Supplementary Table 1. Numbers of quality filtered Illumina reads from ovary, teratocyte, venom gland and larval sequence libraries that were included in the parasitism transcriptome assembly. Single reads had low quality partners that were excluded from the dataset.

Tissue or cell type	**Ovaries**	**Teratocytes**	**Venom gland**	**Larvae**
Read pairs	51,673,982	49,507,250	68,219,085	47,827,562
Single reads	9,781,812	8,154,144	11,029,183	10,286,276
Total reads	113,129,776	107,168,644	147,467,353	105,941,400
Reads Mapped	109,022,310 (96.37%)	95,279,474 (88.91%)	143,699,728 (97.45%)	102,621,862 (96.87%)

Supplementary Table 2. Venom data set. All loci have an RPKM greater than 50 in venom, are upregulated greater than 50-fold compared to ovary expression, and their corresponding protein product is detected in venom gland reservoirs. Abbreviations for species names are as follows: Ci: *Chelonus inanitus,* Cr: *Cotesia rubecula*, Ep1: *Eumenes pomiformis*, Eo: *Eupelmus orentalis*, Hd: *Hyposoter didymator,* Lb: *Leptopilina boulardi,* Ma: *Microctonus aethipoides,* Mh: *Microctonus hyperodae,* Ph: *Pimpla hypochondriaca*, Pp2: *Pteromalus puparum*, and Nv: *Nasonia vitripennis.*

Locus	**Ovaries**	**Teratocytes**	**Venom**	**Larvae**	**Venom unique peptide matches**	**Teratocyte unique peptide matches**	**Putative function**	**Signal peptide**	**Direct orthologs**	**Functional class previously identified in Braconids**	**Functional class previously identified in other parasitic wasps**	**References**
comp33950_c0	5	497	12638	5	8	5	metalloprotease-like, reprolysin family	Y	Ci	Ci	Lb, Lh	[1, 13, 15]
comp40703_c0	1	46	59	8	2	2	esterase/lipase-like, Ci-50	Y	Ci	Ci	Hd, Lb, Lh, Nv	[1-3, 13, 15]
comp36551_c0	5	0	17536	7	9		Ci-48a-like	N	Ma, Mh, Ci, Nv	Ma, Mh, Ci	Nv	[1, 3, 4]
comp17585_c0	3	0	7863	14	13		Ci-48a-like	Y	Ma, Mh, Ci, Nv	Ma, Mh, Ci	Nv	[1, 3, 4]
comp36791_c0	5	0	2439	1	11		Ci-48a-like	Y	Ma, Mh, Ci, Nv	Ma, Mh, Ci	Nv	[1, 3, 4]
comp37198_c0	1	1	725	1	5		Ci-48a-like	N	Ma, Mh, Ci, Nv	Ma, Mh, Ci	Nv	[1, 3, 4]
comp35049_c0	7	2	1170	2	8		Ci-48a-like	Y	Ma, Mh, Ci, Nv	Ma, Mh, Ci	Nv	[1, 3, 4]
comp17908_c0	3	3	3462	5	3		unknown, PBP/GOBP family, baculovirus protein of unknown function (DUF816) domain	Y		Ci		[1]
comp21422_c0	1	8	1414	1	18		seminal fluid protein, glycosyl hydrolase family	Y		Ci	Eo, Lb, Lh	[1, 5, 15]
comp36944_c0	0	1449	922	0	2	4	serine protease snake	Y		Ci, Cr	Nv, Pp2, Ph, Hd, Lh	[1-3, 6-8, 13]
comp37513_c0	1	0	351	0	2		serine carboxypeptidase	Y		Ci, Cr	Nv, Pp2, Ph, Hd, Lh	[1-3, 8, 13]
comp17613_c0	257	2	423421	115	7		unknown, cysteine rich conotoxin superfamily	Y		Ma, Mh, Ci		[1, 4]
comp21557_c0	11	1952	17904	5	19	19	zinc metalloprotease, reprolysin family	Y		Ci	Ep1, Nv, Hd, Ph	[2, 3, 7, 9]

comp36550_c0	12	1052	11067	37	2		viral cysteine rich-domain containing protein	Y		Ma, Mh, Ci		[1, 4]
comp17591_c0	1	41	3172	1	3		serpin	Y			Lb, Lh, Hd	[4, 10, 13, 15]
comp38077_c0	3	0	224	0	3		phospholipase A2	N			Nv	[3]
comp21649_c0	3	3	2847	1	3		conserved protein, domain of unknown function (DUF4339)	N				
comp36655_c0	56	0	6425	4	9		deoxyribonuclease II, plancitoxin	Y				
comp37062_c0	2	653	388	0	10		Nucleopolyhedrovirus p26 protein	Y				
comp37102_c0	17	114	952	18	9		polynucleotide kinase 3 phosphatase domain-containing protein	Y				
comp36886_c0	3	66	2114	1	10		protease domain-containing protein	Y				
comp21649_c1	1	1	1469	0	2		conserved uncharacterized protein	N				
comp36950_c0	1	23	935	11	2		conserved uncharacterized protein	Y				
comp36917_c0	1	1004	116	10	3		conserved uncharacterized protein	Y				
comp29658_c0	33	13629	117556	35	15	9	unknown	Y				
comp36535_c0	38	3	76709	25	12		unknown	Y				
comp36593_c0	1	0	4138	1	2		unknown	N				
comp36807_c0	4	0	3793	1	3		unknown	N				
comp17570_c0	4	88	2519	20	3		unknown	Y				
comp21649_c2	4	2	1884	1	4		unknown	Y				

Supplementary Table 3. Teratocyte data set. All loci have an RPKM greater than 50 in teratocytes, are upregulated greater than 50-fold compared to ovary expression, and their corresponding protein product is detected in teratocyte conditioned media. Abbreviations for species names are as follows: Ci: *Chelonus inanitus,* Cr: *Cotesia rubecula*, Dc: *Dinocampus coccinellae,* Ep1: *Eumenes pomiformis*, Eo: *Eupelmus orentalis*, Hd: *Hyposoter didymator,* Ma: *Microctonus aethipoides,* Mc: *Microplitis crocipes*, Mh: *Microctonus hyperodae,* Ph: *Pimpla hypochondriaca*, Pp2: *Pteromalus puparum*, and Nv: *Nasonia vitripennis.*

