Base change	Modification	Perc Methy	Ref	ALT	Ref-Fwd	Ref-Rev	ALT-Fwd	ALT-Rev	Het Cal
G	Methy	100%	G	G	x	x	-	-	-
G	Methy	50%	G	G,A	x	x	-	x	-
G	Methy	0%	G	G,A	x	-	-	x	-
C	Methy	100%	C	C	x	x	-	-	-
C	Methy	50%	C	C,T	x	x	x	-	-
C	Methy	0%	C	C,T	-	x	x	-	-
G>A	Mut + Methy	100%	G	A	-	-	x	x	FwdALT/FwdTotal
G>A	Mut + Methy	50%	G	G,A	x	x	x	x	FwdALT/FwdTotal
G>A	Mut + Methy	0%	G	G	x	x	-	-	FwdALT/FwdTotal
G>T	Mut + Methy	100%	G	T	-	-	x	x	FwdALT/FwdTotal
G>T	Mut + Methy	50%	G	G,T	x	x	x	x	FwdALT/FwdTotal
G>T	Mut + Methy	0%	G	G	x	x	-	-	FwdALT/FwdTotal
G>C	Methy	100%	G	C	-	-	x	x	
G>C	Methy	50%	G	T,C	-	-	x	x	
G>C	Methy	0%	G	T,C	-	-	x	x	
C>A	Mut + Methy	100%	C	A	-	-	x	x	RevALT/RevTotal
C>A	Mut + Methy	50%	C	C,A	x	x	x	x	RevALT/RevTotal
C>A	Mut + Methy	0%	C	C	x	x	-	-	RevALT/RevTotal
C>T	Mut + Methy	100%	C	T	-	-	x	x	RevALT/RevTotal
C>T	Mut + Methy	50%	C	C,T	x	x	x	x	RevALT/RevTotal
C>T	Mut + Methy	0%	C	C	x	x	-	-	RevALT/RevTotal
C>G	Methy	100%	C	G	-	-	x	x	
C>G	Methy	50%	C	G,A	-	-	x	x	
C>G	Methy	0%	C	G,A	-	-	x	x	
T>A	Mut + Methy	100%	T	A	-	-	x	x	totalALT/Total
T>A	Mut + Methy	50%	T	T,A	x	x	x	x	totalALT/Total
T>A	Mut + Methy	0%	T	T	x	x	-	-	totalALT/Total
T>C	Methy	100%	T	C	-	-	x	x	RevALT/RevTotal
T>C	Methy	50%	T	T,C	x	-	x	x	RevALT/RevTotal
T>C	Methy	0%	T	T,C	x	-	-	x	RevALT/RevTotal
T>G	Methy	100%	T	G	-	-	x	x	FwdALT/FwdTotal
T>G	Methy	50%	T	G,A	-	-	x	x	FwdALT/FwdTotal
T>G	Methy	0%	T	G,A	-	-	x	x	FwdALT/FwdTotal
A>T	Mut + Methy	100%	A	T	-	-	x	x	totalALT/Total
A>T	Mut + Methy	50%	A	A,T	x	x	x	x	totalALT/Total
A>T	Mut + Methy	0%	A	A	x	x	-	-	totalALT/Total
A>G	Methy	100%	A	G	-	-	x	x	FwdALT/FwdTotal
A>G	Methy	50%	A	A,G	-	x	x	x	FwdALT/FwdTotal
A>G	Methy	0%	A	A,G	-	x	x	-	FwdALT/FwdTotal
A>C	Methy	100%	A	C	-	-	x	x	RevALT/RevTotal

A>C	Methy	50%	A	T,C	-	-	x	x	RevALT/RevTotal
A>C	Methy	0%	A	T,C	-	-	x	x	RevALT/RevTotal

Supplementary Table 1: Summary of permutations of bases with possible mutation with methylation (Mut + Methy) and/or methylation (Methy) status. 'x' refers to the presence of reads in the particular DNA strand and base position. '-' refers to the absence of reads. The grey rows refer to the mutations that cannot be distinguished from bisulfite treatment base modifications using mitocall.