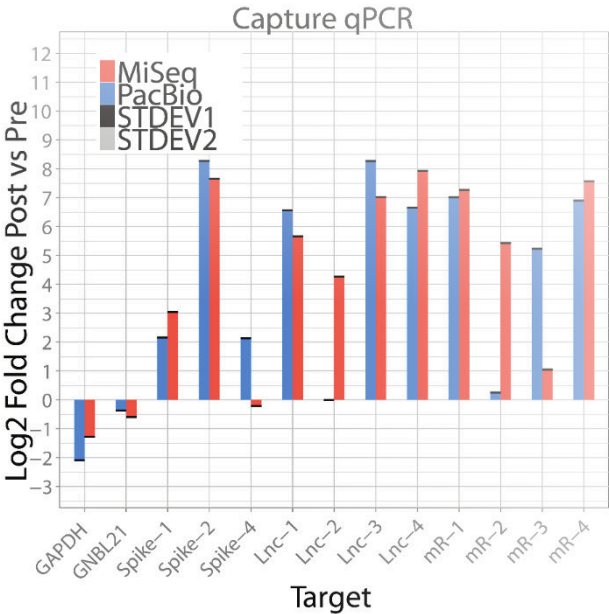
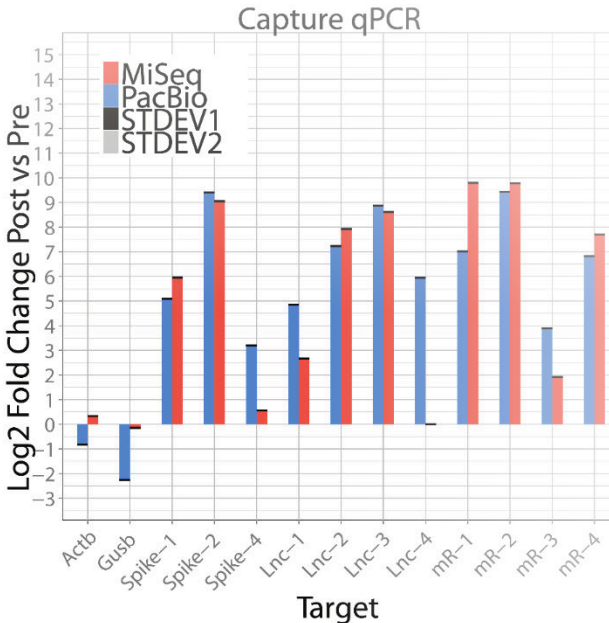


Supplementary Figure S1

Human



Mouse

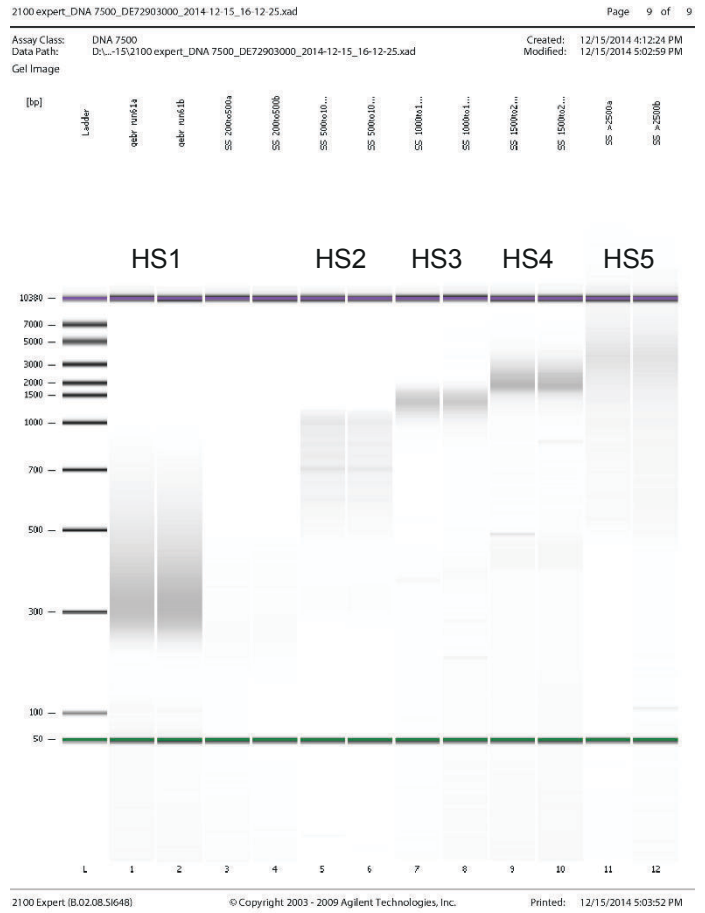


Supplementary Figure S2

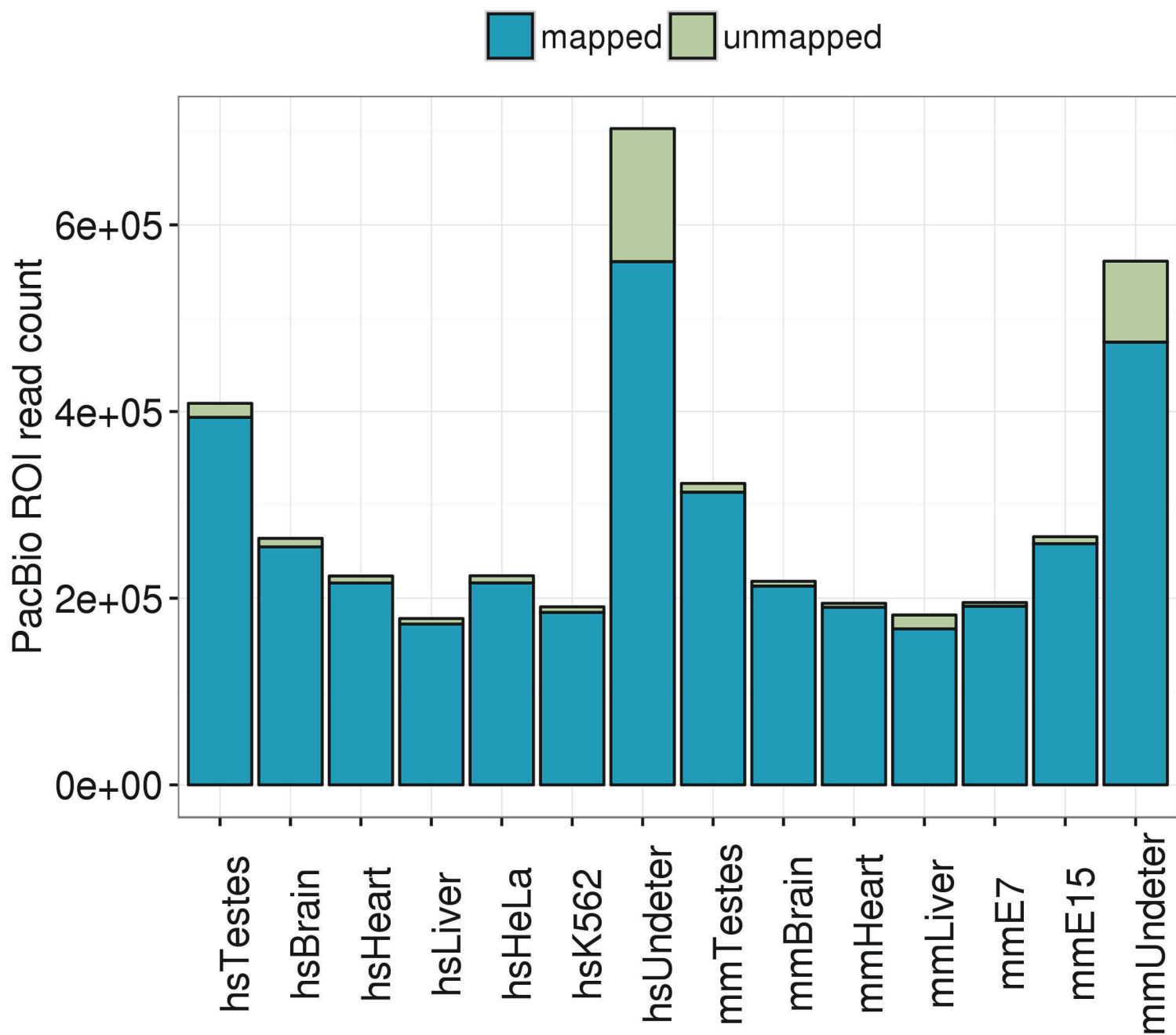
A

	Range (nt)	Human
1	200-500	HS1
2	500-1000	HS2
3	1000-1500	HS3
4	1500-2500	HS4
5	>2500	HS5

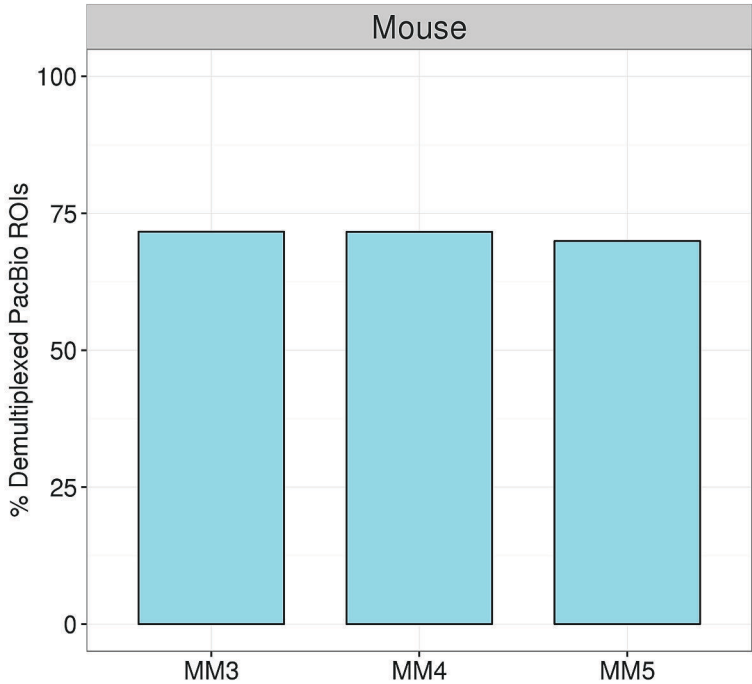
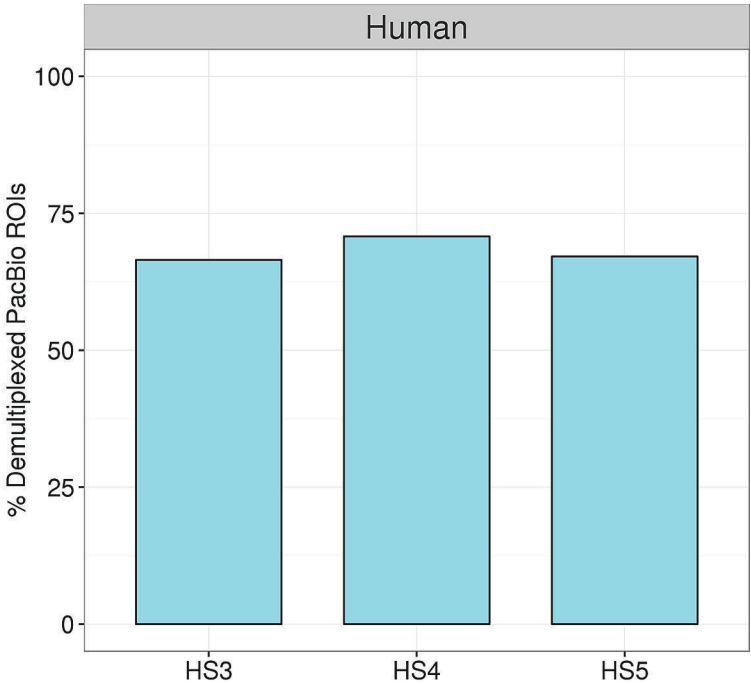
B



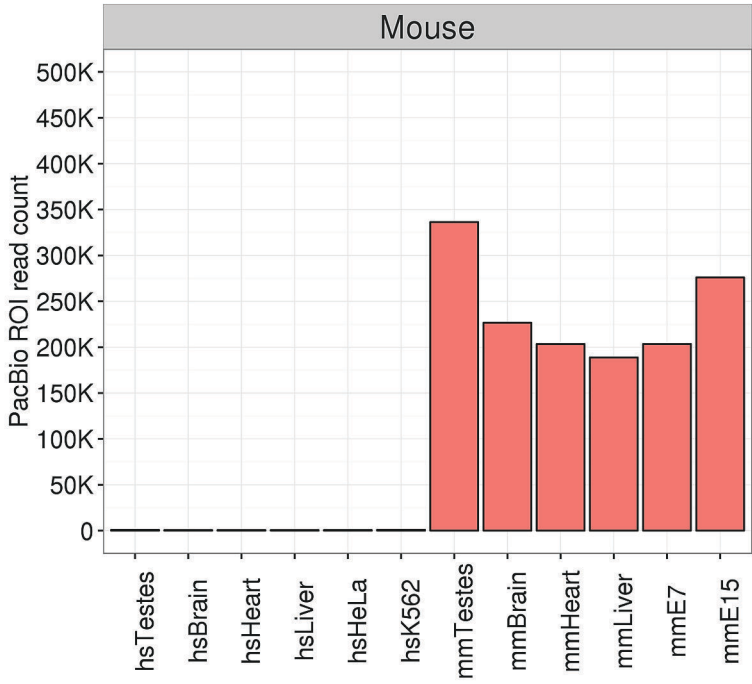
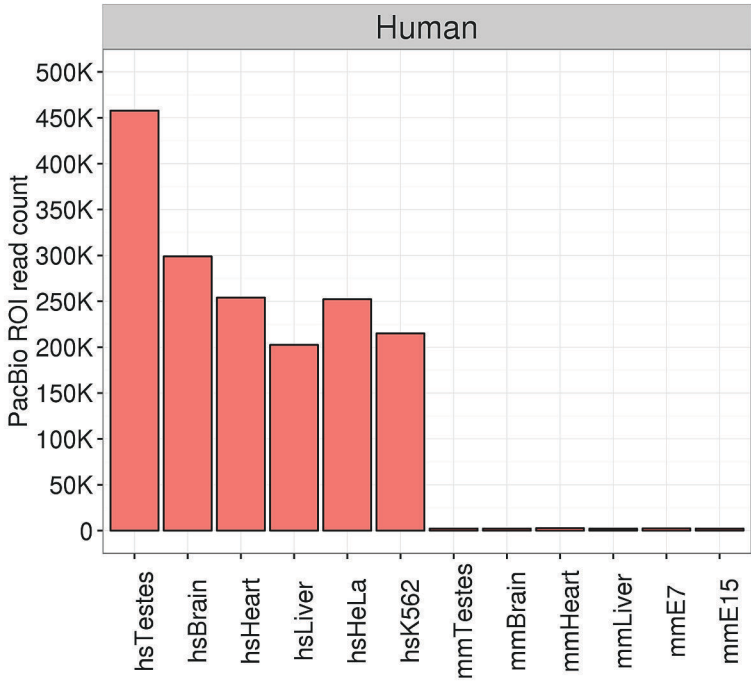
Supplementary Figure S3



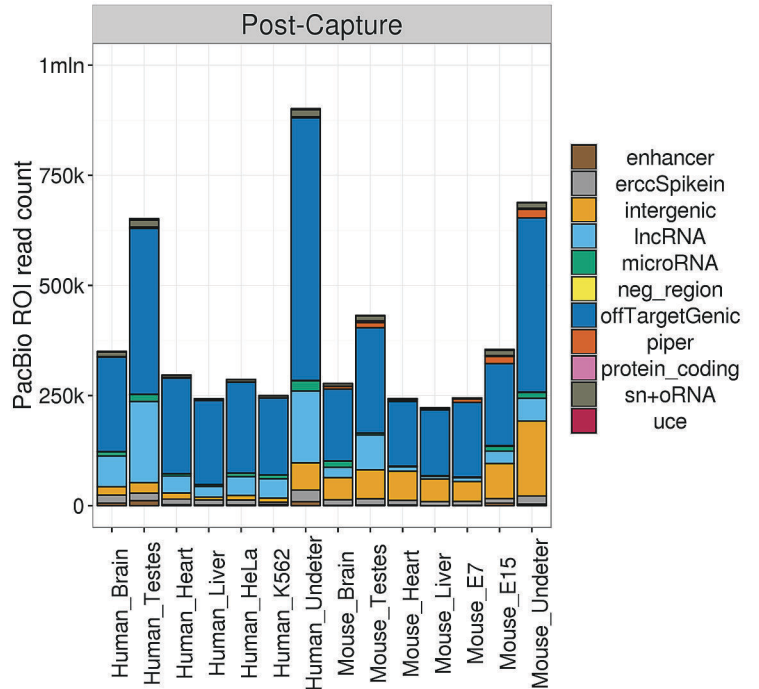
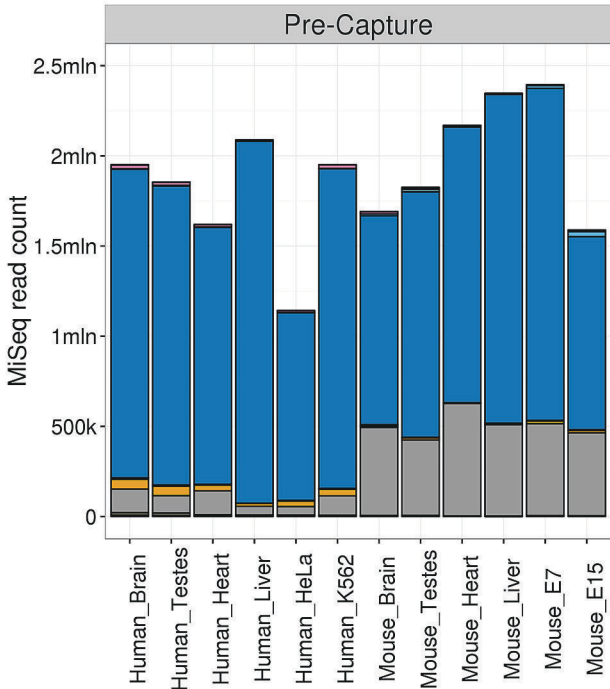
Supplementary Figure S4



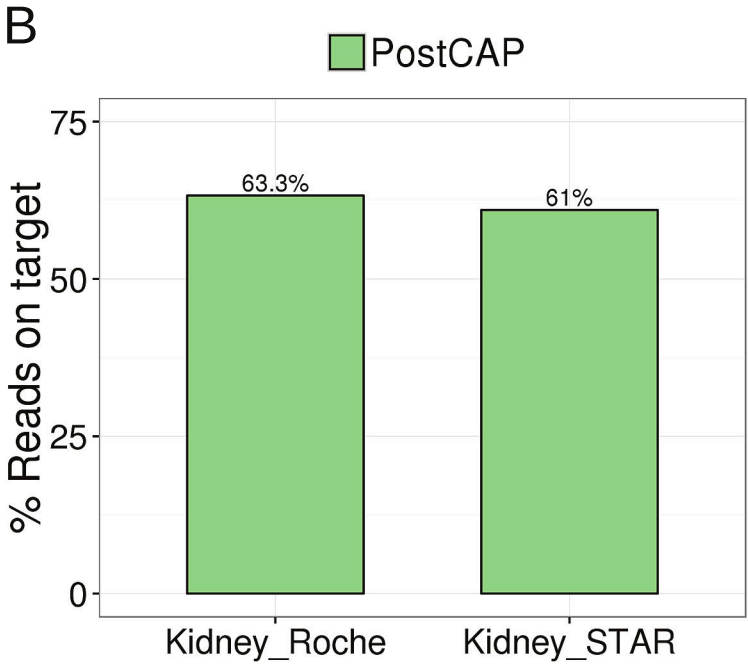
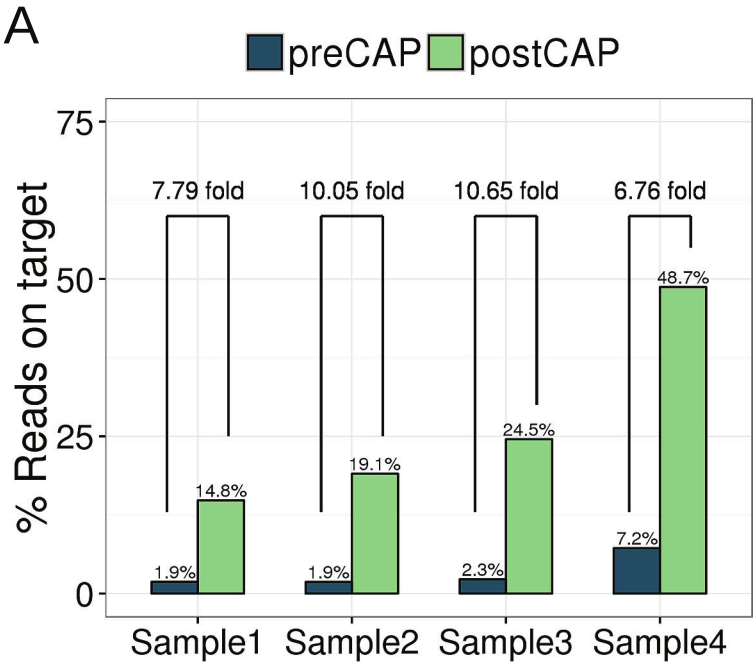
Supplementary Figure S5