Locus	**Ovaries**	**Terato-cytes**	**Venom**	**Larvae**	**Venom unique peptide matches**	**Terato-cyte unique peptide matches**	**Putative function**	**Signal peptide**	**Direct orthologs**	**Functional class previously identified in Braconids**	**Functional class previously identified in other parasitic wasps**	**References**
comp29447_c0	4	2455	184	36		24	esterase FE4-like	Y	Dc	Dc	Nv, Lh	[3, 11, 13, 14]
comp36645_c0	0	9378	0	2		5	TSP14	Y	Mc	Mc		[12]
comp21395_c0	1	566	0	1		2	Chitooligosaccharidolytic beta-N-acetylglucosaminidase-like	Y		Ci	Eo, Lh	[1, 5, 15]
comp17816_c0	0	1347	0	0		7	zinc metalloprotease-like protein	Y		Ci	Ep1, Nv, Hd, Ph, Lb, Lh	[2, 3, 7, 9, 13, 15]
comp34856_c1	2	759	0	1		17	zinc metalloprotease, reprolysin family	Y		Ci	Ep1, Nv, Hd, Ph, Lb, Lh	[2, 3, 7, 9, 13, 15]
comp37629_c0	0	663	0	0		7	zinc metalloprotease, reprolysin family	Y		Ci	Ep1, Nv, Hd, Ph, Lb, Lh	[2, 3, 7, 9, 13, 15]
comp35200_c0	37	21281	1189	2	4	18	zinc metalloprotease, reprolysin family	Y		Ci	Ep1, Nv, Hd, Ph, Lb, Lh	[2, 3, 7, 9, 13, 15]
comp21557_c0	11	1952	17904	5	19	19	zinc metalloprotease, reprolysin family	Y		Ci	Ep1, Nv, Hd, Ph, Lb, Lh	[2, 3, 7, 9, 13, 15]
comp33950_c0	5	497	12638	5	8	5	metalloprotease-like, reprolysin family	Y	Ci	Ci	Ep1, Nv, Hd, Ph, Lb, Lh	[1, 2, 3, 7, 9, 13, 15]
comp35997_c1	0	502	15	1		2	lipase-like	N		Ci	Hd, Nv, Lb, Lh	[1-3, 13, 15]
comp21535_c0	18	14846	0	0		119	Ci-48a-like	Y		Ci		[1]
comp36923_c0	5	3374	0	0		51	Ci-48a-like	Y		Ci		[1]
comp36974_c0	1	2338	0	0		37	Ci-48a-like	Y		Ci		[1]
comp35388_c0	1	4535	0	1		12	Ci-48a-like	Y		Ci		[1]
comp36283_c0	0	908	0	0		31	Ci-48a-like	Y		Ci		[1]
comp38870_c0	0	279	0	1		7	Ci-48a-like	Y		Ci		[1]
comp35119_c0	1	400	10	389		7	Ci-48a-like, cytochrome P450-like	Y		Ci		[1]
comp37086_c0	1	1409	0	1		4	serine protease stubble-like	Y		Ci, Cr	Nv, Pp2, Ph, Hd	[1-3, 6-8]
comp36944_c0	0	1449	922	0	2	4	serine protease snake	Y		Ci, Cr	Nv, Pp2, Ph, Hd	[1-3, 6-8]

comp29745_c0	10	554	404	0		19	Peptidase family M13 domain-containing protein	Y		Ma, Mh		[4]
comp37301_c0	2	241	544	0		30	Peptidase family M13 domain-containing protein	Y		Ma, Mh		[4]
comp30169_c0	0	216	0	0		9	5NUC-like	Y				
comp38689_c0	1	103	2	29		22	aminopeptidase N-like	Y				
comp35353_c0	3	54643	0	1		4	Antimicrobial peptide Hymenoptaecin HD-1	Y				
comp31735_c0	0	10016	0	0		2	Antimicrobial peptide Hymenoptaecin HD-2	Y				
comp33946_c2	1	113	0	1		4	phosphatidylinositol phospholipase C-like	Y			Lb, Lh, Nv	[3, 13, 15]
comp36755_c0	9	5618	1	1		19	phosphatidylinositol phospholipase C-like	Y			Lb, Lh, Nv	[3, 13, 15]
comp37278_c0	0	931	0	8		2	phosphatidylinositol phospholipase C-like	Y			Lb, Lh, Nv	[3, 13, 15]
comp21629_c0	3	4115	0	1		5	chemosensory protein-like	N				
comp21599_c0	2	2220	0	0		16	conserved uncharacterized protein	Y				
comp17486_c0	24	2198	1	1		24	conserved uncharacterized protein	Y				
comp17509_c0	0	2035	0	0		11	conserved uncharacterized protein	N				
comp17643_c0	2	3956	0	0		44	conserved uncharacterized protein	Y				
comp17853_c0	0	1034	0	57		5	conserved uncharacterized protein	Y				
comp21210_c0	0	412	0	0		14	conserved uncharacterized protein	N				
comp21541_c0	0	4353	0	2		27	conserved uncharacterized protein	Y				
comp33911_c0	2	3436	0	0		2	conserved uncharacterized protein	N				
comp35377_c2	3	880	4	2		6	conserved uncharacterized protein	Y				
comp36677_c0	0	1173	0	1292		2	conserved uncharacterized protein	Y				
comp36794_c0	0	4090	0	0		11	conserved uncharacterized protein	Y				
comp37014_c0	0	2027	0	0		3	conserved uncharacterized protein	Y				
comp37136_c0	13	838	0	131		5	conserved uncharacterized protein	Y				
comp30565_c1	1	1297	0	0		7	flavin reductase-like	Y				

