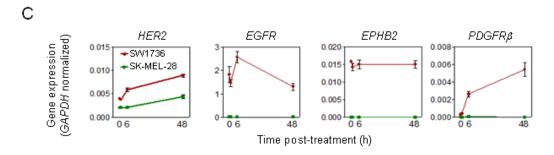


В

Term	List	Term (%) per list	Odds ratio (log <sub>e</sub> )	Adj.pvalue
MAPK signaling pathway (hsa04010	Clusters	1.91	0.63	2.14E-04
	Genome	1.02		
Cytokine-cytokine receptor interaction (hsa04060)	Clusters	2.01	0.69	1.02E-03
	Genome	1.01		
Insulin signaling pathway (hsa04910)	Clusters	1.09	0.86	1.19E-03
	Genome	0.46		
ErbB/HER signaling pathway (hsa04012)	Clusters	0.68	0.86	1.21E-02
	Genome	0.29		



**Figure S2.** PLX4032-treated BRAF mutant thyroid cancer cells show induction or high basal expression of several RTKs compared to melanoma cell lines. **A,** gene expression profiles (Illumina HT-12 v4) of thyroid (SW1736; red) vs melanoma (SK-MEL-28; green) cells at the indicated times after treatment with 2  $\mu$ M PLX4032. Graphs represent the median profiles of gene clusters that are significantly different between the lines. **B,** table shows KEGG terms significantly over-represented in the stated gene clusters vs the rest of the genome by Fisher's exact test. The p-values are adjusted by FDR (B & H). **C,** Technical validation of differentially expressed RTKs identified by expression profiling analysis of SW1736 vs SK-

MEL-28 cells. Cells were treated with 2  $\mu$ M PLX4032 for 1, 6 or 48 h. Points represent RTK/GAPDH Q-RT-PCR values of triplicates assays (mean +/- SD).