Protein-Protein Interaction Network Analysis of Subject Z's Coding SNPs

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Overview

1. Introduction
   - PPI Network and Subject Z's Coding SNPs
   - Project Aims
2. Selected Results
   - Genes with High Centrality
   - Hubs with Coding SNPs
   - Summary for Other Results

PPI Network and Subject Z's Coding SNPs

- Many ways to determine impacts of SNPs
  - Conservation, statistical modeling?.
- Importance of hubs in sparse networks
- Any hubs for genes with SNPs of Carl?
  - A node with many neighbors
  - A node which is centered in communications
- Are they related to disease or any other important traits?
- DIP/MINT PPI Network

Project Aims

- Visualize the PPI networks obtained from the two databases
- Propose a tool that calculates measures of centrality and compare to output from Cytoscape
- Determine distribution of degree centrality and betweenness centrality for PPI networks
- Characterize any statistically significant differences between proteins containing and not containing SNPs in Carl?s genome
- Perform hierarchical analyses on the PPI networks

Genes with High Centrality

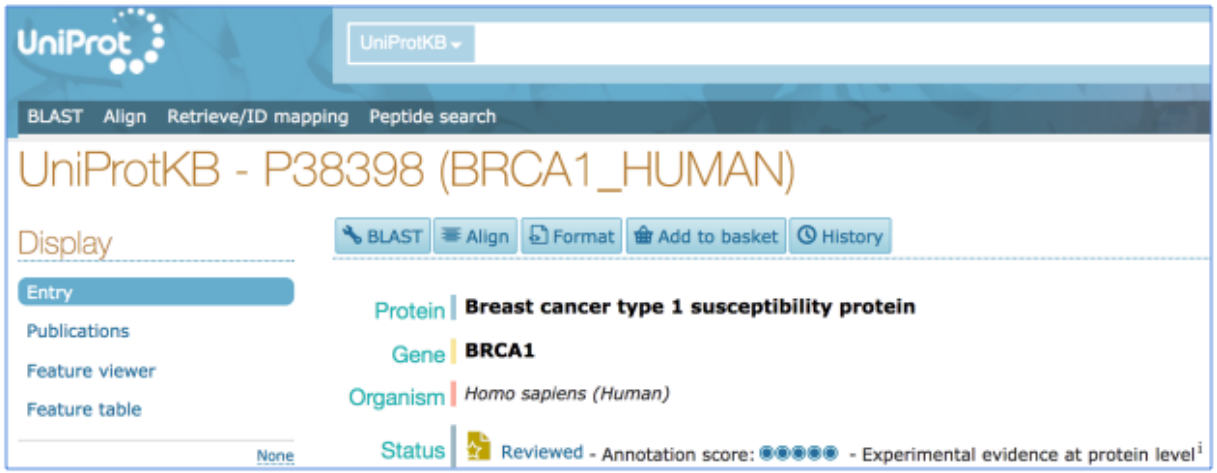
	Cytoscape	Cy.Degree	Coding	Co.Degree
4146	P62988	241	P62988	238
4880	P04637	86	P04637	85
4325	P10275	47	P10275	43
4583	P35222	41	P35222	41
4897	P06400	34	Q00653	37
4288	P38398	33	P06400	34
4468	P01375	32	P01375	32
3501	P62158	31	P38398	31
4889	P04049	31	P19387	30
2831	P19387	30	P63208	30

Table 1: Top 10 Nodes with Highest Degree Centrality in DIP

	Cytoscape	Cy.Betweenness	Coding	Co.Betweenness
2412	Q13573	0.15	Q99459	0.12
1111	Q99459	0.14	P04637	0.07
2469	O95758	0.10	P0CG48	0.06
38	P04637	0.09	O95758	0.06
4531	Q14197	0.07	Q13573	0.06
8	P0CG48	0.07	Q14197	0.05
196	O35182	0.04	O35182	0.03
161	P31947	0.04	P31947	0.03
1275	Q9UL18	0.04	Q9UKV8	0.03
150	P63104	0.03	P63104	0.03

