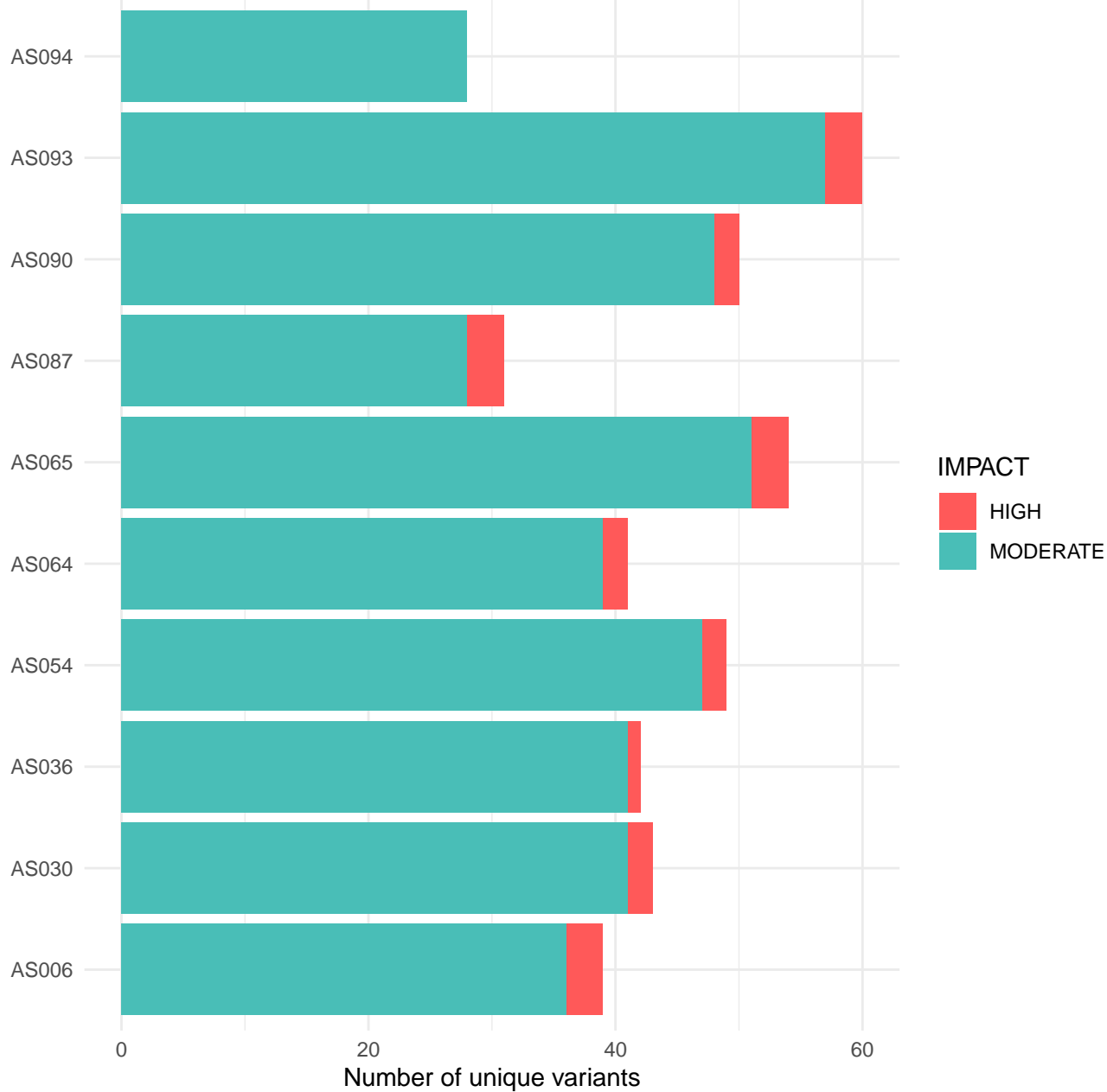
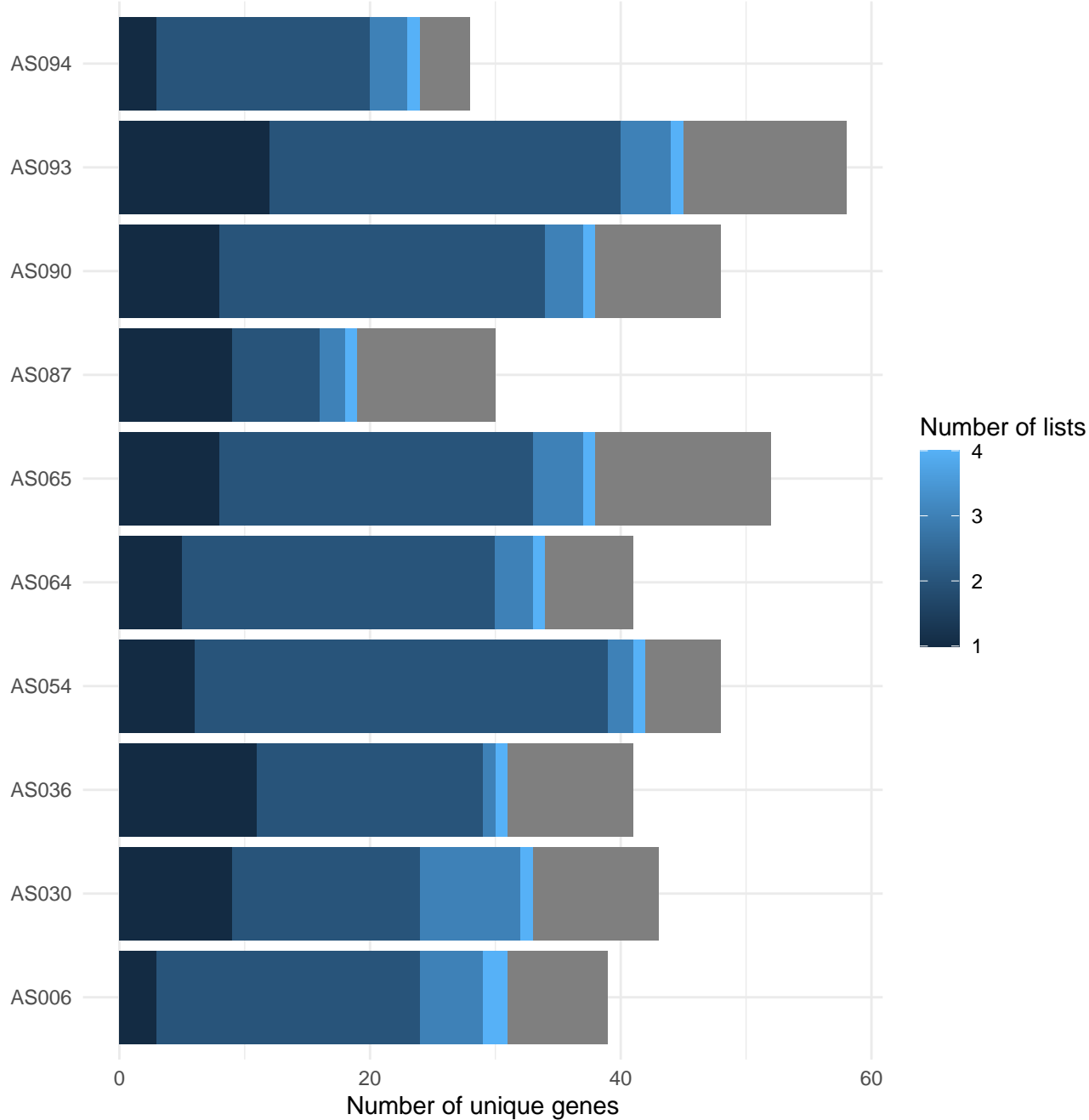
