

Table S1 Studied datasets and their respective access numbers and references. The last column of the table indicates the groups (e.g., control, condition 1, condition 2) belonging to each dataset.

	Access number	Ref. (Code)	Data size	Classes
Bone matrix	GDS928	⁷⁰ (B1)	10499 genes and 6 replica	control (1), temporal groups 1, 2, 3, 4, 5 (5)
	E-MEXP-1618	⁶² (B2)	54675 genes and 84 replica	group 1 (84)
	GSE30322	⁷⁷ (B3)	24747 genes and 31 replica	temporal group 1 (5) and control 1 (5), temporal group 2 (5) and control 2 (5), temporal group 3 (5) and control 3 (5)
	GSE47552	⁷⁶ (B4)	33297 genes and 99 replica	control (5), group 1 (41), group 2 (33), group 3 (20)
Cancer cells	GDS5059	⁶³ (C1)	54675 genes and 30 replica	temporal group 1 (8) and control (2), temporal group 2 (8) and control (2), temporal group 3 (8) and control (2)
	GDS5071	⁷¹ (C2)	33297 genes and 13 replica	control (6), group 1 (7)
	GDS5010	⁵⁹ (C3)	45101 genes and 18 replica	control 1 (3) and group 1 (3), control 2 (3) and group 2 (3), control 3 (3) and group 3 (3)
	GDS5070	⁶⁰ (C4)	54675 genes and 12 replica	control 1 (3) and group 1 (3), control 2 (3) and group 2 (3)
	GSE45016	⁶⁵ (C5)	54675 genes and 11 replica	control (1), group 1 (10)
<i>Drosophila</i> development	GSE9149	⁸³ (D1)	14010 genes and 29 replica	group 1 (6), group 2 (6), group 3 (6), group 4 (6), group 5 (5)
	GSE35240	⁶⁶ (D2)	18952 genes and 15 replica	control 1 (3), control 2 (3), group 1 (3), group 2 (3), group
	GSE31564	⁷⁸ (D3)	18952 genes and 24 replica	2 controls (3) and 6 temporal groups (3)
	GSE18208	⁶⁹ (D4)	18952 genes and 16 replica	control (2), group 1 (7), group 2 (7)
	GSE34400	⁶⁷ (D5)	18952 genes and 44 replica	control (6), group 1 (38)
Neuron cells	GSE28146	⁶¹ (N1)	54657 genes and 30 replica	control (7), group 1 (7), group 2 (8), group 3 (8)
	GSE43578	⁷² (N2)	35557 genes and 18 replica	control 1 (5), group 1 (4), control 2 (3), group 2 (6)
Plant cells	GDS2895	⁷⁴ (P1)	28800 genes and 20 replica	group 1 (4), group 2 (4), group 3 (4), group 4 (4), group 5 (4)
	GSE14304	⁶⁸ (P2)	42537 genes and 16 replica	group 1 (2), group 2 (2), group 3 (2), group 4 (2), group 5 (2), group 6 (2), group 7 (2), group 8 (2)
	GSE14304	⁶⁸ (P3)	57381 genes and 98 replica	group 1 (98)
	GDS2114	⁷³ (P4)	22810 genes and 12 replica	control 1 (1) and group 1(3), control 2 (1) and group 2 (3), control 3 (1) and group 3 (3)
	GDS3244	⁶⁴ (P5)	61170 genes and 160 replica	40 groups (4)

