Table S3. Summary of the frequency of different types of mutations, including base substitution (C>A, C>G, C>T, T>A, T>C, T>G and CC>TT), deletions and insertions, detected in the RMEL3 locus (CTD-2023N9.1), in datasets of cutaneous melanoma samples from the TCGA (450 samples, SKCM) and ICGC (129 samples, MELA-AU project) data portals.

TCGA									
Location	**C>A N (%)**	**C>G N (%)**	**C>T N (%)**	**T>A N (%)**	**T>C N (%)**	**T>G N (%)**	**CC>TT N (%)**	**Deletion N (%)**	**Insertion N (%)**
Upstream	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Downstream	0 (0.00)	0 (0.000	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Intron	52 (50)	1 (0.96)	45(43.23)	1 (0.96)	4 (3.85)	1 (0.96)	0 (0.00)	2 (1.8)	2 (1.8)
Exon	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)

ICGC									
Location	**C>A N (%)**	**C>G N (%)**	**C>T N (%)**	**T>A N (%)**	**T>C N (%)**	**T>G N (%)**	**CC>TT N (%)**	**Deletion N (%)**	**Insertion N (%)**
Upstream	0 (0.00)	0 (0.00)	21 (3.53)	2 (0.34)	2 (0.34)	1 (0.17)	1 (0.17)	0 (0.00)	1 (0.17)
Downstream	0 (0.00)	1 (0.17)	9 (1.51)	2 (0.34)	1 (0.17)	1 (0.17)	0 (0.00)	1 (0.17)	1 (0.00)
Intron	23 (3.87)	6 (1.00)	428 (71.93)	20 (3.36)	29 (4.87)	16 (2.70)	16 (2.70)	10 (1.7)	3 (0.50)
Exon	0 (0.00)	0 (0.00)	1 (0.17)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)