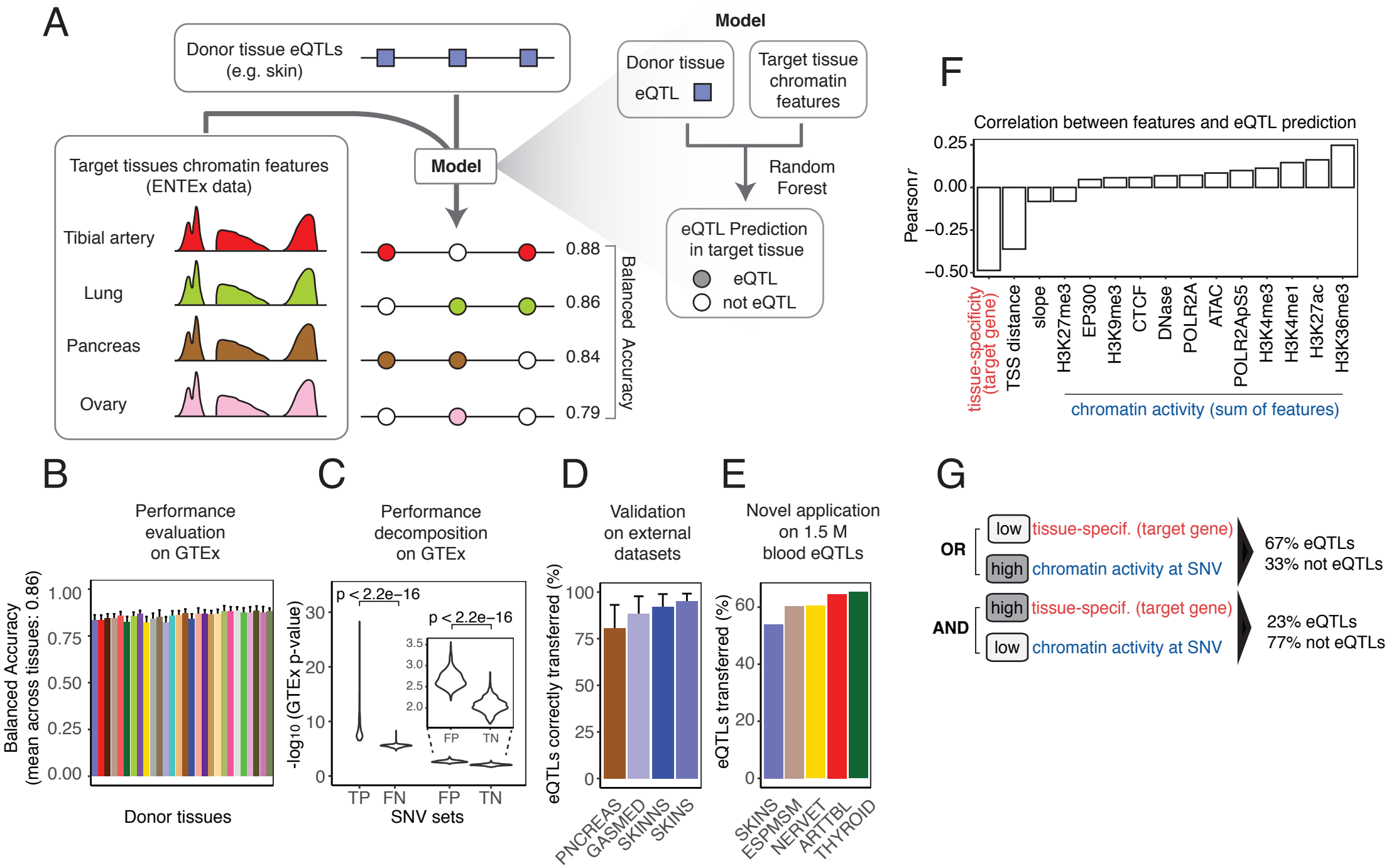
A
Donor tissue eQTLs (e.g. skin)
Target tissues chromatin features (ENTEx data)
Tibial artery
Lung
Pancreas
Ovary
Model
0.88
0.86
0.84
0.79
Balanced Accuracy
Model
Donor tissue eQTL
Target tissue chromatin features
Random Forest
eQTL Prediction in target tissue
eQTL
not eQTL
F
Correlation between features and eQTL prediction
Pearson r
0.25
0.00
−0.25
−0.50
tissue-specificity (target gene)
TSS distance
slope
H3K27me3
EP300
H3K9me3
CTCF
DNase
POLR2A
ATAC
POLR2ApS5
H3K4me3
H3K4me1
H3K27ac
H3K36me3
chromatin activity (sum of features)
B
Performance evaluation on GTEx
Balanced Accuracy (mean across tissues: 0.86)
1.00
0.75
0.50
0.25
0.00
Donor tissues
C
Performance decomposition on GTEx
-log10 (GTEx p-value)
p < 2.2e−16
p < 2.2e−16
TP
FN
FP
TN
SNV sets
D
Validation on external datasets
eQTLs correctly transferred (%)
PNCREAS
GASMED
SKINNS
SKINS
E
Novel application on 1.5 M blood eQTLs
eQTLs transferred (%)
SKINS
ESPMSM
NERVET
ARTTBL
THYROID
G
OR
low
tissue-specif. (target gene)
high
chromatin activity at SNV
67% eQTLs
33% not eQTLs
AND
high
tissue-specif. (target gene)
low
chromatin activity at SNV
23% eQTLs
77% not eQTLs