

| name     | <sup>a</sup> rank_N0 | <sup>b</sup> rank_random | <sup>c</sup> degree | <sup>d</sup> validate |
|----------|----------------------|--------------------------|---------------------|-----------------------|
| TP53     | 0                    | 0.0                      | 615                 | N                     |
| CDC42    | 1                    | 3.4                      | 258                 | N                     |
| FAM48A   | 2                    | 1.1                      | 521                 | N                     |
| INS-IGF2 | 3                    | 3.0                      | 461                 | N                     |
| AKT1     | 4                    | 4.9                      | 497                 | N                     |
| PLEK     | 5                    | 4.2                      | 140                 | N                     |
| RAC1     | 6                    | 6.3                      | 290                 | N                     |
| CALM1    | 7                    | 6.9                      | 265                 | N                     |
| EGFR     | 8                    | 9.4                      | 344                 | N                     |
| ESR1     | 9                    | 10.9                     | 287                 | N                     |
| EGF      | 10                   | 10.4                     | 374                 | N                     |
| DNAH8    | 11                   | 14.9                     | 148                 | N                     |
| CTNNB1   | 12                   | 7.4                      | 369                 | N                     |
| IL6      | 13                   | 16.2                     | 397                 | N                     |
| NFKB1    | 14                   | 15.0                     | 400                 | N                     |
| STAT3    | 15                   | 46.5                     | 282                 | Y                     |
| JUN      | 16                   | 18.8                     | 394                 | N                     |
| SP1      | 17                   | 12.4                     | 352                 | N                     |
| DLG4     | 18                   | 17.7                     | 70                  | N                     |
| IL2      | 19                   | 24.3                     | 309                 | N                     |
| FOS      | 20                   | 31.5                     | 342                 | N                     |
| MYC      | 21                   | 17.7                     | 370                 | N                     |
| FYN      | 22                   | 19.5                     | 233                 | N                     |
| EP300    | 23                   | 27.0                     | 260                 | N                     |
| GRB2     | 24                   | 41.8                     | 242                 | N                     |
| APP      | 25                   | 32.8                     | 334                 | N                     |
| PRKAR2A  | 26                   | 23.2                     | 199                 | N                     |
| CD4      | 27                   | 47.9                     | 253                 | N                     |
| NGF      | 28                   | 39.5                     | 201                 | N                     |