comp22698_c0	0	148	1	2		8	flavin reductase-like	Y				
comp17621_c0	0	9816	0	1		4	MAGE-like	Y				
comp17572_c0	1	6080	0	4		4	NPC2-like	N				
comp29569_c0	0	1245	0	0		3	trypsin domain-containing protein	Y				
comp29658_c0	33	13629	117556	35	15	9	unknown	Y				
comp36540_c1	0	83820	1	3		4	unknown	Y				
comp21548_c0	0	14307	0	1		4	unknown	Y				
comp29700_c0	0	538	0	0		3	unknown	N				
comp21677_c0	0	490	0	0		2	unknown	N				
comp36780_c0	0	6396	0	0		6	unknown	Y				
comp36637_c0	0	8782	0	2		11	unknown	Y				
comp35181_c3	0	4720	0	0		3	unknown	N				
comp31906_c0	0	1778	0	0		32	unknown	N				
comp21677_c2	0	745	0	0		6	unknown	Y				
comp33009_c4	26	7326	3	2		8	unknown	Y				
comp33250_c0	0	749	6	0		14	unknown	Y				
comp21554_c0	1	6989	0	0		4	unknown	Y				
comp17779_c0	3	8468	2	3		7	unknown	N				
comp17801_c0	24	1428	0	0		4	unknown	Y				
comp17803_c0	18	12314	2	3		14	unknown	Y				
comp21210_c1	0	440	0	0		6	unknown	N				
comp21624_c0	1	3835	0	0		3	unknown	Y				
comp29847_c0	1	601	0	0		4	unknown	Y				
comp37154_c0	7	1469	0	7		12	unknown	Y				
comp37519_c0	0	438	0	0		5	unknown	Y				
comp31919_c0	0	215	0	0		11	Vascular endothelial growth factor receptor-like	Y				
comp37158_c0	1	1398	0	0		11	Vascular endothelial growth factor receptor-like	Y				
comp29657_c0	1	9509	0	0		32	viral A-type inclusion protein-like	Y				
comp40453_c0	0	167	0	0		24	vitellogenin-like	Y				

Supplementary Table 4. Loci that are similarly expressed in teratocytes and ovaries (greater than 50 RPKM), and which have a corresponding protein product detected in teratocyte conditioned media. Products from these loci are most likely detected in teratocyte conditioned media because of low level teratocyte mortality during culture.

Locus	Ovaries	Teratocytes	Venom	Larvae	Venom unique peptide matches	Teratocyte unique peptide matches	Putative function	Signal peptide
comp34313_c0	5658	6278	5237	5165		4	Ubiquitin-2 like Rad60 SUMO-like	N
comp34092_c0	180	5044	1570	2		2	NPC2-like	N
comp21579_c0	1600	2752	417	4491		4	40S ribosomal protein S3a	N
comp36568_c0	3706	2619	570	7511		25	elongation factor 1 alpha	N
comp17592_c0	1082	2002	688	4068		6	60S ribosomal protein L7	N
comp17580_c0	1296	1739	370	4092		2	40S ribosomal protein S6	Y
comp36669_c0	1400	1694	543	3597		6	ribosomal protein S3	N
comp36643_c0	1458	1673	375	3558		5	60S ribosomal protein L4-like	Y
comp36714_c0	1081	1613	508	4269		4	60S ribosomal protein L7a	Y
comp36702_c0	2095	1601	312	2814		25	elongation factor 2	N
comp36681_c0	1104	1596	688	3269		2	60S ribosomal protein L10	N
comp36672_c0	1099	1515	919	2871		2	ribosomal protein S15	N
comp18742_c0	1479	1505	462	3235		2	40S ribosomal protein S16	N
comp36744_c0	927	1382	309	3078		6	40S ribosomal protein S4	N
comp36760_c0	522	1244	309	3098		7	40S ribosomal protein SA	N
comp36723_c0	1050	1198	735	2814		2	40S ribosomal protein S17	Y
comp36730_c0	1155	1174	358	2366		3	40S ribosomal protein S13	N
comp36575_c0	1376	1088	442	4264		9	60S acidic ribosomal protein P0-like	N
comp36685_c0	3792	1037	236	2025		2	60S ribosomal protein L13	N
comp21544_c0	1006	1021	443	1919		2	40S ribosomal protein S23	Y
comp36752_c0	820	1021	518	2475		3	40S ribosomal protein S14a	N
comp36845_c0	801	998	362	1236		27	heat shock 70 kDa protein-like	Y
comp21529_c0	829	979	442	2057		2	40S ribosomal protein S10	Y
comp31782_c1	672	932	327	2316		2	60S ribosomal protein L14-like	N
comp36605_c0	1037	894	320	2239		3	40S ribosomal protein S8	N
comp21584_c0	773	856	273	2348		3	60S ribosomal protein L5	N
comp18427_c0	678	854	465	1850		12	Calreticulin	Y
comp32278_c0	3834	837	1098	5059		28	heat shock 70 kDa protein-like	Y
comp36801_c0	809	806	319	1877		2	40S ribosomal protein S20	N
comp29667_c0	1104	784	288	1745		2	40S ribosomal protein S18	N
comp36949_c0	351	659	260	1055		28	disulfide-isomerase A3-like	Y
comp29645_c0	241	641	413	23		2	unknown	N
comp29635_c0	248	530	180	1056		2	SAGA-associated factor 29-like	N
comp18494_c0	924	490	127	1906		2	eukaryotic translation initiation factor 5A-like	N
comp36906_c0	436	414	196	1345		4	60S ribosomal protein L12	Y

