

SUPPLEMENTARY FIGURES

Supplementary Figure 1:

MIRA-seq and bisulfite sequencing of the *MYC* gene.

A. Genome browser view of a melanocyte sample (N) and two melanomas (T).

B. Bisulfite sequencing. After conversion with sodium bisulfite, the hypermethylated *MYC* exon region indicated by the arrow was sequenced in the same samples shown in panel A. Open circles represent unmethylated CpG sequences and closed circles show methylated CpG sequences. The fraction of methylated CpG sites is shown.

Supplementary Figure 2:

Examples of the three gene categories including homeobox genes.

Category 1: Tumor-specific DNA methylation occurs at sequences marked by H3K27me3 in melanocytes. Example, *SHOX2*. Category 2: No tumor-specific DNA methylation occurs near the TSS despite marking with H3K27me3 in melanocytes. Example, *PAX4*. Category 3: Tumor-specific DNA methylation occurs in the absence of H3K27me3 marking in melanocytes. Examples, *PAX3* and *IRX2*.

Supplementary Figure 3:

RNA-seq analysis.

A. Heat map of upregulated (red) and downregulated (green) genes in melanomas (T) and melanocytes (N). The three melanocyte samples are on the right.

B. Principal component analysis of melanocytes and melanomas.

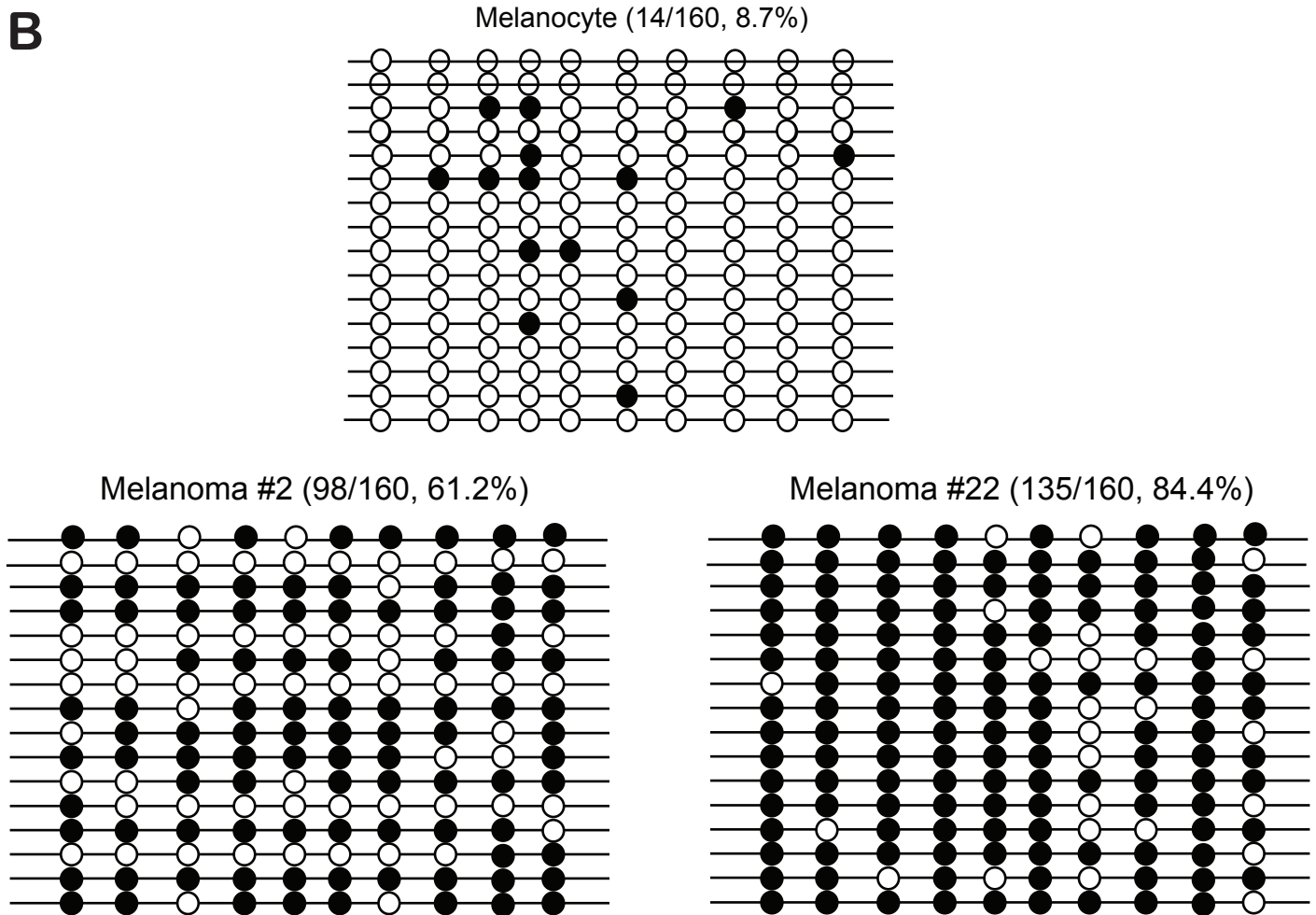
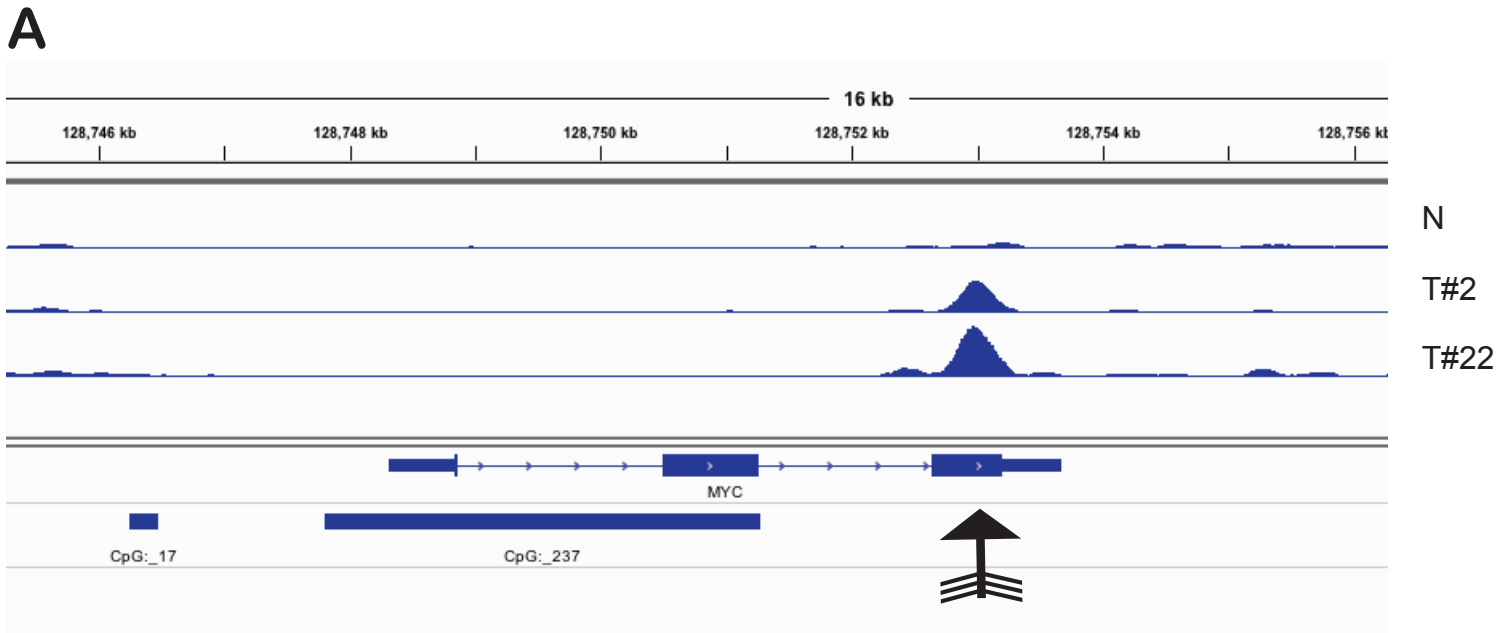


