

Supplementary Figure Legends

Figure S1. Schematic of the modified cytosine PBM methodology. Single-stranded Agilent HK arrays containing 40,000 features were made double-stranded with a nucleotide mix that contains either cytosine, 5mC, or 5hmC using a common primer. An epitope-tagged (GST) TF is allowed to bind to the sequences on the microarray slide. Binding is then detected using a fluor-conjugated antibody to the followed by measurement of bound protein (fluorescence intensities) for each of the array features.

Figure S2. Comparison of CREB1-GST binding to DNA 8-mers between replicates. **A.** Z-scores for CREB1 binding to 8-mers containing cytosine from replicate1 (Y-axis) and cytosine from replicate 2 (X-axis). Three spots are highlighted: 1.the canonical CRE 8-mer TGAC|GTCA (red spot), 2.the CRE|C/EBP chimeric 8-mer TGAC|GCAA (green spot), and the 8-mer TGAT|GCAA (blue spot). **B.** Z-scores for CREB1 binding to 8-mers containing 5mC from replicate1 (Y-axis) and 5mC from replicate 2 (X-axis). **C.** Z-scores for CREB1 binding to 8-mers containing 5hmC from replicate 1 (Y-axis) and 5hmC from replicate 2 (X-axis).

Figure S3. Comparison of ATF1-GST binding to DNA 8-mers between replicates. **A.** Z-scores for ATF1 binding to 8-mers containing cytosine from replicate 1 (Y-axis) and cytosine from replicate 2 (X-axis). **B.** Z-scores for ATF1 binding to 8-mers containing 5mC from replicate1 (Y-axis) and 5mC from replicate 2 (X-axis). **C.** Z-scores for ATF1 binding to 8-mers containing 5hmC from replicate 1 (Y-axis) and 5hmC from replicate 2 (X-axis).

Figure S4. Comparison of JUND-GST binding to DNA 8-mers between replicates. Z-scores for JUND binding to 8-mers containing cytosine from replicate 1 (Y-axis) and cytosine from replicate 2 (X-axis).

Figure S5. Heat-map of enrichment of six motifs in DHS derived from 125 human cells. Hierarchical clustering of enrichment scores for six motifs (CRE, C/EBP, CRE|C/EBP, TGAT|GCAA, and two negative control sequences (-)) in DHS derived from 125 samples in human. Samples were classified according to their karyotype (cancer, normal, brain, ESC or B- or T-cells) as indicated by the color legend.

Figure S6. Enrichment of GO biological process terms of promoters containing TGAT|GCAA. Promoters are defined as -10kbp to +10kbp from the transcription start site.

