|  |
| --- |
| **Supplementary Table 10.** **Interactions between polygenic risk score (PRS) and autosomal mosaic abnormalities on the risk of cirrhosisa,b,c** |
| **Autosomal mosaic abnormalities** | **Multiplicative interaction** | **Additive interaction**  |
| **HR (95% CI)** | ***p* value** | **Intermediate genetic risk** | **High genetic risk** |
| **RERI (95%CI)** | **AP (95%CI)** | **RERI (95%CI)** | **AP (95%CI)** |
| All detectable mCAs  | 0.95 (0.72-1.26) | 0.731 | -0.09 (-0.78,0.61) | -0.06 (-0.52,0.41) | 0.11 (-0.87,1.09) | 0.04 (-0.34,0.43) |
| Cell fraction<10%  | 0.80 (0.56-1.15) | 0.235 | -0.22 (-1.22,0.78) | -0.14 (-0.77,0.50) | -0.45 (-1.76,0.85) | -0.21 (-0.89,0.47) |
| Cell fraction≥10% | 1.18 (0.65-2.12) | 0.589 | -0.40 (-2.05,1.24) | -0.28 (-1.49,0.93) | 1.05 (-1.55,3.66) | 0.29 (-0.29,0.87) |
| Mosaic copy gain | 1.43 (0.67-3.03) | 0.356 | 1.12 (-0.20,2.44) | 0.67 (0.09,1.26) | 1.60 (-0.86,4.06) | 0.56 (0.08,1.04) |
| Cell fraction<10%  | 1.46 (0.54-3.94) | 0.450 | 0.42 (-1.25,2.10) | 0.34 (-0.88,1.57) | 1.27 (-1.78,4.32) | 0.45 (-0.27,1.18) |
| Cell fraction≥10% | 1.37 (0.43-4.35) | 0.594 | 2.87 (0.44,5.31) | 0.95 (0.89,1.00) | 2.52 (-2.23,7.27) | 0.74 (0.37,1.11) |
| Mosaic copy loss | 0.83 (0.44-1.57) | 0.562 | 0.05 (-1.48,1.57) | 0.03 (-1.00,1.06) | -0.24 (-2.24,1.76) | -0.13 (-1.28,1.02) |
| Cell fraction<10%  | 0.66 (0.23-1.86) | 0.429 | 0.89 (-1.25,3.03) | 0.48 (-0.49,1.45) | -0.91 (-3.13,1.31) | -1.21 (-6.05, 3.64) |
| Cell fraction≥10% | 0.95 (0.42-2.16) | 0.910 | -0.67 (-2.98,1.65) | -0.50 (-2.41,1.41) | 0.17 (-3.14,3.48) | 0.06 (-1.03,1.15) |
| Copy-neutral loss of heterozygosity | 0.85 (0.58-1.24) | 0.397 | -0.46 (-1.53,0.62) | -0.31 (-1.08,0.47) | -0.15 (-1.61,1.31) | -0.06 (-0.66,0.54) |
| Cell fraction<10%  | 0.74 (0.49-1.12) | 0.160 | -0.43 (-1.65,0.79) | -0.26 (-1.06,0.53) | -0.68 (-2.24,0.89) | -0.32 (-1.17,0.54) |
| Cell fraction≥10% | 1.70 (0.65-4.43) | 0.277 | -0.91 (-3.62,1.81) | -0.85 (-3.82,2.12) | 2.57 (-2.35,7.49) | 0.49 (-0.14,1.11) |
| Abbreviations: AP, attributable proportion; RERI, relative excess risk due to interaction; HR, hazard ratio; 95% CI, 95% confidence interval.  |
| a Estimates were adjusted for age, age2, sex, smoking status, drinking status, the top 10 principal components of ancestry and genotyping batch. |
| b Genetic risk was categorized into low (bottom quintile), intermediate (quintiles 2-4), and high (top quintile) according to distributions of PRS among individuals without cirrhosis. |
| c When evaluating the interaction effects, 1934 mosaic copy gain carriers, 2781 mosaic copy loss carriers, 7514 mosaic copy-neutral loss of heterozygosity carriers, and 432,675 non-carriers of any mCA types were included, where non-carriers of any mCA types were set as the reference group.  |