

Supporting Information for:
“A deterministic analysis of genome integrity during neoplastic
growth in *Drosophila*”
Table S3

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ID	Coordinates	Genotype	SV type	Length	size on ref. (r)	corrected size (t)	FWD primer	REV primer
1	2L:18578669	Hom	small ins	120	196	316	CCTGGATACCTCTGGCAAAC	AGGAGCCAGTTGAAATTGA
2	2L:21017450	Hom	small ins	133	183	316	TGGGATTAATTTCGCTTTATGA	CAGATGCTGATAAGGGAAAGATG
3	3R:1975276	Hom	small ins	100	127	227	TTTTCTCAGTGCATACTCAGCAG	CTGCCAACTAAAGCAAAGG
4	2L:2646518	Hom	small ins	102	149	251	GGATGCTGTCATTTGCTACG	CACAAACTGCCAGCTACCAA
5	2R:4530459	Het	small ins	114	140	254	TTCAATCTCCTGTGTGCTGAA	CCCAGAAAAATAGGCACCTTC
6	3R:21701316	Het	small ins	114	164	278	AATTATGATTCGGGCCACACC	CCATTGAACAACGCCAATTA
7	2L:3289401	Hom	small ins	25	146	171	TTTTCAAAGCAAAAAGCAGTCC	ATCGGCTGTAGGTCCTTGAA
8	2R:3872130	Hom	small ins	22	124	146	GATTTGGAGGAAATGCTGAA	TGATTATGATAGGCTAAGCAAAGC
9	3L:17484346	Hom	small ins	28	188	216	AGTCGCCACTATCAGCCAGA	TGCACAAATATGCTTCCGTTA
10	3R:1771634	Het	small ins	31	181	212	ACTTTTTCCACTGGGTCCAT	GAAGGCATAAAATAGAAAGCAAA
11	3R:8492543	Hom	del	74	251	177	CGATCAAAGCCATCAAAAT	TGCTTTGTAGATAGTGTCAPTAAAGG
12	3L:10182662	Hom	del	132	298	166	ATGAAAATGCAAGCGACCT	TGCTTAAAGCCCTTTTTCGTT
13	3L:22637989	Het	del	175	317	142	GCCAAAATGGAGTCCGAGT	TCGTTTGTGAATTTATGGGTGA
14	3R:26987829	Het	del	245	368	123	AATTTGGCTGCCAATGAAAG	TGGCAAATGTTTGAGTTTGG
15	3R:22289554	Het	del	120	316	196	GCCTTCCACAGTTCATTGCT	GGCTGTTTCGTAATGATCCA
16	2L:12736726	Hom	del	23	200	177	CTGATCGGTACCCGGAAAAT	TTCGTTAGTCACACAGCGAAAG
17	2L:5757822	Hom	del	22	200	178	GGTAATFTAGTTTCAACCCAGTGC	TTTGGCATTTAAAACAGAAGC
18	3R:3765275	Het	del	22	146	124	TTCTTGTTCGCAAAATAACCA	TCCTGAATTTGTACAPATATTTAATCG
19	2R:8489223	Het	del	25	202	177	TGCTGGGTATGAAAACAAGG	AAAATGCATATTTTCGGTCTG
20	2R:10867320	Het	del	23	206	183	AGCTGAATTTAGAAAGTTGTGGTG	ACAAAAGTACATAGTGTTCCTCA
21	3L:15041213	n.d.	tan dup	418	495	913	TTTCCCATAAAGTATGTCATAAATA	TGACATAGTCCCAATGGTTTCA
22	3R:20192157	n.d.	tan dup	565	648	1213	CTGGCACACAGTTGCAGTTT	GATTTGGGGTCTCCAGATGAA
23	2R:5543741	n.d.	tan dup	889	985	1874	GCCAGGATGGGAATTTTCTT	TGGCACTAAAATGCCAAATGG
24	2L:3026214	n.d.	tan dup	710	773	1483	TAAGGAGGATCGGGAGAGGT	CAAGTCTGCTGAGAAAGC
25	3L:15825407	Het	del	28	205	177	CGAACCCGATTTGTTTTGTT	GCCTGAAAGTTTCTCCACGTC
26	3L:15828140	Het	del	102	215	113	CTTTCTCCACACAGCTGAA	TAGGTAAGCAGCGGTGGATT
27	3L:15826899	n.d.	tan dup	293	442	735	TGGGATGTTGCCAAATGTTA	CTAAGGGCCCAAGCTGAATTT