

Table S1. Primers design of selected genes for RT-qPCR.

Genes	Primer Sequence	
ARF1	Forward: GATGCCGTCCTGTTGATTTT	Reverse: GGCCCAGCTTGTCTGTTATC
HMGR	Forward: TCGCCTGCTTGTCGGTTAT	Reverse: CATACCTGTGTGCGTGGAC
Desaturase	Forward: TGCTTATTTGCACGCCAT CG	Reverse: TCGGTCTCGCTGTACTT GTG
FPPS	Forward: TACCCGGCAAAAATGTT CGT	Reverse: CCTTGGCCACGATATAACTCC

Note: The primer sequences of ARF1 were followed by [32].

Table S2. Statistics of the overall sequences

Categories	Transcript	Unigene
Sequence Number	125338	42389
Max. Length (bp)	32626	32626
Mean Length (bp)	1558.19	1233.27
N50 (bp)	2458	2212
N50 Sequence No.	22645	6340
N90 (bp)	657	449
N90 Sequence No.	81323	28021
GC%	36.33	35.90

Table S3. Annotations of the overall sequences

Database Number Percentage	Database Percentage	Number	Database Number Percentage
NR	16364		38.60
GO	12078		28.49
KEGG	9570		22.58
Pfam	11649		27.48
eggNOG	15674		36.98
Swissprot	12730		30.03
In all database	6474		15.27

Table S4. The most significantly different expression pathway of the KEGG pathway analysis for starved vs normally fed male beetles.

Pathway ID	Pathway	DEG_number	total_number	p-Value	FDR
ko03040	Spliceosome	60	207	6.37×10^{-10}	9.91×10^{-08}
ko00520	Amino sugar and nucleotide sugar	39	107	5.06×10^{-10}	9.91×10^{-08}

	metabolism					
ko00500	Starch and sucrose metabolism	25	69	7.44×10^{-07}	7.72×10^{-05}	
ko03050	Proteasome	23	69	1.04×10^{-05}	0.00081	
ko03008	Ribosome biogenesis in eukaryotes	33	121	1.89×10^{-05}	0.0012	
ko03430	Mismatch repair	13	30	3.95×10^{-05}	0.0020	
ko03030	DNA replication	18	53	7.10×10^{-05}	0.0032	
ko04910	Insulin signaling pathway	39	167	0.00015	0.0060	
ko05134	Legionellosis	20	67	0.00022	0.0076	
	Glycosphingolipid biosynthesis - ganglio series					
ko00604		6	9	0.00028	0.0087	
ko04612	Antigen processing and presentation	25	95	0.00034	0.0097	
ko04141	Protein processing in endoplasmic reticulum	44	209	0.00069	0.017	
ko00052	Galactose metabolism	18	62	0.00065	0.017	
ko04213	Longevity regulating pathway - multiple species	23	91	0.0011	0.024	
	Glycosphingolipid biosynthesis - globo and isoglobo series					
ko00603		6	11	0.0012	0.025	

Table S5. Information of top 10 up-regulated and down-regulated expressed genes (DEGs) in different comparisons.

Gene ID	Description	log ₂ Fold Change	adjustedp- Value	Best Hit
DN36036	Prostatic acid phosphatase	-5.80	0.0010	Tribolium castaneum
DN14259	salivary protein	-2.59	1.75× 10 ⁻⁰⁷	Phlebotomus ariasi
DN63954	putative sugar transporter 25	-2.56	0.00082	Phaedon cochleariae
DN14137	Protein phosphatase 2C containing protein	-2.55	9.92× 10 ⁻⁰⁵	Brugia malayi
DN31519	insulin-degrading enzyme	-2.38	4.95× 10 ⁻¹⁴	Tribolium castaneum
DN21681	3-phosphoinositide-dependent protein kinase 1-like isoform X1	-2.25	0.00080	Priapulus caudatus
DN27944	insulin-degrading enzyme	-2.21	5.25× 10 ⁻⁰⁹	Tribolium castaneum
DN63976	alternative oxidase, mitochondrial-like	-2.19	0.0019	Amphimedon queenslandica
DN59540	Alcohol dehydrogenase [NADP(+)]	-2.06	6.60× 10 ⁻⁰⁶	Strongyloides ratti
DN33569	Serine/threonine-protein kinase Nek8	-1.91	0.0010	Crassostrea gigas
DN9923	glycoside hydrolase family 1	5.90	4.72× 10 ⁻⁰⁶	Phyllotreta striolata
DN8951	cytochrome P450 monooxygenase	4.89	0.00025	Tribolium castaneum
DN26488	glutamate receptor ionotropic, kainate 2 isoform X6	4.37	0.023	Tribolium castaneum
DN3904	chitinase	4.27	2.17× 10 ⁻⁵⁸	Monochamus alternatus
DN14148	transmembrane protease serine 9	4.22	0.030	Tribolium castaneum
DN11370	Potassium channel subfamily T member 1-like Protein	4.18	0.021	Tribolium castaneum
DN13853	vitellogenin receptor	4.08	0.042	Tribolium

