Healthy Ants at 2PM vs Healthy Ants at 10AM

Table 1: Overrepresentation of annotation terms within the total of 77 up-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in healthy *Camponotus castaneus* ant heads at 10 AM (Ant Controls at 10AM samples) compared to gene expression at 2 PM (Ant Controls at 2PM samples)

PFAM Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
PF00650.15 CRAL/TRIO domain	4	73	21	16963	3.790102263	4.51E-06	0.003399132
PF03392.8 Insect pheromone-binding family, A10/OS-D	3	74	9	16975	4.336819571	1.89E-05	0.007110284
PF01401.13 Angiotensin-converting enzyme	2	75	4	16980	4.729156166	0.000298068	0.037407538
PF00917.21 MATH domain	2	75	4	16980	4.729156166	0.000298068	0.037407538
PF07690.11 Major Facilitator Superfamily	5	72	116	16868	2.312355217	0.000217057	0.037407538
PF03765.10 CRAL/TRIO, N-terminal domain	2	75	4	16980	4.729156166	0.000298068	0.037407538

SSP Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
SSP Small Secreted Protein	6	71	305	16679	1.530673538	0.002801902	0.002801902

Secretome Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
secretome Has a SignalP signal sequence	15	62	928	16056	1.431721974	1.72E-05	1.72E-05

Table 2: Overrepresentation of annotation terms within the total of 54 down-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in healthy *Camponotus castaneus* ant heads at 10 AM (Ant Controls at 10AM samples) compared to gene expression at 2 PM (Ant Controls at 2PM samples)

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0055086|nucleobase-containing small molecule metabolic process	6	48	94	16913	3.113101512	7.17E-07	0.000408634
GO:0044281|small molecule metabolic process	8	46	210	16797	2.632648192	3.92E-07	0.000408634
GO:1901564|organonitrogen compound metabolic process	8	46	257	16750	2.427877598	1.71E-06	0.000649606
GO:0072521|purine-containing compound metabolic process	4	50	55	16952	3.20507927	3.59E-05	0.010217626
GO:1901135|carbohydrate derivative metabolic process	5	49	152	16855	2.426139721	0.000136098	0.020708731
GO:0044710|single-organism metabolic process	11	43	911	16096	1.508478333	0.000121765	0.020708731
GO:0044711|single-organism biosynthetic process	5	49	162	16845	2.361830435	0.000181656	0.020708731
GO:0016742|hydroxymethyl-, formyl- and related transferase activity	2	52	3	17004	5.384495063	9.77E-05	0.020708731
GO:0006753|nucleoside phosphate metabolic process	4	50	84	16923	2.779883479	0.000171639	0.020708731
GO:0009117|nucleotide metabolic process	4	50	83	16924	2.79191876	0.000164221	0.020708731
GO:0072522|purine-containing compound biosynthetic process	3	51	36	16971	3.322529002	0.000252698	0.024006266
GO:0016741|transferase activity, transferring one-carbon groups	4	50	92	16915	2.68843886	0.000239985	0.024006266
GO:0008484|sulfuric ester hydrolase activity	2	52	7	17000	4.536961936	0.000348986	0.030603412
GO:0006807|nitrogen compound metabolic process	9	45	739	16268	1.482219434	0.000515393	0.041967712
GO:1901293|nucleoside phosphate biosynthetic process	3	51	54	16953	2.916002698	0.00077716	0.042076237
GO:0006139|nucleobase-containing compound metabolic process	8	46	600	16407	1.559333842	0.000607937	0.042076237
GO:0006163|purine nucleotide metabolic process	3	51	54	16953	2.916002698	0.00077716	0.042076237
GO:0046483|heterocycle metabolic process	8	46	631	16376	1.50706641	0.000841297	0.042076237
GO:0008152|metabolic process	18	36	2496	14511	1.067070351	0.000658862	0.042076237

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0019637|organophosphate metabolic process	4	50	130	16877	2.340443932	0.000848907	0.042076237
GO:0034641|cellular nitrogen compound metabolic process	8	46	631	16376	1.50706641	0.000841297	0.042076237
GO:0009165|nucleotide biosynthetic process	3	51	54	16953	2.916002698	0.00077716	0.042076237
GO:0006725|cellular aromatic compound metabolic process	8	46	618	16389	1.528677345	0.000735934	0.042076237
GO:1901657|glycosyl compound metabolic process	3	51	59	16948	2.827154324	0.000993371	0.045297734
GO:0009116|nucleoside metabolic process	3	51	59	16948	2.827154324	0.000993371	0.045297734
GO:1901360|organic cyclic compound metabolic process	8	46	652	16355	1.473044523	0.001036977	0.045467466
GO:0019438|aromatic compound biosynthetic process	4	50	142	16865	2.251440046	0.0011677	0.049302883

SSP Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
SSP Small Secreted Protein	5	49	306	16701	1.717256389	0.002969093	0.002969093

Healthy Ants at 2PM vs Death After Manipulated Biting Behavior

Table 3: Overrepresentation of annotation terms within the total of 581 up-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in dead *Camponotus castaneus* ant heads after manipulation (Death After Manipulation samples) compared to gene expression in healthy *Camponotus castaneus* ant heads at the same time of day; 2 PM (Ant Controls at 2PM samples)

GO Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
Over-represented							
GO:0003674|molecular_function	300	281	6002	10478	0.622612879	2.60E-13	2.96E-10
GO:0005488|binding	213	368	4115	12365	0.553440294	1.05E-09	3.98E-07
GO:0065007|biological regulation	66	515	804	15676	0.915774732	9.95E-10	3.98E-07
GO:0005515|protein binding	97	484	1459	15021	0.724324024	4.33E-09	8.23E-07
GO:0050789|regulation of biological process	63	518	779	15701	0.896628122	3.90E-09	8.23E-07
GO:0050794|regulation of cellular process	63	518	771	15709	0.907460186	3.03E-09	8.23E-07
GO:0007165|signal transduction	35	546	360	16120	1.05444107	2.54E-07	4.14E-05
GO:0006793|phosphorus metabolic process	35	546	384	16096	0.988412606	1.43E-06	0.000181379
GO:0006796|phosphate-containing compound metabolic process	35	546	382	16098	0.993758797	1.36E-06	0.000181379
GO:0003700|sequence-specific DNA binding transcription factor activity	22	559	182	16298	1.259683973	1.88E-06	0.000194637
GO:0001071|nucleic acid binding transcription factor activity	22	559	182	16298	1.259683973	1.88E-06	0.000194637
GO:0051716|cellular response to stimulus	37	544	446	16034	0.89411646	4.68E-06	0.000445051
GO:0043167|ion binding	100	481	1793	14687	0.53237547	8.00E-06	0.000701855
GO:0050896|response to stimulus	38	543	483	15997	0.84061667	1.12E-05	0.000910377
GO:0036211|protein modification process	30	551	344	16136	0.937628995	1.54E-05	0.001097849
GO:0006464|cellular protein modification process	30	551	344	16136	0.937628995	1.54E-05	0.001097849
GO:0043412|macromolecule modification	31	550	369	16111	0.90052983	1.98E-05	0.00132576
GO:0051171|regulation of nitrogen compound metabolic process	28	553	316	16164	0.951646121	2.57E-05	0.001505275

