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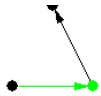
Table S1. All of the identified motifs using FANMOD.

Motif [a]	Type	Number	Frequency [b]	Z-Score [c]	p-Value [d]
	Single input	25	0.056171%	2.6655	0
	Chain	32	0.071899%	3.0889	0
	Chain	17	0.038196%	2.0672	0
	Chain	380	0.8538%	10.559	0
	Chain	30	0.067405%	4.7423	0
	Multiple inputs	11	0.024715%	21.361	0
	Feed forward loop	6	0.013481%	191.77	0
	Multiple inputs	75	0.16851%	3.4083	0
	Feed forward loop	25	0.056171%	46.555	0
	Chain	10	0.022468%	21.361	0
	Feed forward loop	29	0.065158%	101.56	0
	Feed forward loop	87	0.19547%	12.163	0
	Feed forward loop	25	0.056171%	5.5943	0

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	Feed forward loop	28	0.067405%	7.3208	0
	Chain	314	0.70551%	5.4264	0
	Multiple inputs	910	2.0446%	2.4369	0.002
	Multiple inputs	39	0.087627%	2.5049	0
	Chain	155	0.34826%	2.7971	0
	Feed forward loop	26	0.062911%	6.6992	0
	Chain	6	0.013481%	2.3094	0
	Feedback loop	9	0.020222%	undefined	0
	Mixed mode	24	0.053924%	21.361	0
	Mixed mode	6	0.013481%	21.361	0
	Multiple inputs	1742	3.923%	4.0028	0
	Multiple inputs	77	0.17301%	2.2805	0
	Feed forward loop	10	0.022468%	2.6249	0.007
	Mixed mode	7	0.015728%	21.361	0

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	Mixed mode	10	0.022468%	21.361	0
	Mixed mode	18	0.040443%	2.1286	0
	Chain	61	0.13481%	5.1267	0
	Single input	45	0.10111%	2.1088	0
	Mixed mode	10	0.022468%	3.7899	0
	Mixed mode	7	0.015728%	21.361	0
	Multiple inputs	12	0.026962%	21.361	0

[a] The vertices containing cancer genes are represented in green, and the others are represented in black. The three kinds of edges are represented by black (output), green (activation) and red (inhibition) edges, respectively.

[b] The frequency denotes the frequency with which a motif occurred in the original network.

[c] The Z-Score is the original frequency minus the random frequency divided by the standard deviation.

[d] The p-Value of a motif is the number of random networks in which it occurred more often than in the original network, divided by the total number of random networks. Therefore, p-Values range from 0 to 1; the smaller the p-Value, the more significant is the motif.