

Supplementary information for following article

Sublethal effects of imidacloprid on targeting muscle and ribosomal protein related genes in the honey bee *Apis mellifera* L.

Yan-Yan Wu¹, Qi-Hua Luo², Chun-Shen Hou¹, Qiang Wang¹, Ping-Li Dai¹, Jing Gao¹, Yong-Jun Liu¹, Qing-Yun Diao¹,

¹Key Laboratory of Pollinating Insect Biology, Ministry of Agriculture, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences, Beijing 100093, China

² Bureau of Landscape and Forestry, Mi Yun District, Beijing 101500, China

*Corresponding author:

Qing-Yun Diao (Q.Y. Diao)

Key Laboratory of Pollinating Insect Biology, Ministry of Agriculture,
Institute of Apicultural Research, Chinese Academy of Agricultural Sciences,
Beijing 100093,
China

Tel: +8610 62597285

Fax: +8610 62597285

Email: dqyun1@126.com

Table S1. 509 differentially expressed genes between control and imidacloprid treated groups

Gene	SIM_normalize	SCK_normalize	FoldChange	Log ₂ Fold Change	pval	NR:Seq-id	NR:Description
gene3 689	1003.918 525	264.3827 841	3.7972 15951	1.9249420 48	0.000 136	gi 571524910 ref XP_006567203.1	PREDICTED: venom serine protease 34 isoform X1 [Apis mellifera]
gene1 2324	125.3372 686	35.67690 611	3.5131 20455	1.8127530 43	0.000 349	gi 328793159 ref XP_625207.2	PREDICTED: phospholipase B1, membrane-associated-like isoform X3 [Apis mellifera]
gene6 640	4062.789 507	1436.279 536	2.8286 89963	1.5001340 59	2.24E -10	gi 118150502 ref NP_001071288.1	chemosensory protein 1 precursor [Apis mellifera]
gene1 1505	38.40538 04	13.61559 682	2.8206 90192	1.4960482 18	0.018 742	gi 118150512 ref NP_001071293.1	long wavelength sensitive opsin 2 [Apis mellifera]
gene6 088	213.4106 065	81.05746 998	2.6328 30836	1.3966148 29	0.007 057	gi 110758297 ref XP_001120293.1	PREDICTED: phospholipase A2-like [Apis mellifera]
gene4 856	299.8423 02	117.1373 937	2.5597 48791	1.3560022 34	0.001 202	gi 571532643 ref XP_006558886.1	PREDICTED: uncharacterized protein LOC726672 [Apis mellifera]
gene4 913	3164.636 073	1246.956 822	2.5378 87452	1.3436280 91	0.019 333	gi 58585164 ref NP_001011608.1	alpha-glucosidase precursor [Apis mellifera]
gene6 22	7752.783 798	3058.102 863	2.5351 61224	1.3420774 99	0.000 213	gi 110749126 ref XP_394209.2	PREDICTED: glucose dehydrogenase [FAD, quinone] isoform 3 [Apis mellifera]
gene3	2607.675	1055.878	2.4696	1.3043209	0.000	gi 328789967 ref	PREDICTED: laccase-5-like [Apis mellifera]

117	9	357	74544	35	835	XP_625189.2	
gene1 1504	5489.111 853	2268.534 987	2.4196 72557	1.2748118 28	0.001 881	gi 283135098 ref NP_001011639. 2	rhodopsin, long-wavelength [Apis mellifera]
gene9 572	49.36412 267	20.67232 648	2.3879 32616	1.2557621 27	0.003 714	gi 209969890 ref NP_001129681. 1	silk fibroin 4 precursor [Apis mellifera]
gene4 229	38.09507 864	15.98005 68	2.3839 13843	1.2533320 97	0.031 971	gi 645015869 ref XP_001601386. 2	PREDICTED: 40S ribosomal protein S29 [Nasonia vitripennis]
gene1 1561	127.6784 653	54.42497 435	2.3459 53614	1.2301744 88	4.22E -05	gi 571574902 ref XP_006563622. 1	PREDICTED: uncharacterized protein LOC100576330 [Apis mellifera]
gene8 291	4004.018 412	1712.763 153	2.3377 53709	1.2251229 44	0.008 36	gi 66517414 ref XP_623184.1	PREDICTED: arrestin homolog isoform 2 [Apis mellifera]
gene7 311	860.7985 781	372.6899 935	2.3096 90609	1.2076996 11	0.005 136	gi 820836729 ref XP_012346672. 1	PREDICTED: protein takeout-like [Apis florea]
gene9 18	4243.347 557	1870.714 798	2.2683 0277	1.1816132 22	0.031 592	gi 66500020 ref XP_397545.2	PREDICTED: uncharacterized protein LOC409096 [Apis mellifera]
gene1 3571	35.25667 399	15.55119 925	2.2671 35378	1.1808705 42	0.047 74	gi 571579756 ref XP_006572785. 1	PREDICTED: alanine--glyoxylate aminotransferase 2-like [Apis mellifera]
gene7 564	1220.091 073	546.6287 754	2.2320 28624	1.1583555 29	0.000 162	gi 58585118 ref NP_001011589. 1	odorant binding protein 4 precursor [Apis mellifera]

gene8 767	127.0497 722	58.19953 832	2.1830 03093	1.1263141 75	0.006 367	gi 571558341 ref XP_006564092. 1	PREDICTED: pancreatic triacylglycerol lipase-like [Apis mellifera]
gene1 1344	94.33901 449	43.29287 892	2.1790 88498	1.1237247 89	0.000 918	gi 572298283 ref XP_006615299. 1	PREDICTED: uncharacterized protein LOC102672709 [Apis dorsata]
gene4 646	310.3408 783	145.4367 074	2.1338 55228	1.0934622 99	0.007 62	gi 328790707 ref XP_001120503. 2	PREDICTED: transient receptor potential protein [Apis mellifera]
gene6 556	30.09473 295	14.22860 368	2.1150 86879	1.0807169 24	0.033 822	gi 571543586 ref XP_006561486. 1	PREDICTED: ras-like protein family member 11B-like [Apis mellifera]
gene9 140	62.24895 922	29.76868 756	2.0910 88467	1.0642540 99	0.006 037	.	.
gene4 514	106.5166 367	50.98274 518	2.0892 68366	1.0629978 18	0.003 774	gi 110756792 ref XP_001120695. 1	PREDICTED: uncharacterized protein LOC726118 [Apis mellifera]
gene6 036	355.1340 028	170.7369 657	2.0800 06526	1.0565880 55	0.002 322	gi 571539762 ref XP_006565521. 1	PREDICTED: phospholipase B1, membrane-associated-like isoform X1 [Apis mellifera]
gene1 683	254.9297 916	122.8177 222	2.0756 75946	1.0535812 28	0.024 035	gi 218156311 ref NP_001136165. 1	uncharacterized protein LOC100217360 [Apis mellifera]
gene1 2058	918.2284 519	446.4724 505	2.0566 29588	1.0402819 79	0.016 952	gi 58585212 ref NP_001011635. 1	yellow-f precursor [Apis mellifera]

gene1 0921	39.08923 73	19.01873 452	2.0553 01695	1.0393501 81	0.020 81	gi 820852399 ref XP_003694757. 2	PREDICTED: uncharacterized protein LOC100869988 [Apis florea]
gene1 1723	73.50686 947	35.88240 541	2.0485 49105	1.0346024 75	0.012 804	gi 571575711 ref XP_006557840. 1	PREDICTED: elongation of very long chain fatty acids protein AAEL008004-like isoform X2 [Apis mellifera]
gene6 728	1455.333 317	713.0494 787	2.0409 99062	1.0292755 19	0.000 424	gi 328784765 ref XP_624408.2	PREDICTED: trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like [Apis mellifera]
gene1 0514	1140.489 415	567.5426 59	2.0095 21922	1.0068523 16	0.016 271	gi 201023353 ref NP_001128419. 1	esterase A2 [Apis mellifera]
gene1 0882	199.2520 175	99.87751 751	1.9949 63656	0.9963624 64	0.033 733	gi 58585160 ref NP_001011606. 1	opsin, blue-sensitive [Apis mellifera]
gene6 400	250.2774 917	125.5646 715	1.9932 15837	0.9950979 42	5.42E -05	gi 110773269 ref XP_001120568. 1	PREDICTED: cytochrome c oxidase subunit 7C, mitochondrial-like [Apis mellifera]
gene1 1045	776.9336 862	392.1976 598	1.9809 74814	0.9862105 38	3.16E -06	gi 94158709 ref NP_001035295. 1	odorant binding protein 16 precursor [Apis mellifera]
gene1 0777	188.2840 331	95.07633 037	1.9803 46026	0.9857525 35	0.000 113	gi 328785069 ref XP_001121591. 2	PREDICTED: uncharacterized protein LOC725784 isoformX1 [Apis mellifera]
gene1 0174	73.56363 886	37.36558 115	1.9687 54041	0.9772828 84	0.005 558	gi 571567810 ref XP_391975.4	PREDICTED: peptidyl-prolyl cis-trans isomerase, rhodopsin-specific isozyme-like isoform X2 [Apis mellifera]
gene1	184.1792	93.89785	1.9614	0.9719467	0.000	gi 110763495 ref	PREDICTED: MORN repeat-containing protein 4 [Apis mellifera]

1400	861	348	85585	33	129	XP_393307.3	
gene1 1346	105.1018 008	53.82203 235	1.9527 65368	0.9655186 15	0.029 484	gi 328783471 ref XP_001120999. 2	PREDICTED: chymotrypsin inhibitor-like isoform 1 [Apis mellifera]
gene1 3483	118.3173 119	60.69339 245	1.9494 2657	0.9630498 13	0.004 026	gi 66548280 ref XP_624540.1	PREDICTED: dehydrogenase/reductase SDR family member 11-like isoform X2 [Apis mellifera]
gene1 0317	1179.720 156	606.6855 157	1.9445 33247	0.9594239 02	0.000 958	gi 66523006 ref XP_396534.2	PREDICTED: probable cytochrome P450 6a14 isoformX1 [Apis mellifera]
gene6 339	118.4171 544	61.18218 154	1.9354 84342	0.9526946 36	0.002 023	gi 572303416 ref XP_006617694. 1	PREDICTED: uncharacterized protein LOC102676732 [Apis dorsata]
gene5 72	833.5277 943	432.1252 193	1.9289 03376	0.9477808 77	0.000 354	gi 571502919 ref XP_006565388. 1	PREDICTED: uncharacterized protein LOC413056 [Apis mellifera]
gene1 682	104.4473 239	54.49002 32	1.9168 15551	0.9387115 18	0.044 312	gi 820859691 ref XP_003697124. 2	PREDICTED: tetraspanin-7-like [Apis florea]
gene1 1831	242.1671 13	126.6310 374	1.9123 83551	0.9353719 02	0.015 554	gi 328778410 ref XP_001120045. 2	PREDICTED: homeotic protein deformed [Apis mellifera]
gene1 1347	55.20096 445	29.06555 456	1.8991 88413	0.9253830 38	0.036 417	gi 571574368 ref XP_006563415. 1	PREDICTED: mucin-6-like isoform X1 [Apis mellifera]
gene1 2112	428.9224 056	228.5108 154	1.8770 33281	0.9084542 3	4.04E -05	gi 66526281 ref XP_396852.2	PREDICTED: scavenger receptor class B member 1 [Apis mellifera]
gene8	410.0094	219.1903	1.8705	0.9034728	0.000	gi 66534390 ref	PREDICTED: pancreatic triacylglycerol lipase-like isoform X2 [Apis mellifera]

768	572	505	63445	99	127	XP_623663.1	
gene1 3055	825.6577 386	441.7616 678	1.8690 11729	0.9022756 23	2.71E -06	gi 759079256 ref XP_011349442. 1	PREDICTED: 40S ribosomal protein S19-like isoform X1 [Cerapachys biroi]
gene5 792	1438.974 909	776.1995 504	1.8538 72382	0.8905419 34	7.32E -07	gi 307173970 gb EFN64700.1	40S ribosomal protein S15 [Camponotus floridanus]
gene8 719	119.5378 144	64.93917 443	1.8407 65847	0.8803061 22	0.003 015	gi 571558039 ref XP_006562102. 1	PREDICTED: tetratricopeptide repeat protein 39C-like [Apis mellifera]
gene1 1350	1125.545 578	615.3632 538	1.8290 75057	0.8711142 78	0.015 569	gi 571574380 ref XP_006563420. 1	PREDICTED: chymotrypsin inhibitor-like isoform X2 [Apis mellifera]
gene1 0988	857.1372 661	469.5715 307	1.8253 60377	0.8681813 2	2.12E -06	gi 571573277 ref XP_006557994. 1	PREDICTED: CDGSH iron-sulfur domain-containing protein 2 homolog isoform X1 [Apis mellifera]
gene1 1340	171.7511 3	94.40159 593	1.8193 66805	0.8634364 36	0.028 863	gi 110763428 ref XP_001120193. 1	PREDICTED: uncharacterized protein LOC725232 [Apis mellifera]
gene1 3333	51.82689 664	28.52126 477	1.8171 3178	0.8616630 49	0.027 959	gi 48097526 ref XP_391912.1	PREDICTED: alpha-tocopherol transfer protein-like [Apis mellifera]
gene1 1095	132.6212 46	73.38198 13	1.8072 72626	0.8538141 52	0.042 945	gi 66548280 ref XP_624540.1	PREDICTED: dehydrogenase/reductase SDR family member 11-like isoform X2 [Apis mellifera]
gene1 641	272.5564 694	151.6818 442	1.7968 95804	0.8455067 54	0.027 448	gi 571510600 ref XP_006571771. 1	PREDICTED: uncharacterized protein LOC102654257 [Apis mellifera]
gene1	1021.181	572.6309	1.7833	0.8345619	9.09E	gi 328779527 ref	PREDICTED: uncharacterized protein LOC552366 [Apis mellifera]

95	668	468	15543	99	-06	XP_625285.2	
gene1 2553	78.62719 841	44.18166 937	1.7796 33941	0.8315805 19	0.016 661	.	.
gene2 375	121.2298 602	68.12836 747	1.7794 32925	0.8314175 52	0.010 035	gi 571514717 ref XP_006568869. 1	PREDICTED: uncharacterized protein LOC724555 isoform X1 [Apis mellifera]
gene8 822	536.1067 392	302.3450 366	1.7731 62031	0.8263243 76	0.002 126	gi 380029575 ref XP_003698444. 1	PREDICTED: 60S ribosomal protein L32 [Apis florea]
gene8 005	92.50236 257	52.44422 398	1.7638 2365	0.8187063 25	0.009 813	gi 328784573 ref XP_001122994. 2	PREDICTED: serendipity locus protein H-1-like [Apis mellifera]
gene3 674	49959.67 741	28489.18 165	1.7536 36802	0.8103499 8	0.002 401	gi 58585154 ref NP_001011607. 1	melittin precursor [Apis mellifera]
gene1 1047	2087.784 93	1192.114 72	1.7513 28874	0.8084500 26	0.035 956	gi 94158830 ref NP_001035317. 1	odorant binding protein 18 precursor [Apis mellifera]
gene7 65	502.4862 996	287.9221 767	1.7452 15688	0.8034053 47	7.49E -05	gi 571503975 ref XP_006568688. 1	PREDICTED: uncharacterized protein LOC408592 isoform X1 [Apis mellifera]
gene9 451	602.1048 77	346.5165 649	1.7375 93345	0.7970904 83	0.034 942	gi 571563280 ref XP_006558363. 1	PREDICTED: facilitated trehalose transporter Tret1-like [Apis mellifera]
gene1 0415	569.8122 85	328.4087 086	1.7350 7057	0.7949943 42	0.012 279	gi 815768511 ref XP_012231503.	PREDICTED: uncharacterized protein LOC105677458 [Linepithema humile]

