

Table SI. Relevant oligonucleotide sequences of primers.

Genes	Primer sequences (5'→3')
IRAK4	F: CATAACGCAACCTTAATGTGGGG R: GGAAGTGTGATCTGTCGTCG
IRAK1	F: AGCCGAGGTCTGCATTACATT R: TGGCAGTCTGGATAACTGATGA
TAK1	F: TCCAACCGCAGCTACTCTG R: CCCGTACAGGAAGCAGTTATTTT
TRAF6	F: AAAGCGAGAGATTCTTTCCCTG R: ACTGGGGACAATCACTAGAGC
MKK3	F: GCCTCAGACCAAAGGAAAATCC R: GGTGTGGGGTTGGACACAG
TLR4	F: AGCTCCTGACCTTGGTCTTG R: CGCAGGGGAACTCAATGAGG
MyD88	F: TCATGTTCTCCATACCCTTGGT R: AAAGTGCAGTGGGGTCAG
FOS	F: TTGAGCGATCATCCCGGTC R: GCGTGAGTCCATACTGGCAAG
JUN	F: GTGTGGGACGACGATCAAAAAG R: TGACCACTAACAGGGAAAGGAC
MKK7	F: GATGTCGCGTCCTGGTTTAAG R: ACTTGGGAGAAGGTGGGGAA
MAPK1	F: TCAGATGAATTTTCGTTGGCAGA R: GAGCACTTGGGTACTCCACG
MAPK3	F: TCCGCCATGAGAATGTTATAGGC R: GGTGGTGTGATAAGCAGATTGG
β-actin	F: GTGCTGTCCCTGTATGCCTC R: GTTTCATGAATGCCACAGGA

F, forward; R, reverse; IRAK, interleukin1 receptorassociated kinase; TAK1, transforming growth factor-β-activated kinase 1; TRAF6, TNF receptorassociated factor 6; MyD88, myeloid differentiation primary response protein MyD88; MKK3, mitogen-activated protein kinase kinase 3.

Table SII. Terms enriched in GO terms (LPS group vs. LPS+BBR group).

GO ID	Description	Term type
GO:0044848	Biological phase	Biological_process
GO:0032501	Multicellular organismal process	Biological_process
GO:0050789	Regulation of biological process	Biological_process
GO:0048511	Rhythmic process	Biological_process
GO:0040007	Growth	Biological_process
GO:0022414	Reproductive process	Biological_process
GO:0098754	Detoxification	Biological_process
GO:0050896	Response to stimulus	Biological_process
GO:0040011	Locomotion	Biological_process
GO:0071840	Cellular component organization or biogenesis	Biological_process
GO:0000003	Reproduction	Biological_process
GO:0065007	Biological regulation	Biological_process
GO:0051704	Multi-organism process	Biological_process
GO:0022610	Biological adhesion	Biological_process
GO:0099531	Presynaptic process involved in chemical synaptic transmission	Biological_process
GO:0001906	Cell killing	Biological_process
GO:0051179	Localization	Biological_process
GO:0032502	Developmental process	Biological_process
GO:0002376	Immune system process	Biological_process
GO:0048519	Negative regulation of biological process	Biological_process
GO:0098743	Cell aggregation	Biological_process
GO:0044699	Single-organism process	Biological_process
GO:0008152	Metabolic process	Biological_process
GO:0007610	Behavior	Biological_process
GO:0048518	Positive regulation of biological process	Biological_process
GO:0023052	Signaling	Biological_process
GO:0009987	Cellular process	Biological_process
GO:0005623	Cell	Cellular_component
GO:0043226	Organelle	Cellular_component
GO:0044422	Organelle part	Cellular_component
GO:0044464	Cell part	Cellular_component
GO:0016020	Membrane	Cellular_component
GO:0044217	Other organism part	Cellular_component
GO:0045202	Synapse	Cellular_component
GO:0044456	Synapse part	Cellular_component
GO:0005576	Extracellular region	Cellular_component
GO:0099080	Supramolecular complex	Cellular_component
GO:0031974	Membrane-enclosed lumen	Cellular_component
GO:0044425	Membrane part	Cellular_component
GO:0032991	Macromolecular complex	Cellular_component
GO:0044421	Extracellular region part	Cellular_component
GO:0009295	Nucleoid	Cellular_component
GO:0030054	Cell junction	Cellular_component
GO:0044215	Other organism	Cellular_component
GO:0000988	Transcription factor activity, protein binding	Molecular_function
GO:0042056	Chemoattractant activity	Molecular_function
GO:0016015	Morphogen activity	Molecular_function
GO:0001071	Nucleic acid binding transcription factor activity	Molecular_function
GO:0009055	Electron carrier activity	Molecular_function
GO:0005215	Transporter activity	Molecular_function
GO:0005488	Binding	Molecular_function
GO:0003824	Catalytic activity	Molecular_function
GO:0004871	Signal transducer activity	Molecular_function
GO:0005198	Structural molecule activity	Molecular_function
GO:0098772	Molecular function regulator	Molecular_function
GO:0016209	Antioxidant activity	Molecular_function
GO:0045182	Translation regulator activity	Molecular_function
GO:0060089	Molecular transducer activity	Molecular_function
GO:0045499	Chemorepellent activity	Molecular_function

