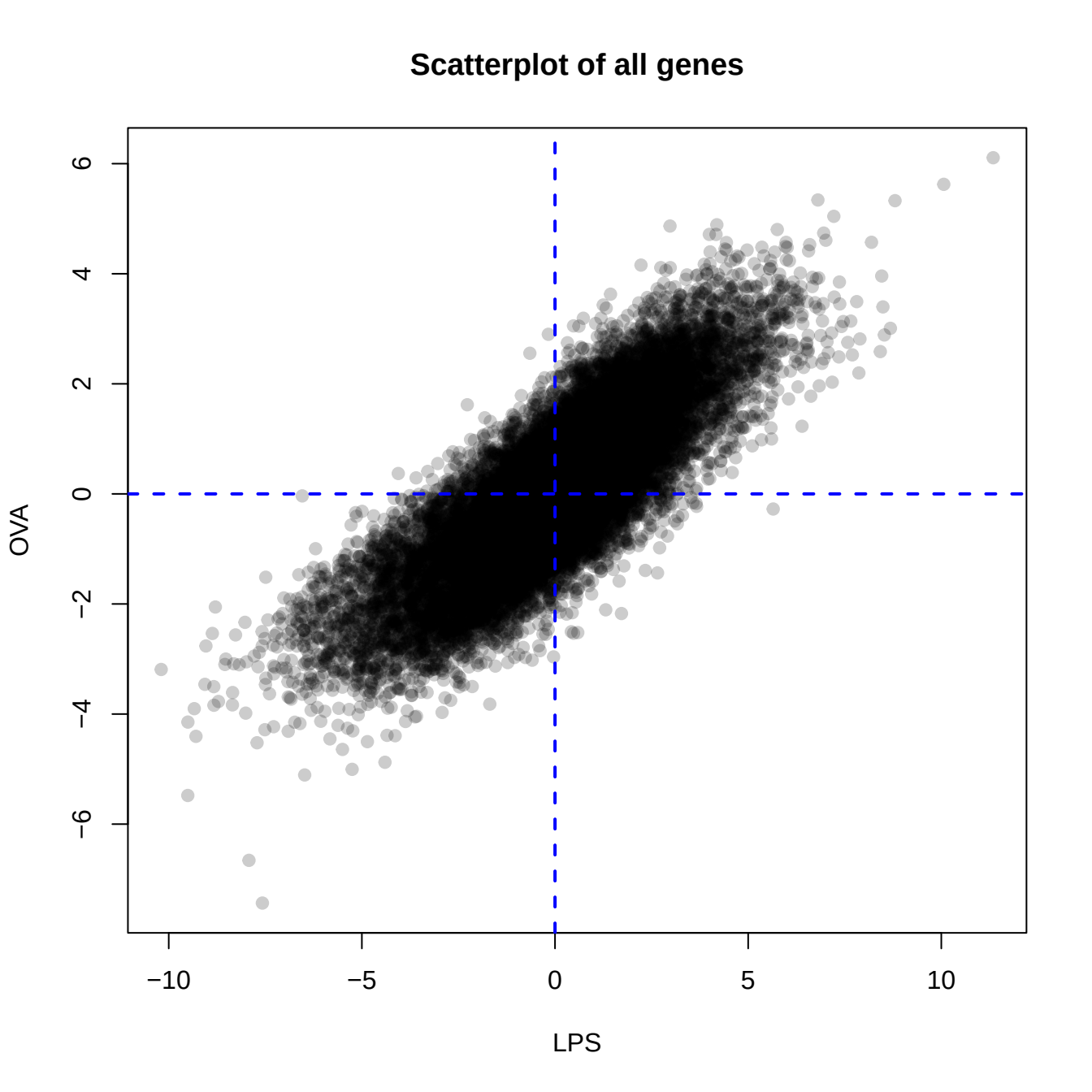
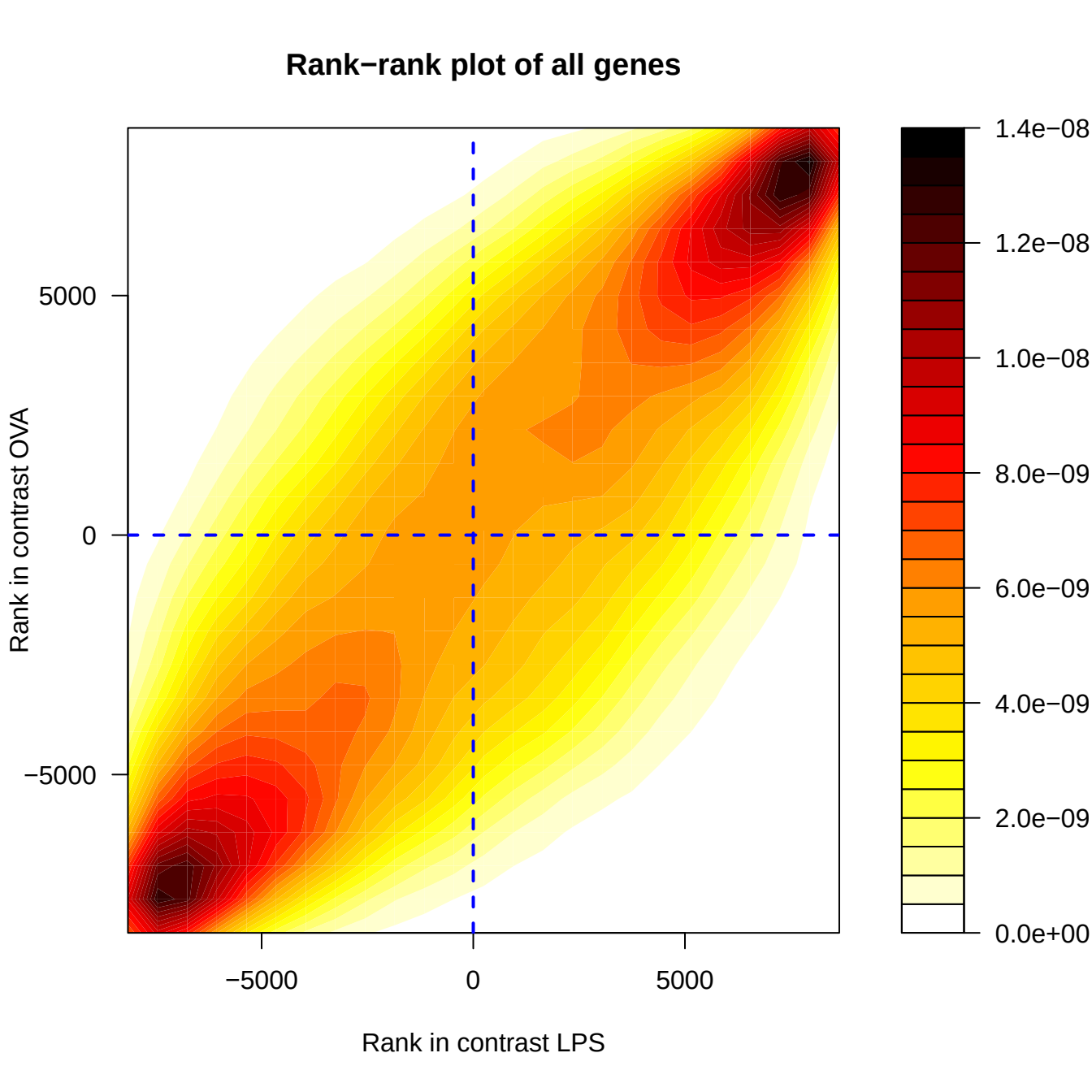
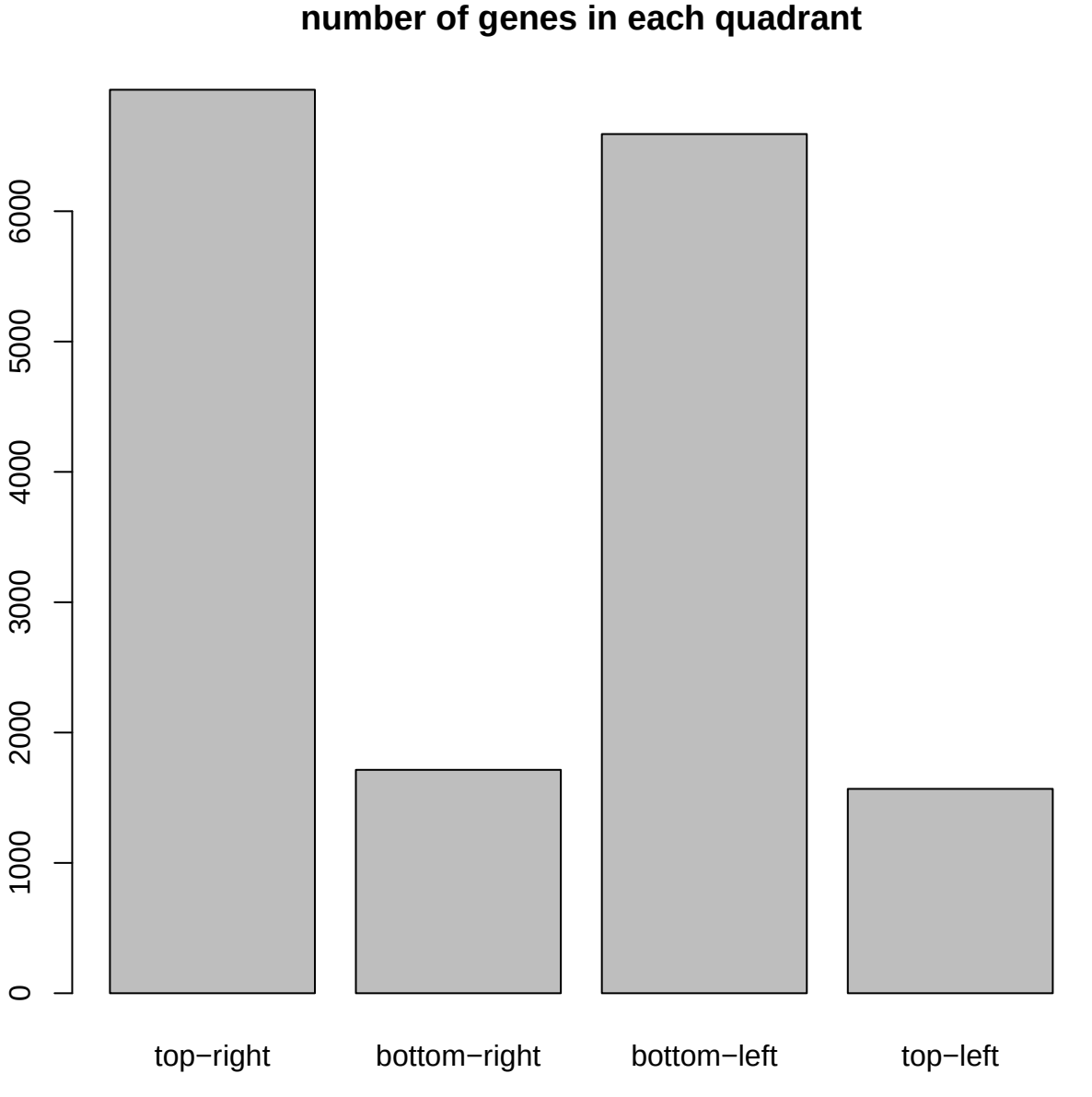
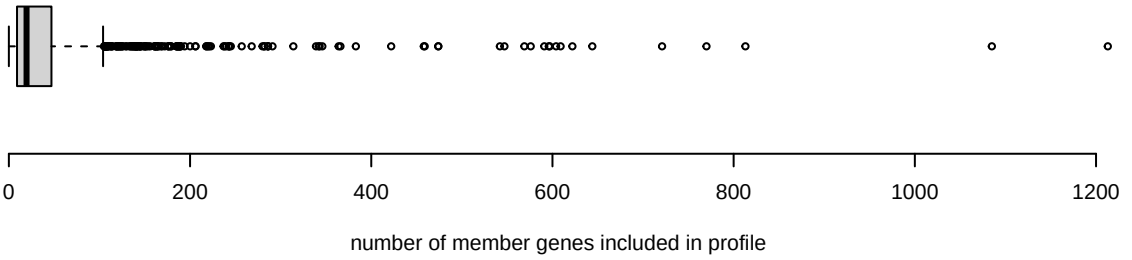

Scatterplot of all genes
OVA
LPS
6
4
2
0
−2
−4
−6
−10
−5
0
5
10

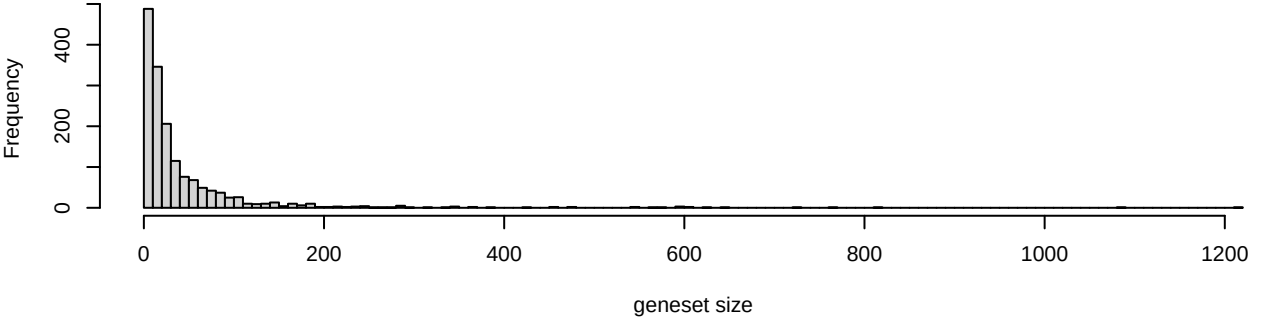

Rank−rank plot of all genes
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00


number of genes in each quadrant
0
1000
2000
3000
4000
5000
6000
top−right
bottom−right
bottom−left
top−left

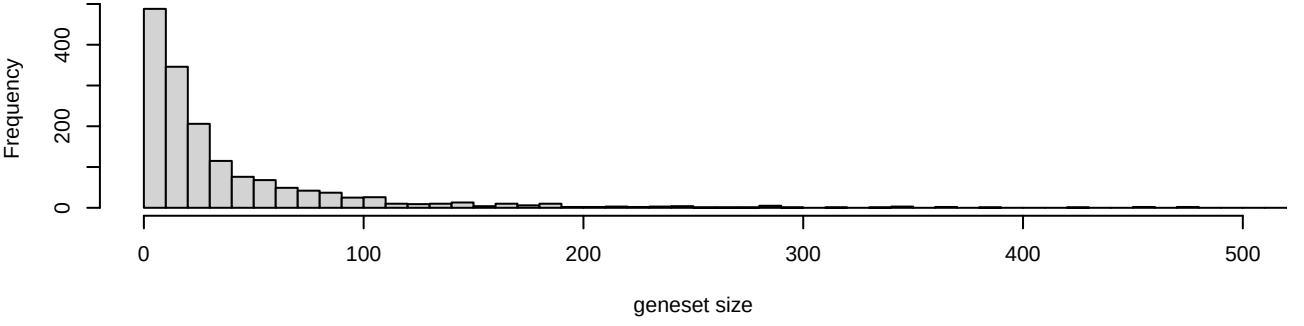
Gene set size

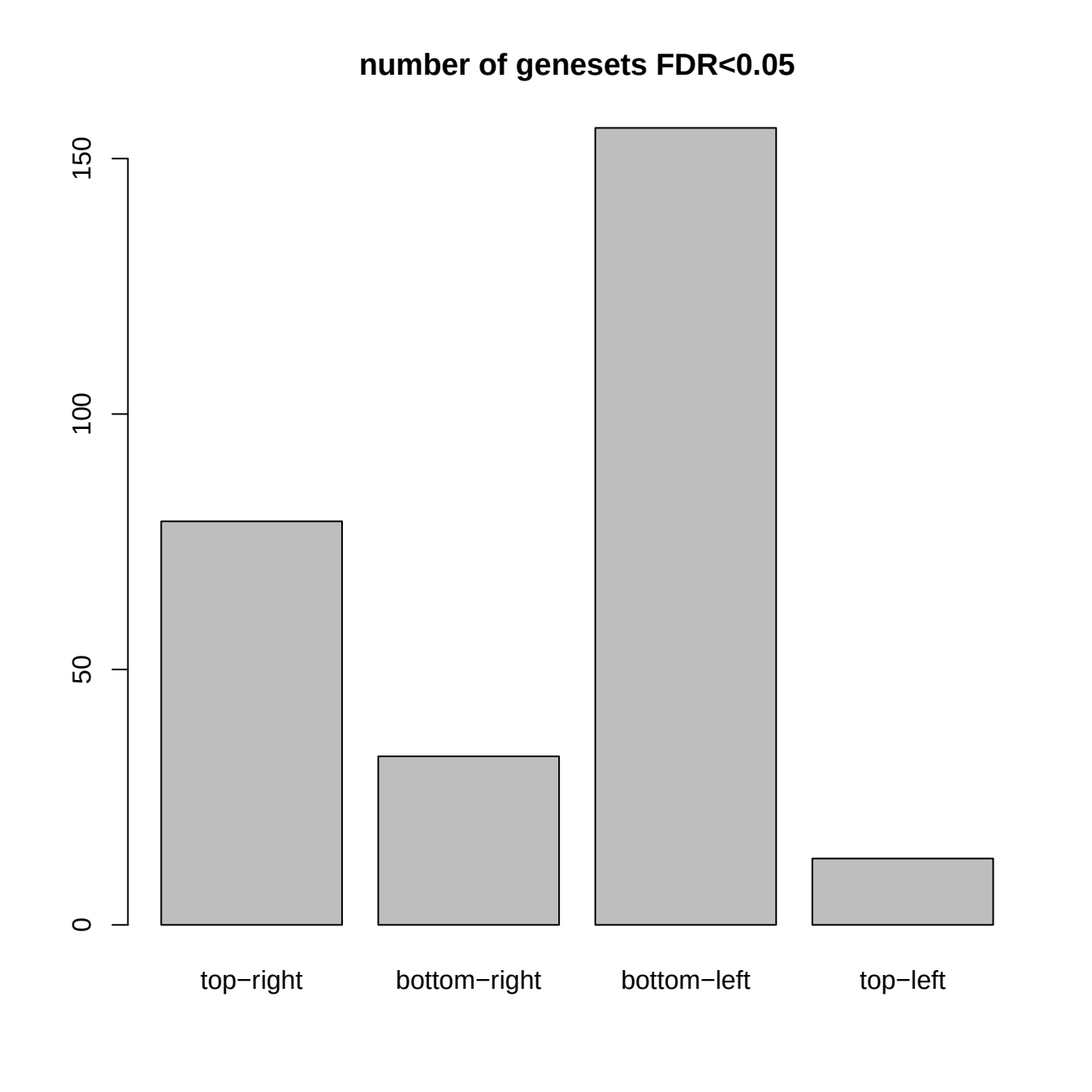


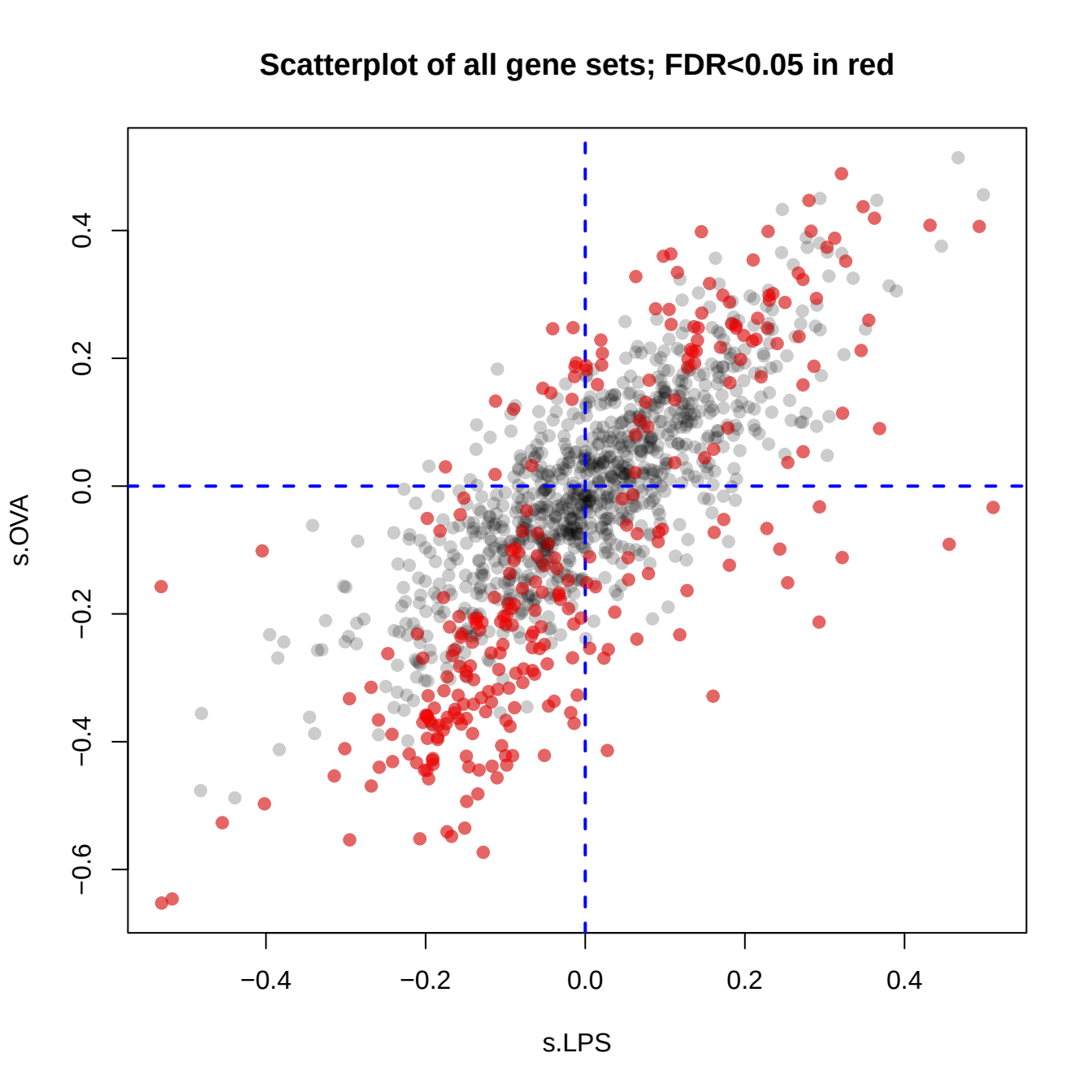
Histogram of geneset size

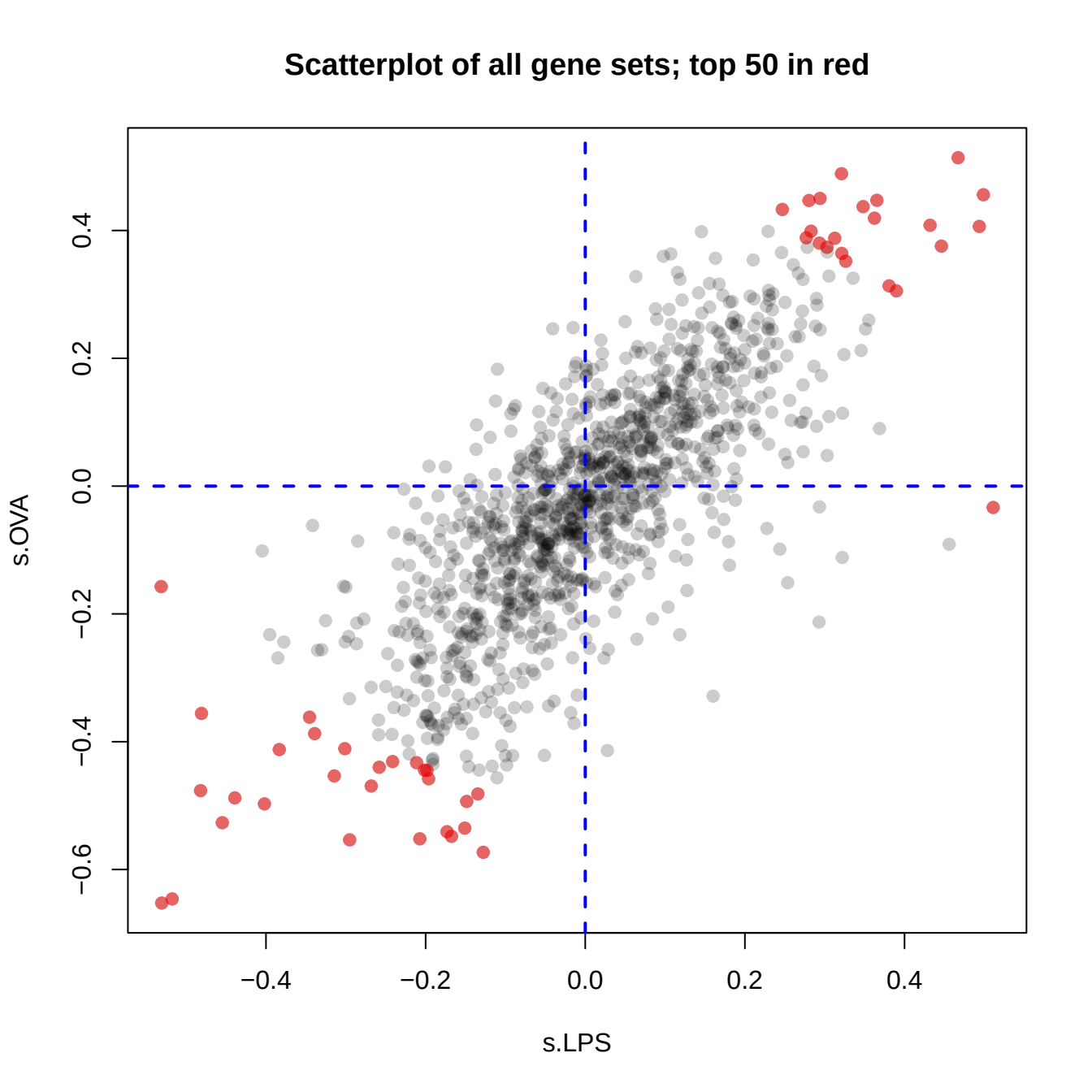


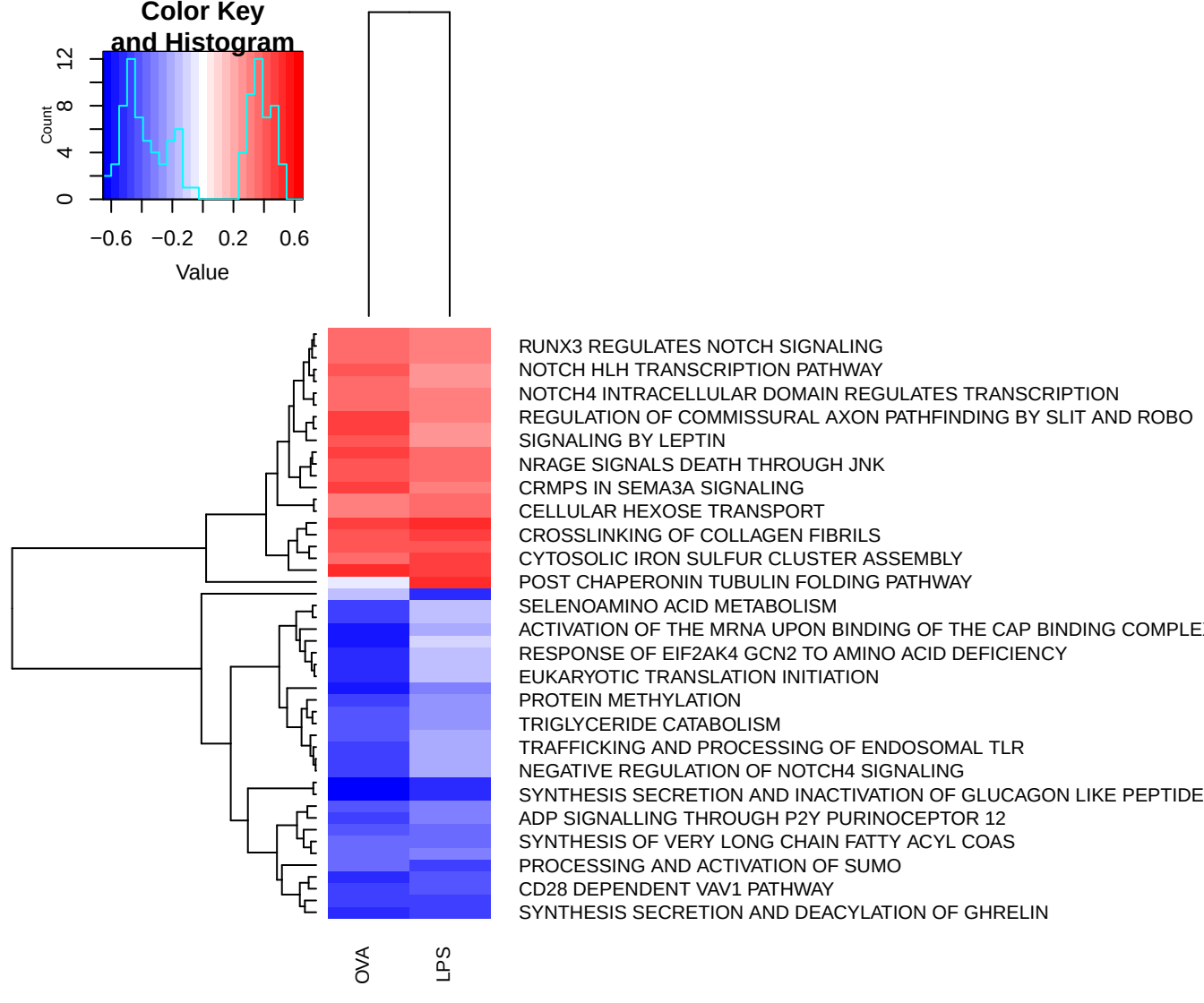
Trimmed histogram of geneset size

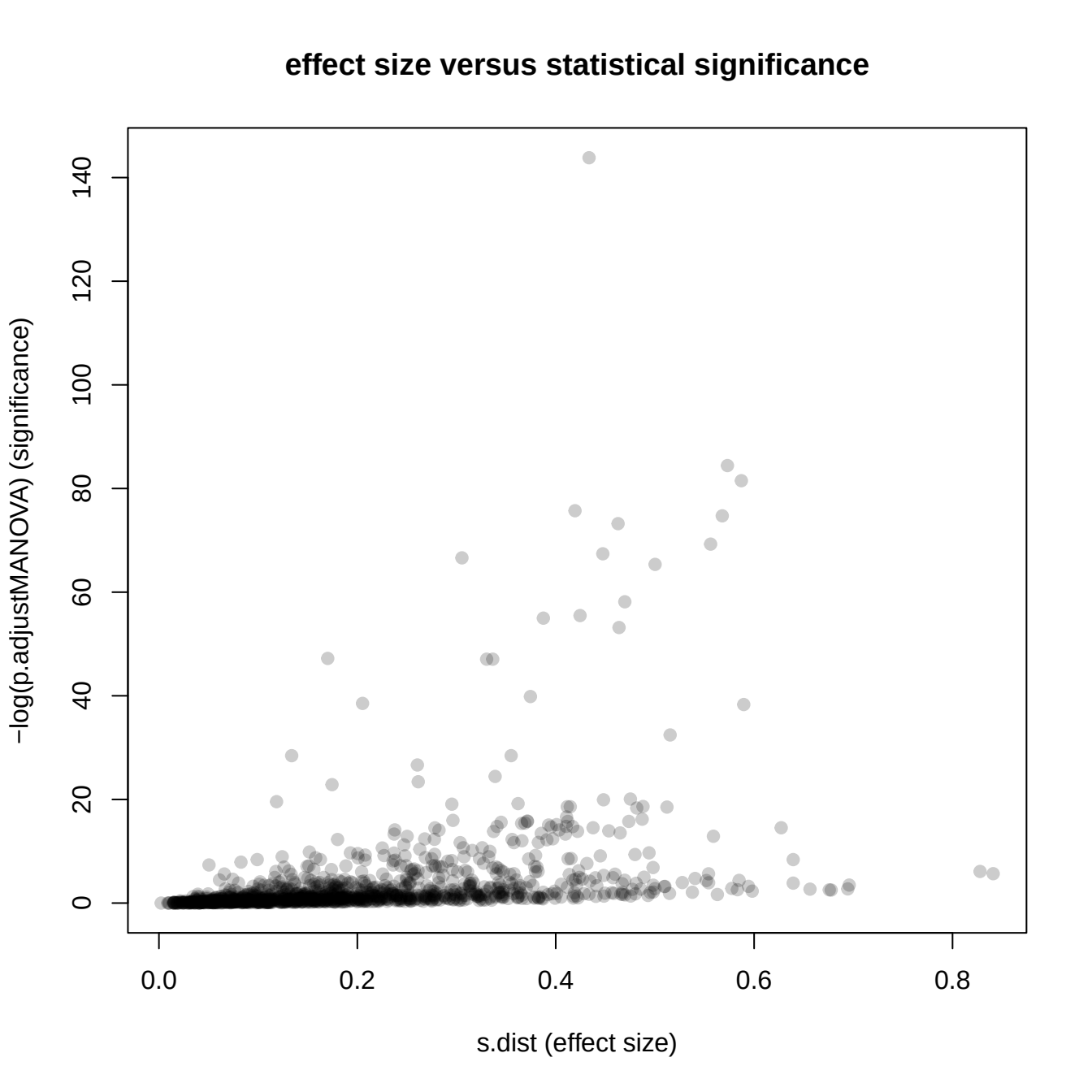


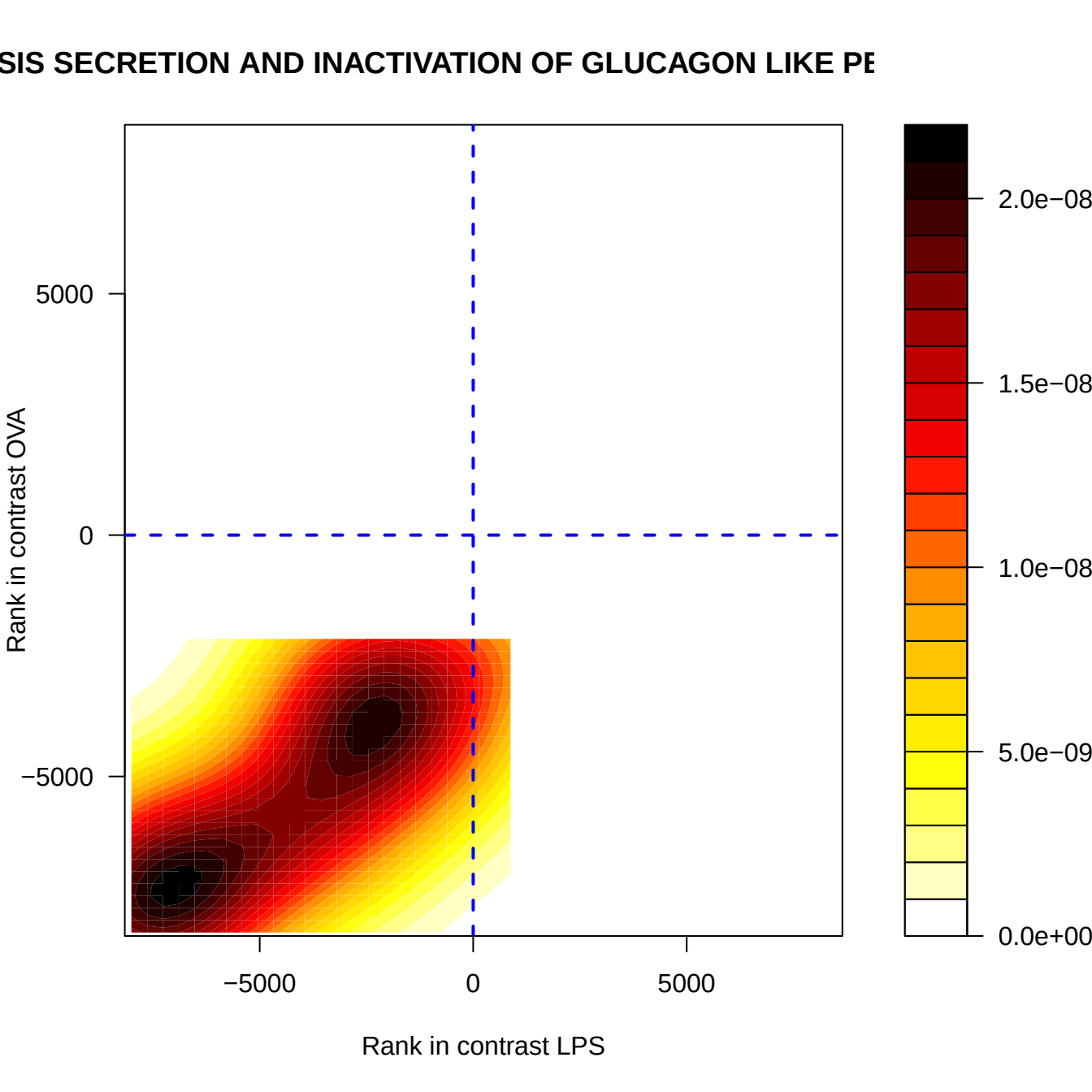

number of genesets FDR<0.05
150
100
50
0
top−right
bottom−right
bottom−left
top−left

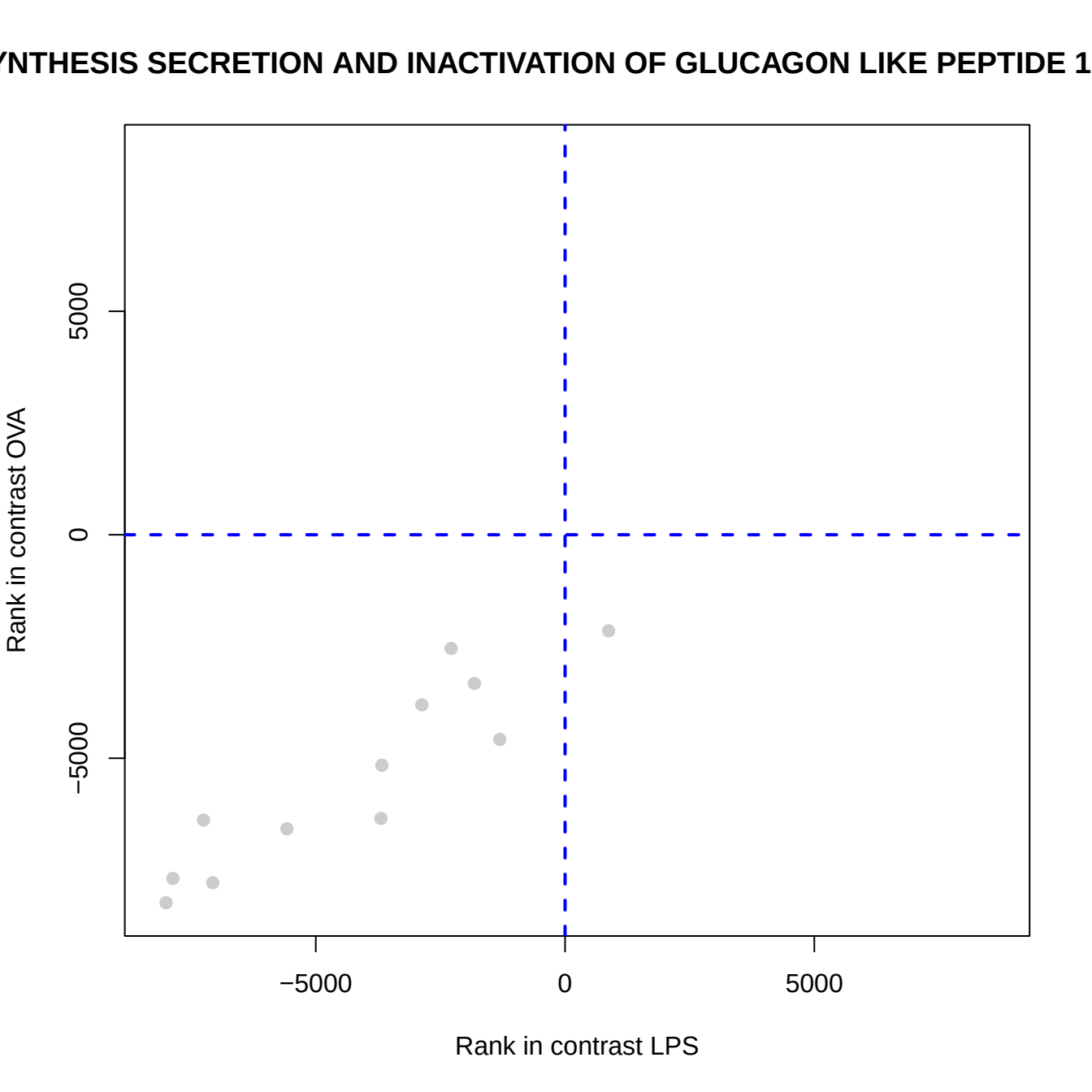

Scatterplot of all gene sets; FDR<0.05 in red
s.OVA
s.LPS
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.4
−0.2
0.0
0.2
0.4

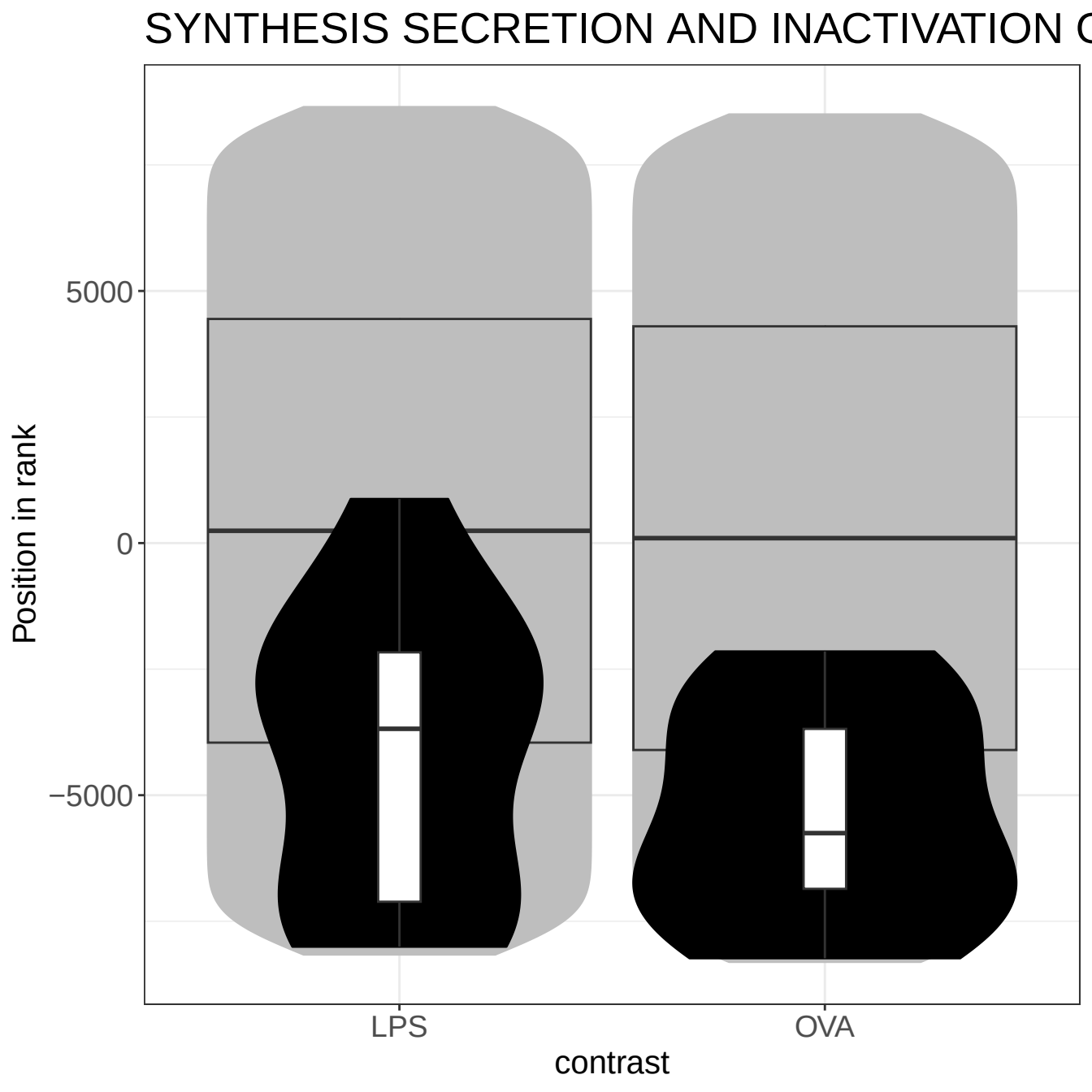

Scatterplot of all gene sets; top 50 in red
s.OVA
s.LPS
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.4
−0.2
0.0
0.2
0.4

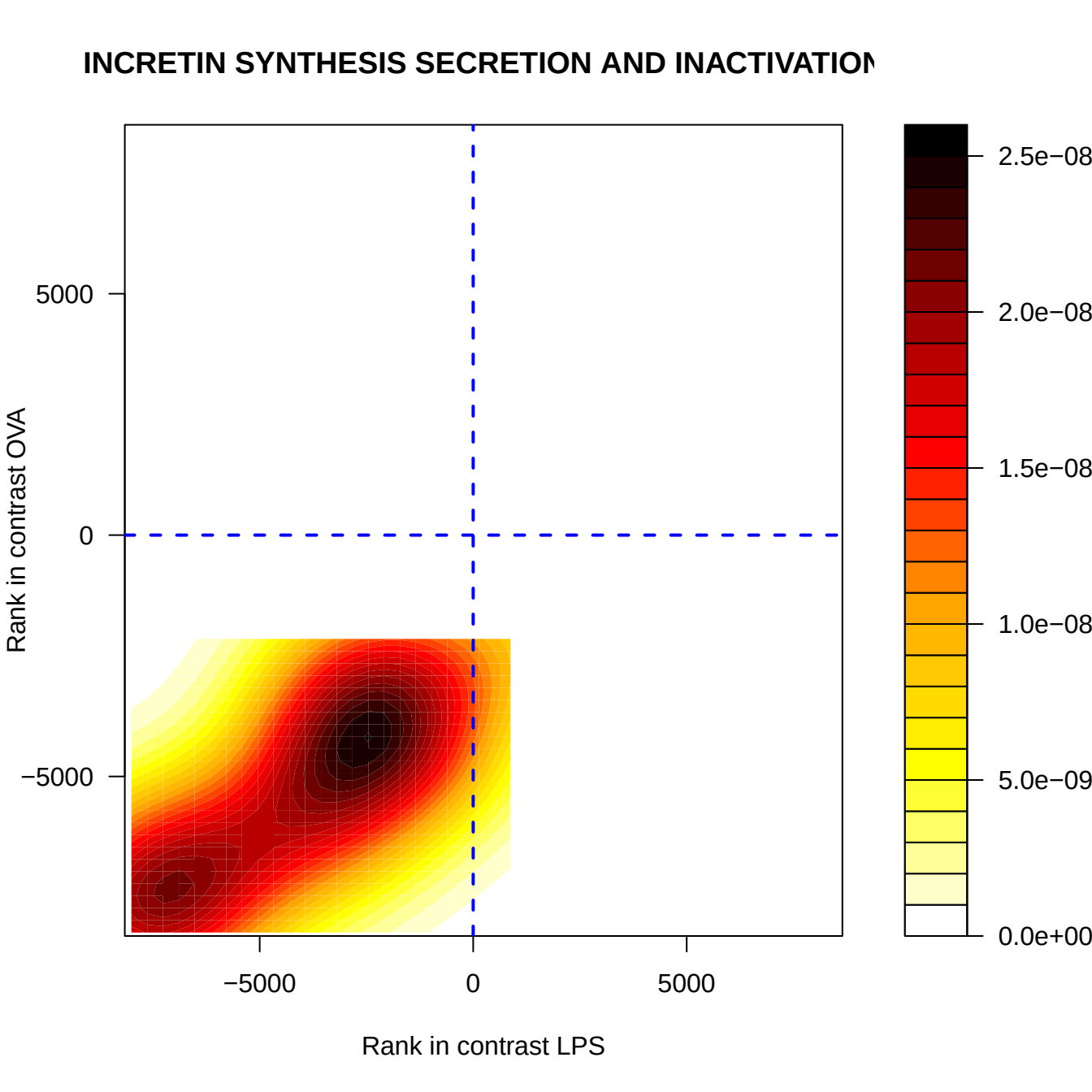

Color Key and Histogram
Count
0
4
8
12
−0.6
−0.2
0.2
0.6
Value
RUNX3 REGULATES NOTCH SIGNALING
NOTCH HLH TRANSCRIPTION PATHWAY
NOTCH4 INTRACELLULAR DOMAIN REGULATES TRANSCRIPTION
REGULATION OF COMMISSURAL AXON PATHFINDING BY SLIT AND ROBO
SIGNALING BY LEPTIN
NRAGE SIGNALS DEATH THROUGH JNK
CRMPS IN SEMA3A SIGNALING
CELLULAR HEXOSE TRANSPORT
CROSSLINKING OF COLLAGEN FIBRILS
CYTOSOLIC IRON SULFUR CLUSTER ASSEMBLY
POST CHAPERONIN TUBULIN FOLDING PATHWAY
SELENOAMINO ACID METABOLISM
ACTIVATION OF THE MRNA UPON BINDING OF THE CAP BINDING COMPLE
RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID DEFICIENCY
EUKARYOTIC TRANSLATION INITIATION
PROTEIN METHYLATION
TRIGLYCERIDE CATABOLISM
TRAFFICKING AND PROCESSING OF ENDOSOMAL TLR
NEGATIVE REGULATION OF NOTCH4 SIGNALING
SYNTHESIS SECRETION AND INACTIVATION OF GLUCAGON LIKE PEPTIDE
ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 12
SYNTHESIS OF VERY LONG CHAIN FATTY ACYL COAS
PROCESSING AND ACTIVATION OF SUMO
CD28 DEPENDENT VAV1 PATHWAY
SYNTHESIS SECRETION AND DEACYLATION OF GHRELIN
OVA
LPS

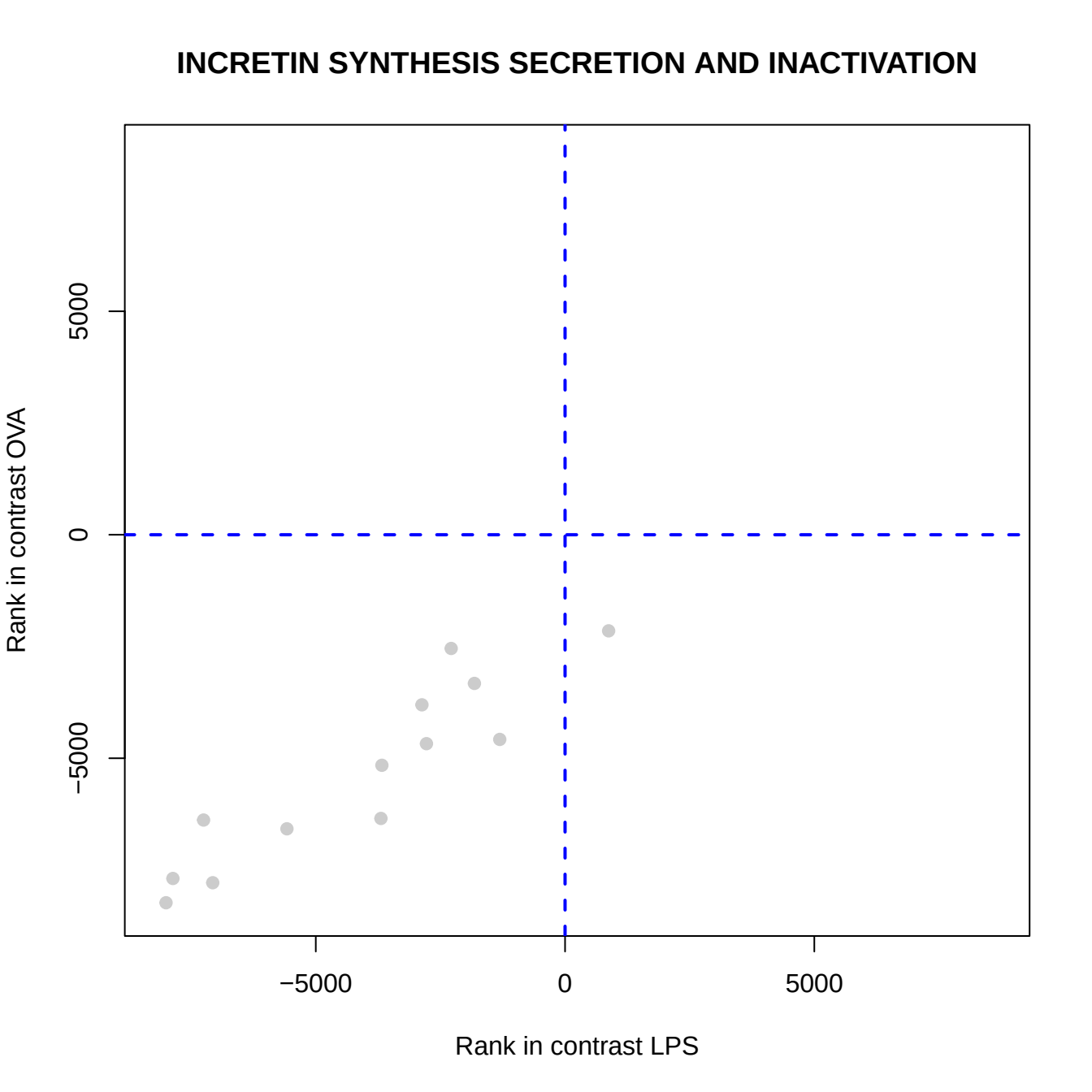

effect size versus statistical significance
−log(p.adjustMANOVA) (significance)
0
20
40
60
80
100
120
140
0.0
0.2
0.4
0.6
0.8
s.dist (effect size)

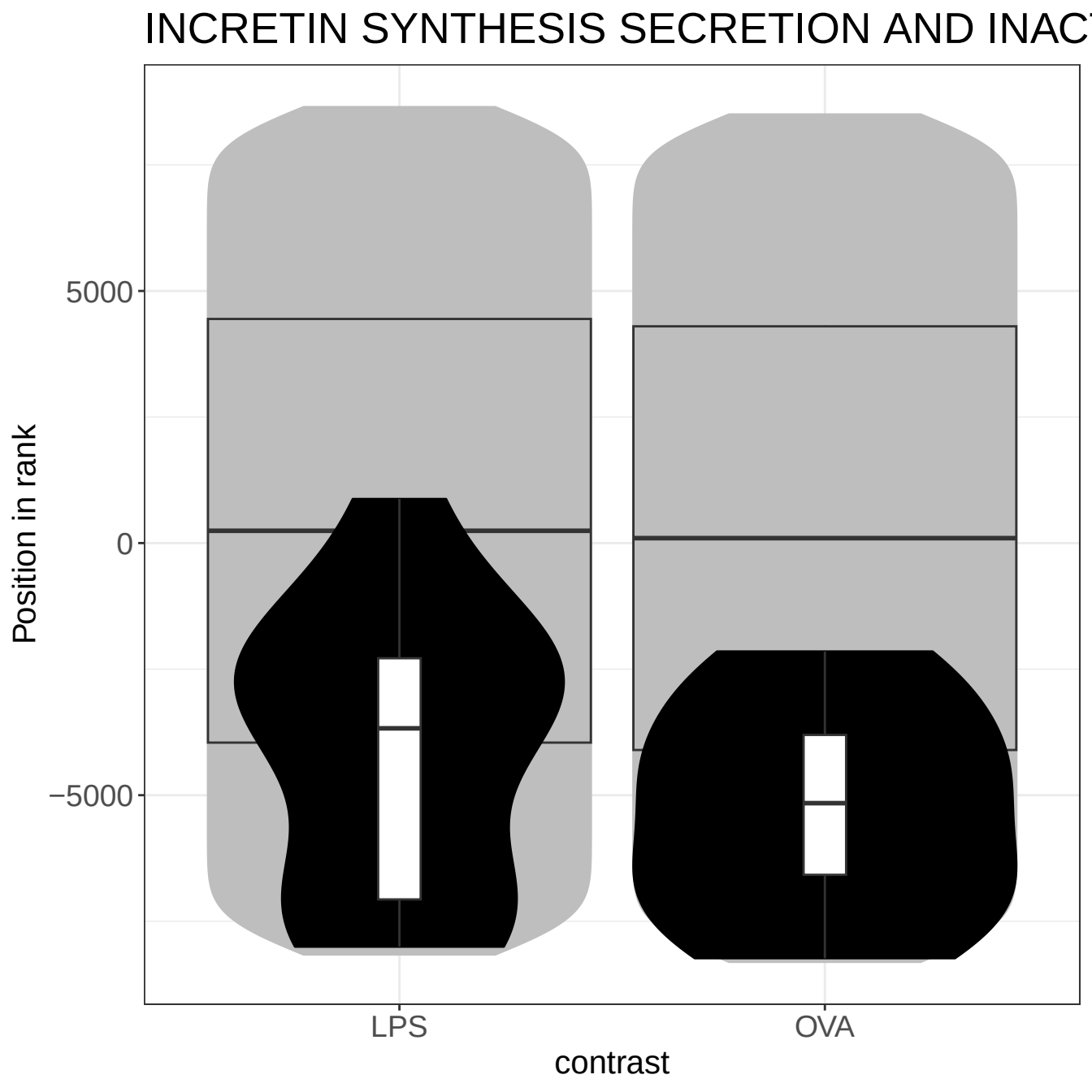

SIS SECRETION AND INACTIVATION OF GLUCAGON LIKE PE
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

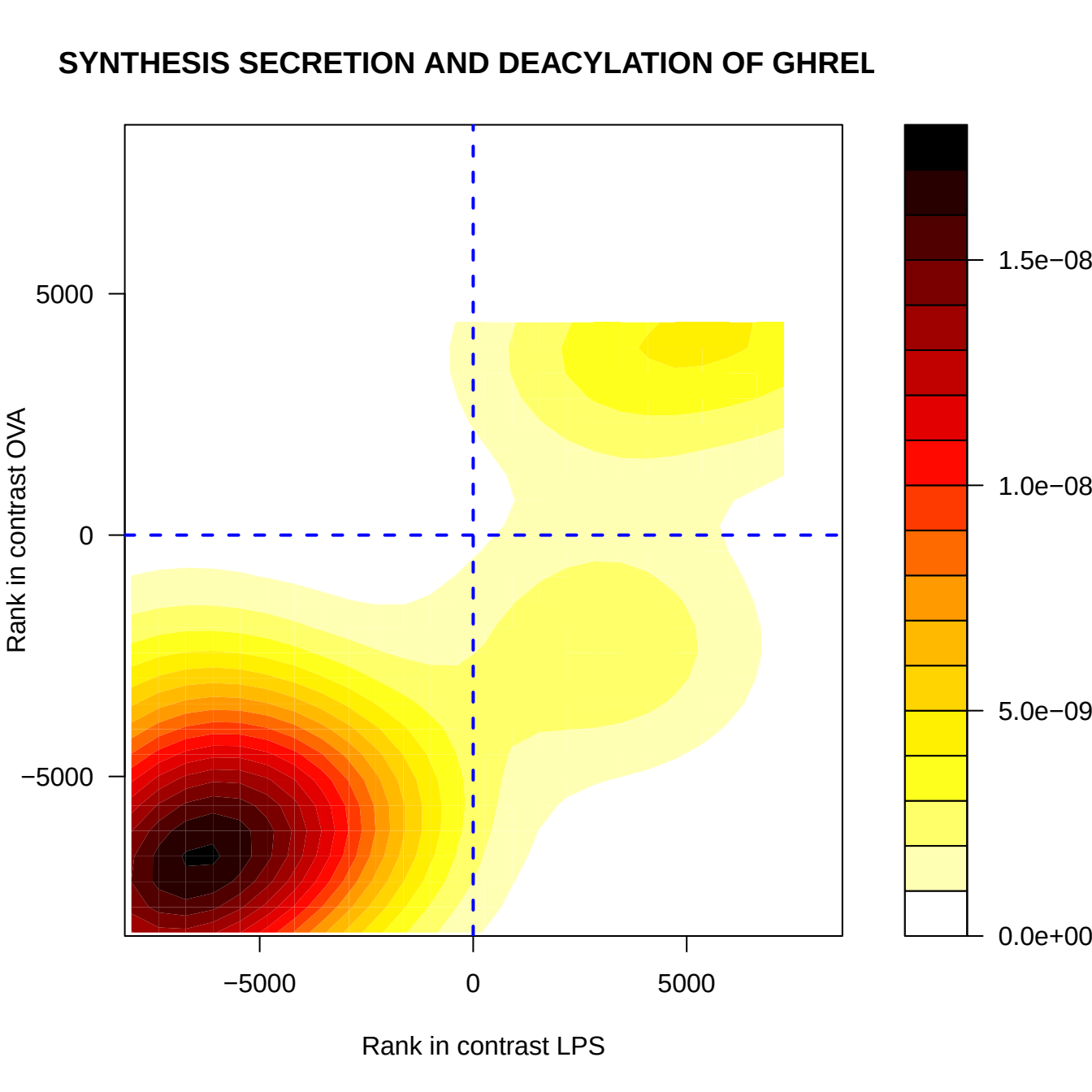

YNTHESIS SECRETION AND INACTIVATION OF GLUCAGON LIKE PEPTIDE 1
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

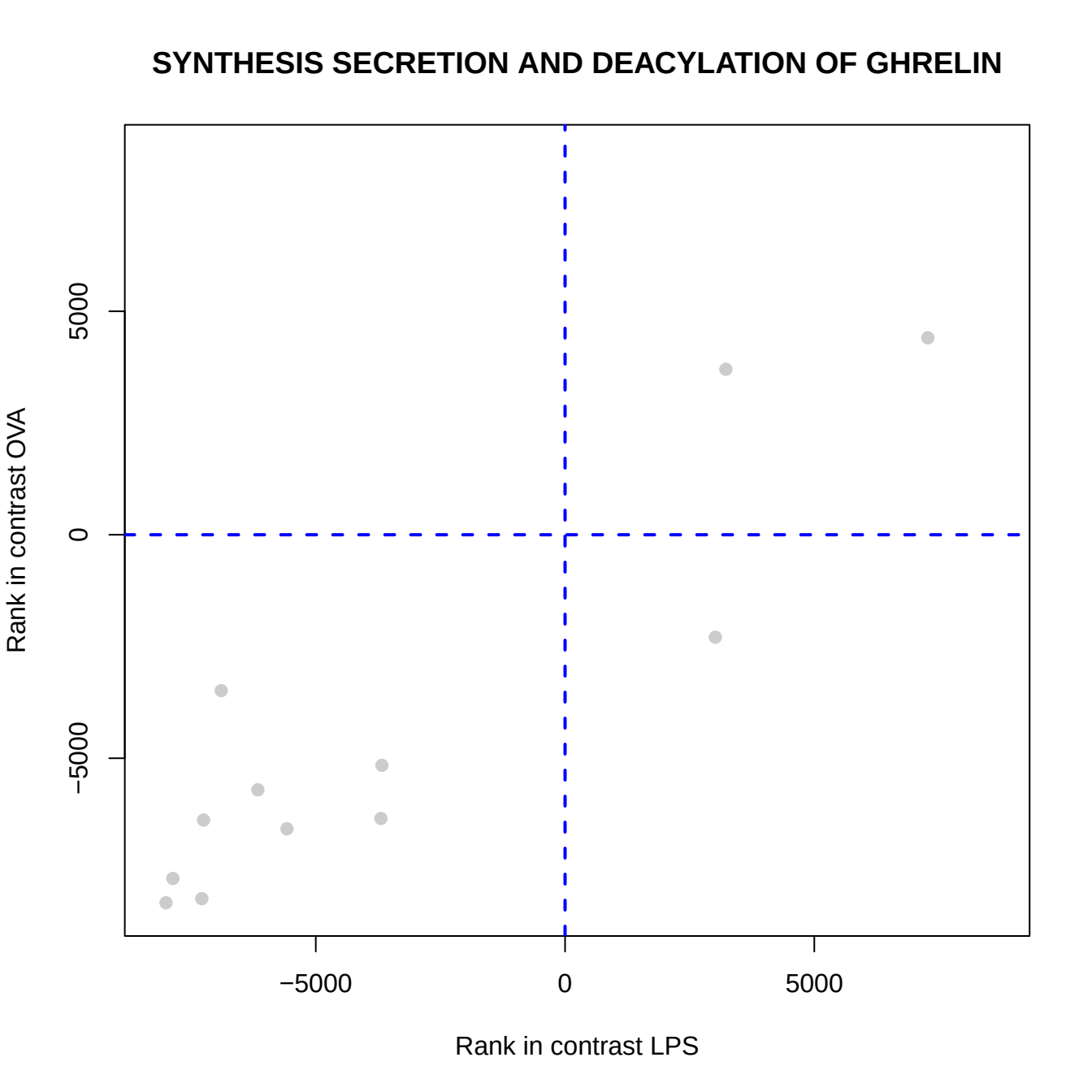

SYNTHESIS SECRETION AND INACTIVATION C
5000
0
−5000
Position in rank
LPS
OVA
contrast

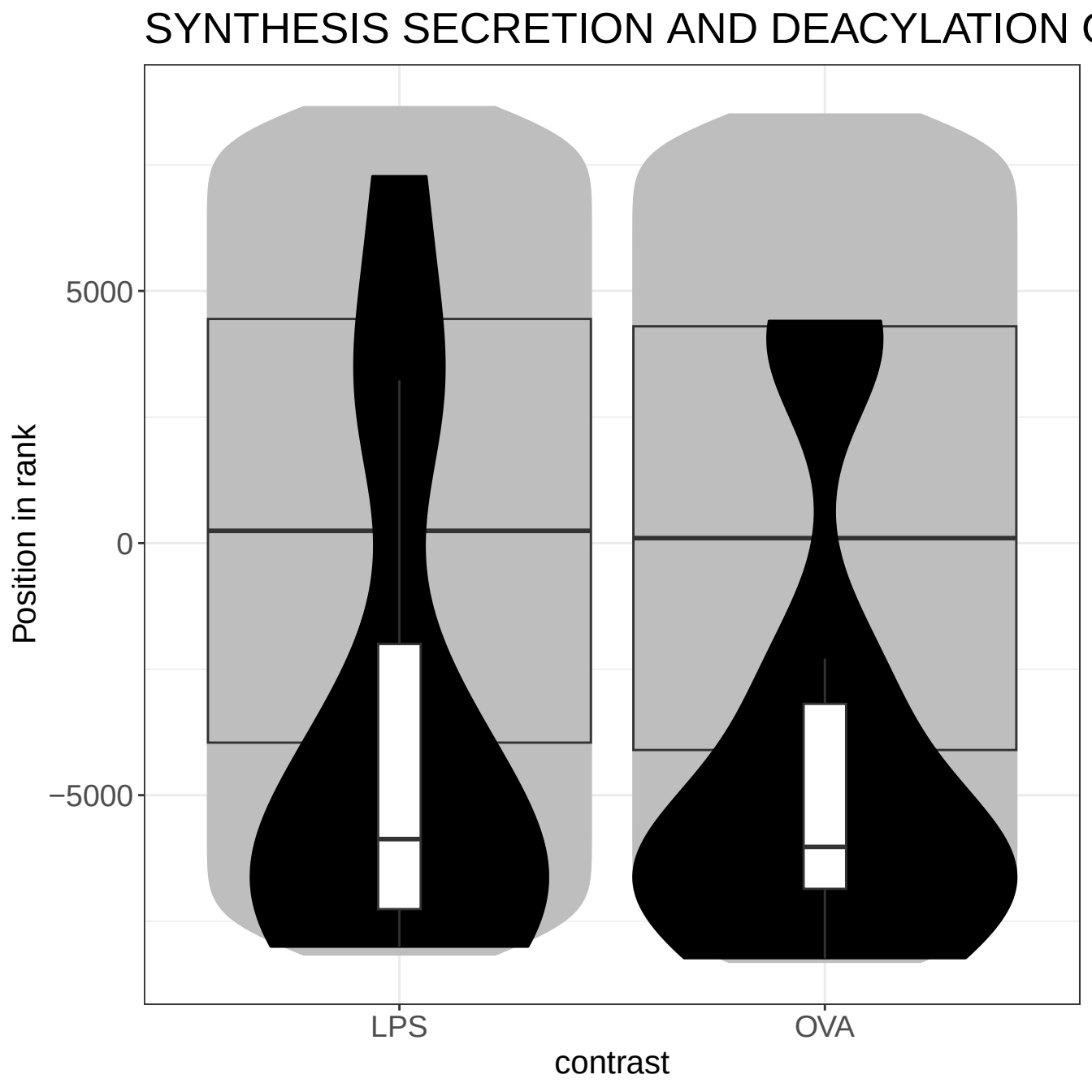

INCRETIN SYNTHESIS SECRETION AND INACTIVATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.5e−08
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

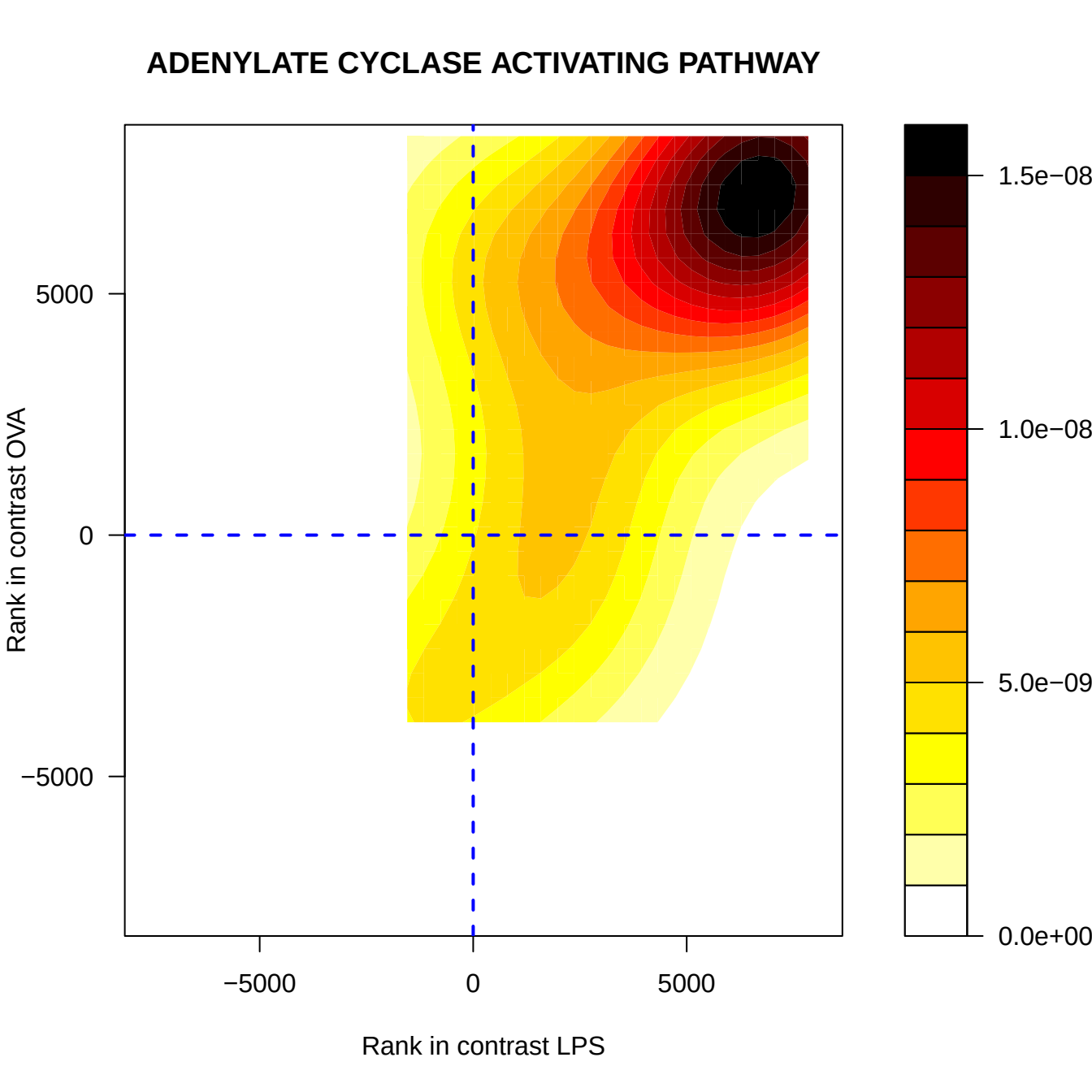

INCRETIN SYNTHESIS SECRETION AND INACTIVATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

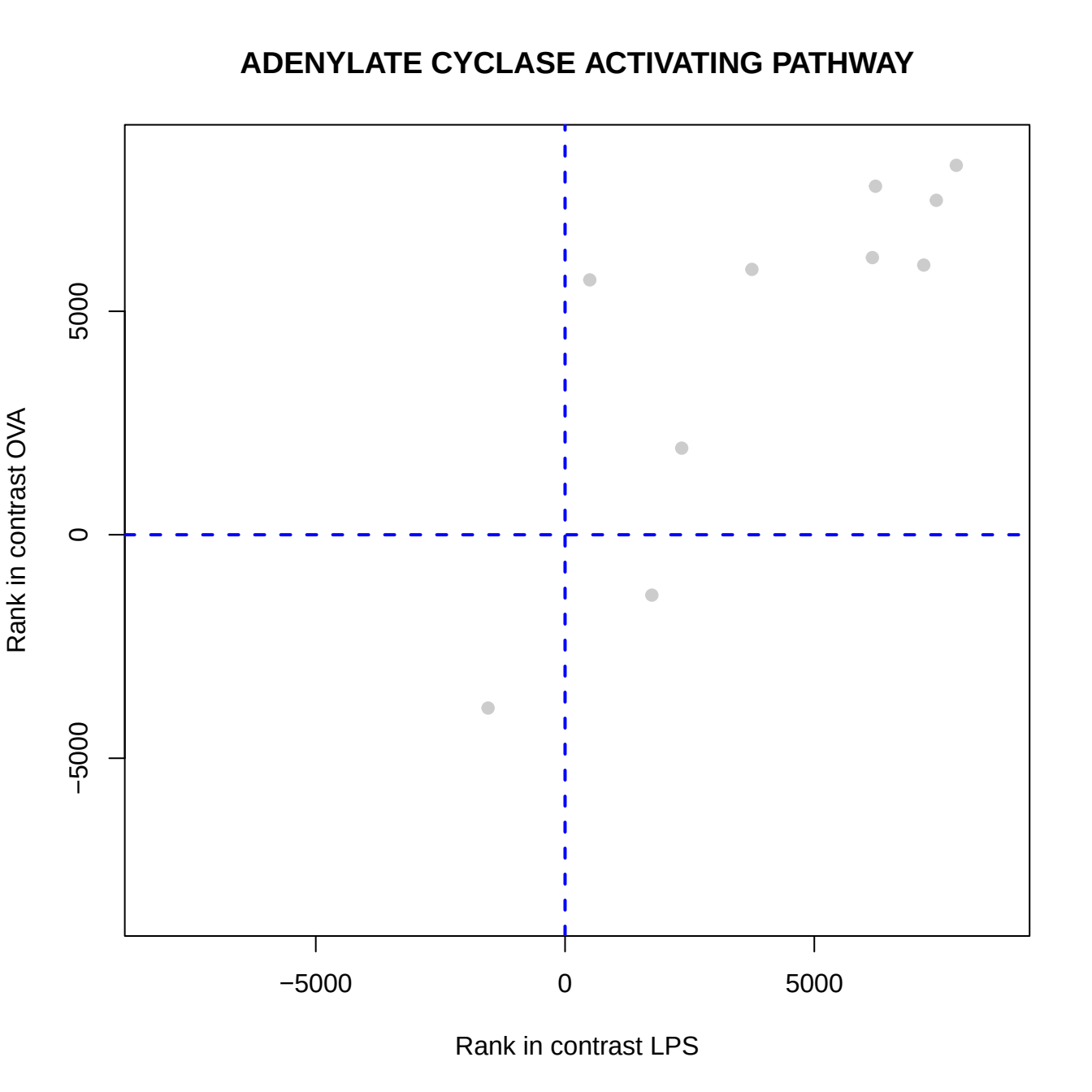

INCRETIN SYNTHESIS SECRETION AND INAC
5000
0
−5000
Position in rank
LPS
OVA
contrast

