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| **Supplementary Table 11. Interactions between polygenic risk score (PRS) and autosomal mosaic abnormalities on the risk of compensated 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  | 1.04 (0.74,1.46) | 0.813 | 0.24 (-0.65,1.13) | 0.13 (-0.34,0.61)  | 0.61 (-0.77,1.98) | 0.19 (-0.19,0.56) |
| Cell fraction<10%  | 0.91 (0.58,1.42) | 0.678 | 0.16 (-1.11,1.43) | 0.08 (-0.56,0.73) | 0.13 (-1.70,1.96) | 0.04 (-0.57,0.65) |
| Cell fraction≥10% | 1.26 (0.60-2.64) | 0.548 | 0.31 (-1.64,2.26) | 0.17 (-0.86,1.20) | 1.52 (-1.88,4.92) | 0.38 (-0.24,0.99) |
| Mosaic copy gain | 1.03 (0.39-2.74) | 0.956 | 0.68 (-1.28,2.64) | 0.42 (-0.62,1.45) | 0.52 (-2.58,3.63) | 0.22 (-0.88,1.32) |
| Cell fraction<10% | 1.08 (0.25-4.62) | 0.917 | -0.69 (-3.18,1.79) | -1.00 (-5.31,3.31) | 0.03 (-3.96,4.02) | 0.01 (-1.67,1.69) |
| Cell fraction≥10% | 0.99 (0.26-3.69) | 0.983 | 4.12 (0.21, -8.04) | 0.93 (0.86,1.00) | 1.67 (-4.20,7.54) | 0.56 (-0.31,1.43) |
| Mosaic copy loss | 1.14 (0.51-2.54) | 0.741 | 1.94 (0.73,3.15) | 0.92 (0.84,1.00) | 1.00 (-1.05,3.04) | 0.48 (-0.04,1.00) |
| Cell fraction<10% | 0.59 (0.18-1.92) | 0.384 | 2.88 (0.56,5.20) | 0.92 (0.85,1.00) | NA | NA |
| Cell fraction≥10% | 1.99 (0.65-6.15) | 0.229 | 1.36 (-0.11,2.84) | 0.81 (0.63,1.00) | 2.72 (-1.25,6.70) | 0.67 (0.35,1.00) |
| Copy-neutral loss of heterozygosity | 0.94 (0.59,1.49) | 0.791 | -0.28 (-1.68,1.13) | -0.16 (-1.01,0.69) | 0.44 (-1.63,2.51) | 0.13 (-0.43,0.69) |
| Cell fraction<10%  | 0.94 (0.58,1.54) | 0.818 | 0.04 (-1.52,1.60) | 0.02 (-0.75,0.79) | 0.45 (-1.83,2.74) | 0.13 (-0.48,0.74) |
| Cell fraction≥10% | 0.91 (0.27,3.09) | 0.884 | -2.49 (-6.99,2.01) | -2.72 (-9.68,4.25) | 0.17 (-6.56,6.91) | 0.04 (-1.40,1.47) |
| *Definition of 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.  |