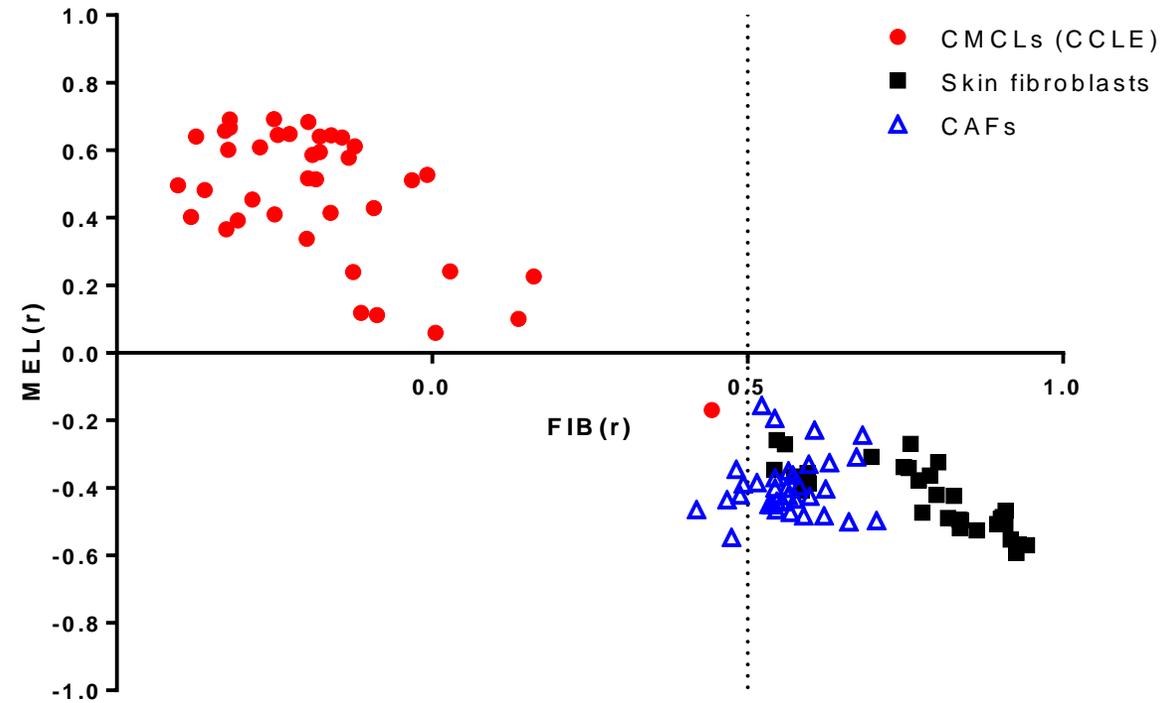
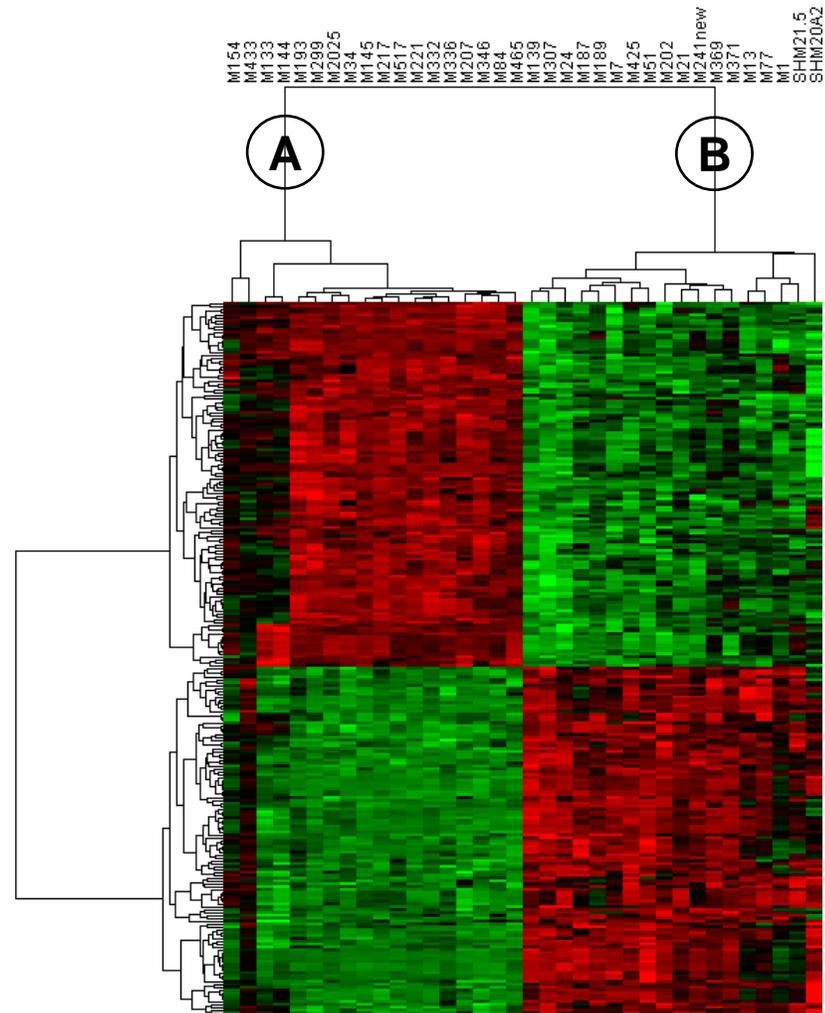
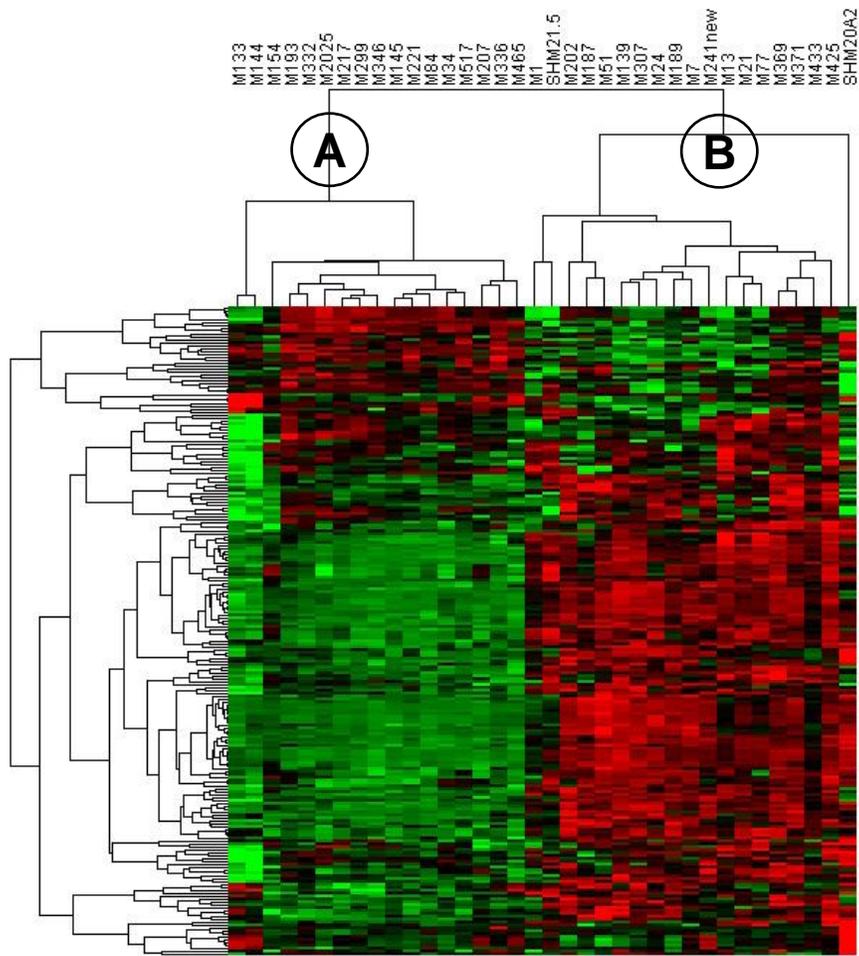


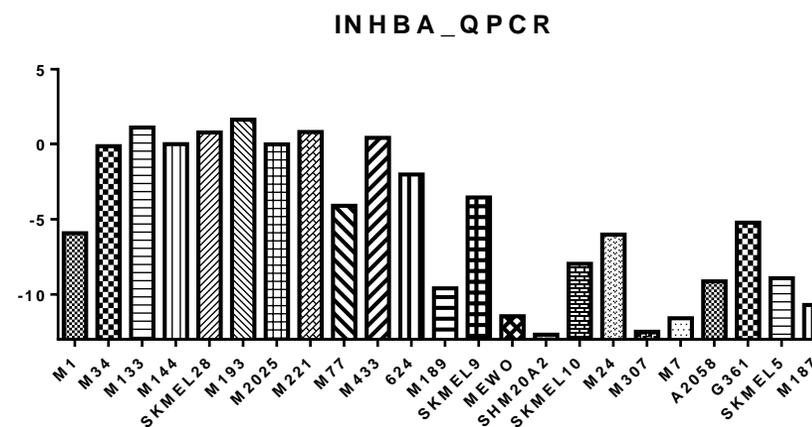
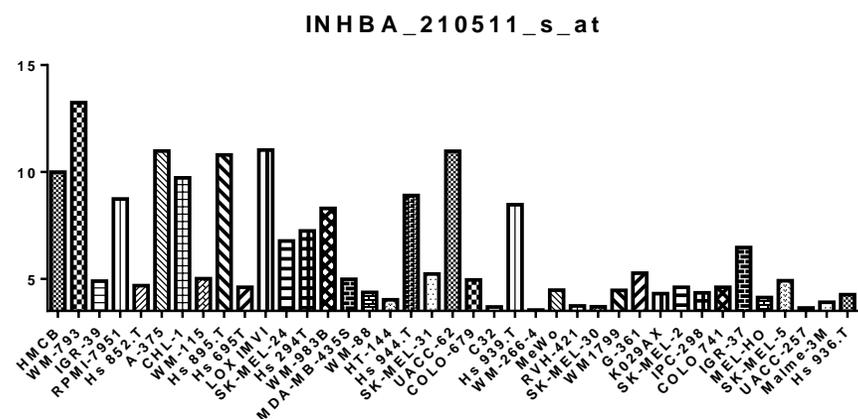
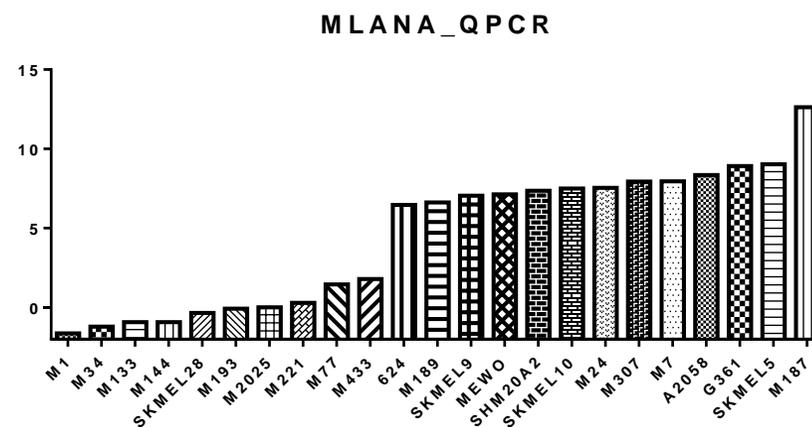
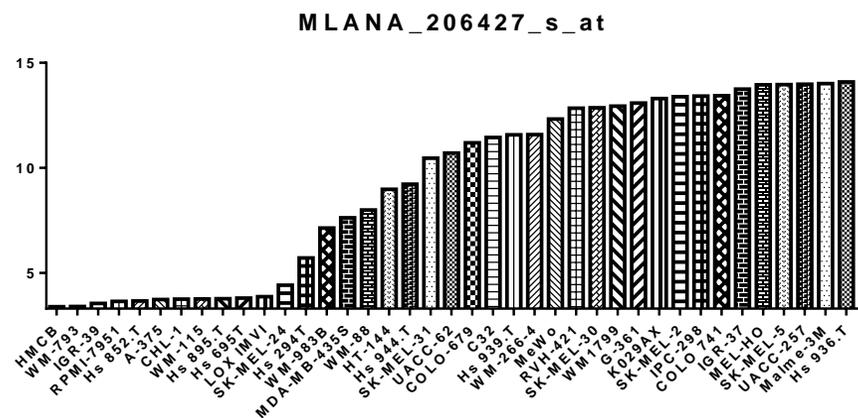
**Supplementary Figure 1a: Fibroblast/Melanoma correlation plot of skin fibroblasts, cancer associated fibroblasts (CAFs) and primary melanoma cell lines (PMCL) from different cohorts.** Similarity to fibroblastoid and melanocytic signature of primary melanoma cell lines were calculated as FIBr and MELr values, using GSE4840, GSE4841 and GSE4843 datasets. Most, if not all of the samples in GSE4841 and GSE4843 were positively correlated with melanocytic signature. Almost half of the samples in GSE4840 dataset were positively correlated with fibroblastoid signature.