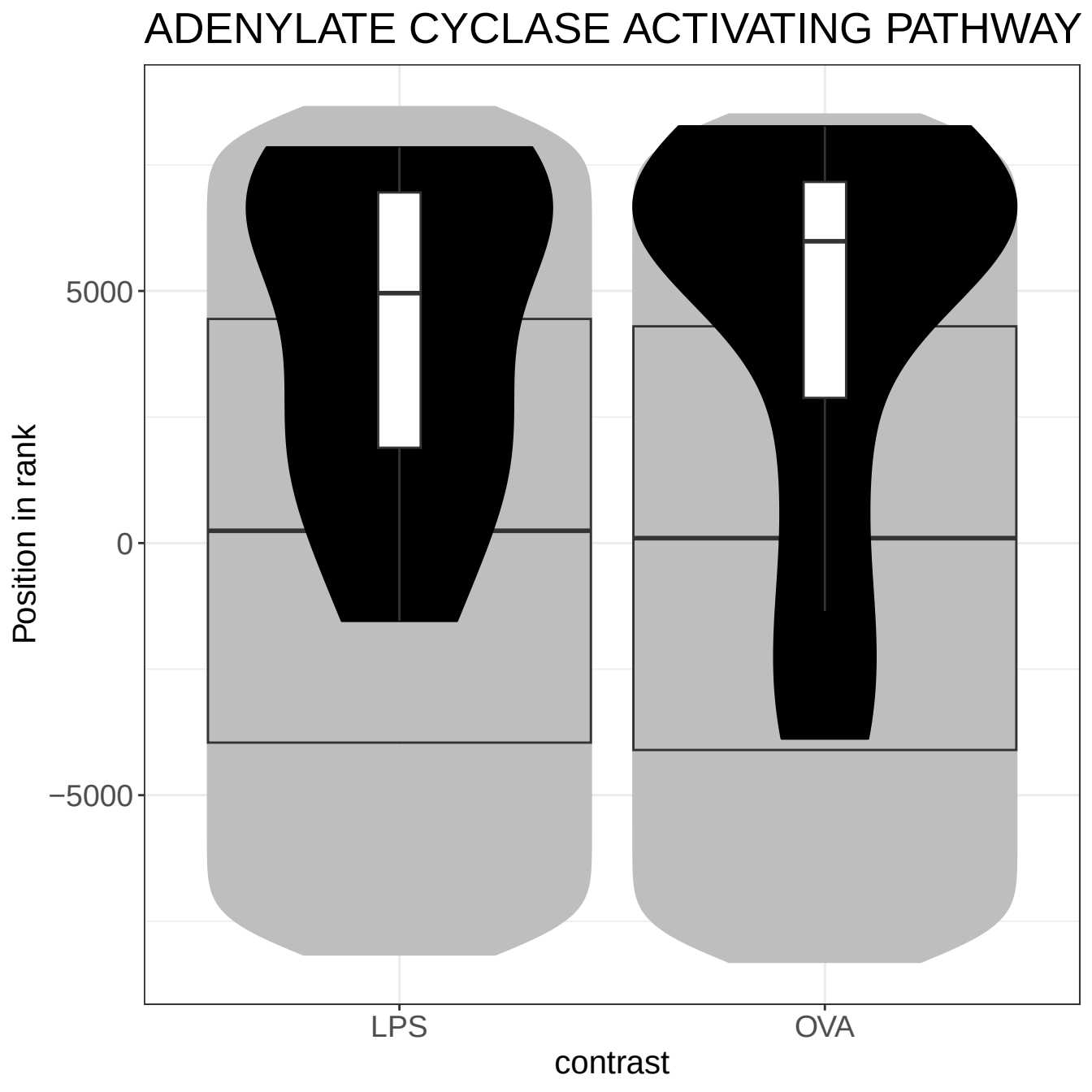

SYNTHESIS SECRETION AND DEACYLATION OF GHREL
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

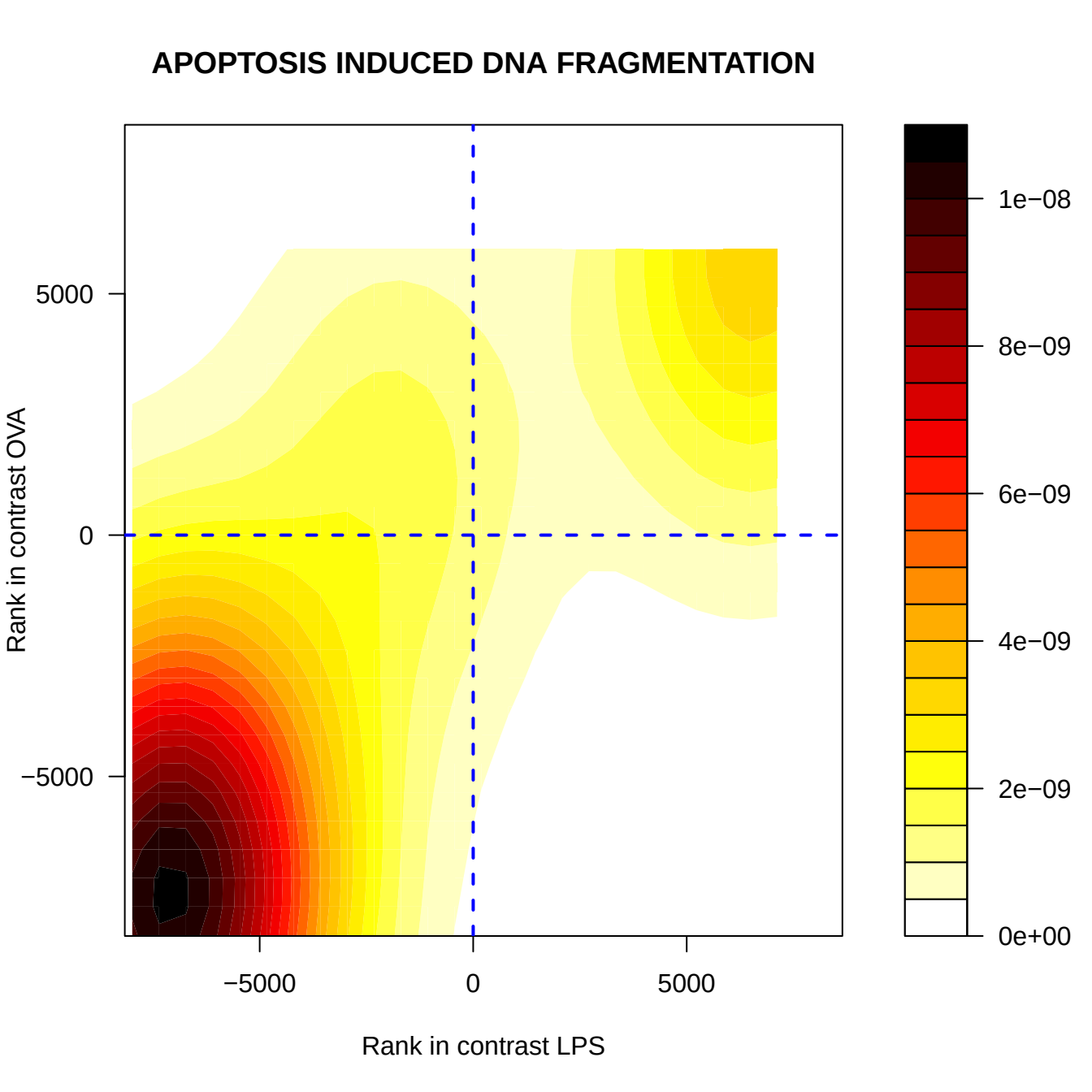

SYNTHESIS SECRETION AND DEACYLATION OF GHRELIN
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

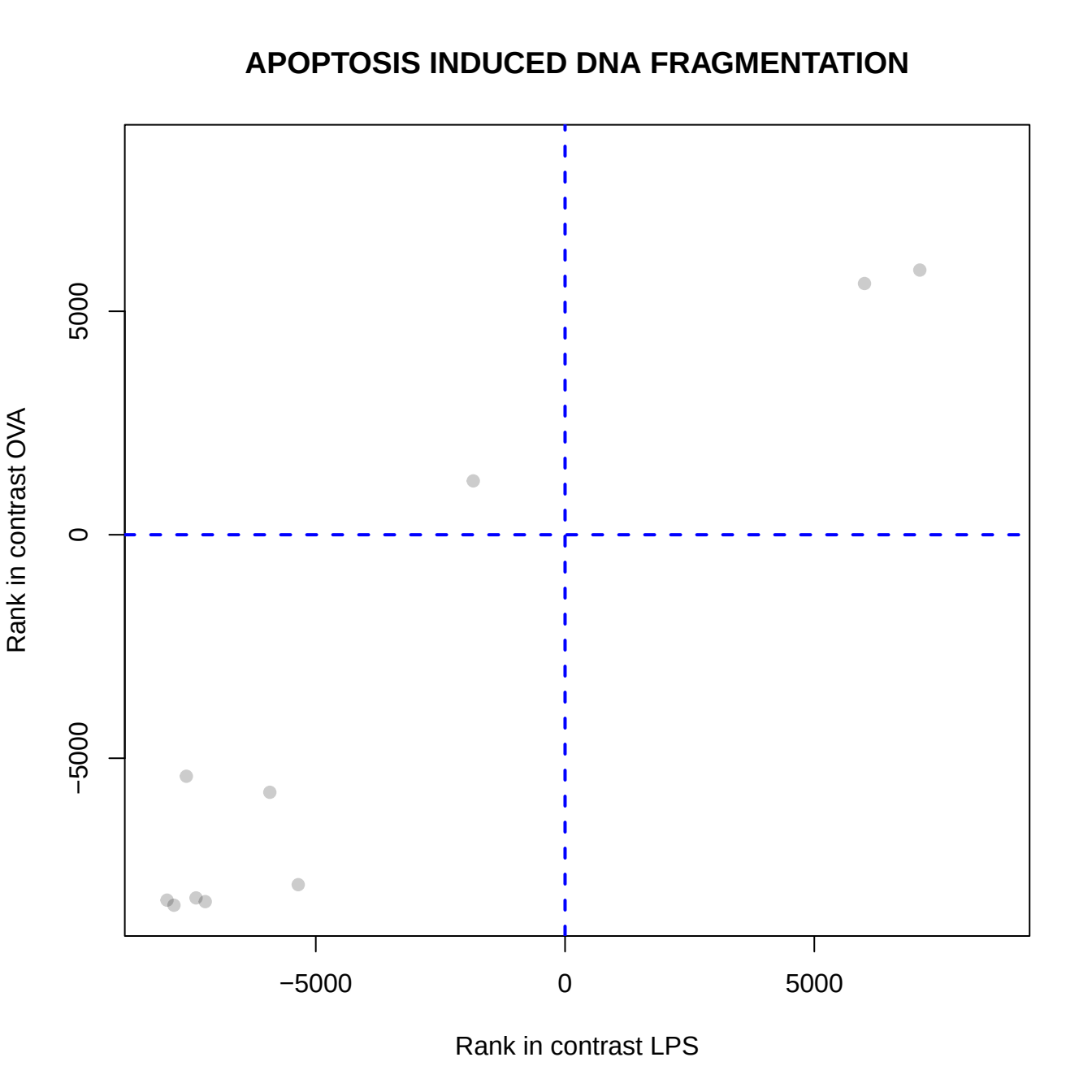

SYNTHESIS SECRETION AND DEACYLATION
5000
0
−5000
Position in rank
LPS
OVA
contrast

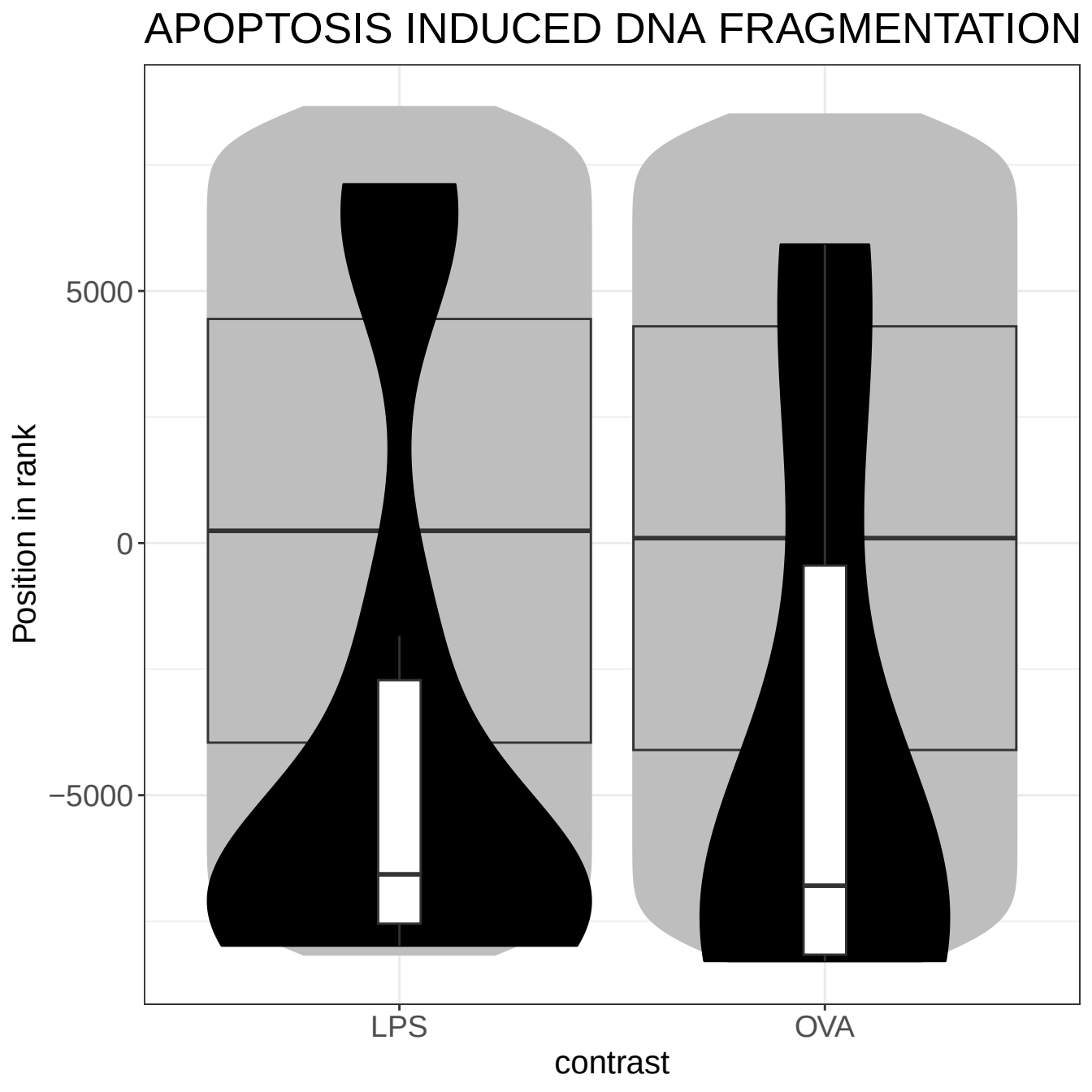

ADENYLATE CYCLASE ACTIVATING PATHWAY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

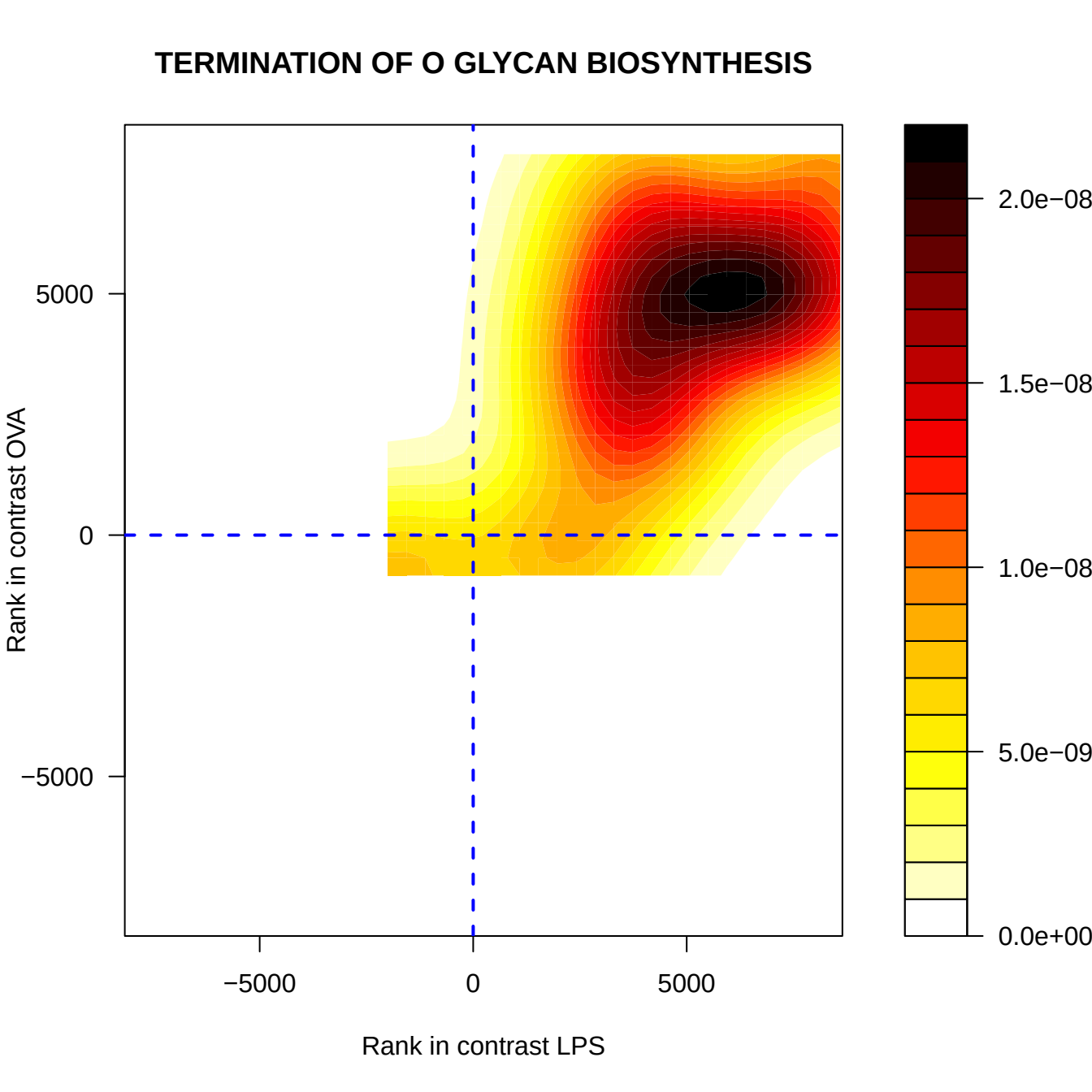

ADENYLATE CYCLASE ACTIVATING PATHWAY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

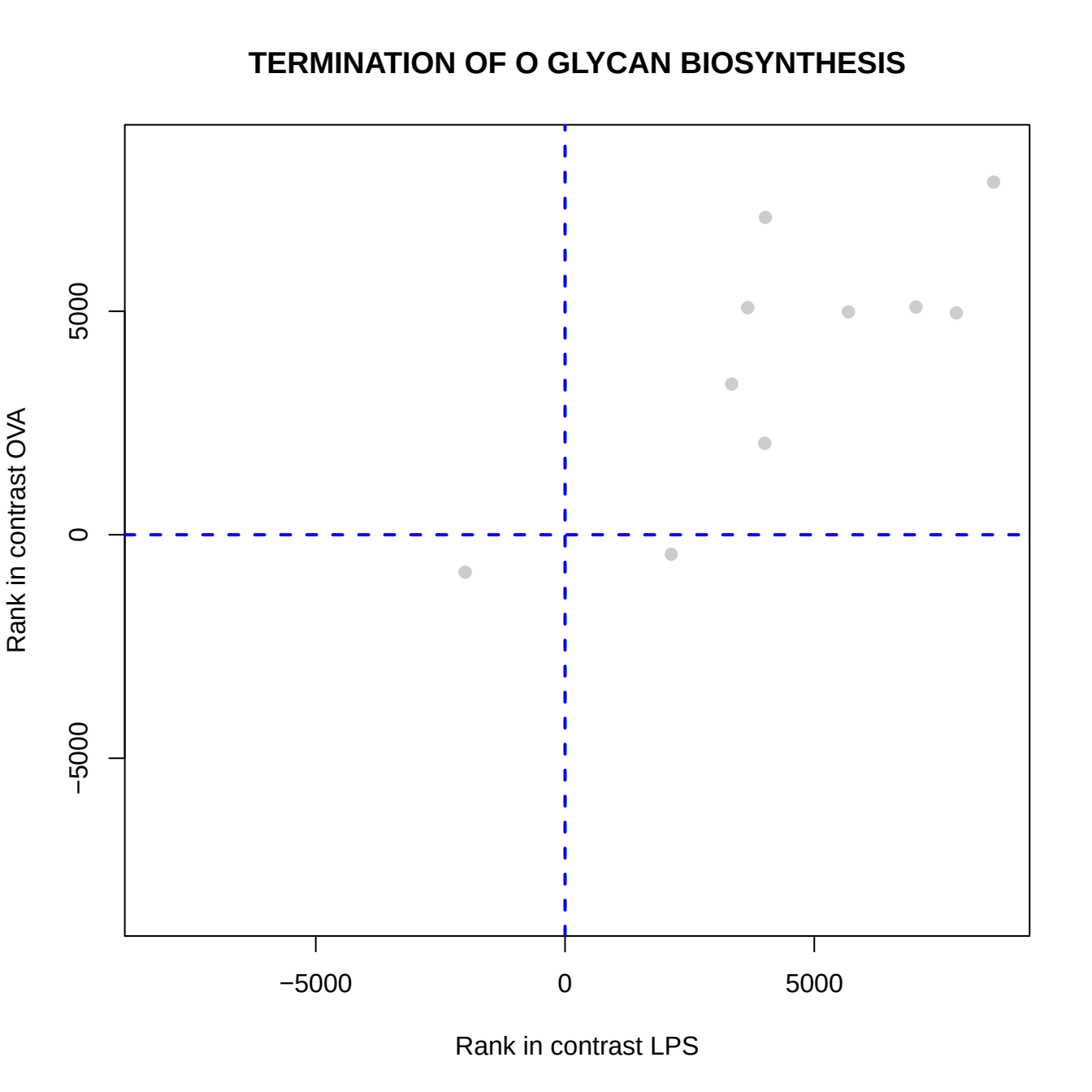

ADENYLATE CYCLASE ACTIVATING PATHWAY
Position in rank
5000
0
−5000
LPS
OVA
contrast

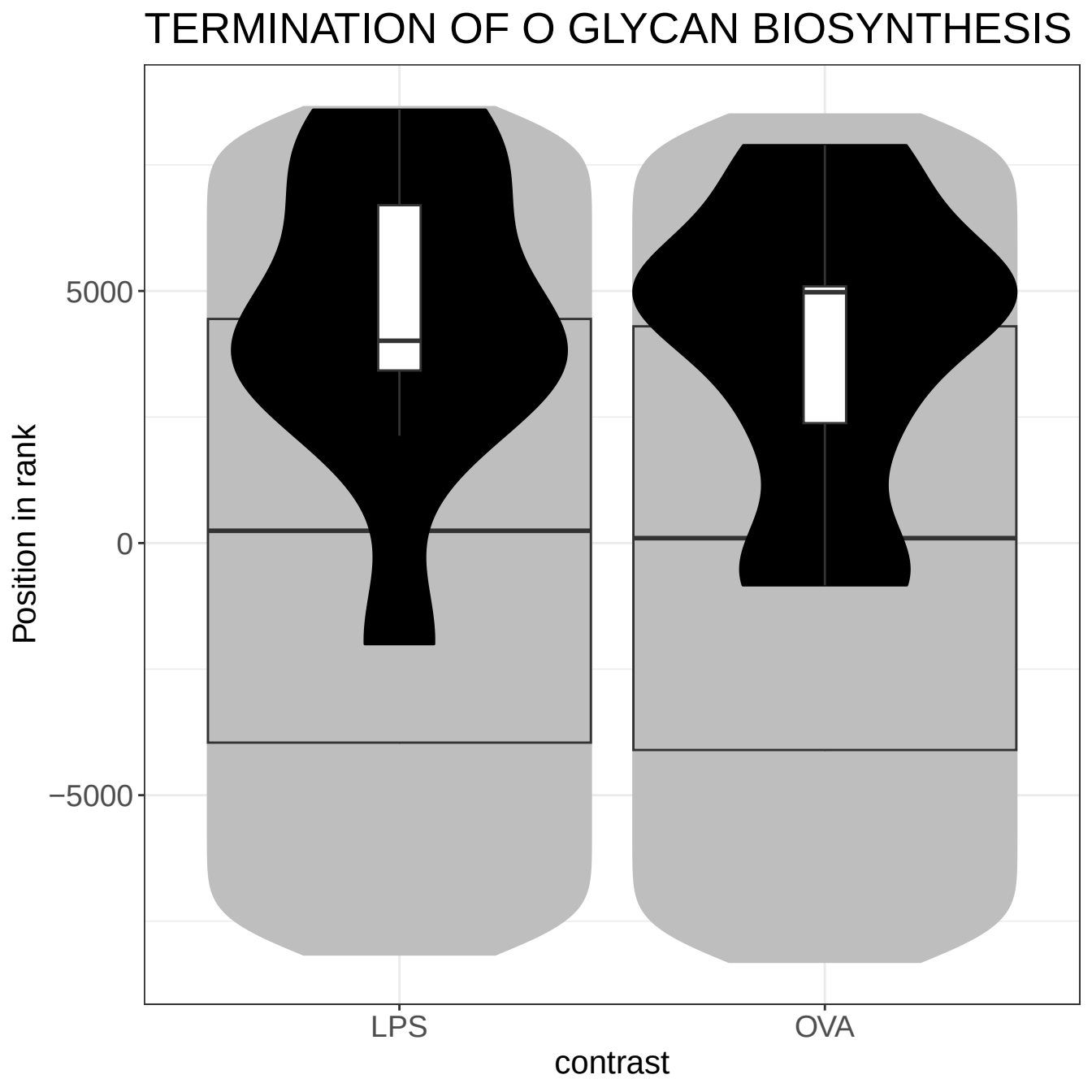

APOPTOSIS INDUCED DNA FRAGMENTATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

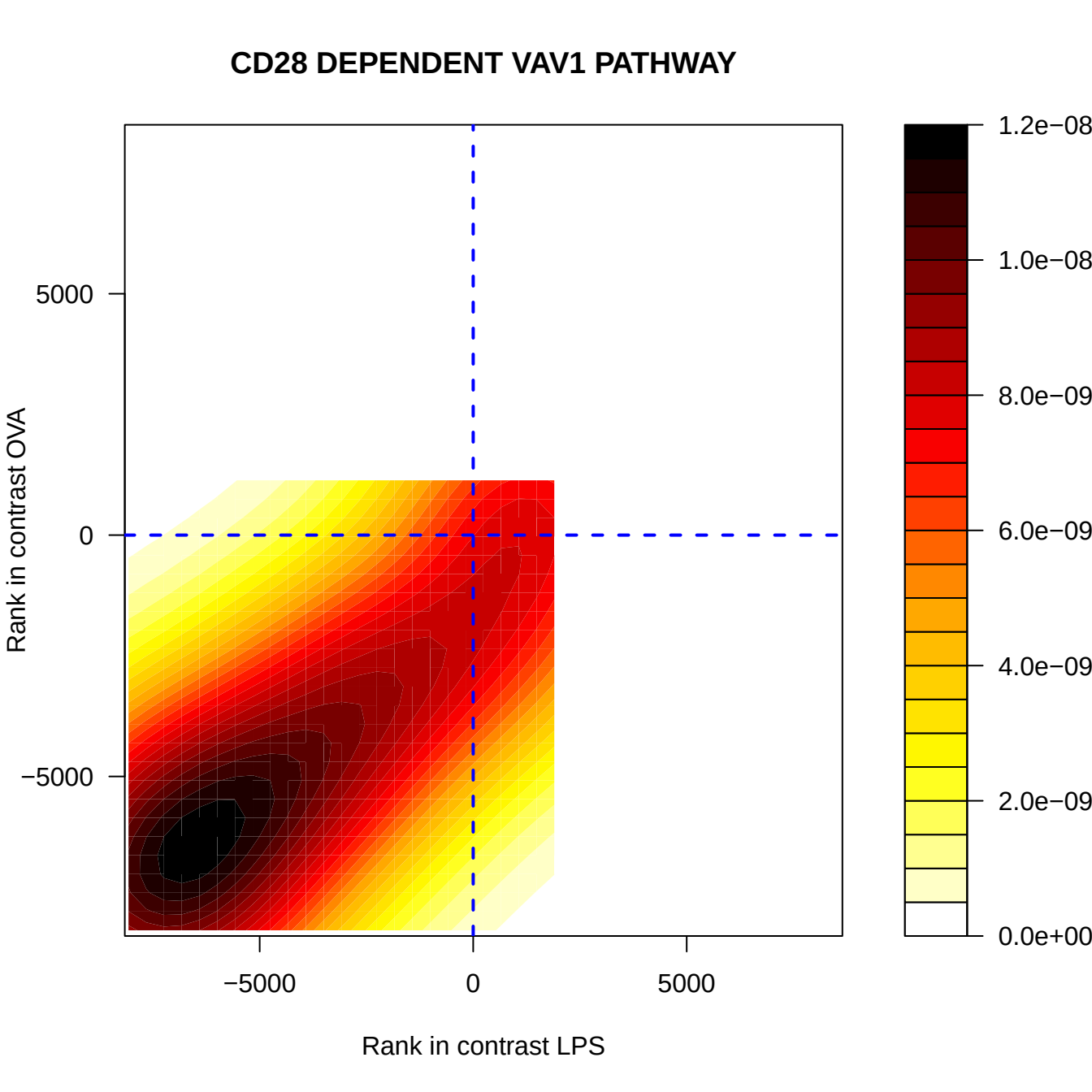

APOPTOSIS INDUCED DNA FRAGMENTATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

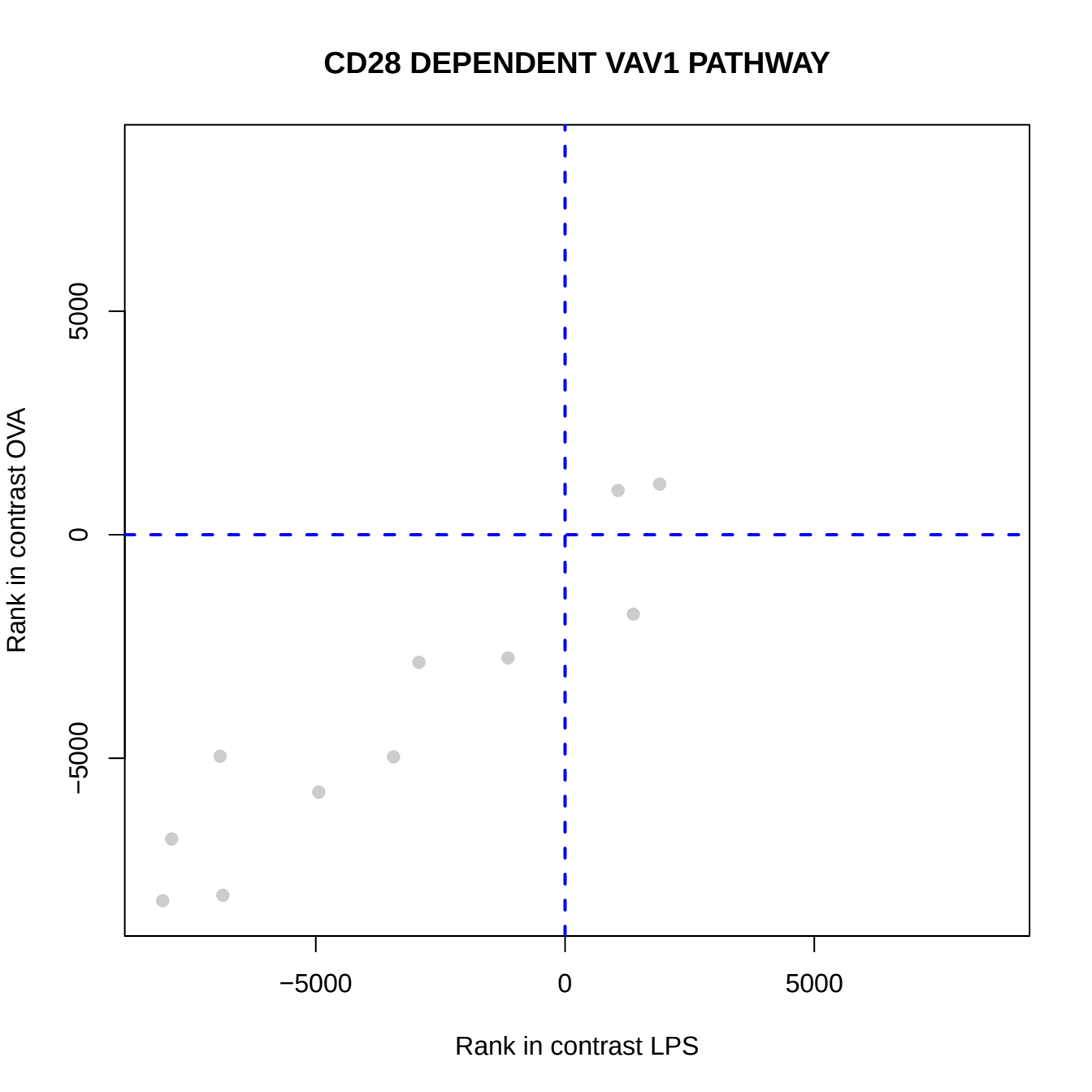

APOPTOSIS INDUCED DNA FRAGMENTATION
5000
0
−5000
Position in rank
LPS
OVA
contrast

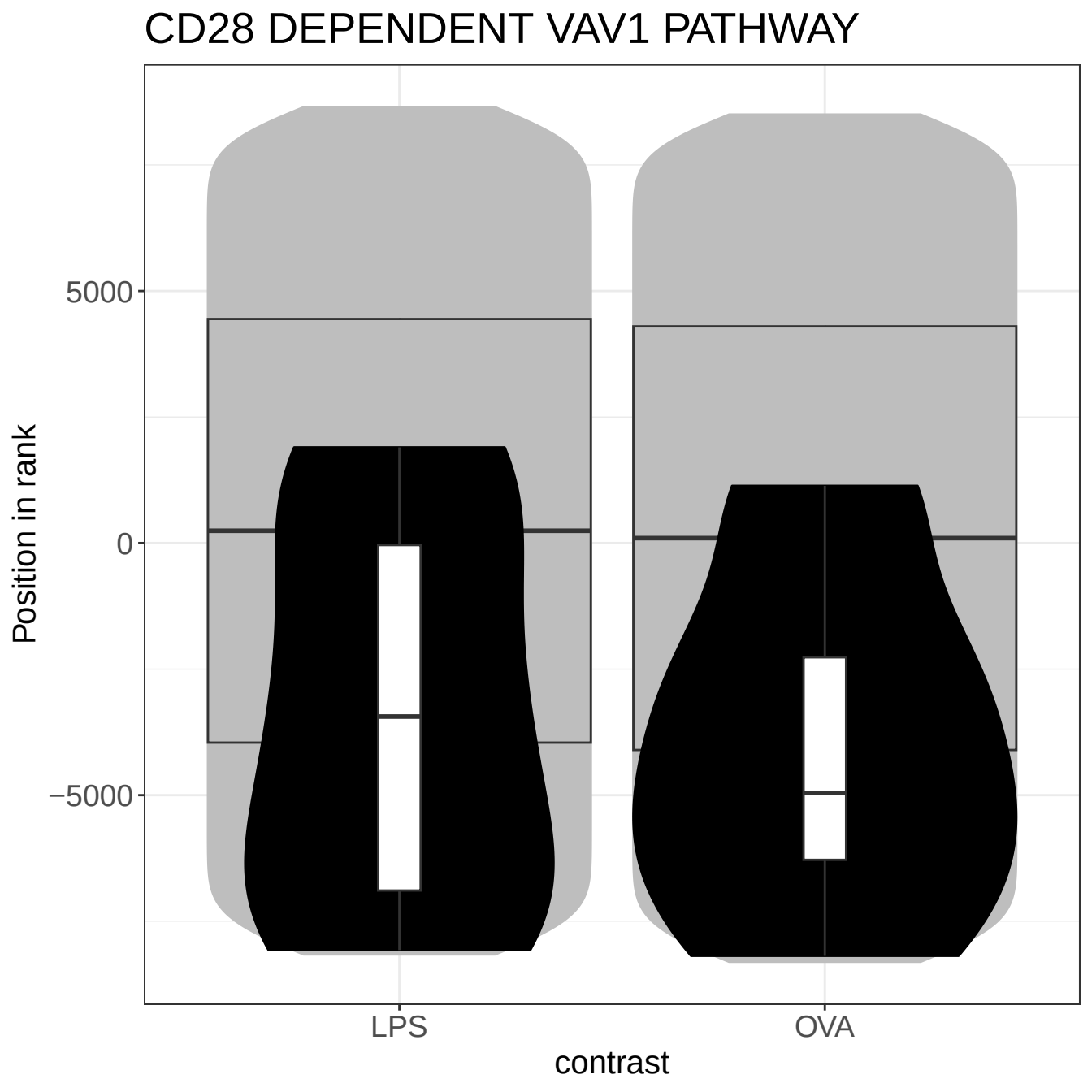

TERMINATION OF O GLYCAN BIOSYNTHESIS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

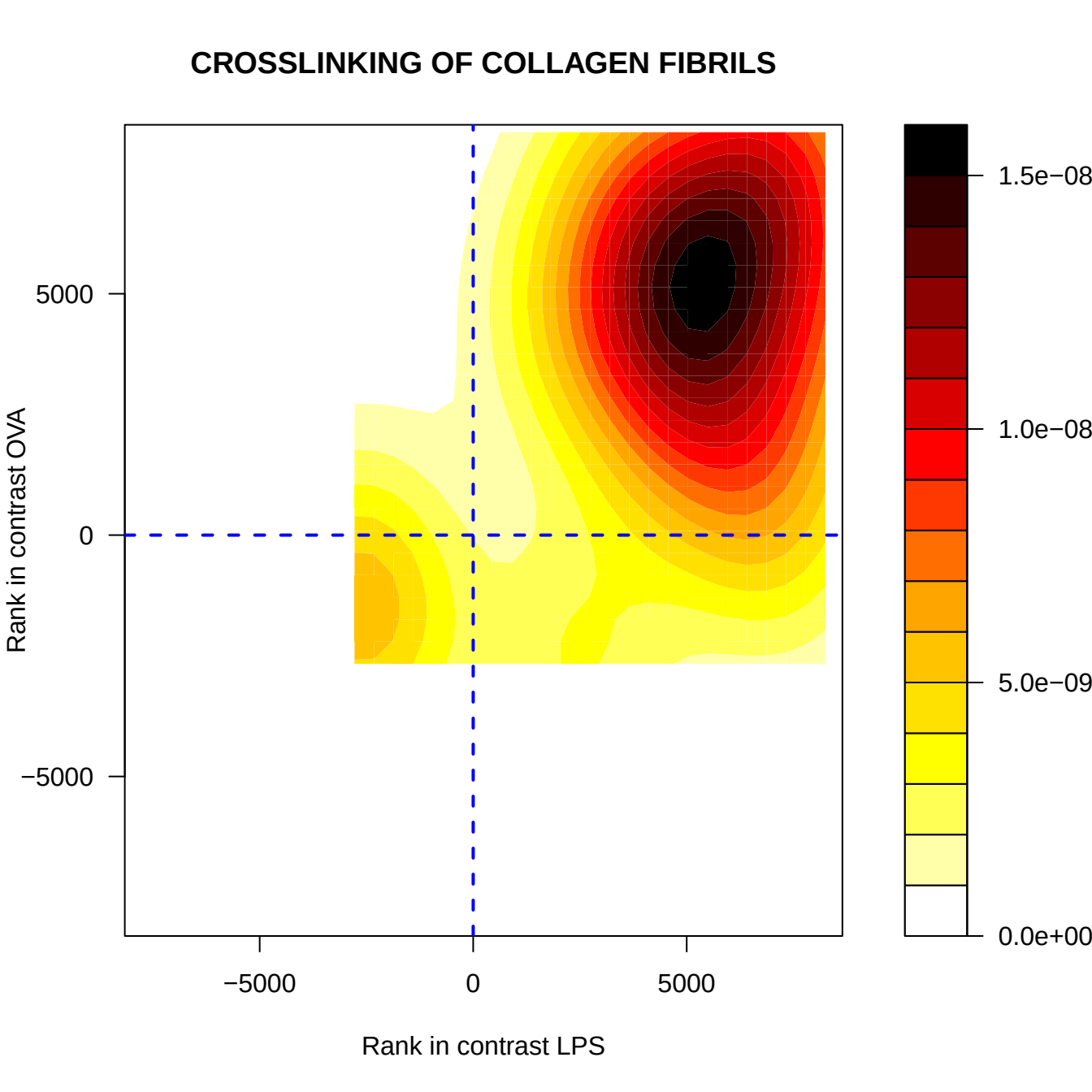

TERMINATION OF O GLYCAN BIOSYNTHESIS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

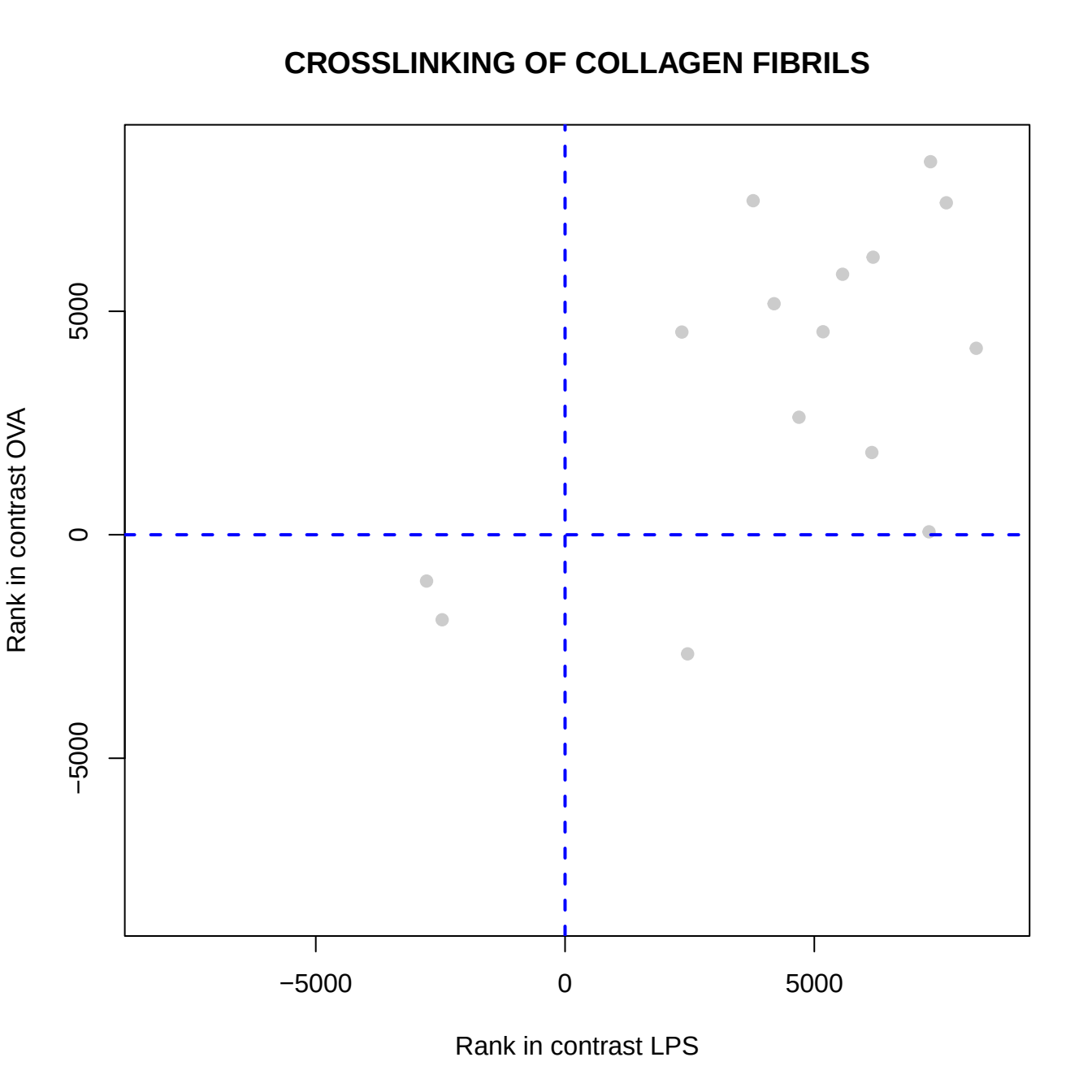

TERMINATION OF O GLYCAN BIOSYNTHESIS
Position in rank
5000
0
−5000
LPS
OVA
contrast

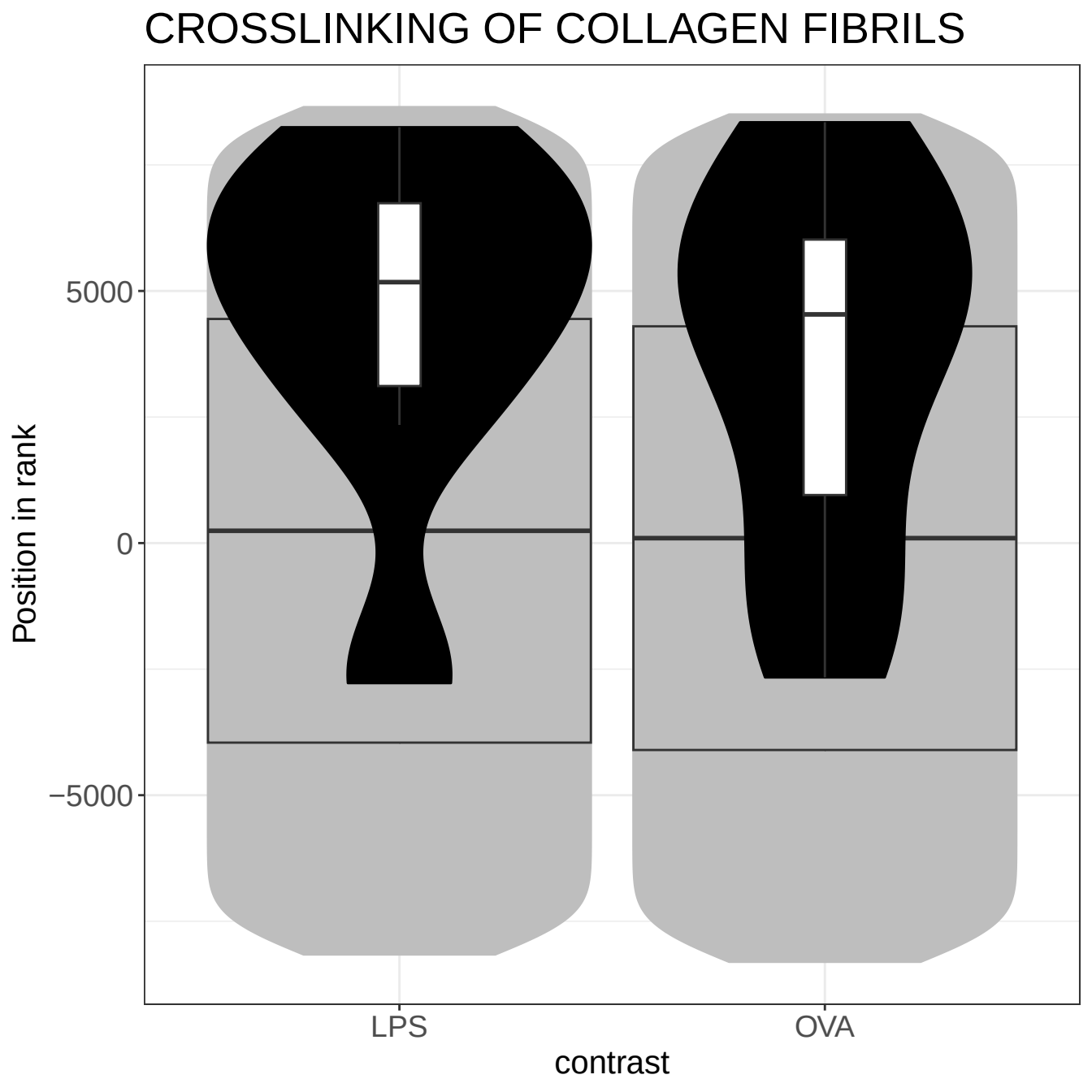

CD28 DEPENDENT VAV1 PATHWAY
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

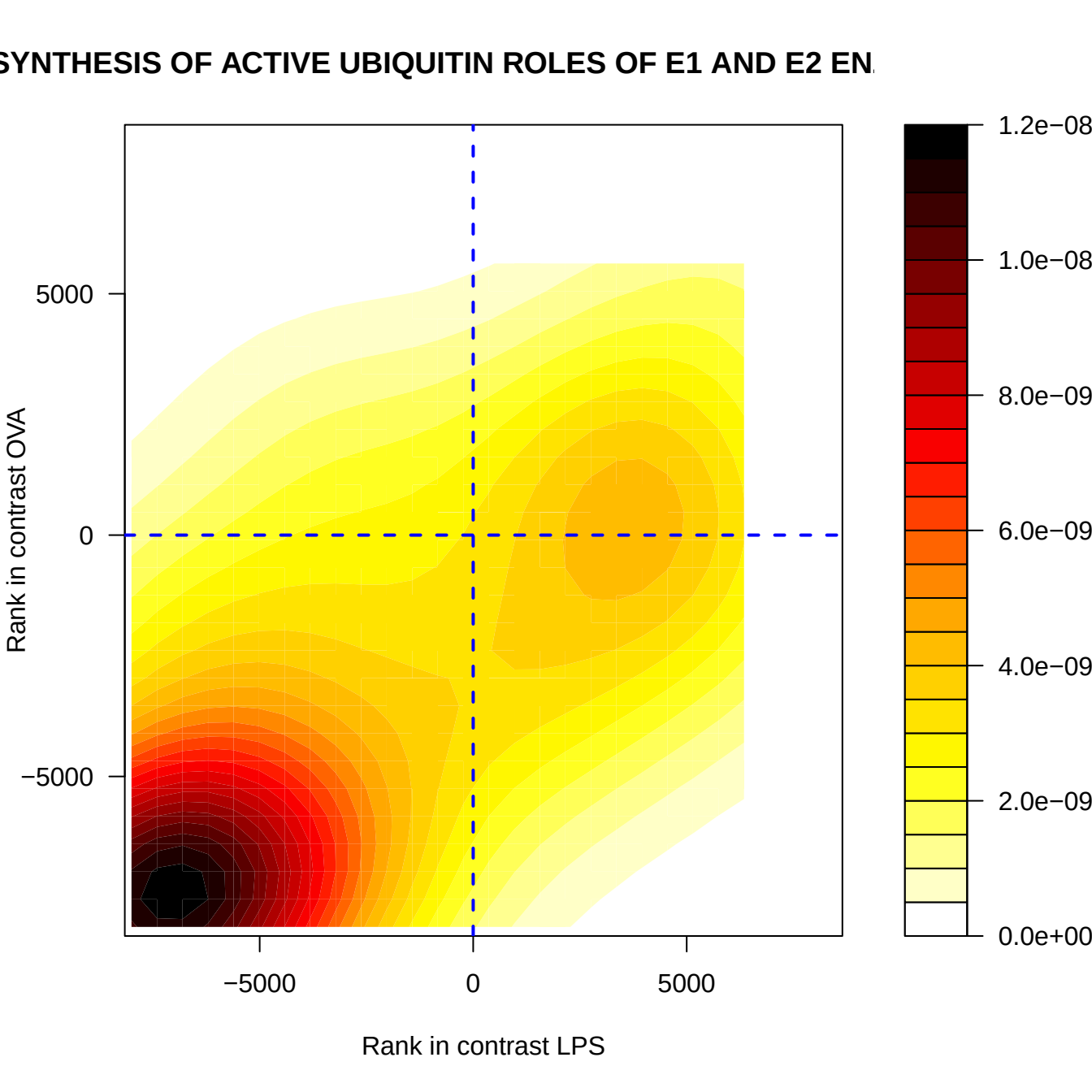

CD28 DEPENDENT VAV1 PATHWAY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS


CD28 DEPENDENT VAV1 PATHWAY
5000
0
−5000
Position in rank
LPS
OVA
contrast

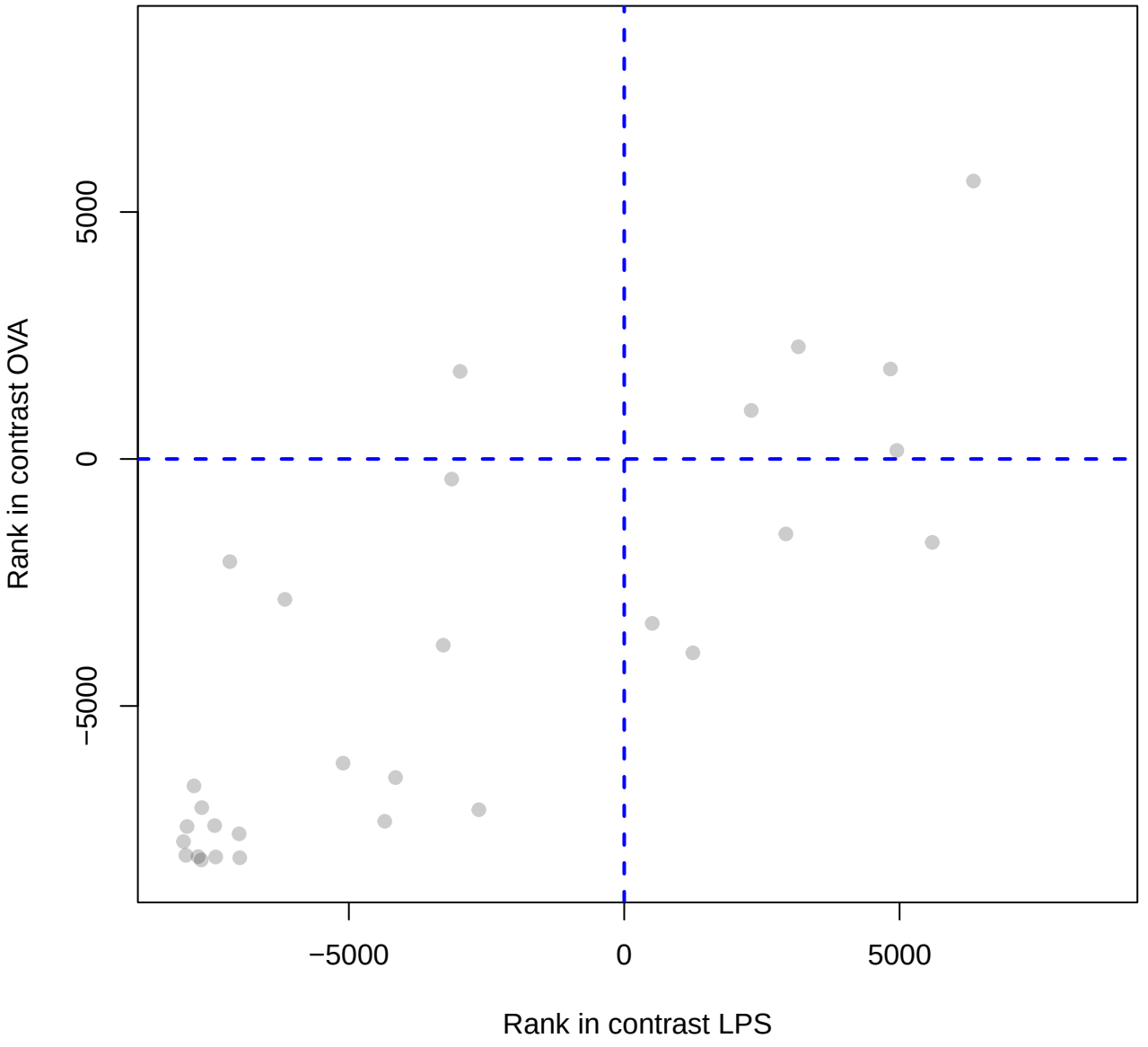

CROSSLINKING OF COLLAGEN FIBRILS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

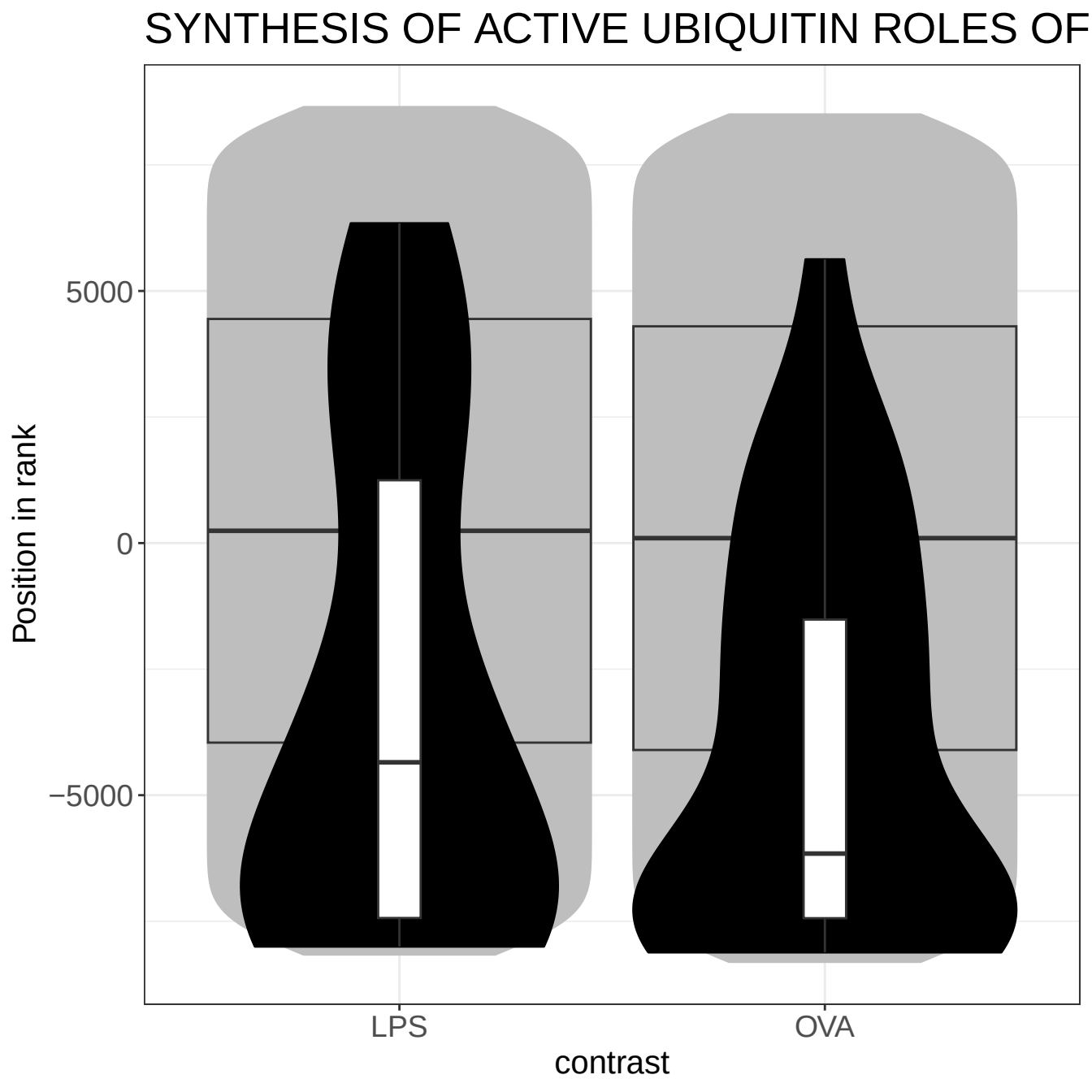

CROSSLINKING OF COLLAGEN FIBRILS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

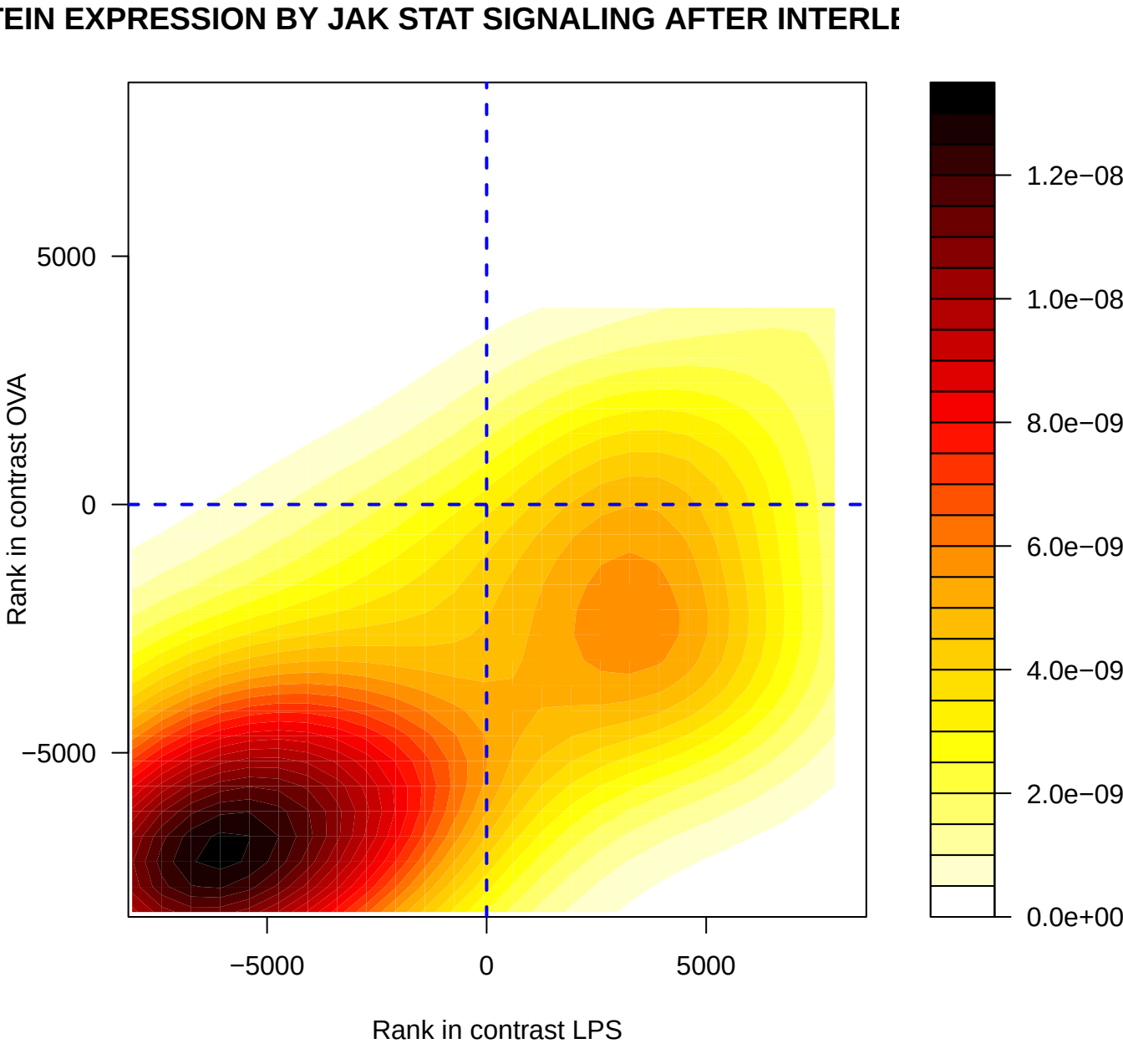

CROSSLINKING OF COLLAGEN FIBRILS
5000
0
−5000
Position in rank
LPS
OVA
contrast

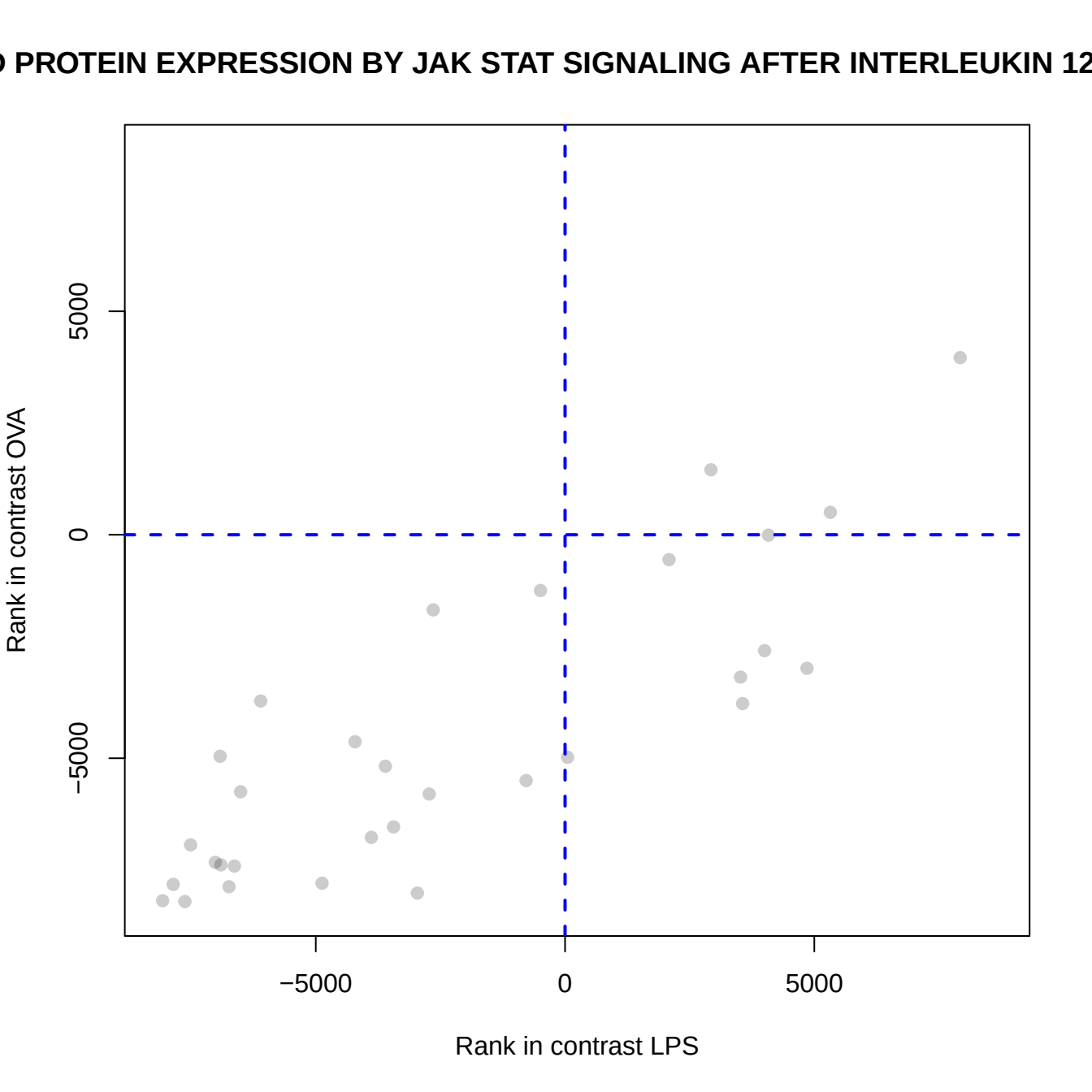

SYNTHESIS OF ACTIVE UBIQUITIN ROLES OF E1 AND E2 EN
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

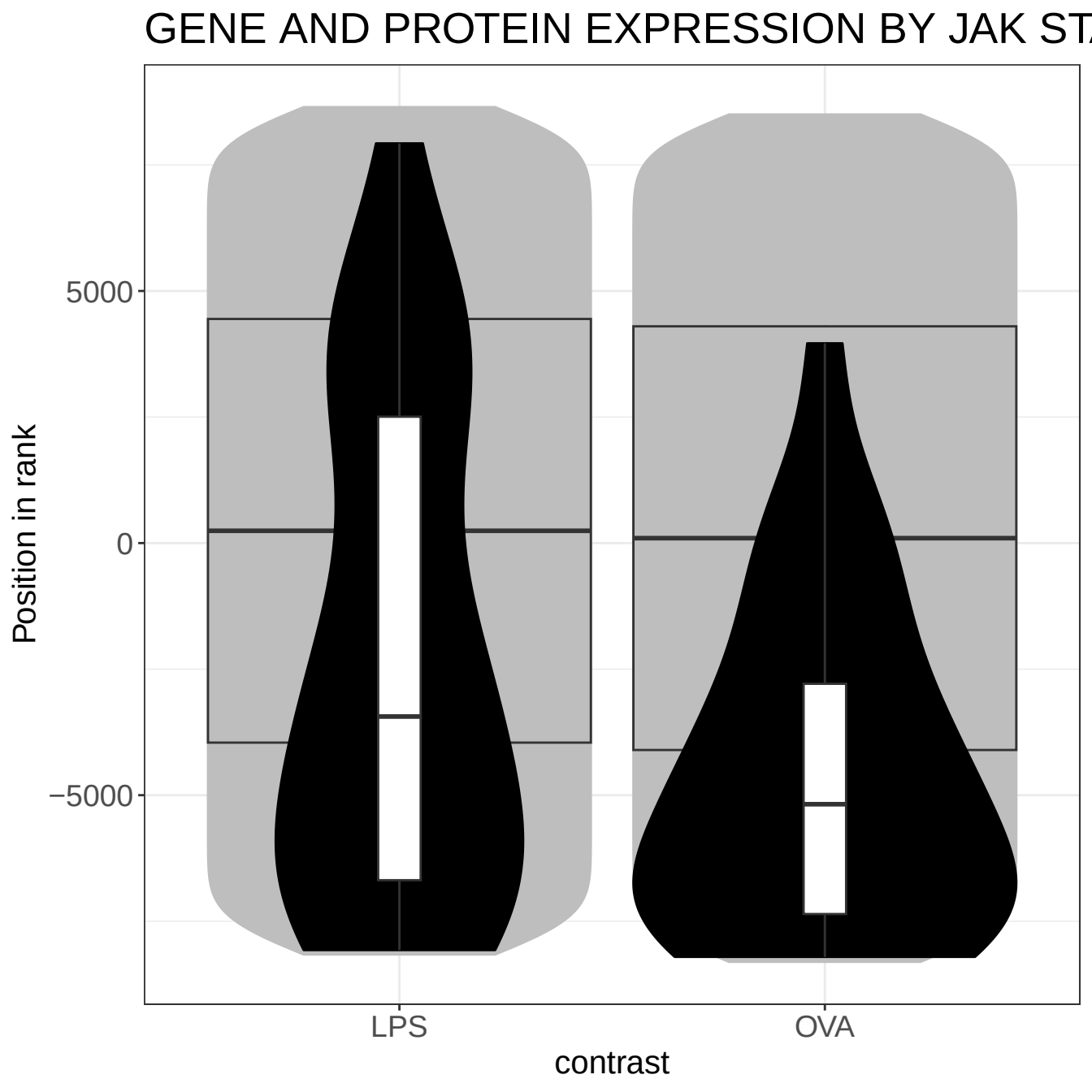
SYNTHESIS OF ACTIVE UBIQUITIN ROLES OF E1 AND E2 ENZYMES

