Supplementary Table 1

Participants’ information and clinical characteristics.

| Characteristics | RA       | OA       | HD       |
|-----------------|----------|----------|----------|
| Number          | 82       | 36       | 64       |
| Age (years)a    | 55(45.25,62.25) | 52.5(35, 62.25) | 50(45.75, 52.75) |
| Sex (M/F)       | 20/62    | 10/26    | 18/46    |
| Anti-CCP(IU/ml)a| 130.6(79.65,174) | /       | /       |
| RF((IU/ml)b     | 123.5(48.63,383.3) | /       | /       |
| CRP(mm/h)b      | 18.18±21.03 | /       | /       |
| ESR(mg/ml)b     | 39.28±24.3 | /       | /       |

a Expressed as the median (25th to 75th percentile).
b Expressed as the means ± SD (standard deviation).

Abbreviations: RA, rheumatoid arthritis; OA, osteoarthritis; HD, healthy donors; anti-CCP, anti-cyclic citrullinated peptide antibody; RF, rheumatoid factor; CRP, C-reactive protein; ESR, erythrocyte sedimentation rate.
**Supplementary Table 2**

| Species  | Gene Name | Sequence (5′-3′)                                      |
|----------|-----------|------------------------------------------------------|
| Homo sapiens | YY1       | Fw: AAAACGACACCAACTTGTTTCATAC                       |
|           |           | Rv: AAGTCCAGTGAAGAGCGGTTCC                         |
|           | T-bet     | Fw: AACCCAGTTCATGCGTGAC                            |
|           |           | Rv: ATGGACTCAAGTGTCTCCCGGAA                        |
|           | IL-17A    | Fw: GCTGGGAGAGATACCTGGTC                           |
|           |           | Rv: TAATGAGTGTAGTCCGAATGAG                         |
|           | IL-22     | Fw: AAATAACAAATTAGATGCCCA                         |
|           |           | Rv: TAAAACAAAGTGGCATAGGT                           |
|           | Foxp3     | Fw: CAAGTTCCACAACATGCCGACC                        |
|           |           | Rv: TCCAGTCATGCCACCGGTCCAC                        |
|           | RORγt     | Fw: GGCACCCTACCTTTACCTG                            |
|           |           | Rv: TCTTGGCCTTCATTGTACCTCT                       |
|           | STAT3     | Fw: TCTGCGCTTTTCTGTAAGCAA                          |
|           |           | Rv: AAAGGCTATGCTGATAACGT                          |
|           | Runx1     | Fw: TTCTGAAAAGCACCAATTAGCC                        |
|           |           | Rv: AAACAAATGTATAGCCTACAGG                        |
|           | GAPDH     | Fw: CACATGGCCTCCAAGAGGATAA                         |
|           |           | Rv: TGAGGGTCTCTCTCTCTTCTCTTG                     |
|           | miR-124-3p| Fw: CGTAAGGCCAGCCGGTAA                             |
|           |           | Rv: AGTGCAGGGTGCGAGGTATT                          |
|           |           | Rr: GTCGTATCCAGTGACCGAGGTATT CTGTCCGACTGGATA       |
|           |           | CGACATGCC                                          |
|           | miR-218-5p| Fw: GCGCGTGTTGCTTTGATCTAA                         |
|           |           | Rv: AGTGCAGGCGTCCAGGTAAT                          |
|           |           | Rr: GTCGTATCCAGTGCAGGGGTCCGAGGTATTCTGCAGCTGGATA   |
|           |           | CGACACATGG                                          |
|           | let-7-5p  | Fw: GCGCGTGAGGTAGTGTTG                            |
|           |           | Rv: AGTGCAGGGTCCAGGTAAT                          |
|           |           | Rr: GTCGTATCCAGTGCAGGGGTCCGAGGTATTCTGCAGCTGGATA   |
|           |           | CGACACACC                                          |
|           | U6        | Fw: AAACGCTCTGCAAAATTTGC                              |
|           |           | Rv: CTCGCTCTGCGACGACA                            |
|           |           | Rr: CTCGCTCTGCGACGACA                            |

Abbreviations: Fw, Forward primer; Rv: Reverse primer; Rt: Reverse transcription primer.
### Supplementary Table 3

Primers used for plasmids cloning.