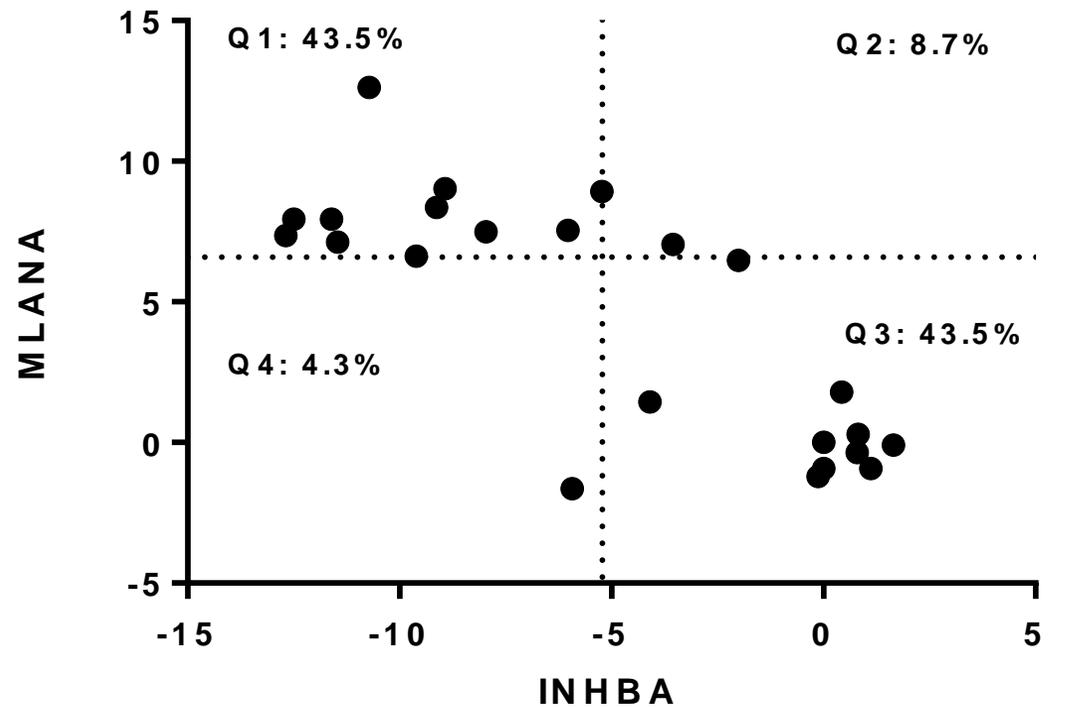
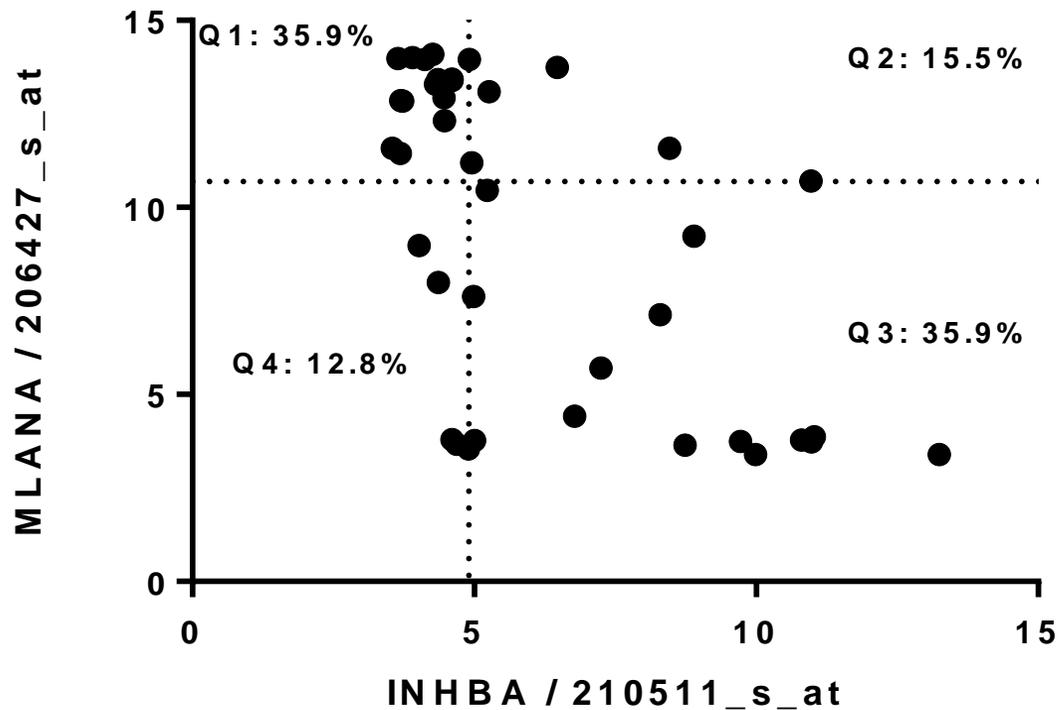
**Supplementary Figure 1b: Fibroblast/Melanoma correlation plot of commercially available melanoma cells lines (CMCLs) , skin fibroblasts and CAFs.** CMCLs screened for 24 different drugs in Cancer Cell Line Encyclopedia (CCLE) database plotted according to their FIB and MEL r values with skin fibroblasts and CAFs (see Figure 1 for explanations).



