

Supplementary Information

Table S1. GenBank accession numbers and abbreviations used for phylogenetic analysis of EpOME synthase *CYP* genes.

Table S2. GenBank accession numbers and abbreviations used for phylogenetic analysis of *sEH*

Table S3. Sequences of primers used in this study and their PCR conditions

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Figure S1. LC-MS/MS of EpOMEs and DiHOMEs of *F. occidentalis*

Figure S2. FISH assay of TSWV titer in *F. occidentalis* in response to arachidonic acid (AA) and AUDA using sense probe specific to TSWV N. the contours are drawn because of no signal. The scale bars represent 0.1mm.

Table S1. GenBank accession numbers and abbreviations used for phylogenetic analysis of EpOME synthase CYP genes.

Species	Abbreviation	Accession number
<i>Frankliniella occidentalis</i>	Fo CYP1	AED99066
<i>Frankliniella occidentalis</i>	Fo CYP2	AED99065
<i>Frankliniella occidentalis</i>	Fo CYP3	KAE8749876
<i>Frankliniella occidentalis</i>	Fo CYP4	KAE8739041
<i>Frankliniella occidentalis</i>	Fo CYP5	XP052132944
<i>Frankliniella occidentalis</i>	Fo CYP6	XP052131731
<i>Frankliniella occidentalis</i>	Fo CYP8	XP026287395
<i>Frankliniella occidentalis</i>	Fo CYP12	XP052132028
<i>Frankliniella occidentalis</i>	Fo CYP18	XP052132697
<i>Frankliniella occidentalis</i>	Fo CYP24	XP052129246
<i>Frankliniella occidentalis</i>	Fo CYP35	XP052127336
<i>Frankliniella occidentalis</i>	Fo CYP40	XP052126914
<i>Frankliniella occidentalis</i>	Fo CYP45	XP052126387
<i>Frankliniella occidentalis</i>	Fo CYP46	XP052124927
<i>Frankliniella occidentalis</i>	Fo CYP47	XP026273658
<i>Frankliniella occidentalis</i>	Fo CYP48	XP026287901
<i>Frankliniella occidentalis</i>	Fo CYP49	XP026284054
<i>Frankliniella occidentalis</i>	Fo CYP50	XP052123820
<i>Homo sapiens</i>	Hs CYP1	NP000766
<i>Homo sapiens</i>	Hs CYP2	NP000752
<i>Homo sapiens</i>	Hs CYP3	NP000764
<i>Homo sapiens</i>	Hs CYP4	NP000762
<i>Homo sapiens</i>	Hs CYP5	NP000761
<i>Mus musculus</i>	Mm CYP1	NP083255
<i>Mus musculus</i>	Mm CYP2	NP067257
<i>Mus musculus</i>	Mm CYP3	NP034137
<i>Mus musculus</i>	Mm CYP4	NP034123
<i>Mus musculus</i>	Mm CYP5	NP034138
<i>Rattus norvegicus</i>	Rn CYP1	NP786942
<i>Spodoptera exigua</i>	Se CYP32	QWM97828

Table S2. GenBank accession numbers and abbreviations used for phylogenetic analysis of sEH

Species	Abbreviation	Accession number
<i>Aedes aegypti</i>	Aaeg PA	AAEL006354
<i>Aedes aegypti</i>	Aaeg PB	EAT42095
<i>Aedes aegypti</i>	Aaeg1	XP001651935
<i>Anopheles gambiae</i>	Agam1	EAA10122
<i>Anopheles gambiae</i>	Agam2	EAL40266
<i>Anopheles gambiae</i>	Agam3	EAL40265
<i>Bombyx mori</i>	mBmori	BAH97088
<i>Bombyx mori</i>	Bm	XP004927786
<i>Bombyx mori</i>	Bmor X1	XP004927786
<i>Bombyx mori</i>	Bmor X2	XP021204834
<i>Caenorhabditis elegans</i>	Cele	CCD61875
<i>Drosophila melanogaster</i>	Dmel	BAD04047
<i>Frankliniella occidentalis</i>	Fo-EH1	XP052128701
<i>Frankliniella occidentalis</i>	Fo-EH2	XP026280634
<i>Frankliniella occidentalis</i>	Fo-EH3	XP026275638
<i>Frankliniella occidentalis</i>	Fo-EH4	KAE8745912
<i>Gallus</i>	Ggal	AAZ38461
<i>Helicoverpa armigera</i>	Harm	XP021183905
<i>Homo sapiens</i>	Hsap	AAC41694
<i>Homo sapiens</i>	Hsap Hs	NP775838
<i>Mus musculus domesticus</i>	Mmus	AAA37555
<i>Plutella xylostella</i>	Pxyl	XP011556182
<i>Rattus norvegicus</i>	sRnor	CAA46211
<i>Rattus norvegicus</i>	mRnor	AAA41585
<i>Spodoptera exigua</i>	Se-JHEH	ABD85119
<i>Spodoptera exigua</i>	Se-sEH	QWM97829
<i>Spodoptera litura</i>	Slit	XP022829648
<i>Strongylocentrotus purpuratus</i>	Spur	NP001121538

