**Suppl Table 4_Gene set enrichment and pathway analysis_10.4.2019**

| Comparison number | Comparison name                        | Number of DEGs | No of enriched GOBPs | No of enriched KEGGs | No of enriched GOBPs | No of enriched KEGGs | No of enriched REACTOME terms |
|-------------------|----------------------------------------|----------------|----------------------|----------------------|----------------------|----------------------|-----------------------------|
| 1                 | Violent vs Control + Non-Violent       | 34             | No significantly enriched | No significantly enriched | 29                   | 8                    | 6                           |
| 2                 | Violent vs Control                     | 4              | No significantly enriched | No significantly enriched | *                    | *                    | *                           |
| 3                 | Non-Violent vs Control                 | 4              | No significantly enriched | No significantly enriched | 165                  | 21                   | 27                          |
| 4                 | Violent vs Non-Violent                 | 28             | No significantly enriched | No significantly enriched | 34                   | 7                    | 9                           |

*Could not be produced because of an internal error. For unidentified reason the test would not run for the gene list.

**NEURONS**
violent vs. control + non-violent

**GOBPs**

| Term ID   | Term Description                                                                 | Gene Set Size | Normalized Enrichment Score (NES) | P-value  | Adjusted P-value |
|-----------|----------------------------------------------------------------------------------|---------------|-----------------------------------|----------|------------------|
| GO:0001817| regulation of cytokine production                                                 | 485           | -1.2110                           | 0.0002   | 0.039            |
| GO:0002250| adaptive immune response                                                          | 268           | -1.3260                           | 0.0002   | 0.039            |
| GO:0002253| activation of immune response                                                     | 435           | -1.2508                           | 0.0002   | 0.039            |
| GO:0002694| regulation of leukocyte activation                                                | 371           | -1.2191                           | 0.0002   | 0.039            |
| GO:0002697| regulation of immune effector process                                             | 275           | -1.2673                           | 0.0002   | 0.039            |
| GO:0002757| immune response-activating signal transduction                                   | 387           | -1.2422                           | 0.0002   | 0.039            |
| GO:0002764| immune response-regulating signaling pathway                                      | 419           | -1.2670                           | 0.0002   | 0.039            |
| GO:0002768| immune response-regulating cell surface receptor signaling pathway                | 304           | -1.2877                           | 0.0002   | 0.039            |
| GO:0009617| response to bacterium                                                             | 369           | -1.2131                           | 0.0002   | 0.039            |
| GO:0019221| cytokine-mediated signaling pathway                                               | 450           | -1.2314                           | 0.0002   | 0.039            |
| GO:0050865| regulation of cell activation                                                     | 404           | -1.2141                           | 0.0002   | 0.039            |
| GO:0050900| leukocyte migration                                                               | 299           | -1.2719                           | 0.0002   | 0.039            |
| GO:0051606| detection of stimulus                                                            | 311           | -1.3092                           | 0.0002   | 0.039            |
| GO:1901615| organic hydroxy compound metabolic process                                        | 383           | -1.2354                           | 0.0002   | 0.039            |
| GO:0002443| leukocyte mediated immunity                                                       | 235           | -1.2774                           | 0.0002   | 0.039            |
| GO:0007606| sensory perception of chemical stimulus                                           | 169           | -1.3329                           | 0.0002   | 0.039            |
| GO:0002460| adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 178 | -1.2706 | 0.0002 | 0.039 |
| GO:0009593| detection of chemical stimulus                                                    | 157           | -1.3543                           | 0.0002   | 0.039            |
| GO:0050906| detection of stimulus involved in sensory perception                              | 171           | -1.3517                           | 0.0002   | 0.039            |
### GO Terms

| Gene ID        | Term Description                                      | Gene Set Size | Normalized Enrichment Score (NES) | P-value | Adjusted P-value |
|---------------|-------------------------------------------------------|---------------|-----------------------------------|---------|------------------|
| GO:0098656    | anion transmembrane transport                         | 182           | -1.2671                           | 0.0002  | 0.039            |
| GO:1901617    | organic hydroxy compound biosynthetic process         | 157           | -1.2999                           | 0.0002  | 0.039            |
| GO:0015698    | inorganic anion transport                             | 139           | -1.3098                           | 0.0002  | 0.039            |
| GO:0009566    | fertilization                                         | 137           | -1.3546                           | 0.0002  | 0.039            |
| GO:0005906    | detection of chemical stimulus involved in sensory perception | 124       | -1.3673                           | 0.0002  | 0.039            |
| GO:0007608    | sensory perception of smell                           | 115           | -1.4028                           | 0.0002  | 0.039            |
| GO:0050911    | detection of chemical stimulus involved in sensory perception of smell | 90            | -1.4285                           | 0.0002  | 0.039            |
| GO:0009988    | cell-cell recognition                                 | 54            | -1.4257                           | 0.0002  | 0.039            |
| GO:0030049    | muscle filament sliding                                | 36            | -1.4492                           | 0.0002  | 0.039            |
| GO:0033275    | actin-myosin filament sliding                         | 36            | -1.4492                           | 0.0002  | 0.039            |

### KEGGs

| Term ID      | Term Description                                      | Gene Set Size | Normalized Enrichment Score (NES) | P-value | Adjusted P-value |
|--------------|-------------------------------------------------------|---------------|-----------------------------------|---------|------------------|
| hsa04740     | Olfactory transduction                                | 127           | -1.4154                           | 0.0002  | 0.031            |
| hsa05152     | Tuberculosis                                           | 153           | -1.3135                           | 0.0002  | 0.031            |
| hsa04060     | Cytokine-cytokine receptor interaction                | 179           | -1.2987                           | 0.0004  | 0.032            |
| hsa02010     | ABC transporters                                      | 44            | -1.4406                           | 0.0004  | 0.032            |
| hsa04650     | Natural killer cell mediated cytotoxicity             | 95            | -1.3552                           | 0.0006  | 0.036            |
| hsa04380     | Osteoclast differentiation                            | 109           | -1.3290                           | 0.0008  | 0.036            |
| hsa04610     | Complement and coagulation cascades                   | 65            | -1.3718                           | 0.0008  | 0.036            |
| hsa00190     | Oxidative phosphorylation                             | 128           | -1.2876                           | 0.0012  | 0.047            |

### REACTOME

| Term ID      | Term Description                                      | Gene Set Size | Normalized Enrichment Score (NES) | P-value | Adjusted P-value |
|--------------|-------------------------------------------------------|---------------|-----------------------------------|---------|------------------|
| 388396       | GPCR downstream signaling                              | 486           | -1.2028                           | 0.0002  | 0.006            |
| 186249       | Innate Immune System                                   | 499           | -1.2041                           | 0.0002  | 0.006            |
| 382551       | Transmembrane transport of small molecules            | 497           | -1.1993                           | 0.0002  | 0.006            |
| 1428517      | The citric acid (TCA) cycle and respiratory electron transport | 136       | -1.3285                           | 0.0006  | 0.013            |
| 1280218      | Adaptive Immune System                                 | 395           | -1.1864                           | 0.0012  | 0.020            |
| 1280215      | Cytokine Signaling in Immune system                    | 247           | -1.2084                           | 0.0034  | 0.040            |