Supplementary Material

Table S1. Transcript derived fragments differentially regulated in *Diuraphis noxia* biotypes SA1 and SAM with the different primer pairs ($P < 0.05$).

Primer pair	***Diuraphis noxia* biotype**	
	SA1	**SAM**
MTG / TGT	1768	1179
MTG / TCA	1664	1750
MGA / TGA	2333	1879

Table S2. Sequenced transcript derived fragments to which putative identity could be assigned following BLASTn and BLASTx searches[56] using BLAST2GO.[57] Sequence name, sequence length, number of hits, mean similarity and E-values, number of GO terms and descriptions, as well as enzyme codes are indicated.

Seq. Name	**Seq. Description**	**Seq. Length**	**#Hits**	**min. E-Value**	**mean Similarity**	**#GOs**	**GOs**	**Enzyme Codes**
11.1_M13R.ab1	laccase 2	614	100	2.05E-95	80.97%	5	F:copper ion binding; F:L-ascorbate oxidase activity; F:hydroquinone:oxygen oxidoreductase activity; P:chitin-based cuticle development; P:oxidation-reduction process	EC:1.10.3.2; EC:1.10.3.3
11.2_M13R.ab1	laccase 2	615	100	4.23E-96	81.33%	5	F:copper ion binding; F:L-ascorbate oxidase activity; F:hydroquinone:oxygen oxidoreductase activity; P:chitin-based cuticle development; P:oxidation-reduction process	EC:1.10.3.2; EC:1.10.3.3
12.1_M13R.ab1	cop9 signalosome complex subunit 5	594	100	5.77E-86	93.19%	24	C:transcription factor complex; C:cytoplasm; C:COP9 signalosome; C:nuclear periphery; F:transcription coactivator activity; F:protein binding; F:metallopeptidase activity; F:NEDD8 activating enzyme activity; F:metal ion binding; P:compound eye photoreceptor cell differentiation; P:proteolysis; P:mitotic G2 DNA damage checkpoint; P:oocyte dorsal/ventral axis specification; P:oocyte anterior/posterior axis specification; P:axonogenesis; P:glial cell migration; P:cullin deneddylation; P:negative regulation of proteasomal ubiquitin-dependent protein catabolic process; P:negative regulation of lamellocyte differentiation; P:negative regulation of hemocyte proliferation; P:positive regulation of cell cycle; P:positive regulation of transcription from RNA polymerase II promoter; P:regulation of JNK cascade; P:protein stabilization	-

