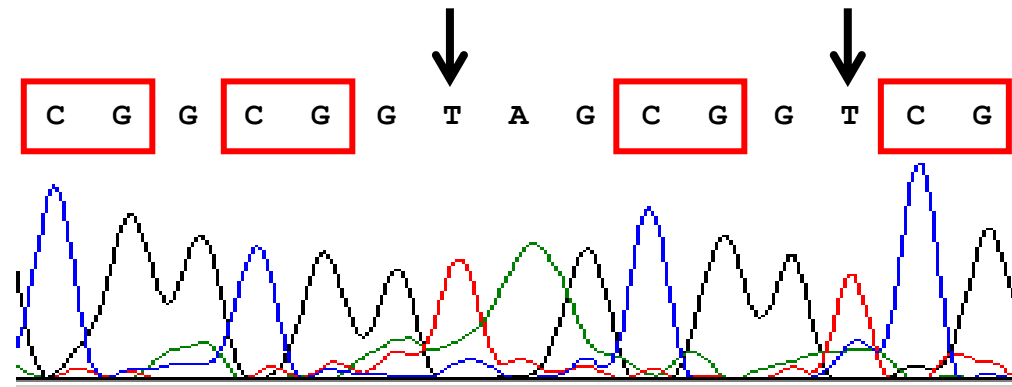
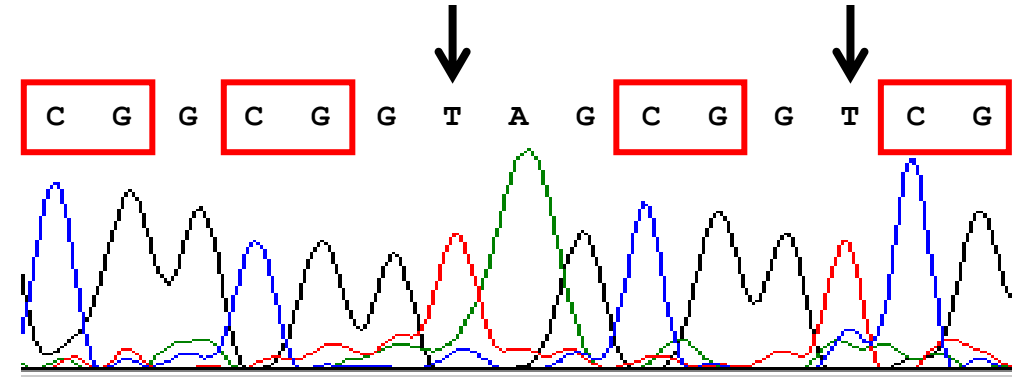


PYCARD

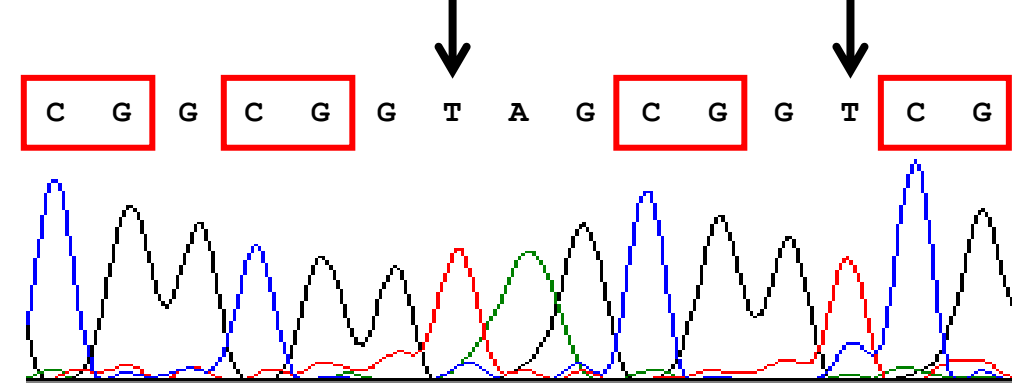
TR9_MeTA14
-Tet 4d



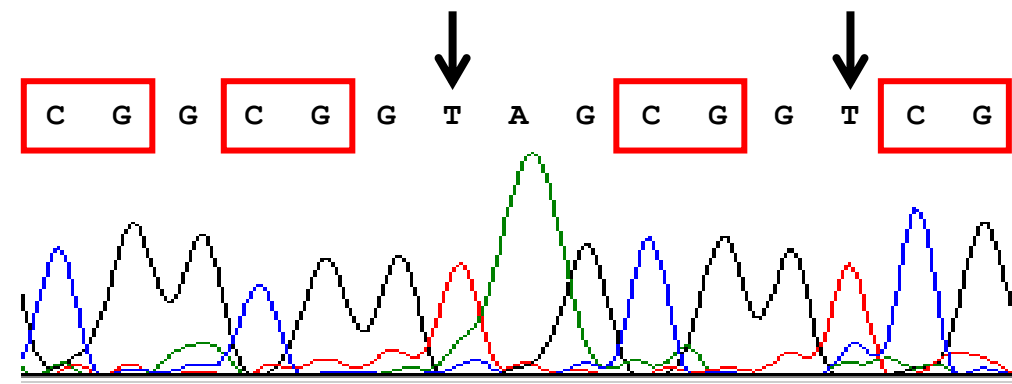
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+Tet 4d



