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Figure 1**A: Yeast-2-Hybrid Screening***Screen Parameters*

Bait Fragment→Homo sapiens –WBP2 (aa 1-261)

Prey Library→Human Breast Tumor Epithelial Cells

cDNA Library

Processed Clones→ 166

Analyzed interactions: 87 millions

Global PBS (for Interactions represented in the Screen)		Nb	%
A	Very high confidence in the interaction	4	13.3%
B	High confidence in the interaction	7	23.3%
C	Good confidence in the interaction	1	3.3%
D	Moderate confidence in the interaction This category is the most difficult to interpret because it mixes two classes of interactions : - False-positive interactions - Interactions hardly detectable by the Y2H technique (low representation of the mRNA in the library, prey folding, prey toxicity in yeast)	17	56.7%
E	Interactions involving highly connected prey domains, warning of non-specific interaction. The threshold for high connectivity is 10 for screens with Human, Mouse, Drosophila and Arabidopsis and 6 for all other organisms. They can be classified in different categories: - Prey proteins that are known to be highly connected due to their biological function - Proteins with a prey interacting domain that contains a known protein interaction motif or a biochemically promiscuous motif	1	3.3%
F	Experimentally proven technical artifacts	0	0.0%

Figure 2

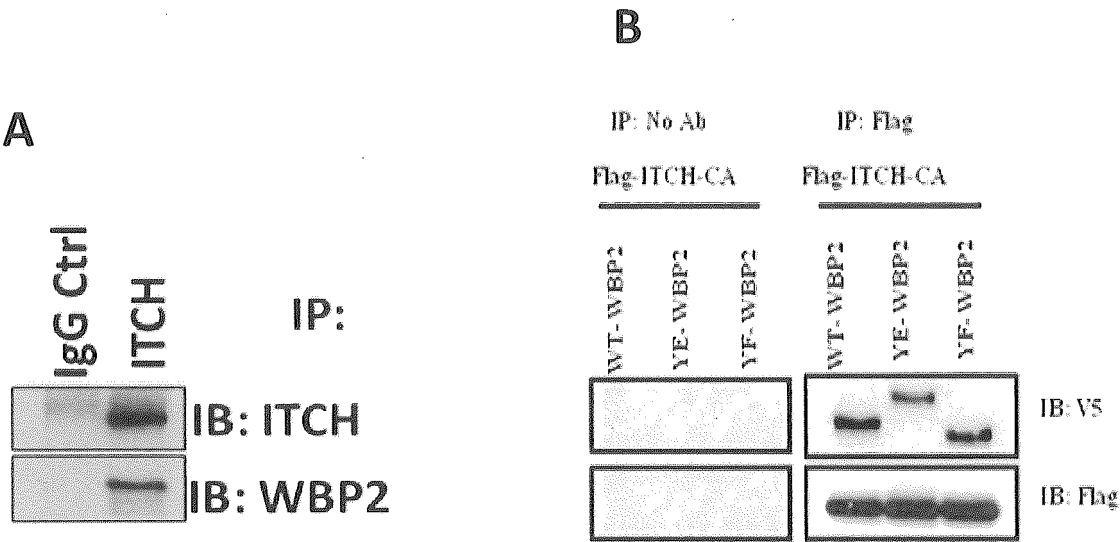
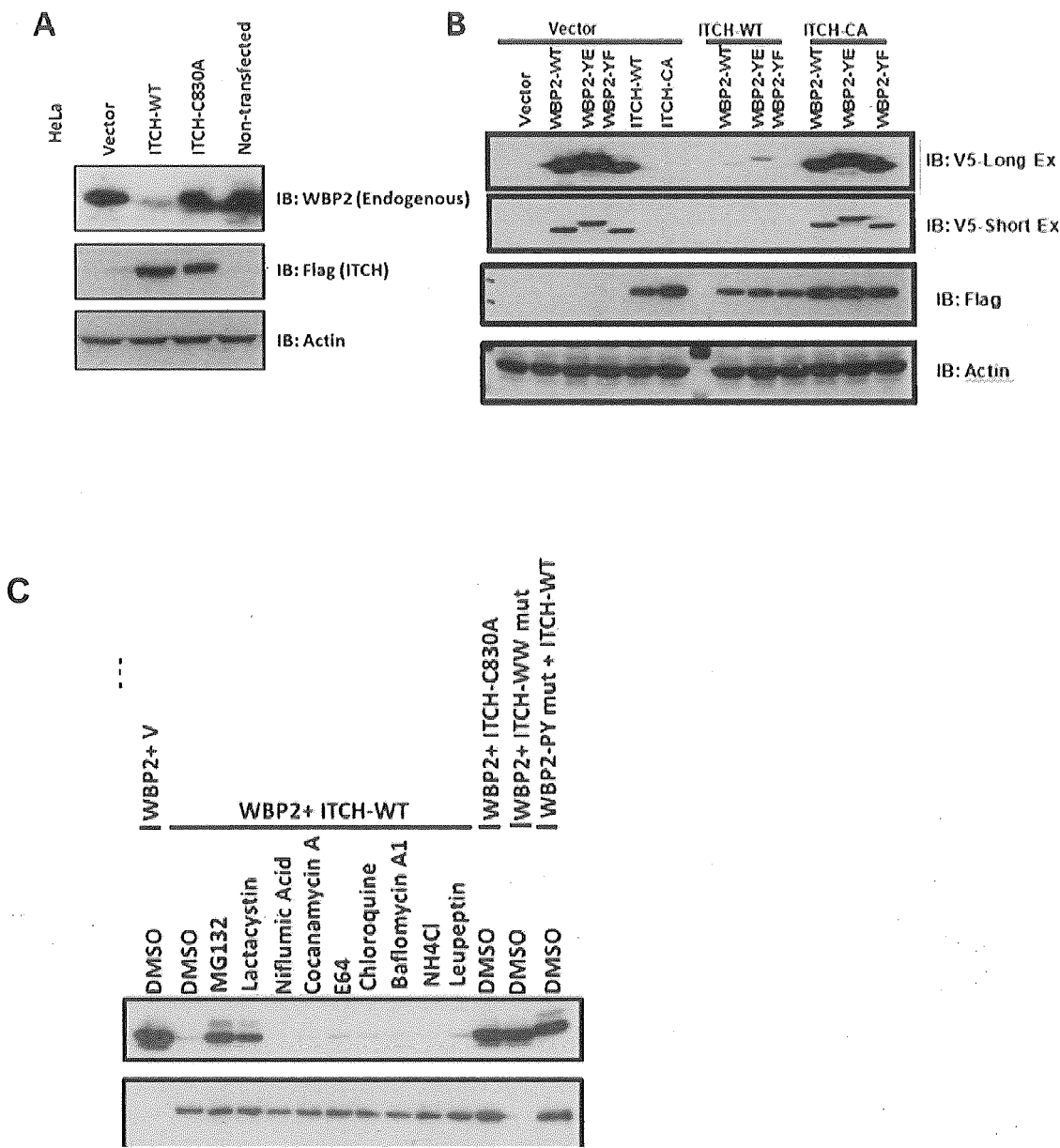


