

# Whole-blood Gene Expression Profiling in Ankylosing Spondylitis Shows Upregulation of Toll-like Receptor 4 and 5

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**ABSTRACT. Objective.** To identify differentially expressed genes in peripheral blood cells (PBC) of patients with ankylosing spondylitis (AS) relative to healthy controls and controls with systemic inflammation.

**Methods.** We investigated PBC samples of 16 patients with AS and 14 matched controls, in addition to systemic lupus erythematosus (SLE) and systemic sclerosis (SSc) samples utilizing Illumina Human Ref-8 BeadChips. Candidate genes were confirmed using quantitative PCR. Subsequently, these genes were also validated in a separate sample of 27 patients with AS [before and after anti-tumor necrosis factor (anti-TNF) treatment] and 27 matched controls.

**Results.** We identified 83 differentially expressed transcripts between AS patients and controls. This gene list was filtered through the lists of differentially expressed transcripts in SLE and SSc, which resulted in identification of 52 uniquely dysregulated transcripts in AS. Many of the differentially expressed genes belonged to Toll-like receptor (TLR) and related pathways. *TLR4* and *TLR5* were the only dysregulated TLR subtypes among AS patients. We confirmed the overexpression of *TLR4* and *TLR5* in AS patients in comparison to controls ( $p = 0.012$  and  $p = 0.006$ , respectively) and SLE ( $p = 0.002$ ,  $p = 0.008$ ) using quantitative PCR in the same sample. Similarly, *TLR4* ( $p = 0.007$ ) and *TLR5* ( $p = 0.012$ ) were significantly upregulated among the AS patients before anti-TNF treatment in the confirmatory sample. *TLR4* ( $p = 0.002$ ) and *TLR5* ( $p = 0.025$ ) decreased significantly after anti-TNF treatment.

**Conclusion.** PBC gene expression profiling in AS shows an upregulation of *TLR4* and *TLR5*. This supports the importance of TLR subtypes in the pathogenesis of AS that are responsible for the immune response to Gram-negative bacteria. (J Rheumatol First Release Oct 15 2010; doi:10.3899/jrheum.100469)

## Key Indexing Terms:

ANKYLOSING SPONDYLITIS      TOLL-LIKE RECEPTORS      IMMUNE SYSTEM  
AUTOIMMUNITY                      BACTERIA                      GENE EXPRESSION PROFILING

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Ankylosing spondylitis (AS) is a chronic inflammatory arthritis with a predilection for the spine and sacroiliac joints that can lead to new bone formation and ultimately ankylosis. AS is the prototype of spondyloarthropathies (SpA), a related family of disorders with common clinical features and with a strong association with HLA-B27. However, HLA-B27 accounts only for ~45% of the genetic risk in AS. Genome-wide association studies have identified several other non-HLA susceptibility genes such as IL23R and ERAP1 in AS<sup>1,2</sup>. Other diseases belonging to the spectrum of SpA are reactive arthritis, psoriatic arthritis, and arthritis in patients with inflammatory bowel disease<sup>3</sup>.

Functional studies also have been undertaken to identify candidate genes and pathways that play a role in the pathogenesis of SpA. Microarray data from synovium suggest a proinflammatory profile. Gu, *et al* demonstrated increased RNA expression of monocyte chemoattractant protein 1

(MCP-1), interleukin 8 (IL-8), IL-1 $\beta$ , endothelial-monocyte activating polypeptide II, interferon- $\gamma$ , tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), and BiP in SpA synovial fluid mononuclear cells<sup>4</sup>. Rihl, *et al* found elevated levels of IL-7 transcript and protein in sacroiliac joint cells<sup>5</sup>. On the other hand, transcriptional profiling of isolated peripheral blood mononuclear cells (PBMC) by several groups showed that transcripts involved in the inflammatory response are differentially expressed in SpA patients, but reports on the nature of these changes seem to vary. The earliest PBMC study indicated increased expression of proinflammatory proteins such as CXCR4/SDF-1<sup>6</sup>. However, recent reports suggest decreased immune responsiveness of the PBMC. Smith, *et al* found a “reverse interferon (IFN) signature” characterized by decreased expression of IFN- $\gamma$  and IFN- $\gamma$ -inducible genes in AS macrophages<sup>7</sup>, and Duan, *et al* found that AS PBMC display an immunosuppressive phenotype as shown by underexpression of NR4A2, TNFAIP3, and CD69<sup>8</sup>.

We investigated the whole-blood gene transcript profile of AS patients in comparison to controls in order to elucidate the gene expression patterns involved in this disease. Unlike previous investigators, we employed a commercially available method to stabilize RNA in the blood immediately upon phlebotomy to minimize artifacts that occur with handling and purification of living PBMC<sup>9</sup>. We compared their transcript profiles to healthy controls; we also compared transcript profiles to those of patients with systemic sclerosis (SSc) and systemic lupus erythematosus (SLE) in order to identify transcripts that were specific to AS and were not related only to the presence of systemic inflammation. We identified 51 genes that were differentially expressed only in AS patients. Many of the differentially expressed genes belonged to Toll-like receptor (TLR) and related pathways. We observed an overexpression of *TLR4* and *TLR5* that was confirmed by quantitative polymerase chain reaction (PCR) in 2 different cohorts of AS patients. We further demonstrated that *TLR4* and *TLR5* transcripts in whole blood decreased significantly after TNF- $\alpha$  inhibitor (anti-TNF) therapy. Our findings provide support for the importance of a pathogen-associated molecular pattern in the pathogenesis of AS.

## MATERIALS AND METHODS

The patients with AS were recruited from the Prospective Study of Outcomes in Ankylosing Spondylitis (PSOAS) study. The PSOAS is a longitudinal study of AS patients from 3 sites in the USA: the University of Texas Health Science Center at Houston, Houston, Texas (UTHSC-H); Cedars-Sinai Medical Center, Los Angeles, California; and the National Institutes of Health, Bethesda, Maryland. All AS patients met the modified New York criteria for the definitive diagnosis of AS<sup>10</sup>. From patients enrolled in PSOAS, we investigated 2 separate groups of patients with AS. In the initial group, no patient was receiving anti-TNF or other immunosuppressive agents. All AS patients in the initial sample set were recruited from the UTHSC-H site. In the second confirmatory cohort, 2 samples were investigated from each patient: the first before initiation of an anti-TNF treatment; the second was obtained after the patient was treated with an

anti-TNF agent for  $\geq 6$  months. AS patients in the confirmatory cohort were recruited from all 3 participating sites. All AS patients enrolled in the discovery group had active disease, defined as Bath AS Disease Activity Index (BASDAI) score  $\geq 3.5$ . Similarly, all AS patients in the confirmatory cohort had a BASDAI  $\geq 3.5$  before the initiation of anti-TNF therapy. In addition to demographic information and BASDAI, we measured C-reactive protein (CRP) at the time of blood draw in AS patients.