DN812	Lipase 3	3.83	1.55× 10 ⁻²⁹	castaneum Zootermopsis nevadensis
DN12993	cytochrome P450 6bq17	3.72	0.013	Leptinotarsa decemlineata
DN39974	general odorant-binding protein 72	3.76	0.012	Tribolium castaneum

Table S6. All the putative genes in pheromone biosynthesis via the MVA pathway in *C. ferrugineus*

Sequence Name	Length(bp)	Description	Best blast Hit
DN8502	2684	3-hydroxy-3-methylglutaryl coenzyme A synthase	gi 859132804 gb AKO63317.1 3-hydroxy-3-methylglutaryl coenzyme A synthase (<i>Leptinotarsa decemlineata</i>)
DN14	3765	3-hydroxy-3-methylglutaryl coenzyme A reductase 2	gi 859132811 gb AKO63319.1 3-hydroxy-3-methylglutaryl coenzyme A reductase 2 (<i>Leptinotarsa decemlineata</i>)
DN13258	2520	acetyl-CoA acetyltransferase 2	gi 983657959 gb AMB37467.1 acetyl-CoA acetyltransferase 2 (<i>Leptinotarsa decemlineata</i>)
DN7232	1958	acetyl-CoA acetyltransferase, mitochondrial isoform X1	gi 189234785 ref XP_975008.2 PREDICTED: acetyl-CoA acetyltransferase, mitochondrial isoform X1 (<i>Tribolium castaneum</i>)
DN4867	1986	mevalonate kinase	gi 859132814 gb AKO63320.1 mevalonate kinase (<i>Leptinotarsa decemlineata</i>)
DN1057	1828	diphosphomevalonate decarboxylase	gi 385200014 gb AFI45055.1 diphosphomevalonate decarboxylase (<i>Dendroctonus ponderosae</i>)
DN14040	2079	geranylgeranyl diphosphate synthase	gi 549439117 gb AGX25357.1 geranylgeranyl diphosphate synthase (<i>Pissodes strobi</i>)
DN43621	412	isopentenyl diphosphate synthase	gi 943360326 gb ALL35402.1 isopentenyl diphosphate synthase (<i>Psylliodes chrysocephalus</i>)
DN34563	1439	isoprenyl diphosphate synthase	gi 449139004 gb AGE89831.1 isoprenyl diphosphate synthase

			(<i>Phaedon cochleariae</i>)
DN17749	1283	isopentenyl diphosphate synthase	gi 943360322 gb ALL35400.1 isopentenyl diphosphate synthase (<i>Phyllotreta striolata</i>)
DN17069	854	farnesyl pyrophosphate synthase	gi 282158091 ref NP_001164089.1 farnesyl pyrophosphate synthase (<i>Tribolium castaneum</i>)
DN3052	2122	farnesyl pyrophosphate synthase	gi 1008444024 ref XP_015836774.1 PREDICTED: farnesyl pyrophosphate synthase isoform X1 (<i>Tribolium castaneum</i>)
DN34020	437	cytochrome P450-4c	gi 936578848 ref XP_014204067.1 PREDICTED: cytochrome P450 4C1- like (<i>Copidosoma floridanum</i>)
DN57140	387	Cytochrome P450-6a	gi 1004399086 gb KYB27039.1 Cytochrome P450 6a2-like Protein (<i>Tribolium castaneum</i>)
DN11348	539	Cytochrome P450-6a	gi 91084707 ref XP_969633.1 PREDICTED: probable cytochrome P450 6a23 (<i>Tribolium castaneum</i>)
DN9170	1751	cytochrome P450-4c	gi 91094839 ref XP_971612.1 PREDICTED: cytochrome P450 4C1 (<i>Tribolium castaneum</i>)
DN1125	319	cytochrome P450 9e	gi 91088761 ref XP_975385.1 PREDICTED: cytochrome P450 9e2 (<i>Tribolium castaneum</i>)
DN25899	463	cytochrome P450 9e	gi 1008450276 ref XP_015838490.1 PREDICTED: cytochrome P450 9e2-like (<i>Tribolium castaneum</i>)
DN14817	414	cytochrome P450 6b	gi 478734979 gb AGJ51945.1 cytochrome P450 CYP6BQ22 (<i>Dastarcus helophoroides</i>)