| CRCT1    | 29                   | 683.5                    | 9                   | N                     |
| IL1B     | 30                   | 36.7                     | 269                 | N                     |
| IFNG     | 31                   | 41.3                     | 297                 | N                     |
| CDH1     | 32                   | 43.6                     | 223                 | N                     |
| VEGFA    | 33                   | 44.5                     | 287                 | N                     |
| NOD2     | 34                   | 1706.6                   | 47                  | Y                     |
| BCL2     | 35                   | 38.7                     | 306                 | N                     |
| PIK3R1   | 36                   | 55.5                     | 263                 | N                     |
| IL23R    | 37                   | 1185.3                   | 61                  | Y                     |

|            |    |        |     |   |
|------------|----|--------|-----|---|
| FN1        | 38 | 24.3   | 243 | N |
| PPARG      | 39 | 29.1   | 253 | N |
| RAC2       | 40 | 34.0   | 144 | N |
| ATG16L1    | 41 | 2690.1 | 20  | Y |
| PTEN       | 42 | 55.5   | 198 | N |
| MAPK1      | 43 | 35.2   | 246 | N |
| CDKN2A     | 44 | 37.2   | 176 | N |
| NKX2-3     | 45 | 4774.5 | 12  | Y |
| ST6GALNAC1 | 46 | 48.4   | 24  | N |
| ABCC11     | 47 | 135.3  | 51  | N |
| FURIN      | 48 | 24.0   | 75  | N |
| TBP        | 49 | 44.2   | 195 | N |
| DAG1       | 50 | 111.4  | 64  | N |
| GNAL       | 51 | 44.0   | 298 | N |
| GRIP1      | 52 | 92.7   | 46  | N |
| GCNT1      | 53 | 41.5   | 25  | N |
| JAK2       | 54 | 104.1  | 231 | Y |
| PARK2      | 55 | 50.7   | 131 | N |
| CCND1      | 56 | 46.7   | 315 | N |
| IGF1       | 57 | 56.0   | 250 | N |
| GSK3B      | 58 | 47.6   | 152 | N |
| B3GNT6     | 59 | 51.2   | 20  | N |
| GNAT3      | 60 | 124.6  | 37  | N |
| C1GALT1    | 61 | 46.5   | 21  | N |
| ACTN2      | 62 | 66.6   | 138 | N |
| VIM        | 63 | 91.9   | 190 | N |
| MTF1       | 64 | 731.9  | 19  | N |
| BMP4       | 65 | 54.7   | 159 | N |
| RELA       | 66 | 87.4   | 244 | N |
| MAPK8      | 67 | 55.4   | 269 | N |
| PTS        | 68 | 45.6   | 46  | N |
| NOTCH1     | 69 | 52.6   | 183 | N |
| RB1        | 70 | 83.8   | 170 | N |
| RHOQ       | 71 | 58.9   | 100 | N |
| RNF31      | 72 | 127.6  | 142 | N |
| PIK3CA     | 73 | 84.6   | 241 | N |
| STAT1      | 74 | 100.6  | 218 | N |
| PRKACG     | 75 | 68.4   | 96  | N |
| CREBBP     | 76 | 153.1  | 172 | N |
| SNAP25     | 77 | 68.3   | 64  | N |

|         |    |        |     |   |
|---------|----|--------|-----|---|
| IL8     | 78 | 78.5   | 267 | N |
| ACTN4   | 79 | 137.7  | 97  | N |
| IL4     | 80 | 94.3   | 218 | N |
| TNFSF15 | 81 | 4351.7 | 16  | Y |
| CBL     | 82 | 124.6  | 180 | N |
| HNF4A   | 83 | 85.9   | 178 | N |
| PCNA    | 84 | 70.2   | 224 | N |
| PPP2R1A | 85 | 123.6  | 124 | N |
| MGAT1   | 86 | 134.8  | 14  | N |
| CD44    | 87 | 74.9   | 217 | N |
| SLC7A13 | 88 | 3495.6 | 2   | N |
| PIK3R2  | 89 | 146.7  | 175 | N |
| ACTG1   | 90 | 200.1  | 92  | N |
| PRKCA   | 91 | 70.8   | 202 | N |
| SCAPER  | 92 | 5318.3 | 2   | N |
| MAPK14  | 93 | 92.5   | 193 | N |
| POMC    | 94 | 135.7  | 256 | N |
