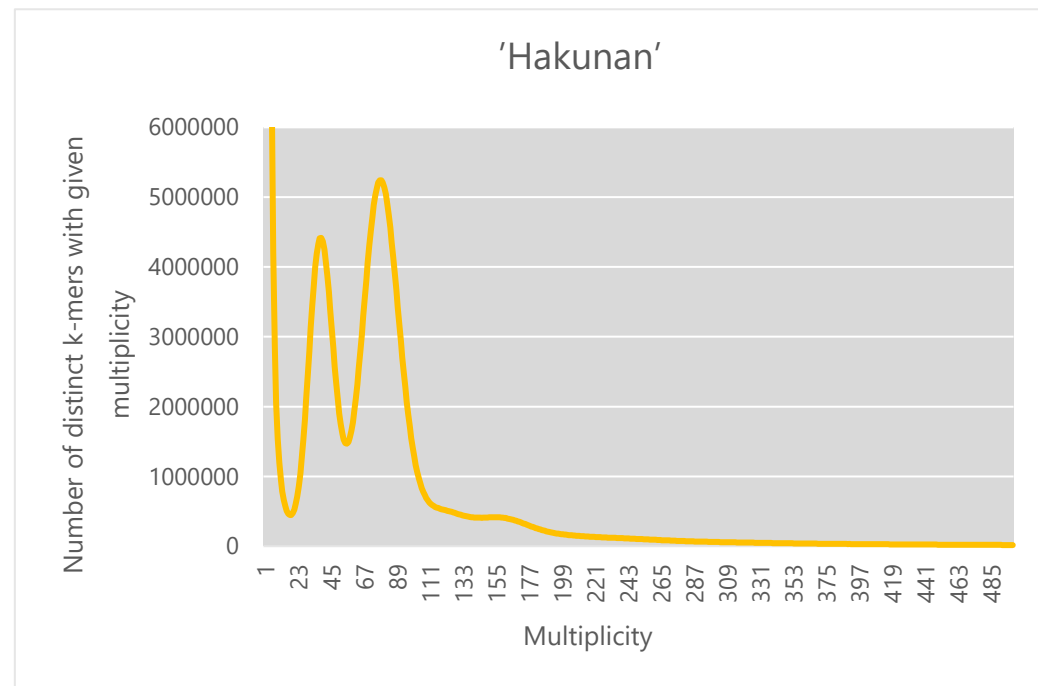


	Peak	Estimated Coverage:	Estimated Genome Size:
Shine_Muscat	111	119.8	999,223,129.4
	225	242.8	492,950,077.2
Akitsu21	58	64.9	1,112,728,631.9
	117	130.9	551,609,065.4
Hakunan	39	43.6	1,116,387,055.0
	79	88.4	551,127,786.8



Supplementary Fig. S1. Genome size estimation using Jellyfish with the distribution of the number of distinct kmers (kmer = 17) with the given multiplicity values.

'Shine Muscat'

AKitsu 21

'Hakunan'

GenomeScope Profile

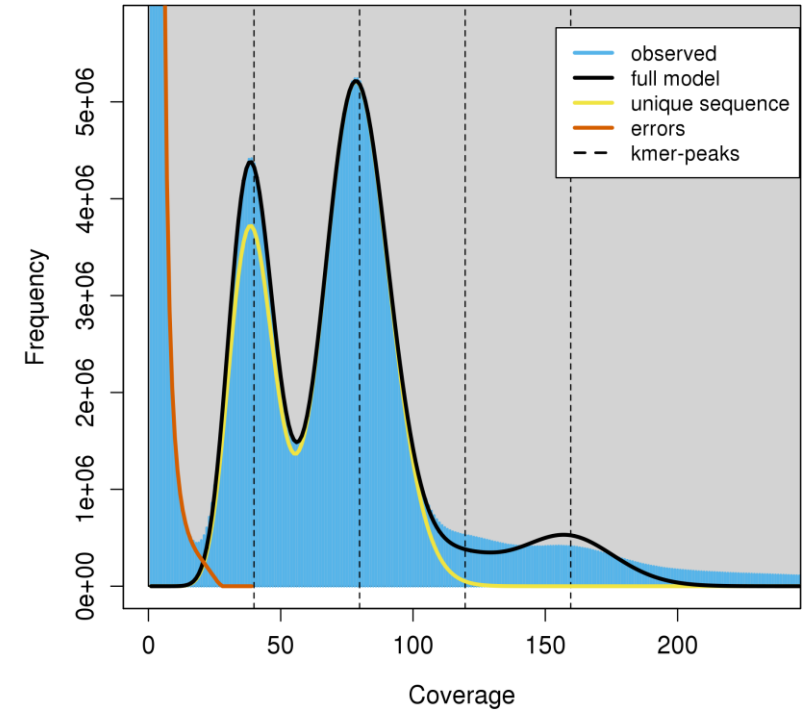
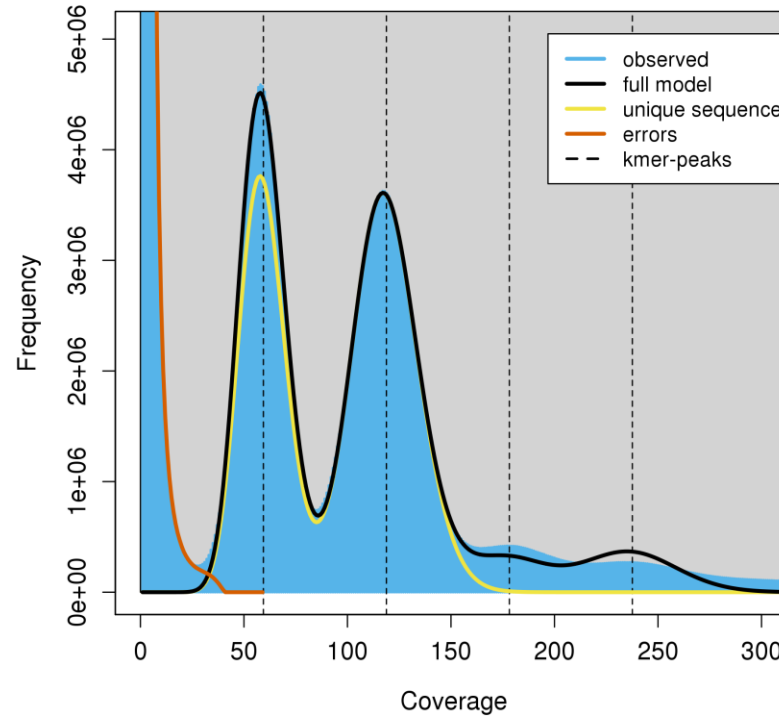
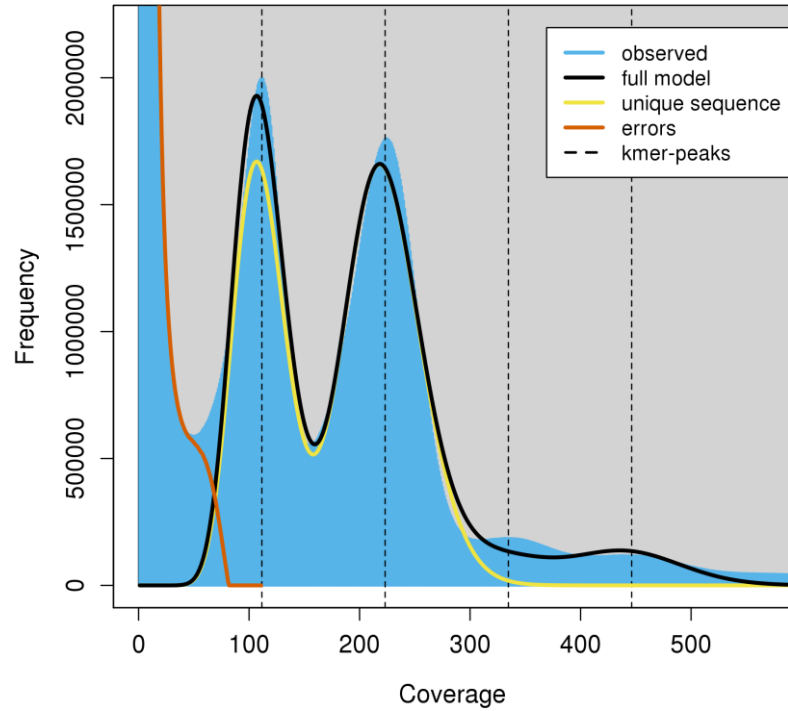
len:374,085,271bp uniq:51.1% het:1.79% kcov:112 err:0.499% dup:4.25% k:17

