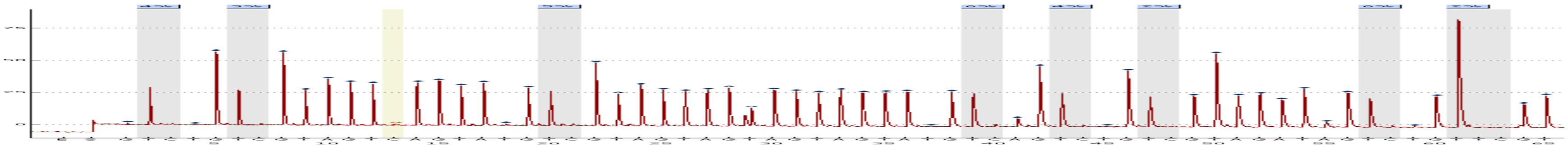
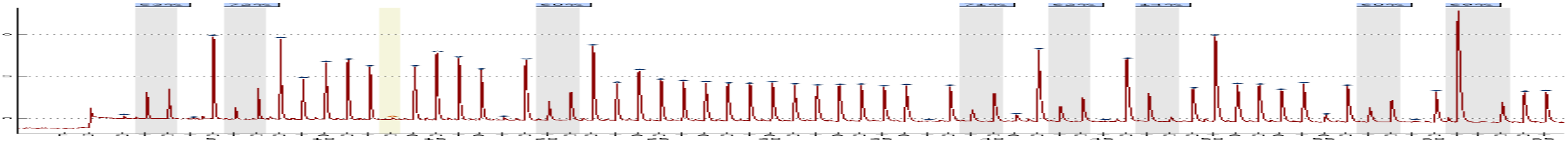
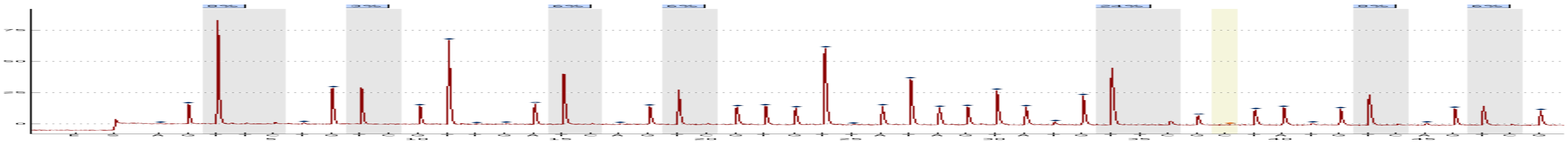
*Leprel1 un*methylated clinical case



