

Skliros et al., 2023. Supplemental Table S4. Single Nucleotide Polymorphisms of resistant strain **VaAthena1_B** for each Contig separately. Tables show Nucleotide shift, position, change, polymorphism, type, variant frequency and in the case of a mutation in a CDS product, protein, effect and protein_id.

Contig 3

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------|----------|--------------------|-------------------|
| A | 2716 | 2716 | 1 | T -> A | 5 | SNP (transversion) | 40.00% |

Contig 6

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|----------|------------|--------------------|-------------------|
| AT | 49 | 50 | 2 | TC -> AT | 155 -> 156 | Substitution | 27.1% -> 27.6% |
| T | 52 | 52 | 1 | C -> T | 160 | SNP (transition) | 28.70% |
| T | 64 | 64 | 1 | A -> T | 183 | SNP (transversion) | 32.20% |

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|---|---------|-----|---|---|---------------------------|-------------------------|------------------------------|
| | | | | | | svers ion) | |
| T | 15 2 | 151 | 0 | | 23 6 | Inser tion | 39. 40 % |
| G | 15 5 | 155 | 1 | A -> G | 23 5 | SNP (tran sition) | 39. 10 % |
| TCA | 15 7 | 159 | 3 | ATT -> TCA | 23 0 - > 23 8 | Subs tituti on | 38. 7% -> 39. 6% |
| GT | 16 2 | 163 | 2 | TC -> GT | 22 6 - > 22 9 | Subs tituti on | 40. 2% -> 40. 7% |
| TTAAAATGGCTACGTAGCTCAGCTGGTTAG AGCACATCACTCATAATGATGGGGTCACAG GTTCGAATCCCGTCGTAGCCACCAT | 16 5 | 165 | 1 | A -> TTAAAATGGCTACGTAGCTCAGCTGGTTAG AGCACATCACTCATAATGATGGGGTCACAG GTTCGAATCCCGTCGTAGCCACCAT | 19 5 - > 22 3 | Inser tion | 30. 8% -> 38. 3% |
| A | 16 6 | 165 | 0 | | 18 9 | Inser tion | 31. 70 % |
| TT | 16 6 | 165 | 0 | | 18 1 - > 18 2 | Inser tion | 28. 7% -> 29. 1% |
| T | 16 6 | 165 | 0 | | 17 9 | Inser tion | 27. 90 % |

| | | | | | | | |
|----|-----|-----|---|----------|------------|--------------------|----------------|
| T | 166 | 165 | 0 | | 172 | Insertion | 25.00% |
| AA | 310 | 311 | 2 | CC -> AA | 142 -> 166 | Substitution | 30.3% -> 38.0% |
| T | 390 | 390 | 1 | C -> T | 186 | SNP (transition) | 54.80% |
| C | 397 | 397 | 1 | T -> C | 158 | SNP (transition) | 36.70% |
| C | 420 | 420 | 1 | T -> C | 351 | SNP (transition) | 51.00% |
| A | 428 | 428 | 1 | T -> A | 391 | SNP (transversion) | 46.50% |
| A | 436 | 436 | 1 | T -> A | 436 | SNP (transversion) | 48.60% |
| C | 437 | 437 | 1 | T -> C | 436 | SNP (transition) | 31.40% |

Contig 7

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|------|---------|---------|--------|--------|----------|--------------------|-------------------|-------------------------------|-------------------|-----------------------------|-------------------------|----------------|------------|
| C | 216879 | 216879 | 1 | T -> C | 418 | SNP (transition) | 41.40 % | 0 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |
| C | 216885 | 216885 | 1 | A -> C | 421 | SNP (transversion) | 40.60 % | 0 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |
| C | 216888 | 216888 | 1 | G -> C | 425 | SNP (transversion) | 41.20 % | 0 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |
| T | 216921 | 216921 | 1 | C -> T | 401 | SNP (transition) | 39.70 % | 0 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |
| T | 216924 | 216924 | 1 | C -> T | 399 | SNP (transition) | 39.30 % | 0 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |
| C | 216927 | 216927 | 1 | G -> C | 401 | SNP (transversion) | 38.90 % | 0 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |
| A | 216942 | 216942 | 1 | T -> A | 385 | SNP (transversion) | 33.80 % | 0 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |
| G | 216951 | 216951 | 1 | A -> G | 414 | SNP (transition) | 29.50 % | 4.0E-320 | | calcium-binding protein CDS | calcium-binding protein | None | KLI72868.1 |

Contig 13

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------|----------|-------------------|-------------------|
|------|---------|---------|--------|--------|----------|-------------------|-------------------|

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|---|--------|--------|---|--------|-----|---------------------|--------|
| A | 286321 | 286321 | 1 | G -> A | 483 | SNP (transition) | 32.10% |
|---|--------|--------|---|--------|-----|---------------------|--------|

Contig 14

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|------|---------|---------|--------|--------------|--------------|--------------------|-------------------|-------------------------------|-------------------|--------------------------|----------------------|----------------|------------|
| A | 7 | 7 | 1 | G -> A | 3598 | SNP (transition) | 38.20% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71769.1 |
| AATC | 10 | 13 | 3 | CACG -> AATC | 3499 -> 3602 | Substitution | 35.5% -> 35.9% | 0 | TV -> TI | hypothetical protein CDS | hypothetical protein | Substitution | KLI71769.1 |
| G | 22 | 22 | 1 | A -> G | 3473 | SNP (transition) | 41.70% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71769.1 |
| G | 31 | 31 | 1 | A -> G | 3465 | SNP (transition) | 81.70% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71769.1 |
| A | 34 | 34 | 1 | G -> A | 3491 | SNP (transition) | 81.90% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71769.1 |
| T | 52 | 52 | 1 | C -> T | 3543 | SNP (transition) | 37.80% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71769.1 |
| C | 55 | 55 | 1 | T -> C | 3588 | SNP (transition) | 37.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71769.1 |
| C | 61 | 61 | 1 | G -> C | 3620 | SNP (transversion) | 63.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71769.1 |