GenomeScope Profile

len:447,230,329bp uniq:43.5% het:1.85% kcov:59.4 err:0.295% dup:1.1% k:17

GenomeScope Profile

len:455,057,695bp uniq:43.6% het:1.32% kcov:39.9 err:0.301% dup:0.865% k:17



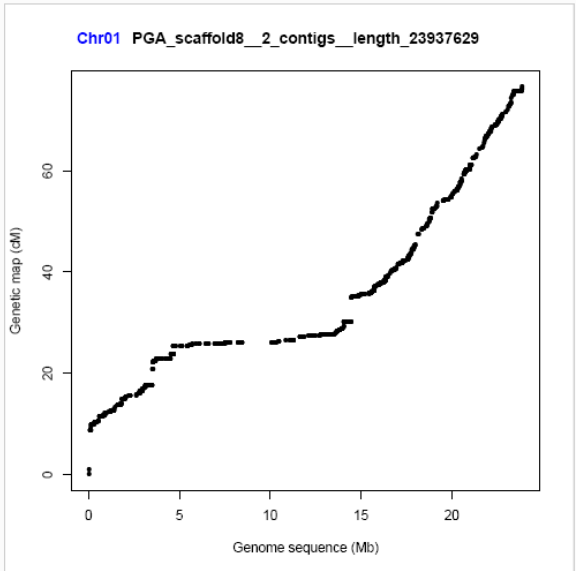
Supplementary Fig. S2. Genome size and heterozygosity estimation using Genomescope 1.0 with the distribution of the number of distinct kmers (kmer = 17) with the given multiplicity values.

Supplementary Fig. S3.

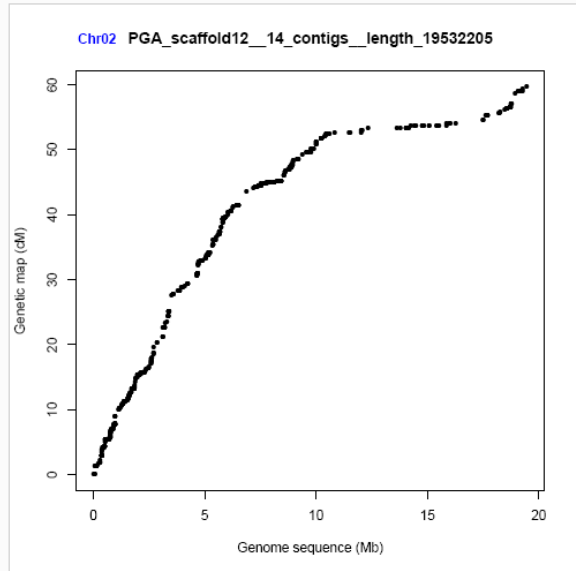
Comparisons of variant positions mapped on the longest 19 Hi-C scaffolds and the integrated linkage map.

The names under the heading 'PGA_scaffold' represents the names of the 19 Hi-C scaffolds. The chromosome numbers given later on the analysis were shown with blue letters.

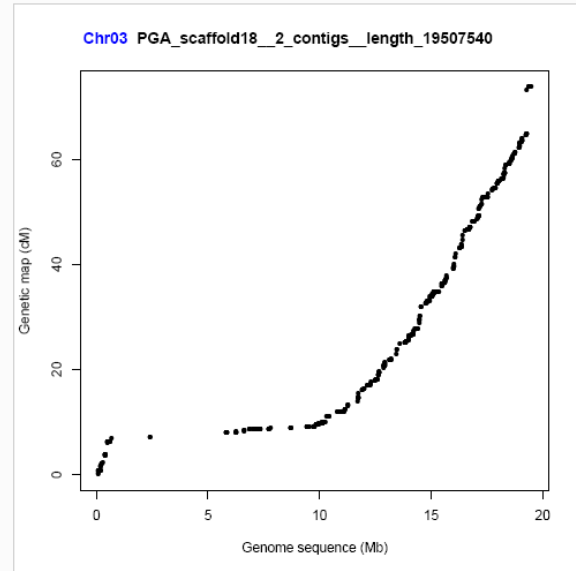
A) Comparison with the integrated linkage map



