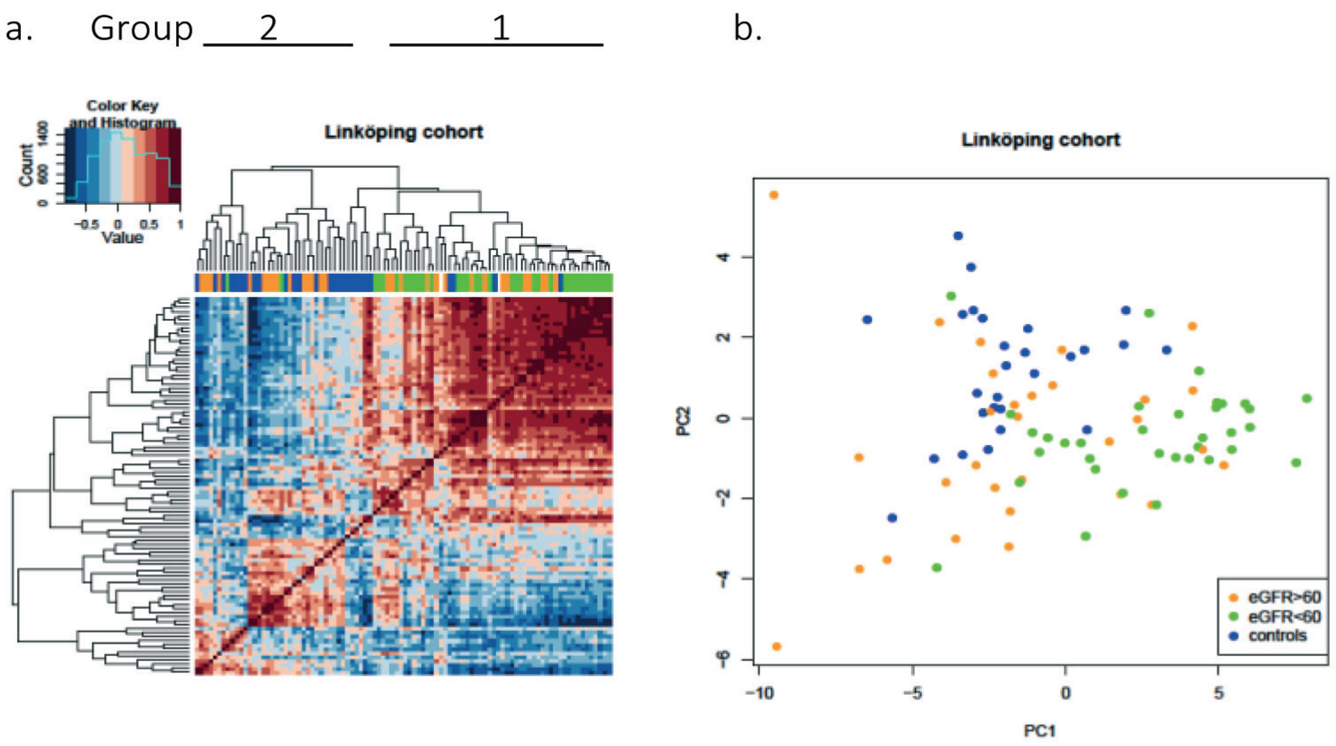
Supplementary Table I. The 35 miRNAs included in the PCR panel, as well as miRBase ID, TaqMan microRNA Assay ID and mature sequence for each miRNA.