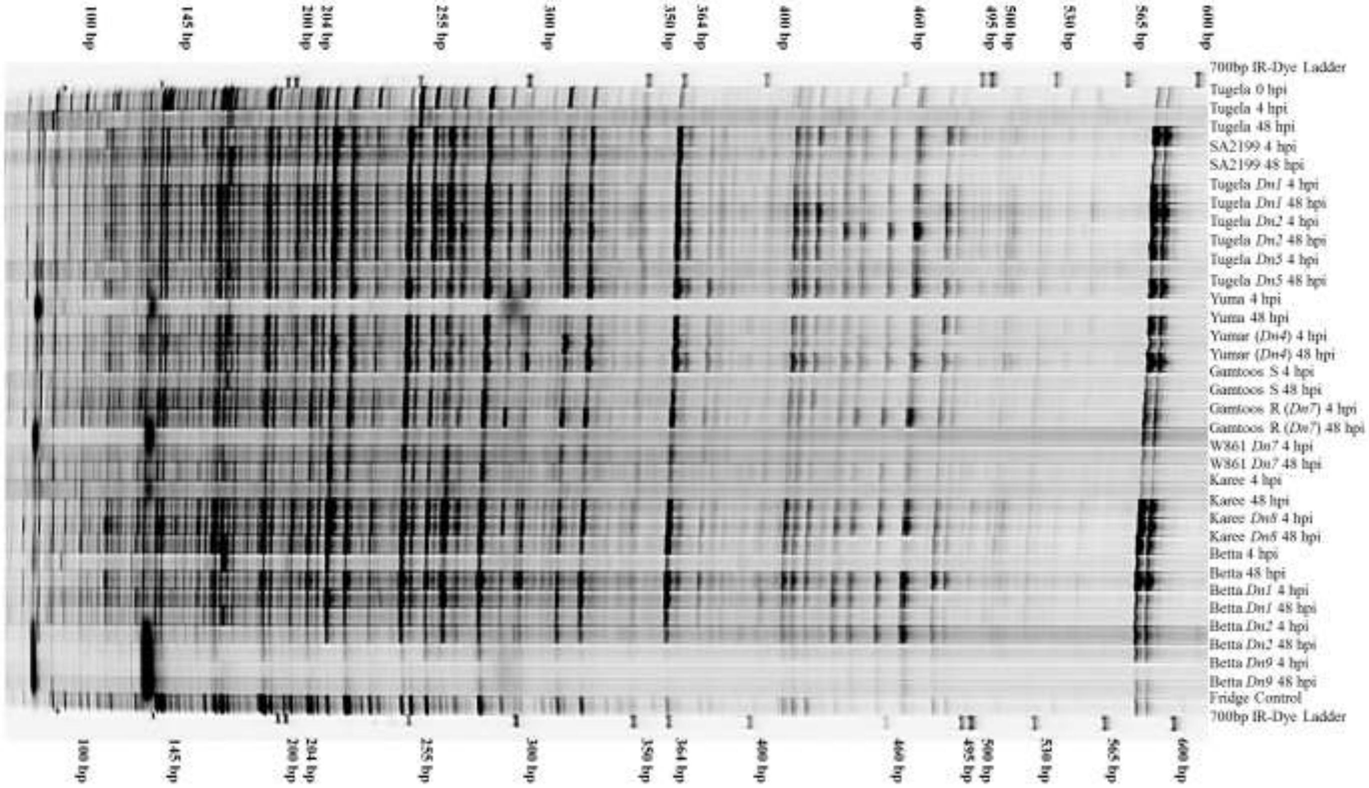
Seq. Name	Seq. Description	Seq. Length	#Hits	min. E-Value	mean Similarity	#GOs	GOs	Enzyme Codes
12.2_M13R.ab1	cop9 signalosome complex subunit 5	592	100	4.88E-86	93.01%	24	C:transcription factor complex; C:cytoplasm; C:COP9 signalosome; C:nuclear periphery; F:transcription coactivator activity; F:protein binding; F:metallopeptidase activity; F:NEDD8 activating enzyme activity; F:metal ion binding; P:compound eye photoreceptor cell differentiation; P:proteolysis; P:mitotic G2 DNA damage checkpoint; P:oocyte dorsal/ventral axis specification; P:oocyte anterior/posterior axis specification; P:axonogenesis; P:glial cell migration; P:cullin deneddylation; P:negative regulation of proteasomal ubiquitin-dependent protein catabolic process; P:negative regulation of lamellocyte differentiation; P:negative regulation of hemocyte proliferation; P:positive regulation of cell cycle; P:positive regulation of transcription from RNA polymerase II promoter; P:regulation of JNK cascade; P:protein stabilization	-
13.1_M13R.ab1	60s ribosomal protein l18	553	100	3.29E-62	78.31%	15	C:membrane; C:cytosolic large ribosomal subunit; C:intracellular membrane-bounded organelle; F:sequence-specific DNA binding transcription factor activity; F:RNA binding; F:structural constituent of ribosome; F:sequence-specific DNA binding; P:mitotic spindle elongation; P:nuclear-transcribed mRNA catabolic process, nonsense-mediated decay; P:regulation of transcription, DNA-dependent; P:translational initiation; P:translational elongation; P:translational termination; P:SRP-dependent cotranslational protein targeting to membrane; P:viral transcription	-
13.2_M13R.ab1	cullin-3	558	100	6.58E-53	86.75%	40	C:nuclear ubiquitin ligase complex; C:Golgi apparatus; C:polar microtubule; C:SCF ubiquitin ligase complex; C:Cul3-RING ubiquitin ligase complex; C:female germline ring canal; F:ubiquitin-protein ligase activity; F:cyclin binding; F:POZ domain binding; F:ubiquitin protein ligase binding; P:G1/S transition of mitotic cell cycle; P:mitotic anaphase; P:protein polyubiquitination; P:cytokinesis; P:compound eye morphogenesis; P:trophectodermal cellular morphogenesis; P:protein monoubiquitination; P:activation of cysteine-type endopeptidase activity involved in apoptotic process; P:cell cycle arrest; P:integrin-mediated signaling pathway; P:sperm individualization; P:gastrulation; P:axonogenesis; P:imaginal disc-derived wing morphogenesis; P:cyclin catabolic process; P:positive regulation of cell proliferation; P:Wnt receptor signaling pathway; P:cell migration; P:stem cell division; P:regulation of proteolysis; P:sleep; P:positive regulation of cytokinesis; P:negative regulation of Rho protein signal transduction; P:embryonic cleavage; P:stress fiber assembly; P:regulation of circadian sleep/wake cycle, sleep; P:locomotor rhythm; P:COPII vesicle coating; P:dendrite morphogenesis; P:intrinsic apoptotic signaling pathway	EC:6.3.2.19