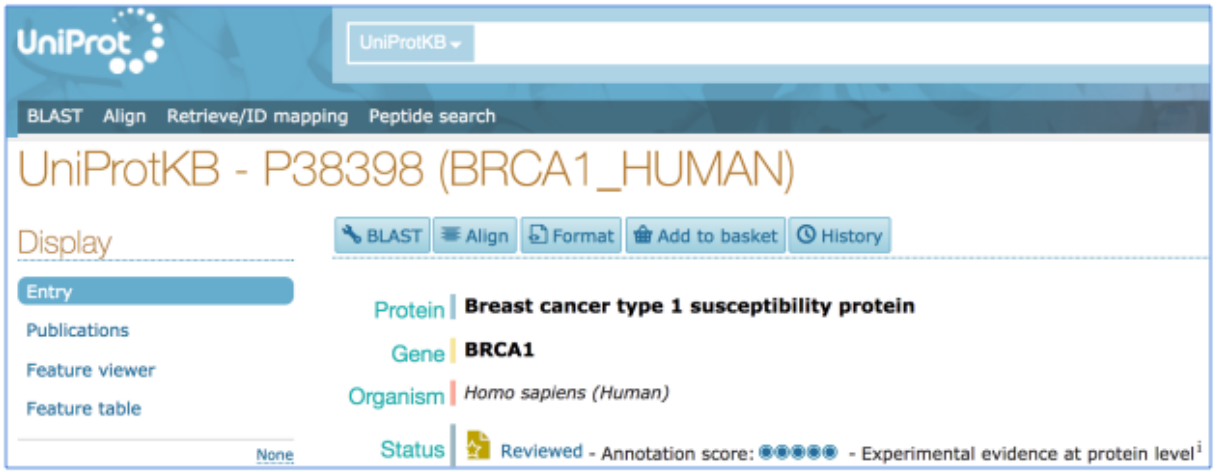
Table 4: Top 10 Nodes with Highest Betweenness Centrality in MINT

Hubs with Coding SNPs



UniProtKB Record

Hubs with Coding SNPs



UniProtKB Record

Function

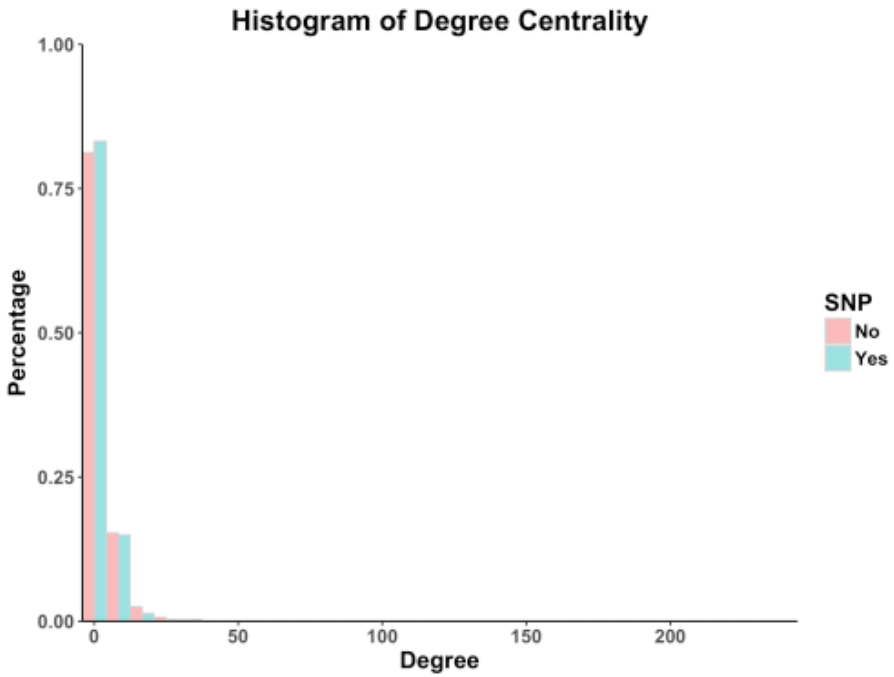
E3 ubiquitin-protein ligase that specifically mediates the formation of 'Lys-6'-linked polyubiquitin chains and plays a central role in DNA repair by facilitating cellular responses to DNA damage. It is unclear whether it also mediates the formation of other types of polyubiquitin chains. The E3 ubiquitin-protein ligase activity is required for its tumor suppressor function. The BRCA1-BARD1 heterodimer coordinates a diverse range of cellular pathways such as DNA damage repair, ubiquitination and transcriptional regulation to maintain genomic stability. Regulates centrosomal microtubule nucleation. Required for normal cell cycle progression from G2 to mitosis. Required for appropriate cell cycle