GO Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0019219|regulation of nucleobase-containing compound metabolic process	28	553	316	16164	0.951646121	2.57E-05	0.001505275
GO:0016310|phosphorylation	23	558	235	16245	1.047090188	2.64E-05	0.001505275
GO:0080090|regulation of primary metabolic process	28	553	324	16156	0.92614977	3.45E-05	0.001870457
GO:0031323|regulation of cellular metabolic process	28	553	327	16153	0.916747408	3.89E-05	0.001976197
GO:0006468|protein phosphorylation	22	559	225	16255	1.044948411	3.99E-05	0.001976197
GO:0019222|regulation of metabolic process	28	553	333	16147	0.898193572	5.02E-05	0.002386647
GO:0004672|protein kinase activity	22	559	231	16249	1.018261917	5.72E-05	0.002577603
GO:0046872|metal ion binding	58	523	930	15550	0.617492878	5.88E-05	0.002577603
GO:2001141|regulation of RNA biosynthetic process	25	556	282	16198	0.948843516	7.60E-05	0.002988165
GO:0051252|regulation of RNA metabolic process	25	556	282	16198	0.948843516	7.60E-05	0.002988165
GO:0006355|regulation of transcription, DNA-templated	25	556	282	16198	0.948843516	7.60E-05	0.002988165
GO:0010556|regulation of macromolecule biosynthetic process	25	556	289	16191	0.923891654	9.51E-05	0.003011545
GO:0006470|protein dephosphorylation	7	574	25	16455	2.082789589	8.21E-05	0.003011545
GO:2000112|regulation of cellular macromolecule biosynthetic process	25	556	289	16191	0.923891654	9.51E-05	0.003011545
GO:0010468|regulation of gene expression	25	556	289	16191	0.923891654	9.51E-05	0.003011545
GO:0009889|regulation of biosynthetic process	25	556	289	16191	0.923891654	9.51E-05	0.003011545
GO:0016020|membrane	40	541	566	15914	0.731820601	8.04E-05	0.003011545
GO:0031326|regulation of cellular biosynthetic process	25	556	289	16191	0.923891654	9.51E-05	0.003011545
GO:0043169|cation binding	58	523	948	15532	0.597164735	0.000100207	0.003087445
GO:0004721|phosphoprotein phosphatase activity	7	574	27	16453	2.005706997	0.00012368	0.003615268
GO:0060255|regulation of macromolecule metabolic process	25	556	299	16181	0.889256951	0.000140394	0.00400124
GO:0004725|protein tyrosine phosphatase activity	6	575	19	16461	2.201699675	0.000154781	0.004303654
GO:0008150|biological_process	184	397	4060	12420	0.34912458	0.00016607	0.004507602
GO:0043565|sequence-specific DNA binding	17	564	170	16310	1.061894351	0.000229955	0.005957921

GO Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0009987|cellular process	109	472	2185	14295	0.412662894	0.000250437	0.006344406
GO:0016311|dephosphorylation	7	574	31	16449	1.867313512	0.000257864	0.006390537
GO:0005575|cellular_component	106	475	2120	14360	0.413154765	0.000270644	0.00656455
GO:0016773|phosphotransferase activity, alcohol group as acceptor	23	558	285	16195	0.851103905	0.000398331	0.009460357
GO:0005509|calcium ion binding	13	568	115	16365	1.180795997	0.000426716	0.009927668
GO:0006811|ion transport	17	564	184	16296	0.981898293	0.000534317	0.012090622
GO:0044765|single-organism transport	30	551	424	16056	0.723567008	0.000540896	0.012090622
GO:0022838|substrate-specific channel activity	11	570	90	16390	1.256875913	0.000644986	0.013368804
GO:0022803|passive transmembrane transporter activity	11	570	90	16390	1.256875913	0.000644986	0.013368804
GO:0015267|channel activity	11	570	90	16390	1.256875913	0.000644986	0.013368804
GO:0005216|ion channel activity	11	570	90	16390	1.256875913	0.000644986	0.013368804
GO:0016301|kinase activity	22	559	277	16203	0.833827163	0.000951108	0.019022159
GO:0006810|transport	36	545	564	15916	0.622759064	0.001163246	0.022476278
GO:0051234|establishment of localization	36	545	566	15914	0.61909357	0.001189083	0.022592586
GO:0016791|phosphatase activity	8	573	56	16424	1.409703093	0.001423183	0.026597182
GO:0055085|transmembrane transport	21	560	273	16207	0.800312385	0.00157278	0.028918857
GO:0006461|protein complex assembly	6	575	33	16447	1.648780236	0.001903759	0.034448974

PFAM Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
PF00069.20 Protein kinase domain	21	560	216	16264	1.038016602	6.40E-05	0.016065116
PF13895.1 Immunoglobulin domain	13	568	93	16387	1.394472062	6.33E-05	0.016065116
PF07714.12 Protein tyrosine kinase	21	560	213	16267	1.052187283	5.32E-05	0.016065116
PF14259.1 RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	11	570	80	16400	1.375268891	0.000260676	0.024536104
PF00102.22 Protein-tyrosine phosphatase	6	575	19	16461	2.201699675	0.000154781	0.024536104
PF13306.1 Leucine rich repeats (6 copies)	7	574	31	16449	1.867313512	0.000257864	0.024536104
PF00036.27 EF hand	6	575	20	16460	2.150345629	0.000195466	0.024536104
PF00076.17 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	12	569	93	16387	1.312670339	0.000236687	0.024536104
PF07716.10 Basic region leucine zipper	5	576	14	16466	2.32332585	0.000351943	0.029445866
PF07647.12 SAM domain (Sterile alpha motif)	5	576	15	16465	2.254272245	0.000456201	0.034109821
PF07679.11 Immunoglobulin I-set domain	11	570	87	16393	1.290960487	0.000498284	0.034109821
PF00105.13 Zinc finger, C4 type (two domains)	5	576	16	16464	2.189672988	0.000582118	0.036527901

Secretome Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
secretome Has a SignalP signal sequence	48	533	895	15585	0.449920061	0.00536912	0.00536912

Table 4: Overrepresentation of annotation terms within the total of 565 down-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in dead *Camponotus castaneus* ant heads after manipulation (Death After Manipulation samples) compared to gene expression in healthy *Camponotus castaneus* ant heads at the same time of day; 2 PM (Ant Controls at 2PM samples)

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0008152|metabolic process	240	325	2274	14222	1.530063407	1.72E-59	1.96E-56
GO:0008150|biological_process	318	247	3926	12570	1.416354973	6.03E-59	3.44E-56
GO:0003824|catalytic activity	245	320	2519	13977	1.446488339	1.07E-54	4.07E-52
GO:0003674|molecular_function	361	204	5941	10555	1.145480176	9.73E-40	2.77E-37
GO:0016491|oxidoreductase activity	90	475	440	16056	1.93355803	5.62E-39	1.28E-36
GO:0044699|single-organism process	160	405	1593	14903	1.307230252	1.81E-34	3.44E-32
GO:0044710|single-organism metabolic process	106	459	816	15680	1.490115823	2.03E-30	3.31E-28
GO:0055114|oxidation-reduction process	69	496	359	16137	1.83307824	1.93E-28	2.75E-26
GO:0044238|primary metabolic process	128	437	1618	14878	0.990789862	1.70E-18	2.15E-16
GO:0071704|organic substance metabolic process	131	434	1704	14792	0.963260855	5.69E-18	6.49E-16
GO:0048037|cofactor binding	32	533	135	16361	1.984595433	6.06E-16	6.28E-14
GO:0050662|coenzyme binding	26	539	99	16397	2.078114787	4.40E-14	4.18E-12
GO:0005975|carbohydrate metabolic process	30	535	153	16343	1.790047663	3.75E-13	3.29E-11
GO:0044281|small molecule metabolic process	32	533	186	16310	1.661001501	1.38E-12	1.13E-10
GO:0044763|single-organism cellular process	75	490	903	15593	0.971937544	8.42E-12	6.40E-10
GO:1901564|organonitrogen compound metabolic process	33	532	232	16264	1.469836056	5.95E-11	4.24E-09
GO:0005506|iron ion binding	25	540	132	16364	1.747343842	6.76E-11	4.53E-09
GO:0016705|oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	25	540	135	16361	1.72468764	1.03E-10	6.52E-09
GO:0043167|ion binding	114	451	1779	14717	0.737682988	1.43E-10	8.58E-09
GO:1901605|alpha-amino acid metabolic process	12	553	20	16476	2.88347643	1.91E-10	1.09E-08