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|----|-----|-----|---|----------|---------------|------------------|-----------------|---|--------|--------------------------|----------------------|--------------|-------------|
| AC | 66 | 67 | 2 | GT -> AC | 3550 - > 3571 | Substitution | 63.4% - > 63.6% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71 769.1 |
| G | 73 | 73 | 1 | A -> G | 3569 | SNP (transition) | 63.50% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71 769.1 |
| C | 120 | 120 | 1 | T -> C | 805 | SNP (transition) | 54.30% | 0 | K -> E | hypothetical protein CDS | hypothetical protein | Substitution | KLI71 769.1 |
| C | 175 | 175 | 1 | T -> C | 578 | SNP (transition) | 49.70% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI71 769.1 |

Contig 15

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------------------------|---------|---------|--------|--|------------|--------------------|-------------------|
| C | 1 | 1 | 1 | A -> C | 169 | SNP (transversion) | 96.40% |
| ATATCAG | 4 | 10 | 7 | CATATCA -> ATATCAG | 169 -> 182 | Substitution | 87.4% -> 94.1% |
| ACG | 12 | 14 | 3 | GAC -> ACG | 183 | Substitution | 87.40% |
| TCAG | 17 | 20 | 4 | GTCA -> TCAG | 186 -> 190 | Substitution | 83.7% -> 85.5% |
| TA | 22 | 23 | 2 | GT -> TA | 193 | Substitution | 81.3% -> 82.4% |
| CATCACTGCTCGCTCTGTCTAT | 26 | 47 | 22 | ACATCACTGCTCGCTCTGTCTA -> CATCACTGCTCGCTCTGTCTAT | 191 -> 206 | Substitution | 70.4% -> 80.3% |
| CT | 49 | 50 | 2 | TC -> CT | 201 -> 203 | Substitution | 69.7% -> 70.9% |

| | | | | | | | |
|----------|-----|-----|---|----------------------|------------|--------------------|----------------|
| GTCTCATA | 52 | 59 | 8 | TGTCTCAT -> GTCTCATA | 191 -> 198 | Substitution | 63.6% -> 68.2% |
| C | 62 | 62 | 1 | A -> C | 197 | SNP (transversion) | 62.90% |
| GCTGA | 64 | 68 | 5 | CGCTG -> GCTGA | 199 -> 203 | Substitution | 59.1% -> 60.8% |
| CACAT | 70 | 74 | 5 | ACACA -> CACAT | 198 -> 201 | Substitution | 55.3% -> 58.7% |
| GA | 76 | 77 | 2 | TG -> GA | 205 | Substitution | 53.20% |
| G | 80 | 80 | 1 | A -> G | 205 | SNP (transition) | 53.20% |
| C | 82 | 82 | 1 | G -> C | 204 | SNP (transversion) | 52.00% |
| ATATA | 84 | 88 | 5 | CATAT -> ATATA | 198 -> 205 | Substitution | 48.8% -> 50.5% |
| CG | 92 | 93 | 2 | AC -> CG | 205 | Substitution | 47.30% |
| CTCAGTAC | 95 | 102 | 8 | GCTCAGTA -> CTCAGTAC | 213 -> 216 | Substitution | 43.5% -> 45.1% |
| A | 104 | 104 | 1 | C -> A | 216 | SNP (transversion) | 42.60% |
| CGT | 107 | 109 | 3 | ACG -> CGT | 211 -> 216 | Substitution | 39.3% -> 41.2% |
| GCACA | 111 | 115 | 5 | TGCAC -> GCACA | 213 -> 214 | Substitution | 37.9% -> 38.0% |
| G | 117 | 117 | 1 | A -> G | 216 | SNP (transition) | 38.00% |
| T | 119 | 119 | 1 | G -> T | 221 | SNP (transversion) | 37.10% |
| CTG | 121 | 123 | 3 | TCT -> CTG | 221 -> 222 | Substitution | 36.2% -> 36.5% |
| TG | 125 | 126 | 2 | GT -> TG | 222 | Substitution | 35.6% -> 36.0% |

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|----------|-----|-----|---|----------------------|------------|--------------------|----------------|
| CTGA | 128 | 131 | 4 | GCTG -> CTGA | 225 -> 228 | Substitution | 33.9% -> 35.1% |
| TCTCA | 133 | 137 | 5 | ATCTC -> TCTCA | 226 -> 233 | Substitution | 31.8% -> 33.3% |
| T | 139 | 139 | 1 | A -> T | 233 | SNP (transversion) | 31.80% |
| ACAC | 141 | 144 | 4 | TACA -> ACAC | 228 -> 232 | Substitution | 30.3% -> 31.2% |
| ATCGCACT | 146 | 153 | 8 | CATCGCAC -> ATCGCACT | 221 -> 226 | Substitution | 24.9% -> 27.6% |

Contig 16

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|------|---------|---------|--------|--------------------------|------------|--------------------------|-------------------|-------------------------------|-------------------|-----------------------------|-------------------------|----------------|------------|
| | 50291 | 50296 | 6 | (CAGAGC)14 -> (CAGAGC)13 | 361 -> 362 | Deletion (tandem repeat) | 98.9% -> 99.2% | 0 | AE P -> A | chemotaxis protein CheW CDS | chemotaxis protein CheW | Deletion | KLI71480.1 |

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|------------|-----------|-----------|---|-------------------------------------|------------------|---------------------------------|----------------------|---|-------------|-----------------------------------|-------------------------------|---------------|--------------------|
| GCC AGA | 5037 9 | 5037 8 | 0 | (CAGAGC)1 4 -> (CAGAGC)1 5 | 361 -> 368 | Insertion (tandem repeat) | 92.8% -> 92.9% | 0 | E -> EPE | chemotaxis protein CheW CDS | chemotaxis protein CheW | Inse rtion | KLI7 1480. 1 |
|------------|-----------|-----------|---|-------------------------------------|------------------|---------------------------------|----------------------|---|-------------|-----------------------------------|-------------------------------|---------------|--------------------|

