Supplemental Table 1: Family, species, collection identifier, collection year, collection country, collection method, voucher identifier, voucher depository, total amount of extract DNA, amount of DNA input to library preparation, post-enrichment method, and MiSeq run of all samples used for target enrichment.

Family	Species	CollnID	CollnYr	Country	CollnMethod	VoucherID	Deposited	DNA (ng)	Lib DNA (ng)	Post enrichment method	MiSeq Run
Andrenidae	*Andrena (Callandrena) asteris*	USGS_DRO_137659	2009	USA	hand net	USNMENT00921242	USNM	6480	486	with bead	R1
Andrenidae	*Andrena (Melandrena) sp*	None	2012	USA	Malaise trap	USNMENT00921243	USNM	693	69	with bead	R1
Apidae	*Bombus pensylvanicus*	USGS_DRO_13724	2009	USA	soapy pan trap	USNMENT00921244	USNM	560	470	with bead	R1
Bradynobaenidae	*Chyphotes mellipes*	PSW14654	2002	USA	unknown	CASENT0106101	CASC	678	498	with bead	R1
Evaniidae	*Evaniella semaeoda*	D. Smith 5	2012	USA	Malaise trap	USNMENT00921245	USNM	2340	503	with bead	R1
Formicidae	*Aphaenogaster albisetosa*	MGB1978	2011	USA	hand collection	USNMENT00921246	USNM	784	500	NaOH	R2
Formicidae	*Aphaenogaster megommata*	PSW16689	2012	Mexico	hand collection	USNMENT00921247	USNM	319	266	NaOH	R2
Formicidae	*Aphaenogaster tennesseensis*	MGB2040	2013	USA	hand collection	USNMENT00921248	USNM	779	500	NaOH	R2
Formicidae	*Aphaenogaster texana*	MGB1983	2011	USA	litter sifting	USNMENT00921249	USNM	736	500	NaOH	R2
Formicidae	*Messor piceus*	TRP-2012a-NPHC(B)	2012	S. Africa	hand collection	USNMENT00921250	USNM	932	500	NaOH	R2
Formicidae	*Pogonomyrmex occidentalis*	MGB2005	2012	USA	hand collection	USNMENT00921251	USNM	1021	500	NaOH	R2
Formicidae	*Sericomyrmex harekulli*	AJ111125-05	2011	Guyana	bait	USNMENT00921252	USNM	843	497	with bead	R1
Formicidae	*Stenamma diecki*	MGB2046	2013	USA	hand collection	USNMENT00921253	USNM	284	237	NaOH	R2
Formicidae	*Stenamma expolitum*	MGB1880	2011	Nicaragua	hand collection	USNMENT00921254	USNM	400	333	NaOH	R2
Formicidae	*Stenamma felixi*	JTL7524	2011	Nicaragua	hand collection	USNMENT00921255	USNM	533	444	NaOH	R2
Formicidae	*Stenamma impar*	MGB2036	2013	USA	hand collection	USNMENT00921256	USNM	262	218	NaOH	R2
Formicidae	*Stenamma megamanni*	Wm-D-05-1-01	2011	Nicaragua	litter sifting	USNMENT00921257	USNM	315	252	with bead	R1
Formicidae	*Stenamma megamanni*	MGB1764	2011	Nicaragua	hand collection	USNMENT00921258	USNM	326	272	NaOH	R2
Formicidae	*Stenamma muralla*	JTL7007	2010	Honduras	hand collection	USNMENT00921259	USNM	181	151	NaOH	R2
Pergidae	*Acordulecera pellucida*	D. Smith 3	2012	USA	Malaise trap	USNMENT00921260	USNM	1060	424	with bead	R1
Pompilidae	*Aporus niger*	ANTC4004	2002	USA	unknown	CASENT0106104	CASC	2120	498	with bead	R1
Pteromalidae	*Nasonia vitripennis***	None	2013	USA	purchased	None	None	3923	500	with bead	R1
Sapygidae	*Sapyga pumila*	ANTC4005	2004	USA	unknown	CASENT0106105	CASC	2270	499	with bead	R1
Scoliidae	*Scolia verticalis*	ANTC4007	2004	Australia	unknown	CASENT0106107	CASC	5550	500	with bead	R1
Sphecidae	*Chalybion californicum*	PSW15440	2005	USA	unknown	CASENT0106103	CASC	3730	506	with bead	R1
Tenthredinidae	*Nematus tibialis*	D. Smith 2	2012	USA	Malaise trap	USNMENT00921261	USNM	2950	502	with bead	R1

Tenthredinidae	*Taxonus pallidicornis*	D. Smith 1	2012	USA	Malaise trap	USNMENT00921262	USNM	6120	490	with bead	R1
Trigonalidae	*Orthogonalys pulchella*	D. Smith 4	2012	USA	Malaise trap	USNMENT00921263	USNM	3390	509	with bead	R1
Vespidae	*Metapolybia cingulata*	ANTC4006	2007	Peru	unknown	CASENT0106106	USNM	749	502	with bead	R1
Vespidae	*Mischocyttarus flavitarsis*	PSW15442	2005	USA	unknown	CASENT0106102	USNM	6480	486	with bead	R1

Supplemental Table 2: Species, genome assembly, genome assembly source, reference, and number of UCE loci in assembly for all genome-enabled taxa.

Species	**Name of assembly**	**Assembly source**	**Reference**	**Unique UCE loci in assembly**
Acromyrmex echinatior	Aech_3.9	Genbank	10.1101/gr.121392.111	774
Apis mellifera	Amel_4.5	Genbank	10.1186/1471-2164-15-86	803
Atta cephalotes	Attacep1.0	Genbank	10.1371/journal.pgen.1002007	748
Camponotus floridanus	CamFlo_1.0	Genbank	10.1126/science.1192428	767
Cerapachys biroi	CerBir1.0	Genbank	10.1016/j.cub.2014.01.018	768
Ceratosolen solmsi	CerSol_1.0	Genbank	10.1186/gb-2013-14-12-r141	897
Harpegnathos saltator	HarSal_1.0	Genbank	10.1126/science.1192428	763
Lasioglossum albipes	ASM34657v1	Genbank	10.1186/gb-2013-14-12-r142	779
Linepithema humile	Lhum_1.0	hymenopteragenome.org	10.1073/pnas.1008617108	762
Nasonia giraulti	Ngir_1.0	Genbank	10.1126/science.1178028	1191
Nasonia longicornis	Nlon_1.0	Genbank	10.1126/science.1178028	1192
Nasonia vitripennis	Nvit_2.0	Genbank	10.1126/science.1178028	1214
Pogonomyrmex barbatus	Pbar_UMD_V03	Genbank	10.1073/pnas.1007901108	666
Solenopsis invicta	Si_gnG	Genbank	10.1073/pnas.1009690108	768

Supplemental Table 3: Quantitative PCR primers used for assessment (relative quantification) of enrichment success and enrichment differences of Cot-1 sources.

