**Supplementary Table 1: FUSION analysis in East Asian COPD patients identified 35 genes across all tissues.**

|  |  |  |
| --- | --- | --- |
| **Items**  | ***P-value*** | ***Z score***  |
| **Adipose** |  |  |
| **Subcustaneous** |  |  |
| *MICA* | 1.50E-07 | -5.25  |
| *CYP2B7P* | 1.71E-07 | 5.23  |
| *LINC02356* | 7.23E-07 | -4.96  |
| *AGER* | 3.91E-06 | 4.62  |
| **Visceral omentum** |  |  |
| *ITPKC* | 2.91E-08 | -5.55  |
| *LINC02356* | 7.54E-07 | -4.95  |
| *CIB2* | 2.97E-06 | -4.67  |
| *MICA* | 5.45E-06 | -4.55  |
| **Adrenal gland** |  |  |
| *LRP11* | 3.18E-08 | 5.53  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Artery** |  |  |
| **Aorta** |  |  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Coronary** |  |  |
| *CYP2T1P* | 6.11E-08 | 5.42  |
| *GNPDA2* | 1.06E-05 | 4.40  |
| **Tibial** |  |  |
| *CYP2T1P* | 9.36E-09 | 5.74  |
| *ITPKC* | 2.00E-07 | -5.20  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Brain** |  |  |
| **Amygdala** |  |  |
| *CIB2* | 2.97E-06 | -4.67  |
| *SH2D7* | 1.64E-05 | -4.31  |
| **Anterior cingulate cortex BA24** |  |  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Caudate basal ganglia** |  |  |
| *CHRNA3* | 3.01E-08 | -5.54  |
| *CYP2B7P* | 1.76E-07 | 5.22  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Cerebellar hemisphere** |  |  |
| *CHRNB2* | 9.00E-08 | -5.35  |
| **Cerebellum** |  |  |
| *CHRNB2* | 9.00E-08 | -5.35  |
| *PSMA4* | 8.96E-07 | -4.91  |
| **Cortex** |  |  |
| *CYP2A7* | 6.53E-07 | -4.97  |
| *SH2D7* | 1.23E-06 | -4.85  |
| **Frontal cortex BA9** |  |  |
| *CYP2T1P* | 4.03E-12 | 6.94  |
| *EGLN2* | 8.88E-07 | 4.92  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Hippocampus** |  |  |
| *PSMA4* | 5.70E-07 | -5.00  |
| *CYP2A7* | 1.17E-06 | -4.86  |
| **Hypothalamus** |  |  |
| *CYP2A7* | 1.18E-06 | -4.86  |
| *CIB2* | 2.27E-06 | -4.73  |
| *CHRNB2* | 9.28E-06 | -4.43  |
| **Nucleus accumbens basal ganglia** |  |  |
| *CYP2A7* | 5.98E-11 | -6.54  |
| *CYP2B7P* | 1.46E-06 | 4.82  |
| *CIB2* | 8.48E-06 | -4.45  |
| **Putamen basal ganglia** |  |  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Spinal cord cervical c-1** |  |  |
| *LY6G5B* | 7.25E-07 | 4.95  |
| *CYP2A7* | 1.25E-06 | -4.85  |
| **Substantia nigra** |  |  |
| *CIB2* | 2.97E-06 | -4.67  |
| *MICA* | 1.27E-05 | -4.37  |
| **Breast mammary tissue** |  |  |
| *MICA* | 3.77E-07 | -5.08  |
| *CIB2* | 1.30E-06 | -4.84  |
| **Cells** |  |  |
| **Cultured fibroblasts** |  |  |
| *ADAM1B* | 1.21E-06 | -4.85  |
| *CIB2* | 2.97E-06 | -4.67  |
| *ITPKC* | 3.32E-06 | -4.65  |