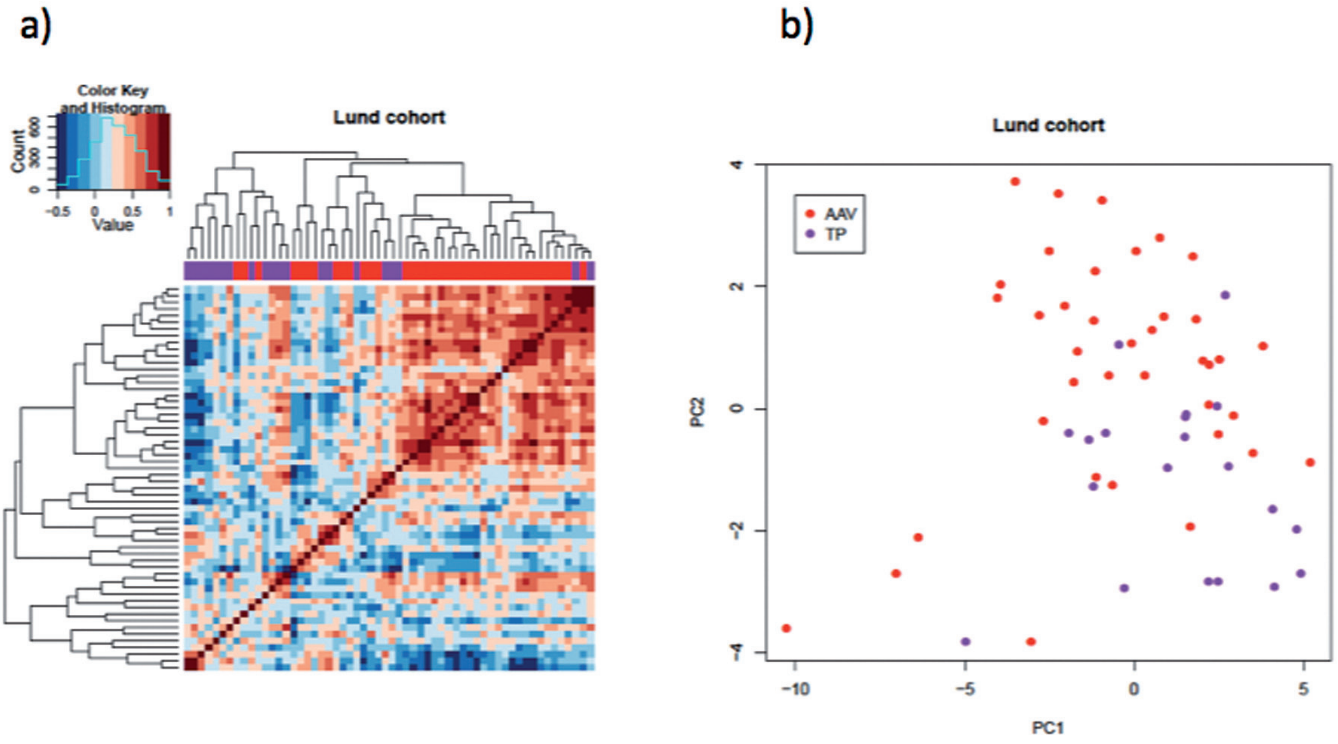
miRNA	miRBase ID	Assay ID	Mature microRNA sequence
hsa-miR-15a	hsa-miR-15a-5p	000389	UAGCAGCACAUAAUGGUUUGUG
hsa-miR-16	hsa-miR-16-5p	000391	UAGCAGCACGUAAAUAUUGGCG
hsa-miR-17	hsa-miR-17-5p	002308	CAAAGUGCUUACAGUGCAGGUAGU
hsa-miR-20a	hsa-miR-20a-5p	000580	UAAAGUGCUUAUAGUGCAGGUAG
hsa-miR-21	hsa-miR-21-5p	000397	UAGCUUAUCAGACUGAUGUUGA
hsa-miR-24	hsa-miR-24-3p	000402	UGGCUCAGUUCAGCAGGAACAG
hsa-miR-29a	hsa-miR-29a-3p	002112	UAGCACCAUCUGAAAUCGGUUA
hsa-miR-34a	hsa-miR-34a-5p	000426	UGGCAGUGUCUUAGCUGGUUGU
hsa-miR-92a	hsa-miR-92a-3p	000431	UAUUGCACUUGUCCCGGCCUGU
hsa-miR-101	hsa-miR-101-3p	002253	UAACAGUACUGUGAUAACUGAA
hsa-miR-106a	hsa-miR-106a-5p	002169	AAAAGUGCUUACAGUGCAGGUAG
hsa-miR-125a-3p	hsa-miR-125a-3p	002199	ACAGGUGAGGUUCUUGGGAGCC
hsa-miR-132	hsa-miR-132-3p	000457	UAACAGUCUACAGCCAUGGUCG
hsa-miR-141	hsa-miR-141-3p	000463	UAACACUGUCUGGUAAAGAUGG
hsa-miR-142-3p	hsa-miR-142-3p	000464	UGUAGUGUUUCCUACUUUAUGGA
hsa-miR-146a	hsa-miR-146a-5p	000468	UGAGAACUGAAUUCCAUGGGUU
hsa-miR-146b	hsa-miR-146b-5p	001097	UGAGAACUGAAUUCCAUAGGCU
hsa-miR-150	hsa-miR-150-5p	000473	UCUCCCAACCCUUGUACCAGUG
hsa-miR-155	hsa-miR-155-5p	002623	UUAAUGCUAAUCGUGAUAGGGGU
hsa-miR-181b	hsa-miR-181b-5p	001098	AACAUUCAUUGCUGUCGGUGGG
hsa-miR-184	hsa-miR-184	000485	UGGACGGAGAACUGAUAAGGGU
hsa-miR-196a	hsa-miR-196a-5p	241070_mat	UAGGUAGUUUCAUGUUGUUGGG
hsa-miR-203	hsa-miR-203a	000507	GUGAAAUGUUUAGGACCACUAG
hsa-miR-221	hsa-miR-221-3p	000524	AGCUACAUUGUCUGCUGGGUUUC
hsa-miR-223	hsa-miR-223-3p	002295	UGUCAGUUUGUCAAAUACCCCA
hsa-miR-342-3p	hsa-miR-342-3p	002260	UCUCACACAGAAAUCGCACCCGU
