

genes	chr	pos	ref	alt	worst_annotation	gnomad-exc	gnomad-ger	topmed	polyphen	sift
KLHDC4	16	87742977	A	G	synonymous_variant	0.0050395	0.0048534	0.0054393		
PIEZO1	16	88793220	G	A	missense_variant	0.0007943	0.0011321	0.0005654		
GALNS,TRAP	16	88923563	C	G	missense_variant	9.74E-06	0	0		

		l1.4	l1.4_gq	l1.4_dp	l1.2	l1.2_gq	l1.2_dp	l1.3	l1.3_gq	l1.3_dp	l1.2	l1.2_gq	l1.2_dp
muttaster	fathmm	G/G	99	38	G/G	99	39	G/G	99	45	A/G	99	45
disease_causing	tolerated	A/A	99	38	A/A	99	40	A/A	99	44	G/A	99	41
disease_causing	damaging	G/G	99	45	G/G	99	33	G/G	99	44	C/G	99	51

l.1	l.1_gq	l.1_dp
A/G	99	39
G/A	99	35
C/G	99	54