| *ACAD10* | 3.60E-06 | -4.63  |
| **EBV-transformed lymphocytes** |  |  |
| *PHETA1* | 4.11E-11 | -6.60  |
| *ITPKC* | 3.69E-06 | -4.63  |
| *CIB2* | 6.94E-06 | -4.50  |
| *MICA* | 7.33E-06 | -4.48  |
| **Colon** |  |  |
| **Sigmoid** |  |  |
| *CHRNA5* | 9.10E-12 | 6.82  |
| *CYP2T1P* | 9.92E-07 | 4.89  |
| *CIB2* | 2.97E-06 | -4.67  |
| *CYP2B7P* | 4.21E-06 | 4.60  |
| **Transverse** |  |  |
| *MAPKAPK5-AS1* | 5.28E-17 | 8.38  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Esophagus** |  |  |
| **Gastroesophageal junction** |  |  |
| *CYP2T1P* | 1.77E-08 | 5.63  |
| *BRD2* | 1.68E-06 | 4.79  |
| *MICA* | 2.10E-06 | -4.74  |
| *SH2D7* | 5.25E-06 | -4.55  |
| *ZBTB44-DT* | 5.96E-06 | 4.53  |
| **Mucosa** |  |  |
| *CYP2T1P* | 3.48E-08 | 5.52  |
| **Muscularis** |  |  |
| *CYP2T1P* | 3.89E-08 | 5.50  |
| **Heart** |  |  |
| **Atrial appendage** |  |  |
| *CIB2* | 2.36E-08 | -5.58  |
| *CYP2T1P* | 8.88E-07 | 4.92  |
| *CYP2B7P* | 1.02E-06 | 4.89  |
| *SPTBN4* | 5.61E-06 | 4.54  |
| **Left ventricle** |  |  |
| *CIB2* | 2.09E-09 | -5.99  |
| *CYP2B7P* | 8.24E-07 | 4.93  |
| *ACAD10* | 1.83E-06 | -4.77  |
| *TMEM116* | 5.36E-06 | -4.55  |
| **Kidney cortex** |  |  |
| NA | NA | NA  |
| **Liver** |  |  |
| *CYP2A7P1* | 1.09E-06 | -4.87  |
| **Lung** |  |  |
| *HECTD4* | 2.99E-20 | -9.22  |
| *CYP2B7P* | 4.64E-12 | -6.92  |
| *C19orf54* | 2.06E-07 | 5.19  |
| *EGLN2* | 8.88E-07 | 4.92  |
| *MICA* | 1.74E-06 | -4.78  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Minor salivary gland** |  |  |
| *MICA* | 5.25E-06 | -4.55  |
| **Muscle skeletal** |  |  |
| *CYP2G1P* | 8.53E-10 | 6.13  |
| *HYKK* | 3.12E-09 | 5.93  |
| *CYP2T1P* | 1.12E-08 | 5.71  |
| *SH2D7* | 2.97E-06 | -4.67  |
| **Tibial Nerve** |  |  |
| *MICA* | 3.37E-07 | -5.10  |
| *ITPKC* | 1.94E-06 | -4.76  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Ovary** |  |  |
| *CIB2* | 2.97E-06 | -4.67  |
| *GUF1* | 9.00E-06 | -4.44  |
| **Pancreas** |  |  |
| *TMEM116* | 4.46E-10 | -6.24  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Pituitary** |  |  |
| *CYP2B7P* | 1.36E-08 | 5.68  |
| *CIB2* | 1.28E-06 | -4.84  |
| *CYP2G1P* | 1.95E-06 | 4.76  |
| *MICA* | 1.96E-06 | -4.76  |
| **Prostate** |  |  |
| *CYP2B7P* | 5.22E-09 | 5.84  |
| *MICA* | 7.62E-08 | -5.38  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Skin** |  |  |
| **Not sun exposed suprapubic** |  |  |
| *CYP2T1P* | 1.02E-08 | 5.73  |
| *RAB4B* | 1.67E-08 | 5.64  |
| *CIB2* | 4.87E-08 | -5.46  |
| *MICA* | 2.93E-07 | -5.13  |
| *MAPKAPK5-AS1* | 5.69E-07 | 5.00  |
| **Sun exposed lower leg** |  |  |