| Species       | Primer Designation | Sequence (5′-3′)                                                                 |
|---------------|--------------------|--------------------------------------------------------------------------------|
| Homo sapiens  | LV-YY1-shRNA       | Fw: GATCC-**GACGACGACTACATTTGAAACAATTTGTAATGCTGCTGTC-TTTTTG**                   |
|               |                    | Rv: AATTCAAAAAAG-CCTCCTGATTATCTCAGATTAT-TCTTCTGAA-**ATATCTGAATAATCAGG-AGGCG**   |
|               | WT-T-bet promoter  | Fw: CGGGGTACCAGGAAAAAGAGGGCAACCCG                                               |
|               | MUT-T-bet promoter | Fw: CCGCTCAGCTCTACTAGCTCAGCGAGCCG                                               |
|               | YY1-let7-WT        | Fw: CACTTGGAATTGCCTCAGGAAAGCTCTGTTAGGAG                                         |
|               |                    | Rv: TCCGAAGCAATCCCAAGTGGGACTCGGTAGGGCG                                           |
|               | YY1-miR-124-WT     | Fw: CCCCTGTGGCTCTGTGGAATTTTGAATGCTTATTTGTGA                                     |
|               |                    | Rv: ATCTGATGAAACATTTAACCCTT                                                    |
|               | YY1-miR-218-WT     | Fw: GAATAGGAAAGCGTCTGTAAGCACGATTTCTTAT                                          |
|               |                    | Rv: TTCCTTTTGTGTCAGAATACT                                                      |
|               | YY1-miR-124-MUT    | Fw: CCCCTGTGGCTCTGTGGAATTTTGAACACGGAATTGTG                                       |
|               | let-7-5p mimics    | Fw: AACGAGGCTCCAGTGCAGAATGCTGTTAGGAG                                          |
|               | 3p mimics         | Rv: AATTCAAAAAAG-GATACCTGGCATTGACCTCT-TTCAAGAG-AGAGGCTCACATGCCAGGTAC-TTTTTG     |
|               | miR-218-5p mimics | Fw: GAATAGGAAAGGGTATGCAGTCTGTAAGCACGATTTCTTAT                                      |
|               | let-7-5p inhibitor | Fw: CCCCTGTGGCTCTGTGGAATTTTGAACACGGAATTGTG                                       |
|               | inhibitor         | Rv: AATTCAAAAAAG-GATACCTGGCATTGACCTCT-TTCAAGAG-AGAGGCTCACATGCCAGGTAC-TTTTTG     |
|               | miR-218-5p inhibitor | Fw: GAATAGGAAAGGGTATGCAGTCTGTAAGCACGATTTCTTAT                                       |
|               | NC mimics         | Fw: CCCCTGTGGCTCTGTGGAATTTTGAACACGGAATTGTG                                       |
|               | inhibitor         | Rv: AATTCAAAAAAG-GATACCTGGCATTGACCTCT-TTCAAGAG-AGAGGCTCACATGCCAGGTAC-TTTTTG     |
| Mus musculus  | LV-YY1-shRNA907    | Fw: GATCC-**GGATACCTGGCATTGACCTCT**-TTCAAGAG-AGAGGCTCACATGCCAGGTAC-TTTTTG     |
|               |                   | Rv: AATTCAAAAAAG-GATACCTGGCATTGACCTCT-TTCAAGAG-AGAGGCTCACATGCCAGGTAC-TTTTTG     |
|               | LV-YY1-shRNA1009  | Fw: GATCC-**GCCCTCATAAAGAGCTGCACAA-**TTCAAGAGA-TTGTGCAGCTTTTATAGGGG-TTTTTTG** |
|               |                   | Rv: AATTCAAAAAAG-GATACCTGGCATTGACCTCT-TTCAAGAG-AGAGGCTCACATGCCAGGTAC-TTTTTG     |

Abbreviations: Fw, forward primer; Rv: reverse primer; WT, wild-type; MUT, mutant; LV, lentivirus; shRNA, short hairpin RNA; NC, normal control.
## Supplementary Table 4

### Primers used for ChIP PCR.

| Primer | Sequence (5’-3’)                      | Product Size(bp) | Position on T-bet Gene Locus |
|--------|---------------------------------------|------------------|-------------------------------|
| P1     | Fw: GGCAAGAACTTCCCTGGTCCT            | 98               | -1821~1724                    |
|        | Rv: CTGGTACTGTCACTGATCCGGT           |                  |                               |
| P2     | Fw: AAATTATATATTGTGCTGTG            | 127              | -1321~1195                    |
|        | Rv: GTGGAATGCGGCTGATTTA            |                  |                               |
| P3     | Fw: CACCCTCTCTGTAAGGCTT            | 100              | -879~780                      |
|        | Rv: GGTGGACTTCAGGCAAGGAA          |                  |                               |
| P4     | Fw: CTTCTAGTGTGCCCCGTGCTC        | 126              | -405~280                      |
|        | Rv: GAGACTTCAAAGCTGGGCTGA        |                  |                               |

Abbreviations: Fw, forward primer; Rv: reverse primer.
Supplementary Figure 1

Supplementary Figure 1. Representative scheme showing the flow-cytometry gating strategy used for the analysis of CD4^+IL17A^+IFN-γ^+ cells or CD4^+IL17A^+GM-CSF^+ cells. The proportions of CD4^+IL17A^+IFN-γ^+ cells or CD4^+IL17A^+GM-CSF^+ cells were determined from PBMCs or polarized naïve CD4^+ cells. Cells were gated by FSC-A/SSC-A (A and F) to exclude debris and then by FSC-H/FSC-W (B and D) to exclude cell doublets. Next, Dead cells were excluded by live/dead staining (C and H) and CD4^+ cells (CD4^+/SSC-A) were further gated (D and I). Lastly, cells to be analysed were gated by IL-17A and IFN-γ/GM-CSF (E and J) to determine the cell proportions.
**Supplementary Figure 2**

Supplementary Figure 2. The sorting efficiency of CD4⁺CD45RA⁺ cells from PBMCs. Human naïve CD4⁺ T cells from PBMCs (A) were purified following manufacturer’s instruction. Purity check was performed after sorting and sorted fractions with ≥ 90% purity (B) were used for further experiments.