Figure S1

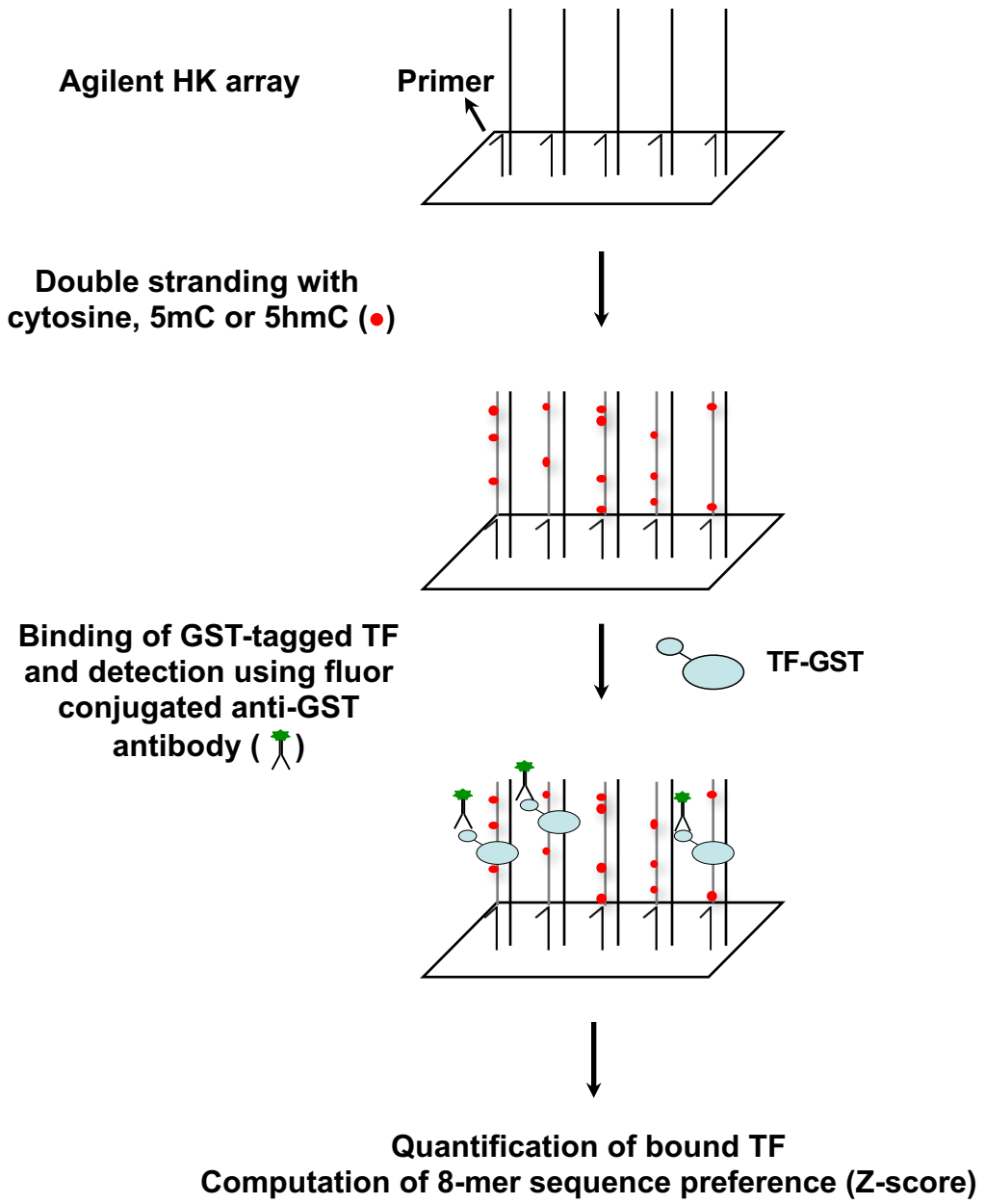


Figure S2

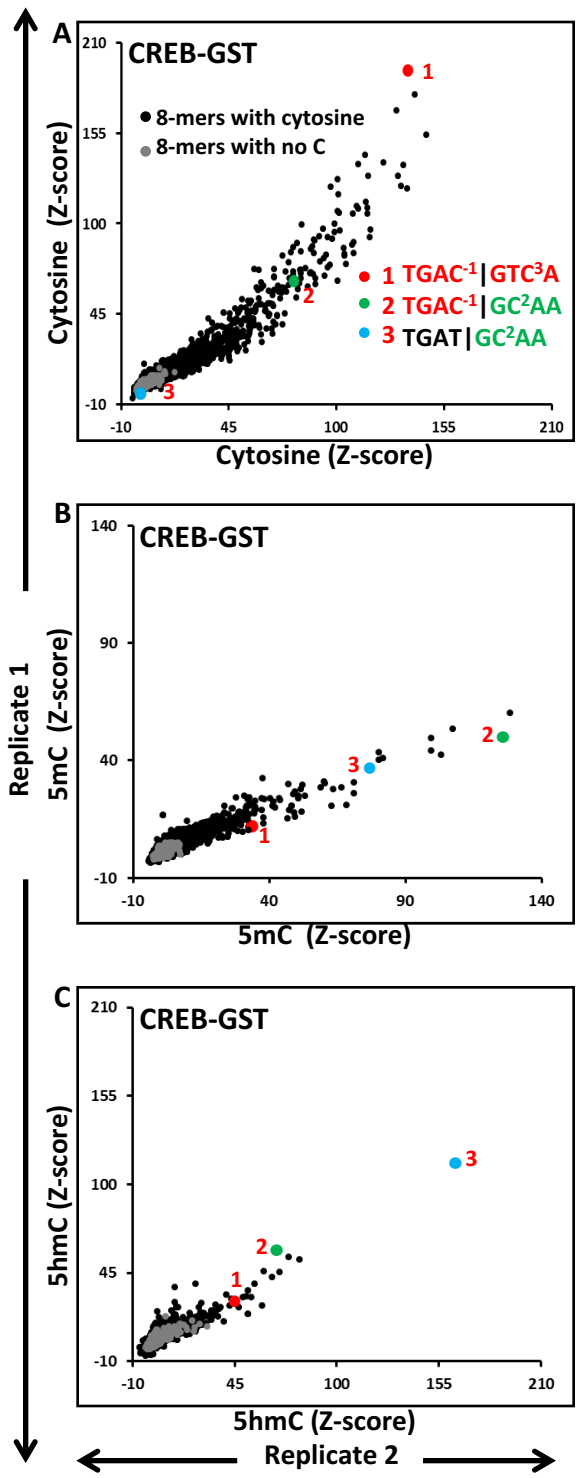


