

**Supplementary table 1. A total of 125 differentially expressed miRNAs in psoriatic involved and psoriatic uninvolved skin with respect to the normal human skin. miRtron and noncanonical miRNAs are highlighted in blue.**

Mature miRNA	Sequence	Normalized no. reads			Fold change			Total reads
		NN <sup>a</sup>	PN <sup>a</sup>	PP <sup>a</sup>	PP/NN	PP/PN	PN/NN	
hsa-mir-31.iso1	GCTATGCCAACATATTGCCATC	10.94	18.91	694.01	63.43	36.71	1.73	723.86
hsa-miR-31	AGGCAAGATGCTGGCATAGCT	1063.44	3255.25	45690.24	42.93	14.03	3.06	55883
hsa-miR-31*	TGCTATGCCAACATATTGCCAT	250.54	358.19	8679.14	34.51	24.17	1.43	10412
hsa-miR-206	TGGAATGTAAGGAAGTGTGTGG	119.25	317.23	1538.82	12.80	4.84	2.65	2156
hsa-miR-6732/miRtron	TAACCCTGTCCTCTCCCTCCCAG	1.00	2.05	11.58	11.58	5.65	2.05	14.63
hsa-miR-21*	CAACACCAGTCGATGGGCTGT	712.24	1032.56	6278.75	8.80	6.08	1.45	8754
hsa-miR-135b*	ATGTAGGGCTAAAAGCCATGGG	62.36	66.18	506.18	8.00	7.55	1.06	694
miR-937/miRtron	ATCCGCGCTCTGACTCTTGCC	3.19	2.05	20.40	6.40	9.95	-1.56	25.64
hsa-miR-33b*	CAGTGCCTCGGCAGTGCAGCCC	61.27	67.23	353.62	5.70	5.20	1.10	521
hsa-miR-135b	TATGGCTTTTCATTCTATGTGA	643.31	682.77	3636.74	5.65	5.32	1.06	5362
hsa-mir-455.iso1	TGCAGTCCATGGGCATATACAC	481.39	563.03	2711.68	5.63	4.82	1.17	3756.10
hsa-miR-222*	CTCAGTAGCCAGTGTAGATCCT	440.91	736.34	2467.41	5.59	3.35	1.67	3902
miR-1983/tRNAIle	CTCACCTGGAGCATGTTTTCT	23.98	25.16	117.40	4.90	4.67	1.05	166.54
hsa-miR-1268	CGGGCGTGGTGGTGGGGG	1514.20	2227.94	6745.25	4.45	3.03	1.47	11154
Novel #6	TAAAAGTAATTGTGGTATTTGC	303.06	370.80	1246.93	4.10	3.36	1.22	2044
hsa-miR-21	TAGCTTATCAGACTGATGTTGA	4091259.64	4176278.01	16177715.35	3.95	3.87	1.02	26060562
hsa-miR-431	TGTCTTGACAGCCGTCATGCA	44.86	54.62	178.13	3.91	3.22	1.21	295
hsa-mir-146a.iso1	TTGAGAACTGAATCCATGGGT	1101.73	1510.50	4294.59	3.90	2.84	1.37	6906.83
hsa-miR-4772	TCTGATCAGGCAAATTGCAG	77.68	68.28	296.30	3.78	4.29	-1.14	472
miRtron #144/miRtron	TTTGCTAACTTTCTTTTCCAAG	22.88	25.16	79.48	3.47	3.16	1.10	127.52
hsa-mir-21.iso1	AGCTTATCAGACTGATGTTGAC	28387.89	20802.53	93943.14	3.31	4.52	0.73	143133.55
hsa-miR-7	TGGAAGACTAGTGATTTTGTGT	9314.93	12290.97	28373.42	3.05	2.31	1.32	52390
