**Supplemental Table 1:** List of SNPs determined GPPAD-02 and risk score calculation

|  |  |  |
| --- | --- | --- |
| **SNP** | **Gene, Allele, or Haplotype** | **Score weight for genotype or per allele** |
| **HLA class II** |  |  |
| rs17426593  rs2187668 rs7454108 | HLA DR4-DQ8/DR4-DQ8 | 3.15 |
| HLA DR3/DR4-DQ8 | 3.98 |
|
| rs3129889 | HLA *DRB1*\*1501 | Exclusion criteria for first degree relatives |
| rs1794265 | HLA *DQB1*\*0503 | Exclusion criteria for first degree relatives |
| **HLA class I** |  |  |
| rs1264813 | HLA A 24 | 0.43 |
| rs2395029 | HLA B 5701 | 0.92 |
| **Non-HLA SNPs** |  |  |
| rs2476601 | *PTPN22* | 0.76 |
| rs2816316 | *RGS1* | 0.16 |
| rs3024505 | *IL10* | 0.22 |
| rs1990760 | *IFIH1* | 0.16 |
| rs3087243 | *CTLA4* | 0.16 |
| rs10517086 | *C4orf52* | 0.19 |
| rs2069763 | *IL2* | 0.11 |
| rs6897932 | *IL7R* | 0.19 |
| rs3757247 | *BACH2* | 0.19 |
| rs9388489 | *C6orf173* | 0.14 |
| rs6920220 | *TNFAIP3* | 0.15 |
| rs1738074 | *TAGAP* | 0.05 |
| rs7804356 | *SCAP2* | 0.15 |
| rs4948088 | *COBL* | 0.17 |
| rs7020673 | *GLIS3* | 0.23 |
| rs12722495 | *IL2RA* | 0.47 |
| rs947474 | *PRKCQ* | 0.15 |
| rs10509540 | *RNLS/C10orf59* | 0.25 |
| rs689 | *INS* | 0.65 |
| rs4763879 | *CD69* | 0.06 |
| rs2292239 | *ERBB3* | 0.36 |
| rs3184504 | *SH2B3* | 0.24 |
| rs1465788 | *ZFP36L1* | 0.13 |
| rs17574546 | *RASGRP1* | 0.13 |
| rs3825932 | *CTSH* | 0.15 |
| rs12708716 | *CLEC16A* | 0.15 |
| rs4788084 | *IL27* | 0.20 |
| rs7202877 | *CTRB2* | 0.19 |
| rs2290400 | *ORMDL3* | 0.25 |
| rs7221109 | *CCR7* | 0.15 |
| rs45450798 | *PTPN2* | 0.09 |
| rs763361 | *CD226* | 0.12 |
| rs425105 | *PRKD2* | 0.21 |
| rs2281808 | *SIRPG* | 0.07 |
| rs3788013 | *UBASH3a* | 0.16 |
| rs5753037 | *RPS3AP51* | 0.15 |
| rs229541 | *IL2B* | 0.18 |
| rs5979785 | *TLR8* | 0.09 |
| rs2664170 | *GAB3* | 0.14 |

The risk score is calculated by multiplying the number of risk alleles (i. e. 0, 1 or 2 for each single SNP) with the weight assigned to each SNP and then summing up the weighted contributions of all SNPs plus an additive constant for each of the two HLA class II categories, 3.15 for infants who have the HLA DR4-DQ8/DR4-DQ8 genotype or 3.98 for infants who have the HLA DR3/DR4-DQ8 genotype or 3.12 for infants who have the HLA DR3/DR3 genotype or 2.08 for infants who have the HLA DR4-DQ8/DRX genotype or 1.55 for infants who have the HLA DR3/DRX genotype.

As an example, the risk score for a child with HLA DR4-DQ8/DR4-DQ8, homozygous for the risk allele of rs1264813 (weight 0.43), heterozygous for the risk allele of rs2395029 (weight 0.92), homozygous for the non-risk allele of rs2476601 (weight 0.76) and for all other SNPs in the genetic risk score is calculated as follows:

Risk score = 3.15 + (2 \* 0.43) + (1 \* 0.92) + (0 \* 0.76) + 0 = 4.93