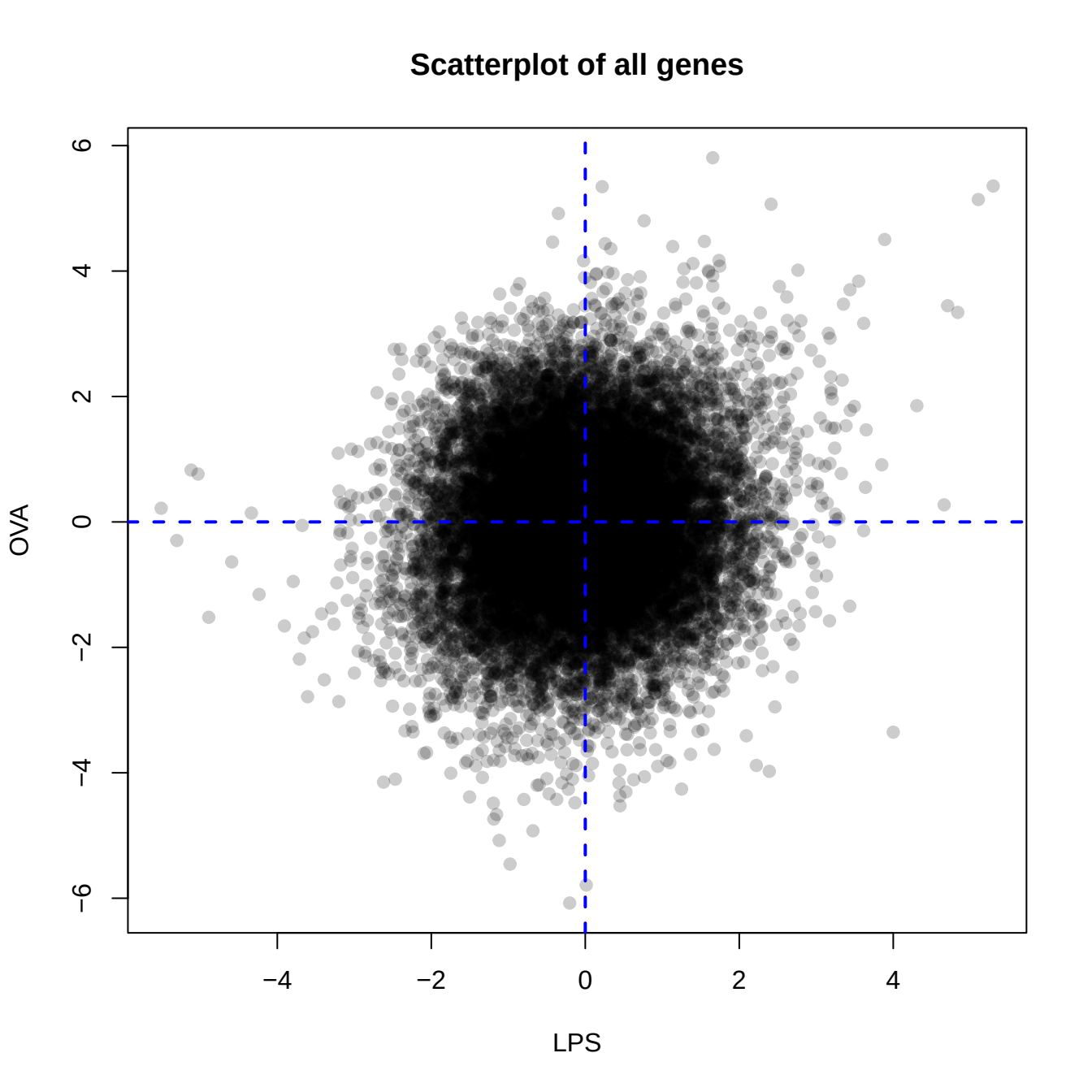
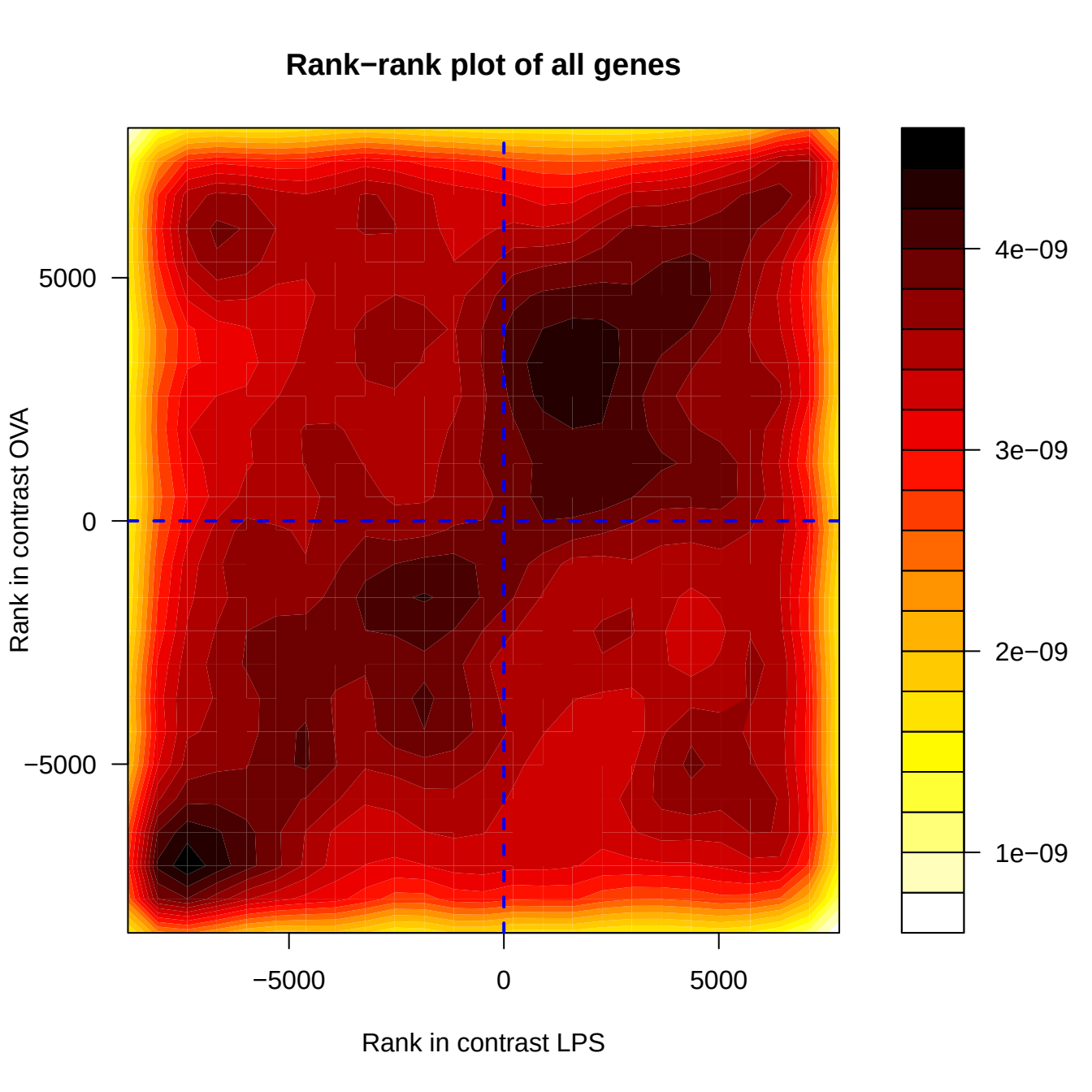
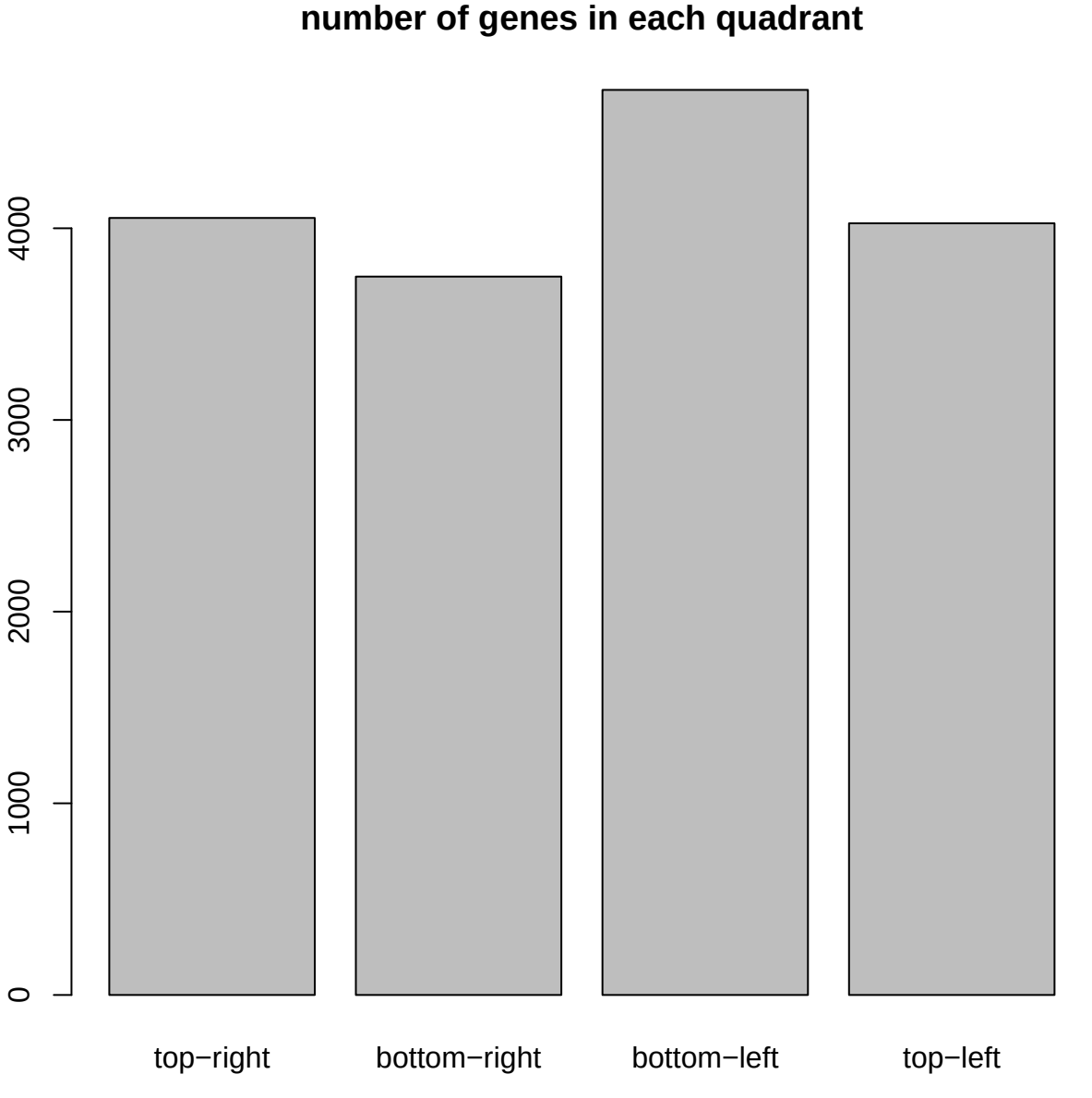
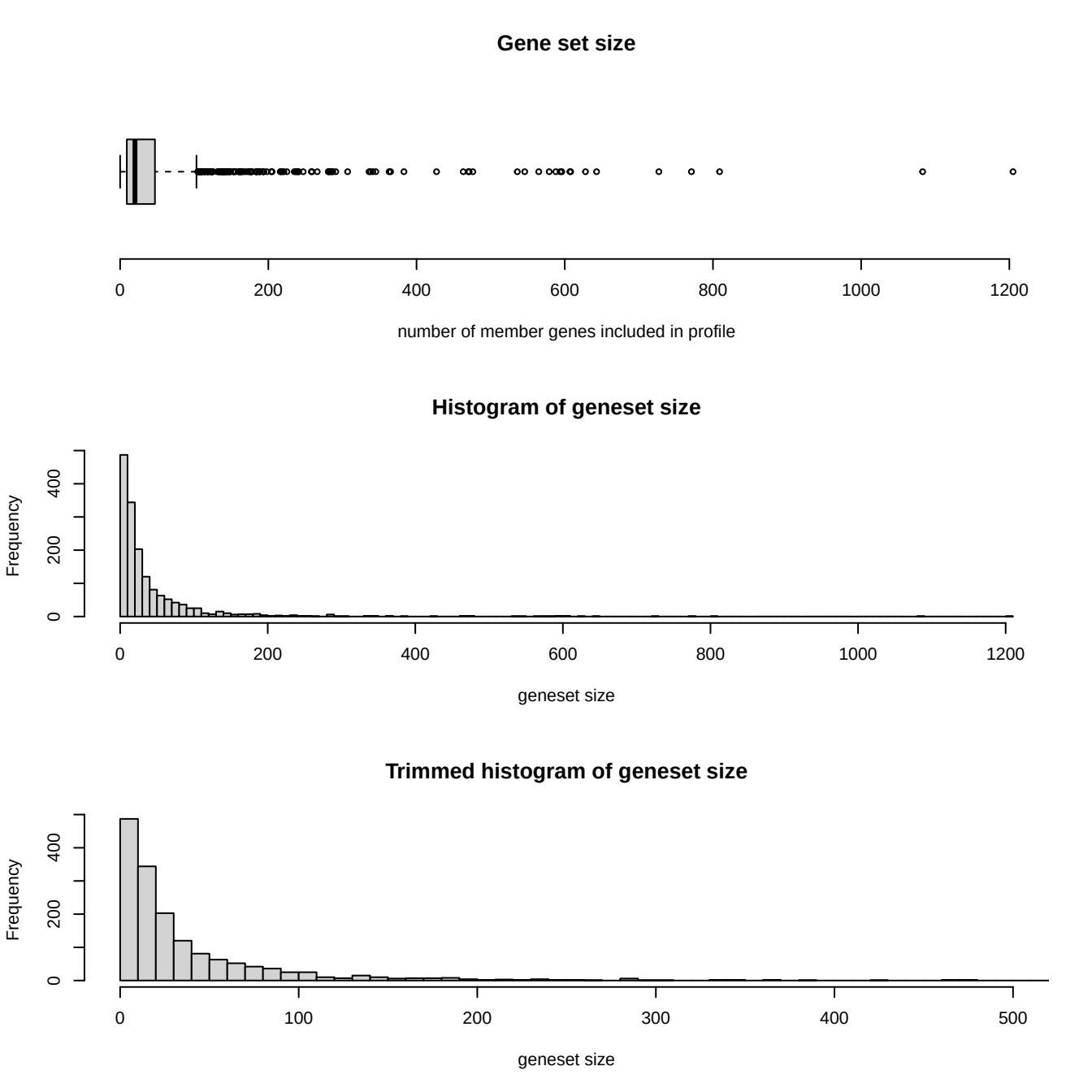
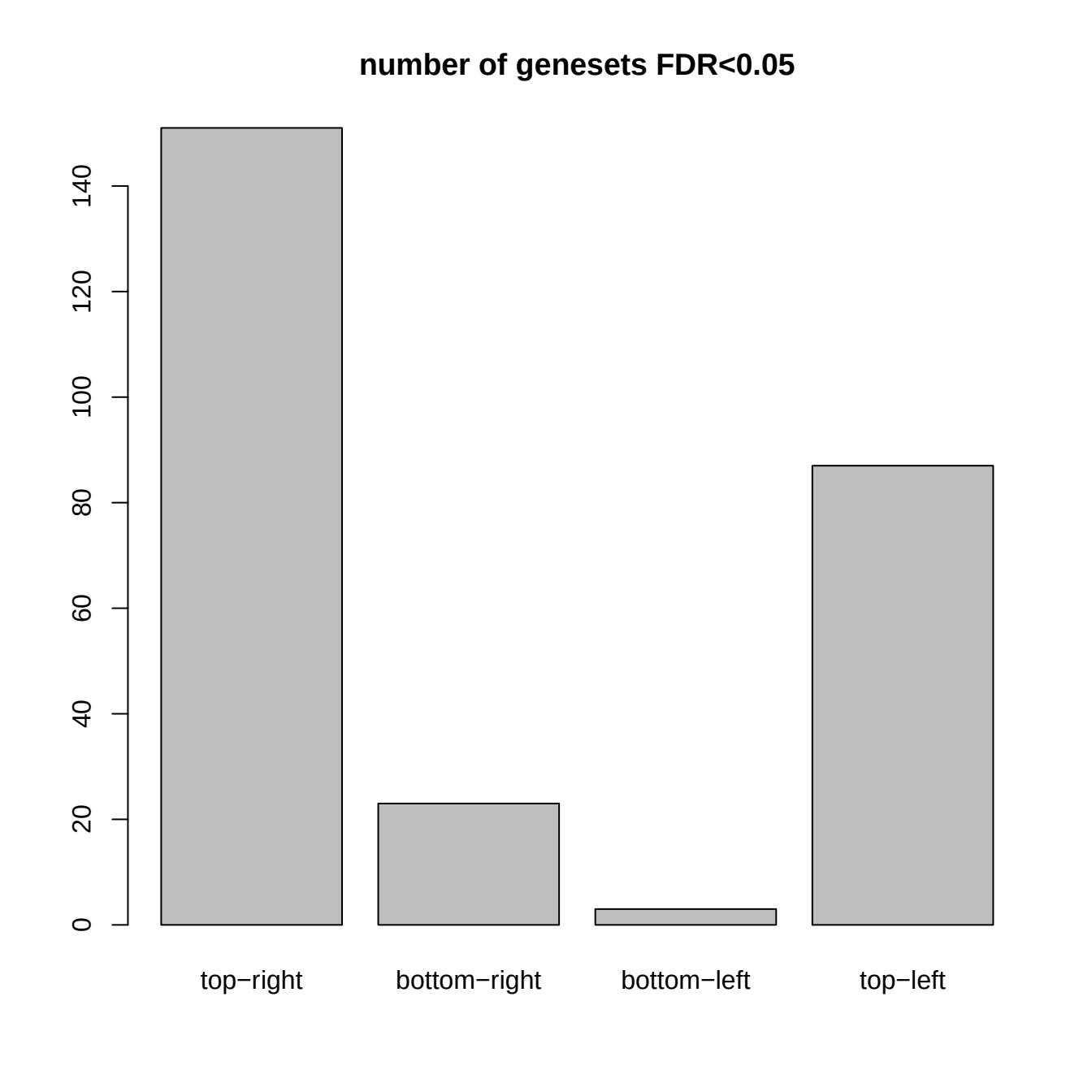
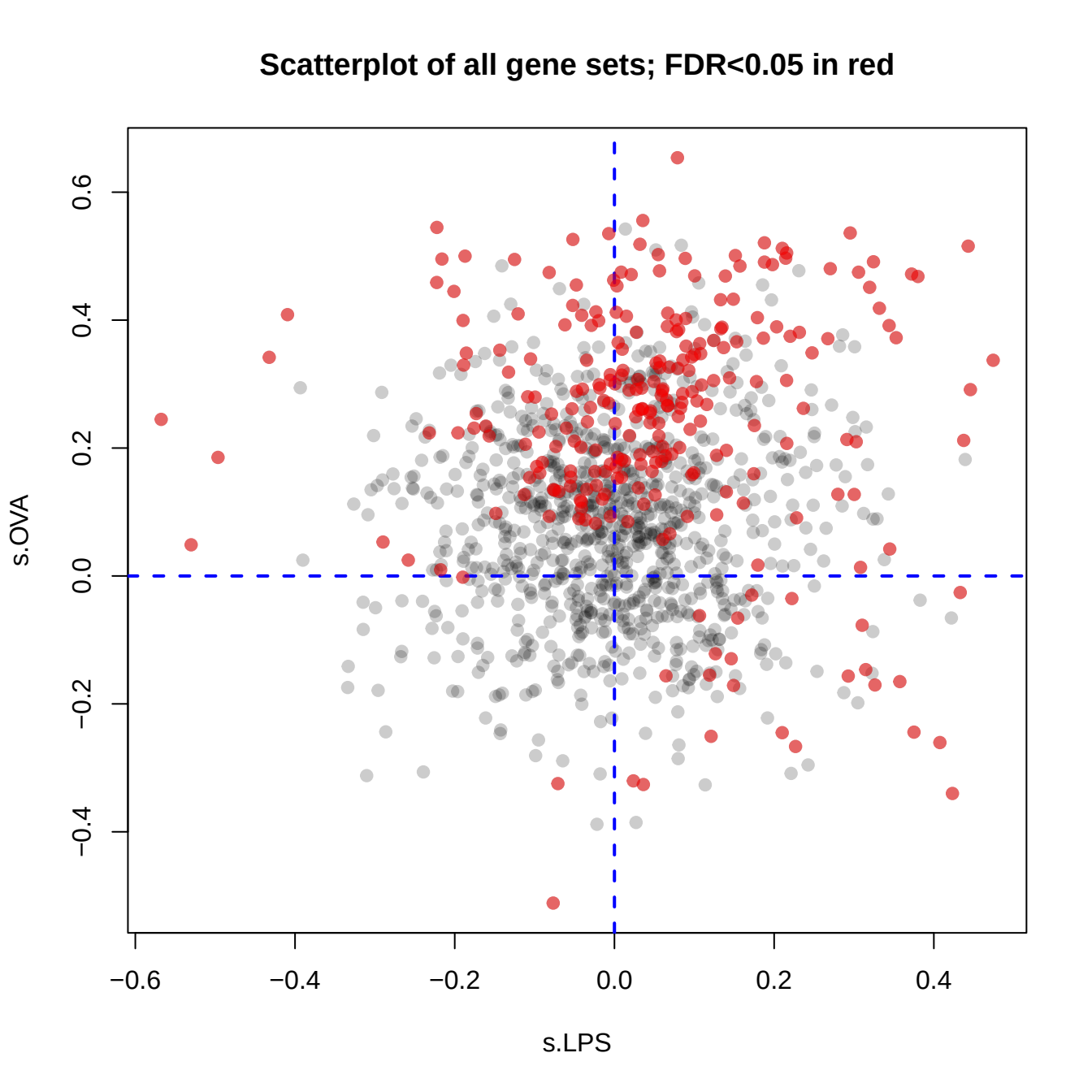

Scatterplot of all genes
OVA
LPS
6
4
2
0
−2
−4
−6
−4
−2
0
2
4

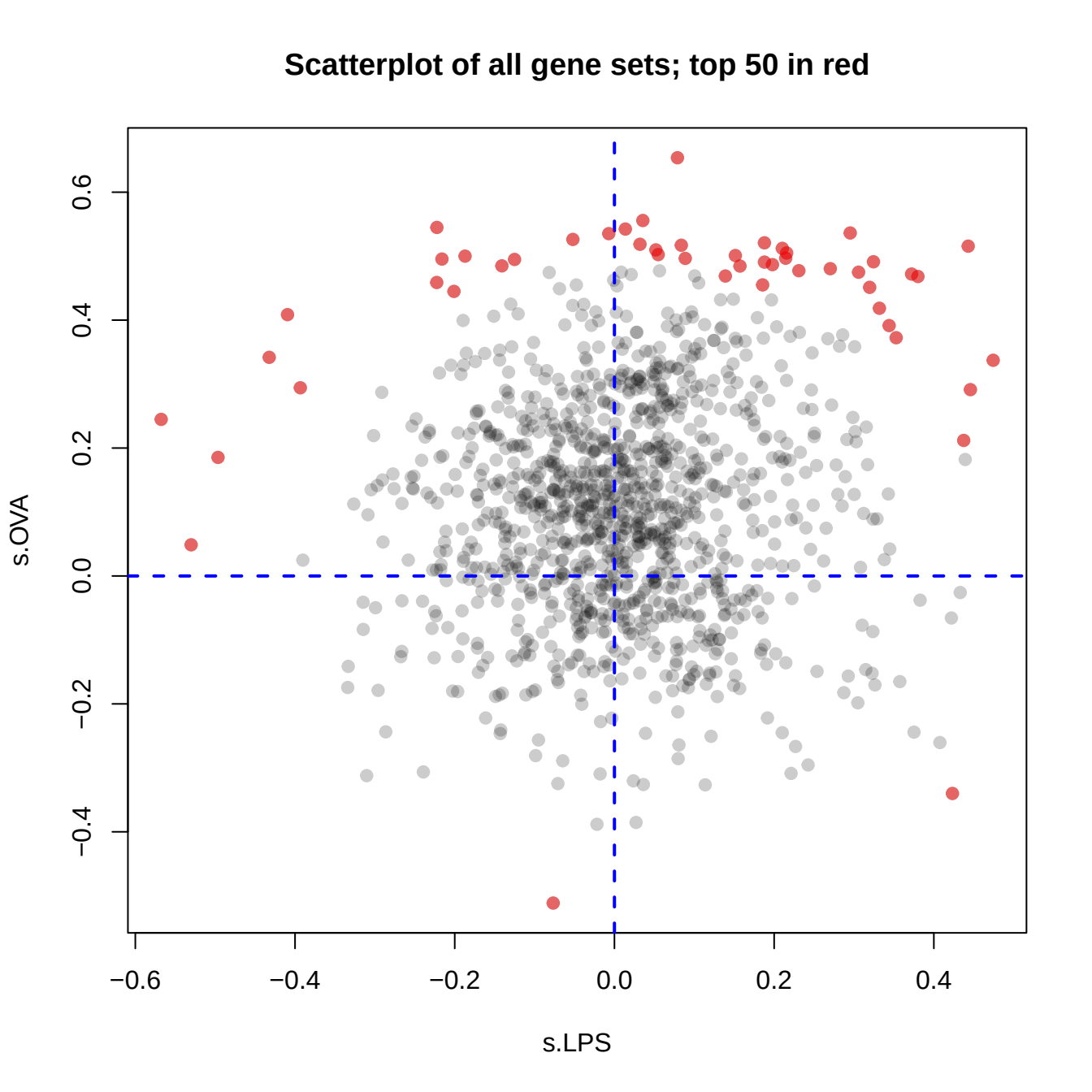

Rank−rank plot of all genes
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
4e−09
3e−09
2e−09
1e−09

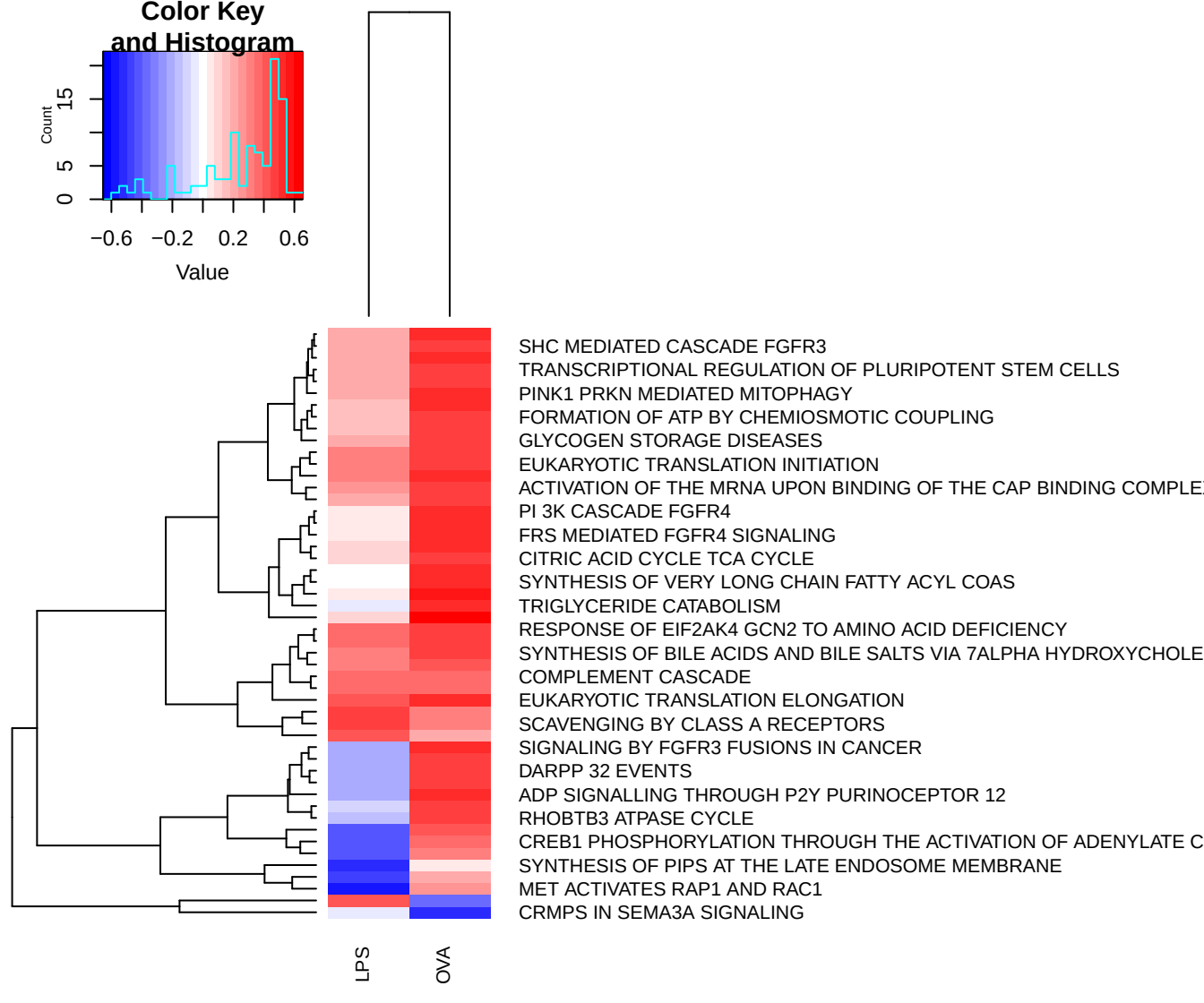

number of genes in each quadrant
0
1000
2000
3000
4000
top−right
bottom−right
bottom−left
top−left

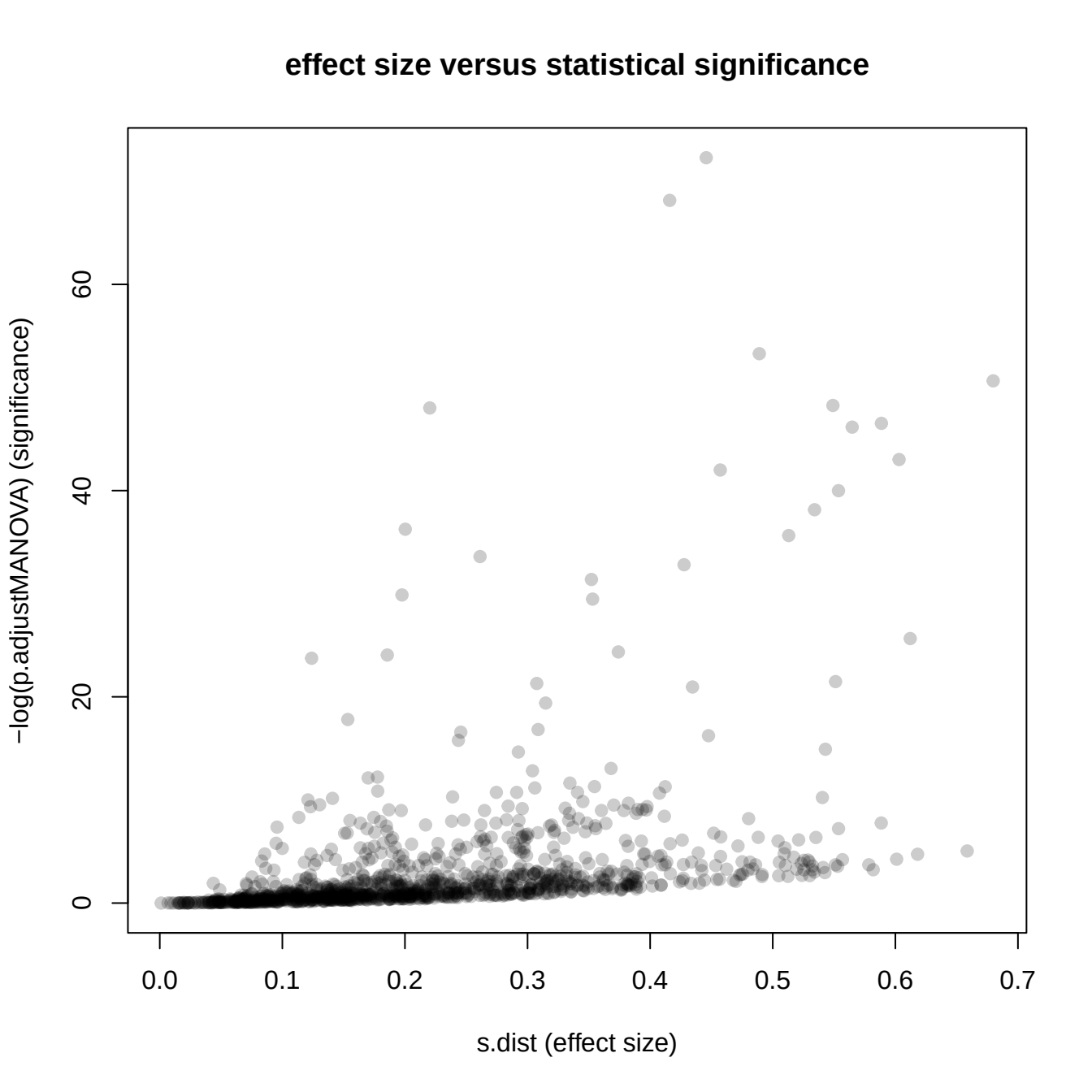

Gene set size
0
200
400
600
800
1000
1200
number of member genes included in profile
Histogram of geneset size
Frequency
0
200
400
0
200
400
600
800
1000
1200
geneset size
Trimmed histogram of geneset size
Frequency
0
200
400
0
100
200
300
400
500
geneset size

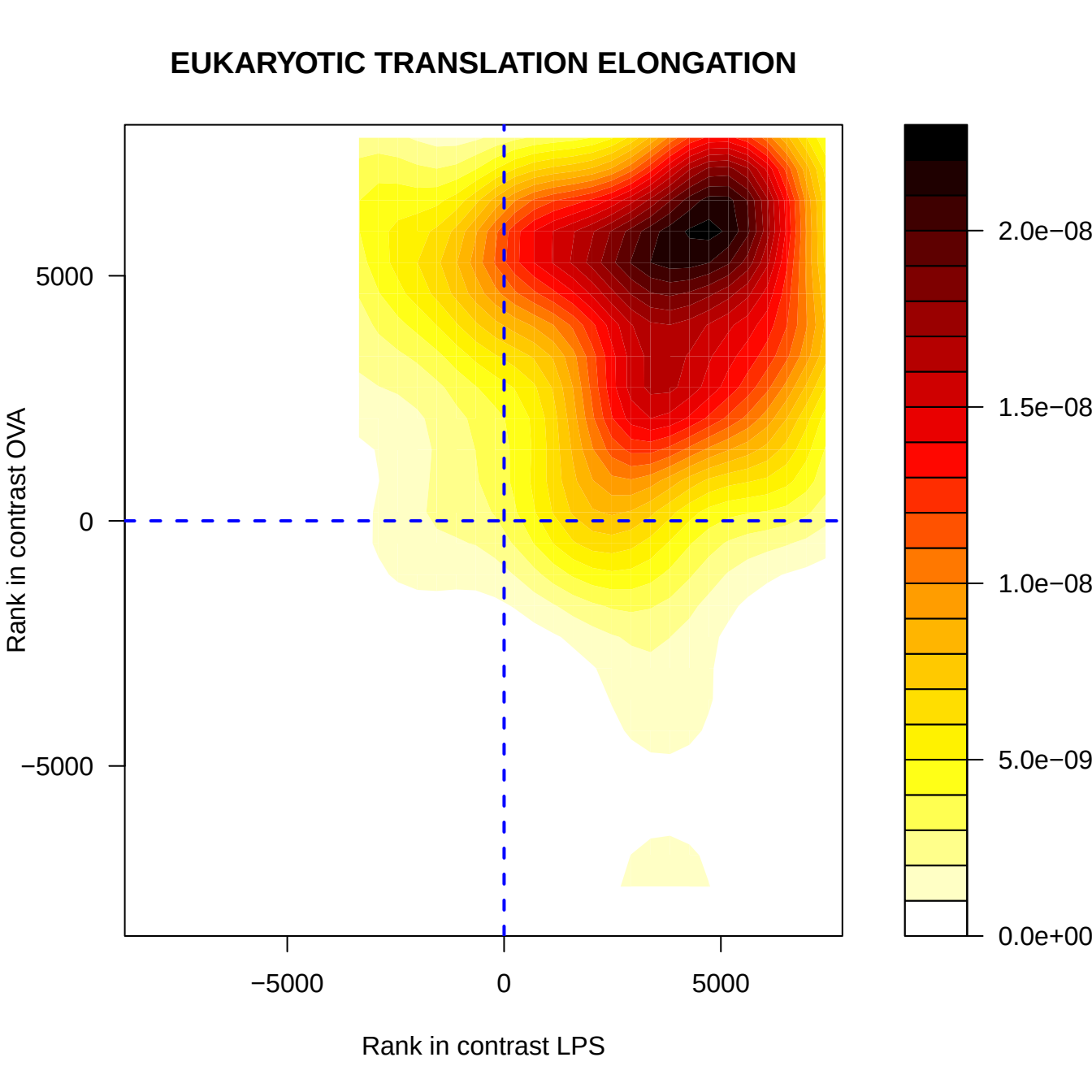

number of genesets FDR<0.05
0
20
40
60
80
100
120
140
top−right
bottom−right
bottom−left
top−left

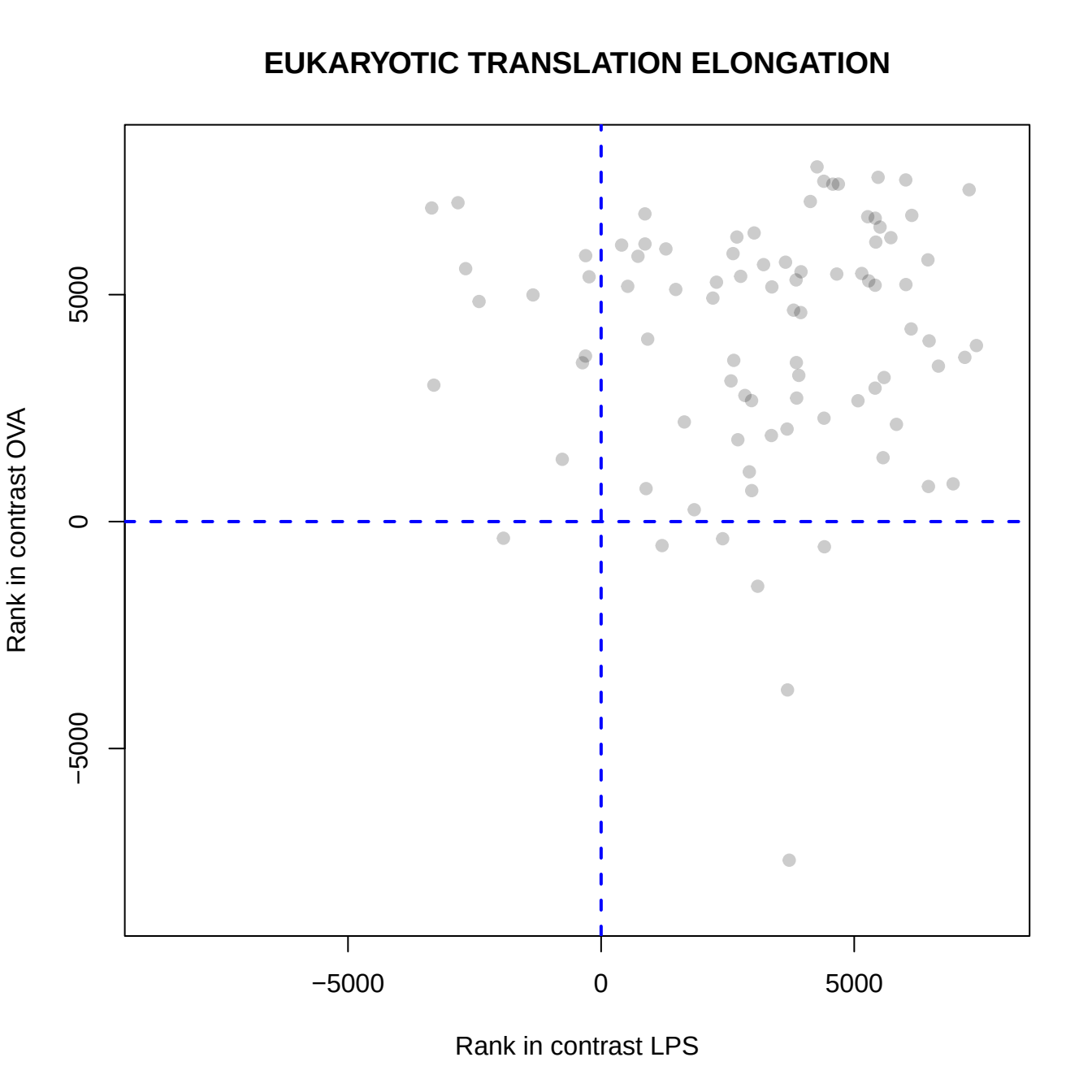

Scatterplot of all gene sets; FDR<0.05 in red
s.OVA
s.LPS
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.4
−0.2
0.0
0.2
0.4

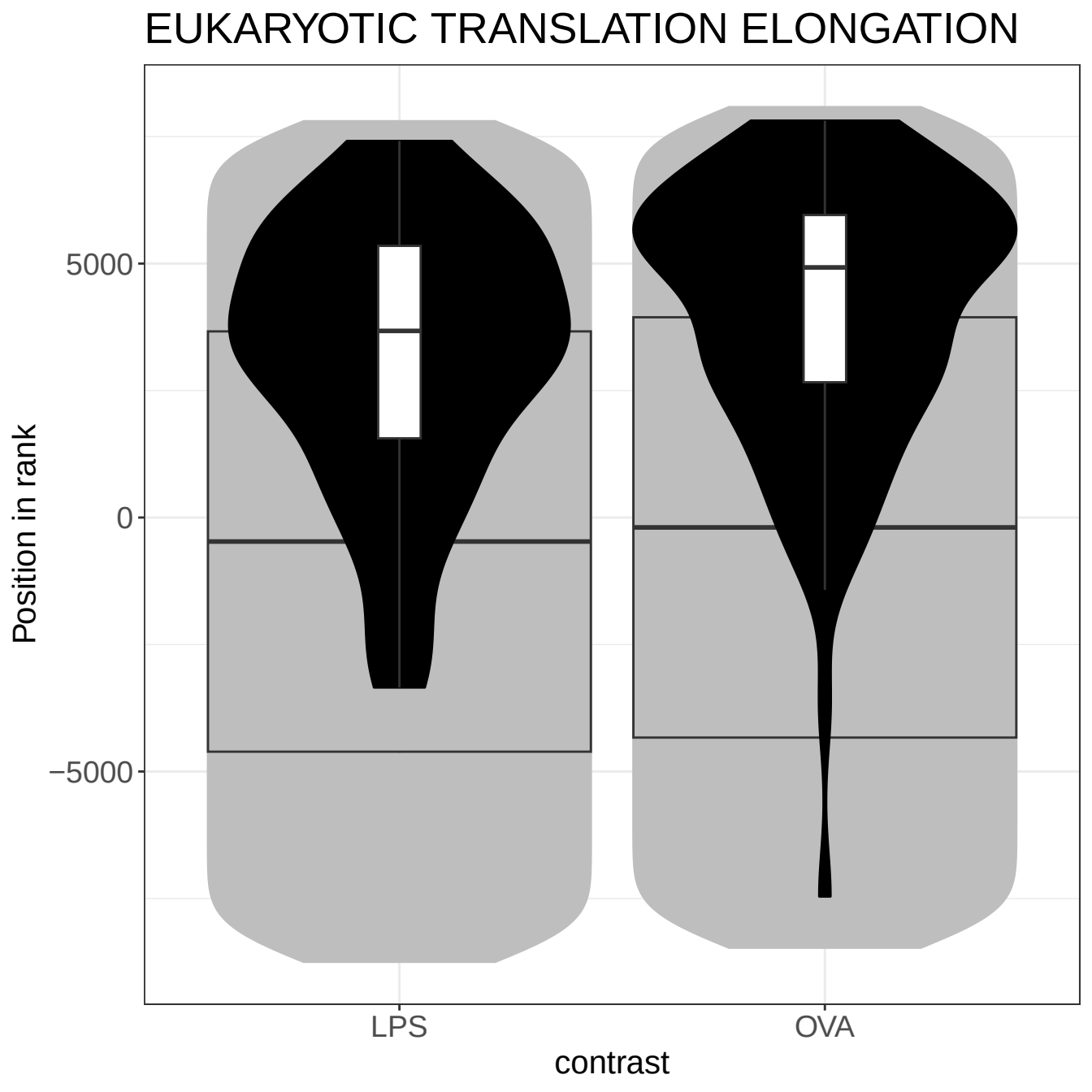

Scatterplot of all gene sets; top 50 in red
s.OVA
s.LPS
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.4
−0.2
0.0
0.2
0.4

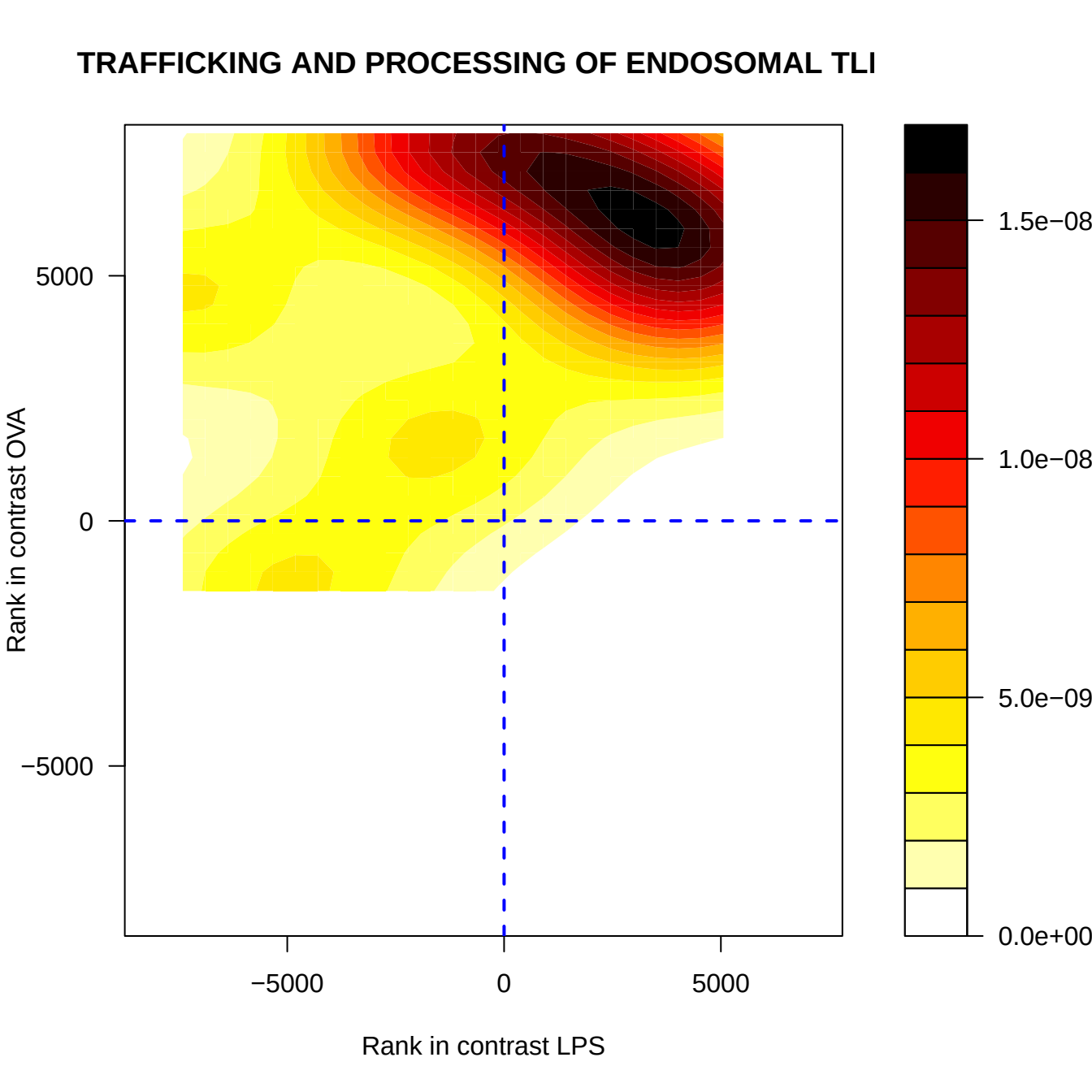

Color Key and Histogram
Count
0
5
15
−0.6
−0.2
0.2
0.6
Value
SHC MEDIATED CASCADE FGFR3
TRANSCRIPTIONAL REGULATION OF PLURIPOTENT STEM CELLS
PINK1 PRKN MEDIATED MITOPHAGY
FORMATION OF ATP BY CHEMIOSMOTIC COUPLING
GLYCOGEN STORAGE DISEASES
EUKARYOTIC TRANSLATION INITIATION
ACTIVATION OF THE MRNA UPON BINDING OF THE CAP BINDING COMPLE
PI 3K CASCADE FGFR4
FRS MEDIATED FGFR4 SIGNALING
CITRIC ACID CYCLE TCA CYCLE
SYNTHESIS OF VERY LONG CHAIN FATTY ACYL COAS
TRIGLYCERIDE CATABOLISM
RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID DEFICIENCY
SYNTHESIS OF BILE ACIDS AND BILE SALTS VIA 7ALPHA HYDROXYCHOLE
COMPLEMENT CASCADE
EUKARYOTIC TRANSLATION ELONGATION
SCAVENGING BY CLASS A RECEPTORS
SIGNALING BY FGFR3 FUSIONS IN CANCER
DARPP 32 EVENTS
ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 12
RHOBTB3 ATPASE CYCLE
CREB1 PHOSPHORYLATION THROUGH THE ACTIVATION OF ADENYLATE C
SYNTHESIS OF PIPS AT THE LATE ENDOSOME MEMBRANE
MET ACTIVATES RAP1 AND RAC1
CRMPS IN SEMA3A SIGNALING
LPS
OVA

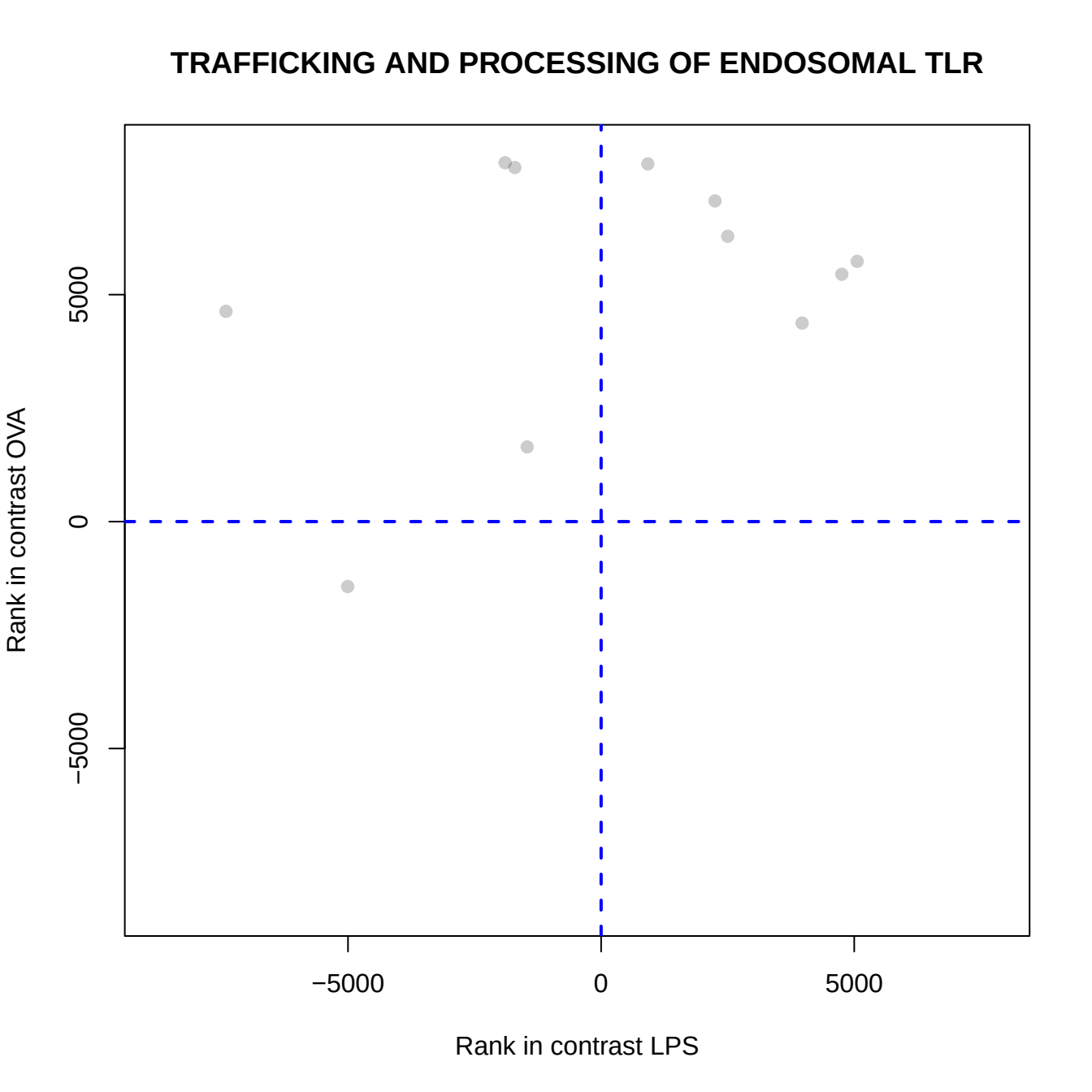

effect size versus statistical significance
−log(p.adjustMANOVA) (significance)
0
20
40
60
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
s.dist (effect size)

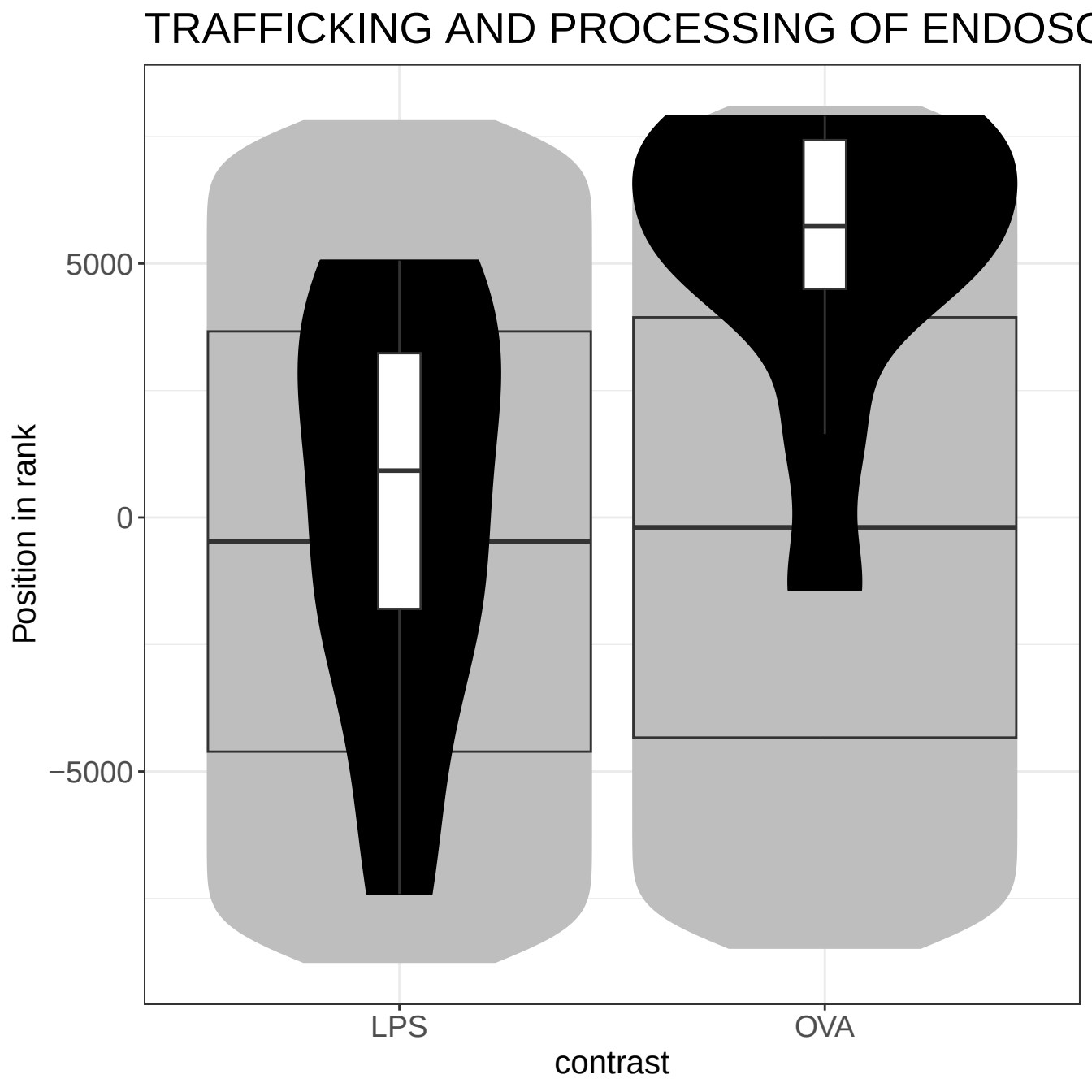

EUKARYOTIC TRANSLATION ELONGATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

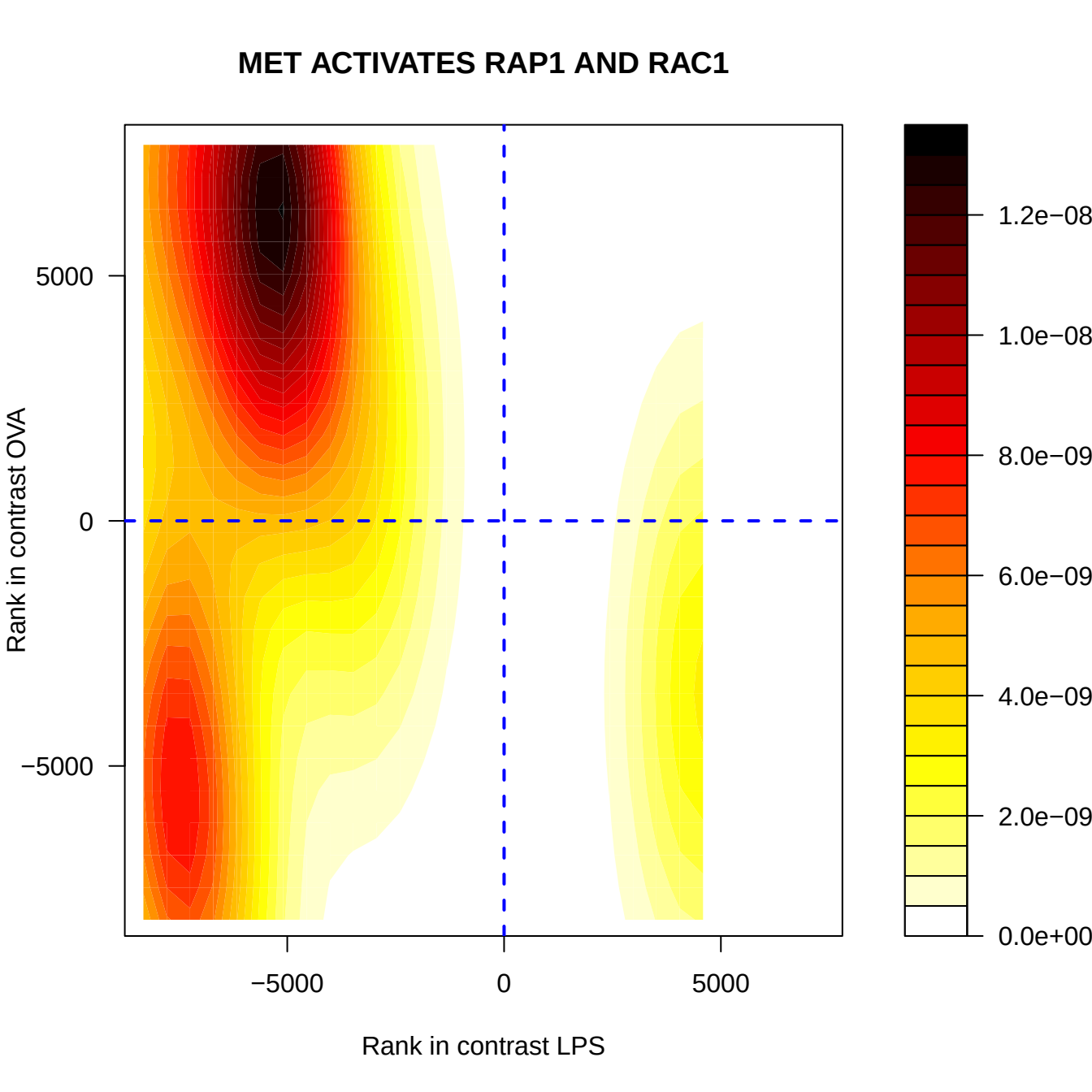

EUKARYOTIC TRANSLATION ELONGATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

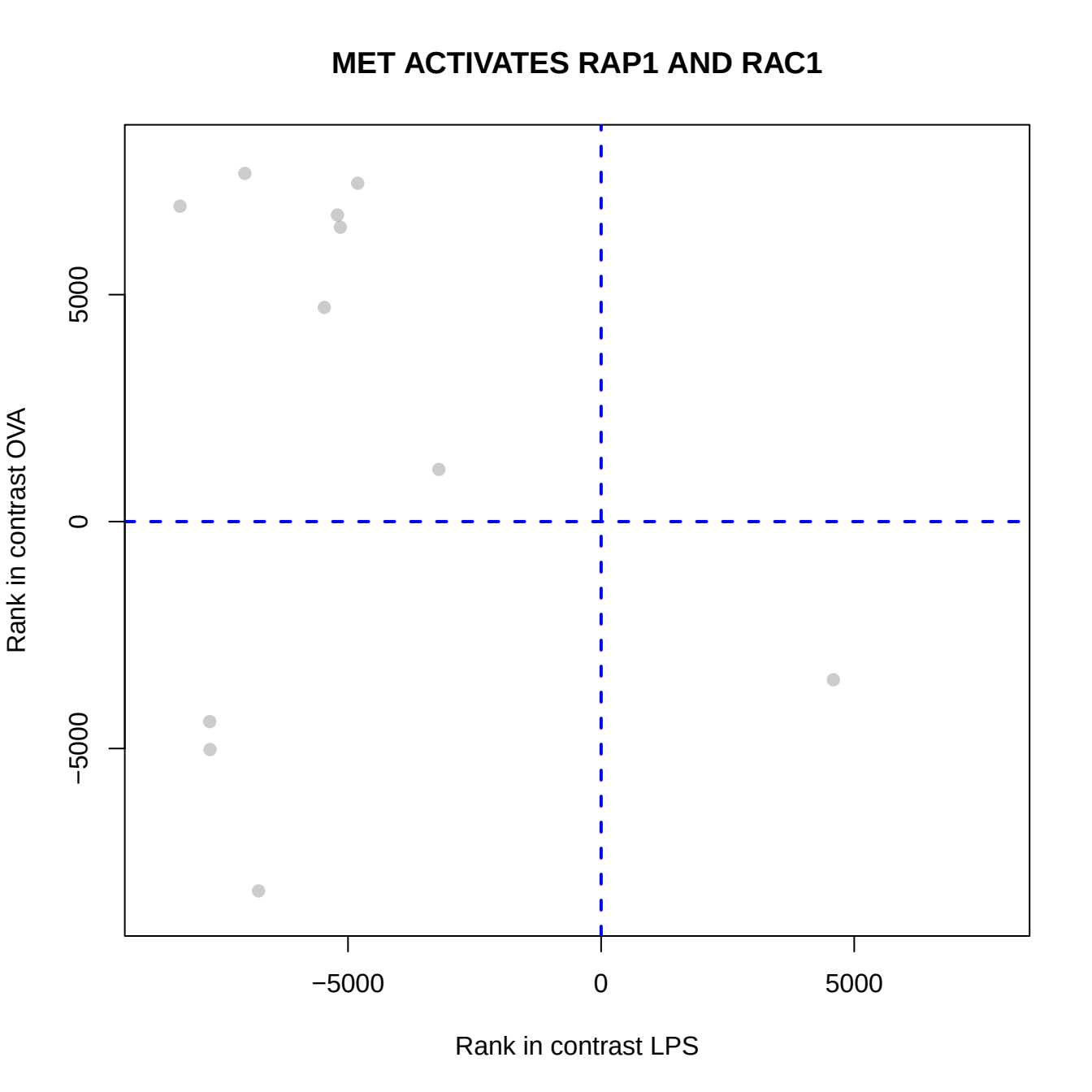

EUKARYOTIC TRANSLATION ELONGATION
5000
0
−5000
Position in rank
LPS
OVA
contrast

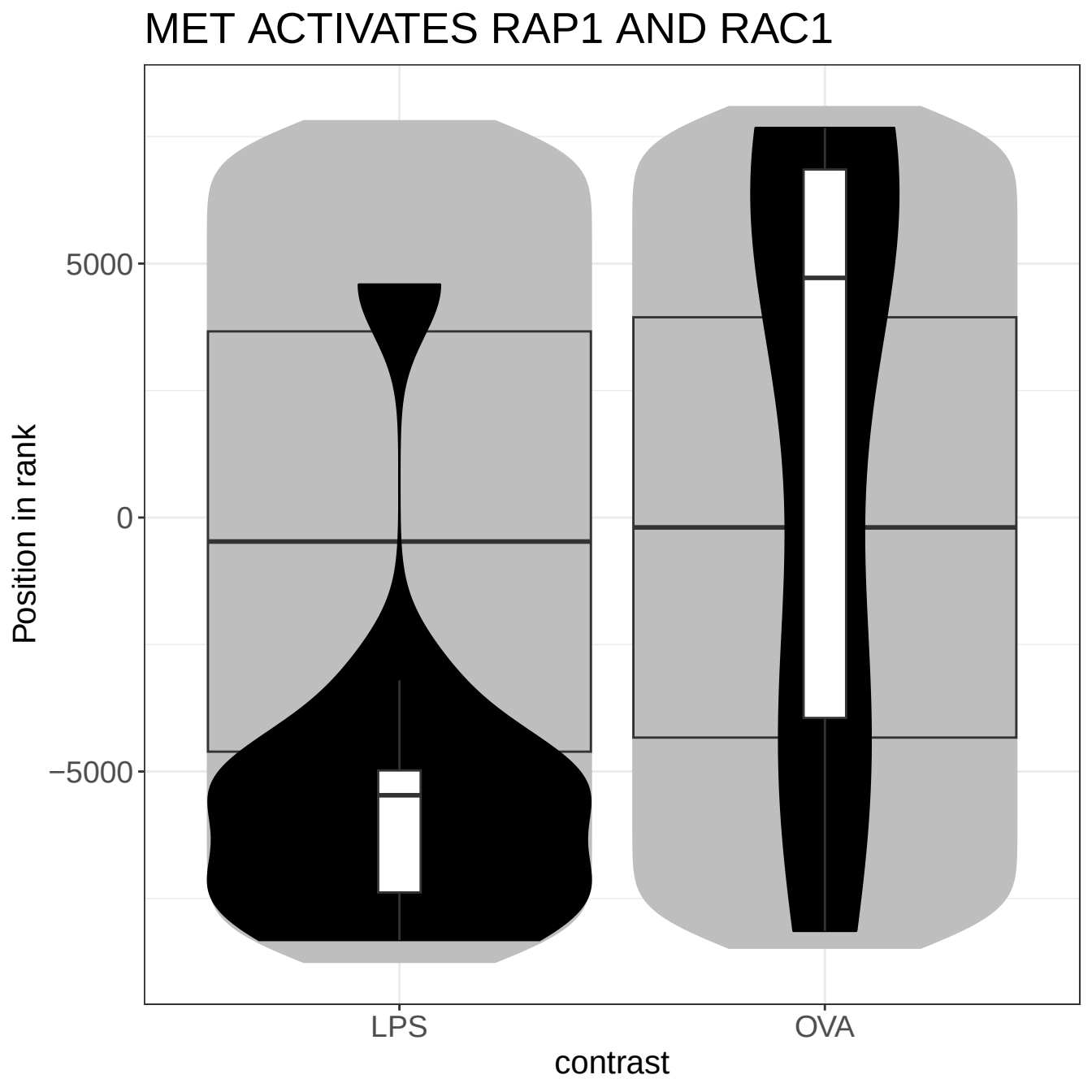

TRAFFICKING AND PROCESSING OF ENDOSOMAL TLI
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

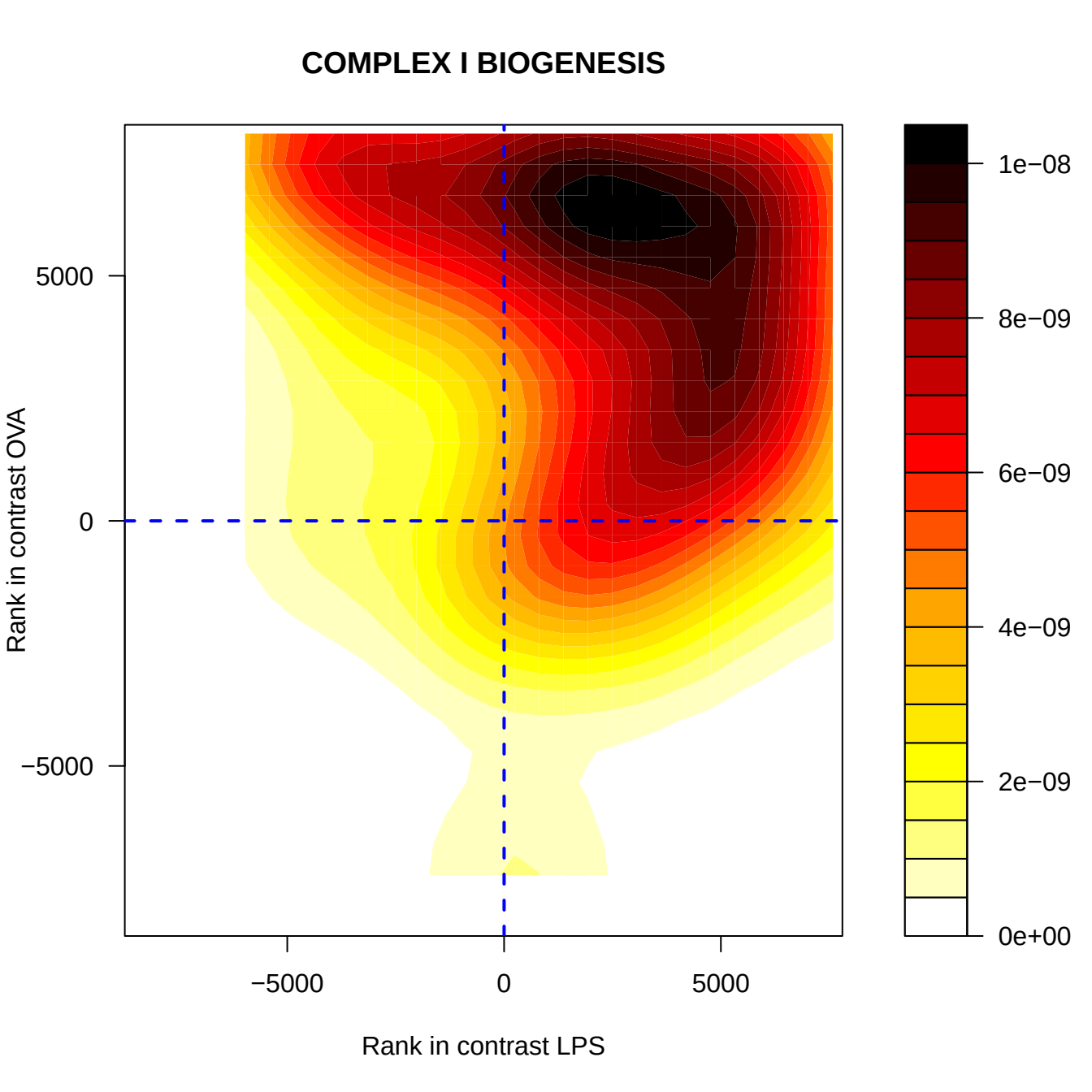

TRAFFICKING AND PROCESSING OF ENDOSOMAL TLR
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

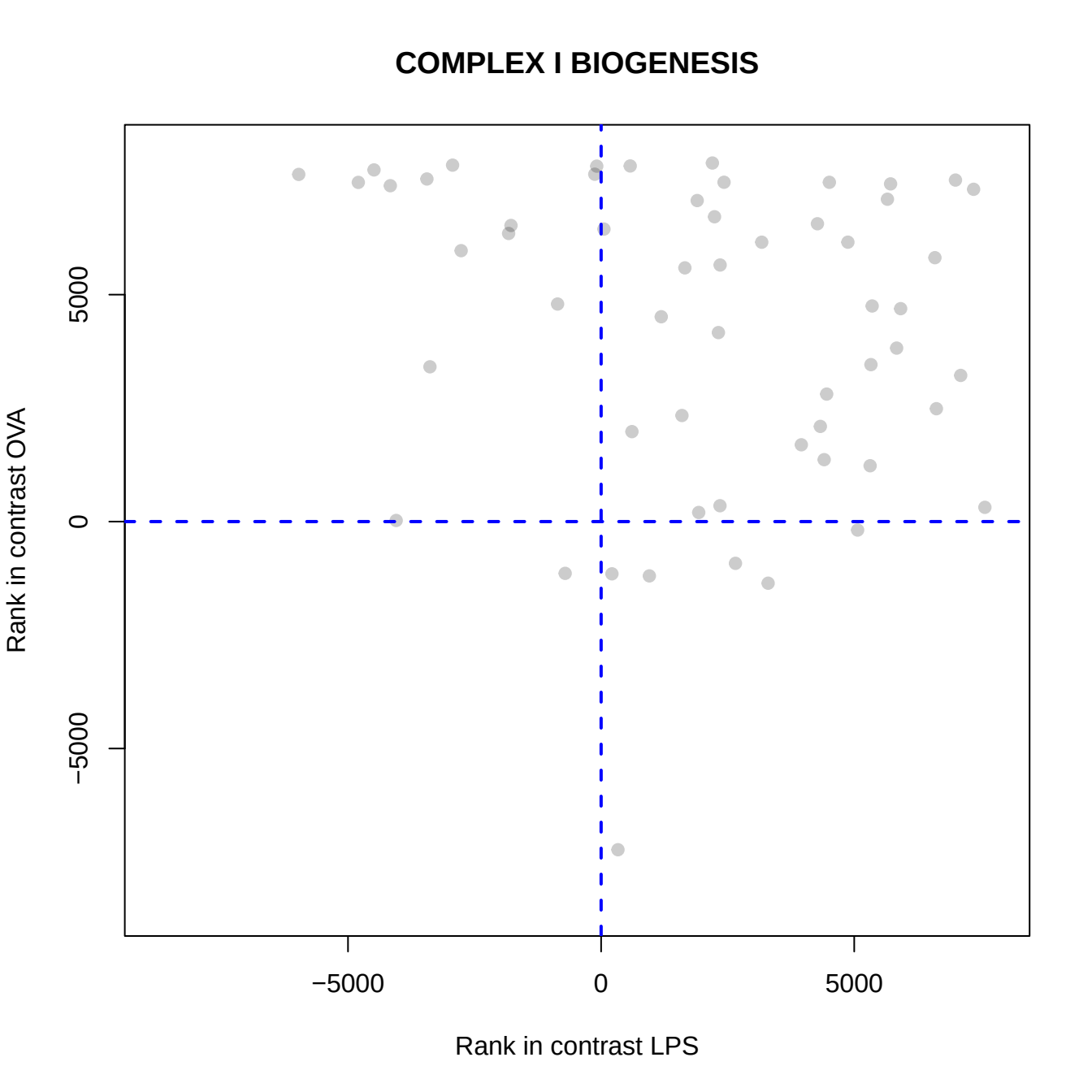

TRAFFICKING AND PROCESSING OF ENDOSO
5000
0
−5000
Position in rank
LPS
OVA
contrast