Figure 3



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Figure 4

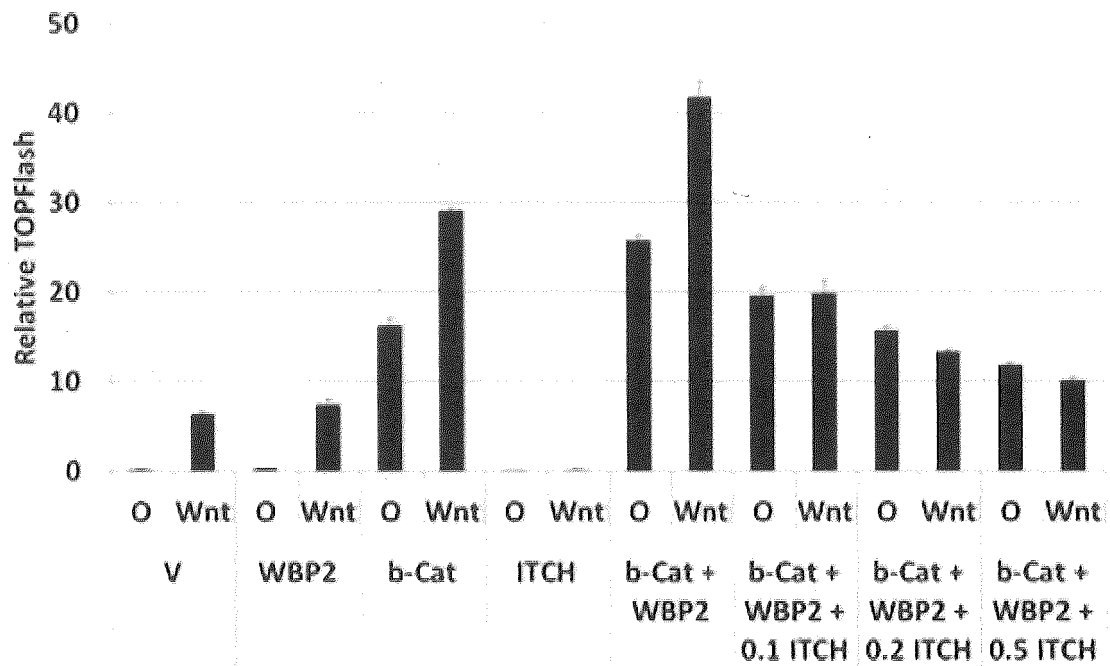


Figure 5

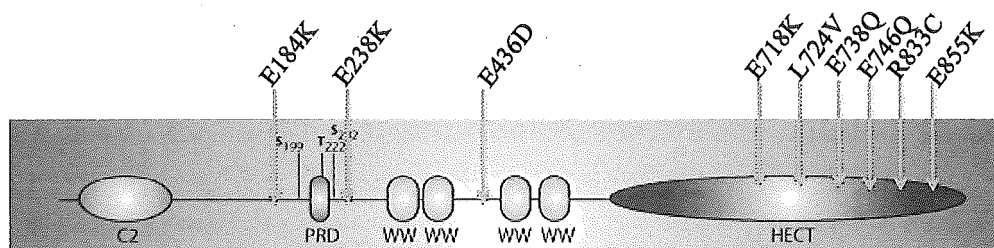


Figure 6

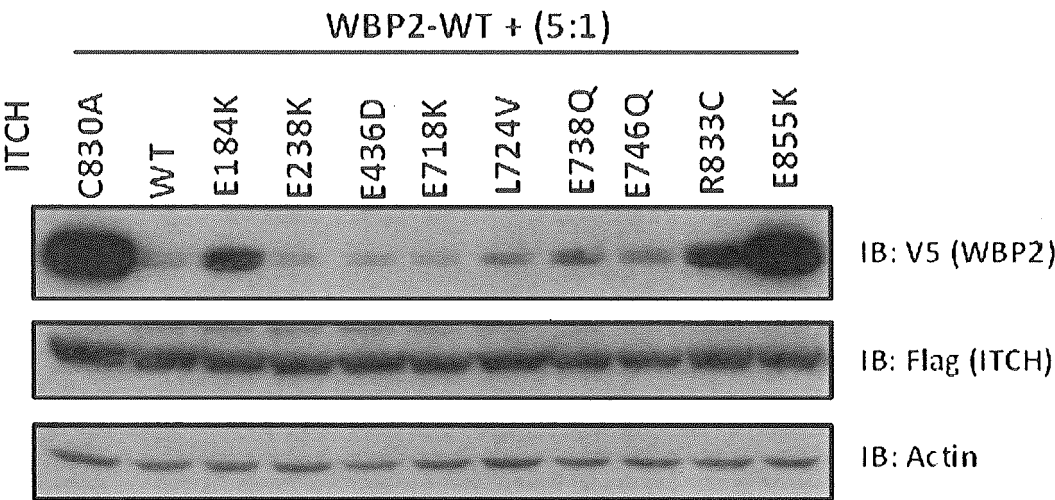
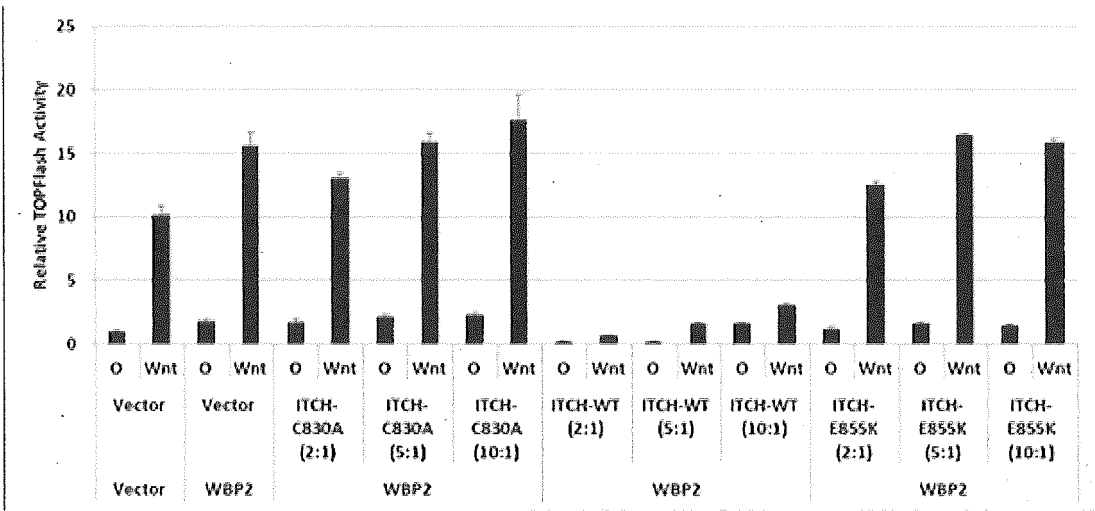


