Supplementary data of:

DGLinker: flexible knowledge-graph prediction of disease-gene associations

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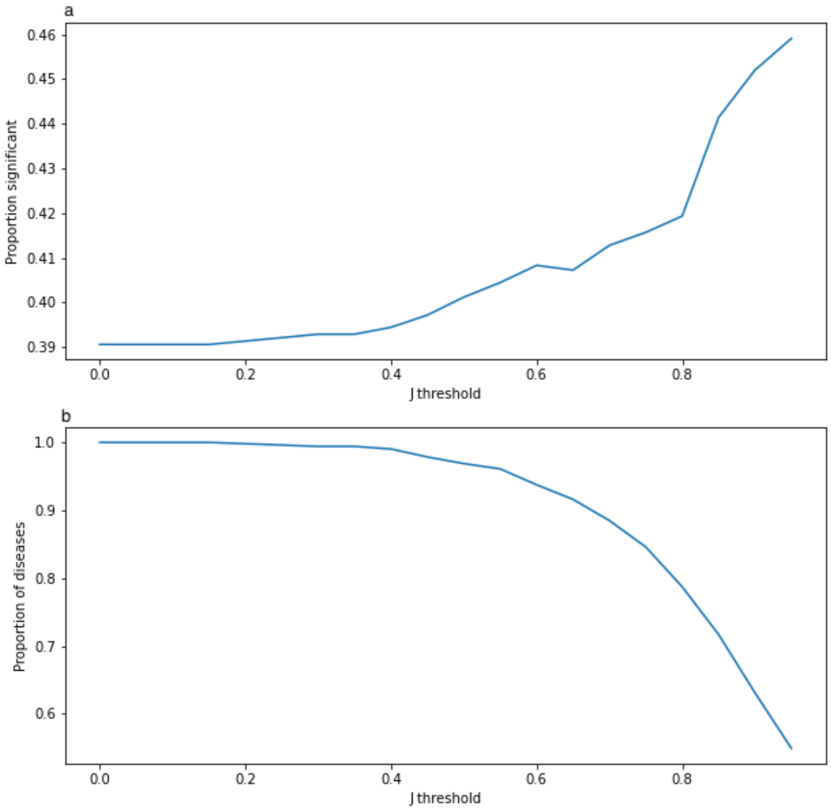

Supplementary figure 1. Effect of J-statistic threshold on model validation and number of models. Analysis performed for all 512 diseases for which the external validation had sufficient statistical power. A) proportion of models with training J >= threshold that are significant. B) proportion of models retained with training J >= threshold.

J threshold	Proportion significant at threshold	Number at threshold	Proportion at threshold
0.00	0.39	512	1.00
0.05	0.39	512	1.00
0.10	0.39	512	1.00
0.15	0.39	512	1.00
0.20	0.39	511	1.00
0.25	0.39	510	1.00
0.30	0.39	509	0.99
0.35	0.39	509	0.99
0.40	0.39	507	0.99
0.45	0.40	501	0.98
0.50	0.40	496	0.97
0.55	0.40	492	0.96
0.60	0.41	480	0.94
0.65	0.41	469	0.92
0.70	0.41	453	0.88
0.75	0.42	433	0.85
0.80	0.42	403	0.79
0.85	0.44	367	0.72
0.90	0.45	323	0.63
0.95	0.46	281	0.55

Supplementary table 1. Effect of J-statistic threshold on validation performance. Analysis performed for all 512 diseases for which the external validation had sufficient statistical power. Models are retained if training J >= threshold for each row.