Contig 17

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|-------------|---------------|-----------------------|----------------------|
| G | 22 | 22 | 1 | A -> G | 165 | SNP (transition) | 41.20% |
| A | 36 | 36 | 1 | G -> A | 164 | SNP (transition) | 35.40% |
| C | 72 | 73 | 2 | AT -> C | 163 -> 166 | Deletion | 30.7% -> 31.3% |
| A | 216849 | 216848 | 0 | | 98 | Insertion | 83.70% |
| T | 216850 | 216850 | 1 | A -> T | 92 | SNP (transversion) | 89.10% |
| | 216856 | 216857 | 2 | | 357 -> 366 | Deletion | 53.3% -> 54.6% |
| A | 216861 | 216861 | 1 | T -> A | 357 | SNP (transversion) | 38.70% |
| C | 216862 | 216862 | 1 | T -> C | 354 | SNP (transition) | 54.00% |
| T | 216864 | 216864 | 1 | G -> T | 354 | SNP (transversion) | 60.50% |
| T | 216866 | 216866 | 1 | G -> T | 359 | SNP (transversion) | 53.50% |
| T | 216868 | 216868 | 1 | C -> T | 364 | SNP (transition) | 53.00% |
| GA | 216871 | 216872 | 2 | TT -> GA | 345 -> 348 | Substitution | 52.8% -> 53.2% |
| AA | 216875 | 216875 | 1 | C -> AA | 329 -> 337 | Insertion | 46.6% -> 46.8% |
| T | 216878 | 216878 | 1 | C -> T | 329 | SNP (transition) | 47.10% |
| G | 216882 | 216882 | 1 | T -> G | 307 | SNP (transversion) | 49.80% |

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|---|--------|--------|---|--------|-----|-----------------------|--------|
| C | 216946 | 216946 | 1 | A -> C | 213 | SNP (transversion) | 34.30% |
| | 216955 | 216955 | 1 | | 196 | Deletion | 26.50% |
| A | 216958 | 216958 | 1 | T -> A | 189 | SNP (transversion) | 27.50% |
| G | 217109 | 217109 | 1 | A -> G | 172 | SNP (transition) | 78.50% |

Contig 18

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|-----------------|----------|-----------------------|----------------------|
| A | 306 | 306 | 1 | C -> A | 183 | SNP (transversion) | 25.70% |
| A | 308 | 308 | 1 | G -> A | 184 | SNP (transition) | 25.00% |
| GTAG | 311 | 314 | 4 | TCTT -> GTAG | 187 | Substitution | 25.70% |

Contig 19

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|-----------------|---------|---------|--------|---------------------------------------|---------------|-----------------------|----------------------|
| GC | 96 | 97 | 2 | CA -> GC | 162 -> 163 | Substitution | 25.8% -> 25.9% |
| A | 99 | 99 | 1 | T -> A | 168 | SNP (transversion) | 29.80% |
| T | 197 | 197 | 1 | C -> T | 143 | SNP (transition) | 28.70% |
| CATTGTTATATCTCA | 200 | 214 | 15 | GCGGAGGCACATATT -> CATTGTTATATCTCA | 112 -> 134 | Substitution | 25.9% -> 30.2% |

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|--------|-----|-----|---|------------------|---------------|--------------|-------------------|
| AAGAGA | 216 | 221 | 6 | CGTTTT -> AAGAGA | 103 -> 112 | Substitution | 25.2% -> 26.9% |
|--------|-----|-----|---|------------------|---------------|--------------|-------------------|

Contig 23

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|-------|---------|---------|--------|-------------------|---------------|-----------------------|-------------------|
| CT | 2 | 3 | 2 | TA -> CT | 270 -> 271 | Substitution | 41.7% -> 41.9% |
| T | 6 | 6 | 1 | G -> T | 278 | SNP (transversion) | 57.20% |
| T | 68 | 68 | 1 | G -> T | 145 | SNP (transversion) | 53.80% |
| C | 70 | 70 | 1 | T -> C | 145 | SNP (transition) | 53.80% |
| GTT | 72 | 74 | 3 | TGC -> GTT | 145 | Substitution | 53.80% |
| C | 78 | 78 | 1 | A -> C | 147 | SNP (transversion) | 62.60% |
| T | 79 | 79 | 1 | A -> T | 147 | SNP (transversion) | 53.10% |
| T | 80 | 80 | 1 | G -> T | 147 | SNP (transversion) | 62.60% |
| GC | 82 | 83 | 2 | TT -> GC | 147 -> 148 | Substitution | 52.7% -> 53.1% |
| CAAAA | 85 | 89 | 5 | TCTCT -> CAAAA | 147 -> 148 | Substitution | 52.0% -> 52.4% |
| GGA | 92 | 94 | 3 | AAG -> GGA | 150 | Substitution | 51.30% |
| C | 98 | 102 | 5 | AGGTG -> C | 150 -> 155 | Deletion | 50.3% -> 52.0% |
| T | 107 | 107 | 1 | C -> T | 156 | SNP (transition) | 58.30% |
| G | 114 | 114 | 1 | T -> G | 160 | SNP (transversion) | 48.80% |
| A | 118 | 118 | 1 | G -> A | 160 | SNP (transition) | 48.10% |

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|--------|-----|-----|---|---------------------|---------------|-----------------------|-------------------|
| A | 119 | 119 | 1 | T -> A | 160 | SNP (transversion) | 56.90% |
| G | 120 | 120 | 1 | T -> G | 160 | SNP (transversion) | 47.50% |
| T | 121 | 121 | 1 | G -> T | 160 | SNP (transversion) | 56.90% |
| T | 132 | 132 | 1 | A -> T | 150 | SNP (transversion) | 44.70% |
| C | 142 | 141 | 0 | +C | 131 | Insertion | 36.60% |
| TTC | 147 | 149 | 3 | AAT -> TTC | 123 -> 124 | Substitution | 39.8% -> 40.3% |
| CAA | 152 | 154 | 3 | TTT -> CAA | 114 -> 121 | Substitution | 33.3% -> 36.4% |
| CGTTTC | 156 | 161 | 6 | TAGAAG -> CGTTTC | 93 -> 106 | Substitution | 29.1% -> 31.2% |
| GC | 163 | 164 | 2 | TT -> GC | 90 -> 92 | Substitution | 26.7% -> 28.3% |
| G | 167 | 167 | 1 | T -> G | 86 | SNP (transversion) | 26.70% |