| *CYP2T1P* | 9.36E-09 | 5.74  |
| *MICA* | 2.95E-07 | -5.13  |
| **Small intestine terminal ileum** |  |  |
| *MICA* | 8.84E-07 | -4.92  |
| *MAPKAPK5* | 5.57E-06 | 4.54  |
| **Spleen** |  |  |
| *RAB4B* | 1.28E-10 | 6.43  |
| *MICA* | 7.88E-08 | -5.37  |
| *RPS23P10* | 1.10E-06 | -4.87  |
| *CYP2T1P* | 4.96E-06 | 4.57  |
| *TMEM116* | 5.63E-06 | -4.54  |
| **Stomach** |  |  |
| *CYP2B7P* | 4.46E-19 | 8.93  |
| *TMEM116* | 4.46E-10 | -6.24  |
| *CIB2* | 2.97E-06 | -4.67  |
| **Testis** |  |  |
| *LINC01405* | 4.86E-07 | -5.03  |
| *MICA* | 7.45E-07 | -4.95  |
| **Uterus** |  |  |
| *CYP2A7* | 1.25E-06 | -4.85  |
| *GNPDA2* | 4.44E-06 | 4.59  |
| **Vagina** |  |  |
| *CYP2A7* | 1.38E-06 | -4.83  |
| **Whole blood** |  |  |
| *EGLN2* | 2.85E-11 | -6.65  |
| *PSMA4* | 2.89E-11 | -6.65  |
| *RAB4B* | 2.41E-10 | 6.33  |
| *MICA* | 1.29E-09 | -6.07  |
| *CIB2* | 2.97E-06 | -4.67  |

COPD: Chronic obstructive pulmonary disease; FUSION: Functional Summary-based Imputation. NA: Not available.

**Supplementary Table 2: UTMOST analysis in East Asian COPD patients identified 34 genes across all tissues.**

|  |  |  |
| --- | --- | --- |
| **Items** | ***P-value*** | ***Z score***  |
| **Adipose** |  |  |
| **Subcutaneous** |  |  |
| *TCTN1* | 2.46E-09 | -5.96  |
| *SNRPA* | 3.57E-09 | 5.90  |
| *FAM109A* | 4.89E-08 | 5.46  |
| *RAB4B* | 1.43E-07 | 5.26  |
| **Visceral omentum** |  |  |
| *SNRPA* | 2.88E-15 | -7.90  |
| *RAB4B* | 2.28E-12 | 7.02  |
| *PKD2* | 9.75E-10 | -6.11  |
| *PPP1CC* | 2.09E-09 | 5.99  |
| *CYP2S1* | 3.03E-07 | 5.12  |
| *PLD3* | 3.08E-07 | -5.12  |
| *FAM216A* | 8.33E-07 | 4.93  |
| *ATXN2* | 1.34E-06 | 4.83  |
| **Adrenal gland** |  |  |
| *SNRPA* | 1.85E-10 | -6.37  |
| *TCTN1* | 6.51E-09 | -5.80  |
| *ADCK4* | 1.51E-06 | -4.81  |
| *EGLN2* | 1.77E-06 | -4.78  |
| *SH2B3* | 1.84E-06 | -4.77  |
| **Artery** |  |  |
| **Aorta** |  |  |
| *TCTN1* | 3.84E-10 | -6.26  |
| *PPP1CC* | 6.78E-09 | 5.80  |
| *HECTD4* | 4.07E-08 | -5.49  |
| **Coronary** |  |  |
| *MYL2* | 8.54E-11 | -6.49  |
| *SNRPA* | 3.37E-10 | -6.28  |
| *TCTN1* | 7.71E-09 | -5.78  |
| *BLVRB* | 9.90E-07 | -4.89  |
| **Tibial** |  |  |
| *FAM109A* | 8.30E-08 | 5.36  |
| *ADCK4* | 9.55E-08 | -5.34  |
| *TCTN1* | 1.83E-07 | -5.22  |
| *MYL2* | 3.08E-06 | 4.67  |
| **Brain** |  |  |
| **Anterior cingulate cortex BA24** |  |  |
| *EGLN2* | 3.49E-09 | 5.91  |
| *TCTN1* | 3.17E-08 | 5.53  |
| *NUMBL* | 4.42E-08 | -5.47  |
| *SH2B3* | 1.74E-07 | -5.23  |
| *MYL2* | 2.74E-07 | -5.14  |
| *PKD2* | 3.34E-07 | 5.10  |
| **Caudate basal ganglia** |  |  |
| *SNRPA* | 3.32E-11 | -6.63  |
