

Supplementary Material

Global miRNA expression profile reveals novel molecular players in aneurysmal subarachnoid haemorrhage

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This PDF file includes 5 supplementary figures and 2 supplementary table:

Supplementary Figure S1: Correlation of miRNA expression by sample.

Supplementary Figure S2: Principal component analysis comprising aSAH patients and control individuals.

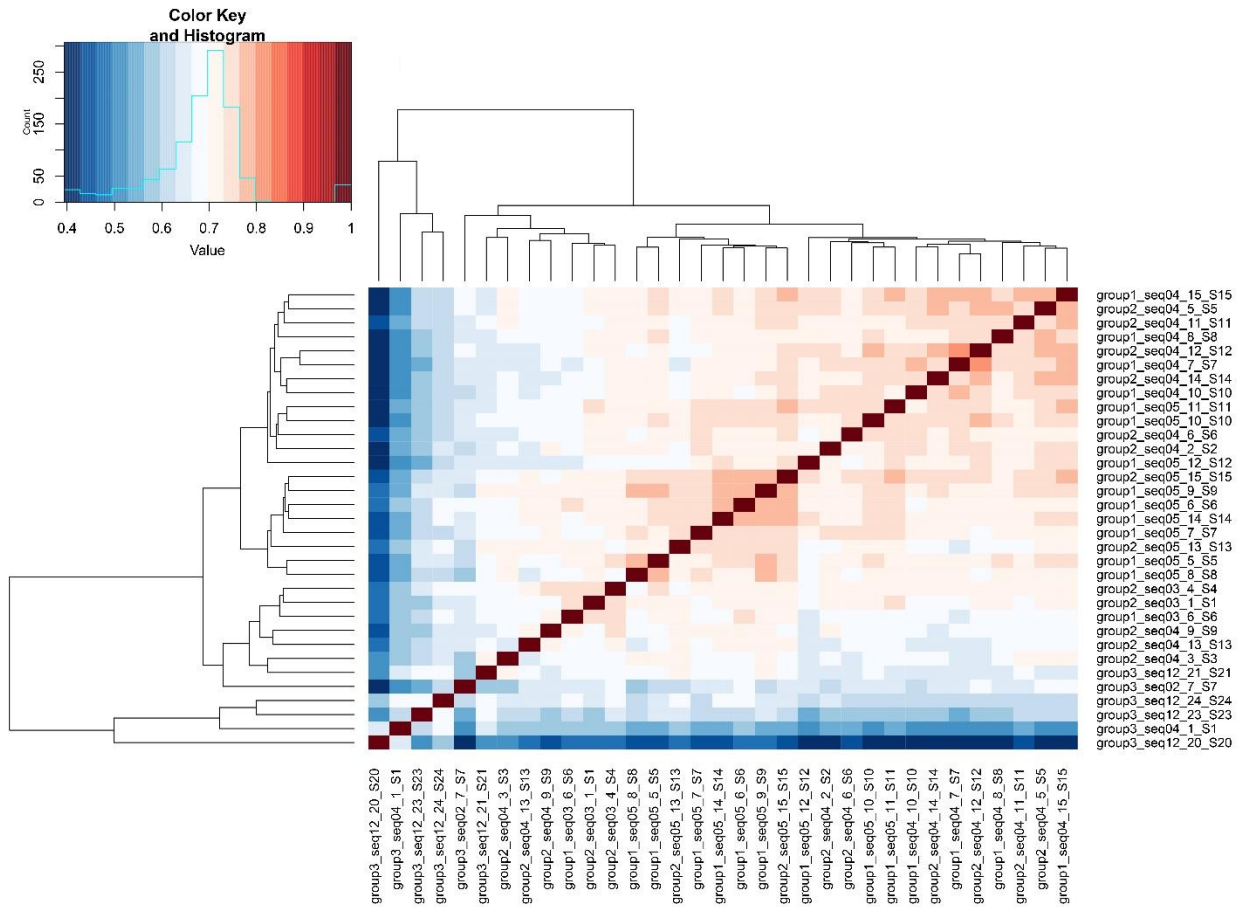
Supplementary Figure S3: Statistics of DE miRNAs between group1 and control.