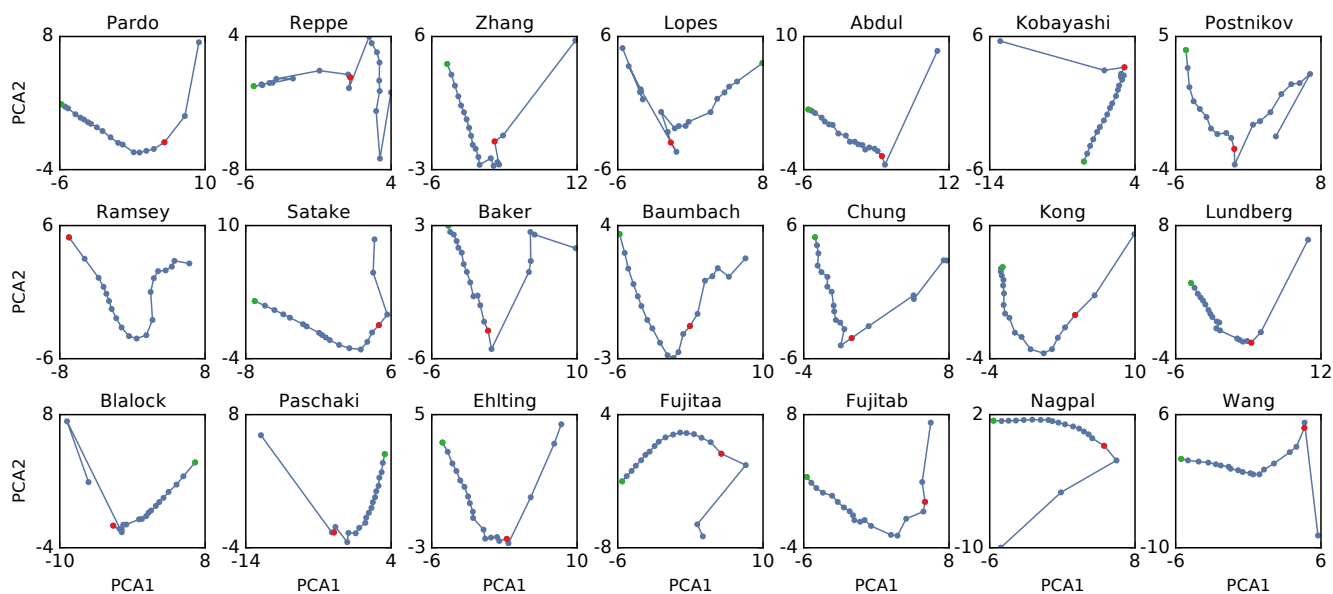


Fig. S1 PCA projections of network properties obtained using distinct threshold values. The name on the top of each plot corresponds to the first author of the dataset were the networks were generated. Green dots indicate the network corresponding to the lowest threshold. Red dots indicate the detected transition from stable to unstable properties.

Table S2 Absolute Pearson correlation coefficients obtained for the relationships between node strength (sum of edge weights) and degree. Green cells indicate values larger than 0.5.

	T variation	T entropy	T comp. 0.4	T comp. 0.6	T comp. 0.8	T deg. 100	T deg. 1000	T power-law
Pardo	0.65	0.65	0.31	0.47	0.47	0.75	0.93	0.31
Reppe	0.16	0.63	0.41	0.58	0.77	0.46	0.84	0.70
Zhang	0.08	0.65	0.36	0.50	0.61	0.61	0.87	0.58
Lopes	0.06	0.82	0.52	0.64	0.75	0.53	0.82	0.33
Abdul	0.19	0.89	0.62	0.77	0.84	0.51	0.75	0.28
Kobayashi	0.28	0.70	0.50	0.56	0.61	0.62	0.81	0.67
Postnikov	0.34	0.65	0.43	0.51	0.55	0.67	0.91	0.91
Ramsey	0.84	0.73	0.57	0.64	0.66	0.50	0.73	0.44
Satake	0.13	0.30	0.16	0.19	0.22	0.40	0.77	0.15
Baker	0.51	0.55	0.40	0.46	0.64	0.31	0.60	0.42
Baumbach	0.77	0.83	0.72	0.77	0.80	0.70	0.80	0.80
Chung	0.62	0.22	0.61	0.60	0.43	0.30	0.94	0.82
Kong	0.56	0.53	0.63	0.78	0.83	0.51	0.78	0.58
Lundberg	0.11	0.92	0.61	0.78	0.87	0.67	0.92	0.78
Blalock	0.09	0.59	0.38	0.42	0.46	0.60	0.89	0.71
Paschaki	0.13	0.63	0.41	0.51	0.59	0.61	0.86	0.68
Ehltting	0.20	0.75	0.49	0.57	0.64	0.67	0.90	0.76
Fujitaa	0.42	0.49	0.38	0.42	0.53	0.35	0.66	0.29
Fujitab	0.00	0.16	0.07	0.03	0.12	0.07	0.55	0.07
Nagpal	0.34	0.71	0.44	0.56	0.63	0.69	0.90	0.58
Wang	0.10	0.72	0.60	0.77	0.89	0.53	0.76	0.38

