Supplementary Table S1. Summary of the lower quality micro-RNA studies.

Publication details and reference	Study population	Epigenetic data: mechanism studied and coverage	Results: Key findings	Repeated epigenetic measures	Replication	JBI percentage and risk of bias
Micro-RNAs - blood						
Sui, W et al. Iranian journal of Kidney Diseases, 2014. [45]	Aged > 18 years MPGN 10; MCD 10; Membranous 10; FSGS 10; Healthy controls 16.	Micro-RNA – blood MiR-181a, miR-483-5p, and miR-557 primer assays.	MiR-181a was significantly upregulated in patients with MCD, MPGN, Membranous and FSGS compared to healthy controls (fold change 19.17, 20.09, 20.20 and 32.92 respectively, all $p < 0.05$). There was no difference in miR-483-5p and miR-557 between people with NS and controls.	No	No	60% Moderate risk
Teng, J et al. International Journal of Clinical & Experimental Pathology, 2015. [46]	No specific age restrictions. NS 25; Healthy controls 20.	Micro-RNA – blood TaqMan Low density Array - 754 human miRNAs.	Participants with NS had higher expression of 35 miRNAs and lower expression of 24 miRNAs. Six of these miRNAs were confirmed with real-time PCR ($p<0.05$) and had fold changes $\geqslant 1.5$: miR-181a, miR-210, miR-30a, miR-942, miR-192 and miR-586.	No	No	20% High risk
Zapata-Benavides, P et al. BioMed Research International, 2017. [47]	No specific age restrictions, only children included. NS 21; Healthy controls 10.	Micro-RNA – serum MiR-15a, miR-16-1, and miR-193a primer assays.	MiR-16-1 was downregulated in NS compared to healthy controls (relative expression 0.54 compared to 1.86, p=0.019).	No	No	60% Moderate risk
Micro-RNAs – urine						
Huang, Z et al. BioMed Research International, 2017. [48]	Aged < 18 years MCD 5; FSGS 8.	Micro-RNA – urinary exosomes MiR-193a primer assay	MiR-193a levels were significantly higher in FSGS compared to MCD (1376 versus 386.3, $p <0.05$).	No	No	60% Moderate risk
Wang, L et al. Frontiers in Cell and Developmental Biology, 2021. [49]	No specific age restrictions, only children included. FSGS (non-monogenic) 8; IgAN 7; MCD 5; Healthy controls 5.	Micro-RNA – urinary exosomes MiR-193a primer assay	MiR-193a levels were significantly higher in FSGS compared to people with IgAN, MCD and healthy controls (1060.4, 423.7, 381.9 and 163.6 respectively, all $p < 0.05$). For people with FSGS, miR-193a levels positively correlated with glomerulosclerosis index ($R^2 = 0.795$, $p < 0.05$).	No	No	50% Moderate risk
Konta, T et al. Clinical & Experimental Nephrology, 2014. [50]	Aged > 18 years MCD 5; IgAN 46; CrGN 9; DN 11; Healthy controls 5.	Micro-RNA – urine Agilent human miRNA array 16.0 - 1257 human miRNAs.	The concentration of total urinary micro-RNAs were increased in patients with renal disease compared to healthy controls (median values mg/gCr: 3.6 in the healthy controls, 5.5 in the MCNS patients, 6.3 in the IgAN patients ($p <0.05$), 9.1 in the CrGN patients ($p <0.05$) and 13.0 in the DMN patients ($p <0.05$). Total urinary micro-RNA concentration was correlated with proteinuria ($R^2 = 0.42$, $p < 0.01$). The microarray analysis detected 39 micro-RNAs that were 100 times greater in renal disease groups than healthy controls. Of these, higher levels of miR-574-3p were detected in all 4 types of renal disease.	No	No	60% Moderate risk
Wang, G et al. Clinica Chimica Acta, 2013. [51]	No specific age restrictions, only adults included. MCD or FSGS 21; Diabetic glomerulosclerosis 20; Membranous 23; Healthy controls 10.	Micro-RNA – urine MiR-21, miR-29a, miR-29b, miR-29c, miR-122, miR-141, miR-150, miR-184, miR-192, miR-198, miR-200a, miR-200b, miR-200c, miR-205, miR-375, miR-429 and miR-638 primer assays	MiR-192 levels were higher in patients with MCD, FSGS, Membranous and healthy controls compared to diabetic glomerulosclerosis (0.88, 0.84, 0.72 and 0.27 respectively, $p = 0.017$). MiR-200c levels were higher in MCD, FSGS and healthy controls and lower in diabetic glomerulosclerosis and membranous (1.63, 1.04, 0.43, 0.42 respectively, $p = 0.034$). In patients with MCD or FSGS, lower miR-184, miR-192, miR-200c and miR-275 expression correlated with lower eGFR ($R^2 = 0.55$, $p = 0.009$; $R^2 = 0.51$, $p = 0.019$; $R^2 = 0.52$, $p = 0.015$; $R^2 = 0.58$, $p = 0.006$ respectively).	No	No	60% Moderate risk

