

894 **SUPPLEMENTARY FIGURE LEGENDS**

895 **Supplementary Fig. 1.** Karyotypes of the three subjects: **(a)** jg1a, **(b)** jg1b, and **(c)** jg1c.

896 The arrow in panel **(a)** indicates the normal variation inv(9)(p12q13).

897

898 **Supplementary Fig. 2.** Harr plot of the alignment between chromosome 9 of GRCh38

899 and two largest scaffolds aligned to chromosome 9 from the **(a)** jg1a, **(b)** jg1b, and **(c)**

900 jg1c assemblies, indicating that the two individual genomes harbor a possible shared

901 inversion. 'Super-scaffold' is the default prefix designated by BionanoSolve software.

902

903 **Supplementary Fig. 3.** Workflow of the construction of JG1. **(a)** Workflow of the

904 construction of each draft assembly. **(b)** Workflow of the integration of three draft

905 assemblies. Rectangles indicate substrates such as reads, contigs, and scaffolds.

906 Rectangles with rounded corners indicate software or processes.

907

908 **Supplementary Fig. 4:** Histogram of PacBio subreads length for **(a)** jg1a, **(b)** jg1b, and

909 **(c)** jg1c. The length of each subread was calculated using the SAMtools (ver. 1.8) faidx

910 command.

911

912 **Supplementary Fig. 5:** Histogram of Bionano data for **(a)** Nt.BspQI of jg1a, **(b)**

913 Nb.BssSI of jg1a, **(c)** jg1b, and **(d)** jg1c. The length of each molecule was extracted from

914 the BNX file.

915

916 **Supplementary Fig. 6:** Majority decision. **(a)** Schematic representation of majority

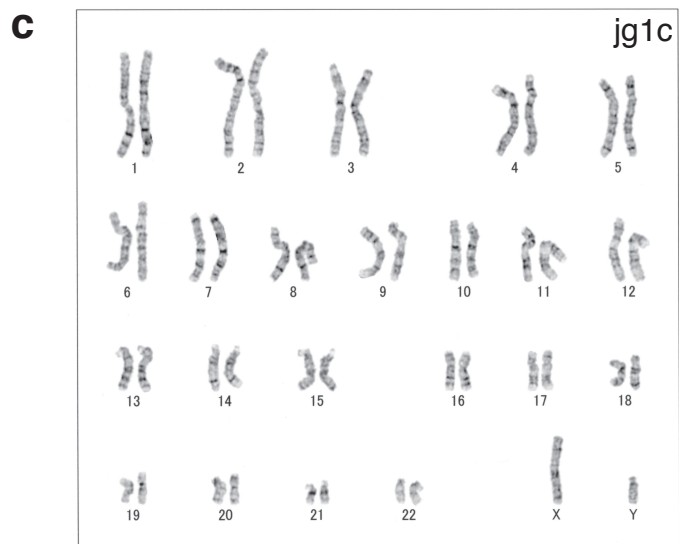
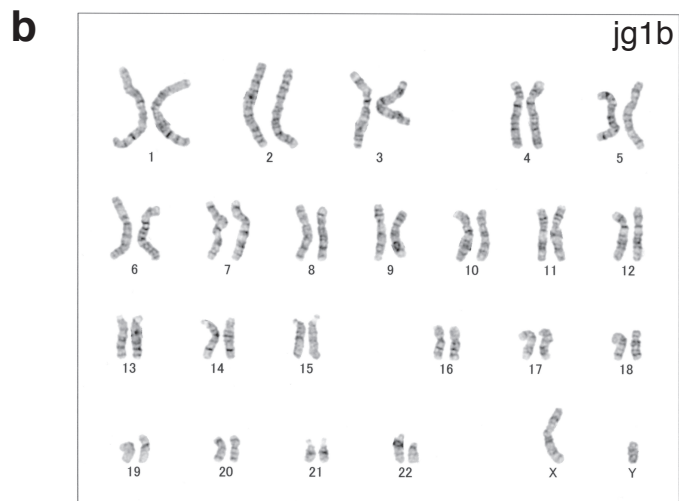
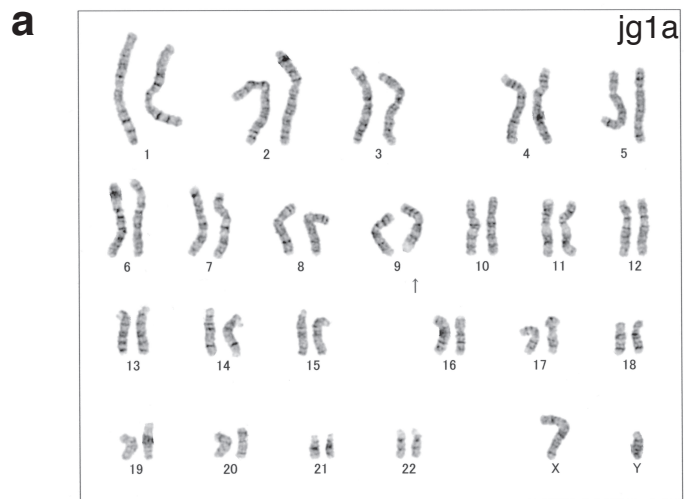
917 decision approach. **(b)** Venn diagram of SNVs detected in JG1, jg1a, jg1b, and jg1c by

