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Supplemental Material to:

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Comparison of epigenetic profiles of human oral epithelial cells from HIV positive (on HAART) and HIV negative subjects

Epigenetics 2013; 8(7)
http://dx.doi.org/10.4161/epi.25028

http://www.landesbioscience.com/journals/epigenetics/article/25028/

Supplementary information:

Table S1: Clinical data for HIV+ (on HAART) samples used in this study

Sample numbers	***CD4 cell (cells/mL)***	***Viral Load (virus/ml)#***	***HAART Regime*****	***Used in Figures***
1	1226	U	Aba/Ten/Efa	**1A; 2;S1**
2	622	U	Ten/Ata/Rit/Aba	**1A;2;4**
3	454	U	Nor/Lex/Tru	**1A;2;4**
4	1170	48	Epz/Ten/Ata/Rit	**1B;4; S1**
5	543	48	Tru/Rit/Ata	**1B; 2; S1**
6	264	48	Rit/Ata	**1B; 2; S1**
7	374	48	Nor/Pre/Sus/Vir	**1B; 2,4; S1**
8	730	48	Atr	**1B; 2; S1**
9	525	48	Epi/Sel/Ise	**1B; 2; S1**
10	361	U	Pre/Tru/Int	**4; S1**
11	480	U	Vir/Ret/Epi	**2;4; S1**
12	834	U	Atr	**4**

***Aba**: Abacavir; **Ata**: Atazanavir; **Atr**: Atripla; **Efa**:Efavirenz; **Epi**: Epivir: **Epz**: Epzicom; **Int**: Intellence; **Ise**: Isentress; **Lex**: Lexiva; **Nor**: Norvir; **Pre**: Prezista; **Ret**: Retrovir; **Rit**: Ritonavir; **Sel**: Selzentry; **Sus**: Sustiva; **Ten**: Tenofovir; **Tru**: Truvada; **Vir**: Viread;
**U= Undetectable

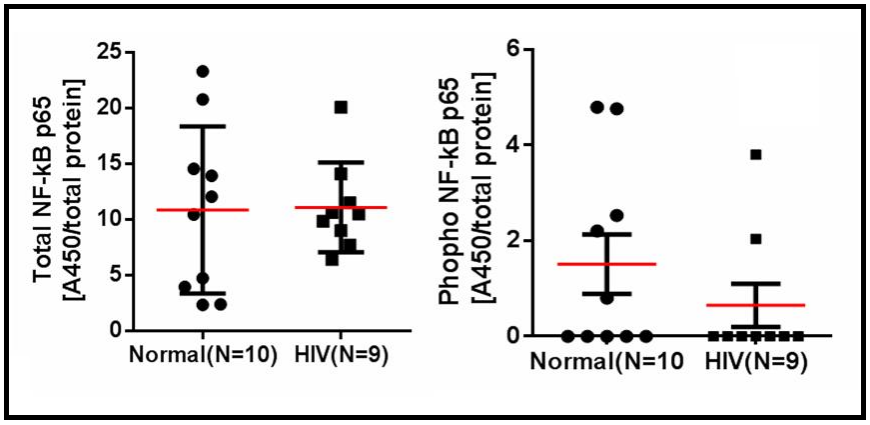

Figure S1: Comparison of endogenous levels of total and phosphor NF-κB in the cell lysates of normal and HIV+ (O/H) subjects. The red bar is the mean values. The red bar is the mean values [*= $p<0.05$, Mann-Whitney t test]. Total and phospho-p65 NF-κB in the cell lysates of were determined by PathScan ELISA (Cell Signaling, Danvers, MA)

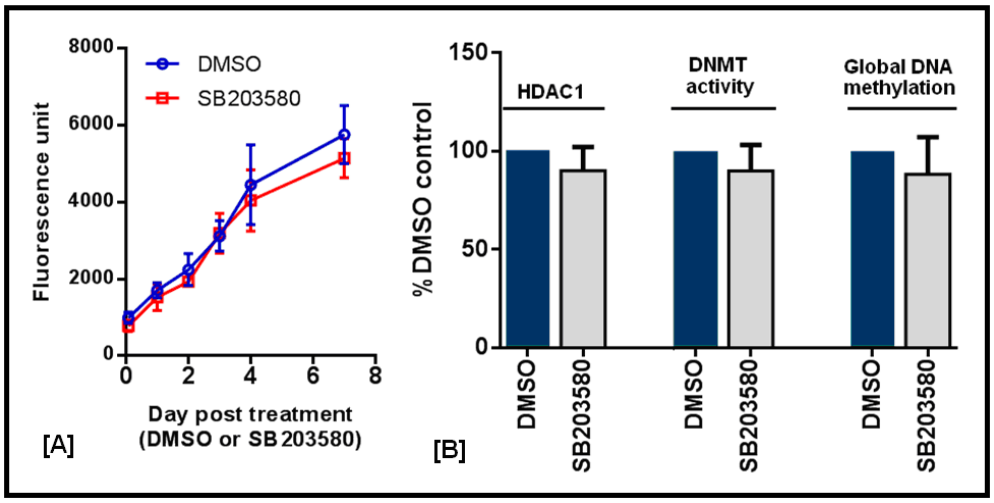

Figure S2: **[A]**. POECs from three healthy individuals were mixed and seeded onto 96 well plates. After 24 hrs the cells were pretreated with either SB SB203580 (10μM) or DMSO (5μl/ml) for 2hrs and cell growth was measured using PrestoBlue® Reagent for 7 days. Results are the mean [±SD] of quadruple wells. **[B]** POECs from healthy subjects were pretreated with either SB SB203580 (10μM) or DMSO (5μl/ml) for 2hrs and then allowed to grow for an additional 24 hrs. The nuclear extracts and genomic DNA were isolated and the levels of HDAC1 and DNMT activity in the nuclear extracts were measured. Global DNA methylation was determined as the percentage of 5-mC in total DNA. The results of HDAC1 levels, DNMT activity and global DNA methylation in SB SB203580 treated cells were expressed as %DMSO control cells. Results are the mean (± SD) of triplicate experiments