Table S1. A list of genes related to pathogen recognition*

Gene name	Domain(s)	Contig(s)	nCF	nCH	nIF	nIH	nIF:nCF	nIH:nC
CTL10	Lectin-C	11458, 14515, 14516, 15639, 17942	675.4	0.0	1788.3	0.0	*2.7*	0/0
Draper	EMI, NIM repeats	1849, 10216	0.0	83.5	18.1	142.9	*1.5*	1.7
Dscam	FN-3, Ig	5244, 7892, 9670	0.0	19.6	24.2	35.0	*2.0*	1.8
Galectin-2	β-propeller repeats	7714	0.0	12.3	0.0	8.7	0/0	0.7
Galectin-4	GLECT	2140	11.8	51.6	24.2	20.4	2.0	0.4
Hemicentin 1	Ig	131, 465, 14278	1729.9	186.7	2319.9	699.9	1.3	3.8
Hemicentin 2	Ig	4353	47.4	267.7	163.1	1545.6	3.4	5.8
Hemolin	Ig	3442	11.8	29.5	8868.8	116.6	748.5	4.0
IML-2		4775	11.8	0.0	537.7	0.0	45.4	0/0
IML-3	Lectin-C	1097, 13163, 14125	1670.6	800.7	2688.4	673.6	1.6	0.8
IML-3a	Lectin-C	13452, 16454	94.8	1078.2	0.0	985.7	0.0	0.9
IML-3b	Lectin-C	6630, 7642, 13397, 18062	165.9	2149.0	350.4	860.3	2.1	0.4
IML-4		4808	0.0	0.0	2573.6	5.8	*217.2*	*2.4*
Lectin		6497	651.7	8397.2	30.2	3893.1	0.0	0.5
Lectin prec.	VWD	14570	545.0	4990.7	6.0	2143.4	0.0	0.4
Leureptin	LRR	4012, 8453, 15857	1978.7	9.8	4392.1	58.3	2.2	5.9
Leureptin2	LRR	2194	177.7	4.9	126.9	0.0	0.7	0.0
NimA	NIM repeats	858	35.5	152.3	0.0	265.4	0.0	1.7
NimB		8820	11.8	90.9	18.1	81.7	1.5	0.9
PGRP-1		13190, 14104	343.6	0.0	1752.0	64.2	5.1	*26.1*
PGRP-2		14700	0.0	0.0	1105.6	5.8	*93.3*	*2.4*
PGRP-3	Amidase 2	14752	0.0	0.0	712.9	5.8	*60.2*	*2.4*
PGRP-D	Amidase 2	575	35.5	0.0	1564.7	14.6	44.0	*5.9*
PGRP-L2	Amidase 2	151	47.4	147.4	24.2	195.4	0.5	1.3
PGRP-L5	Amidase 2	309	201.4	265.3	175.2	268.3	0.9	1.0
PGRP-LC	Amidase 2	3259	0.0	39.3	0.0	23.3	0/0	0.6
PGRP-S1	Amidase 2	11845	0.0	4.9	54.4	49.6	*4.6*	10.1
PGRP-S2	Amidase 2	5684	0.0	2.5	96.7	11.7	*8.2*	4.8
PGRP-S5	Amidase 2	8467	0.0	0.0	682.7	0.0	*57.6*	0/0
SR-C-like	Somatomedin-B, Sushi (SCR repeat), MAM	5933, 8686, 13271, 15116, 15350, 15564	462.1	4573.1	48.3	4068.1	0.1	0.9
TEP1	α2M	9741, 10503, 12298	0.0	9.8	0.0	23.3	0/0	2.4
TEP2	α2M	8026, 8870	23.7	29.5	6.0	37.9	0.3	1.3
βGRP1	GH16-βGRP	2979	580.6	0.0	555.8	11.7	1.0	*4.8*
βGRP2	GH16-βGRP	1326	11.8	22.1	114.8	204.1	9.7	9.2
βGRP3		14744, 14786	308.1	0.0	296.0	0.0	1.0	0/0
βGRP4	GH16-βGRP	4114	213.3	4.9	271.9	17.5	1.3	3.6
MBP		8247	319.9	4.9	737.1	52.5	2.3	10.7

* Genes reported by Zhang et al. (2011) are *underlined*. nCF, nCH, nIF and nIH are normalized read numbers and, for genes with two or more contigs, they represent the total values. When nCF = 0, adjusted NRN for nIF (*italics*) is calculated as nIF × 825/9775; when nCH = 0, adjusted NRN for nIH (*italics*) is calculated as nIH × 3980/9775.

