3
V\$VDR_Q6_01
V\$WT1_Q6
V\$ZIC1_01