Contig 27

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | CDS | product | Protein Effect | protein_id | Amino Acid Change |
|--|---------|---------|--------|---|------------------|------------------------------|-------------------|--------------------------------|-------------------------|----------------|------------|-------------------------------|
| GCAACAGCAACAGCAACA GCAACAGCAACAGCAACA | 27340 | 27339 | 0 | (AACAGCAAC AGCAACAGC) 4 -> (AACAGCAAC AGCAACAGC) 6 | 114 -> 188 | Insertion (tandem repeat) | 86.4% -> 88.8% | hypothetical protein CDS | hypothetical protein | Insertion | KLI70436.1 | Q -> QQQQQQ QQQQQQ Q |

Contig 28

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | CDS | product | Protein Effect | protein_id |
|------|---------|---------|--------|--------|----------|--------------------|-------------------|-------------------------------|-----------------------------|-------------------------|----------------|-------------|
| G | 10120 | 10120 | 1 | T -> G | 1011 | SNP (transversion) | 47.50 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| C | 10129 | 10129 | 1 | G -> C | 987 | SNP (transversion) | 72.70 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| T | 10145 | 10145 | 1 | C -> T | 955 | SNP (transition) | 55.70 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| C | 10153 | 10153 | 1 | T -> C | 962 | SNP (transition) | 58.60 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| T | 10159 | 10159 | 1 | C -> T | 991 | SNP (transition) | 61.00 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| A | 10204 | 10204 | 1 | C -> A | 879 | SNP (transversion) | 33.90 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| C | 10273 | 10273 | 1 | T -> C | 992 | SNP (transition) | 43.00 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |

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|---|-------|-------|---|--------|------|-------------------------|------------|---|-----------------------------------|----------------------------|--------------|----------------|
| G | 10282 | 10282 | 1 | C -> G | 1005 | SNP (transversion) | 43.20 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| T | 10322 | 10322 | 1 | G -> T | 1026 | SNP (transversion) | 27.10 % | 0 | calcium-binding protein CDS | calcium-binding protein | Substitution | KLI704 16.1 |
| T | 10351 | 10351 | 1 | A -> T | 998 | SNP (transversion) | 35.70 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| T | 10360 | 10360 | 1 | C -> T | 1003 | SNP (transition) | 28.60 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| A | 10369 | 10369 | 1 | G -> A | 976 | SNP (transition) | 41.70 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| A | 10387 | 10387 | 1 | G -> A | 1003 | SNP (transition) | 41.30 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| C | 10396 | 10396 | 1 | T -> C | 1084 | SNP (transition) | 45.20 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| G | 10405 | 10405 | 1 | C -> G | 1056 | SNP (transversion) | 56.30 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |
| G | 10414 | 10414 | 1 | A -> G | 1050 | SNP (transition) | 34.50 % | 0 | calcium-binding protein CDS | calcium-binding protein | None | KLI704 16.1 |

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|-----|-------|-------|---|---------------|---------------------|---------------------------|----------------------|---|---------------------------------------|--------------------------------|------------------|----------------|
| T | 10429 | 10429 | 1 | C -> T | 1067 | SNP (transition) | 39.60 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| T | 10432 | 10432 | 1 | C -> T | 1069 | SNP (transition) | 27.50 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| GT | 10434 | 10435 | 2 | CG -> GT | 1067 - > 1069 | Substituti on | 32.7% -> 32.9% | 0 | calcium- binding protein CDS | calcium- binding protein | Substitu tion | KLI704 16.1 |
| G | 10441 | 10441 | 1 | A -> G | 1072 | SNP (transition) | 71.70 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| C | 10444 | 10444 | 1 | A -> C | 1099 | SNP (transvers ion) | 47.10 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| T | 10444 | 10444 | 1 | A -> T | 1099 | SNP (transvers ion) | 26.10 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| C | 10447 | 10447 | 1 | T -> C | 1104 | SNP (transition) | 26.30 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| ACC | 10481 | 10483 | 2 | TCA -> ACC | 1012 - > 1022 | Substituti on | 49.6% -> 50.1% | 0 | calcium- binding protein CDS | calcium- binding protein | Substitu tion | KLI704 16.1 |
| C | 10486 | 10486 | 1 | T -> C | 997 | SNP (transition) | 43.50 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |

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|----------------|-------|-------|---|-------------------------------------|-------------|---------------------------|----------------------|---------------|---------------------------------------|--------------------------------|------------------|----------------|
| C | 10498 | 10498 | 1 | T -> C | 967 | SNP (transition) | 72.00 % | 0 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| A | 10534 | 10534 | 1 | G -> A | 63 | SNP (transition) | 87.30 % | 3.90E- 167 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| C | 10540 | 10540 | 1 | T -> C | 54 | SNP (transition) | 90.70 % | 1.00E- 165 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| T | 10546 | 10546 | 1 | C -> T | 45 | SNP (transition) | 80.00 % | 8.80E- 118 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |
| AG | 10549 | 10550 | 2 | GT -> AG | 33 -> 34 | Substituti on | 36.4% -> 38.2% | 2.90E-37 | calcium- binding protein CDS | calcium- binding protein | Substitu tion | KLI704 16.1 |
| AGCGGA AACG | 10549 | 10558 | 9 | GTCCACT GTT -> AGCGGA AACG | 21 -> 34 | Substituti on | 29.4% -> 43.5% | 8.00E-18 | calcium- binding protein CDS | calcium- binding protein | Substitu tion | KLI704 16.1 |
| G | 10564 | 10564 | 1 | C -> G | 23 | SNP (transvers ion) | 34.80 % | 1.20E-16 | calcium- binding protein CDS | calcium- binding protein | None | KLI704 16.1 |

