

OMTN, Volume 13

Supplemental Information

Circular RNA Transcriptomic Analysis of Primary Human Brain Microvascular Endothelial Cells Infected with Meningitic *Escherichia coli*

Ruicheng Yang, Bojie Xu, Bo Yang, Jiyang Fu, Lu Liu, Nouman Amjad, Aoling Cai, Chen Tan, Huanchun Chen, and Xiangru Wang

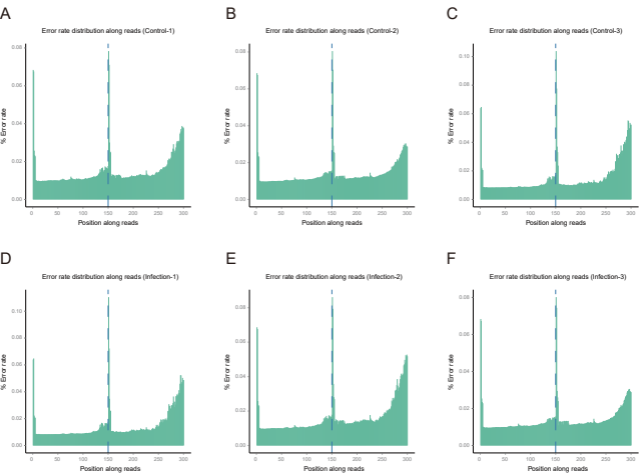
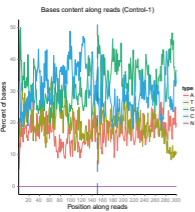
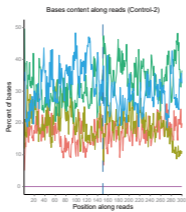


Figure S1. The error rate distribution in each sample

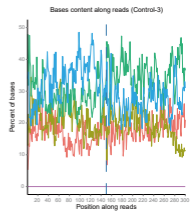
A



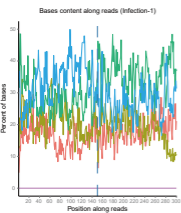
B



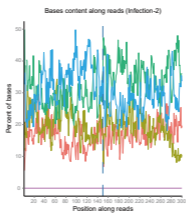
C



D



E



F

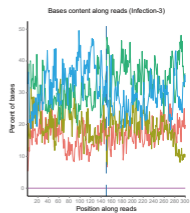
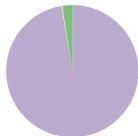


Figure S2. The base content in each sample

A

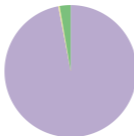
Classification of Raw Reads (Control-1)



Clean Reads (42335456, 97.38%)
 Containing N (90787, 0.21%)
 Low Quality (0.1, 0.00%)
 Adapter Related (1048943, 2.41%)

B

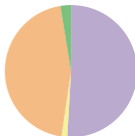
Classification of Raw Reads (Control-2)



Clean Reads (44811438, 97.01%)
 Containing N (142816, 0.31%)
 Low Quality (0.1, 0.00%)
 Adapter Related (1238462, 2.68%)

C

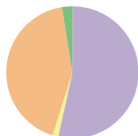
Classification of Raw Reads (Control-3)



Clean Reads (30519992, 50.91%)
 Containing N (837704, 1.40%)
 Low Quality (27041050, 45.11%)
 Adapter Related (11542290, 2.58%)

D

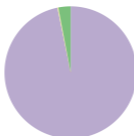
Classification of Raw Reads (Infection-1)



Clean Reads (27121430, 53.45%)
 Containing N (709407, 1.40%)
 Low Quality (21625355, 42.62%)
 Adapter Related (1281691, 2.53%)

E

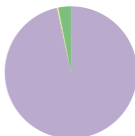
Classification of Raw Reads (Infection-2)



Clean Reads (43476316, 96.80%)
 Containing N (93817, 0.21%)
 Low Quality (0.1, 0.00%)
 Adapter Related (1344024, 2.99%)

F

Classification of Raw Reads (Infection-3)



