**Table EV2 Adaptive mutations identified in clones derived from mixed populations.**

Clones were derived from *tub2-401* populations at the end of the experiment (Gf). We derived them from populations where multiple adaptive mutations have high frequencies (see Figure 3A). For each clone, we tested by Sanger sequencing the presence of individual mutations.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | *Number of clones with mutations in the indicated genes* | | | |  |
| **Populations** | **Recurrently mutated genes** | ***TUB1*** | ***TUB2*** | ***TUB4*** | ***KIP3*** | **Concurrent mutations** |
| C5 | *TUB1, KIP3* | 4 | - | - | 2 | 0 |
| F4 | *TUB2, KIP3* | - | 6 | - | 1 | 0 |
| F5 | *TUB4, KIP3* | - | - | 8 | 0 | 0 |
| G4 | *TUB1, TUB2* | 3 | 4 | - | - | 0 |