

1 **Supplementary figure 1.** Sankey Diagram illustrating prior lines of therapy, between diagnosis (left  
2 side) and start of study treatment (right side).

3 **Supplementary figure 2. A.** The percentage of DC populations in the isolated myDC product was  
4 assessed by flow cytometry. Bars show the percentages of each DC subtype per patient and the  
5 median of all patients (n=7). **B.** and **C.** The maturation status of the isolated myDC product was  
6 evaluated by flow cytometry. Dots show the percentage of cells expressing a marker (**B**) or the mean  
7 fluorescence intensity (MFI) of a marker (**C**) on the CD1c (BDCA-1)<sup>+</sup> and CD141 (BDCA-3)<sup>+</sup>  
8 subpopulations (n=7). **D.** t-SNE plot of the myDC product isolated from patient 8, showing the cDC1,  
9 cDC2 and pDC population and the remaining contaminating CD14<sup>+</sup> cells.

10 **Supplementary figure 3.** Case illustrations and treatment disposition of all patients with exception of  
11 patient 7. Timeline depicts time since first treatment administration. Dots indicate treatment  
12 administration as indicated on day 1 and day 2. Needle indicates injected lesion. SD: stable disease,  
13 PR: partial response, PD: progressive disease, NGS = next generation sequencing results (mutated  
14 genes), TLDD = trametinib + low dose dabrafenib, TMZ = temozolomide (chemotherapy)

15 **Supplementary figure 4.** Immunological blood composition at baseline in responders and non-  
16 responders. **A.** Absolute cell counts of the major blood immune cell types at baseline were  
17 determined using a complete blood count. Data are depicted as cells/mm<sup>3</sup>. **B.** The neutrophil-to-  
18 lymphocyte ratio (NLR) was determined by dividing the absolute neutrophil number by the absolute  
19 lymphocyte number. **C.** Absolute numbers of the distinct lymphocyte subsets were determined by  
20 flow cytometry and the absolute lymphocyte cell count. Data are depicted as cells/mm<sup>3</sup>. **D.**  
21 Frequencies of CD4<sup>+</sup> and CD8<sup>+</sup> T cells as percentage of T cells were calculated by dividing the number  
22 of CD4<sup>+</sup> and CD8<sup>+</sup> T cells by the number of CD3<sup>+</sup> T cells. **E.** The frequency of Tregs as percentage of  
23 CD4<sup>+</sup> T cells was calculated by dividing the number of Tregs by the number of CD4<sup>+</sup> T cells. Each dot  
24 represents one patient (n=6), which are further divided into responders (R) (n=3) and non-  
25 responders (NR) (n=3). Statistical analysis by (a) Mann-Whitney test with p-values corrected for

26 multiple testing by the Holm-Sidak method and (b-e) Mann-Whitney test. CR = complete response;  
27 SD = stable disease; PR = partial response; PD = progressive disease.

28 **Supplementary figure 5.** Evolution of blood composition from baseline to on-treatment in  
29 responders and non-responders. **A.** Absolute cell counts of the major blood immune cell types at  
30 baseline and on-treatment were determined using a complete blood count. Data are depicted as  
31 cells/mm<sup>3</sup>. **B.** Frequencies of different T cell subsets as percentage of CD4<sup>+</sup> T cells (upper panels) or  
32 CD8<sup>+</sup> T cells (lower panels). **C.** Frequencies of DC subsets as percentage of total DCs. All on-treatment  
33 values are depicted as 1 value, being the median of all on-treatment values. Each dot represents one  
34 patient (n=6), which are further divided into responders (R) (n=3) and non-responders (NR) (n=3).  
35 Statistical analysis by paired t-test, both on all data or for responders and non-responders separately.  
36 \* p < 0.05. T<sub>SCM</sub>: stem cell memory T cell; T<sub>N</sub>: naïve T cells; T<sub>TE</sub>: terminally differentiated T cells; T<sub>CM</sub>:  
37 central memory T cells; T<sub>EM</sub>: effector-memory T cells.

38 **Supplementary Figure 6.** Results from multiplex immunohistochemistry analysis. **A.** Upper panel:  
39 proportion of tumor cells (SOX10<sup>+</sup>) in biopsy sample. Middle panel depicts cellular composition of the  
40 tumor area. Lower panel depicts cellular composition of the peritumoral area. Indicated beneath  
41 graph is time on treatment and lesion. **B.** Graphs representing mean distance between SOX10<sup>+</sup>  
42 melanoma cells and CD8<sup>+</sup> (upper panel) or CD4<sup>+</sup> (lower panel) T-cells in patient 2. **C.** Visual  
43 representation of decreasing distance between CD8<sup>+</sup> T-cells and SOX10<sup>+</sup> melanoma cells in patient 2  
44 both at baseline and on-treatment. White lines indicate distance. **D.** Microscopic images of patient 5  
45 suggestive for the phenomena of T-cell exclusion with majority of both CD4<sup>+</sup> and CD8<sup>+</sup> T-cells being  
46 restricted to the peritumoral area. DAPI=4',6-diamidino-2-fenylindool **E.** Graphs representing % of  
47 macrophages as a proportion of total amount of cells in the tumor area, split between CD68<sup>+</sup> cells  
48 and CD68<sup>+</sup> SOX10<sup>+</sup> double positive cells.