918 comparison with hs37d5. The intersection relationship was inferred using the BCFtools

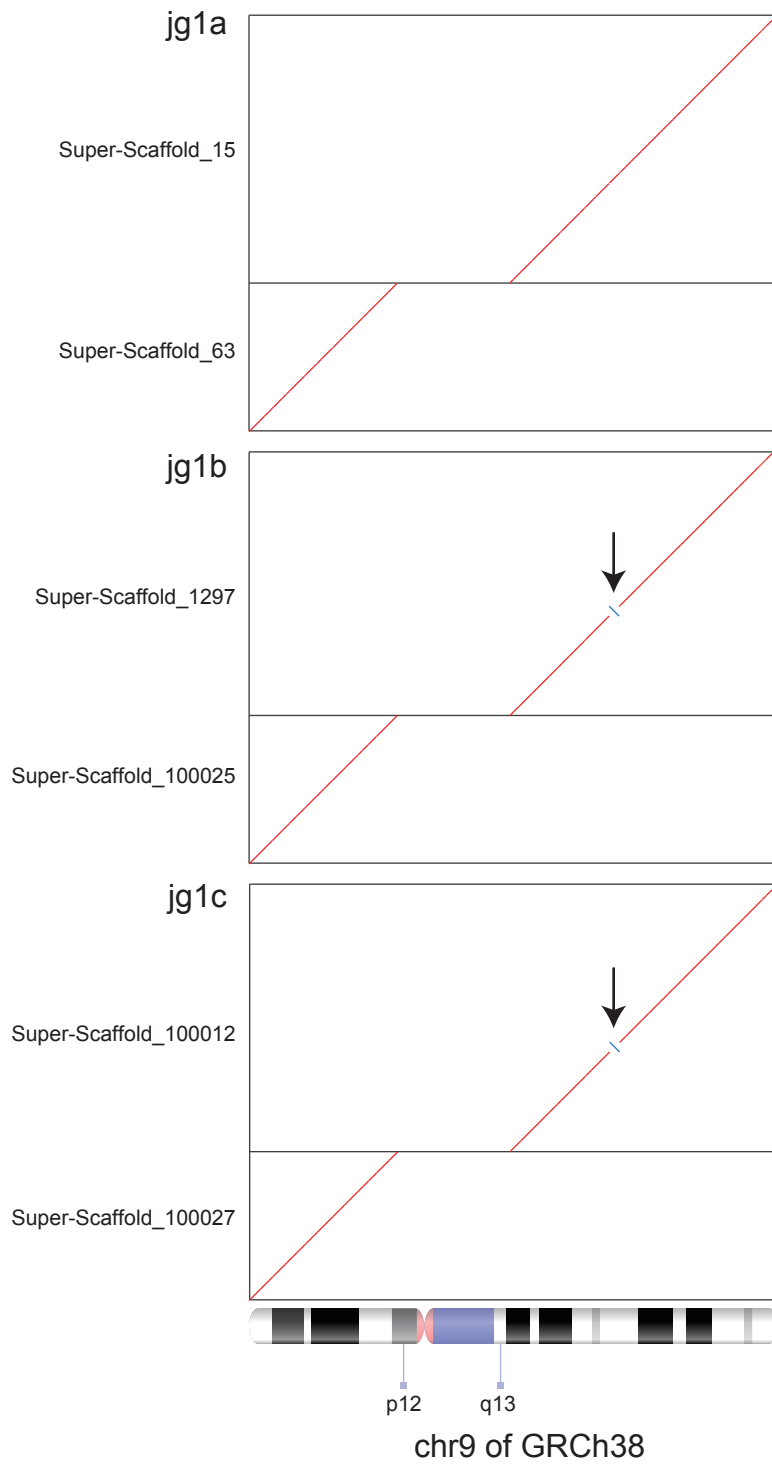
919 (ver. 1.8) isec command.

