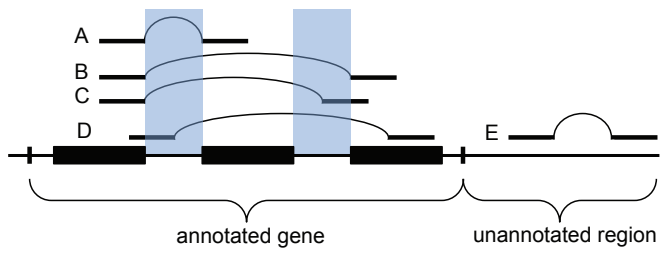


Fig. S12

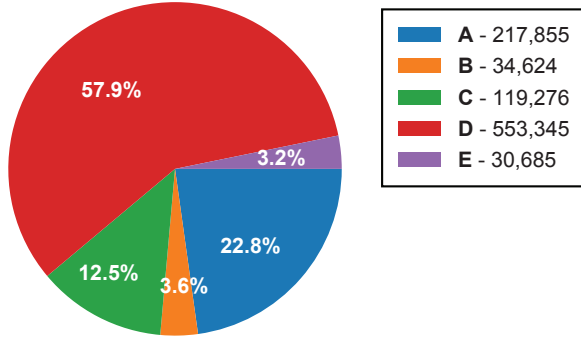
A



- A:** annotated junction
- B:** Both boundaries are annotated but the splice is not
- C:** One boundary is annotated and the other is not
- D:** Neither boundary is annotated but at least one end is in a known gene
- E:** Neither boundary is in a known gene

B

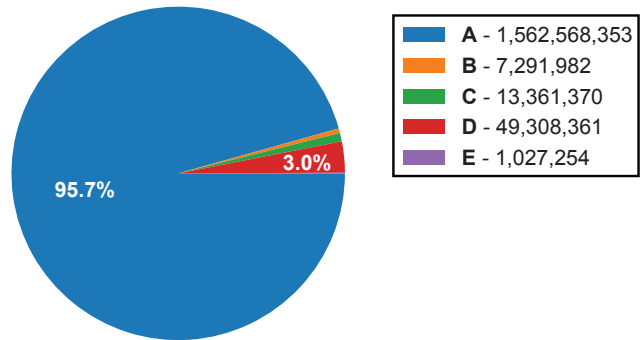
Fraction of junctions in each category



955,785 junctions total

C

Fraction of reads in each category



1,633,557,320 junctions total

D