| ARF6    | 95 | 101.0  | 95  | N |
| STX1A   | 96 | 88.3   | 63  | N |
| PPP1CA  | 97 | 115.5  | 67  | N |
| ARF1    | 98 | 105.0  | 58  | N |
| ABL1    | 99 | 93.3   | 151 | N |

**Table S1**, <sup>a</sup>rank\_N0 is gene rank by posterior scores in networks overlaid by GWAS data (T=1 for propagaion). <sup>b</sup>rank\_random is the average gene rank by posterior scores in networks overlaid by random prior information. <sup>c</sup>degree is the degree of gene in the network, <sup>d</sup>validate denotes whether the gene is reported (Y-Yes, N-No) as association in other Crohn's Disease studies according to GWAS catalog, [www.pnas.org/cgi/doi/10.1073/pnas.0903103106](http://www.pnas.org/cgi/doi/10.1073/pnas.0903103106)

| name     | <sup>a</sup> rank_P | <sup>b</sup> pval | <sup>c</sup> rank_N0 | <sup>d</sup> rank_Ni | <sup>e</sup> validate | <sup>f</sup> PSP |
|----------|---------------------|-------------------|----------------------|----------------------|-----------------------|------------------|
| NOD2     | 0                   | 1.76e-15          | 34                   | 1432.8               | Y                     | 0.0000           |
| ATG16L1  | 1                   | 1.08e-13          | 41                   | 2311.6               | Y                     | 0.0000           |
| IL23R    | 2                   | 2.91e-13          | 37                   | 1258.1               | Y                     | 0.0000           |
| C1orf141 | 3                   | 1.15e-09          | 1853                 | 5869.8               | Y                     | 0.0017           |
| CYLD     | 4                   | 4.49e-09          | 620                  | 4763.9               | Y                     | 0.0000           |
| NKX2-3   | 5                   | 1.61e-08          | 45                   | 4156.3               | Y                     | 0.0000           |
| PTPN2    | 6                   | 4.01e-07          | 234                  | 3668.3               | Y                     | 0.0000           |
| SLC22A5  | 7                   | 4.74e-07          | 224                  | 3987.2               | Y                     | 0.0000           |
| BSN      | 8                   | 6.44e-07          | 351                  | 1259.6               | Y                     | 0.0031           |
| APEH     | 9                   | 6.44e-07          | 2816                 | 6895.4               | N                     | 0.0010           |
| CDKAL1   | 10                  | 4.86e-06          | 768                  | 2806.9               | Y                     | 0.0000           |
| STAT3    | 12                  | 1.12e-05          | 15                   | 44.3                 | Y                     | 0.0000           |
| DAG1     | 13                  | 1.27e-05          | 50                   | 128.8                | N                     | 0.0041           |
| AMT      | 15                  | 1.32e-05          | 481                  | 1419.5               | N                     | 0.0060           |
| GCKR     | 19                  | 1.69e-05          | 1023                 | 3427.9               | Y                     | 0.0005           |
| IL12RB2  | 20                  | 1.89e-05          | 2483                 | 5702.7               | Y                     | 0.0006           |