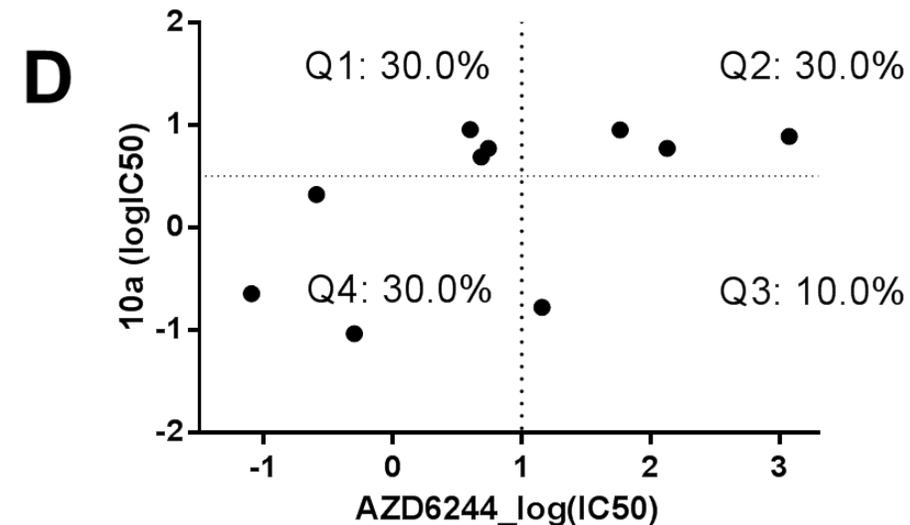
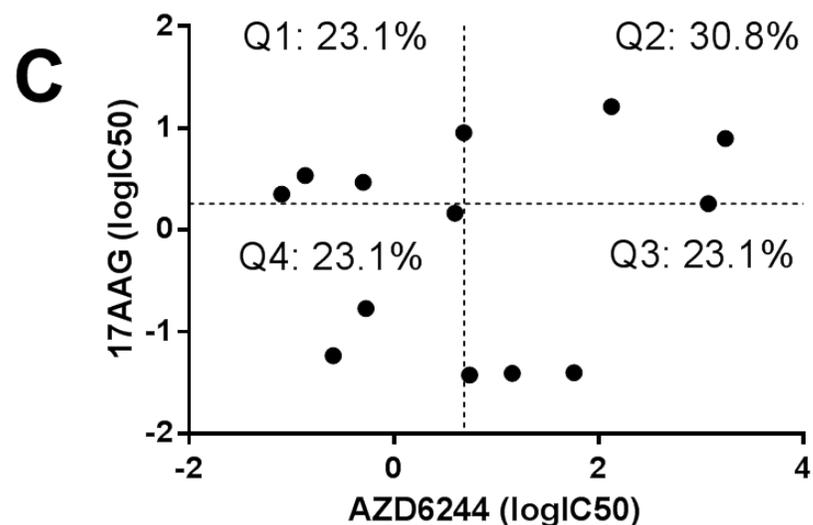
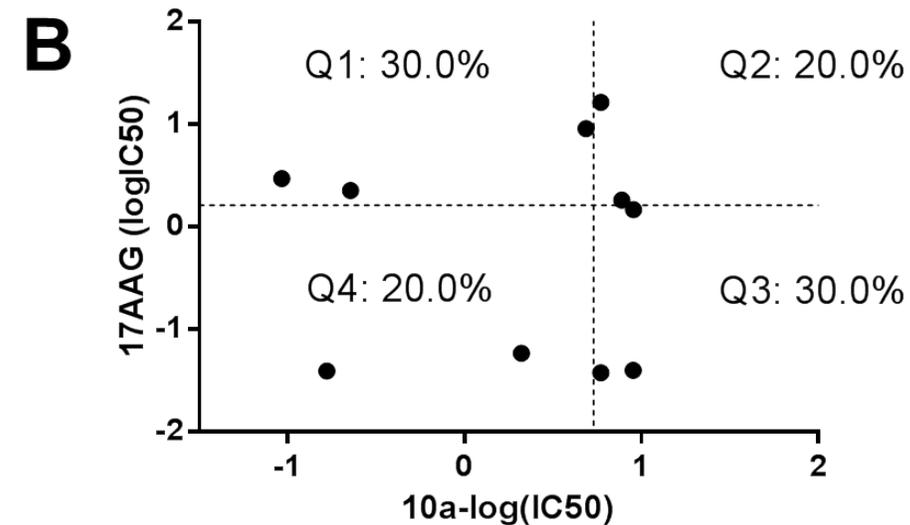
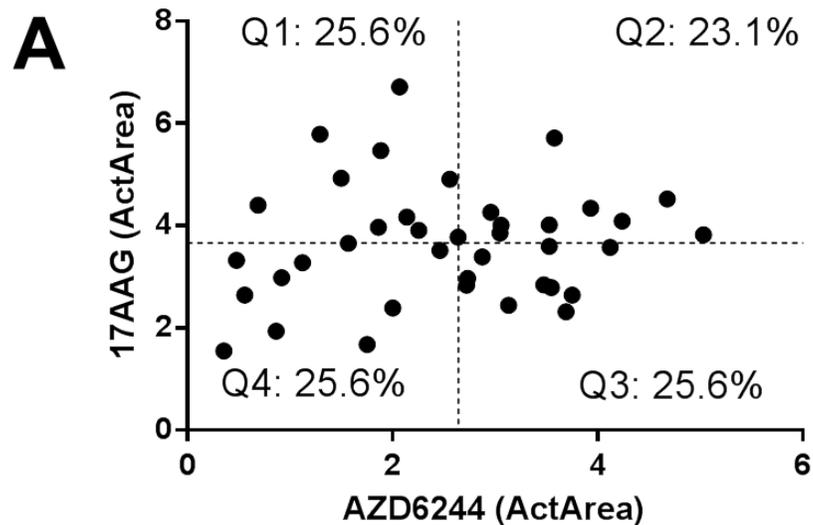
**Supplementary Figure 2: Hierarchical clustering analysis (HCA) of PrMCLs.** HCA based on 223 melanoma specific probesets using C-MAP data identifies two major groups (A and B) (left). Supervised HCA of genes differentially expressed in groups A and B (right).



**Supplementary Figure 3. Inhibin A (INHBA) and MelanA (MLANA) expression in melanoma cell lines.** In silico analysis of gene expression profiles in CMCLs (GSE36133), left panel; and qPCR based gene expression of PrMCLs (right panel) and some CMCLs show expression levels of these two genes are inversely correlated. Pearson's  $r$  and  $p$  values for CMCLs and PrMCLs are  $-0.6$  ( $p < 0.0001$ ) and  $-0.79$  ( $p < 0.0001$ ), respectively.



**Supplementary Figure 4. MLANA and INHBA co-expression of melanoma cell lines and PrMCLs.** Cell lines categorized into quadrants based on expression of MLANA and INHBA. Thresholds correspond to mean expression. In silico analysis of melanoma cell lines (left) and in vitro qPCR based analysis of PrMCLs (right) both show most cells to cluster in quadrants 1 and 3 as expected.



**Supplementary Figure 5. Quadrant plots of sensitivity similarities among melanoma cell lines.** In silico analysis of melanoma cell line drug sensitivity distribution to 17AAG and AZD6244 (**A**). In vitro analysis of sensitivity distribution of PrMCLs (**B-D**). A borderline correlation is observed between IC50 values obtained for 10a and AZD6244 (Pearson's  $r$ : 0.57,  $p$ =0.08)