UCE locus	UCE locus genomic position	UCE locus size	Upper primer (5' - 3')	Tm upper primer	Lower primer (5' - 3')	Tm lower primer	Estimated product size
uce-82	chr1:2966279-2966458	114	GCCGACCCCCTGCTGAAGAG	59.1	AGACTTACGGCGTCTGCCACG	59.2	77
uce-202	chr2:4442225-4442404	170	GCCATGCGTGTTCGCTCTTGC	59.9	TGCATCGGCCCTTGACAGCG	60	162
uce-591	chr2:34873617-34873796	136	GGGCATCTACACATTTGAGTCCGCC	59.9	ACGAAGTCGAGCCAATTCCATGC	58	102
uce-1101	chr4:34336396-34336576	127	CGTAGCCATAACGATCGGTCGCC	59.8	ACACACCACTGTCGGACAAACTGC	59.8	87
uce-1160	chr4:5470676-5470856	125	AGGCTTTGGGTGGGCGTTCG	59.9	TCACAGCACACACTGGGCCG	59.6	121
uce-1196	chr4:4001320-4001500	137	GATTAGGGTTGGGGCCTAGGACAGG	59.8	GGGGGACAGTACGTGGCTCG	58.9	75
uce-1481	ChrUn.Scaffold477:51625-51805	119	TCTTCTGCATGGCGTGGTTGG	57.7	ACAAGTGCGCTTGCAATTTGTTGGG	57.7	75

Supplemental Table 4: Crossing point (C_p) values for quantitative PCR showing the fold enrichment differences between unenriched controls, enrichments using chicken Cot-1 as a blocking agent, enrichments using hymenoptera Cot-1 as a blocking agent, and Δ Cot-1 or the fold-enrichment difference between chicken and hymenoptera Cot-1.

	Unenriched controls		**Used chicken Cot-1**				**Used hymenoptera Cot-1**				**Δ Cot-1**
	Name	**Cp**	**Name**	**Cp**	**Delta Cp**	**Enrichment**	**Name**	**Cp**	**Delta Cp**	**Enrichment**	
Pool 1	c1-1162	21.23	p1c-1162	13.9	7.3	158.7	p1h-1162	14.4	6.8	51.0	107.6
	c1-132	27.27	p1c-132	17.9	9.3	643.6	p1h-132	18.2	9.1	184.6	459.0
	c1-2055	21.82	p1c-2055	13.7	8.1	280.1	p1h-2055	14.3	7.6	78.6	201.5
	c1-2118	21.27	p1c-2118	16.5	4.8	27.3	p1h-2118	16.9	4.4	12.6	14.6
	c1-2173	21.47	p1c-2173	13.9	7.5	184.8	p1h-2173	14.8	6.7	46.5	138.3
	c1-2704	22.10	p1c-2704	14.3	7.8	227.5	p1h-2704	15.0	7.1	59.6	167.9
	c1-539	27.78	p1c-539	18.6	9.2	580.0	p1h-539	19.6	8.2	110.5	469.5
	c1-neg		p1c-neg				p1h-neg				
Pool 2	c2-1162	22.41	p2c-1162	13.6	8.8	455.1	p2h-1162	14.3	8.1	108.0	347.1
	c2-1162-r2	22.26	p2c-1162-r2	13.4	8.8	458.3	p2h-1162-r2	14.0	8.2	114.4	343.8
	c2-132	27.56	p2c-132	17.5	10.1	1067.5	p2h-132	18.7	8.9	168.4	899.1
	c2-132-r2	27.29	p2c-132-r2	17.3	10.0	1031.1	p2h-132-r2	17.5	9.8	284.5	746.6
	c2-2055	23.23	p2c-2055	13.5	9.7	855.1	p2h-2055	14.0	9.2	200.2	655.0
	c2-2055-r2	22.79	p2c-2055-r2	13.4	9.4	661.7	p2h-2055-r2	14.0	8.8	163.6	498.1
	c2-2118	23.51	p2c-2118	17.1	6.4	86.8	p2h-2118	17.8	5.7	27.2	59.6
	c2-2118-r2	23.22	p2c-2118-r2	17.0	6.3	76.6	p2h-2118-r2	17.6	5.7	26.0	50.6
	c2-2173	23.76	p2c-2173	14.6	9.1	564.2	p2h-2173	15.3	8.5	132.1	432.0
	c2-2173-r2	23.56	p2c-2173-r2	14.4	9.1	560.3	p2h-2173-r2	15.0	8.5	136.0	424.3
	c2-2704	23.52	p2c-2704	14.5	9.0	515.6	p2h-2704	15.3	8.2	114.4	401.2
	c2-2704-r2	23.55	p2c-2704-r2	14.5	9.0	519.1	p2h-2704-r2	14.9	8.6	144.9	374.2
	c2-539	31.04	p2c-539	20.0	11.0	2091.0	p2h-539	21.0	10.1	336.3	1754.7
	c2-539-r2	31.07	p2c-539-r2	19.6	11.5	2916.5	p2h-539-r2	20.1	10.9	549.0	2367.4
	c2-neg		p2c-neg				p2h-neg				
	c2-neg-r2		p2c-neg-r2				p2h-neg-r2				

Pool 3	c3-1162	22.90	p3c-1162	14.0	8.9	474.4	p3h-1162	14.3	8.6	145.8		328.7
	c3-132	28.58	p3c-132	17.7	10.9	1910.9	p3h-132	18.0	10.6	448.7		1462.2
	c3-2055	23.29	p3c-2055	13.7	9.6	792.4	p3h-2055	13.8	9.5	240.7		551.6
	c3-2118	23.18	p3c-2118	16.0	7.2	149.1	p3h-2118	16.6	6.6	43.9		105.2
	c3-2173	23.70	p3c-2173	14.1	9.6	797.9	p3h-2173	14.3	9.5	232.5		565.3
	c3-2704	23.14	p3c-2704	13.8	9.3	643.6	p3h-2704	14.1	9.1	185.7		457.9
	c3-539	30.72	p3c-539	19.7	11.0	2105.6	p3h-539	19.5	11.2	641.5		1464.1
	c3-neg		p3c-neg				p3h-neg					
					Avg.	744.1			**Avg.**	178.1	**Avg.**	566.0
					95 CI	259.9			**95 CI**	57.1	**95 CI**	207.0

Supplemental Table 5: Summary values describing the number of reads collected during sequencing of each enriched library.