Figure S1

Category 1

Category 2

Category 3

Category 3

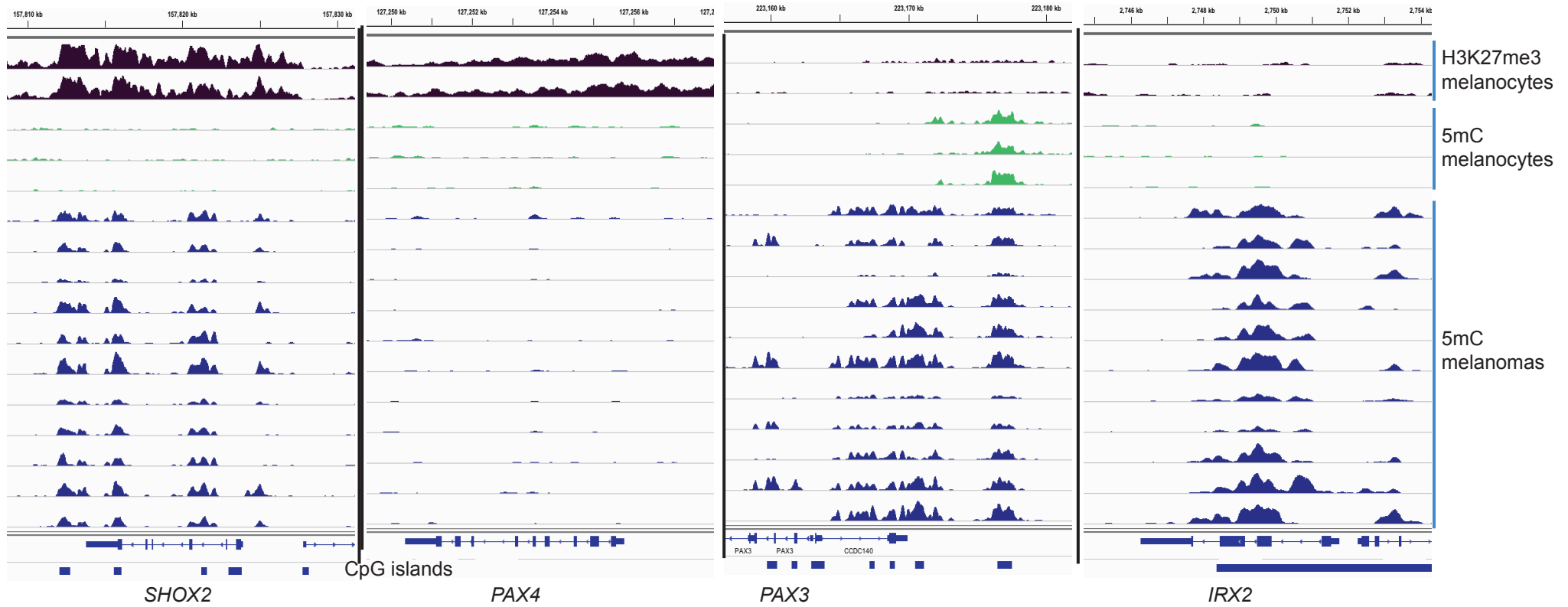
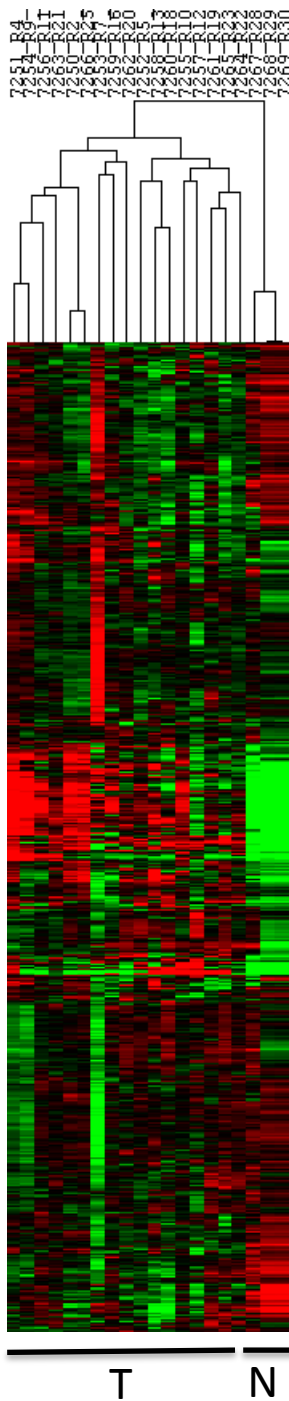


Figure S2

A



B

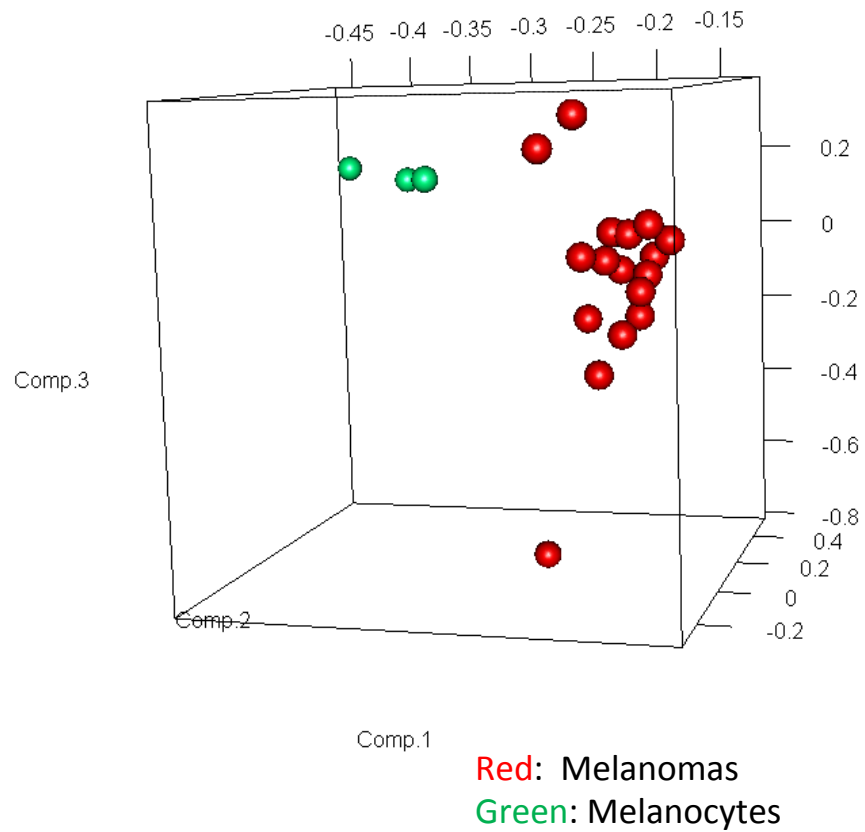


Figure S3