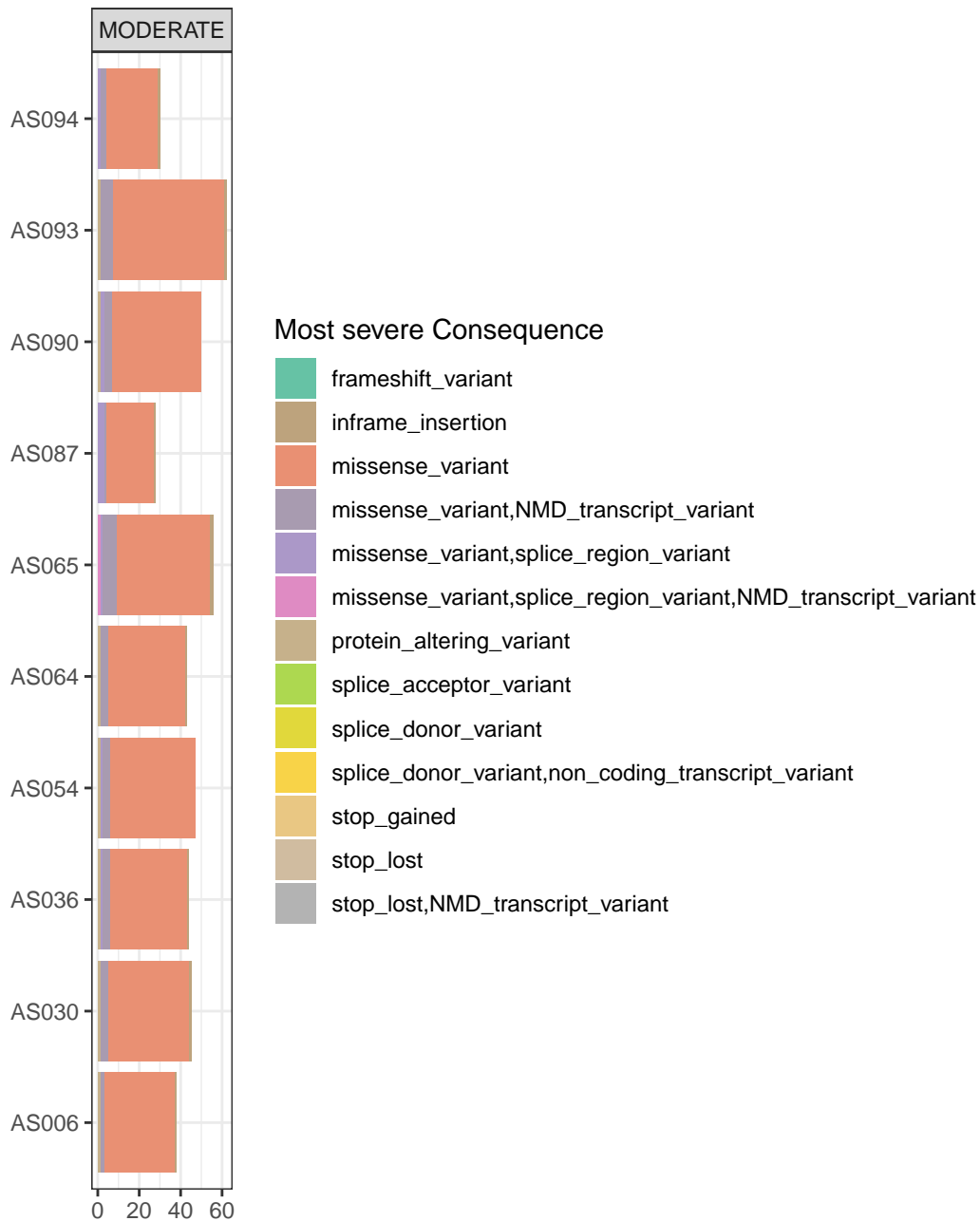
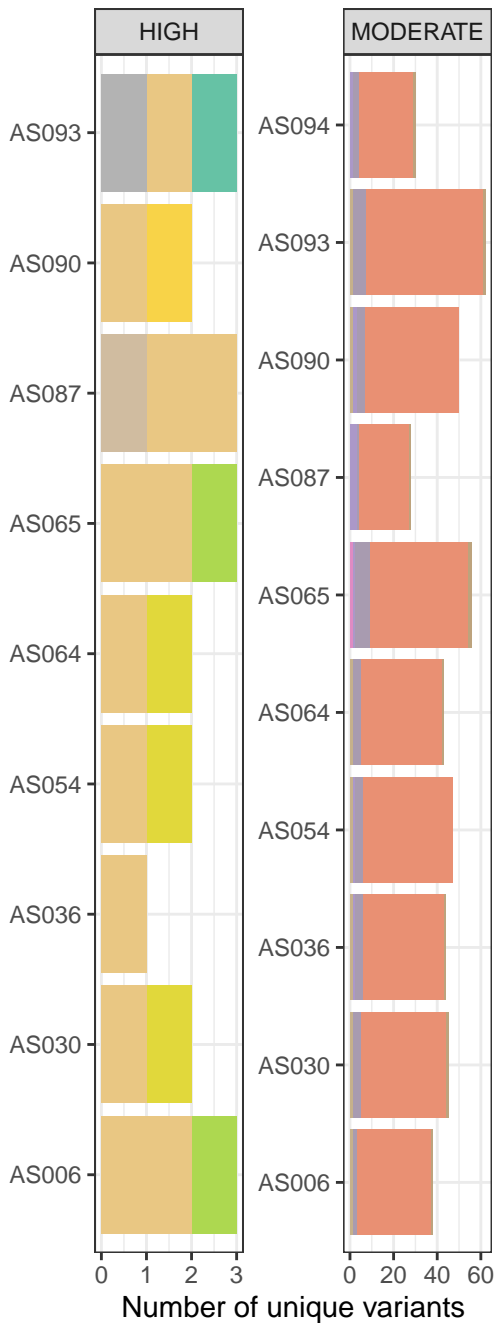


