

**Supplementary Data:** Parameters used for each iteration in scaffolding with LINKS v1.8.5 (Warren et al., 2015).

Iteration	d	t	k	l	a
1	1,000	50	19	5	0.3
2	2,500	25	19	5	0.3
3	5,000	10	19	5	0.3
4	7,500	5	19	5	0.3
5	10,000	5	19	5	0.3
6	15,000	5	19	5	0.3
7	20,000	2	19	5	0.3
8	25,000	2	19	5	0.3
9	30,000	2	19	5	0.3
10	35,000	2	19	5	0.3
11	40,000	2	19	5	0.3
12	45,000	2	19	5	0.3
13	50,000	2	19	5	0.3
14	55,000	2	19	5	0.3
15	60,000	2	19	5	0.3
16	65,000	2	19	5	0.3
17	70,000	2	19	5	0.3
18	75,000	2	19	5	0.3
19	80,000	2	19	5	0.3
20	85,000	2	19	5	0.3

*d* : distance between *k*-mer pairs (ie. target distances to re-scaffold on)  
*t* : step of sliding window when extracting *k*-mer pairs from long reads  
*k* : *k*-mer value  
*l* : minimum number of links (*k*-mer pairs) to compute scaffold (default -l 5)  
*a* : maximum link ratio between two best contig pairs (default -a 0.3)

## References

Warren, R.L., Yang, C., Vandervalk, B.P., Behsaz, B., Lagman, A., Jones, S.J.M., et al. (2015).  
 LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads.  
*GigaScience* 4(1), 35. doi: 10.1186/s13742-015-0076-3.