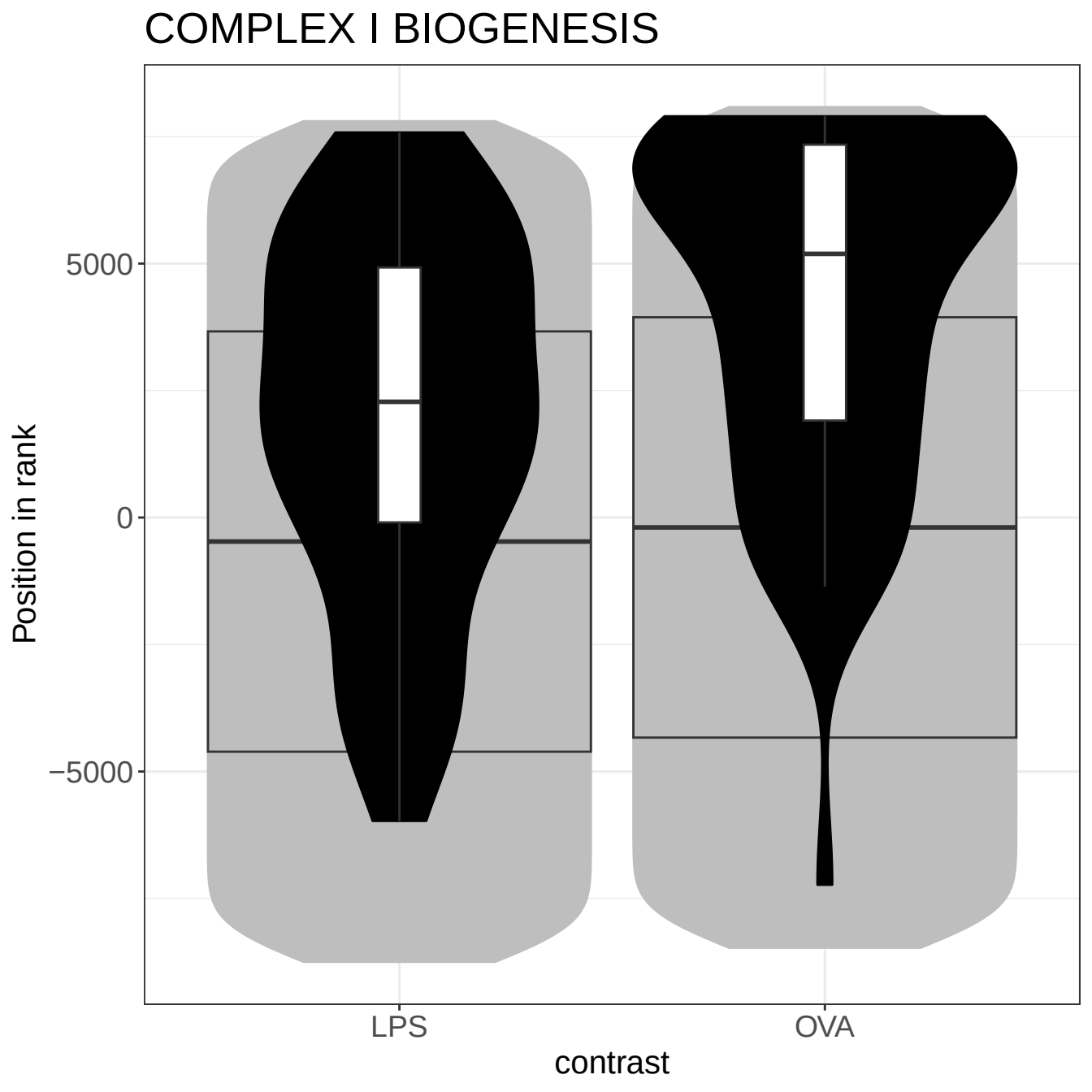

MET ACTIVATES RAP1 AND RAC1
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

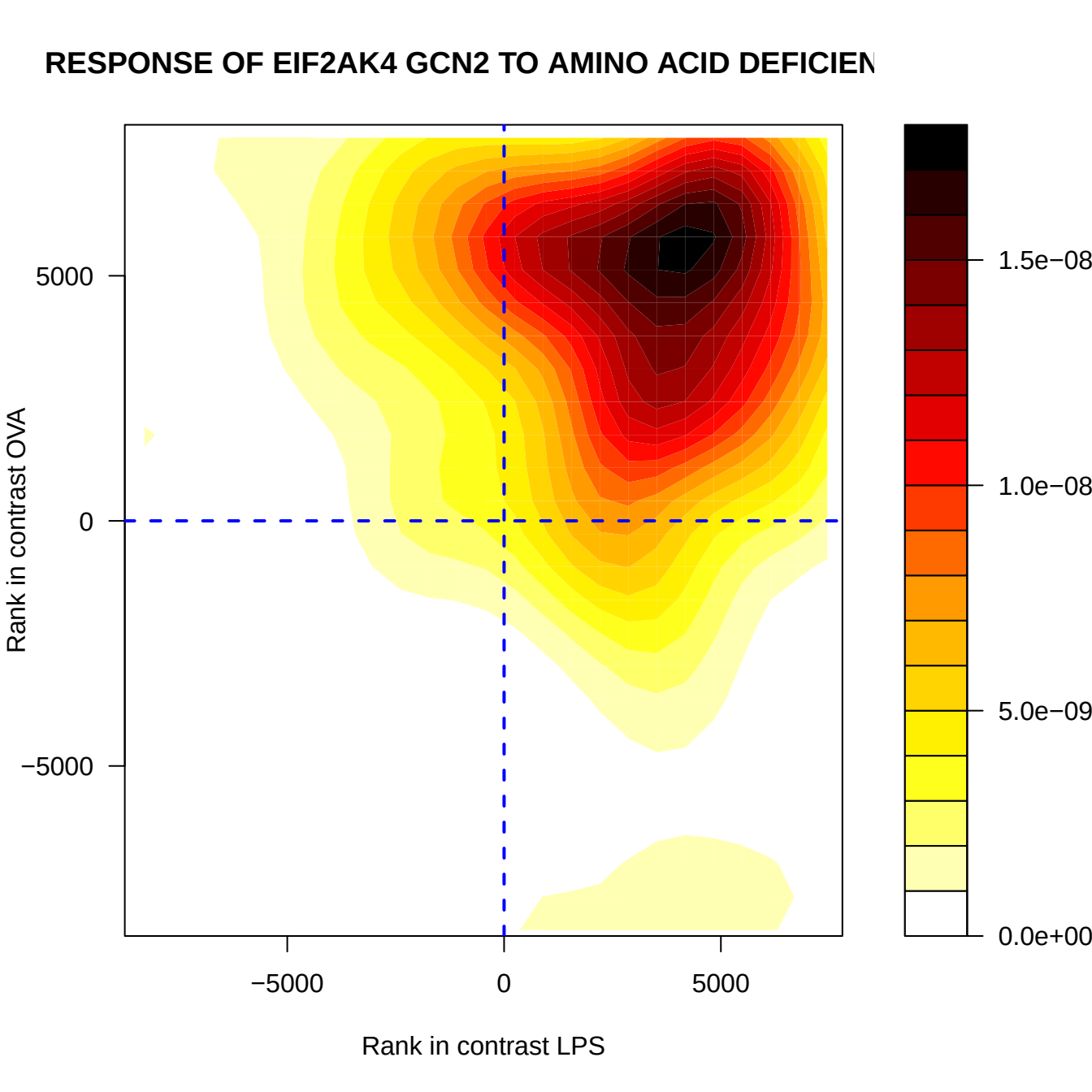

MET ACTIVATES RAP1 AND RAC1
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

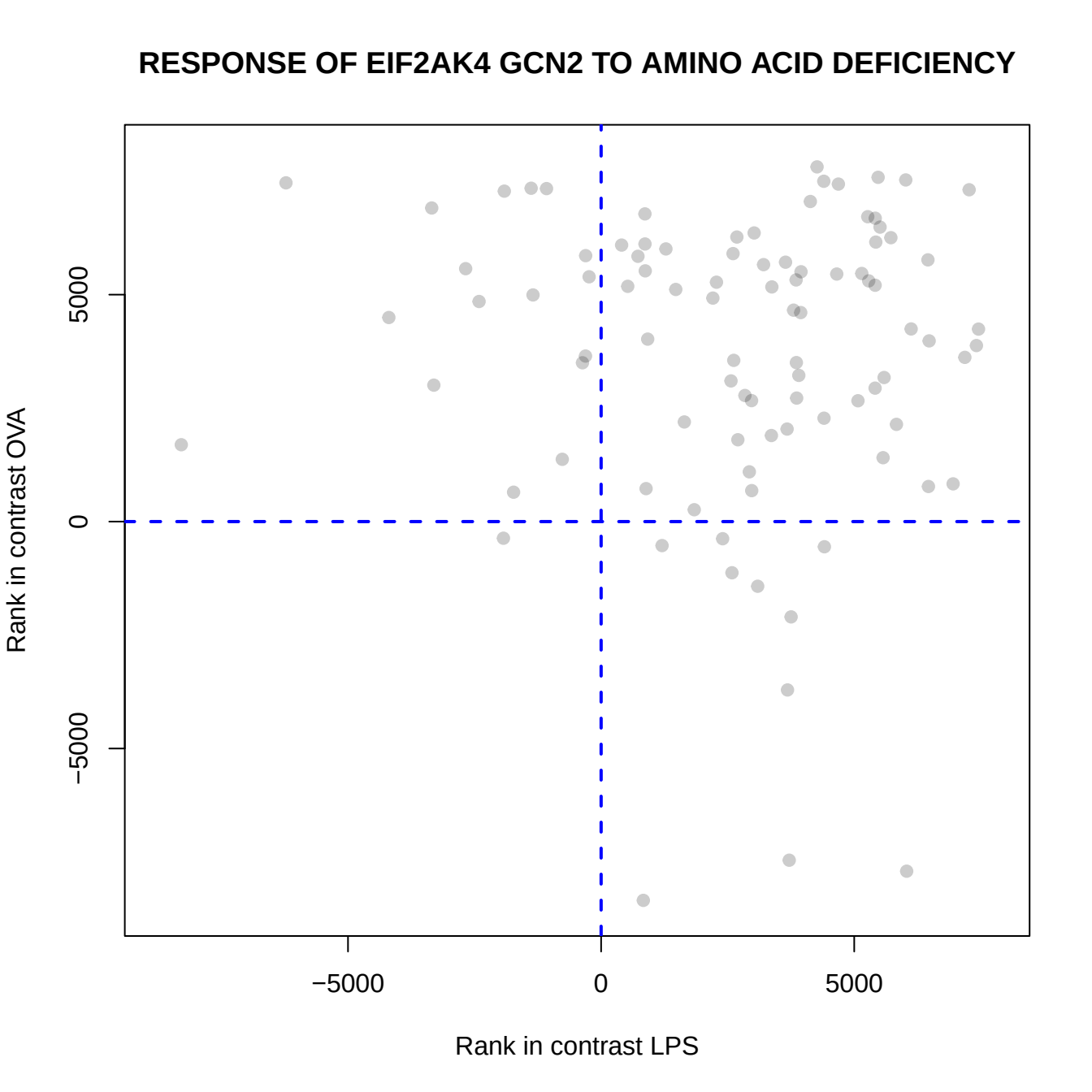

MET ACTIVATES RAP1 AND RAC1
5000
0
−5000
Position in rank
LPS
OVA
contrast

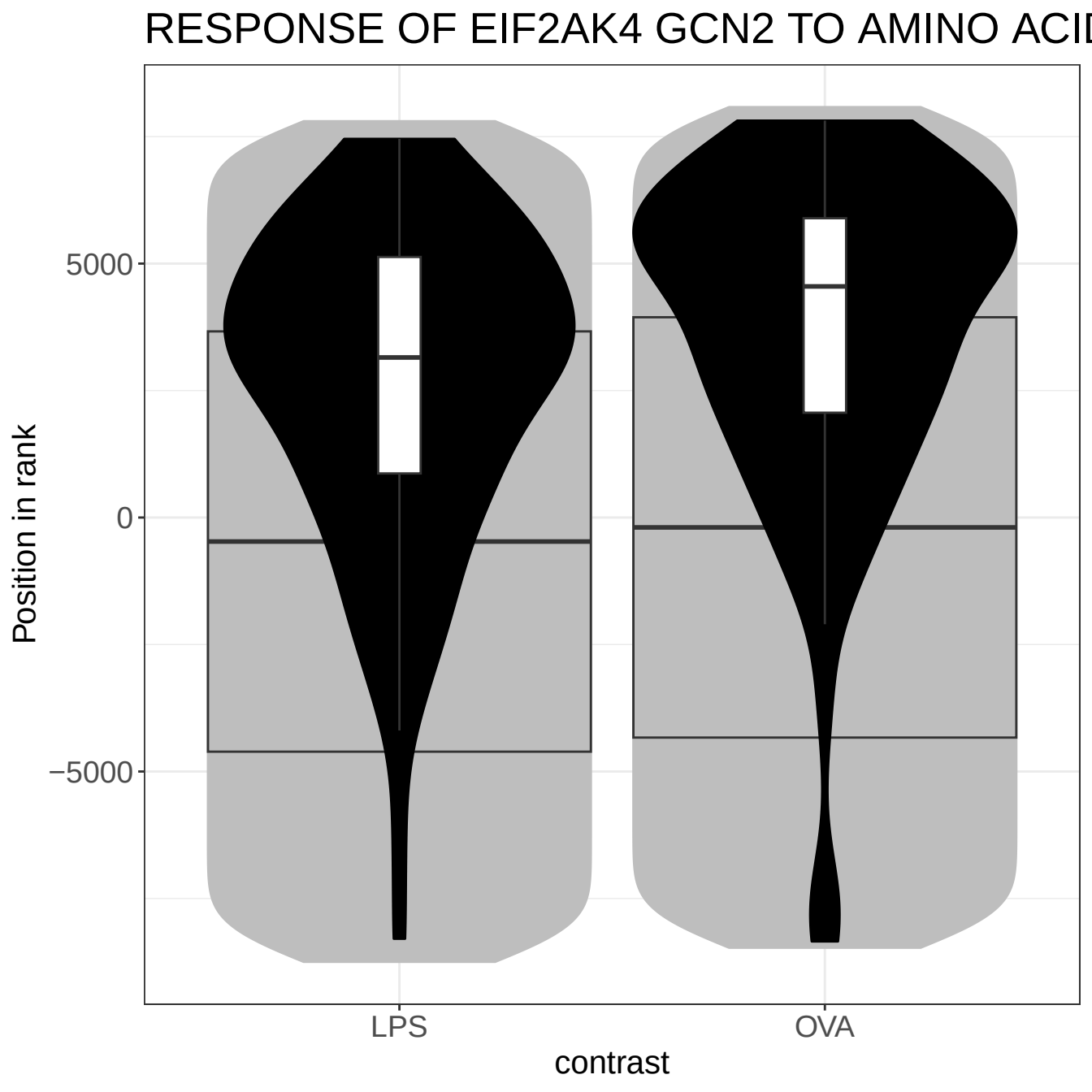

COMPLEX I BIOGENESIS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

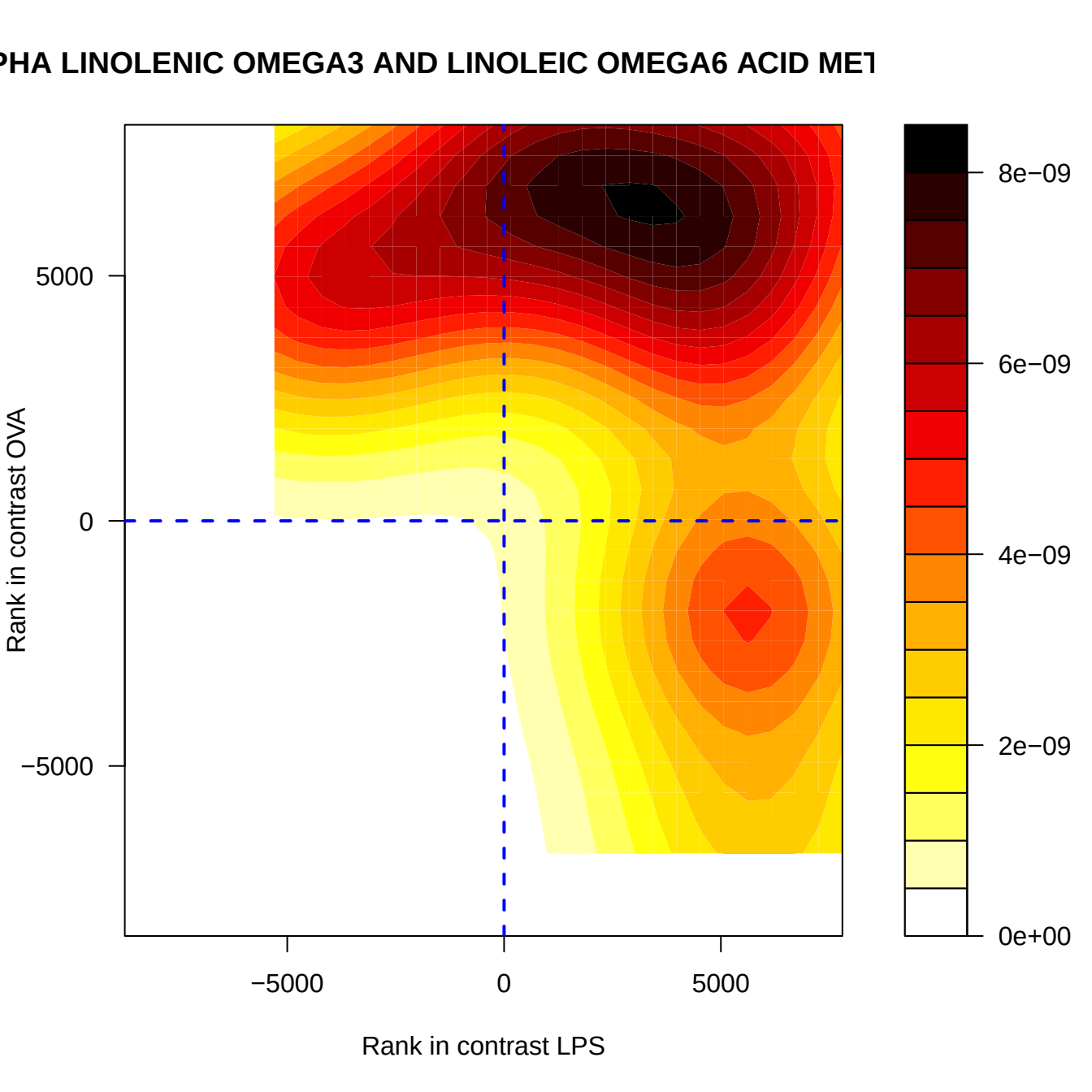

COMPLEX I BIOGENESIS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

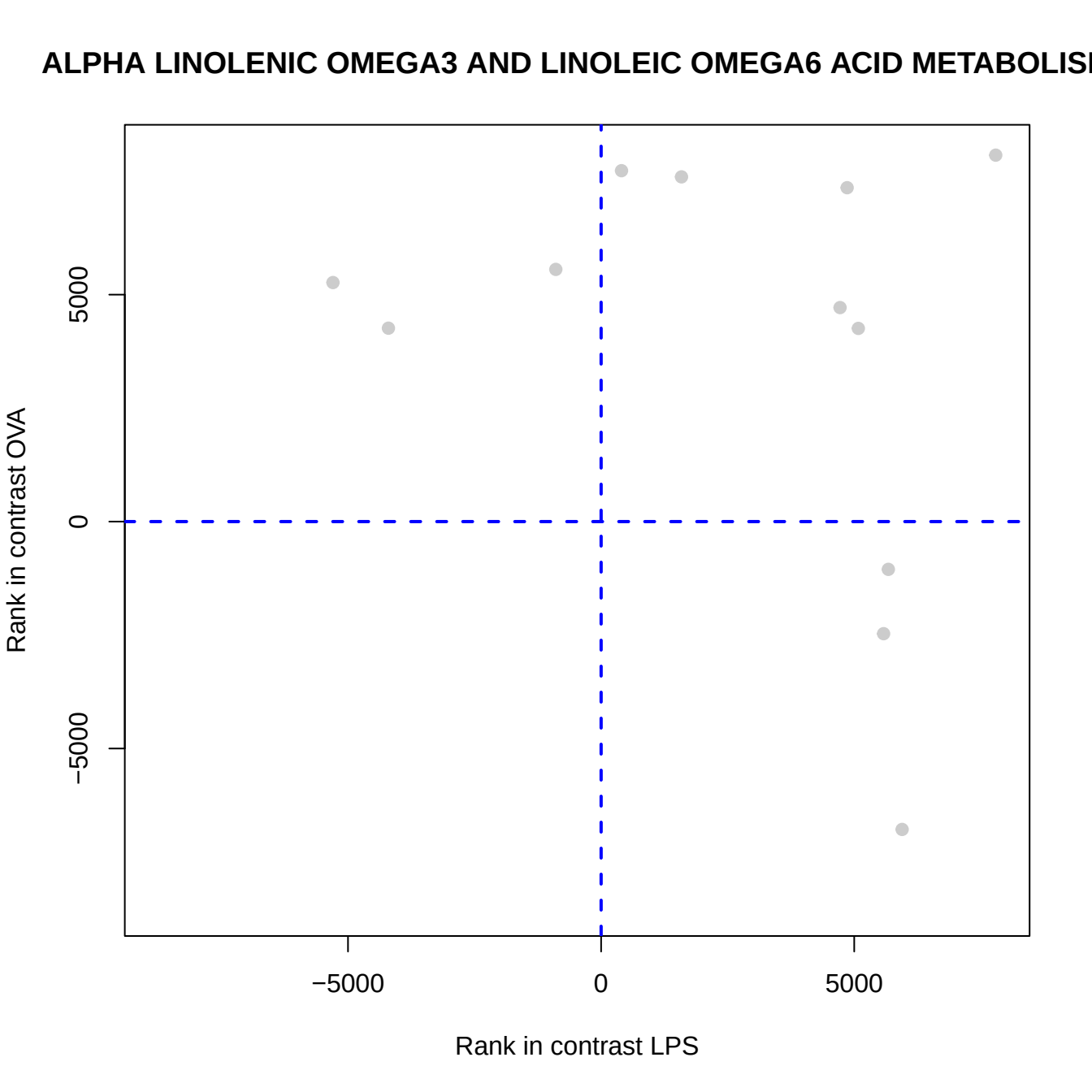

COMPLEX I BIOGENESIS
5000
0
−5000
Position in rank
LPS
OVA
contrast

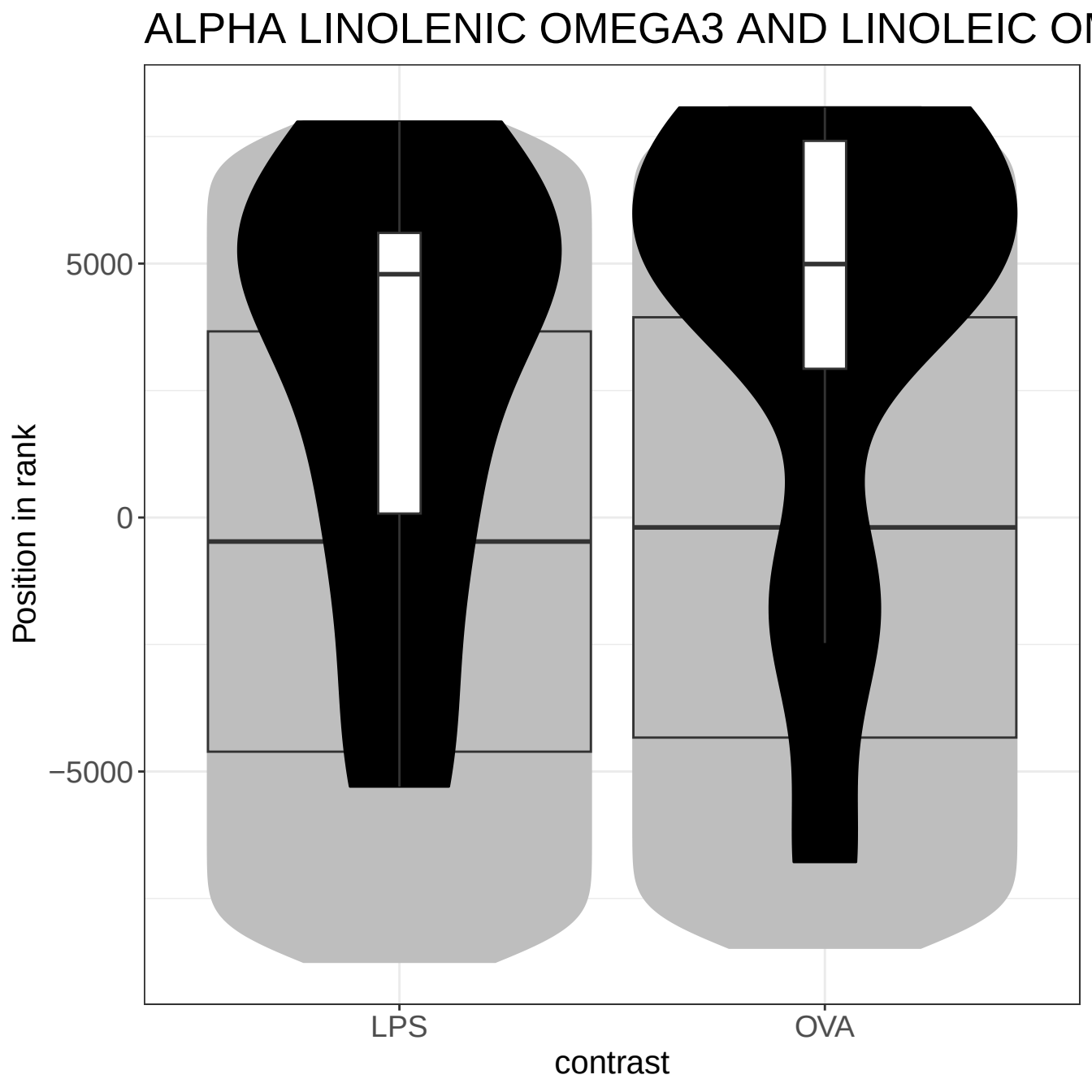

RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID DEFICIEN
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

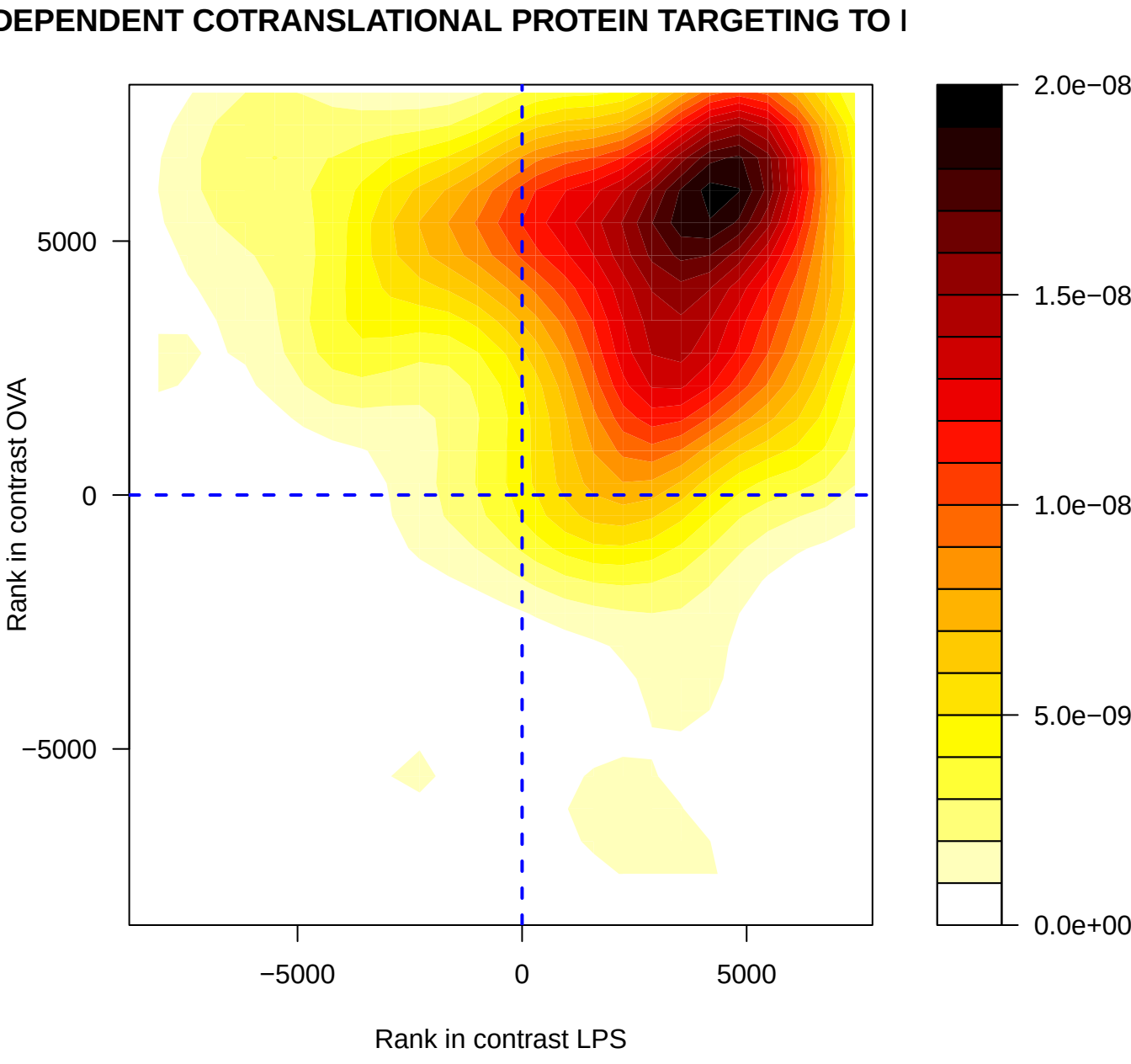

RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID DEFICIENCY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

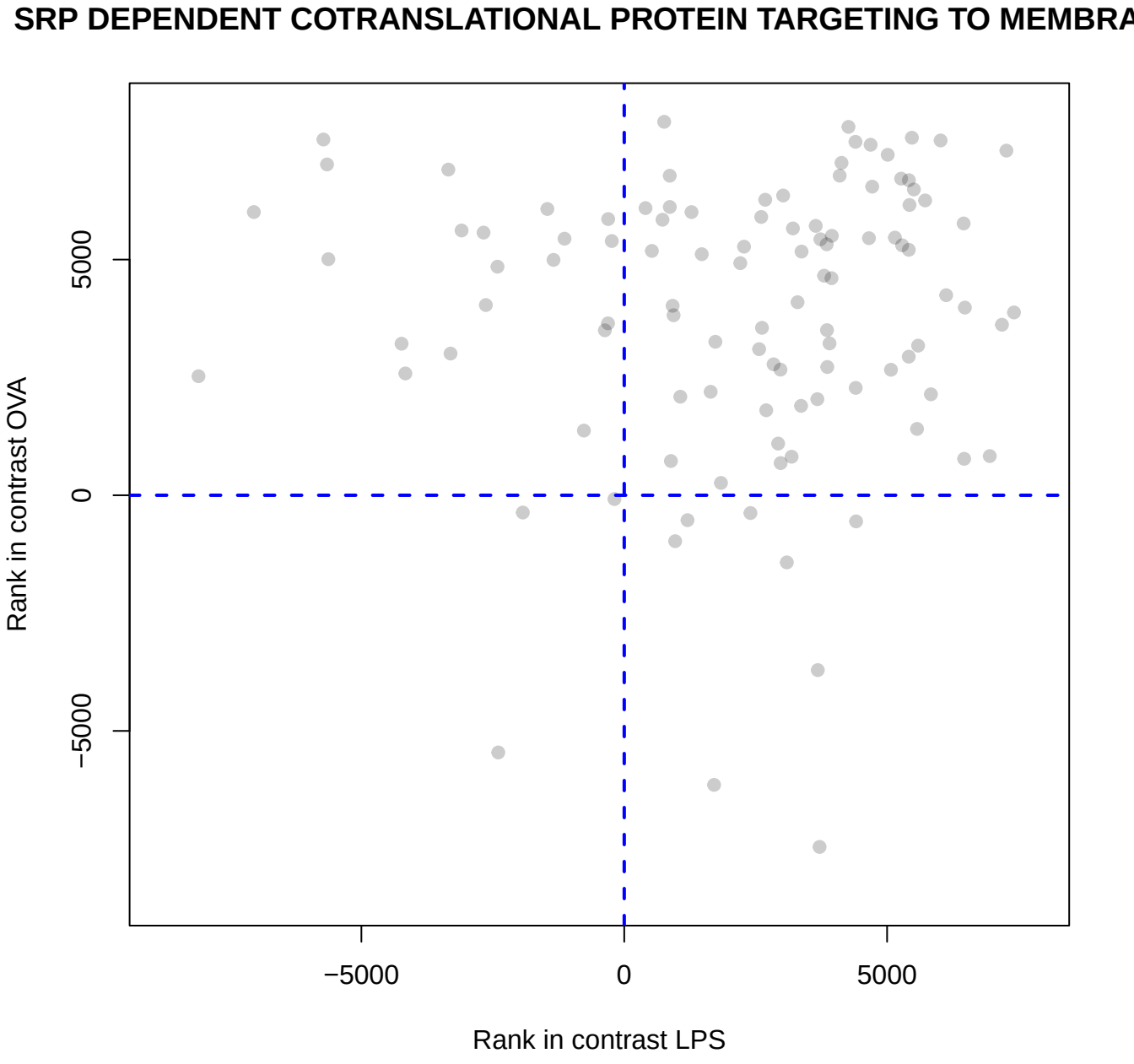

RESPONSE OF EIF2AK4 GCN2 TO AMINO ACID
5000
0
−5000
Position in rank
LPS
OVA
contrast

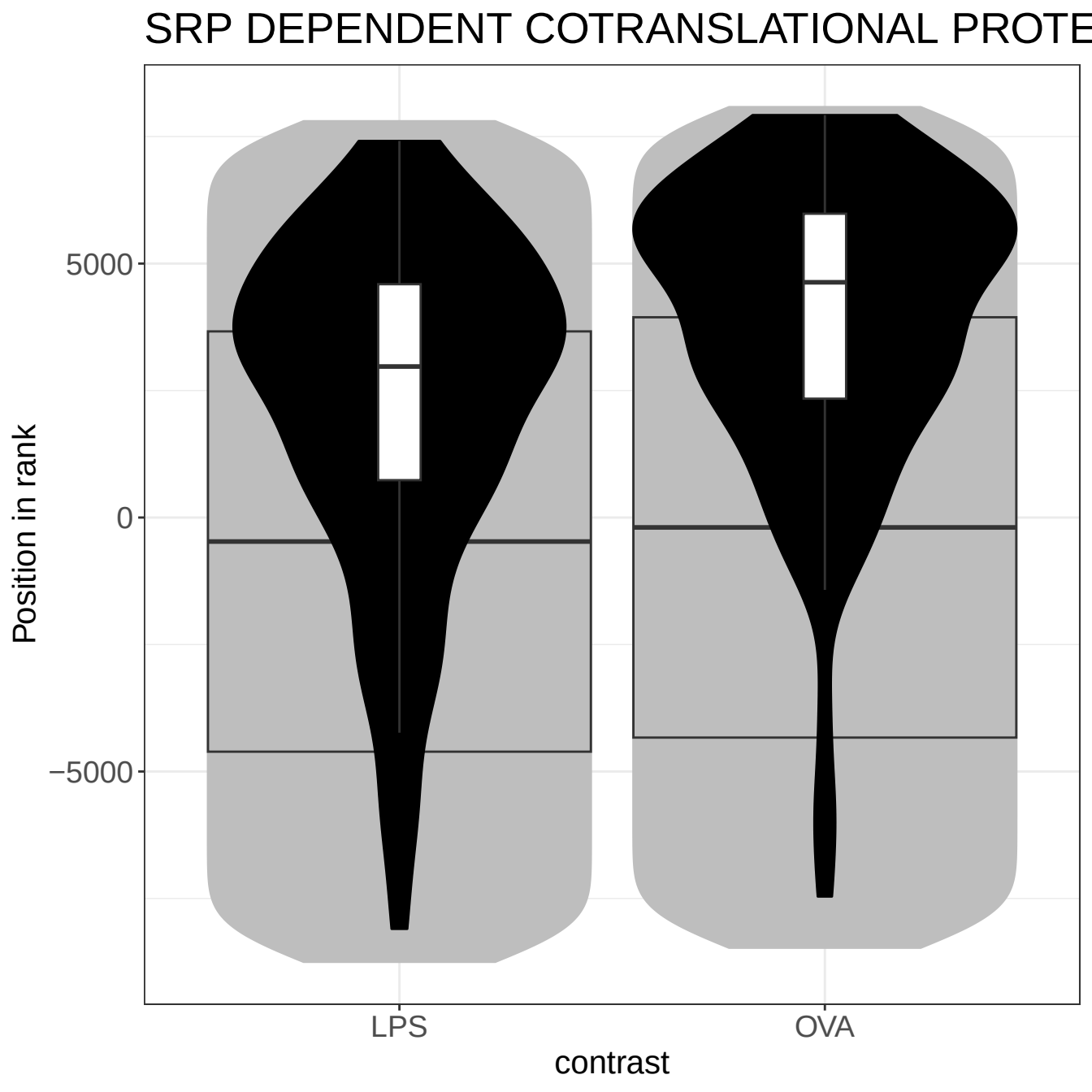

PHA LINOLENIC OMEGA3 AND LINOLEIC OMEGA6 ACID MET
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

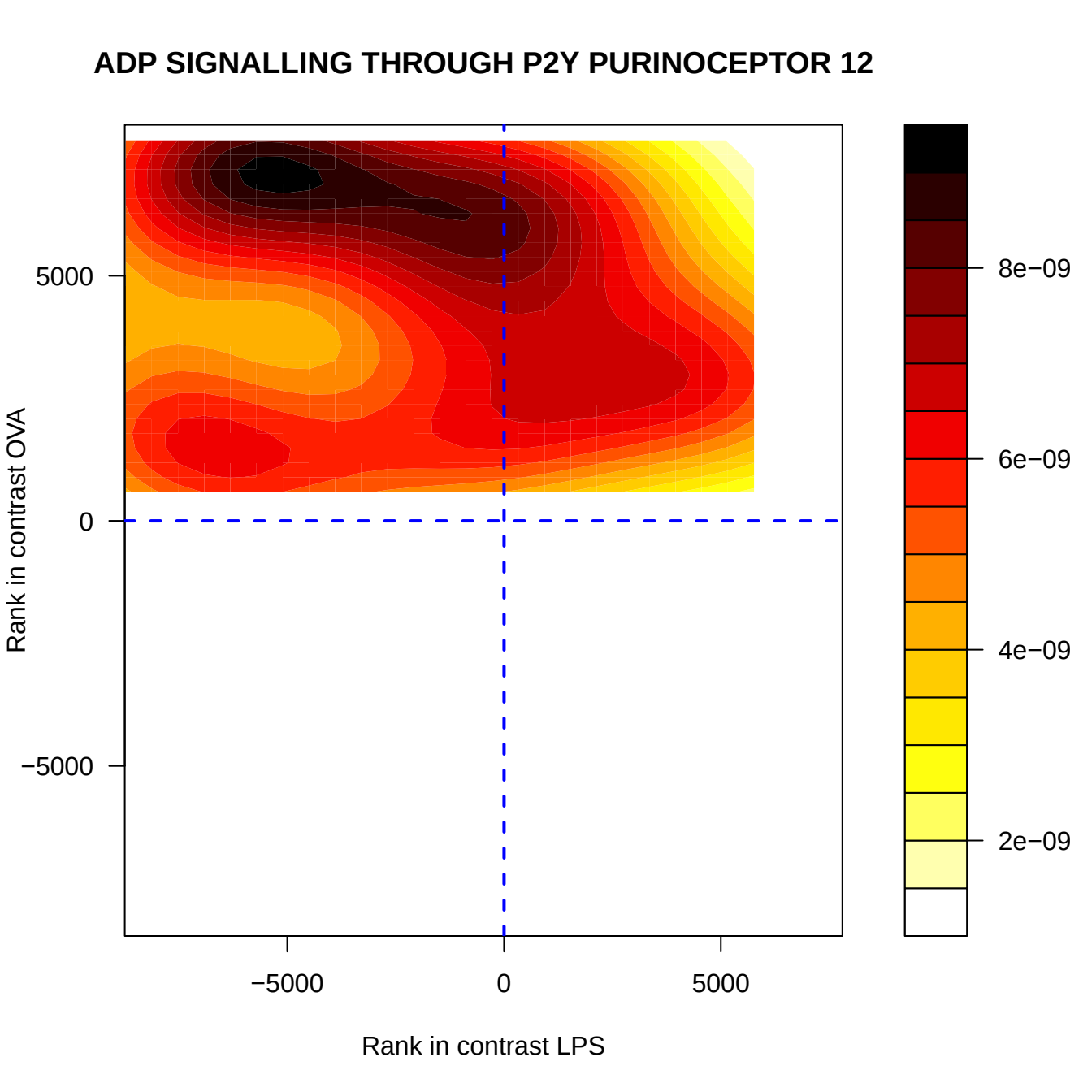

ALPHA LINOLENIC OMEGA3 AND LINOLEIC OMEGA6 ACID METABOLISI
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

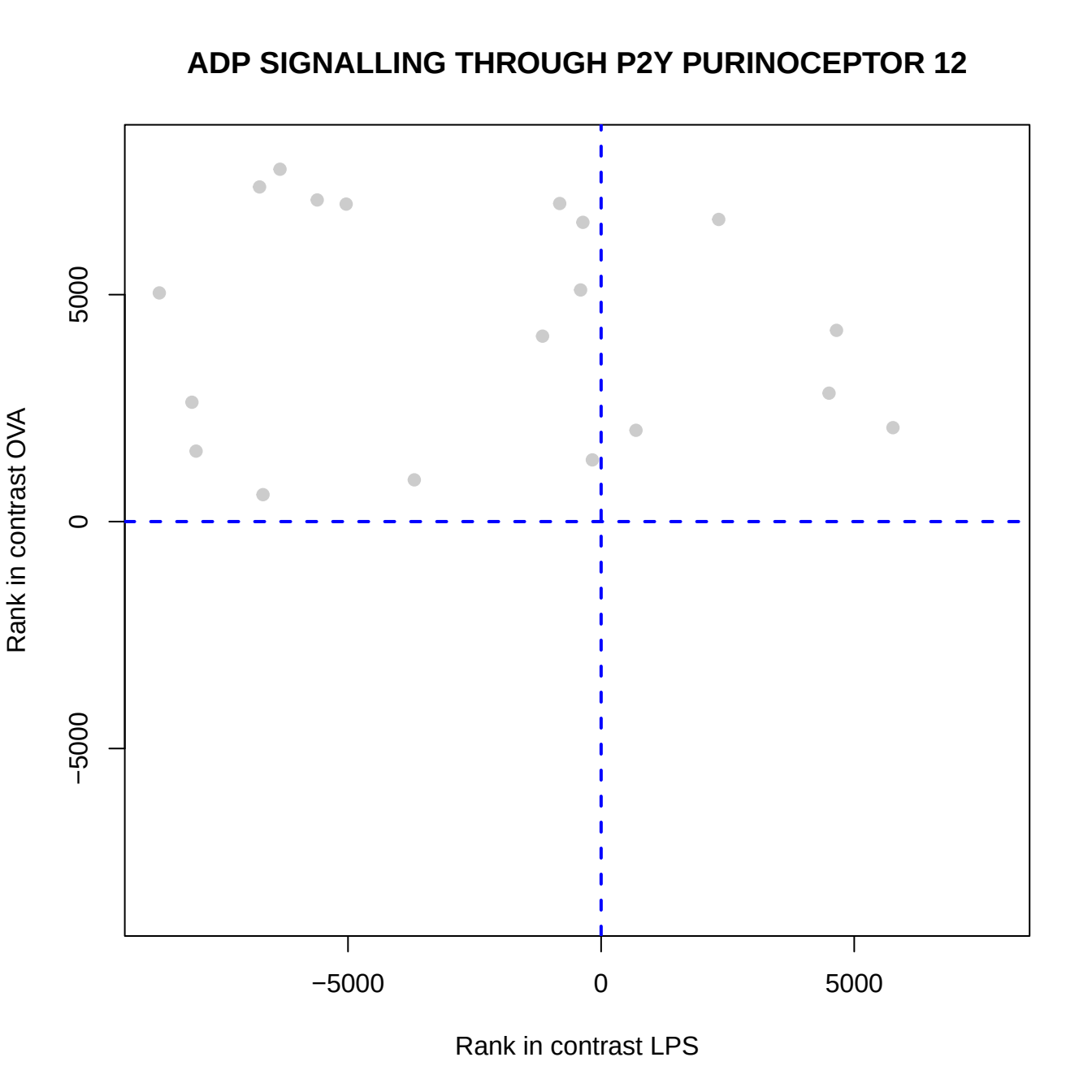

ALPHA LINOLENIC OMEGA3 AND LINOLEIC O
5000
0
−5000
Position in rank
LPS
OVA
contrast

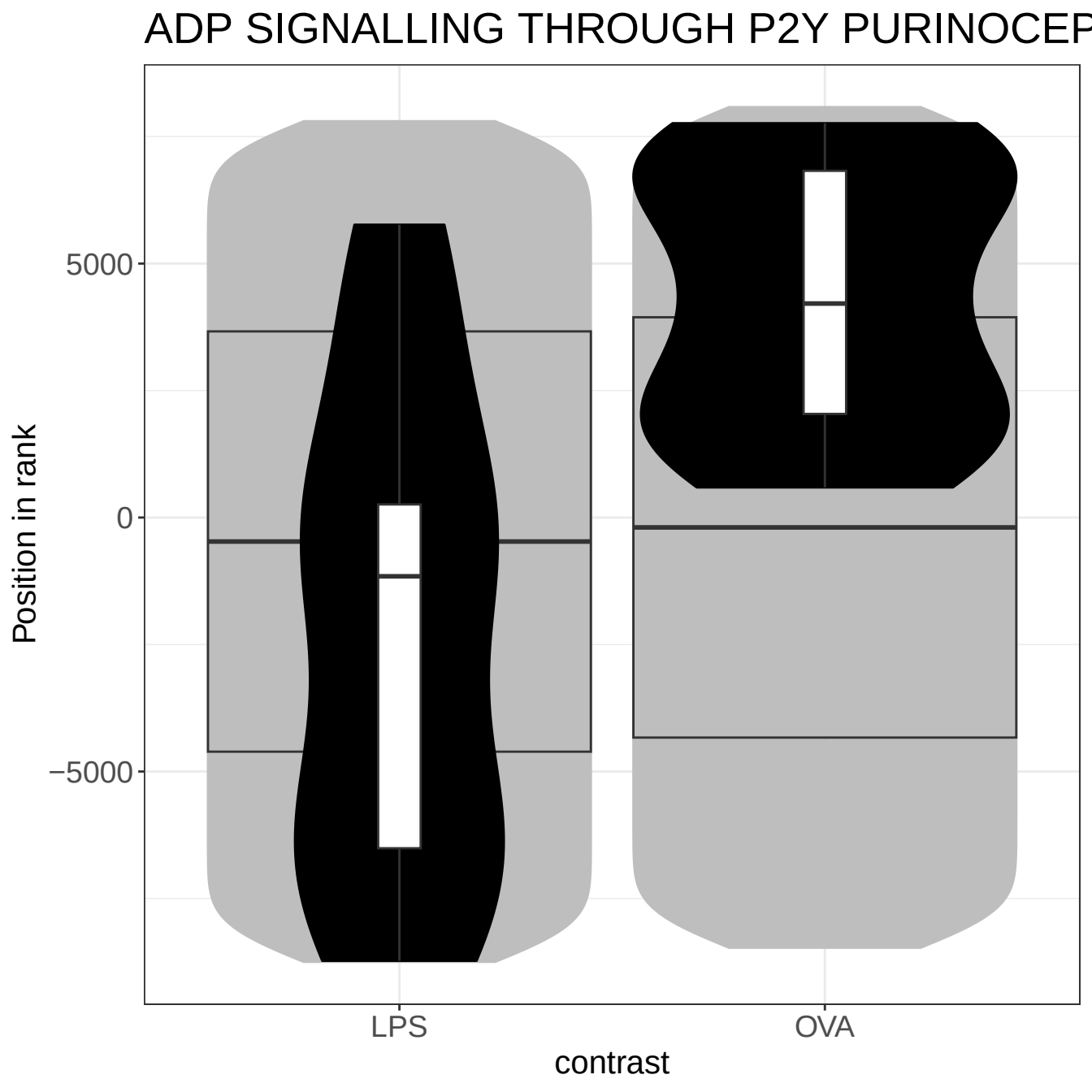

DEPENDENT COTRANSLATIONAL PROTEIN TARGETING TO I
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

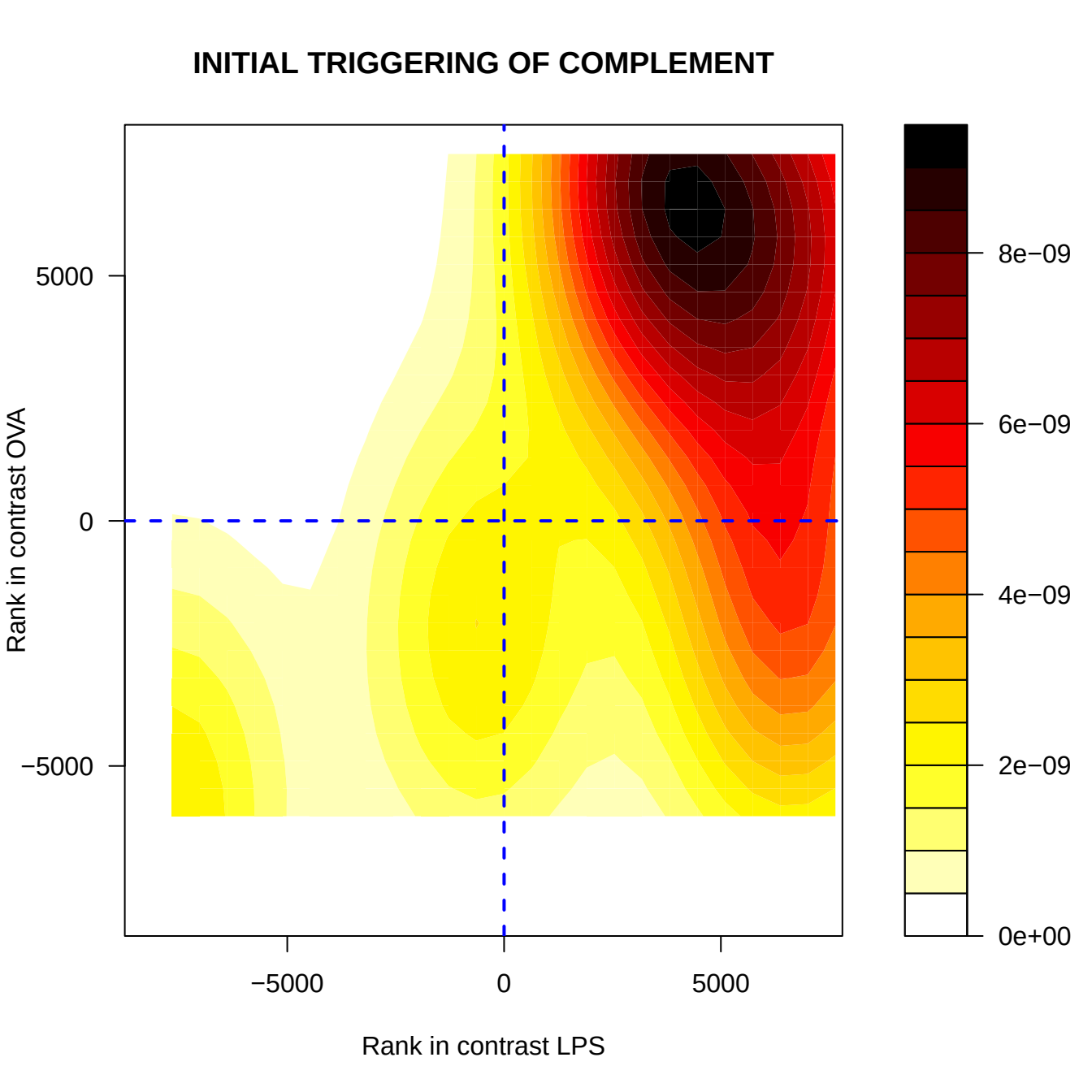

SRP DEPENDENT COTRANSLATIONAL PROTEIN TARGETING TO MEMBRA
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

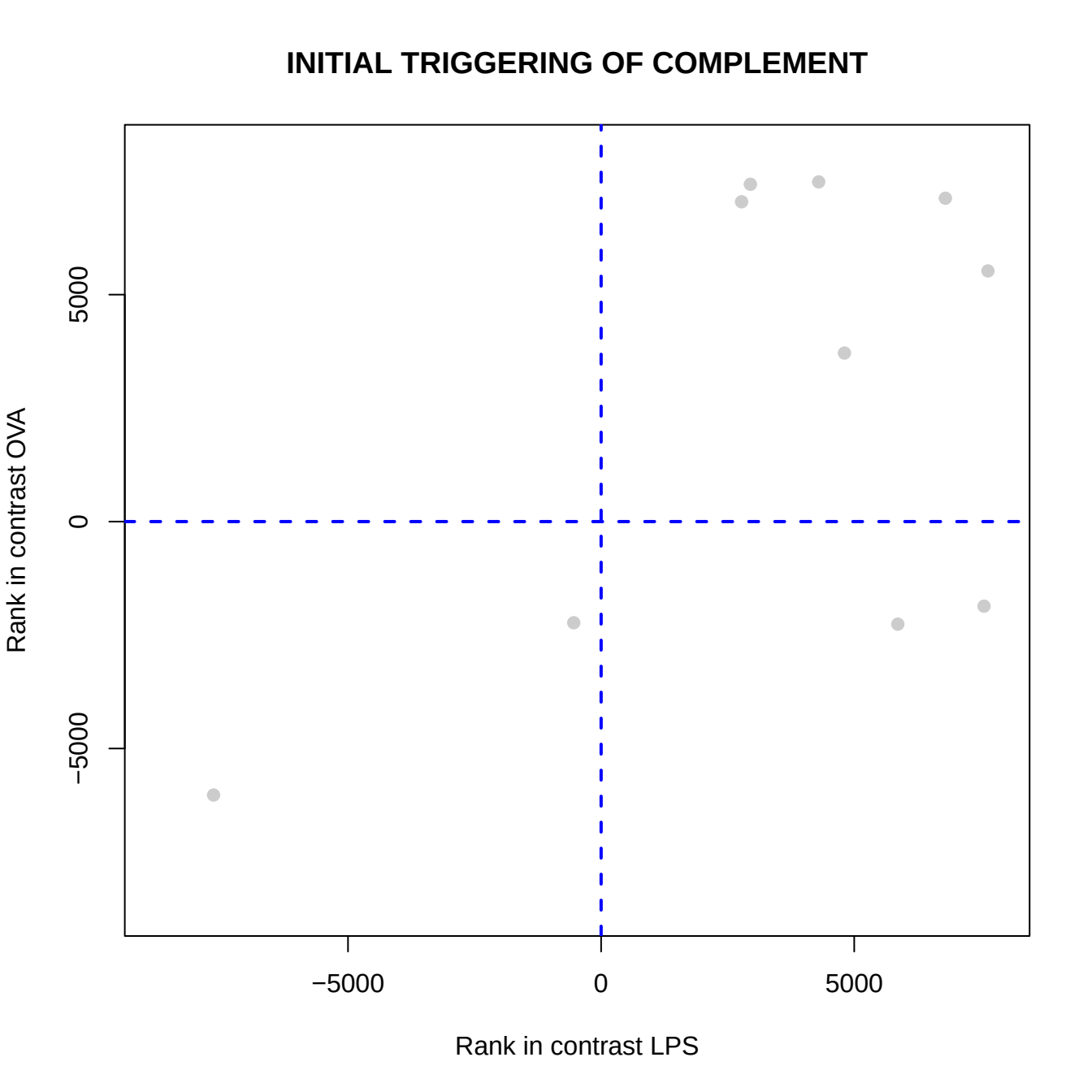

SRP DEPENDENT COTRANSLATIONAL PROTE
5000
0
−5000
Position in rank
LPS
OVA
contrast

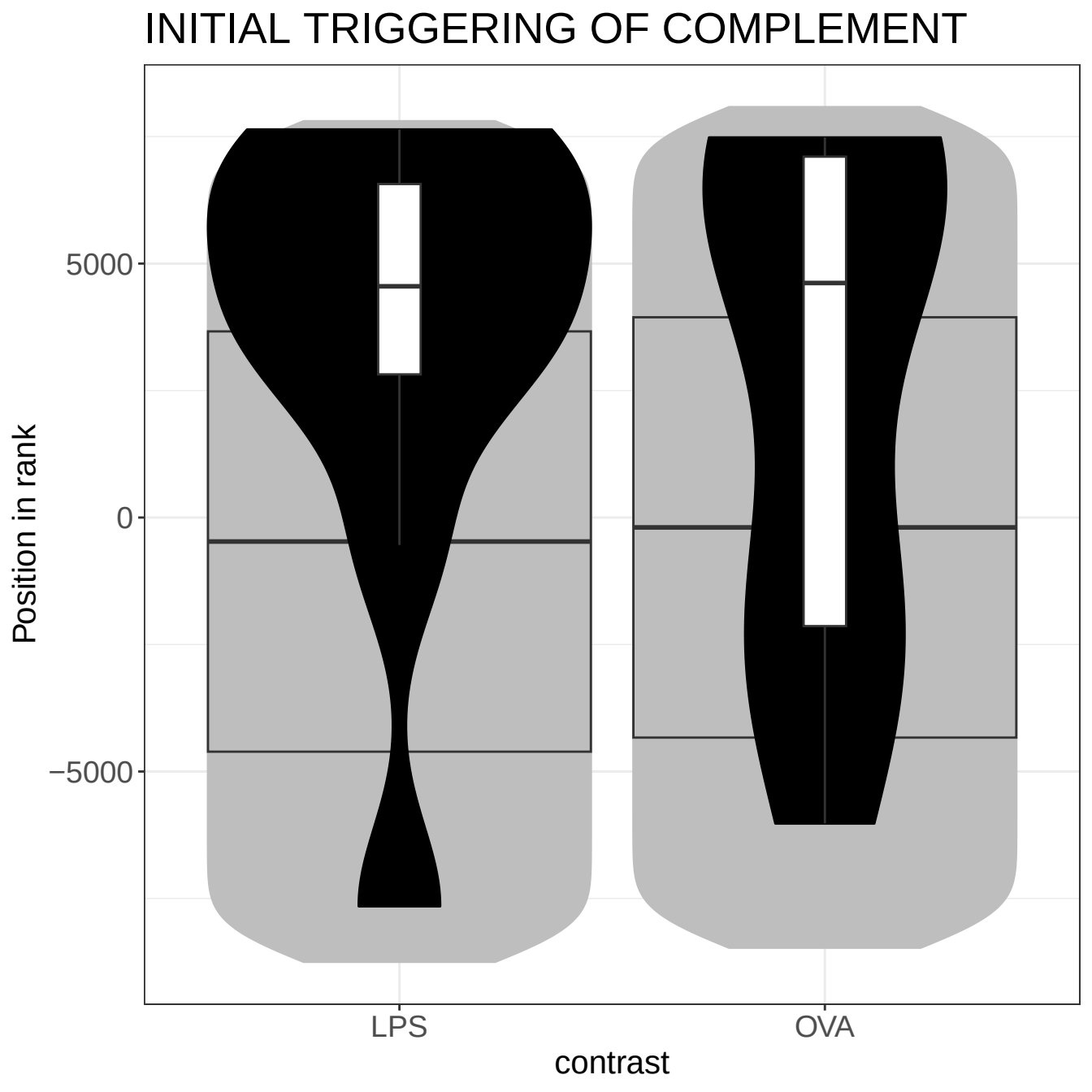

ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 12
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09

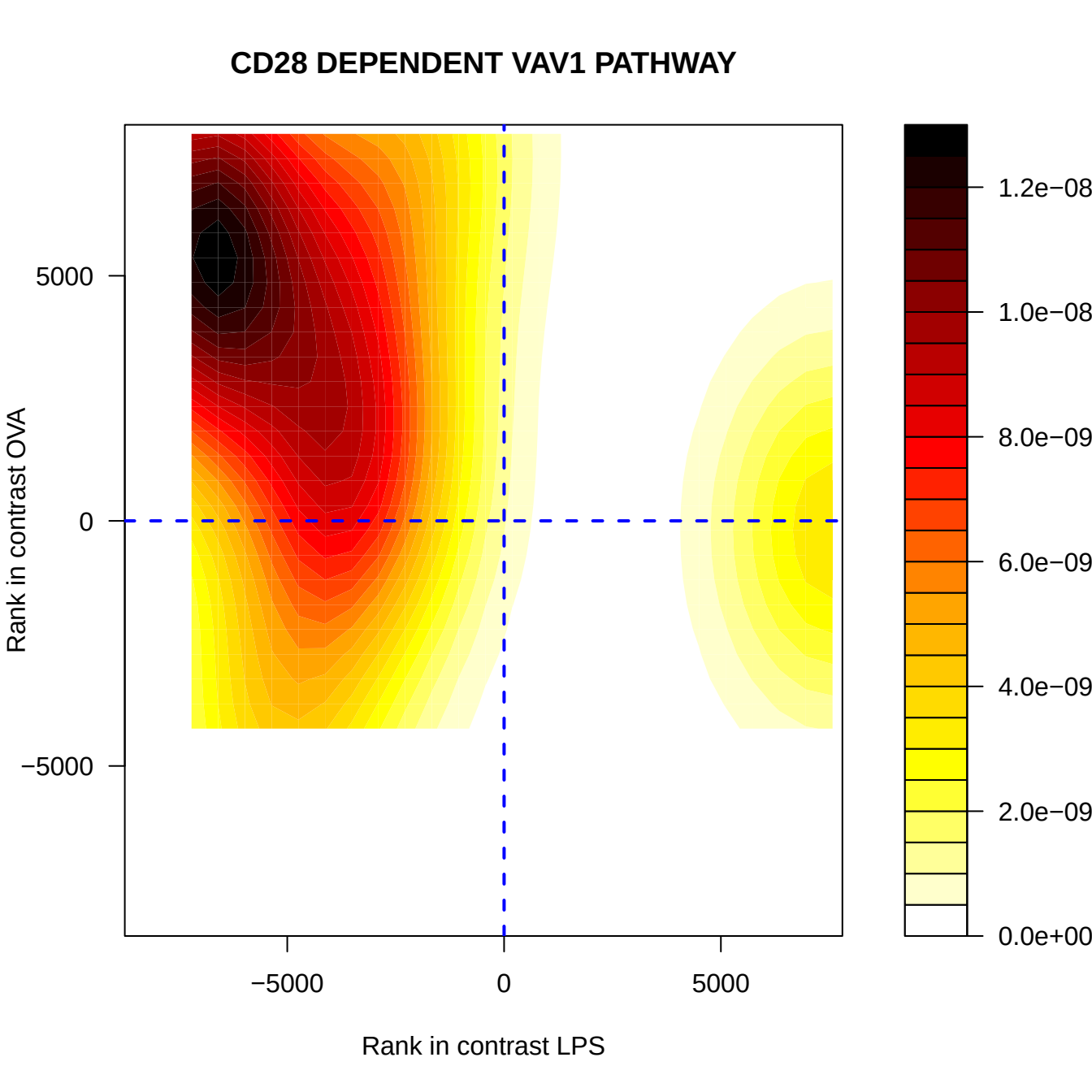

ADP SIGNALLING THROUGH P2Y PURINOCEPTOR 12
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

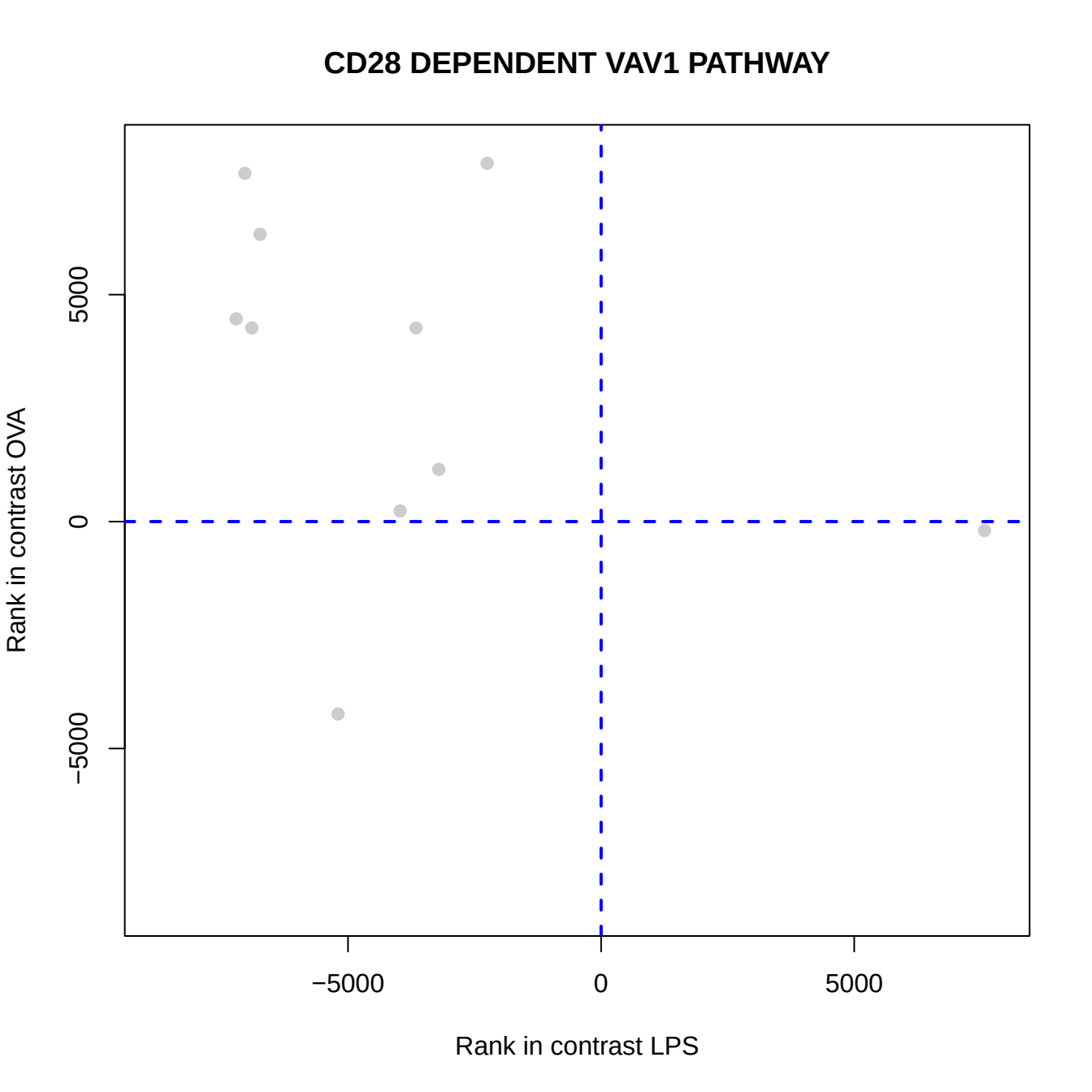

ADP SIGNALLING THROUGH P2Y PURINOCEP
5000
0
−5000
Position in rank
LPS
OVA
contrast

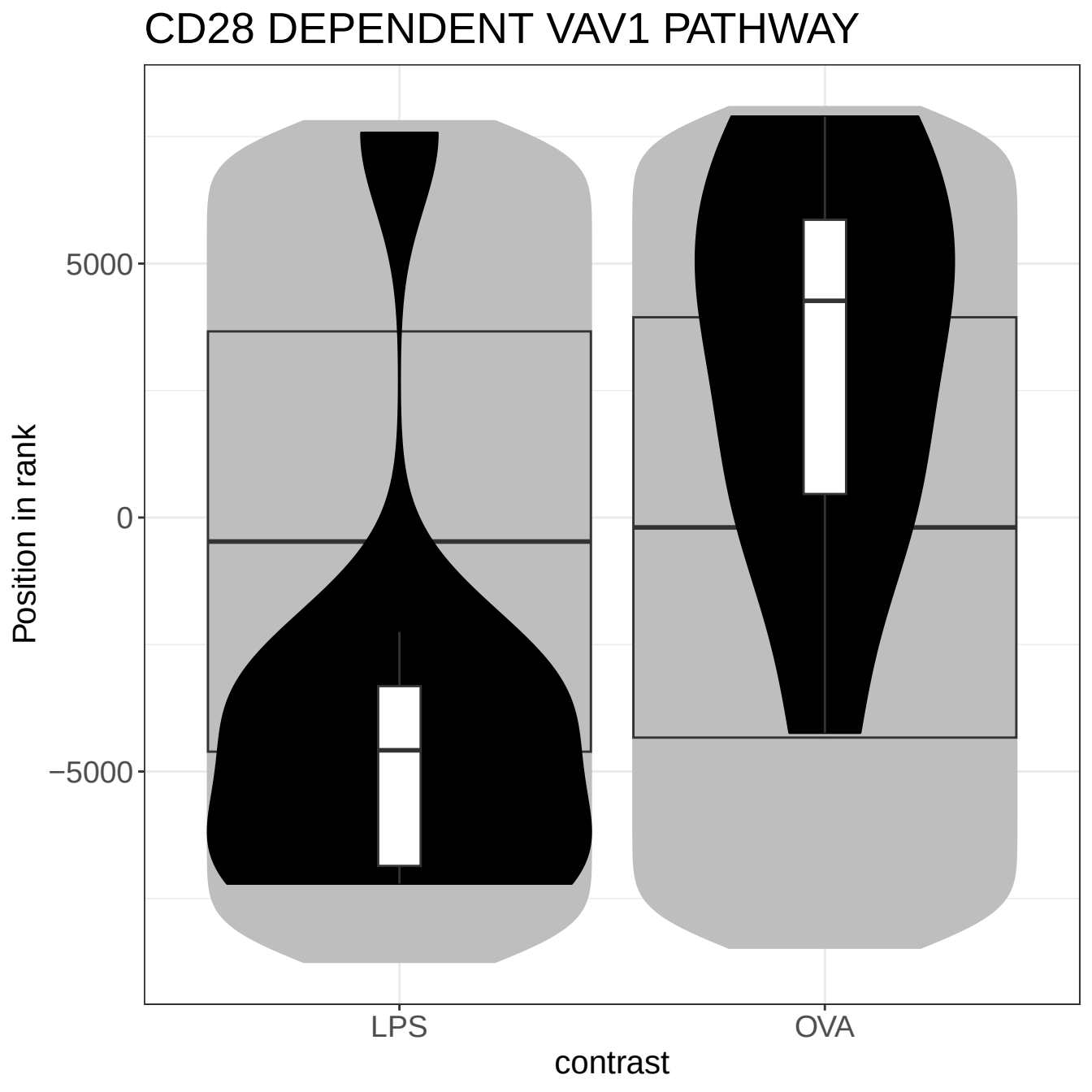

INITIAL TRIGGERING OF COMPLEMENT
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

