**Supplementary Table 2.** Association between secretor MBL2 polymorphisms and disease-specific survival, stratified by study population*

| | Case patients from case–control study | | | | Case-only series | | | |
|---|---|---|---|---|---|---|---|---|
| | White patients | | African American patients | | White patients | | African American patients | |
| Genotype | No. | RR of death† (95% CI) | No. | RR of death (95% CI) | No. | RR of death† (95% CI) | No. | RR of death† (95% CI) |
| Promoter SNP | | | | | | | | |
| mbl2_11 (*rs11003125)* | | | | | | | | |
| C/C *(L/L)* | 140 | 1.0 (referent) | 89 | 1.0 (referent) | 75 | 1.0 (referent) | 31 | 1.0 (referent) |
| C/G *(L/H)* | 159 | 1.10 (0.75 to 1.61) | 35 | 1.08 (0.60 to 1.95) | 79 | 0.72 (0.45 to 1.15) | 9 | 0.64 (0.19 to 2.20) |
| G/G *(H/H)* | 49 | 1.12 (0.67 to 1.89) | 4 | 2.11 (0.63 to 7.04) | 21 | 1.70 (0.89 to 3.26) | 0 | — |
| mbl2_12 *(rs7096206)* | | | | | | | | |
| G/G *(Y/Y)* | 219 | 1.0 (referent) | 93 | 1.0 (referent) | 110 | 1.0 (referent) | 31 | 1.0 (referent) |
| G/C *(Y/X)* | 120 | **0.65 (0.45 to 0.93)** | 31 | 1.07 (0.59 to 1.93) | 60 | **0.56 (0.34 to 0.92)** | 10 | 1.69 (0.57 to 5.01) |
| C/C *(X/X)* | 15 | 0.59 (0.24 to 1.48) | 3 | 1.81 (0.41 to 7.99) | 9 | 0.55 (0.17 to 1.83) | 1 | — |
| G/C + C/C | 135 | **0.64 (0.45 to 0.91)** | 34 | 1.13 (0.64 to 1.99) | 69 | **0.56 (0.35 to 0.90)** | 11 | 1.90 (0.68 to 5.32) |
| Exon 1 SNP | | | | | | | | |
| mbl2_03 (*rs5030737)* | | | | | | | | |
| C/C *(Non-D/Non-D)* | 292 | 1.0 (referent) | 122 | 1.0 (referent) | 155 | 1.0 (referent) | 38 | 1.0 (referent) |
| C/T *(Non-D/D)* | 56 | 0.74 (0.47 to 1.16) | 5 | 0.43 (0.10 to 1.81) | 19 | 1.72 (0.94 to 3.13) | 1 | — |
| T/T *(D/D)* | 3 | 2.82 (0.38 to 20.72) | 0 | — | 1 | — | 0 | — |
| mbl2_01 *(rs1800450)* | | | | | | | | |
| G/G *(Non-B/Non-B)* | 264 | 1.0 (referent) | 117 | 1.0 (referent) | 127 | 1.0 (referent) | 35 | 1.0 (referent) |
| G/A *(Non-B/B)* | 80 | 1.00 (0.67 to 1.51) | 7 | 1.30 (0.29 to 5.81) | 40 | 0.80 (0.48 to 1.34) | 6 | 1.55 (0.49 to 4.92) |
| A/A *(B/B)* | 3 | 3.19 (0.43 to 23.60) | 1 | — | 4 | 1.20 (0.28 to 5.03) | 0 | — |
| mbl2_02 (rs1800451) | | | | | | | | |
| G/G (*Non-C/Non-C)* | 337 | 1.0 (referent) | 73 | 1.0 (referent) | 42 | 1.0 (referent) | 18 | 1.0 (referent) |
| G/A *(Non-C/C))* | 8 | 1.38 (0.50 to 3.77) | 42 | 0.92 (0.53 to 1.59) | 6 | 0.65 (0.09 to 4.95) | 16 | 1.08 (0.37 to 3.09) |
| A/A *(C/C)* | 1 | — | 6 | 0.59 (0.14 to 2.53) | 0 | — | 4 | 7.42 (1.16 to 47.60) |
| Haplotype | | | | | | | | |
| GGCGG *(HYA)* | 192 | 1.0 (referent) | 38 | 1.0 (referent) | 102 | 1.0 (referent) | 8 | 1.0 (referent) |
| CGCGG *(LYA)* | 186 | 1.00 (0.73 to 1.37) | 107 | 0.65 (0.38 to 1.11) | 94 | 1.38 (0.94 to 2.05) | 28 | 0.93 (0.33 to 2.65) |