The healthy controls had no history of autoimmune diseases or spondyloarthritis-related manifestations and were matched for sex, age, and ethnicity to AS patients. Patients with SLE and SSc were also investigated as disease controls in order to identify gene expression patterns that are specific to AS and are not related only to presence of systemic inflammation. Patients with SSc or SLE were recruited from the continuing longitudinal studies or clinical practice of the investigators at UTHSC-H. All SSc patients met the 1980 American College of Rheumatology (ACR) preliminary criteria for the classification of SSc<sup>11</sup>. Similarly, all SLE patients fulfilled the ACR classification criteria for SLE<sup>12</sup> and had signs of active disease in at least 2 categories of the Systemic Lupus Activity Measure-Revised<sup>13</sup>. Patients with SSc or SLE receiving immunosuppressive agents other than low-dose steroids (prednisone  $\leq 5$  mg) and hydroxychloroquine were excluded from the study. The comparison group for the patients with SSc or SLE were healthy controls matched for sex, age, and ethnicity to patients with SSc.

All study subjects provided written informed consent and the study was approved by the institutional review boards of all participating centers.

**Sample processing and microarray experiments.** Whole-blood samples for gene expression studies were drawn directly into PAXgene<sup>TM</sup> tubes (PreAnalytix, Hombrechtikon, Switzerland). All blood samples were processed in the laboratories of the Division of Rheumatology and Clinical Immunogenetics, UTHSC-H. Total RNA was isolated and purified according to the manufacturer's protocol using PAXgene RNA Kit. The RNA quality and yield was assessed by NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA) and Agilent 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA). A globin reduction was not done because this procedure did not increase percentage of present calls in a preliminary experiment with 9 healthy control samples. This finding might be explained by the longer transcript probes printed on the Illumina arrays (50 mer probes) in comparison to Affymetrix arrays.

Two hundred nanograms of total RNA were amplified and purified utilizing Illumina TotalPrep RNA Amplification Kit (Applied Biosystems/Ambion, Austin, TX, USA) according to the manufacturer's instructions. We hybridized the amplified cRNA on Illumina Human Ref-8v2 arrays and extracted the data utilizing the Illumina Beadstudio software (Illumina, San Diego, CA, USA).

**Microarray data analysis.** The raw data were exported into BRB-ArrayTools v. 3.7 (R. Simon and A. Pen Lam, National Cancer Institute, Bethesda, MD, USA).

Probes whose signal detection p values indicated no significant difference from those of the negative controls ( $p < 0.01$ ) were removed from the analysis. In addition, we excluded genes whose expression values were missing or were filtered out in more than 50% of experiments. Expression data were normalized using the median over the entire array. We used less stringent criteria for detection of differentially expressed genes in order to increase detection of any transcripts with altered gene expression. A gene was defined as differentially expressed for all comparisons when the significance level for comparison was  $p < 0.01$ , utilizing a random variance t test<sup>14</sup>. The set of differentially expressed genes was modeled in Ingenuity Pathway Analysis (Ingenuity Systems, Redwood City, CA, USA) to detect pathways or biological processes involving these genes.

**Real-time quantitative PCR.** Quantitative PCR (qPCR) assays for *TLR4* and *TLR5* were designed to confirm the microarray results. The assay details including the primer sequence, lowest limit of detection, and PCR efficiency are shown in Table 1. Each sample was assayed in triplicate plus a control without reverse transcriptase to access DNA contamination. Samples

Table 1. Details of quantitative PCR.

| Gene                 | Accession No. | Primer and Probe   | Amplicon Length | PCR Efficiency | Lower Limit of Detection (molecules) |
|----------------------|---------------|--|-----------------|----------------|--------------------------------------|
| Toll-like receptor 4 | NM_138554     | 500 (+) GAG CCT TTT CTG GAC TAT CAA G*<br>582 (-) TCC AAT GGG GAA GTT CTC TAG*<br>554 (-) FAM-AGA TTT GTC TCC ACA GCC ACC AGC-BHQ1†    | 81 bases        | 95%            | 180                                  |
| Toll-like receptor 5 | NM_003268     | 2209 (+) GCC ATC TGA CTG CAT TAA GG*<br>2284 (-) GCA GGT AAA TCA TTG TGA GAA AG*<br>2237 (+) FAM-CCT CAA CTC CAA CAG GCT GAC AGT-BHQ1† | 84 bases        | 95%            | 170                                  |

\* Primer sequence. † Probe sequence.

were reverse transcribed into cDNA using superscript II reverse transcriptase (Invitrogen, Carlsbad, CA, USA) for 30 min at 50°C in 384-well plates. PCR master mix containing JumpStart Taq Polymerase (Sigma, St. Louis, MO, USA) was added to the samples. Each assembled plate was run in a 7900 real-time instrument using the following PCR conditions: 95°C for 1 min, followed by 40 cycles of 95°C for 12 s and 60°C for 30 s. Results were analyzed utilizing SDS 2.3 (7900) software (Applied Biosystems, Foster City, CA, USA) with FAM reporter and ROX as the reference dye. The final data were normalized to 18s rRNA levels. The final data were presented as the molecules of the transcript divided by the molecules of 18sRNA transcript × 100.

*Statistical analysis.* Continuous variables were analyzed by t test if the dependent variable had a normal distribution. The Mann-Whitney nonparametric test was used if the outcome variable did not have a normal distribution. We compared the gene expression values, CRP, and BASDAI scores between pre- and post-anti-TNF treatment samples utilizing a paired T test if model assumptions were met, otherwise Wilcoxon signed-rank test was applied. Linear regression was used to investigate the relationship among 2 continuous variables. Two-sided p values < 0.05 were considered significant. Analyses were performed utilizing the NCSS 2007 statistical program (NCSS, Kaysville, UT, USA).

## RESULTS

*Characteristics of study groups.* A total of 16 patients with AS and 14 healthy controls were examined in the first group. There were no significant differences in age, sex, and ethnicity between patients and controls. Table 2 shows the demographic characteristics, presence of spondyloarthritis (SpA) related manifestations, and other clinical features in

participants. No control subjects had a SpA-related manifestation. The majority of AS patients (75%) were male. Among AS patients, the mean BASDAI score was 5.31 (± 2.01 SD) and the median CRP was 0.59 mg/dl. All AS patients in this group were HLA-B27-positive. We also investigated the gene expression profile of 74 patients with SSc (female 79.7%, mean age 49.16 yrs), 21 matched controls (female 80.95%, mean age 53.53 yrs), and 17 patients with SLE (female 94.12%, mean age 38.5 yrs).

*Gene expression microarrays show upregulation of nuclear factor-κB and TLR pathways in AS.* A total of 8230 transcripts passed our filtering criteria across all the peripheral blood samples. Clustering analyses according to date of hybridization or chip number indicated no technical artifact.

