Table 4. Logistic regression analyses of associations between SNPs and risk of postoperative inadequate analgesia

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | SNP | Model | Genotype | Adequate analgesia | Inadequate analgesia | OR (95% CI)  unadjusted | P-Value  unadjusted | OR (95% CI) adjusted | P-Value  adjusted |
| ESR1 | rs9340799 | Recessive | A/A-G/A | 99 (91.7%) | 89 (98.9%) | 1.00 | 0.01 | 1.00 | 0.020 |
| G/G | 9 (8.3%) | 1 (1.1%) | 0.12 (0.02-0.99) | 0.13 (0.02-1.08) |
| P2RY12 | rs3732765 | Dominant | G/G | 76 (70.4%) | 75 (83.3%) | 1.00 | 0.031 | 1.00 | 0.180 |
| G/A-A/A | 32 (29.6%) | 15 (16.7%) | 0.48 (0.24-0.95) | 0.61 (0.29-1.28) |
| SCN11A | rs33985936 | Dominant | C/C | 89 (82.4%) | 66 (73.3%) | 1.00 | 0.12 | 1.00 | 0.042 |
| T/C-T/T | 19 (17.6%) | 24 (26.7%) | 1.70 (0.86-3.37) | 2.15 (1.02-4.52) |
|  | rs11709492 | Dominant | C/C | 51 (47.2%) | 56 (62.2%) | 1.00 | 0.03 | 1.00 | 0.005 |
| T/C-T/T | 57 (52.8%) | 34 (37.8%) | 0.54 (0.31-0.96) | 0.41 (0.22-0.77) |
| SCN10A | rs6795970 | Dominant | G/G | 84 (77.8%) | 59 (65.6%) | 1.00 | 0.06 | 1.00 | 0.026 |
| G/A-A/A | 24 (22.2%) | 31 (34.4%) | 1.84 (0.98-3.45) | 2.14 (1.09-4.21) |
| SCN9A | rs6746030 | Dominant | G/G | 94 (87%) | 86 (95.6%) | 1.00 | 0.032 | 1.00 | 0.067 |
| G/A-A/A | 14 (13%) | 4 (4.4%) | 0.31 (0.10-0.99) | 0.35 (0.10-1.16) |
|  | 3312G>T | Dominant | G/G | 96 (88.9%) | 66 (73.3%) | 1.00 | 0.005 | 1.00 | 0.011 |
| T/G-T/T | 12 (11.1%) | 24 (26.7%) | 2.91 (1.36-6.22) | 2.85 (1.25-6.51) |
| TAOK3 | rs1277441 | Dominant | T/T | 33 (30.6%) | 40 (44.4%) | 1.00 | 0.044 | 1.00 | 0.13 |
| T/C-C/C | 75 (69.4%) | 50 (55.6%) | 0.55 (0.31-0.99) | 0.61 (0.32-1.15) |

Abbreviations: CI = confidence intervals; ESR1 = estrogen receptor 1; OR = odds ratios; P2RY12 = purinergic receptor P2Y12; SCN11A = sodium voltage-gated channel alpha subunit 11; SCN10A = sodium voltage-gated channel alpha subunit 10; SCN9A = sodium voltage-gated channel alpha subunit 9; SNP = single nucleotide polymorphism; TAOK3 = TAO kinase 3.