Figure S3

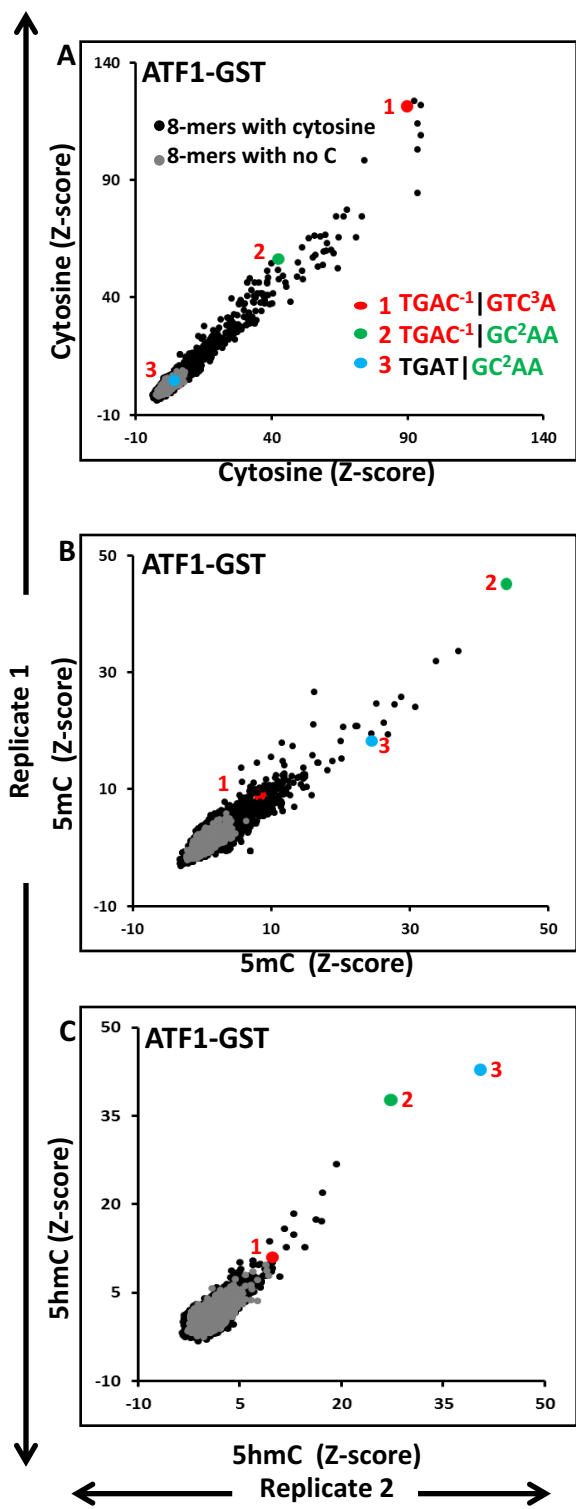


Figure S4

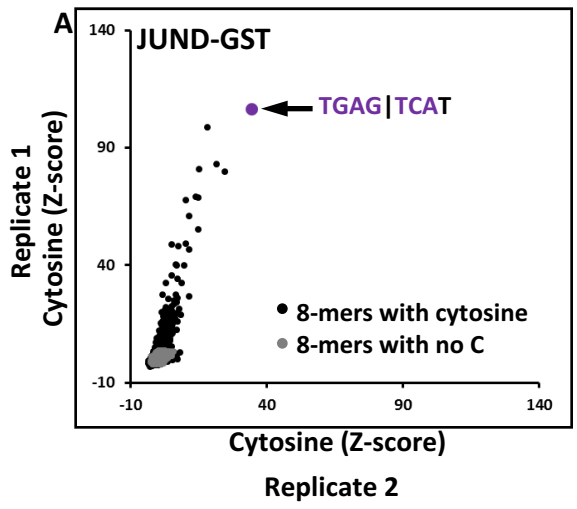
