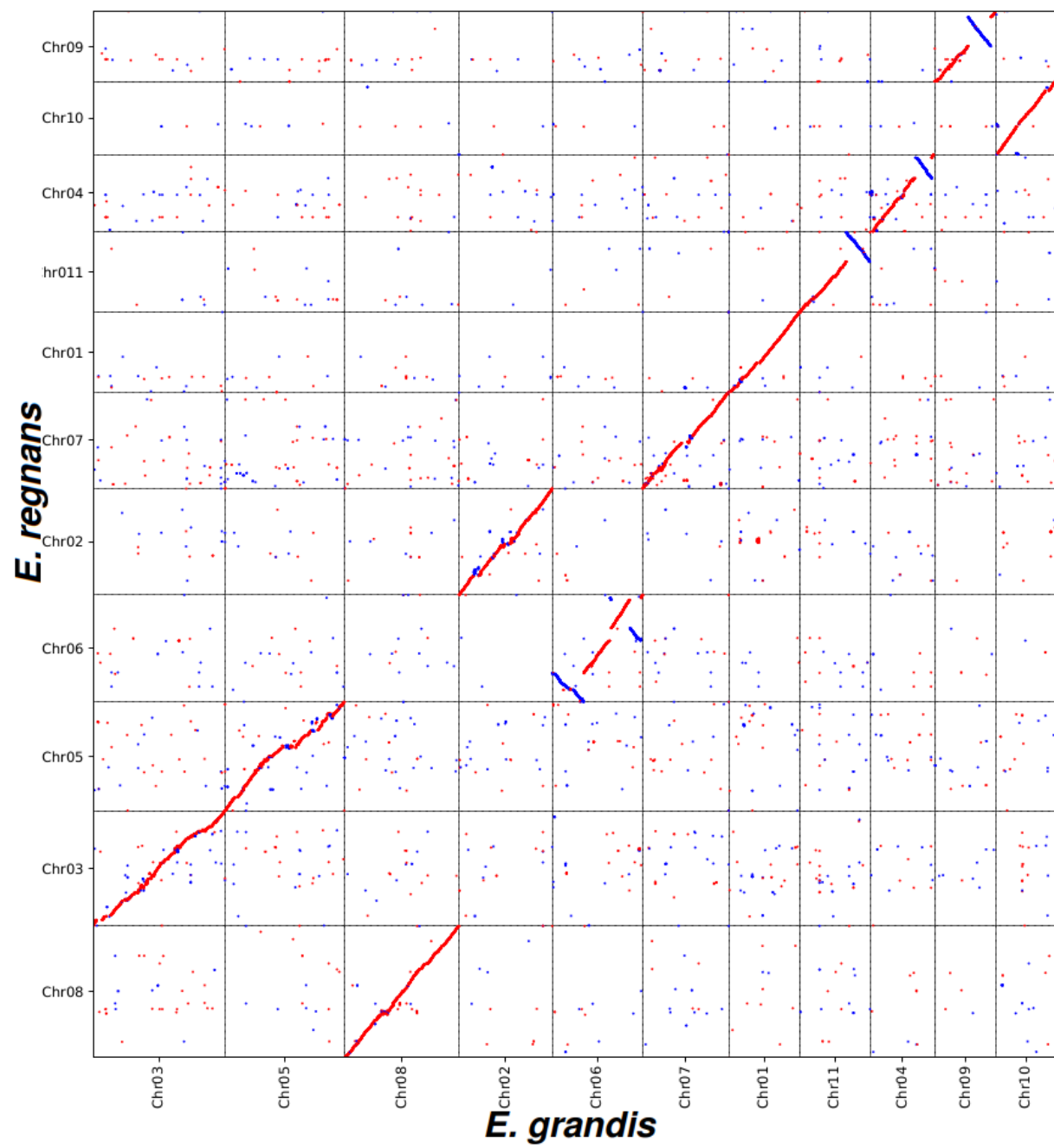


Supplementary Table S1. Genome BUSCO scores.