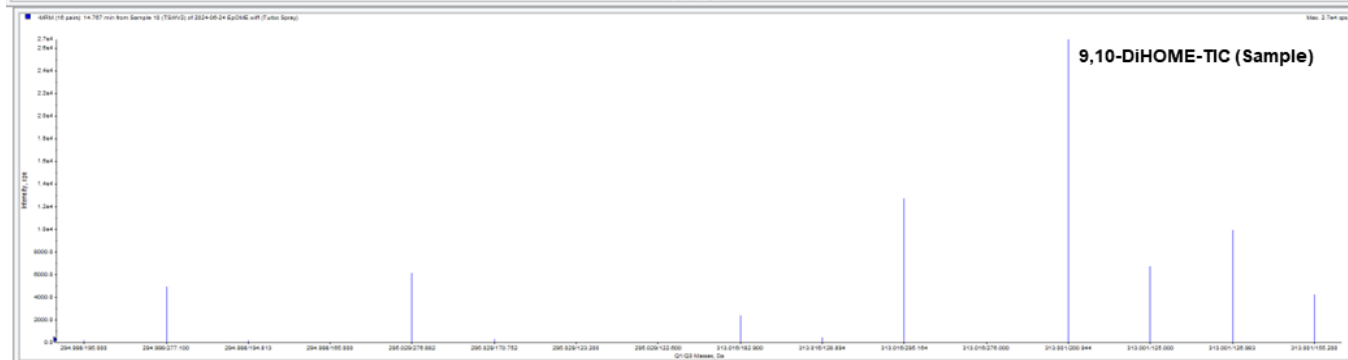
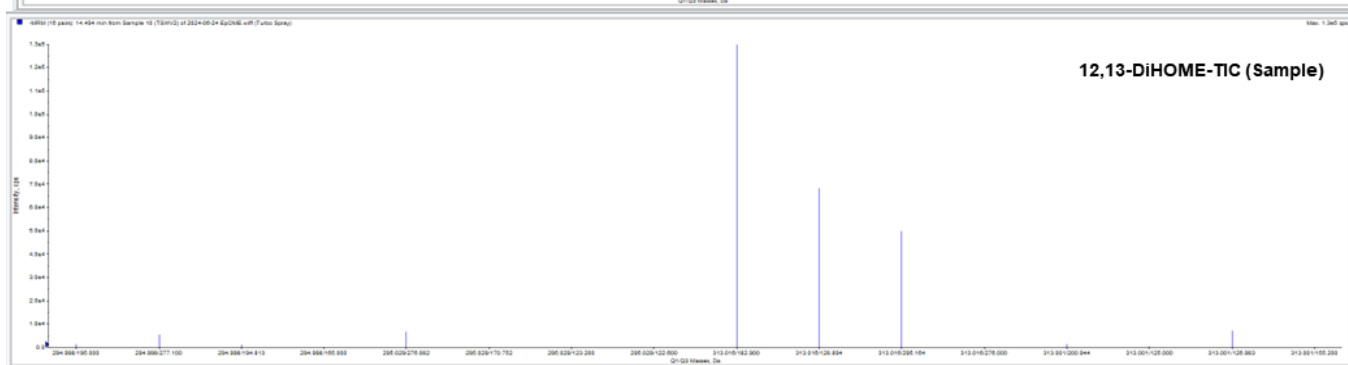
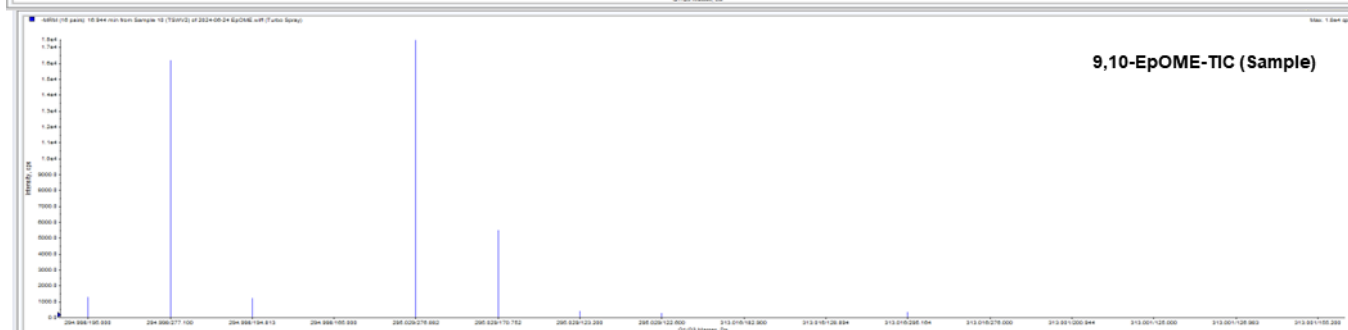
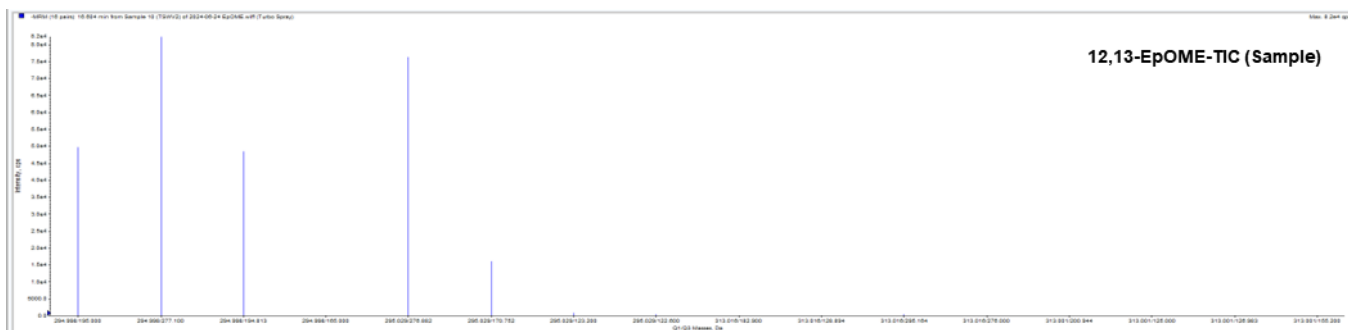
Table S3. Sequences of primers and prob used in this study and their PCR conditions