GREP – Unique variants per sample



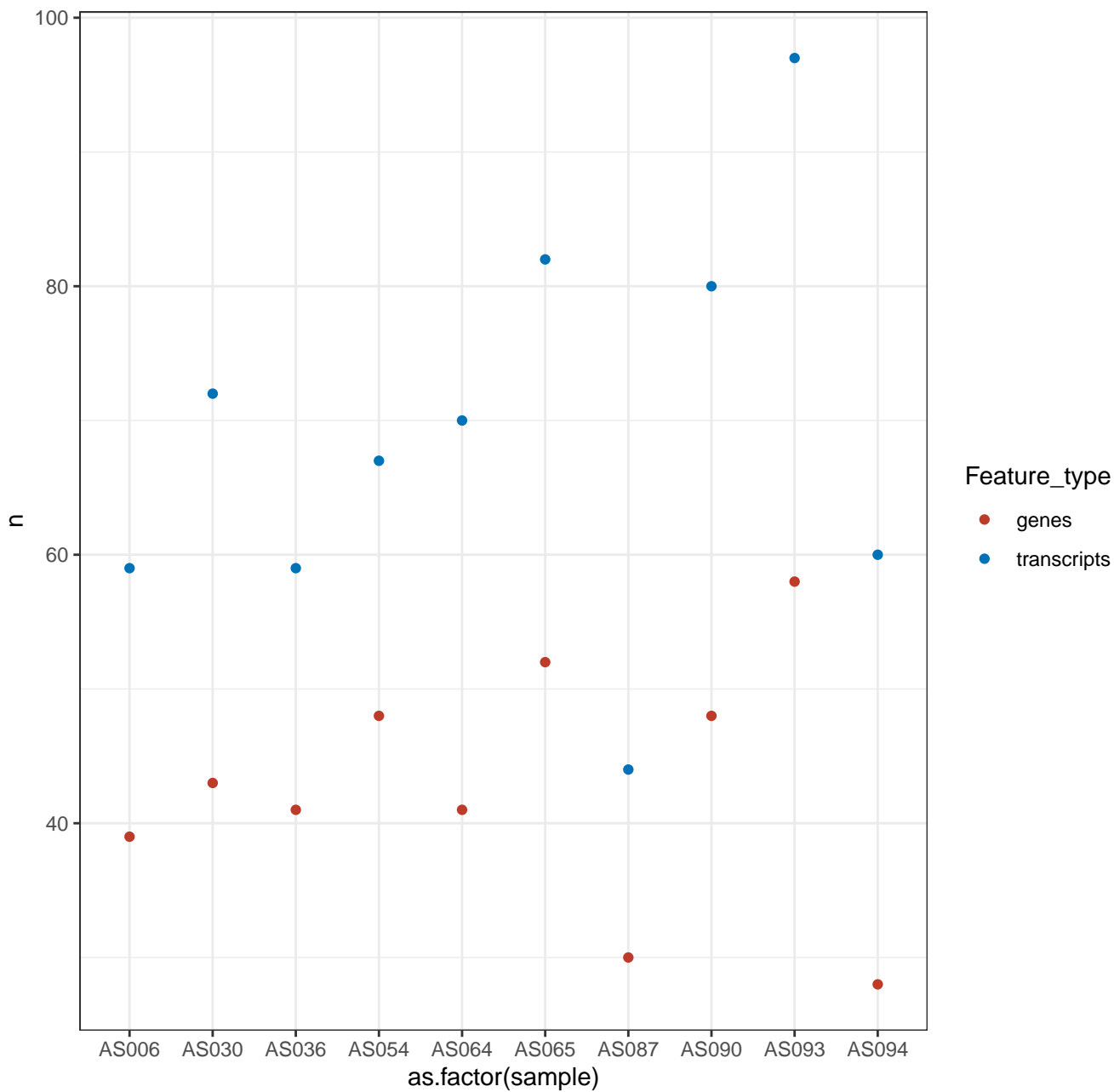




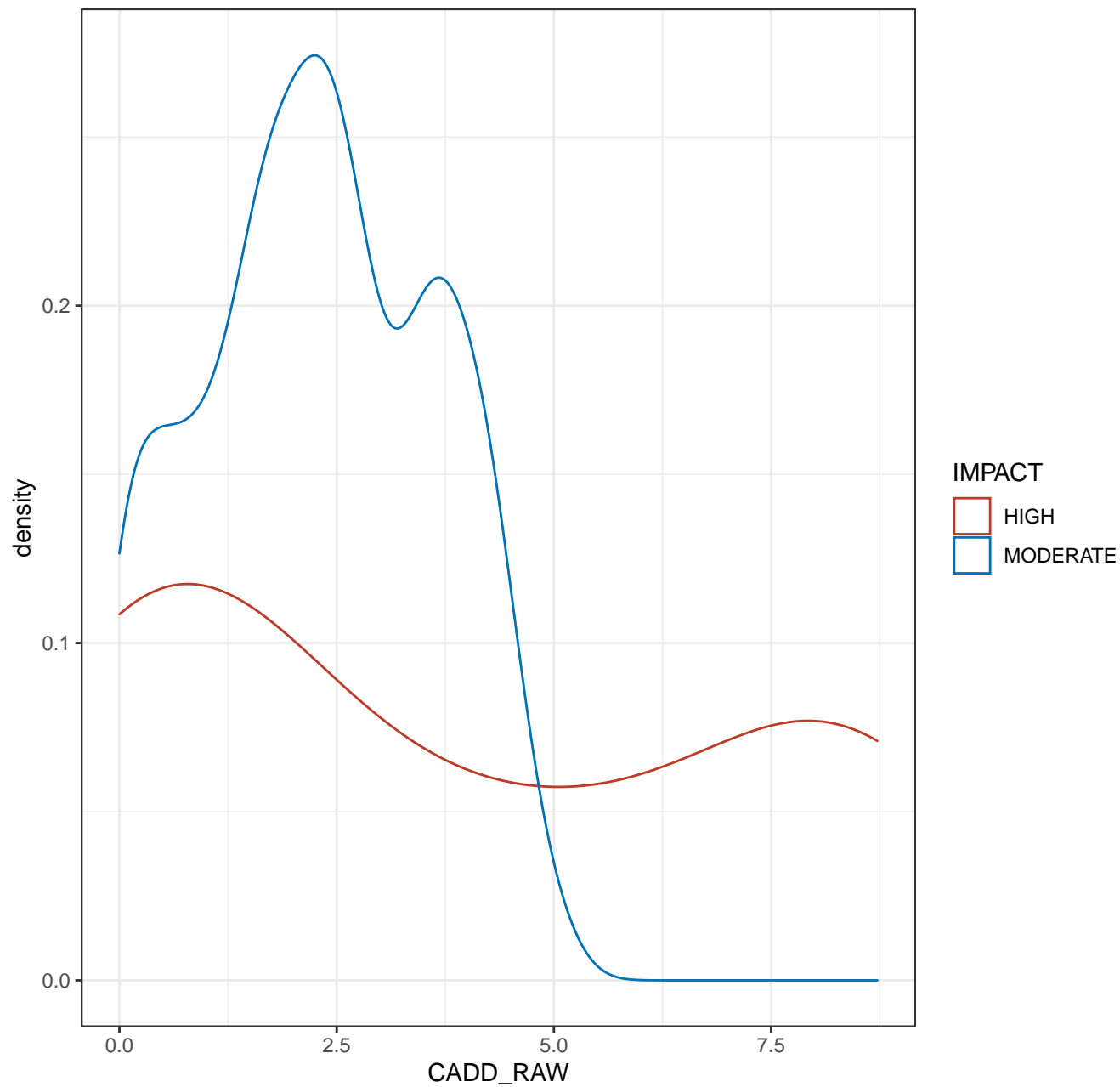
Most severe Consequence

- frameshift_variant
- inframe_insertion
- missense_variant
- missense_variant,NMD_transcript_variant
- missense_variant,splice_region_variant
- missense_variant,splice_region_variant,NMD_transcript_variant
- protein_altering_variant
- splice_acceptor_variant
- splice_donor_variant
- splice_donor_variant,non_coding_transcript_variant
- stop_gained
- stop_lost
- stop_lost,NMD_transcript_variant

