**SUPPLEMENTARY FIGURES AND TABLES**



Supplementary figure 1. Forest plot present the meta-analysis outcomes of pooled studies, showing the relation of cases and control PsA and the *TNF* -238 G>A cytokine



Supplementary figure 2. Forest plot present the meta-analysis outcomes of pooled studies, showing the relation of cases and control PsA and the *TNF* -308 G>A cytokine



Supplementary figure 3. Forest plot present the meta-analysis outcomes of pooled studies, showing the relation of cases and control PsA and the *TNF* -857 C>T cytokine



Supplementary figure 4. Forest plot present the meta-analysis outcomes of pooled studies, showing the relation of cases and control PsA and the *IL12B* (rs6887695) C>G cytokine



Supplementary figure 5. Forest plot present the meta-analysis outcomes of pooled studies, showing the relation of cases and control PsA and the *IL12B* (rs3212227) A>C cytokine



Supplementary figure 6. Forest plot present the meta-analysis outcomes of pooled studies, showing the relation of cases and control PsA and the *IL23A* (rs2066808) A>G cytokine



Supplementary figure 7. Forest plot present the meta-analysis outcomes of pooled studies, showing the relation of cases and control PsA and the *IL23R* (rs11209026) G>A cytokine

NEWCASTLE-OTTAWA QUALITY ASSESSMENT SCALE

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Study/ Year | Selection \*\*\*\* | Comparability\*\* | Exposure\*\*\* | Total |
| Eirís et al., 2014 [34] | \*\*\*\* | \*\* | \*\*\* | 9 |
| Cabaleiro et al., 2013 [35] | \*\*\* | \*\* | \*\*\* | 8 |
| Popa et al., 2013 [41] | \*\*\*\* | \*\* | \*\*\* | 9 |
| Jadon et al., 2013 [40] | \*\* | \* | \*\*\* | 6 |
| Yang et al. 2013 [42] | \*\*\*\* | \*\* | \*\*\* | 9 |
| Giardina et al., 2011[44] | \*\*\*\* | \* | \*\*\* | 8 |
| Bowes et al. 2011 [43] | \*\*\*\* | \* | \*\*\* | 8 |
| Popa et al., 2011 [45] | \*\*\*\* | \* | \*\*\* | 8 |
| Rahman et al., 2009 [47] | \*\*\*\* | \* | \*\*\* | 8 |
| Hüffmeier et al., 2009 [46] | \*\*\*\* | \*\* | \*\*\* | 9 |
| Filer et al., 2008 [36] | \*\*\*\* | \* | \*\*\* | 8 |
| Liu et al.,2008 [37] | \*\*\*\* | \*\* | \*\* | 8 |
| Reich et al., 2007 [39] | \*\*\* | \* | \*\*\* | 7 |
| Chang et al., 2007 [38] | \*\*\* | \* | \*\*\* | 7 |

PUBMED, WEB OF SCIENCE AND SCOPUS DATABASES BLOCKS

|  |  |  |  |
| --- | --- | --- | --- |
|  | **BLOCK 1** | **BLOCK 2** | **BLOCK 3** |
| **PubMed (Mesh)** | Polymorphism, Genetic OR Genotype OR Genetic Techniques | Cytokines | Spondylarthropathies |
| **PubMed (Free Term)** | Polymorphism, Genetic | Cytokines | Spondylarthropathies |
| **PubMed (Free Term)** | Polymorphism, Genetic | Cytokine | Spondylarthropathies |
| **Web of Knowledge (Topic)** | Polymorphism, Genetic OR Genotype OR Genetic Techniques | Cytokines OR Cytokine | Spondylarthropathies OR Spondylitis |
| **Web of Knowledge (Tittle)** | ----- | Cytokines OR Cytokine | Spondylitis OR Spondylarthropathies |
| **Scopus** | ----- | Cytokines OR Cytokine | Spondylarthropathies |

