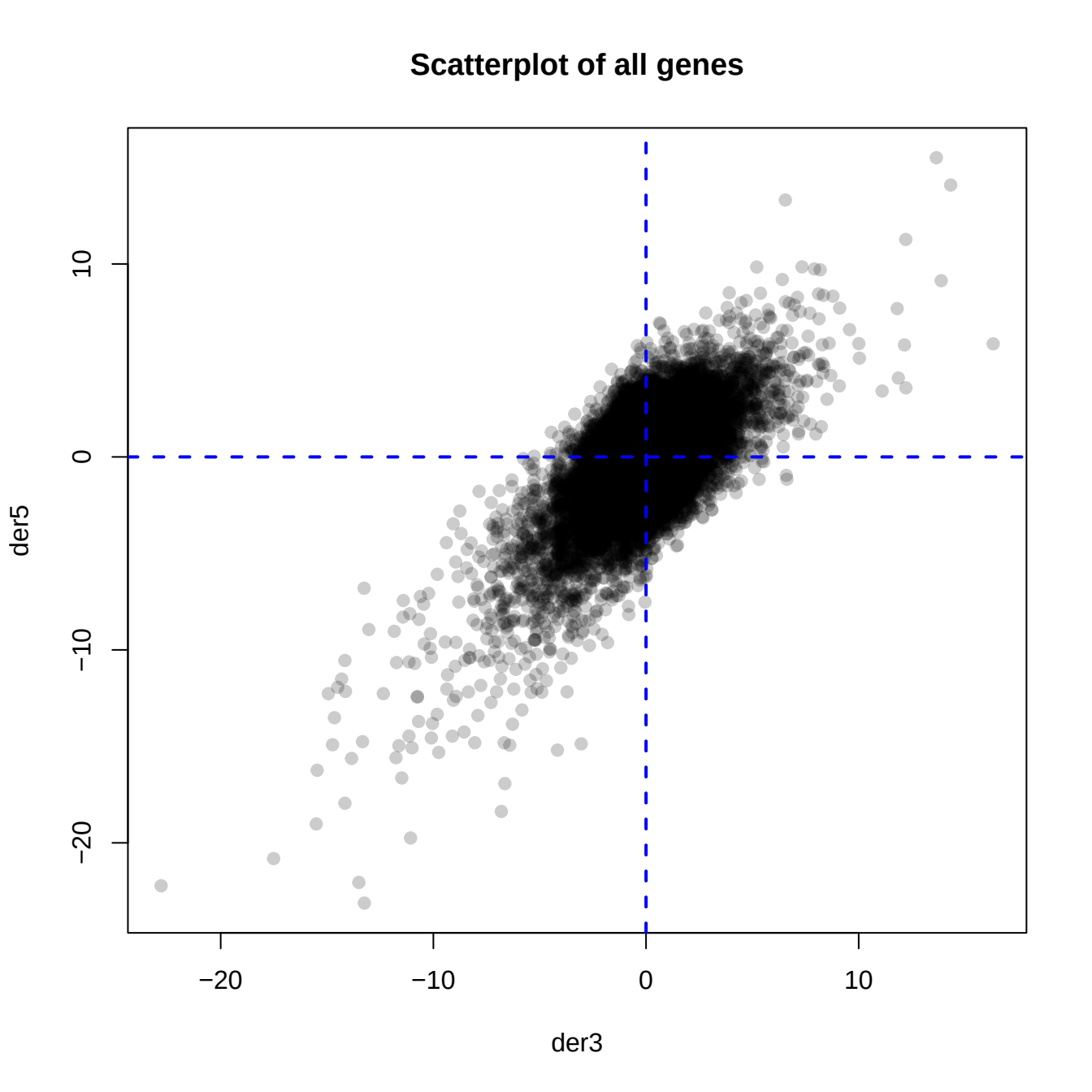
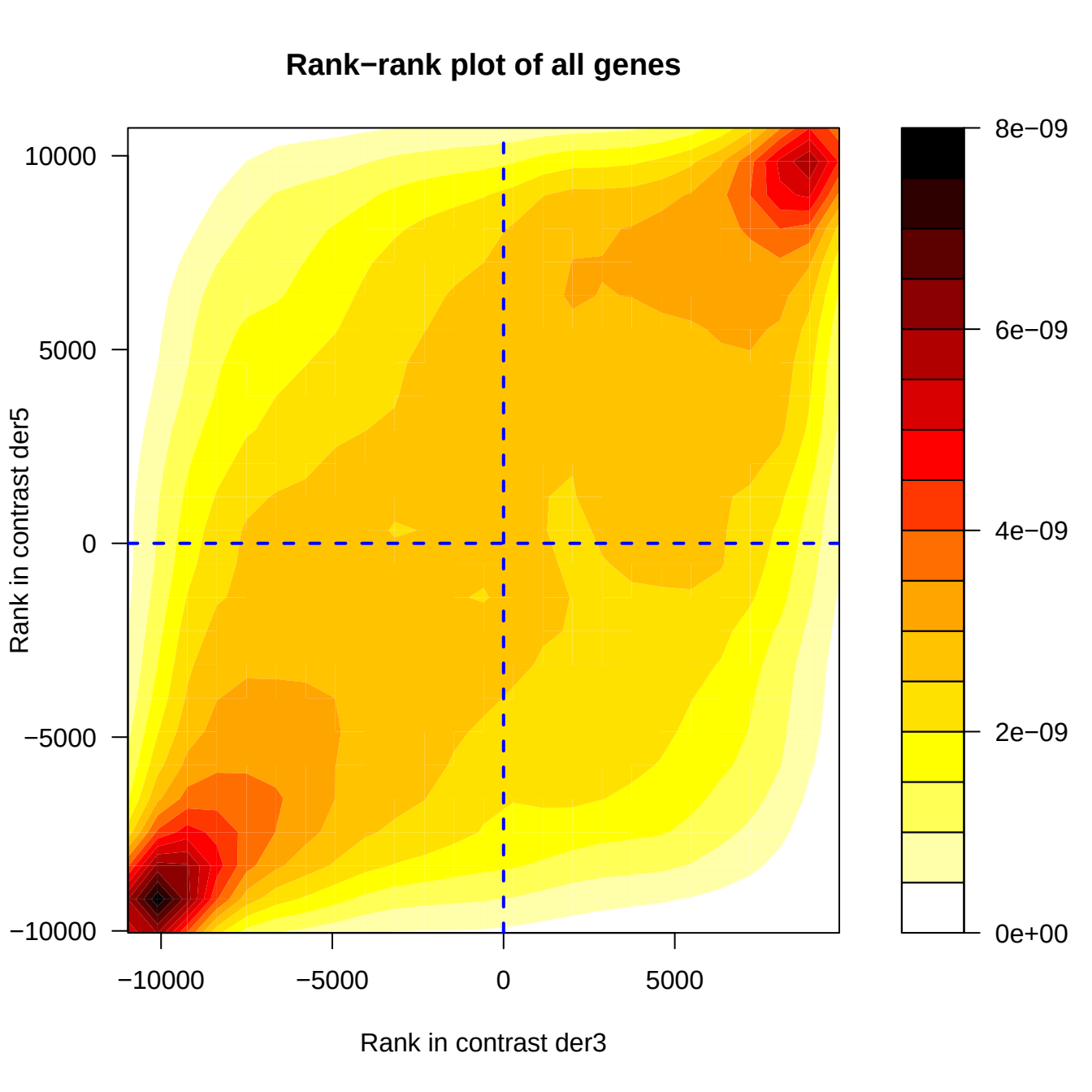
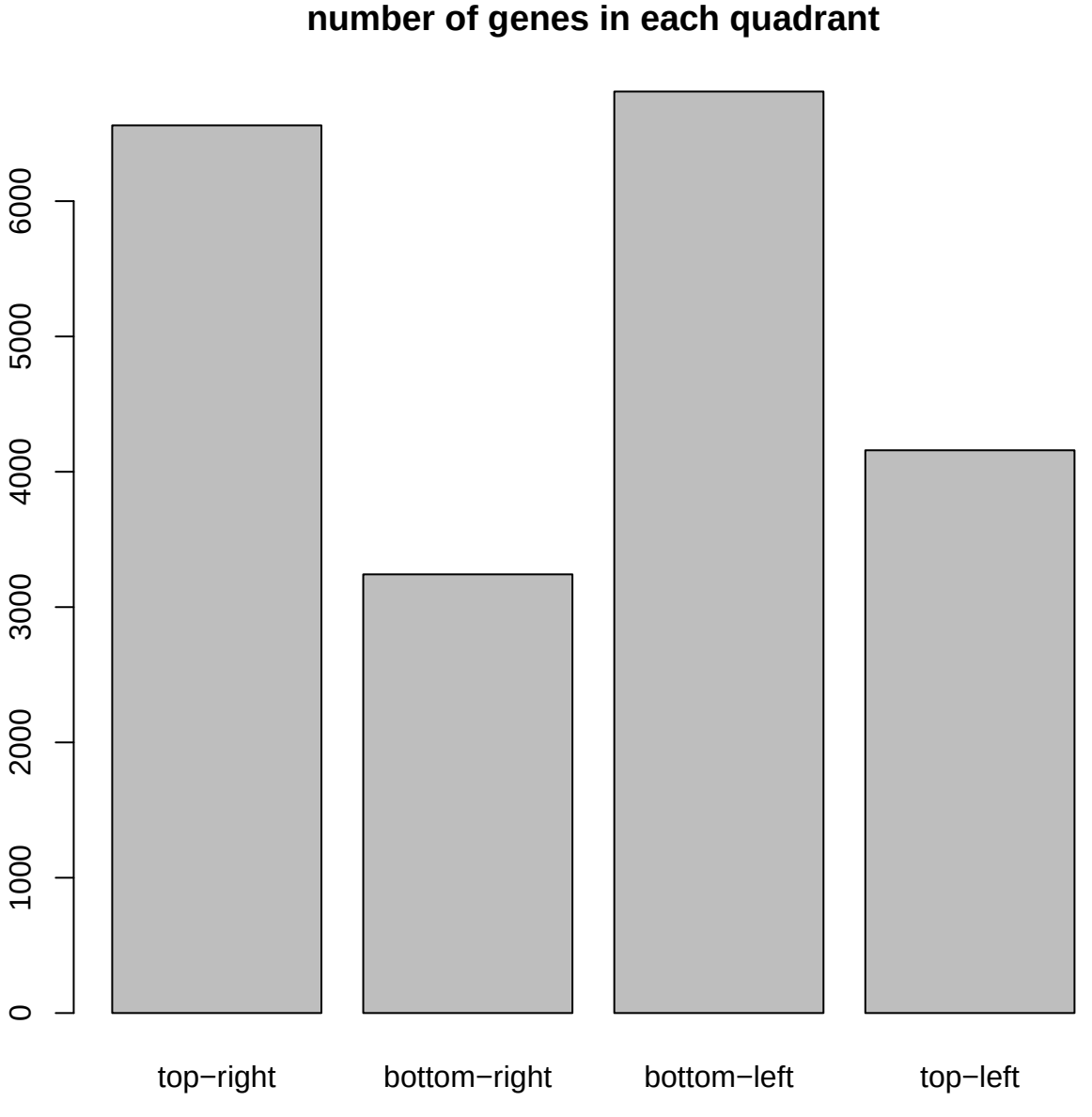
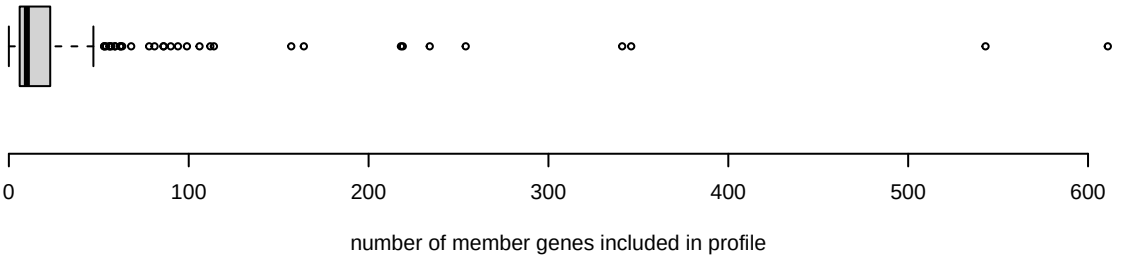

Scatterplot of all genes
der5
der3
10
0
−10
−20
−20
−10
0
10

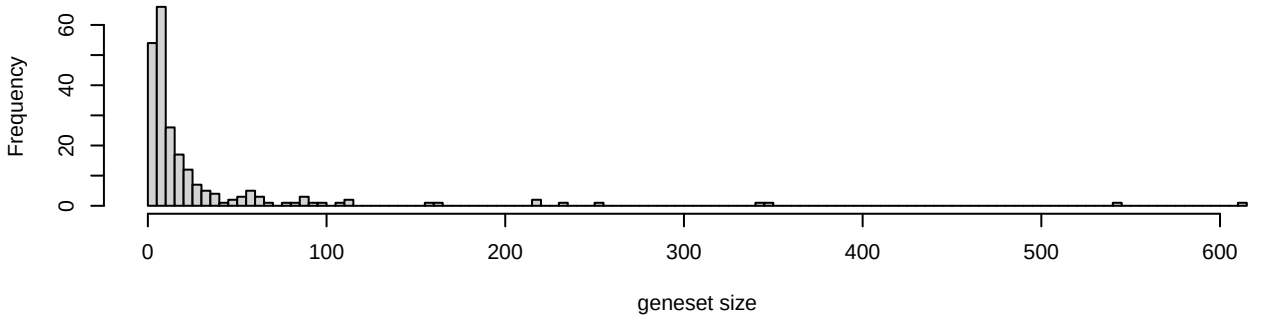

Rank−rank plot of all genes
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
8e−09
6e−09
4e−09
2e−09
0e+00


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

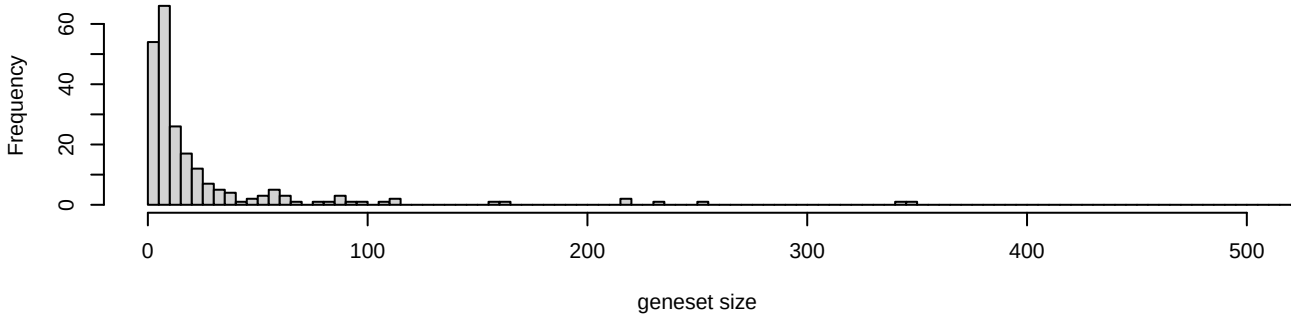
Gene set size

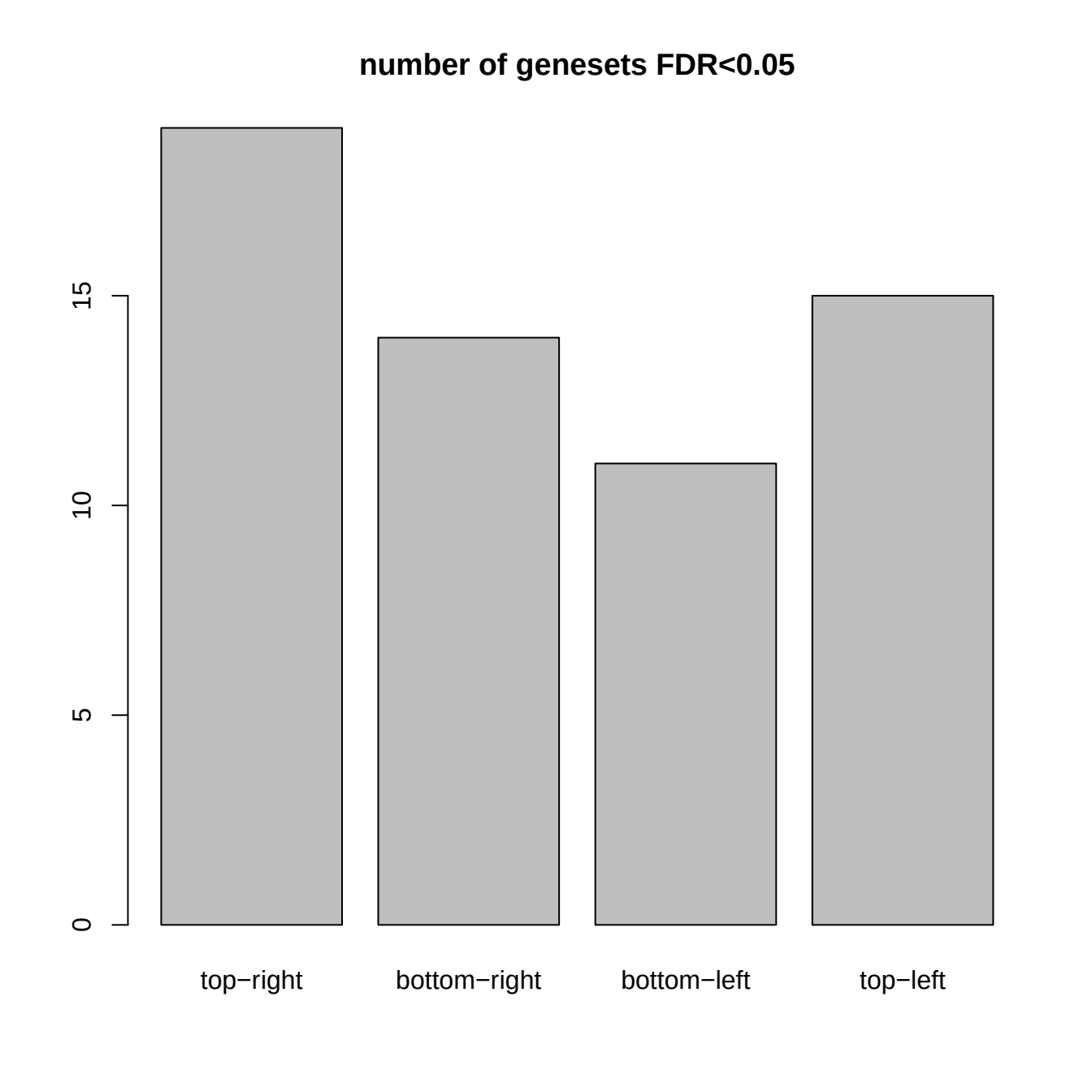


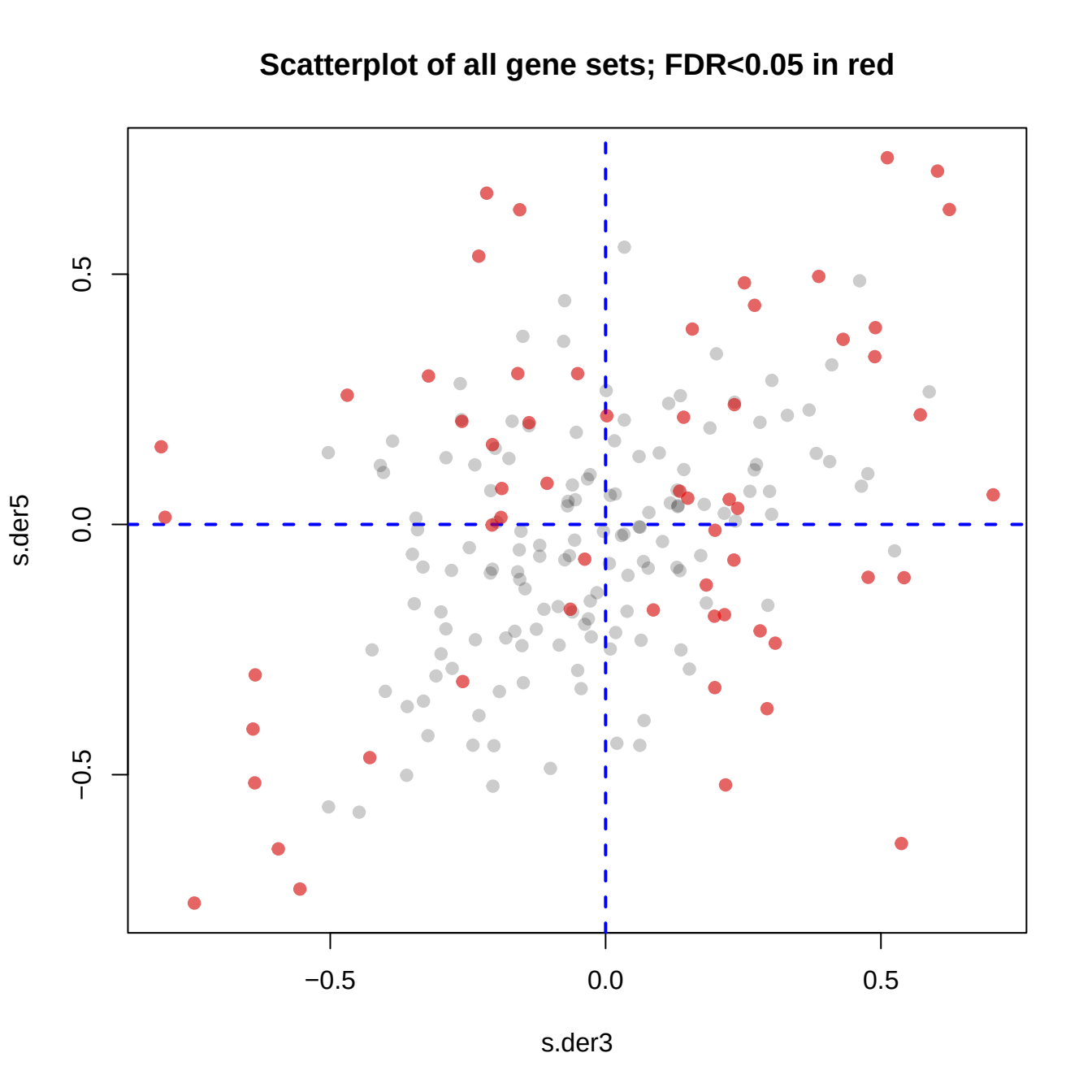
Histogram of geneset size

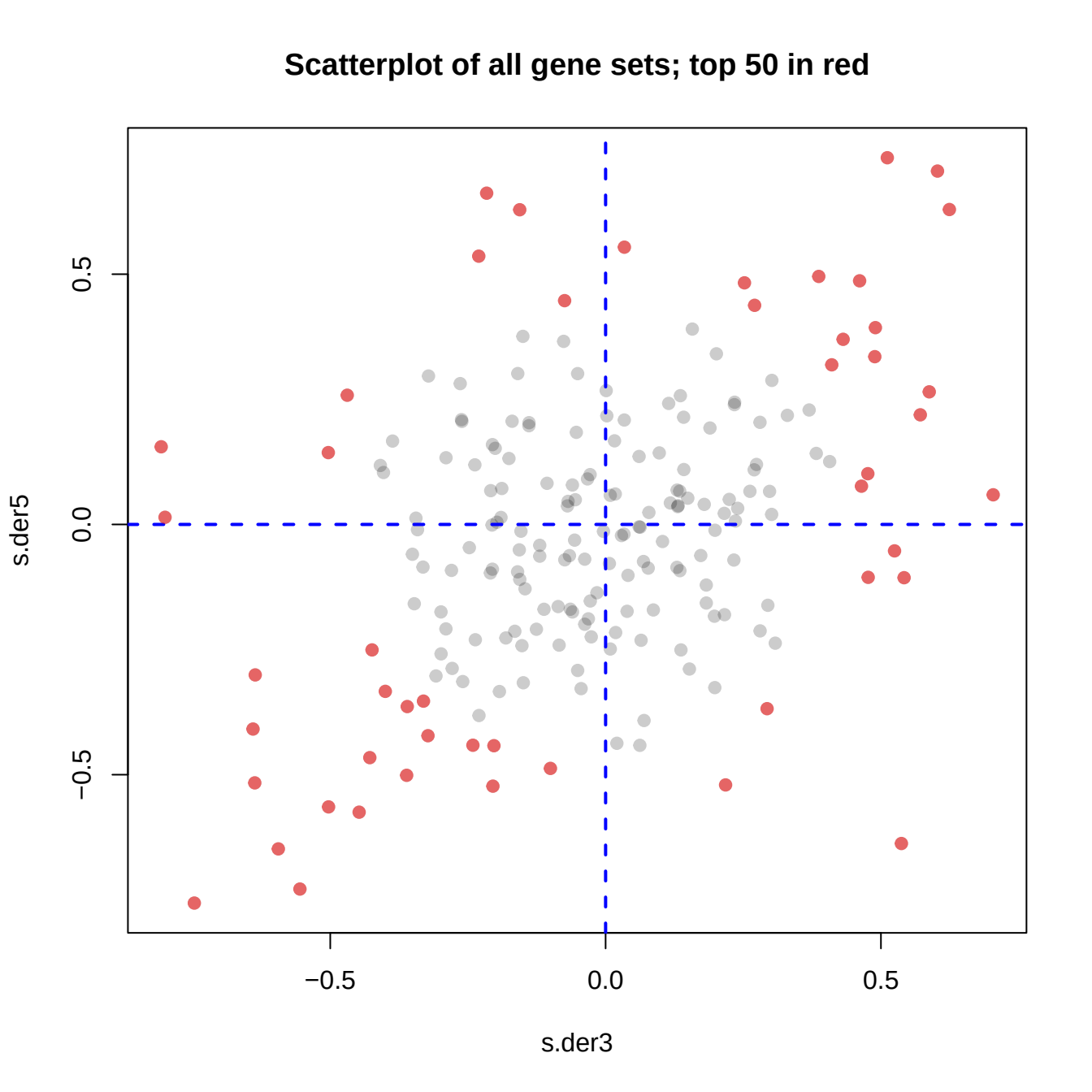


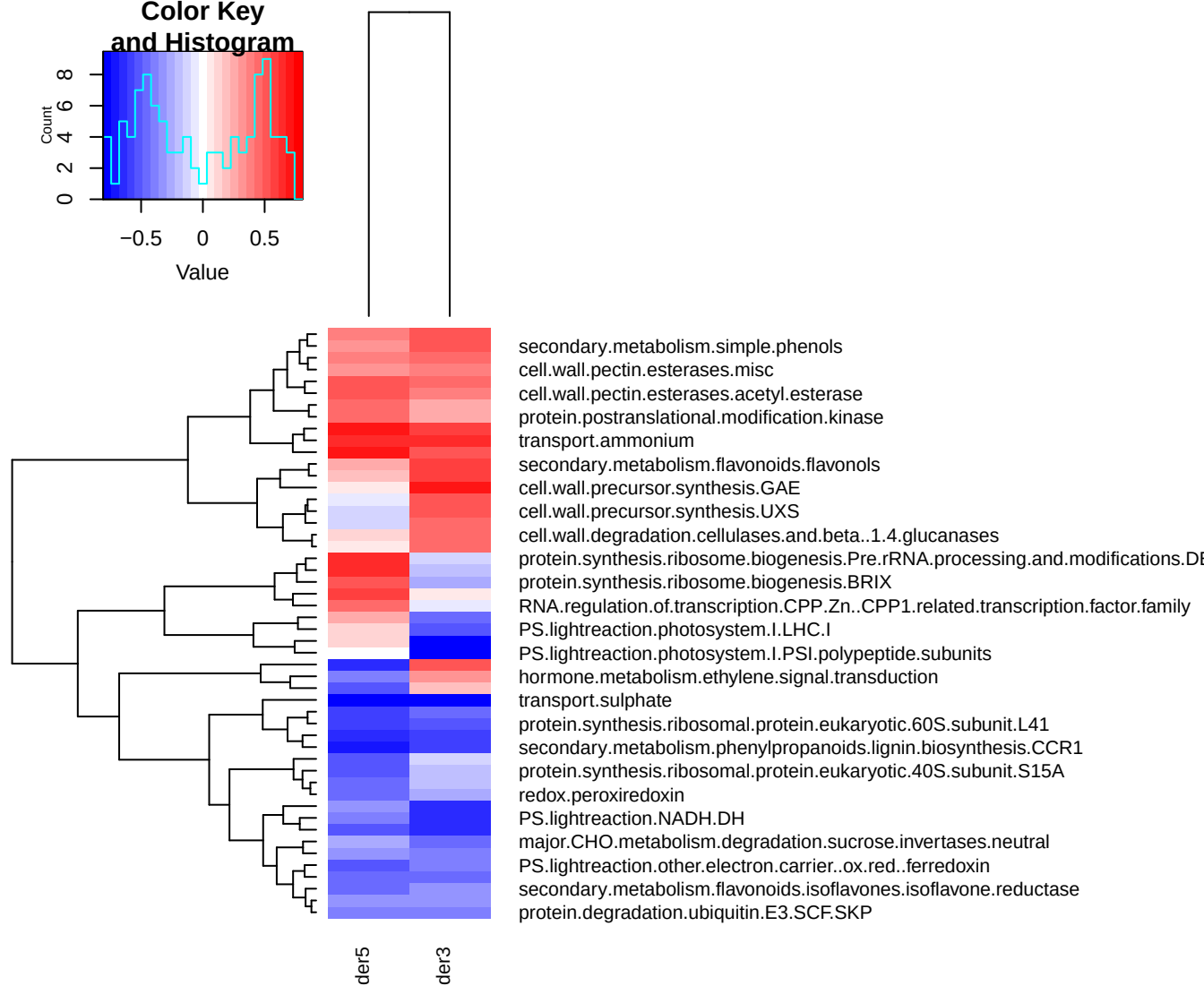
Trimmed histogram of geneset size

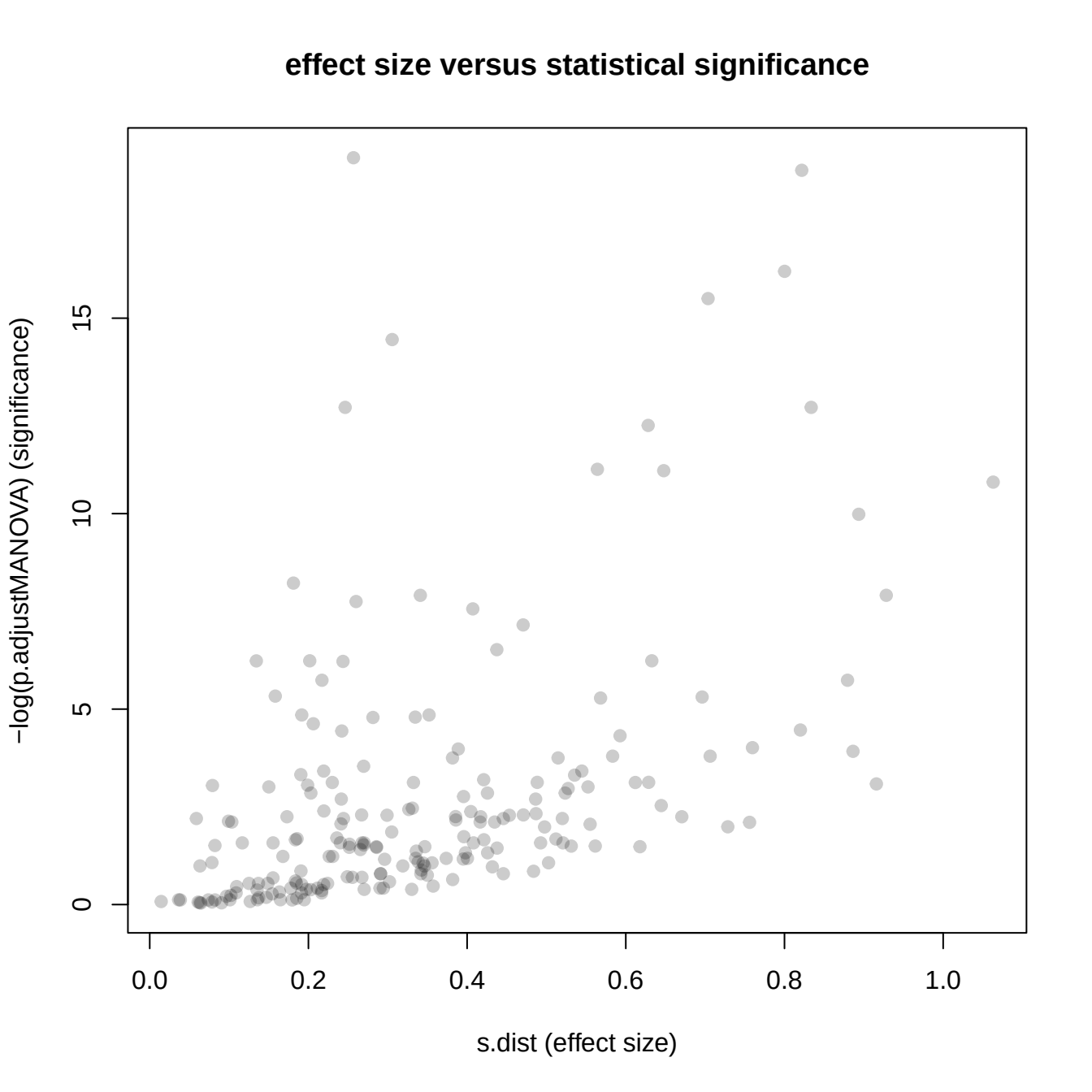


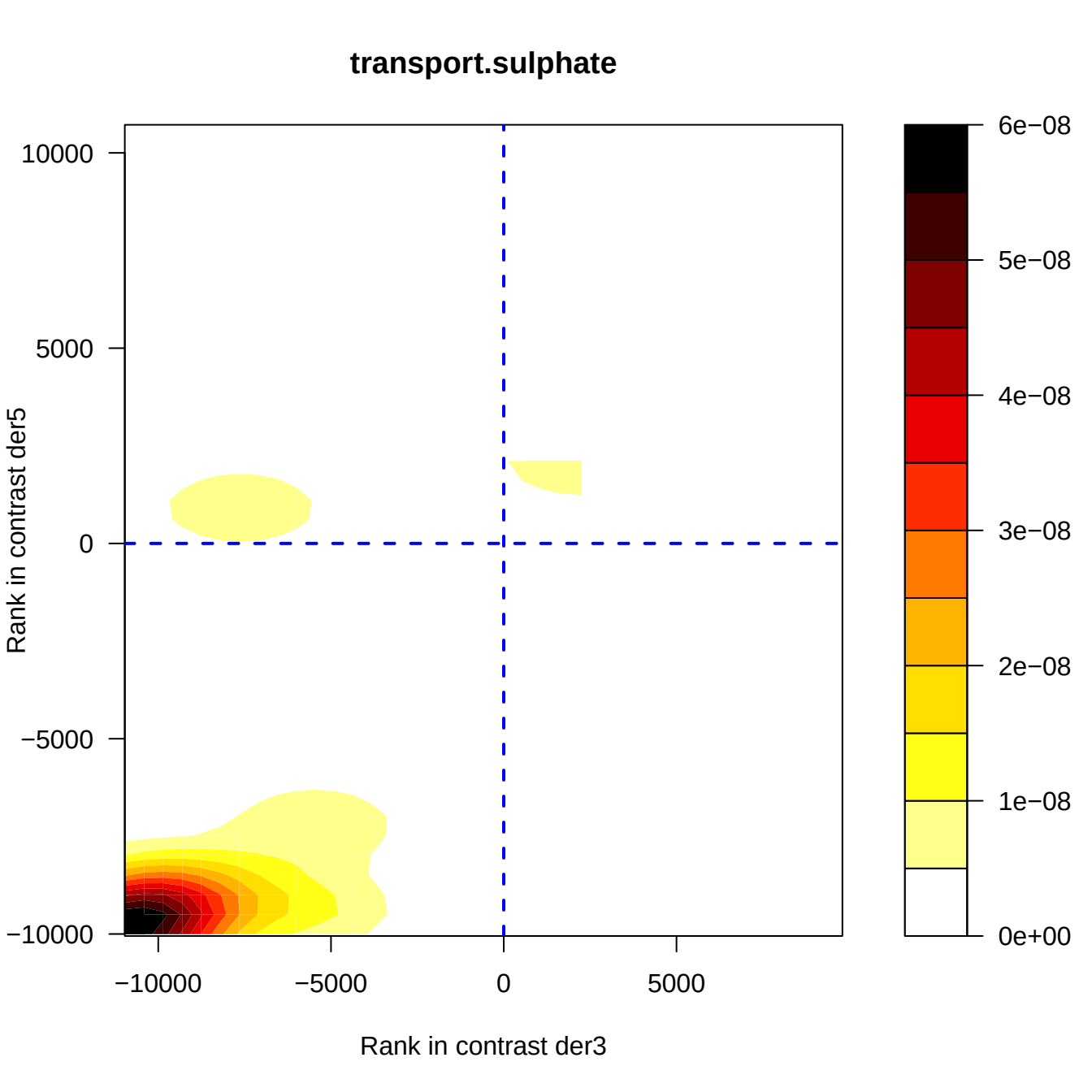

number of genesets FDR<0.05
0
5
10
15
top−right
bottom−right
bottom−left
top−left

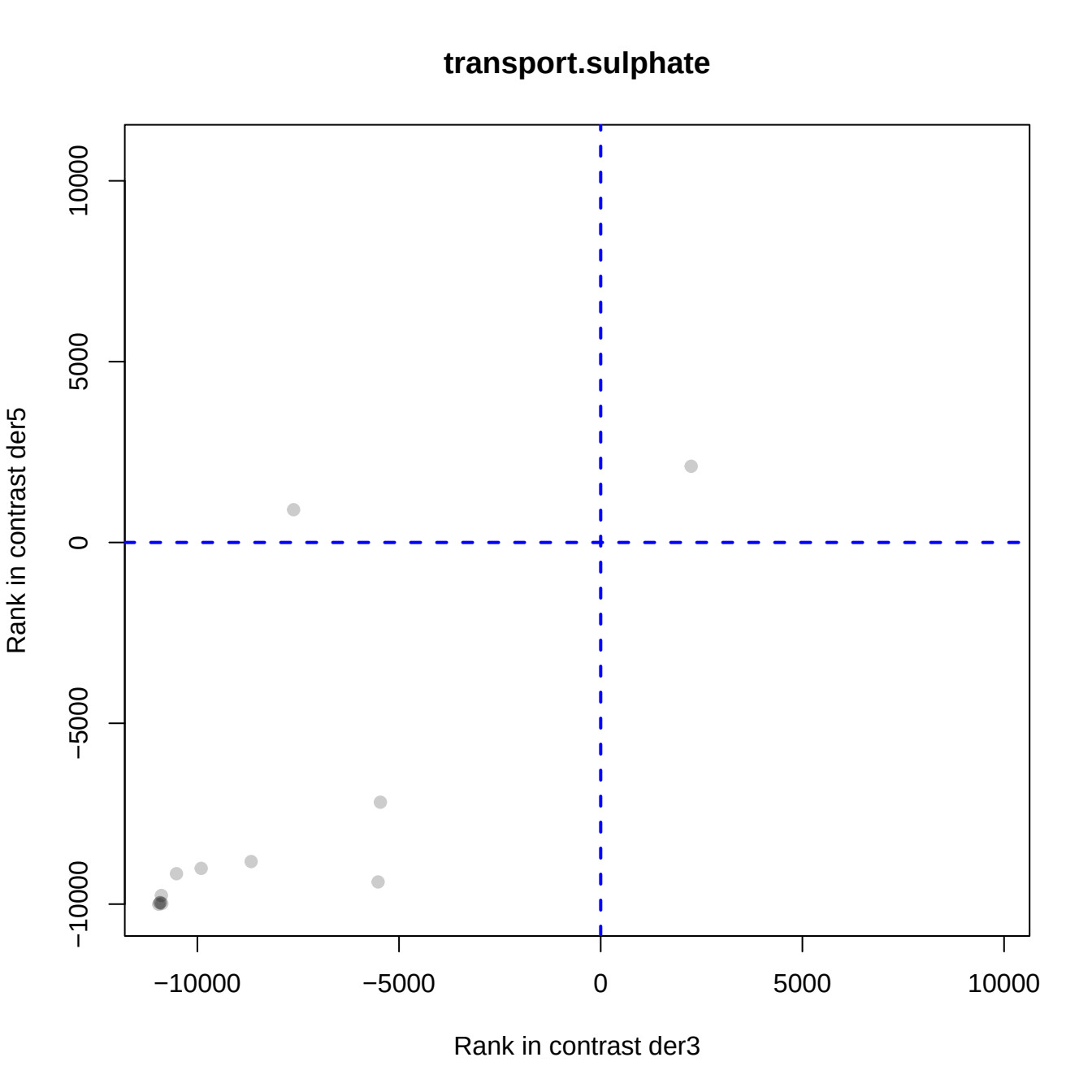

Scatterplot of all gene sets; FDR<0.05 in red
s.der5
s.der3
0.5
0.0
−0.5
−0.5
0.0
0.5

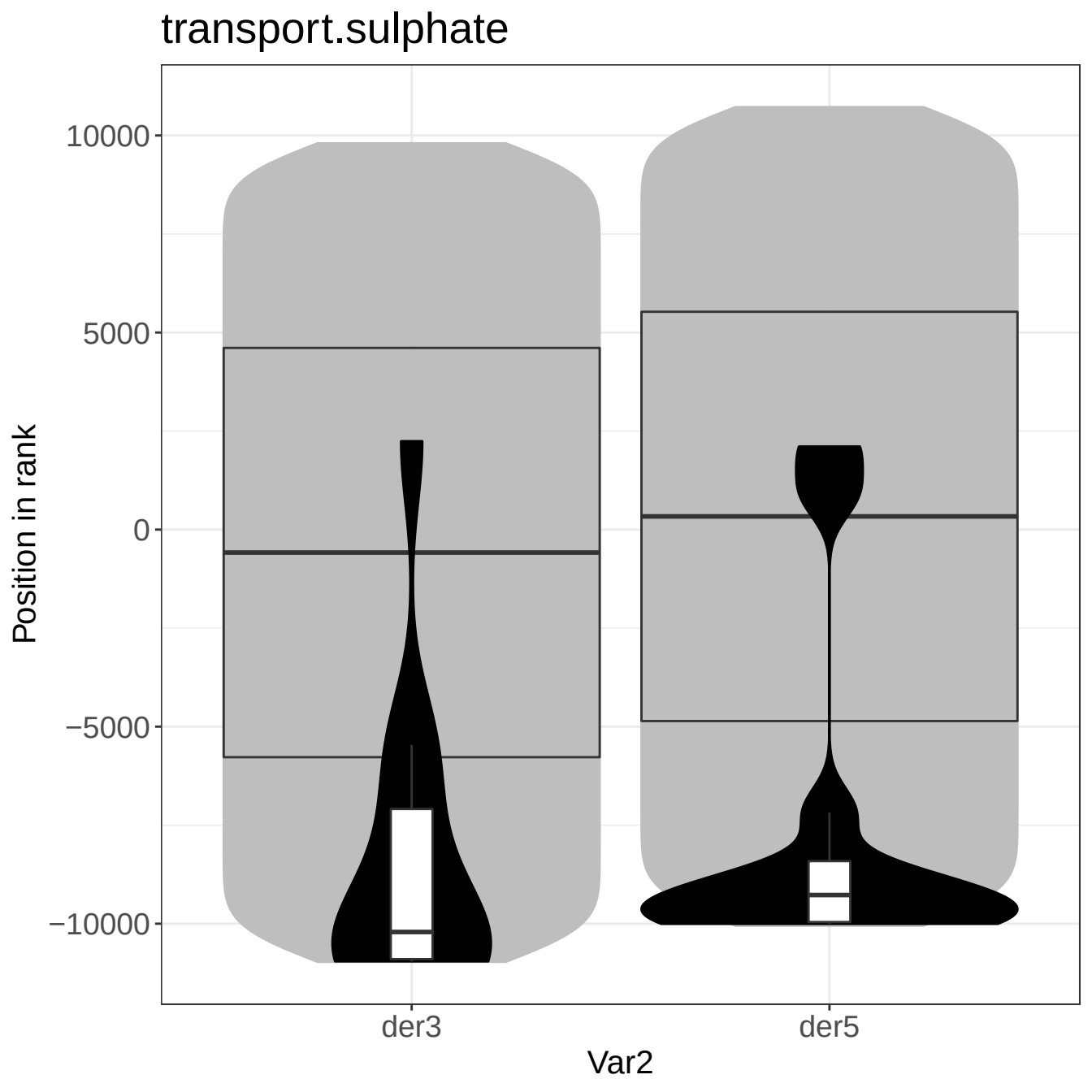

Scatterplot of all gene sets; top 50 in red
s.der5
0.5
0.0
−0.5
−0.5
0.0
0.5
s.der3

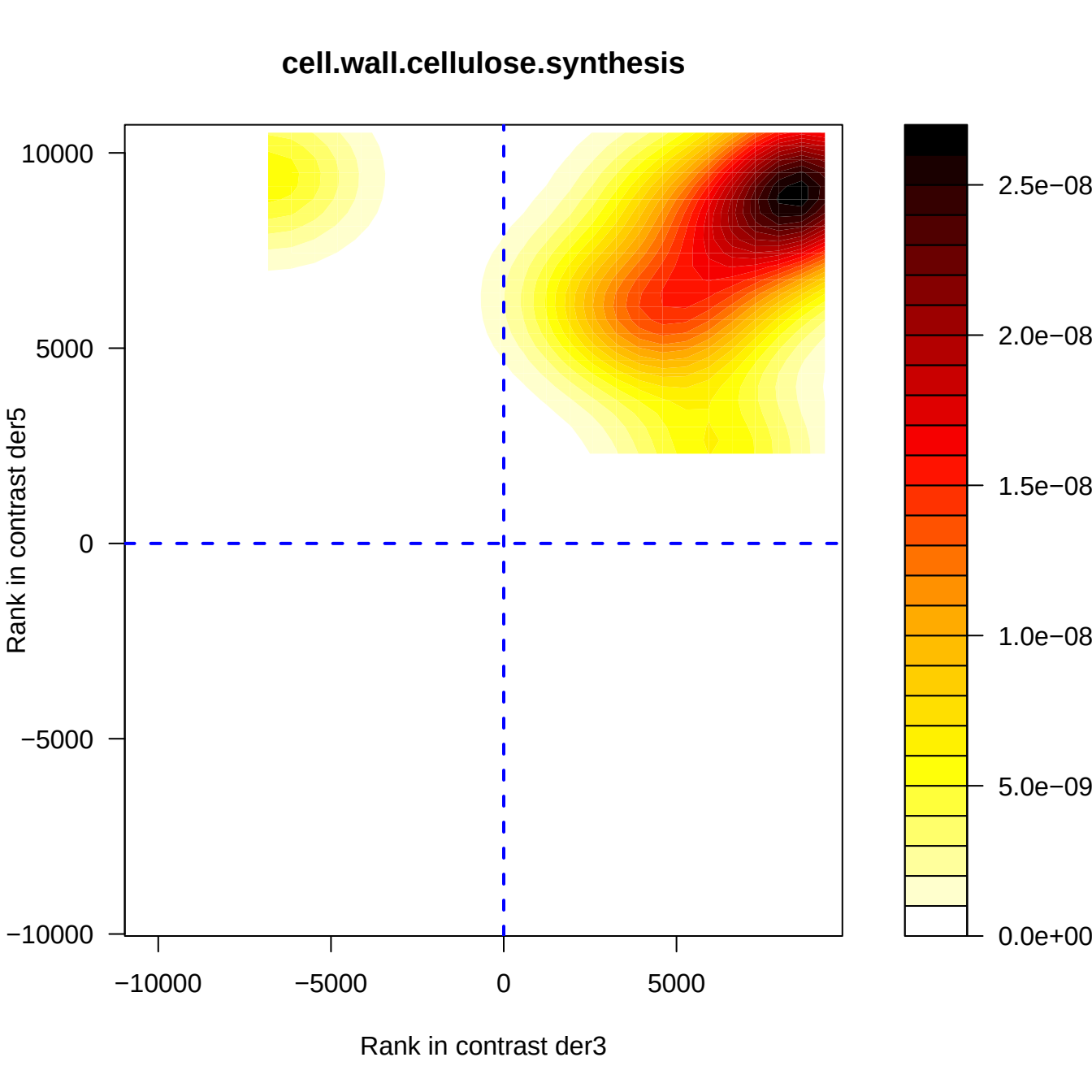

Color Key and Histogram
Count
0
2
4
6
8
−0.5
0
0.5
Value
secondary.metabolism.simple.phenols
cell.wall.pectin.esterases.misc
cell.wall.pectin.esterases.acetyl.esterase
protein.postranslational.modification.kinase
transport.ammonium
secondary.metabolism.flavonoids.flavonols
cell.wall.precursor.synthesis.GAE
cell.wall.precursor.synthesis.UXS
cell.wall.degradation.cellulases.and.beta..1.4.glucanases
protein.synthesis.ribosome.biogenesis.Pre.rRNA.processing.and.modifications.DE
protein.synthesis.ribosome.biogenesis.BRIX
RNA.regulation.of.transcription.CPP.Zn..CPP1.related.transcription.factor.family
PS.lightreaction.photosystem.I.LHC.I
PS.lightreaction.photosystem.I.PSI.polypeptide.subunits
hormone.metabolism.ethylene.signal.transduction
transport.sulphate
protein.synthesis.ribosomal.protein.eukaryotic.60S.subunit.L41
secondary.metabolism.phenylpropanoids.lignin.biosynthesis.CCR1
protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15A
redox.peroxiredoxin
PS.lightreaction.NADH.DH
major.CHO.metabolism.degradation.sucrose.invertases.neutral
PS.lightreaction.other.electron.carrier..ox.red..ferredoxin
secondary.metabolism.flavonoids.isoflavones.isoflavone.reductase
protein.degradation.ubiquitin.E3.SCF.SKP
der5
der3

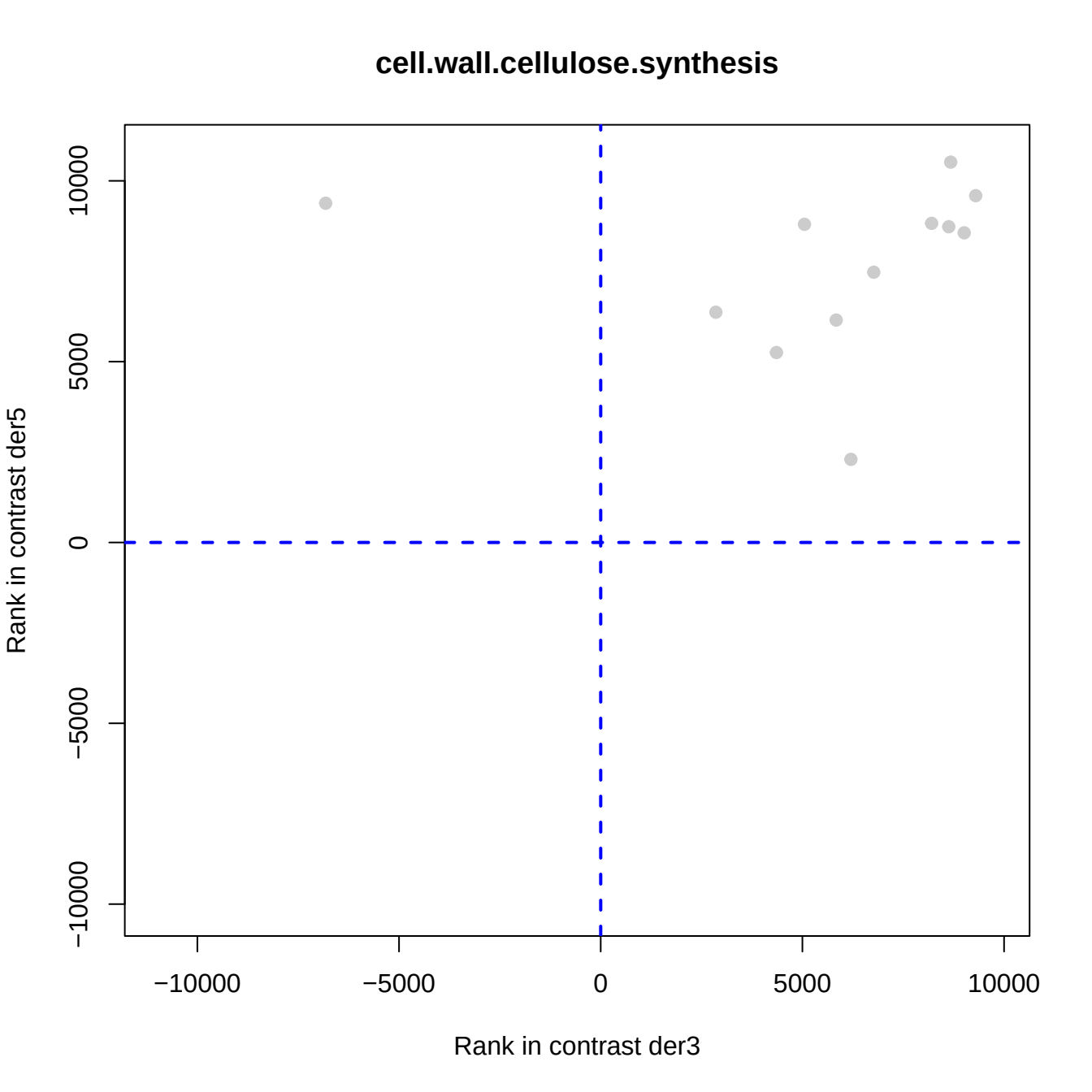

effect size versus statistical significance
−log(p.adjustMANOVA) (significance)
0
5
10
15
0.0
0.2
0.4
0.6
0.8
1.0
s.dist (effect size)

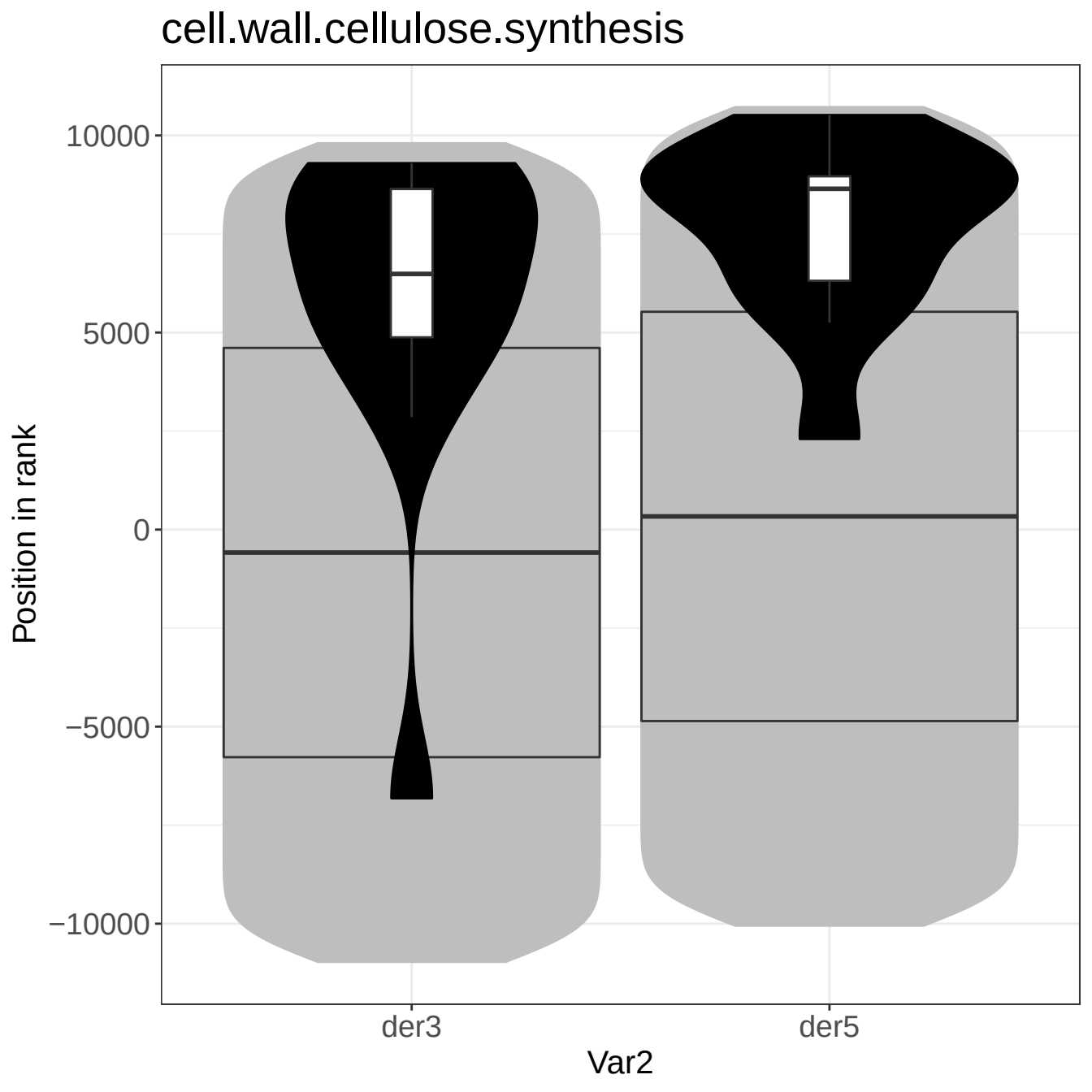

transport.sulphate
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
6e−08
5e−08
4e−08
3e−08
2e−08
1e−08
0e+00

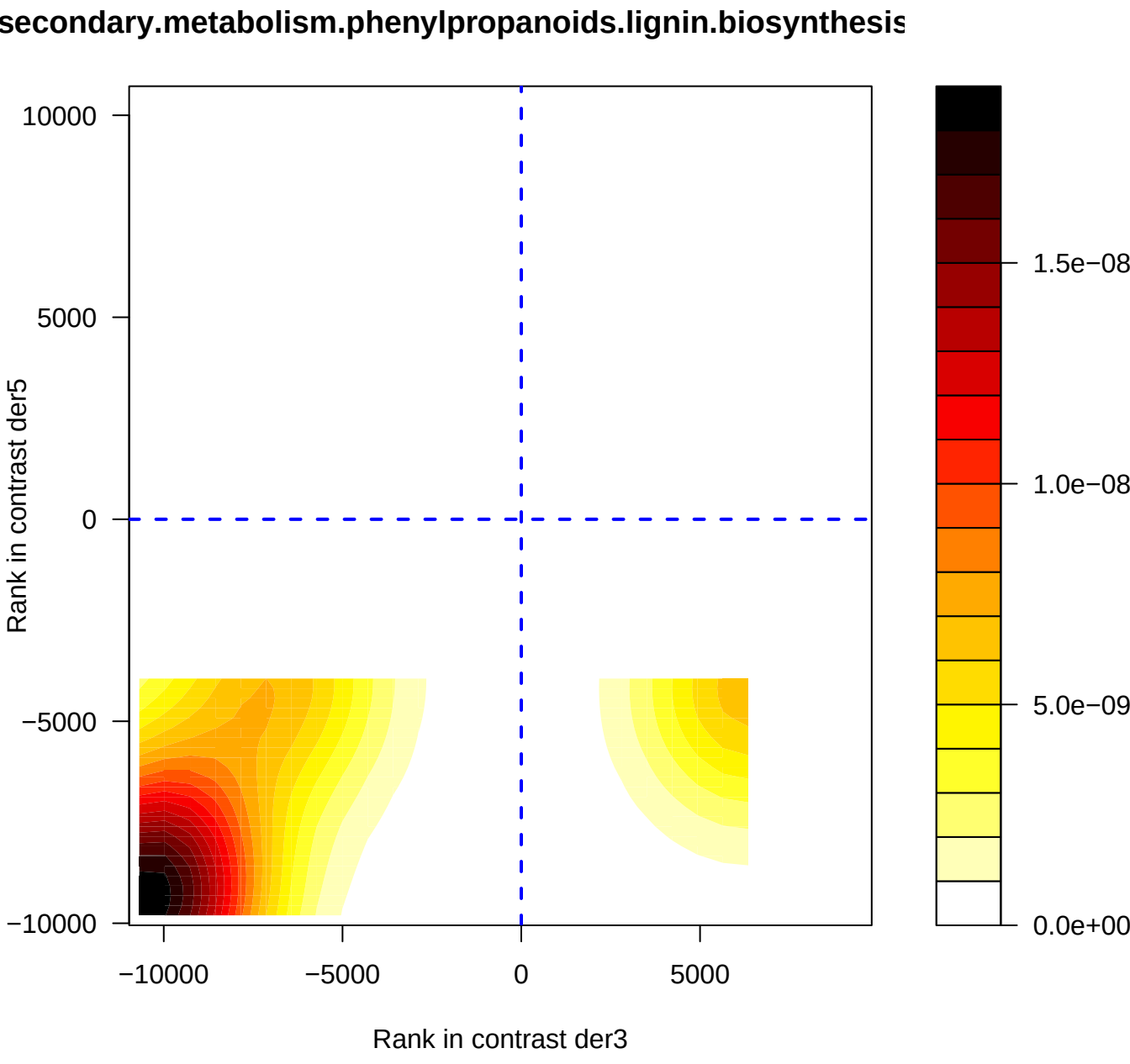

transport.sulphate
Rank in contrast der5
Rank in contrast der3
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

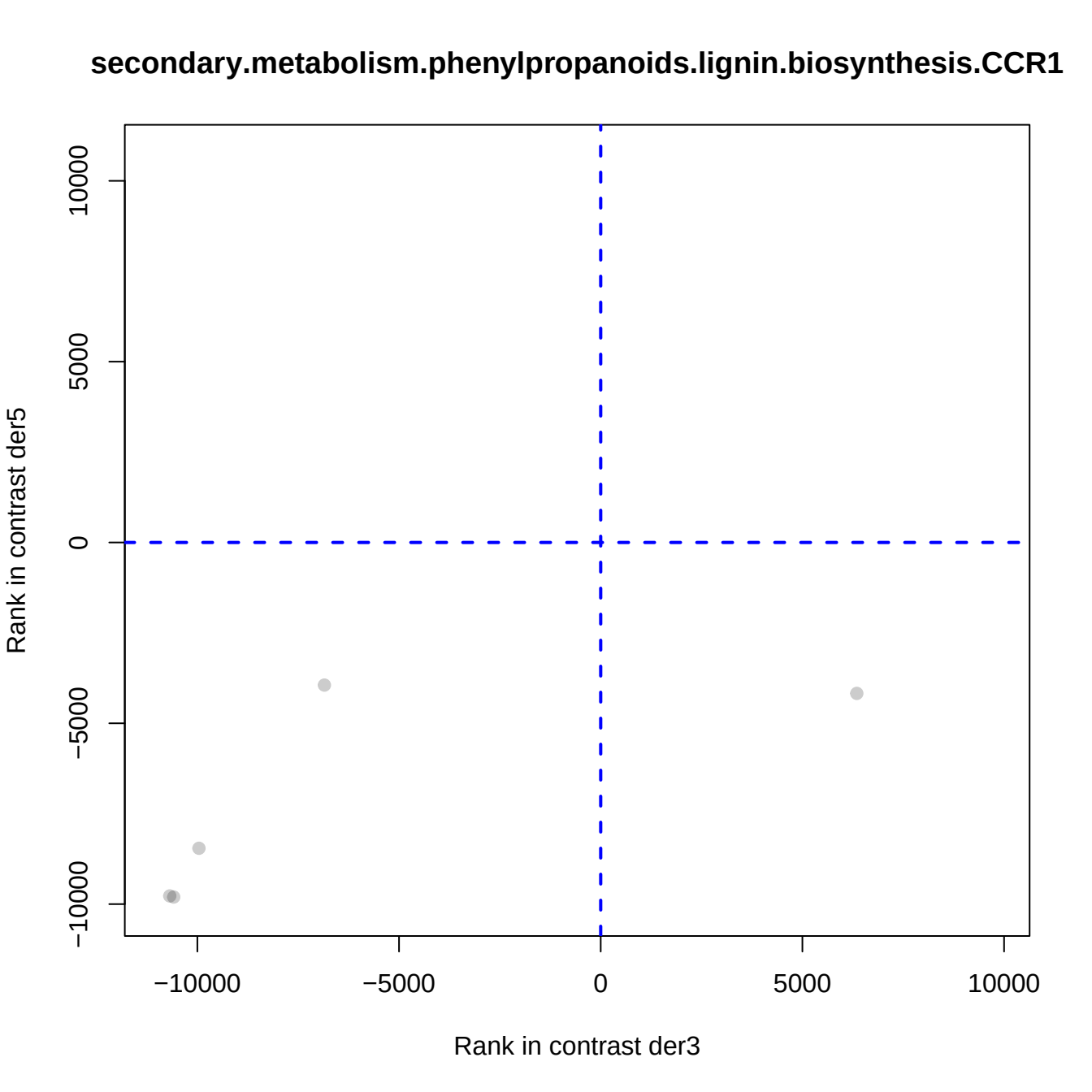

transport.sulphate
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

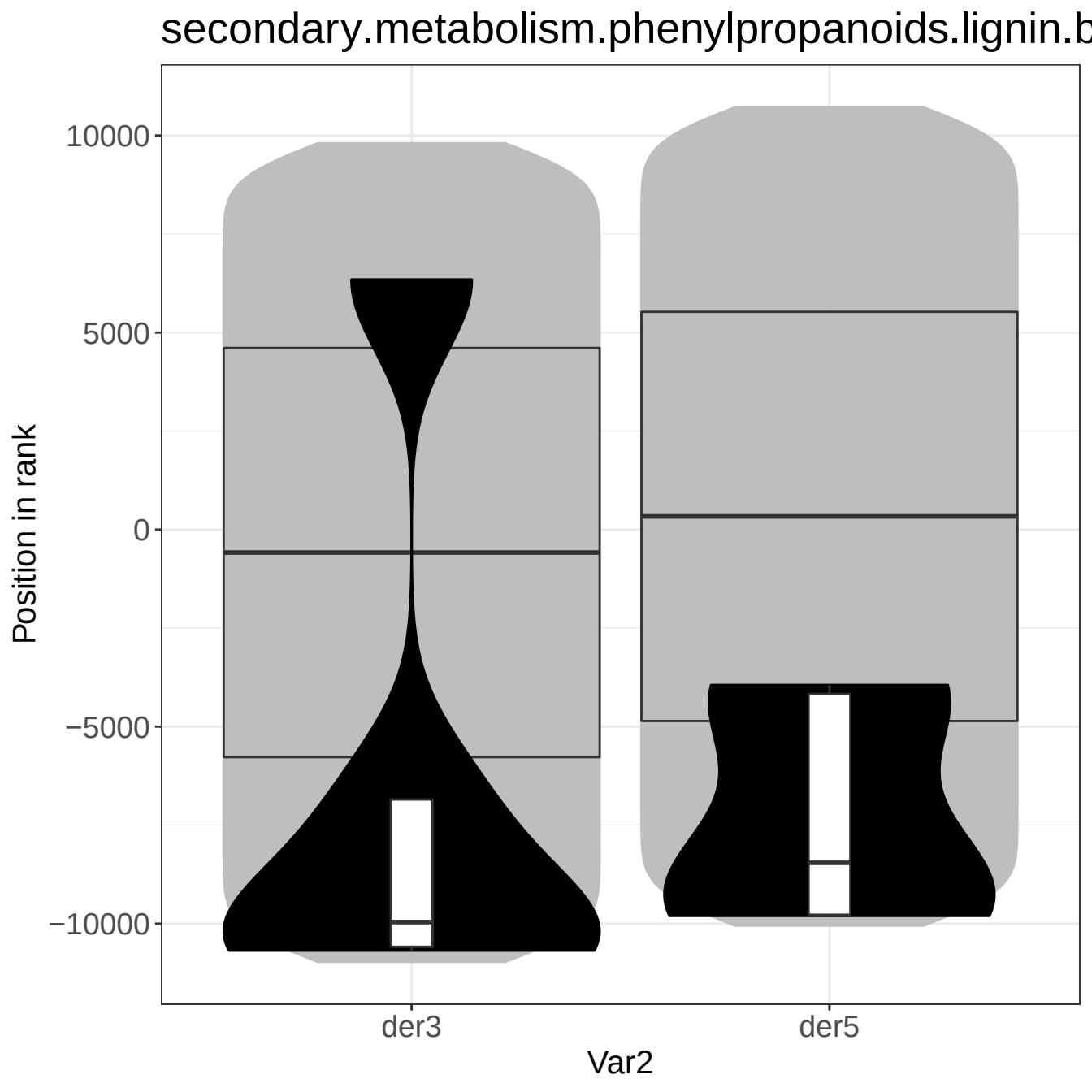

cell.wall.cellulose.synthesis
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
2.5e−08
2.0e−08
1.5e−08
1.0e−08
5.0e−09
0.0e+00

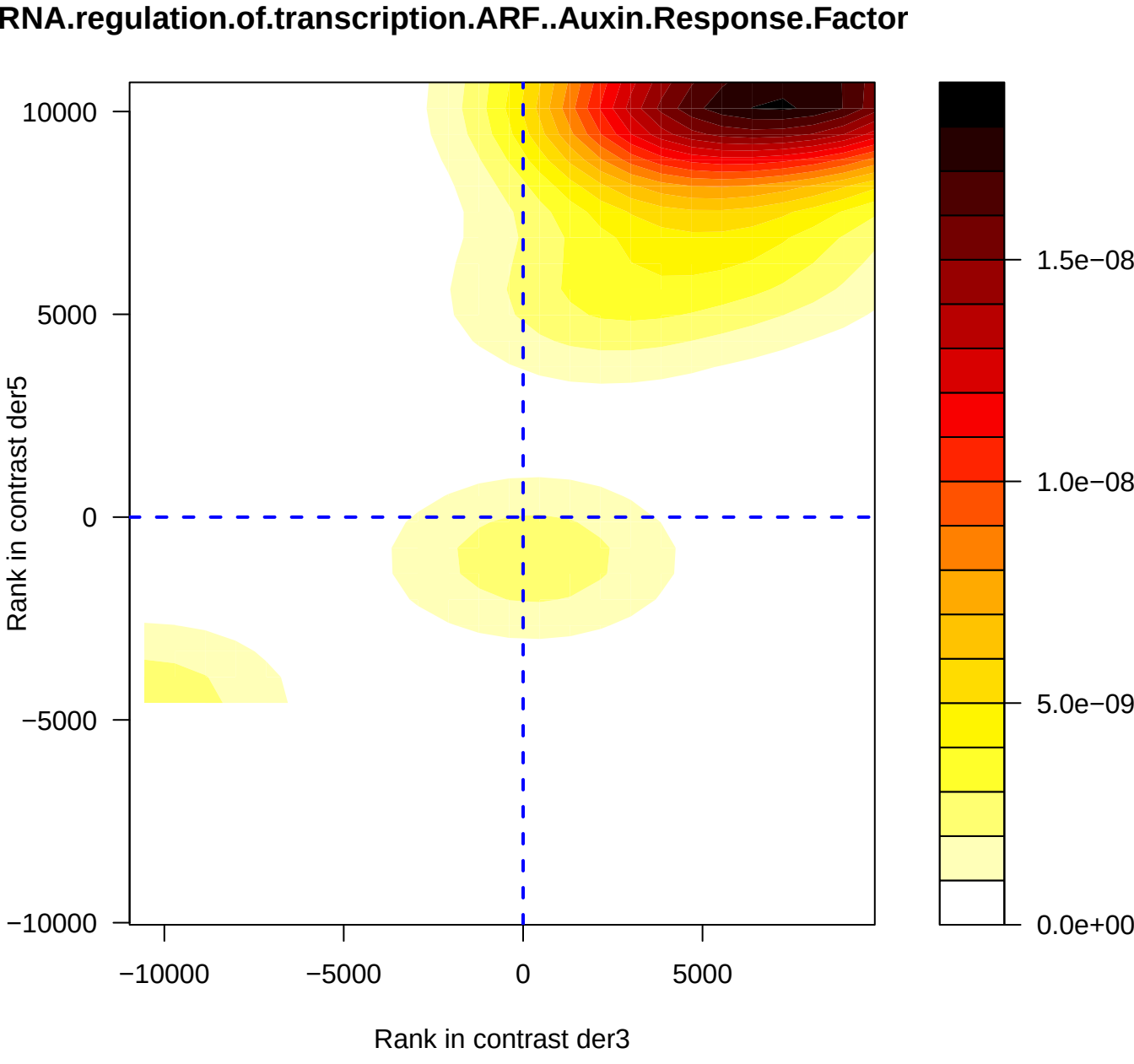

cell.wall.cellulose.synthesis
Rank in contrast der5
Rank in contrast der3
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