Table S2. Hemolymph proteinases, serpins, and other extracellular signaling molecules (see footnote of Table S1)

Gene name	Domain(s)	Contig(s)	nCF	nCH	nIF	nIH	nIF:nCF	nIH:nCH
HP1	Trypsin	8524, 12527, 16264, 16288, 16719, 17102, 18182	876.8	8709.1	42.3	5849.8	0.1	0.7
HP2	Trypsin	6333	35.5	24.6	18.1	40.8	0.5	1.7
HP3	Trypsin	5756	0.0	137.5	0.0	72.9	0/0	0.5
HP4	Trypsin	5654	23.7	167.0	6.0	134.1	0.3	0.8
HP5	CLIP, trypsin	2203	0.0	36.8	30.2	212.9	2.6	5.8
HP6	Trypsin	540	284.4	260.3	447.1	405.3	1.6	1.6
HP7	Trypsin	3018, 3762	11.8	159.6	175.2	256.6	14.8	1.6
HP8	CLIP, trypsin	5370, 9086	379.2	4.9	712.9	29.2	1.9	5.9
HP9	Trypsin	3989	0.0	2.5	48.3	70.0	*4.1*	28.5
HP12	Trypsin	11373	23.7	2.5	30.2	0.0	1.3	0.0
HP13	Trypsin	1094	35.5	191.6	12.1	189.6	0.3	1.0
HP14	LDLa,CCP,	3606, 3785	154.0	14.7	447.1	29.2	2.9	2.0
HP15	Trypsin	4433	0.0	4.9	18.1	32.1	*1.5*	6.5
HP17s	Trypsin	5186, 14177	0.0	0.0	78.5	55.4	*6.6*	*22.6*
HP18	Trypsin	8231	0.0	2.5	0.0	99.1	0/0	40.4
HP19	Trypsin	3199, 6539, 14093	35.5	39.3	235.6	81.7	6.6	2.1
HP20	Trypsin	4242	59.2	0.0	259.8	2.9	4.4	*1.2*
HP21	CLIP, trypsin	2439	319.9	12.3	247.7	37.9	0.8	3.1
HP22	Trypsin	2361	82.9	9.8	422.9	2.9	5.1	0.3
SPH-1a	Trypsin	6149, 14393	272.5	63.9	4941.9	125.4	18.1	2.0
SPH-1b	Trypsin	2813	1279.6	22.1	1891.0	210.0	1.5	9.5
SPH2	Trypsin	2843	876.8	19.6	809.6	8.7	0.9	0.5
SPH4	Trypsin	2985	35.5	0.0	954.5	0.0	26.9	0/0
Serpin1	Serpin	7639	7713.4	0.0	7473.2	40.8	1.0	*16.6*
Serpin2	Serpin	5255, 5821, 14248, 14456, 15111, 15910 16917, 17048, 17058, 17751, 18441	106.6	790.8	302.1	9827.5	2.8	12.4
Serpin3	Serpin	2693	248.8	17.2	1872.8	55.4	7.5	3.2
Serpin4	Serpin	4422	556.9	334.0	2235.3	615.3	4.0	1.8
Serpin5		5831, 13453, 13454	94.8	31.9	1039.1	122.5	11.0	3.8
Serpin6	Serpin	1706	82.9	83.5	163.1	236.2	2.0	2.8
Serpin7	Serpin	8071, 8076	379.2	7.4	773.3	8.7	2.0	1.2
Serpin11	Serpin	6359	0.0	4.9	36.2	32.1	*3.1*	6.5
Serpin12	Serpin	3776, 6215, 6531, 17814	2417.1	19.6	5799.8	148.7	2.4	7.6
Serpin13	Serpin	2184	628.0	4.9	670.6	2.9	1.1	0.6
Serpin22	Serpin	3224	1161.2	0.0	2881.8	0.0	2.5	0/0
PI6		8286	0.0	0.0	839.8	67.1	*70.9*	*27.3*
PI-like		3674, 10722	118.5	7.4	646.4	70.0	5.5	9.5
Trypsin inh. B	Kunitz-BPTI	13936	0.0	0.0	151.0	0.0	*12.8*	0/0
Kazal-type PI	Kazal-1, -2	5197	0.0	0.0	120.8	2.9	*10.2*	*1.2*
Punch	GTP-cyclohydro1	1029	237.0	0.0	350.4	23.3	1.5	*9.5*
Phe hydroxylase	ACT	509	864.9	41.8	2036.0	20.4	2.4	0.5
Tyr hydroxylase	Biopterin-H	2023	11.8	0.0	199.4	20.4	16.8	*8.3*
DDC	DOPA-deC	940	0.0	0.0	1262.7	20.4	*106.6*	*8.3*
PAP1	CLIP, trypsin	3070	94.8	49.1	314.2	61.2	3.3	1.3
PAP2	CLIP, trypsin	1667	0.0	17.2	592.1	96.2	*50.0*	5.6
PAP3	CLIP, trypsin	1818	0.0	63.9	271.9	192.5	*23.0*	3.0
ProPO-p1		17085	616.1	5690.6	24.2	4858.3	0.0	0.9
ProPO-p2		17958	296.2	3249.3	18.1	2741.2	0.1	0.8
Zn proteinase	Peptidase-M14	915	0.0	51.6	126.9	75.8	10.7	1.5
Scolexin	Trypsin	10791, 10792, 16520, 18669, 18670, 18963	23.7	0.0	16650.2	5.8	702.6	*2.4*
Hdd1-like		2382	0.0	4.9	658.5	201.2	*55.6*	41.0
Hdd13-like		5606	11.8	0.0	114.8	11.7	9.7	*4.8*
Hdd23-like		6581	0.0	0.0	78.5	29.2	*6.6*	*11.9*

