S3 Table. Functional gene classification using DAVID. The top three enrichment groups found from the 273 identifiable genes with statistical significance.

| Group | Enrichment Score* | Kappa** | Gene name |
|---|----------------------|---------|--|
| IL-1 Family | 8.851 | 0.97 | IL1F10: interleukin 1 family, member 10 (theta) |
| | | 0.94 | IL1F9: interleukin 1 family, member 9 |
| | | 0.89 | IL1F5: interleukin 1 family, member 5 (delta) |
| | | 0.71 | IL1F8: interleukin 1 family, member 8 (eta) |
| | | 0.57 | IL1RN; interleukin 1 receptor antagonist |
| | | 0.46 | IL33: interleukin 33 |
| Chemokine Family (C-C and C-X-C motif ligand) | 7.078 | 0.83 | CXCL2: chemokine (C-X-C motif) ligand 2 |
| | | 0.82 | CCL20: chemokine (C-C motif) ligand 20 |
| | | 0.81 | CCL3L3/L1: chemokine (C-C motif) ligand 3-like 3/1 |
| | | 0.80 | CXCL5: chemokine (C-X-C motif) ligand 5 |
| | | 0.77 | CXCL1: chemokine (C-X-C motif) ligand 1 |
| | | 0.59 | CCL3: chemokine (C-C motif) ligand 3 |
| | | 0.45 | IL8: interleukin 8 |
| | | 0.41 | GDF15: growth differentiation factor 15 |
| | | 0.38 | CCL5: chemokine (C-C motif) ligand 5 |
| | | 0.35 | IL1RN: interleukin 1 receptor antagonist |
| Histone Family | 3.172 | 0.93 | HIST1H2BD: histone cluster 1, H2bd |
| | | 0.92 | HIST2H2AA3/4: histone cluster 2, H2aa3; H2aa4 |
| | | 0.91 | H2AFJ: H2A histone family, member J |
| | | 0.90 | HIST1H2AC: histone cluster 1, H2ac |
| | | 0.90 | HIST2H2AC: histone cluster 2, H2ac |
| | | 0.88 | HIST1H2BF: histone cluster 1, H2bi |
| | | 0.88 | HIST2H2BE: histone cluster 2, H2be |
| | | 0.73 | HIST1H4J: histone cluster 1, H4I |
| | | 0.73 | H1F0: H1 histone family, member 0 |
| | | 0.51 | HJURP: Holliday junction recognition protein |

^{*}Geometric mean of the overall group significance based on gene EASE scores (modified Fisher Exact P-Value) in -log scale

^{**}Gene-to-gene Similarity Score: **Very high (0.75-1)**, High (0.5-0.75), Moderate (0.25-0.5), Low (<0.25)