## **SUPPLEMENTARY TABLE**

	TCGA cohort			ICGC cohort		
	<i>MUC16</i>		- <i>P</i> value	MUC16		Damhao
-	Mutated	Wild-type	- P value	Mutated	Wild-type	– <i>P</i> value
TP53						
Mutated	57 (16.7%)	7 (5.6%)	0.001	27 (20.5%)	2 (3.9%)	0.006
Wild-type	284 (83.3%)	119 (94.4%)		105 (70.5%)	49 (96.1%)	
POLE						
Mutated	44 (12.9%)	1 (0.8%)	< 0.001	16 (12.1%)	0 (0.0%)	0.007
Wild-type	297 (87.1%)	125 (99.2%)		116 (87.9%)	51 (100.0%)	
BRCA1/2						
Mutated	56 (16.4%)	5 (4.0%)	< 0.001	26 (19.7%)	2 (3.9%)	0.006
Wild-type	285 (83.6%)	121 (96.0%)		106 (80.3%)	49 (96.1%)	
MMR genes						
Mutated	49 (14.4%)	2 (1.6%)	< 0.001	22 (16.7%)	0 (0.0%)	0.001
Wild-type	292 (85.6%)	124 (98.4%)		110 (83.3%)	51 (100.0%)	

## Supplementary Table 1. Cooccurrent mutation of *MUC16* and DNA repair genes.