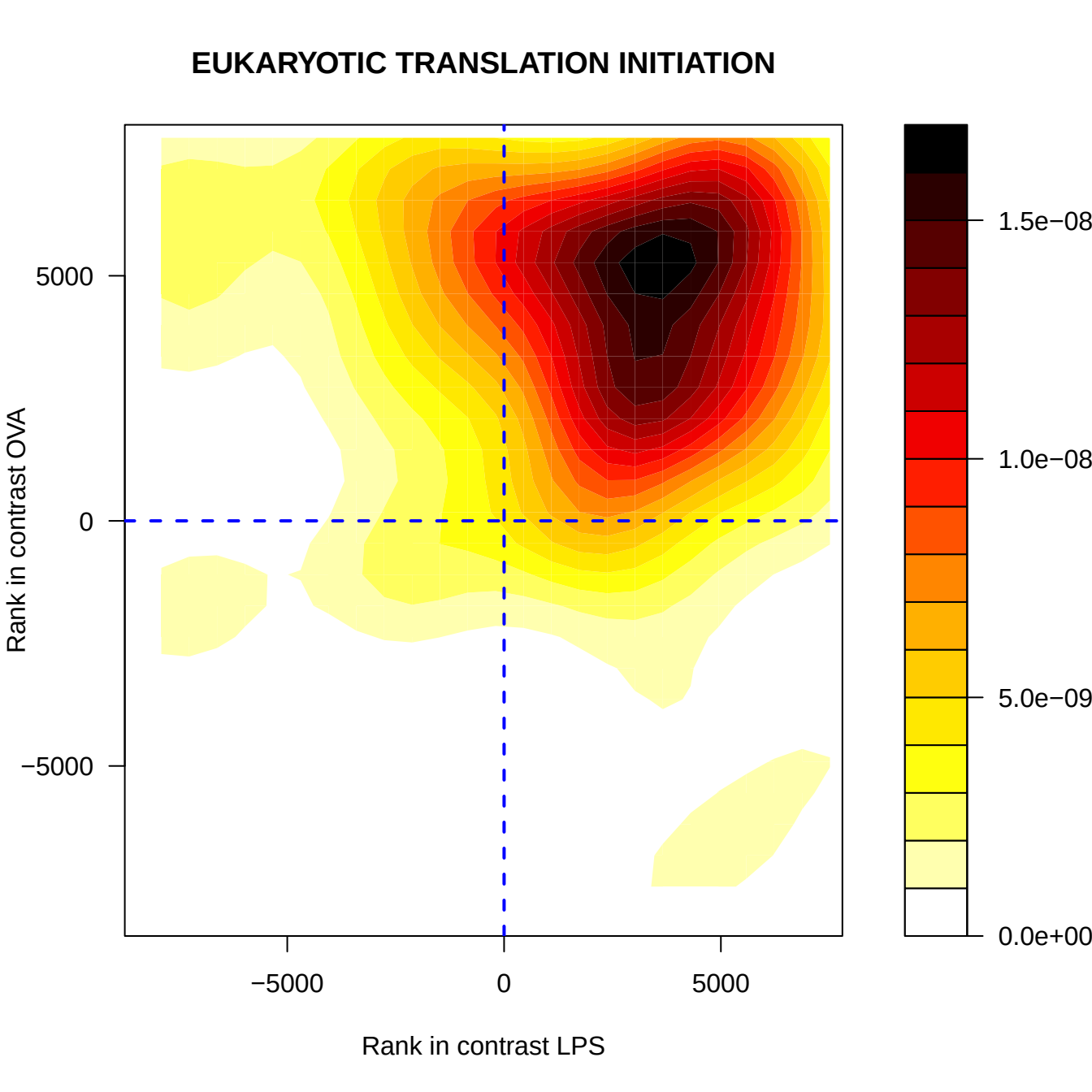

INITIAL TRIGGERING OF COMPLEMENT
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

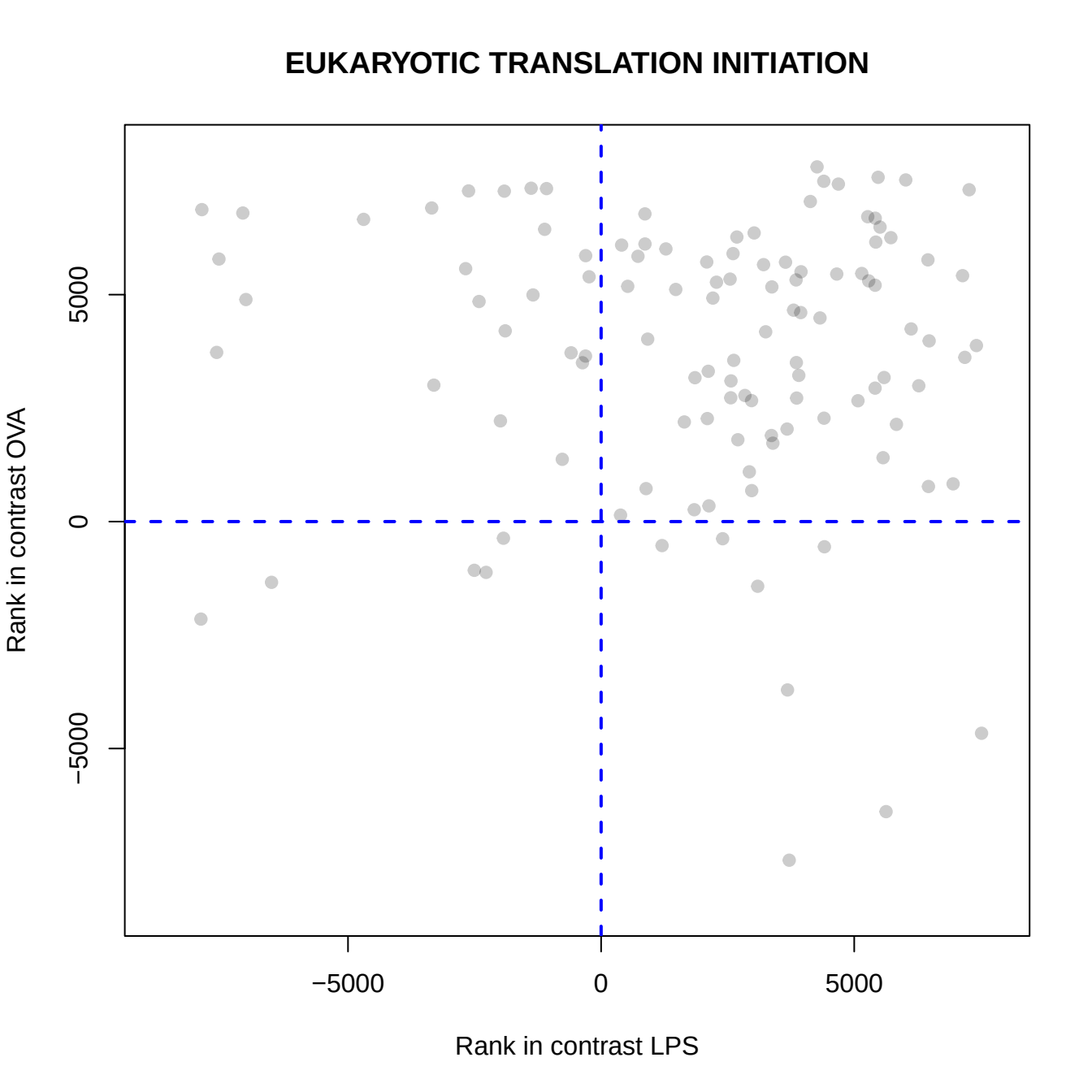

INITIAL TRIGGERING OF COMPLEMENT
5000
0
−5000
Position in rank
LPS
OVA
contrast

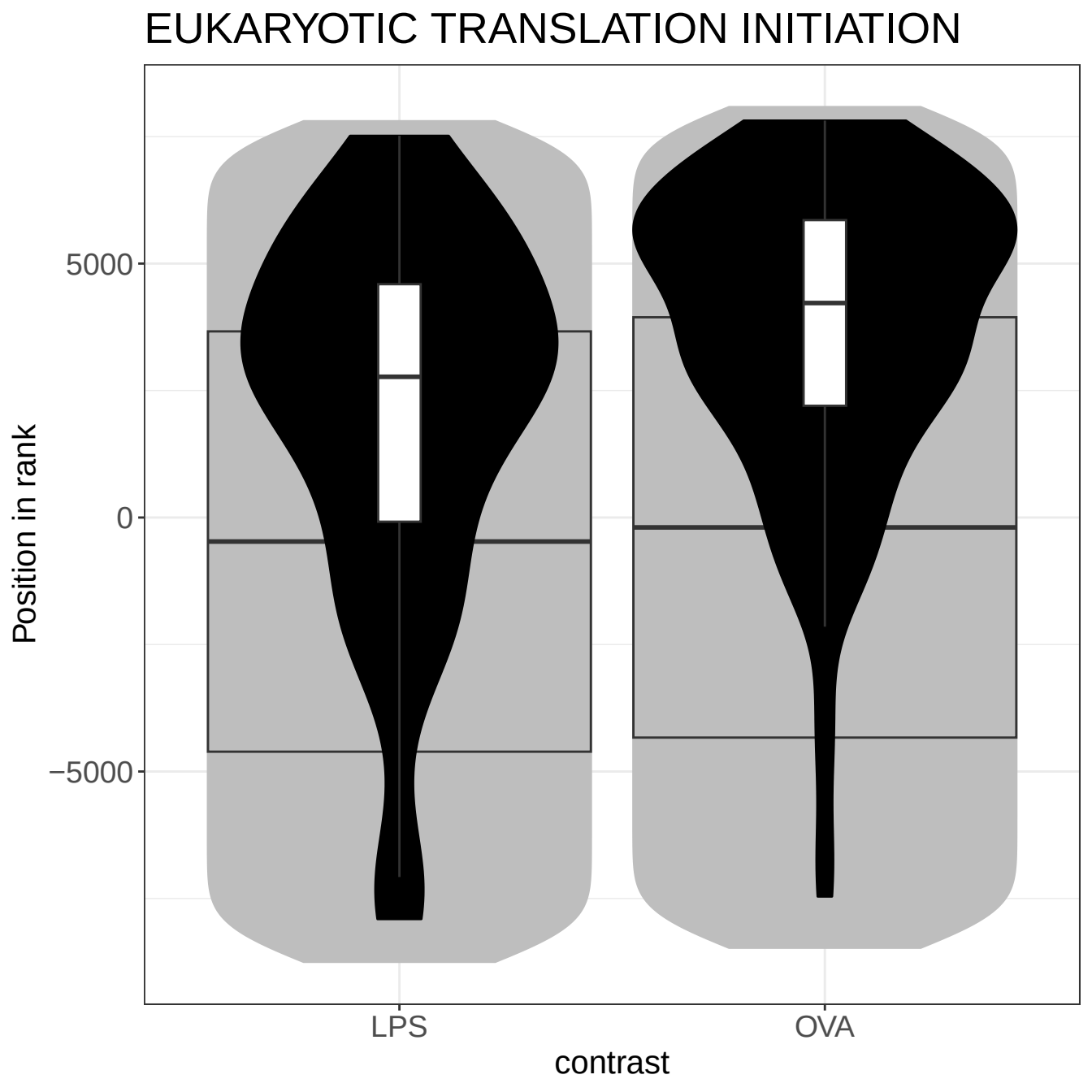

CD28 DEPENDENT VAV1 PATHWAY
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

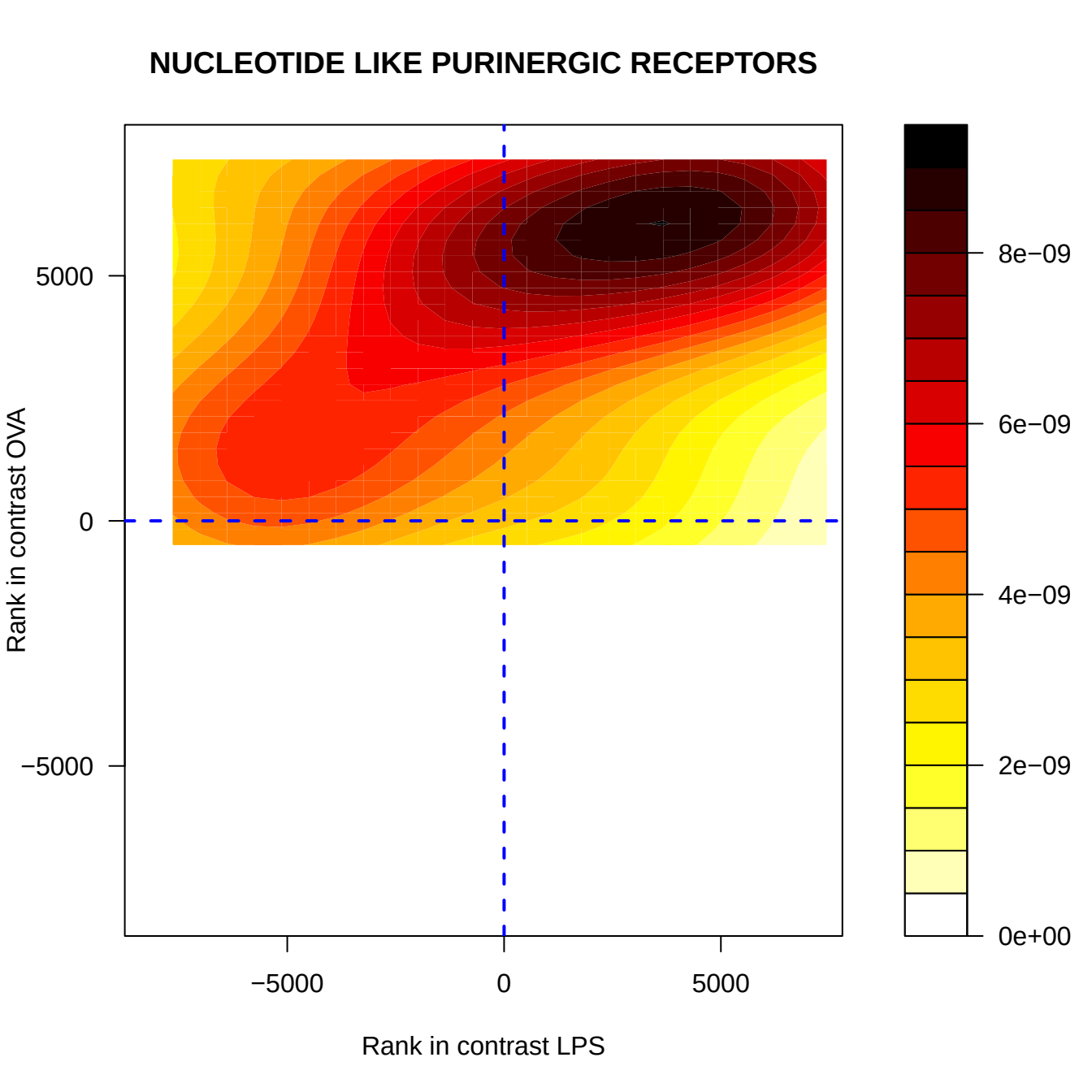

CD28 DEPENDENT VAV1 PATHWAY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

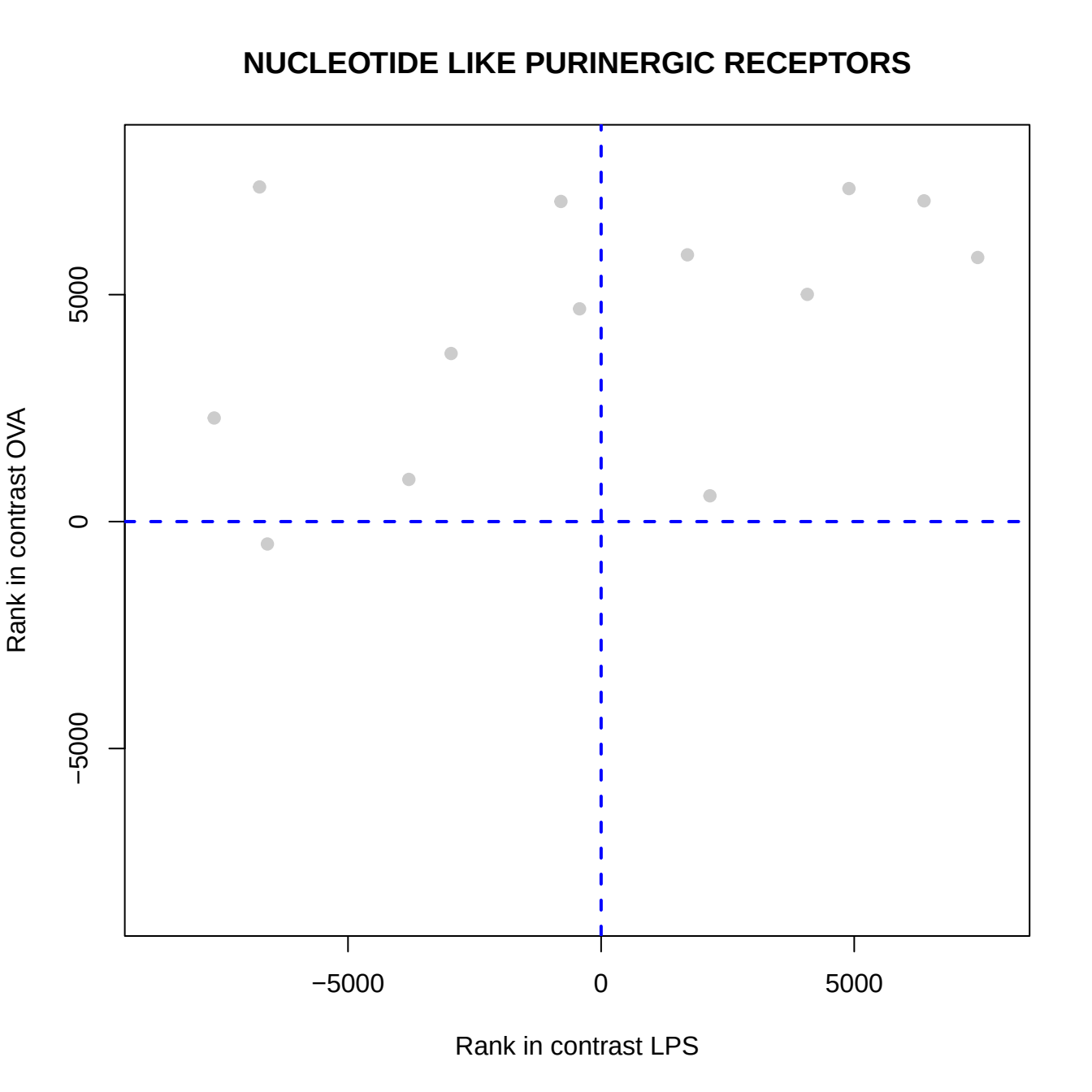

CD28 DEPENDENT VAV1 PATHWAY
5000
0
−5000
Position in rank
LPS
OVA
contrast

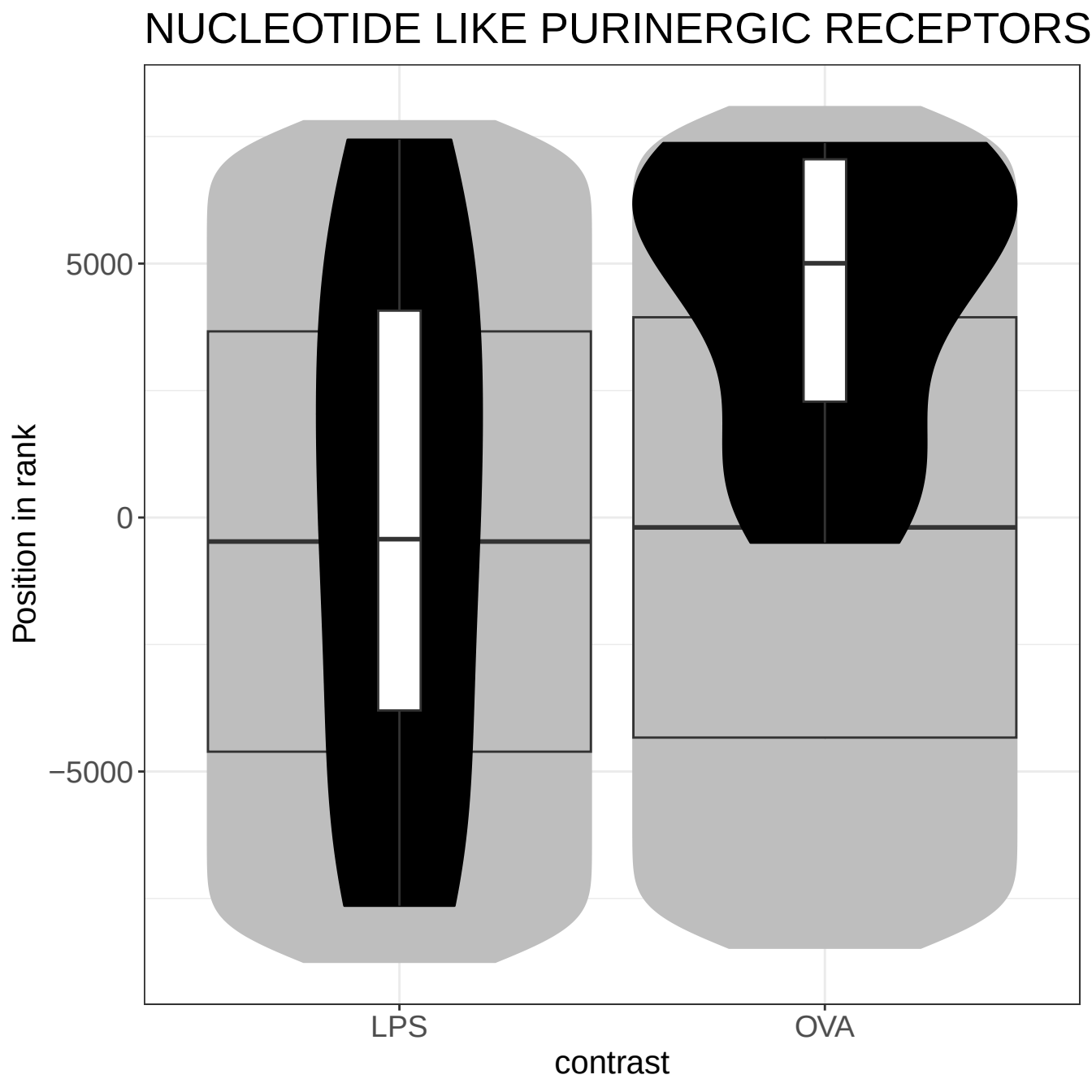

EUKARYOTIC TRANSLATION INITIATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

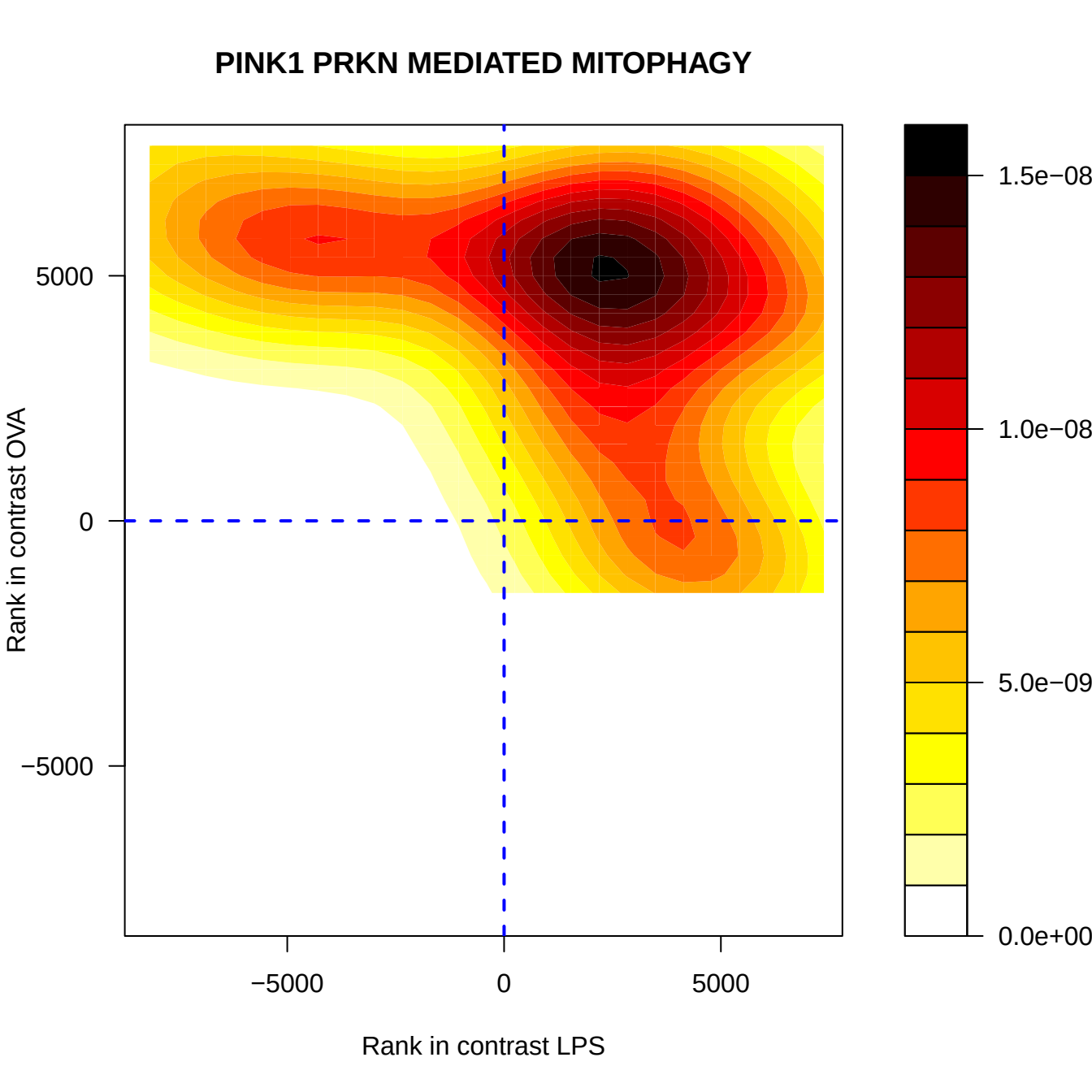

EUKARYOTIC TRANSLATION INITIATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

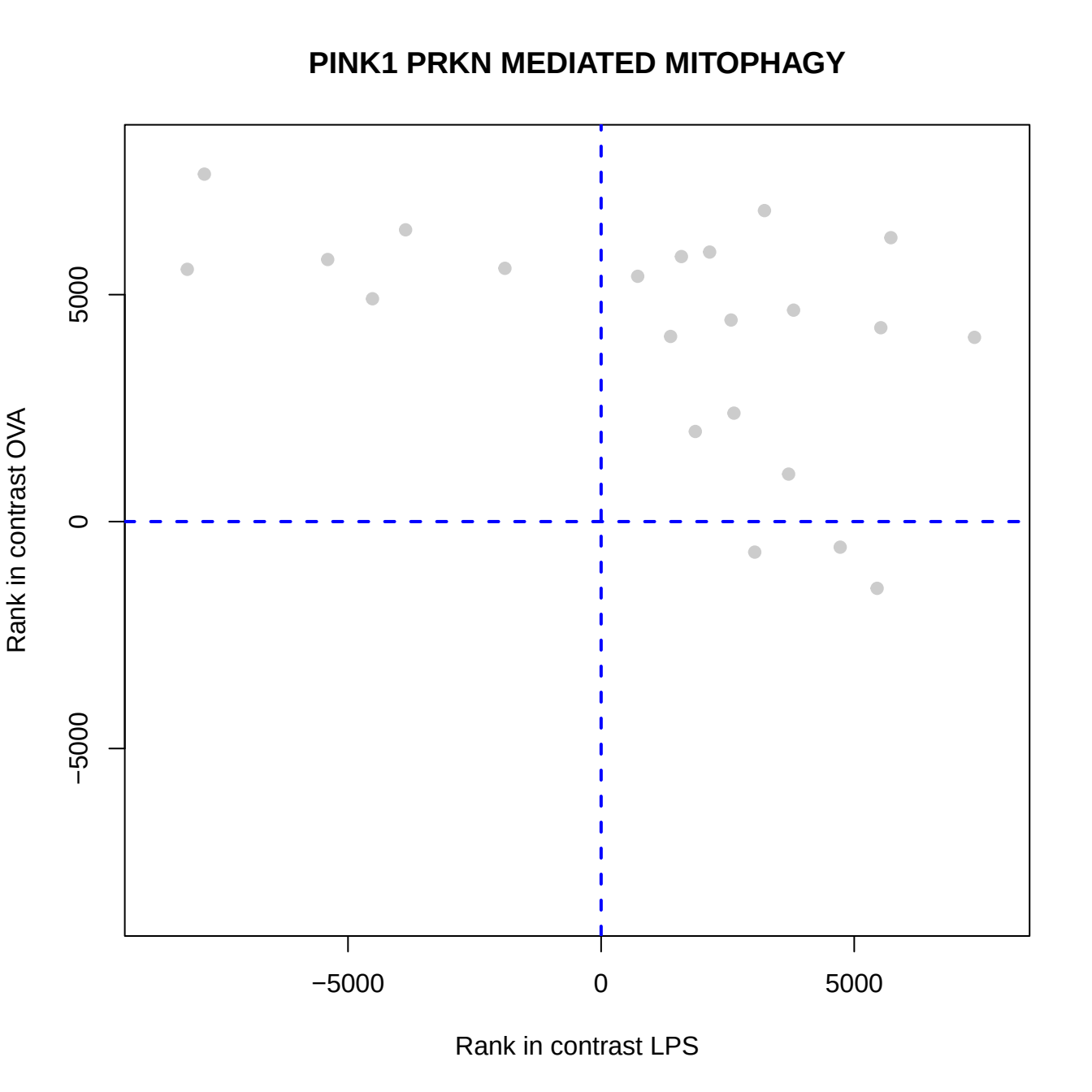

EUKARYOTIC TRANSLATION INITIATION
5000
0
−5000
Position in rank
LPS
OVA
contrast

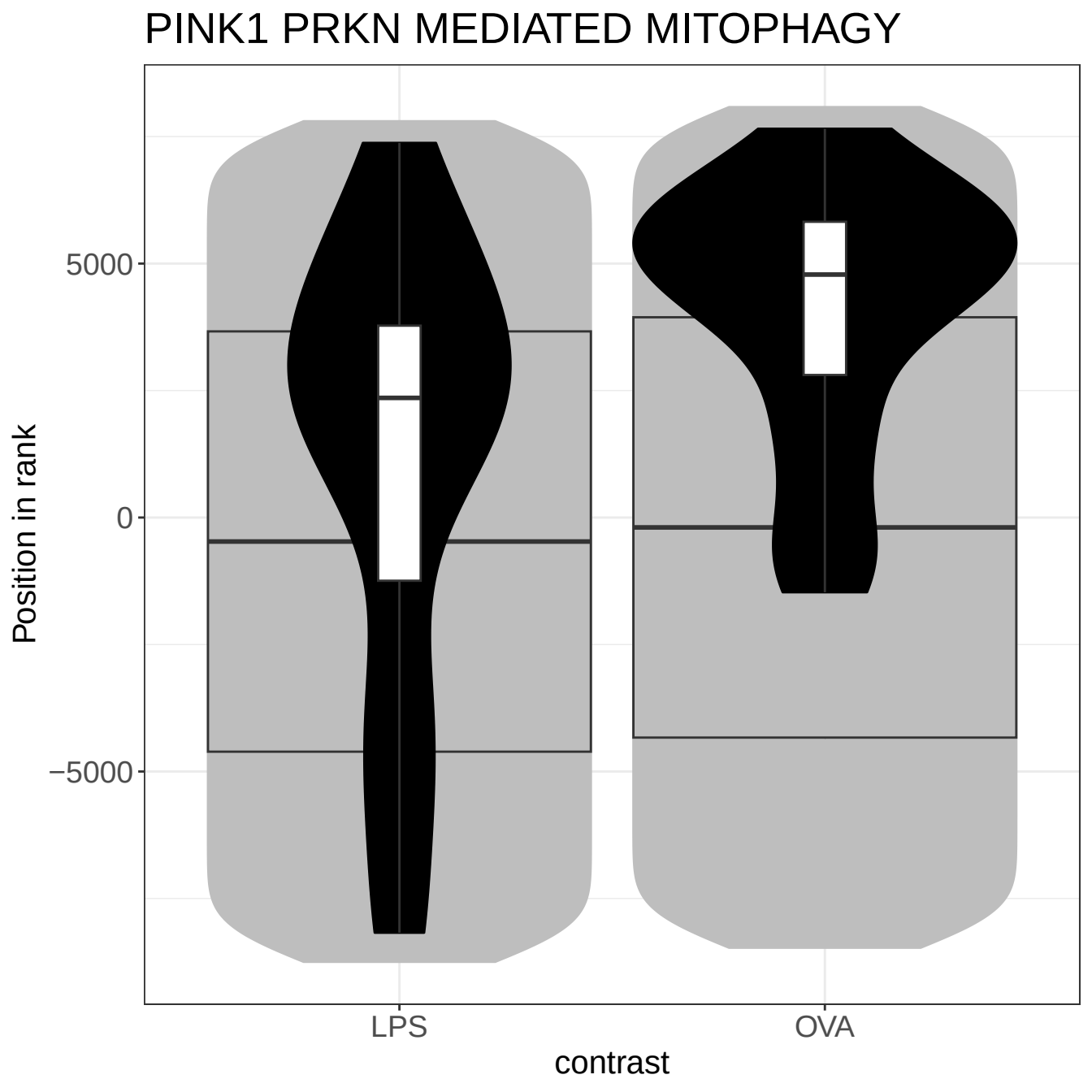

NUCLEOTIDE LIKE PURINERGIC RECEPTORS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

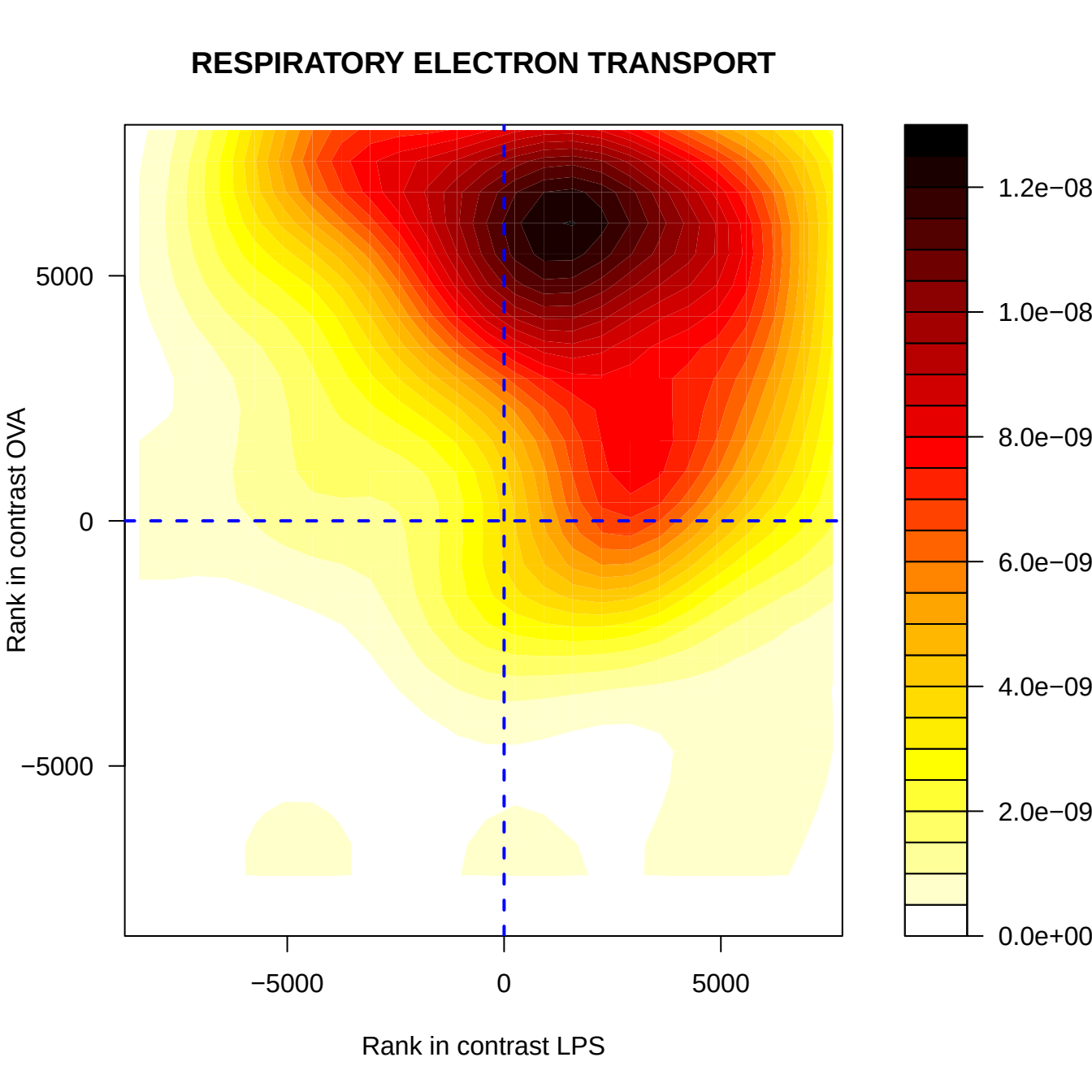

NUCLEOTIDE LIKE PURINERGIC RECEPTORS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

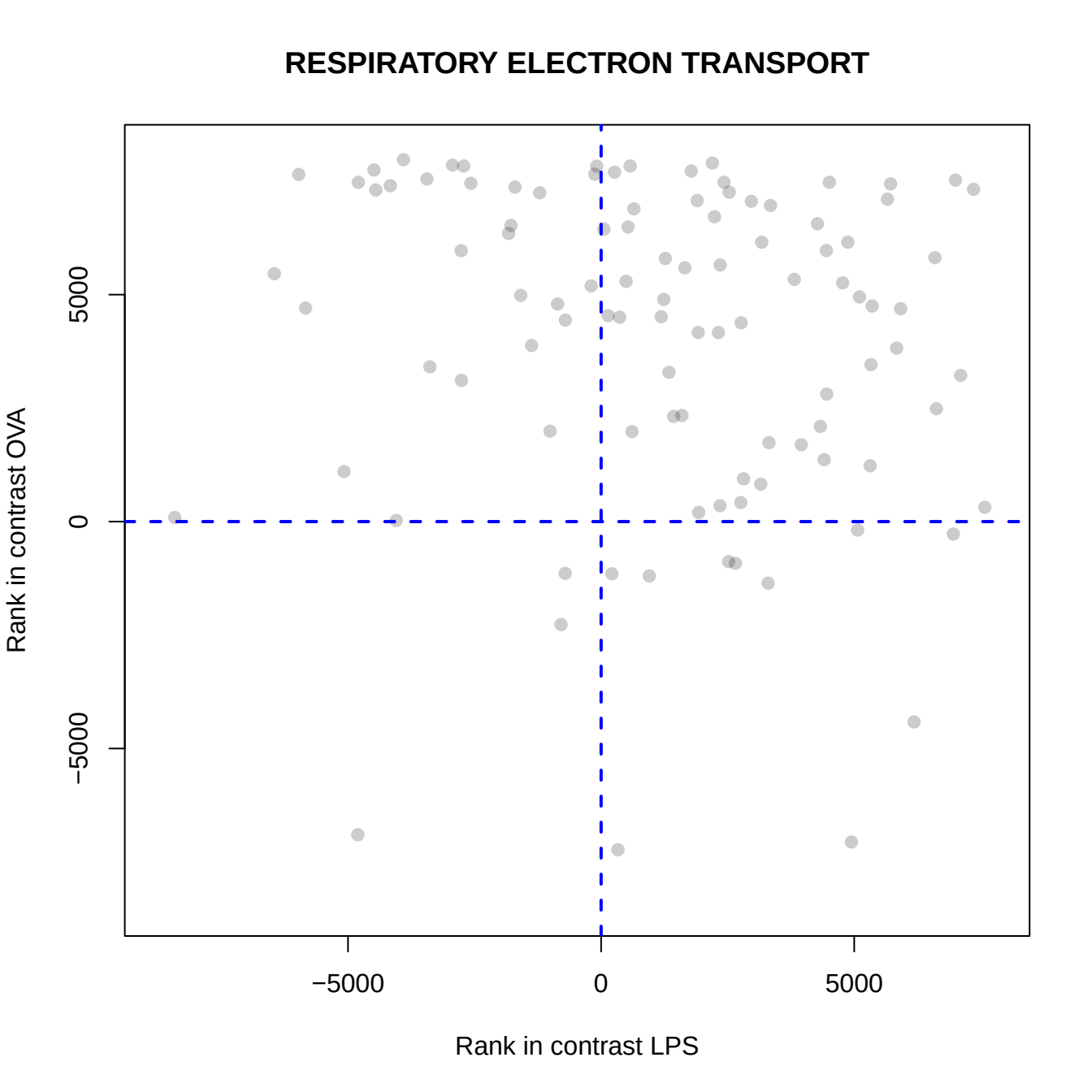

NUCLEOTIDE LIKE PURINERGIC RECEPTORS
Position in rank
5000
0
−5000
LPS
OVA
contrast

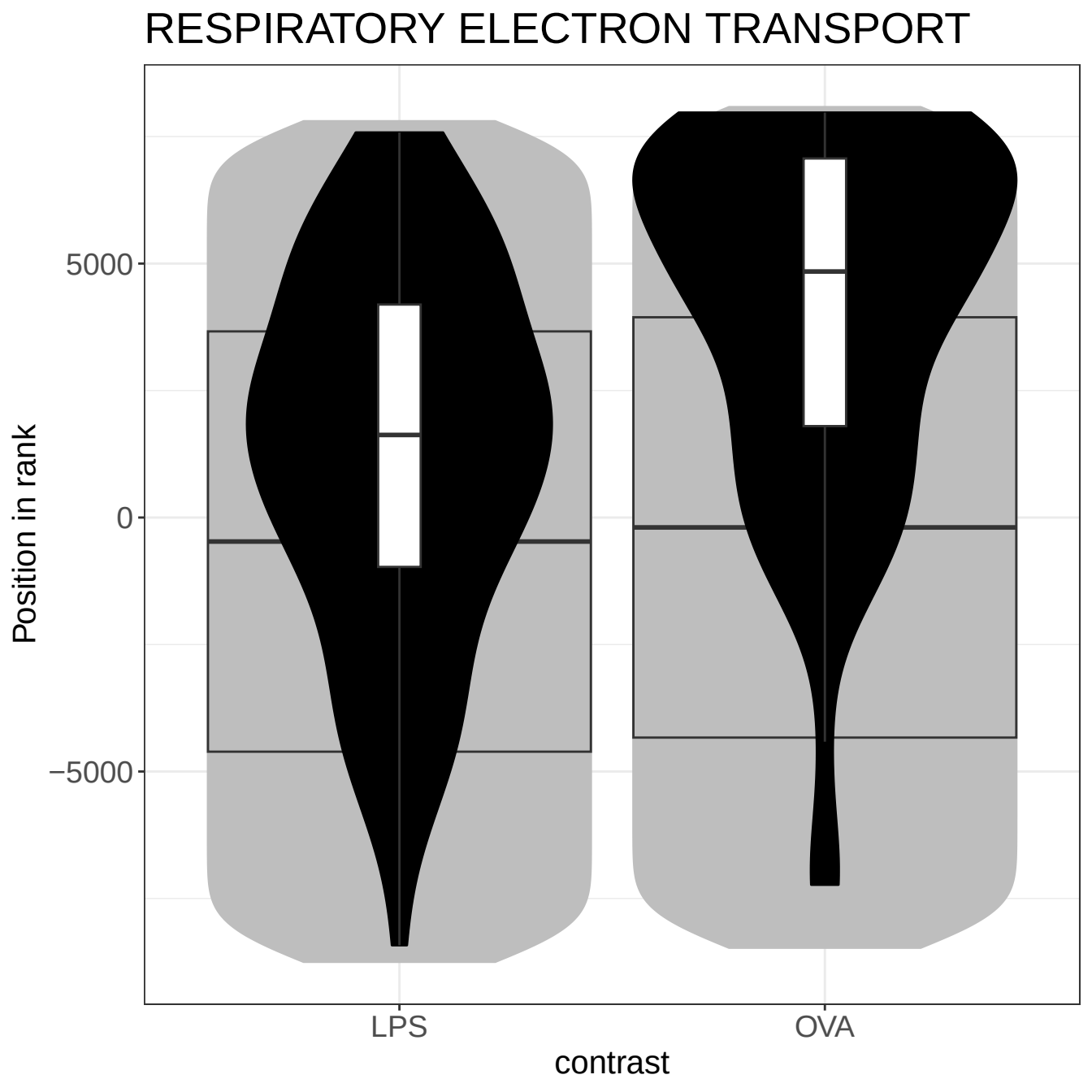

PINK1 PRKN MEDIATED MITOPHAGY
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

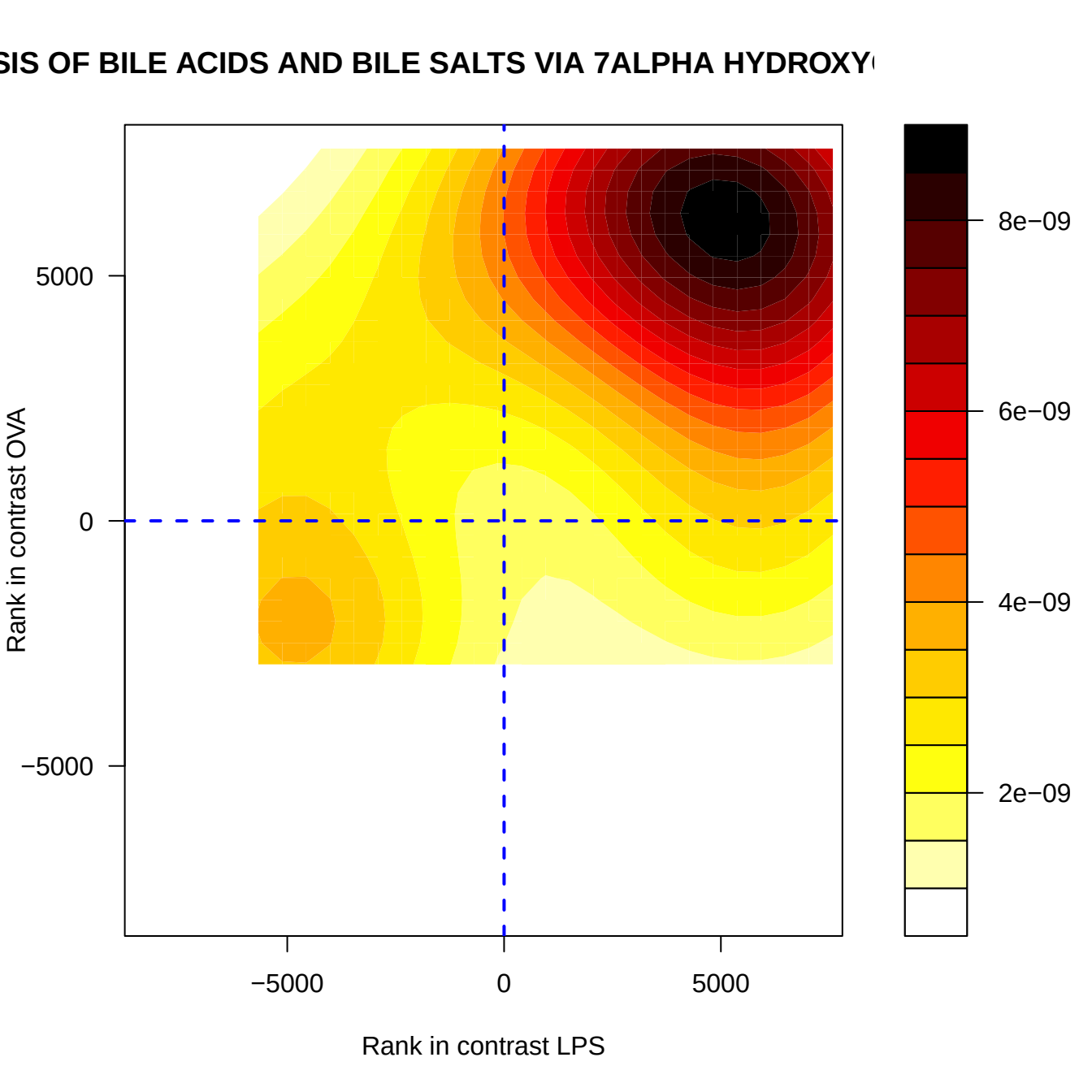

PINK1 PRKN MEDIATED MITOPHAGY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

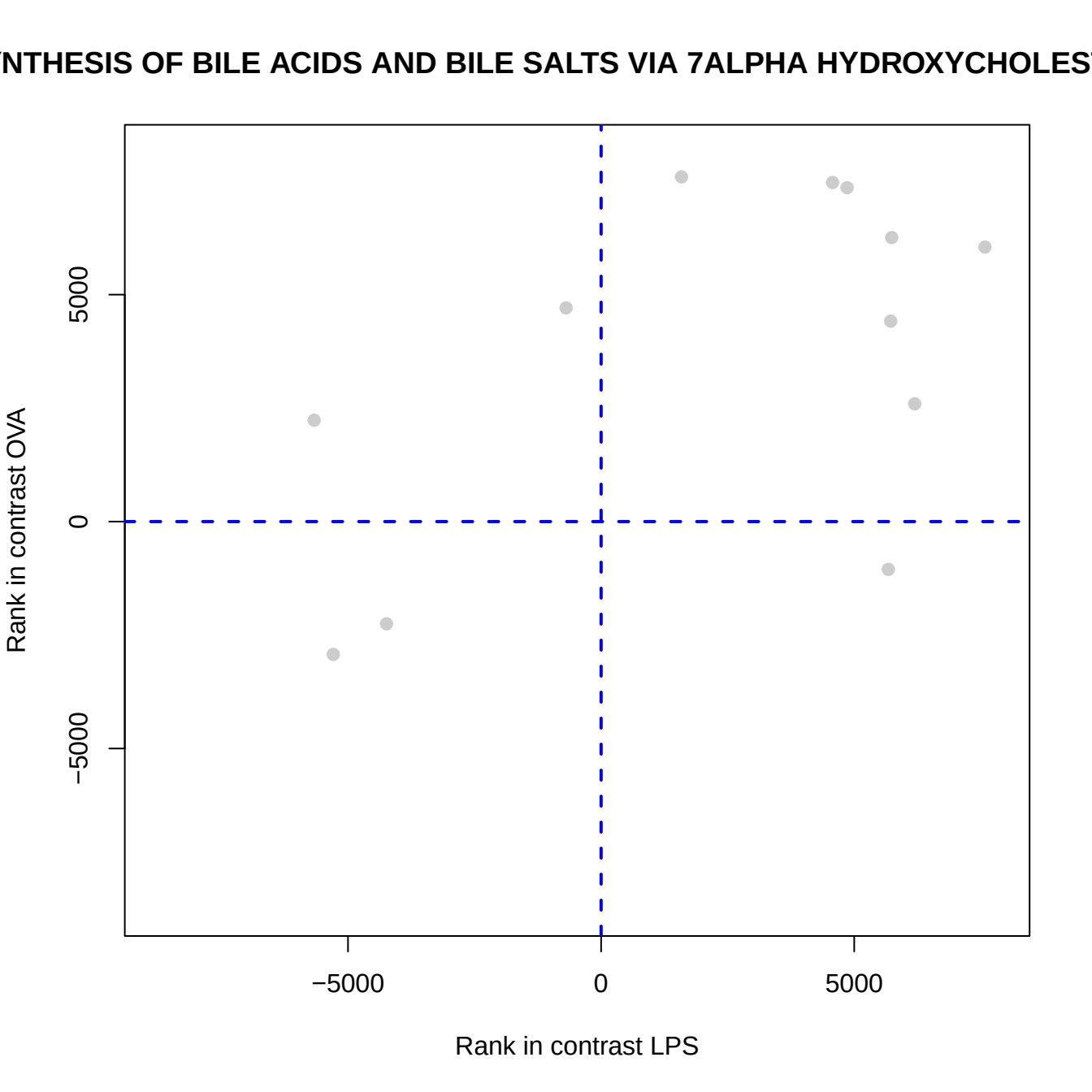

PINK1 PRKN MEDIATED MITOPHAGY
5000
0
−5000
Position in rank
LPS
OVA
contrast

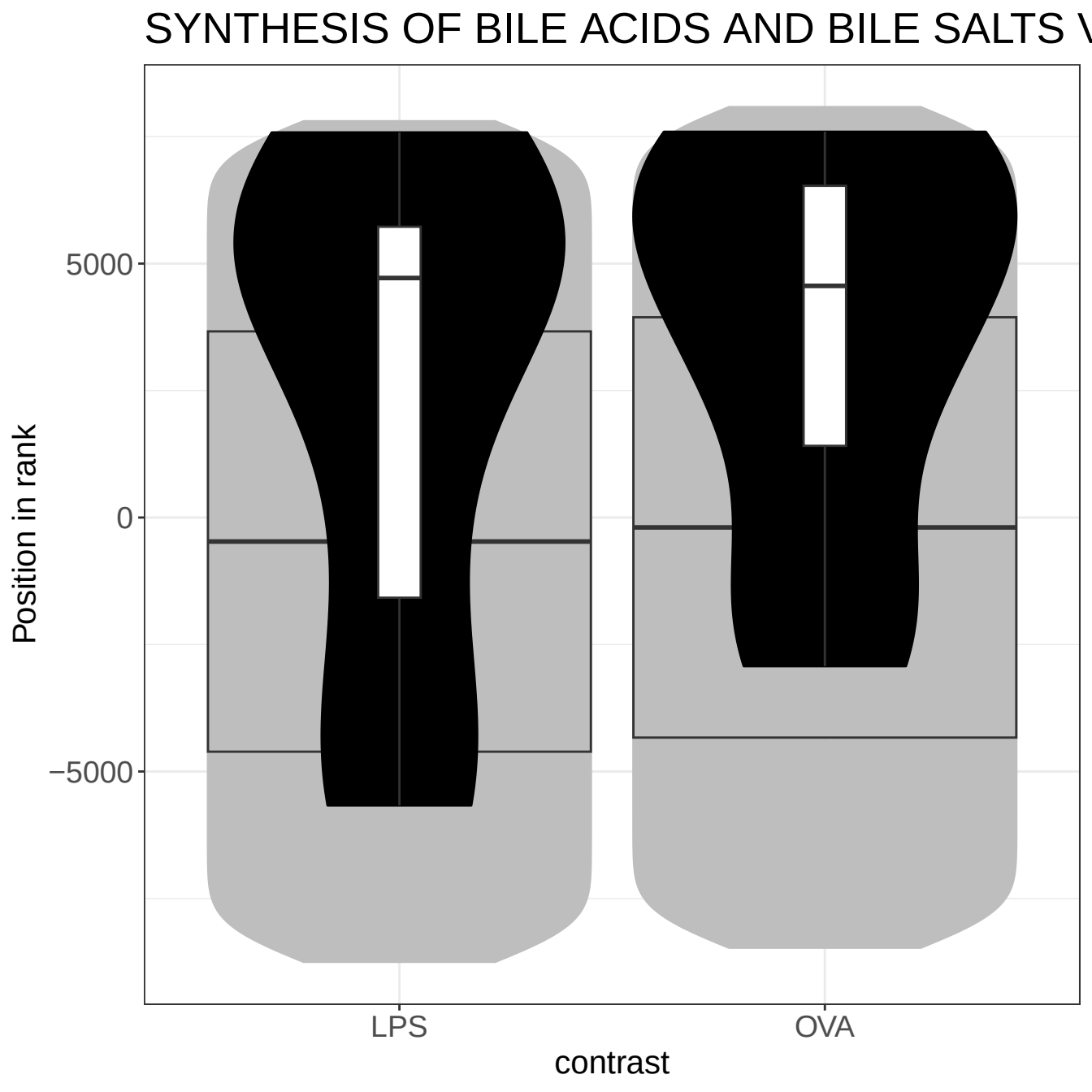

RESPIRATORY ELECTRON TRANSPORT
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

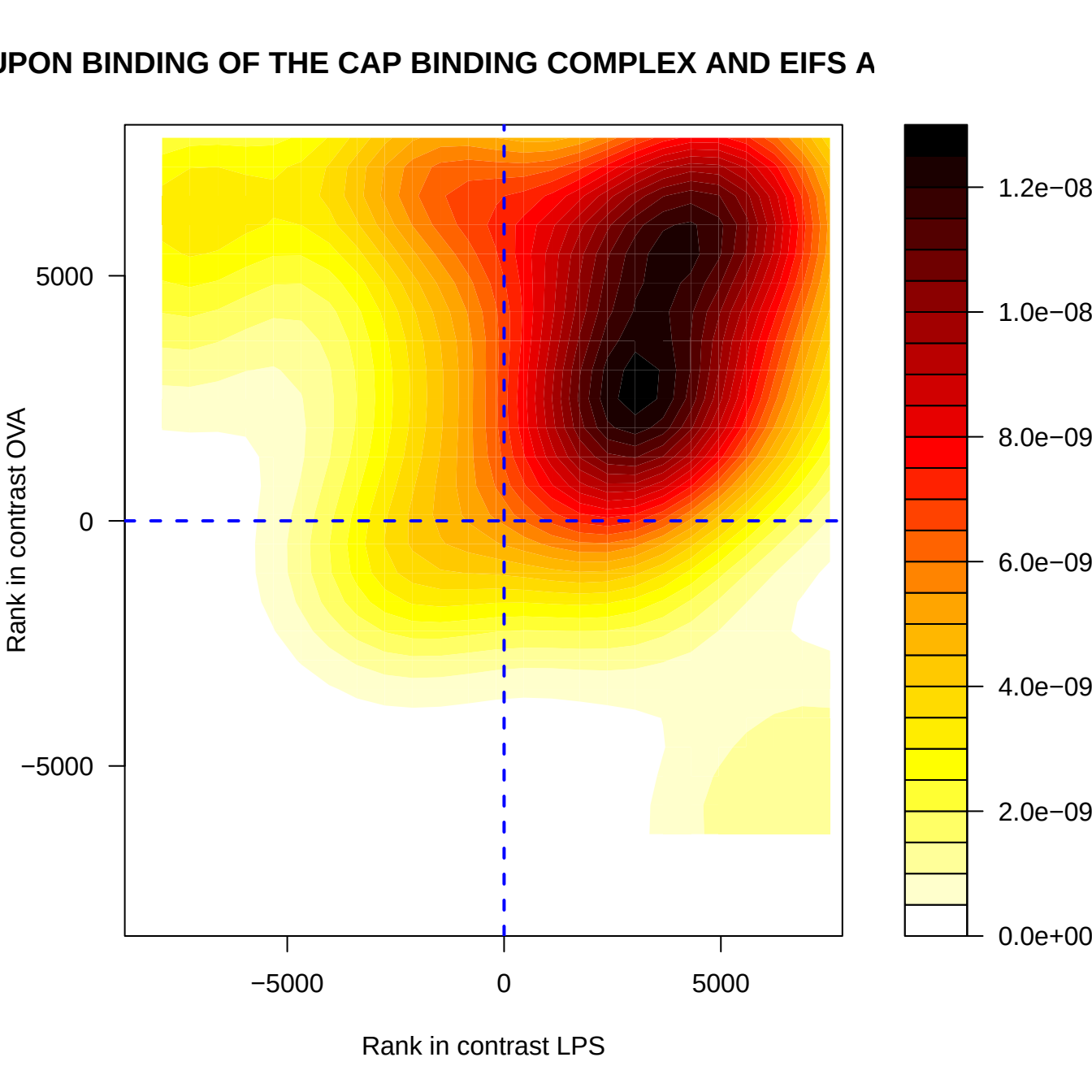

RESPIRATORY ELECTRON TRANSPORT
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

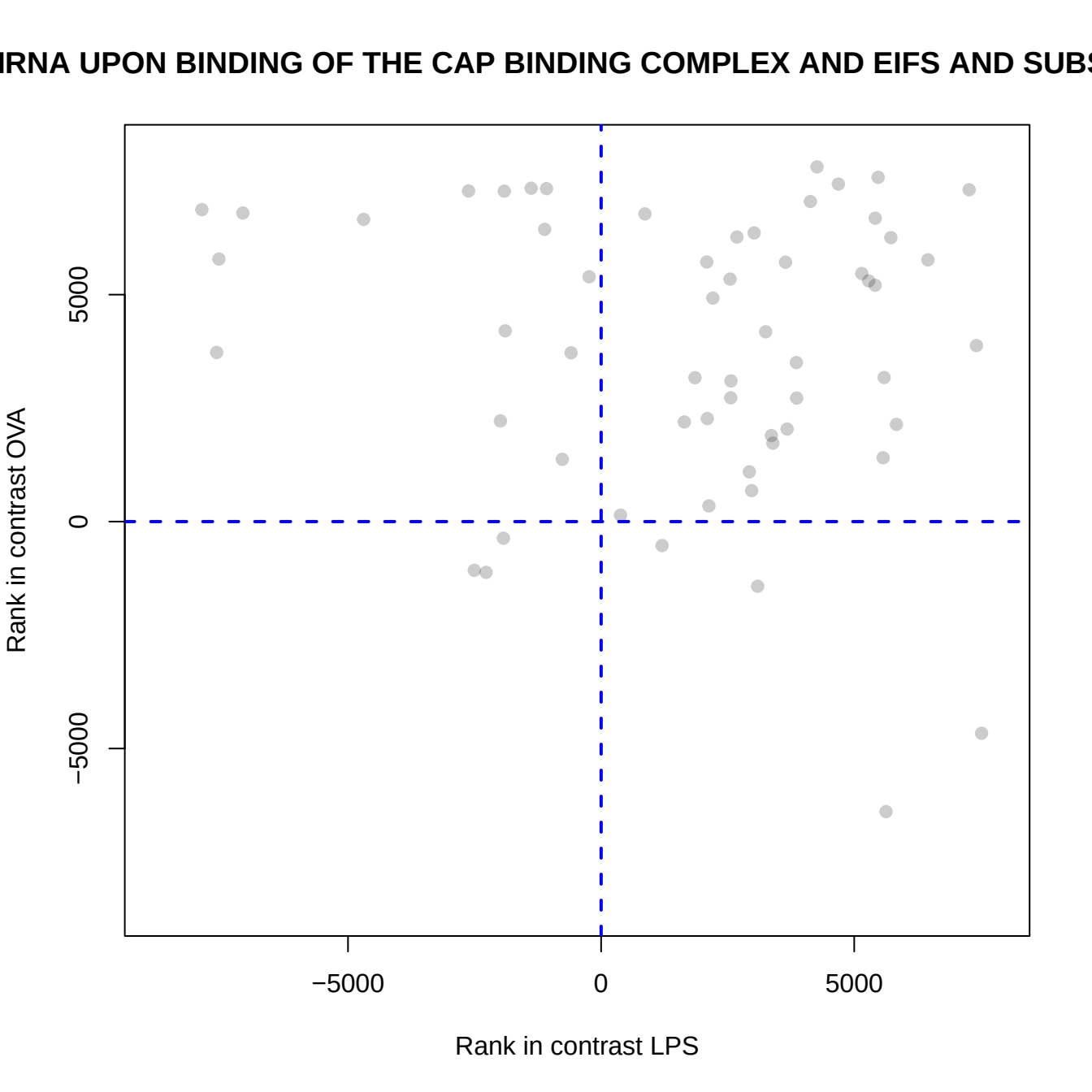

RESPIRATORY ELECTRON TRANSPORT
5000
0
−5000
Position in rank
LPS
OVA
contrast

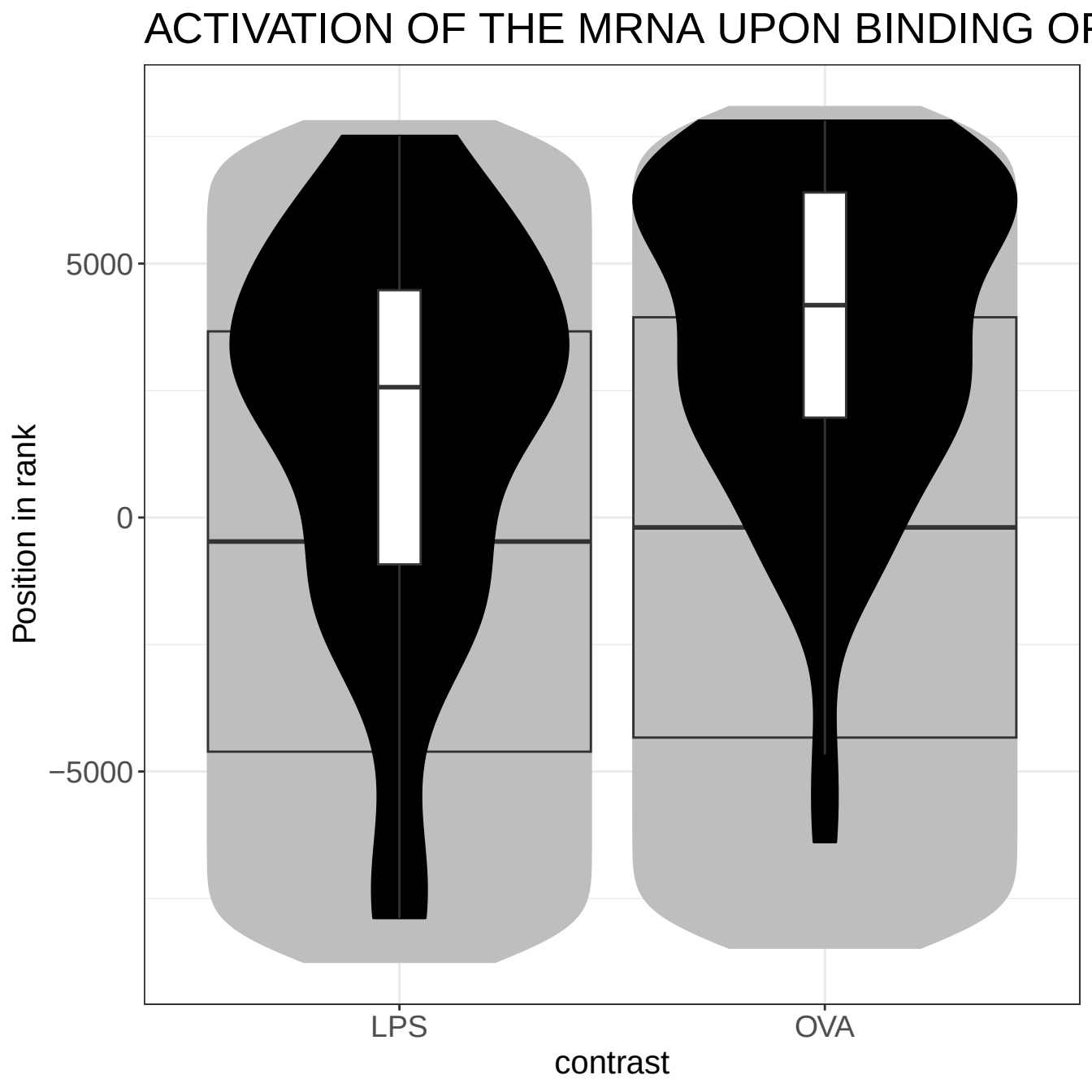

SIS OF BILE ACIDS AND BILE SALTS VIA 7ALPHA HYDROXY(
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09

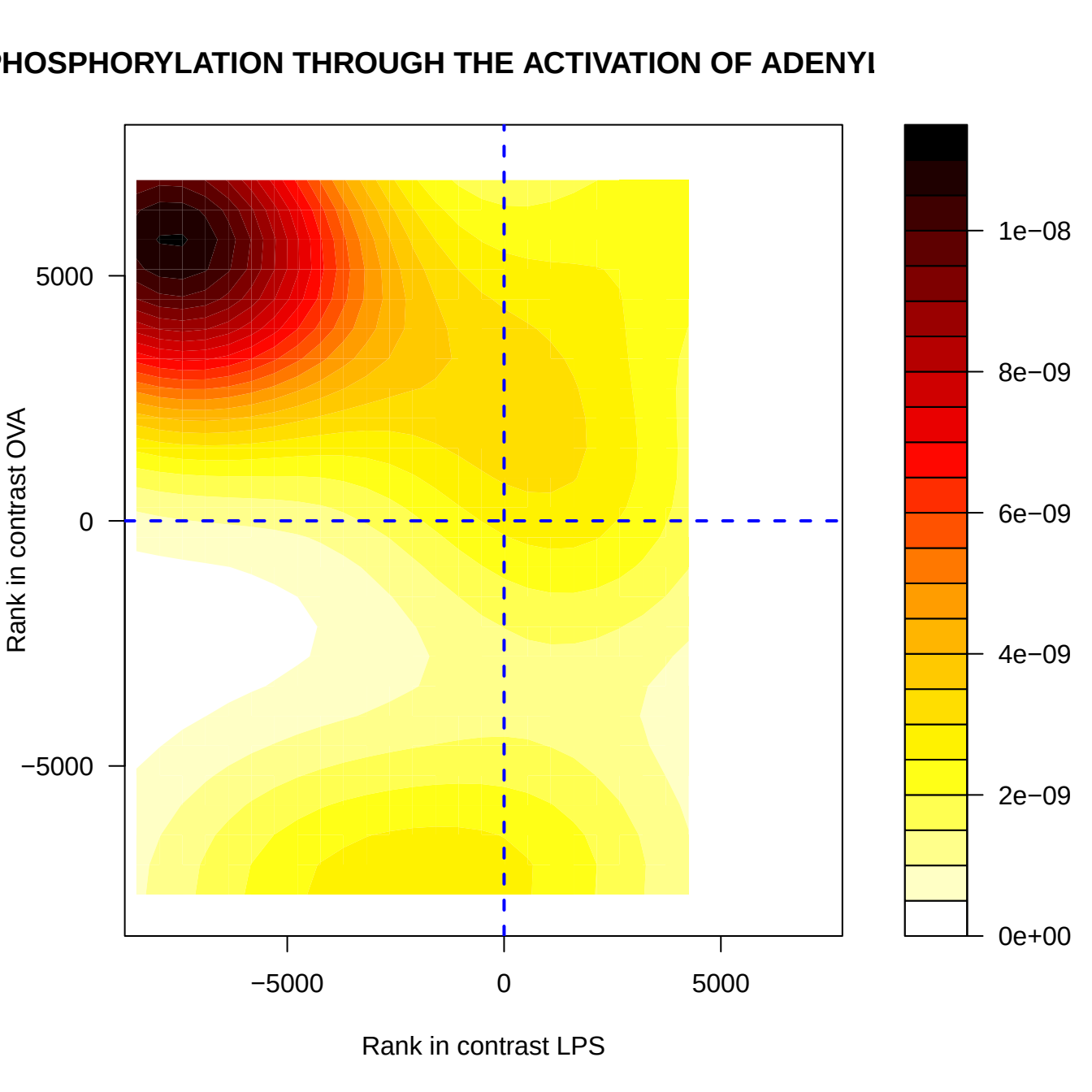

NTHESIS OF BILE ACIDS AND BILE SALTS VIA 7ALPHA HYDROXYCHOLES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

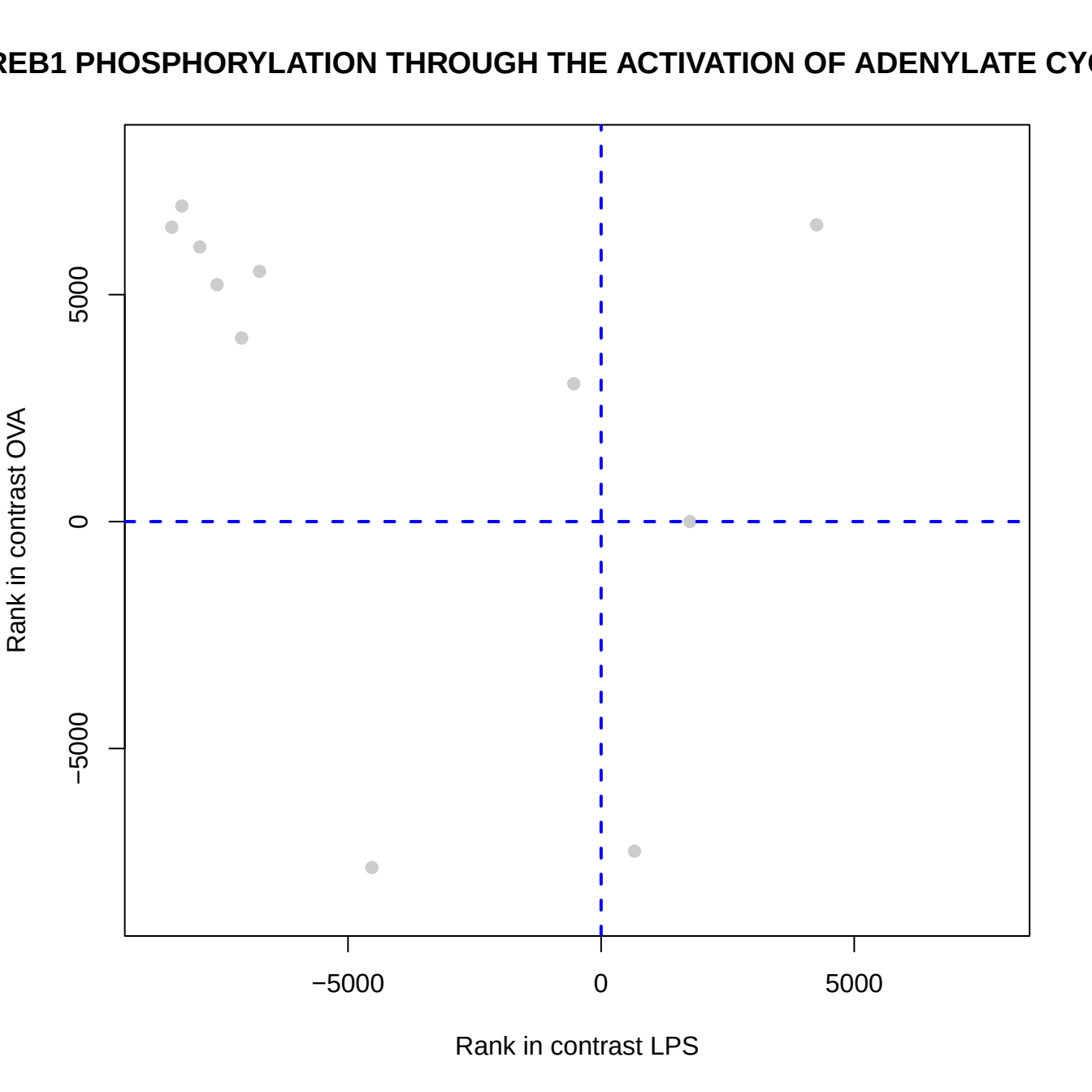

SYNTHESIS OF BILE ACIDS AND BILE SALTS V
5000
0
−5000
Position in rank
LPS
OVA
contrast

