

**Supplementary Table 2. GO analysis on targets of iGrowth associated miRNA in both CEU and YRI samples**

<b>Category</b>	<b>Term</b>	<b>PValue</b>
GOTERM_BP_ALL	immune system process	5.42E-06
GOTERM_BP_ALL	response to oxygen levels	7.47E-05
GOTERM_BP_ALL	regulation of immune system process	1.20E-04
GOTERM_BP_ALL	immune response	5.20E-04
GOTERM_BP_ALL	regulation of lymphocyte activation	5.36E-04
GOTERM_BP_ALL	negative regulation of biological process	5.57E-04
GOTERM_BP_ALL	positive regulation of biological process	0.001138732
GOTERM_BP_ALL	regulation of leukocyte activation	0.001216061
GOTERM_BP_ALL	response to hypoxia	0.001224492
GOTERM_BP_ALL	positive regulation of immune system process	0.001342152
GOTERM_BP_ALL	cellular localization	0.001357963
GOTERM_BP_ALL	response to chemical stimulus	0.001567713
GOTERM_BP_ALL	regulation of cell activation	0.001753154
GOTERM_BP_ALL	response to stimulus	0.002188004
GOTERM_BP_ALL	regulation of T cell activation	0.002426228
GOTERM_BP_ALL	regulation of molecular function	0.002514211
GOTERM_BP_ALL	protein localization	0.002905823
GOTERM_BP_ALL	regulation of cell proliferation	0.002929773
GOTERM_BP_ALL	regulation of cell growth	0.003511074
GOTERM_BP_ALL	negative regulation of cellular process	0.003523066
GOTERM_BP_ALL	establishment of localization in cell	0.003806643
GOTERM_BP_ALL	cellular process	0.004012806
GOTERM_BP_ALL	protein transport	0.004162102
GOTERM_BP_ALL	negative regulation of catalytic activity	0.004309638
GOTERM_BP_ALL	negative regulation of cellular metabolic process	0.004532435
GOTERM_BP_ALL	establishment of protein localization	0.004632976
GOTERM_BP_ALL	proteasomal protein catabolic process	0.005323438
GOTERM_BP_ALL	proteasomal ubiquitin-dependent protein catabolic process	0.005323438
GOTERM_BP_ALL	negative regulation of metabolic process	0.005462267
GOTERM_BP_ALL	negative regulation of macromolecule metabolic process	0.005628749
GOTERM_BP_ALL	negative regulation of gene expression	0.005931185
GOTERM_BP_ALL	negative regulation of molecular function	0.006453741
GOTERM_BP_ALL	regulation of alpha-beta T cell differentiation	0.006752721
GOTERM_BP_ALL	regulation of catalytic activity	0.006986991
GOTERM_BP_ALL	response to extracellular stimulus	0.007919127
GOTERM_BP_ALL	regulation of caspase activity	0.007930912
GOTERM_BP_ALL	positive regulation of macromolecule metabolic process	0.008108493
GOTERM_BP_ALL	regulation of B cell activation	0.008222264
GOTERM_BP_ALL	cellular amino acid biosynthetic process	0.008222264
GOTERM_BP_ALL	regulation of protein kinase activity	0.008297546
GOTERM_BP_ALL	regulation of endopeptidase activity	0.009248302
GOTERM_BP_ALL	macromolecule localization	0.010015986
GOTERM_BP_ALL	positive regulation of protein ubiquitination	0.010205928

GOTERM_BP_ALL	regulation of kinase activity	0.010649083
GOTERM_BP_ALL	system development	0.010724083
GOTERM_BP_ALL	negative regulation of protein modification process	0.011037173
GOTERM_BP_ALL	carboxylic acid biosynthetic process	0.011082968
GOTERM_BP_ALL	organic acid biosynthetic process	0.011082968
GOTERM_BP_ALL	regulation of peptidase activity	0.011229454