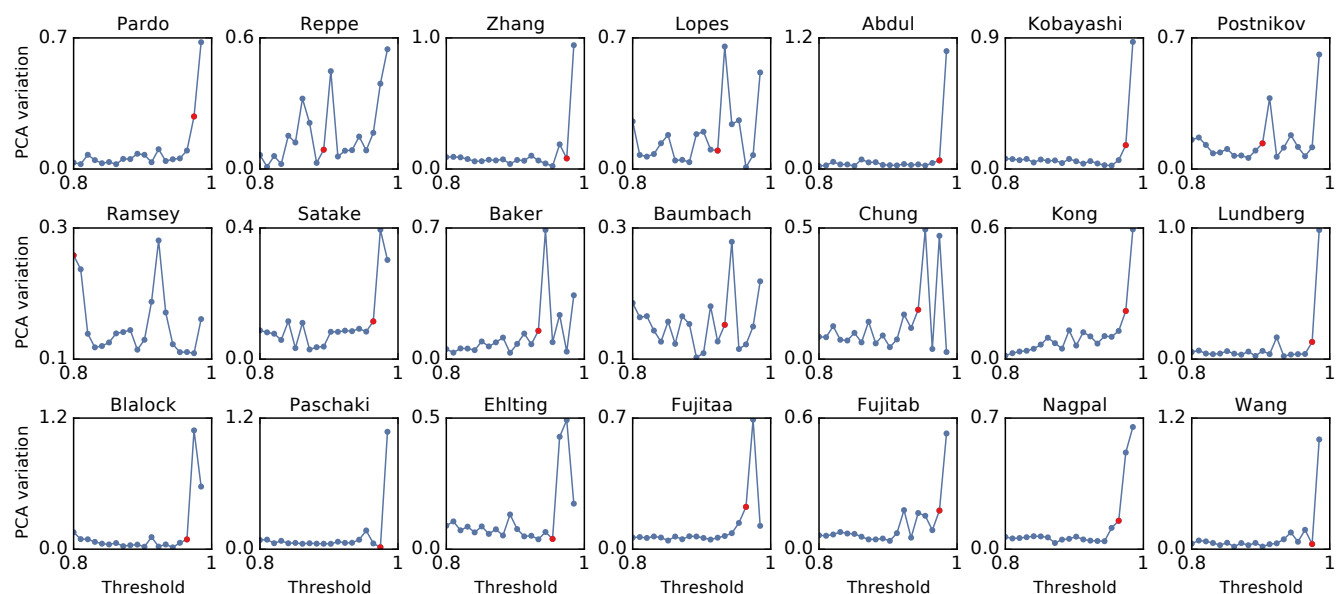


Fig. S2 Variation among consecutive PCA points from Figure S1. The name on the top of each plot corresponds to the first author of the dataset were the networks were generated. Red dots indicate the detected transition from stable to unstable properties.

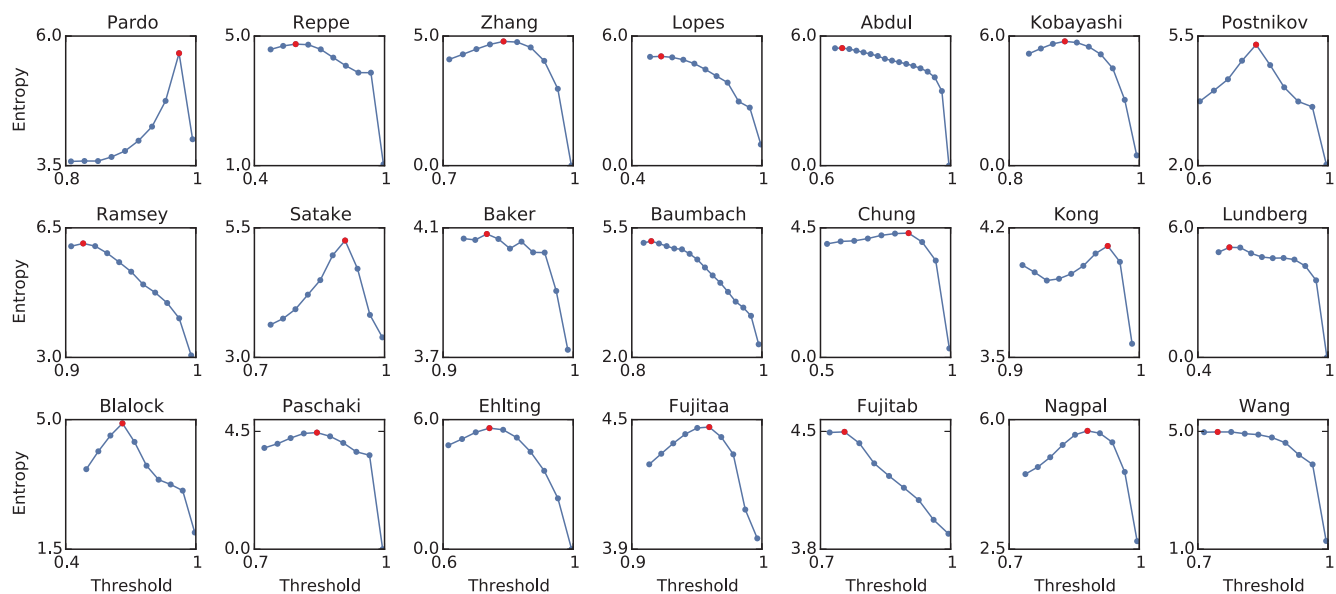


Fig. S3 Entropy values obtained for networks generated by different threshold values. Red dots indicate the maximum entropy reached by each dataset.

