

SUPPLEMENTARY TABLES

Supplementary Table 4. DEGs between AST and LPS samples.

Gene	sampleA	sampleB	baseMeanA	baseMeanB	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ENSMUSG0000022818	AST	LPS	48.41487417	15.22940743	28.89401138	1.021436182	0.212138014	4.814960607	1.47229E-06	0.000673911
ENSMUSG0000059824	AST	LPS	569.0902514	204.3558614	354.5406102	1.022655966	0.202188092	5.057943611	4.23802E-07	0.000231532
ENSMUSG0000060600	AST	LPS	309.7794502	108.9422031	191.6398931	1.081034961	0.19750523	5.473449788	4.41358E-08	3.73742E-05
ENSMUSG0000048498	AST	LPS	342.5834924	70.69719237	182.6503747	1.167546697	0.218068915	5.354026256	8.60184E-08	6.62185E-05
ENSMUSG0000039109	AST	LPS	596.1148924	204.052468	365.4899369	1.167651944	0.188164286	6.205491853	5.45261E-10	9.23454E-07
ENSMUSG0000032915	AST	LPS	613.660102	149.1405857	340.4133277	1.183303614	0.21566635	5.486732691	4.09436E-08	3.73742E-05
ENSMUSG0000027338	AST	LPS	62.4055815	9.174534721	31.09320104	1.194972807	0.216388509	5.522348729	3.34498E-08	3.33238E-05
ENSMUSG0000033227	AST	LPS	19.33965891	1.81051473	9.028397628	1.433440935	0.217019981	6.605110399	3.97221E-11	1.34547E-07
ENSMUSG0000051682	AST	LPS	522.9979615	102.0594688	275.3870835	1.483269424	0.211237851	7.021797556	2.19032E-12	9.96623E-09

Supplementary Table 5. GO analysis of the 11 AST-associated genes.

ID	Description	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0034364	high-density lipoprotein particle	23/23436	5.04E-05	0.000750507	0.000164585	20210/20208	2
GO:0034358	plasma lipoprotein particle	34/23436	0.00011442	0.000750507	0.000164585	20210/20208	2
GO:1990777	lipoprotein particle	34/23436	0.00011442	0.000750507	0.000164585	20210/20208	2
GO:0032994	protein-lipid complex	36/23436	0.000125085	0.000750507	0.000164585	20210/20208	2
GO:0020005	symbiont-containing vacuole membrane	12/23436	0.005619159	0.019216454	0.004214135	634650	1
GO:0020003	symbiont-containing vacuole	14/23436	0.006552889	0.019216454	0.004214135	634650	1
GO:0065010	extracellular membrane-bounded organelle	16/23436	0.007485823	0.019216454	0.004214135	634650	1
GO:0030430	host cell cytoplasm	17/23436	0.007951991	0.019216454	0.004214135	634650	1
GO:0033655	host cell cytoplasm part	17/23436	0.007951991	0.019216454	0.004214135	634650	1
GO:0033646	host intracellular part	20/23436	0.009349301	0.019216454	0.004214135	634650	1
GO:0043656	intracellular region of host	20/23436	0.009349301	0.019216454	0.004214135	634650	1
GO:0033643	host cell part	22/23436	0.010279847	0.019216454	0.004214135	634650	1
GO:0018995	host	24/23436	0.011209598	0.019216454	0.004214135	634650	1
GO:0043657	host cell	24/23436	0.011209598	0.019216454	0.004214135	634650	1
GO:0005881	cytoplasmic microtubule	78/23436	0.036014707	0.04801961	0.010530616	20208	1

Supplementary Table 6. The list of primer sequences used in this study.

1	GAPDH	forward	5' -	AGGTCGGTGTGAACGGATTTG	- 3'
		reverse	5' -	TGTAGACCATGTAGTTGAGGTCA	- 3'
2	Saa3	forward	5' -	AGAGAGGCTGTTCAGAAGTTCA	- 3'
		reverse	5' -	AGCAGGTCGGAAGTGGTTG	- 3'
3	Ly6i	forward	5' -	CTGAGAGGAACCCTTCTCCAA	- 3'
		reverse	5' -	GGTGTTCACACACTACCCC	- 3'
4	Saa1	forward	5' -	TGGCTGGAAAGATGGAGACAA	- 3'
		reverse	5' -	AAAGCTCTCTTGCATCACTG	- 3'
5	Irf7	forward	5' -	GAGACTGGCTATTGGGGGAG	- 3'
		reverse	5' -	GACCGAAATGCTTCCAGGG	- 3'
6	Cxcl5	forward	5' -	GTTCCATCTCGCCATTCATGC	- 3'
		reverse	5' -	GCGGCTATGACTGAGGAAGG	- 3'
7	Ccl7	forward	5' -	GCTGCTTTCAGCATCCAAGTG	- 3'
		reverse	5' -	CCAGGGACACCGACTACTG	- 3'
8	Timp1	forward	5' -	CGAGACCACCTTATACCAGCG	- 3'
		reverse	5' -	ATGACTGGGGTGTAGGCGTA	- 3'
9	Isg15	forward	5' -	AGTGATGCTAGTGGTACAGAACT	- 3'
		reverse	5' -	CAGTCTGCGTCAGAAAGACCT	- 3'
10	Gbp11	forward	5' -	CATTGCAGAGAAGTGCACCAA	- 3'
		reverse	5' -	ATCACAGTCTCTCATTTGCTCC	- 3'
11	Tgtp1	forward	5' -	TGGGACCACTAACTTCACACC	- 3'
		reverse	5' -	GGCCAGTTGTGCATCATTTTC	- 3'
12	Cxcl13	forward	5' -	GGCCACGGTATTCTGGAAGC	- 3'
		reverse	5' -	GGGCGTAACTTGAATCCGATCTA	- 3'