| *TRAFD1* | 1.64E-10 | -6.39  |
| *SH2B3* | 6.79E-07 | -4.97  |
| **Cerebellar hemisphere** |  |  |
| *TCTN1* | 3.12E-08 | 5.54  |
| *SH2B3* | 2.51E-06 | -4.71  |
| **Cerebellum** |  |  |
| NA | NA | NA  |
| **Cortex** |  |  |
| *SNRPA* | 1.52E-08 | -5.66  |
| *MYL2* | 1.40E-06 | -4.83  |
| *ADCK4* | 1.55E-06 | -4.81  |
| **Frontal cortex BA9** |  |  |
| *BRAP* | 1.43E-09 | -6.05  |
| *TRAFD1* | 1.65E-07 | -5.24  |
| **Hippocampus** |  |  |
| *PLD3* | 3.74E-14 | 7.57  |
| *FAM216A* | 7.63E-10 | 6.15  |
| *BRAP* | 2.69E-08 | 5.56  |
| *PPP1CC* | 1.54E-07 | 5.25  |
| *SH2B3* | 2.31E-07 | -5.17  |
| *GABRG2* | 1.22E-06 | -4.85  |
| *CNTD2* | 2.12E-06 | 4.74  |
| **Hypothalamus** |  |  |
| *SNRPA* | 3.06E-09 | 5.93  |
| *ALDH2* | 7.55E-09 | 5.78  |
| *SH2B3* | 1.06E-07 | -5.32  |
| **Nucleus accumbens basal ganglia** |  |  |
| *SH2B3* | 4.04E-07 | -5.07  |
| *TCTN1* | 3.14E-06 | 4.66  |
| **Putamen basal ganglia** |  |  |
| *PLD3* | 1.09E-08 | 5.72  |
| *SNRPA* | 1.35E-07 | 5.27  |
| *PKD2* | 3.79E-07 | -5.08  |
| *ADCK4* | 1.20E-06 | -4.86  |
| **Mammary tissue** |  |  |
| *BRAP* | 2.67E-15 | 7.91  |
| *EGLN2* | 1.27E-12 | -7.10  |
| *FAM109A* | 1.83E-10 | 6.38  |
| *FAM216A* | 3.86E-09 | 5.89  |
| *PPTC7* | 1.92E-06 | 4.76  |
| **Cells**  |  |  |
| **EBV-transformed lymphocytes** |  |  |
| *SNRPA* | 3.66E-15 | 7.87  |
| **Transformed fibroblasts** |  |  |
| *PLD3* | 1.41E-08 | -5.67  |
| *ADCK4* | 2.73E-07 | -5.14  |
| *FAM216A* | 7.15E-07 | 4.96  |
| *TCTN1* | 9.07E-07 | -4.91  |
| *RAB4B* | 1.49E-06 | 4.81  |
| **Colon** |  |  |
| **Sigmoid** |  |  |
| *SNRPA* | 8.69E-13 | -7.15  |
| **Transverse** |  |  |
| *SH2B3* | 4.36E-08 | -5.48  |
| *RAB4B* | 2.10E-07 | 5.19  |
| *SNRPA* | 2.40E-07 | 5.17  |
| **Esophagus** |  |  |
| **Gastroesophageal junction** |  |  |
| *BRAP* | 5.81E-15 | -7.81  |
| *SNRPA* | 2.70E-14 | -7.61  |
| *PKD2* | 2.53E-09 | -5.96  |
| **Mucosa** |  |  |
| *TRAFD1* | 9.98E-07 | 4.89  |
| **Muscularis** |  |  |
| *ADCK4* | 5.99E-11 | -6.54  |
| *PLD3* | 1.02E-08 | -5.73  |
| *PSMC4* | 1.03E-07 | -5.32  |
| *SNRPA* | 1.98E-07 | -5.20  |
| *BRAP* | 3.32E-07 | -5.10  |
| **Heart** |  |  |
| **Atrial appendage** |  |  |
| *HVCN1* | 7.65E-08 | -5.38  |
| **Left ventricle** |  |  |
| *FAM109A* | 1.73E-06 | 4.78  |
| **Liver** |  |  |
| *BRAP* | 9.91E-08 | -5.33  |
| **Lung** |  |  |
| *SNRPA* | 5.60E-09 | -5.83  |
| *RAB4B* | 2.15E-08 | 5.60  |
| *TRAFD1* | 5.53E-08 | 5.43  |
| *EGLN2* | 1.39E-06 | 4.83  |
| **Muscle skeletal** |  |  |
| *BRAP* | 1.83E-23 | 9.98  |
| *TCTN1* | 9.94E-07 | -4.89  |
| *SH2B3* | 2.88E-06 | -4.68  |
