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| **S1 Table. Risk allele effect comparison between lean and non-lean GDM samples.** |
|  |  |  | **Lean**(N=184/125) | **Non-Lean**(N=128/248) |  |
| **GENE** | **SNP** | **A1** | **OR** | ***P* value** | **OR** | ***P* value** | **t test *P* value** |
| *TCF7L2* | rs7901695 | C | 2.649 | **0.001768** | 1.897 | **0.009695** | 0.3957 |
| rs4506565 | T | 2.211 | **0.005541** | 2.03 | **0.003126** | 0.8176 |
| rs7903146 | T | 2.365 | **0.003477** | 1.956 | **0.00634** | 0.618 |
| rs12243326 | C | 2.473 | **0.01136** | 3.327 | **9.87x10-05** | 0.5284 |
| *KCNQ1* | rs2237892 | T | 0.6298 | **0.04575** | 0.5216 | **0.0008519** | 0.5307 |
| rs2237897 | T | 0.6123 | **0.03994** | 0.4698 | **0.0002011** | 0.3956 |
| *CENTD2* | rs1552224 | T | 1.154 | 0.7406 | 1.573 | 0.2567 | 0.5999 |
| *MNTR1B* | rs1387153 | T | 0.888 | 0.6337 | 1.761 | **0.01297** | **0.0432** |
| Logistic regression corrected for age, Native American ancestry and dummy reference hospital. **t test *P* value** of comparison between risk allele effect of lean and non-lean GDM samples. **N** is the sample size of controls/cases used in the analyses. |