GO Annotation term	# down-regulated proteins with annotation term	# down-regulated proteins without annotation term	# other proteins with annotation term	# other proteins without annotation term	log odds ratio	p-value (uncorrected)	p-value (corrected)
GO:0020037|heme binding	25	540	143	16353	1.666628701	3.00E-10	1.56E-08
GO:0046906|tetrapyrrole binding	25	540	143	16353	1.666628701	3.00E-10	1.56E-08
GO:0043436|oxoacid metabolic process	20	545	89	16407	1.911773461	4.16E-10	1.90E-08
GO:0006082|organic acid metabolic process	20	545	89	16407	1.911773461	4.16E-10	1.90E-08
GO:0019752|carboxylic acid metabolic process	20	545	89	16407	1.911773461	4.16E-10	1.90E-08
GO:0006520|cellular amino acid metabolic process	18	547	72	16424	2.015755795	7.25E-10	3.18E-08
GO:0044282|small molecule catabolic process	9	556	8	16488	3.507402864	8.63E-10	3.64E-08
GO:0050660|flavin adenine dinucleotide binding	14	551	39	16457	2.372267072	1.19E-09	4.84E-08
GO:0044765|single-organism transport	42	523	412	16084	1.142645073	1.95E-09	7.65E-08
GO:0009987|cellular process	126	439	2168	14328	0.640193075	5.70E-09	2.16E-07
GO:0016021|integral component of membrane	45	520	486	16010	1.04759386	7.87E-09	2.89E-07
GO:0016740|transferase activity	57	508	714	15782	0.908312187	1.24E-08	4.42E-07
GO:0016054|organic acid catabolic process	8	557	8	16488	3.387822883	1.40E-08	4.70E-07
GO:0046395|carboxylic acid catabolic process	8	557	8	16488	3.387822883	1.40E-08	4.70E-07
GO:0009063|cellular amino acid catabolic process	7	558	6	16490	3.540301133	6.07E-08	1.98E-06
GO:0044712|single-organism catabolic process	13	552	49	16447	2.067479382	9.42E-08	2.98E-06
GO:0016614|oxidoreductase activity, acting on CH-OH group of donors	14	551	62	16434	1.907295774	1.69E-07	5.20E-06
GO:0003995|acyl-CoA dehydrogenase activity	6	559	4	16492	3.789946329	2.41E-07	7.23E-06
GO:0006810|transport	45	520	555	15941	0.91051525	3.11E-07	9.09E-06
GO:0051234|establishment of localization	45	520	557	15939	0.906792653	3.37E-07	9.62E-06
GO:0044425|membrane part	46	519	591	15905	0.8693103	7.02E-07	1.95E-05
GO:0006629|lipid metabolic process	19	546	135	16361	1.439200958	8.31E-07	2.25E-05
GO:1901606|alpha-amino acid catabolic process	6	559	6	16490	3.384359942	1.00E-06	2.65E-05
GO:0055085|transmembrane transport	27	538	267	16229	1.115284692	1.82E-06	4.71E-05

GO Annotation term	# down-regulated proteins with annotation term	# down-regulated proteins without annotation term	# other proteins with annotation term	# other proteins without annotation term	log odds ratio	p-value (uncorrected)	p-value (corrected)
GO:1901565|organonitrogen compound catabolic process	9	556	27	16469	2.289854522	1.90E-06	4.82E-05
GO:0044237|cellular metabolic process	80	485	1344	15152	0.620360038	2.79E-06	6.92E-05
GO:0016787|hydrolase activity	66	499	1038	15458	0.67787953	3.08E-06	7.47E-05
GO:0005215|transporter activity	32	533	360	16136	0.989918527	4.27E-06	0.000101397
GO:0016773|phosphotransferase activity, alcohol group as acceptor	27	538	281	16215	1.063315655	4.39E-06	0.000102112
GO:0016627|oxidoreductase activity, acting on the CH-CH group of donors	7	558	15	16481	2.623464467	4.65E-06	0.00010611
GO:0006544|glycine metabolic process	5	560	5	16491	3.382633273	8.59E-06	0.000192023
GO:0043168|anion binding	56	509	859	15637	0.694529932	9.56E-06	0.000209589
GO:0009069|serine family amino acid metabolic process	5	560	6	16490	3.200251075	1.53E-05	0.000329525
GO:0043169|cation binding	59	506	947	15549	0.649453288	1.70E-05	0.000358108
GO:1901363|heterocyclic compound binding	100	465	1888	14608	0.509184037	1.77E-05	0.000360541
GO:0097159|organic cyclic compound binding	100	465	1888	14608	0.509184037	1.77E-05	0.000360541
GO:0036094|small molecule binding	54	511	839	15657	0.67907713	1.89E-05	0.00037743
GO:0006869|lipid transport	5	560	7	16489	3.046039751	2.55E-05	0.000502142
GO:1901265|nucleoside phosphate binding	53	512	834	15662	0.664726561	2.90E-05	0.000551072
GO:0000166|nucleotide binding	53	512	834	15662	0.664726561	2.90E-05	0.000551072
GO:0009056|catabolic process	15	550	122	16374	1.297560868	4.92E-05	0.000919989
GO:0009071|serine family amino acid catabolic process	4	561	4	16492	3.380909788	7.49E-05	0.00135558
GO:0006546|glycine catabolic process	4	561	4	16492	3.380909788	7.49E-05	0.00135558
GO:0022857|transmembrane transporter activity	26	539	319	16177	0.894535624	9.66E-05	0.001719991
GO:0005488|binding	184	381	4144	12352	0.364292871	9.90E-05	0.001736138
GO:0008272|sulfate transport	4	561	5	16491	3.1577056	0.000131312	0.002169503
GO:0015116|sulfate transmembrane transporter activity	4	561	5	16491	3.1577056	0.000131312	0.002169503

GO Annotation term	# down-regulated proteins with annotation term	# down-regulated proteins without annotation term	# other proteins with annotation term	# other proteins without annotation term	log odds ratio	p-value (uncorrected)	p-value (corrected)
GO:1901682|sulfur compound transmembrane transporter activity	4	561	5	16491	3.1577056	0.000131312	0.002169503
GO:0072348|sulfur compound transport	4	561	5	16491	3.1577056	0.000131312	0.002169503
GO:1901575|organic substance catabolic process	14	551	119	16377	1.251832218	0.000133422	0.002172868
GO:0044711|single-organism biosynthetic process	16	549	151	16345	1.148887763	0.000139337	0.00223724
GO:0016310|phosphorylation	21	544	237	16259	0.97391493	0.000144568	0.002288993
GO:0016746|transferase activity, transferring acyl groups	10	555	65	16431	1.516154783	0.000175242	0.002736658
GO:0016301|kinase activity	23	542	276	16220	0.913827676	0.000203846	0.003140338
GO:0006468|protein phosphorylation	20	545	227	16269	0.967013197	0.000221418	0.003365553
GO:0019538|protein metabolic process	49	516	810	15686	0.609203159	0.000254472	0.003812012
GO:0006820|anion transport	7	558	32	16464	1.864746742	0.000257478	0.003812012
GO:0016616|oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	8	557	44	16452	1.680888997	0.000286579	0.004188463
GO:0016742|hydroxymethyl-, formyl- and related transferase activity	3	562	2	16494	3.784715216	0.000343704	0.00495978
GO:0008236|serine-type peptidase activity	11	554	88	16408	1.308918071	0.000430493	0.006058792
GO:0017171|serine hydrolase activity	11	554	88	16408	1.308918071	0.000430493	0.006058792
GO:0044283|small molecule biosynthetic process	6	559	25	16471	1.956090709	0.000466556	0.006486269
GO:0004672|protein kinase activity	20	545	233	16263	0.940555893	0.000490512	0.006737146
GO:0046872|metal ion binding	53	512	935	15561	0.543943822	0.000635131	0.008518229
GO:0050661|NADP binding	3	562	3	16493	3.379189478	0.000670478	0.008785578
GO:0005319|lipid transporter activity	4	561	9	16487	2.569676349	0.000670277	0.008785578
GO:0046914|transition metal ion binding	36	529	576	15920	0.631754305	0.000788515	0.01021485
GO:0005576|extracellular region	9	556	67	16429	1.378567009	0.000888917	0.011386127
GO:0008509|anion transmembrane transporter activity	6	559	29	16467	1.807427823	0.000919415	0.01151795
GO:1901607|alpha-amino acid biosynthetic process	4	561	10	16486	2.464255177	0.000913942	0.01151795