## Checklist PRISMA and other systematic review files

|  |  |  |  |
| --- | --- | --- | --- |
| **+Section/topic** | **#** | **Checklist item** | **Reported on page #** |
| **TITLE** | | |  |
| Title | 1 | Identify the report as a systematic review, meta-analysis, or both. | 1 |
| **ABSTRACT** | | |  |
| Structured summary | 2 | Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number. | 1 |
| **INTRODUCTION** | | |  |
| Rationale | 3 | Describe the rationale for the review in the context of what is already known. | 2,3 |
| Objectives | 4 | Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS). | N/A |
| **METHODS** | | |  |
| Protocol and registration | 5 | Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number. | No registration of protocol |
| Eligibility criteria | 6 | Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale. | N/A |
| Information sources | 7 | Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched. | 3,4 |
| Search | 8 | Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated. | 3-5 |
| Study selection | 9 | State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis). | 3-5 |
| Data collection process | 10 | Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data from investigators. | 6 |
| Data items | 11 | List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made. | N/A |
| Risk of bias in individual studies | 12 | Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis. | 3-5 |
| Summary measures | 13 | State the principal summary measures (e.g., risk ratio, difference in means). | 5 |
| Synthesis of results | 14 | Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I2) for each meta-analysis. | 5 |
| Risk of bias across studies | 15 | Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies). | N/A |
| Additional analyses | 16 | Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified. | N/A |
| **RESULTS** | | |  |
| Study selection | 17 | Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram. | 5,6 |
| Study characteristics | 18 | For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations. | 5-,8 |
| Risk of bias within studies | 19 | Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12). |  |
| Results of individual studies | 20 | For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot. | 5-8 (Table 2) |
| Synthesis of results | 21 | Present results of each meta-analysis done, including confidence intervals and measures of consistency. | 5-8 (Table 2) |
| Risk of bias across studies | 22 | Present results of any assessment of risk of bias across studies (see Item 15). | N/A |
| Additional analysis | 23 | Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see Item 16]). | N/A |
| **DISCUSSION** | | |  |
| Summary of evidence | 24 | Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers). | 8 - 13 |
| Limitations | 25 | Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias). | 13 |
| Conclusions | 26 | Provide a general interpretation of the results in the context of other evidence, and implications for future research. | 13 |
| **FUNDING** | | |  |
| Funding | 27 | Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review. | 14 |

*From:*  Moher D, Liberati A, Tetzlaff J, Altman DG, The PRISMA Group (2009). Preferred Reporting Items for Systematic Reviews and Meta-Analyses: The PRISMA Statement. PLoS Med 6(7): e1000097. doi:10.1371/journal.pmed1000097

For more information, visit: [**www.prisma-statement.org**](http://www.prisma-statement.org)

