

Supplementary Table 1: Targeted genes and their assay ID in TaqMan assays:

Human TaqMan Assays	
Gene name	TaqMan assay ID
WNT1	Hs01011247_m1
WNT2	Hs00608224_m1
WNT2B	Hs00921614_m1
WNT3	Hs00902257_m1
WNT3A	Hs00263977_m1
WNT4	Hs01573504_m1
WNT5A	Hs00998537_m1
WNT5B	Hs01086864_m1
WNT6	Hs00362452_m1
WNT7A	Hs00171699_m1
WNT7B	Hs00536497_m1
WNT8A	Hs00230534_m1
WNT8B	Hs00610126_m1
WNT9A	Hs00243321_m1
WNT9B	Hs00287409_m1
WNT10A	Hs00228741_m1
WNT10B	Hs00559664_m1
WNT11	Hs00182986_m1
WNT16	Hs00365138_m1
MYC	Hs00153408_m1
GAPDH	Hs02758991_g1

Mouse TaqMan Assays	
Gene name	TaqMan assay ID
APC	Mm00545872_m1
AXIN1	Mm01299060_m1
AXIN2	Mm00443610_m1
β -Catenin	Mm00458117_m1
BMP4	Mm00432087_m1
BRCA1	Mm00515386_m1
CCND1	Mm00432359_m1
CCND2	Mm00438070_m1
CCND3	Mm01612362_m1
CDC42	Mm01194005_g1
CDK4	Mm00726334_s1
CSNK1G2	Mm00506098_m1
DKK1	Mm00438422_m1
DKK2	Mm01322146_m1
DKK4	Mm00461141_m1
DVL1	Mm00438592_m1

DVL2	Mm00432899_m1
DVL3	Mm00432914_m1
EFNB2	Mm00438670_m1
Elf2s3y	Mm01210630_m1
FGF1	Mm00438906_m1
FGF2	Mm00433287_m1
FGF4	Mm00438917_m1
FGF7	Mm00433291_m1
FGF8	Mm00438922_m1
FGF9	Mm00442795_m1
FGFR1	Mm00438930_m1
FGFR2	Mm01269930_m1
FGFR3	Mm00433294_m1
FGFR4	Mm01341852_m1
FOXA2	Mm01976556_s1
FRZB (SFRP3)	Mm00441378_m1
FZD1	Mm00445405_s1
FZD2	Mm02524776_m1
FZD3	Mm00445423_m1
FZD4	Mm00433382_m1
FZD5	Mm00445623_s1
FZD6	Mm00433387_m1
FZD7	Mm00433409_m1
FZD8	Mm01234717_s1
FZD9	Mm01206511_s1
FZD10	Mm00558396_s1
GATA6	Mm00802636_m1
GRB2	Mm03023989_g1
GSK3 β	Mm00444911_m1
IL1A	Mm00439620_m1
IL1B	Mm00434228_m1
IL6	Mm00446190_m1
KCNMA1	Mm01268569_m1
KDR	Mm01222421_m1
KREMEN1	Mm00459616_m1
KREMEN2	Mm01309205_m1
HGF	Mm01135193_m1
LEF1	Mm00550265_m1
LRP5	Mm01227476_m1
LRP6	Mm00999795_m1
MYCBP	Mm01192721_m1
MYCL	Mm03053598_s1
MYCN	Mm00476449_m1