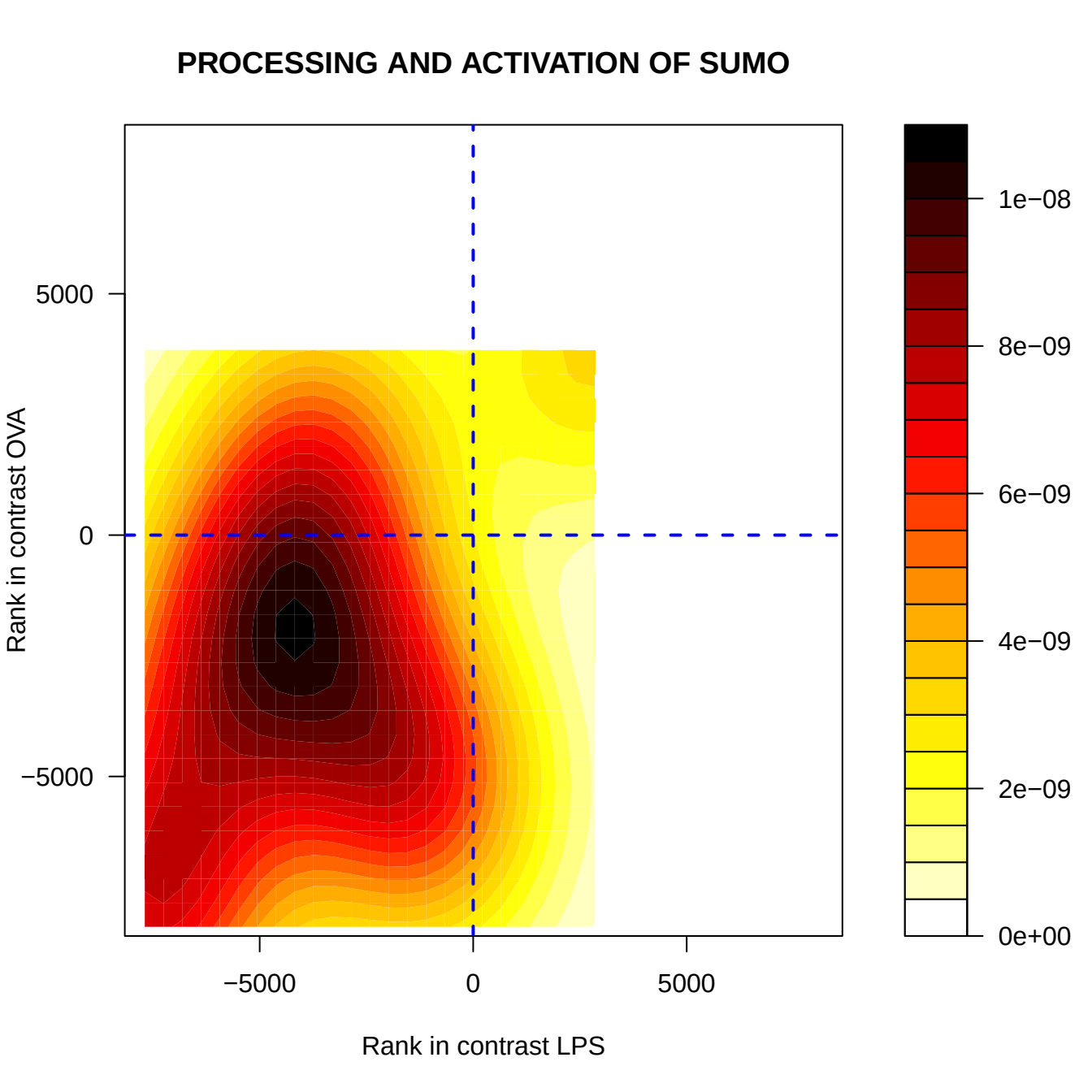


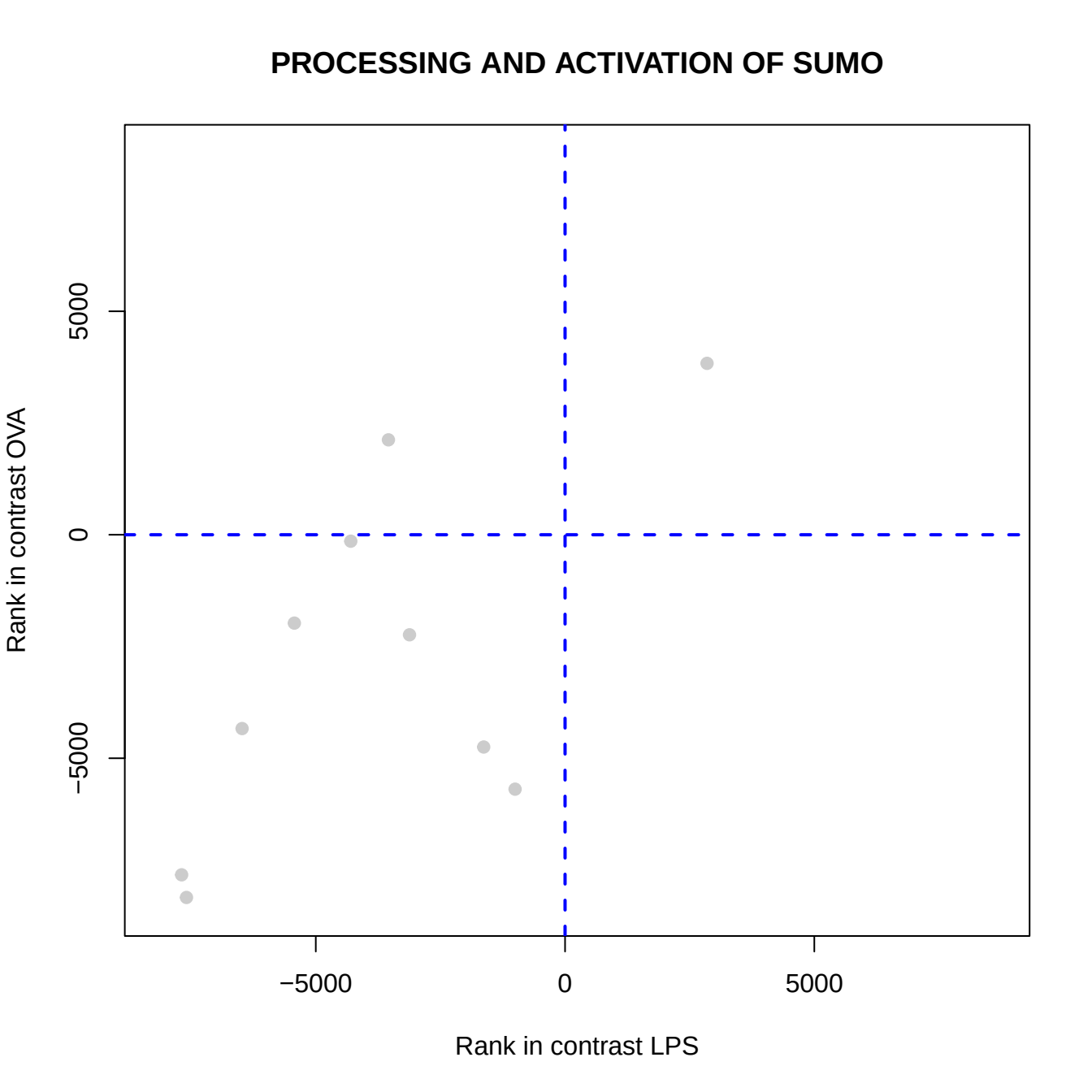

SYNTHESIS OF ACTIVE UBIQUITIN ROLES OF
5000
0
−5000
Position in rank
LPS
OVA
contrast

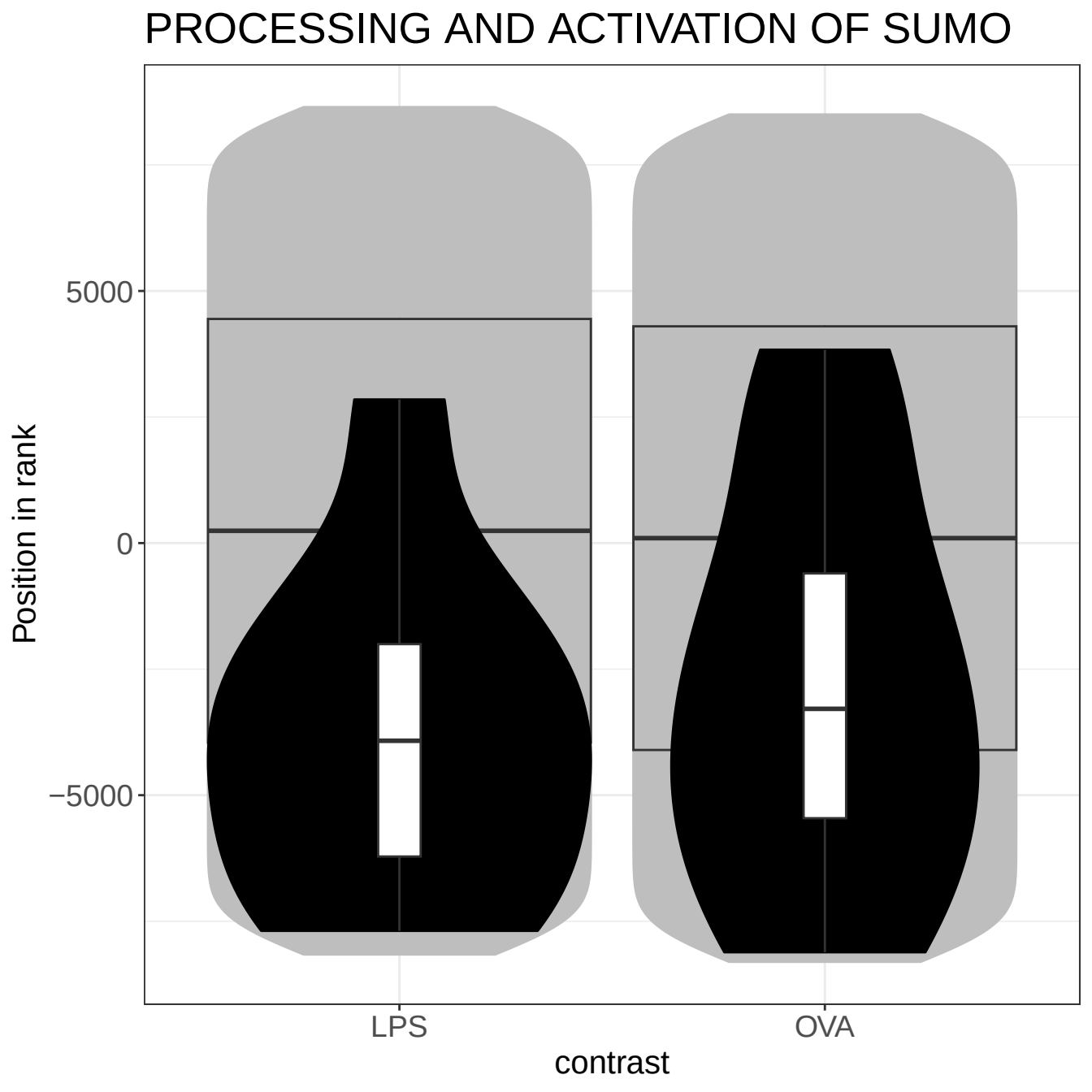

TEIN EXPRESSION BY JAK STAT SIGNALING AFTER INTERLE
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

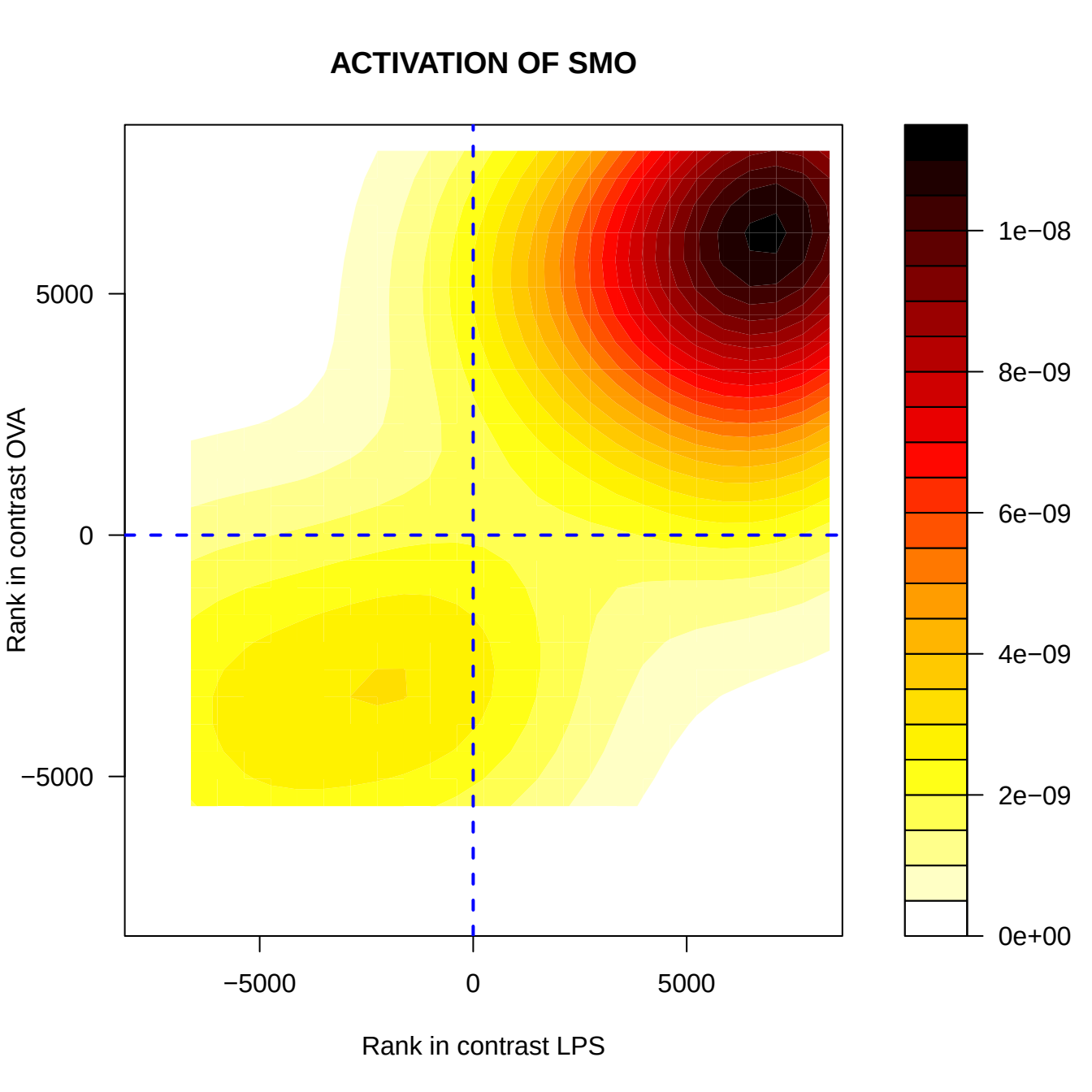

D PROTEIN EXPRESSION BY JAK STAT SIGNALING AFTER INTERLEUKIN 12
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

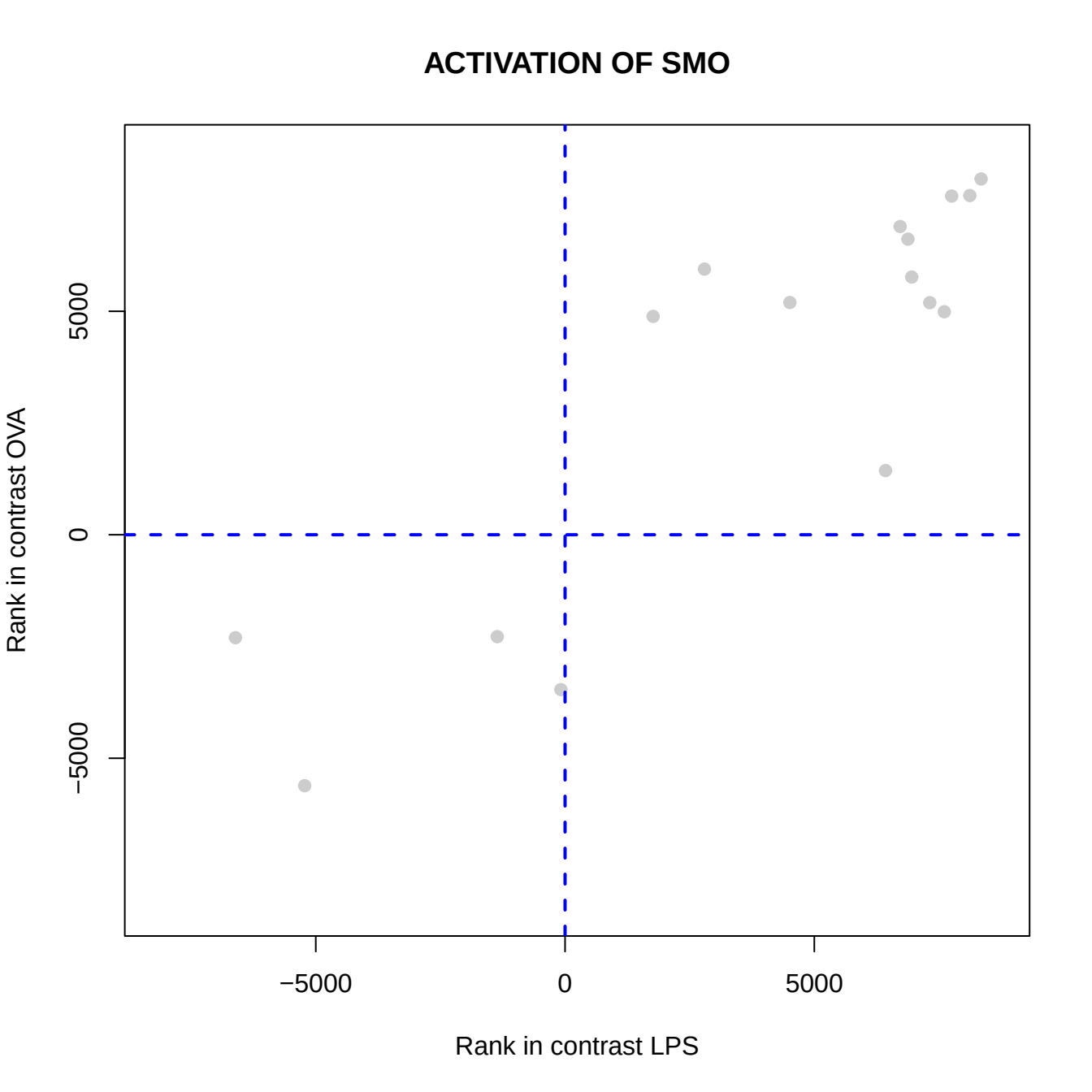

GENE AND PROTEIN EXPRESSION BY JAK ST
5000
0
−5000
Position in rank
LPS
OVA
contrast

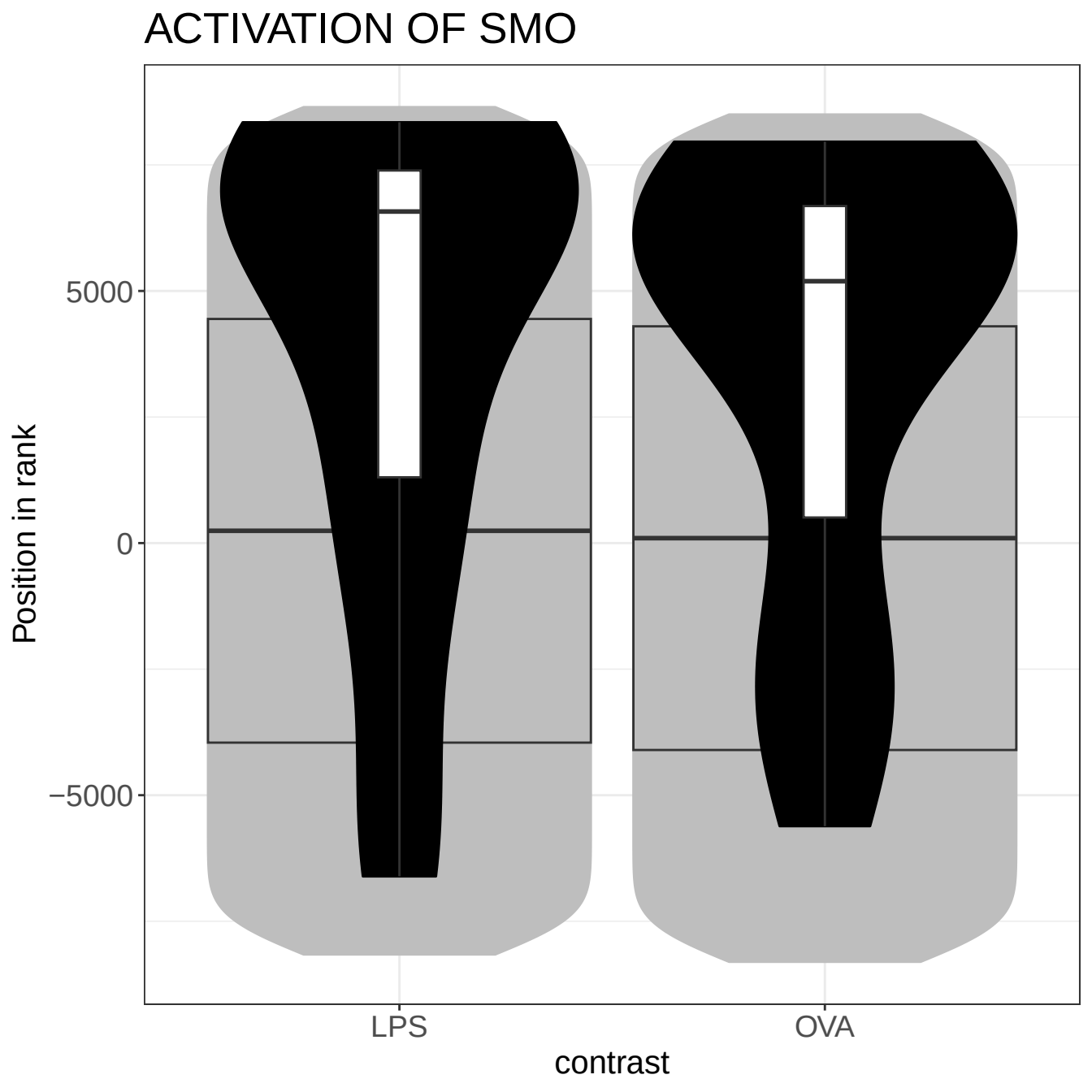

PROCESSING AND ACTIVATION OF SUMO
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

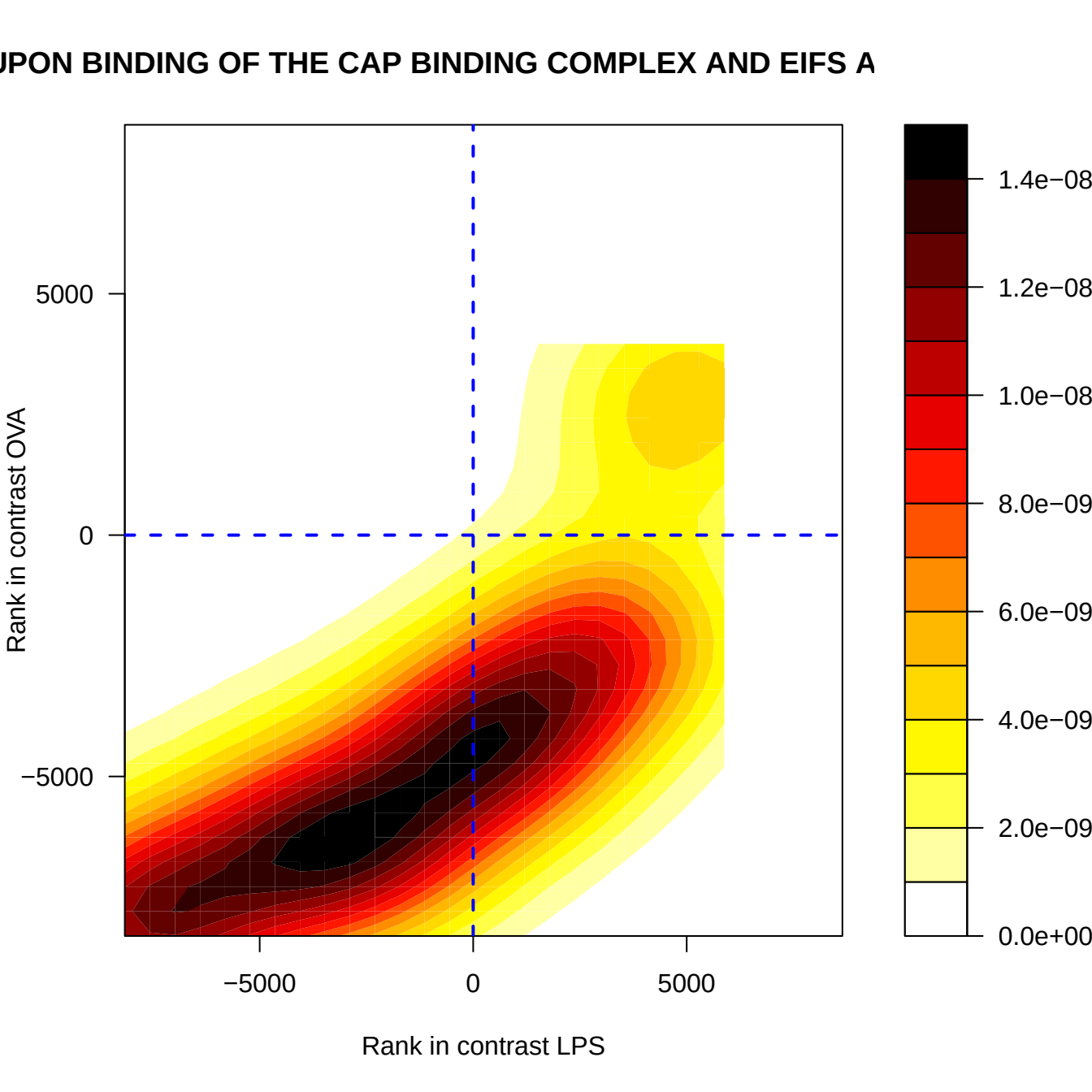

PROCESSING AND ACTIVATION OF SUMO
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

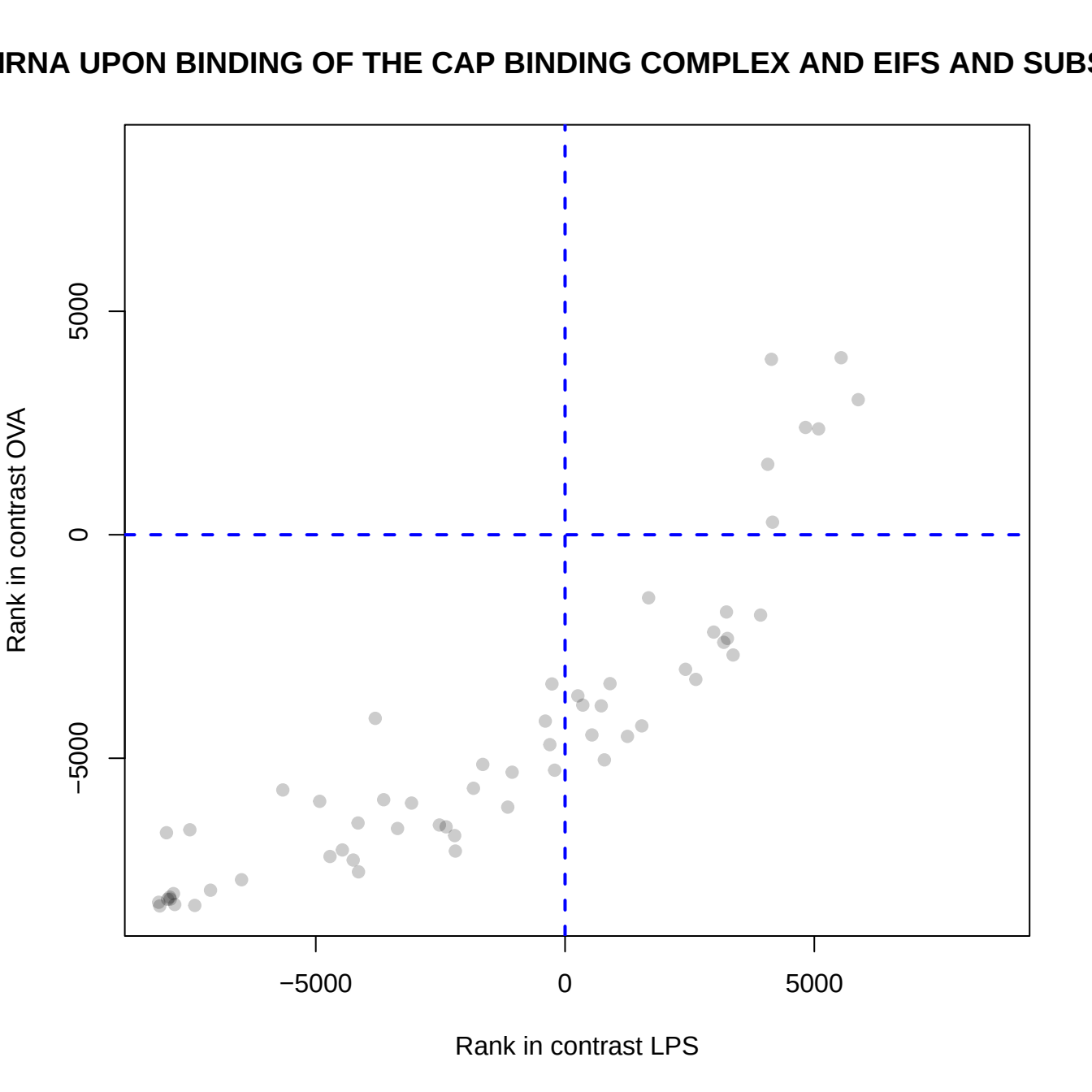

PROCESSING AND ACTIVATION OF SUMO
5000
0
−5000
Position in rank
LPS
OVA
contrast

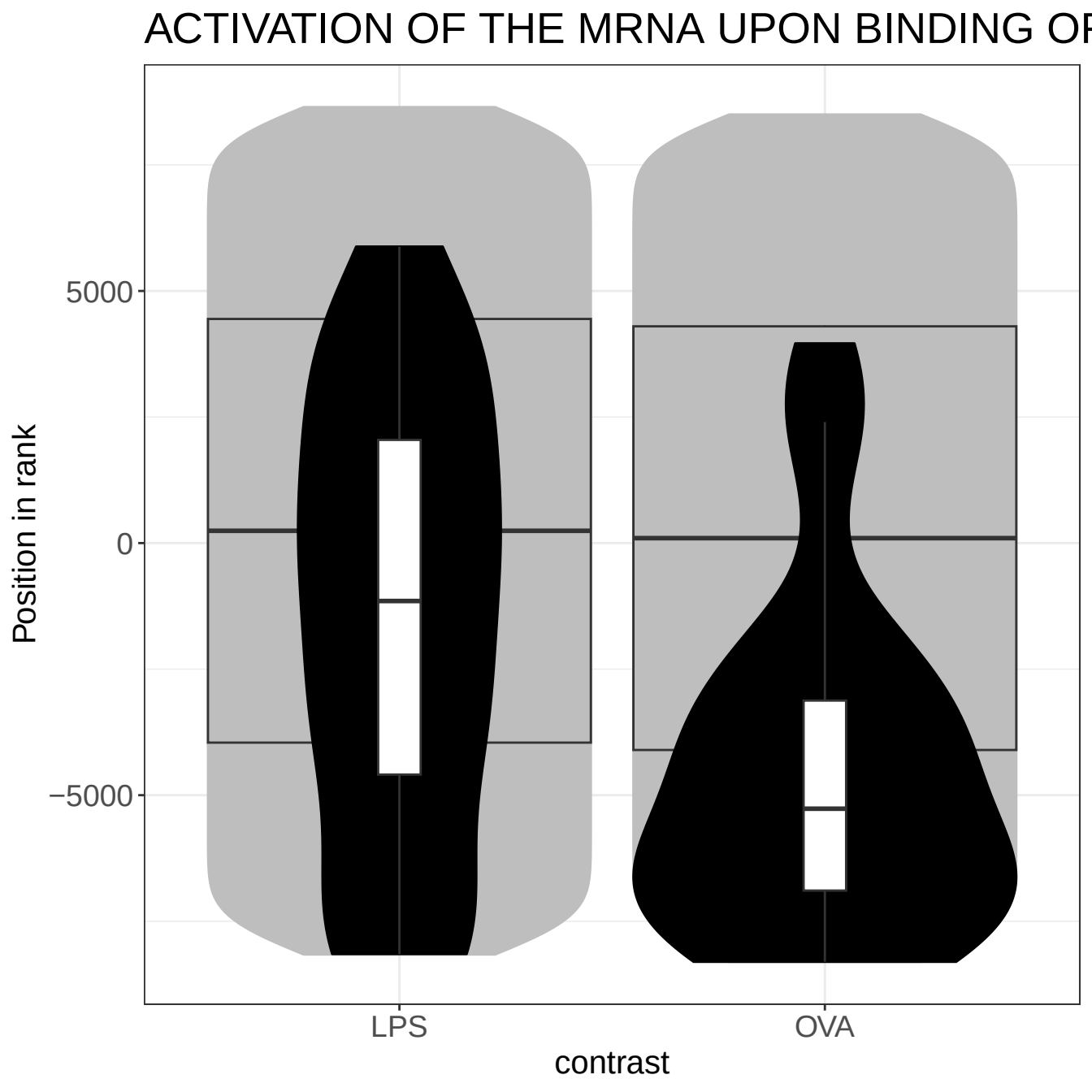

ACTIVATION OF SMO
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

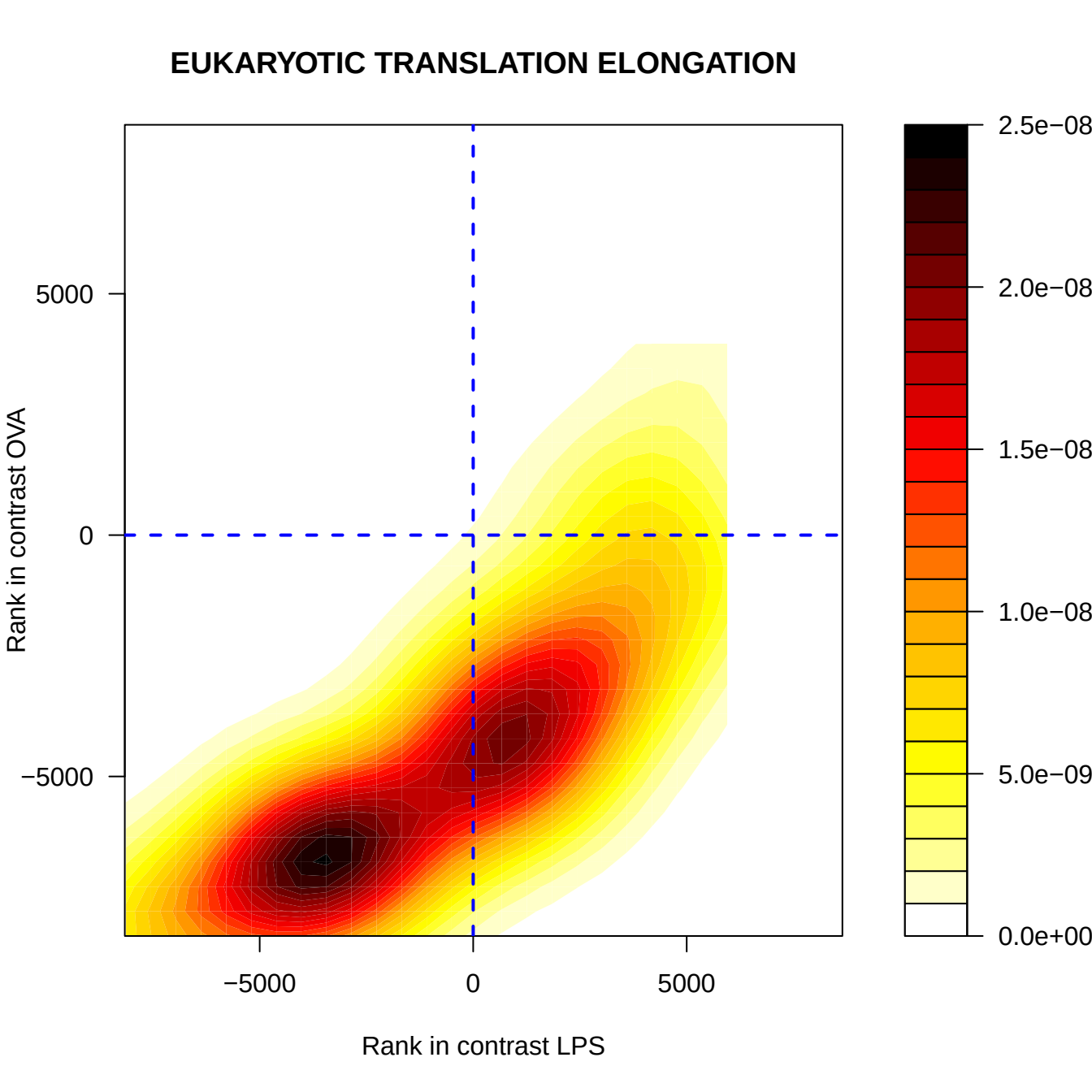

ACTIVATION OF SMO
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

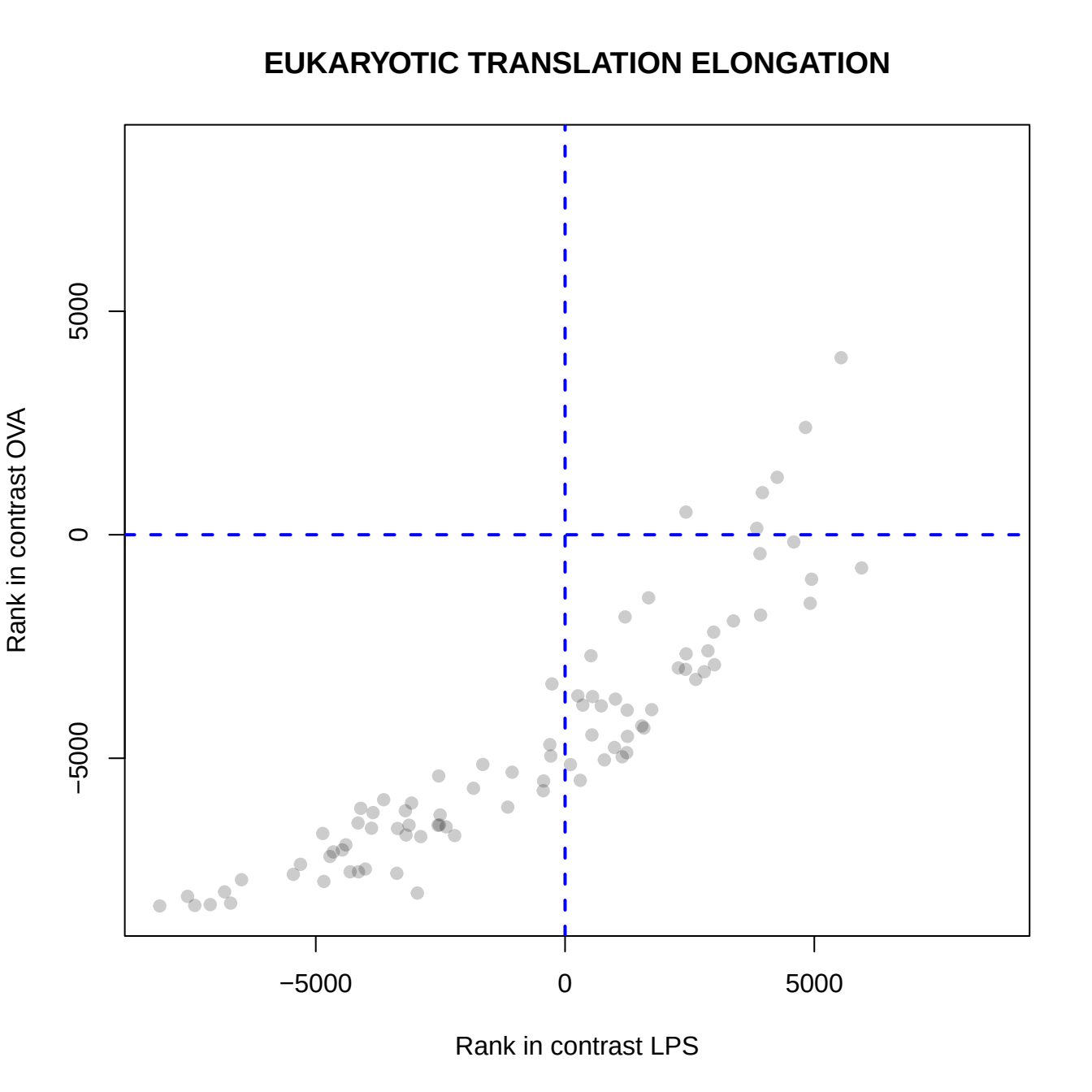

ACTIVATION OF SMO
Position in rank
5000
0
−5000
LPS
OVA
contrast

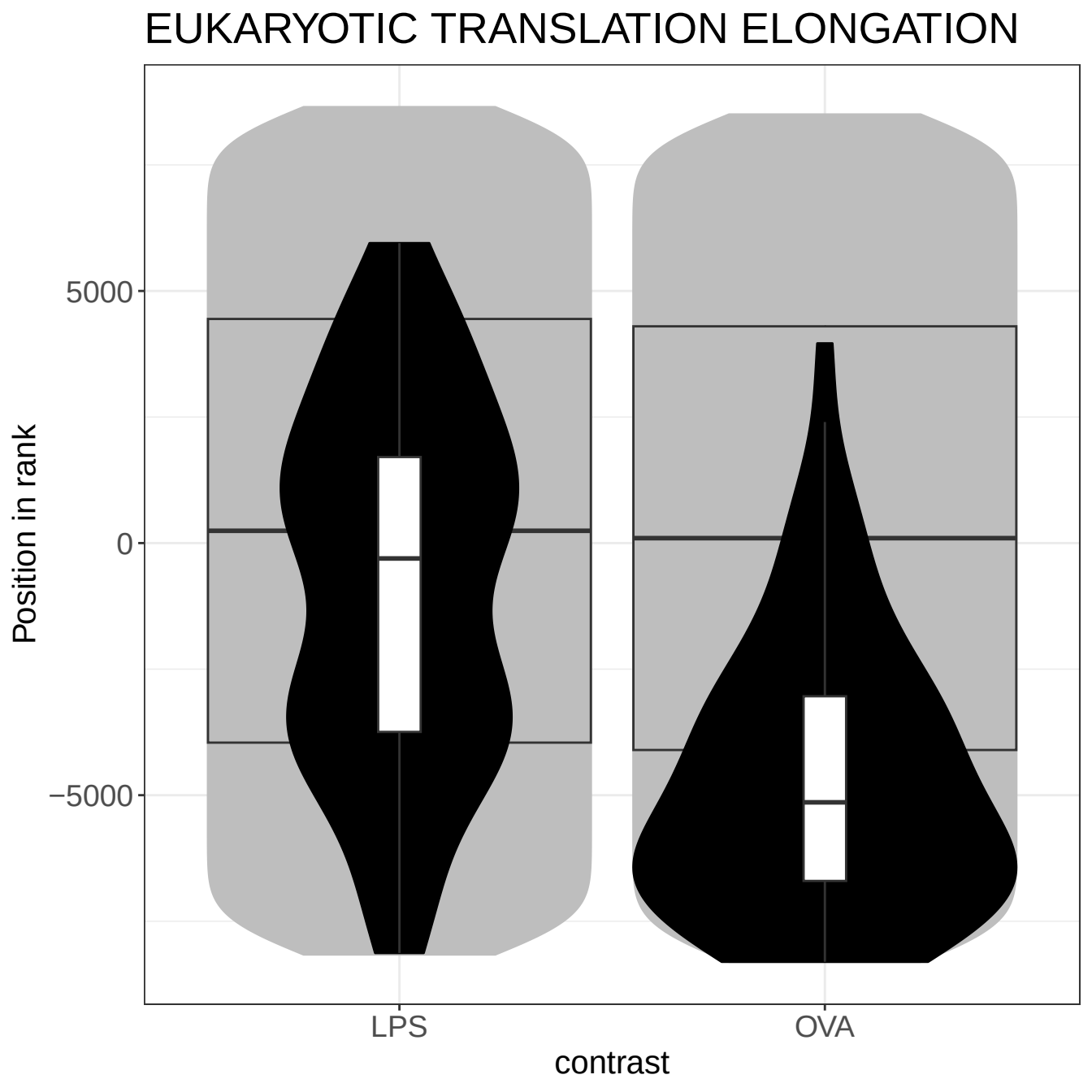

UPON BINDING OF THE CAP BINDING COMPLEX AND EIFS A
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

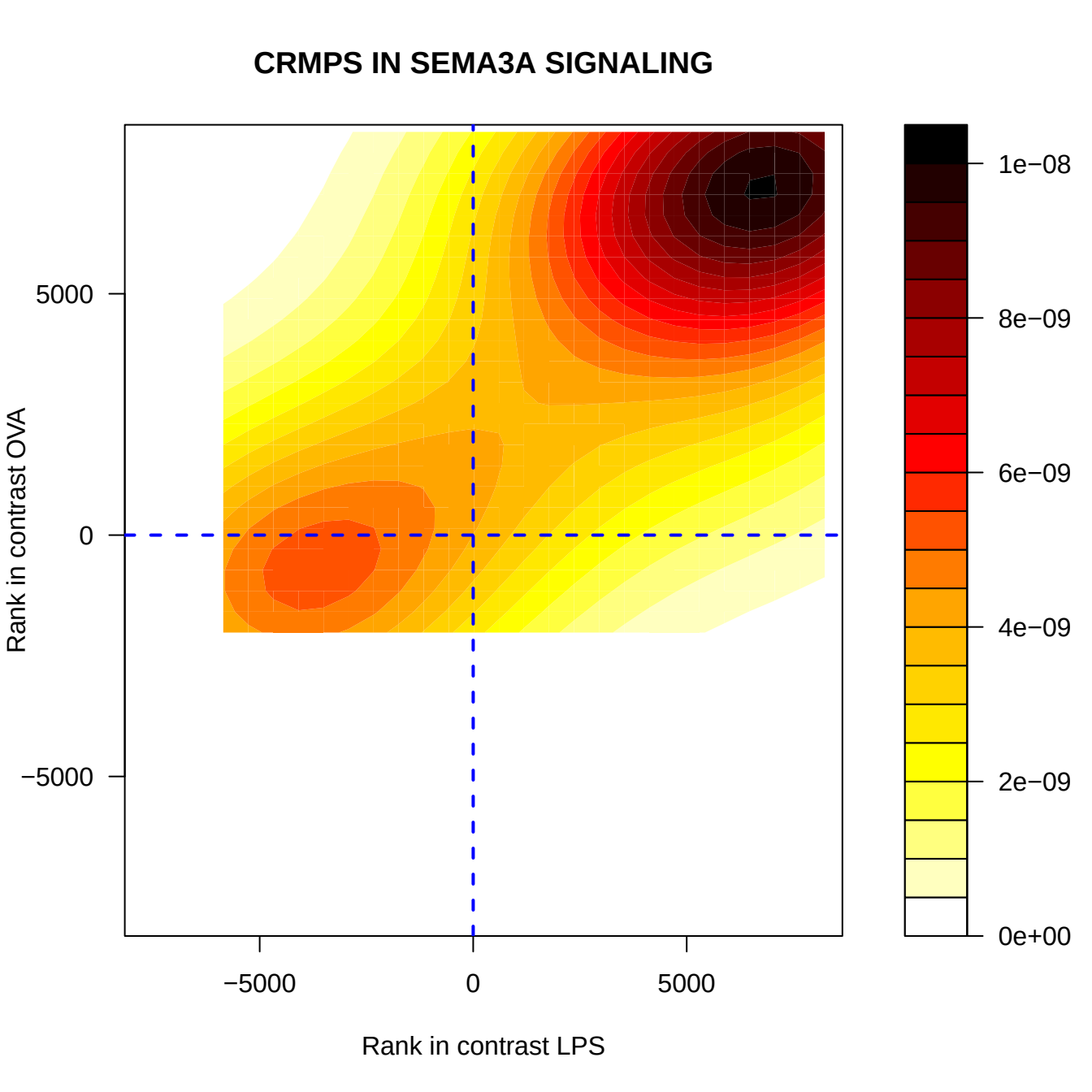

IRNA UPON BINDING OF THE CAP BINDING COMPLEX AND EIFS AND SUBS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

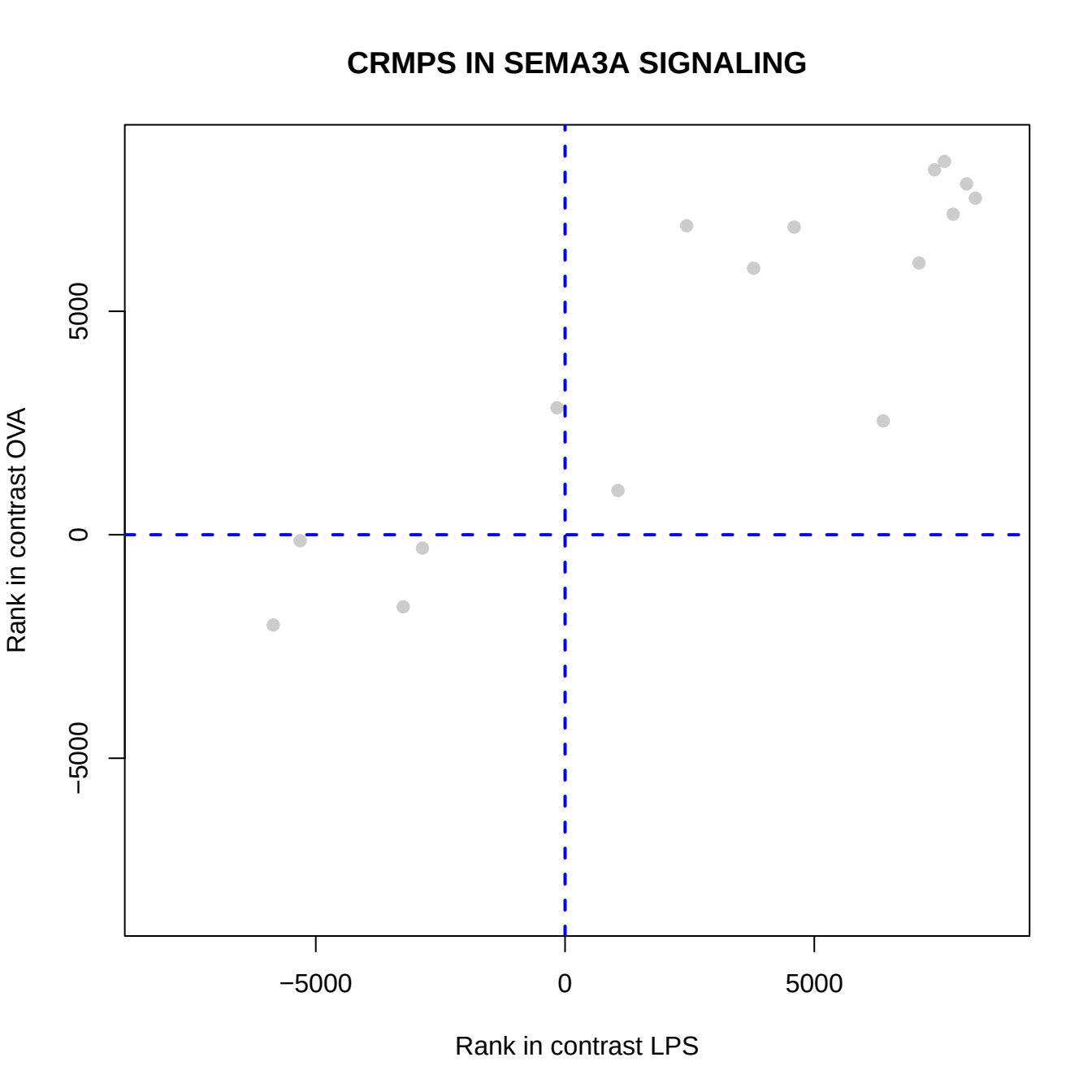

ACTIVATION OF THE MRNA UPON BINDING OF
5000
0
−5000
Position in rank
LPS
OVA
contrast

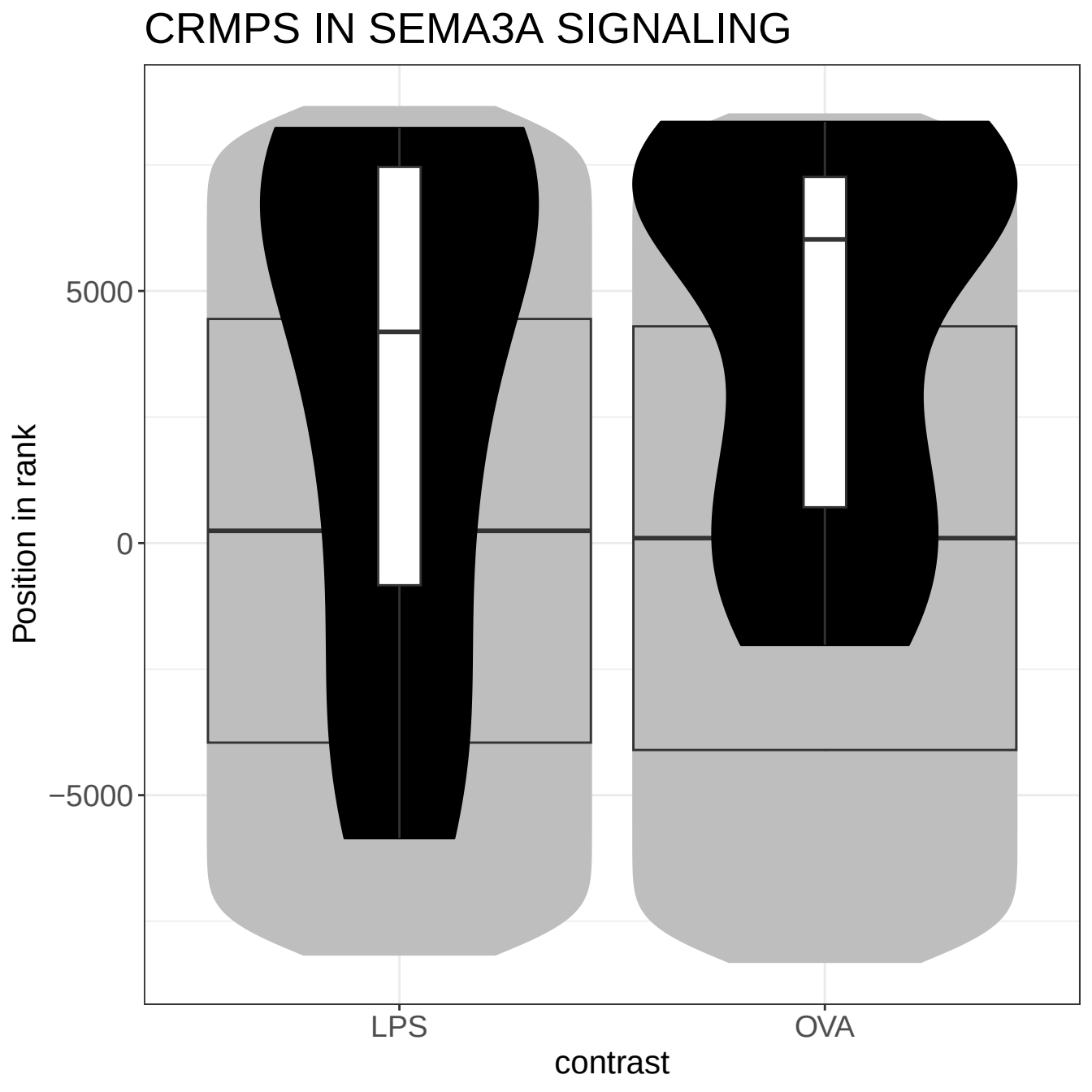

EUKARYOTIC TRANSLATION ELONGATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.5e−08
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

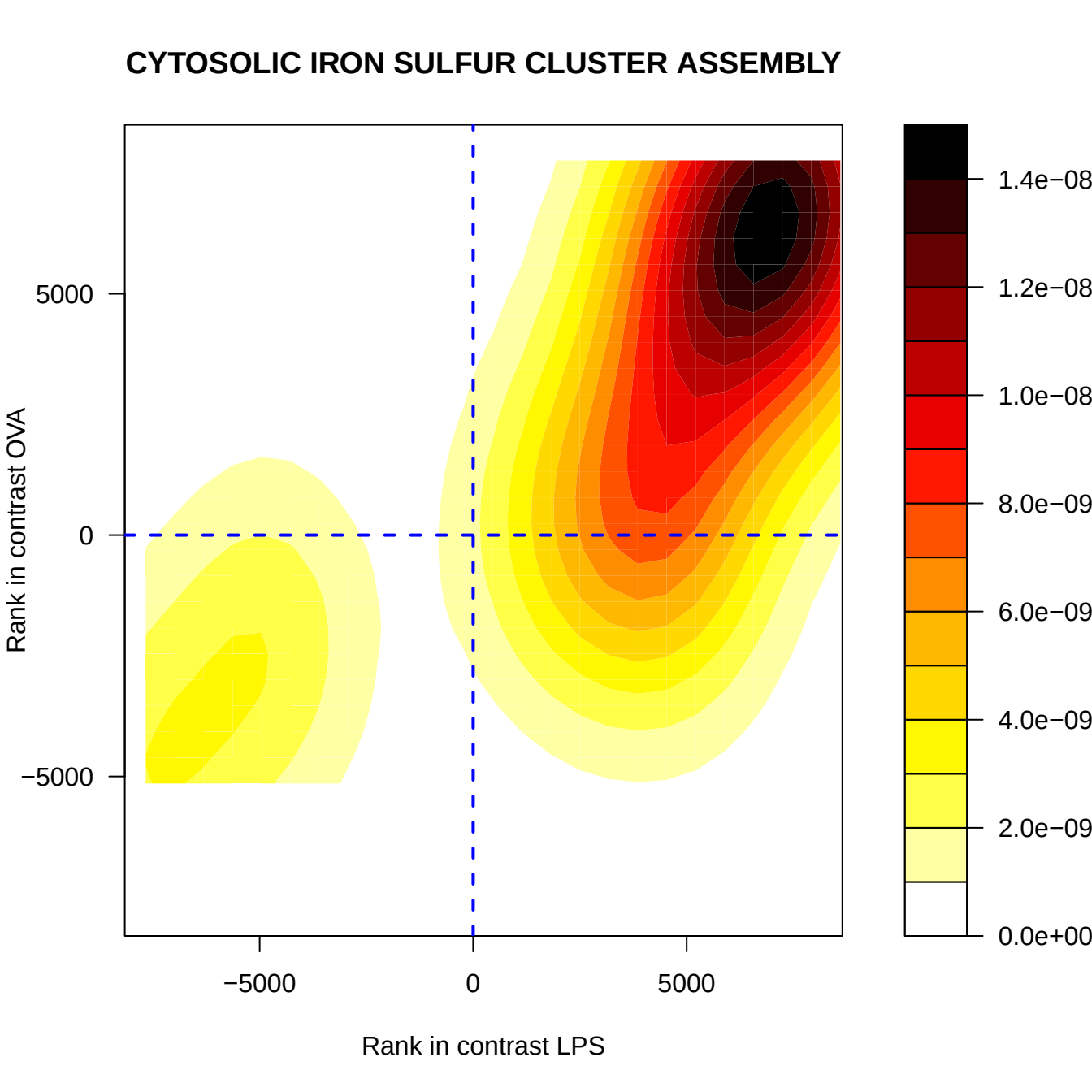

EUKARYOTIC TRANSLATION ELONGATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

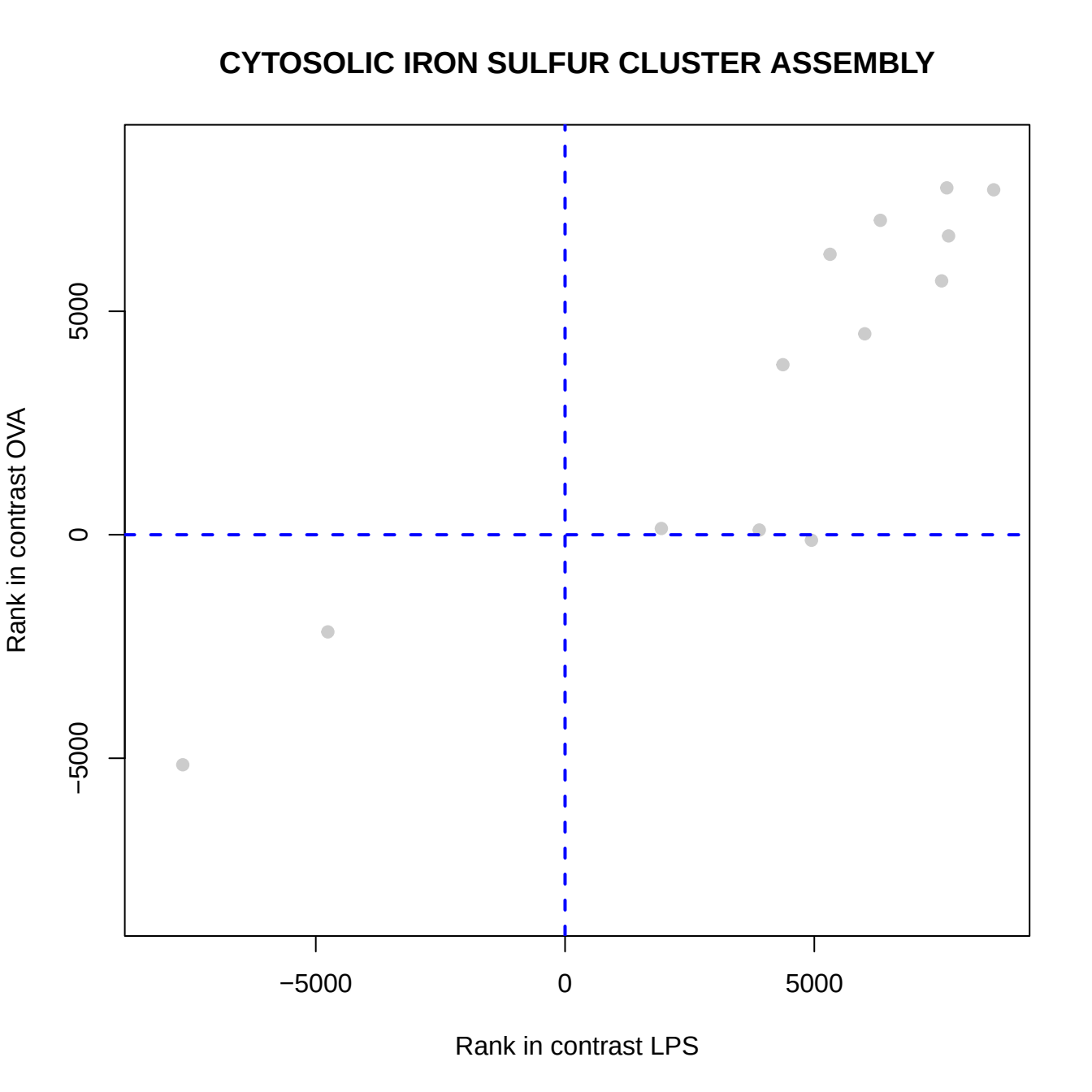

EUKARYOTIC TRANSLATION ELONGATION
Position in rank
5000
0
−5000
LPS
OVA
contrast

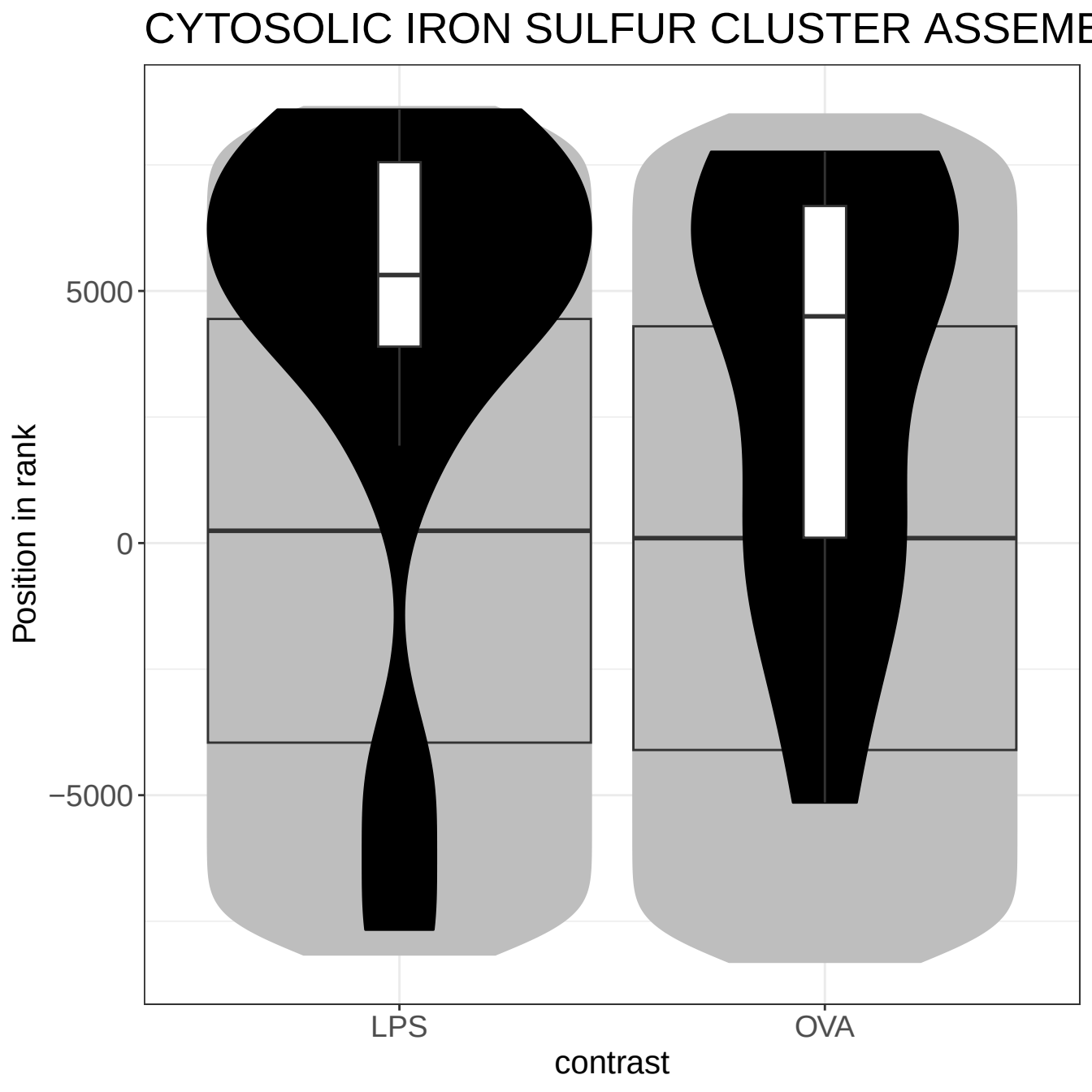

CRMPS IN SEMA3A SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

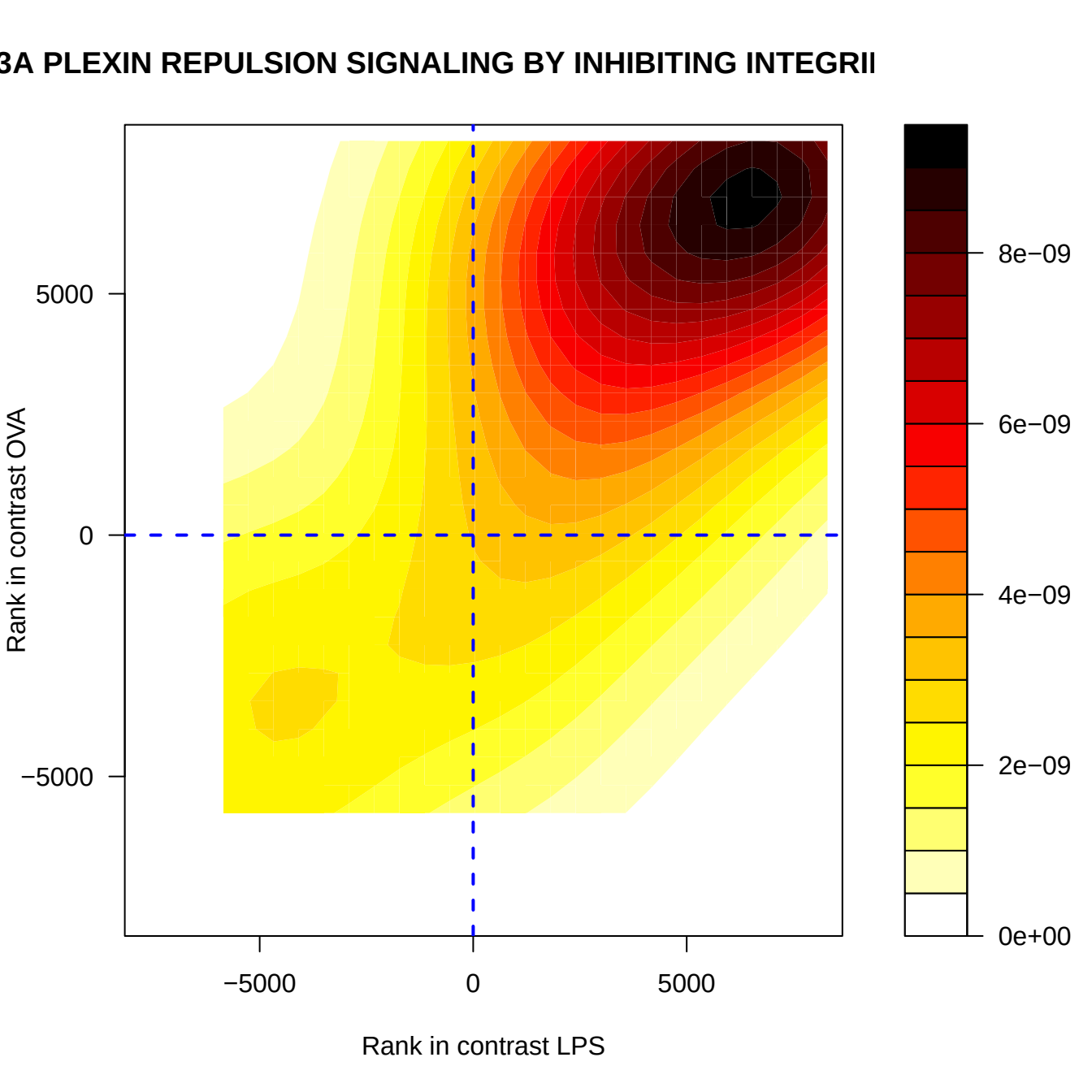

CRMPS IN SEMA3A SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

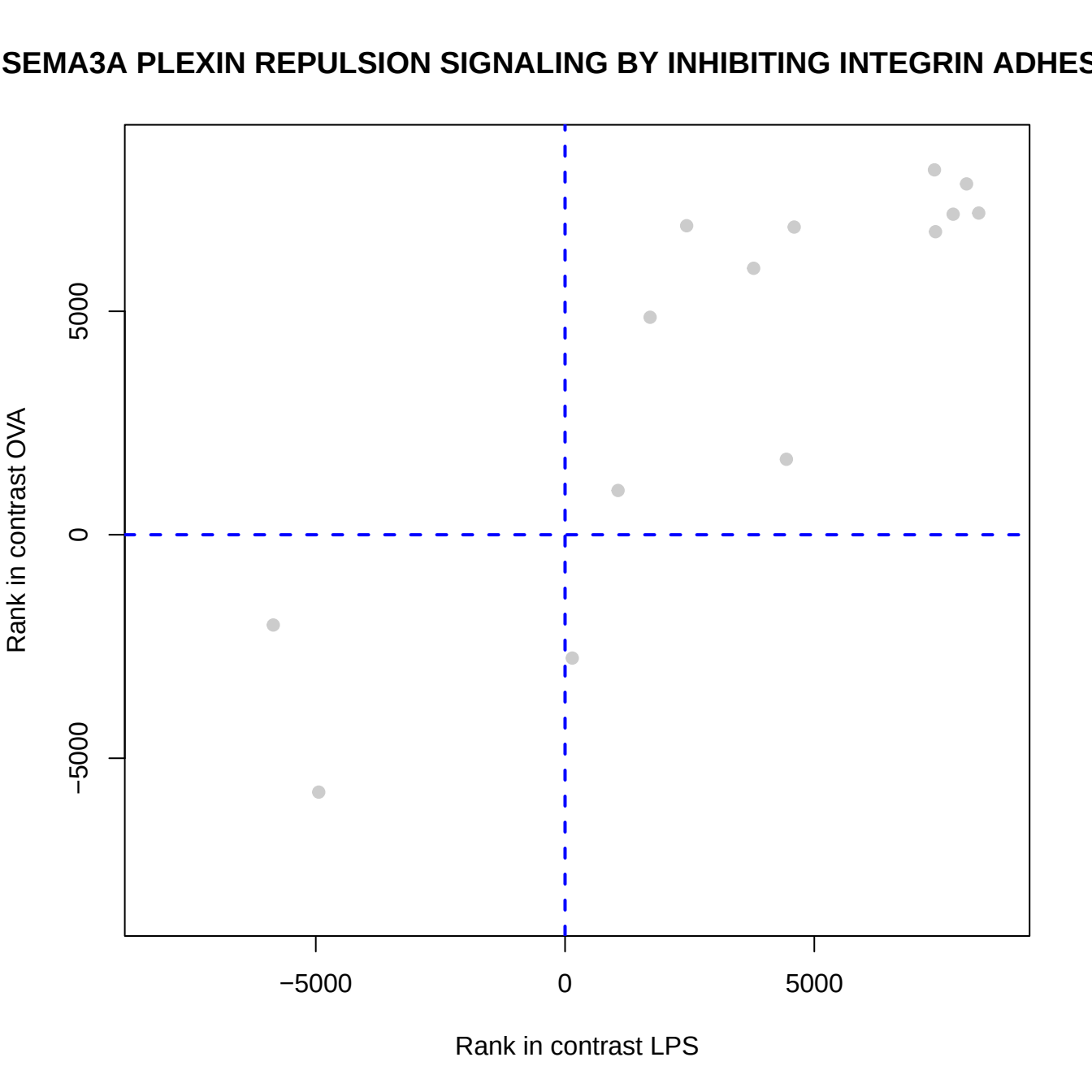

CRMPS IN SEMA3A SIGNALING
Position in rank
5000
0
−5000
LPS
OVA
contrast

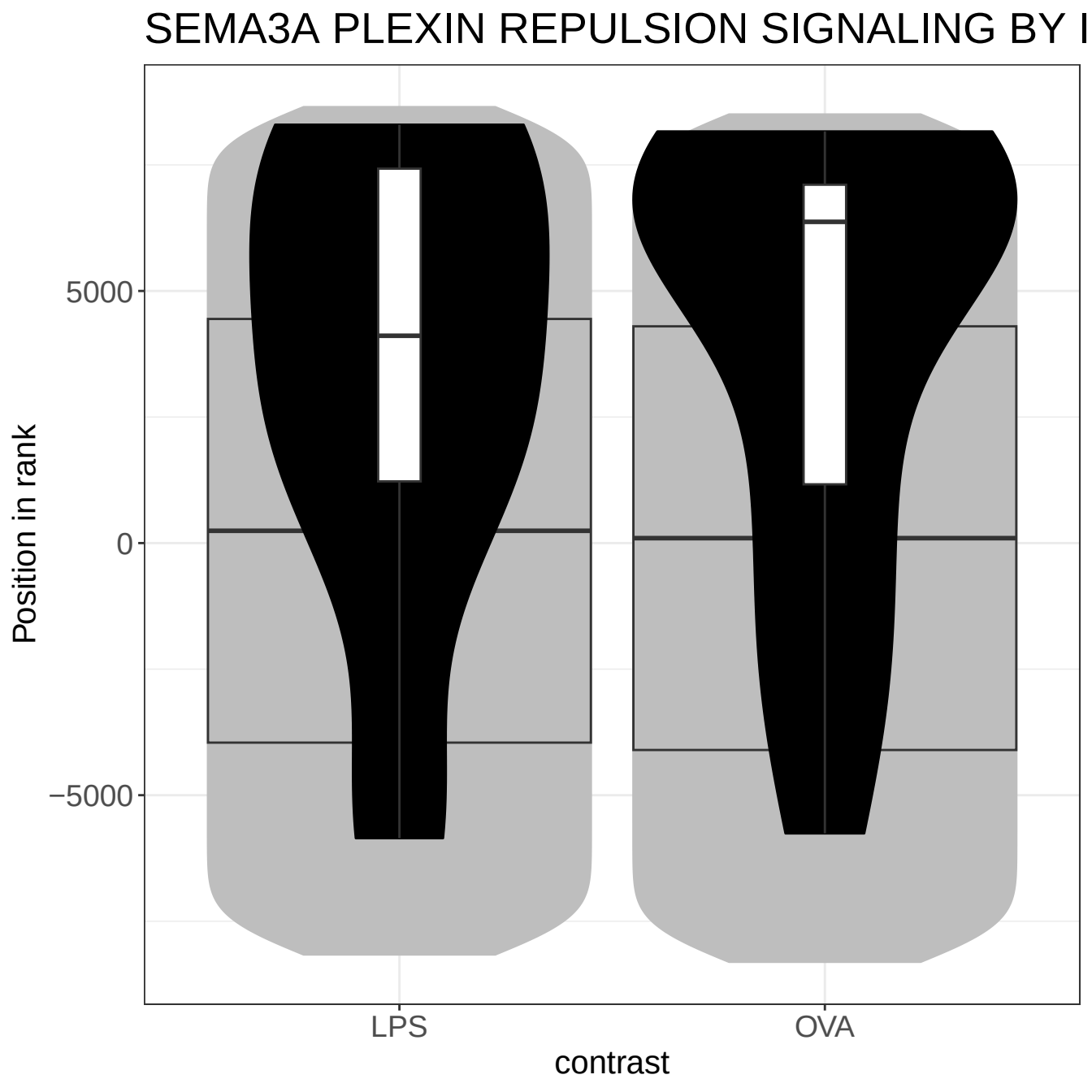

CYTOSOLIC IRON SULFUR CLUSTER ASSEMBLY
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

