

NON_MUT1_CyHV3_ORF78	1	MAPHLRSRSL	TARHLTESRT	EGLSFHGQRP	DGTILAVDRG
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		MAPHLRSRSL	TARHLTESRT	EGLSFHGQRP	DGTILAVDRG
NON_MUT1_CyHV3_ORF78	41	RLLC <sup>+</sup> THADID	ELERTLLGSS	APVSHKDLVP	IYCDRCLPYT
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		RLLC <sup>+</sup> THADID	ELERTLLGSS	APVSHKDLVP	IYCDRCLPYT
NON_MUT1_CyHV3_ORF78	81	LPWSQAPVSH	DRDGLLPAHG	YTVVG <sup>+</sup> TAGVF	SRDLVETKGM
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		LPWSQAPVSH	DRDGLLPAHG	YTVVG <sup>+</sup> TAGVF	SRDLVETKGM
NON_MUT1_CyHV3_ORF78	121	EKTSQHYHLP	LRDLELFTHT	QKSNRVLLVH	CDIPIG <sup>+</sup> SVIC
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		EKTSQHYHLP	LRDLELFTHT	QKSNRVLLVH	CDIPIG <sup>+</sup> SVIC
NON_MUT1_CyHV3_ORF78	161	YWHVHDRENA	HCAVNALIVI	TDQAFHTIFS	RCKGLSWTTT
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		YWHVHDRENA	HCAVNALIVI	TDQAFHTIFS	RCKGLSWTTT
NON_MUT1_CyHV3_ORF78	201	SVVASELSLV	GIPGRASSLI	HSISRLSDLT	QGTLPVSRKP
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		SVVASELSLV	GIPGRASSLI	HSISRLSDLT	QGTLPVSRKP
NON_MUT1_CyHV3_ORF78	241	DLRSLGYGRN	SPRHADV <sup>+</sup> VMA	ALSKGTENPE	ETASDQREW
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		DLRSLGYGRN	SPRHADV <sup>+</sup> VMA	ALSKGTENPE	ETASDQREW
NON_MUT1_CyHV3_ORF78	281	KQMV <sup>+</sup> EMLMGQ	LDLLYEATIA	KGPDDDGQAS	KRYLSEGRDL
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		KQMV <sup>+</sup> EMLMGQ	LDLLYEATIA	KGPDDDGQAS	KRYLSEGRDL
NON_MUT1_CyHV3_ORF78	321	FKKLHELKAH	LEKLESASTP	AAVSAAAPAP	STSVPA <sup>+</sup> PQQT
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		FKKLHELKAH	LEKLESASTP	AAVSAAAPAP	STSVPA <sup>+</sup> PQQT
NON_MUT1_CyHV3_ORF78	361	TETPKEDSRA	GTPEASVTSQ	QAQSAPVPSQ	PVTSVPSQPV
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		TETPKEDSRA	GTPEASVTSQ	QAQSAPVPSQ	PVTSVPSQPV
NON_MUT1_CyHV3_ORF78	401	TSVPSPVTS	VPSQPVTSVP	SQPVTSVPSQ	PVTSVQQPNK
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		TSVPSPVTS	VPSQPVTSVP	SQPVTSVQQP	NKMASSDDIR
NON_MUT1_CyHV3_ORF78	441	MASSDDIRDA	VAKALADV <sup>+</sup> IK	PSIQQYTPPP	QPNHGGGATG
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		DAVAKALADV	IKPSIQQYTP	PPQPNHGGGA	TGFRDFVEMF
NON_MUT1_CyHV3_ORF78	481	FRDFVEMFKL	MQQM <sup>+</sup> HAPAQA	PAPVAAPAPV	VAQVPQSLSH
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		KLMQQMHAPA	QAPAPVAAPA	PVVAQVPQSL	SHHGLVDDEH
NON_MUT1_CyHV3_ORF78	521	HGLVDDEHPS	TSAHQ <sup>+</sup> RGGKR	KLELSDDDIK	LFKKLREQDE
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		PSTSAHQ <sup>+</sup> RGG	KRKLELSDDD	IKLFFKKLREQ	DELSRREKER
NON_MUT1_CyHV3_ORF78	561	LSRREKERLA	LKEELKKEMM	AEFSSSV <sup>+</sup> PQA	AAPVVVPSTS
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		LALKEELKKE	MMAEFSSSV <sup>+</sup> P	QAAAPVVVPS	TSAPAPVTDV
NON_MUT1_CyHV3_ORF78	601	APAPVTDVKQ	LVSEAIKELL	AVQQQQQQQA	VVPAPQGVPG
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		KQLVSEAIKE	LLAVQQQQQQ	QAVVPAPQGV	PGPATTISLP
NON_MUT1_CyHV3_ORF78	641	PATTISLPVA	TLAAATGRSP	AAAAALQSAI	NNVHESASQL
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		VATLAAATGR	SPAAAAALQS	AINNVHESAS	QLVPGGNLNG
NON_MUT1_CyHV3_ORF78	681	VPGGLNLGVA	GVPVNA <sup>+</sup> STVV	STPQPAVPST	STQVVSVSAG
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		VAGVPVNA <sup>+</sup> ST	VVSTPQPAVP	STSTQVVSVS	AGLEVQGGGN
NON_MUT1_CyHV3_ORF78	721	LEVQGGGNKK	SLNDDARKMM	MLMMDH*	
MUT1c1 NC_009127.1_cds_YP_001096113.1_77		KKSLNDDARK	MMMLMMDH*		