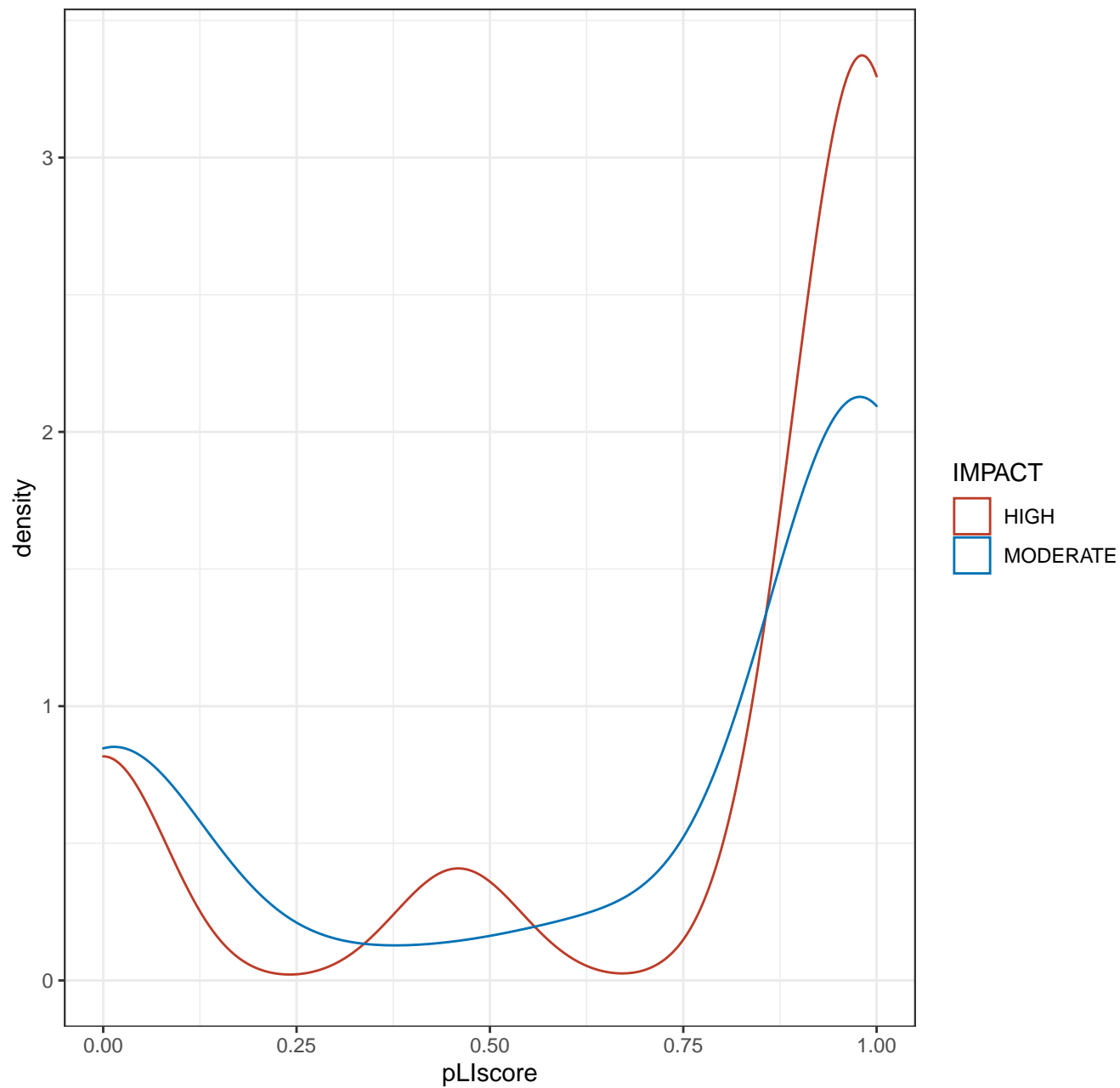
GREP – Genes and transcripts



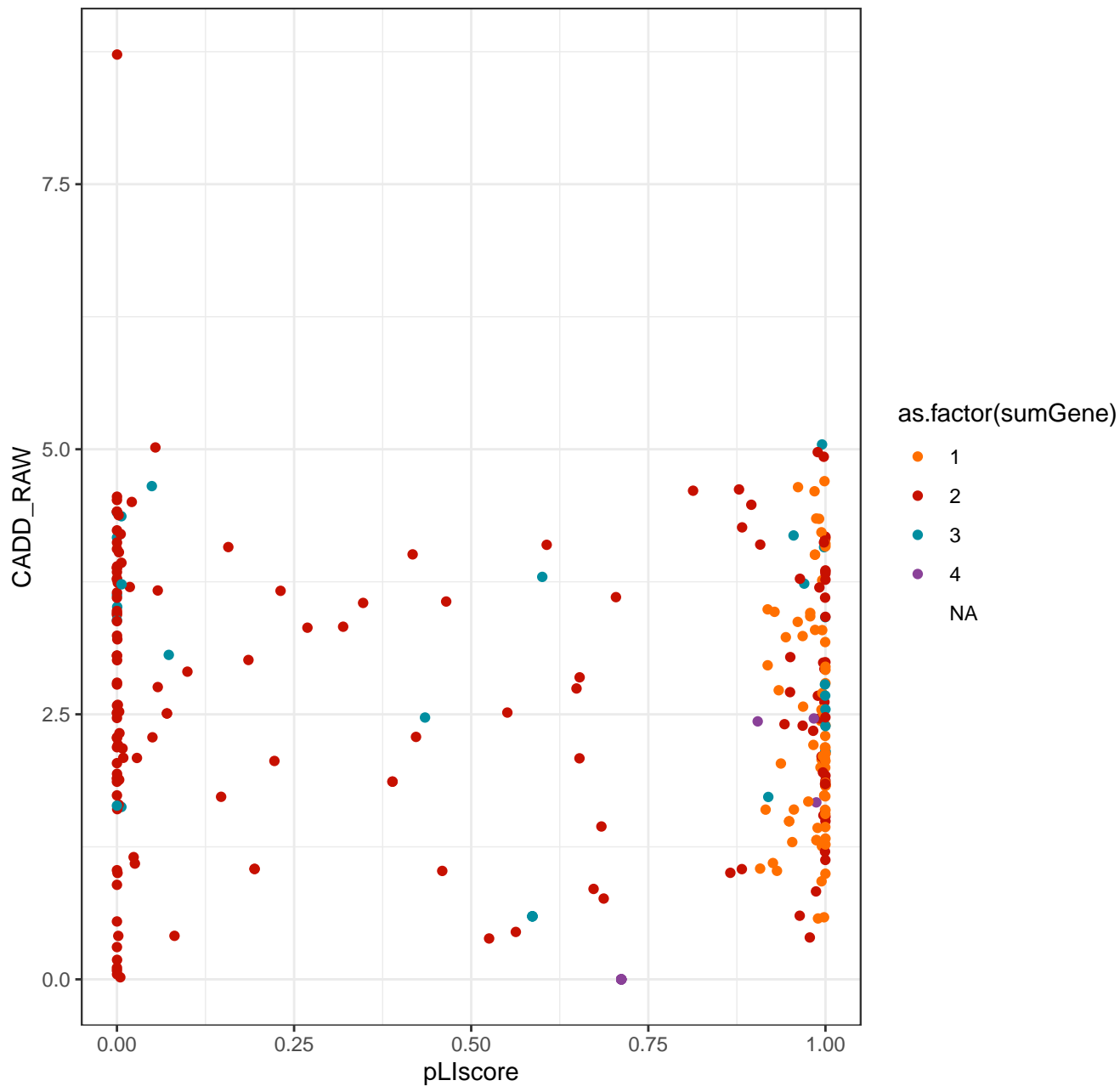
GREP – CADD



GREP – pLI

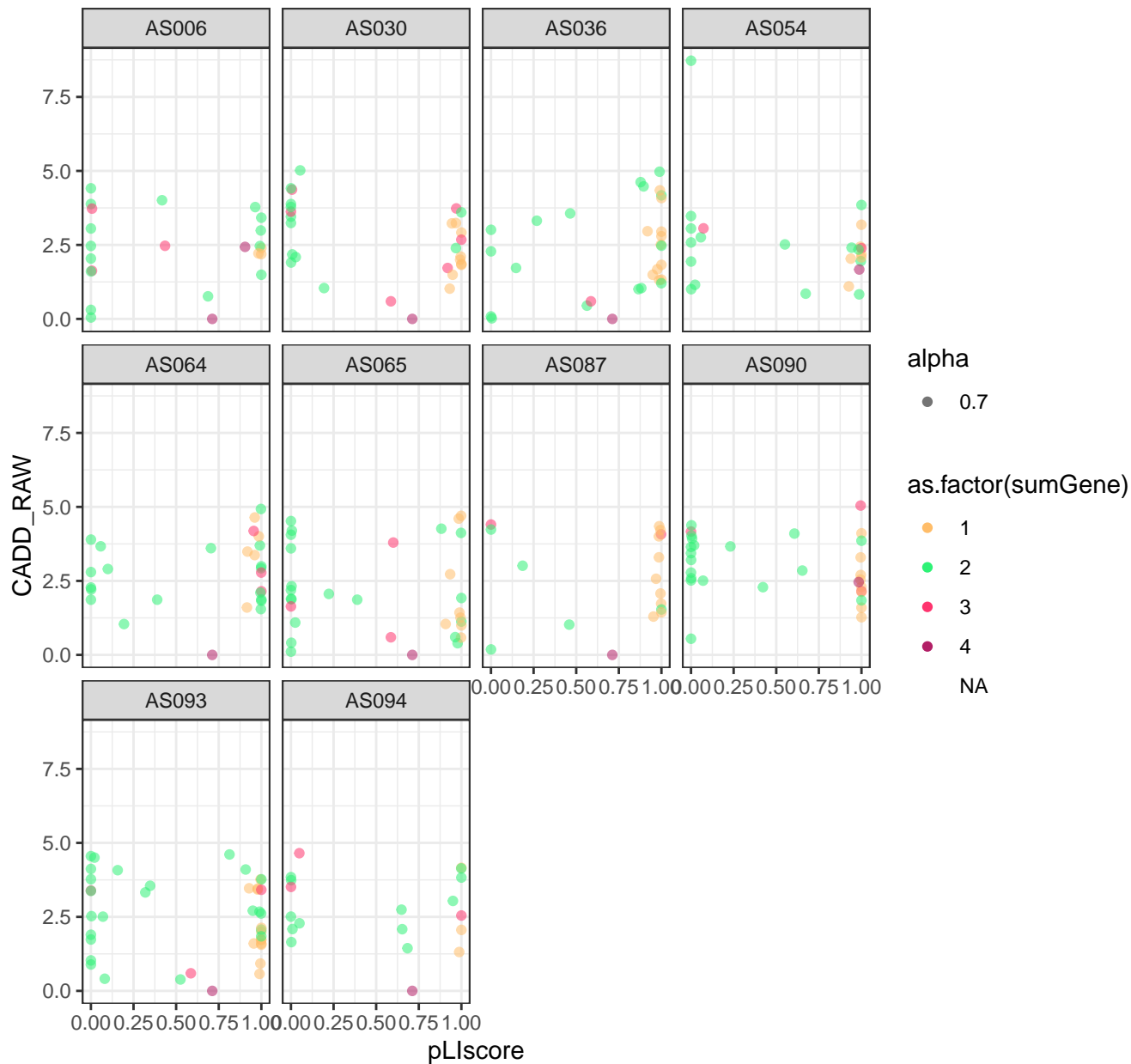


GREP – pLI CADD sumGene



GREPpLI, CADD, gene lists

unique sites with data =331



GREP – Genes shared among samples

HIGH

MODERATE

genes

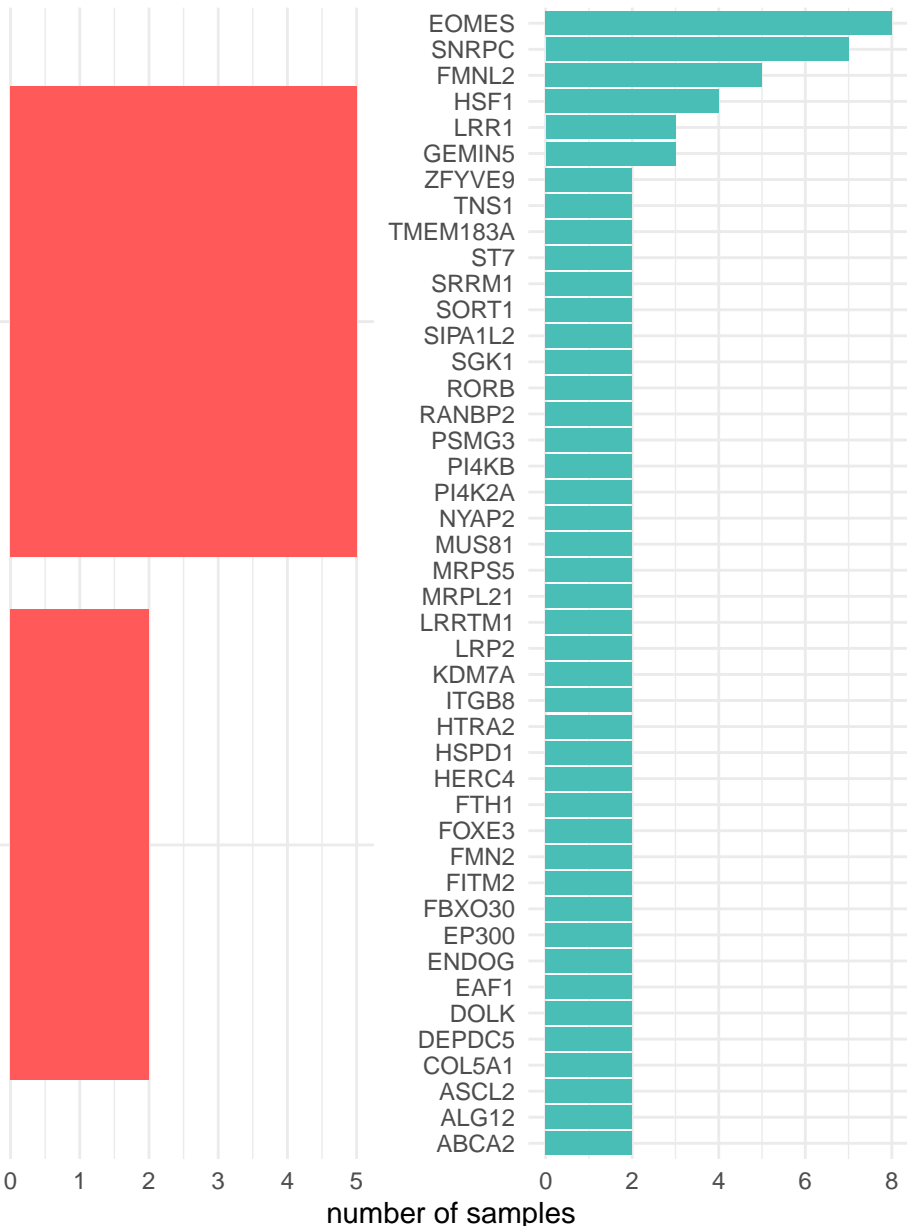
IMPACT

HIGH

MODERATE

FMNL2

FRMPD3



number of samples

GREP – Genes shared among samples

HIGH

MODERATE