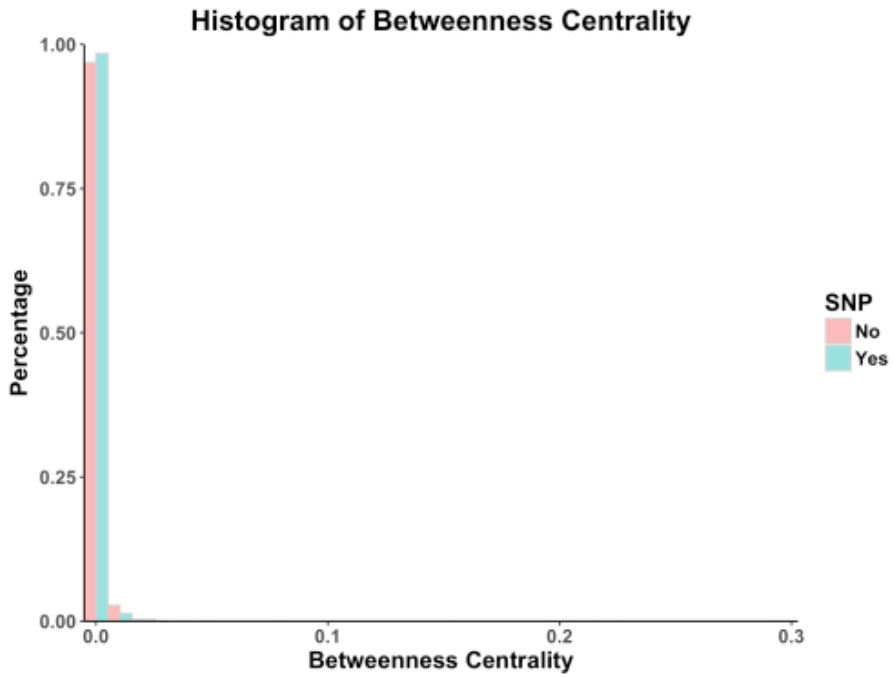
Summary for Other Results

- No statistically significant difference between
  - Distribution of centrality for genes with or without SNPs
  - Hierarchical composition for genes with or without SNPs
- Proposed a tool to calculate centrality for nodes

