**SUPPLEMENTAL TABLES**

**Novel Diagnostic Biomarkers Related to Necroptosis and immune infiltration landscape in Acute Myocardial Infarction**

**Inventory of Supplemental Information**

Supplement table 1: Oligonucleotides used for qPCR.

Supplement table 2: GO functional enrichment analysis for the NRDEGs

Supplement table 3: The KEGG Pathway Enrichment Analysis for the NRDEGs.

Supplement Table 1: Oligonucleotides used for qPCR.

|  |  |  |
| --- | --- | --- |
| mRNA | Forward (5’-3’) | Reverse (5’-3’) |
| TNF | CCTCTCTCTAATCAGCCCTCTG | GAGGACCTGGGAGTAGATGAG |
| IL1B | ATGATGGCTTATTACAGTGGCAA | GTCGGAGATTCGTAGCTGGA |
| TNFAIP3 | TCAACTGGTGTCGAGAAGTCC | CAAGTCTGTGTCCTGAACGC |
| TRAF5 | CCACTCGGTGCTTCACAAC | GTACCGGCCCAGAATAACCT |
| NLRP3 | CGTGAGTCCCATTAAGATGGAGT | CCCGACAGTGGATATAGAACAGA |
| TLR4 | AGACCTGTCCCTGAACCCTAT | CGATGGACTTCTAAACCAGCCA |
| GAPDH | TGTTGCCATCAATGACCCCTT | CTCCACGACGTACTCAGCG |

| Oncology | ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue |
| --- | --- | --- | --- | --- | --- | --- | --- |
| BP | GO:0043122 | regulation of I-kappaB kinase/NF-kappaB signaling | 7/15 | 237/18670 | 2.87E-10 | 4.89E-07 | 1.79E-07 |
| BP | GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 7/15 | 269/18670 | 6.95E-10 | 5.92E-07 | 2.17E-07 |
| BP | GO:0051090 | regulation of DNA-binding transcription factor activity | 7/15 | 432/18670 | 1.85E-08 | 5.27E-06 | 1.93E-06 |
| BP | GO:1904951 | positive regulation of establishment of protein localization | 7/15 | 456/18670 | 2.69E-08 | 6.55E-06 | 2.4E-06 |
| BP | GO:0051092 | positive regulation of NF-kappaB transcription factor activity | 6/15 | 149/18670 | 1.1E-09 | 6.25E-07 | 2.29E-07 |
| BP | GO:0043123 | positive regulation of I-kappaB kinase/NF-kappaB signaling | 6/15 | 183/18670 | 3.8E-09 | 1.62E-06 | 5.92E-07 |
| BP | GO:0051091 | positive regulation of DNA-binding transcription factor activity | 6/15 | 261/18670 | 3.17E-08 | 6.76E-06 | 2.47E-06 |
| BP | GO:0034599 | cellular response to oxidative stress | 6/15 | 302/18670 | 7.55E-08 | 9.89E-06 | 3.62E-06 |
| BP | GO:0009615 | response to virus | 6/15 | 326/18670 | 1.19E-07 | 1.22E-05 | 4.46E-06 |
| BP | GO:0071496 | cellular response to external stimulus | 6/15 | 339/18670 | 1.49E-07 | 1.34E-05 | 4.9E-06 |
| CC | GO:0035631 | CD40 receptor complex | 2/15 | 11/19717 | 2.96E-05 | 0.001628 | 0.001121 |
| CC | GO:0001891 | phagocytic cup | 2/15 | 27/19717 | 0.000188 | 0.005157 | 0.003553 |
| CC | GO:0043209 | myelin sheath | 2/15 | 49/19717 | 0.000622 | 0.011409 | 0.007861 |
| CC | GO:0005791 | rough endoplasmic reticulum | 2/15 | 85/19717 | 0.001859 | 0.025568 | 0.017616 |
| CC | GO:0005635 | nuclear envelope | 3/15 | 464/19717 | 0.004772 | 0.05249 | 0.036165 |
| MF | GO:0005164 | tumor necrosis factor receptor binding | 3/15 | 31/17697 | 2.18E-06 | 0.000181 | 8.47E-05 |
| MF | GO:0002020 | protease binding | 4/15 | 128/17697 | 3.35E-06 | 0.000181 | 8.47E-05 |
| MF | GO:0032813 | tumor necrosis factor receptor superfamily binding | 3/15 | 46/17697 | 7.32E-06 | 0.000263 | 0.000123 |
| MF | GO:0005126 | cytokine receptor binding | 4/15 | 286/17697 | 7.92E-05 | 0.002139 | 0.001001 |
| MF | GO:0031625 | ubiquitin protein ligase binding | 3/15 | 290/17697 | 0.001712 | 0.027456 | 0.012845 |
| MF | GO:0050662 | coenzyme binding | 3/15 | 291/17697 | 0.001729 | 0.027456 | 0.012845 |
| MF | GO:0043130 | ubiquitin binding | 2/15 | 76/17697 | 0.001843 | 0.027456 | 0.012845 |
| MF | GO:0044389 | ubiquitin-like protein ligase binding | 3/15 | 308/17697 | 0.002034 | 0.027456 | 0.012845 |
| MF | GO:0032182 | ubiquitin-like protein binding | 2/15 | 96/17697 | 0.00292 | 0.033968 | 0.015892 |
| MF | GO:0004843 | thiol-dependent ubiquitin-specific protease activity | 2/15 | 106/17697 | 0.003547 | 0.033968 | 0.015892 |