hsa-miR-346	hsa-miR-346	000553	UGUCUGCCCGCAUGCCUGCCUCU
hsa-miR-363	hsa-miR-363-3p	001271	AAUUGCACGGUAAUCCAUCUGUA
hsa-miR-383	hsa-miR-383-5p	000573	AGAUCAGAAGGUGAUUGUGGCU
hsa-miR-409-3p	hsa-miR-409-3p	002332	GAAUGUUGCUCGGUGAACCCCU
hsa-miR-423-5p	hsa-miR-423-5p	002340	UGAGGGGCAGAGAGCGAGACUUU
hsa-miR-638	hsa-miR-638	001582	AGGGAUCGCGGGCGGGUGGCGGCCU
cel-miR-39	cel-miR-39-3p	000200	UCACCGGGUGAAAUCAGCUUG
cel-miR-54	cel-miR-54-3p	001361	UACCCGUAAUCUUCAUAAUCCGAG
cel-miR-238	cel-miR-238-3p	000248	UUUGUACUCCGAUGCCAUUCAGA

Supplementary Table II. P-values and fold changes for the 32 miRNAs for all patients, including those with an active disease state, in the Linköping and Lund cohorts. Values marked in yellow had a *p*-value below 0.05 in an unpaired *t*-test, red indicates significant up-regulation and green significant down-regulation. The 7 miRNAs that were consistently up- or down-regulated in both cohorts are shown in boldface.

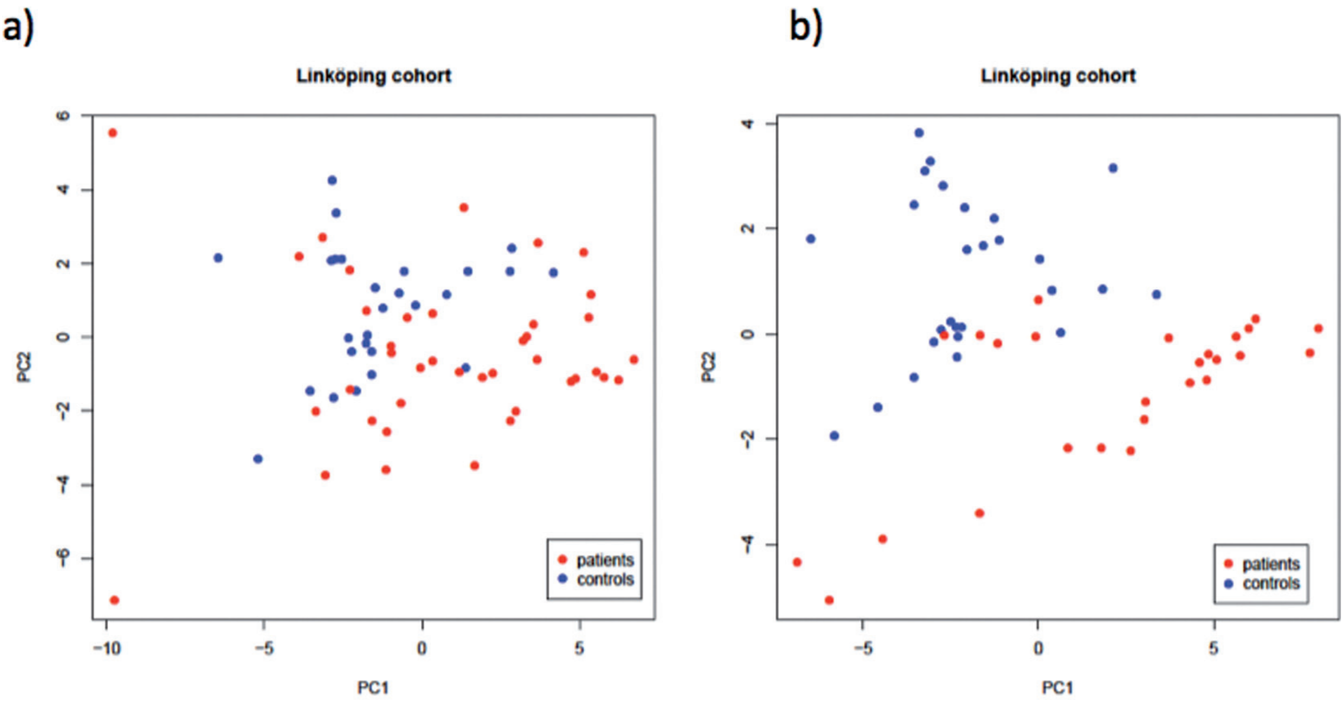
	Linköping cohort		Lund cohort	
miRNA	**p-value**	**Fold change**	**p-value**	**Fold change**
hsa-miR-142-3p	9.76E-13	1.81	0.0084	1.33
hsa-miR-16	1.02E-11	0.36	0.2056	0.81
hsa-miR-181b	2.24E-10	2.56	6.49E-05	0.27
hsa-miR-20a	7.55E-08	0.56	0.0001	0.71
hsa-miR-184	5.60E-06	1.39	0.1622	0.70
hsa-miR-146b	1.99E-05	1.40	0.8538	1.02
hsa-miR-223	4.83E-05	1.47	0.5719	0.93
hsa-miR-17	8.41E-05	0.61	4.77E-05	1.54
hsa-miR-106a	0.0001	0.62	1.76E-05	1.60
hsa-miR-92a	0.0005	0.74	1.96E-07	0.36
hsa-miR-203	0.0020	0.51	0.4220	0.92
hsa-miR-29a	0.0039	1.36	0.0350	1.56
hsa-miR-34a	0.0132	1.31	0.0008	2.08
