

Supplementary Figures and Tables

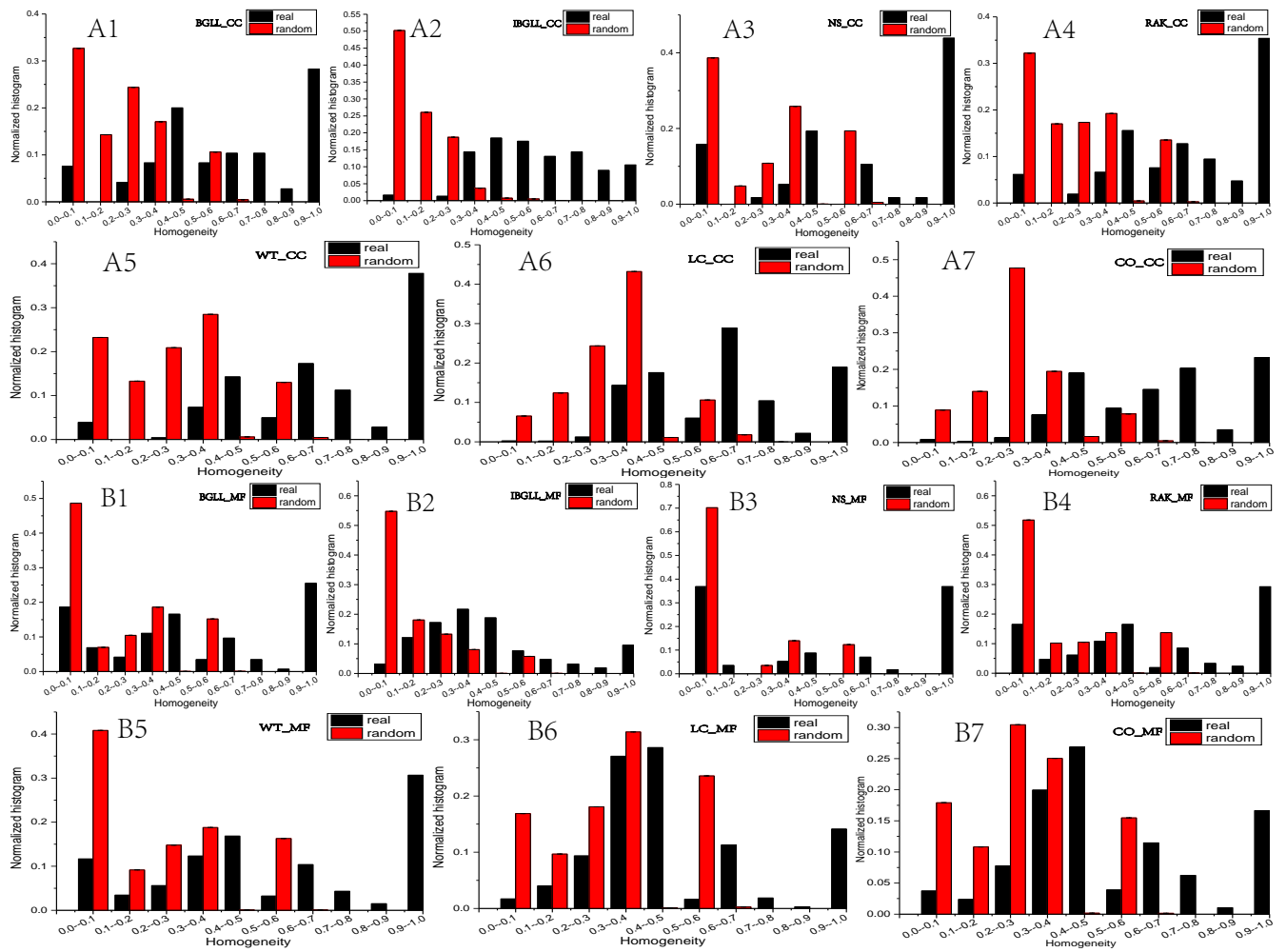


Figure 1. Homogeneity of CC and MF associations at different module sizes.