MST1R	Mm00436382_m1
NMI	Mm00803857_m1
PAK3	Mm01332263_m1
PECAM1	Mm01242576_m1
PLCG1	Mm01247293_m1
PLK3C2G	Mm00440781_m1
RARA	Mm01296312_m1
RARB	Mm01319677_m1
RARRES1	Mm01220691_m1
RARRES2	Mm00503579_m1
RLF	Mm01181427_m1
RSPO1	Mm00507077_m1
RXRB	Mm00441193_m1
SFRP1	Mm00489161_m1
SFRP2	Mm01213947_m1
SFRP4	Mm00840104_m1
SFRP5	Mm01194236_m1
SOSTDC1(WISE)	Mm03024258_s1
SRC	Mm00436785_m1
TCF7	Mm00493445_m1
TCF7L1	Mm01188711_m1
TCF7L2	Mm00501505_m1
TGFA	Mm00446232_m1
TGFB1	Mm00441724_m1
TGFB2	Mm00436955_m1
TGFB3	Mm00436960_m1
TGIF1	Mm01227699_m1
THBS1	Mm00449032_g1
TNF	Mm00443258_m1
VEGFA	Mm00437304_m1
WASF2	Mm00463191_m1
WIF1	Mm00442355_m1
YAP1	Mm01143263_m1
ID2	Mm00711781_m1
BIRC5	Mm00599749_m1
CTGF	Mm01192933_g1
SMAD7	Mm00484742_m1
SMAD2	Mm00487530_m1
SMAD3	Mm01170760_m1
SMAD4	Mm03023996_m1
LATS1	Mm01191886_m1
LATS2	Mm01321138_m1
GAPDH	Mm03302249_g1

Supplementary Table 2: miRNAs expressed at 2-fold or higher in term hAECs compared to preterm hAECs

Gene name	Fold change (Term Vs Preterm hAECs)
hsa-let-7f	73.9252724
hsa-miR-624	11.9606178
hsa-miR-501-5p	11.5893119
hsa-miR-1267	9.40703942
hsa-miR-10a	9.33998835
hsa-miR-30a-5p	9.23908353
hsa-miR-769-3p	6.09007502
hsa-miR-765	5.9368267
hsa-miR-616	5.93591322
hsa-miR-622	5.80398986
hsa-miR-614	5.75760573
hsa-miR-936	5.72195043
hsa-miR-302d	4.83553578
hsa-miR-335	4.73486978
hsa-miR-1260	4.67596701
hsa-miR-320B	4.64558651
hsa-miR-1290	4.63298416
hsa-miR-100	4.58483479
hsa-miR-1291	4.5791212
hsa-miR-135b	4.56791799
hsa-miR-205	4.56299398
hsa-miR-146b-5p	4.52565544
hsa-miR-654-5p	3.10642021
hsa-miR-345	3.03995507
hsa-miR-362-3p	3.01261017
hsa-miR-34a	3.01110705
hsa-miR-590-3P	2.98324197
hsa-miR-604	2.97292486
hsa-miR-496	2.96894013
hsa-miR-500	2.96631334
hsa-miR-515-3p	2.96351426
hsa-miR-483-5p	2.96316713
hsa-miR-638	2.96307676
hsa-miR-491-5p	2.96063779
hsa-miR-886-5p	2.95575768
hsa-miR-548E	2.95336568
hsa-miR-653	2.95306682
hsa-miR-886-3p	2.95226863
hsa-miR-580	2.94765361
hsa-miR-875-5p	2.94732264

hsa-miR-548L	2.94185471
hsa-miR-652	2.93768967
hsa-miR-520g	2.9331686
hsa-miR-942	2.93215018
hsa-miR-572	2.93123168
hsa-miR-603	2.93006161
hsa-miR-601	2.92240879
hsa-miR-483-3p	2.91913716
hsa-miR-550	2.91420628
hsa-miR-660	2.91405276
hsa-miR-532-3p	2.91197102
hsa-miR-564	2.89349069
hsa-miR-9	2.88646754
hsa-miR-625	2.86010874
hsa-miR-429	2.85665141
hsa-miR-1244	2.4558335
hsa-miR-1274B	2.45036175
hsa-miR-24	2.41474149
hsa-miR-126	2.40232568
hsa-miR-1248	2.39443579
hsa-miR-21	2.39229574
hsa-miR-27b	2.38572168
hsa-miR-125b	2.38510826
hsa-miR-200a	2.38357455
hsa-miR-339-3p	2.36985986
hsa-miR-16	2.36078678
hsa-miR-190b	2.35740682
hsa-miR-182	2.35422425
hsa-miR-1282	2.34712512
hsa-miR-183	2.34537522
hsa-miR-29a	2.34277881
hsa-miR-148b	2.33849404
hsa-miR-302a	2.3347608
hsa-miR-210	2.33292956
hsa-miR-136	2.33038569
hsa-miR-15a	2.31586435
hsa-miR-26a	2.31559789
hsa-let-7a	2.3138683
hsa-miR-24-2	2.31292863
hsa-miR-135b	2.31255512
hsa-miR-184	2.3124926
hsa-miR-151-3p	2.31168328
hsa-miR-1303	2.30981251

