

Suppl Table 3: Reactome pathway enrichment analysis of the 366 genes differentially edited between depressed patients (n=26) and controls (n=31)

| Pathway ID    | Pathway name                                     | Event hierarchy                     | Entities ratio | p(FDR)   |
|---------------|--------------------------------------------------|-------------------------------------|----------------|----------|
| R-HSA-202427  | Phosphorylation of CD3 and TCR zeta chains       | Adaptative Immune System            | 16/45          | 8.99E-10 |
| R-HSA-202433  | Generation of second messenger molecules         | Adaptative Immune System            | 16/58          | 1.79E-08 |
| R-HSA-202430  | Translocation of ZAP-70 to Immunological synapse | Adaptative Immune System            | 14/42          | 1.79E-08 |
| R-HSA-389948  | PD-1 signaling                                   | Adaptative Immune System            | 14/45          | 3.27E-08 |
| R-HSA-202403  | TCR signaling                                    | Adaptative Immune System            | 21/146         | 8.91E-07 |
| R-HSA-388841  | Costimulation by the CD28 family                 | Adaptative Immune System            | 19/97          | 1.30E-06 |
| R-HSA-202424  | Downstream TCR signaling                         | Adaptative Immune System            | 17/124         | 3.53E-05 |
| R-HSA-877300  | Interferon gamma signaling                       | Cytokine Signaling in Immune System | 21/250         | 2.73E-03 |
| R-HSA-2132295 | MHC class II antigen presentation                | Adaptative Immune System            | 15/148         | 4.53E-03 |
| R-HSA-9616222 | Transcriptional regulation of granulopoiesis     | Developmental biology               | 9/71           | 2.72E-02 |