

Supplementary Figure 2. Bisulfite analysis of methylated genes. DNA from Caco-2 cell and normal lymphoblasts was treated with Na Bisulfite, amplified using primers specific for 10 different promoters (see below) including 164 individual CpG sites, and then subjected to whole population sequencing analysis without cloning. Two sample promoter (CX36 and KIAA06440) regions are shown for both lymphoblast and Caco-2 DNA. Note that all CpGs have been converted to CA (i.e. 5mC converted to T in the opposite strand) in lymphoblasts, while the same sites are methylated in Caco-2. The original CpG sites are marked with a red line on the lymphoblast sequences. Genes analyzed: CX36 (NM_01487), KIAA0644 (NM_020660), CRHR2 (NM_001883), Glutamate receptor metabotropic 7 (NM_000844), Carbonic anhydrase IV, (NM_900717), HOXD12 (NM_021193), POU4F3 (NM_002700), Procadherin gamma subfamily B5 (NM_018925), EDG8 (NM_030760) and C20 orf55 (NM_031424). Each promoter region was amplified using nested primers (sequences available upon request).