Table S3. Hemocyte adhesion-related genes (see footnote of Table S1)

Gene name	Domain(s)	Contig(s)	nCF	nCH	nIF	nIH	nIF:nCF	nIH:nCH
HAIP	GH-18	2947	6137.5	51.6	5926.6	163.3	1.0	3.2
Hemolectin	C8, EGF, F5_F8-type-C, VWD,	11280, 13813, 14711, 14760, 15506, 15594,	2772.5	34035.7	126.9	13458.1	0.1	0.4
Hemocyte-specific integrin α1	FG-GAP, integrin-α	3997, 4957, 4966	94.8	677.9	36.2	939.0	0.4	1.4
Hemocyte-specific integrin α2	Integrin- α 2	5800, 5860, 8294, 9106	142.2	0.0	175.2	8.7	1.2	*3.6*
Hemocyte-specific integrin α3	Integrin- α, FG-GAP	771	71.1	110.5	84.6	113.7	1.2	1.0
Plasmatocyte-specific integrin β1	Integrin-β, EGF-2	1850, 13553, 18269	118.5	975.0	84.6	1463.9	0.7	1.5
Integrin β1	Integrin-β, -β tail, - β cyt	349	343.6	412.6	350.4	662.0	1.0	1.6
Integrin related-1	Integrin-β-cyt	461	11.8	117.9	84.6	314.9	7.1	2.7
Integrin-linked protein kinase 2	ANK, PTK	2401	71.1	135.1	24.2	204.1	0.3	1.5
Lacunin	Ig, ADAM-spacer1, Kunitz-BPTI, PLAC	15, 2717, 15269, 15273	1410.0	12488.9	120.8	12335.4	0.1	1.0
Laminin	Laminin-G2	4	639.8	4452.8	132.9	4578.4	0.2	1.0
Neuroglian	I-set, FN3	163	165.9	365.9	96.7	609.5	0.6	1.7
Tetraspanin		92, 3559, 4331, 4687, 5512, 6843, 7644, 17721	509.5	1761.0	930.4	2502.1	1.8	1.4
Reeler1/Hdd11	Reeler	3778	0.0	27.0	1160.0	81.7	*97.9*	3.0
Paralytic peptide BP1	Lipoprotein_11	3375, 7873	296.2	852.2	447.1	974.0	1.5	1.1
Paralytic peptide BP2	Lipoprotein_11	3648, 14107, 15055	35.55	331.6	0.0	236.2	0.0	0.7
Paralytic peptide BP3	Lipoprotein_11	4042, 5938, 15696, 16051, 16074, 16096,	2085.3	2512.5	2344.1	5922.7	1.1	2.4
uENF/PSP precursor	GBP-PSP	2651	284.4	0.0	749.1	0.0	2.6	0/0
Thrombospondin	EGF-CA, TSP-C & -3	535	793.8	2.5	604.1	0.0	0.8	0.0