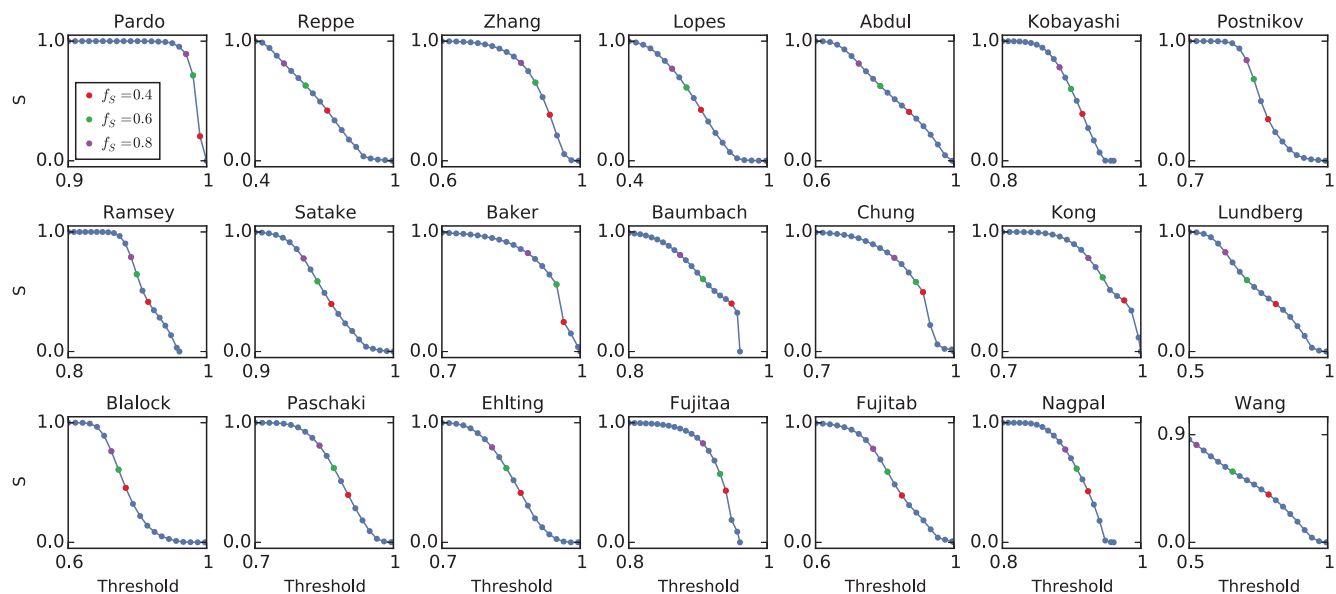


Fig. S4 Network's giant component size as a function of threshold. The size is normalized by the total number of genes studied in each experiment. Colored dots indicate the giant component sizes used in the analysis, represented as f_s .

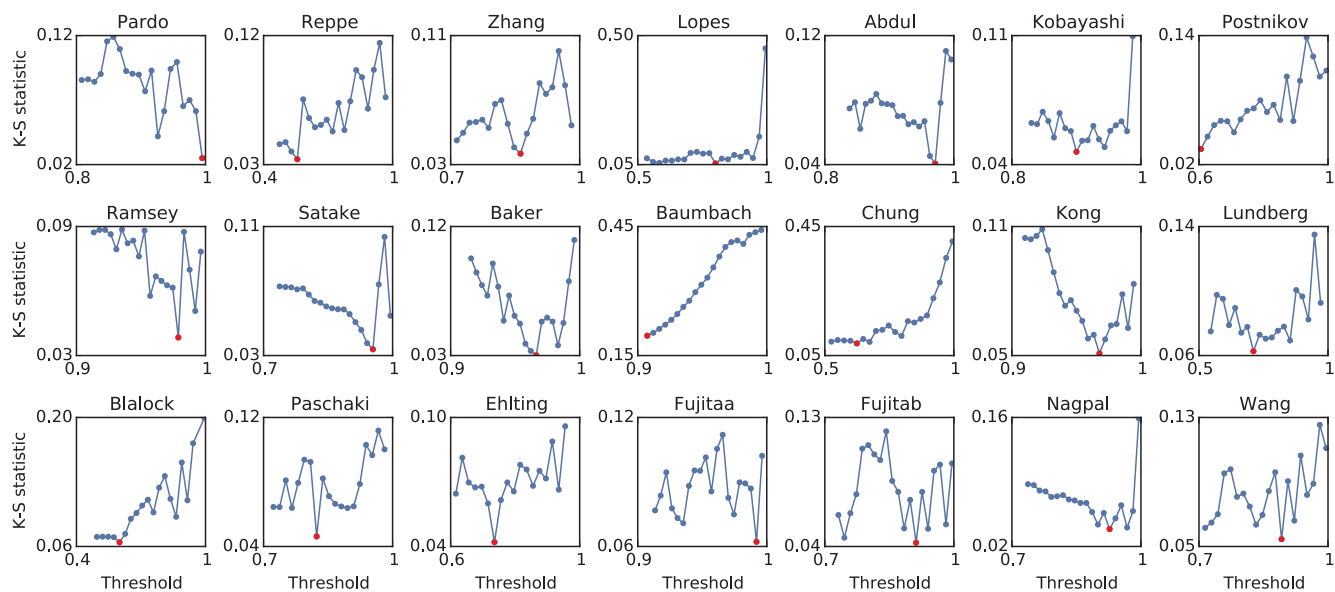


Fig. S5 Kolmogorov-Smirnov statistic comparing the degree distribution of the networks to a power-law function.