						1	
gene7 565	8968.287 148	5173.314 532	1.7335 6696	0.7937435 63	0.013 815	gi 94158729 ref NP_001035311. 1	odorant binding protein 3 precursor [Apis mellifera]
gene1 72	138.2338 759	79.74826 056	1.7333 77943	0.7935862 52	0.007 465	gi 572270852 ref XP_006613410. 1	PREDICTED: pre-mRNA-splicing factor CWC22 homolog isoform X1 [Apis dorsata]
gene4 019	56.93668 085	32.84762 473	1.7333 57627	0.7935693 42	0.048 287	gi 328780013 ref XP_003249736. 1	PREDICTED: uncharacterized protein LOC100577683 [Apis mellifera]
gene4 029	74.56387 108	43.04345 194	1.7322 93014	0.7926829 79	0.030 887	gi 58585100 ref NP_001011575. 1	nicotinic acetylcholine receptor alpha8 subunit [Apis mellifera]
gene5 376	484.1611 425	280.2891 666	1.7273 63024	0.7885713 13	0.001 927	gi 571535759 ref XP_001119990. 2	PREDICTED: uncharacterized protein LOC724221 isoform 1 [Apis mellifera]
gene1 044	58.53595 719	33.94581 154	1.7243 94102	0.7860895 33	0.046 946	gi 733869626 ref XP_010708157. 1	PREDICTED: histone H3-like [Meleagris gallopavo]
gene4 760	61.93738 044	35.96915 12	1.7219 58355	0.7840502 52	0.045 671	gi 380024952 ref XP_003696250. 1	PREDICTED: transcription and mRNA export factor ENY2 [Apis florea]
gene3 838	228.0182 276	132.8743 782	1.7160 43609	0.7790862 16	0.031 991	gi 571525702 ref XP_006567356. 1	PREDICTED: uncharacterized protein LOC102654949 [Apis mellifera]
gene1	73.32726	42.76249	1.7147	0.7780037	0.034	gi 571508217 ref	PREDICTED: uncharacterized protein LOC551357 isoform X1 [Apis mellifera]

294	278	197	5654	58	907	XP_006571299.1	
gene2 309	146.4416 058	85.79326 133	1.7069 12682	0.7713892 58	0.042 146	gi 571515131 ref XP_006568941.1	PREDICTED: soma ferritin [Apis mellifera]
gene1 0274	1276.810 4	748.3118 383	1.7062 54445	0.7708328 05	0.000 994	gi 58585144 ref NP_001011598.1	alpha-amylase precursor [Apis mellifera]
gene1 434	252.6413 77	148.2108 179	1.7046 0821	0.7694401 86	0.013 995	gi 110766219 ref XP_001120479.1	PREDICTED: ribonuclease kappa-like [Apis mellifera]
gene2 279	72.27949 484	42.42015 139	1.7038 95259	0.7688366 54	0.023 574	gi 328789556 ref XP_003251294.1	PREDICTED: uncharacterized protein LOC100576118 isoform X1 [Apis mellifera]
gene1 484	80.96610 154	47.57380 305	1.7019 05174	0.7671506 55	0.016 207	gi 201023329 ref NP_001128406.1	GABA neurotransmitter transporter-1A [Apis mellifera]
gene6 81	129.7908 969	76.56575 205	1.6951 56038	0.7614180 79	0.021 704	gi 48138800 ref XP_396933.1	PREDICTED: cell death-related nuclease 6 isoform X1 [Apis mellifera]
gene1 1923	4183.135 548	2472.690 294	1.6917 34528	0.7585031 94	1.17E -05	gi 66526748 ref XP_624696.1	PREDICTED: 60S ribosomal protein L27a isoform X2 [Apis mellifera]
gene8 055	89.32091 513	52.96326 673	1.6864 69144	0.7540059 23	0.017 993	gi 571553698 ref XP_006565579.1	PREDICTED: uncharacterized protein LOC725578 isoform X1 [Apis mellifera]
gene6 61	119.4236 047	70.88404 328	1.6847 74164	0.7525552 18	0.012 82	gi 328788801 ref XP_001122217.1	PREDICTED: facilitated trehalose transporter Tret1-like [Apis mellifera]

						2	
gene1 0792	211.9464 421	126.4379 328	1.6762 88416	0.7452703 95	0.034 822	gi 328785089 ref XP_394000.3	PREDICTED: carotenoid isomeroxygenase isoform 1 [Apis mellifera]
gene7 304	2040.046 96	1225.067 773	1.6652 52327	0.7357407 98	0.001 374	gi 328781001 ref XP_393105.3	PREDICTED: circadian clock-controlled protein-like isoform 1 [Apis mellifera]
gene2 111	94.90833 311	57.01151 327	1.6647 22223	0.7352814 68	0.047 875	gi 571513290 ref XP_006565983. 1	PREDICTED: chaoptin-like, partial [Apis mellifera]
gene1 2883	6920.564 154	4169.694 29	1.6597 29388	0.7309480 36	0.000 406	gi 110768640 ref XP_001119842. 1	PREDICTED: uncharacterized protein LOC724114 isoform X1 [Apis mellifera]
gene1 1520	105.2494 48	63.46140 389	1.6584 79667	0.7298613 25	0.040 948	gi 571575360 ref XP_006563786. 1	PREDICTED: enteropeptidase-like [Apis mellifera]
gene2 686	310.5977 176	187.6978 287	1.6547 75229	0.7266352 67	0.005 278	gi 755959992 ref XP_011304587. 1	PREDICTED: 60S ribosomal protein L37a [Fopius arisanus]
gene1 627	63.63914 685	38.48005 969	1.6538 21417	0.7258034 58	0.039 18	gi 571510150 ref XP_006571692. 1	PREDICTED: HIG1 domain family member 1B-like [Apis mellifera]
gene3 840	113.6148 063	68.82044 416	1.6508 87432	0.7232417 51	0.012 887	gi 571525805 ref XP_006567379. 1	PREDICTED: alkylglycerol monooxygenase-like [Apis mellifera]
gene1 2219	1591.884 701	968.9893 872	1.6428 29862	0.7161830 76	0.000 137	gi 328793032 ref XP_003251816. 1	PREDICTED: uncharacterized protein LOC100578392 [Apis mellifera]

gene6 373	3424.826 568	2085.309 292	1.6423 59041	0.7157695 53	8.86E -05	gi 292494904 ref NP_001167614. 1	ribosomal protein L35 [Apis mellifera]
gene1 1062	182.7940 141	111.3789 45	1.6411 9003	0.7147422 95	0.008 318	gi 328778021 ref XP_395665.4	PREDICTED: protein brown [Apis mellifera]
gene5 460	162.9473 969	100.0187 726	1.6291 68133	0.7041355	0.043 331	gi 328791967 ref XP_392873.4	PREDICTED: intraflagellar transport protein 74 homolog [Apis mellifera]
gene6 780	506.6409 439	312.6918 118	1.6202 56511	0.6962222 31	0.032 521	gi 110758964 ref XP_001121327. 1	PREDICTED: regucalcin-like [Apis mellifera]
gene3 264	16162.91 477	9983.251 26	1.6190 03103	0.6951057 51	0.004 329	.	.
gene4 622	610.2399 838	377.7869 068	1.6153 021	0.6918040 08	0.015 633	gi 66509585 ref XP_395132.2	PREDICTED: uncharacterized protein LOC411664 isoform X2 [Apis mellifera]
gene6 926	3682.461 504	2281.697 634	1.6139 13013	0.6905628 22	2.32E -05	gi 48142237 ref XP_397314.1	PREDICTED: 60S ribosomal protein L31 isoform 2 [Apis mellifera]
gene1 2255	2214.706 449	1372.287 447	1.6138 79405	0.6905327 79	0.038 978	gi 66558893 ref XP_623595.1	PREDICTED: probable cytochrome P450 6a14 [Apis mellifera]
gene3 735	1085.352 191	673.4438 002	1.6116 44788	0.6885338 04	0.000 325	gi 322788733 gb EFZ14326.1	hypothetical protein SINV_15101, partial [Solenopsis invicta]
gene6 981	70.03160 562	43.58984 274	1.6066 03769	0.6840141 66	0.043 748	gi 328789207 ref XP_395655.4	PREDICTED: jmjC domain-containing protein 4-like isoform 1 [Apis mellifera]
gene7 961	140.6766 141	87.65630 87	1.6048 65824	0.6824526 85	0.015 444	gi 571553130 ref XP_006562937. 1	PREDICTED: uncharacterized protein LOC102656803 [Apis mellifera]
gene1	848.5324	528.8873	1.6043	0.6820094	0.001	gi 66552169 ref	PREDICTED: 60S ribosomal protein L28 [Apis mellifera]

2807	418	265	72802	14	07	XP_625152.1	
gene1 0089	91.37530 037	57.07505 397	1.6009 67393	0.6789439 25	0.025 45	gi 571567042 ref XP_393912.3	PREDICTED: L-threonine 3-dehydrogenase, mitochondrial-like [Apis mellifera]
gene1 1122	270.8088 802	169.5725 443	1.5970 09005	0.6753724 47	0.005 843	gi 572261912 ref XP_006609229. 1	PREDICTED: ABC transporter F family member 4-like isoform X1 [Apis dorsata]
gene1 0156	181.7887 897	113.9685 764	1.5950 78183	0.6736271 4	0.007 145	gi 571568097 ref XP_006560490. 1	PREDICTED: fumarylacetoacetase [Apis mellifera]
gene1 0050	208.8176 948	131.0258 685	1.5937 13495	0.6723922 96	0.019 776	gi 571566849 ref XP_006558585. 1	PREDICTED: G patch domain-containing protein 4-like [Apis mellifera]
gene1 2212	144.3213 196	90.58885 643	1.5931 465	0.6718789 38	0.025 308	.	.
gene4 740	151.8323 459	95.35135 134	1.5923 46031	0.6711538 81	0.021 231	gi 380025726 ref XP_003696619. 1	PREDICTED: adenosine 3'-phospho 5'-phosphosulfate transporter 1-like [Apis florea]
gene1 1955	4973.884 95	3124.167 14	1.5920 67494	0.6709014 99	3.51E -05	gi 571576123 ref XP_624943.3	PREDICTED: 40S ribosomal protein S7 [Apis mellifera]
gene7 309	712.4011 865	447.4915 237	1.5919 88113	0.6708295 64	0.001 033	gi 110766380 ref XP_001122696. 1	PREDICTED: protein takeout-like [Apis mellifera]
gene3 723	1213.706 297	764.3367 455	1.5879 20905	0.6671390 53	0.002 861	gi 571525079 ref XP_392316.4	PREDICTED: protein-L-isoaspartate(D-aspartate) O-methyltransferase-like isoform X5 [Apis mellifera]
gene5 581	4812.736 391	3047.206 045	1.5793 93162	0.6593703 49	0.001 138	gi 48105889 ref XP_393034.1	PREDICTED: 60S ribosomal protein L7a [Apis mellifera]

gene1 769	236.4629 791	150.3283 505	1.5729 76609	0.6534972 17	0.029 966	gi 571511216 ref XP_006559166. 1	PREDICTED: putative leucine-rich repeat-containing protein DDB_G0290503-like isoform X1 [Apis mellifera]
gene1 2935	374.8107 307	238.7255 692	1.5700 48538	0.6508091 6	0.001 416	gi 571578681 ref XP_001123051. 2	PREDICTED: glutamine synthetase 2 cytoplasmic-like, partial [Apis mellifera]
gene7 353	4860.177 505	3095.711 634	1.5699 71005	0.6507379 15	0.000 286	gi 571547971 ref XP_006561561. 1	PREDICTED: 40S ribosomal protein S8 isoform X1 [Apis mellifera]
gene1 2523	508.7198 806	324.2436 817	1.5689 4308	0.6497930 13	0.002 279	gi 110773426 ref XP_001119845. 1	PREDICTED: stress-associated endoplasmic reticulum protein 2-like [Apis mellifera]
gene1 0910	1045.058 07	667.1882 344	1.5663 61659	0.6474173 57	0.000 782	gi 110762954 ref XP_001121176. 1	PREDICTED: 60S ribosomal protein L34 isoformX1 [Apis mellifera]
gene6 927	289.4316 39	185.0682 429	1.5639 18447	0.6451652 83	0.004 629	gi 66514688 ref XP_624939.1	PREDICTED: protein phosphatase 1 regulatory subunit 14C-like isoform X3 [Apis mellifera]
gene6 628	172.4100 579	110.3308 537	1.5626 64043	0.6440076 47	0.023 817	gi 328783839 ref XP_395385.3	PREDICTED: 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial-like isoform X3 [Apis mellifera]
gene6 75	228.6949 349	146.6946 01	1.5589 8672	0.6406086 39	0.006 562	gi 110765976 ref XP_623942.2	PREDICTED: BAG family molecular chaperone regulator 2-like [Apis mellifera]
gene7 830	4771.016 851	3062.029 695	1.5581 22333	0.6398085 08	0.000 392	gi 572268139 ref XP_006612127. 1	PREDICTED: 60S acidic ribosomal protein P0-like [Apis dorsata]
gene1 2536	112.1575 481	72.01196 702	1.5574 84856	0.6392181 35	0.030 947	gi 110769776 ref XP_001123277.	PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1-like [Apis mellifera]

						1	
gene8 178	3302.244 223	2120.849 01	1.5570 38812	0.6388049 07	0.000 388	gi 297591983 ref NP_001172073. 1	60S acidic ribosomal protein P1 [Apis mellifera]
gene5 501	2407.637 324	1549.273 432	1.5540 42866	0.6360262 99	0.000 513	gi 48104663 ref XP_392962.1	PREDICTED: receptor of activated protein kinase C 1 isoformX1 [Apis mellifera]
gene5 872	205.6179 247	132.3768 627	1.5532 76914	0.6353150 52	0.014 82	gi 383855926 ref XP_003703461. 1	PREDICTED: 60S ribosomal protein L29-1 [Megachile rotundata]
gene6 733	214.1447 796	137.9364 547	1.5524 88645	0.6345827 16	0.011 467	gi 66514532 ref XP_624335.1	PREDICTED: guanine nucleotide-binding protein subunit beta-2-like [Apis mellifera]
gene4 916	208.6058 852	134.5900 447	1.5499 35477	0.6322081 58	0.022 409	gi 328780683 ref XP_001121779. 2	PREDICTED: UDP-glucuronosyltransferase 2C1-like [Apis mellifera]
gene1 0905	795.9347 489	513.7851 316	1.5491 58782	0.6314850 22	0.001 858	gi 571572991 ref XP_006565801. 1	PREDICTED: ATP synthase subunit d, mitochondrial [Apis mellifera]
gene1 1421	4588.458 448	2962.781 73	1.5486 99454	0.6310571 97	0.000 268	gi 66525285 ref XP_392071.2	PREDICTED: 60S ribosomal protein L4 isoform 1 [Apis mellifera]
gene1 0316	1107.689 082	715.3997 65	1.5483 49798	0.6307314 38	0.000 873	gi 571568772 ref XP_006565136. 1	PREDICTED: uncharacterized protein LOC724946 [Apis mellifera]
gene5 578	538.5641 202	348.0574 701	1.5473 42512	0.6297925 8	0.023 084	gi 66547599 ref XP_623499.1	PREDICTED: selection and upkeep of intraepithelial T-cells protein 2-like [Apis mellifera]
gene1 2634	2229.472 419	1445.390 181	1.5424 70987	0.6252433 54	0.001 234	gi 380023818 ref XP_003695708.	PREDICTED: 60S ribosomal protein L12 [Apis florea]