hsa-mir-944.iso1	GAAATTATTGTACATCGGATGA	964.97	864.50	2936.55	3.04	3.40	0.90	4766.02
hsa-miR-496	TGAGTATTACATGGCCAATCTC	148.79	190.13	451.51	3.02	2.37	1.28	829
hsa-miR-3065-5p	TCAACAAAATCACTGATGCTGGA	537.19	474.79	1622.60	3.02	3.41	-1.13	2783
hsa-miR-3614	CCACTTGGATCTGAAGGCTGCC	61.27	65.13	183.42	2.96	2.79	1.06	326
hsa-miR-592	TTGTGTCAATATGCGATGATGT	54.70	77.73	161.38	2.92	2.06	1.41	307
hsa-mir-378a.iso1	CTGGACTTGGAGTCAGAAGGC	71843.34	92591.43	206610.53	2.88	2.23	1.29	371045.29
hsa-miR-545*	TCAGTAAATGTTTATTAGATGA	52.52	60.92	151.68	2.85	2.47	1.16	278
hsa-miR-944	AAATTATTGTACATCGGATGAG	8181.47	7959.04	23300.16	2.85	2.93	-1.03	41477

hsa-miR-200c*	CGTCTTACCCAGCAGTGTTTGG	530.62	584.03	1485.03	2.80	2.54	1.10	2725
hsa-miR-940	AAGGCAGGGCCCCGCTCCCC	66.74	66.18	187.83	2.79	2.81	-1.01	337
hsa-miR-147b	GTGTGCGGAAATGCTTCTGCTA	64.55	81.93	181.66	2.79	2.20	1.27	343
miR-203-AS	TTGAACTGTTAAGAACCACTGG	1657.52	2138.66	4597.95	2.77	2.15	1.29	8765
hsa-miR-155	TTAATGCTAATCGTGATAGGGGT	18527.02	19220.60	50098.60	2.70	2.61	1.04	92043
hsa-miR-378	ACTGGACTTGAGTCAGAAGG	1308311.11	1659217.08	3504731.56	2.68	2.11	1.27	6749701
hsa-miR-1303	TTTAGAGACGGGGTCTTGCTCT	100.65	153.36	269.85	2.66	1.75	1.52	544
hsa-miR-3176	ACTGGCCTGGGACTACCGG	87.53	82.98	234.57	2.66	2.80	-1.05	425
hsa-miR-3613	TGTTGTACTTTTTTTTTTGTTC	5674.95	5138.66	14804.44	2.61	2.88	-1.10	26867
hsa-miR-211	TTCCCTTTGTCATCCTTCGCCT	3135.61	6034.67	8157.96	2.60	1.35	1.92	17862
hsa-miR-4802	TACATGGATGGAAACCTTCAAGC	80.96	81.93	207.23	2.54	2.51	1.01	387
hsa-mir-1307.iso1	CTCGGCGTGGCGTGGTCTGG	1329.30	1212.19	3367.77	2.53	2.78	0.91	5909.26
hsa-mir-155.iso1	TAATGCTAATCGTGATAGGGG	169.58	161.76	428.58	2.53	2.65	0.95	759.92
hsa-miR-142-3p	TGTAGTGTTCCTACTTTATGGA	91176.69	77835.12	229401.86	2.52	2.95	-1.17	417574
hsa-mir-223.iso1	GTCAGTTTGTCAAATACCCAA	1369.78	1656.51	3433.91	2.51	2.07	1.21	6460.20
hsa-miR-455-3p	GCAGTCCATGGGCATATACAC	12226.26	11781.52	30044.52	2.46	2.55	-1.04	56461
hsa-miR-18a	TAAGGTGCATCTAGTGCAGATAG	6729.64	7211.14	16350.32	2.43	2.27	1.07	31557
hsa-miR-3150b	TGAGGAGATCGTCGAGTTGGC	59.08	116.60	142.86	2.39	1.22	1.96	327
Novel #116	AAAGGACCTTGTGAGACGGAG	53.61	76.68	128.75	2.38	1.67	1.42	268
