Single gene alteration, HR (95% CI)	PBO+ AAP (N)	NIRA+ AAP (N)	rPFS	TCC	TSP	OS	TPSA	ORR (risk ratio)
HRR-Fanconi group	14	17	0.59 (0.23, 1.45)	0.68 (0.17, 2.74)	0.90 (0.24, 3.37)	0.43 (0.12, 1.50)	0.65 (0.27, 1.59)	1.5 (0.38, 6.00)
BRIP1	4	4	0.23 (0.02, 2.26)	NE	1.14 (0.10, 13.27)	NE	0.98 (0.14, 7.00)	0.5 (0.13, 2.00)
FANCA	6	5	1.07 (0.18, 6.44)	0.51 (0.05, 5.16)	1.23 (0.17, 8.74)	NE	0.66 (0.13, 3.47)	NE
PALB2	4	8	0.59 (0.15, 2.22)	0.39 (0.02, 6.19)	0.41 (0.03, 6.62)	0.27 (0.05, 1.66)	0.59 (0.16, 2.20)	2 (0.33, 11.97)
HRR associated group	23	20	0.64 (0.26, 1.58)	0.72 (0.19, 2.69)	0.58 (0.17, 2.00)	0.43 (0.13, 1.38)	0.43 (0.17, 1.10)	6.4 (0.96, 43.25)
CHEK2	20	18	0.66 (0.25, 1.75)	0.36 (0.07, 1.88)	0.54 (0.14, 2.25)	0.44 (0.12, 1.71)	0.37 (0.14, 0.99)	NE
HDAC2	3	2	0.71 (0.06, 8.02)	NE	0.71 (0.04, 11.79)	0.440 (0.04, 5.13)	NE	NE
ATM	42	43	1.11 (0.63, 1.99)	0.26 (0.08, 0.80)	0.75 (0.28, 2.00)	1.07 (0.44, 2.65)	0.73 (0.39, 1.36)	3 (1.12, 8.13)
CDK12	16	11	1.32 (0.43, 3.92)	1.13 (0.27, 5.70)	1.05 (0.28, 3.94)	1.61 (0.49, 5.33)	0.66 (0.24, 1.80)	2.25 (0.64, 7.97)

NE = not estimable due to few or no events.