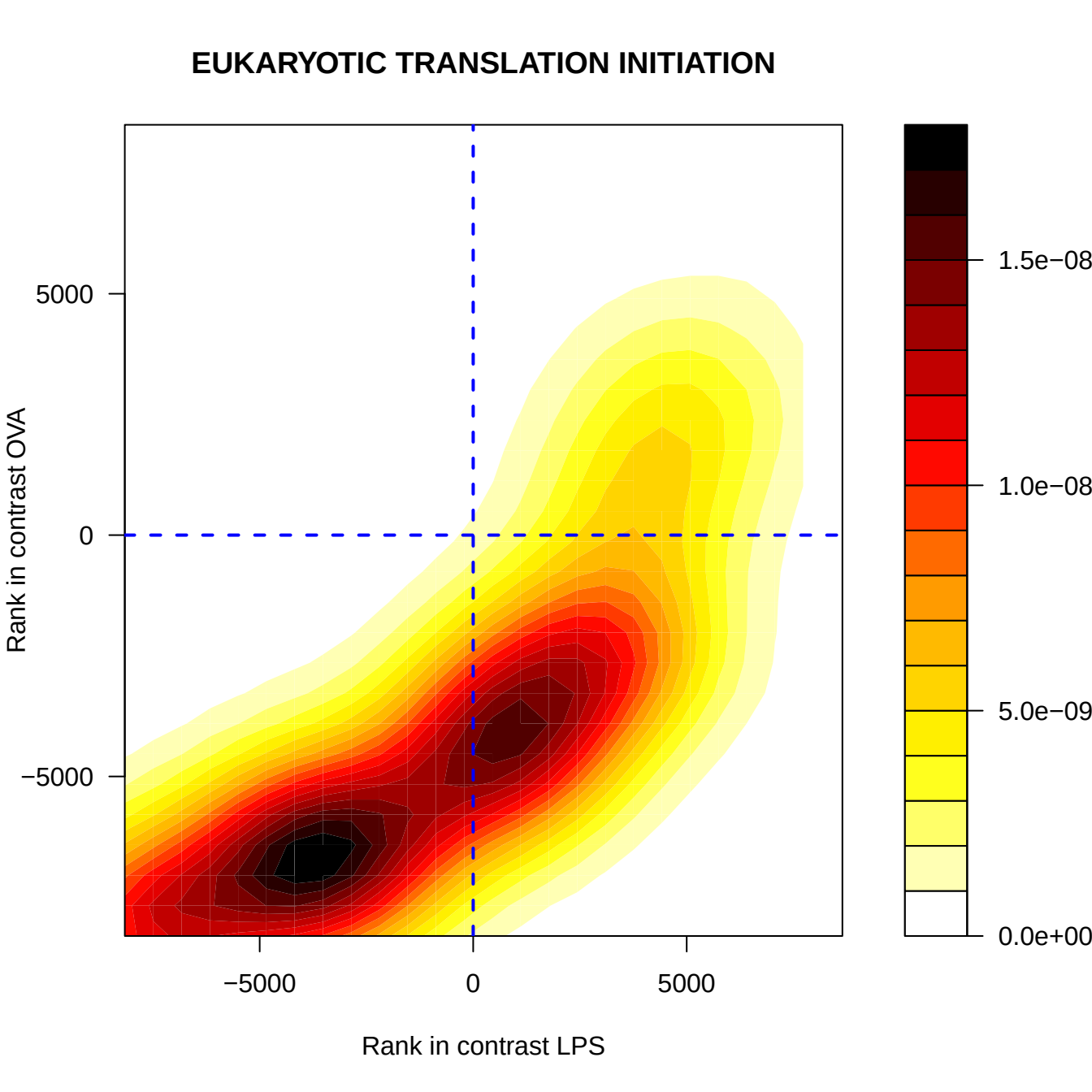

CYTOSOLIC IRON SULFUR CLUSTER ASSEMBLY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

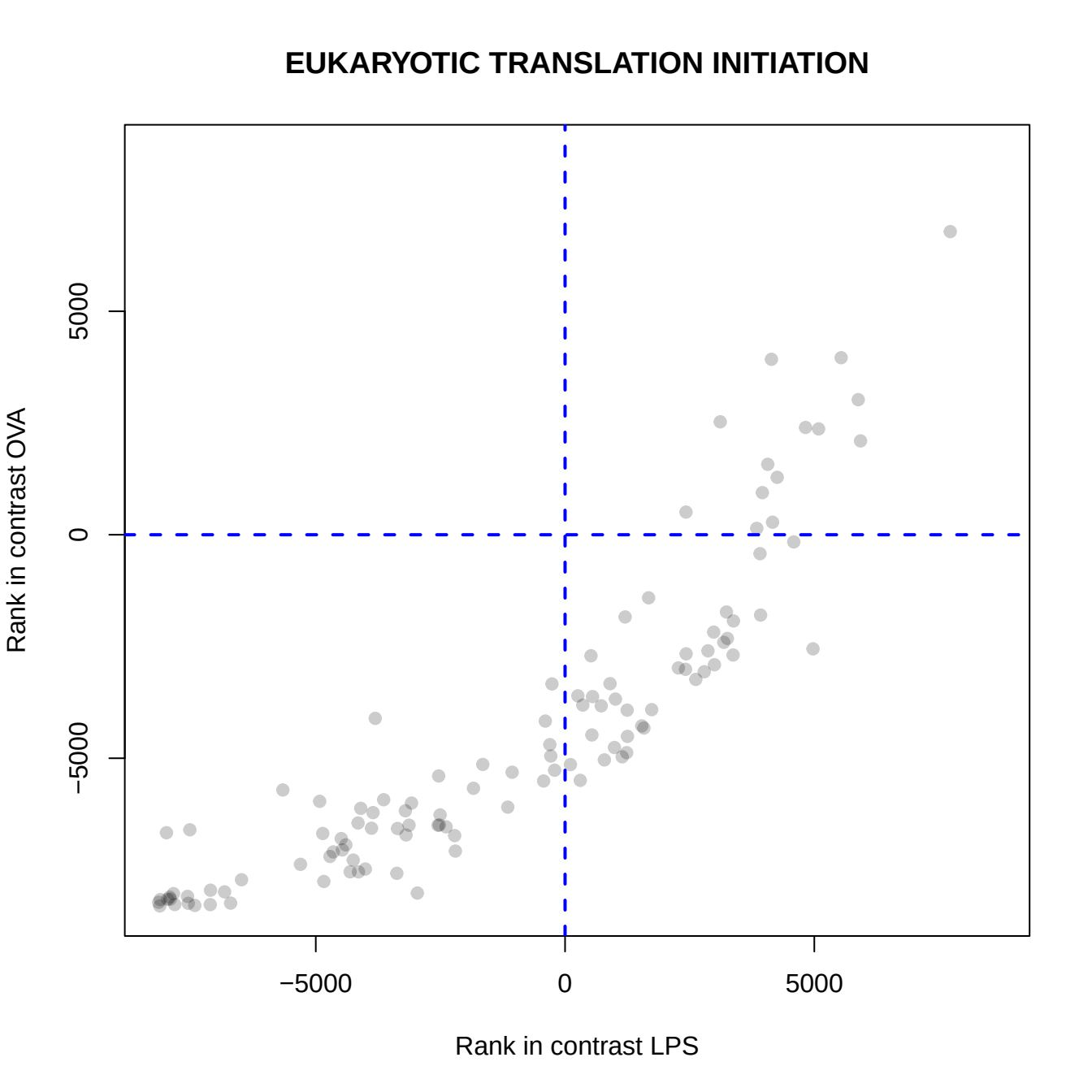

CYTOSOLIC IRON SULFUR CLUSTER ASSEME
5000
0
−5000
Position in rank
LPS
OVA
contrast

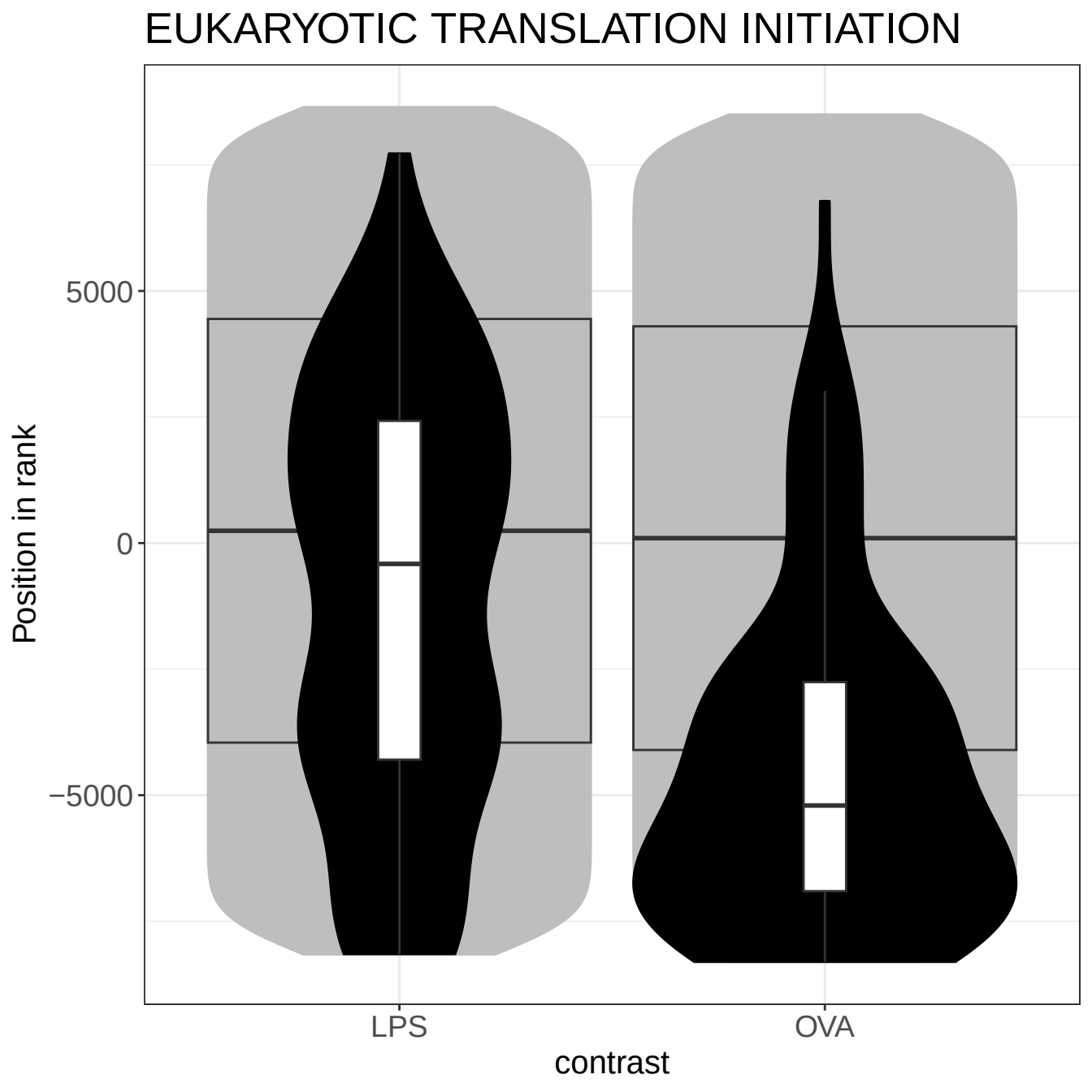

3A PLEXIN REPULSION SIGNALING BY INHIBITING INTEGRII
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

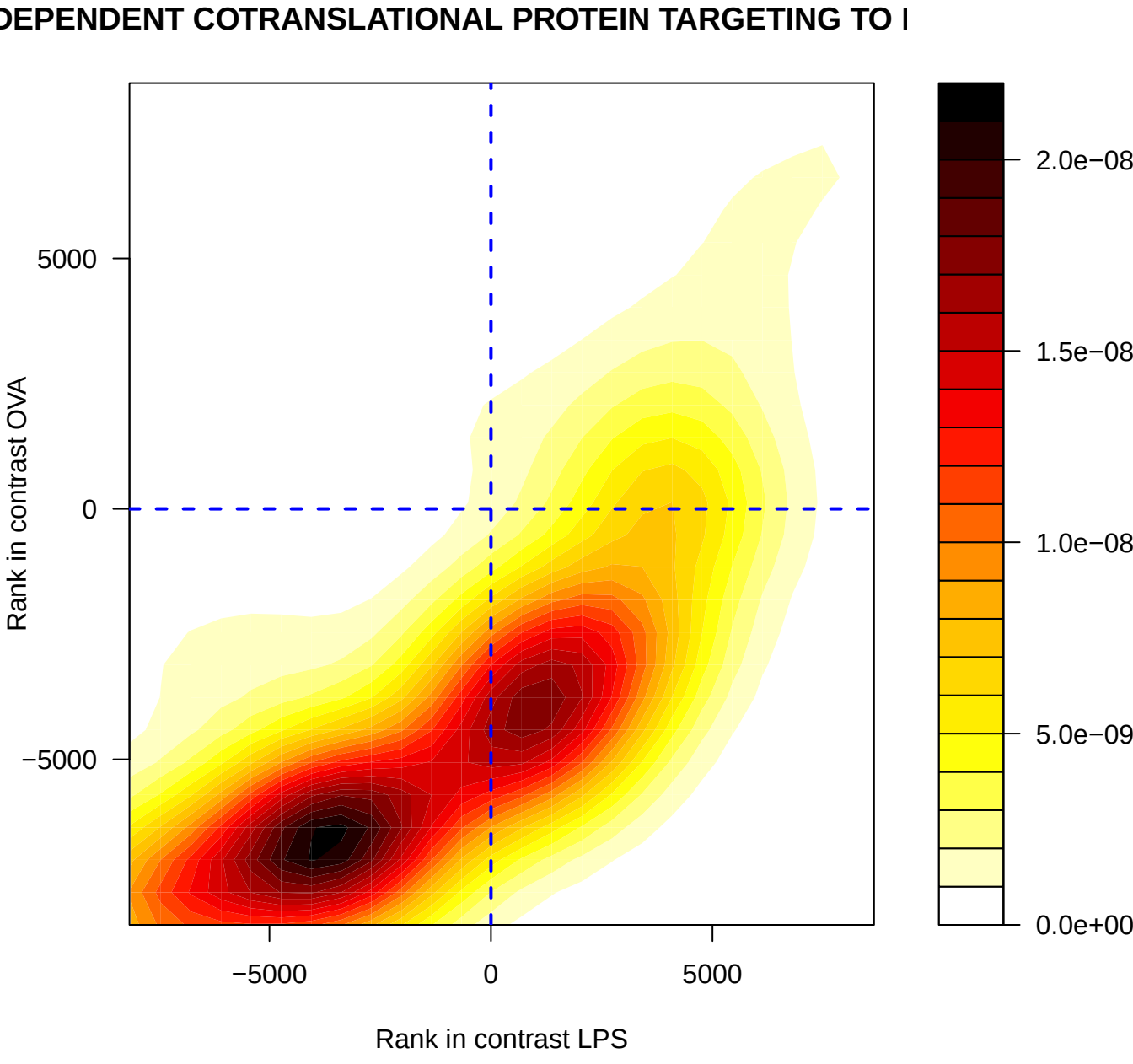

SEMA3A PLEXIN REPULSION SIGNALING BY INHIBITING INTEGRIN ADHES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

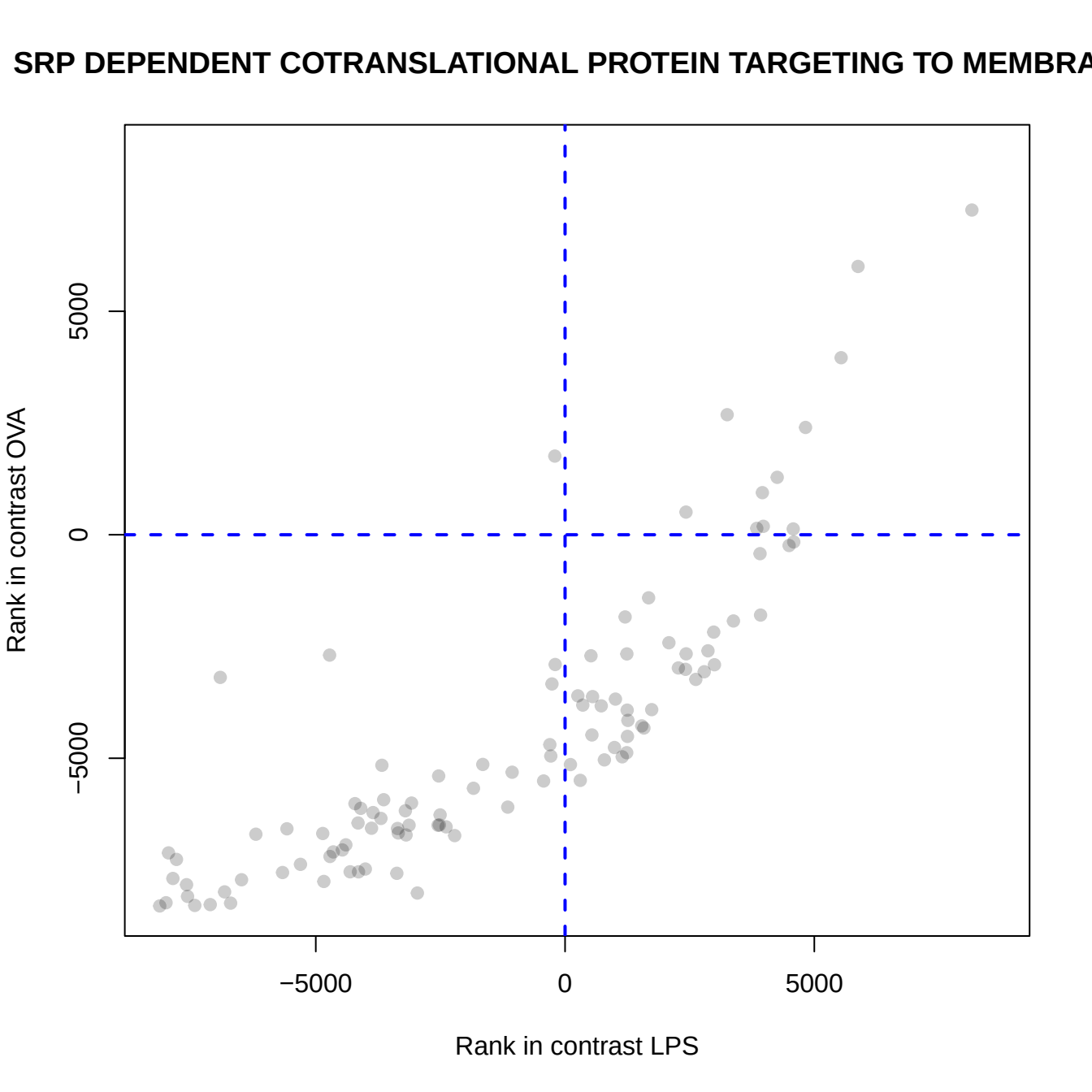

SEMA3A PLEXIN REPULSION SIGNALING BY I
5000
0
−5000
Position in rank
LPS
OVA
contrast

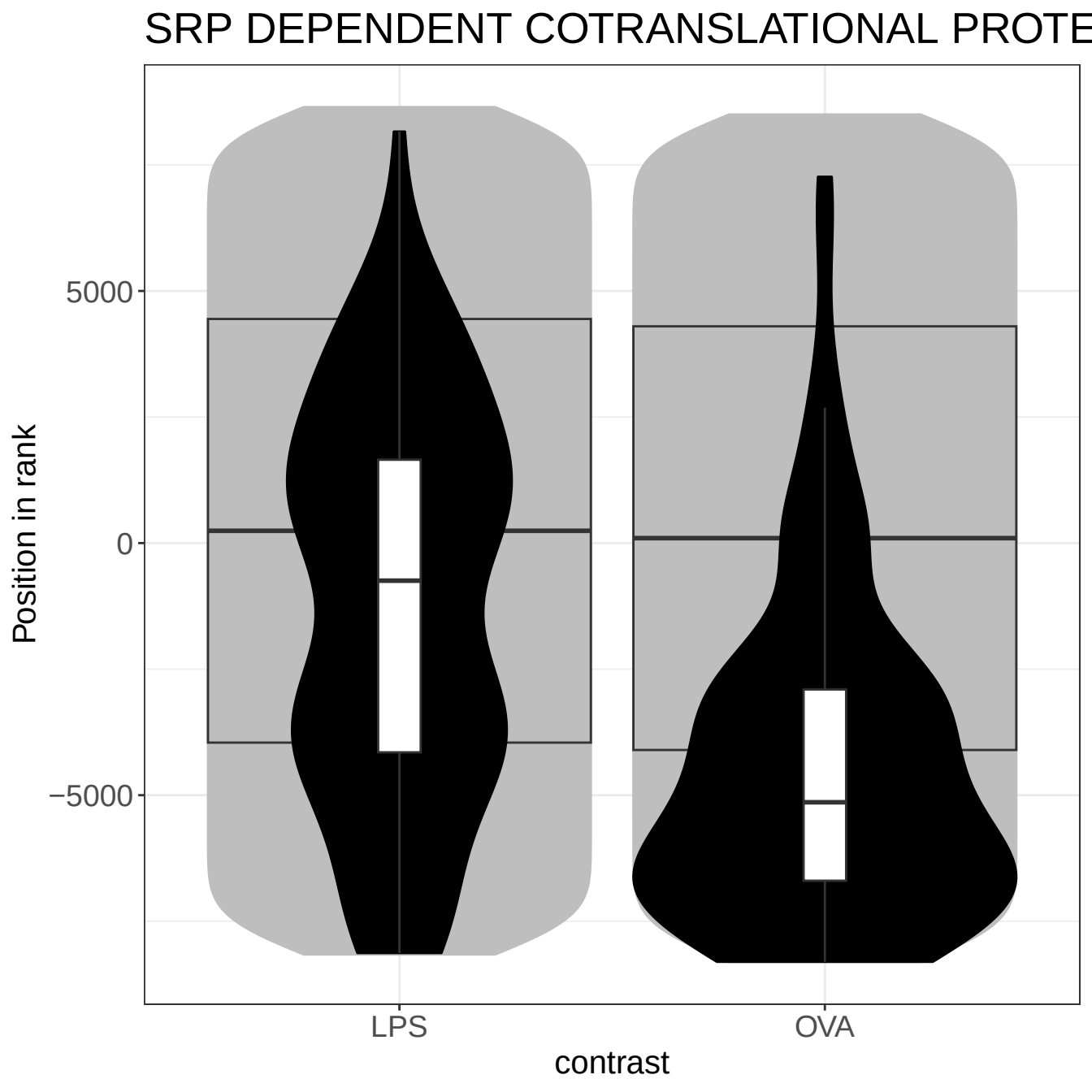

EUKARYOTIC TRANSLATION INITIATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

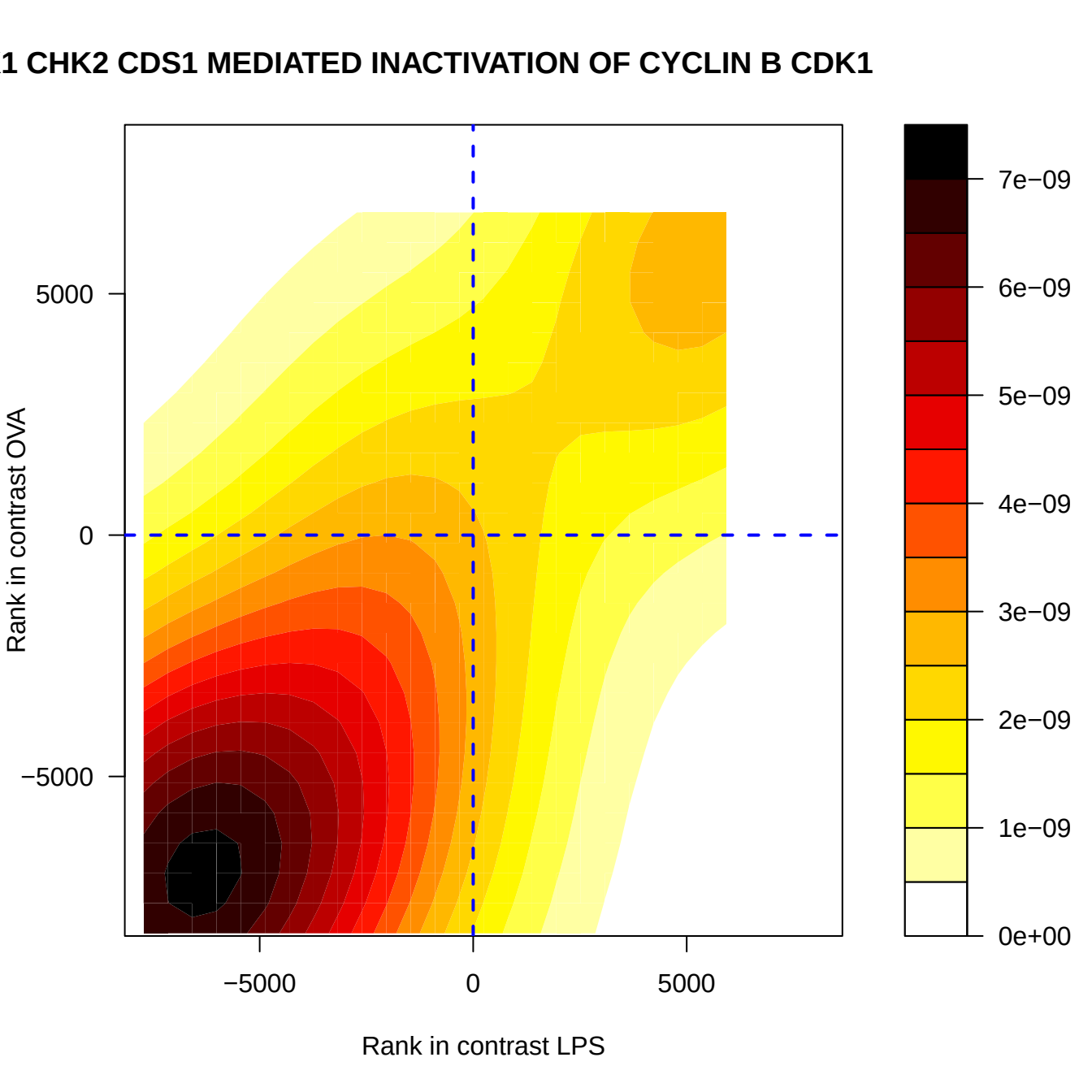

EUKARYOTIC TRANSLATION INITIATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

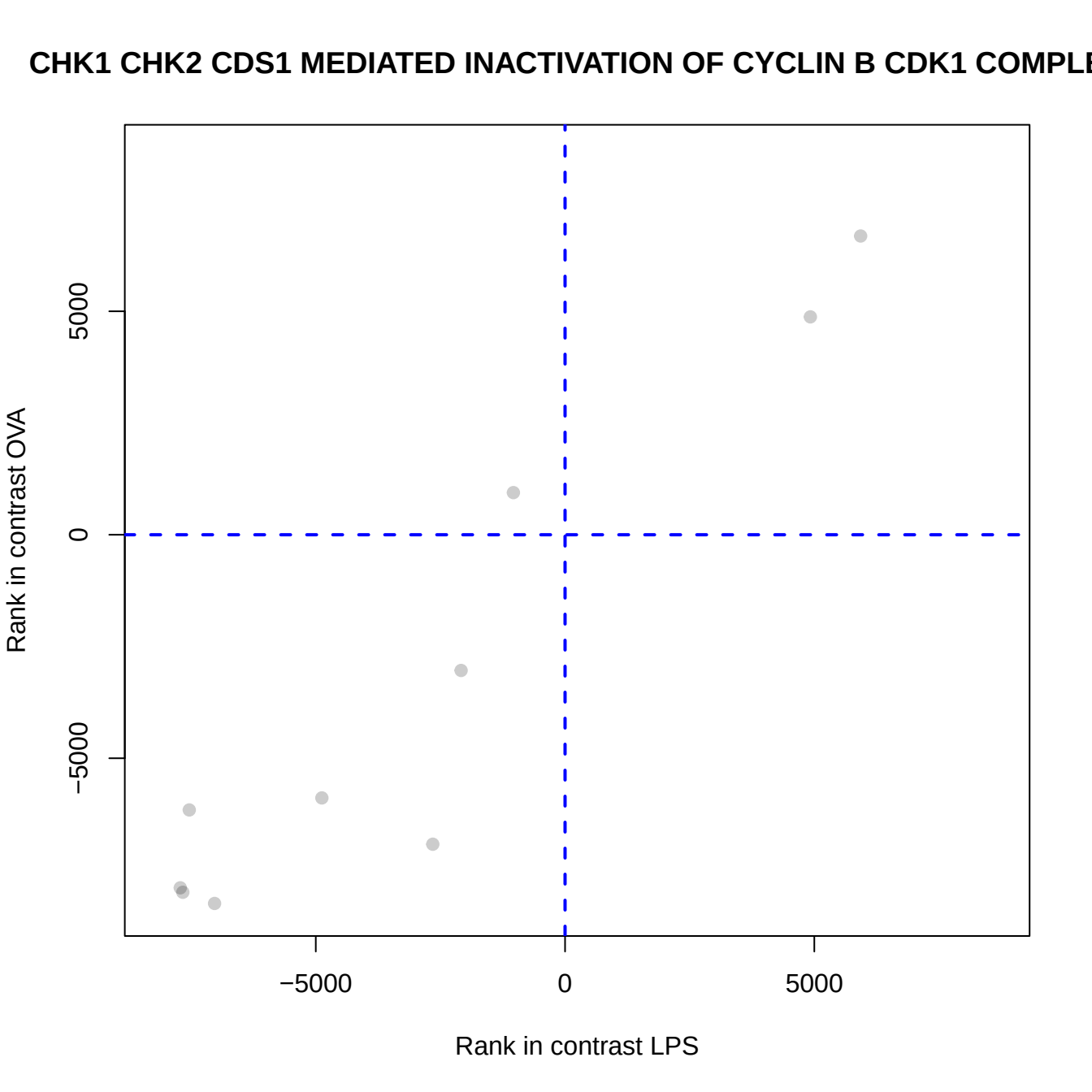

EUKARYOTIC TRANSLATION INITIATION
Position in rank
5000
0
−5000
LPS
OVA
contrast

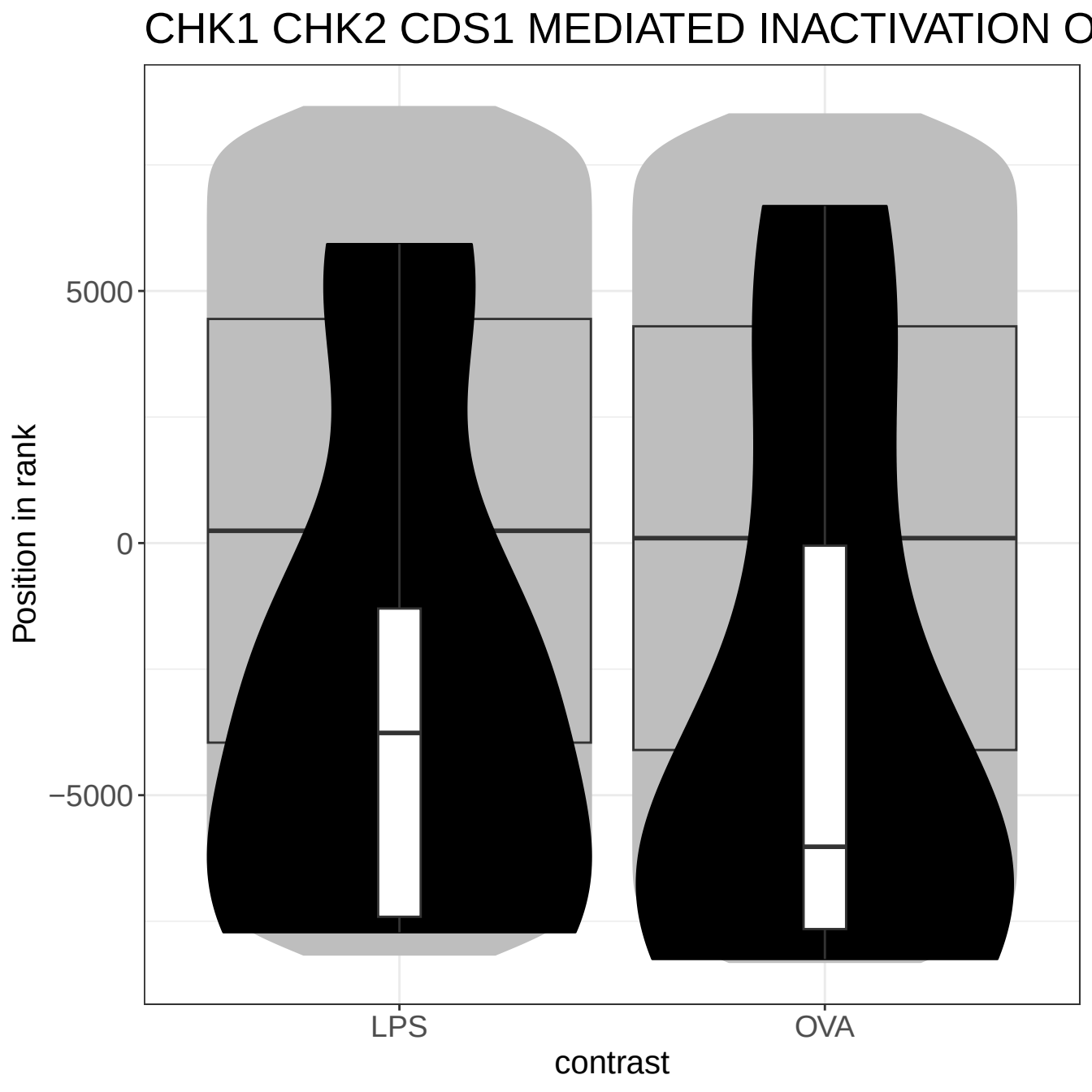

DEPENDENT COTRANSLATIONAL PROTEIN TARGETING TO I
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

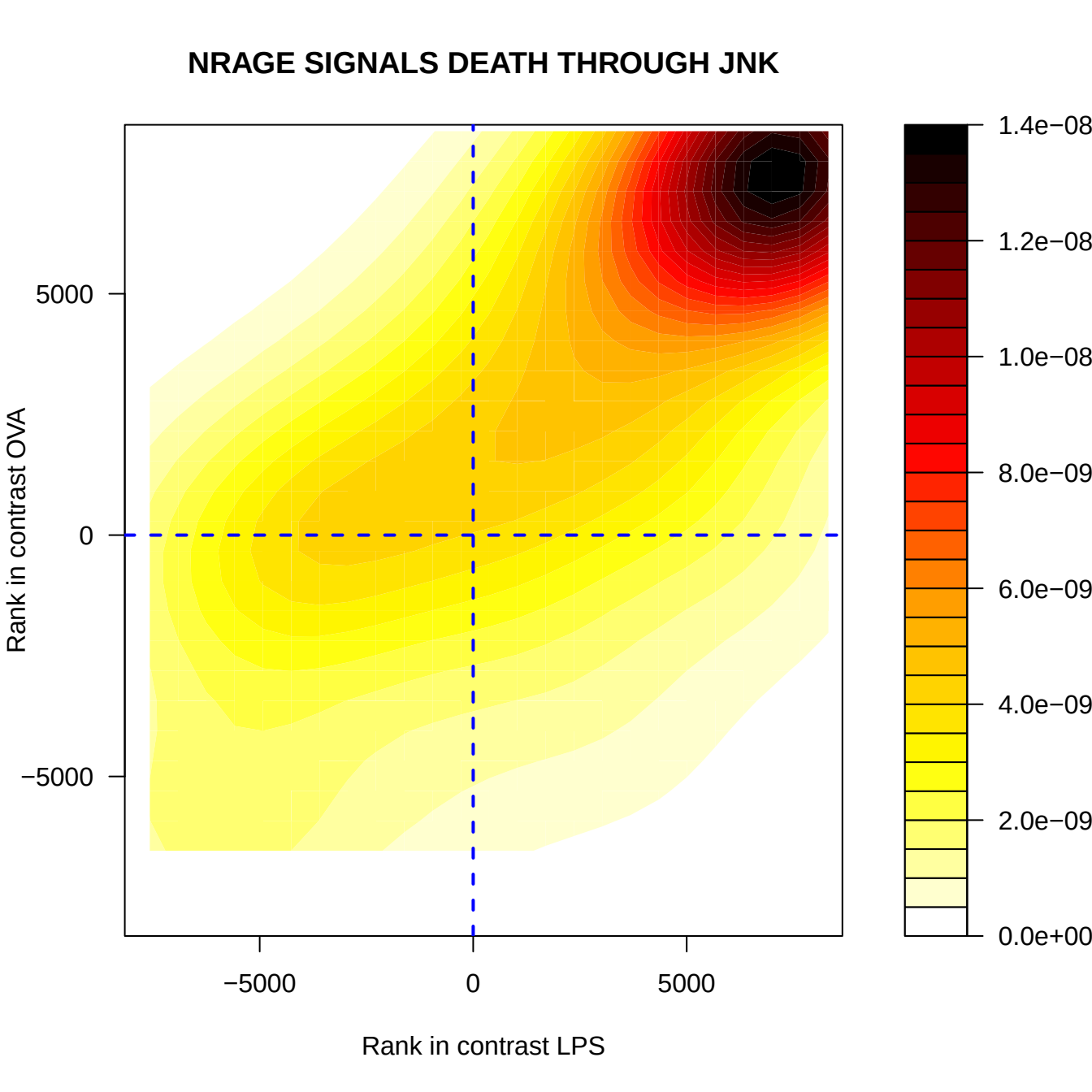

SRP DEPENDENT COTRANSLATIONAL PROTEIN TARGETING TO MEMBRA
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

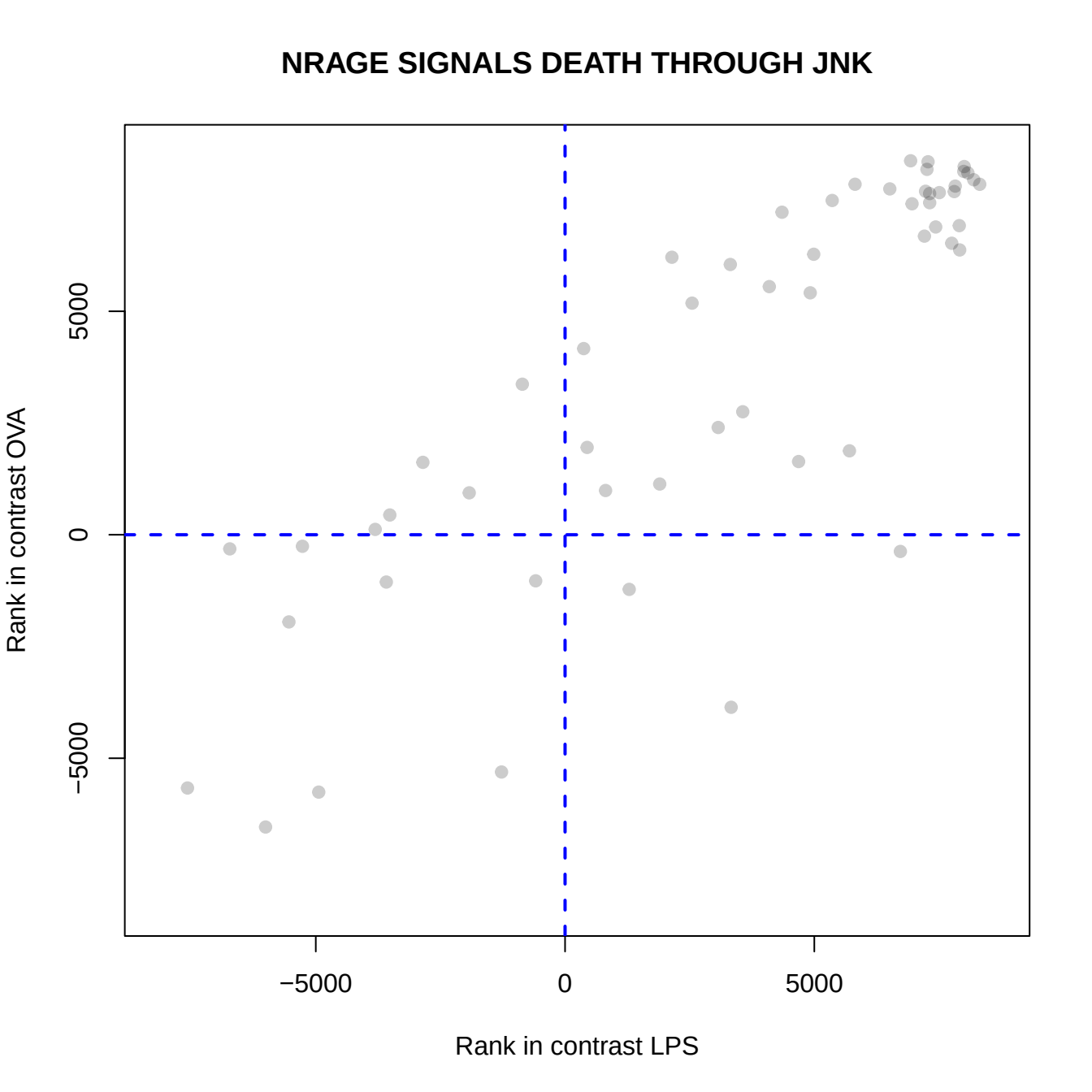

SRP DEPENDENT COTRANSLATIONAL PROTE
5000
0
−5000
Position in rank
LPS
OVA
contrast

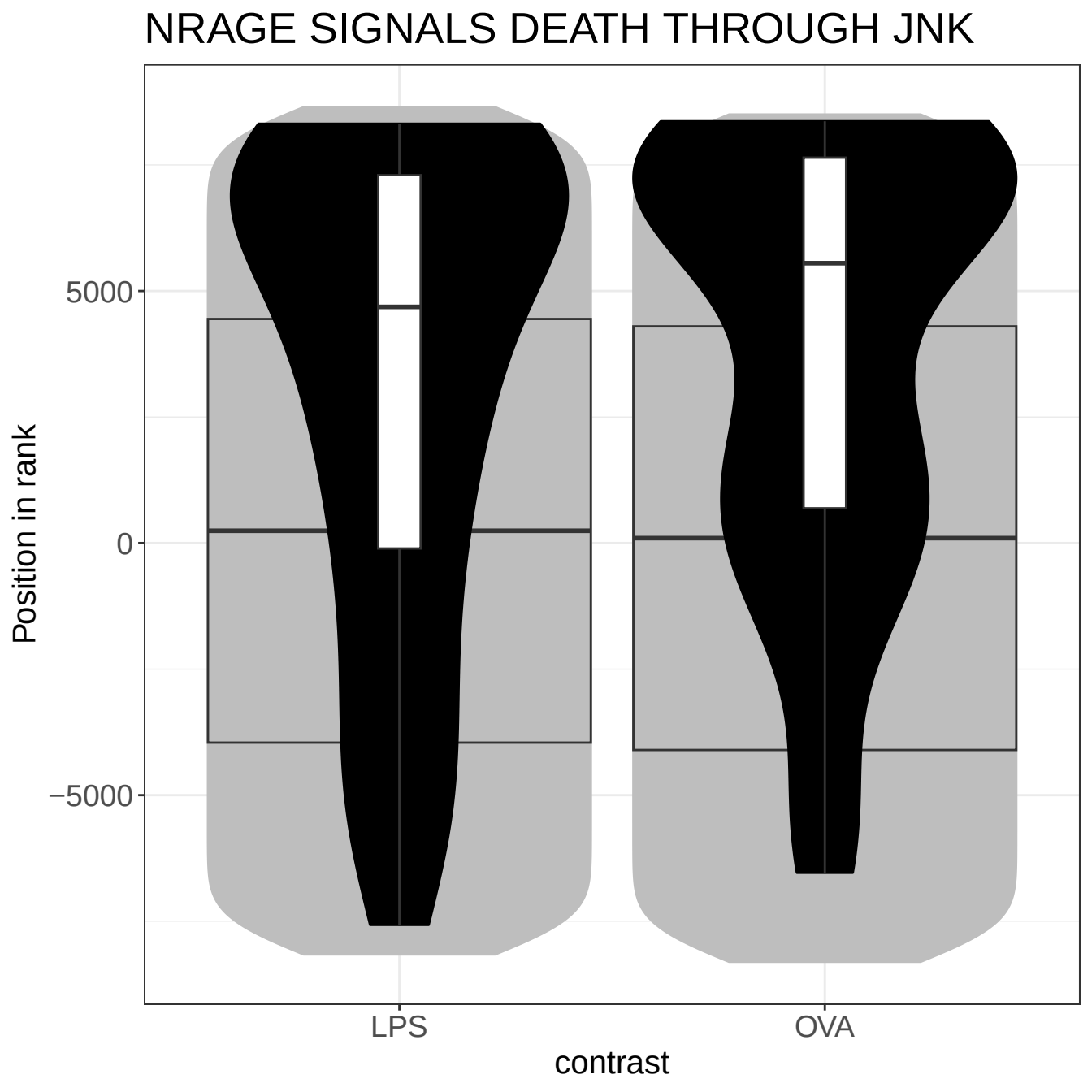

1 CHK2 CDS1 MEDIATED INACTIVATION OF CYCLIN B CDK1
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
7e−09
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

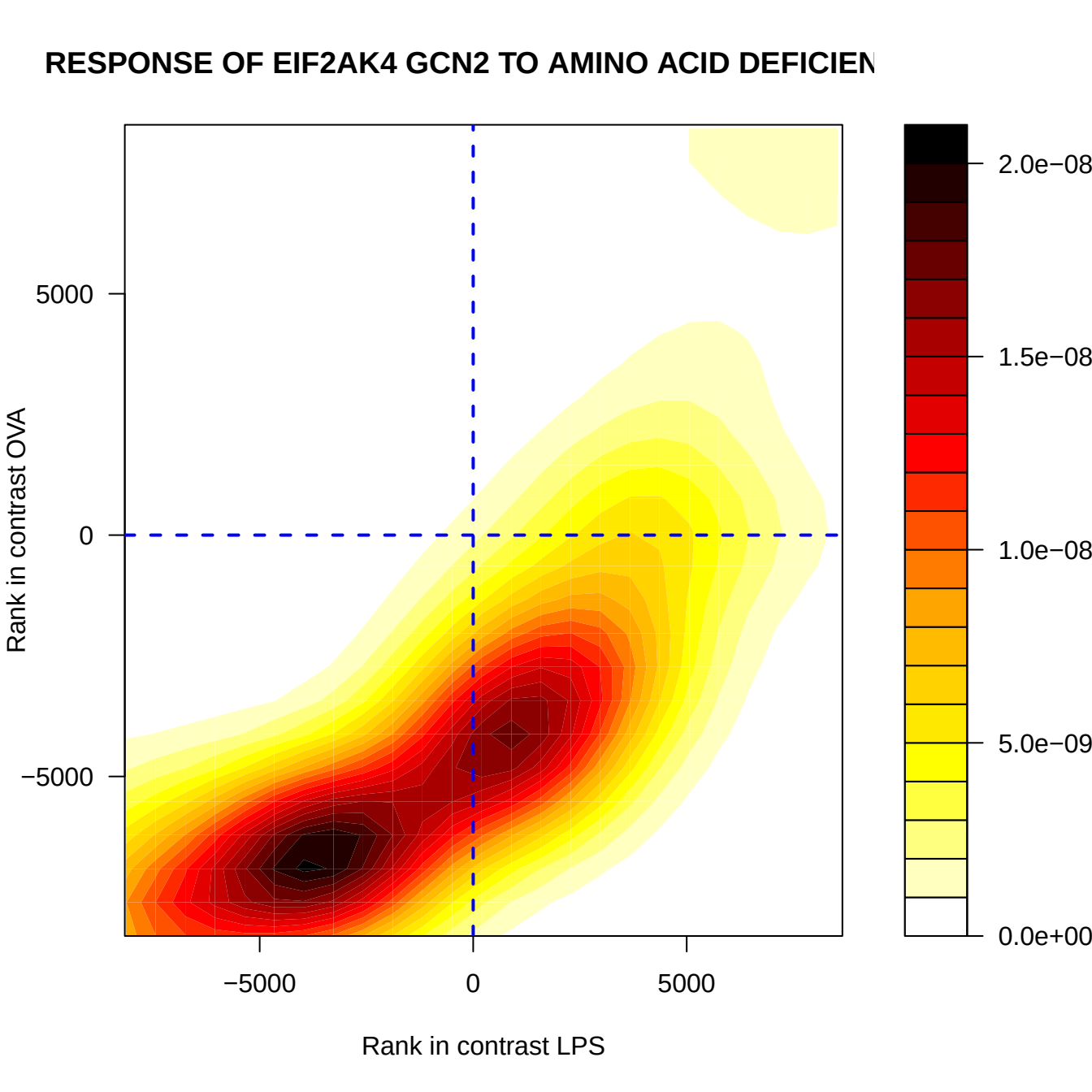

CHK1 CHK2 CDS1 MEDIATED INACTIVATION OF CYCLIN B CDK1 COMPLE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

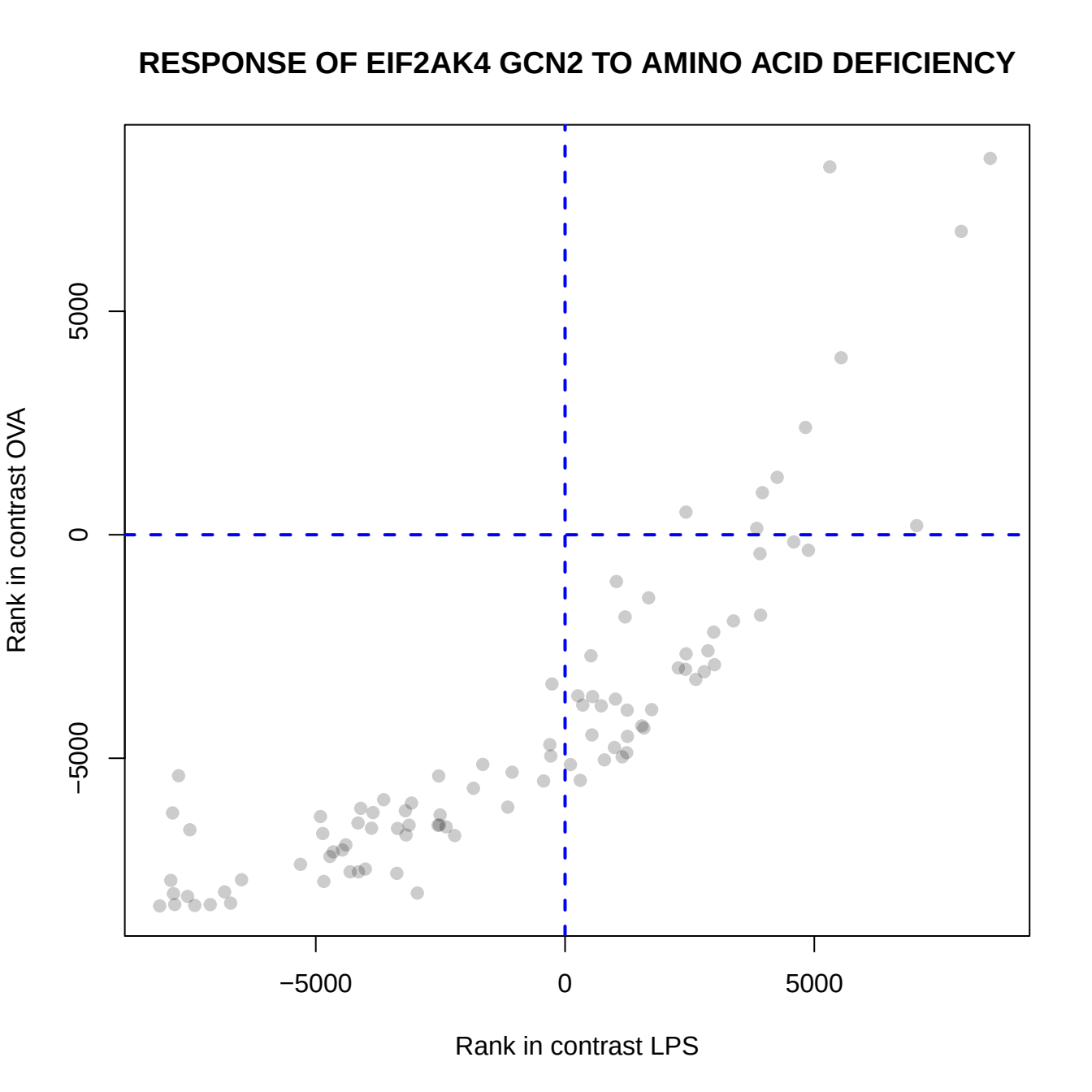

CHK1 CHK2 CDS1 MEDIATED INACTIVATION O
5000
0
−5000
Position in rank
LPS
OVA
contrast

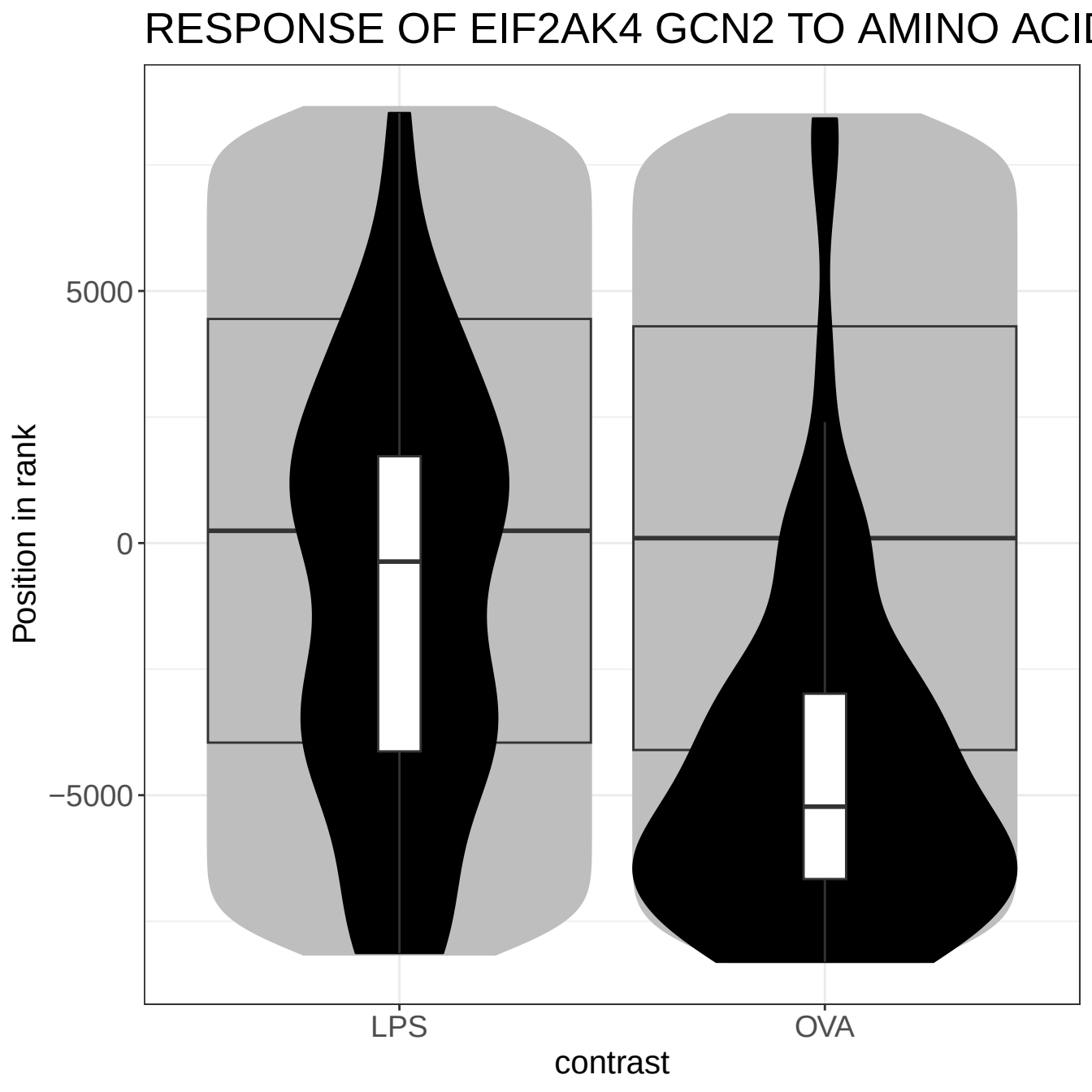

NRAGE SIGNALS DEATH THROUGH JNK
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

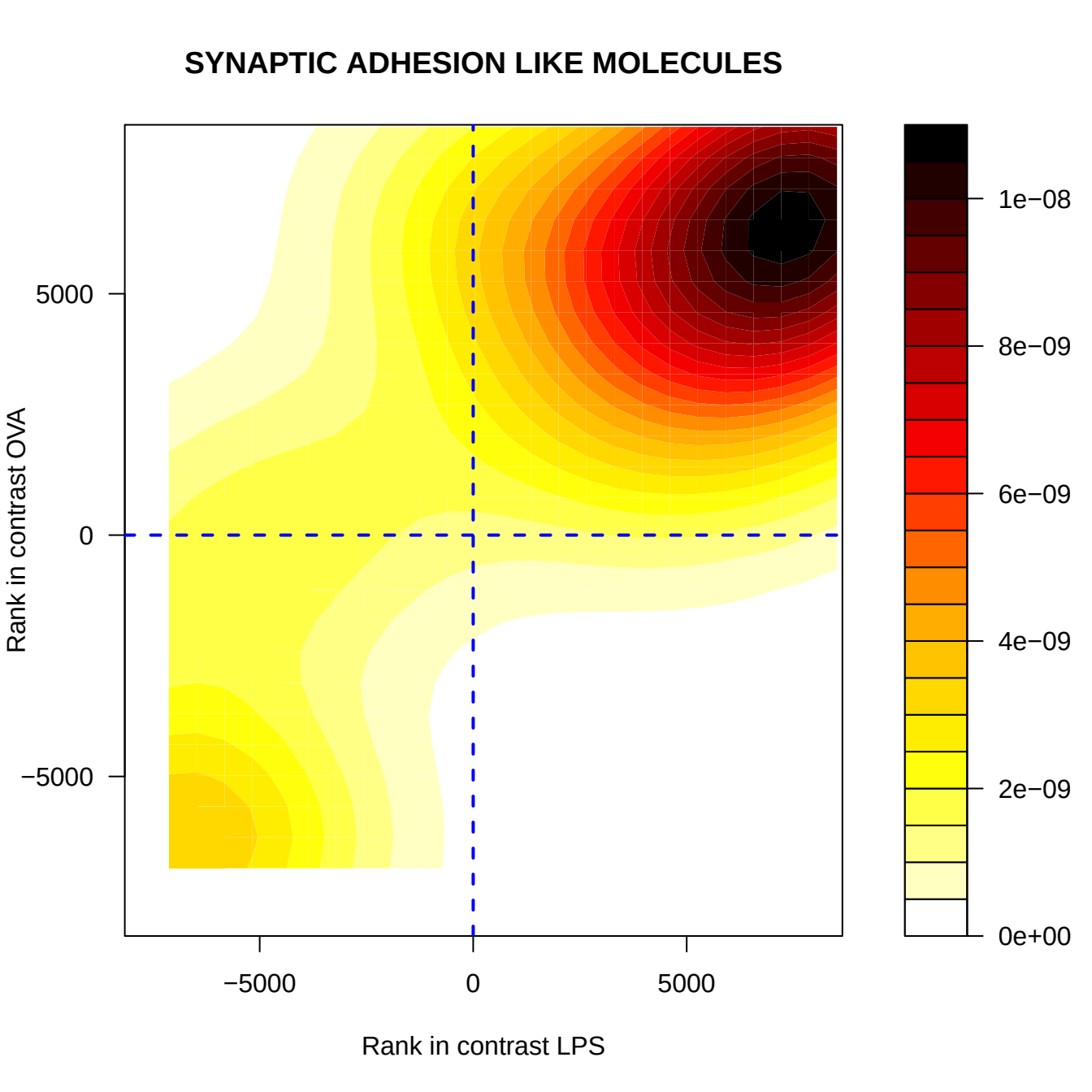

NRAGE SIGNALS DEATH THROUGH JNK
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

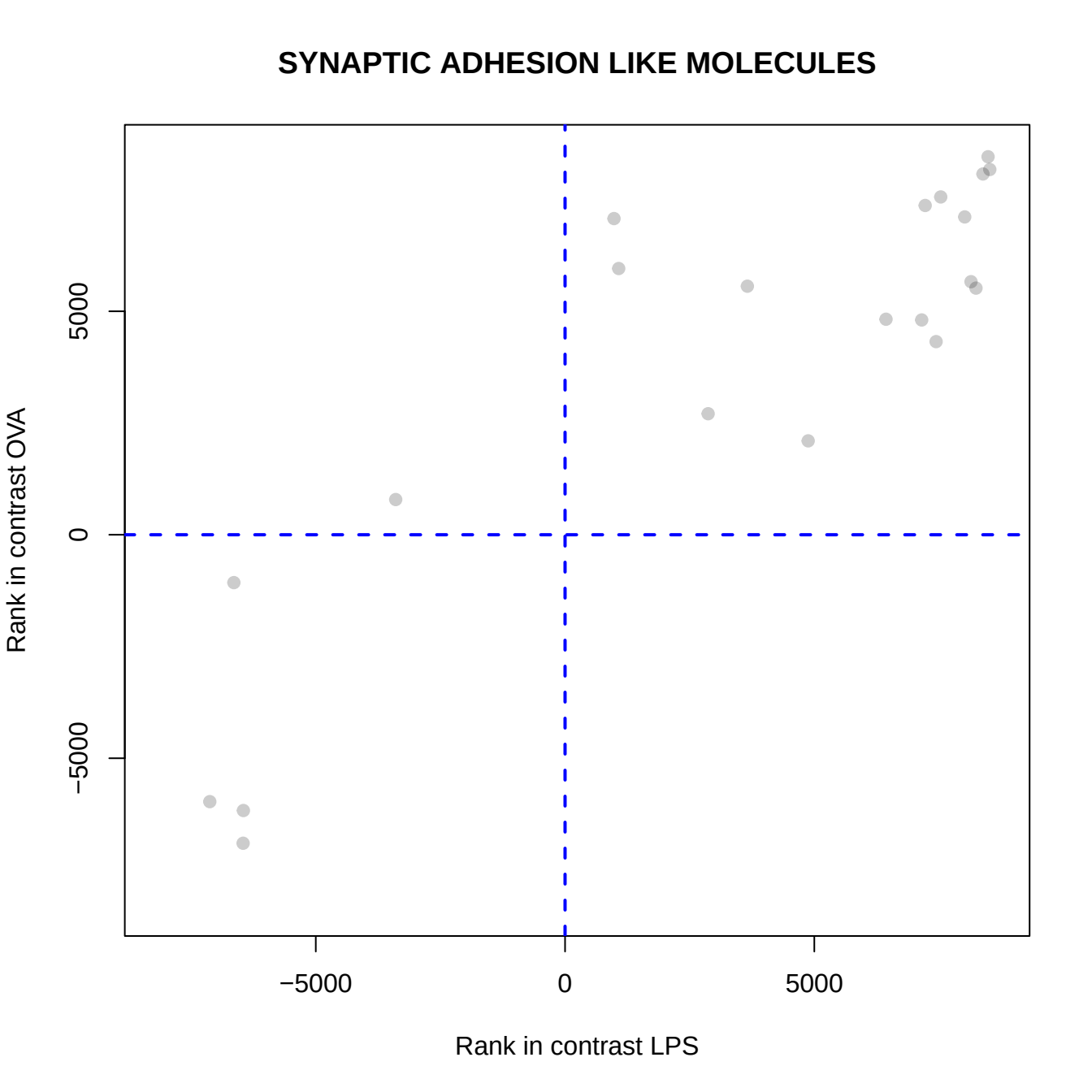

NRAGE SIGNALS DEATH THROUGH JNK
Position in rank
5000
0
−5000
LPS
OVA
contrast

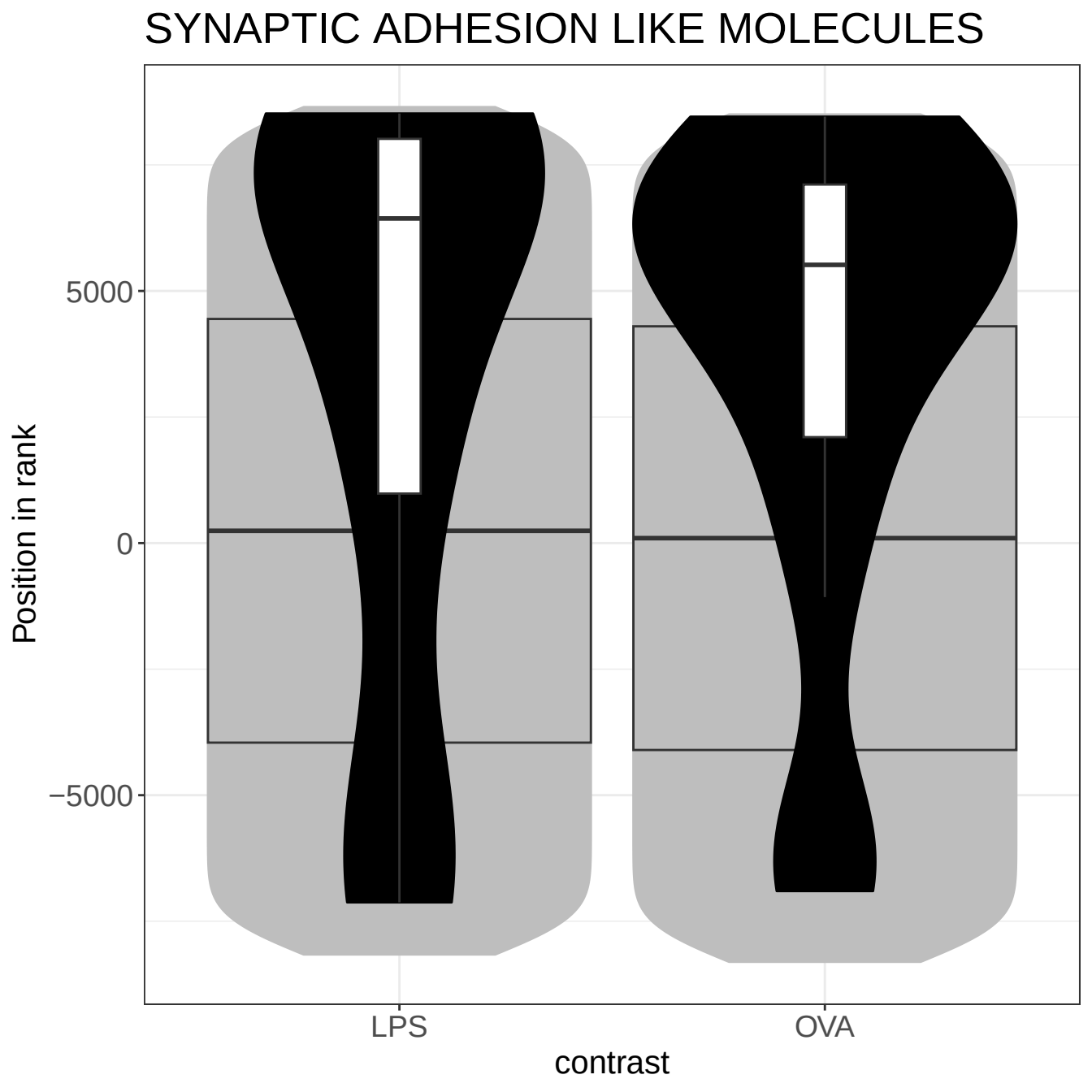

RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID DEFICIEN
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

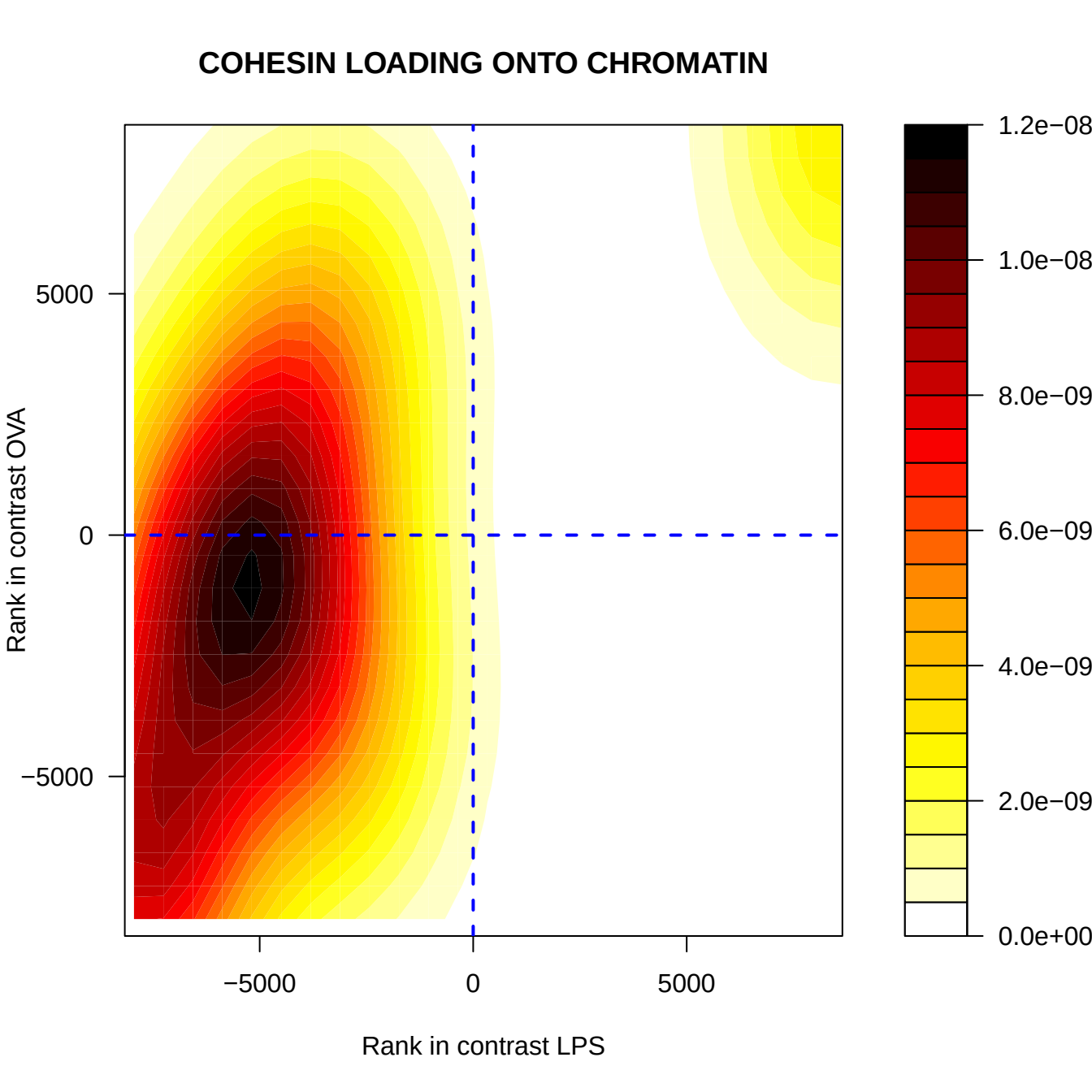

RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID DEFICIENCY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

