Figure S1: In the LPLSG experiment, the proportion of lncRNAs and proteins in negative samples to the total sample category is shown in the figure, which the blue area represents 79% of the total sample proportion, and the orange region represents the sample category that has not been selected.

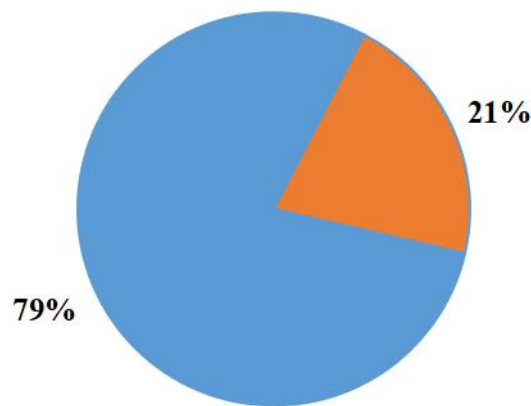

Proportion of LPLSG sample data categories

Figure S2: lncRNA-lncRNA similarity calculation process. (1)The binary matrix represents the known lnRNA-protein associations; (2) The green arrows are the process of the starting node lncRNAs to the proteins resource propagation,$(1/2)l_1$ represents the propagation proportion of $l_1 \rightarrow p_1$; The yellow arrows are the proteins to the lncRNAs resource propagation process,$(1/2)[(1/2)l_1+(1/2)l_2]$ represents the propagation proportion of $p_1 \rightarrow l_1$; (3)Represent the similarity between lncRNA -lncRNA calcualted by the Resource Allocation algorithm.
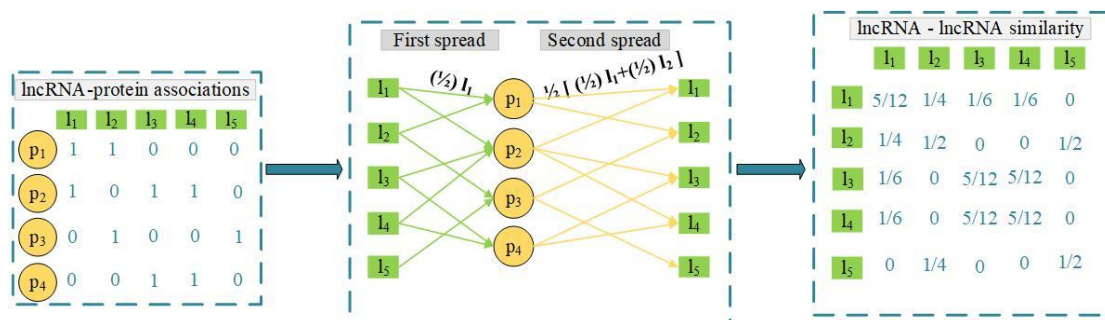

Figure S2: In the figure, matrix formula 1 indicates that the $Score_{lp}$ prediction score matrix is calculated by taking the lncRNA data set L in the binary network as the starting node set. Matrix formula 2 indicates that the $Score_{pl}$ prediction score matrix is obtained by taking the protein data set P in the binary network as the starting node set. It can be seen from the figure that $Score_{lp}$ and $Score_{pl}$ are not equal and asymmetric, so our proposed LPLSG fusion $Score_{lp}$ and $Score_{pl}$ is not redundant and feasible.

$$(1). \quad \begin{pmatrix} 1 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{pmatrix} \xrightarrow{Score_{lp}} \begin{pmatrix} 0 & 0 & 0.17 & 0.17 & 0.4 \\ 0 & 0.25 & 0 & 0 & 0 \\ 0.2 & 0 & 0 & 0 & 0 \\ 0.33 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$(2). \quad \begin{pmatrix} 1 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 1 & 1 & 0 \end{pmatrix} \xrightarrow{Score_{pl}} \begin{pmatrix} 0 & 0 & 0.18 & 0.18 & 0.27 \\ 0 & 0.2 & 0 & 0 & 0 \\ 0.25 & 0 & 0 & 0 & 0 \\ 0.4 & 0 & 0 & 0 & 0 \end{pmatrix}$$

Table S1: according to the experimental evaluation results of RWR algorithm under different restart probability w,the vertical axis index represents 6 evaluation indicators, and the horizontal axis indicator represents w with different values $(0 < w < 1)$.

	AUPR	AUC	F1_Score	Acc	Recall	Precision
w=0.1	**0.280**	**0.801**	**0.350**	**0.945**	**0.362**	**0.340**
w=0.2	0.268	0.798	0.340	0.942	0.364	0.324
w=0.3	0.256	0.795	0.324	0.940	0.355	0.300
w=0.4	0.243	0.791	0.302	0.933	0.351	0.269
w=0.5	0.230	0.786	0.285	0.929	0.341	0.256
w=0.6	0.216	0.779	0.267	0.922	0.345	0.228
w=0.7	0.202	0.772	0.251	0.915	0.340	0.216
w=0.8	0.189	0.762	0.235	0.902	0.360	0.192
w=0.9	0.174	0.750	0.220	0.916	0.287	0.193

Table S2: according to the experimental evaluation results of LP (label propagation) algorithm under different propagation probability p, the vertical axis index represents 6 evaluation indicators, and the horizontal axis indicator represents p with different values $(0 < p < 1)$.

	AUPR	AUC	F1_Score	Acc	Recall	Precision
p=0.1	**0.233**	**0.809**	**0.319**	**0.932**	**0.387**	**0.271**
p=0.2	0.229	0.808	0.315	0.931	0.387	0.266
p=0.3	0.224	0.806	0.312	0.933	0.374	0.272
p=0.4	0.215	0.804	0.309	0.938	0.341	0.285
p=0.5	0.207	0.801	0.303	0.932	0.360	0.266
p=0.6	0.201	0.780	0.295	0.934	0.340	0.270
p=0.7	0.195	0.793	0.281	0.932	0.325	0.254

p=0.8	0.188	0.788	0.271	0.927	0.335	0.233
p=0.9	0.182	0.780	0.263	0.933	0.292	0.252