



Figure 3 – figure supplement 2. Transcriptional programs distinguish M and NM basal cells. **(A)** Principal components analysis (PCA) scatter plot of 42 basal cells (points), showing that the distribution (top and side density histograms) of M and NM basal cells (color legend) is strongly associated with the first principal component. **(B)** Accuracy (y axis) of a machine learning (*k*-nearest neighbor) classifier in distinguishing M from NM basal cells using the top *n* most differentially expressed genes (x axis). The high accuracy indicates that M and NM clusters are well separated in transcriptional space.