**Table 2.** Summary of the most highly associated regions at *P* < 1 × 10-5 identified in Phase 1 for each of the 4 traits analysed genome-wide.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  | **Phase 1** | | | | **Phase 2a** | | **Phase 2b** | | |  |
| **Trait** | **Marker** | **Chr** | **Position** | **Effect Allele** | **Allele Frequency** | **𝛃a (95% CI)** | **P-value** | **I2 (%)** | **𝛃a (95% CI)** | **P-value** | **𝛃a (95% CI)** | | **P-value** | **Genesb** |
| DAS28 | rs2372751 | 3 | 81124821 | C | 0.49 | 0.17 (0.10, 0.24) | 2.8 ×10-6 | 0 | -0.02 (-0.14, 0.10) | 0.77 | 0.13 (-0.08, 0.34) | | 0.23 | *LINC02027* |
|  | rs58840038 | 5 | 125773164 | T | 0.31 | -0.17 (-0.24, -0.09) | 8.0 ×10-6 | 0 | -0.04 (-0.16, 0.09) | 0.57 | 0.03 (-0.16, 0.23) | | 0.73 | *GRAMD3* |
|  | rs6903359 | 6 | 21986214 | C | 0.13 | -0.23 (-0.34, -0.13) | 7.4 ×10-6 | 0 | 0.07 (-0.12, 0.27) | 0.46 | 0.10 (-0.17, 0.38) | | 0.45 | *CASC15* |
|  | rs168201 | 10 | 84610081 | G | 0.48 | 0.18 (0.12, 0.25) | 9.8 ×10-8 | 0 | -0.10 (-0.21, 0.02) | 0.091 | 0.08 (-0.10, 0.26) | | 0.38 | *NRG3* |
|  | rs57816977 | 18 | 4012466 | C | 0.18 | -0.22 (-0.31, -0.12) | 5.3 ×10-6 | 0 | 0.12 (-0.03, 0.27) | 0.10 | 0.00 (-0.24, 0.25) | | 1.00 | *DLGAP1* |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| loge(CRP+1) | rs79244342 | 6 | 54660244 | G | 0.09 | -0.26 (-0.37, -0.15) | 3.3 ×10-6 | 0 | -0.05 (-0.24, 0.13) | 0.57 | 0.02 (-0.34, 0.37) | | 0.93 | *KRASP1* |
|  | rs1889339 | 9 | 96053928 | G | 0.18 | 0.19 (0.11, 0.27) | 5.7 ×10-6 | 0 | -0.06 (-0.20, 0.07) | 0.38 | 0.17 (-0.05, 0.39) | | 0.14 | *WNK2* |
|  |  |  |  |  |  |  |  |  |  |  |  | |  |  |
| SJC28 | rs35179427 | 1 | 95670888 | A | 0.08 | 0.21 (0.12, 0.30) | 7.8 ×10-6 | 0 | -0.05 (-0.20, 0.09) | 0.49 | -0.25 (-0.54, 0.04) | | 0.10 | *RWDD3 TMEM56-RWDD3* |
|  | rs1453301 | 2 | 138080695 | A | 0.16 | 0.15 (0.09, 0.22) | 7.1 ×10-6 | 0 | -0.05 (-0.16, 0.06) | 0.39 | -0.03 (-0.22, 0.17) | | 0.79 | *THSD7B* |
|  | rs77458347 | 4 | 109896081 | T | 0.14 | 0.18 (0.10, 0.26) | 6.7 ×10-6 | 0 | -0.02 (-0.14, 0.10) | 0.77 | 0.18 (-0.10, 0.47) | | 0.21 | *COL25A1* |
|  | rs144940912 | 4 | 155092290 | T | 0.07 | 0.26 (0.15, 0.36) | 1.4 ×10-6 | 16 | 0.11 (-0.05, 0.27) | 0.20 | 0.11 (-0.32, 0.53) | | 0.62 |  |
|  | rs12663189 | 6 | 162730663 | C | 0.43 | 0.12 (0.07, 0.17) | 2.0 ×10-6 | 0 | -0.01 (-0.09, 0.08) | 0.87 | 0.04 (-0.12, 0.20) | | 0.64 | *PARK2* |
