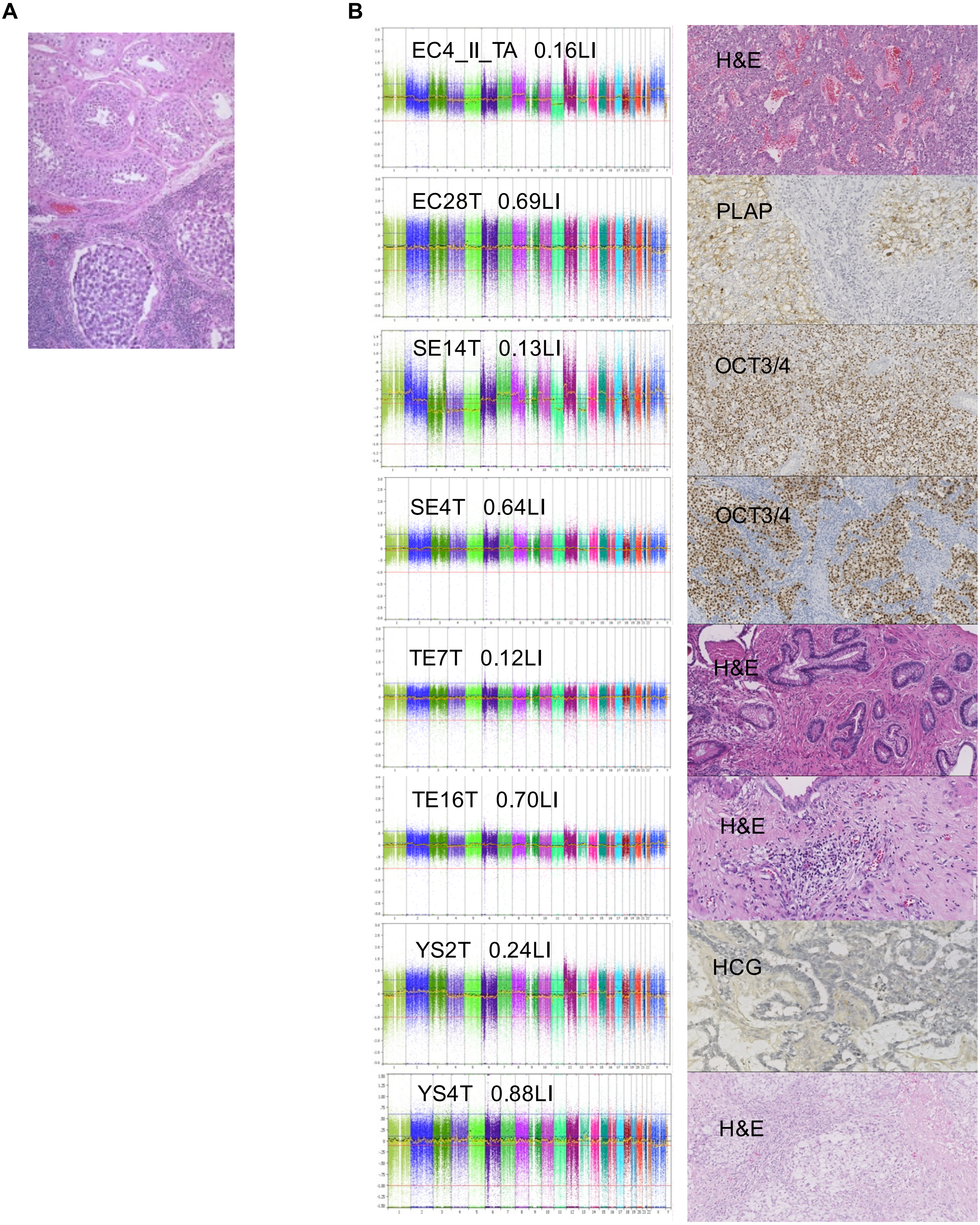
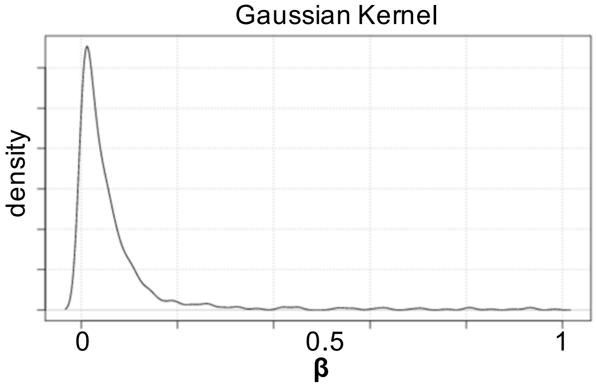
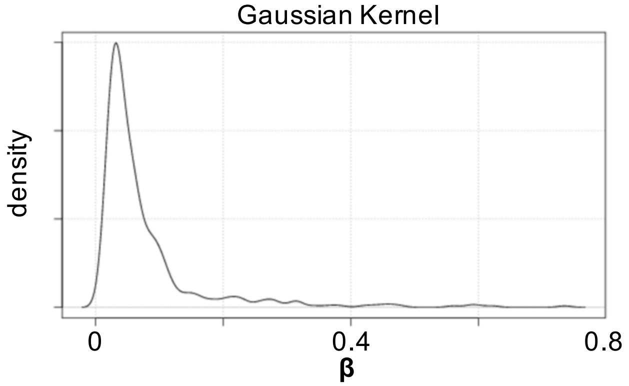

A
B
EC4_II_TA 0.16LI
H&E
EC28T 0.69LI
PLAP
SE14T 0.13LI
OCT3/4
SE4T 0.64LI
OCT3/4
TE7T 0.12LI
H&E
TE16T 0.70LI
H&E
YS2T 0.24LI
HCG
YS4T 0.88LI
H&E