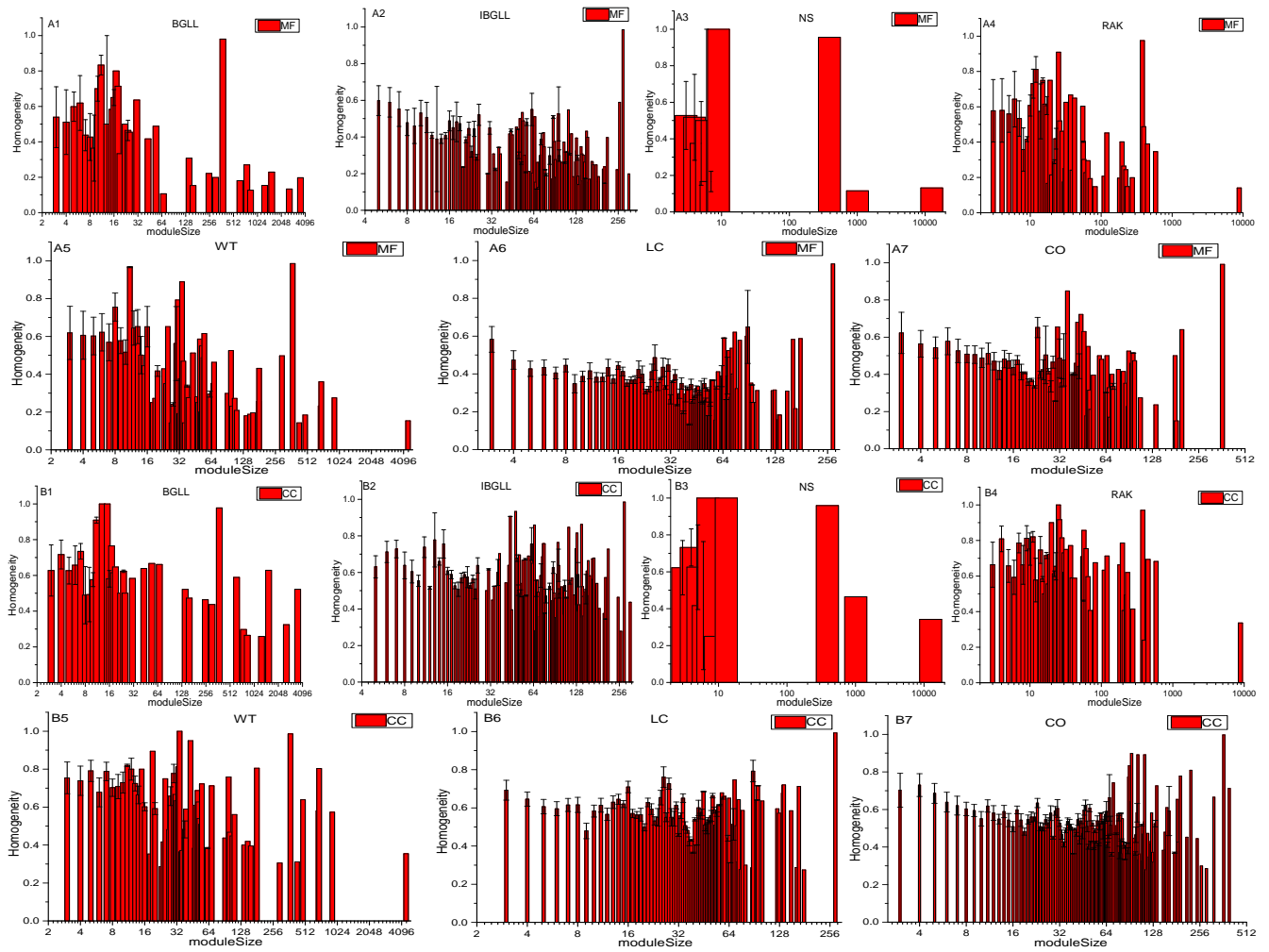


Figure 2. Homogeneity of MF and CC associations at different module sizes.