Primer	Use	Orientation	Sequence (5'-3')	Annealing temperature (°C)	Amplicon (bp)
EF1	qPCR	Forward	TCA AGG AAC TGC GTC GTG GAT	52	130
		Reverse	ACA GGG GTG TAG CCG TTA GAG		
Fo-CYP24	qPCR	Forward	CGCCGCACTCAAGAACT	54	304
		Reverse	CAAGAAGGGCAGGAAGTTGA		
Fo-CYP40	qPCR	Forward	CACCCTCATCTTCCTGAACAAC	54	248
		Reverse	TGTAGTCTCGGCCTTGGATAG		
Fo-sEH1	qPCR	Forward	AAGTTCATTCTTGTGCACACG	52	388
		Reverse	TTGAAGGCCTCGATGTCTTCC		
Fo-sEH2	qPCR	Forward	TTCTTCCTGTTCCAAGTGCCTT	52	752
		Reverse	TTCTCATCCGAGTGAATTCCTTC		
Fo-sEH3	qPCR	Forward	GGTAGAGATCGTCCCCTTATTC	52	348
		Reverse	ACAAGGAACCATCCCAGAAG		
Fo-JHEH	qPCR	Forward	AACATCCCCGACTCAGTGATC	52	523
		Reverse	TTGACGTGAATGAAGTGGAGG		
T7- Fo-CYP24	RNAi	Forward	TAATACGACTCACTATAGGGAGACG CCGCACTCAAGAACT	54	354
		Reverse	TAATACGACTCACTATAGGGAGACA AGAAGGGCAGGAAGTTGA		
T7- Fo-CYP40	RNAi	Forward	TAATACGACTCACTATAGGGAGACA CCCTCATCTTCCTGAACAAC	54	250
		Reverse	TAATACGACTCACTATAGGGAGATG TAGTCTCGGCCTTGGATAG		
T7- Fo-sEH1	RNAi	Forward	TAATACGACTCACTATAGGGAGATG CATTGCGCAGAAGAATCAG	52	367
		Reverse	TAATACGACTCACTATAGGGAGAGC TTAAGAAATGAACGCATTGC		
T7- Fo-sEH2	RNAi	Forward	TAATACGACTCACTATAGGGAGATT CTTCCTGTTCCAAGTGCCTT	52	800
		Reverse	TAATACGACTCACTATAGGGAGATT CTCATCCGGAGTGATTCTTC		
T7- Fo-sEH3	RNAi	Forward	TAATACGACTCACTATAGGGAGAGG TAGAGATCGTCCCCTTATTC	52	398
		Reverse	TAATACGACTCACTATAGGGAGAAC AAGGAACCATCCCAGAAG		
T7- Fo-JHEH	RNAi	Forward	TAATACGACTCACTATAGGGAGAAA CATCCCCGACTCAGTGATC	52	321
		Reverse	TAATACGACTCACTATAGGGAGATT GACGTGAATGAAGTGGAGG		
Fo-Caspase1	qPCR	Forward	CCCAGAAGATGGCACATGGT	55	176
		Reverse	ACAATTGAGGGCACCTGCTT		
Fo-Caspase2	qPCR	Forward	ACTGCCACACTCATCTGCAA	55	148
		Reverse	CCACAATGCGGGGAGATGAT		
Fo-Caspase3	qPCR	Forward	ACTGAACTATGCGAGCCCAA	55	183
		Reverse	TTGGGGAAGAACTGCGACTC		
Fo-Caspase4	qPCR	Forward	CAGTGATGGGAGATAGGCCG	55	222

