Table S3. The percentages of subgroups of DDR gene mutations by clinical factors in the patients

Genes		Histology			FIGO stage		Tumor grade		Recurrence		Death	
		OSA	OEA	OCCA	Early	Advanced	Low	High	No	Yes	No	Yes
	172	69	39	64	69	103	29	143	70	102	96	76
HR												
Wild type	154	58	36	60	64	90	26	128	64	90	89	65
	89.5%	84.1%	92.3%	93.8%	92.8%	87.4%	89.7%	89.5%	91.4%	88.2%	92.7%	85.5%
Mutation	18	11	3	4	5	13	3	15	6	12	7	11
	10.5%	15.9%	7.7%	6.3%	7.2%	12.6%	10.3%	10.5%	8.6%	11.8%	7.3%	14.5%
P value*				0.154		0.259		0.981		0.502		0.126
NHEJ												
Wild type	170	68	39	63	69	101	29	141	70	100	96	74
	98.8%	98.6%	100.0%	98.4%	100.0%	98.1%	100.0%	98.6%	100.0%	98.0%	100.0%	97.4%
Mutation	2	1	0	1	0	2	0	2	0	2	0	2
	1.2%	1.4%	0.0%	1.6%	0.0%	1.9%	0.0%	1.4%	0.0%	2.0%	0.0%	2.6%
P value*				0.742		0.244		0.522		0.239		0.11
MMR												
Wild type	161	67	33	61	65	96	24	137	66	95	91	70
	93.6%	97.1%	84.6%	95.3%	94.2%	93.2%	82.8%	95.8%	94.3%	93.1%	94.8%	92.1%
Mutation	11	2	6	3	4	7	5	6	4	7	5	6
	6.4%	2.9%	15.4%	4.7%	5.8%	6.8%	17.2%	4.2%	5.7%	6.9%	5.2%	7.9%

P value*				0.03		0.793		0.009		0.762		0.475
BER												
Wild type	160	65	37	58	65	95	27	133	66	94	91	69
	93.0%	94.2%	94.9%	90.6%	94.2%	92.2%	93.1%	93.0%	94.3%	92.2%	94.8%	90.8%
Mutation	12	4	2	6	4	8	2	10	4	8	5	7
	7.0%	5.8%	5.1%	9.4%	5.8%	7.8%	6.9%	7.0%	5.7%	7.8%	5.2%	9.2%
P value*				0.631		0.619		0.985		0.59		0.306
NER												
Wild type	167	66	39	62	67	100	29	138	67	100	93	74
	97.1%	95.7%	100.0%	96.9%	97.1%	97.1%	100.0%	96.5%	95.7%	98.0%	96.9%	97.4%
Mutation	5	3	0	2	2	3	0	5	3	2	3	2
	2.9%	4.3%	0.0%	3.1%	2.9%	2.9%	0.0%	3.5%	4.3%	2.0%	3.1%	2.6%
P value*				0.43		0.996		0.307		0.373		0.848
TLS												
Wild type	171	69	39	63	69	102	29	142	70	101	96	75
	99.4%	100.0%	100.0%	98.4%	100.0%	99.0%	100.0%	99.3%	100.0%	99.0%	100.0%	98.7%
Mutation	1	0	0	1	0	1	0	1	0	1	0	1
	0.6%	0.0%	0.0%	1.6%	0.0%	1.0%	0.0%	0.7%	0.0%	1.0%	0.0%	1.3%
P value*				0.428		0.412		0.652		0.406		0.26
CCR												
Wild type	119	29	30	60	60	59	24	95	57	62	74	45
	69.2%	42.0%	76.9%	93.8%	87.0%	57.3%	82.8%	66.4%	81.4%	60.8%	77.1%	59.2%

Mutation	53	40	9	4	9	44	5	48	13	40	22	31
	30.8%	58.0%	23.1%	6.3%	13.0%	42.7%	17.2%	33.6%	18.6%	39.2%	22.9%	40.8%
P value*				<0.001		<0.001		0.083		0.004		0.012

Note: OSA: ovarian serous carcinoma; OEA: ovarian endometrioid carcinoma; OCCA: ovarian clear cell carcinoma; HR: homologous recombination; NHEJ: nonhomologous DNA end joining; MMR: mismatch repair; BER: base excision repair; NER: nucleotide excision repair; TLS: translesion synthesis; CCR: cell cycle regulation;*Pearson's chi-squared test