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| **S4 Table. Functional annotation of the genetic variants associated to the risk of GDM and related metabolic traits in Mexican women.** |
| **GENE** | **CHR** | **BAND** | **SNP** | **ALLELE** | **STRAND** | **PREDICTED FUNCTION** | **cDNA POS** | **SPLICE DISTANCE** |
| *CENTD2* | 11 | q13.4 | rs1552224 | A|C | 1 | 5’UTR | 306 | NA |
| *KCNQ1* | 11 | p15.4 | rs2237892 | C|T | 1 | Intronic | NA | 29246 |
| rs2237897 | C|T | 1 | Intronic | NA | 10451 |
| *MTNR1B* | 11 | q14.3 | rs1387153 | C|T | 1 | Intergenic | NA | NA |
| *TCF7L2* | 10 | q25.2 | rs12243326 | T|C | 1 | Intronic | NA | 10969 |
| rs4506565 | A|T | 1 | Intronic | NA | 31658 |
| rs7901695 | T|GCA | 1 | Intronic | NA | 29705 |
| rs7903146 | C|T | 1 | Intronic | NA | 33966 |
| **ALLELE:** Examined alleles (reference allele/observed allele)**STRAND:** 1, forward; -1, reverse**PREDICTED FUNCTION:** Predicted function of the SNP based on its location on the transcript**cDNA POS:** SNP position on cDNA, if the prediction function is coding, 3’ UTR or 5’ UTR**SPLICE DISTANCE:** Distance to splice junction, if the predicted function is intronic\* rs7901695 studied alleles are T/C |