						1	
gene1 59	6613.180 983	4288.531 006	1.5420 62066	0.6248608 33	0.000 635	gi 110767080 ref XP_001120419. 1	PREDICTED: 40S ribosomal protein S6-like [Apis mellifera]
gene8 665	100.8168 581	65.39677 75	1.5416 18134	0.6244454 47	0.036 965	gi 571557896 ref XP_006559087. 1	PREDICTED: uncharacterized protein LOC551609 [Apis mellifera]
gene4 123	2453.098 591	1595.197 363	1.5378 02562	0.6208702 88	0.000 481	gi 572272221 ref XP_006614024. 1	PREDICTED: 40S ribosomal protein S11-like isoform X1 [Apis dorsata]
gene1 2761	512.9703 758	333.9740 527	1.5359 58772	0.6191394 92	0.002 126	gi 572316891 ref XP_006624058. 1	PREDICTED: opsin, ultraviolet-sensitive-like [Apis dorsata]
gene3 15	210.9857 635	137.5455 267	1.5339 34025	0.6172364 33	0.009 767	gi 571501317 ref XP_006562598. 1	PREDICTED: eyes absent homolog 4 isoform X1 [Apis mellifera]
gene1 0549	6640.047 713	4334.924 239	1.5317 56346	0.6151868 29	0.000 668	gi 66524293 ref XP_393965.2	PREDICTED: 40S ribosomal protein SA [Apis mellifera]
gene9 835	3515.794 923	2295.783 193	1.5314 14174	0.6148645 15	0.030 337	gi 571565205 ref XP_006566903. 1	PREDICTED: cytochrome P450 6AQ1 isoform X1 [Apis mellifera]
gene5 558	150.9899 175	98.80574 639	1.5281 49151	0.6117853 61	0.022 225	gi 328791922 ref XP_395661.4	PREDICTED: transcriptional adapter 1-like isoform 1 [Apis mellifera]
gene7 95	2379.977 355	1558.660 928	1.5269 37201	0.6106407 29	0.000 95	gi 805784468 ref XP_003703131. 2	PREDICTED: 60S ribosomal protein L9 [Megachile rotundata]

gene3 323	134.6853 094	88.39353 334	1.5237 00935	0.6075797 65	0.036 614	gi 571522164 ref XP_623316.3	PREDICTED: cell division cycle protein 16 homolog isoform X2 [Apis mellifera]
gene1 560	109.3595 296	71.81670 235	1.5227 58996	0.6066876 27	0.049 548	gi 118150500 ref NP_001071287. 1	chemosensory protein 6 precursor [Apis mellifera]
gene1 0647	5327.139 446	3504.063 774	1.5202 74684	0.6043320 14	0.000 892	gi 66551967 ref XP_624896.1	PREDICTED: 60S ribosomal protein L13 isoform 1 [Apis mellifera]
gene1 0797	2393.566 045	1575.001 743	1.5197 22791	0.6038081 89	0.001 877	gi 110762813 ref XP_625009.2	PREDICTED: 60S ribosomal protein L22 isoform 1 [Apis mellifera]
gene3 414	3586.784 712	2368.188 378	1.5145 69004	0.5989073 09	0.002 158	gi 156554296 ref XP_001602465. 1	PREDICTED: 40S ribosomal protein S14 [Nasonia vitripennis]
gene3 87	2204.721 783	1459.620 292	1.5104 76248	0.5950034 98	0.000 74	gi 571501696 ref XP_006563278. 1	PREDICTED: 60S ribosomal protein L10a [Apis mellifera]
gene1 1506	377.0098 466	249.9222 387	1.5085 08601	0.5931229 22	0.007 848	gi 66525117 ref XP_625185.1	PREDICTED: prefoldin subunit 6-like isoform X2 [Apis mellifera]
gene2 03	546.6532 49	362.5128 886	1.5079 55348	0.5925937 1	0.004 989	gi 572272330 ref XP_006614075. 1	PREDICTED: uncharacterized protein LOC102676956 [Apis dorsata]
gene5 557	370.7927 7	246.3909 339	1.5048 96159	0.5896639 41	0.006 421	gi 66564836 ref XP_624899.1	PREDICTED: AP-3 complex subunit mu-1-like isoform X2 [Apis mellifera]
gene7 437	368.7736 118	245.1387 924	1.5043 46204	0.5891366 21	0.010 134	gi 571549345 ref XP_006561839. 1	PREDICTED: probable elongation factor 1-delta isoform X1 [Apis mellifera]
gene5	1736.076	1154.644	1.5035	0.5883813	0.008	gi 58585214 ref	FABP-like protein [Apis mellifera]

01	667	95	5888	65	493	NP_001011636.1	
gene3 500	3250.027 054	2162.707 953	1.5027 58174	0.5876128 67	0.001 585	gi 571523338 ref XP_006562063.1	PREDICTED: ribosome biogenesis protein NSA2 homolog isoform X1 [Apis mellifera]
gene7 763	5586.913 719	3718.362 951	1.5025 19736	0.5873839 41	0.001 188	gi 571551848 ref XP_006560185.1	PREDICTED: peroxisomal hydratase-dehydrogenase-epimerase-like [Apis mellifera]
gene7 324	2895.001 686	1927.235 422	1.5021 52592	0.5870313 73	0.001 351	gi 571548748 ref XP_006561728.1	PREDICTED: 60S ribosomal protein L35a isoform X1 [Apis mellifera]
gene2 92	5213.762 025	3472.328 928	1.5015 1732	0.5864211 16	0.000 959	gi 350404704 ref XP_003487192.1	PREDICTED: 40S ribosomal protein S17 [Bombus impatiens]
gene7 079	223.7018 804	149.0716 845	1.5006 32941	0.5855711 33	0.017 671	gi 328790583 ref XP_624669.3	PREDICTED: serine/threonine-protein phosphatase 4 catalytic subunit B-like, partial [Apis mellifera]
gene8 922	1257.721 632	1889.859 54	0.6655 1064	-0.5874663 63	0.001 647	gi 328787292 ref XP_003250919.1	PREDICTED: LOW QUALITY PROTEIN: ral guanine nucleotide dissociation stimulator [Apis mellifera]
gene2 241	1260.805 484	1897.689 482	0.6643 89773	-0.5898982 3	0.007 999	gi 572313600 ref XP_006622495.1	PREDICTED: retinal-specific ATP-binding cassette transporter-like [Apis dorsata]
gene6 631	696.7102 089	1048.727 575	0.6643 386	-0.5900093 53	0.017 337	gi 571544325 ref XP_006563880.1	PREDICTED: plasma membrane calcium-transporting ATPase 3 isoform X3 [Apis mellifera]
gene9	385.8362	581.4370	0.6635	-0.5916341	0.027	gi 571563105 ref	PREDICTED: dynein heavy chain 7, axonemal-like [Apis mellifera]

337	693	111	90831	43	38	XP_006570553.1	
gene5 589	208.6096 514	314.3808 929	0.6635 57029	-0.5917076 32	0.019 658	gi 571536790 ref XP_006571000.1	PREDICTED: LON peptidase N-terminal domain and RING finger protein 3-like isoform X1 [Apis mellifera]
gene7 736	605.8484 711	913.8552 149	0.6629 58925	-0.5930086 06	0.006 1	gi 571551614 ref XP_006559285.1	PREDICTED: SNF-related serine/threonine-protein kinase-like [Apis mellifera]
gene2 453	2119.286 37	3200.208 476	0.6622 33847	-0.5945873 45	0.013 316	gi 571514351 ref XP_006568803.1	PREDICTED: uncharacterized protein LOC410793 [Apis mellifera]
gene1 0937	744.5965 592	1124.502 932	0.6621 56174	-0.5947565 68	0.017 533	gi 571573081 ref XP_006565834.1	PREDICTED: transcription factor Sp1-like [Apis mellifera]
gene5 720	508.9623 143	769.4301 774	0.6614 79533	-0.5962315 77	0.008 766	gi 328777755 ref XP_396693.2	PREDICTED: carboxylesterase 5A [Apis mellifera]
gene1 1518	973.7595 348	1472.114 539	0.6614 69953	-0.5962524 71	0.006 147	gi 571574799 ref XP_006563582.1	PREDICTED: STE20-like serine/threonine-protein kinase-like isoform X1 [Apis mellifera]
gene1 601	533.5376 994	806.8457 359	0.6612 6358	-0.5967026 51	0.015 182	gi 571510304 ref XP_006571710.1	PREDICTED: short spindle protein 4 isoform X1 [Apis mellifera]
gene1 228	36762.01 204	55614.13 429	0.6610 19227	-0.5972358 6	0.002 89	gi 571507693 ref XP_006571189.1	PREDICTED: titin-like isoform X1 [Apis mellifera]
gene7	2027.470	3069.567	0.6605	-0.5983547	0.012	gi 328781112 ref	PREDICTED: leukocyte receptor cluster member 8 homolog isoform X1 [Apis

387	269	713	06774	37	592	XP_001121422.2	mellifera]
gene6 17	3034.557 521	4596.369 716	0.6602 07448	-0.5990086 8	0.003 329	gi 380027719 ref XP_003697566.1	PREDICTED: 3-phosphoinositide-dependent protein kinase 1 isoform X1 [Apis florea]
gene9 638	1123.906 313	1702.936 543	0.6599 81323	-0.5995028 97	0.002 223	gi 571564323 ref XP_006562313.1	PREDICTED: metalloproteinase inhibitor 3-like isoform X2 [Apis mellifera]
gene4 103	743.3420 354	1127.512 202	0.6592 76267	-0.6010449 48	0.005 713	gi 571527866 ref XP_006562261.1	PREDICTED: putative leucine-rich repeat-containing protein DDB_G0290503-like [Apis mellifera]
gene3 287	236.8097 03	359.7960 822	0.6581 77548	-0.6034512 82	0.015 084	gi 571521962 ref XP_006558737.1	PREDICTED: POU domain, class 2, transcription factor 1-like isoform X2 [Apis mellifera]
gene3 055	145.2674 98	220.9723 452	0.6574 01259	-0.6051538 74	0.037 812	gi 861649330 gb KMQ96764.1	hypothetical protein RF55_2936, partial [Lasius niger]
gene1 317	1113.354 915	1694.109 271	0.6571 91914	-0.6056133 65	0.002 624	gi 571508489 ref XP_006571351.1	PREDICTED: actin-binding LIM protein 2-like isoform X2 [Apis mellifera]
gene4 669	303.3761 928	461.6768 516	0.6571 18051	-0.6057755 22	0.005 701	gi 301601654 ref NP_001013377.2	venom acid phosphatase AcpH-1 precursor [Apis mellifera]
gene1 1283	279.7410 828	425.8461 851	0.6569 06396	-0.6062402 82	0.022 387	gi 328780356 ref XP_624636.3	PREDICTED: serine/arginine repetitive matrix protein 2-like isoformX2 [Apis mellifera]
gene1 139	2125.234 073	3236.130 269	0.6567 20804	-0.6066479 36	0.005 314	gi 571506210 ref XP_006570777.	PREDICTED: apoptosis 2 inhibitor-like [Apis mellifera]

						1	
gene9 274	1495.522 346	2278.895 388	0.6562 48792	-0.6076852 32	0.002 727	gi 66519258 ref XP_625210.1	PREDICTED: glycine N-methyltransferase-like [Apis mellifera]
gene5 244	329.0128 635	502.0608 797	0.6553 24637	-0.6097183 25	0.022 638	gi 571534392 ref XP_006565398. 1	PREDICTED: uncharacterized protein LOC100577669 isoform X2 [Apis mellifera]
gene1 51	738.4531 787	1128.155 878	0.6545 66619	-0.6113880 65	0.009 483	gi 571500407 ref XP_006559949. 1	PREDICTED: protein muscleblind-like [Apis mellifera]
gene1 0984	1126.669 035	1722.070 033	0.6542 52739	-0.6120800 37	0.009 733	gi 571573297 ref XP_006558002. 1	PREDICTED: histone-lysine N-methyltransferase 2C [Apis mellifera]
gene4 169	89.01634 454	136.1354 228	0.6538 8084	-0.6129003 46	0.036 949	gi 571527928 ref XP_006564221. 1	PREDICTED: estradiol 17-beta-dehydrogenase 2 [Apis mellifera]
gene9 757	247.2242 566	378.1922 026	0.6537 00036	-0.6132993 18	0.026 58	gi 571564875 ref XP_006565275. 1	PREDICTED: myelin regulatory factor-like isoform X1 [Apis mellifera]
gene2 671	104.0874 874	159.4890 74	0.6526 30834	-0.6156609 44	0.037 144	gi 48095402 ref XP_392288.1	PREDICTED: TNF receptor-associated factor 4-like isoform X4 [Apis mellifera]
gene8 689	549.5118 987	842.7640 115	0.6520 35316	-0.6169779 88	0.030 695	gi 571557908 ref XP_006559090. 1	PREDICTED: anion exchange protein 2-like [Apis mellifera]
gene6 347	190.3543 911	292.0276 264	0.6518 36929	-0.6174170 07	0.033 644	gi 328777846 ref XP_395849.4	PREDICTED: transient receptor potential cation channel trpm isoform X10 [Apis mellifera]
gene8	643.9774	988.2161	0.6516	-0.6178165	0.007	gi 571557888 ref	PREDICTED: serine/threonine-protein kinase N [Apis mellifera]

590	264	718	56434	47	631	XP_006559086.1	
gene2 113	1180.002 995	1811.574 578	0.6513 68709	-0.6184536 78	0.002 875	gi 328786226 ref XP_392617.4	PREDICTED: neurotrimin [Apis mellifera]
gene1 1918	930.8721 797	1433.029 81	0.6495 83263	-0.6224136 35	0.006 096	gi 571576060 ref XP_006559482.1	PREDICTED: protein sprouty, partial [Apis mellifera]
gene8 760	1301.985 088	2004.762 925	0.6494 45913	-0.6227187 15	0.001 89	gi 571558282 ref XP_006563373.1	PREDICTED: uncharacterized protein LOC412215 isoform X1 [Apis mellifera]
gene9 813	319.1079 968	491.3766 104	0.6494 16334	-0.6227844 24	0.008 513	gi 328785548 ref XP_003250614.1	PREDICTED: uncharacterized protein LOC100576266 isoform X1 [Apis mellifera]
gene1 342	991.8351 702	1527.884 322	0.6491 55931	-0.6233630 31	0.007 096	gi 571508634 ref XP_006571379.1	PREDICTED: LOW QUALITY PROTEIN: endoribonuclease Dicer-like [Apis mellifera]
gene1 135	206.7467 424	318.7626 945	0.6485 914	-0.6246182	0.008 32	gi 571506988 ref XP_006570927.1	PREDICTED: uncharacterized protein LOC411996 [Apis mellifera]
gene8 482	120.4238 029	185.8702 875	0.6478 91627	-0.6261755 83	0.029 855	gi 571556504 ref XP_003249116.2	PREDICTED: dentin sialophosphoprotein-like isoform X1 [Apis mellifera]
gene3 884	419.9787 278	648.8468 691	0.6472 69406	-0.6275617 79	0.008 279	gi 571526129 ref XP_006569380.1	PREDICTED: focal adhesion kinase 1 isoform X1 [Apis mellifera]
gene1	139.2713	215.4316	0.6464	-0.6293312	0.018	gi 328782396 ref	PREDICTED: uncharacterized protein LOC412825 isoform X2 [Apis mellifera]

