

Supplementary Materials

Transcriptional landscape of *BRAF* wild type metastatic melanoma

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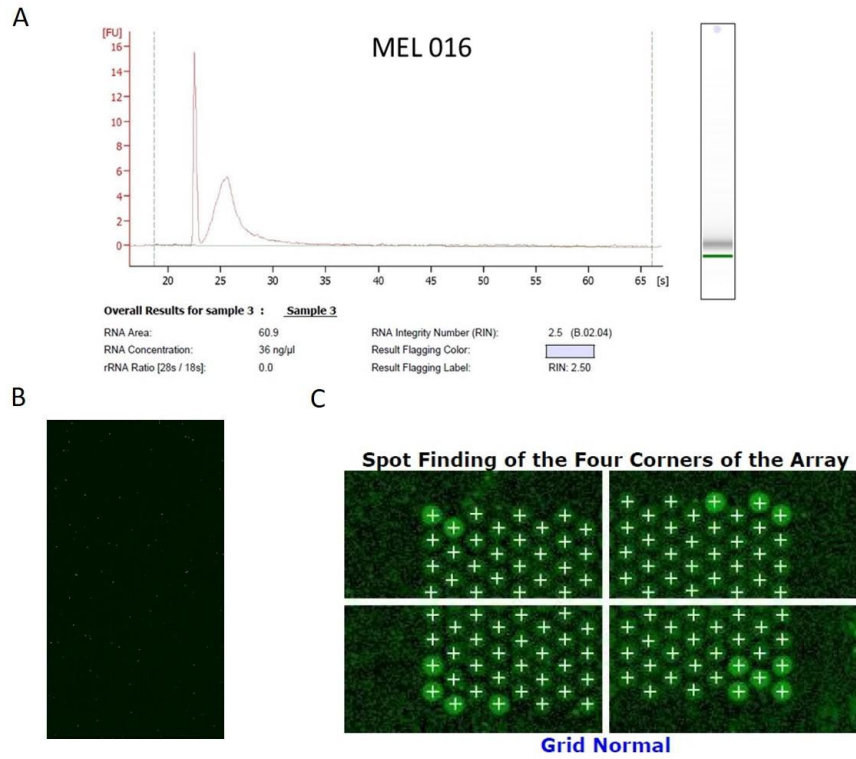


Figure S1. Evaluation of RNA quality and microarray hybridisation. *A)* Agilent 2100 Bioanalyzer analysis of a representative specimen showing RNA Integrity Number (RIN = 2.5) consistent with the values generally expected for paraffin-embedded tissues. *B)* Representative scanning of a microarray slide after hybridisation. *C)* Magnification of the four corners of the slide in B showing reference probes for grid positioning.

