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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Locus | Model | Genotype | Sample size | | | Prostate cancers vs Controls | | BPH vs Controls | |
|  | | | Prostate cancer | BPH | Control | Odds Ratio | P value | Odds Ratio | P value |
| UGT2B28 | Allele | Ins | 207 (86.2%) | 203 (84.6%) | 203 (84.6%) | 1 | 0.6 | 1 | 1 |
| Del | 33 (13.8%) | 37 (15.4%) | 37 (15.4%) | 0.87 (0.53-1.45) |  | 1 (0.61-1.64) |  |
| Codominant | Ins/Ins | 90 (75%) | 87 (72.5%) | 88 (73.3%) | 1 | 0.77 | 1 | 0.91 |
| Ins/Del | 27 (22.5%) | 29 (24.2%) | 27 (22.5%) | 0.98 (0.53-1.8) |  | 1.09 (0.59-1.98) |  |
| Del/Del | 3 (2.5%) | 4 (3.3%) | 5 (4.2%) | 0.59 (0.14-2.53) |  | 0.81 (0.21-3.11) |  |
| Dominant | Ins/Ins | 90 (75%) | 87 (72.5%) | 88 (73.3%) | 1 | 0.77 | 1 | 0.88 |
| Ins/Del + Del/Del | 30 (25%) | 33 (27.5%) | 32 (26.7%) | 0.92 (0.51-1.63) |  | 1.04 (0.59-1.84) |  |
| Recessive | Ins/Ins + Ins/Del | 117 (97.5%) | 116 (96.7%) | 115 (95.8%) | 1 | 0.47 | 1 | 0.73 |
| Del/Del | 3 (2.5%) | 4 (3.3%) | 5 (4.2%) | 0.59 (0.14-2.53) |  | 0.79 (0.21-3.03) |  |
| Overdominant | Ins/Ins + Del/Del | 93 (77.5%) | 91 (75.8%) | 93 (77.5%) | 1 | 1 | 1 | 0.76 |
| Ins/Del | 27 (22.5%) | 29 (24.2%) | 27 (22.5%) | 1 (0.55-1.83) |  | 1.1 (0.6-2) |  |
| Log-Additive |  | | | | 0.88 (0.54-1.44) | 0.62 | 1 (0.62-1.6) | 1 |
| UGT2B17 | Allele | Ins | 165 (68.8%) | 143 (59.6%) | 181 (75.4%) | 1 | 0.1 | 1 | <0.0001 |
| Del | 75 (31.2%) | 97 (40.4%) | 59 (24.6%) | 1.39 (0.93-2.08) |  | 2.08 (1.41-3.08) |  |
| Codominant | Ins/Ins | 53 (44.2%) | 43 (35.8%) | 66 (55%) | 1 | 0.22 | 1 | 5e-04 |
| Ins/Del | 59 (49.1%) | 57 (47.5%) | 49 (40.8%) | 1.5 (0.89-2.53) |  | 1.79 (1.04-3.07) |  |
| Del/Del | 8 (6.7%) | 20 (16.7%) | 5 (4.2%) | 1.99 (0.62-6.45) |  | 6.14 (2.14-17.59) |  |
| Dominant | Ins/Ins | 53 (44.2%) | 43 (35.8%) | 66 (55%) | 1 | 0.09 | 1 | 0.002 |
| Ins/Del + Del/Del | 67 (55.8%) | 77 (64.2%) | 54 (45%) | 1.55 (0.93-2.57) |  | 2.19 (1.3-3.67) |  |
| Recessive | Ins/Ins + Ins/Del | 112 (93.3%) | 100 (83.3%) | 115 (95.8%) | 1 | 0.39 | 1 | 0.001 |
| Del/Del | 8 (6.7%) | 20 (16.7%) | 5 (4.2%) | 1.64 (0.52-5.17) |  | 4.6 (1.67-12.71) |  |
| Overdominant | Ins/Ins + Del/Del | 61 (50.9%) | 63 (52.5%) | 71 (59.2%) | 1 | 0.19 | 1 | 0.3 |
| Ins/Del | 59 (49.1%) | 57 (47.5%) | 49 (40.8%) | 1.4 (0.84-2.33) |  | 1.31 (0.79-2.18) |  |
| Log-Additive |  | | | | 1.46 (0.95-2.25) | 0.08 | 2.14 (1.42-3.22) | 2e-04 |
| UGT2B15 | Allele | T | 157 (65.4%) | 124 (51.7%) | 153 (63.8%) | 1 | 0.7 | 1 | 0.007 |
| G | 83 (34.6%) | 116 (48.3%) | 87 (36.2%) | 0.93 (0.64-1.35) |  | 1.64 (1.14-2.37) |  |
| Codominant | TT | 47 (39.2%) | 30 (25%) | 44 (36.7%) | 1 | 0.91 | 1 | 0.012 |
| TG | 63 (52.5%) | 64 (53.3%) | 65 (54.1%) | 0.91 (0.53-1.55) |  | 1.44 (0.81-2.57) |  |
| GG | 10 (8.3%) | 26 (21.7%) | 11 (9.2%) | 0.85 (0.33-2.2) |  | 3.47 (1.49-8.06) |  |
| Dominant | TT | 47 (39.2%) | 30 (25%) | 44 (36.7%) | 1 | 0.69 | 1 | 0.05 |
| TG+GG | 73 (60.8%) | 90 (75%) | 76 (63.3%) | 0.9 (0.53-1.52) |  | 1.74 (1-3.03) |  |
| Recessive | TT+TG | 110 (91.7%) | 94 (78.3%) | 109 (90.8%) | 1 | 0.82 | 1 | 0.0066 |
| GG | 10 (8.3%) | 26 (21.7%) | 11 (9.2%) | 0.9 (0.37-2.21) |  | 2.74 (1.29-5.84) |  |
| Overdominant | TT+GG | 57 (47.5%) | 56 (46.7%) | 55 (45.9%) | 1 | 0.8 | 1 | 0.9 |
| TG | 63 (52.5%) | 64 (53.3%) | 65 (54.1%) | 0.94 (0.56-1.55) |  | 0.97 (0.58-1.61) |  |
| Log-Additive |  | | | | 0.92 (0.61-1.38) | 0.68 | 1.76 (1.18-2.62) | 0.0045 |