|  | rs314637 | 7 | 4421893 | A | 0.22 | 0.15 (0.08, 0.21) | 2.9 ×10-6 | 13 | 0.08 (-0.02, 0.18) | 0.11 | 0.19 (-0.01, 0.38) | | 0.06 |  |
|  | rs113798271 | 7 | 145059089 | G | 0.21 | 0.14 (0.08, 0.21) | 9.4 ×10-6 | 29 | 0.02 (-0.08, 0.12) | 0.67 | 0.02 (-0.16, 0.21) | | 0.81 |  |
|  | rs1175813 | 19 | 49737486 | G | 0.11 | 0.20 (0.12, 0.29) | 1.4 ×10-6 | 0 | -0.15 (-0.27, -0.03) | 0.012 | 0.00 (-0.24, 0.25) | | 0.98 |  |
|  | rs1042579 | 20 | 23028724 | A | 0.23 | 0.15 (0.08, 0.21) | 6.9 ×10-6 | 0 | 0.02 (-0.09, 0.12) | 0.76 | 0.24 (0.04, 0.44) | | 0.020 | *THBD* |
|  | rs2836915 | 21 | 40509189 | T | 0.31 | -0.13 (-0.18, -0.07) | 4.5 ×10-6 | 0 | -0.05 (-0.14, 0.04) | 0.26 | -0.06 (-0.24, 0.12) | | 0.51 |  |
|  |  |  |  |  |  |  |  |  |  |  |  | |  |  |
| TJC28 | rs10058818 | 5 | 56808696 | G | 0.21 | 0.17 (0.10, 0.25) | 2.4 ×10-6 | 8 | 0.06 (-0.06, 0.17) | 0.31 | -0.10 (-0.32, 0.12) | | 0.37 | *LINCR-0003* |
|  | rs10515242 | 5 | 95982675 | C | 0.06 | 0.28 (0.16, 0.40) | 4.8 ×10-6 | 0 | 0.17 (-0.01, 0.35) | 0.069 | -0.08 (-0.42, 0.26) | | 0.64 |  |
|  | rs2026708 | 6 | 21986895 | G | 0.14 | -0.22 (-0.31, -0.13) | 1.9 ×10-6 | 0 | 0.02 (-0.14, 0.19) | 0.78 | 0.06 (-0.19, 0.30) | | 0.65 | *CASC15* |
|  | rs2776898 | 6 | 37541111 | T | 0.35 | 0.16 (0.10, 0.23) | 9.9 ×10-7 | 0 | -0.11 (-0.21, -0.01) | 0.027 | 0.14 (-0.03, 0.32) | | 0.11 |  |
|  | rs114461403 | 7 | 16547268 | T | 0.33 | 0.15 (0.08, 0.21) | 7.5 ×10-6 | 0 | 0.00 (-0.11, 0.10) | 0.98 | -0.12 (-0.30, 0.07) | | 0.21 |  |
|  | rs28442057 | 15 | 55110958 | T | 0.34 | 0.14 (0.08, 0.21) | 7.9 ×10-6 | 0 | -0.01 (-0.11, 0.09) | 0.82 | 0.04 (-0.15, 0.22) | | 0.68 |  |
|  | rs12446816 | 16 | 14092341 | G | 0.38 | 0.15 (0.09, 0.21) | 5.1 ×10-6 | 0 | -0.01 (-0.11, 0.08) | 0.77 | 0.01 (-0.16, 0.17) | | 0.95 |  |
|  | rs9910936 | 17 | 42949168 | T | 0.28 | 0.15 (0.09, 0.22) | 6.7 ×10-6 | 0 | 0.05 (-0.06, 0.16) | 0.38 | 0.08 (-0.11, 0.28) | | 0.40 | *CCDC103 EFTUD2 GFAP KIF18B* |
| Abbreviations: DAS28, disease activity score in 28 joints; CRP, C-reactive protein; SJC28, swollen joint count 28; TJC tender joint count 28; Chr chromosome; 𝛃 beta; CI confidence interval; I2 Heterogeneity statistica Per-allele for change in outcome in number of standard deviations, positive values correspond to worse response. b SNP or supporting SNPs with P<5x10-5 located within gene. | | | | | | | | | | | | | | |