Supplementary Materials

Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity

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Supplementary Table S1. Summary of cell-type specific miRNA expression data used in MIGWAS.

Anatomical category	Cell names	No. highly and specifically expressed miRNAs	Library ID
bone	annulus pulposus cell	167	SRhi10004.TTAGGC.11248,SRhi10004.CTTGTA.11463
bone	bone cell	169	SRhi10006.CAGATC.11219,SRhi10003.CAGATC.11536,SRhi10010.GTTTCG.11697,SRhi10013.GGTAGC.11464
bone	chondrocyte	167	SRhi10011.TTAGGC.11261,SRhi10011.CTTGTA.11338,SRhi10012.GTGAAA.11410,SRhi10012.TTAGGC.11262,SRhi10012.CTTGTA.11339,SRhi10013.GTGAAA.11411
bone	fibroblast of periodontium	170	SRhi10007.ACAGTG.11238,SRhi10004.AGTTCC.11319,SRhi10003.GTTTCG.11395
bone	human chondrocyte de-differentiated sample	164	SRhi10011.TTAGGC.11261,SRhi10011.CTTGTA.11338,SRhi10012.GTGAAA.11410
bone	human chondrocyte re-differentiated sample	165	SRhi10012.TTAGGC.11262,SRhi10012.CTTGTA.11339,SRhi10013.GTGAAA.11411
bone	nucleus pulposus cell of intervertebral disc	195	SRhi10013.ATGTCA.11252,SRhi10014.CAGATC.11462
bone	osteoblast	168	SRhi10014.ATGTCA.11276,SRhi10003.CGTACG.11353,SRhi10015.CAGATC.11425,SRhi10015.ATGTCA.11277,SRhi10004.CGTACG.11354,SRhi10002.ACTTGA.11426
bone	trabecular meshwork cell	175	SRhi10008.GTCCGC.11532,SRhi10005.GGTAGC.11612
bone	vertebral mesenchymal stem cell	93	SRhi10006.CAGATC.11219
brain	astrocyte of the cerebellum	168	SRhi10005.TTAGGC.11500,SRhi10006.GTGAAA.11661
brain	astrocyte of the cerebral cortex	169	SRhi10006.TTAGGC.11235,SRhi10006.CTTGTA.11316,SRhi10007.GTGAAA.11392
brain	brain macroglial cell	168	SRhi10005.TTAGGC.11500,SRhi10006.GTGAAA.11661,SRhi10006.TTAGGC.11235,SRhi10006.CTTGTA.11316,SRhi10007.GTGAAA.11392
brain	central nervous system pericyte	176	SRhi10002.CCGTCC.11491,SRhi10004.ACTTGA.11652
brain	fibroblast of choroid plexus	146	SRhi10014.TGACCA.11492
brain	glial cell (sensu Vertebrata)	168	SRhi10005.TTAGGC.11500,SRhi10006.GTGAAA.11661,SRhi10006.TTAGGC.11235,SRhi10006.CTTGTA.11316,SRhi10007.GTGAAA.11392,SRhi10008.GATCAG.11498
brain	human diencephalon - adult sample	168	SRhi10006.ACTTGA.10160,SRhi10007.ACTTGA.10162
brain	human pineal gland - adult sample	162	SRhi10006.ACTTGA.10160
brain	human pituitary gland - adult sample	172	SRhi10007.ACTTGA.10162
brain	human spinal cord - adult sample	162	SRhi10003.GGCTAC.10159
brain	leptomeningeal cell	168	SRhi10011.GCCAAT.11493,SRhi10002.ATGTCA.11573
brain	neural cell	168	SRhi10005.TTAGGC.11500,SRhi10006.GTGAAA.11661,SRhi10006.TTAGGC.11235,SRhi10006.CTTGTA.11316,SRhi10007.GTGAAA.11392,SRhi10014.TGACCA.11492,SRhi10011.GCCAAT.11493,SRhi10002.ATGTCA.11573,SRhi10014.GTTTCG.11352,SRhi10012.CAGATC.11424,SRhi10002.CCGTCC.11491,SRhi10004.ACTTGA.11652,SRhi10015.CCGTCC.11215,SRhi10015.CGTACG.11528,SRhi10007.GATCAG.11608,SRhi10008.GATCAG.11498,SRhi10011.GTAGAG.11234,SRhi10009.GAGTGG.11315,SRhi10003.TAGCTT.11391
brain	neuronal stem cell	164	SRhi10014.GTTTCG.11352,SRhi10012.CAGATC.11424
brain	Schwann cell	176	SRhi10008.GATCAG.11498
cardiac	cardiocyte	168	SRhi10013.TGACCA.11268,SRhi10012.AGTCAA.11345,SRhi10011.GTGGCC.11417,SRhi10014.GTAGAG.11286,SRhi10012.GAGTGG.11363,SRhi10007.TAGCTT.11435
cardiac	fibroblast of cardiac tissue	169	SRhi10013.TGACCA.11268,SRhi10012.AGTCAA.11345,SRhi10011.GTGGCC.11417
cardiac	smooth muscle cell of the coronary artery	178	SRhi10014.GTAGAG.11286,SRhi10012.GAGTGG.11363,SRhi10007.TAGCTT.11435
eye	corneal epithelial cell	167	SRhi10015.TTAGGC.11526,SRhi10014.CTTGTA.11606,SRhi10015.GTGAAA.11687
eye	fibroblast of the conjunctiva	178	SRhi10015.TGACCA.11531
eye	retinal pigment epithelial cell	168	SRhi10015.CCGTCC.11215,SRhi10015.CGTACG.11528,SRhi10007.GATCAG.11608
fat	acinar cell of sebaceous gland	168	SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378
fat	adipocyte of breast	170	SRhi10011.CGATGT.11376,SRhi10013.GGCTAC.11327
fat	adipocyte of omentum tissue	168	SRhi10012.CGATGT.11473,SRhi10014.GGCTAC.11474,SRhi10002.GTGAAA.11475

fat	fat cell	168	SRhi10011.CGATGT.11376,SRhi10013.GGCTAC.11327,SRhi10012.CGATGT.11473,SRhi10014.GGCTAC.11474,SRhi10002.GTGAAA.11475,SRhi10013.CGATGT.11476,SRhi10014.CGATGT.11259,SRhi10015.GGCTAC.11336,SRhi10003.GTGAAA.11408
fat	fibroblast of mammary gland	166	SRhi10006.ACAGTG.11540,SRhi10003.AGTTCC.11620,SRhi10002.GTTTCG.11701
fat	mammary gland epithelial cell	162	SRhi10007.GCCAAT.11273,SRhi10013.AGTTCC.11350,SRhi10007.GTTTCG.11422
fat	mesenchymal stem cell of adipose	165	SRhi10012.GCCAAT.11217,SRhi10015.GCCAAT.11537,SRhi10003.ATGTCA.11617
fat	omentum preadipocyte	168	SRhi10006.CCGTCC.11468,SRhi10008.CGTACG.11329,SRhi10010.ACTTGA.11403
fat	perirenal adipocyte cell	179	SRhi10013.CGATGT.11476
fat	perirenal preadipocyte	181	SRhi10011.ACTTGA.11469
fat	preadipocyte	168	SRhi10007.CGTACG.11328,SRhi10006.CCGTCC.11468,SRhi10008.CGTACG.11329,SRhi10010.ACTTGA.11403,SRhi10011.ACTTGA.11469,SRhi10007.CCGTCC.11279,SRhi10009.CGTACG.11356,SRhi10012.ACTTGA.11428,SRhi10008.CCGTCC.11280,SRhi10010.CGTACG.11357,SRhi10013.ACTTGA.11429
fat	preadipocyte of the breast	187	SRhi10007.CGTACG.11328
fat	subcutaneous fat cell	160	SRhi10014.CGATGT.11259,SRhi10015.GGCTAC.11336,SRhi10003.GTGAAA.11408
fat	subcutaneous preadipocyte	169	SRhi10007.CCGTCC.11279,SRhi10009.CGTACG.11356,SRhi10012.ACTTGA.11428
fat	visceral preadipocyte	169	SRhi10008.CCGTCC.11280,SRhi10010.CGTACG.11357,SRhi10013.ACTTGA.11429
fetal	amnion mesenchymal stem cell	169	SRhi10002.CAGATC.11547,SRhi10004.ATGTCA.11627,SRhi10003.TTAGGC.12237
fetal	chorionic membrane mesenchymal stem cell	173	SRhi10013.TTAGGC.12240
fetal	embryonic stem cell	168	SRhi10037.AGTTCC.3902,SRhi10037.CGTACG.3903,SRhi10037.GGTAGC.3904
fetal	endothelial cell of umbilical vein	171	SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400
fetal	epithelial cell of amnion	169	SRhi10002.TTAGGC.11533,SRhi10003.CTTGTA.11613,SRhi10005.GTGAAA.11694
fetal	extraembryonic cell	168	SRhi10002.TTAGGC.11533,SRhi10003.CTTGTA.11613,SRhi10005.GTGAAA.11694,SRhi10010.ACAGTG.11535,SRhi10007.CAGATC.11548,SRhi10002.CAGATC.11547,SRhi10004.ATGTCA.11627,SRhi10014.GCCAAT.11214,SRhi10005.CAGATC.11539,SRhi10006.ATGTCA.11619,SRhi10011.GTTTCG.11700,SRhi10008.ATGTCA.11549,SRhi10009.CAGATC.11629,SRhi10004.CCGTCC.11278,SRhi10006.CGTACG.11355,SRhi10008.ACTTGA.11427,SRhi10003.TTAGGC.12237,SRhi10013.TTAGGC.12240
fetal	human amniotic membrane cell- Amnion sample	166	SRhi10003.TTAGGC.12237
fetal	human amniotic membrane cell- fetal sample	176	SRhi10002.CAGATC.11547,SRhi10004.ATGTCA.11627
fetal	human mesenchymal stem cell of umbilical cord- Sciencell sample	168	SRhi10007.CAGATC.11548,SRhi10014.GCCAAT.11214,SRhi10005.CAGATC.11539,SRhi10006.ATGTCA.11619,SRhi10011.GTTTCG.11700
fetal	mesenchymal stem cell of umbilical cord	168	SRhi10007.CAGATC.11548,SRhi10014.GCCAAT.11214,SRhi10005.CAGATC.11539,SRhi10006.ATGTCA.11619,SRhi10011.GTTTCG.11700,SRhi10008.ATGTCA.11549,SRhi10009.CAGATC.11629
fetal	mesenchymal stem cell of Whartons jelly	167	SRhi10007.CAGATC.11548
fetal	placental epithelial cell	168	SRhi10004.CCGTCC.11278,SRhi10006.CGTACG.11355,SRhi10008.ACTTGA.11427
fetal	smooth muscle cell of the umbilical artery	166	SRhi10015.TAGCTT.11212,SRhi10005.GTCCGC.11290,SRhi10003.GGTAGC.11367,SRhi10014.TAGCTT.11439
fetal	fibroblast of villous mesenchyme	189	SRhi10010.ACAGTG.11535
gastrointestinal	epithelial cell of alimentary canal	168	SRhi10011.TGACCA.11507,SRhi10010.AGTCAA.11587,SRhi10011.ACAGTG.11302,SRhi10006.AGTTCC.11379,SRhi10002.GCCAAT.11246,SRhi10004.GCCAAT.11251
gastrointestinal	epithelial cell of esophagus	171	SRhi10011.TGACCA.11507,SRhi10010.AGTCAA.11587
gastrointestinal	fibroblast of gingiva	160	SRhi10003.ACAGTG.11237,SRhi10014.AGTCAA.11318,SRhi10013.GTGGCC.11394
gastrointestinal	gingival epithelial cell	157	SRhi10011.ACAGTG.11302,SRhi10006.AGTTCC.11379
gastrointestinal	intestinal epithelial cell	169	SRhi10002.GCCAAT.11246
gastrointestinal	keratinized cell of the oral mucosa	173	SRhi10004.GCCAAT.11251
gastrointestinal	smooth muscle cell of the esophagus	159	SRhi10008.TAGCTT.11508