| USP4     | 26                  | 2.89e-05          | 2094                 | 6179.7               | N                     | 0.0002           |
| CREM     | 30                  | 3.88e-05          | 422                  | 2606.5               | Y                     | 0.0000           |
| BSG      | 31                  | 4.11e-05          | 1580                 | 4417.7               | N                     | 0.0008           |
| DGKD     | 33                  | 4.21e-05          | 1098                 | 3136.3               | Y                     | 0.0005           |
| ERC2     | 39                  | 6.30e-05          | 827                  | 3233.7               | N                     | 0.0085           |
| SLC22A4  | 40                  | 6.77e-05          | 268                  | 3734.8               | Y                     | 0.0000           |
| ACSL6    | 42                  | 7.24e-05          | 861                  | 2682.4               | Y                     | 0.0098           |
| IP6K1    | 46                  | 7.52e-05          | 819                  | 5268.6               | N                     | 0.0005           |
| TNFSF15  | 48                  | 7.85e-05          | 81                   | 4020.5               | Y                     | 0.0000           |
| TNFRSF6B | 51                  | 8.17e-05          | 883                  | 5865.4               | N                     | 0.0014           |
| SP110    | 54                  | 8.63e-05          | 2386                 | 5565.9               | N                     | 0.0091           |
| POU2F1   | 56                  | 1.10e-04          | 2432                 | 4856.6               | N                     | 0.0056           |
| MAPT     | 61                  | 1.55e-04          | 126                  | 464.5                | N                     | 0.0007           |
| CRHR1    | 67                  | 1.89e-04          | 1174                 | 6646.3               | N                     | 0.0014           |
| WNT3     | 69                  | 1.99e-04          | 1917                 | 5421.9               | N                     | 0.0015           |
| VWF      | 70                  | 2.00e-04          | 658                  | 1626.3               | N                     | 0.0058           |
| N4BP1    | 83                  | 2.39e-04          | 766                  | 3780.5               | N                     | 0.0037           |
| MOGS     | 87                  | 2.67e-04          | 1882                 | 6474.9               | N                     | 0.0014           |
| GRB2     | 89                  | 2.71e-04          | 24                   | 36.9                 | N                     | 0.0076           |
| MYH3     | 90                  | 2.71e-04          | 2635                 | 5539.0               | N                     | 0.0033           |
| DLG5     | 91                  | 2.80e-04          | 114                  | 5814.4               | N                     | 0.0000           |
| USP1     | 92                  | 2.84e-04          | 2462                 | 5958.0               | N                     | 0.0005           |

|                 |     |          |      |        |   |        |
|-----------------|-----|----------|------|--------|---|--------|
| P4HA2           | 99  | 3.26e-04 | 1028 | 6499.5 | Y | 0.0001 |