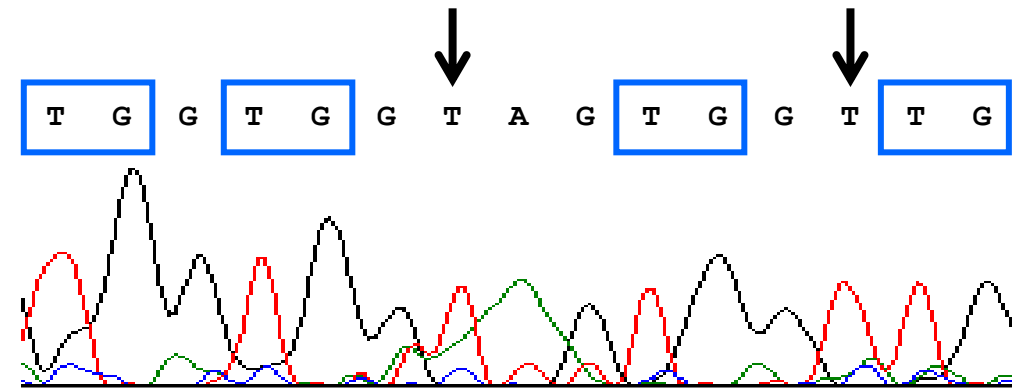
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-Tet 4d



