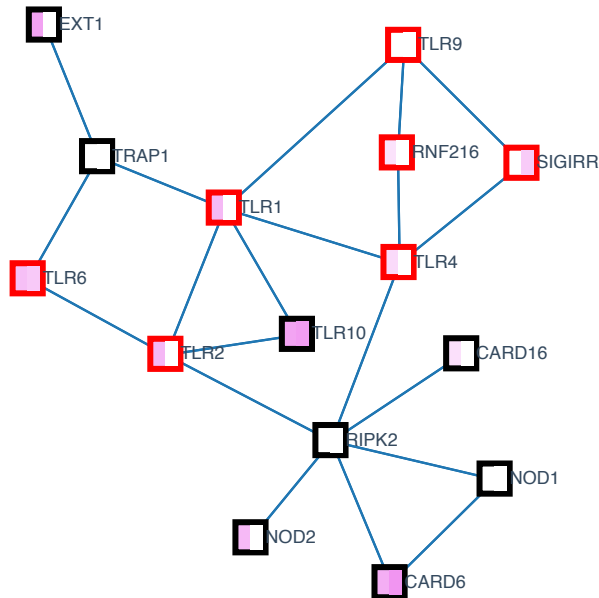


# Top 19 densely connected subnetworks by gene ranking

Pathways: Regulation of toll-like receptor signaling pathway\_Homo sapiens\_WP1449 1.0e-11 [Download as text file](#)

— Network



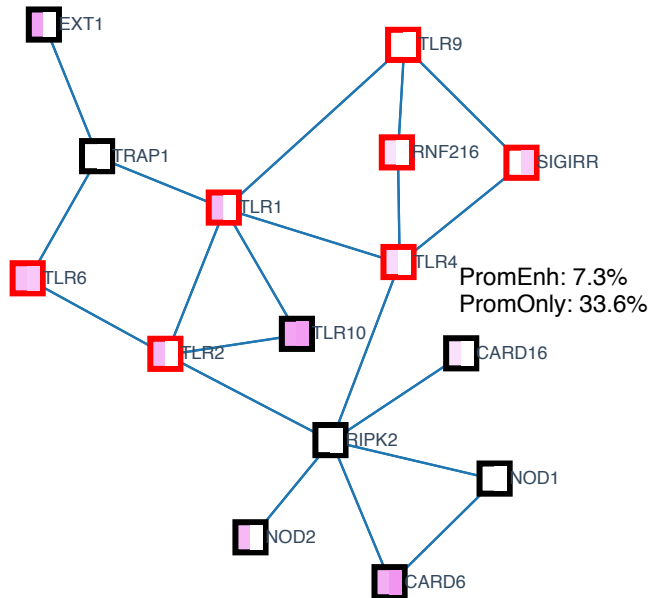
The colors of node represent the rankings of the gene (PromEnh: scored from both its promoter and enhancers, PromOnly: scored from its promoter only). User can drag the nodes for a better layout.



# Top 19 densely connected subnetworks by gene ranking

Pathways: Regulation of toll-like receptor signaling pathway\_Homo sapiens\_WP1449 1.0e-11 [Download as text file](#)

— Network



Only genes in the top 10% of the rankings are colored. Move mouse over a node, the positions of its rankings will pop up.

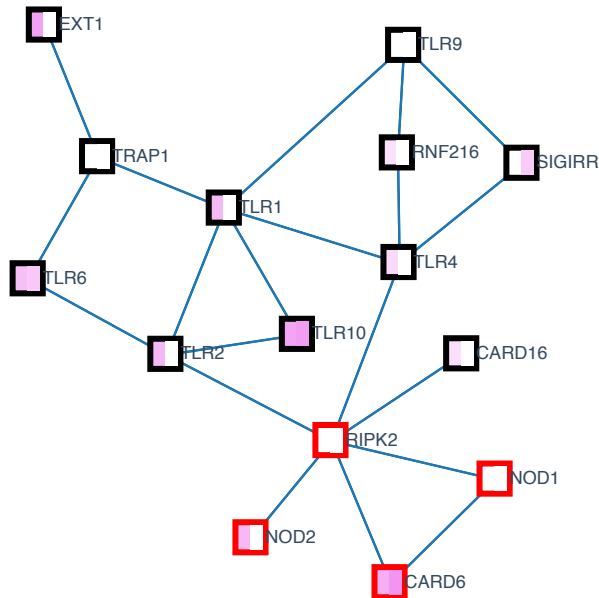


# Top 19 densely connected subnetworks by gene ranking

Pathways: NOD-like receptor signaling pathway\_Homo sapiens\_hsa04621 7.9e-07

[Download as text file](#)