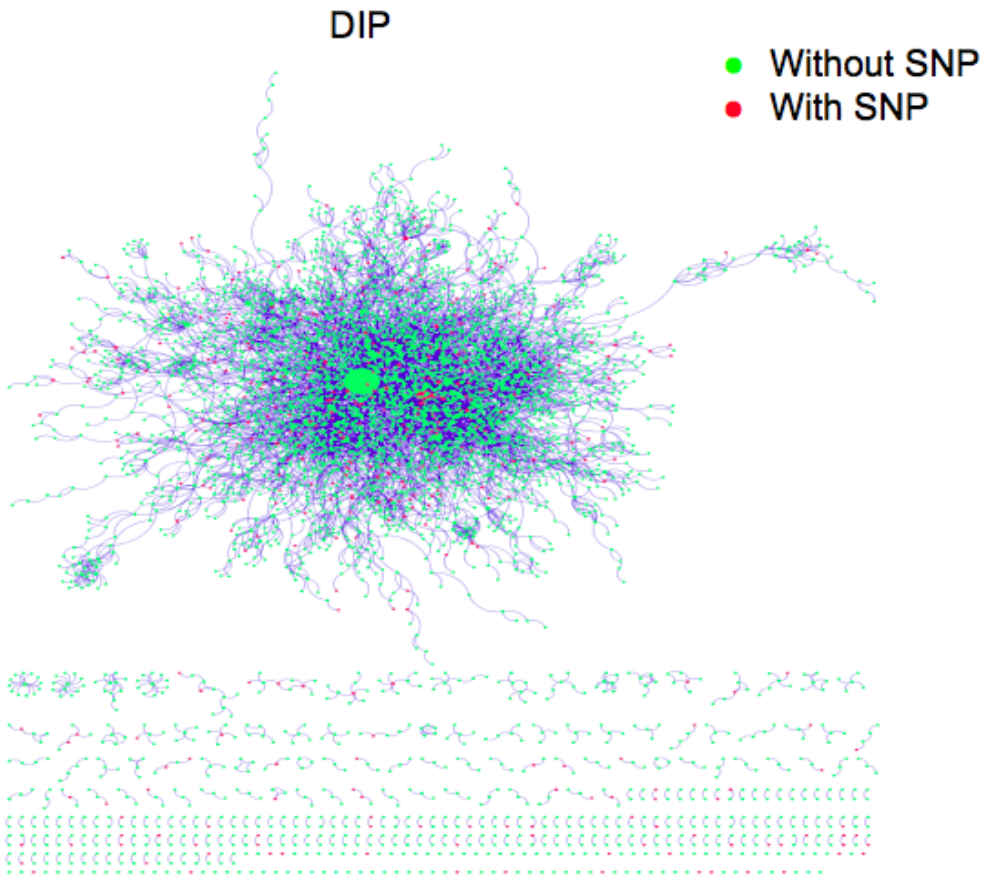
The End

Centrality

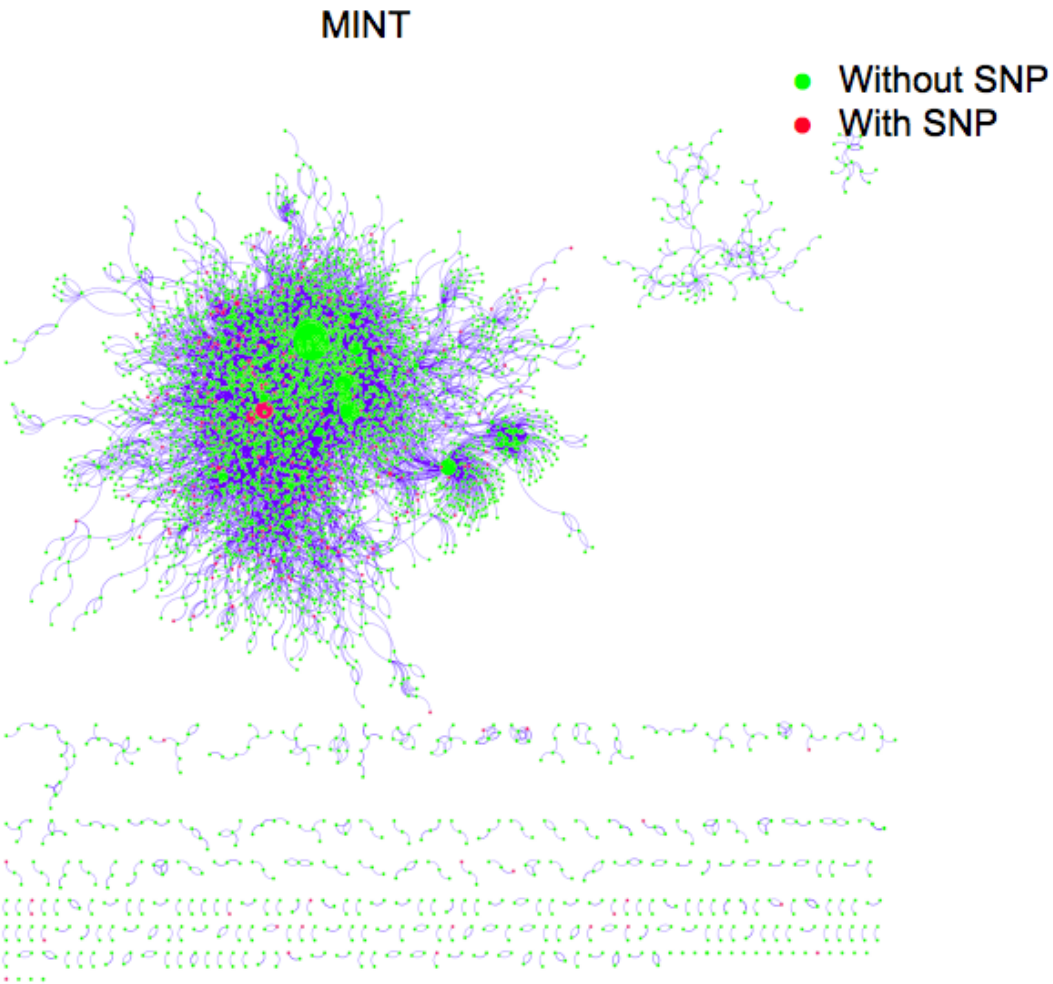

Histogram of Degree Centrality
Percentage
1.00
0.75
0.50
0.25
0.00
0
50
100
150
200
Degree
SNP
No
Yes


Histogram of Betweenness Centrality
Percentage
1.00
0.75
0.50
0.25
0.00
0.0
0.1
0.2
0.3
Betweenness Centrality
SNP
No
Yes

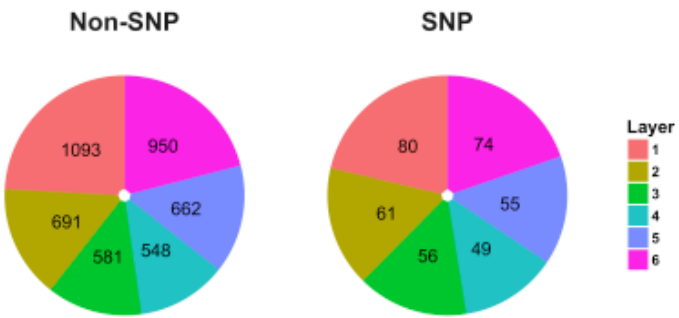
DIP



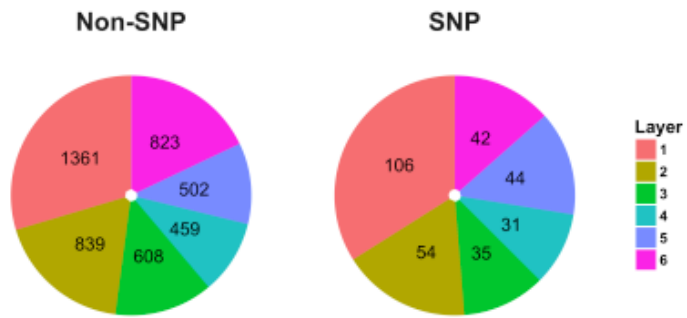
MINT



Hierarchical Composition



DIP



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