

Supplementary File 3: Diagnostic SNP analysis confirms source populations match the RNA-seq samples.

Table S3.1: RNAseq samples were genotyped relative to protein coding WGS SNPs from individuals from the source populations in Panama. Both SNPs were contained in the protein coding sequence of the gene *Cortex*. Individuals from the RNAseq experiment match the genotype of the source populations.

Sequence	Race	Individual	Informative site, scaffold 215006	
			1207068	1210502
WGS	<i>melpomene</i>	P3_1	TT	TT
		P3_2	TT	TT
		P3_3	TC	TC
WGS	<i>rosina</i>	ros10_1	CC	CC
		ros10_2	CC	CC
		ros10_3	CC	CC
		ros10_4	CC	CC
		ros10_5	CC	CC
		ros10_6	CC	CC
		ros10_7	CC	CC
		ros10_8	CC	CC
		ros10_9	CC	CC
		ros10_10	CC	CC
RNAseq	<i>melpomene</i>	49	TT	TT
		52	TT	TT
		54	TT	TT
		55	TT	TT
		56	TT	TT
		61	TT	TT
		62	TT	TT
RNAseq	<i>rosina</i>	13	CC	CC
		14	CC	CC
		15	CC	CC
		16	CC	CC
		17	CC	CC
		24	CC	CC

Table S3.2: This was repeated for the *H. erato* samples; here, only one informative protein-coding SNP was found, in the gene *parn*. Once again, all individuals match the expected genotype.

Informative site, scaffold 1505			
Sequence	Race	Individual	2306177
WGS	<i>hydara</i>	STRI_WOM_0039	AA
		STRI_WOM_0040	AA
		STRI_WOM_0042	AA
		STRI_WOM_0088	AA
		STRI_WOM_5193	AA
		STRI_WOM_5351	AA
WGS	<i>demophoon</i>	Pet_ED3	GG
		Pet_ED4	GG
		Pet_ED5	GG
		Pet_ED6	GG
		STRI_WOM_0033	GG
		STRI_WOM_0082	GG
		STRI_WOM_0087	GG
		STRIWOM1284	GG
		STRIWOM5353	GG
		STRIWOM5362	GG
RNAseq	<i>hydara</i>	17	AA
		25	AA
		33	AA
		34	AA
		36	AA
RNAseq	<i>demophoon</i>	A4	GG
		D2	GG
		D6	GG
		D9	GG
		C6	GG
		H3	GG
		A4	GG