TR15_MeTA5
+Tet 4d

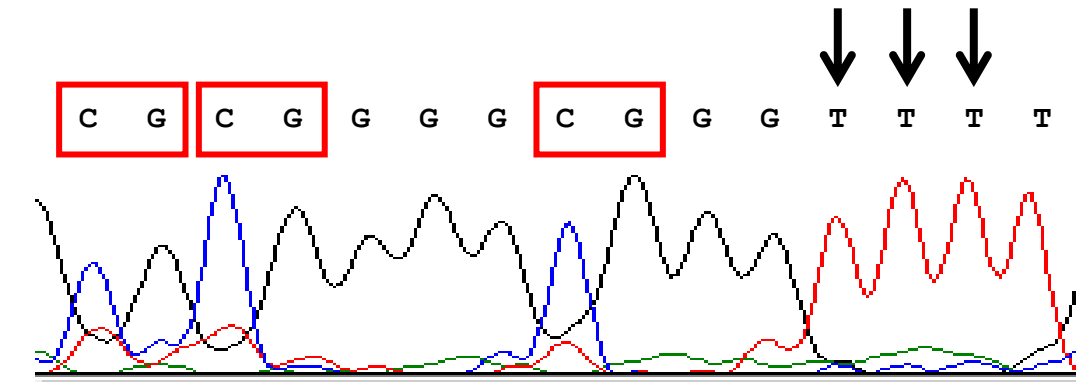


RWPE-1

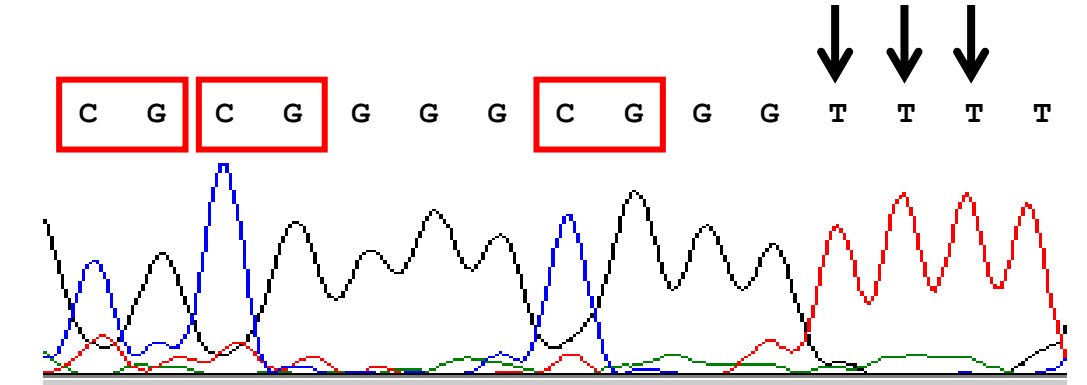


TNFRSF25

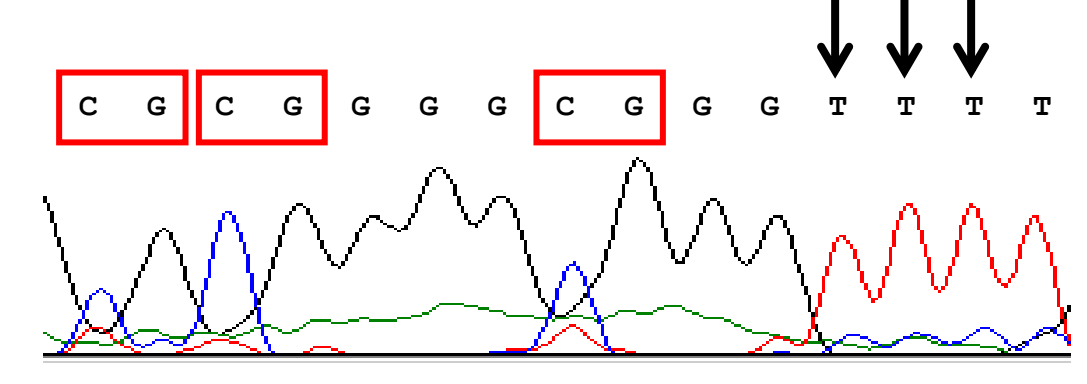
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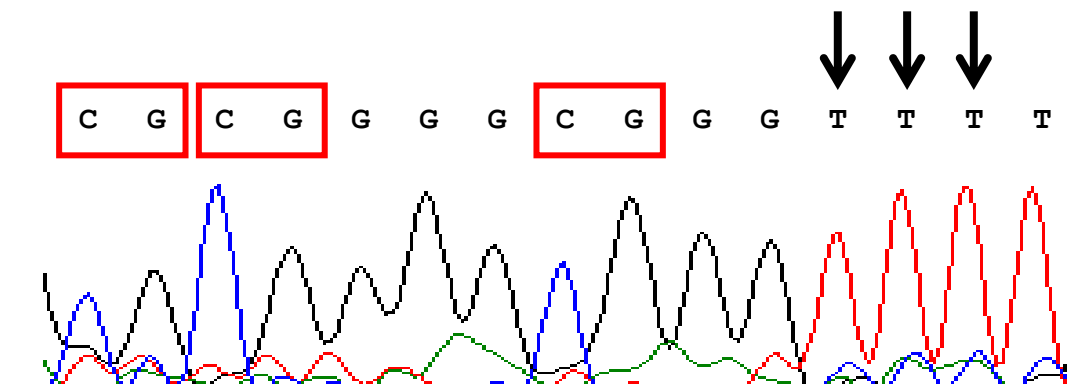
TR9_MeTA14
+Tet 4d



TR15_MeTA5
-Tet 4d



TR15_MeTA5
+Tet 4d



RWPE-1

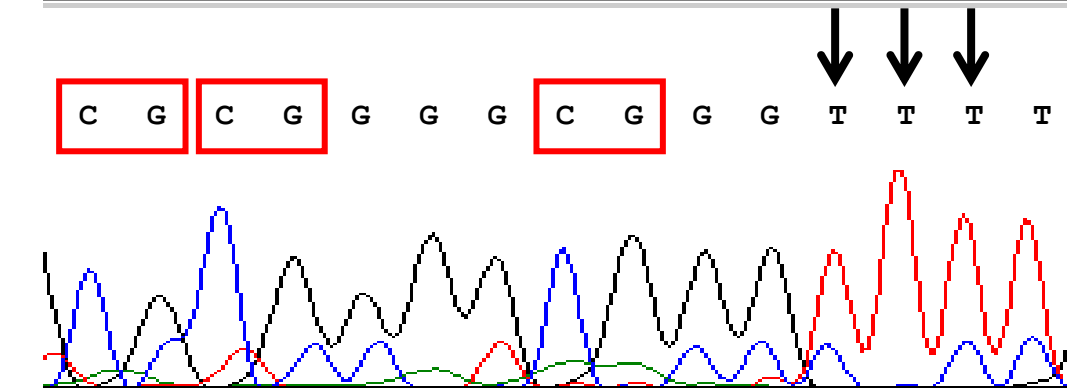


Figure S2. Representative bisulfite sequencing results of *PYCARD* (left) and *TNFRSF25* (right) promoter regions. *PYCARD* promoter region was highly methylated in LNCaP-derived prostate cancer cells but not in RWPE-1 normal prostate epithelial cells. Genomic DNAs were treated with sodium bisulfite and the promoter CGIs of *PYCARD* were sequenced. *TNFRSF25* promoter region was highly methylated both in LNCaP-derived prostate cancer cells and in RWPE-1 normal prostate epithelial cells. Arrows indicate the positions of cytosine residue converted by sodium bisulfite. Methylated CpG sites are boxed with red, and unmethylated CpG sites are boxed with blue.