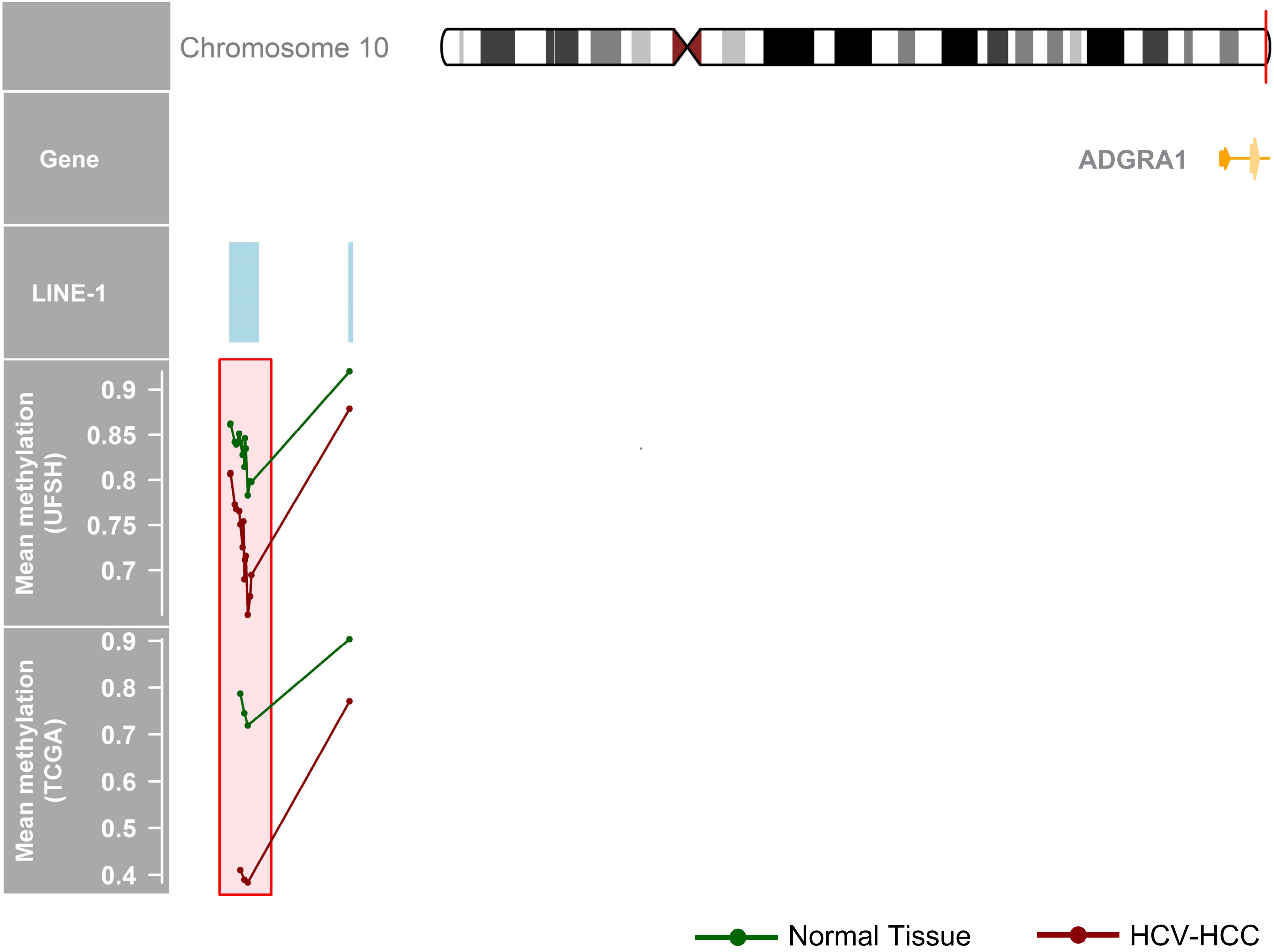
Extended Figures

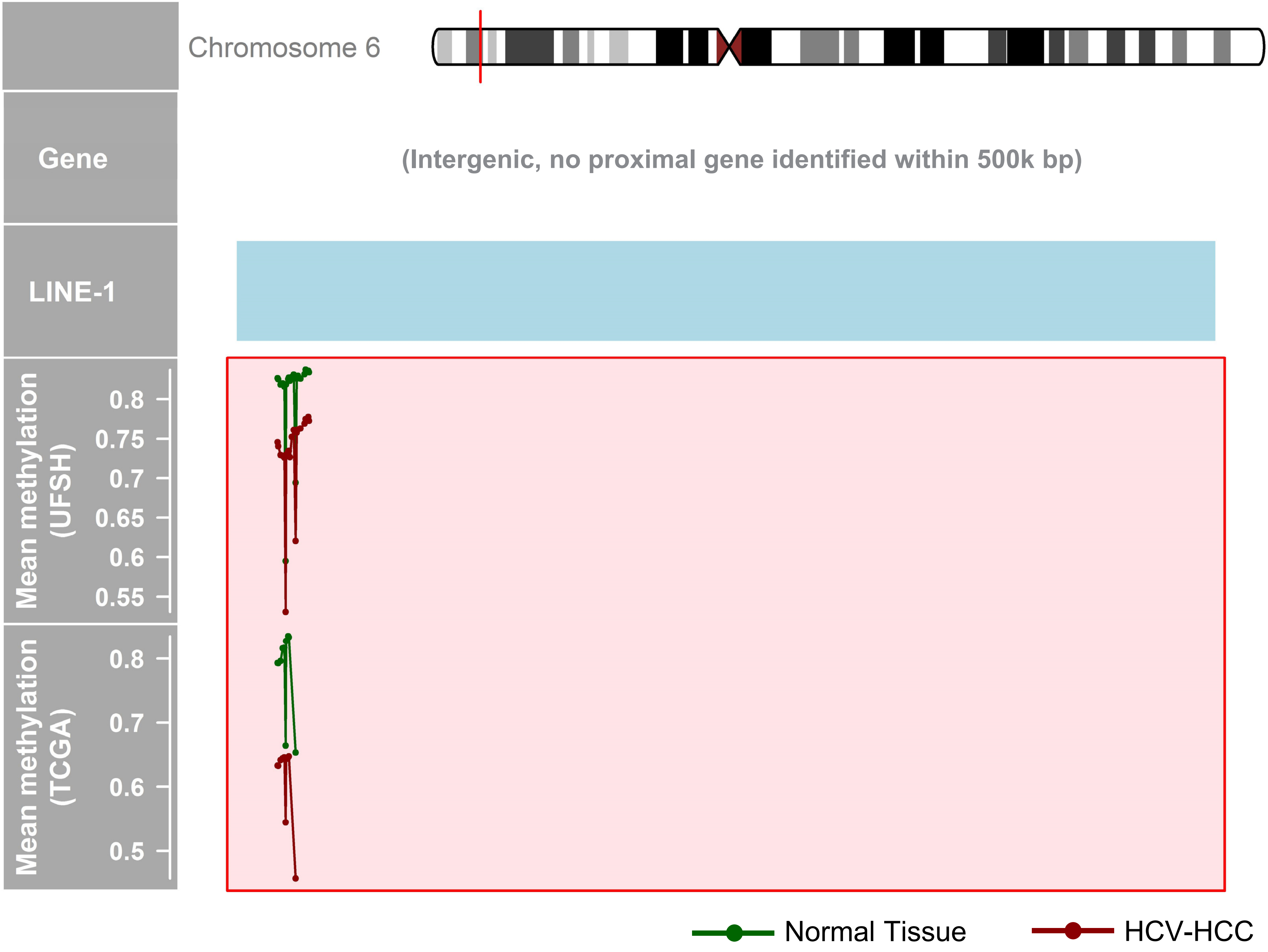
Zheng et. al.
DNA Methylation of Individual Repetitive Elements in Hepatitis C Virus Infection-Induced Hepatocellular Carcinoma

