Table SI. List of gout candidate genes.

| A1CF  | GCKR  | NIPAL1 | SLC16A5 | SLC2A1 |
|-------|-------|--------|---------|--------|
| ABC4  | GEF   | NLRP3  | SLC16A6 | SLC2A10|
| ABCG2 | HADH  | NOD2   | SLC16A7 | SLC2A11|
| ACADS | HIST1H2BF | NRG4  | SLC16A8 | SLC2A12|
| ACVR1B| HIST1H4E | OSTC  | SLC16A9 | SLC2A13|
| ACVR2A|  HLF  | P2RX7  | SLC17A1 | SLC2A14|
| ACVRL1| HNF1B | P2X7R  | SLC17A2 | SLC2A2 |
| ADRB3 | HNF4G | PDK2   | SLC17A3 | SLC2A3 |
| AGL   | HPRT1 | PDZK1  | SLC17A4 | SLC2A3P1|
| ALDH16A1| IGF1R | PKFM   | SLC17A5 | SLC2A3P2|
| ALDH2 | IGF1R | PKLR   | SLC17A6 | SLC2A3P4|
| ALDOB | IL12B | PLA2G12A| SLC17A7 | SLC2A4 |
| ALPK1 | IL18R1| PPARC1A| SLC17A8 | SLC2A5 |
| AMPD1 | IL1A  | PPARC1B| SLC17A9 | SLC2A6 |
| AXO1  | IL1B  | PKRAG2 | SLC22A1 | SLC2A7 |
| ASAH2 | IL23R | PRKG2  | SLC22A10| SLC2A8 |
| ATXN2 | IL33  | PRPS1  | SLC22A11| SLC2A9 |
| B3GNT4| IL8   | PRPSAP1| SLC22A12| SLC2AXP1|
| BAZ1B | INHBB | PTPN11 | SLC22A13| SLC27A4|
| BCA53 | INHBC | PYGM   | SLC22A14| STAT4  |
| C1orf82|ITPR1 | R3HDM2 | SLC22A15| STC1   |
| CARD15| JAK2  | REN    | SLC22A16| TGFBI  |
| CARD8 | KCNQ1 | RXF3   | SLC22A17| TGM4   |
| CD14  | LEF1  | RREB1  | SLC22A18| TLR2   |
| CLNK  | LRP2  | SFBMT1 | SLC22A2 | TLR4   |
| CNINH2| LRRC16A| SGK1   | SLC22A20| TMEM171|
| CNTN4 | LTBP3 | SGMS2  | SLC22A23| TNXIP  |
| COMT  | MAF   | SLC16A1| SLC22A24| TRIM46 |
| CPT2  | MEFV  | SLC16A10| SLC22A25| UBE2Q2 |
| CUX2  | MLXIPL| SLC16A11| SLC22A3 | UGT1A  |
| CYP2U1| MOCOS | SLC16A12| SLC22A31| UMOD   |
| DAPK1 | MTHFR | SLC16A13| SLC22A4 | UOX    |
| DCP1A | MUST1 | SLC16A14| SLC22A5 | VEGFA  |
| EGF   | MYD88 | SLC16A14P1| SLC22A6 | VEGFA  |
| ELOVL6| MYL2  | SLC16A2 | SLC22A7 | WDR1   |
| FAM35A| NCF1  | SLC16A3 | SLC22A8 | XDH    |
| G6PC  | NFAT5 | SLC16A4 | SLC22A9 | ZNF518B|
Table SII. Results of conventional radiography, autoantibodies and HLA-B27 tests of patients with gout in three gout pedigrees.

| Individual ID | HLA-B27 | ANA+ENA | Joint X-ray |
|---------------|---------|---------|-------------|
| F1_I:1        | -       | -       | +           |
| F1_II:1       | -       | -       | +           |
| F2_I:1        | -       | -       | +           |
| F2_II:1       | -       | -       | NA          |
| F2_II:7       | -       | -       | -           |
| F2_III:1      | -       | -       | NA          |
| F2_III:9      | -       | -       | -           |
| F3_1:1        | -       | -       | +           |
| F3_41         | -       | -       | +           |
| F3_45         | -       | -       | -           |
| F3_II:2       | -       | -       | +           |
| F3_III:2      | -       | -       | NA          |
| F3_III:3      | -       | -       | NA          |

Joint X-ray ‘+’ means the patient has the typical manifestation of cortical erosion, soft tissue swelling, tophi or wormy appearance. NA, not applicable; HLA-B27, human leukocyte antigen B27; ANA, antinuclear antibody; ENA, extractable nuclear antigen.