1331	628	036	76007	68	388	XP_396277.4	
gene2 978	709.9991 47	1098.639 27	0.6462 53203	-0.6298285 69	0.027 198	gi 328787394 ref XP_001120785. 2	PREDICTED: zinc finger protein 704-like isoform X1 [Apis mellifera]
gene1 1974	99.80772 077	154.9822 329	0.6439 94598	-0.6348795 09	0.044 001	gi 328780859 ref XP_623612.3	PREDICTED: uncharacterized protein LOC551214 [Apis mellifera]
gene1 451	992.1353 899	1543.807 685	0.6426 54781	-0.6378841 31	0.004 004	gi 820854688 ref XP_012344633. 1	PREDICTED: sarcoplasmic reticulum histidine-rich calcium-binding protein-like [Apis florea]
gene9 992	370.4742 15	576.9541 378	0.6421 20735	-0.6390835 09	0.011 378	gi 571566328 ref XP_006557910. 1	PREDICTED: probable serine/threonine-protein kinase CG32666-like isoform X1 [Apis mellifera]
gene4 099	421.2642 988	656.1754 337	0.6419 99498	-0.6393559 26	0.003 739	gi 571527860 ref XP_006562260. 1	PREDICTED: putative leucine-rich repeat-containing protein DDB_G0290503-like [Apis mellifera]
gene2 765	400.1117 635	623.6461 057	0.6415 68607	-0.6403245 44	0.003 744	gi 572300533 ref XP_006616356. 1	PREDICTED: guanylate cyclase 32E-like [Apis dorsata]
gene3 605	373.3388 511	582.4810 282	0.6409 45942	-0.6417254 12	0.034 388	gi 571523965 ref XP_006562759. 1	PREDICTED: rap guanine nucleotide exchange factor 6-like isoform X5 [Apis mellifera]
gene3 639	888.7253 551	1386.782 416	0.6408 54214	-0.6419318 95	0.025 267	gi 328785371 ref XP_001121634. 2	PREDICTED: beta-1,3-glucan-binding protein [Apis mellifera]
gene1 0139	163.6633 409	255.4125 379	0.6407 80372	-0.6420981 39	0.041 345	gi 571567534 ref XP_006560383.	PREDICTED: uncharacterized protein LOC410462 [Apis mellifera]

						1	
gene1 017	230.9547 054	361.3424 517	0.6391 5741	-0.6457568 18	0.030 7	gi 571506073 ref XP_006570707. 1	PREDICTED: myogenic-determination protein [Apis mellifera]
gene6 481	231.4456 644	362.3720 395	0.6386 96255	-0.6467981 05	0.020 154	gi 571543074 ref XP_392487.4	PREDICTED: uncharacterized protein C20orf1 12 homolog isoform X3 [Apis mellifera]
gene2 167	1609.150 936	2521.328 659	0.6382 15462	-0.6478845 33	0.002 763	gi 328788856 ref XP_003251195. 1	PREDICTED: uncharacterized protein LOC410867 [Apis mellifera]
gene8 102	14585.81 003	22867.27 822	0.6378 46353	-0.6487191 5	0.023 674	gi 571555466 ref XP_006566278. 1	PREDICTED: lorocrin-like isoform X1 [Apis mellifera]
gene7 68	1630.065 966	2562.125 116	0.6362 1638	-0.6524105 79	0.003 778	gi 571503986 ref XP_006568691. 1	PREDICTED: triple functional domain protein isoform X1 [Apis mellifera]
gene9 842	3410.973 436	5365.197 228	0.6357 59188	-0.6534476 87	0.000 341	gi 328787572 ref XP_393878.3	PREDICTED: IGF-II mRNA-binding protein isoform X4 [Apis mellifera]
gene6 686	147.8046 081	232.6498 4	0.6353 09305	-0.6544689 46	0.012 271	gi 66514147 ref XP_396290.2	PREDICTED: alpha-mannosidase 2 isoform X5 [Apis mellifera]
gene1 472	2314.129 305	3645.182 416	0.6348 45953	-0.6555215 34	0.003 05	gi 48094759 ref XP_392183.1	PREDICTED: quinone oxidoreductase-like isoformX1 [Apis mellifera]
gene3 047	243.4078 469	383.5271 4	0.6346 56121	-0.6559529 95	0.003 119	gi 48095262 ref XP_394396.1	PREDICTED: putative inorganic phosphate cotransporter-like isoform X2 [Apis mellifera]
gene6 910	580.1977 958	914.2378 647	0.6346 24552	-0.6560247 57	0.003 506	gi 66555130 ref XP_394934.2	PREDICTED: sterol regulatory element-binding protein cleavage-activating protein-like isoform X5 [Apis mellifera]
gene1	196.5258	309.6814	0.6346	-0.6560658	0.022	gi 571568747 ref	PREDICTED: putative polypeptide N-acetylgalactosaminyltransferase 9-like isoform

0269	321	049	06499		169	XP_006565129.1	X1 [Apis mellifera]
gene3 702	238.6390 384	376.5313 923	0.6337 82583	-0.6579400 82	0.008 501	gi 571524982 ref XP_392312.3	PREDICTED: signal-induced proliferation-associated 1-like protein 2-like isoform X3 [Apis mellifera]
gene1 166	1611.667 51	2543.790 164	0.6335 69361	-0.6584255 25	0.004 672	gi 571507165 ref XP_006571083.1	PREDICTED: calponin homology domain-containing protein DDB_G0272472-like isoform X1 [Apis mellifera]
gene9 071	2739.972 881	4326.543 743	0.6332 93697	-0.6590533 75	0.023 743	gi 571560383 ref XP_006566549.1	PREDICTED: ataxin-2 homolog isoform X2 [Apis mellifera]
gene1 1309	222.1247 696	350.7890 256	0.6332 14706	-0.6592333 34	0.009 07	gi 66547762 ref XP_395162.2	PREDICTED: E3 ubiquitin-protein ligase KCMF1-like isoform X2 [Apis mellifera]
gene1 1476	152.5791 903	241.4160 78	0.6320 17518	-0.6619635 49	0.027 074	.	.
gene4 884	165.9914 729	263.6013 762	0.6297 06397	-0.6672487 72	0.012 946	gi 571532845 ref XP_006560108.1	PREDICTED: dynein heavy chain 5, axonemal [Apis mellifera]
gene6 337	319.9521 158	508.1625 498	0.6296 25532	-0.6674340 5	0.019 576	gi 328777836 ref XP_397383.3	PREDICTED: myocyte-specific enhancer factor 2 isoform X6 [Apis mellifera]
gene6 461	125.4262 07	199.3830 756	0.6290 71483	-0.6687041 32	0.047 356	gi 571542912 ref XP_006559626.1	PREDICTED: protein SMG9-like [Apis mellifera]
gene2 362	285.9674 696	456.1506 057	0.6269 14589	-0.6736591 91	0.009 382	gi 66557637 ref XP_395638.2	PREDICTED: SH3 domain-containing RING finger protein 3 isoformX2 [Apis mellifera]
gene4 360	1484.316 847	2371.109 793	0.6260 00893	-0.6757633 81	0.000 762	gi 328788553 ref XP_392382.4	PREDICTED: protein similar-like [Apis mellifera]

gene1 779	597.7658 412	955.5302 369	0.6255 85479	-0.6767210 69	0.003 902	gi 571511127 ref XP_006559148. 1	PREDICTED: ALK tyrosine kinase receptor-like isoform X1 [Apis mellifera]
gene8 110	879.6185 029	1406.161 808	0.6255 45722	-0.6768127 58	0.001 491	gi 571555411 ref XP_006566271. 1	PREDICTED: RNA-binding protein 24-like isoform X3 [Apis mellifera]
gene7 438	993.4827 362	1589.249 13	0.6251 27123	-0.6777784 96	0.001 275	gi 571549403 ref XP_006561854. 1	PREDICTED: solute carrier organic anion transporter family member 5A1-like isoform X1 [Apis mellifera]
gene4 782	227.0690 198	363.8224 03	0.6241 20499	-0.6801034 97	0.022 237	gi 571531755 ref XP_006570259. 1	PREDICTED: lutropin-choriogonadotropic hormone receptor-like isoform X2 [Apis mellifera]
gene2 015	182.5369 452	292.6248 582	0.6237 91657	-0.6808638 38	0.010 76	gi 571512920 ref XP_006565932. 1	PREDICTED: dihydropyrimidinase-like isoform X2 [Apis mellifera]
gene3 659	12445.81 341	19966.66 673	0.6233 29551	-0.6819329 84	0.000 657	gi 571524355 ref XP_006566009. 1	PREDICTED: microtubule-associated protein futsch [Apis mellifera]
gene1 062	263.0838 868	422.1214 878	0.6232 4211	-0.6821353 81	0.011 145	gi 571506745 ref XP_006570883. 1	PREDICTED: shootin-1-like isoform X1 [Apis mellifera]
gene1 0306	309.6483 173	496.8460 343	0.6232 27914	-0.6821682 44	0.034 398	gi 48105753 ref XP_395996.1	PREDICTED: long-chain-fatty-acid--CoA ligase 6-like isoform X5 [Apis mellifera]
gene1 492	472.6985 722	759.2866 228	0.6225 56171	-0.6837240 84	0.011 794	gi 571509864 ref XP_006571637. 1	PREDICTED: serine protease snake isoform X2 [Apis mellifera]

gene1 0793	412.7201 068	663.2559 784	0.6222 63681	-0.6844020 5	0.012 998	gi 328785091 ref XP_392015.3	PREDICTED: chloride channel protein 2-like isoform X5 [Apis mellifera]
gene2 647	748.1476 116	1204.593 328	0.6210 78993	-0.6871513 23	0.028 392	gi 328778864 ref XP_397465.4	PREDICTED: ATP-binding cassette sub-family A member 2-like isoform X2 [Apis mellifera]
gene5 083	753.2765 479	1212.884 917	0.6210 61848	-0.6871911 49	0.000 612	gi 820849087 ref XP_012342290. 1	PREDICTED: protein fem-1 homolog CG6966 isoform X1 [Apis florea]
gene6 694	321.2426 928	517.4803 033	0.6207 82454	-0.6878403 13	0.008 905	gi 571544009 ref XP_006563828. 1	PREDICTED: forkhead box protein I1-like isoform X1 [Apis mellifera]
gene8 608	93.95164 715	151.3934 962	0.6205 7915	-0.6883128 69	0.013 545	gi 571557367 ref XP_006559002. 1	PREDICTED: homeobox protein caupolican isoform X1 [Apis mellifera]
gene8 965	535.4672 792	864.5323 06	0.6193 72203	-0.6911214 57	0.001 139	gi 328786814 ref XP_391908.4	PREDICTED: RB1-inducible coiled-coil protein 1 isoform X3 [Apis mellifera]
gene8 175	578.8175 925	935.6506 948	0.6186 25728	-0.6928612 59	0.005 85	gi 571555016 ref XP_006566205. 1	PREDICTED: serine/threonine-protein kinase mig-15 isoform X1 [Apis mellifera]
gene6 564	792.0705 929	1280.728 85	0.6184 52995	-0.6932641 47	0.001 607	gi 571543610 ref XP_006561489. 1	PREDICTED: protein unc-13 homolog D isoform X1 [Apis mellifera]
gene1 1549	265.2728 322	429.0484 764	0.6182 81725	-0.6936637 31	0.015 935	gi 571574890 ref XP_006563617. 1	PREDICTED: atrial natriuretic peptide receptor 1-like isoform X1 [Apis mellifera]
gene6 58	371.7259 21	601.3951 999	0.6181 059	-0.6940740 6	0.002 041	gi 328788793 ref XP_396802.3	PREDICTED: ubiquitin carboxyl-terminal hydrolase 31-like isoform 1 [Apis mellifera]

gene3 755	185.5576 605	300.2353 322	0.6180 40719	-0.6942262 04	0.044 007	gi 571524747 ref XP_006567170. 1	PREDICTED: NF-kappa-B inhibitor cactus 1 isoform X1 [Apis mellifera]
gene1 637	101.0548 568	163.7289 17	0.6172 08363	-0.6961704 85	0.035 418	gi 328792845 ref XP_393414.4	PREDICTED: leishmanolysin-like peptidase [Apis mellifera]
gene5 650	551.5399 004	896.6670 204	0.6151 00018	-0.7011070 77	0.020 003	gi 571537270 ref XP_006557373. 1	PREDICTED: dentin sialophosphoprotein-like isoform X1 [Apis mellifera]
gene1 161	1046.258 023	1701.806 552	0.6147 9257	-0.7018283 66	0.040 891	gi 328792136 ref XP_397003.4	PREDICTED: uncharacterized protein R02F2.2-like isoform X5 [Apis mellifera]
gene1 2102	215.5989 798	351.0136 041	0.6142 18302	-0.7031765 94	0.010 742	gi 571576575 ref XP_006563214. 1	PREDICTED: uncharacterized protein LOC724469 isoform X1 [Apis mellifera]
gene3 261	51.35972 251	83.62975 91	0.6141 32135	-0.703379	0.037 528	gi 571521847 ref XP_006558249. 1	PREDICTED: uncharacterized protein LOC100576135 [Apis mellifera]
gene9 471	320.1715 281	521.5858 046	0.6138 42488	-0.7040595 87	0.023 819	gi 571563474 ref XP_006558394. 1	PREDICTED: uncharacterized protein LOC725246 [Apis mellifera]
gene9 913	405.4579 153	660.8610 95	0.6135 29709	-0.7047948 9	0.016 983	gi 571565878 ref XP_006567026. 1	PREDICTED: tolkin isoform X1 [Apis mellifera]
gene9 160	258.9864	422.3264 113	0.6132 37517	-0.7054821 32	0.013 645	.	.
gene9 918	50.16886 892	81.85240 702	0.6129 18676	-0.7062324 3	0.038 787	gi 571565909 ref XP_006567030.	PREDICTED: protein tracheless-like isoform X1 [Apis mellifera]

						1	
gene1 1752	447.3820 239	730.8174 613	0.6121 66577	-0.7080038 15	0.004 821	gi 571575649 ref XP_006557820. 1	PREDICTED: mitogen-activated protein kinase-binding protein 1-like isoform X1 [Apis mellifera]
gene1 177	173.8495 484	284.3633 121	0.6113 64199	-0.7098960 24	0.034 172	gi 328792187 ref XP_003251692. 1	PREDICTED: uncharacterized protein LOC100577522 isoform X1 [Apis mellifera]
gene8 414	220.4216 443	360.9995 773	0.6105 86987	-0.7117312 52	0.018 656	gi 328789808 ref XP_393661.3	PREDICTED: disks large homolog 5-like isoform X6 [Apis mellifera]
gene9 910	82.97990 821	135.9211 379	0.6105 00394	-0.7119358 7	0.023 396	gi 571566042 ref XP_006567059. 1	PREDICTED: uncharacterized protein LOC726758 [Apis mellifera]
gene3 817	655.1878 775	1074.566 329	0.6097 23067	-0.7137739 69	0.028 089	gi 572307746 ref XP_006619721. 1	PREDICTED: CCAAT/enhancer-binding protein-like [Apis dorsata]
gene1 1522	8045.384 023	13203.68 287	0.6093 28784	-0.7147072 03	0.025 278	gi 328783370 ref XP_001121121. 2	PREDICTED: trypsin-1-like isoform X1 [Apis mellifera]
gene6 05	47.49572 922	77.98080 358	0.6090 69502	-0.7153212 28	0.043 962	gi 571502866 ref XP_006565377. 1	PREDICTED: golgin subfamily A member 6-like protein 2-like isoform X1 [Apis mellifera]
gene7 184	74.17648 672	121.7934 879	0.6090 34917	-0.7154031 53	0.033 584	gi 820866416 ref XP_012349637. 1	PREDICTED: uncharacterized protein LOC105737031 [Apis florea]
gene3 596	4591.144 077	7542.208 999	0.6087 26711	-0.7161334 22	0.000 404	gi 328782416 ref XP_001120871.	PREDICTED: uncharacterized protein LOC724971 isoform X1 [Apis mellifera]