genitourinary	epithelial cell of prostate	169	SRhi10009.CCGTCC.11253,SRhi10011.CGTACG.11331,SRhi10014.ACTTGA.11404
genitourinary	prostate stromal cell	165	SRhi10010.CCGTCC.11254,SRhi10012.CGTACG.11332,SRhi10003.CGATGT.11405
genitourinary	Sertoli cell	190	SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333
genitourinary	smooth muscle cell of prostate	168	SRhi10002.GTCCGC.11257,SRhi10014.GAGTGG.11335,SRhi10010.TAGCTT.11465
genitourinary	urothelial cell	176	SRhi10009.GGCTAC.11216,SRhi10013.GTCCGC.11520,SRhi10010.GGTAGC.11600
genitourinary	uterine smooth muscle cell	166	SRhi10006.GTCCGC.11258,SRhi10002.GGCTAC.11466
immune	B cell	168	SRhi10066.TAGCTT.11544,SRhi10066.GGCTAC.11624,SRhi10066.CTTGTA.11705,SRhi10084.CCGTCC.4534
immune	CD14-positive CD16-negative classical monocyte	172	SRhi10064.CAGATC.11857
immune	CD4-positive alpha-beta T cell	168	SRhi10009.TTAGGC.11225,SRhi10009.CTTGTA.11306,SRhi10010.GTGAAA.11382
immune	CD8-positive alpha-beta T cell	168	SRhi10010.TTAGGC.11226,SRhi10010.CTTGTA.11307,SRhi10011.GTGAAA.11383
immune	endothelial cell of lymphatic vessel	167	SRhi10005.TGACCA.11236,SRhi10004.AGTCAA.11317,SRhi10005.GTGGCC.11393
immune	fibroblast of lymphatic vessel	164	SRhi10005.ACAGTG.11506,SRhi10002.AGTTCC.11586,SRhi10015.GTGGCC.11667
immune	human CD14-positive monocyte sample	168	SRhi10008.TTAGGC.11224,SRhi10008.CTTGTA.11305,SRhi10009.GTGAAA.11381
immune	immature conventional dendritic cell	168	SRhi10002.TGACCA.11227,SRhi10015.CTTGTA.11308,SRhi10002.GTGGCC.11384
immune	leukocyte	168	SRhi10008.TTAGGC.11224,SRhi10008.CTTGTA.11305,SRhi10009.GTGAAA.11381,SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386,SRhi10064.CAGATC.11857,SRhi10066.TAGCTT.11544,SRhi10066.GGCTAC.11624,SRhi10066.CTTGTA.11705,SRhi10009.TTAGGC.11225,SRhi10009.CTTGTA.11306,SRhi10010.GTGAAA.11382,SRhi10010.TTAGGC.11226,SRhi10010.CTTGTA.11307,SRhi10011.GTGAAA.11383,SRhi10002.TGACCA.11227,SRhi10015.CTTGTA.11308,SRhi10002.GTGGCC.11384,SRhi10006.GCCAAT.11232,SRhi10012.AGTTCC.11313,SRhi10006.GTTTCG.11389,SRhi10008.GCCAAT.11487,SRhi10009.GCCAAT.11565,SRhi10014.AGTTCC.11566,SRhi10008.GTTTCG.11567,SRhi10010.ATGTCA.11230,SRhi10013.GTTTCG.11311,SRhi10011.CAGATC.11387,SRhi10012.ATGTCA.11233,SRhi10015.GTTTCG.11314,SRhi10013.CAGATC.11390,SRhi10003.CCGTCC.11231,SRhi10005.CGTACG.11312,SRhi10005.ACTTGA.11388,SRhi10084.CCGTCC.4534,SRhi10042.AGTCAA.3997
immune	lymphocyte	168	SRhi10066.TAGCTT.11544,SRhi10066.GGCTAC.11624,SRhi10066.CTTGTA.11705,SRhi10009.TTAGGC.11225,SRhi10009.CTTGTA.11306,SRhi10010.GTGAAA.11382,SRhi10010.TTAGGC.11226,SRhi10010.CTTGTA.11307,SRhi10011.GTGAAA.11383,SRhi10010.ATGTCA.11230,SRhi10013.GTTTCG.11311,SRhi10011.CAGATC.11387,SRhi10084.CCGTCC.4534,SRhi10042.AGTCAA.3997
immune	macrophage	171	SRhi10006.GCCAAT.11232,SRhi10012.AGTTCC.11313,SRhi10006.GTTTCG.11389
immune	mast cell	168	SRhi10008.GCCAAT.11487,SRhi10009.GCCAAT.11565,SRhi10014.AGTTCC.11566,SRhi10008.GTTTCG.11567
immune	mast cell- stimulated sample	131	SRhi10008.GCCAAT.11487
immune	mature alpha-beta T cell	168	SRhi10009.TTAGGC.11225,SRhi10009.CTTGTA.11306,SRhi10010.GTGAAA.11382,SRhi10010.TTAGGC.11226,SRhi10010.CTTGTA.11307,SRhi10011.GTGAAA.11383
immune	mesenchymal stem cell of the bone marrow	168	SRhi10003.CAGATC.11536,SRhi10010.GTTTCG.11697,SRhi10013.GGTAGC.11464
immune	monocyte	168	SRhi10008.TTAGGC.11224,SRhi10008.CTTGTA.11305,SRhi10009.GTGAAA.11381,SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386,SRhi10064.CAGATC.11857,SRhi10002.TGACCA.11227,SRhi10015.CTTGTA.11308,SRhi10002.GTGGCC.11384
immune	mononuclear cell	168	SRhi10003.CCGTCC.11231,SRhi10005.CGTACG.11312,SRhi10005.ACTTGA.11388
immune	myeloid leukocyte	168	SRhi10008.TTAGGC.11224,SRhi10008.CTTGTA.11305,SRhi10009.GTGAAA.11381,SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386,SRhi10064.CAGATC.11857,SRhi10002.TGACCA.11227,SRhi10015.CTTGTA.11308,SRhi10002.GTGGCC.11384,SRhi10006.GCCAAT.11232,SRhi10012.AGTTCC.11313,SRhi10006.GTTTCG.11389,SRhi10008.GCCAAT.11487,SRhi10009.GCCAAT.11565,SRhi10014.AGTTCC.11566,SRhi10008.GTTTCG.11567,SRhi10012.ATGTCA.11233,SRhi10015.GTTTCG.11314,SRhi10013.CAGATC.11390
immune	natural killer cell	168	SRhi10010.ATGTCA.11230,SRhi10013.GTTTCG.11311,SRhi10011.CAGATC.11387
immune	neutrophil	168	SRhi10012.ATGTCA.11233,SRhi10015.GTTTCG.11314,SRhi10013.CAGATC.11390
immune	nongranular leukocyte	168	SRhi10008.TTAGGC.11224,SRhi10008.CTTGTA.11305,SRhi10009.GTGAAA.11381,SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386,SRhi10064.CAGATC.11857,SRhi10066.TAGCTT.11544,

			SRhi10066.GGCTAC.11624,SRhi10066.CTTGTA.11705,SRhi10009.TTAGGC.11225,SRhi10009.CTTGTA.11306,SRhi10010.GTGAAA.11382,SRhi10010.TTAGGC.11226,SRhi10010.CTTGTA.11307,SRhi10011.GTGAAA.11383,SRhi10002.TGACCA.11227,SRhi10015.CTTGTA.11308,SRhi10002.GTGGCC.11384,SRhi10010.ATGTCA.11230,SRhi10013.GTTTCG.11311,SRhi10011.CAGATC.11387,SRhi10003.CCGTCC.11231,SRhi10005.CGTACG.11312,SRhi10005.ACTTGA.11388,SRhi10084.CCGTCC.4534,SRhi10042.AGTCAA.3997
immune	phagocyte	168	SRhi10064.CAGATC.11857,SRhi10006.GCCAAT.11232,SRhi10012.AGTTCC.11313,SRhi10006.GTTTCG.11389
joint	synovial cell	169	SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440
kidney	epithelial cell of nephron	168	SRhi10002.GATCAG.11516,SRhi10011.CCGTCC.11517,SRhi10003.GATCAG.11597,SRhi10012.CCGTCC.11514,SRhi10004.GATCAG.11594,SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676
kidney	epithelial cell of proximal tubule	167	SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676
kidney	glomerular endothelial cell	157	SRhi10012.CCGTCC.11514,SRhi10004.GATCAG.11594
kidney	human renal cortical epithelial cell sample	168	SRhi10002.GATCAG.11516,SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676
kidney	mesangial cell	157	SRhi10013.CCGTCC.11518,SRhi10013.CGTACG.11598
kidney	nephron tubule epithelial cell	168	SRhi10002.GATCAG.11516,SRhi10011.CCGTCC.11517,SRhi10003.GATCAG.11597,SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676
kidney	renal cortical epithelial cell	168	SRhi10002.GATCAG.11516,SRhi10012.CCGTCC.11514,SRhi10004.GATCAG.11594,SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676
liver	endothelial cell of hepatic sinusoid	166	SRhi10014.ACAGTG.11521,SRhi10008.AGTTCC.11601
liver	hepatic mesenchymal stem cell	168	SRhi10013.GCCAAT.11218,SRhi10004.CAGATC.11538
liver	hepatic stellate cell	163	SRhi10015.ACAGTG.11524,SRhi10009.AGTTCC.11604
liver	hepatocyte	168	SRhi10066.AGTCAA.11523,SRhi10066.AGTTCC.11603,SRhi10066.ATGTCA.11684
lung	airway epithelial cell	168	SRhi10007.TTAGGC.11511,SRhi10007.CTTGTA.11591,SRhi10008.GTGAAA.11453,SRhi10007.GTAGAG.11256,SRhi10006.GAGTGG.11334,SRhi10014.GGTAGC.11406,SRhi10006.GGTAGC.11369,SRhi10005.CGATGT.11441
lung	bronchial epithelial cell	168	SRhi10007.TTAGGC.11511,SRhi10007.CTTGTA.11591,SRhi10008.GTGAAA.11453
lung	bronchial smooth muscle cell	198	SRhi10004.TAGCTT.11512
lung	epithelial cell of tracheobronchial tree	168	SRhi10007.TTAGGC.11511,SRhi10007.CTTGTA.11591,SRhi10008.GTGAAA.11453,SRhi10006.GGTAGC.11369,SRhi10005.CGATGT.11441
lung	fibroblast of lung	176	SRhi10004.ACAGTG.11270,SRhi10015.AGTCAA.11347,SRhi10014.GTGGCC.11419
lung	fibroblast of pulmonary artery	91	SRhi10008.ACAGTG.11250
lung	pneumocyte	168	SRhi10015.CGATGT.11510,SRhi10002.CTTGTA.11590,SRhi10004.GTGAAA.11671
lung	smooth muscle cell of the pulmonary artery	168	SRhi10003.GTCCGC.11288,SRhi10015.GAGTGG.11365,SRhi10011.TAGCTT.11437
lung	smooth muscle cell of trachea	158	SRhi10013.TAGCTT.11513
lung	tracheal epithelial cell	168	SRhi10006.GGTAGC.11369,SRhi10005.CGATGT.11441
muscle	cell of skeletal muscle	168	SRhi10005.GTAGAG.11281,SRhi10004.GAGTGG.11358,SRhi10012.GATCAG.11430,SRhi10006.GTAGAG.11240,SRhi10005.GAGTGG.11321,SRhi10013.GATCAG.11397,SRhi10004.GTAGAG.11282,SRhi10003.GAGTGG.11359
muscle	muscle cell	168	SRhi10004.GTAGAG.11282,SRhi10003.GAGTGG.11359,SRhi10009.GTAGAG.11210,SRhi10008.GTAGAG.11283,SRhi10007.GAGTGG.11360,SRhi10010.GTAGAG.11284,SRhi10008.GAGTGG.11361,SRhi10002.TAGCTT.11433,SRhi10011.GTAGAG.11234,SRhi10009.GAGTGG.11315,SRhi10003.TAGCTT.11391,SRhi10004.TAGCTT.11512,SRhi10012.GTAGAG.11285,SRhi10010.GAGTGG.11362,SRhi10013.GTAGAG.11239,SRhi10011.GAGTGG.11320,SRhi10006.TAGCTT.11396,SRhi10014.GTAGAG.11286,SRhi10012.GAGTGG.11363,SRhi10007.TAGCTT.11435,SRhi10008.TAGCTT.11508,SRhi10015.GTAGAG.11287,SRhi10013.GAGTGG.11364,SRhi10009.TAGCTT.11436,SRhi10002.GTCCGC.11257,SRhi10014.GAGTGG.11335,SRhi10010.TAGCTT.11465,SRhi10003.GTCCGC.11288,SRhi10015.GAGTGG.11365,SRhi10011.TAGCTT.11437,SRhi10004.GTCCGC.11289,SRhi10002.GGTAGC.11366,SRhi10012.TAGCTT.11438,SRhi10013.TAGCTT.11513,SRhi10015.TAGCTT.11212,SRhi10005.GTCCGC.11290,SRhi10003.GGTAGC.11367,SRhi10014.TAGCTT.11439,SRhi10006.GTCCGC.11258,SRhi10002.GGCTAC.11466
muscle	muscle precursor cell	168	SRhi10009.ATGTCA.11241,SRhi10012.GTTTCG.11322,SRhi10010.CAGATC.11398,SRhi10006.GTAGAG.11240,SRhi10005.GAGTGG.11321,SRhi10013.GATCAG.11397
muscle	myotube	170	SRhi10004.GTAGAG.11282,SRhi10003.GAGTGG.11359