GO, Gene Ontology; LPS, lipopolysaccharide; BBR, berberine.

Table SIII. GO annotation of Vasn, Acvr1b, NFκBIA, Pnp and Adam17.

A, Vasn	
GO ID	Description
GO:0007166	Cell surface receptor signaling pathway
GO:0009987	Cellular process
GO:0010719	Negative regulation of epithelial to mesenchymal transition
GO:0030512	Negative regulation of transforming growth factor beta receptor signaling pathway
GO:0048523	Negative regulation of cellular process
GO:0050896	Response to stimulus
GO:0070887	Cellular response to chemical stimulus
GO:0071456	Cellular response to hypoxia
GO:0071461	Cellular response to redox state
B, Acvr1b	
GO ID	Description
GO:0000082	G1/S transition of mitotic cell cycle
GO:0001701	<i>In utero</i> embryonic development
GO:0001942	Hair follicle development
GO:0006355	Regulation of transcription, DNA-templated
GO:0006468	Protein phosphorylation
GO:0007165	Signal transduction
GO:0007178	Transmembrane receptor protein serine/threonine kinase signaling pathway
GO:0007179	Transforming growth factor beta receptor signaling pathway
GO:0007389	Pattern specification process
GO:0007417	Central nervous system development
GO:0009966	Regulation of signal transduction
GO:0010628	Positive regulation of gene expression
GO:0010629	Negative regulation of gene expression
GO:0010862	Positive regulation of pathway-restricted SMAD protein phosphorylation
GO:0016310	Phosphorylation
GO:0018107	Peptidyl-threonine phosphorylation
GO:0023014	Signal transduction by protein phosphorylation
GO:0030308	Negative regulation of cell growth
GO:0032924	Activin receptor signaling pathway
GO:0032927	Positive regulation of activin receptor signaling pathway
GO:0038092	Nodal signaling pathway
GO:0045648	Positive regulation of erythrocyte differentiation
GO:0045944	Positive regulation of transcription from RNA polymerase II promoter
GO:0046545	Development of primary female sexual characteristics
GO:0046777	Protein autophosphorylation
GO:0097191	Extrinsic apoptotic signaling pathway
GO:1901165	Positive regulation of trophoblast cell migration
C, NFκBIA	
GO ID	Description
GO:0000060	Protein import into nucleus, translocation
GO:0007253	Cytoplasmic sequestering of NF-κB
GO:0010745	Negative regulation of macrophage derived foam cell differentiation
GO:0010875	Positive regulation of cholesterol efflux
GO:0010888	Negative regulation of lipid storage
GO:0031663	Lipopolysaccharide-mediated signaling pathway
GO:0032088	Negative regulation of NF-kappaB transcription factor activity
GO:0032270	Positive regulation of cellular protein metabolic process
GO:0032495	response to muramyl dipeptide
GO:0034142	toll-like receptor 4 signaling pathway

Table III. Continued.

