

# Asiatic Acid Attenuates Inflammation Induced by *Salmonella* via Upregulating LncRNA TVX1 in Microglia

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Figure S1. Raw data of lncRNA sequencing. Data represent the control, *S.T* and AA + *S.T*, n=3 per group.



Figure S2. Error rate distribution map of lncRNA sequencing. X-axis is the base position of reads, Y-axis is the single base error rate. Data represent the control, *S.T* and AA + *S.T*, n=3 per group.

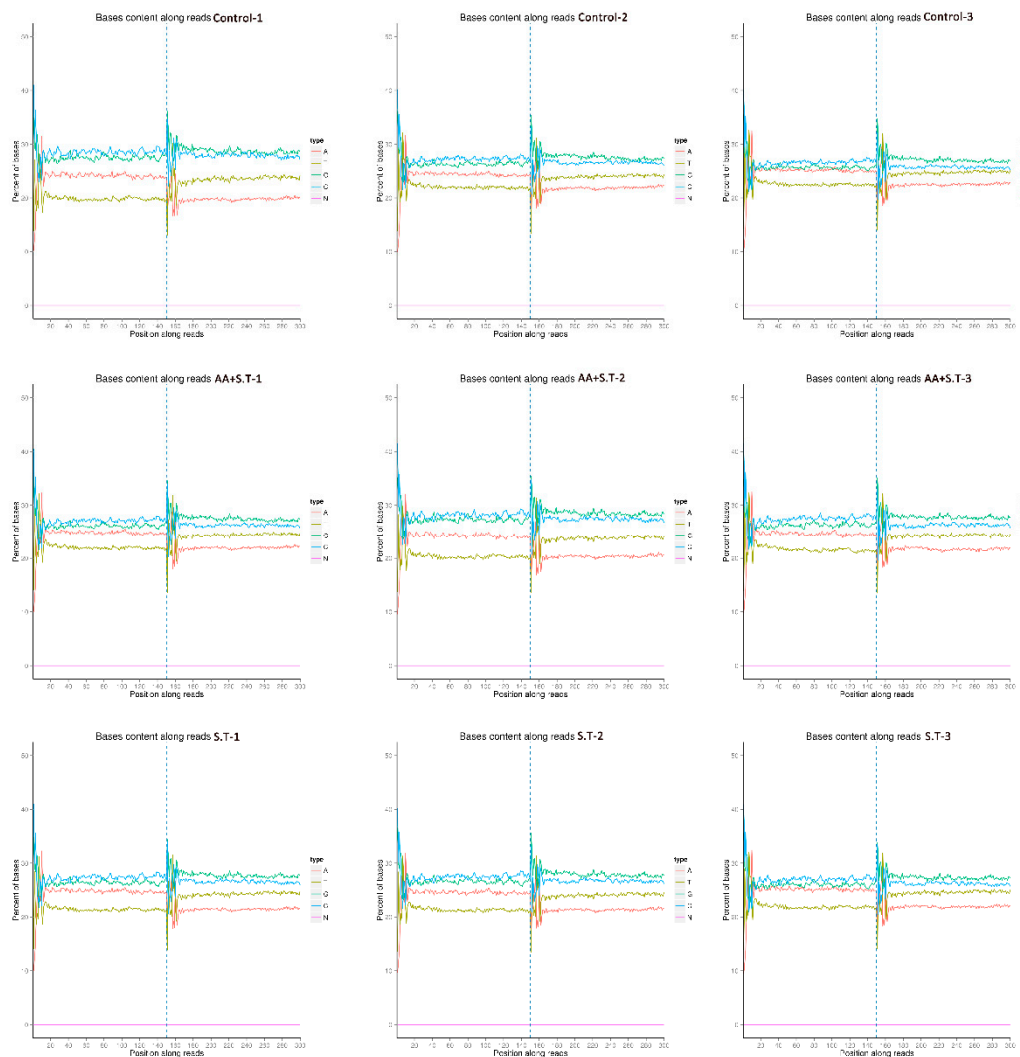


Figure S3. GC content of lncRNA sequencing. X-axis is the base position of reads, Y-axis is the proportion of the base. Data represent the control, *S.T* and AA + *S.T*, n=3 per group.