Clean Reads (41596127, 96.61%)
 Containing N (132028, 0.31%)
 Low Quality (0.1, 0.00%)
 Adapter Related (1325368, 3.08%)

Figure S3. the raw read classification in each sample

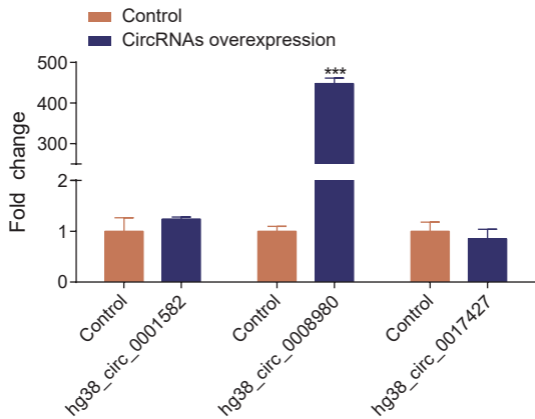


Figure S4. Overexpression of the circRNAs shown in Figure 6B. Data were expressed as the mean \pm SEM from three independent assays. *** indicated $p < 0.001$.

Table S1. Quality list of data output

Sample	Raw Reads	Clean Reads	Clean Bases	Error Rate(%)	Q20(%)	Q30(%)	GC Content(%)
Control-1-1	43475186	42335456	6.35G	0.02	98.57	95.74	62.64
Control-1-2	43475186	42335456	6.35G	0.03	96.11	90.74	63.4
Control-2-1	46192716	44811438	6.72G	0.02	98.63	95.84	63.14
Control-2-2	46192716	44811438	6.72G	0.02	96.42	91.68	63.74
Control-3-1	59943036	30519992	4.58G	0.02	99.44	97.97	62.01
Control-3-2	59943036	30519992	4.58G	0.03	97.1	90.58	62.66
Infection-1-1	50737883	27121430	4.07G	0.02	99.4	97.83	62.31
Infection-1-2	50737883	27121430	4.07G	0.03	97.21	90.9	63.03
Infection-2-1	44914157	43476316	6.52G	0.02	98.57	95.77	63.12
Infection-2-2	44914157	43476316	6.52G	0.03	94.89	88.26	63.93
Infection-3-1	43053523	41596127	6.24G	0.02	98.68	95.96	63.34
Infection-3-2	43053523	41596127	6.24G	0.02	96.4	91.66	63.97

Table S4. Primers used for real-time PCR in this study

Primers	Nucleotide sequence (5'-3')	Amplified fragments
P1	TGCCAGACTGATTGTCAT	
P2	TCTTCTCATTGATGGATGGA	hg38_circ_0000395
P3	ATTAGCCCAGAGTCCTTAT	
P4	GCATAATACAGTCACACCAG	hg38_circ_0008815
P5	GACGAGCCTACTTCAAGA	
P6	CAACCTTATCATAGCCATACC	hg38_circ_0033002
P7	ACAGCCTCACCATCATT	
P8	TTCAGCAACCAGTTCTCT	hg38_circ_0014254
P9	ATAACCTCGGCTGTTTACA	
P10	GCTTCCAGATCCTGACTC	hg38_circ_0019064
P11	AGTCACATCTTCTGCTT	
P12	CTGTTGTCATCAATGCCTT	hg38_circ_0035876
P13	AGTCAAGAGCCATCTGTAG	
P14	GAAGCCTACAACATTGG	hg38_circ_0001582
P15	CTCCACCAGATGTCAGTT	
P16	TACAGGCAGAGGGTATTTG	hg38_circ_0008980
P17	CCAGAAGAAGAGGAAGAAGA	
P18	CTCAGTGTTCCAGTCAT	hg38_circ_0017427
P19	CTGAACCCTGTAACCTTTCC	
P20	AGACATCTGGCGTTGGTACATA	ETV1
P21	TGCCTCCTGCACCACCACT	
P22	CGCCTGCTTCACCACCTTC	GAPDH