Supplementary table 1. Characteristics of the individual studies for PsA included in the meta-analysis of cytokine *TNFA*.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | -238G>A (rs361525) | | | | | | | | | | | | -308G>A (rs1800629) | | | | | | | | | | | | -857C>T (rs1799724) | | | | | | | | | | | | -1031T>C (rs1799964) | | | | | | | | | | | |  |
| Study (Year) | Population | Genotyping methods | HWE | Sample sizes | | G allele | | A allele | | Case | | | Control | | | Sample sizes | | G allele | | A allele | | Case | | | Control | | | Sample sizes | | C allele | | T allele | | Case | | | Control | | | Sample sizes | | T allele | | C allele | | Case | | | Control | | |  |
|  |  |  |  | C | Cc | C | Cc | C | Cc | GG | GA | AA | GG | GA | AA | C | Cc | C | Cc | C | Cc | GG | GA | AA | GG | GA | AA | C | Cc | C | Cc | C | Cc | CC | CT | TT | CC | CT | TT | C | Cc | C | Cc | C | Cc | TT | TC | CC | TT | TC | CC |  |
| Cabaleiro et al. (2013)[35] | Spanish (Caucasian) | PCR and Sequencing | Y | 33 | 160 | 0.88 | 0.85 | 0.12 | 0.15 | 26 | 6 | 1 | 128 | 17 | 15 | 33 | 160 | 0.92 | 0.81 | 0.08 | 0.19 | 28 | 5 | 0 | 115 | 29 | 16 | 33 | 160 | 0.76 | 0.88 | 0.24 | 0.12 | 18 | 14 | 1 | 135 | 13 | 12 | 33 | 160 | 0.77 | 0.73 | 0.23 | 0.27 | 20 | 11 | 2 | 88 | 57 | 15 |  |
| Giardina et al. (2011)\*[44] | German, Italian and English | TaqMan® and SSP-PCR | Y | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 895 | 1314 | 0.85 | 0.88 | 0.15 | 0.12 | 644 | 230 | 21 | 1032 | 261 | 21 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |  |
| Popa et al. (2011)[45] | Romanian | TaqMan® and RT-PCR | Y | 86 | 147 | 0.95 | 0.98 | 0.05 | 0.02 | 78 | 8 | 0 | 141 | 6 | 0 | 86 | 142 | 0.9 | 0.86 | 0.1 | 0.14 | 71 | 13 | 2 | 107 | 30 | 5 | 86 | 147 | 0.72 | 0.81 | 0.28 | 0.19 | 46 | 32 | 8 | 95 | 41 | 6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |  |
| Reich et al. (2007)[39] | German | TaqMan® assays | Y | 368 | 372 | 0.91 | 0.95 | 0.09 | 0.05 | 303 | 60 | 5 | 338 | 32 | 2 | 361 | 370 | 0.87 | 0.83 | 0.13 | 0.17 | 275 | 76 | 10 | 253 | 107 | 10 | 370 | 373 | 0.87 | 0.92 | 0.13 | 0.08 | 275 | 92 | 3 | 317 | 55 | 1 | 367 | 368 | 0.81 | 0.76 | 0.19 | 0.24 | 237 | 119 | 11 | 212 | 138 | 18 |  |
| Chang et al. (2007)[38] | Chinese | Sequencing | Y | 102 | 210 | 0.97 | 0.98 | 0.03 | 0.02 | NR | NR | NR | NR | NR | NR | 102 | 210 | 0.97 | 0.91 | 0.03 | 0.09 | NR | NR | NR | NR | NR | NR | 102 | 210 | 0.84 | 0.9 | 0.16 | 0.1 | NR | NR | NR | NR | NR | NR | 102 | 210 | 0.81 | 0.8 | 0.19 | 0.2 | NR | NR | NR | NR | NR | NR |  |

\* The values correspond to the sum of the three populations studied: German, Italian and English. C: case; Cc: control; HWE: Hardy-Weinberg equilibrium; Y: yes; N: no; NR: not reported; NA: not applicable; PCR: Polymerase Chain Reaction; MALDI-TOF: matrix-assisted laser desorption ionization-time of flight ; SSP-PCR: Single Specific Primer-Polymerase Chain Reaction; RT-PCR: Real Time-Polymerase Chain Reaction; RFLP-PCR: Restriction Fragment Length Polymorphism-Polymerase Chain Reaction.