Contig 29

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------|----------|----------------------|----------------------|
| G | 133 | 133 | 1 | A -> G | 227 | SNP (transition) | 36.60% |

| | | | | | | | |
|------|-----|-----|----|--------------|------------|--------------------|----------------|
| T | 135 | 135 | 1 | A -> T | 233 | SNP (transversion) | 35.60% |
| T | 137 | 136 | 0 | | 221 | Insertion | 27.60% |
| T | 141 | 141 | 1 | C -> T | 207 | SNP (transition) | 30.00% |
| T | 142 | 142 | 1 | C -> T | 206 | SNP (transition) | 40.30% |
| C | 143 | 143 | 1 | T -> C | 206 | SNP (transition) | 53.90% |
| C | 145 | 145 | 1 | T -> C | 207 | SNP (transition) | 52.70% |
| CG | 147 | 148 | 2 | TC -> CG | 208 -> 210 | Substitution | 29.5% -> 29.8% |
| A | 151 | 151 | 1 | G -> A | 206 | SNP (transition) | 39.30% |
| C | 154 | 154 | 1 | T -> C | 206 | SNP (transition) | 41.70% |
| C | 165 | 165 | 1 | A -> C | 186 | SNP (transversion) | 37.10% |
| T | 168 | 168 | 1 | G -> T | 170 | SNP (transversion) | 53.50% |
| A | 250 | 250 | 1 | T -> A | 147 | SNP (transversion) | 51.70% |
| AG | 252 | 253 | 2 | TT -> AG | 146 | Substitution | 51.40% |
| TCTC | 255 | 258 | 4 | ATAA -> TCTC | 144 -> 150 | Substitution | 48.0% -> 50.0% |
| C | 260 | 260 | 1 | T -> C | 148 | SNP (transition) | 47.30% |
| GT | 262 | 263 | 2 | AA -> GT | 144 -> 145 | Substitution | 46.5% -> 46.9% |
| C | 265 | 265 | 1 | G -> C | 140 | SNP (transversion) | 48.60% |
| | 266 | 279 | 14 | | 137 -> 161 | Deletion | 33.5% -> 39.4% |
| T | 281 | 281 | 1 | C -> T | 157 | SNP (transition) | 46.50% |
| GT | 286 | 287 | 2 | AA -> GT | 169 -> 172 | Substitution | 44.8% -> 45.6% |
| C | 290 | 290 | 1 | T -> C | 179 | SNP (transition) | 43.60% |
| AC | 291 | 292 | 2 | GA -> AC | 181 | Substitution | 51.40% |
| AT | 294 | 295 | 2 | GC -> AT | 194 -> 195 | Substitution | 37.9% -> 38.1% |

| | | | | | | | |
|--|-----|-----|---|--|-----|----------|--------|
| | 298 | 299 | 2 | | 212 | Deletion | 35.80% |
|--|-----|-----|---|--|-----|----------|--------|

Contig 31

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|--------|---------|---------|--------|--------------------------------|-------------------|------------------------------|-------------------|-------------------------------|-------------------|--------------------------------------|-------------------------------|----------------|------------|
| | 16050 | 16055 | 6 | (TCTGCT)11 -> (TCTGCT)10 | 775 | Deletion (tandem repeat) | 99.00% | 0 | EA E -> E | cell division protein FtsY CDS | cell division protein FtsY | Deletion | KLI70360.1 |
| TCTGCT | 16116 | 16115 | 0 | (TCTGCT)11 -> (TCTGCT)12 | 812 - > 826 | Insertion (tandem repeat) | 95.00% | 0 | P -> PAE | cell division protein FtsY CDS | cell division protein FtsY | Insertion | KLI70360.1 |

Contig 34

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|------|---------|---------|--------|-----------|----------|---------------------|-------------------|-------------------------------|-------------------|-------------------------------|------------------------|----------------|------------|
| G | 3957 | 3957 | 1 | A -> G | 186 | SNP (transition) | 52.70% | 6.80E-299 | | nucleoside permease CDS | nucleoside permease | None | KLI70272.1 |

| | | | | | | | | | | | | | |
|----|------|------|---|--------------|---------------|---------------------------|--------------------|-----------|--------------|------------------------------------|--------------------------------|------------------|----------------|
| AT | 3996 | 3997 | 2 | GC - > AT | 156 -> 157 | Substitutio n | 50.0% - > 50.3% | 1.10E-234 | RH - > RY | nucleosi de permeas e CDS | nucleosi de permeas e | Substitut ion | KLI7027 2.1 |
| G | 4024 | 4024 | 1 | T -> G | 138 | SNP (transversi on) | 43.50% | 7.20E-177 | E -> D | nucleosi de permeas e CDS | nucleosi de permeas e | Substitut ion | KLI7027 2.1 |
| A | 7429 | 7429 | 1 | G -> A | 162 | SNP (transition) | 25.30% | 1.10E-109 | | | | | |
| A | 7436 | 7436 | 1 | T -> A | 161 | SNP (transversi on) | 26.10% | 1.50E-104 | | | | | |
| AA | 7441 | 7442 | 2 | CG - > AA | 158 | Substitutio n | 27.20% | 3.20E-112 | | | | | |
| A | 7444 | 7444 | 1 | C -> A | 160 | SNP (transversi on) | 26.90% | 6.00E-112 | | | | | |
| G | 7448 | 7448 | 1 | T -> G | 163 | SNP (transversi on) | 26.40% | 7.60E-116 | | | | | |
| A | 7454 | 7454 | 1 | C -> A | 164 | SNP (transversi on) | 26.80% | 1.80E-114 | | | | | |
| T | 7474 | 7474 | 1 | G -> T | 159 | SNP (transversi on) | 30.20% | 1.30E-127 | | | | | |
| A | 7486 | 7486 | 1 | G -> A | 163 | SNP (transition) | 31.90% | 3.40E-129 | | | | | |

Contig 38

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------|----------|----------------------|----------------------|
| G | 22 | 22 | 1 | A -> G | 212 | SNP (transition) | 31.10% |

| | | | | | | | |
|------|----|----|---|-----------------|---------------|-----------------------|-------------------|
| G | 30 | 31 | 2 | AA -> G | 195 -> 198 | Deletion | 26.7% -> 27.3% |
| TGCT | 35 | 38 | 4 | AATC -> TGCT | 186 -> 193 | Substitution | 25.3% -> 27.1% |
| C | 41 | 41 | 1 | G -> C | 184 | SNP (transversion) | 25.50% |