						2	
gene1 0161	252.5057 419	414.8681 55	0.6086 40935	-0.7163367 27	0.005 515	gi 66522653 ref XP_391978.2	PREDICTED: LIM domain-containing protein jub-like [Apis mellifera]
gene2 559	470.3899 273	773.1466 82	0.6084 09682	-0.7168849 82	0.001 302	gi 328777221 ref XP_397251.4	PREDICTED: formin-binding protein 1 homolog isoform X8 [Apis mellifera]
gene5 499	1277.131 669	2100.269 493	0.6080 79903	-0.7176671 86	0.016 907	gi 571537009 ref XP_006571028. 1	PREDICTED: CD109 antigen [Apis mellifera]
gene1 1597	180.3892 695	296.8062 949	0.6077 67667	-0.7184081 68	0.013 864	gi 571575051 ref XP_006563676. 1	PREDICTED: disintegrin and metalloproteinase domain-containing protein 10 isoform X1 [Apis mellifera]
gene3 385	616.0233 045	1013.825 983	0.6076 22328	-0.7187532 09	0.001 636	gi 572299676 ref XP_006615958. 1	PREDICTED: uncharacterized protein LOC102675370 [Apis dorsata]
gene7 317	998.5994 946	1643.693 259	0.6075 33972	-0.7189630 11	0.000 477	gi 571548729 ref XP_006561725. 1	PREDICTED: microtubule-associated protein futsch isoform X3 [Apis mellifera]
gene3 6	193.6319 435	318.9445 73	0.6071 02174	-0.7199887 56	0.013 724	gi 571499372 ref XP_006557431. 1	PREDICTED: LOW QUALITY PROTEIN: probable E3 ubiquitin-protein ligase MYCBP2-like [Apis mellifera]
gene1 0696	71.06284 036	117.1301 334	0.6066 99901	-0.7209450 19	0.042 748	gi 571571591 ref XP_006563142. 1	PREDICTED: flocculation protein FLO11-like, partial [Apis mellifera]
gene4 197	338.2446 956	558.0638 059	0.6061 03983	-0.7223627 71	0.013 235	gi 571528328 ref XP_006564287. 1	PREDICTED: ral GTPase-activating protein subunit alpha-1-like [Apis mellifera]

gene9 303	1357.214 374	2240.471 674	0.6057 71718	-0.7231538 71	0.002 075	gi 571562868 ref XP_006570507. 1	PREDICTED: histone deacetylase 5 isoform X1 [Apis mellifera]
gene4 612	132.0186 994	218.1163 086	0.6052 67438	-0.7243553 54	0.012 24	gi 571531460 ref XP_006570008. 1	PREDICTED: phosphoinositide 3-kinase adapter protein 1-like isoform X1 [Apis mellifera]
gene1 444	269.1543 242	444.7627 554	0.6051 63811	-0.7246023 78	0.003 659	gi 571509220 ref XP_006571490. 1	PREDICTED: glutamate receptor ionotropic, kainate 2-like isoform X1 [Apis mellifera]
gene6 289	66.64707 816	110.3271 855	0.6040 85728	-0.7271747 92	0.015 377	gi 328777523 ref XP_001121647. 2	PREDICTED: uncharacterized protein LOC725844 [Apis mellifera]
gene1 0038	854.6436 3	1415.040 13	0.6039 71302	-0.7274480 93	0.001 61	gi 571566790 ref XP_006558573. 1	PREDICTED: transmembrane protein 132C-like isoform X1 [Apis mellifera]
gene2 727	1938.121 704	3213.243 44	0.6031 66781	-0.7293711 19	0.000 605	gi 571518233 ref XP_006560559. 1	PREDICTED: uncharacterized protein LOC413858 isoform X1 [Apis mellifera]
gene1 2472	168.1755 813	279.0546 382	0.6026 61839	-0.7305793 81	0.012 083	gi 328793368 ref XP_001122855. 2	PREDICTED: uncharacterized protein C9orf85 homolog [Apis mellifera]
gene6 707	1362.075 38	2264.995 041	0.6013 591	-0.7337013 44	0.004 769	gi 571544563 ref XP_006563931. 1	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein-like [Apis mellifera]
gene5 936	78357.23 001	130709.5 025	0.5994 76155	-0.7382257 25	0.005 507	gi 571539411 ref XP_006564376.	PREDICTED: titin isoform X14 [Apis mellifera]

						1	
gene1 0768	186.7431 317	312.0300 478	0.5984 78041	-0.7406297 82	0.021 968	gi 328785145 ref XP_003250547. 1	PREDICTED: uncharacterized protein LOC100578776 isoform X1 [Apis mellifera]
gene5 703	409.4730 53	685.4657 536	0.5973 64713	-0.7433160 77	0.002 266	gi 328776788 ref XP_396348.4	PREDICTED: octopamine receptor beta-2R isoformX5 [Apis mellifera]
gene3 054	557.4711 172	933.8435 121	0.5969 6417	-0.7442837 52	0.007 447	gi 571520595 ref XP_006568504. 1	PREDICTED: uncharacterized protein LOC725508 isoform X1 [Apis mellifera]
gene1 528	658.1839 158	1104.107 168	0.5961 23216	-0.7463175 35	0.007 504	gi 328792704 ref XP_003251765. 1	PREDICTED: G-protein coupled receptor Mth2-like [Apis mellifera]
gene4 097	3975.288 999	6675.929 408	0.5954 66003	-0.7479089 53	0.001 414	gi 571527472 ref XP_006562194. 1	PREDICTED: muscle M-line assembly protein unc-89 isoform X1 [Apis mellifera]
gene7 931	766.5217 484	1289.277 169	0.5945 36044	-0.7501638 17	0.017 306	gi 571552976 ref XP_006562907. 1	PREDICTED: microtubule-associated protein futsch-like isoform X1 [Apis mellifera]
gene7 351	48.61301 972	81.81063 941	0.5942 13907	-0.7509457 23	0.033 365	gi 571548873 ref XP_006561744. 1	PREDICTED: uncharacterized protein LOC102654791 isoform X1 [Apis mellifera]
gene1 983	119.8910 223	201.7896 673	0.5941 3856	-0.7511286 71	0.012 49	gi 571512714 ref XP_006565907. 1	PREDICTED: uncharacterized protein LOC100578356 isoform X1 [Apis mellifera]
gene7 569	419.9354 931	707.6226 704	0.5934 45505	-0.7528125 38	0.006 059	gi 328788058 ref XP_003251054.	PREDICTED: protein sprint-like [Apis mellifera]

						1	
gene8 280	150.7346 158	254.4962 887	0.5922 86106	-0.7556338 52	0.019 855	gi 328786663 ref XP_001121883. 2	PREDICTED: trichohyalin isoform X1 [Apis mellifera]
gene2 350	594.0028 259	1002.967 681	0.5922 45231	-0.7557334 18	0.017 572	gi 571514834 ref XP_006568889. 1	PREDICTED: bestrophin-2-like isoform X1 [Apis mellifera]
gene9 824	574.5077 208	970.4640 229	0.5919 92807	-0.7563484 49	0.009 484	gi 820860434 ref XP_012347067. 1	PREDICTED: hairy/enhancer-of-split related with YRPW motif protein 1 isoform X1 [Apis florea]
gene4 751	428.2637 754	723.8136 737	0.5916 76824	-0.7571187 1	0.000 898	gi 571532211 ref XP_006570323. 1	PREDICTED: myosin-VIIa [Apis mellifera]
gene1 87	112.2280 872	189.8431 325	0.5911 62218	-0.7583740 28	0.011 205	gi 571500415 ref XP_006559951. 1	PREDICTED: translation initiation factor eIF-2B subunit epsilon-like [Apis mellifera]
gene7 791	114.3814 26	193.6603 448	0.5906 29053	-0.7596757 72	0.007 605	gi 571552109 ref XP_003249836. 2	PREDICTED: O-glucosyltransferase rumi homolog isoform X1 [Apis mellifera]
gene7 087	242.5186 845	412.5713 616	0.5878 22391	-0.7665477 79	0.006 393	gi 571547082 ref XP_006569898. 1	PREDICTED: dentin sialophosphoprotein [Apis mellifera]
gene2 789	211.6413 505	360.3941 357	0.5872 49707	-0.7679540 07	0.002 026	gi 571518556 ref XP_006560971. 1	PREDICTED: ATP-binding cassette sub-family C member Sur isoform X1 [Apis mellifera]
gene1	1504.814	2563.186	0.5870	-0.7683532	9.20E	gi 571574872 ref	PREDICTED: DE-cadherin-like isoform X1 [Apis mellifera]

1545	321	982	87221	41	-05	XP_006563610.1	
gene1 772	602.3701 865	1026.229 275	0.5869 74277	-0.7686308 14	0.007 414	gi 328778092 ref XP_003249448.1	PREDICTED: putative transcription factor capicua-like isoform X1 [Apis mellifera]
gene5 535	50.92504 592	86.80138 106	0.5866 84743	-0.7693426 21	0.025 136	.	.
gene6 228	55.18665 674	94.06699 037	0.5866 73992	-0.7693690 58	0.034 56	gi 328790219 ref XP_003251395.1	PREDICTED: uncharacterized protein LOC100578532 [Apis mellifera]
gene7 489	74.25034 434	126.7310 416	0.5858 89167	-0.7713003 21	0.007 608	gi 328781401 ref XP_001120510.2	PREDICTED: neprilysin-2 isoform X1 [Apis mellifera]
gene2 216	2694.368 596	4603.078 505	0.5853 4057	-0.7726518 19	0.029 946	gi 571515814 ref XP_006569086.1	PREDICTED: ryanodine receptor 44F isoform X1 [Apis mellifera]
gene1 0713	187.6079 999	321.8287 202	0.5829 43622	-0.7785717 31	0.012 493	gi 571571585 ref XP_006563140.1	PREDICTED: uncharacterized protein LOC408462 [Apis mellifera]
gene4 165	1290.149 797	2220.898 284	0.5809 13501	-0.7836047 35	0.000 319	gi 571527923 ref XP_006564220.1	PREDICTED: ribosome-releasing factor 2, mitochondrial-like [Apis mellifera]
gene2 90	123.3381 322	212.3288 265	0.5808 82654	-0.7836813 45	0.023 111	gi 571500821 ref XP_006561977.1	PREDICTED: uncharacterized protein LOC102653658 [Apis mellifera]
gene5	67.13570	115.6059	0.5807	-0.7840632	0.015	.	.

120	96	356	28915	25	785		
gene8 393	46.84174 775	80.87903 085	0.5791 58124	-0.7879708 03	0.034 656		
gene1 0034	44.24382 777	76.39871 617	0.5791 17425	-0.7880721 89	0.047 631		
gene3 079	117.6367 821	203.9695 793	0.5767 36896	-0.7940147 75	0.027 589	gi 571520772 ref XP_006568534. 1	PREDICTED: succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial-like [Apis mellifera]
gene2 321	1166.830 139	2027.456 931	0.5755 14143	-0.7970767 12	0.000 216	gi 571515056 ref XP_006568926. 1	PREDICTED: uncharacterized protein LOC725893 isoform X2 [Apis mellifera]
gene1 2892	183.9954 124	320.0585 348	0.5748 80506	-0.7986659 85	0.006 475	gi 571578616 ref XP_006572452. 1	PREDICTED: filamin-A-like [Apis mellifera]
gene1 0195	110.9936 395	193.8242 462	0.5726 50954	-0.8042720 49	0.007 103	gi 328779553 ref XP_001121446. 2	PREDICTED: lachesin-like [Apis mellifera]
gene2 328	2411.604 985	4214.758 495	0.5721 8106	-0.8054563 5	0.000 144	gi 571514985 ref XP_006568907. 1	PREDICTED: microtubule-associated protein futsch-like isoform X1 [Apis mellifera]
gene2 730	95.24785 639	166.6885 839	0.5714 11996	-0.8073967 72	0.012 745	gi 571518206 ref XP_006560552. 1	PREDICTED: dual oxidase isoform X1 [Apis mellifera]
gene3 256	138.8088 097	243.0170 749	0.5711 89534	-0.8079585 5	0.002 468	gi 328776907 ref XP_624136.3	PREDICTED: transcriptional activator cubitus interruptus isoform X2 [Apis mellifera]
gene9	1026.303	1797.468	0.5709	-0.8085087	0.000	gi 571562942 ref	PREDICTED: uncharacterized protein LOC408333 isoform X1 [Apis mellifera]

296	46	067	71735	67	46	XP_006570521.1	
gene7 413	53.33314 305	93.42692 334	0.5708 54109	-0.8088060 07	0.019 58	gi 571549265 ref XP_006561821.1	PREDICTED: uncharacterized protein LOC100578091 [Apis mellifera]
gene7 676	131.9770 873	231.3469 165	0.5704 72645	-0.8097703 87	0.014 535	gi 571550740 ref XP_006567539.1	PREDICTED: transcription factor Sp8-like [Apis mellifera]
gene1 1165	77.65491 069	136.3422 605	0.5695 58627	-0.8120837 42	0.018 024	gi 328779954 ref XP_394109.3	PREDICTED: G protein-coupled receptor kinase 2 isoform X2 [Apis mellifera]
gene5 940	13158.27 386	23235.23 383	0.5663 06926	-0.8203439 19	0.015 201	gi 571539415 ref XP_006564377.1	PREDICTED: titin-like [Apis mellifera]
gene1 1835	121.6574 978	215.6097 719	0.5642 48534	-0.8255973 29	0.018 19	gi 328778440 ref XP_623903.2	PREDICTED: homeotic protein Sex combs reduced [Apis mellifera]
gene1 856	979.8056 918	1743.035 347	0.5621 26117	-0.8310342 49	0.008 518	gi 328780582 ref XP_393610.4	PREDICTED: rho guanine nucleotide exchange factor 12 isoform X4 [Apis mellifera]
gene1 1699	245.7112 455	437.8011 755	0.5612 39346	-0.8333119 41	0.013 403	gi 66554761 ref XP_397331.2	PREDICTED: ankyrin repeat and SOCS box protein 16-like isoform X2 [Apis mellifera]
gene3 967	1112.705 355	1983.131 479	0.5610 85014	-0.8337087 13	0.026 652	gi 571526651 ref XP_006557955.1	PREDICTED: uncharacterized protein LOC102655788 [Apis mellifera]
gene3 829	647.9128 849	1156.454 344	0.5602 58075	-0.8358365 56	0.000 248	gi 334724440 ref NP_001229316.1	filamin-like [Apis mellifera]
gene3	1191.702	2128.499	0.5598	-0.8368121	0.001	gi 571521734 ref	PREDICTED: zinc finger protein 1-like [Apis mellifera]