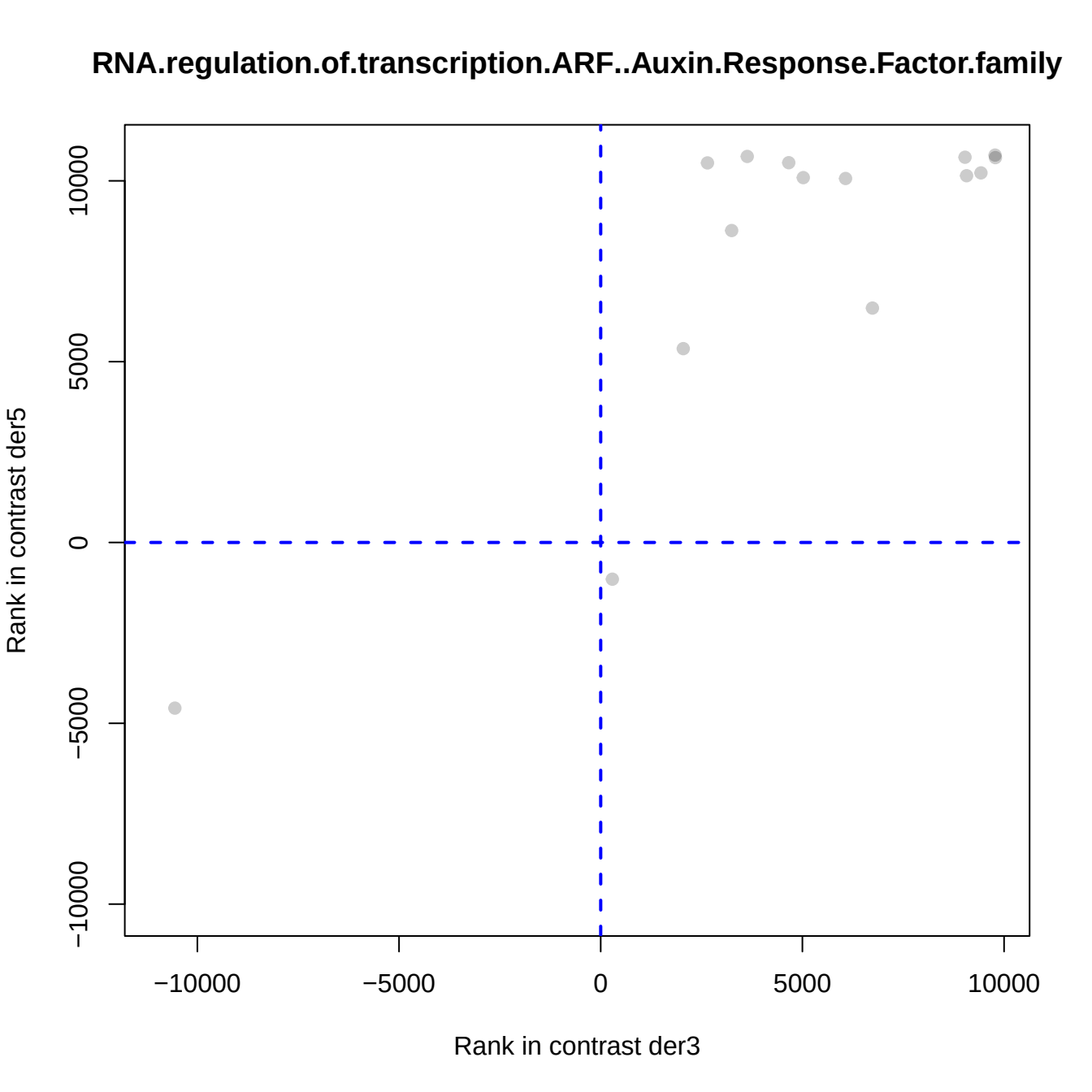

cell.wall.cellulose.synthesis
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

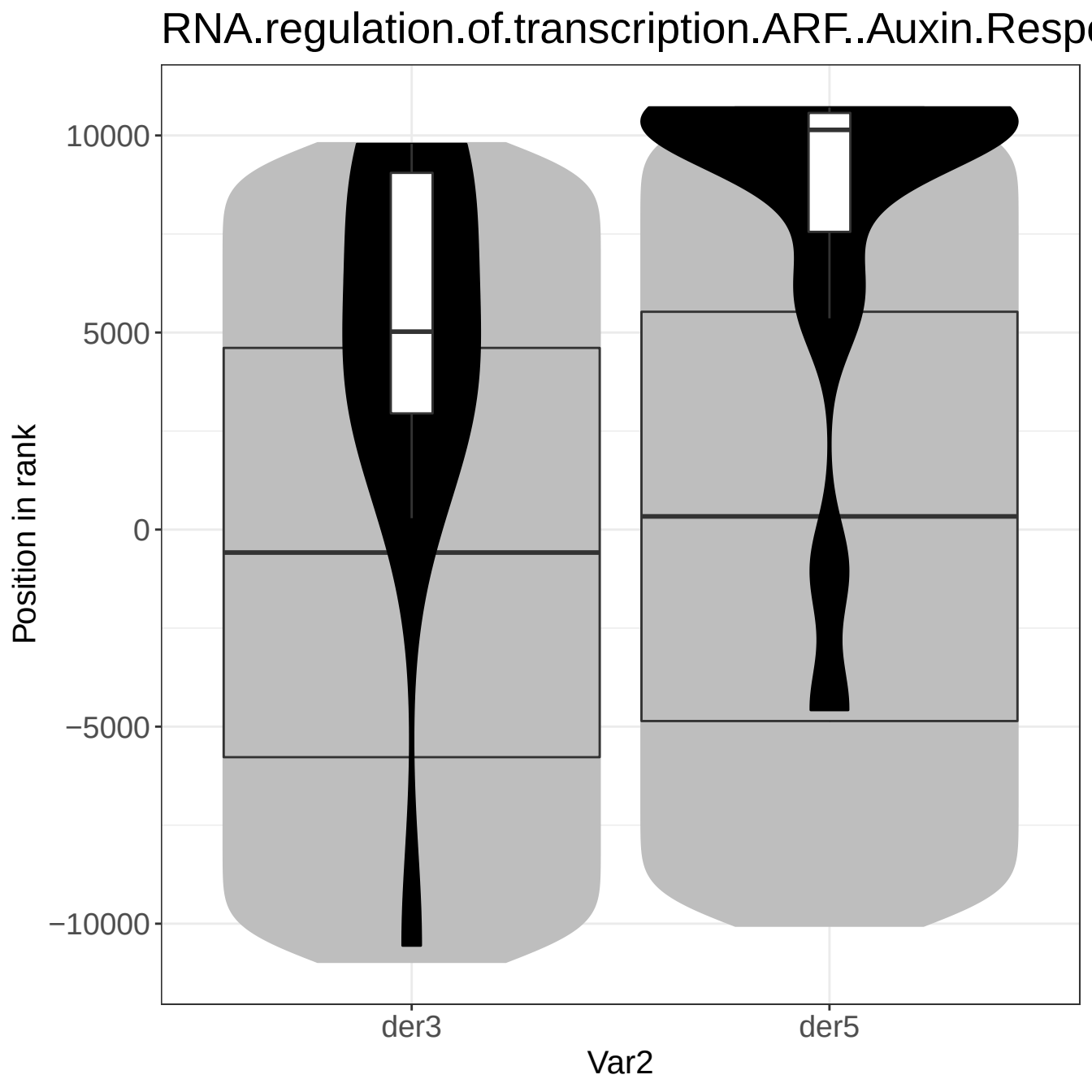

secondary.metabolism.phenylpropanoids.lignin.biosynthesis
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
1.5e−08
1.0e−08
5.0e−09
0.0e+00

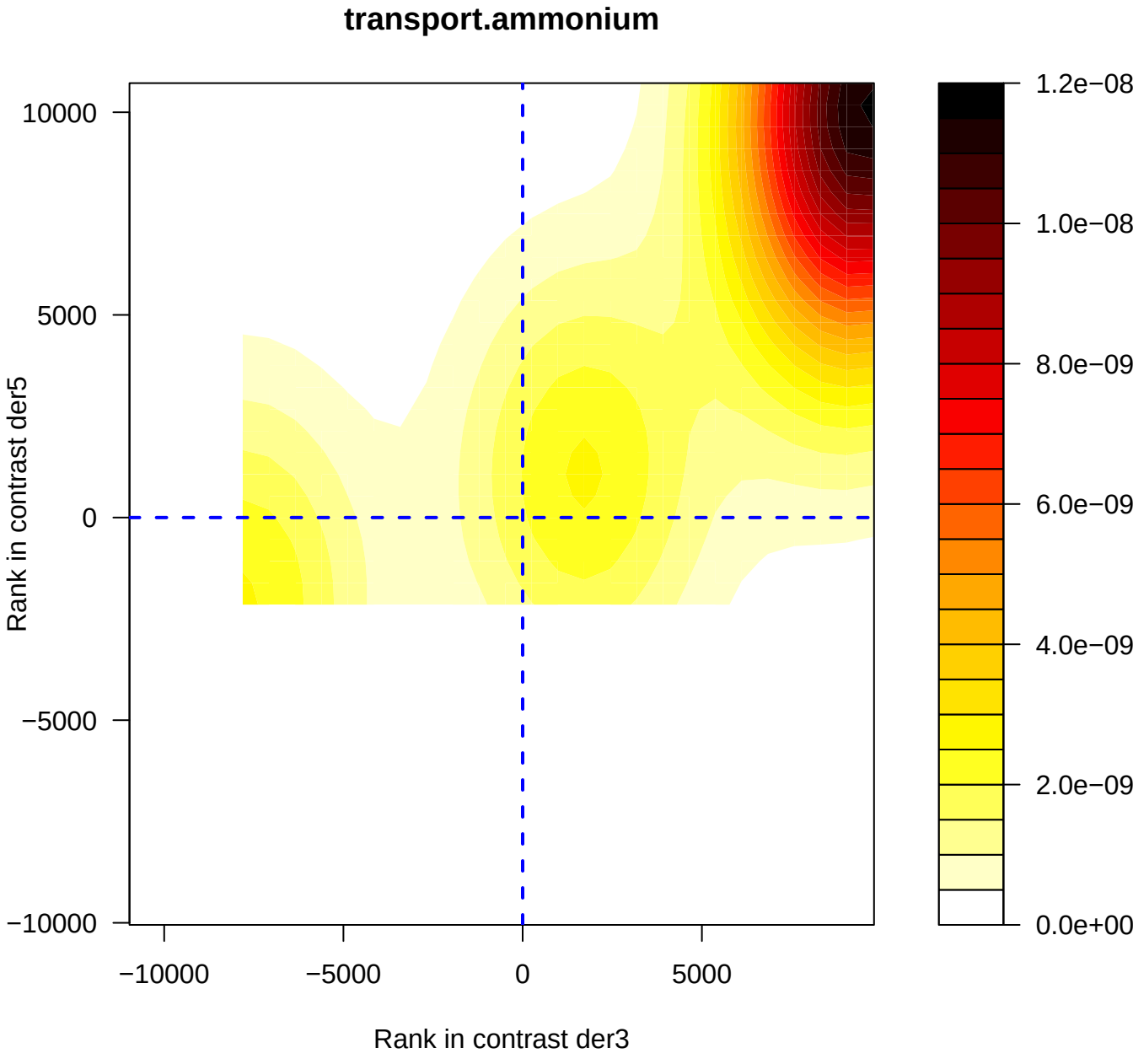

secondary.metabolism.phenylpropanoids.lignin.biosynthesis.CCR1
Rank in contrast der5
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
Rank in contrast der3

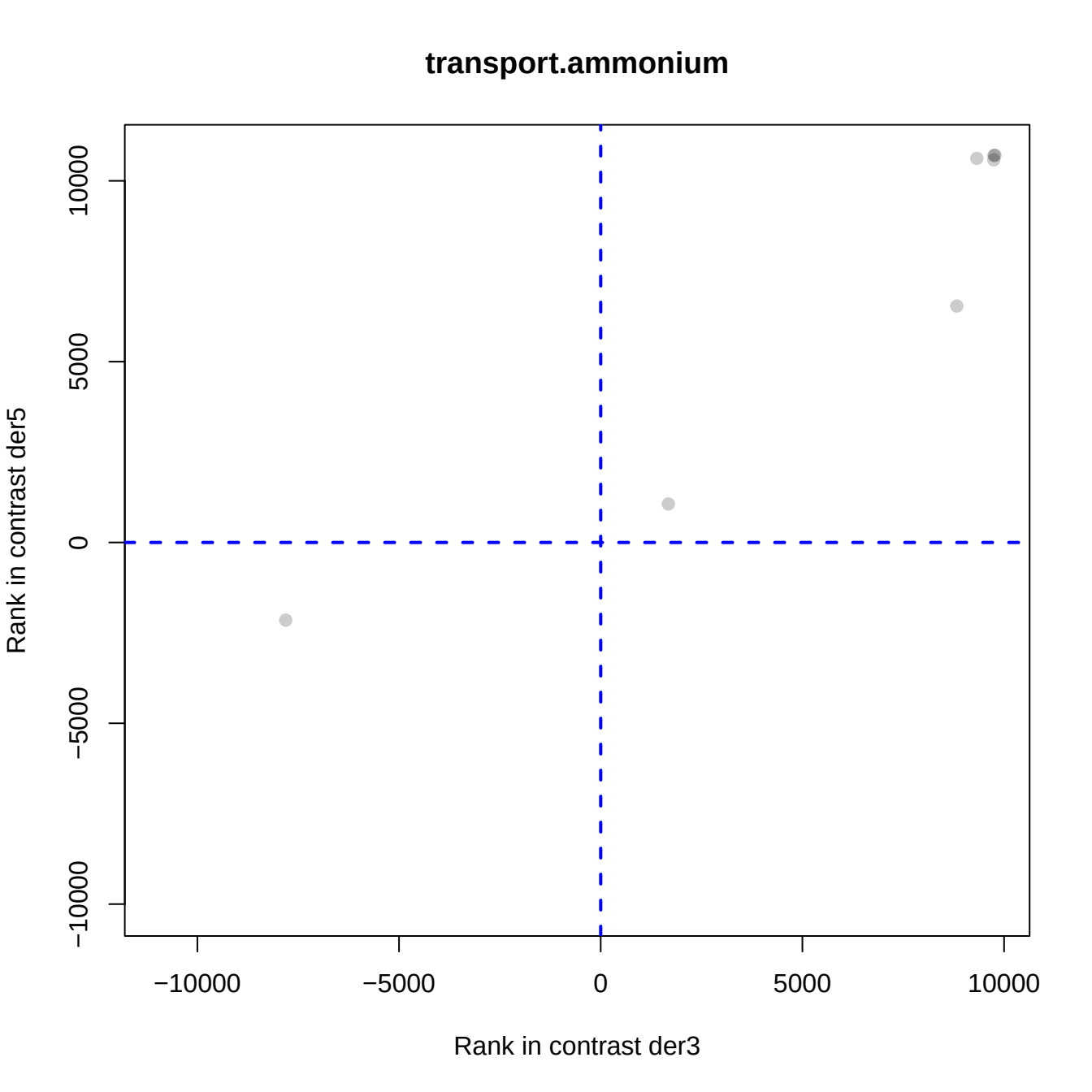

secondary.metabolism.phenylpropanoids.lignin.b
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

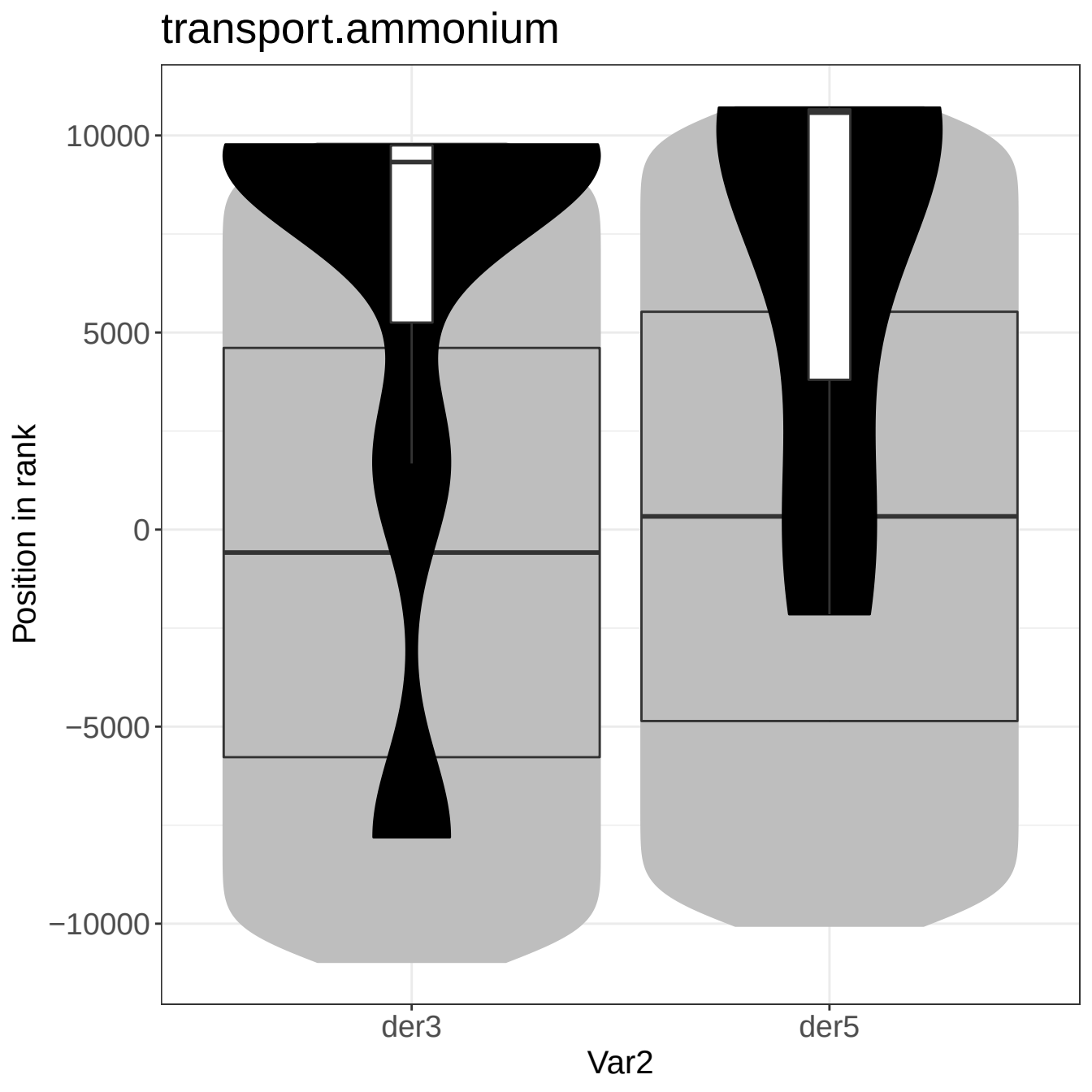

RNA.regulation.of.transcription.ARF..Auxin.Response.Factor
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
1.5e−08
1.0e−08
5.0e−09
0.0e+00

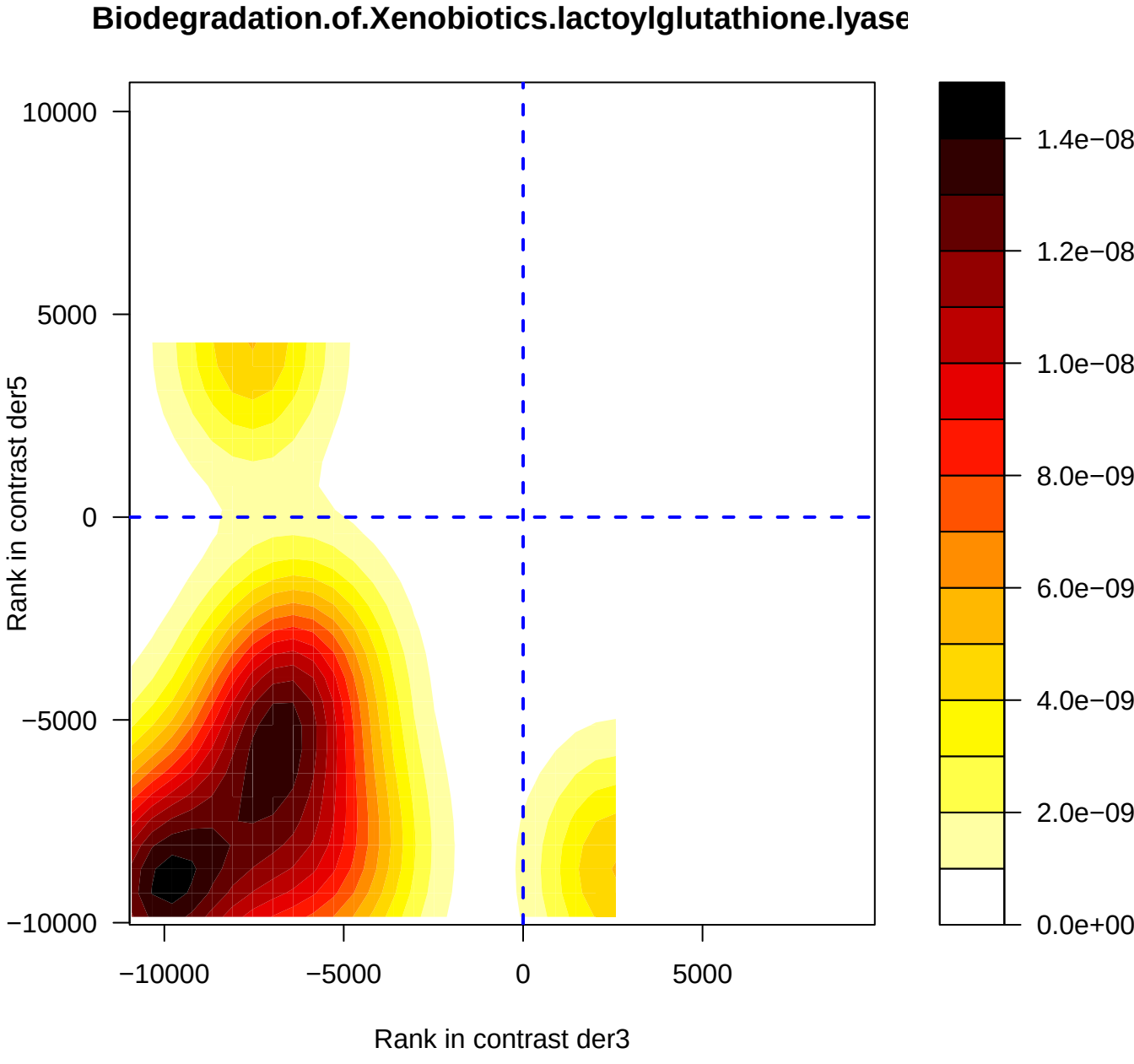

RNA.regulation.of.transcription.ARF..Auxin.Response.Factor.family
Rank in contrast der5
Rank in contrast der3
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

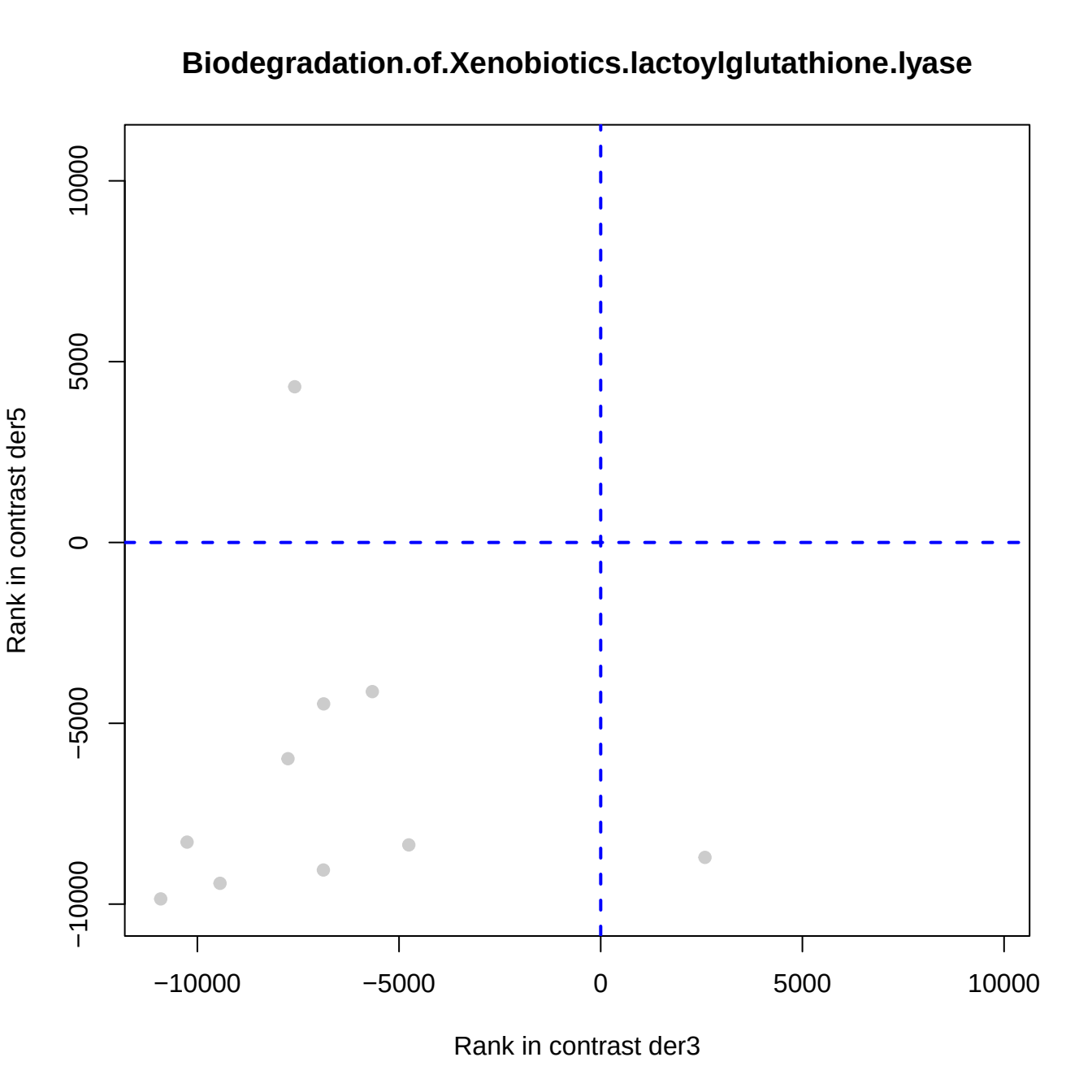

RNA.regulation.of.transcription.ARF..Auxin.Resp
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

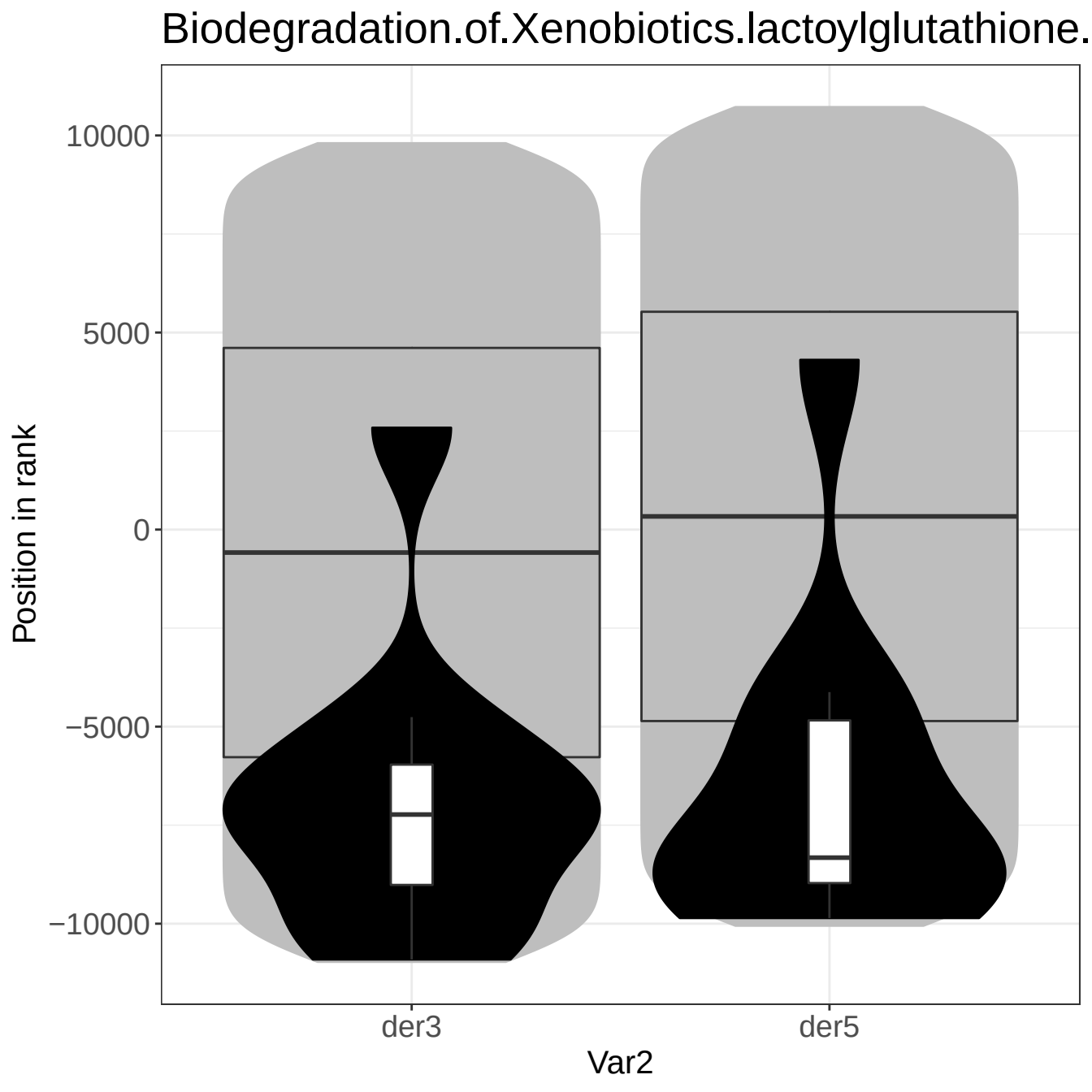

transport.ammonium
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

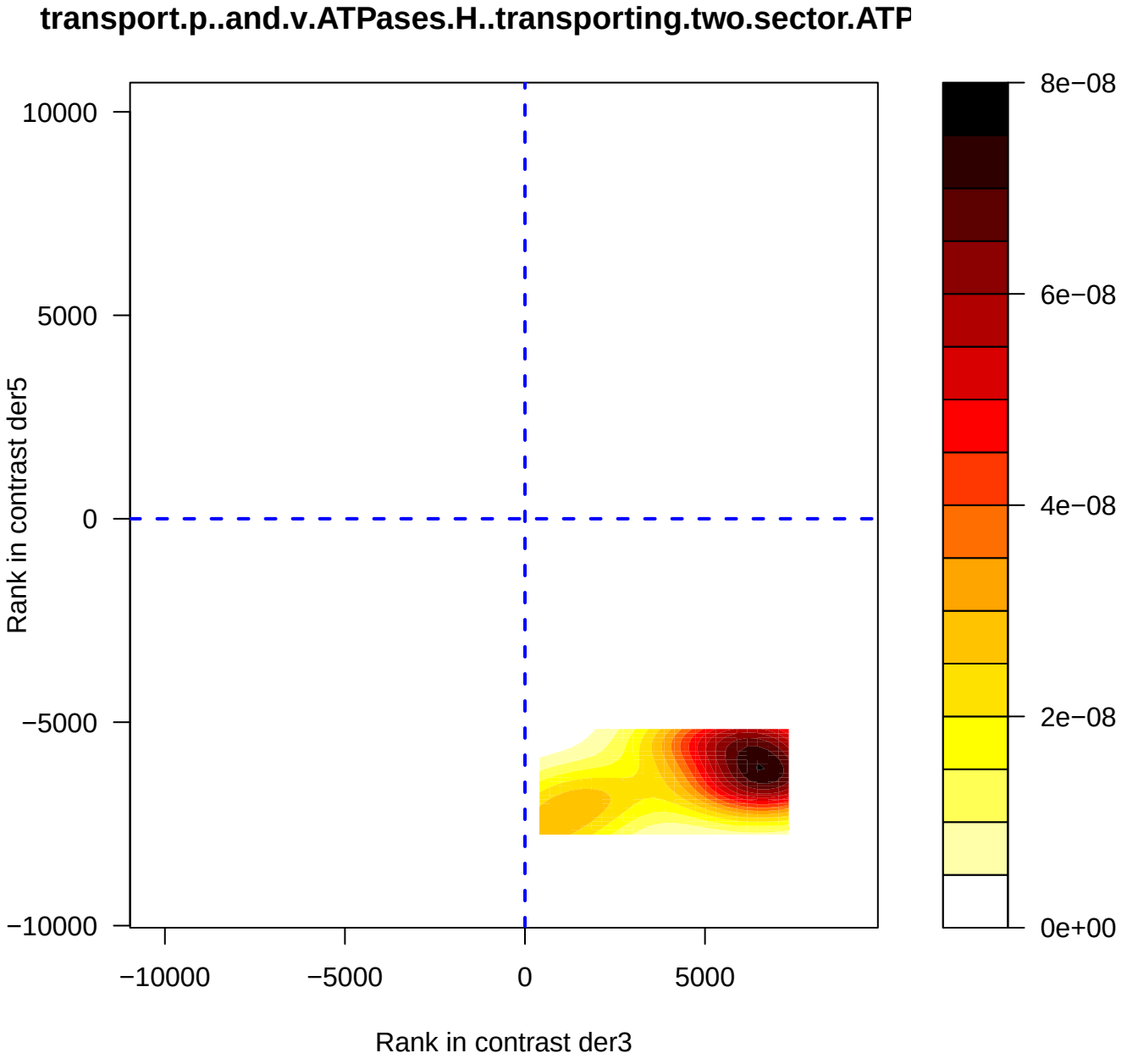

transport.ammonium
Rank in contrast der5
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
Rank in contrast der3

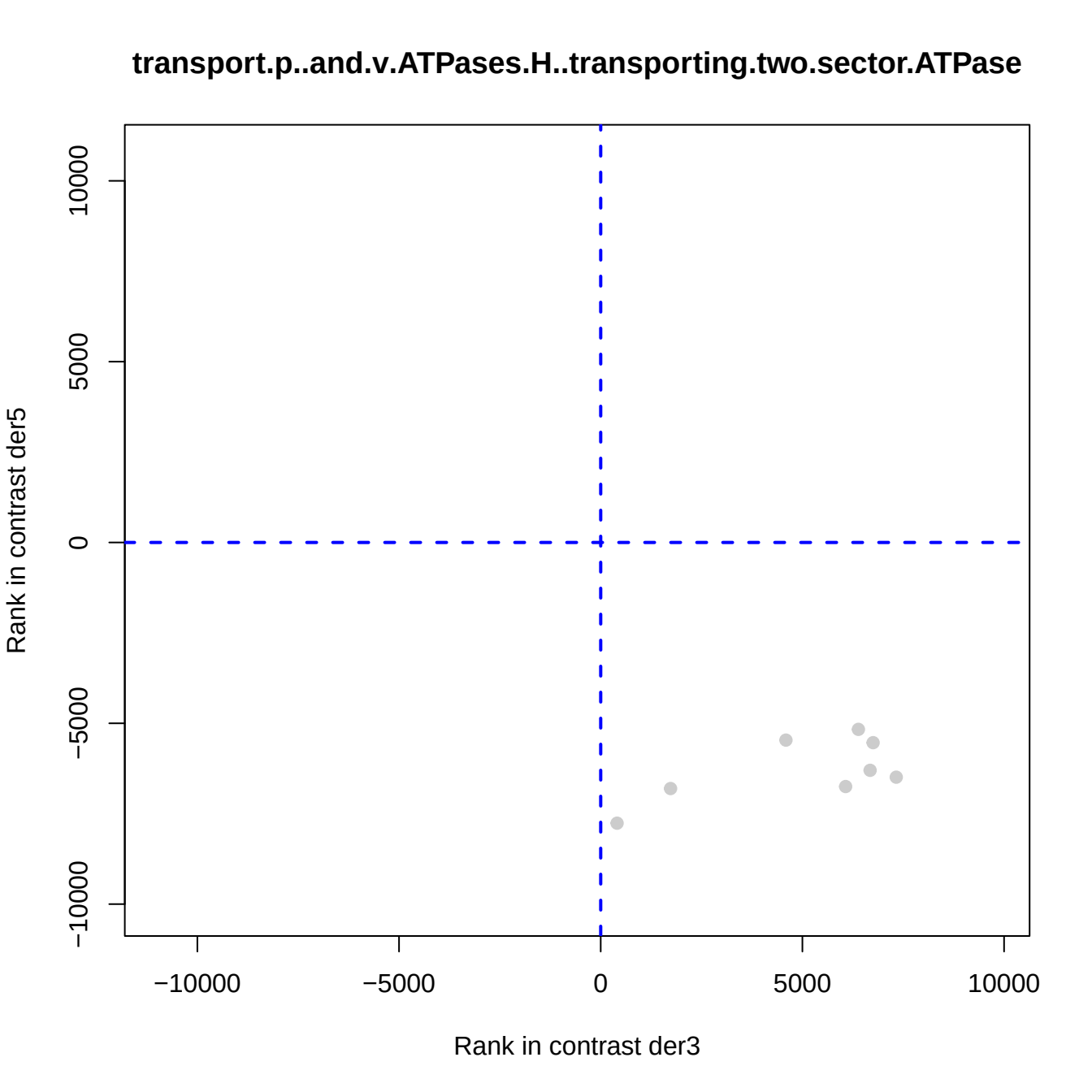

transport.ammonium
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

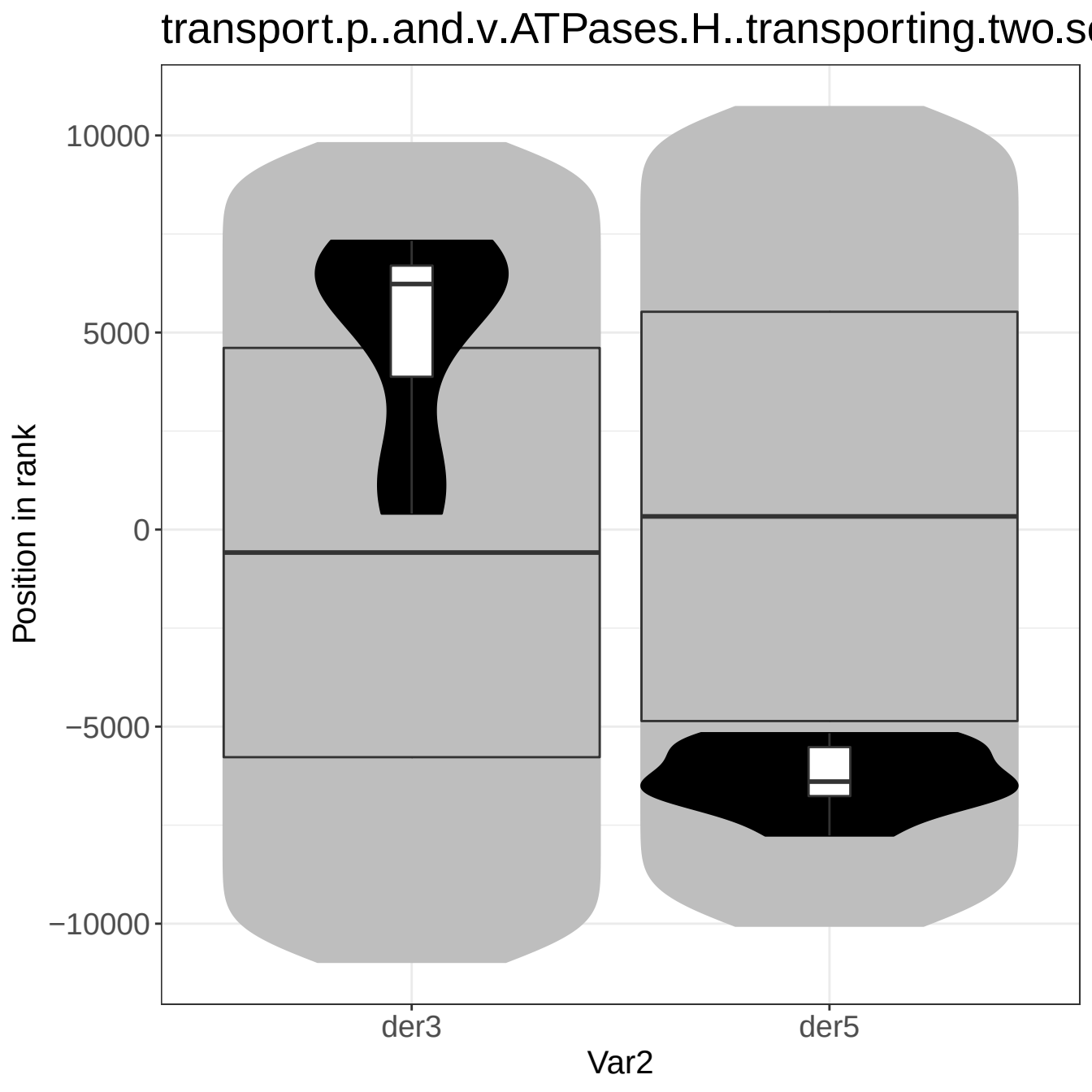

Biodegradation.of.Xenobiotics.lactoylglutathione.lyase
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
1.4e−08
1.2e−08
1.0e−08
8.0e−09
6.0e−09
4.0e−09
2.0e−09
0.0e+00

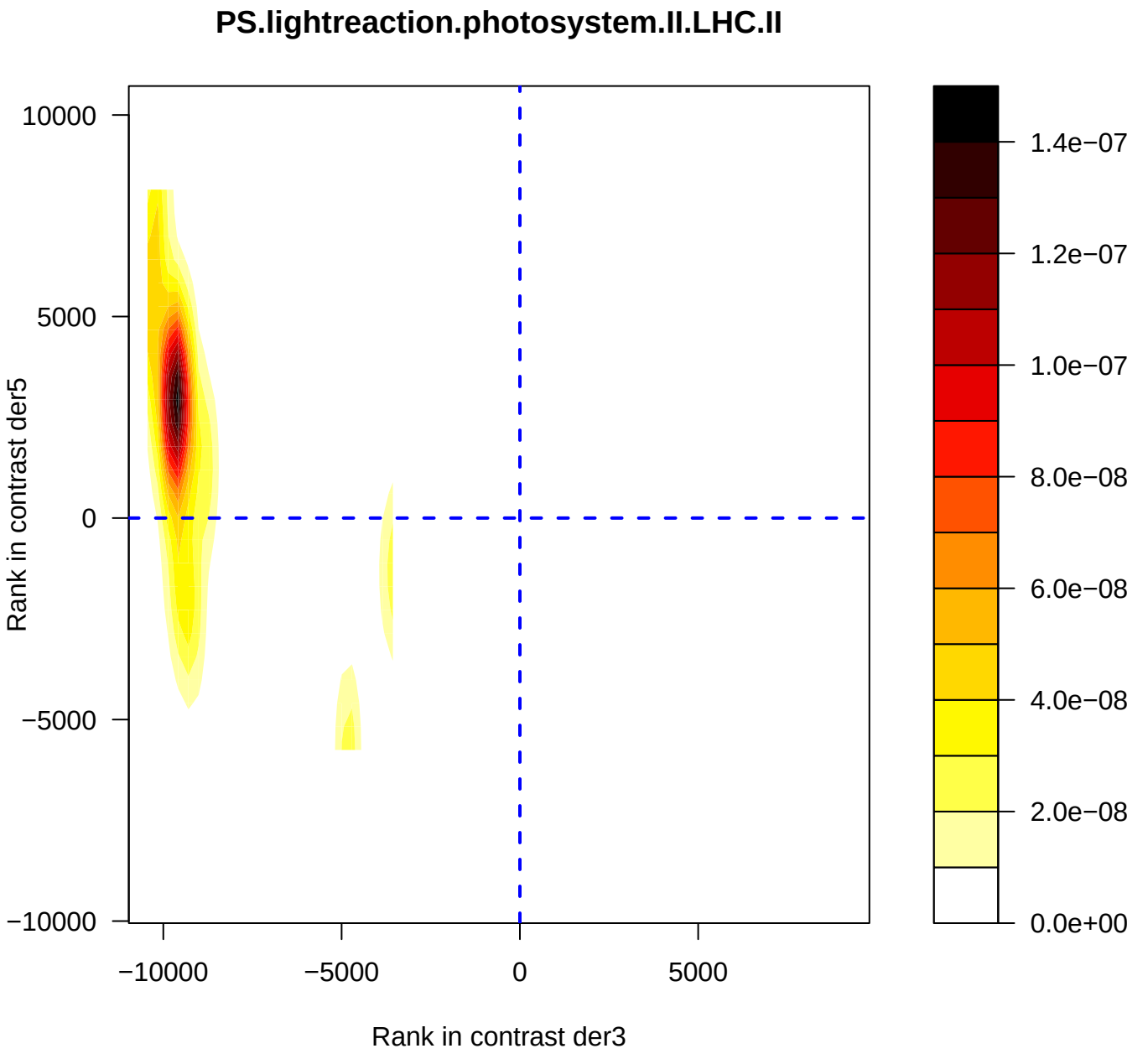

Biodegradation.of.Xenobiotics.lactoylglutathione.lyase
Rank in contrast der5
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
Rank in contrast der3

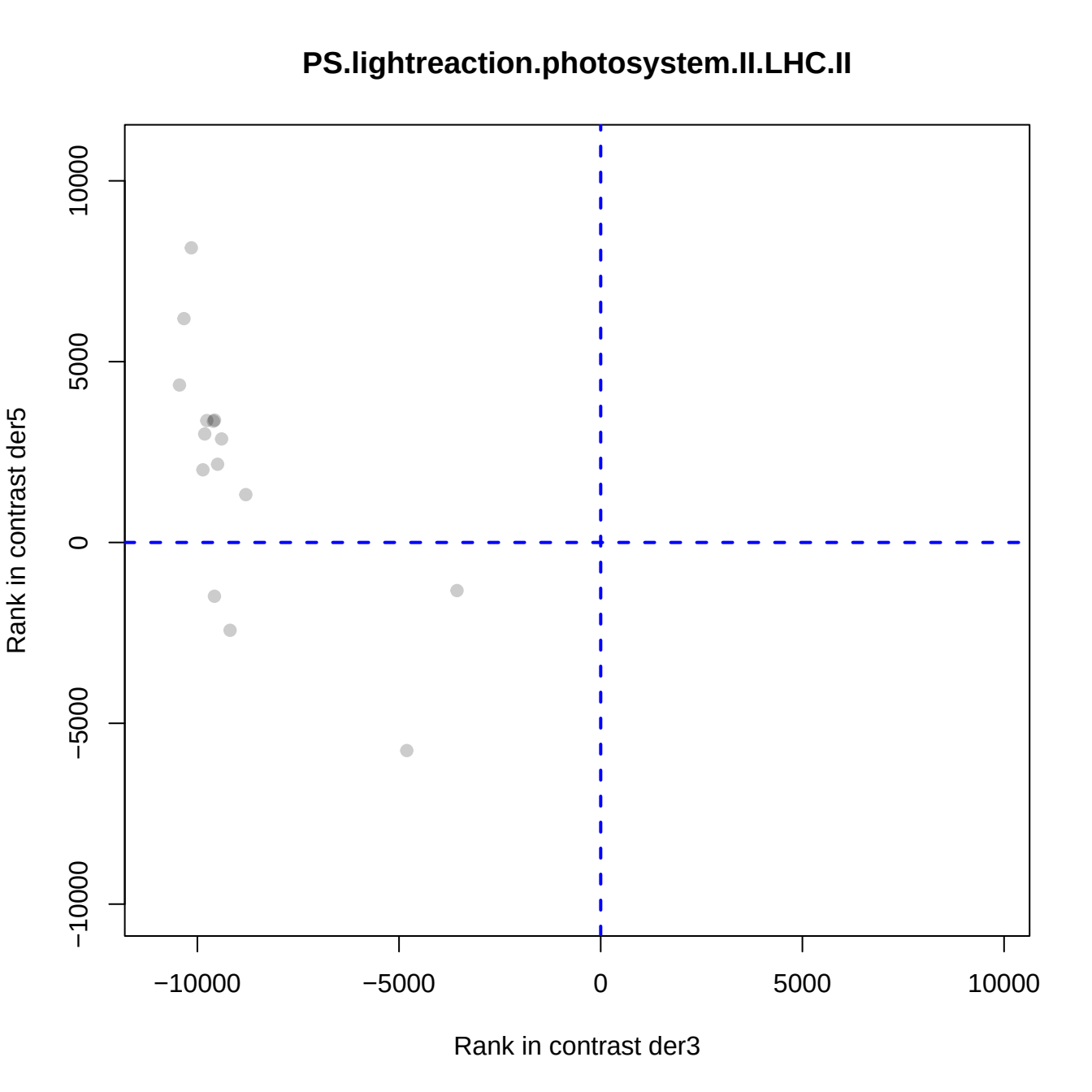

Biodegradation.of.Xenobiotics.lactoylglutathione.
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

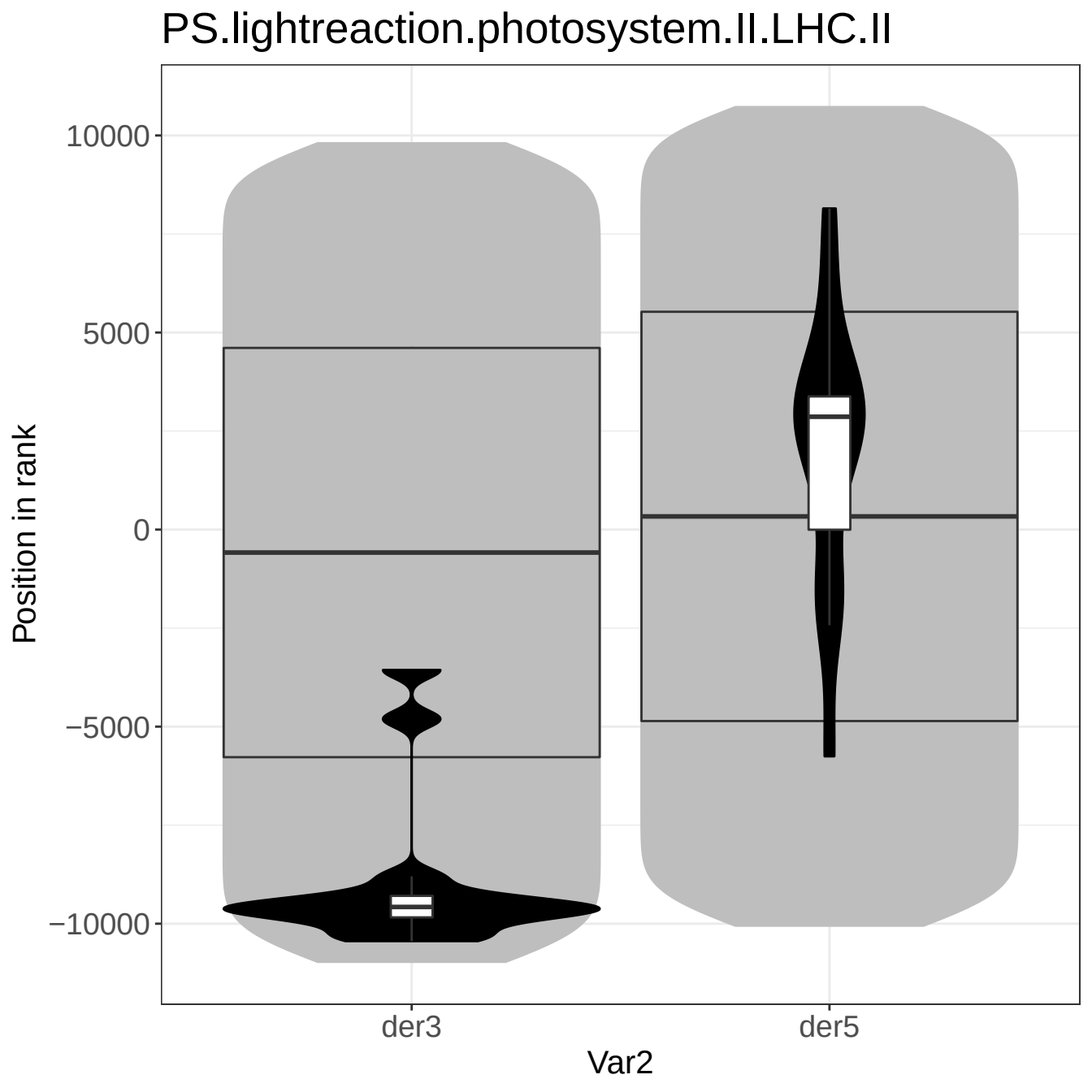

transport.p..and.v.ATPases.H..transporting.two.sector.ATP
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
8e−08
6e−08
4e−08
2e−08
0e+00

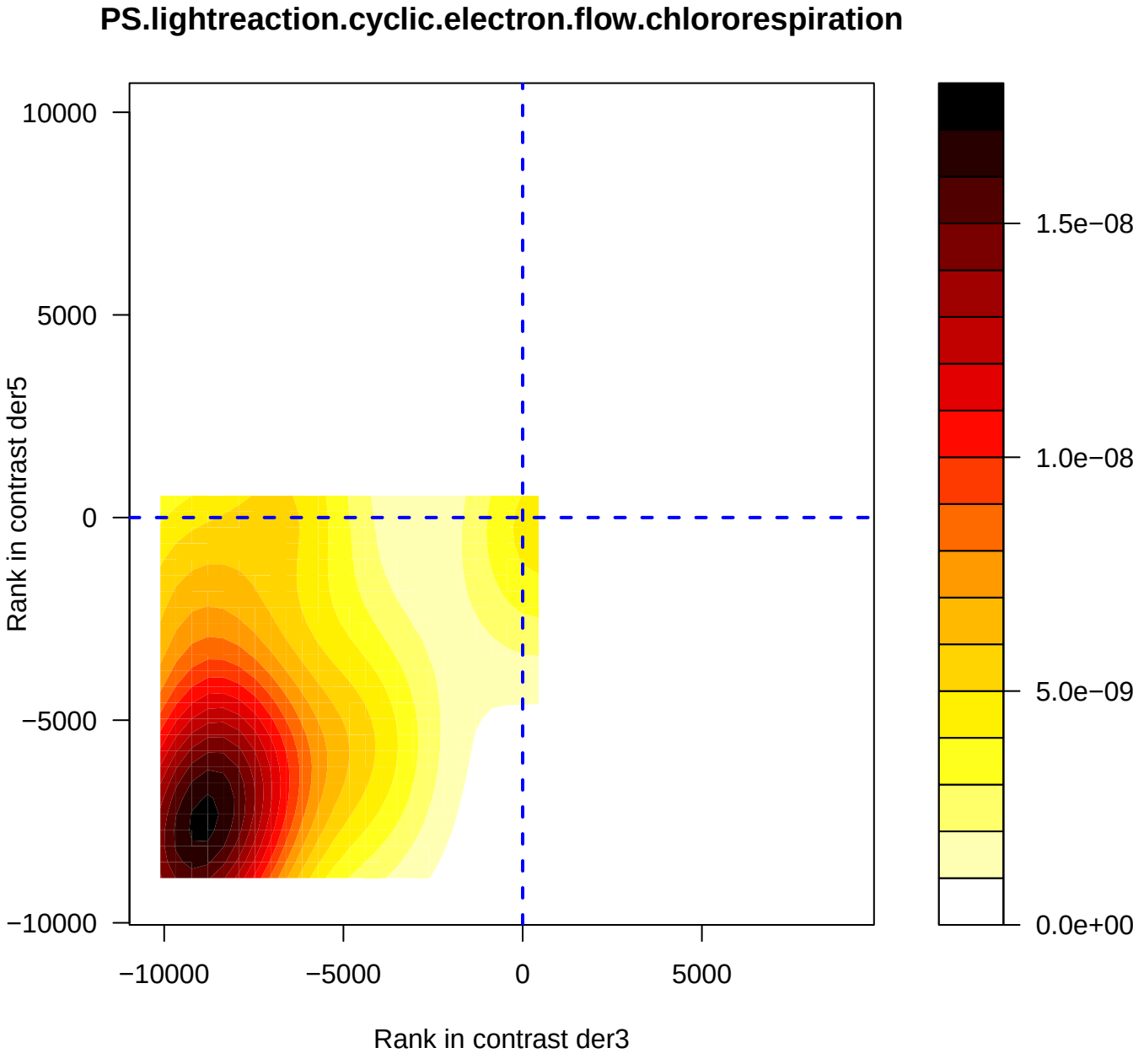

transport.p..and.v.ATPases.H..transporting.two.sector.ATPase
Rank in contrast der5
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
Rank in contrast der3

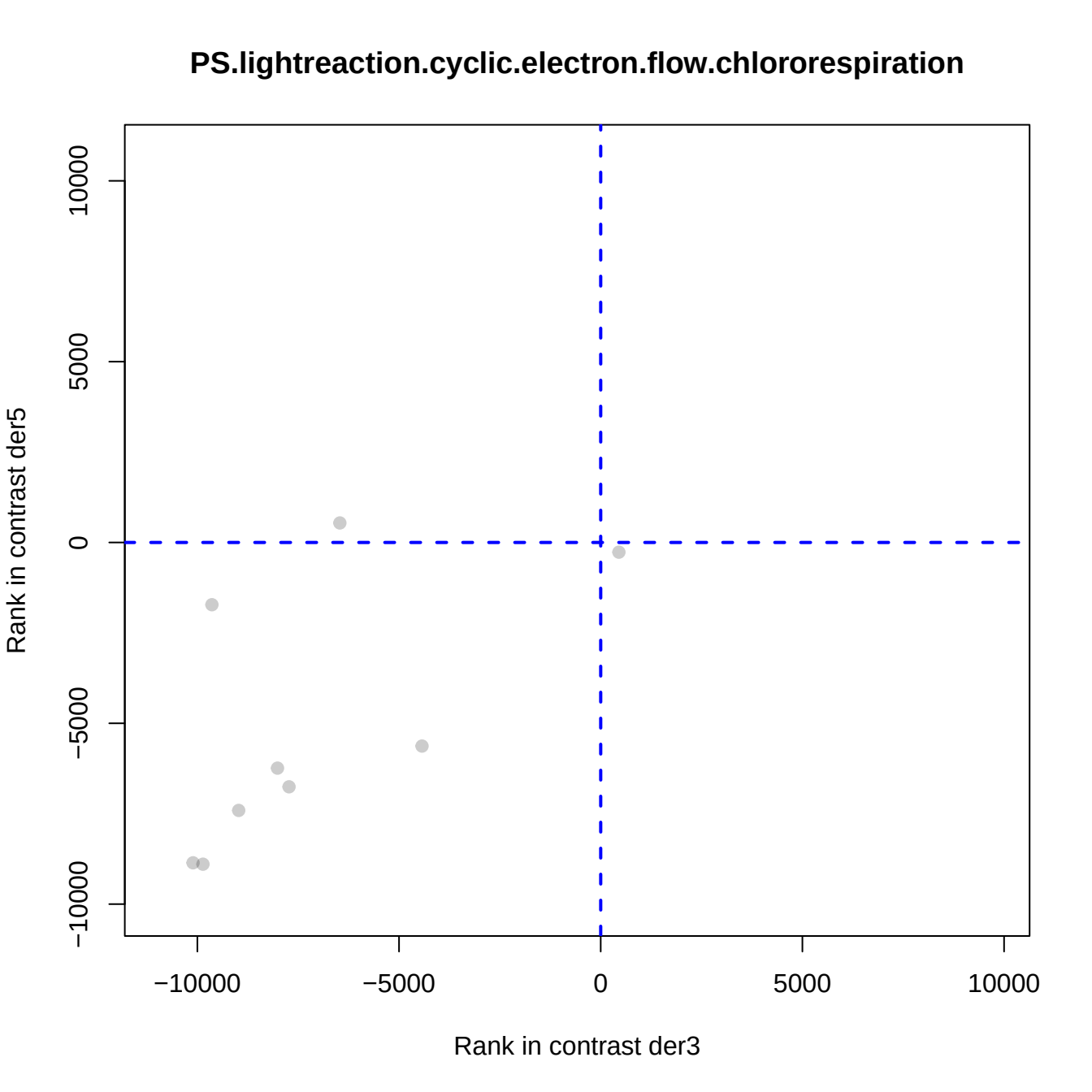

transport.p..and.v.ATPases.H..transporting.two.s
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

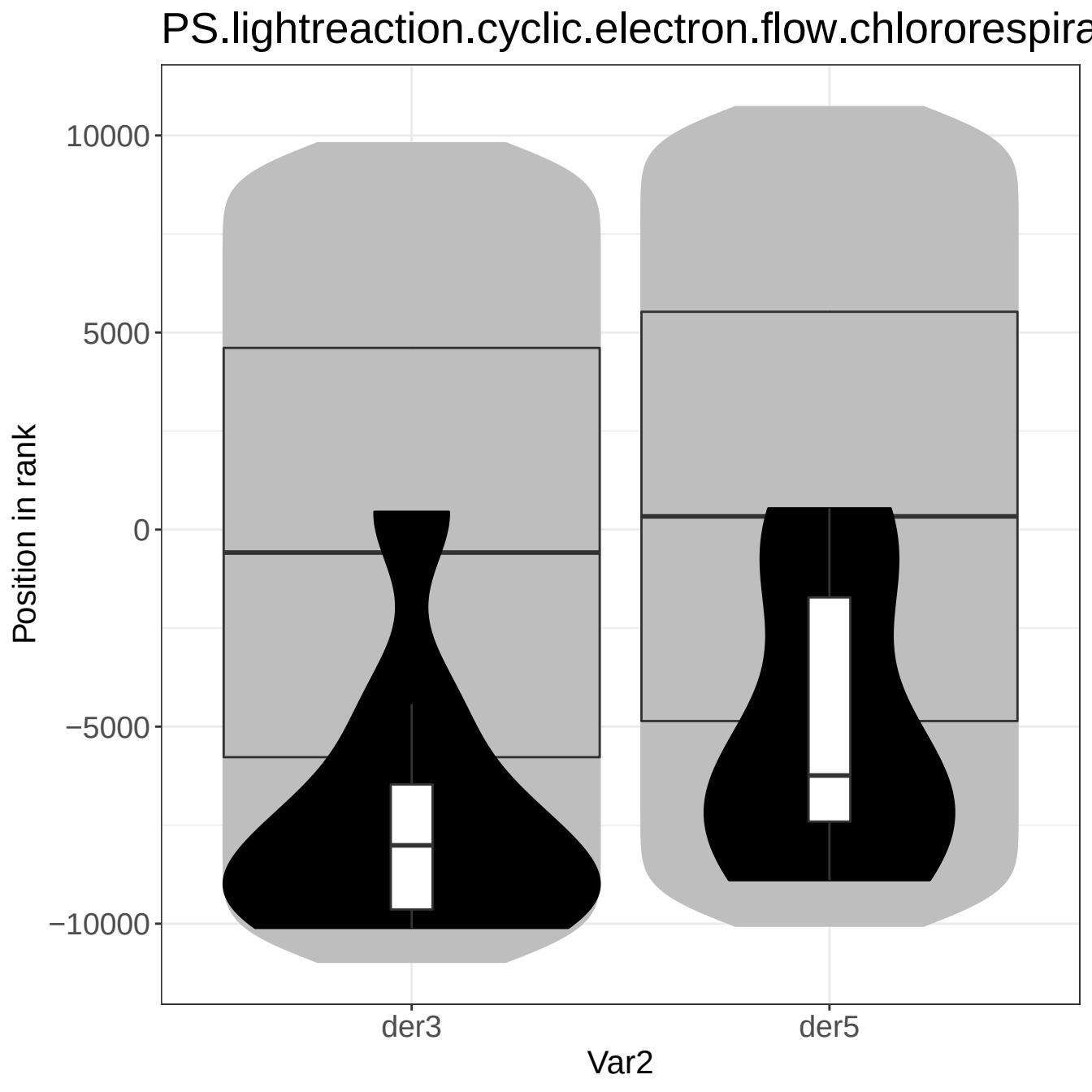

PS.lightreaction.photosystem.II.LHC.II
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
1.4e−07
1.2e−07
1.0e−07
8.0e−08
6.0e−08
4.0e−08
2.0e−08
0.0e+00

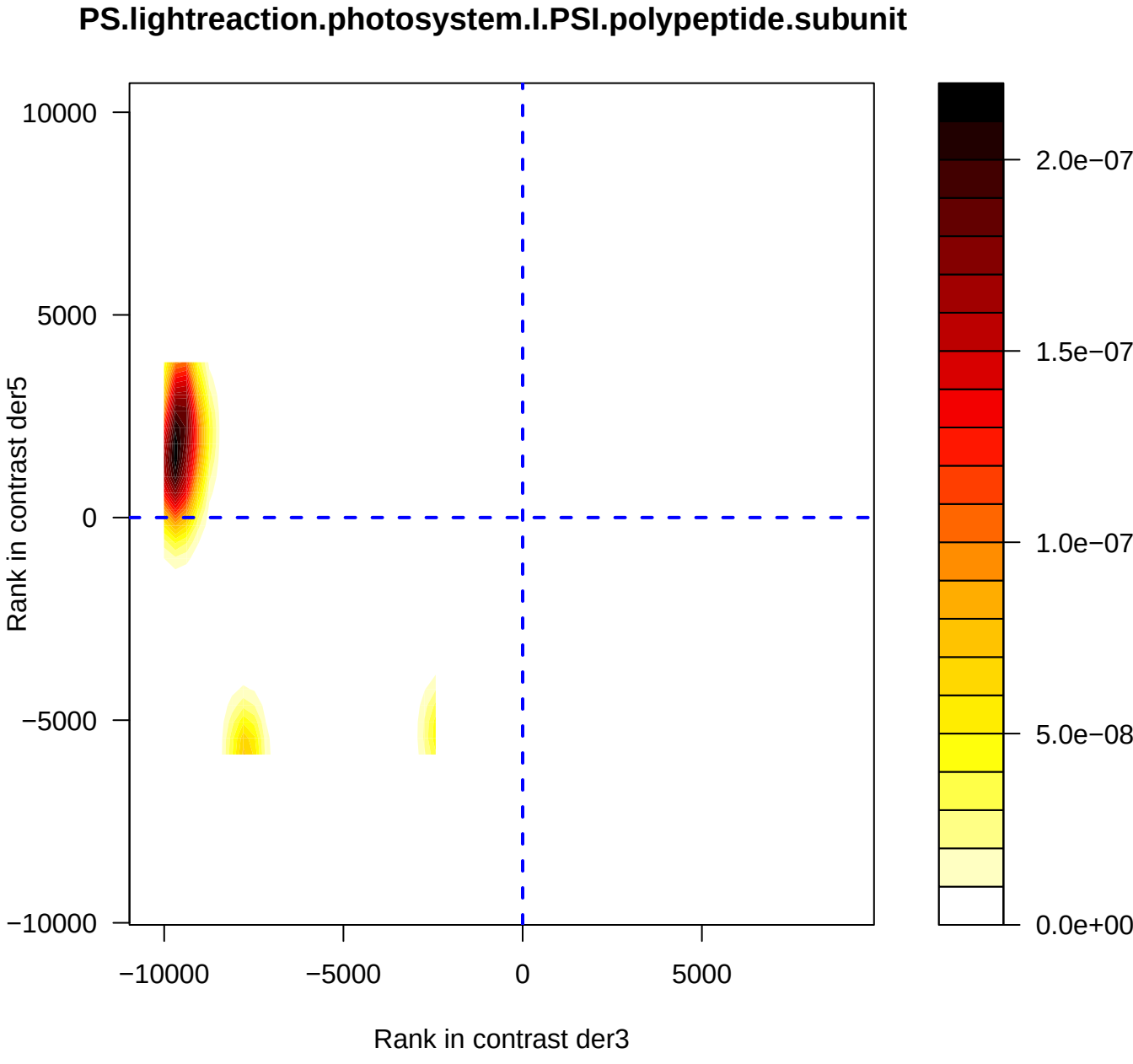

PS.lightreaction.photosystem.II.LHC.II
Rank in contrast der5
Rank in contrast der3
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000

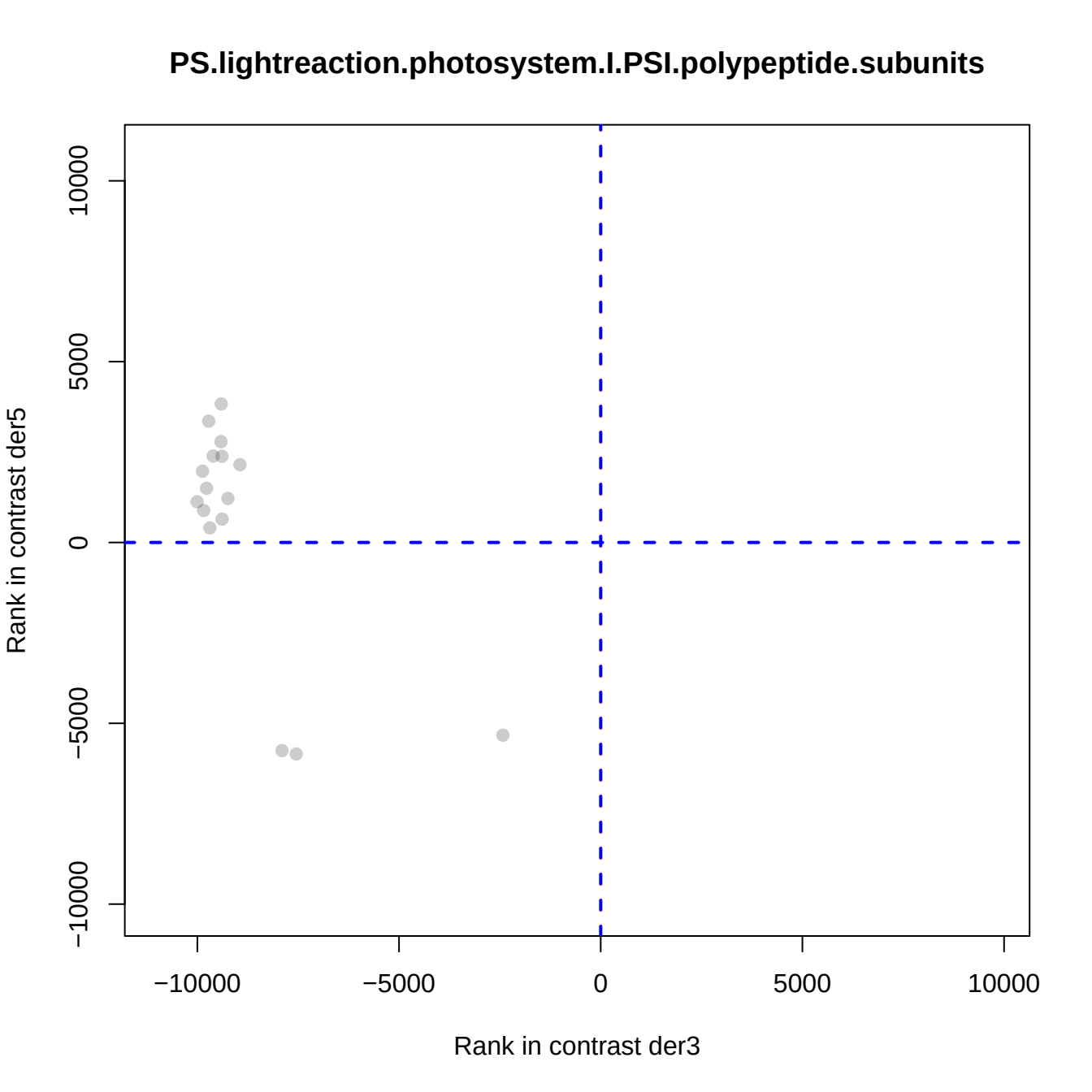

PS.lightreaction.photosystem.II.LHC.II
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2

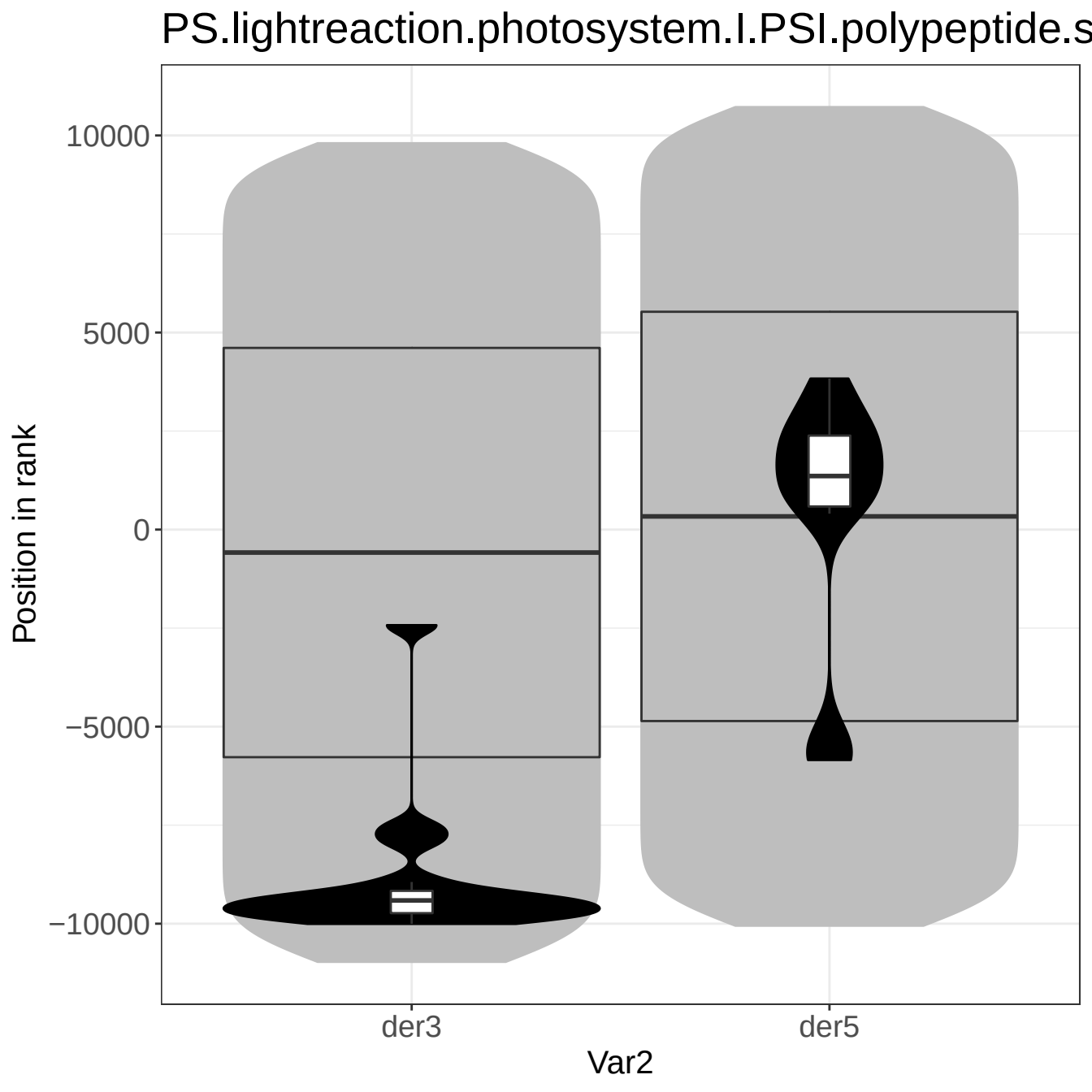

PS.lightreaction.cyclic.electron.flow.chlororespiration
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
1.5e−08
1.0e−08
5.0e−09
0.0e+00