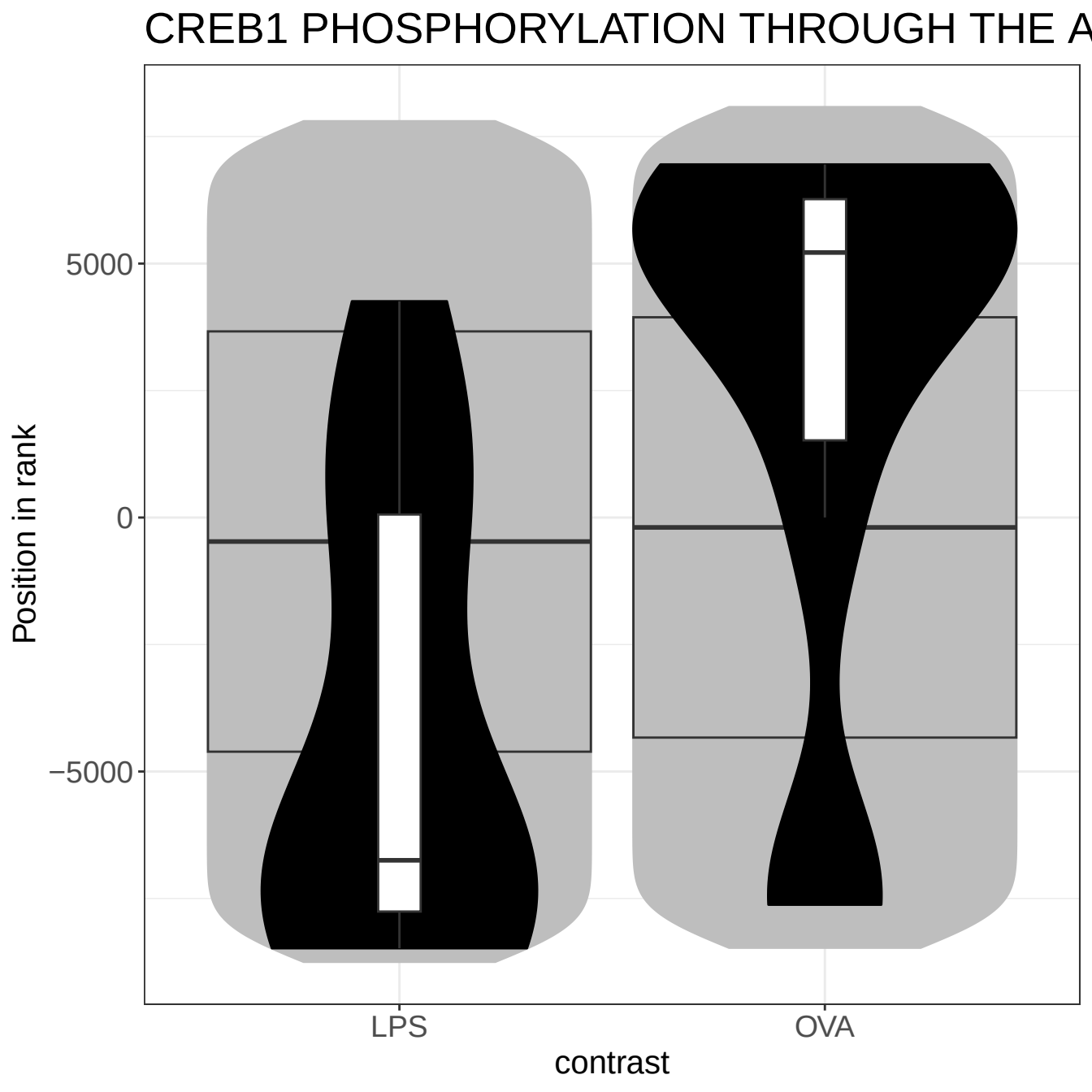

UPON BINDING OF THE CAP BINDING COMPLEX AND EIFS A
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

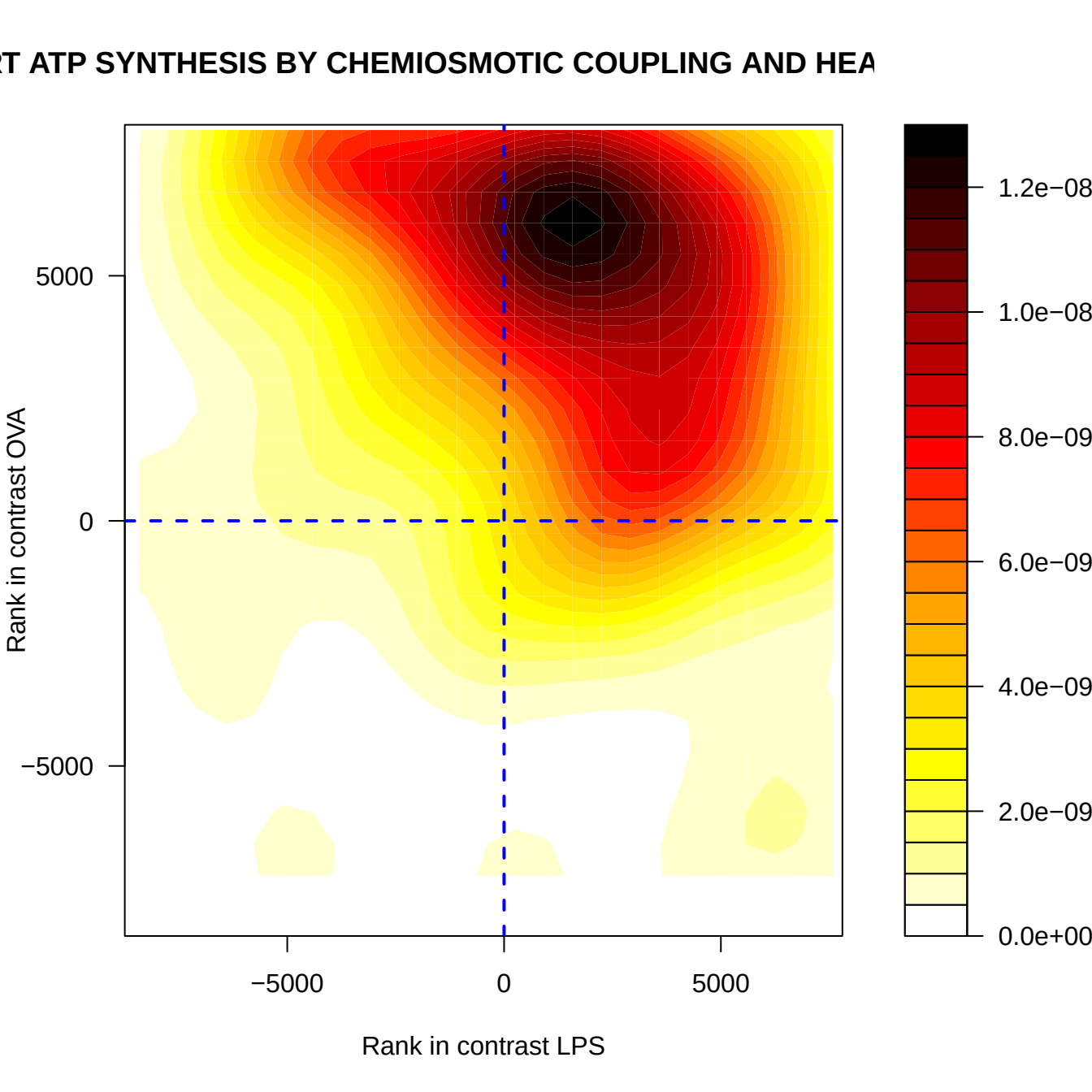

IRNA UPON BINDING OF THE CAP BINDING COMPLEX AND EIFS AND SUBS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

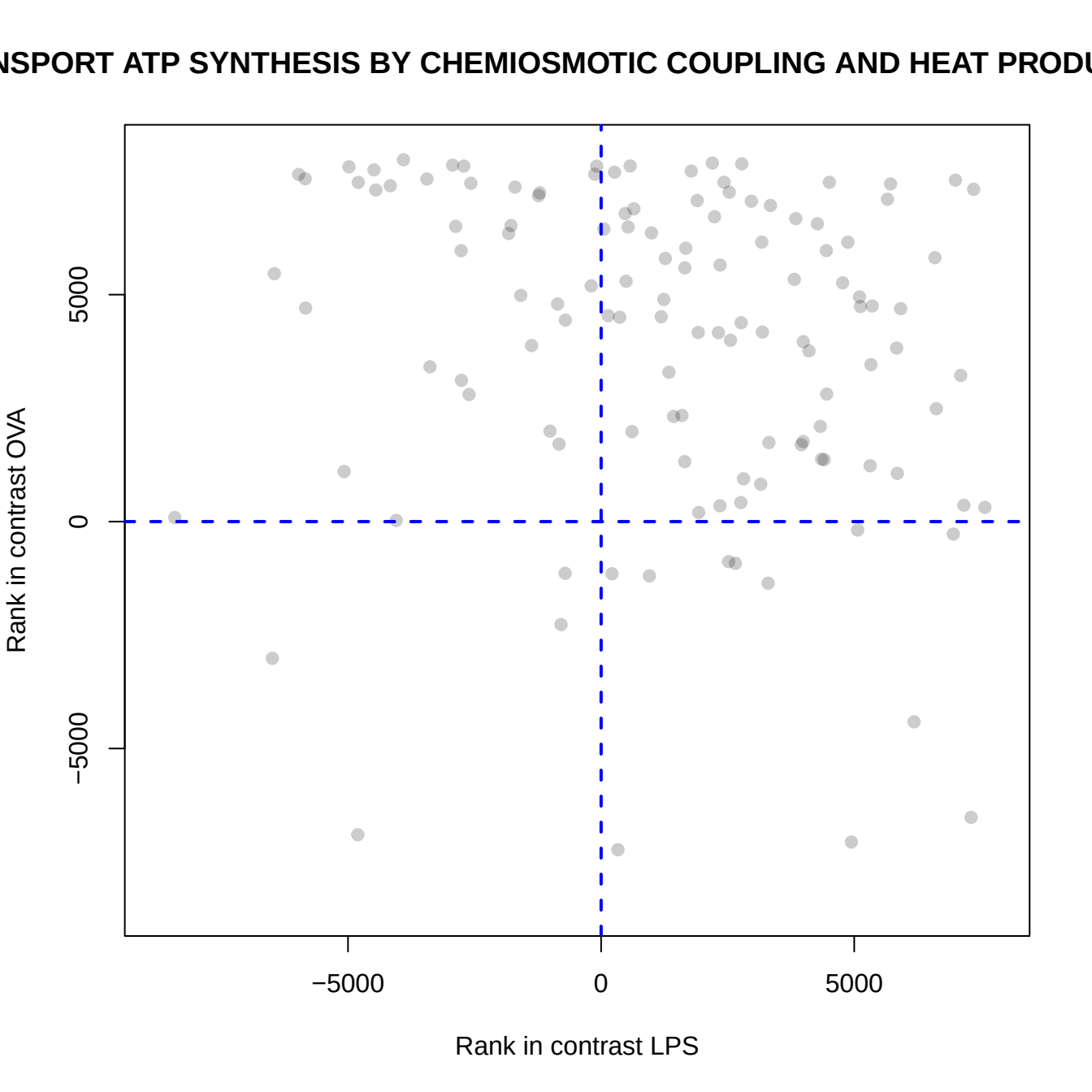

ACTIVATION OF THE MRNA UPON BINDING OF
5000
0
−5000
Position in rank
LPS
OVA
contrast

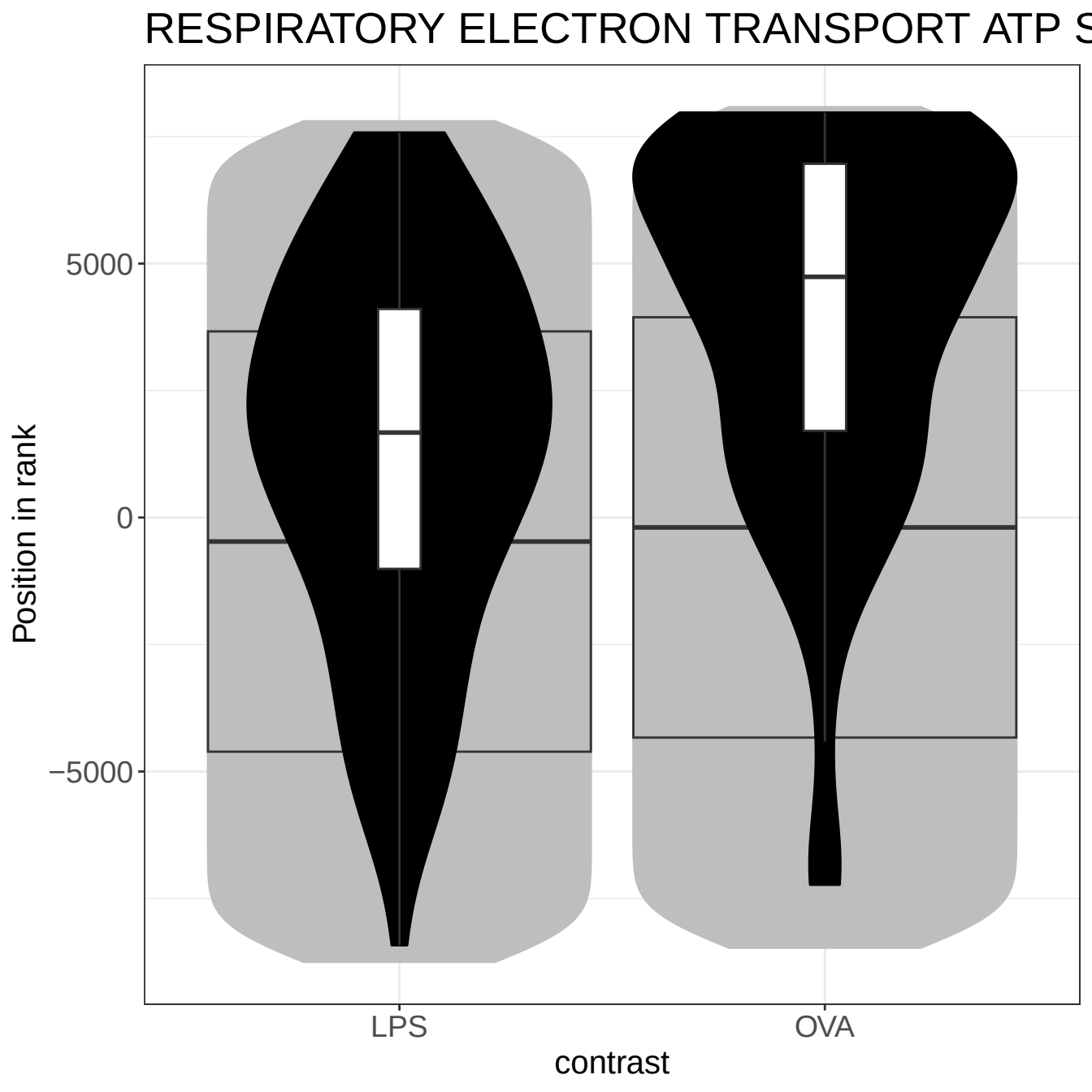

PHOSPHORYLATION THROUGH THE ACTIVATION OF ADENYI
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

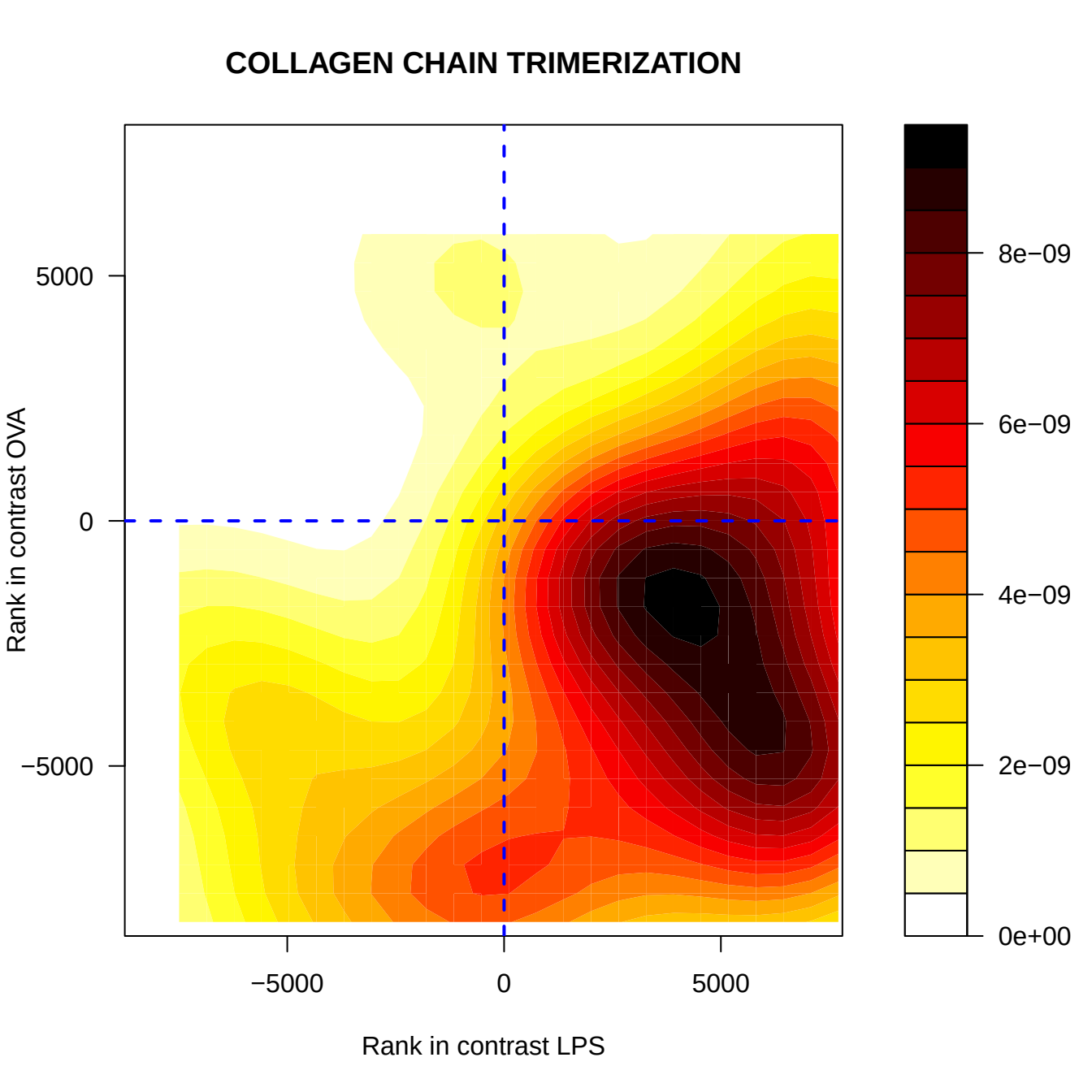

REB1 PHOSPHORYLATION THROUGH THE ACTIVATION OF ADENYLATE CY
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

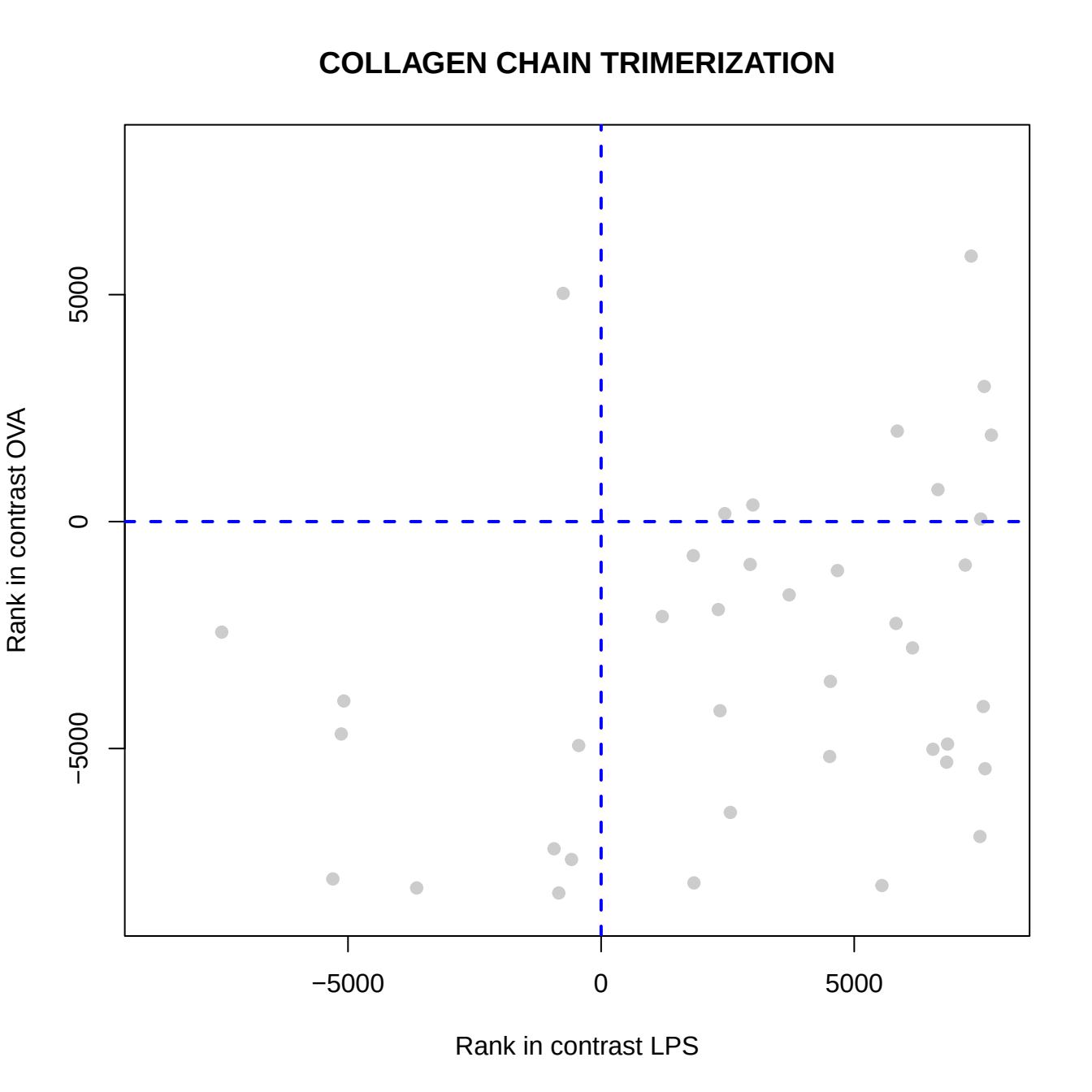

CREB1 PHOSPHORYLATION THROUGH THE A
5000
0
−5000
Position in rank
LPS
OVA
contrast

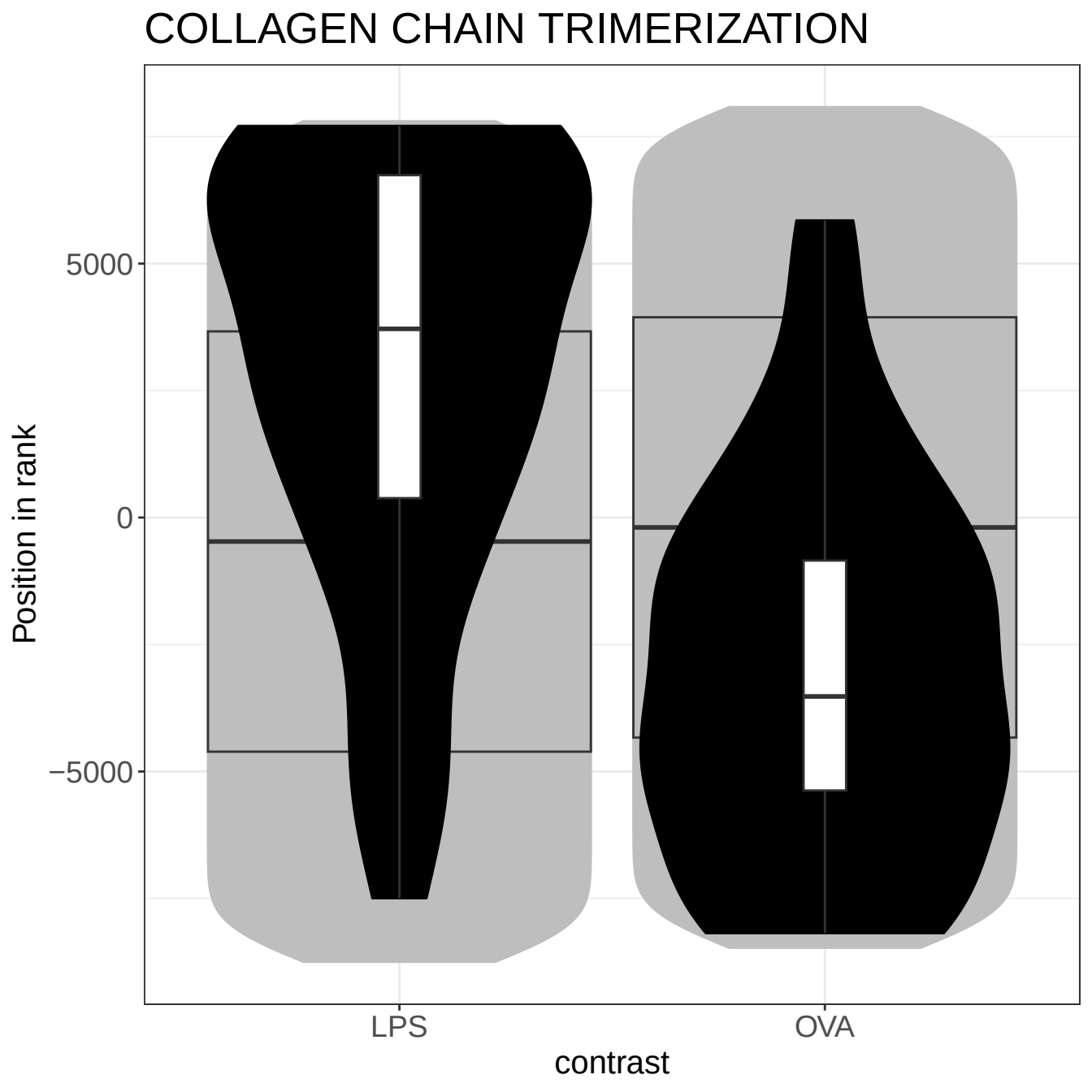

RT ATP SYNTHESIS BY CHEMIOSMOTIC COUPLING AND HEA
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

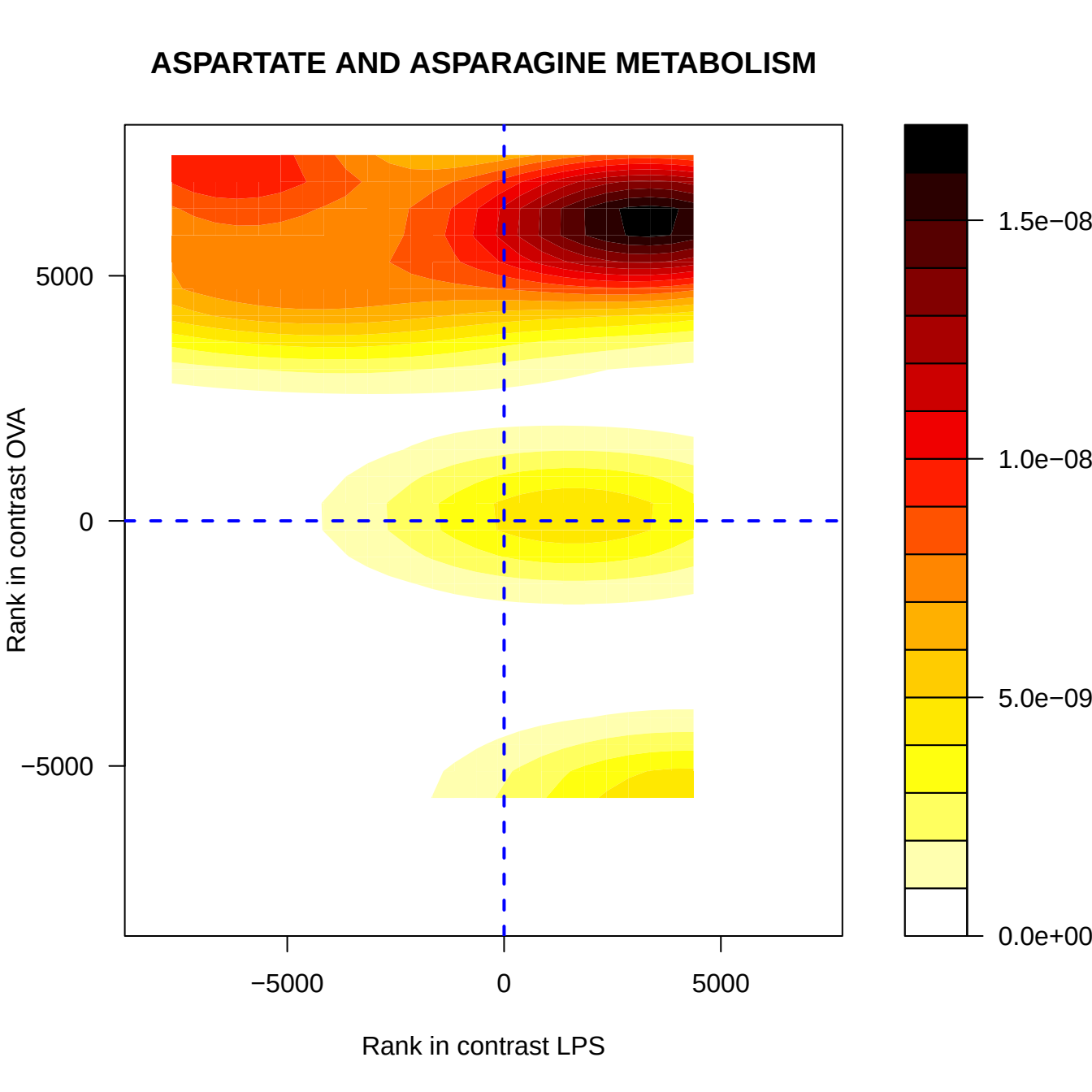

NSPORT ATP SYNTHESIS BY CHEMIOSMOTIC COUPLING AND HEAT PRODU
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

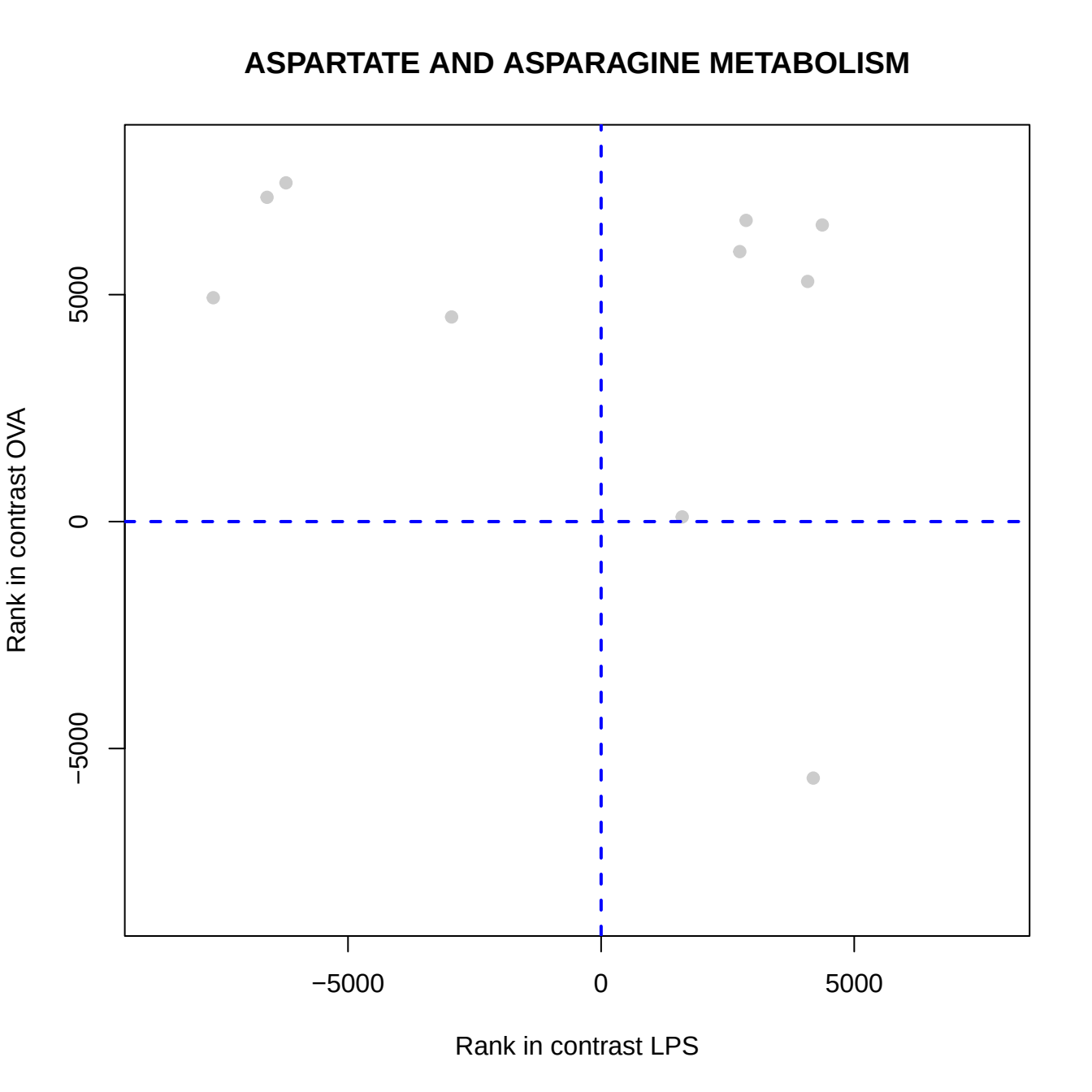

RESPIRATORY ELECTRON TRANSPORT ATP S
5000
0
−5000
Position in rank
LPS
OVA
contrast

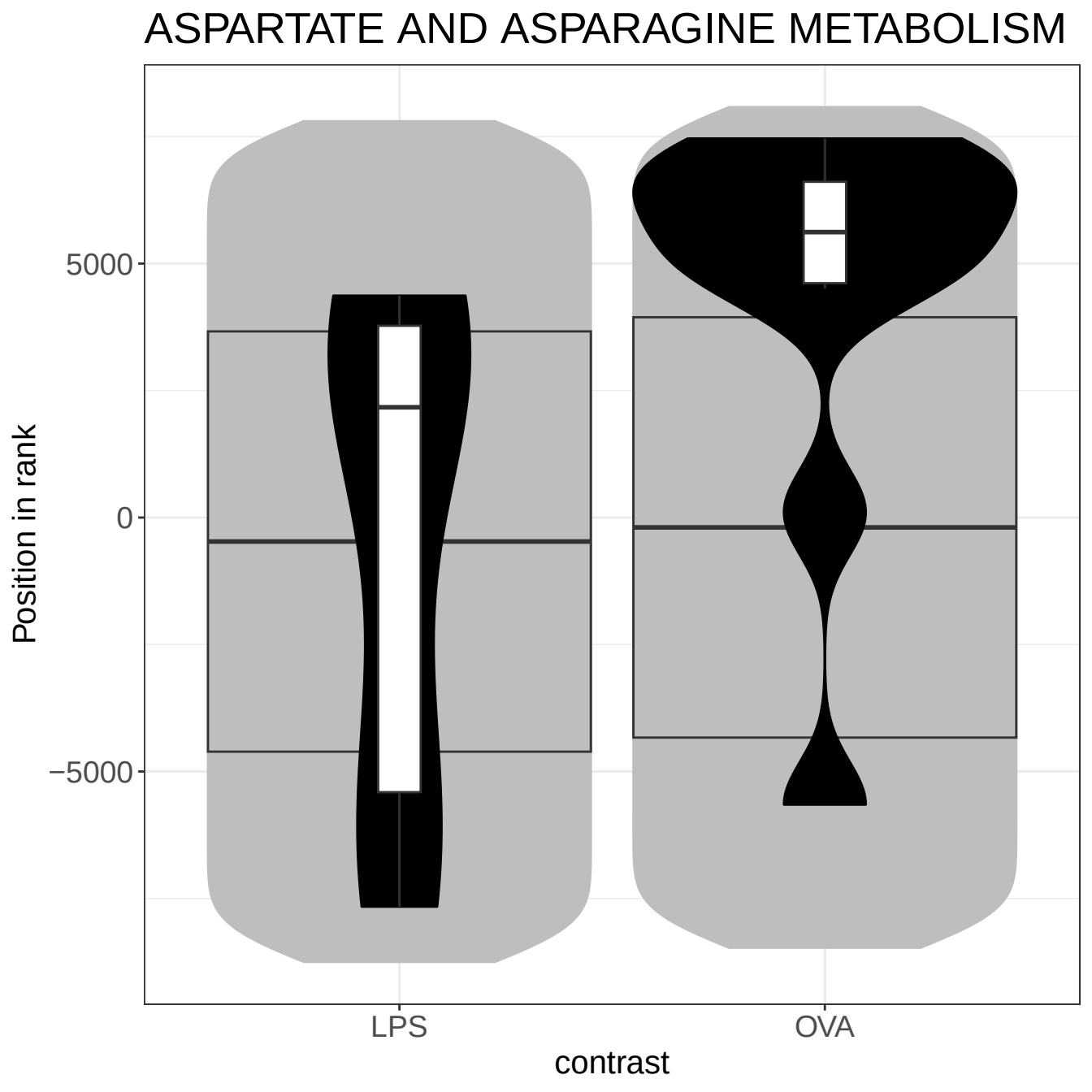

COLLAGEN CHAIN TRIMERIZATION
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

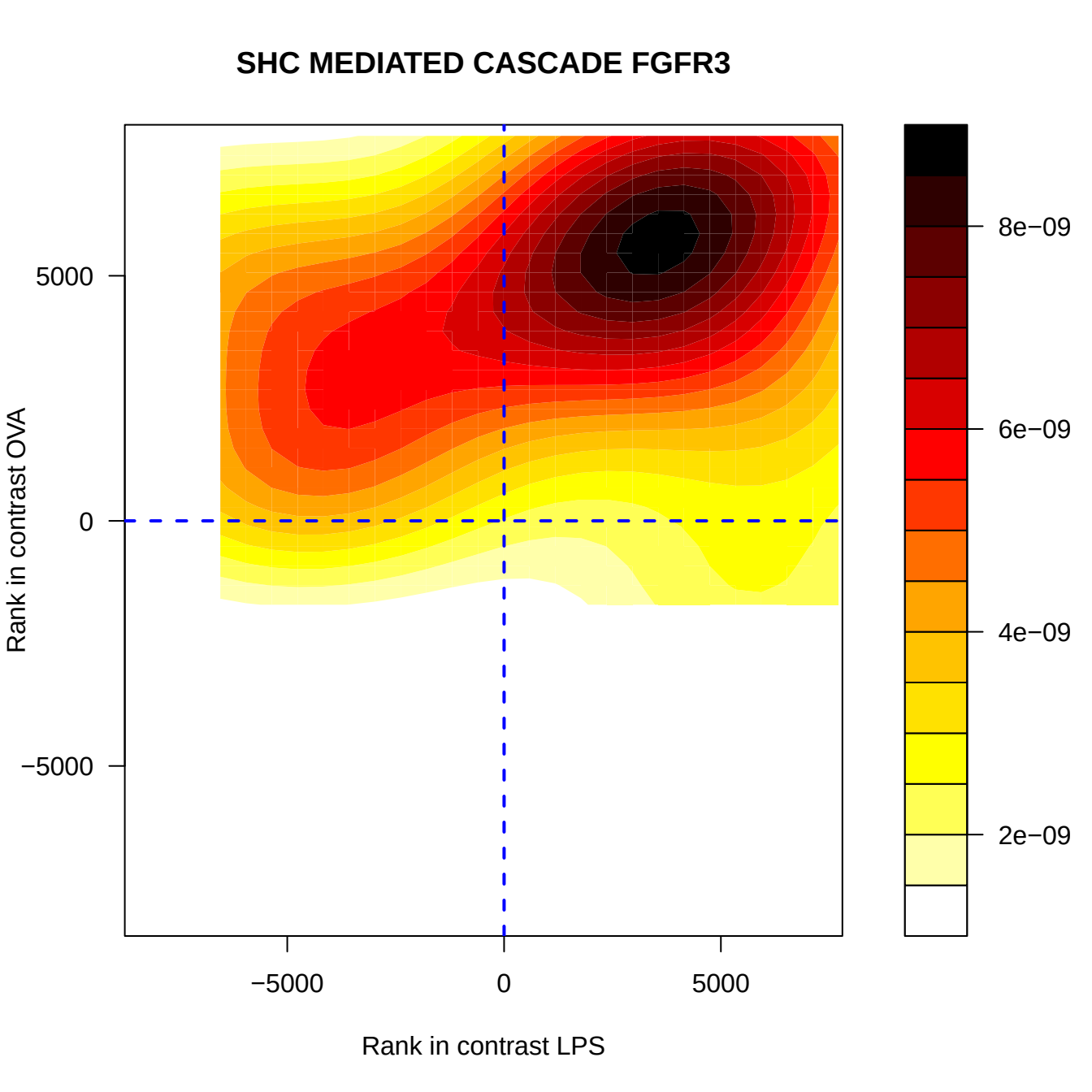

COLLAGEN CHAIN TRIMERIZATION
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

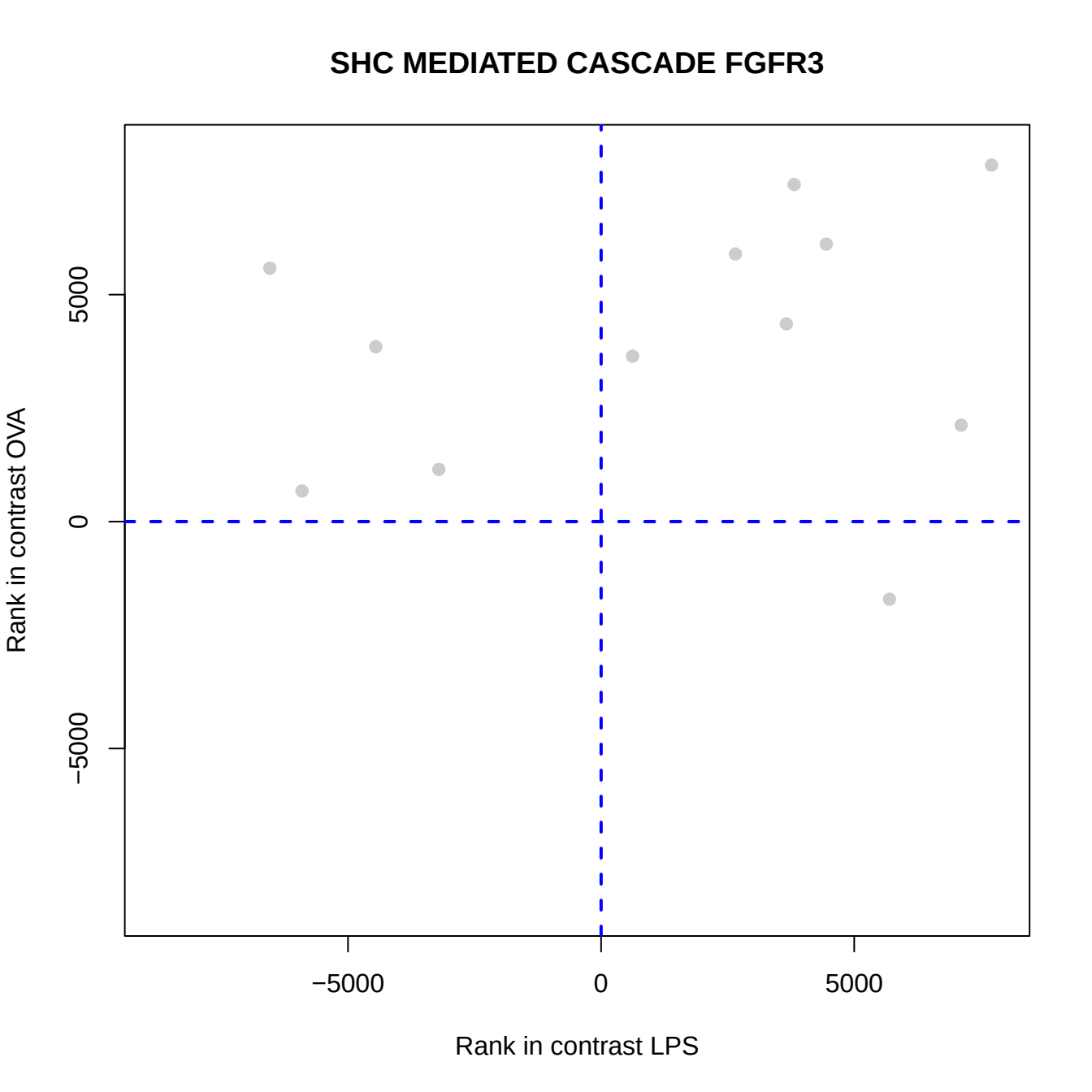

COLLAGEN CHAIN TRIMERIZATION
5000
0
−5000
Position in rank
LPS
OVA
contrast

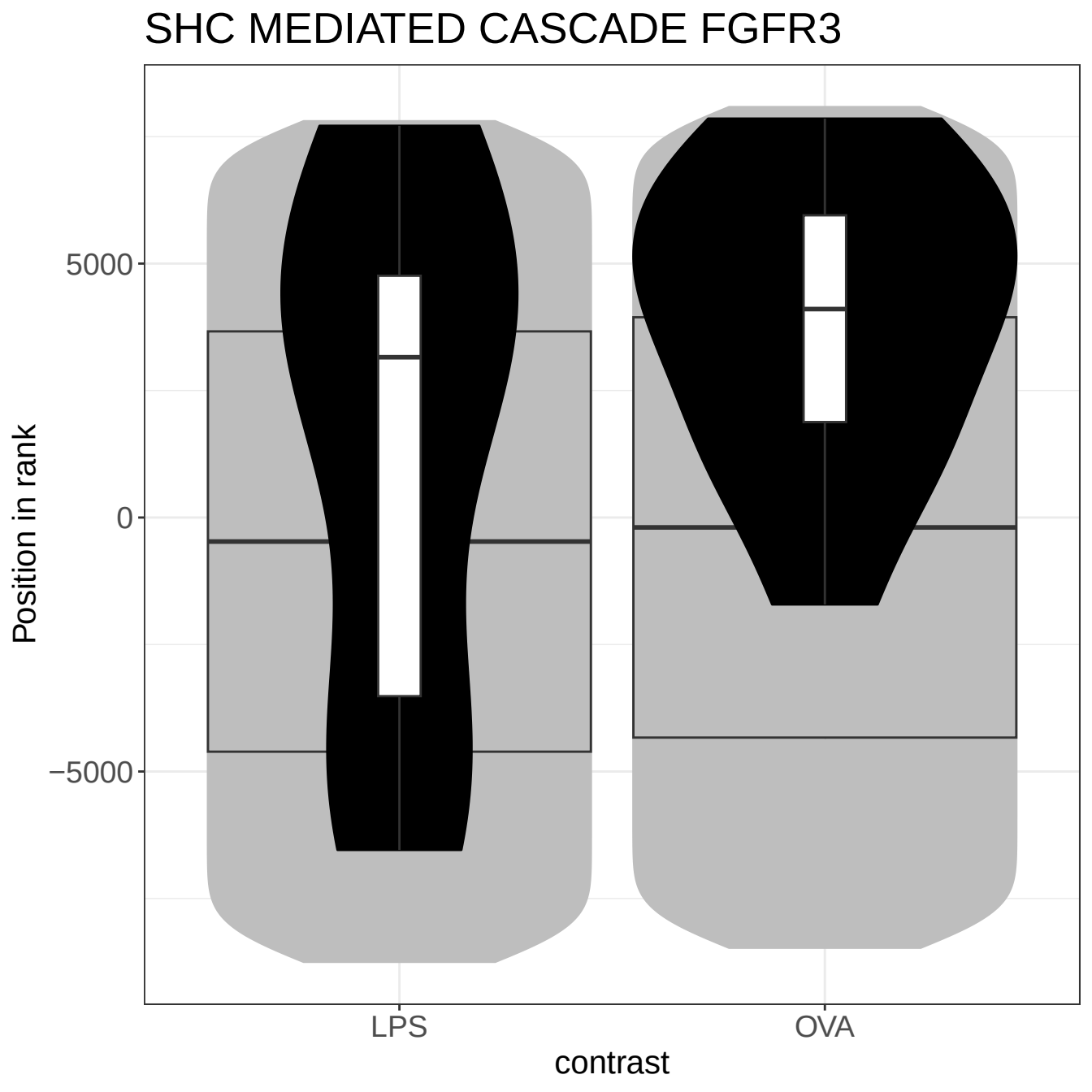

ASPARTATE AND ASPARAGINE METABOLISM
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

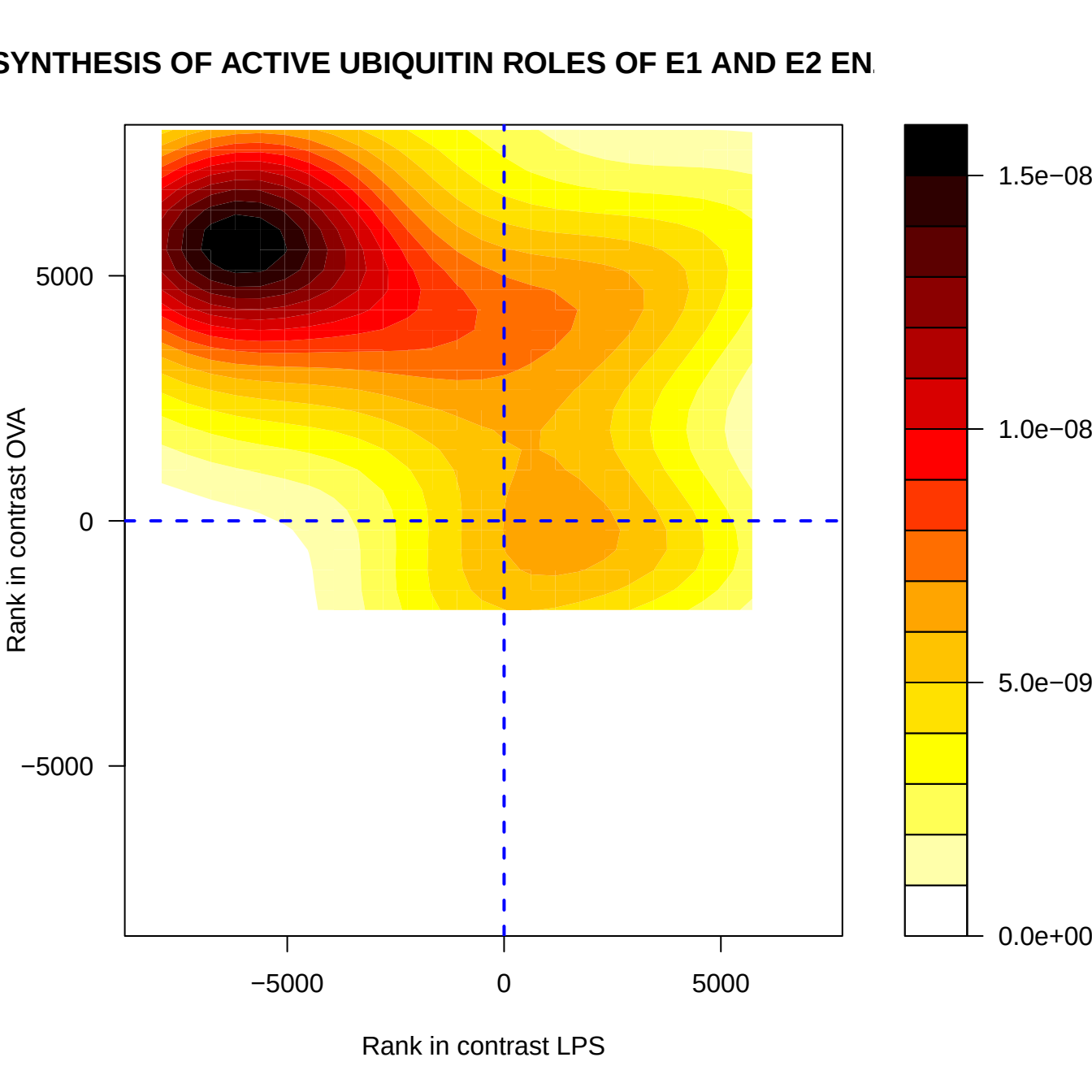

ASPARTATE AND ASPARAGINE METABOLISM
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS


ASPARTATE AND ASPARAGINE METABOLISM
5000
0
−5000
Position in rank
LPS
OVA
contrast

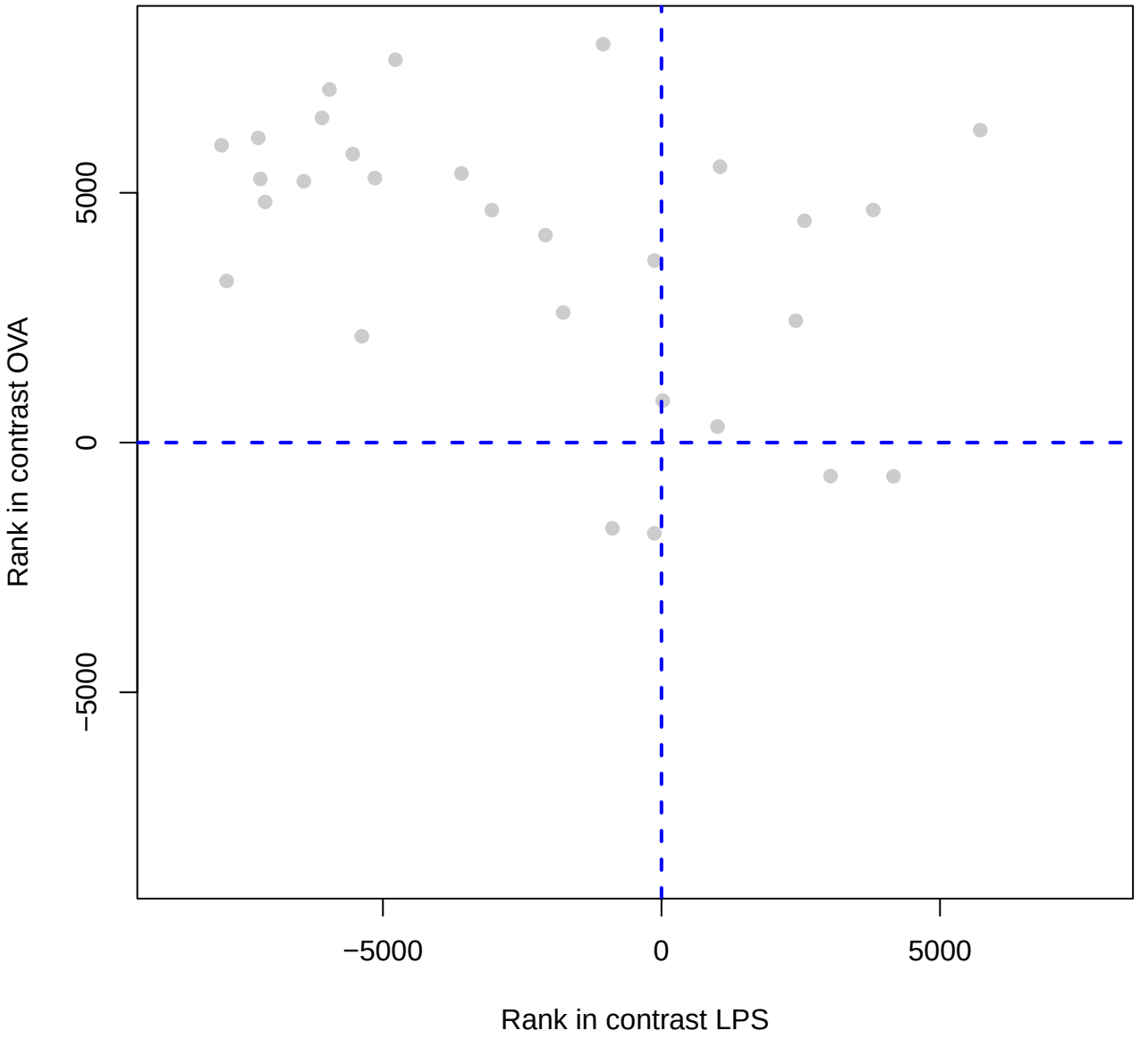

SHC MEDIATED CASCADE FGFR3
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09

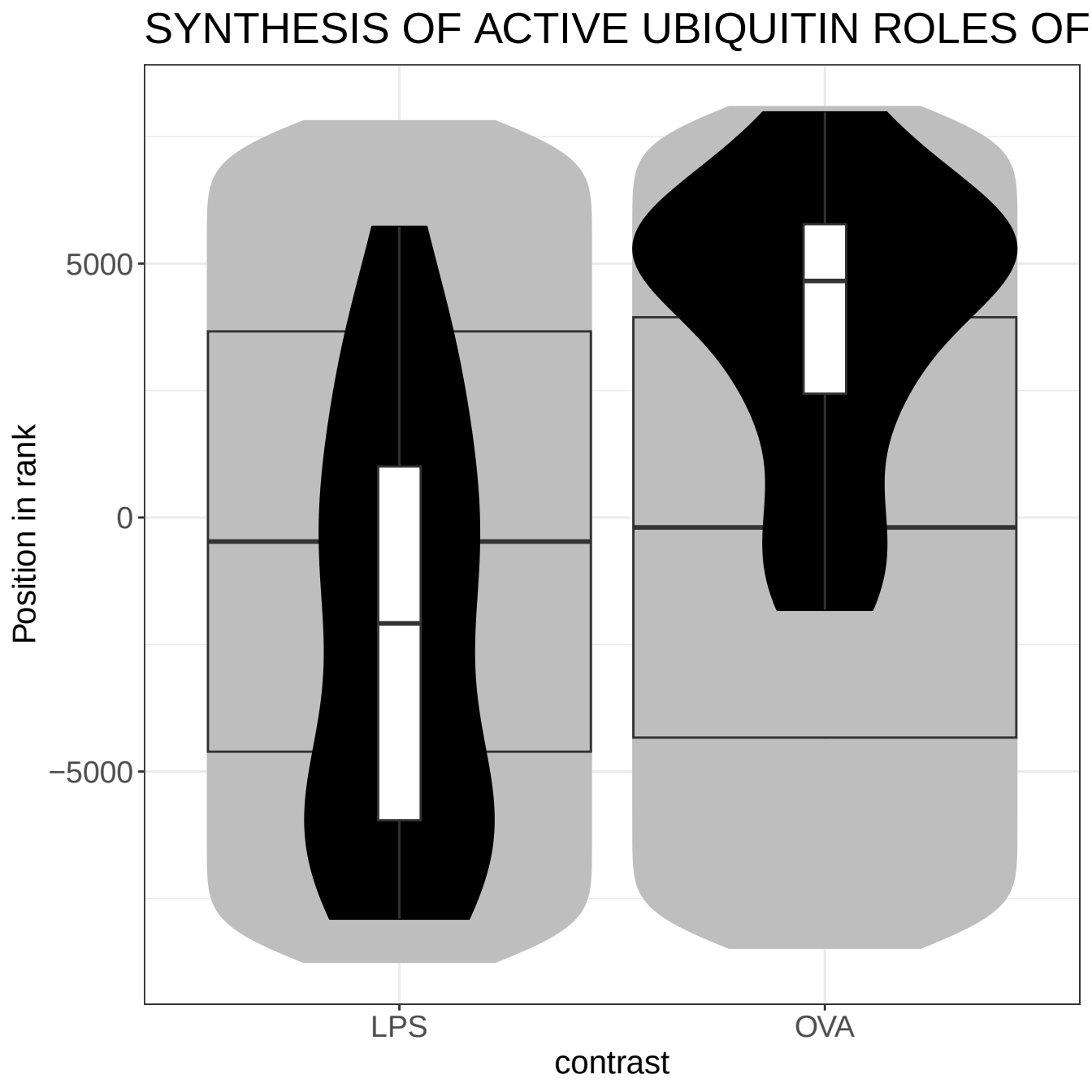

SHC MEDIATED CASCADE FGFR3
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

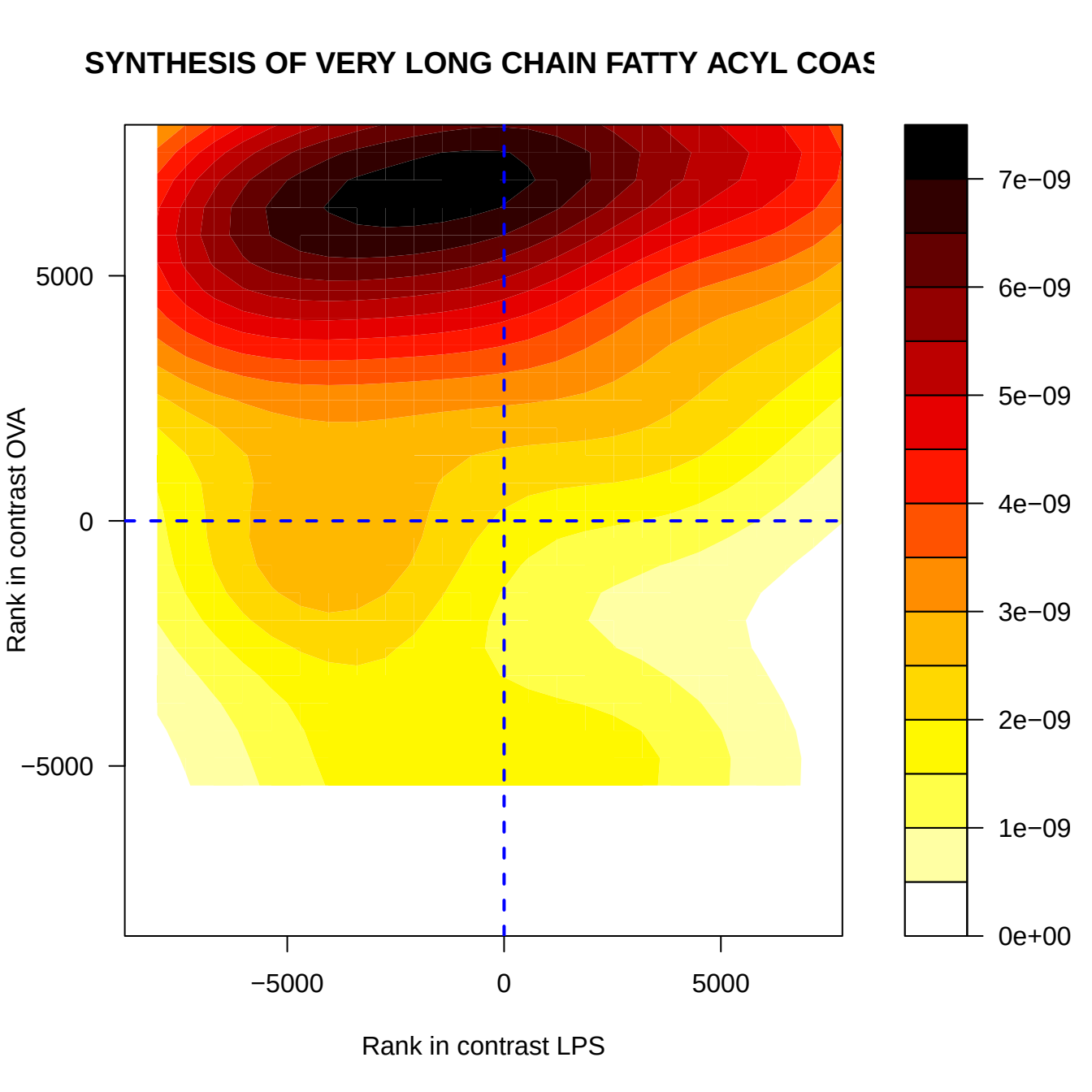

SHC MEDIATED CASCADE FGFR3
5000
0
−5000
Position in rank
LPS
OVA
contrast

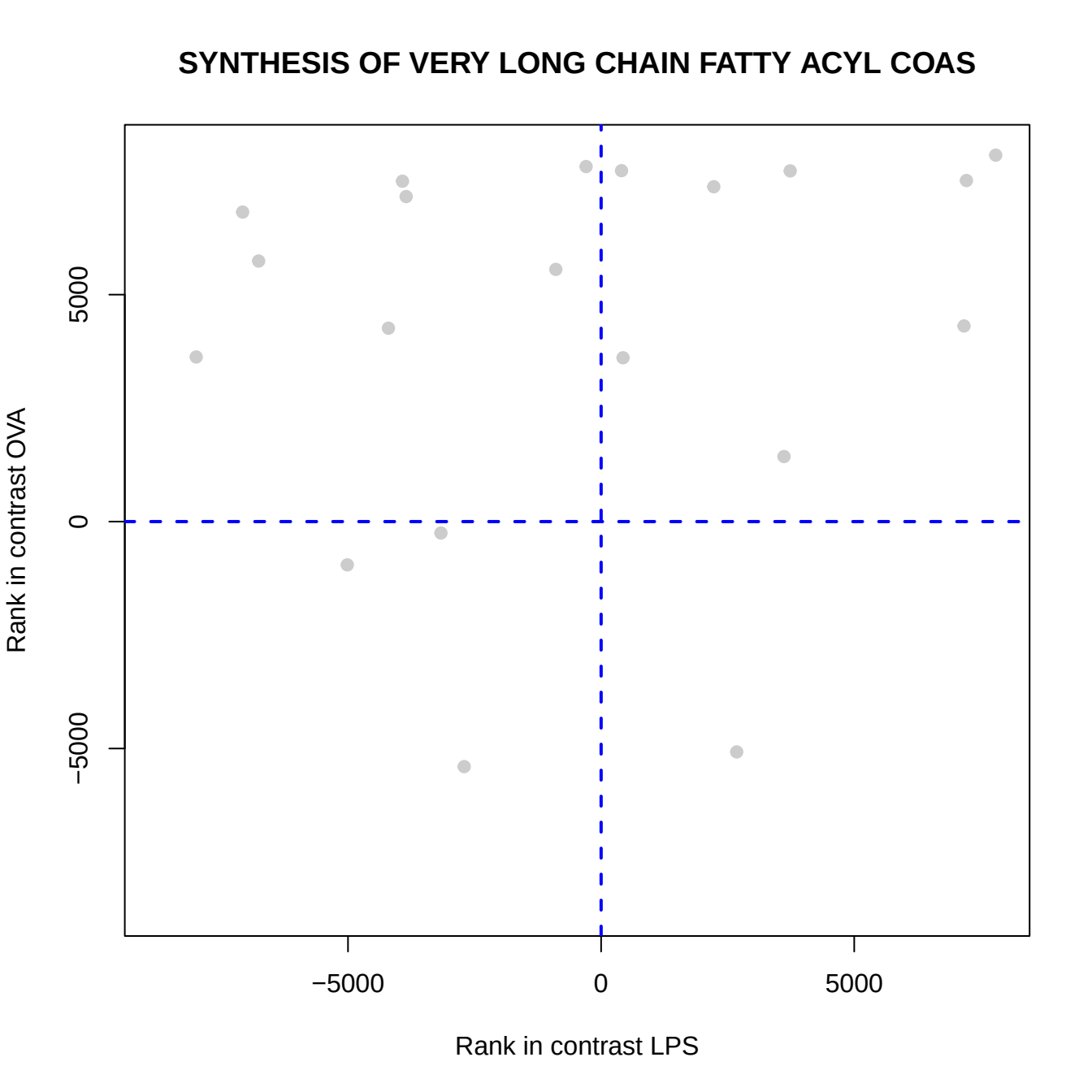

SYNTHESIS OF ACTIVE UBIQUITIN ROLES OF E1 AND E2 EN
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

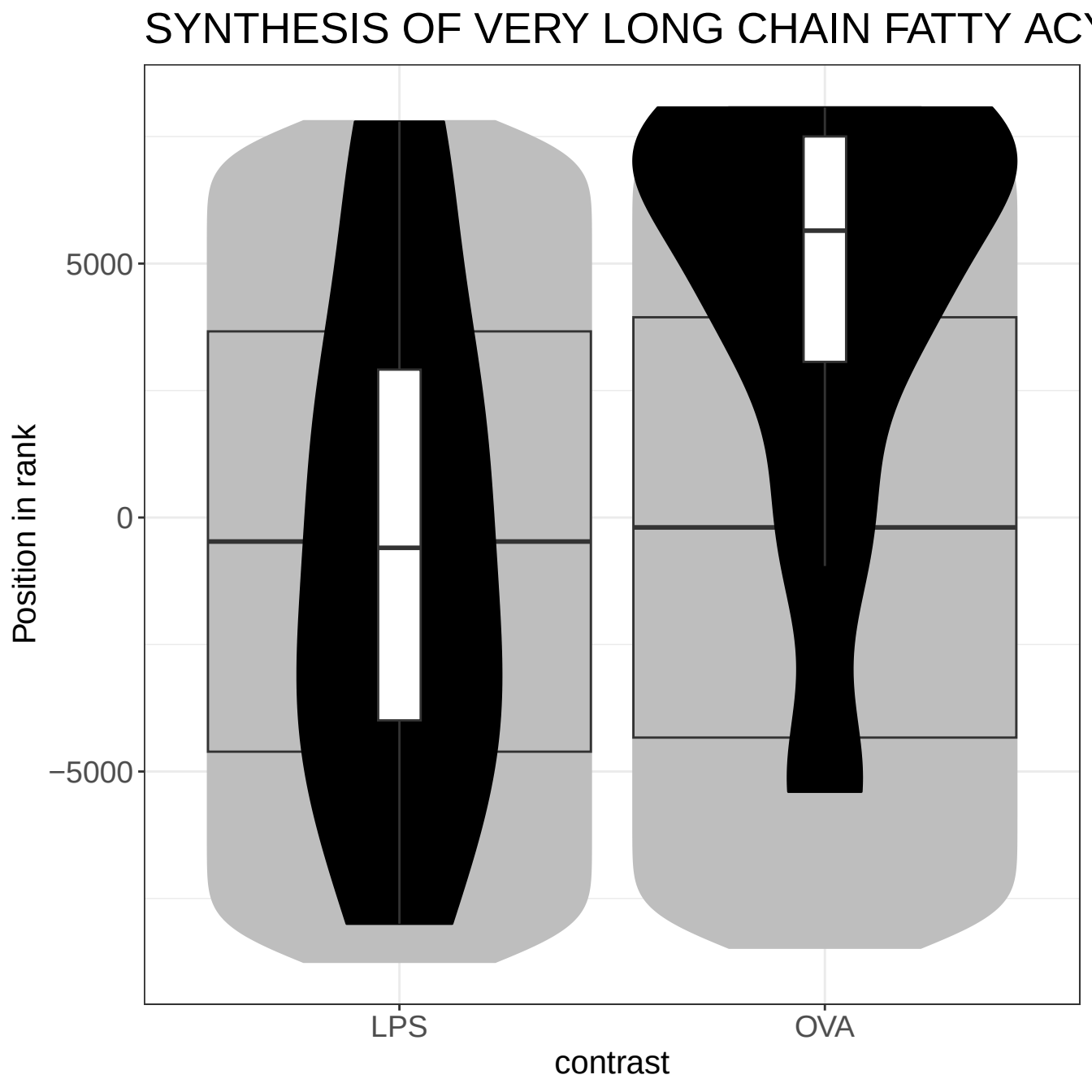
SYNTHESIS OF ACTIVE UBIQUITIN ROLES OF E1 AND E2 ENZYMES

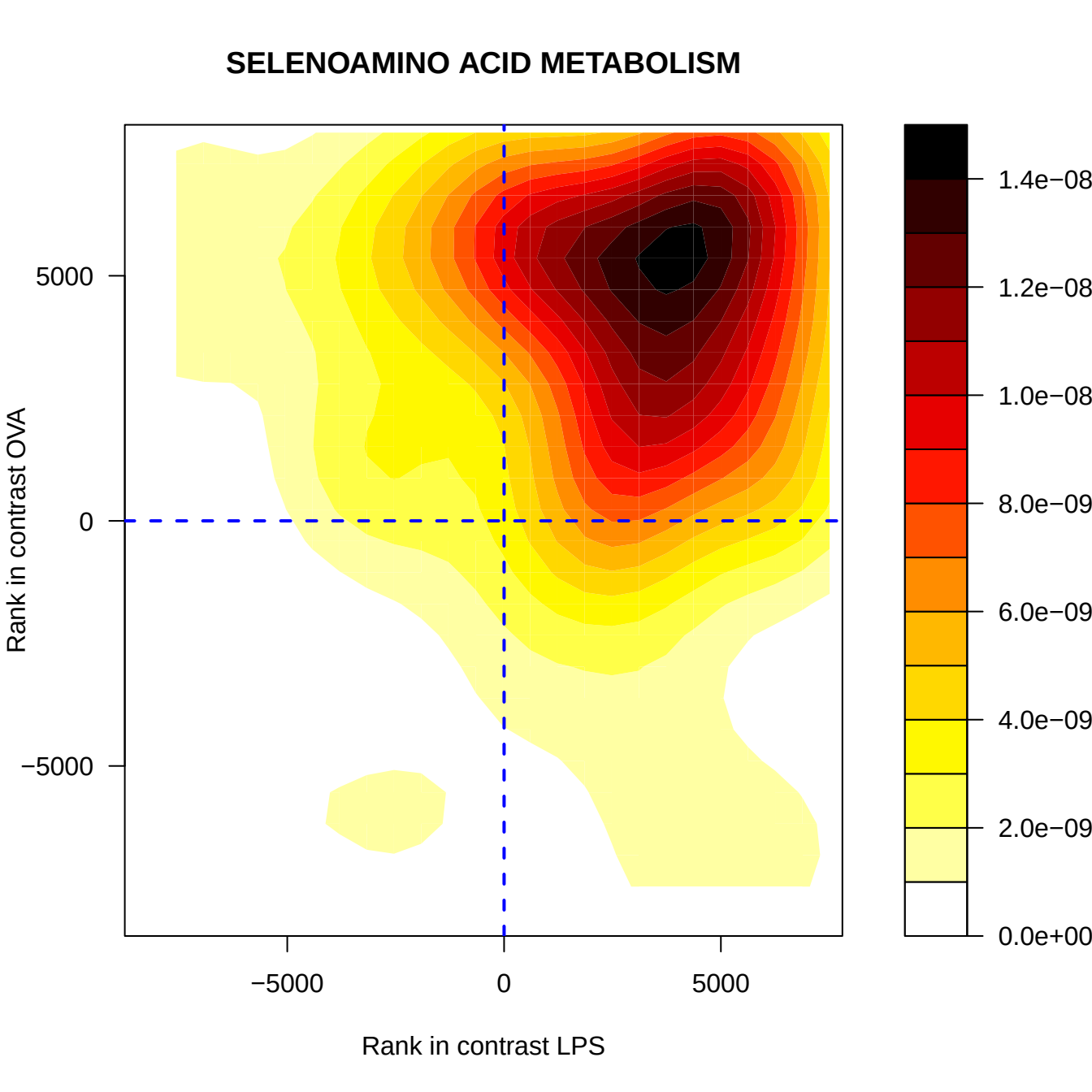


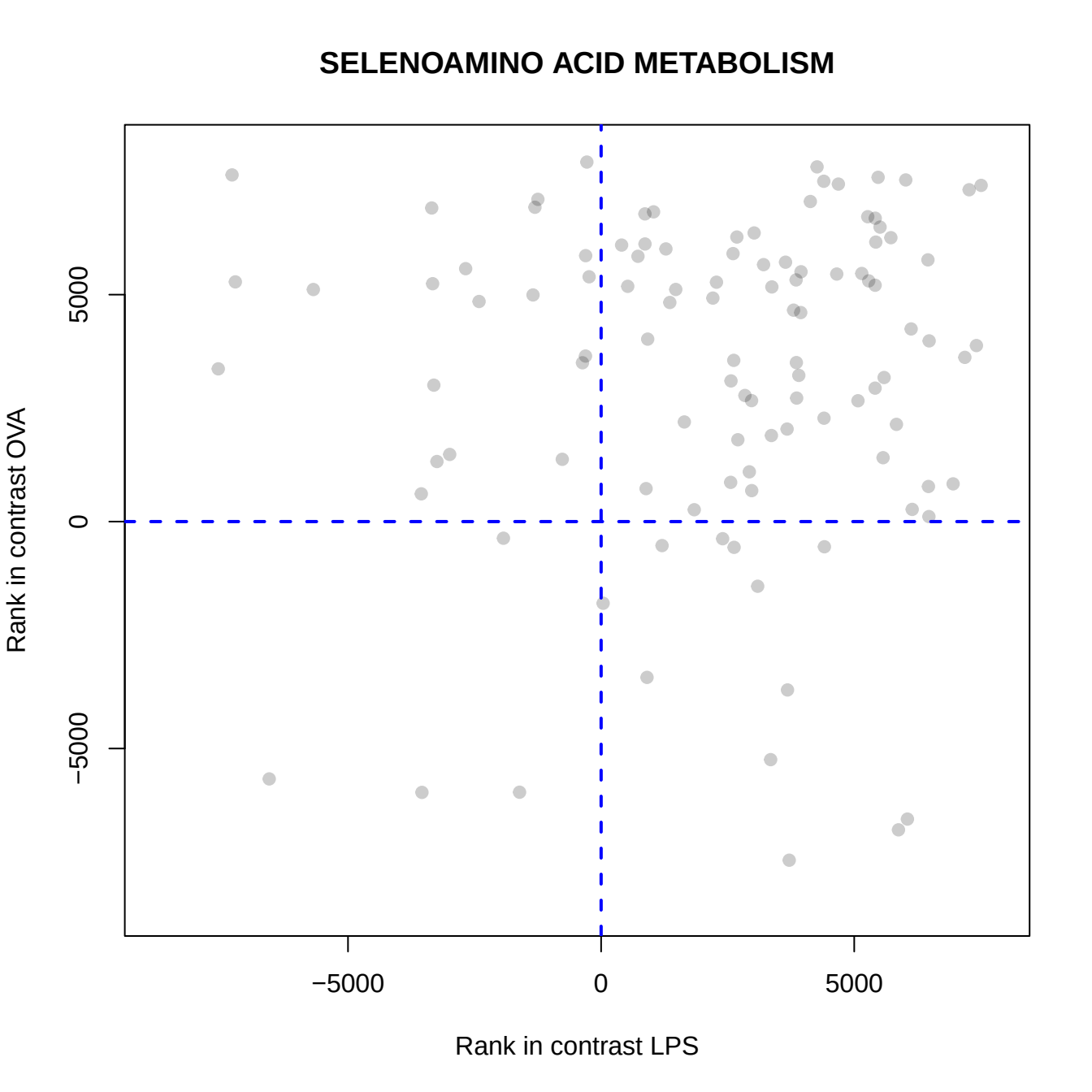

SYNTHESIS OF ACTIVE UBIQUITIN ROLES OF
5000
0
−5000
Position in rank
LPS
OVA
contrast

