Supplementary Table 1. Eighteen miRNAs whose expression levels are correlated with iGrowth in both CEU and YRI samples

miRNA	iGrowth raw p values	
	CEU	*YRI*
hsa-let-7d	0.02833046	0.1196481
hsa-miR-148b	0.0029303	0.00465769
hsa-miR-185*	0.0068943	0.03976238
hsa-miR-18a	0.00920889	1.53E-06
hsa-miR-18b	0.03720755	2.48E-06
hsa-miR-193b	0.02716574	0.02180195
hsa-miR-196a*	0.00478224	0.03530713
hsa-miR-210	0.0004309	1.41E-06
hsa-miR-331-3p	0.04736953	0.12969614
hsa-miR-34a	0.00800108	0.08214981
hsa-miR-365	0.01005646	0.02635361
hsa-miR-518a-5p/hsa-miR-527	0.04660004	0.00041619
hsa-miR-600	0.00182647	0.01054308
hsa-miR-765	0.03224653	4.72E-05
hsa-miR-768-3p	0.03623567	0.00058002
hsa-miR-768-5p	0.00244068	6.51E-06
hsa-miR-939	0.03461726	0.02167831
miRPlus_42521	0.04934229	0.03895866

In YRI samples, all identified miRNAs are correlated with iGrowth at FDR<0.05; while in CEU samples, raw p<0.05 was used for data filtering.