muscle	skeletal muscle myoblast	165	SRhi10009.ATGTCA.11241,SRhi10012.GTTTCG.11322,SRhi10010.CAGATC.11398
muscle	skeletal muscle satellite cell	167	SRhi10006.GTAGAG.11240,SRhi10005.GAGTGG.11321,SRhi10013.GATCAG.11397
muscle	smooth muscle cell of colon	166	SRhi10013.GTAGAG.11239,SRhi10011.GAGTGG.11320,SRhi10006.TAGCTT.11396
muscle	smooth muscle cell sample	168	SRhi10009.GTAGAG.11210,SRhi10008.GTAGAG.11283,SRhi10007.GAGTGG.11360,SRhi10010.GTAGAG.11284,SRhi10008.GAGTGG.11361,SRhi10002.TAGCTT.11433,SRhi10011.GTAGAG.11234,SRhi10009.GAGTGG.11315,SRhi10003.TAGCTT.11391,SRhi10012.GTAGAG.11285,SRhi10010.GAGTGG.11362,SRhi10014.GTAGAG.11286,SRhi10012.GAGTGG.11363,SRhi10007.TAGCTT.11435,SRhi10008.TAGCTT.11508,SRhi10015.GTAGAG.11287,SRhi10013.GAGTGG.11364,SRhi10009.TAGCTT.11436,SRhi10002.GTCCGC.11257,SRhi10014.GAGTGG.11335,SRhi10010.TAGCTT.11465,SRhi10003.GTCCGC.11288,SRhi10015.GAGTGG.11365,SRhi10011.TAGCTT.11437,SRhi10004.GTCCGC.11289,SRhi10002.GGTAGC.11366,SRhi10012.TAGCTT.11438,SRhi10013.TAGCTT.11513,SRhi10005.GTCCGC.11290,SRhi10006.GTCCGC.11258,SRhi10002.GGCTAC.11466
others	adult endothelial progenitor cell	168	SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386
others	columnar/cuboidal epithelial cell	168	SRhi10014.TTAGGC.11242,SRhi10013.CTTGTA.11323,SRhi10014.GTGAAA.11399,SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676
others	connective tissue cell	168	SRhi10011.CGATGT.11376,SRhi10013.GGCTAC.11327,SRhi10012.CGATGT.11473,SRhi10014.GGCTAC.11474,SRhi10002.GTGAAA.11475,SRhi10013.CGATGT.11476,SRhi10014.CGATGT.11259,SRhi10015.GGCTAC.11336,SRhi10003.GTGAAA.11408,SRhi10004.TTAGGC.11248,SRhi10004.CTTGTA.11463,SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386,SRhi10011.TTAGGC.11261,SRhi10011.CTTGTA.11338,SRhi10012.GTGAAA.11410,SRhi10012.TTAGGC.11262,SRhi10012.CTTGTA.11339,SRhi10013.GTGAAA.11411,SRhi10012.TGACCA.11245,SRhi10011.AGTCAA.11326,SRhi10012.GGTAGC.11401,SRhi10013.TGACCA.11268,SRhi10012.AGTCAA.11345,SRhi10011.GTGGCC.11417,SRhi10014.TGACCA.11492,SRhi10015.TGACCA.11531,SRhi10002.ACAGTG.11269,SRhi10013.AGTCAA.11346,SRhi10012.GTGGCC.11418,SRhi10003.ACAGTG.11237,SRhi10014.AGTCAA.11318,SRhi10013.GTGGCC.11394,SRhi10004.ACAGTG.11270,SRhi10015.AGTCAA.11347,SRhi10014.GTGGCC.11419,SRhi10005.ACAGTG.11506,SRhi10002.AGTTCC.11586,SRhi10015.GTGGCC.11667,SRhi10006.ACAGTG.11540,SRhi10003.AGTTCC.11620,SRhi10002.GTTTCG.11701,SRhi10007.ACAGTG.11238,SRhi10004.AGTTCC.11319,SRhi10003.GTTTCG.11395,SRhi10008.ACAGTG.11250,SRhi10010.ACAGTG.11535,SRhi10013.ACAGTG.11271,SRhi10007.AGTTCC.11348,SRhi10004.GTTTCG.11420,SRhi10015.ACAGTG.11524,SRhi10009.AGTTCC.11604,SRhi10005.GCCAAT.11527,SRhi10011.AGTTCC.11607,SRhi10011.GCCAAT.11493,SRhi10002.ATGTCA.11573,SRhi10006.CAGATC.11219,SRhi10007.CAGATC.11548,SRhi10012.GCCAAT.11217,SRhi10015.GCCAAT.11537,SRhi10003.ATGTCA.11617,SRhi10002.CAGATC.11547,SRhi10004.ATGTCA.11627,SRhi10003.CAGATC.11536,SRhi10010.GTTTCG.11697,SRhi10013.GGTAGC.11464,SRhi10013.GCCAAT.11218,SRhi10004.CAGATC.11538,SRhi10014.GCCAAT.11214,SRhi10005.CAGATC.11539,SRhi10006.ATGTCA.11619,SRhi10011.GTTTCG.11700,SRhi10008.ATGTCA.11549,SRhi10009.CAGATC.11629,SRhi10013.ATGTCA.11252,SRhi10014.CAGATC.11462,SRhi10014.ATGTCA.11276,SRhi10003.CGTACG.11353,SRhi10015.CAGATC.11425,SRhi10015.ATGTCA.11277,SRhi10004.CGTACG.11354,SRhi10002.ACTTGA.11426,SRhi10003.ACTTGA.11249,SRhi10002.CCGTCC.11491,SRhi10004.ACTTGA.11652,SRhi10007.CGTACG.11328,SRhi10006.CCGTCC.11468,SRhi10008.CGTACG.11329,SRhi10010.ACTTGA.11403,SRhi10011.ACTTGA.11469,SRhi10007.CCGTCC.11279,SRhi10009.CGTACG.11356,SRhi10012.ACTTGA.11428,SRhi10008.CCGTCC.11280,SRhi10010.CGTACG.11357,SRhi10013.ACTTGA.11429,SRhi10010.CCGTCC.11254,SRhi10012.CGTACG.11332,SRhi10003.CGATGT.11405,SRhi10013.CCGTCC.11518,SRhi10013.CGTACG.11598,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440,SRhi10003.TTAGGC.12237,SRhi10013.TTAGGC.12240,SRhi10042.GAGTGG.3952+3953
others	contractile cell	168	SRhi10002.CCGTCC.11491,SRhi10004.ACTTGA.11652,SRhi10013.CCGTCC.11518,SRhi10013.CGTACG.11598,SRhi10004.GTAGAG.11282,SRhi10003.GAGTGG.11359,SRhi10009.GTAGAG.11210,SRhi10008.GTAGAG.11283,SRhi10007.GAGTGG.11360,SRhi10010.GTAGAG.11284,SRhi10008.GAGTGG.11361,SRhi10002.TAGCTT.11433,SRhi10011.GTAGAG.11234,SRhi10009.GAGTGG.11315,SRhi10003.TAGCTT.11391,SRhi10004.TAGCTT.11512,SRhi10012.GTAGAG.11285,SRhi10010.GAGTGG.11362,SRhi10013.GTAGAG.11239,SRhi10011.GAGTGG.11320,SRhi10006.TAGCTT.11396,SRhi10014.GTAGAG.11286,SRhi10012.GAGTGG.11363,SRhi10007.TAGCTT.11435,SRhi10008.TAGCTT.11508,SRhi10015.GTAGAG.11287,SRhi10013.GAGTGG.11364,SRhi10009.TAGCTT.11436,SRhi10002.GTCCGC.11257,SRhi10014.GAGTGG.11335,SRhi10010.TAGCTT.11465,SRhi10003.GTCCGC.11288,SRhi10015.GAGTGG.11365,SRhi10011.TAGCTT.11437,SRhi10004.GTCCGC.11289,SRhi10002.GGTAGC.11366,SRhi10012.TAGCTT.11438,SRhi10013.TAGCTT.11513,SRhi10015.TAGCTT.11212,SRhi10005.GTCCGC.11290,SRhi10003.GGTAGC.11367,SRhi10014.TAGCTT.11439,SRhi10006.GTCCG