Seq. Name	Seq. Description	Seq. Length	#Hits	min. E-Value	mean Similarity	#GOs	GOs	Enzyme Codes
14.1_M13R.ab1	voltage-gated potassium channel subunit beta-2 isoform x2	289	3	5.71E-16	91.33%	0	-	-
14.2_M13-R.ab1	collagen alpha-1 partial	508	100	3.73E-70	79.96%	14	C:collagen type IV; C:basal lamina; C:endoplasmic reticulum lumen; C:neuromuscular junction; F:extracellular matrix structural constituent; F:hydrolase activity; F:platelet-derived growth factor binding; P:angiogenesis; P:axon guidance; P:neuromuscular junction development; P:extracellular matrix disassembly; P:collagen catabolic process; P:epithelial cell differentiation; P:cellular response to amino acid stimulus	-
15.1_M13-R.ab1	collagen alpha-1 chain	505	100	1.55E-69	80.76%	14	C:collagen type IV; C:basal lamina; C:endoplasmic reticulum lumen; C:neuromuscular junction; F:extracellular matrix structural constituent; F:hydrolase activity; F:platelet-derived growth factor binding; P:angiogenesis; P:axon guidance; P:neuromuscular junction development; P:extracellular matrix disassembly; P:collagen catabolic process; P:epithelial cell differentiation; P:cellular response to amino acid stimulus	-
15.2_M13-R.ab1	transmembrane protein mitochondrial isoform x2	512	100	2.58E-73	56.39%	13	C:mitochondrial inner membrane; C:integral to membrane; C:sarcoplasmic reticulum; C:sarcomere; C:filamentous actin; C:investment cone; F:actin filament binding; P:glucose metabolic process; P:mitochondrion organization; P:regulation of lamellipodium assembly; P:pole plasm oskar mRNA localization; P:negative regulation of transcription, DNA-dependent; P:dendrite morphogenesis	-
16.1_M13-R.ab1	acidic mammalian chitinase-like	499	100	9.68E-67	78.70%	7	C:extracellular region; C:integral to membrane; F:chitinase activity; F:chitin binding; F:heparin binding; P:carbohydrate metabolic process; P:chitin catabolic process	EC:3.2.1.14
16.2_M13-R.ab1	monocarboxylate transporter	504	100	9.11E-66	79.69%	3	C:integral to membrane; F:secondary active monocarboxylate transmembrane transporter activity; P:transmembrane transport	-
17.2_M13-R.ab1	isoform b	479	100	6.89E-55	73.89%	8	C:apical plasma membrane; F:Notch binding; F:calcium ion binding; F:carbohydrate binding; P:cell adhesion; P:regulation of tube architecture, open tracheal system; P:negative regulation of Notch signaling pathway; P:muscle cell cellular homeostasis	-
17.3_M13-R.ab1	midnolin	473	100	4.25E-54	76.30%	2	C:nucleolus; P:lateral inhibition	-

