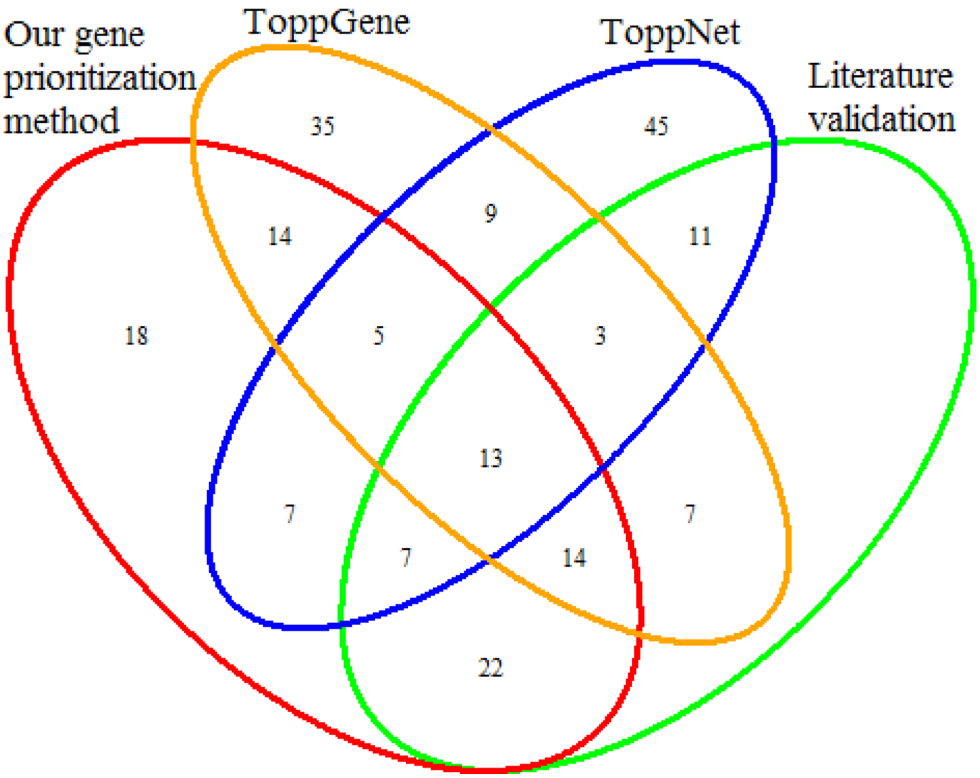
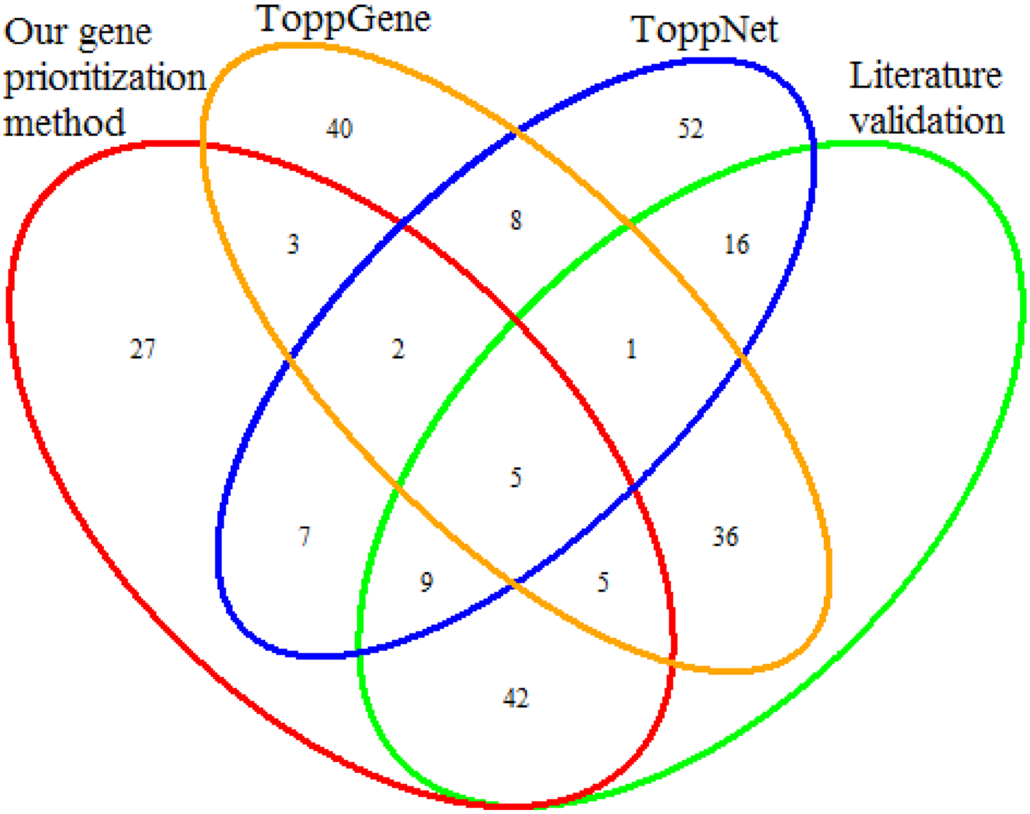
Prioritizing chronic obstructive pulmonary disease (COPD) candidate genes in COPD-related networks

SUPPLEMENTARY MATERIALS



Supplementary Figure 1: Overlap of top 100 genes from our gene prioritization method, ToppGene and ToppNet, and their literature validation for the COPD-related metabolic network.



Supplementary Figure 2: Overlap of top 100 genes from our gene prioritization method, ToppGene and ToppNet, and their literature validation the COPD-related PPI network.

Supplementary Table 1: The number of significantly enriched functions and pathways, and the number and proportion of COPD-related functions and pathways in these significantly enriched functions and pathways, for top 100 genes from our gene prioritization method, ToppGene and ToppNet in COPD-related metabolic and PPI networks

		Function		Pathway	
		Significantly enriched	**COPD- related (proportion)**	**Significantly enriched**	**COPD- related (proportion)**
COPD-related metabolic network	**Our gene prioritization method**	143	86 (60.140%)	34	32 (94.118%)
	ToppGene	100	55 (55%)	20	15 (75%)
	ToppNet	75	42 (56%)	19	9 (47.368%)
COPD-related PPI network	**Our gene prioritization method**	541	223 (41.220%)	104	78 (75%)
	ToppGene	307	175 (57.003%)	53	42 (79.245%)
	ToppNet	134	76 (56.716%)	40	32 (80%)