PS.lightreaction.cyclic.electron.flow.chlororespiration
Rank in contrast der5
Rank in contrast der3
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000


PS.lightreaction.cyclic.electron.flow.chlororespira
10000
5000
0
−5000
−10000
Position in rank
der3
der5
Var2


PS.lightreaction.photosystem.I.PSI.polypeptide.subunit
10000
5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
0
5000
Rank in contrast der3
2.0e−07
1.5e−07
1.0e−07
5.0e−08
0.0e+00


PS.lightreaction.photosystem.I.PSI.polypeptide.subunits
Rank in contrast der5
10000
5000
0
−5000
−10000
−10000
−5000
0
5000
10000
Rank in contrast der3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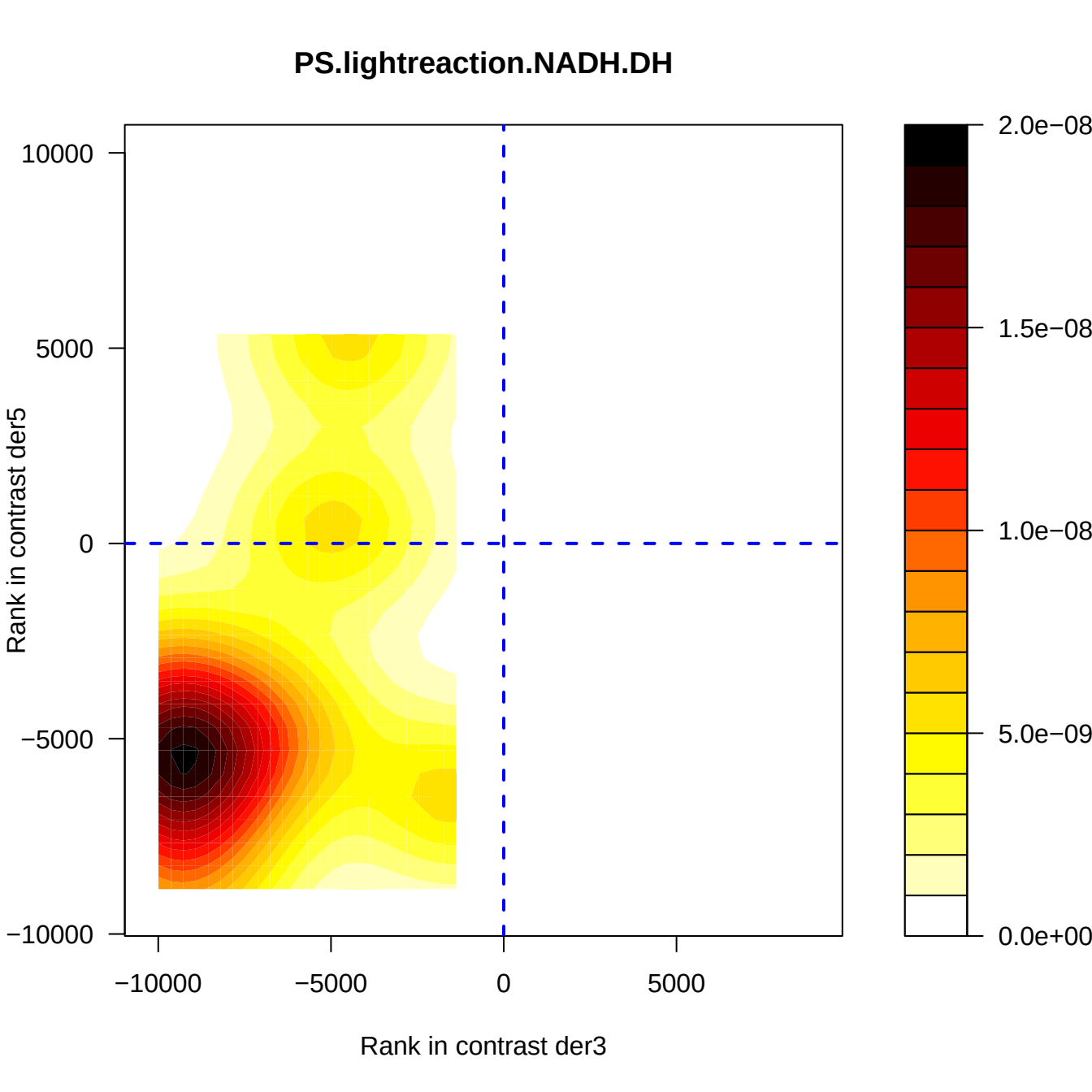
Position in rank
der3
der5
Var2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Rank in contrast der3
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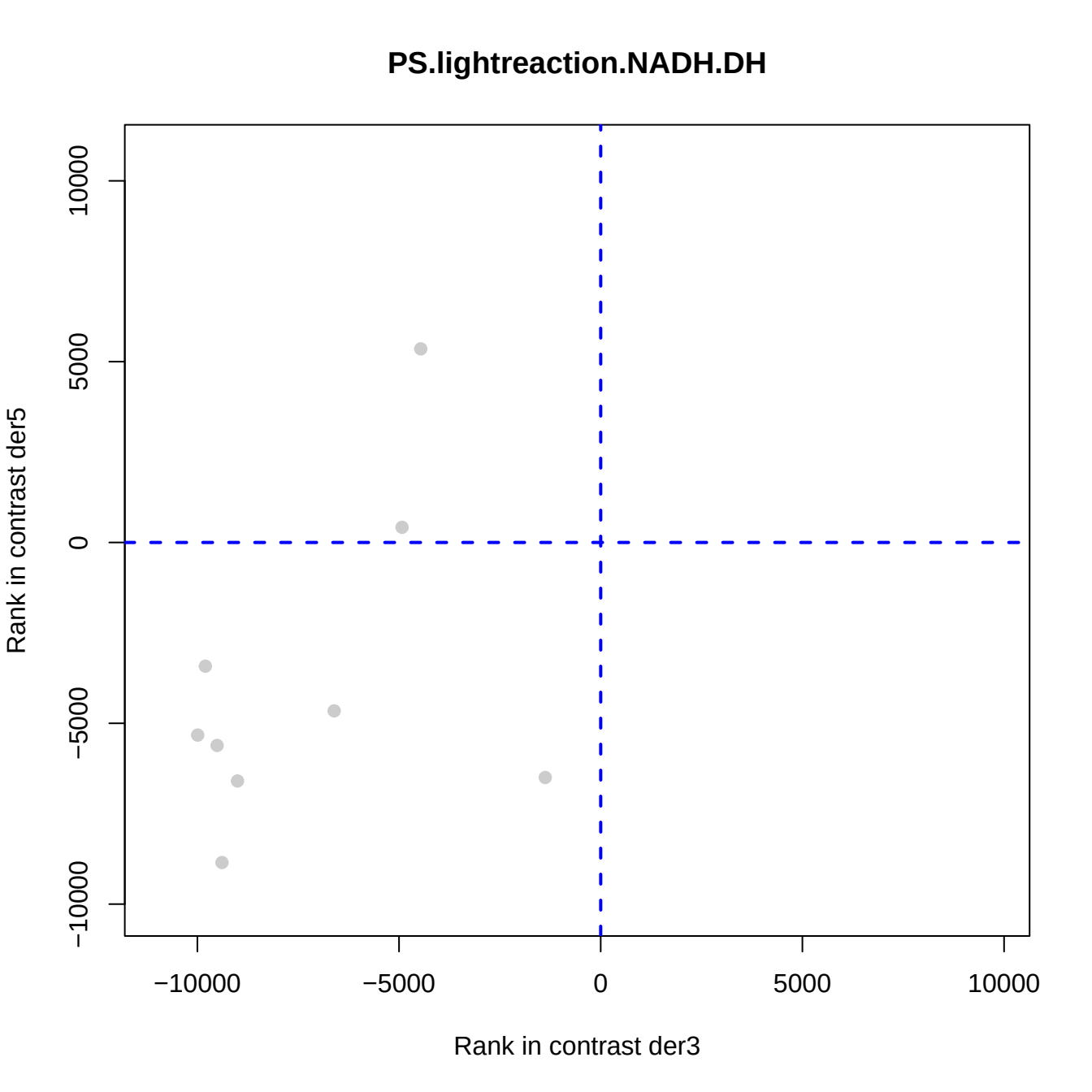
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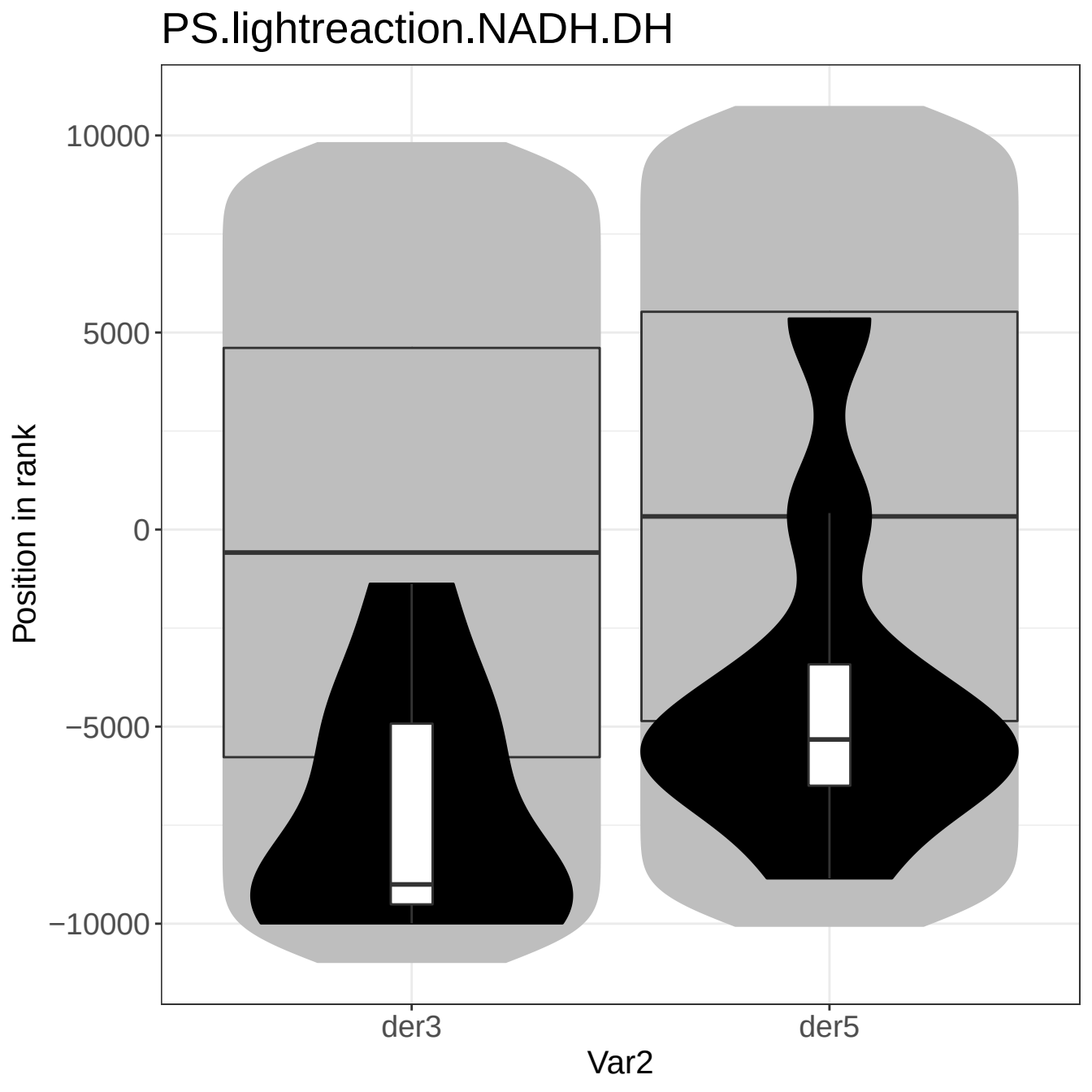
Rank in contrast der3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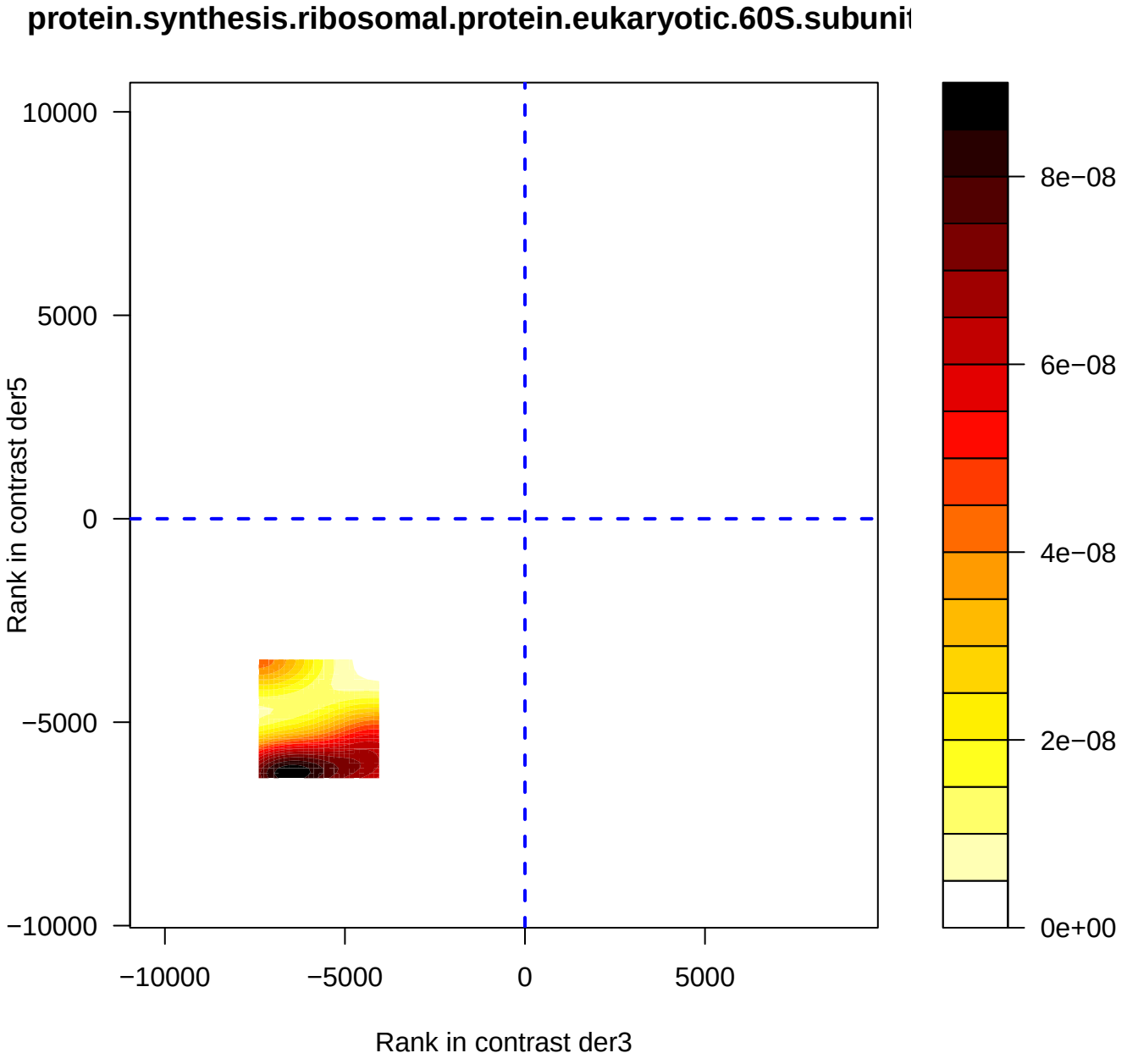
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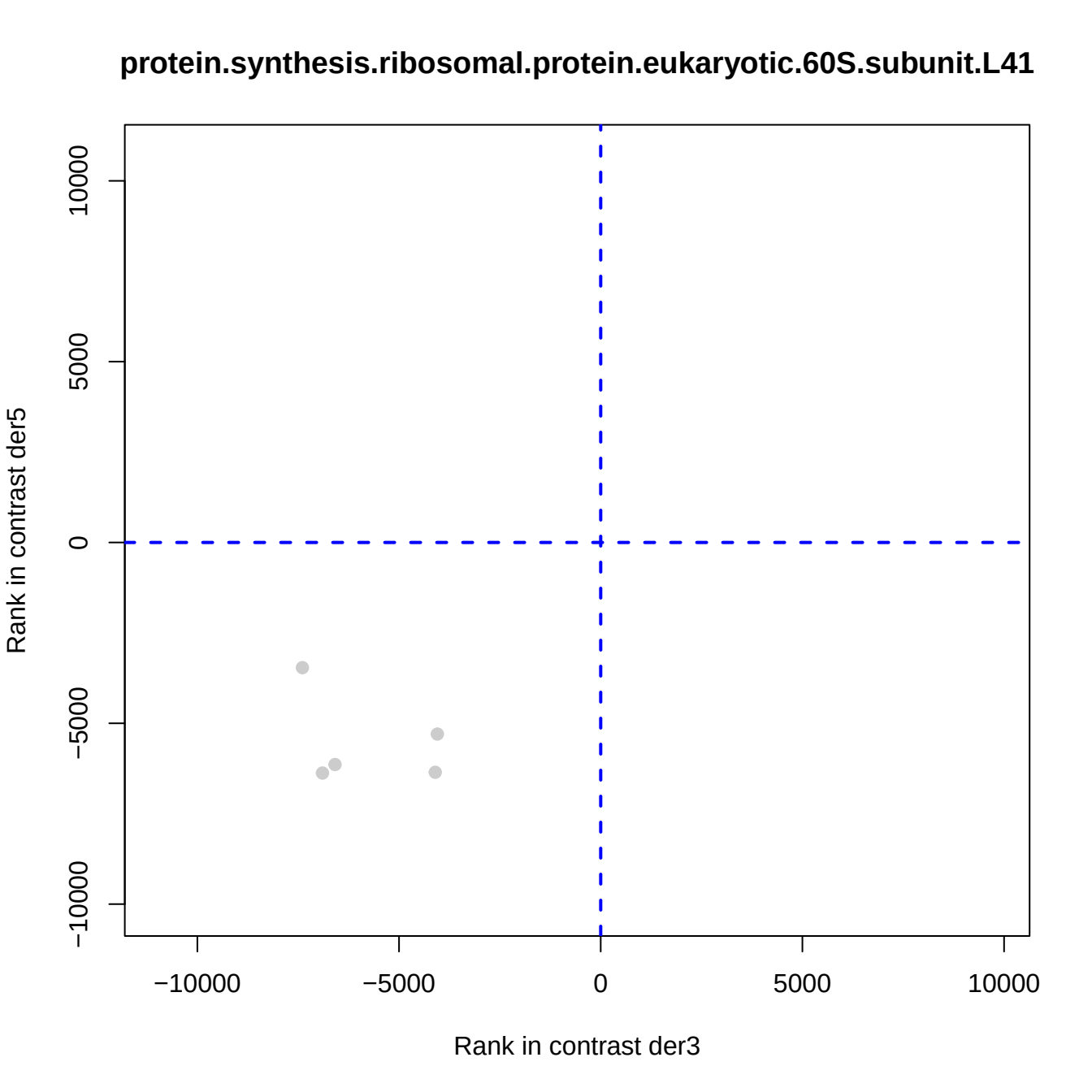
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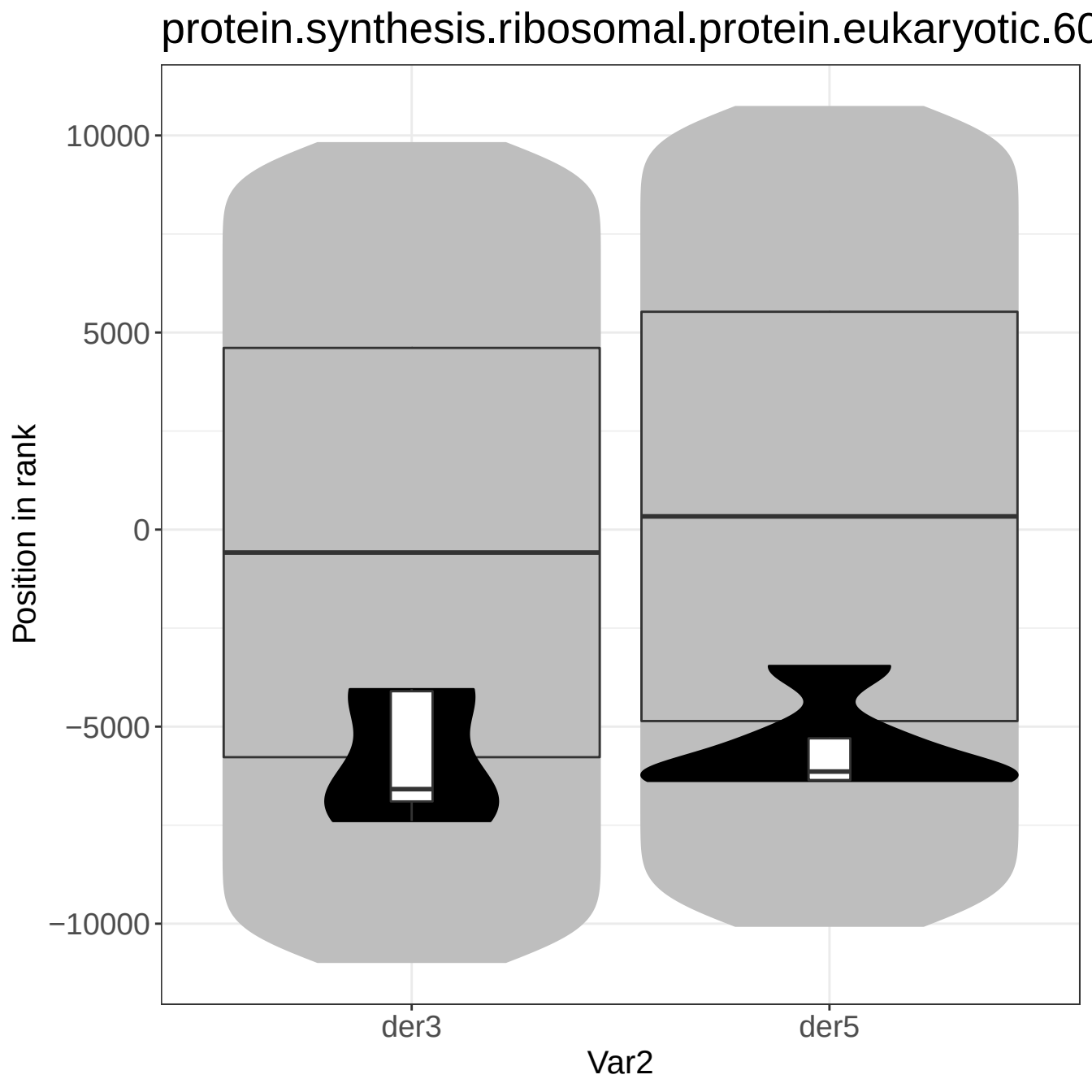
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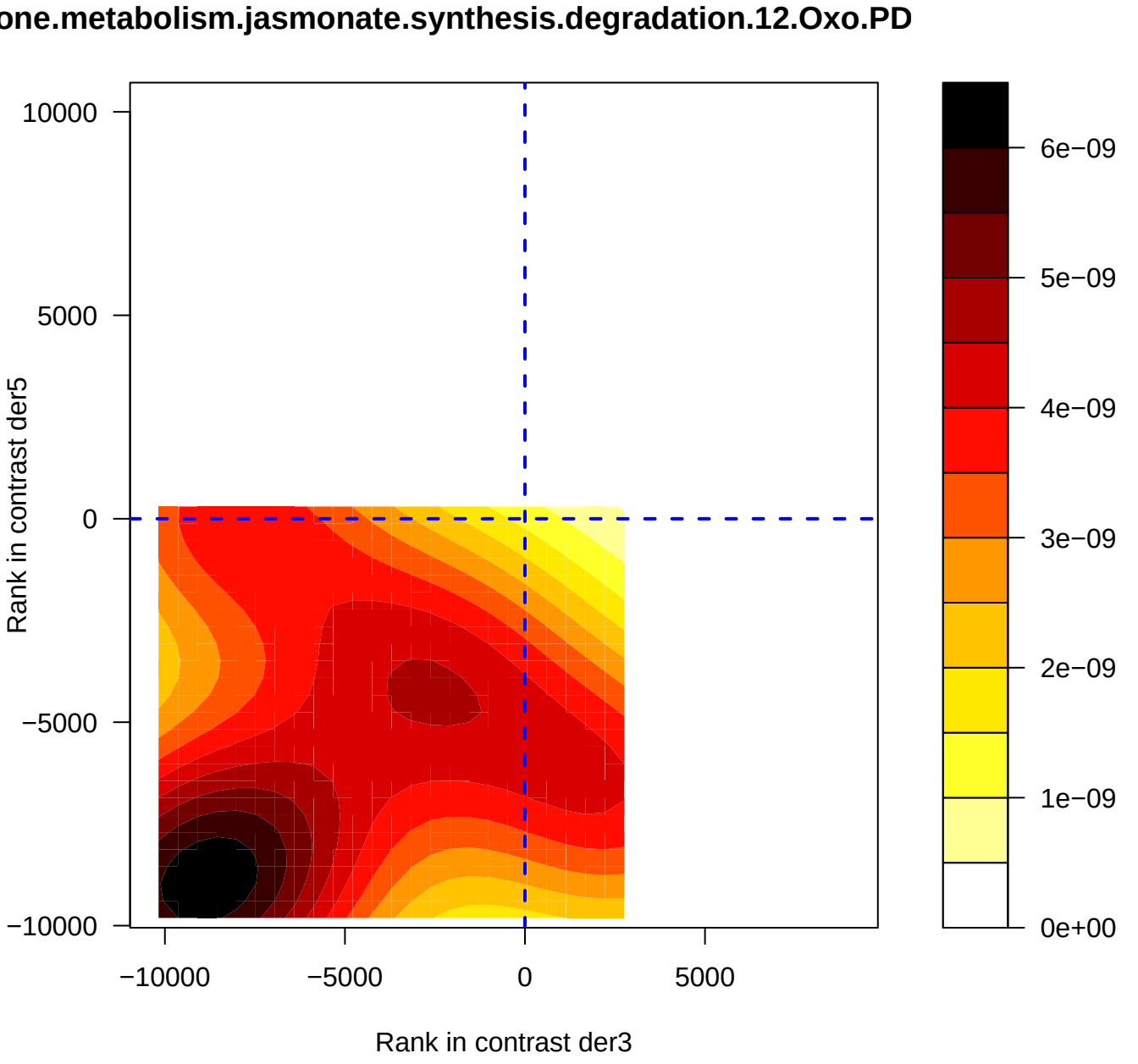
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Rank in contrast der3
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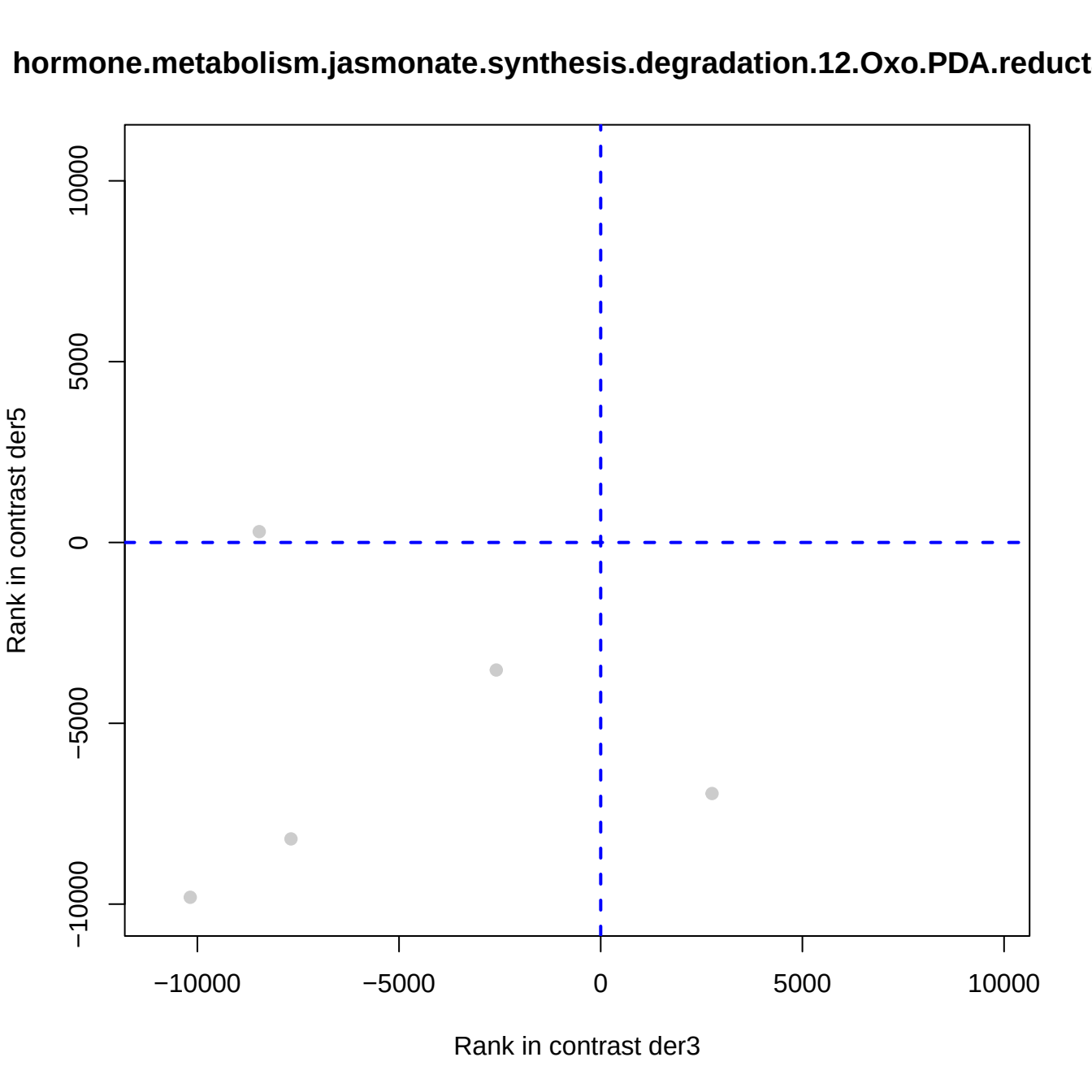
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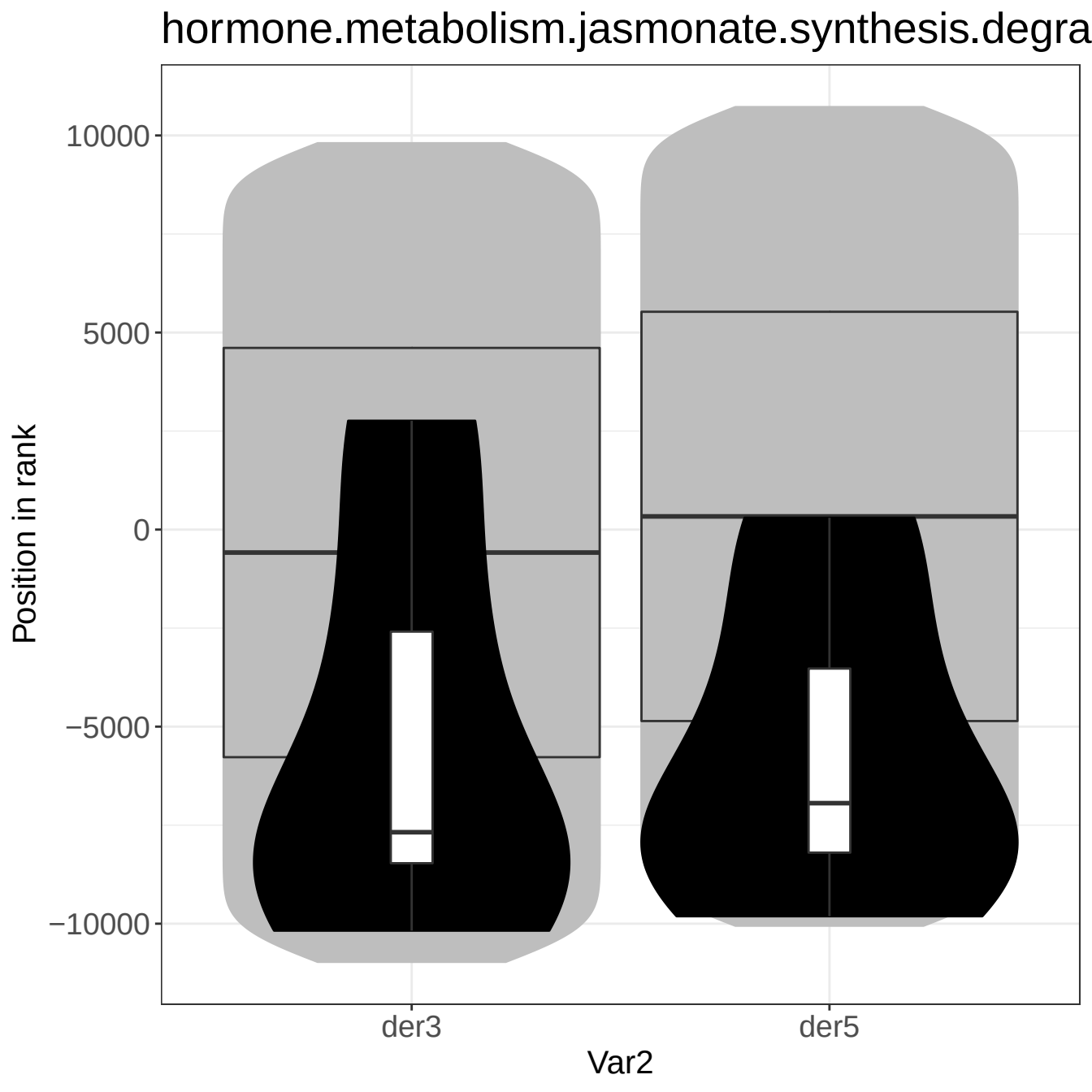
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Position in rank
der3
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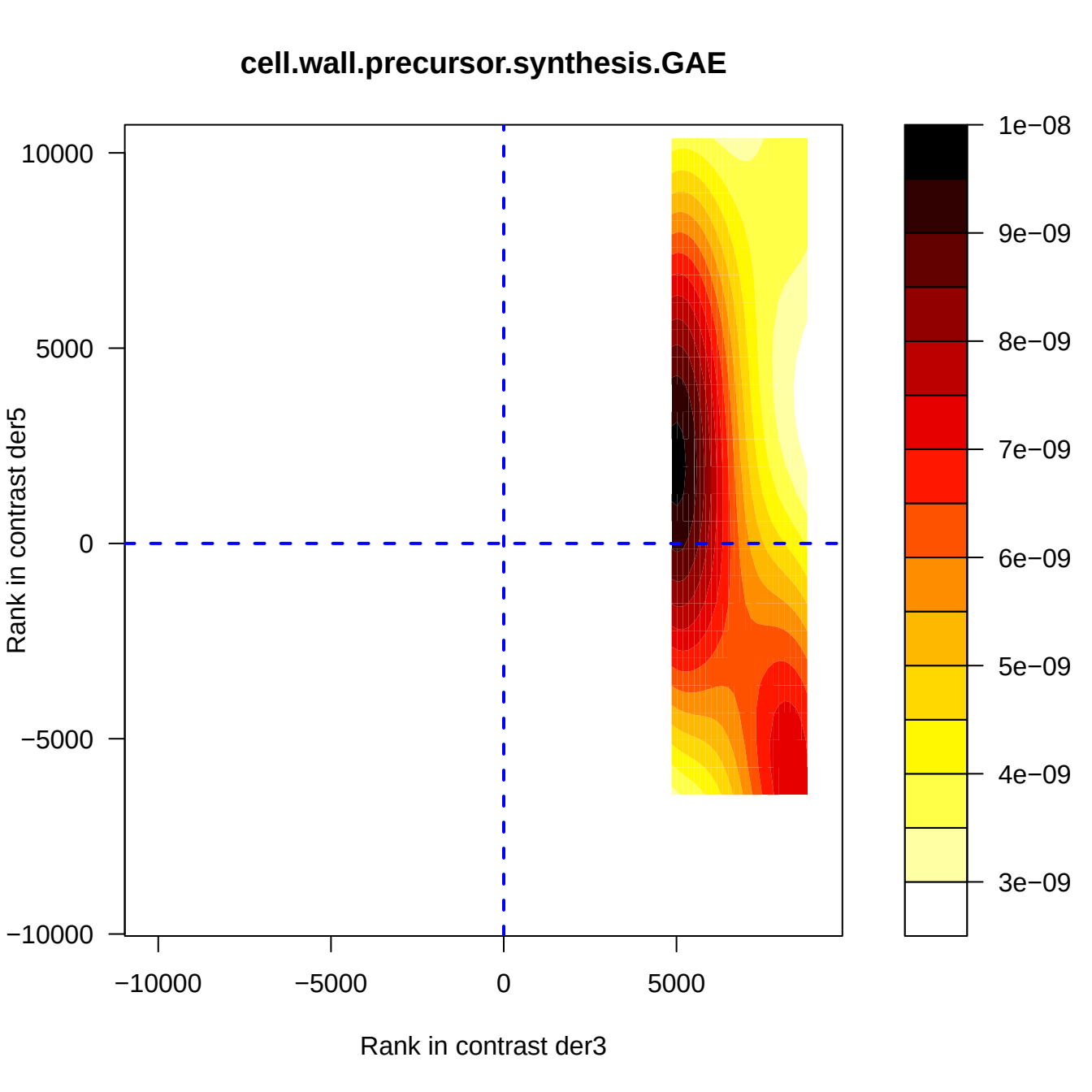
Var2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9e−09
8e−09
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6e−09
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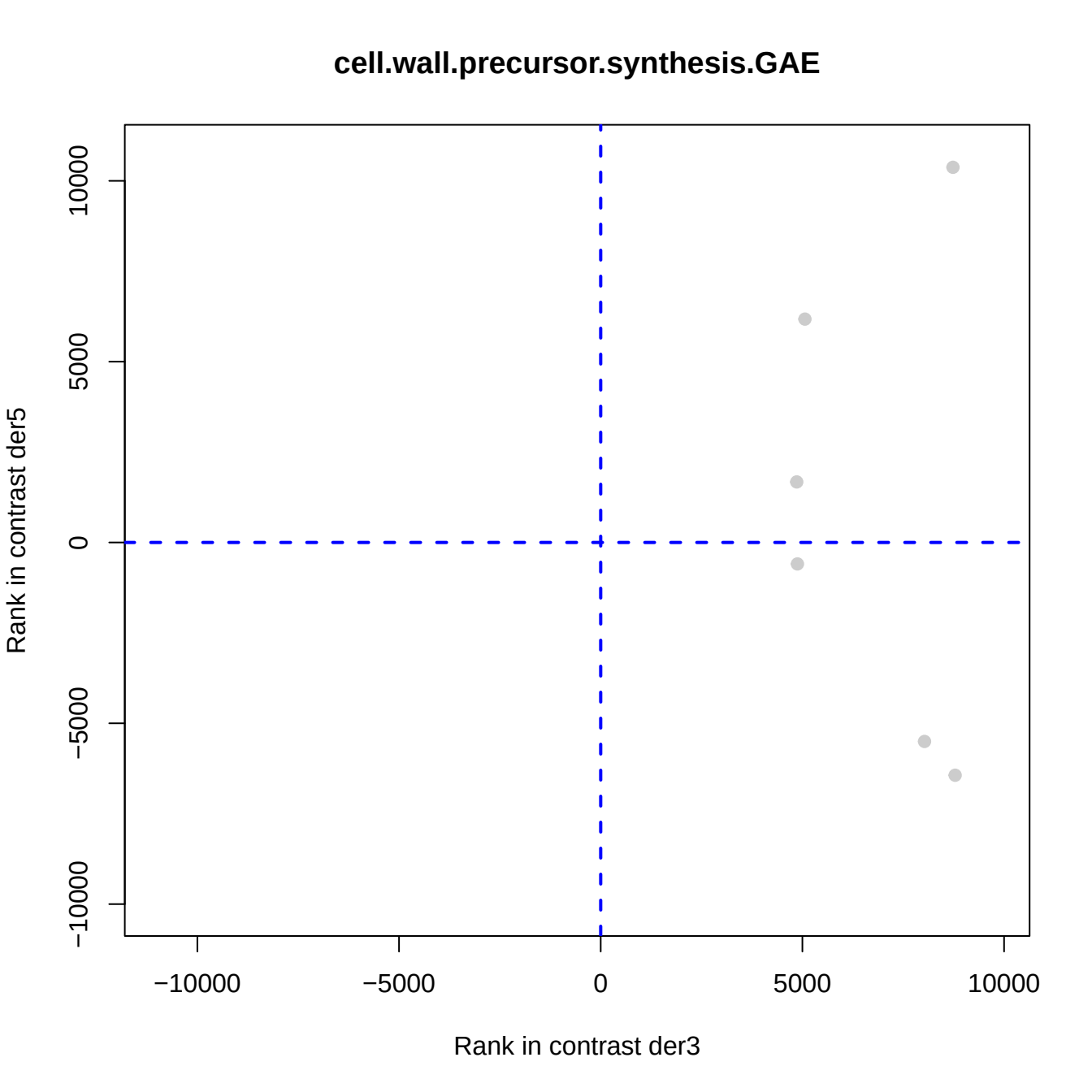
4e−09
3e−09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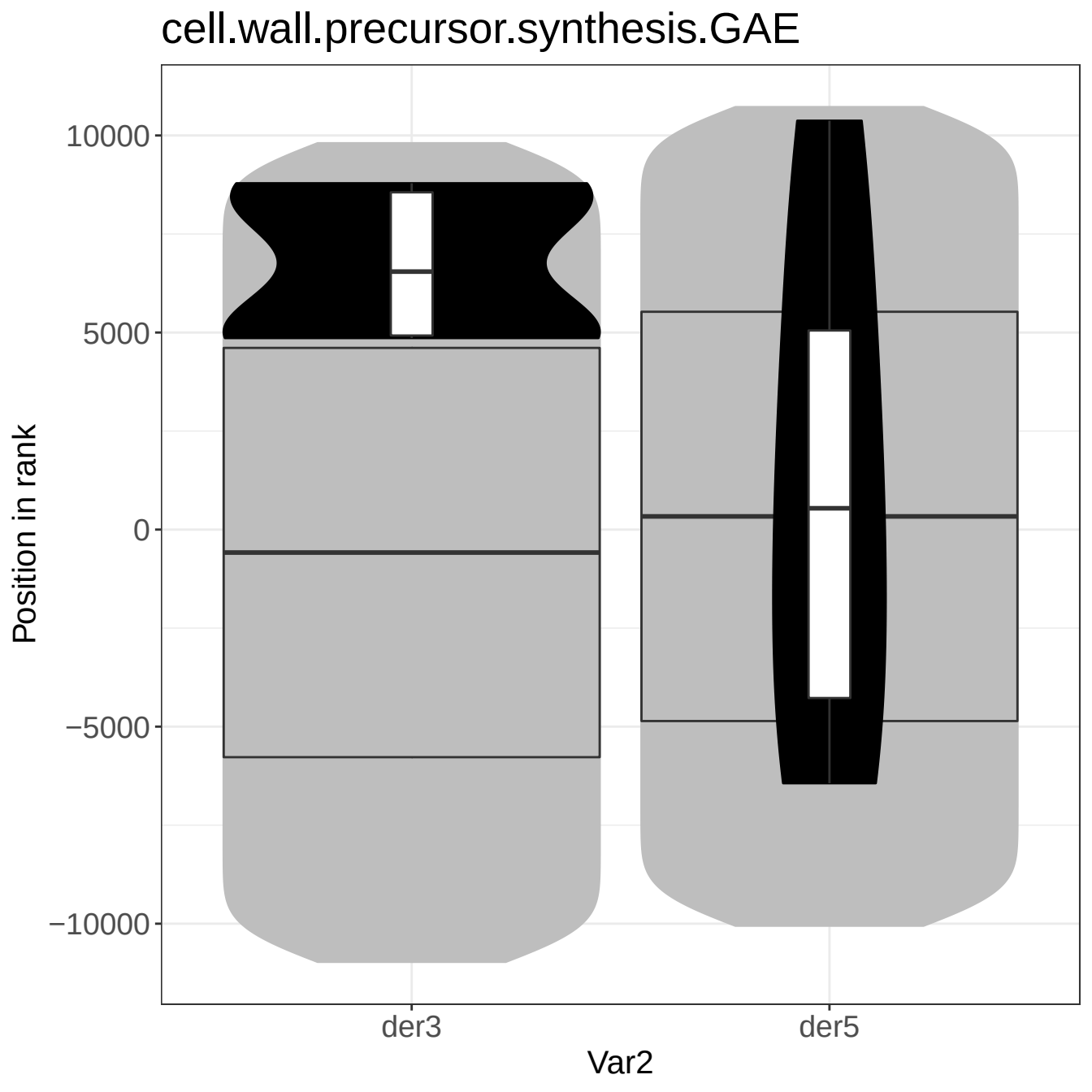
Rank in contrast der3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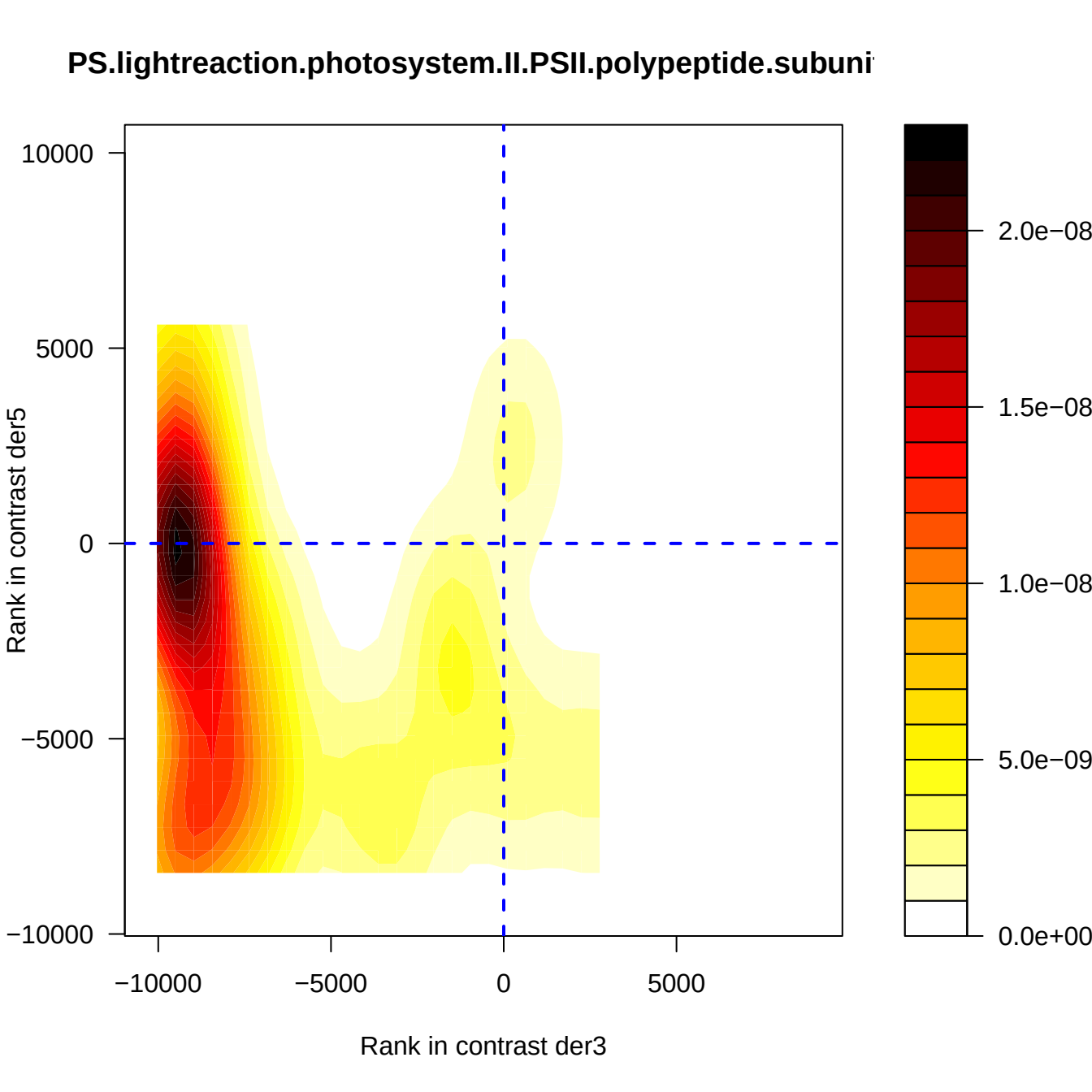
Position in rank
der3
der5
Var2


PS.lightreaction.photosystem.II.PSII.polypeptide.subuni
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Rank in contrast der5
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Rank in contrast der3
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1.5e−08
1.0e−08
5.0e−09
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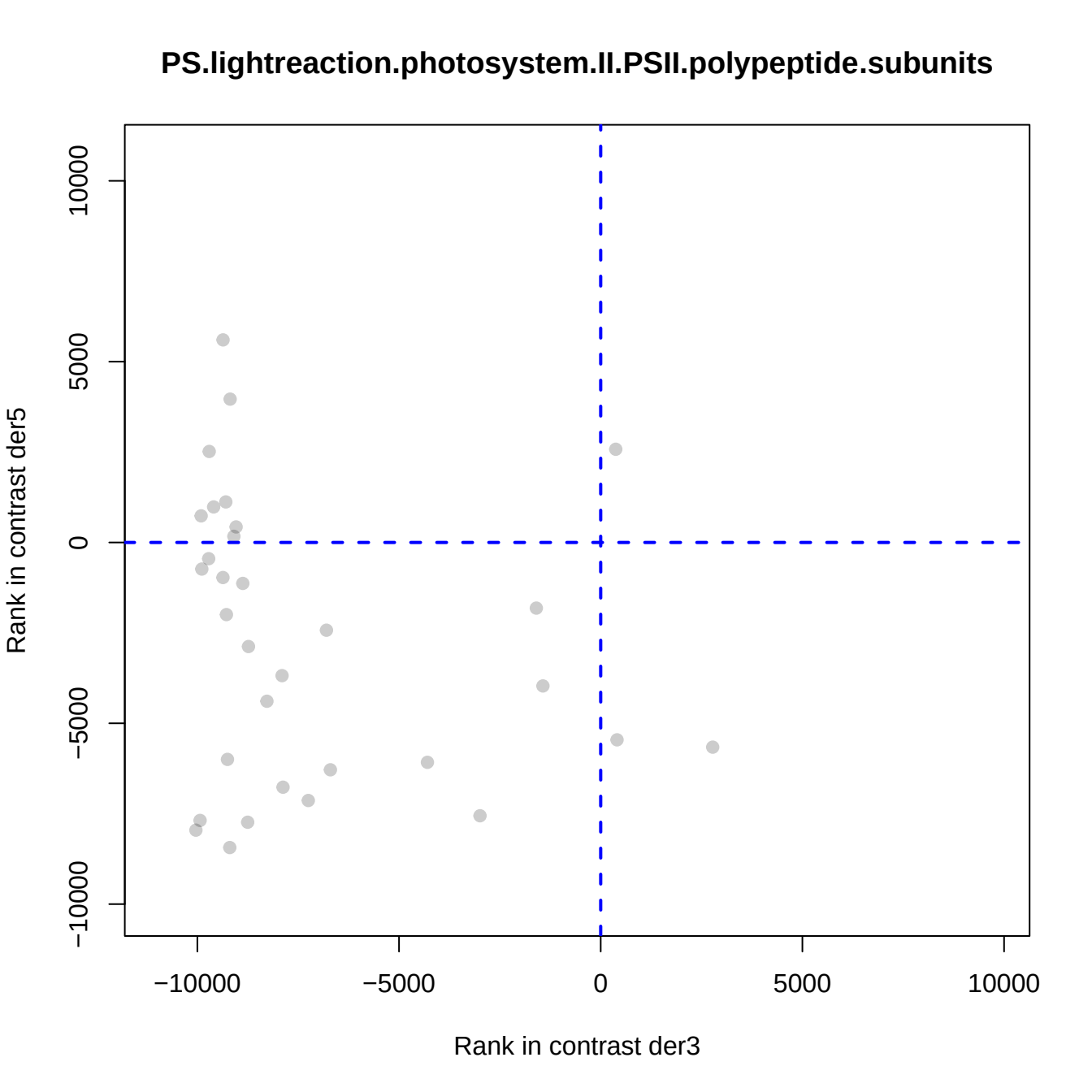
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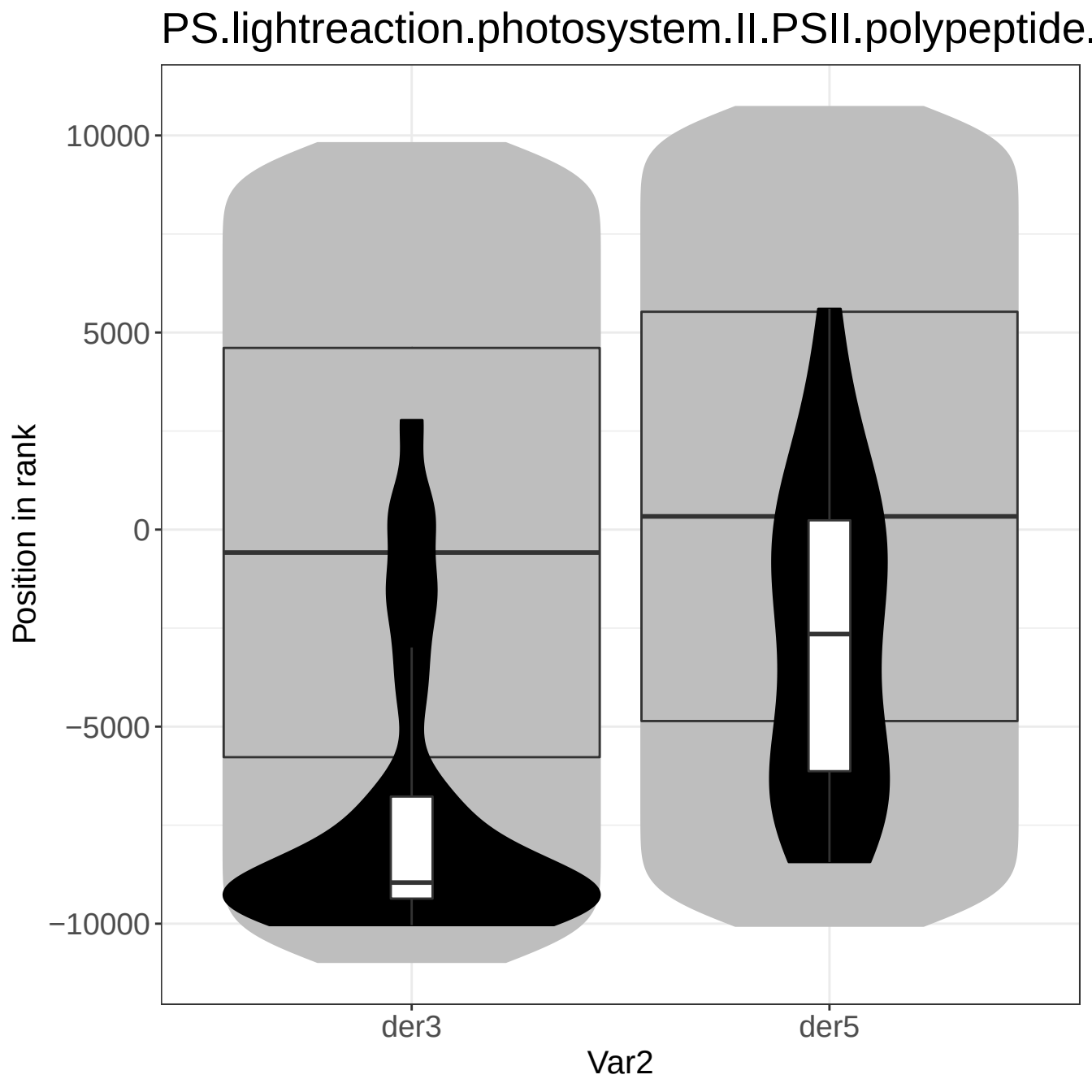
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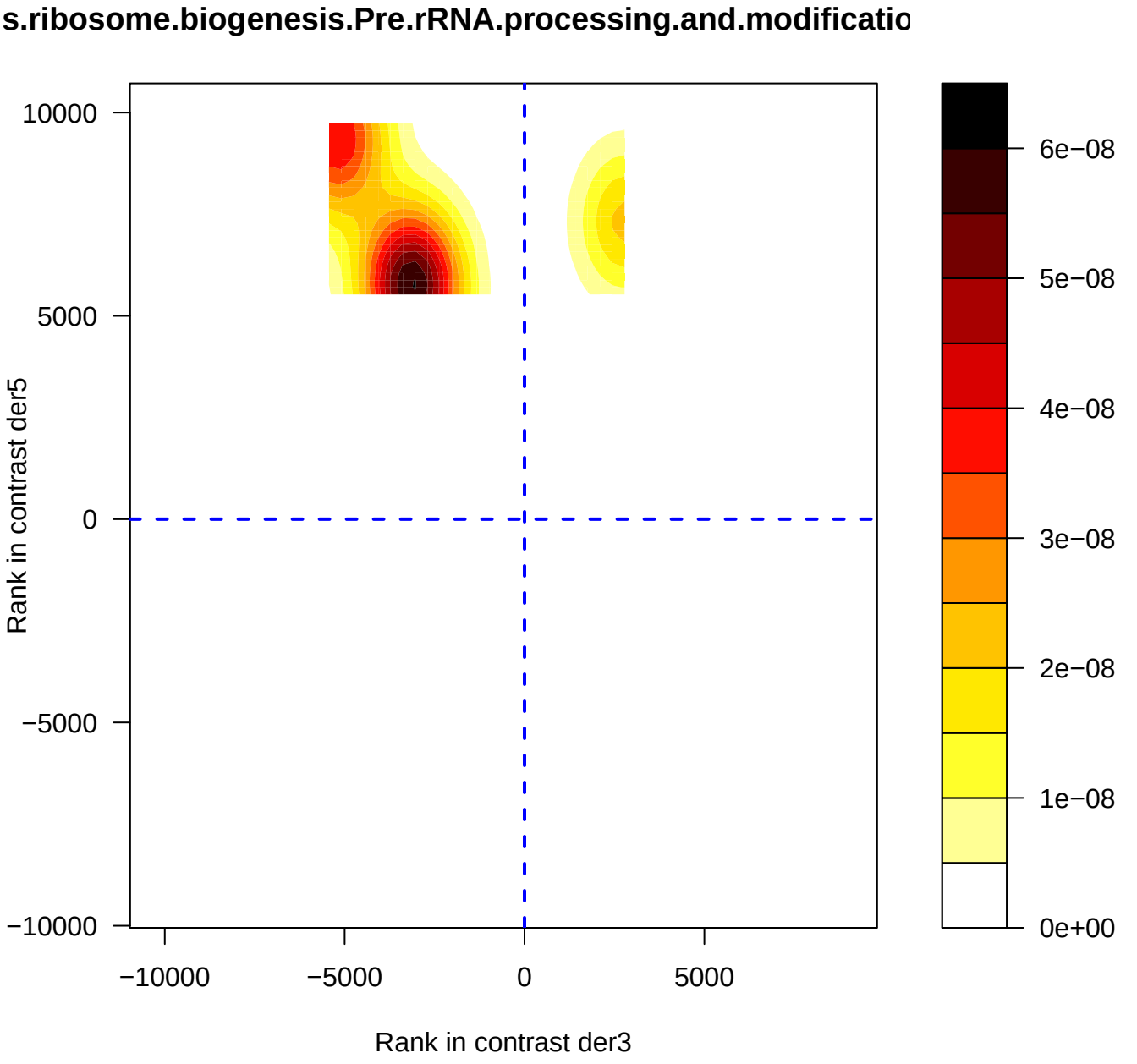
Position in rank
der3
der5
Var2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Rank in contrast der3
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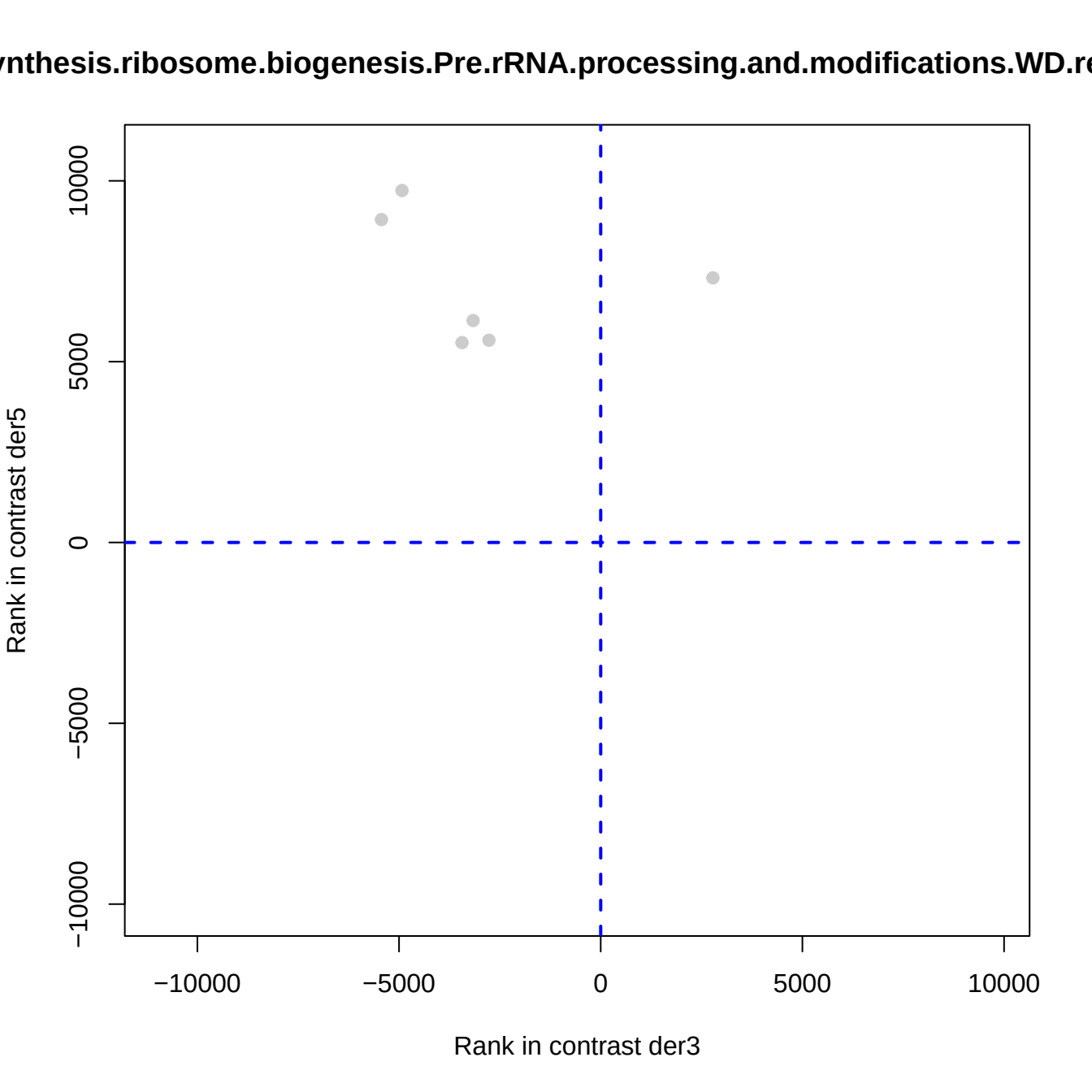
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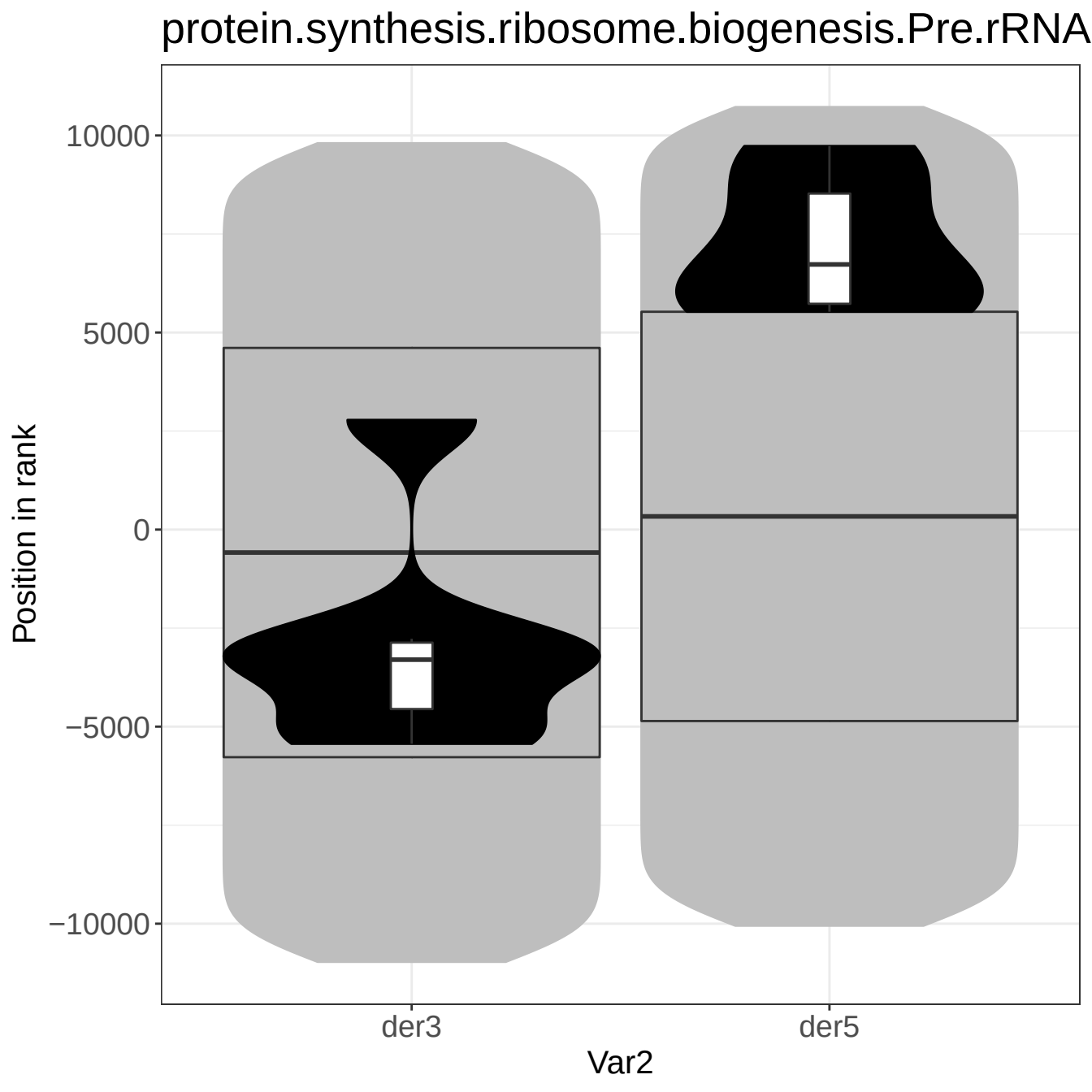
Rank in contrast der3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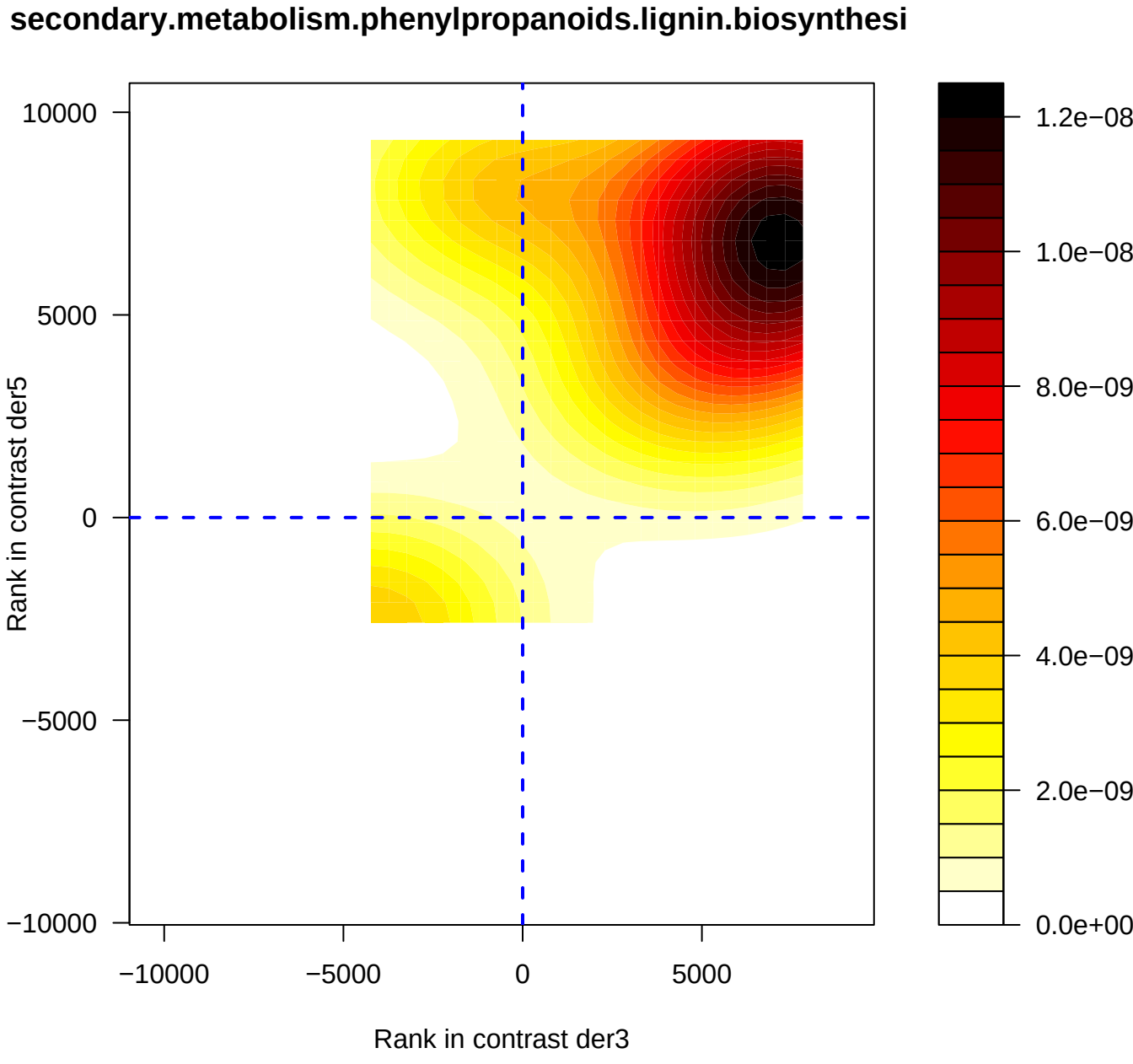
Position in rank
der3
der5
Var2