Table S7. All the putative genes in pheromone biosynthesis via the FAS pathway in *C. ferrugineus*

Sequence Name	Length	Description	Best blast Hit
DN26988	5727	acetyl-CoA carboxylase	gi 919000753 ref XP_013405631.1 PREDICTED: acetyl-CoA carboxylase-like, partial (<i>Lingula anatina</i>)
DN2984	5449	acetyl-CoA carboxylase	gi 919033674 ref XP_013400502.1 PREDICTED: acetyl-CoA carboxylase-like isoform X1 (<i>Lingula</i>

			<i>anatina</i>)
DN4246	8236	acetyl-CoA carboxylase	gi 642926044 ref XP_008194742.1 PREDICTED: acetyl-CoA carboxylase isoform X4 (<i>Tribolium castaneum</i>)
DN451	7614	fatty acid synthase	gi 998254491 gb AMK38868.1 fatty acid synthase 1 (<i>Colaphellus bowringi</i>)
DN451	448	fatty acid synthase	gi 478250393 gb ENN70888.1 hypothetical protein YQE_12293, partial (<i>Dendroctonus ponderosae</i>)
DN5055	7842	fatty acid synthase	gi 546672885 gb ERL84608.1 hypothetical protein D910_02036 (<i>Dendroctonus ponderosae</i>)
DN13200	2686	fatty acid synthase	gi 936579093 ref XP_014204155.1 PREDICTED: fatty acid synthase-like isoform X1 (<i>Copidosoma floridanum</i>)
DN13306	898	fatty acid synthase	gi 478252126 gb ENN72557.1 hypothetical protein YQE_10897, partial (<i>Dendroctonus ponderosae</i>)
DN13809	4400	fatty acid synthase	gi 833654169 gb AKM28424.1 fatty acid synthase 2 (<i>Aphis gossypii</i>)
DN14149	720	fatty acid synthase	gi 478250393 gb ENN70888.1 hypothetical protein YQE_12293, partial (<i>Dendroctonus ponderosae</i>)
DN14585	637	fatty acid synthase	gi 808127224 ref XP_012166572.1 PREDICTED: LOW QUALITY PROTEIN: fatty acid synthase (<i>Bombus terrestris</i>)
DN17237	853	fatty acid synthase	gi 350407733 ref XP_003488176.1 PREDICTED: fatty acid synthase (<i>Bombus impatiens</i>)
DN20777	1243	fatty acid synthase	gi 1008441829 ref XP_015836196.1 PREDICTED: fatty acid synthase (<i>Tribolium castaneum</i>)
DN2296	6583	fatty acid synthase	gi 642914795 ref XP_008190356.1 PREDICTED: fatty acid synthase (<i>Tribolium castaneum</i>)
DN24241	430	fatty acid synthase	gi 827552646 ref XP_012548082.1 PREDICTED: LOW QUALITY PROTEIN: p270 isoform X1 (<i>Bombyx mori</i>)
DN24375	356	fatty acid synthase	gi 939666222 ref XP_014280344.1 PREDICTED: fatty acid synthase-like

			(<i>Halyomorpha halys</i>)
DN24459	327	fatty acid synthase	gi 998254491 gb AMK38868.1 fatty acid synthase 1 (<i>Colaphellus bowringi</i>)
DN26951	397	fatty acid synthase	gi 970895185 ref XP_015113057.1 PREDICTED: fatty acid synthase-like (<i>Diachasma alloeum</i>)
DN27948	1080	fatty acid synthase	gi 478250393 gb ENN70888.1 hypothetical protein YQE_12293, partial (<i>Dendroctonus ponderosae</i>)
DN3683	8015	fatty acid synthase	gi 642910328 ref XP_008200285.1 PREDICTED: fatty acid synthase (<i>Tribolium castaneum</i>)
DN37960	1788	fatty acid synthase	gi 972194346 ref XP_015179002.1 PREDICTED: fatty acid synthase (<i>Polistes dominula</i>)
DN38748	329	fatty acid synthase	gi 998254491 gb AMK38868.1 fatty acid synthase 1 (<i>Colaphellus bowringi</i>)
fatty acid transport protein			
DN805	2935	fatty acid transport protein	gi 642923280 ref XP_008193688.1 PREDICTED: long-chain fatty acid transport protein 4 isoform X1 (<i>Tribolium castaneum</i>)
DN18413	396	fatty acid transport protein	gi 642923280 ref XP_008193688.1 PREDICTED: long-chain fatty acid transport protein 4 isoform X1 (<i>Tribolium castaneum</i>)
DN2523	2017	fatty acid transport protein	gi 91086105 ref XP_967675.1 PREDICTED: long-chain fatty acid transport protein 4 (<i>Tribolium castaneum</i>)
Acyl-CoA dehydrogenase			
DN2581	3478	Acyl-CoA dehydrogenase	gi 642938637 ref XP_008197587.1 PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial (<i>Tribolium castaneum</i>)
DN348	1959	Acyl-CoA dehydrogenase	gi 91079744 ref XP_970506.1 PREDICTED: probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial (<i>Tribolium castaneum</i>)
DN5059	2150	Acyl-CoA dehydrogenase	gi 642915063 ref XP_008190394.1 PREDICTED: acyl-CoA