Supplementary Figure S4: Statistics of DE miRNAs between group2 and control.

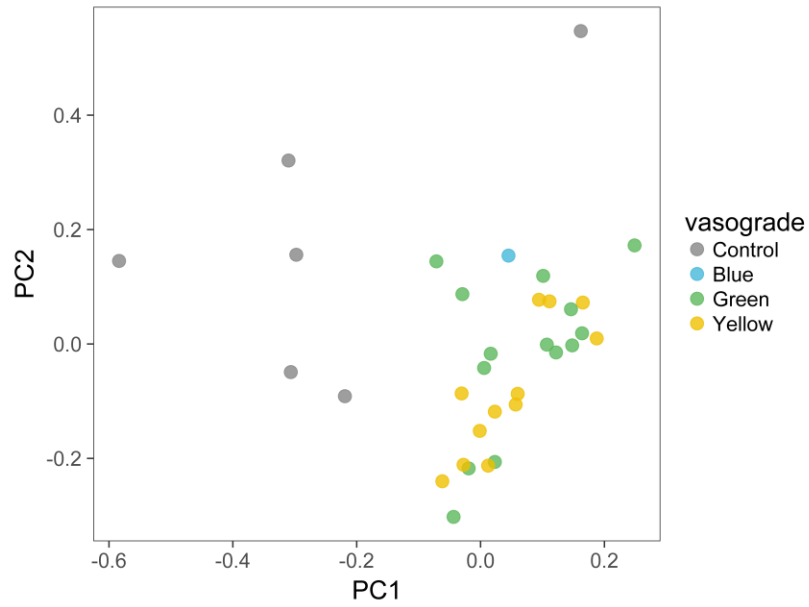
Supplementary Figure S5: Total number of reads mapped to novel miRNAs by sample.

Supplementary Table S1: Statistical power analysis for sample sizes.

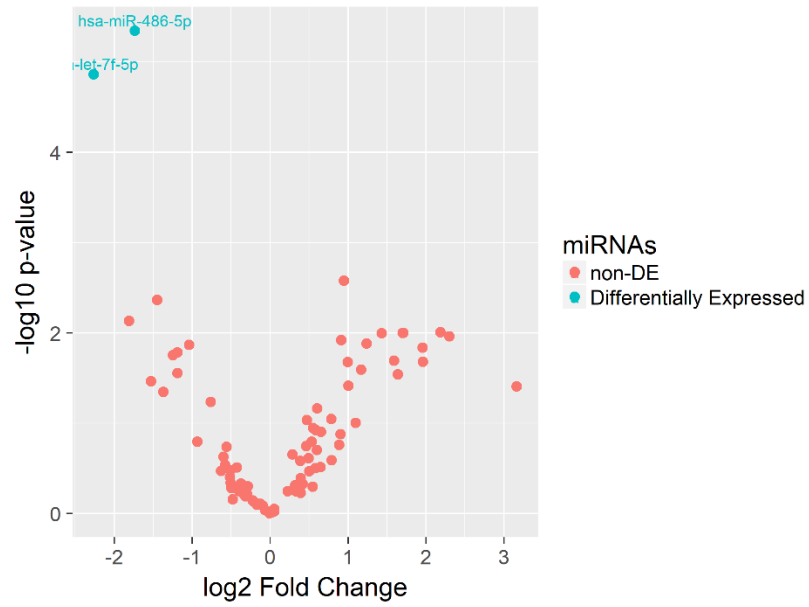
Supplementary Table S2: DE miRNAs between aSAH patients and control group from edgeR software.



