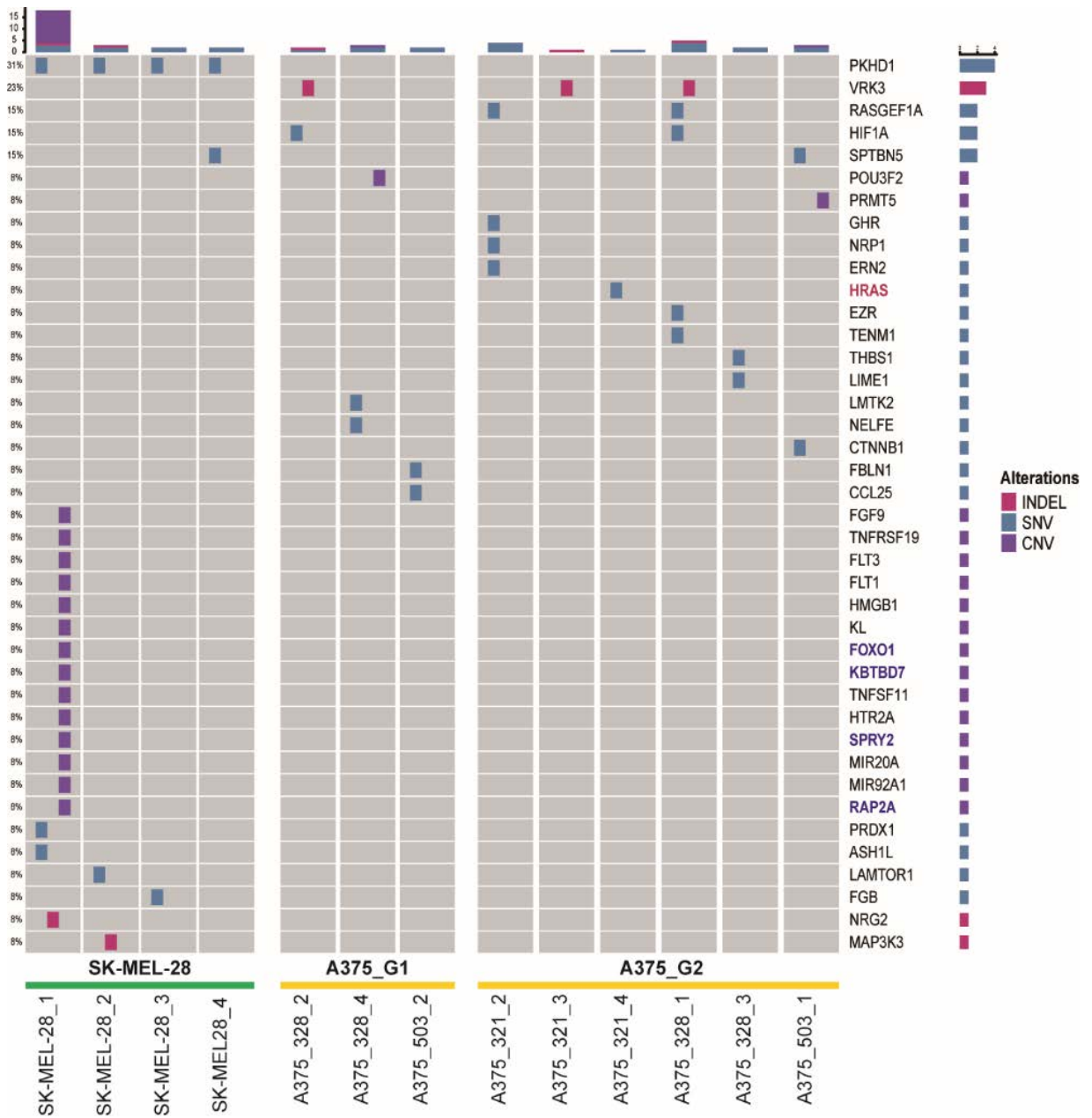
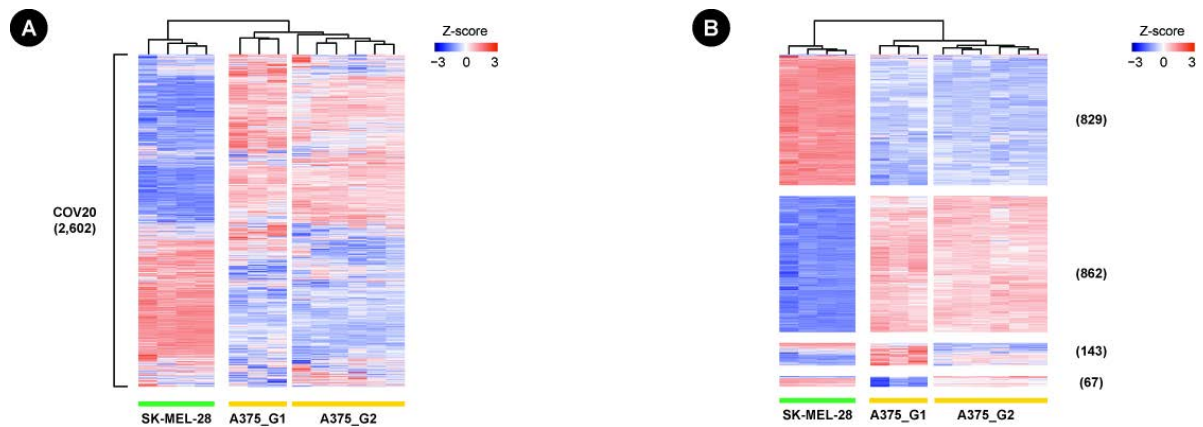


ION	0.10	0.10	0.13	0.09	05	04		
KEGG_PROGESTER	-	-	-	-	8.84E-	4.57E-	-	-
ONE_MEDIATED_	0.12	0.12	0.19	0.09	04	03		
OOCYTE_MATUR								
ATION								

Terms with both case columns indicate the overlapping terms in results from t-test analysis. GSVA, gene set variation analysis; FDR, false discovery rate.



**Supplementary Fig. 1.** Somatic variations from exome sequencing analysis. Mutation plot showing the single nucleotide variants (SNVs), indels, and copy number variations. The genes on the row are from the collection of mitogen-activated protein kinase pathway, receptor tyrosine kinase, and microphthalmia-associated transcription factor (*MITF*) regulations. All SNVs are over the allele frequency of 0.1. The insertion/deletion variations were below the allele frequency of 0.1. Copy number variations (CNVs) were copy number loss events.



**Supplementary Fig. 2.** Hierarchical clustering of resistant cells. (A) Hierarchical clustering with the top 20% in the coefficient of variation (COV20) genes yielded three sample groups where SK-MEL-28 and A375 cells were divided. A375 cells were further divided into two subgroups. (B) Hierarchical clustering with differentially expressed genes (DEGs) obtained by comparing (1) SK-MEL-28 vs. A375 cells and (2) A375 group 1 vs. A375 group 2 cells. Numbers in parentheses indicate the number of DEGs (upregulated and downregulated in the two comparisons).