Table S3.1 CRISPR-Cas9 deletion alleles and associated sequences

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| **Strain** | **Allele** | **Gene Target** | **Phenotype** | **Fails to Complement** | **Guide RNA Sequence #1** | **Guide RNA Sequence #2** | **Left Flanking Sequence****(30 bp)** | **Right Flanking Sequence****(30 bp)** |
| VC4612 | gk5682 | C34D4.4 | unfertilized oocytes laid | GE2840, GE2890 | GCATACCGTACTTTTCCCGG | GTGGTGGTTGTTGAGCACGG | AAAAGCGAAAATTTCCGGAGCGTTCCCCCG | TGCTCAACAACCACCACAAGAATATCAAAA |
| VC4606 | gk5676 | F56D5.2 | unfertilized oocytes laid | GE2837 | TATTTCAGGACACCACGGAA | GAAGGTTCACTCAGTCTGAT | TACAGTGGAAAATATTTCAGGACACCACGG | ATTGGTTCAAAAGTGGCGGTACGAGTCGCT |
| VC4645 | gk5714 | nstp-2 | exploded through vulva or bagged with few late-stage dead embryos | GE2091, GE2288 | CTTCTTCTCATCTTGCTTGT | GAAATGTAGAAAATGTCATC | TATCTACTGTTTCTTCTTCTCATCTTGCTT | TCAGGTTCATGGCAGATGGCTCTTGTCTGT |

Table S3.2 Overrepresented Biological Process GO terms and associated genes

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| **Biological Process GO Term** | **Associated Gene(s)** |
| DNA repair (GO:0006281) | wapl-1; rad-50; cra-1; atl-1; mre-11; rad-51 |
| nucleobase-containing compound metabolic process (GO:0006139) | csr-1; atl-1; cra-1; div-1; dlat-1; F21D5.1; lis-1; mel-32; mre-11; rad-50; rad-51; sqv-4; top-3; wapl-1 |
| regulation of cell cycle (GO:0051726) | air-1; wapl-1; hcp-3; atl-1; mre-11; such-1; zyg-8 |
| DNA recombination (GO:0006310) | rad-50; cra-1; mre-11; rad-51; lis-1 |
| organelle disassembly (GO:1903008) | atg-7; cpl-1; mbk-2; ccz-1 |
| regulation of cellular component organization (GO:0051128) | atg-7; wapl-1; cpl-1; tlk-1; unc-112; cup-5; cyk-3; such-1; zyg-8 |
| establishment of mitotic spindle localization (GO:0040001) | cls-2; mom-2; let-99; zyg-8; lis-1 |
| cell division (GO:0051301) | cls-2; rmd-1; gsp-2; let-99; cyk-3; such-1; lis-1; mbk-2 |
| cellular metabolic process (GO:0044237) | atg-7; air-1; atl-1; bckd-1A; C56A3.8; cept-2; cpl-1; cpt-2; cra-1; csr-1; cyk-3; dgtr-1; div-1; dlat-1; F21D5.1; gsp-2; gsr-1; lis-1; mbk-2; mel-32; mre-11; rad-50; rad-51; sqv-4; such-1; tlk-1; top-3; vps-39; wapl-1; zyg-8 |
| chromosome segregation (GO:0007059) | csr-1; cls-2; tlk-1; hcp-3; rmd-1; cra-1; atl-1; lis-1 |
| embryo development (GO:0009790) | atg-7; atl-1; csr-1; cyk-3; hcp-3; lis-1; mbk-2; mel-32; mom-2; pos-1; rad-51; sqv-4 |
| meiotic cell cycle process (GO:1903046) | klp-18; rad-50; klp-19; cls-2; atl-1; mre-11; rad-51; lis-1 |
| organelle assembly (GO:0070925) | atg-7; klp-18; air-1; csr-1; klp-19; cls-2; hcp-3; sas-5; lis-1; ccz-1 |
| spindle organization (GO:0007051) | klp-18; air-1; klp-19; cls-2; hcp-3; rmd-1; lis-1 |
| reproductive process (GO:0022414) | klp-18; atl-1; cls-2; cra-1; csr-1; gsp-2; klp-19; lis-1; mbk-2; mre-11; rad-50; rad-51; sqv-4; such-1; unc-112; wapl-1 |
| nuclear division (GO:0000280) | klp-18; air-1; csr-1; klp-19; cls-2; hcp-3; rmd-1; atl-1; rad-51; lis-1 |
| chromosome organization (GO:0051276) | air-1; atl-1; cls-2; csr-1; gsp-2; hcp-3; klp-19; lis-1; mre-11; rad-50; rad-51; rmd-1; top-3 |
| cytoskeleton organization (GO:0007010) | klp-18; air-1; cls-2; cyk-3; hcp-3; klp-19; let-99; lis-1; mom-2; pod-1; rmd-1; sas-5; zyg-8 |
| microtubule-based process (GO:0007017) | klp-18; air-1; cls-2; cyk-3; hcp-3; klp-19; let-99; lis-1; mbk-2; mom-2; rmd-1; sas-5; zyg-8 |
| mitotic cell cycle process (GO:1903047) | air-1; cls-2; csr-1; cyk-3; hcp-3; let-99; lis-1; mbk-2; mom-2; mre-11; rad-51; rmd-1; zyg-8 |
| organelle organization (GO:0006996) | atg-7; air-1; atl-1; C56A3.8; ccz-1; cls-2; cpl-1; csr-1; cup-5; cyk-3; gsp-2; hcp-3; klp-18; klp-19; let-99; lis-1; mbk-2; mom-2; mre-11; pod-1; rad-50; rad-51; rmd-1; sas-5; top-3; unc-112; vps-39; zyg-8 |
| cell cycle (GO:0007049) | klp-18; air-1; atl-1; cls-2; cra-1; csr-1; cyk-3; gsp-2; hcp-3; klp-19; let-99; lis-1; mbk-2; mom-2; mre-11; rad-50; rad-51; rmd-1; sas-5; such-1; wapl-1; zyg-8 |

