

Supplementary data for the manuscript titled: 'Redefining metamorphosis in spiny lobsters: molecular analysis of the phyllosoma to puerulus transition in *Sagmariasus verreauxi*' (Authors: Tomer Ventura, Quinn P. Fitzgibbon, Stephen C. Battaglene and Abigail Elizur)

Includes: Table S1, Figure S1-S2. Table S2 (a large dataset) is submitted separately as an excel file.

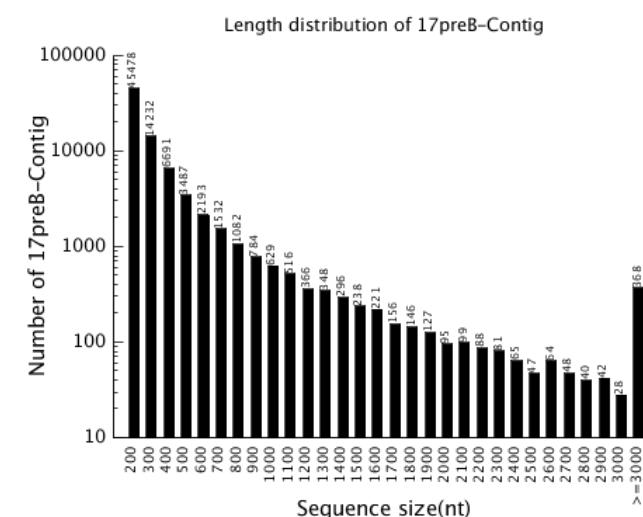
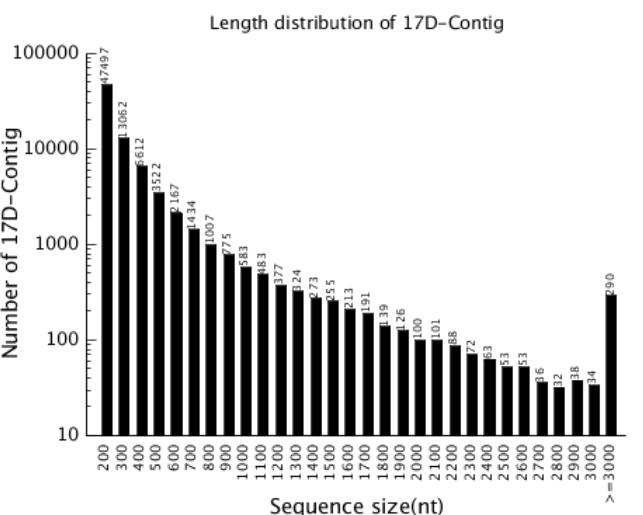
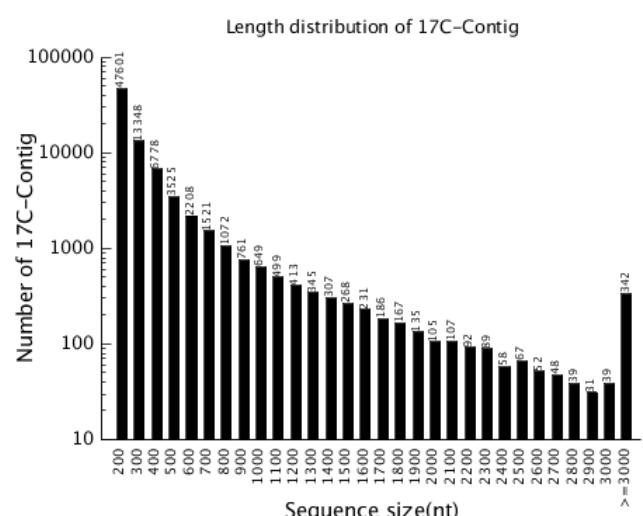
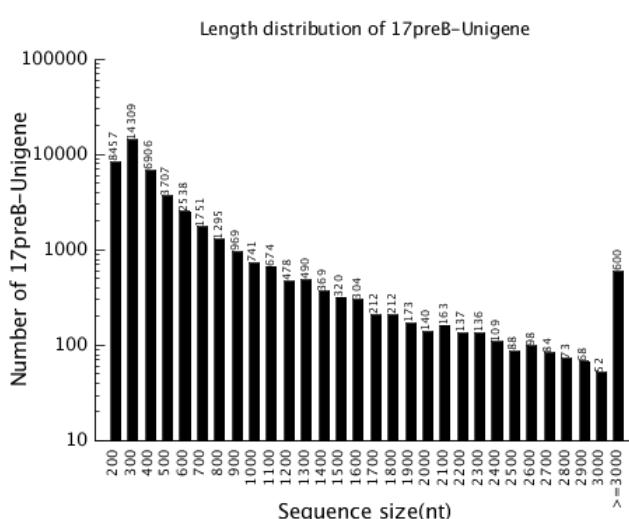
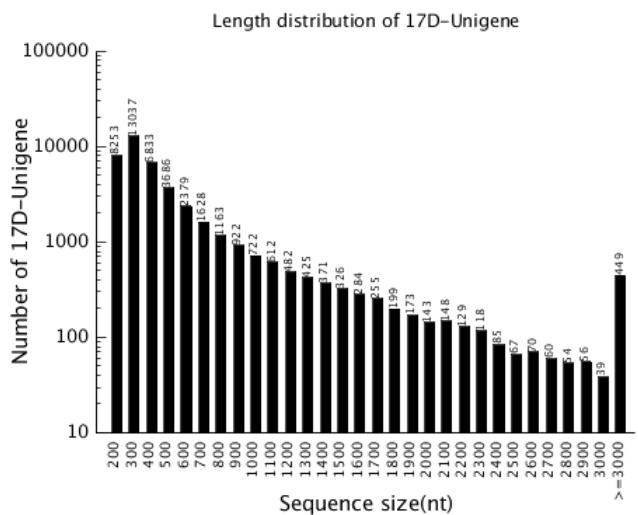
