

S3 Table. Results of the multivariate logistic regression analyses for male and female patients.

| A. Male cases (n=255) + male controls (n=242) | | | | | |
|-----------------------------------------------------------------------------------------------------------------------------|-----------------|-------------|---------------|---------------|----------------|
| Variables | Category | * OR | 95% CI | | p value |
| | | | lower | higher | |
| <i>BRM-741</i> (co-dominant model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 1 vs 0 | 1.00 | 0.65 | 1.53 | 0.99 |
| | 2 vs 0 | 1.07 | 0.64 | 1.79 | 0.79 |
| <i>BRM-1321</i> (co-dominant model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 1 vs 0 | 1.14 | 0.76 | 1.73 | 0.52 |
| | 2 vs 0 | 1.10 | 0.66 | 1.85 | 0.71 |
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Both Del/Del; 1=No Ins/Ins; 2=One Ins/Ins; 3=Both Ins/Ins) | 1 vs 0 | 1.17 | 0.72 | 1.91 | 0.52 |
| | 2 vs 0 | 1.42 | 0.81 | 2.52 | 0.22 |
| | 3 vs 0 | 1.02 | 0.51 | 2.05 | 0.95 |
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Others; 1=Both Ins/Ins) | 1 vs 0 | 0.86 | 0.47 | 1.56 | 0.62 |
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Both Del/Del; 1=Others) | 1 vs 0 | 1.21 | 0.77 | 1.91 | 0.41 |
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Others; 1=At least one Ins/Ins) | 1 vs 0 | 1.14 | 0.77 | 1.68 | 0.51 |
| <i>BRM-741</i> (dominant model; 0=Del/Del; 1=Others) | 1 vs 0 | 1.02 | 0.68 | 1.53 | 0.92 |
| <i>BRM-741</i> (recessive model; 0=Others; 1=Ins/Ins) | 1 vs 0 | 1.07 | 0.70 | 1.66 | 0.75 |
| <i>BRM-741</i> (additive model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 2 vs 1 vs 0 | 1.03 | 0.80 | 1.33 | 0.80 |
| <i>BRM-1321</i> (dominant model; 0=Del/Del; 1=Others) | 1 vs 0 | 1.13 | 0.77 | 1.67 | 0.53 |
| <i>BRM-1321</i> (recessive model; 0=Others; 1=Ins/Ins) | 1 vs 0 | 1.02 | 0.65 | 1.60 | 0.94 |
| <i>BRM-1321</i> (additive model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 2 vs 1 vs 0 | 1.06 | 0.82 | 1.37 | 0.65 |
| B. Female cases (n=172) + female controls (n=166) | | | | | |
| Variables | Category | * OR | 95% CI | | p value |
| | | | lower | higher | |
| <i>BRM-741</i> (co-dominant model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 1 vs 0 | 1.14 | 0.67 | 1.97 | 0.62 |
| | 2 vs 0 | 0.75 | 0.38 | 1.46 | 0.40 |
| <i>BRM-1321</i> (co-dominant model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 1 vs 0 | 1.29 | 0.78 | 2.16 | 0.32 |
| | 2 vs 0 | 0.69 | 0.35 | 1.34 | 0.28 |

| | | | | | |
|-----------------------------------------------------------------------------------------------------------------------------|-------------|------|------|------|------|
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Both Del/Del; 1=No Ins/Ins; 2=One Ins/Ins; 3=Both Ins/Ins) | 1 vs 0 | 1.66 | 0.87 | 3.20 | 0.12 |
| | 2 vs 0 | 1.16 | 0.54 | 2.52 | 0.70 |
| | 3 vs 0 | 0.69 | 0.26 | 1.75 | 0.44 |
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Others; 1=Both Ins/Ins) | 1 vs 0 | 0.49 | 0.22 | 1.06 | 0.08 |
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Both Del/Del; 1=Others) | 1 vs 0 | 1.38 | 0.75 | 2.59 | 0.31 |
| Genotype combination of <i>BRM-741</i> and <i>BRM-1321</i> (0=Others; 1=At least one Ins/Ins) | 1 vs 0 | 0.66 | 0.40 | 1.09 | 0.11 |
| <i>BRM-741</i> (dominant model; 0=Del/Del; 1=Others) | 1 vs 0 | 1.01 | 0.61 | 1.70 | 0.96 |
| <i>BRM-741</i> (recessive model; 0=Others; 1=Ins/Ins) | 1 vs 0 | 0.69 | 0.39 | 1.20 | 0.19 |
| <i>BRM-741</i> (additive model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 2 vs 1 vs 0 | 0.88 | 0.63 | 1.22 | 0.45 |
| <i>BRM-1321</i> (dominant model; 0=Del/Del; 1=Others) | 1 vs 0 | 1.09 | 0.67 | 1.77 | 0.72 |
| <i>BRM-1321</i> (recessive model; 0=Others; 1=Ins/Ins) | 1 vs 0 | 0.59 | 0.33 | 1.07 | 0.08 |
| <i>BRM-1321</i> (additive model; 0=Del/Del; 1=Ins/Del; 2=Ins/Ins) | 2 vs 1 vs 0 | 0.89 | 0.64 | 1.22 | 0.46 |

CI, confidence interval; Del, deletion; Ins, insertion; OR, odds ratio.

* Adjusted for age, number of first degree relatives with colorectal cancer, smoking status, and body mass index.