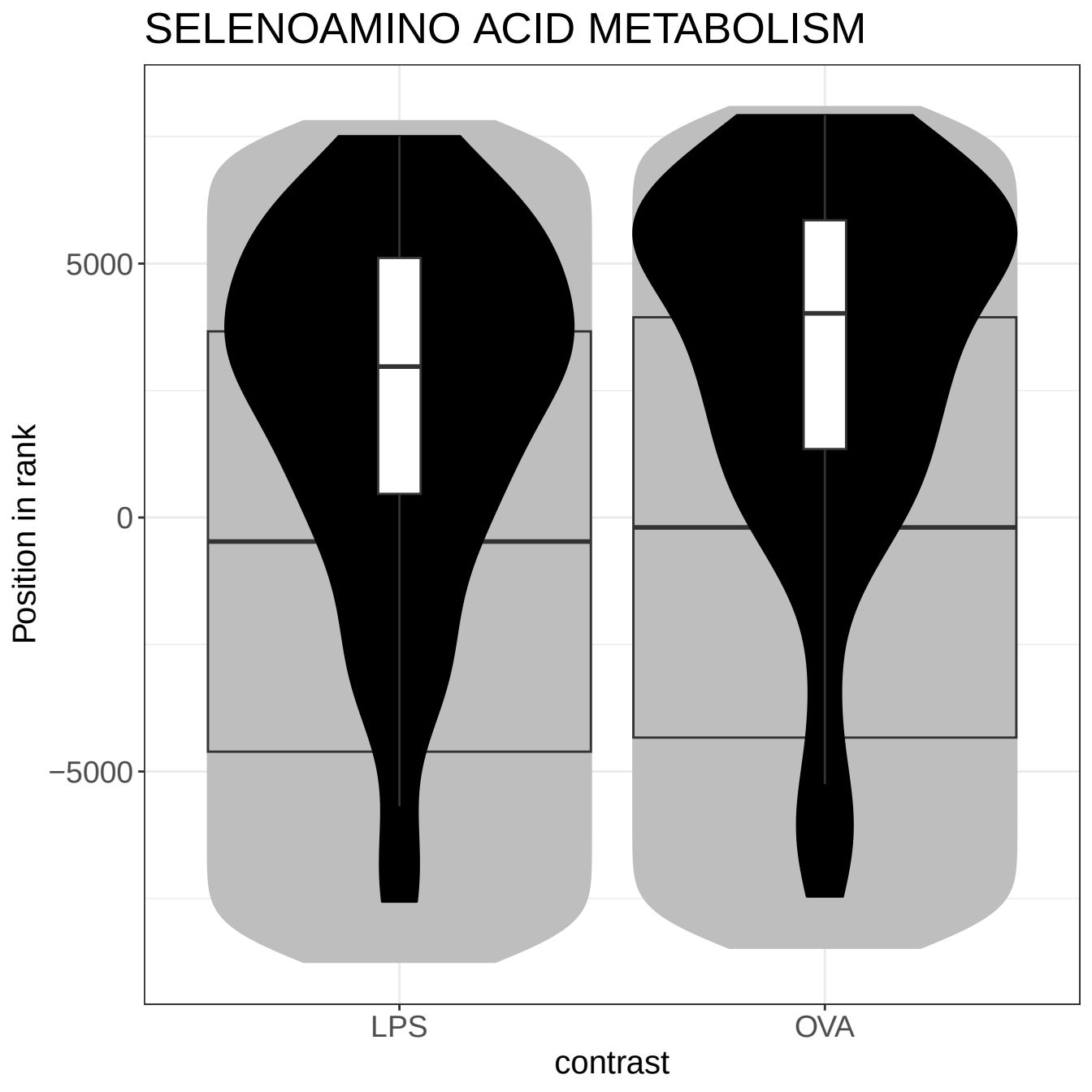

SYNTHESIS OF VERY LONG CHAIN FATTY ACYL COAS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
7e−09
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

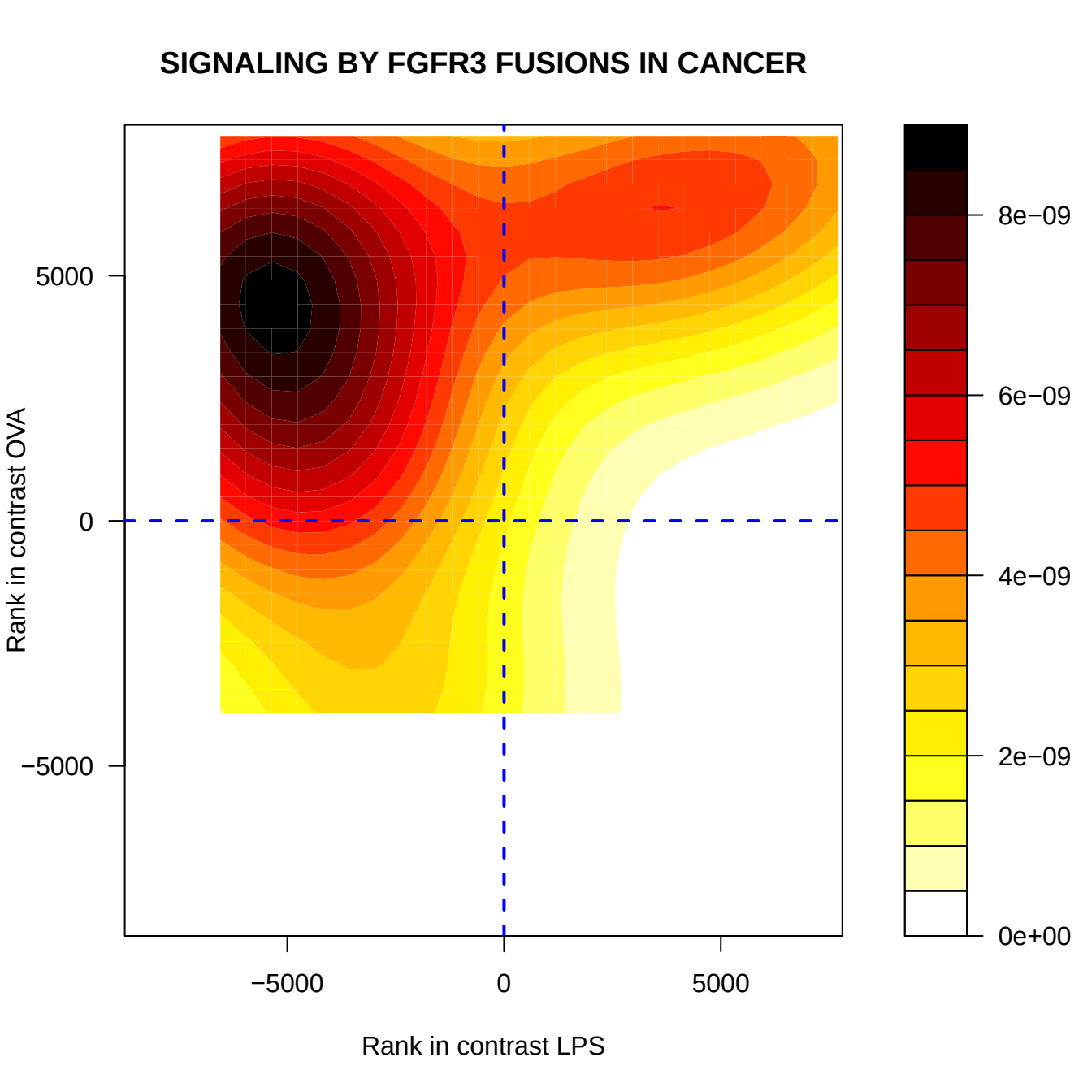

SYNTHESIS OF VERY LONG CHAIN FATTY ACYL COAS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

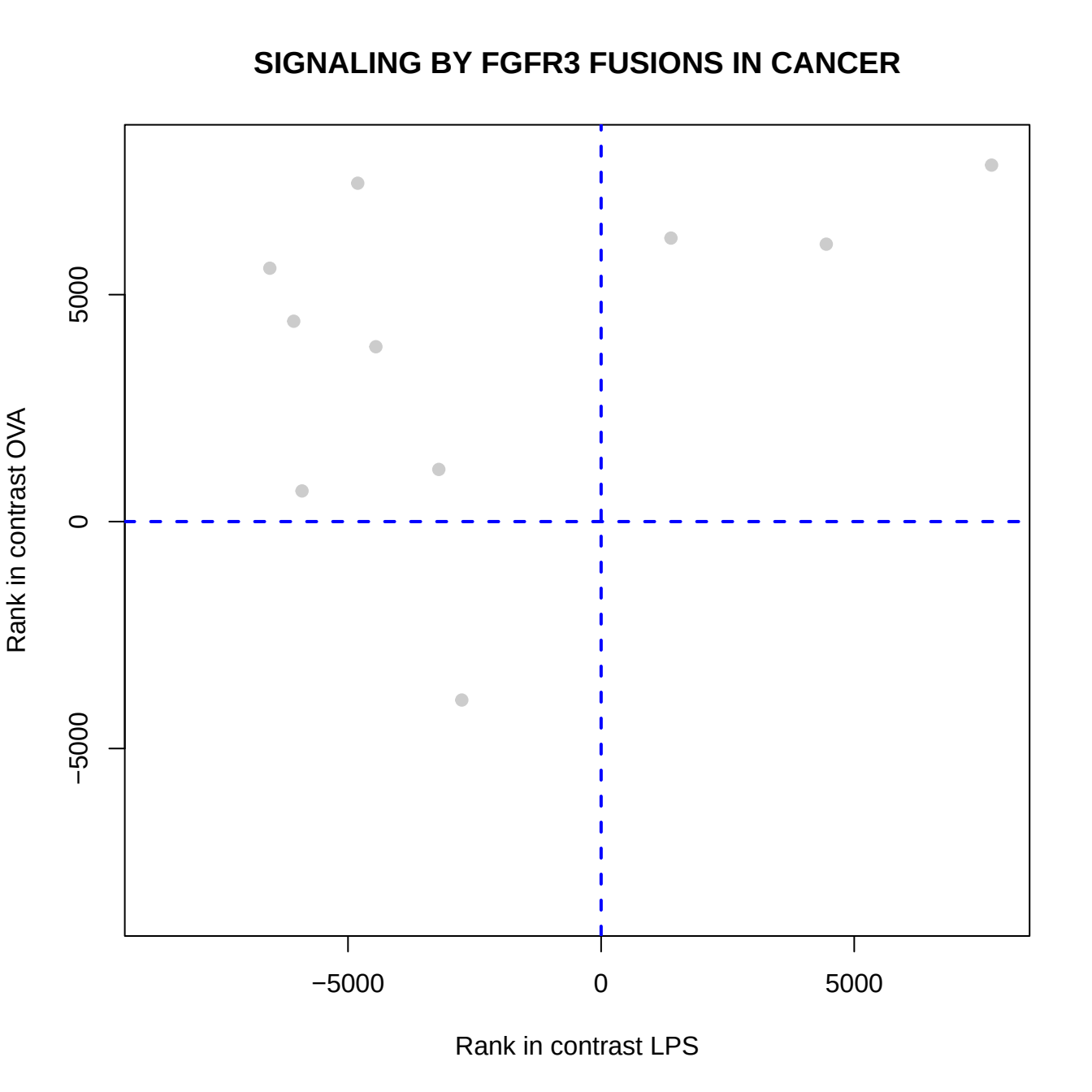

SYNTHESIS OF VERY LONG CHAIN FATTY ACY
5000
0
−5000
Position in rank
LPS
OVA
contrast

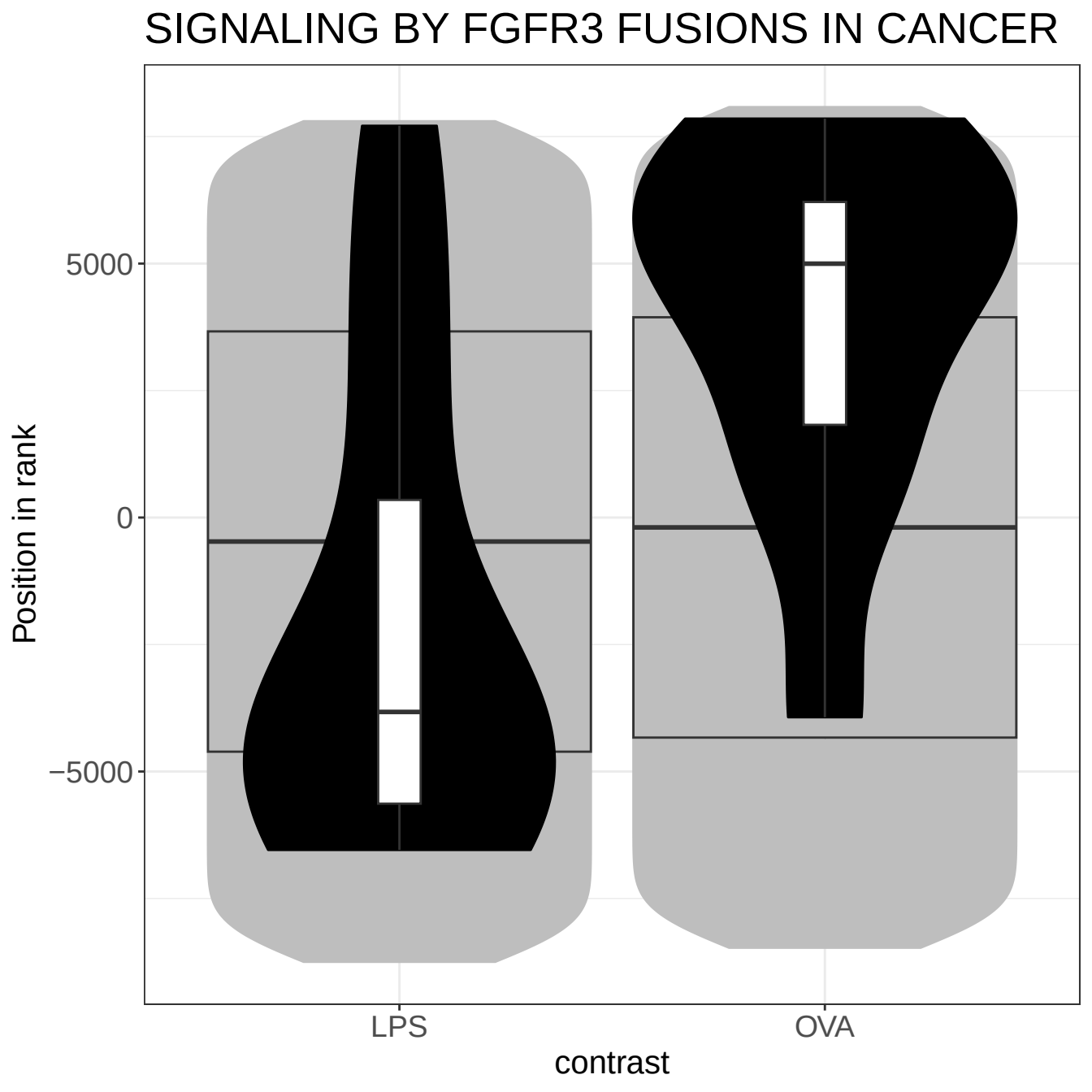

SELENOAMINO ACID METABOLISM
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

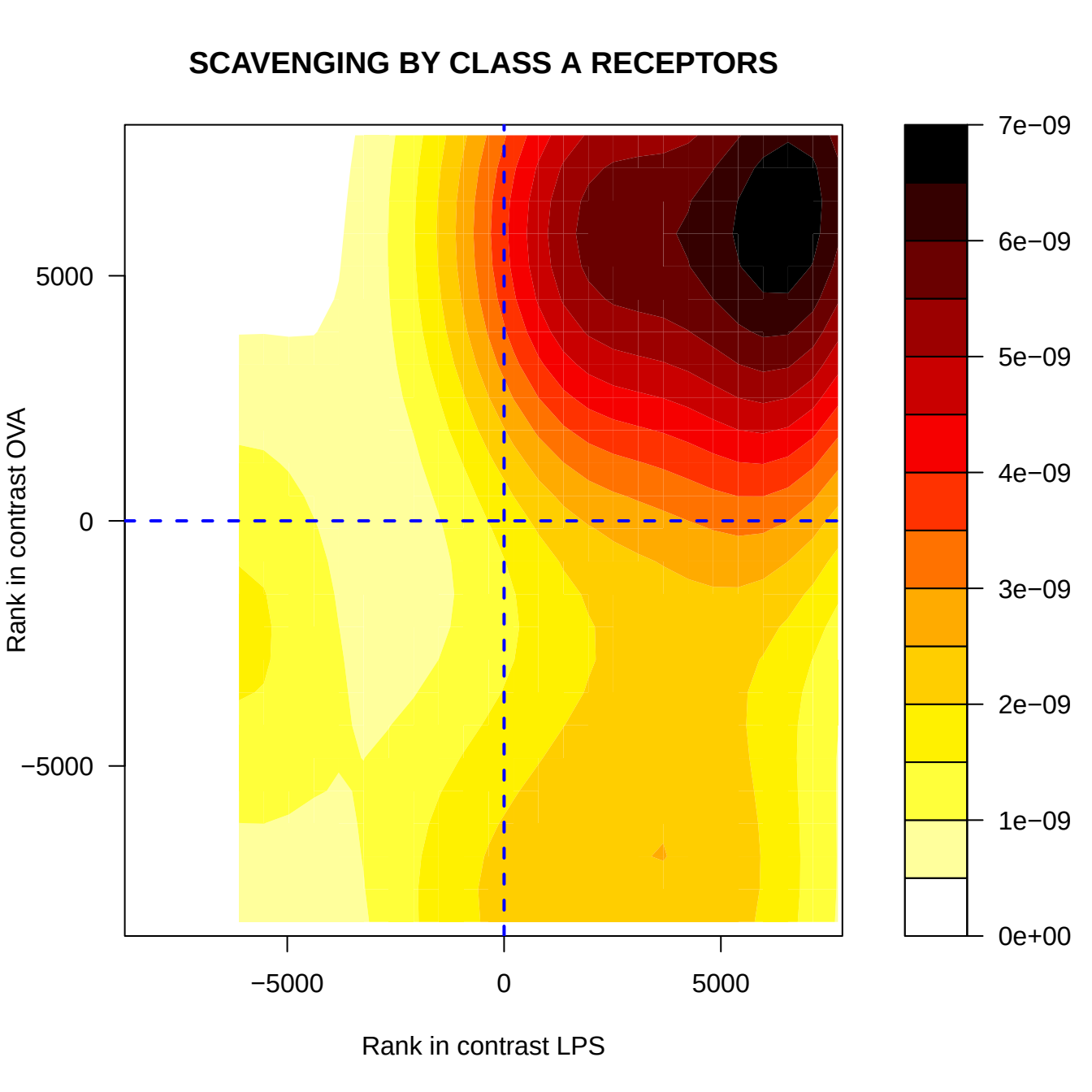

SELENOAMINO ACID METABOLISM
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

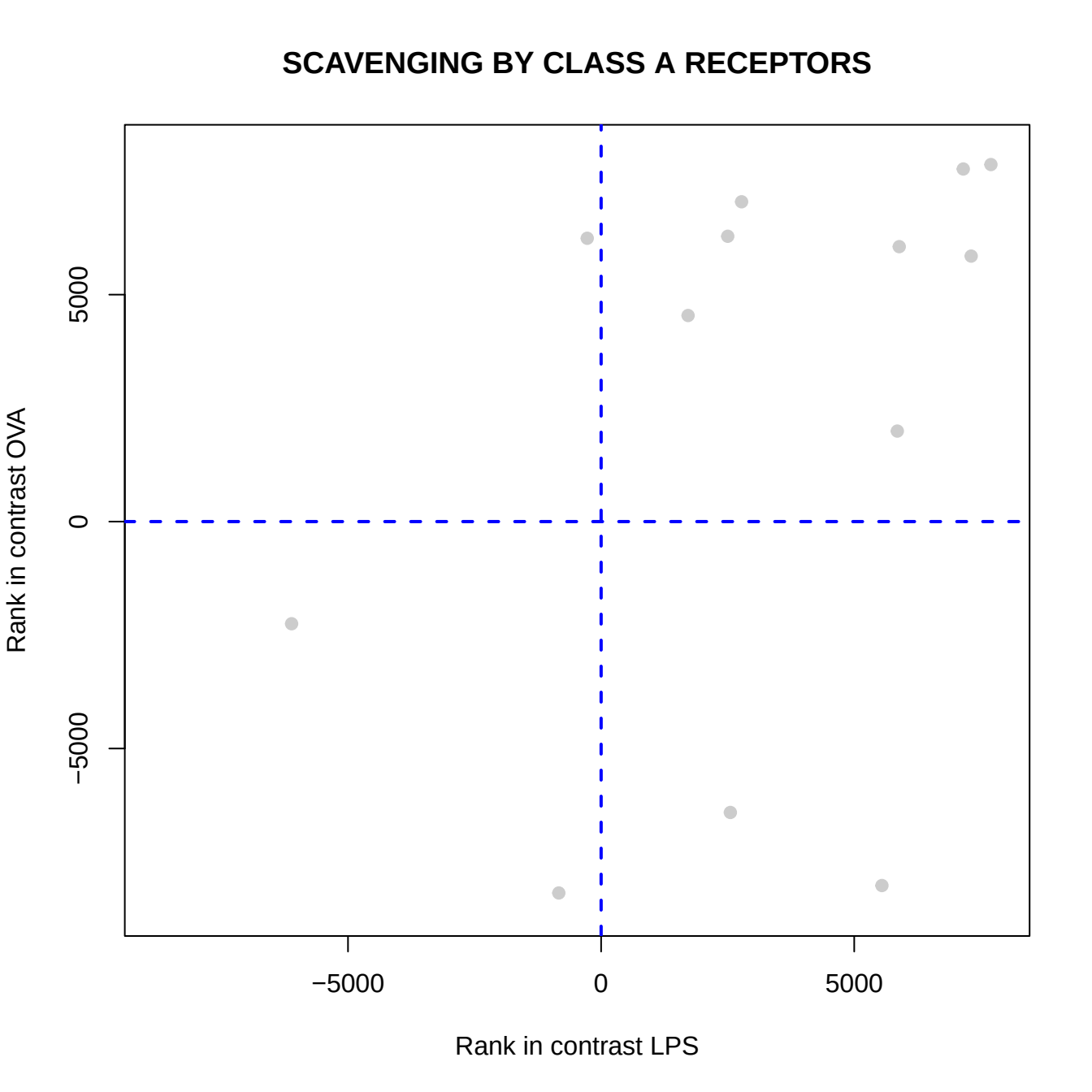

SELENOAMINO ACID METABOLISM
5000
0
−5000
Position in rank
LPS
OVA
contrast

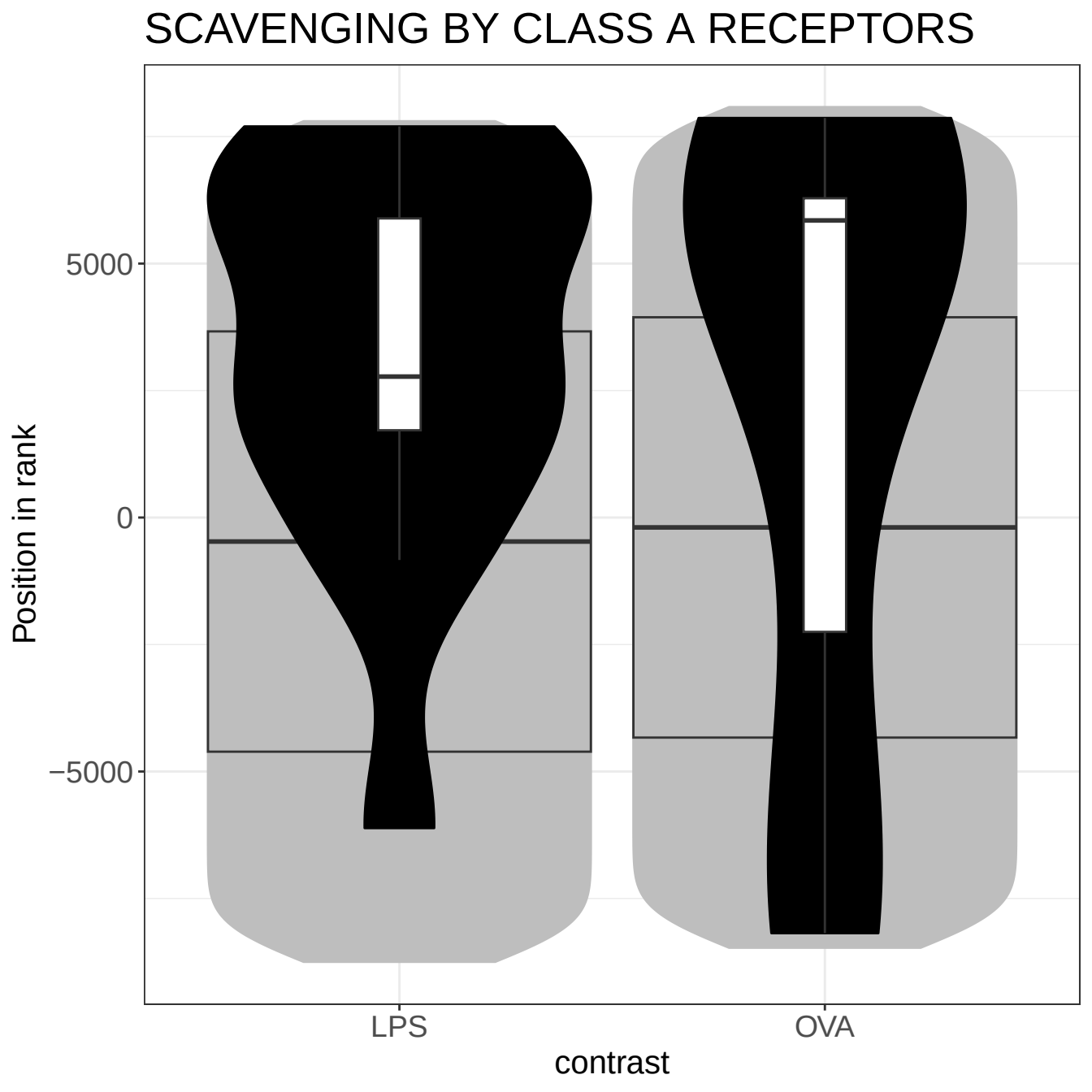

SIGNALING BY FGFR3 FUSIONS IN CANCER
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00

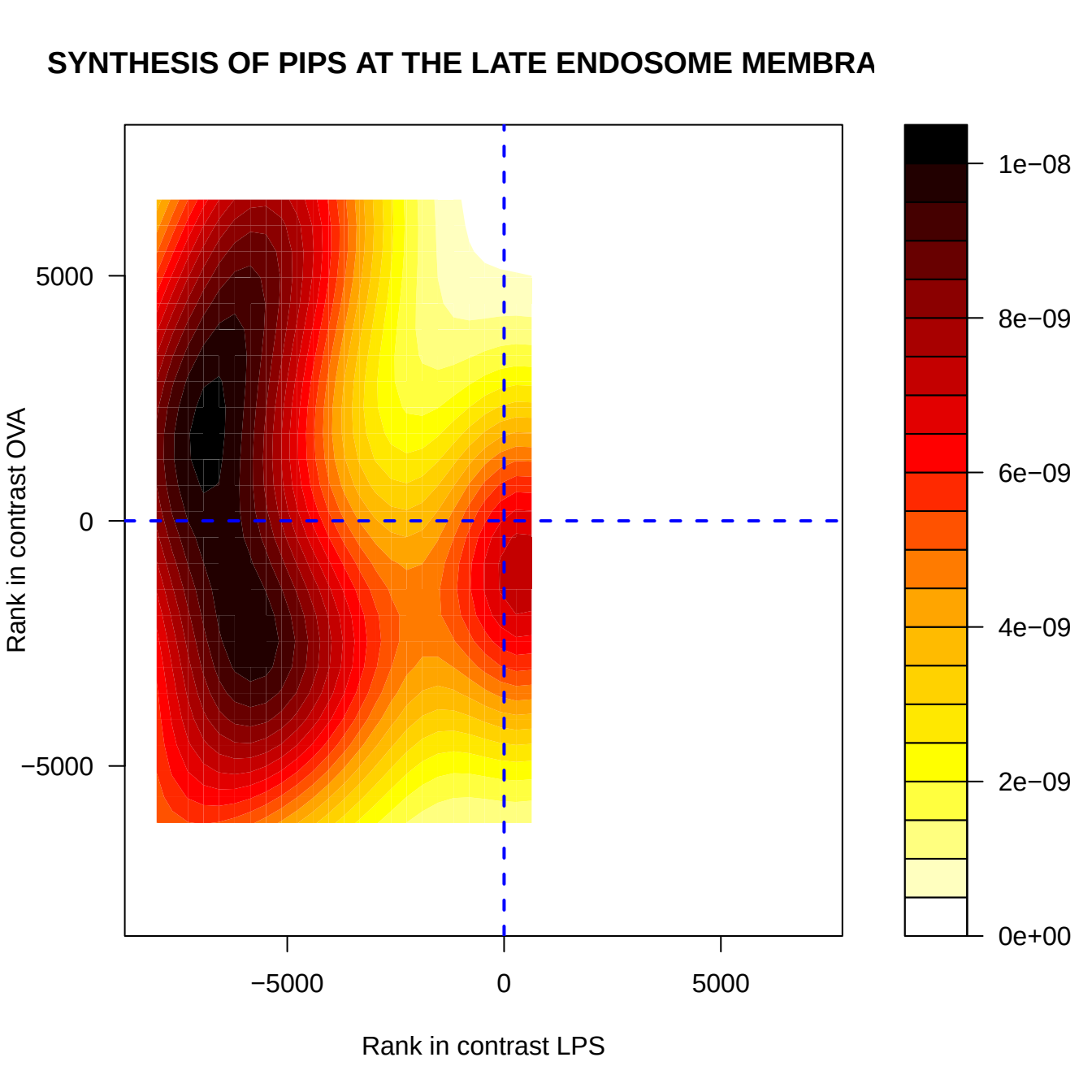

SIGNALING BY FGFR3 FUSIONS IN CANCER
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

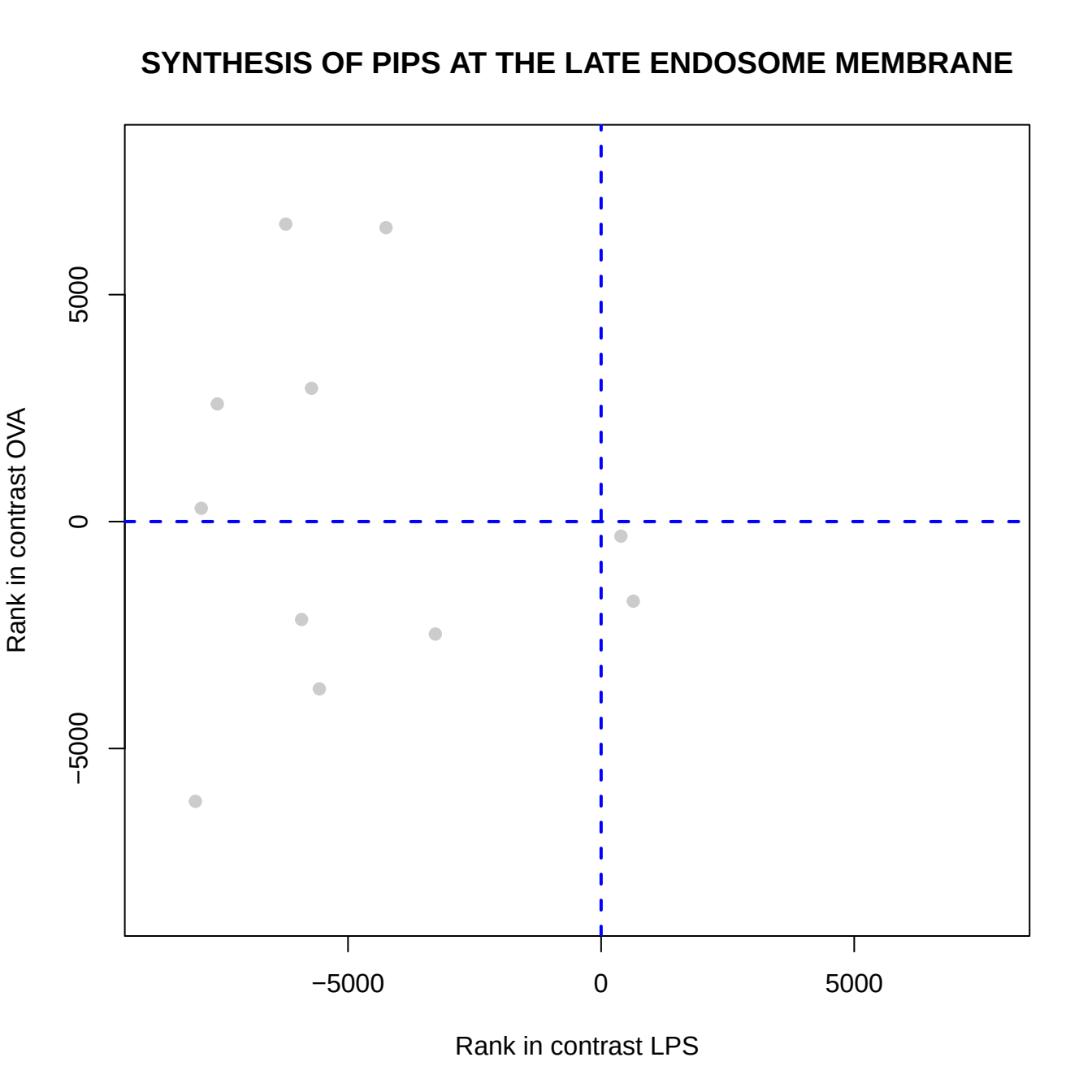

SIGNALING BY FGFR3 FUSIONS IN CANCER
5000
0
−5000
Position in rank
LPS
OVA
contrast

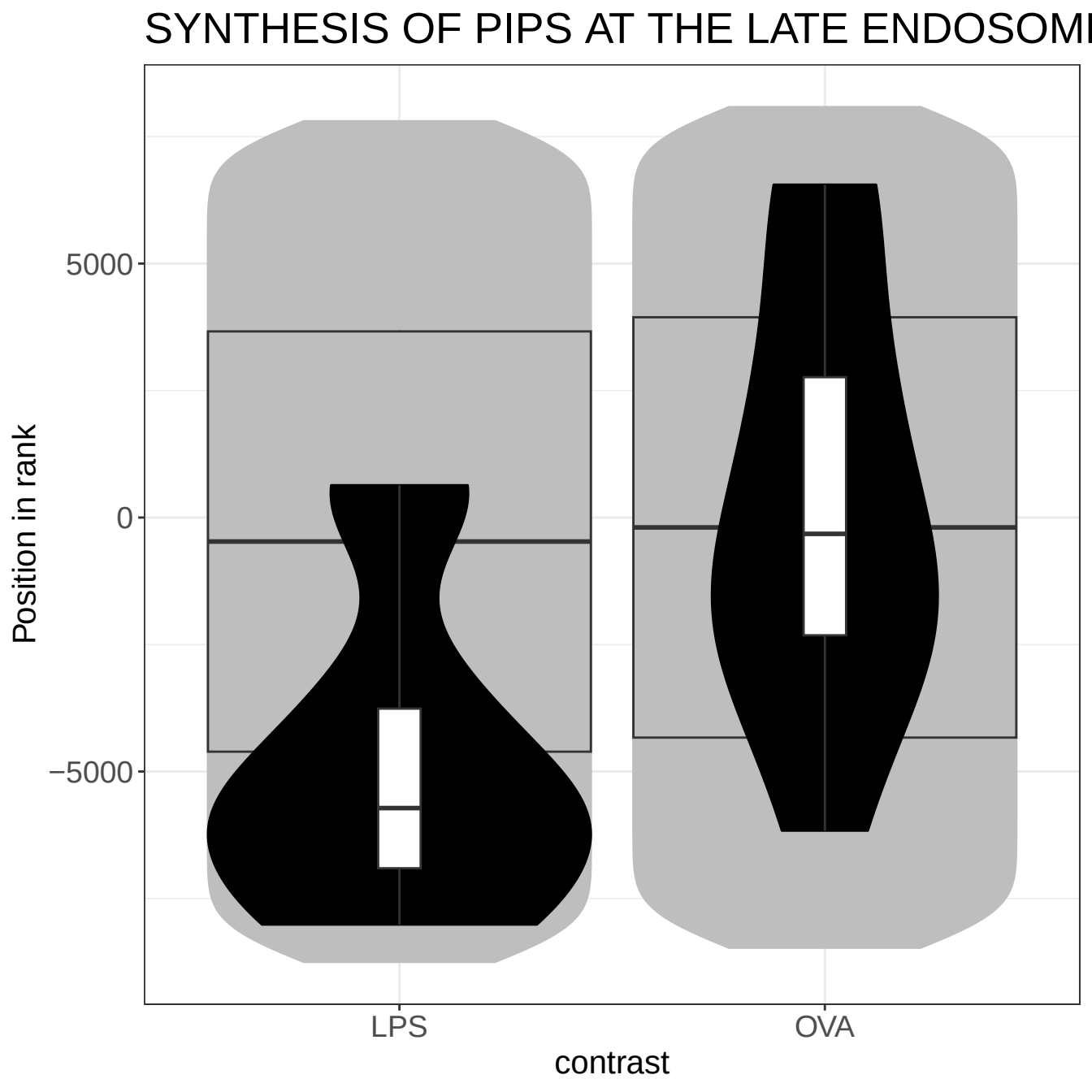

SCAVENGING BY CLASS A RECEPTORS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
7e−09
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

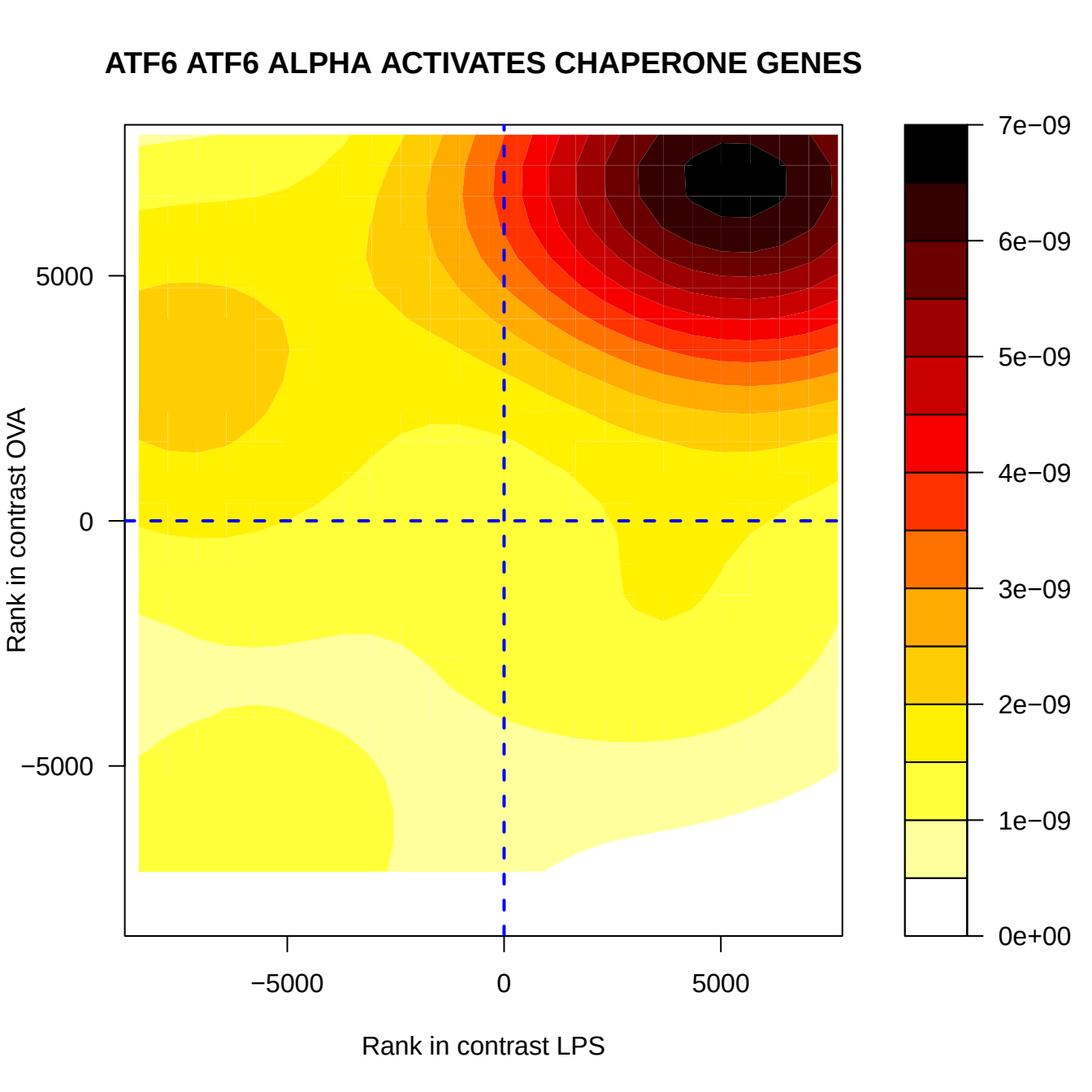

SCAVENGING BY CLASS A RECEPTORS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

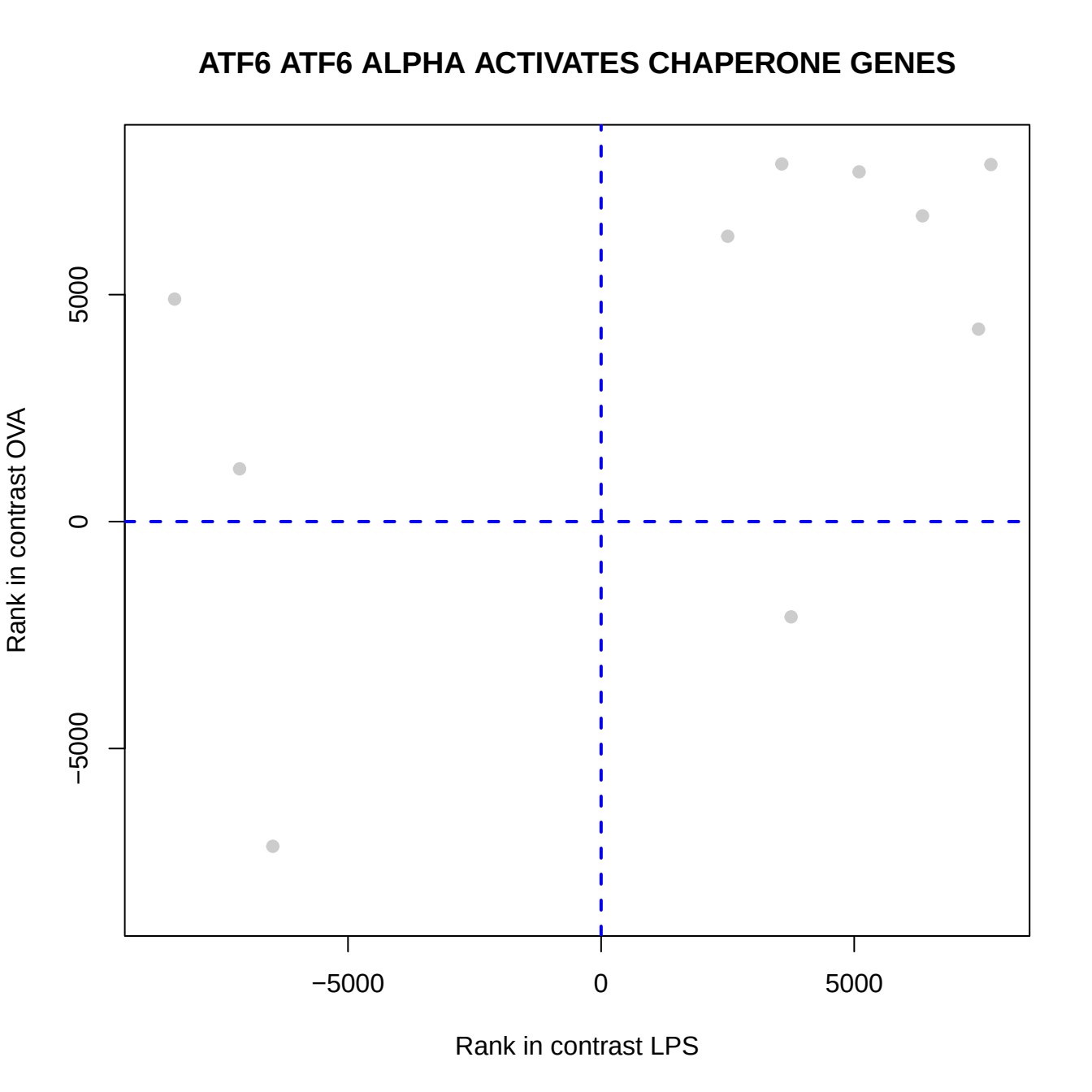

SCAVENGING BY CLASS A RECEPTORS
5000
0
−5000
Position in rank
LPS
OVA
contrast

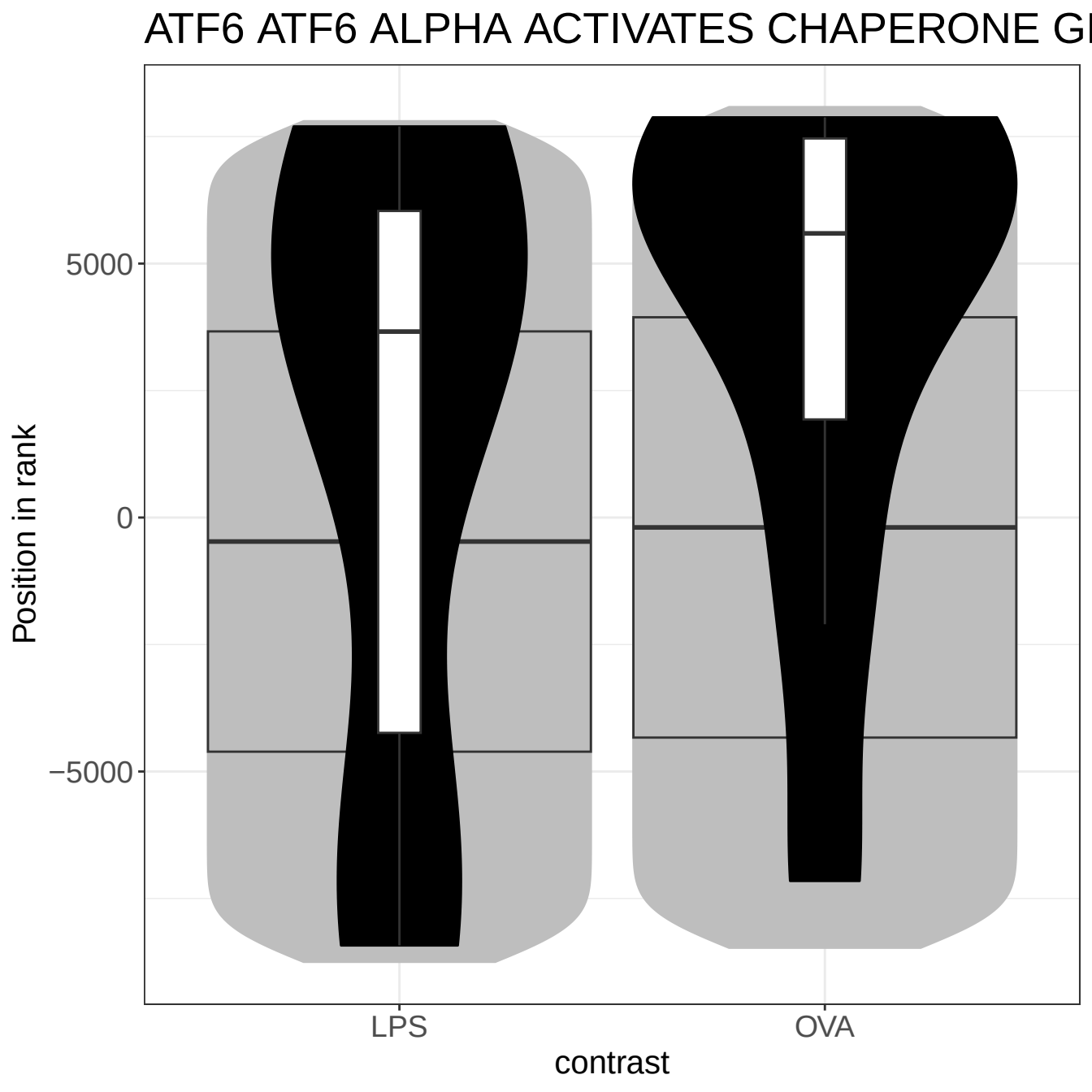

SYNTHESIS OF PIPS AT THE LATE ENDOSOME MEMBRA
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

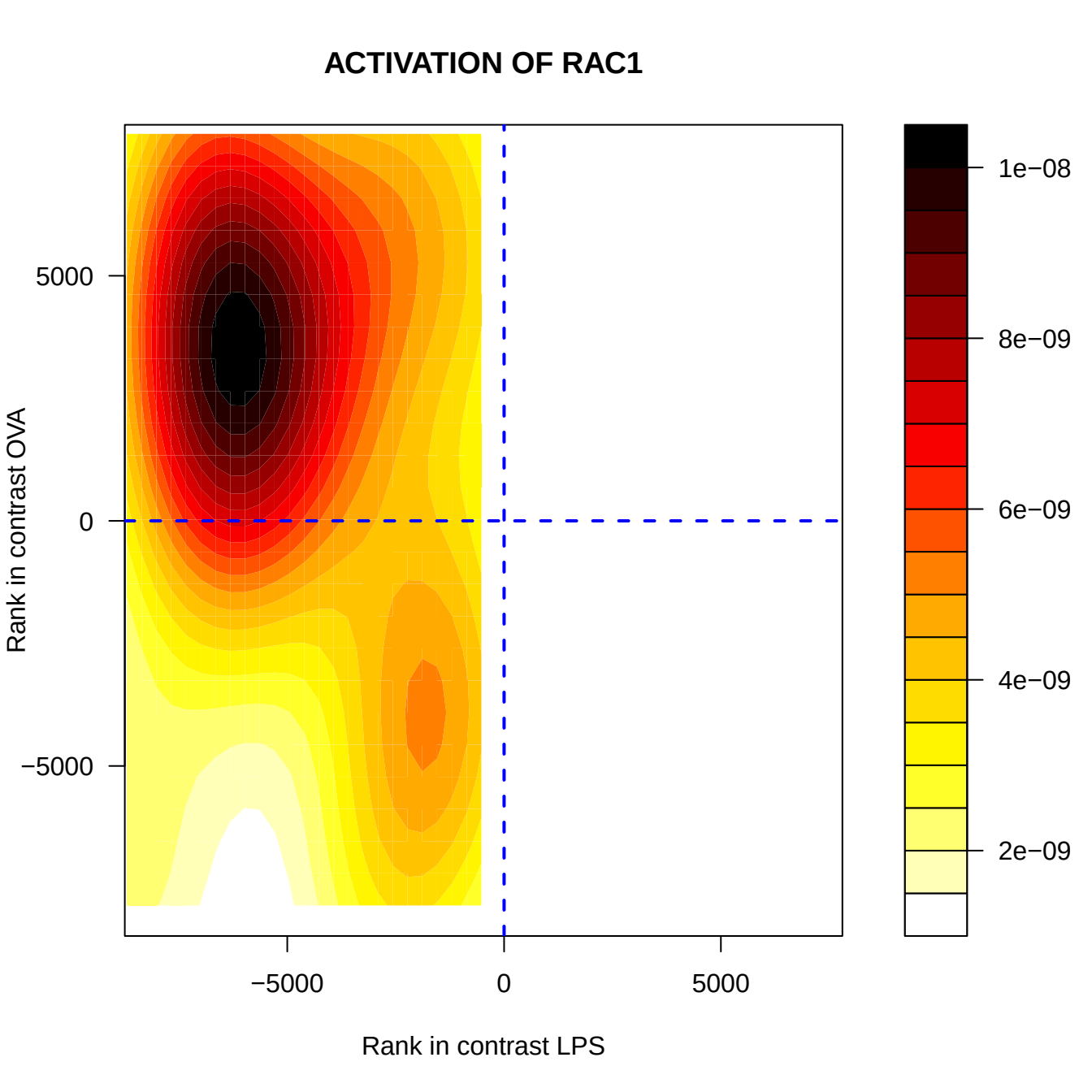

SYNTHESIS OF PIPS AT THE LATE ENDOSOME MEMBRANE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

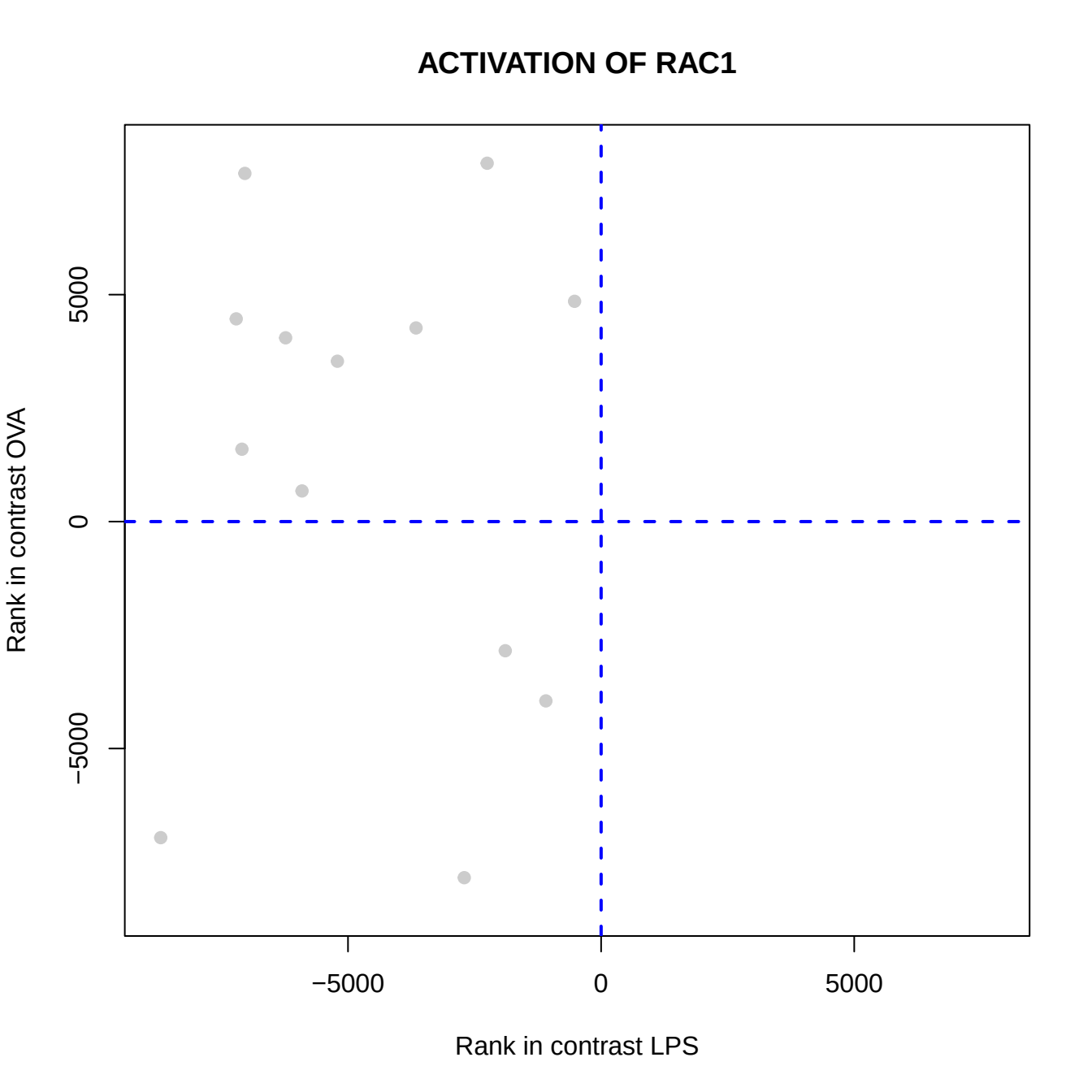

SYNTHESIS OF PIPS AT THE LATE ENDOSOMI
5000
0
−5000
Position in rank
LPS
OVA
contrast

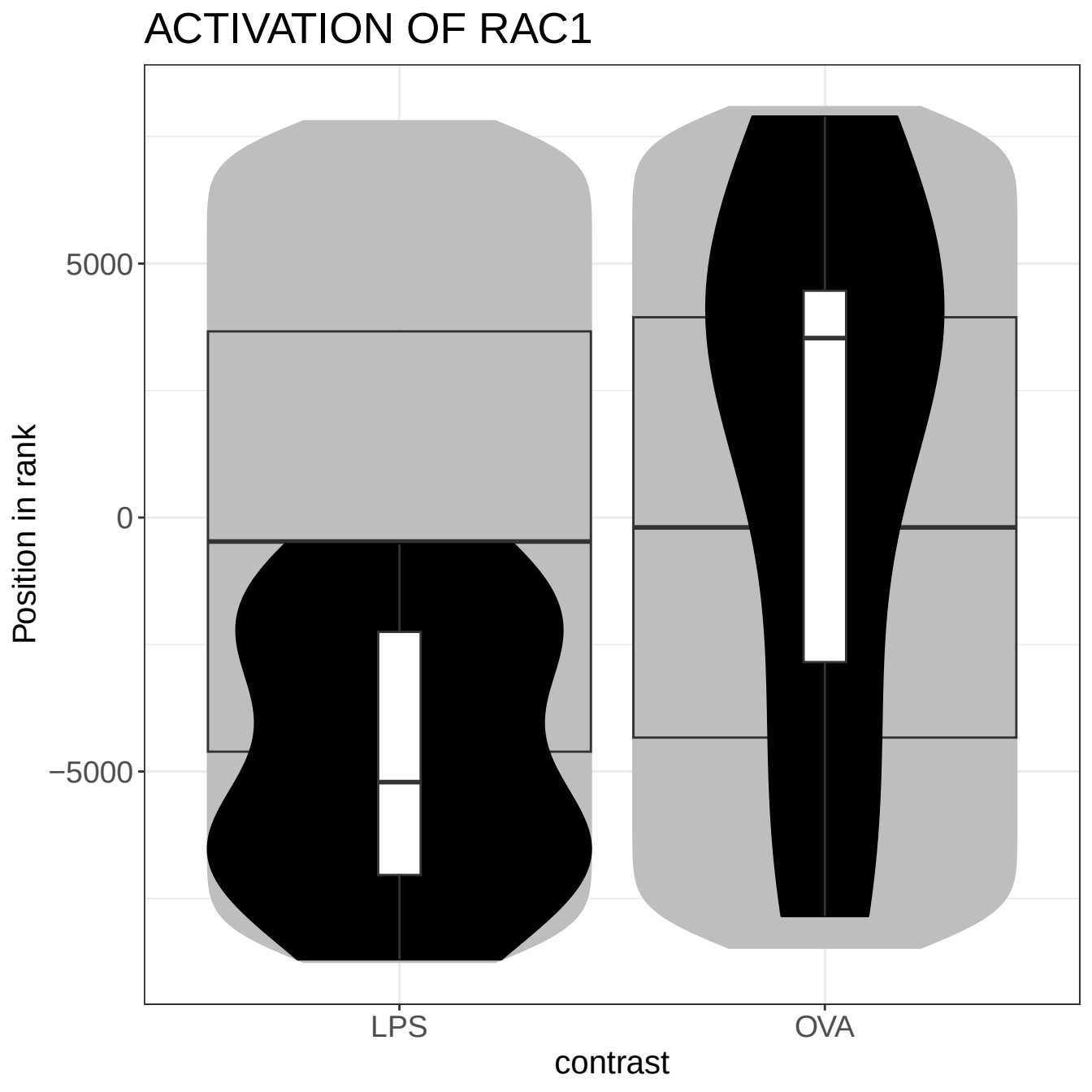

ATF6 ATF6 ALPHA ACTIVATES CHAPERONE GENES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
7e−09
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

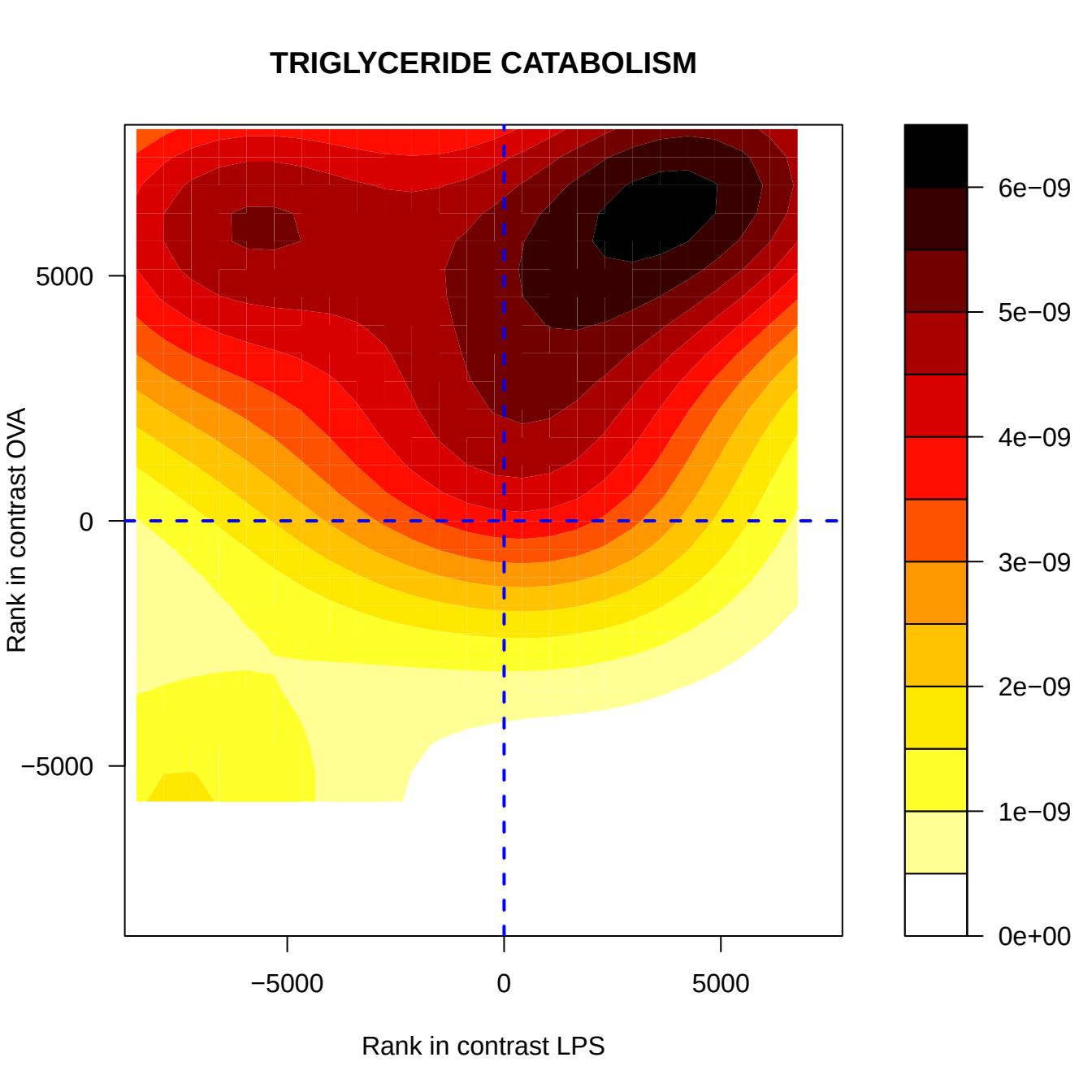

ATF6 ATF6 ALPHA ACTIVATES CHAPERONE GENES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

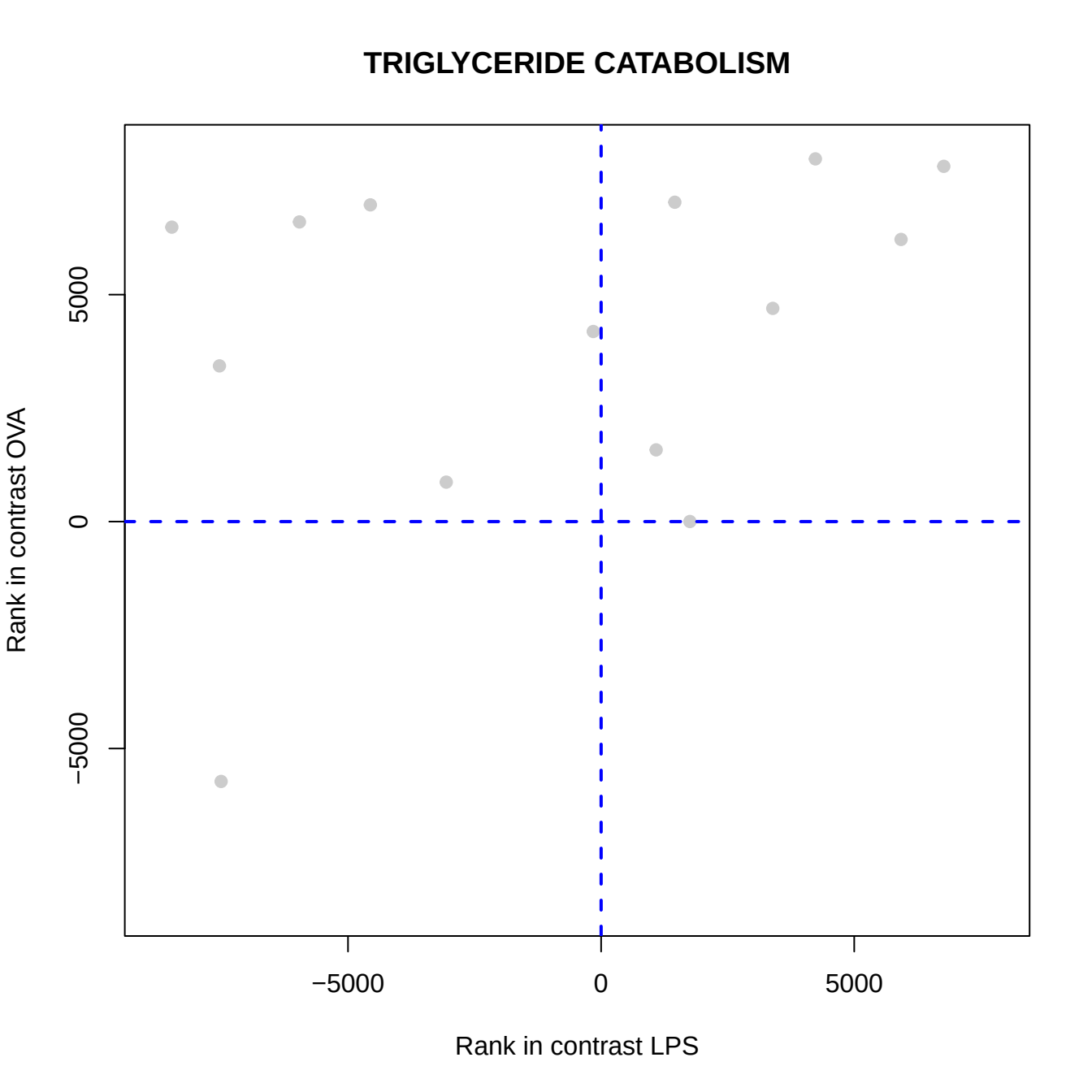

ATF6 ATF6 ALPHA ACTIVATES CHAPERONE GE
5000
0
−5000
Position in rank
LPS
OVA
contrast