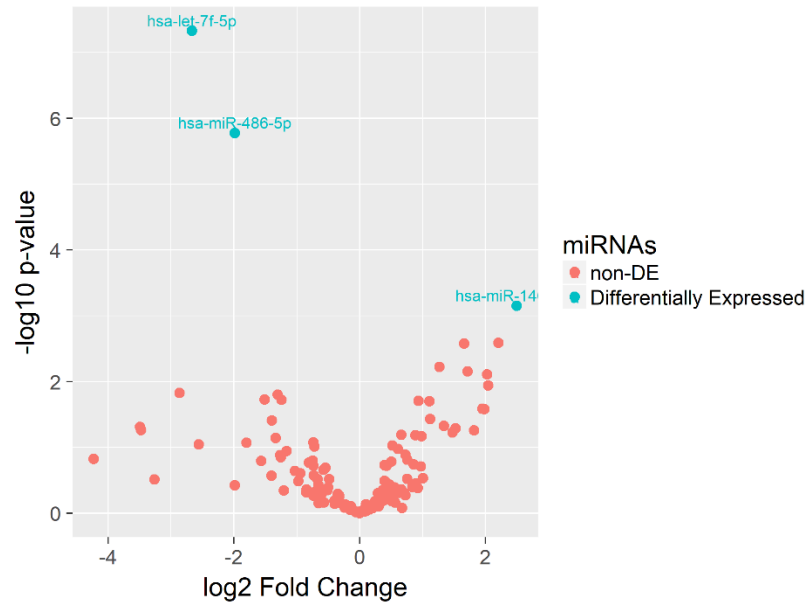
Supplementary Figure S1: Correlation of miRNA expression by sample. Heatmap shows Spearman correlation of miRNA expression of 33 samples comprising aSAH patients in group1 (n = 14), group2 (n = 13) and control individuals (n = 6). **Dark-red** colors correspond to maximum correlation, **dark-blue** colors minimum correlation and white corresponds to average correlation.



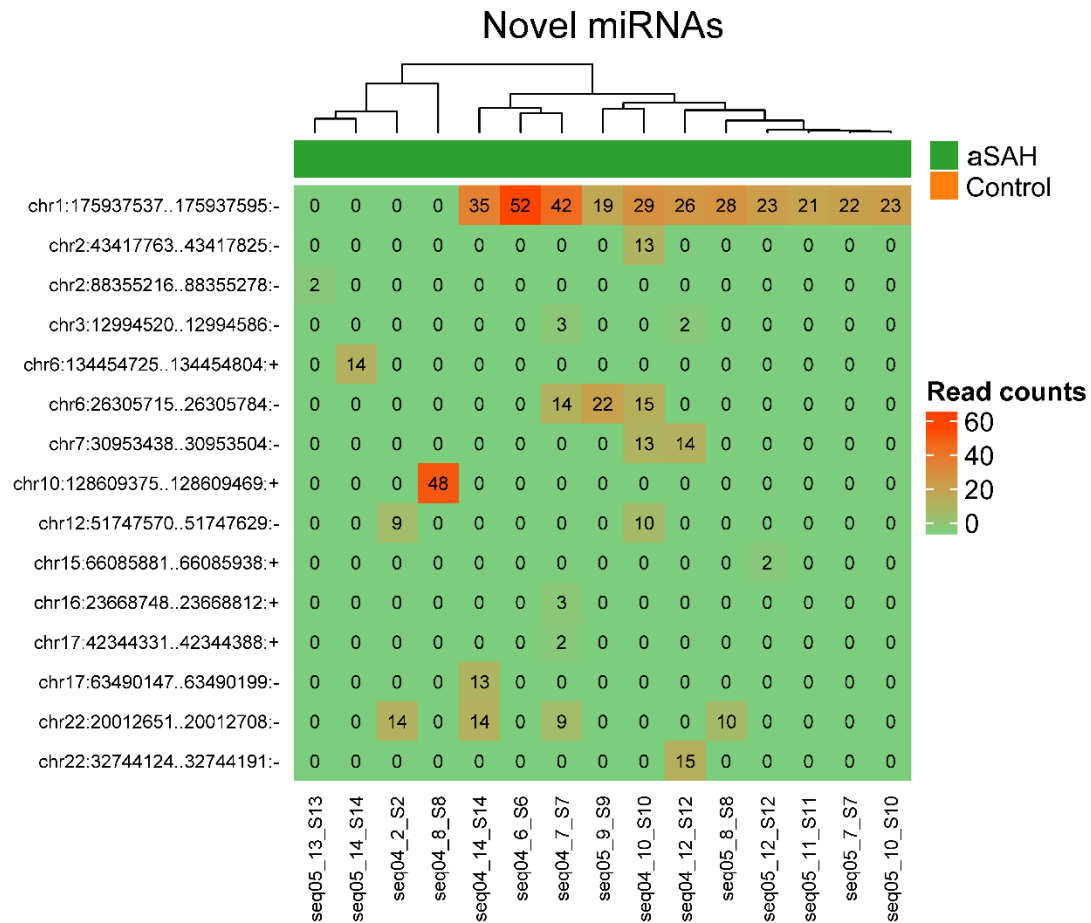
Supplementary Figure S2: Principal component analysis comprising aSAH patients and control individuals. The dots are colored according to vasograde scale described in Table 1 of clinical parameters (main article).



