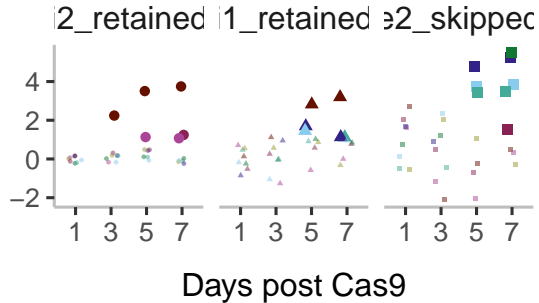


isoform / total



fct_rev(isoform)

- i2_retained
- ▲ i1_retained
- e2_skipped

as.factor(sig)

- 1
- 2

gene

- SF3B1
- SF3B2
- SF3B3
- SF3B4
- SF3B5
- SF3B6
- SF3B7
- AQR