Table S2 Detailed results of split-read mutation detection

Linkage Group	Start	Stop	Size	Score	Predicted in:	Homozygous in:
I	1580676	1580681	5	10	Both	Both
I	6151523	6151526	3	10	Both	Both
I	10948442	10948685	243	2	Both	Both
II	563219	563256	37	2	*sy745*	Both
II	4117187	4117193	6	2	*sy740*	Both
II	4611574	4611595	21	4	*sy745*	Both
IV	3036896	3036902	6	2	Both	Both
IV	8121709	8121716	7	5	*sy740*	Both
IV	8578126	8580609	2483	2	Both	Both
V	931548	931552	4	2	Both	Both
V	1645712	1647498	1786	9	Both	Both
V	5625703	5625715	12	12	Both	Both
V	5755542	5756050	508	3	Both	Both
V	6081823	6094837	13014	7	Both	Both
V	7725877	7725881	4	2	Both	Both
V	9026726	9026729	3	6	Both	Both
V	9063330	9063335	5	13	Both	Both
V	15434910	15434919	9	10	Both	Both
V	19820304	19820370	66	2	Both	Both
X	2002626	2002632	6	4	Both	Both
X	4938588	4938592	4	8	Both	Both
X	8941405	8941409	4	12	Both	Both
X	8941405	8941409	4	8	Both	Both
X	14432312	14432326	14	5	Both	Both
I	230840	231919	1079	7	Both	Neither
I	232747	237780	5033	2	Both	Neither
I	238430	238468	38	4	Both	Neither
I	246119	246175	56	3	*sy745*	Neither*
I	3812704	4548148	735444	13	Both	Neither
I	13156287	13156436	149	4	Both	Neither
I	14169356	14386795	217439	2	Both	Neither
II	2220320	2221389	1069	2	Both	Neither
II	3775873	7422381	3646508	2	*sy745*	Neither
II	6187749	6187758	9	2	*sy740*	Neither*
II	12009805	12009852	47	2	*sy740*	Neither*
II	12572308	12573728	1420	4	Both	Neither
III	13032636	13032832	196	4	*sy740*	Neither
IV	7727245	7727296	51	3	Both	Neither
IV	11071120	11072356	1236	11	Both	Neither
IV	14320741	14356442	35701	2	*sy745*	Neither
IV	15438235	16899372	1461137	4	*sy745*	Neither
V	3707494	3707683	189	2	Both	Neither
V	13646108	13646149	41	8	Both	Neither*
V	17344382	17344476	94	2	*sy745*	Neither*
X	1614748	1615141	393	2	*sy740*	Neither*
X	1614997	1615141	144	4	Both	Neither*
X	7077853	7077873	20	3	*sy740*	Neither
X	16014052	16014197	145	2	*sy740*	Neither*

The 48 candidate deletions predicted by split-read analysis in the *dpy-11(sy740)* and/or *dpy-11(sy745)* strains on the basis of two or more reads ("Score" in the table) are listed by linkage group, start site, end site, and size. Each was manually curated by examination of reads aligned to the reference sequence using the Burrows-Wheeler aligner. 24 of the 48 candidate deletions were homozygous in both strains; the other 24 had reads consistent with the presence of wild-type sequence at these coordinates in both strains, and so are marked as

being homozygous in neither strain. Predicted deletions in this latter class could have been represented by sequencing reads if they were present as heterozygotes, but such reads would not have been mapped to the corresponding site in the genome by the Burrows-Wheeler aligner. The candidate deletions marked with an asterisk (*) were tested using PCR to seek smaller products as predicted (see Table S4); of these, only one was present, the predicted deletion starting at 13646108 on LGV; that deletion was predicted in both strains and was detectable by PCR in both strains, indicating that it did not result from CRISPR-Cas nuclease activity.