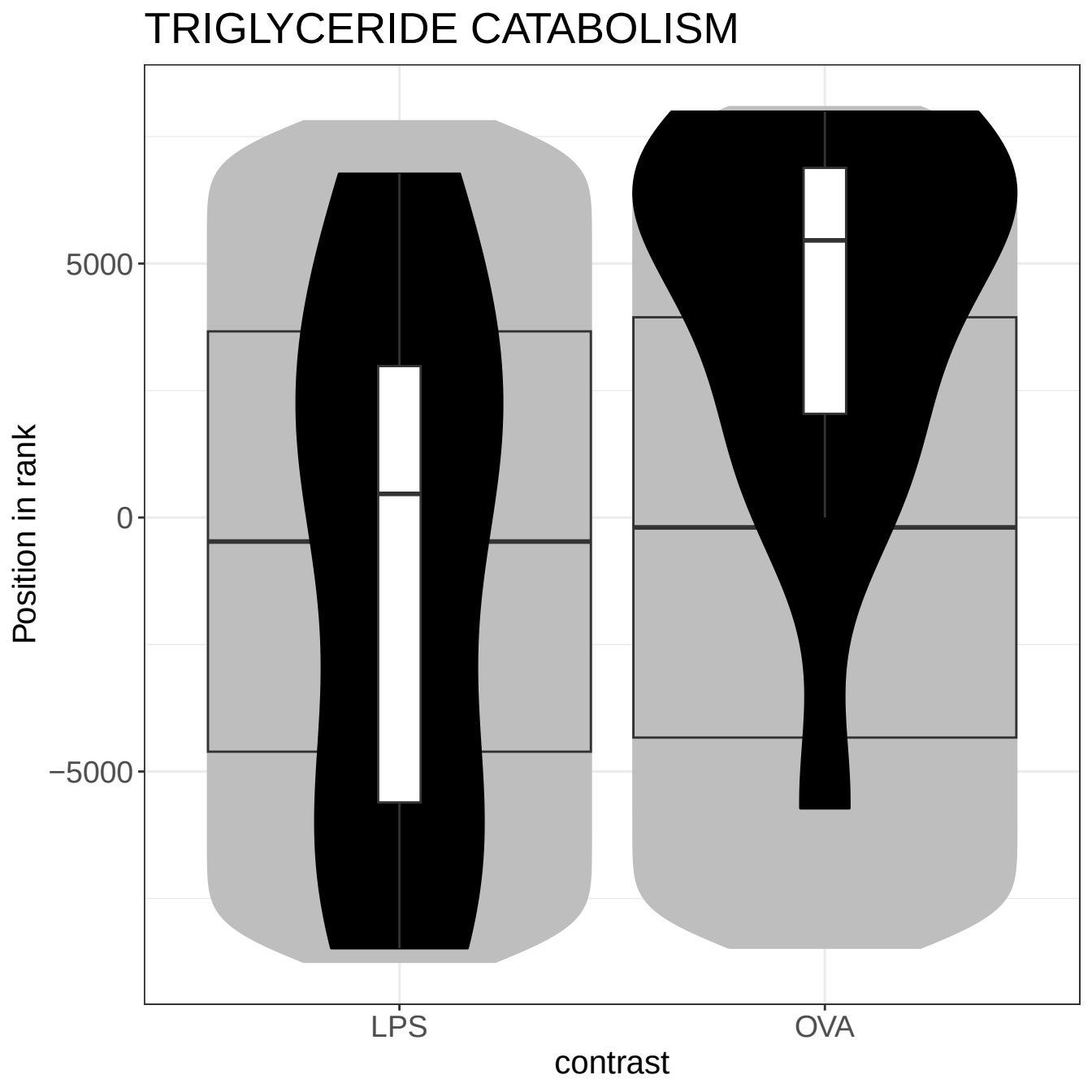

ACTIVATION OF RAC1
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09

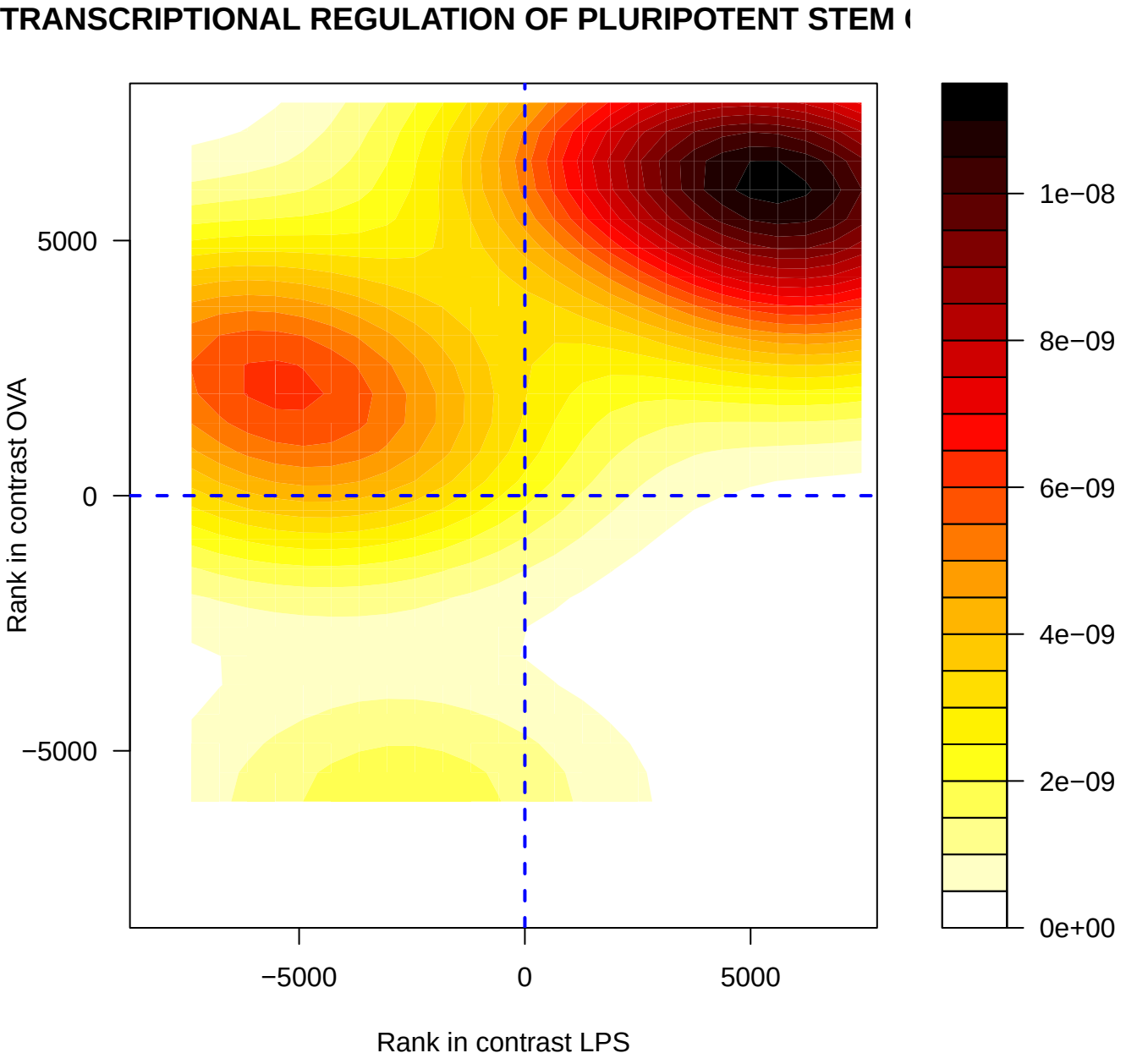

ACTIVATION OF RAC1
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

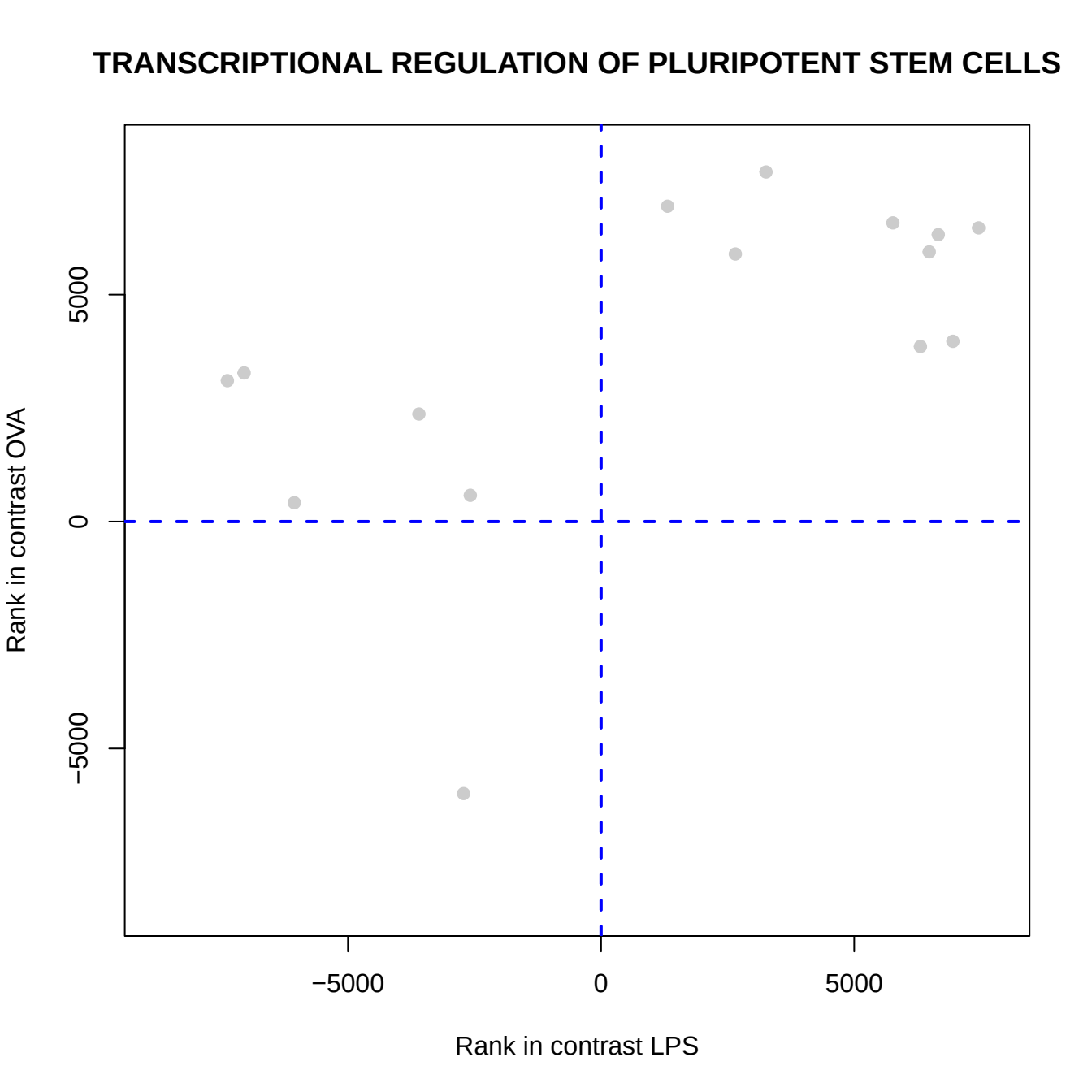

ACTIVATION OF RAC1
5000
0
−5000
Position in rank
LPS
OVA
contrast

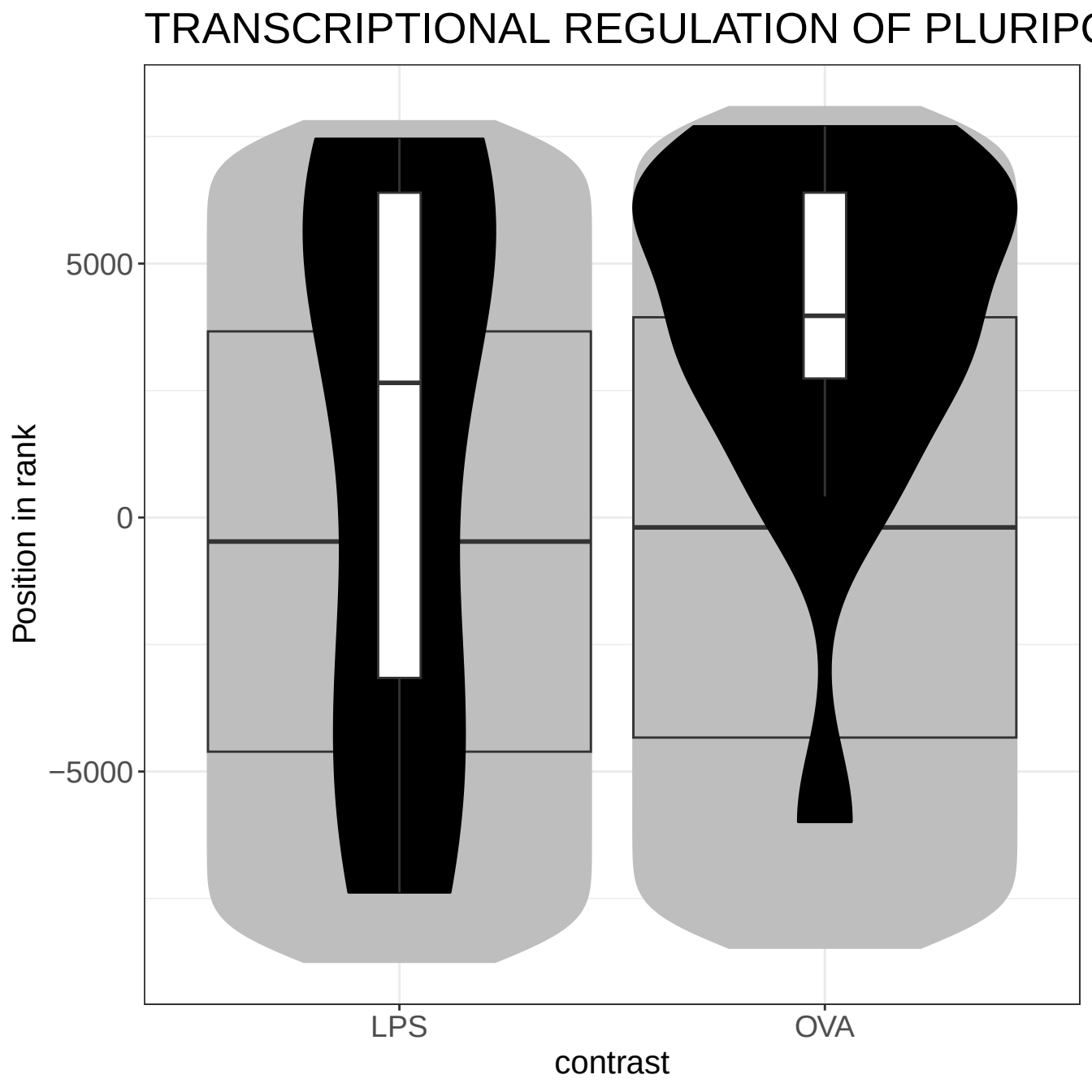

TRIGLYCERIDE CATABOLISM
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

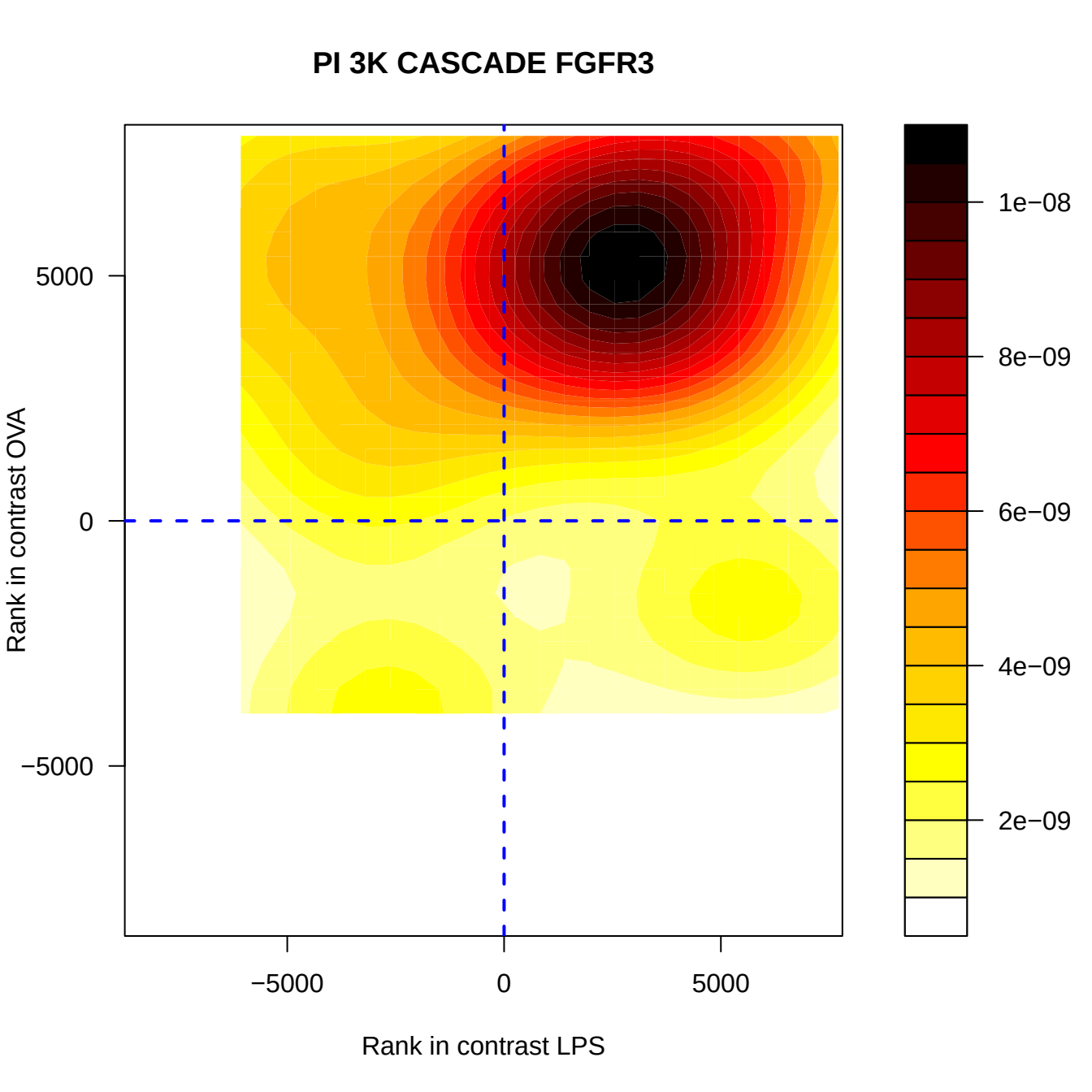

TRIGLYCERIDE CATABOLISM
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

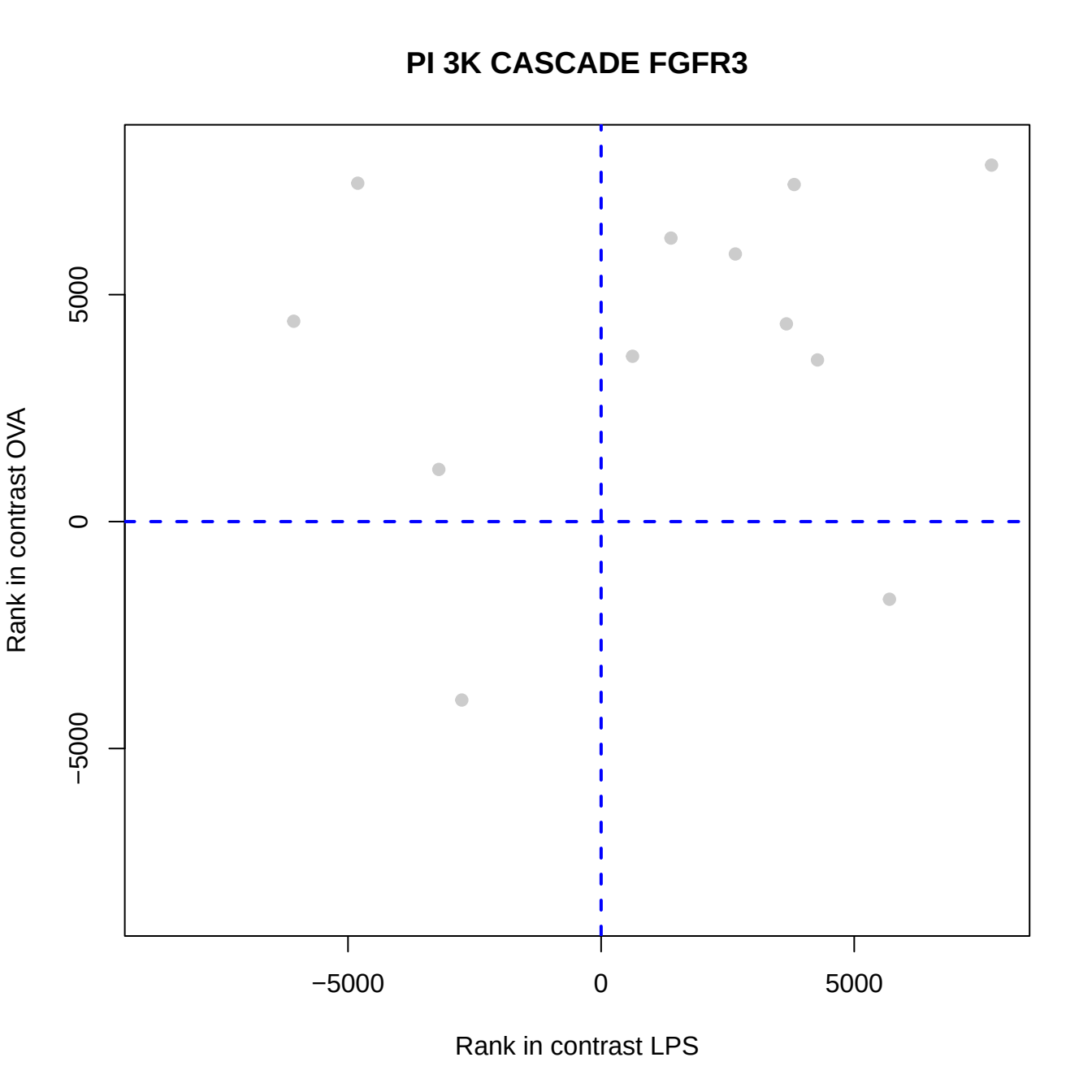

TRIGLYCERIDE CATABOLISM
5000
0
−5000
Position in rank
LPS
OVA
contrast

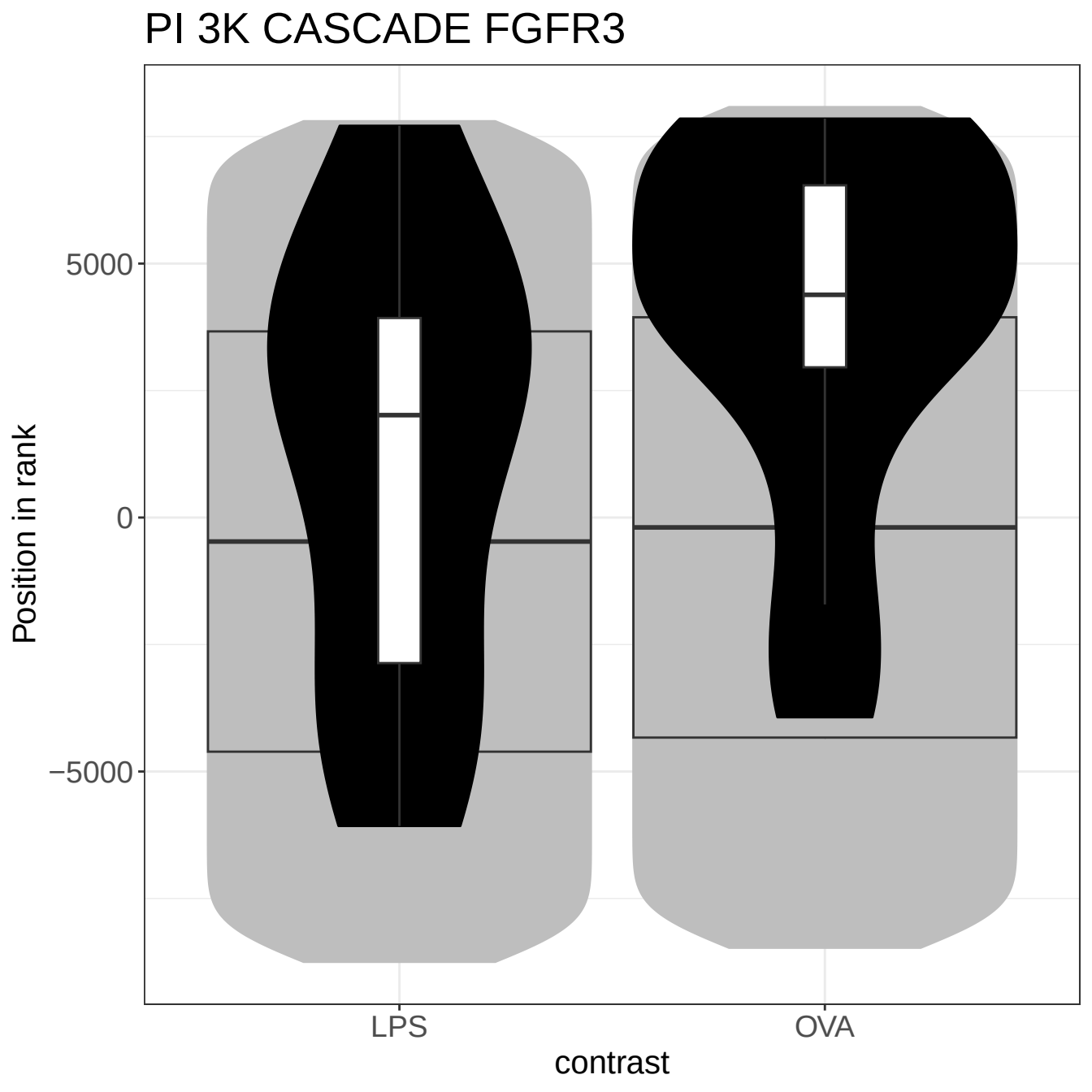

TRANSCRIPTIONAL REGULATION OF PLURIPOTENT STEM (
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

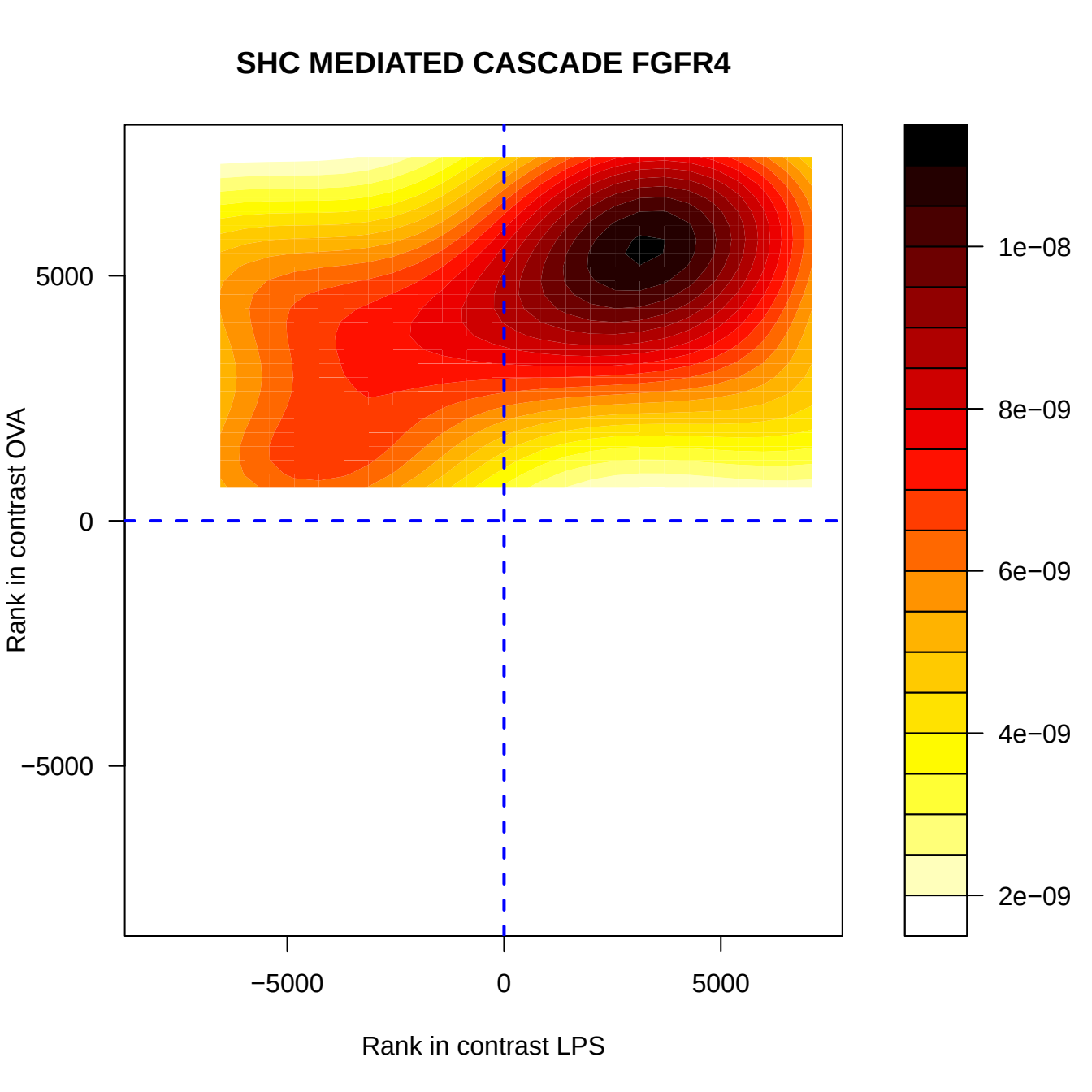

TRANSCRIPTIONAL REGULATION OF PLURIPOTENT STEM CELLS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

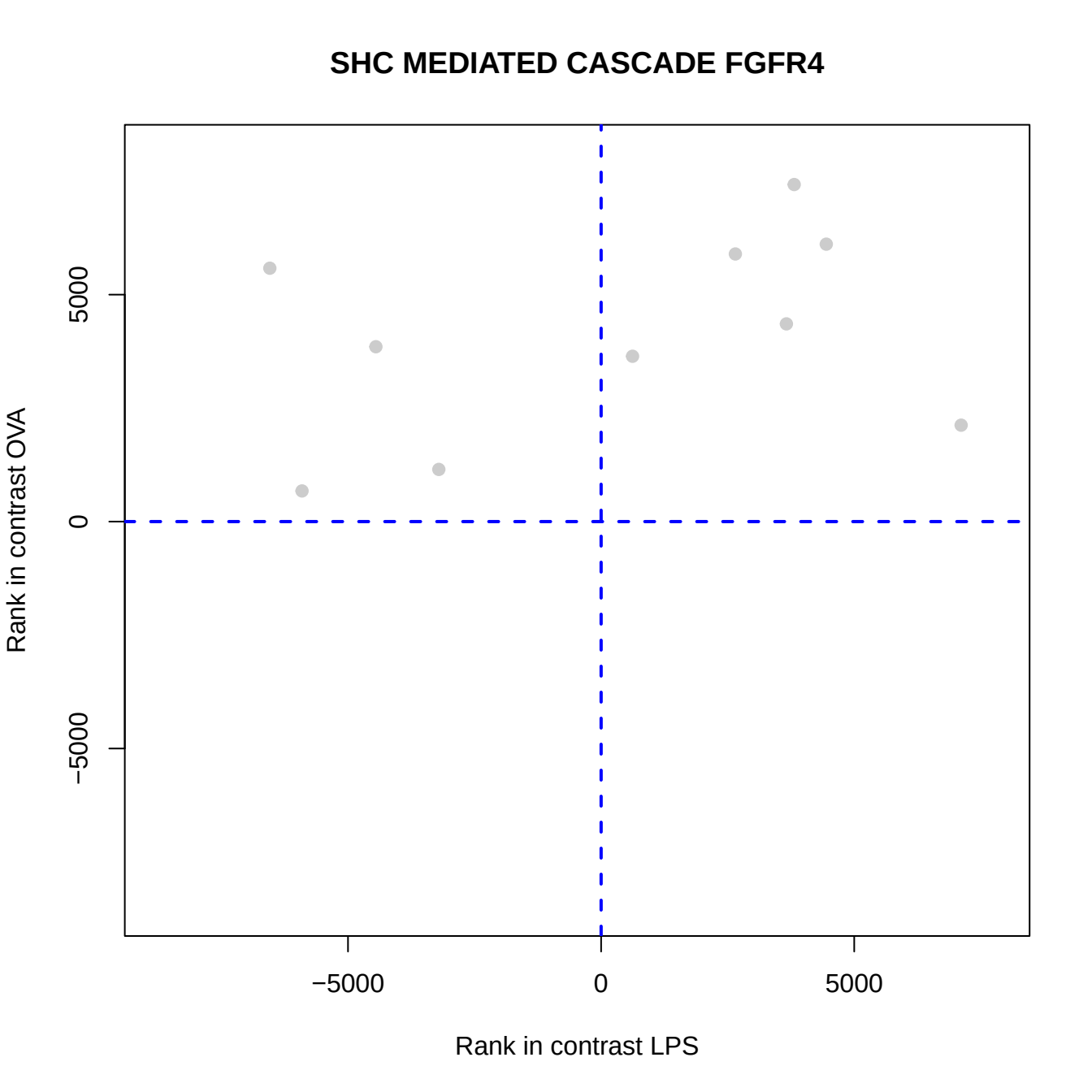

TRANSCRIPTIONAL REGULATION OF PLURIPO
5000
0
−5000
Position in rank
LPS
OVA
contrast

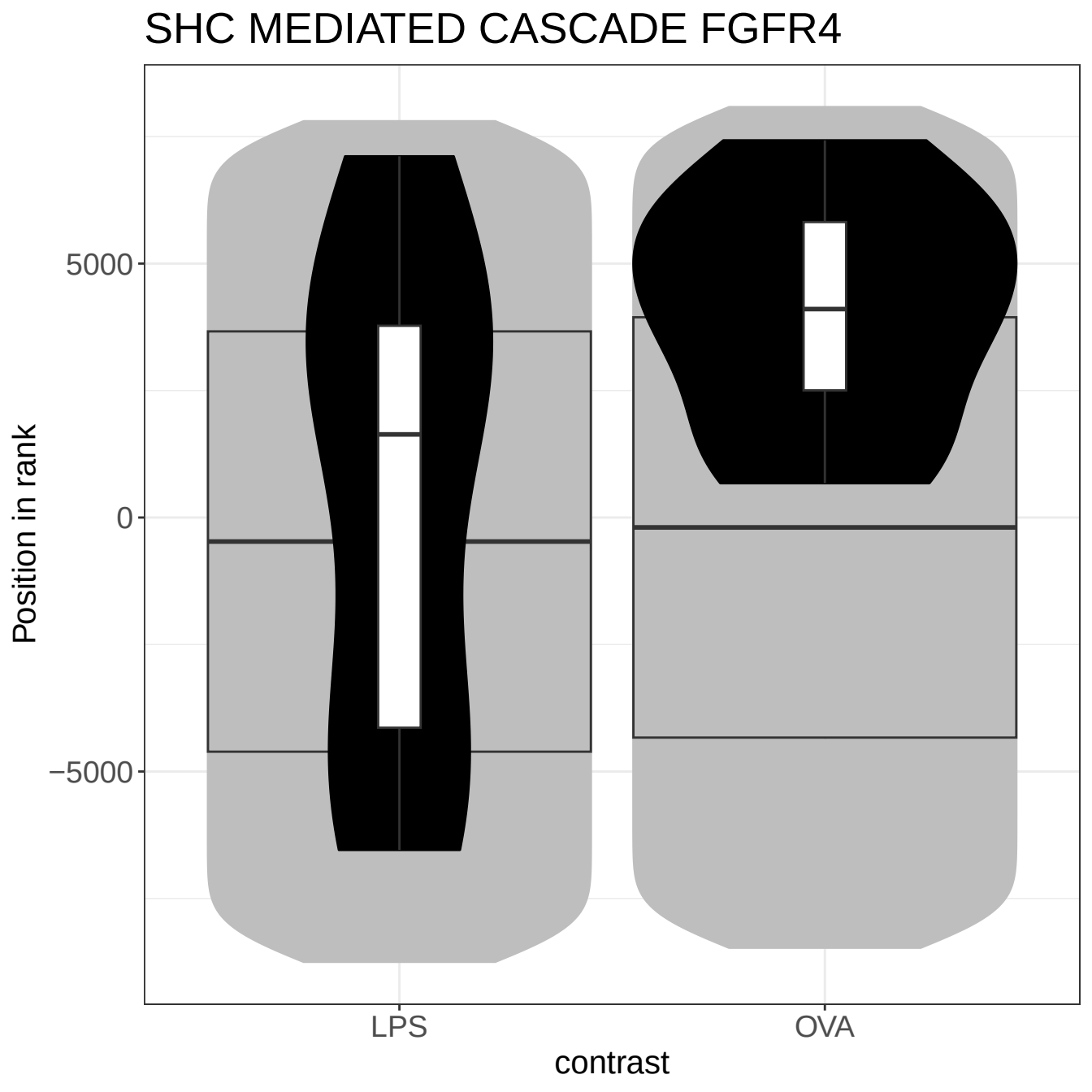

PI 3K CASCADE FGFR3
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09

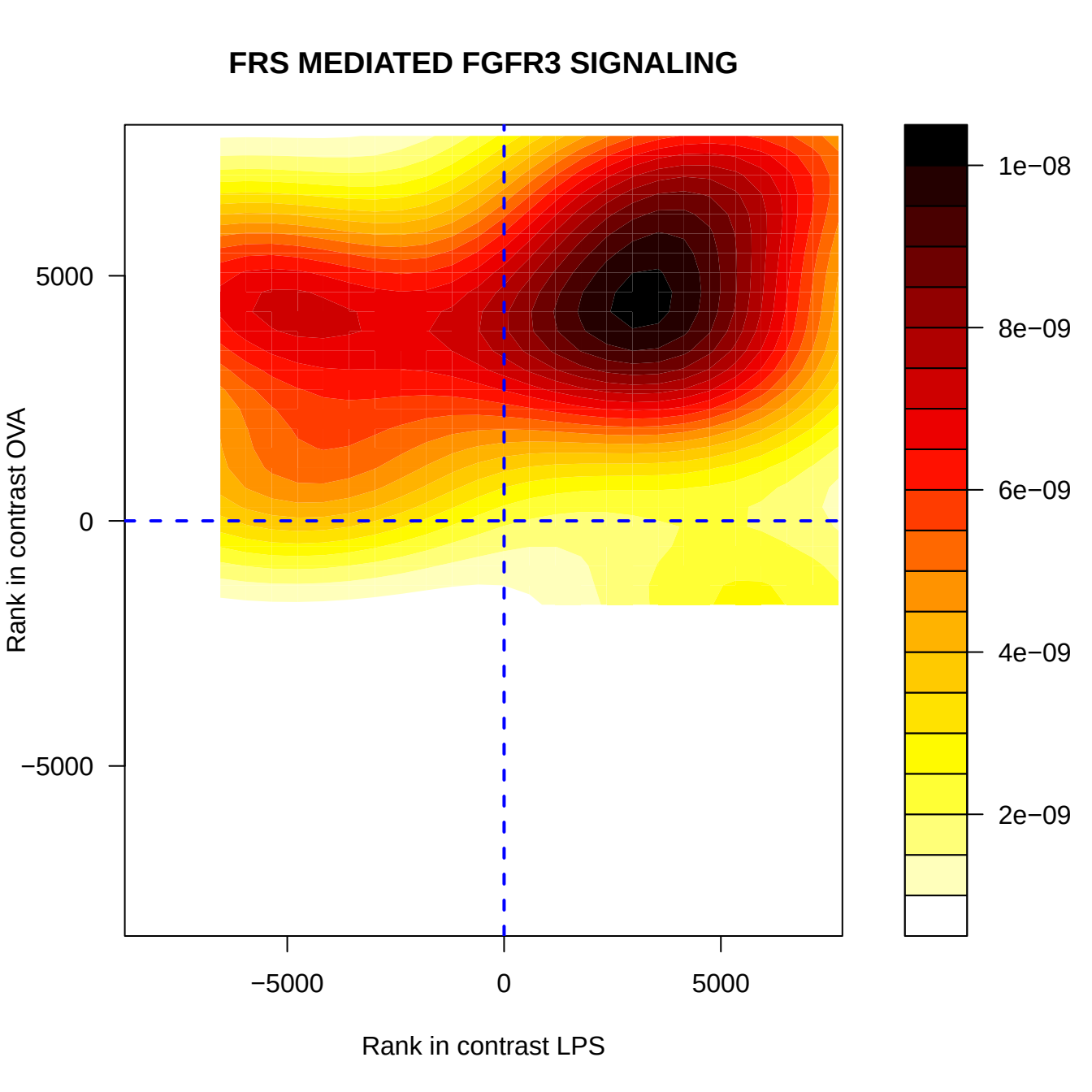

PI 3K CASCADE FGFR3
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

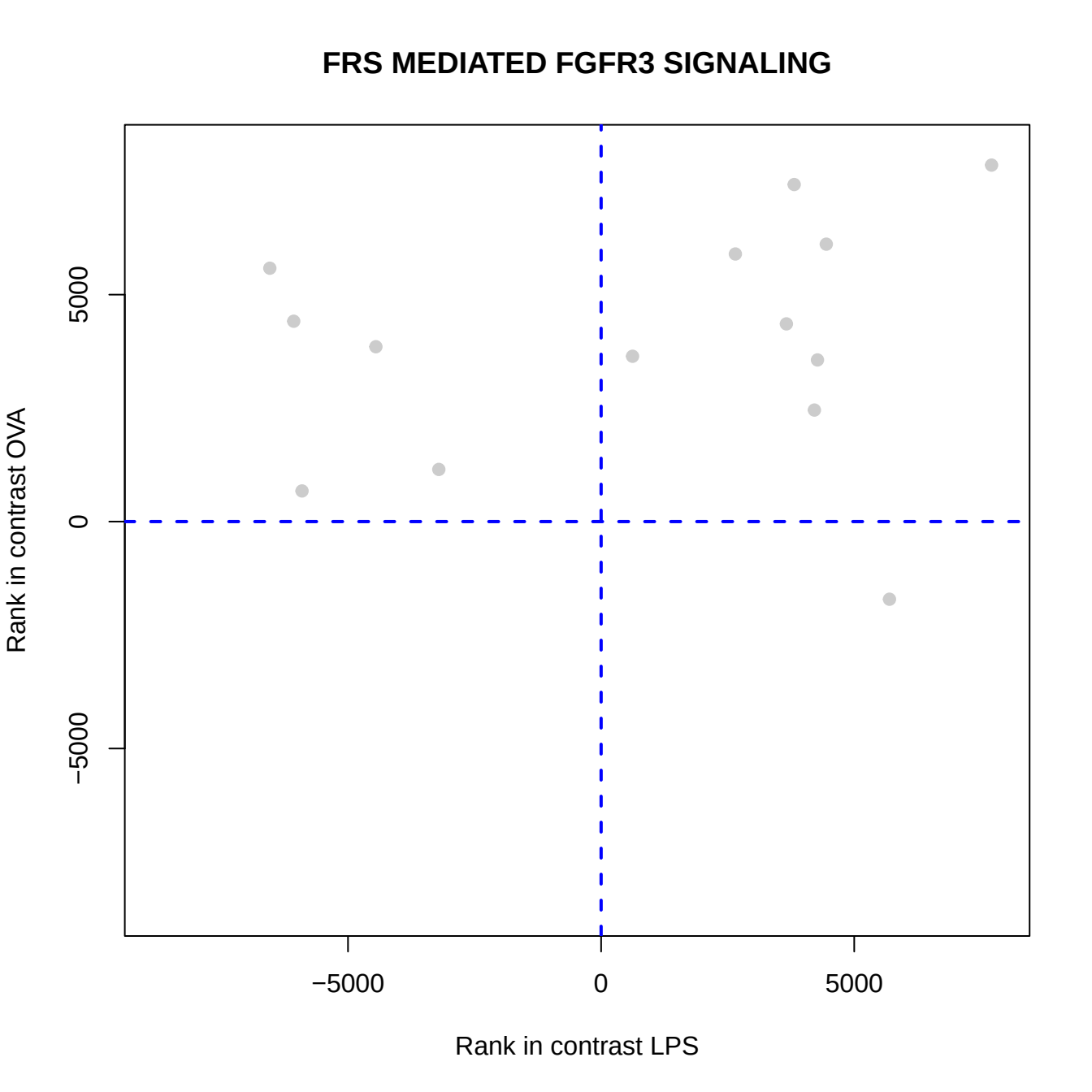

PI 3K CASCADE FGFR3
5000
0
−5000
Position in rank
LPS
OVA
contrast

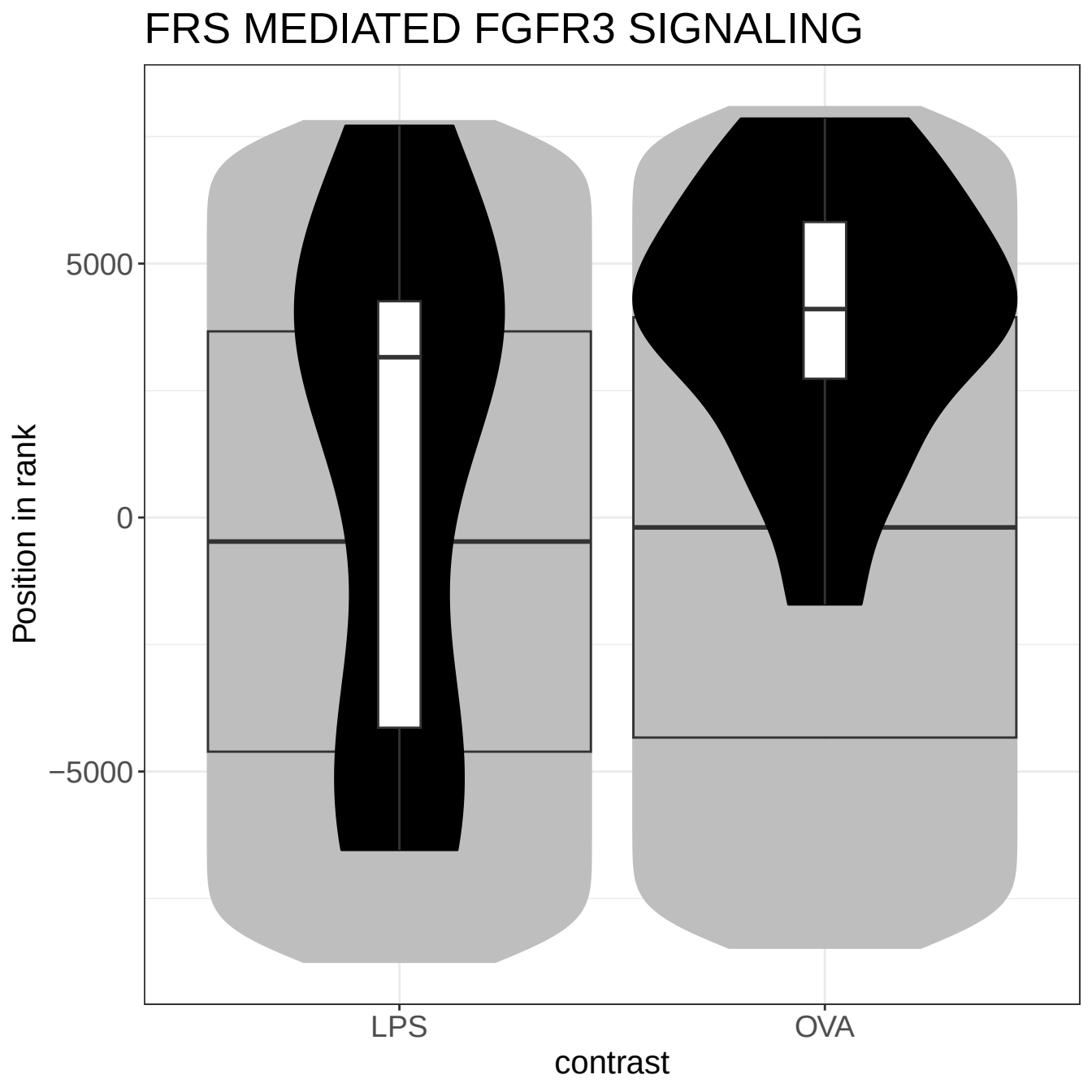

SHC MEDIATED CASCADE FGFR4
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09