secondary.metabolism.phenylpropanoids.lignin.biosynthesi
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Rank in contrast der5
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5000
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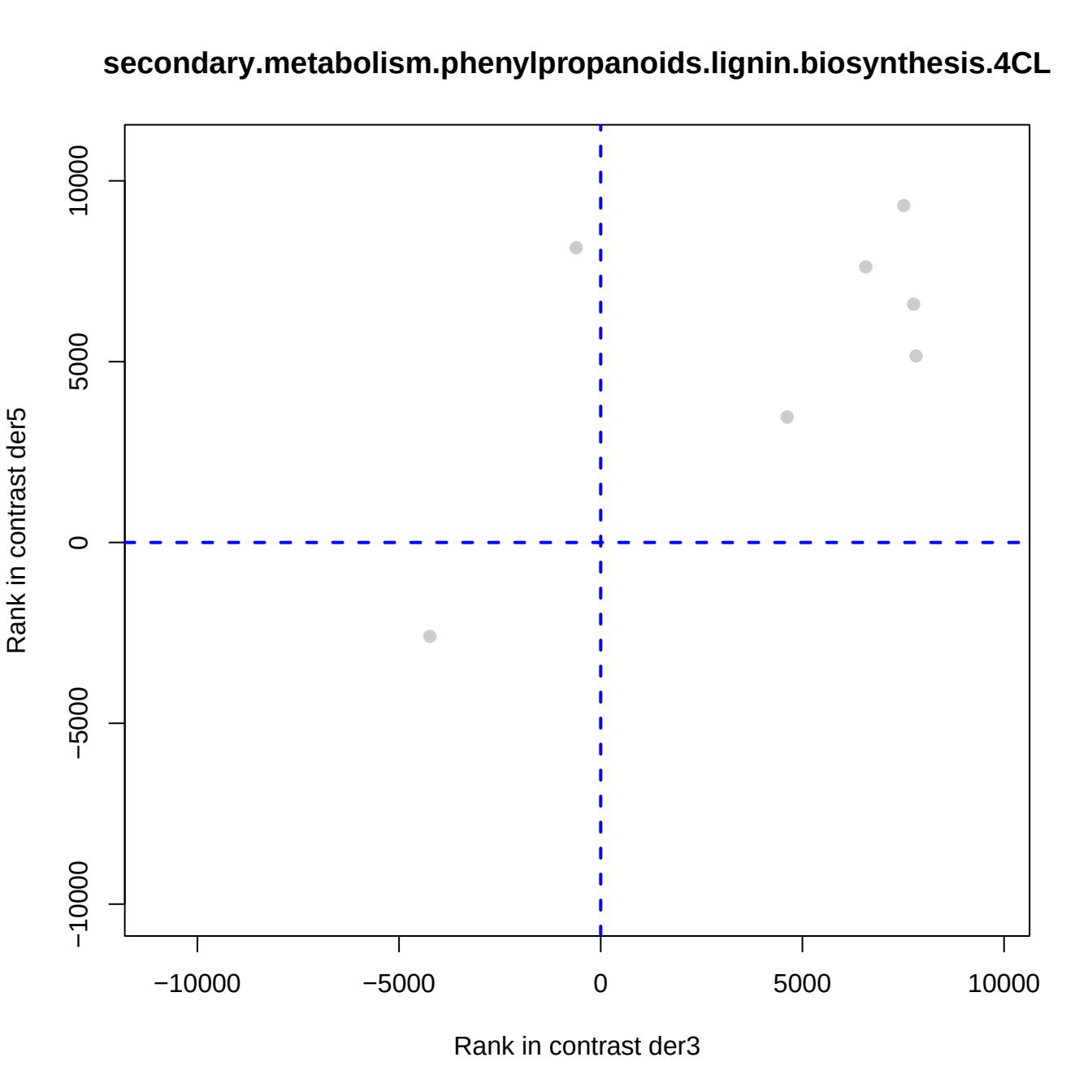
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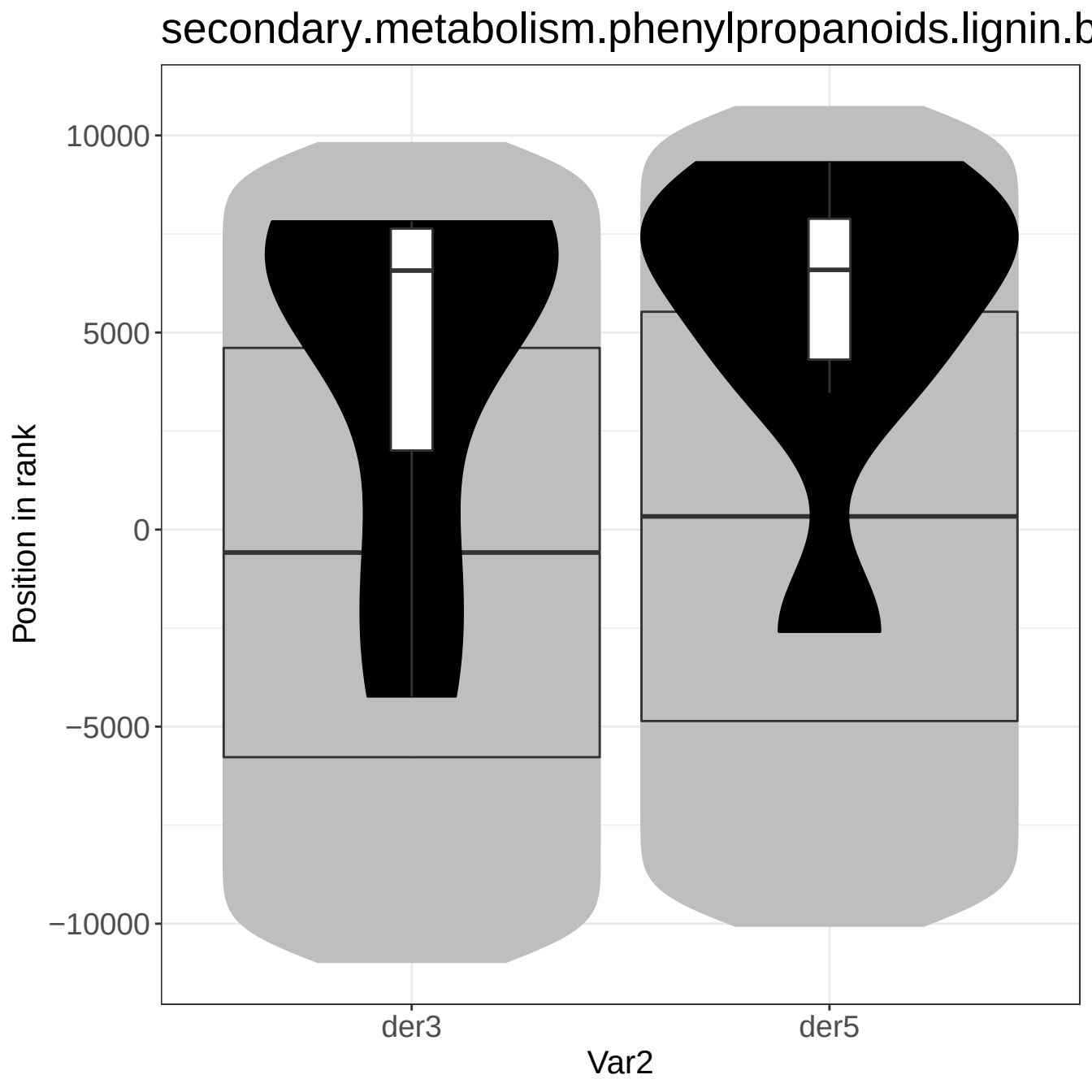
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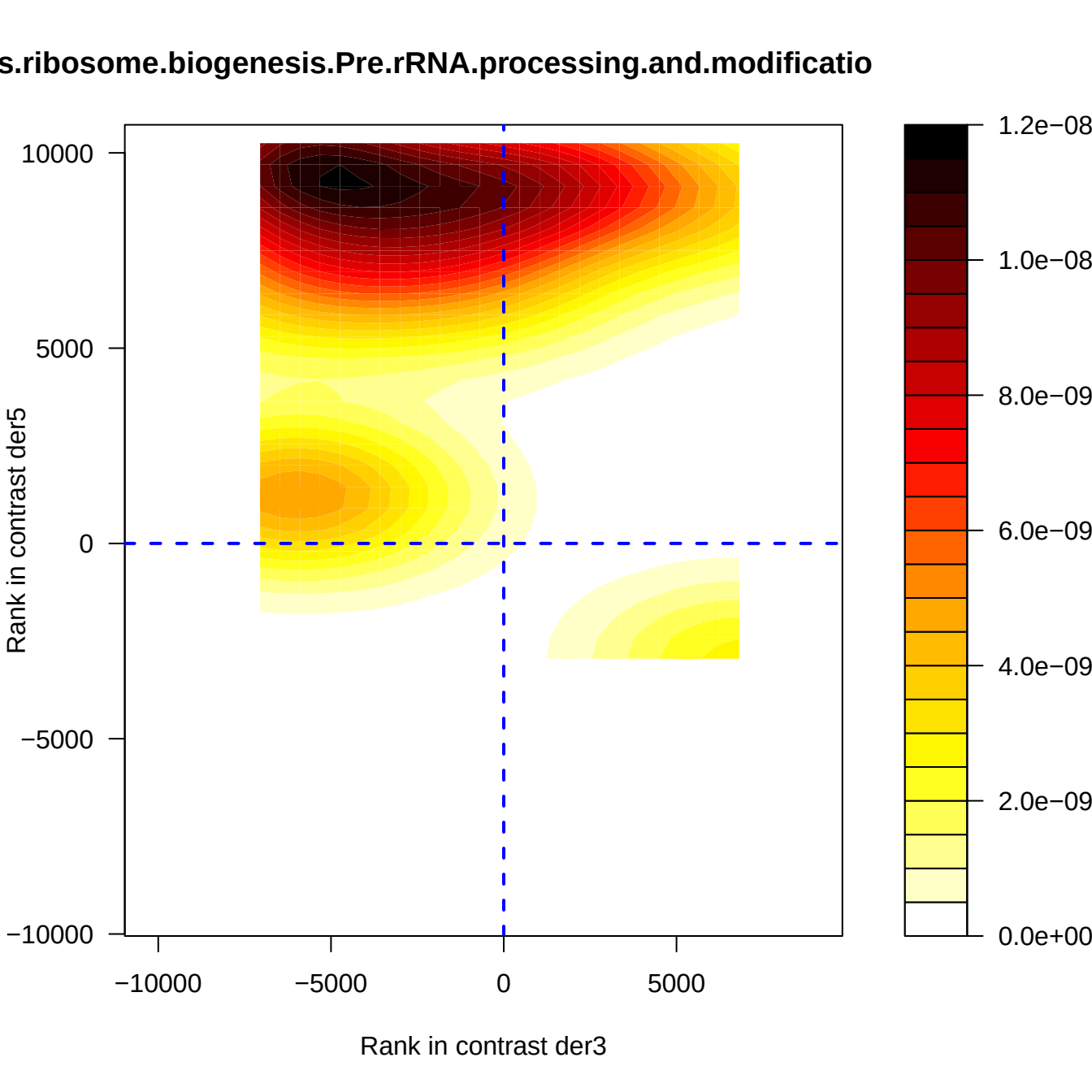
Position in rank
der3
der5
Var2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4.0e−09
2.0e−09
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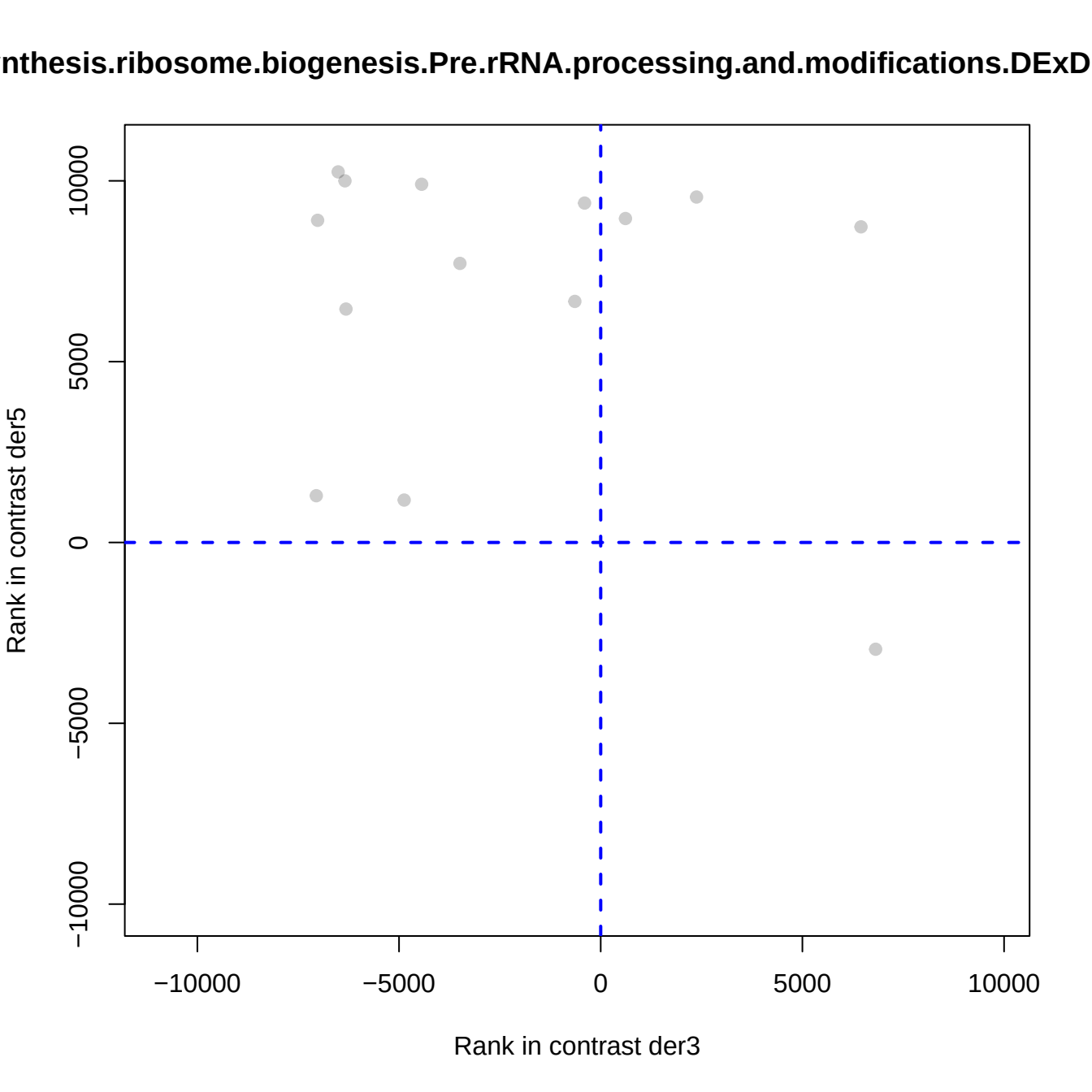
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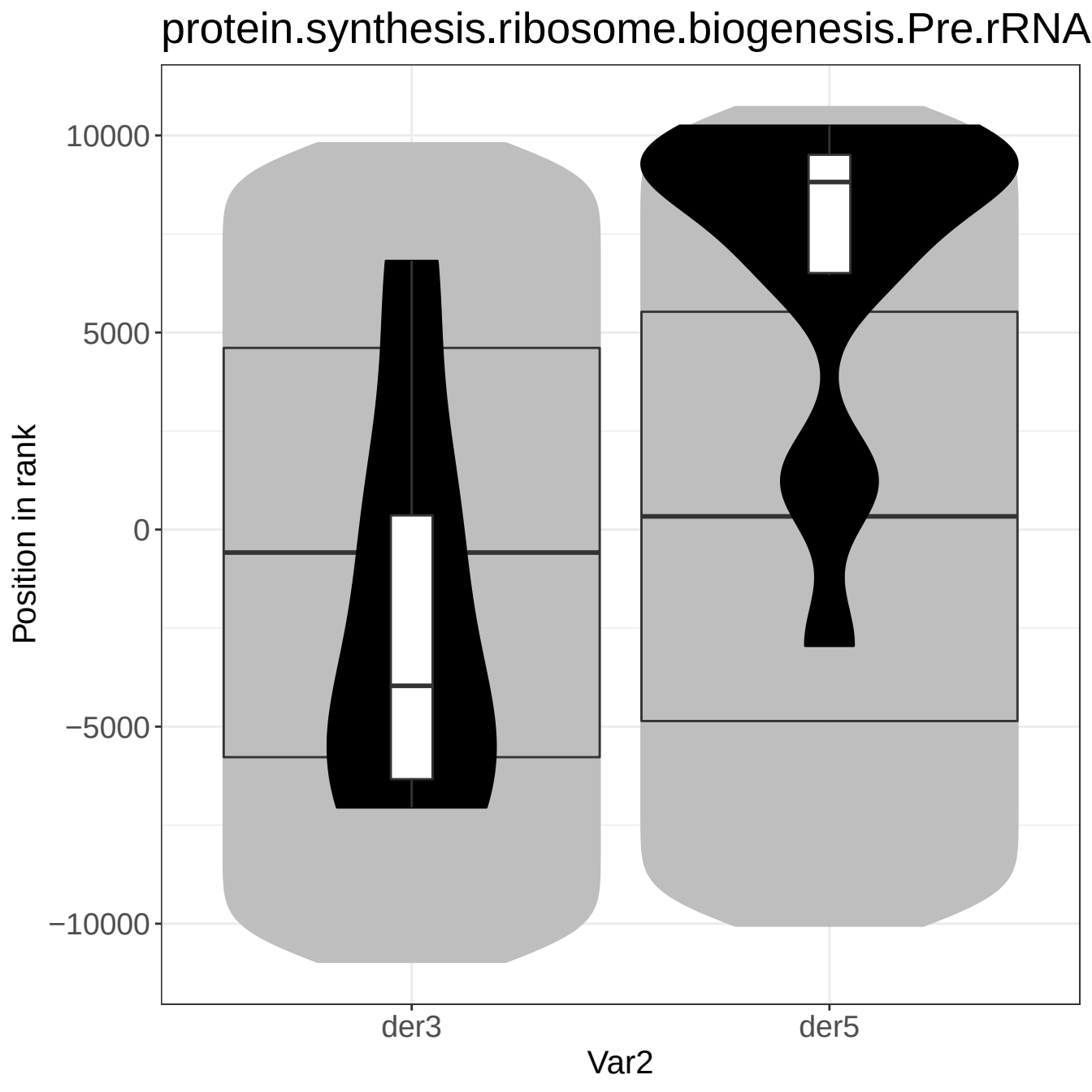
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Position in rank
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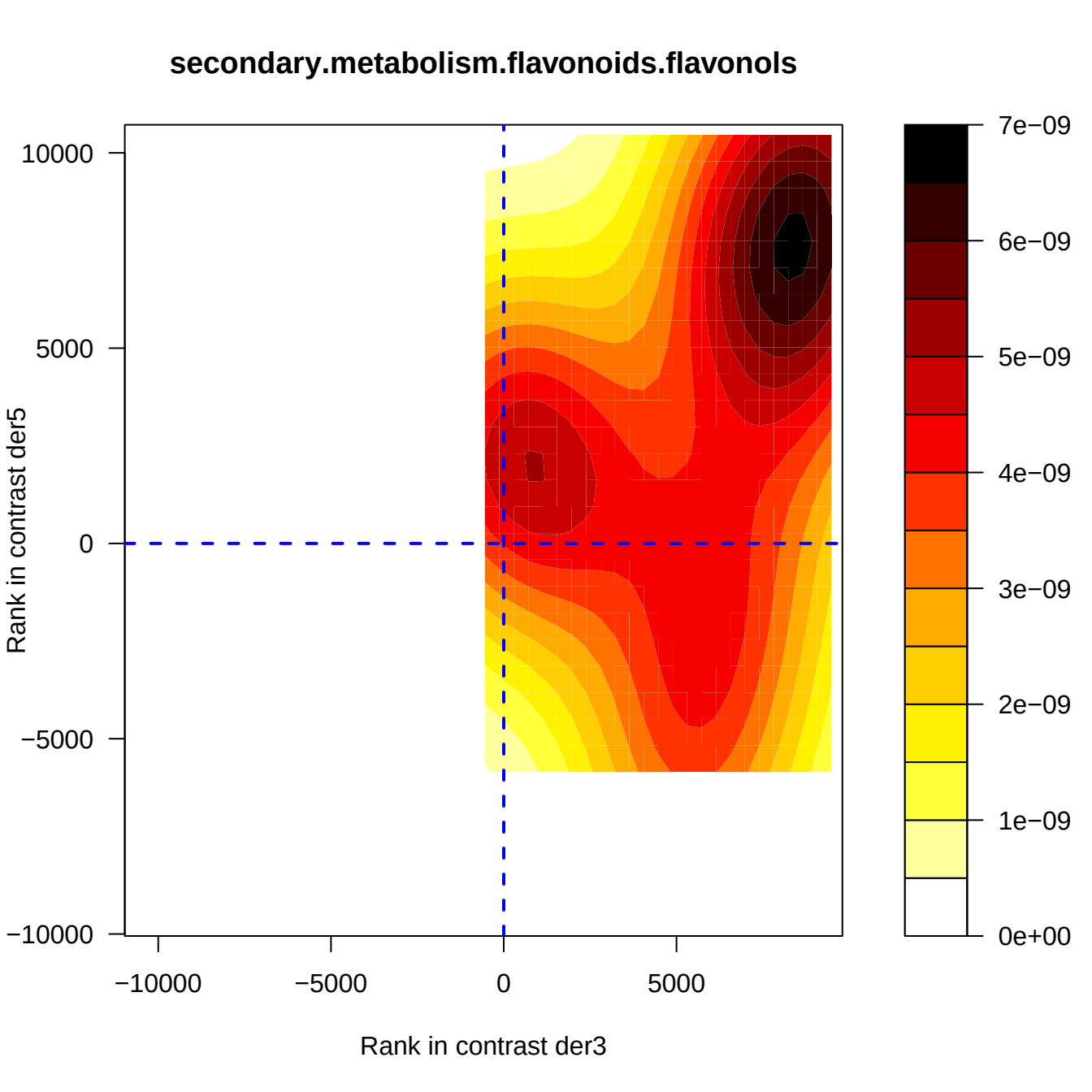
Var2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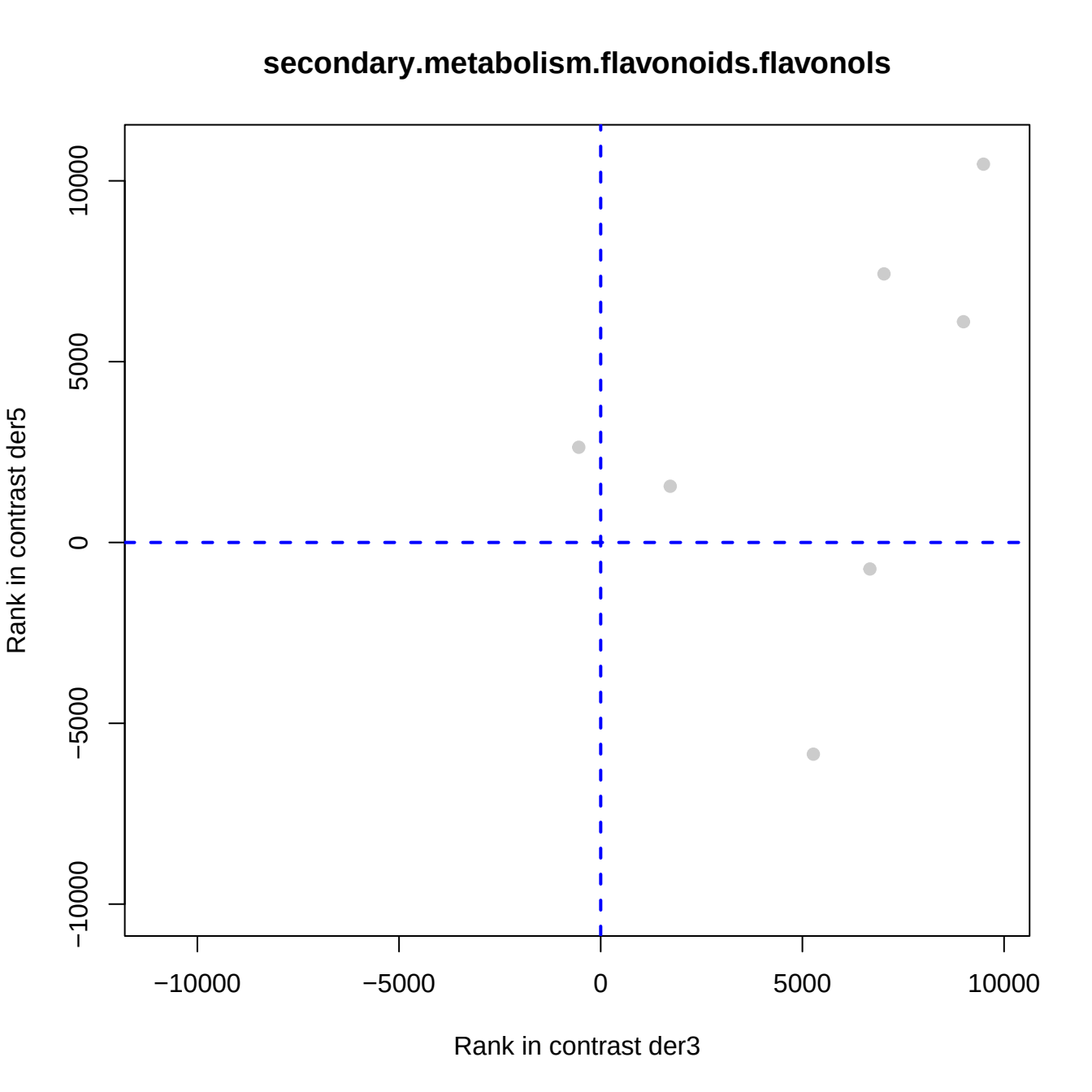
secondary.metabolism.flavonoids.flavonols
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Rank in contrast der3
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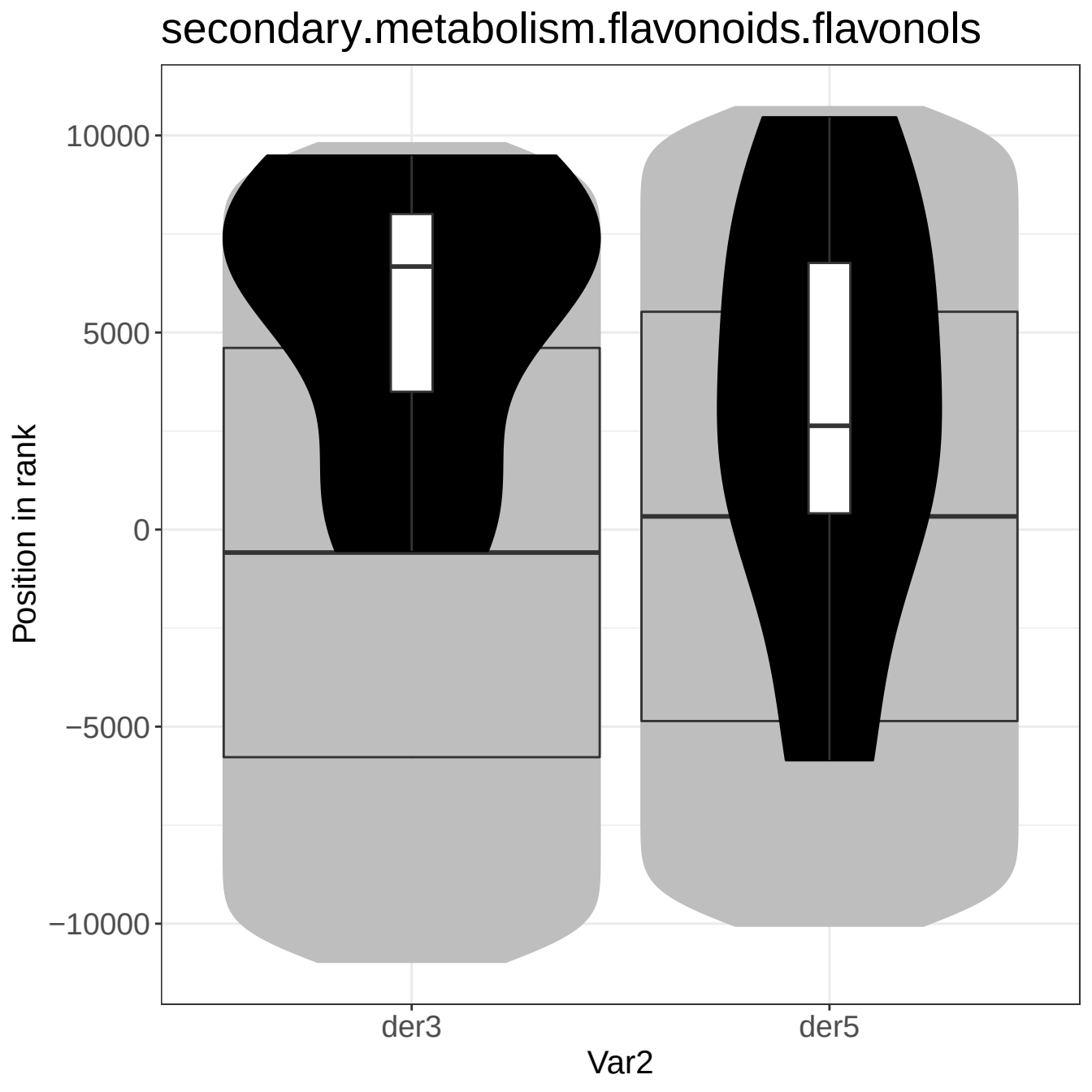
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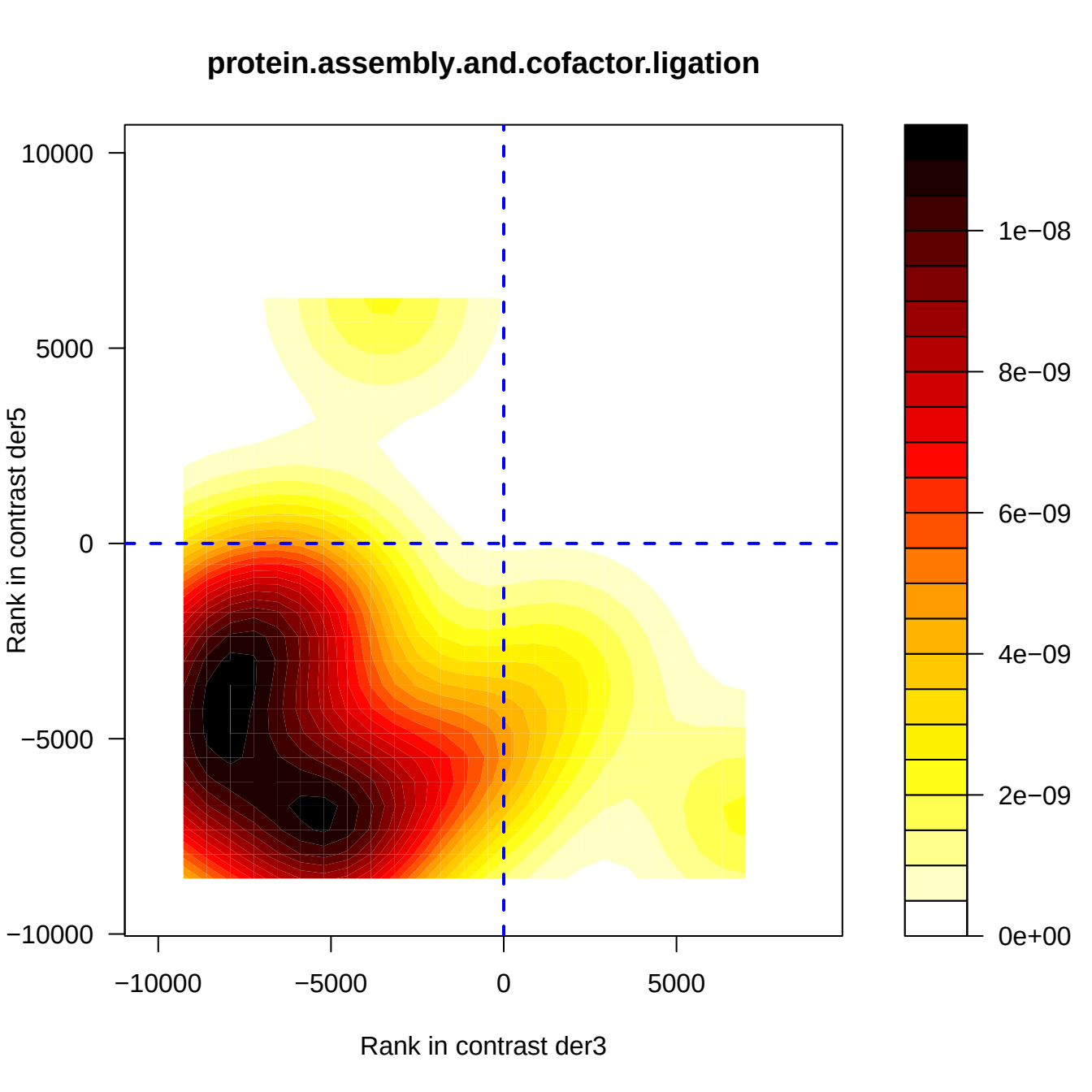
Position in rank
der3
der5
Var2


protein.assembly.and.cofactor.ligation
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Rank in contrast der3
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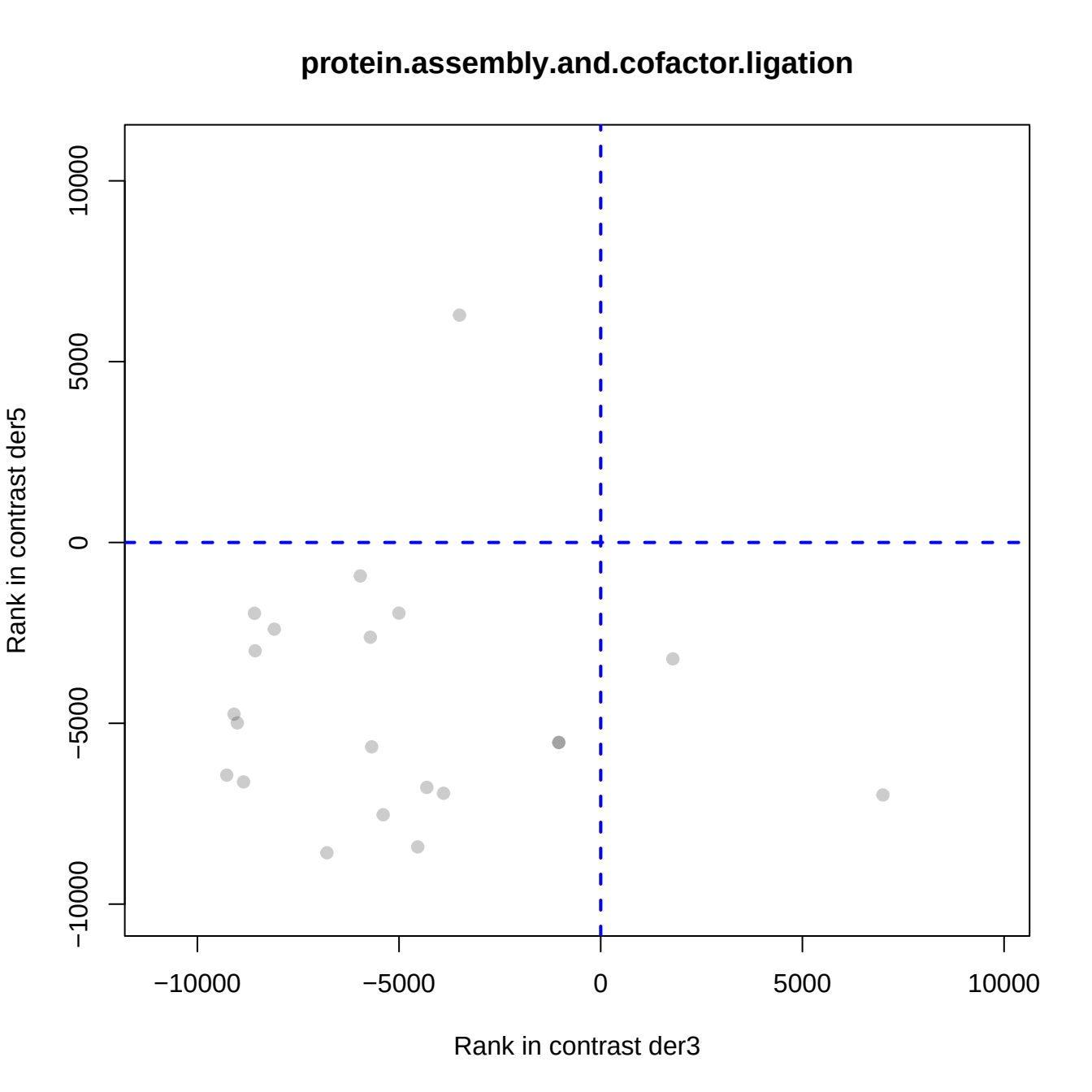
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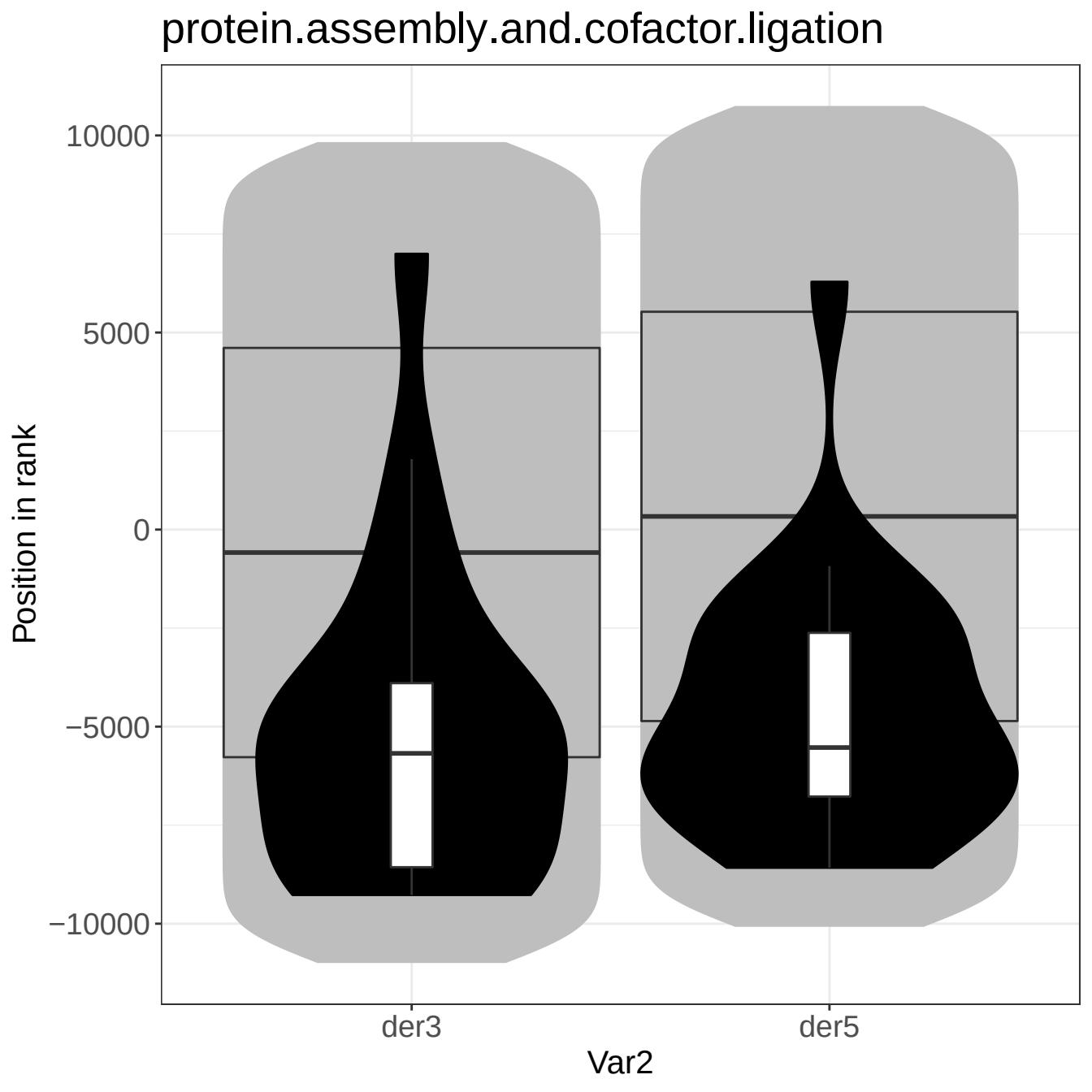
Rank in contrast der3


protein.assembly.and.cofactor.ligation
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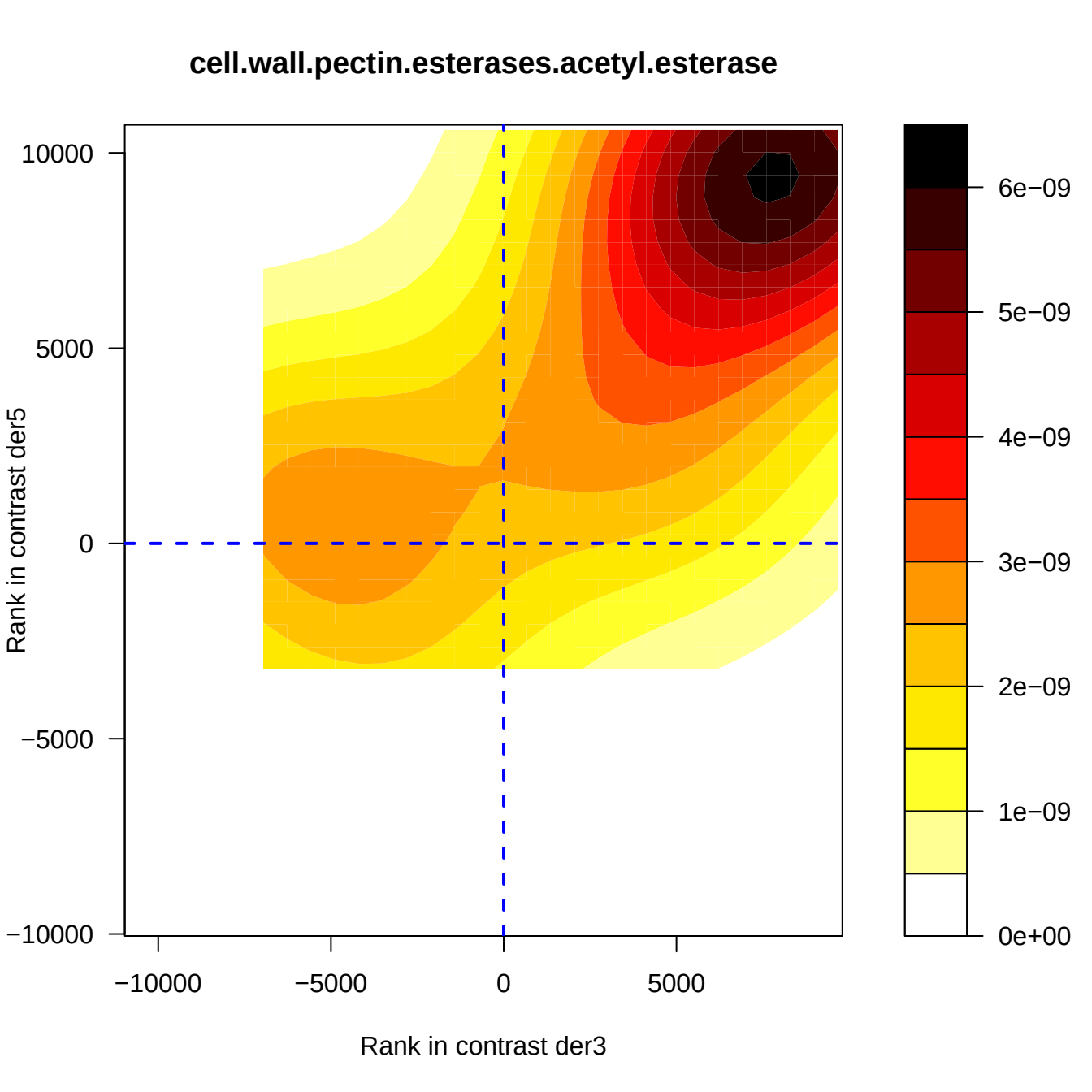
Position in rank
der3
der5
Var2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Rank in contrast der3
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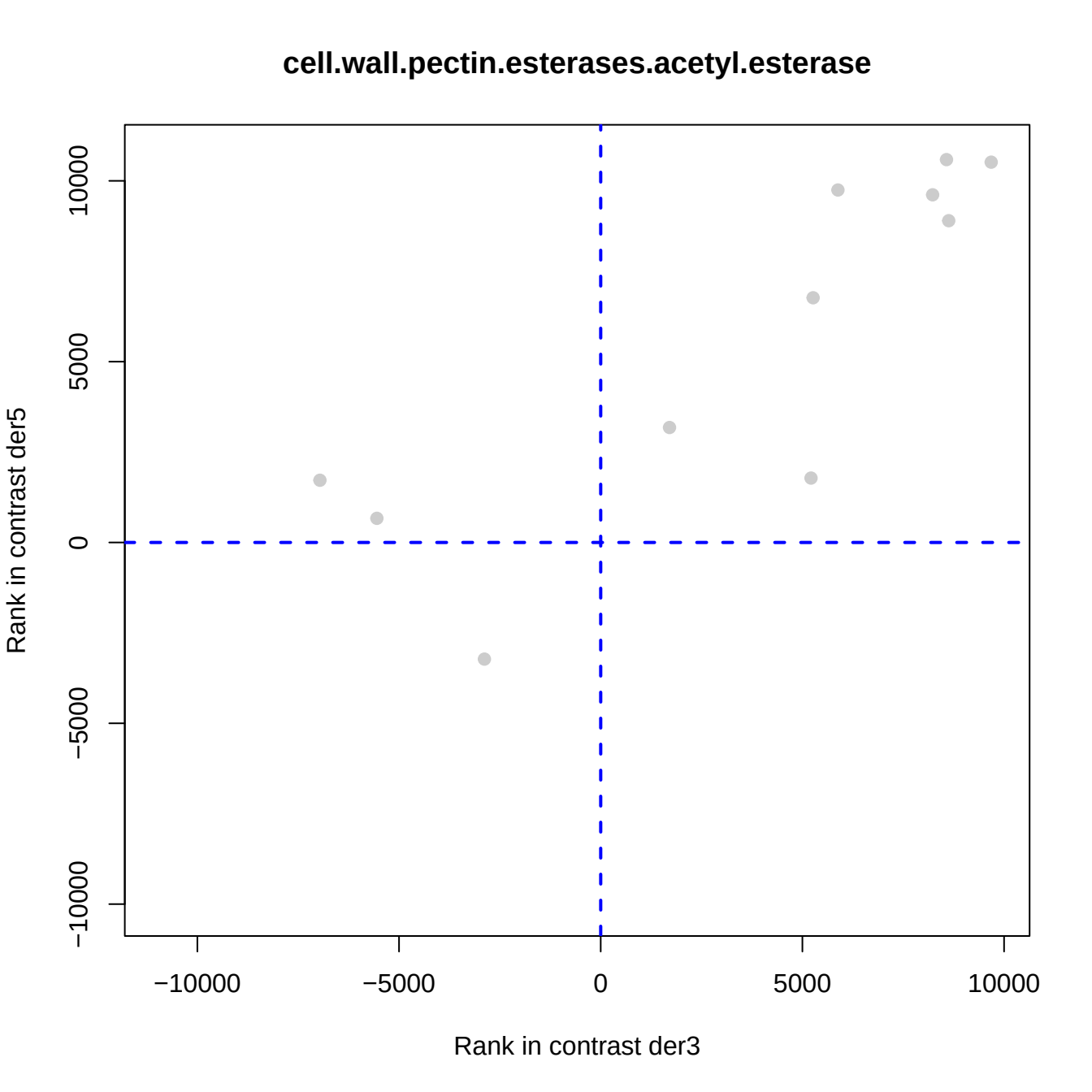
cell.wall.pectin.esterases.acetyl.esterase
Rank in contrast der5
Rank in contrast der3
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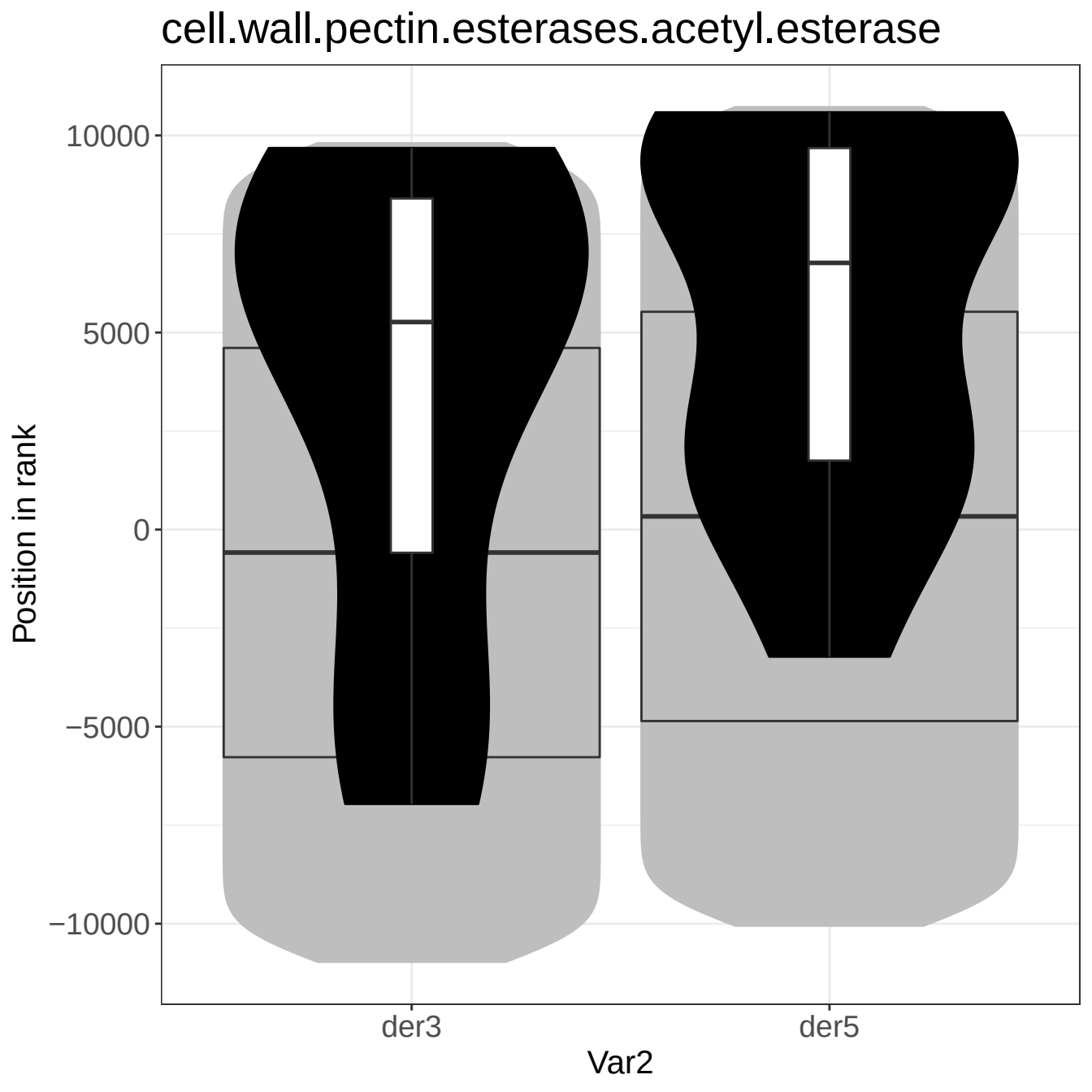
cell.wall.pectin.esterases.acetyl.esterase
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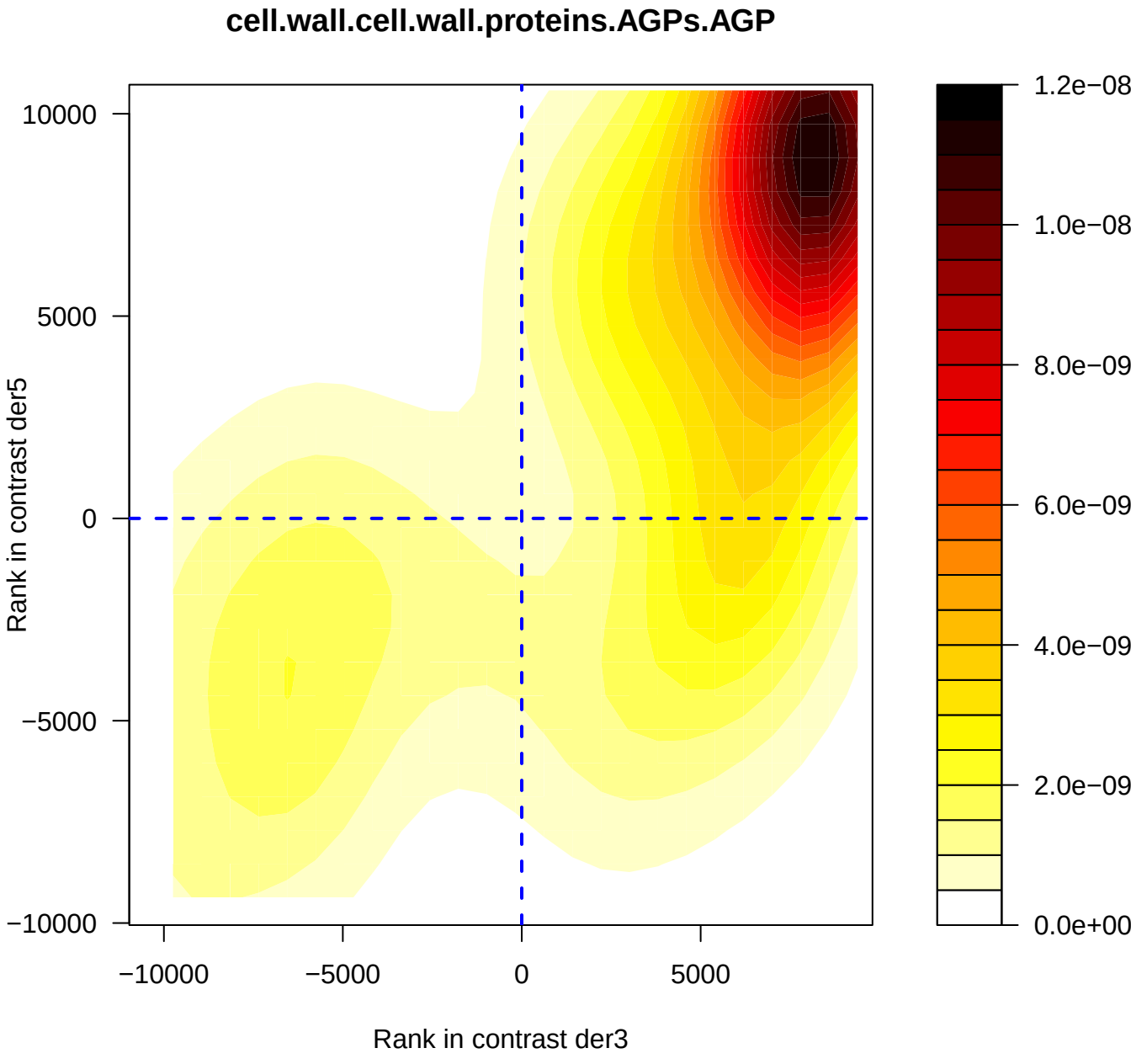
Position in rank
der3
der5
Var2


cell.wall.cell.wall.proteins.AGPs.AGP
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5000
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4.0e−09
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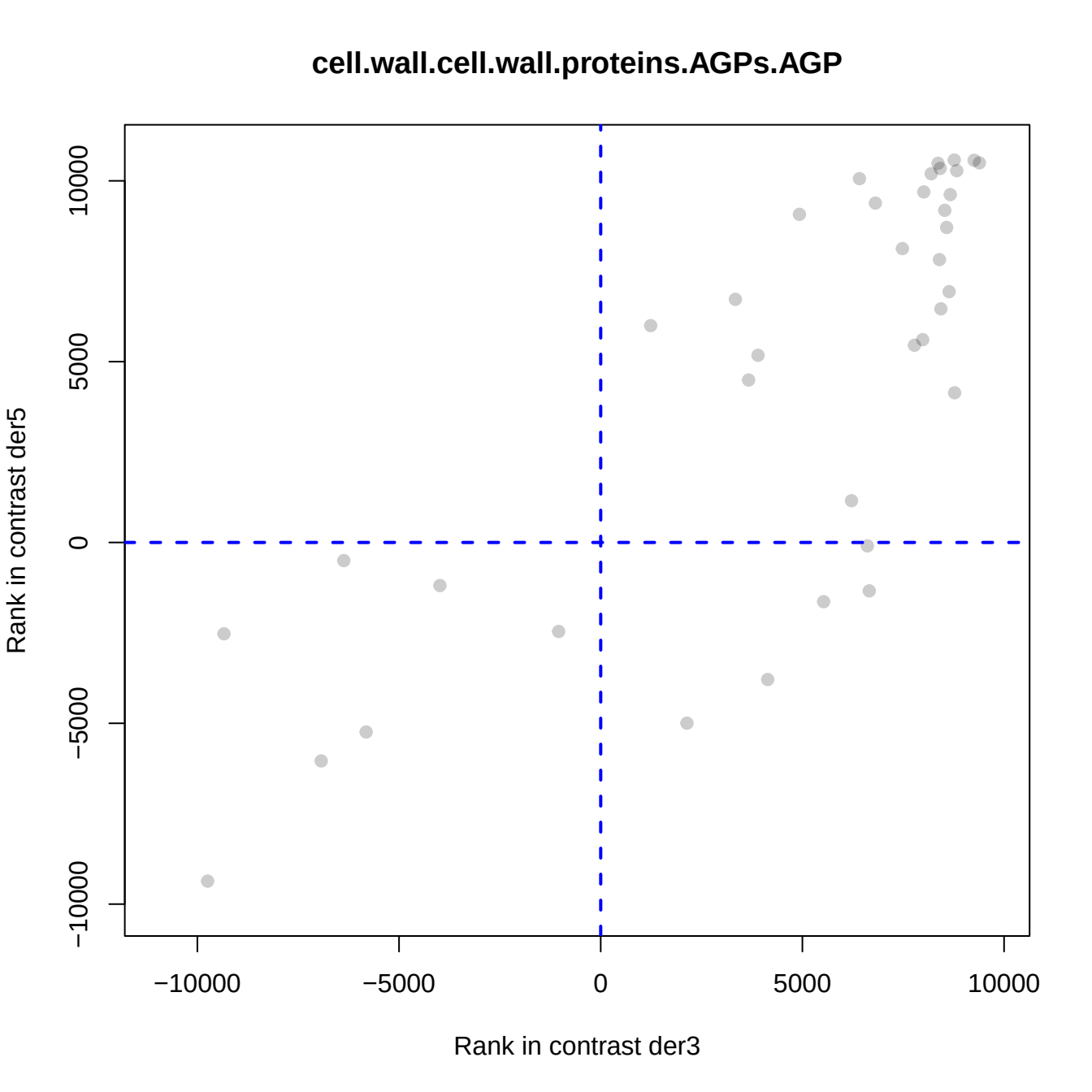
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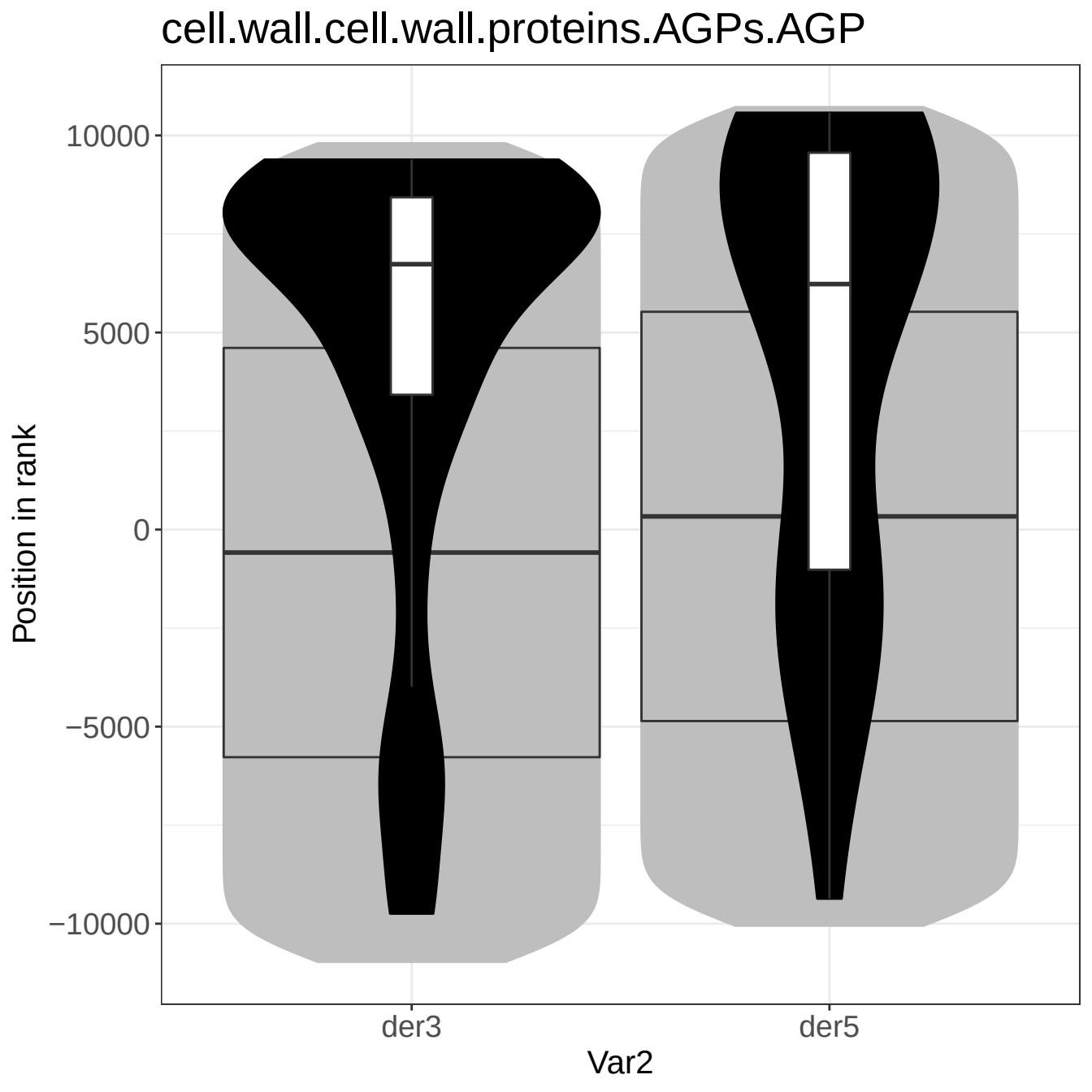
Rank in contrast der3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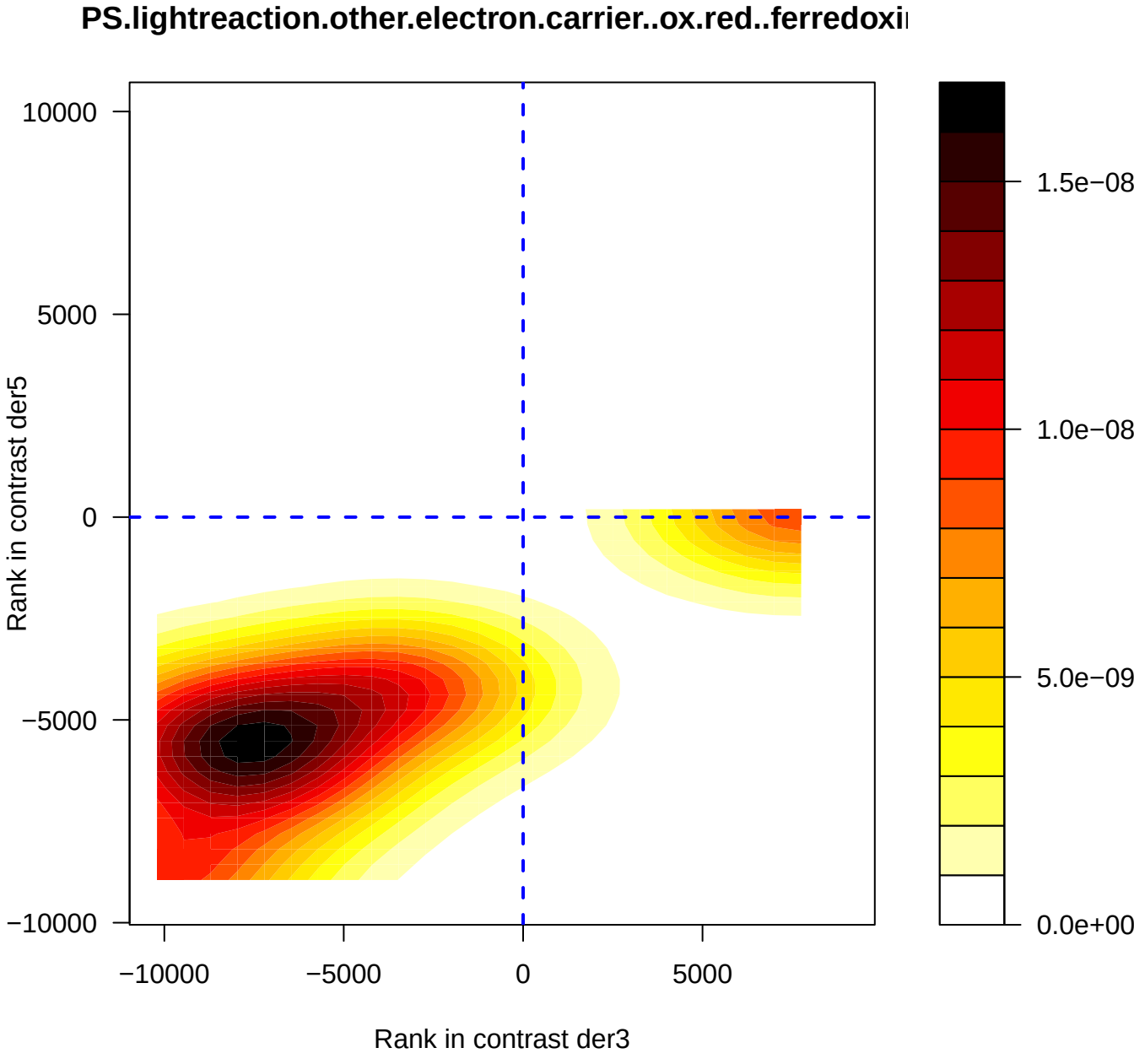
−5000
−10000
Position in rank
der3
der5
Var2