Supplementary Figure S6

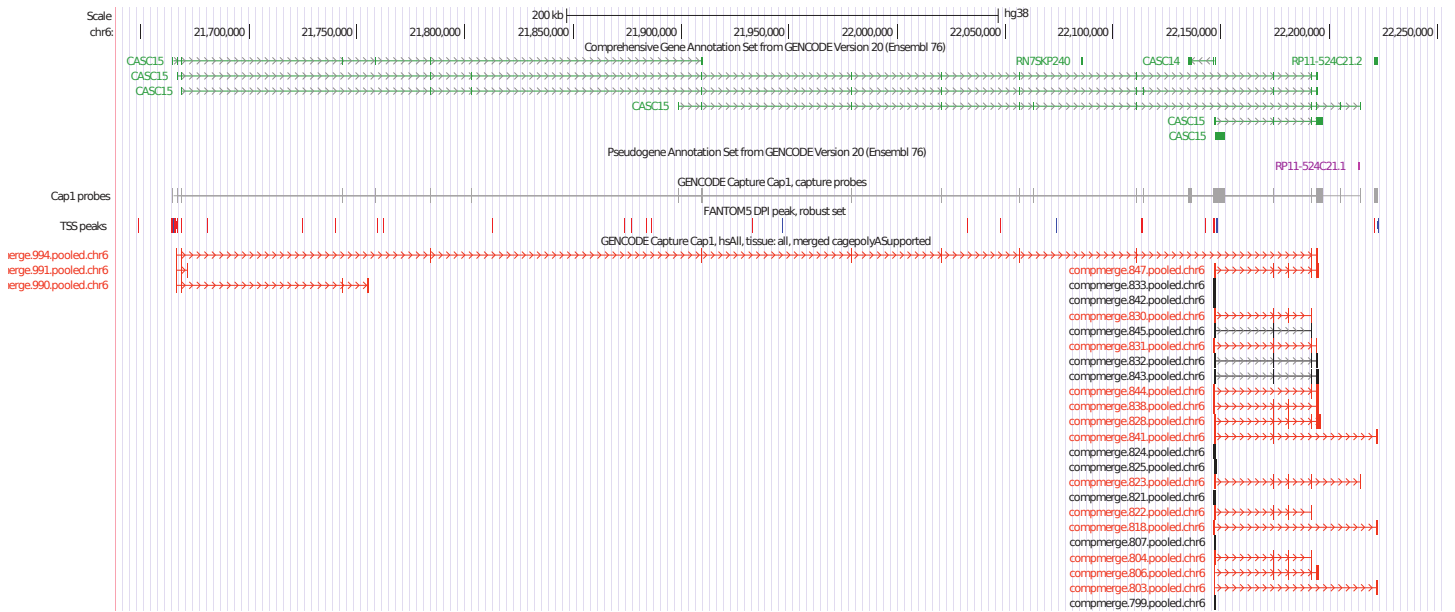


Supplementary Figure S7

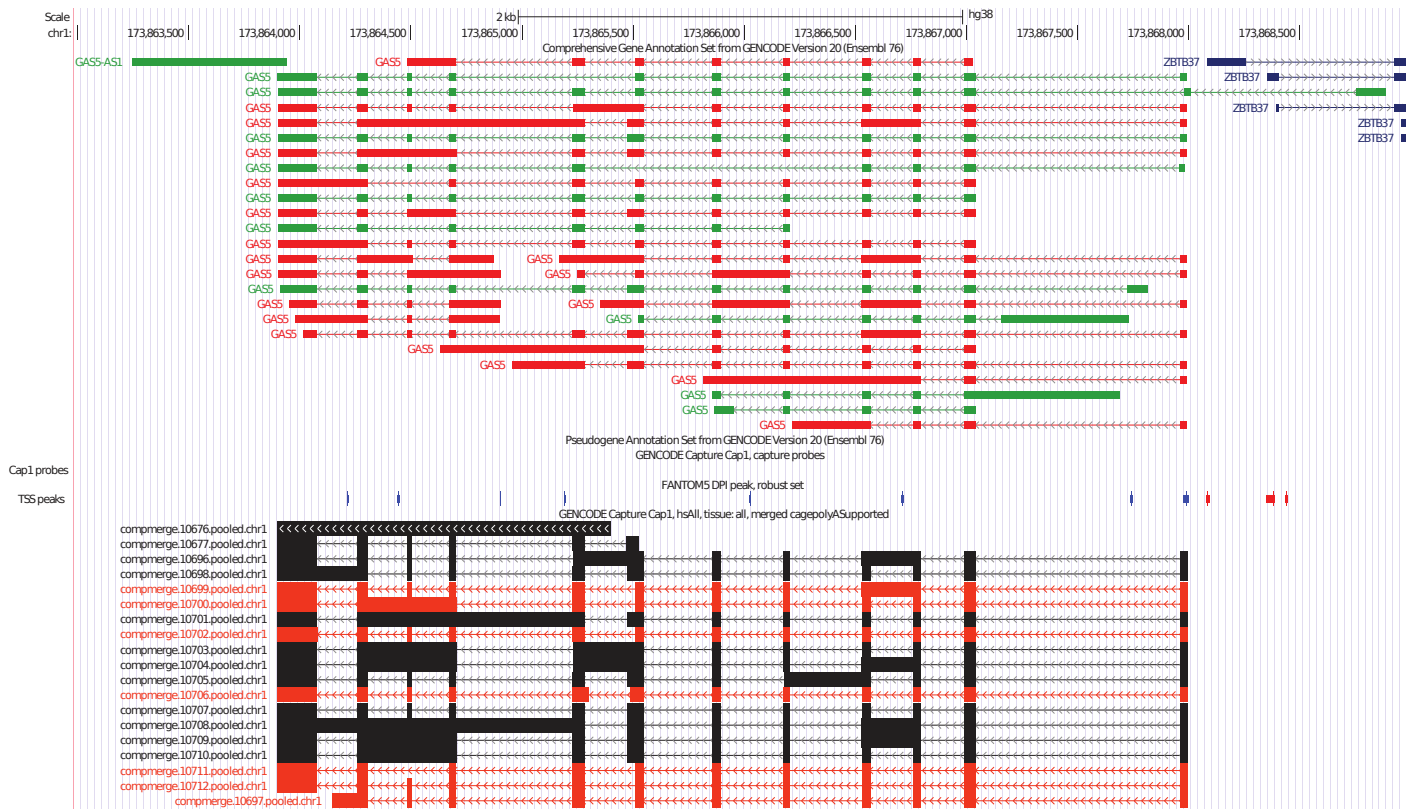


Supplementary Figure S8

CASC15 / ENSG00000272168

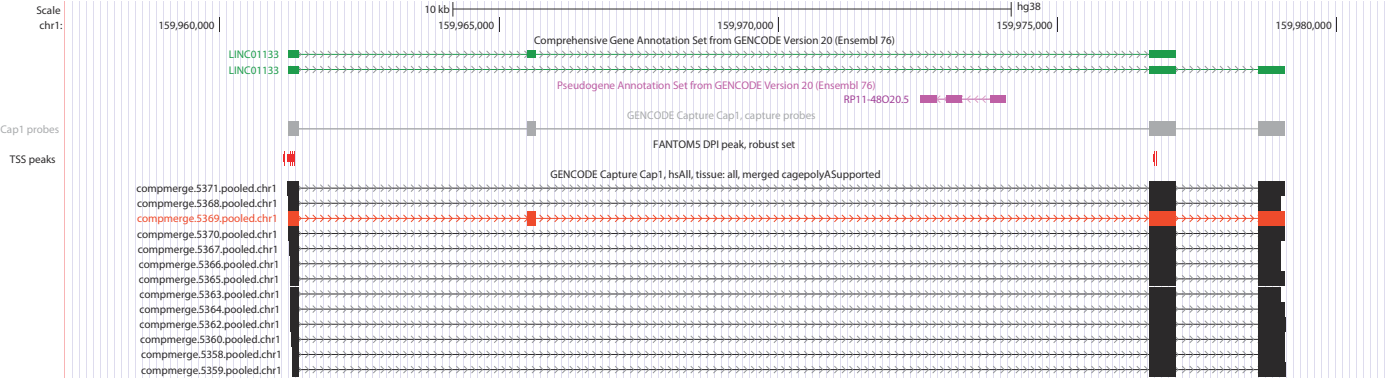


GAS5 / ENSG00000234741



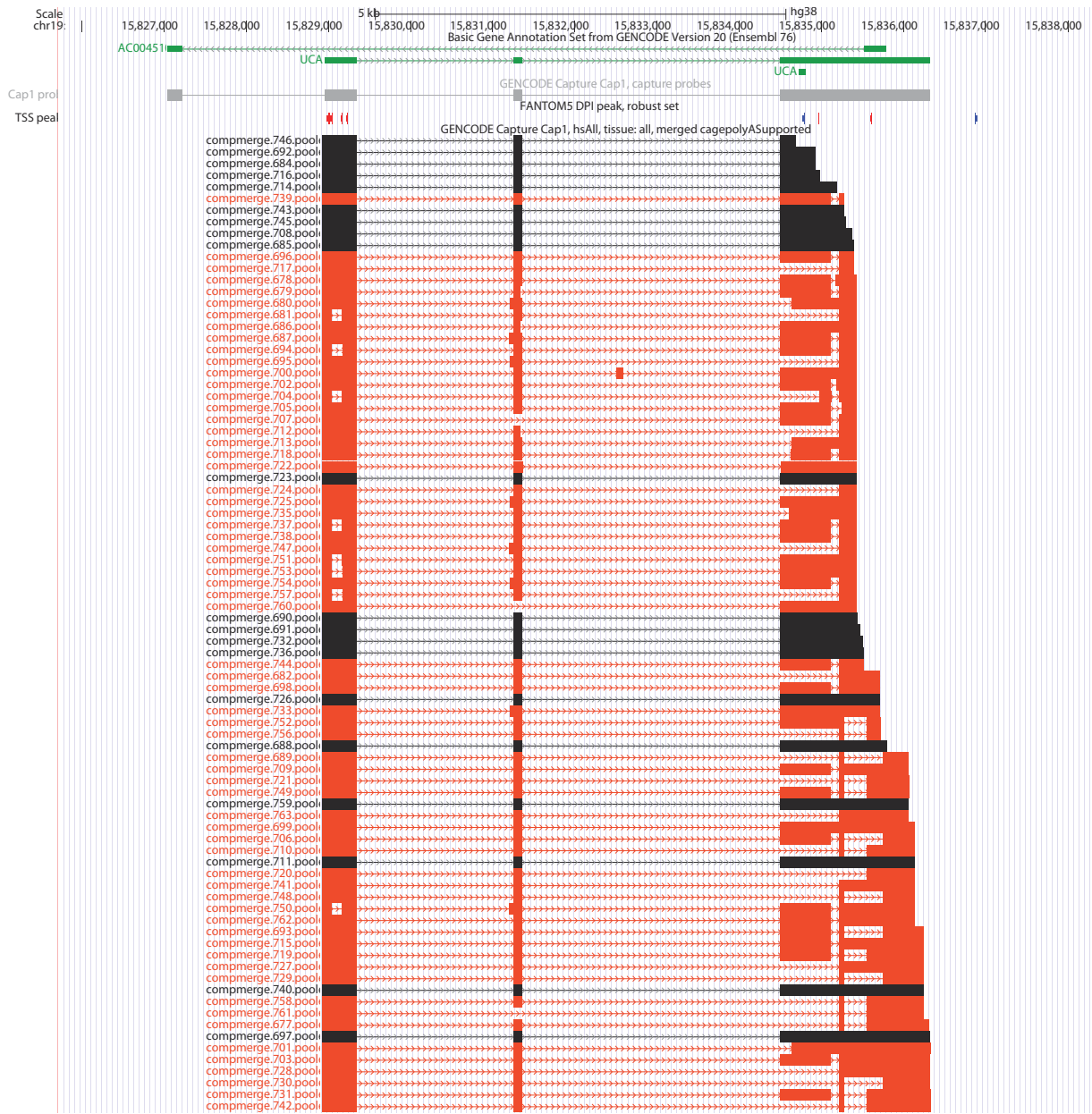
Supplementary Figure S9

LINC01133 / ENSG00000224259



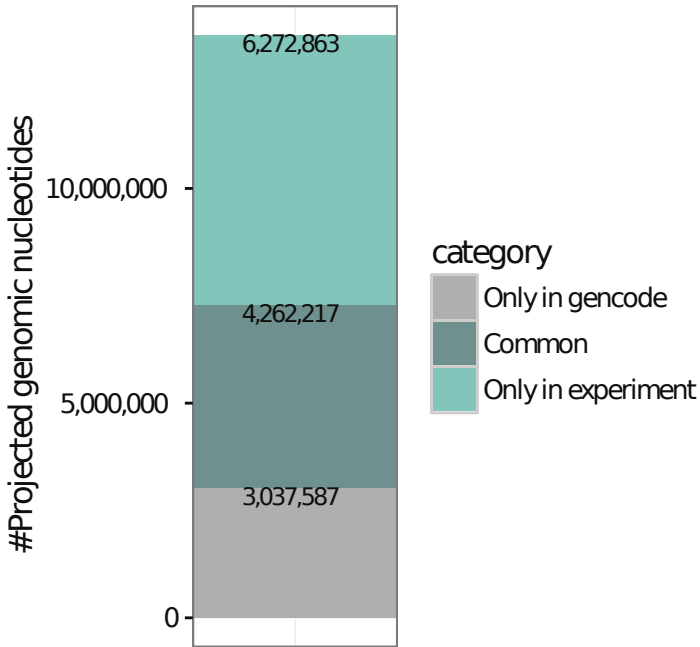
Supplementary Figure S10

UCA1 / ENSG00000214049

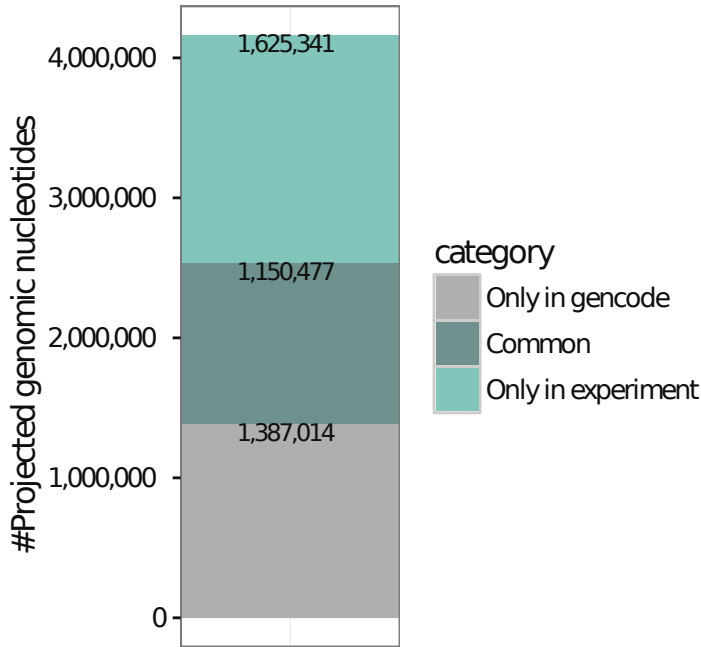


Supplementary Figure S11

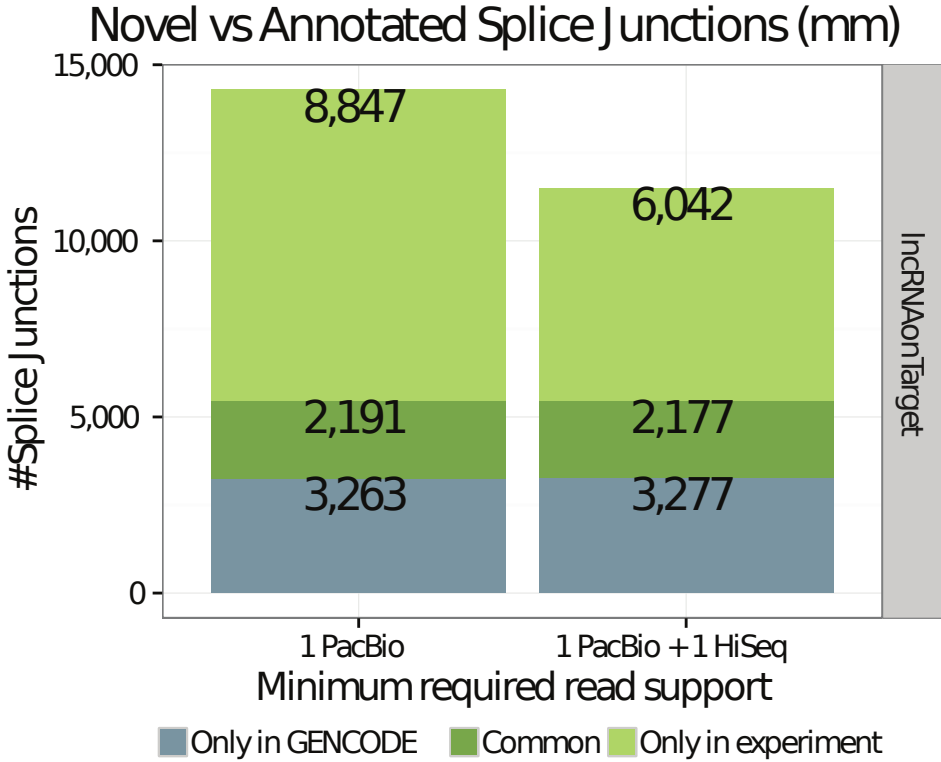
Novel vs Annotated Exonic lncRNA Nucleotides (hs)



Novel vs Annotated Exonic lncRNA Nucleotides (mm)