Contig 40

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------|----------|-----------------------|----------------------|
| C | 66081 | 66081 | 1 | G -> C | 178 | SNP (transversion) | 43.30% |
| G | 66087 | 66087 | 1 | A -> G | 176 | SNP (transition) | 43.80% |
| A | 66092 | 66092 | 1 | G -> A | 175 | SNP (transition) | 44.00% |
| T | 66114 | 66114 | 1 | C -> T | 169 | SNP (transition) | 45.60% |

Contig 46

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|-----------------|---------------|-----------------------|----------------------|
| A | 1999 | 1999 | 1 | C -> A | 248 | SNP (transversion) | 31.50% |
| G | 2012 | 2012 | 1 | A -> G | 247 | SNP (transition) | 27.50% |
| GCCC | 2599 | 2602 | 4 | ATTT -> GCCC | 359 -> 365 | Substitution | 25.6% -> 26.0% |
| T | 2604 | 2604 | 1 | C -> T | 360 | SNP (transition) | 26.10% |
| AGT | 2607 | 2609 | 3 | CTG -> AGT | 362 -> 384 | Substitution | 26.2% -> 27.8% |
| A | 2616 | 2616 | 1 | G -> A | 380 | SNP (transition) | 27.40% |
| T | 2619 | 2619 | 1 | A -> T | 365 | SNP (transversion) | 28.50% |

Contig 49

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|------|---------|---------|--------|----------|------------|--------------------|-------------------|-------------------------------|-------------------|--------------------------|----------------------|----------------|------------|
| C | 8 | 8 | 1 | G -> C | 1375 | SNP (transversion) | 25.20% | 0 | D -> E | hypothetical protein CDS | hypothetical protein | Substitution | KLI70043.1 |
| A | 53 | 53 | 1 | G -> A | 894 | SNP (transition) | 32.90% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| G | 59 | 59 | 1 | A -> G | 853 | SNP (transition) | 29.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| G | 62 | 62 | 1 | A -> G | 828 | SNP (transition) | 27.50% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| GA | 73 | 74 | 2 | AG -> GA | 801 -> 803 | Substitution | 25.6% - 25.8% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| G | 101 | 101 | 1 | A -> G | 971 | SNP (transition) | 41.50% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| CA | 109 | 110 | 2 | TC -> CA | 938 -> 945 | Substitution | 38.0% - 38.1% | 0 | AI -> AV | hypothetical protein CDS | hypothetical protein | Substitution | KLI70043.1 |
| G | 113 | 113 | 1 | C -> G | 913 | SNP (transversion) | 37.60% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| A | 116 | 116 | 1 | G -> A | 886 | SNP (transition) | 37.10% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |

| | | | | | | | | | | | | | |
|----------|-----|-----|---|--------------------|---------------------|---------------------------|--------------------|---|-----------------|-----------------------------|--------------------------|------------------|----------------|
| CTT | 121 | 123 | 3 | TGG - -> CTT | 824 -> 854 | Substituti on | 34.6% - > 35.7% | 0 | TN - > KD | hypothetical protein CDS | hypothetica l protein | Substit ution | KLI70 043.1 |
| T | 125 | 125 | 1 | C -> T | 821 | SNP (transition) | 34.70% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| G | 143 | 143 | 1 | C -> G | 810 | SNP (transvers ion) | 31.40% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| T | 348 | 348 | 1 | C -> T | 1711 | SNP (transition) | 69.10% | 0 | G -> D | hypothetical protein CDS | hypothetica l protein | Substit ution | KLI70 043.1 |
| A | 374 | 374 | 1 | G -> A | 1683 | SNP (transition) | 69.20% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| C | 386 | 386 | 1 | T -> C | 1652 | SNP (transition) | 70.30% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| T | 392 | 392 | 1 | G -> T | 2218 | SNP (transvers ion) | 77.50% | 0 | N -> K | hypothetical protein CDS | hypothetica l protein | Substit ution | KLI70 043.1 |
| A | 395 | 395 | 1 | G -> A | 2213 | SNP (transition) | 65.70% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| A | 407 | 407 | 1 | G -> A | 2124 | SNP (transition) | 33.40% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| C | 413 | 413 | 1 | T -> C | 2099 | SNP (transition) | 75.10% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| T | 416 | 416 | 1 | A -> T | 2039 | SNP (transvers ion) | 64.00% | 0 | | hypothetical protein CDS | hypothetica l protein | None | KLI70 043.1 |
| CGC T | 419 | 422 | 3 | GGTA -> CGCT | 1939 - > 4249 | Substituti on | 17.7% - > 38.8% | 0 | VT - > VA | hypothetical protein CDS | hypothetica l protein | Substit ution | KLI70 043.1 |

| | | | | | | | | | | | | | |
|-----|-----|-----|---|------------|--------------|--------------------|----------------|---|----------|--------------------------|----------------------|--------------|------------|
| CT | 421 | 422 | 2 | TA -> CT | 1939 -> 4249 | Substitution | 27.1% -> 42.6% | 0 | VT -> VA | hypothetical protein CDS | hypothetical protein | Substitution | KLI70043.1 |
| T | 425 | 425 | 1 | C -> T | 4308 | SNP (transition) | 63.00% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| G | 428 | 428 | 1 | A -> G | 4275 | SNP (transition) | 82.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| C | 452 | 452 | 1 | T -> C | 3641 | SNP (transition) | 49.10% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| A | 455 | 455 | 1 | G -> A | 3646 | SNP (transition) | 37.20% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| A | 470 | 470 | 1 | G -> A | 3517 | SNP (transition) | 34.10% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| G | 473 | 473 | 1 | C -> G | 3509 | SNP (transversion) | 51.80% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| G | 479 | 479 | 1 | C -> G | 3482 | SNP (transversion) | 54.80% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| TAG | 482 | 484 | 2 | CAA -> TAG | 3410 -> 3426 | Substitution | 25.9% -> 26.0% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| G | 484 | 484 | 1 | A -> G | 3410 | SNP (transition) | 31.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |
| GGT | 485 | 487 | 2 | CGC -> GGT | 3408 -> 3414 | Substitution | 25.50% | 0 | A -> T | hypothetical protein CDS | hypothetical protein | Substitution | KLI70043.1 |
| C | 509 | 509 | 1 | G -> C | 2780 | SNP (transversion) | 36.50% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70043.1 |