Note: The following figures provide the genomic views of the identified 15 HCV-HCC-associated RE and their proximal gene within 500 kb (one gene per figure; presented as the same order as Table 2). Mean methylation levels for each CpGs in REs across HCV-HCC and normal liver tissue are plotted to demonstrate the hypo-/hyper-methylation patterns. The identified differentially methylated RE region(s) are highlighted by red shaded frame(s). Both UFSH and TCGA results are shown.

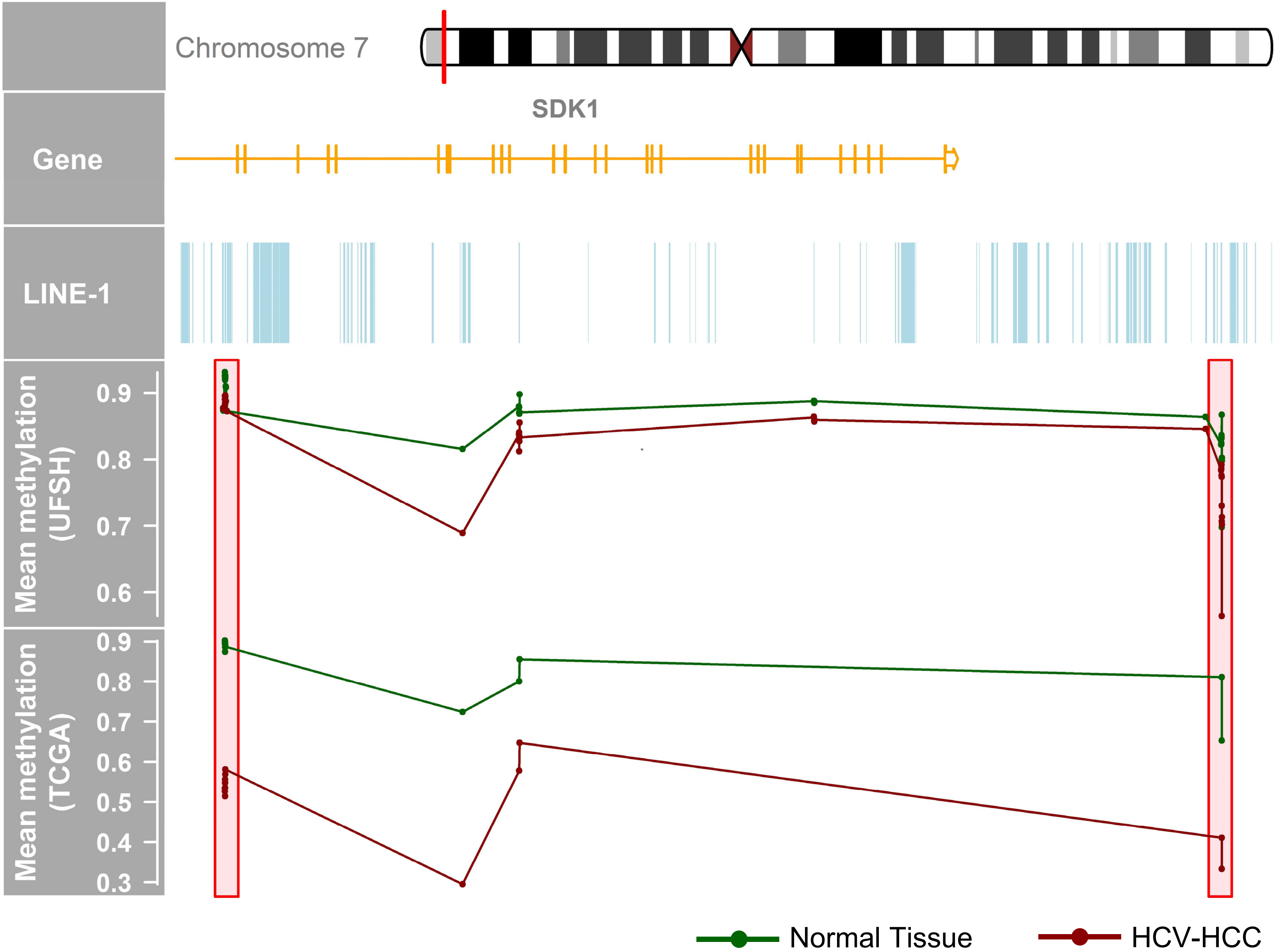
LINE-1 chr10:134875427-134876211