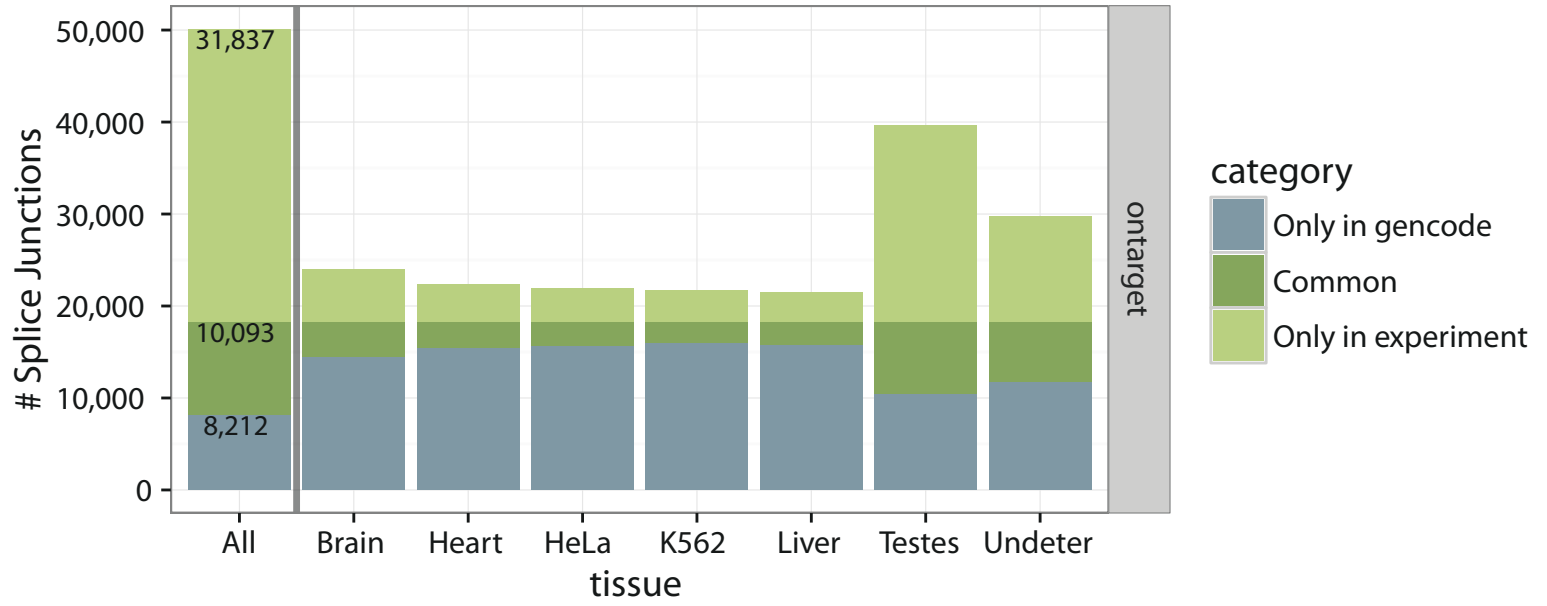


Supplementary Figure S12

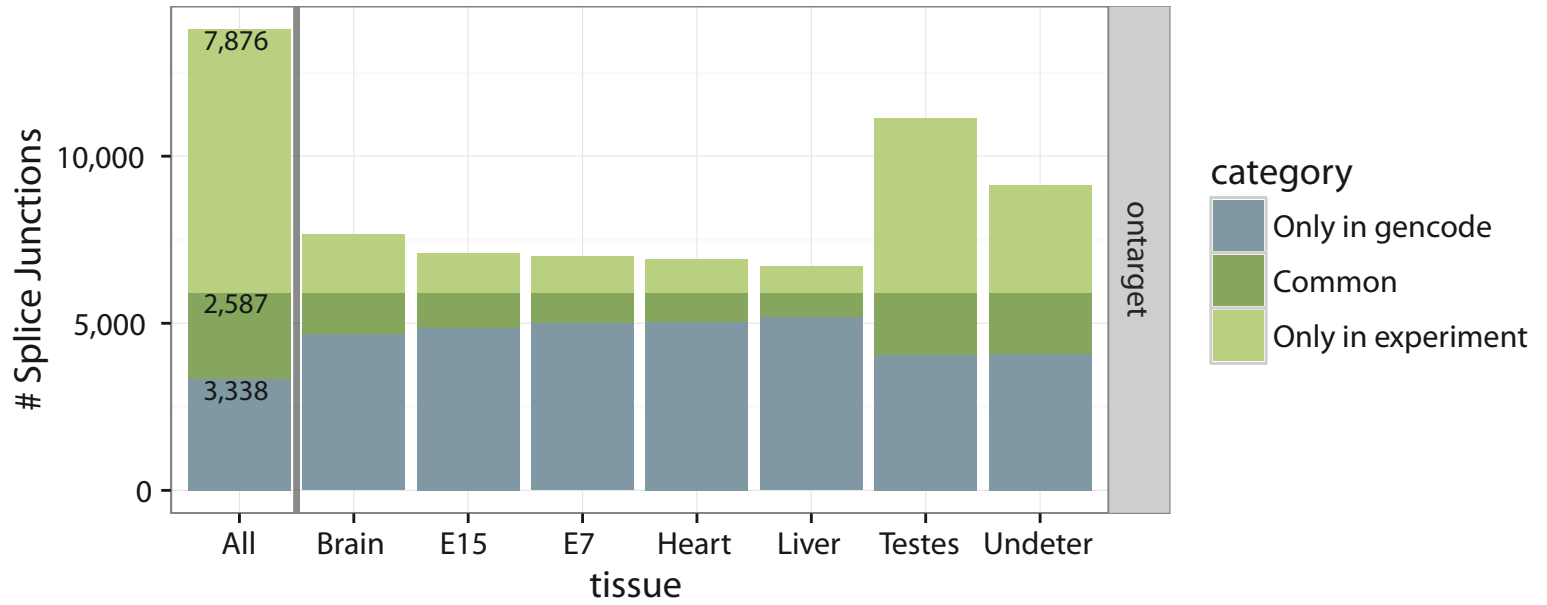


Supplementary Figure S13

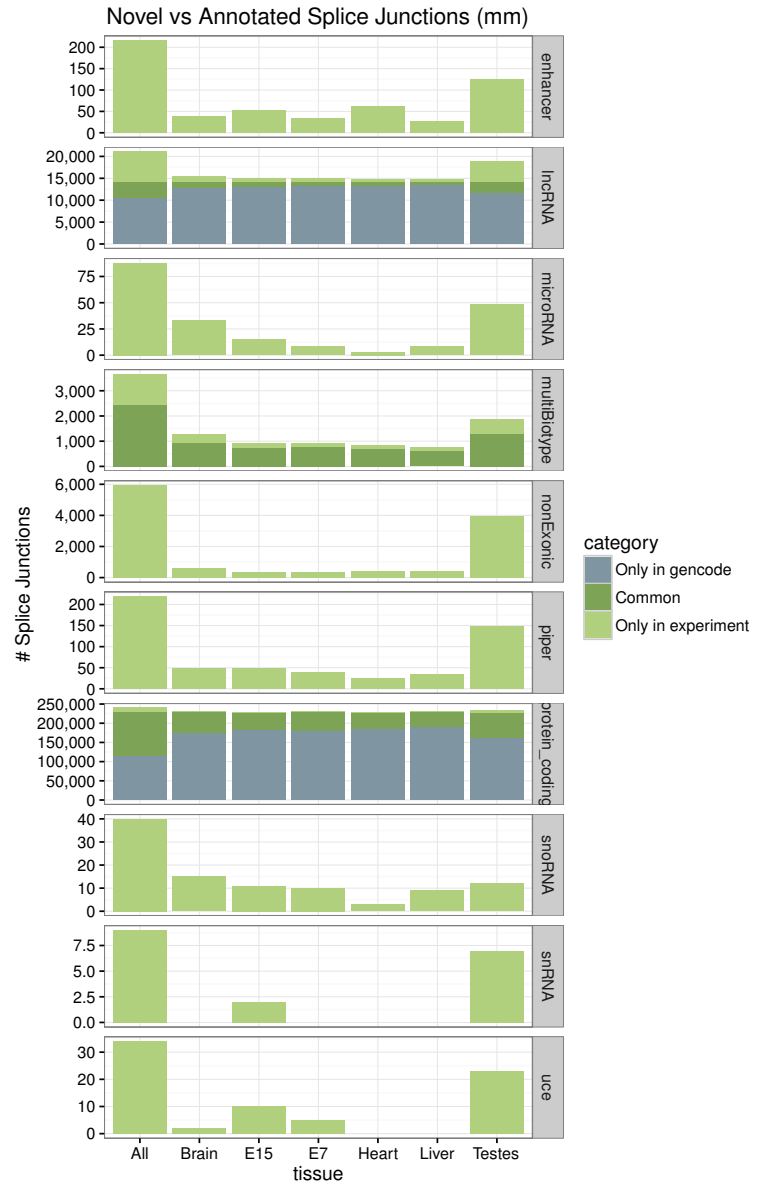
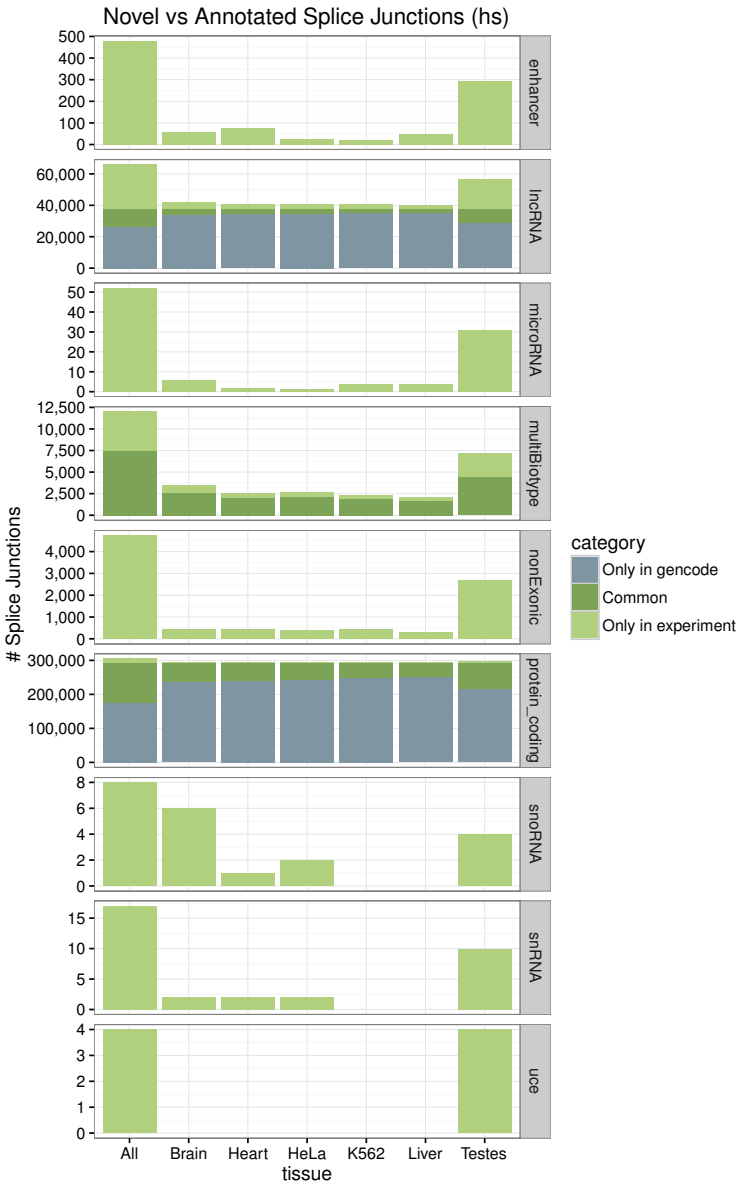
Novel vs Annotated Splice Junctions (hs)



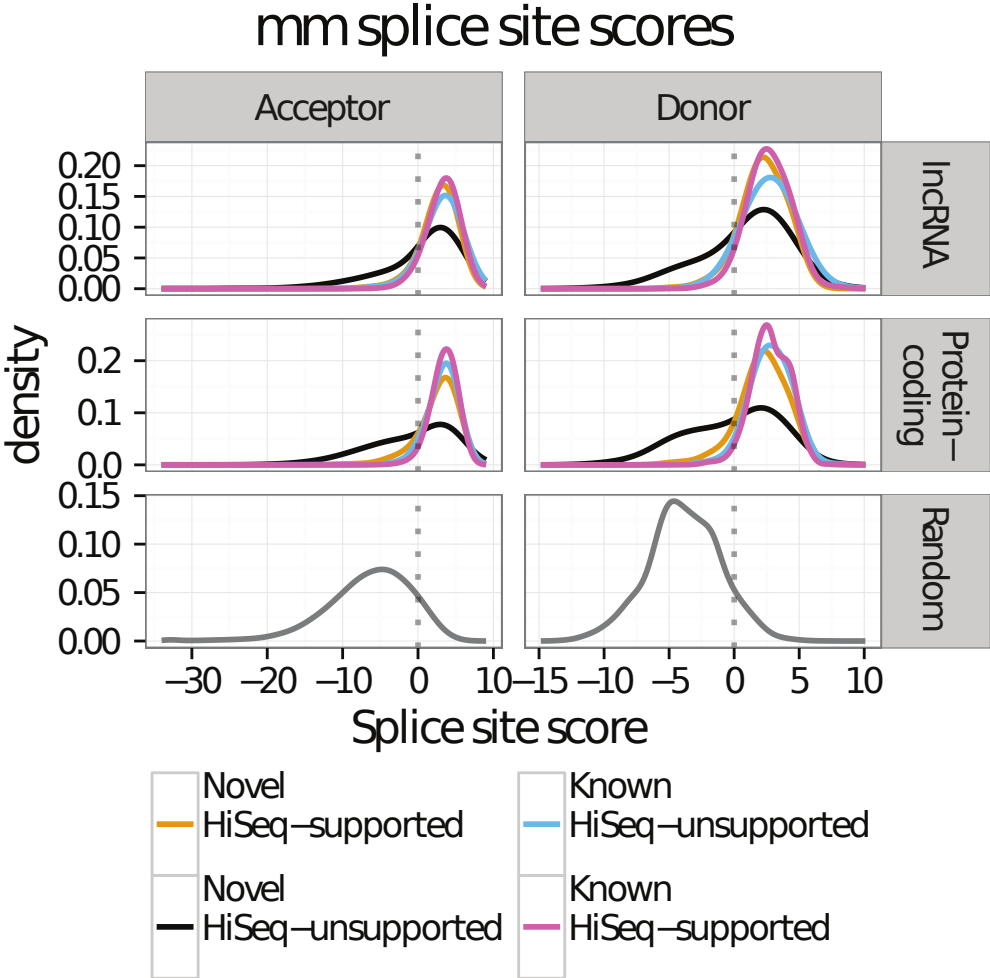
Novel vs Annotated Splice Junctions (mm)



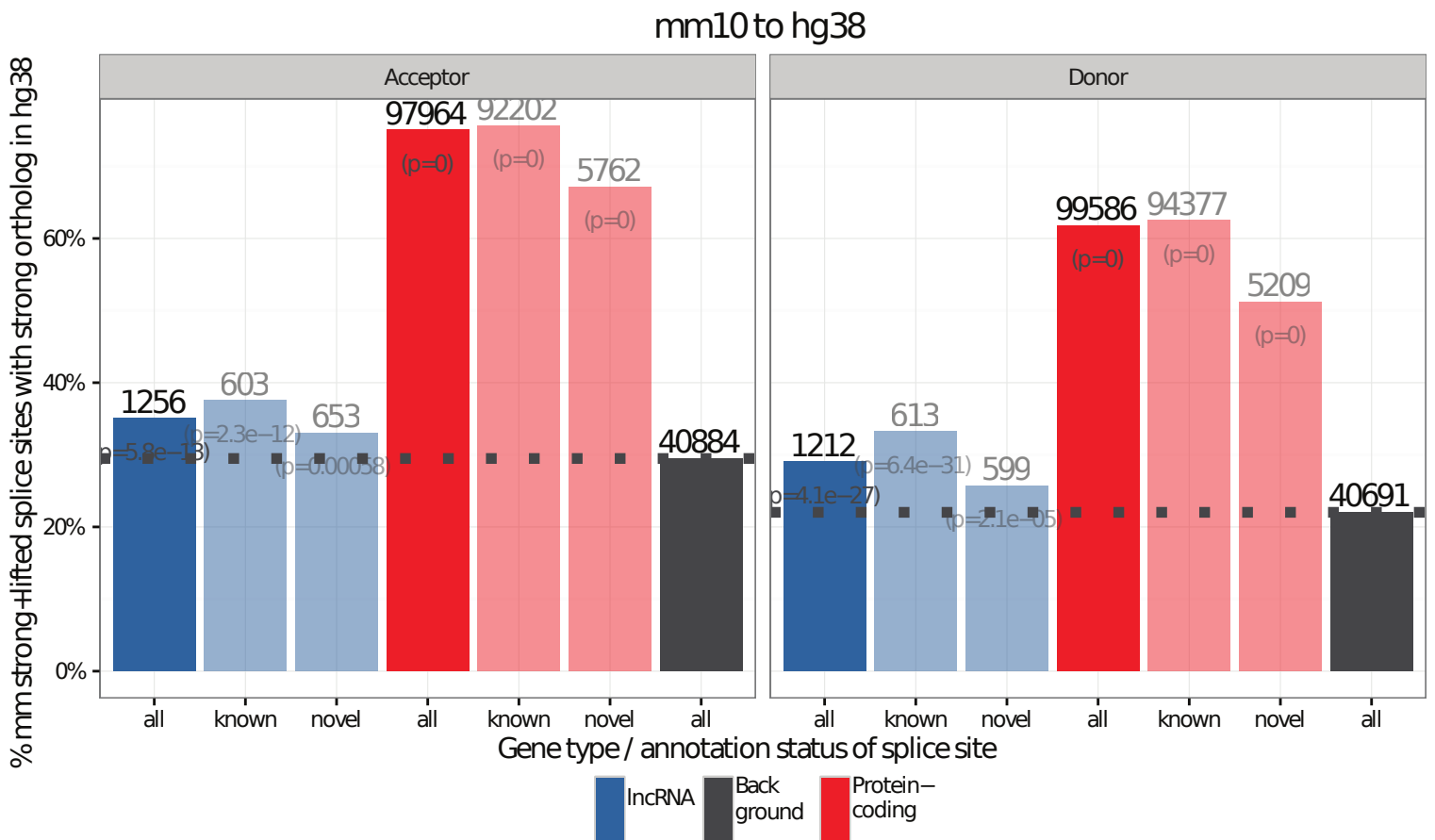
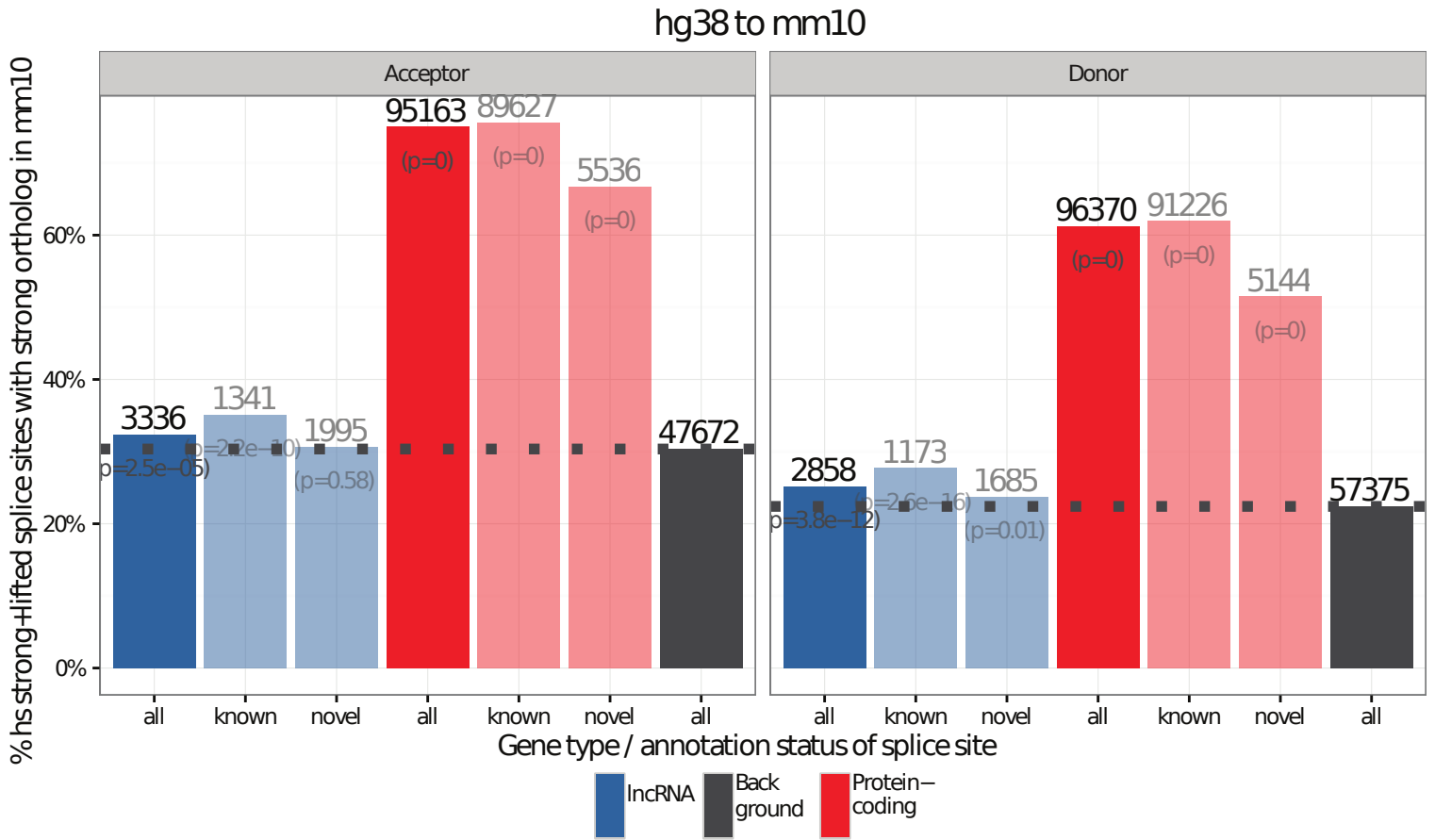
Supplementary Figure S14