PS.lightreaction.other.electron.carrier..ox.red..ferredoxi
10000
5000
0
−5000
−10000
Rank in contrast der5
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−5000
0
5000
Rank in contrast der3
1.5e−08
1.0e−08
5.0e−09
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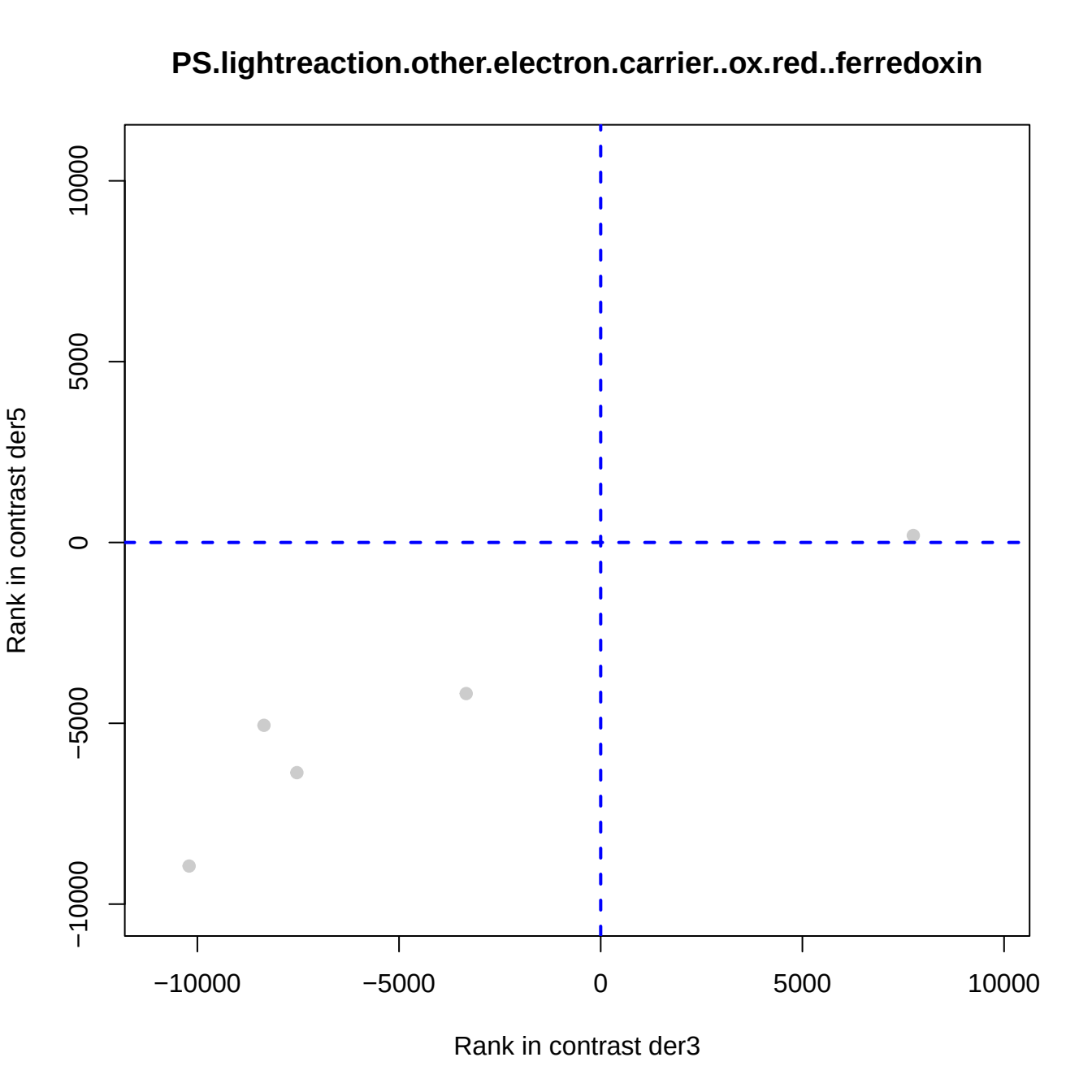
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Rank in contrast der3
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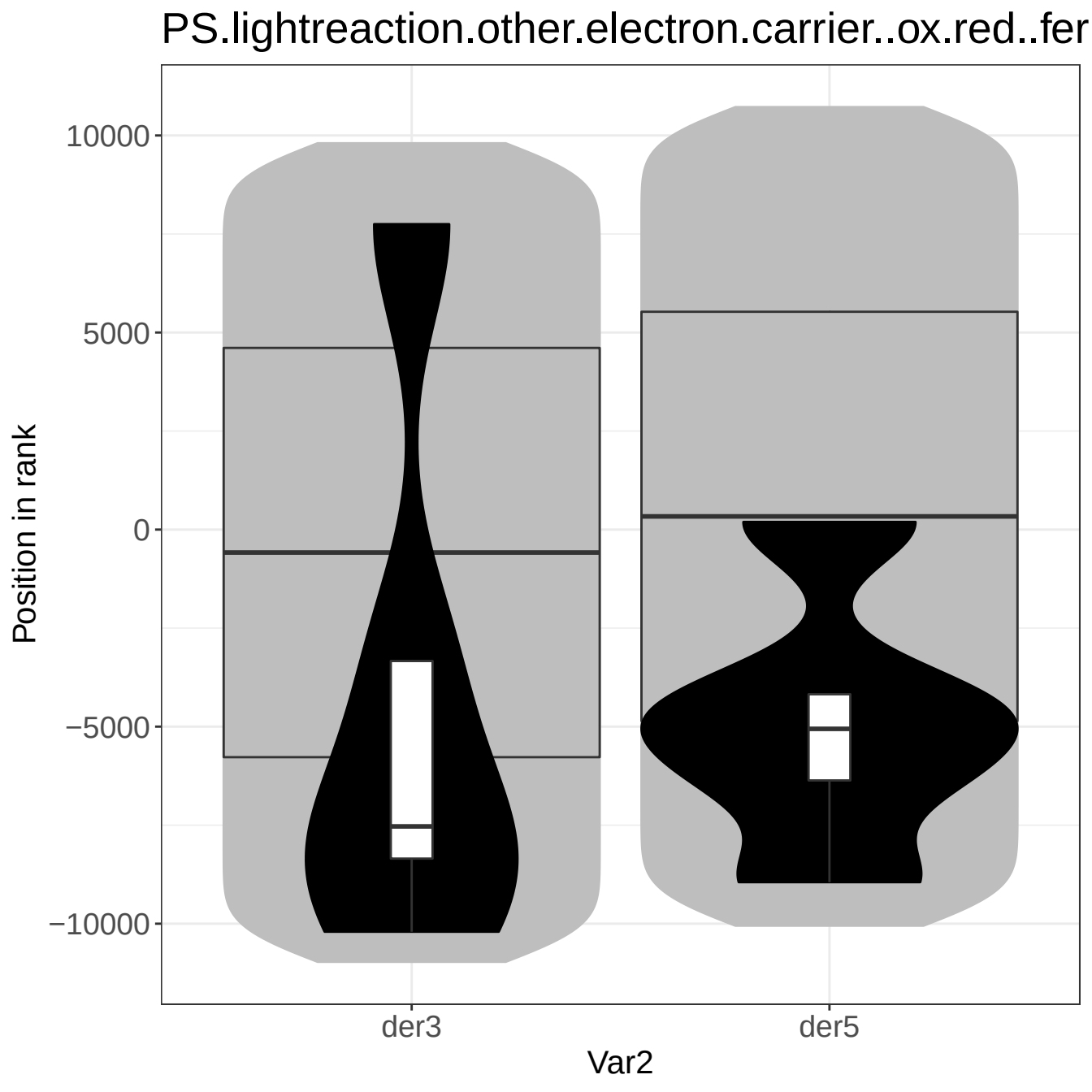
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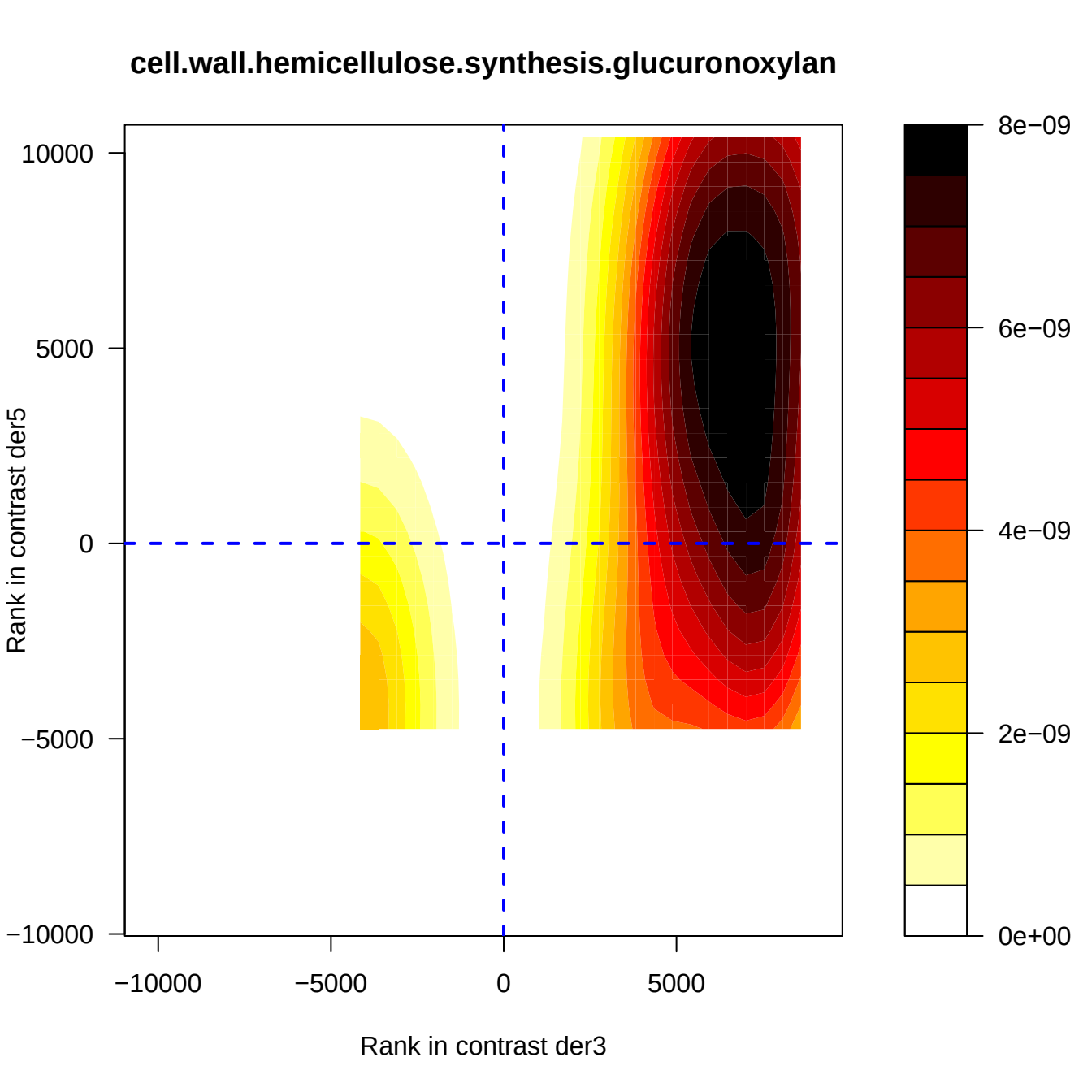
Position in rank
der3
der5
Var2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Rank in contrast der3
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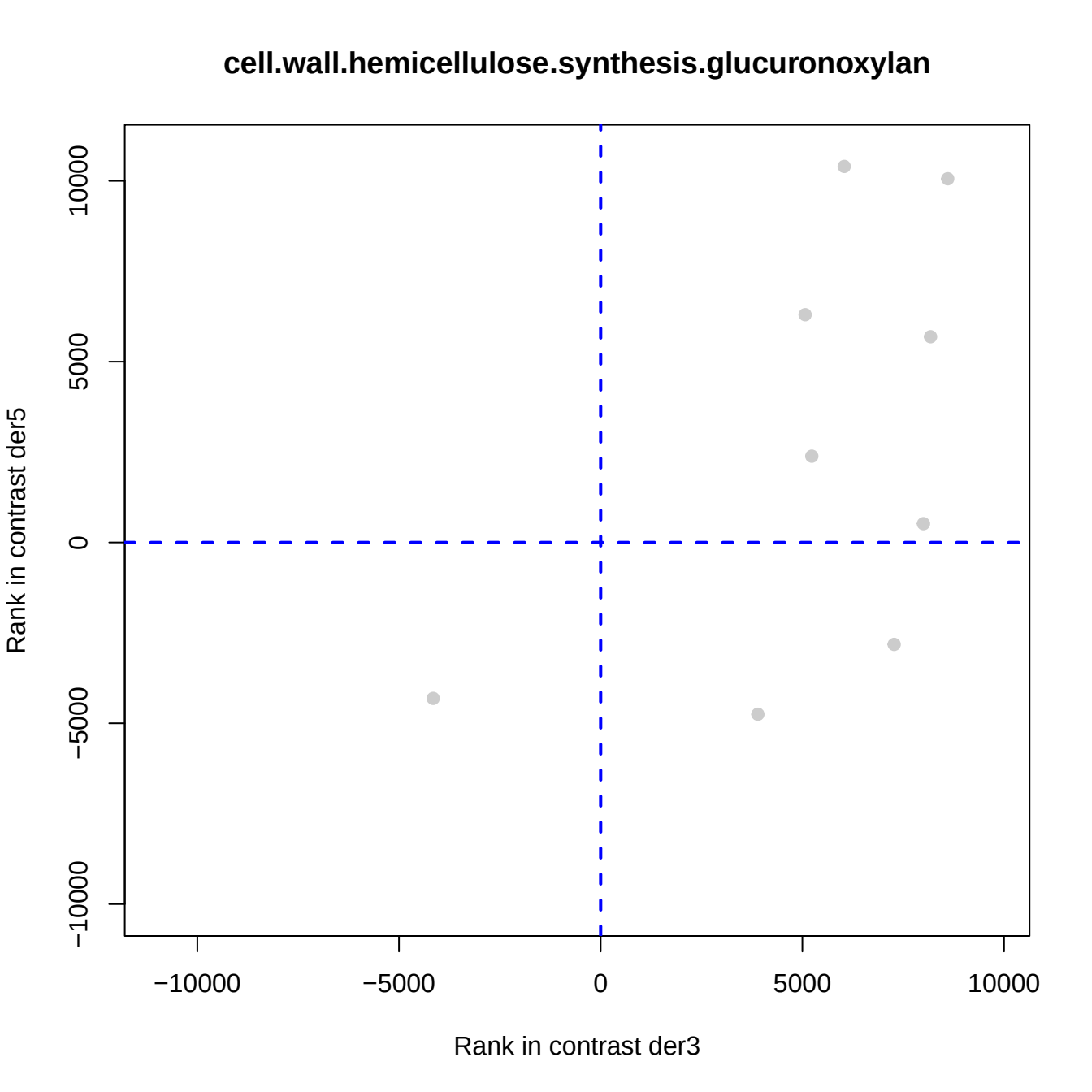
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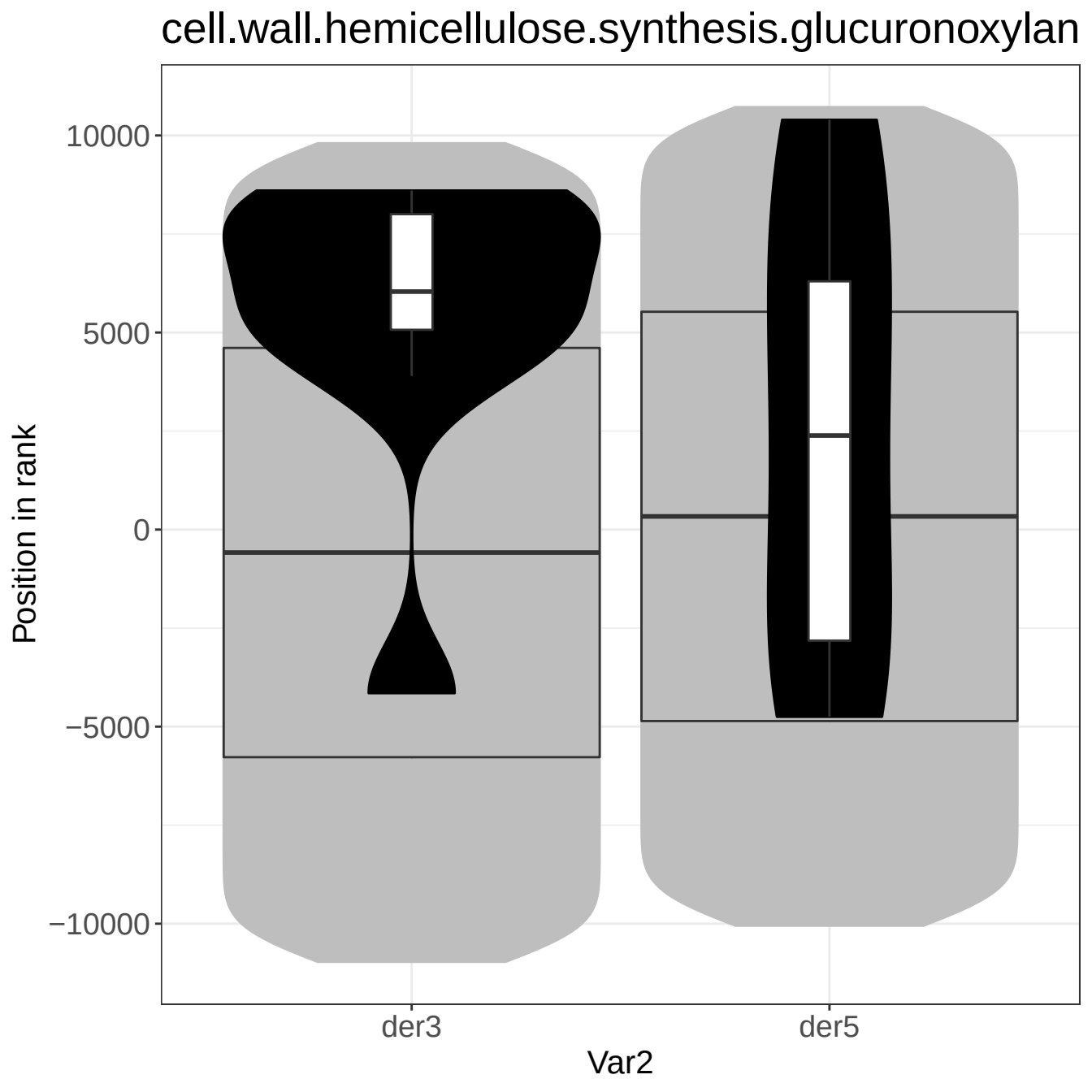
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der5
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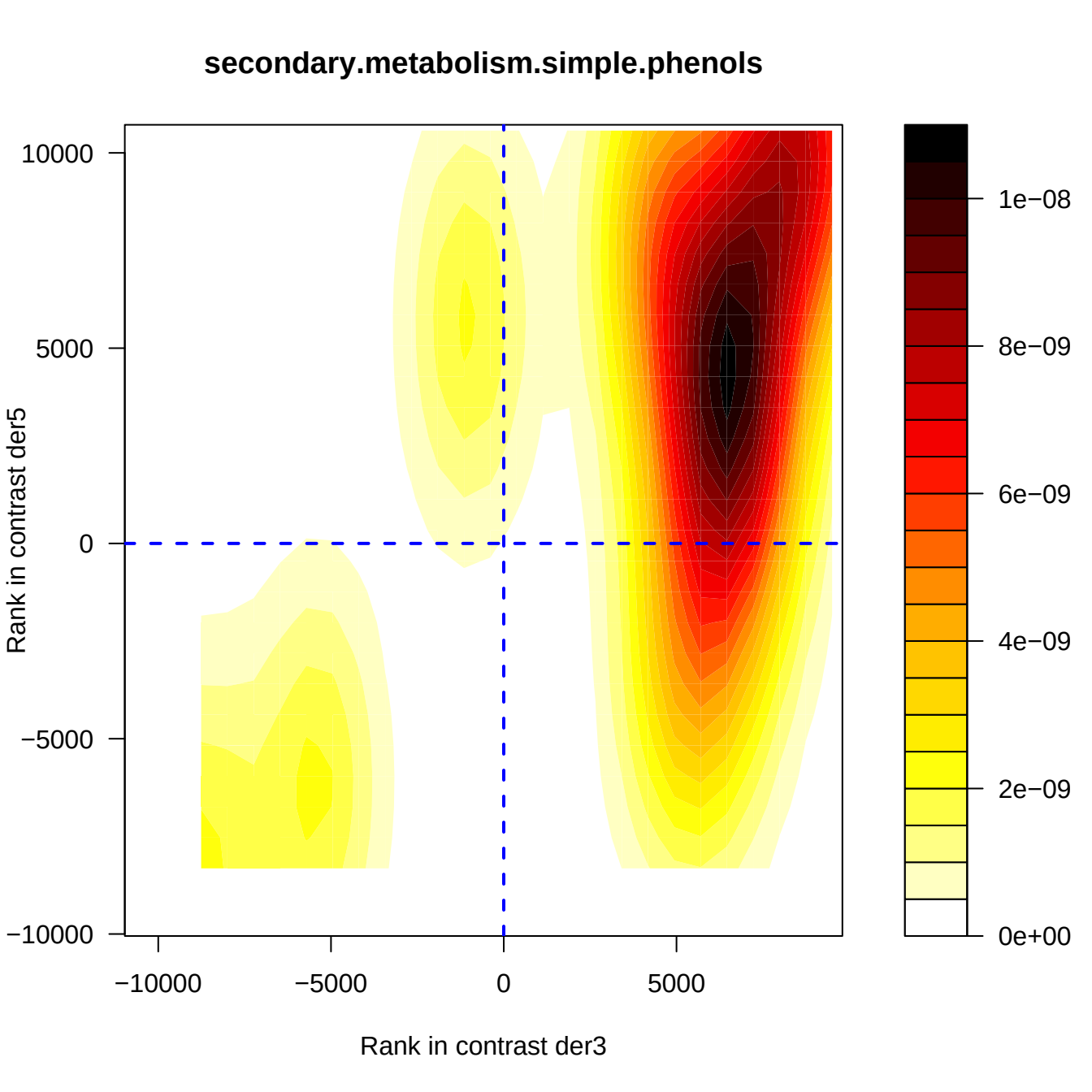
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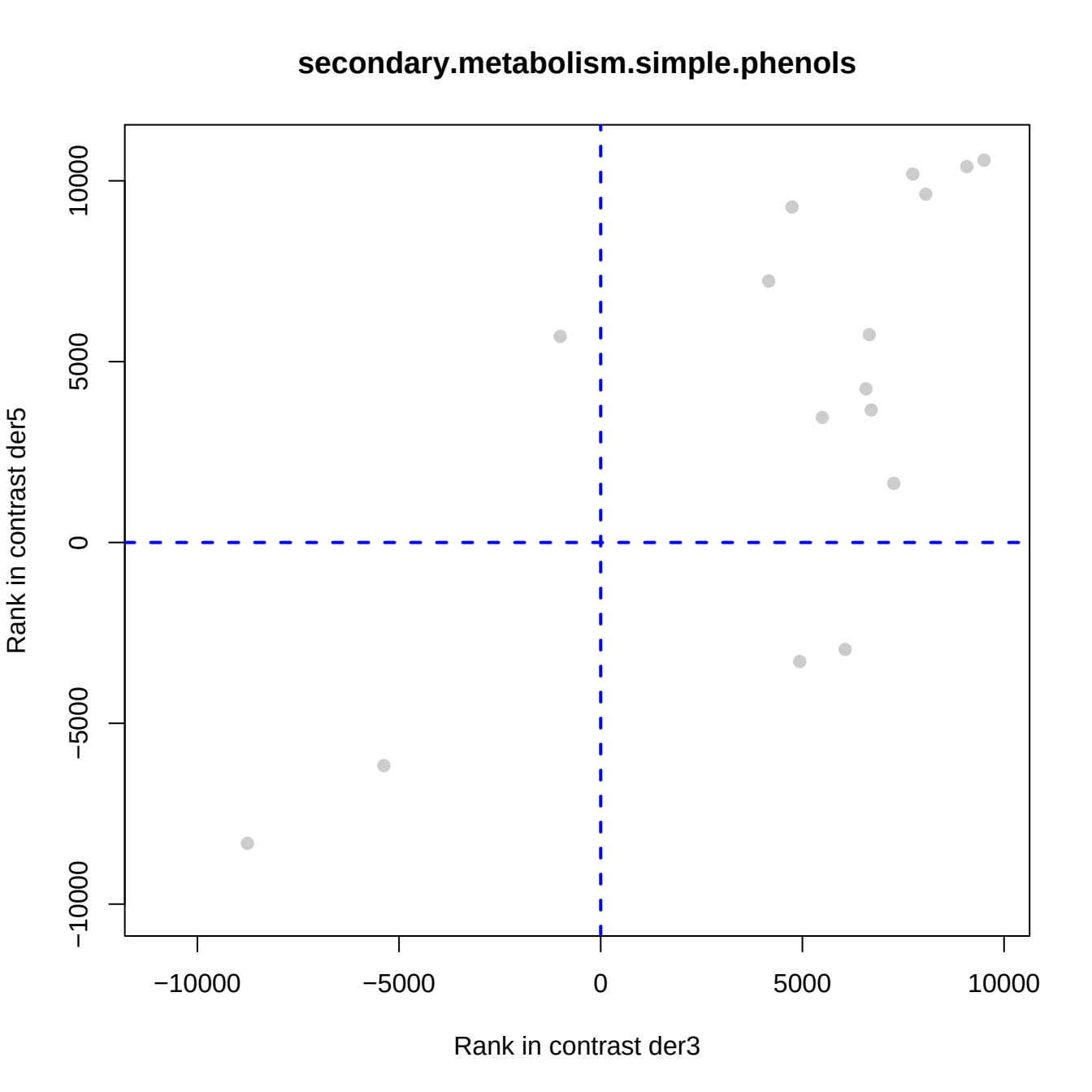
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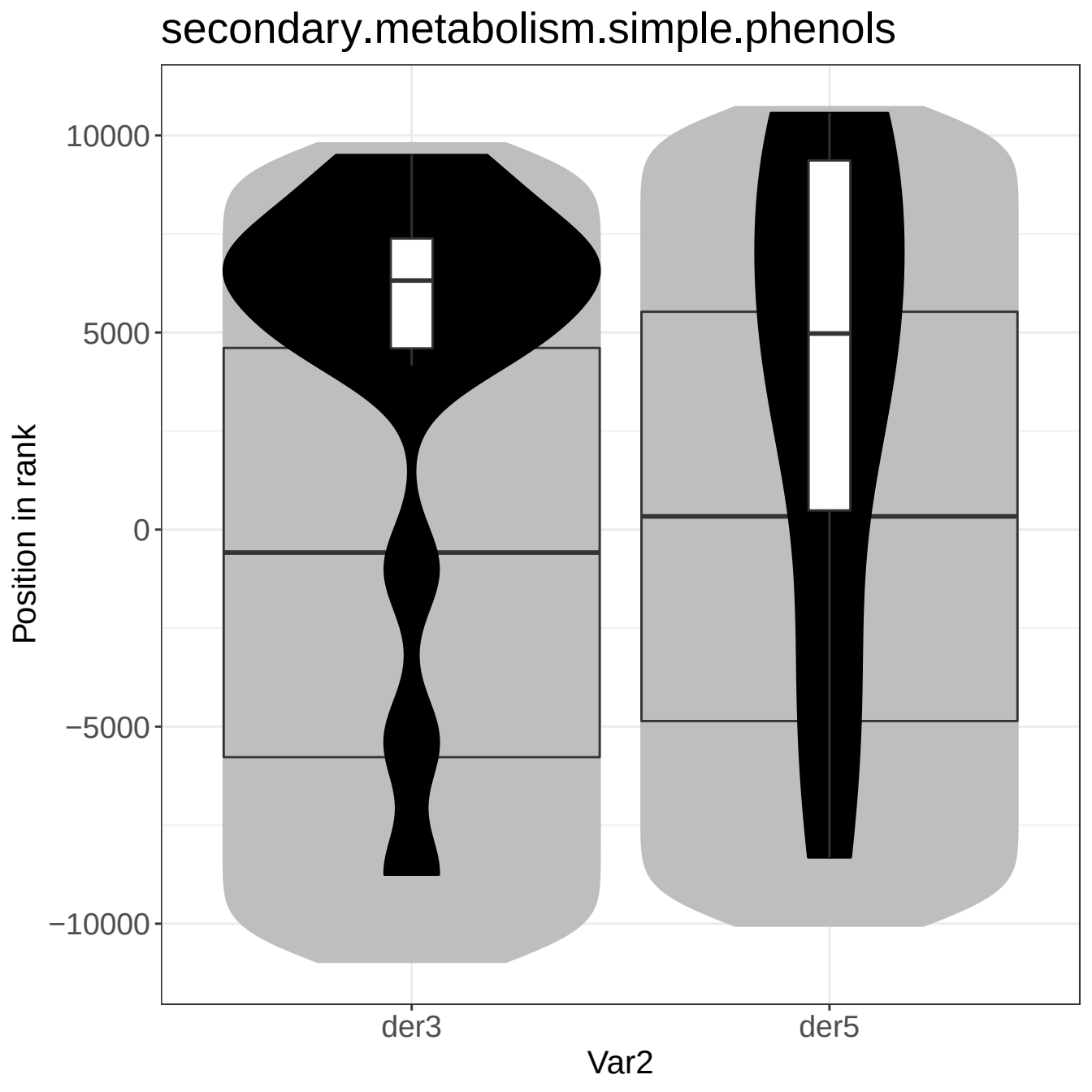
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Position in rank
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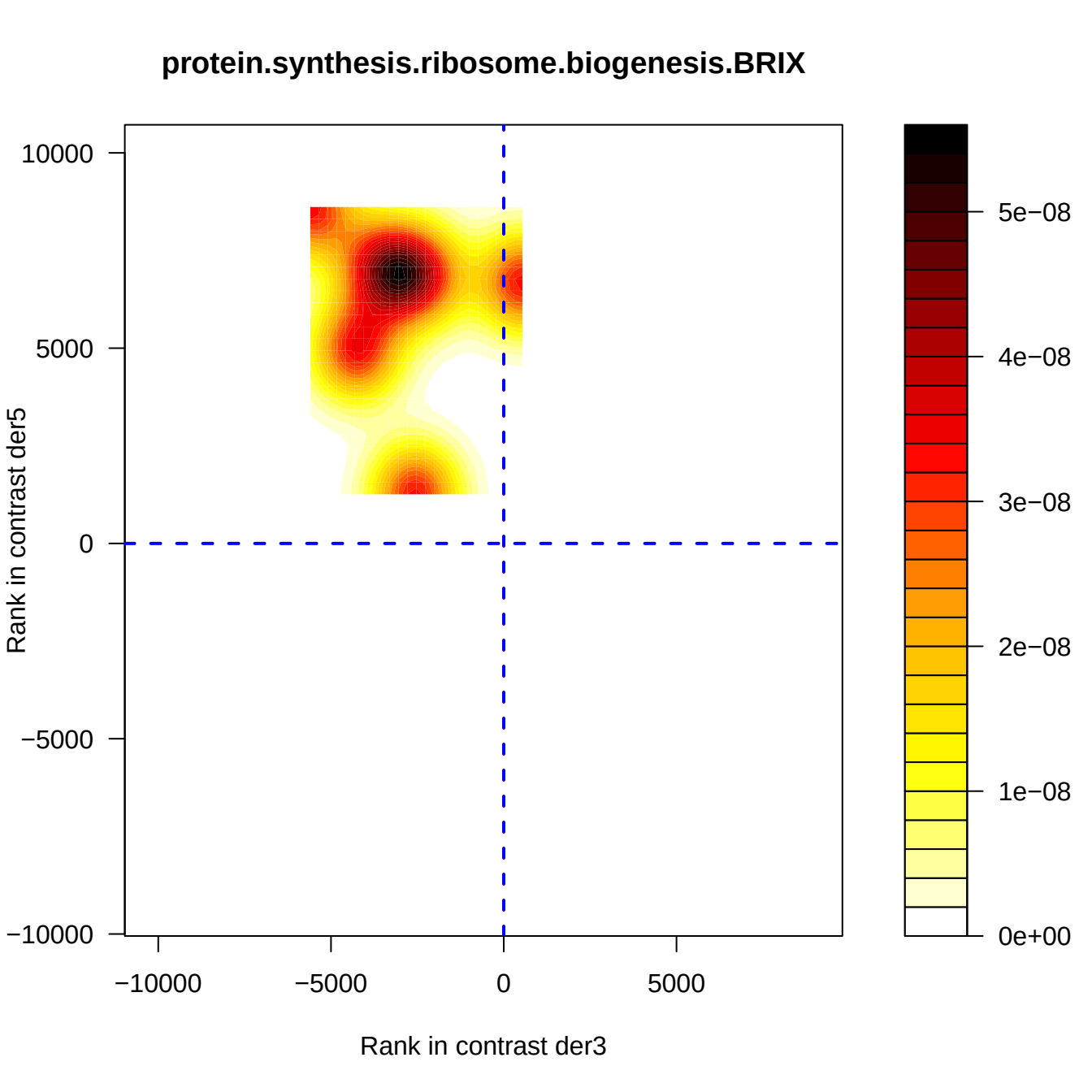
protein.synthesis.ribosome.biogenesis.BRIX
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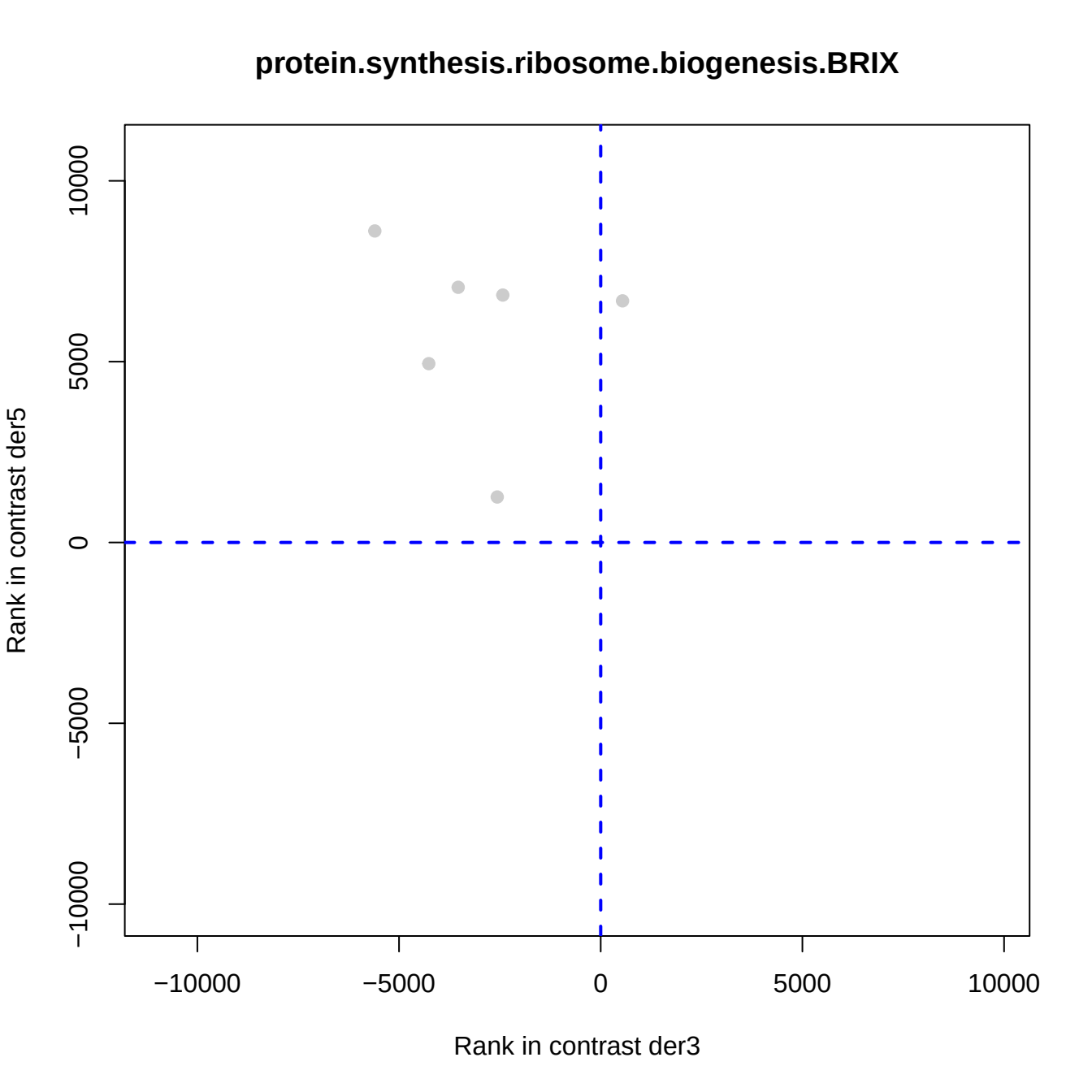
protein.synthesis.ribosome.biogenesis.BRIX
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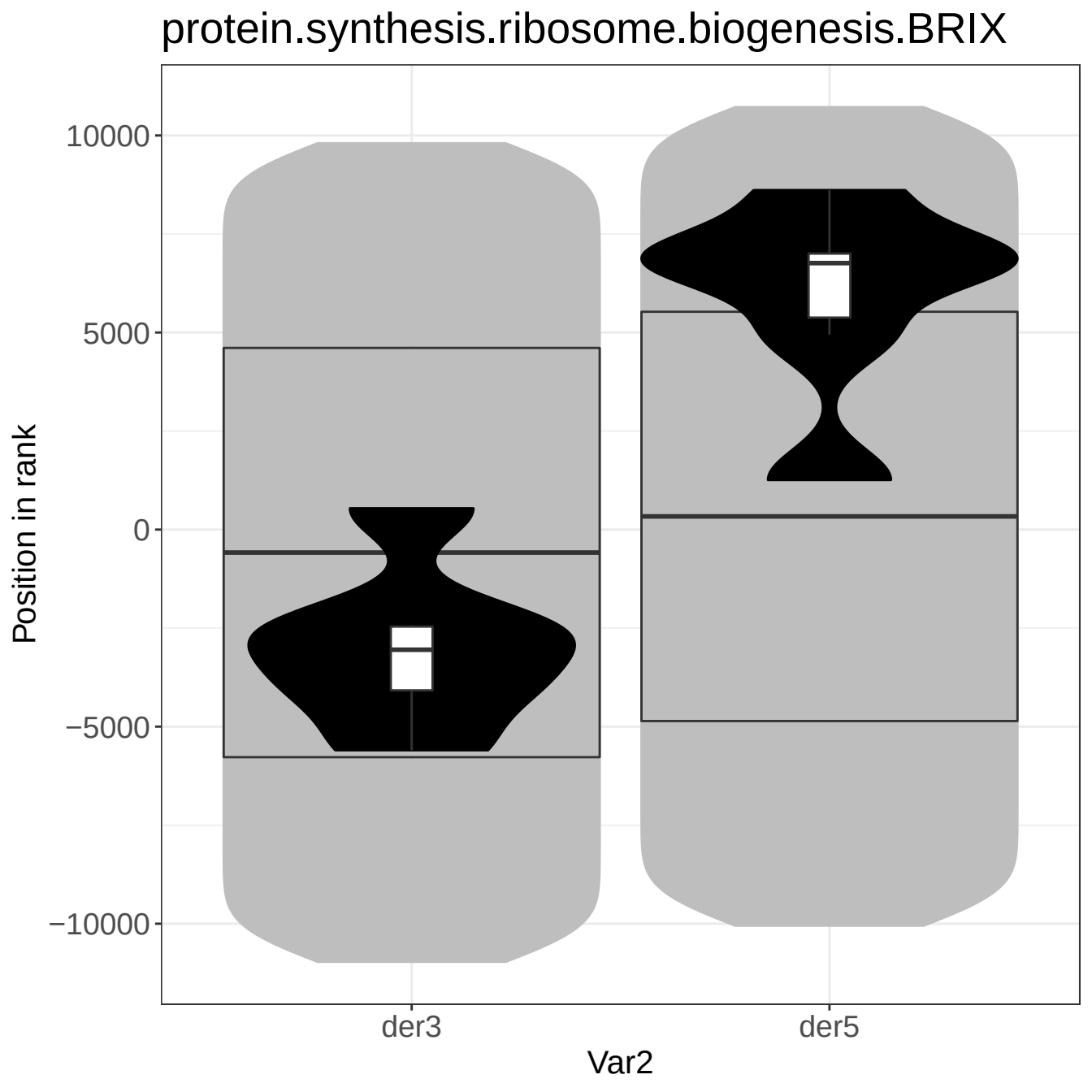
Rank in contrast der3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der3
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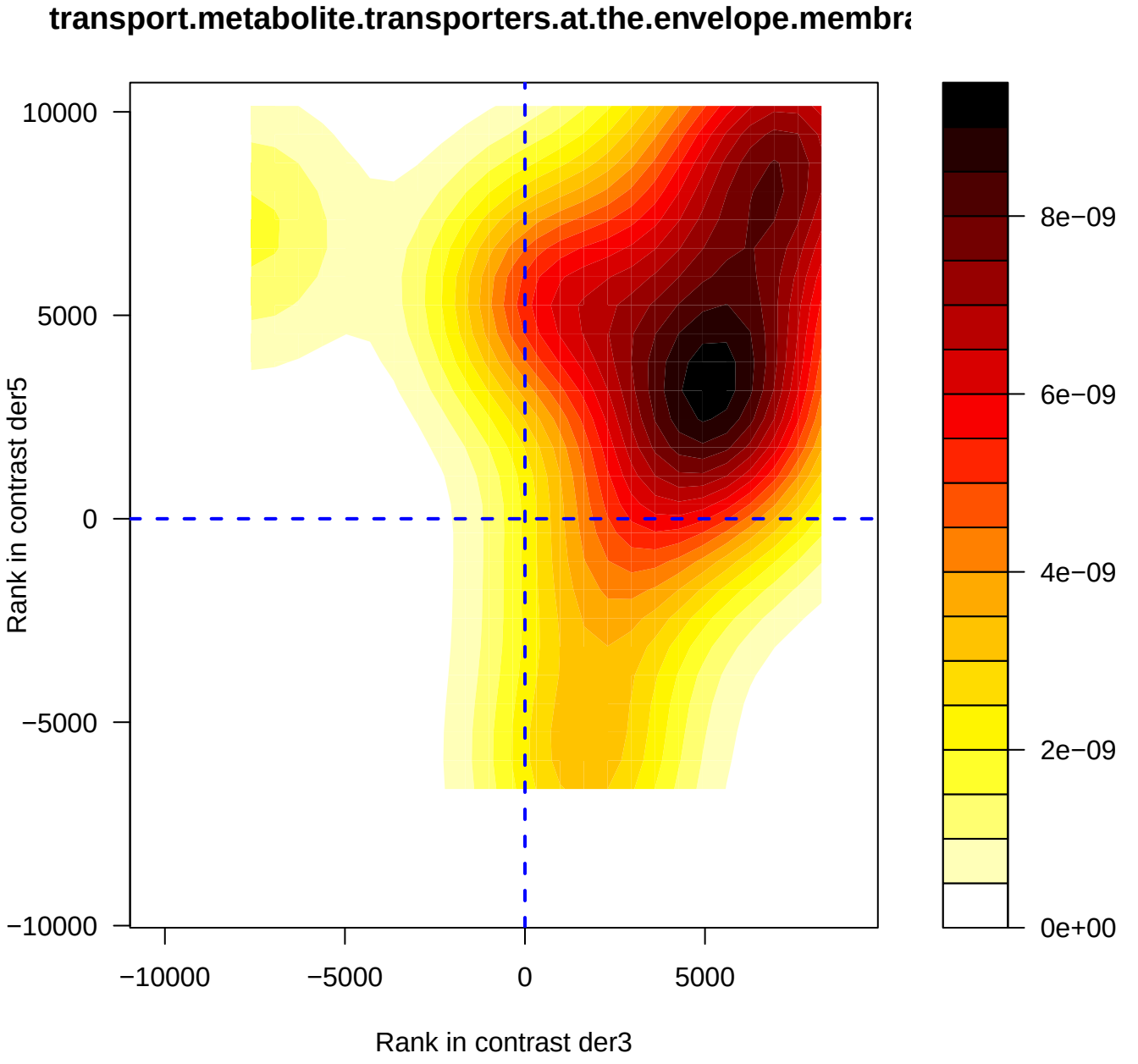
Var2


transport.metabolite.transporters.at.the.envelope.membra
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Rank in contrast der3
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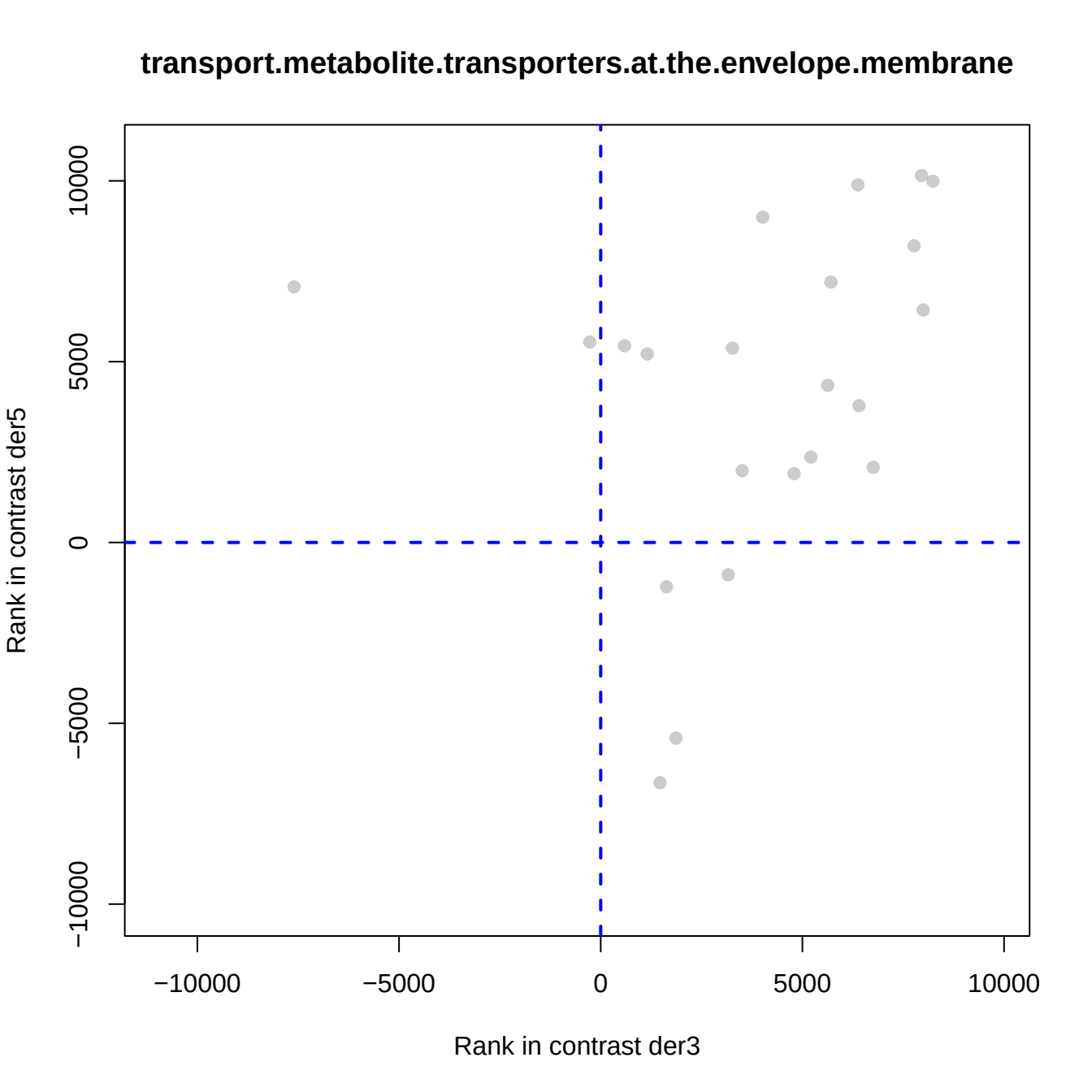
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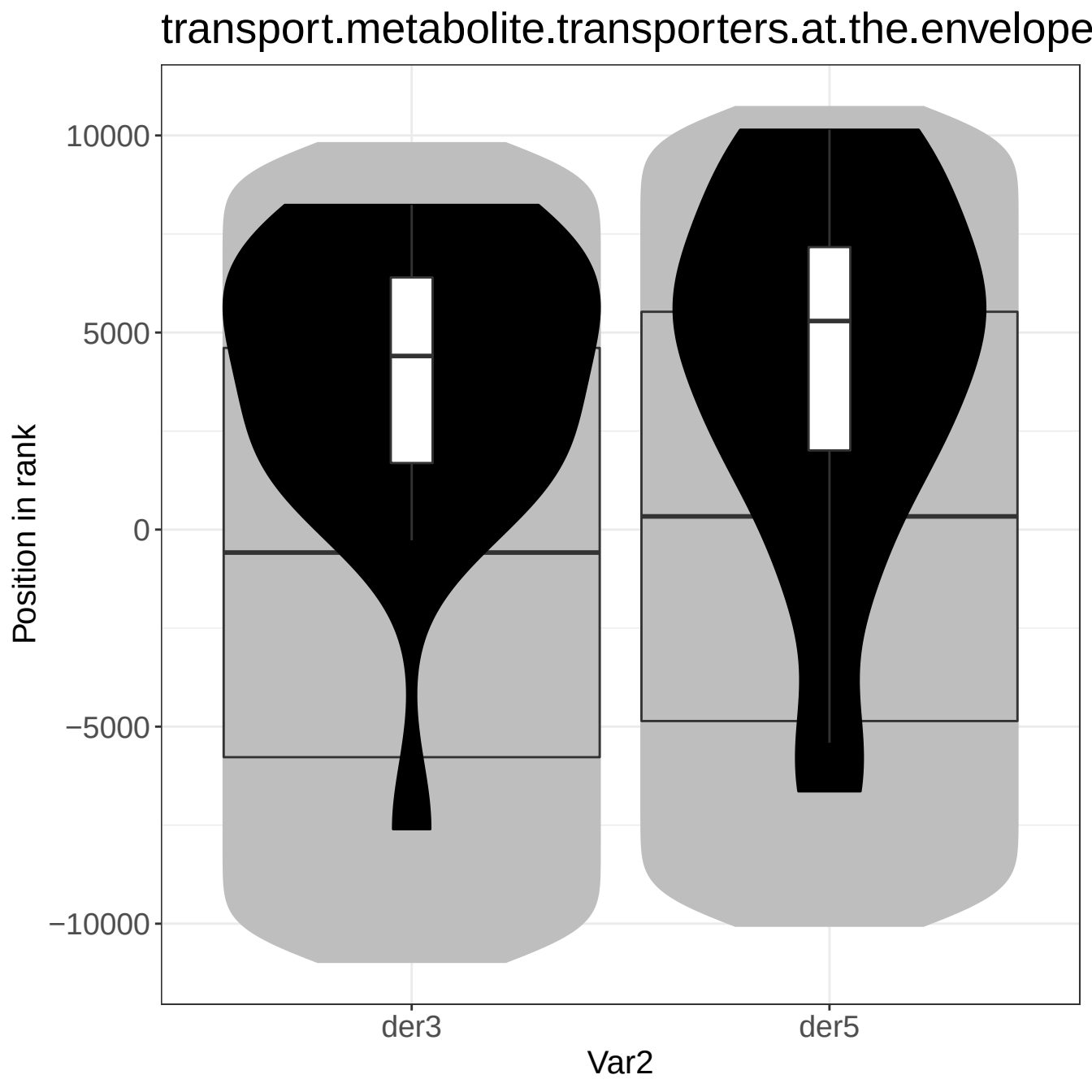
transport.metabolite.transporters.at.the.envelope
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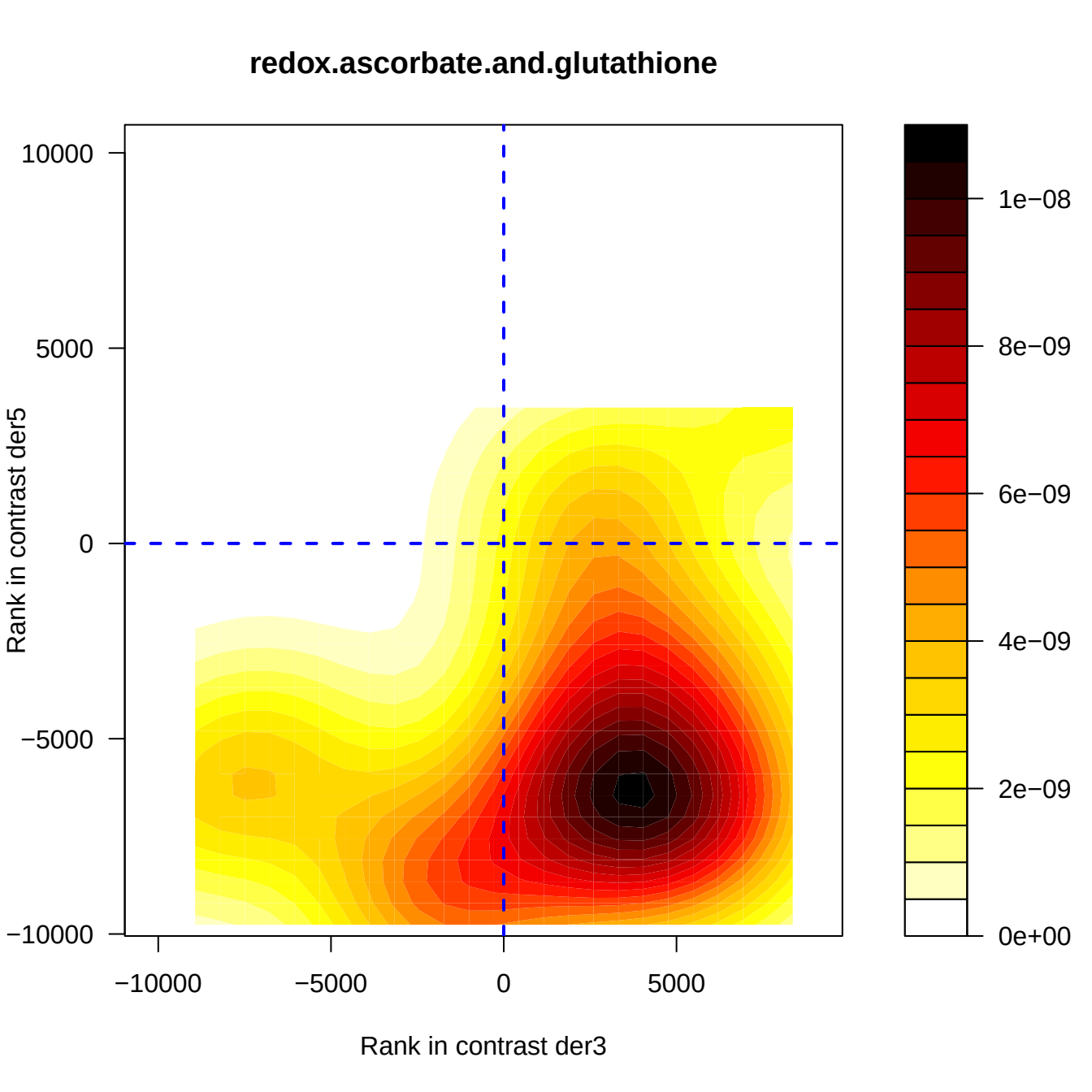
Position in rank
der3
der5
Var2


redox.ascorbate.and.glutathione
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Rank in contrast der5
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Rank in contrast der3
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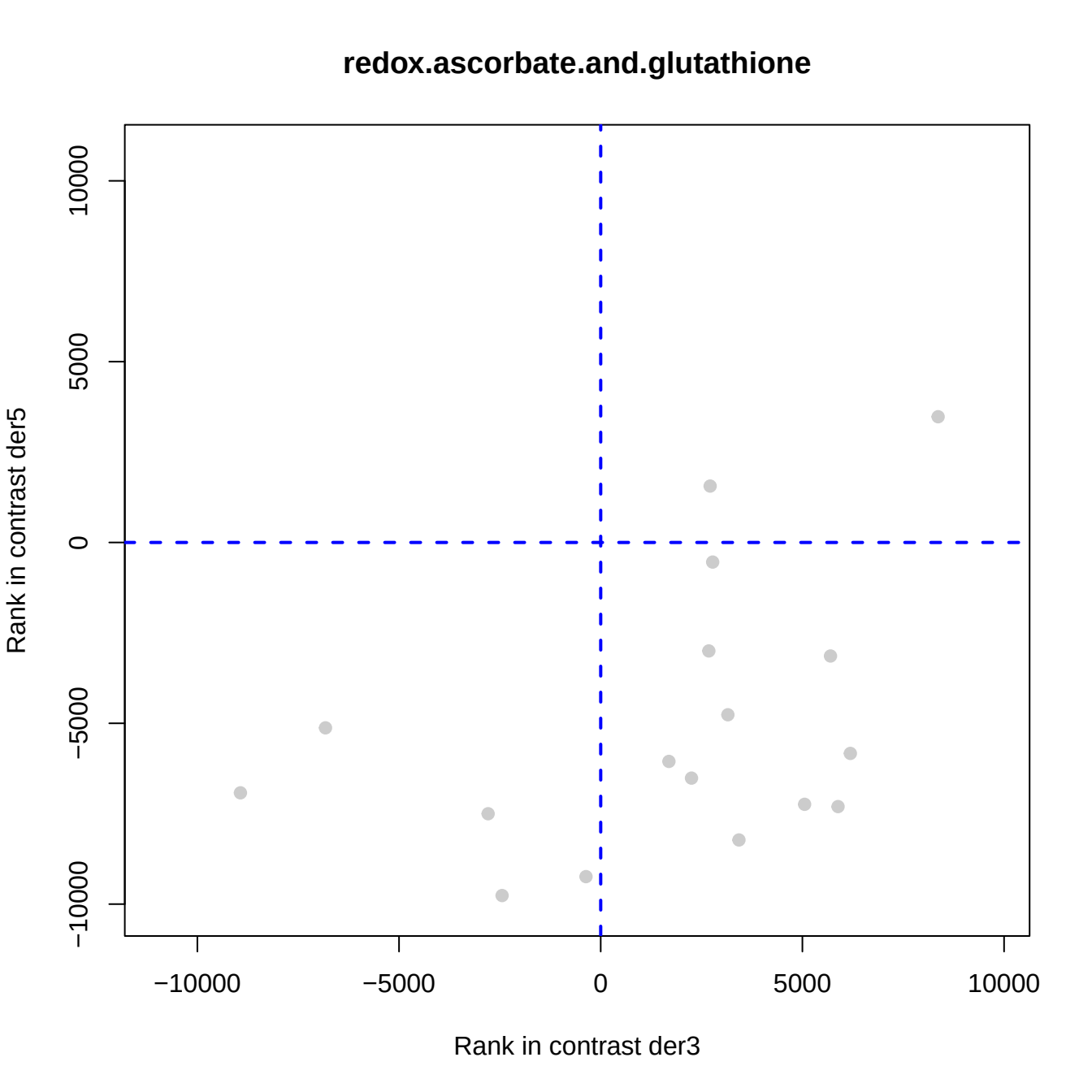
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5000
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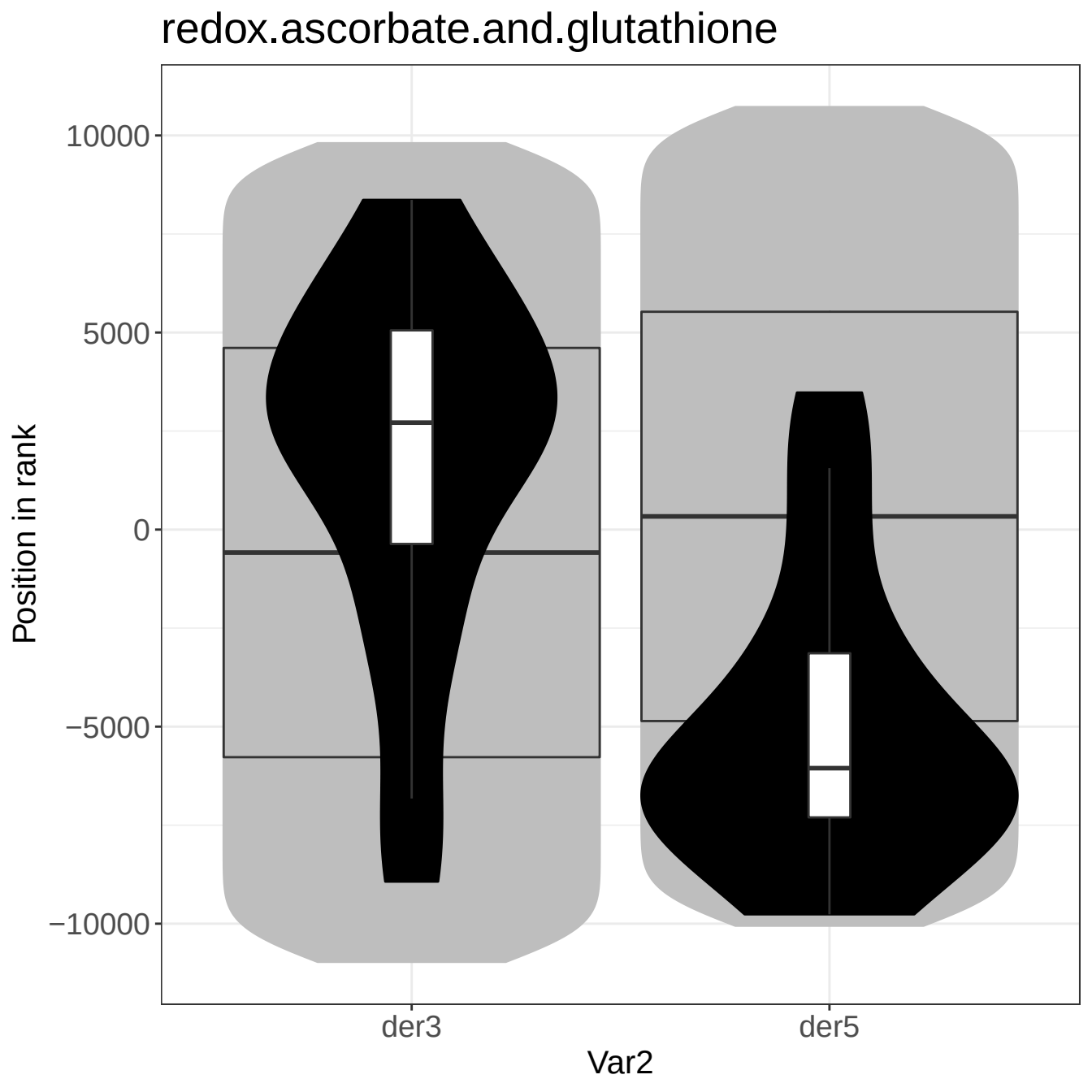
Rank in contrast der3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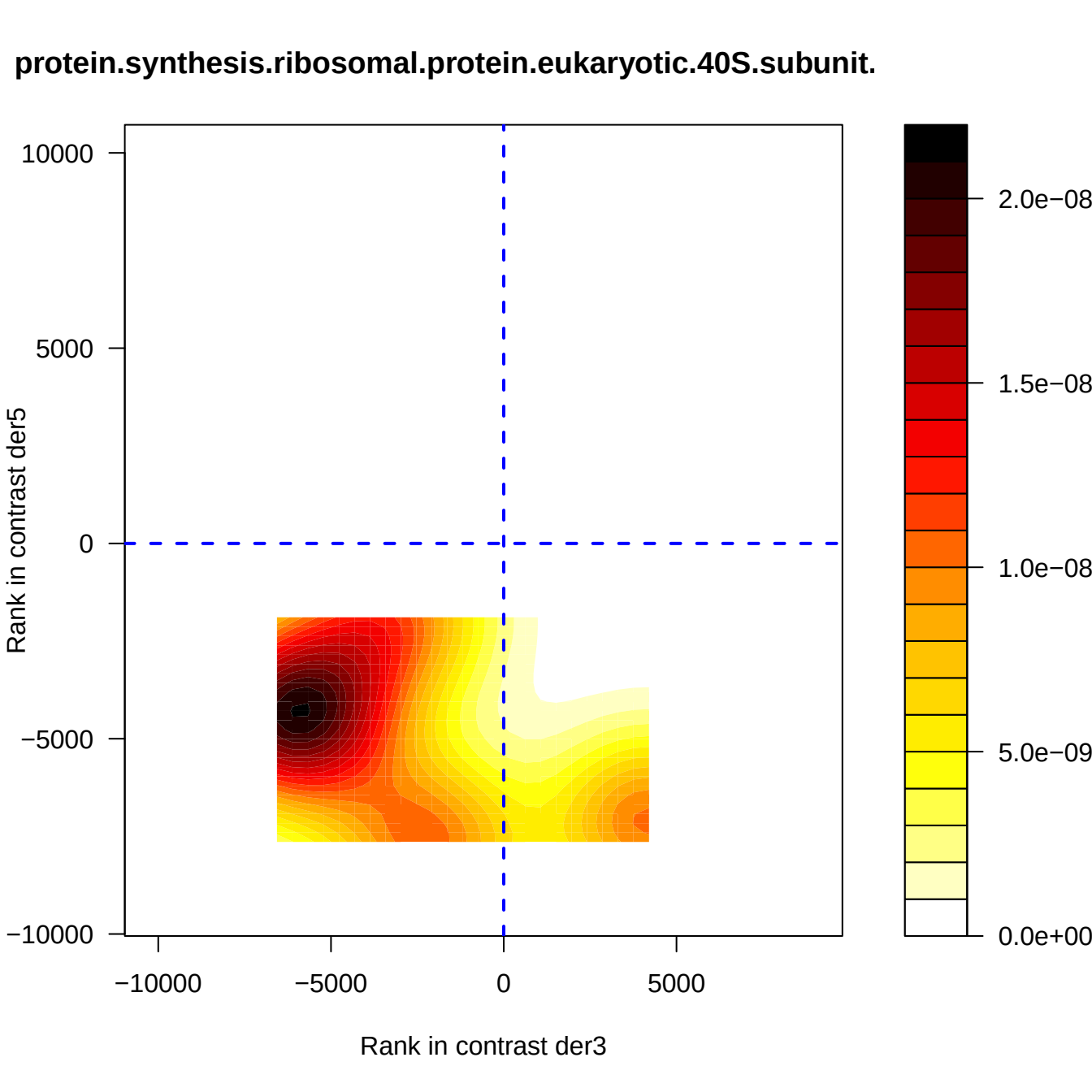
Position in rank
der3
der5
Var2


protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.
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−5000
−10000
Rank in contrast der5
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−5000
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Rank in contrast der3
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1.0e−08
5.0e−09
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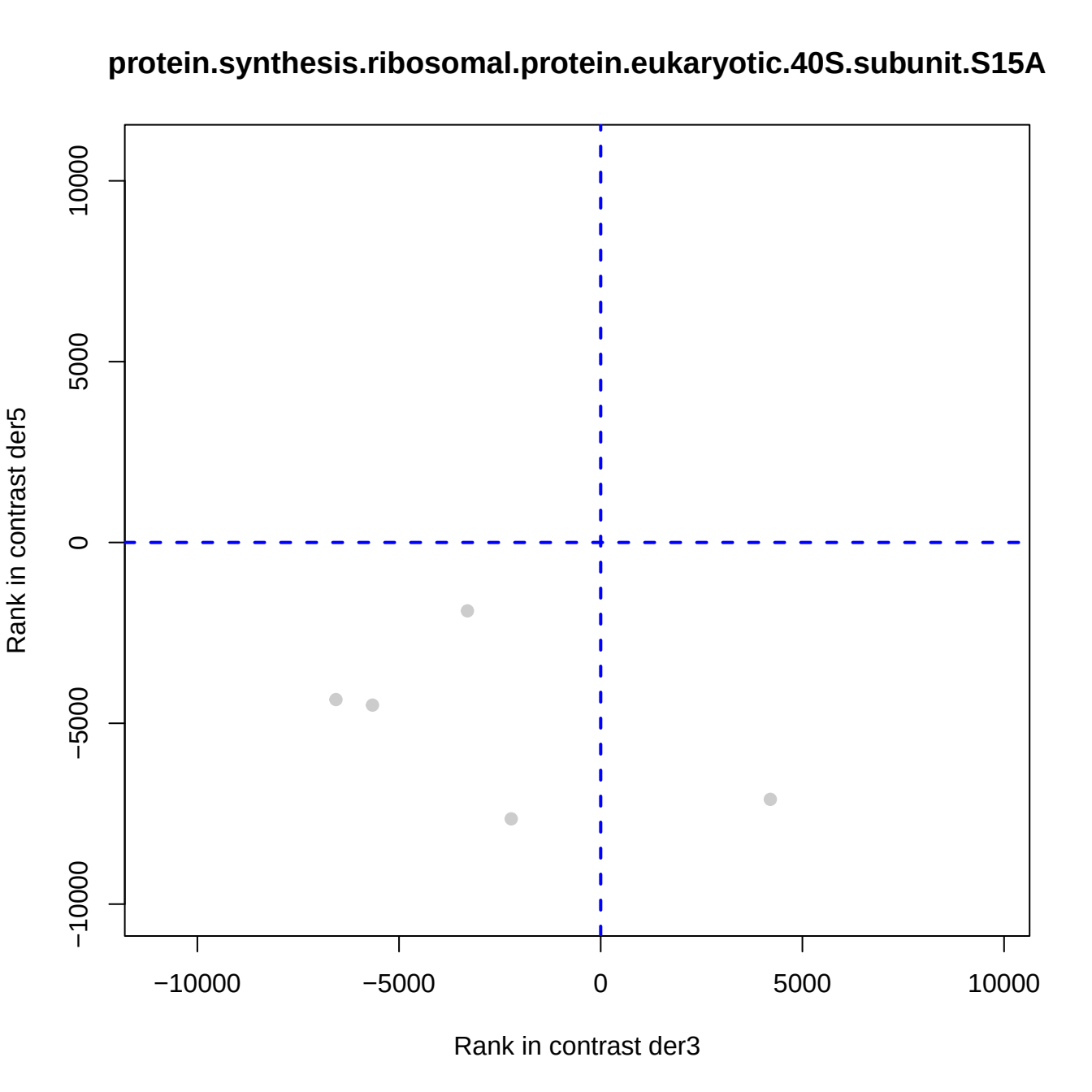
protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S15A
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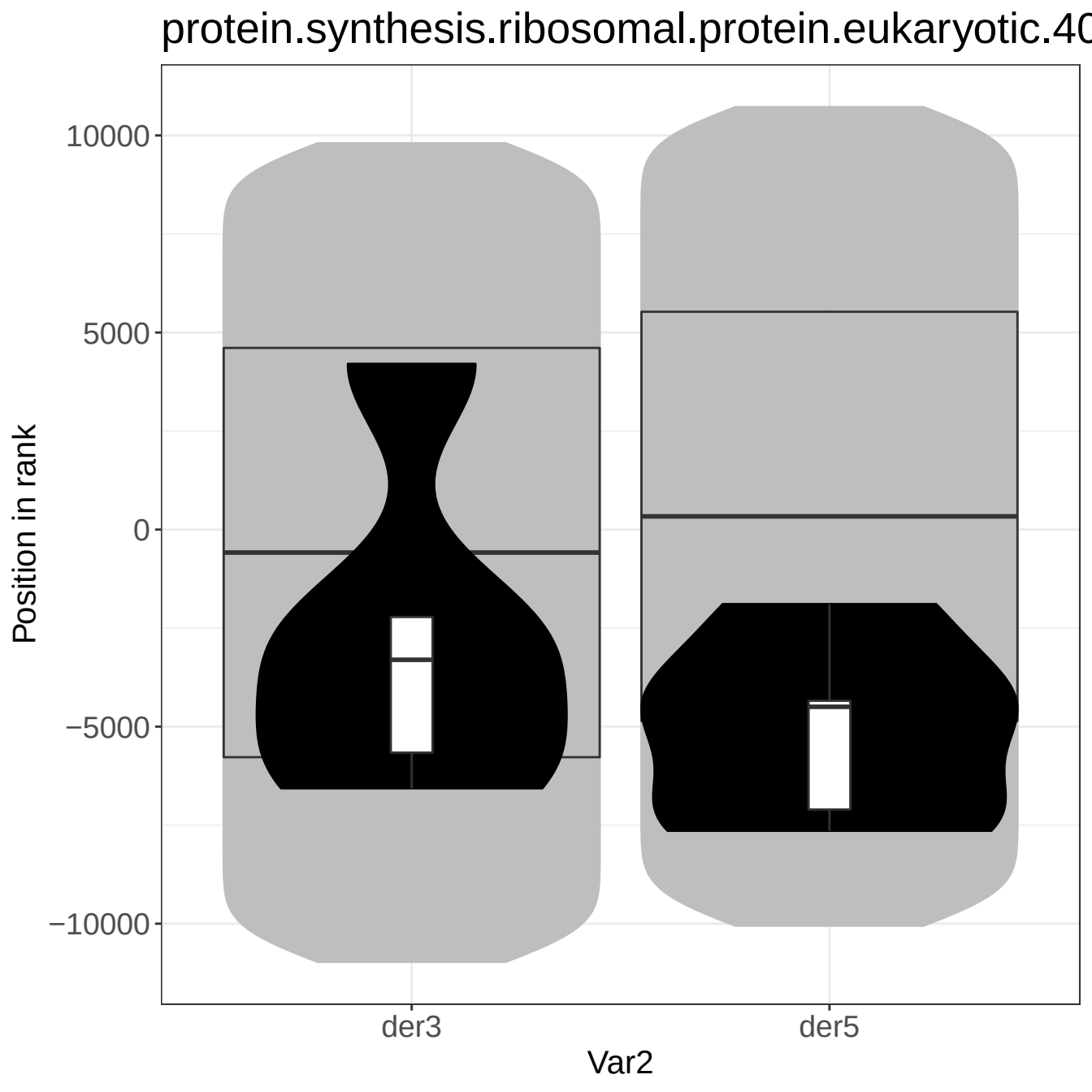
Rank in contrast der3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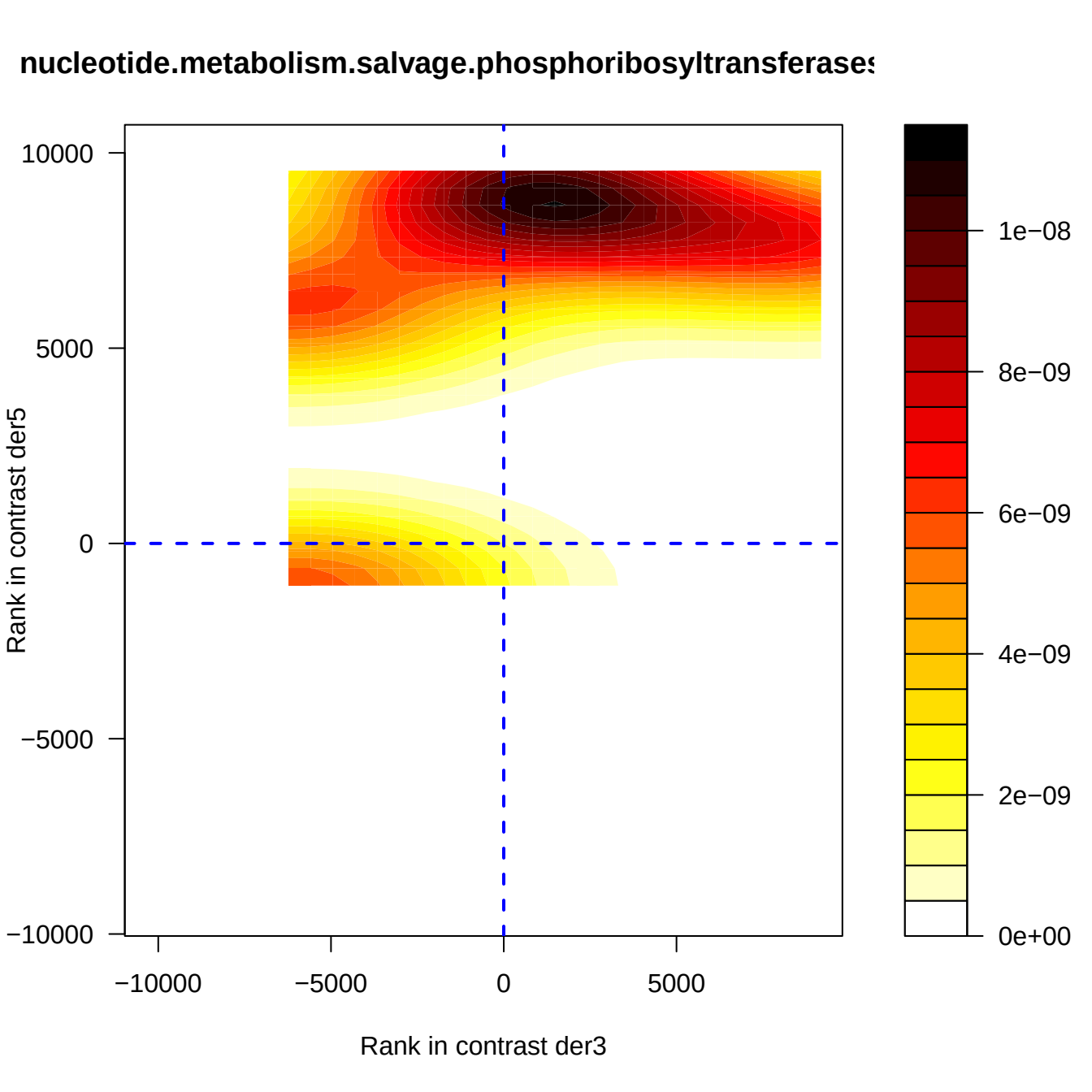
Position in rank
der3
der5
Var2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−10000
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Rank in contrast der3
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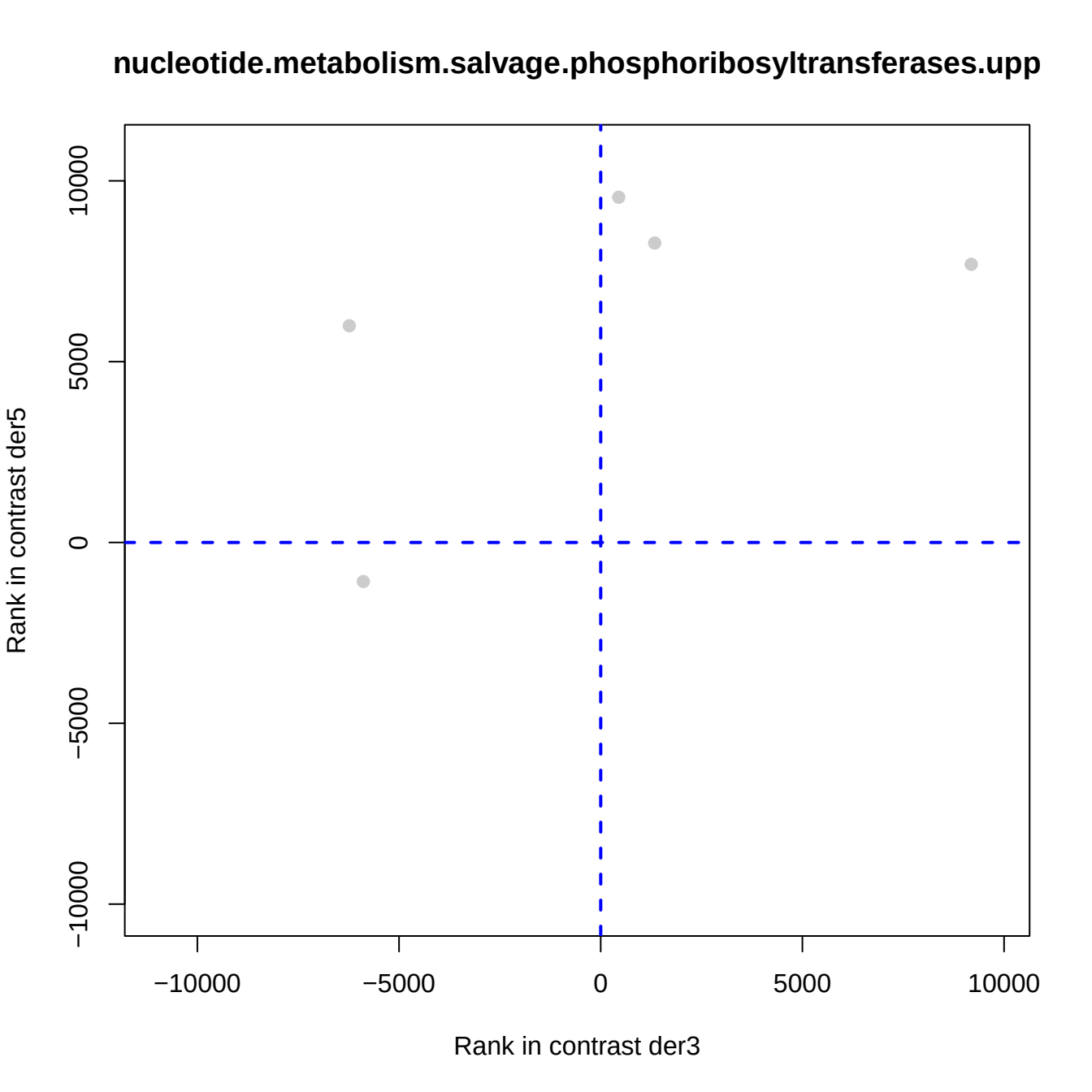
2e−09
0e+00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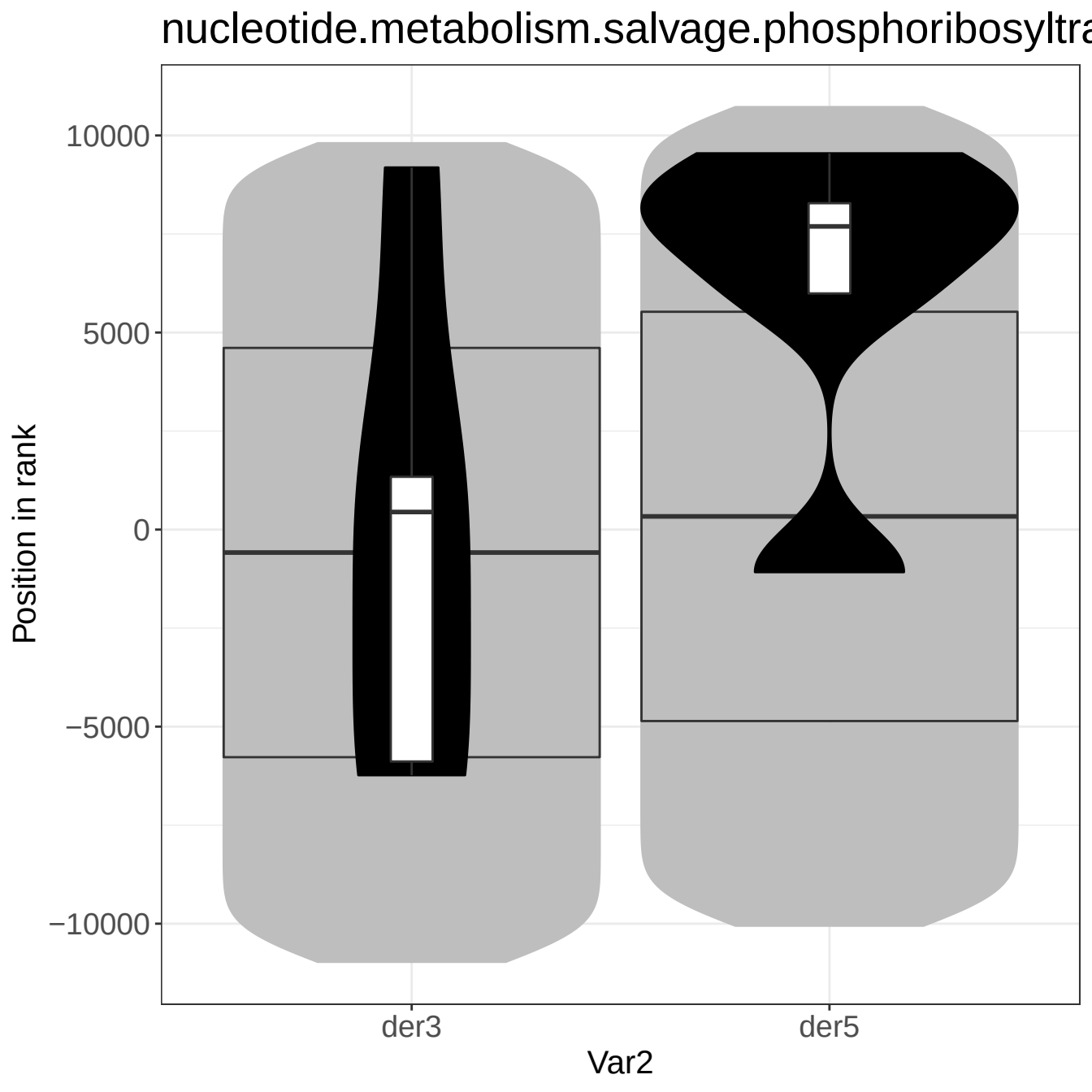
Rank in contrast der3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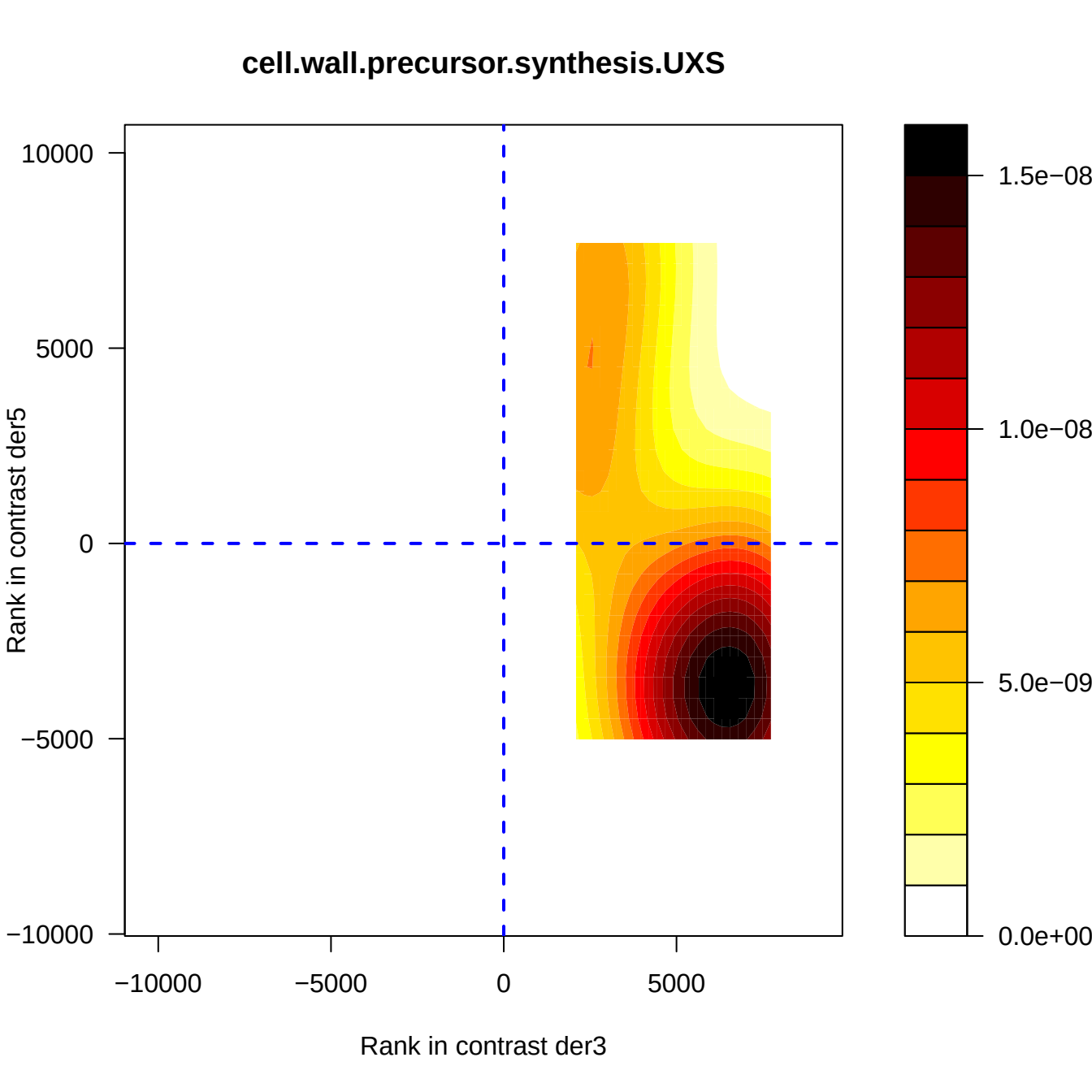
Position in rank
der3
der5
Var2


