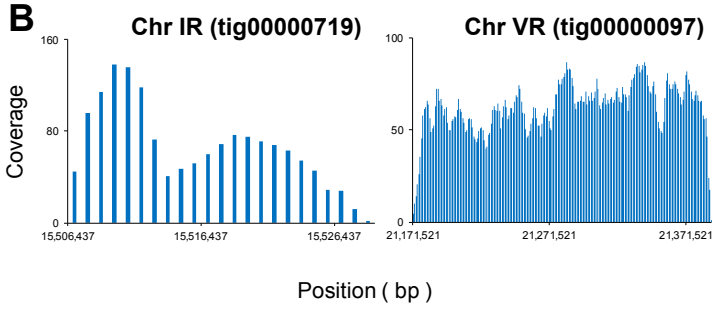
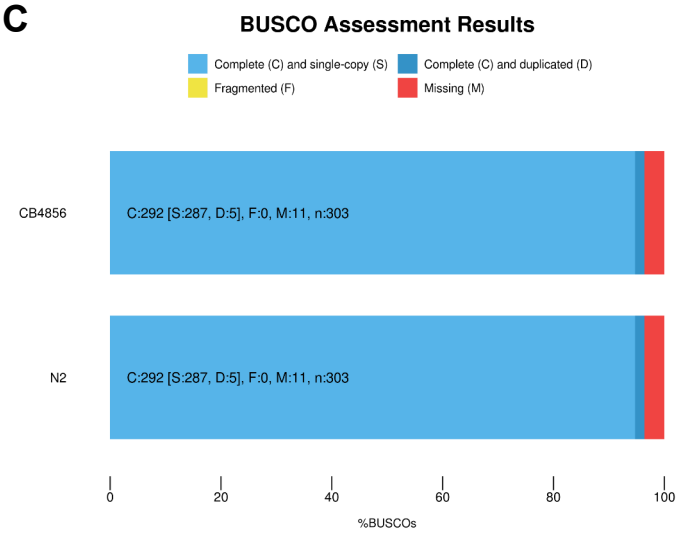
A

	I	I	I	I:720	I:719	V	V	V:97
Position (bp)	13,515,166	14,529,568	15,452,510	15,502,000	15,519,000	19,390,823	20,391,131	21,282,521
CB4856	0/0	0/0	0/0	C	C	0/0	0/0	C
N2	1/1	1/1	1/1	N	N	1/1	1/1	N
QX104	0/0	0/0	0/0	C	C	QX101	0/0	0/0	C
QX164	0/0	0/0	0/0	C	C	QX102	0/0	0/0	C
QX166	0/0	0/0	0/0	C	C	QX104	0/0	0/0	C
QX202	0/0	0/0	0/0	C	C	QX193	0/0	0/0	C
QX34	0/0	0/0	0/0	C	C	QX198	0/0	0/0	C
QX37	0/0	0/0	0/0	C	C	QX207	0/0	0/0	C
QX41	0/0	0/0	0/0	C	C	QX412	0/0	0/0	C
QX412	0/0	0/0	0/0	C	C	QX6	0/0	0/0	C
QX413	0/0	0/0	0/0	C	C	QX66	0/0	0/0	C
QX423	0/0	0/0	0/0	C	C	QX70	0/0	0/0	C
QX48	0/0	0/0	0/0	C	C	QX75	0/0	0/0	C
QX9	0/0	0/0	0/0	C	C	QX9	0/0	0/0	C
QX98	0/0	0/0	0/0	C	C	QX11	1/1	0/0	C
QX101	1/1	0/0	0/0	C	C	QX12	1/1	0/0	C
QX487	1/1	0/0	0/0	C	C	QX128	1/1	0/0	C
QX174	1/1	1/1	0/0	C	C	QX204	1/1	0/0	C
QX42	1/1	1/1	0/0	C	C	QX65	1/1	0/0	C
QX45	1/1	1/1	0/0	C	C	QX71	1/1	0/0	C
QX6	1/1	1/1	0/0	C	C	QX131	1/1	1/1	N
QX102	1/1	1/1	1/1	N	N	QX132	1/1	1/1	N
QX103	1/1	1/1	1/1	N	N	QX176	1/1	1/1	N
QX132	1/1	1/1	1/1	N	N	QX202	1/1	1/1	N
QX176	1/1	1/1	1/1	N	N	QX34	1/1	1/1	N
QX204	1/1	1/1	1/1	N	N	QX37	1/1	1/1	N
QX39	1/1	1/1	1/1	N	N	QX39	1/1	1/1	N
QX66	1/1	1/1	1/1	N	N	QX41	1/1	1/1	N
QX71	1/1	1/1	1/1	N	N	QX413	1/1	1/1	N
QX75	1/1	1/1	1/1	N	N	QX42	1/1	1/1	N
QX91	1/1	1/1	1/1	N	N	QX487	1/1	1/1	N
QX93	1/1	1/1	1/1	N	N	QX69	1/1	1/1	N
QX131	0/0	0/0	1/1	N	N	QX8	1/1	1/1	N
QX193	0/0	0/0	1/1	N	N	QX93	1/1	1/1	N
QX207	0/0	0/0	1/1	N	N	QX98	1/1	1/1	N
QX70	0/0	0/0	1/1	N	N	QX164	0/0	1/1	N
QX8	0/0	0/0	1/1	N	N	QX166	0/0	1/1	N
QX11	1/1	0/0	1/1	N	N	QX423	0/0	1/1	N
QX198	1/1	0/0	1/1	N	N	QX44	0/0	1/1	N
QX44	1/1	0/0	1/1	N	N	QX45	0/0	1/1	N
QX12	1/1	1/1	1/1	C	C	QX48	0/0	1/1	N
QX128	1/1	1/1	1/1	C	C	QX103	0/0	0/0	N
QX65	1/1	1/1	1/1	C	C	QX174	0/0	0/0	N
QX69	1/1	1/1	1/1	C	C	QX91	1/1	0/0	N
Segregant ratio	5/42	12/42	4/42	0/42	21/42		13/42	3/42