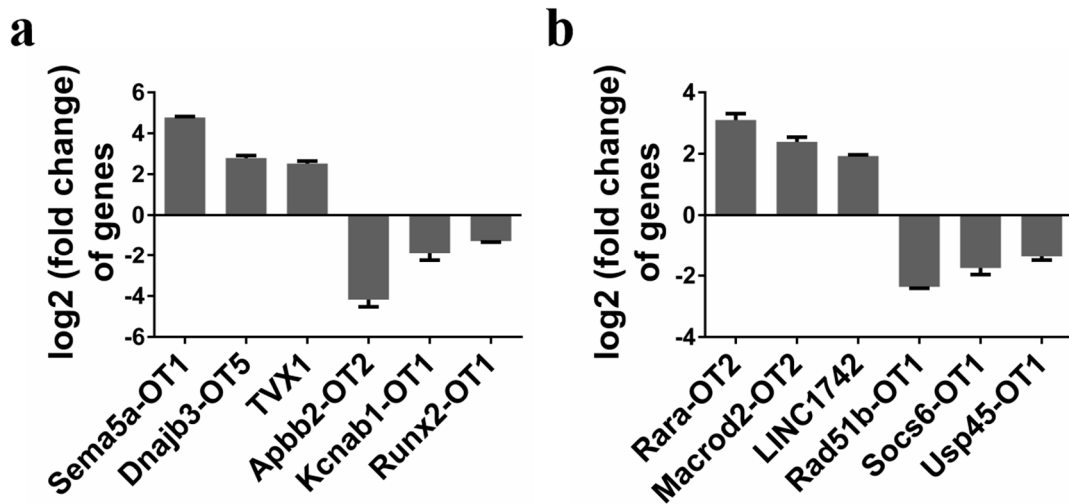


Figure S4 Verification of lncRNA sequencing results using qPCR.

(a) Differential lncRNAs between *S.T* and control. (b) Differential lncRNAs between *S.T* and AA + *S.T*.

Values are expressed as the mean  $\pm$  SEM (n = 3 per group).

**Table S1.** The primers for RT-q PCR used in present study

Name	Primer sequence (5' - 3')
$\beta$ -actin	F: CCACCATGTACCCAGGCATT
	R: AGGGTGTAACACGCAGCTCA
Runx2-OT1	F: AAGCCATCCCACTCCTTCGGTAG
	R: TCCAGCCCTGCCACATCAGAG
Apbb2-OT2	F: GAATCTCGCTGCCGCTGCTC
	R: GCTCCCAGGTCTCGCAGTCC
Kcnab1-OT1	F: TCCTCCTCGGACTGCTGCTTG
	R: CCTTCCCTGCCTCCCTGCTC
TVX1	F: GCCGAGCCTCAGCCACATAATC
	R: TGTGTCTCTTACTCCTGCGTCTCC
Sema5a-OT1	F: AGCCGCACGCATTTCATACCC
	R: ATCACTCCCCTCCAACAGTTCCTC
Dnajb3-OT5	F: GGCATCATCACCATCGGAACTCC
	R: GACTCGGGCATTATCACACACTC

Socs6-OT1	F: CGATGAAGCACAGTGAGTGAGACC R: GACACCATGCAGACACCTGACAG
Rad51b-OT1	F: GAAACTGAAGGCGGCCATGG R: GCTCTGCTCCGAAGTGAGGT
Usp45-OT1	F: ACCTGCTGAGTGATGGTGGC R: AACCTFCTCTGTGGACCAGG
Rara-OT2	F: CCCCATGCCCCGAGGAAGAG R: CCAAGCAGCCACAGTCAGAAGAG
MacroD2-OT2	F: AGGCTCTGAGGTGCTGCTGTG R: CTCGGGAGGGAAAAGTGCAAAGG
LINC1742	F: GCATGTATGTCAGGGCACCAGATG R: GCATGTATGTCAGGGCACCAGATG
IL-1 $\beta$	CACTACAGGCTCCGAGATGAACAAC TGTCGTTGCTTGGTTCTCCTTGTAC
IL-6	CTCCCAACAGACCTGTCTATAC CCATTGCACAACCTCTTTTCTCA
IL-18	AGACCTGGAATCAGACAACCTT TCAGTCATATCCTCGAACACAG

**Table S2.** Quality assessment of lncRNA sequencing.

Sample	Raw	Clean	Raw	Clean	Error	Q20 (%)	Q30 (%)	GC
name	reads	reads	bases (G)	bases (G)	rate (%)			content (%)
A 1	90261956	87689564	13.54	13.15	0.02	98.38	94.98	56.45
A 2	78390842	75957418	11.76	11.39	0.02	98.50	95.26	53.99
A 3	91410330	88895678	13.71	13.33	0.02	98.43	95.05	52.68
B 1	78957812	76018072	11.84	11.40	0.02	98.39	94.95	53.57
B 2	95474126	91590888	14.32	13.74	0.02	98.39	95.03	55.75
B 3	88416854	84915634	13.26	12.74	0.02	98.83	96.25	53.98
C 1	80497734	77584648	12.07	11.64	0.02	98.68	95.90	54.16

C 2	89036448	84586346	13.36	12.69	0.02	98.90	96.34	54.46
C 3	81207732	77293500	12.18	11.59	0.02	98.45	95.10	53.38

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