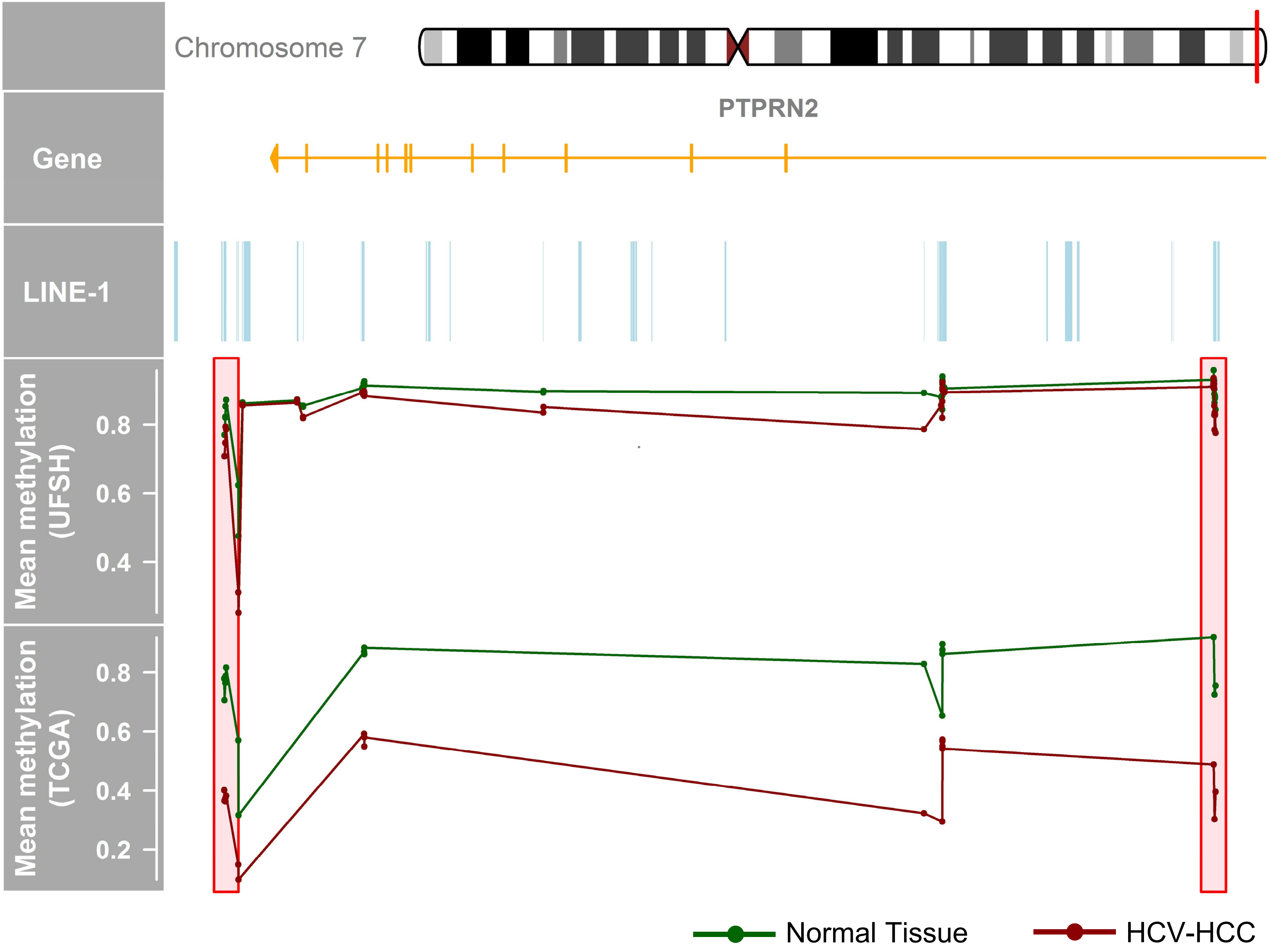
LINE-1 chr6:9810984-9817010



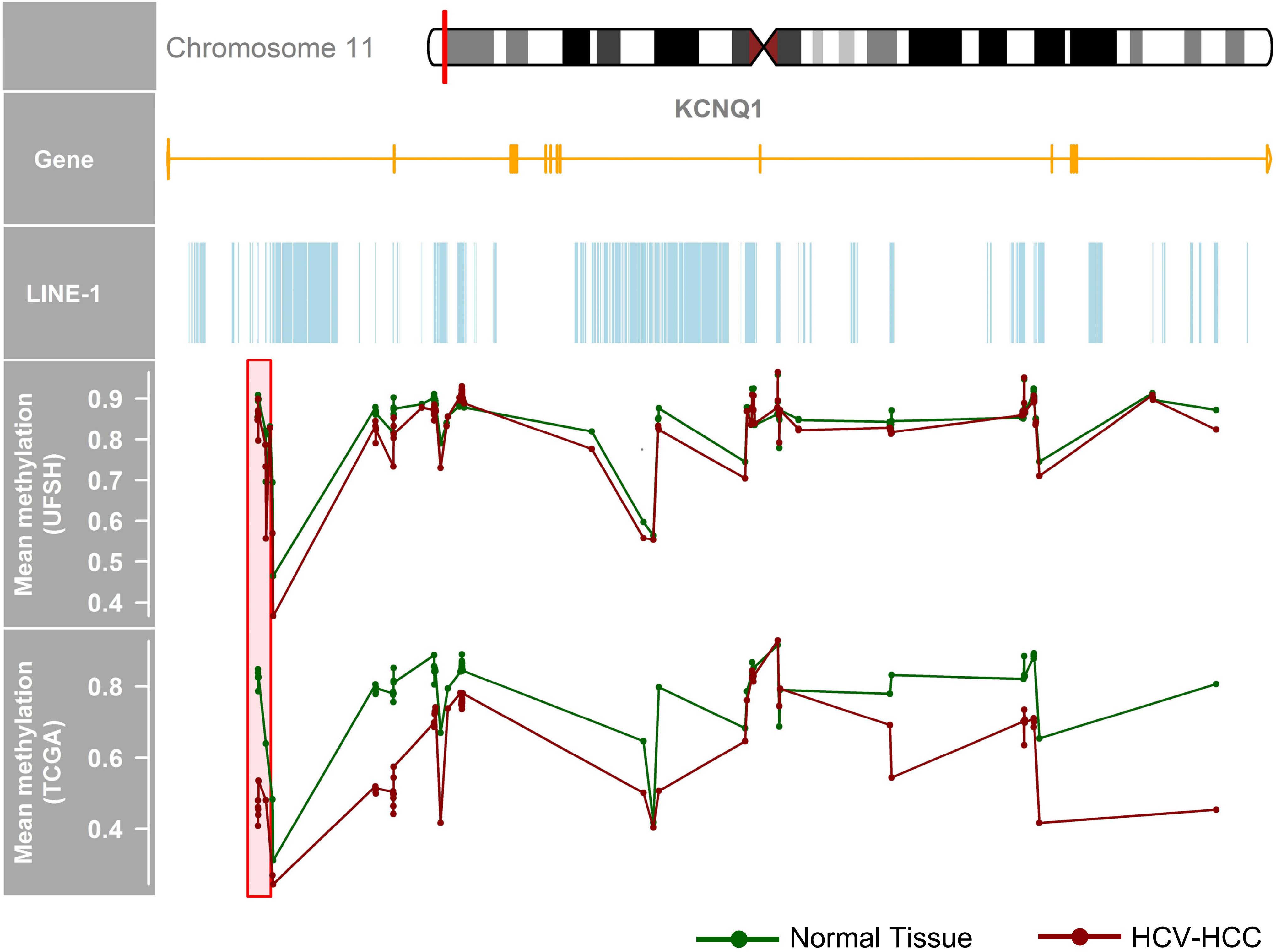
LINE-1 chr7:4388884-4389235 LINE-1 chr7:4085177-4085587



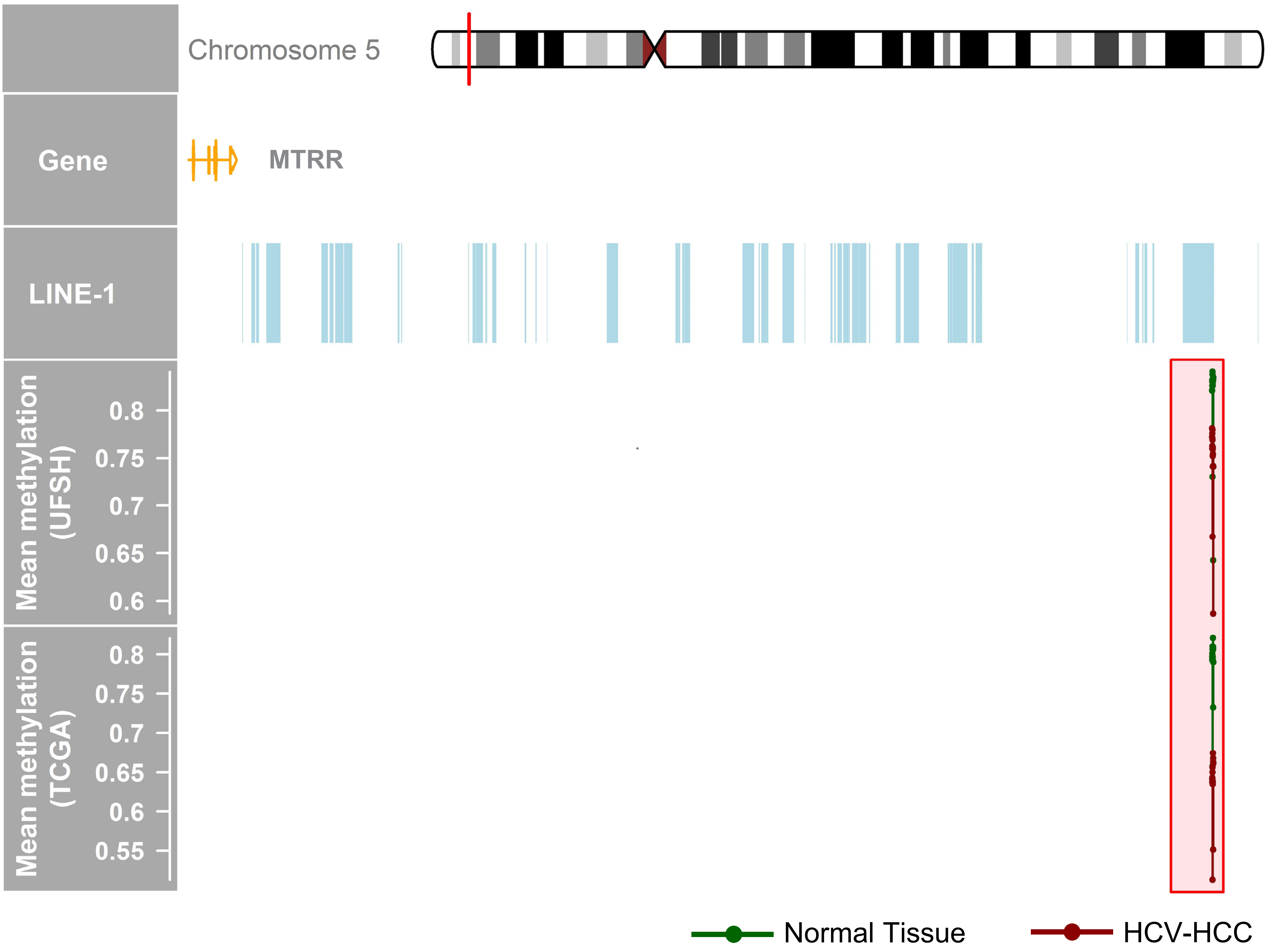
LINE-1 chr7:157594780-157595648 LINE-1 chr7:157318533-157319261