Table S4. Autophagy-related genes (see footnote of Table S1)

Gene name	Domain(s)	Contig(s)	nCF	nCH	nIF	nIH	nIF:nCF	nIH:nCH
Atg2	Chorein-N	15384	71.1	0.0	30.2	0.0	0.4	0/0
Atg2 like	Apt1	8264	94.8	2.5	42.3	0.0	0.5	0.0
Atg3	Autophagy-N & -C, BUD22, act-C	392	414.7	144.9	145.0	140.0	0.4	1.0
Atg4	Peptidase-C54	4329	213.3	2.5	60.4	5.8	0.3	2.4
Atg4-like	Peptidase-C54	11947	94.8	4.9	24.2	0.0	0.3	0.0
Atg5	APG5	5386, 5513	343.6	7.4	78.5	17.5	0.2	2.4
Atg6	APG6	12191, 14634	201.4	0.0	48.3	2.9	0.2	*1.2*
Atg8	Atg8	7383	59.2	105.6	181.2	64.2	3.1	0.6
Atg12	APG12	12607	106.6	2.5	12.1	2.9	0.1	1.2

Table S5. Genes of AMPs and other effector proteins (see footnote of Table S1)

Gene name	Domain(s)	Contig(s)	nCF	nCH	nIF	nIH	nIF:nCF	nIH:nCH
Attacin-1	Attacin N&C	8902, 14343	0.0	0.0	2114.5	61.2	*178.5*	*24.9*
Attacin-2	Attacin N&C	11040, 11711, 17135	0.0	49.1	1443.9	7940.7	*121.9*	161.7
Attacin-3	Attacin N&C	6782, 16576, 17705	0.0	0.0	833.7	102.1	*70.4*	*41.6*
Attacin-4	Attacin N&C	7203, 14641, 18324	23.7	7.4	2984.5	64.2	125.9	8.7
Attacin-5	Attacin N&C	13563, 17350	0.0	0.0	5207.7	0.0	*439.5*	0/0
Attacin-6	Attacin C	15159, 15744	0.0	0.0	0.0	145.8	0/0	*59.4*
Cecropin-6	Cecropin	14997	0.0	0.0	205.4	29.2	17.3	11.9
Cecropin B precursor		13894	0.0	0.0	290.0	84.6	*24.5*	*34.4*
Cecropin-like peptide B-5		12151, 15041	0.0	0.0	1141.8	0.0	*96.4*	0/0
Gallerimycin		10234	0.0	2.5	1504.3	20.4	*127.0*	8.3
Gloverin		2067	11.8	0.0	1691.6	239.1	142.8	*97.4*
Putative PI	TIL	16018	0.0	0.0	241.7	35.0	*20.4*	*14.3*
Immune related protein		15998, 17184, 18819	0.0	39.3	821.6	2519.6	*69.4*	64.1
IMPI		3142	11.8	17.2	2537.4	352.9	214.2	20.5
Lebocin-A precursor		13916, 17301, 17434	35.5	0.0	8017.0	0.0	225.5	0/0
Lebocin-B precursor		10853	0.0	0.0	682.7	2.9	*57.6*	*1.2*
Lebocin C precursor		4903	0.0	0.0	1685.6	17.5	*142.3*	*7.1*
Lebocin-D precursor		7116	11.8	9.8	5449.4	8.7	459.9	0.9
Lysozyme-like protein 1	LYZ1	1285	284.4	113.0	428.9	140.0	1.5	1.2
Lysozyme	LYZ	8421, 15931, 16133	1078.2	235.8	19640.7	2633.3	18.2	11.2
Moricin		9484	11.8	0.0	809.6	163.3	68.3	*66.5*
Moricin-like		17439	0.0	0.0	592.1	90.4	*50.0*	*36.8*
Possible AMP	Toxin_2	3746, 14568, 16292, 18150, 18699	0.0	19.6	507.5	1816.8	*42.8*	92.5
Secreted peptide 30		6597	710.9	0.0	1208.3	0.0	1.7	0/0
Salivary Cys-rich peptide	WAP	4175	0.0	17.2	241.7	131.2	*20.4*	7.6
Peptidase inhibitor precursor	WAP	12848	0.00	39.3	0.0	2.9	0/0	0.1
Peptidase inhibitor-like	WAP	14536	71.09	0.0	48.3	0.0	0.7	0/0
Antileukoproteinase precursor	WAP	15064	0.00	0.0	90.6	0.0	*7.7*	0/0
Putative WAP-2 isoform 1	WAP	13827	0.00	0.0	42.3	0.0	*3.6*	0/0
Transferrin	Transferrin	2145, 11027, 14937, 16606, 17206, 18239, 18308	1196.7	36.8	8542.6	277.0	7.1	7.5

