

Clustering of phosphorylation site abundance matrix supports distinct signaling state of persistent cells. (A) Clustered phosphorylation site abundance matrix for parental (P) and short-term persistent (S) M229, M238, and M249 melanoma cells. Quantile normalized data was log-transformed and filtered for a Bonferroni-corrected ANOVA p-value less than 0.1 (grouped by samples). Complete linkage clustering of centered and scaled data by row with correlation based distance metric. (B) Clustering of the pair-wise Pearson correlation matrix. Quantile normalized data was log transformed, filtered for a Bonferroni-corrected ANOVA p-value less than 0.1 (grouped by samples) and centered before calculation of Pearson correlation coefficients. Correlation coefficients were complete linkage clustered with Euclidean distance metric.