Micro-RNAs – renal tissue						
Baker, M et al. Journal of the American Society of Nephrology, 2017. [52]	No specific age restrictions - only adults included. DN 23; FSGS 19; IgAN 18; MPGN 19; Healthy controls 14. Validation cohort: DN 19; FSGS 21.	Micro-RNA - Renal - glomeruli and proximal tubules Illumina TruSeq small RNA - whole transcriptome.	Compared with control glomeruli, DN, FSGS, IgAN, and MPGN glomeruli exhibited differential expression of 18, 12, 2, and 17 known micro-RNAs, respectively. Compared with control or FSGS glomeruli, IgAN glomeruli exhibited downregulated expression of hsa-miR-3182. Compared with control proximal tubules, DN, FSGS, IgAN, and MPGN proximal tubules had differential expression of 13, 14, 8, and 8 micro-RNAs, respectively, but expression of micro-RNAs did not differ significantly between the disease groups.	No	Yes	40% High risk
Lu, M et al. Experimental & Molecular Pathology, 2015. [53]	No specific age restrictions - only children included. MPGN 22; MCD 8; ECPGN 11; FSGS 4; Membranous 3; Glomerular minor lesions 4; Healthy controls 8.	Micro-RNA – renal. MiR-191, miR-151-3p, miR-150, miR-30a-5p and miR-19b primer assays.	MiR-191 and miR-151-3p intrarenal levels were higher in all 6 kidney disease groups compared to healthy controls. MiR-19b levels were higher in membranous, MPGN and ECPGN (2.5-3 fold, $p < 0.05$]. MiR-30a-5p levels were lower in FSGS and glomerular minor lesions (0.25 and 0.5, $p < 0.05$). MiR-150 levels were lower in MPGN, MCD, FSGS and glomerular minor lesions (0.25-0.66, $p < 0.05$).	No	No	60% Moderate risk
Gebeshuber, C et al. Nature Medicine, 2013. [54]	No specific age restrictions - adults and children included. FSGS 48 (4 with pathogenic genetic variants, 4 with HIV); MCD 17; Membranous 10; IgAN 10; Healthy controls 5.	Micro-RNA – renal – glomeruli. MiR-193a primer assay and FISH.	MiR-193a was over expressed in glomeruli from individuals with FSGS compared to disease or healthy controls ($p<0.0001$).	No	No	60% Moderate risk
Yang, X et al. International Journal of Molecular Medicine, 2015. [55]	No specific age restrictions. FSGS 3; Healthy controls 3.	Micro-RNA – renal – glomeruli. MiR-135a and miR-135b primer assays.	MiR-135a and miR-135b levels were higher in FSGS glomeruli compared to healthy controls ($p < 0.01$).	No	No	50% Moderate risk
Yang, X et al. International Journal of Molecular Medicine, 2017. [56]	No specific age restrictions. FSGS 3; Healthy controls 3.	Micro-RNA – renal – glomeruli. MiR-135a primer assay.	Patients with FSGS had higher levels of miR-135a compared to healthy controls ($p<0.05$).	No	No	50% Moderate risk
Peng, R et al. International Journal of Molecular Sciences, 2015. [57]	No specific age restrictions. FSGS 1; Healthy control 1.	Micro-RNA – renal – glomeruli. MiR-30a primer assay.	Expression of miR-30a was lower in FSGS glomeruli compared to healthy control ($p<0.05$).	No	No	20% High risk
Muller-Deile, J et al. Kidney International, 2017. [58]	No specific age restrictions. FSGS 7; Membranous 9; MCD 6; IgAN 6; DN 7; Healthy controls 9.	Micro-RNA – renal – glomeruli. In situ hybridization for miR-378a-3p.	FSGS and membranous glomeruli had increased miR-378a-3p expression compared to healthy controls ($p<0.05$).	No	No	20% High risk
Wu, J et al. Journal of the American Society of Nephrology, 2014. [59]	No specific age restrictions - only adults included. FSGS 16; Healthy controls 6.	Micro-RNA – renal – glomeruli. MiR-30a, miR-30b, miR-30c, miR-30d, and miR-30e primer assays.	MiR-30a, miR-30b, miR-30c, miR-30d, and miR-30e levels were lower in FSGS glomeruli compared to healthy controls ($p<0.05$ for all micro-RNAs).	No	No	60% Moderate risk
Micro-RNAs – blood and urine						
Wang, N et al. PloS ONE, 2012. [60]	No specific age restrictions, only adults included. FSGS 16;	Micro-RNA – blood and urine. MiR-10a and miR-30d TaqMan probe assays	Urinary miR-10a and miR-30d levels were higher in FSGS patients compared to healthy controls ($p<0.01$).	No	No	70% Low risk