Fo-IAP	qPCR	Reverse	ACCCCATGAGCAAGTATGGC	52	267
		Forward	CTAGCGATTCCCAAGGAGTATTT		
TWSV-N	qPCR	Reverse	CACACAGTTGACACAAGAAACC	52	777
		Forward	ATGTCTAAGGTTAAGCTCACTAAGGAA		
TWSV-NSm	qPCR	Reverse	TTAAGCAAGTTCTGCAAGTATTGCC TG	52	372
		Forward	GAAGGGTCAAGGGACAATAAC		
TWSV-NSs	qPCR	Reverse	CCTTCCTCCTCTTCTTCAAATG	52	439
		Forward	GCCTGCATTCCAAACCATAAC		
T7-TWSV-N	RNAi	Reverse	CCCTGGCAAAGTCTATCTTCC	52	827
		Forward	TAATACGACTCACTATAGGGAGAATGTCTAAGGTTAAGCTCACTAAGGA A		
T7-TWSV-NSm	RNAi	Reverse	TAATACGACTCACTATAGGGAGATT AAGCAAGTTCTGCAAGTATTGCCTG	52	422
		Forward	TAATACGACTCACTATAGGGAGAGAAGGGTCAAGGGACAATAAC		
T7-TWSV-NSs	RNAi	Reverse	TAATACGACTCACTATAGGGAGACCTTCCTCCTCTTCTTCAAATG	52	489
		Forward	TAATACGACTCACTATAGGGAGAGCCTGCATTCCAAACCATAAC		
		Reverse	TAATACGACTCACTATAGGGAGACCTGGCAAAGTCTATCTTCC		