Taxon	Trimmed reads	Total BP	Mean length	95 % CI	Min lengths	Max length	Median length
Acordulecera pellucida	408,901	86,125,439	210.6	0.1	40	251	250
Andrena (Callandrena) asteris	83,975	15,540,798	185.1	0.2	40	251	199
Andrena (Melandrena) sp	410,453	84,592,764	206.1	0.1	40	251	232
Aphaenogaster albisetosa	2,217,687	426,328,391	192.2	0.0	40	251	207
Aphaenogaster megommata	2,047,669	386,980,038	189.0	0.0	40	251	198
Aphaenogaster tennesseensis	1,625,068	281,397,272	173.2	0.0	40	251	173
Aphaenogaster texana	1,059,887	182,422,784	172.1	0.1	40	251	171
Aporus niger	398,607	74,624,652	187.2	0.1	40	251	195
Bombus pensylvanicus	301,910	63,481,685	210.3	0.1	40	251	250
Chalybion californicus	654,184	117,929,426	180.3	0.1	40	251	183
Chyphotes mellipes	1,664,263	322,103,690	193.5	0.0	40	251	208
Evaniella semaeoda	414,086	78,104,105	188.6	0.1	40	251	202
Messor piceus	1,710,354	331,117,936	193.6	0.0	40	251	209
Metapolybia cingulata	719,460	142,797,714	198.5	0.1	40	251	220
Mischocyttarus flavitarsis	307,969	61,394,499	199.4	0.1	40	251	223
Nasonia vitripennis	528,367	99,597,773	188.5	0.1	40	251	199
Nematus tibialis	703,569	135,792,550	193.0	0.1	40	251	213
Orthogonalys pulchella	1,822,967	354,456,435	194.4	0.0	40	251	214
Pogonomyrmex occidentalis	2,129,915	406,383,752	190.8	0.0	40	251	203
Sapyga pumila	1,732,085	311,775,579	180.0	0.0	40	251	180
Scolia verticalis	907,356	178,554,253	196.8	0.1	40	251	221
Sericomyrmex harekulli	327,399	64,865,315	198.1	0.1	40	251	214
Stenamma diecki	1,579,469	314,662,462	199.2	0.0	40	251	218
Stenamma expolitum	1,847,383	362,261,429	196.1	0.0	40	251	211
Stenamma felixi	2,001,433	356,384,998	178.1	0.0	40	251	179
Stenamma impar	1,541,096	293,383,544	190.4	0.0	40	251	199
Stenamma megamanni	2,179,975	395,476,057	181.4	0.0	40	251	181
Stenamma megamanni2	801,435	169,627,489	211.7	0.1	40	251	250
Stenamma muralla	1,237,264	238,365,794	192.7	0.1	40	251	203
Taxonus pallidicornis	577,999	119,464,673	206.7	0.1	40	251	250

Supplemental Table 6: Summary values describing the number of contigs assembled by ABySS from adapter- and quality-trimmed reads ("All" contigs), their average coverage, the mean length of All contigs, the count of unique reads aligned to All contigs, the number of UCE contigs identified from the pool of All contigs, the mean length of UCE contigs, the average UCE contig sequencing coverage, and the percentage of unique reads that aligned to UCE contigs (this is a percentage of the percentage of unique reads aligning to All contigs).

Taxon	**All contigs**	**All contigs coverage**	**All contigs coverage 95 CI**	**All contigs mean length**	**All contigs mean length 95 CI**	**All contigs unique reads aligned**	**UCE contigs**	**UCE contigs mean length**	**UCE contigs coverage**	**UCE contigs unique reads aligned**
Acordulecera pellucida	62,419	3.4	0.1	197.4	0.8	85.6%	319	705.0	30.3	12.1%
Andrena (Callandrena) asteris	9,027	4.6	0.3	208.6	2.4	79.3%	714	437.1	11.5	36.9%
Andrena (Melandrena) sp	69,660	3.3	0.2	194.1	0.7	88.2%	704	636.9	19.9	17.4%
Aphaenogaster albisetosa	275,539	4.1	0.0	218.5	0.4	87.4%	302	654.7	43.9	2.8%
Aphaenogaster megommata	230,940	4.1	0.1	201.2	0.4	81.0%	323	725.1	46.8	4.3%
Aphaenogaster tennesseensis	184,108	4.2	0.1	186.7	0.4	82.4%	412	678.6	44.9	7.2%
Aphaenogaster texana	126,796	4.0	0.1	179.4	0.4	82.6%	348	522.8	30.3	5.1%
Aporus niger	37,593	5.0	1.0	193.1	1.0	84.1%	725	559.6	17.1	18.5%
Bombus pensylvanicus	55,323	3.0	0.1	197.4	0.8	88.9%	703	632.0	23.9	23.7%
Chalybion californicus	91,078	3.5	0.2	196.6	0.6	80.1%	660	614.1	34.1	18.1%
Chyphotes mellipes	191,326	4.4	0.3	222.8	0.6	89.5%	472	808.1	59.7	9.2%
Evaniella semaeoda	43,255	4.4	0.2	193.8	1.1	85.9%	515	702.8	30.9	22.1%
Messor piceus	190,453	4.5	0.2	194.0	0.4	82.8%	423	693.8	43.7	6.5%
Metapolybia cingulata	131,497	3.1	0.0	197.7	0.5	88.3%	562	618.4	38.2	13.2%
Mischocyttarus flavitarsis	37,614	4.4	0.3	194.0	1.0	88.1%	616	519.3	33.0	24.5%
Nasonia vitripennis	69,994	3.8	0.1	180.0	0.6	87.0%	756	463.1	45.5	22.8%
Nematus tibialis	101,439	3.4	0.1	197.3	0.7	85.4%	324	683.6	47.1	10.6%
Orthogonalys pulchella	174,934	3.9	0.1	251.1	0.8	83.8%	266	807.8	74.1	4.6%
Pogonomyrmex occidentalis	266,414	3.9	0.0	220.1	0.4	86.2%	293	658.2	56.6	3.1%
Sapyga pumila	215,619	3.7	0.1	210.1	0.5	84.4%	349	596.3	71.1	5.7%
Scolia verticalis	105,754	3.9	0.1	208.1	0.7	84.4%	516	794.1	49.2	16.2%

Sericomyrmex harekulli	61,272	3.1	0.0	185.4	0.8	89.4%	663	606.1	24.6	22.1%
Stenamma diecki	194,733	4.0	0.1	207.0	0.5	85.5%	523	820.2	46.6	10.0%
Stenamma expolitum	236,274	3.9	0.0	214.7	0.5	86.9%	376	785.6	50.3	5.4%
Stenamma felixi	277,927	3.5	0.0	203.8	0.4	85.1%	263	603.4	35.6	2.2%
Stenamma impar	180,786	4.3	0.1	197.9	0.5	86.6%	524	727.8	45.4	9.6%
Stenamma megamanni	140,321	3.0	0.0	209.4	0.6	87.9%	544	803.3	35.1	12.9%
Stenamma megamanni2	285,366	3.5	0.0	213.0	0.4	86.3%	314	765.0	45.6	3.8%
Stenamma muralla	188,981	3.2	0.0	205.8	0.4	85.1%	392	713.3	46.6	7.5%
Taxonus pallidicornis	79,453	3.5	0.1	202.9	0.8	82.5%	416	737.2	40.1	15.7%

Supplemental Table 7: Summary values describing attributes of the UCE contigs assembled by Trinity.

