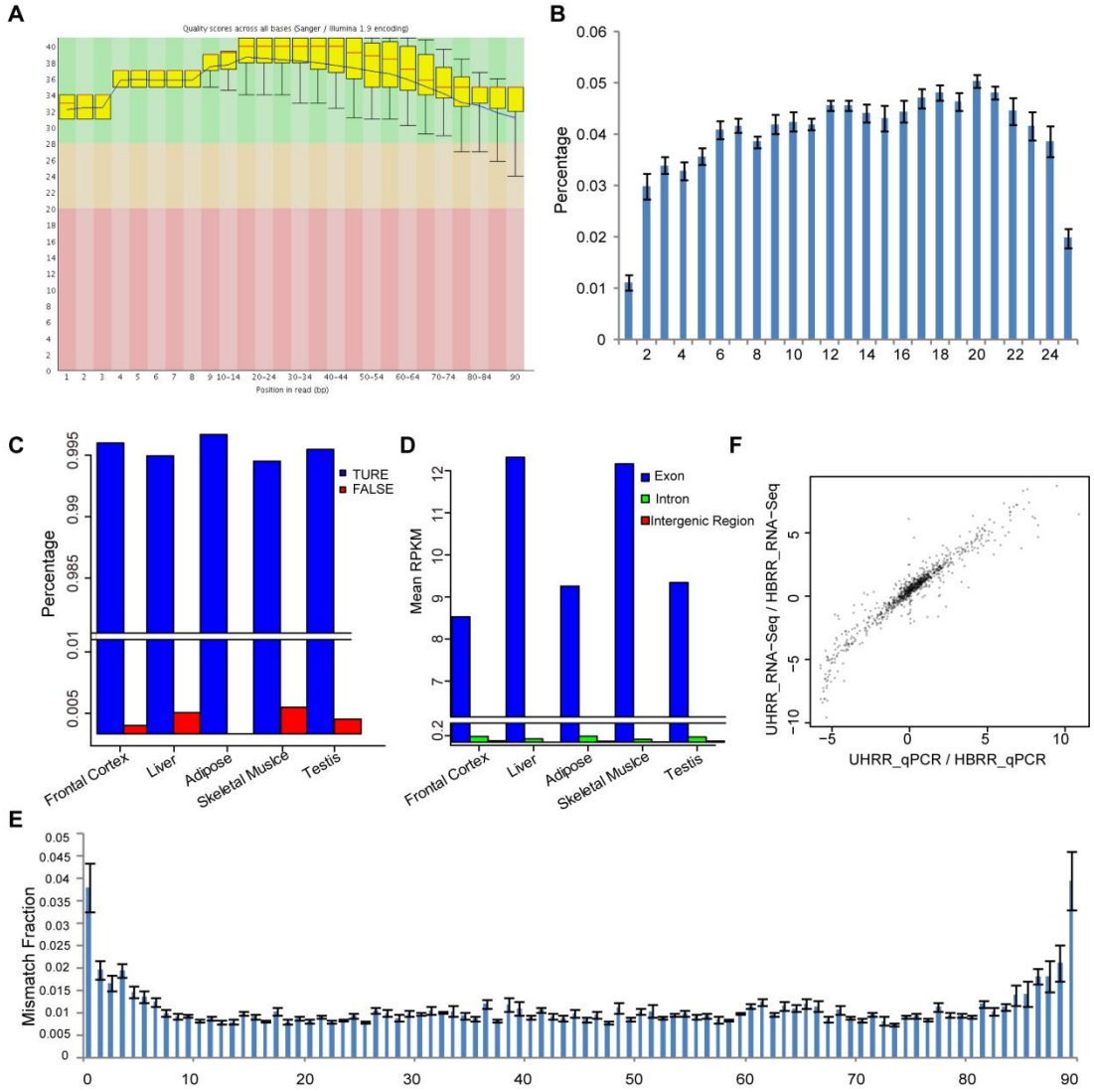
Figure S1


A
Quality scores across all bases (Sanger / Illumina 1.9 encoding)
Position in read (bp)
B
Percentage
C
Percentage
TURE
FALSE
Frontal Cortex
Liver
Adipose
Skeletal Muscle
Testis
D
Mean RPKM
Exon
Intron
Intergenic Region
Frontal Cortex
Liver
Adipose
Skeletal Muscle
Testis
F
UHRR_RNA-Seq / HBRR_RNA-Seq
UHRR_qPCR / HBRR_qPCR
E
Mismatch Fraction