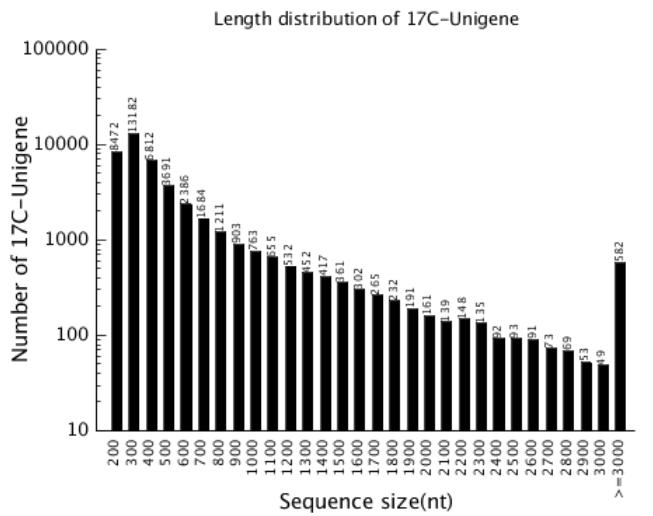
Table S1: List of proteins used in the phylogenetic trees in Figures 4, 5, 6

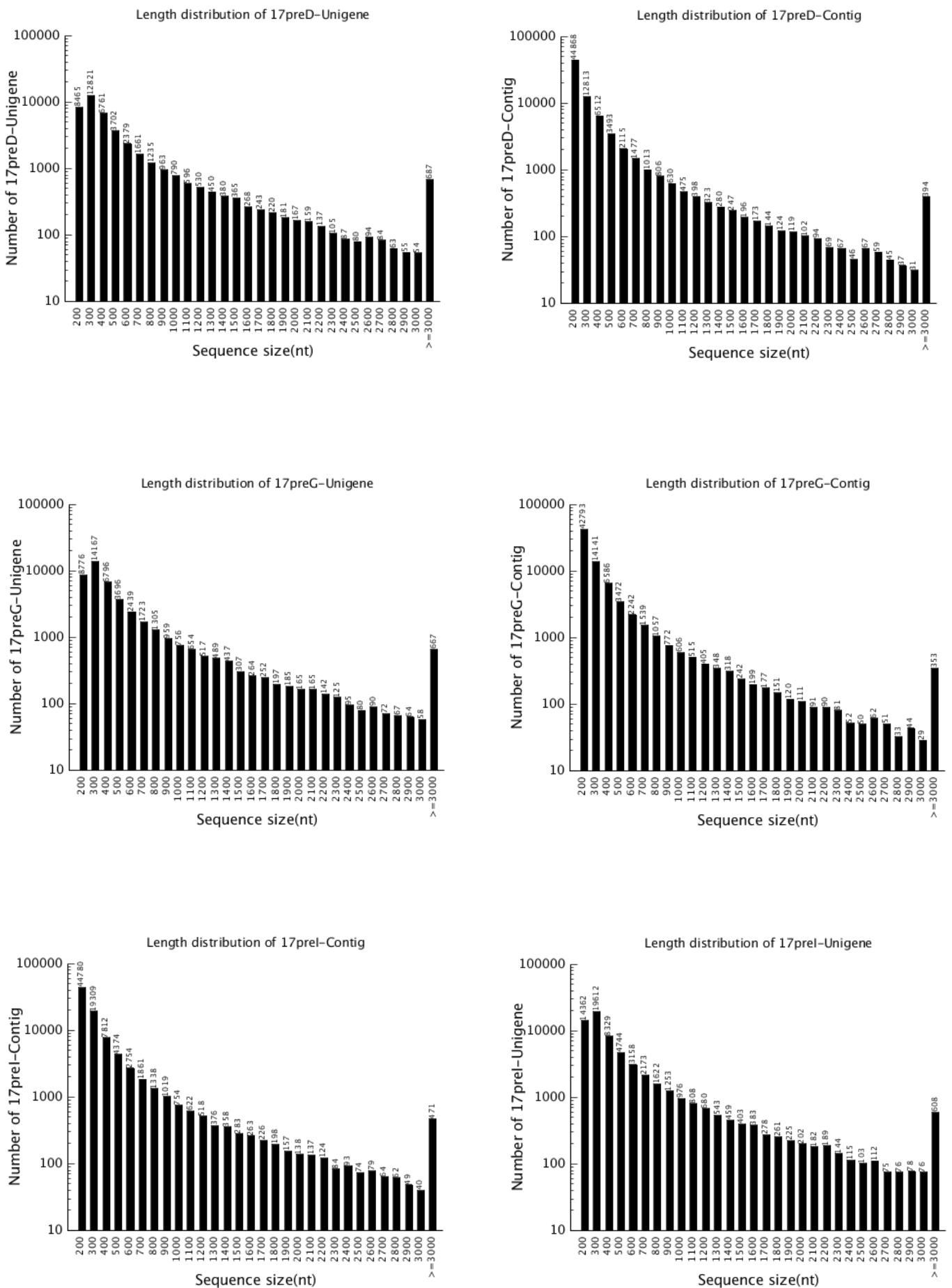
Species	Common name	Protein	Accession Number (NCBI GenBank)	Figure
<i>Drosophila melanogaster</i>	Common fruit fly	CYP6A2	AAB36782	4C
<i>Bombyx mori</i>	The silk moth	CYP303a1-like	XP_004932789	4C
<i>Acyrthosiphon pisum</i>	Pea aphid	CYP303a1	XP_001951093	4C
<i>Tribolium castaneum</i>	Flour beetle	CYP303a1	XP_008200616	4C
<i>Drosophila melanogaster</i>	Common fruit fly	Cyp303a1, isoform B	NP_001285977	4C
