GWAS summary statistics for basal cell carcinoma (BCC)

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This file contains association summary statistics for the genome-wide association studies (GWAS) of basal cell carcinoma (BCC), published in Adolphe & Xue et al. (*Genome Medicine*. 2020).

We conducted a genome-wide association studies (GWAS) with ~7 million genetic variants in 392K participants (17,416 cases and 375,455 controls) of European ancestry, from the full cohort v2 release of the UK Biobank (UKB). Details of genotyping, quality control (QC), association analysis for the study are provided in the Methods section of Adolphe & Xue et al. (*Genome Medicine*. 2020).

Here, we provided the GWAS results for ~7 million common (minor allele frequency >= 0.01) SNPs.

For each SNP, we have provided the following information:

- CHR: Chromosome
- BP: Base-pairs position (build 37)
- SNP: rsID
- A1: minor allele
- A2: major allele
- Frq_A1: allele frequency of A1
- b: effect size of A1
- se: standard error of b
- P: p-value
- N: total sample size (not effective N)

Reference: Christelle Adolphe[#], Angli Xue[#], Atefeh Taherian Fard , Laura A. Genovesi, Jian Yang[*] and Brandon J. Wainwright[*]. Genetic and functional interaction network analysis reveals global enrichment of regulatory T Cell genes influencing basal cell carcinoma susceptibility. *Genome Medicine*. (2020)

Please refer any queries to: Brandon Wainwright (b.wainwright@imb.uq.edu.au) or Jian Yang (jian.yang@westlake.edu.cn)