235	967	676	79327	83	162	XP_006557404.1	
gene4 934	308.6458 936	551.9530 034	0.5591 8872	-0.8385928 35	0.000 5	gi 571533018 ref XP_006561305.1	PREDICTED: probable phospholipid-transporting ATPase ID-like isoform X1 [Apis mellifera]
gene8 463	2340.853 831	4195.204 192	0.5579 83289	-0.8417061 81	0.009 457	gi 571556170 ref XP_006569704.1	PREDICTED: abaecin isoform X1 [Apis mellifera]
gene3 140	121.2763 199	217.4227 238	0.5577 90454	-0.8422048 5	0.009 17	gi 328789915 ref XP_001120679.2	PREDICTED: G-protein coupled receptor Mth2-like [Apis mellifera]
gene3 491	346.3923 036	621.1596 051	0.5576 54266	-0.8425571 37	0.001 539	gi 110755844 ref XP_396884.3	PREDICTED: protein kibra-like isoformX2 [Apis mellifera]
gene1 0281	451.8555 21	811.0068 634	0.5571 53757	-0.8438525 74	0.000 865	gi 328785317 ref XP_001120437.2	PREDICTED: integrin alpha-PS2 isoform X1 [Apis mellifera]
gene7 848	241.6271 2	433.8862 796	0.5568 90437	-0.8445345 75	0.000 728	gi 571552520 ref XP_006562428.1	PREDICTED: gamma-tubulin complex component 5-like, partial [Apis mellifera]
gene8 361	1624.112 131	2916.713 903	0.5568 29427	-0.8446926 39	0.000 147	gi 571555508 ref XP_006566284.1	PREDICTED: LOW QUALITY PROTEIN: kinase D-interacting substrate of 220 kDa-like [Apis mellifera]
gene5 038	437.1798 776	786.1936 402	0.5560 71501	-0.8466576 95	0.000 375	gi 328782190 ref XP_394861.4	PREDICTED: nose resistant to fluoxetine protein 6-like [Apis mellifera]
gene1 1810	465.4494 826	837.9655 602	0.5554 51805	-0.8482663 58	0.003 422	gi 571575481 ref XP_006557753.1	PREDICTED: growth factor receptor-bound protein 14-like isoform X2 [Apis mellifera]

						1	
gene7 921	920.7560 859	1662.295 165	0.5539 06493	-0.8522856 44	0.003 657	gi 328782724 ref XP_393711.3	PREDICTED: protein kinase DC2 isoform X2 [Apis mellifera]
gene3 655	120.1303 151	217.5027 851	0.5523 16215	-0.8564336 11	0.019 218	gi 571524339 ref XP_006566006. 1	PREDICTED: ETS-like protein pointed, isoform P1-like isoform X1 [Apis mellifera]
gene2 93	214.7277 095	389.1927 684	0.5517 25846	-0.8579765 28	0.007 644	gi 571500707 ref XP_006561972. 1	PREDICTED: furin-like isoform X1 [Apis mellifera]
gene7 729	38.81224 861	70.40892 821	0.5512 40441	-0.8592463 62	0.037 266	gi 66518356 ref XP_395932.2	PREDICTED: knirps-related protein isoform X3 [Apis mellifera]
gene4 104	1330.572 987	2420.827 967	0.5496 35499	-0.8634529 1	8.94E -05	gi 571527532 ref XP_006562205. 1	PREDICTED: dentin sialophosphoprotein-like [Apis mellifera]
gene4 810	1774.559 912	3232.714 016	0.5489 38107	-0.8652846 02	7.58E -05	gi 58585174 ref NP_001011615. 1	hymenoptaecin preproprotein [Apis mellifera]
gene2 45	27.81387 623	50.69561 74	0.5486 4459	-0.8660562 15	0.037 025	gi 571501010 ref XP_006562006. 1	PREDICTED: autophagy-related protein 23-like isoform X1 [Apis mellifera]
gene8 442	26.27644 332	48.09953 033	0.5462 93137	-0.8722527 95	0.026 813	gi 328790437 ref XP_623893.3	PREDICTED: Bardet-Biedl syndrome 5 protein homolog [Apis mellifera]
gene5 125	464.9121 149	851.6184 251	0.5459 15989	-0.8732491 42	0.009 325	gi 571533916 ref XP_006564143. 1	PREDICTED: sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1-like isoform X1 [Apis mellifera]
gene1	92.87560	170.4184	0.5449	-0.8757099	0.011	gi 328792499 ref	PREDICTED: major facilitator superfamily domain-containing protein 12-like

435	616	576	85605	72	766	XP_624057.2	isoform X2 [Apis mellifera]
gene7 497	269.5589 499	495.0417 992	0.5445 17554	-0.8769495 35	0.001 779	gi 571549689 ref XP_006561911.1	PREDICTED: organic solute transporter alpha-like protein-like [Apis mellifera]
gene3 479	191.0674 834	351.1611 622	0.5441 01979	-0.8780510 19	0.000 407	gi 571523199 ref XP_006562043.1	PREDICTED: kinetochore-associated protein 1-like [Apis mellifera]
gene2 437	5390.454 677	9907.457 278	0.5440 80537	-0.8781078 74	0.000 939	gi 571514423 ref XP_006568818.1	PREDICTED: LOW QUALITY PROTEIN: twitchin [Apis mellifera]
gene7 226	352.1656 826	649.4281 216	0.5422 70454	-0.8829155 28	0.006 065	gi 571548223 ref XP_006561630.1	PREDICTED: la-related protein 4-like isoform X1 [Apis mellifera]
gene2 936	210.1127 632	388.4259 669	0.5409 33874	-0.8864758 5	0.014 878	gi 571519626 ref XP_003250376.2	PREDICTED: uncharacterized protein LOC100577178 isoform X1 [Apis mellifera]
gene3 179	591.5339 784	1095.332 288	0.5400 49796	-0.8888356 56	0.000 232	gi 572297383 ref XP_006614882.1	PREDICTED: protein crumbs-like isoform X1 [Apis dorsata]
gene7 000	40.52292 013	75.23391 33	0.5386 25712	-0.8926449 94	0.020 759	gi 571546304 ref XP_006568595.1	PREDICTED: cAMP-specific 3',5'-cyclic phosphodiesterase, isoforms N/G isoform X9 [Apis mellifera]
gene1 2577	122.0396 975	226.8014 939	0.5380 9036	-0.8940796 34	0.000 831	gi 328793514 ref XP_395995.3	PREDICTED: organic cation transporter protein-like isoform 1 [Apis mellifera]
gene4 978	385.6083 453	716.7141 701	0.5380 22494	-0.8942616 03	0.043 769	gi 571533289 ref XP_006561360.	PREDICTED: uncharacterized protein LOC725964 isoform X1 [Apis mellifera]

gene1 3340	85.37982 222	158.8080 02	0.5376 2922	-0.8953165 44	0.022 628	gi 328794317 ref XP_001123227. 2	PREDICTED: short spindle protein 4-like [Apis mellifera]
gene4 364	364.0765 407	677.6822 877	0.5372 37799	-0.8963672 81	0.000 117	gi 571529190 ref XP_006567731. 1	PREDICTED: centrosomal and chromosomal factor-like isoform X1 [Apis mellifera]
gene1 1853	44.49606 611	82.98266 06	0.5362 09201	-0.8991321 21	0.037 561	.	.
gene1 1391	68.98188 973	128.7376 318	0.5358 33142	-0.9001442 79	0.024 847	gi 571575347 ref XP_006563782. 1	PREDICTED: neurofilament medium polypeptide-like [Apis mellifera]
gene1 209	8231.385 857	15384.16 287	0.5350 55819	-0.9022386 89	0.000 565	gi 328792196 ref XP_001121241. 2	PREDICTED: probable serine/threonine-protein kinase clkA-like [Apis mellifera]
gene7 811	23.10989 267	43.29933 462	0.5337 23968	-0.9058342 96	0.035 218	gi 572305324 ref XP_006618592. 1	PREDICTED: uncharacterized protein LOC102678905 [Apis dorsata]
gene3 021	377.4088 751	707.7993 651	0.5332 14487	-0.9072121 18	0.010 986	gi 571520122 ref XP_006568040. 1	PREDICTED: guanine nucleotide-releasing factor 2-like isoform X1 [Apis mellifera]
gene1 537	571.5571 532	1076.599 089	0.5308 91359	-0.9135114 36	0.000 687	gi 66501273 ref XP_392808.2	PREDICTED: tribbles homolog 2 isoform X2 [Apis mellifera]
gene1 0957	74.49084 601	140.3371 073	0.5307 99355	-0.9137614 78	0.007 081	gi 571573151 ref XP_006565859. 1	PREDICTED: facilitated trehalose transporter Tret1-like isoform X1 [Apis mellifera]

gene1 0825	255.6422 321	483.1018 137	0.5291 68438	-0.9182010 8	0.000 672	gi 571572421 ref XP_006565003. 1	PREDICTED: protein ccsmt1-like isoform X2 [Apis mellifera]
gene7 264	35.40543 977	67.05525 795	0.5280 03931	-0.9213794 25	0.045 847	gi 571548069 ref XP_006561588. 1	PREDICTED: sodium channel protein paralytic isoform X16 [Apis mellifera]
gene1 592	437.2792 416	829.8480 737	0.5269 38913	-0.9242923 73	0.031 172	gi 328792769 ref XP_003251772. 1	PREDICTED: uncharacterized protein LOC100578606 isoform X1 [Apis mellifera]
gene6 984	88.52572 791	168.4609 885	0.5254 96904	-0.9282458 3	0.028 175	gi 66535525 ref XP_624087.1	PREDICTED: thioredoxin domain-containing protein 9-like [Apis mellifera]
gene4 765	20923.09 459	39855.49 85	0.5249 73853	-0.9296825 27	1.97E -06	gi 572315326 ref XP_006623317. 1	PREDICTED: uncharacterized protein LOC102673964 [Apis dorsata]
gene1 829	664.3570 676	1265.994 895	0.5247 70732	-0.9302408 36	0.000 111	gi 571511699 ref XP_006561153. 1	PREDICTED: pleckstrin homology-like domain family B member 2-like isoform X1 [Apis mellifera]
gene3 362	346.0527 325	659.7843 173	0.5244 93722	-0.9310025 9	0.013 257	gi 571523080 ref XP_006560680. 1	PREDICTED: protein held out wings [Apis mellifera]
gene4 164	1181.265 858	2259.040 136	0.5229 06096	-0.9353762 06	0.011 032	gi 571527908 ref XP_006564216. 1	PREDICTED: transcription factor kayak isoform X1 [Apis mellifera]
gene8 785	191.6641 266	367.0591 328	0.5221 61443	-0.9374321 63	0.001 683	gi 328784384 ref XP_003250447. 1	PREDICTED: transcriptional regulator Myc-B-like [Apis mellifera]

gene1 1296	143.9526 46	275.8066 402	0.5219 33213	-0.9380628 83	0.001 711	gi 571574152 ref XP_006561080. 1	PREDICTED: protein TANC2-like isoform X1 [Apis mellifera]
gene1 0294	74.50743 025	142.9572 212	0.5211 86895	-0.9401272 86	0.003 518	gi 110762343 ref XP_001120949. 1	PREDICTED: protein odd-skipped-like [Apis mellifera]
gene7 453	75.87599 362	145.6163 151	0.5210 67942	-0.9404565 98	0.012 307	gi 571549438 ref XP_006561864. 1	PREDICTED: DBF4-type zinc finger-containing protein 2 homolog isoform X1 [Apis mellifera]
gene8 492	2108.704 491	4047.854 954	0.5209 43689	-0.9408006 62	3.87E -05	gi 571556561 ref XP_006557505. 1	PREDICTED: protein-methionine sulfoxide oxidase Mical isoform X1 [Apis mellifera]
gene8 982	440.4994 557	847.7738 227	0.5195 95491	-0.9445391 83	0.015 187	.	.
gene4 446	57.61611 763	110.9036 011	0.5195 153	-0.9447618 56	0.035 495	gi 328788288 ref XP_003251097. 1	PREDICTED: solute carrier family 52, riboflavin transporter, member 3-A-like [Apis mellifera]
gene1 316	58.47442 53	113.1183 084	0.5169 31575	-0.9519547 68	0.007 694	gi 328792339 ref XP_396231.3	PREDICTED: chondroitin sulfate proteoglycan 4 isoform X3 [Apis mellifera]
gene1 204	111.3118 639	216.0035 464	0.5153 24242	-0.9564476 33	0.007 917	gi 571507384 ref XP_006571131. 1	PREDICTED: tropomyosin-2-like [Apis mellifera]
gene7 954	128.1357 518	248.7649 421	0.5150 8766	-0.9571101 18	0.000 369	gi 572299973 ref XP_006616097. 1	PREDICTED: G-protein coupled receptor moody-like isoform X1 [Apis dorsata]
gene7	259.1346	503.2459	0.5149	-0.9575616	0.018	gi 571552117 ref	PREDICTED: matrix metalloproteinase-14-like isoform X1 [Apis mellifera]

792	618	475	26475	47	441	XP_006561295.1	
gene3 541	82.22652 874	160.1168 054	0.5135 40903	-0.9614489 06	0.004 823	gi 571523594 ref XP_006562689.1	PREDICTED: PHD finger protein rhinoceros-like isoform X1 [Apis mellifera]
gene7 062	1599.908 367	3124.904 822	0.5119 86271	-0.9658229 7	0.000 48	gi 110759161 ref XP_394764.3	PREDICTED: uncharacterized protein LOC411290 isoform X4 [Apis mellifera]
gene1 219	54.71316 557	106.9464 721	0.5115 93926	-0.9669289 59	0.039 829	gi 328792207 ref XP_623471.3	PREDICTED: diacylglycerol kinase 1 isoform X4 [Apis mellifera]
gene9 639	33.25978 011	65.06106 237	0.5112 08685	-0.9680157 49	0.020 281	.	.
gene1 2547	191.7600 221	376.9126 195	0.5087 65194	-0.9749281 19	0.006 026	gi 571577791 ref XP_006572178.1	PREDICTED: uncharacterized protein LOC552030 isoform X1 [Apis mellifera]
gene7 816	418.2899 358	822.8447 861	0.5083 46097	-0.9761170 33	5.75E -05	gi 571552186 ref XP_006562089.1	PREDICTED: uncharacterized protein LOC412101 isoform X1 [Apis mellifera]
gene2 242	202.8623 71	399.4236 025	0.5078 87791	-0.9774183 02	0.000 773	.	.
gene6 240	24.09454 014	47.47878 843	0.5074 80097	-0.9785768 54	0.025 873	gi 571540842 ref XP_006569464.1	PREDICTED: uncharacterized protein LOC102656235 [Apis mellifera]
gene7 256	633.1860 671	1253.845 826	0.5049 95155	-0.9856585 48	2.40E -05	gi 571548368 ref XP_006561662.1	PREDICTED: uncharacterized protein LOC100576640 isoform X3 [Apis mellifera]
gene7	27.14715	53.77944	0.5047	-0.9862536	0.024	gi 571550528 ref	PREDICTED: dynein heavy chain 10, axonemal-like [Apis mellifera]