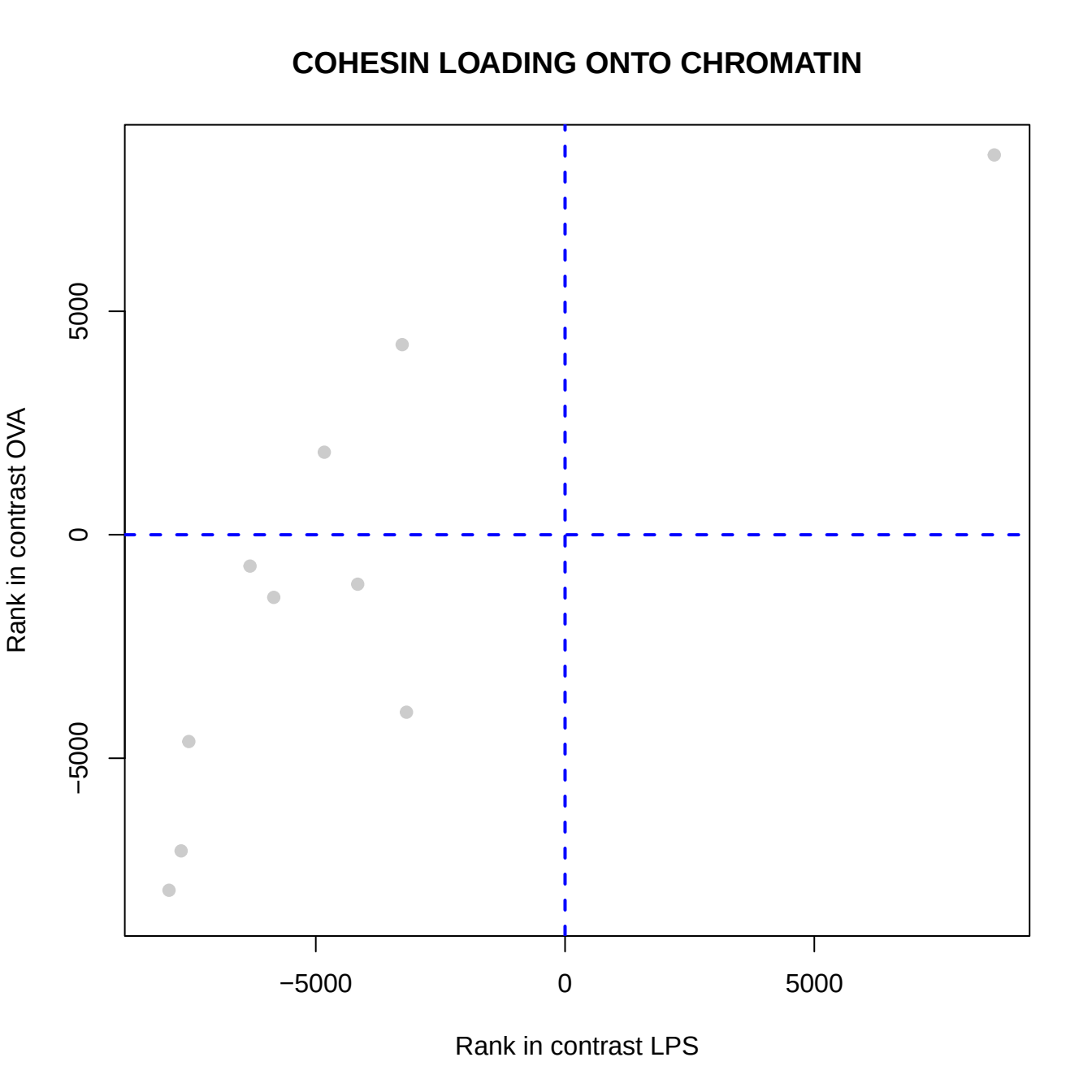

RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID
5000
0
−5000
Position in rank
LPS
OVA
contrast

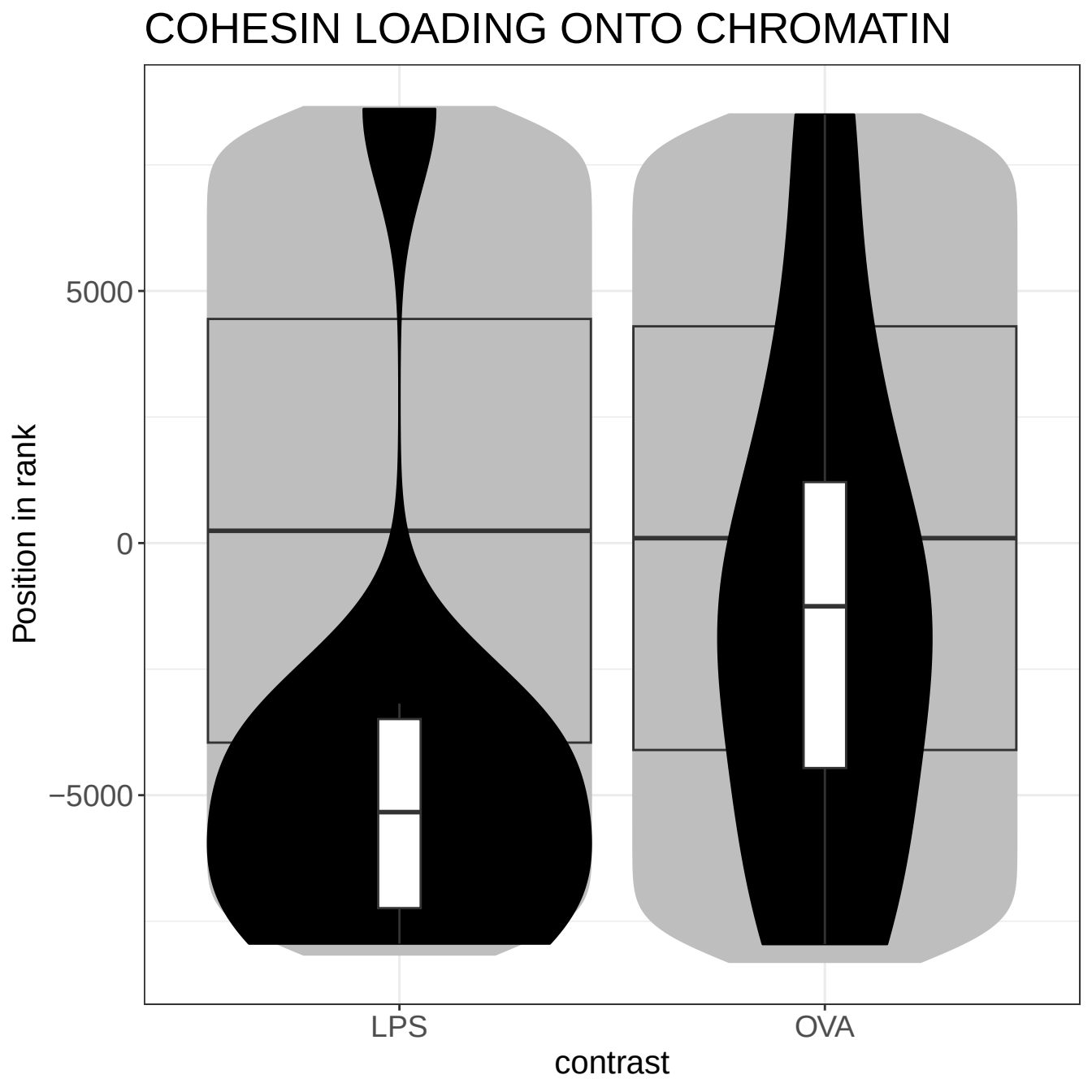

SYNAPTIC ADHESION LIKE MOLECULES
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

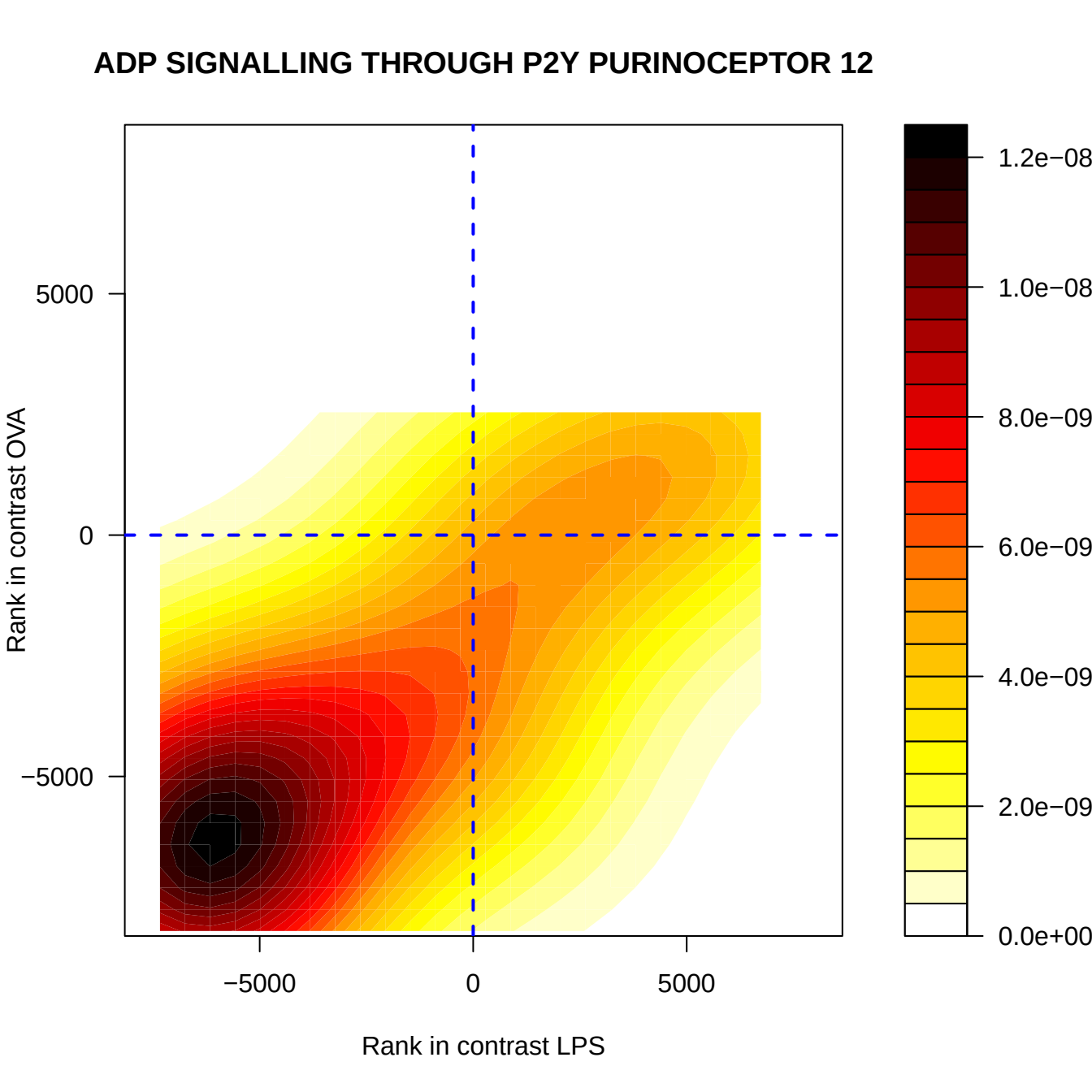

SYNAPTIC ADHESION LIKE MOLECULES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

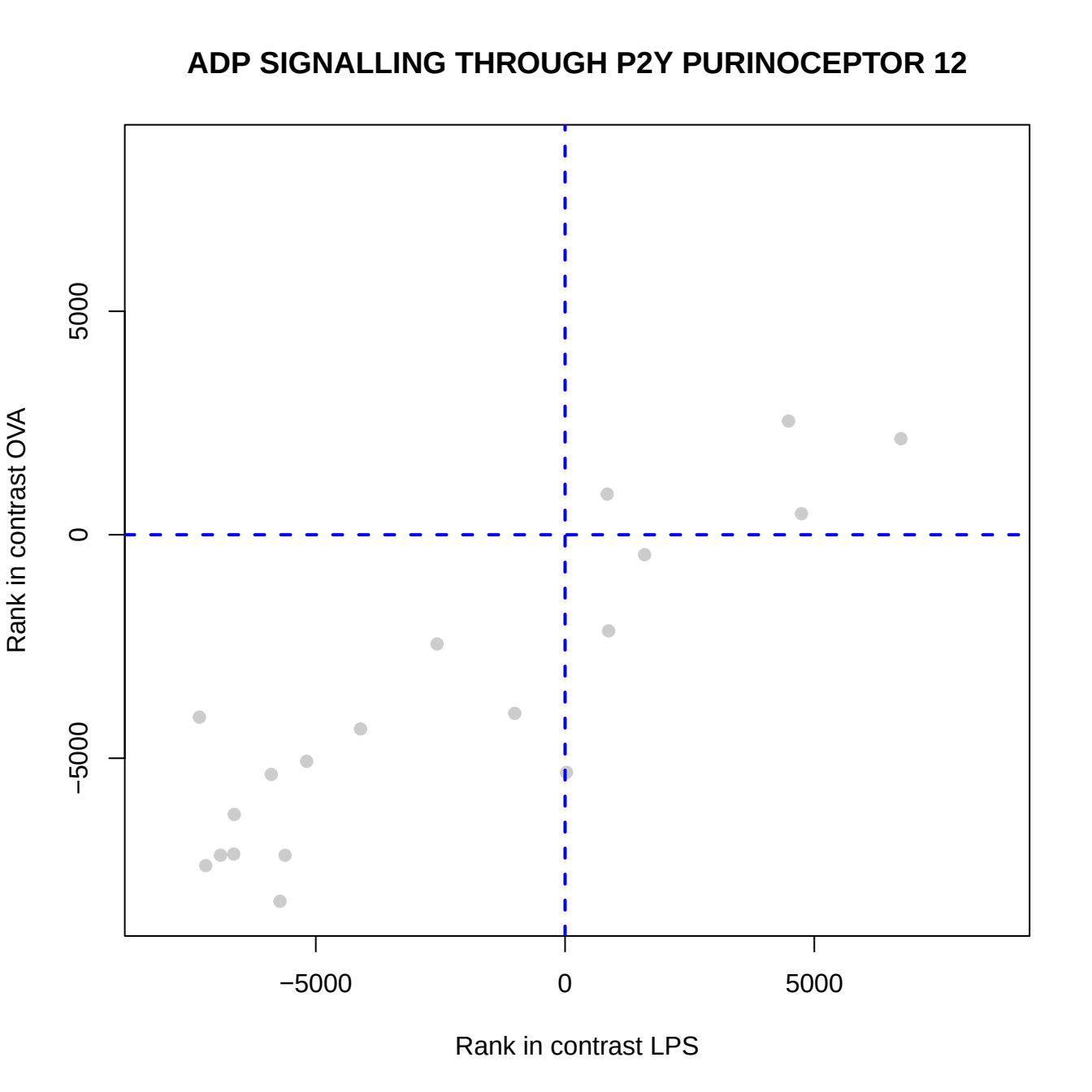

SYNAPTIC ADHESION LIKE MOLECULES
Position in rank
5000
0
−5000
LPS
OVA
contrast

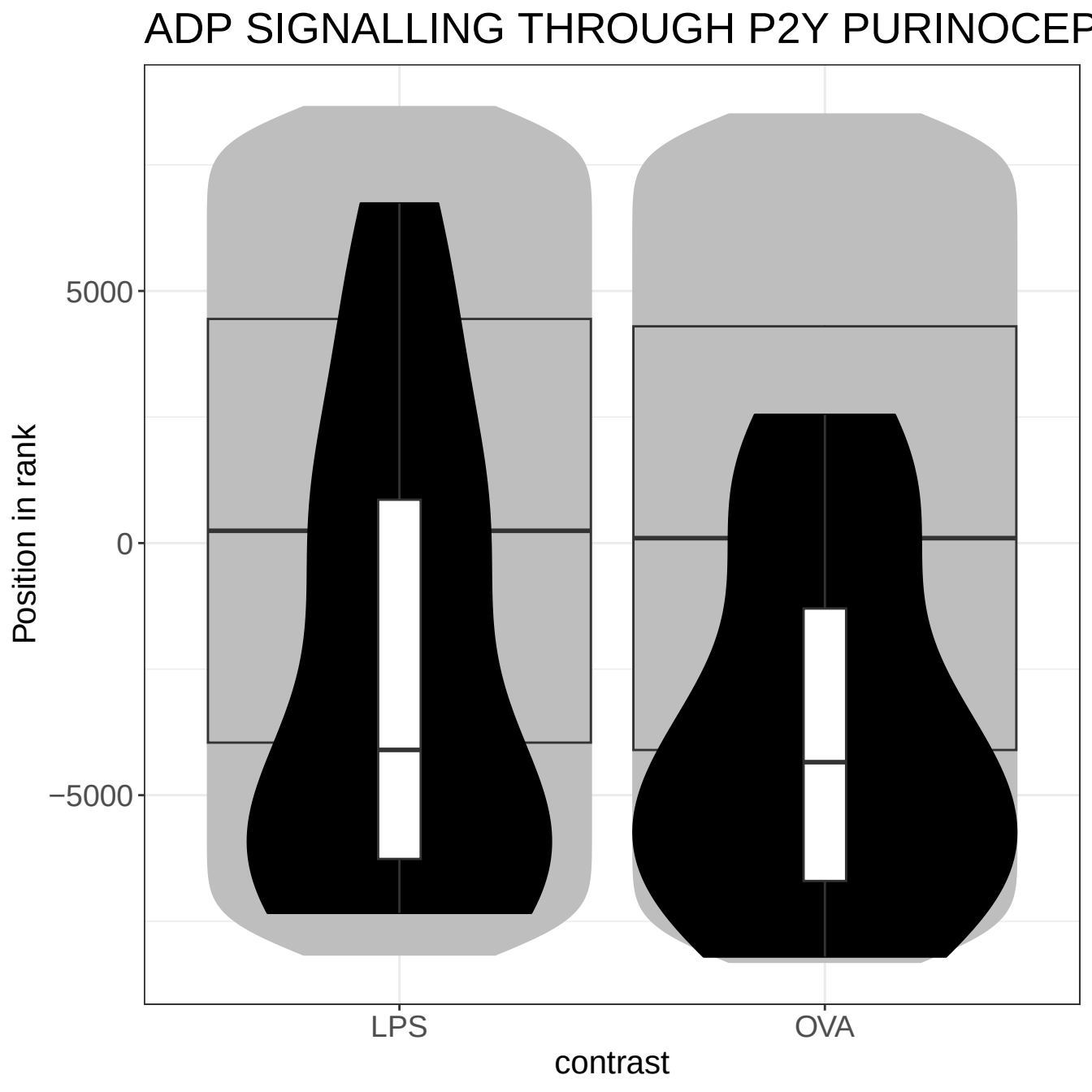

COHESIN LOADING ONTO CHROMATIN
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

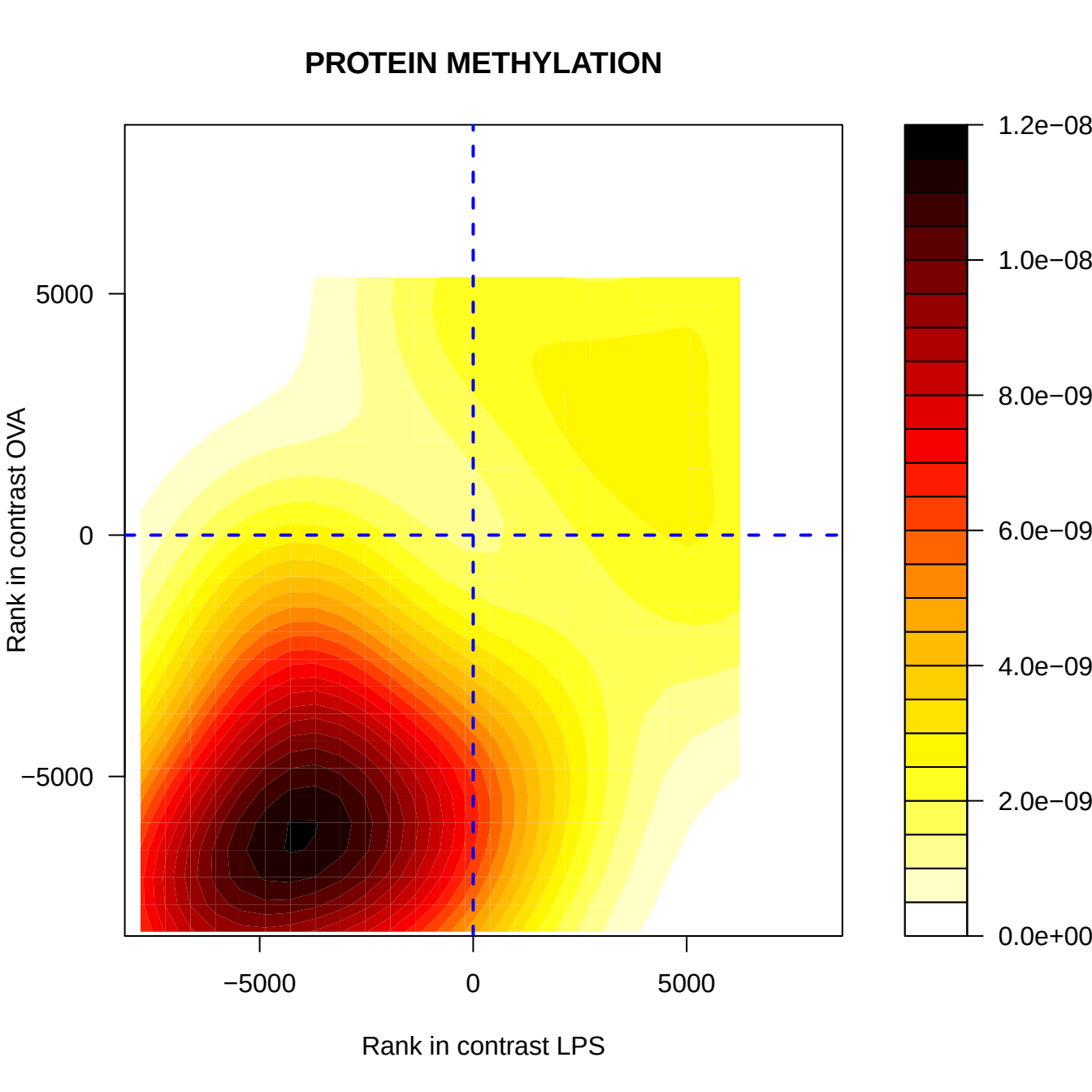

COHESIN LOADING ONTO CHROMATIN
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

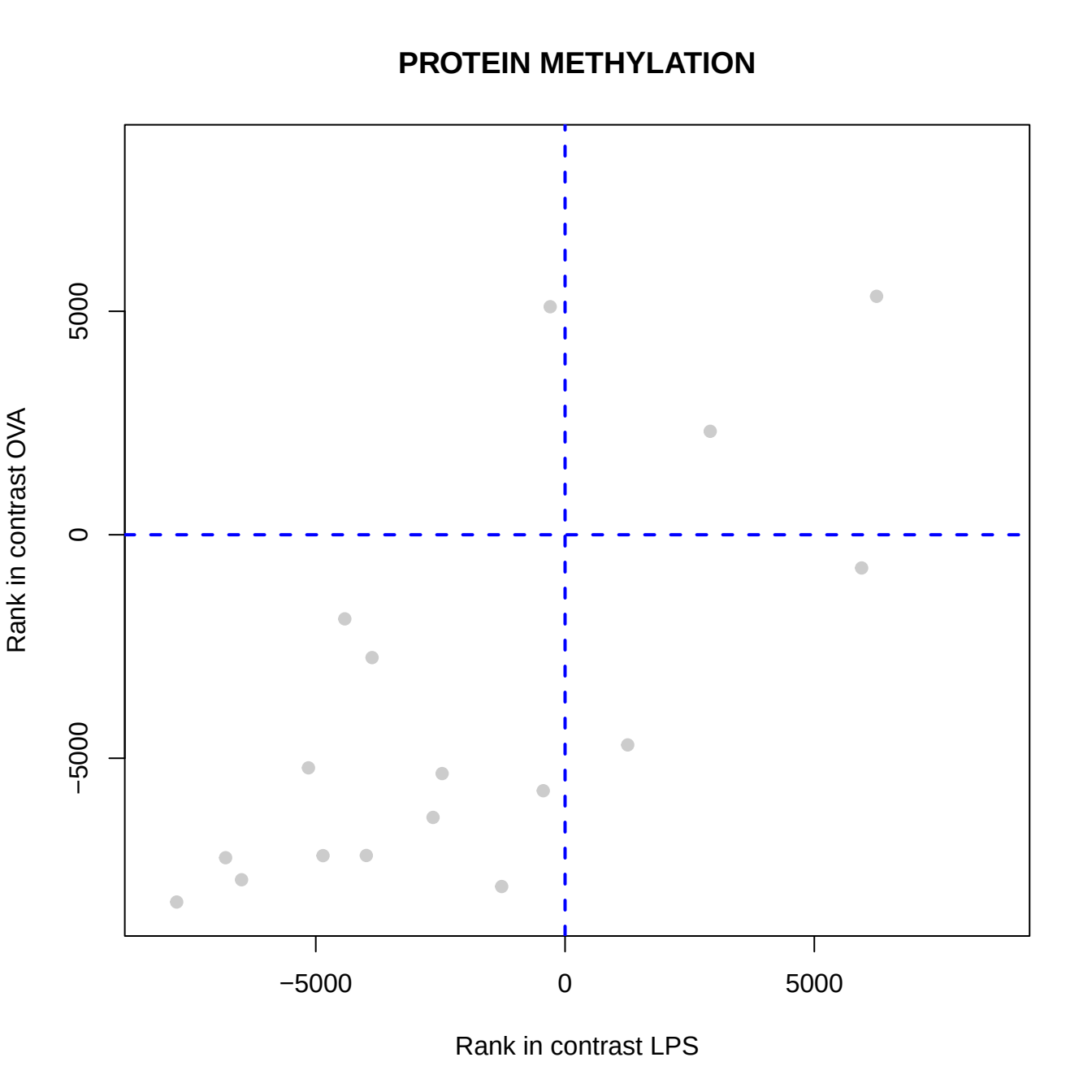

COHESIN LOADING ONTO CHROMATIN
5000
0
−5000
Position in rank
LPS
OVA
contrast

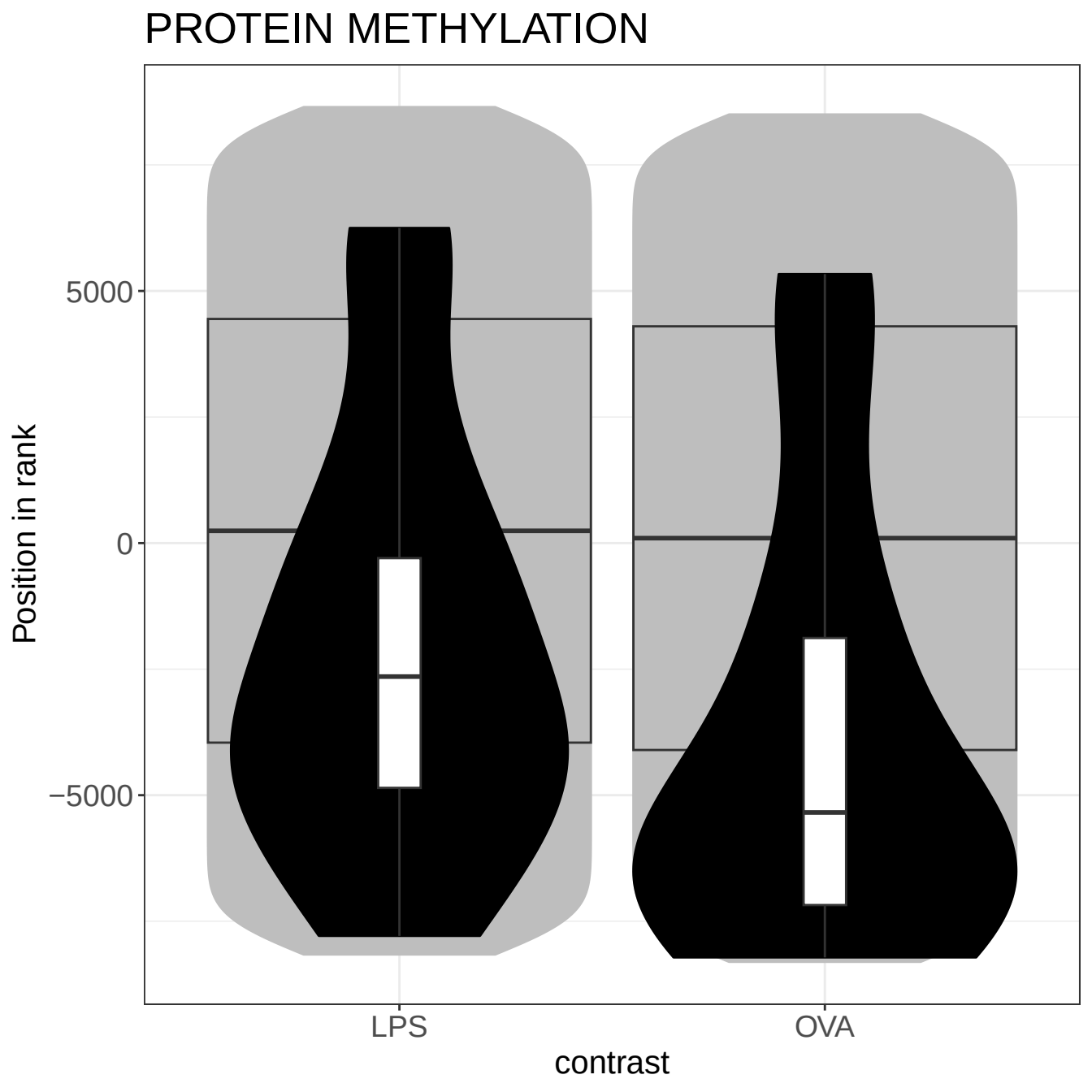

ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 12
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

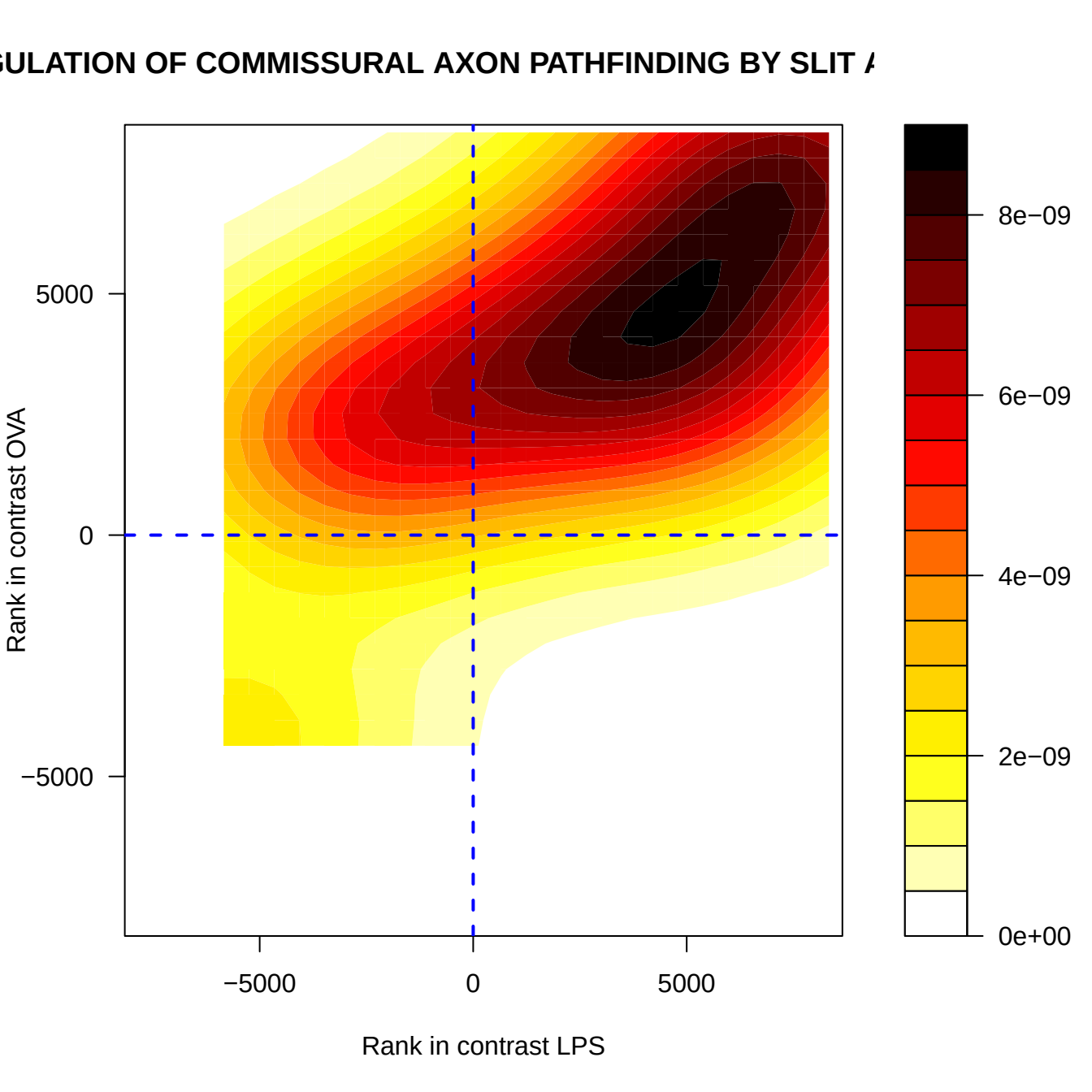

ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 12
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

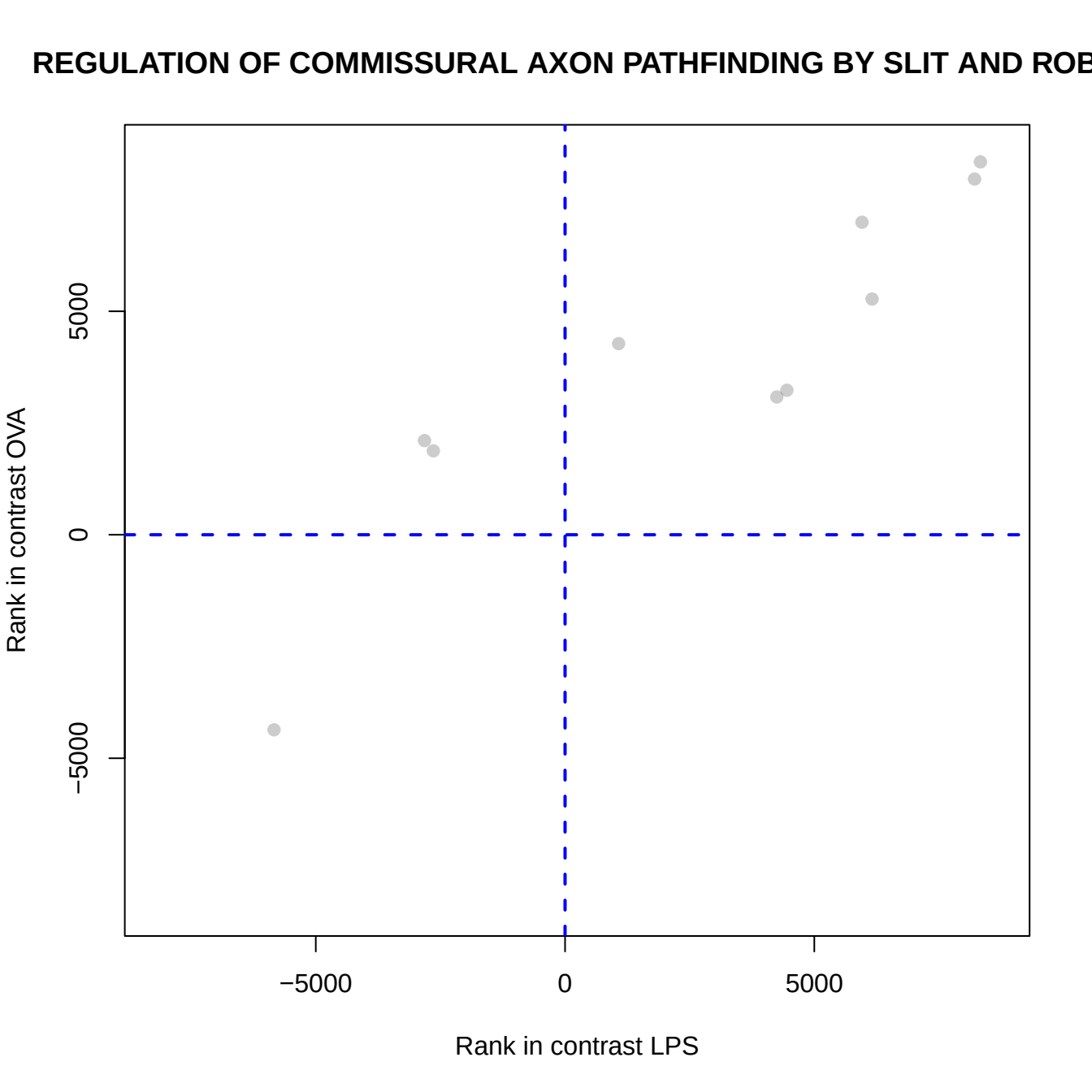

ADP SIGNALLING THROUGH P2Y PURINOCEP
Position in rank
5000
0
−5000
LPS
OVA
contrast

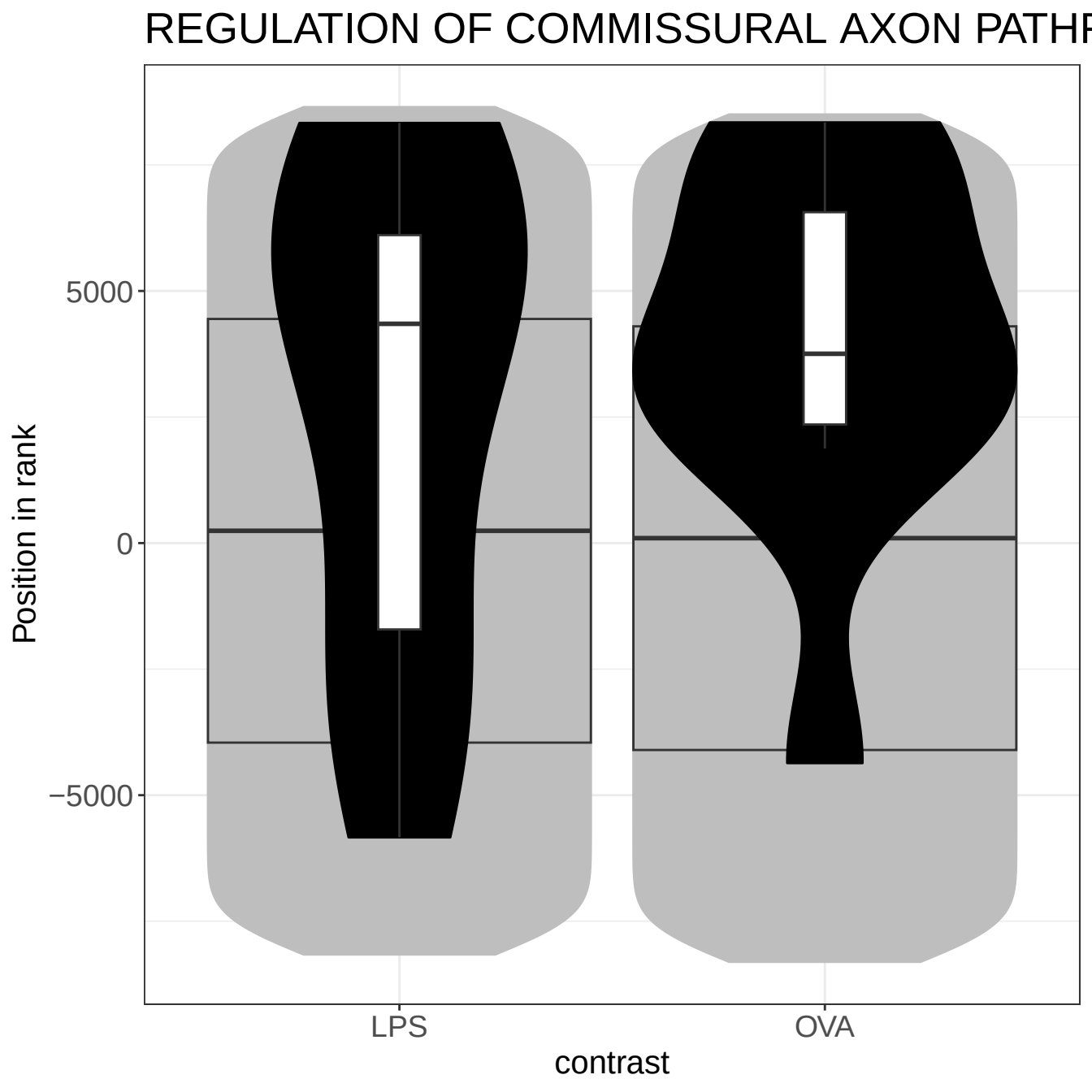

PROTEIN METHYLATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

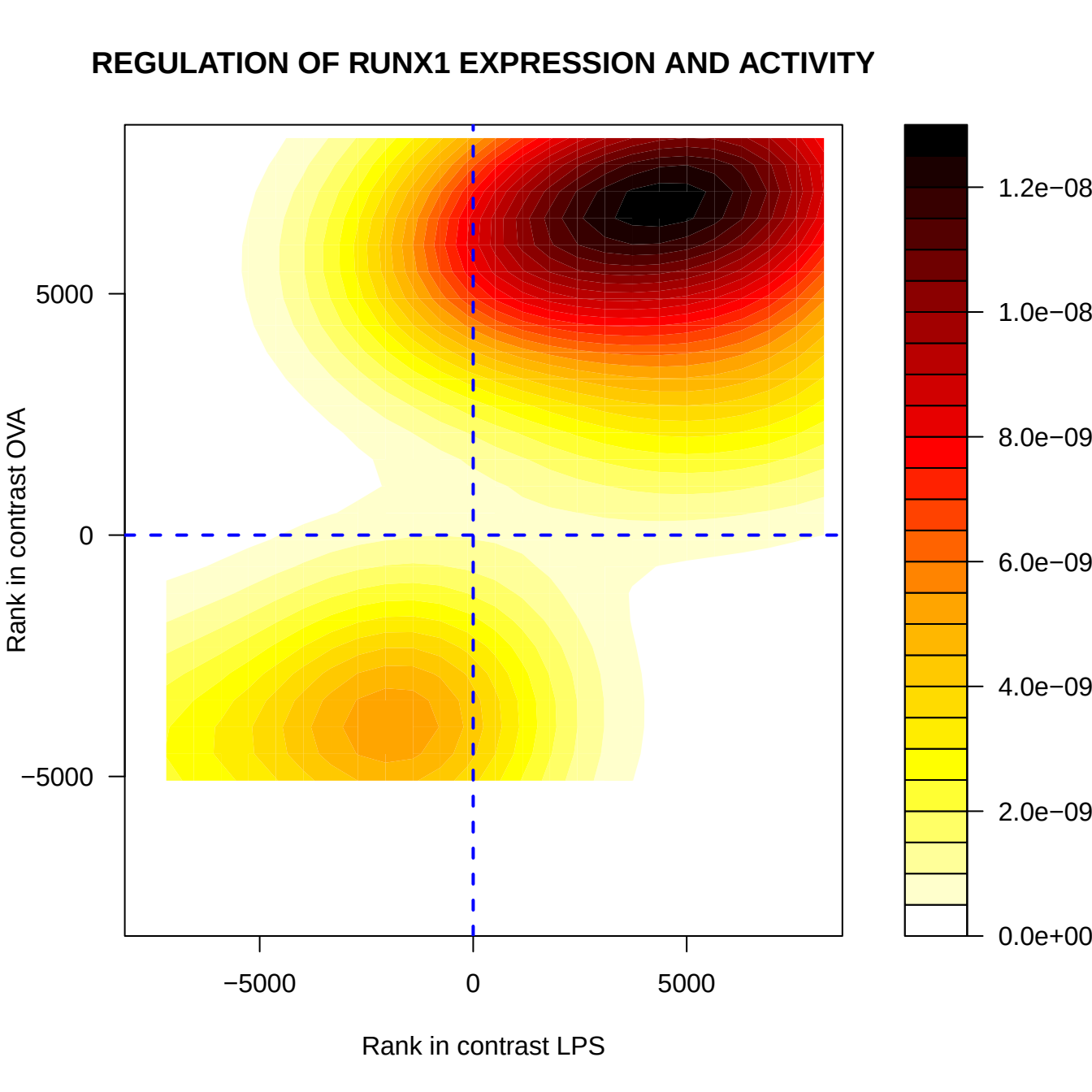

PROTEIN METHYLATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

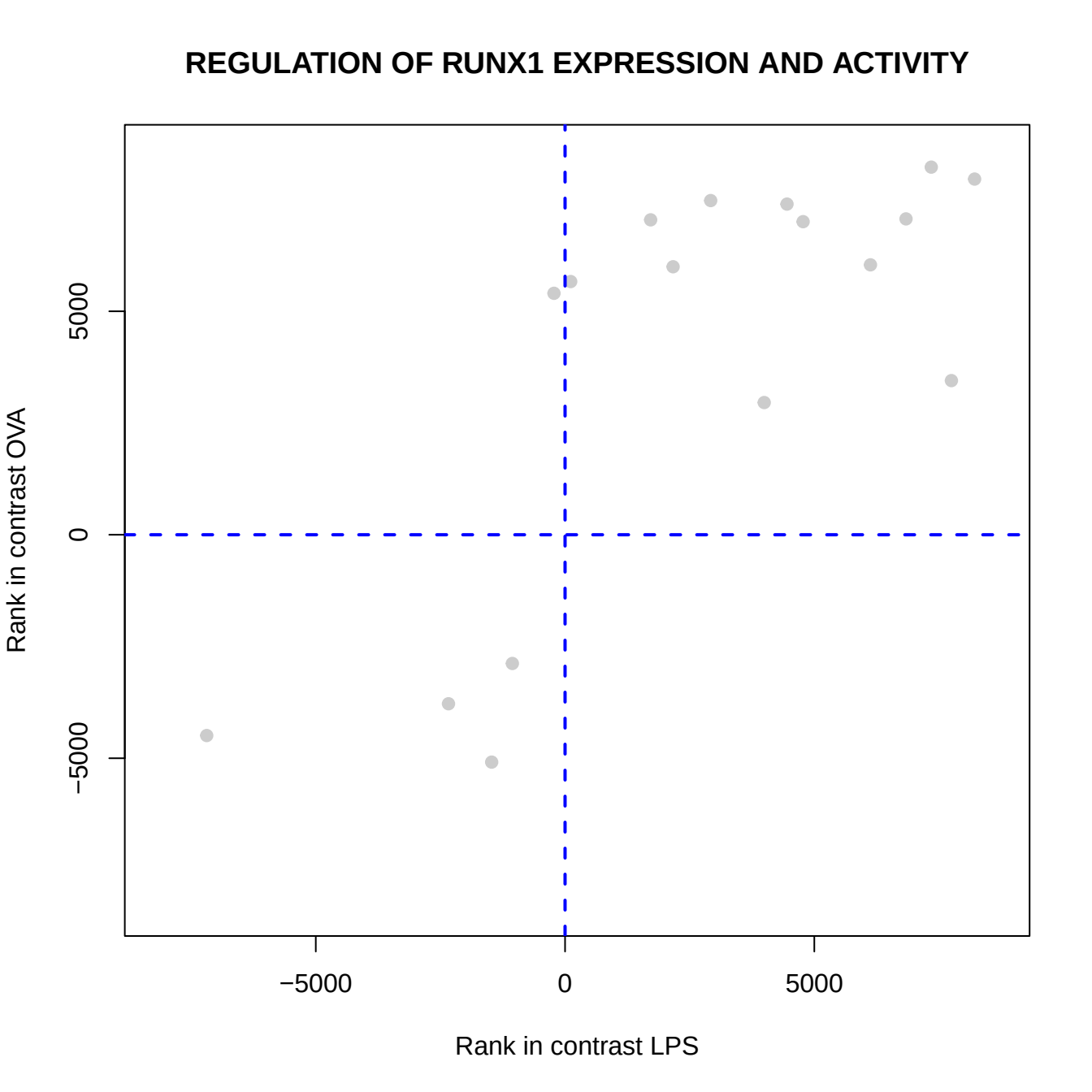

PROTEIN METHYLATION
5000
0
−5000
Position in rank
LPS
OVA
contrast

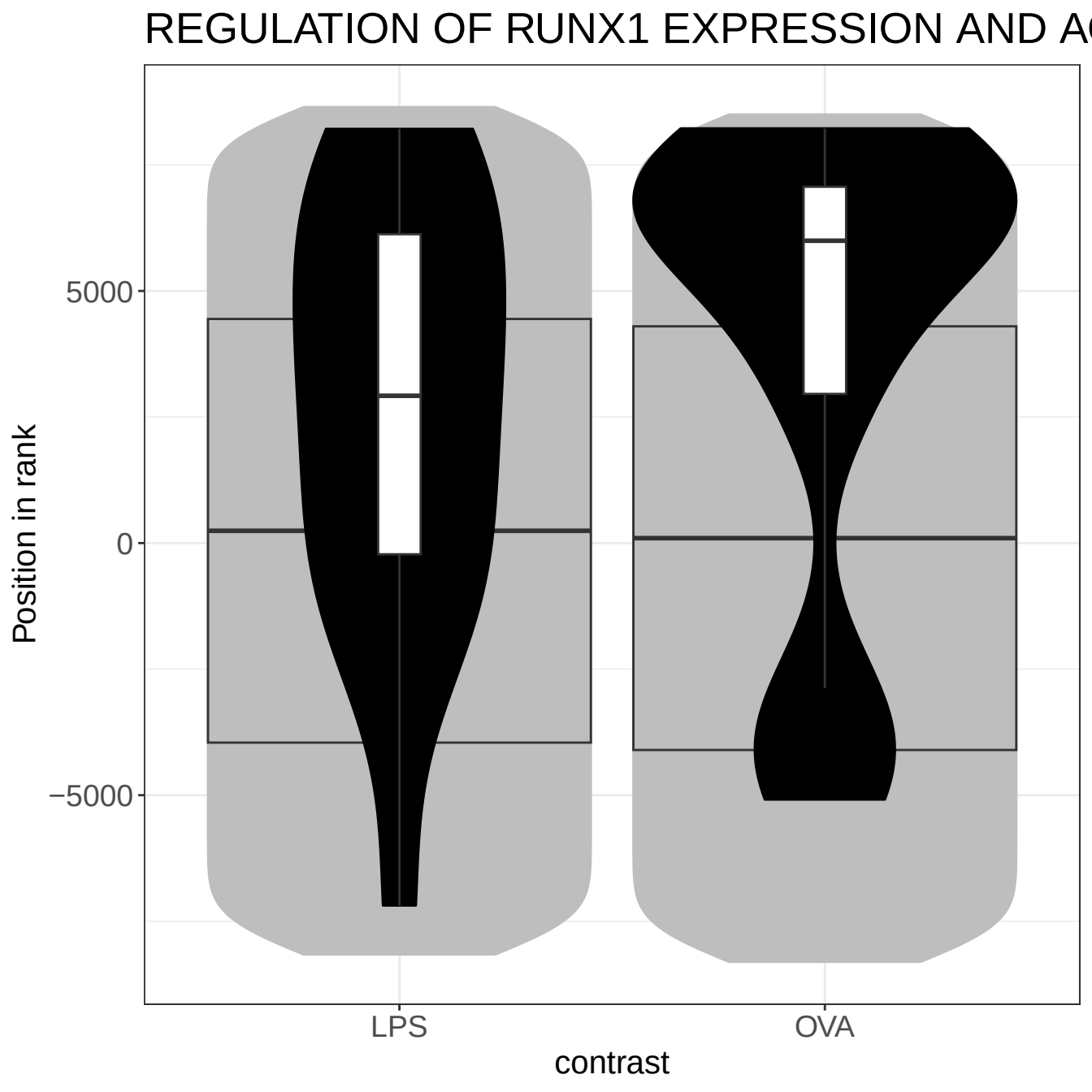

GULATION OF COMMISSURAL AXON PATHFINDING BY SLIT A
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

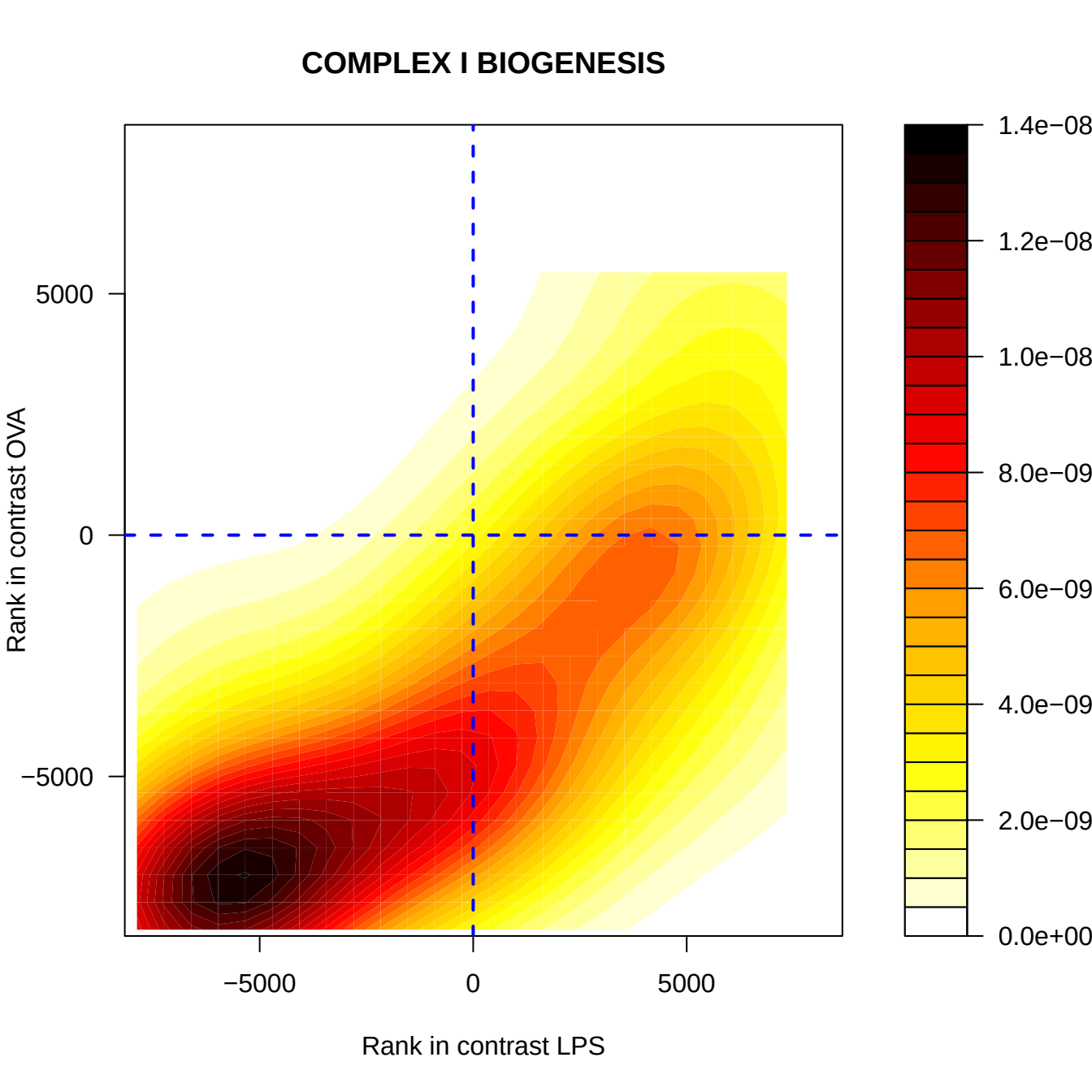

REGULATION OF COMMISSURAL AXON PATHFINDING BY SLIT AND ROB
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

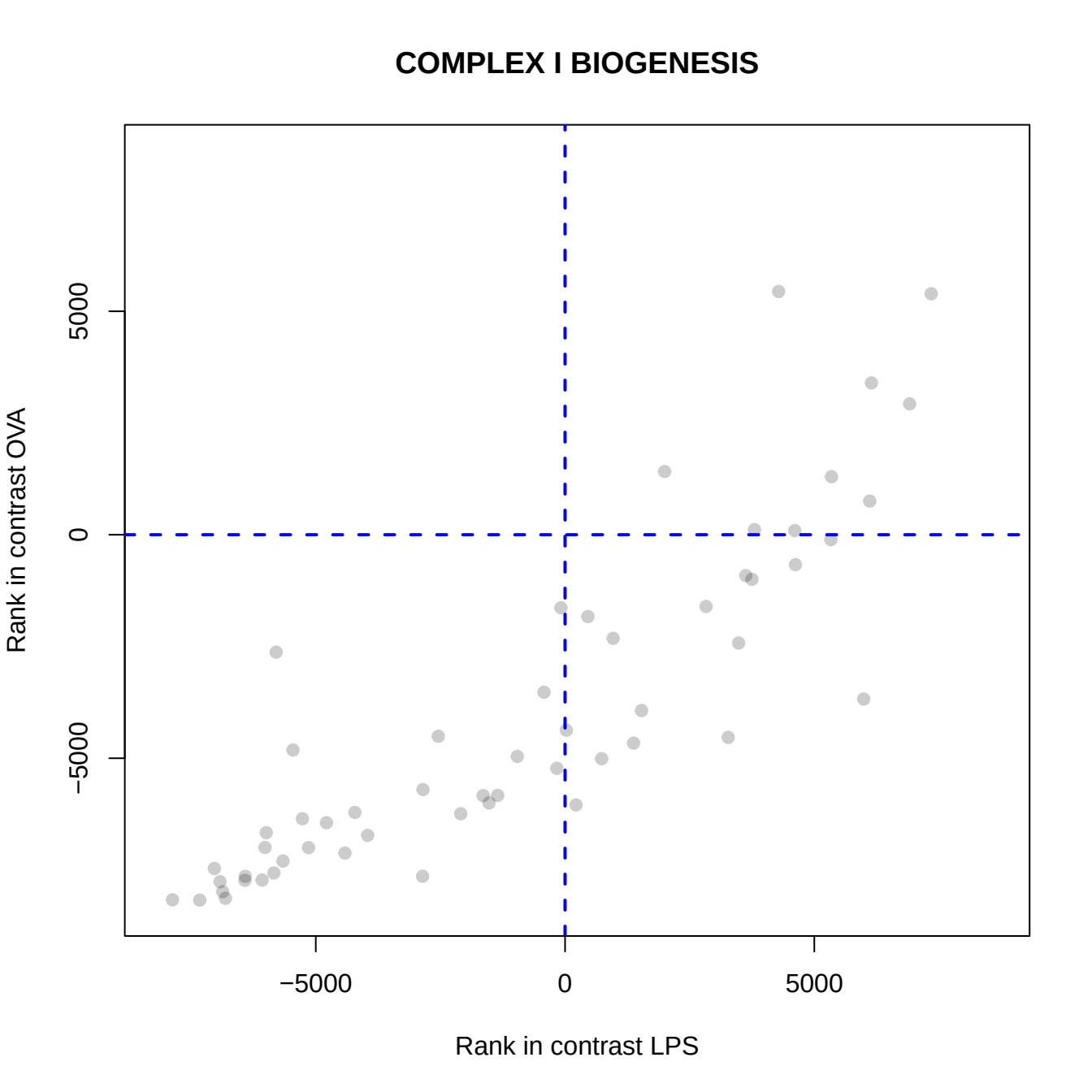

REGULATION OF COMMISSURAL AXON PATHF
5000
0
−5000
Position in rank
LPS
OVA
contrast

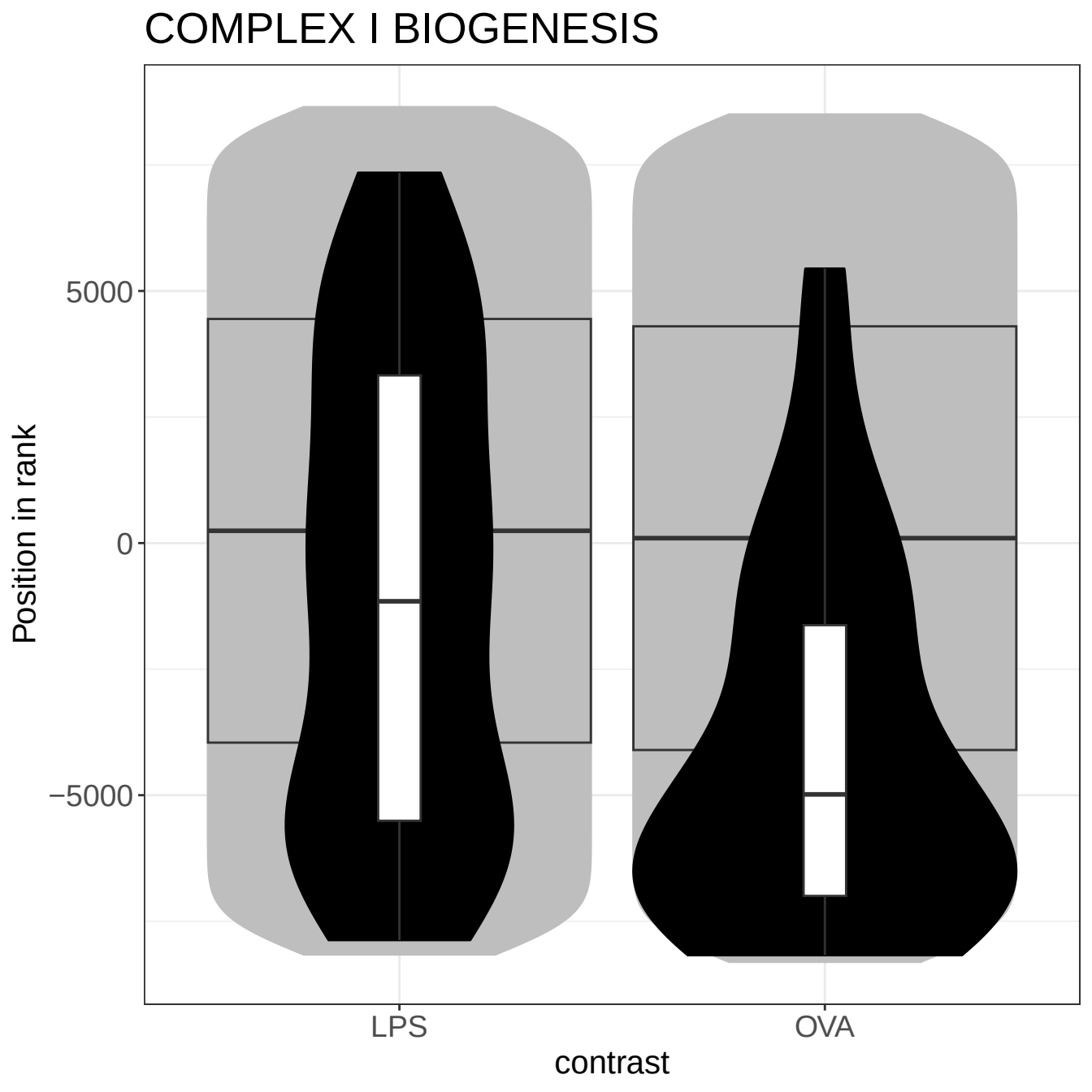

REGULATION OF RUNX1 EXPRESSION AND ACTIVITY
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

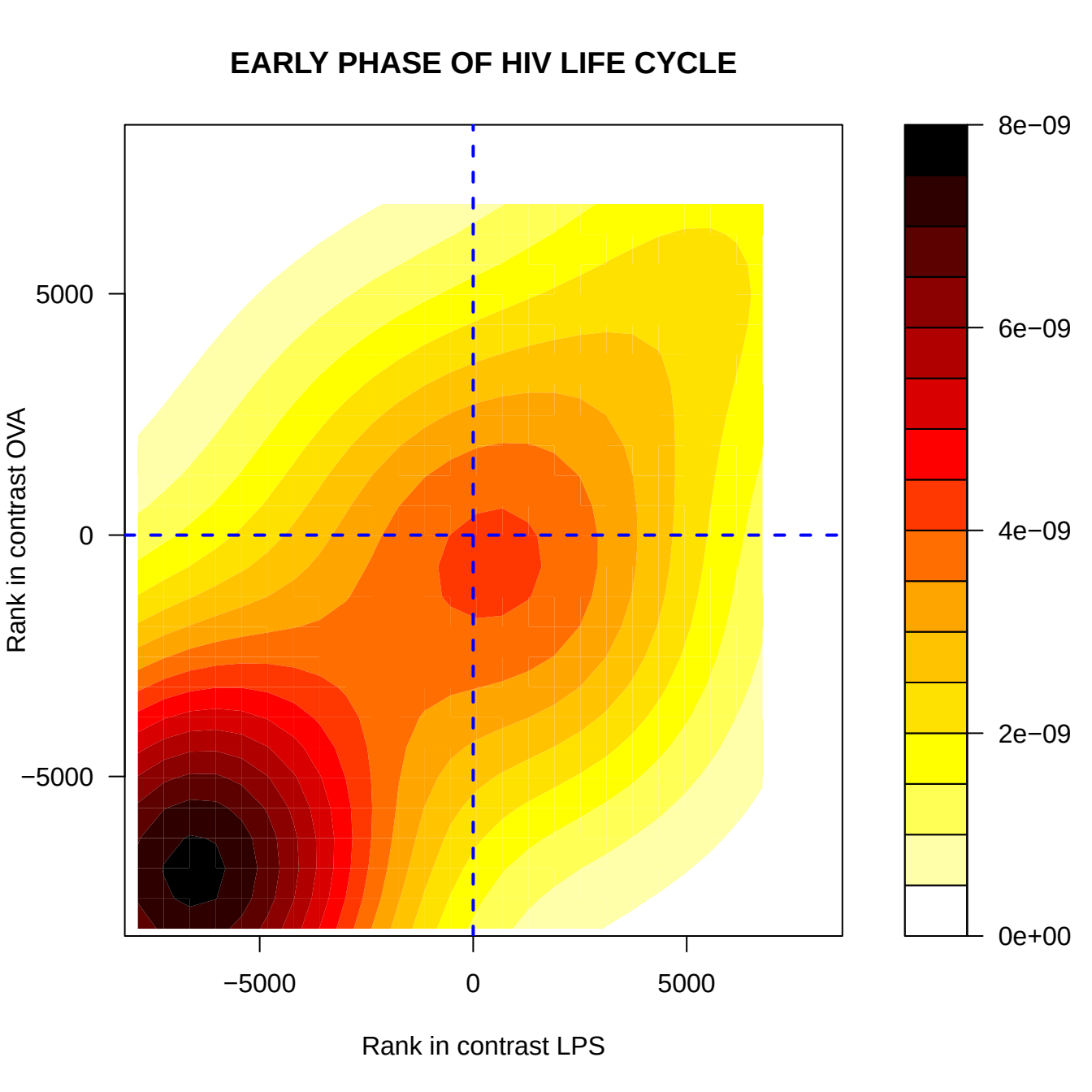

REGULATION OF RUNX1 EXPRESSION AND ACTIVITY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

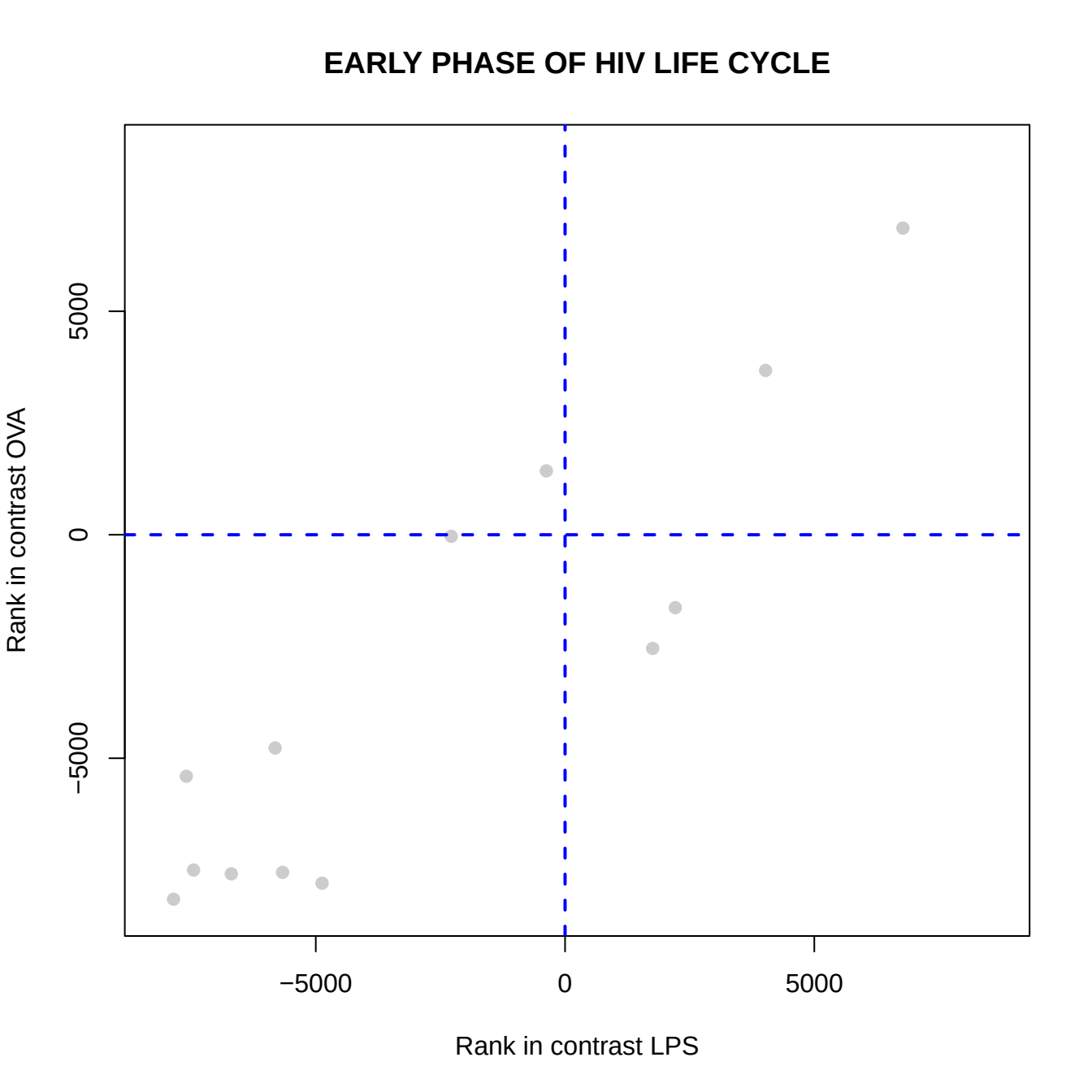

REGULATION OF RUNX1 EXPRESSION AND A
5000
0
−5000
Position in rank
LPS
OVA
contrast

