Table 1. Assembly statistics and BUSCO analysis for *B. affinis* in comparison to other *Bombus* genomes. NA = Not Available.

| | Subgenus | **Assembly statistics** | | | | | | **BUSCO results**[a] | | |
		Length (Mb)	N50 (Mb)	L50	No. contigs	Largest contig (Mb)	GC%	Complete [single, duplicated]	Fragmented	Missing
B. affinis	*Bombus*	365.1	12.3	11	858	20.817111	37.4	98.9% [98.1%, 0.4%]	0.00%	1.10%
B. terrestris[b]	*Bombus*	393.0	14.6	10	250	25.524254	38.7	98.4 [98.1%, 0.3%]	0.50%	1.10%
B. ignitus[c]	*Bombus*	242.6	15.2	8	748	19.827955	37.6	97.0% [96.9%, 0.1%]	1.20%	1.80%
B. impatiens[d]	*Pyrobombus*	246.9	1.4	53	5460	5.46609	37.8	98.3% [98.1%, 0.2%]	0.70%	1.00%
B. terricola[e]	*Bombus*	239.9	0.3	NA	1448	NA	37.5	NA	NA	NA

(a) Analysis run using OrthoDB v.10, Hymenoptera dataset (hymenoptera_odb10) containing 5,991 genes

(b) *Bombus terrestris* genome assembly version: 1.2

(c) *Bombus ignitus* genome assembly version: 1.0

(d) *Bombus impatiens* genome assembly version: 2.2

(e) *Bombus terricola* genome assembly data presented in Kent et al. (2018); Complete assembly unavailable for download on NCBI (https://www.ncbi.nlm.nih.gov/genome/), and thus unavailable for analysis