comp29651_c0	1042	353	348	2130		7	peptidyl-prolyl cis-trans isomerase-like	N
comp36741_c0	332	350	198	871		2	mitochondrial GTPase 1-like	N
comp17558_c0	345	340	241	967		26	protein disulfide-isomerase-like	N
comp21436_c0	514	334	153	367		2	peptidyl-prolyl cis-trans isomerase B-like	Y
comp17891_c0	449	317	254	1909		17	Glyceraldehyde-3-phosphate dehydrogenase-like	N
comp34100_c2	1278	310	160	1898		19	tubulin beta-1 chain-like	Y
comp36889_c0	474	292	70	1361		11	Elongation factor 1-gamma	N
comp36956_c0	277	287	64	1932		4	nucleoside diphosphate kinase-like	N
comp29620_c0	249	286	169	285		8	protein disulfide-isomerase A6-like	Y
comp17599_c0	2262	246	158	2756		12	actin related protein	N
comp20412_c0	167	237	100	376		26	endoplasmin	Y
comp17662_c0	1774	236	139	1643		14	alpha-tubulin	N
comp21625_c0	930	228	160	974		7	6-phosphofructokinase-like	Y
comp31722_c0	783	221	465	1243		2	polyadenylate-binding protein 1-like	N
comp31812_c1	388	198	34	345		4	fatty acid synthase-like	Y
comp22551_c0	94	196	144	183		3	C-factor-like	Y
comp20922_c0	298	185	310	87		2	conserved uncharacterized protein	Y
comp37151_c0	383	183	106	703		2	glutathione S-transferase S3	N
comp36792_c0	2094	181	149	1747		12	heat shock 90 kDa protein-like	Y
comp36043_c1	144	173	79	397		26	Fructose-bisphosphate aldolase	N
comp20947_c0	112	173	1	101		21	L-lactate dehydrogenase-like	N
comp37049_c0	397	164	109	593		5	Peroxiredoxin 1	N
comp21426_c1	295	161	102	406		2	thioredoxin-like protein	N
comp17560_c0	385	152	96	1513		8	ATP synthase beta subunit	N
comp36958_c0	371	135	56	1033		3	ATP synthase alpha subunit	Y
comp18839_c0	224	135	146	172		6	Cathepsin L	Y
comp17797_c1	495	129	52	693		13	heat shock 70 kDa protein-like	N
comp31846_c0	541	127	65	964		4	ATP-dependent RNA helicase WM6-like	Y
comp30000_c1	293	127	60	314		17	pyruvate kinase-like	Y
comp36998_c0	133	117	48	499		3	syntenin-1-like	Y
comp21157_c1	457	116	73	1268		9	conserved uncharacterized protein	N
comp19329_c0	338	116	92	325		3	farnesoic acid methyltransferase-like	N
comp37675_c0	82	115	82	180		2	chloride intracellular channel exc-4	Y
comp29619_c0	228	112	63	271		17	neutral alpha-glucosidase AB-like	Y
comp21856_c1	206	102	28	618		23	tudor staphylococcus/micrococcal nuclease	Y
comp17797_c0	244	101	44	587		5	heat shock 70 kDa protein-like	N
comp36608_c0	622	99	136	797		2	conserved uncharacterized protein	Y
comp18352_c0	67	99	9	9		19	aldehyde dehydrogenase X, mitochondrial-like	Y
comp36093_c0	522	97	92	865		3	Eukaryotic initiation factor 4A-II	N
comp31602_c2	431	97	125	322		12	transitional endoplasmic reticulum	N
comp21759_c0	155	93	44	184		5	asparaginyl-tRNA synthetase	N
comp37537_c0	169	92	57	246		11	phosphoglycerate kinase-like	N
comp17666_c0	693	89	76	914		2	RNA-binding protein squid-like	N
comp33893_c8	946	88	99	486		4	histone H3.3	Y
comp35264_c12	155	85	54	186		2	protein transport protein Sec23A-like	Y
comp29648_c0	531	82	47	901		2	nucleosome assembly protein 1-like	N

comp37182_c0	252	76	264	75		2	cathepsin L-like	Y
comp35274_c2	156	75	61	452		10	Malate dehydrogenase, mitochondrial	N
comp18235_c0	221	71	23	220		4	ATP-citrate synthase-like	N
comp37489_c0	155	70	24	246		5	6-phosphogluconate dehydrogenase, decarboxylating-lik	N
comp37473_c0	118	70	18	271		26	glucose-6-phosphate isomerase	Y
comp21596_c2	222	69	21	612		7	La autoantigen homolog (ssb gene)	N
comp31773_c1	147	69	37	153		3	glucosidase 2 subunit beta-like	Y
comp29595_c0	120	69	45	240		2	annexin-B9-like	Y
comp37055_c1	328	67	66	620		14	enolase-like	Y
comp29617_c2	68	67	45	53		7	hexokinase type 2-like	N
comp35103_c6	375	66	101	239		2	moesin/ezrin/radixin-like	Y
comp35427_c12	242	64	54	204		2	SDA1-like protein	Y
comp30297_c0	96	64	32	104		13	Hypoxia up-regulated protein-like	Y
comp39545_c0	59	64	22	105		5	Asparagine synthetase	N
comp38174_c0	82	63	62	171		2	coatomer subunit delta-like	Y
comp36141_c1	51	63	1	33		8	histone H2B-like protein	Y
comp22309_c3	168	61	36	449		2	eukaryotic translation initiation factor 2 subunit 1-like	Y
comp29812_c1	293	60	23	293		5	eukaryotic translation initiation factor 3 subunit A-like	Y
comp21640_c0	636	59	40	1442		4	nascent polypeptide-associated complex subunit	N
comp37144_c0	350	54	40	731		7	T-complex protein 1 subunit epsilon	N
comp17761_c0	299	54	29	216		5	citrate synthase, mitochondrial-like	Y
comp20381_c0	363	53	40	506		10	T-complex protein 1 subunit gamma	N
comp37518_c0	232	52	37	414		14	T-complex protein 1 subunit eta	N
comp21888_c0	266	51	75	216		15	thioredoxin reductase 2, mitochondrial-like	Y
comp35886_c6	157	51	39	117		17	puromycin-sensitive aminopeptidase-like	Y
comp36402_c2	65	51	5	169		9	inositol-3-phosphate synthase 1-B-like	Y

Supplementary Table 5. Loci that have a corresponding protein product detected in teratocyte conditioned media, that do not belong to the differentially upregulated or similarly expressed groups in a pairwise teratocyte and ovaries comparison. These loci have low teratocyte RPKM values and low fold change values relative to ovaries, suggesting that they do not encode secretory products. Products from these loci are most likely detected in teratocyte conditioned media because of low level teratocyte mortality during culture.

