

S1 Table. Distribution of alteration of somatic signatures

Variable	NDLC (n=41, 46.6%)	DLC (n=47, 53.4%)	p-value
Aging			
No altered	27 (65.9)	33 (70.2)	0.819
altered	14 (34.1)	14 (29.8)	
APOBEC			
No altered	38 (92.7)	47 (100)	0.097
altered	3 (7.3)	0	
Smoking			
No altered	31 (75.6)	25 (53.2)	0.045
altered	10 (24.4)	22 (46.8)	
BRCA1/2			
No altered	41 (100)	46 (97.9)	> 0.99
altered	0	1 (2.1)	
MMR			
No altered	8 (19.5)	17 (36.2)	0.101
altered	33 (80.5)	30 (63.8)	
UV			
No altered	41 (100)	45 (95.7)	0.497
altered	0	2 (4.3)	
POLE			
No altered	38 (92.7)	45 (95.7)	0.661
altered	3 (7.3)	2 (4.3)	
TMZ			
No altered	40 (97.6)	44 (93.6)	0.620
altered	1 (2.4)	3 (6.4)	
NRF			
No altered	26 (63.4)	35 (74.5)	0.354
altered	15 (36.6)	12 (25.5)	
DNA repair			
No altered	19 (46.3)	11 (23.4)	0.027
altered	22 (53.7)	36 (76.6)	
AR			
No altered	36 (87.8)	37 (78.7)	0.395
altered	5 (12.2)	10 (21.3)	
PI3K			
No altered	23 (56.1)	21 (44.7)	0.393
altered	18 (43.9)	26 (55.3)	
RTK-RAS			
No altered	6 (14.6)	6 (12.8)	> 0.99
altered	35 (85.4)	41 (87.2)	
TP53			
No altered	8 (19.5)	11 (23.4)	0.796
altered	33 (80.5)	36 (76.6)	
Cell cycle			
No altered	24 (58.5)	28 (59.6)	> 0.99
altered	17 (41.5)	19 (40.4)	
NOTCH			
No altered	10 (24.4)	10 (21.3)	0.802

altered

31 (75.6)

37 (78.7)

Values are presented as number (%). p-value was estimate by Fisher's exact test. AR, androgen receptor; DLC, durable local control group; MMR, mismatch repair; NDLC, non-durable local control group; PI3K, phosphoinositide 3-kinase; RTK, receptor tyrosine kinase; TMZ, temozolomide; UV, ultraviolet.