

Position in genome	Gene	Amino acid variant	Reference base	Variant base	Predicted effect	Cat 5	Cat 6
9246	nsp4	A231V	C	T	missense	0.109848	0.12967
11083	nsp6	L37F	G	T	missense	0.048263	0.0570735
13394	nsp10	K124E	A	G	missense	0.037975	0
15036	nsp12	K532N	A	C	missense	0.058824	0
15106	nsp12	T556P	A	C	missense	0.031782	0
15168	nsp12	L576L	G	A	synonymo us	0.045752	0
15940	nsp12	P834S	C	T	missense	0.057109	0.0478295
19983	nsp15	D124fs	C	CT	frameshift variant & stop gained	--	0.060126
21768	S	H69R	A	G	missense	1	0.9924445
23282	S	D574Y	G	T	missense	0.040634	0.0493335
23403	S	D614G	A	G	missense	0.989247	0.9833965