Supplementary Figure S15

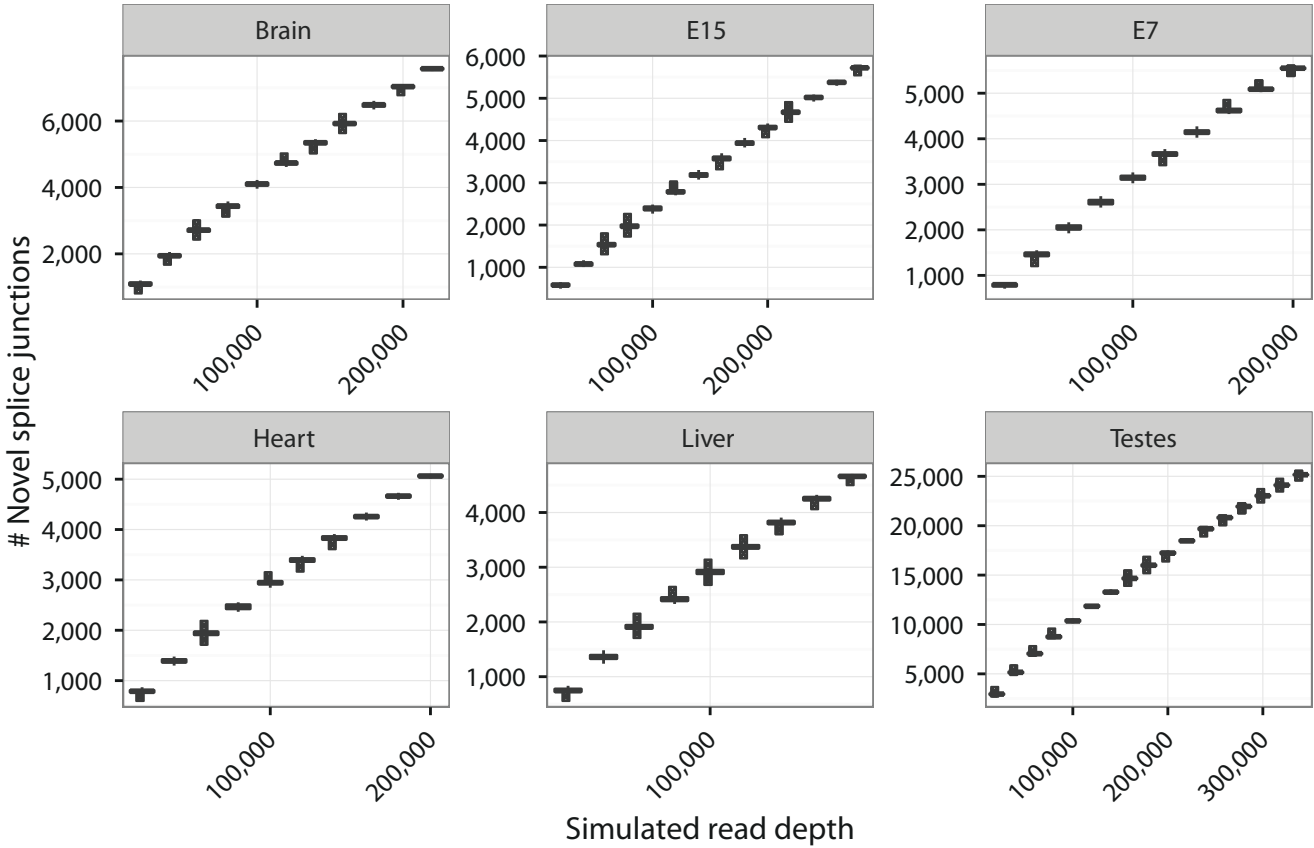


Supplementary Figure S16



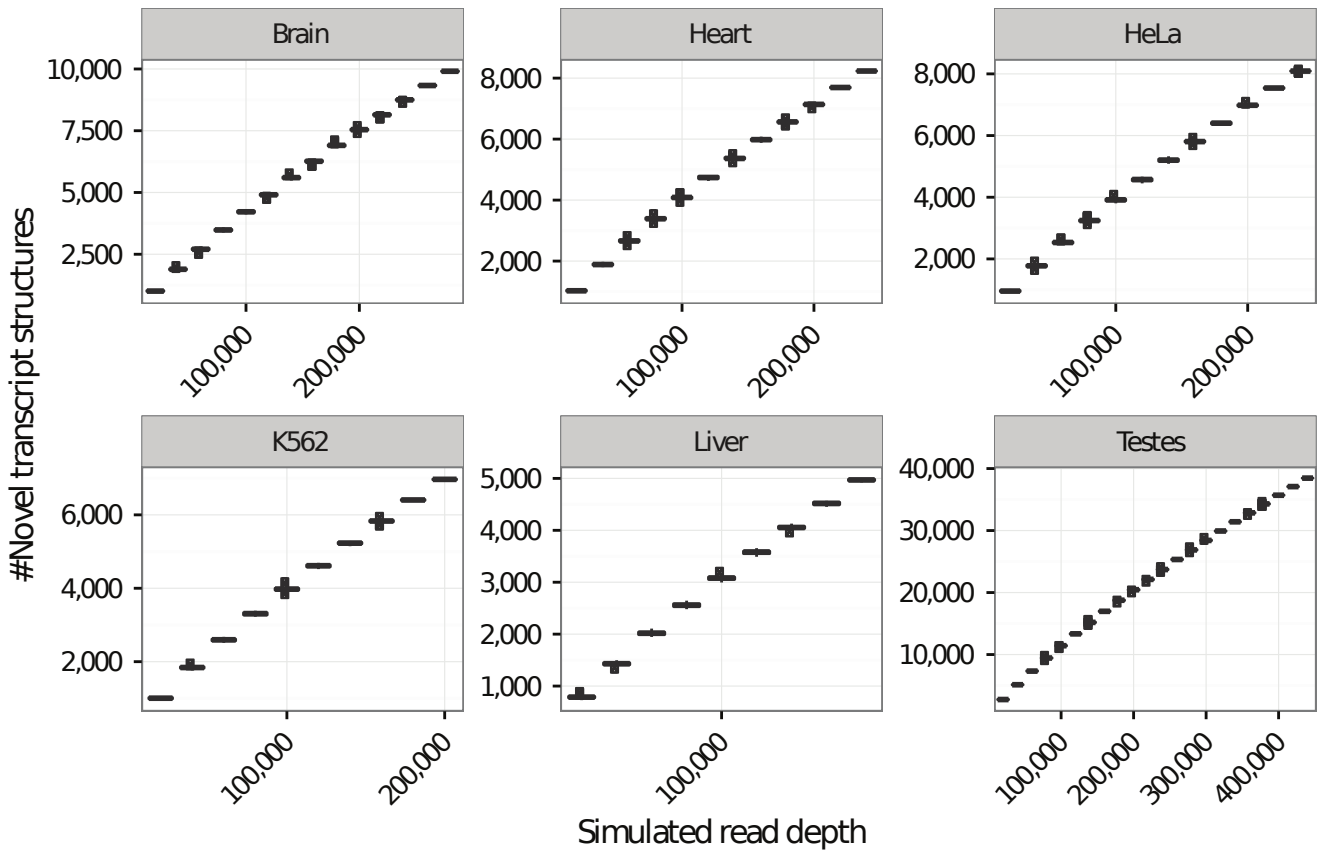
Supplementary Figure S17

Simulated read depth vs novel splice junction discovery (mm)

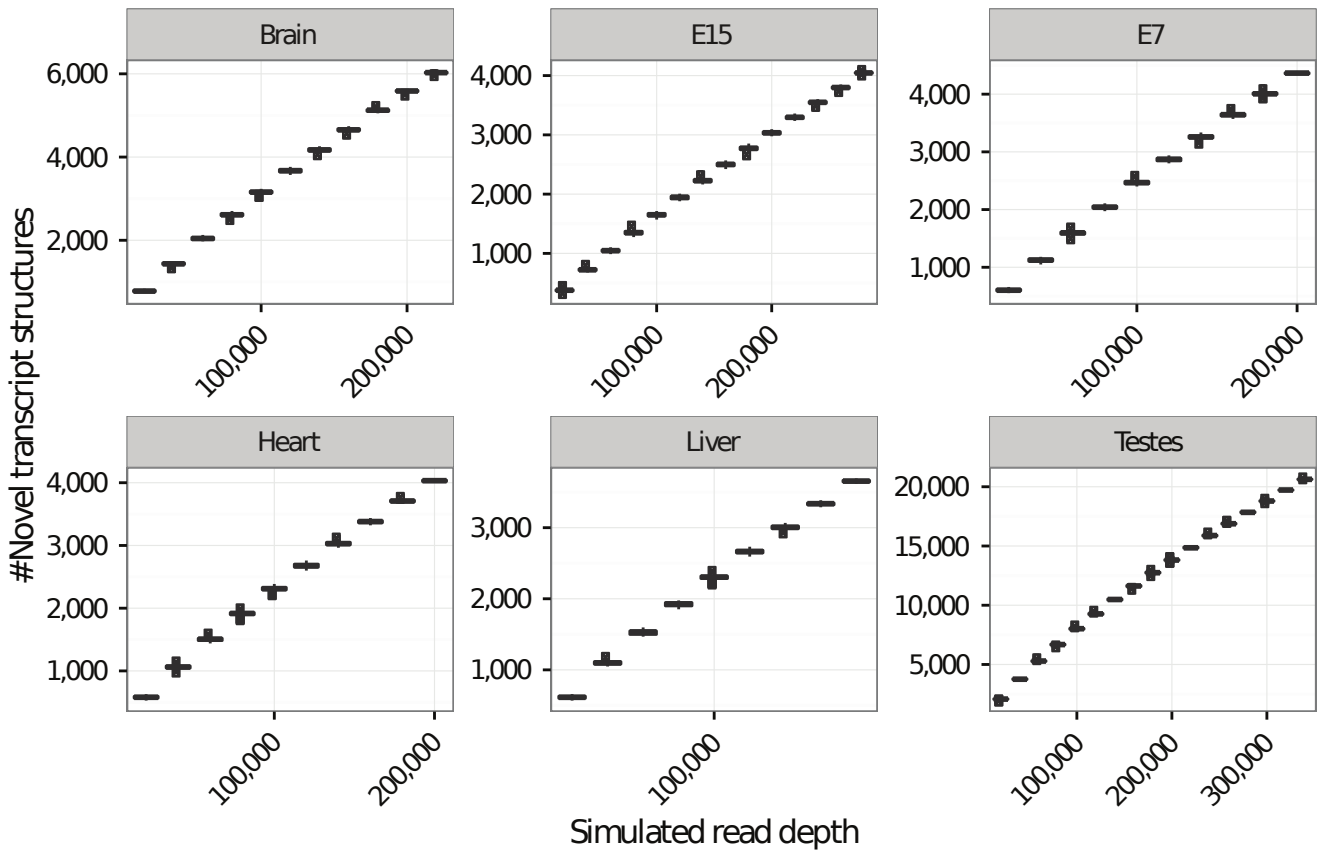


Supplementary Figure S18

Simulated read depth vs novel transcript discovery (hs)



Simulated read depth vs novel transcript discovery (mm)

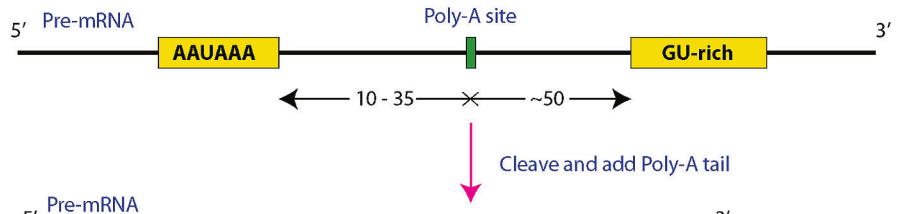


Supplementary Figure S20

A

- Canonical polyA signals:**
- AACAAA
 - AATAAA**
 - AATACA
 - AATAGA
 - AATATA
 - AATGAA
 - ACTAAA
 - AGTAAA
 - ATTAAT**
 - CATAAA
 - GATAAA
 - TATAAA
 - TTTAAA

B



C



Species	Set	Total # sites	# Sites with Poly-A signal upstream (-10 to -50 nts)	% Sites with Poly-A signal upstream (-10 to -50 nts)
Human	Poly-A sites	35,092	30,301	86%
	Control	203,303	30,519	15%
Mouse	Poly-A sites	27,152	23,249	86%
	Control	175,240	20,423	12%

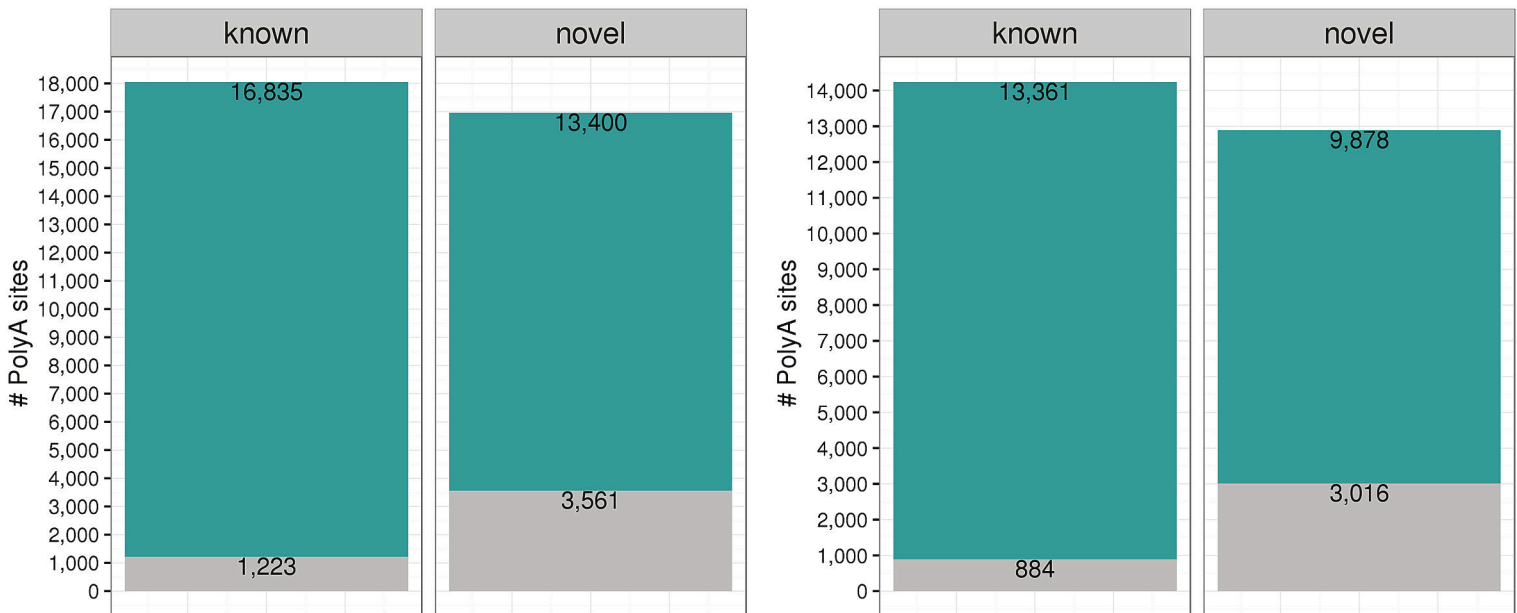
D

Human

Mouse

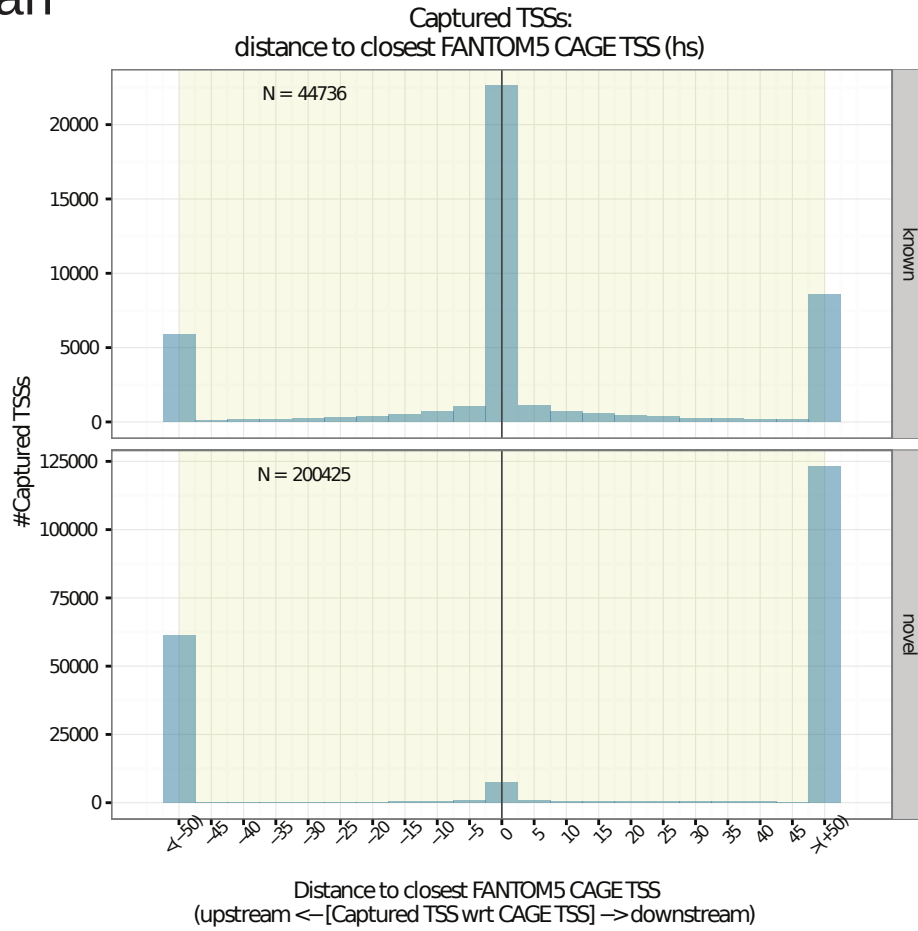
Motif upstream No motif upstream

Motif upstream No motif upstream

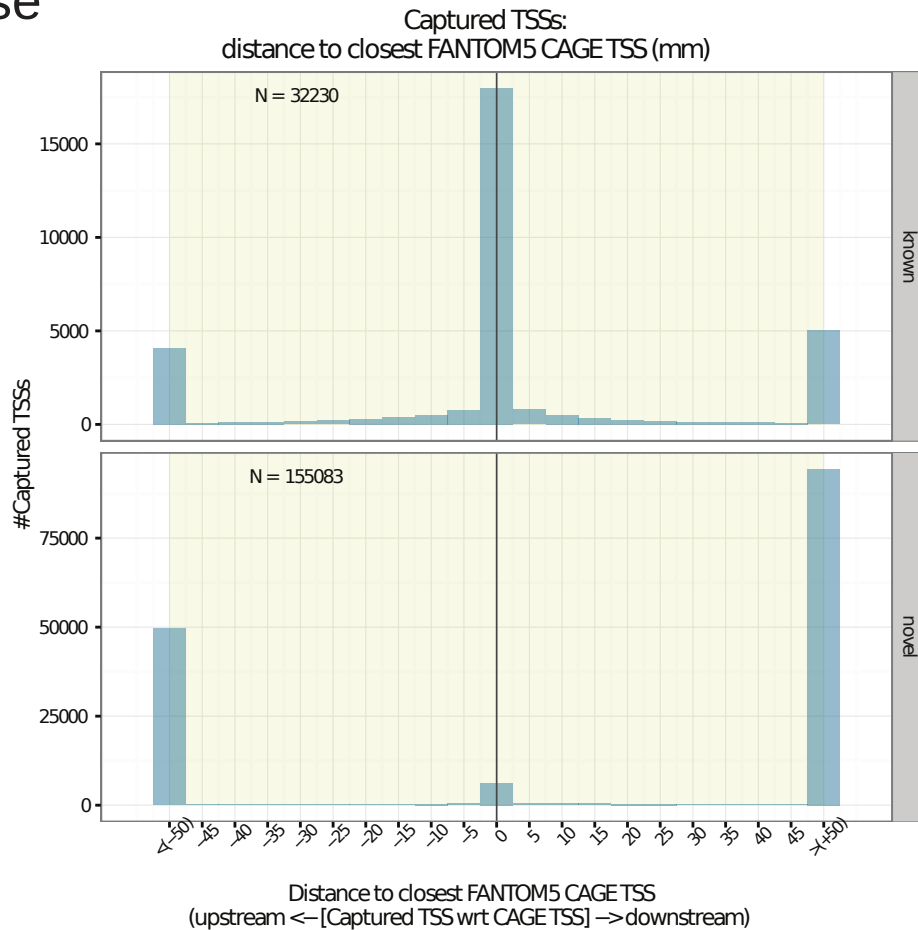


Supplementary Figure S21

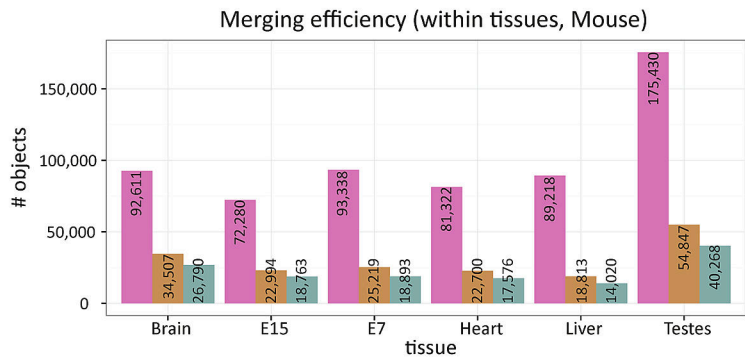
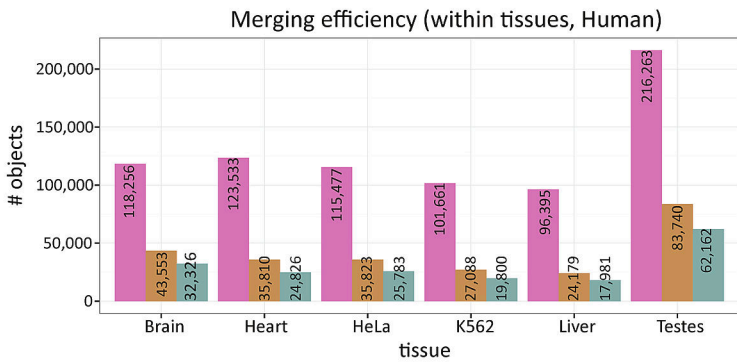
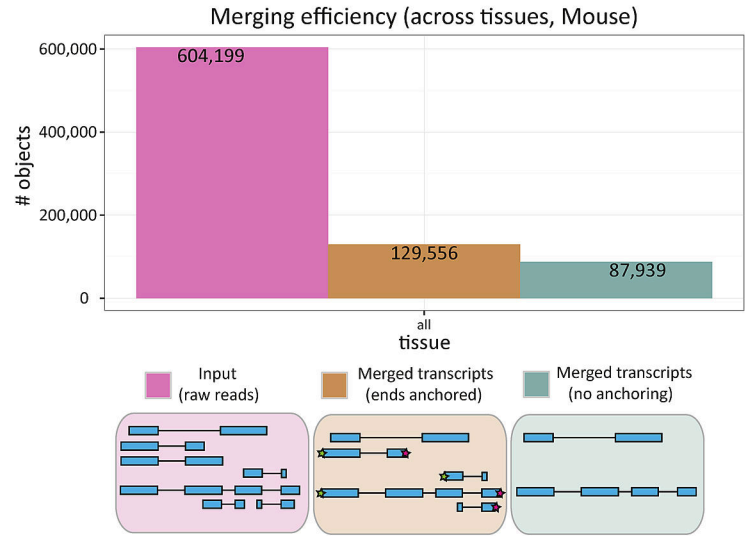
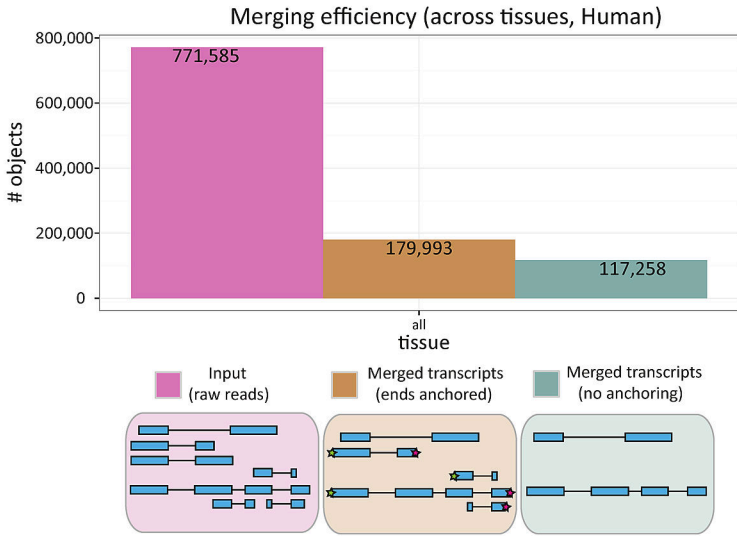
Human