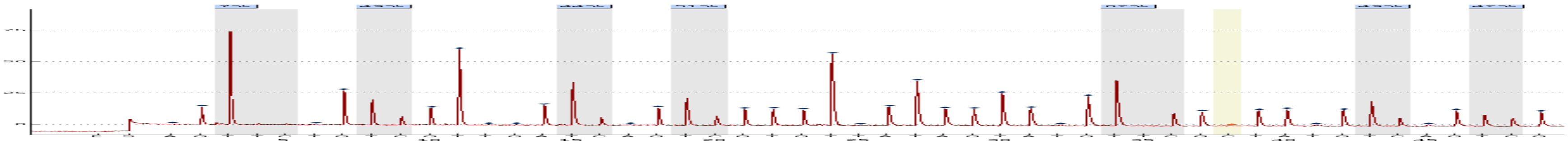
*Leprel1* methylated clinical case



*P4HA3* unmethylated clinical case

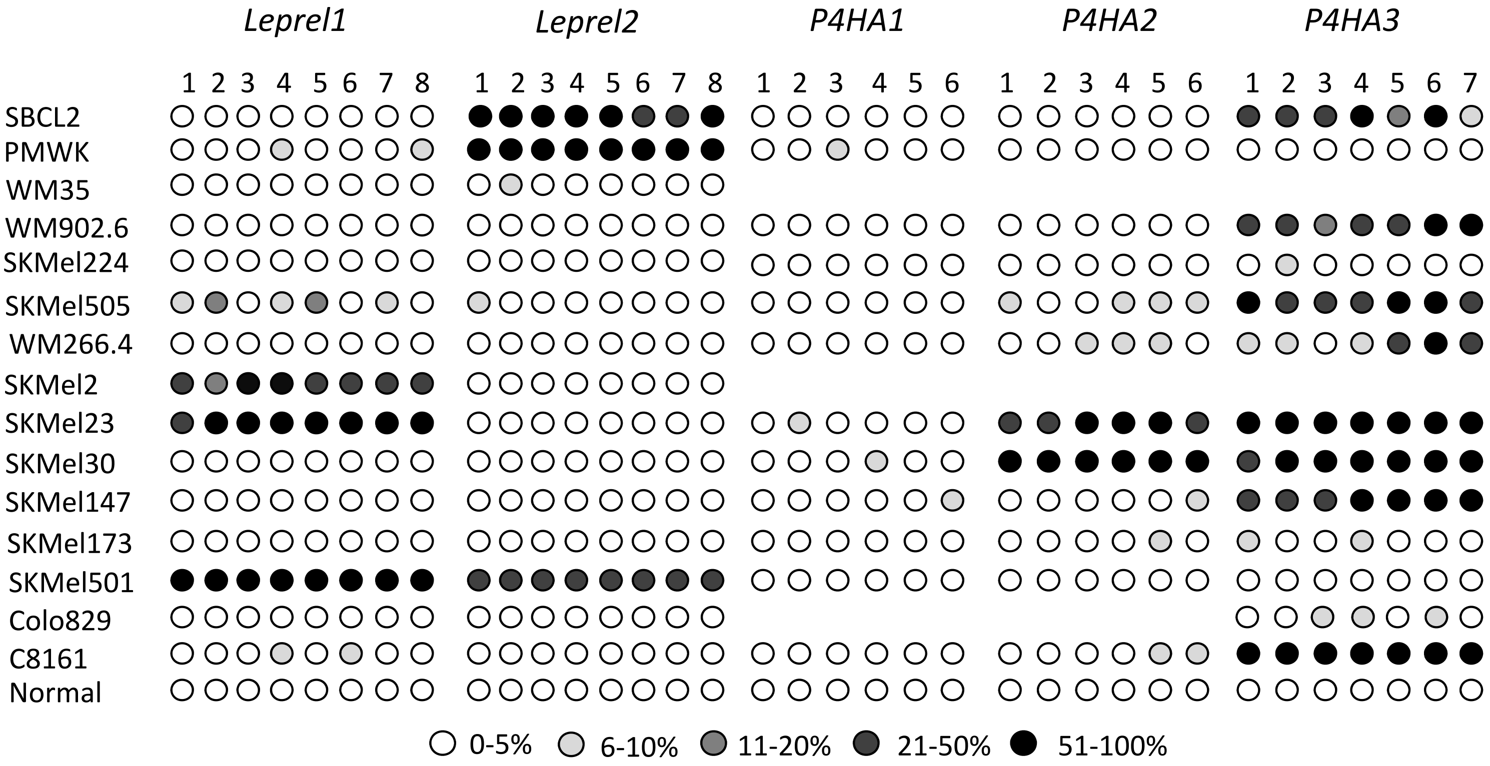


*P4HA3* methylated clinical case



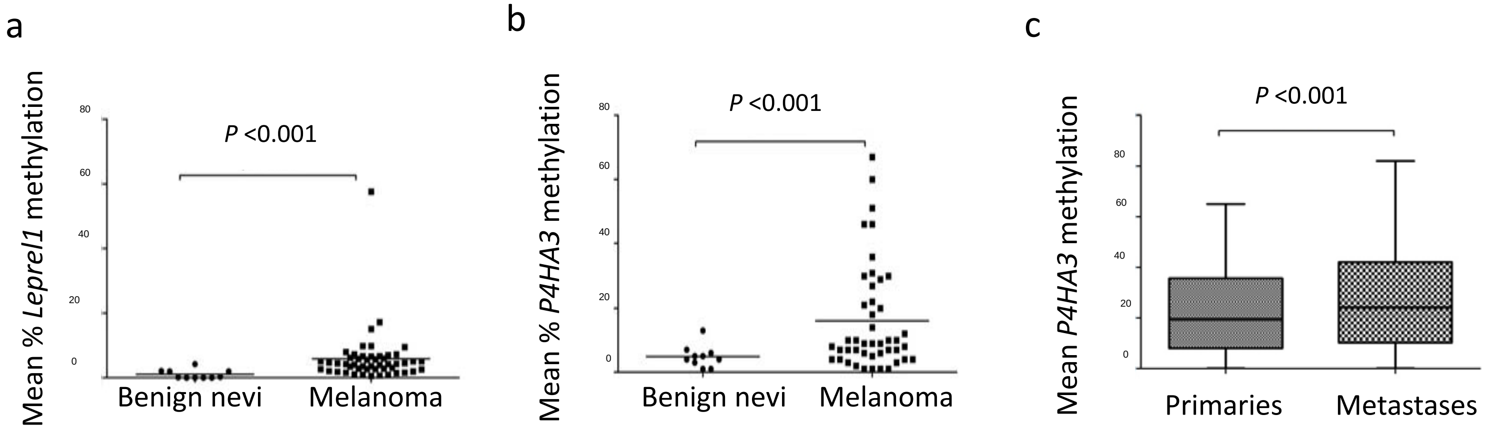
**Supplementary Figure 1**

Representative pyrograms for *Leprel1* and *P4HA3*.



**Supplementary Figure 2**

Expression of specific *C-P3H* and *C-P4H* genes is subject to methylation-dependent transcriptional silencing in melanoma. Data shows methylation profiles of each gene in the melanoma cell line panel. Five levels of methylation are represented, methylation increasing with the intensity of shading in the circles as shown.



**Supplementary Figure 3**

a: Mann-Whitney analysis of *Leprel1 in* CpG island methylation in benign nevi and melanoma tissue samples. Methylation is significantly higher in melanomas. b: Mann-Whitney analysis of *P4HA3 in* CpG island methylation in benign nevi and melanoma tissue samples. Methylation is significantly higher in melanomas. c: Average methylation in *P4HA3* in primary and metastatic melanoma.