<i>Musca domestica</i>	Common house fly	CYP303a1-like	XP_005184173	4C
<i>Macrobrachium rosenbergii</i>	Giant freshwater prawn	Mr-CYP15A1	na	4C
<i>Drosophila melanogaster</i>	Common fruit fly	Cyp305a1	NP_649151	4C
<i>Ceratitis capitata</i>	Mediterranian fruit fly	CYP305a1-like	XP_004537734	4C
<i>Diploptera punctata</i>	Cockroach	CYP15A1	AAS13464	4C
<i>Reticulitermes flavipes</i>	Eastern subterranean termite	CYP15A1	C1K313	4C
<i>Schistocerca gregaria</i>	Desert locust	Methyl farnesoate epoxidase	ADV17351	4C
<i>Tribolium castaneum</i>	Flour beetle	CYP15A1	D6WFY6	4C
<i>Acyrthosiphon pisum</i>	Pea aphid	CYP305a1	XP_001952620	4C
<i>Apis florea</i>	Dwarf honey bee	CYP305a1	XP_003693154	4C
<i>Nasonia vitripennis</i>	Parasitoid wasp	CYP303a1	XP_001605585	4C
<i>Microplitis demolitor</i>	Parasitoid wasp	CYP305a1	XP_008549892	4C
<i>Metaseiulus occidentalis</i>	Predatory mite	CYP307a1-like	XP_003747195	4C
<i>Bombus terrestris</i>	Buff-tailed bumblebee	CYP307a1-like	XP_003400661	4C
<i>Nasonia vitripennis</i>	Parasitoid wasp	CYP307a1	XP_008211923	4C
<i>Tribolium castaneum</i>	Flour beetle	CYP307a1	XP_008200059	4C
<i>Acyrthosiphon pisum</i>	Pea aphid	CYP307a1	XP_008179686	4C

