

S6 Table. SNVs according to number of non-*BRCA1/2* HR-related gene aberrations

Non- <i>BRCA1/2</i> HR-related gene aberrations	0	1	≥ 2	p-value ^{a)}
Mean	14.15	14.77	26.88	0.002
SD	4.70	5.49	28.20	
	a	a	b	

HR, homologous recombination; SD, standard deviation. ^{a)}p-value by Kruskal–Wallis test. a, b: Different letters indicate statistically significant differences between multiple comparisons ($p < 0.05$).