| ENSP00000332488 | 101 | 3.49e-04 | 2526 | 7770.8 | N | 0.0026 |
| CD48            | 119 | 4.92e-04 | 1978 | 4466.6 | N | 0.0028 |
| PCDH15          | 128 | 5.97e-04 | 270  | 727.4  | N | 0.0067 |
| IL18RAP         | 144 | 7.42e-04 | 382  | 3619.9 | Y | 0.0000 |
| PTGFR           | 163 | 8.46e-04 | 1593 | 2982.6 | N | 0.0094 |
| NEDD4L          | 173 | 9.08e-04 | 433  | 1213.3 | N | 0.0015 |
| GRAP2           | 175 | 9.24e-04 | 2559 | 4973.3 | N | 0.0042 |
| STX2            | 176 | 9.30e-04 | 548  | 1428.8 | N | 0.0059 |
| ADCY3           | 182 | 9.62e-04 | 403  | 895.3  | N | 0.0056 |
| IRF1            | 188 | 1.00e-03 | 781  | 2086.7 | Y | 0.0031 |
| CAMK2G          | 199 | 1.10e-03 | 763  | 2074.0 | N | 0.0037 |
| IL12B           | 214 | 1.28e-03 | 334  | 1887.7 | Y | 0.0000 |
| CREBBP          | 227 | 1.39e-03 | 76   | 152.6  | N | 0.0016 |
| STX16           | 236 | 1.44e-03 | 1214 | 3354.3 | N | 0.0033 |
| UBE2Q1          | 256 | 1.57e-03 | 1515 | 7958.1 | N | 0.0015 |
| UTS2            | 257 | 1.57e-03 | 1818 | 4044.9 | N | 0.0022 |
| HERC2           | 259 | 1.59e-03 | 144  | 839.9  | N | 0.0004 |
| INPP5E          | 261 | 1.64e-03 | 1297 | 3595.8 | N | 0.0058 |
| PTGER4          | 263 | 1.64e-03 | 749  | 2115.6 | Y | 0.0021 |
| CAPN10          | 288 | 1.91e-03 | 859  | 5083.2 | N | 0.0036 |
| DEFA5           | 293 | 1.94e-03 | 1312 | 6235.9 | N | 0.0001 |
| CDC37           | 298 | 1.97e-03 | 2517 | 5162.5 | N | 0.0070 |
| FZD6            | 303 | 2.01e-03 | 423  | 1067.2 | N | 0.0084 |
| CCNY            | 305 | 2.01e-03 | 239  | 3945.7 | N | 0.0000 |
| DCTN1           | 330 | 2.19e-03 | 119  | 320.2  | N | 0.0033 |
| SLC8A1          | 331 | 2.23e-03 | 806  | 2927.4 | N | 0.0053 |
| Clorf43         | 337 | 2.25e-03 | 840  | 7057.2 | N | 0.0005 |
| POMT2           | 371 | 2.45e-03 | 614  | 2444.7 | N | 0.0075 |
| KAT2A           | 373 | 2.46e-03 | 733  | 1800.2 | N | 0.0044 |
| RRAS            | 408 | 2.78e-03 | 1181 | 2943.6 | N | 0.0060 |
| IL18R1          | 417 | 2.81e-03 | 1109 | 3342.2 | Y | 0.0028 |
| PIM1            | 468 | 3.34e-03 | 1123 | 3365.2 | N | 0.0011 |
| AHCYL1          | 475 | 3.42e-03 | 1801 | 4357.3 | N | 0.0093 |
| FOS             | 477 | 3.43e-03 | 20   | 31.5   | N | 0.0036 |
| ASAH1           | 483 | 3.47e-03 | 1151 | 2913.4 | N | 0.0103 |
| KIAA0564        | 495 | 3.67e-03 | 805  | 2226.1 | N | 0.0098 |
| PRMT5           | 504 | 3.82e-03 | 413  | 1171.4 | N | 0.0062 |
| ST6GAL2         | 527 | 4.05e-03 | 295  | 4923.5 | N | 0.0006 |
| CHDH            | 605 | 5.01e-03 | 2631 | 5462.3 | N | 0.0039 |

|          |      |          |      |        |   |        |
|----------|------|----------|------|--------|---|--------|
| IL12RB1  | 627  | 5.23e-03 | 1432 | 3865.7 | N | 0.0002 |
| MAP3K7   | 648  | 5.42e-03 | 242  | 685.7  | N | 0.0015 |
| ZFAND6   | 673  | 5.75e-03 | 2113 | 6879.9 | N | 0.0011 |
| CD3G     | 744  | 6.65e-03 | 2197 | 4901.5 | N | 0.0080 |
| CD3D     | 745  | 6.65e-03 | 1045 | 3601.1 | N | 0.0006 |
| LAMA5    | 780  | 7.13e-03 | 1412 | 3080.9 | N | 0.0042 |
| SEC13    | 817  | 7.56e-03 | 399  | 921.8  | N | 0.0028 |
| RORC     | 885  | 8.41e-03 | 740  | 1789.7 | N | 0.0082 |
| TRAF1    | 975  | 9.45e-03 | 380  | 1357.1 | N | 0.0001 |
| S100B    | 988  | 9.59e-03 | 323  | 1093.3 | N | 0.0042 |
| ELAVL4   | 1054 | 1.09e-02 | 191  | 804.9  | N | 0.0091 |
