**GWAS summary statistics of intracranial germ cell tumors in Japanese**

**General information:**

* **Sample size**: 133 cases vs. 762 controls
* **Genotyping array**: Infinium Asian Screening Array
* **Sample QC**: We excluded individuals (i) with genotyping call rate < 0.97, (ii) in close kinship (PI\_HAT > 0.17), and (iii) estimated of non-East Asian ancestry.
* **Variant QC**: We excluded variants with (i) genotyping call rate < 0.99, (ii) minor allele count < 5, (iii) *P* value for Hardy–Weinberg equilibrium < 1.0 × 10−5 in controls, and (iv) > 10% allele frequency difference with the imputation reference panel or the allele frequency panel of Tohoku Medical Megabank Project.
* **Phasing and imputation**: SHAPEIT2 and Minimac3
* **Imputation reference**: Combined panel of 1000 Genomes Project Phase 3 version 5 genotype (*n* = 2,504) and Japanese whole-genome sequencing data (*n* = 1,037)
* **Post-imputation QC**: We excluded imputed variants with Rsq < 0.7 and minor allele frequency < 0.5%.
* **Association test**: We performed an association test by a logistic regression model including the top 20 principal components as covariates using PLINK2.

**Uploaded files**

| **File name** | **Descriptions** |
| --- | --- |
| GWASsummary\_IGCT\_Japanese\_SoneharaNatCommun2022.autosome.txt.gz | Results for 7,803,874 autosomal variants |
| GWASsummary\_IGCT\_Japanese\_SoneharaNatCommun2022.chrX.txt.gz | Results for 181,867 X chromosome variants (males, females, and meta-analysis of males and females) |

**Columns**

**Autosomal variants**

| **#** | **column name** | **Descriptions** |
| --- | --- | --- |
| 1 | SNP | marker name (CHR:POS:REF:ALT) |
| 2 | CHR | chromosome |
| 3 | POS | position (hg19) |
| 4 | A1 | effect allele (ALT) |
| 5 | A2 | other allele (REF) |
| 6 | N\_CASE | number of cases |
| 7 | N\_CONTROL | number of controls |
| 8 | FREQ\_A1\_CASE | effect allele frequency in cases |
| 9 | FREQ\_A1\_CONTROL | effect allele frequency in controls |
| 10 | RSQ | imputation Rsq value |
| 11 | BETA | log(odds ratio) for effect allele |
| 12 | SE | standard error of log(odds ratio) for effect allele |
| 13 | P | P value |

**X chromosome variants**

| **#** | **column name** | **Descriptions** |
| --- | --- | --- |
| 1 | SNP | marker name (CHR:POS:REF:ALT) |
| 2 | CHR | chromosome |
| 3 | POS | position (hg19) |
| 4 | A1 | effect allele (ALT) |
| 5 | A2 | other allele (REF) |
| 6 | M\_N\_CASE | number of cases in males |
| 7 | M\_N\_CONTROL | number of controls in males |
| 8 | M\_FREQ\_A1\_CASE | effect allele frequency in cases in males |
| 9 | M\_FREQ\_A1\_CONTROL | effect allele frequency in controls in males |
| 10 | M\_RSQ | imputation Rsq value in males |
| 11 | M\_BETA | log(odds ratio) for effect allele in males |
| 12 | M\_SE | standard error of log(odds ratio) for effect allele in males |
| 13 | M\_P | P value in males |
| 14 | F\_N\_CASE | number of cases in females |
| 15 | F\_N\_CONTROL | number of controls in females |
| 16 | F\_FREQ\_A1\_CASE | effect allele frequency in cases in females |
| 17 | F\_FREQ\_A1\_CONTROL | effect allele frequency in controls in females |
| 18 | F\_RSQ | imputation Rsq value in females |
| 19 | F\_BETA | log(odds ratio) for effect allele in females |
| 20 | F\_SE | standard error of log(odds ratio) for effect allele in females |
| 21 | F\_P | P value in females |
| 22 | BETA | log(odds ratio) for effect allele in meta-analysis of sexes |
| 23 | SE | standard error of log(odds ratio) for effect allele in meta-analysis of sexes |
| 24 | P | P value in meta-analysis of sexes |