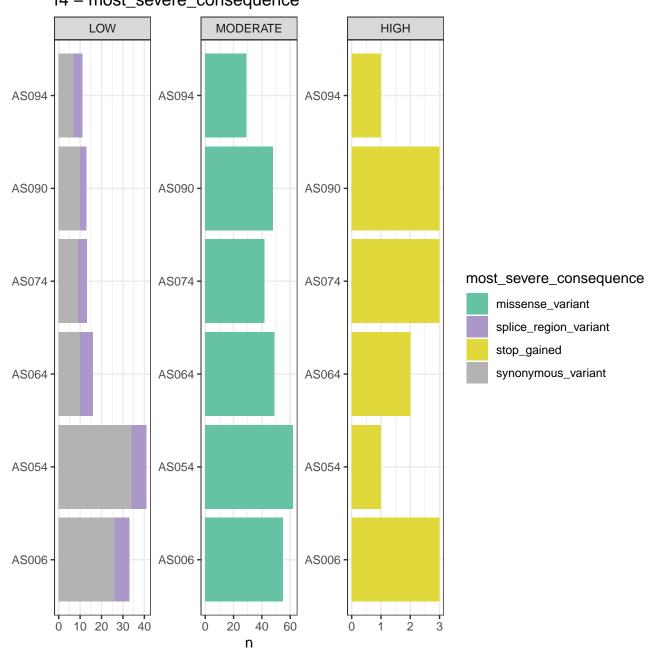
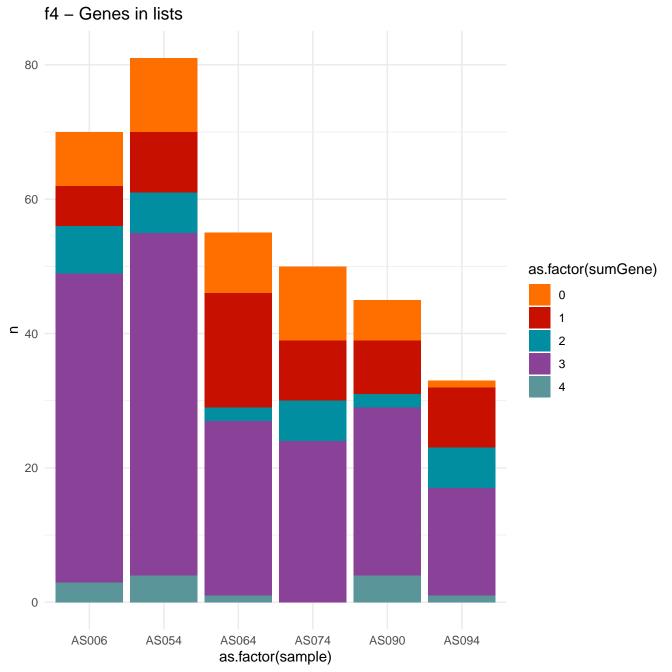
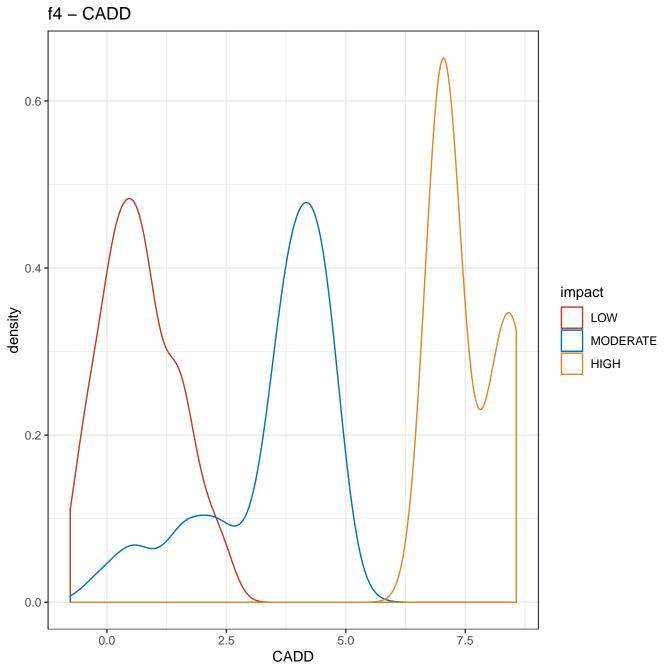


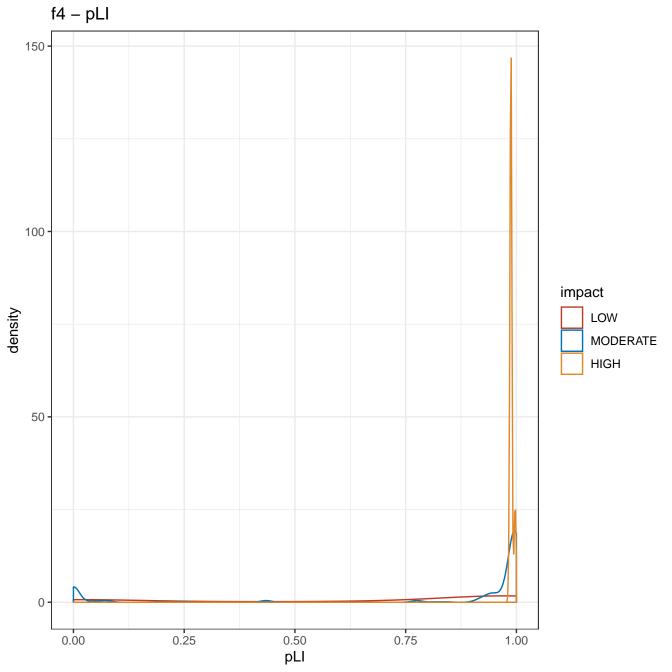
f4 - most_severe_consequence



f4 - Genes and transcripts 80 -70 -60 type \subseteq genes transcripts 50 -40 -AS006 AS054 AS064 AS074 AS090 AS094 as.factor(sample)

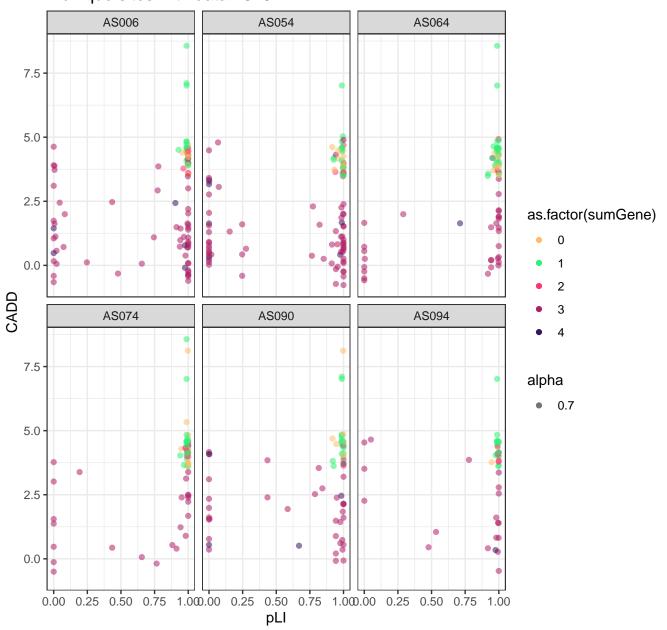






f4 - pLI CADD sumGene 7.5 -5.0 as.factor(sumGene) 0 2.5 0.0 0.00 0.25 0.50 1.00 0.75 pLI

f4pLI, CADD, gene lists # unique sites with data =373



f4 – Genes shared among samples