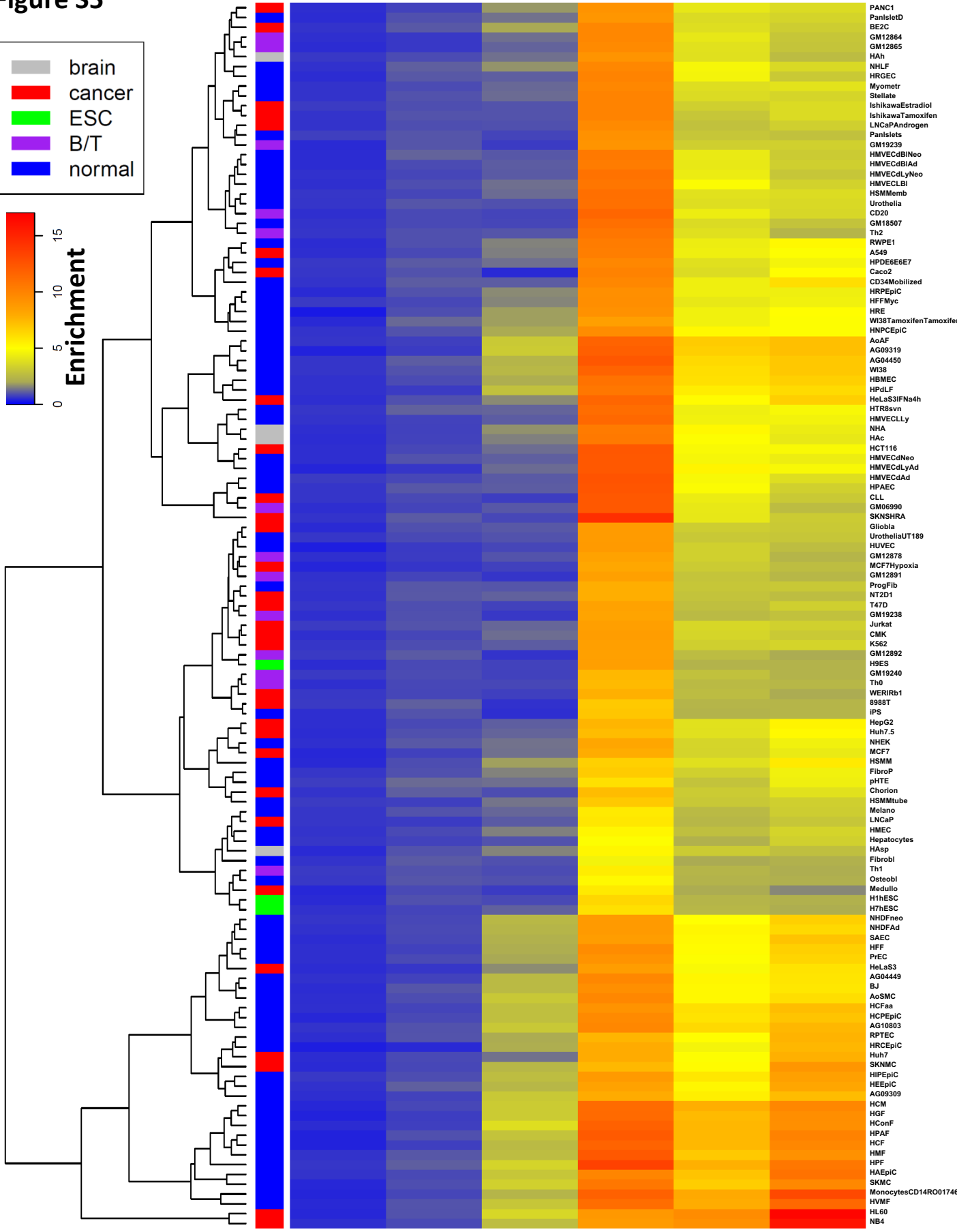
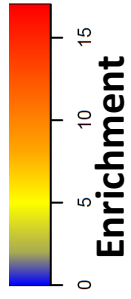
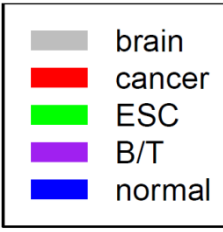


