

Table S2. Detailed information on 13 predicted genes (C1-C13) within the candidate regions and reasons for further screening or otherwise

Candidate	Gene name*	Length (bp)	Annotation: best hit with E-value	Exclusion reason
C1	BGIBMGA008531	303	Myb-MuvB complex subunit Lin-52 [<i>B. mori</i>] (E-value: 2.00E-39)	Two <i>Dazao</i> -specific SNPs
C2	BGIBMGA008532	564	N-acetyltransferase [<i>B. mori</i>] (E-value: 5.00E-103)	Identical to <i>Dazao</i>
C3	BGIBMGA008324	246	AGAP002567-PA [<i>A. gambiae</i>] (E-value: 8.00E-05)	Two silent SNPs
C4	BGIBMGA008533	1326	Similar to AGAP001885-PA [<i>T. castaneum</i>] (E-value: 3.00E-90)	Irrelevant expression pattern
C5	BGIBMGA008323	249	Hypothetical protein SS1G_04978 [<i>S. sclerotiorum</i>] (E-value: 4.3)	Irrelevant expression pattern
C6	BGIBMGA008322	216	Similar to GA18100-PA [<i>N. vitripennis</i>] (E-value: 2.00E-20)	Three silent SNPs
C7	BGIBMGA008534	1116	GK25744 [<i>D. willistoni</i>] (E-value: 6.00E-110)	Non- <i>mln</i> -specific insertion; irrelevant expression pattern
C8	BGIBMGA008535	252	Snrnp48 protein [<i>D. rerio</i>] (E-value: 1.2)	One <i>Dazao</i> -specific SNP; one <i>Dazao</i> -specific deletion
C9	BGIBMGA008536	1131	Similar to zinc-finger CCCH-type containing 14 [<i>T. castaneum</i>] (E-value: 4.00E-27)	Irrelevant expression pattern
C10	BGIBMGA008537	1350	Conserved hypothetical protein [<i>C. quinquefasciatus</i>] (E-value: 3.00E-33)	Irrelevant expression pattern
C11	BGIBMGA008538	787	Arylalkylamine N-acetyltransferase [<i>B. mori</i>] (E-value: 2.00E-107)	<i>mln</i> -specific 126 bp deletion; coincident expression pattern
C12	BGIBMGA008539	660	Arylalkylamine N-acetyltransferase [<i>A. pernyi</i>] (E-value: 3.00E-30)	Identical to <i>Dazao</i>
C13	BGIBMGA008540	390	Similar to AGAP003014-PA [<i>T. castaneum</i>] (E-value: 1.00E-28)	Identical to <i>Dazao</i>

*Duan et al. (2010).