Seq. Name	**Seq. Description**	**Seq. Length**	**#Hits**	**min. E-Value**	**mean Similarity**	**#GOs**	**GOs**	**Enzyme Codes**
18.1_M13-R.ab1	fatty acid synthase	448	100	6.62E-51	81.15%	13	F:NADPH:quinone reductase activity; F:[acyl-carrier-protein] S-acetyltransferase activity; F:[acyl-carrier-protein] S-malonyltransferase activity; F:3-oxoacyl-[acyl-carrier-protein] synthase activity; F:3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity; F:3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity; F:enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity; F:oleoyl-[acyl-carrier-protein] hydrolase activity; F:zinc ion binding; F:myristoyl-[acyl-carrier-protein] hydrolase activity; F:palmitoyl-[acyl-carrier-protein] hydrolase activity; P:biosynthetic process; P:oxidation-reduction process	EC:2.3.1.41; EC:4.2.1.61; EC:3.1.2.14; EC:2.3.1.38; EC:1.1.1.100; EC:2.3.1.39; EC:1.6.5.5; EC:1.3.1.10
18.2_M13-R.ab1	fatty acid synthase	447	100	1.11E-51	81.90%	14	C:lipid particle; F:NADPH:quinone reductase activity; F:[acyl-carrier-protein] S-acetyltransferase activity; F:[acyl-carrier-protein] S-malonyltransferase activity; F:3-oxoacyl-[acyl-carrier-protein] synthase activity; F:3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity; F:3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity; F:enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity; F:oleoyl-[acyl-carrier-protein] hydrolase activity; F:zinc ion binding; F:myristoyl-[acyl-carrier-protein] hydrolase activity; F:palmitoyl-[acyl-carrier-protein] hydrolase activity; P:biosynthetic process; P:oxidation-reduction process	EC:2.3.1.41; EC:4.2.1.61; EC:3.1.2.14; EC:2.3.1.38; EC:1.1.1.100; EC:2.3.1.39; EC:1.6.5.5; EC:1.3.1.10
22.1_M13-R.ab1	acidic mammalian chitinase-like	498	100	2.52E-65	78.55%	7	C:extracellular region; C:integral to membrane; F:chitinase activity; F:chitin binding; F:heparin binding; P:carbohydrate metabolic process; P:chitin catabolic process	EC:3.2.1.14
22.2_M13-R.ab1	voltage-gated potassium channel subunit beta-2 isoform x2	297	3	6.11E-16	91.33%	0	-	-
24.1_M13-R.ab1	acidic mammalian chitinase-like	499	100	8.18E-67	78.77%	7	C:extracellular region; C:integral to membrane; F:chitinase activity; F:chitin binding; F:heparin binding; P:carbohydrate metabolic process; P:chitin catabolic process	EC:3.2.1.14
24.2_M13-R.ab1	acidic mammalian chitinase-like	499	100	3.33E-66	78.80%	7	C:extracellular region; C:integral to membrane; F:chitinase activity; F:chitin binding; F:heparin binding; P:carbohydrate metabolic process; P:chitin catabolic process	EC:3.2.1.14
31.1_M13R.ab1	AF253496_1beta-galactosidase	454	2	9.37E-09	73.00%	0	-	-
42.2_M13-R.ab1	voltage-gated potassium channel subunit beta-2 isoform x2	401	3	9.13E-16	91.00%	0	-	-

Seq. Name	Seq. Description	Seq. Length	#Hits	min. E-Value	mean Similarity	#GOs	GOs	Enzyme Codes
42.3_M13-R.ab1	---NA---	297	0			0	-	-
44.2_M13-R.ab1	cytochrome oxidase subunit partial	296	4	1.13E-05	71.25%	3	F:ATPase activity; F:ATP binding; P:ATP catabolic process	
44.3_M13-R.ab1	protein	439	50	1.44E-10	78.10%	0	-	-
61.1_M13R.ab1	6-phosphogluconate decarboxylating	496	100	1.89E-60	87.99%	26	C:mitochondrion; F:phosphogluconate dehydrogenase (decarboxylating) activity; F:phosphoglycerate dehydrogenase activity; F:phospholipid binding; F:phosphogluconate 2-dehydrogenase activity; F:protein heterodimerization activity; F:NADP binding; F:NAD binding; P:nematode larval development; P:glutamine metabolic process; P:glycine metabolic process; P:L-serine biosynthetic process; P:threonine metabolic process; P:pentose-phosphate shunt, oxidative branch; P:gamma-aminobutyric acid metabolic process; P:regulation of gene expression; P:molting cycle, collagen and cuticulin-based cuticle; P:pentose biosynthetic process; P:D-gluconate metabolic process; P:taurine metabolic process; P:spinal cord development; P:glial cell development; P:neural tube development; P:neuron projection development; P:cellular response to oxidative stress; P:G1 to G0 transition	EC:1.1.1.43; EC:1.1.1.44; EC:1.1.1.95
61.2_M13R.ab1	PREDICTED: uncharacterized protein LOC100159805 isoform X2	600	3	4.46E-43	77.67%	0	-	-
62.1_M13R.ab1	PREDICTED: uncharacterized protein LOC100159805 isoform X2	599	2	1.21E-43	80.00%	0	-	-
63.2_M13-R.ab1	eukaryotic translation initiation factor 3 subunit b	614	100	5.09E-74	72.74%	11	C:cytosol; C:eukaryotic translation initiation factor 3 complex; C:eukaryotic 43S preinitiation complex; C:eukaryotic 48S preinitiation complex; F:nucleotide binding; F:mRNA binding; F:translation initiation factor activity; F:translation initiation factor binding; F:protein complex scaffold; P:formation of translation preinitiation complex; P:regulation of translational initiation	-
63.5_M13-R.ab1	beta-galactosidase	251	2	1.63E-07	78.00%	0	-	
64.2_M13-R.ab1	proton-associated sugar transporter a-like	557	100	2.29E-62	70.00%	9	C:integral to membrane; C:cytoplasmic vesicle; C:apical part of cell; F:glucose transmembrane transporter activity; F:sucrose:hydrogen symporter activity; P:glucose transport; P:sucrose transport; P:cell redox homeostasis; P:transmembrane transport	-

