Description	**p-value**	**corr p-value**	**Cluster freq**
proteolysis	5.42E-24	4.17E-21	26/41 63.4%
protein metabolic process	2.71E-12	1.04E-09	28/41 68.2%
macromolecule metabolic process	2.62E-09	6.72E-07	30/41 73.1%
regulation of response to external stimulus	5.72E-08	1.10E-05	8/41 19.5%
primary metabolic process	9.29E-08	1.43E-05	32/41 78.0%
digestion	2.40E-07	3.08E-05	6/41 14.6%
regulation of response to stimulus	1.61E-06	1.77E-04	10/41 24.3%
metabolic process	2.23E-06	2.14E-04	32/41 78.0%
respiratory gaseous exchange	3.20E-06	2.74E-04	4/41 9.7%
modification by host of symbiont morphology or physiology	6.13E-06	4.71E-04	3/41 7.3%
interaction with symbiont	1.73E-05	1.21E-03	3/41 7.3%
cleavage of cytoskeletal proteins involved in apoptosis	2.40E-05	1.23E-03	2/41 4.8%
cleavage of lamin	2.40E-05	1.23E-03	2/41 4.8%
neutrophil mediated killing of symbiont cell	2.40E-05	1.23E-03	2/41 4.8%
neutrophil mediated cytotoxicity	2.40E-05	1.23E-03	2/41 4.8%
regulation of response to stress	3.01E-05	1.45E-03	7/41 17.0%
modification of morphology or physiology of other organism involved in symbiotic interaction	3.24E-05	1.47E-03	3/41 7.3%
killing by host of symbiont cells	7.97E-05	2.88E-03	2/41 4.8%
disruption by host of symbiont cells	7.97E-05	2.88E-03	2/41 4.8%
regulation of growth of symbiont in host	7.97E-05	2.88E-03	2/41 4.8%
negative regulation of growth of symbiont in host	7.97E-05	2.88E-03	2/41 4.8%
protein maturation by peptide bond cleavage	8.24E-05	2.88E-03	4/41 9.7%
acute inflammatory response	1.19E-04	3.67E-03	4/41 9.7%
modulation of growth of symbiont involved in interaction with host	1.19E-04	3.67E-03	2/41 4.8%
negative regulation of growth of symbiont involved in interaction with host	1.19E-04	3.67E-03	2/41 4.8%
regulation of inflammatory response	1.24E-04	3.67E-03	4/41 9.7%
disruption of cells of other organism involved in symbiotic interaction	1.67E-04	4.58E-03	2/41 4.8%
killing of cells in other organism involved in symbiotic interaction	1.67E-04	4.58E-03	2/41 4.8%
regulation of blood coagulation	1.86E-04	4.93E-03	3/41 7.3%
regulation of symbiosis, encompassing mutualism through parasitism	2.22E-04	5.59E-03	2/41 4.8%
protein processing	2.25E-04	5.59E-03	4/41 9.7%
regulation of wound healing	2.49E-04	5.80E-03	3/41 7.3%
regulation of coagulation	2.49E-04	5.80E-03	3/41 7.3%
protein maturation	3.19E-04	7.03E-03	4/41 9.7%
defense response	3.20E-04	7.03E-03	8/41 19.5%
negative regulation of multi-organism process	3.55E-04	7.39E-03	2/41 4.8%
negative regulation of fibrinolysis	3.55E-04	7.39E-03	2/41 4.8%
regulation of chemokine biosynthetic process	4.34E-04	8.55E-03	2/41 4.8%
leukocyte mediated cytotoxicity	4.34E-04	8.55E-03	2/41 4.8%