920

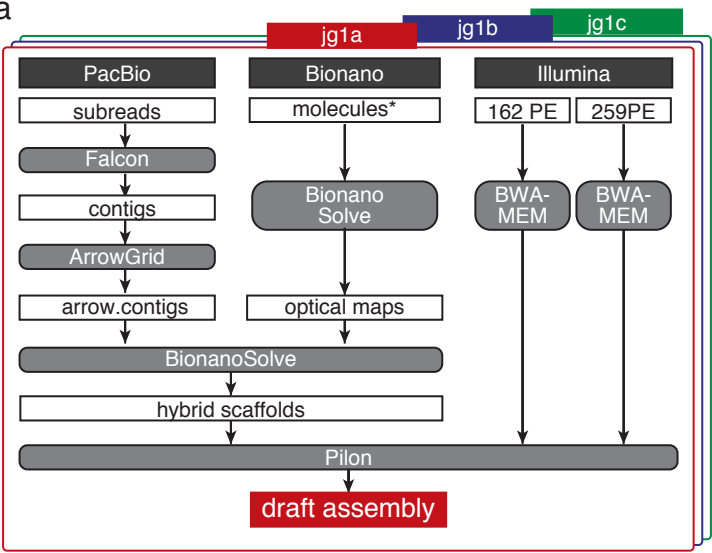
921 **Supplementary Fig. 7:** Length distributions of detected transposable elements in the
922 GRCh38 and JG1 genomes. Shown are *Alu*, SVA, and LINE1. Transposable elements and
923 their subclasses were identified using RepeatMasker software (ver. 4.0.7) with the '-
924 species human' option. The resulting OUT format files were converted to BED format
925 using the `rmsk2bed` command of BEDOPS software⁵⁹ (ver. 2.4.35). Transposable
926 elements disrupted by other elements were counted as distinct.
927



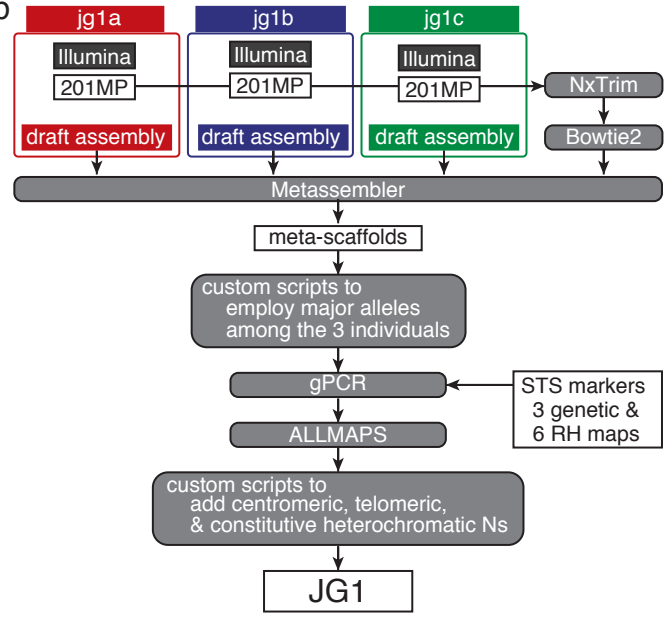
Supplementary Fig. 1; Takayama et al.