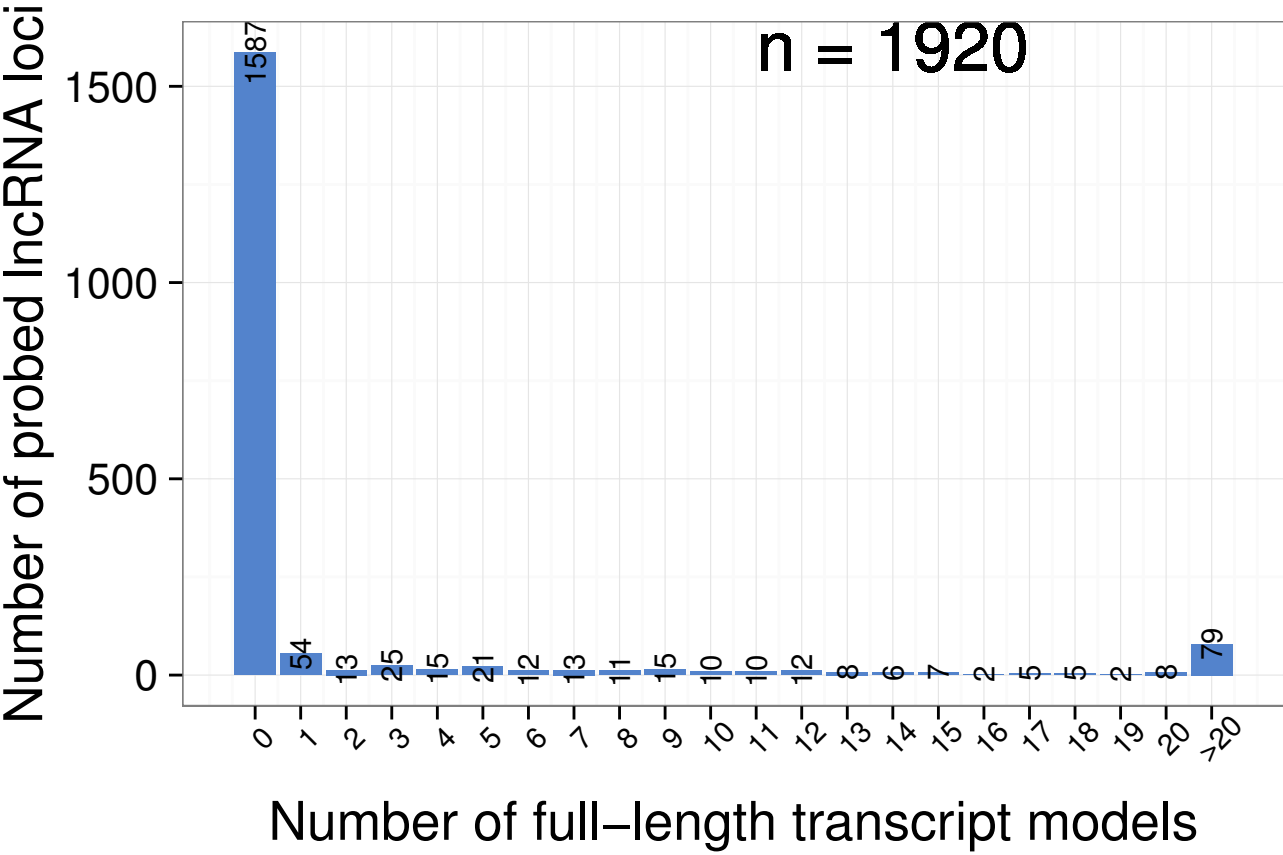
Mouse



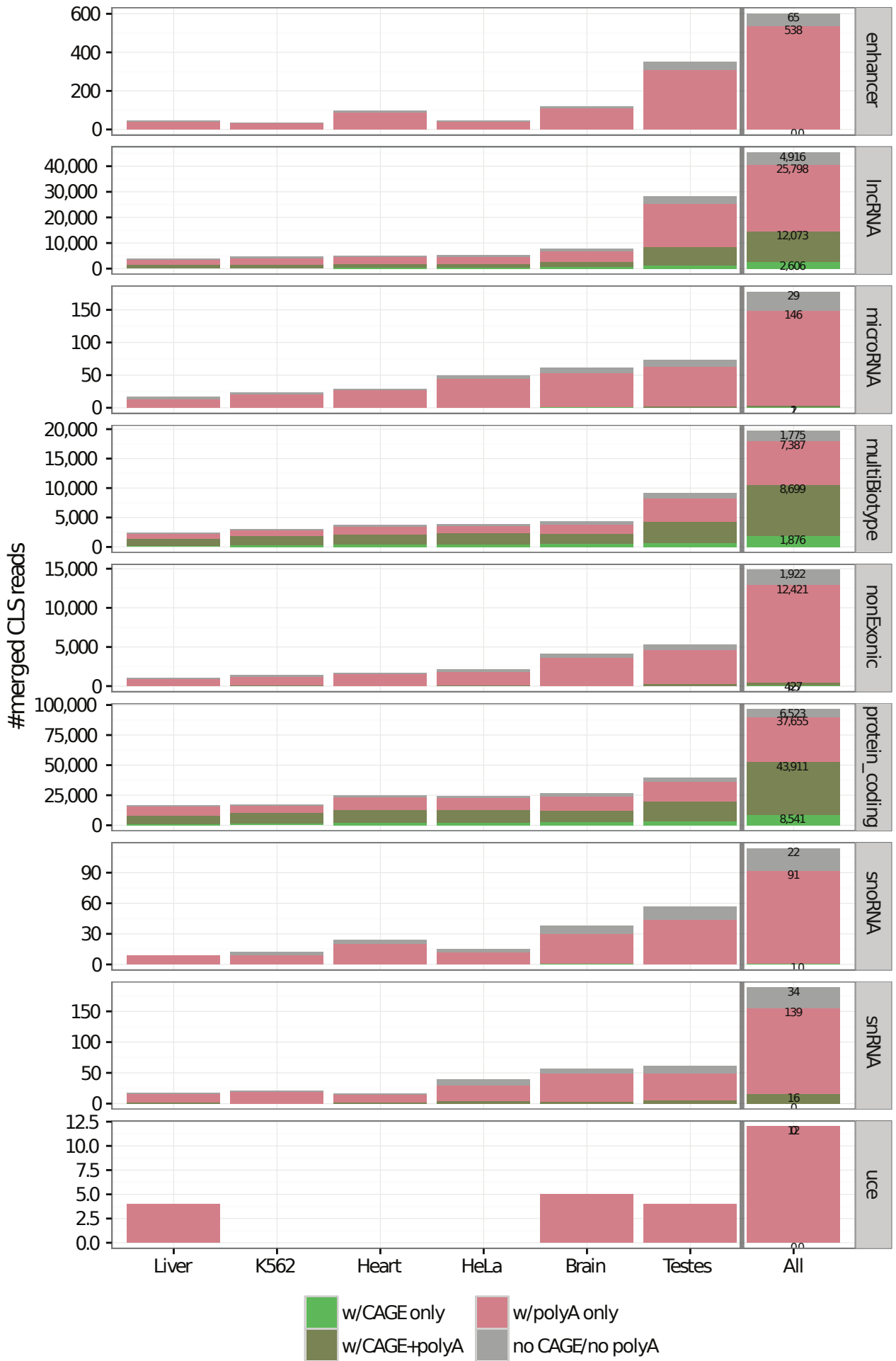
Supplementary Figure S22



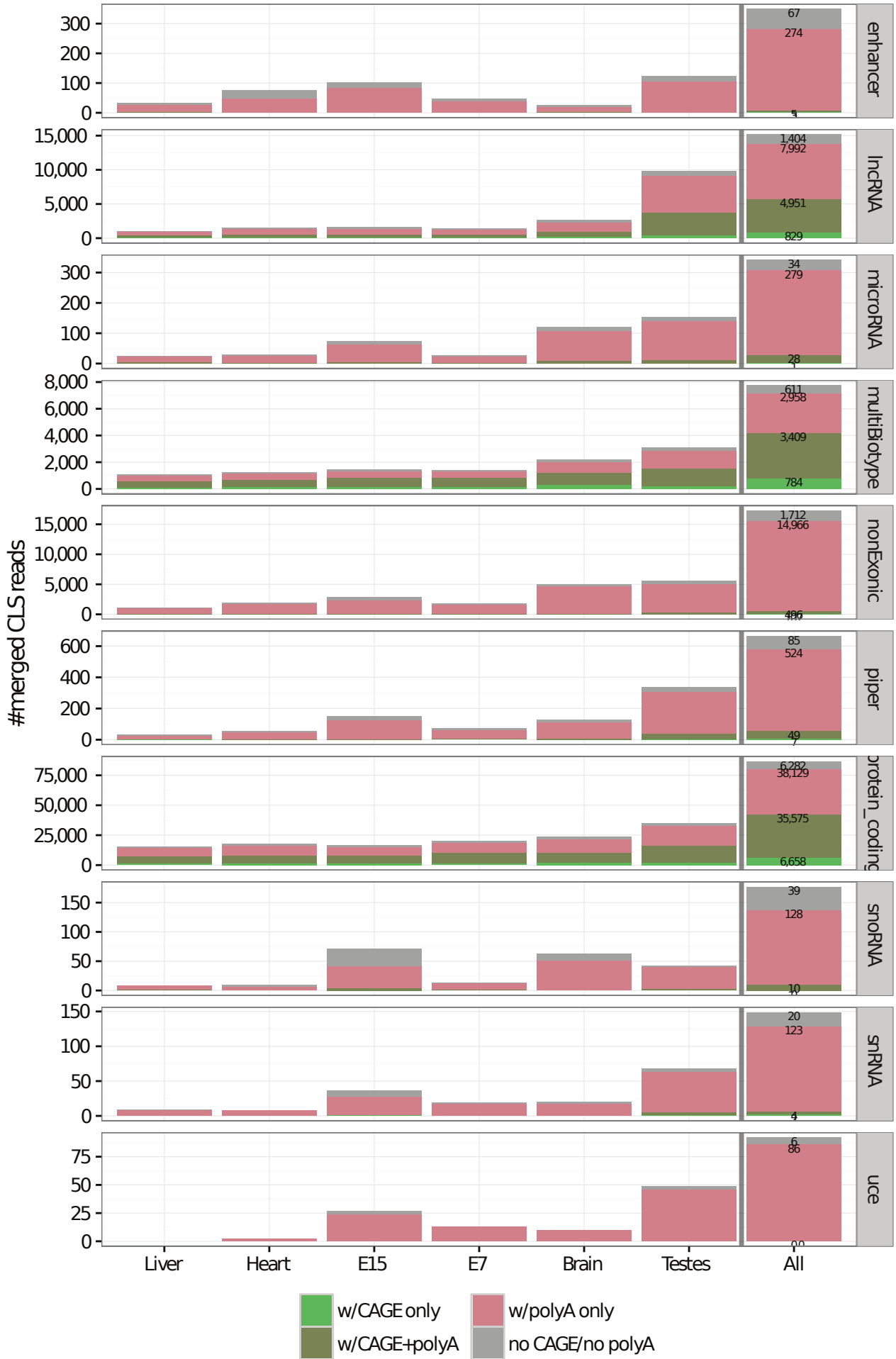
Supplementary Figure S23



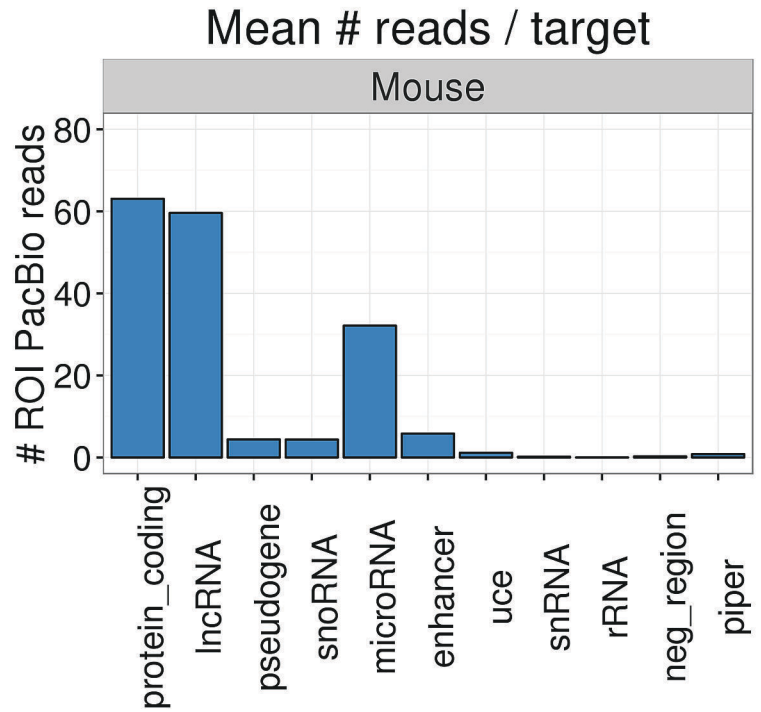
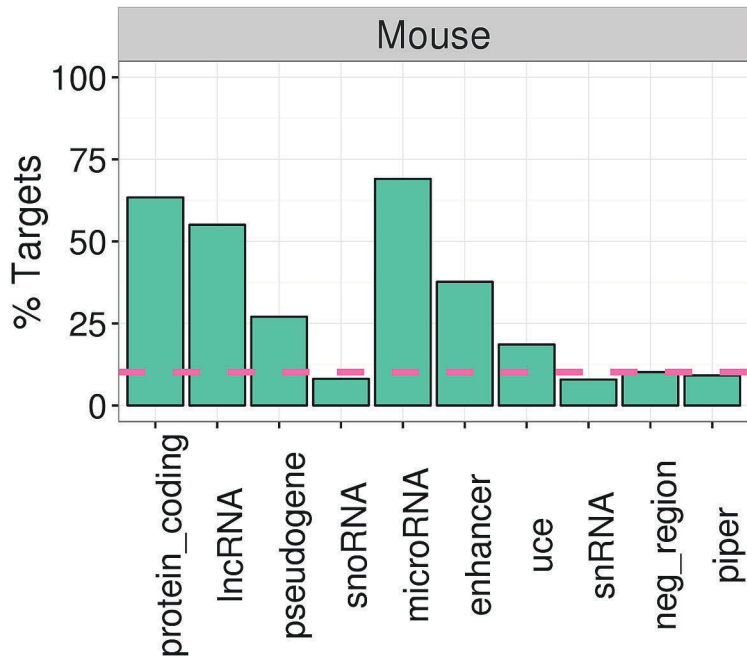
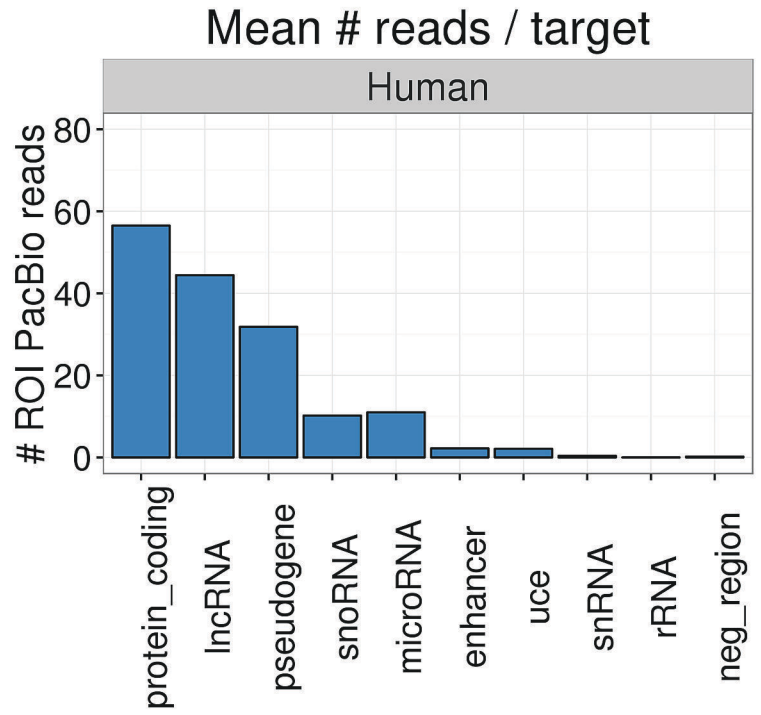
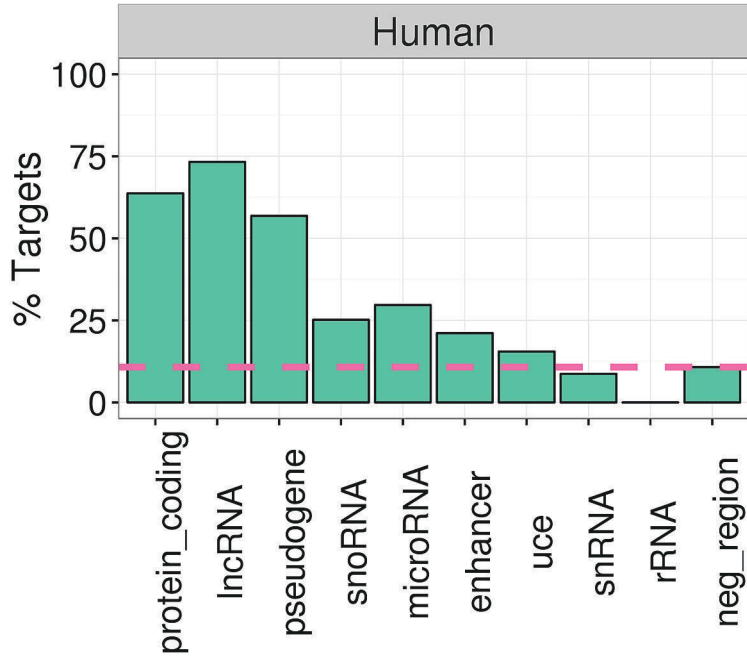
Supplementary Figure S24



