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| **Supplementary Table 9. Gene set enrichment analysis (MAGENTA) for European Americans of biological pathways with at least one gene from the confirmed loci1.** |
| Database | Gene set | Original No. of genes in gene set | No. of genes in gene set analyzed by MAGENTA | Nominal GSEA P value | FDR q-value2 | No. of genes expected above 75th percentile cutoff | No. of genes observed above 75th percentile cutoff | Genes within 300 kb from the confirmed SNPs |
| BIOCARTA |   |   |   |   |   |   |   |   |
|   | VEGF\_PATHWAY | 29 | 27 | 0.05 | 0.36 | 7 | 11 | EIF2S1 |
| GOTERM |   |   |   |   |   |   |   |   |
|   | catalytic activity | 122 | 113 | 0.03 | 0.27 | 28 | 38 | PIGH |
|   | actin cytoskeleton organization | 119 | 104 | 0.03 | 0.27 | 26 | 35 | PLEK2 |
|   | ATPase activity, coupled to transmembrane movement of substances | 31 | 24 | 0.05 | 0.36 | 6 | 10 | ATP6V1D |
| 1. Pathways with a nominal P value < 0.05 are summarized. |
| 2. Multiple testing correction was conducted separately for each database due to considerable overlap of gene sets between databases. |