

Table S1. The GO functional analysis of DEGs in Module-Up-A and Module-Down-A. (Shown top 5)

Category	Term	Description	P Value
Module-Up-A			
Biological Process	GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	3.82E-06
Biological Process	GO:0006886	intracellular protein transport	6.86E-06
Molecular Function	GO:0016175	superoxide-generating NADPH oxidase activity	5.87E-05
Biological Process	GO:0042554	superoxide anion generation	1.22E-04
Biological Process	GO:0006801	superoxide metabolic process	2.53E-04
Module-Down-A			
Biological Process	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	2.12E-05
Biological Process	GO:0009303	rRNA transcription	1.88E-04
Biological Process	GO:0051966	regulation of synaptic transmission, glutamatergic	7.12E-04
Biological Process	GO:0071222	cellular response to lipopolysaccharide	9.54E-04
Biological Process	GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled	1.06E-03

Table S2. The KEGG pathway analysis of DEGs in Module-Up-A and Module-Down-A. (Shown top 5)

Category	Term	Description	P Value
Module-Up-A			
Pathway	hsa04961	Endocrine and other factor-regulated calcium reabsorption	4.13E-03
Pathway	hsa05016	Huntington's disease	7.51E-03
Pathway	hsa04721	Synaptic vesicle cycle	7.96E-03
Pathway	hsa04144	Endocytosis	1.68E-02
Pathway	hsa04380	Osteoclast differentiation	3.19E-02
Module-Down-A			
Pathway	hsa04020	Calcium signaling pathway	7.96E-06
Pathway	hsa04022	cGMP-PKG signaling pathway	8.72E-05
Pathway	hsa05142	Chagas disease (American trypanosomiasis)	3.13E-03
Pathway	hsa05200	Pathways in cancer	4.42E-03
Pathway	hsa04270	Vascular smooth muscle contraction	4.58E-03

Supplementary Figure Legends

Figure S1.

The significant modules in the up-regulated protein-protein interaction network with MCODE score >4 and node >6 . (A). Module-Up-A. (B). Module-Down-A.

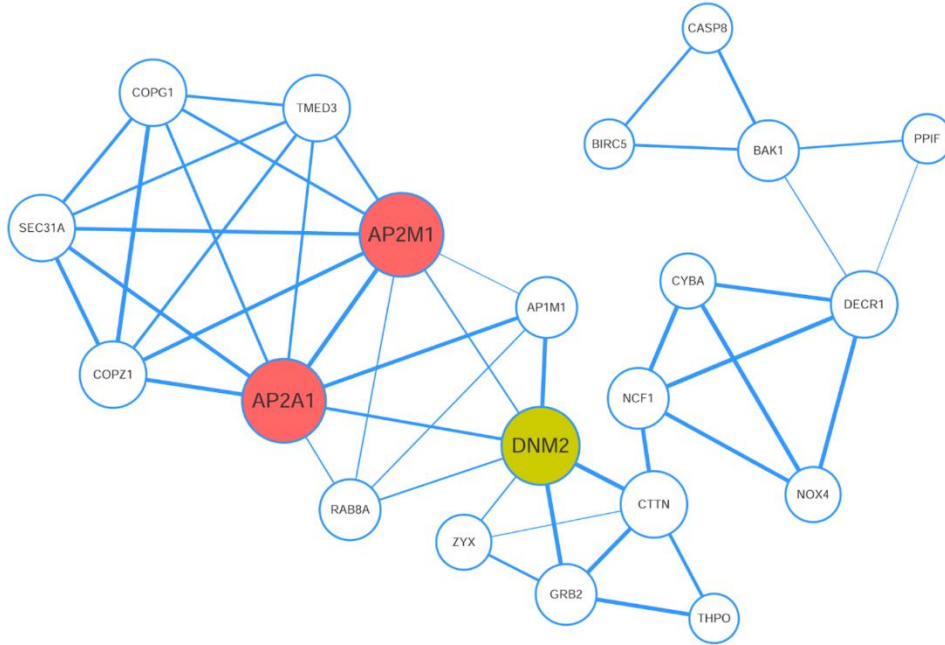
MCODE: molecular complex detection. Molecules in red, yellow and green indicated star molecules and width of edge was determined to the combined score of the protein-protein interaction relationship.

Figure S2.

Protein expression level detected using Reverse Phase Protein Array was compared by Student's t test between groups (*BAP1* mutated versus *BAP1* wild-type). (A). TP53 protein level was not significantly different between groups. (B). CTNNB1 protein level was significantly higher in *BAP1* wild-type tumor samples. Note: We excluded each protein expression level in the highest 5% or the lowest 5% among all patients studied to avoid measurement errors.

Figure S1

A



B

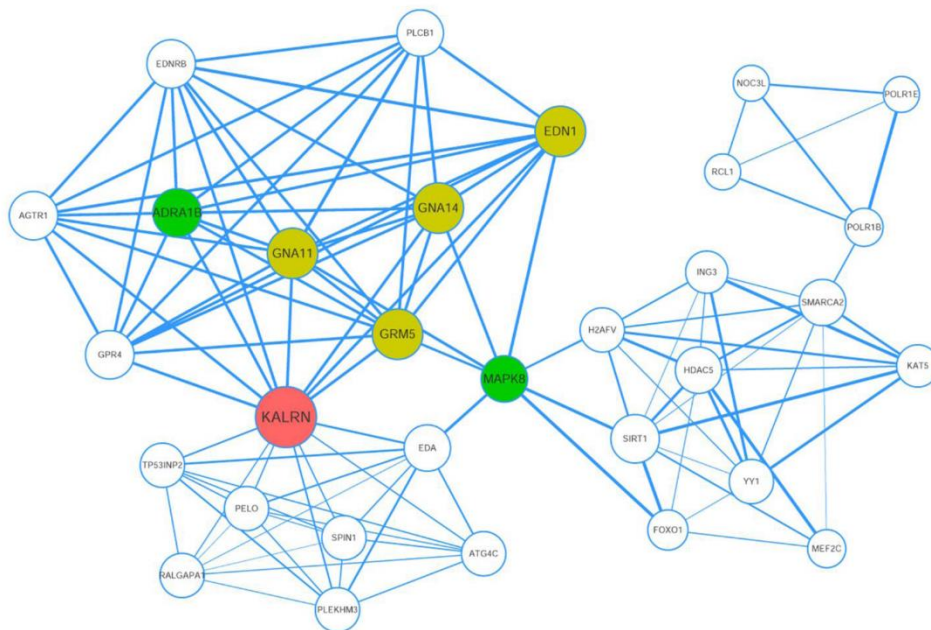


Figure S2