Taxon	**UCE contigs**	**UCE contigs total BP**	**UCE contigs mean length**	**UCE contigs mean length 95 CI**	**UCE contigs min length**	**UCE contigs max length**	**UCE contigs median length**	**UCE contigs > 1kb**	**UCE contigs coverage**	**UCE contigs unique reads aligned**
Acordulecera pellucida	341	349,519	1,025.0	19.7	206	2,504	1,054.0	198	26.3	18.4%
Andrena (Callandrena) asteris	740	425,271	574.7	7.0	202	1,447	558.0	16	9.8	44.4%
Andrena (Melandrena) sp	774	663,345	857.0	9.9	208	2,253	861.5	234	18.2	25.9%
Aphaenogaster albisetosa	764	862,282	1,128.6	20.8	223	11,435	1,124.5	461	88.3	26.0%
Aphaenogaster megommata	751	889,250	1,184.1	16.2	230	2,776	1,170.0	484	79.2	28.8%
Aphaenogaster tennesseensis	751	793,300	1,056.3	14.8	210	2,493	1,051.0	412	62.4	30.5%
Aphaenogaster texana	750	693,422	924.6	12.8	207	2,645	906.0	281	51.5	33.2%
Aporus niger	740	528,399	714.1	9.1	205	1,981	717.0	71	14.5	17.7%
Bombus pensylvanicus	780	670,544	859.7	9.2	206	2,036	879.0	228	21.4	35.0%
Chalybion californicus	778	631,930	812.2	10.4	205	1,968	809.0	201	33.2	29.6%
Chyphotes mellipes	774	916,382	1,184.0	13.0	294	3,189	1,185.0	558	66.2	26.6%
Evaniella semaeoda	638	619,918	971.7	11.6	220	2,229	978.5	301	31.1	39.1%
Messor piceus	730	811,543	1,111.7	15.7	210	3,730	1,119.5	441	58.9	26.2%
Metapolybia cingulata	685	563,953	823.3	12.8	207	2,103	801.0	211	40.1	24.7%
Mischocyttarus flavitarsis	634	450,896	711.2	11.6	203	2,687	676.5	110	30.0	32.4%
Nasonia vitripennis	1,166	899,101	771.1	7.7	202	1,672	763.0	237	46.9	57.1%
Nematus tibialis	453	475,444	1,049.5	17.9	209	3,894	1,070.0	265	47.9	26.4%
Orthogonalys pulchella	706	962,959	1,364.0	16.5	205	2,998	1,352.0	569	109.0	35.0%
Pogonomyrmex occidentalis	741	846,554	1,142.4	16.2	231	3,190	1,124.0	457	97.5	26.8%
Sapyga pumila	720	753,734	1,046.9	13.4	224	2,743	1,078.0	428	86.4	28.6%
Scolia verticalis	760	813,497	1,070.4	12.2	286	2,877	1,078.0	461	56.6	36.0%
Sericomyrmex harekulli	744	606,204	814.8	9.7	205	2,099	830.5	177	22.3	33.5%
Stenamma diecki	751	857,659	1,142.0	15.0	209	3,188	1,167.0	488	53.5	23.7%
Stenamma expolitum	749	907,836	1,212.1	15.7	205	2,690	1,216.0	520	69.3	25.7%

Stenamma felixi	762	816,726	1,071.8	14.2	209	3,469	1,056.0	433	75.3	25.1%
Stenamma impar	741	782,478	1,056.0	14.1	229	2,846	1,046.0	428	49.8	22.4%
Stenamma megamanni	754	858,069	1,138.0	14.5	217	3,227	1,166.5	502	37.8	28.6%
Stenamma megamanni2	756	932,105	1,232.9	20.0	204	9,956	1,218.0	525	87.5	28.7%
Stenamma muralla	734	830,910	1,132.0	14.8	221	3,299	1,113.0	480	61.6	30.6%
Taxonus pallidicornis	459	523,674	1,140.9	21.6	205	3,001	1,173.0	282	37.7	27.5%

Supplemental Table 8: Summary values describing attributes of the UCE contigs assembled by ABySS.

Taxon	**UCE contigs**	**UCE contigs total BP**	**UCE contigs mean length**	**UCE contigs mean length 95 CI**	**UCE contigs min length**	**UCE contigs max length**	**UCE contigs median length**	**UCE contigs > 1kb**	**UCE contigs coverage**	**UCE contigs unique reads aligned**
Acordulecera pellucida	319	224,885	705.0	17.0	102	1,774	737.0	52	30.3	12.1%
Andrena (Callandrena) asteris	714	312,069	437.1	5.5	102	901	431.0	0	11.5	36.9%
Andrena (Melandrena) sp	705	449,059	637.0	9.3	103	1,577	635.0	47	19.9	17.4%
Aphaenogaster albisetosa	302	197,727	654.7	19.3	105	2,072	621.0	48	43.9	2.8%
Aphaenogaster megommata	323	234,220	725.1	19.5	103	1,818	687.0	63	46.8	4.3%
Aphaenogaster tennesseensis	413	280,246	678.6	15.5	101	1,800	647.0	71	44.9	7.2%
Aphaenogaster texana	348	181,931	522.8	13.5	104	1,714	496.0	12	30.3	5.1%
Aporus niger	726	406,631	560.1	7.6	101	1,230	547.5	12	17.1	18.5%
Bombus pensylvanicus	703	444,314	632.0	8.3	101	1,521	635.0	26	23.9	23.7%
Chalybion californicus	660	405,336	614.1	9.5	101	1,336	616.0	34	34.1	18.1%
Chyphotes mellipes	472	381,416	808.1	17.1	102	2,063	829.5	140	59.7	9.2%
Evaniella semaeoda	515	361,966	702.8	12.1	104	2,191	721.0	61	30.9	22.1%
Messor piceus	424	294,305	694.1	16.1	101	2,044	669.5	62	43.7	6.5%
Metapolybia cingulata	563	348,507	619.0	12.4	101	1,677	604.0	62	38.2	13.2%
Mischocyttarus flavitarsis	617	320,960	520.2	9.3	101	1,878	503.0	13	33.0	24.5%
Nasonia vitripennis	756	350,095	463.1	8.7	101	1,368	450.5	17	45.5	22.8%
Nematus tibialis	325	222,333	684.1	18.4	101	1,972	713.0	53	47.1	10.6%
Orthogonalys pulchella	266	214,864	807.8	28.4	102	2,303	826.5	96	74.1	4.6%
Pogonomyrmex occidentalis	293	192,855	658.2	19.9	106	2,134	632.0	36	56.6	3.1%
Sapyga pumila	349	208,097	596.3	16.5	102	1,533	555.0	35	71.1	5.7%
Scolia verticalis	516	409,772	794.1	13.8	101	1,857	803.0	137	49.2	16.2%
Sericomyrmex harekulli	663	401,814	606.1	8.8	101	1,613	618.0	22	24.6	22.1%
Stenamma diecki	524	429,972	820.6	15.2	101	1,850	818.0	164	46.6	10.0%
Stenamma expolitum	376	295,389	785.6	18.5	101	2,136	764.0	95	50.3	5.4%

Stenamma felixi	263	158,700	603.4	17.4	103	1,843	558.0	21	35.6	2.2%
Stenamma impar	524	381,375	727.8	13.7	102	2,480	690.5	107	45.4	9.6%
Stenamma megamanni2	314	240,207	765.0	20.2	102	1,980	719.5	67	45.6	3.8%
Stenamma megamanni	545	437,935	803.6	15.5	101	2,653	793.0	164	35.1	12.9%
Stenamma muralla	392	279,628	713.3	16.1	102	2,114	664.0	70	46.6	7.5%
Taxonus pallidicornis	416	306,665	737.2	18.8	102	2,906	724.5	100	40.1	15.7%

Supplemental Table 9: Model structure, AIC, number of parameters, AICc, and Akaike weight (w_i) for general linear models of parameters affecting the mean number of UCE contigs captured.

