Figure S1

Supplemental Figure 1. *TNBC Subpopulations Are Genotypically Similar But Epigenetically Distinct.* (A) Differential regions of H3K27ac enrichment in POS and NEG cells. Regions with an adjusted p-value < 0.05 and $\log_2$ fold change greater 0 are enriched in POS cells (blue), regions with an adjusted p-value < 0.05 and $\log_2$ fold change less than zero are enriched in NEG cells (red). (B) Comparison of gene expression in the POS subpopulation FACS-sorted from SUM-229PE cells with POS cells cultured in isolation for 6 weeks (left). Pearson correlation coefficient = 0.91. Comparison of gene expression in the NEG subpopulation FACS-sorted from SUM-229PE with NEG cells cultured in isolation for 6 weeks (right). Pearson correlation coefficient = 0.95. (C) GO analysis of the molecular function of genes enriched in POS cells identified in Fig. 1G (D) Expression of genes in POS cells relative to NEG cells in the Heterotypic Cell-Cell Adhesion GO term identified in Fig. S1C. (E) Expression of genes in POS cells relative to NEG cells in the Cadherin Binding in Cell-Cell Adhesion GO term identified in Fig. S1C. (F) GO analysis of the molecular function of genes enriched in NEG subpopulation identified in Fig. 1G. (G) Expression of genes in POS cells relative to NEG cells in the Collagen Binding GO term in Fig. S1F. (H) Expression of genes in POS cells relative to NEG cells in the TGFβ II Receptor Binding GO term in Fig. S1F. (I) Expression of genes in POS cells relative to NEG cells in the PDGF Receptor Binding GO term in Fig. S1F. (J) Comparison of the differentially expressed genes in POS and NEG cells with genes identified by DESeq2 in the mesenchymal breast cancer cell line SUM-159PT and the basal like breast cancer cell line HCC-1806. (K) Row-mean normalized expression of genes from the mesenchymal breast cancer geneset in POS and NEG cells. Maximal expression indicated in yellow. Unexpressed genes indicated in grey. (L) Row-mean normalized expression of genes from the basal breast cancer geneset in POS and NEG cells. Maximal expression indicated in yellow. Unexpressed genes indicated in grey. (M) Flow cytometry of SUM-149PT basal-like breast cancer cells stained for EpCAM and CD49f (ITGA6). Subpopulation frequencies indicated in upper right corner of quadrant.