Table S4. Probe sequences used in FISH assay

Gene	Probes	Sequence (5' - 3')
<i>TSWV-N</i>	Antisense	FITC-TTT-TTAAGCAAGTTCTGCAAGTATTGCCTG
	Sense	FITC-AAA-CAGGCAATACTTGCAGAACTTGCTTAA



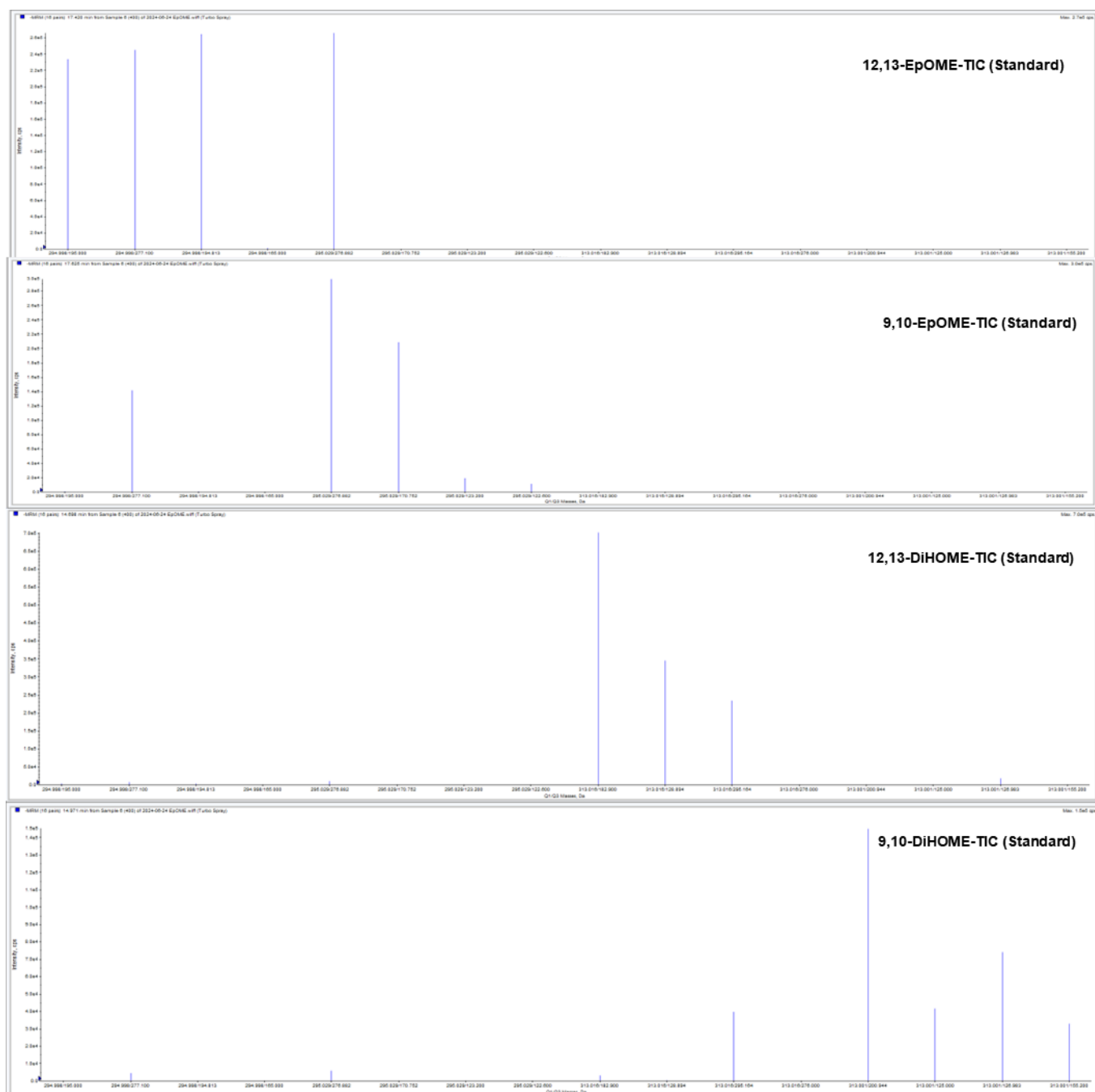


Figure S1

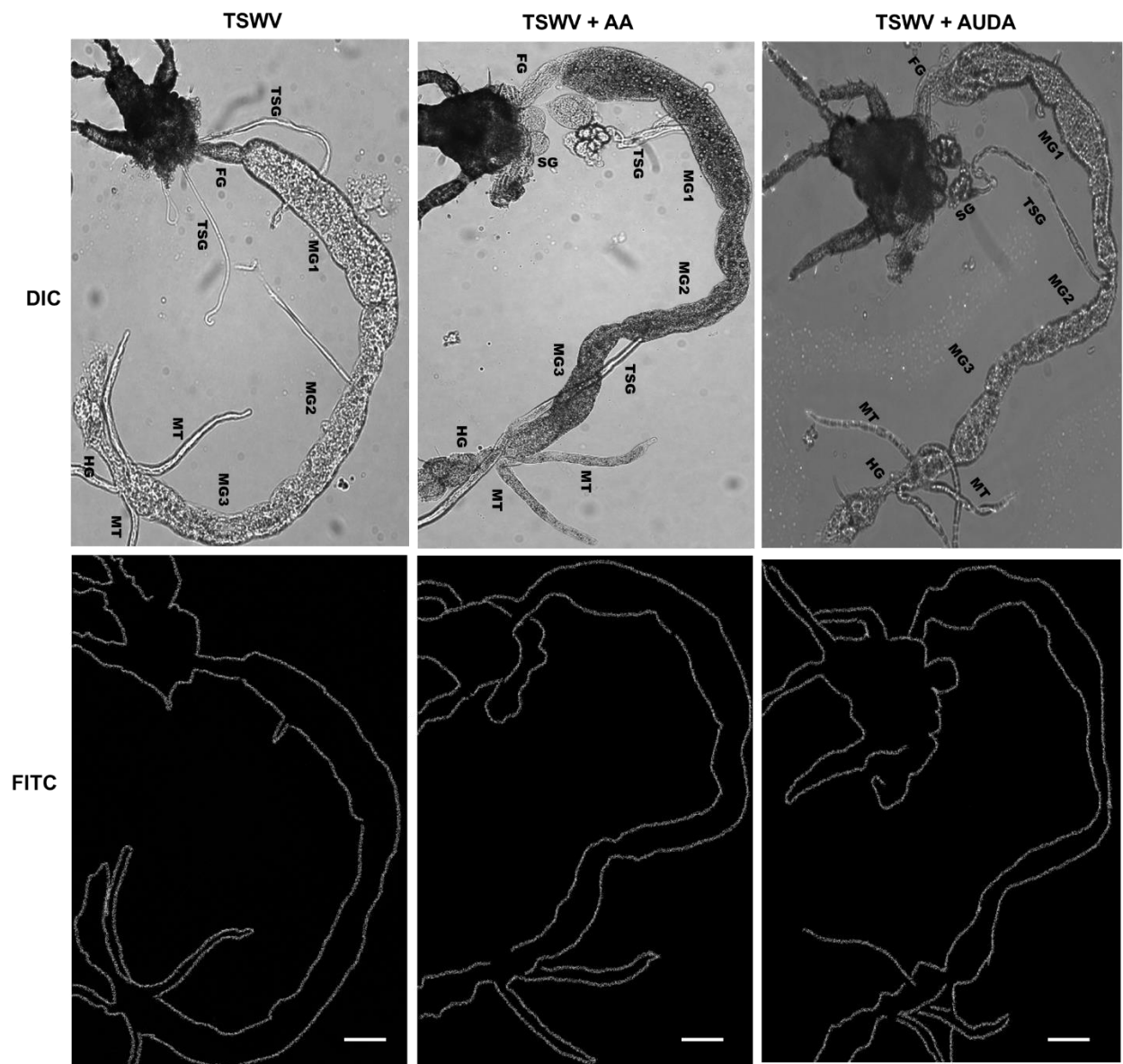


Figure S2