A

TCGA TGCT SE 100%
TCGA TGCT EC 100%
TCGA TGCT TE >90%
TCGA TGCT YST >80%

DPPA3

1
0.5
0

B

CpH

C

GNAS
GRB10
HM13
HYMAI
KCNQ1
KCNQ1OT1
L3MBTL
MAGEL2
MEST
MESTIT1
NAP1L5
NDN
PEG10
PLAGL1
SGCE
SNRPN
TRAPPC9
ZNF331

H19

Supplemental Fig. S7. Validation of key methylation findings in independent TGCT dataset from TCGA. Public level 1 Illumina 450K methylation data were downloaded, and samples were selected for analysis based on annotated purity for histologic subtypes as indicated in samples color legend. **A**. *DPPA3* methylation is erased. **B**. mCH targets are specifically methylated in EC. **C**. Globally imprints are erased, with focal, recurrent imprinted gene hypermethylation, notably *HM13* in NS (purple rectangle), and *H19* in TE (orange rectangle).