	Healthy controls 16.					

Abbreviations: Area under curve, AUC; crescentic glomerulonephritis, CrGN; diabetic nephropathy, DN; endocapillary proliferative glomerulonephritis, ECPGN; focal segmental glomerulosclerosis, FSGS; human immunodeficiency virus, HIV; IgA nephropathy, IgAN; JBI, Joanna Briggs Institute; membranoproliferative glomerulonephritis MPGN; minimal change disease, MCD; nephrotic syndrome NS; peripheral blood mononuclear cells, PBMCs.

Supplementary Table S2. Summary of the lower quality DNA methylation and small RNA studies.

Publication details and reference	Study population	Epigenetic data: mechanism studied and coverage	Results: Key findings	Repeated epigenetic measures	Replication	JBI percentage and risk of bias
DNA methylation						
Kobayashi, Y et al. BMC Research Notes, 2017. [61]	MCD patients aged < 16 years. MCD 6; Healthy controls 5.	DNAm – monocytes and naïve T helper cells. Microarray-based integrated analysis of methylation by isoschizomers (MIAMI) - genome wide.	In monocytes, there was differing DNAm between MCD relapse and remission (210 sites), MCD relapse and healthy controls (391 sites) and MCD remission and healthy controls (286 sites). In naïve T cells, there was differing DNAm between MCD relapse and remission (469 sites), MCD relapse and healthy controls (445 sites) and MCD remission and healthy controls (291 sites).	Yes - paired relapse and remission	No	80% Low risk
Zaorska, K et al. Journal of Translational Medicine, 2021. [62]	No specific age restrictions - only children included. SRNS 53; SSNS 71; Healthy controls 55.	DNAm – blood. CpG islands for SOCS3 and SOCS5 methylation primers.	SOCS3.2 promoter was 15-fold more frequently unmethylated in SRNS compared to SSNS ($p<0.0001$). The best performing steroid resistance prediction model included *ABCB1* rs1922240, rs1045642 and rs2235048, *CD73* rs9444348 and rs4431401, serum creatinine and unmethylated SOCS3 promoter region, AUC = 0.78.	No	No	60% Moderate risk
Kobayashi, Y et al. Pediatric Nephrology, 2012. [63]	Aged < 16 years. MCD 6 - monocytes, 4 of these - naïve T helper cells.	DNAm – monocytes and naïve T helper cells. MIAMI - genome wide.	Three gene loci (*GATA2*, *PBX4*, and *NYX*) were significantly less methylated in naïve T helper cells during MCD relapse compared to remission. There were no differences in DNAm in monocytes between MCD relapse and remission.	Yes – paired relapse and remission	No	50% Moderate risk
Histone modifications						
Zhang, L et al. American Journal of Nephrology, 2009. [64]	No specific age restrictions - only adults included. MCD 15; Healthy controls 15.	DNAm – PBMCs. UNH Human CpG Island Microarray (12,000 sites).	There were significant differences in H3K4me3 between people with MCD and healthy controls (848 increased probes and 231 decreased probes). There were positive correlations between mRNA and H3K4me3 levels and an inverse relationship between promoter DNAm and H3K4me3.	No	No	100% Low risk