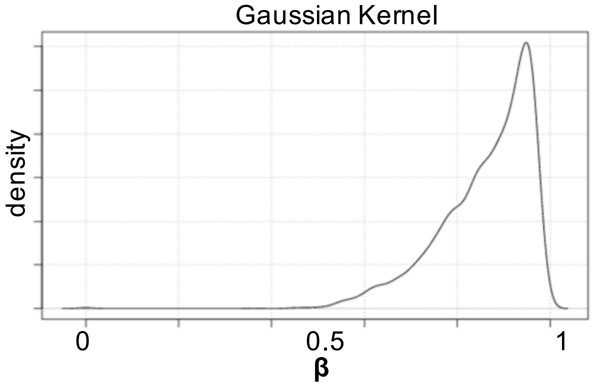
C Somatic primary cell lines



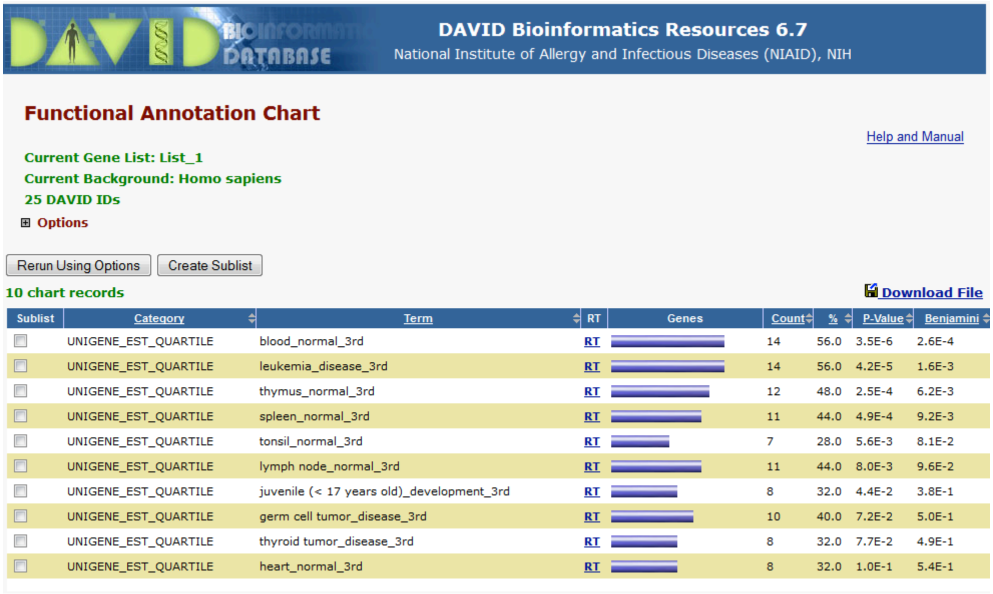
D TGCT cell lines



E Leukocytes



F



DAVID Bioinformatics Resources 6.7
National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Chart

Help and Manual

Current Gene List: List_1
Current Background: Homo sapiens
25 DAVID IDs
⊞ **Options**

10 chart records

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
☐	UNIGENE_EST_QUARTILE	blood_normal_3rd	RT	▬	14	56.0	3.5E-6	2.6E-4
☐	UNIGENE_EST_QUARTILE	leukemia_disease_3rd	RT	▬	14	56.0	4.2E-5	1.6E-3
☐	UNIGENE_EST_QUARTILE	thymus_normal_3rd	RT	▬	12	48.0	2.5E-4	6.2E-3
☐	UNIGENE_EST_QUARTILE	spleen_normal_3rd	RT	▬	11	44.0	4.9E-4	9.2E-3
☐	UNIGENE_EST_QUARTILE	tonsil_normal_3rd	RT	▬	7	28.0	5.6E-3	8.1E-2
☐	UNIGENE_EST_QUARTILE	lymph node_normal_3rd	RT	▬	11	44.0	8.0E-3	9.6E-2
☐	UNIGENE_EST_QUARTILE	juvenile (< 17 years old)_development_3rd	RT	▬	8	32.0	4.4E-2	3.8E-1
☐	UNIGENE_EST_QUARTILE	germ cell tumor_disease_3rd	RT	▬	10	40.0	7.2E-2	5.0E-1
☐	UNIGENE_EST_QUARTILE	thyroid tumor_disease_3rd	RT	▬	8	32.0	7.7E-2	4.9E-1
☐	UNIGENE_EST_QUARTILE	heart_normal_3rd	RT	▬	8	32.0	1.0E-1	5.4E-1

Supplemental Fig. S3. Lymphoid infiltration index (LI) corresponds with histological lymphoid infiltrate and SCNA suppression in array profiles. **A**. SE engulfed in lymphocytes. **B**. SCNA profile and histology are shown for representative low-and high-LI cases. Tumor histology and SCNA plots were inspected for correspondence with LI, which confirmed the expected elevated lymphoid frequency and impaired detection of SCNA in these specimens, further validating exclusion of 12p-neutral TGCT (n=22). Overall, tumor tissue methylation data were found to be amenable to correction for lymphoid cell frequency, more accurately reflecting intrinsic tumor-cell target methylation. **C-E.** Further validations of leukocyte-specificity of LS36 allelic methylation targets used to measure TGCT tissue infiltrates. **C**. Near absent allelic methylation (Kernel density estimation (KDE)) of LS36 in somatic primary specimens (n=22, GSE30654). **D**. Near absent allelic methylation (KDE) of LS36 in TGCT cell lines (n=12, GSE60787). **E**. Biallelic methylation of LS36 (KDE) in leukocyte reference panel (n=117, GSE67393). **F**. Gene functional annotation analysis on the LS36 showed significant enrichment for leukocyte related annotations.