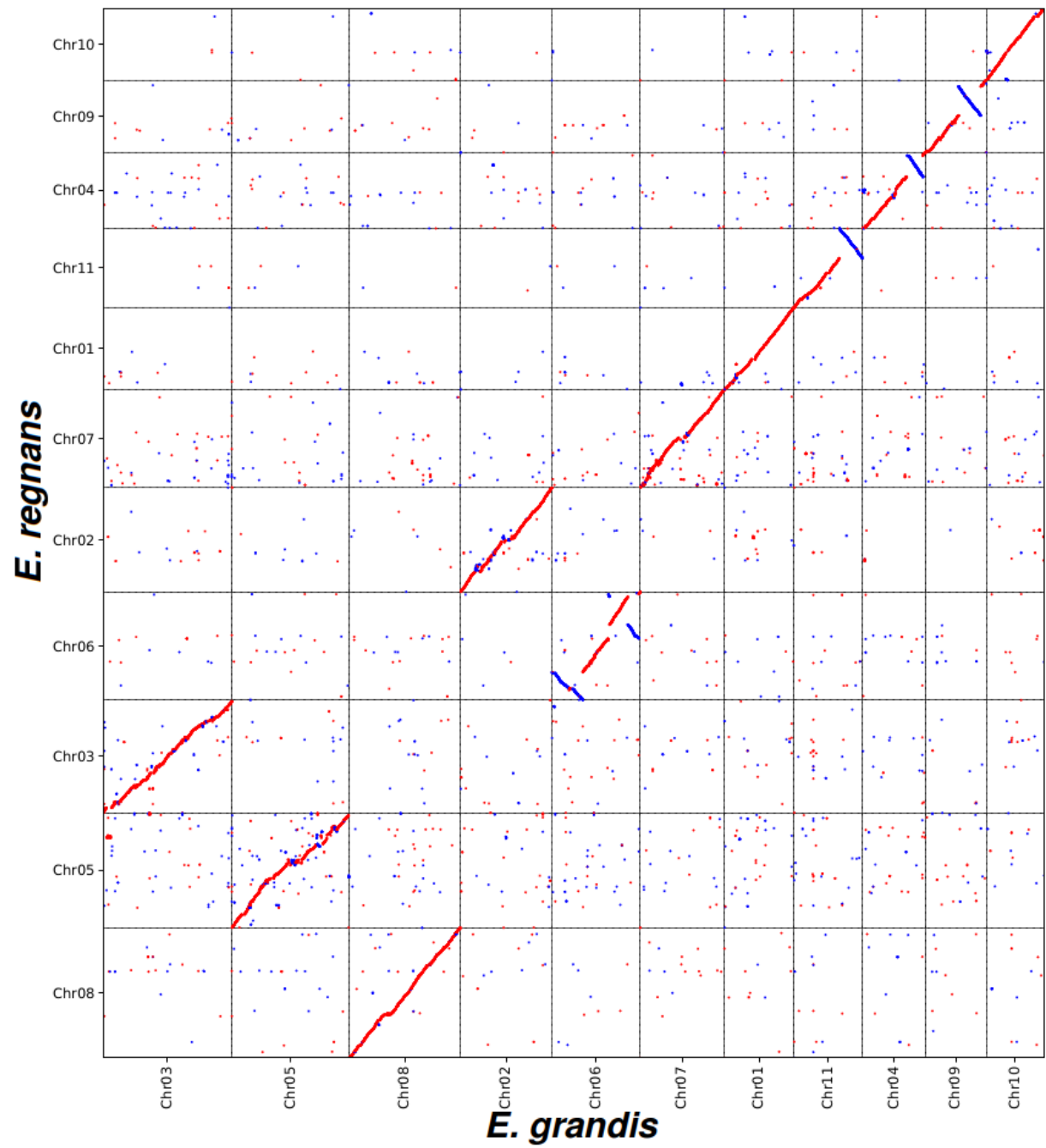
	Haplotype 1		Haplotype 2	
	Count	Percent	Count	Percent
Complete	2,262	97.25%	2,215	95.23%
Complete and single-copy	1,938	83.32%	1,924	82.72%
Complete and duplicated	324	13.93%	291	12.51%
Fragmented	22	0.95%	42	1.81%
Missing	42	1.81%	69	2.97%

Supplementary Table S2. Telomere location and length.