		se	dehydrogenase family member 9, mitochondrial (<i>Tribolium castaneum</i>)
DN811	2224	Acyl-CoA dehydrogenase	gi 91088951 ref XP_973830.1 PREDICTED: short-chain specific acyl-CoA dehydrogenase, mitochondrial (<i>Tribolium castaneum</i>)
DN9993	534	Acyl-CoA dehydrogenase	gi 662190906 ref XP_008468241.1 PREDICTED: probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial (<i>Diaphorina citri</i>)
DN10841	2696	Acyl-CoA dehydrogenase	gi 91076006 ref XP_966406.1 PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial (<i>Tribolium castaneum</i>)
DN1273	1691	Acyl-CoA dehydrogenase	gi 91079744 ref XP_970506.1 PREDICTED: probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial (<i>Tribolium castaneum</i>)
DN13359	326	Acyl-CoA dehydrogenase	gi 642938637 ref XP_008197587.1 PREDICTED: short/branched chain specific acyl-CoA dehydrogenase, mitochondrial (<i>Tribolium castaneum</i>)
DN9959	2483	3-ketoacyl-CoA thiolase	gi 91087491 ref XP_968373.1 PREDICTED: 3-ketoacyl-CoA thiolase, mitochondrial (<i>Tribolium castaneum</i>)
DN16536	474	3-ketoacyl-CoA thiolase	gi 663287133 ref XP_008500452.1 PREDICTED: 3-ketoacyl-CoA thiolase, peroxisomal (<i>Calypte anna</i>)
3-hydroxyacyl-CoA dehydrogenase			
DN164	3279	3-hydroxyacyl-CoA dehydrogenase	gi 91078584 ref XP_971954.1 PREDICTED: 3-hydroxyacyl-CoA dehydrogenase type-2 (<i>Tribolium castaneum</i>)
enoyl-CoA hydratase			
DN3785	1584	3-hydroxyacyl-CoA dehydrogenase	gi 91076844 ref XP_974775.1 PREDICTED: probable enoyl-CoA hydratase (<i>Tribolium castaneum</i>)

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DN10753	1604	Desaturase	gi 328722879 ref XP_003247697.1 PREDICTED: acyl-CoA Delta (11) desaturase isoform X1 (<i>Acyrtosiphon pisum</i>)
DN14591	2190	Desaturase	gi 302371202 ref NP_001180578.1 Z9 acyl-CoA desaturase B (<i>Tribolium castaneum</i>)
DN35858	786	Desaturase	gi 768419096 ref XP_011550250.1 PREDICTED: stearyl-CoA desaturase 5-like (<i>Plutella xylostella</i>)
DN4192	2745	Desaturase	gi 984880662 ref NP_001306191.1 acyl-CoA Delta(11) desaturase (<i>Tribolium castaneum</i>)
DN6011	2756	Desaturase	gi 907678927 ref XP_013106080.1 PREDICTED: acyl-CoA Delta(11) desaturase (<i>Stomoxys calcitrans</i>)
DN7337	1764	Desaturase	gi 1000734683 ref XP_015589799.1 PREDICTED: acyl-CoA Delta(11) desaturase isoform X1 (<i>Cephus cinctus</i>)
DN748	2342	Desaturase	gi 984880672 ref NP_001306192.1 acyl-CoA Delta(11) desaturase-like (<i>Tribolium castaneum</i>)
DN1161	2785	Fatty acyl- CoA reductase	gi 642916861 ref XP_008199532.1 PREDICTED: putative fatty acyl- CoA reductase CG5065 isoform X2 (<i>Tribolium castaneum</i>)
DN12539	2315	Fatty acyl- CoA reductase	gi 1008443007 ref XP_008194927.2 PREDICTED: fatty acyl-CoA reductase 1 isoform X1 (<i>Tribolium castaneum</i>)
DN12880	1378	Fatty acyl- CoA reductase	gi 189239820 ref XP_971534.2 PREDICTED: putative fatty acyl- CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN12939	2465	Fatty acyl- CoA reductase	gi 985386804 ref XP_015371677.1 PREDICTED: putative fatty acyl- CoA reductase CG5065 (<i>Diuraphis noxia</i>)
DN17133	303	Fatty acyl- CoA	gi 939637560 ref XP_014294630.1 PREDICTED: putative fatty acyl-