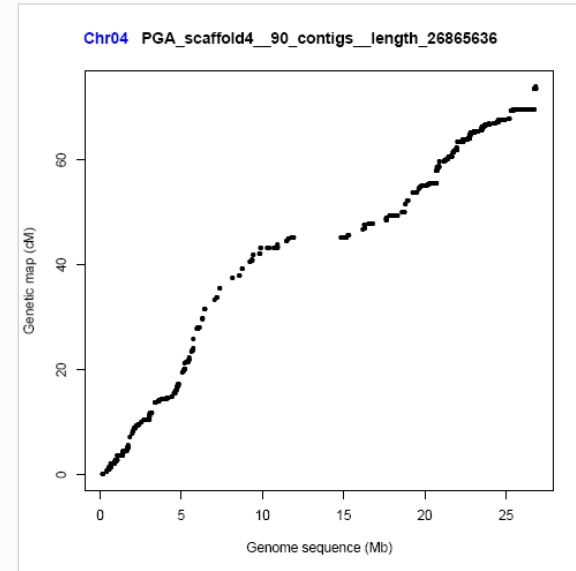
1



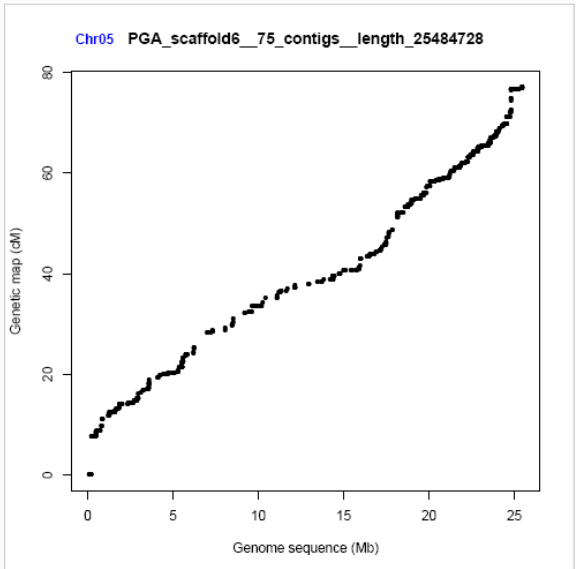
2



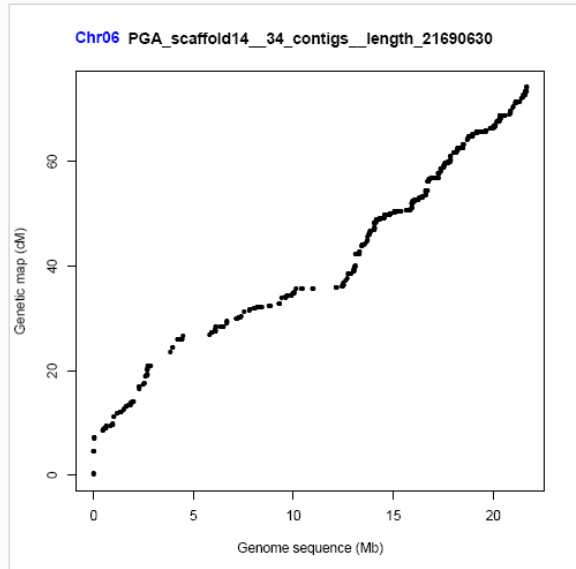
3



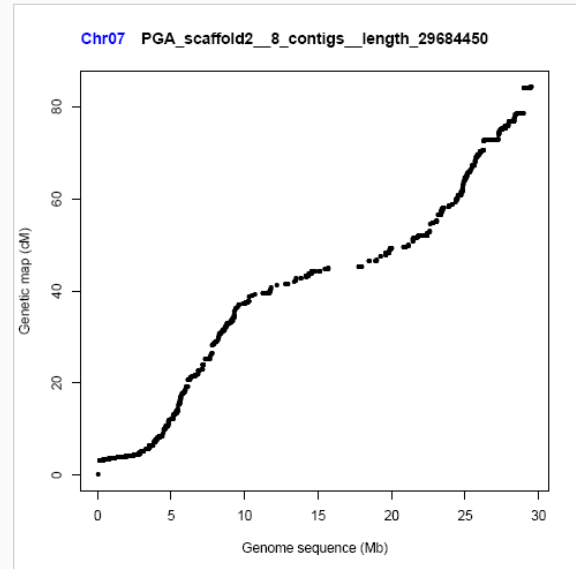
4



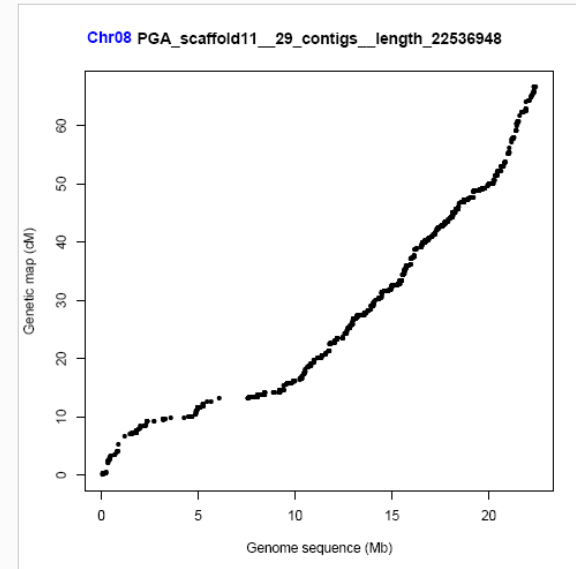
5



6

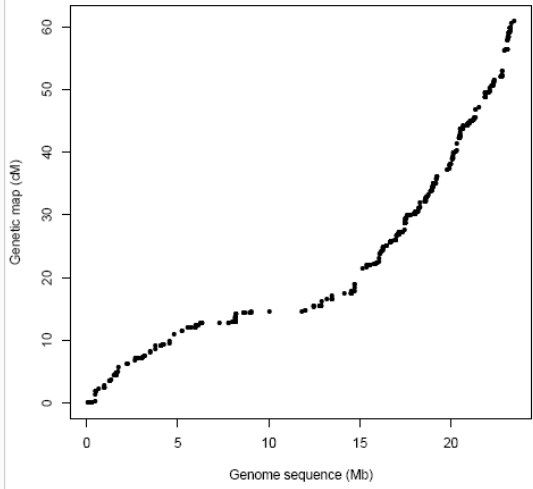


7



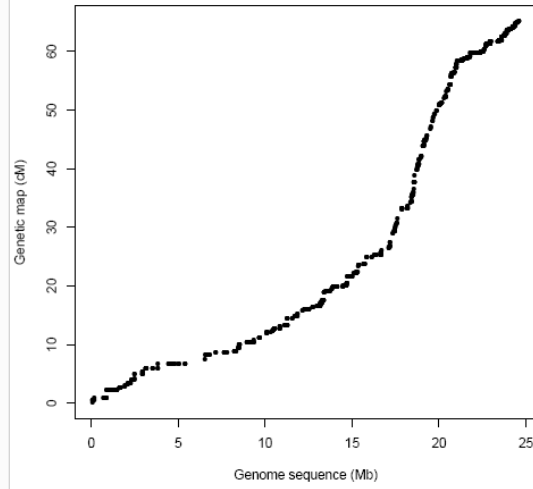
8

Chr09 PGA_scaffold9_80_contigs_length_23488122



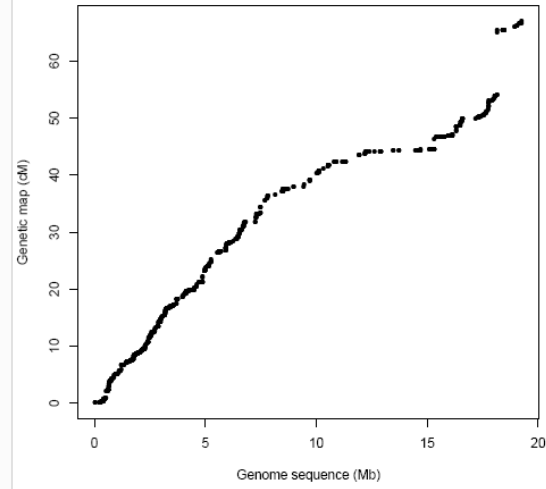
9

Chr10 PGA_scaffold7_6_contigs_length_24671681



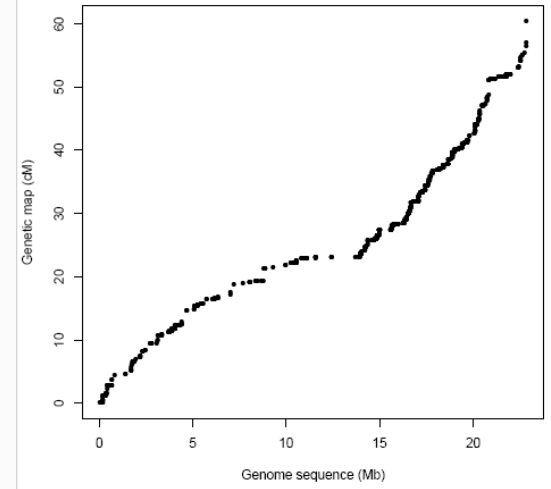
10

Chr11 PGA_scaffold16_8_contigs_length_19281646



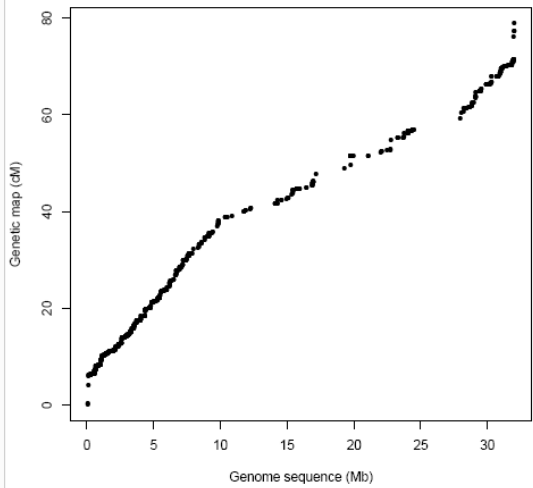
11

Chr12 PGA_scaffold10_3_contigs_length_22859447



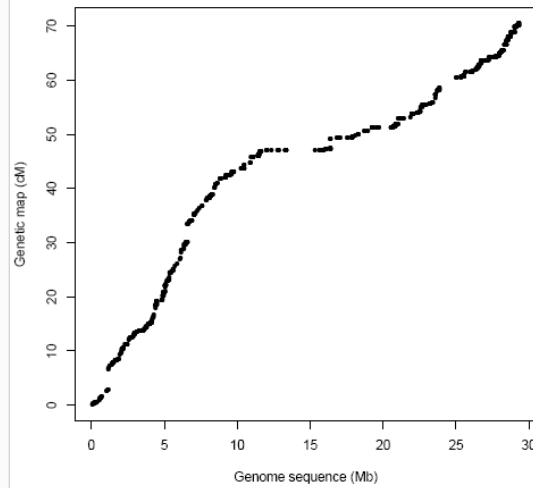
12

Chr13 PGA_scaffold0_5_contigs_length_32036281



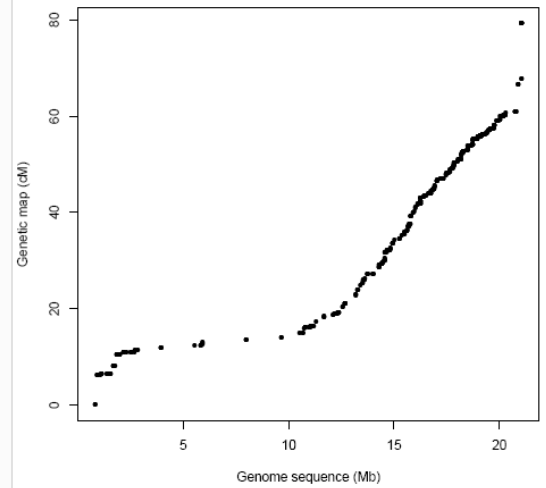
13

Chr14 PGA_scaffold3_5_contigs_length_29504403



