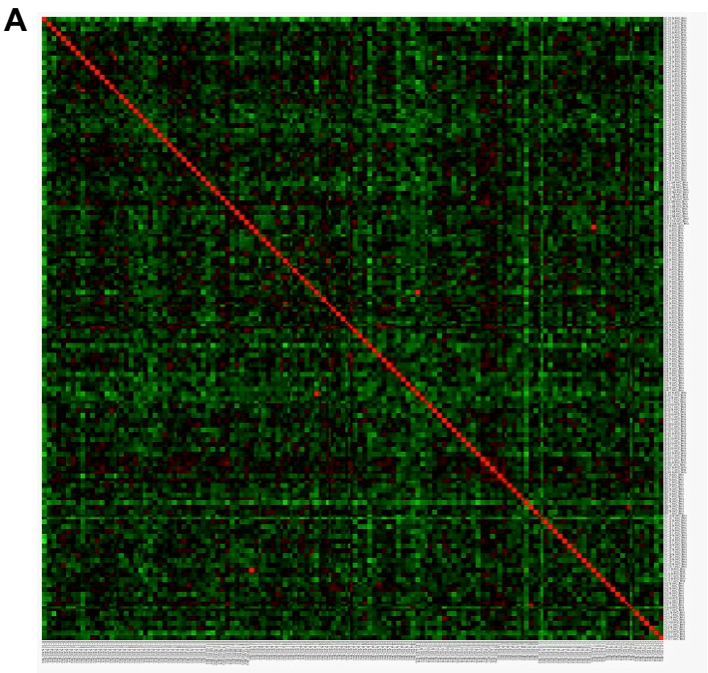
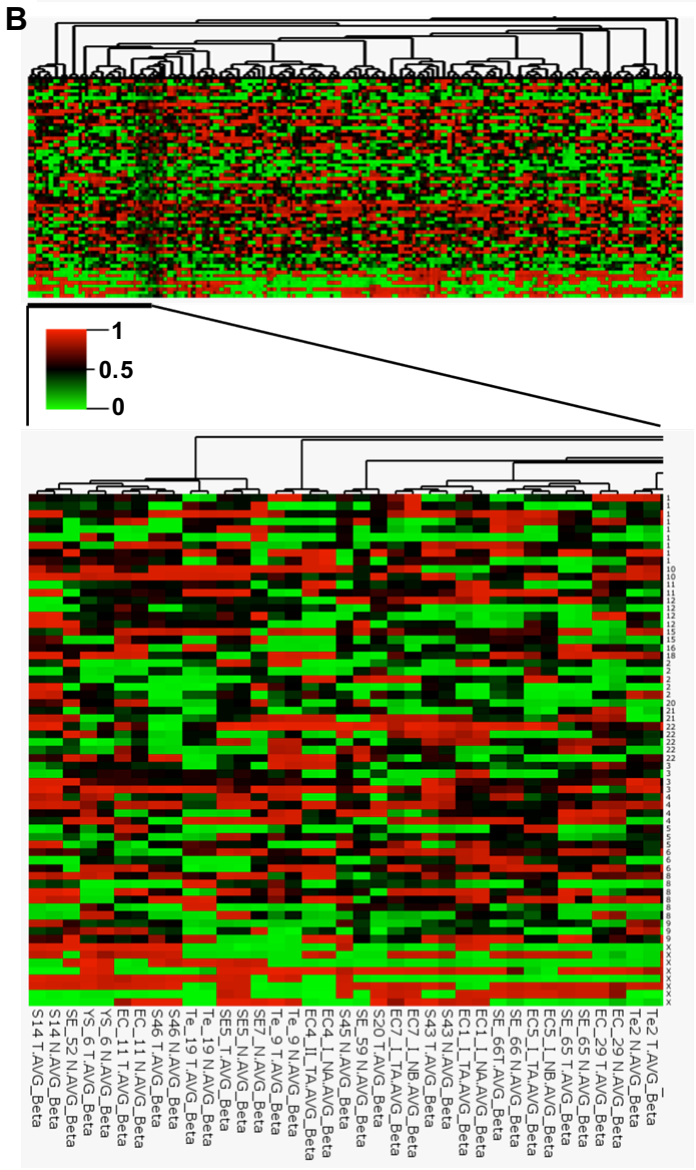

