**Supplementary Table 7.** Association between the genotypes of SNPs in LGALS3 gene and glioma risk

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genomic model | Genotype | Control | Case | p value (2df)  | Logistic regression  |
| No. (%) | No. (%) | OR (95% CI) | p value |
|  | **rs4652** |  |  |  |  |  |
| Codominant | AA | 513 (38.3%) | 329 (34.2%) | 0.085 | 1.00 (reference) |  |
|  | CA | 634 (47.3%) | 473 (49.1%) |  | 1.16 (0.97-1.40) | 0.113 |
|  | CC | 193 (14.4%) | 161 (16.7%) |  | 1.29 (1.00-1.67) | 0.054 |
| Dominant | CA+CC | 827 (61.7%) | 634 (65.8%) | 0.043 | 1.19 (1.00-1.42) | 0.051 |
|  |  |  |  |  |  |  |
|  | **rs4644** |  |  |  |  |  |
| Codominant | CC | 931 (68.9%) | 635 (65.9%) | 0.019 | 1.00 (reference) |  |
|  | AC | 396 (29.3%) | 294 (30.5%) |  | 1.09 (0.90-1.30) | 0.393 |
|  | AA | 24 (1.8%) | 34 (3.5%) |  | 2.15(1.25-3.72) | 0.006 |
| Recessive | CC+AC | 1327 (98.2%) | 929 (96.5%) | 0.008 | 2.10 (1.22-3.62) | 0.007 |
|  |  |  |  |  |  |  |
|  | **rs7157768** |  |  |  |  |  |
| Codominant | GG | 999 (74.6%) | 698 (73.2%) | 0.074 | 1.00 (reference) |  |
|  | CG | 309 (23.1%) | 243 (25.5%) |  | 1.10 (0.90-1.35) | 0.333 |
|  | CC | 32 (2.4%) | 12 (1.3%) |  | 0.49 (0.24-0.97) | 0.039 |
| Dominant | CG+CC | 341 (25.4%) | 255 (26.8%) | 0.481 | 1.04 (0.86-1.27) | 0.669 |
|  |  |  |  |  |  |  |
|  | **rs17128230** |  |  |  |  |  |
| Codominant | CC | 1159 (85.9%) | 809 (84.1%) | 0.068 | 1.00 (reference) |  |
|  | TC | 178 (13.2%) | 150 (15.6%) |  | 1.21 (0.95-1.54) | 0.122 |
|  | TT | 12 (0.9%) | 3 (0.3%) |  | 0.44 (0.12-1.59) | 0.212 |
| Dominant | TC+TT | 190 (14.1%) | 153 (15.9%) | 0.225 | 1.17 (0.92-1.48) | 0.205 |
|  |  |  |  |  |  |  |
|  | **rs8013027** |  |  |  |  |  |
| Codominant | CC | 620 (46.3%) | 408 (42.7%) | 0.2 | 1.00 (reference) |  |
|  | GC | 589 (44.0%) | 440 (46.1%) |  | 1.10 (0.92-1.32) | 0.302 |
|  | GG | 131 (9.8%) | 107 (11.2%) |  | 1.22 (0.91-1.63) | 0.182 |
| Dominant | GC+GG | 720 (53.7%) | 547 (57.3%) | 0.092 | 1.12 (0.95-1.33) | 0.19 |