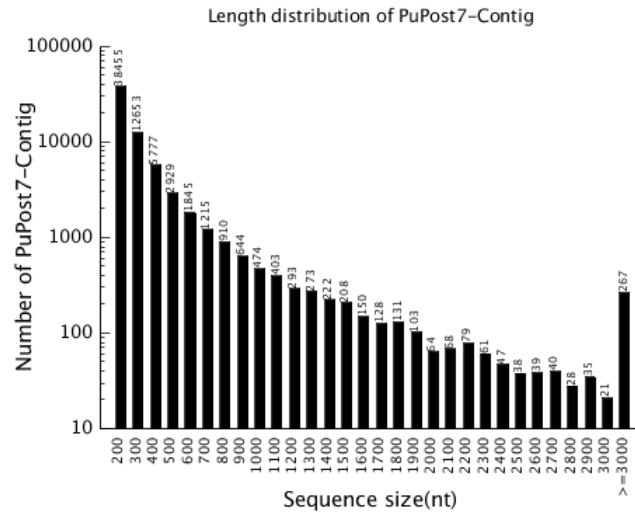
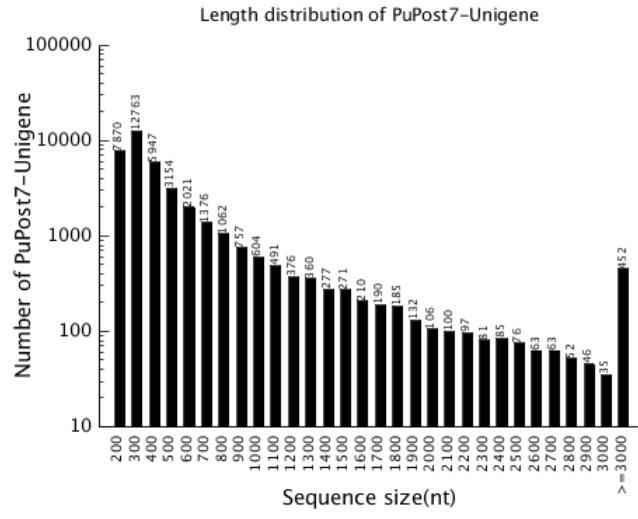
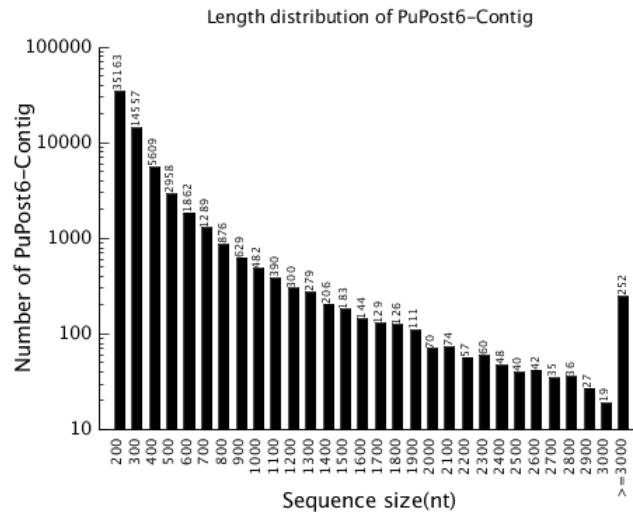
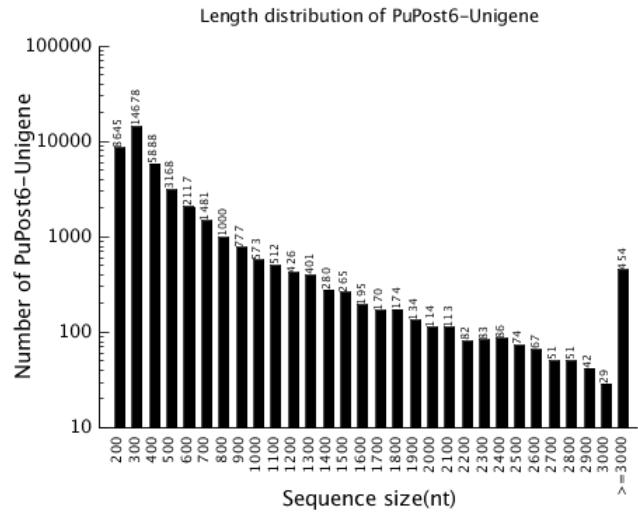
Figure S1: Length distribution of contigs and unigenes across all ten samples:

Key to library names:

1. Intermolt phyllosoma 17: 17D, 17D.
2. 20% retracting phyllosoma 17: 17preB, 17preD.
3. 80% retracting phyllosoma 17: 17preG, 17preI.
4. Post-molt puerulus: PuPost6, PuPost7.
5. H-phase puerulus: PuH1, PuH2.







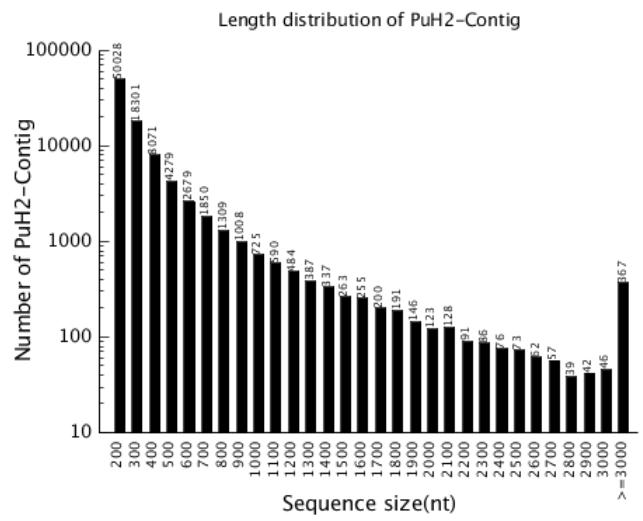
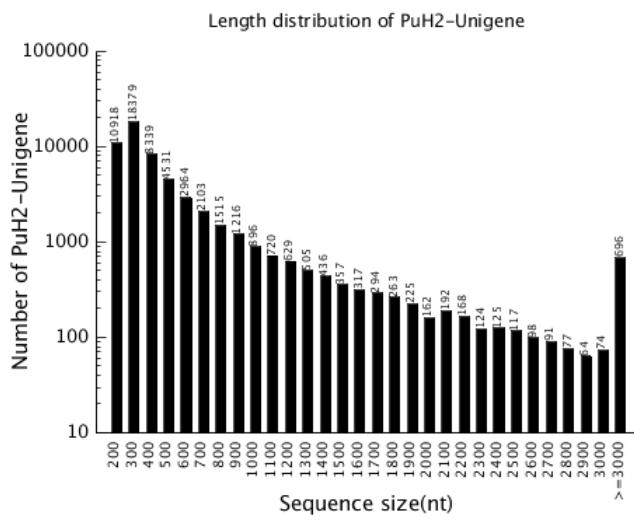