Supplementary Figure S25



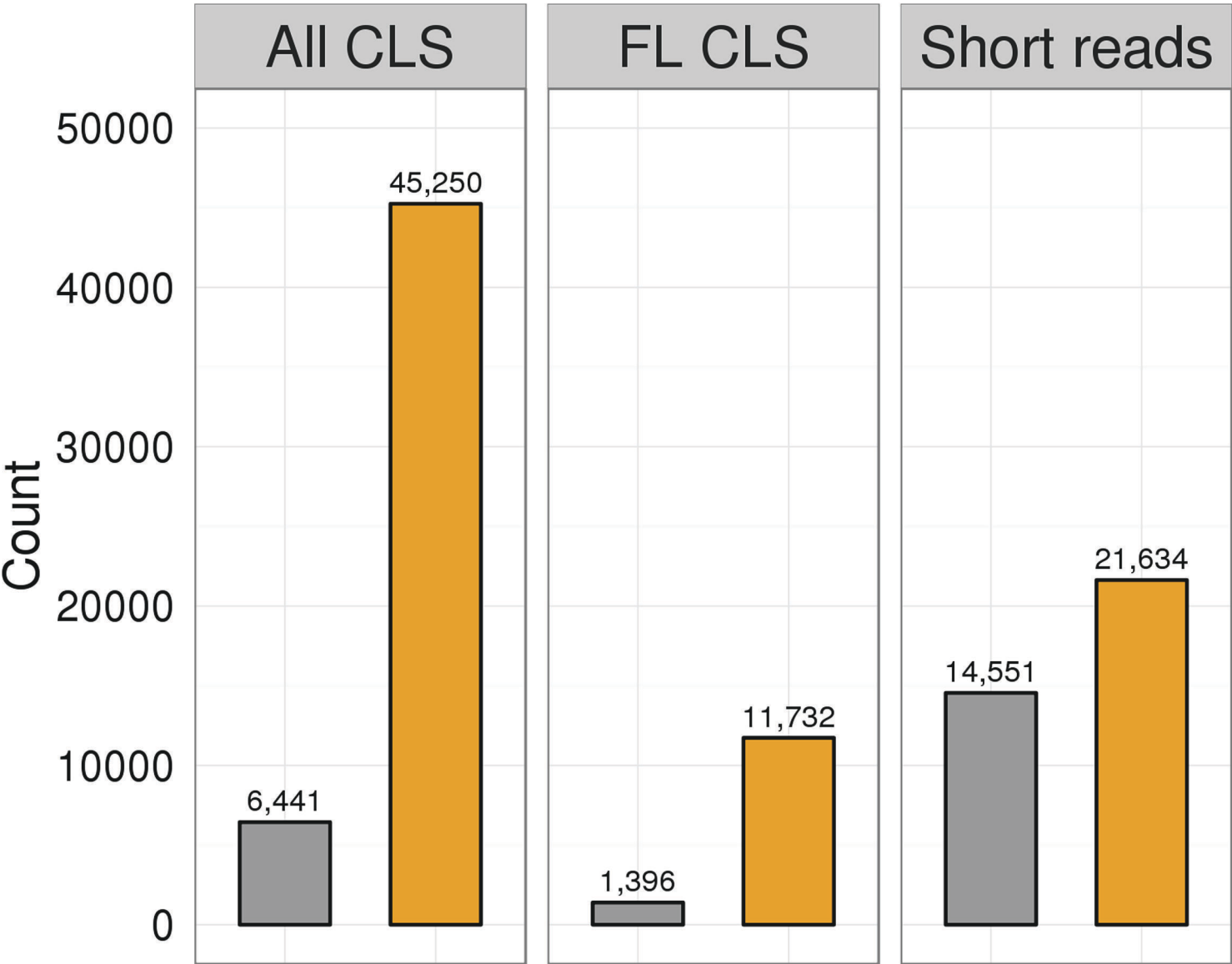
Supplementary Figure S26



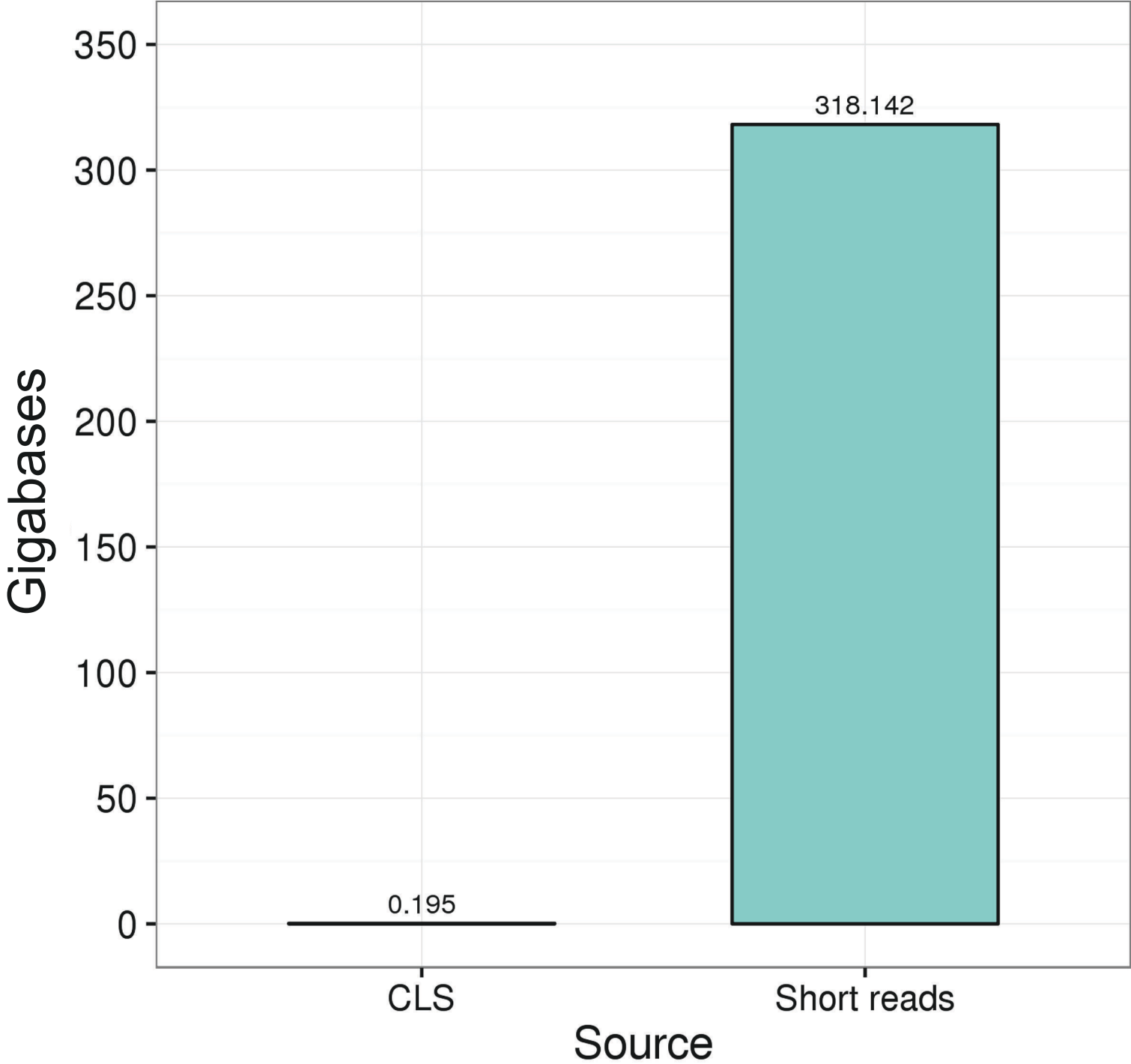
Supplementary Figure S27

Comparison of CLS and Short Read Transcript Discovery

Known transcripts (unique) Novel transcripts (unique)

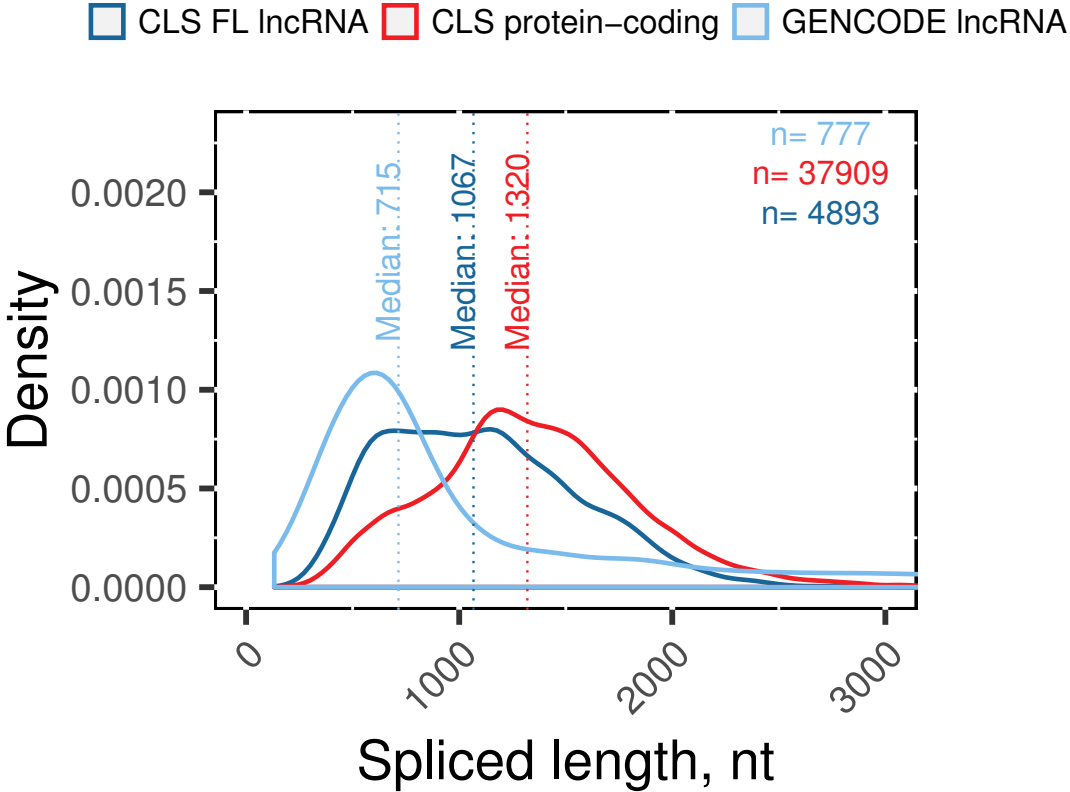


Supplementary Figure S28

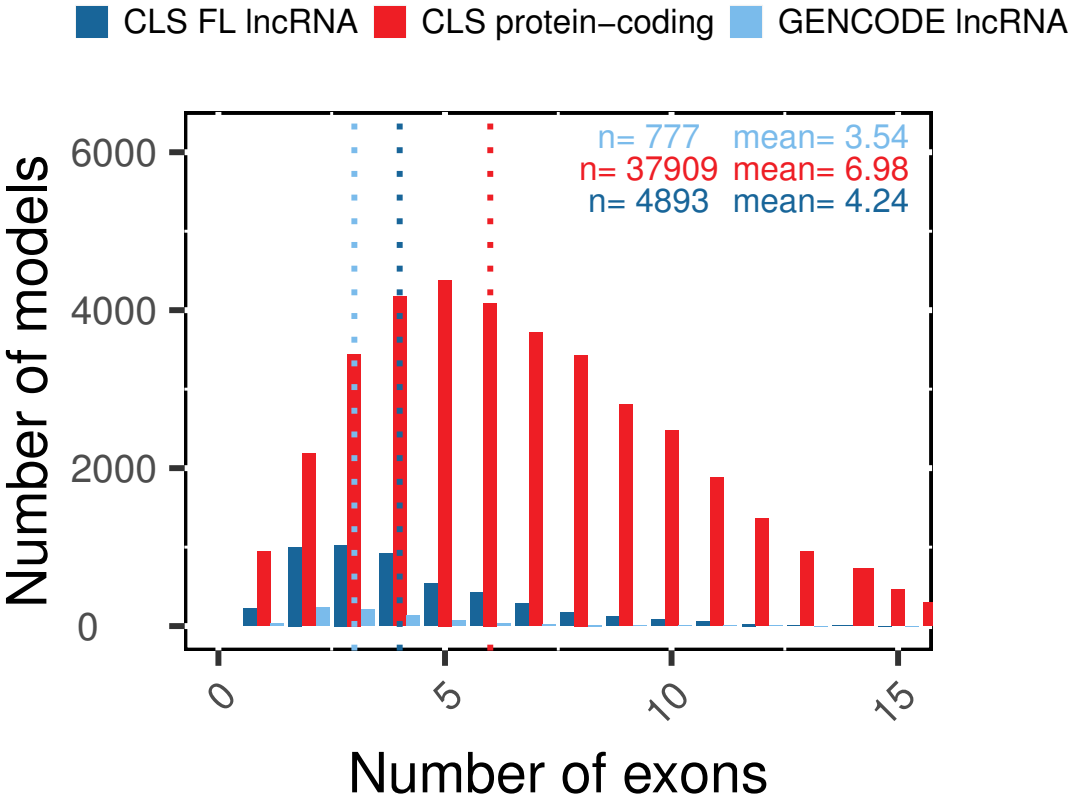


Supplementary Figure S29

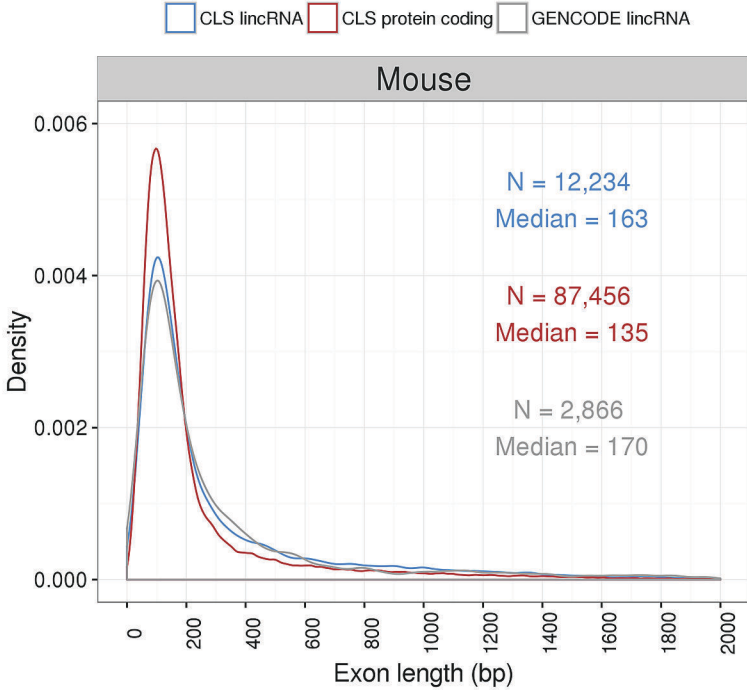
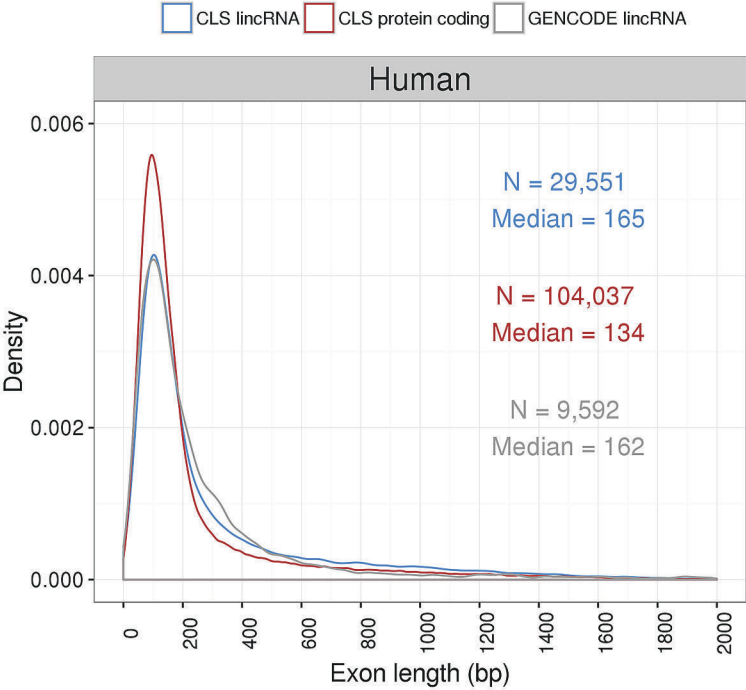
A



B

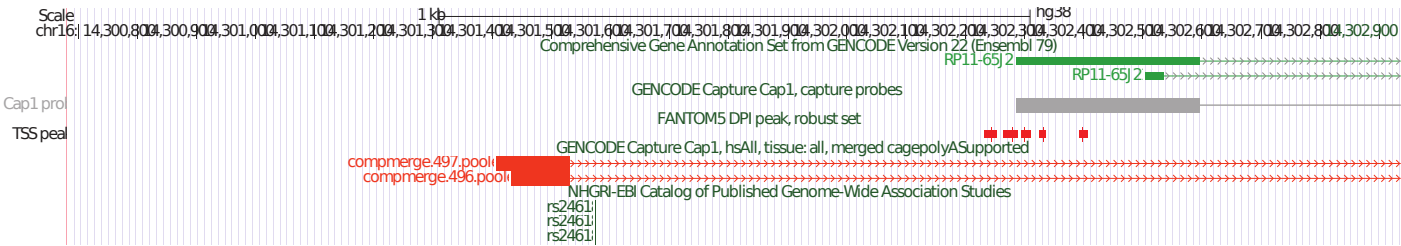


Supplementary Figure S30

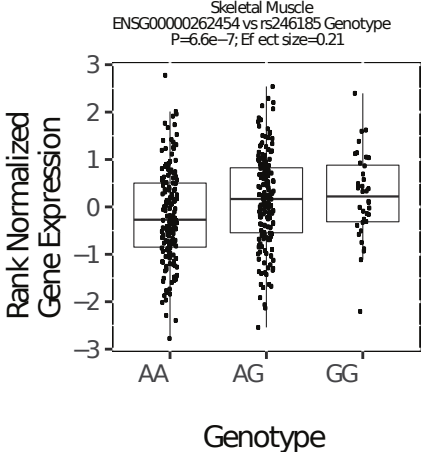


Supplementary Figure S31

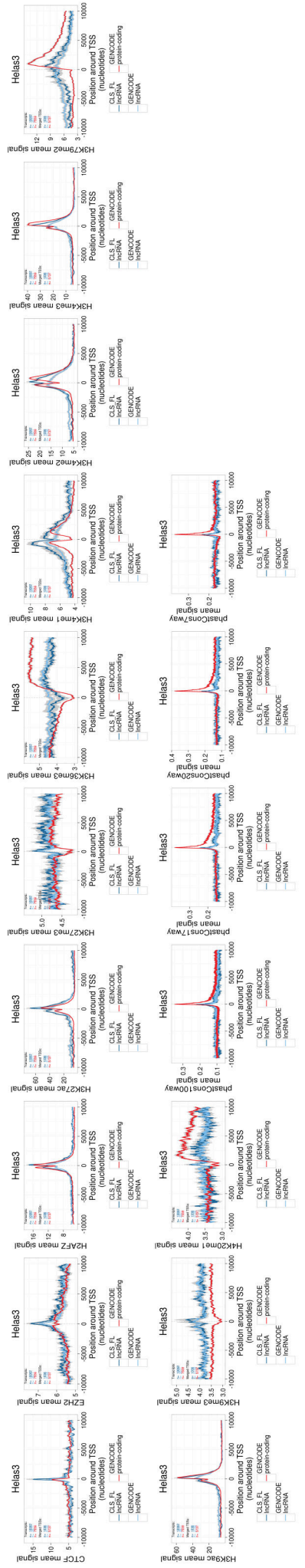
A



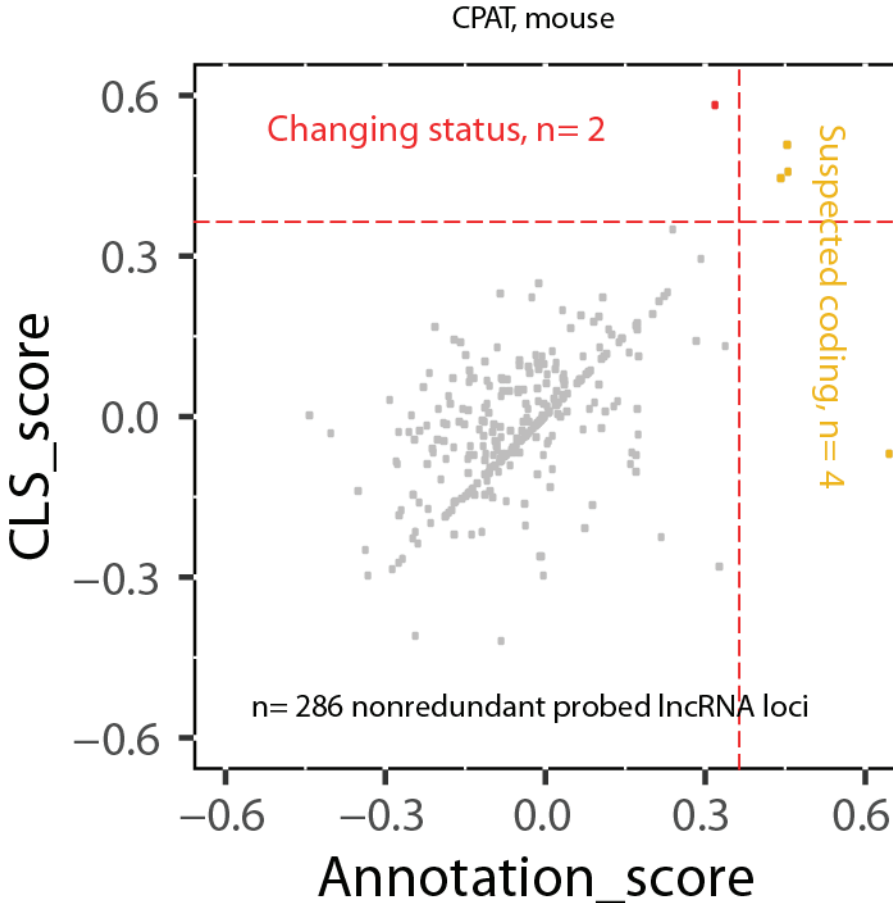
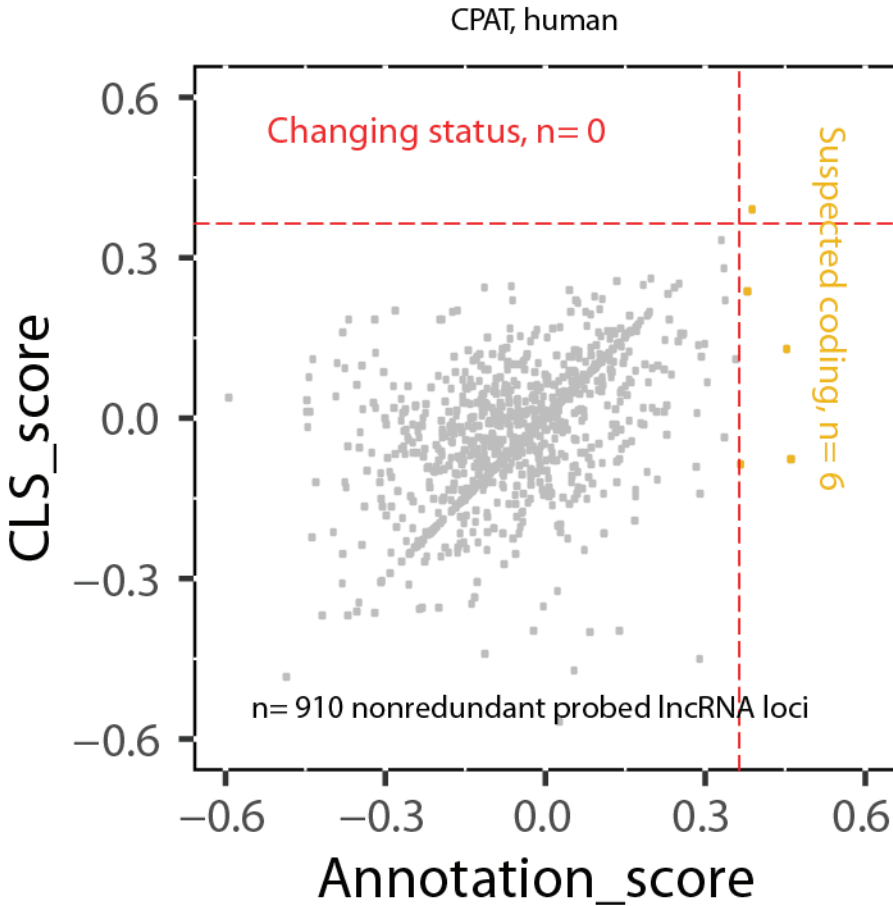
B