| TWSG1    | 1057 | 1.09e-02 | 757  | 2290.9 | N | 0.0036 |
| IL15     | 1184 | 1.28e-02 | 804  | 1863.1 | N | 0.0048 |
| ABCC11   | 1232 | 1.35e-02 | 47   | 178.0  | N | 0.0002 |
| WBP4     | 1339 | 1.52e-02 | 215  | 856.7  | N | 0.0069 |
| CLCN1    | 1356 | 5.59e-03 | 975  | 3401.0 | N | 0.0054 |
| JAK1     | 1505 | 1.79e-02 | 145  | 332.3  | N | 0.0020 |
| PIP5K1A  | 1589 | 1.91e-02 | 2701 | 5339.7 | N | 0.0051 |
| CTDSP2   | 1605 | 1.94e-02 | 1064 | 3294.8 | N | 0.0023 |
| SEC23B   | 1608 | 1.95e-02 | 2353 | 5739.1 | N | 0.0028 |
| PHYH     | 1650 | 2.01e-02 | 349  | 1540.8 | N | 0.0058 |
| PPIP5K1  | 1658 | 2.02e-02 | 472  | 3820.2 | N | 0.0000 |
| CD4      | 1731 | 2.15e-02 | 27   | 52.6   | N | 0.0022 |
| TNFRSF8  | 1766 | 2.21e-02 | 1190 | 2540.9 | N | 0.0078 |
| OSM      | 1862 | 2.38e-02 | 1487 | 3085.3 | N | 0.0090 |
| CX3CR1   | 1919 | 2.48e-02 | 1459 | 3318.6 | N | 0.0068 |
| IL1R1    | 1951 | 2.55e-02 | 458  | 1599.0 | N | 0.0001 |
| SCAPER   | 2034 | 2.70e-02 | 92   | 4137.7 | N | 0.0006 |
| C20orf54 | 2043 | 2.72e-02 | 1781 | 6844.2 | N | 0.0076 |
| UBFD1    | 2116 | 2.91e-02 | 330  | 1958.7 | N | 0.0073 |
| GPT      | 2163 | 3.02e-02 | 2251 | 4594.1 | N | 0.0066 |
| IPPK     | 2165 | 3.03e-02 | 905  | 4736.9 | N | 0.0006 |
| LIMCH1   | 2242 | 3.17e-02 | 170  | 3303.0 | N | 0.0101 |
| SOCS4    | 2330 | 3.36e-02 | 1021 | 2636.7 | N | 0.0035 |
| NCKAP1   | 2361 | 3.43e-02 | 865  | 3057.7 | N | 0.0069 |
| CD3E     | 2621 | 4.04e-02 | 1654 | 3943.6 | N | 0.0051 |
| FKBP4    | 2704 | 4.33e-02 | 2629 | 6167.0 | N | 0.0020 |
| TMC8     | 2869 | 4.74e-02 | 1812 | 7839.2 | N | 0.0043 |
| TMC6     | 2870 | 4.74e-02 | 1811 | 7700.6 | N | 0.0045 |
| FAM92B   | 2880 | 4.75e-02 | 102  | 5654.4 | N | 0.0001 |

|           |       |          |      |        |   |        |
|-----------|-------|----------|------|--------|---|--------|
| SSU72     | 2885  | 4.78e-02 | 416  | 3835.6 | N | 0.0000 |
| SEC24D    | 2933  | 4.88e-02 | 2360 | 5425.9 | N | 0.0085 |
| IP6K3     | 3052  | 5.21e-02 | 1042 | 6119.4 | N | 0.0001 |
| JAK2      | 3063  | 5.23e-02 | 54   | 100.2  | Y | 0.0025 |
| IL5       | 3137  | 5.43e-02 | 440  | 1009.2 | N | 0.0101 |
| UBAC1     | 3232  | 5.64e-02 | 1081 | 5968.7 | N | 0.0027 |
| SEC23A    | 3285  | 5.80e-02 | 1500 | 4870.5 | N | 0.0031 |
| RHOC      | 3352  | 5.97e-02 | 1463 | 4109.1 | N | 0.0089 |
| PTPN22    | 3390  | 6.09e-02 | 651  | 2025.7 | Y | 0.0015 |
| ESYT3     | 3425  | 6.20e-02 | 2424 | 6008.4 | N | 0.0091 |
| GABARAPL2 | 3580  | 6.62e-02 | 546  | 2401.3 | N | 0.0064 |
| HIST1H4A  | 3616  | 6.71e-02 | 1860 | 6167.5 | N | 0.0008 |
| TMEM39A   | 3650  | 6.81e-02 | 530  | 6071.9 | N | 0.0016 |
| IL13      | 3734  | 7.07e-02 | 932  | 2662.1 | N | 0.0022 |
| PPAP2A    | 3741  | 7.09e-02 | 193  | 543.5  | N | 0.0044 |
| C10orf107 | 3760  | 7.17e-02 | 634  | 2249.5 | N | 0.0066 |
| FECH      | 3825  | 7.37e-02 | 1933 | 4514.8 | N | 0.0071 |
| ACTG1     | 4576  | 1.01e-01 | 90   | 200.7  | N | 0.0084 |
| IL23A     | 4657  | 1.04e-01 | 489  | 1467.1 | N | 0.0012 |
| CXCR4     | 4821  | 1.11e-01 | 252  | 598.3  | N | 0.0088 |
| SLC7A13   | 5476  | 1.41e-01 | 88   | 3944.4 | N | 0.0005 |
| RIMS2     | 5769  | 1.56e-01 | 345  | 1720.0 | N | 0.0007 |
| KPNA7     | 5815  | 7.68e-02 | 2007 | 7231.5 | N | 0.0048 |
| CRCT1     | 6411  | 1.94e-01 | 29   | 1282.8 | N | 0.0003 |