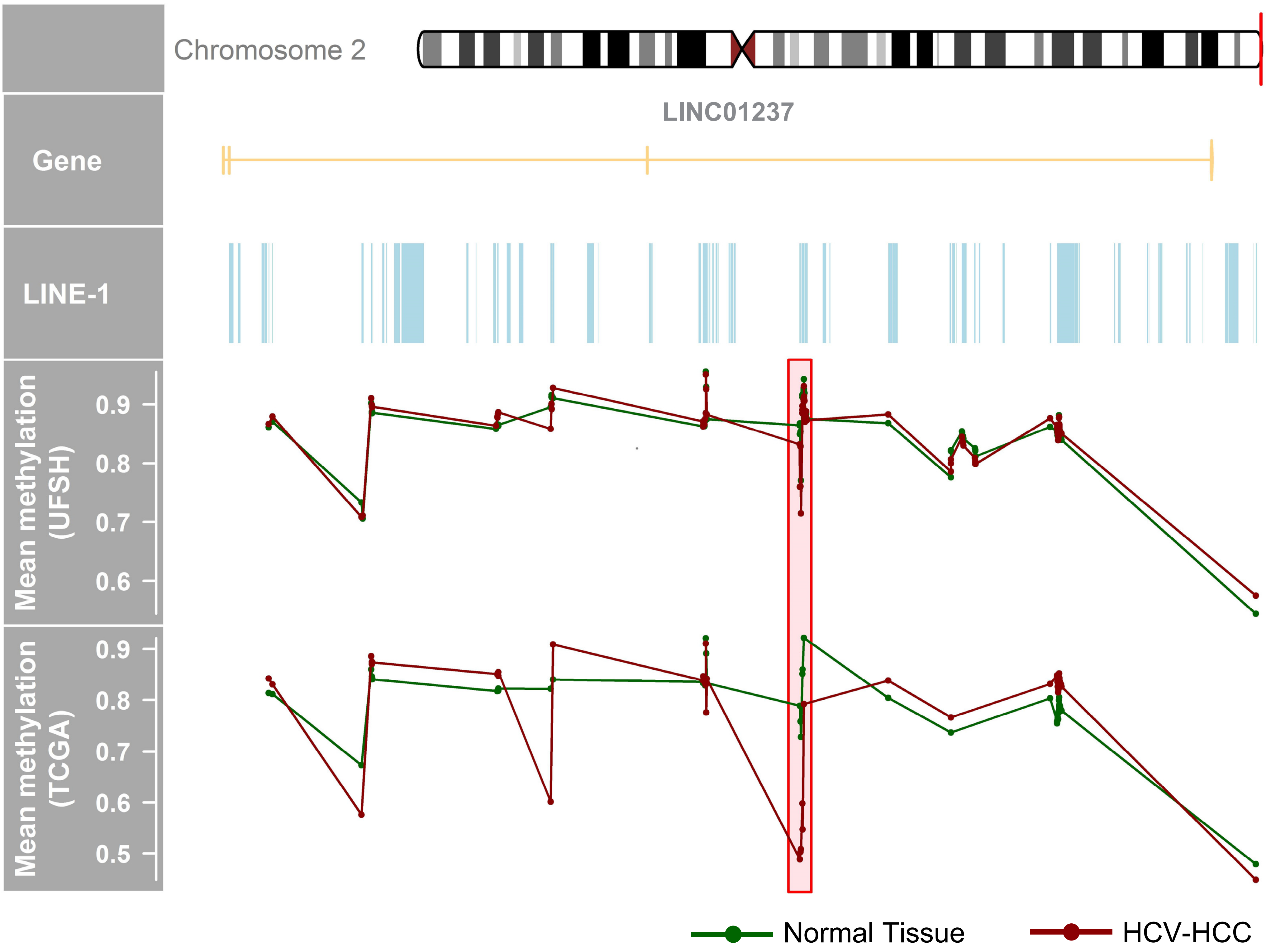
LINE-1 chr11:2499185-2499531



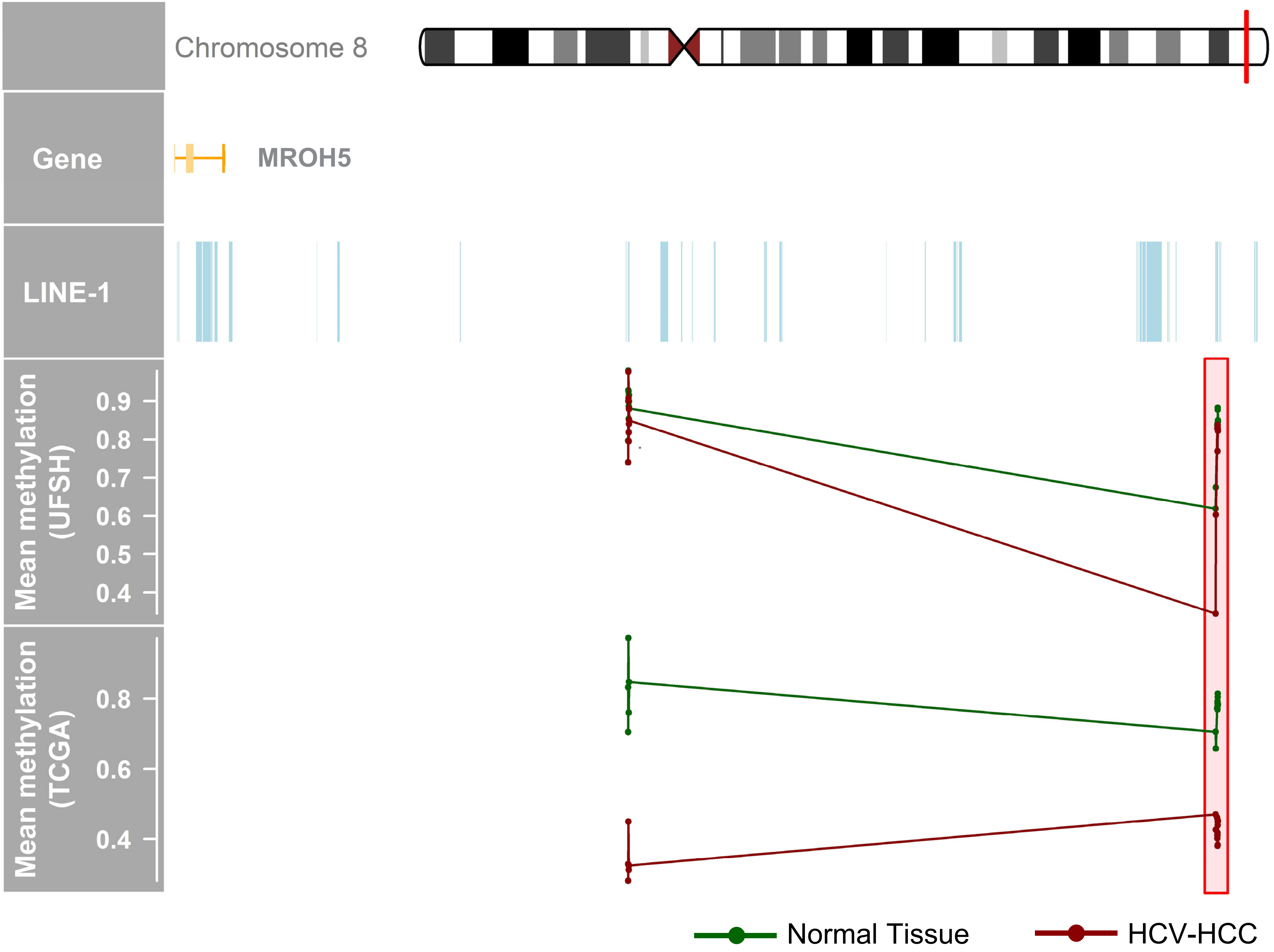
LINE-1 chr5:8084329-8090357