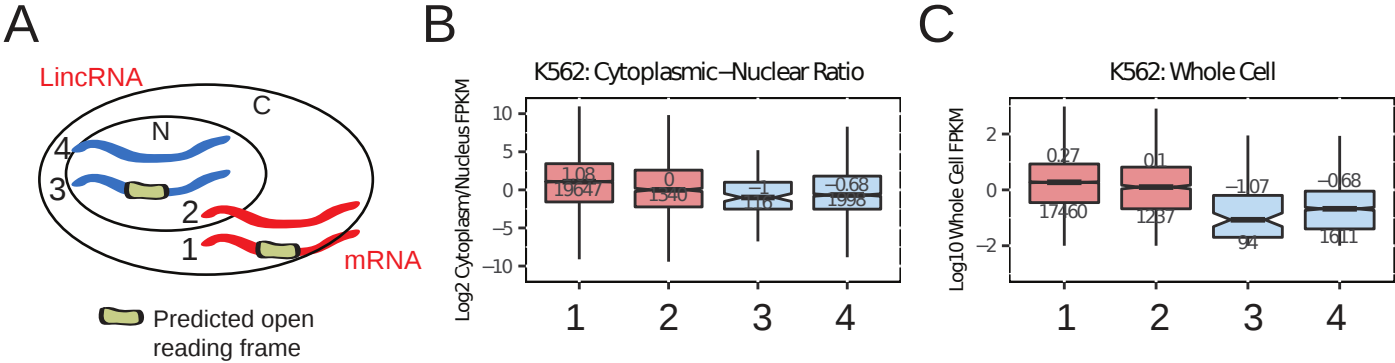
Supplementary Figure S32



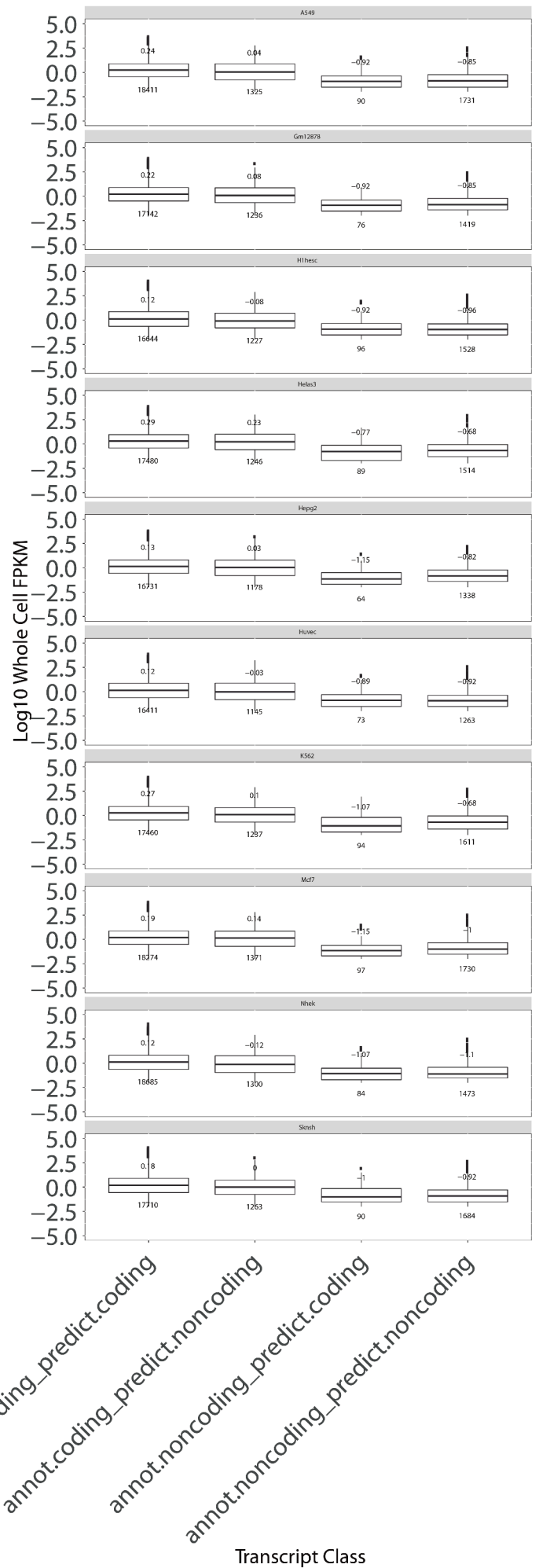
Supplementary Figure S34



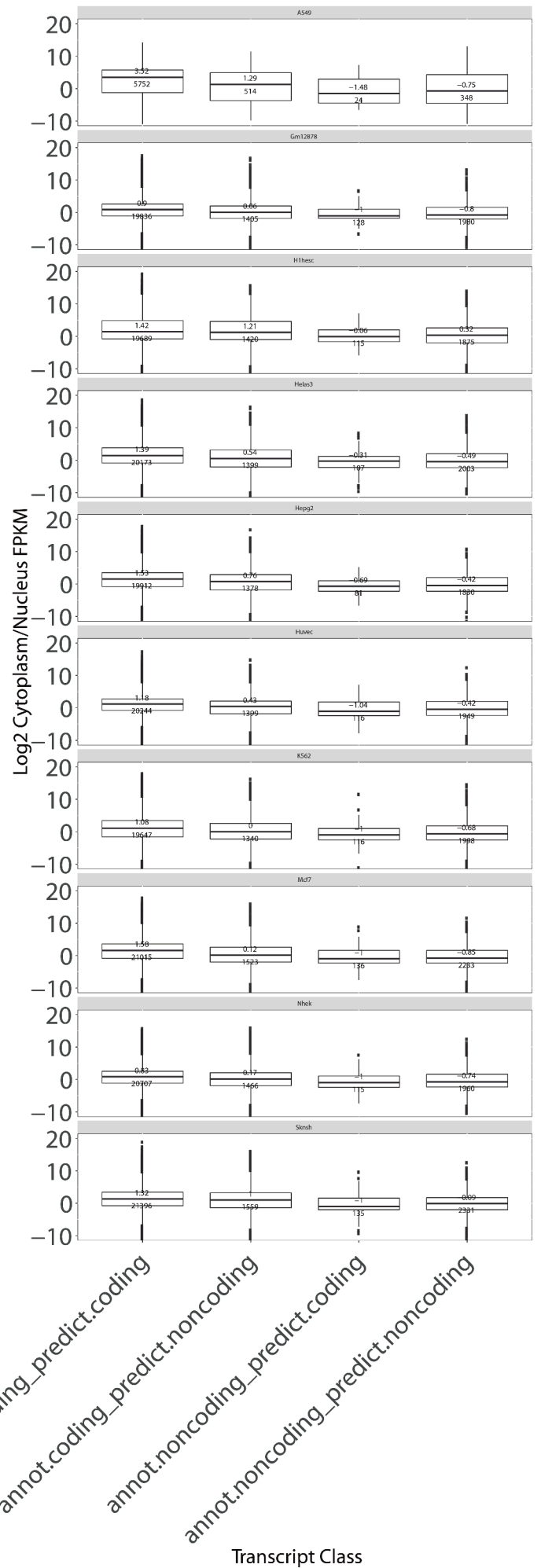
Supplementary Figure S36



Supplementary Figure S37

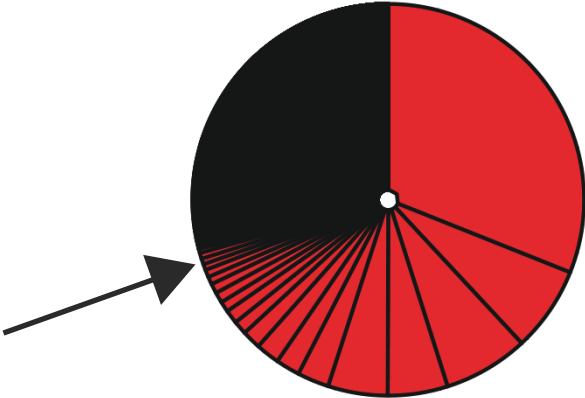


Supplementary Figure S38



Supplementary Figure S39

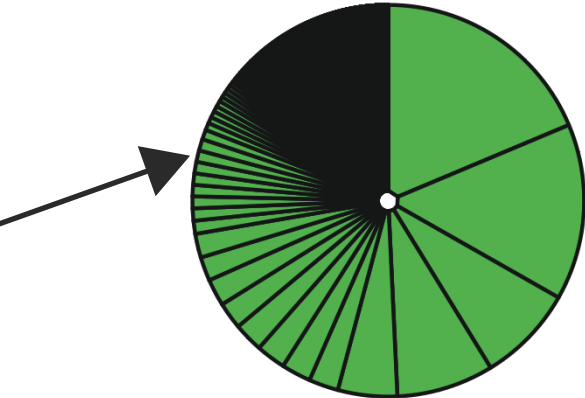
Human candidates



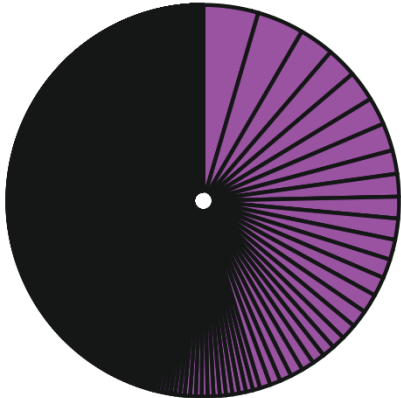
Human targets



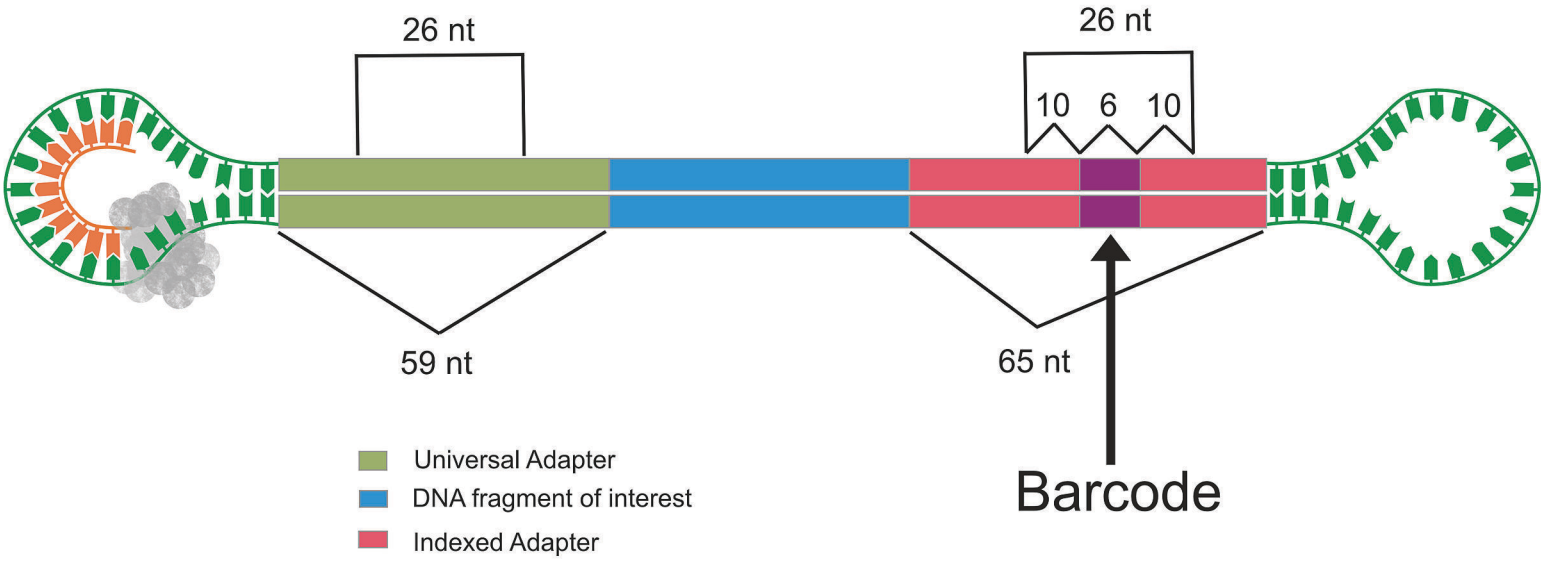
Mouse candidates



Mouse targets



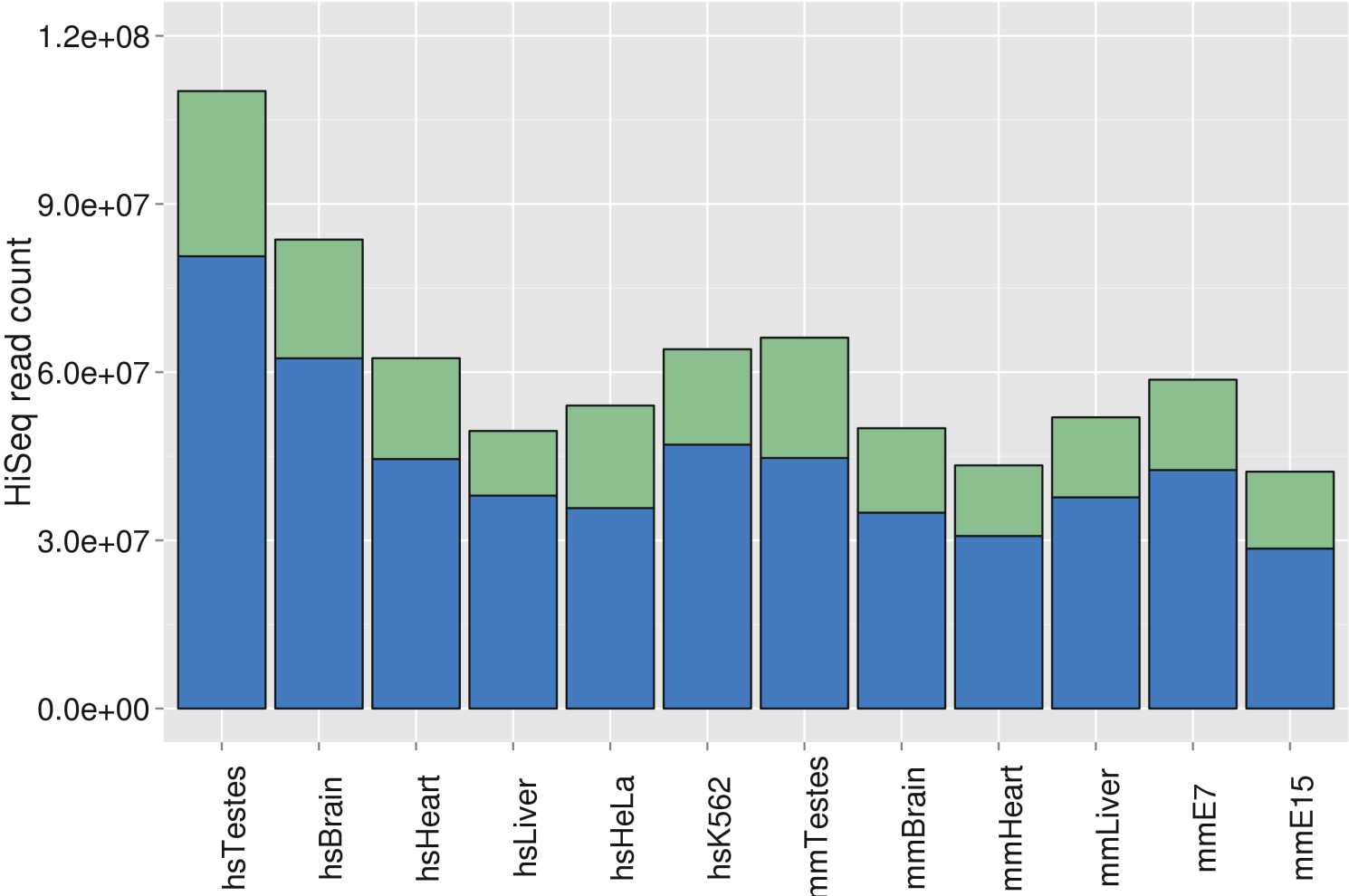
Supplementary Figure S40



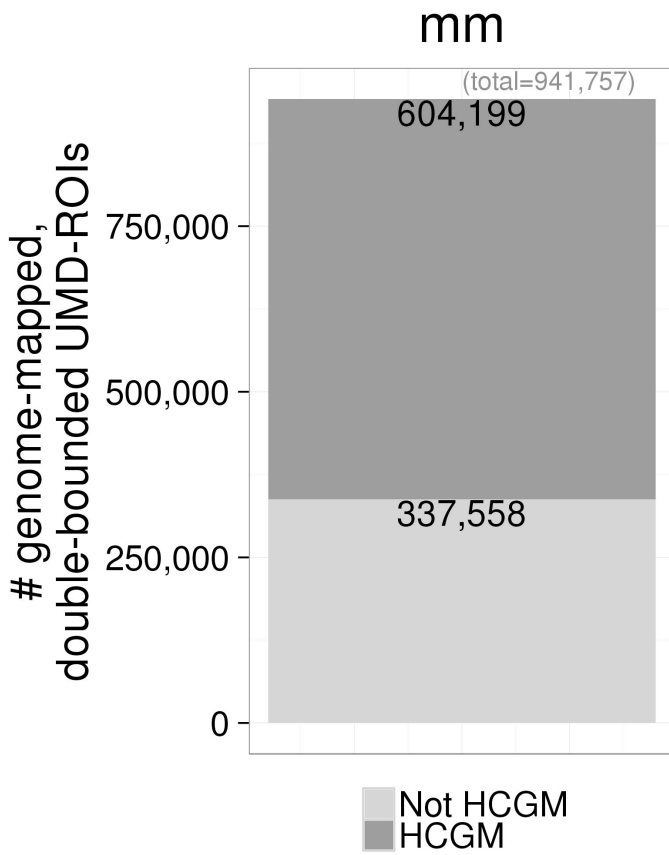
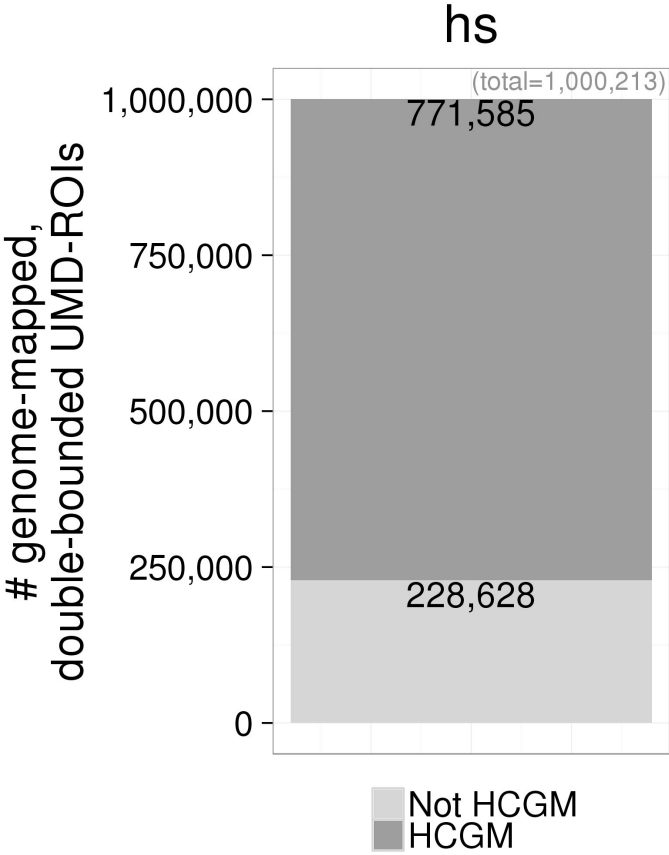
Supplementary Figure S41