A comparison of 16 AS patients with their matched controls revealed 83 differentially expressed transcripts. An unsupervised hierarchical clustering of these genes in AS patients and their controls is shown in Figure 1. A list of these genes is provided in Appendix 1. In a similar analysis, comparison of SLE and SSc samples to their matched controls resulted in 936 and 530 differentially expressed transcripts, respectively. The most prominent gene expression pattern among SLE and SSc patients consisted of upregulation of genes belonging IFN-related pathways<sup>15</sup>, whereas we did not observe an overrepresentation of up- or down-

Table 2. Demographic features of patients with AS and their matched controls in both samples.

| Feature                           | Discovery Group |                 | Confirmation Group |                 |
|-----------------------------------|-----------------|-----------------|--------------------|-----------------|
|                                   | AS, n = 16      | Control, n = 14 | AS, n = 27         | Control, n = 27 |
| Age, mean (SD) yrs                | 36.01 (11.94)   | 32.11 (7.34)    | 36.08 (11.4)       | 37.21 (10.68)   |
| No. male (%)                      | 12 (75)         | 10 (71.43)      | 14 (51.85)         | 14 (51.85)      |
| No. Caucasian (%)                 | 13 (81.25)      | 11 (78.57)      | 17 (62.96)         | 17 (62.96)      |
| Disease duration                  | 16.09 (12.87)   | NA              | 11.55 (5.86)       | NA              |
| BASDAI*                           | 5.31 (2.01)     | NA              | 5.93 (1.35)        | NA              |
| C-reactive protein                | 1.4 (2.23)      | NA              | 1.56 (2.17)        | NA              |
| Uveitis                           | 3 (18.75)       | 0               | 14 (51.85)         | 0               |
| Psoriasis                         | 1 (6.25)        | 0               | 3 (11.11)          | 0               |
| Peripheral inflammatory arthritis | 10 (62.5)       | 0               | 7 (25.93)          | 0               |
| Crohn's disease                   | 0               | 0               | 3 (11.11)          | 0               |

BASDAI: Bath Ankylosing Spondylitis Disease Activity Index; NA: not applicable.

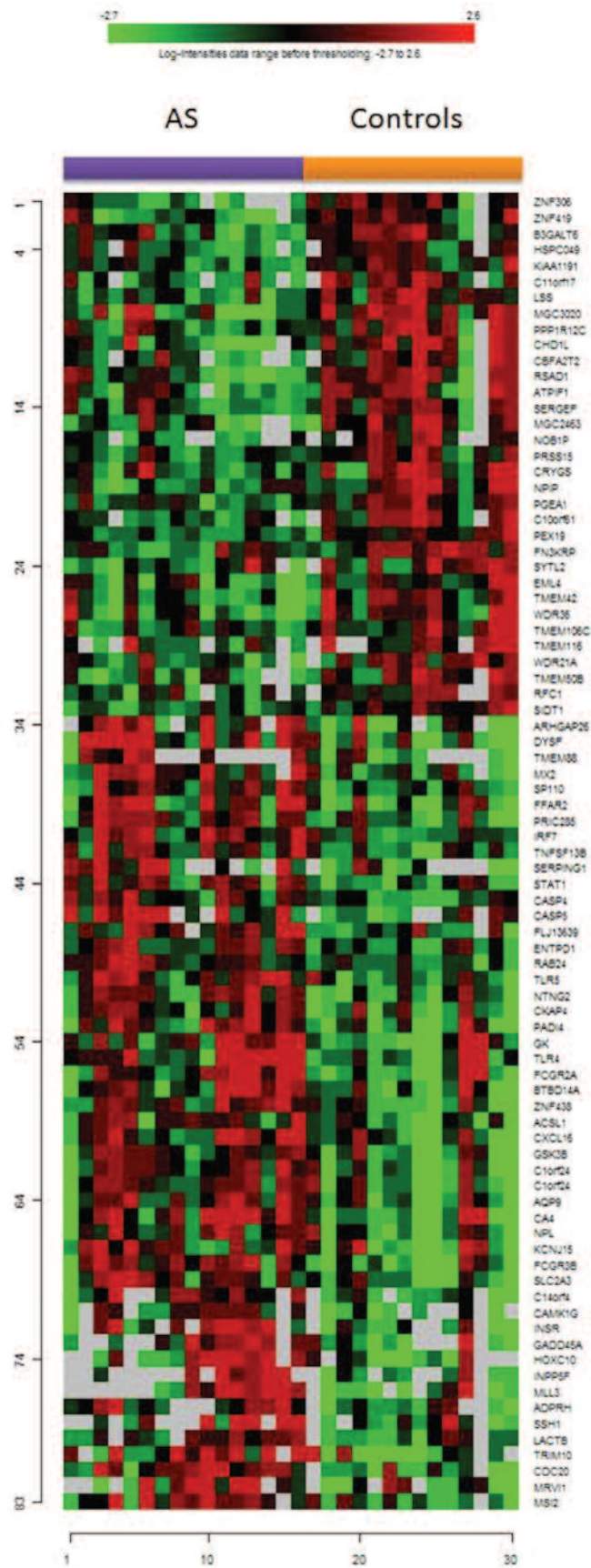


Figure 1. Unsupervised hierarchical clustering of 83 genes identified as differentially expressed between patients with AS and controls.

regulated genes belonging to IFN pathways in comparisons of AS patients to controls in the Ingenuity Pathway Analysis.

Then we filtered the differentially expressed genes in AS through the lists of differentially expressed transcripts in SLE and SSc, which resulted in 52 transcripts corresponding to 51 genes that were uniquely differentially expressed among AS patients (Appendix 2). Ingenuity Pathway Analysis of these 52 transcripts demonstrated overrepresentation of transcripts belonging to pathways involved in TLR signaling. *TLR4* ( $p = 0.008$ ) and *TLR5* ( $p = 0.006$ ) were overexpressed in AS patients but not in patients with SLE or SSc. No other subtype of *TLR* was differentially expressed in AS patients.

The significantly dysregulated pathways were nuclear factor- $\kappa$ B signaling, dendritic cell maturation, TLR, TREM1 signaling, and BRCA1 in DNA damage (Table 3). It is notable that TLR play a major role in the activation of the first 4 pathways. Specifically, *TLR4* and *TLR5* were the only dysregulated genes that were present in all these 4 pathways.

We next assessed *TLR4* and *TLR5* levels in patients with AS, their matched controls, and patients with SLE using qPCR. In agreement with the microarray results, AS patients had higher *TLR4* ( $p = 0.012$ ) and *TLR5* ( $p = 0.006$ ) levels than controls. Similarly, in comparison to SLE, AS patients showed overexpression of *TLR4* ( $p = 0.002$ ) and *TLR5* ( $p = 0.008$ ), whereas *TLR4* ( $p = 0.203$ ) and *TLR5* ( $p = 0.383$ ) levels did not differ significantly between SLE patients and controls. Figure 2 shows the *TLR4* and *TLR5* levels among these 3 study groups. Further, *TLR4* and *TLR5* levels correlated highly with each other ( $p < 0.001$ ,  $r^2 = 0.62$ ).

*Overexpression of TLR4 and TLR5 was confirmed in a separate group of AS patients.* We next examined the *TLR4* and *TLR5* levels in a second larger sample of 27 patients with AS and 27 matched healthy controls. A total of 22 patients with AS (81.5%) were HLA-B27-positive; characteristics of patients and controls in the confirmation group are shown in Table 2. One sample before and another one after anti-TNF treatment were investigated on each AS patient. The CRP and BASDAI score of AS patients before anti-TNF treatment were 0.791 mg/dl (median) and  $5.93 \pm 1.35$  (mean  $\pm$  SD), respectively. As expected, both CRP ( $p = 0.005$ ) and BASDAI score ( $p < 0.001$ ) decreased significantly upon anti-TNF treatment to 0.095 mg/dl (median) and  $3.49 \pm 2.33$  (mean  $\pm$  SD), respectively.