Locus	**Ovaries**	**Teratocytes**	**Venom**	**Larvae**	**Venom unique peptide matches**	**Teratocyte unique peptide matches**	**Putative function**	**Signal peptide**
comp38335_c0	18	340	24	2		19	membrane metallo-endopeptidase-like	N
comp29445_c1	13	192	14	10		6	neural/ectodermal development factor IMP-L2-like	Y
comp31811_c0	30	153	15	1		10	unknown	Y
comp35146_c2	41	111	19	100		6	histone-like	Y
comp40745_c0	5	107	0	2		2	unknown	Y
comp39677_c0	23	92	23	13		4	endoplasmic reticulum oxidoreductin-1-like	Y
comp36269_c3	30	57	22	27		3	gamma-glutamyl hydrolase A-like	Y
comp34347_c0	100	49	53	133		3	protein transport protein Sec24C-like	Y
comp34541_c0	282	48	26	462		13	T-complex protein 1 subunit theta-like	N
comp38669_c0	54	47	46	81		3	venom serine carboxypeptidase-like	Y
comp40703_c0	1	46	59	8	2	2	esterase/lipase-like, Ci-50	Y
comp37647_c0	173	44	45	322		4	translation initiation factor 2 gamma subunit	N
comp38007_c0	121	43	37	319		6	Dihydrolipoyl dehydrogenase, mitochondrial	Y
comp35378_c7	97	42	31	104		2	acetyl-CoA acetyltransferase, cytosolic-like	Y
comp29391_c0	139	42	26	142		2	dipeptidyl peptidase 3-like	Y
comp36094_c0	30	41	2	26		5	unknown	
comp37698_c0	225	40	22	349		8	T-complex protein 1 subunit zeta-like	N
comp35596_c10	173	40	2	61		11	Insulin-like growth factor-like	N
comp29837_c0	374	39	25	214		5	97 kDa heat shock protein-like	Y
comp29837_c2	398	38	21	189		8	heat shock 70 kDa protein 4L-like	N
comp38080_c0	124	37	44	249		3	proteasome subunit alpha type-4-like	N
comp37760_c0	159	37	30	162		5	Isocitrate dehydrogenase [NADP] cytoplasmic	N
comp30773_c0	190	35	36	183		4	Phosphoglycerate mutase-like	Y
comp21723_c0	125	35	49	178		7	V-type proton ATPase subunit B-like	N
comp20153_c0	251	35	47	378		11	triosephosphate isomerase-like	N
comp37002_c0	1379	33	9	329		6	heat shock protein 83-like	N
comp20709_c0	298	33	66	306		10	V-type proton ATPase catalytic subunit A-like	N
comp37851_c0	129	32	59	262		2	Proteasome subunit alpha type-5	Y
comp20425_c0	215	32	21	359		7	T-complex protein 1 subunit alpha-like	N
comp32652_c1	81	32	19	98		9	Histidyl-tRNA synthetase, cytoplasmic	N
comp34190_c1	87	30	49	417		2	cytoplasmic aconitate hydratase-like	Y

comp21730_c0	156	30	44	250		2	transaldolase-like	N
comp29800_c0	290	30	33	150		3	Ubiquitin-like modifier-activating enzyme	N
comp36460_c1	63	30	9	70		4	isoleucine--tRNA ligase	Y
comp21803_c0	186	30	25	214		10	e3 ubiquitin-protein ligase RFWD2-like	Y
comp19665_c0	242	30	26	432		14	T-complex protein 1 subunit delta	Y
comp17397_c0	171	28	25	84		3	spectrin alpha chain-like	Y
comp40186_c0	46	27	29	36		6	unknown	
comp21801_c0	114	27	47	82		2	cytosolic non-specific dipeptidase-like	Y
comp21667_c0	147	27	20	145		2	26S proteasome non-ATPase regulatory subunit 12-like	Y
comp21118_c0	67	25	33	63		4	programmed cell death 6-interacting protein-like	Y
comp28412_c1	44	24	19	39		2	unknown	
comp32131_c0	114	24	21	134		4	ubiquitin carboxyl-terminal hydrolase 14-like	N
comp29417_c0	43	23	8	107		2	Aspartate aminotransferase, cytoplasmic	N
comp20156_c0	103	23	16	78		2	leucyl-tRNA synthetase, cytoplasmic-lik	Y
comp22761_c0	96	23	52	160		20	unknown	Y
comp22243_c0	30	22	11	74		5	Adenosine kinase	N
comp37680_c0	156	21	24	157		2	26S proteasome non-ATPase regulatory subunit 1-like	Y
comp21206_c0	164	20	6	121		2	importin subunit beta-1-like	Y
comp36989_c0	365	20	8	1265		18	60 kDa heat shock protein, mitochondrial	Y
comp19857_c0	103	18	14	224		2	3-hydroxyacyl-CoA dehydrogenase	N
comp38578_c0	84	17	32	141		3	26S proteasome non-ATPase regulatory subunit 3-like	N
comp38339_c0	166	17	23	100		3	bifunctional aminoacyl-tRNA synthetase-like	Y
comp17700_c0	182	17	12	775		16	transketolase-like protein	Y
comp37879_c0	136	16	17	268		12	T-complex protein 1 subunit beta-like	N
comp38172_c0	128	15	15	83		3	cullin-associated NEDD8-dissociated protein	N
comp34165_c0	209	15	8	229		4	heterogeneous nuclear ribonucleoprotein	Y
comp19472_c0	34	13	11	46		2	unknown	
comp18768_c0	75	11	22	67		22	NADP-dependent malic enzyme-like	N
comp29304_c0	83	8	4	138		2	uridine 5'-monophosphate synthase-like	N
comp21462_c1	332	8	5	95		3	piwi-like	Y
comp21743_c0	72	6	87	51		3	Translational activator GCN1	Y
comp38771_c0	52	4	24	187		9	cystathionine beta-synthase-like	N
comp22875_c0	69	3	61	112		2	Antithrombin-III	Y
comp31759_c3	18	3	17	108		3	adenylosuccinate lyase-like	N
comp38123_c0	4	1	1	408		3	conserved uncharacterized protein	Y
comp22689_c1	110	1	18	100		6	conserved uncharacterized protein	N
comp31654_c1	20	1	290	233		7	conserved uncharacterized protein	Y
comp22459_c0	10	0	297	70		2	venom protein Vn50-like	Y
comp38046_c0	7	0	3	288		2	apolipophorins-like	Y
comp35347_c6	139	0	68	477		6	chitinase	Y

Supplementary Table 6. Loci with RPKM greater than 50 and differentially upregulated greater than 50-fold in larvae compared to ovaries. No proteins were detected in larval conditioned media, suggesting that these loci are not secretory products.