| Sample   | Clean data (Gb) | Initial bases on target (Mb) | Alignment rate (%) | Base covered on target (Gb) | Fraction of effective bases on target (%) | Mean sequencing depth | 4x coverage (%) | 10x coverage (%) | 20x coverage (%) |
|----------|-----------------|------------------------------|--------------------|-------------------------------|------------------------------------------|----------------------|----------------|-----------------|-----------------|
| F1:II:1  | 13.44           | 50.34                        | 98.68              | 5.52                          | 44.60                                    | 97.53                | 99.00          | 98.50           | 97.20           |
| F2:II:1  | 13.91           | 50.34                        | 98.81              | 6.20                          | 44.70                                    | 123.26               | 99.00          | 98.60           | 97.70           |
| F3:II:1  | 13.24           | 50.34                        | 98.70              | 4.91                          | 39.10                                    | 109.70               | 99.00          | 98.60           | 97.60           |
| Mean     | 13.53           | 50.34                        | 98.73              | 5.54                          | 42.80                                    | 110.16               | 99.00          | 98.57           | 97.50           |
| Standard deviation | 0.35   | 0.00                         | 0.07               | 0.65                          | 3.20                                     | 12.87                | 0.00           | 0.06            | 0.26            |
Table SIV. Disease ontology enrichment analysis of genes in the coexpression network.

| Description                        | GeneRatio | BgRatio | P-value     | Adjust     | q-value   | Count |
|-------------------------------------|-----------|---------|-------------|------------|-----------|-------|
| Hyperuricemia                       | 9/40      | 20/8018 | 1.18x10^{-16} | 8.02E-14   | 2.51E-14  | 9     |
| Gout                                | 9/40      | 29/8018 | 6.80x10^{-15} | 2.32E-12   | 7.26E-13  | 9     |
| Acquired metabolic disease          | 25/40     | 930/8018| 2.18x10^{-14} | 4.97E-12   | 1.56E-12  | 25    |
| Disease of metabolism               | 26/40     | 1111/8018 | 1.22x10^{-13} | 2.08E-11   | 6.52E-12  | 26    |
| Obesity                             | 15/40     | 313/8018| 8.89x10^{-12} | 1.21E-09   | 3.80E-10  | 15    |
| Overnutrition                       | 15/40     | 322/8018| 1.34x10^{-11} | 1.52E-09   | 4.76E-10  | 15    |
| Nutrition disease                   | 15/40     | 338/8018| 2.68x10^{-11} | 2.61E-09   | 8.17E-10  | 15    |
| Artery disease                      | 22/40     | 961/8018| 5.78x10^{-11} | 4.93E-09   | 1.54E-09  | 22    |
| Hypertension                        | 18/40     | 594/8018| 8.52x10^{-11} | 6.46E-09   | 2.02E-09  | 18    |
| Cardiovascular system disease       | 24/40     | 1333/8018| 6.83x10^{-10} | 4.66E-08   | 1.46E-08  | 24    |
| GO ID      | Term                                      | Term P-value | Adjusted term P-value | Group P-value | Adjust group P-value | GO groups | % Associated genes | Number of genes |
|------------|-------------------------------------------|--------------|-----------------------|---------------|---------------------|-----------|--------------------|-----------------|
| GO:0015747 | Urate transport                           | 6.5x10^-21   | 2.3E-19               | 2.1E-21       | 1.7E-20             | Group0    | 90.00              | 9.00            |
| GO:0043252 | Sodium-independent organic anion transport | 2.2x10^-19   | 4.0E-18               | 2.1E-21       | 1.7E-20             | Group0    | 39.29              | 11.00           |