cell.wall.precursor.synthesis.UXS
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Rank in contrast der3
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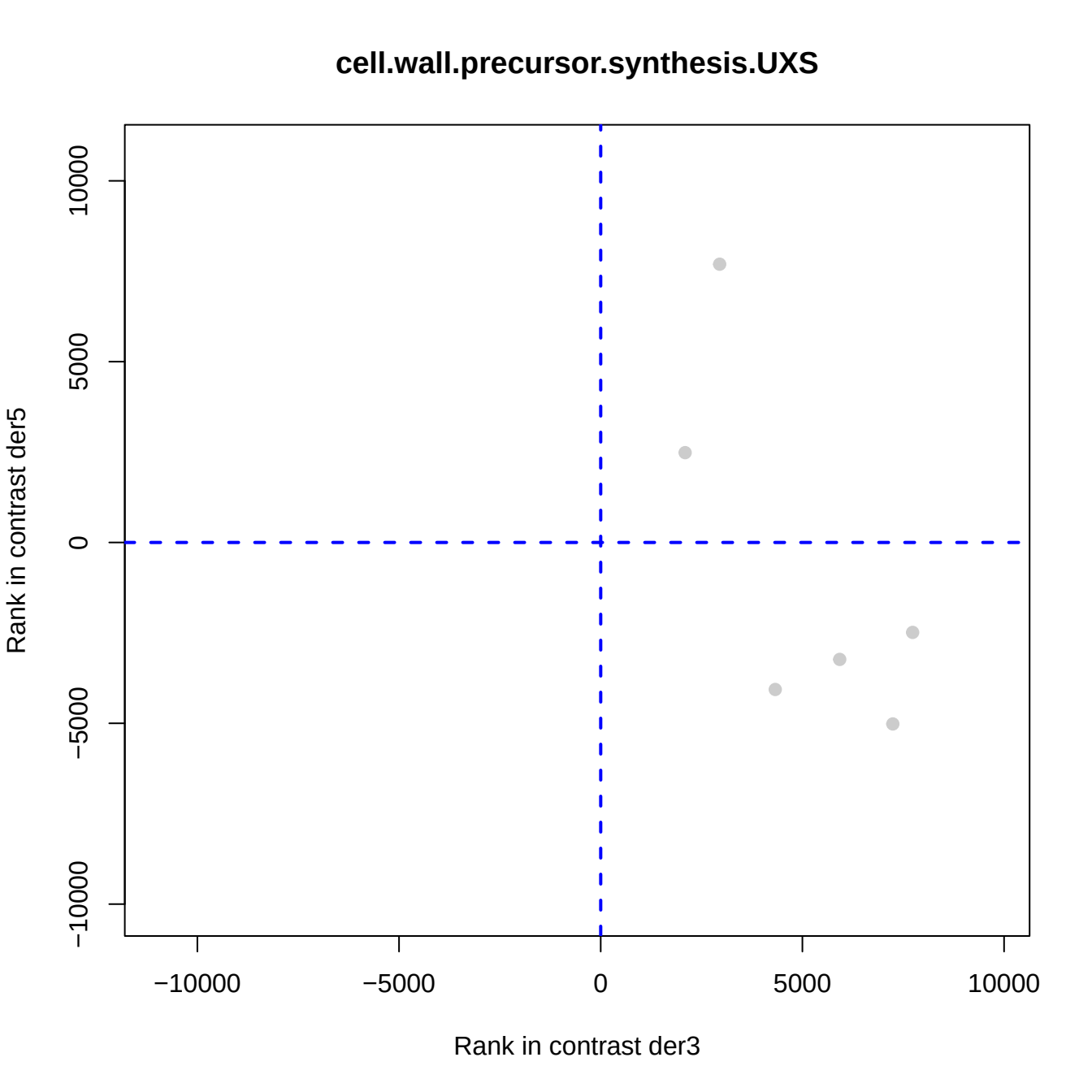
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−5000
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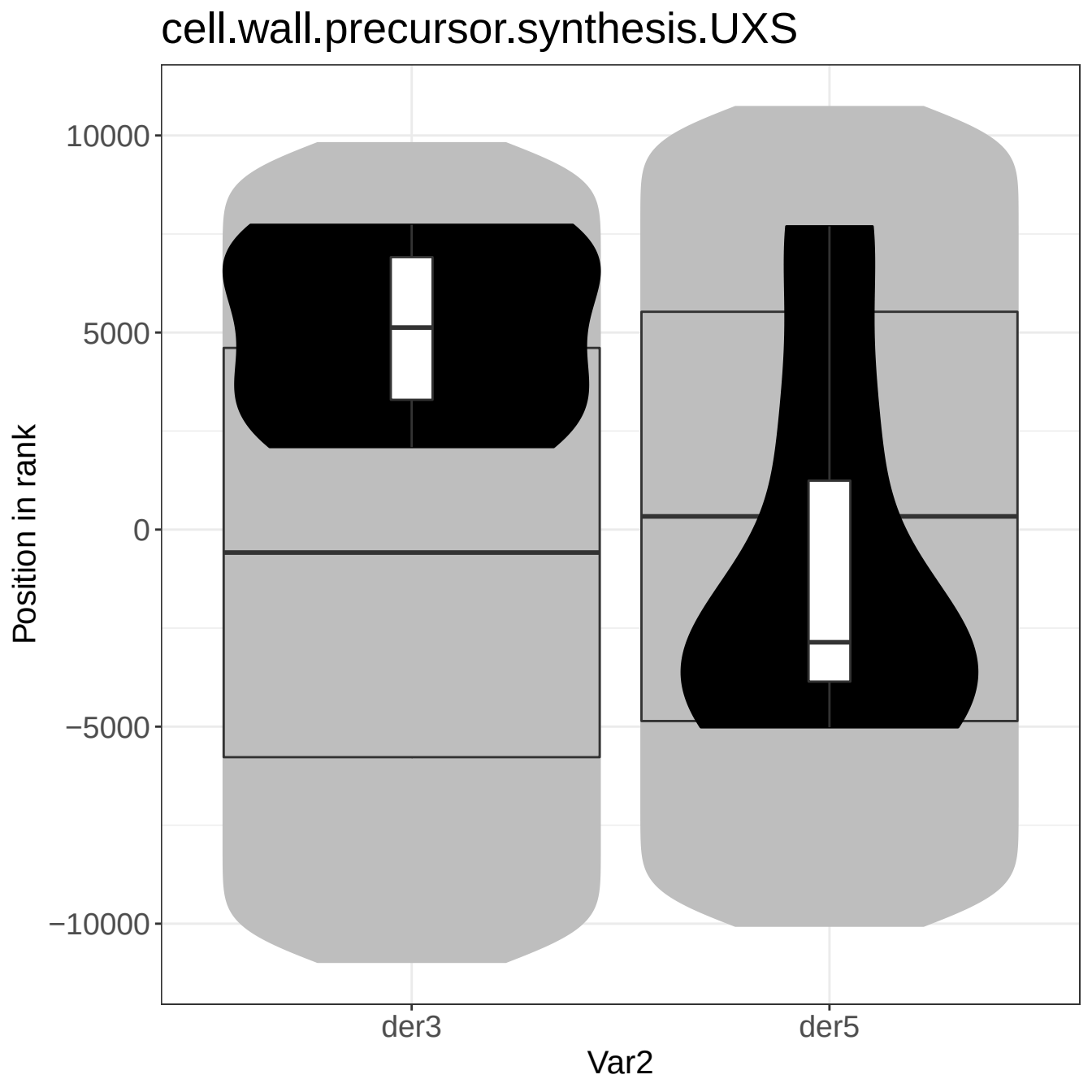
5000
10000
Rank in contrast der3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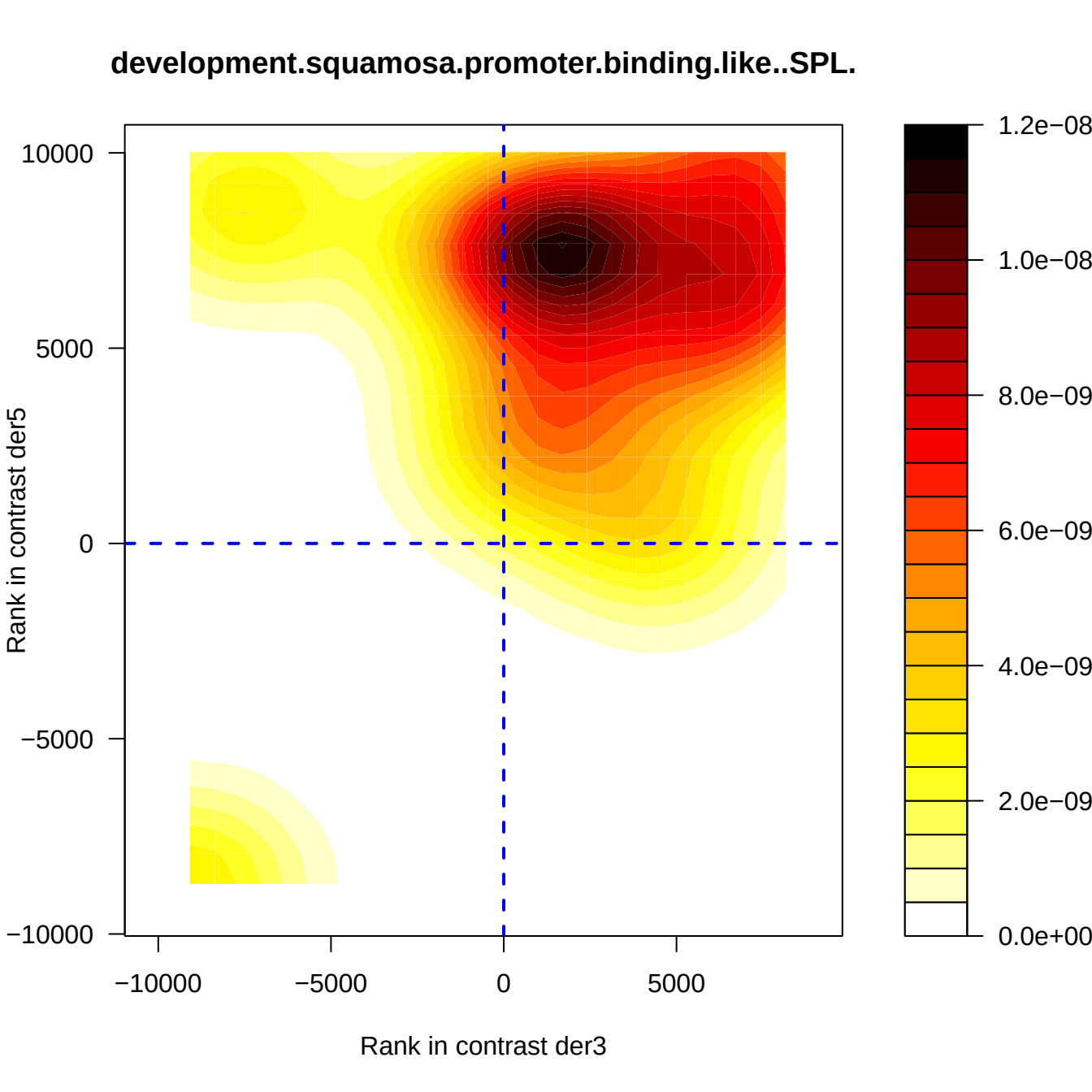
Position in rank
der3
der5
Var2


development.squamosa.promoter.binding.like..SPL.
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Rank in contrast der5
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−5000
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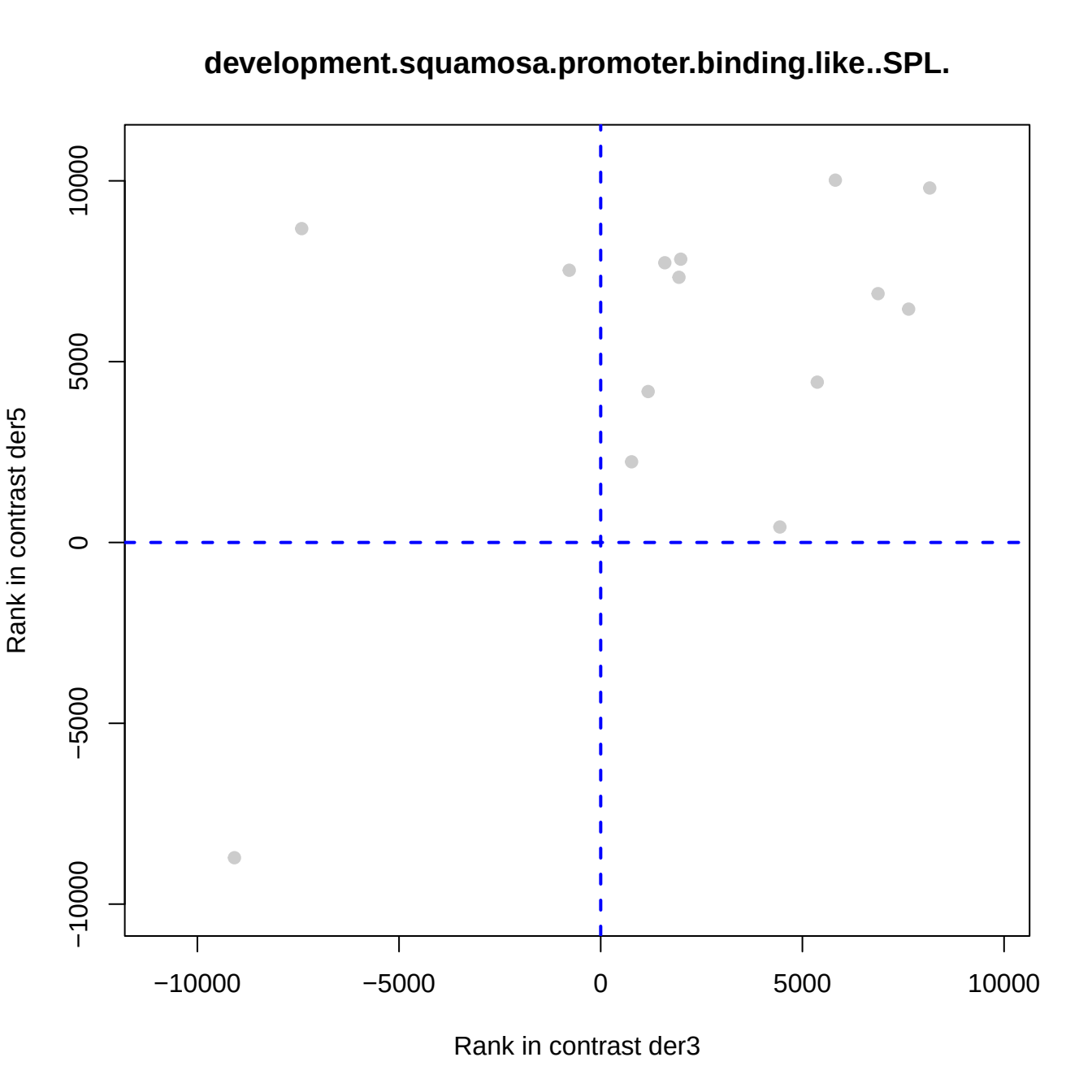
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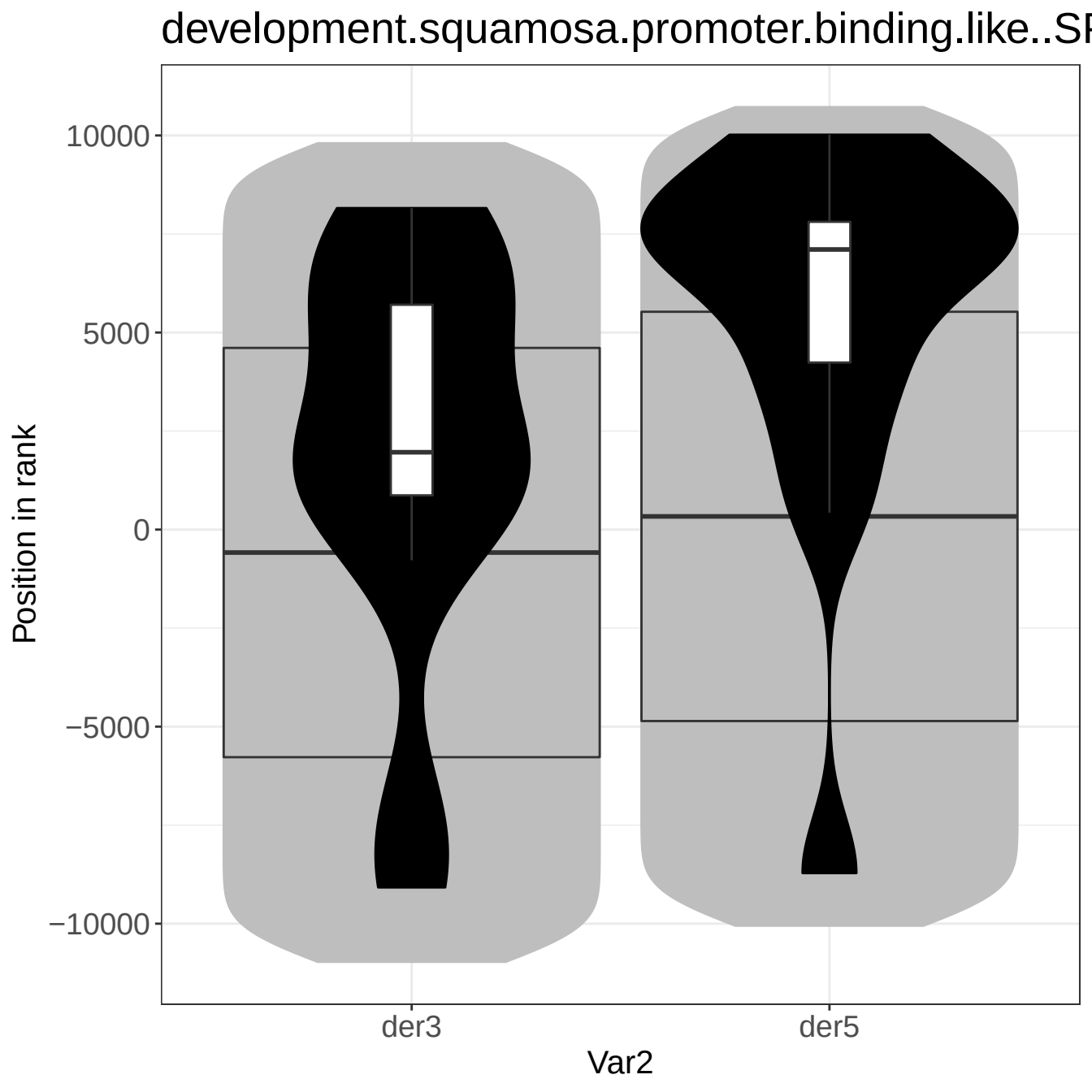
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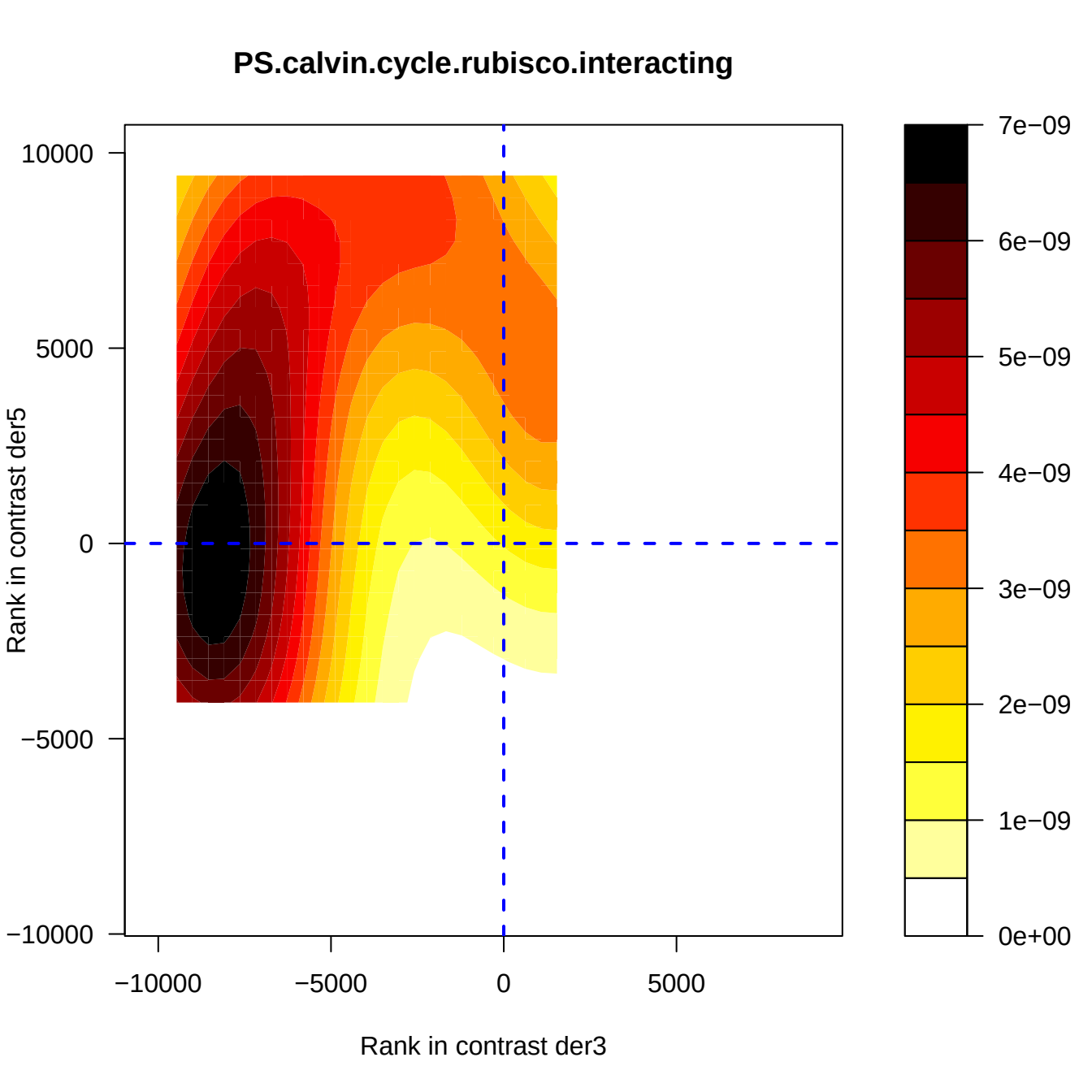
Position in rank
der3
der5
Var2


PS.calvin.cycle.rubisco.interacting
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Rank in contrast der5
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−5000
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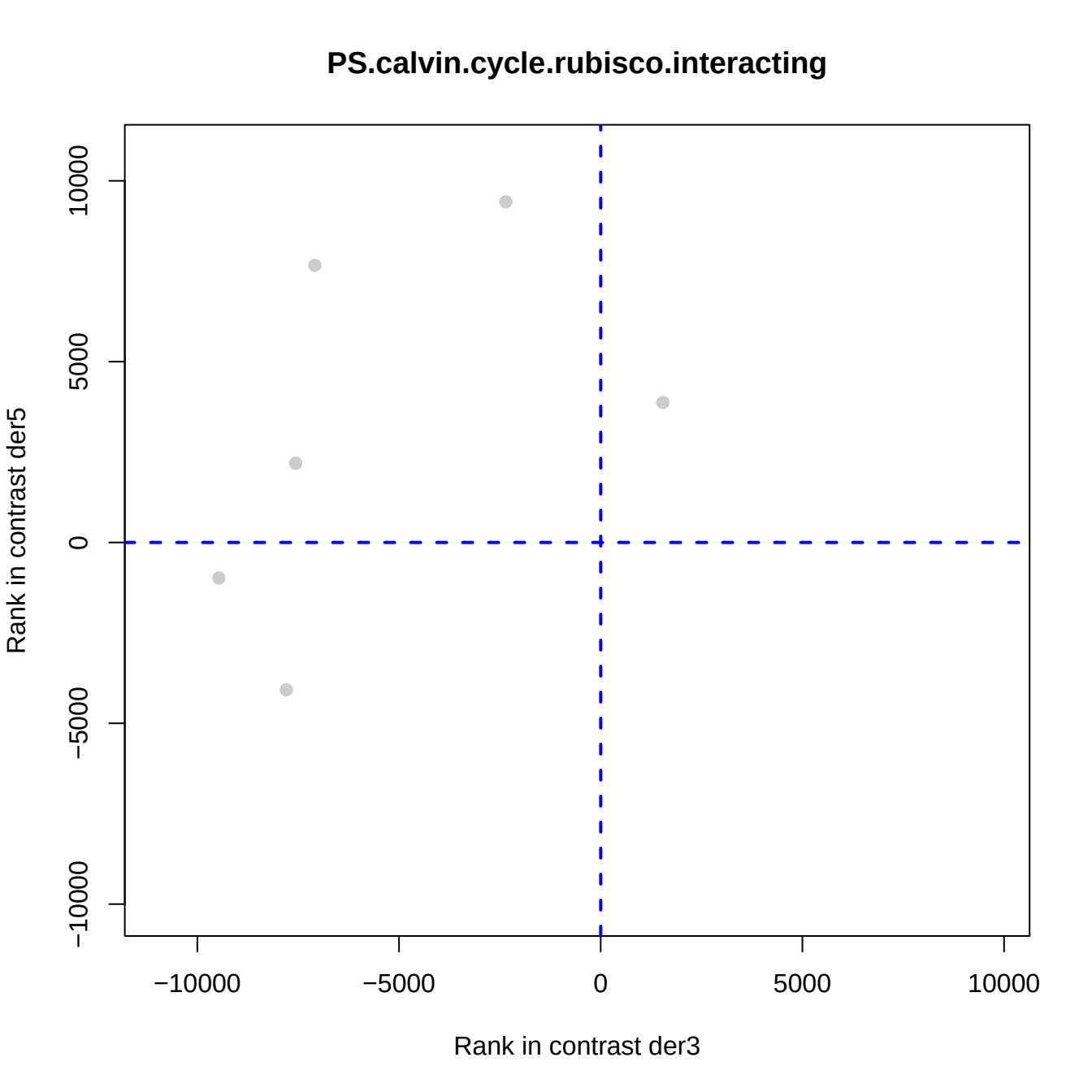
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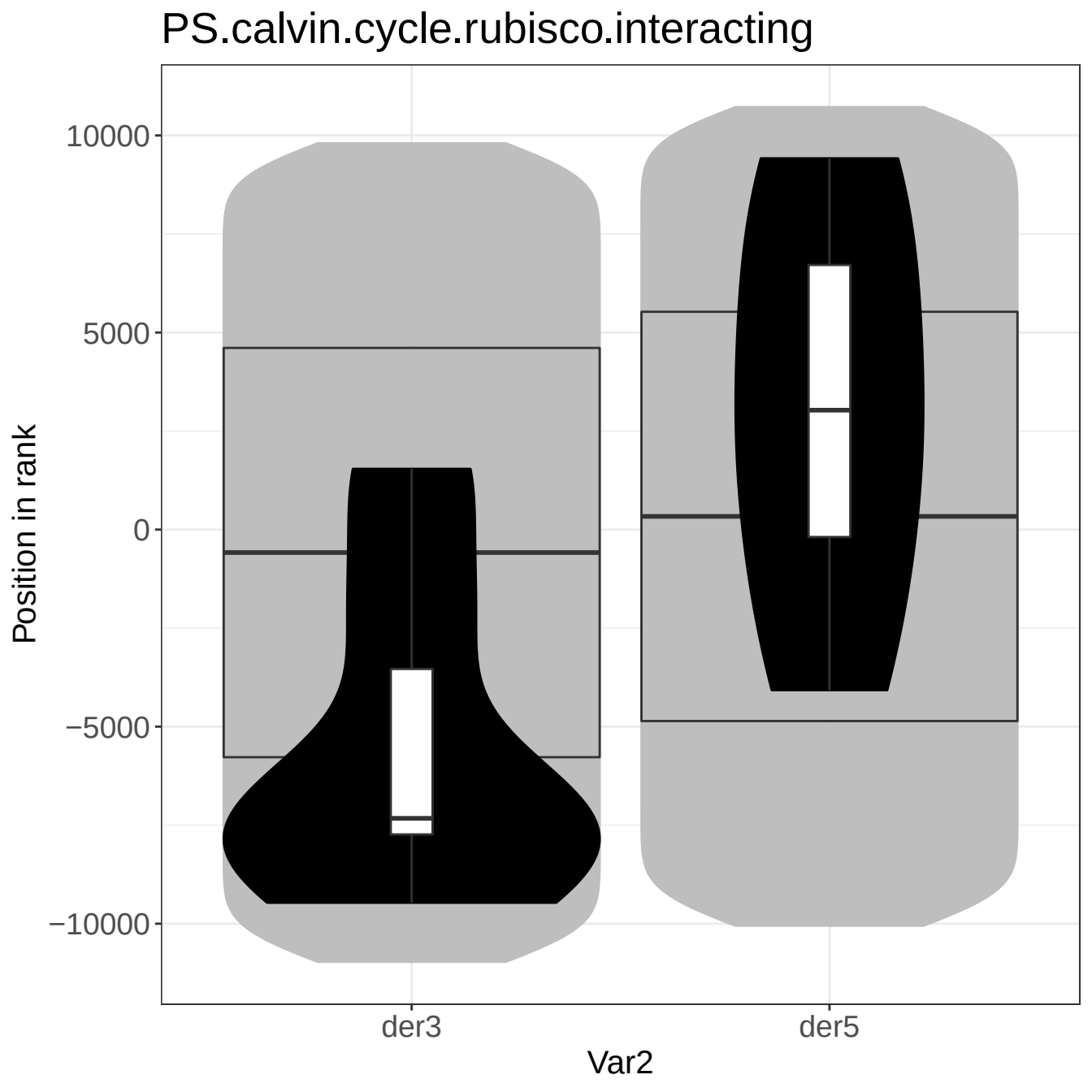
Rank in contrast der3


PS.calvin.cycle.rubisco.interacting
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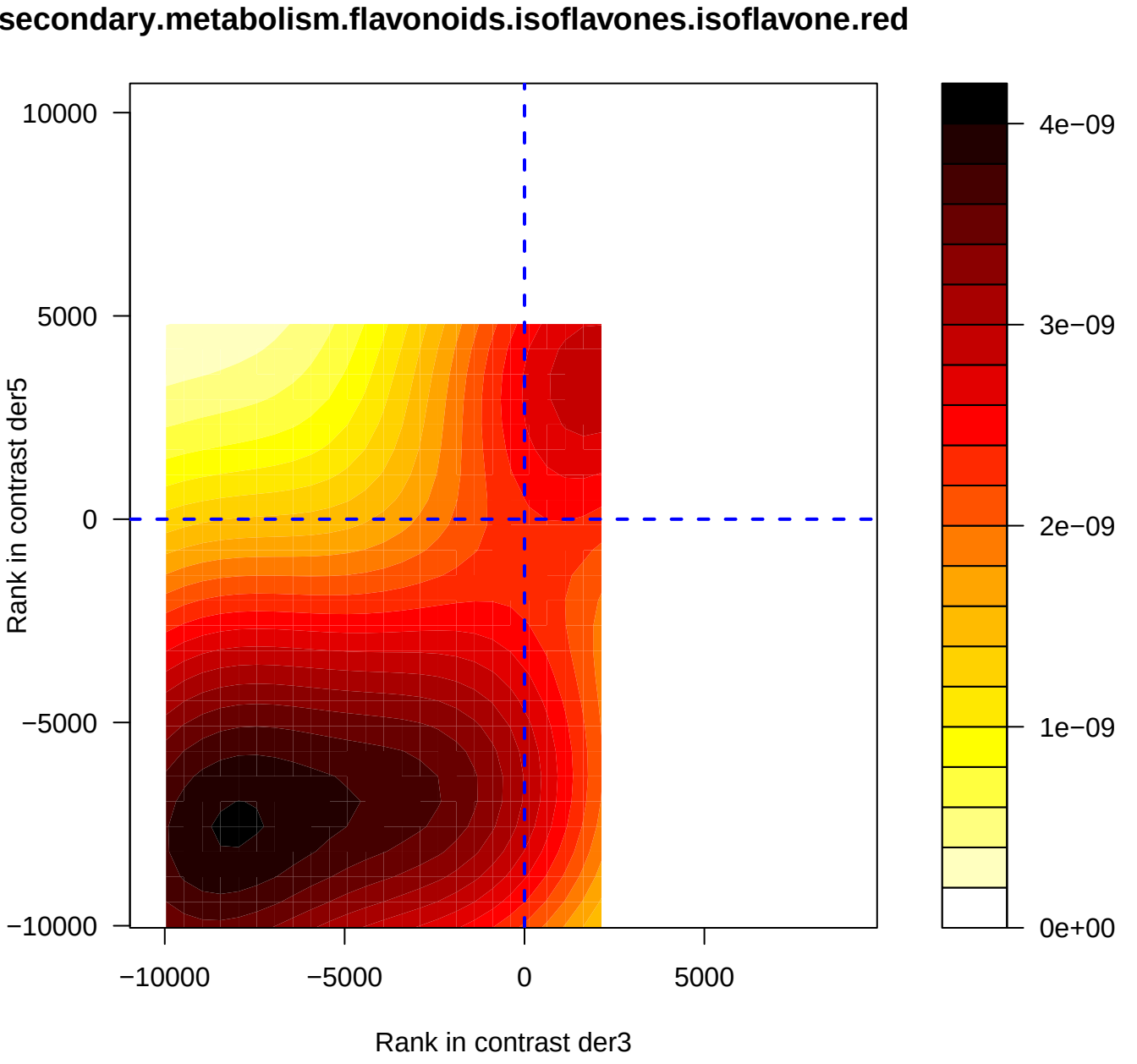
Position in rank
der3
der5
Var2


secondary.metabolism.flavonoids.isoflavones.isoflavone.red
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−5000
−10000
Rank in contrast der5
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−5000
0
5000
Rank in contrast der3
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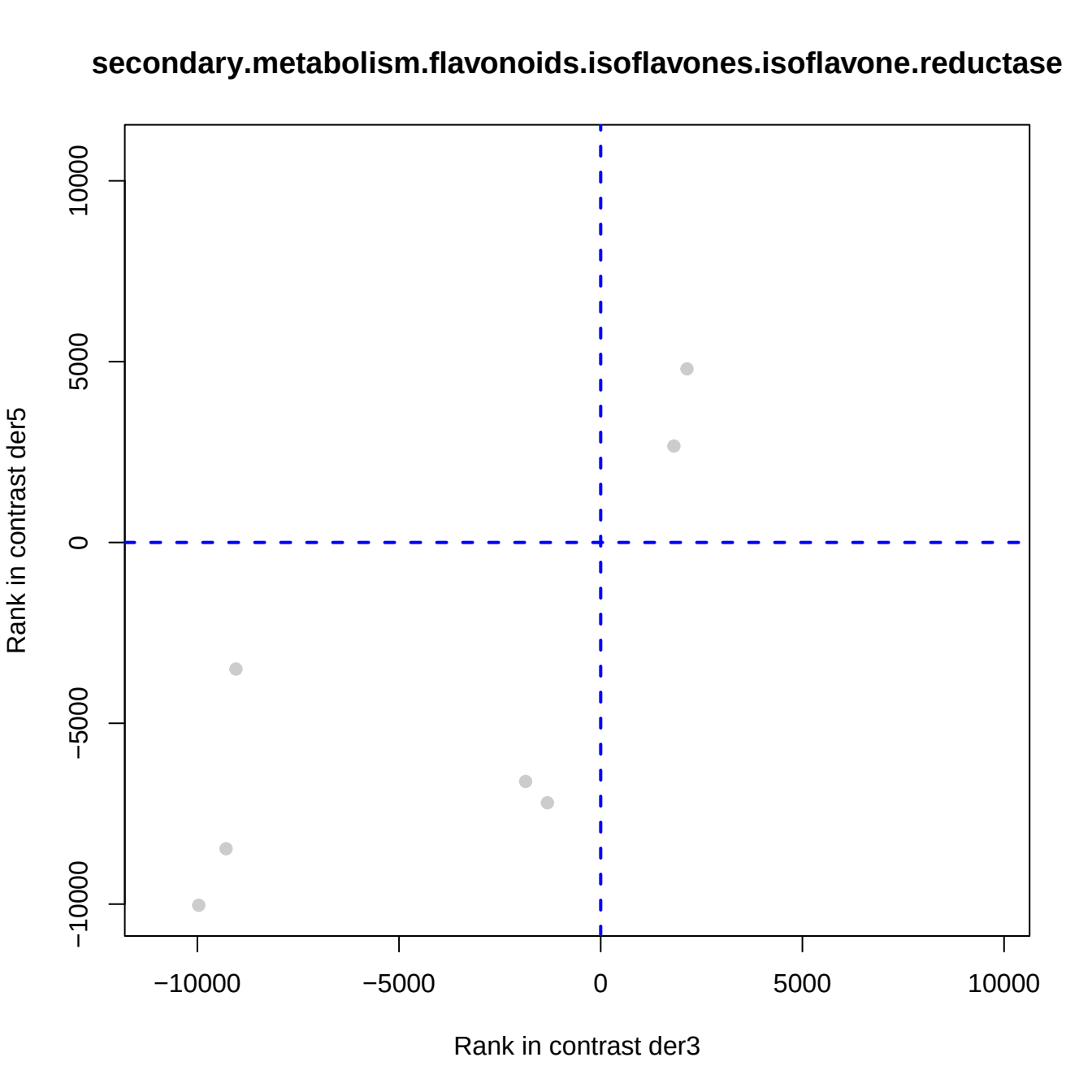
3e−09
2e−09
1e−09
0e+00


secondary.metabolism.flavonoids.isoflavones.isoflavone.reductase
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Rank in contrast der3
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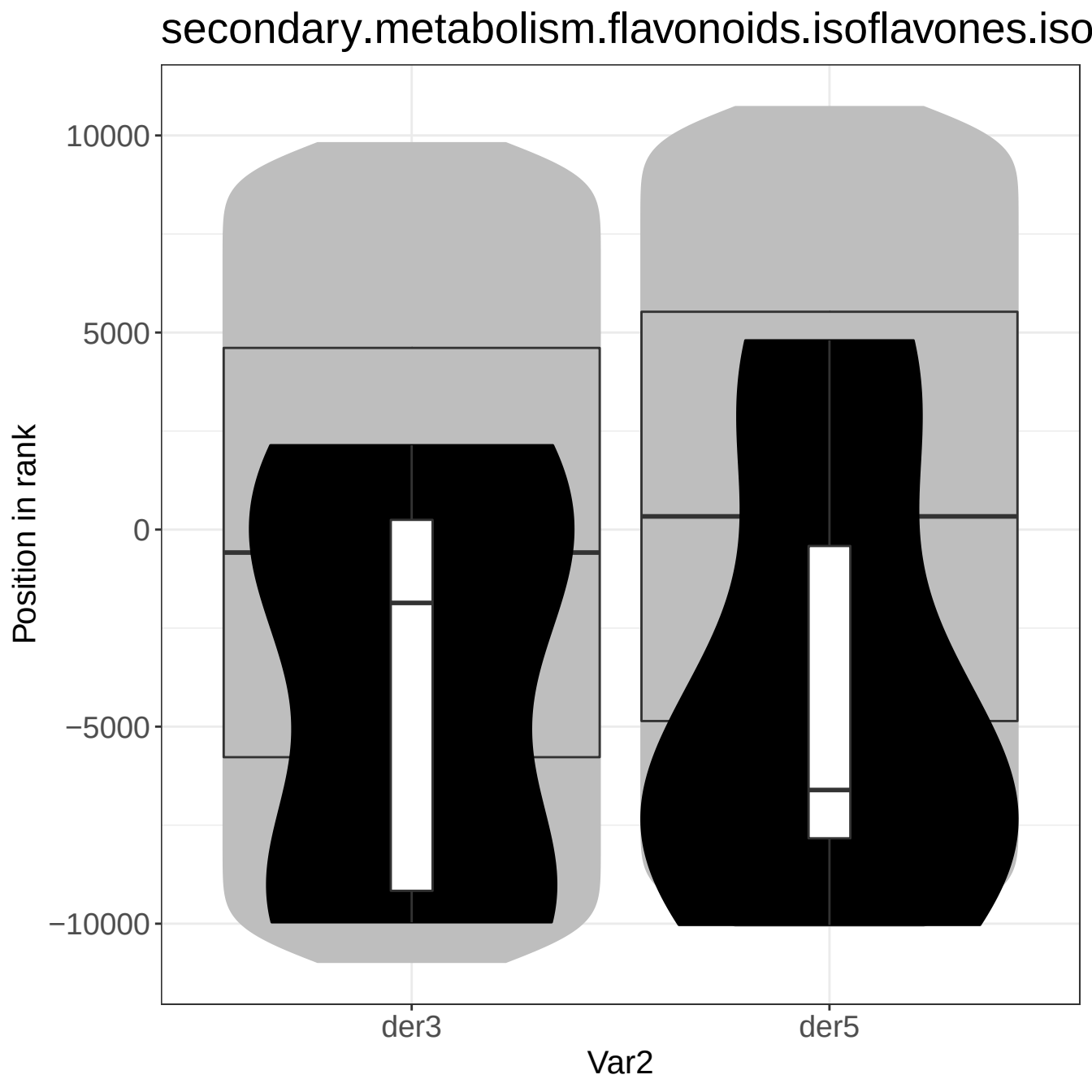
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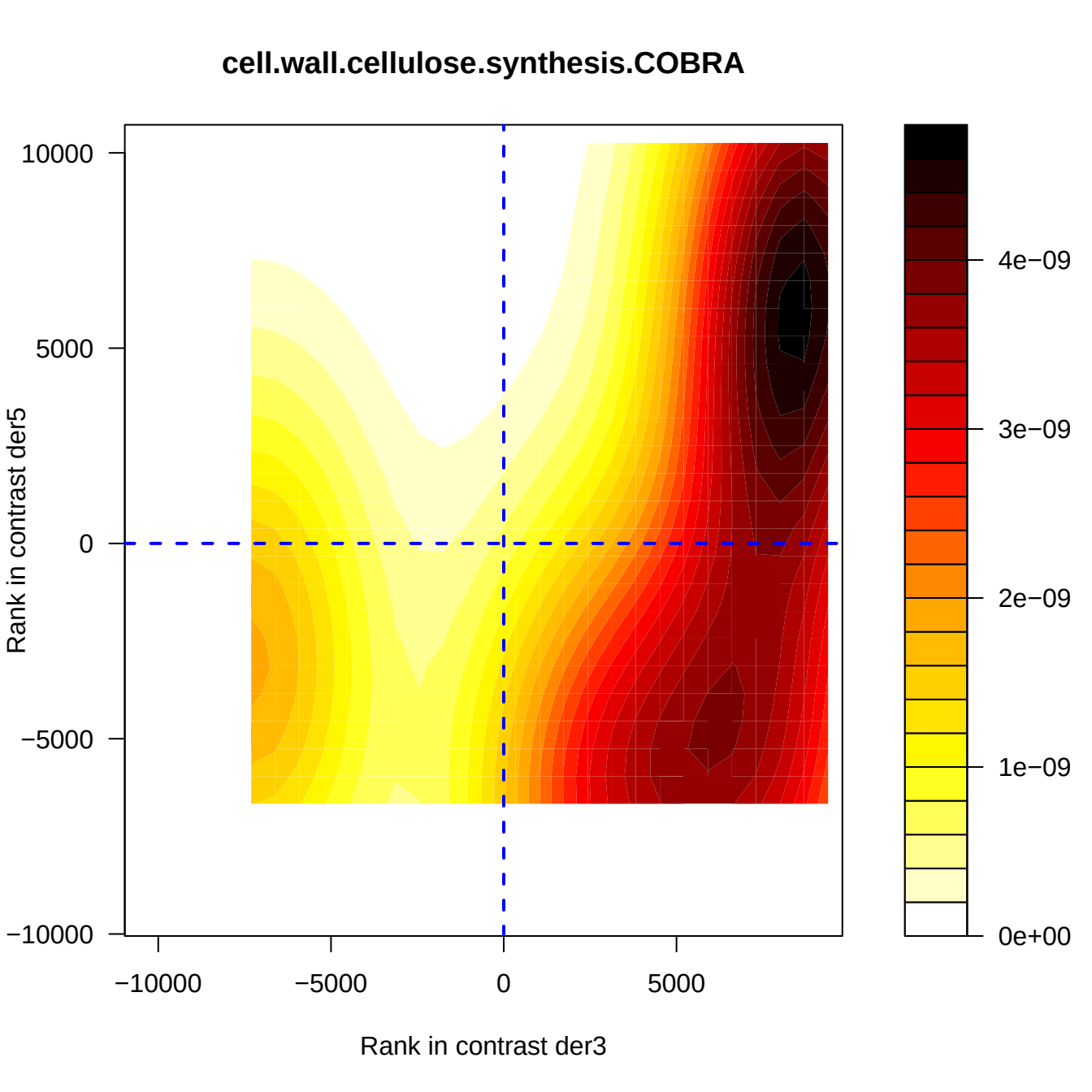
Position in rank
der3
der5
Var2


cell.wall.cellulose.synthesis.COBRA
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Rank in contrast der3
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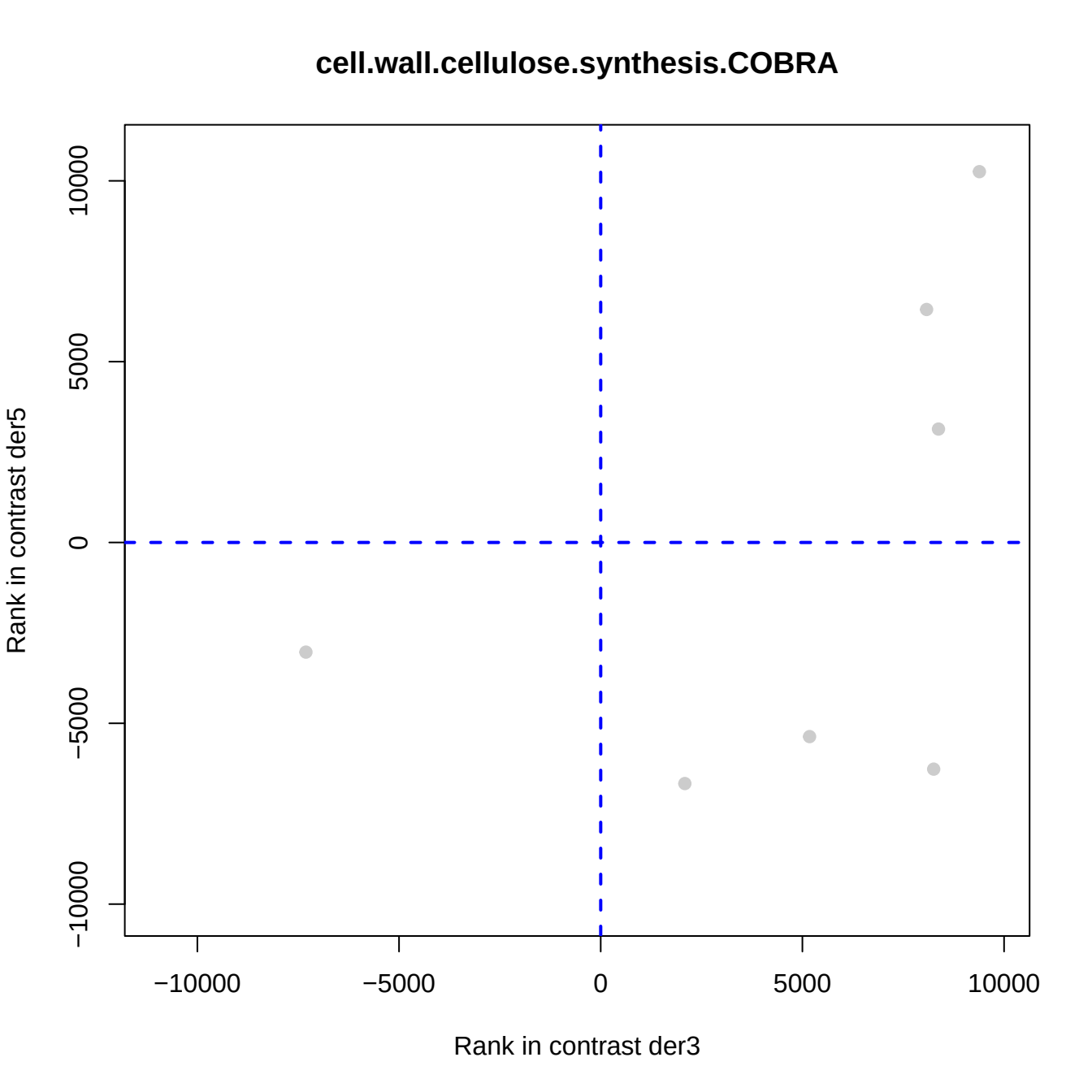
cell.wall.cellulose.synthesis.COBRA
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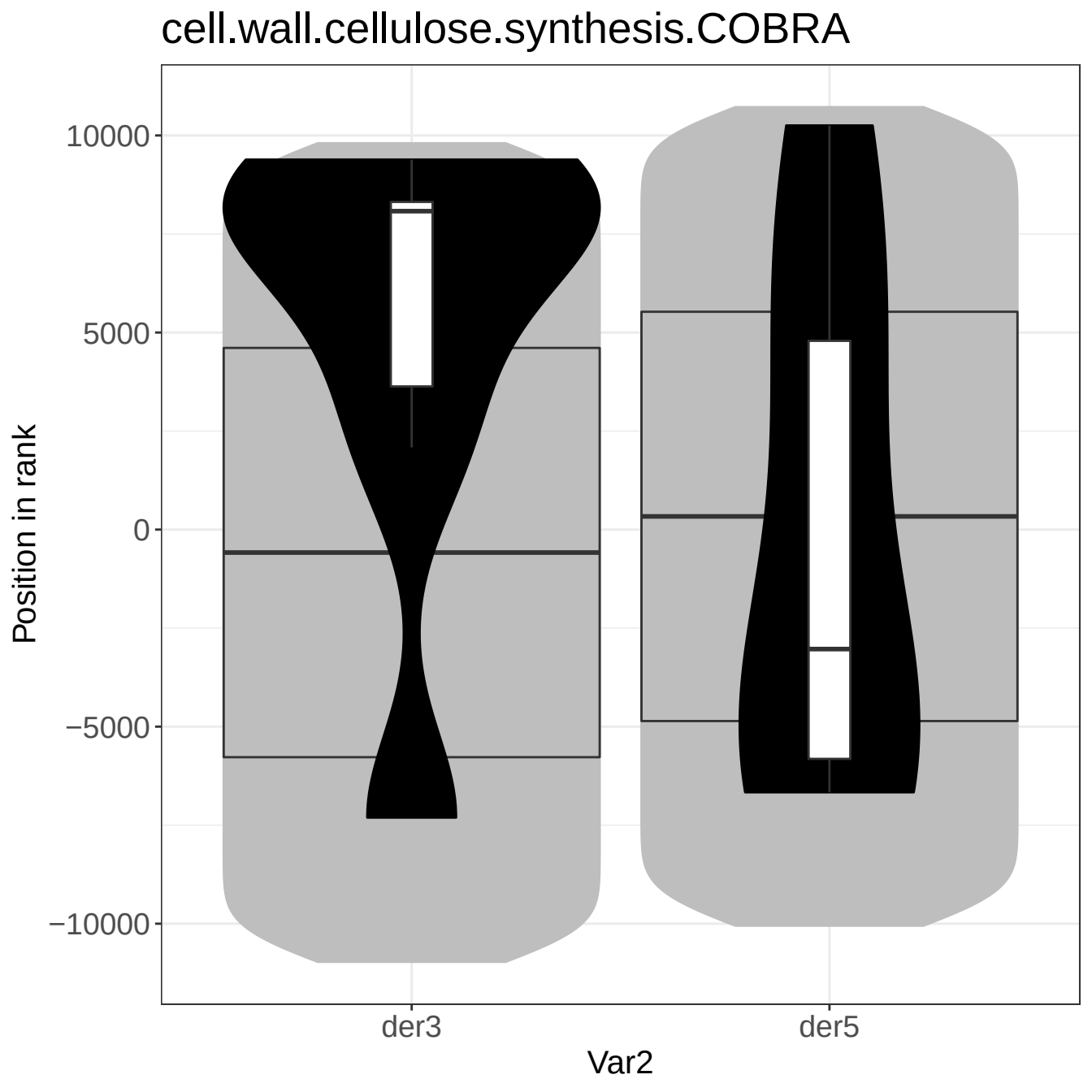
Rank in contrast der3


cell.wall.cellulose.synthesis.COBRA
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−5000
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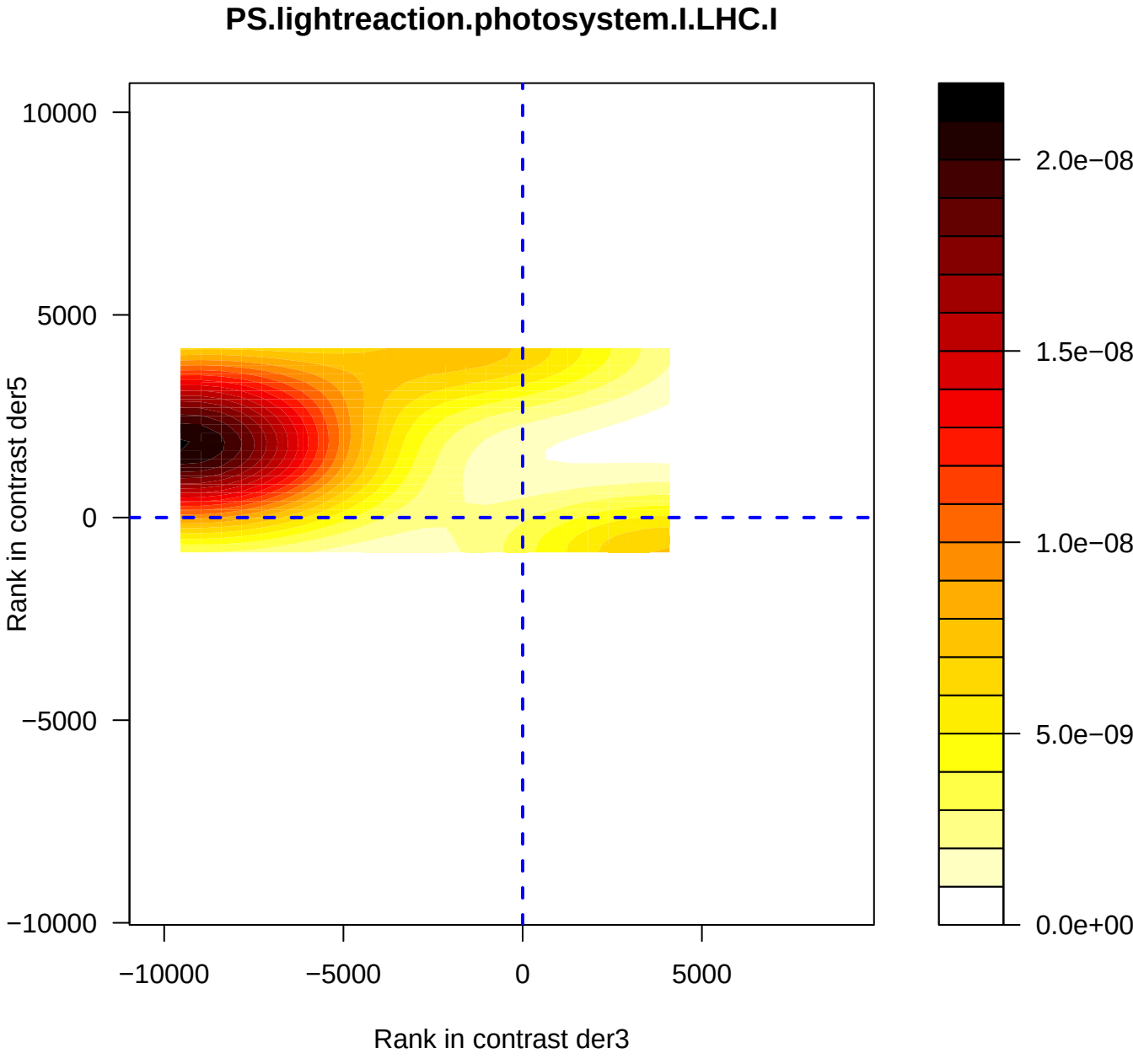
Position in rank
der3
der5
Var2