GOTERM_BP_ALL	negative regulation of cell proliferation	0.011624372
GOTERM_BP_ALL	hemopoiesis	0.012134482
GOTERM_BP_ALL	serine family amino acid biosynthetic process	0.012227795
GOTERM_BP_ALL	positive regulation of cellular process	0.012546559
GOTERM_BP_ALL	response to UV	0.013596973
GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	0.014149512
GOTERM_BP_ALL	regulation of transferase activity	0.014375562
GOTERM_BP_ALL	antigen receptor-mediated signaling pathway	0.014619119
GOTERM_BP_ALL	regulation of phosphorylation	0.015137765
GOTERM_BP_ALL	intracellular transport	0.015183409
GOTERM_BP_ALL	myeloid cell differentiation	0.015358871
GOTERM_BP_ALL	response to endoplasmic reticulum stress	0.01585234
GOTERM_BP_ALL	regulation of programmed cell death	0.016442017
GOTERM_BP_ALL	protein homooligomerization	0.016702558
GOTERM_BP_ALL	regulation of lymphocyte differentiation	0.016960008
GOTERM_BP_ALL	positive regulation of vasoconstriction	0.016988597
GOTERM_BP_ALL	positive regulation of coagulation	0.016988597
GOTERM_BP_ALL	leukocyte differentiation	0.017061078
GOTERM_BP_ALL	regulation of cell death	0.01706239
GOTERM_BP_ALL	cellular response to extracellular stimulus	0.017874774
GOTERM_BP_ALL	positive regulation of metabolic process	0.017910354
GOTERM_BP_ALL	regulation of protein modification process	0.017991242
GOTERM_BP_ALL	regulation of alpha-beta T cell activation	0.018489367
GOTERM_BP_ALL	regulation of growth	0.018718333
GOTERM_BP_ALL	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	0.018819708
GOTERM_BP_ALL	negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	0.018819708
GOTERM_BP_ALL	cortical cytoskeleton organization	0.019617866
GOTERM_BP_ALL	anatomical structure development	0.019872646
GOTERM_BP_ALL	positive regulation of cellular metabolic process	0.020171528
GOTERM_BP_ALL	organ development	0.020229469
GOTERM_BP_ALL	regulation of protein ubiquitination	0.020397465
GOTERM_BP_ALL	response to stress	0.020624116
GOTERM_BP_ALL	regulation of phosphate metabolic process	0.020660391
GOTERM_BP_ALL	regulation of phosphorus metabolic process	0.020660391
GOTERM_BP_ALL	negative regulation of ligase activity	0.020801086
GOTERM_BP_ALL	negative regulation of ubiquitin-protein ligase activity	0.020801086
GOTERM_BP_ALL	hemopoietic or lymphoid organ development	0.021432588
GOTERM_BP_ALL	regulation of multicellular organismal process	0.0214391
GOTERM_BP_ALL	positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	0.021837997

GOTERM_BP_ALL	positive regulation of molecular function	0.022005495
GOTERM_BP_ALL	response to pH	0.022405414
GOTERM_BP_ALL	cell cycle arrest	0.022852076
GOTERM_BP_ALL	immune response-activating cell surface receptor signaling pathway	0.022873678
GOTERM_BP_ALL	negative regulation of cellular protein metabolic process	0.023267352
GOTERM_BP_ALL	positive regulation of ubiquitin-protein ligase activity	0.024005319
GOTERM_BP_ALL	regulation of ubiquitin-protein ligase activity during mitotic cell cycle	0.025136107
GOTERM_BP_ALL	multicellular organismal development	0.027257334
GOTERM_BP_ALL	regulation of apoptosis	0.027403533
GOTERM_BP_ALL	positive regulation of ligase activity	0.027492773