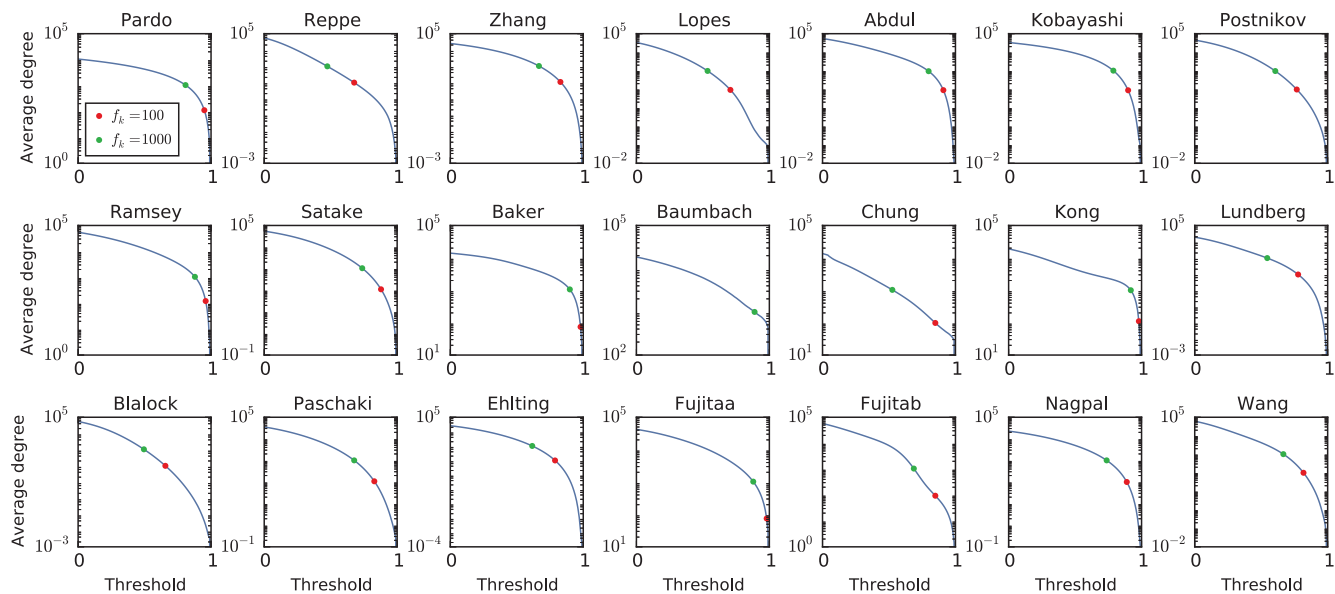


Fig. S6 Average degree of the networks obtained by different thresholds. The dots indicate the chosen average degree for analyzing this criterion, represented as f_k .

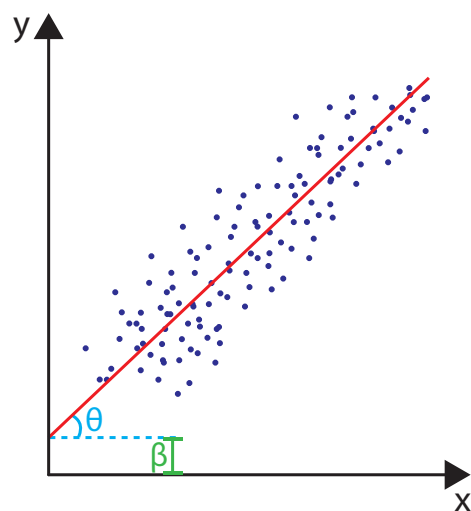


Fig. S7 Meaning of the angular (α) and linear (β) coefficients. The red line represents a linear regression of the blue points. β is given by the y value where the red line intercepts the y axis. θ is the angle between the red line and the x axis. α is calculated as $\alpha = \tan(\theta)$.

Table S4 Pearson correlation values between the methods shown in Figure S8.

	T variation	T entropy	T comp 0.4	T comp 0.6	T comp 0.8	T deg. 100	T deg. 1000	T power-law
T variation	1	0.05	0.09	0.05	0.02	0.02	-0.03	0.14
T entropy	0.05	1	0.92	0.93	0.90	0.80	0.75	0.61
T comp 0.4	0.09	0.92	1	0.97	0.93	0.89	0.79	0.64
T comp 0.6	0.05	0.93	0.97	1	0.99	0.80	0.71	0.56
T comp 0.8	0.02	0.90	0.93	0.99	1	0.73	0.66	0.51
T deg. 100	0.02	0.80	0.89	0.80	0.73	1	0.95	0.83
T deg. 1000	-0.03	0.75	0.79	0.71	0.66	0.95	1	0.88
T power-law	0.14	0.61	0.64	0.56	0.51	0.83	0.88	1

Table S5 Alpha values ($\tilde{\alpha}$) for the methods shown in Figure S8.

