Fig. S5. Bisulfite sequencing of selected regions within cuticular protein genes

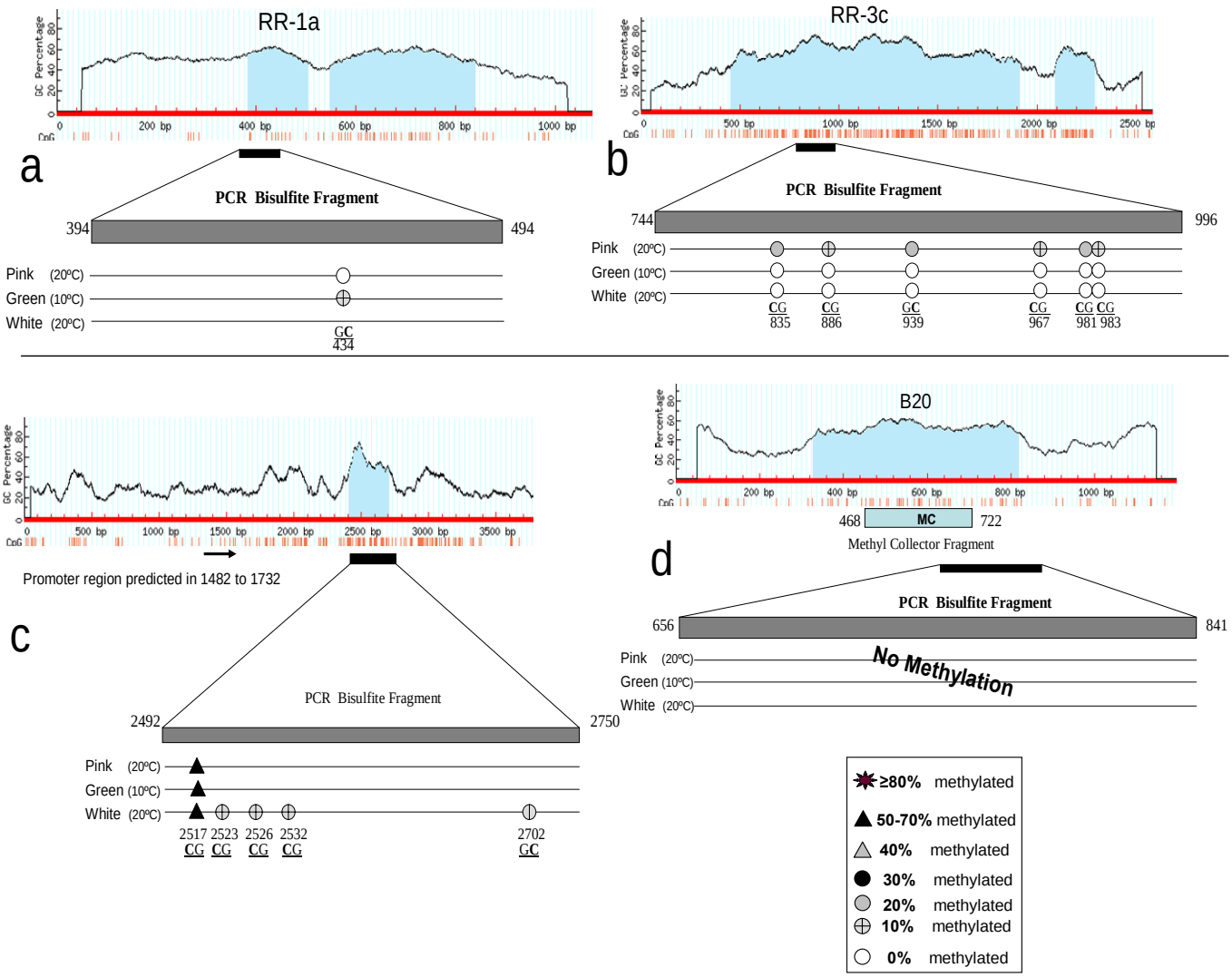

Figure S5. Bisulfite sequencing of fragments showing low levels of methylation

Prediction of the CpG Island and the design of primers for bisulfite sequencing were performed using the MethPrimer program http://www.urogene.org/methprimer/index1.html. Quantification of the methylation percentage was calculated by direct bisulfite sequencing of 10 independent clones. **(a)**, an RR-1 cuticular protein gene located at gi|171829605: position 22358-22862 Contig16053. **(b)**, an RR-3 cuticular protein gene located at gi|171829029:61577-62329 Contig16630. **(c)**, a promoter prediction of the reverse complementary sequence of the region between 18611 and 22481 at gi|171845529|gb|ABLF01000124.1 The promoter region was predicted using the WWW Promoter Scan program http://www-bimas.cit.nih.gov/molbio/proscan/ [The promoter was identified on the forward strand from1482 to 1732, the Promoter Score was 62.10 (Promoter Cutoff = 53.000000) and a TATA motif was found at 1710, Est.TSS = 1740]. **(d)**, the affinity precipitated B19 fragment was found to be unmethylated.