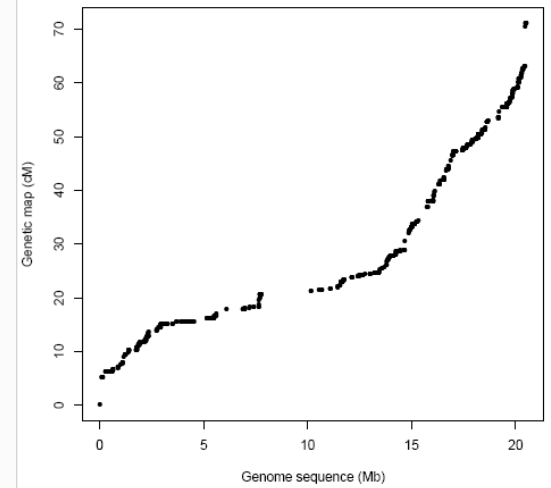
14

Chr15 PGA_scaffold15_11_contigs_length_21074376



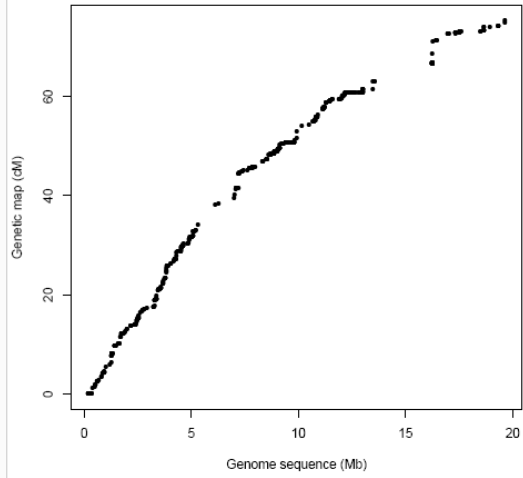
15

Chr16 PGA_scaffold17_11_contigs_length_20575746



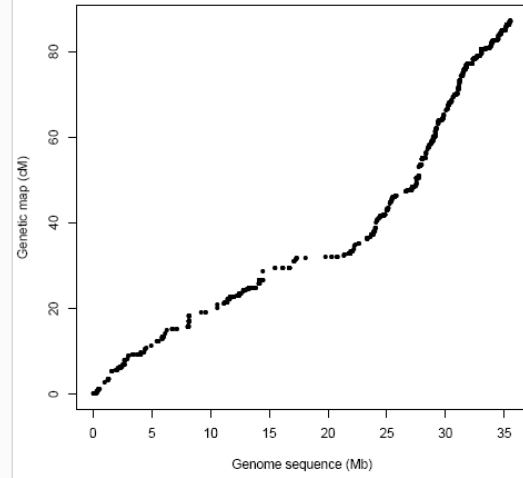
16

Chr17 PGA_scaffold13_5_contigs_length_20111917



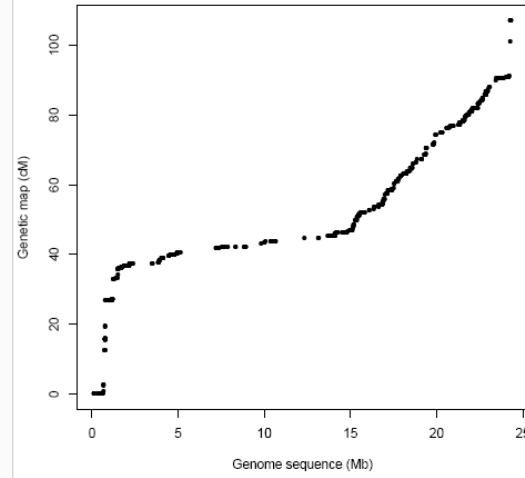
17

Chr18 PGA_scaffold1_41_contigs_length_35651461

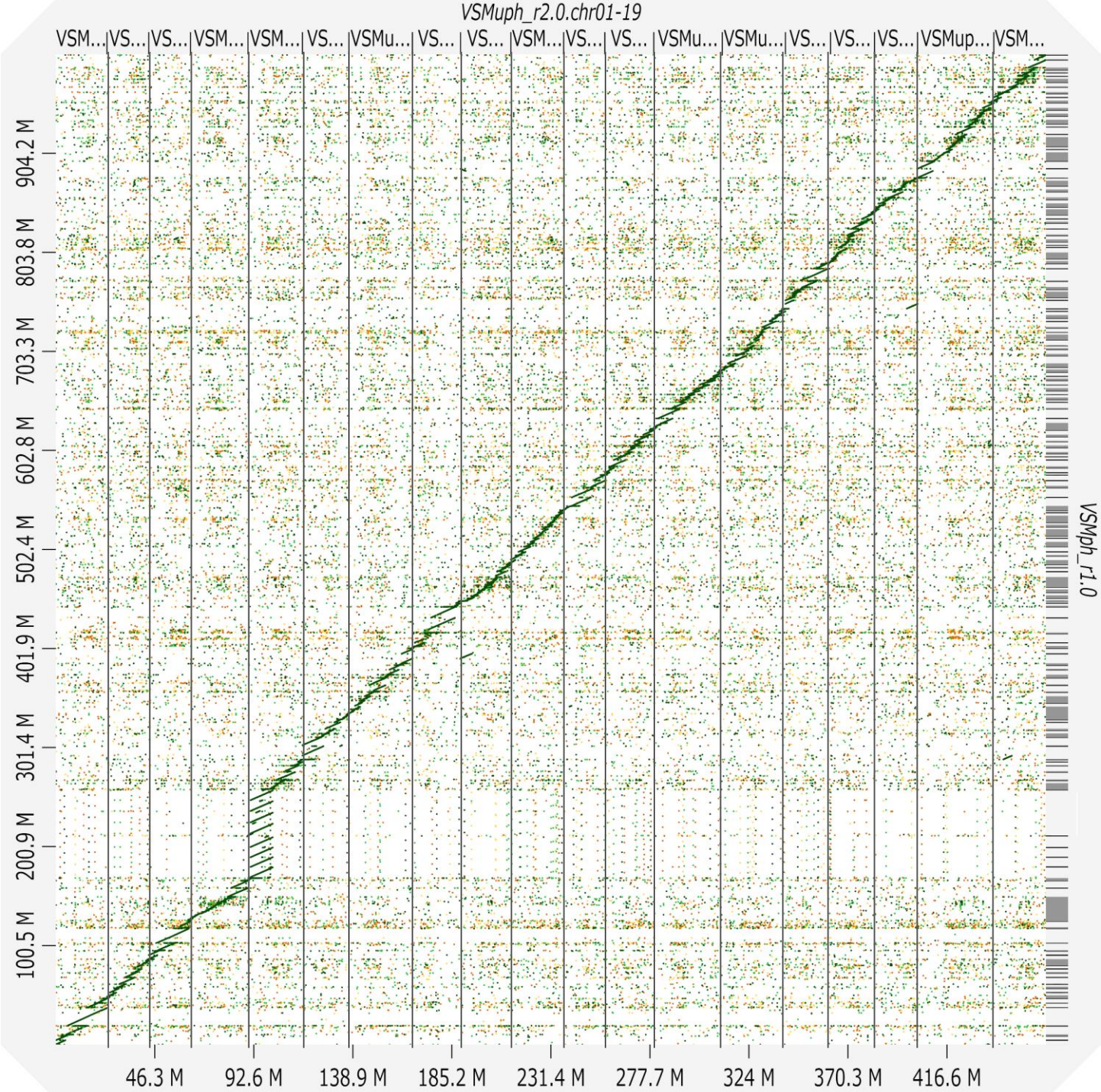


18

Chr19 PGA_scaffold5_62_contigs_length_24390762



19

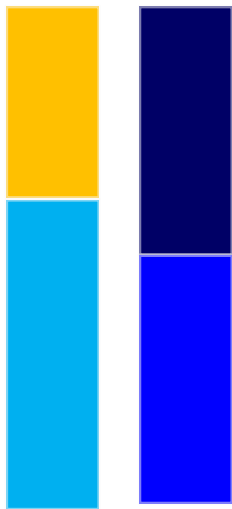


Supplementary Fig. S4. The genome sequences comparisons between the 19 pseudomolecules in VSMuph_r2.0 (unphased) and VSMph_r1.0 (phased) sequences.

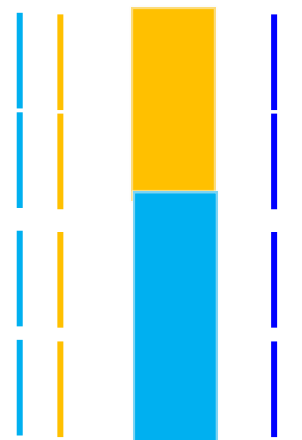
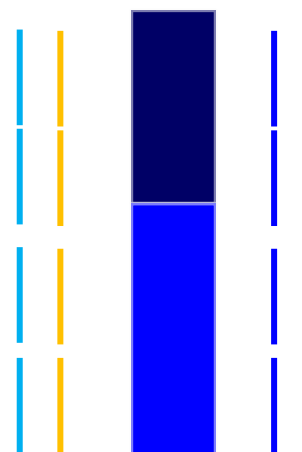
A)

Akitsu 21
V. labruscana × *V. vinifera*'Hakunan'
V. vinifera

'Shine Muscat'



B)

Mapping
Akitsu 21 reads**Expected allele type**Major: Hetero
Minor: Ref homo
Few: Alt homo*Few Alt homo allele were identified because of sequence differences between *V. labruscana* and *V. vinifera*.Scaffold from
Akitsu 21Mapping
'Hakunan' reads**Expected allele type**Major: Ref homo
Minor: Hetero
Few: Alt homoScaffold from
'Hakunan'**Expected allele type**Major: Alt homo
Minor: Hetero
Few: Ref homo**Expected allele type**Major: Ref homo
Minor: Hetero
Few: Alt homo

Supplementary Fig. S5. A schematic diagram of parental rads mapped onto the 'Shine Muscat' unphased genome and expected allele types on the variants. A) The haploid genome structure of the 'Shine Muscat' and the parental genomes. B) Expected allele types of Akitsu 21 and 'Hakunan' identified on the unphased 'Shine Muscat' genome sequences.