	T variation	T entropy	T comp. 0.4	T comp. 0.6	T comp. 0.8	T deg. 100	T deg. 1000	T power-law
T variation	1.00	0.02	0.04	0.02	0.01	0.01	-0.01	0.04
T entropy	0.16	1.00	1.39	1.09	0.87	1.06	0.70	0.57
T comp. 0.4	0.19	0.60	1.00	0.75	0.60	0.77	0.48	0.39
T comp. 0.6	0.12	0.78	1.25	1.00	0.81	0.89	0.56	0.45
T comp. 0.8	0.06	0.93	1.47	1.20	1.00	0.99	0.63	0.50
T deg. 100	0.04	0.61	1.02	0.71	0.53	1.00	0.67	0.59
T deg. 1000	-0.10	0.81	1.29	0.90	0.69	1.34	1.00	0.88
T power-law	0.49	0.65	1.04	0.71	0.53	1.17	0.87	1.00

Table S6 Beta values ($\tilde{\beta}$) for the methods shown in Figure S8.

	T variation	T entropy	T comp. 0.4	T comp. 0.6	T comp. 0.8	T deg. 100	T deg. 1000	T power-law
T variation	0.00	0.94	0.91	0.93	0.94	0.94	0.95	0.91
T entropy	0.64	0.00	-0.45	-0.13	0.09	-0.11	0.30	0.31
T comp. 0.4	0.71	0.41	0.00	0.25	0.41	0.23	0.55	0.56
T comp. 0.6	0.73	0.22	-0.27	0.00	0.19	0.08	0.45	0.47
T comp. 0.8	0.75	0.07	-0.50	-0.21	-0.00	-0.04	0.35	0.39
T deg. 100	0.82	0.38	-0.05	0.25	0.43	0.00	0.38	0.36
T deg. 1000	0.80	0.07	-0.44	-0.06	0.16	-0.44	-0.00	-0.03
T power-law	0.38	0.32	-0.09	0.23	0.41	-0.17	0.22	0.00

Table S7 Chosen thresholds by the different criteria for each experiment.

	T variation	T entropy	T comp. 0.4	T comp. 0.6	T comp. 0.8	T deg. 100	T deg. 1000	T power-law
Pardo	0.974	0.974	0.995	0.990	0.990	0.949	0.808	0.995
Reppe	0.892	0.590	0.711	0.616	0.521	0.677	0.475	0.557
Zhang	0.974	0.813	0.911	0.869	0.827	0.828	0.667	0.839
Lopes	0.923	0.535	0.711	0.648	0.584	0.707	0.535	0.801
Abdul	0.974	0.667	0.869	0.784	0.721	0.909	0.798	0.964
Kobayashi	0.974	0.857	0.942	0.921	0.900	0.899	0.788	0.875
Postnikov	0.903	0.779	0.869	0.837	0.821	0.768	0.606	0.606
Ramsey	0.800	0.879	0.942	0.921	0.911	0.960	0.879	0.971
Satake	0.964	0.909	0.953	0.942	0.932	0.879	0.737	0.954
Baker	0.933	0.920	0.963	0.948	0.884	0.980	0.899	0.960
Baumbach	0.933	0.830	0.984	0.932	0.890	0.990	0.889	0.889
Chung	0.944	0.838	0.932	0.916	0.869	0.848	0.525	0.624
Kong	0.974	0.978	0.963	0.916	0.884	0.980	0.919	0.971
Lundberg	0.974	0.545	0.811	0.706	0.627	0.778	0.545	0.711
Blalock	0.964	0.662	0.763	0.742	0.721	0.657	0.495	0.600
Paschaki	0.974	0.818	0.900	0.869	0.837	0.828	0.677	0.794
Ehltling	0.954	0.742	0.869	0.837	0.806	0.788	0.616	0.736
Fujitaa	0.964	0.943	0.974	0.963	0.932	0.980	0.879	0.989
Fujitab	0.974	0.755	0.848	0.806	0.763	0.848	0.687	0.898
Nagpal	0.964	0.880	0.953	0.932	0.911	0.889	0.737	0.927
Wang	0.974	0.703	0.784	0.653	0.521	0.818	0.667	0.874

