

**Supplementary Table 2.** Statistical univariate analysis with patient paired design for before and after liraglutide treatment

Gene	Base mean	Log <sub>2</sub> fold change (lfc)	SE (lfc)	P value	P adj. value (BH)
hsa-miR-142-5p	912	0.375	0.102	0.000	0.042
hsa-miR-423-3p	581	-0.452	0.132	0.001	0.057
hsa-miR-320a-3p	2,455	-0.287	0.096	0.003	0.126
hsa-miR-126-5p	2,285	0.352	0.117	0.003	0.126
hsa-miR-19a-3p	139	0.435	0.148	0.003	0.126
hsa-miR-29b-3p	172	0.333	0.121	0.006	0.182
hsa-miR-23b-3p	156	-0.343	0.130	0.008	0.196
hsa-miR-19b-3p	760	0.391	0.147	0.008	0.196
hsa-miR-1307-3p	701	-0.349	0.137	0.011	0.227
hsa-miR-185-3p	62	-0.328	0.137	0.017	0.248
hsa-miR-484	1,077	-0.263	0.107	0.014	0.248
hsa-miR-150-5p	6,871	0.214	0.090	0.017	0.248
hsa-miR-375-3p	191	0.398	0.166	0.017	0.248
hsa-miR-320b	60	-0.288	0.125	0.021	0.278
hsa-miR-181a-5p	347	-0.219	0.096	0.022	0.278
hsa-miR-425-5p	2,884	-0.243	0.109	0.025	0.284
hsa-miR-206	104	0.427	0.190	0.025	0.284
hsa-miR-182-5p	667	0.344	0.158	0.029	0.307
hsa-miR-1260b	29	-0.629	0.292	0.031	0.313
hsa-miR-181a-2-3p	48	-0.317	0.155	0.041	0.371
hsa-miR-423-5p	10,687	-0.180	0.087	0.040	0.371
hsa-miR-3615	696	-0.197	0.098	0.045	0.386
hsa-miR-101-3p	2,449	0.313	0.160	0.050	0.400
hsa-miR-16-5p	294,166	0.339	0.177	0.055	0.400
hsa-miR-148a-3p	2,294	0.254	0.132	0.055	0.400
hsa-miR-7-5p	297	0.294	0.151	0.052	0.400
hsa-miR-335-5p	233	0.245	0.130	0.059	0.414
hsa-miR-194-5p	417	0.277	0.148	0.061	0.414
hsa-miR-22-3p	665	-0.215	0.119	0.070	0.457
hsa-miR-320d	62	-0.233	0.146	0.109	0.478
hsa-miR-320c	216	-0.213	0.130	0.100	0.478
hsa-miR-652-3p	44	-0.276	0.158	0.081	0.478
hsa-miR-485-5p	31	-0.390	0.229	0.089	0.478
hsa-miR-222-3p	99	-0.158	0.098	0.106	0.478
hsa-miR-221-3p	1,472	-0.270	0.160	0.090	0.478
hsa-miR-93-5p	8,457	0.169	0.107	0.113	0.478
hsa-miR-301a-3p	36	0.251	0.142	0.076	0.478
hsa-miR-15b-3p	43	0.223	0.141	0.112	0.478
hsa-miR-486-3p	152	-0.221	0.135	0.100	0.478
hsa-miR-29c-3p	657	0.190	0.118	0.108	0.478
hsa-miR-339-5p	374	-0.261	0.161	0.106	0.478

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**Supplementary Table 2.** Continued