Supplementary table 2. Characteristics of the individual studies for PsA included in the meta-analysis of cytokine *IL12B*.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | IL-12β (rs6887695) | | | | | | | | | | | | IL-12β (rs3212227) | | | | | | | | | | |  |
| Study (Year) | Population | Genotyping methods | HWE | Sample sizes | | G allele | | C allele | | Cases | | | Control | | | Sample sizes | | A allele | | C allele | | Cases | | | Control | | |
|  |  |  |  | C | Cc | C | Cc | C | Cc | GG | GC | CC | GG | GC | CC | C | Cc | C | Cc | C | Cc | AA | AC | CC | AA | AC | CC |
| Eirís et al. (2014)[34] | Northern Spanish | RT-PCR | Y | 91 | 426 | 0.75 | 0.61 | 0.25 | 0.39 | 48 | 41 | 2 | 167 | 187 | 72 | 91 | 426 | 0.83 | 0.83 | 0.17 | 0.17 | 64 | 23 | 4 | 294 | 115 | 17 |
| Jadon et al. (2013)[40] | English | iPLEX Sequenom MassARRAY® | Y | 261 | 5422 | 0.58 | 0.55 | 0.42 | 0.45 | NR | NR | NR | NR | NR | NR | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| Popa et al. (2013)[41] | Romanian | MassARRAY® using allele-specific MALDI-TOF | Y | 94 | 161 | 0.27 | 0.33 | 0.73 | 0.67 | NR | NR | NR | NR | NR | NR | 94 | 161 | 0.23 | 0.27 | 0.77 | 0.73 | NR | NR | NR | NR | NR | NR |
| Filer et al. (2008)[36] | British | MassARRAY® | Y | 519 | 2239 | 0.74 | 0.68 | 0.26 | 0.32 | 283 | 207 | 29 | 1021 | 1006 | 212 | 527 | 4681 | 0.85 | 0.81 | 0.15 | 0.19 | 382 | 136 | 9 | 3032 | 1478 | 171 |
| Liu et al. (2008)[37] | North-West region of England | Illumina HumanHap300 | Y | 576 | 480 | 0.79 | 0.72 | 0.21 | 0.28 | NR | NR | NR | NR | NR | NR |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | T allele | | G allele | | Cases | | | Control | | |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | C | Cc | C | Cc | TT | TG | GG | TT | TG | GG |
| Cabaleiro et al. (2013)[35] | Spanish (Caucasian) | TaqMan® Probes | Y | 33 | 160 | 0.67 | 0.69 | 0.33 | 0.31 | 13 | 17 | 3 | 81 | 60 | 19 | 33 | 160 | 0.85 | 0.80 | 0.15 | 0.20 | 24 | 8 | 1 | 99 | 54 | 4 |
| Hüffmeier et al. (2009)[46] | German | RT-PCR | Y | 723 | 926 | 0.77 | 0.69 | 0.23 | 0.31 | NR | NR | NR | NR | NR | NR | 732 | 913 | 0.85 | 0.79 | 0.15 | 0.21 | NR | NR | NR | NR | NR | NR |

C: case; Cc: control; HWE: Hardy-Weinberg equilibrium; Y: yes; N: no; NR: not reported; NA: not applicable; MALDI-TOF: matrix-assisted laser desorption ionization-time of flight ; RT-PCR: Real Time-Polymerase Chain Reaction; RFLP-PCR: Restriction Fragment Length Polymorphism-Polymerase Chain Reaction

Supplementary table 3. Characteristics of the individual studies for PsA included in the meta-analysis of cytokine *IL23A*.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | IL-23A (rs2066808) | | | | | | | | | | | | IL-23A (rs11171806) | | | | | | | | | | | |
| Study (Year) | Population | Genotyping methods | HWE | Sample sizes | | A allele | | G allele | | Cases | | | Control | | | Sample sizes | | A allele | | G allele | | Cases | | | Control | | |
|  |  |  |  | C | Cc | C | Cc | C | Cc | AA | AG | GG | AA | AG | GG | C | Cc | C | Cc | C | Cc | AA | AG | GG | AA | AG | GG |
| Eirís et al. (2014)[34] | Northern Spanish | RT-PCR | Y | 91 | 426 | 0.97 | 0.92 | 0.03 | 0.08 | 86 | 5 | 0 | 362 | 63 | 1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| Bowes et al. (2011)[43] | English and Irish | Sequencing | Y | 902 | 5529 | 0.96 | 0.93 | 0.04 | 0.07 | 832 | 68 | 2 | 4770 | 733 | 26 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
|  |  |  |  |  | | C allele | | T allele | |  | | |  | | |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  | C | Cc | C | Cc | CC | CT | TT | CC | CT | TT |  |  |  |  |  |  |  |  |  |  |  |  |
| Popa et al. (2013)[41] | Romanian | MassARRAY® using allele-specific MALDI-TOF | Y | 94 | 161 | 0.96 | 0.92 | 0.04 | 0.08 | NR | NR | NR | NR | NR | NR | 94 | 161 | 0.03 | 0.08 | 0.97 | 0.92 | NR | NR | NR | NR | NR | NR |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

C: case; Cc: control; HWE: Hardy-Weinberg equilibrium; Y: yes; N: no; NR: not reported; NA: not applicable; MALDI-TOF: matrix-assisted laser desorption ionization-time of flight ; RT-PCR: Real Time-Polymerase Chain Reaction.