immune effector process	4.94E-04	9.49E-03	4/41	9.7%
neutrophil mediated immunity	5.19E-04	9.74E-03	2/41	4.8%
symbiosis, encompassing mutualism through parasitism	5.45E-04	9.98E-03	3/41	7.3%
regulation of fibrinolysis	6.13E-04	1.10E-02	2/41	4.8%
positive regulation of blood coagulation	7.14E-04	1.25E-02	2/41	4.8%
positive regulation of immune response	7.86E-04	1.34E-02	4/41	9.7%
complement activation, alternative pathway	8.22E-04	1.34E-02	2/41	4.8%
defense response to fungus	8.22E-04	1.34E-02	2/41	4.8%
positive regulation of phagocytosis	9.38E-04	1.50E-02	2/41	4.8%
positive regulation of response to stimulus	9.60E-04	1.51E-02	5/41	12.1%
positive regulation of coagulation	1.06E-03	1.63E-02	2/41	4.8%
regulation of defense response	1.13E-03	1.71E-02	4/41	9.7%
regulation of immune system process	1.22E-03	1.81E-02	6/41	14.6%
myeloid leukocyte mediated immunity	1.33E-03	1.86E-02	2/41	4.8%
cytolysis	1.33E-03	1.86E-02	2/41	4.8%
killing of cells of another organism	1.33E-03	1.86E-02	2/41	4.8%
regulation of phagocytosis	1.47E-03	2.02E-02	2/41	4.8%
collagen catabolic process	1.63E-03	2.19E-02	2/41	4.8%
leukocyte mediated immunity	1.71E-03	2.27E-02	3/41	7.3%
regulation of chemokine production	1.95E-03	2.51E-02	2/41	4.8%
inflammatory response	1.96E-03	2.51E-02	5/41	12.1%
negative regulation of blood coagulation	2.13E-03	2.59E-02	2/41	4.8%
negative regulation of coagulation	2.49E-03	2.59E-02	2/41	4.8%
response to fungus	2.49E-03	2.59E-02	2/41	4.8%
cellular response to extracellular stimulus	2.60E-03	2.59E-02	3/41	7.3%
regulation of cytokine production	2.60E-03	2.59E-02	4/41	9.7%
cellular response to external stimulus	2.67E-03	2.59E-02	3/41	7.3%
cellular component disassembly involved in apoptosis	2.69E-03	2.59E-02	2/41	4.8%
multicellular organismal catabolic process	2.69E-03	2.59E-02	2/41	4.8%
regulation of fractalkine production	2.87E-03	2.59E-02	1/41	2.4%
negative regulation of interleukin-13 production	2.87E-03	2.59E-02	1/41	2.4%
negative regulation of interleukin-5 production	2.87E-03	2.59E-02	1/41	2.4%
regulation of systemic arterial blood pressure by atrial natriuretic peptide	2.87E-03	2.59E-02	1/41	2.4%
positive regulation of interleukin-1 biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
regulation of interleukin-1 biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
regulation of fractalkine biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
positive regulation of fractalkine biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
regulation of interleukin-1 beta biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
interleukin-1 beta biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
positive regulation of interleukin-1 beta biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
positive regulation of myeloid leukocyte mediated immunity	2.87E-03	2.59E-02	1/41	2.4%
positive regulation of type II hypersensitivity	2.87E-03	2.59E-02	1/41	2.4%
regulation of type II hypersensitivity	2.87E-03	2.59E-02	1/41	2.4%
positive regulation of type IIa hypersensitivity	2.87E-03	2.59E-02	1/41	2.4%
regulation of type IIa hypersensitivity	2.87E-03	2.59E-02	1/41	2.4%
interleukin-1 biosynthetic process	2.87E-03	2.59E-02	1/41	2.4%
response to stress	3.16E-03	2.83E-02	12/41	29.2%
regulation of biological quality	3.27E-03	2.89E-02	11/41	26.8%
collagen metabolic process	3.31E-03	2.90E-02	2/41	4.8%
cell killing	3.76E-03	3.25E-02	2/41	4.8%

multicellular organismal macromolecule metabolic process	4.00E-03	3.42E-02	2/41	4.8%
regulation of immune response	4.46E-03	3.77E-02	4/41	9.7%
multicellular organismal process	4.57E-03	3.82E-02	21/41	51.2%
immune system process	4.87E-03	3.86E-02	8/41	19.5%
positive regulation of endocytosis	5.28E-03	3.86E-02	2/41	4.8%
acute-phase response	5.28E-03	3.86E-02	2/41	4.8%
multicellular organismal metabolic process	5.55E-03	3.86E-02	2/41	4.8%
negative regulation of growth	5.57E-03	3.86E-02	3/41	7.3%
positive regulation of complement activation	5.72E-03	3.86E-02	1/41	2.4%
positive regulation of transcription by glucose	5.72E-03	3.86E-02	1/41	2.4%
positive regulation of transcription from RNA polymerase II promoter by glucose	5.72E-03	3.86E-02	1/41	2.4%
positive regulation of transcription from RNA polymerase II promoter by carbon catabolites	5.72E-03	3.86E-02	1/41	2.4%
regulation of transcription from RNA polymerase II promoter by carbon catabolites	5.72E-03	3.86E-02	1/41	2.4%
regulation of transcription from RNA polymerase II promoter by glucose	5.72E-03	3.86E-02	1/41	2.4%
positive regulation of transcription by carbon catabolites	5.72E-03	3.86E-02	1/41	2.4%
negative regulation of interleukin-8 biosynthetic process	5.72E-03	3.86E-02	1/41	2.4%
positive regulation of hypersensitivity	5.72E-03	3.86E-02	1/41	2.4%
neutrophil mediated killing of bacterium	5.72E-03	3.86E-02	1/41	2.4%
neutrophil mediated killing of gram-positive bacterium	5.72E-03	3.86E-02	1/41	2.4%
neutrophil mediated killing of fungus	5.72E-03	3.86E-02	1/41	2.4%
viral genome expression	5.72E-03	3.86E-02	1/41	2.4%
viral transcription	5.72E-03	3.86E-02	1/41	2.4%
late viral mRNA transcription	5.72E-03	3.86E-02	1/41	2.4%
regulation of activation of membrane attack complex	5.72E-03	3.86E-02	1/41	2.4%
positive regulation of activation of membrane attack complex	5.72E-03	3.86E-02	1/41	2.4%
complement activation	5.84E-03	3.90E-02	2/41	4.8%
activation of plasma proteins involved in acute inflammatory response	6.12E-03	4.06E-02	2/41	4.8%
positive regulation of immune system process	6.81E-03	4.47E-02	4/41	9.7%
regulation of multi-organism process	7.66E-03	4.99E-02		