Gene	Base mean	Log <sub>2</sub> fold change (lfc)	SE (lfc)	P value	P adj. value (BH)
hsa-let-7g-5p	2,603	0.190	0.115	0.097	0.478
hsa-miR-30c-5p	180	-0.142	0.089	0.111	0.478
hsa-miR-30e-5p	3,926	0.152	0.087	0.078	0.478
hsa-miR-26b-5p	4,655	0.156	0.097	0.107	0.478
hsa-miR-501-3p	64	-0.190	0.122	0.120	0.481
hsa-miR-378a-3p	184	-0.229	0.146	0.118	0.481
hsa-miR-20b-5p	274	0.242	0.156	0.122	0.481
hsa-miR-4433b-5p	844	-0.336	0.219	0.125	0.485
hsa-miR-107	108	-0.172	0.113	0.130	0.492
hsa-miR-4508	151	-0.196	0.131	0.133	0.492
hsa-miR-1301-3p	90	-0.338	0.226	0.135	0.492
hsa-let-7d-5p	1,340	-0.158	0.109	0.147	0.508
hsa-miR-744-5p	823	-0.249	0.171	0.145	0.508
hsa-miR-584-5p	518	-0.195	0.134	0.146	0.508
hsa-miR-32-5p	74	0.235	0.166	0.157	0.533
hsa-miR-100-5p	51	-0.272	0.203	0.181	0.534
hsa-miR-130a-3p	129	0.160	0.119	0.180	0.534
hsa-miR-532-3p	97	-0.156	0.115	0.175	0.534
hsa-miR-193b-5p	79	-0.281	0.209	0.180	0.534
hsa-miR-126-3p	20,400	0.140	0.102	0.171	0.534
hsa-miR-30d-5p	11,516	-0.123	0.091	0.175	0.534
hsa-miR-142-3p	2,613	-0.168	0.126	0.183	0.534
hsa-miR-27a-3p	251	0.139	0.103	0.177	0.534
hsa-miR-2110	79	-0.145	0.107	0.175	0.534
hsa-miR-18a-5p	58	0.171	0.133	0.197	0.554
hsa-miR-3613-5p	145	0.222	0.171	0.194	0.554
hsa-miR-361-5p	274	-0.133	0.104	0.198	0.554
hsa-miR-15a-5p	488	0.177	0.142	0.214	0.589
hsa-miR-106b-3p	366	-0.164	0.136	0.229	0.605
hsa-miR-92a-3p	32,206	-0.159	0.132	0.228	0.605
hsa-miR-1180-3p	91	-0.184	0.152	0.226	0.605
hsa-miR-99a-5p	116	-0.168	0.149	0.258	0.624
hsa-miR-671-5p	38	-0.184	0.167	0.270	0.624
hsa-miR-30e-3p	46	0.138	0.126	0.272	0.624
hsa-miR-151a-5p	86	-0.154	0.141	0.272	0.624
hsa-miR-127-3p	250	-0.248	0.221	0.260	0.624
hsa-let-7e-5p	309	-0.166	0.150	0.270	0.624
hsa-miR-190a-5p	66	-0.181	0.156	0.247	0.624
hsa-miR-24-3p	1,535	-0.115	0.101	0.256	0.624
hsa-miR-134-5p	170	-0.190	0.170	0.263	0.624
hsa-miR-197-3p	315	-0.136	0.117	0.244	0.624
hsa-miR-133a-3p	43	0.212	0.180	0.240	0.624

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Supplementary Table 2. Continued