hsa-miR-125a-5p	2.30917378
hsa-miR-30d	2.30753055
hsa-miR-33a	2.30252808
hsa-miR-21	2.29932237
hsa-miR-1285	2.29742498
hsa-miR-126	2.29467963
hsa-miR-1243	2.29330581
hsa-miR-203	2.29226645
hsa-let-7b	2.29098935
hsa-miR-152	2.28618595
hsa-miR-23a	2.27398344
hsa-miR-193b	2.26861493
hsa-miR-148b	2.24852161
hsa-miR-206	2.24723773
hsa-miR-338-5P	2.15202934
hsa-miR-193a-5p	2.0961773

Supplementary Table 3: Pathways union of 22 most upregulated miRNAs in term hAECs compared to preterm hAECs

KEGG pathway	p-value	#genes	#miRNAs
Hippo signaling pathway	1.87e-10	97	11
Proteoglycans in cancer	2.22e-16	128	10
Lysine degradation	3.22e-10	27	8
Adherens junction	2.43e-09	49	8
Glioma	1.2e-10	42	7
Transcriptional misregulation in cancer	2.92e-06	68	7
Colorectal cancer	4.26e-07	42	5
Central carbon metabolism in cancer	0.000551468	35	5
Oocyte meiosis	0.01050969	52	5
Fatty acid biosynthesis	0	4	4
Pathways in cancer	0	170	4
Fatty acid metabolism	2.46e-14	12	4
ECM-receptor interaction	2.25e-07	41	4
Viral carcinogenesis	1.69e-05	76	4
Pancreatic cancer	3.84e-05	39	4
Cell cycle	0.001057385	56	4
p53 signaling pathway	0.008877096	31	4
TGF-beta signaling pathway	0.009077201	23	4
Bladder cancer	0.0303866	27	4
Chronic myeloid leukemia	8.52e-07	36	3
Steroid biosynthesis	1.08e-06	13	3
MicroRNAs in cancer	2.61e-05	31	3
Signaling pathways regulating pluripotency of stem cells	0.000101375	56	3
Hepatitis B	0.000116071	65	3
Non-small cell lung cancer	0.00106916	19	3
Wnt signaling pathway	0.001600731	34	3
Mucin type O-Glycan biosynthesis	0.01146427	15	3
Prostate cancer	0.01627984	41	3
Endometrial cancer	0.01806197	24	3
Protein processing in endoplasmic reticulum	0.03844125	64	3