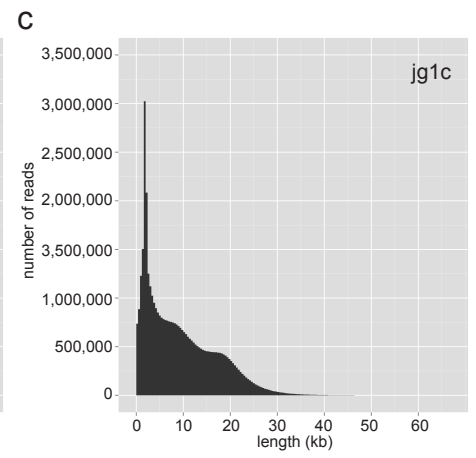
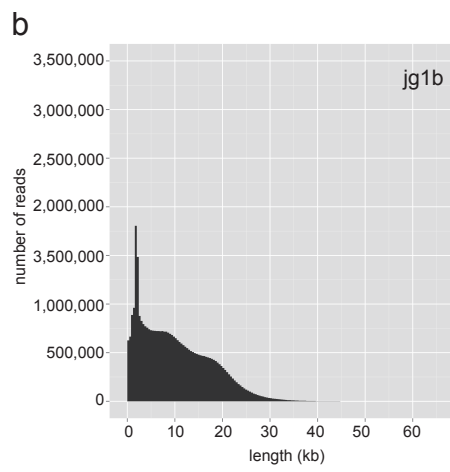
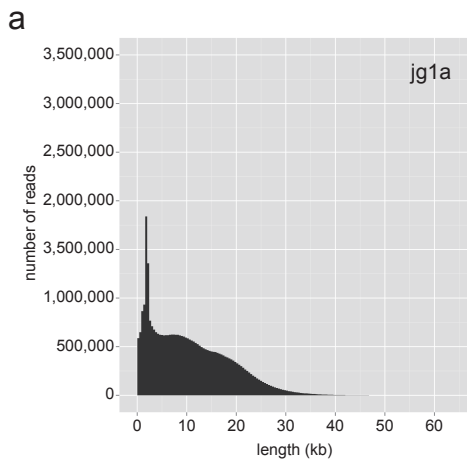
Supplementary Fig. 2
Takayama et al.