**Table 3:** Results of correlation analysis between UGT2B28, UGT2B17, UGT2B15, rs1800629 and rs361525 polymorphisms and risk of BPH and prostate cancer

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
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| rs1800629 | Allele | G | 184 (92%) | | 204 (92.7%) | | 206 (93.6%) | 1 | 0.51 | 1 | 0.7 |
| A | 16 (8%) | | 16 (7.3%) | | 14 (6.4%) | 1.28 (0.61-2.69) |  | 1.15 (0.55-2.43) |  |
| Codominant | GG | 84 (84%) | | 94 (85.5%) | | 96 (87.3%) | 1 | 0.5 | 1 | 0.69 |
| AG | 16 (16%) | | 16 (14.5%) | | 14 (12.7%) | 1.31 (0.6-2.83) |  | 1.7 (0.54-2.52) |  |
| AA | - | | - | | - | - |  | - |  |
| Dominant | GG | - | | - | | - | - | - | - | - |
| AG+AA | - | | - | | - | - |  | - |  |
| Recessive | GG+AG | - | | - | | - | - | - | - | - |
| AA | - | | - | | - | - |  | - |  |
| Overdominant | GG+AA | - | | - | | - | - | - | - | - |
| AG | - | | - | | - | - |  | - |  |
| Log-Additive |  | | | | | | - | - | - | - |
| rs361525 | Allele | G | 190 (95%) | 213 (96.8%) | | 215 (97.7%) | | 1 | 013 | 1 | 0.56 |
| A | 10 (5%) | 7 (3.2%) | | 5 (2.3%) | | 2.26 (0.76-6.74) |  | 1.41 (0.44-4.52) |  |
| Codominant | GG | 90 (90%) | 103 (93.6%) | | 105 (95.5%) | | 1 | 0.12 | 1 | 0.55 |
| AG | 10 (10%) | 7 (6.4%) | | 5 (4.5%) | | 2.33 (0.77-7.08) |  | 1.43 (0.44-4.64) |  |
| AA | - | - | | - | | - |  | - |  |
| Dominant | GG | - | - | | - | | - | - | - | - |
| AG+AA | - | - | | - | | - |  | - |  |
| Recessive | GG+AG | - | - | | - | | - | - | - | - |
| AA | - | - | | - | | - |  | - |  |
| Overdominant | GG+AA | - | - | | - | | - | - | - | - |
| AG | - | - | | - | | - |  | - |  |
| Log-Additive |  | | | | | | - | - | - | - |

\*In this table, the allelic and genotypic frequency comparison of the cancer group to control and the BPH group to controls is given in one table. Yellow columns are the frequency of genotypes and alleles in each study group. Gray shows the comparison between PCa and control, and Orange indicates a comparison of BPH with the control group.

\*As is considered, UGT2B17 was associated with the risk of BPH in allelic, Codominant, Recessive, and Log-Additive modes of inheritances. The G allele was more prevalent among BPH cases compared with controls (OR (95% CI) =1.64 (1.14-2.37), P value = <0.0001. For example, in the codominant model, individuals carrying the GG genotype had a significantly higher risk of BPH in comparison with those who carry the TT genotype (GG versus TT: OR (95% CI) = 3.47 (1.49-8.06), P value 0.012). Also, UGT2B15 was associated with the risk of BPH in allelic, Codominant, Recessive, and Log-Additive modes of inheritances (P value= 0.007).  
\*rs1800629 and rs361525 show no significant association with PCa or BPH in any of the inheritance models. Dash lines: no genotype or allele.