			C.11258,SRhi10002.GGCTAC.11466
others	ecto-epithelial cell	168	SRhi10014.TTAGGC.11242,SRhi10013.CTTGTA.11323,SRhi10014.GTGAAA.11399,SRhi10015.TTAGGC.11526,SRhi10014.CTTGTA.11606,SRhi10015.GTGAAA.11687,SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421,SRhi10004.GCCAAT.11251,SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378
others	endo-epithelial cell	168	SRhi10007.TTAGGC.11511,SRhi10007.CTTGTA.11591,SRhi10008.GTGAAA.11453,SRhi10011.TGACCA.11507,SRhi10010.AGTCAA.11587,SRhi10011.ACAGTG.11302,SRhi10006.AGTTCC.11379,SRhi10002.GCCAAT.11246,SRhi10004.GCCAAT.11251,SRhi10009.CCGTCC.11253,SRhi10011.CGTACG.11331,SRhi10014.ACTTGA.11404,SRhi10007.GTAGAG.11256,SRhi10006.GAGTGG.11334,SRhi10014.GGTAGC.11406,SRhi10006.GGTAGC.11369,SRhi10005.CGATGT.11441
others	endothelial cell	168	SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10005.TGACCA.11236,SRhi10004.AGTCAA.11317,SRhi10005.GTGGCC.11393,SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343,SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416,SRhi10014.ACAGTG.11521,SRhi10008.AGTTCC.11601,SRhi10012.CCGTCC.11514,SRhi10004.GATCAG.11594,SRhi10008.GTCCGC.11532,SRhi10005.GGTAGC.11612
others	epidermal cell	168	SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421,SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378
others	epithelial cell	168	SRhi10015.CGATGT.11510,SRhi10002.CTTGTA.11590,SRhi10004.GTGAAA.11671,SRhi10002.TTAGGC.11533,SRhi10003.CTTGTA.11613,SRhi10005.GTGAAA.11694,SRhi10007.TTAGGC.11511,SRhi10007.CTTGTA.11591,SRhi10008.GTGAAA.11453,SRhi10014.TTAGGC.11242,SRhi10013.CTTGTA.11323,SRhi10014.GTGAAA.11399,SRhi10015.TTAGGC.11526,SRhi10014.CTTGTA.11606,SRhi10015.GTGAAA.11687,SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10005.TGACCA.11236,SRhi10004.AGTCAA.11317,SRhi10005.GTGGCC.11393,SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343,SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416,SRhi10011.TGACCA.11507,SRhi10010.AGTCAA.11587,SRhi10011.ACAGTG.11302,SRhi10006.AGTTCC.11379,SRhi10014.ACAGTG.11521,SRhi10008.AGTTCC.11601,SRhi10066.AGTCAA.11523,SRhi10066.AGTTCC.11603,SRhi10066.ATGTCA.11684,SRhi10002.GCCAAT.11246,SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421,SRhi10004.GCCAAT.11251,SRhi10007.GCCAAT.11273,SRhi10013.AGTTCC.11350,SRhi10007.GTTTCG.11422,SRhi10008.CAGATC.11247,SRhi10007.ATGTCA.11402,SRhi10004.CCGTCC.11278,SRhi10006.CGTACG.11355,SRhi10008.ACTTGA.11427,SRhi10009.CCGTCC.11253,SRhi10011.CGTACG.11331,SRhi10014.ACTTGA.11404,SRhi10002.GATCAG.11516,SRhi10011.CCGTCC.11517,SRhi10003.GATCAG.11597,SRhi10012.CCGTCC.11514,SRhi10004.GATCAG.11594,SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676,SRhi10015.CCGTCC.11215,SRhi10015.CGTACG.11528,SRhi10007.GATCAG.11608,SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333,SRhi10007.GTAGAG.11256,SRhi10006.GAGTGG.11334,SRhi10014.GGTAGC.11406,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440,SRhi10008.GTCCGC.11532,SRhi10005.GGTAGC.11612,SRhi10006.GGTAGC.11369,SRhi10005.CGATGT.11441,SRhi10009.GGCTAC.11216,SRhi10013.GTCCGC.11520,SRhi10010.GGTAGC.11600
others	exocrine cell	168	SRhi10015.ACAGTG.11524,SRhi10009.AGTTCC.11604,SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378
others	extracellular matrix secreting cell	168	SRhi10011.TTAGGC.11261,SRhi10011.CTTGTA.11338,SRhi10012.GTGAAA.11410,SRhi10012.TTAGGC.11262,SRhi10012.CTTGTA.11339,SRhi10013.GTGAAA.11411,SRhi10015.ACAGTG.11524,SRhi10009.AGTTCC.11604,SRhi10011.GCCAAT.11493,SRhi10002.ATGTCA.11573,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440
others	fibroblast	168	SRhi10012.TGACCA.11245,SRhi10011.AGTCAA.11326,SRhi10012.GGTAGC.11401,SRhi10013.TGACCA.11268,SRhi10012.AGTCAA.11345,SRhi10011.GTGGCC.11417,SRhi10014.TGACCA.11492,SRhi10015.TGACCA.11531,SRhi10002.ACAGTG.11269,SRhi10013.AGTCAA.11346,SRhi10012.GTGGCC.11418,SRhi10003.ACAGTG.11237,SRhi10014.AGTCAA.11318,SRhi10013.GTGGCC.11394,SRhi10004.ACAGTG.11270,SRhi10015.AGTCAA.11347,SRhi10014.GTGGCC.11419,SRhi10005.ACAGTG.11506,SRhi10002.AGTTCC.11586,SRhi10015.GTGGCC.11667,SRhi10006.ACAGTG.11540,SRhi10003.AGTTCC.11620,SRhi10002.GTTTCG.11701,SRhi10007.ACAGTG.11238,SRhi10004.AGTTCC.11319,SRhi10003.GTTTCG.11395,SRhi10008.ACAGTG.11250,SRhi10010.ACAGTG.11535,SRhi10015.ACAGTG.11524,SRhi10009.AGTTCC.11604,SRhi10005.GCCAAT.11527,SRhi10011.AGTTCC.11607,SRhi10007.CGTACG.11328,SRhi10006.CCGTCC.11468,SRhi10008

			.CGTACG.11329,SRhi10010.ACTTGA.11403,SRhi10011.ACTTGA.11469,SRhi10007.CCGTCC.11279,SRhi10009.CGTACG.11356,SRhi10012.ACTTGA.11428,SRhi10008.CCGTCC.11280,SRhi10010.CGTACG.11357,SRhi10013.ACTTGA.11429,SRhi10042.GAGTGG.3952+3953
others	GAG secreting cell	168	SRhi10011.TTAGGC.11261,SRhi10011.CTTGTA.11338,SRhi10012.GTGAAA.11410,SRhi10012.TTAGGC.11262,SRhi10012.CTTGTA.11339,SRhi10013.GTGAAA.11411,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440
others	general ecto-epithelial cell	168	SRhi10015.TTAGGC.11526,SRhi10014.CTTGTA.11606,SRhi10015.GTGAAA.11687,SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421,SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378
others	iPS	168	SRhi10043.GTGAAA.4080+4081,SRhi10043.GTTTCG.4084,SRhi10043.GTAGAG.4082+4083
others	keratinizing barrier epithelial cell	169	SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421,SRhi10004.GCCAAT.11251
others	lining cell	168	SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10005.TGACCA.11236,SRhi10004.AGTCAA.11317,SRhi10005.GTGGCC.11393,SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343,SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416,SRhi10014.ACAGTG.11521,SRhi10008.AGTTCC.11601,SRhi10008.CAGATC.11247,SRhi10007.ATGTCA.11402,SRhi10012.CCGTCC.11514,SRhi10004.GATCAG.11594,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440,SRhi10008.GTCCGC.11532,SRhi10005.GGTAGC.11612
others	mesenchymal stem cell	168	SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386,SRhi10013.ACAGTG.11271,SRhi10007.AGTTCC.11348,SRhi10004.GTTTCG.11420,SRhi10006.CAGATC.11219,SRhi10007.CAGATC.11548,SRhi10012.GCCAAT.11217,SRhi10015.GCCAAT.11537,SRhi10003.ATGTCA.11617,SRhi10002.CAGATC.11547,SRhi10004.ATGTCA.11627,SRhi10003.CAGATC.11536,SRhi10010.GTTTCG.11697,SRhi10013.GGTAGC.11464,SRhi10013.GCCAAT.11218,SRhi10004.CAGATC.11538,SRhi10014.GCCAAT.11214,SRhi10005.CAGATC.11539,SRhi10006.ATGTCA.11619,SRhi10011.GTTTCG.11700,SRhi10008.ATGTCA.11549,SRhi10009.CAGATC.11629,SRhi10003.TTAGGC.12237,SRhi10013.TTAGGC.12240
others	meso-epithelial cell	168	SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10005.TGACCA.11236,SRhi10004.AGTCAA.11317,SRhi10005.GTGGCC.11393,SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343,SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416,SRhi10014.ACAGTG.11521,SRhi10008.AGTTCC.11601,SRhi10012.CCGTCC.11514,SRhi10004.GATCAG.11594,SRhi10014.CCGTCC.11515,SRhi10014.CGTACG.11595,SRhi10006.GATCAG.11676,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440,SRhi10008.GTCCGC.11532,SRhi10005.GGTAGC.11612
others	mesothelial cell	168	SRhi10008.CAGATC.11247,SRhi10007.ATGTCA.11402,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333
others	multi fate stem cell	168	SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi10009.GTGGCC.11386,SRhi10013.ACAGTG.11271,SRhi10007.AGTTCC.11348,SRhi10004.GTTTCG.11420,SRhi10006.CAGATC.11219,SRhi10007.CAGATC.11548,SRhi10012.GCCAAT.11217,SRhi10015.GCCAAT.11537,SRhi10003.ATGTCA.11617,SRhi10002.CAGATC.11547,SRhi10004.ATGTCA.11627,SRhi10003.CAGATC.11536,SRhi10010.GTTTCG.11697,SRhi10013.GGTAGC.11464,SRhi10013.GCCAAT.11218,SRhi10004.CAGATC.11538,SRhi10014.GCCAAT.11214,SRhi10005.CAGATC.11539,SRhi10006.ATGTCA.11619,SRhi10011.GTTTCG.11700,SRhi10008.ATGTCA.11549,SRhi10009.CAGATC.11629,SRhi10014.GTTTCG.11352,SRhi10012.CAGATC.11424,SRhi10003.TTAGGC.12237,SRhi10013.TTAGGC.12240
others	non-terminally differentiated cell	168	SRhi10009.ATGTCA.11241,SRhi10012.GTTTCG.11322,SRhi10010.CAGATC.11398,SRhi10014.ATGTCA.11276,SRhi10003.CGTACG.11353,SRhi10015.CAGATC.11425,SRhi10015.ATGTCA.11277,SRhi10004.CGTACG.11354,SRhi10002.ACTTGA.11426,SRhi10006.GTAGAG.11240,SRhi10005.GAGTGG.11321,SRhi10013.GATCAG.11397
others	pericyte cell	168	SRhi10002.CCGTCC.11491,SRhi10004.ACTTGA.11652,SRhi10013.CCGTCC.11518,SRhi10013.CGTACG.11598
others	pigment cell	168	SRhi10010.GCCAAT.11274,SRhi10015.AGTTCC.11351,SRhi10009.GTTTCG.11423,SRhi10015.CCGTCC.11215,SRhi10015.CGTACG.11528,SRhi10007.GATCAG.11608
others	pluripotent stem cell	168	SRhi10037.AGTTCC.3902,SRhi10037.CGTACG.3903,SRhi10037.GGTAGC.3904,SRhi10043.GTGAAA.4080+4081,SRhi10043.GTTTCG.4084,SRhi10043.GTAGAG.4082+4083
others	precursor cell	168	SRhi10008.TTAGGC.11224,SRhi10008.CTTGTA.11305,SRhi10009.GTGAAA.11381,SRhi10010.TGACCA.11229,SRhi10009.AGTCAA.11310,SRhi1000