— Network

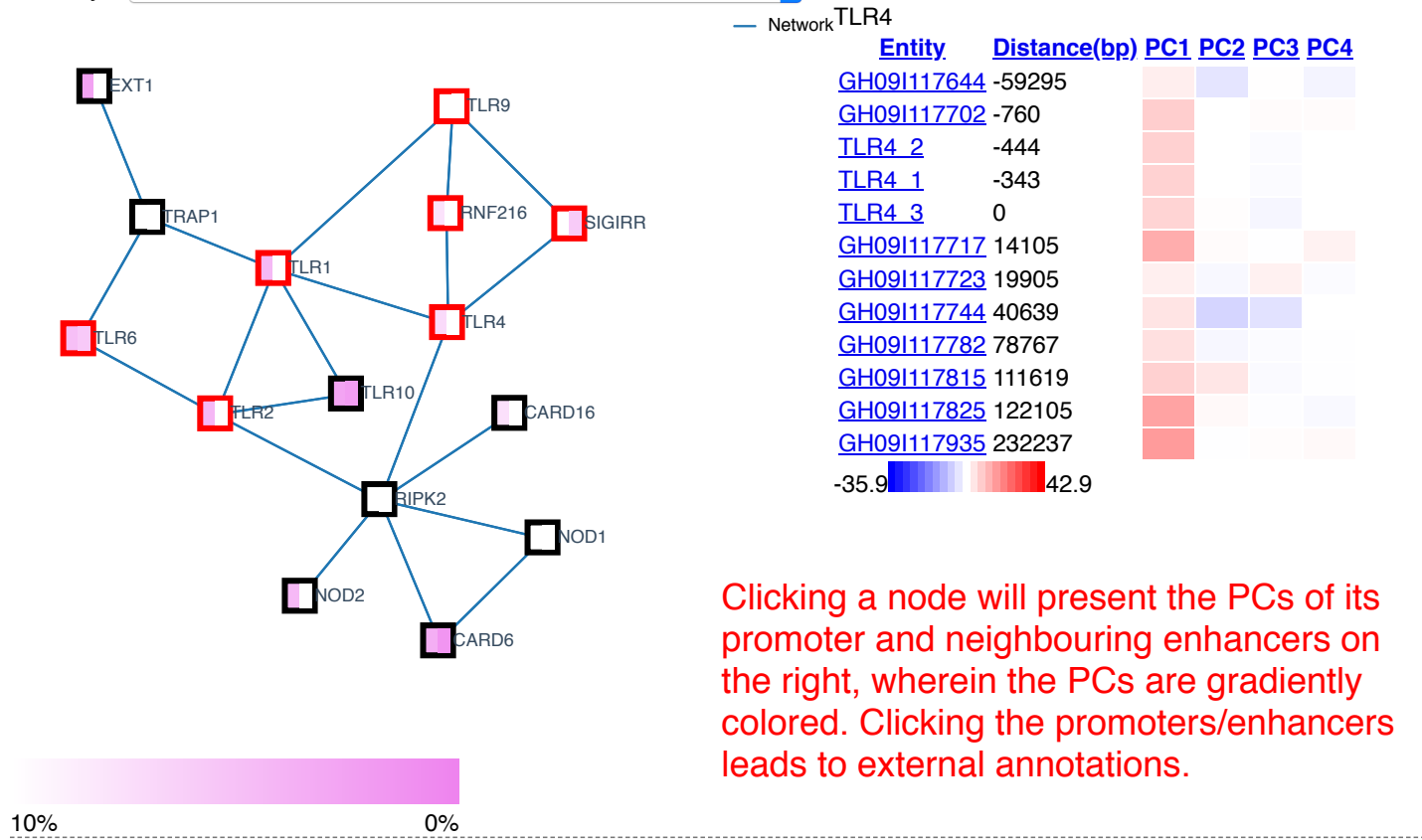


The boundaries of the nodes are colored in red if the corresponding genes are belong to the pathway in the drop list. User can know the p-value of a pathway and its gene sets by selecting an item in the drop list.



# Top 19 densely connected subnetworks by gene ranking

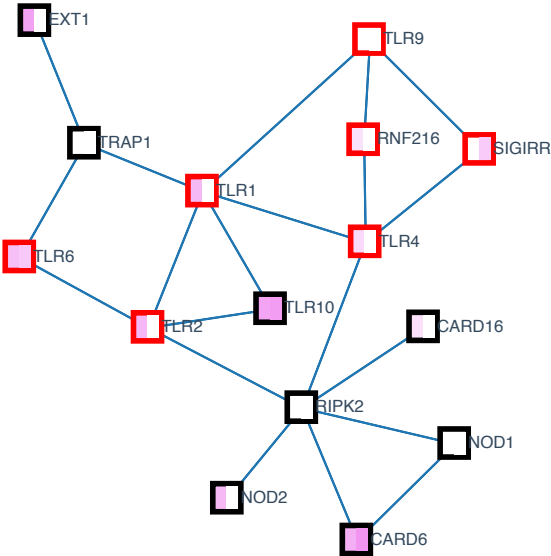
Pathways:  [Download as text file](#)



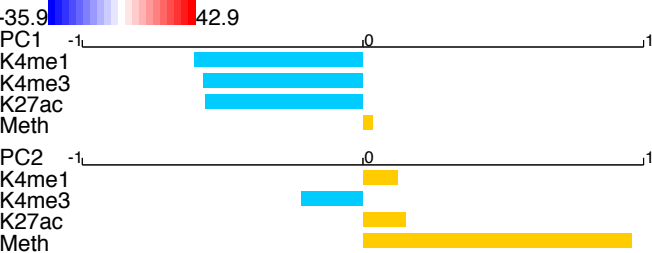
# Top 19 densely connected subnetworks by gene ranking

Pathways: Regulation of toll-like receptor signaling pathway\_Homo sapiens\_WP1449 1.0e-1 [Download as text file](#)

— Network TLR4



Entity	Distance(bp)	PC1	PC2	PC3	PC4
<a href="#">GH09I117644</a>	-59295				
<a href="#">GH09I117702</a>	-760				
<a href="#">TLR4_2</a>	-444				
<a href="#">TLR4_1</a>	-343				
<a href="#">TLR4_3</a>	0				
<a href="#">GH09I117717</a>	14105				
<a href="#">GH09I117723</a>	19905				
<a href="#">GH09I117744</a>	40639				
<a href="#">GH09I117782</a>	78767				
<a href="#">GH09I117815</a>	111619				
<a href="#">GH09I117825</a>	122105				
<a href="#">GH09I117935</a>	232237				



Legend of the PC pops upon clicking the corresponding PC, showing the composition of epigenetic marks.