Gene	Base mean	Log <sub>2</sub> fold change (lfc)	SE (lfc)	P value	P adj. value (BH)
hsa-miR-941	127	0.090	0.084	0.285	0.629
hsa-miR-342-3p	4,810	0.104	0.098	0.284	0.629
hsa-miR-629-5p	223	-0.126	0.117	0.284	0.629
hsa-miR-21-5p	2,494	-0.090	0.088	0.304	0.639
hsa-miR-942-5p	68	0.127	0.124	0.303	0.639
hsa-miR-185-5p	2,181	0.115	0.112	0.306	0.639
hsa-miR-193a-5p	357	-0.156	0.150	0.299	0.639
hsa-miR-4732-5p	281	0.164	0.159	0.303	0.639
hsa-miR-1908-5p	41	-0.199	0.197	0.313	0.646
hsa-miR-17-5p	210	0.117	0.122	0.339	0.693
hsa-miR-30b-5p	34	0.145	0.154	0.345	0.698
hsa-miR-421	48	0.129	0.138	0.350	0.700
hsa-miR-379-5p	54	-0.201	0.220	0.361	0.715
hsa-miR-93-3p	85	-0.111	0.125	0.374	0.732
hsa-miR-192-5p	790	0.128	0.147	0.384	0.745
hsa-miR-224-5p	338	-0.178	0.209	0.395	0.746
hsa-miR-125a-5p	3,997	-0.087	0.103	0.399	0.746
hsa-miR-205-5p	54	-0.136	0.161	0.400	0.746
hsa-miR-431-5p	104	-0.186	0.219	0.394	0.746
hsa-miR-99b-5p	563	-0.104	0.128	0.415	0.758
hsa-miR-10b-5p	411	-0.081	0.101	0.423	0.758
hsa-miR-183-5p	331	0.129	0.160	0.419	0.758
hsa-miR-92b-3p	73	-0.122	0.150	0.418	0.758
hsa-miR-1306-5p	193	0.108	0.139	0.438	0.770
hsa-miR-223-5p	235	0.094	0.122	0.438	0.770
hsa-miR-363-3p	210	-0.103	0.147	0.484	0.771
hsa-miR-103a-3p	4,978	-0.082	0.113	0.470	0.771
hsa-miR-25-3p	9,941	0.094	0.125	0.455	0.771
hsa-miR-323b-3p	29	-0.175	0.255	0.491	0.771
hsa-miR-326	95	-0.187	0.264	0.479	0.771
hsa-miR-328-3p	1,126	-0.110	0.147	0.455	0.771
hsa-miR-485-3p	220	0.164	0.224	0.464	0.771
hsa-miR-145-5p	64	0.112	0.147	0.447	0.771
hsa-miR-140-3p	1,009	0.108	0.151	0.474	0.771
hsa-miR-454-3p	214	0.135	0.183	0.461	0.771
hsa-miR-148b-3p	574	0.066	0.095	0.491	0.771
hsa-miR-152-3p	133	0.092	0.133	0.486	0.771
hsa-miR-486-5p	153,091	-0.099	0.133	0.454	0.771
hsa-let-7i-5p	11,533	0.061	0.090	0.500	0.772
hsa-miR-1-3p	50	0.148	0.219	0.498	0.772
hsa-miR-576-5p	65	0.089	0.139	0.525	0.779

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Supplementary Table 2. Continued

Gene	Base mean	Log <sub>2</sub> fold change (lfc)	SE (lfc)	P value	P adj. value (BH)
hsa-miR-191-5p	9,192	0.098	0.153	0.522	0.779
hsa-miR-199a-5p	58	-0.109	0.171	0.522	0.779
hsa-miR-345-5p	75	-0.107	0.167	0.521	0.779
hsa-miR-769-5p	37	-0.141	0.218	0.520	0.779
hsa-miR-432-5p	580	-0.118	0.189	0.532	0.783
hsa-miR-574-3p	166	0.081	0.140	0.561	0.808
hsa-miR-532-5p	249	0.079	0.137	0.562	0.808
hsa-miR-370-3p	88	-0.106	0.182	0.561	0.808
hsa-miR-196b-5p	73	0.085	0.150	0.573	0.812
hsa-miR-339-3p	50	0.099	0.176	0.572	0.812
hsa-miR-1246	191	-0.059	0.116	0.612	0.820
hsa-miR-382-5p	424	-0.089	0.177	0.614	0.820
hsa-miR-625-3p	448	-0.085	0.171	0.619	0.820
hsa-miR-144-3p	187	0.088	0.177	0.622	0.820
hsa-miR-660-5p	413	-0.058	0.111	0.599	0.820
hsa-miR-483-3p	323	0.086	0.163	0.600	0.820
hsa-let-7a-5p	22,856	-0.078	0.147	0.593	0.820
hsa-miR-223-3p	23,375	0.074	0.141	0.602	0.820
hsa-miR-340-5p	58	0.085	0.170	0.619	0.820
hsa-miR-26a-5p	4,602	0.054	0.100	0.590	0.820
hsa-miR-331-3p	28	0.095	0.201	0.636	0.833
hsa-miR-885-3p	51	-0.131	0.286	0.648	0.835
hsa-miR-20a-5p	584	0.060	0.131	0.647	0.835
hsa-miR-11400	31	-0.115	0.258	0.655	0.835
hsa-miR-30a-5p	652	0.054	0.121	0.654	0.835
hsa-miR-324-5p	155	-0.045	0.108	0.675	0.853
hsa-miR-15b-5p	337	0.035	0.085	0.678	0.853
hsa-miR-181b-5p	76	-0.043	0.109	0.691	0.861
hsa-miR-23a-3p	1,345	-0.038	0.104	0.716	0.861
hsa-miR-186-5p	438	0.036	0.105	0.729	0.861
hsa-miR-28-3p	490	-0.046	0.135	0.734	0.861
hsa-miR-29a-3p	863	0.040	0.115	0.728	0.861
hsa-miR-628-3p	47	-0.061	0.164	0.710	0.861
hsa-let-7f-5p	9,320	-0.056	0.162	0.732	0.861
hsa-let-7c-5p	788	-0.053	0.142	0.707	0.861
hsa-miR-34a-5p	117	-0.071	0.205	0.730	0.861
hsa-miR-374a-5p	62	0.055	0.157	0.725	0.861
hsa-miR-27b-3p	685	0.053	0.137	0.696	0.861
hsa-miR-143-3p	760	0.042	0.138	0.759	0.884
hsa-miR-10a-5p	425	-0.027	0.091	0.764	0.885
hsa-miR-199a-3p	2,453	0.038	0.136	0.778	0.894

