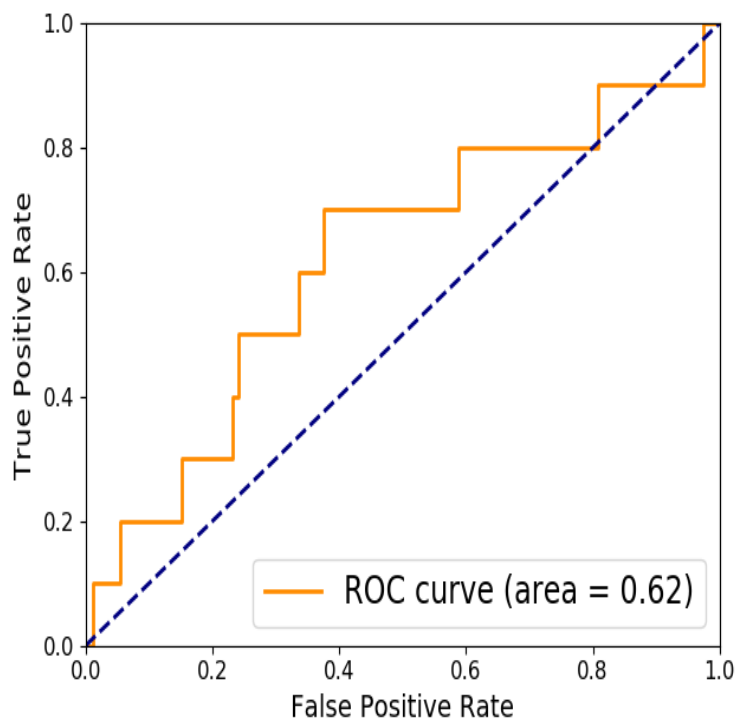
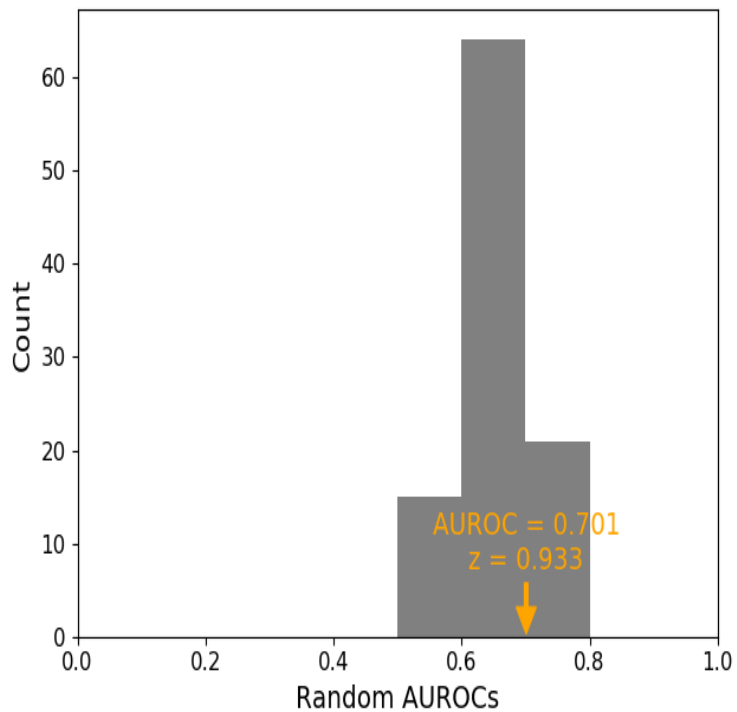