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0016772|transferase activity, transferring phosphorus-containing groups	30	535	450	16046	0.692897928	0.001011475	0.01253349
GO:0016798|hydrolase activity, acting on glycosyl bonds	8	557	55	16441	1.457076611	0.001072976	0.013152608
GO:0006796|phosphate-containing compound metabolic process	27	538	390	16106	0.728778719	0.001168704	0.014173645
GO:0006793|phosphorus metabolic process	27	538	392	16104	0.723539433	0.001200915	0.01441098
GO:0006575|cellular modified amino acid metabolic process	4	561	11	16485	2.368884338	0.001213856	0.014414545
GO:0030170|pyridoxal phosphate binding	6	559	31	16465	1.740614986	0.001245165	0.0146339
GO:0005575|cellular_component	100	465	2126	14370	0.374033201	0.001443121	0.01678733
GO:0015103|inorganic anion transmembrane transporter activity	4	561	12	16484	2.281812298	0.001576411	0.018037545
GO:0006807|nitrogen compound metabolic process	41	524	707	15789	0.558118491	0.001582241	0.018037545
GO:0046394|carboxylic acid biosynthetic process	5	560	22	16474	1.899997335	0.00172567	0.019286905
GO:0016053|organic acid biosynthetic process	5	560	22	16474	1.899997335	0.00172567	0.019286905
GO:0044248|cellular catabolic process	10	555	90	16406	1.189209709	0.00175263	0.019398044
GO:0016701|oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	3	562	5	16491	2.868242583	0.001786232	0.019579855
GO:0003854|3-beta-hydroxy-delta5-steroid dehydrogenase activity	4	561	13	16483	2.201708924	0.002007945	0.020809616
GO:0033764|steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	4	561	13	16483	2.201708924	0.002007945	0.020809616
GO:0016229|steroid dehydrogenase activity	4	561	13	16483	2.201708924	0.002007945	0.020809616
GO:0019318|hexose metabolic process	4	561	13	16483	2.201708924	0.002007945	0.020809616
GO:0015698|inorganic anion transport	4	561	13	16483	2.201708924	0.002007945	0.020809616
GO:0004252|serine-type endopeptidase activity	9	556	77	16419	1.238845341	0.002144514	0.022024743
GO:0016903|oxidoreductase activity, acting on the aldehyde or oxo group of donors	5	560	24	16472	1.812864547	0.002403927	0.024468542
GO:0006694|steroid biosynthetic process	4	561	14	16482	2.127540281	0.002514704	0.02514704
GO:0005996|monosaccharide metabolic process	4	561	14	16482	2.127540281	0.002514704	0.02514704

GO Annotation term	# down-regulated proteins with annotation term	# down-regulated proteins without annotation term	# other proteins with annotation term	# other proteins without annotation term	log odds ratio	p-value (uncorrected)	p-value (corrected)
GO:0008652|cellular amino acid biosynthetic process	4	561	15	16481	2.058486736	0.003102797	0.030493008
GO:0008202|steroid metabolic process	4	561	15	16481	2.058486736	0.003102797	0.030493008
GO:0004553|hydrolase activity, hydrolyzing O-glycosyl compounds	7	558	52	16444	1.378023416	0.003231489	0.031486306
GO:0016853|isomerase activity	6	559	39	16457	1.510554548	0.003490194	0.033156846
GO:0005509|calcium ion binding	11	554	117	16379	1.022311957	0.003526464	0.03322454
GO:0009064|glutamine family amino acid metabolic process	3	562	7	16489	2.531649061	0.003642507	0.033759818
GO:0006006|glucose metabolic process	3	562	7	16489	2.531649061	0.003642507	0.033759818
GO:0009058|biosynthetic process	30	535	491	16005	0.603142959	0.003793597	0.034597603
GO:0080019|fatty-acyl-CoA reductase (alcohol-forming) activity	4	561	16	16480	1.993887537	0.003778169	0.034597603
GO:0016747|transferase activity, transferring acyl groups other than amino-acyl groups	6	559	40	16456	1.485175973	0.003903686	0.035319061
GO:0044267|cellular protein metabolic process	30	535	495	16001	0.594779371	0.003963554	0.035578363
GO:0016620|oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	4	561	18	16478	1.875983135	0.005413517	0.0467531

PFAM Annotation term	# down-regulated proteins with annotation term	# down-regulated proteins without annotation term	# other proteins with annotation term	# other proteins without annotation term	log odds ratio	p-value (uncorrected)	p-value (corrected)
PF00067.17 Cytochrome P450	22	543	110	16386	1.797635358	3.85E-10	2.90E-07
PF00650.15 CRAL/TRIO domain	10	555	15	16481	2.985530259	3.06E-09	1.15E-06
PF00441.19 Acyl-CoA dehydrogenase, C-terminal domain	6	559	3	16493	4.077689035	9.91E-08	2.49E-05
PF02770.14 Acyl-CoA dehydrogenase, middle domain	6	559	4	16492	3.789946329	2.41E-07	3.63E-05
PF08028.6 Acyl-CoA dehydrogenase, C-terminal domain	5	560	1	16495	4.992313712	2.28E-07	3.63E-05
PF07859.8 alpha/beta hydrolase fold	9	556	22	16474	2.494952489	4.72E-07	4.65E-05
PF07690.11 Major Facilitator Superfamily	17	548	104	16392	1.587095848	4.94E-07	4.65E-05
PF02958.15 Ecdysteroid kinase	8	557	15	16481	2.758789582	4.35E-07	4.65E-05
PF08659.5 KR domain	12	553	50	16446	1.965363208	7.38E-07	6.17E-05
PF00106.20 short chain dehydrogenase	13	552	63	16433	1.815313372	1.13E-06	8.53E-05
PF00083.19 Sugar (and other) transporter	13	552	66	16430	1.76861078	1.79E-06	0.000122302
PF02771.11 Acyl-CoA dehydrogenase, N-terminal domain	5	560	3	16493	3.893580167	2.02E-06	0.000126605
PF01370.16 NAD dependent epimerase/dehydratase family	9	556	29	16467	2.21827411	3.10E-06	0.00017983
PF00378.15 Enoyl-CoA hydratase/isomerase family	5	560	5	16491	3.382633273	8.59E-06	0.000462047
PF13561.1 Enoyl-(Acyl carrier protein) reductase	9	556	35	16461	2.029857447	1.13E-05	0.000515536
PF07914.6 Protein of unknown function (DUF1679)	6	559	11	16485	2.777920879	1.16E-05	0.000515536
PF00128.19 Alpha amylase, catalytic domain	6	559	11	16485	2.777920879	1.16E-05	0.000515536
PF03765.10 CRAL/TRIO, N-terminal domain	4	561	2	16494	4.074178232	1.69E-05	0.000708228
PF02719.10 Polysaccharide biosynthesis protein	5	560	9	16487	2.794604022	6.11E-05	0.002422004
PF01347.17 Lipoprotein amino terminal region	4	561	4	16492	3.380909788	7.49E-05	0.002742374
PF00501.23 AMP-binding enzyme	6	559	17	16479	2.342238774	8.01E-05	0.002742374
PF00732.14 GMC oxidoreductase	6	559	17	16479	2.342238774	8.01E-05	0.002742374
PF13792.1 Sulfate transporter N-terminal domain with GLY motif	4	561	5	16491	3.1577056	0.000131312	0.003409584