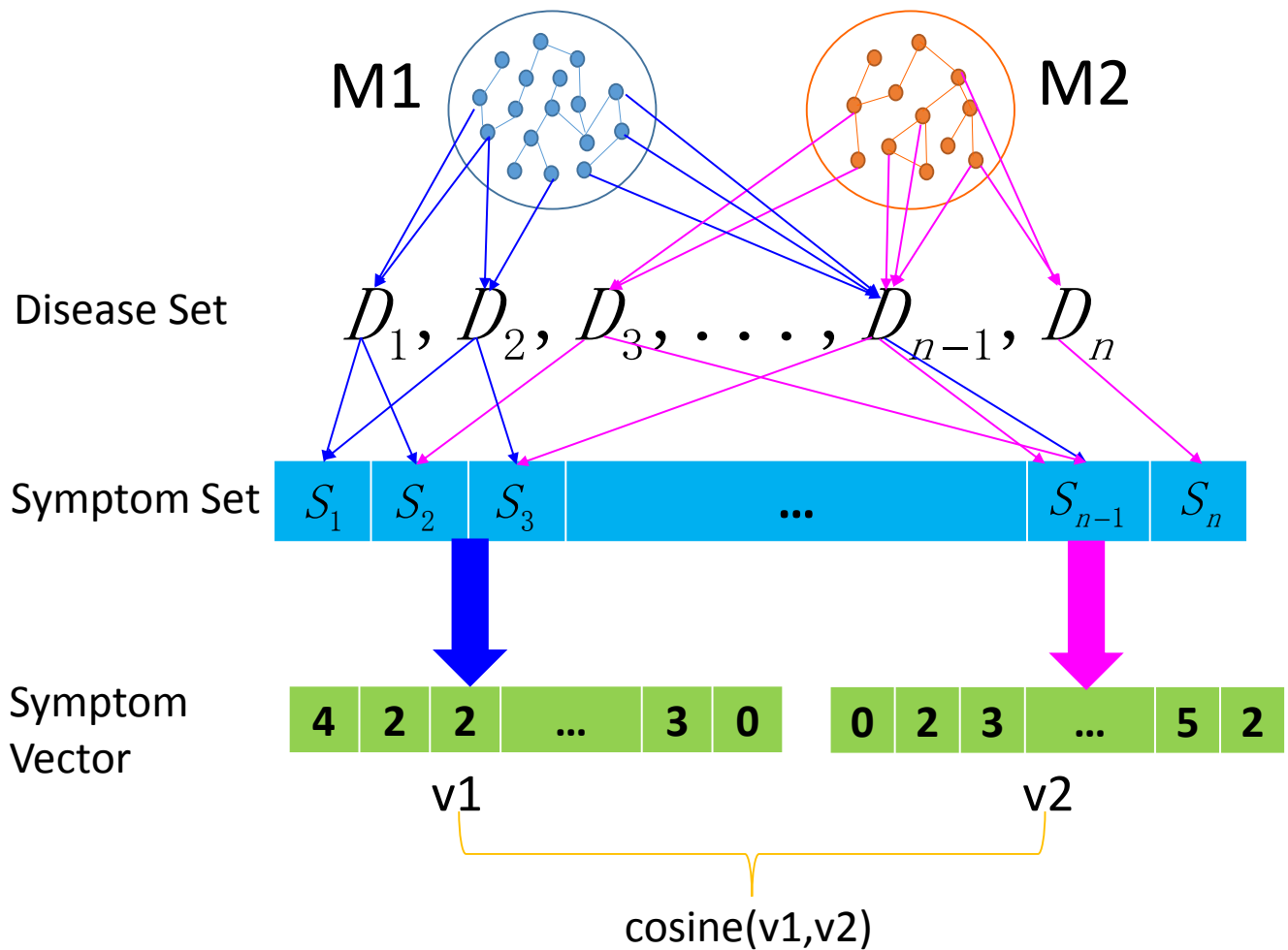


Figure 3. The process of symptom vector constructed for a module.

| Method | BP | CC | MF | Pathway |
|--------|--------------|--------------|--------------|-----------------|
| BGLL | -0.21 (0.01) | -0.16 (0.05) | -0.17 (0.04) | 0.16 (0.04) |
| RAK | -0.14 (0.05) | -0.07 (0.31) | -0.11 (0.10) | 0.26 (1.40E-04) |
| NS | 0.10 (0.45) | 0.11 (0.41) | 0.13 (0.32) | 0.48 (1.98E-03) |
| WT | -0.15 (0.01) | -0.09 (0.03) | -0.13 (0.09) | 0.07 (1.33E-03) |

Table 1. Correlation between module size and homogeneity. PCC(p-value)

| Method | BP | CC | MF | Pathway |
|--------|-----------------|-----------------|-------------|------------------|
| BGLL | 0.15 (0.07) | 0.16 (0.04) | 0.11 (0.21) | -0.31 (1.51E-04) |
| RAK | 0.11 (0.12) | 0.15 (0.03) | 0.16 (0.02) | -0.15 (2.27E-03) |
| NS | -0.17 (0.21) | 0.07 (0.61) | 0.09 (0.50) | -0.16 (2.34E-04) |
| WT | 0.18 (6.93E-05) | 0.19 (2.76E-05) | 0.11 (0.02) | -0.23 (6.59E-07) |