PS.lightreaction.photosystem.I.LHC.I
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5000
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−5000
−10000
Rank in contrast der5
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−5000
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5000
Rank in contrast der3
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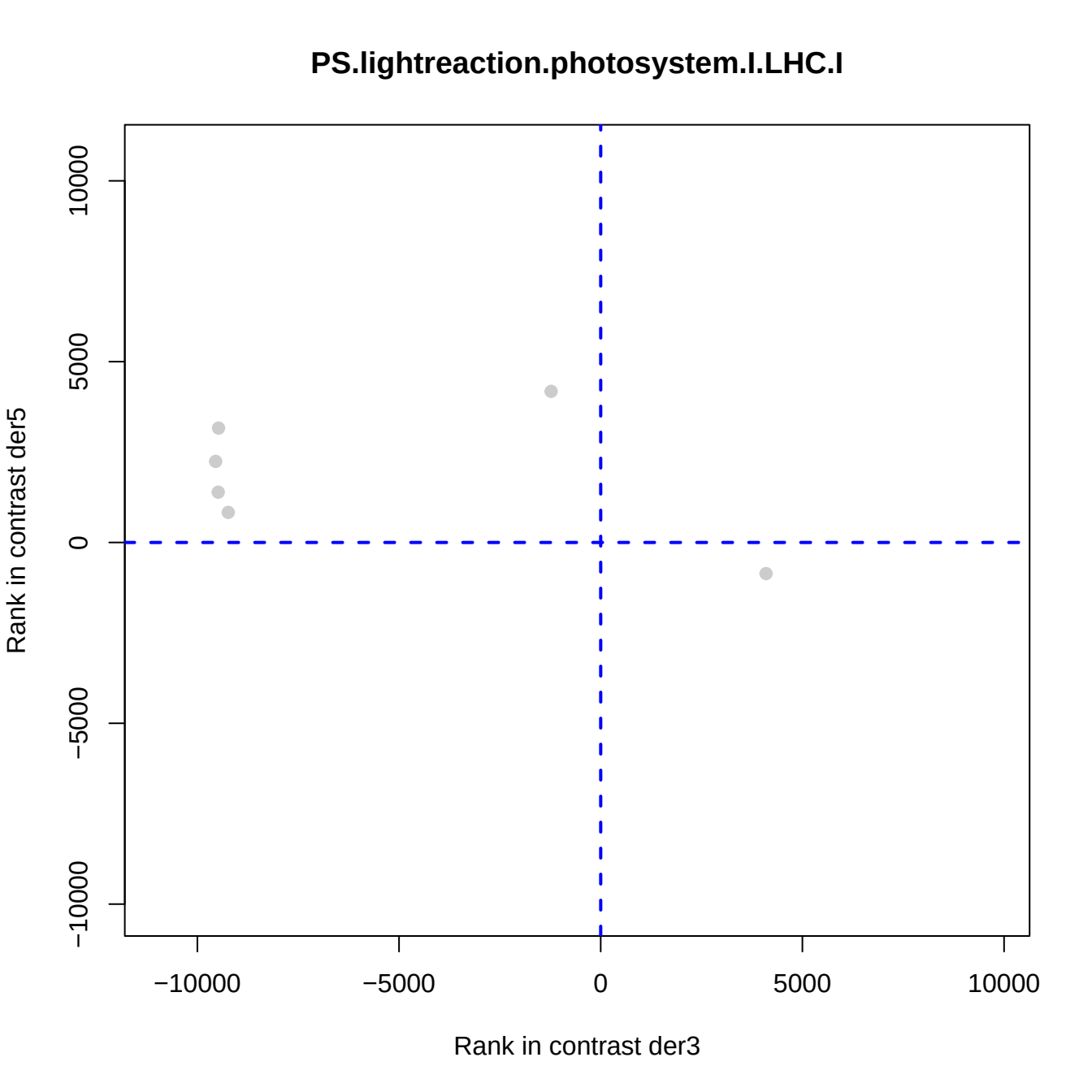
1.5e−08
1.0e−08
5.0e−09
0.0e+00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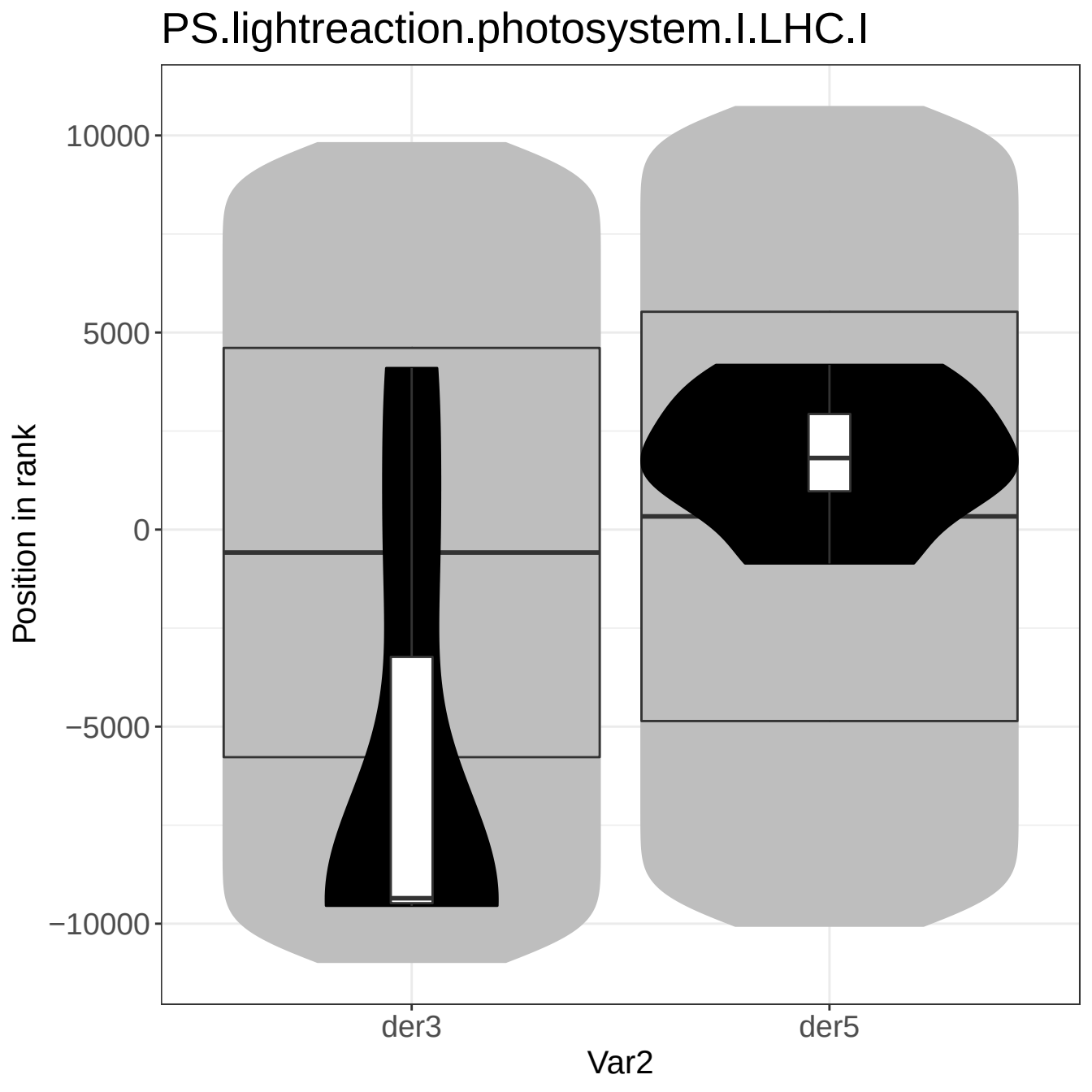
Rank in contrast der3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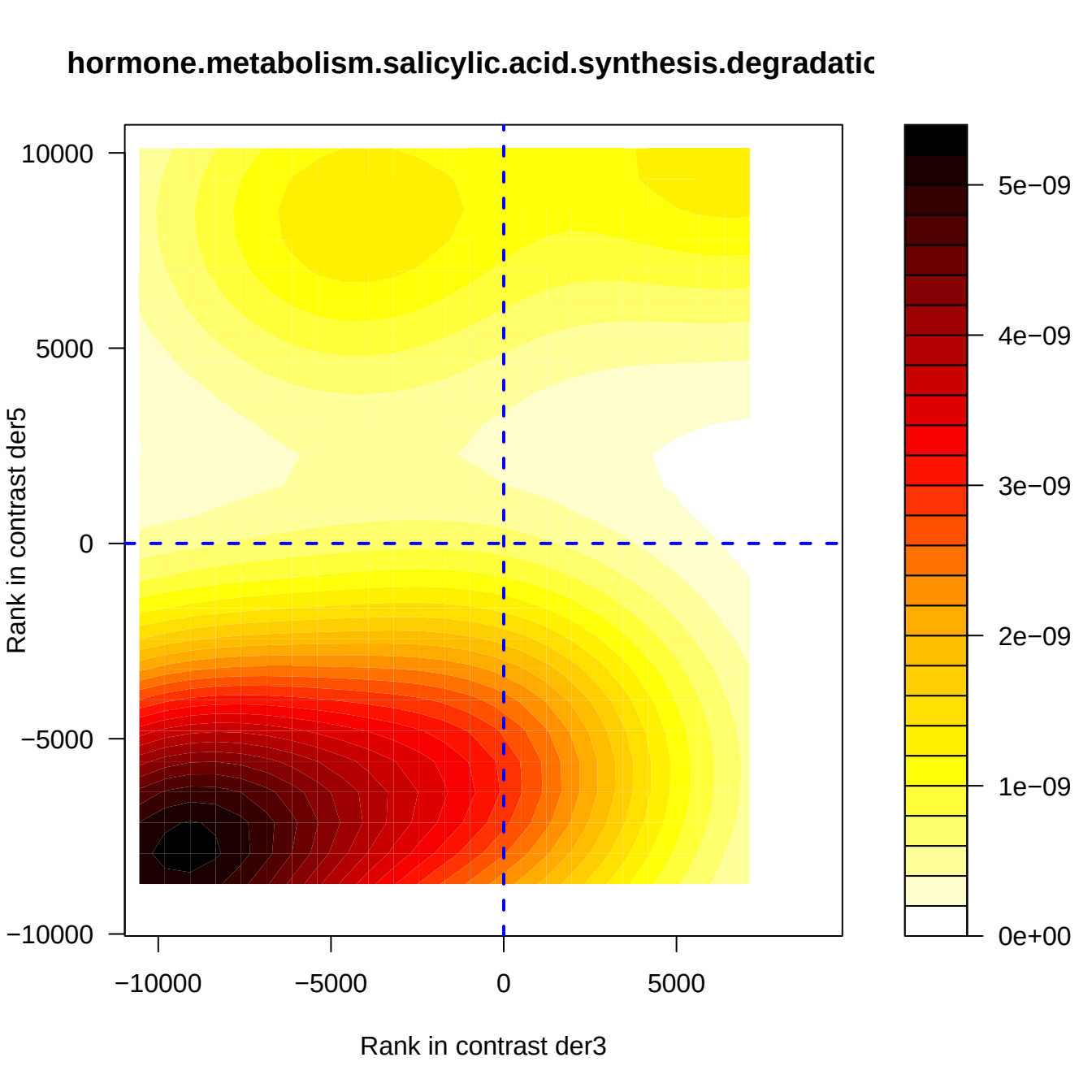
Position in rank
der3
der5
Var2


hormone.metabolism.salicylic.acid.synthesis.degradatic
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5000
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−5000
−10000
Rank in contrast der5
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5000
Rank in contrast der3
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4e−09
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1e−09
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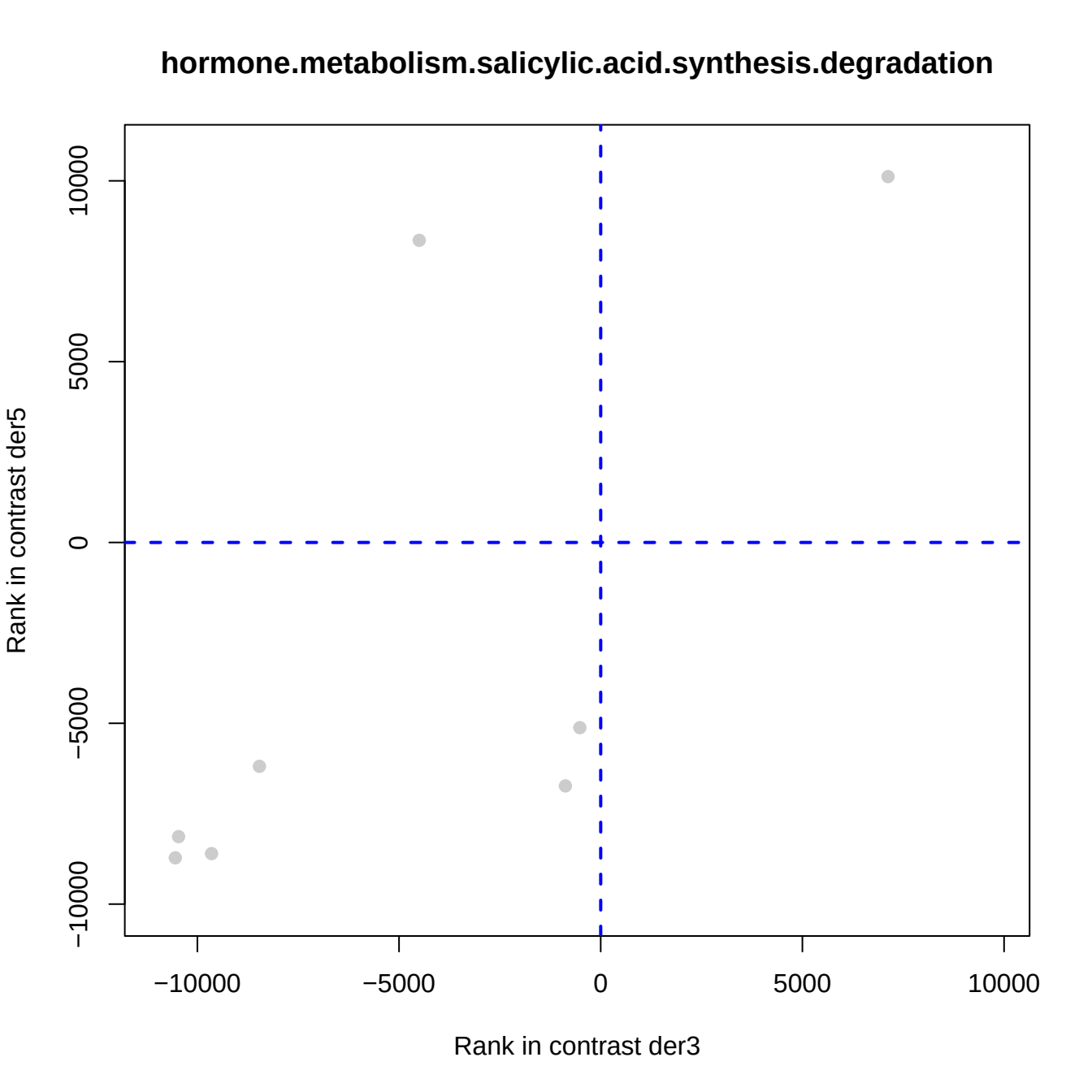
hormone.metabolism.salicylic.acid.synthesis.degradation
Rank in contrast der5
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−5000
−10000
−10000
−5000
0
5000
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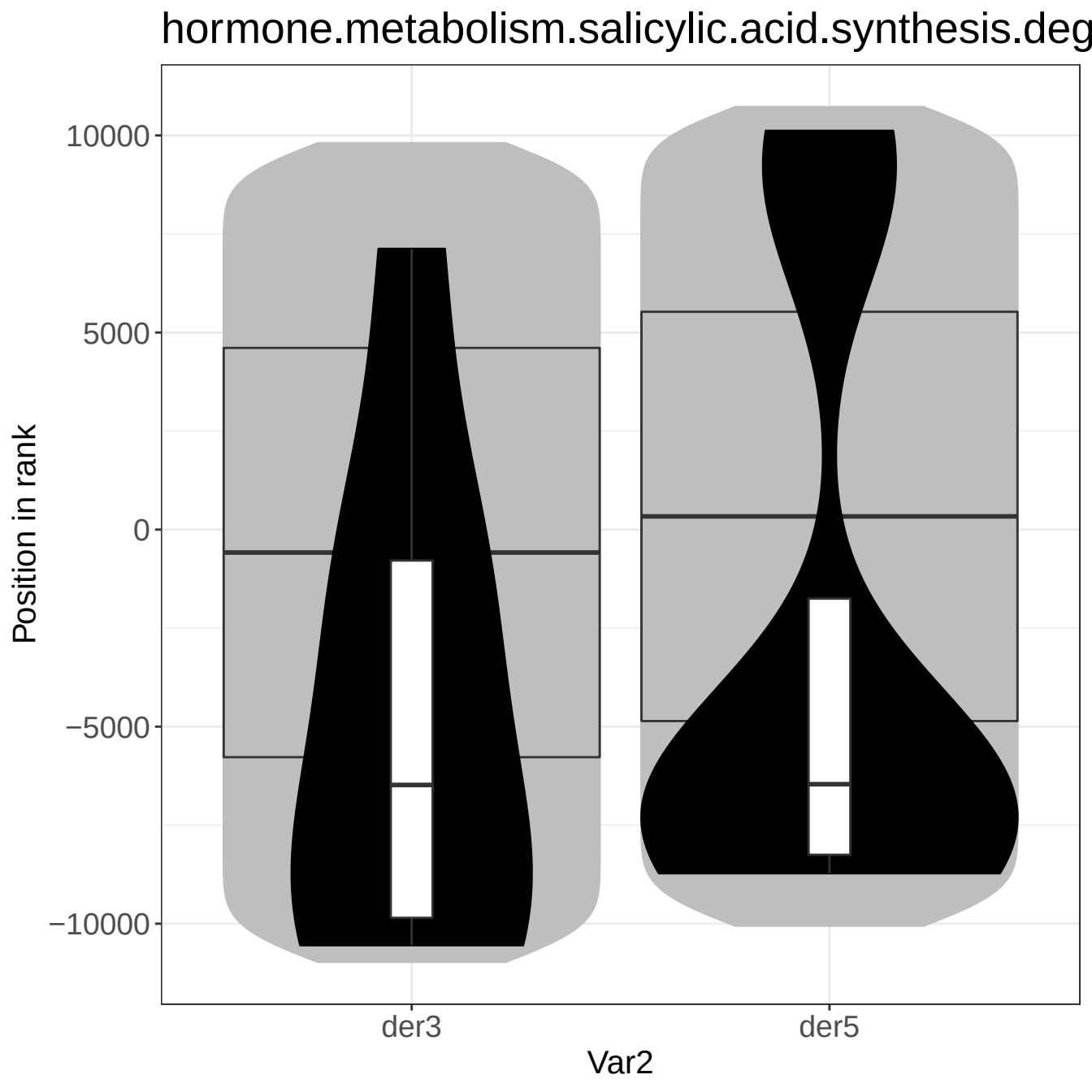
Rank in contrast der3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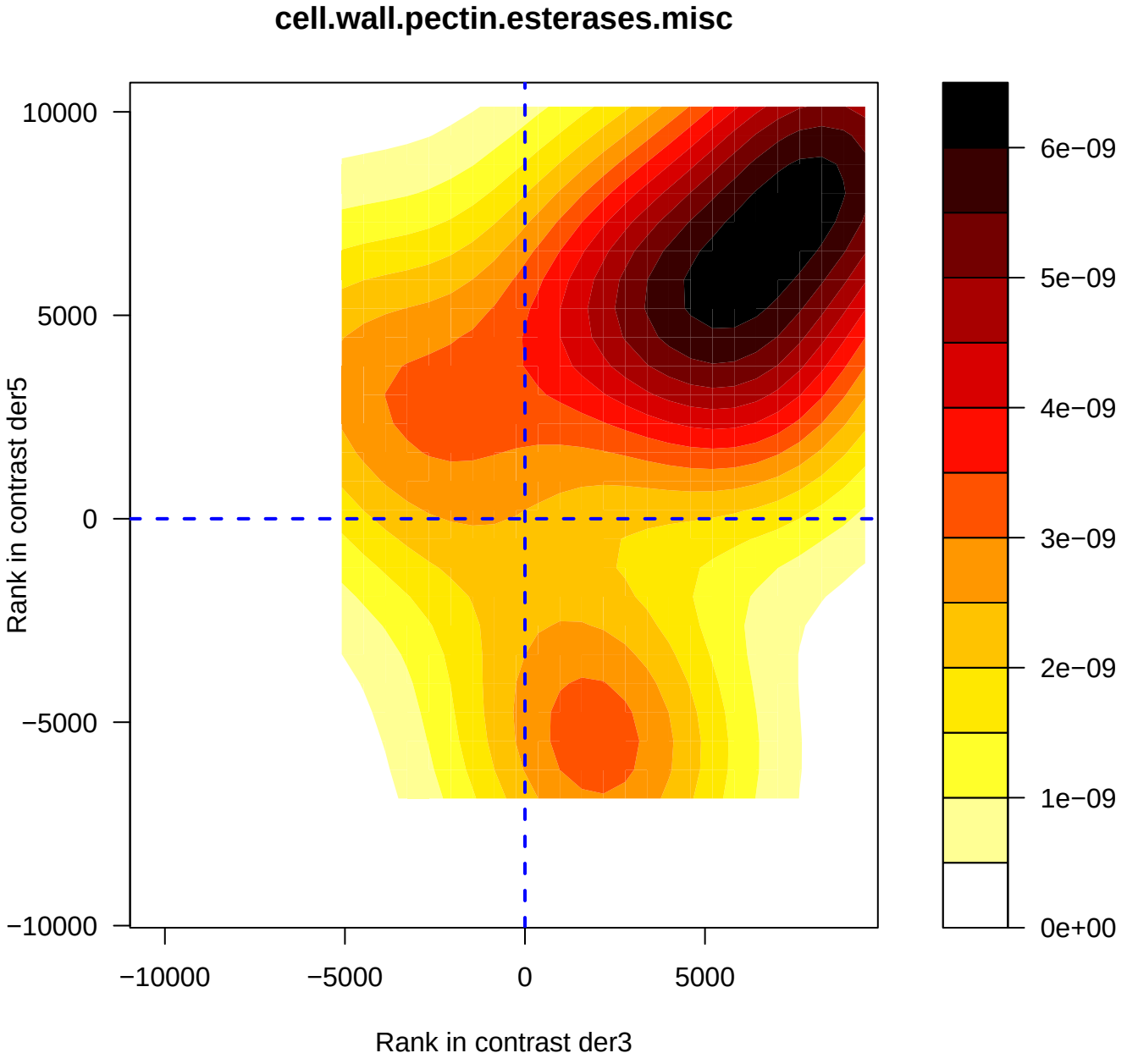
Position in rank
der3
der5
Var2


cell.wall.pectin.esterases.misc
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Rank in contrast der3
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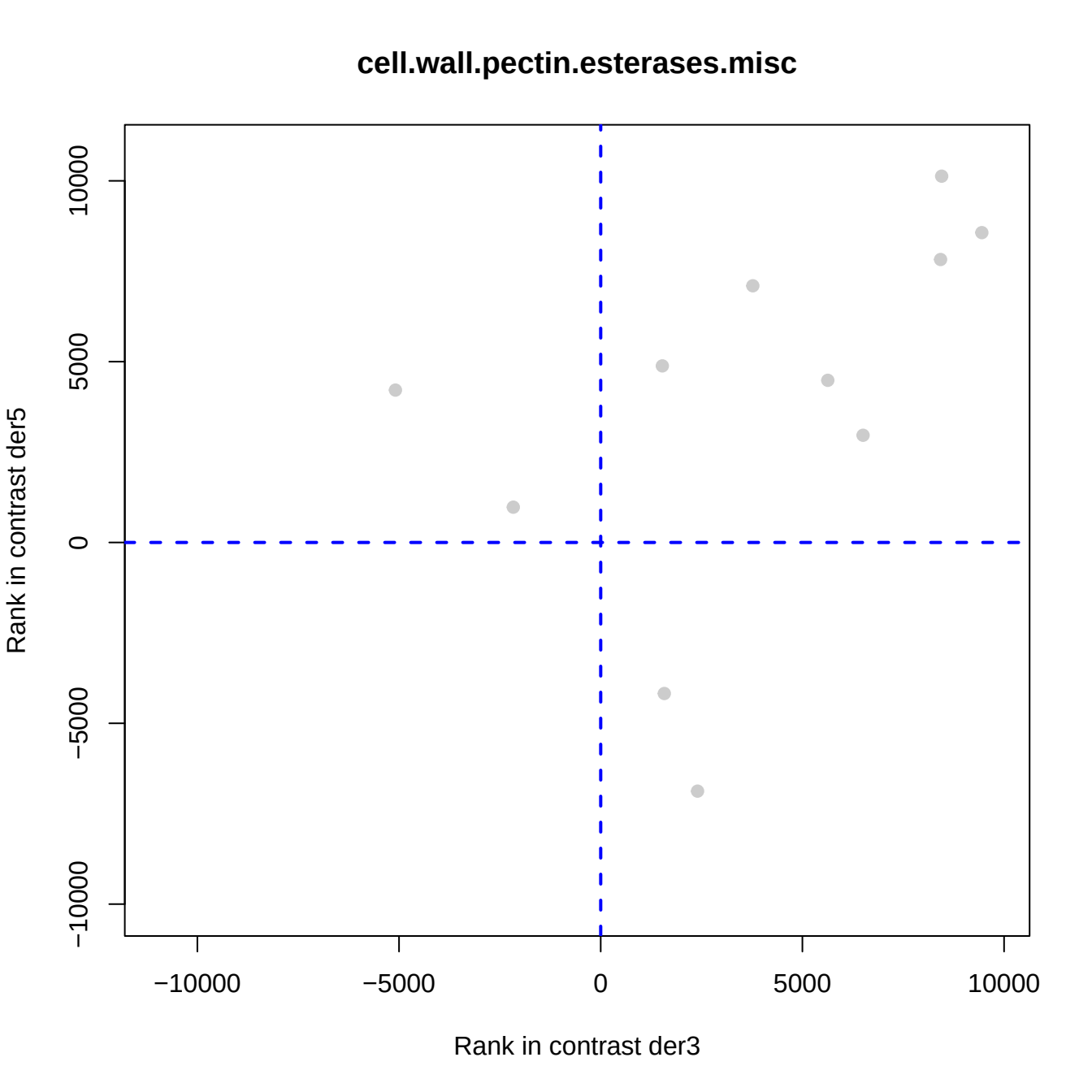
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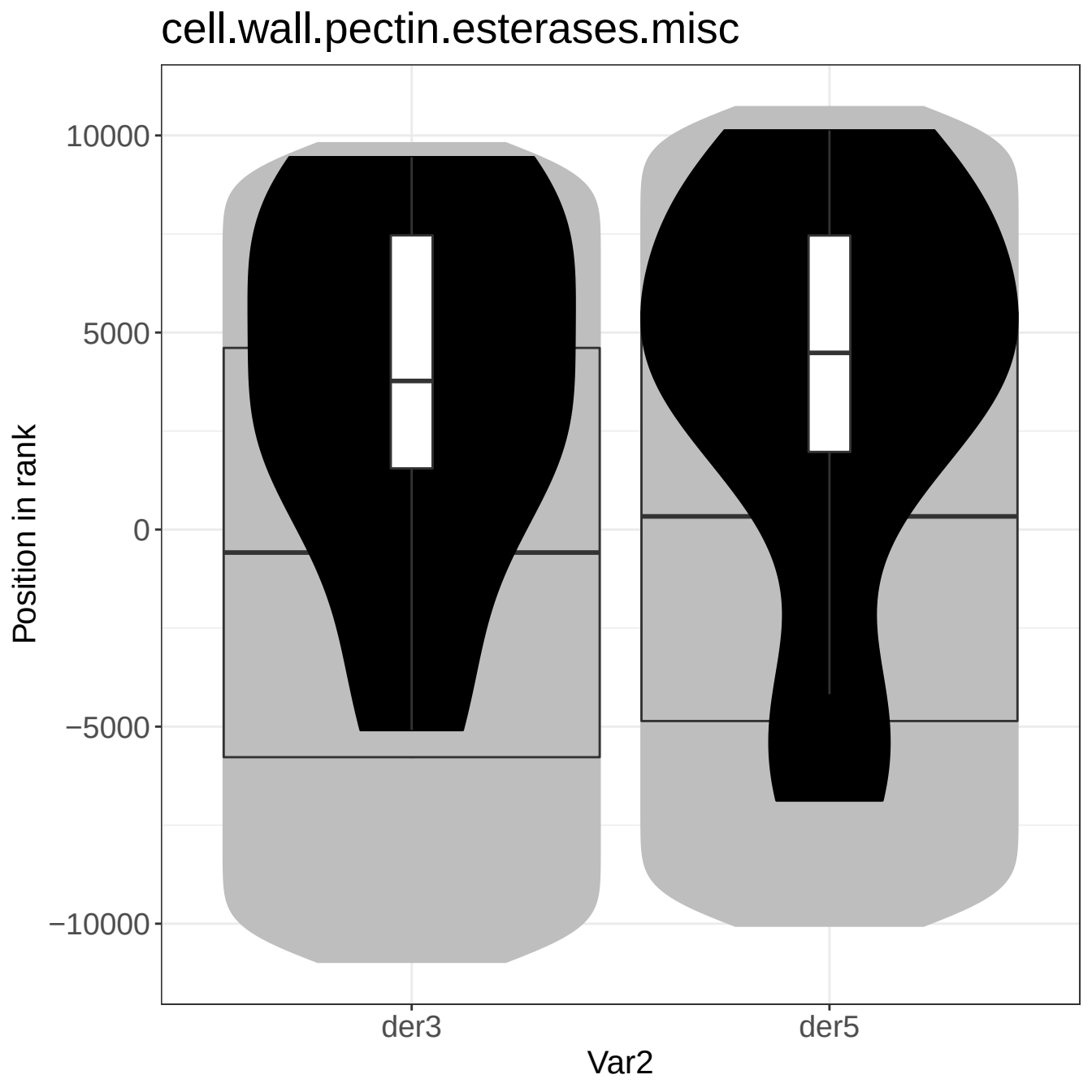
Rank in contrast der3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Position in rank
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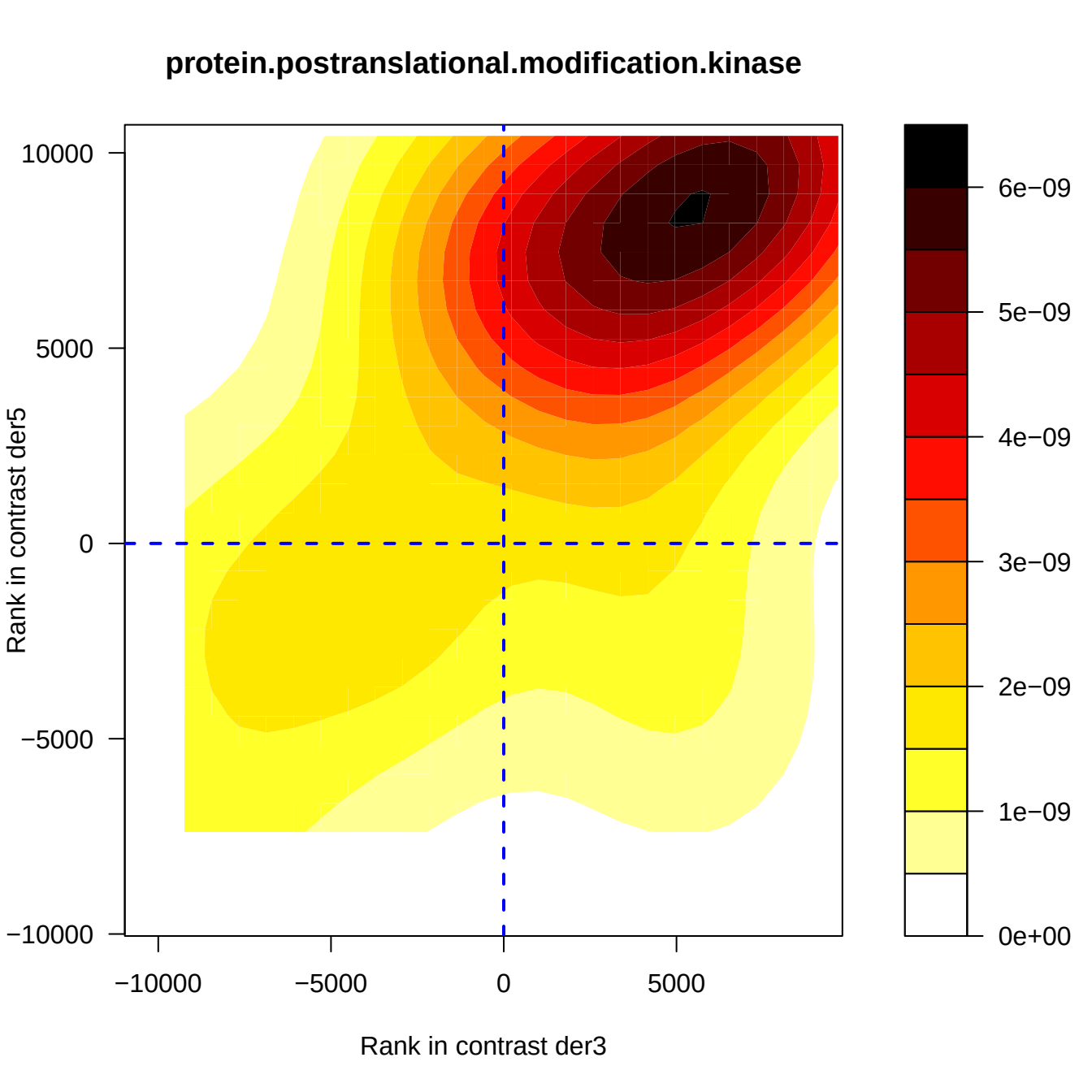
der5
Var2


protein.postranslational.modification.kinase
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Rank in contrast der5
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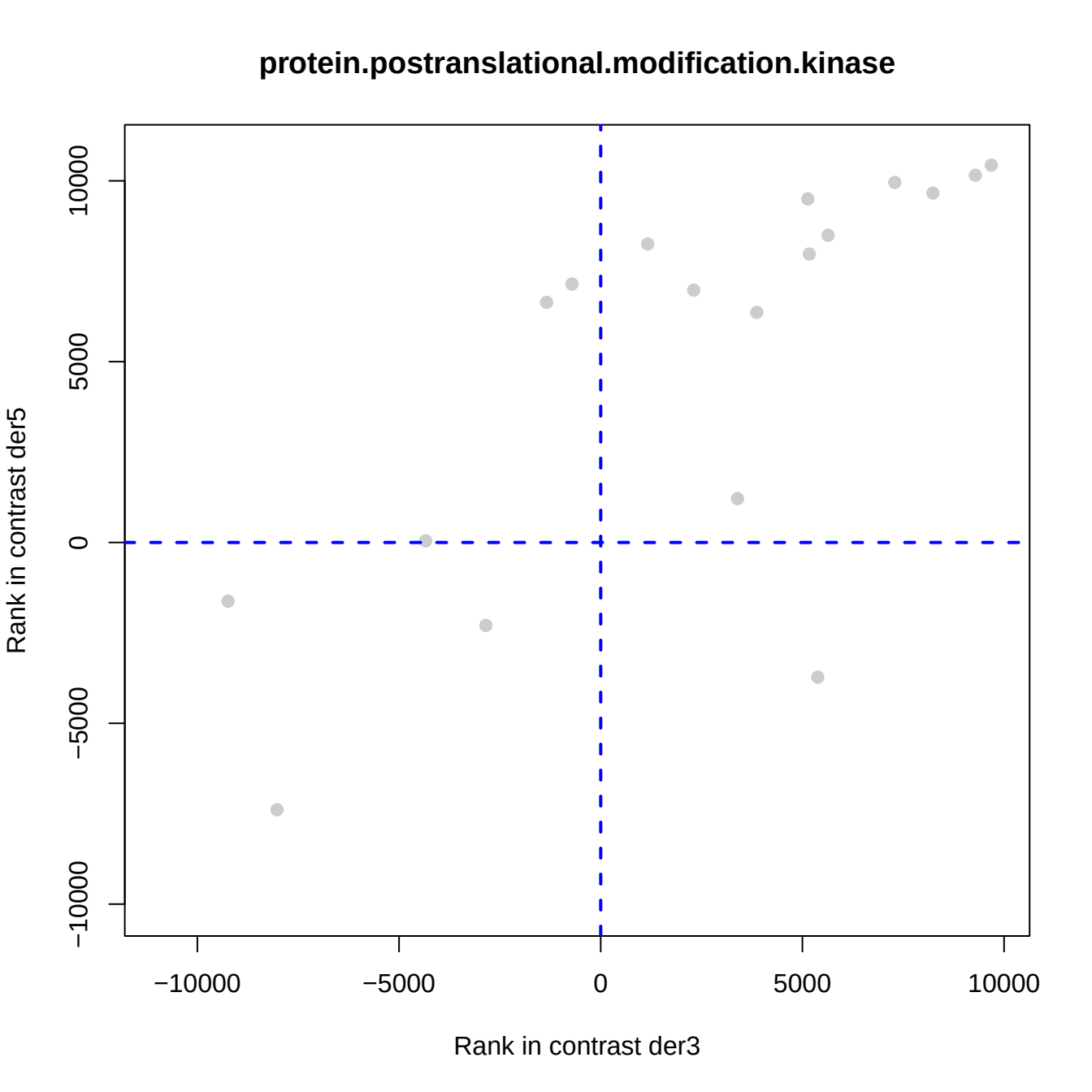
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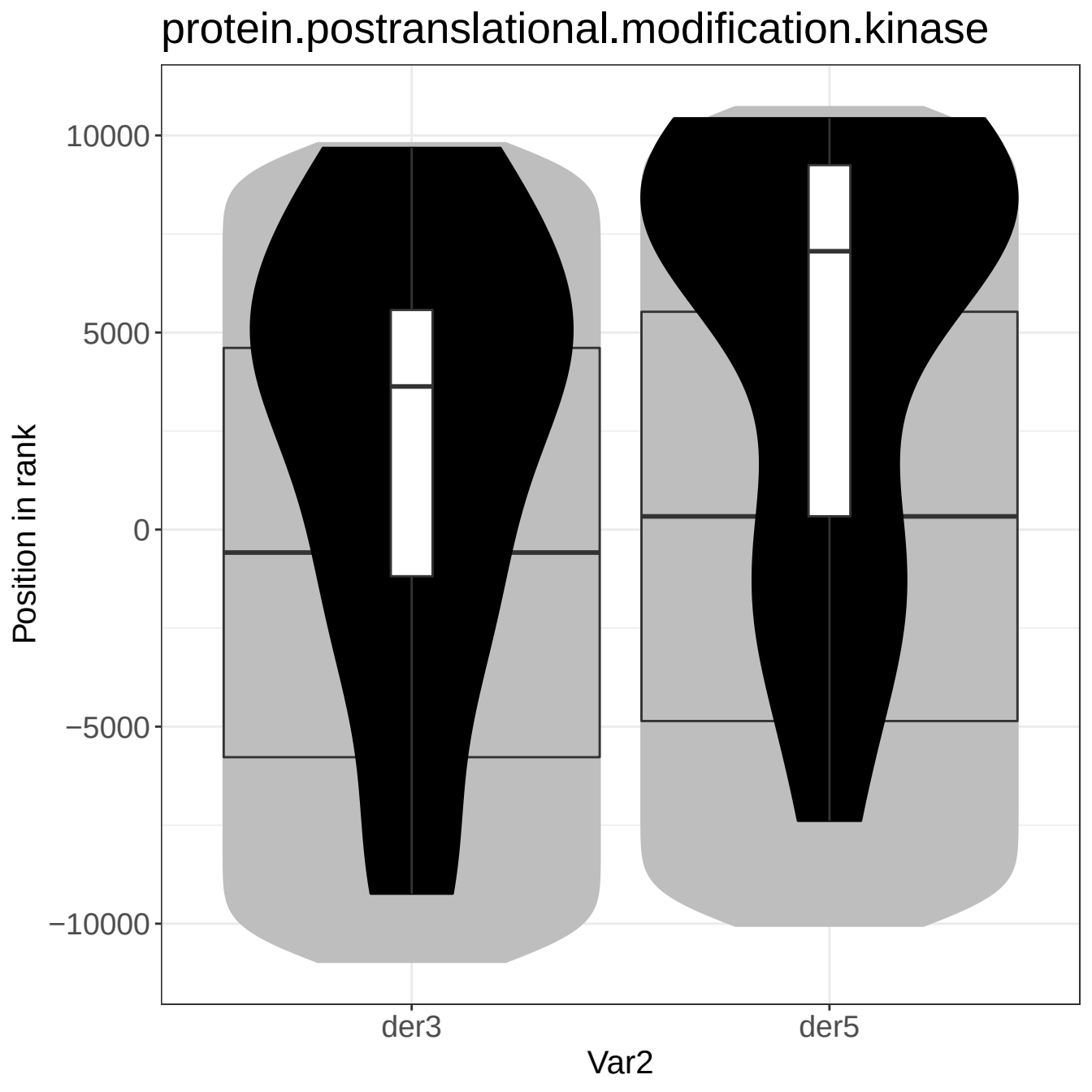
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Position in rank
der3
der5
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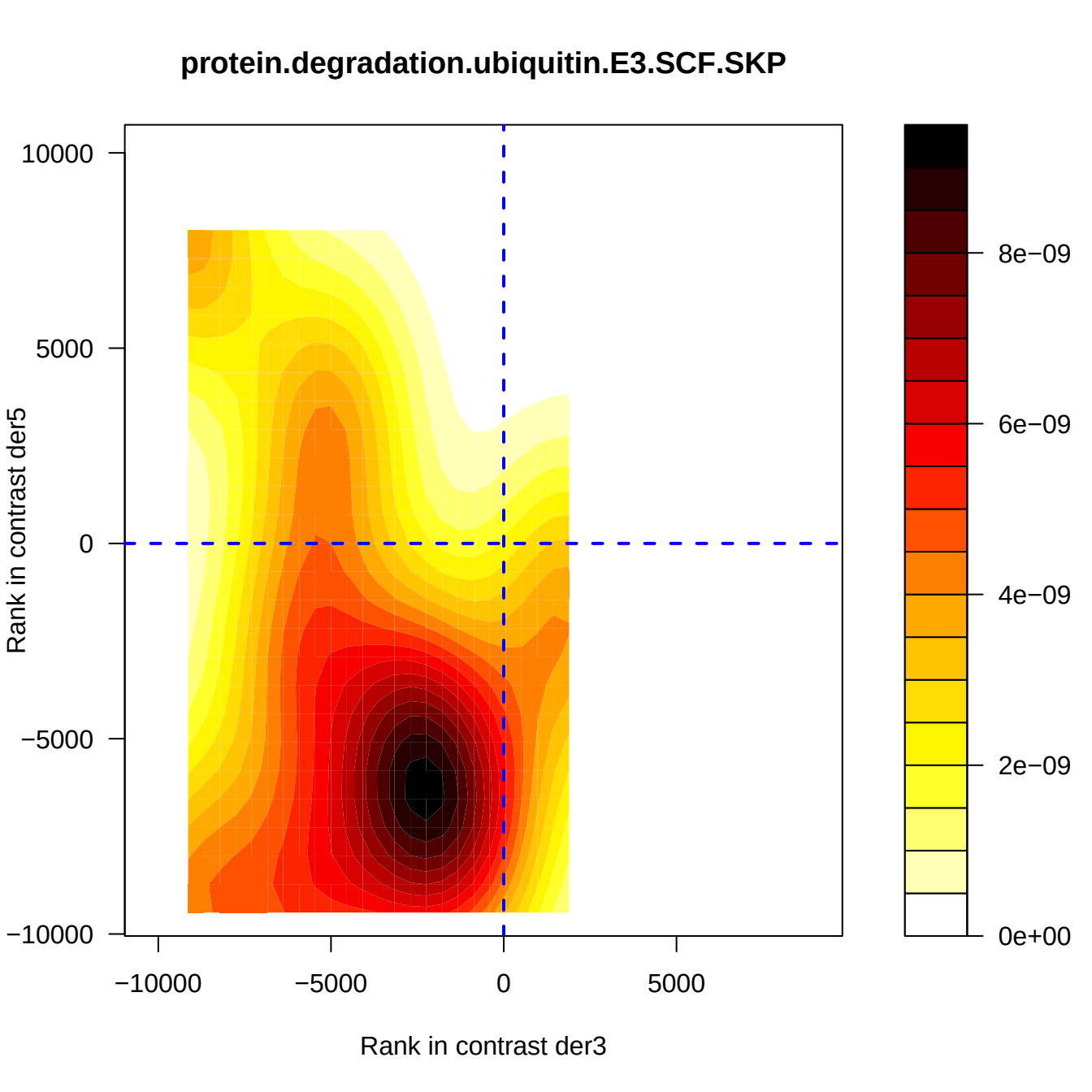
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Rank in contrast der5
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Rank in contrast der3
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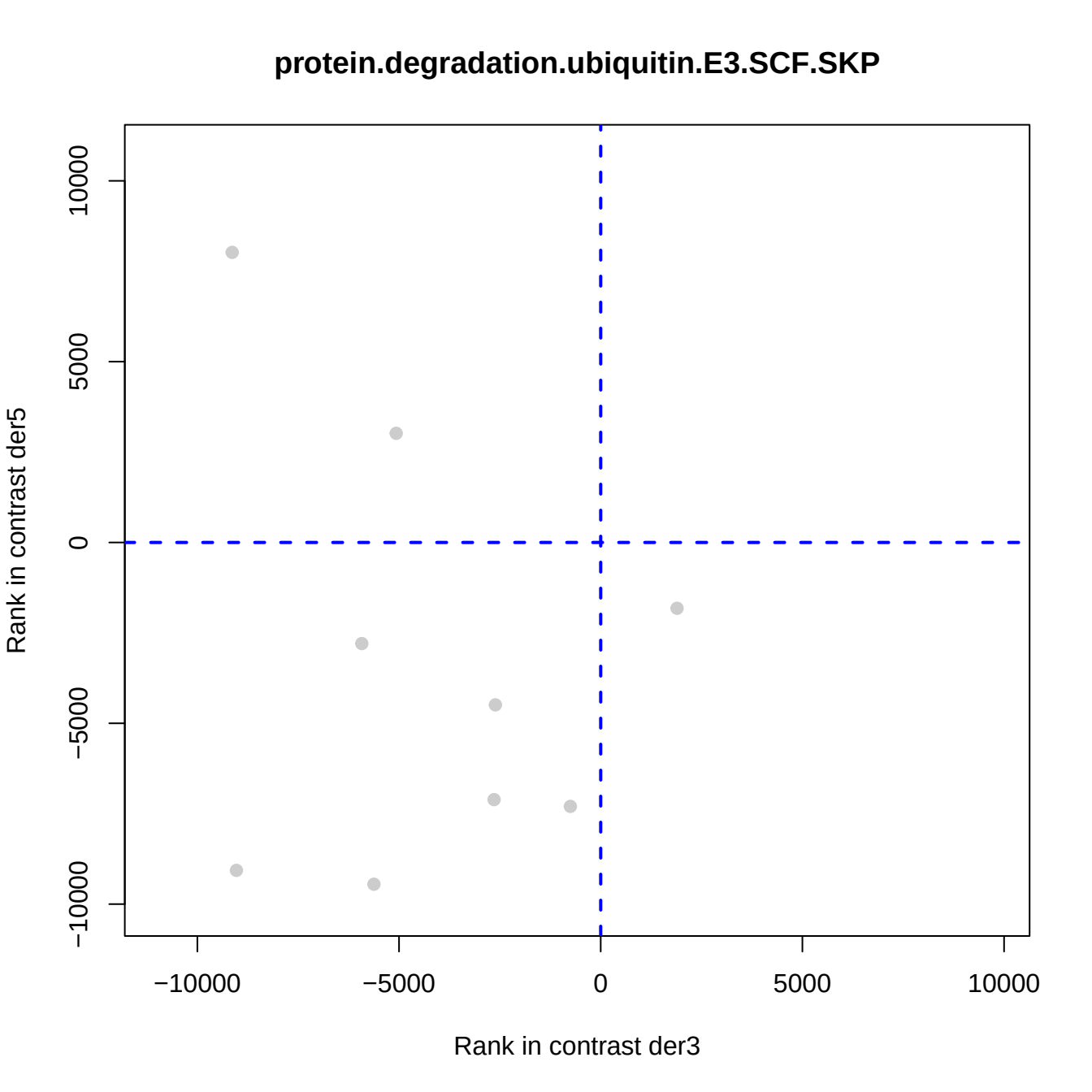
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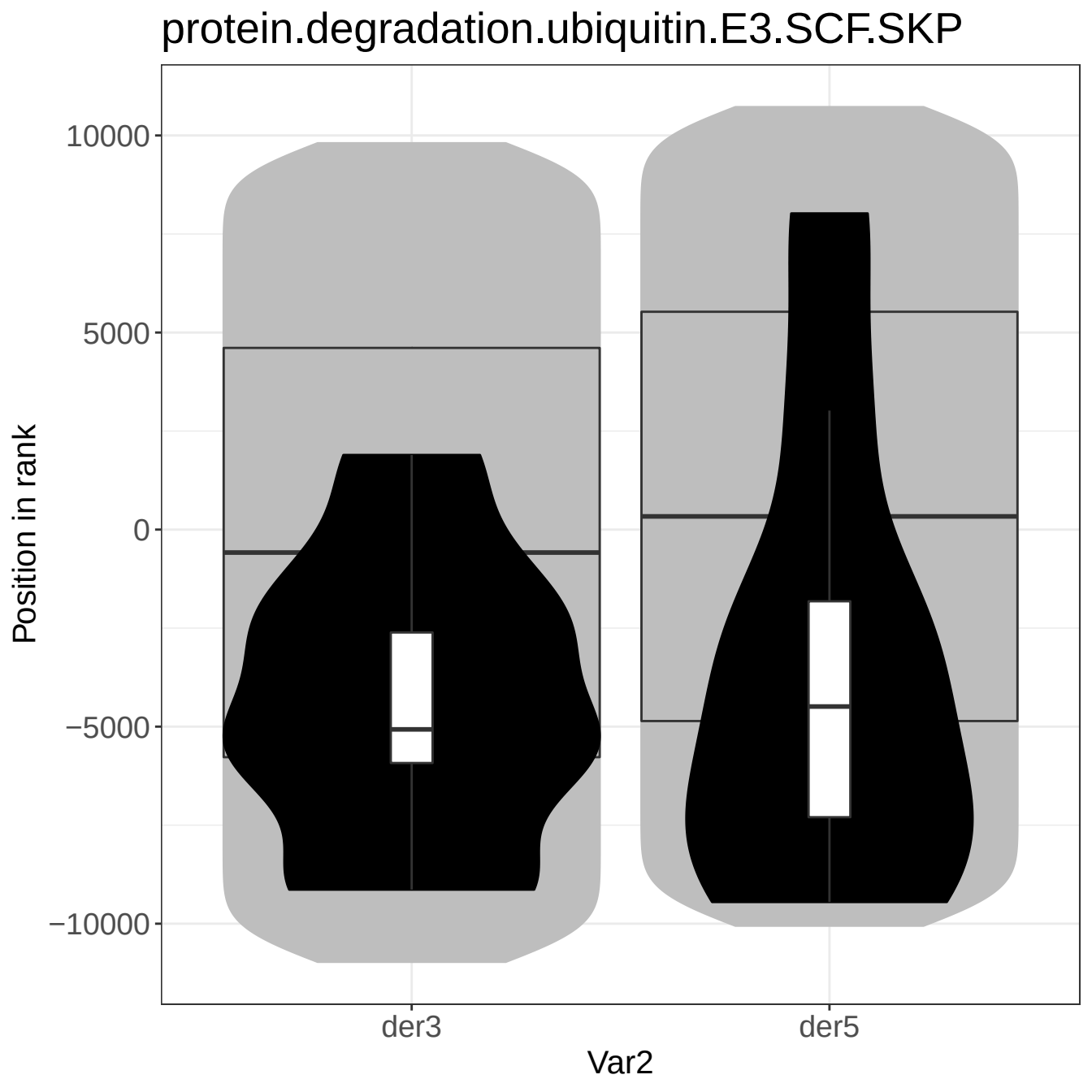
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Position in rank
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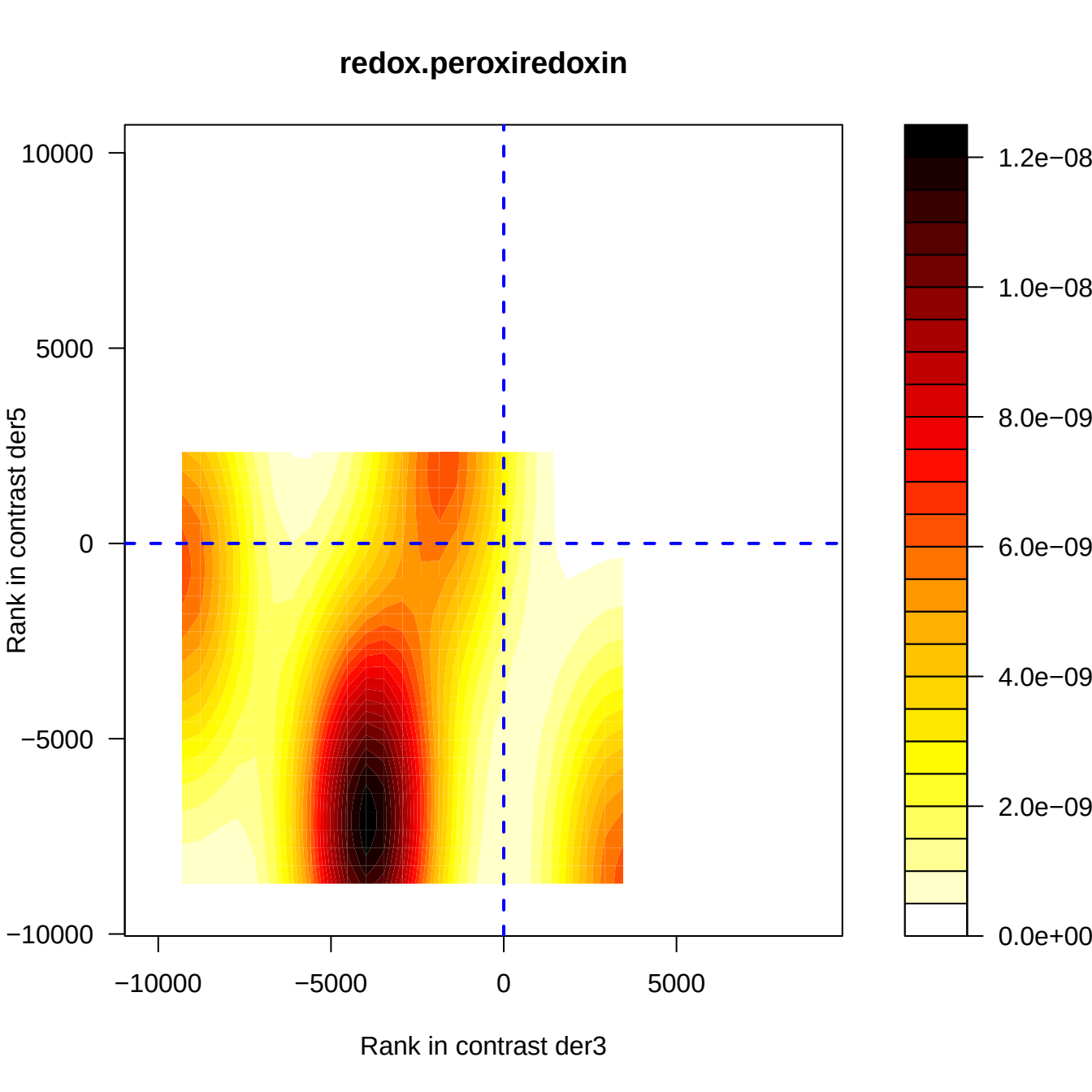
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−5000
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5000
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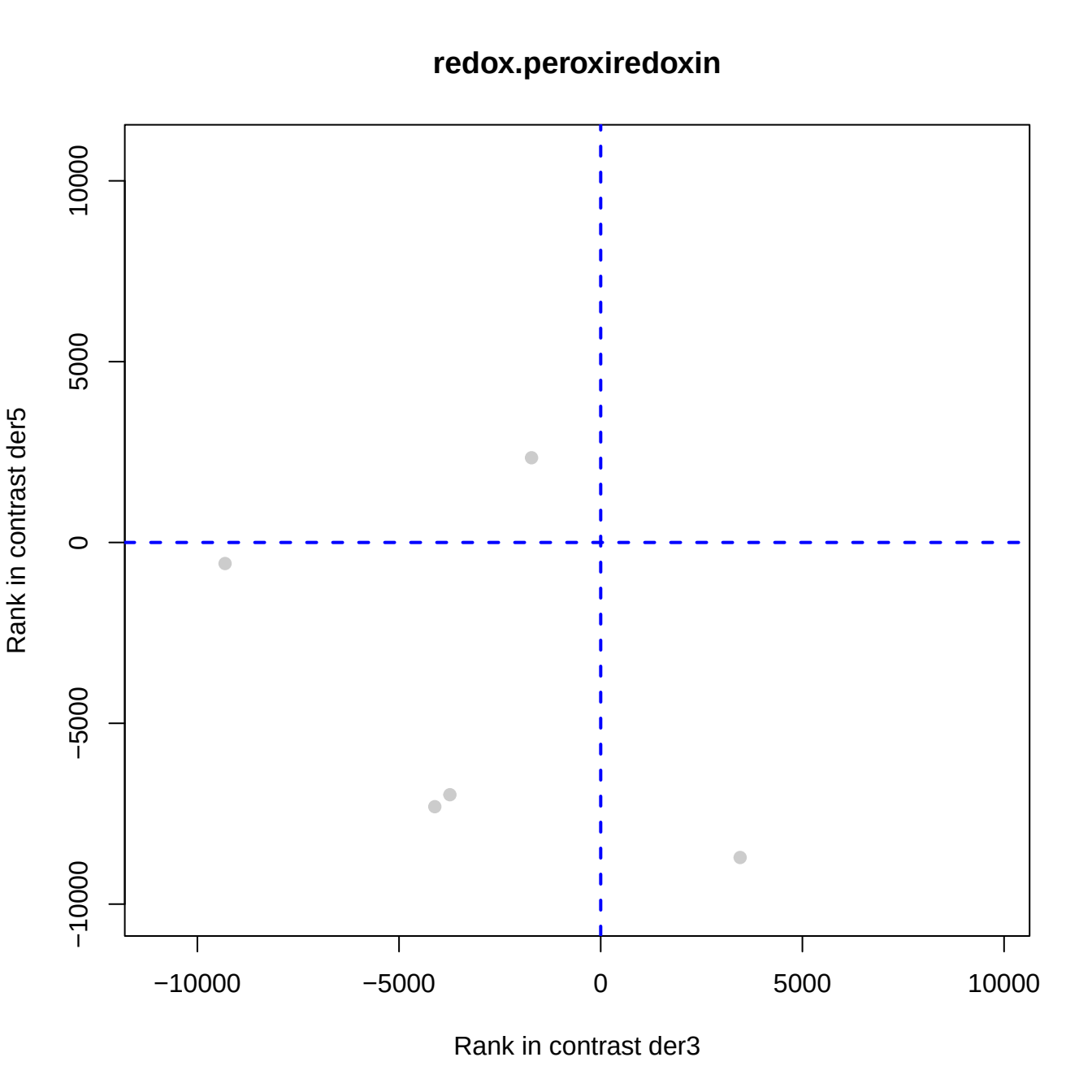
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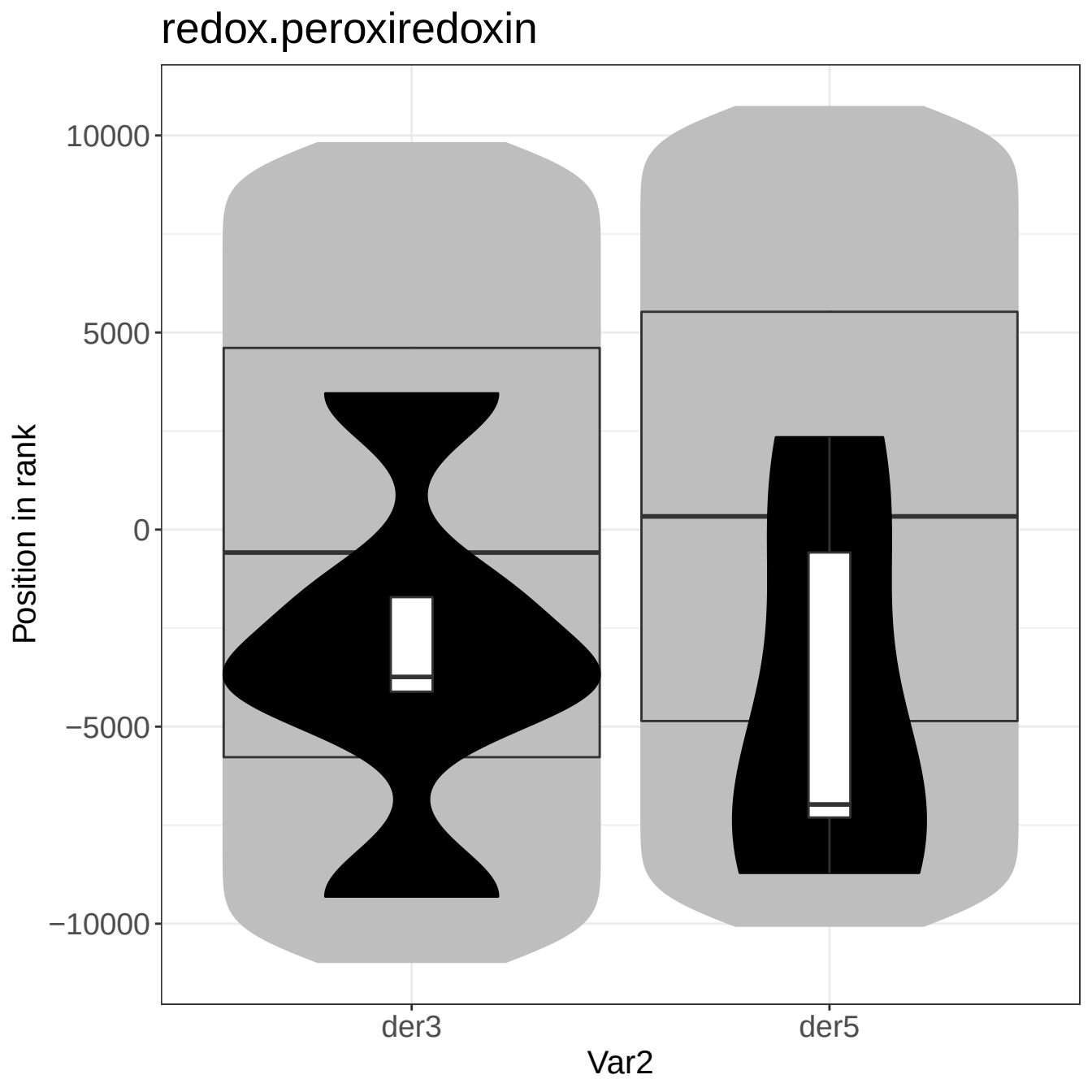
5000
10000
Rank in contrast der3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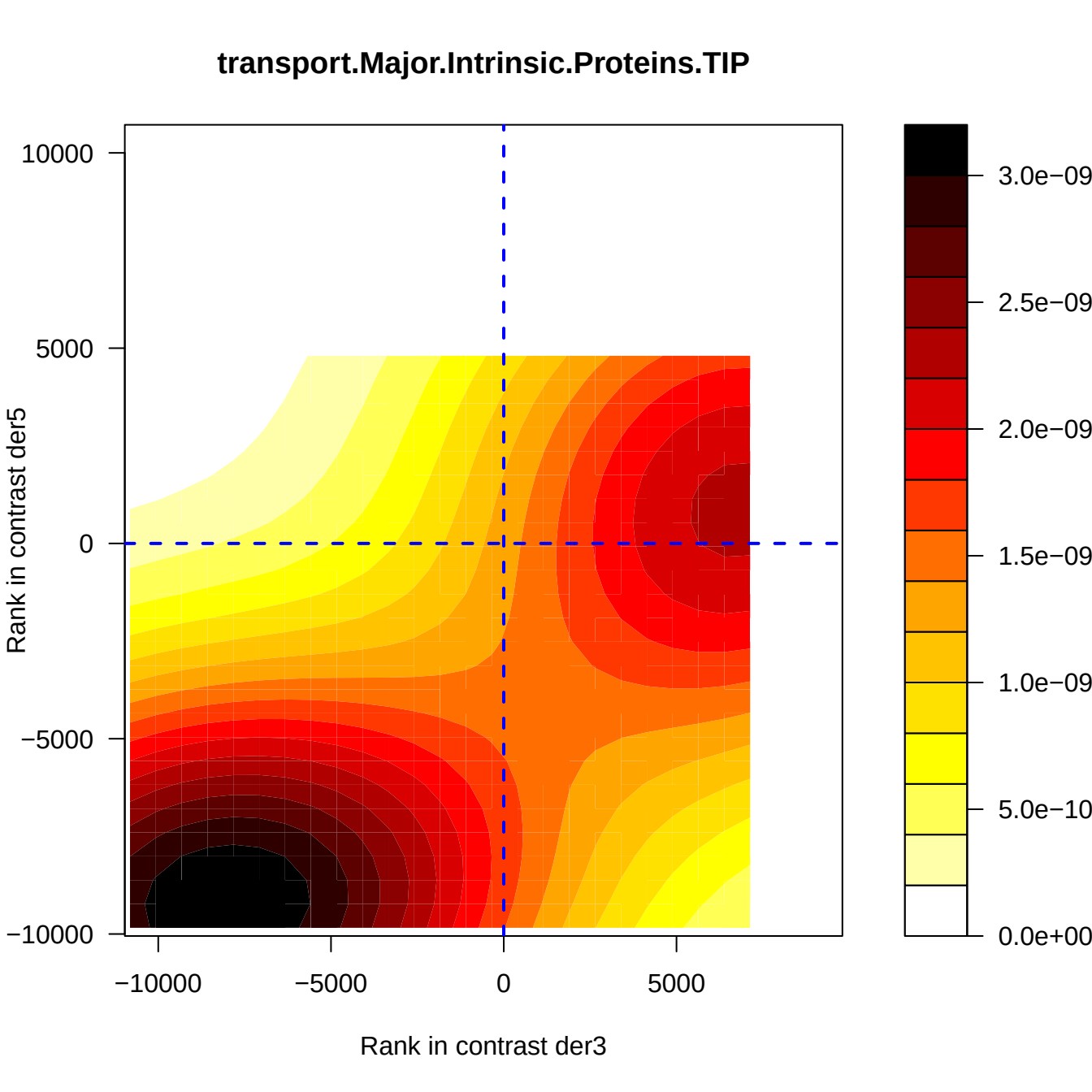
Position in rank
der3
der5
Var2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Rank in contrast der5
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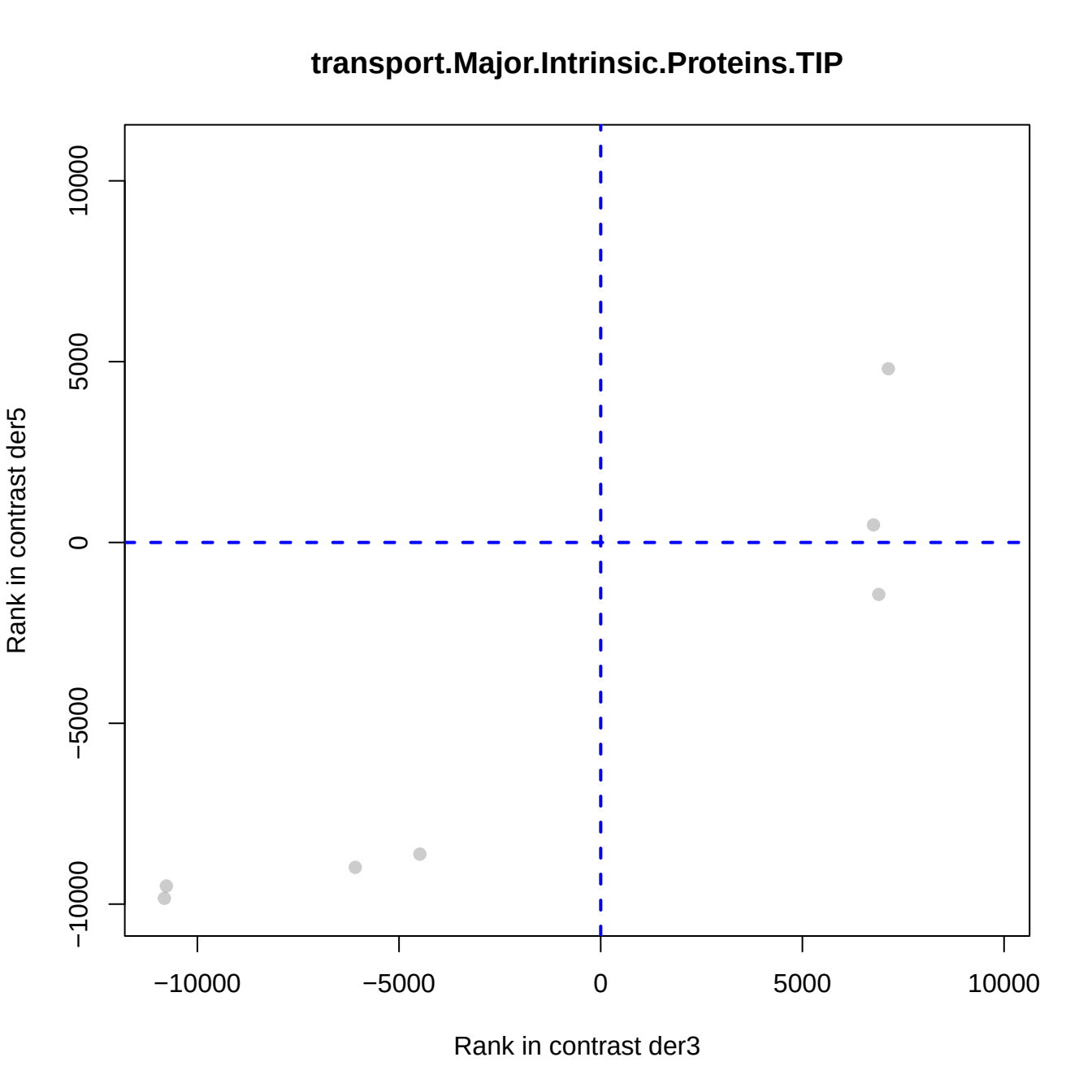
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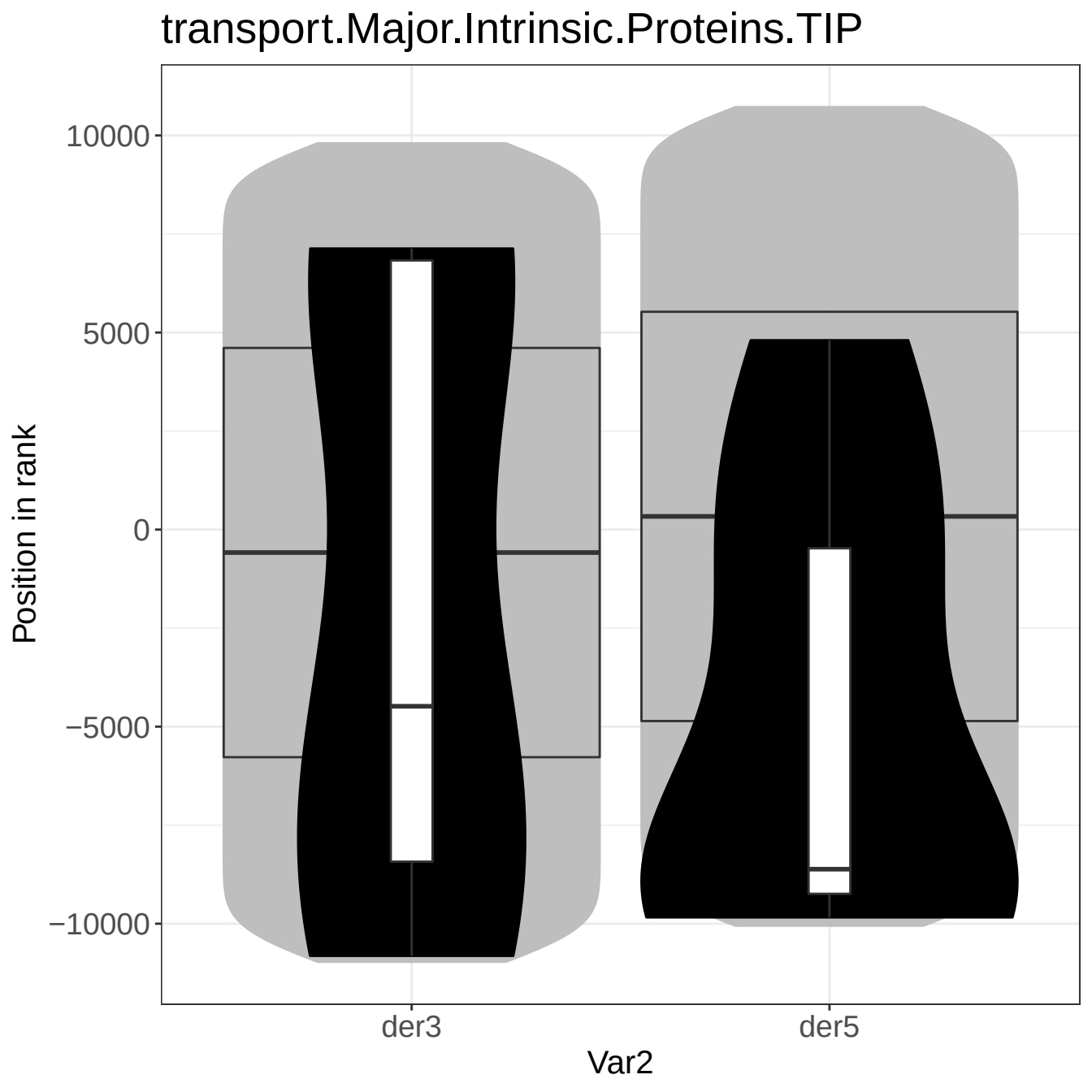
Rank in contrast der3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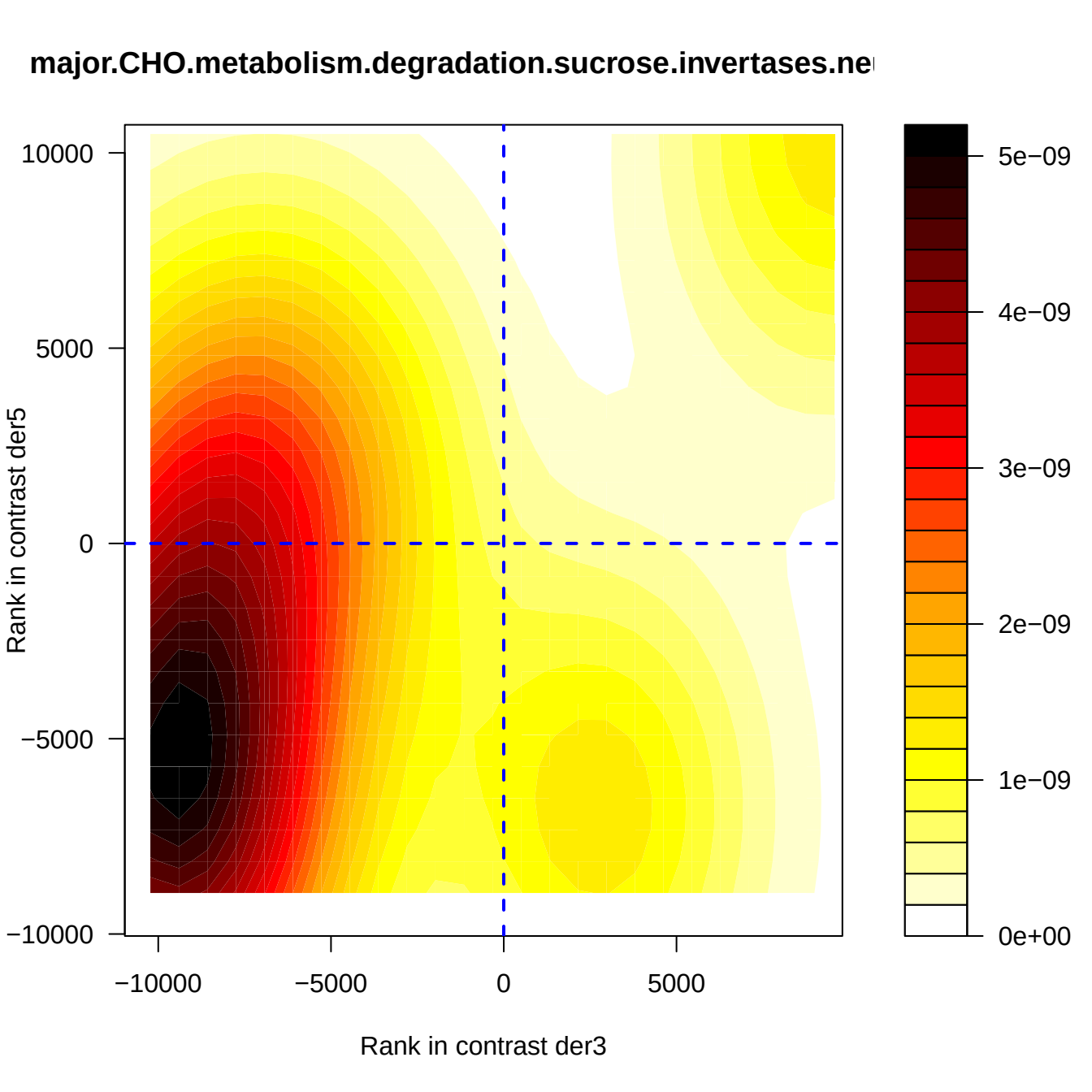
Position in rank
der3
der5
Var2