| | | | | | | | | | | | | | |
|---|-----|-----|---|--------|------|-----------------------|--------|---|-----------|-----------------------------|-------------------------|--------------|----------------|
| G | 530 | 530 | 1 | C -> G | 4717 | SNP (transversion) | 35.40% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 563 | 563 | 1 | G -> A | 5010 | SNP (transition) | 31.70% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 608 | 608 | 1 | G -> A | 5144 | SNP (transition) | 41.40% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| G | 614 | 614 | 1 | A -> G | 5105 | SNP (transition) | 33.20% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| T | 623 | 623 | 1 | C -> T | 5180 | SNP (transition) | 26.60% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| C | 628 | 628 | 1 | T -> C | 5060 | SNP (transition) | 42.00% | 0 | N -> D | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |
| G | 671 | 671 | 1 | A -> G | 5212 | SNP (transition) | 33.00% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| T | 675 | 675 | 1 | C -> T | 5085 | SNP (transition) | 25.30% | 0 | S -> N | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |
| A | 677 | 677 | 1 | G -> A | 5114 | SNP (transition) | 39.20% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 722 | 722 | 1 | G -> A | 5483 | SNP (transition) | 26.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| T | 728 | 728 | 1 | C -> T | 5444 | SNP (transition) | 25.50% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 737 | 737 | 1 | G -> A | 5487 | SNP (transition) | 72.80% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |

| | | | | | | | | | | | | | |
|----|-----|-----|---|-------------|---------------|-----------------------|-----------------------|---|-----------------|-----------------------------|-------------------------|--------------|----------------|
| C | 752 | 752 | 1 | G -> C | 1840 | SNP (transversion) | 44.70% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 755 | 755 | 1 | C -> A | 1865 | SNP (transversion) | 45.10% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| G | 806 | 806 | 1 | C -> G | 1894 | SNP (transversion) | 69.60% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| C | 823 | 823 | 1 | T -> C | 1930 | SNP (transition) | 56.90% | 0 | I -> V | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |
| T | 834 | 834 | 1 | G -> T | 1944 | SNP (transversion) | 67.50% | 0 | T -> K | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |
| C | 844 | 844 | 1 | T -> C | 1412 | SNP (transition) | 66.80% | 0 | T -> A | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |
| A | 854 | 854 | 1 | G -> A | 1387 | SNP (transition) | 66.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 881 | 881 | 1 | G -> A | 1452 | SNP (transition) | 60.50% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 887 | 887 | 1 | G -> A | 1456 | SNP (transition) | 65.90% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| G | 896 | 896 | 1 | A -> G | 1486 | SNP (transition) | 67.00% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| CA | 943 | 944 | 2 | TC -> CA | 774 -> 775 | Substitution | 36.7% - > 36.8% | 0 | AI - > AV | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |
| G | 947 | 947 | 1 | C -> G | 794 | SNP (transversion) | 38.40% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |

| | | | | | | | | | | | | | |
|---|------|------|---|--------|------|-----------------------|--------|---|-----------|-----------------------------|-------------------------|--------------|----------------|
| G | 974 | 974 | 1 | A -> G | 1902 | SNP (transition) | 39.40% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| C | 977 | 977 | 1 | G -> C | 1906 | SNP (transversion) | 41.30% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| C | 983 | 983 | 1 | T -> C | 1956 | SNP (transition) | 62.40% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| C | 986 | 986 | 1 | G -> C | 1964 | SNP (transversion) | 62.40% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| T | 1013 | 1013 | 1 | C -> T | 2498 | SNP (transition) | 49.10% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| C | 1016 | 1016 | 1 | T -> C | 2538 | SNP (transition) | 32.00% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| G | 1025 | 1025 | 1 | C -> G | 2636 | SNP (transversion) | 26.40% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| T | 1025 | 1025 | 1 | C -> T | 2636 | SNP (transition) | 49.00% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| T | 1054 | 1054 | 1 | C -> T | 2945 | SNP (transition) | 60.10% | 0 | A -> T | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |
| A | 1055 | 1055 | 1 | C -> A | 2950 | SNP (transversion) | 34.90% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| G | 1055 | 1055 | 1 | C -> G | 2950 | SNP (transversion) | 41.70% | 0 | | hypothetical protein CDS | hypothetical protein | None | KLI70 043.1 |
| A | 1062 | 1062 | 1 | T -> A | 2947 | SNP (transversion) | 51.80% | 0 | Y -> F | hypothetical protein CDS | hypothetical protein | Substitution | KLI70 043.1 |

Contig 53

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------|----------|--------------------|-------------------|
| A | 36 | 36 | 1 | G -> A | 347 | SNP (transition) | 31.70% |
| T | 856 | 856 | 1 | A -> T | 6324 | SNP (transversion) | 26.60% |
| C | 1196 | 1196 | 1 | A -> C | 5751 | SNP (transversion) | 50.50% |
| A | 2748 | 2748 | 1 | C -> A | 5867 | SNP (transversion) | 32.90% |
| A | 2757 | 2757 | 1 | G -> A | 5907 | SNP (transition) | 32.70% |
| C | 2759 | 2759 | 1 | T -> C | 5796 | SNP (transition) | 32.90% |

Contig 54

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------------------------------------|------------|---------------------------|-------------------|
| G | 61 | 61 | 1 | A -> G | 1275 | SNP (transition) | 32.20% |
| T | 72 | 72 | 1 | C -> T | 1186 | SNP (transition) | 33.30% |
| G | 1153 | 1153 | 1 | A -> G | 8706 | SNP (transition) | 34.40% |
| T | 1172 | 1172 | 1 | C -> T | 8585 | SNP (transition) | 28.00% |
| C | 1173 | 1173 | 1 | T -> C | 8488 | SNP (transition) | 43.40% |
| G | 1550 | 1550 | 1 | A -> G | 4407 | SNP (transition) | 25.80% |
| A | 1679 | 1678 | 0 | (A) ₂ -> (A) ₃ | 1338 | Insertion (tandem repeat) | 39.00% |
| CGAA | 1707 | 1710 | 4 | TTTC -> CGAA | 836 -> 846 | Substitution | 33.9% -> 34.1% |