		reductase	CoA reductase CG5065, partial (<i>Halyomorpha halys</i>)
DN18398	850	Fatty acyl-CoA reductase	gi 91087837 ref XP_967757.1 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN18398	935	Fatty acyl-CoA reductase	gi 817187712 ref XP_012288416.1 PREDICTED: fatty acyl-CoA reductase 1 (<i>Orussus abietinus</i>)
DN2670	2084	Fatty acyl-CoA reductase	gi 91085011 ref XP_973467.1 PREDICTED: putative fatty acyl-CoA reductase CG8306 (<i>Tribolium castaneum</i>)
DN33105	2209	Fatty acyl-CoA reductase	gi 1008441937 ref XP_015836217.1 PREDICTED: fatty acyl-CoA reductase 1 isoform X2 (<i>Tribolium castaneum</i>)
DN36061	884	Fatty acyl-CoA reductase	gi 951561237 ref XP_014479570.1 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Dinoponera quadriceps</i>)
DN4075	2799	Fatty acyl-CoA reductase	gi 189238048 ref XP_001811309.1 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN4372	2406	Fatty acyl-CoA reductase	gi 189239820 ref XP_971534.2 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN4479	1174	Fatty acyl-CoA reductase	gi 659495078 gb AID66650.1 fatty acyl reductase (<i>Agrotis segetum</i>)
DN4898	2435	Fatty acyl-CoA reductase	gi 270008526 gb EFA04974.1 Putative fatty acyl-CoA reductase CG5065-like Protein (<i>Tribolium castaneum</i>)
DN50015	389	Fatty acyl-CoA reductase	gi 985386804 ref XP_015371677.1 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Diuraphis noxia</i>)
DN510	1975	Fatty acyl-CoA reductase	gi 572270973 ref XP_006613464.1 PREDICTED: putative fatty acyl-CoA reductase CG5065-like (<i>Apis dorsata</i>)

DN6636	2182	Fatty acyl-CoA reductase	gi 91084843 ref XP_966905.1 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN666	3915	Fatty acyl-CoA reductase	gi 91084571 ref XP_973790.1 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN7489	2261	Fatty acyl-CoA reductase	gi 189239820 ref XP_971534.2 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN9924	1623	Fatty acyl-CoA reductase	gi 91087837 ref XP_967757.1 PREDICTED: putative fatty acyl-CoA reductase CG5065 (<i>Tribolium castaneum</i>)
DN5736	1725	acyl-CoA-binding protein	gi 91090704 ref XP_974824.1 PREDICTED: putative acyl-CoA-binding protein (<i>Tribolium castaneum</i>)
DN1181	5019	acyl-CoA-binding protein	gi 676433961 ref XP_009047071.1 hypothetical protein LOTGIDRAFT_205113 (<i>Lottia gigantea</i>)
DN13258	2520	acetyl-CoA acetyltransferase (ACAT)	gi 983657959 gb AMB37467.1 acetyl-CoA acetyltransferase 2 (<i>Leptinotarsa decemlineata</i>)
DN7232	1958	acetyl-CoA acetyltransferase (ACAT)	gi 189234785 ref XP_975008.2 PREDICTED: acetyl-CoA acetyltransferase, mitochondrial isoform X1 (<i>Tribolium castaneum</i>)

Reference

1. Zhang, M.; Du, M.-Y.; Wang, G.-X.; Wang, Z.-Y.; Lu, Y.-J. Identification, mRNA expression, and functional analysis of chitin synthase 2 gene in the rusty grain beetle, *Cryptolestes ferrugineus*. *J. Stored Prod. Res.* **2020**, *87*, 101622. <https://doi.org/10.1016/j.jspr.2020.101622>.