| **Tibial nerve** |  |  |
| *FAM109A* | 9.52E-13 | 7.14  |
| *BRAP* | 8.10E-10 | -6.14  |
| *TCTN1* | 2.78E-09 | -5.94  |
| *CNTD2* | 1.64E-08 | -5.65  |
| *MIA* | 2.65E-07 | -5.15  |
| **Ovary** |  |  |
| *PLD3* | 4.72E-13 | -7.23  |
| *ALDH2* | 2.17E-12 | -7.02  |
| *PKD2* | 7.04E-10 | 6.17  |
| *ADCK4* | 8.14E-09 | -5.77  |
| *SH2B3* | 8.45E-09 | -5.76  |
| *NUMBL* | 1.25E-07 | -5.29  |
| *TCTN1* | 2.24E-07 | -5.18  |
| *ACAD10* | 8.92E-07 | -4.91  |
| **Pancreas** |  |  |
| *SNRPA* | 8.02E-12 | -6.84  |
| *TCTN1* | 3.06E-09 | -5.93  |
| *FAM216A* | 1.28E-06 | 4.84  |
| **Pituitary** |  |  |
| *SNRPA* | 9.77E-18 | -8.58  |
| *ADCK4* | 1.73E-12 | -7.06  |
| *EGLN2* | 1.58E-09 | 6.04  |
| *SH2B3* | 1.35E-06 | -4.83  |
| *NUMBL* | 2.30E-06 | -4.73  |
| *RAB4B* | 3.21E-06 | 4.66  |
| **Prostate** |  |  |
| *PKD2* | 4.14E-10 | -6.25  |
| *RAB4B* | 2.48E-09 | 5.96  |
| *IDH3A* | 2.01E-08 | 5.61  |
| *ATP2A2* | 3.08E-07 | 5.12  |
| **Skin** |  |  |
| **Not sun exposed suprapubic** |  |  |
| *RAB4B* | 7.92E-08 | 5.37  |
| **Sun exposed lower leg** |  |  |
| *SH2B3* | 1.49E-14 | -7.69  |
| *BRAP* | 3.65E-10 | -6.27  |
| *TCTN1* | 1.73E-08 | -5.64  |
| *CIB2* | 2.63E-07 | -5.15  |
| *NUMBL* | 3.06E-07 | -5.12  |
| *RAB4B* | 3.71E-07 | 5.08  |
| **Small intestine terminal ileum** |  |  |
| *RAB4B* | 1.45E-09 | 6.05  |
| *PPP1CC* | 1.45E-08 | 5.67  |
| **Spleen** |  |  |
| *PPP1CC* | 6.87E-11 | -6.52  |
| *RAB4B* | 3.23E-09 | 5.92  |
| *NUMBL* | 2.98E-08 | -5.54  |
| *BTN1A1* | 7.53E-07 | -4.95  |
| **Stomach** |  |  |
| *ADCK4* | 9.98E-08 | -5.33  |
| *CEACAM5* | 1.32E-07 | 5.28  |
| *FAM109A* | 2.88E-06 | 4.68  |
| **Testis** |  |  |
| *SNRPA* | 4.19E-12 | -6.93  |
| *PPP1CC* | 1.28E-10 | 6.43  |
| *CYP2F1* | 4.92E-08 | -5.45  |
| *RAB4B* | 1.11E-07 | 5.31  |
| **Thyroid** |  |  |
| *PLD3* | 1.11E-10 | 6.45  |
| *SNRPA* | 2.07E-08 | 5.61  |
| *RAB4B* | 9.64E-08 | 5.33  |
| *EGLN2* | 1.59E-07 | 5.24  |
| *HVCN1* | 6.63E-07 | -4.97  |
| **Uterus** |  |  |
| *SNRPA* | 1.85E-11 | 6.72  |
| *ADCK4* | 3.11E-06 | -4.66  |
| **Vagina** |  |  |
| *NUMBL* | 9.06E-15 | -7.75  |
| *EGLN2* | 1.08E-11 | -6.80  |
| *FAM216A* | 5.29E-07 | 5.02  |
| *C11orf80* | 1.28E-06 | -4.84  |
| **Whole blood** |  |  |
| *NUMBL* | 3.91E-18 | 8.68  |
| *EGLN2* | 3.56E-11 | -6.62  |
| *TRAFD1* | 7.43E-08 | -5.38  |
| *PKD2* | 1.25E-06 | -4.85  |

COPD: Chronic obstructive pulmonary disease; UTMOST: Unified Test for Molecular Signatures. NA: Not available.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Items**  | **Description** | **Count** | **Ratio** | **Log10(*P*)** |