Table 3. Dysregulated pathways in comparison of patients with AS and unaffected controls according to Ingenuity Pathway Analysis.

| Canonical Pathways                   | P      |
|--------------------------------------|--------|
| Nuclear factor- $\kappa$ B signaling | 0.0006 |
| Dendritic cell maturation            | 0.008  |
| Toll-like receptor signaling         | 0.008  |
| TREM1 signaling                      | 0.01   |
| BRCA1 in DNA damage response         | 0.009  |

Compared to their matched controls, we again observed higher *TLR4* ( $p = 0.007$ ) and *TLR5* ( $p = 0.012$ ) levels in AS patients before initiation of the anti-TNF treatment. However, *TLR4* and *TLR5* levels in AS samples after anti-TNF treatment did not differ significantly from controls ( $p = 0.126$ ,  $p = 0.173$ , respectively). Figure 3 shows *TLR4* and *TLR5* levels in the AS samples before and after initiation of anti-TNF treatment and in controls. Similarly to the initial sample, *TLR4* and *TLR5* levels also correlated significantly with each other ( $p < 0.001$ ,  $r^2 = 0.44$ ).

*TLR4 and TLR5 levels decreased significantly after TNF blockade.* *TLR4* levels decreased significantly after initiation of anti-TNF treatment from 0.072 to 0.046 ( $p = 0.002$ ) in patients with AS. Similarly, the *TLR5* levels also declined significantly on treatment with anti-TNF from 0.005 to 0.0038 ( $p = 0.025$ ; Figure 3). Further, the percentage changes in *TLR4* and *TLR5* after TNF blockade correlated highly with each other ( $p < 0.001$ ,  $r^2 = 0.75$ ).

*TLR4 and TLR5 levels in relationship with clinical features.* BASDAI scores did not correlate with *TLR4* and *TLR5* levels in either study cohort (data not shown). Although CRP levels correlated with *TLR4* and *TLR5* levels in the initial sample ( $p = 0.015$ ,  $r^2 = 0.4$  and  $p = 0.001$ ,  $r^2 = 0.6$ , respectively), we could not confirm this finding among pre-TNF samples in the second study group ( $p = 0.833$  for *TLR4*,  $p = 0.753$  for *TLR5*). Among the patients with AS, history of uveitis, psoriasis, peripheral inflammatory arthritis, or Crohn's disease did not correlate with *TLR4* and *TLR5* levels in the 2 study cohorts (data not shown). Further, there was no significant difference in *TLR4* and *TLR5* levels between the HLA-B27-positive and HLA-B27-negative AS patients ( $p = 0.454$ ,  $p = 0.319$ , respectively).

## DISCUSSION

We observed that PBC global gene expression profiling of patients with AS showed a dysregulation of TLR-related pathways. We specifically identified an overexpression of *TLR4* and *TLR5*, which also was confirmed by qPCR in the initial and a separate confirmatory sample. Differential regulation of these genes appeared to be unique to AS and was not observed in SLE or SSc. Our study is the first report of increased expression of *TLR5* in AS.

An abnormal host response against pathogens has been implicated in the pathogenesis of AS and other SpA subtypes. Further, 60% of patients with SpA without evidence of clinical Crohn's disease have endoscopic or histological signs of gut inflammation<sup>16</sup>. Moreover, studies with B27-transgenic rats provide support for the role of commensal gut flora in the pathogenesis of HLA-B27-associated gut and joint manifestations. The B27-transgenic rats do not develop inflammatory intestinal or peripheral joint disease in a germ-free environment<sup>17</sup>.

TLR are primarily involved in innate immune responses to microbial pathogens by recognition of conserved pathogen-

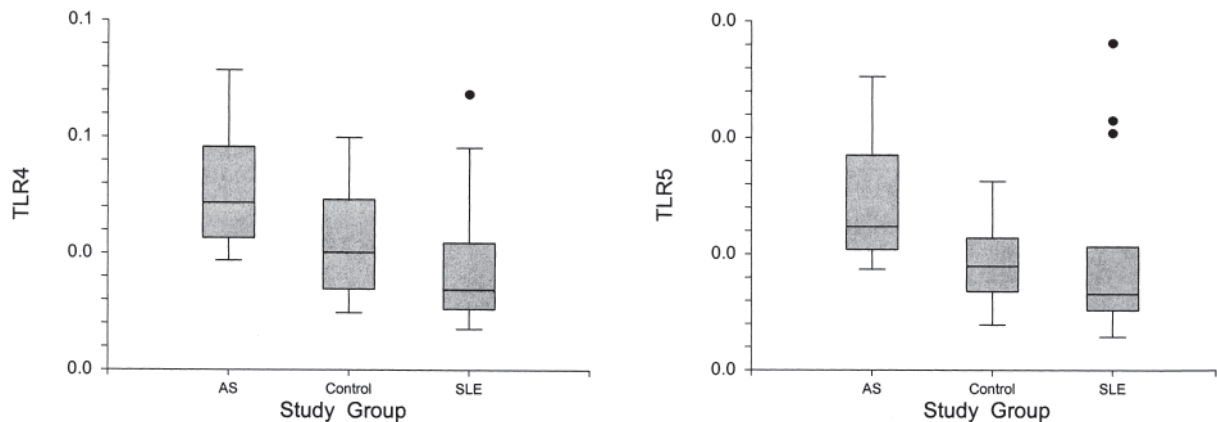


Figure 2. Gene expression levels of *TLR4* and *TLR5* in AS, SLE, and controls by qPCR in the first study sample. Expression of both genes is higher in AS patients in comparison to controls and SLE patients, while there was no significant difference between SLE patients and controls.

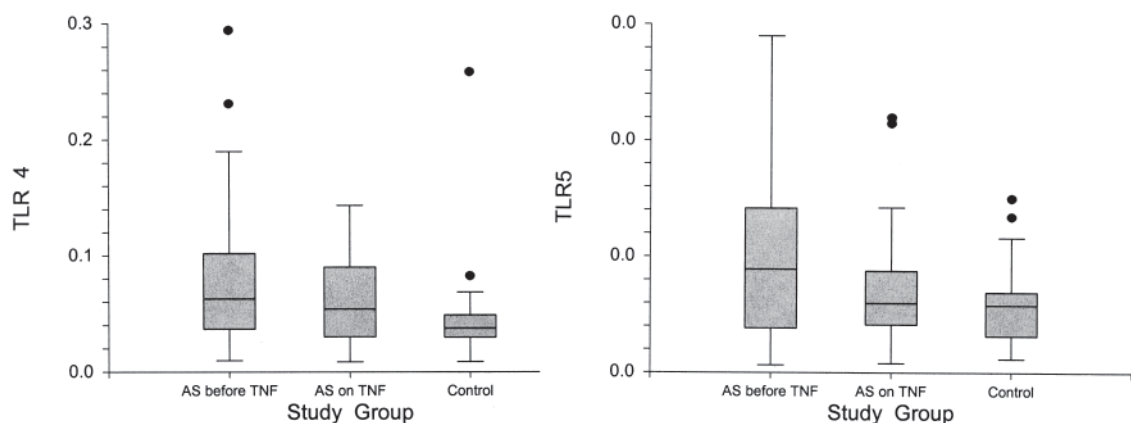


Figure 3. Gene expression levels of *TLR4* and *TLR5* in patients with AS before and during anti-TNF treatment, as well as controls, in the second study sample. Gene expression levels of both genes decreased significantly after anti-TNF treatment among AS patients. Again, before anti-TNF treatment, samples showed higher *TLR4* and *TLR5* levels than controls. After anti-TNF treatment, there was no significant difference between AS patients and controls.

