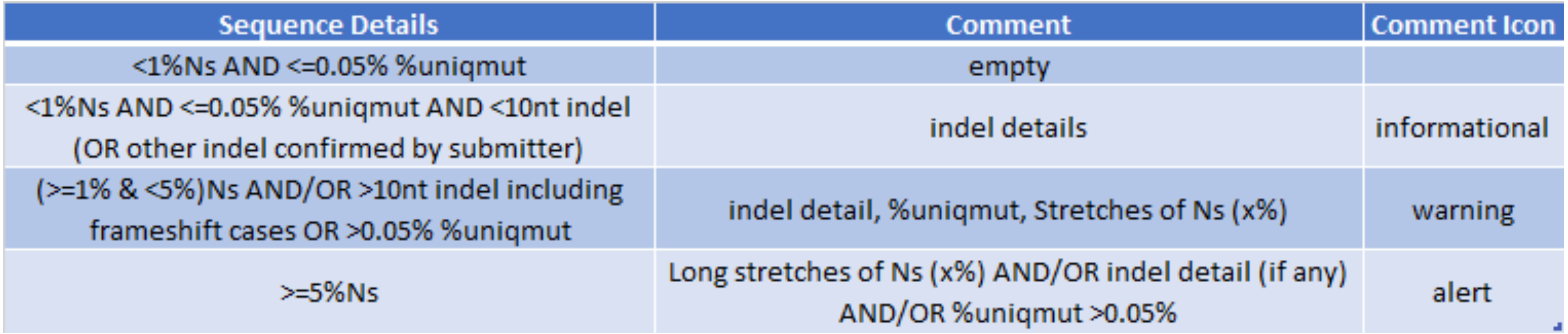
Inclusion Criteria

hCoV-19 genomes:

- Length >100 nucleotides;
- Stretches <50% of Ns

Sequences pending confirmation:

- Sequences with frameshift (nucleotide insertion, or deletions that are not dividable by three);
- Sequences with early STOP codon in the Spike, causing the truncation of the protein.



Sequence Details	Comment	Comment Icon	
<1%Ns AND <=0.05% %uniqmut	empty		
<1%Ns AND <=0.05% %uniqmut AND <10nt indel (OR other indel confirmed by submitter)	indel details	informational	ℹ
(>=1% & <5%)Ns AND/OR >10nt indel including frameshift cases OR >0.05% %uniqmut	indel detail, %uniqmut, Stretches of Ns (x%)	warning	◆
>=5%Ns	Long stretches of Ns (x%) AND/OR indel detail (if any) AND/OR %uniqmut >0.05%	alert	⚠

NOTE: the %uniqmut (% unique mutations) refers to those changes in the amino acid that have not been detected in more than two shared sequences. The threshold of 0.05% indicates 5 unique amino acid changes per genome.