			9.GTGGCC.11386,SRhi10064.CAGATC.11857,SRhi10002.TGACCA.11227,SRhi10015.CTTGTA.11308,SRhi10002.GTGGCC.11384,SRhi10013.ACAGTG.11271,SRhi10007.AGTTCC.11348,SRhi10004.GTTTCG.11420,SRhi10006.CAGATC.11219,SRhi10007.CAGATC.11548,SRhi10012.GCCAAT.11217,SRhi10015.GCCAAT.11537,SRhi10003.ATGTCA.11617,SRhi10002.CAGATC.11547,SRhi10004.ATGTCA.11627,SRhi10003.CAGATC.11536,SRhi10010.GTTTCG.11697,SRhi10013.GGTAGC.11464,SRhi10013.GCCAAT.11218,SRhi10004.CAGATC.11538,SRhi10014.GCCAAT.11214,SRhi10005.CAGATC.11539,SRhi10006.ATGTCA.11619,SRhi10011.GTTTCG.11700,SRhi10008.ATGTCA.11549,SRhi10009.CAGATC.11629,SRhi10009.ATGTCA.11241,SRhi10012.GTTTCG.11322,SRhi10010.CAGATC.11398,SRhi10014.GTTTCG.11352,SRhi10012.CAGATC.11424,SRhi10014.ATGTCA.11276,SRhi10003.CGTACG.11353,SRhi10015.CAGATC.11425,SRhi10015.ATGTCA.11277,SRhi10004.CGTACG.11354,SRhi10002.ACTTGA.11426,SRhi10006.GTAGAG.11240,SRhi10005.GAGTGG.11321,SRhi10013.GATCAG.11397,SRhi10003.TTAGGC.12237,SRhi10013.TTAGGC.12240
others	protein secreting cell	168	SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333
others	secretory cell	168	SRhi10011.TTAGGC.11261,SRhi10011.CTTGTA.11338,SRhi10012.GTGAAA.11410,SRhi10012.TTAGGC.11262,SRhi10012.CTTGTA.11339,SRhi10013.GTGAAA.11411,SRhi10015.ACAGTG.11524,SRhi10009.AGTTCC.11604,SRhi10008.GCCAAT.11487,SRhi10009.GCCAAT.11565,SRhi10014.AGTTCC.11566,SRhi10008.GTTTCG.11567,SRhi10011.GCCAAT.11493,SRhi10002.ATGTCA.11573,SRhi10002.GTAGAG.11220,SRhi10002.GAGTGG.11301,SRhi10009.GATCAG.11378,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440
others	smooth muscle cell	168	SRhi10009.GTAGAG.11210,SRhi10008.GTAGAG.11283,SRhi10007.GAGTGG.11360,SRhi10010.GTAGAG.11284,SRhi10008.GAGTGG.11361,SRhi10002.TAGCTT.11433,SRhi10011.GTAGAG.11234,SRhi10009.GAGTGG.11315,SRhi10003.TAGCTT.11391,SRhi10004.TAGCTT.11512,SRhi10012.GTAGAG.11285,SRhi10010.GAGTGG.11362,SRhi10013.GTAGAG.11239,SRhi10011.GAGTGG.11320,SRhi10006.TAGCTT.11396,SRhi10014.GTAGAG.11286,SRhi10012.GAGTGG.11363,SRhi10007.TAGCTT.11435,SRhi10008.TAGCTT.11508,SRhi10015.GTAGAG.11287,SRhi10013.GAGTGG.11364,SRhi10009.TAGCTT.11436,SRhi10002.GTCCGC.11257,SRhi10014.GAGTGG.11335,SRhi10010.TAGCTT.11465,SRhi10003.GTCCGC.11288,SRhi10015.GAGTGG.11365,SRhi10011.TAGCTT.11437,SRhi10004.GTCCGC.11289,SRhi10002.GGTAGC.11366,SRhi10012.TAGCTT.11438,SRhi10013.TAGCTT.11513,SRhi10015.TAGCTT.11212,SRhi10005.GTCCGC.11290,SRhi10003.GGTAGC.11367,SRhi10014.TAGCTT.11439,SRhi10006.GTCCGC.11258,SRhi10002.GGCTAC.11466
others	squamous epithelial cell	168	SRhi10015.TTAGGC.11526,SRhi10014.CTTGTA.11606,SRhi10015.GTGAAA.11687,SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343,SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416,SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421,SRhi10004.GCCAAT.11251,SRhi10008.CAGATC.11247,SRhi10007.ATGTCA.11402,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333
others	stromal cell	168	SRhi10011.TTAGGC.11261,SRhi10011.CTTGTA.11338,SRhi10012.GTGAAA.11410,SRhi10012.TTAGGC.11262,SRhi10012.CTTGTA.11339,SRhi10013.GTGAAA.11411,SRhi10015.ACAGTG.11524,SRhi10009.AGTTCC.11604,SRhi10011.GCCAAT.11493,SRhi10002.ATGTCA.11573,SRhi10003.ACTTGA.11249,SRhi10010.CCGTCC.11254,SRhi10012.CGTACG.11332,SRhi10003.CGATGT.11405,SRhi10007.GTCCGC.11291,SRhi10004.GGTAGC.11368,SRhi10004.GGCTAC.11440
others	stuff accumulating cell	168	SRhi10011.CGATGT.11376,SRhi10013.GGCTAC.11327,SRhi10012.CGATGT.11473,SRhi10014.GGCTAC.11474,SRhi10002.GTGAAA.11475,SRhi10013.CGATGT.11476,SRhi10014.CGATGT.11259,SRhi10015.GGCTAC.11336,SRhi10003.GTGAAA.11408,SRhi10064.CAGATC.11857,SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421,SRhi10004.GCCAAT.11251,SRhi10006.GCCAAT.11232,SRhi10012.AGTTCC.11313,SRhi10006.GTTTCG.11389,SRhi10010.GCCAAT.11274,SRhi10015.AGTTCC.11351,SRhi10009.GTTTCG.11423,SRhi10015.CCGTCC.11215,SRhi10015.CGTACG.11528,SRhi10007.GATCAG.11608
others	supportive cell	168	SRhi10012.TGACCA.11245,SRhi10011.AGTCAA.11326,SRhi10012.GGTAGC.11401,SRhi10002.CCGTCC.11491,SRhi10004.ACTTGA.11652,SRhi10013.CCGTCC.11518,SRhi10013.CGTACG.11598,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333
pancreas	stromal cell of pancreas	179	SRhi10003.ACTTGA.11249
skin	fibroblast of dermis	167	SRhi10002.ACAGTG.11269,SRhi10013.AGTCAA.11346,SRhi10012.GTGGCC.11418,SRhi10042.GAGTGG.3952+3953
skin	hair follicle dermal papilla cell	167	SRhi10013.ACAGTG.11271,SRhi10007.AGTTCC.11348,SRhi10004.GTTTCG.11420
skin	keratinocyte	168	SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421

			10013.CCGTCC.11518,SRhi10013.CGTACG.11598,SRhi10003.GTAGAG.11255,SRhi10010.GATCAG.11333
pancreas	stromal cell of pancreas	179	SRhi10003.ACTTGA.11249
skin	fibroblast of dermis	167	SRhi10002.ACAGTG.11269,SRhi10013.AGTCAA.11346,SRhi10012.GTGGCC.11418,SRhi10042.GAGTGG.3952+3953
skin	hair follicle dermal papilla cell	167	SRhi10013.ACAGTG.11271,SRhi10007.AGTTCC.11348,SRhi10004.GTTTCG.11420
skin	keratinocyte	168	SRhi10003.GCCAAT.11272,SRhi10010.AGTTCC.11349,SRhi10005.GTTTCG.11421
skin	keratocyte	162	SRhi10005.GCCAAT.11527,SRhi10011.AGTTCC.11607
skin	light melanocyte	168	SRhi10010.GCCAAT.11274,SRhi10015.AGTTCC.11351,SRhi10009.GTTTCG.11423
skin	non-pigmented ciliary epithelial cell	166	SRhi10014.TTAGGC.11242,SRhi10013.CTTGTA.11323,SRhi10014.GTGAAA.11399
vascular	aortic endothelial cell	168	SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343
vascular	aortic smooth muscle cell	170	SRhi10009.GTAGAG.11210,SRhi10008.GTAGAG.11283,SRhi10007.GAGTGG.11360
vascular	blood vessel endothelial cell	168	SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343,SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416
vascular	capillary endothelial cell	166	SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414
vascular	endothelial cell of artery	168	SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343
vascular	endothelial cell of vascular tree	168	SRhi10003.TGACCA.11207,SRhi10002.AGTCAA.11263,SRhi10003.GTGGCC.11340,SRhi10011.GGTAGC.11412,SRhi10004.TGACCA.11264,SRhi10003.AGTCAA.11341,SRhi10004.GTGGCC.11413,SRhi10005.TGACCA.11236,SRhi10004.AGTCAA.11317,SRhi10005.GTGGCC.11393,SRhi10006.TGACCA.11265,SRhi10006.GTGGCC.11414,SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343,SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416
vascular	fibroblast of the aortic adventitia	155	SRhi10012.TGACCA.11245,SRhi10011.AGTCAA.11326,SRhi10012.GGTAGC.11401
vascular	smooth muscle cell of the brachiocephalic vasculature	168	SRhi10010.GTAGAG.11284,SRhi10008.GAGTGG.11361,SRhi10002.TAGCTT.11433
vascular	smooth muscle cell of the brain vasculature	166	SRhi10011.GTAGAG.11234,SRhi10009.GAGTGG.11315,SRhi10003.TAGCTT.11391
vascular	smooth muscle cell of the carotid artery	182	SRhi10012.GTAGAG.11285,SRhi10010.GAGTGG.11362
vascular	smooth muscle cell of the internal thoracic artery	168	SRhi10015.GTAGAG.11287,SRhi10013.GAGTGG.11364,SRhi10009.TAGCTT.11436
vascular	smooth muscle cell of the subclavian artery	168	SRhi10015.GTAGAG.11287,SRhi10013.GAGTGG.11364,SRhi10009.TAGCTT.11436,SRhi10004.GTCCGC.11289,SRhi10002.GGTAGC.11366,SRhi10012.TAGCTT.11438
vascular	thoracic aorta endothelial cell	159	SRhi10007.TGACCA.11266,SRhi10006.AGTCAA.11343
vascular	vascular associated smooth muscle cell	168	SRhi10009.GTAGAG.11210,SRhi10008.GTAGAG.11283,SRhi10007.GAGTGG.11360,SRhi10010.GTAGAG.11284,SRhi10008.GAGTGG.11361,SRhi10002.TAGCTT.11433,SRhi10011.GTAGAG.11234,SRhi10009.GAGTGG.11315,SRhi10003.TAGCTT.11391,SRhi10012.GTAGAG.11285,SRhi10010.GAGTGG.11362,SRhi10014.GTAGAG.11286,SRhi10012.GAGTGG.11363,SRhi10007.TAGCTT.11435,SRhi10015.GTAGAG.11287,SRhi10013.GAGTGG.11364,SRhi10009.TAGCTT.11436,SRhi10003.GTCCGC.11288,SRhi10015.GAGTGG.11365,SRhi10011.TAGCTT.11437,SRhi10004.GTCCGC.11289,SRhi10002.GGTAGC.11366,SRhi10012.TAGCTT.11438,SRhi10015.TAGCTT.11212,SRhi10005.GTCCGC.11290,SRhi10003.GGTAGC.11367,SRhi10014.TAGCTT.11439
vascular	vein endothelial cell	168	SRhi10008.TGACCA.11243,SRhi10007.AGTCAA.11324,SRhi10007.GTGGCC.11400,SRhi10009.TGACCA.11267,SRhi10008.AGTCAA.11344,SRhi10008.GTGGCC.11416

Supplementary Table S2. A list of the miRNA-target gene prediction databases.

Database	No. miRNAs	No. target genes	Reference PMID	Accessed date	Website
TargetScan Human	1,530	18,366	26267216	2012/7/11	http://www.targetscan.org/vert_72/
DIANA-TarBase	1,918	18,475	22135297	2014/1/23	http://diana.imis.athena-innovation.gr/DianaTools/index.php
PITA	670	16,942	17893677	2014/12/15	https://genie.weizmann.ac.il/pubs/mir07/mir07_data.html
miRDB	1,916	16,655	25378301	2014/10/29	http://www.mirdb.org/

Supplementary Table S3. Summary of the GWAS used in the current study.