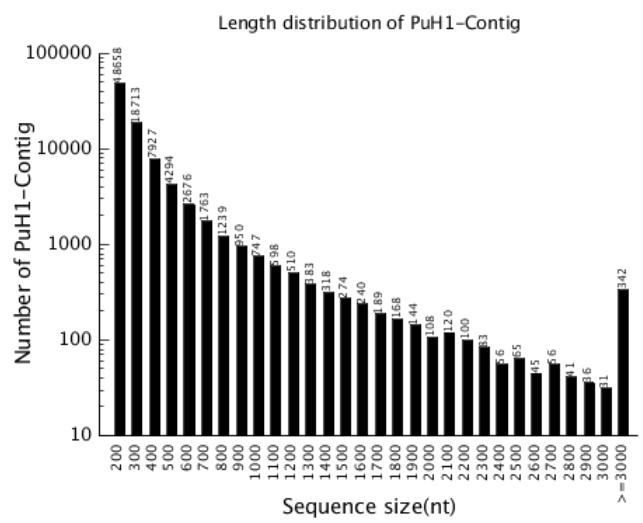
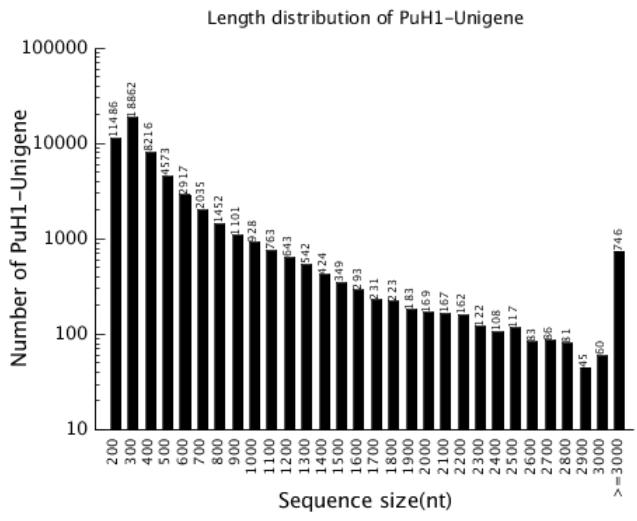
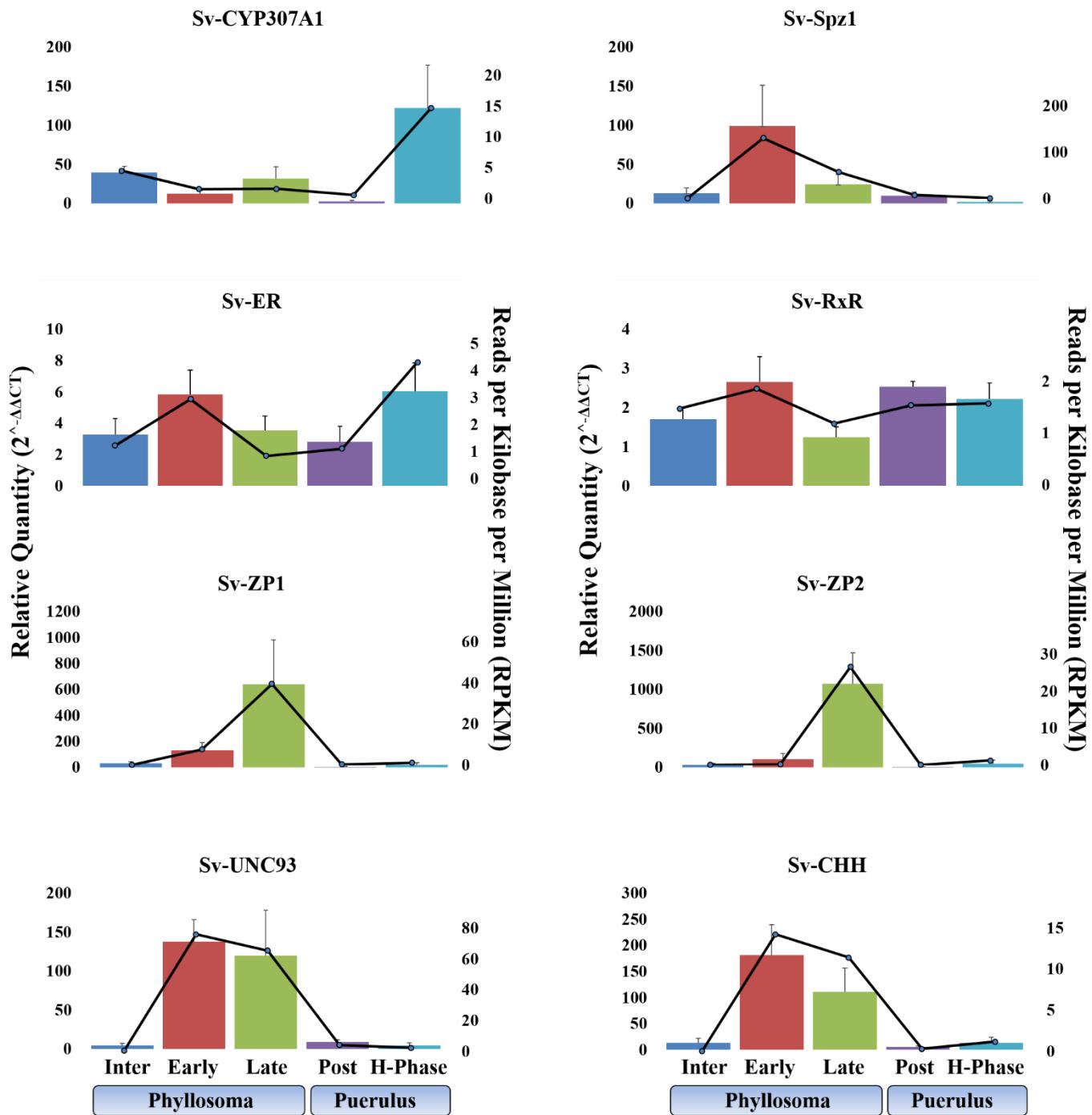


Figure S2: Relative quantification of key genes using qPCR (columns) and RPKM values (line), throughout metamorphosis:



Details of genes, primers and probes used for qPCR analysis in Figure S2:

Gene name	GenBank accession no. / unigene	Forward primer (5' to 3')	Reverse primer (5' to 3')	Probe
Sv-18S	KF828103	ggtgcatggccgttctta	tggagatccgtcgactagttaat	22
Sv-FAMeT1	Unigene44448	ccacgttgcctcacttc	ttcttgaacctgatggctga	22
Sv-CYP15A1	CL6907.Contig1	cgtgggtcatggacgact	ttcagagtggcatccgtgta	1
Sv-CYP307A1	Unigene44916	ggaggatcttgggtggat	agggttgtggaggatgtac	156
Sv-ER	CL5835.contig4	aacagccagtaacatccaaa	tcacactcaagaacaagcgact	142
Sv-RxR	CL4526.contig2	cagtccctgtctccaccac	acagacatgacggcgttctc	157
Sv-ZP1	Unigene50269	agcgaccccaactgtgtg	agctgttgaggtagatgtcgaa	116
Sv-ZP2	Unigene30964	acccggcccagtcatagt	tgggtggctgactggatta	78
Sv-UNC93	CL5857.Contig2	ccaggttggtgatgttgtt	ctctcctgcgggtcaactt	78
Sv-Spz1	CL5710.Contig1_All	ctaccgacatccatgtaacac	agcagttctccagtcatctcg	86
Sv-CHH	Unigene30324	gagggaaagccacgagagac	ggtgaacctgacaacaccaa	51