**Supplementary Figure S1.** **A.** Expression of *MITF*-high and *MITF*-low marker genes in *MITF*-high 501Mel cells and *MITF*-low MM099 and MM047 cells. **B.** RTqPCR performed on bulk RNA from 501Mel, MM047 and MM099 cells as indicated using the same SOX9 and SOX10 primers as used in single cell RTqPCR analyses.

**Supplementary Figure S2.** Comparsion of gene expression in primary melanomas 1 and 2. Heatmap illustrating gene expression values in primary melanomas 1 and 2 (after clustering calculated on the ranked data as described in (14)). At the bottom of the panel \*\* indicates cells from tumour 1 that segregate with tumour 2 and cells from tumour 2 that segregate with tumour 1.

**Supplementary Figure S3.** **A-C**. Gene expression in the indicated primary melanomas. Heatmaps illustrate gene expression in single cells after clustering of cells and genes.

**Supplementary Figure S4.** Gene expression in 501Mel and MM099 cells. The indicated cells were labelled with the RNAscope probes. Expression of *MITF* and *SOX10* was restricted to 501Mel cells and *BIRC3* and *SOX9* to MM099 cells. Magnification 40X.

**Supplementary Figure S5.** Subpopulations of cells in cutaneous metastases expressing *MITF*-high and *MITF*-low markers. **A-C.** Sections from a cutaneous metastasis were labelled with RNAscope probes for the indicated genes and images were captured by fluorescent (panels A and B) or confocal microscopy (panel C). Arrowheads show representative double labelled cells. All panels show 40X magnification.

**Supplementary Figure S6.** *SOX9* and *SOX10* expression in sweat glands. **A-B.** Sections from a cutaneous metastasis were labelled with RNAscope probes for the indicated genes revealing gland-like structures labelled by *SOX10*, *SOX9* and *BIRC3*. Arrowheads show representative double labelled cells. **C.**  Sections viewed by confocal microscopy where the right panel shows a high magnification view of the boxed area. **D**. Hematoxylinandeosin stained section of the same cutaneous metastases. 10X and 20X magnification. Arrowheads show representative sweat glands. **E**. High magnification views of two representative structures, with the corresponding brightfield views. Panels A-C 40 X magnification, E 100X magnification.

**Supplementary Dataset 1.** A list of the assayed genes along with the primer sequences used.