	model	**AIC**	**Params**	**AICc**	**Δ_i**	**w_i**
1	contigs ~ distance + reads + assembly + mean	1241.0	6	1244.7	0.0	1.0
2	contigs ~ distance + reads + mean	1250.6	5	1253.1	8.4	0.0
3	contigs ~ distance + assembly + mean	1579.9	5	1582.4	337.7	0.0
4	contigs ~ distance + mean	1683.0	4	1684.6	439.9	0.0
5	contigs ~ distance + reads + assembly	1744.7	5	1747.2	502.5	0.0
6	contigs ~ distance + assembly	1755.0	4	1756.6	511.9	0.0
7	contigs ~ reads + assembly + mean	2593.5	5	2596.0	1351.3	0.0
8	contigs ~ reads + assembly	2609.5	4	2611.1	1366.4	0.0
9	contigs ~ assembly + mean	2629.4	4	2631.0	1386.3	0.0
10	contigs ~ assembly	2757.2	3	2758.1	1513.5	0.0
11	contigs ~ distance + reads	3147.4	4	3149.0	1904.3	0.0
12	contigs ~ distance	3157.7	3	3158.6	1914.0	0.0
13	contigs ~ reads + mean	3235.8	4	3237.4	1992.7	0.0
14	contigs ~ mean	3801.1	3	3802.0	2557.4	0.0
15	contigs ~ reads	4100.1	3	4101.0	2856.4	0.0

Supplemental Table 10: Model structure, AIC, number of parameters, AICc, and Akaike weight (*w*$_i$) for general linear models of parameters affecting the number of UCE contigs captured among Trinity (only) assemblies.

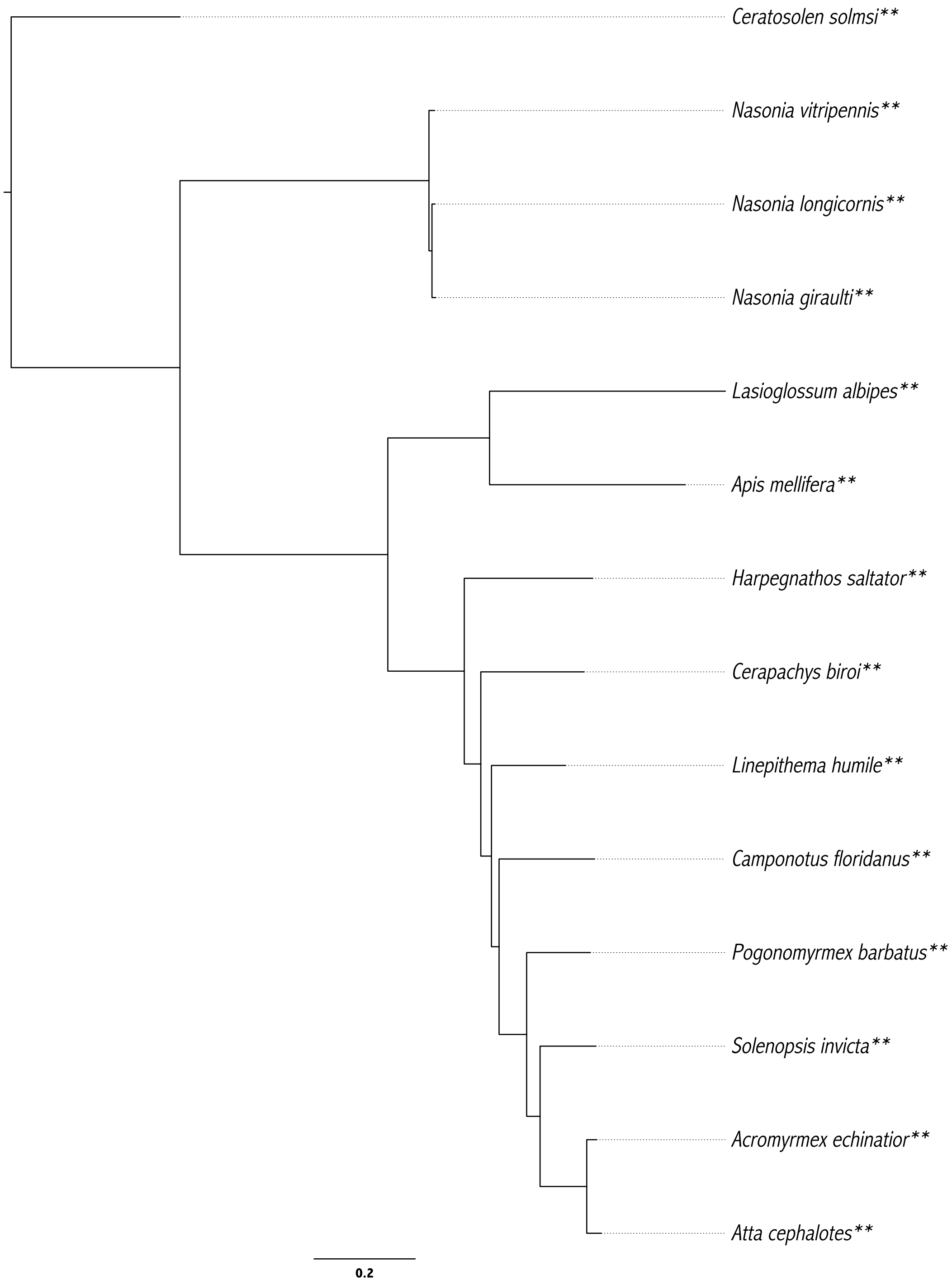
	model	**AIC**	**Params**	**AICc**	**Δ_i**	**w_i**
1	contigs ~ distance + mean	424.2	3	425.2	0.0	0.8
2	contigs ~ distance + reads + mean	426.2	4	427.8	2.6	0.2
3	contigs ~ distance + reads	457.3	3	458.2	33.0	0.0
4	contigs ~ distance	571.9	2	572.3	147.2	0.0
5	contigs ~ reads + mean	829.3	3	830.3	405.1	0.0
6	contigs ~ reads	997.8	2	998.2	573.1	0.0
7	contigs ~ mean	998.8	2	999.3	574.1	0.0

Supplemental Table 11: Model structure, AIC, number of parameters, AICc, and Akaike weight (*w*ᵢ) for general linear models of parameters affecting the length of UCE contigs captured.