Locus	Ovaries	Teratocytes	Venom	Larvae	Venom unique peptide matches	Teratocyte unique peptide matches	Putative function	Signal peptide
comp27562_c0	0.1	0	0	106			Annexin-B9-like	Y
comp37746_c0	0.1	0	0	403			apolipoprotein D-like	Y
comp38433_c0	0.1	222	1	87			apolipoprotein D-like	Y
comp17852_c0	15	0	1	1064			apolipoprotein D-like	N
comp36851_c0	5	0	24	2255			B1 protein-like	Y
comp16179_c0	0.1	0	0	157			carboxypeptidase B-like	Y
comp21690_c1	3	0	1	155			carboxypeptidase B-like	Y
comp18591_c0	5	0	597	389			Chemosensory protein, Ci-14a	Y
comp35119_c0	1	400	10	389		7	Ci-48a-like, cytochrome P450-like	Y
comp36677_c0	0.1	1173	0	1292		2	conserved uncharacterized protein	Y
comp20551_c0	0.1	0	0	1104			conserved uncharacterized protein	Y
comp30268_c0	0.1	0	0	604			conserved uncharacterized protein	Y
comp38288_c0	0.1	0	0	465			conserved uncharacterized protein	Y
comp19237_c0	0.1	0	0	306			conserved uncharacterized protein	Y
comp18727_c0	0.1	0	0	303			conserved uncharacterized protein	Y
comp37169_c0	1	0	0	1094			conserved uncharacterized protein	Y
comp42762_c0	0.1	0	0	103			conserved uncharacterized protein	N
comp34270_c1	0.1	12	0	87			conserved uncharacterized protein	N
comp17853_c0	0.1	1034	0	57		5	conserved uncharacterized protein	Y
comp29466_c0	1	0	0	279			conserved uncharacterized protein	Y
comp35060_c0	1	0	0	231			conserved uncharacterized protein	Y
comp17284_c0	2	39	0	281			conserved uncharacterized protein	Y
comp22684_c1	3	0	0	272			conserved uncharacterized protein	Y
comp16315_c0	1	0	29	64			conserved uncharacterized protein	Y
comp38404_c0	0.1	0	1	372			cuticle protein-like	Y
comp38051_c0	0.1	0	0	354			cuticle protein-like	Y
comp34221_c0	0.1	0	0	302			cuticle protein-like	Y
comp18319_c0	0.1	0	0	167			cuticle protein-like	N
comp40683_c0	0.1	0	0	116			cuticle protein-like	Y
comp22841_c0	0.1	0	0	98			cuticle protein-like	N
comp42237_c0	0.1	1	2	96			cuticle protein-like	N
comp39420_c0	0.1	0	87	92			cuticle protein-like	Y
comp16287_c0	1	0	0	159			cuticle protein-like	Y
comp38084_c0	0.1	99	0	290			egf-like	N
comp22721_c0	0.1	0	0	617			Endocuticle structural glycoprotein SgAbd-1	Y
comp37936_c0	0.1	0	1	428			Endocuticle structural glycoprotein SgAbd-1	Y
comp31666_c2	1	0	1	2142			Endocuticle structural glycoprotein SgAbd-1	Y

comp36399_c0	2	0	0	301			fatty acid synthase-like	Y
comp37362_c0	2	1	1	724			Fatty acid-binding protein-like	N
comp18559_c0	0.1	0	1	4105			hexamerin	N
comp36892_c0	1	0	1	3958			hexamerin	Y
comp29446_c0	1	0	0	297			hexamerin	Y
comp19037_c0	9	0	0	555			hexamerin	Y
comp29574_c0	0.1	0	0	882			hypothetical protein	N
comp18539_c0	0.1	0	0	728			hypothetical protein	Y
comp37716_c0	0.1	0	0	710			hypothetical protein	Y
comp37603_c0	0.1	0	0	584			hypothetical protein	Y
comp37454_c0	0.1	0	0	570			hypothetical protein	N
comp37840_c0	0.1	0	0	406			hypothetical protein	N
comp31666_c1	0.1	0	0	260			hypothetical protein	N
comp19005_c0	0.1	0	0	205			hypothetical protein	Y
comp23029_c0	0.1	0	0	203			hypothetical protein	Y
comp22937_c0	0.1	0	0	182			hypothetical protein	Y
comp21665_c0	0.1	0	0	167			hypothetical protein	N
comp18319_c1	0.1	0	0	143			hypothetical protein	N
comp38086_c0	0.1	62	0	135			hypothetical protein	N
comp22956_c0	0.1	0	0	132			hypothetical protein	Y
comp40819_c0	0.1	0	0	128			hypothetical protein	Y
comp41282_c0	0.1	1	0	127			hypothetical protein	Y
comp22956_c1	0.1	0	0	122			hypothetical protein	N
comp41083_c0	0.1	0	0	97			hypothetical protein	Y
comp37474_c0	1	0	0	701			hypothetical protein	Y
comp17718_c0	1	206	1	633			hypothetical protein	Y
comp34190_c0	1	0	0	259			hypothetical protein	N
comp39376_c0	1	0	0	221			hypothetical protein	Y
comp37818_c0	2	0	1	404			hypothetical protein	Y
comp33398_c0	1	1	0	188			hypothetical protein	Y
comp39794_c0	1	1	23	163			hypothetical protein	Y
comp40372_c0	1	0	0	136			hypothetical protein	N
comp37546_c0	2	1	0	269			hypothetical protein	Y
comp37903_c0	5	0	0	511			hypothetical protein	Y
comp38123_c0	4	1	1	408		3	hypothetical protein	Y
comp34034_c0	1	0	0	99			hypothetical protein	Y
comp37781_c0	3	0	33	247			hypothetical protein	Y
comp34190_c2	7	0	0	562			hypothetical protein	Y
comp22918_c1	4	0	2	303			hypothetical protein	N
comp18648_c0	3	1	1	188			hypothetical protein	N
comp40523_c0	0.1	0	0	141			metalloprotease-like	Y
comp19031_c0	2	41	0	161			Monocarboxylate transporter-like	N
comp37854_c0	0.1	0	0	421			Peritrophin-1-like	Y
comp18994_c0	0.1	0	0	481			putative mucin-like protein	N
comp19348_c0	0.1	0	0	397			putative mucin-like protein	Y
comp22425_c0	2	0	1	179			Serine proteinase stubble-like	Y

comp18480_c0	2	0	1	152			Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Y
comp37382_c0	2	353	136	114			Thioredoxin	Y
comp40598_c0	0.1	0	0	148			vitellin-degrading protease-like	Y

Supplementary Table 7. Nudivirus-like genes detected in the venom, teratocyte, ovary and larval transcriptome dataset. Several nudivirus-like genes were not detected in the transcriptome dataset, from which low abundance loci had been removed. For nudivirus-like genes represented in the dataset, no expression was observed (RPKM < 3) in teratocytes, venom or larval samples, with the exception of *pif-5*.