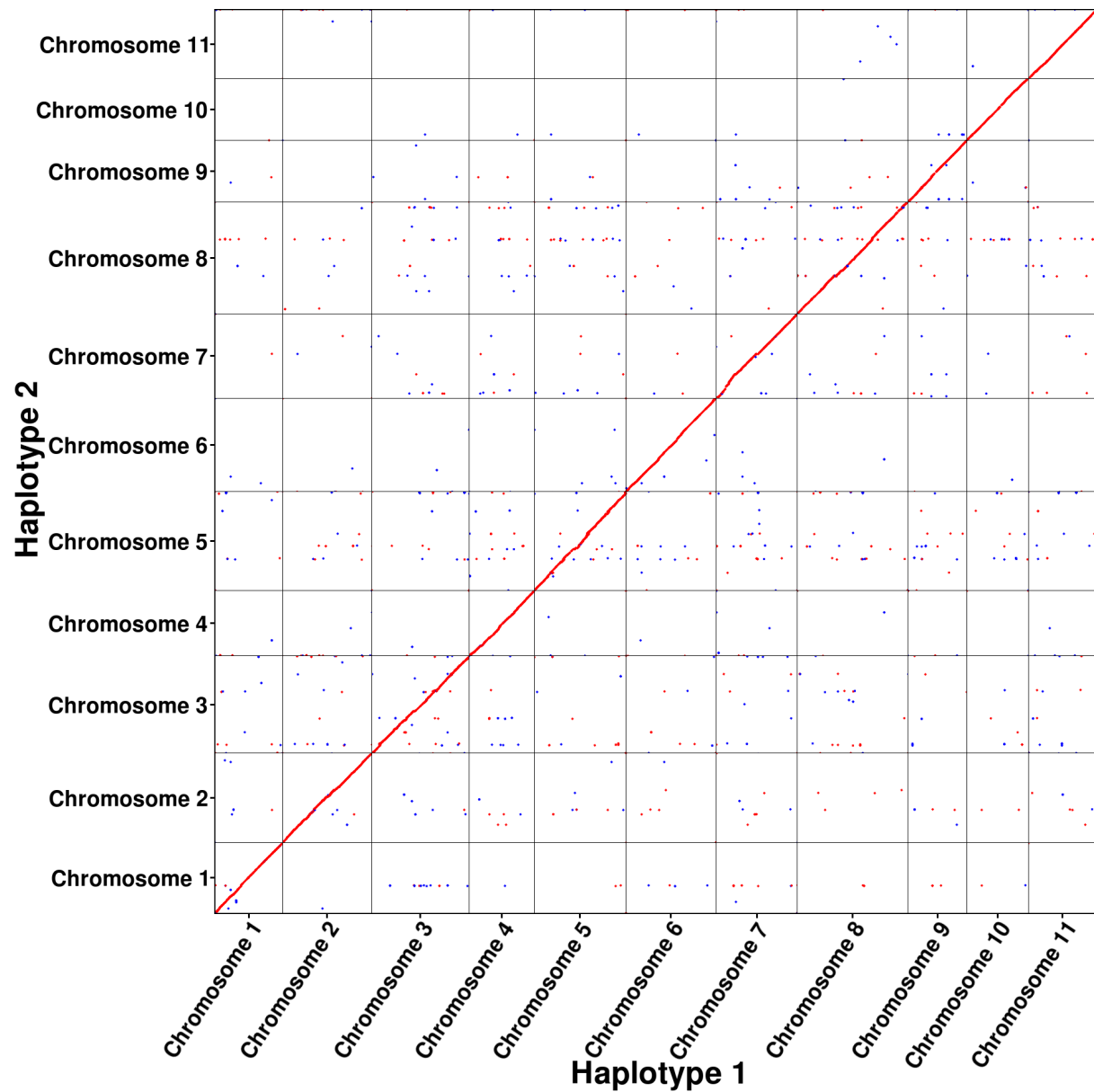
	Haplotype 1				Haplotype 2			
	5'		3'		5'		3'	
	Position	Length (bp)	Position	Length (bp)	Position	Length (bp)	Position	Length (bp)
Chr01	5' - 9,733	9,733	36,815,509 - 3'	9,529	5' - 5,338	5,338	37,746,093 - 3'	2,333
Chr02	5' - 9,448	9,448	48,724,974 - 3'	8,923	5' - 8,720	8,720	48,106,521 - 3'	11,331
Chr03	5' - 7,256	7,256	52,851,340 - 3'	7,232	5' - 9,615	9,615	52,049,455 - 3'	10,349
Chr04	5' - 14,330	14,330			5' - 12,787	12,787	34,897,684 - 3'	3,291
Chr05	5' - 10,596	10,596	49,832,280 - 3'	8,800	5' - 6,990	6,990	53,041,714 - 3'	12,845
Chr06	5' - 11,159	11,159	48,960,576 - 3'	7,914	5' - 6,148	6,148	50,009,749 - 3'	6,336
Chr07	5' - 11,183	11,183	439,73,121 - 3'	12,046	5' - 13,620	13,620	45,390,053 - 3'	12,046
Chr08	5' - 12,104	12,104	60,201,552 - 3'	5,894	5' - 12,660	12,660	60,120,395 - 3'	14,493
Chr09	5' - 2,283	2,283	32,173,511 - 3'	6,622	5' - 9,936	9,936	33,249,521 - 3'	4,468
Chr10	5' - 5,118	5,118	33,492,389 - 3'	12,715	5' - 7,850	7,850	33,213,086 - 3'	9,566
Chr11	5' - 12,497	12,497	36,717,888 - 3'	13,192	5' - 12,497	12,497	36,807,481 - 3'	885



Supplementary Figure S1. *E. regnans* haplotype 1 compared to *E. grandis*



Supplementary Figure S2. *E. regnans* haplotype 2 compared to *E. grandis*



Supplementary Figure S3. *E. regnans* haplotype 1 compared to haplotype 2.
Confirmation that haplotypes were identically scaffolded.