635	86	306	86905	11	726	XP_006567505.1	
gene1 1798	296.5403 31	588.8148 421	0.5036 22378	-0.9895857 05	0.000 267	gi 571575747 ref XP_006557850.1	PREDICTED: microtubule-associated protein futsch-like [Apis mellifera]
gene4 200	93.82113 071	186.3316 695	0.5035 16825	-0.9898881 07	0.006 872	gi 571528133 ref XP_006564252.1	PREDICTED: homeobox protein SIX2-like isoform X1 [Apis mellifera]
gene7 405	53.39629 754	106.2002 16	0.5027 88973	-0.9919750 86	0.007 054	gi 571549180 ref XP_006561803.1	PREDICTED: uncharacterized protein LOC411336 isoform X1 [Apis mellifera]
gene5 111	178.9338 348	356.2924 304	0.5022 10599	-0.9936356 19	0.001 876	gi 571533996 ref XP_006564155.1	PREDICTED: probable serine/threonine-protein kinase dyrk2-like isoform X2 [Apis mellifera]
gene1 0175	1919.455 095	3834.484 238	0.5005 77125	-0.9983357 3	0.002 087	gi 571567823 ref XP_006560440.1	PREDICTED: piezo-type mechanosensitive ion channel component 2 isoform X1 [Apis mellifera]
gene1 2075	1812.873 106	3623.007 821	0.5003 77917	-0.9989099 74	0.000 286	gi 328782977 ref XP_392097.4	PREDICTED: collagen alpha-1(IV) chain-like isoform 1 [Apis mellifera]
gene4 431	2687.497 961	5413.604 42	0.4964 34123	-1.0103258 12	0.000 344	gi 571529759 ref XP_006567837.1	PREDICTED: dual specificity protein phosphatase 10 [Apis mellifera]
gene1 1110	222.8969 045	449.6028 539	0.4957 63989	-1.0122746 12	0.000 393	gi 328779092 ref XP_624412.2	PREDICTED: putative amino acid permease F13H10.3-like [Apis mellifera]
gene3 277	667.4635 441	1347.672 757	0.4952 7123	-1.0137092 77	0.001 33	gi 572268404 ref XP_006612252.1	PREDICTED: vesicular glutamate transporter 2-like isoform X1 [Apis dorsata]

						1	
gene1 0310	270.4031 593	550.8279 852	0.4909 03089	-1.0264898 51	0.000 182	gi 571568775 ref XP_006565137. 1	PREDICTED: talin-1-like [Apis mellifera]
gene1 1284	25.13949 354	51.23555 25	0.4906 65023	-1.0271896 63	0.032 538	.	.
gene9 887	116.8886 776	238.4525 218	0.4901 96861	-1.0285668 5	0.012 51	gi 571565676 ref XP_006566994. 1	PREDICTED: putative fatty acyl-CoA reductase CG5065-like [Apis mellifera]
gene4 038	144.5028 094	295.1621 575	0.4895 70921	-1.0304102 25	0.005 257	gi 328780431 ref XP_396579.2	PREDICTED: putative ferric-chelate reductase 1 homolog isoformX1 [Apis mellifera]
gene2 768	566.8317 017	1161.851 99	0.4878 69114	-1.0354339 41	0.001 104	gi 571518921 ref XP_006561030. 1	PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC551170 [Apis mellifera]
gene6 632	30.42797 002	62.43042 601	0.4873 90075	-1.0368512 22	0.021 06	.	.
gene5 706	18.70612 763	38.52910 469	0.4855 06419	-1.0424377 26	0.035 403	.	.
gene3 912	19.61234 743	40.46336 872	0.4846 93886	-1.0448542 1	0.030 864	.	.
gene3 890	156.3884 642	322.6821 988	0.4846 51663	-1.0449798 93	6.30E -05	gi 328790075 ref XP_001120790. 2	PREDICTED: laccase-1-like [Apis mellifera]
gene1 2968	25.41525 625	52.58473 349	0.4833 20054	-1.0489492 37	0.034 378	gi 571578735 ref XP_006572484. 1	PREDICTED: uncharacterized protein LOC102655303 isoform X1 [Apis mellifera]

gene4 877	22.29722 38	46.14229 002	0.4832 27508	-1.0492255 13	0.026 667	gi 571532839 ref XP_006560106. 1	PREDICTED: epidermal growth factor receptor-like, partial [Apis mellifera]
gene1 43	102.1782 889	212.0880 153	0.4817 73045	-1.0535744 18	0.024 064	gi 571499603 ref XP_006558614. 1	PREDICTED: uncharacterized protein LOC102656689 isoform X1 [Apis mellifera]
gene1 0626	1486.847 807	3104.263 423	0.4789 69599	-1.0619940 07	0.000 576	gi 571571446 ref XP_006563114. 1	PREDICTED: protein Malvolio isoform X1 [Apis mellifera]
gene1 1412	24.68536 712	51.81603 494	0.4764 04016	-1.0697425 21	0.023 582	gi 94158832 ref NP_001035315. 1	odorant binding protein 9 precursor [Apis mellifera]
gene8 912	57.81279 874	121.5300 99	0.4757 07658	-1.0718528 45	0.002 858	gi 571559390 ref XP_006566381. 1	PREDICTED: protein apterous isoform X1 [Apis mellifera]
gene1 0238	18.60393 21	39.19115 654	0.4746 97195	-1.0749205 69	0.019 753	gi 48097975 ref XP_393944.1	PREDICTED: protein escargot [Apis mellifera]
gene4 4	14.51937 393	30.76668 337	0.4719 18723	-1.0833896 84	0.036 384	.	.
gene1 203	22.11475 152	47.02613 292	0.4702 65151	-1.0884536 68	0.017 434	.	.
gene1 2060	88.13765 559	187.5772 372	0.4698 73941	-1.0896543 38	0.011 911	gi 571576451 ref XP_006563160. 1	PREDICTED: putative uncharacterized protein DDB_G0282133-like isoform X1 [Apis mellifera]
gene5 670	22.48889 572	47.90380 8	0.4694 59458	-1.0909275 23	0.024 834	gi 110757922 ref XP_001122422.	PREDICTED: uncharacterized protein LOC726699 isoform X1 [Apis mellifera]

						1	
gene9 765	43.17633 249	92.05866 312	0.4690 08902	-1.0923127 9	0.005 313	gi 571564846 ref XP_006565269. 1	PREDICTED: uncharacterized protein LOC102654968 [Apis mellifera]
gene1 246	1152.300 995	2464.357 319	0.4675 86817	-1.0966938 38	0.000 335	gi 571508040 ref XP_003251700. 2	PREDICTED: uncharacterized protein LOC100576169 [Apis mellifera]
gene3 488	98.75870 984	212.5422 38	0.4646 54512	-1.1057696 78	0.002 537	gi 571523231 ref XP_006562047. 1	PREDICTED: target of Myb protein 1-like isoform X1 [Apis mellifera]
gene5 937	78.09882 095	168.3762 846	0.4638 35041	-1.1083162 79	0.049 596	gi 571539358 ref XP_006564362. 1	PREDICTED: uncharacterized protein LOC102655685 isoform X1 [Apis mellifera]
gene6 609	11.62572 04	25.09526 828	0.4632 63444	-1.1100952 52	0.047 049	gi 571544547 ref XP_006563926. 1	PREDICTED: uncharacterized protein LOC413106 isoform X1 [Apis mellifera]
gene1 1968	136.4073 412	294.7759 828	0.4627 49169	-1.1116976 95	0.000 352	gi 571576379 ref XP_396342.5	PREDICTED: A disintegrin and metalloproteinase with thrombospondin motifs 3-like [Apis mellifera]
gene2 464	266.2319 138	578.9697 424	0.4598 37353	-1.1208044 33	5.56E -05	gi 328789675 ref XP_001122118. 2	PREDICTED: bone morphogenetic protein 2-B isoform X1 [Apis mellifera]
gene1 469	28.56497 918	62.16860 434	0.4594 7596	-1.1219387 13	0.013 205	gi 572269672 ref XP_006612850. 1	PREDICTED: uncharacterized protein LOC102673414 [Apis dorsata]
gene4 778	538.8726 037	1174.725 653	0.4587 22088	-1.1243077 2	0.000 253	gi 110757136 ref XP_625175.2	PREDICTED: ETS homologous factor-like [Apis mellifera]

gene5 776	193.0432 995	421.8704 516	0.4575 89051	-1.1278755 63	0.001 873	gi 571538195 ref XP_006559876. 1	PREDICTED: calcium release-activated calcium channel protein 1-like [Apis mellifera]
gene1 0110	115.2733 891	251.9724 688	0.4574 84064	-1.1282066 05	5.94E -05	gi 571567206 ref XP_006560128. 1	PREDICTED: uncharacterized protein PF11_0207-like isoform X1 [Apis mellifera]
gene6 235	147.0143 961	322.0994 285	0.4564 2551	-1.1315486 66	3.31E -06	gi 571540827 ref XP_394662.5	PREDICTED: L-lactate dehydrogenase-like isoform X2 [Apis mellifera]
gene4 562	315.0313 134	694.1185 326	0.4538 58093	-1.1396868 12	1.83E -05	gi 571530638 ref XP_006567976. 1	PREDICTED: uncharacterized protein LOC552512 isoform X1 [Apis mellifera]
gene1 0057	89.85052 176	198.0327 334	0.4537 15506	-1.1401401 31	0.003 738	gi 571566871 ref XP_006558588. 1	PREDICTED: uncharacterized protein LOC102654964 isoform X1 [Apis mellifera]
gene8 011	20.54973 671	45.29353 02	0.4537 0137	-1.1401850 78	0.019 103	gi 328784632 ref XP_003250475. 1	PREDICTED: pair-rule protein odd-paired-like [Apis mellifera]
gene1 229	6117.113 171	13512.03 818	0.4527 158	-1.1433224 38	6.76E -06	gi 571507718 ref XP_006571196. 1	PREDICTED: nesprin-1-like [Apis mellifera]
gene7 605	31.93808 152	71.44282 877	0.4470 4391	-1.1615115 5	0.042 063	gi 571550280 ref XP_006567453. 1	PREDICTED: peroxiredoxin 1-like [Apis mellifera]
gene1 2207	44.56437 651	99.96281 422	0.4458 09543	-1.1655005 96	0.036 532	gi 571576963 ref XP_006571904. 1	PREDICTED: EKC/KEOPS complex subunit TPRKB-like [Apis mellifera]

gene6 156	22.63864 399	50.86836 345	0.4450 43686	-1.1679811 34	0.019 068	gi 380018207 ref XP_003693026. 1	PREDICTED: GTP-binding protein REM 1 [Apis florea]
gene3 255	741.7174 058	1670.296 402	0.4440 63344	-1.1711626 08	0.007 496	gi 571521844 ref XP_006558248. 1	PREDICTED: intracellular protein transport protein USO1-like [Apis mellifera]
gene8 080	16.31159 921	36.91915 252	0.4418 19438	-1.1784712 03	0.037 615	.	.
gene7 880	1031.128 389	2345.292 742	0.4396 58713	-1.1855440 34	0.000 11	gi 571552621 ref XP_006562848. 1	PREDICTED: mucin-2-like [Apis mellifera]
gene1 1598	15.44117 847	35.38611 01	0.4363 62698	-1.1964003 16	0.025 822	.	.
gene3 014	11.96588 059	27.51965 981	0.4348 12082	-1.2015360 65	0.045 689	.	.
gene9 598	26.13841 47	60.21932 788	0.4340 53577	-1.2040549 62	0.037 328	gi 571563998 ref XP_006561270. 1	PREDICTED: protein penguin [Apis mellifera]
gene7 059	100.8806 665	233.7943 605	0.4314 93156	-1.2125904 18	0.004 964	gi 571546747 ref XP_006569833. 1	PREDICTED: dynein beta chain, ciliary-like [Apis mellifera]
gene8 418	16.95482 65	39.39281 786	0.4304 04003	-1.2162365 99	0.013 774	.	.
gene1 0783	1103.660 831	2576.024 9	0.4284 35622	-1.2228496 57	0.000 468	gi 571572211 ref XP_006564974. 1	PREDICTED: probable cation-transporting ATPase 13A3-like isoform X1 [Apis mellifera]

gene1 1710	23.18321 227	54.15541 765	0.4280 86667	-1.2240251 91	0.006 229	gi 571575429 ref XP_006557360. 1	PREDICTED: uncharacterized protein LOC102655415 [Apis mellifera]
gene3 045	72.25783 656	169.2231 722	0.4269 97294	-1.2277011 69	0.001 679	gi 571520736 ref XP_006568529. 1	PREDICTED: protein tramtrack, alpha isoform-like isoform X7 [Apis mellifera]
gene4 905	308.6638 4	724.8615 703	0.4258 24533	-1.2316690 23	0.001 088	gi 571532896 ref XP_006560793. 1	PREDICTED: uncharacterized protein LOC102653609 [Apis mellifera]
gene6 18	29.54960 964	69.80424 923	0.4233 21072	-1.2401757 89	0.005 363	.	.
gene4 647	74.77944 377	177.1245 188	0.4221 85727	-1.2440502 88	0.000 812	gi 571531318 ref XP_006569990. 1	PREDICTED: cytochrome b5-like [Apis mellifera]
gene1 0231	1651.657 061	3925.735 726	0.4207 25483	-1.2490488 9	5.85E -07	gi 571568232 ref XP_006562813. 1	PREDICTED: uncharacterized protein LOC413596 isoform X1 [Apis mellifera]
gene8 480	178.8879 748	427.8545 885	0.4181 04608	-1.2580641 53	0.003 556	gi 571556476 ref XP_006557488. 1	PREDICTED: uncharacterized protein LOC100577693 [Apis mellifera]
gene5 984	35.80179 73	85.87472 005	0.4169 07296	-1.2622014 76	0.003 819	gi 571540045 ref XP_006565578. 1	PREDICTED: discoidin domain-containing receptor 2-like [Apis mellifera]
gene2 691	1367.423 015	3283.304 882	0.4164 77624	-1.2636891 09	0.000 206	gi 571517921 ref XP_394430.5	PREDICTED: LOW QUALITY PROTEIN: sterile alpha and TIR motif-containing protein 1 [Apis mellifera]
gene1	221.9638	540.4771	0.4106	-1.2839092	2.78E	gi 328792883 ref	PREDICTED: uncharacterized protein LOC100577920 [Apis mellifera]

659	056	699	81187	35	-06	XP_003251794.1	
gene6 514	247.8474 535	604.1695 905	0.4102 28282	-1.2855011 35	0.006 187	gi 571543280 ref XP_006559685.1	PREDICTED: spondin-1-like isoform X1 [Apis mellifera]
gene1 1908	20.95938 544	51.90638 989	0.4037 92009	-1.3083157 36	0.005 155	gi 571575979 ref XP_006559456.1	PREDICTED: cytosolic carboxypeptidase NnaD-like isoform X1 [Apis mellifera]
gene7 583	25.38256 627	62.87708 347	0.4036 8549	-1.3086963 62	0.020 234	gi 571550230 ref XP_394770.5	PREDICTED: protein fork head-like isoform 1 [Apis mellifera]
gene8 076	27.32298 528	67.76251 681	0.4032 16801	-1.3103723 4	0.006 192	gi 571553830 ref XP_006565605.1	PREDICTED: paired box pox-meso protein isoform X1 [Apis mellifera]
gene8 626	128.6299 188	322.4101 005	0.3989 63676	-1.3256706 95	0.001 55	gi 571557263 ref XP_006558991.1	PREDICTED: yellow-e3 isoform X1 [Apis mellifera]
gene5 985	464.6782 132	1164.947 414	0.3988 83424	-1.3259609 23	9.84E -05	gi 328785804 ref XP_003250660.1	PREDICTED: uncharacterized protein LOC100578816 [Apis mellifera]
gene1 2931	86.33212 53	217.4337 801	0.3970 50197	-1.3326066 82	0.001 154	gi 571539407 ref XP_006564375.1	PREDICTED: titin isoform X13 [Apis mellifera]
gene1 2730	1281.379 704	3243.389 993	0.3950 74199	-1.3398044 63	0.001 478	gi 571578283 ref XP_006572347.1	PREDICTED: laminin subunit alpha [Apis mellifera]
gene7	12.32697	31.35438	0.3931	-1.3468481	0.023	gi 571549449 ref	PREDICTED: putative uncharacterized protein DDB_G0271606-like [Apis