| | Case patients from case–control study | | | | Case-only series | | | |
|---|---|---|---|---|---|---|---|---|
| | White patients | | African American patients | | White patients | | African American patients | |
| Genotype | No. | RR of death† (95% CI) | No. | RR of death (95% CI) | No. | RR of death† (95% CI) | No. | RR of death† (95% CI) |
| CCCGG *(LXA)* | 142 | **0.69 (0.48 to 0.99)** | 34 | 0.72 (0.38 to 1.35) | 78 | 0.70 (0.44 to 1.12) | 12 | 2.31 (0.73 to 7.34) |
| CGCAG *(LYB)* | 84 | 1.03 (0.69 to 1.54) | 9 | 0.56 (0.13 to 2.48) | 51 | 0.96 (0.59 to 1.55) | 6 | 1.67 (0.43 to 6.48) |
| CGCGA *(LYC)* | 10 | 1.17 (0.42 to 3.20) | 53 | 0.58 (0.32 to 1.06) | 6 | 0.52 (0.07 to 3.82) | 23 | 1.22 (0.43 to 3.44) |
| GGTGG *(HYD)* | 60 | 0.73 (0.46 to 1.16) | 5 | 0.31 (0.07 to 1.37) | 21 | 1.85 (0.99 to 3.34) | 1 | — |
| Diplotype | | | | | | | | |
| YA/YA | 98 | 1.0 | 40 | 1.0 | 61 | 1.0 | 6 | 1.0 |
| YA/XA | 85 | 0.72 (0.45 to 1.16) | 25 | 1.30 (0.64 to 2.64) | 39 | 0.65 (0.35 to 1.21) | 6 | 1.30 (0.64 to 2.64) |
| XA/XA | 14 | 0.61 (0.23 to 1.59) | 2 | — | 9 | 0.56 (0.16 to 1.90) | 1 | — |
| YA/B | 52 | 1.27 (0.77 to 2.10) | 4 | 0.96 (0.12 to 7.61) | 26 | 0.81 (0.43 to 1.54) | 3 | 0.96 (0.12 to 7.61) |
| XA/B | 19 | **0.30 (0.09 to 0.99)** | 0 | — | 11 | 0.37 (0.13 to 1.06) | 2 | — |
| YA/C | 6 | 1.57 (0.48 to 5.18) | 33 | 1.15 (0.59 to 2.25) | 2 | — | 14 | 1.15 (0.59 to 2.25) |
| YA/D | 39 | 0.65 (0.36 to 1.17) | 3 | 0.26 (0.03 to 1.99) | 7 | **3.03 (1.22 to 7.52)** | 1 | — |
| XA/D | 9 | 0.59 (0.21 to 1.67) | 0 | — | 8 | 0.58 (0.17 to 1.91) | 0 | — |
| XA/C | 1 | — | 5 | 0.32 (0.07 to 1.46) | 2 | — | 2 | — |
| O/O | 14 | 0.80 (0.31 to 2.10) | 11 | 0.62 (0.18 to 2.17) | 11 | 1.36 (0.60 to 3.08) | 4 | 0.62 (0.18 to 2.17) |

*RR = risk ratio; CI = confidence interval; SNP = single-nucleotide polymorphism; — = insufficient data. Statistically significant associations are in boldface type.

†Risk ratio of death was adjusted for sex, stage (III–IV vs. I–II), age at diagnosis, current smoking status, and pack-years of smoking.