Table S4. Expression analysis of *D. v. virgifera* GH family genes identified in this study.[a]

Genes	Length (AA)[b]	Egg (38,657,737)[c]		Neonate (21,864,095)[c]		3rd-instar midgut (40,096,158)[c]	
		Read[d]	RPKM	Read[d]	RPKM	Read[d]	RPKM
GH45-1	720 (239)	1	0.04	4053	258.59	888	30.89
GH45-2	741 (246)	2	0.07	343	21.26	485	16.39
GH45-3	729 (242)	3	0.11	9	0.57	142	4.88
GH45-4	741 (246)	5	0.18	2135	132.30	26621	899.63
GH45-5	729 (242)	0	0	12	0.76	79	2.71
GH45-6*	615 (204)	1	0.04	15	1.12	538	21.92
GH45-7	720 (239)	2	0.07	61252	3907.24	228852	7960.36
GH45-8	717 (238)	6	0.19	14	0.89	86	3.00
GH45-9	720 (239)	0	0	796	50.78	2473	86.02
GH45-10	717 (238)	4	0.14	11641	745.75	67084	2343.23
GH45-11	735 (244)	2	0.07	31	1.94	656	22.35
GH48-1	1926 (641)	1	0.01	3	0.07	26	0.33
GH48-2*	374 (124)	1	0.06	0	0	2	0.13
GH48-3	1926 (641)	2	0.02	302	7.18	965	12.51
GH28-1	1098 (365)	0	0	171	7.14	319	7.27
GH28-2	1098 (365)	0	0	384	16.04	1098	25.01
GH28-3	1116 (371)	0	0	36	1.48	175	3.92
GH28-4*	1097 (365)	21	0.50	3	0.13	221	5.03
GH28-5	1062 (353)	0	0	55	2.38	294	6.92
GH28-6	1092 (363)	2	0.05	707	29.69	11750	269.09
GH28-7	1071 (356)	1	0.02	18	0.77	192	4.48
GH28-8*	855 (284)	5	0.15	1	0.05	3	0.08
GH28-9	1101 (366)	6	0.14	184	7.66	1105	25.10
GH28-10*	813 (270)	22	0.70	1	0.06	4	0.12
GH28-11	1062 (353)	4	0.09	2	0.09	8	0.18
GH28-12	1068 (355)	1	0.02	3	0.13	18	0.42
GH28-13	1104 (367)	1	0.02	28	1.16	15	0.33
GH28-14*	366 (122)	0	0	3	0.37	3	0.20
GH16-1	1125 (374)	3	0.07	36861	1502.60	39623	880.75
GH16-2	1116 (371)	668	15.53	497	20.42	1297	29.06
GH16-3	1119 (372)	614	14.23	501	20.53	1425	31.85
GH16-4	1113 (370)	573	13.35	262	10.80	31	0.70
GH16-5	1149 (382)	69	1.56	5	0.20	331	7.20
GH16-6*	696 (232)	0	0	0	0	1071	38.38
GH16-7*	448 (149)	1	0.06	6	0.61	2	0.11
GH16-8*	925 (307)	69	1.93	506	25.02	31	0.84
GH16-9*	842 (280)	10	0.31	4	0.22	13	0.39
GNBP-1	1353 (450)	40	0.76	173	5.85	34	0.63
GNBP-2	1500 (499)	301	5.19	53	1.62	48	0.80
GNBP-3	1671 (556)	408	6.32	0	0	0	0
GH5*	317 (105)	6	0.49	0	0	0	0

GH1-1	1491 (496)	1	0.02	27	0.83	5	0.08
GH1-2	1458 (485)	1	0.02	558	17.50	2637	45.11
GH1-3	1497 (498)	1	0.02	158	4.83	533	8.88
GH1-4	1494 (497)	2	0.03	1561	47.79	303	5.06
GH1-5	1509 (502)	5	0.09	2787	84.47	7932	131.10
GH1-6	1458 (485)	0	0	56	1.76	1117	19.11
GH1-7	1542 (513)	4	0.07	193	5.72	4099	66.30
GH1-8	1584 (527)	5	0.08	501	14.47	76	1.20
GH1-9	1686 (561)	3	0.05	2016	54.69	53	0.78
GH1-10	1461 (486)	3	0.05	64	2.00	429	7.32
GH1-11	2073 (690)	95	1.19	3	0.07	0	0
GH1-12	1551 (516)	357	5.95	1	0.03	11	0.18
GH1-13	1464 (487)	29	0.51	202	6.31	1232	20.99
GH1-14	1452 (483)	1	0.02	338	10.65	1735	29.80
GH1-15	1494 (497)	2	0.03	321	9.83	4033	67.32
GH1-16	1479 (492)	0	0	314	9.71	2494	42.06
GH1-17	1524 (507)	2	0.03	2137	64.13	6239	102.10
GH1-18	1491 (496)	5	0.09	5590	171.48	15378	257.23
GH1-19	1488 (495)	0	0	1855	57.02	8355	140.04
GH1-20	1539 (512)	19	0.32	68	2.02	13	0.21
GH1-21	1494 (497)	0	0	162	4.96	2340	39.06
GH1-22	1530 (509)	0	0	309	9.24	521	8.49
GH1-23	1024 (340)	0	0	1	0.04	2	0.05
GH1-24*	1280 (426)	12	0.24	185	6.61	339	6.61
GH1-25*	515 (171)	0	0	0	0	1	0.05
GH1-26*	1345 (448)	5	0.10	0	0	0	0
GH1-27*	491 (162)	2	0.11	23	2.14	67	3.40
GH1-28*	625 (208)	8	0.33	62	4.54	135	5.39
GH31-1	3033 (1010)	239	2.04	64	0.97	171	1.41
GH31-2	2727 (908)	9758	92.56	2607	43.72	11733	107.31
GH31-3	2574 (857)	2926	29.41	2823	50.16	9145	88.61
GH31-4	2625 (874)	829	8.17	6016	104.82	7971	75.73
GH31-5	2559 (852)	424	4.29	258	4.61	2352	22.92
GH31-6	1881 (626)	17	0.23	328	7.98	4535	60.13
GH31-7	1917 (638)	27	0.36	1280	30.54	30747	400.02
GH31-8	1941 (646)	19	0.25	73	1.72	397	5.10
GH31-9	1908 (635)	361	4.89	493	11.82	1175	15.36
GH31-10*	2781 (927)	56	0.52	566	9.31	7182	64.41
GH27-1	1236 (411)	1870	39.11	1396	51.62	12256	247.10
GH27-2	1338 (445)	94	1.82	70	2.39	217	4.04

[a] Genes considered as not expressed (RPKM < 0.3 or the number of reads < 10) are marked with grey shade.

[b] Lengths of the transcript (bp) as well as its translated protein in parentheses (amino acids) are shown.

[c] The total numbers of paired-end reads before filtering are shown in parentheses. Note that although the reads were not filtered, we used 0 mismatch to map the reads to the assembled transcriptome. Thus reads that included any ambiguity including unknown nucleotide 'N' were not counted.

[d] The number of paired-end reads mapped.

*The partial ORFs, not including from start to stop codons.