Majumder, S et al. Journal of Clinical Investigation, 2018. [65]	Aged > 18 years. FSGS 10; DN 12; Healthy controls 21.	DNAm – glomeruli. H3K27me3 immunofluorescence	There was Increased H3K4me3 in FSGS and DN compared to healthy controls ($p<0.01$).	No	No	70% Low risk
Long non-coding RNA						
Han, R et al. Scientific Reports, 2019. [66]	Aged > 18 years. FSGS 5; Healthy controls 5.	LncRNA – tubules. Affymetrix HTA2.0 microarrays - whole transcriptome	LOC105375913 expression was increased in tubular cells of FSGS patients compared to healthy controls (fold change > 1.5 and false discovery rate adjusted p value < 0.05).	No	Yes	90% Low risk
Hu, S et al. Journal of Biological Chemistry, 2018. [67]	No specific age restrictions - only adults included. FSGS 5; Healthy controls 5.	LncRNA – glomeruli. Affymetrix HTA2.0 microarrays - whole transcriptome and in situ hydridization staining	LOC105374325 expression was increased in glomeruli of FSGS patients compared to healthy controls ($p <0.05$).	No	Yes	90% Low risk
Salazar-Torres, F et al. Biomedical Reports, 2021. [68]	No specific age restrictions - only adults included. FSGS 5; Lupus 3; ANCA vasculitis 1;	LncRNA – urine. LncRNA TUG1 primer assay	Urinary expression of long non-coding RNA taurine upregulated gene 1 was significantly lower in patients with renal disease ($p=0.015$), in particular FSGS ($p<0.01$), compared to healthy controls.	No	No	70% Low risk

	Advanced global sclerosis 1; Healthy controls 11.					
Xu, J et al. Medical Science Monito, 2020. [69]	No specific age restrictions - only children included. NS 30; Healthy controls 30.	Long non-coding RNA – PBMCs. H19 primer assay	LncRNA H19 expression was lower in PBMCs of children with NS compared to healthy controls ($p<0.001$).	No	No	30% High risk
Circular RNA						
Cui, X et al. Biochemical & Biophysical Research Communications, 2020. [70]	Aged > 18 years FSGS 6; Healthy controls 6.	Circular RNA – glomeruli. CircZNF609 FISH.	There was increased expression of circZNF609 in FSGS glomeruli compared to healthy glomeruli.	No	No	60% Moderate risk
Abbreviations: Area under curve, AUC; diabetic nephropathy, DN; DNA methylation, DNAm; fluorescence in situ hybridization, FISH;, focal segemental glomerulosclerosis, FSGS; IgA nephropathy, IgAN; JBI, Joanna Briggs Institute Long non-coding RNA (lncRNA; minimal change disease, MCD; membranoproliferative glomerulonephritis MPGN; nephrotic syndrome, NS; peripheral blood mononuclear cells, PBMCs; steroid resistant NS, SRNS; steroid sensitive NS, SSNS.						

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