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| Supplementary Table 4-1. Enrichment analysis for KEGG pathway with the GWAS results: all subjects | | |
| Gene category | Number of genes | P-value |
| Styrene degradation | 4 | 0.001 |
| Bisphenol A degradation | 13 | 0.006 |
| Methionine metabolism | 15 | 0.010 |
| Glycosylphosphatidylinositolgpianchor biosynthesis | 20 | 0.020 |
| Selenoamino acid metabolism | 33 | 0.024 |
| Metabolism of xenobiotics by cytochrome P450 | 65 | 0.030 |
| Glutathione metabolism | 33 | 0.035 |
| Cysteine metabolism | 24 | 0.035 |
| Cytokinecytokine receptor interaction | 236 | 0.036 |
| Chondroitin sulfate biosynthesis | 16 | 0.037 |
| Synthesis and degradation of ketone bodies | 8 | 0.037 |
| Gammahexachlorocyclohexane degradation | 24 | 0.042 |
| TGFbeta signaling pathway | 82 | 0.047 |
| Ecmreceptor interaction | 84 | 0.048 |
| No gene category was significantly associated after multiple testing correction (P > 0.05/168) | | |
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| Supplementary Table 4-2. Enrichment analysis for KEGG pathway with the GWAS results: older subjects (age>56 ) | | |
| Gene category | Number of genes | P-value |
| Styrene degradation | 4 | 0.003 |
| Riboflavin metabolism | 16 | 0.004 |
| Fluorene degradation | 2 | 0.007 |
| Methionine metabolism | 15 | 0.010 |
| Thiamine metabolism | 5 | 0.013 |
| Gammahexachlorocyclohexane degradation | 24 | 0.029 |
| Cytokinecytokine receptor interaction | 236 | 0.038 |
| Custom calcium channel | 26 | 0.038 |
| Glycosaminoglycan degradation | 14 | 0.039 |
| Chondroitin sulfate biosynthesis | 16 | 0.039 |
| Maturity onset diabetes of the young | 22 | 0.041 |
| No gene category was significantly associated after multiple testing correction (P > 0.05/168) | | |
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| Supplementary Table 4-3. Enrichment analysis for KEGG pathway with the GWAS results: younger subjects (age≦56) | | |
| Gene category | Number of genes | P-value |
| Glycerolipid metabolism | 53 | 0.001 |
| Reductive carboxylate cycle CO2 fixation | 11 | 0.010 |
| Ubiquinone biosynthesis | 7 | 0.015 |
| Starch and sucrose metabolism | 74 | 0.019 |
| Pyruvate metabolism | 42 | 0.032 |
| Porphyrin and chlorophyll metabolism | 32 | 0.037 |
| Bile acid biosynthesis | 40 | 0.039 |
| Antigen processing and presentation | 66 | 0.045 |
| Nglycan degradation | 16 | 0.048 |
| No gene category was significantly associated after multiple testing correction (P > 0.05/168) | | |