

Table S3: Number of distinct genes (prior to slash) and intergenic regions (after slash) containing at least one probe flagged as having a significant fitness effect in selections of transposon-mutagenized libraries. “Unique” indicates the set of genes which contained one or more significant probes in one genetic background (WT or *rho**) but not the other. “Strict” indicates that the threshold for significance calling was relaxed for the background not being considered (*e.g.*, the entry for “WT unique (strict)” contains the number of genes which had significant probes using the strict criteria in the WT selection, but no significant probes using relaxed criteria in the corresponding *rho** selection); see Section 1.5 for details.

| Condition | WT | WT unique | WT unique (strict) | <i>rho</i> * | <i>rho</i> * unique | <i>rho</i> * unique (strict) |
|-----------|-----------|--------------|--------------------------|--------------|------------------------|------------------------------------|
| CML | 202 / 32 | 139 / 27 | 40 / 16 | 380 / 65 | 317 / 60 | 155 / 42 |
| STP | 239 / 48 | 220 / 45 | 144 / 32 | 148 / 19 | 129 / 16 | 62 / 11 |
| AKG | 341 / 77 | 235 / 63 | 81 / 39 | 347 / 64 | 241 / 50 | 88 / 22 |
| NADM | 511 / 164 | 309 / 89 | 61 / 37 | 464 / 188 | 262 / 113 | 33 / 32 |