Trait category	Trait	Study model	No. samples	No. SNPs	Ethnicity	Reference PMID
Anthropometric	Height	quantitative	253,288	2,550,858	European	25282103
	Height	quantitative	159,148	5,961,600	Japanese	-
	BMI	quantitative	339,224	2,555,510	European	25673413
	BMI	quantitative	158,284	5,961,600	Japanese	28892062
Immune/Allergy	Rheumatoid arthritis	case/control	80,799	9,739,303	Trans-ethnic	24390342
	Systemic lupus erythematosus	case/control	6,899	7,793,762	Japanese	-
	Graves' disease	case/control	9,929	6,020,808	Japanese	-
	Crohn's disease	case/control	30,740	953,241	European	23128233
	Ulcerative colitis	case/control	26,897	1,428,749	European	23128233
	Atopic dermatitis	case/control	9,438	6,031,258	Japanese	26482879
	Asthma	case/control	36,440	5,961,330	Japanese	-
	Pollinosis	case/control	34,406	5,961,329	Japanese	-
Metabolic	Type 2 diabetes	case/control	110,452	2,915,011	European	24509480
	Type 2 diabetes	case/control	65,702	5,961,329	Japanese	-
	LDL cholesterol	quantitative	188,577	2,692,564	European	20686565
	HDL cholesterol	quantitative	188,577	2,692,429	European	20686565
	Triglycerides	quantitative	188,577	2,692,560	European	20686565
Musculoskeletal	Bone mineral density	quantitative	32,961	2,554,591	European	22504420
	Osteoporosis	case/control	35,969	5,961,329	Japanese	-
Neuropsychiatric	Schizophrenia	case/control	81,080	9,444,230	European	25056061
	Epilepsy	case/control	30,979	5,961,329	Japanese	-
	Alzheimer's disease	case/control	54,162	7,055,881	European	24162737
Eye-related	Age-related macular degeneration	case/control	56,494	2,399,382	European	23455636
	Glaucoma	case/control	22,795	5,961,599	Japanese	-
Cardiovascular	Arteriosclerosis obliterans	case/control	32,252	5,961,329	Japanese	-
	Myocardial infarction	case/control	4,864	4,773,769	Japanese	24916648
	Coronary artery disease	case/control	194,427	9,455,778	European	23202125
	Atrial fibrillation	case/control	36,792	5,018,048	Japanese	28416822
	Cerebral aneurysm	case/control	31,467	5,961,329	Japanese	-
	Ischemic stroke	case/control	43,550	5,961,330	Japanese	-
	Systolic blood pressure	quantitative	69,395	2,650,287	European	21909115
	Diastolic blood pressure	quantitative	69,395	2,673,126	European	21909115
Lung-related	COPD	case/control	31,920	5,961,329	Japanese	-
Kidney-related	Uric acid	quantitative	110,347	2,207,610	European	23263486
	eGFR	quantitative	67,093	2,724,035	European	20383146
Liver-related	Chronic hepatitis B	case/control	29,962	5,961,329	Japanese	-

	Chronic hepatitis C	case/control	33,858	5,961,329	Japanese	-
Genitourinary	Age at menarche	quantitative	182,416	2,441,815	European	25231870
	Uterine fibroid	case/control	23,212	5,961,329	Japanese	-
	Urolithiasis	case/control	35,116	5,961,329	Japanese	-
Hematological	Red blood cell	quantitative	71,861	2,589,454	European	23222517
	Platelet	quantitative	66,867	2,703,393	European	22139419
Malignancy	Lung cancer	case/control	31,052	5,932,052	Japanese	-
	Esophageal cancer	case/control	28,403	5,932,052	Japanese	-
	Gastric cancer	case/control	33,349	5,932,052	Japanese	-
	Colorectal cancer	case/control	33,870	5,932,052	Japanese	-
	Breast cancer	case/control	21,768	5,932,052	Japanese	-
	Endometrial cancer	case/control	19,423	5,961,329	Japanese	-
	Prostate cancer	case/control	15,770	5,932,052	Japanese	-

BMI; body mass index, LDL cholesterol; low-density lipoprotein cholesterol, HDL cholesterol; high-density lipoprotein cholesterol, COPD; chronic obstructive pulmonary disease, eGFR; estimated glomerular filtration rate.

Supplementary Table S4. Characteristics of the patients and control subject enrolled in differentially expressed miRNA analysis.

	RA (*n* = 30)	**HC (*n* = 33)**
Age, years	67 (57-75)	37 (33-55)
Sex, % female	83.3	39.4
Duration of symptoms, months	12 (6-12)	NA
RF positive, %	83.3	NA
ACPA positive, %	56.7	NA
DAS28-CRP	3.66 (2.98-4.80)	NA
miRNA-seq raw read count, million	6.29 (5.47-8.12)	5.34 (3.98-6.37)
Mapped rate to miRNA, %	4.81 (3.97-6.44)	9.10 (5.62-11.22)

Values are the median (interquartile range).

RA; rheumatoid arthritis, HC; healthy control, RF; rheumatoid factor, ACPA; anti–citrullinated protein antibody, DAS; disease activity score, CRP; C-reactive protein.

Supplementary Table S5. Meta-analysis of the rheumatoid arthritis (RA) GWAS and the *in silico* replication study at three genetic loci containing candidate biomarker miRNA.

rsID	Chr	Position	Allele 1/2	Gene	Stage	Cohort	No. subjects		Allele 1 frequency		OR (95%CI)	*P*
							RA cases	Controls	RA cases	Controls		
rs34130487	7	99,759,205	C/T	*MIR95-MIR106B*	GWAS	Brass	483	1,631	0.739	0.739	1.05 (0.88-1.25)	0.57
						Canada	589	1,554	0.725	0.737	0.94 (0.81-1.10)	0.44
						Eira	1,097	1,044	0.741	0.723	1.10 (0.96-1.26)	0.16
						Narac1	863	1,191	0.726	0.746	0.91 (0.77-1.08)	0.29
						Narac2	896	6,603	0.739	0.729	1.11 (0.99-1.25)	0.081
						Wtccc	1,520	10,507	0.727	0.709	1.10 (1.00-1.20)	0.039
						ReAct	275	804	0.752	0.715	1.20 (0.97-1.50)	0.099
						Dutch	1,172	1,684	0.720	0.693	1.18 (1.04-1.33)	0.0098
						ACR-Ref	347	264	0.731	0.743	0.98 (0.71-1.33)	0.88
						Corrona	894	1,838	0.725	0.725	0.99 (0.87-1.13)	0.91
						Vandy	739	2,247	0.709	0.724	0.93 (0.82-1.06)	0.27
						iChip_ES	-	-	-	-	-	-
						iChip_NL	-	-	-	-	-	-
						iChip_SE-E	-	-	-	-	-	-
						iChip_SE-U	-	-	-	-	-	-
						iChip_UK	-	-	-	-	-	-
						iChip_US	-	-	-	-	-	-
						iChip_i2b2	-	-	-	-	-	-
						BBJ	2,414	14,245	0.532	0.512	1.08 (1.02-1.16)	0.011
						Kyoto	1,237	2,087	0.545	0.505	1.19 (1.07-1.33)	0.0015
						Korea	799	751	0.475	0.459	1.07 (0.93-1.24)	0.35
					Replication	IORRA2	2,354	5,252	0.550	0.516	1.13 (1.06-1.22)	5.0.E-04
						BBJ3	954	3,105	0.532	0.518	1.06 (0.95-1.18)	0.29
					Meta-analysis	-	16,633	54,807	0.627	0.620	1.08 (1.05-1.11)	3.3.E-08
rs56656810	16	30,788,759	A/C	*MIR762*	GWAS	Brass	483	1,631	0.287	0.261	1.13 (0.94-1.35)	0.18
						Canada	589	1,554	0.287	0.265	1.10 (0.95-1.29)	0.21
						Eira	1,097	1,044	0.283	0.263	1.11 (0.97-1.27)	0.15
						Narac1	863	1,191	0.263	0.270	1.01 (0.86-1.20)	0.89
						Narac2	896	6,603	0.256	0.271	0.95 (0.85-1.07)	0.42
						Wtccc	1,520	10,507	0.279	0.258	1.12 (1.02-1.22)	0.015
						ReAct	275	804	0.294	0.253	1.28 (1.02-1.59)	0.030
						Dutch	1,172	1,684	0.261	0.251	1.08 (0.95-1.22)	0.24
						ACR-Ref	347	264	0.285	0.268	1.12 (0.83-1.51)	0.46
						Corrona	894	1,838	0.283	0.262	1.12 (0.98-1.27)	0.10
						Vandy	739	2,247	0.256	0.255	1.00 (0.88-1.15)	0.9562
						iChip_ES	397	399	0.283	0.263	1.11 (0.86-1.42)	0.42
						iChip_NL	303	2,001	0.264	0.251	1.06 (0.85-1.33)	0.60
						iChip_SE-E	740	1,117	0.276	0.265	1.05 (0.91-1.22)	0.52
						iChip_SE-U	522	962	0.306	0.273	1.20 (1.00-1.43)	0.044
						iChip_UK	1,645	6,082	0.275	0.252	1.11 (1.01-1.22)	0.023
						iChip_US	997	2,132	0.292	0.277	1.09 (0.96-1.23)	0.20
						iChip_i2b2	882	1,863	0.274	0.261	1.08 (0.95-1.23)	0.23
						BBJ	2,414	14,245	0.087	0.087	1.00 (0.90-1.12)	1.00
						Kyoto	1,237	2,087	0.089	0.069	1.33 (1.09-1.62)	0.0042
						Korea	799	751	0.091	0.082	1.16 (0.88-1.53)	0.30
					Replication	IORRA2	2,354	5,252	0.093	0.084	1.14 (1.00-1.29)	0.046
						BBJ3	954	3,105	0.094	0.089	1.08 (0.90-1.29)	0.43
					Meta-analysis	-	22,119	69,363	0.211	0.196	1.09 (1.05-1.12)	3.6.E-08
rs11089637	22	21,979,096	C/T	*MIR301B*	GWAS	Brass	483	1,631	0.172	0.165	1.12 (0.91-1.37)	0.28
						Canada	589	1,554	0.171	0.157	1.17 (0.96-1.42)	0.12
						Eira	1,097	1,044	0.193	0.189	1.05 (0.89-1.23)	0.57
						Narac1	863	1,191	0.186	0.157	1.27 (1.03-1.57)	0.027
						Narac2	896	6,603	0.166	0.163	1.04 (0.90-1.20)	0.62
						Wtccc	1,520	10,507	0.182	0.166	1.14 (1.03-1.28)	0.017
						ReAct	275	804	0.168	0.159	1.08 (0.81-1.44)	0.60
						Dutch	1,172	1,684	0.191	0.187	1.03 (0.88-1.21)	0.68
						ACR-Ref	347	264	0.174	0.170	0.92 (0.60-1.40)	0.70
						Corrona	894	1,838	0.173	0.157	1.12 (0.96-1.31)	0.14
						Vandy	739	2,247	0.167	0.154	1.10 (0.94-1.30)	0.23
						iChip_ES	397	399	0.188	0.158	1.15 (0.85-1.55)	0.36
						iChip_NL	303	2,001	0.173	0.162	1.13 (0.87-1.45)	0.36
						iChip_SE-E	740	1,117	0.183	0.183	1.00 (0.84-1.18)	0.95
						iChip_SE-U	522	962	0.178	0.179	1.02 (0.83-1.26)	0.85
						iChip_UK	1,645	6,082	0.175	0.150	1.20 (1.08-1.33)	0.0010
						iChip_US	997	2,132	0.171	0.160	1.10 (0.94-1.28)	0.23
						iChip_i2b2	882	1,863	0.174	0.166	1.15 (0.99-1.35)	0.071
						BBJ	2,414	14,245	0.472	0.464	1.03 (0.97-1.10)	0.33
						Kyoto	1,237	2,087	0.459	0.454	1.02 (0.91-1.14)	0.73
						Korea	799	751	0.440	0.419	1.09 (0.95-1.26)	0.23
					Replication	IORRA2	2,354	5,252	0.484	0.468	1.06 (0.99-1.14)	0.12
						BBJ3	954	3,105	0.473	0.468	1.02 (0.92-1.13)	0.66
					Meta-analysis	-	22,119	69,363	0.280	0.273	1.07 (1.05-1.10)	3.7.E-07

Details of the study cohorts were described in Okada et al. ***Nature*** 2014 (GWAS) and Okada et al. ***Am J Hum Genet*** 2016 (replication study). Since all the RA cases of one GWAS cohort (*n* = 423 in IORRA) were also included in the replication cohort (IORRA2), we removed the former one in the meta-analysis. SNP genotype data of rs34130487 was not available in the cohorts genotyped using the ImmunoChip platform.

Supplementary Table S6. The result of the tissue-specific MIGWAS.