a

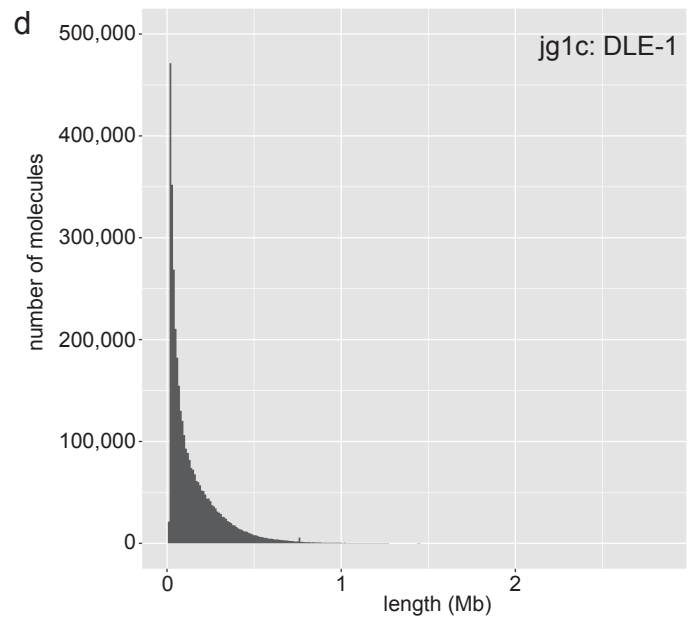
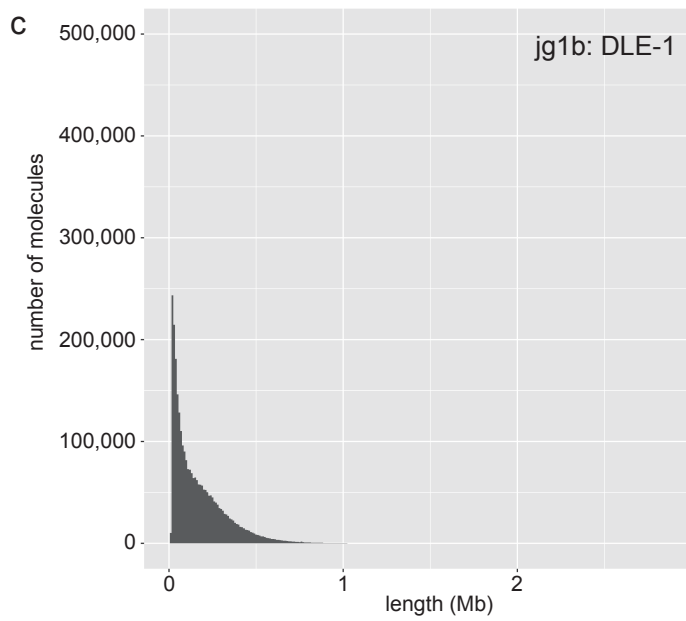
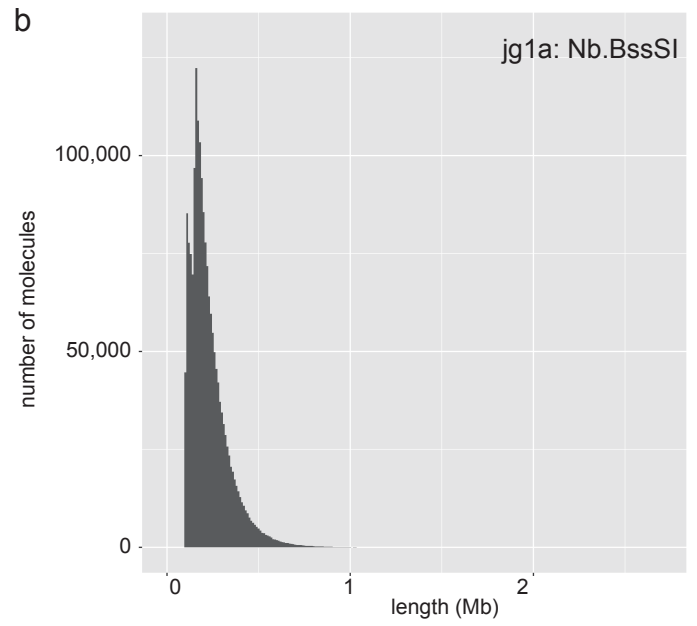
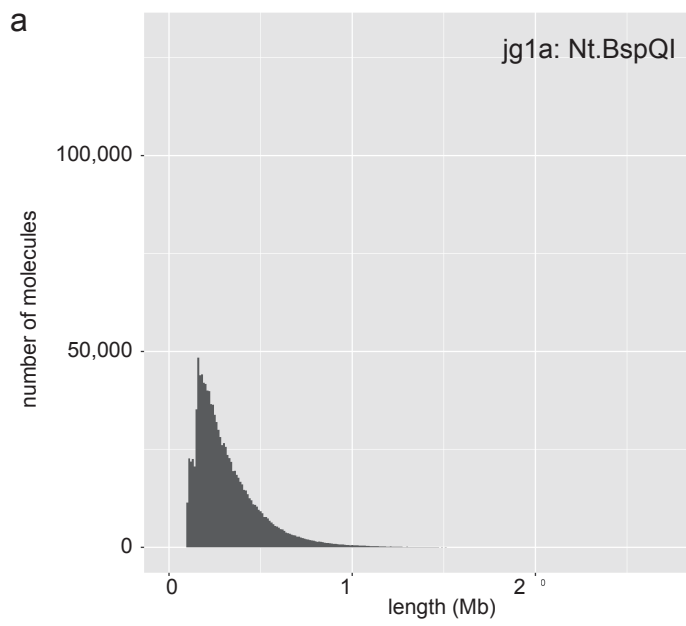
*: Two enzymes (BspQI & BssSI) for jg1a; one enzyme (DEL-1) for jg1b and jg1c

