Supplemental Figure Legends:

**Supplemental Figure 1:** Methylation analysis of CpG sites located close to the *hsa-miR-181c* in LCLs from healthy donors and FA patients. a) MSP analysis of the methylated and unmethylated sequences of *hsa-miR-181c*. b) Pyrosequencing analysis of 4 CpG dinucleotides directly located in the genomic sequence of *hsa-miR-181c*. Analysis was conducted in LCLs from two healthy donors (HD 1 and HD 2) and two FA-A patients (FA-88 and FA-56).

**Supplemental Figure 2:** Analysis of TNFα expression in a FA-C LCL transfected with a Pre-miR control and Pre-miR-181c. As previously described in Figure 2, TNFα expression was measured in a FA-C LCL transfected either with a Pre-miR control (white bar) or Pre-miR-181c (black bar).

**Supplemental Figure 3:** Representative analysis of TNFα expression in PMA-activated BM cells from a FA patient (FA-467). Samples were transduced with a control lentiviral vector expressing EGFP (EGFP LV; gray histogram) or with a vector expressing both the PremiR-181c and EGFP (Pre-miR-181c-EGFP LV; black line in the histogram). Histograms represent TNFα expression in EGFP+ cells after activation with PMA.
Suppl. 1

(a) LCLs

- MSP-methylated
- MSP-unmethylated

(b) Bar graph showing % hsa-miR-181c methylation levels for CpG1, CpG2, CpG3, and CpG4 across different samples:
  - HD 1
  - HD 2
  - FA-88
  - FA-56