genes

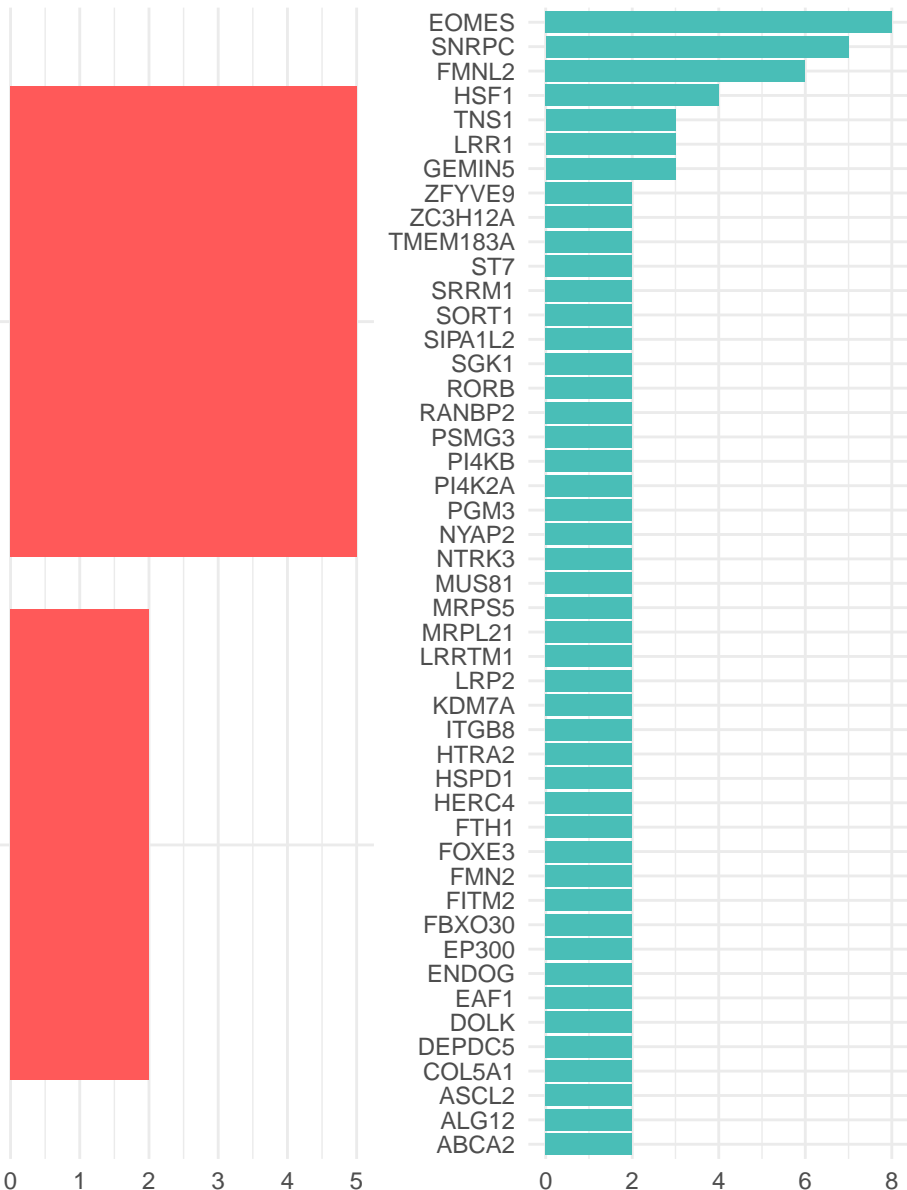
IMPACT

HIGH

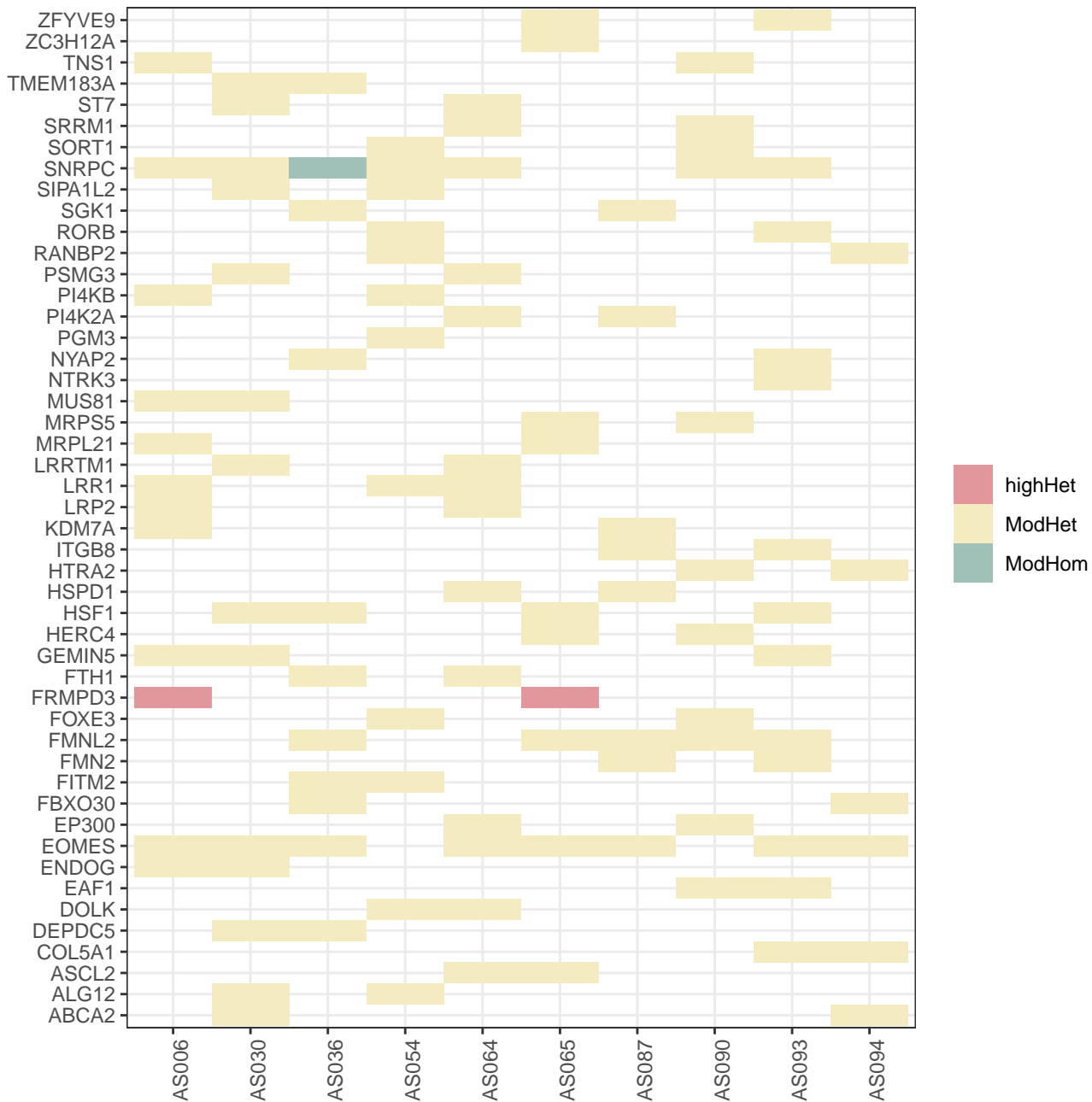
MODERATE

FMNL2

FRMPD3



number of samples



YY1	ZNF750	VPS16	SUZ12	ZNF638	TUT7	ZNHIT6	ZBED4	UTP25
YIPF5	WDR24	TSG101		XPOT		ZEB1	XRN2	
UBR3	WBP11	TRAPPC11	SRGAP1	XPNPEP3	TBC1D22A	UFC1	VIRMA	SPI1
		TMEM131L	SP1	WDR75		TRIM33	USP25	
STAG2	TRAPPC11	SACM1L	SNRPA1	UBE3C	SPEG	SYDE1	UMPS	SOS1
SRF	TLE4	RRS1		TUBGCP4		SOX13	TULP4	
SLAIN1	TGFB2	RNF4	SLC13A4	TTI2	SNX13	SLC33A1	TTF1	SDHB