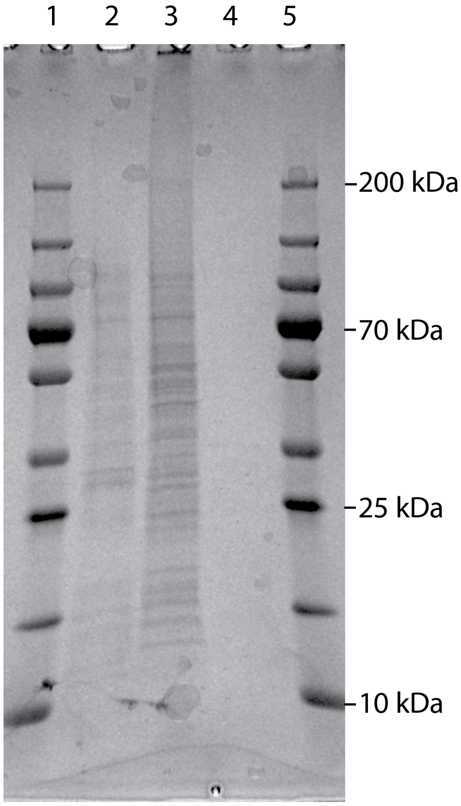
Locus name in transcriptome	**Ovaries RPKM**	**Teratocytes RPKM**	**Venom RPKM**	**Larvae RPKM**	**Nudivirus-like gene**	**Accession number**
comp36928_c0	1995	0	1	0	*17a*	JR139426
comp17471_c0	213	0	0	0	*27b-like*	JO935730
comp35907_c0	306	0	0	0	*35a*	JO965152
comp35095_c5	210	1	1	3	*35a*	JO967015
comp35095_c6	165	0	0	0	*35a*	JO967014
comp23093_c0	284	0	0	0	*35a*	JO957783
comp38425_c0	167	0	0	0	*35a*	JO951116
comp22772_c0	240	1	1	2	*35a*	JO941132
comp35095_c5	210	1	1	3	*35a*	JO967015
comp33171_c0	238	0	0	0	*35a*	JO915239
comp22099_c0	124	0	0	0	*35a*	JO957609
comp35095_c5	210	1	1	3	*35a*	JO967015
comp29688_c1	762	0	0	0	*38K*	JO947012
comp38381_c0	158	0	0	0	*ac92-like-1*	JO941840
comp37183_c0	537	0	0	0	*HzNVorf106-like*	JO948842
comp22792_c1	180	0	0	0	*HzNVorf118-like (PmV-like)*	JO972194
comp22792_c0	297	0	0	0	*HzNVorf118-like (PmV-like)*	JO972194
comp35354_c0	183	2	1	1	*HzNVorf128-like*	JO979913
comp36966_c0	1020	0	0	0	*HzNVorf64-like (p51)*	JO913493
comp21596_c1	1008	0	0	0	*HzNVorf9-like 1*	JO913494
comp21596_c0	232	0	0	0	*HzNVorf9-like 1*	JO913494
comp20060_c0	464	0	0	0	*HzNVorf9-like 2*	JO913495
comp22897_c0	110	0	0	0	*30b*	JO919922
comp35642_c1	138	0	0	0	*lef-5*	JO963952
comp35354_c0	183	2	1	1	*lef-8*	JO979913
comp17941_c0	147	0	0	0	*odv-e66*	JO941547
comp21307_c0	325	0	0	0	*odv-e66*	JO954076
comp21804_c0	352	0	0	0	*odv-e66*	JO928249
comp22420_c0	794	0	0	0	*odv-e66*	JO943687
comp29934_c0	255	0	0	0	*odv-e66*	JO960812
comp31454_c0	1170	0	1	0	*odv-e66*	JO940281
comp34506_c0	976	0	0	0	*odv-e66*	JO933415
comp34506_c0	976	0	0	0	*odv-e66*	JO933415
comp34757_c0	117	0	0	0	*odv-e66*	JO916892
comp36214_c0	384	0	0	0	*odv-e66*	JO951907
comp36214_c1	1503	0	0	0	*odv-e66*	JO921937
comp36214_c2	796	0	1	0	*odv-e66*	JO978990
comp37041_c0	1756	0	1	0	*odv-e66*	JO974925
comp37264_c0	276	0	0	0	*odv-e66*	JO929681
comp38624_c0	282	0	0	0	*odv-e66*	JO944999
comp39237_c0	188	0	0	0	*odv-e66*	JO955987
comp40103_c0	129	0	0	0	*odv-e66*	JO936339
comp17101_c0	308	0	0	0	*p47*	JO979914
comp17155_c0	349	0	0	0	*p74*	JO979915
comp18516_c0	258	0	0	0	*pif-1*	JO979916
comp19798_c1	258	0	0	0	*pif-2*	JO935365
comp37728_c0	184	0	0	0	*pif-3*	JO972553
comp17377_c0	284	0	0	0	*pif-4*	JO913492
comp17357_c0	214	0	0	0	*pif-5*	JO915573
comp36349_c0	**472**	**3**	**1020**	**1**	***pif-5***	**JO923318**

comp35642_c1	138	0	0	0	*vlf-1*	JO963952
comp37375_c0	374	0	0	0	*vlf-1b-2*	JO944220
comp17495_c0	2592	0	2	0	*vp39*	JR139430