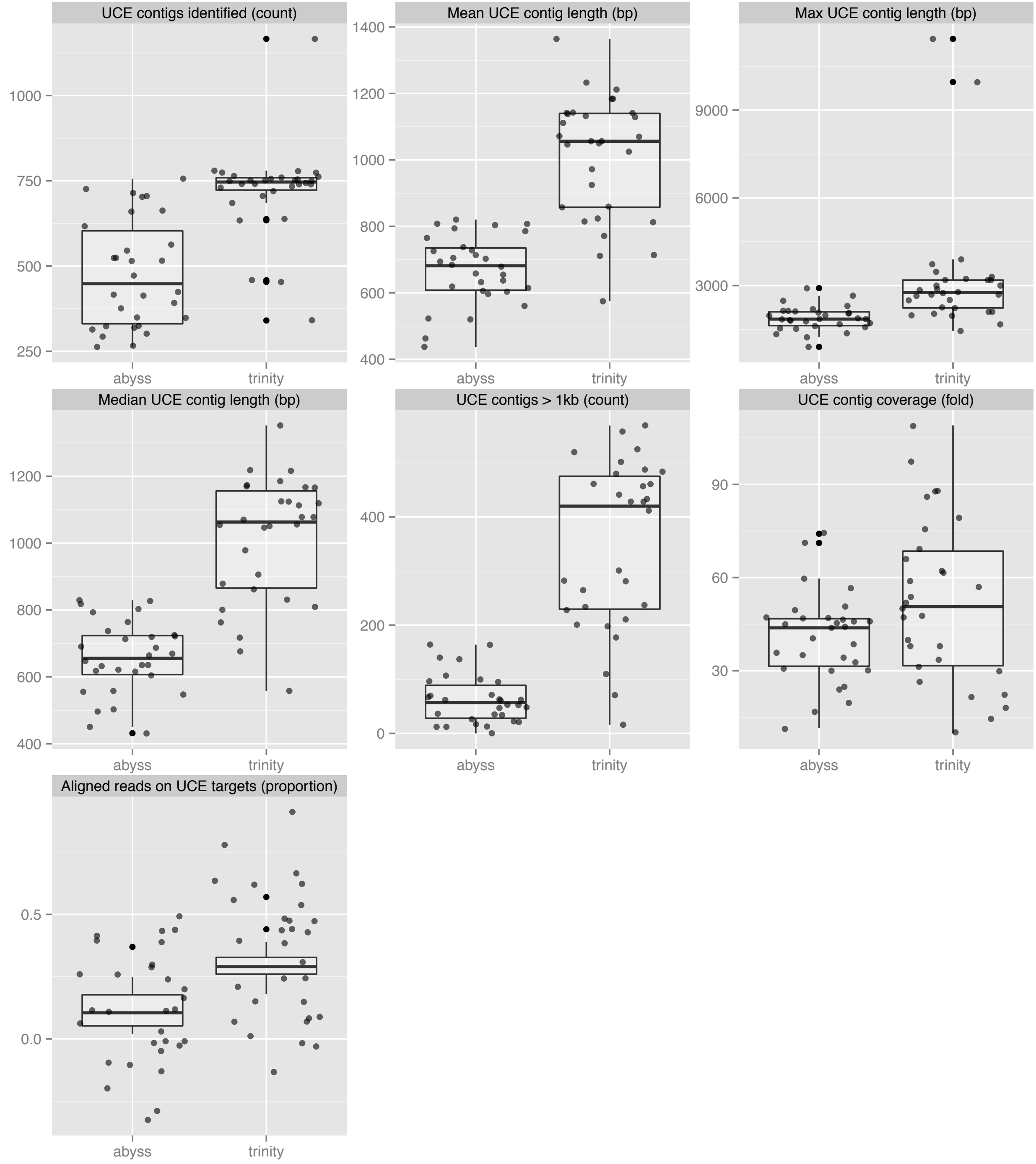
	model	**AIC**	**Params**	**AICc**	**Δi**	w_i
1	mean ~ distance + reads + assembly	687.3	5	689.8	0.0	1.0
2	mean ~ distance + assembly	721.6	4	723.2	33.3	0.0
3	mean ~ reads + assembly	744.9	4	746.5	56.6	0.0
4	mean ~ assembly	775.2	3	776.1	86.3	0.0
5	mean ~ distance + reads	781.5	4	783.1	93.3	0.0
6	mean ~ distance	788.4	3	789.3	99.5	0.0
7	mean ~ reads	814.7	3	815.6	125.8	0.0

Supplemental Table 12: Model structure, AIC, number of parameters, AICc, and Akaike weight (w_i) for general linear models of parameters affecting the length of UCE contigs captured among Trinity (only) assemblies.

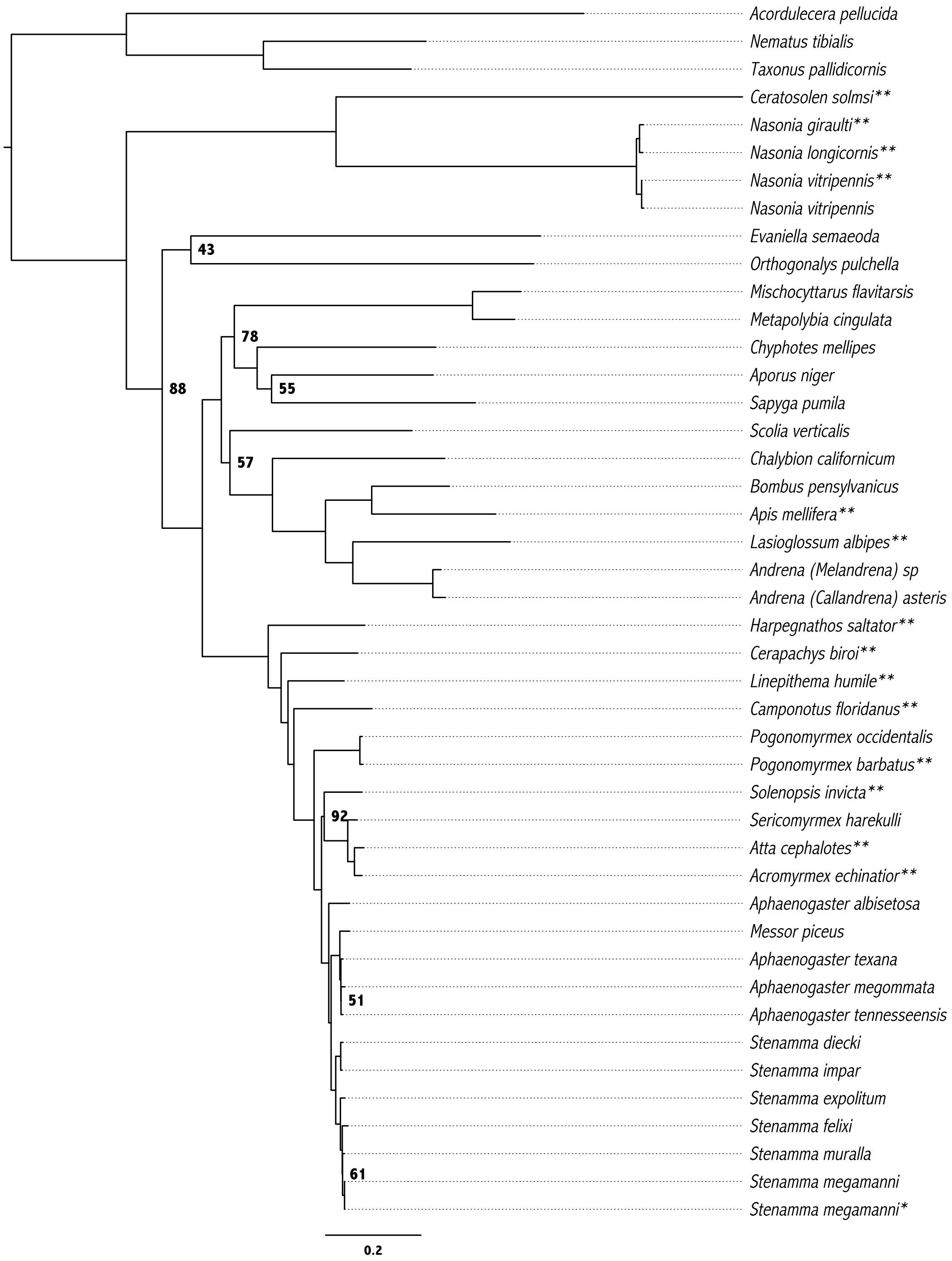
	model	**AIC**	**Params**	**AICc**	**Δ_i**	**w_i**
1	contig length ~ distance + reads	333.1	3	334.0	0.0	1.00
2	contig length ~ distance	373.6	2	374.0	40.0	0.00
3	contig length ~ reads	375.8	2	376.3	42.3	0.00