SDF2L1	SULF2	RCC1L	SENP6	TRIM46		RASA1	SURF6	
		POLR3H		TOMM40	RFC2	RACGAP1	SIK2	RXYLT1
RAN	SLIT2	PIM3	SEL1L	TFPI	RAB11FIP2	PPAT	RYL2	
POGK	SLC4A4	PEX5	SCUBE1	SOS2		PLXNA3	RTL9	PPP1CA
		PAX8		SEN2	PTPMT1	PEX3	RSPRY1	
PHF12	SLC35C1	NOL4	PSME3IP1	RBM19		OPA1	RHOT1	PNISR
PEX12	SEMA4C	NFYC	PRPF18	RAPGEF6	PRR14L	OBSL1	RFWD3	
		NFAT5		RAD1		MTERF3	PSAP	PLAA
PAFAH1B1	SCN1A	NCAPD3	PLOD1	RAB21	PAK3	MOGS	POLR1E	
		MRPL18	PHC1	PPCS		MLLT3	PHF21A	PKN2
NELL2	RTN4RL2	MMP14	NR5A2	PPARGC1B	MEGF10	MED30	NPR3	
MRPS10	ROR2	MED17	MGAT2	PLEKHA6		MARK4	MYBL1	PIK3CD
		MARCHF6		OPN1LW	L1CAM	LRP1B	MED24	
MBD3	PREP	LYL1	MAP3K12	MTMR3		KIF22	MBD2	PHF21B
		LRP12	KANSL3	MRPS34	HCN1	INTS4	LSG1	
MAP2	PPP6R1	IPO11		MRPL53	GID4	IDH3A	INTS5	NCAPH2
MAN1A2	PCDH11X	ECE1	GRM3	METTL17		HOXD9	INTS13	
		HECW2	DCLK1	MED24	ECE1	GGA1	IL25	MED19
FUT7	NDUFB7	DGP2		LNPEP	DDHD1	DIP2B	HK2	
FOXA1	MAP2K4	DBN1	COQ2	LCP2		COQ5	GJB5	FLVCR2
		CELSR1		IGF2R	COPG1	CCDC22	GDF3	
FLAD1	IKZF3	BNIP1		IL3		ATF7IP	GBF1	EML1
		BBS4		HAUS3	CDC6	CCDC22	DVL1	
ELMO1	HES3	ARHGAP21		GTPBP4		ATANKD1	DHX35	DNLZ
		AC008695.1		HAUS3			COX19	
ECEL1	ESCO1			GNL2			CMPK1	DLST
CLSTN3	EPC2			GDA			CLUH	
CCDC6	EIF5B			FANCE			CLK3	CFAP298
				DYRK2			CFAP47	
BUB1	DDX20			DYNCL1I1			ATAD2B	CENPH
BORA	CRNKL1			COL4A5			ALAS1	
				CEBPZ			AGAP3	CACNA1I
BHLHE40	COL4A1			ARHGAP21			ADAMTS2	
				ALX1			ADAM22	ALG9
ASPM	ATP6V1F			AC008695.1			ACSL4	
AHCY	ATG4B						ABCF2	AFDN