Supplementary Figure S3: Statistics of DE miRNAs between group1 and control. The x-axis represents the values of $\log_2(\text{fold change})$ and y-axis are p-value in the scale of $\log_{10}$. Blue dots are the DE miRNAs, and red dots are non-DE miRNAs.



Supplementary Figure S4: Statistics of DE miRNAs between group2 and control. The x-axis represents the values of log2(fold change) and y-axis are p-value in the scale of log10. Blue dots are the DE miRNAs, and red dots are non-DE miRNAs.



Supplementary Figure S5: Total number of reads mapped to novel miRNAs by sample. Novel miRNAs were identified using miRDeep2 with a score higher than 5. miRNAs with overlapping regions were merged, resulting in 15 final miRNAs (showed in Figure). Top bar represents sample group (aSAH patients and control individuals). X-axis: sample name; Y-axis: chromosome position. Heatmap **green** color indicates 0 or few reads; **Orange**: Maximum number of reads aligned in that position.

Supplementary Table S1: Statistical power analysis for sample sizes

Fold change	Power		
	FDR $\alpha < 0.1$	FDR $\alpha < 0.05$	FDR $\alpha < 0.01$
1.25	0.2440176	0.1565958	0.05214386
1.5	0.5334426	0.4085860	0.19848390
1.75	0.7707074	0.6649709	0.42473400
2	0.9049893	0.8402304	0.64785659

Note: power values were estimated using RNASeqPower R package considering unpaired sample sizes of 27 aSAH patients and 6 controls and the average expression data of eight differentially expressed miRNAs found using DESeq2 (see Methods section for details).

Supplementary Table S2: DE miRNAs between aSAH patients and control individuals identified with edgeR software

