The paper, “Genome-wide transcriptional analysis of T cell activation reveals differential gene expression associated with psoriasis”, asserts several genes are significantly upregulated or down regulated in patients with psoriasis compared to those who don’t . these results were found by first pruning the data by removing all genes that were not expressed in at least 3 patients. Then the average expression rate of those who had the disease was computed and compared to the average expression rate of those who didn’t have the gene. This was used to produce tables of relative fold changes. Attempts to reproduce these results were made however results differ from the paper. Table – shows the 13 most upregulated gene indicators as a result of this analysis.

"ILMN\_2058782" "ILMN\_2305112" "ILMN\_1701789" "ILMN\_2410826" "ILMN\_1721113"

“ILMN\_1658247" "ILMN\_2054297" "ILMN\_2184373" "ILMN\_1739428" "ILMN\_1729749"

“ILMN\_1700967" "ILMN\_2347798" "ILMN\_1670134"

The results from Table – differ from the results displayed in the paper. In the paper the principle gene discussed is SPATS2L, which the paper presented as being upregulated 1.37 fold in patients with psoriasis, however in our analysis, the gene was only upregulated 1.003101 fold. The cause of this discrepancy is unknown.