

Supplementary figure S1. Detection of melanoma cells spiked into PBMCs from normal blood. Melanoma cells from the melanoma cell lines WM1617, WM278 and WM1789 were spiked at different concentrations into PBMCs from a NBD in triplicate with 0, 10, 25, 50, 100 and 500 melanoma cells for each melanoma cell line. The expected number of cells spiked is plotted versus the number of cells detected using the CMC assay.

Supplementary figure S2. DNA copy number profile of the ‘excluded candidate cells’. Representative DNA CNV profiles (left) and merged color images (right) of 3 ‘excluded candidate’ cells from patient #37. Adjusted \log_{10} ratio of read depth of sequencing data are plotted for individual bins (y axis) across genomic regions (x axis). Red: CSPG4, white: HMB-45 green: CD45, blue: Hoechst. RNS: relative nuclear size.

Supplementary table S1. Novel chromosomal amplifications and candidate genes. Bold: reported cancer genes (UCSC genome browser).