PFAM Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
PF13716.1 Divergent CRAL/TRIO domain	5	560	11	16485	2.593812011	0.000126193	0.003409584
PF00171.17 Aldehyde dehydrogenase family	4	561	5	16491	3.1577056	0.000131312	0.003409584
PF01740.16 STAS domain	4	561	5	16491	3.1577056	0.000131312	0.003409584
PF00069.20 Protein kinase domain	20	545	217	16279	1.012680338	0.000127143	0.003409584
PF00916.15 Sulfate transporter family	4	561	5	16491	3.1577056	0.000131312	0.003409584
PF07714.12 Protein tyrosine kinase	20	545	214	16282	1.026785946	0.000106862	0.003409584
PF05199.8 GMC oxidoreductase	5	560	14	16482	2.352467954	0.000309354	0.007764787
PF01130.16 CD36 family	4	561	8	16488	2.687520036	0.000476464	0.011321638
PF00135.23 Carboxylesterase family	7	558	36	16460	1.746720722	0.000481132	0.011321638
PF00370.16 FGGY family of carbohydrate kinases, N-terminal domain	3	562	3	16493	3.379189478	0.000670478	0.014424863
PF00294.19 pfkB family carbohydrate kinase	3	562	3	16493	3.379189478	0.000670478	0.014424863
PF00089.21 Trypsin	9	556	64	16432	1.424559132	0.000661171	0.014424863
PF13193.1 AMP-binding enzyme C-terminal domain	4	561	10	16486	2.464255177	0.000913942	0.019116628
PF00248.16 Aldo/keto reductase family	3	562	4	16492	3.091446771	0.001144488	0.023291875
PF00155.16 Aminotransferase class I and II	4	561	12	16484	2.281812298	0.001576411	0.031237826
PF02782.11 FGGY family of carbohydrate kinases, C-terminal domain	3	562	5	16491	2.868242583	0.001786232	0.033625825
PF01633.15 Choline/ethanolamine kinase	3	562	5	16491	2.868242583	0.001786232	0.033625825
PF06585.6 Haemolymph juvenile hormone binding protein (JHBP)	4	561	13	16483	2.201708924	0.002007945	0.035999592
PF01073.14 3-beta hydroxysteroid dehydrogenase/isomerase family	4	561	13	16483	2.201708924	0.002007945	0.035999592
PF00005.22 ABC transporter	6	559	36	16460	1.590779532	0.002443631	0.04279195
PF01061.19 ABC-2 type transporter	4	561	14	16482	2.127540281	0.002514704	0.043035729

SSP Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
SSP Small Secreted Protein	19	546	292	16204	0.658079605	0.009701656	0.009701656

Secretome Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
secretome Has a SignalP signal sequence	83	482	860	15636	1.141295331	1.95E-16	1.95E-16

Healthy Ants at 10AM vs Manipulated Biting Behavior

Table 5: Overrepresentation of annotation terms within the total of 377 up-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in live manipulated *Camponotus castaneus* ant heads (Manipulated Biting Behavior samples) compared to gene expression in healthy *Camponotus castaneus* ant heads at the same time of day; 10 AM (Ant Controls at 10AM samples)

GO Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0003674|molecular_function	202	175	6100	10584	0.694536379	3.17E-11	3.62E-08
GO:0065007|biological regulation	49	328	821	15863	1.060028213	1.59E-09	9.05E-07
GO:0050794|regulation of cellular process	47	330	787	15897	1.05671239	3.49E-09	1.32E-06
GO:0050789|regulation of biological process	47	330	795	15889	1.046095157	4.72E-09	1.34E-06
GO:0019222|regulation of metabolic process	26	351	335	16349	1.285101795	1.38E-07	1.15E-05
GO:2001141|regulation of RNA biosynthetic process	24	353	283	16401	1.371236463	9.30E-08	1.15E-05
GO:0051252|regulation of RNA metabolic process	24	353	283	16401	1.371236463	9.30E-08	1.15E-05
GO:0010556|regulation of macromolecule biosynthetic process	24	353	290	16394	1.346375544	1.42E-07	1.15E-05
GO:0006355|regulation of transcription, DNA-templated	24	353	283	16401	1.371236463	9.30E-08	1.15E-05
GO:0031323|regulation of cellular metabolic process	26	351	329	16355	1.303541504	9.91E-08	1.15E-05
GO:2000112|regulation of cellular macromolecule biosynthetic process	24	353	290	16394	1.346375544	1.42E-07	1.15E-05
GO:0010468|regulation of gene expression	24	353	290	16394	1.346375544	1.42E-07	1.15E-05
GO:0009889|regulation of biosynthetic process	24	353	290	16394	1.346375544	1.42E-07	1.15E-05
GO:0031326|regulation of cellular biosynthetic process	24	353	290	16394	1.346375544	1.42E-07	1.15E-05
GO:0051171|regulation of nitrogen compound metabolic process	25	352	319	16365	1.292953733	2.04E-07	1.45E-05
GO:0019219|regulation of nucleobase-containing compound metabolic process	25	352	319	16365	1.292953733	2.04E-07	1.45E-05
GO:0060255|regulation of macromolecule metabolic process	24	353	300	16384	1.311863827	2.53E-07	1.56E-05
GO:0036211|protein modification process	26	351	348	16336	1.246234375	2.75E-07	1.56E-05

GO Annotation term	# up-regulated proteins with annotation term	# up-regulated proteins without annotation term	# other proteins with annotation term	# other proteins without annotation term	log odds ratio	p-value (uncorrected)	p-value (corrected)
GO:0005488|binding	140	237	4188	12496	0.566767582	3.15E-07	1.56E-05
GO:0043412|macromolecule modification	27	350	373	16311	1.215920298	2.91E-07	1.56E-05
GO:0016310|phosphorylation	21	356	237	16447	1.409429934	3.07E-07	1.56E-05
GO:0006464|cellular protein modification process	26	351	348	16336	1.246234375	2.75E-07	1.56E-05
GO:0080090|regulation of primary metabolic process	25	352	327	16357	1.267695698	3.14E-07	1.56E-05
GO:0003700|sequence-specific DNA binding transcription factor activity	18	359	186	16498	1.492297136	6.72E-07	2.84E-05
GO:0001071|nucleic acid binding transcription factor activity	18	359	186	16498	1.492297136	6.72E-07	2.84E-05
GO:0006796|phosphate-containing compound metabolic process	27	350	390	16294	1.170309193	6.59E-07	2.84E-05
GO:0006468|protein phosphorylation	20	357	227	16457	1.401552672	6.40E-07	2.84E-05
GO:0006793|phosphorus metabolic process	27	350	392	16292	1.165071341	7.23E-07	2.94E-05
GO:0004672|protein kinase activity	20	357	233	16451	1.375099583	9.34E-07	3.67E-05
GO:0016301|kinase activity	21	356	278	16406	1.247372994	3.35E-06	0.000127159
GO:0043565|sequence-specific DNA binding	15	362	172	16512	1.380754181	1.81E-05	0.000627713
GO:0005515|protein binding	60	317	1496	15188	0.653153551	1.80E-05	0.000627713
GO:0016773|phosphotransferase activity, alcohol group as acceptor	20	357	288	16396	1.159828693	1.82E-05	0.000627713
GO:0008150|biological_process	129	248	4115	12569	0.462978289	3.95E-05	0.001325418
GO:0019538|protein metabolic process	37	340	822	15862	0.741913491	0.000107687	0.003494178
GO:0008610|lipid biosynthetic process	8	369	59	16625	1.809770319	0.000110342	0.003494178
GO:0044267|cellular protein metabolic process	26	351	499	16185	0.876544385	0.000121136	0.003732313
GO:0004725|protein tyrosine phosphatase activity	5	372	20	16664	2.415817768	0.000189296	0.005678882
GO:0044255|cellular lipid metabolic process	8	369	66	16618	1.69723188	0.000222979	0.006517833