b

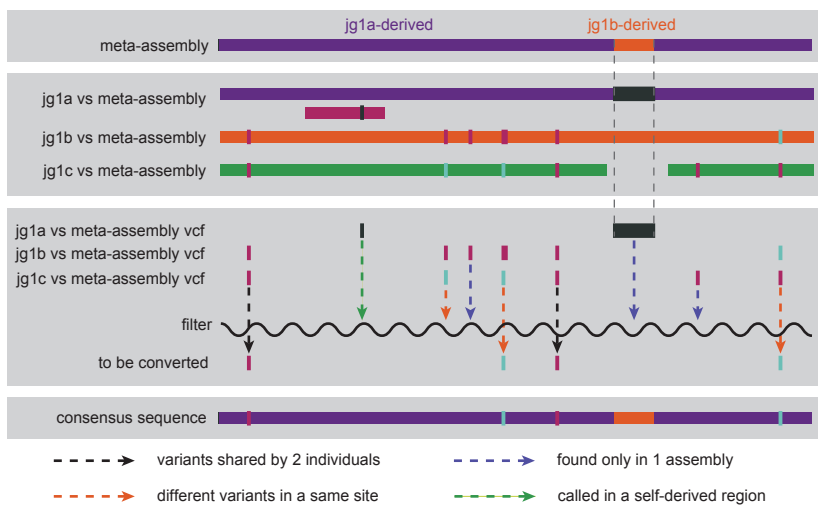
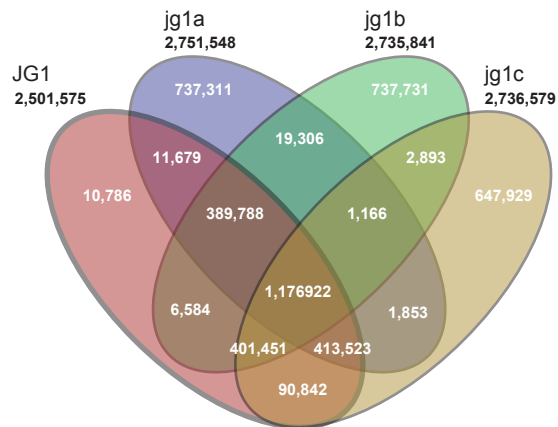
Supplementary Fig. 3; Takayama et al



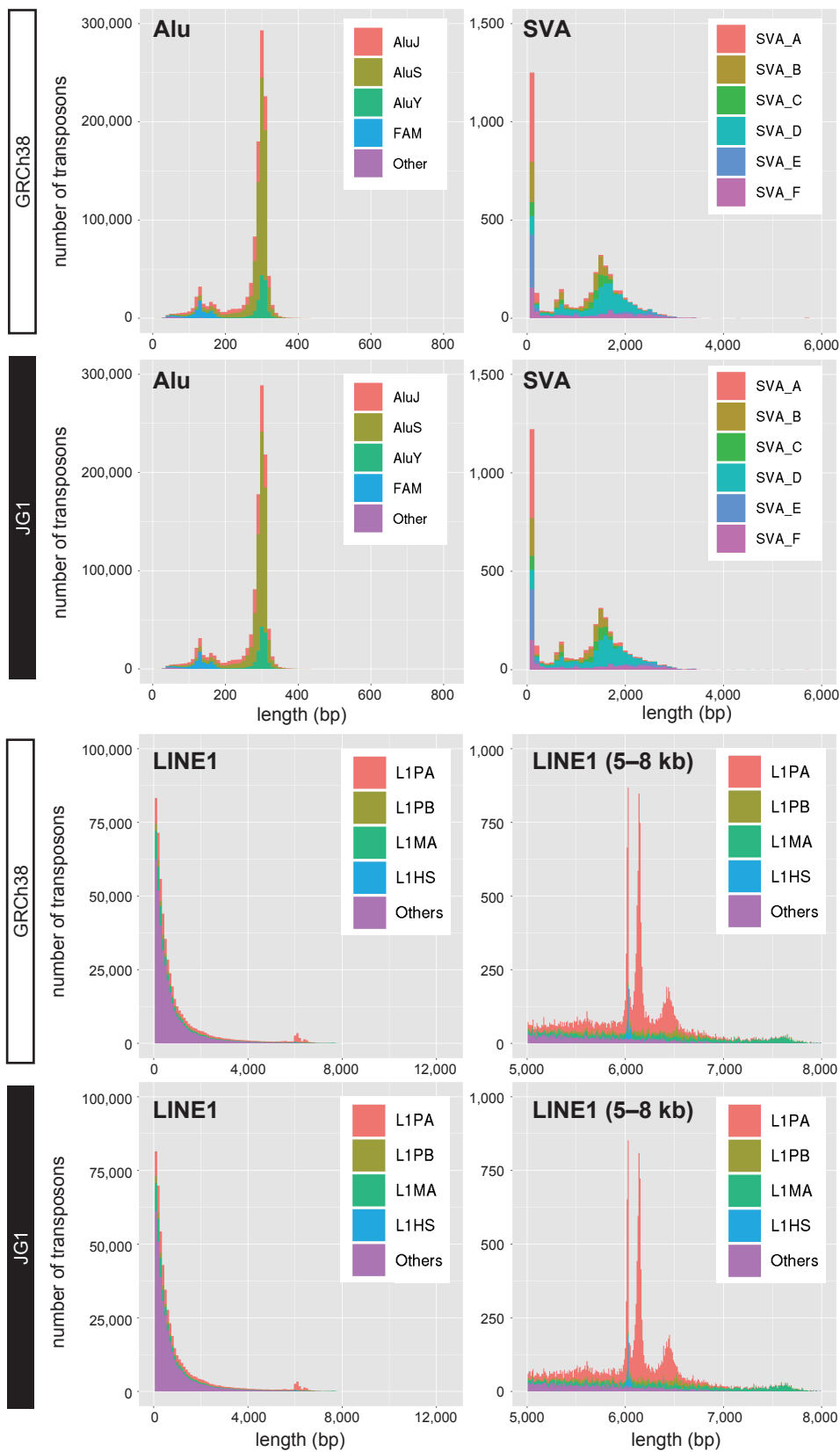
Supplementary Fig. 4
Takayama et al.