Table S6. Other putative immunity-related genes (see footnote of Table S1)

Gene name	Domain(s)	Contig(s)	nCF	nCH	nIF	nIH	nIF:nCF	nIH:nCH
FAK	FERM-M, PK-Tyr, Focal-AT	82	11.8	365.9	42.3	355.8	3.6	1.0
Alk	SH3	8785	0.0	12.3	0.0	0.0	0/0	0.2
Pvr	Ig, PTK	222	94.8	385.6	90.6	501.6	1.0	1.3
Serrate	EGF-Lam, LDLa	49	7109.1	830.1	4428.4	793.2	0.6	1.0
Notch	ANK, EGF-CA	6	35.5	808.0	24.2	842.8	0.7	1.0
Dicer-2	ResIII, Helicase C, dsRNA binding, PAZ	412, 824	71.1	275.1	90.6	402.4	1.3	1.5
Argonaute 1	PAZ-argonaute-like	10180	0.0	7.4	6.0	17.5	*0.5*	2.4
NOS	NO synthase, flavodoxin1	6991, 11493, 11623	0.0	22.1	48.3	29.2	*1.4*	1.3
Peroxiredoxin	PRX-1cys	8403	11.8	14.7	18.1	17.5	1.5	1.2
Thioredoxin POD1	PRX-Typ2cys	6299	35.5	31.9	30.2	52.5	0.8	1.6
Thioredoxin POD2	PRX-Typ2cys	8926	82.9	498.6	48.3	650.3	0.6	1.3
Thioredoxin POD3	PRX-Typ2cys	2937	59.2	147.4	126.9	166.2	2.1	1.1
Brahma	HSA, BRK, SNF2-N, HELIC, Bromodomain, TCH	291	142.2	218.6	102.7	189.6	0.7	0.9
Cationic peptide-8	amfpi-1	16281, 17312	4241.8	0.0	3268.4	0.0	0.8	0/0
DVA-AP3		7139	248.8	1883.8	12.1	764.0	0.0	0.4
Aminoacylase	Peptidase-M20	3287	82.9	1210.8	0.0	691.1	0.0	0.6
Hypoth. protein	Destabilase	6175	130.3	0.0	314.2	2.9	2.4	*1.2*
GL21066		7671	2689.6	7.4	2718.6	8.7	1.0	1.2
~GA16498-PA	Ig	5348	592.4	0.0	404.8	0.0	0.7	0/0
Protein PTase-2c		11311	0.0	2.5	18.1	26.2	*1.5*	10.7
Ral G-exch factor	RasGEF-N, RasGEF,	671	11.8	29.5	60.4	134.1	5.1	4.6
G-exch factor	RhoGEF, SH3	1970	11.8	39.3	72.5	84.6	6.1	2.2
Arf6 G-exch factor		11356	0.0	2.5	24.2	20.4	*2.0*	8.3
Vrille	βZIP-2	1390	11.8	76.1	84.6	55.4	7.1	0.7
Ankyrin repeat pr.		13966	0.0	2.5	0.0	26.2	0/0	10.7
Ankyrin domain 54		6868	0.0	2.5	6.0	32.1	*0.5*	13.1
Dipeptidyl peptidase 4	DPPIV-N	6304	11.8	0.0	66.5	2.9	5.6	*1.2*
TcasGA2-TC008649		537	11.8	78.6	60.4	93.3	5.1	1.2

Figure Legends

Fig. 1. Distribution of 232 *M. sexta* immunity-related genes. The pie chart shows gene number, contig number, and percentage of genes in each functional category relative to the entire set. The category of "intracellular signal transduction" is further divided into pathways (*right*).

Fig. 2. Expression analysis of cellular components (CC, *top*), molecular functions (MF, *middle*), and biological processes (BP, *bottom*) at GO level 2. The bar graph is generated using data from the sum of NRNs for each annotated gene. Each GO term is comprised of four