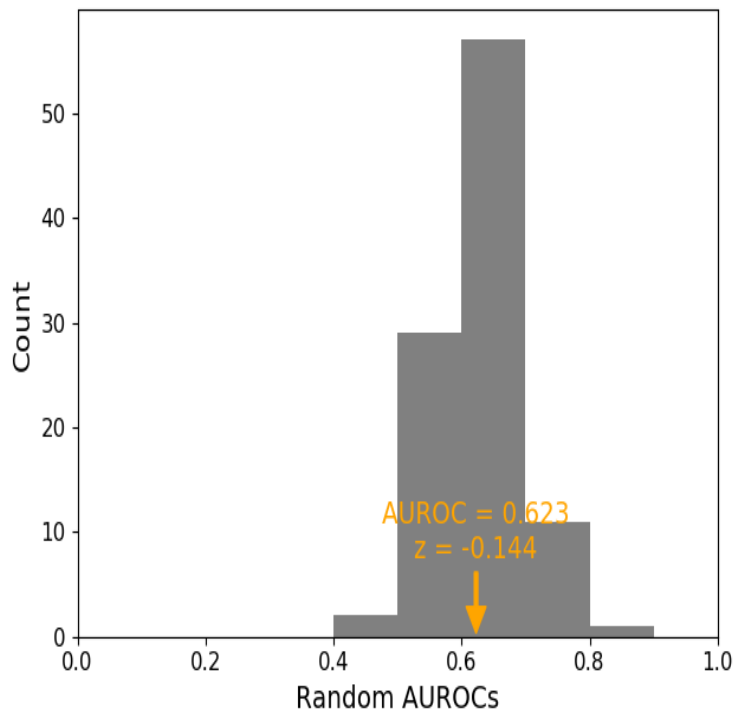
show_1_Diffusion ROC from Gene2axis to Gene1axis STRING10_combined



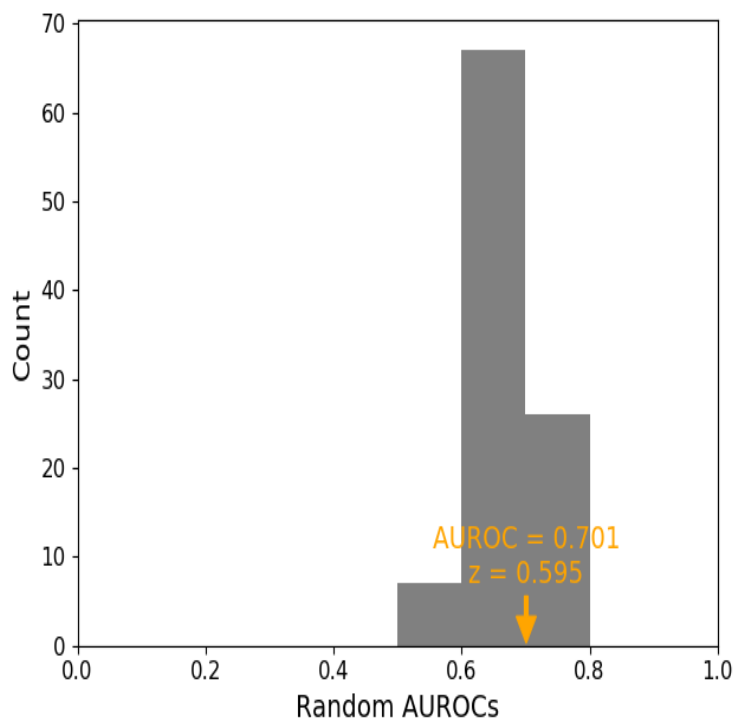
show_21_Zt_degree-matched_from Gene1axis to Gene2axis.png