| GO:0060986 | Endocrine hormone secretion               | 8.5x10^-5    | 1.2E-4                | 1.3E-6        | 1.8E-6              | Group1    | 8.00               | 4.00            |
| GO:0050796 | Regulation of insulin secretion           | 3.1x10^-6    | 6.9E-6                | 1.3E-6        | 1.8E-6              | Group1    | 4.17               | 8.00            |
| GO:0015697 | Quaternary ammonium group transport       | 4.3x10^-15   | 3.9E-14               | 2.7E-12       | 1.0E-11             | Group2    | 70.00              | 7.00            |
| GO:0015838 | Amino-acid betaine transport              | 6.5x10^-9    | 2.1E-8                | 2.7E-12       | 1.0E-11             | Group2    | 66.67              | 4.00            |
| GO:0072488 | Ammonium transmembrane transport          | 1.5x10^-10   | 6.7E-10               | 2.7E-12       | 1.0E-11             | Group2    | 33.33              | 6.00            |
| GO:0015789 | Carnitine transport                       | 2.1x10^-9    | 7.8E-9                | 2.7E-12       | 1.0E-11             | Group2    | 80.00              | 4.00            |
| GO:0046942 | Carboxylic acid transport                 | 2.8x10^-11   | 1.7E-10               | 2.2E-11       | 5.8E-11             | Group3    | 4.55               | 15.00           |
| GO:0015718 | Monocarboxylic acid transport             | 2.2x10^-10   | 9.0E-10               | 2.2E-11       | 5.8E-11             | Group3    | 6.79               | 11.00           |
| GO:0015908 | Fatty acid transport                      | 1.1x10^-3    | 1.2E-3                | 2.2E-11       | 5.8E-11             | Group3    | 5.66               | 6.00            |
| GO:1905039 | Carboxylic acid transmembrane transport   | 1.0x10^-5    | 1.8E-5                | 2.2E-11       | 5.8E-11             | Group3    | 6.66               | 6.00            |
| GO:0006090 | Pyruvate metabolic process                | 3.7x10^-5    | 6.2E-5                | 2.2E-11       | 5.8E-11             | Group3    | 4.04               | 4.00            |
| GO:0090100 | Positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 8.9x10^-6 | 1.6E-5 | 4.8E-5 | 5.5E-5 | Group4 | 5.77 | 6.00 |
| GO:0032924 | Activin receptor signaling pathway        | 3.1x10^-5    | 5.4E-5                | 4.8E-5        | 5.5E-5              | Group4    | 10.26              | 4.00            |
| GO:0060389 | Pathway-restricted SMAD protein phosphorylation | 6.1x10^-7 | 1.5E-6 | 4.8E-5 | 5.5E-5 | Group4 | 9.09 | 6.00 |
| GO:0060393 | Regulation of pathway-restricted SMAD protein phosphorylation | 4.6x10^-7 | 1.2E-6 | 4.8E-5 | 5.5E-5 | Group4 | 9.52 | 6.00 |
| GO:0010862 | Positive regulation of pathway-restricted SMAD protein phosphorylation | 7.8x10^-8 | 2.3E-7 | 4.8E-5 | 5.5E-5 | Group4 | 12.77 | 6.00 |
| GO:008645  | Hexose transport                          | 3.2x10^-11   | 1.6E-10               | 3.2E-11       | 6.5E-11             | Group5    | 6.78               | 12.00           |
| GO:1905950 | Monosaccharide transmembrane transport    | 1.8x10^-16   | 2.2E-15               | 3.2E-11       | 6.5E-11             | Group5    | 42.86              | 9.00            |
| GO:0015758 | Glucose transport                         | 2.8x10^-11   | 2.0E-10               | 3.2E-11       | 6.5E-11             | Group5    | 6.86               | 12.00           |
| GO:0035428 | Hexose transmembrane transport            | 1.8x10^-16   | 2.2E-15               | 3.2E-11       | 6.5E-11             | Group5    | 42.86              | 9.00            |
| GO:0046323 | Glucose import                            | 4.7x10^-5    | 7.4E-5                | 3.2E-11       | 6.5E-11             | Group5    | 5.88               | 5.00            |
| GO:1904659 | Glucose transmembrane transport           | 1.8x10^-16   | 2.2E-15               | 3.2E-11       | 6.5E-11             | Group5    | 42.86              | 9.00            |