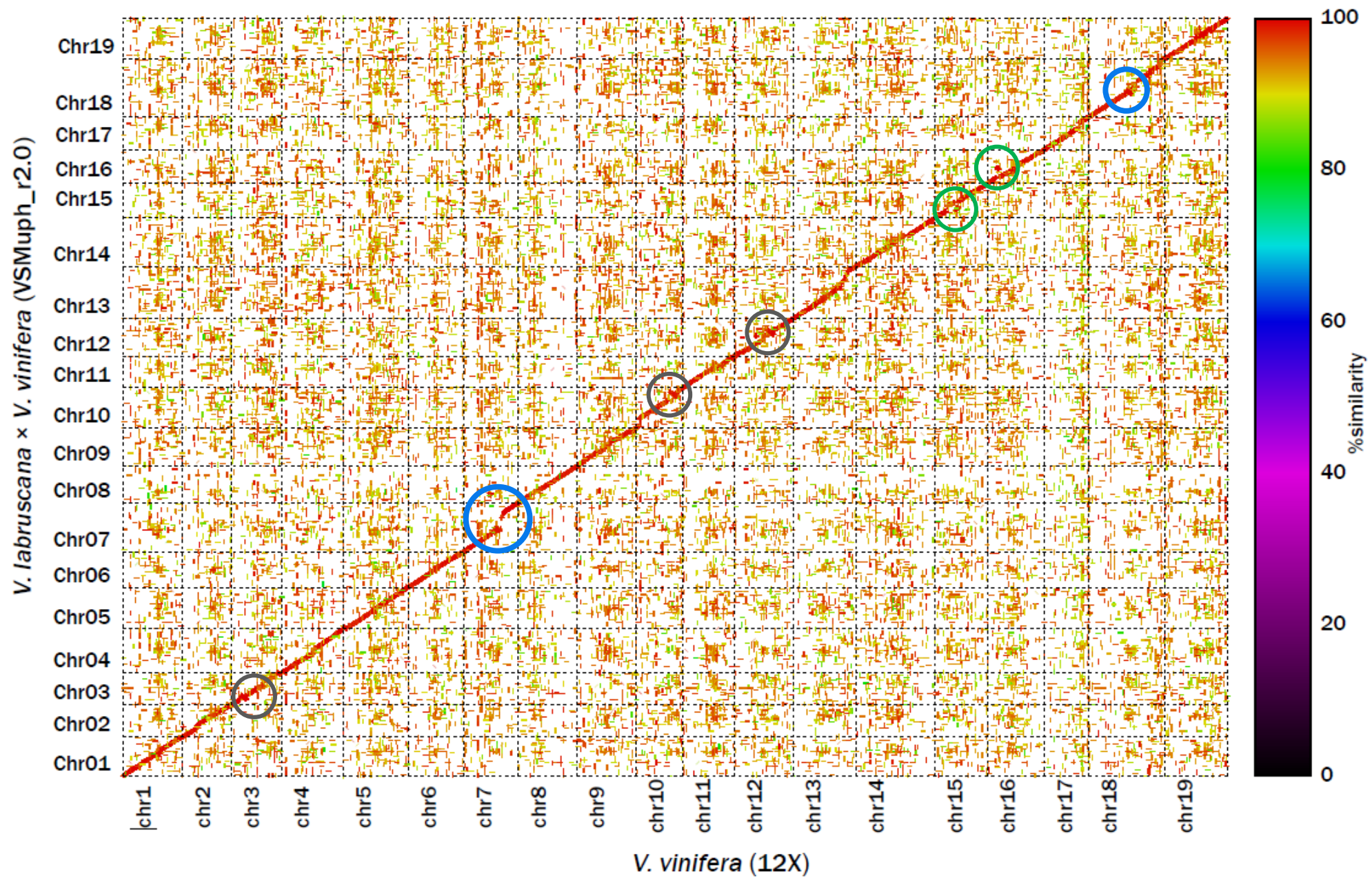
Supplementary Fig. S6. The genome sequences comparisons between the 19 pseudomolecules in VSMuph_r2.0 and those in *V. vinifera*, *V. vinifera* subsp *sylvestrie* and *V. riparia*. Blue, green and black circles show genome regions observed possible deletion, duplication and inversion on VSMuph_r2.0 against the compared sequences.

A) *V. vinifera* (12X) vs *V. labruscana* × *V. vinifera* (VSMuph_r2.0)

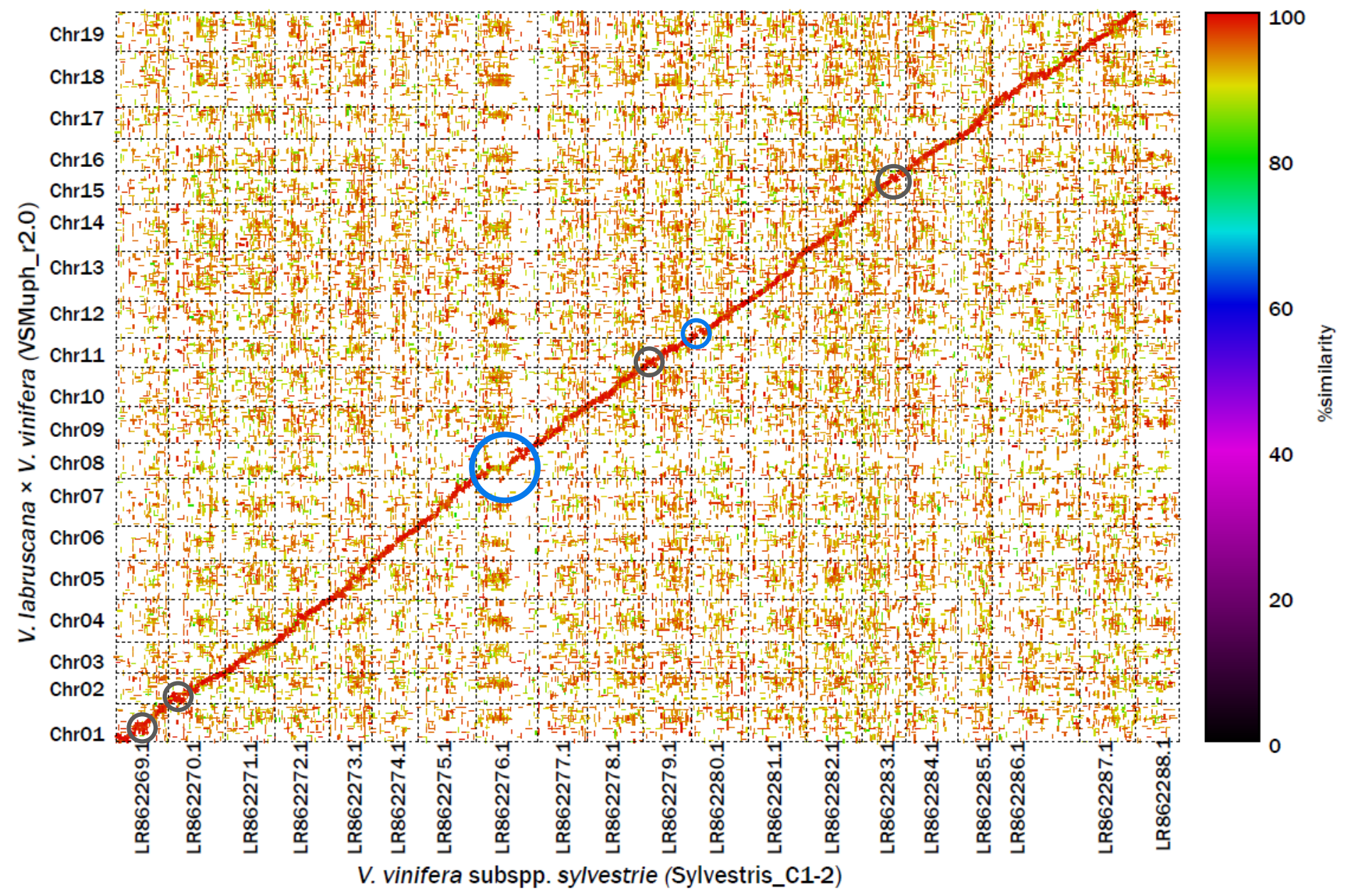
B) *V. vinifera* subsp. *sylvestrie* (Sylvestris_C1-2) vs *V. labruscana* × *V. vinifera* (VSMuph_r2.0)