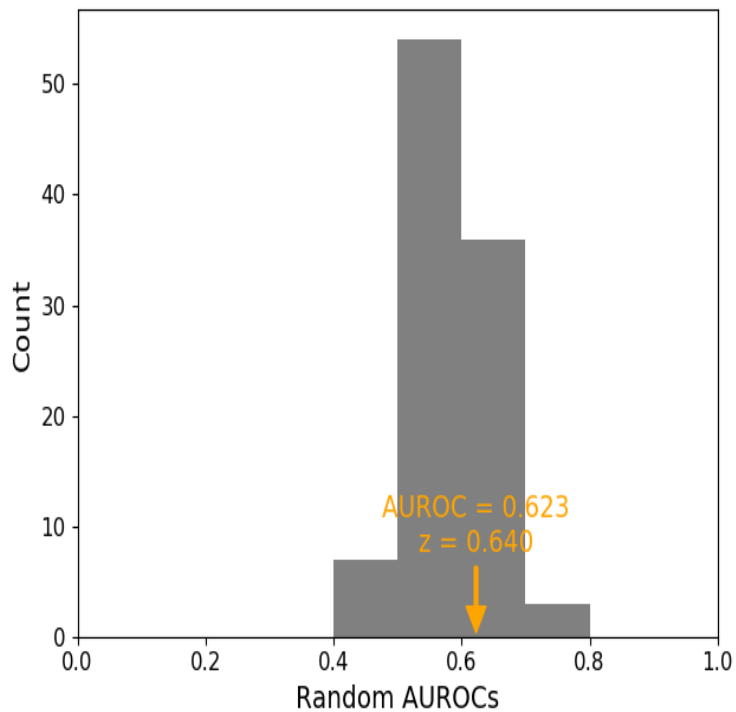
show_11_Zt_degree-matched_from Gene2axis to Gene1axis.png



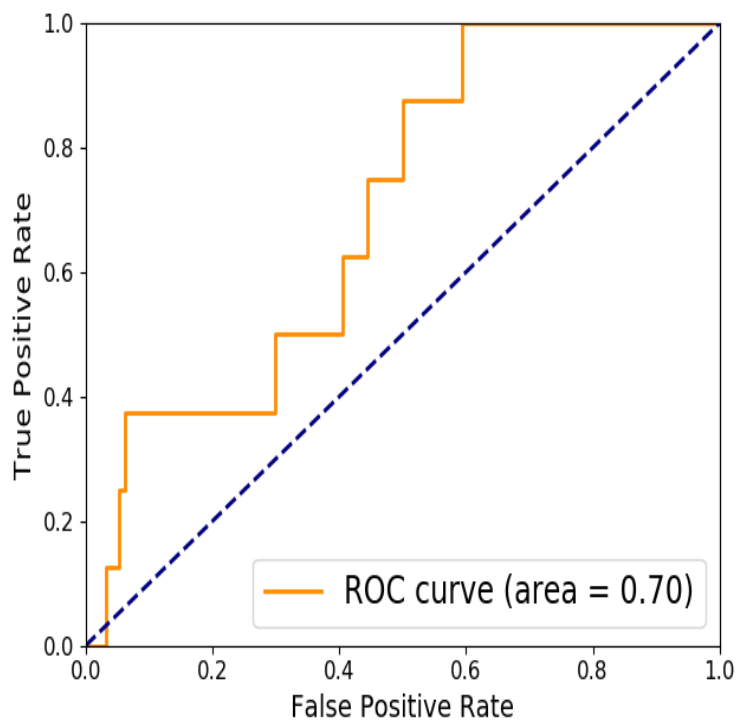
show_22_Zf_degree-matched_from Gene1axis to Gene2axis.png



show_12_Zf_degree-matched_from Gene2axis to Gene1axis.png



show_2_Diffusion ROC from Gene1axis to Gene2axis STRING10_combined



Diffusion	Diffusion	AUROC	Zt	Zt	Zf	Zf (unif)
FROM	TO		(degree-	(uniform)	(degree-	orm)
		matched)	matched)			
Gene2axis	Gene1axis	0.623	-0.144	1.351	0.640	1.064
Gene1axis	Gene2axis	0.701	0.933	1.987	0.595	0.535

Z-scores are computed for the experimental AUROC based on distributions of the random AUROCs

Zf : when randomizing source genes (Diffusion FROM)

Zf : when randomizing recipient genes (Diffusion TO)

Random genes are selected either uniformly or degree matched

* : Distribution of random AUROC is not Gaussian

**	#Mapped	#Total	Not mapped genes
Gene2axis	8	10	B3GNTL1P1;YTHDF3 N/A
Gene1axis	10	10	N/A

(end of file)