| GO:0042345 | Regulation of NF-kB import into nucleus   | 7.2x10^-5    | 1.0E-4                | 5.4E-5        | 5.4E-5              | Group6    | 8.33               | 4.00            |
| GO:0042990 | Regulation of transcription factor import into nucleus | 1.2x10^-3 | 1.2E-3 | 5.4E-5 | 5.4E-5 | Group6 | 4.00 | 4.00 |
| GO:0031663 | Lipopolysaccharide-mediated signaling pathway | 1.6x10^-4 | 2.0E-4 | 5.4E-5 | 5.4E-5 | Group6 | 6.78 | 4.00 |
| GO:0031058 | Positive regulation of histone modification | 9.7x10^-4 | 1.0E-3 | 5.4E-5 | 5.4E-5 | Group6 | 4.26 | 4.00 |
| GO:1905491 | Positive regulation of protein import     | 1.3x10^-4    | 1.7E-4                | 5.4E-5        | 5.4E-5              | Group6    | 4.72               | 5.00            |
| GO:0042307 | Positive regulation of protein import into nucleus | 1.2x10^-4 | 1.6E-4 | 5.4E-5 | 5.4E-5 | Group6 | 4.81 | 5.00 |
| GO:0042348 | Nuclear factor-kB import into nucleus     | 7.2x10^-5    | 1.0E-4                | 5.4E-5        | 5.4E-5              | Group6    | 8.33               | 4.00            |
| GO:0031663 | Lipopolysaccharide-mediated signaling pathway | 1.6x10^-4 | 2.0E-4 | 6.0E-9 | 9.6E-9 | Group7 | 6.78 | 4.00 |
| GO:0009124 | Nucleoside monophosphate biosynthetic process | 8.0x10^-12 | 1.6E-5 | 6.0E-9 | 9.6E-9 | Group7 | 5.88 | 6.00 |
| GO:0009142 | Nucleoside triphosphate biosynthetic process | 6.9x10^-4 | 7.5E-4 | 6.0E-9 | 9.6E-9 | Group7 | 4.65 | 4.00 |
| GO:0035085 | Positive regulation of histone modification | 9.7x10^-4 | 1.0E-3 | 6.0E-9 | 9.6E-9 | Group7 | 4.26 | 4.00 |
| GO:1905039 | Carboxylic acid transmembrane transport   | 1.0x10^-5    | 1.8E-5                | 6.0E-9        | 9.6E-9              | Group7    | 5.66               | 6.00            |
| GO ID       | GOTerm                                         | Term P-value | Adjusted term P-value | Group P-value | Adjust group P-value | GO groups | % Associated genes | Number of genes |
|-------------|------------------------------------------------|--------------|-----------------------|---------------|---------------------|-----------|-------------------|-----------------|
| GO:0006090  | Pyruvate metabolic process                     | 3.7x10^-5    | 6.2E-5                | 6.0E-9        | 9.6E-9              | Group7    | 4.48              | 6.00            |
| GO:0009127  | Purine nucleoside monophosphate biosynthetic process | 2.0x10^-6    | 5.0E-6                | 6.0E-9        | 9.6E-9              | Group7    | 7.41              | 6.00            |
| GO:0009145  | Purine nucleoside triphosphate biosynthetic process | 2.8x10^-4    | 3.3E-4                | 6.0E-9        | 9.6E-9              | Group7    | 5.88              | 4.00            |
| GO:0009156  | Ribonucleoside monophosphate biosynthetic process | 4.9x10^-6    | 1.0E-5                | 6.0E-9        | 9.6E-9              | Group7    | 6.38              | 6.00            |
| GO:0009201  | Ribonucleoside triphosphate biosynthetic process | 4.1x10^-4    | 4.6E-4                | 6.0E-9        | 9.6E-9              | Group7    | 5.33              | 4.00            |
| GO:0009168  | Purine ribonucleoside monophosphate biosynthetic process | 2.0x10^-6    | 5.0E-6                | 6.0E-9        | 9.6E-9              | Group7    | 7.41              | 6.00            |
| GO:0009206  | Purine ribonucleoside triphosphate biosynthetic process | 2.6x10^-4    | 3.2E-4                | 6.0E-9        | 9.6E-9              | Group7    | 5.97              | 4.00            |
| GO:0006754  | ATP biosynthetic process                       | 1.0x10^-4    | 1.3E-4                | 6.0E-9        | 9.6E-9              | Group7    | 7.69              | 4.00            |

GO, gene ontology.