Total freq
732/14305 5.1%

2612/14305 18.2%

4018/14305 28.0%

191/14305 1.3%
5289/14305 36.9%

93/14305 0.6%
524/14305 3.6%
5960/14305 41.6%

36/14305 0.2%
13/14305 0.0%
18/14305 0.1%
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319/14305 2.2%
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39/14305 0.2%
8/14305 0.0%

105/14305 0.7%
43/14305 0.3%
43/14305 0.3%
115/14305 0.8%
620/14305 4.3%
10/14305 0.0%
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129/14305 0.9%
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1542/14305 10.7%
30/14305 0.2%
32/14305 0.2%

33/14305 0.2%
235/14305 1.6%
4377/14305 30.5%

948/14305 6.6%
38/14305 0.2%
38/14305 0.2%
39/14305 0.2%
126/14305 0.8%
2/14305 0.0%
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40/14305 0.2%
41/14305 0.2%

265/14305 1.8%

Genes
CORIN PRTN3 MMP9 PGC PRSS1 AZU1 PRSS3 KLK12 PGA3 PGA4 PGA5 CFD TPSB2 HPN GZMA ELANE GZMB NAPSA PROC GZMK F2 BACE1 CTSD CMA1 TPSAB1 CTSG
CORIN C3 PRTN3 MMP9 PGC PRSS1 AZU1 PRSS3 KLK12 PGA3 PGA4 PGA5 TPSB2 CFD FN1 HPN GZMA ELANE GZMB NAPSA PROC GZMK F2 BACE1 CTSD CMA1 TPSAB1 CTSG
CORIN C3 PRTN3 MMP9 PGC PRSS1 SCGB1A1 AZU1 PRSS3 KLK12 PGA3 PGA4 PGA5 TPSB2 CFD FN1 HPN GZMA ELANE GZMB NAPSA USF1 PROC GZMK BACE1 F2 CTSD CMA1 TPSAB1 CTSG
AZU1 C3 F2 ELANE CMA1 USF1 SCGB1A1 PROC
CORIN C3 PRTN3 MMP9 PGC PRSS1 SCGB1A1 AZU1 ITGB8 PRSS3 KLK12 PGA3 PGA4 PGA5 TPSB2 CFD SFTPB FN1 HPN GZMA ELANE GZMB NAPSA USF1 PROC GZMK BACE1 F2 CTSD CMA1 TPSAB1 CTSG
PGC PRSS3 PRSS1 PGA3 PGA4 PGA5
AZU1 C3 F2 ELANE CMA1 CFD USF1 SCGB1A1 CTSG PROC
CORIN C3 PRTN3 MMP9 PGC PRSS1 SCGB1A1 AZU1 ITGB8 PRSS3 KLK12 PGA3 PGA4 PGA5 TPSB2 CFD SFTPB FN1 HPN GZMA ELANE GZMB NAPSA USF1 PROC GZMK BACE1 F2 CTSD CMA1 TPSAB1 CTSG
SFTPA2 SFTPC SFTPA1 SFTPB
SP1 ELANE CTSG
SP1 ELANE CTSG
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C3 F2 ELANE CMA1 USF1 SCGB1A1 PROC
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AZU1 HERPUD1 HPN SP1 CORIN F2 ELANE SIPA1 USF1 CTSG FN1
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ESRRA CORIN PRTN3 PGC MMP9 PRSS1 SFTPA1 SCGB1A1 AZU1 SP1 ITGB8 SFTPA2 F2 PRSS3 SFTPC PGA3
CMA1 PGA4 PGA5 SFTPB FN1
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