



**Figure 5—figure supplement 1.**

Heat-map of normalized read counts of FACS sorted cells based on CD44 and CD24 surface markers from patient tumor and H1650 derived isogenic cell line H1650-Isg-E4.

Heat-map of normalized read counts across segment breakpoints (using Euclidian distance and ward clustering method) of CD44+/ CD24- cells and CD44-/ CD24+ cells sorted from a (A) NSCL tumor (patient #4) and (B) H1650 derived isogenic cell line (H1650-isg-E4) is displayed. CD44-/ CD24+ cells are marked with a blue circle and CD44+/ CD24- cells are marked with an orange circle. The cluster dendrogram and heat-map of normalized read counts were generated using Ginkgo, an open-source web platform for interactive analyses of CNA. (Garvin et al., 2015) (<http://qb.cshl.edu/ginkgo>).