miRNA ^a	log2FoldChange	log(CPM) ^b	Adjusted <i>p</i> -value	<i>p</i> -value
<i>hsa-miR-15b-3p</i>	6.918817	3.503655	1.11E-15	1.11E-15
<i>hsa-miR-142-5p</i>	6.621679	7.045975	7.05E-22	7.05E-22
<i>hsa-miR-1306-5p</i>	-5.00408	3.175254	0.002968	0.002968
<i>hsa-miR-3200-3p</i>	-5.00224	3.188815	0.004988	0.004988
<i>hsa-miR-503-5p</i>	-4.50662	2.841098	0.031649	0.031649
<i>hsa-miR-374b-5p</i>	4.477083	2.004457	5.72E-08	5.72E-08
<i>hsa-miR-126-5p</i>	4.291935	3.640621	4.01E-13	4.01E-13
<i>hsa-miR-122-5p</i>	3.946439	2.115645	4.19E-07	4.19E-07
<i>hsa-miR-16-2-3p</i>	3.801885	2.243513	0.00031	0.00031
<i>hsa-miR-144-5p</i>	3.54505	4.863662	7.60E-12	7.60E-12
<i>hsa-miR-769-5p</i>	-3.53025	4.262203	0.000853	0.000853
<i>hsa-miR-664a-3p</i>	2.999453	2.371334	2.62E-05	2.62E-05
<i>hsa-miR-185-3p</i>	-2.82041	4.479448	0.000997	0.000997
<i>hsa-miR-942-5p</i>	-2.68145	4.933603	0.000502	0.000502
<i>hsa-miR-146a-5p</i>	-2.41456	5.845715	0.000186	0.000186
<i>hsa-miR-16-5p</i>	2.382268	9.082687	1.28E-08	1.28E-08
<i>hsa-miR-93-3p</i>	2.362859	2.748328	0.000512	0.000512
<i>hsa-miR-500a-3p</i>	-2.34557	5.025987	0.000498	0.000498
<i>hsa-miR-19b-3p</i>	2.343083	3.363962	8.54E-05	8.54E-05
<i>hsa-miR-222-3p</i>	-2.30259	4.982155	0.000383	0.000383
<i>hsa-miR-100-5p</i>	2.098872	3.463587	0.027679	0.027679
<i>hsa-let-7f-5p</i>	2.0946	7.682596	4.75E-09	4.75E-09
<i>hsa-miR-589-5p</i>	-2.05657	5.468522	0.000448	0.000448
<i>hsa-miR-425-5p</i>	2.010978	7.201045	1.64E-06	1.64E-06
<i>hsa-miR-324-5p</i>	-1.86763	4.626887	0.017297	0.017297
<i>hsa-miR-486-5p</i>	1.864753	20.10242	2.44E-10	2.44E-10
<i>hsa-miR-196b-5p</i>	-1.83641	3.470993	0.044455	0.044455
<i>hsa-miR-451a</i>	1.826463	9.238277	0.000465	0.000465
<i>hsa-miR-130b-5p</i>	-1.73826	3.876097	0.040365	0.040365
<i>hsa-miR-941</i>	-1.70564	7.29286	0.003041	0.003041
<i>hsa-miR-5010-3p</i>	1.574023	2.593417	0.038678	0.038678
<i>hsa-miR-185-5p</i>	1.559669	6.777627	2.20E-05	2.20E-05
<i>hsa-miR-3158-3p</i>	-1.53803	5.69166	0.0175	0.0175
<i>hsa-miR-148a-3p</i>	-1.49503	5.478709	0.02025	0.02025
<i>hsa-miR-186-5p</i>	-1.47238	8.682725	0.002121	0.002121
<i>hsa-miR-126-3p</i>	1.455186	3.167767	0.038516	0.038516
<i>hsa-miR-423-3p</i>	-1.3496	8.817697	0.0058	0.0058
<i>hsa-miR-221-3p</i>	-1.30789	6.821661	0.003564	0.003564
<i>hsa-miR-324-3p</i>	-1.24013	4.561812	0.048358	0.048358
<i>hsa-miR-10a-5p</i>	1.235061	3.965005	0.010349	0.010349
<i>hsa-miR-27b-3p</i>	-1.1963	6.35751	0.004691	0.004691
<i>hsa-miR-15a-5p</i>	1.185337	4.099445	0.008867	0.008867
<i>hsa-miR-182-5p</i>	-1.14964	11.30623	0.000711	0.000711
<i>hsa-miR-574-3p</i>	1.144766	5.511526	0.04399	0.04399
<i>hsa-miR-17-5p</i>	1.088197	5.144431	0.007741	0.007741
<i>hsa-miR-151a-3p</i>	1.030884	6.28436	0.010824	0.010824
<i>hsa-miR-128-3p</i>	-1.0236	5.31245	0.035364	0.035364

^a miRNAs also found by DESeq2 are indicated in bold.

^b log(CPM) represents log2 of counts-per-million (see Methods section).