

Additional file 14. Characteristics of the libraries used for genome assembly.

Table S14. *Campoletis sonorensis* genome

	Library ID	Insert size (bp)	Read length (bp)	Data (Gb)	Sequence depth (X)
Paired-ends	CS_WGS_001	250	150	19.18	74.05

Table S15. *Hyposoter didymator* genome

	Insert size (bp)	Read length (bp)	Data (Gb)	Sequence depth (X)	Experiment ID (NCBI SRA)
Paired-ends	250	135_145	6.96	19.89	SRX7136286
	500	100_110	1.52	4.33	SRX7136287
	800	100	3.01	8.60	SRX7136288
Mate-pairs	2,000	100	7.93	22.66	SRX7136289
	5,000	100	5.20	14.85	SRX7136290