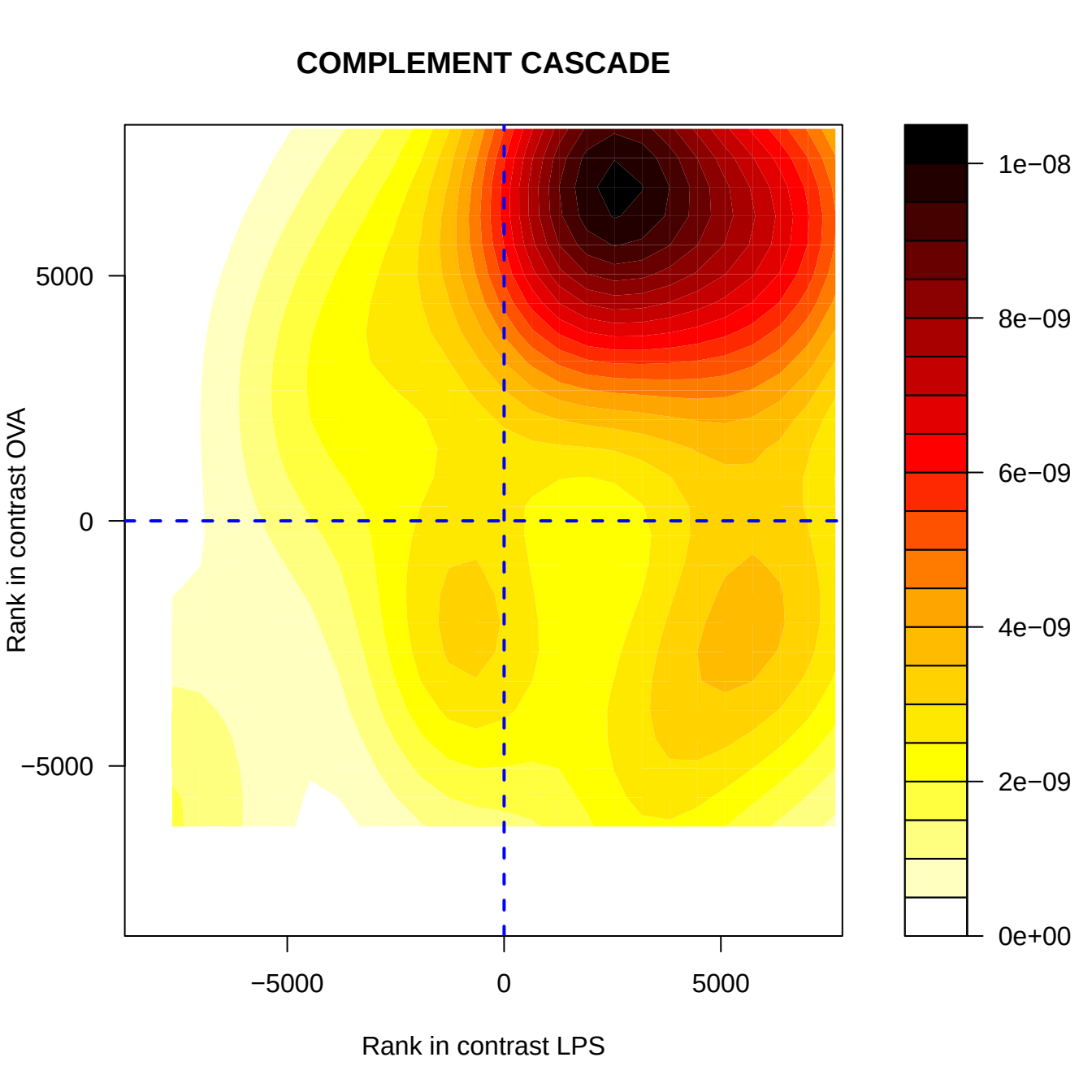

SHC MEDIATED CASCADE FGFR4
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

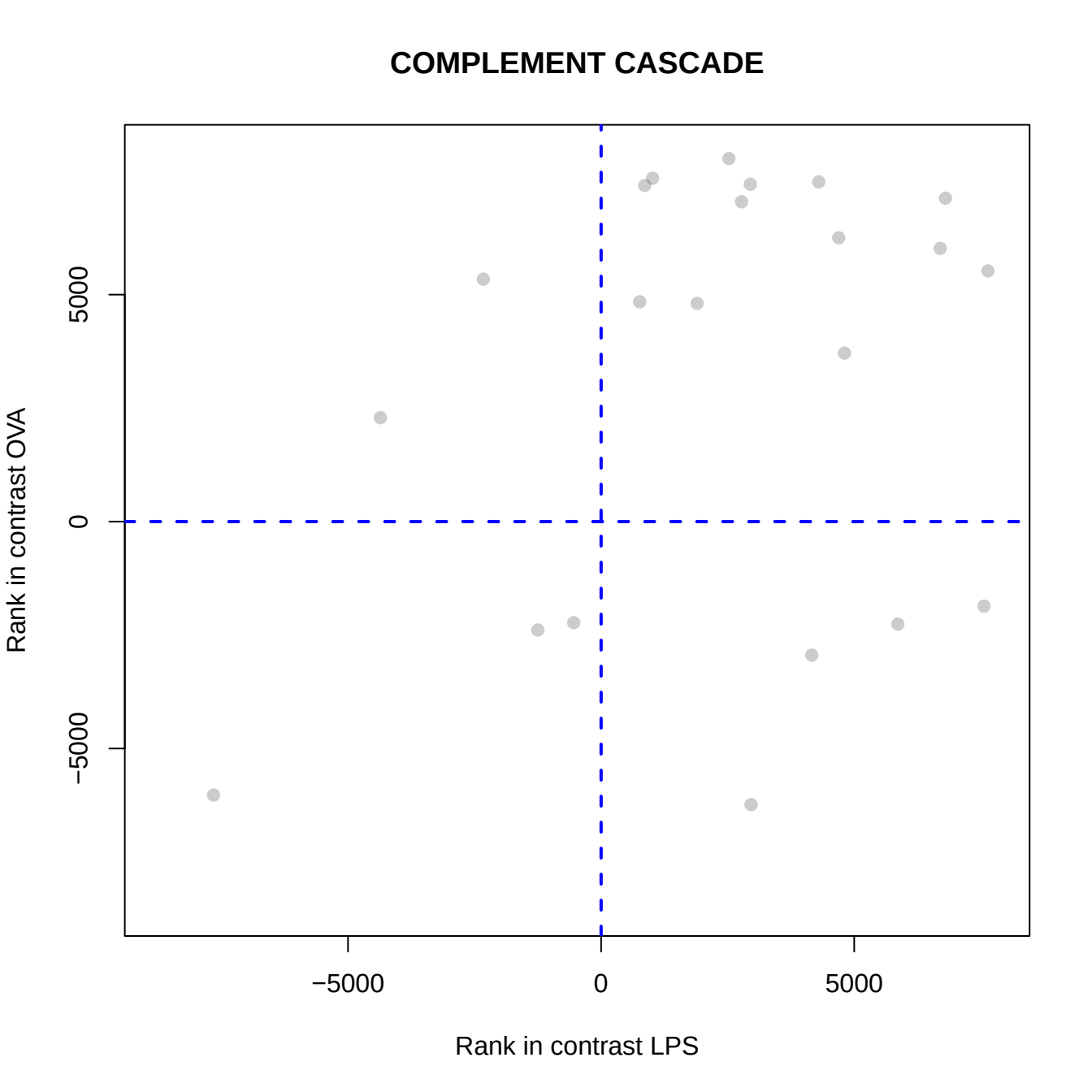

SHC MEDIATED CASCADE FGFR4
5000
0
−5000
Position in rank
LPS
OVA
contrast

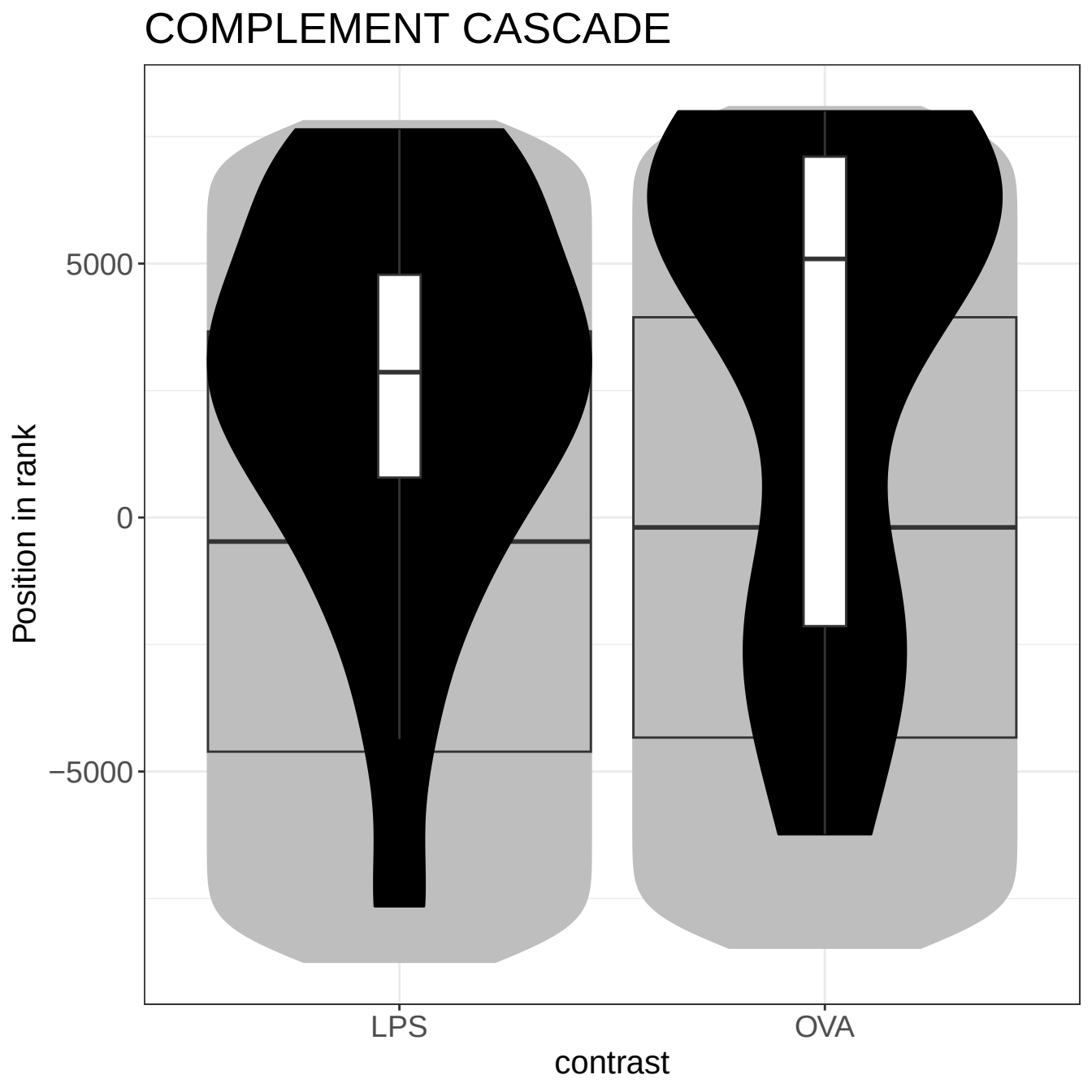

FRS MEDIATED FGFR3 SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09

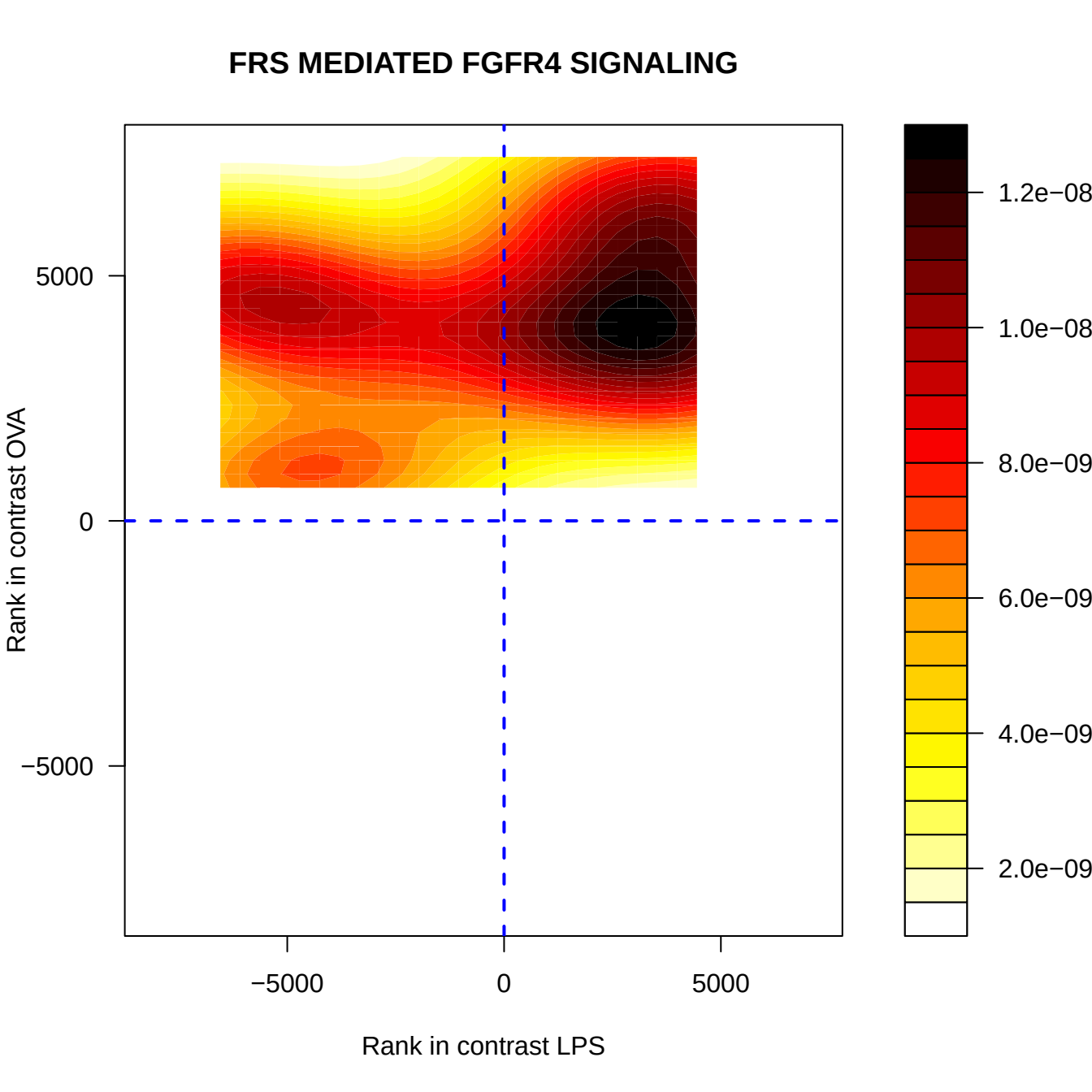

FRS MEDIATED FGFR3 SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

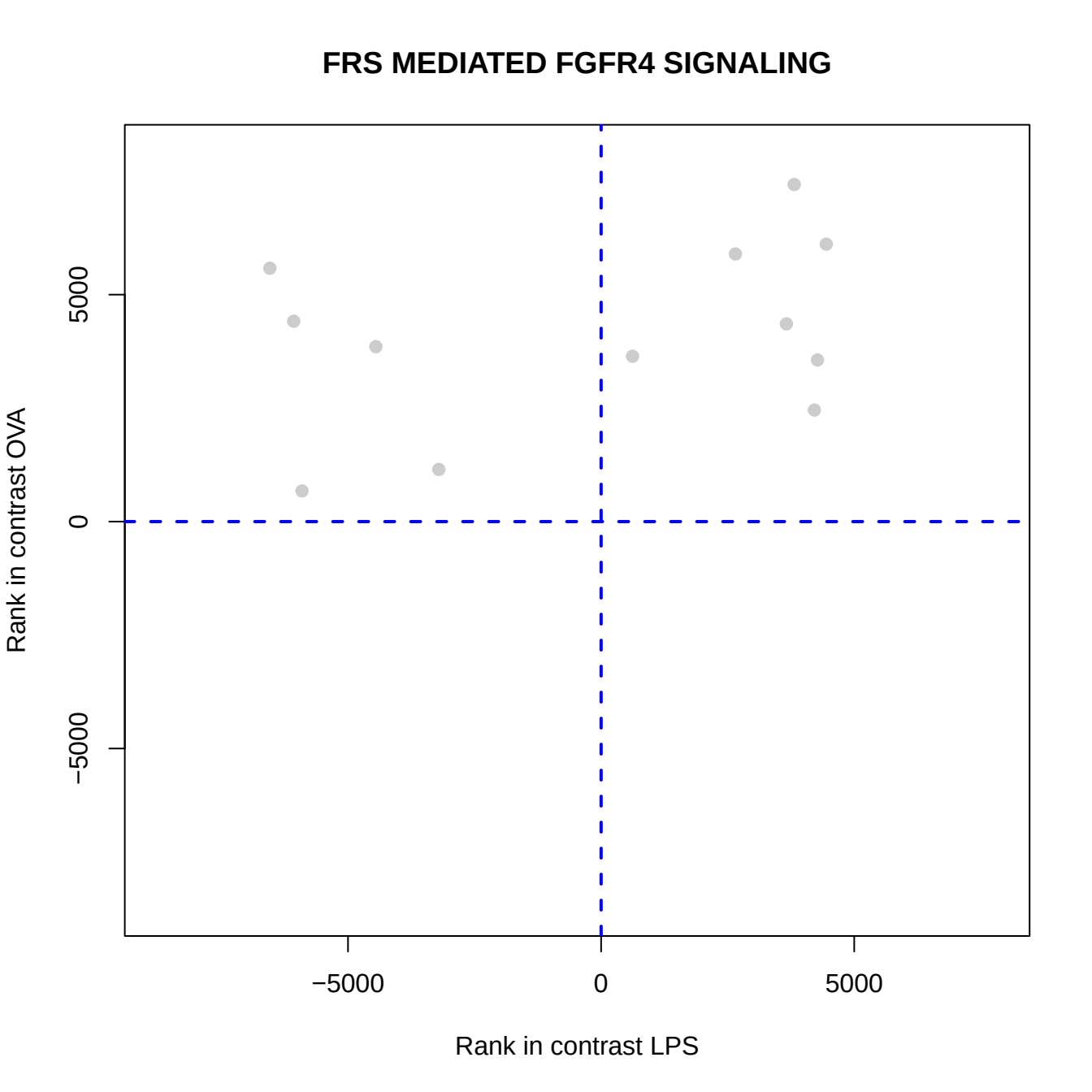

FRS MEDIATED FGFR3 SIGNALING
5000
0
−5000
Position in rank
LPS
OVA
contrast

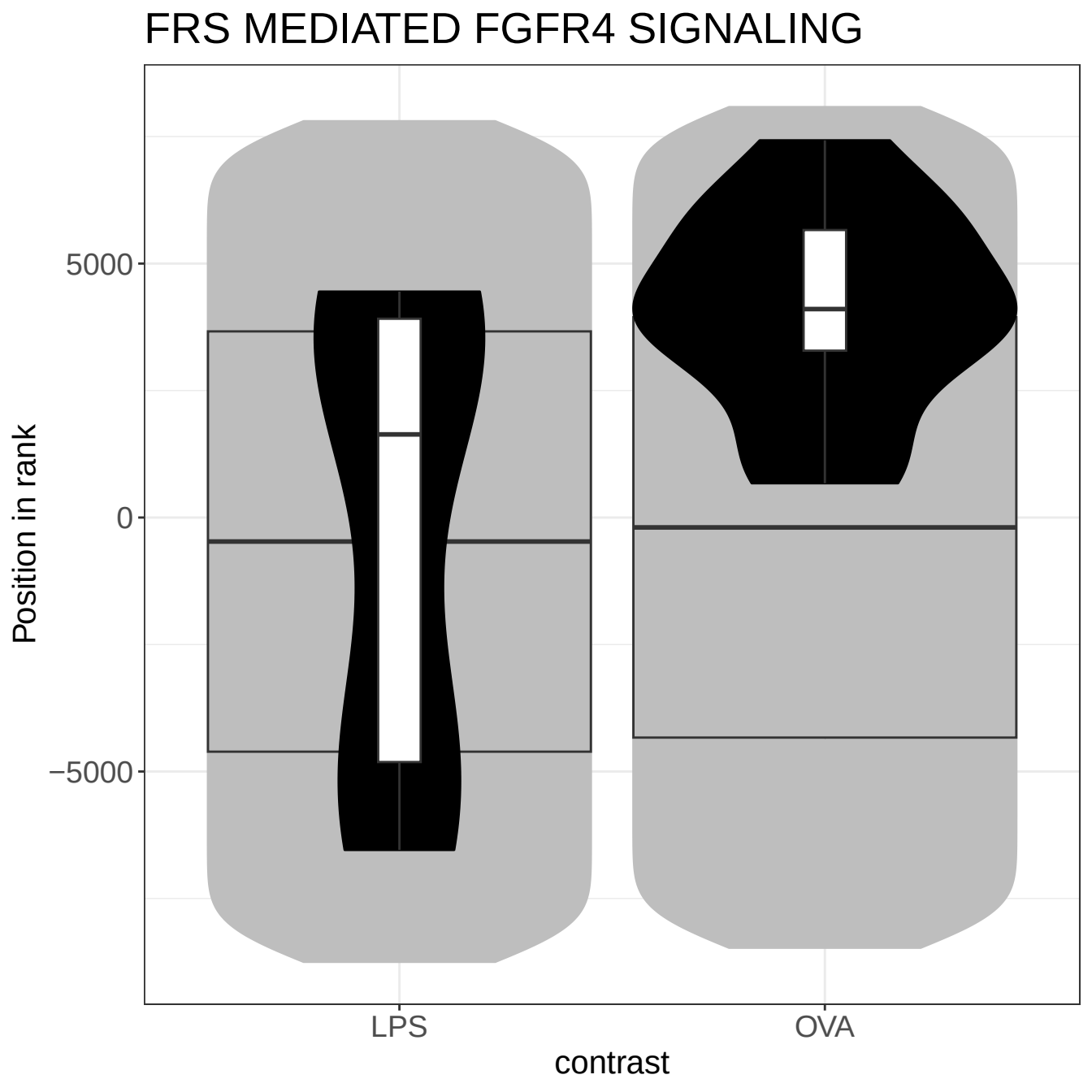

COMPLEMENT CASCADE
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

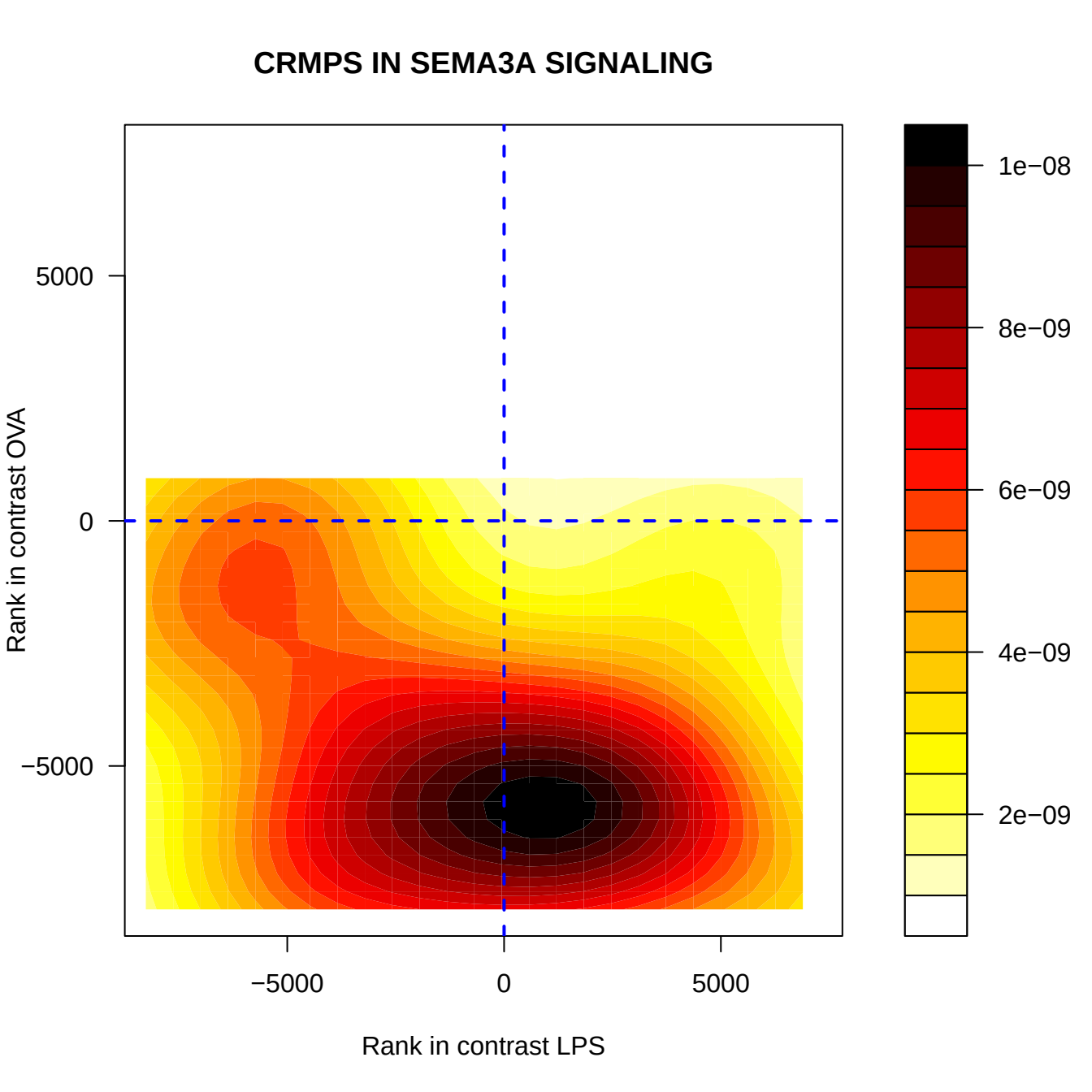

COMPLEMENT CASCADE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

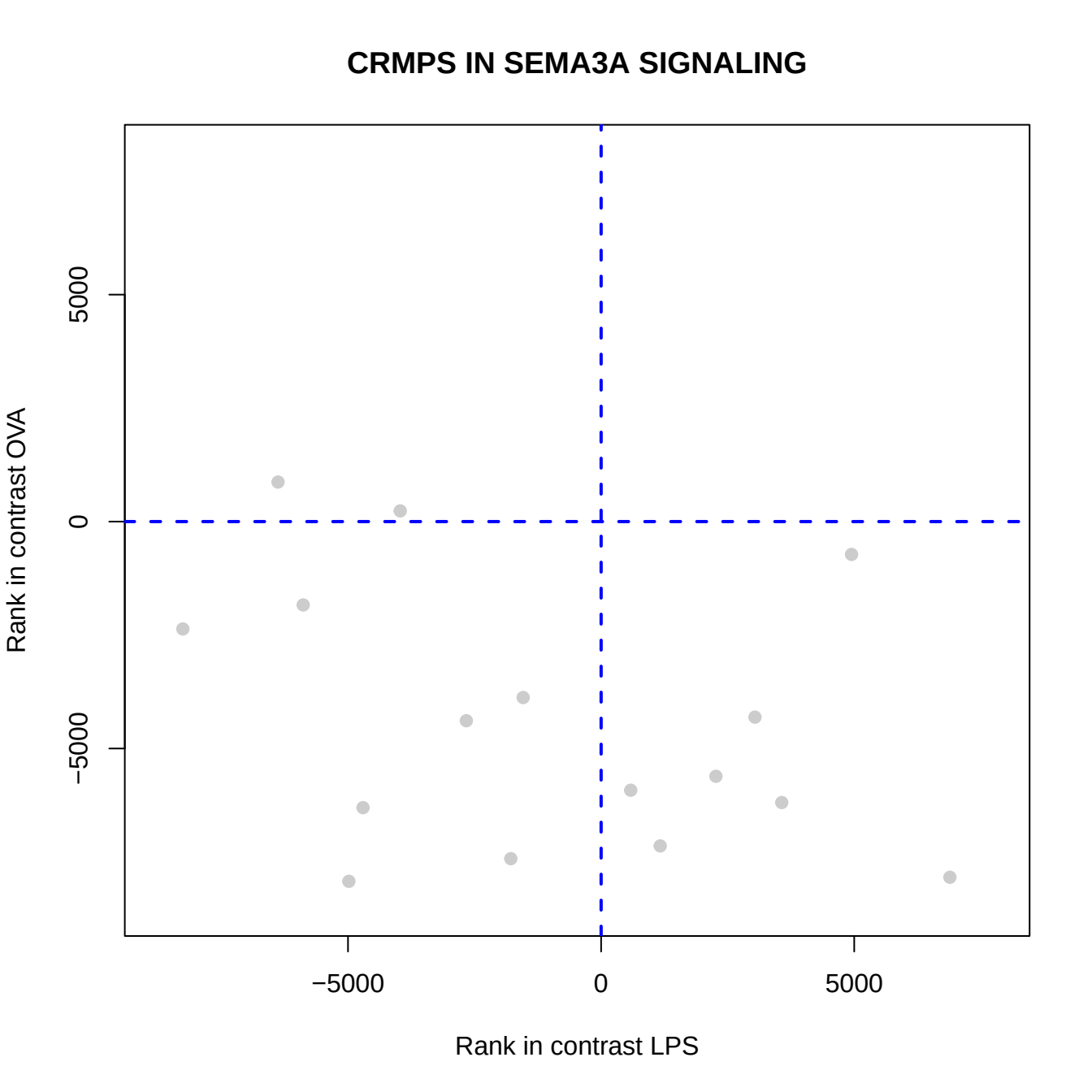

COMPLEMENT CASCADE
5000
0
−5000
Position in rank
LPS
OVA
contrast

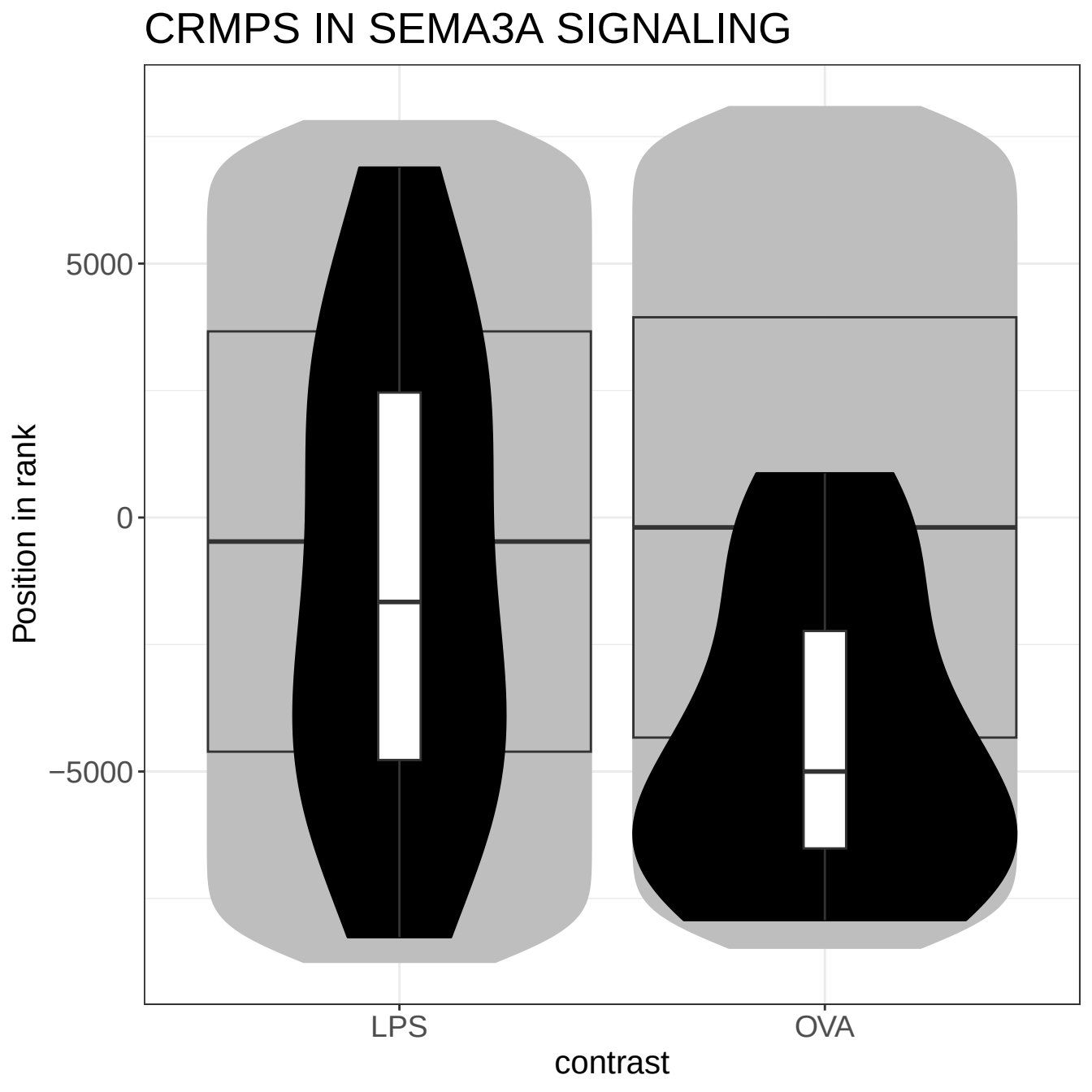

FRS MEDIATED FGFR4 SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09

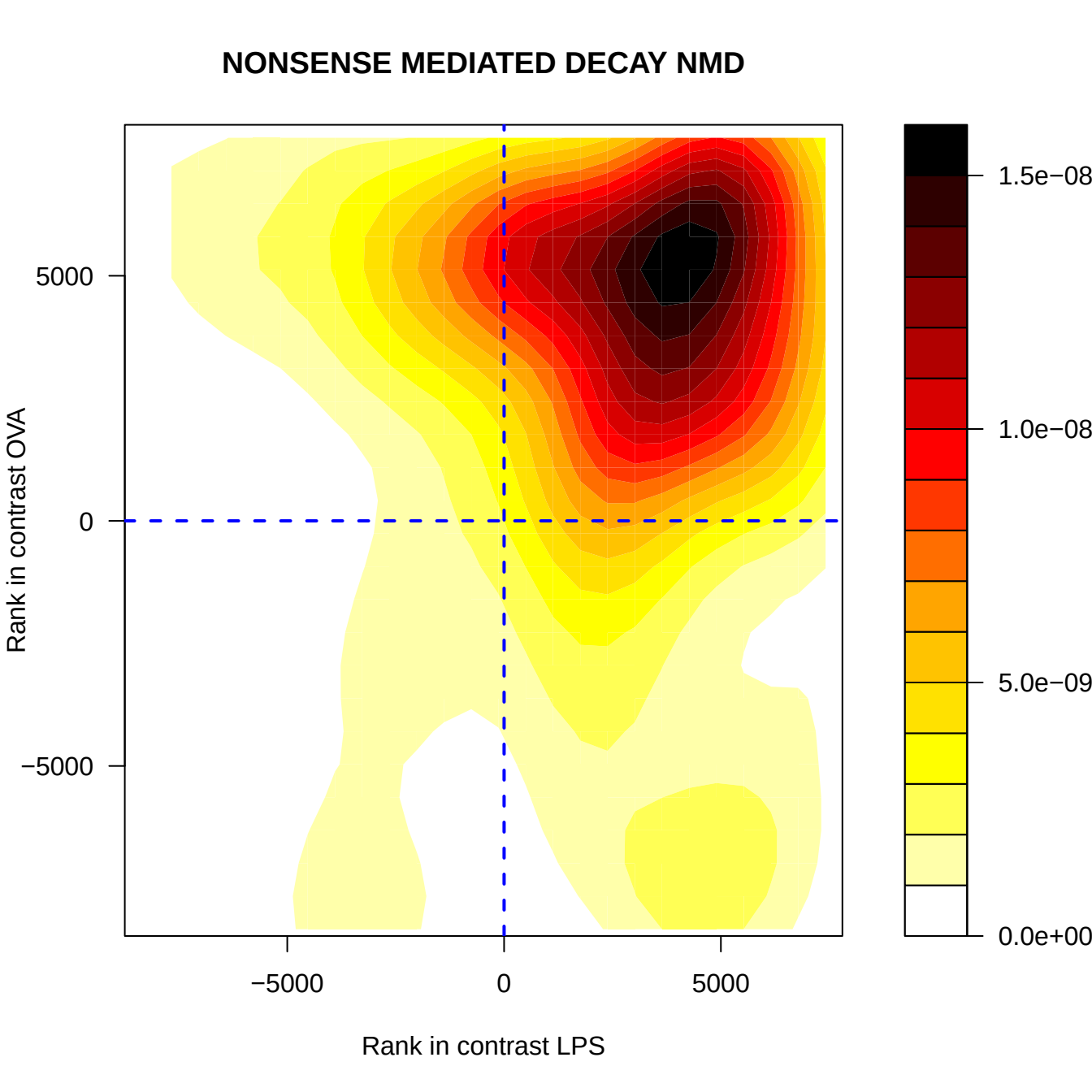

FRS MEDIATED FGFR4 SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

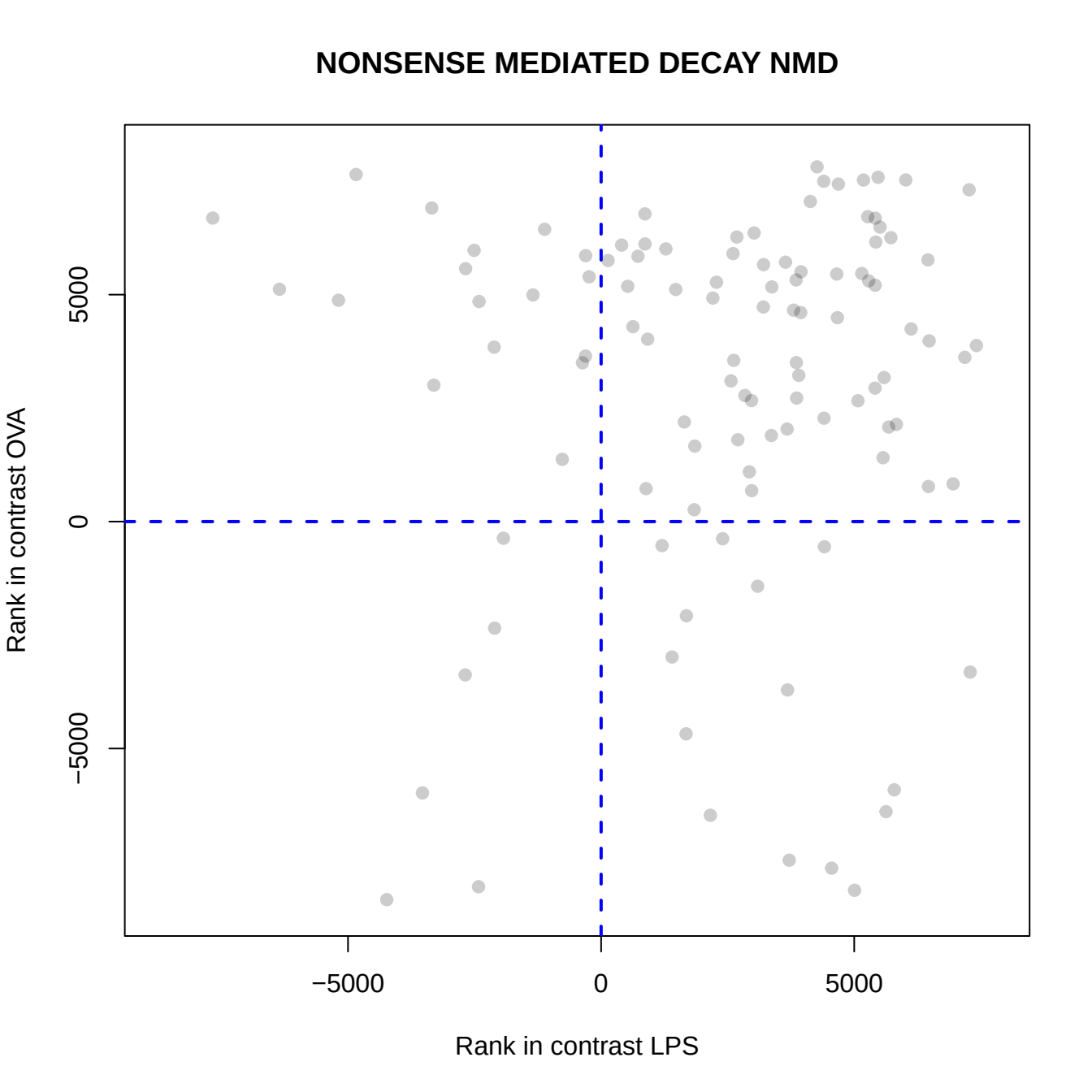

FRS MEDIATED FGFR4 SIGNALING
5000
0
−5000
Position in rank
LPS
OVA
contrast

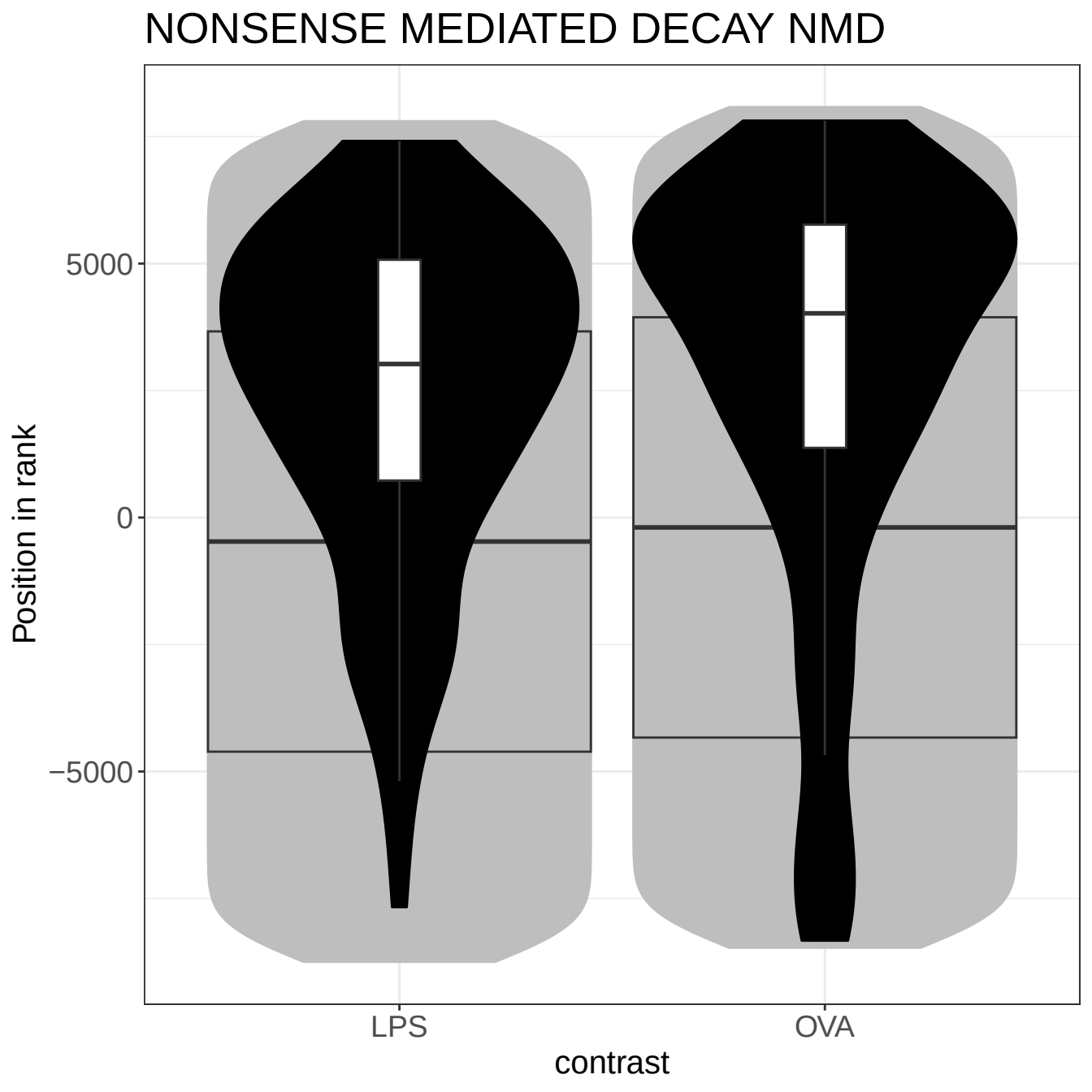

CRMPS IN SEMA3A SIGNALING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09

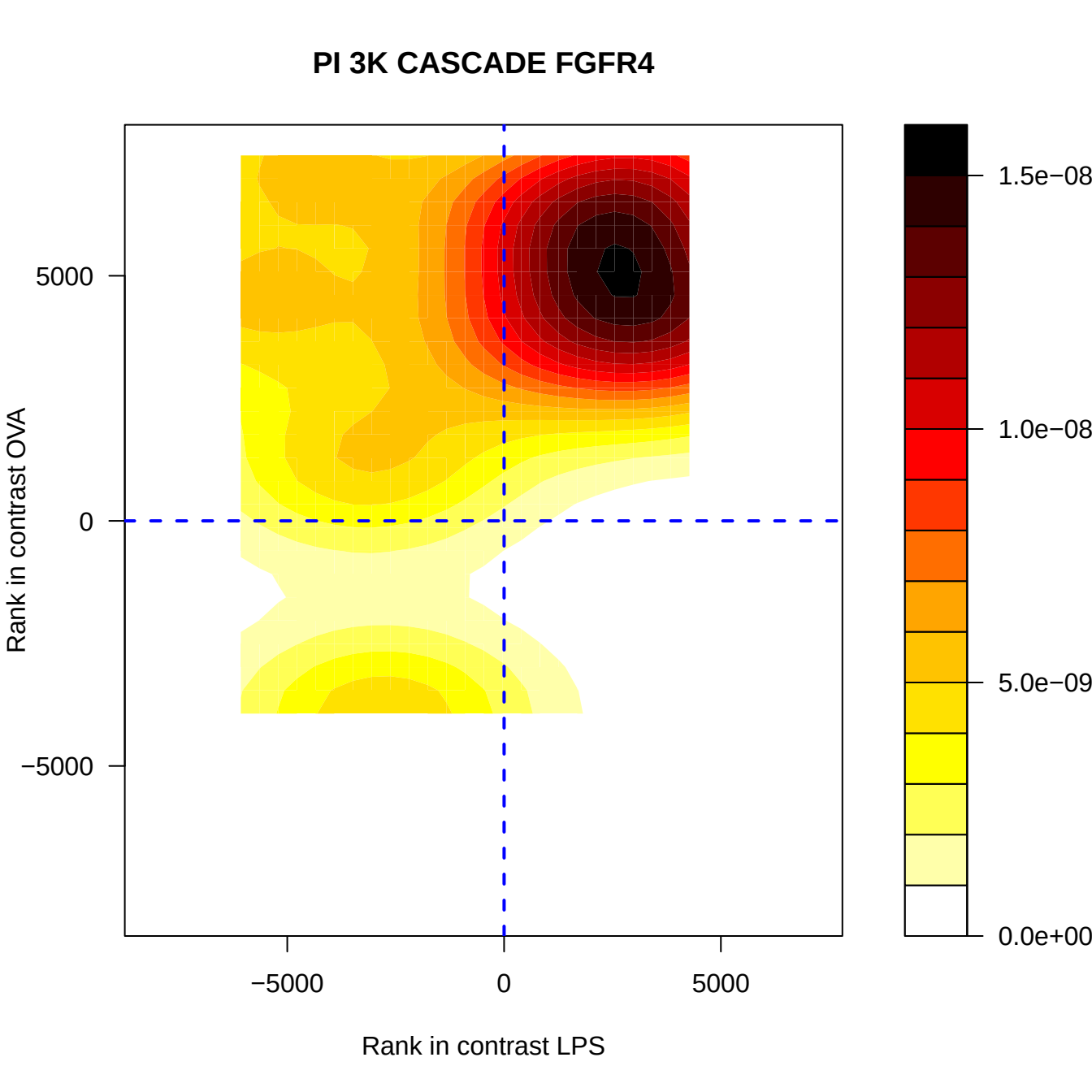

CRMPS IN SEMA3A SIGNALING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

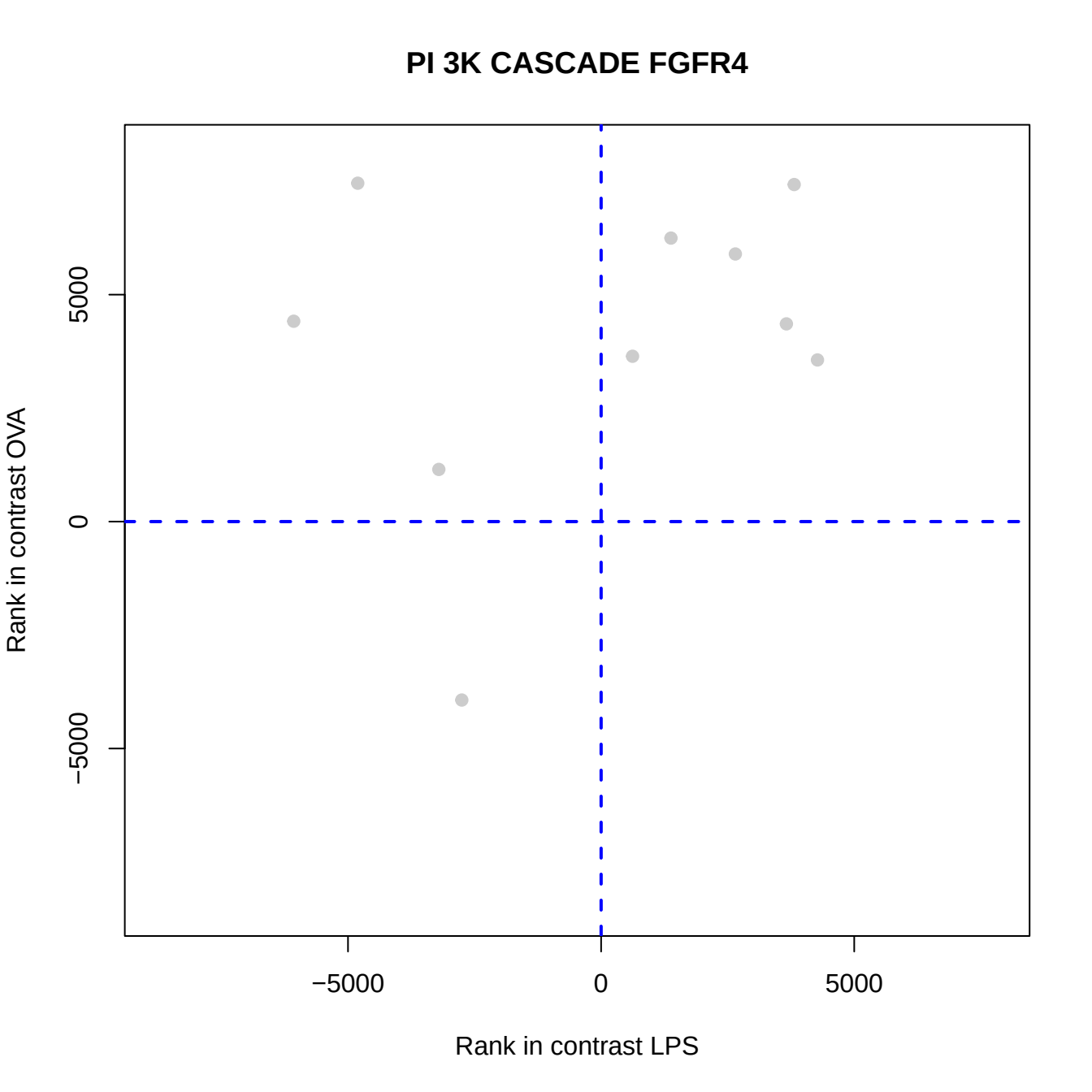

CRMPS IN SEMA3A SIGNALING
5000
0
−5000
Position in rank
LPS
OVA
contrast

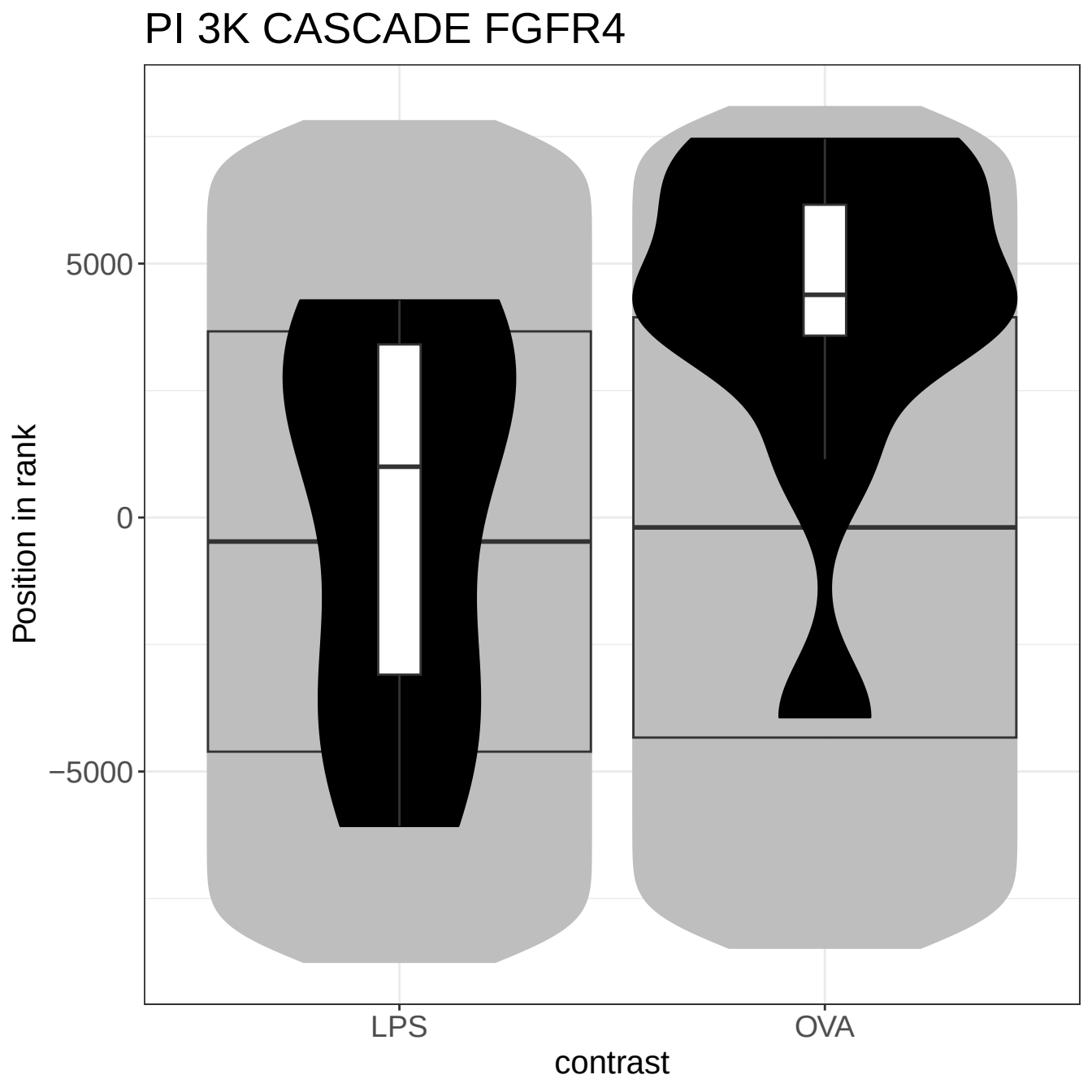

NONSENSE MEDIATED DECAY NMD
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

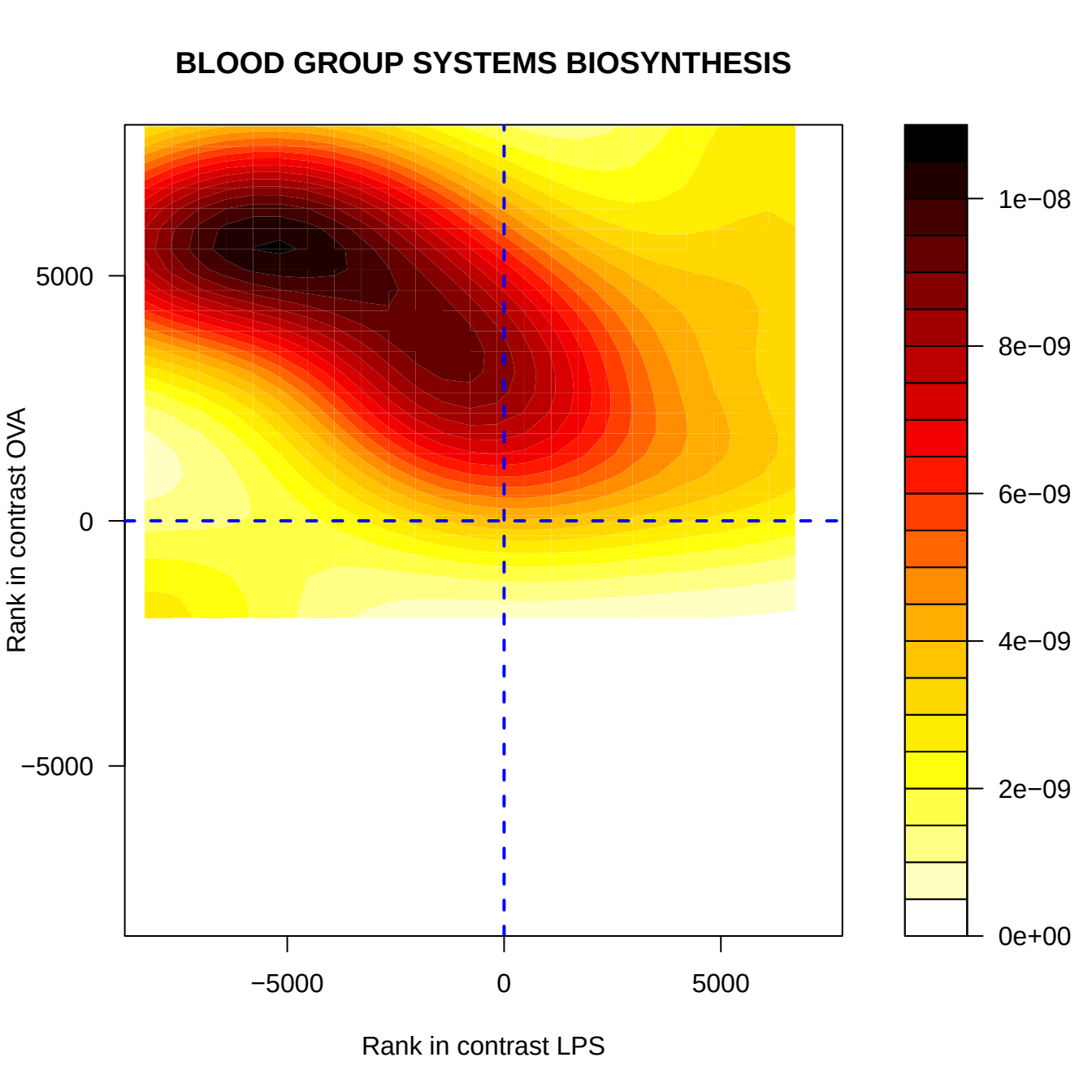

NONSENSE MEDIATED DECAY NMD
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

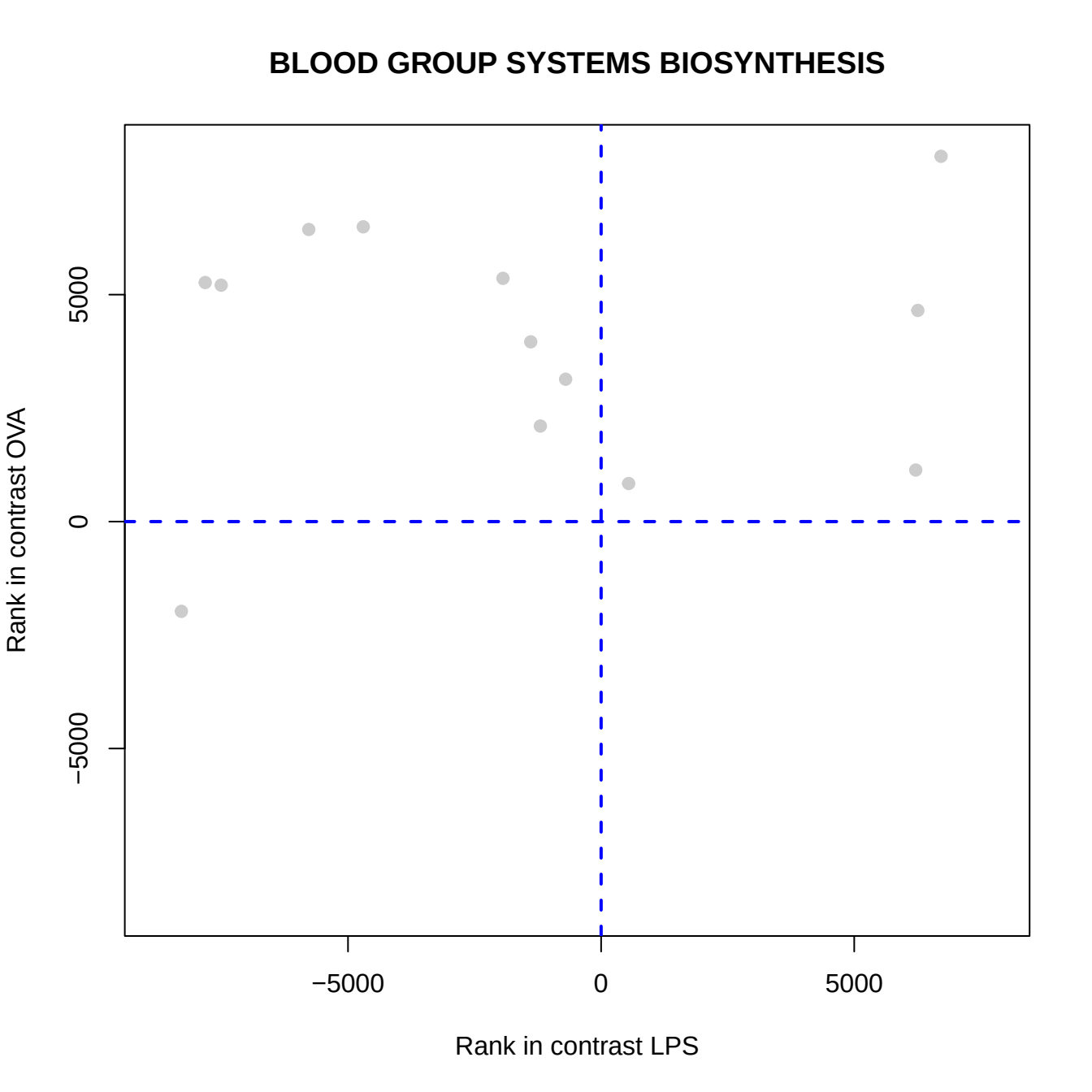

NONSENSE MEDIATED DECAY NMD
5000
0
−5000
Position in rank
LPS
OVA
contrast

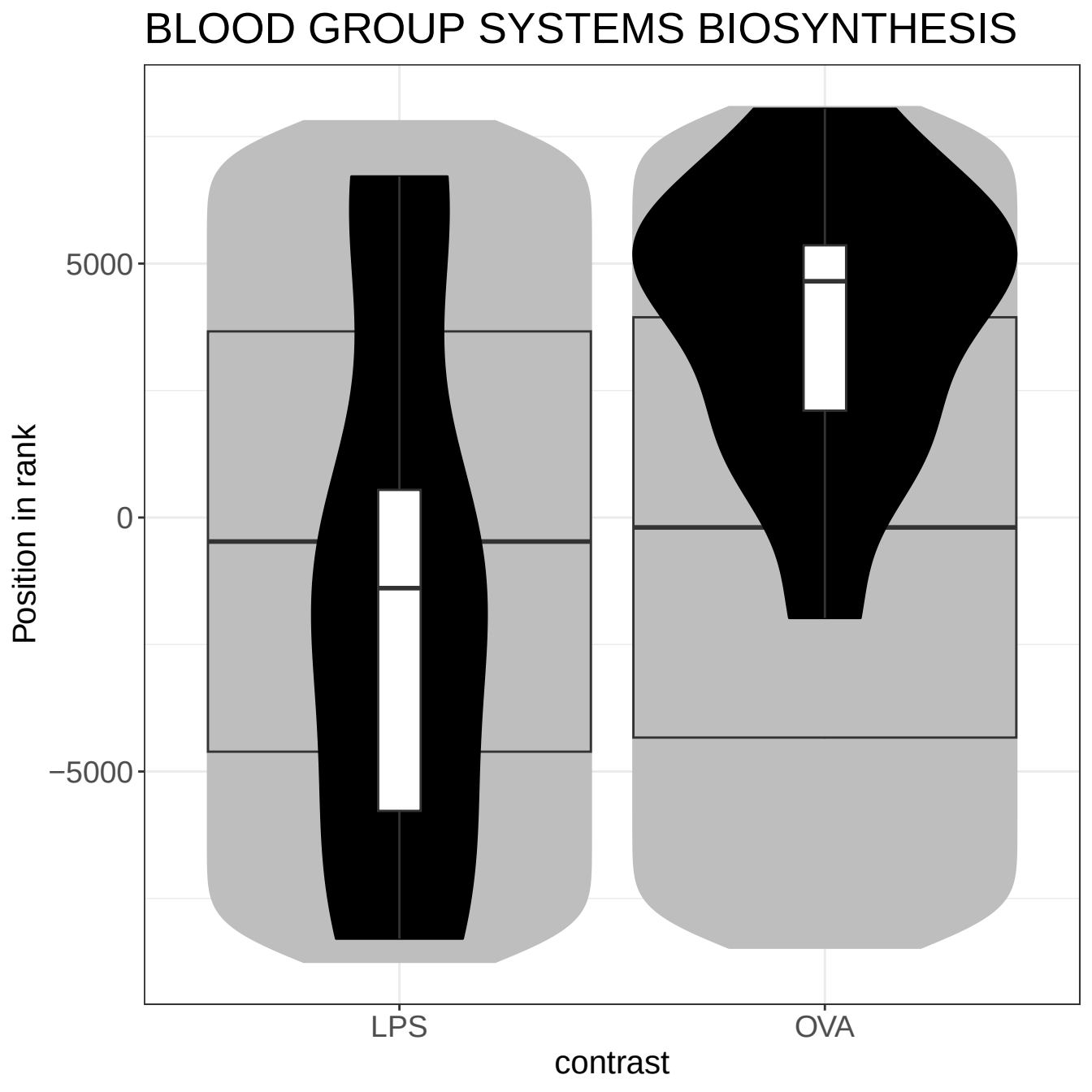

PI 3K CASCADE FGFR4
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1.5e−08
1.0e−08
5.0e−09
0.0e+00

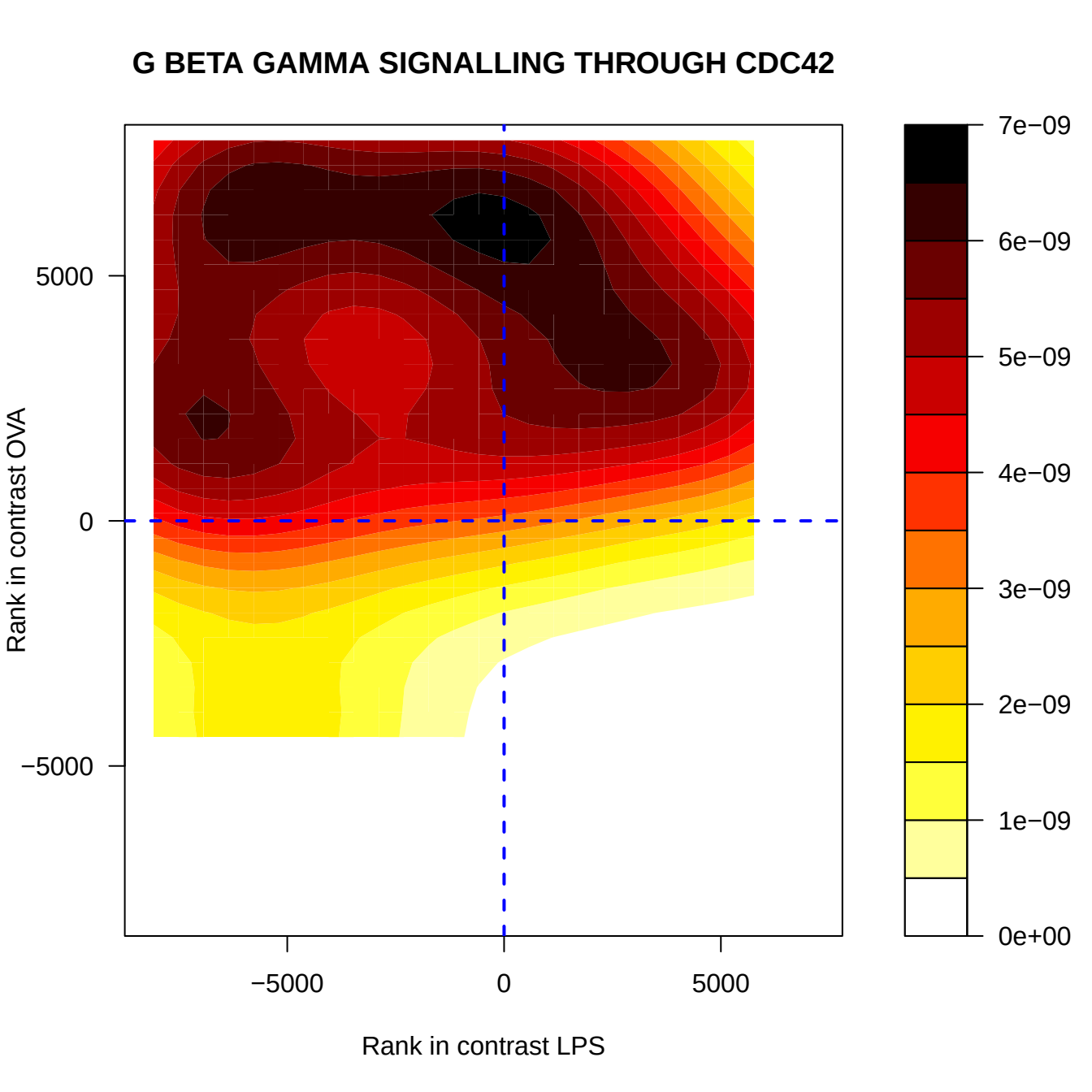

PI 3K CASCADE FGFR4
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

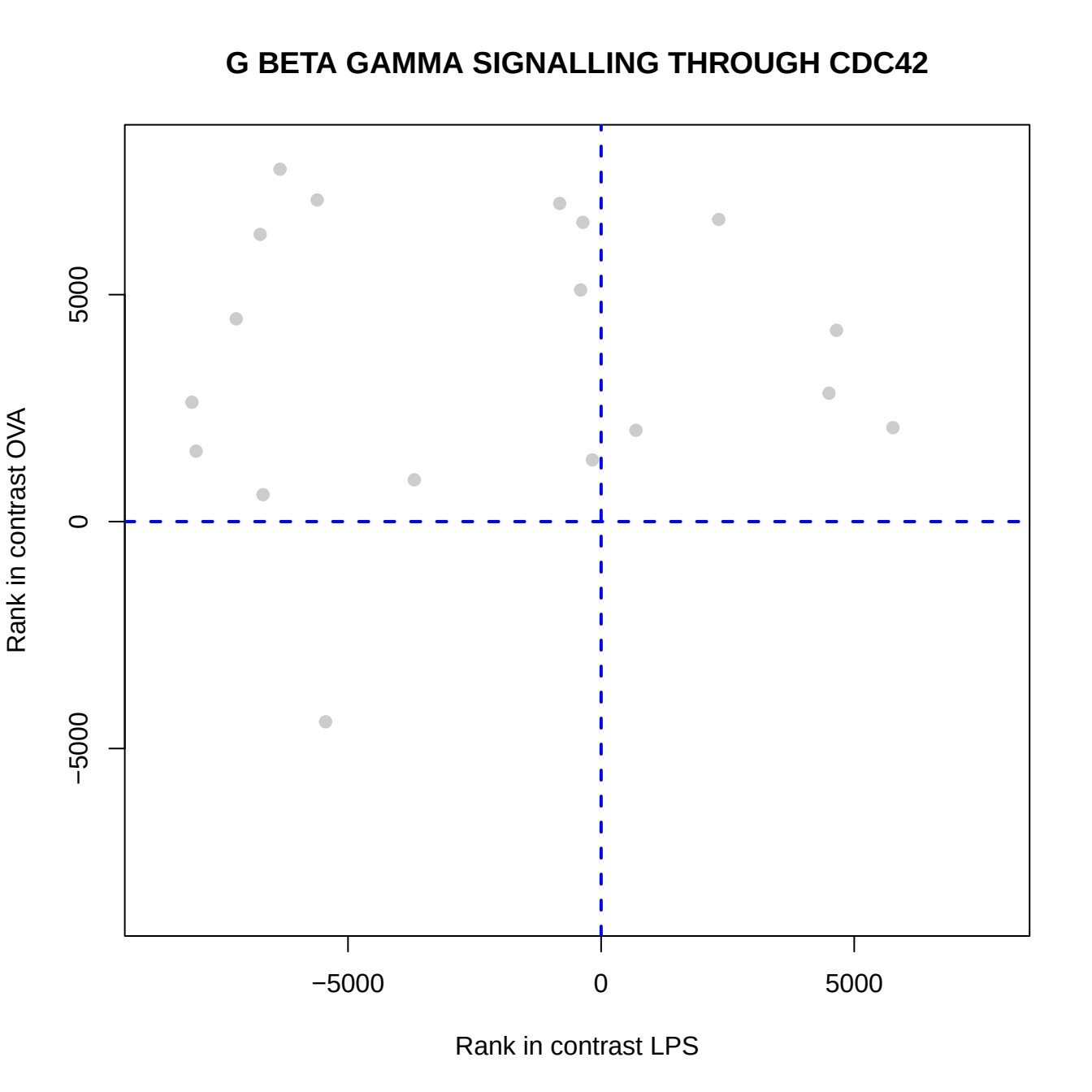

PI 3K CASCADE FGFR4
5000
0
−5000
Position in rank
LPS
OVA
contrast

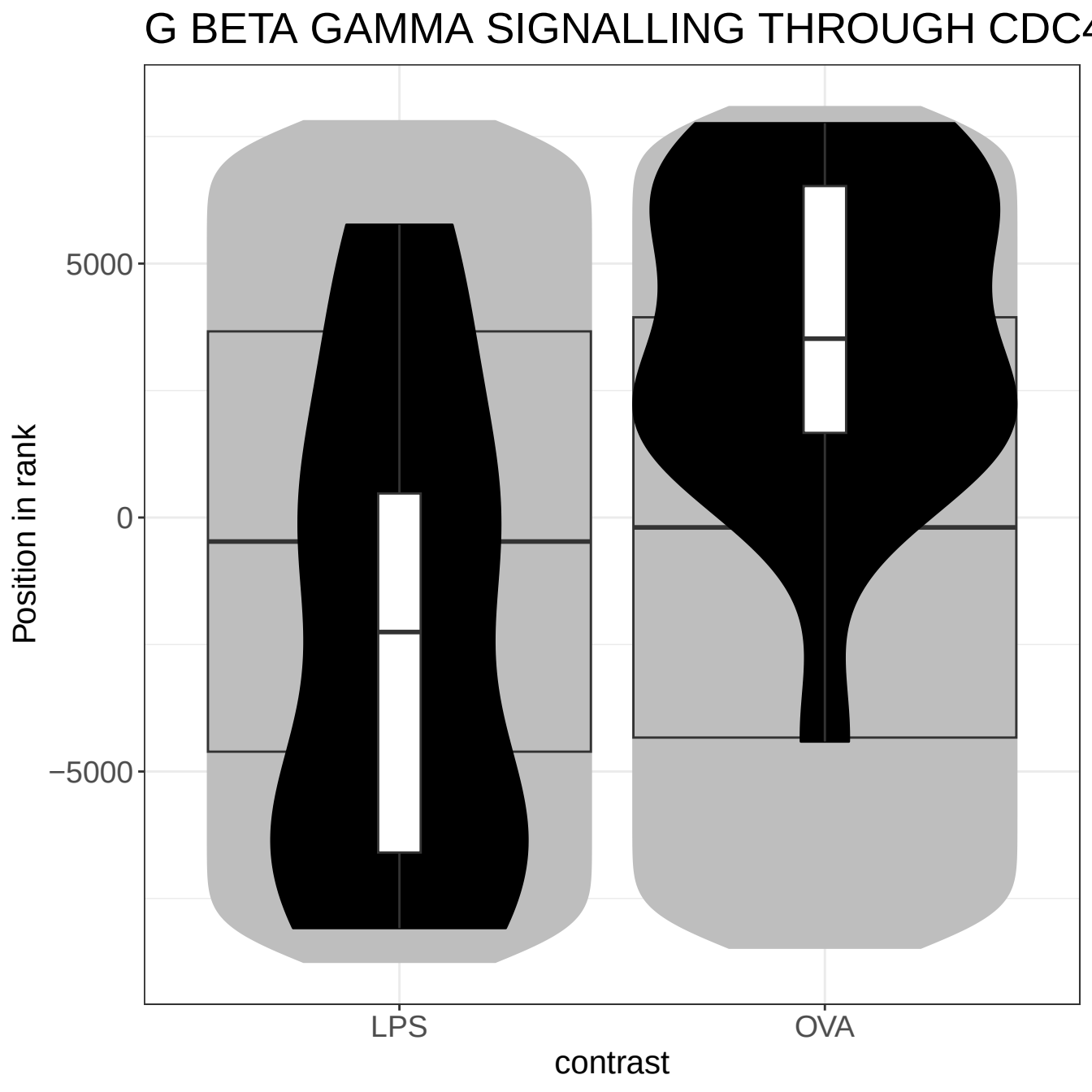

BLOOD GROUP SYSTEMS BIOSYNTHESIS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

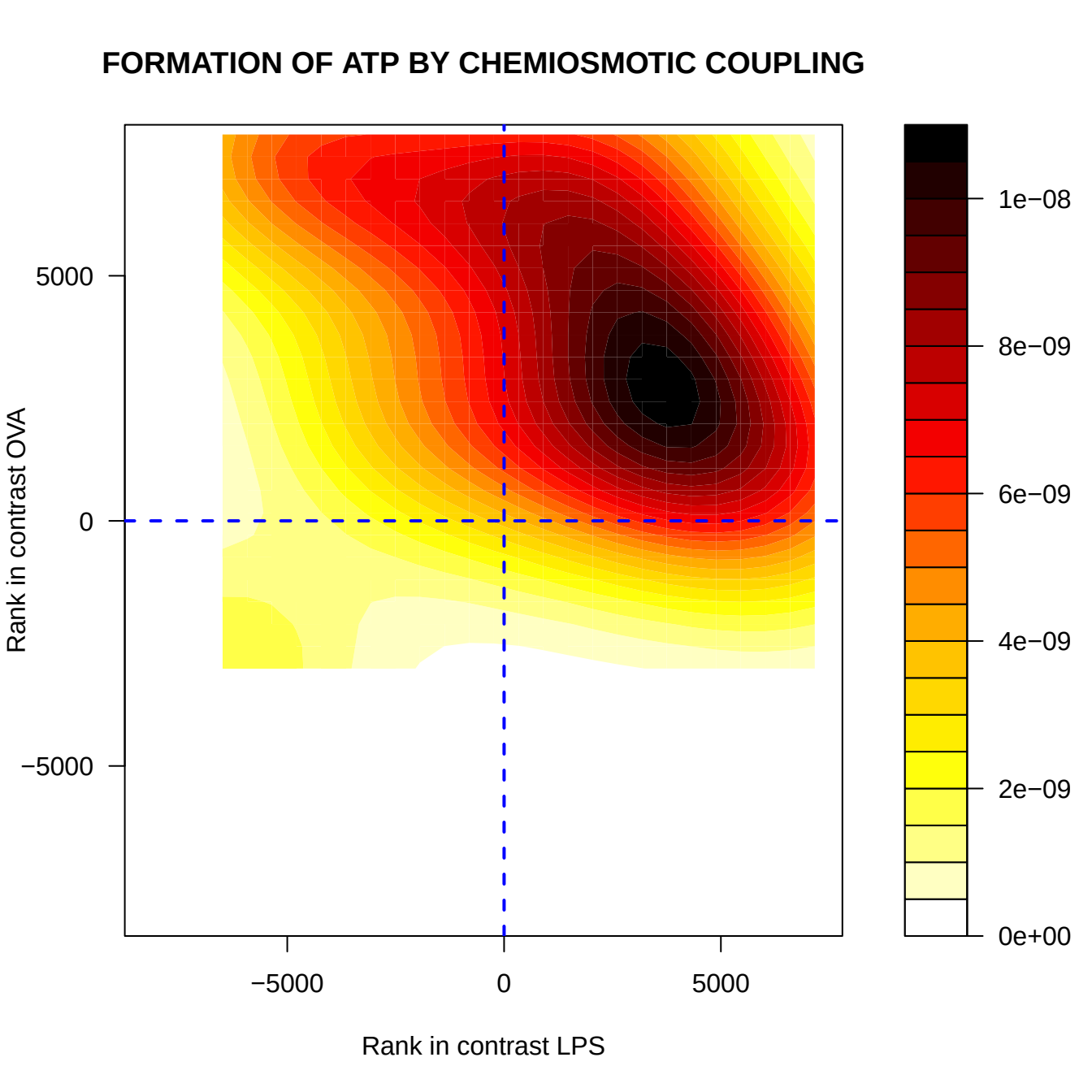

BLOOD GROUP SYSTEMS BIOSYNTHESIS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

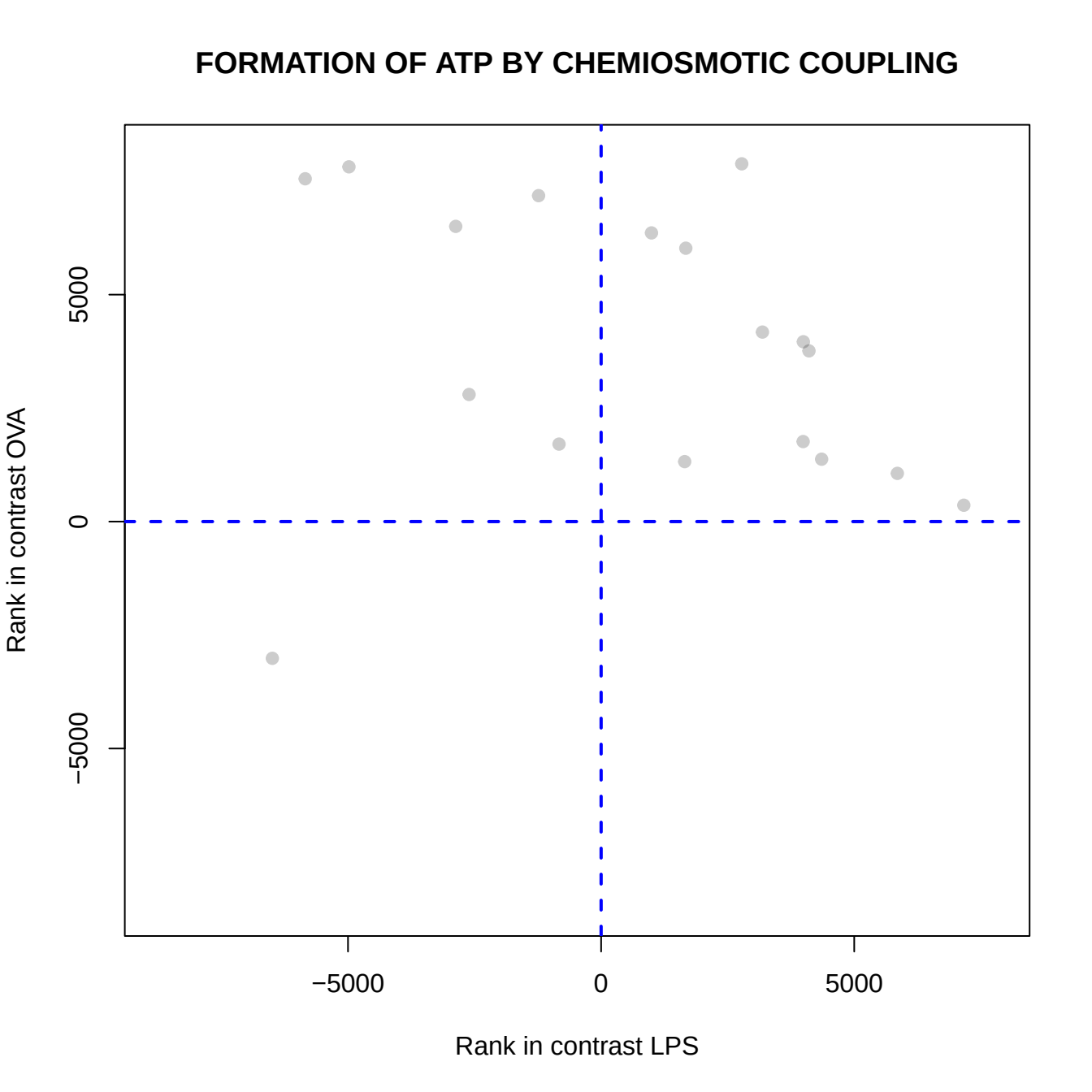

BLOOD GROUP SYSTEMS BIOSYNTHESIS
5000
0
−5000
Position in rank
LPS
OVA
contrast

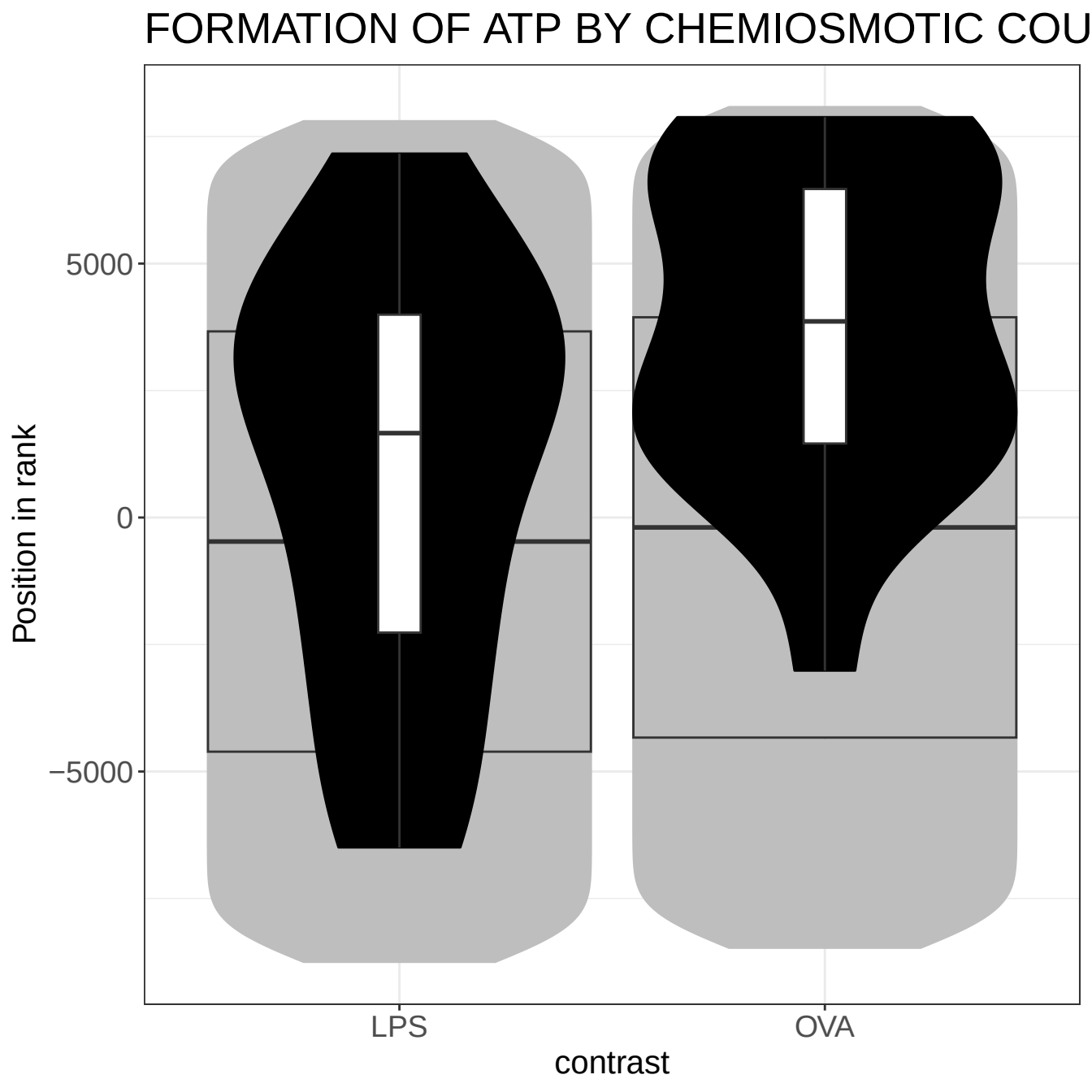

G BETA GAMMA SIGNALLING THROUGH CDC42
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
7e−09
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

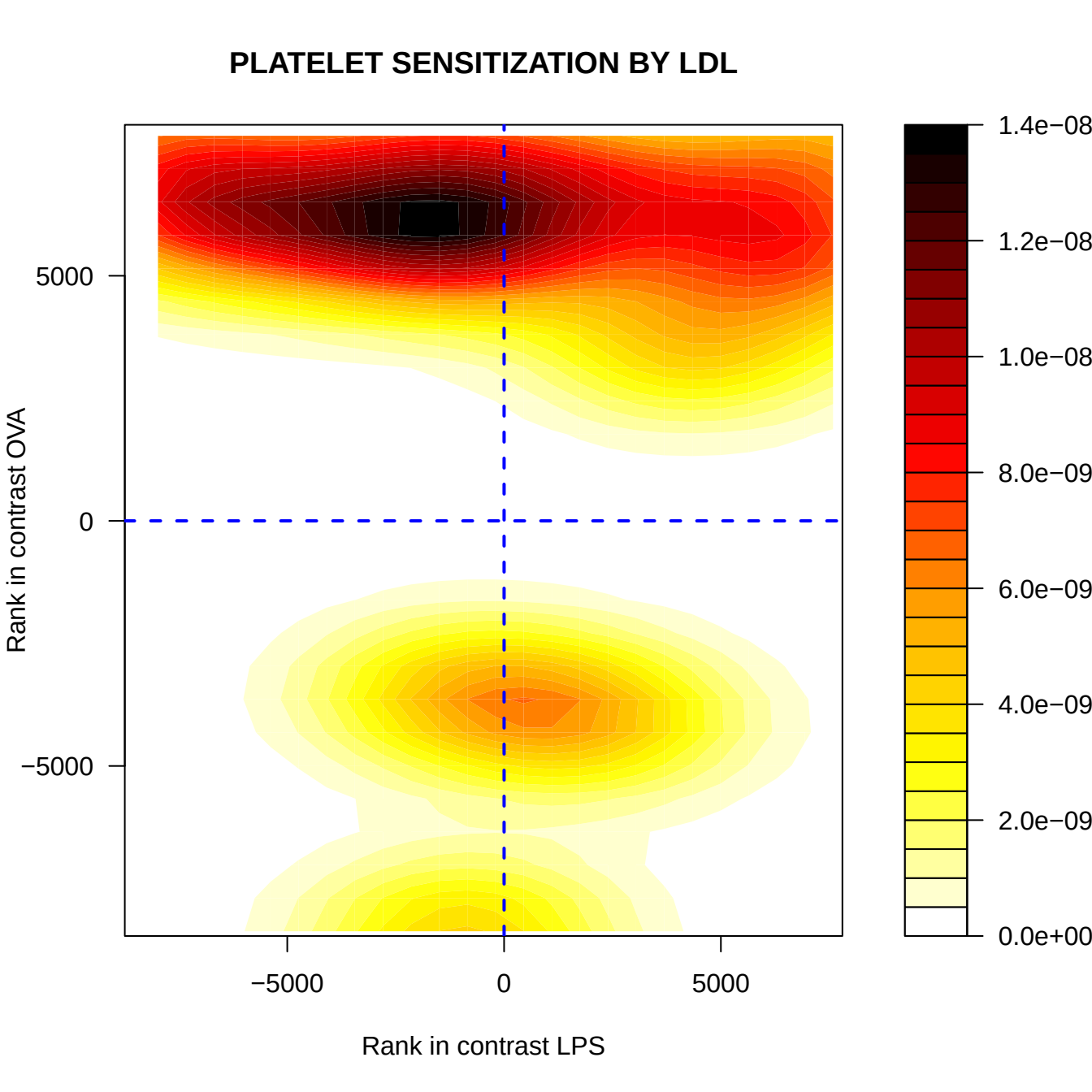

G BETA GAMMA SIGNALLING THROUGH CDC42
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

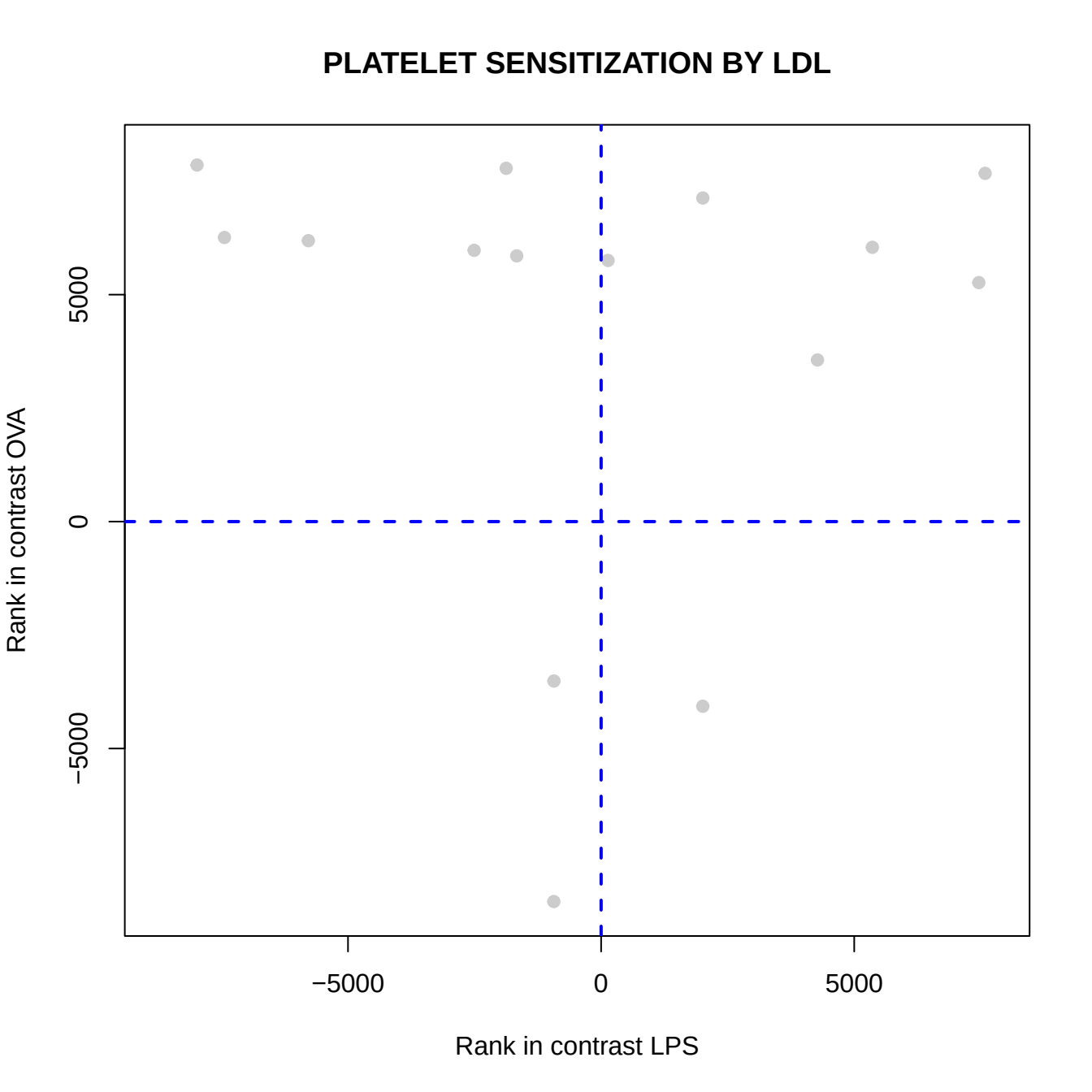

G BETA GAMMA SIGNALLING THROUGH CDC4
5000
0
−5000
Position in rank
LPS
OVA
contrast

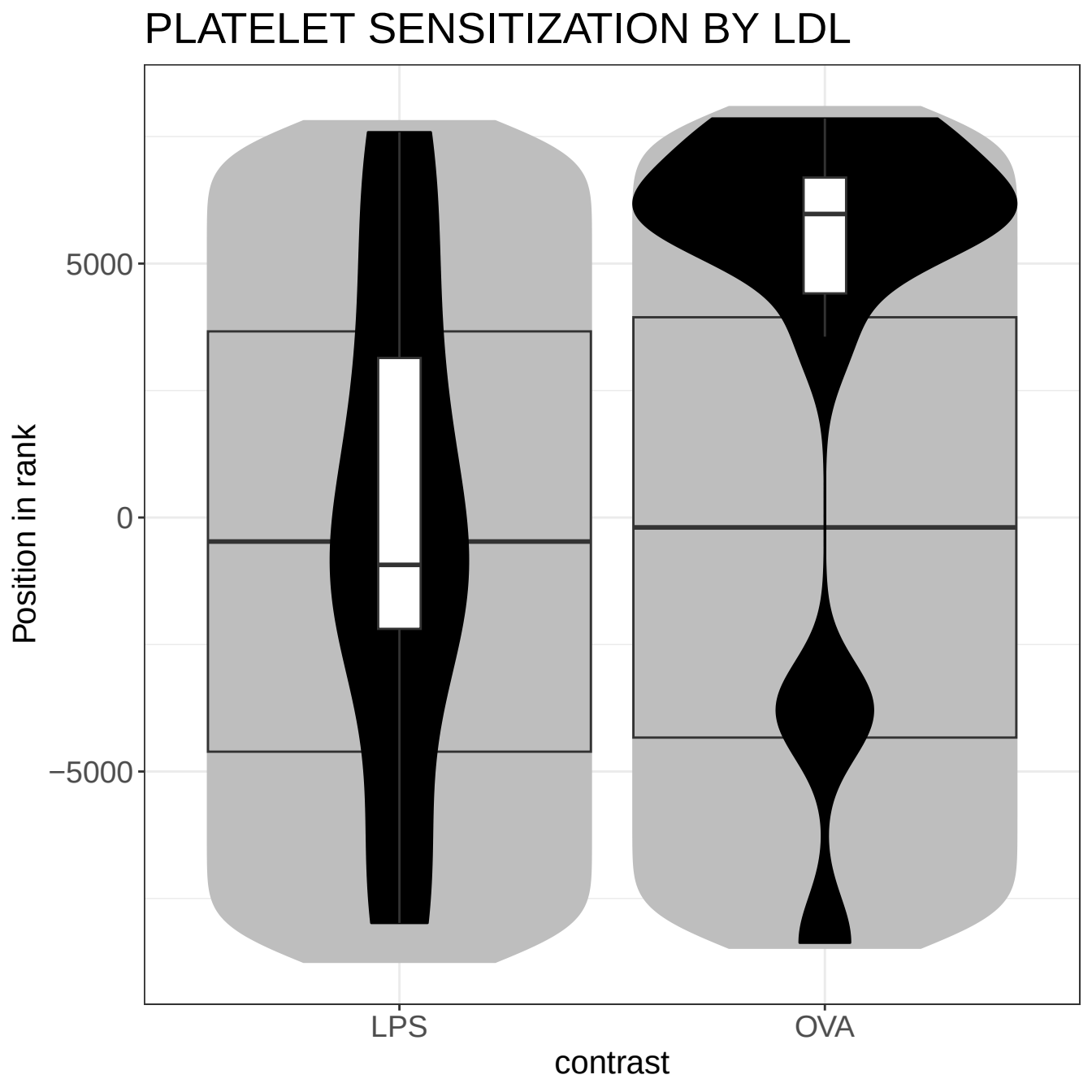

FORMATION OF ATP BY CHEMIOSMOTIC COUPLING
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
1e−08
8e−09
6e−09
4e−09
2e−09
0e+00

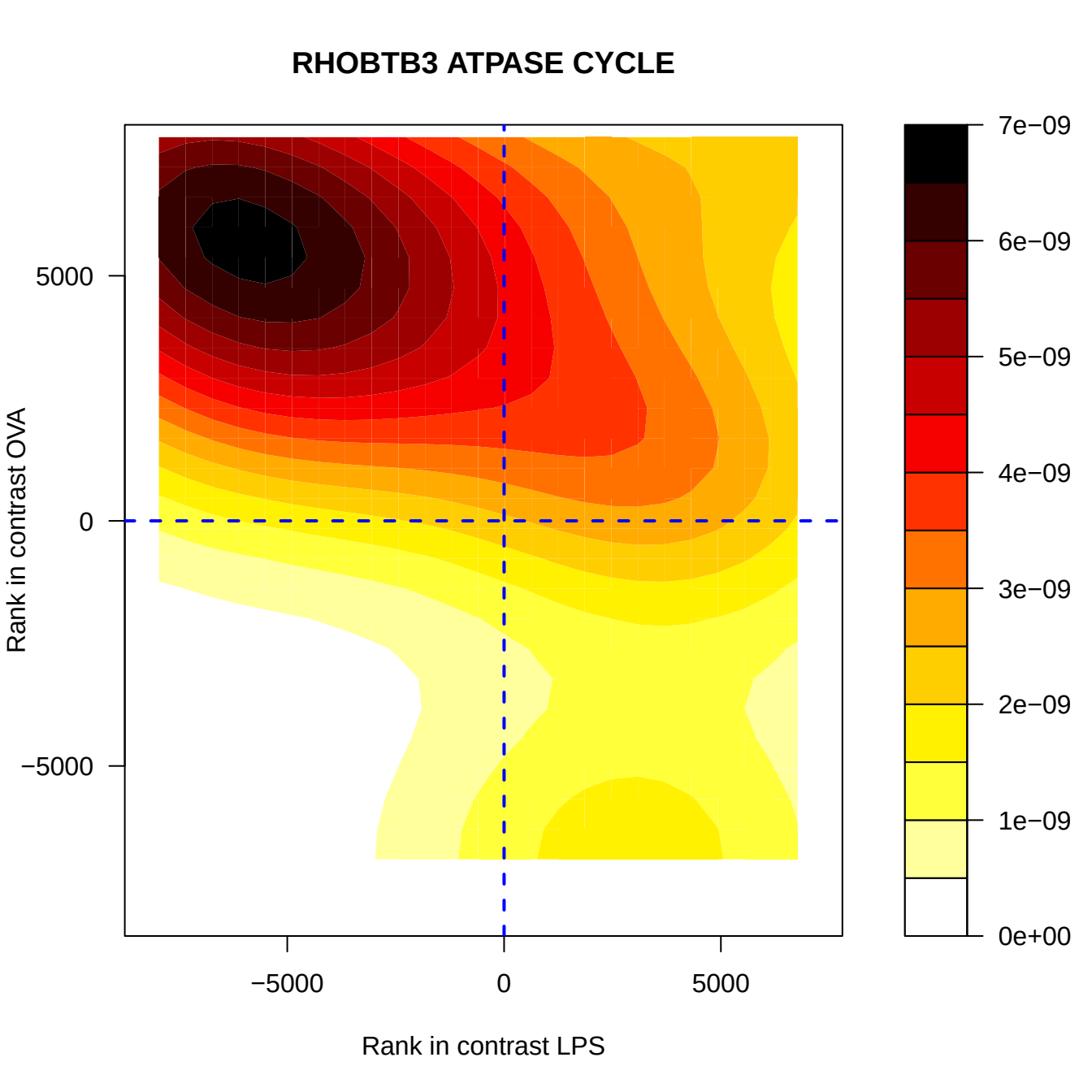

FORMATION OF ATP BY CHEMIOSMOTIC COUPLING
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

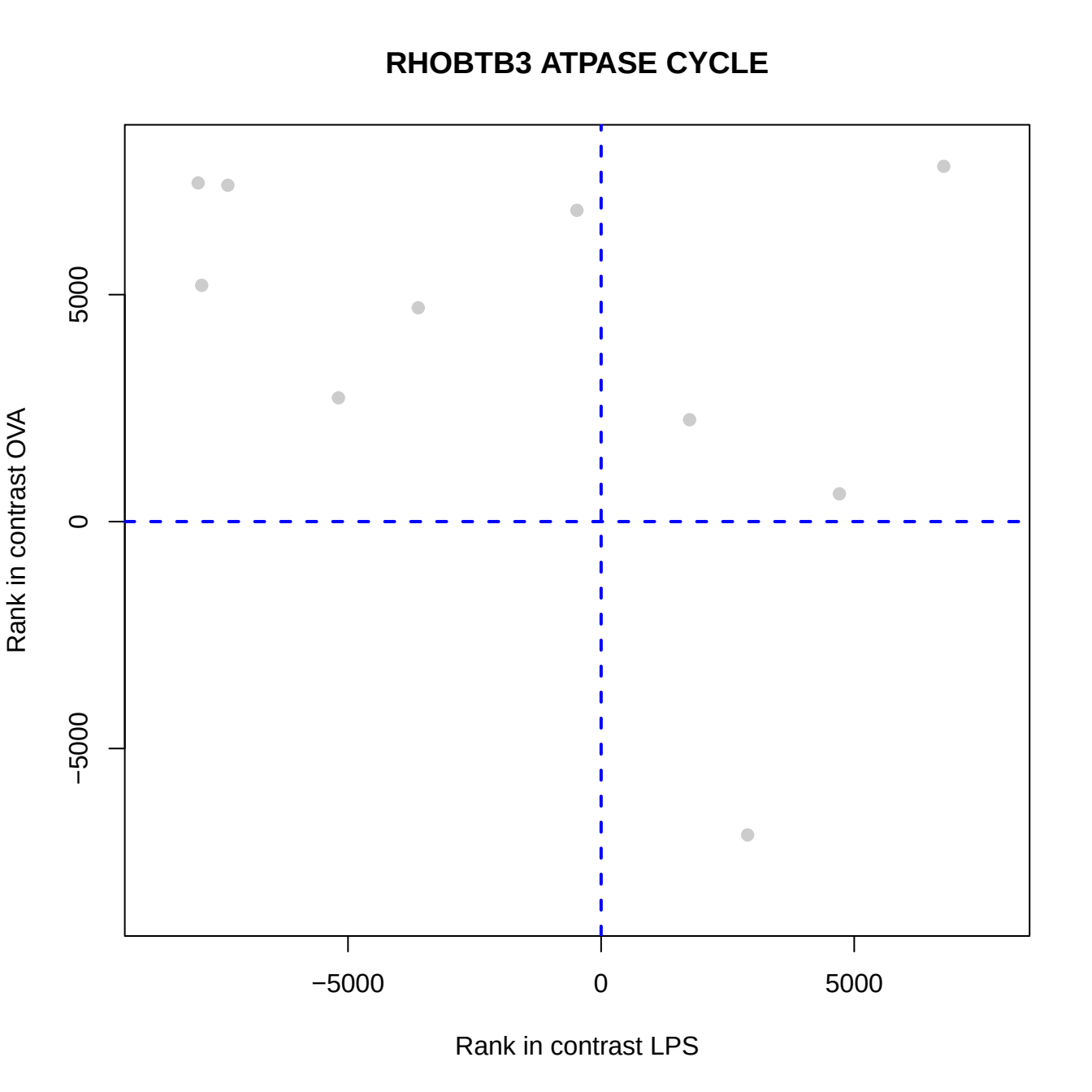

FORMATION OF ATP BY CHEMIOSMOTIC COU
5000
0
−5000
Position in rank
LPS
OVA
contrast