A


B
1
0.5
0
S14 T.AVG_Beta
S14 N.AVG_Beta
SE_52 N.AVG_Beta
YS_6 T.AVG_Beta
YS_6 N.AVG_Beta
EC_11 T.AVG_Beta
EC_11 N.AVG_Beta
S46 T.AVG_Beta
S46 N.AVG_Beta
Te_19 T.AVG_Beta
Te_19 N.AVG_Beta
SE5_T.AVG_Beta
SE5_N.AVG_Beta
SE7_N.AVG_Beta
Te_9 T.AVG_Beta
Te_9 N.AVG_Beta
EC4_II_TA.AVG_Beta
EC4_I_NA.AVG_Beta
S45 N.AVG_Beta
SE_59 N.AVG_Beta
S20 T.AVG_Beta
EC7_I_TA.AVG_Beta
EC7_I_NB.AVG_Beta
S43 T.AVG_Beta
S43 N.AVG_Beta
EC1_I_TA.AVG_Beta
EC1_I_NA.AVG_Beta
SE_66T.AVG_Beta
SE_66 N.AVG_Beta
EC5_I_TA.AVG_Beta
EC5_I_NB.AVG_Beta
SE_65 T.AVG_Beta
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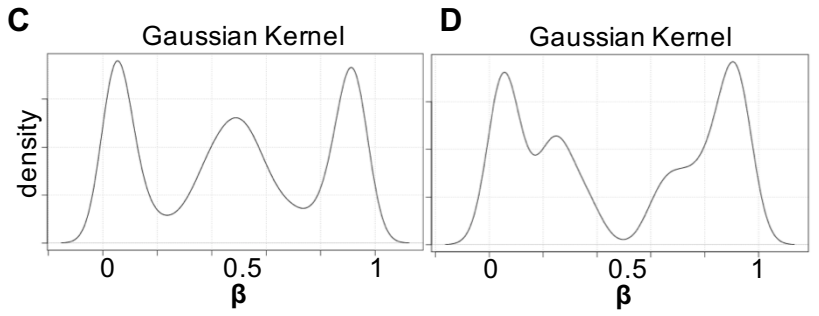
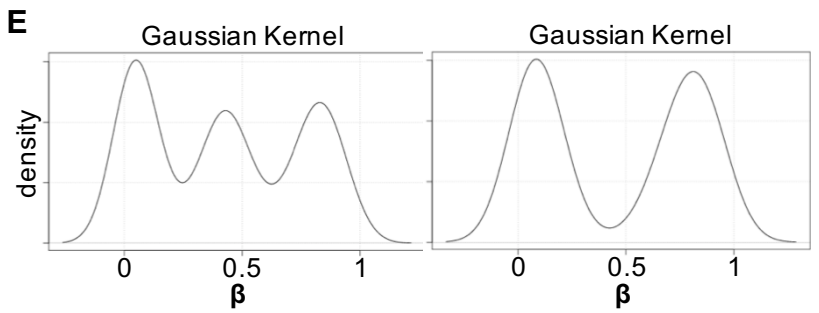
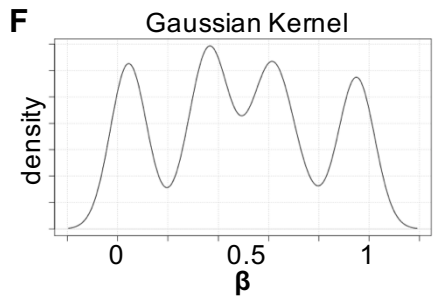
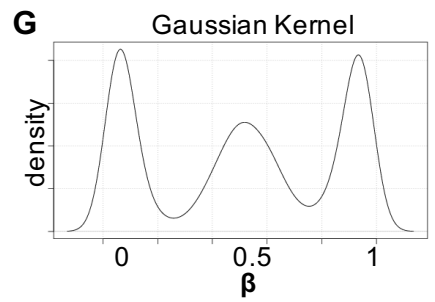
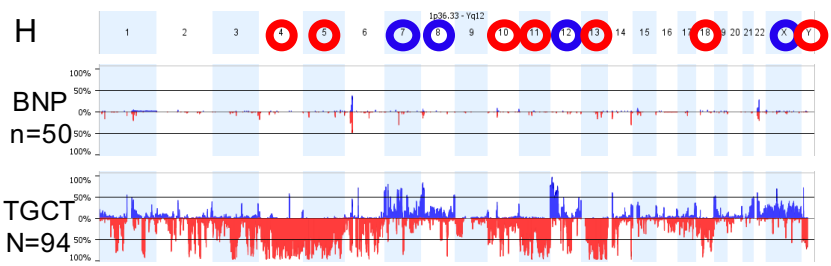
EC_29 T.AVG_Beta
EC_29 N.AVG_Beta
Te2 N.AVG_Beta
Te2 T.AVG_Beta


C
Gaussian Kernel
density
0
0.5
1
β
D
Gaussian Kernel
0
0.5
1
β


E
Gaussian Kernel
density
0
0.5
1
β
Gaussian Kernel
0
0.5
1
β


F
Gaussian Kernel
density
0
0.5
1
β


G
Gaussian Kernel
density
0
0.5
1
β


H
BNP
n=50
TGCT
N=94

Supplemental Fig. S1. **A**. SNP-based matching QC. Pearson correlation of tumor/normal (T/N) pairs (top panel) shows expected matching based on 65 "rs" SNP targets. **B.** Furthermore, Tumor (n=130) and BNT (benign neighboring testis specimens, n=128) were hierarchical clustered with the 65 "rs" 450K array targets (lower two panels), which confirmed sample identity continuity from tissue through to array profiles. Observed homozygosity for the chromosome X targets is as expected for male patients. Equivalent heterozygosity between tumor and normal for autosomal targets indicates a somatic/pre-meiotic origin for the tumors. **C-F**: Representative meiosis patterns by Kernel density estimation (KDE) plots of the 65 SNPs present on the 450K methylation array. **C**. Trimodal methylation beta distribution observed 108 individual TGCT samples with central peak at 0.5 is consistent with pre-meiotic state. **D**. Simulation of a 50:50 mixture of post-meiotic cells (genome-wide UPD reference data) and somatic cells generates a tetramodal pattern with loss of heterozygosity. Note: admixture of pre- and post-meiotic cells from same genetic background eliminates allele frequencies of 0.5. **E**. *In vivo* pre- and post-meiosis ovarian teratoma germ cell tumors (n=6 (left panel) and 3 (right panel), respectively) provide negative and positive control tissues for these states. **F**. Tetramodal peak pattern as seen in triploid placental samples assayed by 450K array (GSE74738, n=10 (5 digynic and, 5 diandric)). **G**. Validation of trimodal methylation beta distribution at SNP loci in independent TGCT dataset (n=94). **H**. Validation of SCNA-calling algorithm in TCGA TGCT dataset (n=94) with benign neighboring prostate (BNP, n=50) from TCGA used as reference baseline; circles around chromosomes indicate recurrent gains (blue) and losses (red) and recapitulate original findings.