**Supplementary Table 1. Pathway analysis of SNPH-associated proteins.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Group** | **N Proteins** | **Ingenuity Pathway Name** | **Name** | ***p* value** | **FDR** | **N Proteins Total** | **N Proteins unique** |
| **Ubiquitination** | 34 | **Protein Ubiquitination Pathway** | **Protein Ubiquitination** | **1E-19** | 0.00% | **27** | **13** |
| Aldosterone Signaling in Epithelial Cells | Aldosterone Signaling | 7E-06 | 0.02% | 10 | 1 |
| Unfolded protein response | Unfolded protein response | 2E-05 | 0.04% | 6 | 0 |
| eNOS Signaling | eNOS | 0.0014 | 1.58% | 7 | 1 |
| NRF2-mediated Oxidative Stress Response | Oxidative Stress response | 0.0007 | 0.79% | 8 | 3 |
| **RNA translation** | 29 | **EIF2 Signaling** | **EIF2** | **2E-19** | 0.00% | **25** | **14** |
| Regulation of eIF4 and p70S6K Signaling | eIF4/p70S6K | 5E-08 | 0.00% | 12 | 0 |
| mTOR Signaling | mTOR | 1E-07 | 0.00% | 13 | 0 |
| **DNA damage** | 13 | **Cell Cycle: G2/M DNA Damage Checkpoint Regulation** | **G2/M DNA damage checkpoint** | **5E-07** | 0.00% | **7** | **2** |
| HIPPO signaling | HIPPO | 2E-07 | 0.00% | 9 | 1 |
| PI3K/AKT Signaling | PI3K/AKT | 0.0015 | 1.58% | 6 | 1 |
| p70S6K Signaling | p70S6K | 0.002 | 1.82% | 6 | 1 |
| **Cytoskeleton** | 17 | **Breast Cancer Regulation by Stathmin1** | **Stathmin** | **4E-05** | 0.07% | **10** | **1** |
| 14-3-3-mediated Signaling | 14-3-3-mediated Signaling | 6E-06 | 0.02% | 9 | 0 |
| Phagosome Maturation | Phagosome maturation | 0.0001 | 0.18% | 8 | 1 |
| Epithelial Adherens Junction Signaling | Epithelial Adherens Junction | 0.0006 | 0.78% | 7 | 1 |
| Germ Cell-Sertoli Cell Junction Signaling | Germ Cell-Sertoli Cell Junction | 0.0017 | 1.62% | 7 | 0 |
| Remodeling of Epithelial Adherens Junctions | Remodeling of Epithelial Adherens Junction | 6E-05 | 0.11% | 6 | 0 |
| **Mitochondrial** | 7 | **Mitochondrial Dysfunction** | **Mitochondrial dysfunction** | **0.0016** | 1.58% | **7** | **6** |
| **Endocytosis** | 6 | **Caveolar-mediated Endocytosis Signaling** | **Caveolar-mediated Endocytosis** | **7E-05** | 0.12% | **6** | **5** |

Enrichment of canonical pathways among the list of SNPH-associated proteins was done using Ingenuity Pathway Analysis software (IPA®, QIAGEN Redwood City, [www.qiagen.com/ingenuity](http://www.qiagen.com/ingenuity)). Pathways with FDR <5% and more than 5 genes were considered as significant. The number of overlapped proteins was used to group pathways with at least 50% overlap, resulting in 6 groups. The main pathway for each group was selected as a pathway with the most unique proteins (best significance in case of pathways with the same number of unique proteins).