Seq. Name	**Seq. Description**	**Seq. Length**	**#Hits**	**min. E-Value**	**mean Similarity**	**#GOs**	**GOs**	**Enzyme Codes**
64.4_M13-R.ab1	lipid storage droplets surface-binding protein 1	568	66	5.01E-84	58.41%	8	C:lipid particle; C:protein-lipid complex; P:triglyceride mobilization; P:regulation of lipid storage; P:positive regulation of triglyceride catabolic process; P:neurogenesis; P:lipid particle organization; P:protein localization to lipid particle	-
65.1_M13-R.ab1	protein	557	100	2.30E-37	85.71%	5	C:nucleus; F:transcription regulatory region sequence-specific DNA binding; F:sequence-specific DNA binding transcription factor activity; P:regulation of transcription, DNA-dependent; P:multicellular organismal development	-
65.2_M13-R.ab1	lipid storage droplets surface-binding protein 1	567	66	5.70E-83	57.82%	3	P:macromolecule localization; P:single-organism cellular process; P:regulation of biological process	-
69.2_M13-R.ab1	AF310245_1beta-galactosidase	408	1	5.44E-04	73.00%	0	-	
69.4_M13-R.ab1	AF310245_1beta-galactosidase	371	1	2.79E-05	74.00%	0	-	
72.2_M13R.ab1	sphingomyelin phosphodiesterase	308	73	1.64E-19	81.71%	2	F:sphingomyelin phosphodiesterase activity; P:sphingomyelin catabolic process	EC:3.1.4.12
73.1_M13R.ab1	AF310245_1beta-galactosidase	318	1	2.06E-05	74.00%	0	-	
73.2_M13R.ab1	monocarboxylate transporter	322	100	2.09E-22	79.84%	3	C:integral to membrane; F:secondary active monocarboxylate transmembrane transporter activity; P:transmembrane transport	-
74.1_M13R.ab1	atp-binding cassette sub-family g member 4	317	3	2.86E-17	77.33%	0	-	
74.2_M13R.ab1	AF310245_1beta-galactosidase	311	1	1.98E-05	74.00%	0	-	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145 bp
200 bp
204 bp
255 bp
300 bp
350 bp
364 bp
400 bp
460 bp
495 bp
500 bp
530 bp
565 bp
600 bp
700bp IR-Dye Ladder
Tugela 0 hpi
Tugela 4 hpi
Tugela 48 hpi
SA2199 4 hpi
SA2199 48 hpi
Tugela *Dn1* 4 hpi
Tugela *Dn1* 48 hpi
Tugela *Dn2* 4 hpi
Tugela *Dn2* 48 hpi
Tugela *Dn5* 4 hpi
Tugela *Dn5* 48 hpi
Yuma 4 hpi
Yuma 48 hpi
Yumar (*Dn4*) 4 hpi
Yumar (*Dn4*) 48 hpi
Gamtoos S 4 hpi
Gamtoos S 48 hpi
Gamtoos R (*Dn7*) 4 hpi
Gamtoos R (*Dn7*) 48 hpi
W861 *Dn7* 4 hpi
W861 *Dn7* 48 hpi
Karee 4 hpi
Karee 48 hpi
Karee *Dn8* 4 hpi
Karee *Dn8* 48 hpi
Betta 4 hpi
Betta 48 hpi
Betta *Dn1* 4 hpi
Betta *Dn1* 48 hpi
Betta *Dn2* 4 hpi
Betta *Dn2* 48 hpi
Betta *Dn9* 4 hpi
Betta *Dn9* 48 hpi
Fridge Control
700bp IR-Dye Ladder
100 bp
145 bp
200 bp
204 bp
255 bp
300 bp
350 bp
364 bp
400 bp
460 bp
495 bp
500 bp
530 bp
565 bp
600 bp

Supp. Fig. 1


Data Distribution
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7.5
10.0
12.5
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17.5
20.0
22.5
25.0
27.5
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32.5
35.0
37.5
40.0
42.5
Total
With Blast (without hits)
With Blast Hits
With Mapping
With GO Annotation

Supp. Fig. 2