| PMM2      | 6910  | 2.27e-01 | 496  | 1918.6 | N | 0.0060 |
| PPIP5K2   | 8248  | 3.29e-01 | 1611 | 5902.5 | N | 0.0005 |
| C1orf64   | 8316  | 3.35e-01 | 637  | 7746.2 | N | 0.0033 |
| FASLG     | 8483  | 3.54e-01 | 227  | 711.3  | Y | 0.0007 |
| TRAPPC1   | 9276  | 4.48e-01 | 1972 | 6522.3 | N | 0.0060 |
| GKN2      | 10028 | 5.55e-01 | 589  | 4442.7 | N | 0.0033 |
| MTERF     | 10454 | 1.61e-01 | 2818 | 8682.0 | N | 0.0075 |
| IGHJ6     | 10958 | 7.78e-01 | 324  | 6174.5 | N | 0.0060 |

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**Table S2**, <sup>a</sup>rank\_P is rank of genes based on gene level  $p$  values from GWAS, <sup>b</sup>pval is  $p$  values from GWAS, <sup>c</sup>rank\_N0 is rank of posterior scores in network overlaid by GWAS prior, <sup>d</sup>rank\_Ni is average gene rank by posterior scores in networks overlaid by random prior information. <sup>e</sup>validate denotes whether the gene is reported (Y-Yes, N-No) as association in other Crohn's Disease studies according to GWAS catalog, [www.pnas.org/cgi/doi/10.1073/pnas.0903103106](http://www.pnas.org/cgi/doi/10.1073/pnas.0903103106). <sup>f</sup> is the  $p$  value of posterior score, based on 10000 permutations, calculated as the proportion of occurrence of larger posterior scores in the permutation.

| IL12_pathway | rank_GWAS | <sup>a</sup> rank_N0 | <sup>b</sup> rank_random |
|--------------|-----------|----------------------|--------------------------|
| JUN          | 2916      | 16                   | 18.2                     |
| MAP2K6       | 2025      | 970                  | 718.2                    |
| IL12A        | 9016      | 3527                 | 4461.9                   |
| IL12B        | 214       | 334                  | 1887.7                   |
| CD3E         | 2621      | 1654                 | 3943.6                   |
| CD3G         | 744       | 2197                 | 4901.5                   |
| MAPK8        | 9032      | 67                   | 56.8                     |
| ETV5         | 6467      | 1994                 | 1884.1                   |
| IFNG         | 9837      | 31                   | 44.9                     |
| STAT4        | 5617      | 1007                 | 1323.9                   |
| IL12RB1      | 627       | 1432                 | 3865.7                   |
| MAPK14       | 3010      | 93                   | 93.0                     |
| CD247        | 2277      | 1016                 | 1756.3                   |
| IL12RB2      | 20        | 2483                 | 5702.7                   |
| IL18         | 5164      | 293                  | 612.7                    |
| TYK2         | 9622      | 499                  | 781.9                    |
| JAK2         | 3063      | 54                   | 100.2                    |
| IL18R1       | 417       | 1109                 | 3342.2                   |
| CD3D         | 745       | 1045                 | 3601.1                   |

**Table S3** Ranks of IL12 pathway genes in GWAS and network propagation ( $T = 1$ ), GWAS rank of gene is based on the most significant SNPs. <sup>a</sup>rank\_N0 is gene rank by posterior scores in network of GWAS prior. <sup>b</sup>rank\_random is the average gene rank by posterior scores in networks of random prior. 15 out of 19 genes have a rank increase in the network of GWAS prior.