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A comprehensive selection of single nucleotide polymorphisms to predict genetic risks of developing common chronic diseases in Japanese

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Recently a number of susceptible loci for common chronic diseases and related disorders have been identified by genome-wide association studies (GWAS). Although the effect size of each SNP differs among different ethnics, abundant literatures allow us to assess each risk in a certain ethnic group. We here report a system to determine genetic risks of developing various disorders among Japanese people, using relevant allele frequencies and odds ratios of selected SNPs.

First we surveyed published papers for GWAS and smaller-scale studies conducted predominantly in Japan, and built a database of disease-susceptible SNPs, curating positions on the human genome, gene names, allele frequencies, odds ratios, p-values, and calculated relative risk to the general population. SNPs verified by replication studies, meta-analysis or multiple studies were preferentially chosen and used for calculating genetic risks. Linkage disequilibrium was considered to remove duplicate SNPs in a susceptible locus. As a result, 128 SNPs were selected for a total of 28 common diseases and related disorders. Among them 93 SNPs were from the results of GWAS with replication studies. Other 26 SNPs were from studies for more than 300 cases followed by replication or another studies, where statistical significance was found and p-values were less than 0.05. Remaining 9 SNPs were from smaller-scale studies with some reliability. Finally 1 to 14 SNPs per disorder were employed for risk calculation of these 28 disorders. Next, segregation ratios of each genotype and relative risks to the general population were calculated and integration of relative risks for each genotype was plotted.

The database with selected SNPs should be useful for predicting risks of developing disorders for Japanese individuals and are ready for the validation of the system.