

Identification of significantly mutated subnetworks in the breast cancer genome

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Additional File 1: Table S1. Parameters used to run Hotnet2

Step 1: Influence Matrix Creation			
Dataset	Parameter Name	Value	Description
Discovery	Edge swap constant, Q	115	The software performs $Q \times$ <i>no of edges</i> swaps
	Number of permutations	1000	Number of permuted networks to create
Validation	Edge swap constant, Q	115	The software performs $Q \times$ <i>no of edges</i> swaps
	Number of permutations	800	Number of permuted networks to create
Step 2: Heat Score Generation			
Discovery	Minimum Heat Score	1	The minimum score for the gene- specific mutation frequency
Validation	Minimum Heat Score	1	The minimum score for the gene- specific mutation frequency
Step 3: Delta Selection			
Discovery	Minimum Network Size	3	Minimum size of the connected components that should be returned
Validation	Minimum Network Size	3	Minimum size of the connected components that should be returned

Additional File 2: Table S2. Calculation of sample-specific mutation score

	<i>KCNRG</i> <i>f</i> = 0.3	<i>TRIM13</i> <i>f</i> = 0.6	<i>DGCR6L</i> <i>f</i> = 0.25	<i>RIMBP3</i> <i>f</i> = 0.38	<i>NOXA1</i> <i>f</i> = 0.2	<i>RAC2</i> <i>f</i> = 0.4	<i>ICMT</i> <i>f</i> = 0.5	Mutation score
Sample 1	1	0	0	-1	0	0	1	1.18
Sample 2	0	1	-1	1	1	0	0	1.43
Sample 3	1	1	0	0	0	1	1	1.80
Sample 4	0	-1	1	0	-1	-1	-1	1.95
Sample 5	0	0	0	1	0	0	0	0.38
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Sample <i>n</i>	-1	0	0	0	1	-1	0	0.9