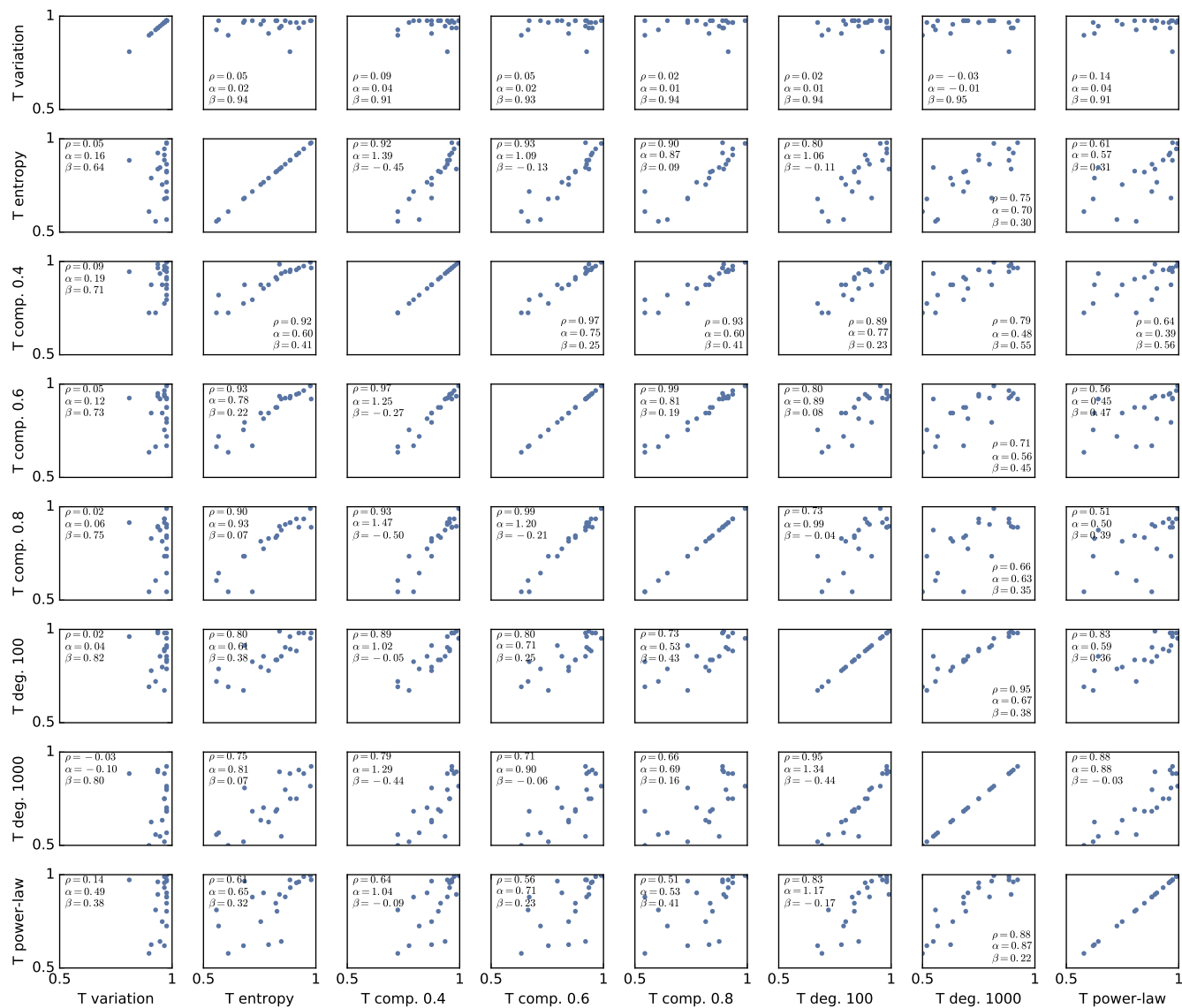


Fig. S8 Scatter plots between the threshold values chosen by different criteria. Each point corresponds to a dataset. Please refer to the main text for the meaning of the axes names. ρ indicates the Pearson correlation coefficient between the plotted values, α indicates the angular coefficient, and β the linear coefficient of a straight line least squares fit of the data.