| **GO functional and KEGG pathway enrichment analyses** |
| GO:0035095 | Behavioral response to nicotine | 3 | 8.57 | −7.10 |
| GO:0046395 | Carboxylic acid catabolic process | 3 | 8.57 | −2.68 |
| GO:0001666 | Response to hypoxia | 3 | 8.57 | −2.41 |
| GO:0006631 | Fatty acid metabolic process | 3 | 8.57 | −2.20 |
| R-HSA-5683057 | MAPK family signaling cascades | 3 | 8.57 | −2.20 |
| **The summary of the enrichment analysis in DisGeNET** |
| C1519383 | Smoking behaviors | 9 | 26.00 | −11.00 |
| C0016529 | Forced expiratory volume function | 7 | 20.00 | −7.60 |
| C0037369 | Smoking | 7 | 20.00 | −6.50 |
| C1861063 | Tobacco addiction, susceptibility to tabacco | 3 | 8.60 | −6.50 |
| C3696898 | Autosomal dominant nocturnal frontal lobe epilepsy | 3 | 8.60 | −6.00 |

**Supplementary Table 3: Top five clusters with their representative enriched terms (one per cluster) and top five enrichment analysis in DisGeNET (FUSION).**

Count: The number of genes in the user-provided lists with membership in the given ontology term; Ratio: The percentage of all the user-provided genes that are found in the given ontology term; FUSION: Functional Summary-based Imputation; Log10(P): The p-value in log base 10.

**Supplementary Table 4: Top five clusters with their representative enriched terms (one per cluster) and top five enrichment analysis in DisGeNET (UTMOST).**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Items**  | **Description** | **Count** | **Ratio** | **Log10(*P*)** |
| **GO functional and KEGG pathway enrichment analysis** |
| R-HSA-211945 | Phase I – functionalization of compounds | 3 | 8.82 | −3.63 |
| hsa05017 | Spinocerebellar ataxia | 3 | 8.82 | −3.25 |
| hsa04261 | Adrenergic signaling in cardiomyocytes | 3 | 8.82 | −3.19 |
| GO:0005975 | Carbohydrate metabolic process | 4 | 11.76 | −2.76 |
| GO:0071407 | Cellular response to organic cyclic compound | 4 | 11.76 | −2.62 |
| **The summary of the enrichment analysis in DisGeNET** |
| C0013124 | Drinking behavior processes | 4 | 12.00 | −10.00 |
| C0202239 | Uric acid measurement (procedure) | 8 | 24.00 | −9.30 |
| C0001948 | Alcohol consumption | 6 | 18.00 | −6.90 |
| C0032181 | Platelet count measurement | 6 | 18.00 | −6.30 |
| C0200638 | Eosinophil count procedure | 7 | 21.00 | −5.40 |

Count: The number of genes in the user-provided lists with membership in the given ontology term; Ratio: The percentage of all the user-provided genes that are found in the given ontology term; UTMOST: Unified Test for MOlecular SignaTures; Log10(P): The p-value in log base 10.