HiSeq mapping stats

■ mapped ■ unmapped

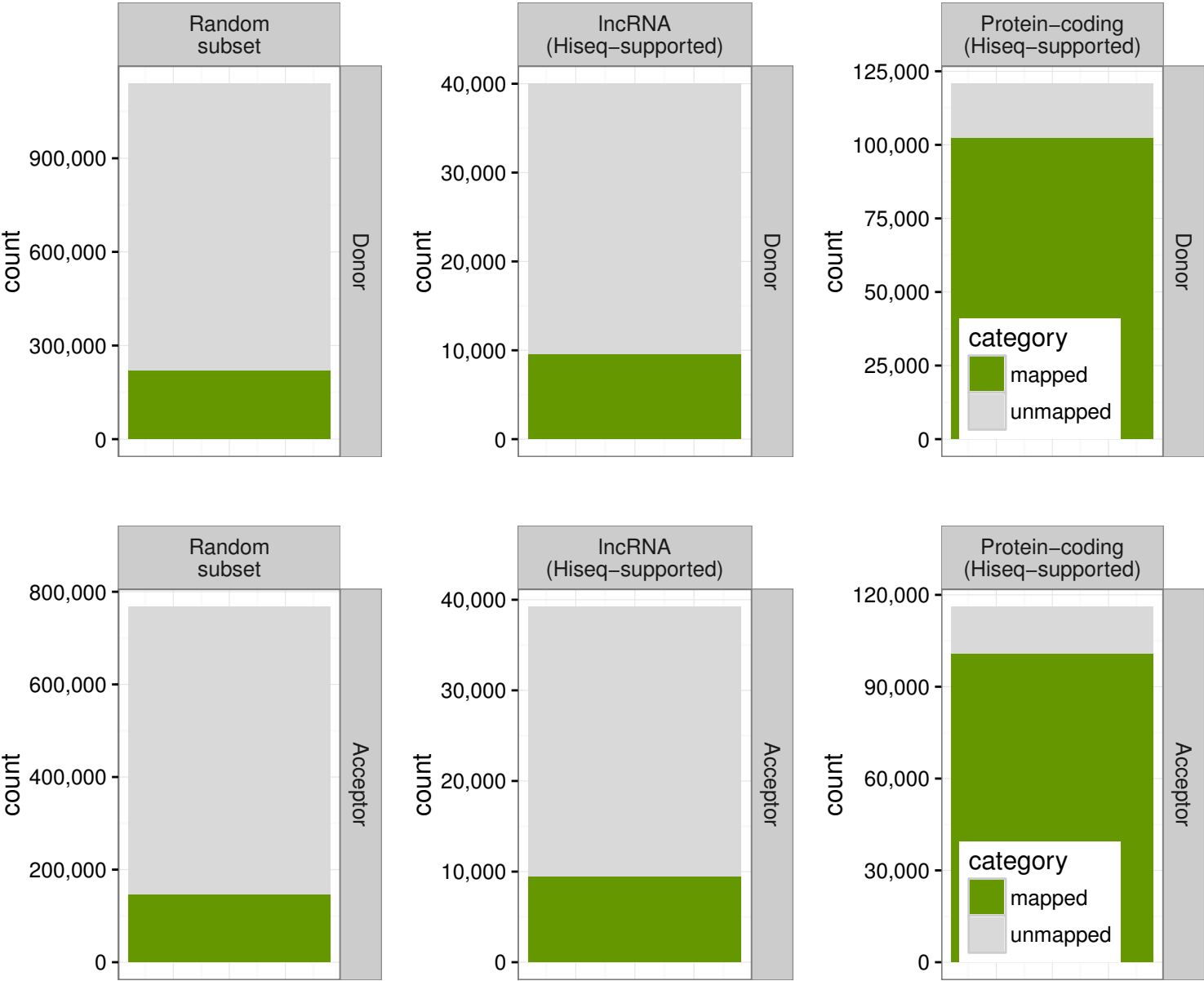


Supplementary Figure S42



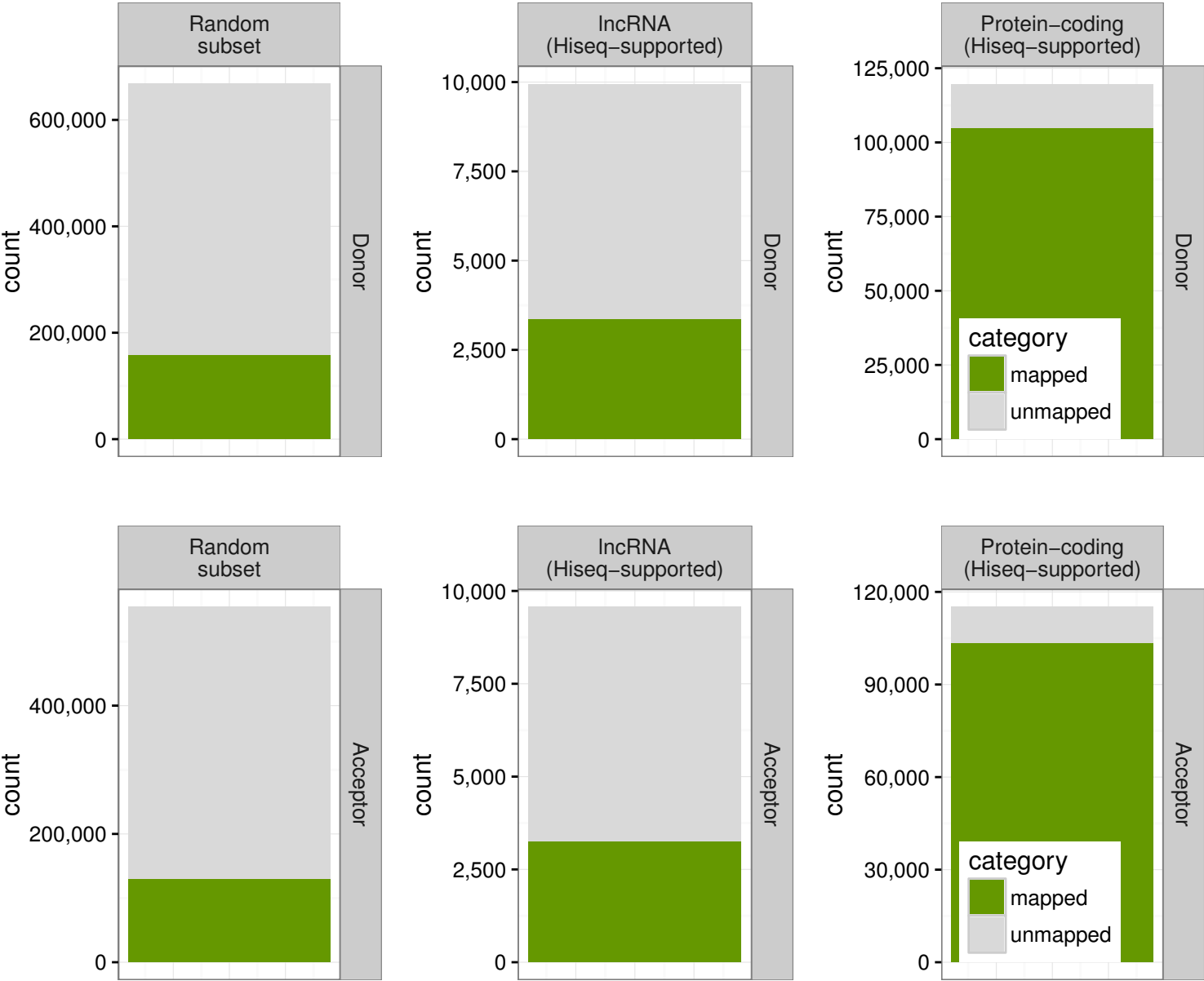
Supplementary Figure S43

hg38 to mm10 splice site liftOver mappings stats



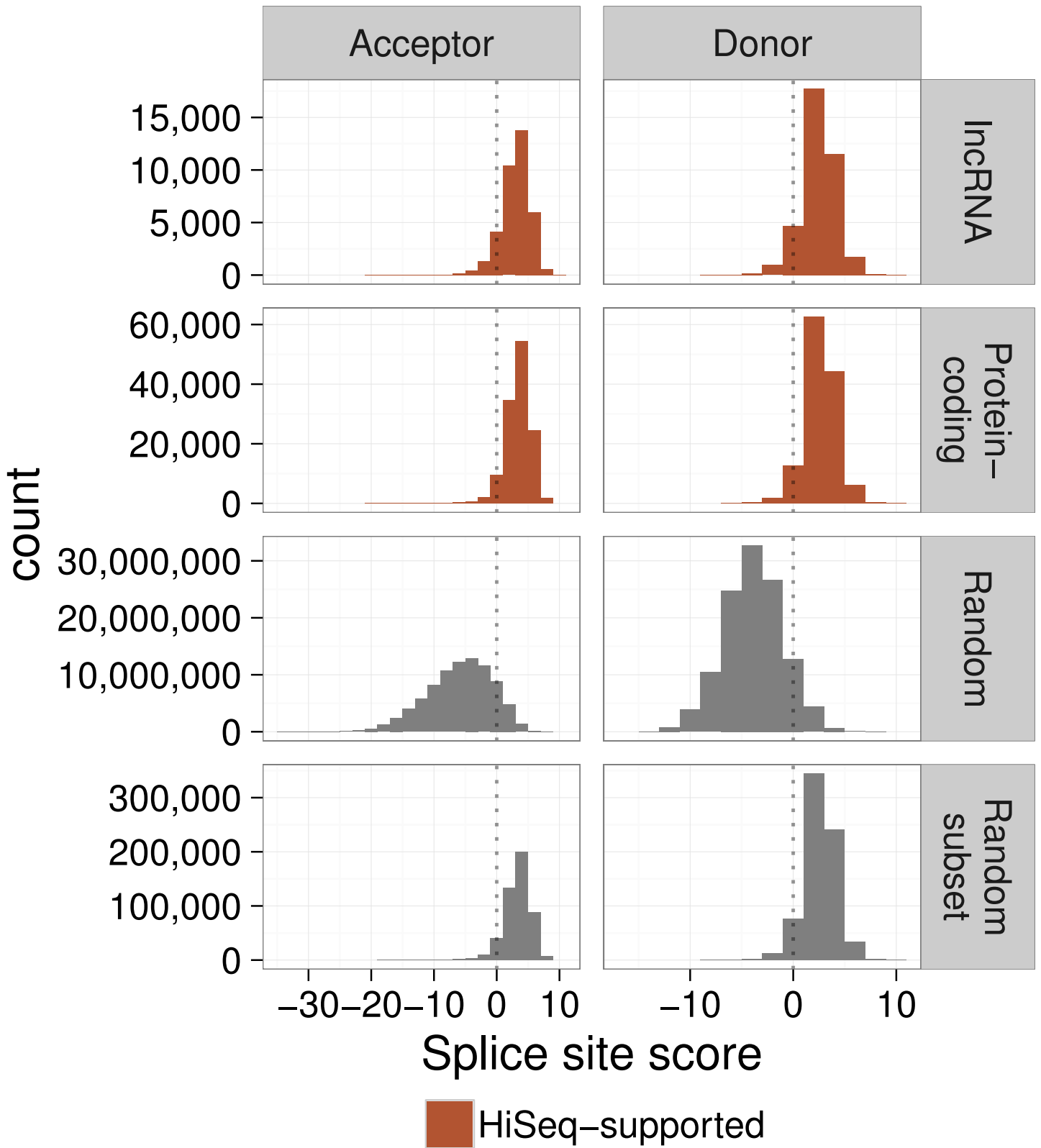
Supplementary Figure S44

mm10 to hg38 splice site liftOver mappings stats



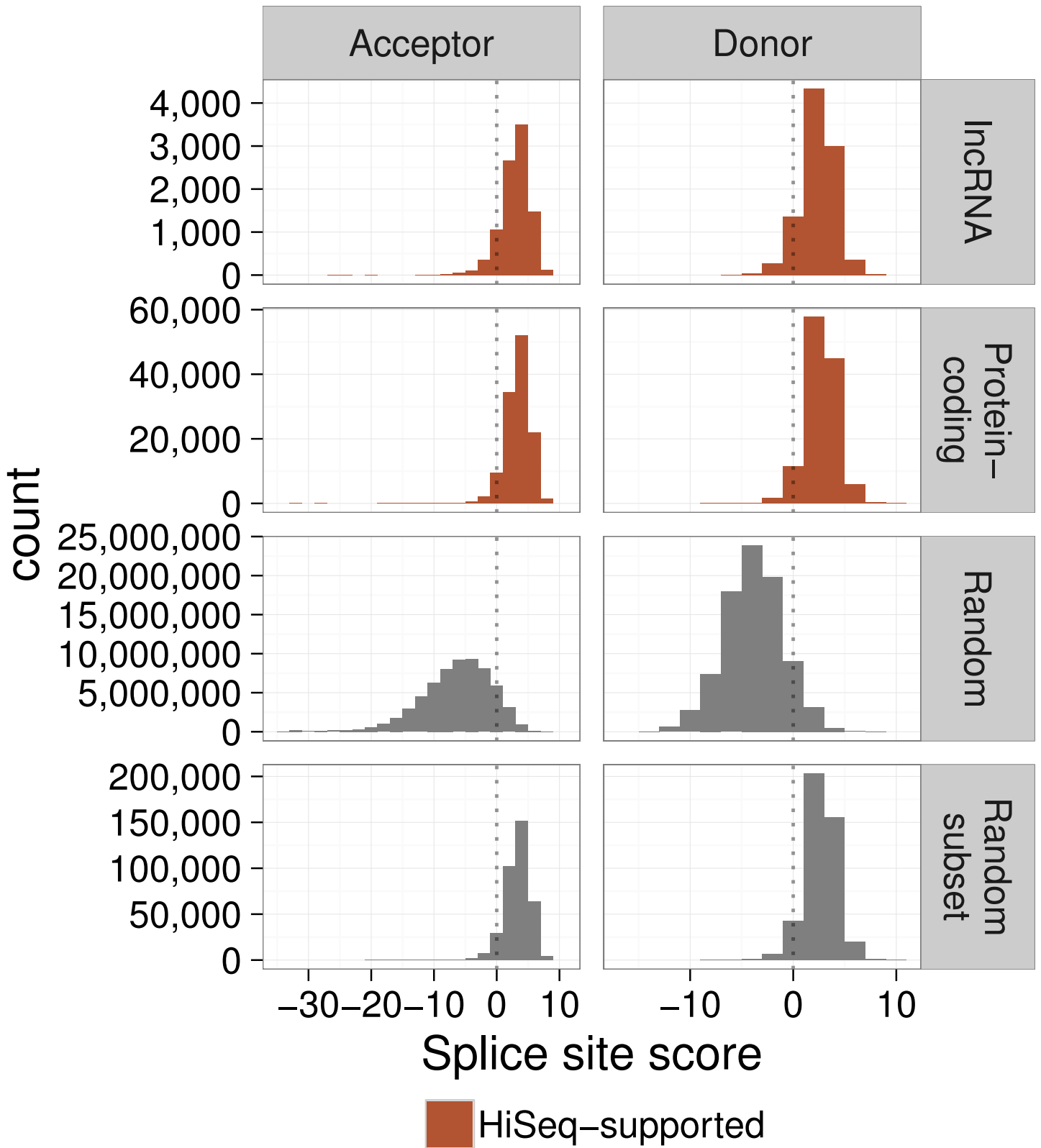
Supplementary Figure S45

hs splice site scores

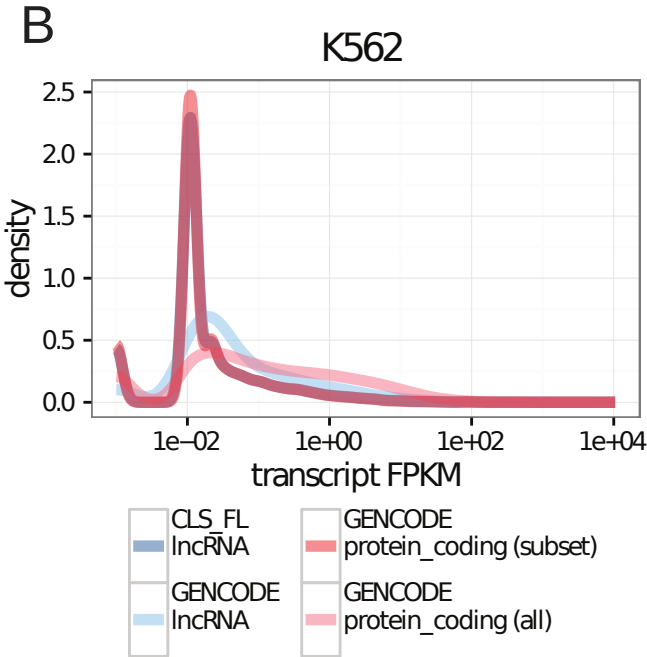
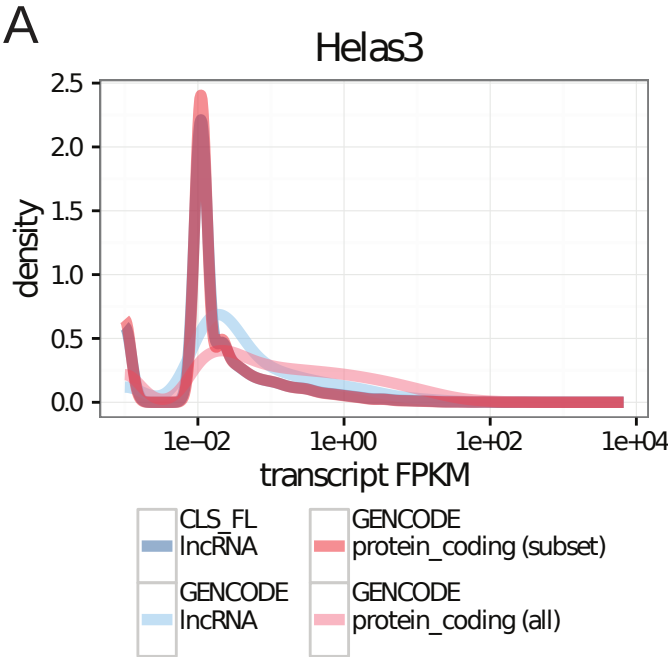


Supplementary Figure S46

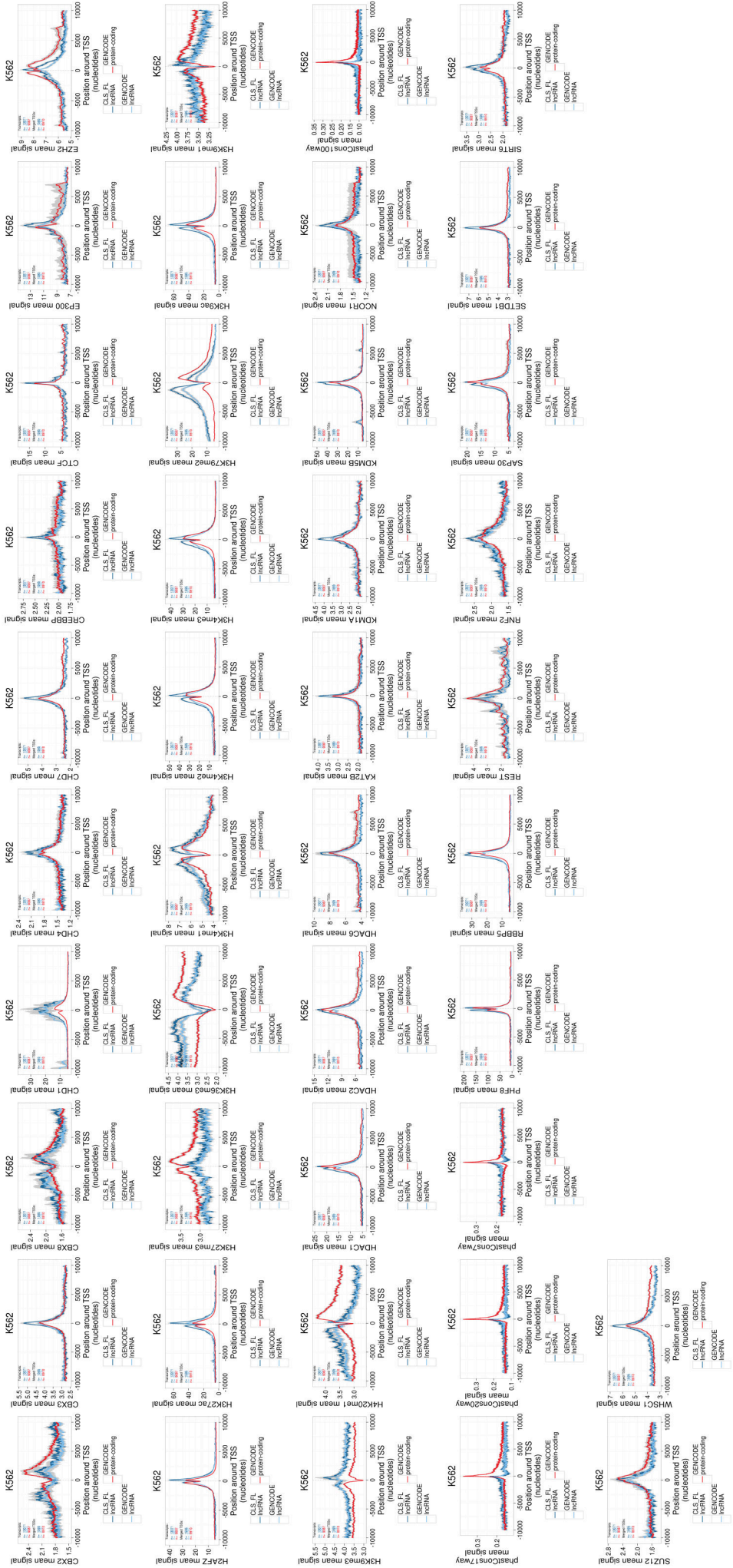
mm splice site scores



Supplementary Figure S47



Supplementary Figure S49



Supplementary Figure S50

