

# Phase I SNPs in PPI and regulatory networks

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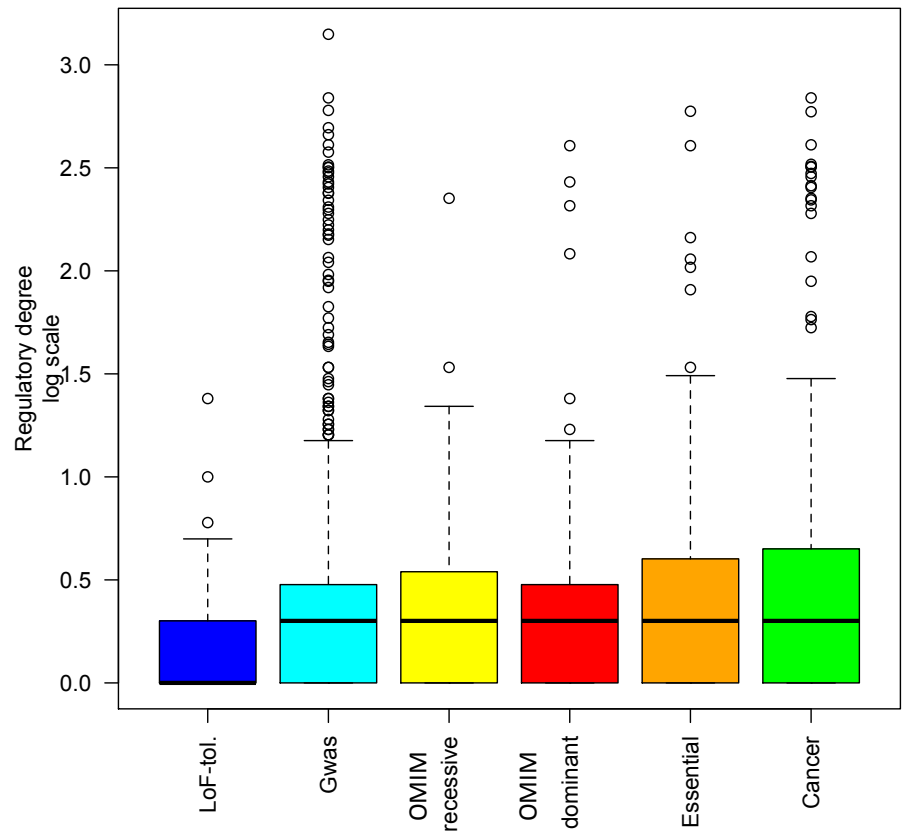
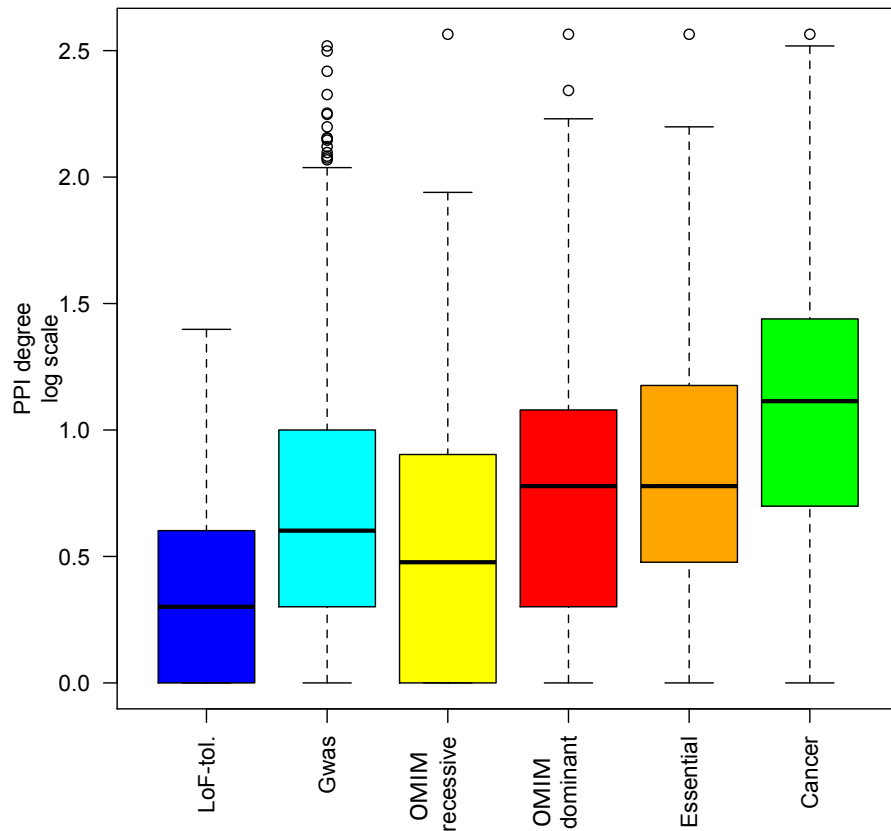
# Network data

