

Supplementary Figure 1: The Pathway analysis usage of cytoscape ClueGO plugin (<https://cytoscape.org/>) (1,2).

The ClueGO plugin visualize to identify enriched pathways amongst all statistically significant proteins. Nodes containing proteins from related KEGG terms are colored the same. The crosslink figure of pathways using ClueGO indicate several genes such as MAGE-A6 and MAGE-A11 are interconnected to BC samples. This bladder cancer related network genes were designed based on TCGA dataset”.

1.Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, et al. Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res.* 2003;13(11):2498-504.

2.Bindea G, Mlecnik B, Hackl H, Charoentong P, Tosolini M, Kirilovsky A, et al: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks. *Bioinformatics.* 2009 ;25(8):1091-3.