associated molecular patterns<sup>18,19</sup>. More than 10 TLR subtypes have been identified. In our study, *TLR4* and *TLR5* were the only TLR subtypes that were overexpressed among patients with AS. Lipopolysaccharide (LPS) in the outer membrane of Gram-negative bacteria is the main ligand of *TLR4*<sup>19</sup>. In animal models, *TLR4* plays a critical role in the early cytokine response of phagocytes upon infection with reactive arthritis-associated Gram-negative bacteria such as *Yersinia*, *Salmonella*, and *Chlamydia*<sup>20,21,22</sup>. An upregulation of *TLR4* among patients with AS has been previously reported. De Rycke, *et al* reported increased expression of *TLR4* but not *TLR2* on PBMC of patients with SpA in comparison to controls<sup>23</sup>. Yang, *et al* showed that the expression of *TLR4* on lymphocytes, monocytes, and neutrophils was all significantly increased among patients with AS<sup>24</sup>.

The main ligand for *TLR5* is flagellin, a primary component of bacterial flagella that extend from the outer mem-

brane of Gram-negative bacteria. Flagella are known to be major antigens of Gram-negative bacteria like *Salmonella*, *Escherichia coli*, and *Yersinia*, where its antigenicity serves as the basis for H serotyping<sup>25,26,27</sup>. There are no published reports on the role of *TLR5* in AS or other SpA subtypes. However, both *TLR5* and flagellin have been implicated in the pathogenesis of Crohn's disease (reviewed by Gewirtz<sup>28</sup>). A study investigating the proteins of commensal microflora that were reactive with antisera from a colitic mouse model identified flagellins as the dominant antigen. Further, serum IgG to these flagellins was elevated in patients with Crohn's disease but not in patients with ulcerative colitis or controls<sup>29</sup>. In another study, flagellin exposure to injured mouse colon *in vivo*, but not intact colon, significantly worsened colonic inflammation, whereas *TLR2*-specific agonists did not have a similar effect<sup>30</sup>. A *TLR5* stop-polymorphism was negatively associated with

Crohn's disease in Ashkenazi Jewish patients, raising the possibility that a downregulation in *TLR5* provides protection against development of Crohn's disease<sup>31</sup>.

AS and Crohn's disease share common clinical features and genetic background. Up to one-third of patients with Crohn's disease have sacroiliac joint involvement similar to AS on computer tomography<sup>32</sup>, whereas roughly 60% of patients with SpA have subclinical colitis by biopsy<sup>16</sup>. These similarities, along with our data, suggest that the role of *TLR5* in the pathogenesis of AS should be further explored in mechanistic studies. We did not observe any significant difference in *TLR5* levels between the AS patients with and those without Crohn's disease in our study ( $p = 0.769$ ). This finding suggests that the overexpression of *TLR5* in AS is independent of the presence of clinically apparent Crohn's disease. However, our study might have been underpowered to detect a relationship between *TLR5* expression and presence of Crohn's disease in patients with AS.

Activation of the innate immune system such as polymorphonuclear cells and macrophages plays an important role in AS-related inflammation. Patients with SpA have significantly higher neutrophil counts and lower lymphoid aggregates than patients with rheumatoid arthritis (RA) on synovial histology<sup>33</sup>. Further, macrophages expressing the hemoglobin scavenger receptor CD163 are increased in the synovial lining of patients with SpA compared to RA patients. CD163+ macrophages also are increased in the colonic lamina propria in SpA patients compared to controls, supporting the hypothesis of a recirculation of similar clones in the intestinal mucosa and synovium<sup>34</sup>. Of interest, both *TLR4* and *TLR5* can induce an acute shedding of CD163 from human monocytes. As well, these 2 TLR subtypes have a synergistic effect on upregulation of CD163, whereas exogenous recombinant IFN- $\gamma$  leads to downregulation of CD163<sup>35</sup>. Global gene expression studies of macrophages derived from AS patients reveal a "reverse" IFN signature, with IFN- $\gamma$  upregulated genes being downregulated<sup>7</sup>. The observed upregulation of *TLR4* and *TLR5* in our study, along with the reported "reverse" IFN- $\gamma$  in AS, are both potential mechanisms that could lead to overexpression CD163+ macrophages in this disease. However, this hypothesis needs to be verified by further mechanistic studies. We did not observe a "reverse" IFN signature in whole-blood samples as described by Smith, *et al* in macrophages of patients with AS<sup>7</sup>.

We observed downregulation of *TLR4* and *TLR5* after initiation of anti-TNF treatment in patients with AS. Both *TLR4* and *TLR5* can induce secretion of TNF- $\alpha$  and other proinflammatory cytokines<sup>30,36</sup>. The expression of *TLR4* on PBMC decreases gradually after treatment of SpA patients with anti-TNF agents *in vivo*. These PBMC have a functional impairment in their capacity to produce TNF- $\alpha$  after stimulation with LPS *in vitro*<sup>23</sup>. Further, *TLR4* mRNA correlated closely with serum TNF- $\alpha$  levels among patients

with AS<sup>24</sup>. These findings suggest that TNF blockade attenuates a self-perpetuating activation of the innate immune system via the TLR pathway.

The *TLR4* and *TLR5* levels and their percentage changes after TNF blockade correlated closely with each other, which raises the possibility that they are both triggered by the same mechanism, whereas we did not observe such a strong correlation of these 2 transcripts with general markers of inflammation such as CRP.

The data on correlation of *TLR4* and *TLR5* levels with CRP in our study were not consistent. While we observed a significant correlation in the first sample, we could not confirm this finding in the second cohort. These results did not change even after we excluded the HLA-B27-negative patients from the analysis (data not shown). Similarly, De Rycke, *et al*<sup>23</sup> did not observe a correlation of *TLR4* expression with CRP in SpA, whereas Yang, *et al*<sup>24</sup> reported correlation of *TLR4* mRNA levels with CRP in HLA-B27-positive patients with AS. Studies with larger sample sizes are needed to resolve this issue.

Potential limitations of our study are that we used less stringent criteria for identification of differentially expressed genes in microarray data analysis in order to increase our ability to detect dysregulated genes and pathways. However, we verified the overexpression of *TLR4* and *TLR5* with qPCR in the same sample in addition to a separate confirmatory cohort. We compared the global gene expression of AS patients to transcriptomes of patients with SLE and SSc. These comparative studies should be extended to patients with other rheumatological diseases such as RA in future investigations. Further, the observed fold-changes in *TLR4* and *TLR5* between AS patients and controls were relatively small (< 2-fold). However, whole-blood samples consist of heterogeneous populations of white blood cell subtypes. It is possible the observed differential expression levels in whole blood are secondary to much higher-fold changes in a particular subset of white blood cells. We focused on dysregulation of TLR transcripts. However, the other observed differentially expressed transcripts and pathways in this study also could play an important role in the pathogenesis of AS. For example, the observed dysregulations in the dendritic cell maturation pathway may provide further support for the importance of defective functional capacity of dendritic cells in SpA<sup>37</sup>.