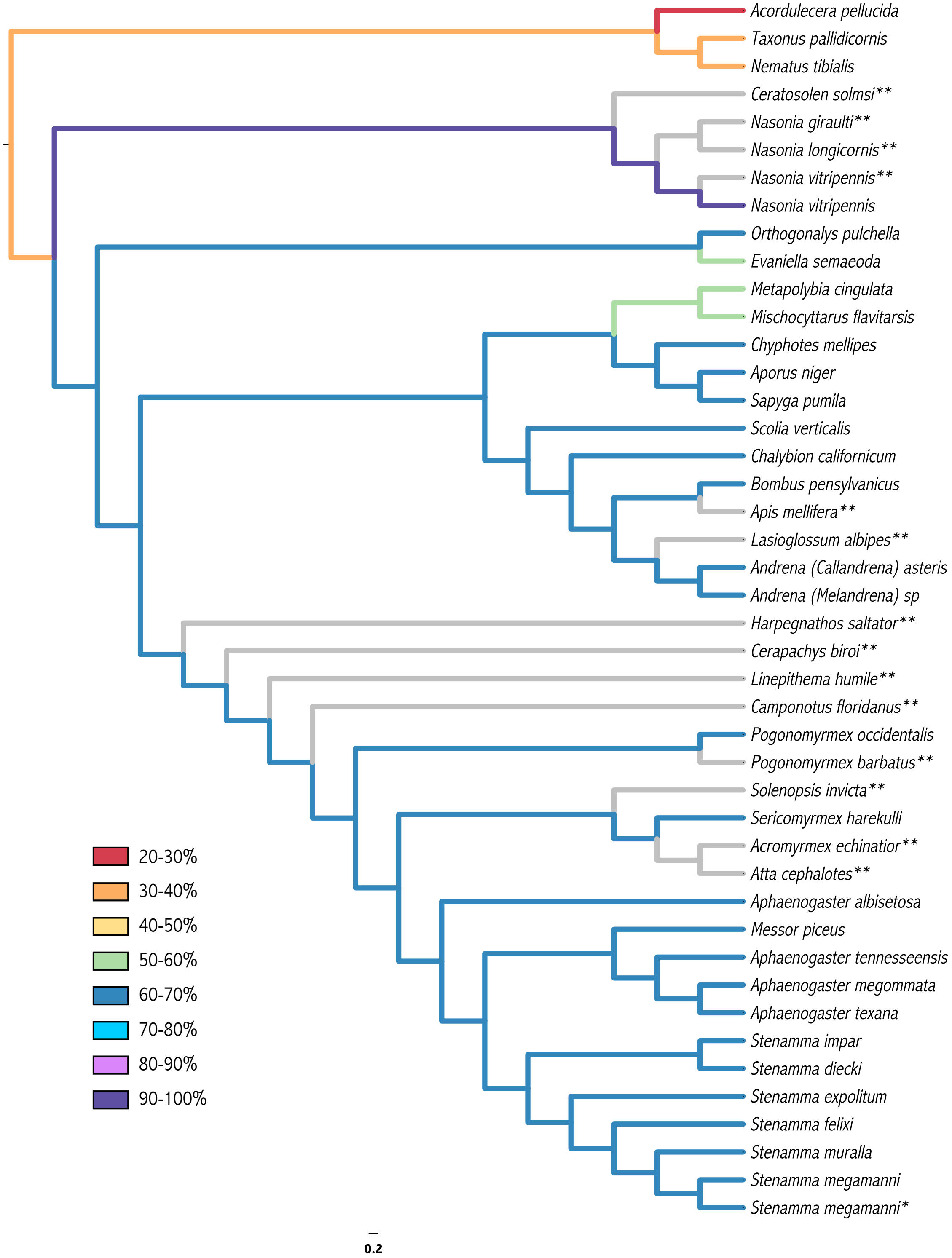
Supplemental Figure 1: Maximum likelihood phylogeny inferred from a 75% complete supermatrix containing data from ultraconserved elements identified in 14 genome-enabled taxa. We show bootstrap support values only where support is < 100%. Although genome assemblies exist for additional hymenopteran taxa, we were not granted permission to include these data in our analyses.



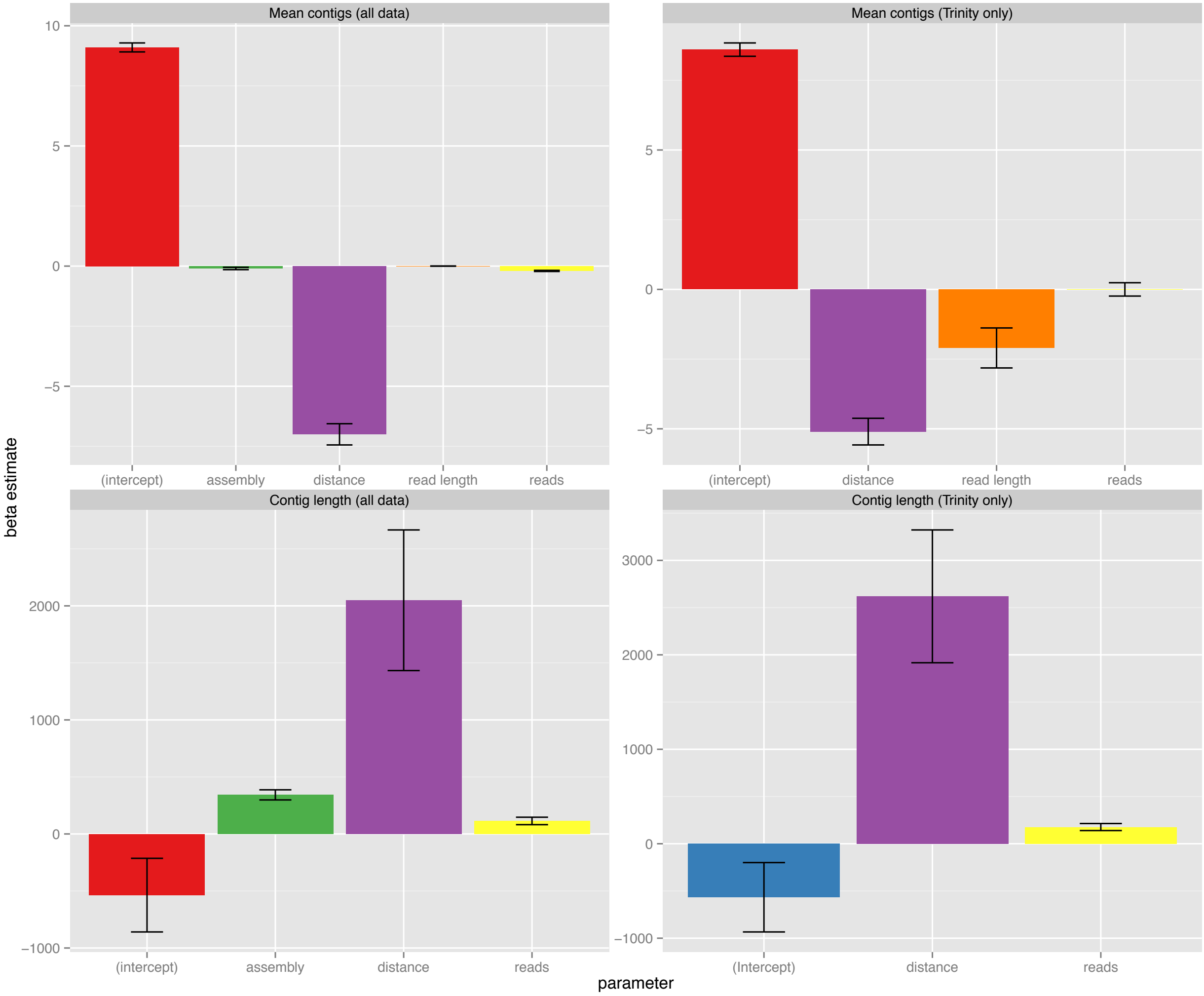
Supplemental Figure 2: Box plots showing differences in standard metrics among UCE contigs assembled by Trinity or ABySS. Jittered dots indicate a given value for each taxon. Values correspond to those in Supplemental Table 7 and Supplemental Table 8.