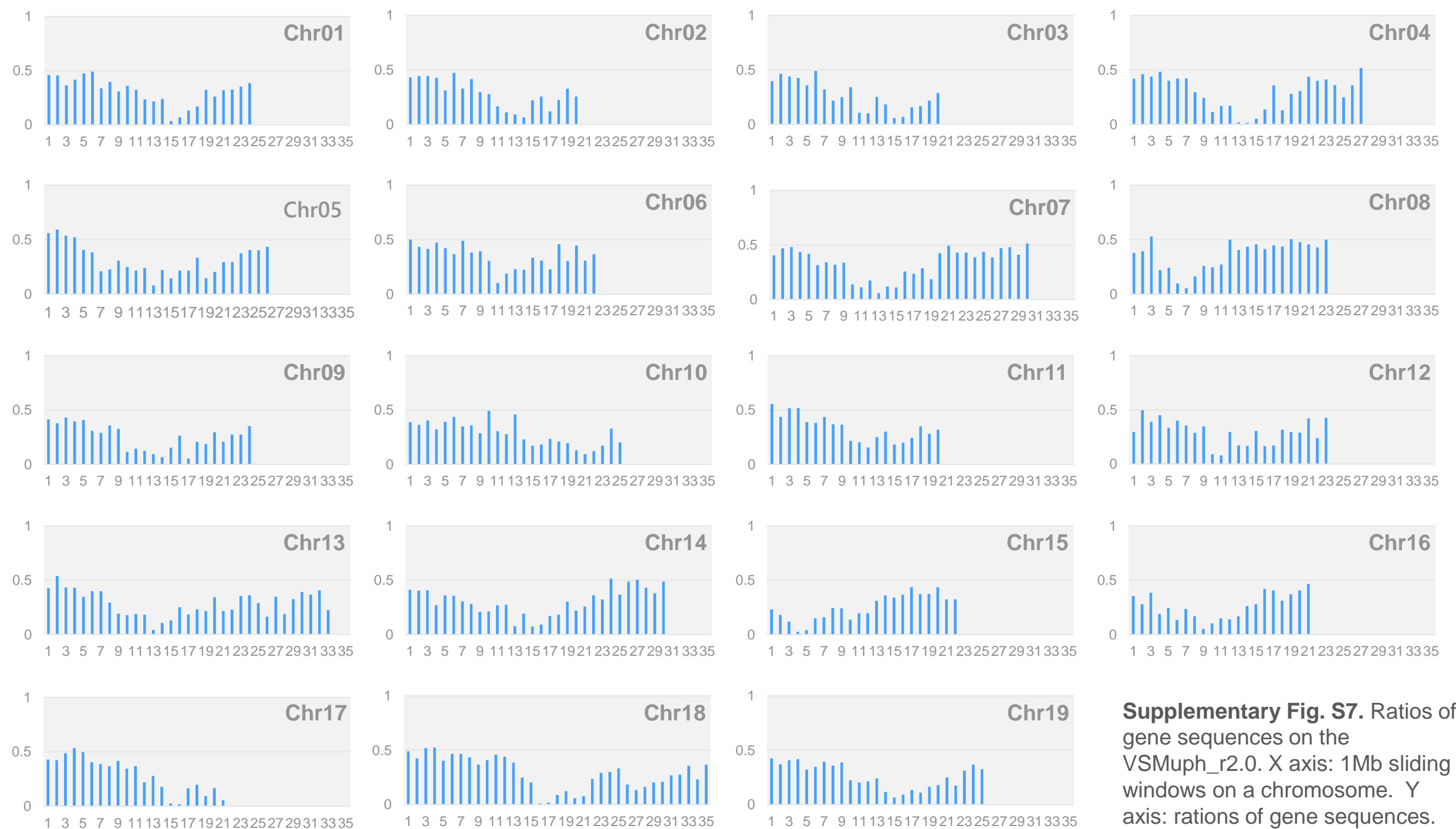
C) *V. riparia* (EGFV_Vit.rip_1.0) vs *V. labruscana* × *V. vinifera* (VSMuph_r2.0)

A) *V. vinifera* (12X) vs *V. labruscana* × *V. vinifera* (VSMuph_r2.0)