Melanoma	0.05479326	29	3
Thyroid hormone signaling pathway	0.07510067	43	3
MAPK signaling pathway	0.2362782	55	3
Thyroid cancer	0.2421421	17	3
RNA transport	0.2476021	47	3
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.2902186	14	3
Epstein-Barr virus infection	0.8280952	69	3
Small cell lung cancer	0.001958015	39	2
ErbB signaling pathway	0.2967561	20	2
HIF-1 signaling pathway	0.4232772	20	2
Estrogen signaling pathway	0.5800298	15	2
Prolactin signaling pathway	0.7940552	12	2
Base excision repair	0.9166133	9	2
Ribosome	0.9359495	27	2
Circadian rhythm	0.9375584	12	2
PI3K-Akt signaling pathway	0.9446857	81	2
Endocytosis	0.955366	42	2
Parkinson's disease	0.965306	11	2
Pyrimidine metabolism	0.9999214	11	2
Acute myeloid leukemia	0.02043816	16	1
Renal cell carcinoma	0.03886262	13	1
FoxO signaling pathway	0.2141295	32	1
HTLV-I infection	0.2418832	21	1
Ubiquitin mediated proteolysis	0.2485583	42	1
Biotin metabolism	0.6066103	1	1
Basal cell carcinoma	0.7988809	15	1
Ras signaling pathway	0.8403023	20	1
Bacterial invasion of epithelial cells	0.8754792	15	1
Focal adhesion	0.9008744	18	1
Spliceosome	0.9298831	14	1
TNF signaling pathway	0.9391868	10	1
Shigellosis	0.9656469	7	1
Leukocyte transendothelial migration	0.9689753	5	1
Apoptosis	0.9782784	17	1

Toxoplasmosis	0.9879972	13	1
Neurotrophin signaling pathway	0.9880193	12	1
mTOR signaling pathway	0.9896191	8	1
mRNA surveillance pathway	0.9918225	23	1
Nucleotide excision repair	0.9934617	8	1
Sphingolipid signaling pathway	0.9941056	11	1
VEGF signaling pathway	0.9951137	9	1
Gap junction	0.9965675	1	1
NF-kappa B signaling pathway	0.9973862	7	1
Melanogenesis	0.9987607	13	1
Glycosphingolipid biosynthesis - lacto and neolacto series	0.9989954	2	1
Cytokine-cytokine receptor interaction	0.9995343	61	1
Choline metabolism in cancer	0.9995538	11	1
Chagas disease (American trypanosomiasis)	0.9998149	11	1
Proteasome	0.9998363	6	1
Valine, leucine and isoleucine biosynthesis	0.9999118	1	1
Huntington's disease	0.9999144	28	1
Fc epsilon RI signaling pathway	0.9999492	11	1
Oxidative phosphorylation	0.9999511	11	1
D-Glutamine and D-glutamate metabolism	0.9999547	1	1
Thyroid hormone synthesis	0.9999614	11	1
Cell adhesion molecules (CAMs)	0.9999652	29	1
2-Oxocarboxylic acid metabolism	0.9999719	2	1
Carbon metabolism	0.9999867	9	1
Amoebiasis	0.9999911	11	1
DNA replication	0.9999984	5	1
Biosynthesis of amino acids	0.9999985	8	1
One carbon pool by folate	0.9999993	1	1
Purine metabolism	0.9999996	15	1
Other types of O-glycan biosynthesis	0.9999998	2	1
Toll-like receptor signaling pathway	0.9999999	10	1
Primary bile acid biosynthesis	1	6	1

Sulfur metabolism	1	2	1
Homologous recombination	1	4	1
Salivary secretion	1	27	1

Supplementary Table 4: miRNAs expressed at 2-fold decrease or lower in term hAECs compared to preterm hAECs

Gene name	Fold change (Term Vs Preterm hAECs)
hsa-miR-520c-3p	0.004527985
hsa-miR-519b-3p	0.018013443
hsa-miR-520h	0.03558593
hsa-miR-520D-3P	0.035845622
hsa-miR-10b	0.140716436
hsa-miR-145	0.270838877
hsa-miR-668	0.2731444
hsa-miR-454	0.284359666
hsa-miR-409-3p	0.286356399
hsa-miR-29b-1	0.28661137
hsa-miR-770-5p	0.287529871
hsa-miR-34b	0.287689555
hsa-miR-27a	0.28903032
hsa-miR-370	0.356659671
hsa-miR-520e	0.359573349
hsa-miR-200b	0.361049863
hsa-miR-127-3p	0.362306602
hsa-miR-487b	0.364577643
hsa-miR-25	0.365880137

Supplementary Table 5: Pathways union of 2-fold decrease or lower expressed miRNAs in term hAECs compared to preterm hAECs