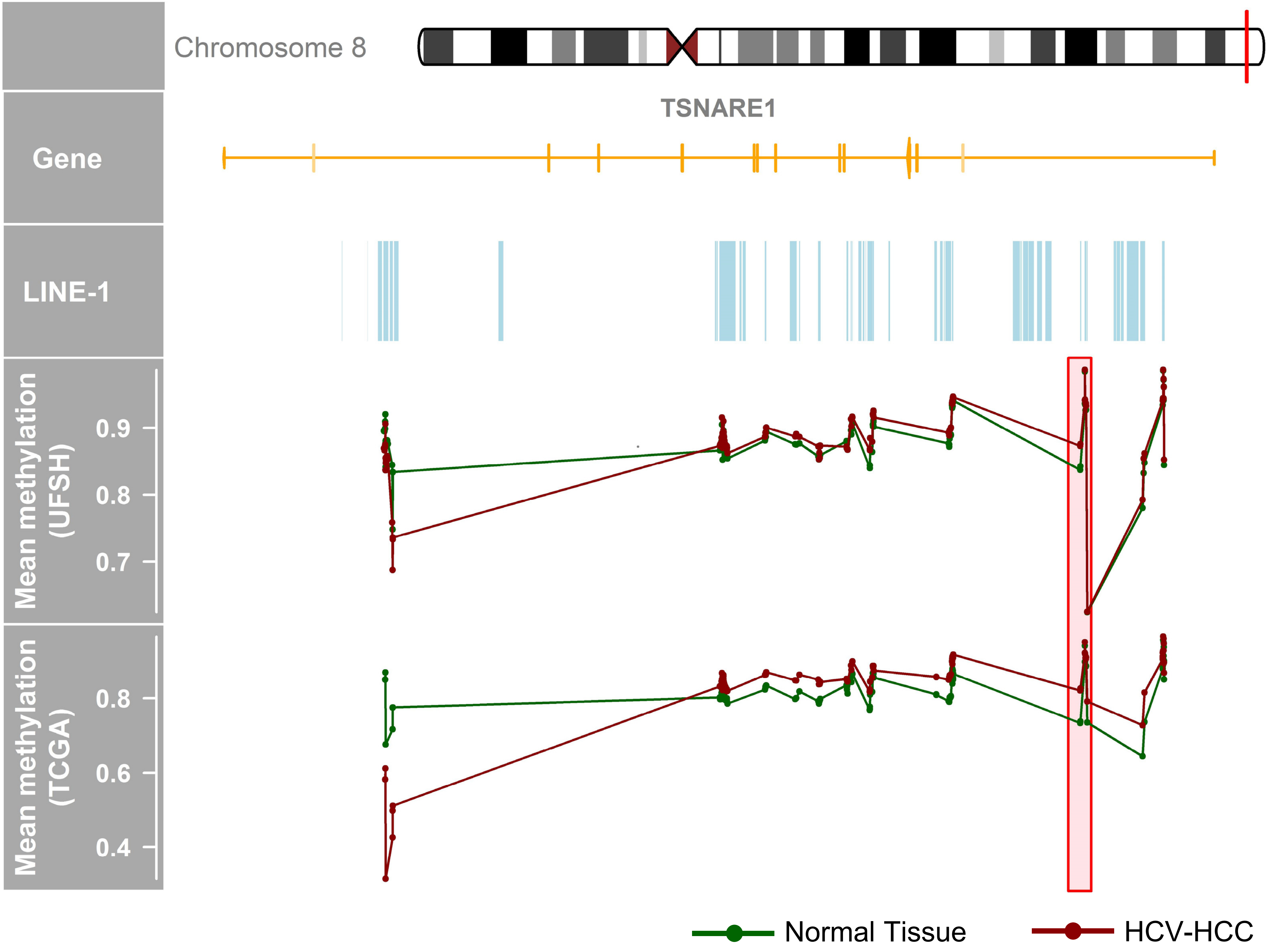
LINE-1 chr2:242938503-242938722



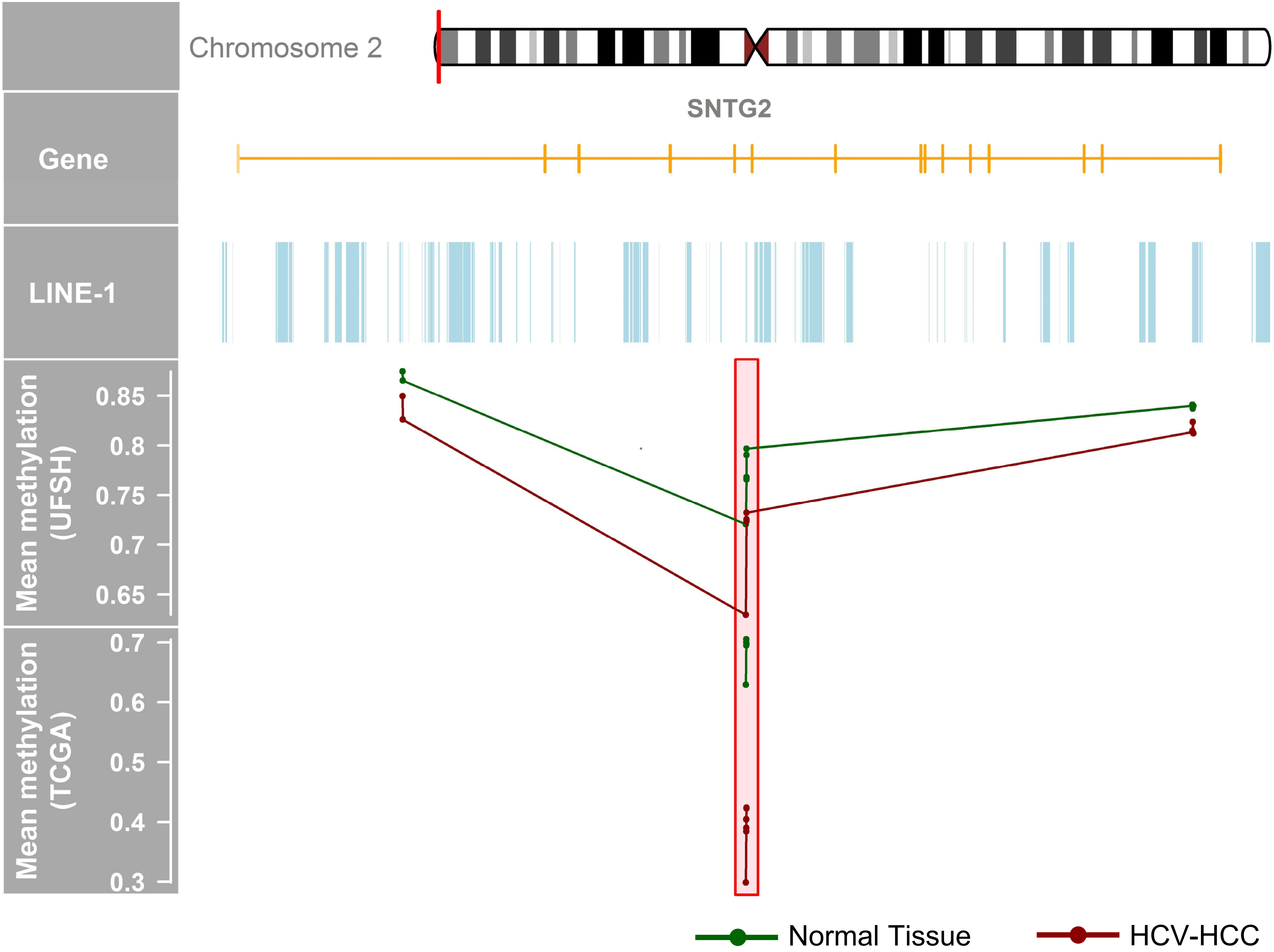