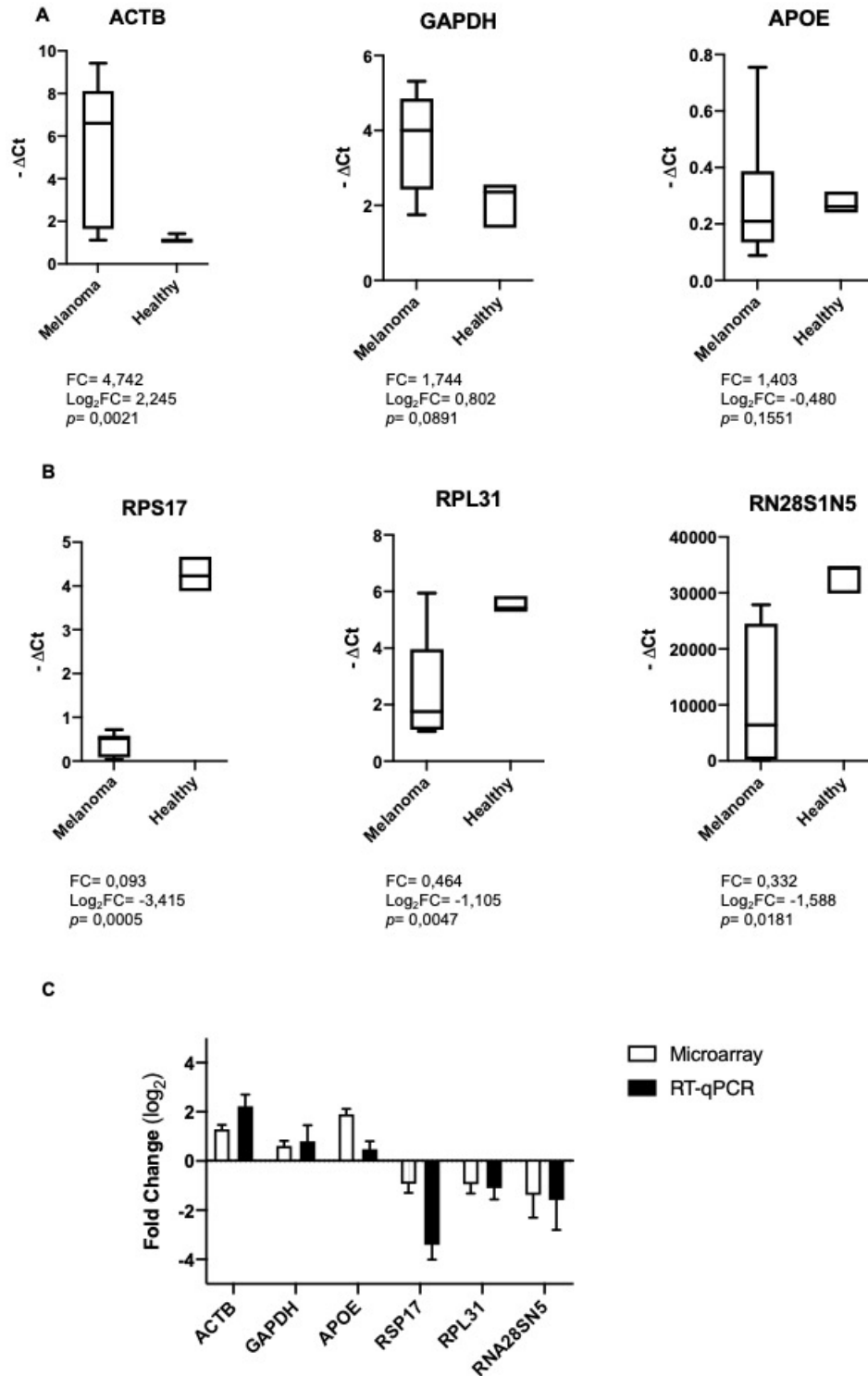


Figure S2. Microarray validation results. A) RT-qPCR results for a selection of three DEGs up-regulated in melanoma compared to healthy control, using a sample subset ($n = 4$) from microarray experiment. B) RT-qPCR results for a selection of three DEGs down-regulated in melanoma compared to healthy control, using a sample subset ($n = 4$) from microarray experiment. Data presented as median and interquartile range (IQR). Ct, threshold cycle; Fold Change $\Delta\Delta Ct$ method of relative quantification; p = p-value (Mann-Whitney U-test). C) Relative expression fold change (log₂) values comparison between microarray and PCR. Data presented as mean \pm SEM.

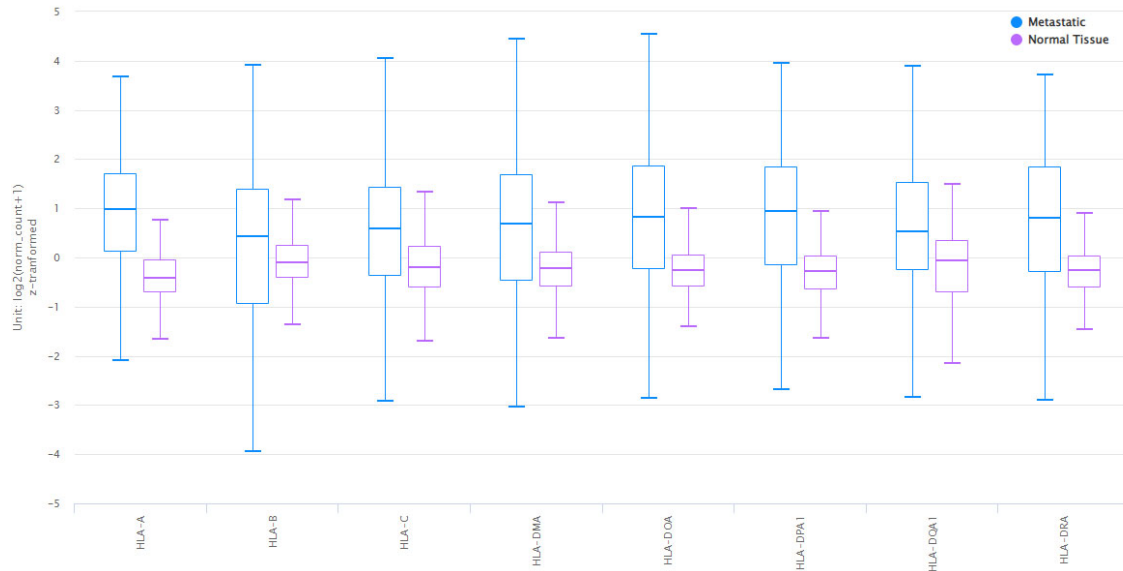


Figure S3. MHC gene expression from TCGA/GTEx databases for metastatic melanoma samples and normal tissues. A systematic overexpression of all the MHC class I genes (HLA-A, HLA-B, HLA-C), as well as MHC class II (HLA-DMA, HLA-DOA, HLA-DPA1, HLA-DQA1, HLA-DRA) could be confirmed, comparing BRAF-wild type metastatic melanoma samples with healthy skin tissue. Xena browser was used to filter TCGA samples and keep only data from Skin Cutaneous Melanoma studies, of metastatic type, and with no mutations in BRAF gene. The final cohort featured 179 tumour samples from TCGA and 557 healthy samples from GTEx, for a total sample size of $n = 736$.