In summary, our global gene expression analysis revealed the TLR-related pathways as the most prominently dysregulated biological process in AS. We identified *TLR4* and *TLR5* as the only dysregulated subtypes of TLR in AS. We confirmed the overexpression of these 2 genes among patients with AS in the same sample and in a confirmatory cohort. We showed that the expression of both receptors decreased after initiation of anti-TNF treatment. Our findings provide further support for the importance of TLR subtypes responsive to Gram-negative bacteria in the pathogen-

esis of AS. Mechanistic studies are needed to elucidate the role of these TLR subtypes in the development of AS.

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Appendix 1. Differentially expressed genes in AS compared to controls.

| Parametric p value | Geom mean of intensities in class 1 (AS) | Geom mean of intensities in class 2 (control) | Fold-change | GB acc       | Gene symbol | Defined Gene list   |
|--------------------|--|---|-------------|--------------|-------------|---|
| 0.000478           | 137.0849484                              | 191.4323799                                   | 0.7161012   | NM_002340    | LSS         | Biosynthesis of steroids  |
| 0.0006957          | 9364.319315                              | 4899.472307                                   | 1.9112914   | NM_000570    | FCGR3B      | Natural killer cell mediated cytotoxicity, immunology   |
| 0.0009312          | 70.135071                                | 39.2769027                                    | 1.7856569   | NM_198330    | INPP5F      |   |
| 0.0010988          | 71.4184127                               | 45.7446495                                    | 1.5612408   | NM_001255    | CDC20       | Cell cycle, Ubiquitin mediated proteolysis  |
| 0.0011141          | 52.8656567                               | 70.9770793                                    | 0.7448272   | NM_001013840 | C10orf61    |   |
| 0.0011586          | 392.3825626                              | 275.9854116                                   | 1.4217511   | NM_182755    | ZNF438      |   |
| 0.0017355          | 61.4036443                               | 44.5498863                                    | 1.378312    | NM_001125    | ADPRH       |   |
| 0.0018922          | 87.5243114                               | 47.5085126                                    | 1.8422869   | NM_170606    | MLL3        | Lysine degradation  |
| 0.002143           | 53.3984454                               | 71.3663158                                    | 0.7482304   | NM_014062    | NOB1P       |   |
| 0.0021903          | 233.0709896                              | 183.0490111                                   | 1.273271    | NM_001031677 | RAB24       |   |
| 0.002331           | 78.1171224                               | 97.3888835                                    | 0.8021154   | NM_017699    | SIDT1       |   |
| 0.002457           | 55.4244192                               | 75.0410081                                    | 0.7385884   | NM_020642    | C11orf17    |   |
| 0.0025345          | 956.4176519                              | 673.3678999                                   | 1.4203493   | NM_033405    | PRIC285     |   |
| 0.002748           | 111.8853999                              | 65.758725                                     | 1.7014533   | NM_015071    | ARHGAP26    |   |
| 0.002797           | 77.7048739                               | 43.8710092                                    | 1.7712124   | NM_018984    | SSH1        | Regulation of actin cytoskeleton  |
| 0.0031593          | 96.3060504                               | 70.9280275                                    | 1.3577996   | NM_001031719 | FLJ13639    |   |
| 0.0032597          | 74.3860187                               | 107.9506798                                   | 0.6890741   | NM_006134    | TMEM50B     |   |
| 0.0034606          | 144.2016183                              | 198.6110208                                   | 0.7260504   | NM_144638    | TMEM42      | Role of Ran in mitotic spindle regulation   |
| 0.0035429          | 121.5756396                              | 65.759618                                     | 1.8487887   | NM_052828    | TRIM10      |   |
| 0.0035783          | 76.7861621                               | 100.233922                                    | 0.7660696   | NM_181340    | WDR21A      |   |
| 0.0037429          | 1428.384827                              | 1074.9697                                     | 1.3287675   | NM_006573    | TNFSF13B    | TACI and BCMA stimulation of B cell immune responses., Cytokine-cytokine receptor interaction |
| 0.0038303          | 2308.950828                              | 1401.307414                                   | 1.6477118   | NM_003494    | DYSF        |   |
| 0.003983           | 287.009692                               | 225.0477753                                   | 1.2753278   | NM_001776    | ENTPD1      |   |
| 0.004009           | 136.1716197                              | 185.1636214                                   | 0.7354124   | NM_006985    | NPIP        |   |
| 0.0040379          | 89.442346                                | 60.228624                                     | 1.4850471   | NM_002463    | MX2         | cell_signaling  |
| 0.0041087          | 636.3160782                              | 820.7957534                                   | 0.7752429   | NM_024619    | FN3KRP      |   |
| 0.0041129          | 54.5849904                               | 70.7770909                                    | 0.771224    | NM_024493    | ZNF306      |   |
| 0.0042             | 129.564397                               | 206.5903427                                   | 0.6271561   | NM_024048    | MGC3020     |   |
| 0.0043066          | 77.2854192                               | 113.9056458                                   | 0.6785039   | NM_004284    | CHD1L       |   |
| 0.0044582          | 313.8851602                              | 213.5519415                                   | 1.4698305   | NM_000167    | GK          | Glycerolipid metabolism, PPAR signaling pathway   |
| 0.004488           | 106.5122966                              | 151.1224528                                   | 0.7048079   | NM_018346    | RSAD1       |   |
| 0.0045615          | 64.1665543                               | 96.0495151                                    | 0.668057    | NM_138341    | TMEM116     |   |
| 0.0051912          | 433.4919731                              | 308.0187609                                   | 1.4073557   | NM_002093    | GSK3B       |   |
| 0.0053976          | 83.1198159                               | 48.5045894                                    | 1.7136485   | NM_203411    | TMEM88      |   |
| 0.0054644          | 249.0470921                              | 304.1155458                                   | 0.8189226   | NM_020444    | KIAA1191    |   |
| 0.0057117          | 1224.60185                               | 822.4718523                                   | 1.4889286   | NM_022059    | CXCL16      |   |
| 0.0057841          | 110.4525818                              | 142.0882007                                   | 0.7773522   | NM_080605    | B3GALT6     | Chondroitin sulfate biosynthesis, Glycan structures - biosynthesis 1                          |
| 0.0059993          | 6755.193466                              | 4676.588102                                   | 1.4444705   | NM_006931    | SLC2A3      | Vitamin C in the Brain, cell_signaling, misc, pharmacology                                    |
| 0.0060617          | 57.8154193                               | 37.7067951                                    | 1.5332891   | NM_020439    | CAMK1G      |   |
| 0.0062033          | 107.4822883                              | 141.3133872                                   | 0.7605952   | NM_024691    | ZNF419      |   |
| 0.0062233          | 393.164908                               | 285.6590853                                   | 1.3763431   | NM_003268    | TLR5        | Toll-like receptor signaling pathway, immunology  |
| 0.006241           | 706.5141744                              | 366.4292943                                   | 1.9281051   | NM_000717    | CA4         | Nitrogen metabolism   |
| 0.0062475          | 4308.608064                              | 2917.50243                                    | 1.4768139   | NM_021642    | FCGR2A      | immunology  |
| 0.0063598          | 1500.259142                              | 1159.001672                                   | 1.2944409   | NM_004031    | IRF7        | gene_regulation, transcription  |
| 0.0064295          | 4468.985126                              | 3070.56217                                    | 1.455429    | NM_012387    | PADI4       |   |
| 0.0065349          | 162.9657928                              | 206.0056073                                   | 0.7910745   | NM_012139    | SERGEF      |   |
| 0.0065475          | 3763.198465                              | 2463.563116                                   | 1.5275429   | NM_022083    | C1orf24     |   |
| 0.0065818          | 169.8341703                              | 202.8024016                                   | 0.8374367   | NM_002857    | PEX19       |   |
| 0.0068421          | 121.5985049                              | 67.4619564                                    | 1.8024752   | NM_130385    | MRVI1       |   |