hsa-miR-19b-1*	AGTTTTGCAGTTTGCATCCAGC	273.52	388.66	649.04	2.37	1.67	1.42	1356
hsa-miR-146a	TGAGAACTGAATTCCATGGGTT	257981.11	310479.12	609439.89	2.36	1.96	1.20	1222470
hsa-miR-188-5p	CATCCCTTGCATGGTGGAGGG	630.19	668.07	1486.79	2.36	2.22	1.06	2898
hsa-miR-376a*	GTAGATTCTCCTTCTATGAGTA	1596.25	1683.82	3748.73	2.35	2.23	1.05	7313
hsa-miR-665	ACCAGGAGGCTGAGGCCCT	159.73	218.49	374.78	2.34	1.71	1.37	779
hsa-miR-4423	AGTTGCCTTTTTGTCCCATGC	59.08	131.30	139.33	2.34	1.06	2.20	337
hsa-miR-548f	AAAAACTGTAATTACTTTT	70.02	72.48	164.02	2.32	2.25	1.03	319
hsa-miR-369-3p	AATAATACATGGTTGATCTTT	3427.73	2759.45	7933.98	2.31	2.87	-1.24	14757
hsa-miR-449a	TGGCAGTGTATTGTTAGCTGGT	119.25	157.56	276.02	2.30	1.75	1.32	572
U60 miRNA-5p/snoRNA	AGTCTGTGATGAATTGCTTTGA	4673445.23	7641212.21	10813232.65	2.30	1.41	1.64	23127890.09
hsa-miR-33a*	CAATGTTTCCACAGTGCATCAC	582.05	689.08	1319.24	2.26	1.91	1.18	2684
hsa-mir-142.iso1	GTAGTGTTCCTACTTTATGG	28092.49	19933.83	63264.57	2.25	3.17	0.71	111290.89
hsa-miR-33b	GTGCATTGCTGTTGCATTGC	284.46	273.11	634.93	2.23	2.32	-1.04	1240
hsa-miR-18a*	ACTGCCCTAAGTGCTCCTTCTGG	253.82	367.65	565.26	2.22	1.54	1.45	1223
hsa-miR-23a*	GGGGTTCCTGGGGATGGGATTT	217.72	348.74	485.02	2.22	1.39	1.60	1081

hsa-miR-223*	CGTGTATTTGACAAGCTGAGTT	479.20	446.43	1050.28	2.19	2.35	-1.07	2054
hsa-miR-187	TCGTGTCTTGTGTTGCAGCCGG	630.19	744.75	1371.27	2.17	1.84	1.18	2840
hsa-miR-1276	TAAAGAGCCCTGTGGAGACA	107.22	91.39	230.16	2.14	2.50	-1.17	446
hsa-miR-223	TGTCAGTTTGTCAAATACCCCA	18027.03	17264.71	38451.16	2.13	2.23	-1.04	76516
hsa-miR-154*	AATCATACACGGTTGACCTATT	261.48	239.50	557.33	2.13	2.32	-1.09	1099
hsa-mir-7.iso1	AACAAATCACAGTCTGCCATA	176.15	185.92	373.90	2.12	2.01	1.06	735.97
hsa-miR-487a	AATCATACAGGGACATCCAGTT	370.89	432.77	785.73	2.12	1.81	1.17	1642
hsa-miR-6515/miRtron	TTGGAGGGTGTGGAAGACATC	75.49	79.83	160.50	2.11	2.00	1.06	327
hsa-miR-19b	TGTGCAAATCCATGCAAACTGA	47813.14	45453.80	100637.24	2.10	2.21	-1.05	201095
hsa-miR-212	TAACAGTCTCCAGTCACGGCC	251.64	226.89	525.58	2.08	2.31	-1.11	1042
hsa-miR-92a-1*	AGGTTGGGATCGGTTGCAATGCT	354.48	436.97	731.05	2.06	1.67	1.23	1569