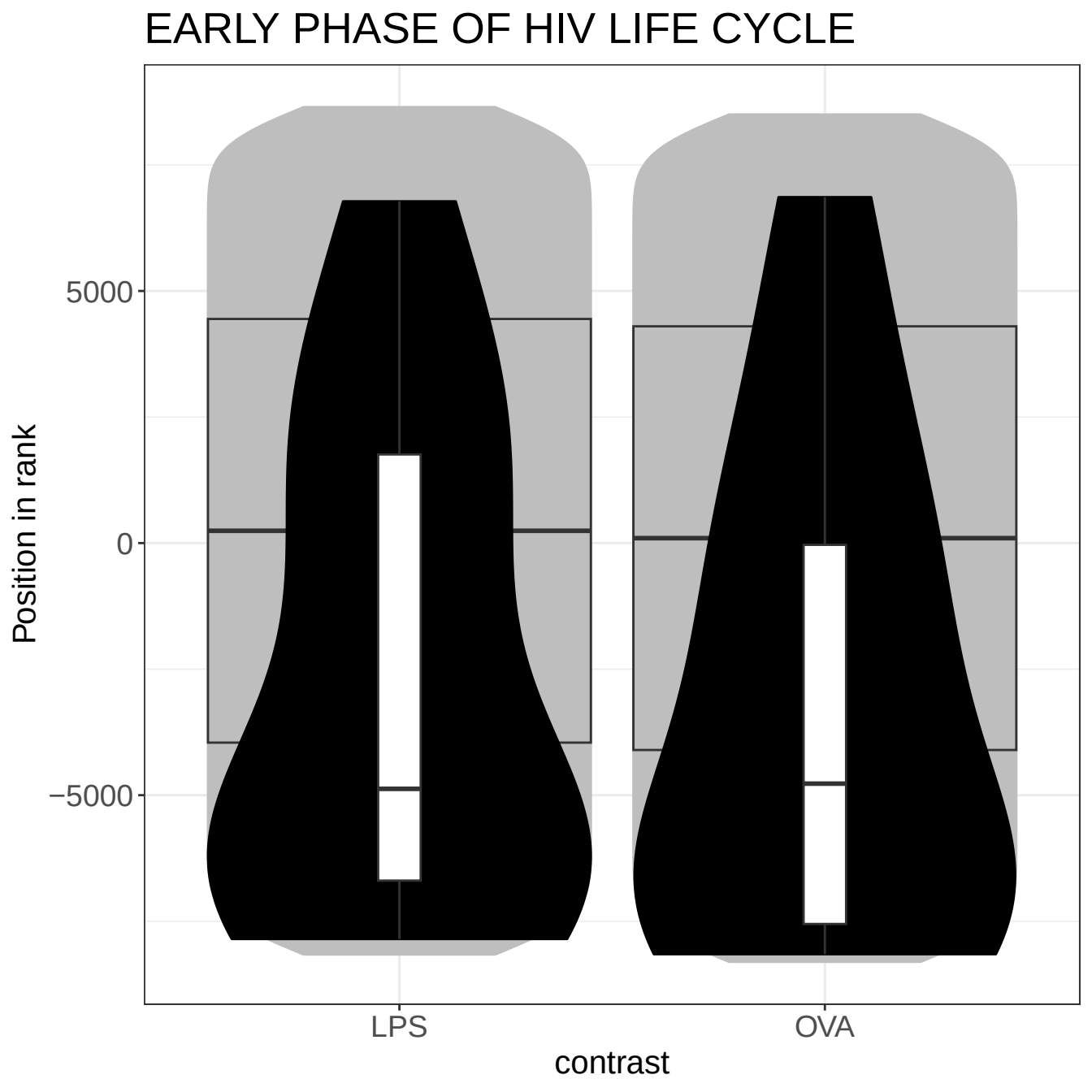

COMPLEX I BIOGENESIS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

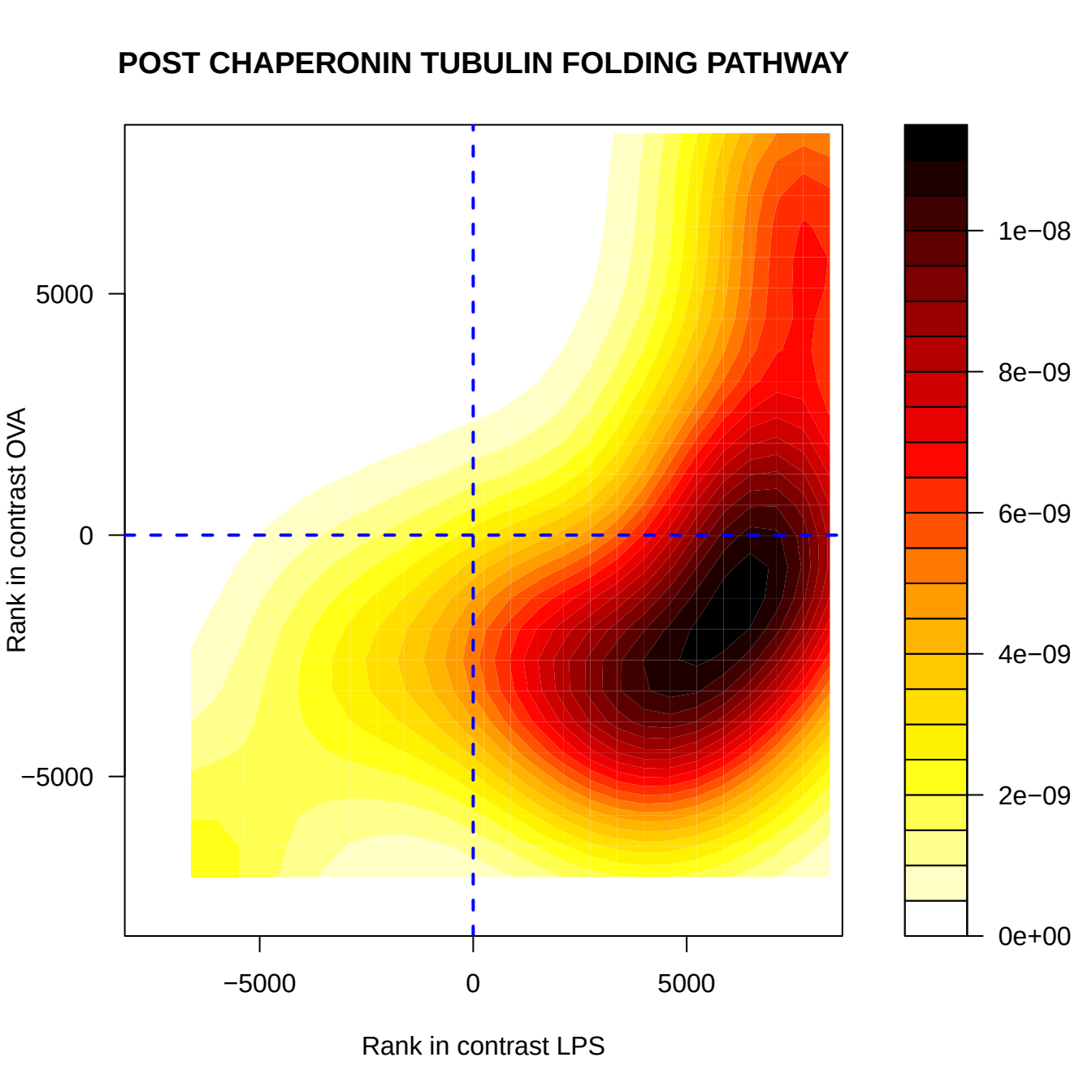

COMPLEX I BIOGENESIS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

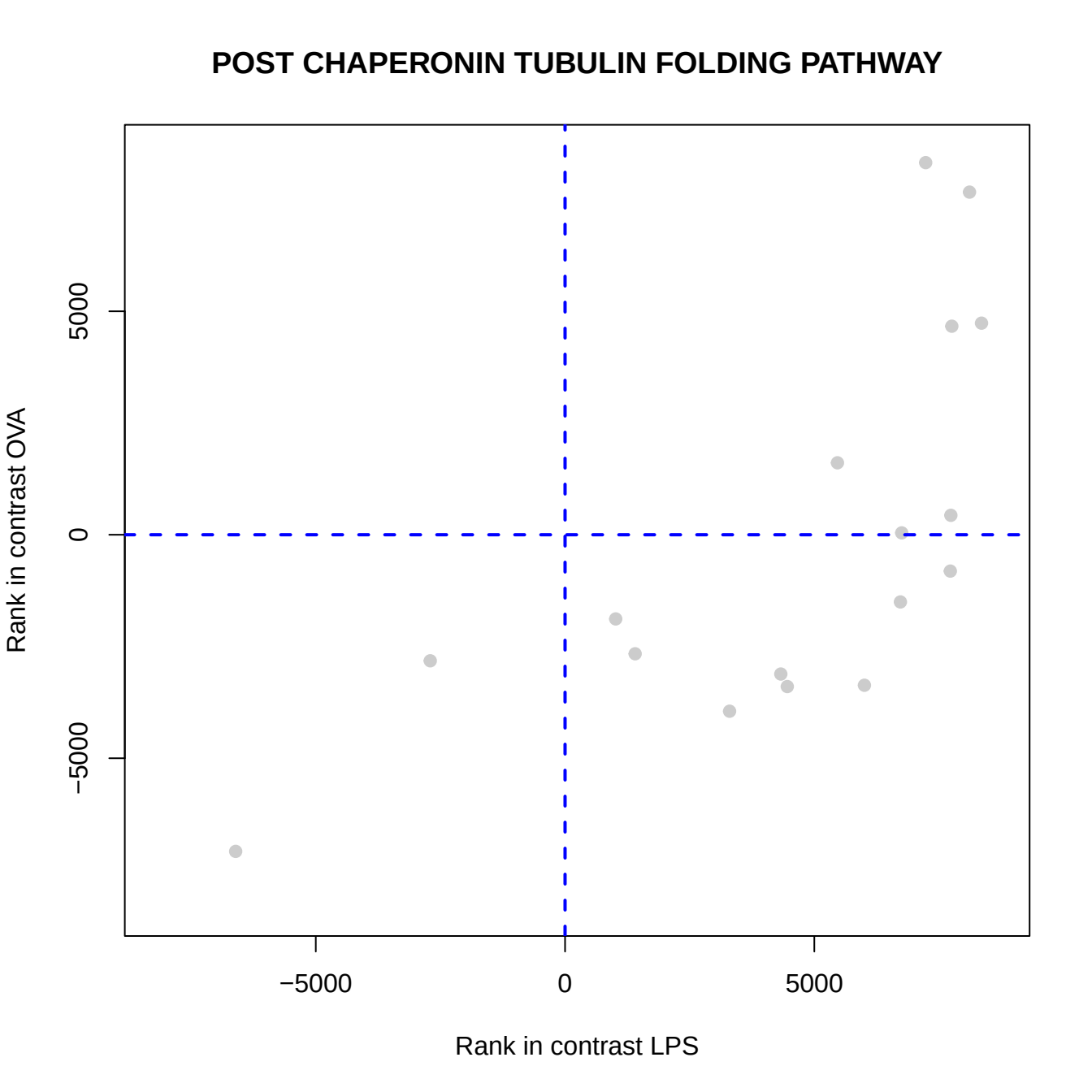

COMPLEX I BIOGENESIS
5000
0
−5000
Position in rank
LPS
OVA
contrast

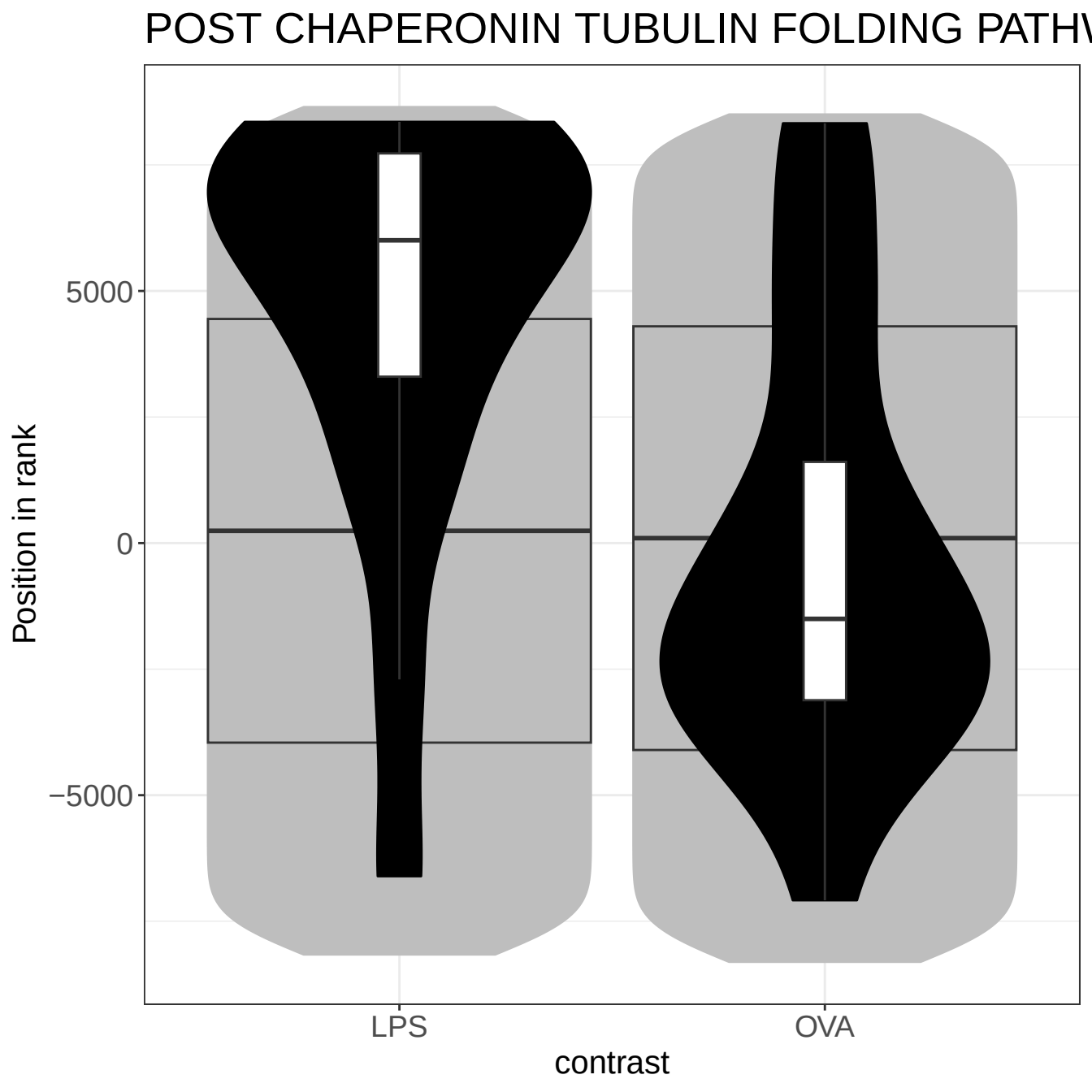

EARLY PHASE OF HIV LIFE CYCLE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

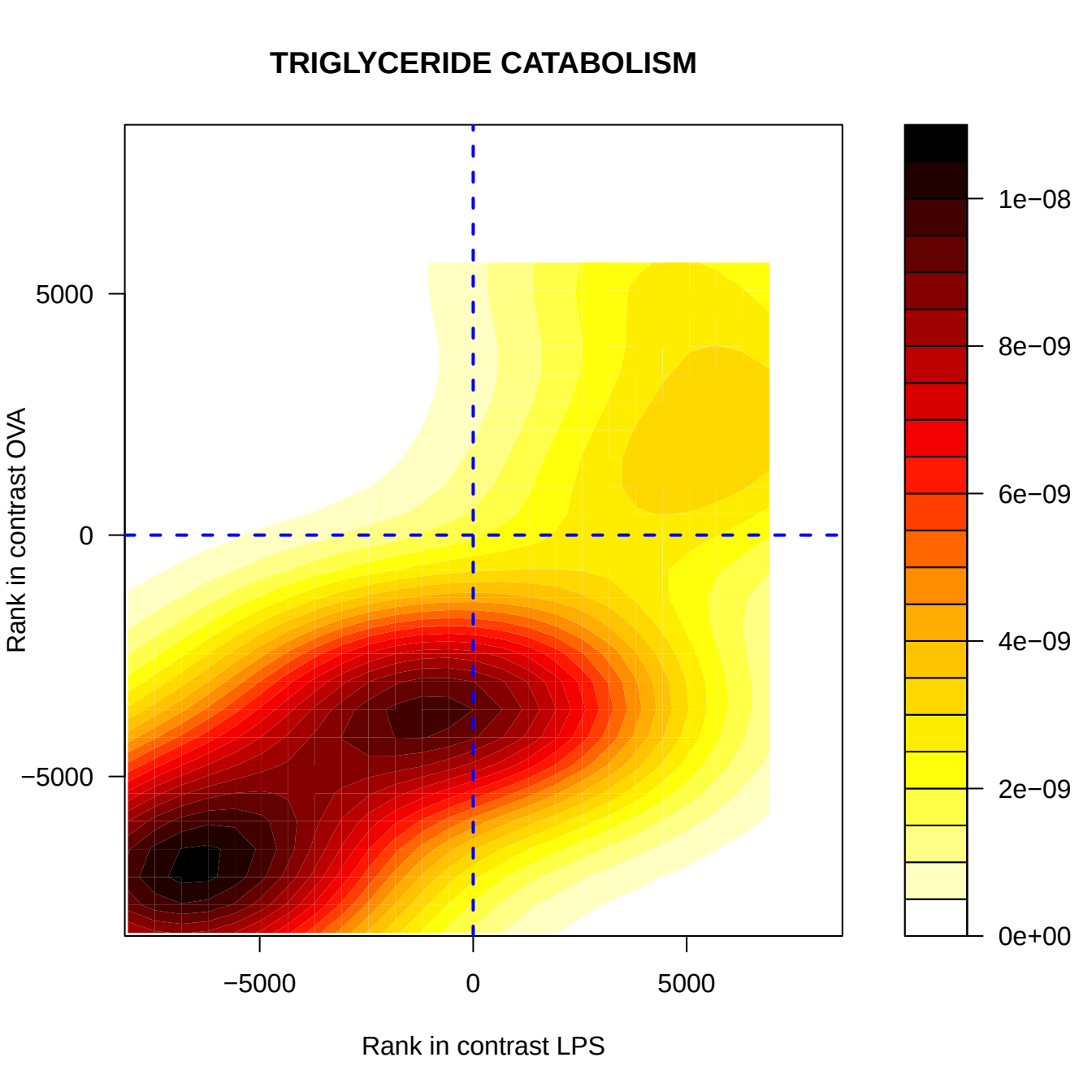

EARLY PHASE OF HIV LIFE CYCLE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

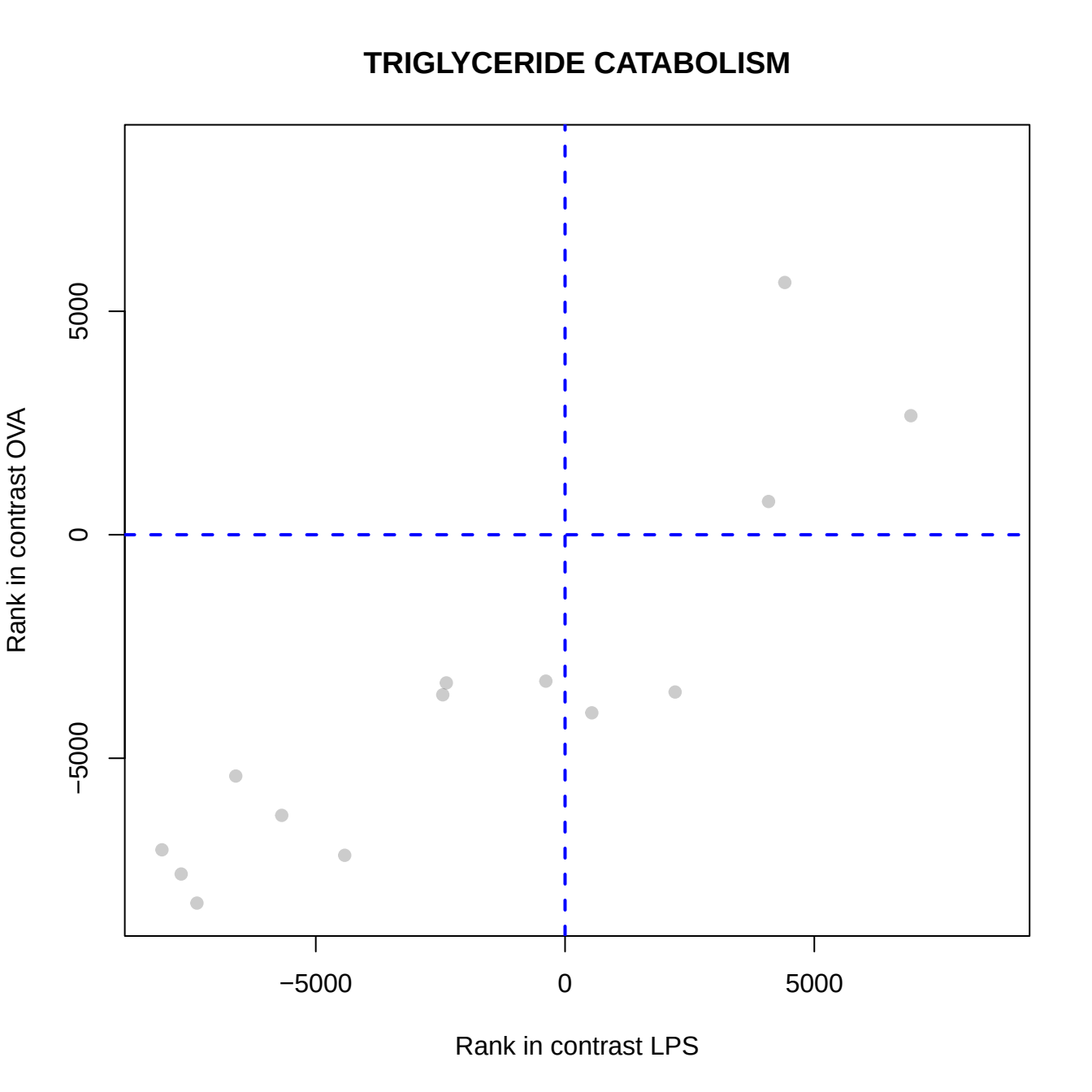

EARLY PHASE OF HIV LIFE CYCLE
Position in rank
5000
0
−5000
LPS
OVA
contrast

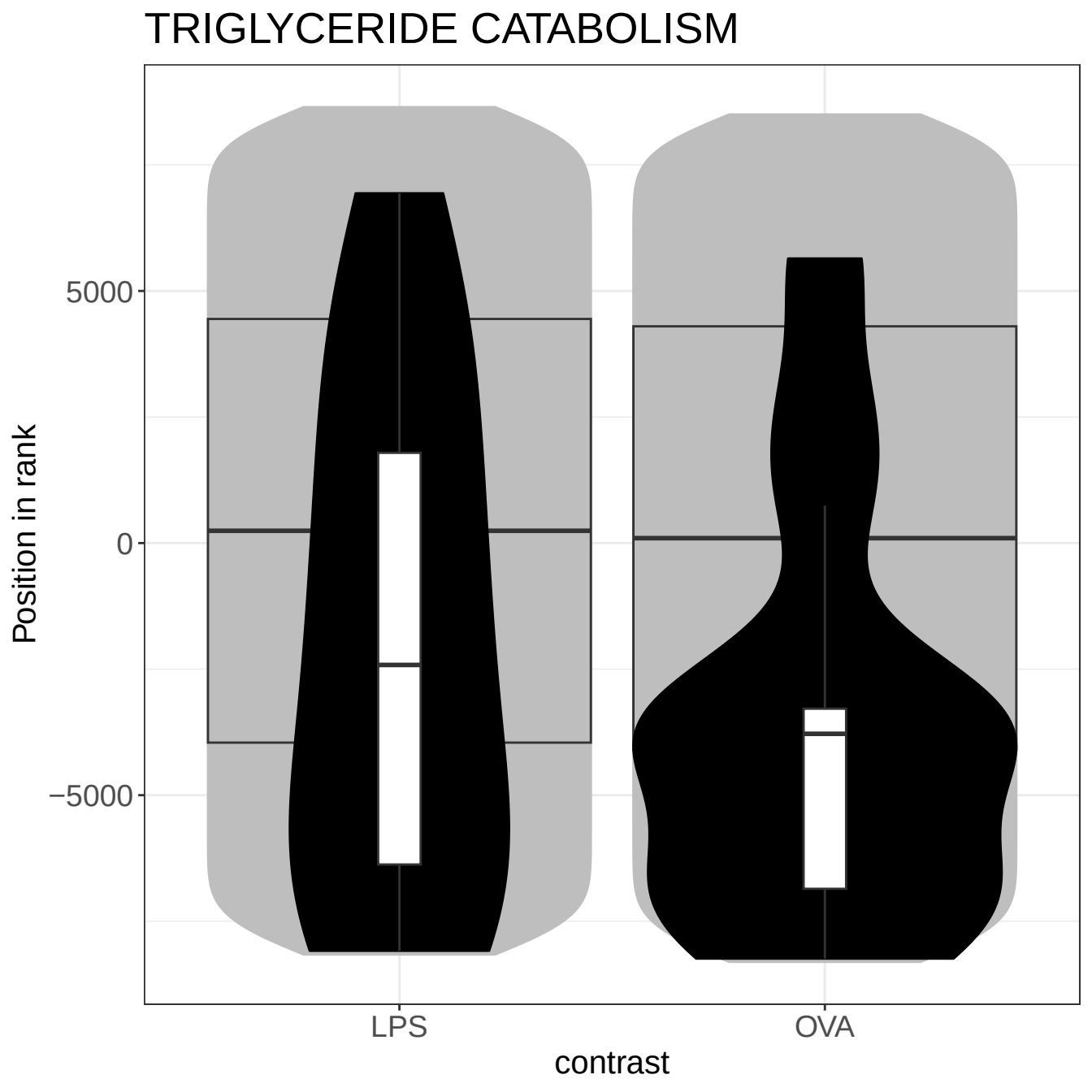

POST CHAPERONIN TUBULIN FOLDING PATHWAY
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

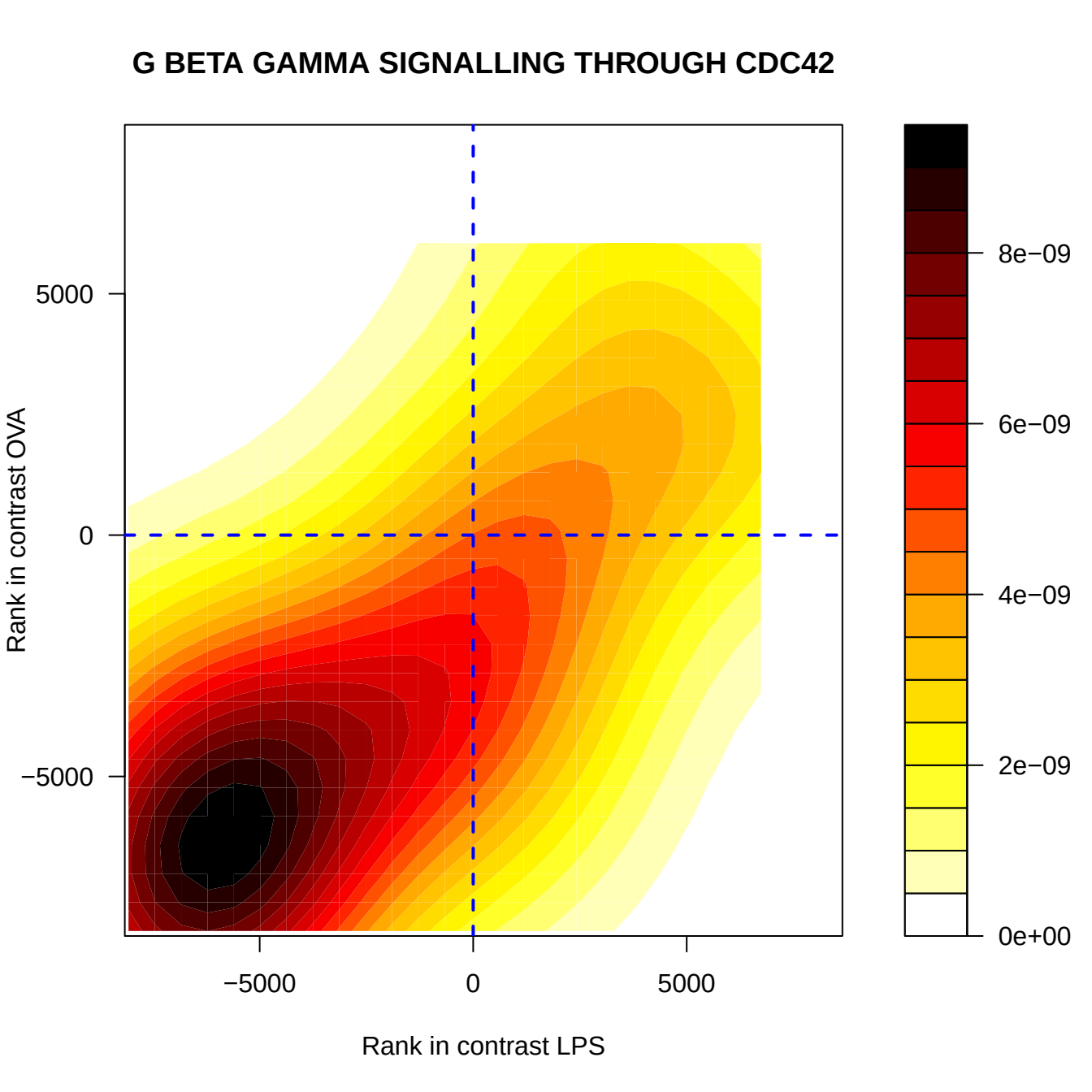

POST CHAPERONIN TUBULIN FOLDING PATHWAY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

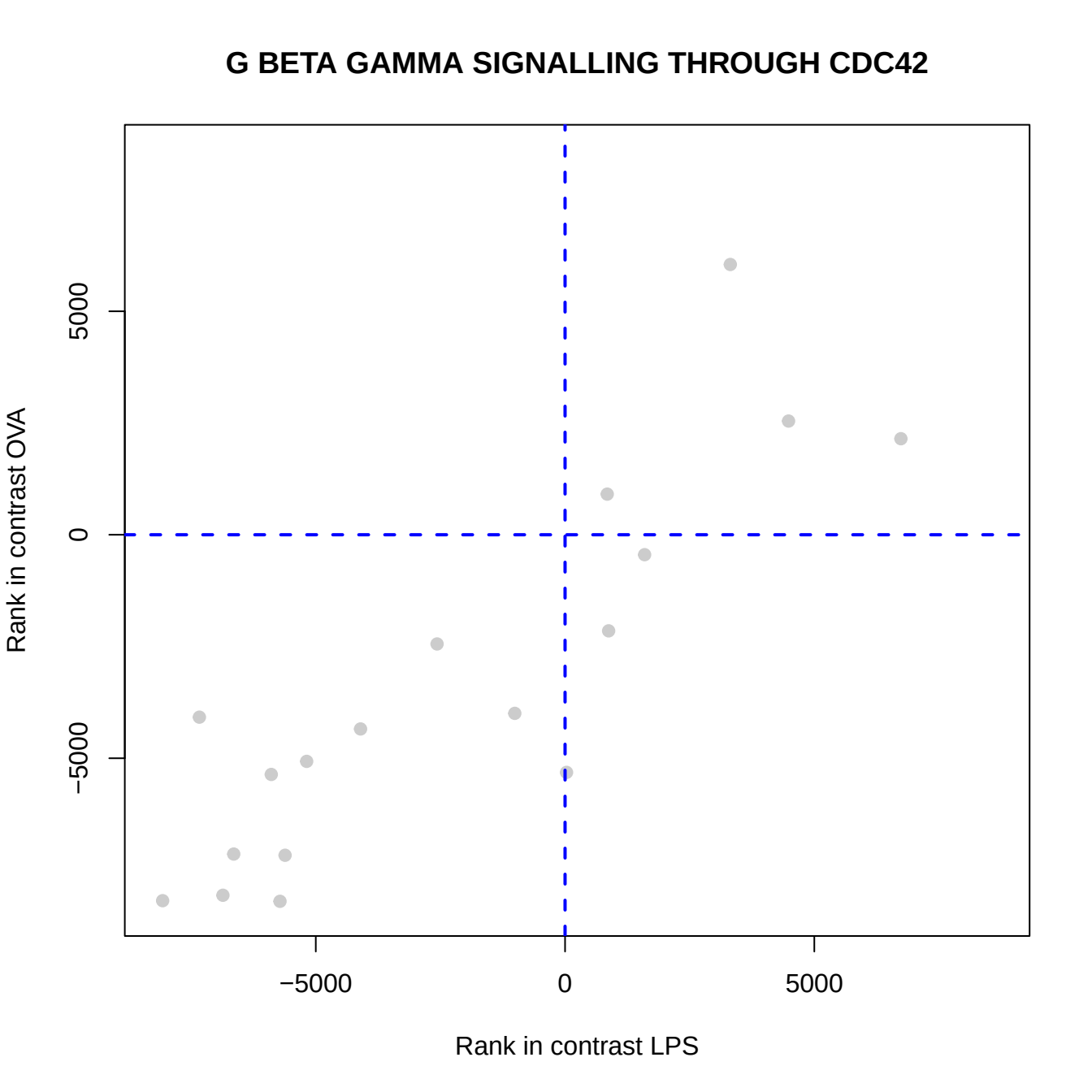

POST CHAPERONIN TUBULIN FOLDING PATHW
5000
0
−5000
Position in rank
LPS
OVA
contrast

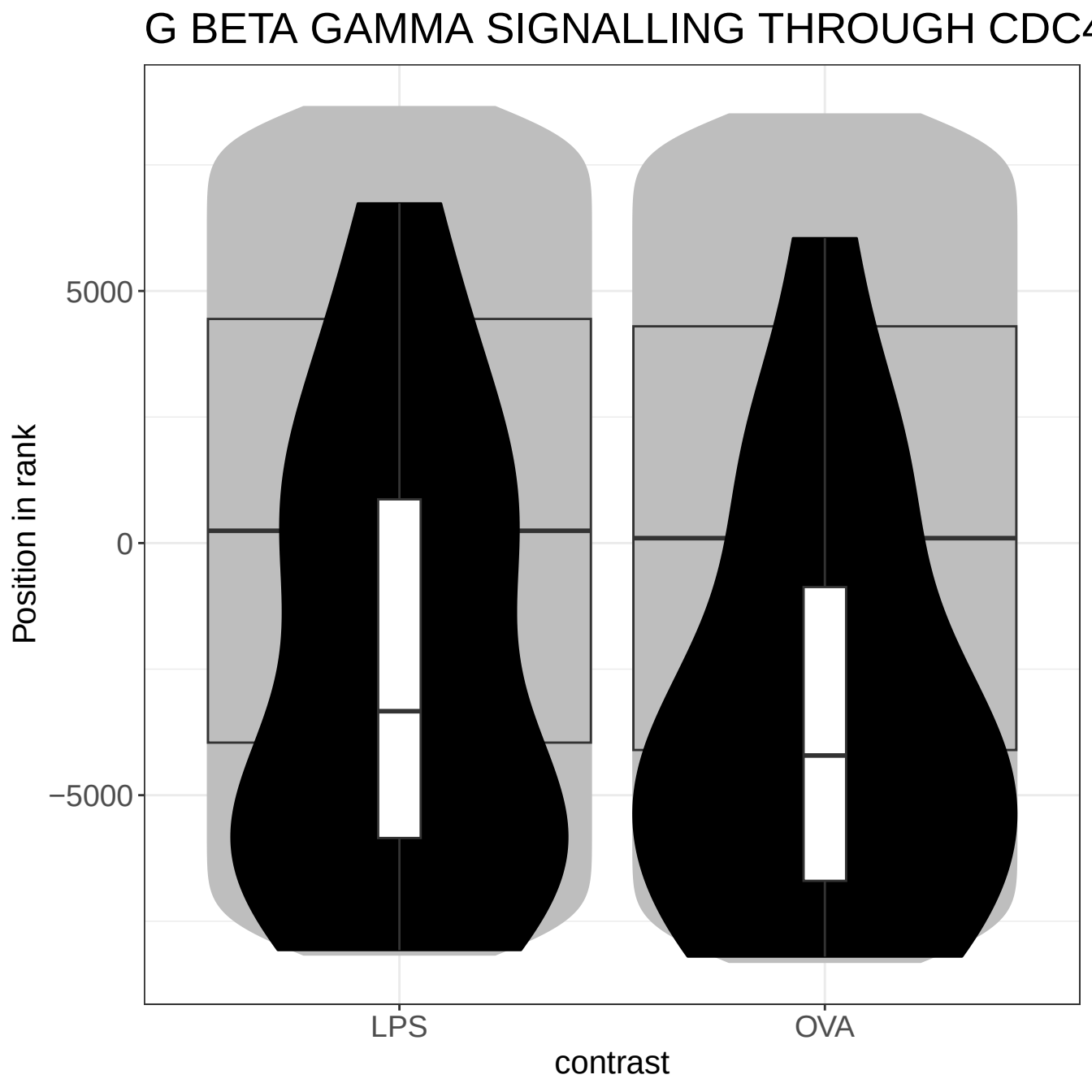

TRIGLYCERIDE CATABOLISM
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

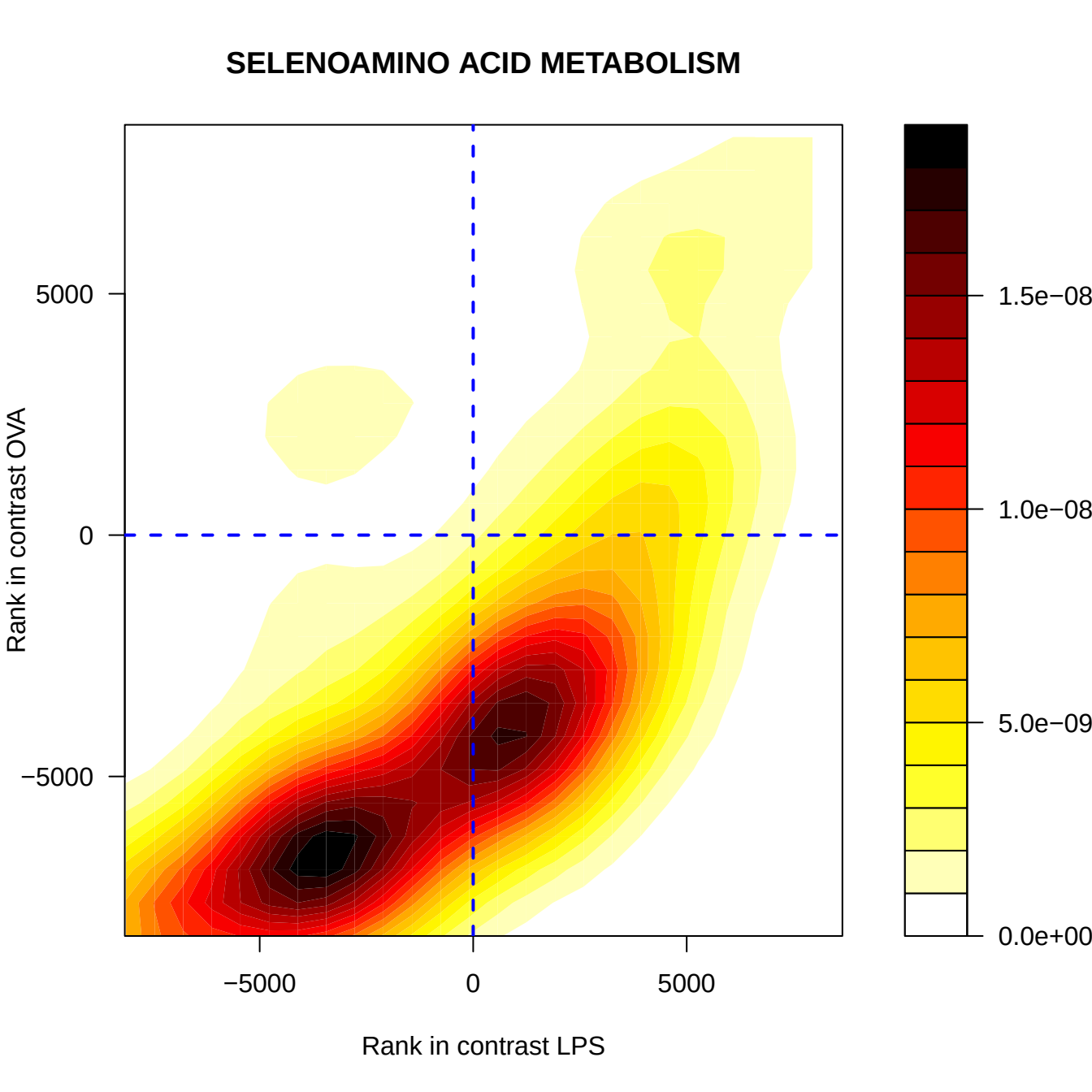

TRIGLYCERIDE CATABOLISM
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

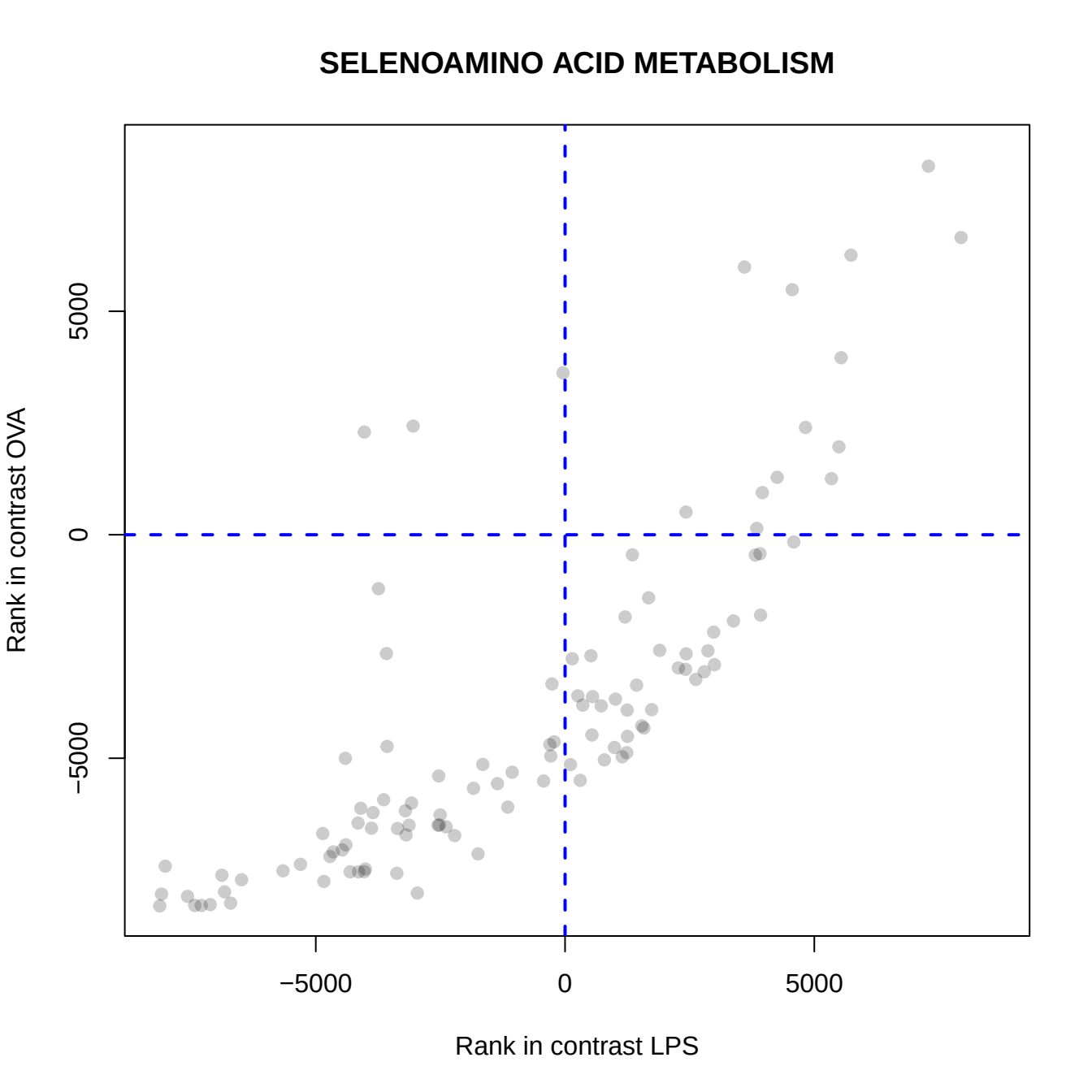

TRIGLYCERIDE CATABOLISM
5000
0
−5000
Position in rank
LPS
OVA
contrast

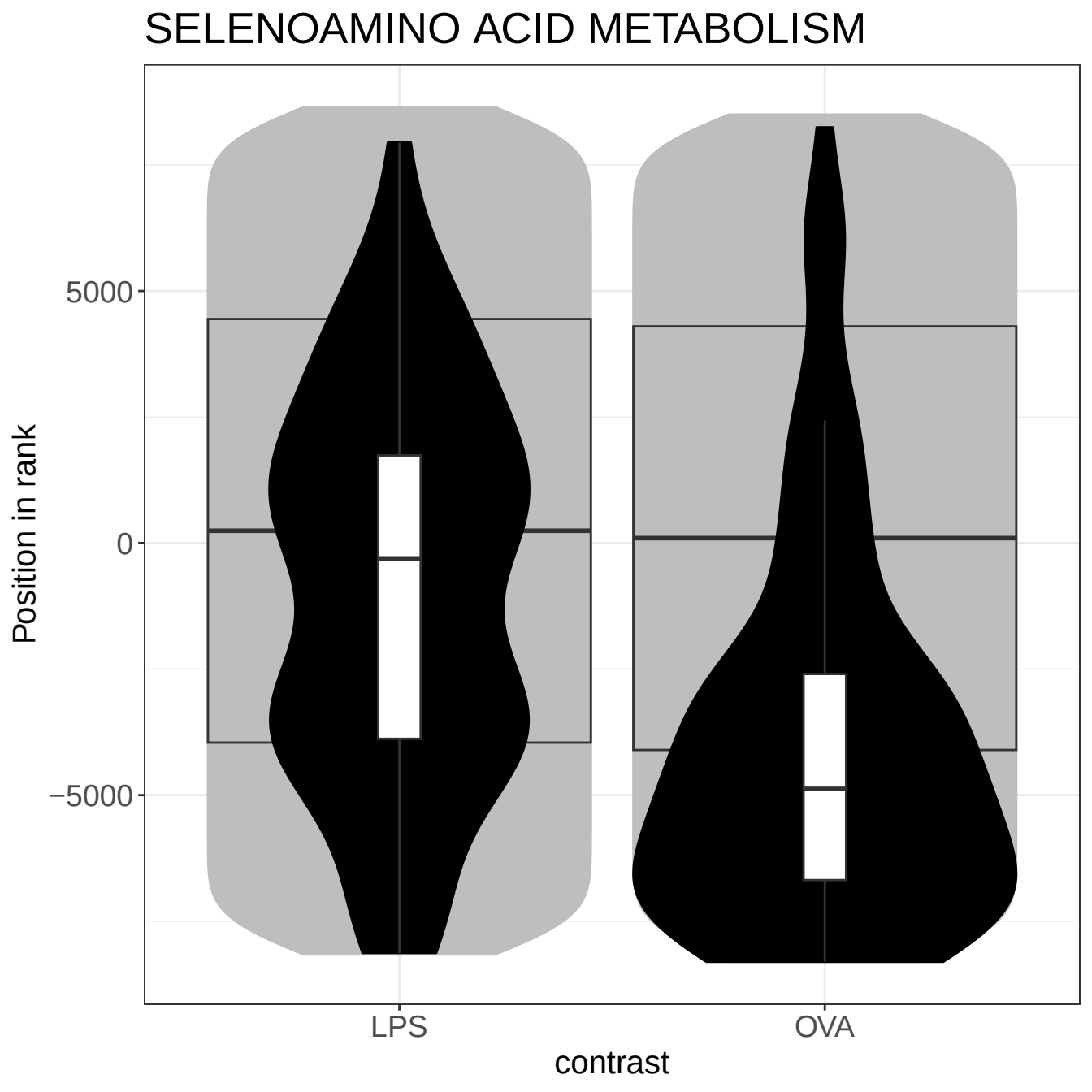

G BETA GAMMA SIGNALLING THROUGH CDC42
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

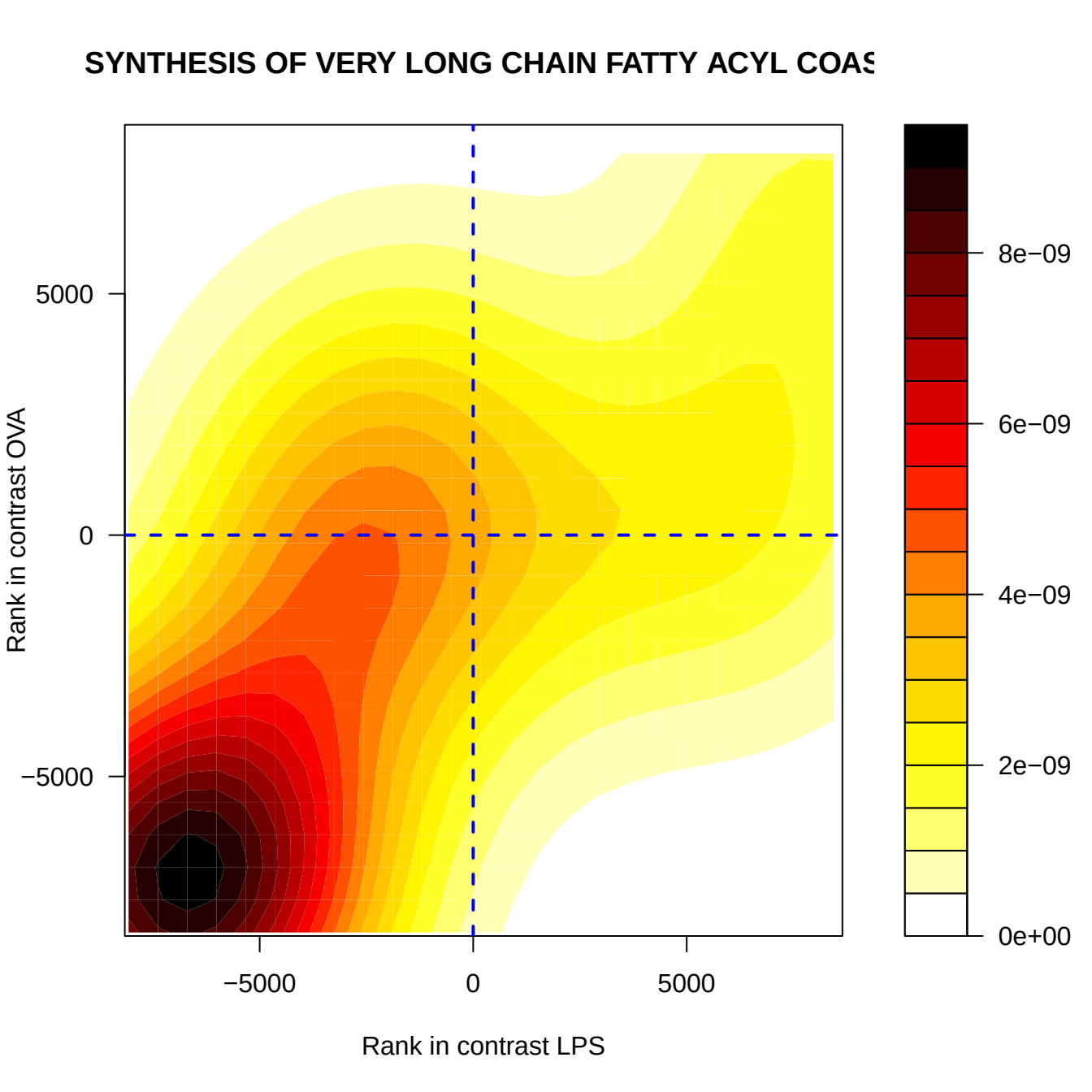

G BETA GAMMA SIGNALLING THROUGH CDC42
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

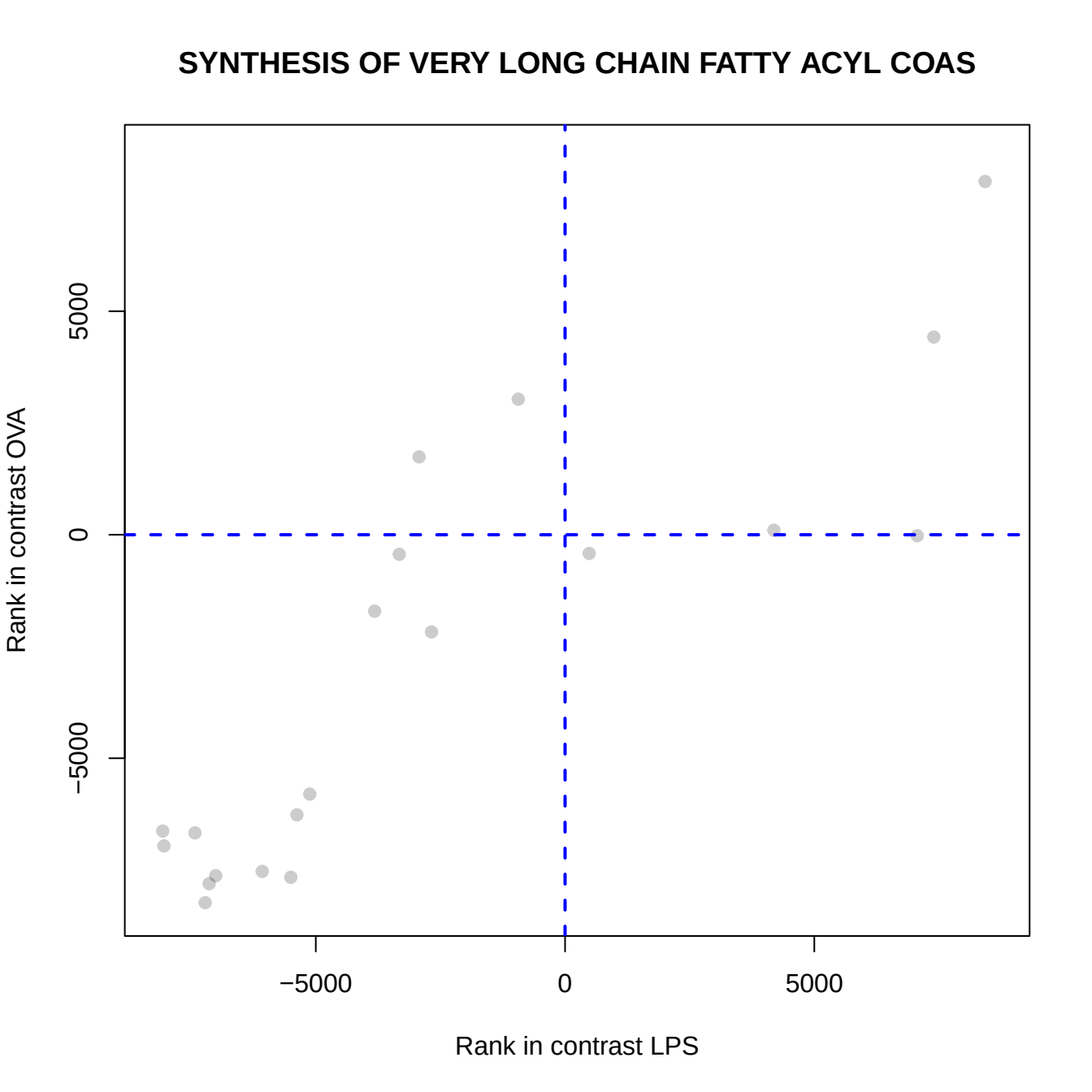

G BETA GAMMA SIGNALLING THROUGH CDC4
5000
0
−5000
Position in rank
LPS
OVA
contrast

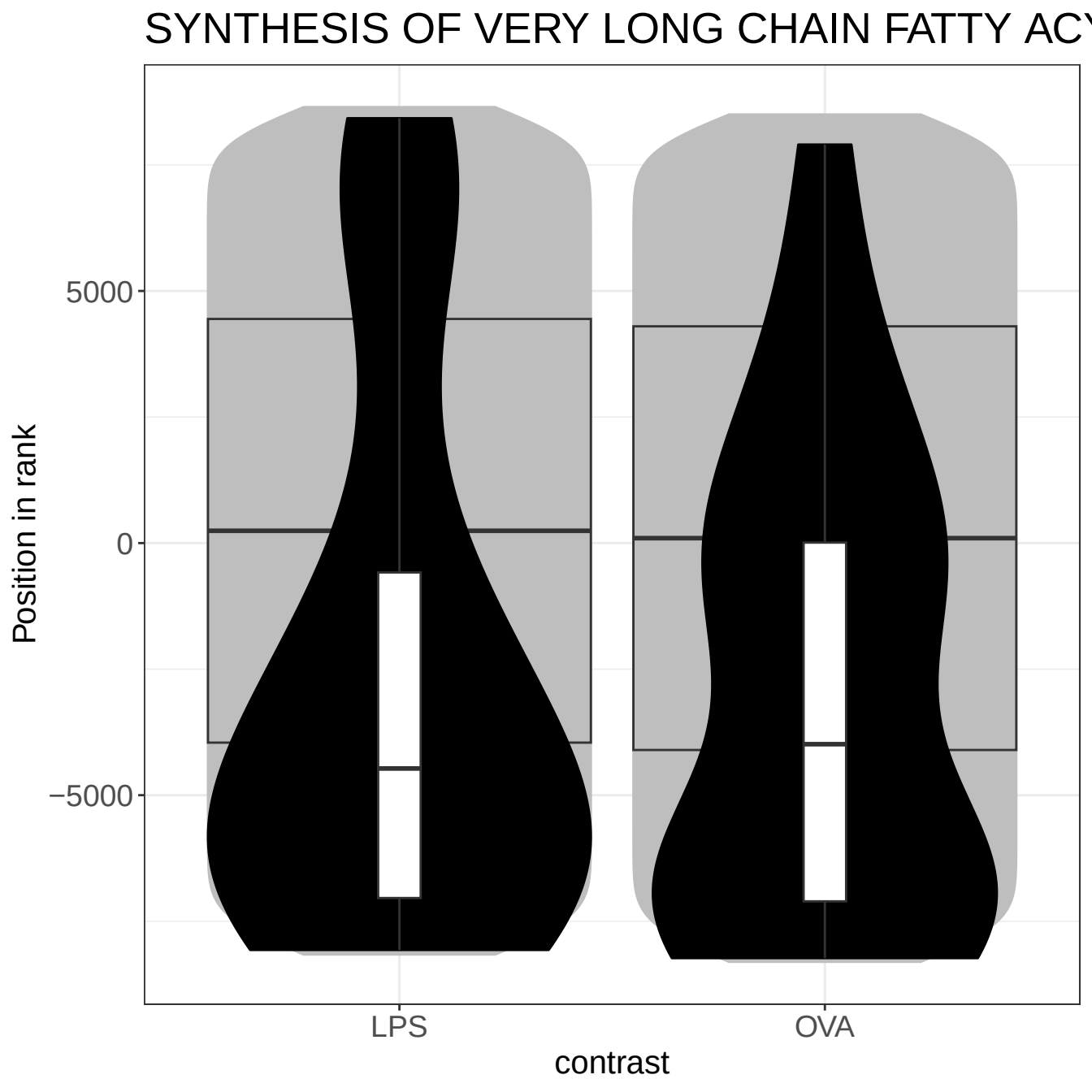

SELENOAMINO ACID METABOLISM
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

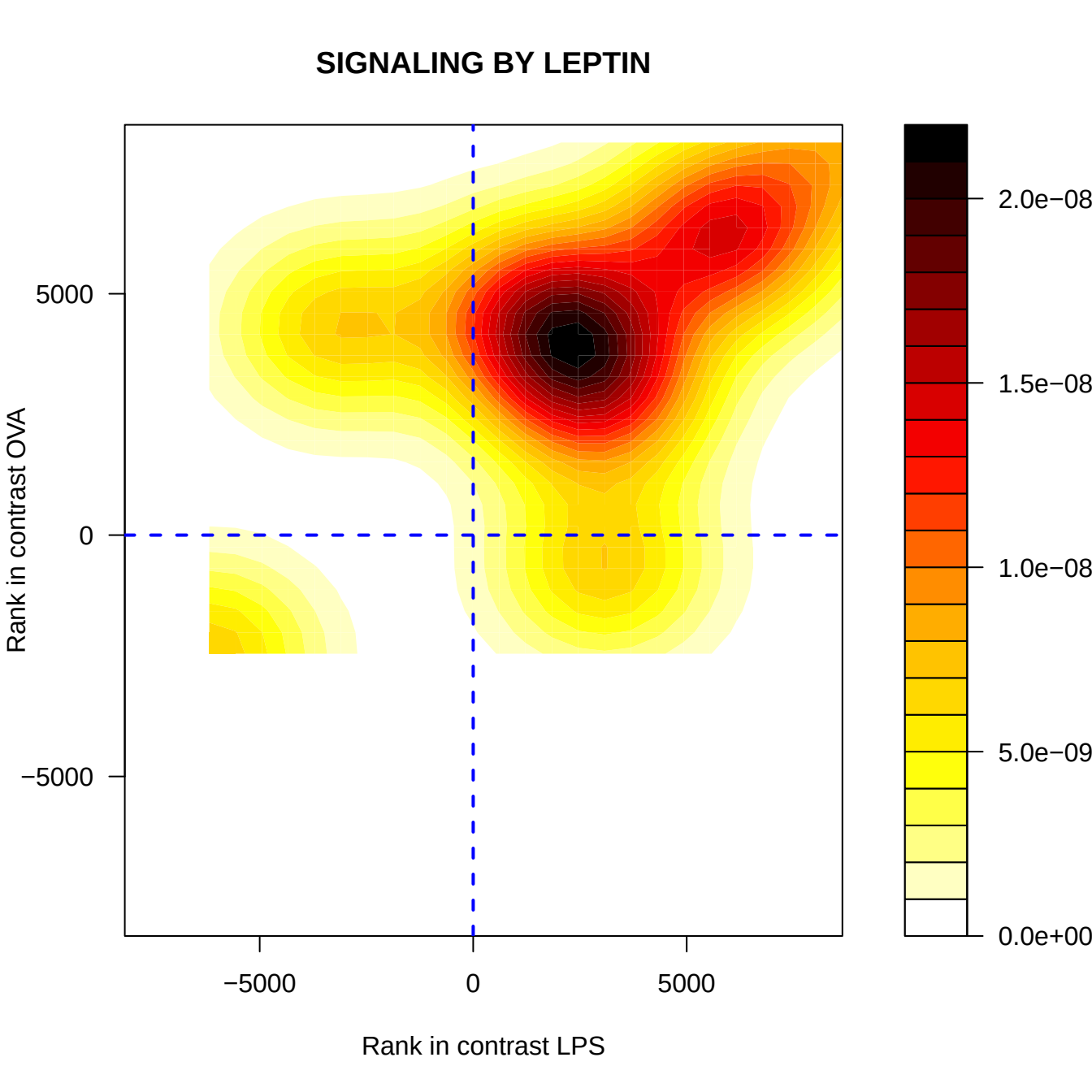

SELENOAMINO ACID METABOLISM
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

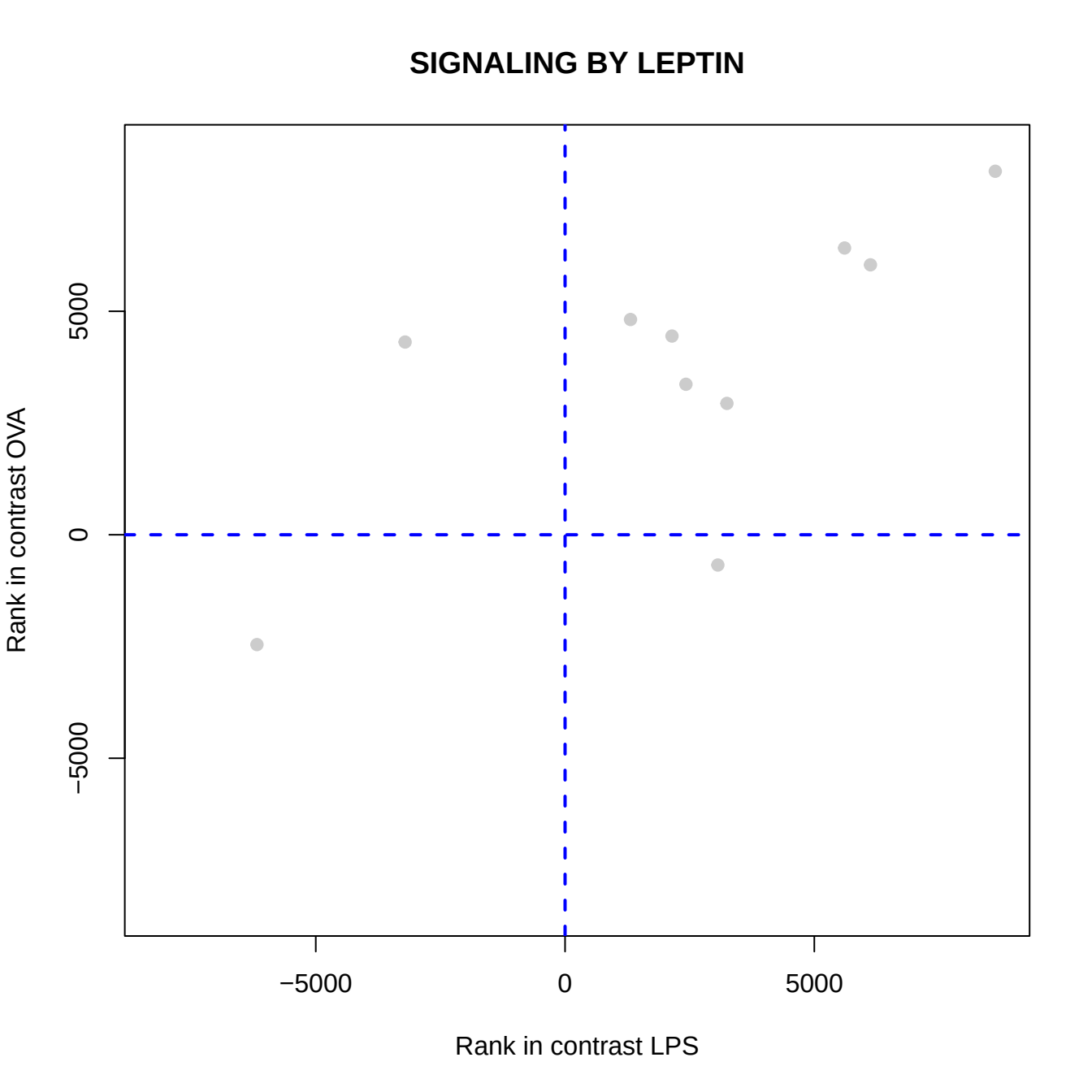

SELENOAMINO ACID METABOLISM
5000
0
−5000
Position in rank
LPS
OVA
contrast

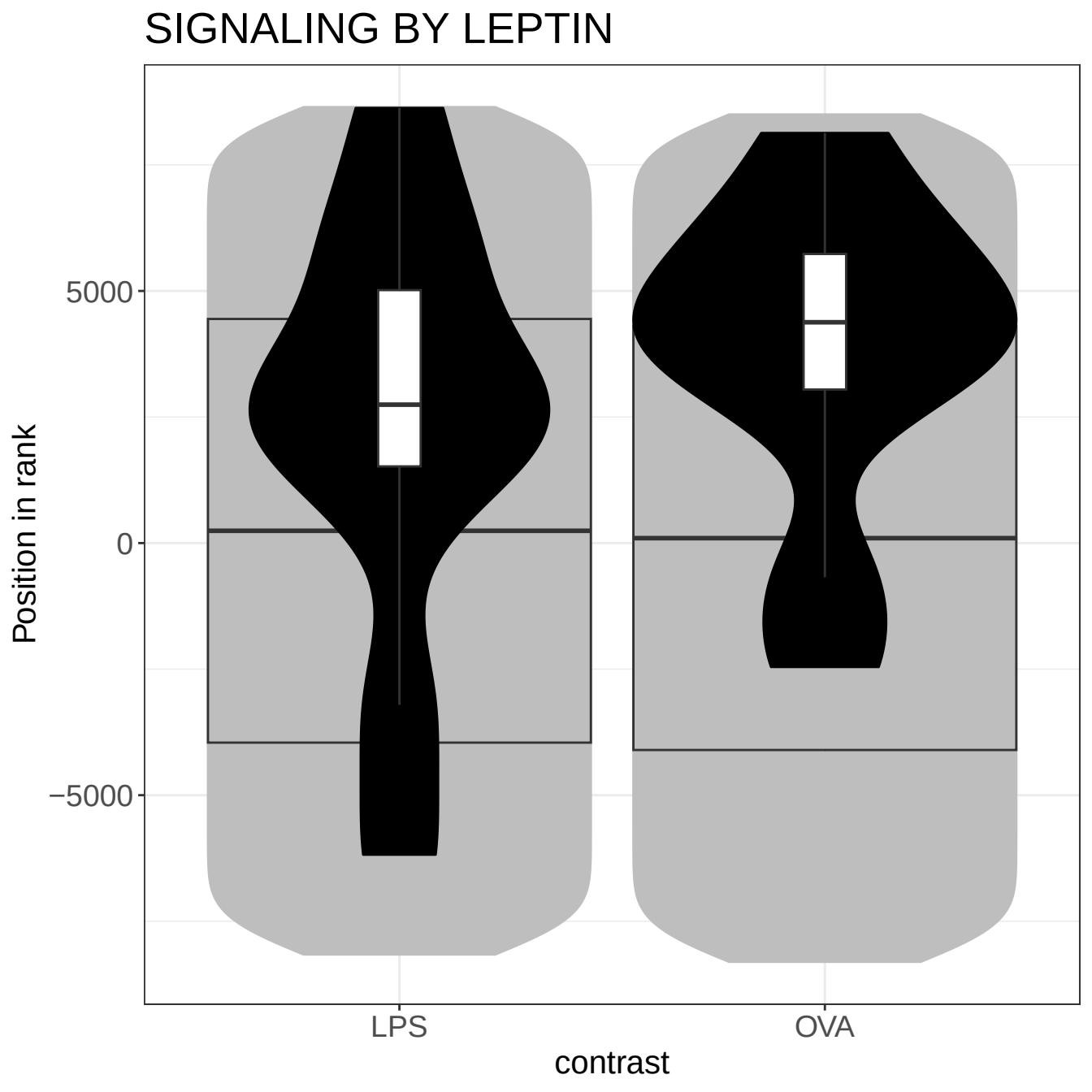

SYNTHESIS OF VERY LONG CHAIN FATTY ACYL COAS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

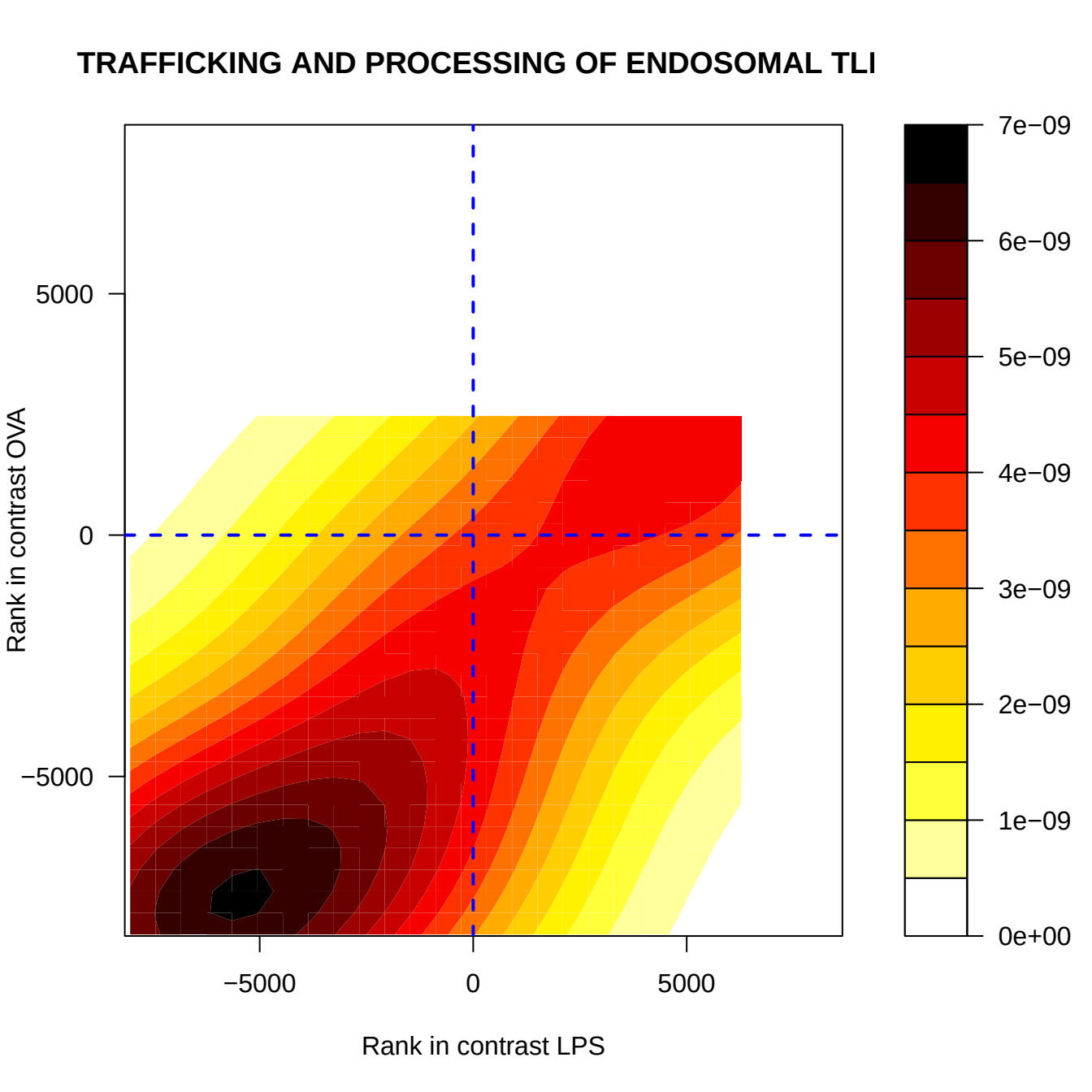

SYNTHESIS OF VERY LONG CHAIN FATTY ACYL COAS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

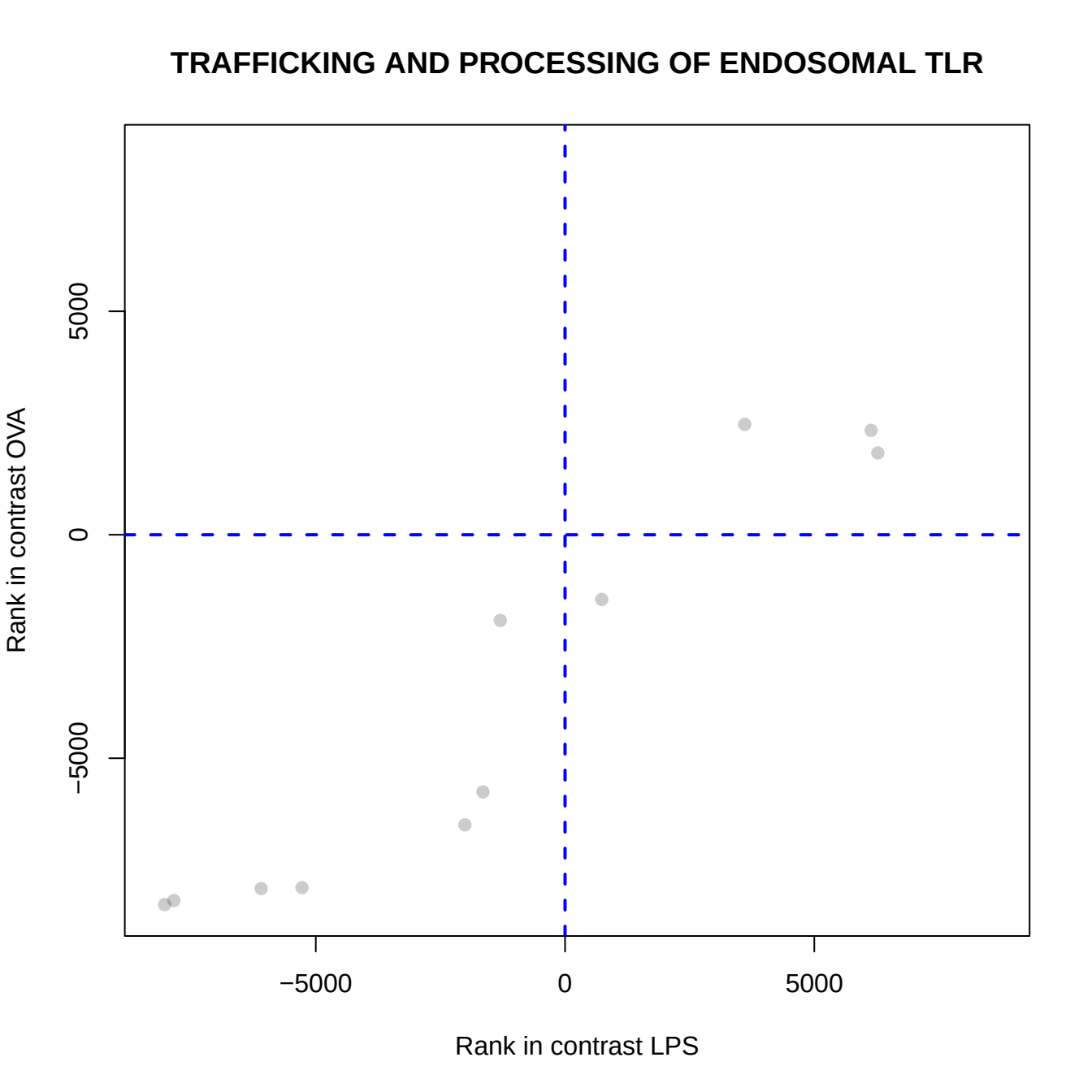

SYNTHESIS OF VERY LONG CHAIN FATTY AC
5000
0
−5000
Position in rank
LPS
OVA
contrast