Contig 57

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|------|---------|---------|--------|--------|----------|--------------------|-------------------|-------------------------------|-------------------|---------------|-----------|----------------|-------------|
| G | 159 | 159 | 1 | T -> G | 371 | SNP (transversion) | 59.60% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| G | 173 | 173 | 1 | A -> G | 394 | SNP (transition) | 59.60% | 0 | D -> G | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| A | 201 | 201 | 1 | G -> A | 421 | SNP (transition) | 40.10% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| G | 363 | 363 | 1 | A -> G | 560 | SNP (transition) | 55.50% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| G | 427 | 427 | 1 | A -> G | 545 | SNP (transition) | 52.80% | 0 | I -> V | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| C | 437 | 437 | 1 | T -> C | 537 | SNP (transition) | 52.10% | 0 | L -> S | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| G | 723 | 723 | 1 | A -> G | 648 | SNP (transition) | 57.60% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| G | 728 | 728 | 1 | T -> G | 654 | SNP (transversion) | 56.40% | 0 | V -> G | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| A | 745 | 745 | 1 | G -> A | 659 | SNP (transition) | 56.90% | 0 | A -> T | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |

| | | | | | | | | | | | | | |
|---|------|------|---|--------|-----|--------------------|--------|---|--------|---------------|-----------|--------------|-------------|
| A | 840 | 840 | 1 | G -> A | 618 | SNP (transition) | 56.80% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| C | 986 | 986 | 1 | T -> C | 585 | SNP (transition) | 48.00% | 0 | I -> T | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| T | 1019 | 1019 | 1 | C -> T | 594 | SNP (transition) | 49.30% | 0 | T -> M | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| C | 1122 | 1122 | 1 | A -> C | 677 | SNP (transversion) | 47.30% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| A | 1159 | 1159 | 1 | G -> A | 678 | SNP (transition) | 50.40% | 0 | A -> T | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| G | 1191 | 1191 | 1 | A -> G | 646 | SNP (transition) | 50.20% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| T | 1323 | 1323 | 1 | C -> T | 488 | SNP (transition) | 54.10% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| C | 1353 | 1353 | 1 | T -> C | 459 | SNP (transition) | 55.80% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |
| T | 1418 | 1418 | 1 | C -> T | 437 | SNP (transition) | 39.10% | 0 | S -> L | RTX toxin CDS | RTX toxin | Substitution | KLI6996 8.1 |
| G | 1425 | 1425 | 1 | A -> G | 427 | SNP (transition) | 37.90% | 0 | | RTX toxin CDS | RTX toxin | None | KLI6996 8.1 |

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|-------|---------|---------|--------|----------------|------------|--------------------|-------------------|
| ACAAA | 17 | 21 | 5 | GTTGT -> ACAAA | 106 -> 111 | Substitution | 50.0% -> 51.8% |
| T | 22 | 22 | 1 | G -> T | 99 | SNP (transversion) | 69.70% |
| T | 23 | 23 | 1 | G -> T | 99 | SNP (transversion) | 47.50% |
| TCA | 25 | 27 | 3 | CGG -> TCA | 90 -> 96 | Substitution | 45.8% -> 46.7% |
| C | 28 | 28 | 1 | T -> C | 88 | SNP (transition) | 64.80% |
| TA | 29 | 30 | 2 | AT -> TA | 87 -> 88 | Substitution | 44.3% -> 44.8% |
| AC | 33 | 34 | 2 | TA -> AC | 83 | Substitution | 45.80% |
| T | 35 | 35 | 1 | A -> T | 83 | SNP (transversion) | 66.30% |
| T | 36 | 36 | 1 | G -> T | 76 | SNP (transversion) | 50.00% |
| AG | 37 | 38 | 2 | GA -> AG | 69 -> 74 | Substitution | 64.9% -> 68.1% |
| T | 39 | 39 | 1 | G -> T | 67 | SNP (transversion) | 52.20% |
| T | 41 | 41 | 1 | A -> T | 58 | SNP (transversion) | 65.50% |
| T | 44 | 44 | 1 | G -> T | 57 | SNP (transversion) | 52.60% |
| A | 45 | 45 | 1 | T -> A | 57 | SNP (transversion) | 64.90% |
| T | 47 | 47 | 1 | C -> T | 44 | SNP (transition) | 38.60% |
| AT | 48 | 49 | 2 | GA -> AT | 36 -> 38 | Substitution | 47.4% -> 50.0% |

Contig 60

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|--------|----------|-------------------|-------------------|
| C | 98 | 98 | 1 | T -> C | 122 | SNP (transition) | 43.40% |

Contig 62

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency |
|------|---------|---------|--------|----------|----------|--------------------|-------------------|
| CG | 2723 | 2724 | 2 | TT -> CG | 30 | Substitution | 96.70% |
| T | 2728 | 2728 | 1 | C -> T | 29 | SNP (transition) | 100.00% |
| T | 2744 | 2744 | 1 | A -> T | 23 | SNP (transversion) | 100.00% |
| A | 2747 | 2747 | 1 | G -> A | 22 | SNP (transition) | 100.00% |

Contig 63

| Name | Minimum | Maximum | Length | Change | Coverage | Polymorphism Type | Variant Frequency | Variant P-Value (approximate) | Amino Acid Change | CDS | product | Protein Effect | protein_id |
|------------------|---------|---------|--------|--------------------------|------------|---------------------------|-------------------|-------------------------------|-------------------|--------------------------|----------------------|----------------|------------|
| GCAACA GCAACA | 89 | 88 | 0 | (AGCAAC)14 -> (AGCAAC)16 | 193 -> 199 | Insertion (tandem repeat) | 100.00% | 0 | Q -> QQQ QQ | hypothetical protein CDS | hypothetical protein | Insertion | KLI69899.1 |