Supplementary table 4. Characteristics of the individual studies for PsA included in the meta-analysis of cytokine *IL23R* (SNP rs11209026. rs7530511, rs2201841)

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  | IL-23R (rs11209026) | | | | | | | | | | | | IL-23R (rs7530511) | | | | | | | | | | | | IL-23R (rs2201841) | | | | | | | | | | | |
| Study (Year) | Population | Genotyping methods | HWE | Sample sizes | | A allele | | G allele | | Cases | | | Control | | | Sample sizes | | C allele | | T allele | | Cases | | | Control | | | Sample sizes | | C allele | | T allele | | Cases | | | Control | | |
|  |  |  |  | C | Cc | C | Cc | C | Cc | AA | AG | GG | AA | AG | GG | C | Cc | C | Cc | C | Cc | CC | CT | TT | CC | CT | TT | C | Cc | C | Cc | C | Cc | CC | CT | TT | CC | CT | TT |
| Yang et al. (2013)[42] | Chinese | MassARRAY® | Y | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 379 | 1181 | 0.7 | 0.73 | 0.3 | 0.27 | NR | NR | NR | NR | NR | NR |
| Jadon et al. (2013)[40] | English | iPLEX Sequenom MassARRAY® | Y | 261 | 4941 | 0.12 | 0.12 | 0.88 | 0.88 | NR | NR | NR | NR | NR | NR | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| Popa et al. (2013)[41] | Romanian | MassARRAY® using allele-specific MALDI-TOF | Y | 94 | 161 | 0.95 | 0.94 | 0.05 | 0.06 | NR | NR | NR | NR | NR | NR | 94 | 161 | 0.12 | 0.12 | 0.88 | 0.88 | NR | NR | NR | NR | NR | NR | 94 | 161 | 0.37 | 0.34 | 0.63 | 0.66 | NR | NR | NR | NR | NR | NR |
| Cabaleiro et al. (2013)[35] | Spanish (Caucasian) | TaqMan® Probes | Y | 33 | 160 | 0.02 | 0.07 | 0.98 | 0.93 | 0 | 1 | 32 | 1 | 20 | 138 | 33 | 160 | 0.85 | 0.86 | 0.15 | 0.14 | 24 | 8 | 1 | 118 | 40 | 2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| Hüffmeier et al. (2009)[46] | German | RT-PCR | Y | 732 | 924 | 0.05 | 0.07 | 0.95 | 0.93 | NR | NR | NR | NR | NR | NR | 739 | 931 | 0.88 | 0.87 | 0.12 | 0.13 | NR | NR | NR | NR | NR | NR | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| Rahman et al. (2009)\*[47] | Canadian (Northern European ancestry) | MassARRAY® | Y | 247 | 228 | 0.04 | 0.08 | 0.96 | 0.92 | NR | NR | NR | NR | NR | NR | 247 | 228 | 0.88 | 0.87 | 0.12 | 0.13 | NR | NR | NR | NR | NR | NR | 247 | 228 | 0.30 | 0.31 | 0.70 | 0.69 | NR | NR | NR | NR | NR | NR |
| Rahman et al. (2009)\*\*[47] |  |  |  | 249 | 248 | 0.04 | 0.07 | 0.96 | 0.93 | NR | NR | NR | NR | NR | NR | 249 | 248 | 0.88 | 0.9 | 0.12 | 0.10 | NR | NR | NR | NR | NR | NR | 249 | 248 | 0.30 | 0.33 | 0.70 | 0.67 | NR | NR | NR | NR | NR | NR |
| Filer et al. (2008)[36] | British | MassARRAY® | Y | 519 | 2209 | 0.05 | 0.07 | 0.95 | 0.93 | 2 | 48 | 469 | 10 | 277 | 1922 | 510 | 2147 | 0.1 | 0.12 | 0.9 | 0.88 | 7 | 88 | 415 | 36 | 448 | 1663 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | A allele | | G allele | |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | C | Cc | C | Cc | AA | AG | GG | AA | AG | GG |
| Eirís et al. (2014)[34] | Northern Spanish | RT-PCR | Y | 91 | 426 | 0.03 | 0.08 | 0.97 | 0.92 | 0 | 6 | 85 | 4 | 60 | 362 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 91 | 426 | 0.74 | 0.65 | 0.26 | 0.35 | 50 | 34 | 7 | 175 | 200 | 51 |
|  |  |  |  |  |  | G allele | | T allele | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  | C | Cc | C | Cc | GG | GT | TT | GG | GT | TT |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Liu et al. (2008)[37] | North-West of England | Illumina HumanHap300 | Y | 576 | 480 | 0.96 | 0.92 | 0.04 | 0.08 | NR | NR | NR | NR | NR | NR | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

