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| **Supplementary Table 1.** Univariate analysis for each specific genomic alteration encompassed in the AMNESIA panel in terms of both PFS and OS. P-values were adjusted using the FDR method |
| **AMNESIA genomic alterations** | **PFS** | **OS** |
| **Gene** | **Alteration type** | ***n* altered (%)** | **HR** | ***p*** | **HR** | ***p*** |
| *KRAS* | snv | 11 (3.4) | 2.78 (1.47-5.27) | 0.004 | 2.35 (1.24-4.47) | 0.022 |
| *MET* | snv | 1 (0.3) | NA | NA | NA | NA |
| *PIK3CA* | snv | 15 (4.6) | 1.14 (0.66-1.95) | 0.78 | 1.06 (0.58-1.94) | 0.86 |
| *EGFR* | amp | 12 (3.7) | 0.91 (0.47-1.77) | 0.78 | 0.87 (0.41-1.86) | 0.86 |
| *KRAS* | amp | 9 (2.8) | 1.5 (0.74-3.04) | 0.43 | 2.11 (0.93-4.78) | 0.121 |
| *MET* | amp | 6 (1.8) | 4.04 (1.77-9.19) | 0.004 | 4.3 (1.89-9.79) | 0.003 |
| Snv, single nucleotide variant; amp, amplification; NE, non assessable. |