hsa-miR-383	0.0245	1.20	2.53E-08	1.86
hsa-miR-221	0.0312	0.64	2.41E-06	0.38
hsa-miR-101	0.0422	0.62	0.6084	0.86
hsa-miR-342-3p	0.0677	0.86	0.1916	0.86
hsa-miR-141	0.0786	1.59	0.0003	2.24
hsa-miR-132	0.0801	2.21	0.0869	0.64
hsa-miR-150	0.0840	1.15	0.0041	1.26
hsa-miR-15a	0.0922	1.23	2.36E-12	2.20
hsa-miR-125a-3p	0.0923	1.21	0.0959	0.65
hsa-miR-409-3p	0.1014	1.19	0.9658	1.00
hsa-miR-155	0.1883	1.15	0.2655	1.11
hsa-miR-346	0.2100	1.65	0.9791	0.99
hsa-miR-363	0.3293	1.21	0.6260	1.08
hsa-miR-24	0.3323	0.89	0.1841	0.87
hsa-miR-423-5p	0.5676	0.93	0.0153	0.61
hsa-miR-21	0.6962	1.04	0.0630	0.58
hsa-miR-638	0.7039	0.97	0.0001	0.59
hsa-miR-146a	0.7201	0.95	0.0010	0.53
hsa-miR-196a	0.9673	0.99	0.0002	2.19



Supplementary Fig. 1. Correlation plot with hierarchic clustering for the Linköping cohort (**a**), where patients with estimated glomerular filtration rate (eGFR) <60 (green) cluster (in the group 1 area) while patients with eGFR>60 (orange) do not. In (**b**) a principal component analysis plot is shown, also indicating clustering of patients with low eGFR. Healthy controls are marked in blue in the band below the dendrogram.



Supplementary Fig. 2. Correlation plot with hierarchical clustering (**a**) and principal component analysis (**b**) for AAV patients (shown in red in the band below the dendrogram) and kidney transplanted patients (TP, purple) in the Lund cohort.



Supplementary Fig. 3. Principal component analysis for PR3-ANCA positive (**a**) and MPO-ANCA positive (**b**) patients together with healthy controls from the Linköping cohort.