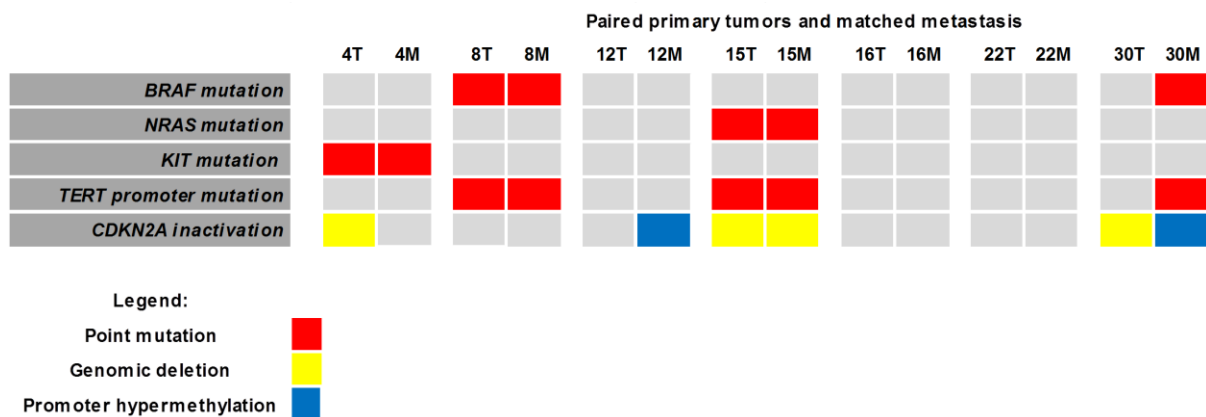


Supplementary Figure 1: Panel of CM driver alterations investigated in seven primary tumors and their paired metastatic tissues.

In this panel, each sample is represented in one column, and the primary tumors (T) are paired with their respective metastatic tissues (M). Mutations in hotspots of the *BRAF*, *NRAS*, and *KIT* genes, and in the *TERT* promoter were tested by capillary sequencing, whereas *CDKN2A* deletions and promoter methylation were investigated by MLPA and pyrosequencing, respectively. The color scheme is indicated in the figure.



Supplementary Figure 2: Analysis of *LINE-1* methylation levels of the primary cutaneous melanomas grouped according to T staging and mitotic rate.

The statistical testing was performed comparing tumors with distinct tumor thickness (T1: <1mm; T2: 1-2mm; T3: 2-4mm; T4: >4mm), and with distinct mitotic rate (number of mitotic cells/mm²). n= number of patients.

