Figure S1: Joint hierarchical clustering of transcriptomes of all patient-matched melanoma metastases and normal tissue samples. The tissue type bar below the dendrogram represents the type of the sample either metastasis tissue (red, sample names starting with P) or normal tissue (grey, sample names starting with N). The origin of the tissue is represented by the origin bar below the dendrogram: brain (B, grey) lung (Lun, blue), lymph node (Lym, green), skin (Ski, yellow), liver (Liv, pink), small intestine (Smi, lightgreen) or soft tissue (Sof, purple). Stability of individual clusters is quantified by the red AU-value, where 100 means that a cluster was perfectly stable. A clear separation between metastasis and normal tissue samples is observed, except for the lymph node metastasis of patient P6.