- PPI network from BIOGRID containing 43,722 interactions between 9,612 genes
- Regulatory network from Gerstein et al (Nature, in press) containing 27,914 interactions between 9,314 genes (118 transcription factors and their targets)

Non-syn SNPs in more connected genes tend to be rare and show less population differentiation

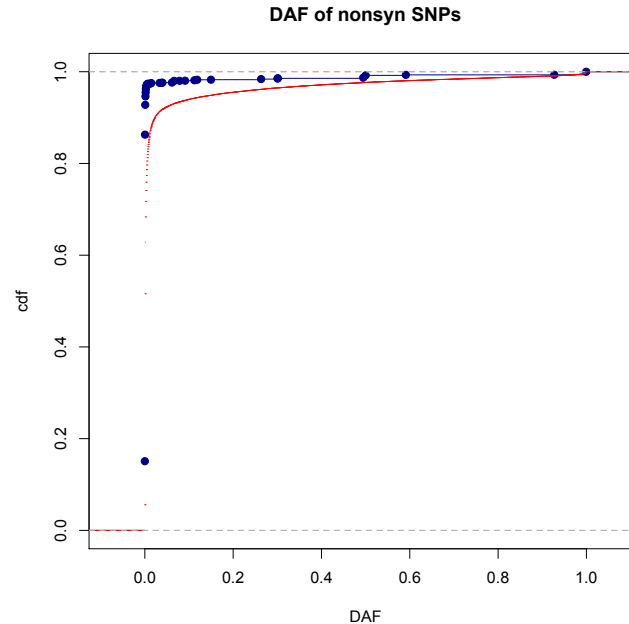
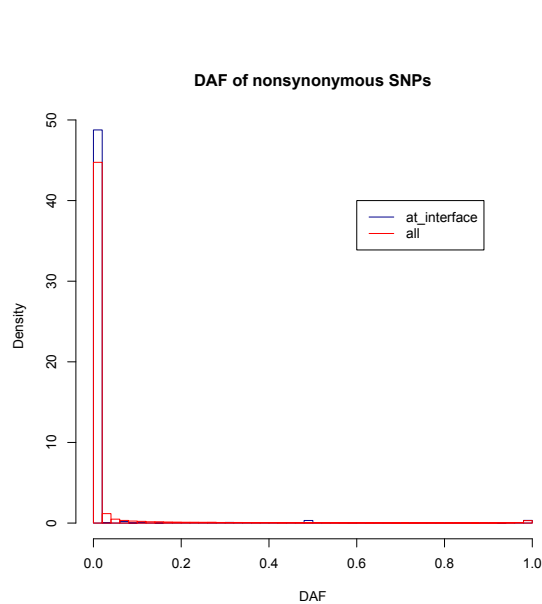
	Corr with PPI degree	pval	Corr with Reg degree	pval
DAF	-0.050	<2.2e-16	-0.018	7.33e-10
AFR_EUR_Fst	-0.043	<2.2e-16	-0.016	5.35e-6
AFR_ASN_Fst	-0.042	<2.2e-16	-0.018	8.14e-7
EUR_ASN_Fst	-0.037	<2.2e-16	-0.018	1..4e-6

# Degree centralities of different gene categories



Gene lists from Hyun  
LoF-tolerant genes from Suganthi

# Structural Interaction Network: SNPs at interaction interfaces tend to be rare



DAF of nonsyn SNPs at interaction interfaces is significantly lower than all nonsyn SNPs (pvalue <2.2 e-16) both Wilcoxon rank and KS-test

# More network related analysis

- How do SNPs at interaction interfaces disrupt protein interactions across these categories: rare SNPs, common SNPs, SNPs overlapping with HGMD data (some case studies) (Validation by Haiyuan)
- Do LoF-tolerant genes show reduced tendency to interact with Mendelian disease genes; Does tendency to interact with Mendelian disease genes vary for three non-synonymous SNP categories: common, low-frequency and rare (Kasper)