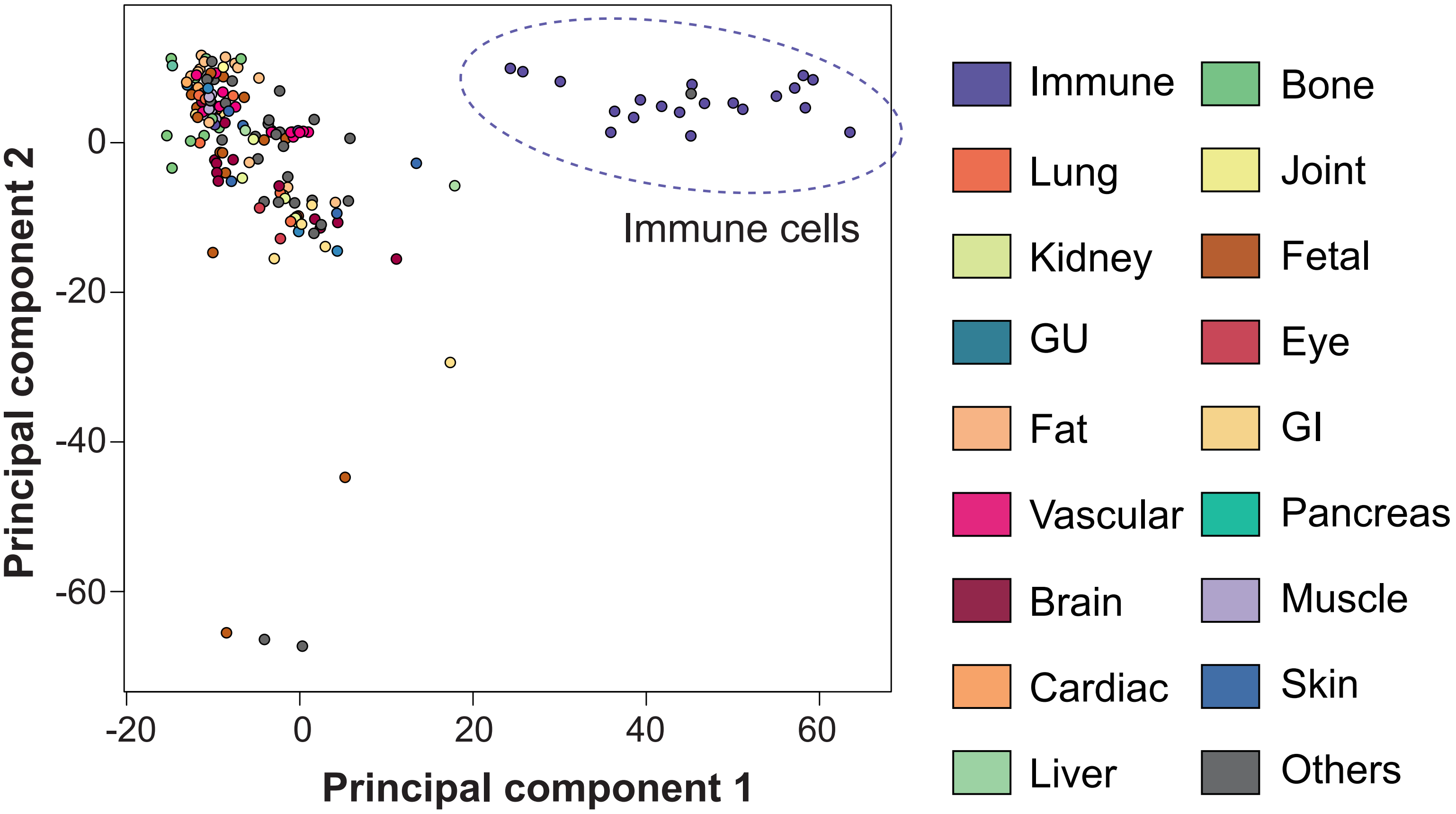
Category	Trait	Immune-related cells	Top-associated tissue	Top-associated cell name
Anthropometric	Height (European)	-	skin	hair follicle dermal papilla cell
	Height (Japanese)	-	fat	preadipocyte of the breast
	BMI (European)	neutrophil	bone	human chondrocyte de-differentiated sample
	BMI (Japansese)	-	skin	light melanocyte
Immune/Allergy	Rheumatoid arthritis	phagocyte	lung	bronchial smooth muscle cell
	Systemic lupus erythematosus	mast cell	immune	mast cell
	Graves' disease	CD14-positive CD16-negative classical monocy	immune	CD14-positive CD16-negative classical monocy
	Crohn's disease	mast cell	immune	mast cell
	Ulcerative colitis	-	muscle	skeletal muscle myoblast
	Atopic dermatitis	mesenchymal stem cell of the bone marrow	bone	bone cell
	Asthma	neutrophil	immune	neutrophil
	Pollinosis	-	kidney	human renal cortical epithelial cell sample
Metabolic	Type 2 diabetes (European)	fibroblast of lymphatic vessel	brain	Schwann cell
	Type 2 diabetes (Japanese)	mast cell- stimulated sample	fetal	human amniotic membrane cell- Amnion sample
	Bone mineral density	fibroblast of lymphatic vessel	skin	keratinocyte
	Osteoporosis	-	fat	fibroblast of mammary gland
	LDL cholesterol	-	fat	subcutaneous fat cell
	HDL cholesterol	natural killer cel	immune	natural killer cel
	Triglycerides	-	brain	central nervous system pericyte
Neuropsychiatric	Schizophrenia	CD14-positive CD16-negative classical monocyte	immune	CD14-positive CD16-negative classical monocyte
	Epilepsy	myeloid leukocyte	immune	myeloid leukocyte
	Alzheimer's disease	B cell	immune	B cell
Eye-related	Age-related macular degeneration	-	fetal	fibroblast of villous mesenchyme
	Glaucoma	mature alpha-beta T cell	skin	keratinocyte
Cardiovascular	Arteriosclerosis obliterans	fibroblast of lymphatic vessel	gastrointestinal	smooth muscle cell of the esophagus
	Myocardial infarction	-	immune	mesenchymal stem cell of the bone marrow
	Coronary artery disease	immature conventional dendritic cell	fat	subcutaneous fat cell
	Atrial fibrillation	-	immune	CD4-positive alpha-beta T cell
	Cerebral aneurysm	-	fetal	iPS
	Ischemic stroke	-	bone	human chondrocyte re-differentiated sample
	Systolic blood pressure	-	muscle	skeletal muscle satellite cell
	Diastolic blood pressure	B cell	brain	Schwann cell
Lung-related	COPD	-	eye	fibroblast of the conjunctiva
Kidney-related	Uric acid	CD14-positive CD16-negative classical monocyte	others	GAG secreting cell
	eGFR	-	cardiac	fibroblast of cardiac tissue
Liver-related	Chronic hepatitis B	phagocyte	fetal	human amniotic membrane cell- Amnion sample
	Chronic hepatitis C	mast cell- stimulated sample	immune	mast cell- stimulated sample
Genitourinary	Age at menarche	-	brain	human pituitary gland - adult sample
	Uterine fibroid	-	fetal	fibroblast of villous mesenchyme
	Urolithiasis	-	fetal	fibroblast of villous mesenchyme
Hematological	Red blood cell	human CD14-positive monocyte sample	immune	human CD14-positive monocyte sample
	Platelet	-	gastrointestinal	keratinized cell of the oral mucosa
Malignancy	Lung cancer	-	brain	human diencephalon - adult sample
	Esophageal cancer	-	lung	bronchial smooth muscle cell
	Gastric cancer	-	fat	perirenal preadipocyte
	Colorectal cancer	-	bone	nucleus pulposus cell of intervertebral disc
	Breast cancer	-	vascular	smooth muscle cell of the subclavian artery
	Endometrial cancer	neutrophil	liver	endothelial cell of hepatic sinusoid
	Prostate cancer	-	fetal	embryonic stem cell

Supplementary Table S7. The result of summary-level data Mendelian randomization.

Gene	Top SNP	Allele 1	Allele 2	Freq	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI
CPNE5	rs1064827	T	C	0.251	0.033	0.018	6.5E-02	0.191	0.031	1.3E-09	0.171	0.097	7.7E-02	3.8E-01
DAP	rs5745297	A	G	0.080	-0.023	0.048	6.3E-01	0.873	0.051	3.6E-66	-0.027	0.055	6.3E-01	6.2E-01
FADS2	rs968567	T	C	0.150	-0.104	0.021	7.3E-07	0.458	0.038	7.8E-33	-0.227	0.050	4.8E-06	5.1E-01
GATS	rs2528900	A	G	0.268	-0.057	0.017	6.6E-04	0.911	0.032	4.3E-184	-0.062	0.018	7.2E-04	7.1E-02
INPP5B	rs28525112	C	G	0.445	-0.093	0.018	1.4E-07	-0.595	0.028	2.2E-100	0.156	0.031	3.1E-07	4.5E-02
IQGAP1	rs2074585	G	A	0.466	-0.056	0.018	1.5E-03	-0.522	0.027	2.2E-80	0.108	0.034	1.7E-03	1.2E-01
IRF5	rs10954215	T	C	0.368	-0.055	0.013	4.6E-05	1.173	0.027	0.0E+00	-0.047	0.011	4.9E-05	1.9E-12
ITSN1	rs2300375	T	C	0.304	-0.054	0.017	1.0E-03	-0.525	0.030	1.6E-68	0.104	0.032	1.3E-03	2.0E-02
PADI2	rs11576552	C	A	0.368	-0.089	0.016	5.2E-08	-0.517	0.029	3.7E-73	0.172	0.033	1.8E-07	5.0E-04
PFKL	rs2838547	C	G	0.161	0.070	0.020	4.1E-04	0.340	0.041	5.4E-17	0.205	0.063	1.1E-03	1.3E-01
PGAP3	rs2934951	A	G	0.318	-0.083	0.014	2.3E-09	0.471	0.030	3.0E-57	-0.177	0.032	2.2E-08	2.0E-03
RAF1	rs12629082	G	A	0.432	0.052	0.018	3.8E-03	0.280	0.028	8.1E-24	0.187	0.067	5.3E-03	3.0E-01
SLC25A23	rs393375	A	T	0.469	-0.007	0.021	7.3E-01	-0.309	0.028	9.9E-29	0.024	0.069	7.3E-01	1.2E-01
SLC44A2	rs78671428	T	G	0.087	0.046	0.029	1.1E-01	-0.972	0.053	2.5E-75	-0.048	0.030	1.2E-01	5.9E-01
SYNGR1	rs2069235	A	G	0.299	0.113	0.016	7.6E-13	0.394	0.030	1.3E-38	0.288	0.046	3.5E-10	2.7E-01
TMPRSS3	rs2277798	A	G	0.374	-0.010	0.014	4.6E-01	-0.290	0.028	1.6E-25	0.035	0.048	4.6E-01	7.5E-05
TNFRSF14	rs7544646	C	G	0.531	0.057	0.013	2.3E-05	-0.445	0.028	1.5E-57	-0.128	0.031	4.3E-05	2.3E-04
TRAF1	rs4310279	G	A	0.278	0.063	0.015	2.5E-05	-0.418	0.031	9.6E-42	-0.152	0.038	5.7E-05	5.6E-02
TSPAN33	rs12667978	C	T	0.458	0.046	0.021	2.7E-02	0.293	0.029	3.7E-24	0.158	0.073	3.0E-02	1.1E-02
UBASH3A	rs1893592	C	A	0.276	-0.106	0.015	3.7E-12	0.464	0.031	1.1E-50	-0.228	0.036	3.0E-10	5.8E-07
UTP11L	rs35129114	T	C	0.264	-0.101	0.020	2.8E-07	-0.243	0.030	9.5E-16	0.417	0.096	1.5E-05	5.8E-02