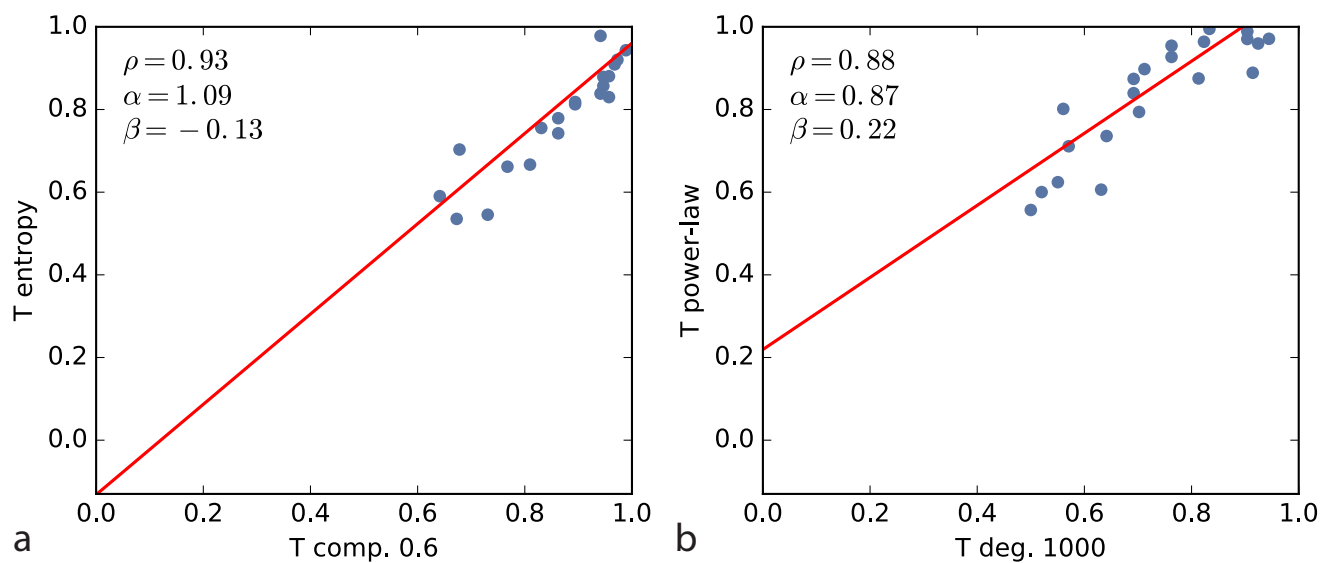


Fig. S9 Correlation between criteria: entropy versus component 60% (a), and power-law versus average degree 1000 (b). ρ corresponds to the Pearson correlation coefficient, α to the angular coefficient and β to the linear coefficient. The red line indicates the best straight line fit using least squares.

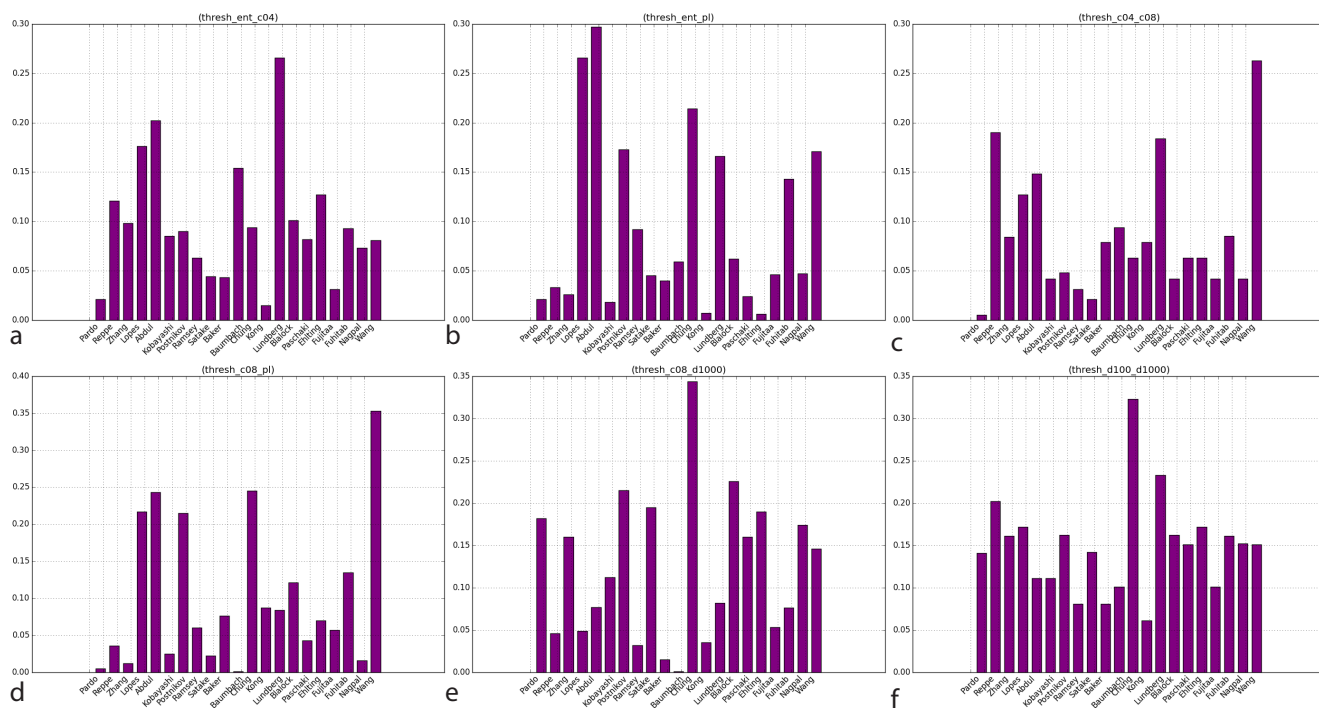


Fig. S10 Difference between the threshold values chosen by two criteria. This comparison considered the criteria that had the largest divergences in Figure 9. (a) entropy X component 40%, (b) entropy X power-law, (c) component 40% X component 80%, (d) component 80% X power-law, (e) component 80% X average degree 1000, (f) average degree 1000 X average degree 100.