Figure 7



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Figure 8

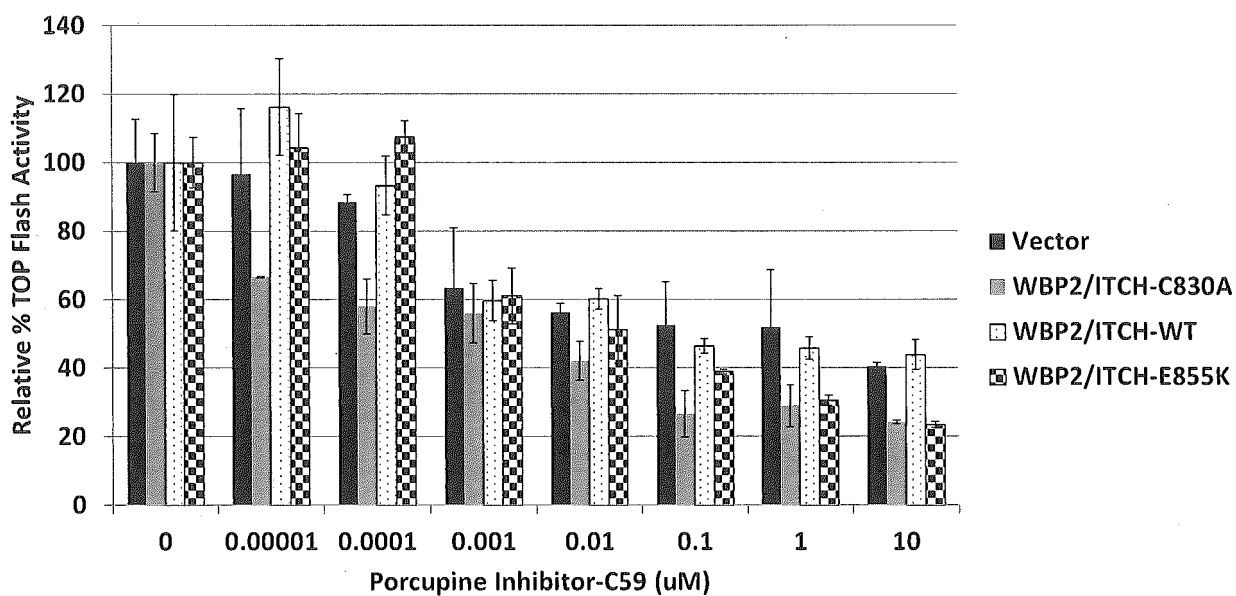


Figure 9

