

## SUPPLEMENTARY INFORMATION – S11

### Description of Selected GWAS summary statistics datasets of Type 1 Diabetes Mellitus.

- *A genome-wide association study identifies KIAA0350 as a type 1 diabetes gene (PMID: 17632545).*

Study participants from the Canadian cohort consist of 1,120 nuclear family trios and 267 independent T1D cases; the Type 1 Diabetes Genetics Consortium cohort consists of 549 families (2,350 individuals) in Europe, North America and Australia, and most subjects were of European ancestry. The control group includes 1,146 subjects from the Caucasian population-based cohort in the GWA study. Genotyping was performed using Illumina Infinium Hap500 high-density oligonucleotide microarrays and matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry using the Sequenom iPLEX system. In total, 1,146 control subjects and 563 individual subjects plus 483 complete T1D family trios with T1DM of European ancestry participated in the study.<sup>1</sup>

- *Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes (PMID: 19430480).*

This meta-analysis combines two previous studies (PMID: 17554300 & PMID: 17554260). The study participants are from the British cohort, including 7,514 T1DM cases and 9,045 control samples. Overall, 841,622 SNP genotyping was performed using the Affymetrix 500K platform and Illumina 550K platform.<sup>2</sup>

- *Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls (PMID: 17554300).*

In this GWA study, conducted on seven major diseases including bipolar disorder, coronary artery disease, Crohn's disease, hypertension, rheumatoid arthritis, type 1 diabetes mellitus, and type 2 diabetes mellitus, approximately 2,000 individual cases were examined for each disease, and 3,000 controls from the British population.

All 500,568 SNPs from 17,000 samples were genotyped using the GeneChip 500K Mapping Array Set (Affymetrix chip).<sup>3</sup>

- *Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes (PMID: 17554260).*

In total, 4,000 individuals with T1DM, 5,000 controls, and 2,997 independent family trios from the British 1958 Birth Cohort were considered for this analysis. Genotyping analysis of 13,378 SNPs completed by Affymetrix 500K Mapping Array GWA GeneChip, and TaqMan assay.<sup>4</sup>

- *Meta-analysis of genome-wide association study data identifies additional type 1 diabetes risk loci (PMID: 18978792).*

The meta-analysis of GWAS contains 3,561 T1DM cases and 4,646 controls from European ancestry under the British 1958 Birth Cohort. All 305,090 SNPs genotyping was performed using the Affymetrix 500K SNP chipset.<sup>5</sup>

- *A novel susceptibility locus for type 1 diabetes on Chr12q13 identified by a genome-wide association study (PMID: 18198356).*

The GWA study consists of 563 T1DM patients and 1,146 control subjects, all of European ancestry from Type 1 Diabetes Genetics Consortium replication cohort and Canadian replication cohort. Genotypes were performed using the Sequenom iPLEX assay (Sequenom, Cambridge, MA).<sup>6</sup>

- *Follow-up analysis of genome-wide association data identifies novel loci for type 1 diabetes (PMID: 31740837).*

The GWA study has a Canadian cohort consisting of 1,120 nuclear family trios and 267 independent T1DM cases, and Type 1 Diabetes Genetics Consortium cohort consisting of 2,350 individual T1DM cases from 549 families, and a type 1 diabetes cohort composed of 103 T1DM cases and 2,024 control cases from Canadian cohort. Variant genotyping was completed using the Illumina Infinium II HumanHap550 Bead Chip technology.<sup>7</sup>

- *The imprinted DLK1-MEG3 gene region on chromosome 14q32.2 alters susceptibility to type 1 diabetes (PMID: 19966805).*

The GWA study includes the Wellcome Trust Case Control Consortium and Type 1 Diabetes Genetics Consortium cohort, comprising 7514 cases and 9045 control samples from White European ancestry.<sup>8</sup>

- *A genome-wide meta-analysis of six type 1 diabetes cohorts identifies multiple associated loci (PMID: 21980299).*

In total, 61,427 participants, including 16,159 T1D cases, 25,386 controls and 6,143 trio families from European, African Admixed, Finnish, East Asian and other admixed population ancestry, were considered for this GWA study. Genotyping was performed for 140,333 variants using the Illumina ImmunoChip.<sup>9</sup>

- *Rare genetic variants of large effect influence risk of type 1 diabetes (PMID: 32005708).*

The meta-analysis has 6,511 T1DM cases and 9,745 control subjects from the European cohort, Diabetes Control and Complications Trial–Epidemiology of Diabetes Interventions and Complications (DCCT-EDIC) cohort, Wellcome Trust Case Control Consortium (WTCCC), Genetics of Kidneys in Diabetes (GoKinD) and T1DGC. The SNP variants were genotyped using Illumina arrays (HumanHap550 or Human1-2M-DuoCustom\_v1\_A) and Affymetrix 500K array.<sup>10</sup>

- *Fine-mapping, trans-ancestral and genomic analyses identify causal variants, cells, genes and drug targets for type 1 diabetes (PMID: 34127860).*

Overall, 61,427 participants, consisting of 16,159 T1D cases, 25,386 controls and 6,143 trio families from European, African Admixed, Finnish, East Asian, and Other Admixed ancestry, participated in this study. 140,333 variants genotyped the Illumina ImmunoChip.<sup>11</sup>

- *Analysis of overlapping genetic association in type 1 and type 2 diabetes PMID: 33830302.*

Type 1 diabetes meta-analysis summary statistics were generated using genome-wide association study (GWAS) data from 3983 cases and 3994 controls from the UK (genotyped using the Illumina Infinium

550K platform), 1926 cases and 3342 controls from the UK (genotyped using the Affymetrix GeneChip 500K platform) and 1558 cases and 2882 controls from Sardinia (genotyped using the Affymetrix 6.0 and Illumina Omni Express platforms), totalling 7467 cases and 10,218 controls.<sup>12</sup>

## References

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