

Table S1. Probes and primers of Q-PCR for human DUSP mRNA levels

| Gene | Accession Number | Probe Sequence | Sense Primer Sequence | Anti-sense Primer Sequence |
|-------------|-------------------------|-----------------------------|------------------------------|-----------------------------------|
| DUSP1 | NM_004417 | AACTCAGCACATTTCGGGACCAAT | GCAGTTATGGTGATGACTTA | CGGGAATAATACTGGTAGG |
| DUSP2 | NM_004418 | TGAAAGGCTCACAGACAGACACAC | GATGGGTGTGTCATGTTG | CTGAGCACAAATAATTTTCCA |
| DUSP3 | NM_004090 | CCCAGTTGTCCTGTTTCTGTA ACTT | GCACATAAAGAAGCTTGC | GCATCTTAGGCCTTACAC |
| DUSP4 | NM_001394 | TGTATTCGGAGTCCTTATTGCCATTCT | CTCCTTCCCCATCATTTC | GCTCTAAGTTGGAGTGTTT |
| DUSP5 | NM_004419 | AGAGCCCTCATCAGCCAGTG | GGATGTAAAACCCATTTTAC | AGCTGACATTTACCACTG |
| DUSP6 | NM_001946 | TTCCGCACTTGGTAACCTTGTCTA | TCTGCAATCTACGTGAAA | GGAGCAAATCTCTCTGTTA |
| DUSP7 | NM_001947 | TCGCCTGTGATGACTGCTGC | CAGTCTGACTTAGCTCTG | GGCAGAAAATGCAAAGAC |
| DUSP8 | NM_004420 | AGTCCTGTTCCCGTTCCTCT | CTGTCATCCCTCCTTTCA | AACGCAACAGACATATGG |
| DUSP9 | NM_001395 | CCCAGTGATCCCGTCAAGACAT | GTCACCTCCCTGTTTCTC | CACCCTCACTACAAAGA |
| DUSP10 | NM_007207 | AGCCACTGACAGCAACAAGCA | GGCCTGTTCAACTACAAG | GCTTCCTCAATGAACTCA |
| DUSP11 | NM_003584 | CAACCAGTCCACAATAAGCCTGTAA | CCAGGTCAAGTGATTTTG | GATGGTGTCTCTGGTAAA |
| DUSP12 | NM_007240 | TGTGCTGCCTTTGCTTCTTATCATTC | GGAAGAACTTGCAGATG | CCATGTAAAGCATAGTTTCC |
| DUSP13 | NM_001007271 | CCTAGAGCCTGCTACTCCATCTG | CACAGAAGATGGTGGAAG | CACACTTGATGCTGTTTC |
| DUSP14 | NM_007026 | TTAGTGCCACTGAAGCCTGC | ACACCTGATGCCTTACTG | CCTCCCTCCCTATCTCTTA |
| DUSP15 | NM_080611 | ATCCACTGCTGCCGCCTTAAT | GCACTTCAAAGAATGTATCA | CGTCACAGTCATCACATA |
| DUSP16 | NM_030640 | TTCCCGTGACCTGTTCTCTGAC | GAGAGCCCCTTTGAAAAG | CCGAAAAGCTAGACTGAC |
| DUSP18 | NM_152511 | ACCCTGGCTCAACCTGTTACCCG | CGTTGCCGTAGAGATGG | GGTCTTCAGAGAAATCCTGG |
| DUSP19 | NM_080876 | CTCTTGATATGTACGAAGCTGCTCCAT | TCCTGATGAATTCTGAACAA | CCTGTATTCTGTCCACTTA |
| DUSP21 | NM_022076 | CCCTTTAACAAGGCACCATCCG | GCACCAAGACTGAACTTG | CGTTCAAAACTCCAACCC |
| DUSP22 | NM_020185 | AATATGTGTCACCTTGTTCTTGCTCA | CCCTGTAACATGCCATAG | GCACTATCATGGACAGAC |
| DUSP23 | NM_017823 | AGCAGTCTTCCAGTTCTACCAGC | GAGACCTATGAGCAGGAG | CAGTGTCTTCAGCCAATG |
| DUSP24 | NM_016086 | CATCACCTTGGCTCTGTCATTCTG | GTGTCACTTCATTGAAATTCA | TGAGGTAGGCTATGATGG |
| DUSP26 | NM_024025 | TCTCTTCGCTGTCTGTCTCTATGCT | CTCTCTCCCTCACCAAAA | GGGTTCTCTGTCTGGTTC |
| DUSP27 | NM_001080426 | AGACCTCATCCACCTCATTCCAG | TCAGGGAGAAGATGGATG | CACACTTCTCAGCTATG |
| GAPDH | NM_002046 | CCTTCATTGACCTCAACTACATGGTT | CTGGTAAAGTGGATATTGTTG | CCCCTTATTGTTTGGAG |

Table S2. Demographic characteristics of the second batch of AS patients and healthy controls

| | AS N = 9 | Healthy controls N = 4 | <i>p</i> value |
|--------------------------|-------------------|---------------------------|----------------|
| Age, years | 49.8 ± 12.4 | 41.5 ± 2.1 | 0.148 |
| Gender, male | 4 (44.4) | 2 (50.0) | 1.000 |
| Disease duration, years | 17.0 (10.5, 25.5) | - | - |
| HLA-B27 positivity | 9 (100.0) | - | - |
| mSASSS (0-72) | 2 (0, 19) | - | - |
| Sacroiliitis grade (0-4) | 2 (2, 3.5) | - | - |
| ESR, mm/hour | 13.6 ± 9.0 | - | - |
| CRP, mg/dl | 0.1 (0.1, 0.4) | - | - |
| BASDAI (0-10) | 2.0 ± 0.8 | - | - |
| BASFI score (0-10) | 2.9 ± 1.9 | - | - |
| BAS-G score (0-10) | 2.4 ± 1.9 | - | - |
| Biologic used | 0 (0.0%) | - | - |

Abbreviation: BASDAI, Bath Ankylosing Spondylitis Disease Activity Index; BASFI, BAS Functional Index; BAS-G, BAS Patient Global Score; CRP, C-reactive protein; ESR, erythrocyte sedimentation rate; HLA, human leukocyte antigen; mSASSS, modified Stokes Ankylosing Spondylitis Spinal Score. Data are presented as frequency (percentage), mean ± standard deviation, or median (interquartile range).