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|           |             |             |           |              |          |   |
|-----------|-------------|-------------|-----------|--------------|----------|---|
| 0.0069067 | 4094.439362 | 3127.288913 | 1.3092616 | NM_139266    | STAT1    | Apoptotic Signaling in Response to DNA Damage, EGF Signaling Pathway, IFN alpha signaling pathway, IFN gamma signaling pathway, IL22 Soluble Receptor Signaling Pathway, Inhibition of Cellular Proliferation by Gleevec, MAPKinase Signaling Pathway, p38 MAPK Signaling Pathway, PDGF Signaling Pathway, TPO Signaling Pathway, Jak-STAT signaling pathway, Toll-like receptor signaling pathway, angiogenesis, immunology, signal_transduction |
| 0.0069214 | 79.185264   | 50.4842138  | 1.5685153 | NM_004347    | CASP5    | MAPK signaling pathway, apoptosis, immunology   |
| 0.0069767 | 2792.841513 | 2234.522646 | 1.2498605 | NM_033306    | CASP4    | Caspase Cascade in Apoptosis, MAPK signaling pathway, apoptosis, immunology   |
| 0.0069791 | 57.8324274  | 41.4198501  | 1.3962491 | NM_024496    | C14orf4  |   |
| 0.0070874 | 458.6254977 | 334.7400414 | 1.3700945 | NM_032536    | NTNG2    |   |
| 0.0072365 | 309.1783279 | 239.2651331 | 1.2921997 | NM_080424    | SP110    |   |
| 0.0075236 | 2360.736625 | 1641.346746 | 1.4382924 | NM_001995    | ACSL1    | Perou's- Intrinsic- Breast-Cancer-Genes, Adipocytokine signaling pathway, Fatty acid metabolism, PPAR signaling pathway   |
| 0.0075429 | 101.3066589 | 143.8378404 | 0.7043116 | NM_016311    | ATPIF1   |   |
| 0.0075842 | 55.9221565  | 71.0356931  | 0.7872402 | NM_002913    | RFC1     |   |
| 0.007629  | 284.5814239 | 197.0116273 | 1.4444905 | NM_138557    | TLR4     | immunology  |
| 0.0078644 | 8192.608896 | 5797.077578 | 1.4132309 | NM_020980    | AQP9     |   |
| 0.0079295 | 352.6683885 | 228.2252792 | 1.5452644 | NM_002243    | KCNJ15   |   |
| 0.0079915 | 69.4960341  | 55.0535557  | 1.2623351 | NM_171846    | LACTB    |   |
| 0.0080308 | 4230.418121 | 2883.942998 | 1.4668869 | NM_022083    | C1orf24  |   |
| 0.0080335 | 61.6309441  | 80.2352561  | 0.768128  | NM_001032999 | CBFA2T2  | cell_cycle, immunology  |
| 0.0080701 | 78.1569398  | 53.726485   | 1.454719  | NM_001924    | GADD45A  | ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway, Cell cycle, MAPK signaling pathway   |
| 0.0083262 | 1358.69924  | 985.1936551 | 1.379119  | NM_030769    | NPL      |   |
| 0.0084262 | 961.6377224 | 682.6056177 | 1.408775  | NM_006825    | CKAP4    |   |
| 0.0084503 | 87.9484113  | 65.2853476  | 1.3471386 | NM_138962    | MSI2     |   |
| 0.0085554 | 597.6472872 | 398.0354876 | 1.5014925 | NM_005306    | FFAR2    |   |
| 0.0087672 | 95.5304166  | 51.085383   | 1.8700147 | NM_000062    | SERPING1 | Intrinsic Prothrombin Activation Pathway, Complement and coagulation cascades   |
| 0.0090354 | 158.4764733 | 192.559439  | 0.8230003 | NM_004793    | PRSS15   |   |
| 0.0091097 | 198.4911419 | 136.4177609 | 1.4550242 | NM_144653    | BTBD14A  |   |
| 0.009238  | 83.129073   | 110.3058286 | 0.7536236 | NM_017607    | PPP1R12C |   |
| 0.0092556 | 126.8566834 | 181.5263622 | 0.6988334 | NM_139281    | WDR36    |   |
| 0.0092918 | 70.2149582  | 85.965983   | 0.8167761 | NM_014149    | HSPC049  |   |
| 0.0093926 | 117.3907998 | 154.3682162 | 0.7604597 | NM_017541    | CRYGS    |   |
| 0.0095282 | 154.6194436 | 194.177994  | 0.7962769 | NM_024056    | TMEM106C |   |
| 0.0095422 | 122.7966001 | 150.2197121 | 0.8174466 | NM_001002880 | PGEA1    |   |
| 0.0095887 | 892.9376363 | 1196.945428 | 0.7460137 | NM_019063    | EML4     |   |
| 0.0096633 | 89.6226922  | 56.5656362  | 1.5844017 | NM_017409    | HOXC10   | development   |
| 0.0096843 | 85.2460615  | 116.6847675 | 0.7305672 | NM_024070    | MGC2463  |   |
| 0.0097158 | 114.2832903 | 153.2233268 | 0.7458609 | NM_206930    | SYTL2    |   |
| 0.0097279 | 59.7622428  | 38.6757469  | 1.5452124 | NM_000208    | INSR     | Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Growth Hormone Signaling Pathway, Insulin Signaling Pathway, Adherens junction, Dentatorubropallidolusian atrophy (DRPLA), Insulin signaling pathway, Type II diabetes mellitus, immunology  |

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Appendix 2. Genes that were only differentially expressed in AS.