Supplement table 2: GO functional enrichment analysis for the NRDEGs.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| ONTOLOGY | ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue |
| KEGG | hsa04217 | Necroptosis | 15/15 | 159/8076 | 1.33E-26 | 1.43E-24 | 7.82E-25 |
| KEGG | hsa04621 | NOD-like receptor signaling pathway | 11/15 | 181/8076 | 6.68E-16 | 3.61E-14 | 1.97E-14 |
| KEGG | hsa04064 | NF-kappa B signaling pathway | 8/15 | 104/8076 | 3.44E-12 | 1.24E-10 | 6.76E-11 |
| KEGG | hsa05131 | Shigellosis | 7/15 | 246/8076 | 1.17E-07 | 3.15E-06 | 1.72E-06 |
| KEGG | hsa04657 | IL-17 signaling pathway | 5/15 | 94/8076 | 5.26E-07 | 1.14E-05 | 6.2E-06 |
| KEGG | hsa04668 | TNF signaling pathway | 5/15 | 112/8076 | 1.26E-06 | 2.27E-05 | 1.24E-05 |
| KEGG | hsa05132 | Salmonella infection | 6/15 | 249/8076 | 3.21E-06 | 4.41E-05 | 2.41E-05 |
| KEGG | hsa04210 | Apoptosis | 5/15 | 136/8076 | 3.3E-06 | 4.41E-05 | 2.41E-05 |
| KEGG | hsa05162 | Measles | 5/15 | 139/8076 | 3.67E-06 | 4.41E-05 | 2.41E-05 |
| KEGG | hsa05133 | Pertussis | 4/15 | 76/8076 | 9.14E-06 | 9.14E-05 | 4.99E-05 |
| KEGG | hsa05140 | Leishmaniasis | 4/15 | 77/8076 | 9.63E-06 | 9.14E-05 | 4.99E-05 |
| KEGG | hsa05164 | Influenza A | 5/15 | 171/8076 | 1.02E-05 | 9.14E-05 | 4.99E-05 |
| KEGG | hsa05152 | Tuberculosis | 5/15 | 180/8076 | 1.3E-05 | 0.000108 | 5.91E-05 |
| KEGG | hsa05130 | Pathogenic Escherichia coli infection | 5/15 | 197/8076 | 2.02E-05 | 0.000156 | 8.51E-05 |
| KEGG | hsa05169 | Epstein-Barr virus infection | 5/15 | 202/8076 | 2.28E-05 | 0.000164 | 8.96E-05 |
| KEGG | hsa04215 | Apoptosis - multiple species | 3/15 | 32/8076 | 2.49E-05 | 0.000167 | 9.13E-05 |
| KEGG | hsa04933 | AGE-RAGE signaling pathway in diabetic complications | 4/15 | 100/8076 | 2.72E-05 | 0.000167 | 9.13E-05 |
| KEGG | hsa05170 | Human immunodeficiency virus 1 infection | 5/15 | 212/8076 | 2.88E-05 | 0.000167 | 9.13E-05 |

Supplement table 3: The KEGG Pathway Enrichment Analysis for the NRDEGs.