## Molecular characterization of transgenic loci from 3 phenotypic classes

| | | | Donor/Target | Donor/Reporter |
|---|---|---|---|---|
| **GFP+ RFP+ CFP+** | Sequencing of PCR products (Primerset 1a) | | 36 | 20 |
| | GFP WT sequence | (uncut) | 7 | 0 |
| | GFP Deletions | (<10bp) | 7 | 0 |
| | GFP Deletions | (>10bp) | 3 | 4 |
| | GFP Insertions | (<10bp) | 4 | 1 |
| | GFP Insertions | (>10bp) | 1 | 0 |
| | CFP like sequence* | | 14 | 15 |
| **GFP- RFP+ CFP+** | PCR (Primerset 1a) and *Not*I digest of PCR product | | 156 | |
| | Donor sized (HEG+) | | 152 | |
| | | *Not*I marker present | 25 | |
| | | *Not*I marker absent | 127 | |
| | Target sized (HEG-) | | 4 | |
| **GFP- RFP- CFP+** | Sequencing of PCR products (Primers: 2 fwd-1a rev) | | 15 | |
| | GFP/CFP recombination** | | 5 | |
| | no PCR product | | 10 | |

* Synthesis-dependent strand annealing using the 3xP3-CFP locus as template could account for these repair events

** The structure of these events indicates that they might have originated through intramolecular recombination via single strand annealing between the homologous regions of the 3xP3-GFP and 3xP3-CFP genes leading to the loss of the interjacent RFP marker.