GO Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0043167|ion binding	64	313	1829	14855	0.507247032	0.000475476	0.013551071
GO:0008653|lipopolysaccharide metabolic process	4	373	14	16670	2.547024588	0.000561663	0.015245138
GO:0009103|lipopolysaccharide biosynthetic process	4	373	14	16670	2.547024588	0.000561663	0.015245138
GO:0006629|lipid metabolic process	11	366	143	16541	1.246014735	0.000635726	0.01647108
GO:0006470|protein dephosphorylation	5	372	27	16657	2.11529302	0.000631971	0.01647108
GO:0003677|DNA binding	23	354	464	16220	0.820313078	0.000746099	0.018901164
GO:0004721|phosphoprotein phosphatase activity	5	372	29	16655	2.043713979	0.000842221	0.020872432
GO:0046872|metal ion binding	38	339	950	15734	0.618703323	0.001073346	0.026034339
GO:0019199|transmembrane receptor protein kinase activity	3	374	7	16677	2.950232146	0.00114436	0.027178541
GO:0043169|cation binding	38	339	968	15716	0.598788546	0.001217949	0.028335946
GO:0016311|dephosphorylation	5	372	33	16651	1.91426205	0.00141342	0.031594104

PFAM Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotati on term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
PF07716.10 Basic region leucine zipper	7	370	12	16672	3.268986438	9.75E-08	7.34E-05
PF00170.16 bZIP transcription factor	6	371	10	16674	3.294578213	7.43E-07	0.000267124
PF00069.20 Protein kinase domain	19	358	218	16466	1.388463858	1.42E-06	0.000267124
PF07714.12 Protein tyrosine kinase	19	358	215	16469	1.40250307	1.17E-06	0.000267124
PF01094.23 Receptor family ligand binding region	5	372	19	16665	2.46717107	0.000154213	0.023224514
PF00102.22 Protein-tyrosine phosphatase	5	372	20	16664	2.415817768	0.000189296	0.023756658
PF06293.9 Lipopolysaccharide kinase (Kdo/WaaP) family	4	373	13	16671	2.621192546	0.000444554	0.047821334

Table 6: Overrepresentation of annotation terms within the total of 391 down-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in live manipulated *Camponotus castaneus* ant heads (Manipulated Biting Behavior samples) compared to gene expression in healthy *Camponotus castaneus* ant heads at the same time of day; 10 AM (Ant Controls at 10AM samples)

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0008150|biological_process	226	165	4018	12652	1.461620564	1.46E-44	1.66E-41
GO:0003824|catalytic activity	174	217	2590	14080	1.472255421	1.05E-40	5.97E-38
GO:0008152|metabolic process	165	226	2349	14321	1.49314776	1.92E-40	7.31E-38
GO:0003674|molecular_function	261	130	6041	10629	1.26200251	1.82E-33	5.19E-31
GO:0044699|single-organism process	126	265	1627	15043	1.480727019	2.78E-33	6.34E-31
GO:0044710|single-organism metabolic process	79	312	843	15827	1.558950328	5.74E-25	1.09E-22
GO:0016491|oxidoreductase activity	58	333	472	16198	1.787964592	1.57E-23	2.55E-21
GO:0055114|oxidation-reduction process	48	343	380	16290	1.791606013	5.17E-20	7.37E-18
GO:0044763|single-organism cellular process	66	325	912	15758	1.255293021	1.70E-15	2.15E-13
GO:0071704|organic substance metabolic process	94	297	1741	14929	0.998408613	3.58E-14	3.71E-12
GO:0044238|primary metabolic process	91	300	1655	15015	1.012325724	3.55E-14	3.71E-12
GO:0044281|small molecule metabolic process	27	364	191	16479	1.856251692	9.44E-13	8.97E-11
GO:0044765|single-organism transport	38	353	416	16254	1.436527154	5.44E-12	4.77E-10
GO:0005975|carbohydrate metabolic process	23	368	160	16510	1.863958999	3.51E-11	2.86E-09
GO:1901564|organonitrogen compound metabolic process	27	364	238	16432	1.633398257	9.35E-11	7.11E-09
GO:0006810|transport	41	350	559	16111	1.216746987	4.29E-10	2.92E-08
GO:0009987|cellular process	98	293	2196	14474	0.790511282	4.35E-10	2.92E-08
GO:0051234|establishment of localization	41	350	561	16109	1.213051408	4.74E-10	3.00E-08
GO:0005506|iron ion binding	19	372	138	16532	1.811344615	3.49E-09	2.10E-07
GO:0043167|ion binding	82	309	1811	14859	0.778104534	1.12E-08	6.39E-07

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0016787|hydrolase activity	56	335	1048	15622	0.91301775	1.77E-08	9.59E-07
GO:0016021|integral component of membrane	35	356	496	16174	1.165001698	2.19E-08	1.14E-06
GO:0043436|oxoacid metabolic process	15	376	94	16576	1.950877421	2.77E-08	1.26E-06
GO:0006082|organic acid metabolic process	15	376	94	16576	1.950877421	2.77E-08	1.26E-06
GO:0019752|carboxylic acid metabolic process	15	376	94	16576	1.950877421	2.77E-08	1.26E-06
GO:0020037|heme binding	18	373	150	16520	1.670485091	6.16E-08	2.60E-06
GO:0046906|tetrapyrrole binding	18	373	150	16520	1.670485091	6.16E-08	2.60E-06
GO:0044425|membrane part	38	353	599	16071	1.060628189	7.46E-08	3.04E-06
GO:0043169|cation binding	51	340	955	15715	0.903539624	9.11E-08	3.58E-06
GO:0006869|lipid transport	6	385	6	16664	3.767762649	1.15E-07	4.23E-06
GO:0005215|transporter activity	28	363	364	16306	1.239936226	1.15E-07	4.23E-06
GO:0006520|cellular amino acid metabolic process	13	378	77	16593	2.002985939	1.31E-07	4.68E-06
GO:0044712|single-organism catabolic process	11	380	51	16619	2.244200285	1.42E-07	4.90E-06
GO:0055085|transmembrane transport	23	368	271	16399	1.330268093	3.26E-07	1.09E-05
GO:1901605|alpha-amino acid metabolic process	8	383	24	16646	2.673277948	4.60E-07	1.50E-05
GO:0016705|oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	16	375	144	16526	1.588539574	8.58E-07	2.72E-05
GO:0004576|oligosaccharyl transferase activity	4	387	1	16669	5.149175654	1.33E-06	4.11E-05
GO:0044282|small molecule catabolic process	6	385	11	16659	3.161326752	1.39E-06	4.18E-05
GO:0009069|serine family amino acid metabolic process	5	386	6	16664	3.582847057	2.54E-06	7.43E-05
GO:0046872|metal ion binding	47	344	941	15729	0.825824226	2.62E-06	7.47E-05
GO:0044237|cellular metabolic process	60	331	1364	15306	0.710049536	4.32E-06	0.000119991
GO:0005575|cellular_component	83	308	2143	14527	0.602543095	6.16E-06	0.000167218
GO:0005319|lipid transporter activity	5	386	8	16662	3.295044958	6.82E-06	0.000180696