KEGG pathway	p-value	#genes	#miRNAs
Pathways in cancer	7.09736e-09	123	5
Adherens junction	7.230013e-09	34	5
Viral carcinogenesis	2.314077e-08	58	5
Hippo signaling pathway	9.020322e-06	55	5
Chronic myeloid leukemia	0.01043694	34	5
Fatty acid metabolism	3.321574e-05	10	4
Lysine degradation	0.0001861324	15	4
Glioma	0.0007934242	26	4
TGF-beta signaling pathway	0.00299193	30	4
p53 signaling pathway	0.0153499	30	4
Prostate cancer	0.04877802	37	4
Bacterial invasion of epithelial cells	0.07623696	36	4
Thyroid hormone signaling pathway	0.08919184	37	4
FoxO signaling pathway	0.1396272	45	4
MicroRNAs in cancer	0	47	3
Fatty acid elongation	2.221477e-05	3	3
Signaling pathways regulating pluripotency of stem cells	8.977921e-05	42	3
Focal adhesion	0.0009282172	66	3
Colorectal cancer	0.001894819	27	3
Transcriptional misregulation in cancer	0.003153647	31	3
Endometrial cancer	0.009056928	20	3
Hepatitis B	0.009636186	35	3
PI3K-Akt signaling pathway	0.1100134	89	3
Central carbon metabolism in cancer	0.2034327	18	3
Cell cycle	0.8333105	34	3
Fatty acid biosynthesis	0	2	2
Bladder cancer	0.008888864	14	2
Fatty acid degradation	0.1516373	6	2
Melanoma	0.1939439	16	2
Small cell lung cancer	0.2118684	29	2
Amoebiasis	0.252933	27	2

Wnt signaling pathway	0.3382355	27	2
Protein processing in endoplasmic reticulum	0.5435447	18	2
Non-small cell lung cancer	0.5459003	15	2
Pancreatic cancer	0.6407905	20	2
Renal cell carcinoma	0.800708	18	2
ErbB signaling pathway	0.8720876	22	2
Axon guidance	0.9803328	20	2
Endocytosis	0.1280316	21	1
Ubiquitin mediated proteolysis	0.366851	23	1
HTLV-I infection	0.6535317	36	1
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.7019688	12	1
Thyroid cancer	0.8192068	4	1
Cell adhesion molecules (CAMs)	0.8207323	1	1
HIF-1 signaling pathway	0.8268555	12	1
N-Glycan biosynthesis	0.8416644	1	1
Prolactin signaling pathway	0.8454987	15	1
Oocyte meiosis	0.8486408	17	1
AMPK signaling pathway	0.9244279	3	1
Neurotrophin signaling pathway	0.9315332	14	1
Glycosaminoglycan degradation	0.9651712	3	1
Rap1 signaling pathway	0.9888523	1	1
Pathogenic Escherichia coli infection	0.9919459	7	1
Inflammatory bowel disease (IBD)	0.9962719	7	1
Dorso-ventral axis formation	0.9977154	6	1
Ras signaling pathway	0.9978458	23	1
Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	0.9984241	1	1
Huntington's disease	0.9991098	7	1
Steroid biosynthesis	0.9992379	3	1
Mucin type O-Glycan biosynthesis	0.9995166	1	1
Dilated cardiomyopathy	0.9999237	13	1
Fc gamma R-mediated phagocytosis	0.999948	11	1
Pyrimidine metabolism	0.9999537	7	1
Other glycan degradation	0.9999543	1	1

Inositol phosphate metabolism	0.9999657	1	1
Hypertrophic cardiomyopathy (HCM)	0.9999665	12	1
Valine, leucine and isoleucine degradation	0.9999786	5	1
Leukocyte transendothelial migration	0.9999984	13	1
Other types of O-glycan biosynthesis	0.9999994	2	1
Glycosphingolipid biosynthesis - lacto and neolacto series	0.9999998	2	1
Sulfur metabolism	1	2	1