GOTERM_BP_ALL	immune response-regulating cell surface receptor signaling pathway	0.02777343
GOTERM_BP_ALL	negative regulation of protein metabolic process	0.027897387
GOTERM_BP_ALL	antigen processing and presentation of peptide antigen via MHC class I	0.028433265
GOTERM_BP_ALL	negative regulation of protein ubiquitination	0.028718942
GOTERM_BP_ALL	negative regulation of transcription	0.028941206
GOTERM_BP_ALL	response to external stimulus	0.029346351
GOTERM_BP_ALL	induction of apoptosis	0.029368234
GOTERM_BP_ALL	induction of programmed cell death	0.029966795
GOTERM_BP_ALL	sphingolipid metabolic process	0.029977172
GOTERM_BP_ALL	immune system development	0.030135354
GOTERM_BP_ALL	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.030699914
GOTERM_BP_ALL	cysteine biosynthetic process	0.031067968
GOTERM_BP_ALL	nuclear fragmentation during apoptosis	0.031067968
GOTERM_BP_ALL	hydrogen sulfide metabolic process	0.031067968
GOTERM_BP_ALL	hydrogen sulfide biosynthetic process	0.031067968
GOTERM_BP_ALL	induction of apoptosis by extracellular signals	0.031334576
GOTERM_BP_ALL	hexose metabolic process	0.031340337
GOTERM_BP_ALL	negative regulation of caspase activity	0.03166286
GOTERM_BP_ALL	cellular response to stress	0.032420957
GOTERM_BP_ALL	cellular response to stimulus	0.032770008
GOTERM_BP_ALL	regulation of ubiquitin-protein ligase activity	0.033945252
GOTERM_BP_ALL	negative regulation of nitrogen compound metabolic process	0.033985071
GOTERM_BP_ALL	response to organic substance	0.034361393
GOTERM_BP_ALL	regulation of tissue remodeling	0.035029312
GOTERM_BP_ALL	response to nutrient levels	0.035526271
GOTERM_BP_ALL	developmental process	0.0362001
GOTERM_BP_ALL	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.036398398
GOTERM_BP_ALL	macromolecule catabolic process	0.037749702
GOTERM_BP_ALL	alcohol metabolic process	0.037835313
GOTERM_BP_ALL	amine biosynthetic process	0.038205004
GOTERM_BP_ALL	regulation of ligase activity	0.038205004
GOTERM_BP_ALL	membrane lipid metabolic process	0.038205004
GOTERM_BP_ALL	positive regulation of apoptosis	0.038438035
GOTERM_BP_ALL	positive regulation of alpha-beta T cell differentiation	0.038527585

GOTERM_BP_ALL	carbohydrate metabolic process	0.039454337
GOTERM_BP_ALL	positive regulation of gene expression	0.040003278
GOTERM_BP_ALL	positive regulation of RNA metabolic process	0.040132115
GOTERM_BP_ALL	positive regulation of programmed cell death	0.040138723
GOTERM_BP_ALL	positive regulation of cell death	0.040777725
GOTERM_BP_ALL	regulation of lymphocyte proliferation	0.04120748
GOTERM_BP_ALL	antigen processing and presentation	0.04120748
GOTERM_BP_ALL	cellular carbohydrate metabolic process	0.041618989
GOTERM_BP_ALL	negative regulation of peptidase activity	0.042152766
GOTERM_BP_ALL	regulation of leukocyte proliferation	0.042757558
GOTERM_BP_ALL	regulation of mononuclear cell proliferation	0.042757558
GOTERM_BP_ALL	regulation of T cell differentiation	0.04552474
GOTERM_BP_ALL	lung alveolus development	0.045900064
GOTERM_BP_ALL	regulation of cell differentiation	0.046153779
GOTERM_BP_ALL	positive regulation of nitrogen compound metabolic process	0.046217463