452	708	413	50031	28	757	XP_006561867.1	mellifera]
gene5 912	522.6240 462	1339.171 374	0.3902 59272	-1.3574951 84	0.000 838	gi 66512834 ref XP_395069.2	PREDICTED: uridine phosphorylase 2-like isoform X2 [Apis mellifera]
gene1 0235	112.0288 382	287.6034 814	0.3895 2532	-1.3602109 84	8.49E -05	gi 571579119 ref XP_003252014.2	PREDICTED: uncharacterized protein LOC100578648, partial [Apis mellifera]
gene1 0209	14.91728 6	38.77830 284	0.3846 8125	-1.3782645 84	0.013 166	gi 571568011 ref XP_006560472.1	PREDICTED: neuroendocrine convertase 1-like [Apis mellifera]
gene6 695	46.15792 488	122.6017 594	0.3764 86643	-1.4093294 11	0.000 564	.	.
gene6 179	411.0725 185	1093.118 204	0.3760 54956	-1.4109845 83	9.30E -06	gi 66512130 ref XP_623621.1	PREDICTED: probable cytochrome P450 305a1 [Apis mellifera]
gene1 826	23.91336 19	64.47366 658	0.3709 01225	-1.4308930 63	0.018 669	.	.
gene1 0410	15.02233 01	41.38212 495	0.3630 14952	-1.4618991 23	0.034 95	gi 571569216 ref XP_006558826.1	PREDICTED: dynein intermediate chain 3, ciliary-like [Apis mellifera]
gene1 2187	11.04152 201	30.83016 5	0.3581 40218	-1.4814035 58	0.027 203	gi 328792988 ref XP_001122709.2	PREDICTED: endocuticle structural glycoprotein SgAbd-8-like isoform X1 [Apis mellifera]
gene7 444	62.74017 873	175.2635 379	0.3579 7622	-1.4820643 42	0.012 542	gi 571549427 ref XP_006561861.1	PREDICTED: hydrocephalus-inducing protein-like [Apis mellifera]
gene9	146.1462	410.1990	0.3562	-1.4889113	2.56E	gi 328791431 ref	PREDICTED: single Ig IL-1-related receptor-like [Apis mellifera]

381	518	559	81297	42	-06	XP_003251562. 1	
gene3 198	341.8965 932	961.0077 082	0.3557 68835	-1.4909879 56	0.000 497	gi 571521398 ref XP_006569925. 1	PREDICTED: LOW QUALITY PROTEIN: formin-like protein CG32138-like [Apis mellifera]
gene5 32	13.55184 871	38.42967 631	0.3526 40199	-1.5037311 5	0.013 275	gi 571502582 ref XP_006565052. 1	PREDICTED: glucose dehydrogenase [FAD, quinone] isoform X1 [Apis mellifera]
gene1 0630	31.67407 249	90.26973 802	0.3508 82513	-1.5109400 47	0.000 715	gi 571571370 ref XP_006563100. 1	PREDICTED: zinc finger protein 423 isoform X1 [Apis mellifera]
gene6 153	13.16469 083	38.05631 945	0.3459 26538	-1.5314624	0.029 13	gi 571540063 ref XP_006568339. 1	PREDICTED: uncharacterized protein LOC100576948 isoform X1 [Apis mellifera]
gene1 657	15.16134 121	44.70687 994	0.3391 27696	-1.5600994 81	0.023 624	gi 571510690 ref XP_006571789. 1	PREDICTED: uncharacterized protein LOC102655202 [Apis mellifera]
gene1 1355	32.67047 365	96.74080 887	0.3377 11396	-1.5661372 3	7.90E -05	.	.
gene1 3195	97.29592 46	288.6430 16	0.3370 80474	-1.5688350 37	0.002 167	gi 571579119 ref XP_003252014. 2	PREDICTED: uncharacterized protein LOC100578648, partial [Apis mellifera]
gene1 0056	39.12225 584	118.7470 751	0.3294 5869	-1.6018305 13	0.001 056	gi 571566904 ref XP_006558594. 1	PREDICTED: uncharacterized protein LOC100577569 [Apis mellifera]
gene1	20.18070	62.18972	0.3245	-1.6236999	0.000	gi 571578992 ref	PREDICTED: A disintegrin and metalloproteinase with thrombospondin motifs

3120	058	55	02165	9	533	XP_623804.2	14-like isoform 1 [Apis mellifera]
gene2 834	126.1246 183	393.6529 704	0.3203 95444	-1.6420744 62	0.010 328	gi 571518900 ref XP_006561027. 1	PREDICTED: sterile alpha and TIR motif-containing protein 1-like, partial [Apis mellifera]
gene7 174	16.21194 07	51.11779 043	0.3171 48698	-1.6567686 73	0.006 201	gi 48132776 ref XP_396702.1	PREDICTED: uncharacterized protein LOC413256 isoformX1 [Apis mellifera]
gene7 467	10.91426 458	34.58878 417	0.3155 43458	-1.6640893 8	0.004 085	.	.
gene8 868	11.82150 09	37.83324 908	0.3124 63275	-1.6782414 62	0.048 231	gi 571559117 ref XP_006566323. 1	PREDICTED: uncharacterized protein LOC413109 [Apis mellifera]
gene7 443	1603.344 513	5158.180 867	0.3108 35264	-1.6857779 08	7.49E -05	gi 571549367 ref XP_006561846. 1	PREDICTED: fibroin heavy chain isoform X2 [Apis mellifera]
gene1 880	13.21835 114	43.09203 928	0.3067 46939	-1.7048791 48	0.003 037	gi 571512020 ref XP_006561218. 1	PREDICTED: uncharacterized protein LOC725506 isoform X3 [Apis mellifera]
gene1 363	655.4129 007	2145.746 971	0.3054 47431	-1.7110039 87	1.66E -12	gi 571508732 ref XP_001120032. 3	PREDICTED: kynurenine/alpha-aminoadipate aminotransferase, mitochondrial-like [Apis mellifera]
gene6 906	10.05559 751	33.44306 053	0.3006 78148	-1.7337080 7	0.002 316	gi 19570323 dbj BAB86288.1	mariner transposase [Apis cerana]
gene1 0169	17.99085 777	64.55634 557	0.2786 84576	-1.8432949 39	0.000 567	.	.
gene2 80	13.24310 149	49.00560 397	0.2702 36471	-1.8877057	0.015 052	gi 571500862 ref XP_006561982.	PREDICTED: chaperone protein dnaJ 1, mitochondrial-like [Apis mellifera]

						1	
gene1 0019	56.14144 579	246.8273 148	0.2274 52322	-2.1363639 34	1.61E -11	gi 571566714 ref XP_006558560. 1	PREDICTED: cyclin-dependent kinase 6 isoform X1 [Apis mellifera]
gene1 658	12.28225 59	59.08787 112	0.2078 64248	-2.2662864 54	6.51E -05	gi 571510683 ref XP_006571787. 1	PREDICTED: uncharacterized protein LOC100577882 isoform X1 [Apis mellifera]
gene4 432	17.21091 291	86.88849 089	0.1980 80468	-2.3358414 69	0.025 08	gi 571529755 ref XP_006567836. 1	PREDICTED: uncharacterized protein LOC102653871 [Apis mellifera]
gene4 929	13.41665 165	70.86385 448	0.1893 29973	-2.4010252 72	6.97E -05	gi 328780665 ref XP_003249840. 1	PREDICTED: uncharacterized protein LOC100577819 [Apis mellifera]

Table S2. 22 down-regulated genes that related to the function of muscle Go term enriched in imidacloprid treatment groups

Gene	Putative function	NR:Seq-id	NR:Description
gene6235	somatic muscle development	gi 571540827 ref XP_394662.5	PREDICTED: L-lactate dehydrogenase-like isoform X2 [Apis mellifera]
gene10281	muscle attachment	gi 328785317 ref XP_001120437.2	PREDICTED: integrin alpha-PS2 isoform X1 [Apis mellifera]
gene151	muscle attachment	gi 571500407 ref XP_006559949.1	PREDICTED: protein muscleblind-like [Apis mellifera]
gene3021	muscle attachment	gi 571520122 ref XP_006568040.1	PREDICTED: guanine nucleotide-releasing factor 2-like isoform X1 [Apis mellifera]
gene3362	muscle attachment	gi 571523080 ref XP_006560680.1	PREDICTED: protein held out wings [Apis mellifera]
gene4877	muscle attachment	gi 571532839 ref XP_006560106.1	PREDICTED: epidermal growth factor receptor-like, partial [Apis mellifera]
gene13340	microtubule related	gi 328794317 ref XP_001123227.2	PREDICTED: short spindle protein 4-like [Apis mellifera]
gene1601	microtubule	gi 571510304 ref XP_006571710.1	PREDICTED: short spindle protein 4 isoform X1 [Apis mellifera]
gene10161	actin binding	gi 66522653 ref XP_391978.2	PREDICTED: LIM domain-containing protein jub-like [Apis mellifera]
gene10310	actin binding	gi 571568775 ref XP_006565137.1	PREDICTED: talin-1-like [Apis mellifera]
gene1229	actin binding	gi 571507718 ref XP_006571196.1	PREDICTED: nesprin-1-like [Apis mellifera]
gene12892	actin binding	gi 571578616 ref XP_006572452.1	PREDICTED: filamin-A-like [Apis mellifera]
gene1317	actin binding	gi 571508489 ref XP_006571351.1	PREDICTED: actin-binding LIM protein 2-like isoform X2 [Apis mellifera]
gene3198	actin binding	gi 571521398 ref XP_006569925.1	PREDICTED: formin-like protein CG32138-like [Apis mellifera]
gene3829	actin binding	gi 334724440 ref NP_001229316.1	PREDICTED: filamin-like [Apis mellifera]
gene3884	actin binding	gi 571526129 ref XP_006569380.1	PREDICTED: focal adhesion kinase 1 isoform X1 [Apis mellifera]
gene8492	actin binding	gi 571556561 ref XP_006557505.1	PREDICTED: protein-methionine sulfoxide oxidase Mical isoform X1 [Apis mellifera]
gene1228	titin-like	gi 571507693 ref XP_006571189.1	PREDICTED: titin-like isoform X1 [Apis mellifera]
gene12931	titin-like	gi 571539407 ref XP_006564375.1	PREDICTED: titin isoform X13 [Apis mellifera]
gene5936	titin-like	gi 571539411 ref XP_006564376.1	PREDICTED: titin isoform X14 [Apis mellifera]
gene7087		gi 571547082 ref XP_006569898.1	PREDICTED: dentin sialophosphoprotein [Apis mellifera]
gene8280		gi 328786663 ref XP_001121883.2	PREDICTED: trichohyalin isoform X1 [Apis mellifera]

Table S3. 28 overexpressed ribosomal protein genes Go term enriched in imidacloprid treatment groups

Gene	NR:Seq-id	NR:Description
gene5792	gi 307173970 gb EFN64700.1	40S ribosomal protein S15 [Camponotus floridanus]
gene11955	gi 571576123 ref XP_624943.3	40S ribosomal protein S7 [Apis mellifera]
gene10549	gi 66524293 ref XP_393965.2	40S ribosomal protein SA [Apis mellifera]
gene4123	gi 572272221 ref XP_006614024.1	40S ribosomal protein S11-like isoform X1 [Apis dorsata]
gene3414	gi 156554296 ref XP_001602465.1	40S ribosomal protein S14 [Nasonia vitripennis]
gene292	gi 350404704 ref XP_003487192.1	40S ribosomal protein S17 [Bombus impatiens]
gene13055	gi 759079256 ref XP_011349442.1	40S ribosomal protein S19-like isoform X1 [Cerapachys biroi]
gene4229	gi 645015869 ref XP_001601386.2	40S ribosomal protein S29 [Nasonia vitripennis]
gene159	gi 110767080 ref XP_001120419.1	40S ribosomal protein S6-like [Apis mellifera]
gene7353	gi 571547971 ref XP_006561561.1	40S ribosomal protein S8 isoform X1 [Apis mellifera]
gene10910	gi 110762954 ref XP_001121176.1	60S ribosomal protein L34 isoformX1 [Apis mellifera]
gene7830	gi 572268139 ref XP_006612127.1	60S acidic ribosomal protein P0-like [Apis dorsata]
gene387	gi 571501696 ref XP_006563278.1	60S ribosomal protein L10a [Apis mellifera]
gene12634	gi 380023818 ref XP_003695708.1	60S ribosomal protein L12 [Apis florea]
gene12807	gi 66552169 ref XP_625152.1	60S ribosomal protein L28 [Apis mellifera]
gene5872	gi 383855926 ref XP_003703461.1	60S ribosomal protein L29-1 [Megachile rotundata]
gene6926	gi 48142237 ref XP_397314.1	60S ribosomal protein L31 isoform 2 [Apis mellifera]
gene8822	gi 380029575 ref XP_003698444.1	60S ribosomal protein L32 [Apis florea]
gene7324	gi 571548748 ref XP_006561728.1	60S ribosomal protein L35a isoform X1 [Apis mellifera]
gene2686	gi 755959992 ref XP_011304587.1	60S ribosomal protein L37a [Fopius arisanus]
gene11421	gi 66525285 ref XP_392071.2	60S ribosomal protein L4 isoform 1 [Apis mellifera]
gene795	gi 805784468 ref XP_003703131.2	60S ribosomal protein L9 [Megachile rotundata]
gene8178	gi 297591983 ref NP_001172073.1	60S acidic ribosomal protein P1 [Apis mellifera]

gene10647	gi 66551967 ref XP_624896.1	60S ribosomal protein L13 isoform 1 [Apis mellifera]
gene10797	gi 110762813 ref XP_625009.2	60S ribosomal protein L22 isoform 1 [Apis mellifera]
gene11923	gi 66526748 ref XP_624696.1	60S ribosomal protein L27a isoform X2 [Apis mellifera]
gene3735	gi 322788733 gb EFZ14326.1	hypothetical protein SINV_15101, partial [Solenopsis invicta]
gene6373	gi 292494904 ref NP_001167614.1	ribosomal protein L35 [Apis mellifera]

Table S4. Sequences of primers for the genes tested

Gene Name	Gene ID-F(R)	Primers	Product length (bp)
AADAT	gene1363-F	GCTCAATCGTATTCTCTGTCT	195
	gene1363-R	CTTTCACCTTTCTTTACCTTC	
Cdk6	gene10019-F	GTTGCCTGAGAACACGATTG	192
	gene10019-R	TTCTGCCCGCTGTACTTCAT	
RpS19	gene13055-F	CTACATTCGCAGCCCAATCG	117
	gene13055-R	GCCTTACGTGCAACACCACC	
Syne1	gene1229-F	ATTGAGAACTTCCGTAATCGC	240
	gene1229-R	TGAACAGTAACATCCTGAGCCA	
RpL31	gene6926-F	AGTGCTATGAGCGAGGTTGTG	142
	gene6926-R	CATCTGGAGTTCCCATTTGTT	
RpS7	gene11955-F	CTGGAATTGGAAATGAATAGCG	128
	gene11955-R	GCCTTTAACTTTGGCATGGGTA	
Bmp7	gene2464-F	CAGAGGAAGGGATCAAACAGAT	263
	gene2464-R	AAGCATGAAGTAAGGGACTG	
RPL35	gene6373-F	CCTTTTTCCGTTGAAGAGGTAT	138
	gene6373-R	ACTTTTGCCACTCGAAGATTTG	
SP28	gene3689-F	CTGTCTACCGTTCCAACACTCG	126

	gene3689-R	AGCACGCTCACCGTAACTTTCT	
mapf	gene2328-F	TTCTCTCTCCCTAACACCTTGC	145
	gene2328-R	AGATAAATTCGATCATCCCGTC	
β -actin	actin-F	TTGGTATGCCAACACTGTCCTTT	120
	actin-R	TGGCGCGATGATCTTAATTT	