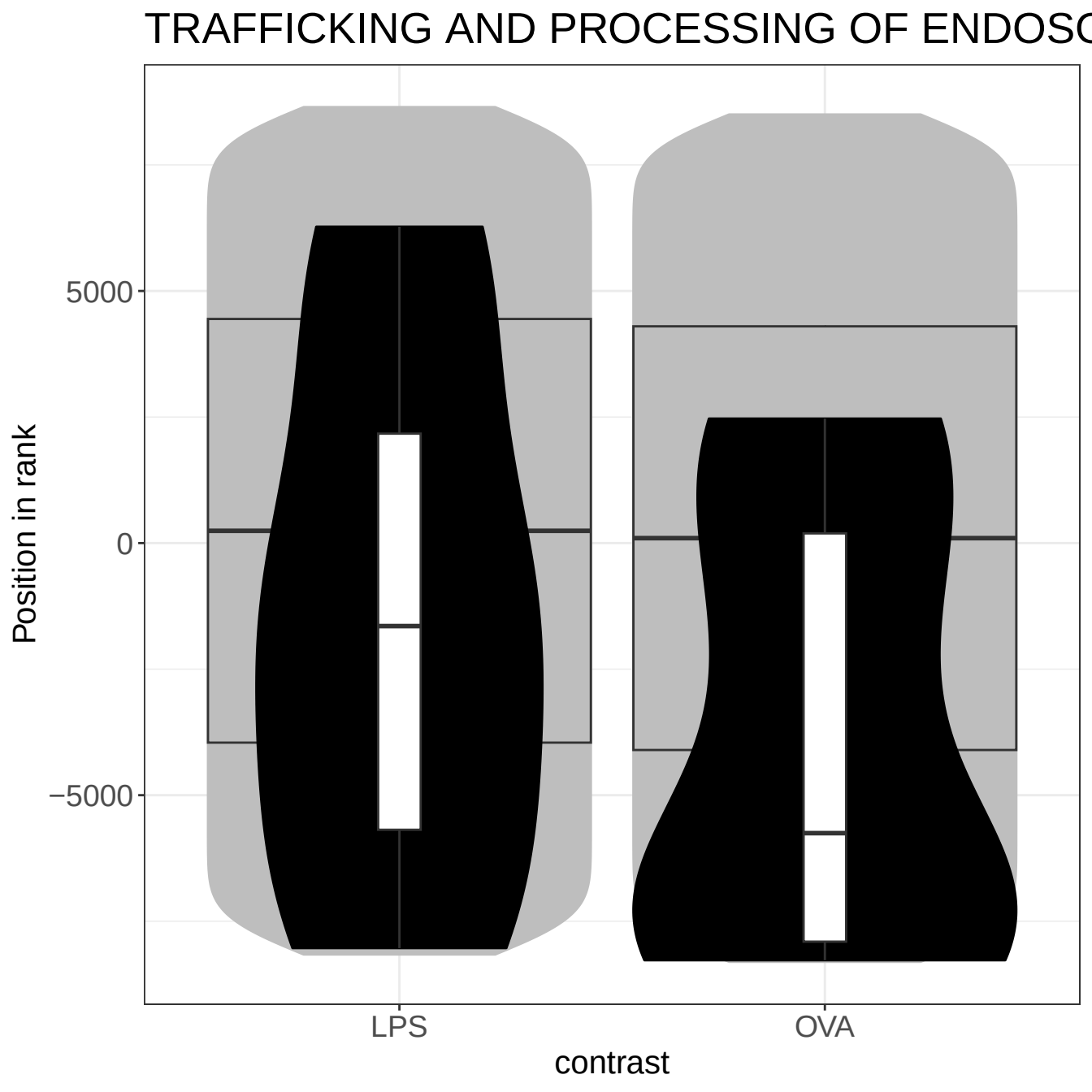

SIGNALING BY LEPTIN
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

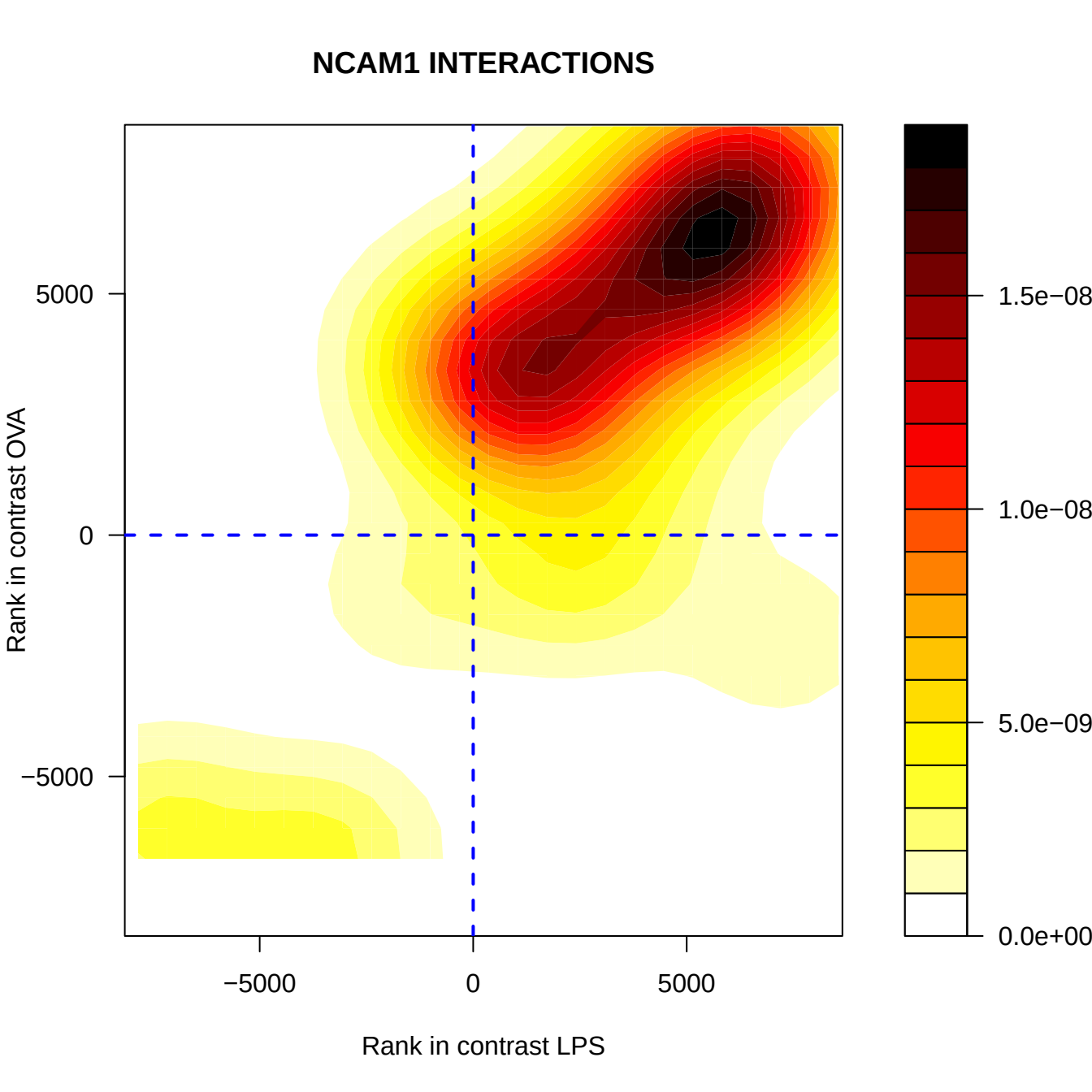

SIGNALING BY LEPTIN
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

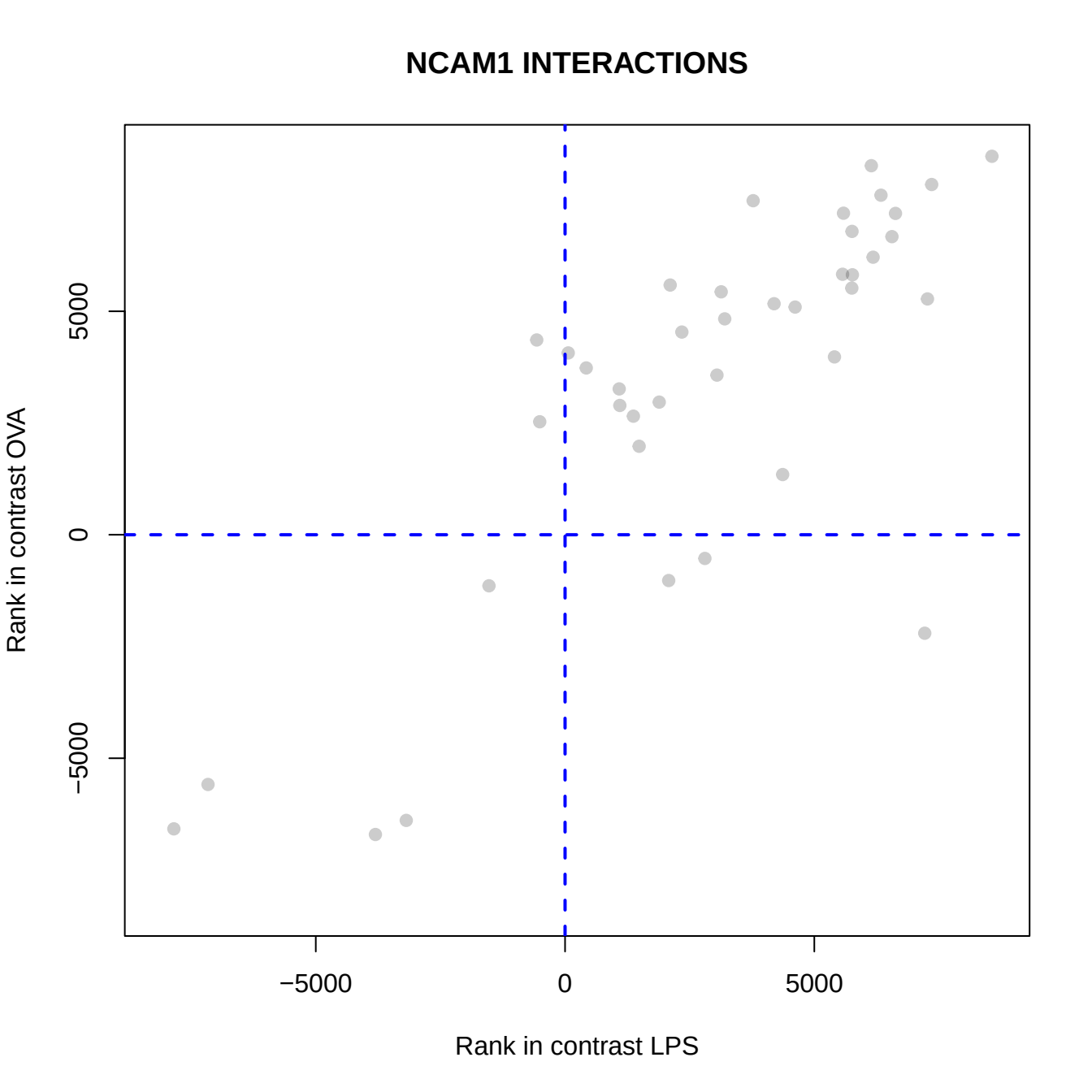

SIGNALING BY LEPTIN
5000
0
−5000
Position in rank
LPS
OVA
contrast

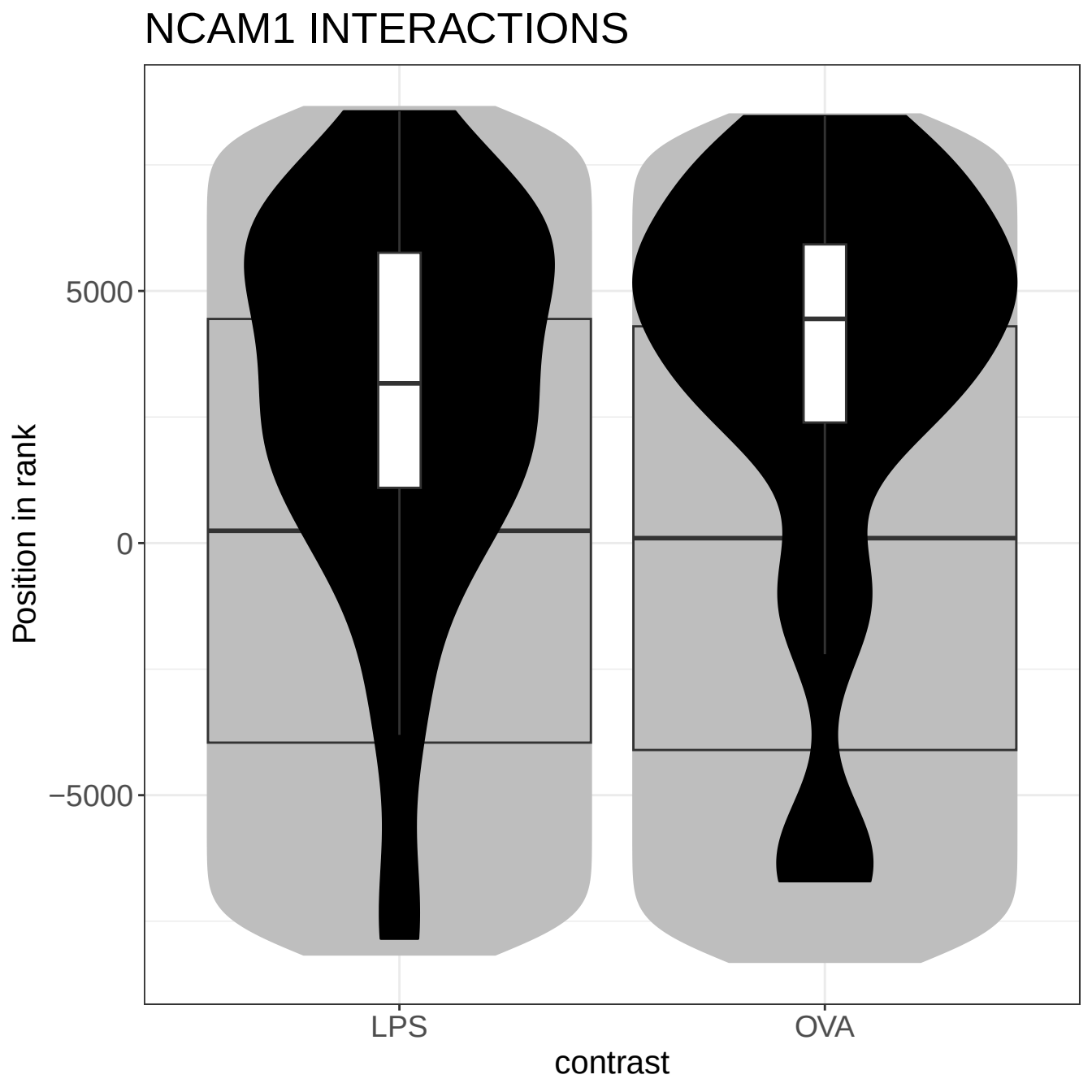

TRAFFICKING AND PROCESSING OF ENDOSOMAL TLI
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
7e−09
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

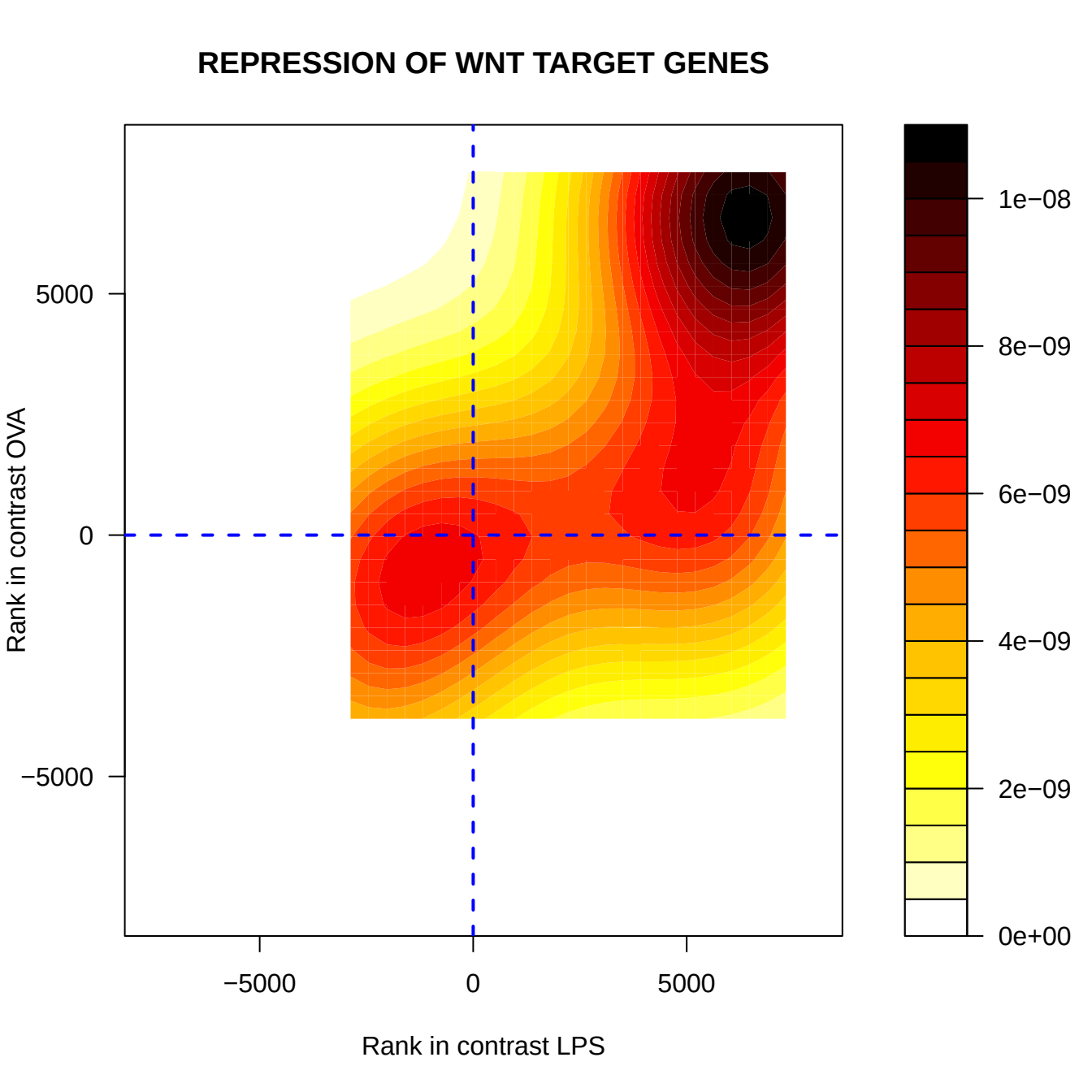

TRAFFICKING AND PROCESSING OF ENDOSOMAL TLR
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

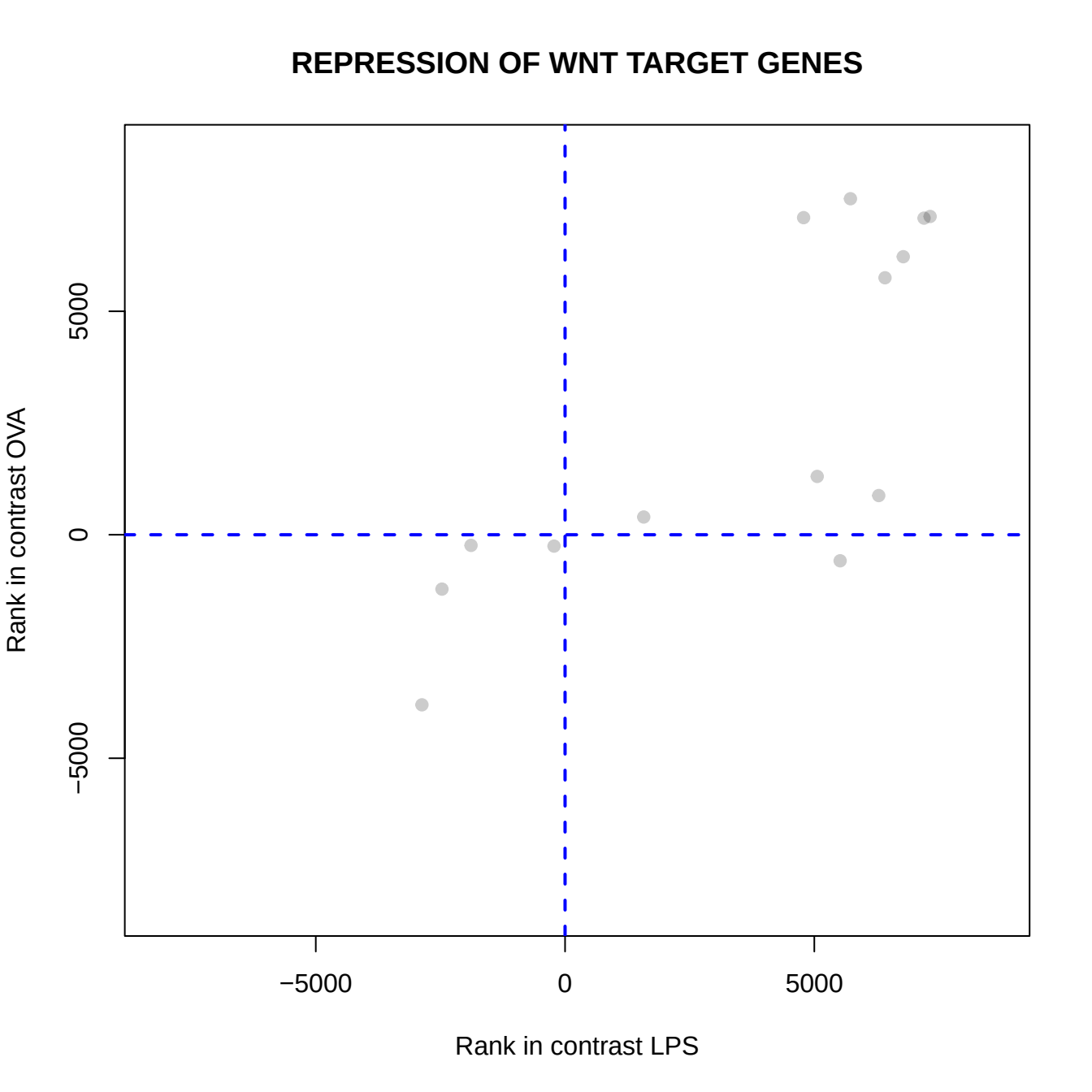

TRAFFICKING AND PROCESSING OF ENDOSO
5000
0
−5000
Position in rank
LPS
OVA
contrast

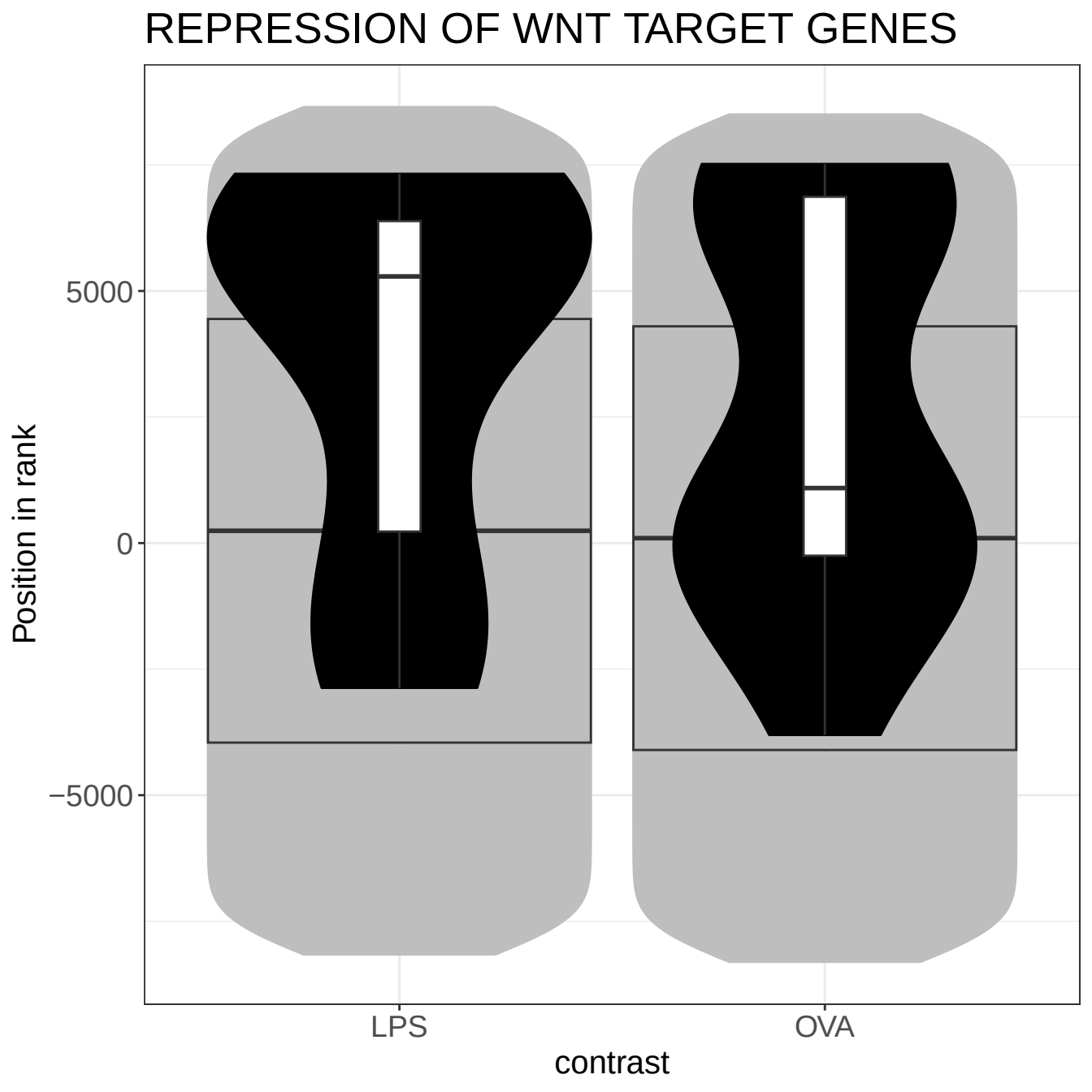

NCAM1 INTERACTIONS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

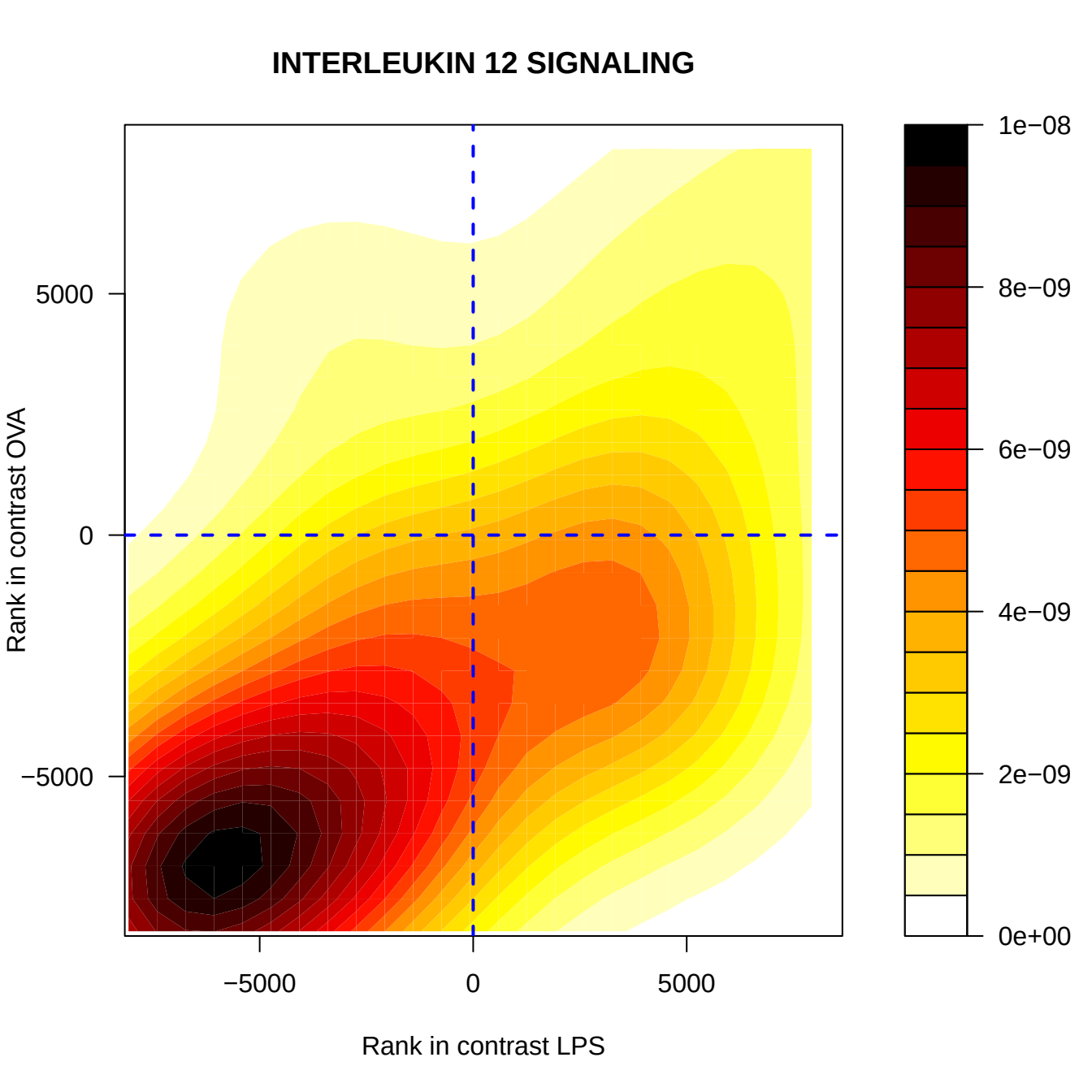

NCAM1 INTERACTIONS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

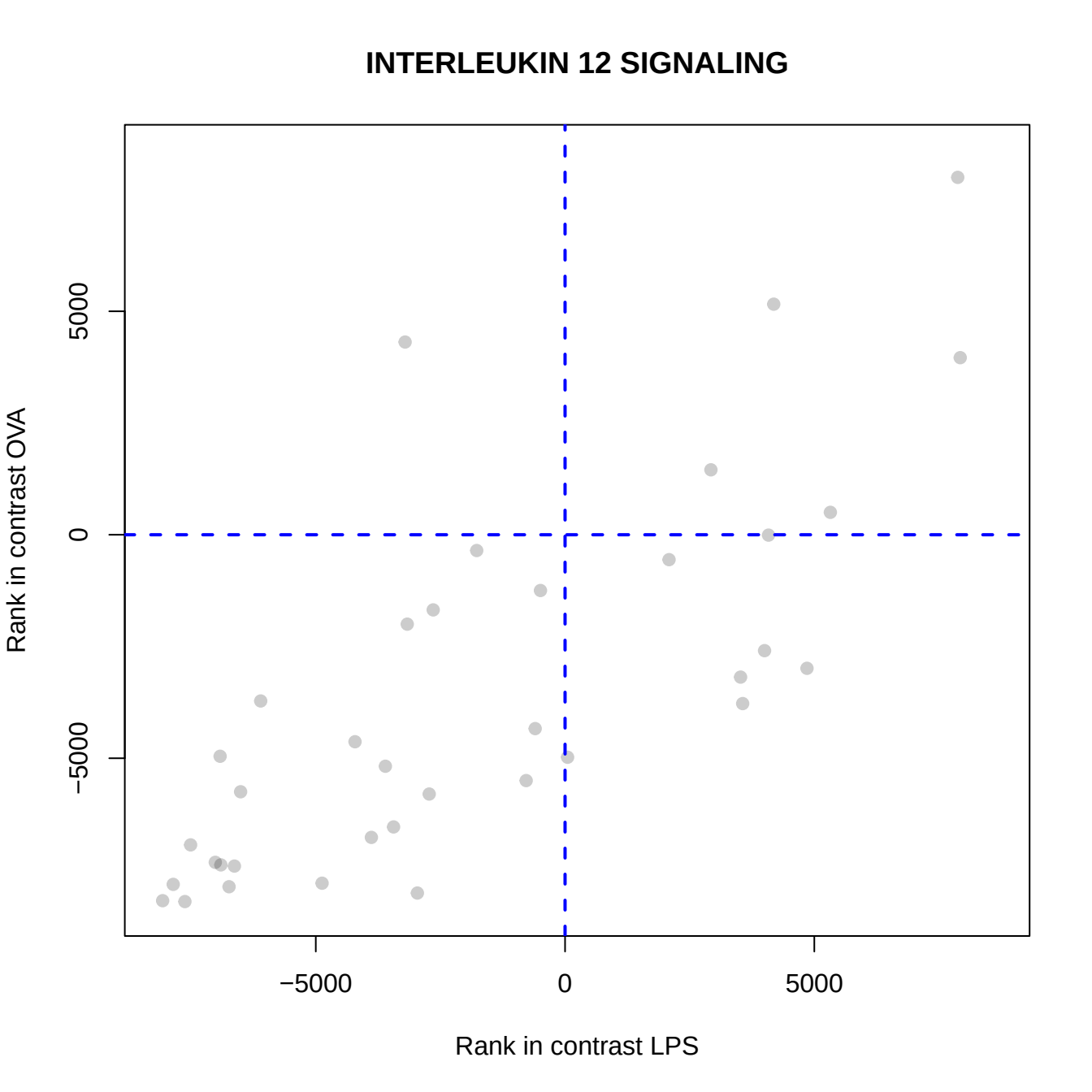

NCAM1 INTERACTIONS
5000
0
−5000
Position in rank
LPS
OVA
contrast

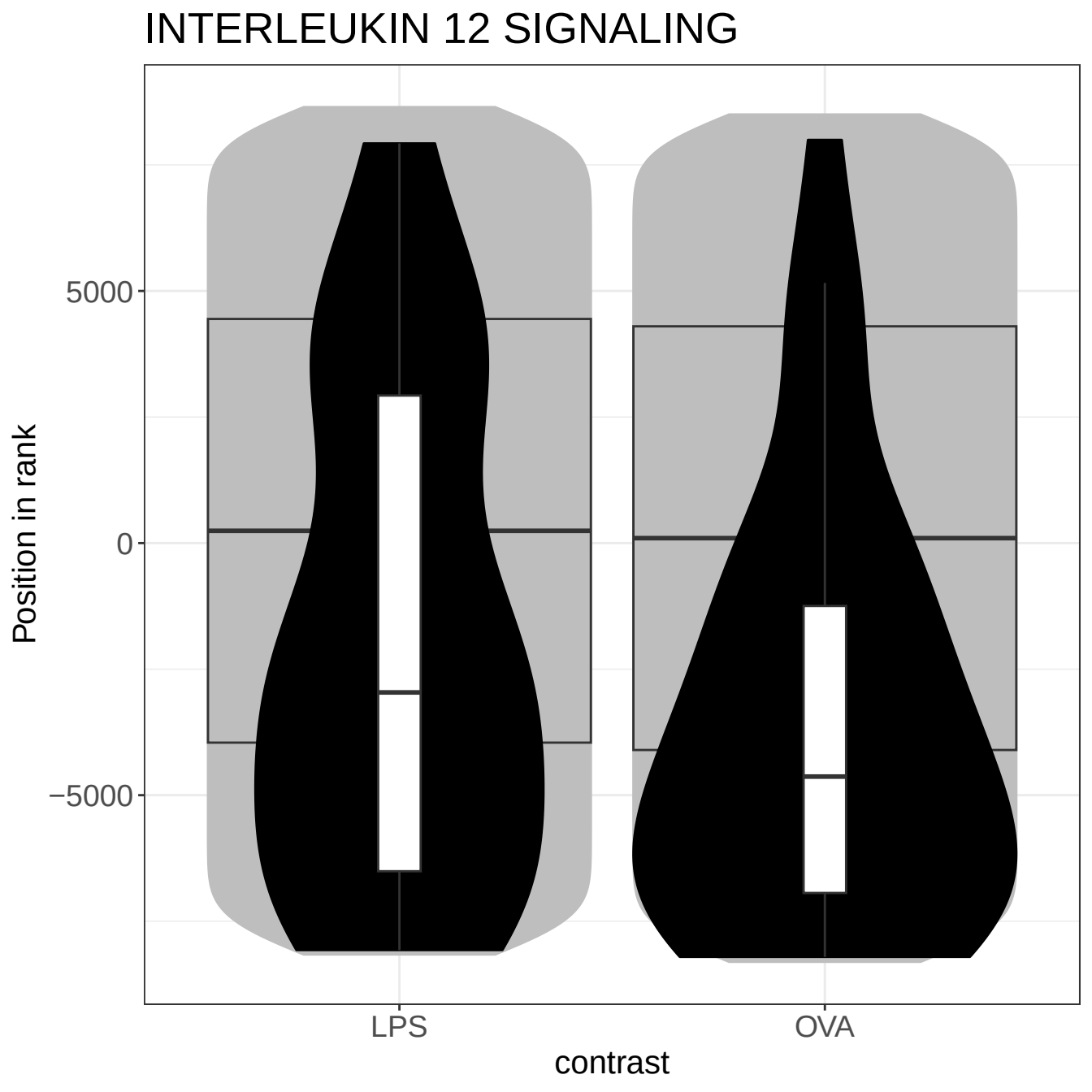

REPRESSION OF WNT TARGET GENES
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

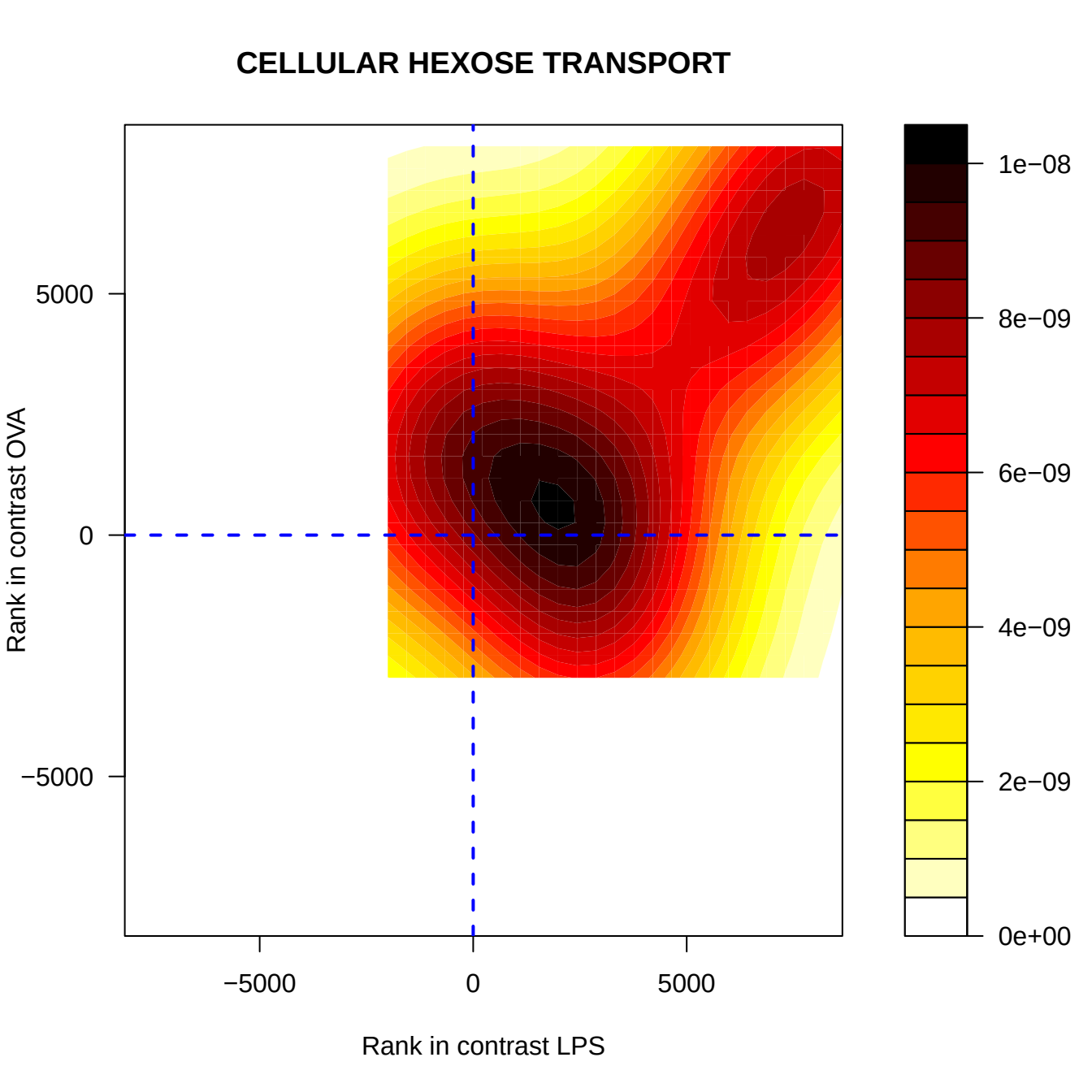

REPRESSION OF WNT TARGET GENES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

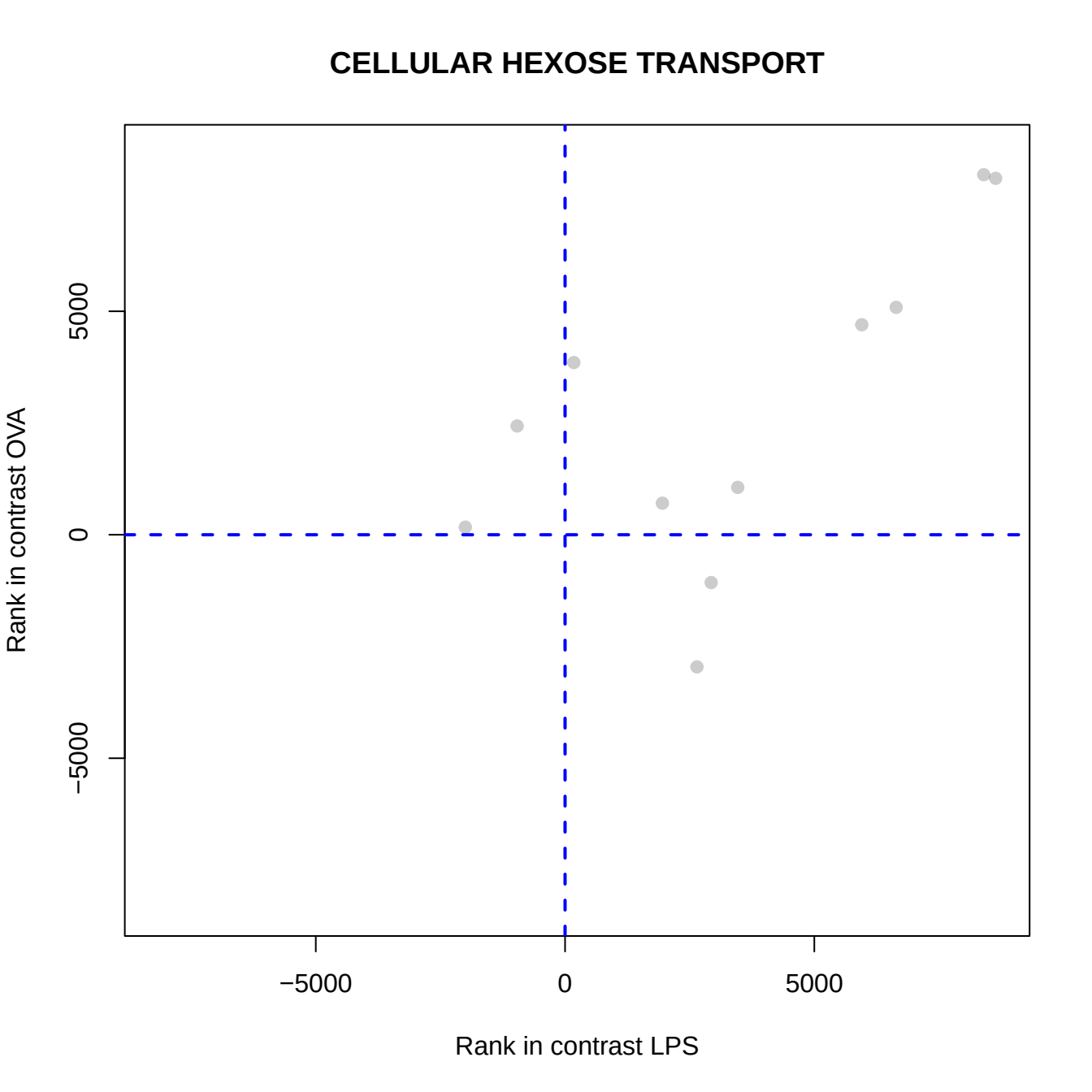

REPRESSION OF WNT TARGET GENES
5000
0
−5000
Position in rank
LPS
OVA
contrast

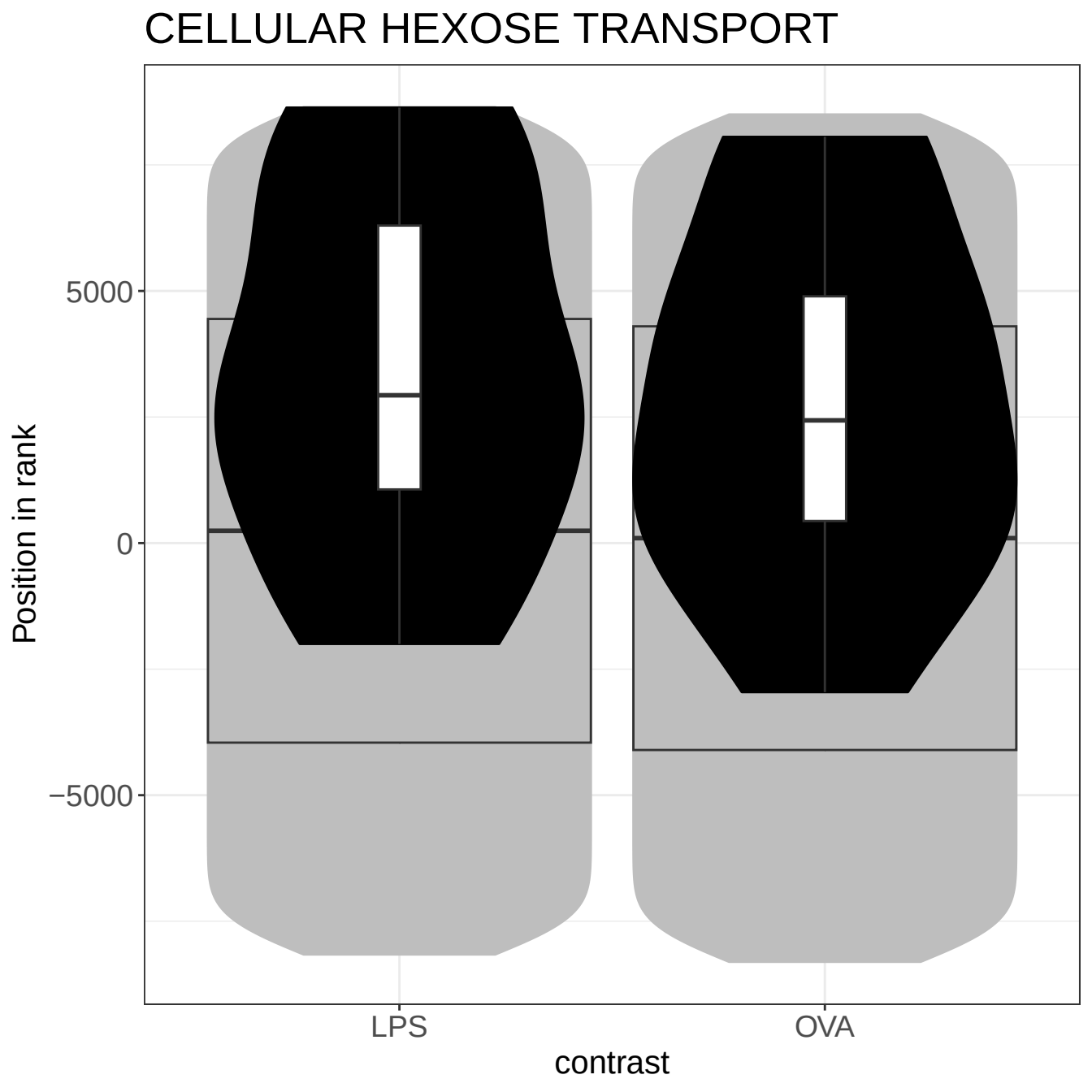

INTERLEUKIN 12 SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

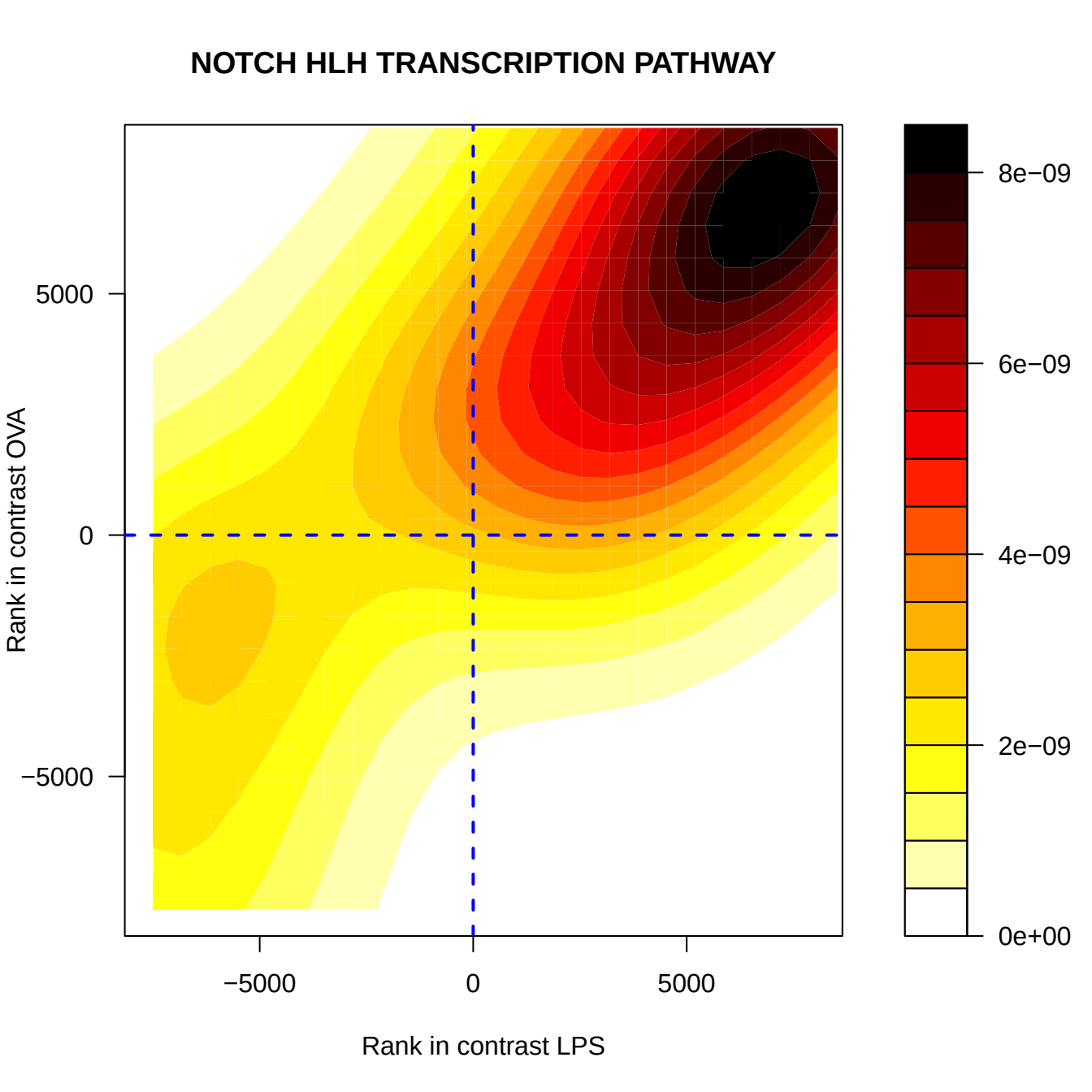

INTERLEUKIN 12 SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

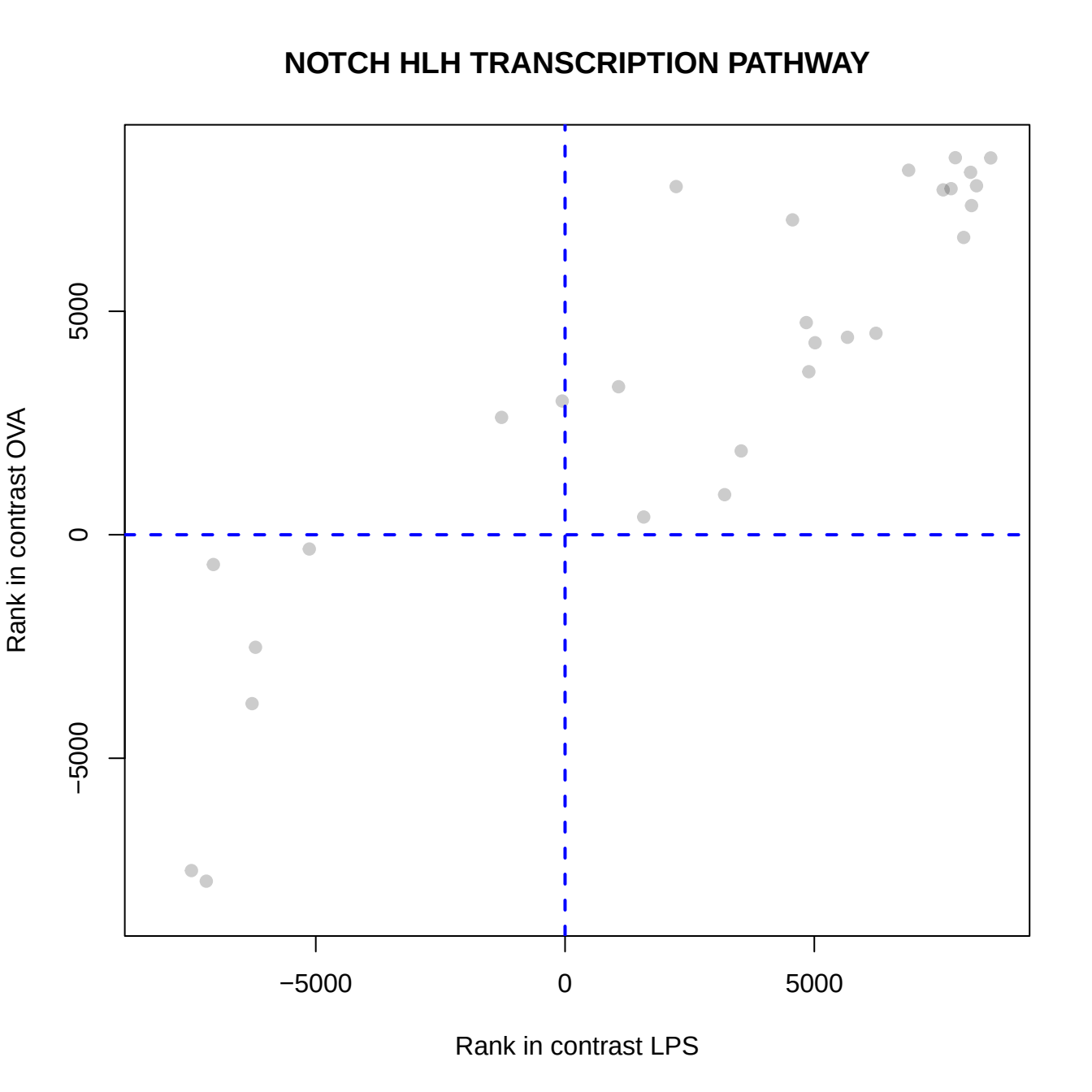

INTERLEUKIN 12 SIGNALING
5000
0
−5000
Position in rank
LPS
OVA
contrast

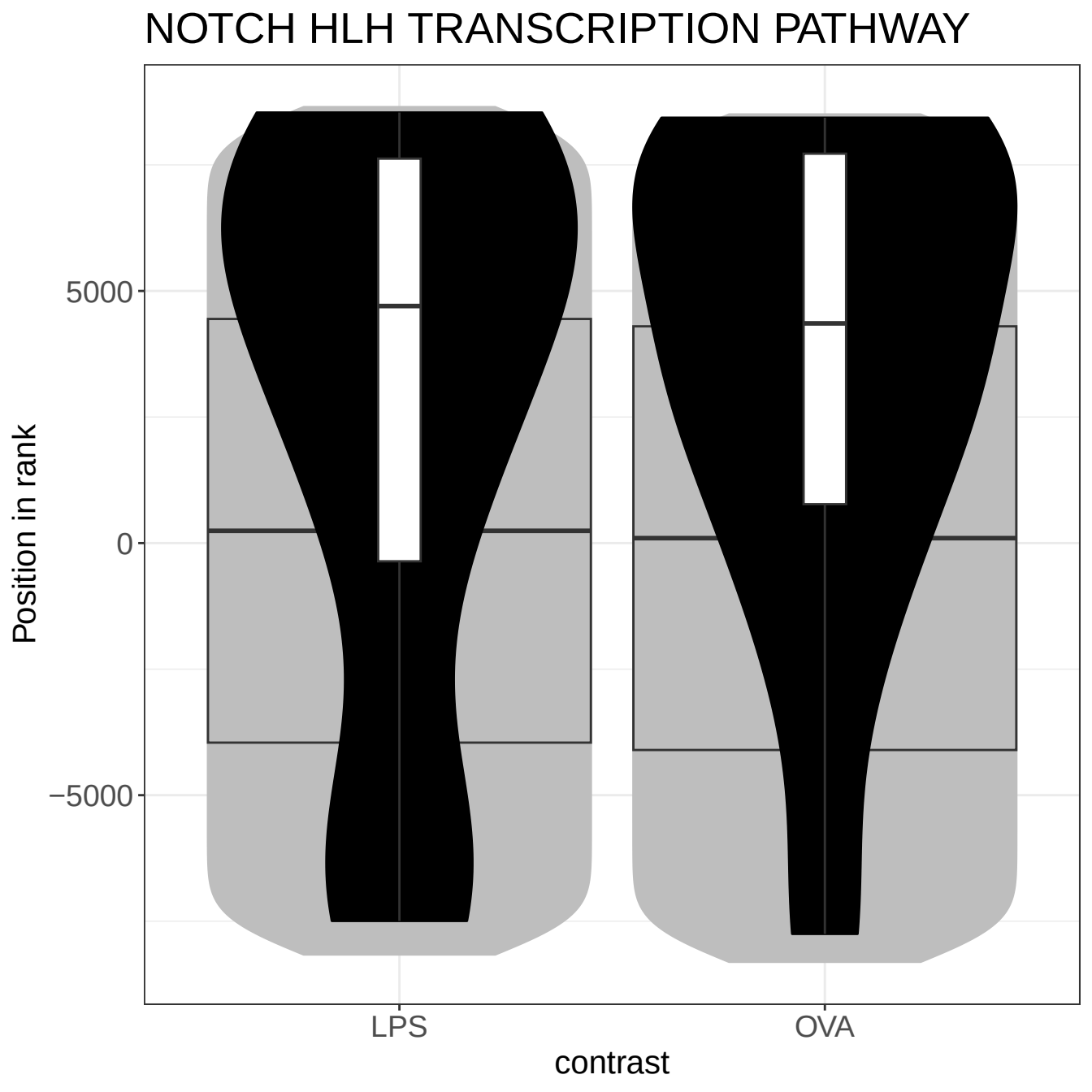

CELLULAR HEXOSE TRANSPORT
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

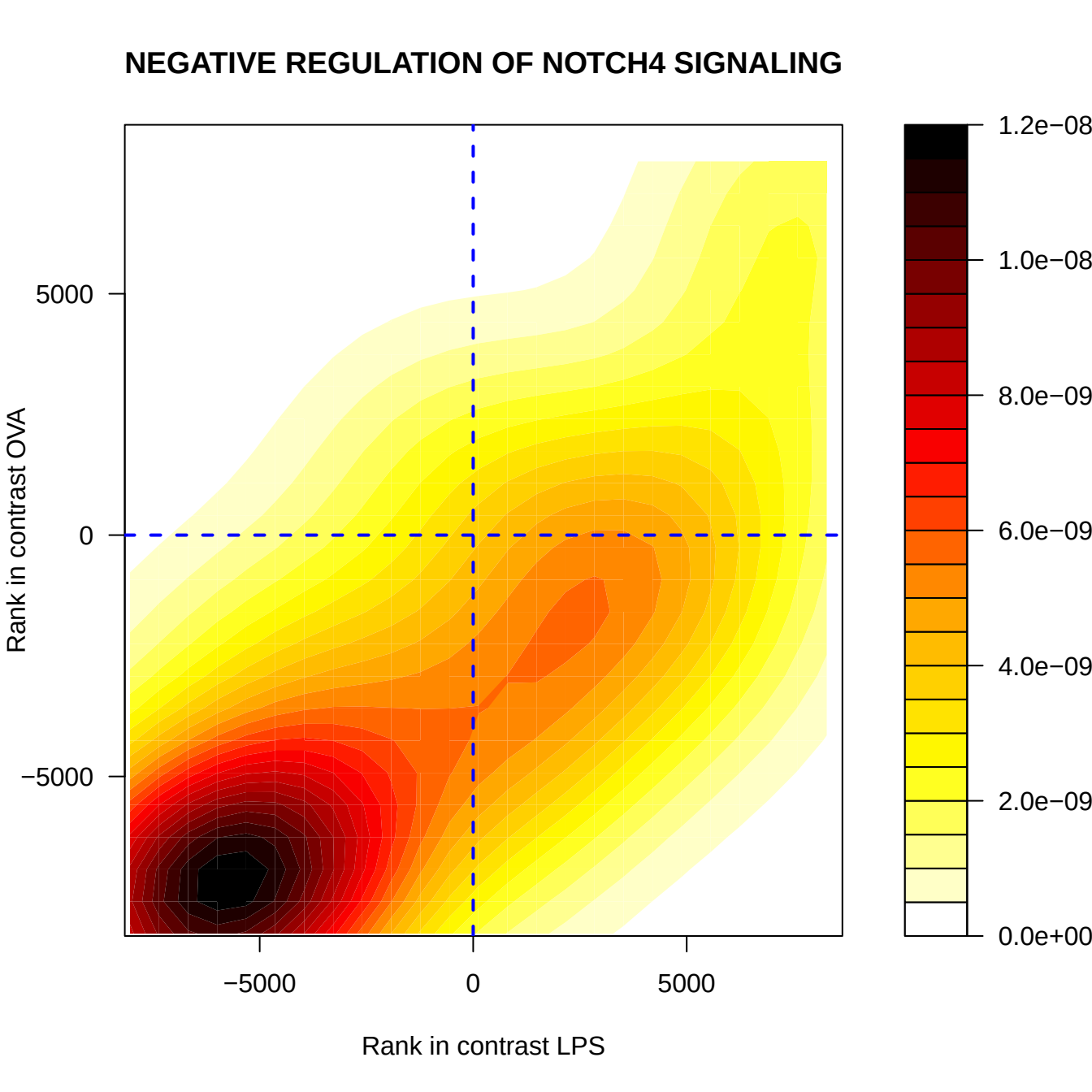

CELLULAR HEXOSE TRANSPORT
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

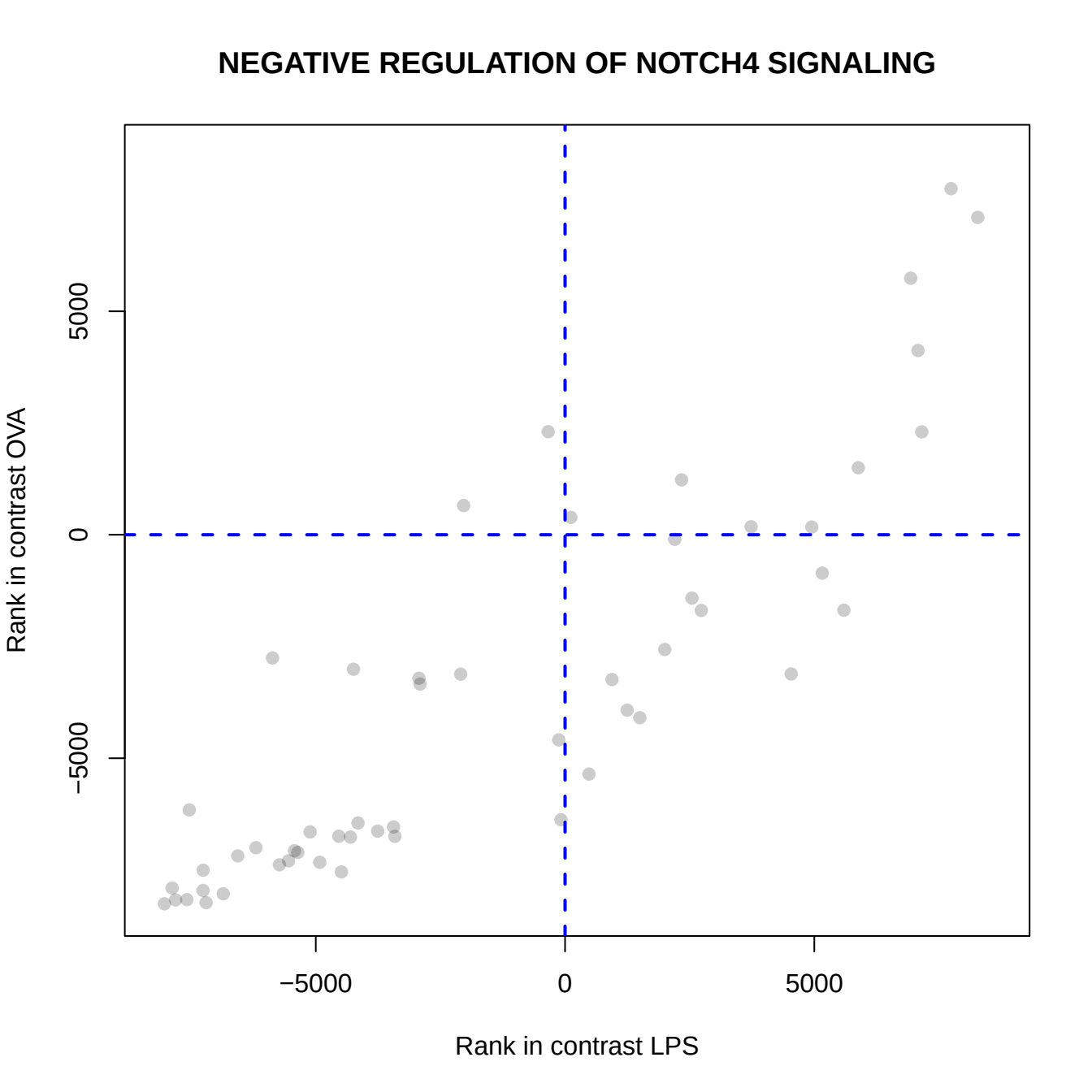

CELLULAR HEXOSE TRANSPORT
Position in rank
5000
0
−5000
LPS
OVA
contrast

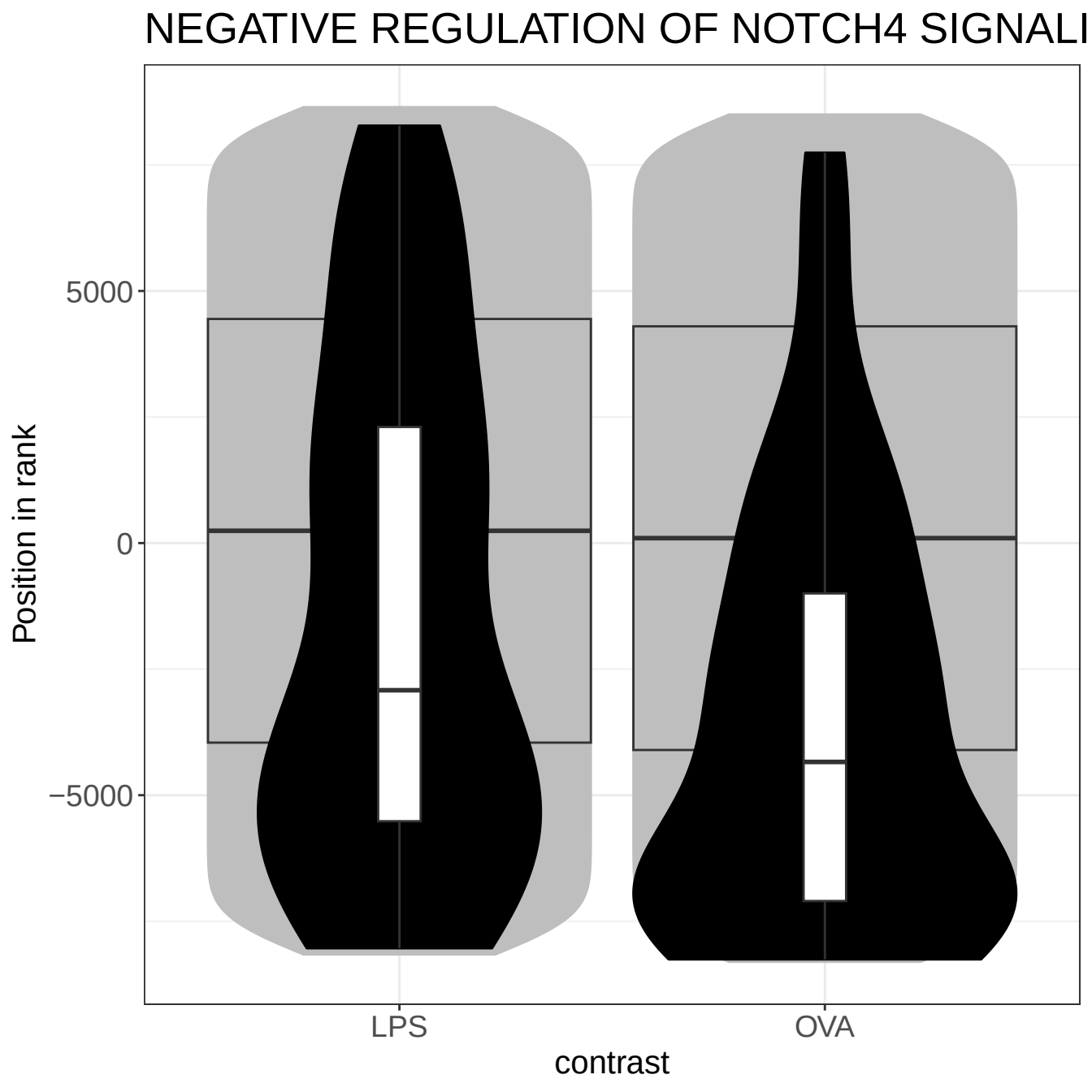

NOTCH HLH TRANSCRIPTION PATHWAY
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

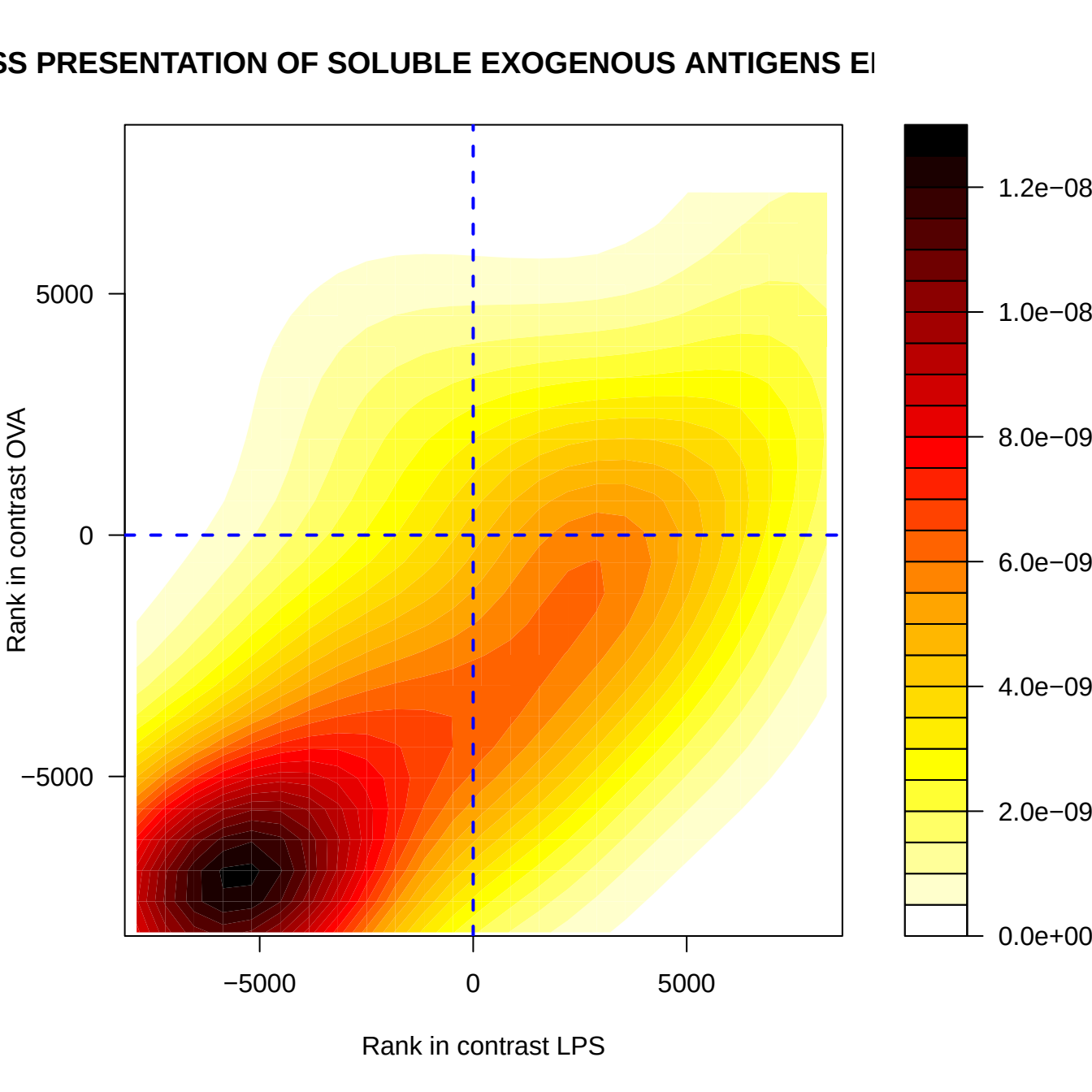

NOTCH HLH TRANSCRIPTION PATHWAY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