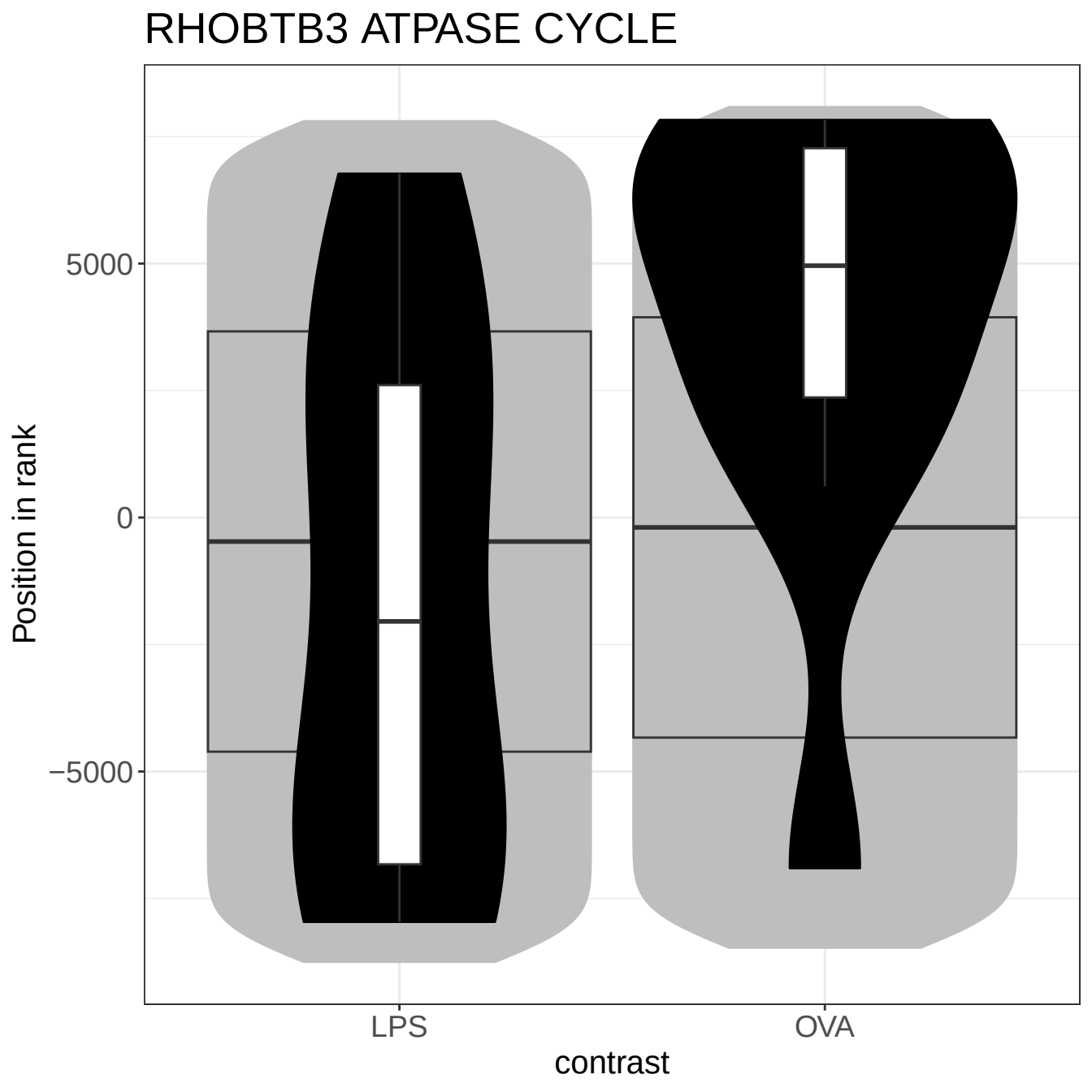

PLATELET SENSITIZATION BY LDL
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

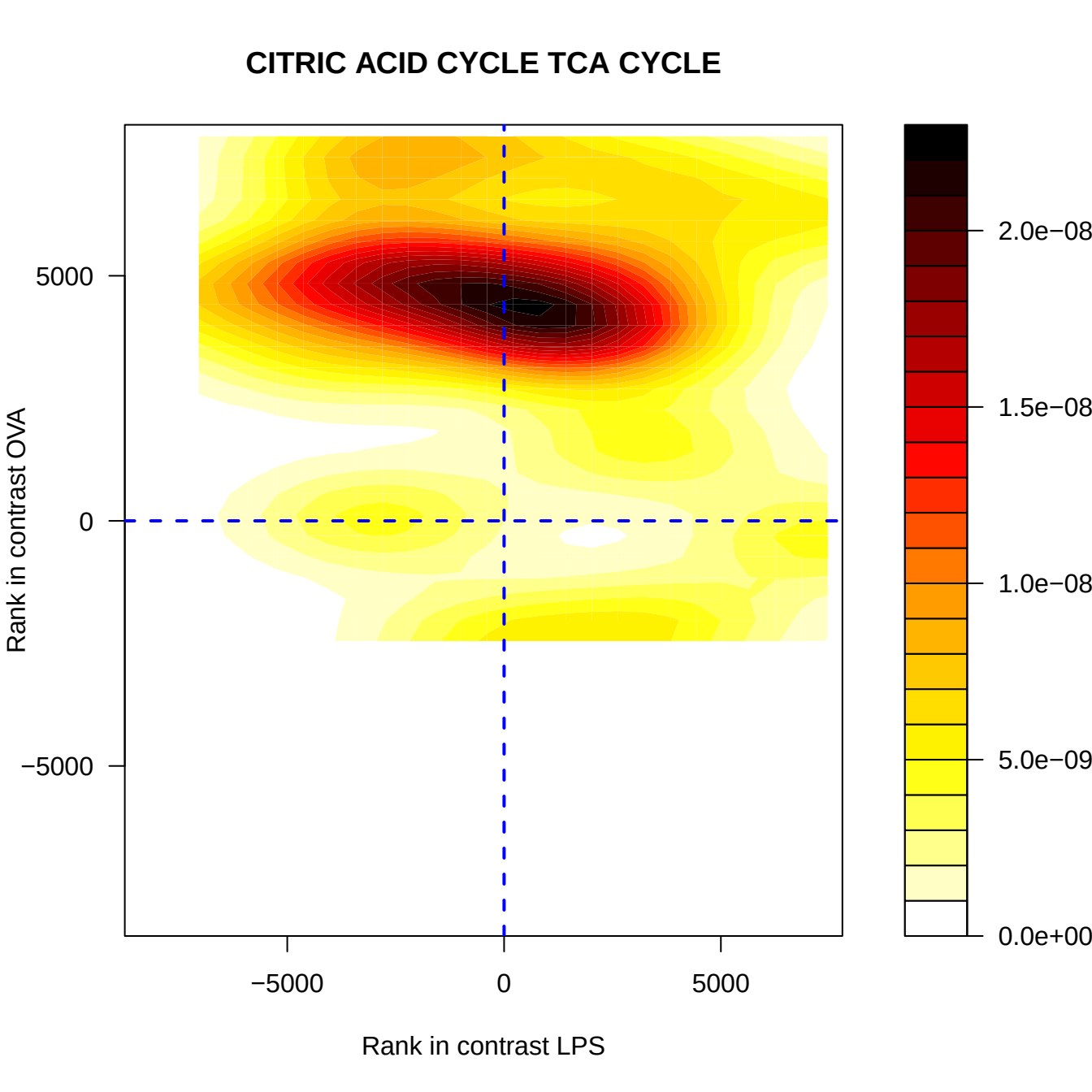

PLATELET SENSITIZATION BY LDL
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

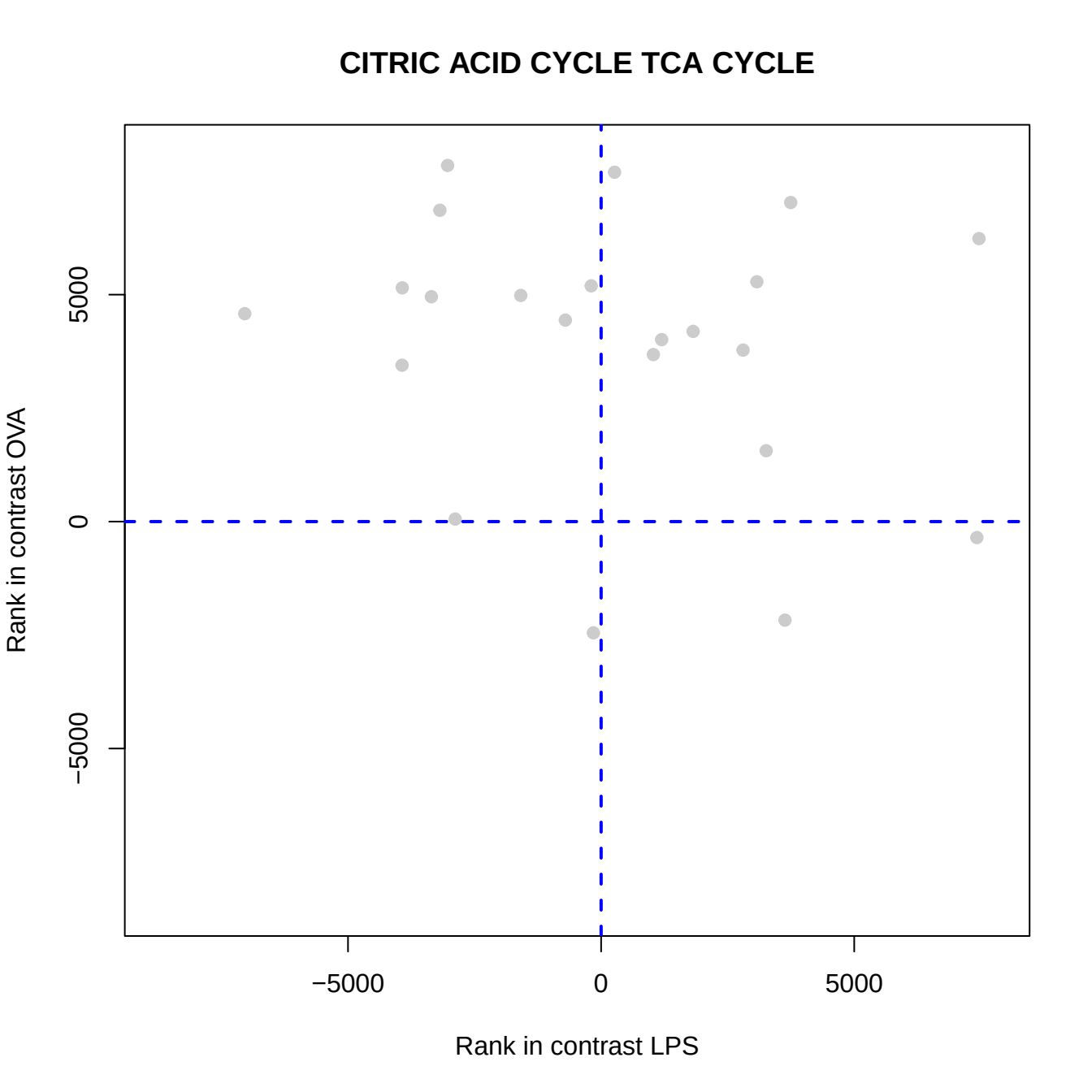

PLATELET SENSITIZATION BY LDL
5000
0
−5000
Position in rank
LPS
OVA
contrast

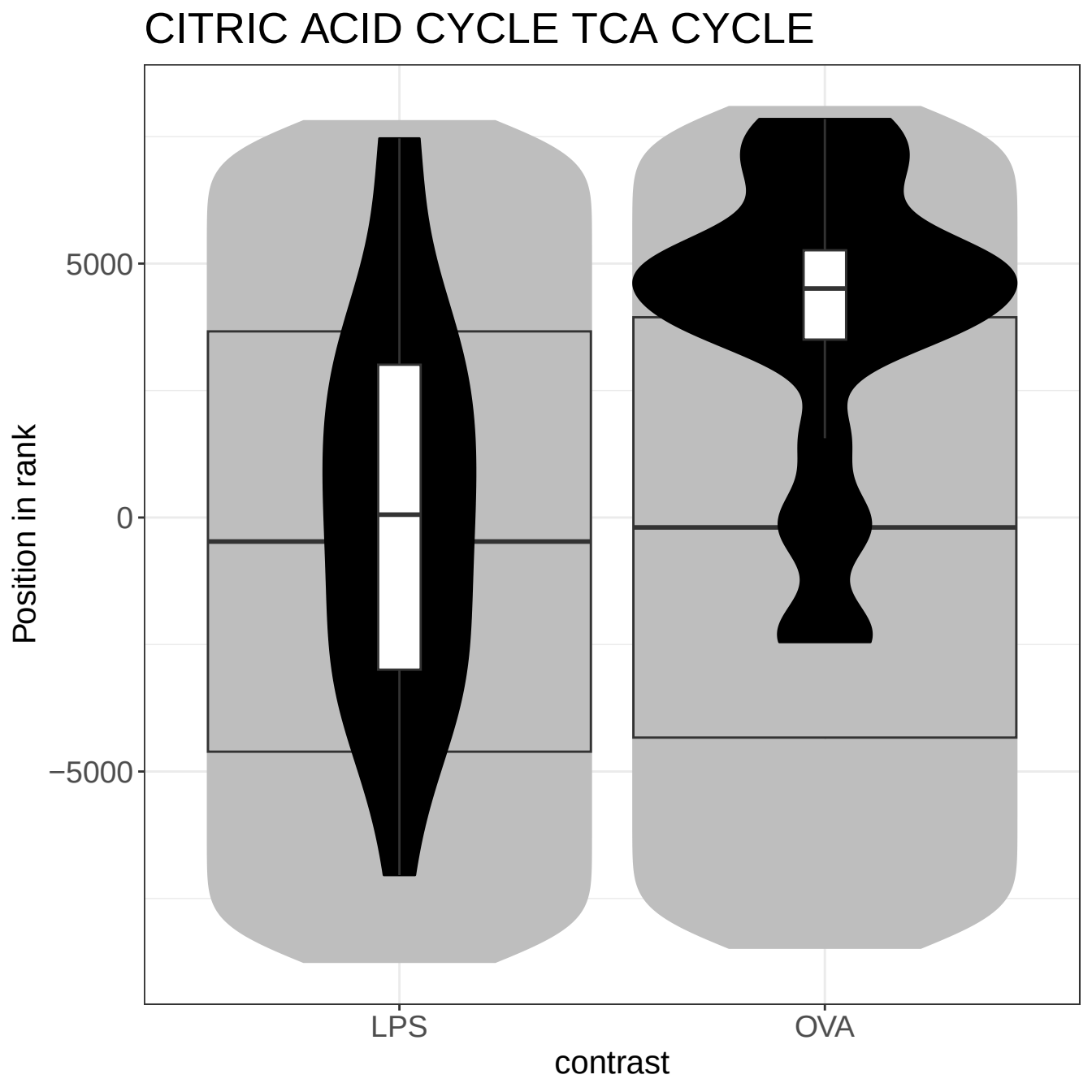

RHOBTB3 ATPASE CYCLE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
7e−09
6e−09
5e−09
4e−09
3e−09
2e−09
1e−09
0e+00

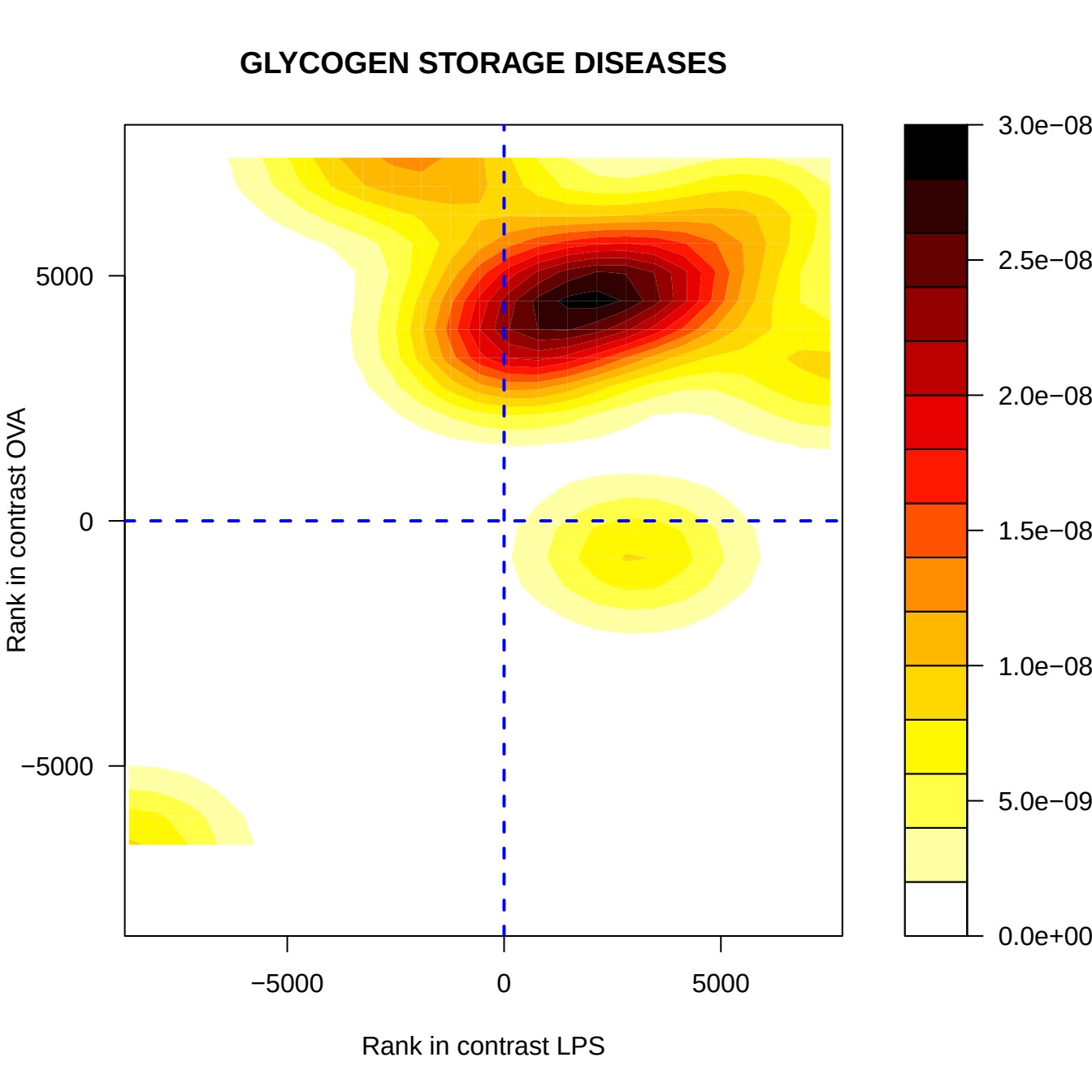

RHOBTB3 ATPASE CYCLE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

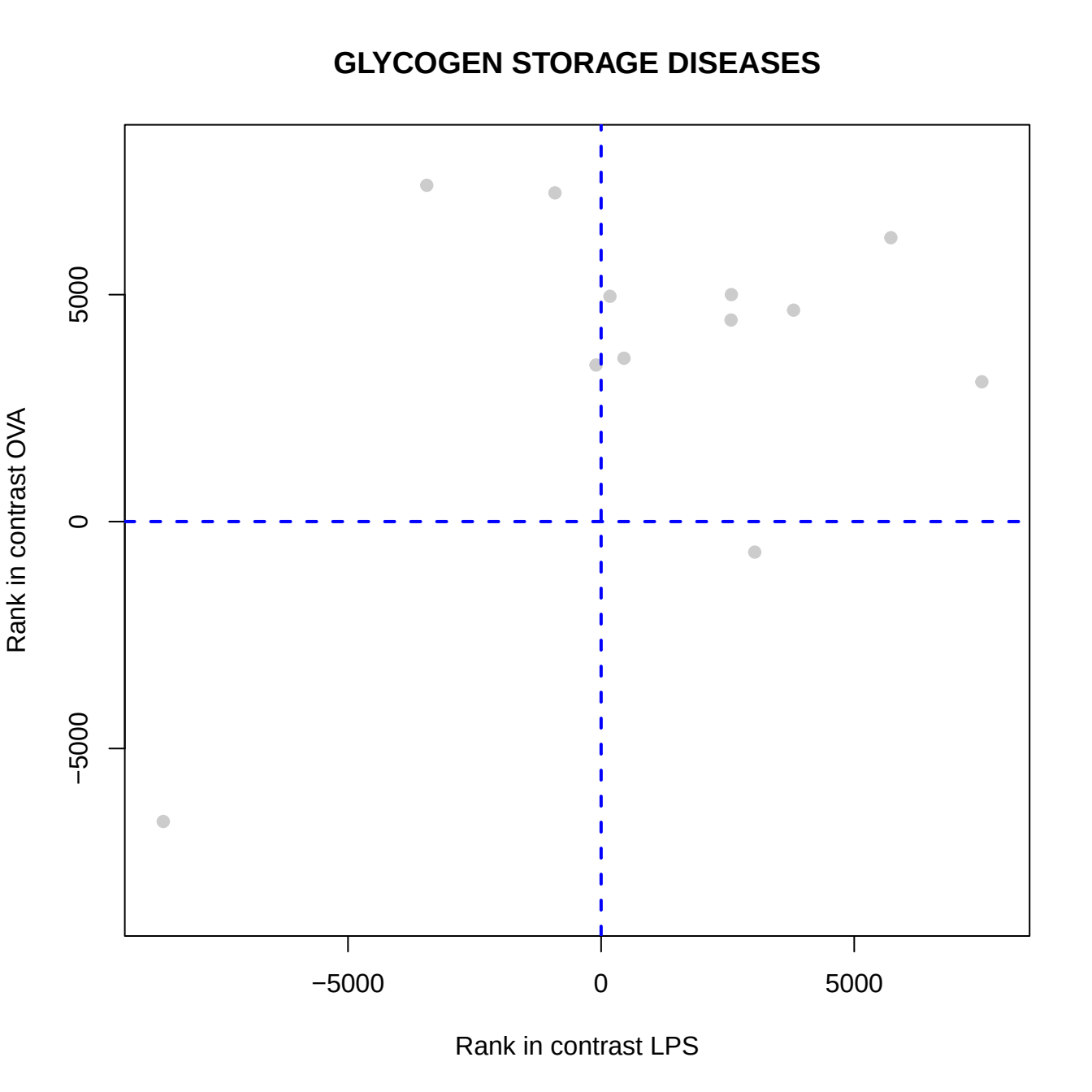

RHOBTB3 ATPASE CYCLE
5000
0
−5000
Position in rank
LPS
OVA
contrast

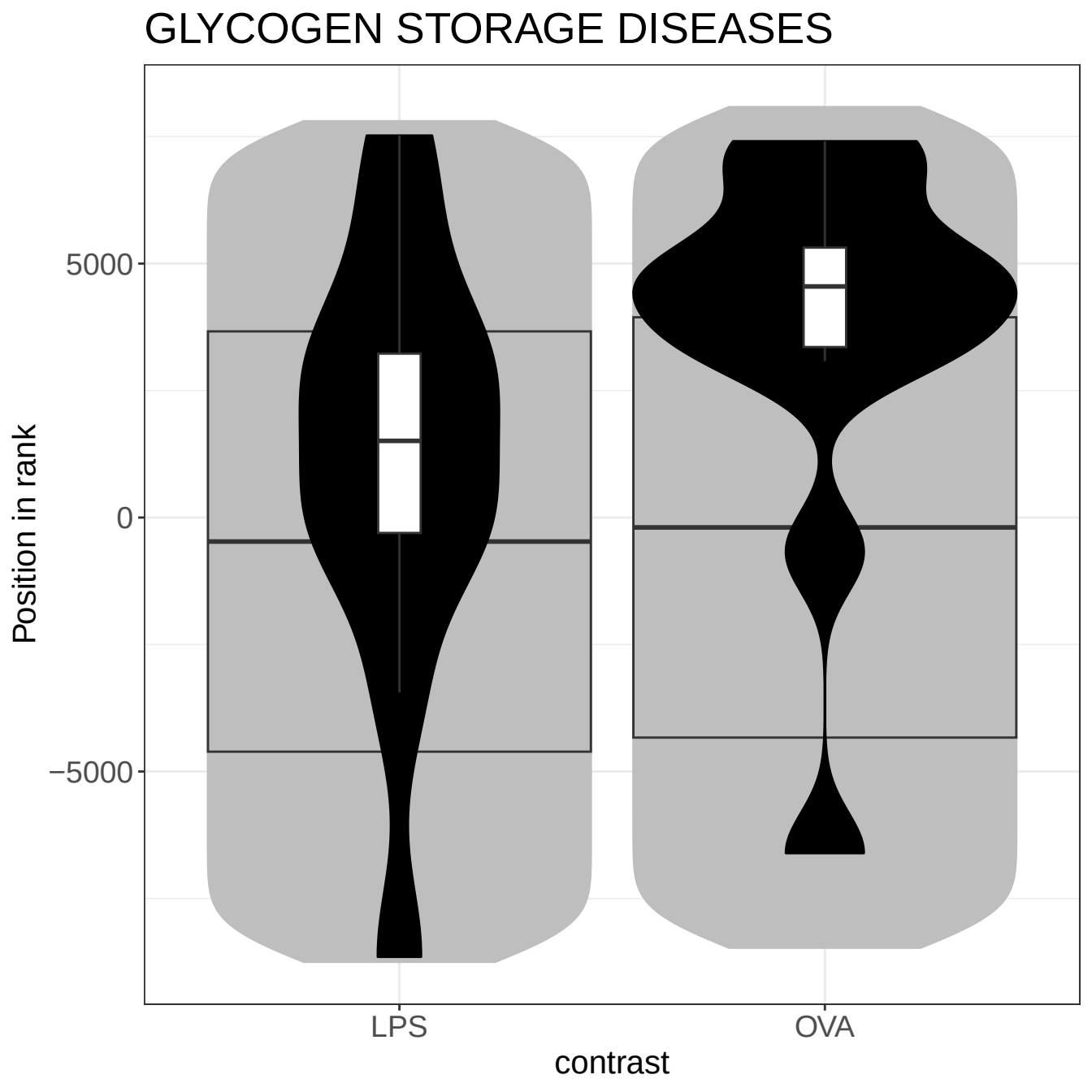

CITRIC ACID CYCLE TCA CYCLE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

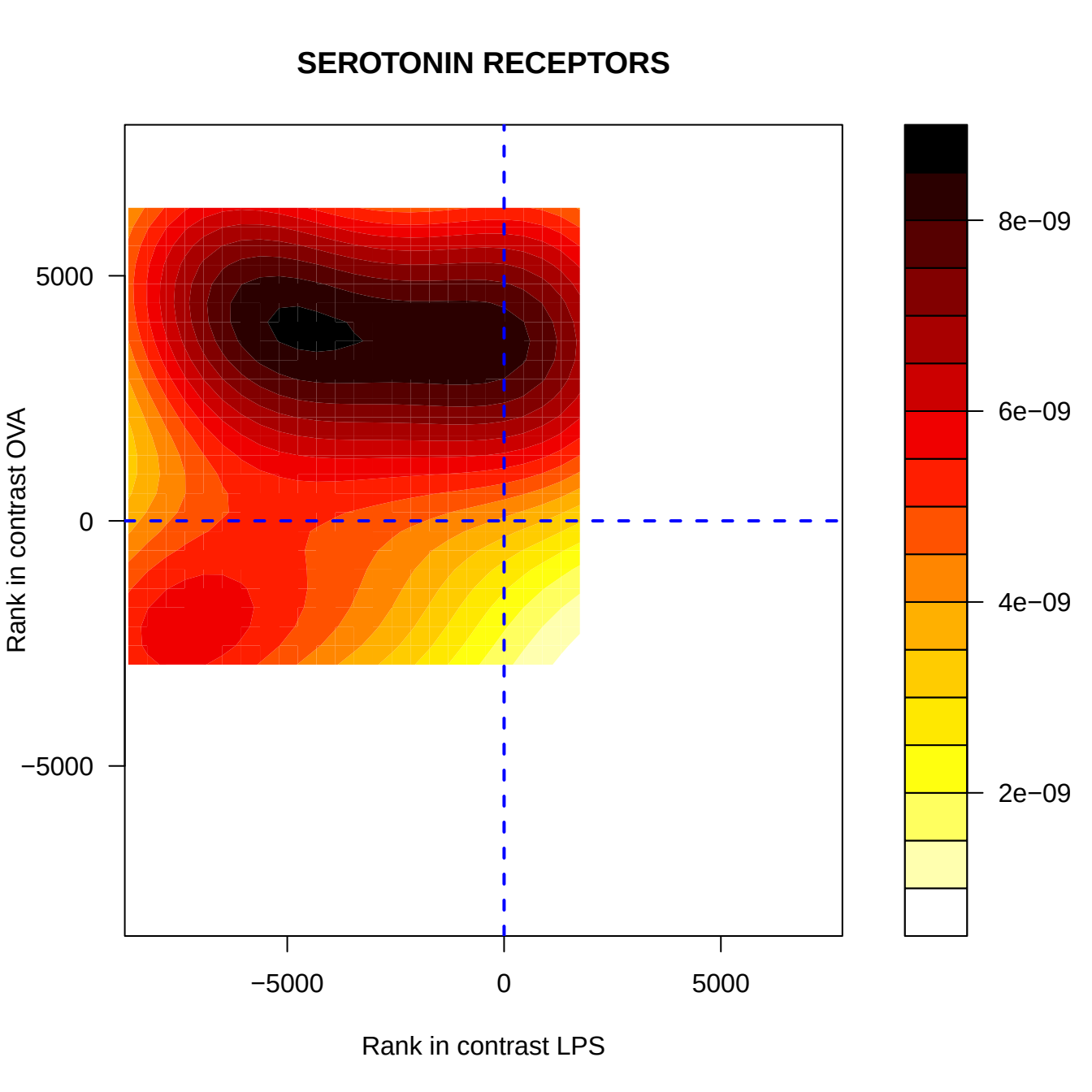

CITRIC ACID CYCLE TCA CYCLE
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

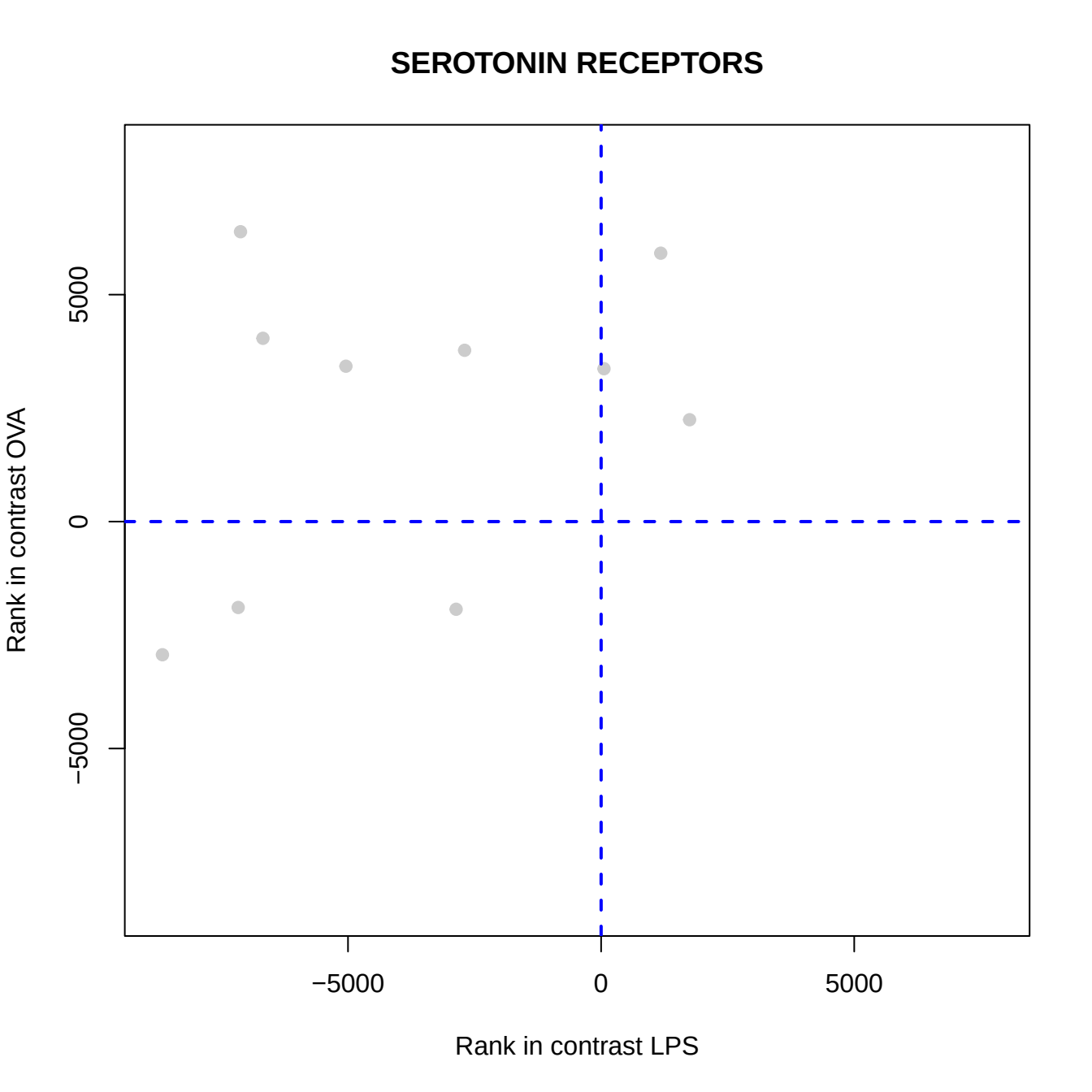

CITRIC ACID CYCLE TCA CYCLE
5000
0
−5000
Position in rank
LPS
OVA
contrast

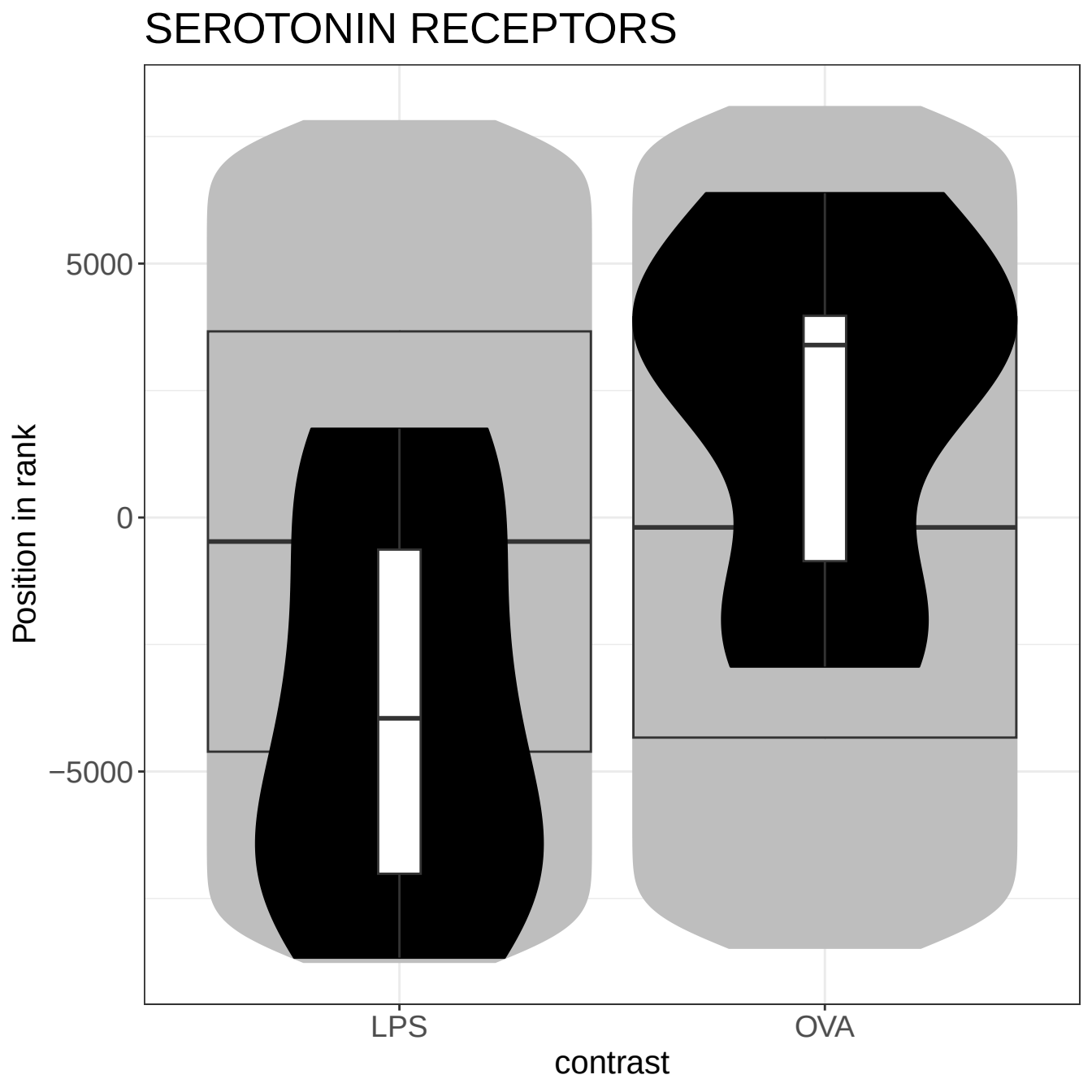

GLYCOGEN STORAGE DISEASES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
3.0e−08
2.5e−08
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

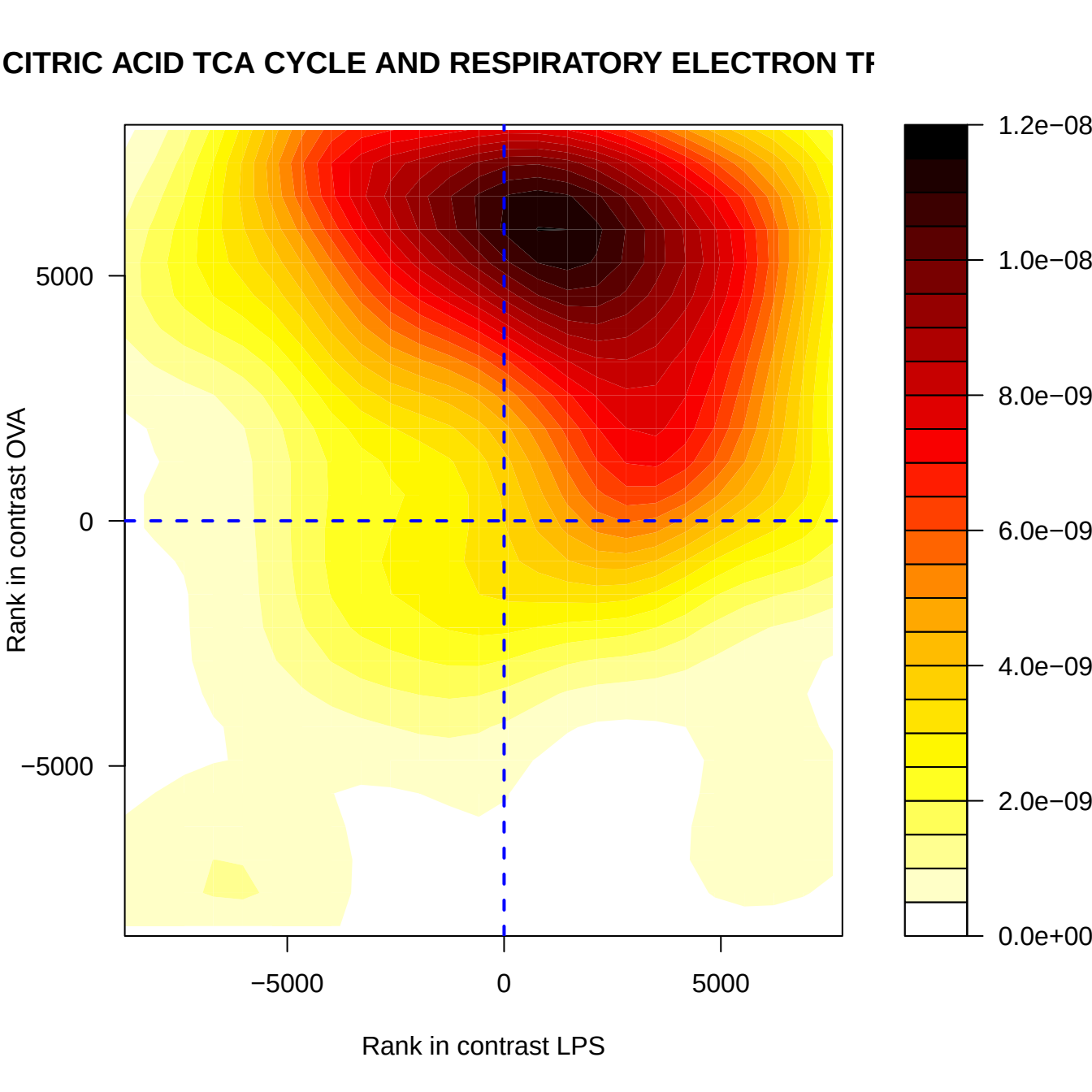

GLYCOGEN STORAGE DISEASES
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

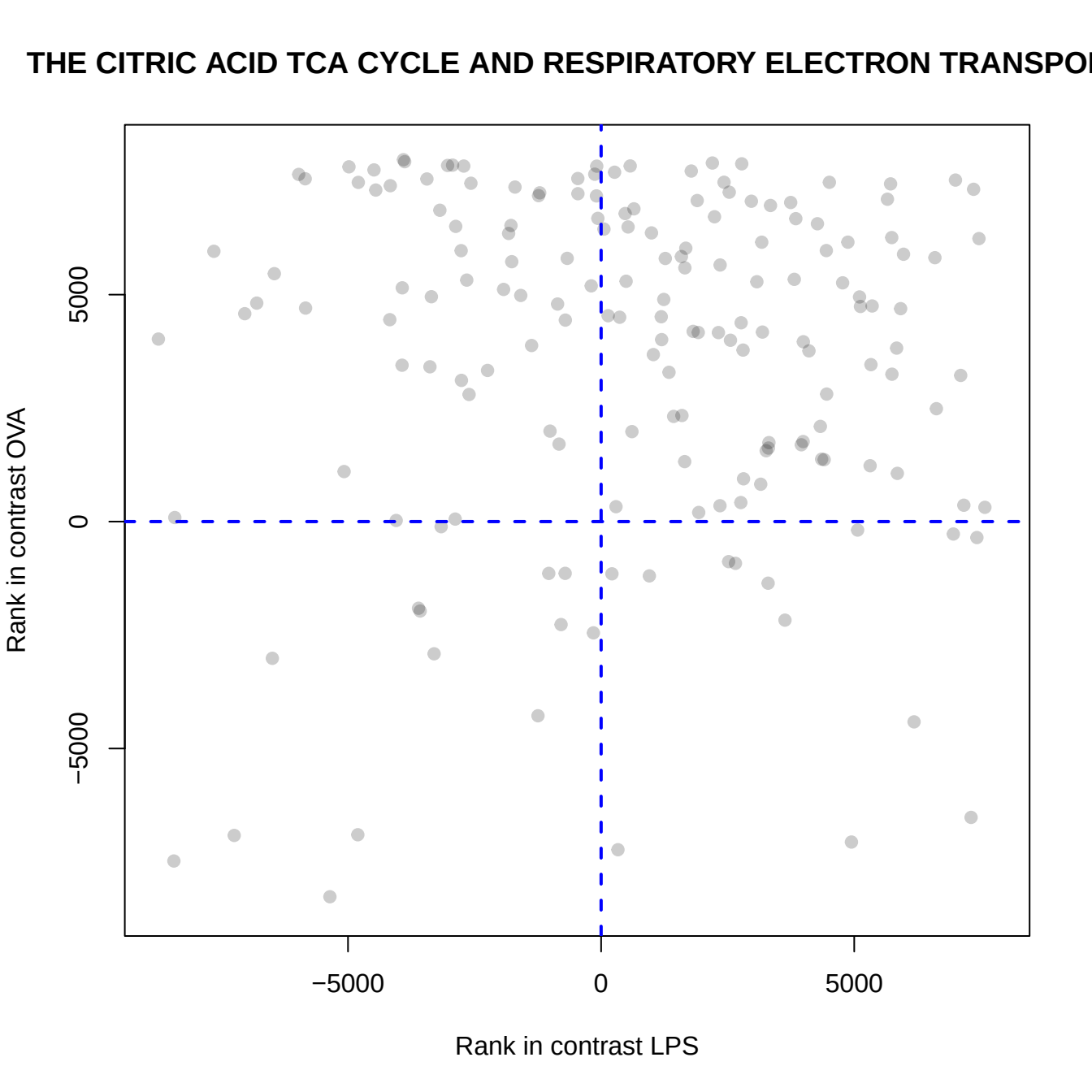

GLYCOGEN STORAGE DISEASES
Position in rank
5000
0
−5000
LPS
OVA
contrast

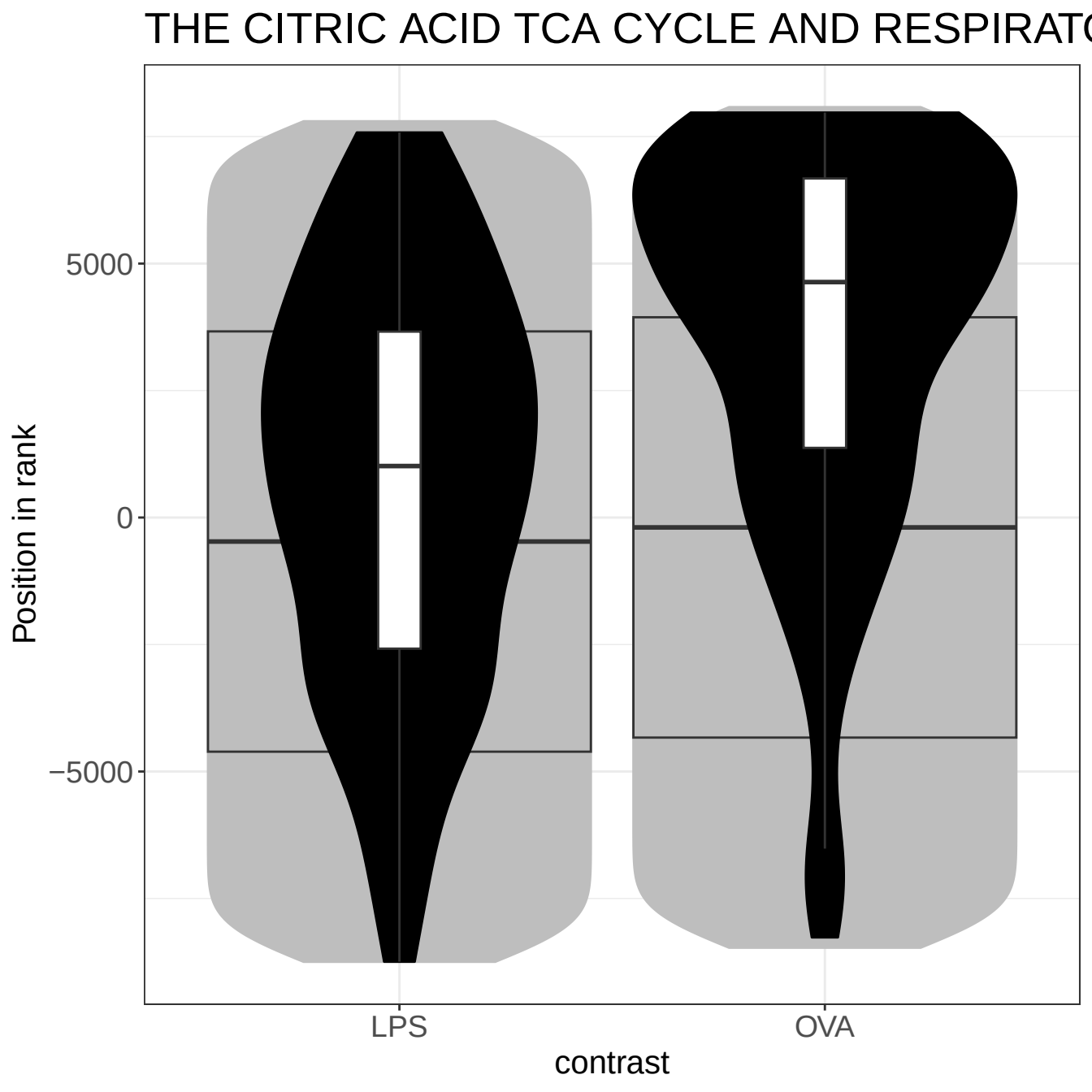

SEROTONIN RECEPTORS
5000
0
−5000
Rank in contrast OVA
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09

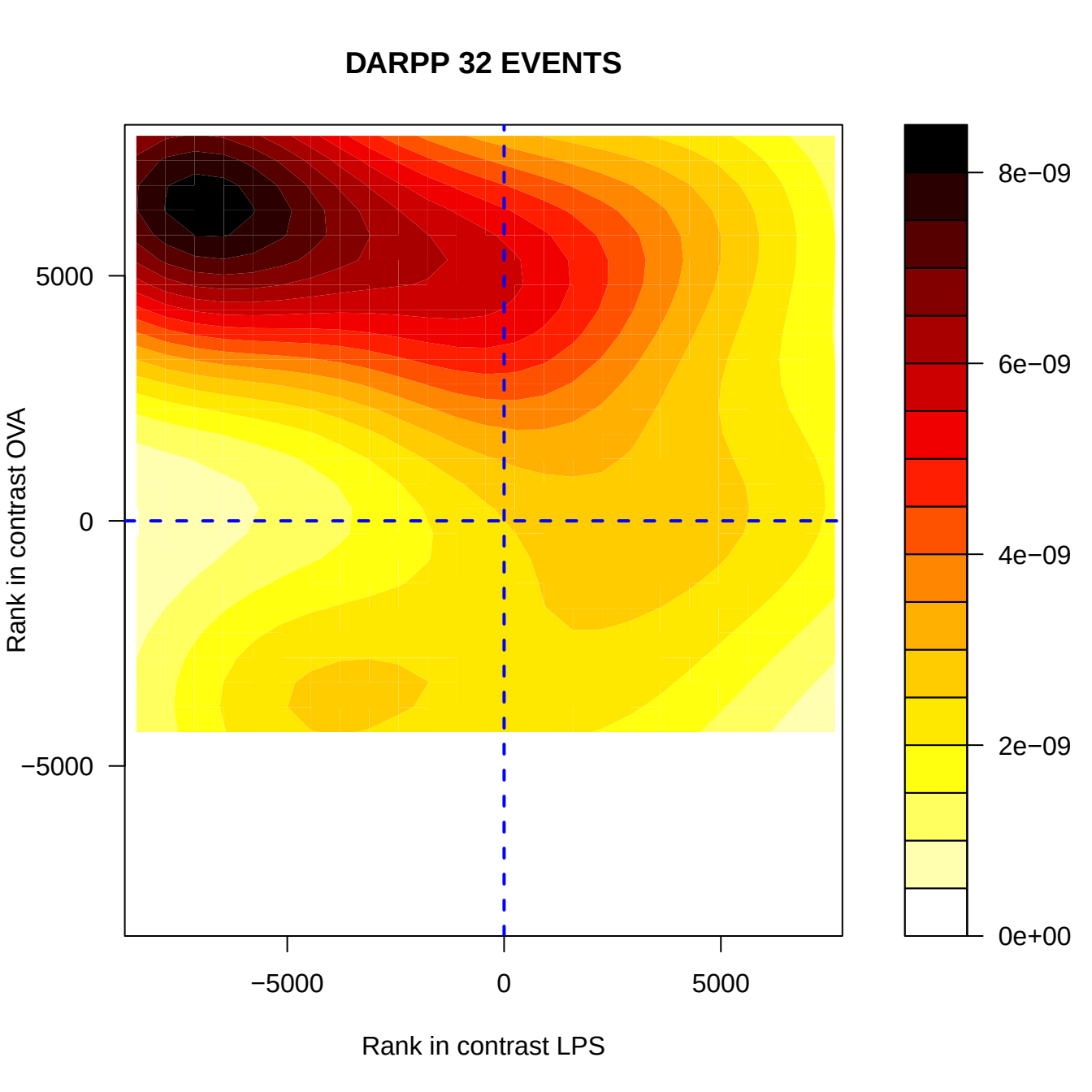

SEROTONIN RECEPTORS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

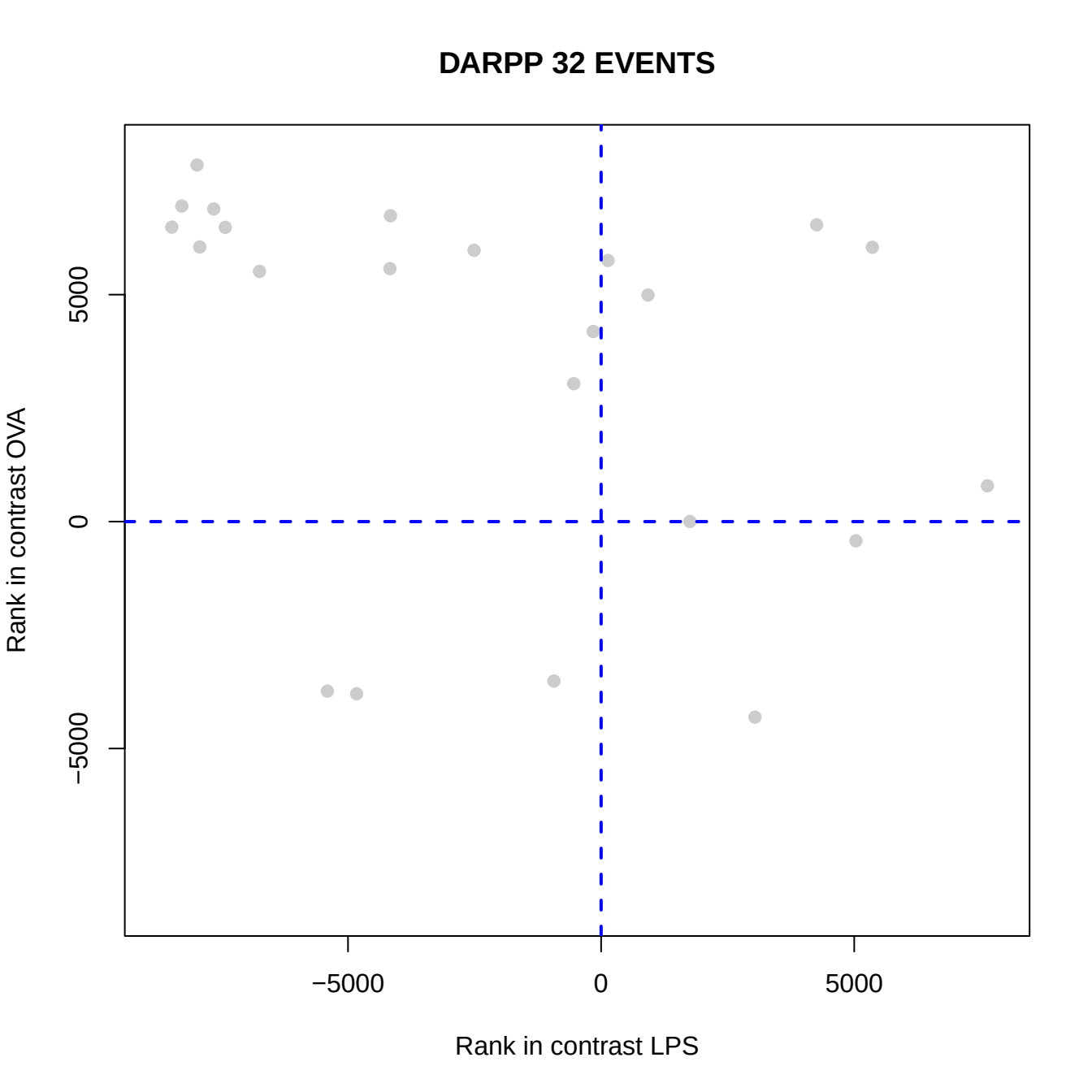

SEROTONIN RECEPTORS
5000
0
−5000
Position in rank
LPS
OVA
contrast

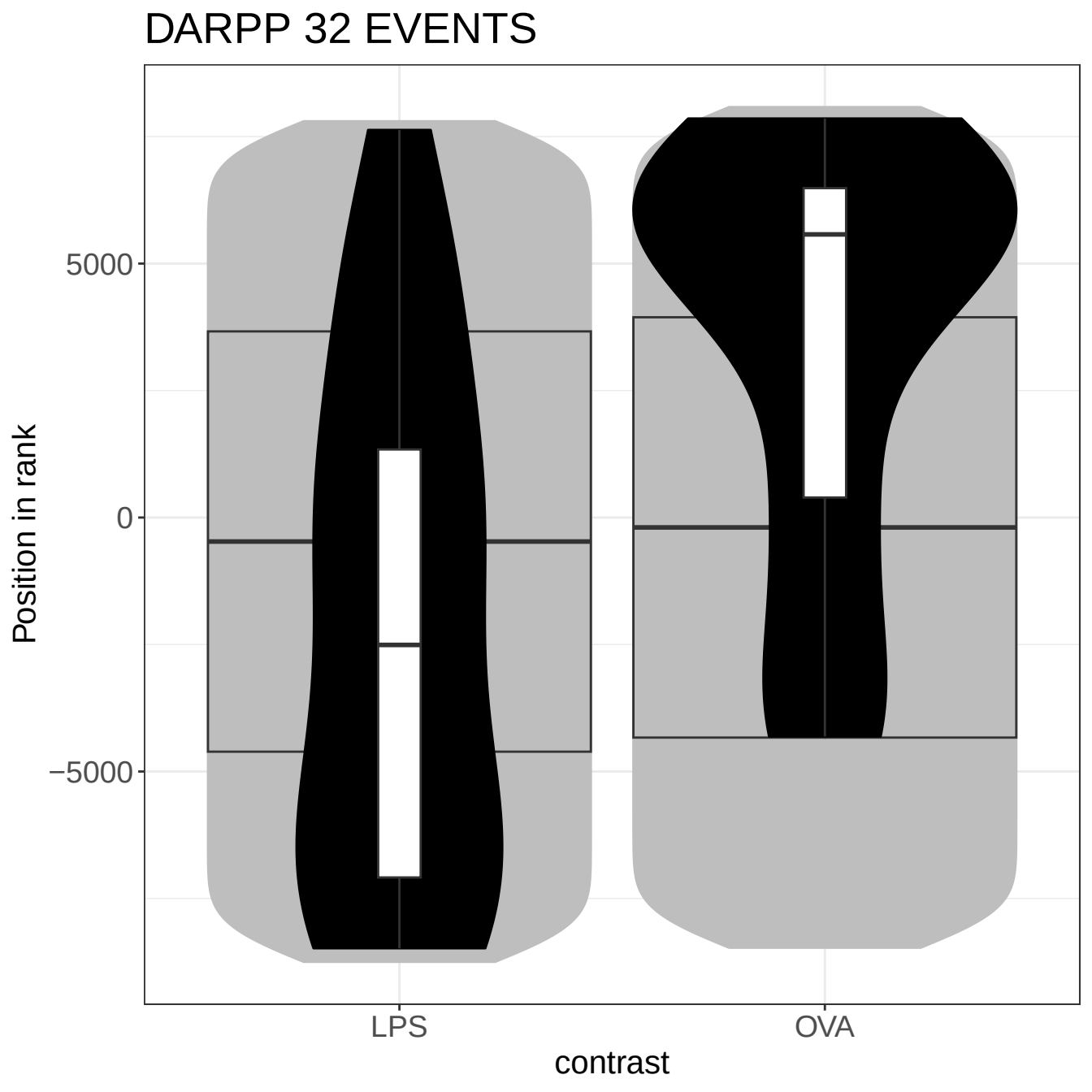

CITRIC ACID TCA CYCLE AND RESPIRATORY ELECTRON TR
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

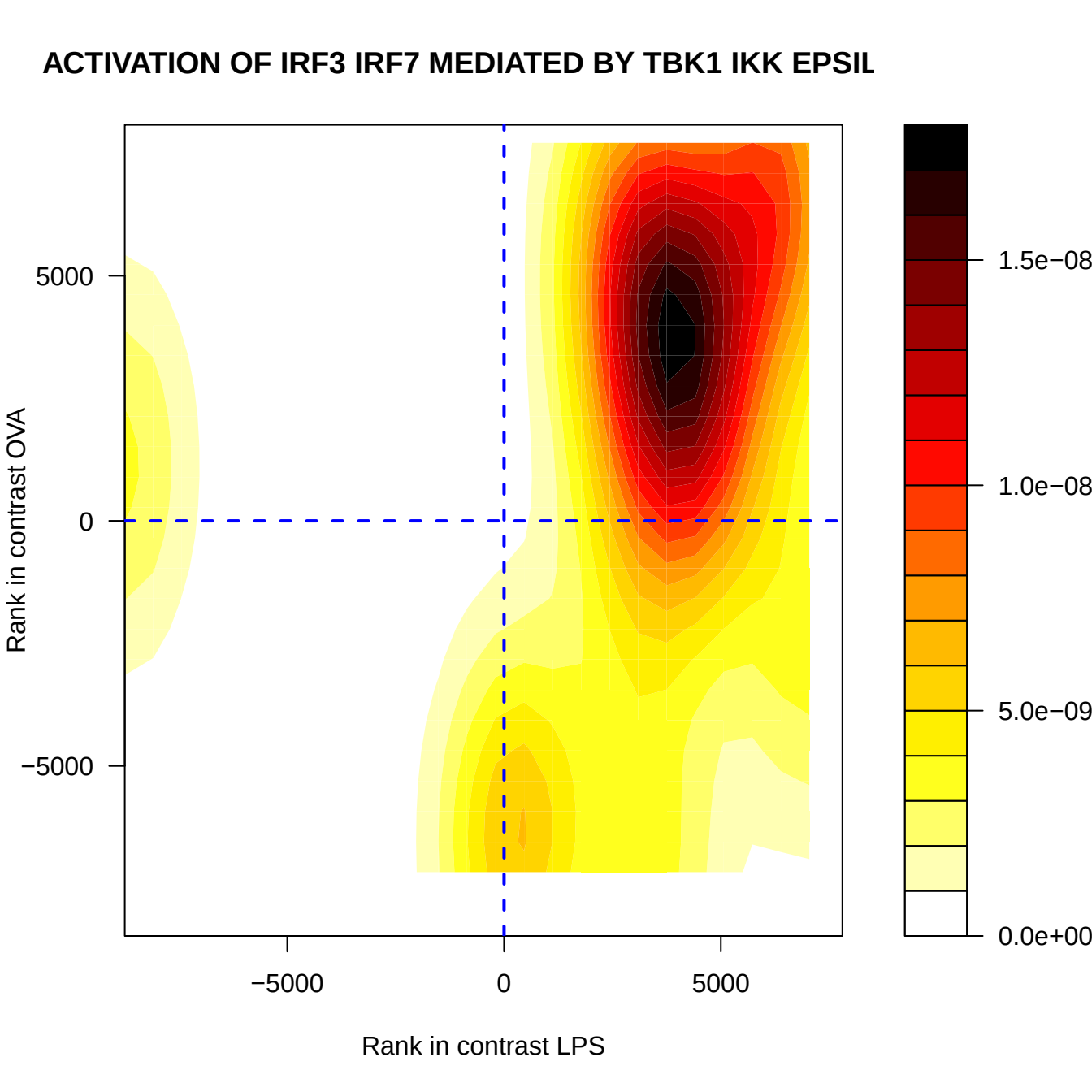

THE CITRIC ACID TCA CYCLE AND RESPIRATORY ELECTRON TRANSPO
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS

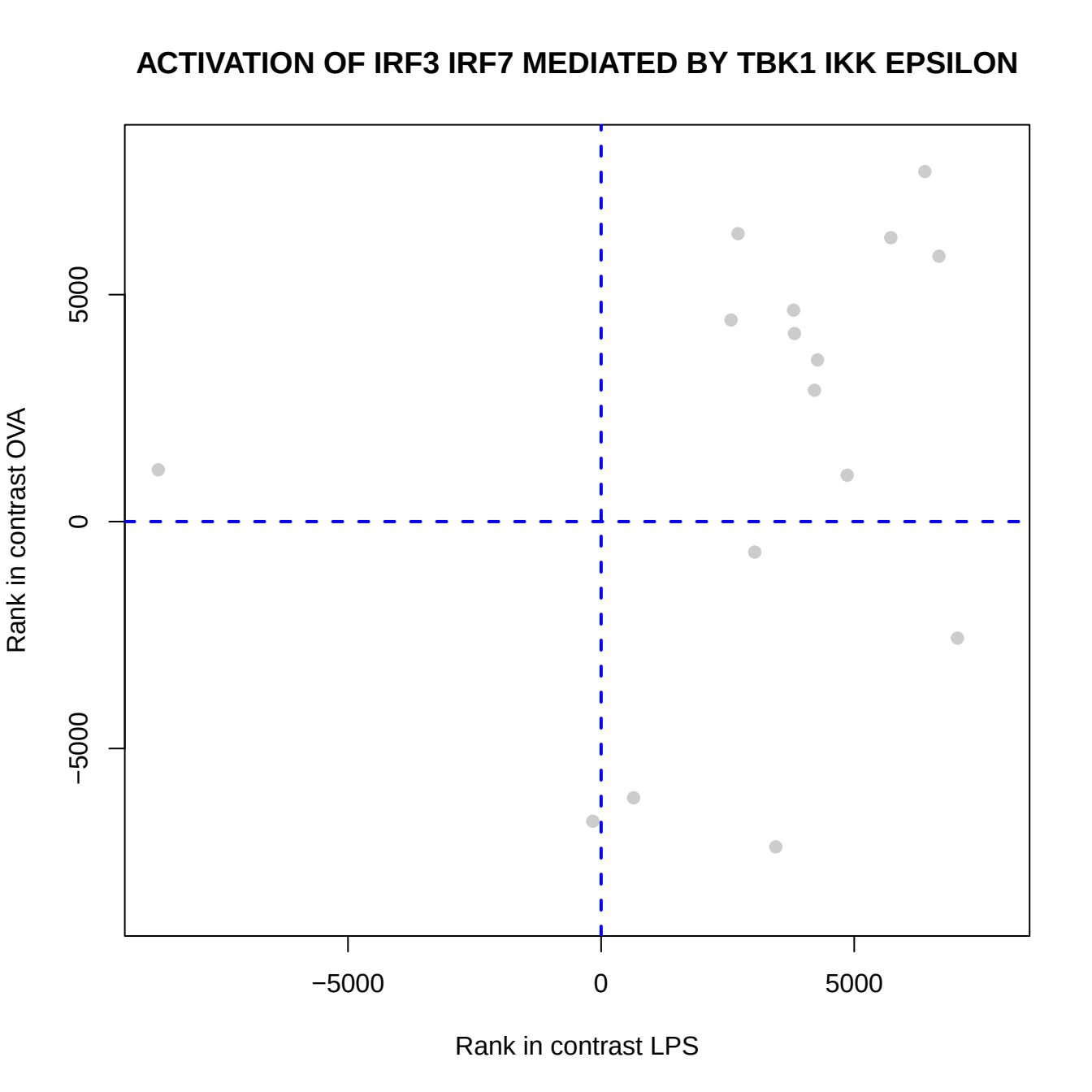

THE CITRIC ACID TCA CYCLE AND RESPIRAT
5000
0
−5000
Position in rank
LPS
OVA
contrast

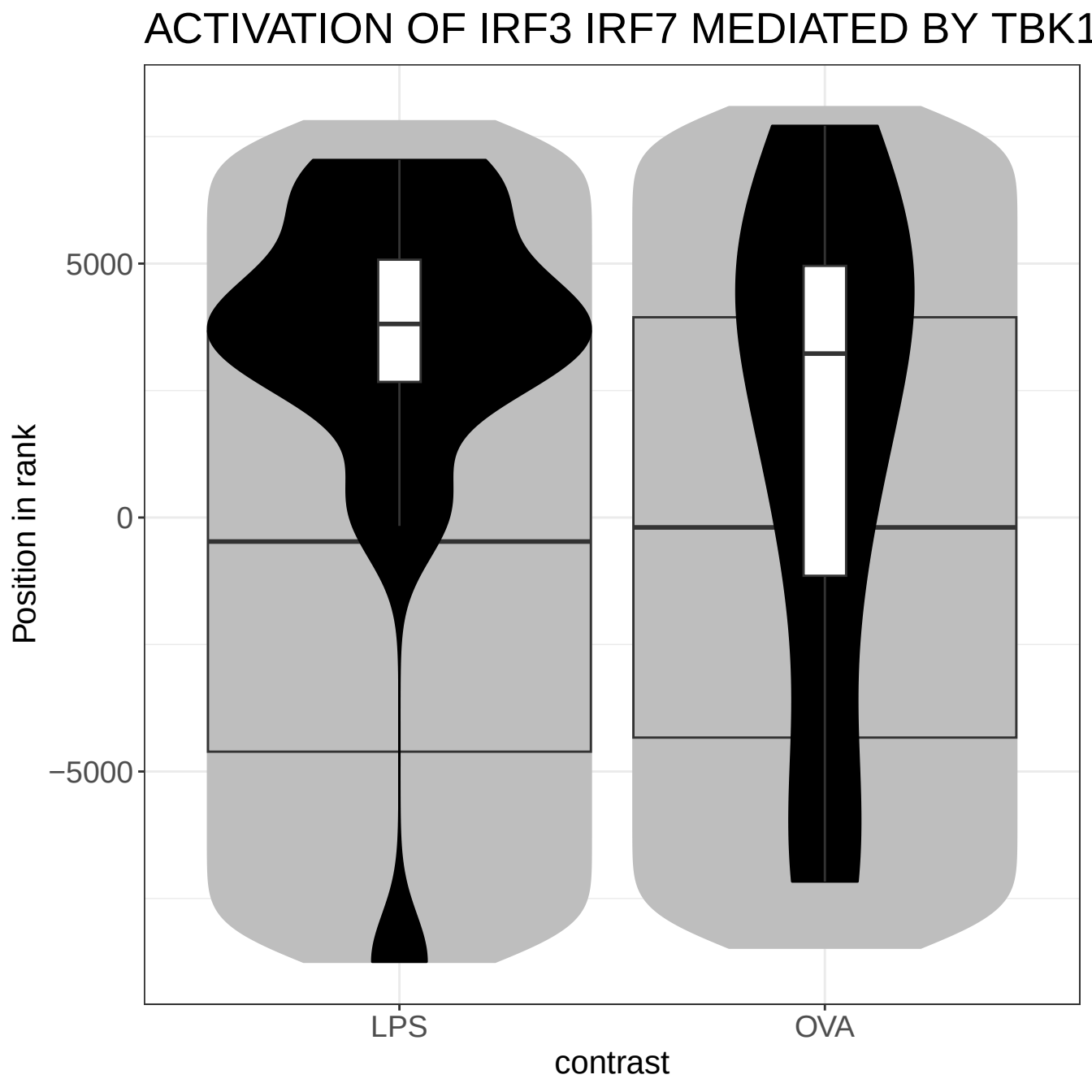

DARPP 32 EVENTS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS
8e−09
6e−09
4e−09
2e−09
0e+00


DARPP 32 EVENTS
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS


DARPP 32 EVENTS
5000
0
−5000
Position in rank
LPS
OVA
contrast


ACTIVATION OF IRF3 IRF7 MEDIATED BY TBK1 IKK EPSIL
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


ACTIVATION OF IRF3 IRF7 MEDIATED BY TBK1 IKK EPSILON
Rank in contrast OVA
5000
0
−5000
−5000
0
5000
Rank in contrast LPS


ACTIVATION OF IRF3 IRF7 MEDIATED BY TBK1
5000
0
−5000
Position in rank
LPS
OVA
contrast