Table S3.3 Overrepresented Molecular Function GO terms and associated genes

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| **Molecular Function GO Term** | **Associated Gene(s)** |
| microtubule binding (GO:0008017) | klp-18; klp-19; cls-2; rmd-1; zyg-8; lis-1 |
| tubulin binding (GO:0015631) | klp-18; klp-19; cls-2; rmd-1; zyg-8; lis-1 |
| cytoskeletal protein binding (GO:0008092) | klp-18; pod-1; klp-19; cls-2; rmd-1; zyg-8; lis-1 |
| protein binding (GO:0005515) | klp-18; air-1; ccz-1; cls-2; cpl-1; dlat-1; gsp-2; hcp-3; klp-19; let-99; lis-1; mbk-2; mel-32; mex-5; mom-2; pod-1; rad-51; rmd-1; sas-5; spn-4; sqv-4; tlk-1; unc-112; vps-33.1; vps-39; zyg-8 |
| binding (GO:0005488) | aptf-2; air-1; atl-1; bckd-1A; C56A3.8; ccz-1; cls-2; cpl-1; csr-1; cup-5; cyk-3; div-1; dlat-1; F21D5.1; gsp-2; gsr-1; hcp-3; klp-18; klp-19; let-99; lis-1; mbk-2; mel-32; mex-5; mom-2; mre-11; perm-5; pod-1; pos-1; rad-50; rad-51; rmd-1; sas-5; spn-4; sqv-4; tlk-1; top-3; unc-112; vps-33.1; vps-39; zyg-8 |
| catalytic activity (GO:0003824) | atg-7; air-1; atl-1; bckd-1A; C56A3.8; cept-2; cpl-1; cpt-2; cra-1; csr-1; cyk-3; dgtr-1; dlat-1; F21D5.1; gsp-2; gsr-1; klp-18; klp-19; mbk-2; mel-32; mre-11; rad-50; rad-51; sqv-4; tlk-1; top-3; trcs-1; zyg-8 |