Supplementary Fig. 5
Takayama et al.

a**b**

Supplementary Fig. 6
Takayama et al.



Supplementary Fig. 7
Takayama et al.

Supplementary Table 1. Basic statistics of PacBio subreads.

Individual	Number of subreads	Sum of subread length (bp)	depth*
hg1a	34,445,474	364,777,563,591	122X
hg1b	36,798,731	370,437,373,175	123X
hg1c	41,535,337	383,220,406,482	128X

* Depth is calculated by assuming the genome size = 3.0 Gb.

Supplementary Table 2. Basic statistics of Bionano molecules.

Individual	Enzyme	Number of molecules	Sum of molecule length (bp)	depth*
hg1a	BspQI	1,156,682	368,075,072,000	123X
	BssSI	1,834,771	418,513,858,000	140X
hg1b	DLE-1	2,840,733	480,476,071,000	160X
hg1c	DLE-1	3,594,225	524,851,027,000	175X

* Depth is calculated by assuming the genome size = 3.0 Gb.

Supplementary Table 3. Basic statistics of Illumina paired-end and mate-pair reads.

Method	Individual	read length (bp)	# of reads	Sum of read length (bp)	depth*
paired end	hg1a	162	543,599,992	88,063,198,704	29X
		259	303,625,608	78,639,032,472	26X
	hg1b	162	578,161,124	93,662,102,088	31X
		259	319,177,020	82,666,848,180	28X
	hg1c	162	571,414,220	92,569,103,640	31X
		259	302,332,088	78,304,010,792	26X
mate pair**	hg1a	201	189,189,310	38,027,051,310	13X
	hg1b		184,346,446	37,053,635,646	12X
	hg1c		185,928,504	37,371,629,304	12X

* Depth is calculated by assuming the genome size = 3.0 Gb.

**all reads (before library separation)

Supplementary Table 4. Basic statistics of Bionano assembly.

Individual	Enzyme	# of fragments	N50 (Mb)	Total length (Mb)
cg1a	BspQI	4,761	1.179	3846.912
cg1a	BssSI	4,392	1.034	3202.036
cg1b	DLE-1	581	41.761	3194.487
cg1c	DLE-1	496	64.293	3481.086

Supplementary Table 5. Length of consecutive Ns inserted manually.

chr	pter (bp)	cen (bp)	qter (bp)	References
1	10,000	30,000,000	10,000	48–50
2	10,000	3,000,000	10,000	
3	10,000	3,000,000	10,000	
4	10,000	3,000,000	10,000	
5	10,000	3,000,000	10,000	
6	10,000	3,000,000	10,000	
7	10,000	3,000,000	10,000	
8	10,000	-	10,000	
9	10,000	30,000,000	10,000	48–50
10	10,000	3,000,000	10,000	
11	10,000	-	10,000	
12	10,000	3,000,000	10,000	
13	16,000,000	-	10,000	50
14	16,000,000	-	10,000	50
15	17,000,000	-	10,000	50
16	10,000	20,000,000	10,000	48–50
17	10,000	3,000,000	10,000	
18	10,000	3,000,000	10,000	
19	10,000	3,000,000	10,000	
20	10,000	3,000,000	10,000	
21	11,000,000	-	10,000	
22	13,000,000	-	10,000	
X	10,000	3,000,000	10,000	
Y	2,260,577	3,000,000	30,000,000	48, 51–53