**Supp. Table 3. Unique nucleotide (Nt) and predicted amino acid (AA) substitutions common to 15a MERS-CoV NRC-2015 genomes.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Genome regionb** | **Genome positionc** | **Nt substitution** | **AA substitution** |
| 3' UTR | 241 | C > T | non coding region |
| ORF1a | 750 | T > G | F158V |
| ORF1a | 2774 | T > C | syn |
| ORF1a | 6173 | T > C | syn |
| ORF1a | 6635 | G > T | M2119I |
| S | 21713 | T > C | syn |
| ORF5 | 27067 | G > T | syn |
| M | 28219 | T > A | F123I |
| M | 28290 | C > T | syn |

aNRC-2015 genomes obtained from humans in this study (KT806053, KT806052, KT806051, KT806048, KT806044, KT806054, KT806049, KT806045, KT806047, KT806046) and previously published (KT029139, KT006149, KT026453, KT026454, KT225476.2)

b3' UTR, 3' untranslated region; ORF 1a, replicase polyprotein; S, spike protein; ORF 5, accessory protein; M, matrix protein

cPosition numbering based on reference genome NC\_019843.3