hsa-miR-378*	CTCCTGACTCCAGGTCCTGTGT	1417.92	1373.95	2899.51	2.04	2.11	-1.03	5892
hsa-mir-203.iso1	TGAAATGTTTAGGACCACTAG	1828790.75	1919175.17	3728148.32	2.04	1.94	1.05	7476114.24
hsa-miR-205*	GATTTCACTGGAGTGAAGTTC	549.22	597.69	1118.18	2.03	1.87	1.09	2339
hsa-miR-1308	GCATGGGTGGTTCAGTGG	2130.16	2262.61	4330.75	2.03	1.91	1.06	9012
hsa-miR-1307	ACTCGGCGTGGCGTCCGGTCTGTG	7732.90	6553.57	15201.27	1.97	2.32	-1.18	30545
hsa-miR-362-3p	AACACACCTATTCAAGGATTCA	405.90	391.81	793.66	1.95	2.02	-1.04	1644
hsa-miR-6513/miRtron	TTTGGGATTGACGCCACATGTCT	74.30	82.93	143.86	1.94	1.73	1.12	301.09
hsa-miR-590-3p	TAATTTTATGTATAAGCTAGT	1237.40	886.55	2400.39	1.94	2.71	-1.40	4697
hsa-miR-19a	TGTGCAAATCTATGCAAACTGA	2609.36	2141.81	4938.34	1.89	2.31	-1.22	10024
miRtron #323/miRtron	TCAGGGAGAAAGAAGGGTTATT	17.41	11.50	32.75	1.88	2.85	-1.67	61.66
hsa-miR-3065-3p	TCAGCACCAGGATATTGTTGGAG	562.35	480.04	1044.99	1.86	2.17	-1.17	2156
hsa-miR-377	ATCACACAAAGGCAACTTTTGT	912.46	768.91	1651.70	1.81	2.15	-1.19	3439
hsa-miR-376b	ATCATAGAGGAAAATCCATGTT	716.62	582.98	1241.64	1.73	2.13	-1.23	2618
hsa-miR-509-5p	TACTGCAGACAGTGGCAATCA	352.29	720.59	567.91	1.61	-1.27	2.04	1652
hsa-miR-542-3p	TGTGACAGATTGATAACTGAAA	5650.88	3641.81	7399.58	1.31	2.03	-1.55	17023
hsa-miR-2110	TTGGGGAAACGGCCGCTGAGTG	1932.13	2987.40	1227.53	-1.57	-2.43	1.55	6002
hsa-miR-4520a	TTGGACAGAAAACACGCAGGA	1284.44	1554.62	746.92	-1.72	-2.08	1.21	3501
hsa-miR-486-5p	TCCTGTAAGAGTGGCAGTCGA	134809.38	148860.36	74411.99	-1.81	-2.00	1.10	349315
hsa-miR-628-3p	TCTAGTAAGAGTGGCAGTCGA	587.52	689.08	313.94	-1.87	-2.19	1.17	1549
hsa-miR-1179	AAGCATTCTTTCATTGGTTGG	152.08	86.13	74.96	-2.02	-1.15	-1.76	306
hsa-miR-99a	AACCCGTAGATCCGATCTTGTG	400593.41	260932.88	195318.48	-2.05	-1.34	-1.54	836045
hsa-mir-628.iso1	TTCTAGTAAGAGTGGCAGTCGA	192.56	245.80	92.59	-2.08	-2.65	1.28	530.95
hsa-miR-3617-5p	AAAGACATAGTTGCAAGATGGG	246.17	263.66	117.29	-2.09	-2.24	1.07	609

hsa-miR-6508-3p	TGGGCCATGCATTTCTAGAACT	135.66	114.50	64.37	-2.09	-1.77	-1.18	306
Novel #333	TCTCTGCCGGCTTGATGGGCTAGC	164.11	131.30	77.60	-2.10	-1.68	-1.25	363
has-miR-1468	CTCCGTTTGCCTGTTTCGCTG	133.48	105.04	59.97	-2.21	-1.74	-1.27	290