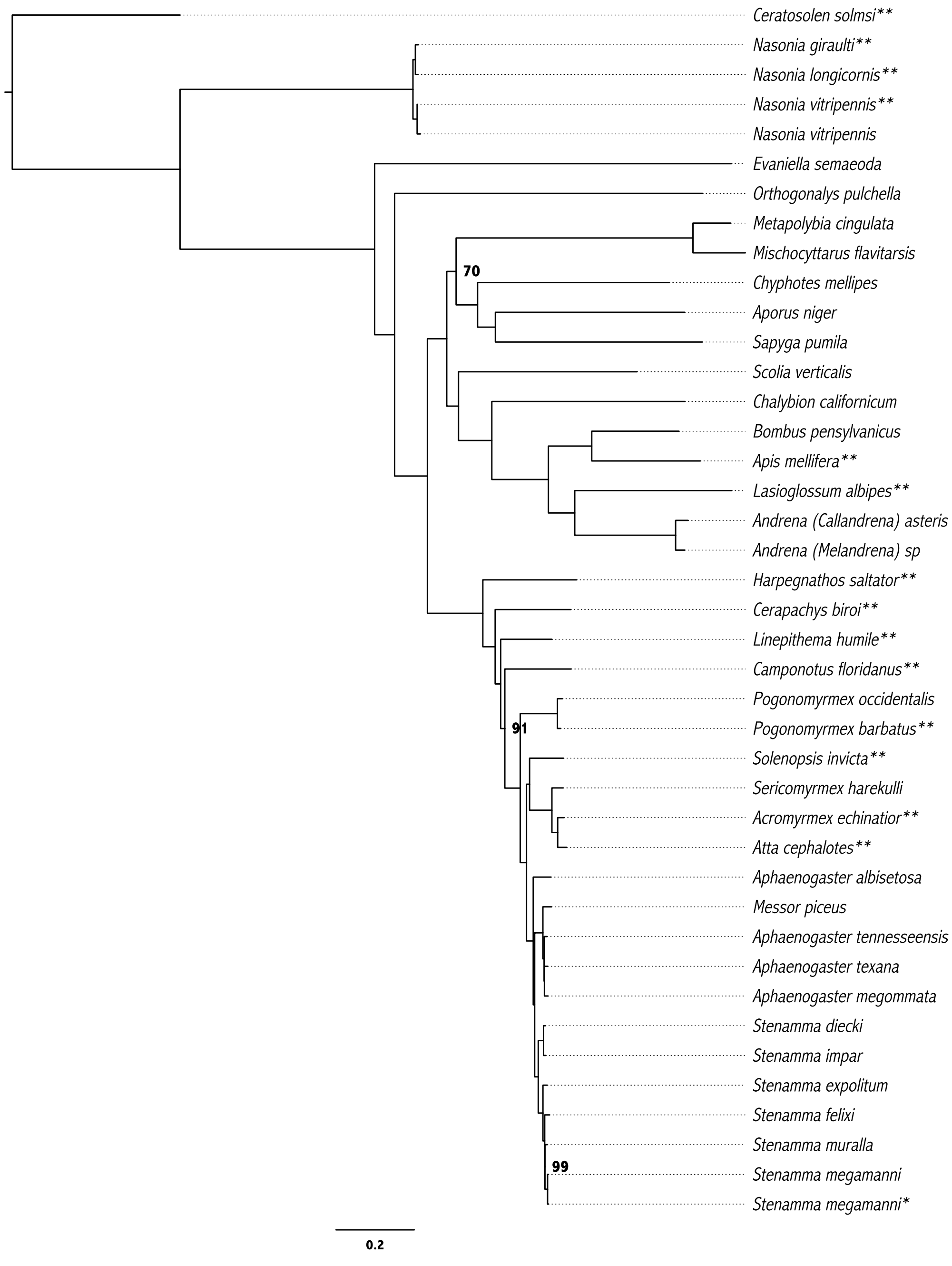
Supplemental Figure 3: Maximum likelihood phylogeny inferred from a 75% complete supermatrix containing data from 14 genome-enabled taxa (identified by double-asterisks) and 30 taxa from which we enriched and assembled (ABySS) ultraconserved element loci. We show bootstrap support values only where support is < 100%, and the single asterisk beside *Stenamma megamanni* denotes that this sample represents a different population of the same species.



Supplemental Figure 4: The topology from Figure 1, with branches colored to indicate the approximate number of ultraconserved element loci we captured, by taxon, relative to the total number of loci captured from *Nasonia vitripennis* (n=1,166).



Supplemental Figure 5: Bar plots comparing parameter (β) estimates (± 95% CI) from general linear models of factors affecting the number of UCE contigs enriched and the length of enriched UCE contigs. Note that the y-axis differs across sub-panels.



Supplemental Figure 6: Maximum likelihood phylogeny inferred from a 75% complete supermatrix containing data from 14 genome-enabled taxa (identified by double-asterisks) and 27 taxa from which we enriched and assembled (Trinity) ultraconserved element loci. To infer this tree, we removed three sawfly taxa from consideration, re-identified UCE loci, re-extracted relevant UCE contigs, and re-aligned the extracted data, resulting in a slightly larger data matrix from that in Figure 1. We show bootstrap support values only where support is < 100%, and the single asterisk beside *Stenamma megamanni* denotes that this sample represents a different population of the same species.