**Table S1. Sequencing results of 64 selected clones**

| | [a]Amino acid deletion/change | [b]Nucleotide deletion | Frequency |
|---|---|---|---|
| Fluorescent | M1Δ[c] | 1 atg 3 | 1 |
| | S2/K3→R | 1 ATG AGt aaA GGA 12 | 4 |
| | G4Δ | 7 AAA gga GAA GAA 18 | 11 |
| | E5Δ | 10 GGA gaa GAA CTT 21 | 3 |
| | F8/T9→S | 19 CTT Ttc aCT GGA 30 | 1 |
| | C48Δ | 136 TTT ATt tgC ACT 147 | 1 |
| | P75/D76→H | 220 TAT Ccg gAT CAT 231 | 1 |
| | P75Δ | 220 TAT ccg GAT CAT 231 | 1 |
| | E172Δ | 508 AAC ATt gaA GAT 519 | 1 |
| | S175/V176→F | 520 GGA Tcc gTT CAA 531 | 1 |
| | A227Δ | 676 ACT GCT gct GGG 687 | 2 |
| | G228Δ | 676 GCT GCt ggG ATT 687 | 4 |
| | G228/I229→V | 679 GCT Ggg aTT ACA 690 | 2 |
| Non-fluorescent | G10Δ | 22 TTC ACt ggA GTT 33 | 1 |
| | D21Δ | 55 GAT GGT gat GTT 60 | 2 |
| | G24Δ | 64 GTT AAT ggg CAC 75 | 1 |
| | E34Δ | 94 GAG GGt gaA GGT 105 | 3 |
| | P58Δ | 166 CCA TGG cca ACA 177 | 1 |
| | P89/E90→Q | 262 ATG Ccc gAA GGT 273 | 1 |
| | T203Δ | 601 CTG TCG ACA CAA 612 | 1 |
| Unexpected | No deletions | NA | 7 |
| | Stop codon | 544 TAtcaA 549 | 1 |
| | 4 bp deletion | NA | 13 |

[a] Triplet nucleotide deletions can occur in one in-frame codon or two neighboring codons, which may result in amino acid mutations.

[b] Deleted nucleotides are lowercased.

[c] This mutant is not subject to further analysis due to deletion in start codon.