**TABLE S1**

**Summary of WGS metrics**

| | *fp6* | *fp9* | *fp12* |
|---|---|---|---|
| Total number of reads | 109 801 600 | 110 380 600 | 106 231 800 |
| % of reads aligned to N2 (wild-type var. Bristol) | 88.01 | 92.79 | 93.89 |
| % of reads aligned to *E. coli* (*C. elegans* diet) | 6.02 | 2.85 | 2.60 |
| % of reads unaligned | 5.97 | 4.36 | 3.51 |
| % GC content[a] | 37.19 | 37.09 | 35.85 |
| % N content | 0.01 | 0.01 | 0.01 |
| Number of clusters/lane (2 lanes for each mutant)[b] | 26 995 200 | 27 572 600 | 26 318 100 |
| | 27 905 600 | 27 617 700 | 26 797 800 |
| Number of common variants vs. N2 reference genome (total)[c] | 1317 (1477) | 1352 (1477) | 1311 (1477) |
| % of reads matching multiple locations | 2.54 | 2.51 | 2.22 |

[a]N2 wild-type genome contains ~36% GC content. [b]Number of clusters are shown after being purity filtered during Illumina pipeline. [c]High quality variants (MAQgene mapping score of 63 with 0 wild-type reads) shared in at least 2 of three mutants sequenced. We found that a total of 1477 high quality variants were identified to be common in at least 2 out of the 3 mutants. The common variants from our backcrossed mutants represent SNPs present in our starting strain (PS3662). Note that these numbers highlight how different our starting strain is in terms of variants, from the reference genome. This might be also true for many strains made in the N2 background, a fact that will be confirmed with additional sequencing of other backgrounds.