| Parametric p value | Geom mean of intensities in class 1 (AS) | Geom mean of intensities in class 2 (control) | Fold-change | GB acc       | Gene symbol | Defined Gene list  | Gene involved in the dysregulated pathways in Table 3          |
|--------------------|--|---|-------------|--------------|-------------|--|--|
| 0.0006957          | 9364.31931                               | 4899.47231                                    | 1.9112914   | NM_000570    | FCGR3B      | Natural killer cell mediated cytotoxicity, immunology                | Dendritic Cell Maturation                                      |
| 0.0009312          | 70.135071                                | 39.2769027                                    | 1.7856569   | NM_198330    | INPP5F      |  |  |
| 0.0011141          | 52.8656567                               | 70.9770793                                    | 0.7448272   | NM_001013840 | C10orf61    |  |  |
| 0.0017355          | 61.4036443                               | 44.5498863                                    | 1.378312    | NM_001125    | ADPRH       |  |  |
| 0.0018922          | 87.5243114                               | 47.5085126                                    | 1.8422869   | NM_170606    | MLL3        | Lysine degradation   |  |
| 0.002143           | 53.3984454                               | 71.3663158                                    | 0.7482304   | NM_014062    | NOB1P       |  |  |
| 0.0021903          | 233.07099                                | 183.049011                                    | 1.273271    | NM_001031677 | RAB24       |  |  |
| 0.002331           | 78.1171224                               | 97.3888835                                    | 0.8021154   | NM_017699    | SIDT1       |  |  |
| 0.002457           | 55.4244192                               | 75.0410081                                    | 0.7385884   | NM_020642    | C11orf17    |  |  |
| 0.002748           | 111.8854                                 | 65.758725                                     | 1.7014533   | NM_015071    | ARHGAP26    |  |  |
| 0.002797           | 77.7048739                               | 43.8710092                                    | 1.7712124   | NM_018984    | SSH1        | Regulation of actin cytoskeleton                                     |  |
| 0.0031593          | 96.3060504                               | 70.9280275                                    | 1.3577996   | NM_001031719 | FLJ13639    |  |  |
| 0.0035429          | 121.57564                                | 65.759618                                     | 1.8487887   | NM_052828    | TRIM10      |  |  |
| 0.0035783          | 76.7861621                               | 100.233922                                    | 0.7660696   | NM_181340    | WDR21A      |  |  |
| 0.0038303          | 2308.95083                               | 1401.30741                                    | 1.6477118   | NM_003494    | DYSF        |  |  |
| 0.0041087          | 636.316078                               | 820.795753                                    | 0.7752429   | NM_024619    | FN3KRP      |  |  |
| 0.0041129          | 54.5849904                               | 70.7770909                                    | 0.771224    | NM_024493    | ZNF306      |  |  |
| 0.0043066          | 77.2854192                               | 113.905646                                    | 0.6785039   | NM_004284    | CHD1L       |  |  |
| 0.0044582          | 313.88516                                | 213.551942                                    | 1.4698305   | NM_000167    | GK          | Glycerolipid metabolism, PPAR signaling pathway                      |  |
| 0.004488           | 106.512297                               | 151.122453                                    | 0.7048079   | NM_018346    | RSAD1       |  |  |
| 0.0045615          | 64.1665543                               | 96.0495151                                    | 0.668057    | NM_138341    | TMEM116     |  |  |
| 0.0051912          | 433.491973                               | 308.018761                                    | 1.4073557   | NM_002093    | GSK3B       |  |  |
| 0.0053976          | 83.1198159                               | 48.5045894                                    | 1.7136485   | NM_203411    | TMEM88      |  |  |
| 0.0057841          | 110.452582                               | 142.088201                                    | 0.7773522   | NM_080605    | B3GALT6     | Chondroitin sulfate biosynthesis, Glycan structures - biosynthesis 1 |  |
| 0.0059993          | 6755.19347                               | 4676.5881                                     | 1.4444705   | NM_006931    | SLC2A3      | Vitamin C in the Brain, cell_signaling, misc, pharmacology           |  |
| 0.0062233          | 393.164908                               | 285.659085                                    | 1.3763431   | NM_003268    | TLR5        | Toll-like receptor signaling pathway, immunology                     | NF-κB Signaling, Toll-like Receptor Signaling, TREM1 Signaling |
| 0.006241           | 706.514174                               | 366.429294                                    | 1.9281051   | NM_000717    | CA4         | Nitrogen metabolism  |  |
| 0.0062475          | 4308.60806                               | 2917.50243                                    | 1.4768139   | NM_021642    | FCGR2A      | immunology   | Dendritic Cell Maturation                                      |
| 0.0064295          | 4468.98513                               | 3070.56217                                    | 1.455429    | NM_012387    | PADI4       |  |  |
| 0.0065349          | 162.965793                               | 206.005607                                    | 0.7910745   | NM_012139    | SERGEF      |  |  |

cell-surface Toll-like receptors. *J Leukoc Biol* 2007;81:663-71.

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|           |            |            |           |           |          |  |
|-----------|------------|------------|-----------|-----------|----------|--|
| 0.0065349 | 162.965793 | 206.005607 | 0.7910745 | NM_012139 | SERGEF   |  |
| 0.0065475 | 3763.19846 | 2463.56312 | 1.5275429 | NM_022083 | C1orf24  |  |
| 0.0065818 | 169.83417  | 202.802402 | 0.8374367 | NM_002857 | PEX19    |  |
| 0.0068421 | 121.598505 | 67.4619564 | 1.8024752 | NM_130385 | MRV11    |  |
| 0.0069791 | 57.8324274 | 41.4198501 | 1.3962491 | NM_024496 | C14orf4  |  |
| 0.0075236 | 2360.73663 | 1641.34675 | 1.4382924 | NM_001995 | ACSL1    | Perou's- Intrinsic- Breast-Cancer-Genes, Adipocytokine signaling pathway, Fatty acid metabolism, PPAR signaling pathway  |
| 0.0075429 | 101.306659 | 143.83784  | 0.7043116 | NM_016311 | ATPIF1   |  |
| 0.0075842 | 55.9221565 | 71.0356931 | 0.7872402 | NM_002913 | RFC1     |  |
| 0.007629  | 284.581424 | 197.011627 | 1.4444905 | NM_138557 | TLR4     | immunology   |
| 0.0078644 | 8192.6089  | 5797.07758 | 1.4132309 | NM_020980 | AQP9     |  |
| 0.0079295 | 352.668389 | 228.225279 | 1.5452644 | NM_002243 | KCNJ15   |  |
| 0.0079915 | 69.4960341 | 55.0535557 | 1.2623351 | NM_171846 | LACTB    |  |
| 0.0080308 | 4230.41812 | 2883.943   | 1.4668869 | NM_022083 | C1orf24  |  |
| 0.0080701 | 78.1569398 | 53.726485  | 1.454719  | NM_001924 | GADD45A  | ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway, Cell cycle, MAPK signaling pathway  |
| 0.0083262 | 1358.69924 | 985.193655 | 1.379119  | NM_030769 | NPL      |  |
| 0.0090354 | 158.476473 | 192.559439 | 0.8230003 | NM_004793 | PRSS15   |  |
| 0.0091097 | 198.491142 | 136.417761 | 1.4550242 | NM_144653 | BTBD14A  |  |
| 0.009238  | 83.129073  | 110.305829 | 0.7536236 | NM_017607 | PPP1R12C |  |
| 0.0092556 | 126.856683 | 181.526362 | 0.6988334 | NM_139281 | WDR36    |  |
| 0.0095282 | 154.619444 | 194.177994 | 0.7962769 | NM_024056 | TMEM106C |  |
| 0.0095887 | 892.937636 | 1196.94543 | 0.7460137 | NM_019063 | EML4     |  |
| 0.0096633 | 89.6226922 | 56.5656362 | 1.5844017 | NM_017409 | HOXC10   | development  |
| 0.0097279 | 59.7622428 | 38.6757469 | 1.5452124 | NM_000208 | INSR     | Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Growth Hormone Signaling Pathway, Insulin Signaling Pathway, Adherens junction, Dentatorubropallidolusian atrophy (DRPLA), Insulin signaling pathway, Type II diabetes mellitus, immunology |

BRCA1 in DNA Damage Response

NF-κB Signaling, Dendritic Cell Maturation, Toll-like Receptor Signaling, TREM1 Signaling

BRCA1 in DNA Damage Response

NF-κB Signaling