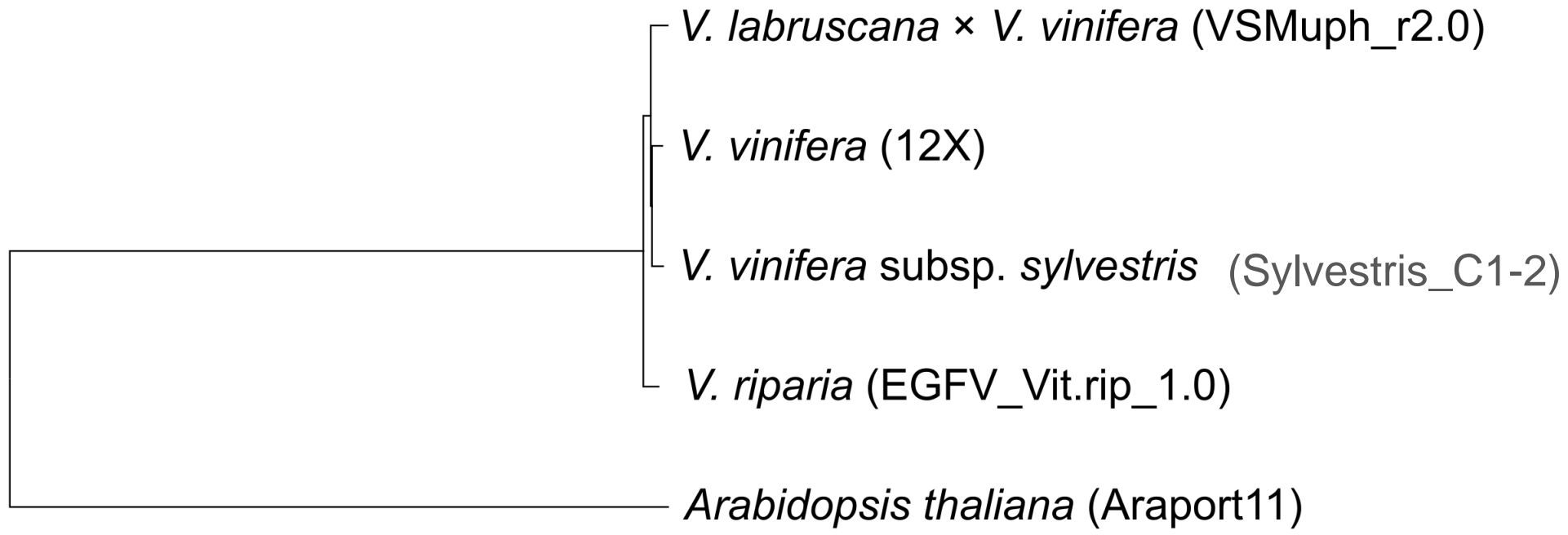


B) *V. vinifera* subsp. *sylvestrie* (Sylvestris_C1-2) vs *V. labruscana* × *V. vinifera* (VSMuph_r2.0)





Supplementary Fig. S7. Ratios of gene sequences on the VSMuph_r2.0. X axis: 1Mb sliding windows on a chromosome. Y axis: ratios of gene sequences.



0.050

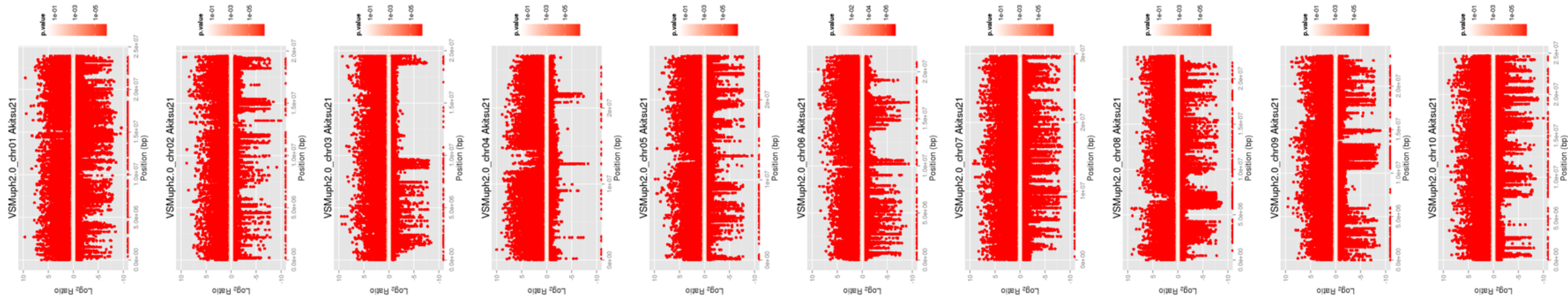
Supplementary Fig. S8. A phylogenetic tree of 956 common single copy genes of the four *Vitis* species *A. thaliana*.

Supplementary Fig. S9. Copy Number Variation of Akitsu 21 and 'Hakunan' against the unphased 'Shine Muscat' genome, VSMuph_r2.0.

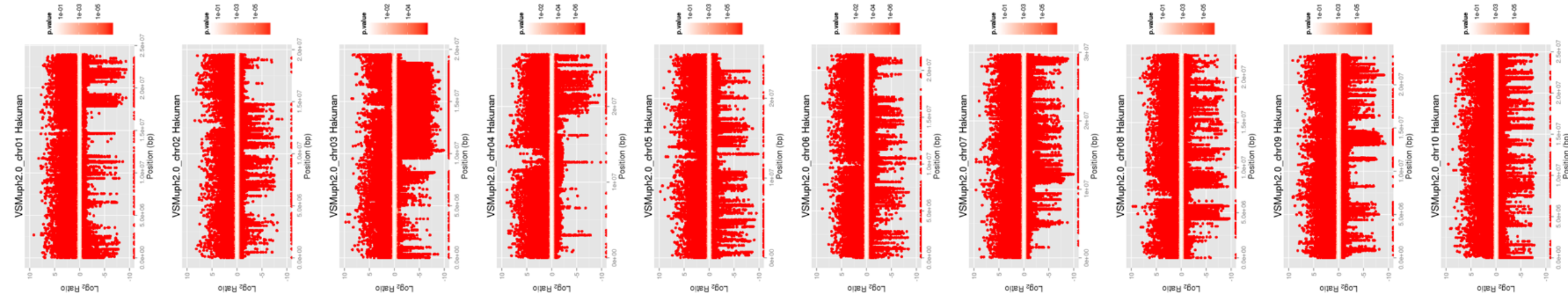
The Log_2 ratio and p values was estimated by CNV-Seq software, based on mapped read count in each 1Mb sliding window.

Chr01-Chr10

Akitsu 21

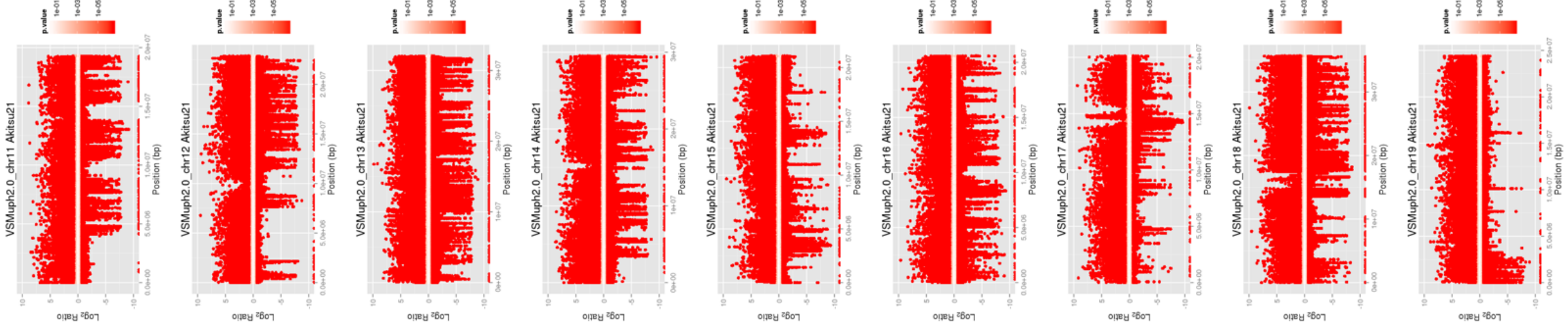


Hakunan



Chr11-Chr19

Akitsu 21



Hakunan