LINE-1 chr8:142852678-142853054



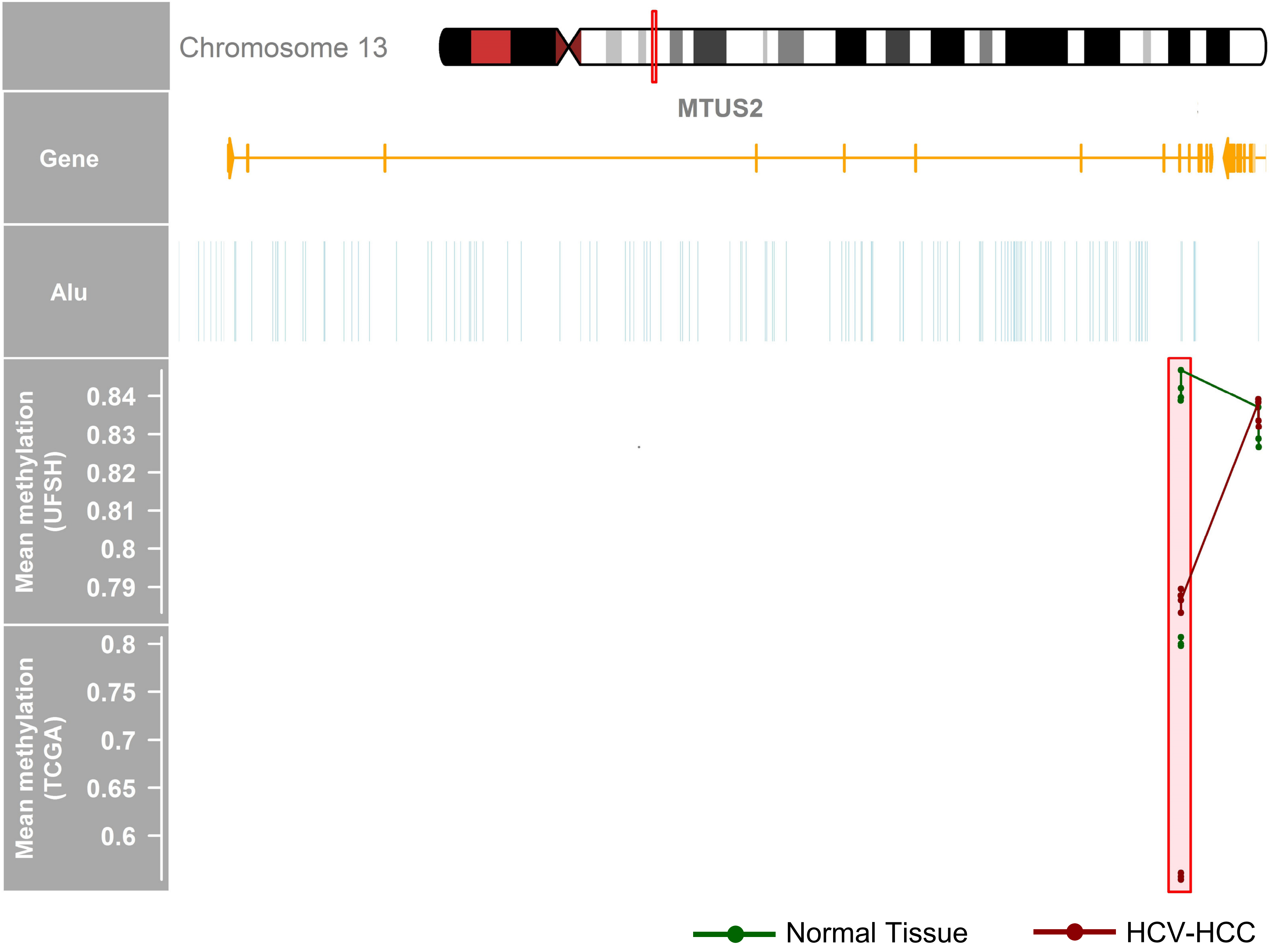
LINE-1 chr8:143458657-143458848



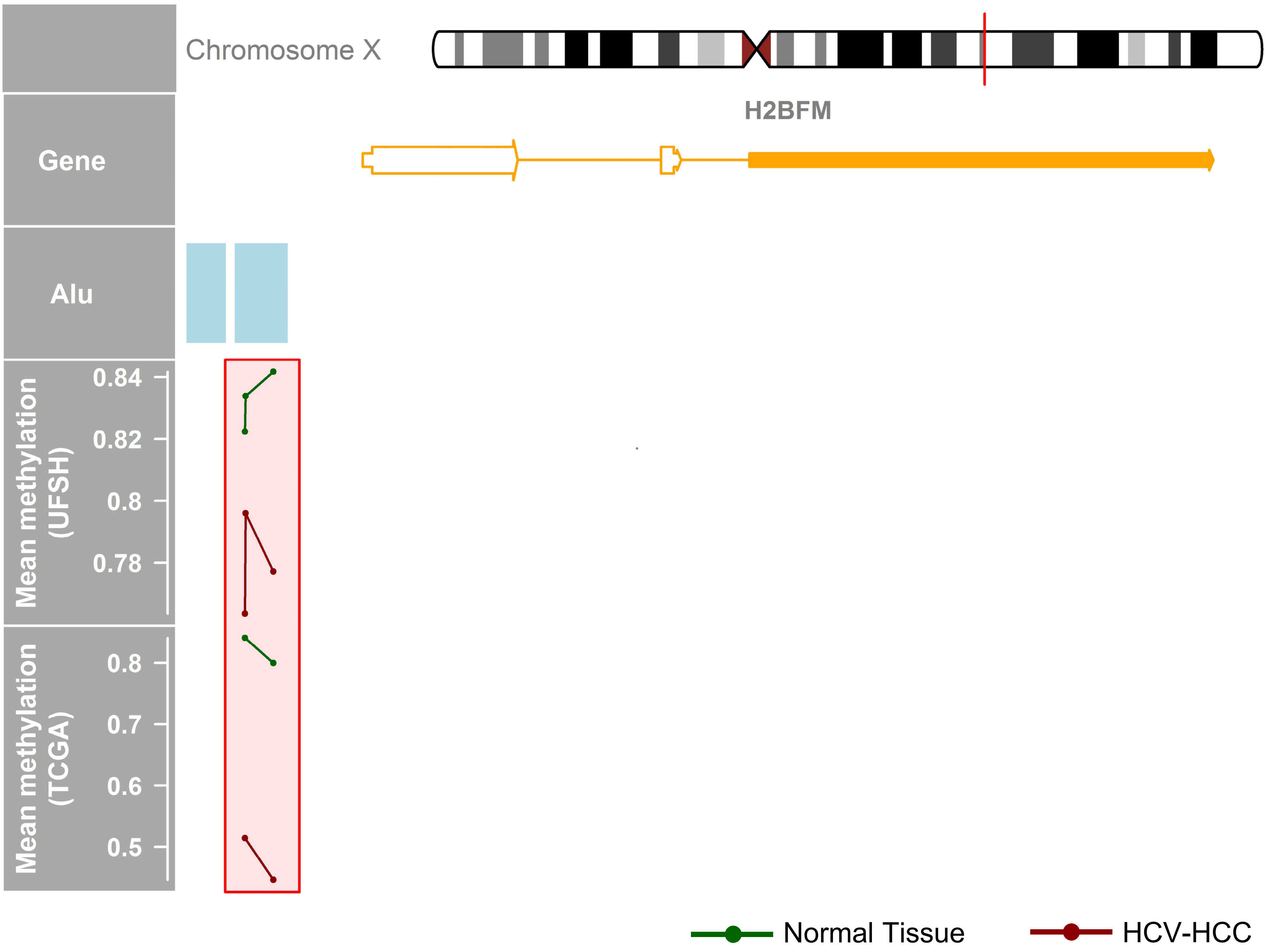
LINE-1 chr2:1166233-1166668



Alu   chr13:30062564-30062769



Alu chrX:103294139-103294294



Alu chr6:31598686-31598816