

Novel cell 'switches' found to promote lung cancer growth, treatment resistance



SCLC cell lines have divergent gene regulatory networks and phenotypes. (A) Hierarchical clustering was performed using 53 SCLC cell lines. Silhouette widths, which measure the likeness within each cluster, were calculated. j, cluster number; n_i, number of samples in each cluster; aveSi, average silhouette width for each cluster. (B) The log fold change (FC) for fate-defining TFs in the indicated cluster versus the rest. (C) Representative cell lines, with cluster membership shown in parentheses, were profiled for cluster-defining proteins by immunoblot. WCL, whole cell lysate. (D) Proportion of adherent samples for

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each cluster as annotated by the Cancer Cell Line Encyclopedia (CCLE). Bars represent the means, and the Mann-Whitney test was used for statistical analysis. *P

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