hsa-mir-10a.iso1	ACCCTGTAGATCCGAATTTGTG	295988.08	194267.94	131798.17	-2.25	-1.47	-1.52	622054.19
hsa-miR-6500-3p	ACACTTGTGGGATGACCTGC	275.71	191.18	119.05	-2.30	-1.60	-1.44	569
hsa-miR-10a	TACCCTGTAGATCCGAATTTGTG	1435203.78	942025.60	621943.60	-2.31	-1.51	-1.52	2913882
hsa-miR-100	AACCCGTAGATCCGAACTTGTG	838053.76	608920.42	362352.60	-2.31	-1.68	-1.38	1756589
hsa-miR-137	TTATTGCTTAAGAATACGCGTAG	529.53	419.12	223.11	-2.37	-1.87	-1.26	1136
hsa-miR-181a-2*	ACCACTGACCGTTGACTGTACC	20226.11	18849.80	8401.35	-2.41	-2.24	-1.07	45959
hsa-miR-375	TTTGTTTCGTTCCGGCTCGCGTGA	16394.67	14909.67	6790.22	-2.41	-2.20	-1.10	36879
hsa-miR-5010-5p/miRtron	AGGGGGATGGCAGACAAAATT	99.56	146.01	40.56	-2.42	-3.54	1.46	276
hsa-miR-5010-3p/miRtron	TTTTGTGTCTCCCATTCGCCAG	28.35	33.56	11.58	-2.43	-2.86	1.18	73.49
hsa-mir-181a.iso1	ACATTCACGCTGTCGGTGAG	2390.55	1255.25	970.03	-2.46	-1.29	-1.90	4615.83
hsa-miR-885-5p	TCCATTACACTACCCTGCCTCT	393.87	358.19	153.44	-2.56	-2.33	-1.10	875
hsa-miR-486-3p	CGGGGCAGCTCAGTACAGGAT	933.24	861.34	363.32	-2.56	-2.37	-1.08	2085
hsa-miR-129-5p	CTTTTTGCGGTCTGGGCTTGC	913.55	1569.33	347.45	-2.62	-4.51	1.72	2723
hsa-mir-375.iso1	TTGTTCGTTCCGGCTCGCGTGA	444.19	373.95	158.73	-2.80	-2.36	-1.19	976.88
hsa-miR-483-3p	TCACTCCTCTCCTCCCGTCTT	159.73	87.18	53.79	-2.93	-1.61	-1.82	290
hsa-miR-6510-3p/miRtron	CACCGACTCTGTCTCCTGCAG	3080.91	2169.12	1057.33	-2.94	-2.04	-1.43	6080
hsa-mir-486.iso1	CCTGTAAGGCTGCCCCGAG	797.58	486.34	264.55	-3.01	-1.84	-1.64	1548.48
hsa-miR-6721-5p/miRtron	TGGGCAGGGGCTTATTGTAGGA	34.92	20.96	10.70	-3.23	-1.96	-1.67	66.58
hsa-mir-100.iso1	ACCCGTAGATCCGAACTTGT	5351.11	2860.30	1566.16	-3.42	-1.83	-1.87	9777.56
hsa-miR-5089-5p	TGGGATTTCTGAGTAGCATCC	143.32	141.81	37.04	-3.79	-3.75	-1.01	308
hsa-miR-548az-5p	AAAAGTGATTGTGGTTTTTGTCT	212.25	192.23	50.27	-4.16	-3.77	-1.10	434
hsa-miR-675*	CTGTATGCCCTCACCGCTCA	387.30	173.32	86.42	-4.44	-1.99	-2.23	617
hsa-miR-124	TAAGGCACGCGGTGAATGCC	2829.27	1455.88	481.49	-5.87	-3.02	-1.94	4518
hsa-miR-4490	TCTGGTAAGAGATTTGGGCAT	184.90	138.66	22.05	-8.07	-6.06	-1.33	326

<sup>3</sup>Normal skin, NN; psoriatic uninvolved skin, PN; psoriatic Involved skin, PP.