All the genes in the annotation file
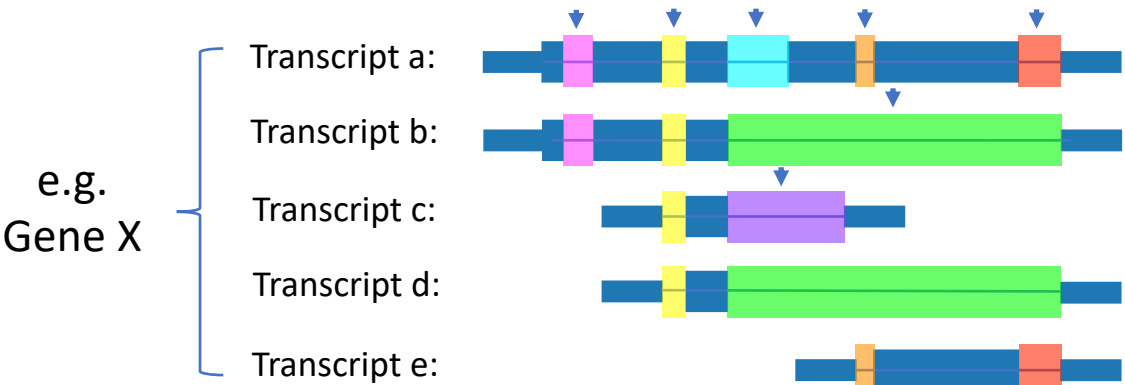
Select the genes that have expression in ≥ 1 sample(s)

1	0	0	3	0	1	0
0	0	0	0	0	0	0
5	0	10	0	0	0	2
0	0	0	0	0	0	0

Get the set of unique introns from all the transcripts of each gene

e.g.
Gene X

Transcript a:

Transcript b:

Transcript c:

Transcript d:

Transcript e:

Keep the introns with length > 30

Total number: *335,436*