

Supplementary Table 2 Polymorphic sites in the L segment of ANG0206 (KWAV)

| Position in the L segment | Location in the L segment | Change | Codon Change | Coverage | Protein Effect | Amino Acid* Change | Variant Frequency |
|---------------------------|---------------------------|---------|--------------|-----------|----------------|--------------------|-------------------|
| 91 | 5' end | T → C | - | 3548 | - | - | 34.1% |
| 673 | L gene | T → C | ACC → GCC | 1399 | Substitution | T → A | 46% |
| 790 | L gene | T → C | AGT → GGT | 1487 | Substitution | S → G | 39.5% |
| 890 | L gene | T → C | GAA → GAG | 1442 | None | - | 43.1% |
| 1297 | L gene | T → C | ATT → GTT | 2289 | Substitution | I → V | 38.4% |
| 1322-1323 | L gene | GG → AC | ACC → AGT | 2097-2108 | Substitution | T → S | 33.3% - 33.4% |
| 2160 | L gene | A → G | GTT → GCT | 2104 | Substitution | V → A | 35.9% |
| 2393 | L gene | G → A | TCC → TCT | 2467 | None | - | 33.8% |
| 3971 | L gene | G → A | CAC → CAT | 1758 | None | - | 28.4% |
| 4004 | L gene | G → A | TGC → TGT | 2457 | None | - | 37% |
| 4121 | L gene | C → T | CAG → CAA | 5400 | None | - | 37.5% |
| 4371 | L gene | T → C | AAA → AGA | 3751 | Substitution | K → R | 36.6% |
| 5687 | L gene | T → C | AAA → AAG | 387 | None | - | 39% |
| 6023 | L gene | C → T | GTG → GTA | 1604 | None | - | 41.6% |
| 6698 | L gene | G → A | GCC → GCT | 806 | None | - | 36.4% |

* A = Alanine, G = Glycine, I = Isoleucine, K = Lysine, R = Arginine, S = Serine, T = Threonine, V = Valine