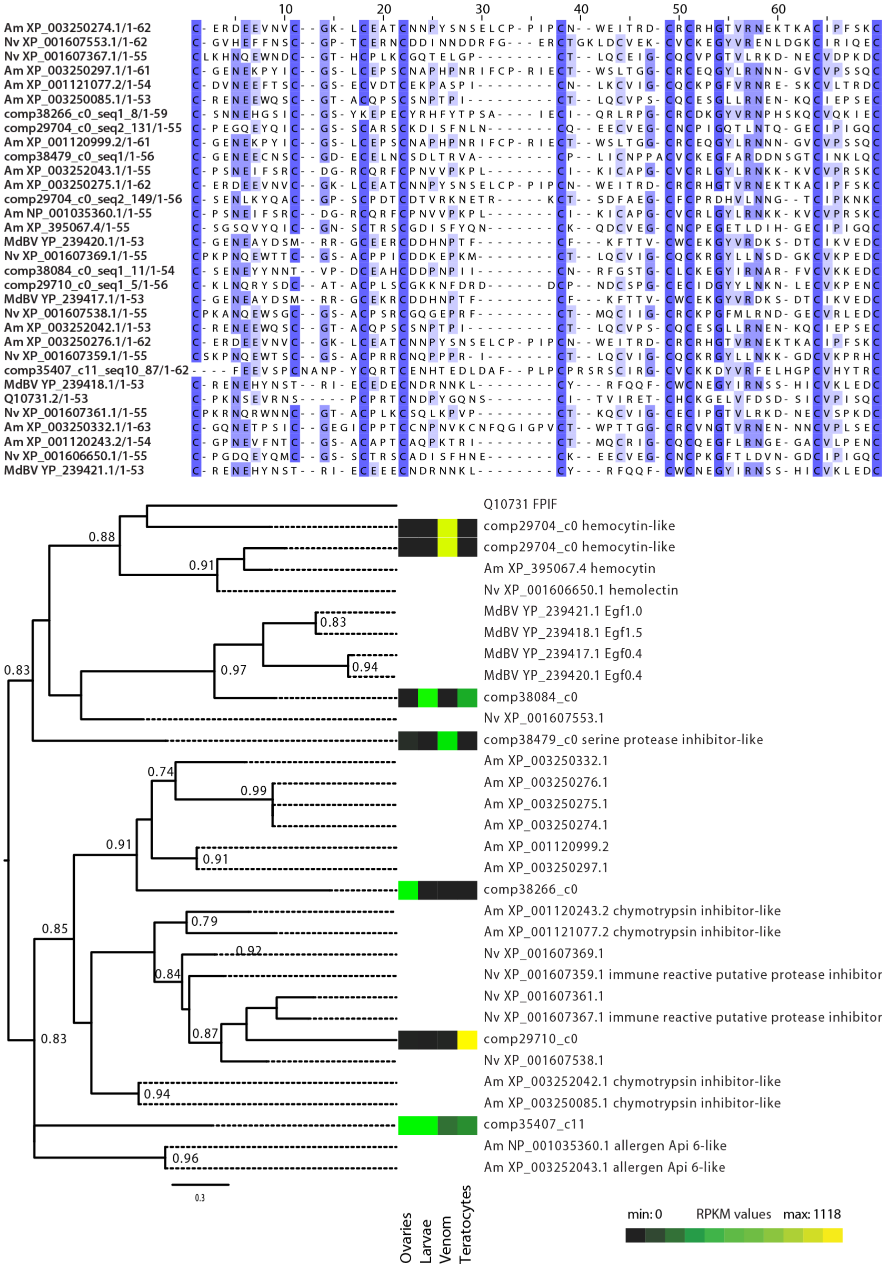
Supplementary Table 8. Matches to MdBV proteins in the venom, teratocyte, ovary and larval transcriptome dataset. Prior studies have shown that most MdBV genes are expressed at zero or low levels in wasps, and consistent with this, most MdBV protein queries had no match in the transcriptome dataset, from which low abundance loci had been removed. Only one MdBV gene was identified in the transcriptome dataset (*egf0.4*), plus several putative MdBV gene relatives located elsewhere in the *M. demolitor* genome. Each locus with a match to an MdBV protein is listed with RPKM values for expression and its best MdBV match. BLAST of MdBV matches against the NCBI non-redundant database (nr) identified three loci (comp36989_c1, comp30193_c0 and comp32277_c5) as more similar to homologs in other hymenopteran species than to MdBV genes, suggesting they are of insect rather than viral origin.

Locus	**Ovaries RPKM**	**Teratocytes RPKM**	**Venom RPKM**	**Larvae RPKM**	**MdBV relative**	**Accession**	**BLAST % identity**	**Best nr BLAST hit**
comp35738_c4	111	24	17	50	*egf0.4*	YP_239420.1 YP_239417.1	102/103 (99%)	Egf0.4
comp38084_c0	**0**	**99**	**0**	**290**	***egf1.0***	**YP_239421.1**	**44/107 (41%)**	**Egf1.5**
					egf1.5	**YP_239418.1** **YP_239416.1**	**45/107 (42%)**	
comp36989_c1	86	6	7	22	*ptp-H1*	YP_239381.1	70/268 (26%)	PTP corkscrew-like (*Megachile rotundata*) 542/618 (88%)
comp30193_c0	57	14	9	54	*ptp-H3*	YP_239383.1	92/269 (34%)	Putative PTP non-receptor type 61F-like (*Nasonia vitripennis*) 318/456 (70%)
comp32277_c5	42	555	22	22	*ank-G3*	YP_239379.1	28/93 (30%)	NF-kappa-B transcription factor relish (*Bombus terrestris*) 412/804 (51%)
					ank-C1	YP_239368.1	28/91 (30%)	
					ank-C2	YP_239369.1	27/82 (32%)	

Supplementary Figure 1. SDS-PAGE analysis of proteins in larva-conditioned media. Lanes 1 and 5: PageRuler Plus Prestained marker, lane 2: teratocyte-conditioned media, lane 3: protein from whole larvae, lane 4: larva-conditioned media. Teratocyte and larva-conditioned media were derived using the methods described in the results, by incubation in media for 72 hours. The gel was loaded with equivalent amounts of conditioned media, and stained with InstantBlue Coomassie-based stain.



Supplementary Figure 2. Alignment and phylogenetic analysis of proteins related to MdBV *egf* genes in *M. demolitor* and other select hymenopteran species. A. An alignment of "CD" regions of *egf* family members and relatives, with conserved sites highlighted in blue. MdBV: *Microplitis demolitor* bracovirus, Am: *Apis mellifera*, Nv: *Nasonia vitripennis*. Expression values (RPKM) for each *M. demoltior* locus are shown using a heat-map. B. Phylogenetic reconstruction of the evolutionary history of *egf* relatives, using the same organism abbreviations as in A. comp38084_c0 is the closest currently known relative of MdBV *egf* genes.



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