B

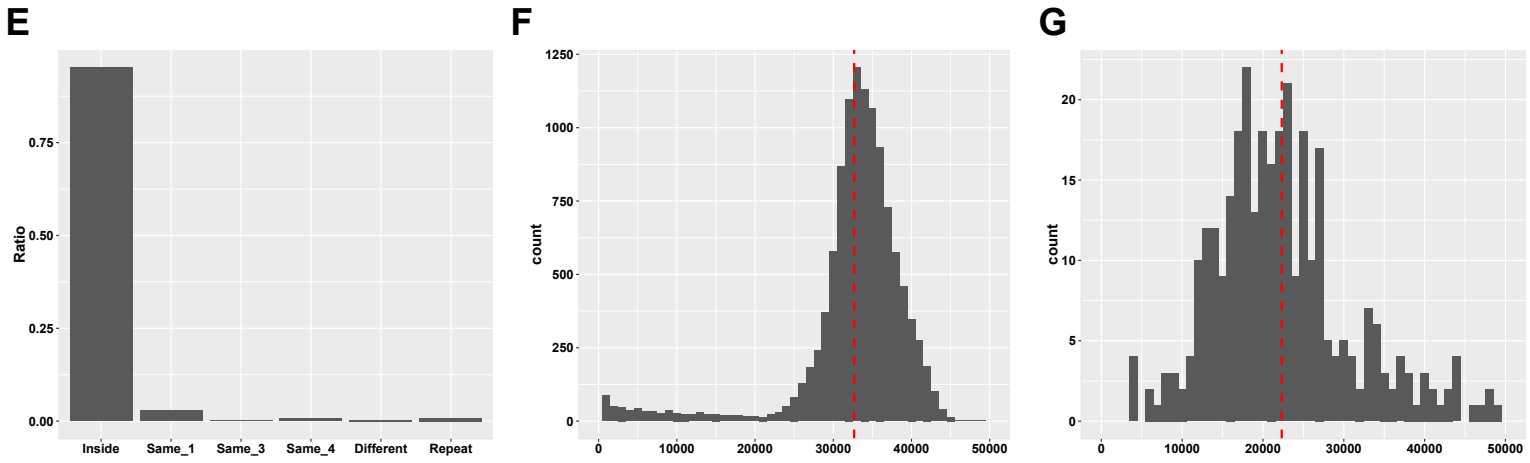


C



D

	Contig name	Contig size (bp)	Start of telomeric array	End of telomeric array	Telomeric repeat sequence	Telomere length (bp)	Position of telomere on contig	Number of canonical telomeric repeats
IL	tig00000193	1,021,041	1,018,151	1,021,041	TTAGGC	2,886	End	481
IR	tig00000719	22,460	1	3,348	GCCTAA	3,348	Start	508
IIL	tig00000150	1,498,322	1	3,979	GCCTAA	3,979	Start	587
IIR	tig00000156	1,307,113	1,303,937	1,307,113	TTAGGC	3,177	End	473
IIIL	tig00000201	999,175	1	3,121	GCCTAA	3,121	Start	480
IIIR	tig00000291	205,719	1	2,524	GCCTAA	2,524	Start	390
IVL	tig00000324	22,756	19,410	22,755	TTAGGC	3,347	End	532
IVR	tig00000212	451,830	1	2,772	GCCTAA	2,772	Start	399
VL	tig00000764	282,952	280,057	282,952	TTAGGC	2,896	End	401
VR	tig00000097	218,346	216,009	218,346	TTAGGC	2,338	End	344
XL	tig00000307	97,378	1	3,259	GCCTAA	3,259	Start	516
XR	tig00000073	2,855,796	2,853,115	2,855,796	TTAGGC	2,682	End	386



Supplemental Figure S2. Linkage map and genome quality. *(A)* Linkage map of Chr IR and Chr VR ends. Blue: CB4856 alleles; yellow: N2 alleles. 0/0: homozygous for CB4856 alleles; 1/1 homozygous for N2 alleles as a result of variant calling with GATK. C, homozygous for CB4856; or N, homozygous for N2 alleles, based on whether each strain contains CB4856-specific sequences (N2 has zero coverage in this region). Segregant ratio represents the number of strains that have different allele types between positions. For example, 21/42 in the middle of the graph indicates that 21 strains have N2 and CB4856 allele types (or vice versa) in Chr I and Chr V, respectively, but not N2 and N2 or CB4856 and CB4856 alleles. tig00000719 and tig00000097 were not placed on the N2 genome, but they are highly linked with chrIR and chrVR ends, respectively. *(B)* Coverage plot of both contigs. *(C)* BUSCO assessment of CB4856 and N2 genomes. *(D)* Telomere lengths and telomere-containing contigs. *(E)* Fosmid alignment to the Kim et al., 2019 genome. Inside, fosmids aligned within a single contig ; Same_1, fosmid aligned to two adjacent contigs; Same_3, the distance between two ends of the fosmid was longer than 3 contigs; Same_4, longer than 4 contigs; different, one fosmid aligned to two different contigs; repeat, fosmid sequence from repeat sequences. *(F)* length distribution of ‘inside’ fosmids, which are contained within a single contig. *(G)* length distribution of fosmids that are aligned to two adjacent contigs.