Figure S5



- PANC1
- PanIsletD
- BE2C
- GM12884
- GM12865
- HAh
- NHLF
- HRGEC
- Myometr
- Stellate
- IshikawaEstradiol
- LNCaPAAndrogen
- PanIslets
- GM19239
- HMVEcdBINeo
- HMVEcdBIAd
- HMVEcdLyNeo
- HMVECLBI
- HSMMemb
- Urothelia
- CD20
- GM18507
- Th2
- RWPE1
- A549
- HPDE6E6E7
- Caco2
- CD34Mobilized
- HRPEpic
- FFMyc
- HRE
- W38TamoxifenTamoxifen
- HNPCePic
- AoAF
- AG09319
- AG04450
- W38
- HBMEC
- HPdLF
- HeLaS3IFNa4h
- HTR8svn
- HMVECLLy
- NHA
- HAc
- HCT116
- HMVEcdNeo
- HMVEcdLyAd
- HMVEcdAd
- HPAEC
- CLL
- GM06990
- SKNSHRA
- Globla
- UrotheliaUT189
- HUVEC
- GM12878
- MCF7Hypoxia
- GM12891
- ProgFib
- NT2D1
- T47D
- GM19238
- Jurkat
- CMK
- K562
- GM12892
- H9ES
- GM19240
- Th0
- WERIRb1
- 898T
- IPS
- HepG2
- Huh7.5
- NHEK
- MCF7
- HSMM
- FibroP
- pHTE
- Chorion
- HSMMtube
- Melano
- LNCaP
- HMEC
- Hepatocytes
- HAsp
- Fibrobl
- Th1
- Osteobl
- Medullo
- HiHESC
- H7HESC
- NHDFneo
- NHDFAd
- SAEC
- HFF
- PvEC
- HeLaS3
- AG04449
- BJ
- AsSMC
- HCFaa
- HCPEpic
- AG10803
- RPTEC
- HRCEpic
- Huh7
- SKNMC
- HIPEpic
- HEPEpic
- AG09309
- HCM
- HGF
- HConF
- HPAF
- HCF
- HMF
- HPF
- HAPEpic
- SKMC
- MonocytesCD14RO01746
- HVMF
- HL60
- NB4

Figure S6

#motif=13,994, #promoters=7,090