Table 2. Correlation between edge density and homogeneity. PCC(p-value)

| Method | PCC (p-value) |
|--------|-----------------|
| BGLL | 0.44 (<1E-127) |
| RAK | 0.39 (<1E-127) |
| NS | 0.45 (4.49E-76) |
| WT | 0.31 (<1E-127) |

Table 3. Correlation between module distance and phenotypic similarity. PCC(p-value)

| Method | BP | CC | MF | Pathway |
|--------|-------------|-------------|-----------------|-------------|
| BGLL | 0.06 (0.45) | 0.06 (0.46) | 0.01 (0.93) | 0.04 (0.58) |
| RAK | 0.04 (0.48) | 0.05 (0.45) | 8.18E-03 (0.91) | 0.11 (0.65) |
| NS | 0.12 (0.35) | 0.08 (0.56) | 4.75E-03 (0.76) | 0.02 (0.86) |
| WT | 0.09 (0.04) | 0.07 (0.12) | 0.07 (0.19) | 0.09 (0.05) |

Table 4. Correlation between disease ratio and homogeneity. PCC(p-value)

| number of proteins annotated by (or participated in) r GO terms (pathways) | PCC(p-value) | | | | |
|--|--------------|----------------|----------------|-----------------|----------------|
| | BP | CC | MF | pathway | |
| BGLL | 1 | 0.40(7.55E-07) | 0.31(2.04E-04) | 0.30(3.14E-04) | 0.78(1.28E-29) |
| | 2 | 0.25(2.29E-03) | 0.13(0.12) | 0.36(8.63E-06) | 0.36(1.07E-05) |
| | 3 | 0.14(0.09) | 0.02(0.84) | 0.22(8.41E-03) | 0.25(0.00326) |
| | 4 | 0.10(0.23) | 0.11(0.20) | -0.01(0.95) | 0.06(0.47) |
| | >=5 | -0.049(0.56) | 0.02(0.86) | -0.02(0.78) | 0.28(7.75E-04) |
| RAK | 1 | 0.42(2.44E-10) | 0.15(0.03) | 0.30(7.91E-06) | 0.81(2.93E-50) |
| | 2 | 0.24(3.64E-4) | 0.15(0.03) | 0.22(1.23E-03) | 0.29(1.44E-05) |
| | 3 | 0.14(0.04) | 0.07(0.30) | 0.21(1.92E-03) | 0.22(1.13E-03) |
| | 4 | 0.14(0.04) | 0.11(0.09) | 0.09(0.17) | 0.26(1.43E-04) |
| | >=5 | 0.01(0.88) | 0.10(0.14) | 0.07(0.32) | 0.25(2.84E-04) |
| NS | 1 | 0.59(1.62E-06) | 0.37(6.0E-03) | 0.56(9.51E-06) | 0.90(7.38E-21) |
| | 2 | 0.31(0.02) | 0.27(0.04) | 0.41(2.14E-03) | NaN |
| | 3 | 0.19(0.16) | 0.06(0.67) | 0.27(0.05) | NaN |
| | 4 | 0.12(0.40) | 0.19(0.16) | -2.16E-03(0.98) | 0.41(1.88E-03) |
| | >=5 | 0.14(0.30) | 9.72E-02(0.48) | 0.05(0.71) | 0.41(1.88E-03) |
| WT | 1 | 0.27(5.72E-09) | 0.11(0.02) | 0.31(9.31E-12) | 0.81(5.2E-17) |
| | 2 | 0.18(7.68E-05) | 0.10(0.03) | 0.18(1.28E-04) | 0.37(1.99E-16) |
| | 3 | 0.05(0.29) | 0.07(0.11) | 0.09(0.05) | 0.21(6.03E-06) |
| | 4 | 0.089(0.06) | 0.09(0.06) | 0.07(0.13) | 0.16(6.51E-04) |
| | >=5 | 7.83E-03(0.87) | 0.04(0.35) | 0.02(0.71) | 0.14(3.10E-03) |

Table 5. Correlation between the number of GO terms at different levels and homogeneity in terms of BP, CC, MF and pathway. PCC(p-value)