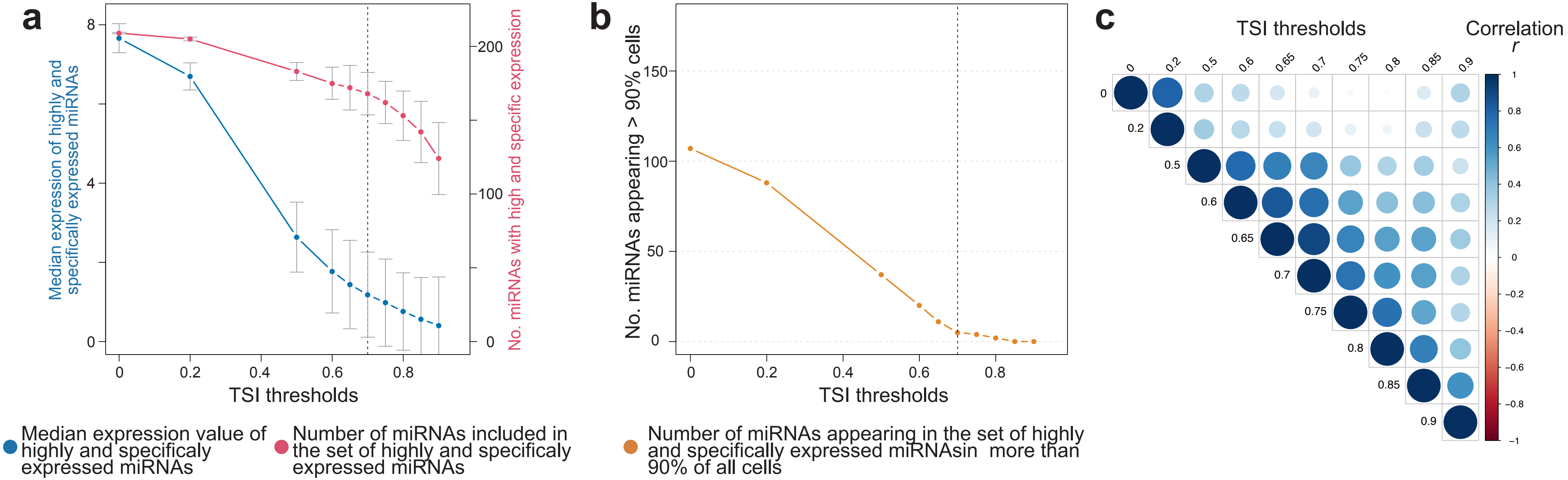
Freq; allele frequency of allele 1, b_GWAS; beta coefficient of allele 1 in GWAS, se_GWAS; standard error in GWAS, p_GWAS; *P* value in GWAS, b_eQTL; beta coefficient of allele 1 in eQTL, se_eQTL; standard error in eQTL, p_eQTL; *P* value in eQTL, b_SMR; beta coefficient of allele 1 in SMR, se_SMR; standard error in SMR, p_SMR; *P* value in SMR, p_HEIDI; *P* value in HEIDI analysis.

Supplementary Figure S1. The principal component analysis on the expression profiles of mature miRNAs.



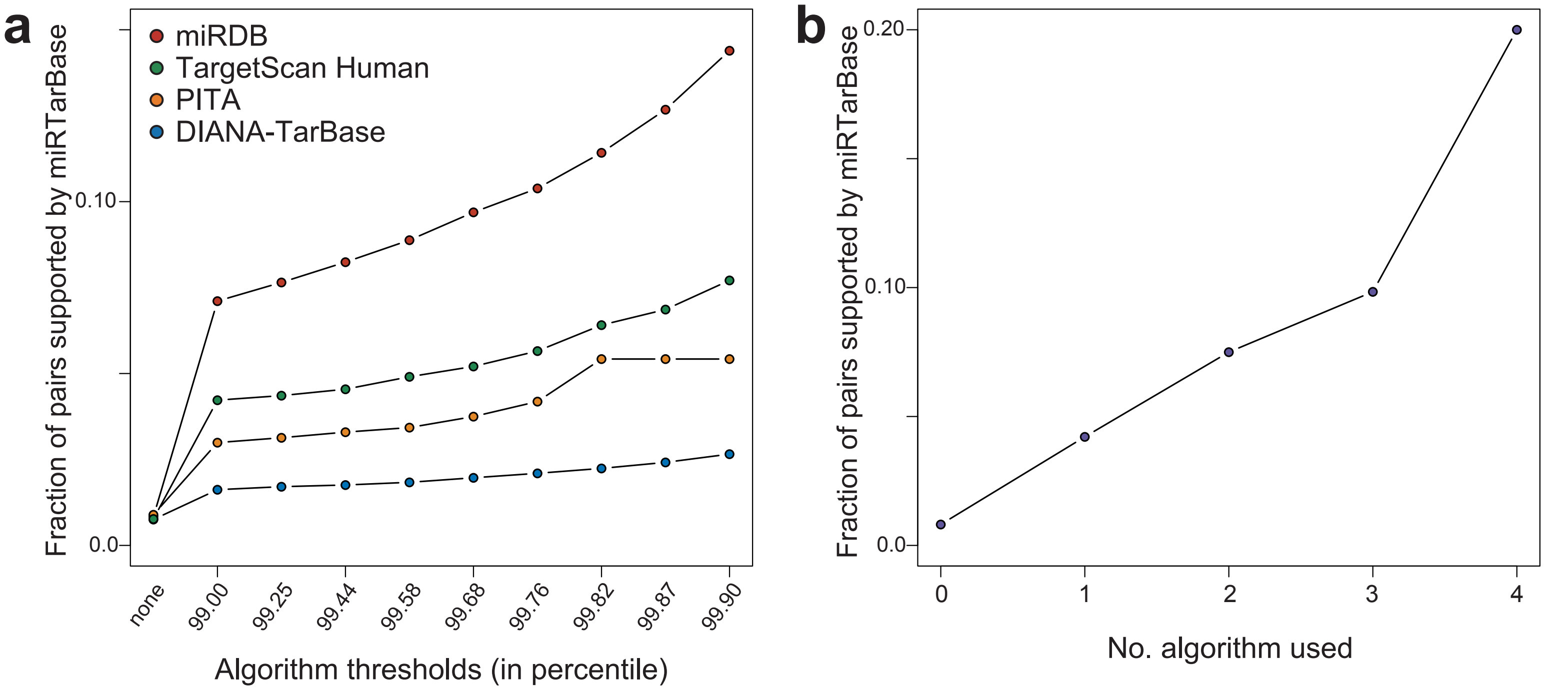
Each circle represents the principal component 1 and 2 of the miRNA expression profile in each cell. The color of each circle indicates the tissue which the cell was collected from. GU; genitourinary, GI; gastrointestinal.

Supplementary Figure S2. The effect of the tissue specificity index (TSI) threshold on the set of highly and specifically expressed miRNAs and on the statistics from MIGWAS.



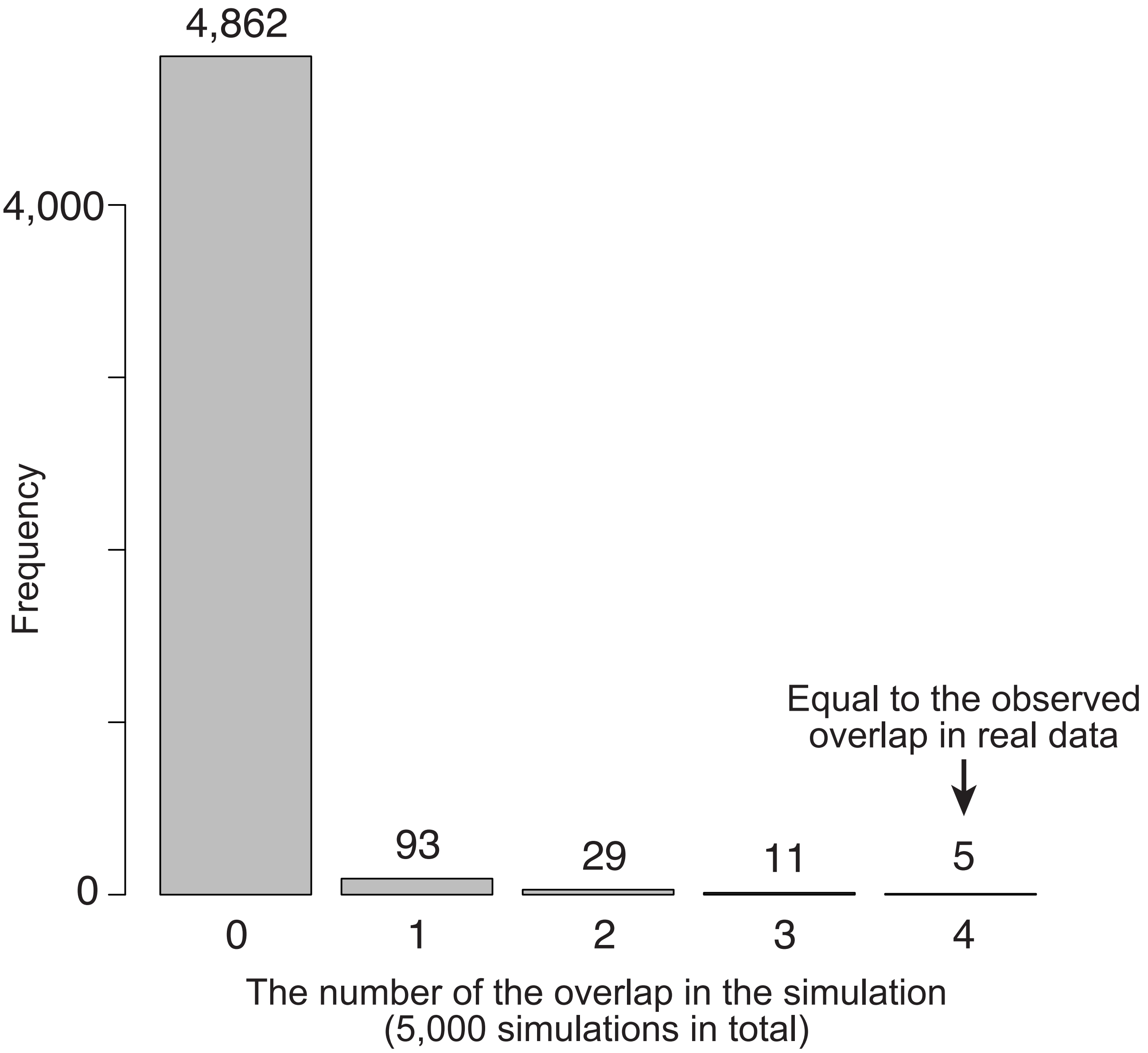
(**a**) Blue circles are the median expression counts and their standard deviations (bars) of highly and specifically expressed miRNAs by the TSI thresholds. Red circles are the median numbers of miRNAs and their standard deviations (bars) with high and specific expression in each cell by the TSI thresholds. (**b**) The number of miRNAs included in a set of highly and specifically expressed miRNAs in more than 90% of 179 cells. (**c**) The correlation plot of MIGWAS statistics by the TSI thresholds. Color intensity and the size of the circles are proportional to the correlation coefficients.

Supplementary Figure S3. *In vitro* support of *in silico* miRNA-gene target prediction algorithms.



The fraction of *in silico* predicted miRNA-gene target pairs supported by miRTarBase (either reporter assay, western blot, microarray or next-generation sequencing) by the thresholds in percentile for each algorithm (**a**) and by the number of algorithms used (**b**).

Supplementary Figure S4. A histogram of the number of the overlapped miRNAs from MIGWAS pipeline and the differential expression analysis by the permutation procedure.



Bars represent the distribution of the number of the overlapped miRNAs included both in MIGWAS candidate miRNAs for RA and the differential expression experiment of RA and HC samples in 5,000 permutation steps. The number shown above each bar is the number of permutation steps within each bin. The rightmost bin, with four overlapped miRNAs, was equal to the observed overlap in real data.