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Supplementary Table 2. Continued

Gene	Base mean	Log <sub>2</sub> fold change (lfc)	SE (lfc)	P value	P adj. value (BH)
hsa-miR-98-5p	161	-0.037	0.134	0.782	0.894
hsa-miR-483-5p	539	0.039	0.161	0.806	0.899
hsa-miR-664a-5p	86	0.033	0.139	0.811	0.899
hsa-miR-409-3p	648	-0.053	0.204	0.795	0.899
hsa-miR-144-5p	106	0.044	0.184	0.813	0.899
hsa-miR-365a-3p	38	-0.064	0.262	0.808	0.899
hsa-miR-361-3p	413	-0.026	0.111	0.814	0.899
hsa-miR-139-3p	209	-0.030	0.138	0.827	0.909
hsa-miR-324-3p	46	0.033	0.165	0.840	0.912
hsa-miR-155-5p	370	-0.027	0.132	0.837	0.912
hsa-let-7d-3p	359	0.017	0.104	0.874	0.938
hsa-miR-654-3p	94	-0.036	0.226	0.873	0.938
hsa-miR-425-3p	94	0.023	0.161	0.885	0.944
hsa-miR-451a	6,659	0.015	0.146	0.918	0.957
hsa-miR-151a-3p	2,367	0.011	0.122	0.926	0.957
hsa-miR-4732-3p	238	0.013	0.149	0.932	0.957
hsa-miR-128-3p	516	-0.011	0.092	0.909	0.957
hsa-let-7b-5p	34,576	0.010	0.118	0.931	0.957
hsa-miR-122-5p	62,092	-0.021	0.212	0.922	0.957
hsa-miR-96-5p	90	0.023	0.202	0.907	0.957
hsa-miR-4454	44	0.005	0.176	0.977	0.989
hsa-miR-146b-5p	375	0.004	0.139	0.978	0.989
hsa-miR-146a-5p	6,025	0.005	0.147	0.971	0.989
hsa-miR-381-3p	33	0.003	0.221	0.991	0.992
hsa-miR-125b-5p	1,570	-0.001	0.120	0.992	0.992

MiRNAs with a mean total read count  $\geq 50$  were used as input for fitting a patient paired design model (design: patient+gender+cardiovascular disease background+treatment). Differential expression was set to an absolute value of fold change  $> 1.5$  and the Benjamini-Hochberg (BH) adjusted  $P < 0.05$ .

SE, standard error.