GO Annotation term	# down-regulated proteins with annotation term	# down-regulated proteins without annotation term	# other proteins with annotation term	# other proteins without annotation term	log odds ratio	p-value (uncorrected)	p-value (corrected)
GO:0009056|catabolic process	13	378	124	16546	1.523673256	1.62E-05	0.000419096
GO:0016740|transferase activity	37	354	734	15936	0.819447951	2.08E-05	0.000527463
GO:0016054|organic acid catabolic process	5	386	11	16659	2.97641116	2.19E-05	0.000530068
GO:0046395|carboxylic acid catabolic process	5	386	11	16659	2.97641116	2.19E-05	0.000530068
GO:0048037|cofactor binding	14	377	153	16517	1.388519653	3.14E-05	0.000745073
GO:0005509|calcium ion binding	12	379	116	16554	1.508163297	3.85E-05	0.000895968
GO:0003995|acyl-CoA dehydrogenase activity	4	387	6	16664	3.357116182	5.11E-05	0.001143056
GO:0006544|glycine metabolic process	4	387	6	16664	3.357116182	5.11E-05	0.001143056
GO:1901575|organic substance catabolic process	12	379	121	16549	1.465660855	5.62E-05	0.00121639
GO:0004553|hydrolase activity, hydrolyzing O-glycosyl compounds	8	383	51	16619	1.917882818	5.66E-05	0.00121639
GO:0071702|organic substance transport	12	379	125	16545	1.432895928	7.50E-05	0.001583916
GO:0046914|transition metal ion binding	30	361	582	16088	0.831677907	8.88E-05	0.001839779
GO:0016798|hydrolase activity, acting on glycosyl bonds	8	383	55	16615	1.842134548	9.12E-05	0.001856638
GO:0019538|protein metabolic process	38	353	821	15849	0.731456679	9.59E-05	0.001918921
GO:0055086|nucleobase-containing small molecule metabolic process	10	381	90	16580	1.575928476	9.85E-05	0.001936513
GO:0016742|hydroxymethyl-, formyl- and related transferase activity	3	388	2	16668	4.165705761	0.000115429	0.002230332
GO:0070085|glycosylation	5	386	18	16652	2.483514393	0.000147487	0.002802248
GO:1901565|organonitrogen compound catabolic process	6	385	30	16640	2.156883468	0.000151722	0.002835465
GO:0005783|endoplasmic reticulum	4	387	9	16661	2.951471029	0.000164845	0.002982918
GO:0009063|cellular amino acid catabolic process	4	387	9	16661	2.951471029	0.000164845	0.002982918
GO:0006820|anion transport	6	385	33	16637	2.061392983	0.000239841	0.004272169
GO:0022857|transmembrane transporter activity	19	372	326	16344	0.94026388	0.000405491	0.007111682
GO:0008236|serine-type peptidase activity	9	382	90	16580	1.467946727	0.000447407	0.007612595
GO:0017171|serine hydrolase activity	9	382	90	16580	1.467946727	0.000447407	0.007612595

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0050662|coenzyme binding	10	381	115	16555	1.329297039	0.000609175	0.009999287
GO:0009071|serine family amino acid catabolic process	3	388	5	16665	3.249235027	0.000613991	0.009999287
GO:0006546|glycine catabolic process	3	388	5	16665	3.249235027	0.000613991	0.009999287
GO:0005488|binding	129	262	4199	12471	0.380027448	0.000633388	0.010169897
GO:0006807|nitrogen compound metabolic process	32	359	716	15954	0.686198208	0.000657242	0.010406333
GO:0016758|transferase activity, transferring hexosyl groups	7	384	58	16612	1.652705191	0.000698182	0.01090311
GO:0006811|ion transport	13	378	188	16482	1.103637354	0.000767556	0.011824511
GO:0006486|protein glycosylation	4	387	15	16655	2.440285218	0.000801369	0.012020536
GO:0043413|macromolecule glycosylation	4	387	15	16655	2.440285218	0.000801369	0.012020536
GO:0008272|sulfate transport	3	388	6	16664	3.066853463	0.000905363	0.012901429
GO:0015116|sulfate transmembrane transporter activity	3	388	6	16664	3.066853463	0.000905363	0.012901429
GO:1901682|sulfur compound transmembrane transporter activity	3	388	6	16664	3.066853463	0.000905363	0.012901429
GO:0072348|sulfur compound transport	3	388	6	16664	3.066853463	0.000905363	0.012901429
GO:0044723|single-organism carbohydrate metabolic process	8	383	81	16589	1.453452502	0.000992824	0.013973075
GO:0022892|substrate-specific transporter activity	15	376	246	16424	0.97962848	0.001054266	0.014656863
GO:0008509|anion transmembrane transporter activity	5	386	30	16640	1.971967876	0.001135492	0.015595914
GO:0008233|peptidase activity	19	372	355	16315	0.853267544	0.00122575	0.01663518
GO:0050660|flavin adenine dinucleotide binding	6	385	47	16623	1.706911091	0.001289267	0.017291344
GO:0016627|oxidoreductase activity, acting on the CH-CH group of donors	4	387	18	16652	2.257783519	0.001432468	0.018988527
GO:0005576|extracellular region	7	384	69	16601	1.478379305	0.001768975	0.022658783
GO:1901566|organonitrogen compound biosynthetic process	8	383	89	16581	1.358782923	0.001734733	0.022658783
GO:0016614|oxidoreductase activity, acting on CH-OH group of donors	7	384	69	16601	1.478379305	0.001768975	0.022658783
GO:0044248|cellular catabolic process	8	383	92	16578	1.32544977	0.002105411	0.026668541

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0070011|peptidase activity, acting on L-amino acid peptides	18	373	347	16323	0.819798993	0.002183406	0.027352558
GO:1901606|alpha-amino acid catabolic process	3	388	9	16661	2.66120831	0.002252818	0.027615189
GO:0016042|lipid catabolic process	3	388	9	16661	2.66120831	0.002252818	0.027615189
GO:0019725|cellular homeostasis	5	386	36	16634	1.789285677	0.002342959	0.028414606
GO:0051604|protein maturation	17	374	321	16349	0.839438436	0.00250631	0.029762433
GO:0016485|protein processing	17	374	321	16349	0.839438436	0.00250631	0.029762433
GO:0016757|transferase activity, transferring glycosyl groups	7	384	75	16595	1.394636207	0.002737391	0.032171395
GO:0016773|phosphotransferase activity, alcohol group as acceptor	16	375	292	16378	0.872603144	0.002814561	0.032740814
GO:1901135|carbohydrate derivative metabolic process	10	381	147	16523	1.08186176	0.003379579	0.03891636
GO:1901607|alpha-amino acid biosynthetic process	3	388	11	16659	2.460417566	0.003602643	0.040663492
GO:0006790|sulfur compound metabolic process	3	388	11	16659	2.460417566	0.003602643	0.040663492
GO:0006575|cellular modified amino acid metabolic process	3	388	12	16658	2.37334616	0.004427438	0.049483128