GOTERM_BP_ALL	homocysteine metabolic process	0.046239711
GOTERM_BP_ALL	cellular cation homeostasis	0.046865071
GOTERM_BP_ALL	immune response-activating signal transduction	0.047773167
GOTERM_BP_ALL	T cell activation	0.04802654
GOTERM_CC_ALL	cytoplasmic part	1.60E-07
GOTERM_CC_ALL	endoplasmic reticulum	2.63E-05
GOTERM_CC_ALL	endoplasmic reticulum part	8.99E-05
GOTERM_CC_ALL	cytoplasm	2.73E-04
GOTERM_CC_ALL	intracellular membrane-bounded organelle	2.81E-04
GOTERM_CC_ALL	membrane-bounded organelle	2.96E-04
GOTERM_CC_ALL	membrane part	3.51E-04
GOTERM_CC_ALL	lytic vacuole	4.10E-04
GOTERM_CC_ALL	lysosome	4.10E-04
GOTERM_CC_ALL	integral to membrane	0.001159476
GOTERM_CC_ALL	endoplasmic reticulum lumen	0.001398051
GOTERM_CC_ALL	vacuole	0.001750685
GOTERM_CC_ALL	membrane	0.001778966
GOTERM_CC_ALL	protein complex	0.003599049
GOTERM_CC_ALL	intracellular organelle	0.003696815
GOTERM_CC_ALL	cytosol	0.003801611
GOTERM_CC_ALL	organelle	0.003966721
GOTERM_CC_ALL	intrinsic to membrane	0.004070481
GOTERM_CC_ALL	organelle lumen	0.004111415
GOTERM_CC_ALL	membrane-enclosed lumen	0.005797016
GOTERM_CC_ALL	MHC class I peptide loading complex	0.007794194
GOTERM_CC_ALL	intracellular organelle lumen	0.007898877
GOTERM_CC_ALL	intracellular part	0.008132916
GOTERM_CC_ALL	endoplasmic reticulum membrane	0.008523363
GOTERM_CC_ALL	nuclear envelope-endoplasmic reticulum network	0.012175058
GOTERM_CC_ALL	cell part	0.013320629
GOTERM_CC_ALL	cell	0.013443724

GOTERM_CC_ALL	proteasome complex	0.014046142
GOTERM_CC_ALL	plasma membrane part	0.01599541
GOTERM_CC_ALL	macromolecular complex	0.017563509
GOTERM_CC_ALL	plasma membrane	0.019757215
GOTERM_CC_ALL	integral to plasma membrane	0.024686834
GOTERM_CC_ALL	cell fraction	0.025574162
GOTERM_CC_ALL	intracellular	0.027360263
GOTERM_CC_ALL	transcription elongation factor complex	0.030270781
GOTERM_CC_ALL	intrinsic to plasma membrane	0.031601698
GOTERM_CC_ALL	insoluble fraction	0.032689935
GOTERM_CC_ALL	mitochondrion	0.044119777
GOTERM_CC_ALL	Golgi apparatus	0.045452489
GOTERM_MF_ALL	protein binding	0.002116542
GOTERM_MF_ALL	calcium ion binding	0.008269431
GOTERM_MF_ALL	lyase activity	0.009079115
GOTERM_MF_ALL	ATPase activity	0.014946622
GOTERM_MF_ALL	purine ribonucleotide binding	0.015298056
GOTERM_MF_ALL	ribonucleotide binding	0.015298056
GOTERM_MF_ALL	nucleotide binding	0.016959136
GOTERM_MF_ALL	nucleoside-triphosphatase activity	0.018085786
GOTERM_MF_ALL	ATP binding	0.019597188
GOTERM_MF_ALL	adenyl ribonucleotide binding	0.023316895
GOTERM_MF_ALL	catalytic activity	0.025609681
GOTERM_MF_ALL	pyrophosphatase activity	0.025789427
GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	0.026772356
GOTERM_MF_ALL	hydrolase activity, acting on acid anhydrides	0.028048324
GOTERM_MF_ALL	purine nucleotide binding	0.028976348
GOTERM_MF_ALL	hydrolase activity	0.033158964
GOTERM_MF_ALL	protein domain specific binding	0.033334378
GOTERM_MF_ALL	purine nucleoside binding	0.034467633
GOTERM_MF_ALL	nucleoside binding	0.037486804
GOTERM_MF_ALL	hydrolase activity, hydrolyzing N-glycosyl compounds	0.037629334
GOTERM_MF_ALL	peptide binding	0.038452539
GOTERM_MF_ALL	adenyl nucleotide binding	0.044063242