\*NewFoundland; \*\* Toronto; C: case; Cc: control; HWE: Hardy-Weinberg equilibrium; Y: yes; N: no; NR: not reported; NA: not applicable; PCR: Polymerase Chain Reaction; MALDI-TOF: matrix-assisted laser desorption ionization-time of flight ; RT-PCR: Real Time-Polymerase Chain Reaction.

Supplementary table 5. Characteristics of the individual studies for PsA included in the meta-analysis of cytokine *IL23R* (SNP rs7517847. rs1004819, rs10489629, rs11465804. rs1495965, rs10889677 and rs1343151)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Study (Year) |  | Popa et al. (2013)[41] | Rahman et al. (2009)\*[47] | Rahman et al. (2009)\*\*[47] |
| IL-23R (rs7517847) |  |  |  |  |
| Sample sizes | C | 94 | 247 | 249 |
| Cc | 161 | 228 | 248 |
| G allele | C | 0.36 | 0.44 | 0.46 |
| Cc | 0.35 | 0.44 | 0.45 |
| T allele | C | 0.64 | 0.56 | 0.54 |
| Cc | 0.65 | 0.56 | 0.55 |
| IL-23R (rs1004819) |  |  |  |  |
| Sample sizes | C | 94 | 247 | 249 |
| Cc | 161 | 228 | 248 |
| C allele | C | 0.41 | 0.69 | 0.72 |
| Cc | 0.34 | 0.69 | 0.68 |
| T allele | C | 0.59 | 0.31 | 0.28 |
| Cc | 0.66 | 0.31 | 0.32 |
| IL-23R (rs10489629) |  |  |  |  |
| Sample sizes | C | 94 | 247 | 249 |
| Cc | 161 | 228 | 248 |
| A allele | C | 0.43 | 0.54 | 0.52 |
| Cc | 0.42 | 0.52 | 0.54 |
| G allele | C | 0.57 | 0.46 | 0.48 |
| Cc | 0.58 | 0.48 | 0.46 |
| IL-23R (rs11465804) |  |  |  |  |
| Sample sizes | C | 94 | NA | NA |
| Cc | 161 | NA | NA |
| G allele | C | 0.05 | NA | NA |
| Cc | 0.06 | NA | NA |
| T allele | C | 0.95 | NA | NA |
| Cc | 0.94 | NA | NA |
| IL-23R (rs1495965) |  |  |  |  |
| Sample sizes | C | 94 | 247 | 249 |
| Cc | 161 | 228 | 248 |
| A allele | C | 0.48 | 0.56 | 0.57 |
| Cc | 0.47 | 0.55 | 0.59 |
| G allele | C | 0.52 | 0.44 | 0.43 |
| Cc | 0.53 | 0.46 | 0.41 |
| IL-23R (rs10889677) |  |  |  |  |
| Sample sizes | C | 94 | 247 | 249 |
| Cc | 161 | 228 | 248 |
| A allele | C | 0.38 | 0.70 | 0.70 |
| Cc | 0.34 | 0.69 | 0.67 |
| C allele | C | 0.62 | 0.30 | 0.30 |
| Cc | 0.66 | 0.31 | 0.33 |
| IL-23R (rs1343151) |  |  |  |  |
| Sample sizes | C | 94 | 247 | 249 |
| Cc | 161 | 228 | 248 |
| C allele | C | 0.28 | 0.70 | 0.65 |
| Cc | 0.30 | 0.66 | 0.66 |
| T allele | C | 0.72 | 0.31 | 0.35 |
| Cc | 0.70 | 0.34 | 0.34 |

\*NewFoundland; \*\* Toronto; C: case; Cc: control; NA: not applicable.