PFAM Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
PF01347.17 Lipoprotein amino terminal region	5	386	3	16667	4.27617425	3.26E-07	0.000136976
PF00067.17 Cytochrome P450	15	376	117	16553	1.730609756	3.64E-07	0.000136976
PF07859.8 alpha/beta hydrolase fold	7	384	24	16646	2.537138992	5.15E-06	0.000968643
PF07690.11 Major Facilitator Superfamily	13	378	108	16562	1.662790128	4.13E-06	0.000968643
PF00441.19 Acyl-CoA dehydrogenase, C-terminal domain	4	387	5	16665	3.539497746	3.12E-05	0.004705816
PF02770.14 Acyl-CoA dehydrogenase, middle domain	4	387	6	16664	3.357116182	5.11E-05	0.005500848
PF00135.23 Carboxylesterase family	7	384	36	16634	2.13095273	4.98E-05	0.005500848
PF00501.23 AMP-binding enzyme	5	386	18	16652	2.483514393	0.000147487	0.013882191
PF13193.1 AMP-binding enzyme C-terminal domain	4	387	10	16660	2.846050491	0.000226622	0.017087785
PF08028.6 Acyl-CoA dehydrogenase, C-terminal domain	3	388	3	16667	3.760180656	0.000226929	0.017087785
PF00106.20 short chain dehydrogenase	8	383	68	16602	1.629177296	0.000342917	0.022611685
PF13848.1 Thioredoxin-like domain	3	388	4	16666	3.472438583	0.000390374	0.022611685
PF01395.17 PBP/GOBP family	3	388	4	16666	3.472438583	0.000390374	0.022611685
PF13405.1 EF-hand domain	6	385	38	16632	1.920013805	0.000471257	0.023657078
PF00083.19 Sugar (and other) transporter	8	383	71	16599	1.585824407	0.000447046	0.023657078
PF00128.19 Alpha amylase, catalytic domain	4	387	13	16657	2.583506138	0.000510241	0.024013223
PF02771.11 Acyl-CoA dehydrogenase, N-terminal domain	3	388	5	16665	3.249235027	0.000613991	0.027196204
PF13792.1 Sulfate transporter N-terminal domain with GLY motif	3	388	6	16664	3.066853463	0.000905363	0.034086933
PF01740.16 STAS domain	3	388	6	16664	3.066853463	0.000905363	0.034086933
PF00916.15 Sulfate transporter family	3	388	6	16664	3.066853463	0.000905363	0.034086933

SSP Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
SSP Small Secreted Protein	22	369	289	16381	1.217696527	3.15E-06	3.15E-06

Secretome Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
secretome Has a SignalP signal sequence	79	312	864	15806	1.53301679	2.46E-24	2.46E-24

Manipulated Biting Behavior vs Death After Manipulated Biting Behavior

Table 7: Overrepresentation of annotation terms within the total of 104 up-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in dead *Camponotus castaneus* ant heads after manipulation (Death After Manipulation samples) compared to gene expression in live manipulated *Camponotus castaneus* ant heads (Manipulated Biting Behavior samples)

No overrepresented annotation terms

Table 8: Over- and under-representation of annotation terms within the total of 224 down-regulated *Camponotus floridanus* homologs (2-fold and significant Q<0.05, minimum expression of 4) in dead *Camponotus castaneus* ant heads after manipulation (Death After Manipulation samples) compared to gene expression in live manipulated *Camponotus castaneus* ant heads (Manipulated Biting Behavior samples)

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0008152|metabolic process	79	145	2435	14402	1.170134439	1.28E-14	1.46E-11
GO:0008150|biological_process	107	117	4137	12700	1.032286006	1.08E-13	4.11E-11
GO:0016491|oxidoreductase activity	33	191	497	16340	1.737015476	9.30E-14	4.11E-11
GO:0055114|oxidation-reduction process	28	196	400	16437	1.769915474	2.53E-12	7.20E-10
GO:0003824|catalytic activity	78	146	2686	14151	1.0348344	6.90E-12	1.57E-09
GO:0044699|single-organism process	56	168	1697	15140	1.089865973	2.09E-10	3.98E-08
GO:0044710|single-organism metabolic process	38	186	884	15953	1.304784602	2.95E-10	4.81E-08
GO:0003674|molecular_function	125	99	6177	10660	0.778859589	1.10E-08	1.56E-06
GO:0048037|cofactor binding	13	211	154	16683	1.898284137	3.20E-07	4.06E-05
GO:0050662|coenzyme binding	10	214	115	16722	1.916157446	5.92E-06	0.000675093
GO:0016705|oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	11	213	149	16688	1.755101978	8.75E-06	0.000906458
GO:0004252|serine-type endopeptidase activity	8	216	78	16759	2.074145014	1.72E-05	0.001629806
GO:0008236|serine-type peptidase activity	8	216	91	16746	1.91921833	4.78E-05	0.003635707
GO:0005506|iron ion binding	10	214	147	16690	1.668741508	4.34E-05	0.003635707
GO:0017171|serine hydrolase activity	8	216	91	16746	1.91921833	4.78E-05	0.003635707
GO:0016614|oxidoreductase activity, acting on CH-OH group of donors	7	217	69	16768	2.059133878	6.21E-05	0.00442227
GO:0020037|heme binding	10	214	158	16679	1.595919767	7.69E-05	0.004867452
GO:0046906|tetrapyrrole binding	10	214	158	16679	1.595919767	7.69E-05	0.004867452
GO:0016701|oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	3	221	5	16832	3.82204879	0.000119119	0.007147118
GO:0005576|extracellular region	6	218	70	16767	1.885937112	0.000486998	0.027758884

GO Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
GO:0005975|carbohydrate metabolic process	9	215	174	16663	1.388477222	0.00071331	0.037848536
GO:0004497|monooxygenase activity	3	221	11	16826	3.033234902	0.00073041	0.037848536
GO:0016787|hydrolase activity	28	196	1076	15761	0.738377923	0.000841252	0.041696861
GO:0051213|dioxygenase activity	3	221	12	16825	2.946164092	0.000904201	0.042949564
GO:0006629|lipid metabolic process	8	216	146	16691	1.443181443	0.000985527	0.044940051

PFAM Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
PF00089.21 Trypsin	8	216	65	16772	2.257241972	5.03E-06	0.002527436
PF07993.7 Male sterility protein	6	218	30	16807	2.73561777	6.71E-06	0.002527436
PF00550.20 Phosphopantetheine attachment site	4	220	10	16827	3.42082174	2.61E-05	0.004916277
PF02719.10 Polysaccharide biosynthesis protein	4	220	10	16827	3.42082174	2.61E-05	0.004916277
PF01370.16 NAD dependent epimerase/dehydratase family	5	219	33	16804	2.453230853	0.00013155	0.019811459
PF00266.14 Aminotransferase class-V	3	221	7	16830	3.485457725	0.000250334	0.031416953
PF00650.15 CRAL/TRIO domain	4	220	21	16816	2.67823047	0.000294647	0.031695642
PF01130.16 CD36 family	3	221	9	16828	3.234024455	0.000450111	0.042366706

SSP Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
SSP Small Secreted Protein	11	213	300	16537	1.046176206	0.002782488	0.002782488

Secretome Annotation term	**# down-regulated proteins with annotation term**	**# down-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
secretome Has a SignalP signal sequence	50	174	893	15944	1.635218987	1.08E-17	1.08E-17

Healthy Ants at 10AM vs Manipulated Biting Behavior vs Death After Manipulated Biting Behavior

Table 9: Overrepresentation of annotation terms within the total of 52 *Camponotus floridanus* homologs that are up-regulated in live manipulated *Camponotus castaneus* ant heads (Manipulated Biting Behavior samples) compared to gene expression in healthy *Camponotus castaneus* ant heads sampled at the same time of day (Healthy Ant Controls at 10AM samples) and down-regulated again after manipulation (Death After Manipulation samples) (2-fold and significant Q<0.05, minimum expression of 4)

Secretome Annotation term	**# up-regulated proteins with annotation term**	**# up-regulated proteins without annotation term**	**# other proteins with annotation term**	**# other proteins without annotation term**	**log odds ratio**	**p-value (uncorrected)**	**p-value (corrected)**
secretome Has a SignalP signal sequence	8	44	935	16074	1.139663717	0.007306394	0.007306394

Table 10: Overrepresentation of annotation terms within the total of 12 *Camponotus floridanus* homologs that are <u>down-regulated</u> in live manipulated *Camponotus castaneus* ant heads (Manipulated Biting Behavior samples) compared to gene expression in healthy *Camponotus castaneus* ant heads sampled at the same time of day (Healthy Ant Controls at 10AM samples) and <u>up-regulated</u> again after manipulation (Death After Manipulation samples) (2-fold and significant Q<0.05, minimum expression of 4)

No overrepresented annotation terms