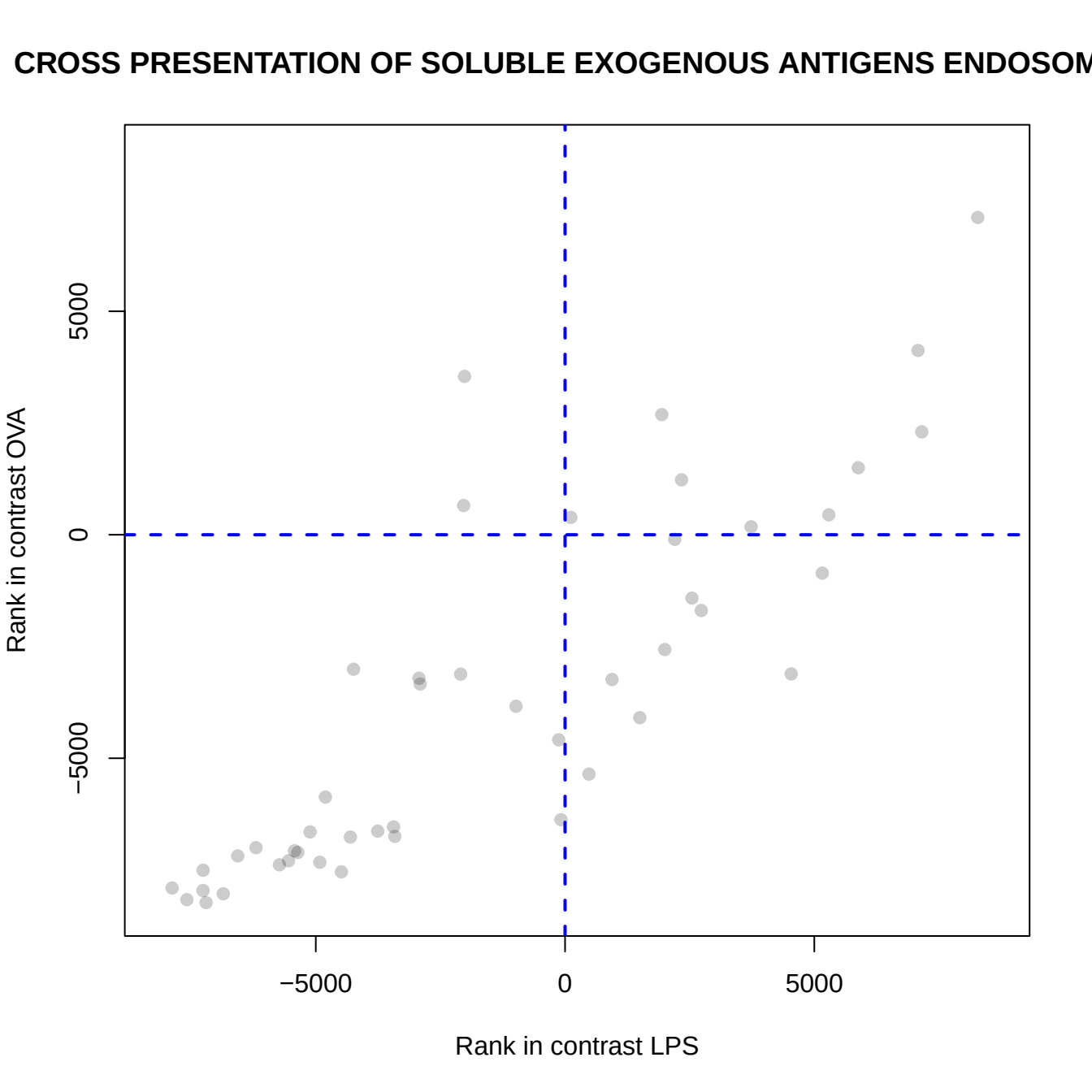

NOTCH HLH TRANSCRIPTION PATHWAY
5000
0
−5000
Position in rank
LPS
OVA
contrast

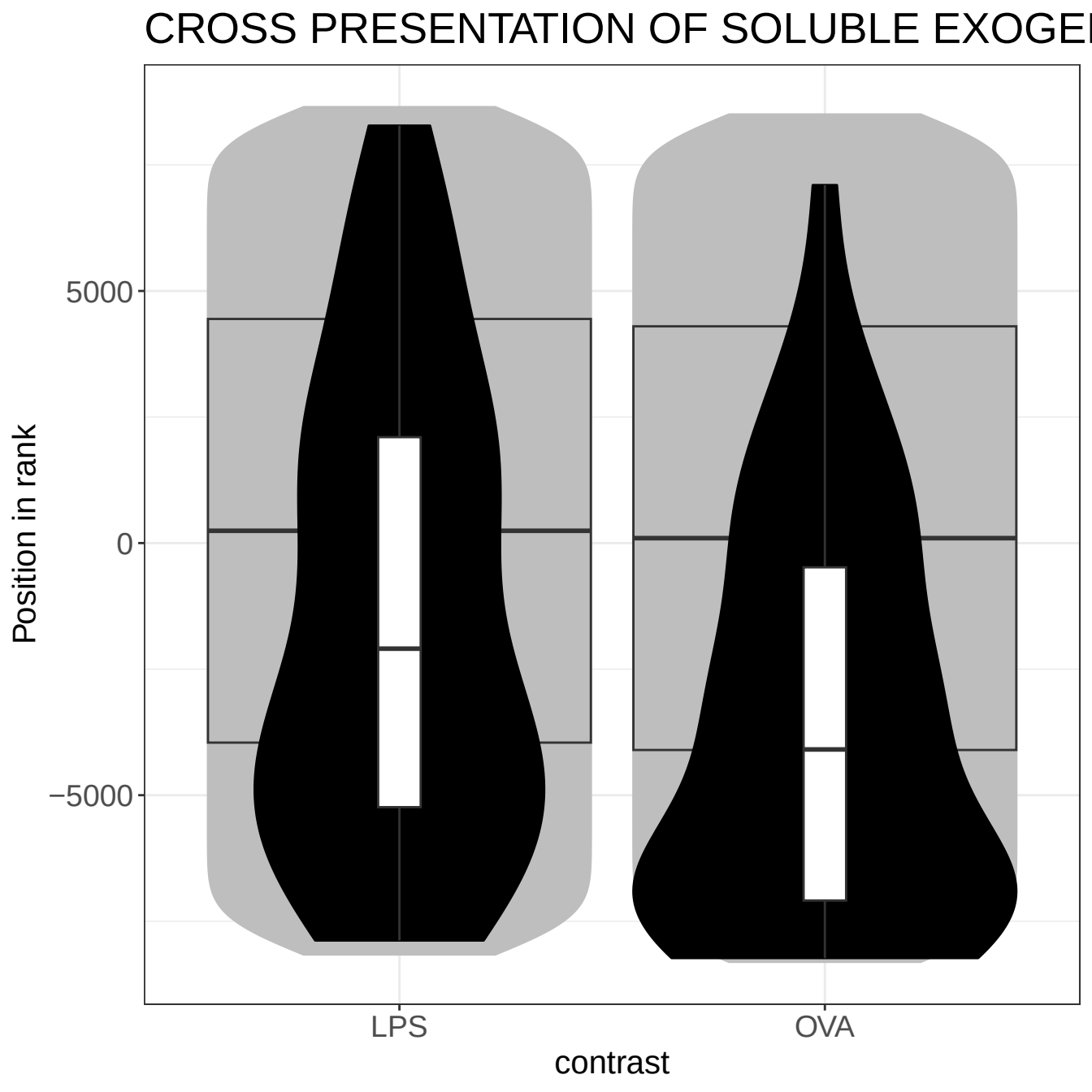

NEGATIVE REGULATION OF NOTCH4 SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

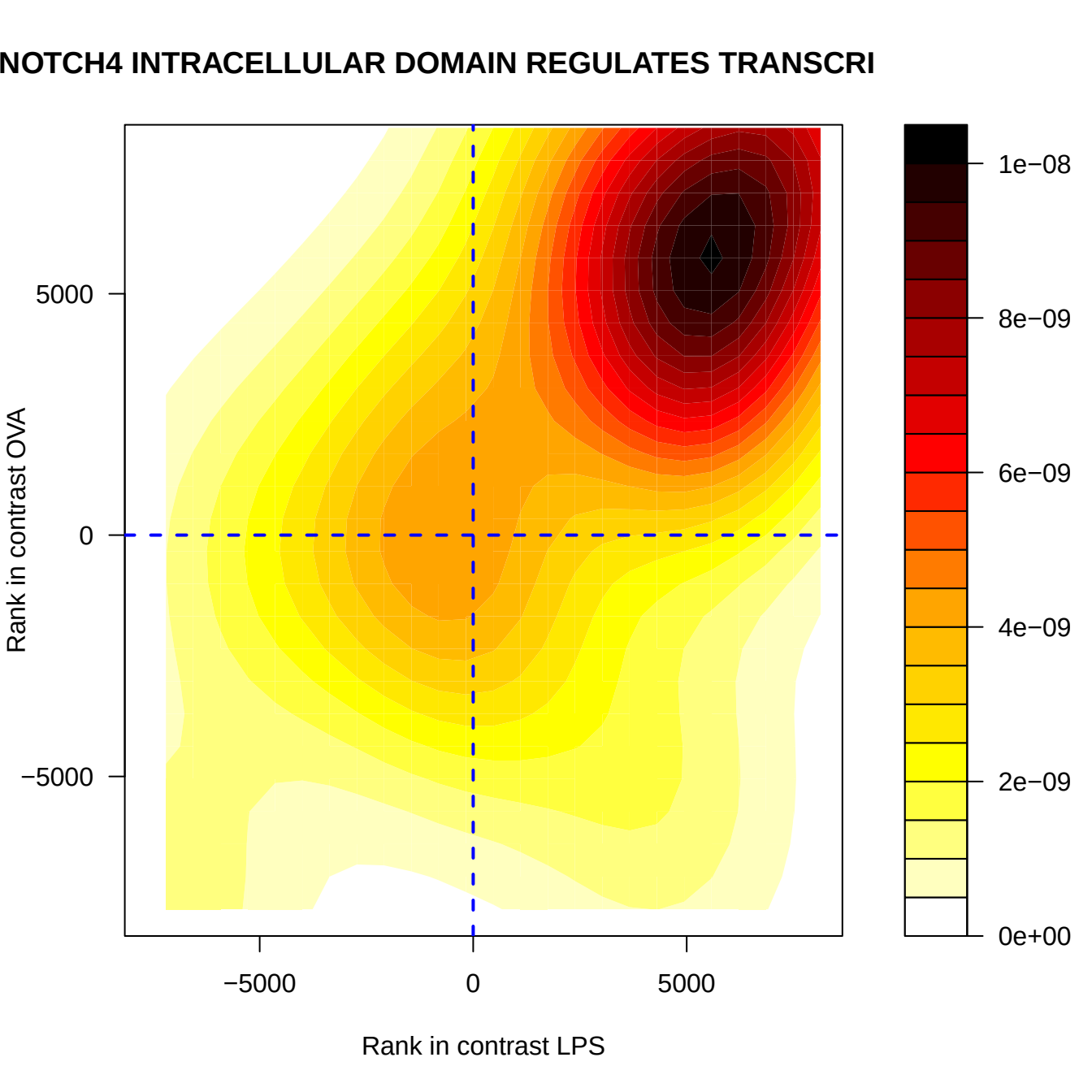

NEGATIVE REGULATION OF NOTCH4 SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

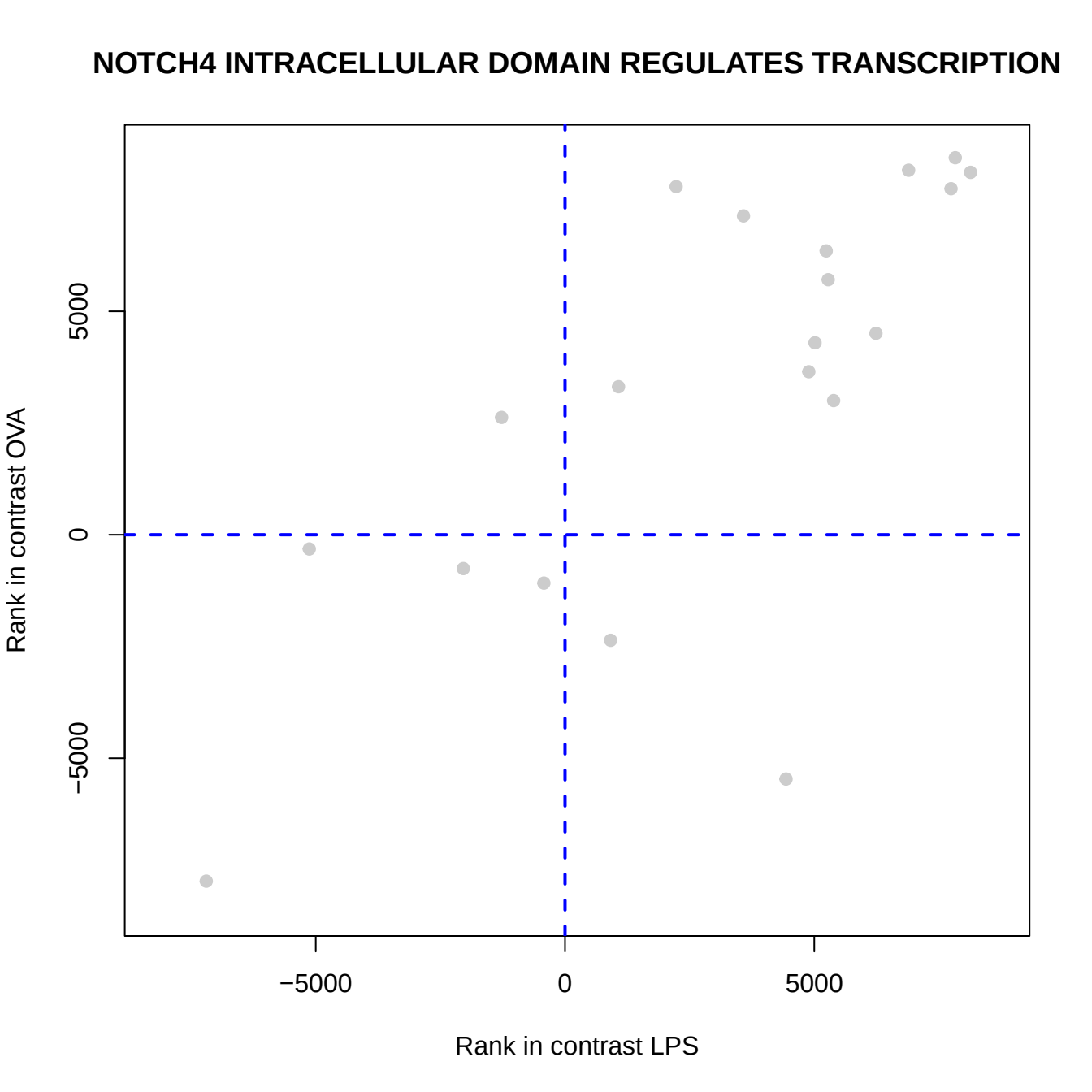

NEGATIVE REGULATION OF NOTCH4 SIGNALI
5000
0
−5000
Position in rank
LPS
OVA
contrast

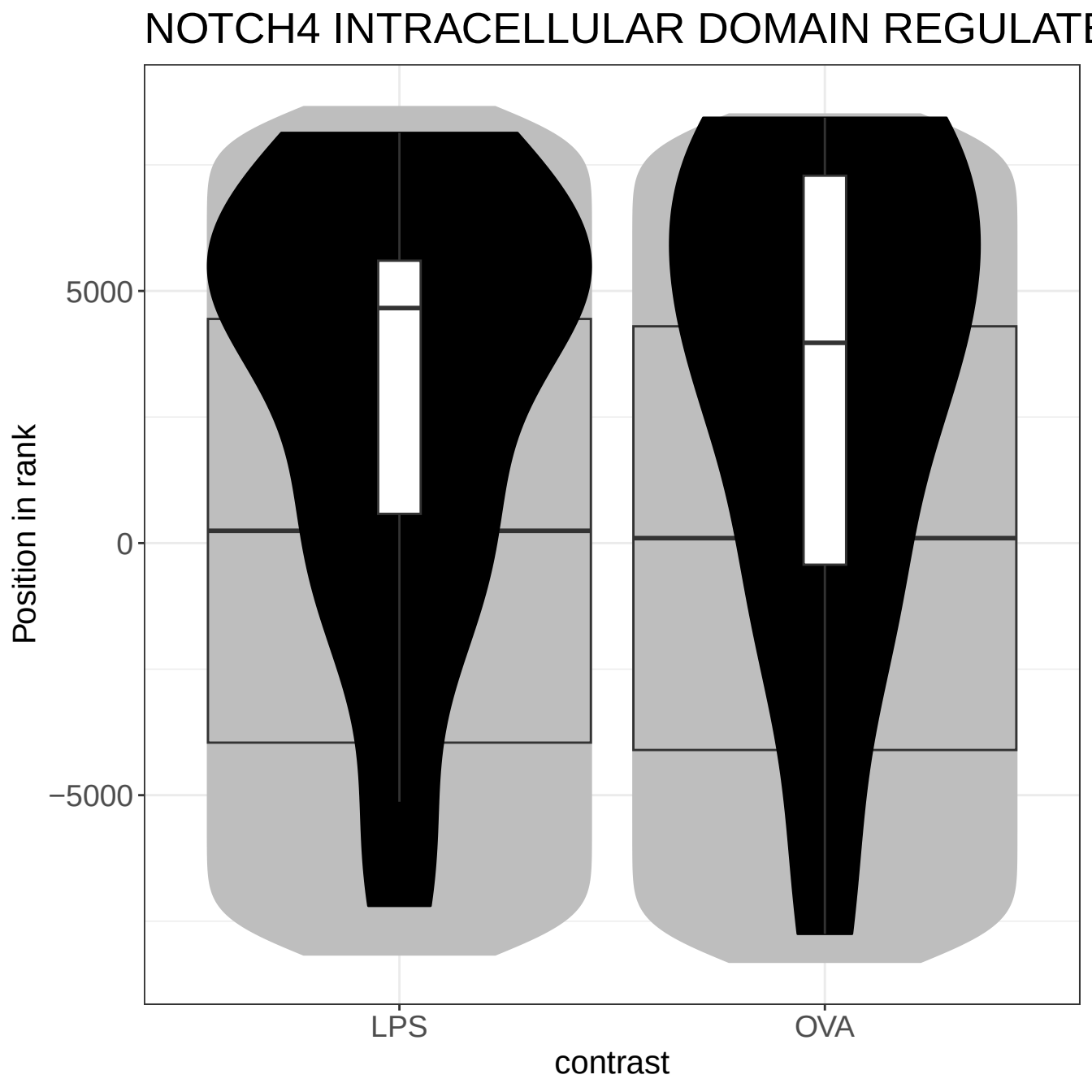

SS PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS EI
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

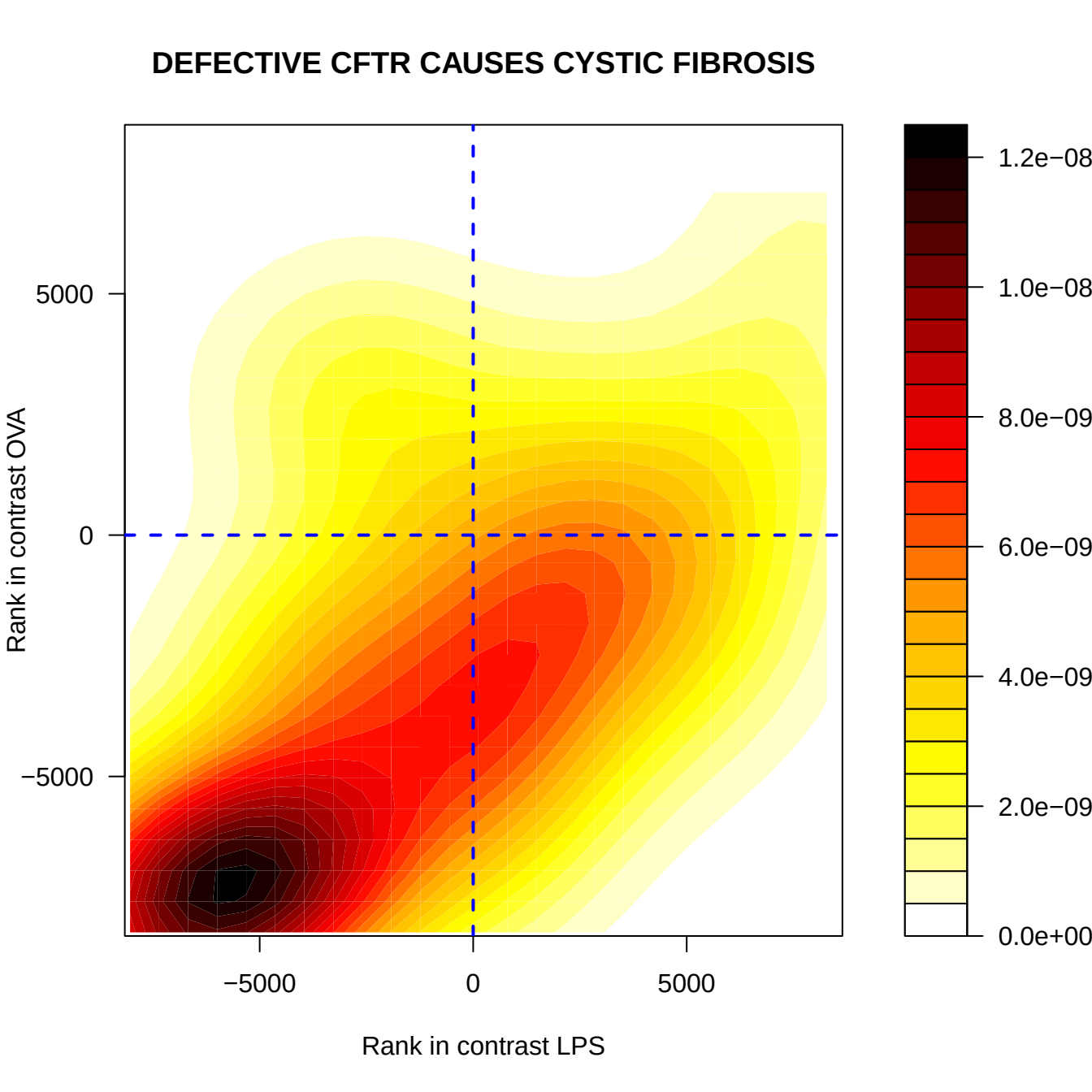

CROSS PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS ENDOSOM
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

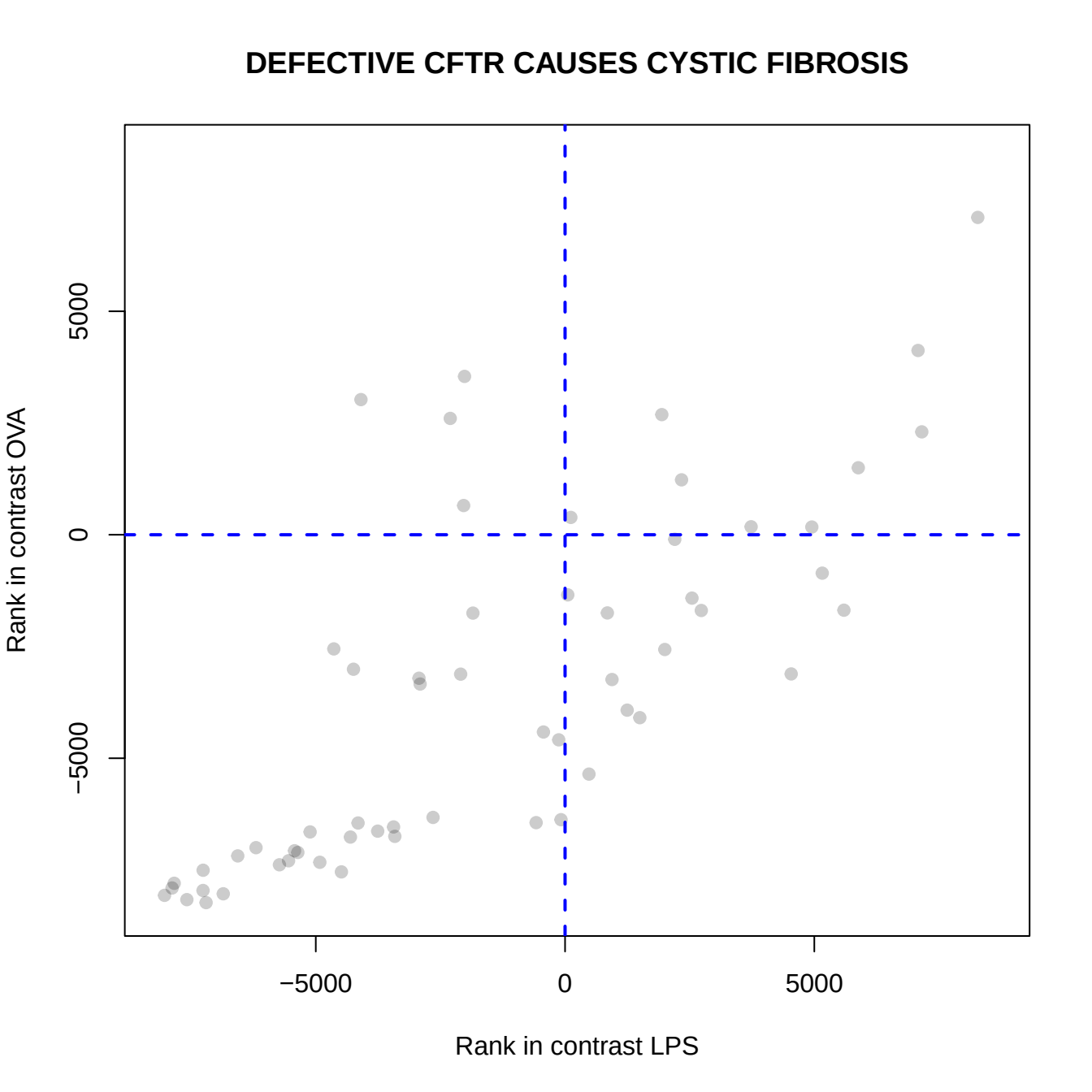

CROSS PRESENTATION OF SOLUBLE EXOGE
5000
0
−5000
Position in rank
LPS
OVA
contrast

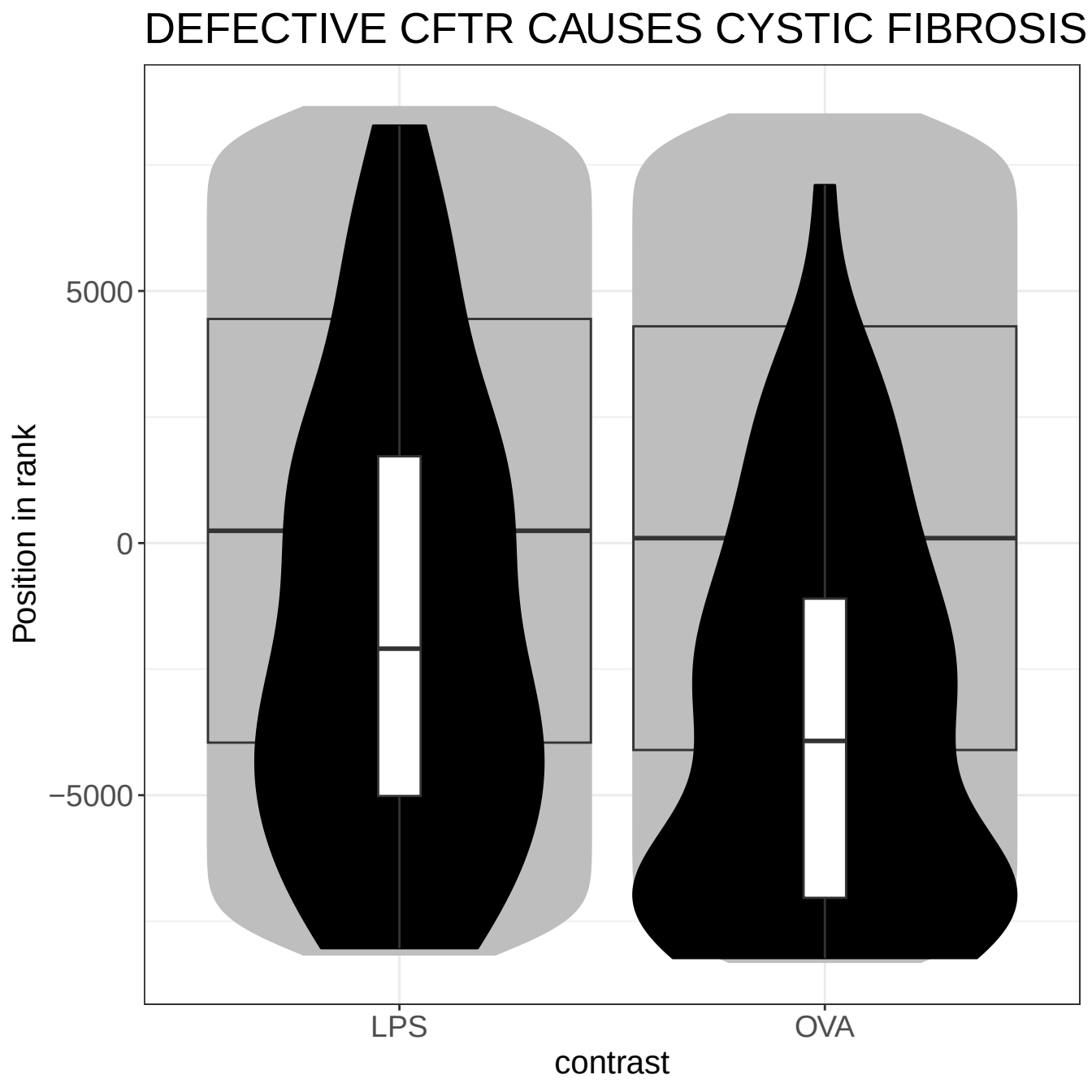

NOTCH4 INTRACELLULAR DOMAIN REGULATES TRANSCRI
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

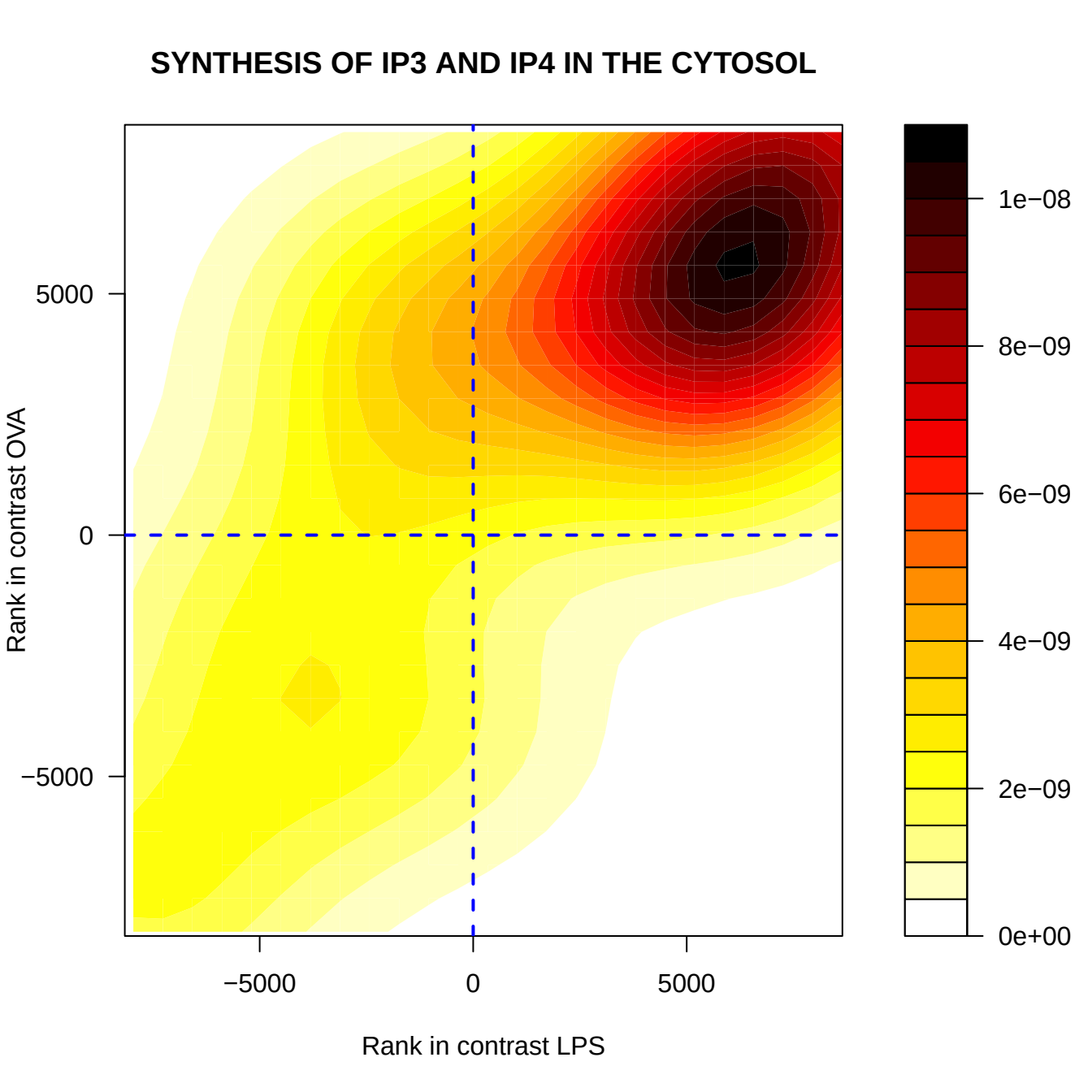

NOTCH4 INTRACELLULAR DOMAIN REGULATES TRANSCRIPTION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

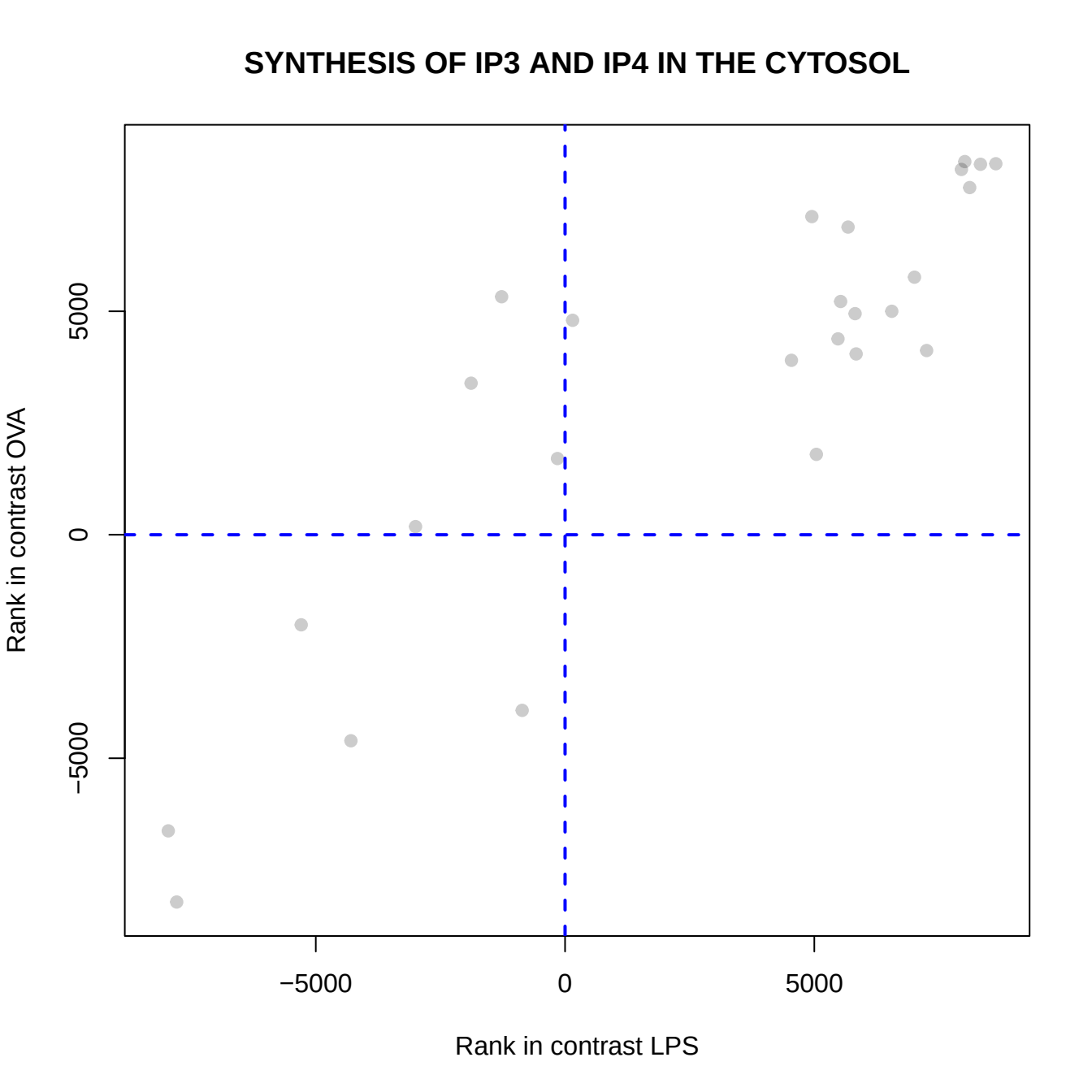

NOTCH4 INTRACELLULAR DOMAIN REGULATE
5000
0
−5000
Position in rank
LPS
OVA
contrast

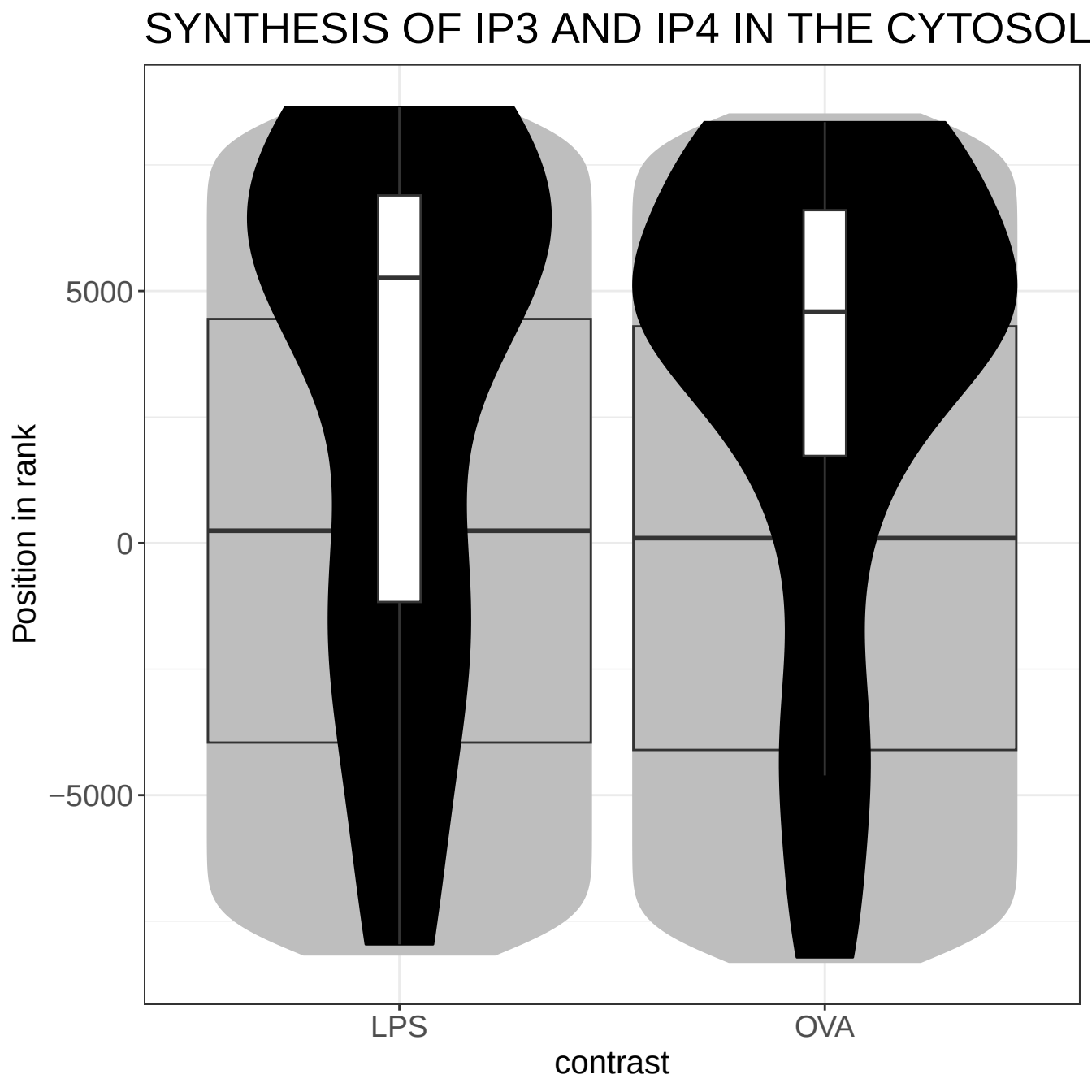

DEFECTIVE CFTR CAUSES CYSTIC FIBROSIS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

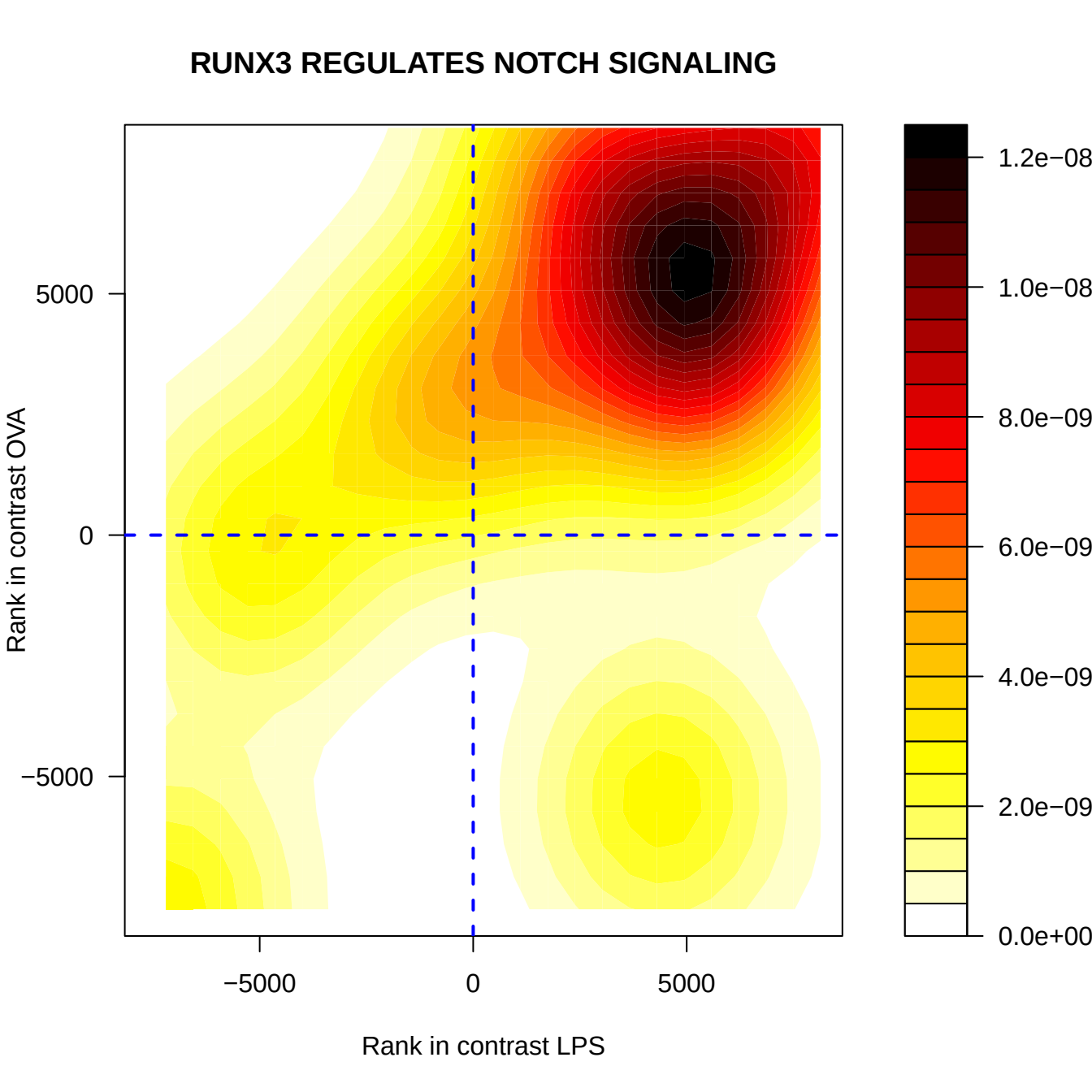

DEFECTIVE CFTR CAUSES CYSTIC FIBROSIS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

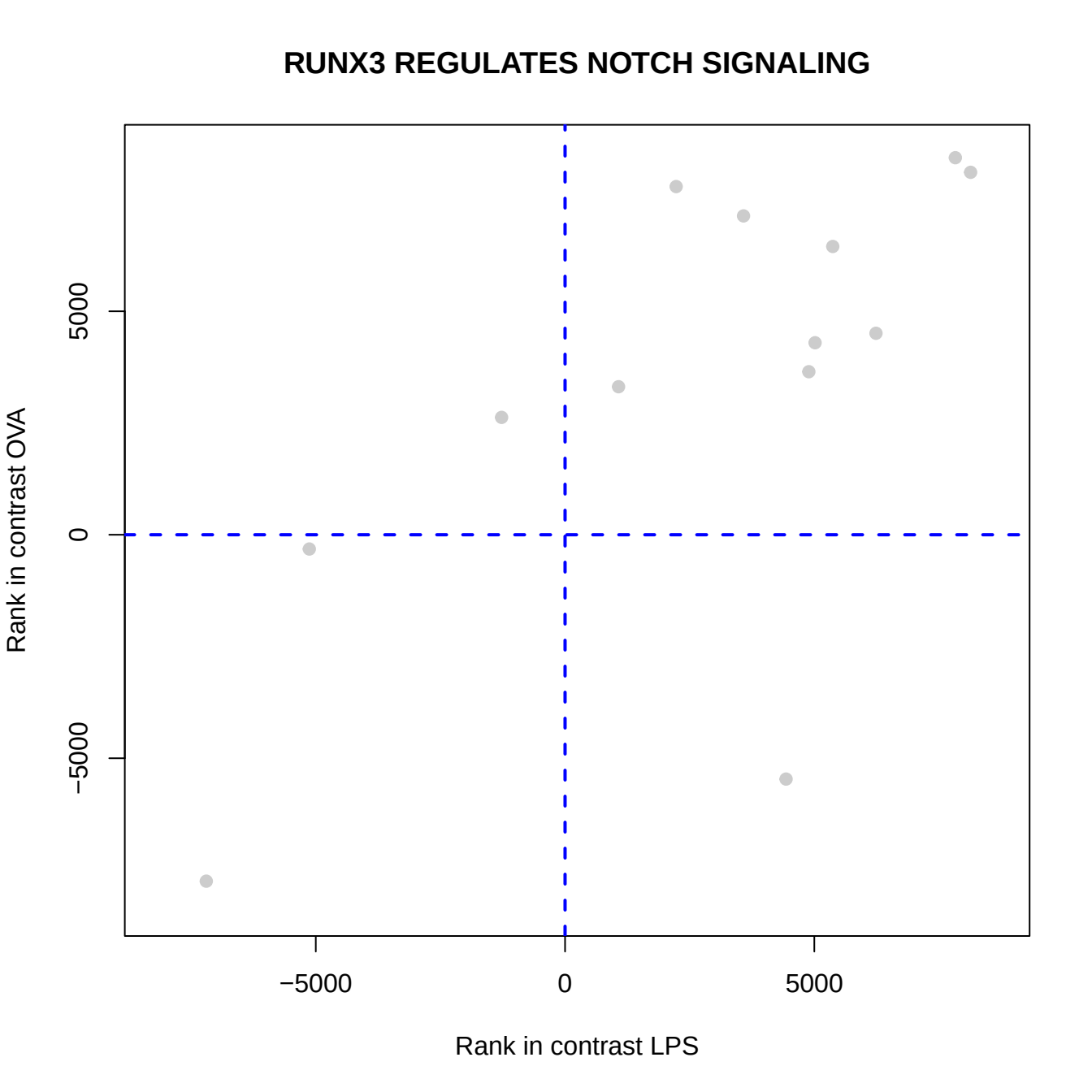

DEFECTIVE CFTR CAUSES CYSTIC FIBROSIS
5000
0
−5000
Position in rank
LPS
OVA
contrast

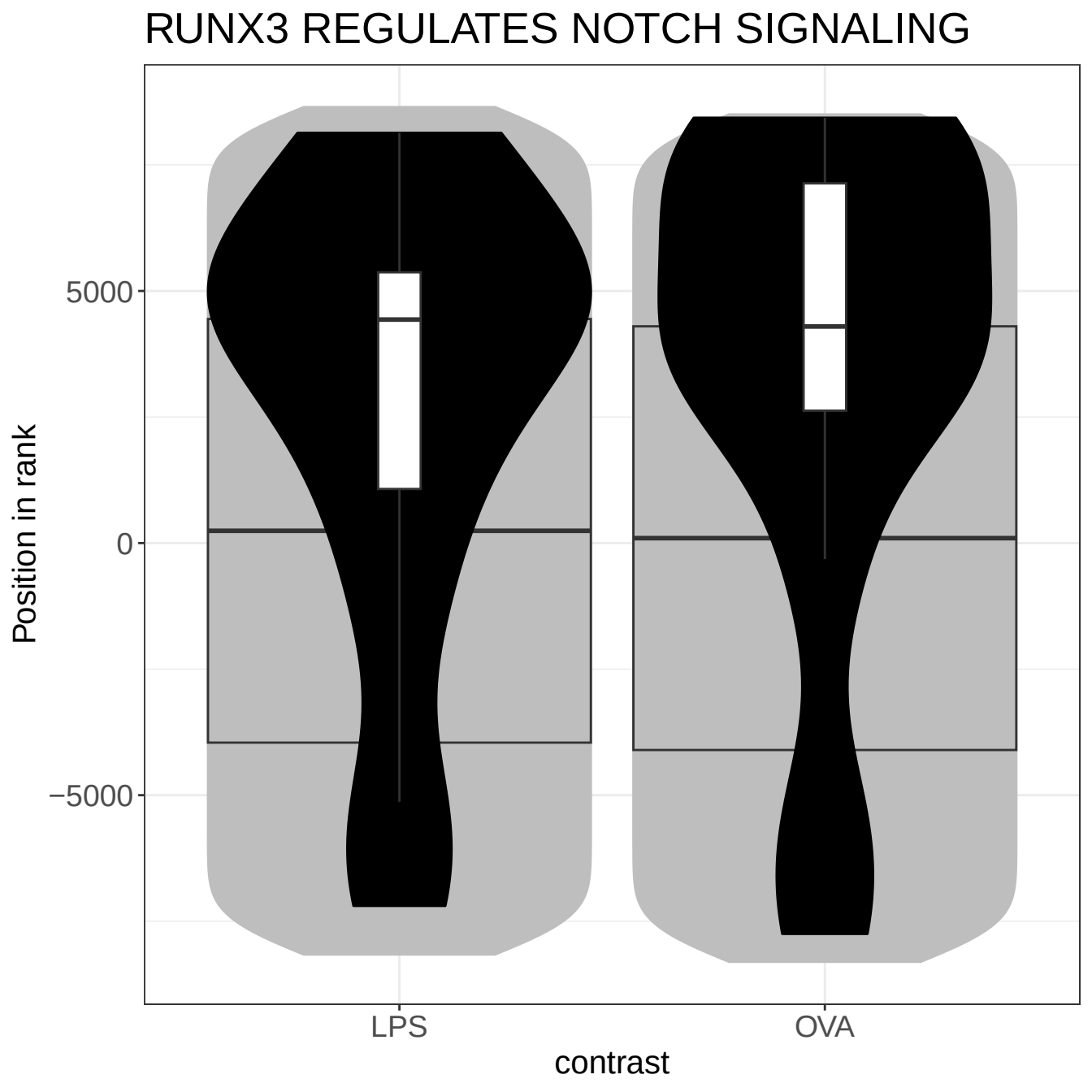

SYNTHESIS OF IP3 AND IP4 IN THE CYTOSOL
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

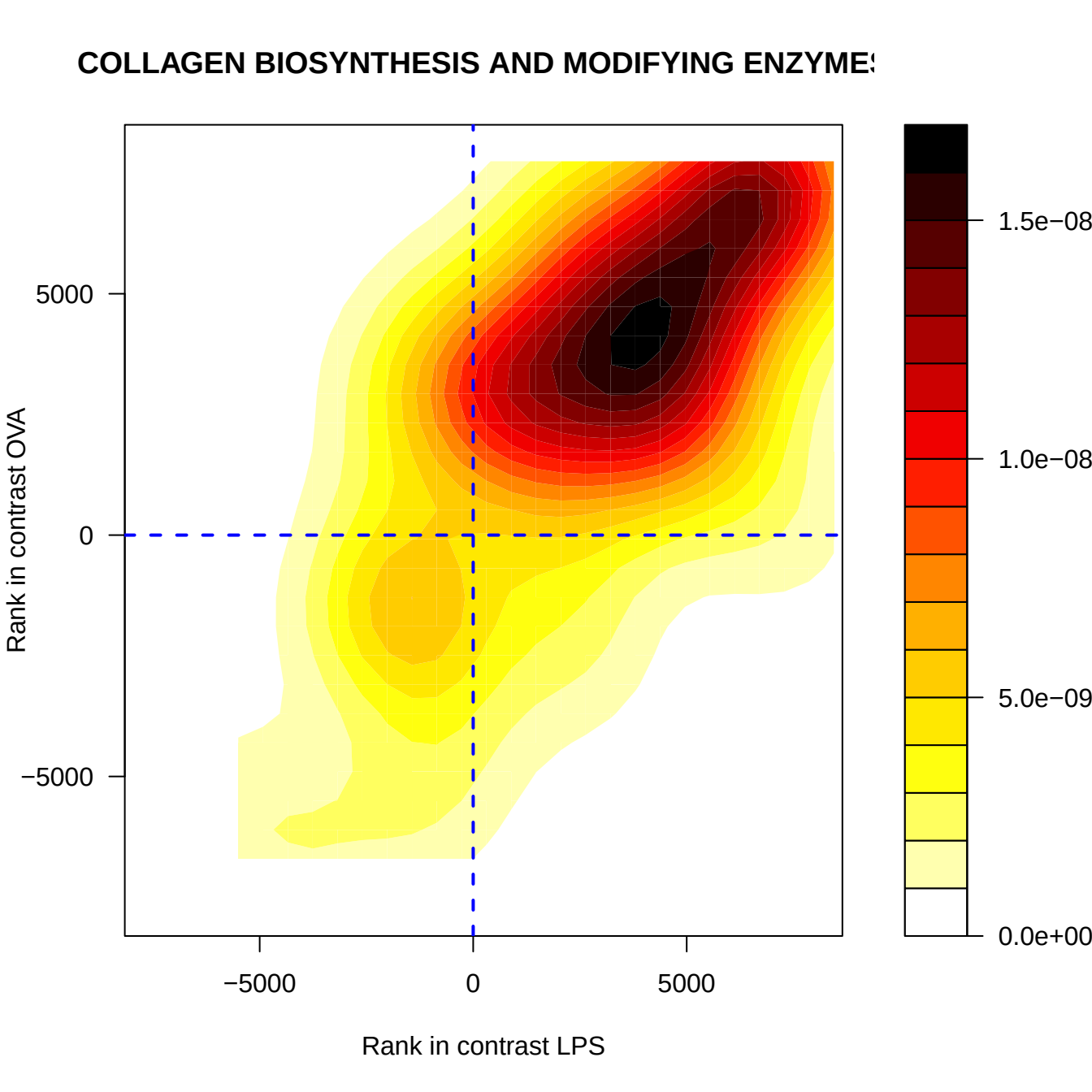

SYNTHESIS OF IP3 AND IP4 IN THE CYTOSOL
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

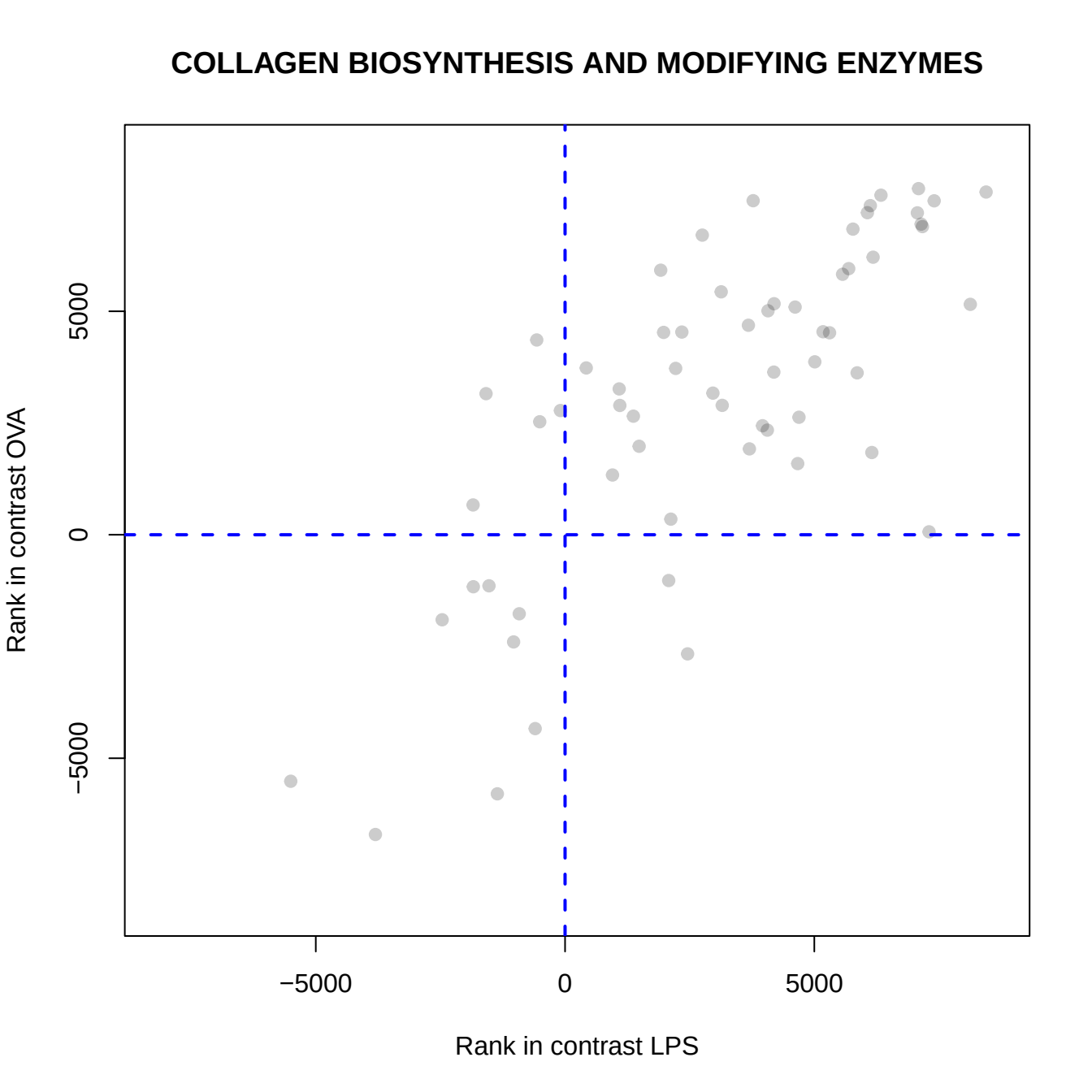

SYNTHESIS OF IP3 AND IP4 IN THE CYTOSOL
5000
0
−5000
Position in rank
LPS
OVA
contrast

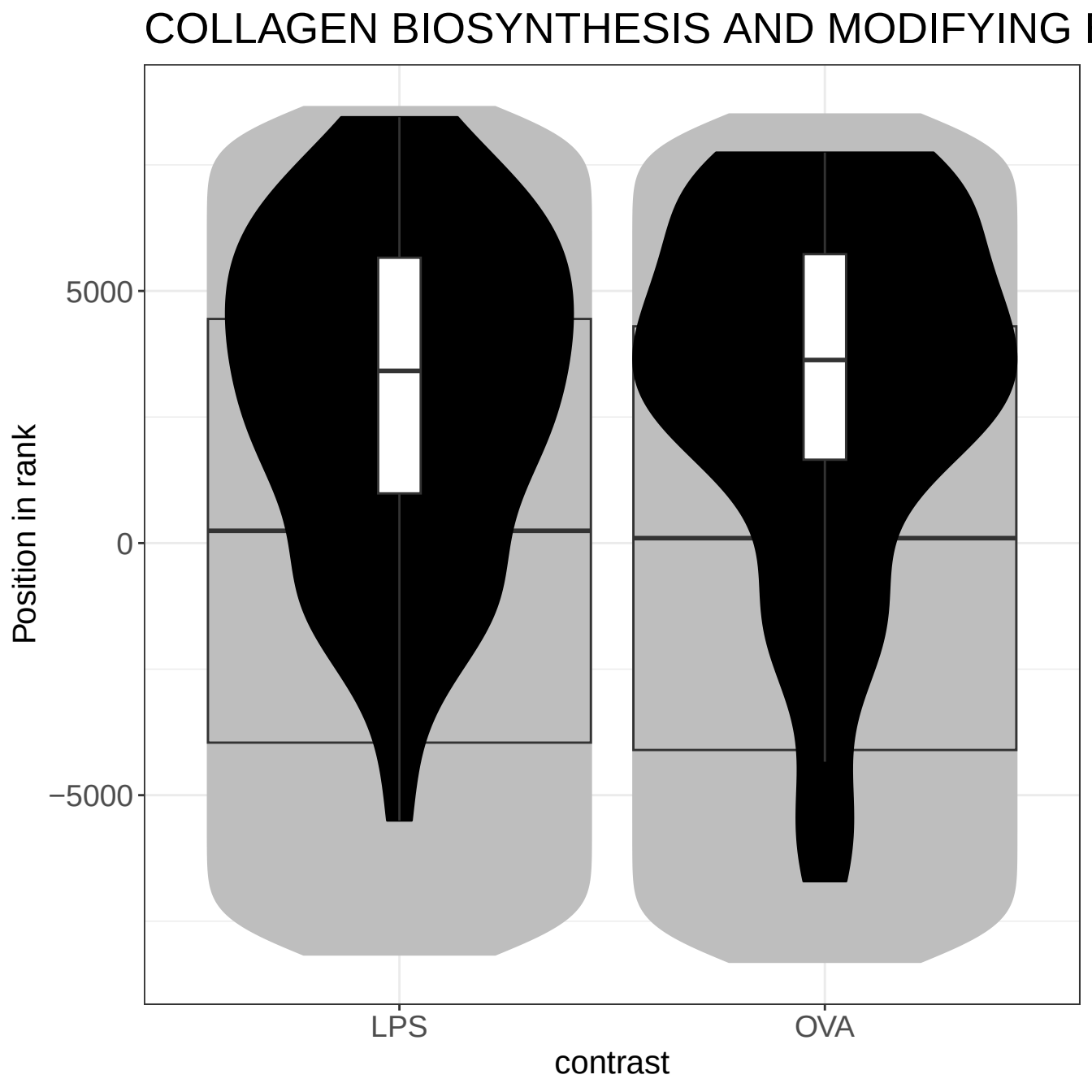

RUNX3 REGULATES NOTCH SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

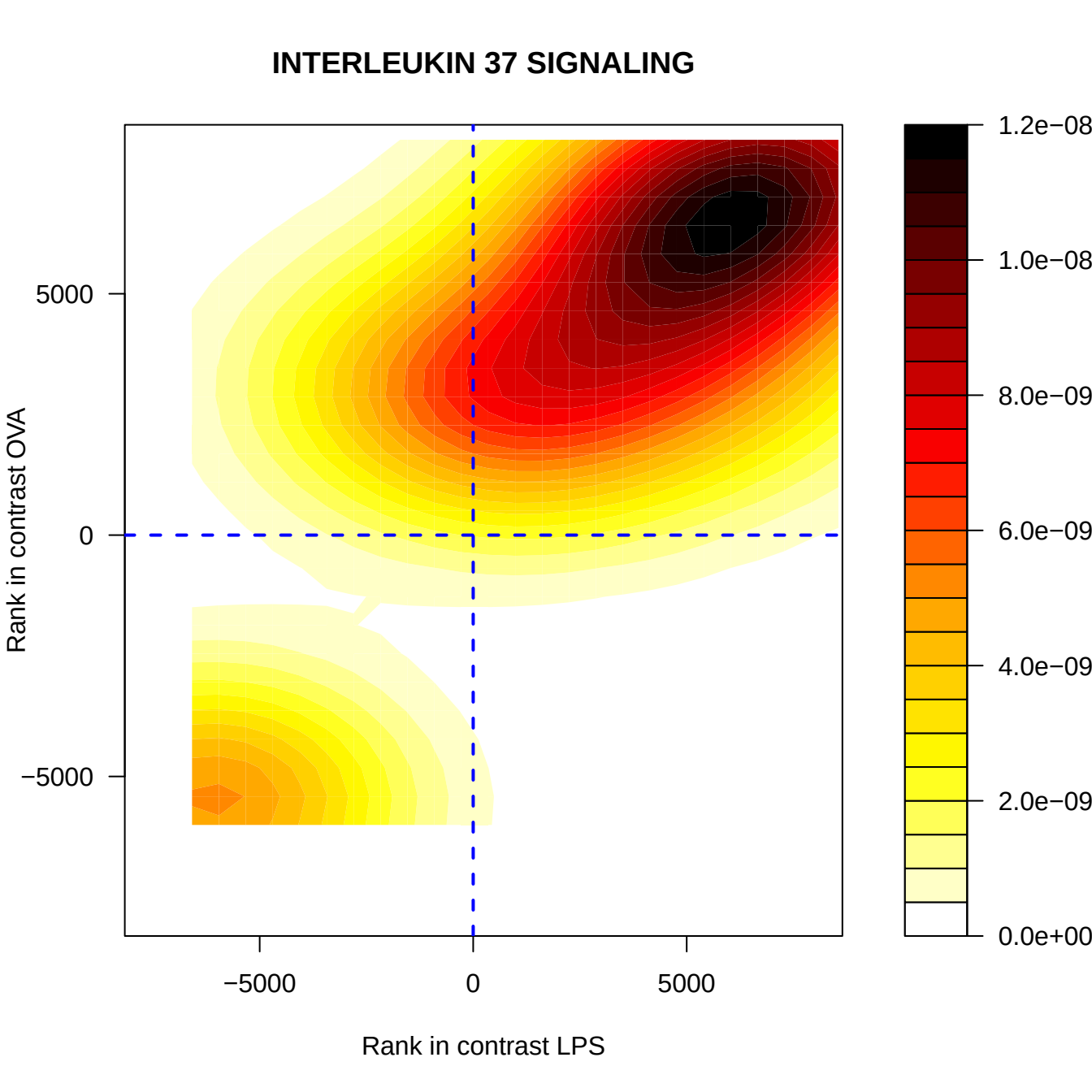

RUNX3 REGULATES NOTCH SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

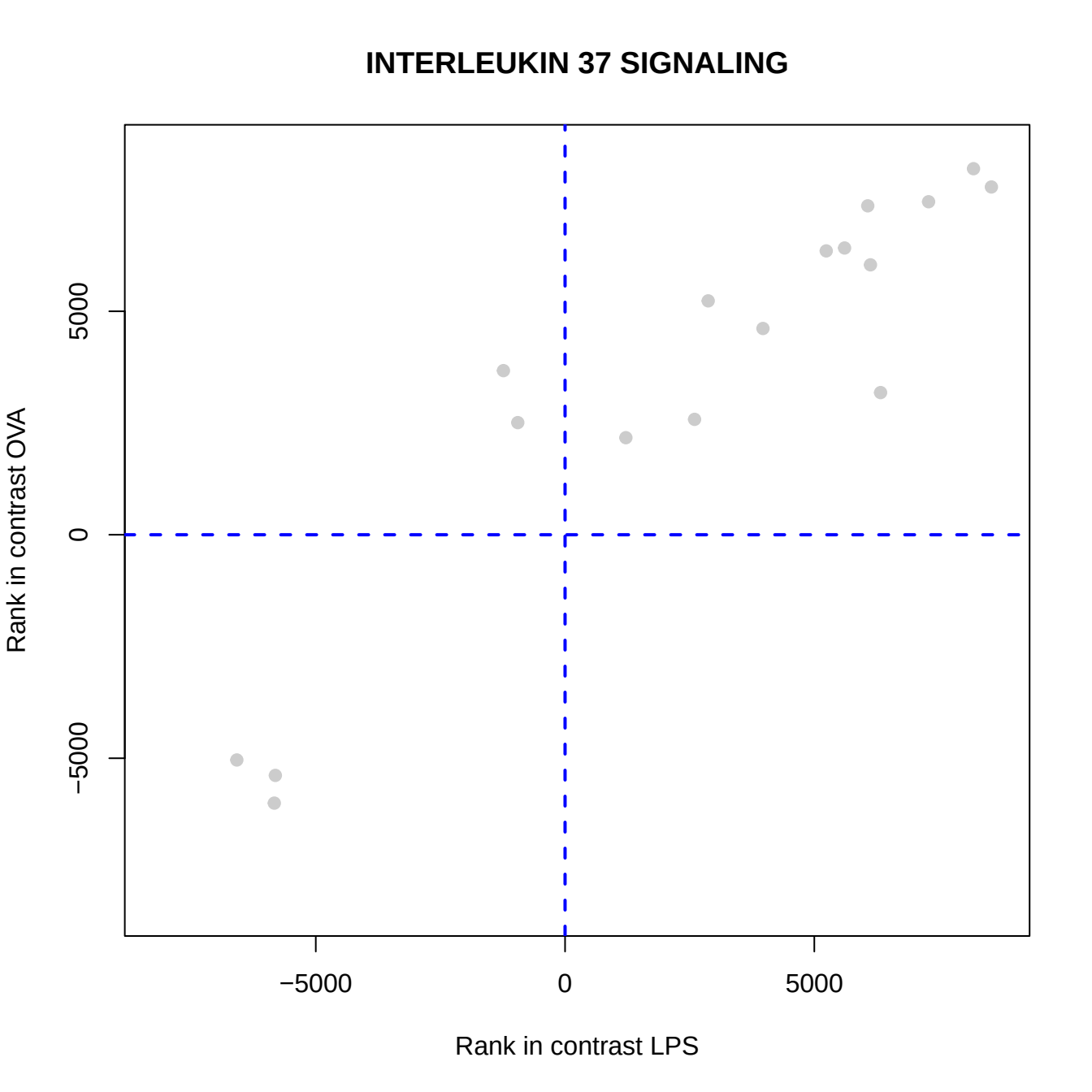

RUNX3 REGULATES NOTCH SIGNALING
5000
0
−5000
Position in rank
LPS
OVA
contrast

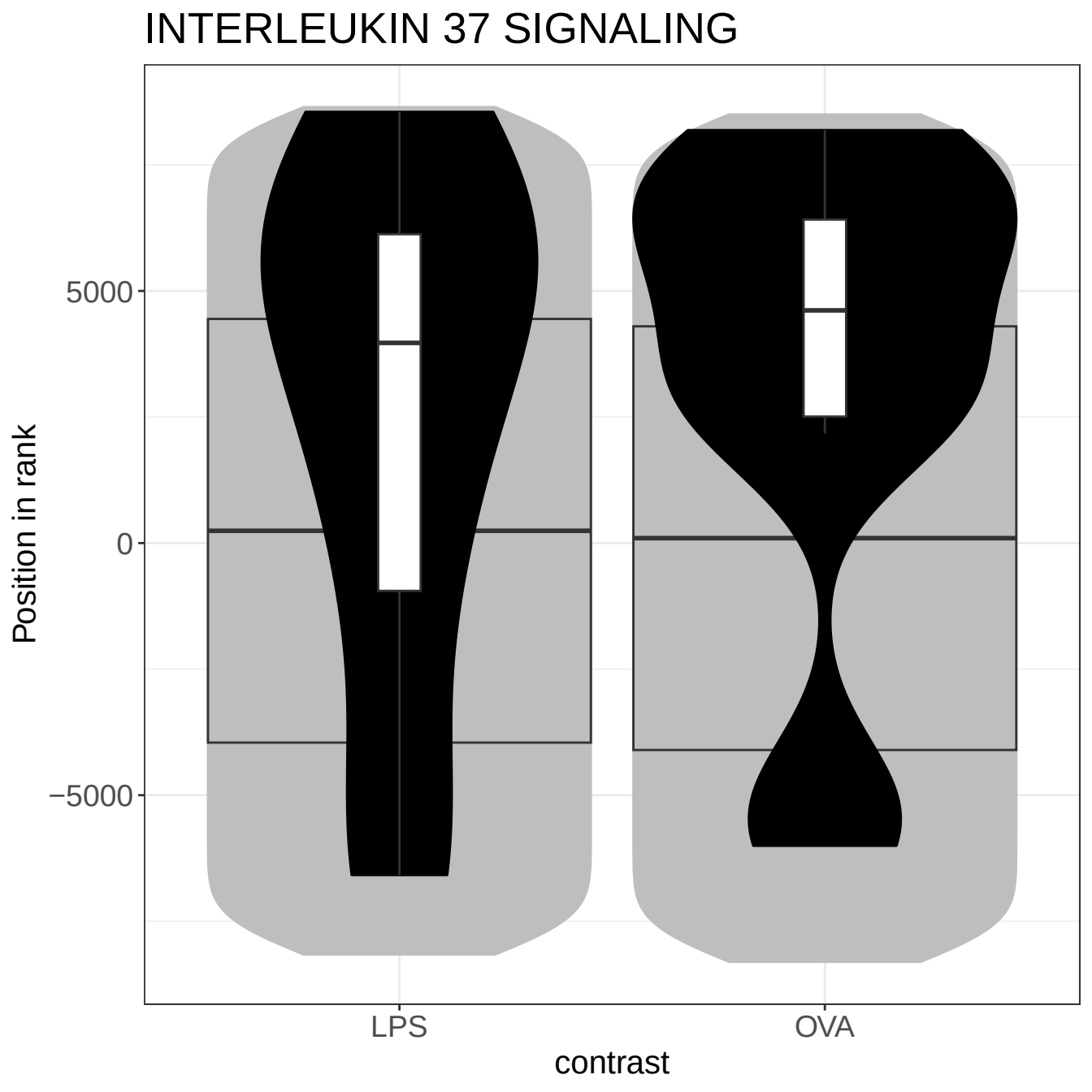

COLLAGEN BIOSYNTHESIS AND MODIFYING ENZYME
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00


COLLAGEN BIOSYNTHESIS AND MODIFYING ENZYMES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS


COLLAGEN BIOSYNTHESIS AND MODIFYING
5000
0
−5000
Position in rank
LPS
OVA
contrast


INTERLEUKIN 37 SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00


INTERLEUKIN 37 SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS


INTERLEUKIN 37 SIGNALING
5000
0
−5000
Position in rank
LPS
OVA
contrast