C, NFκBIA	
GO ID	Description
GO:0035994	Response to muscle stretch
GO:0042127	Regulation of cell proliferation
GO:0043330	Response to exogenous dsRNA
GO:0045638	Negative regulation of myeloid cell differentiation
GO:0045746	Negative regulation of Notch signaling pathway
GO:0045944	Positive regulation of transcription from RNA polymerase II promoter
GO:0070427	Nucleotide-binding oligomerization domain containing 1 signaling pathway
GO:0070431	Nucleotide-binding oligomerization domain containing 2 signaling pathway
GO:0071345	Cellular response to cytokine stimulus
GO:0071407	Cellular response to organic cyclic compound
GO:0097421	Liver regeneration
D, Pnp	
GO ID	Description
GO:0006139	Nucleobase-containing compound metabolic process
GO:0006148	Inosine catabolic process
GO:0006738	Nicotinamide riboside catabolic process
GO:0006955	Immune response
GO:0009116	Nucleoside metabolic process
GO:0034356	NAD biosynthesis via nicotinamide riboside salvage pathway
GO:0034418	Urate biosynthetic process
GO:0042102	Positive regulation of T cell proliferation
GO:0042278	Purine nucleoside metabolic process
GO:0042493	Response to drug
GO:0043101	Purine-containing compound salvage
GO:0046638	Positive regulation of alpha-beta T cell differentiation
GO:0070970	Interleukin-2 secretion
E, Adam17	
GO ID	Description
GO:0001666	Response to hypoxia
GO:0001934	Positive regulation of protein phosphorylation
GO:0006508	Proteolysis
GO:0006509	Membrane protein ectodomain proteolysis
GO:0007155	Cell adhesion
GO:0007173	Epidermal growth factor receptor signaling pathway
GO:0007219	Notch signaling pathway
GO:0007220	Notch receptor processing
GO:0007229	Integrin-mediated signaling pathway
GO:0008284	Positive regulation of cell proliferation
GO:0010820	Positive regulation of T cell chemotaxis
GO:0030307	Positive regulation of cell growth
GO:0030335	Positive regulation of cell migration
GO:0030512	Negative regulation of transforming growth factor beta receptor signaling pathway
GO:0031659	Positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G1/S transition of mitotic cell cycle
GO:0032496	Response to lipopolysaccharide
GO:0032722	Positive regulation of chemokine production
GO:0033627	Cell adhesion mediated by integrin
GO:0035313	Wound healing, spreading of epidermal cells
GO:0035624	Receptor transactivation
GO:0035625	Epidermal growth factor-activated receptor transactivation by G-protein coupled receptor signaling pathway

Table III. Continued.

E, Adam17

GO ID	Description
GO:0043536	Positive regulation of blood vessel endothelial cell migration
GO:0045737	Positive regulation of cyclin-dependent protein serine/threonine kinase activity
GO:0045741	Positive regulation of epidermal growth factor-activated receptor activity
GO:0050830	Defense response to Gram-positive bacterium
GO:0051088	PMA-inducible membrane protein ectodomain proteolysis
GO:0055099	Response to high density lipoprotein particle
GO:0071403	Cellular response to high density lipoprotein particle stimulus
GO:1900087	Positive regulation of G1/S transition of mitotic cell cycle
GO:1903265	Positive regulation of tumor necrosis factor-mediated signaling pathway
GO:1905564	Positive regulation of vascular endothelial cell proliferation

GO, Gene Ontology; Vasn, vasorin; Acvr1b, activin A receptor type 1B; NFκBIA, NFκB inhibitor α; Pnp, purine nucleoside phosphorylase; Adam17, ADAM metallopeptidase domain 17.