major.CHO.metabolism.degradation.sucrose.invertases.ne
10000
5000
0
−5000
−10000
Rank in contrast der5
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Rank in contrast der3
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4e−09
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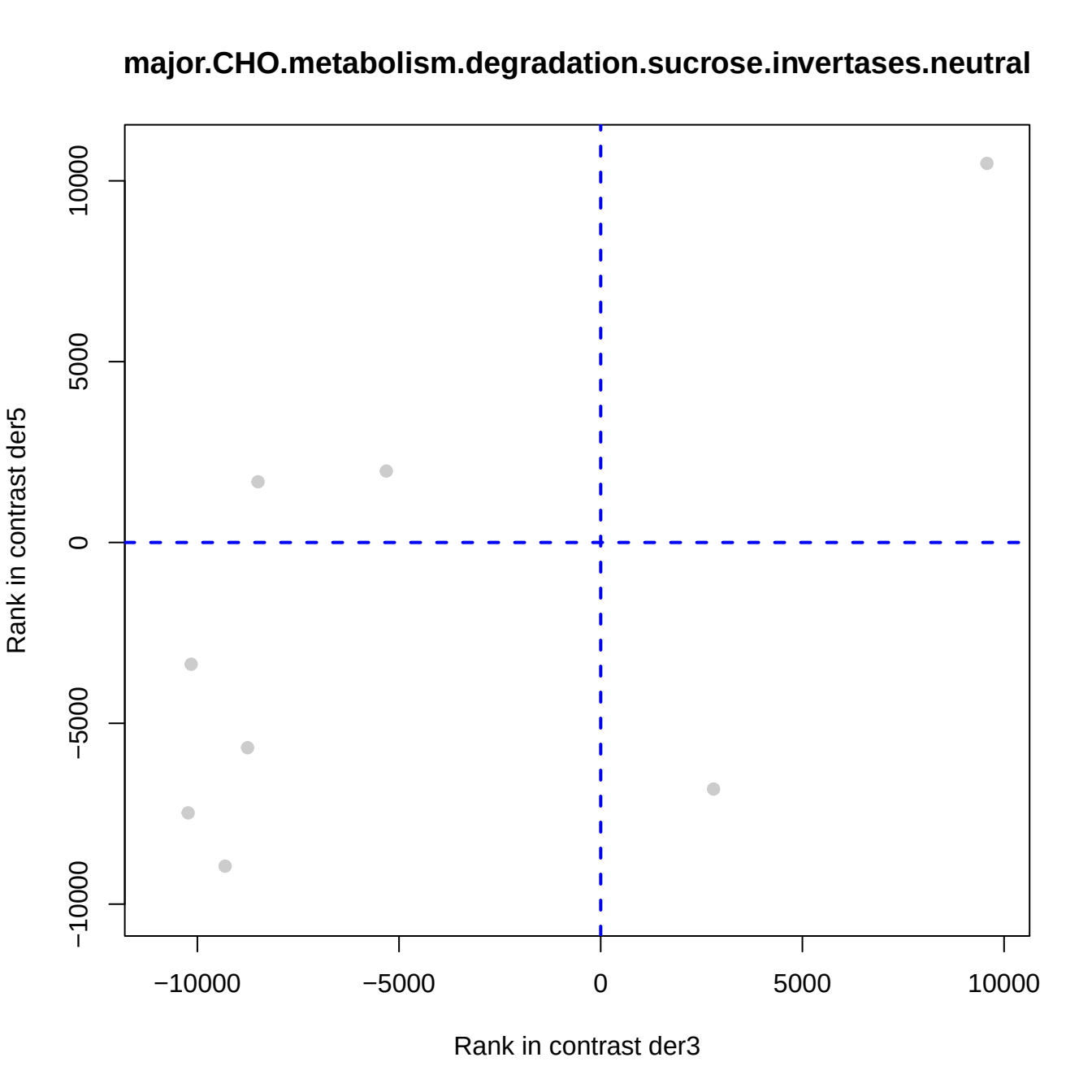
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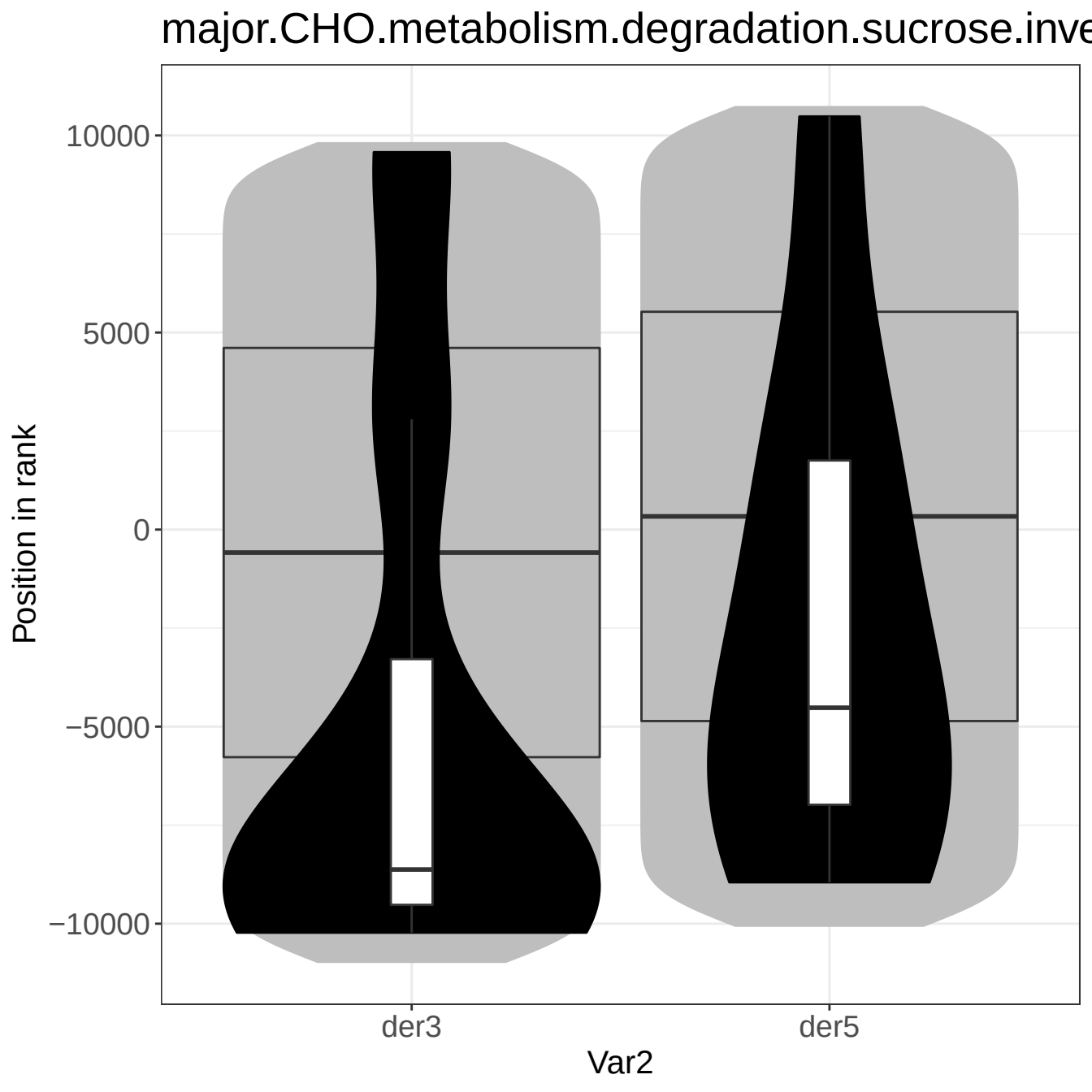
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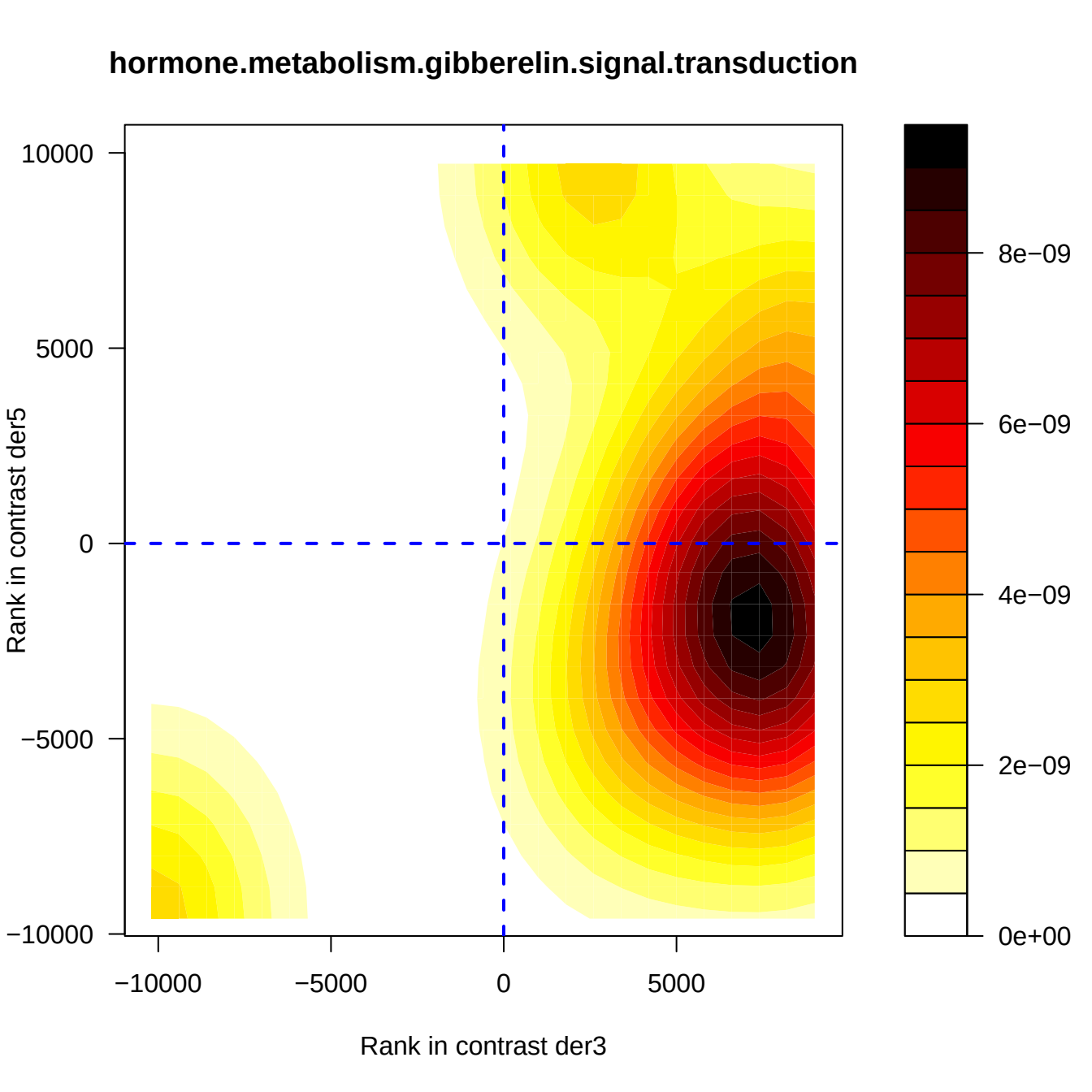
Position in rank
der3
der5
Var2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Rank in contrast der5
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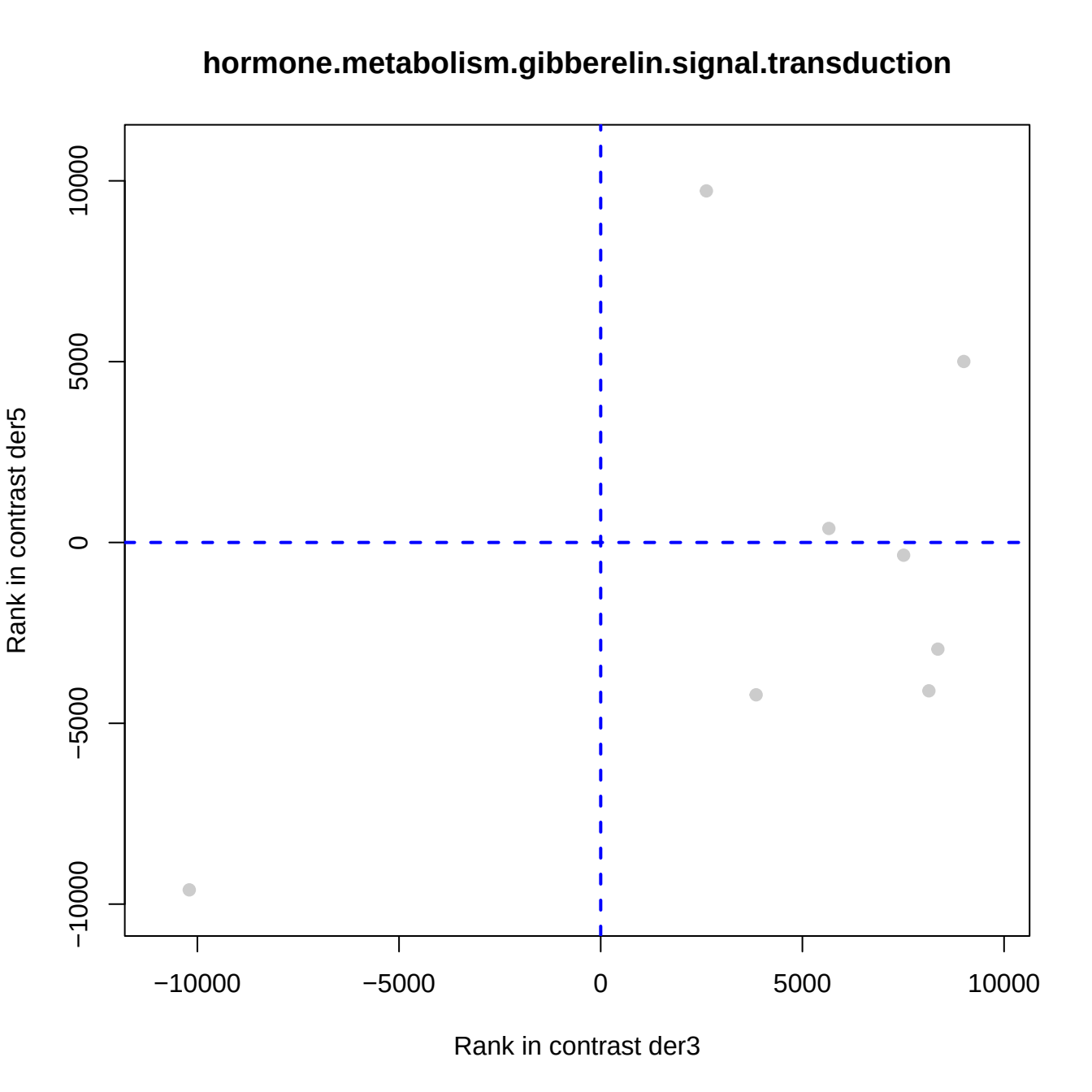
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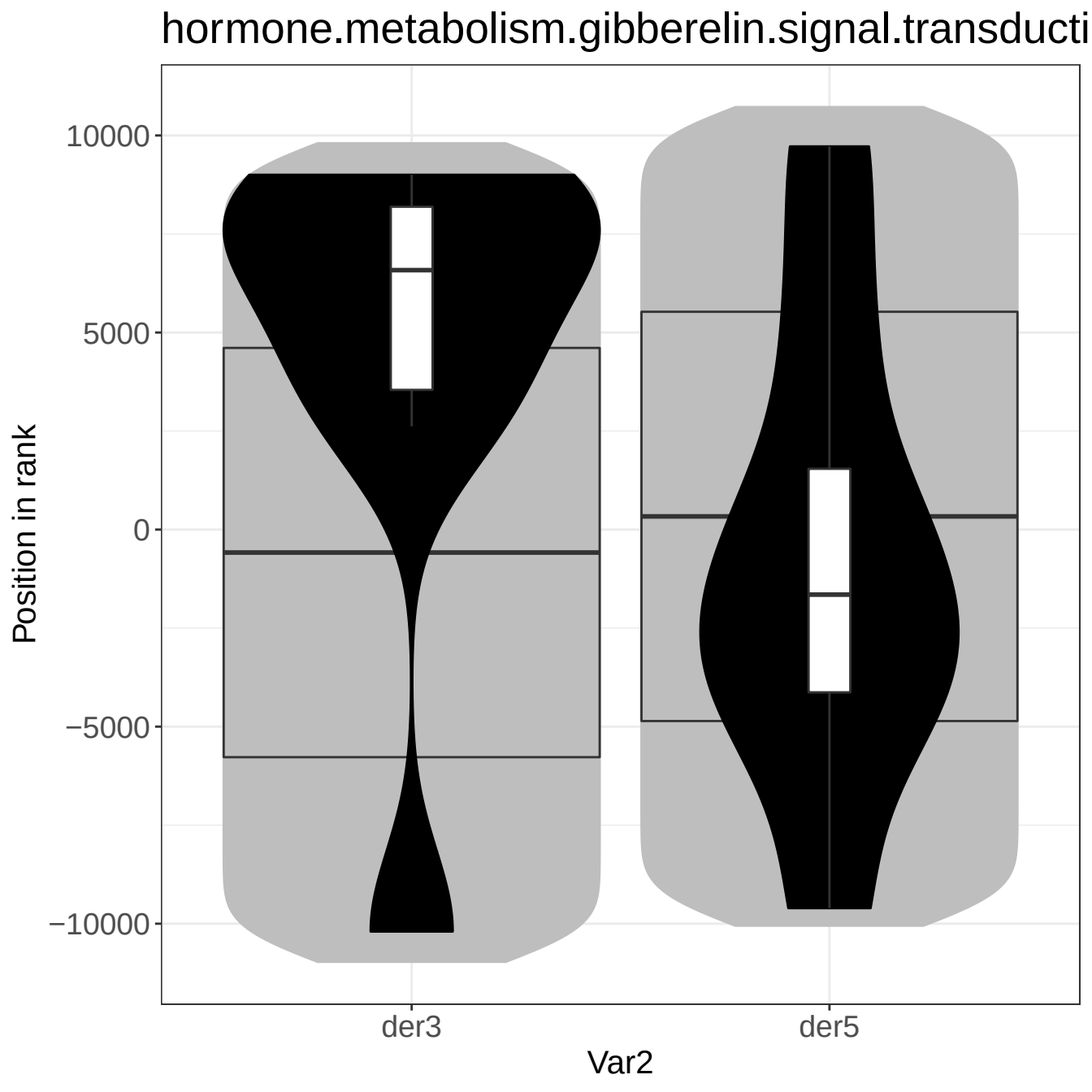
Rank in contrast der3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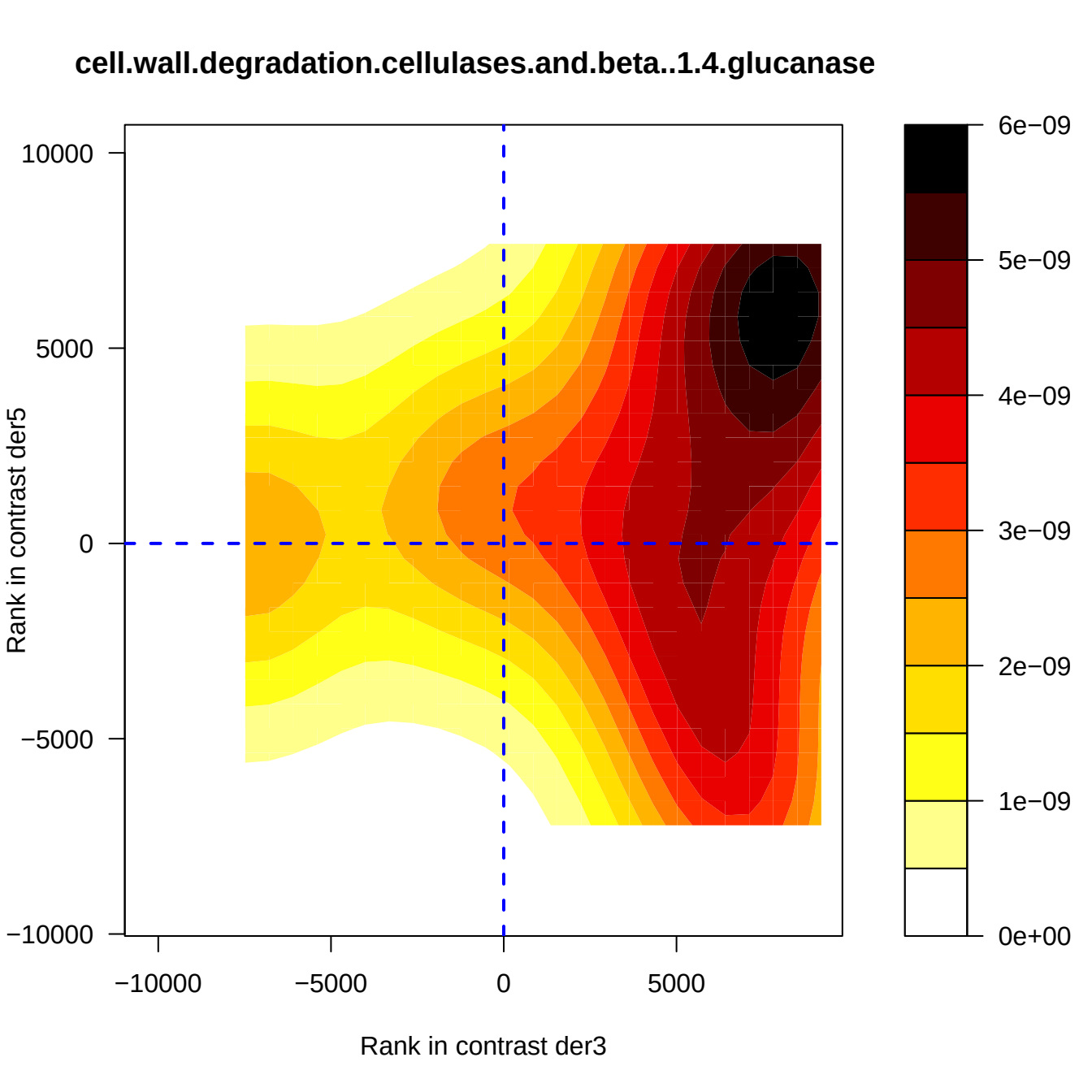
Position in rank
der3
der5
Var2


cell.wall.degradation.cellulases.and.beta..1.4.glucanase
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−5000
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Rank in contrast der5
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Rank in contrast der3
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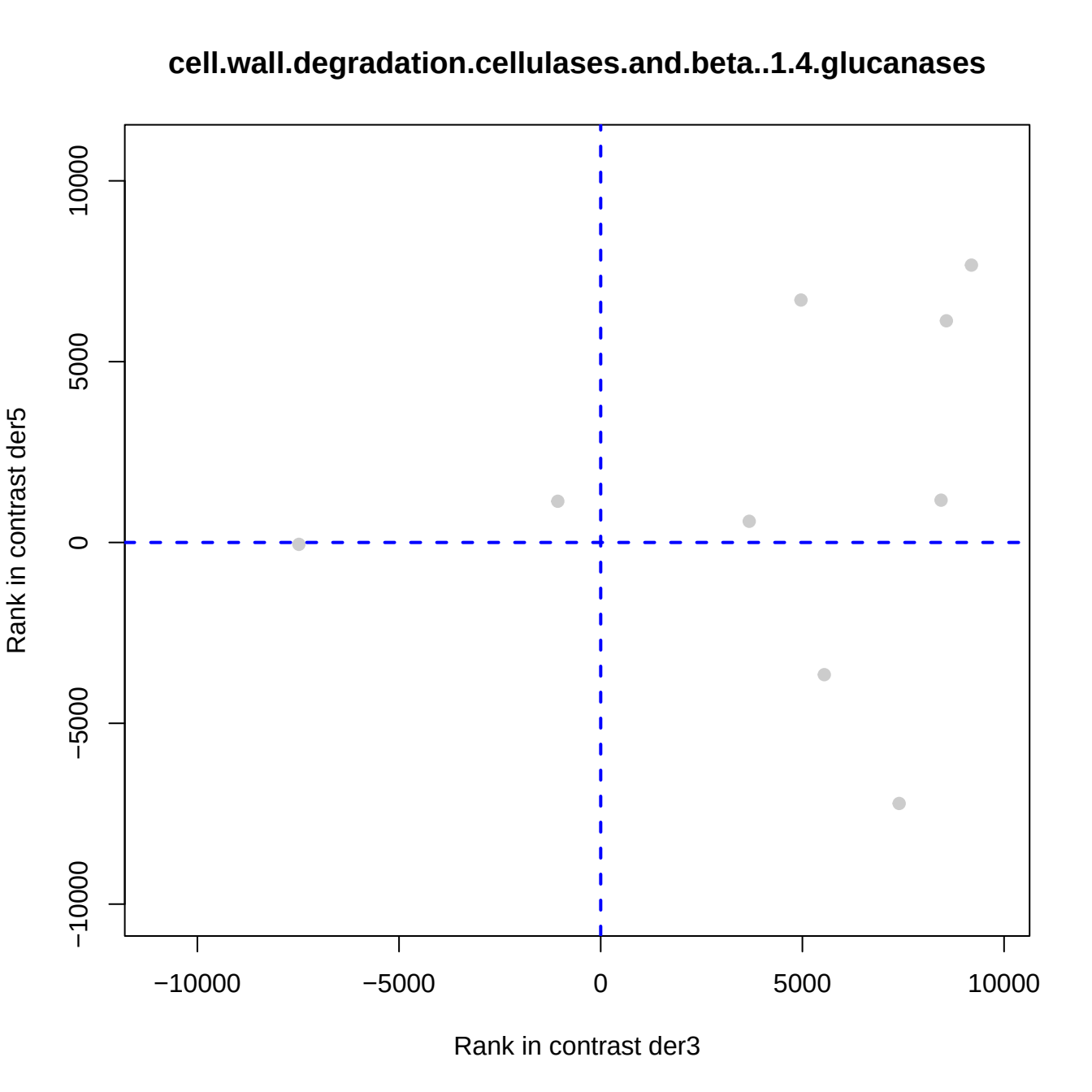
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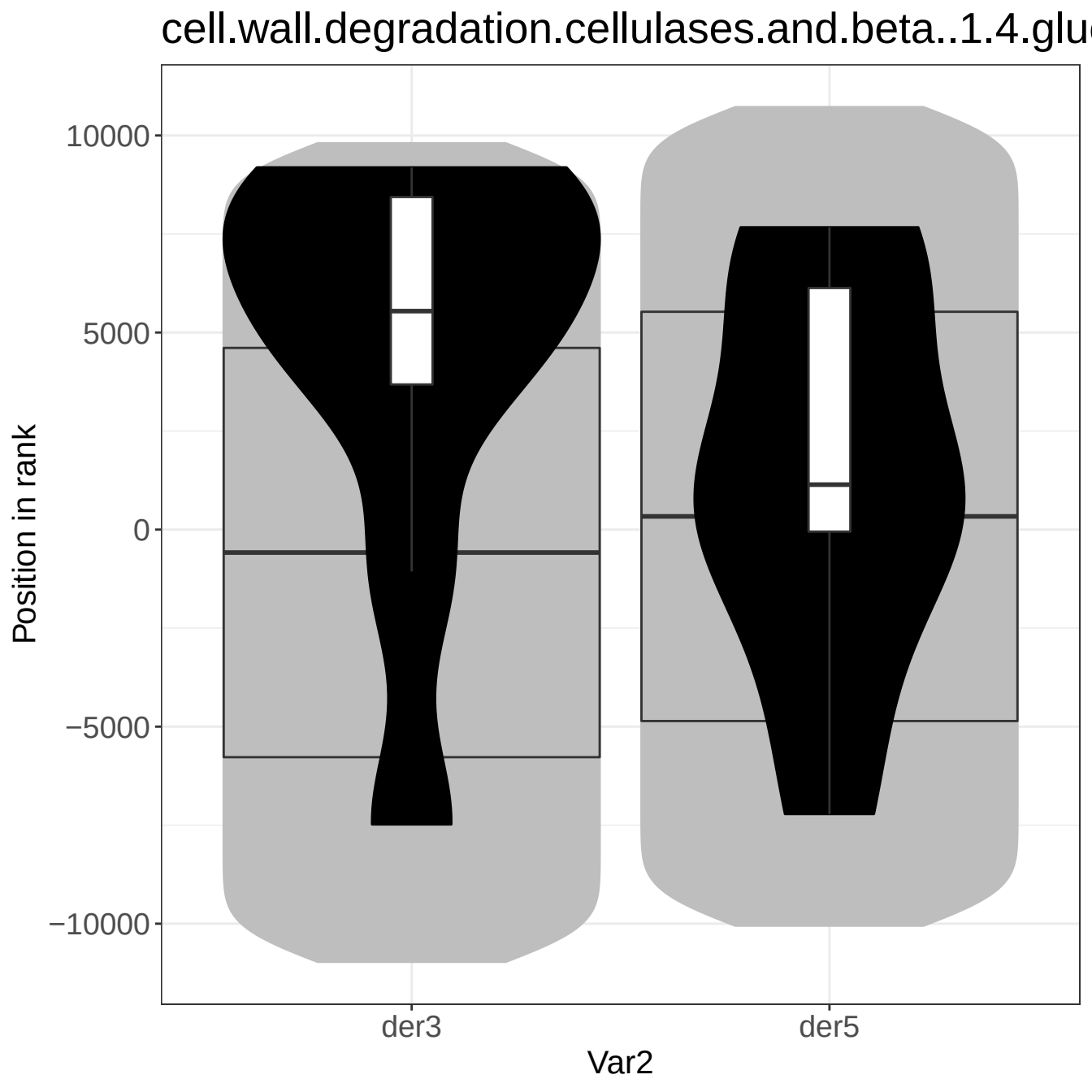
Rank in contrast der3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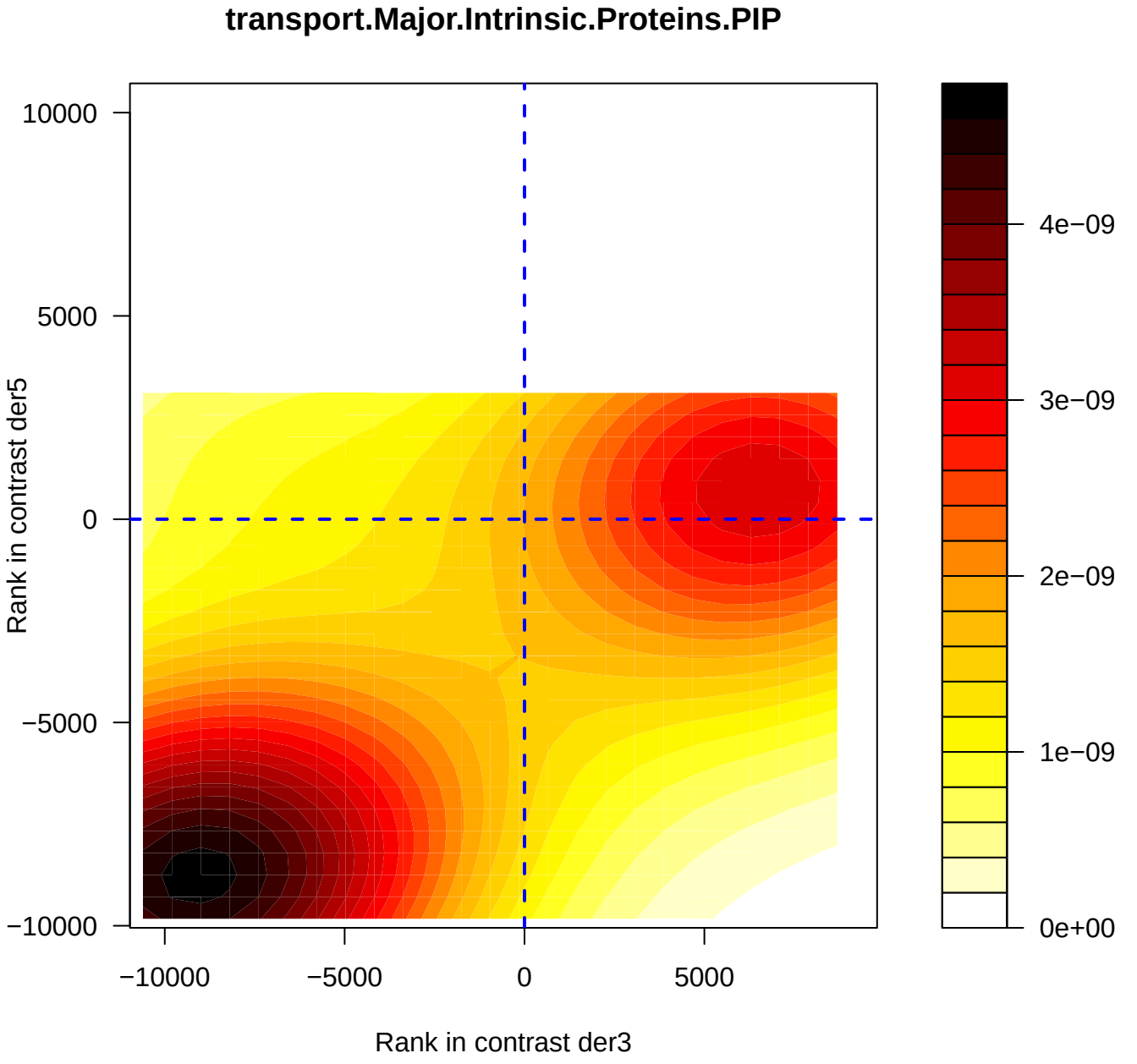
Position in rank
der3
der5
Var2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−5000
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Rank in contrast der3
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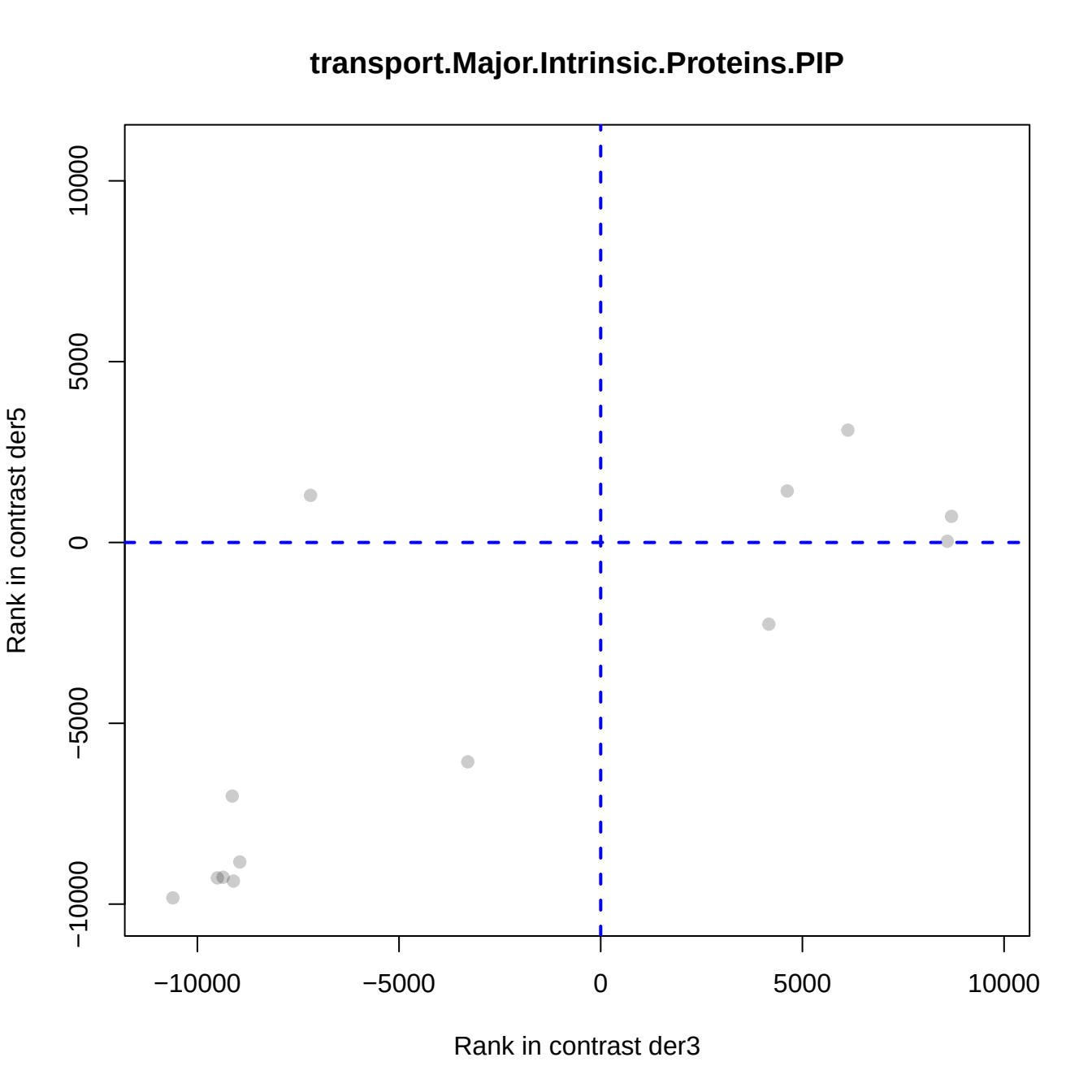
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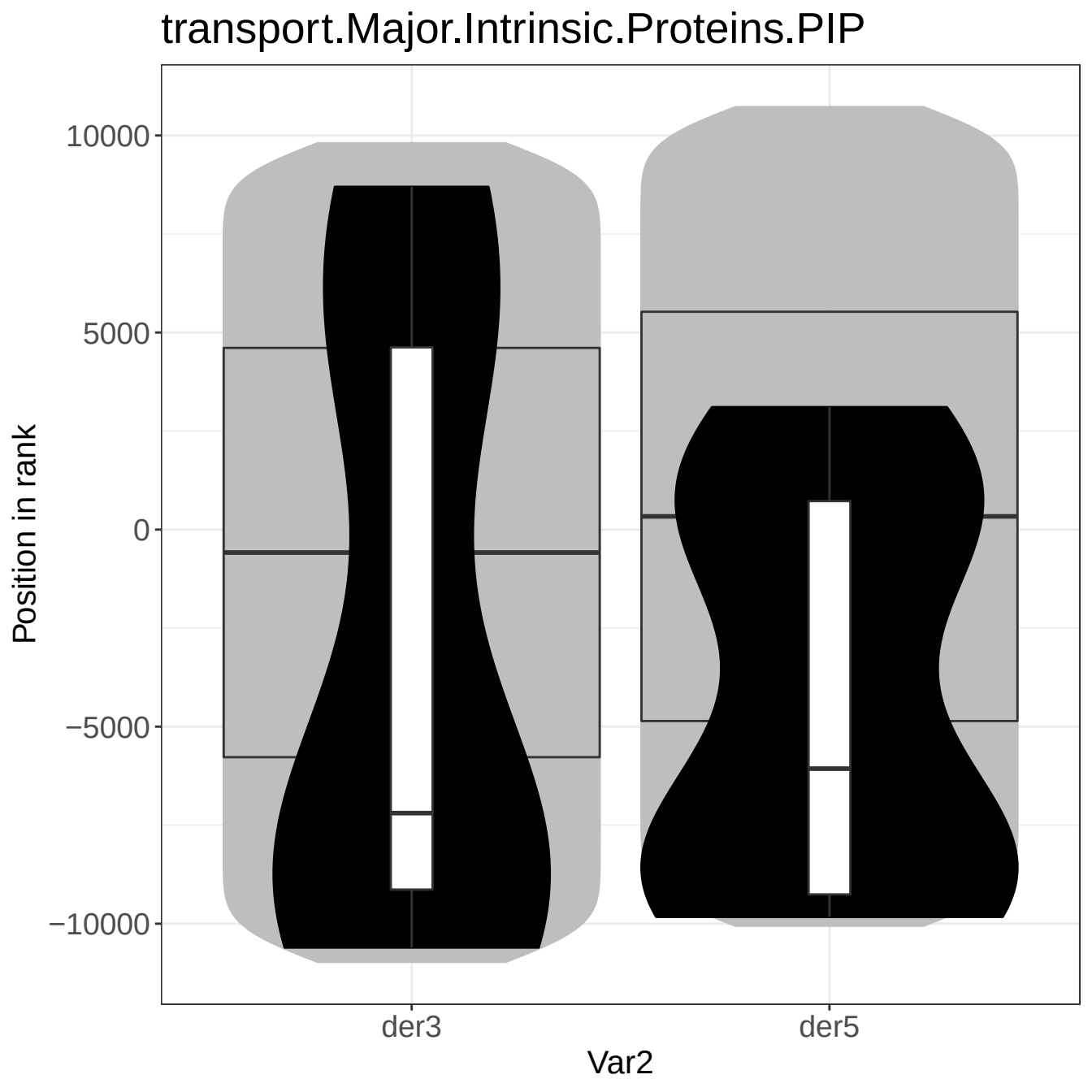
Rank in contrast der3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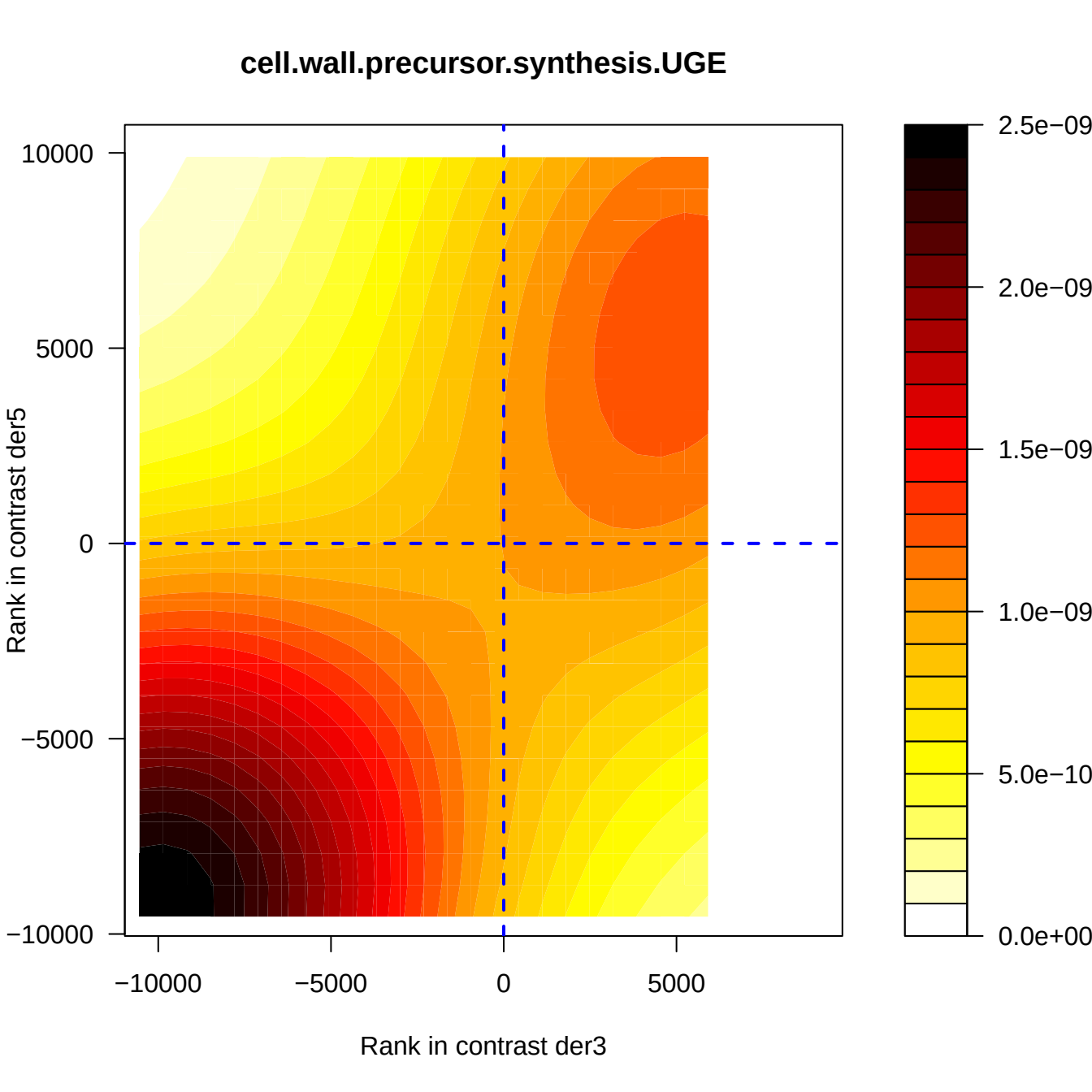
Position in rank
der3
der5
Var2


cell.wall.precursor.synthesis.UGE
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−5000
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−5000
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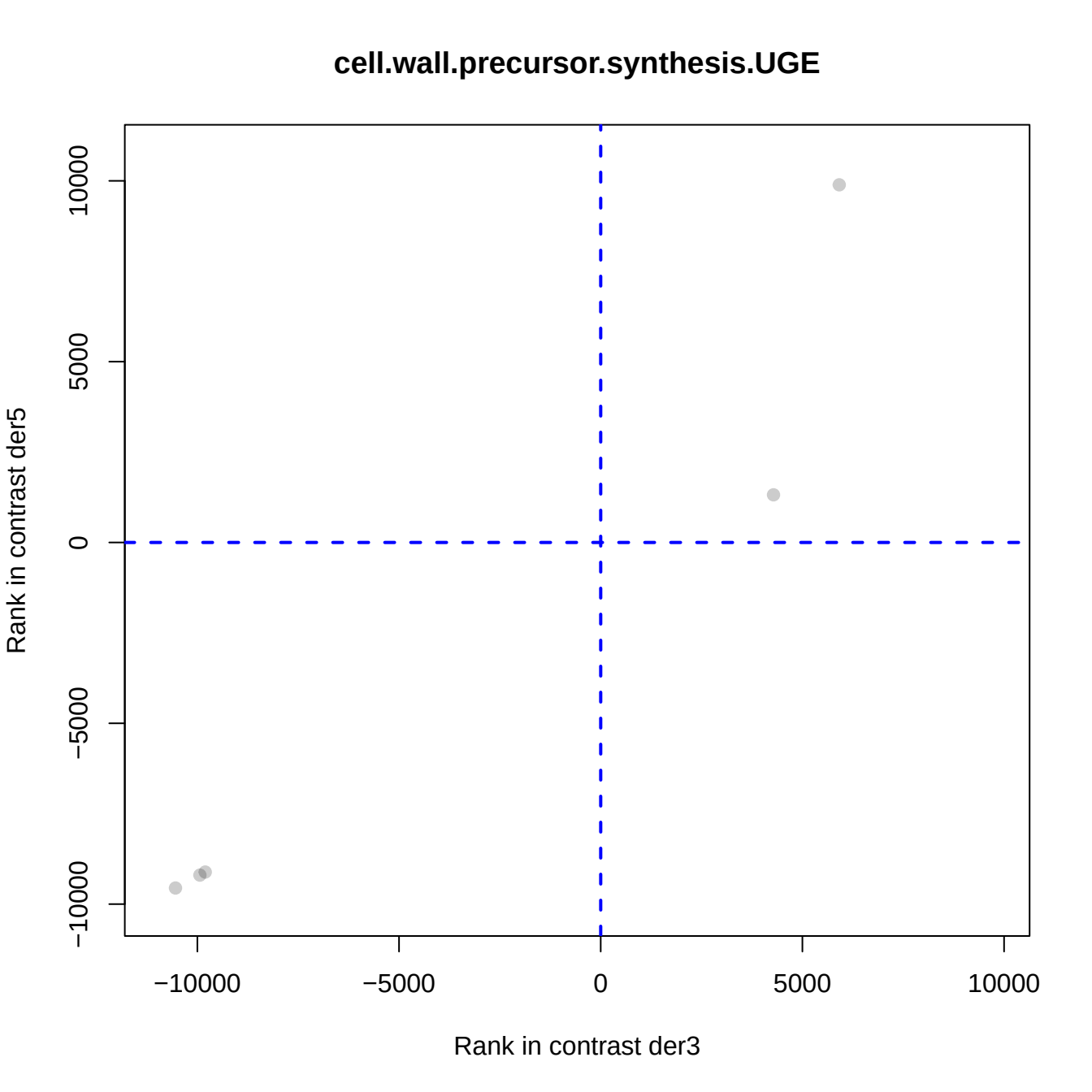
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Rank in contrast der3
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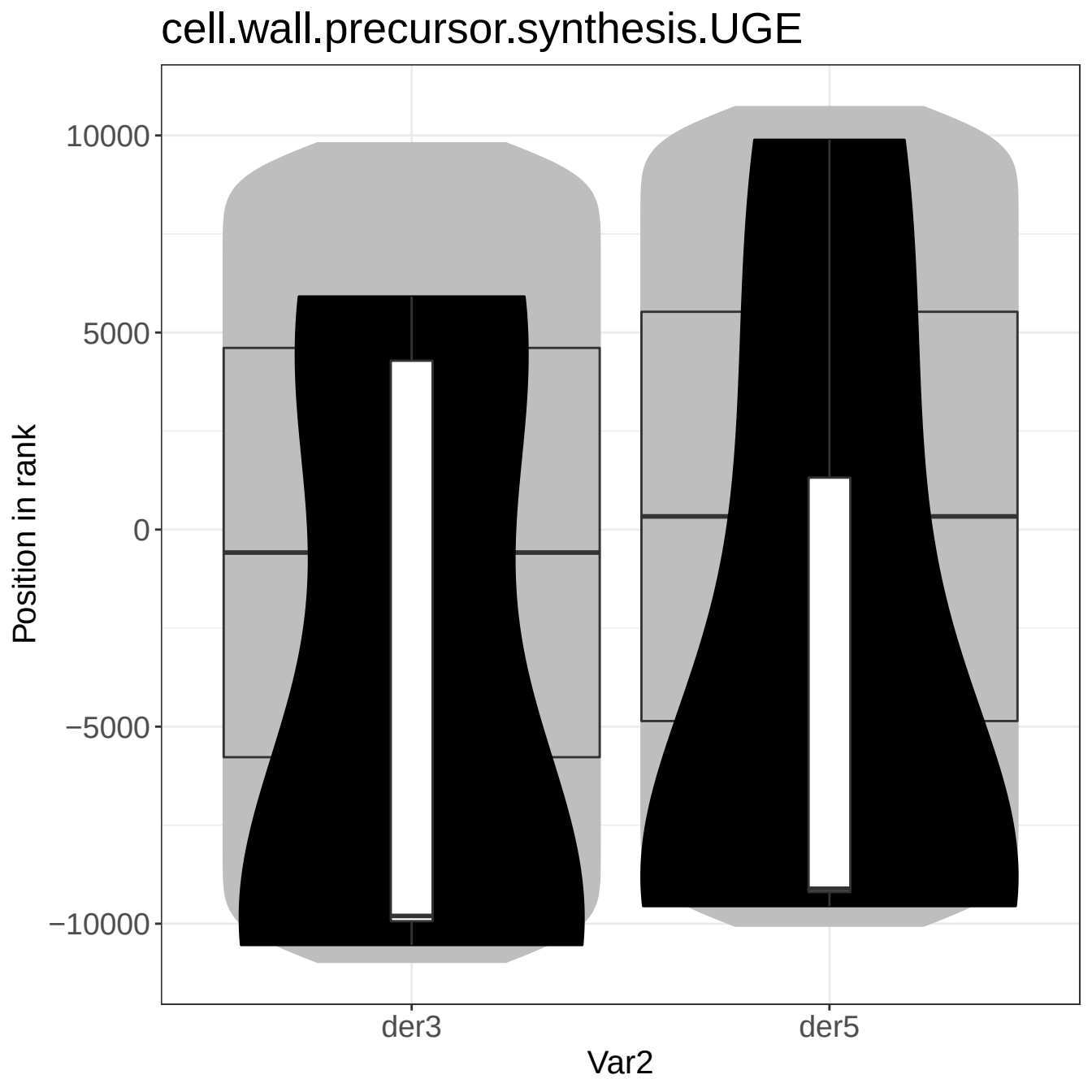
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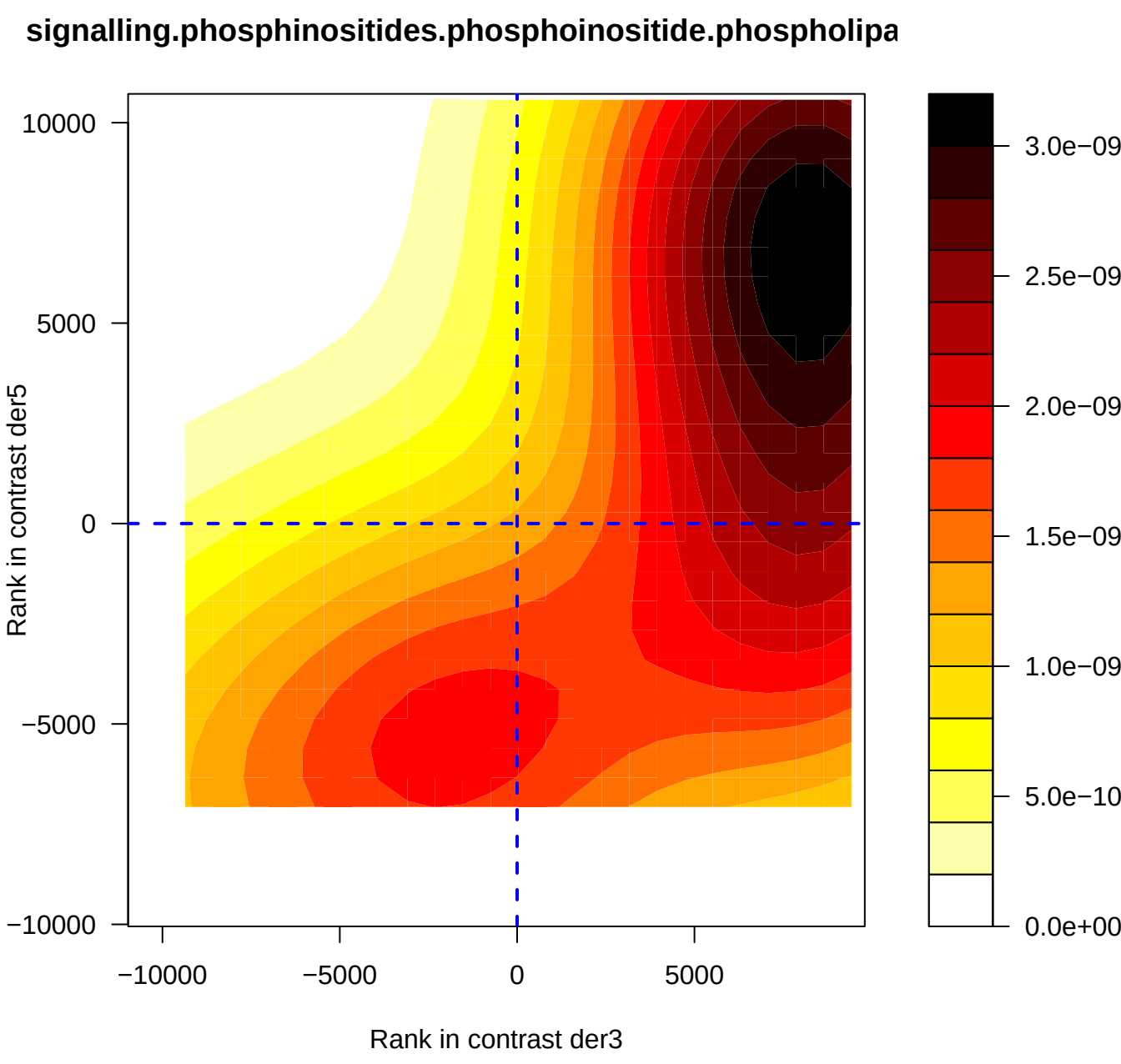
Position in rank
der3
der5
Var2


signalling.phosphinositides.phosphoinositide.phospholipa
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5000
0
−5000
−10000
Rank in contrast der5
−10000
−5000
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5000
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2.5e−09
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1.0e−09
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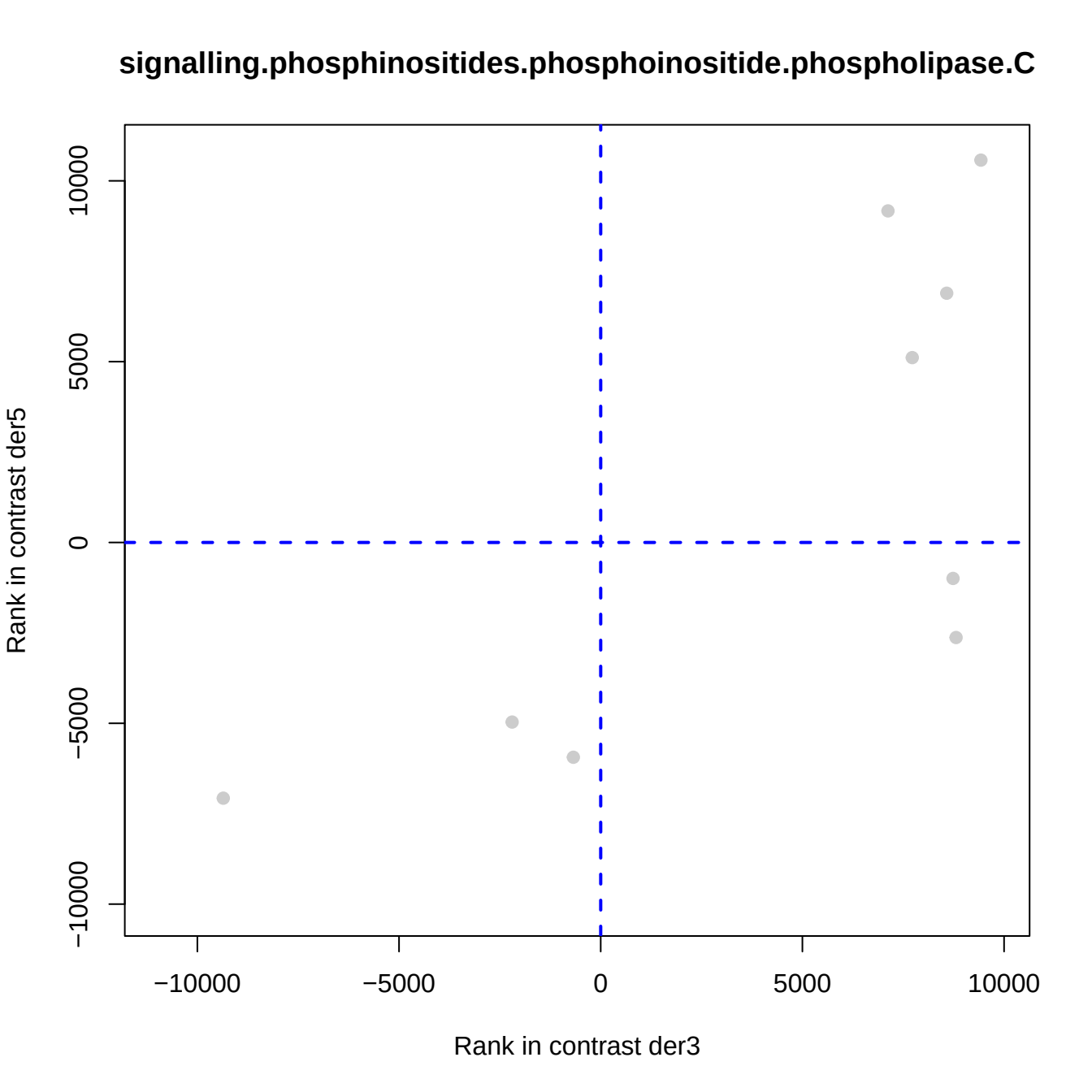
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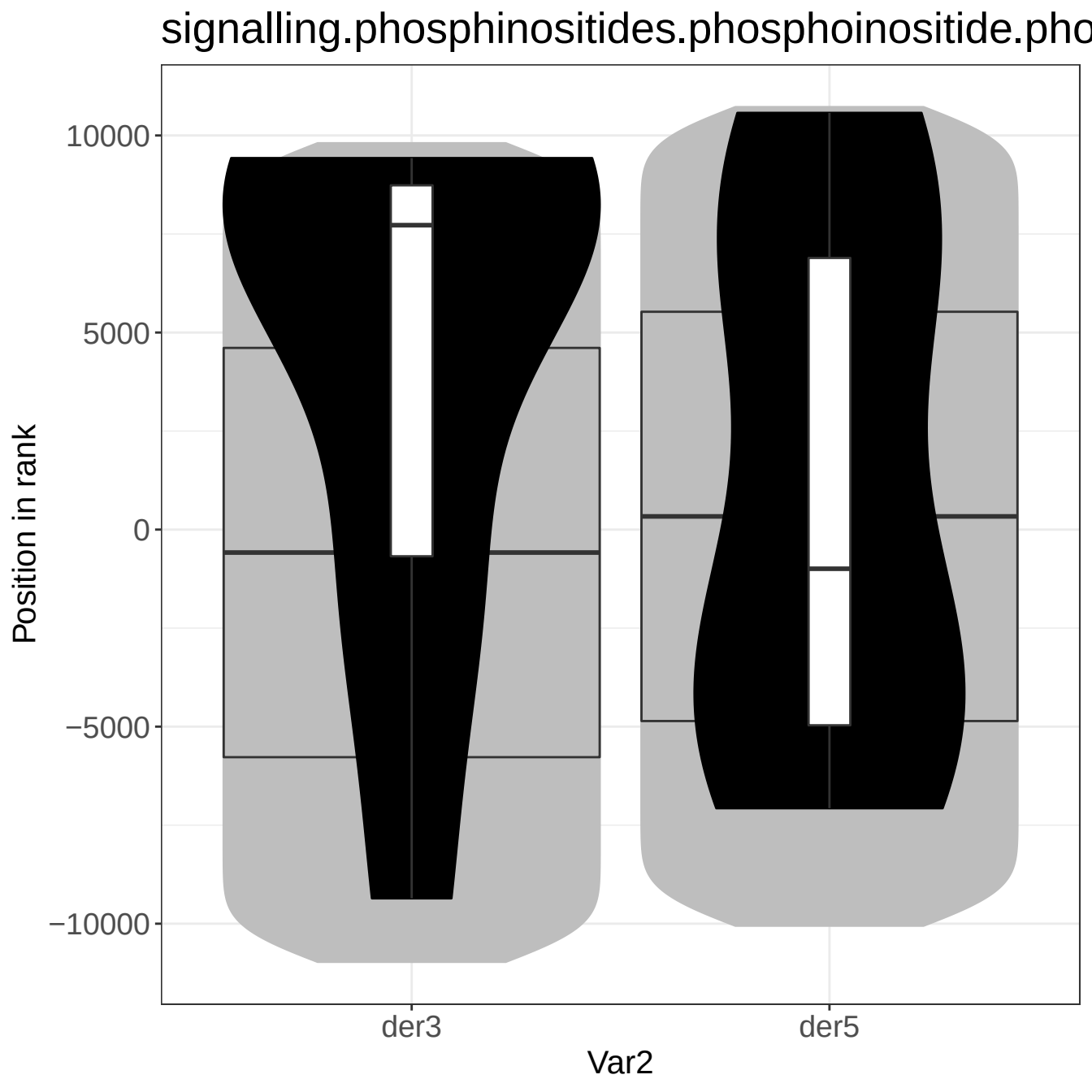
Rank in contrast der3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10000
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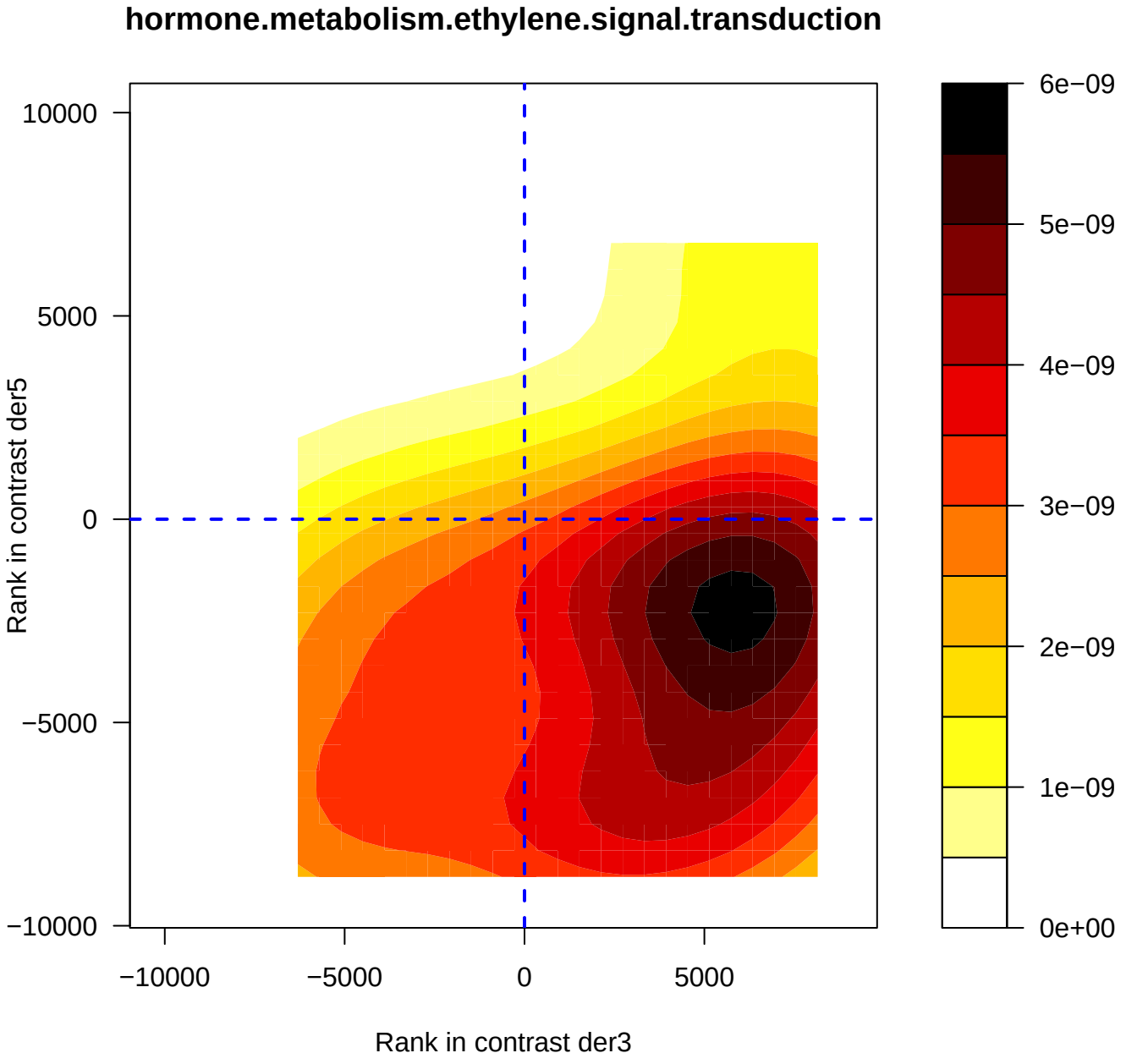
Position in rank
der3
der5
Var2


hormone.metabolism.ethylene.signal.transduction
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−5000
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Rank in contrast der5
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Rank in contrast der3
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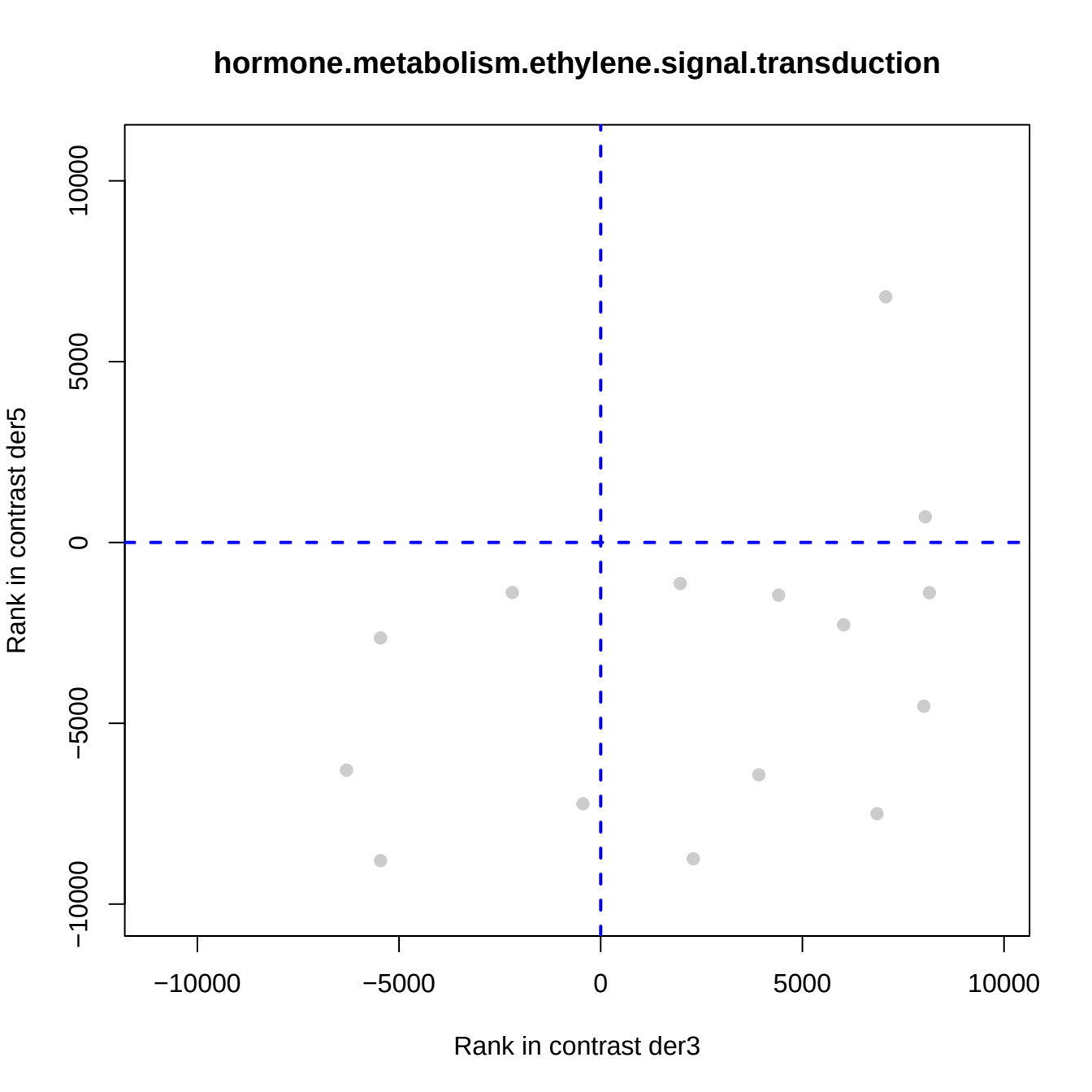
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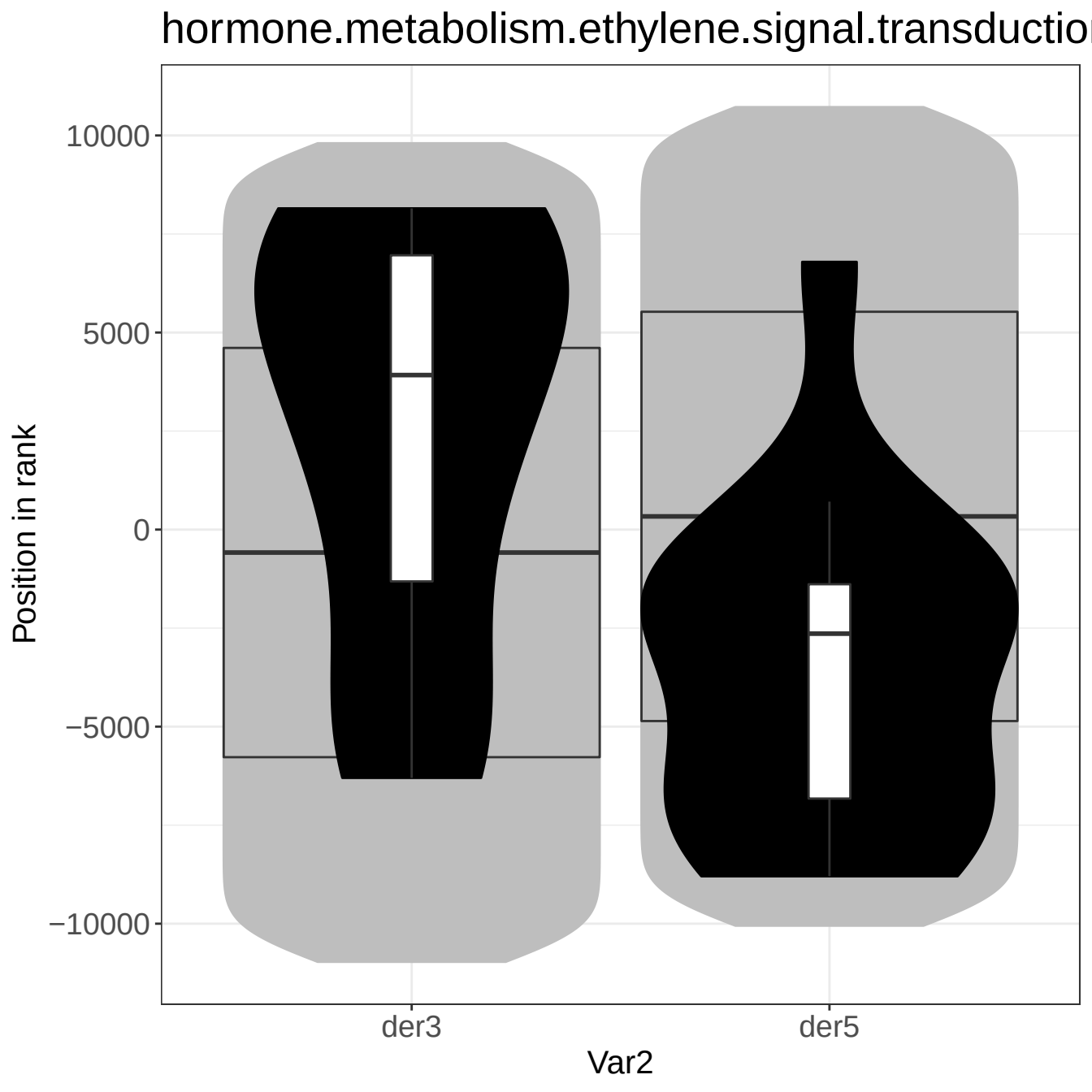
Rank in contrast der3


hormone.metabolism.ethylene.signal.transductio
10000
5000
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−5000
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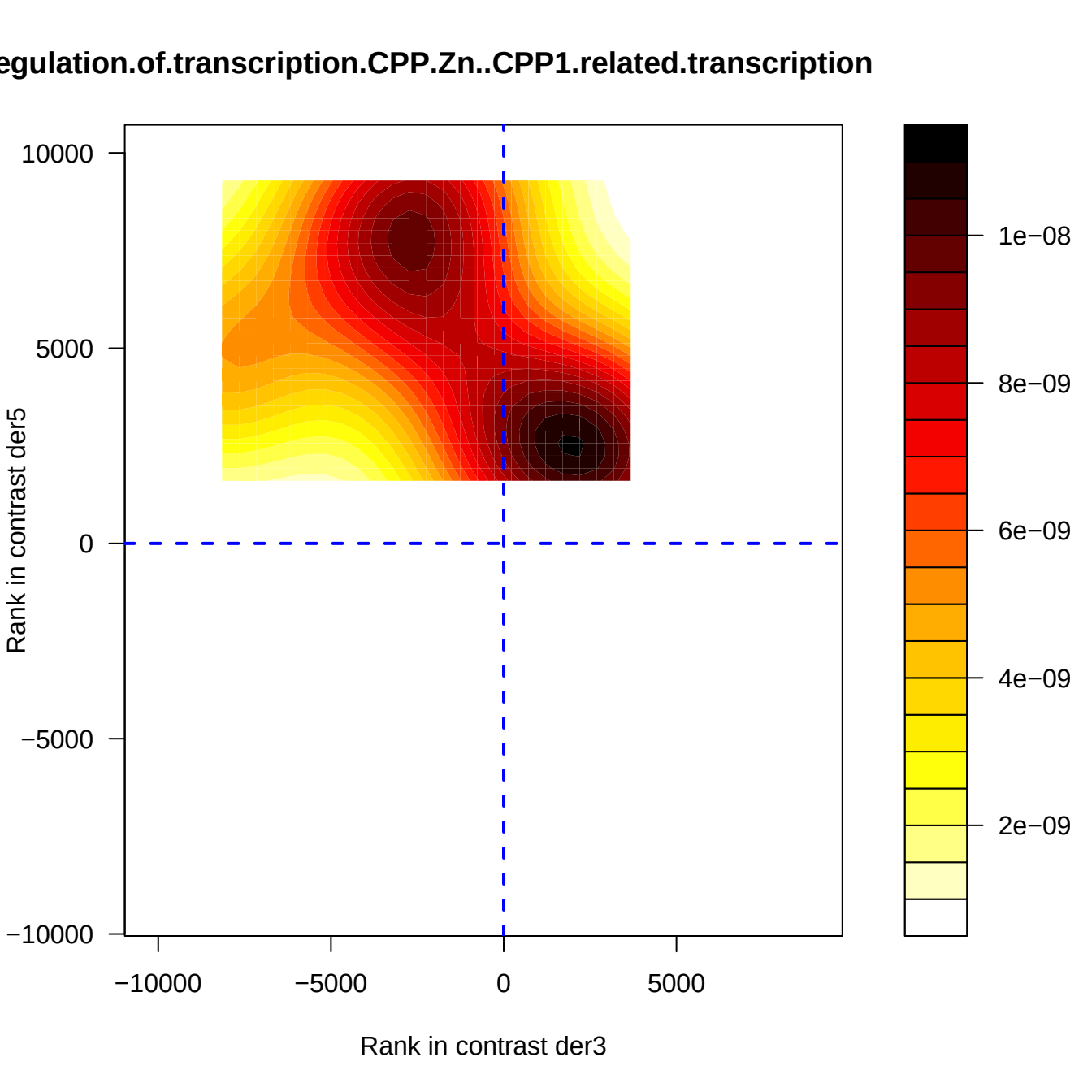
Position in rank
der3
der5
Var2


egulation.of.transcription.CPP.Zn..CPP1.related.transcription
10000
5000
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−5000
−10000
Rank in contrast der5
−10000
−5000
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5000
Rank in contrast der3
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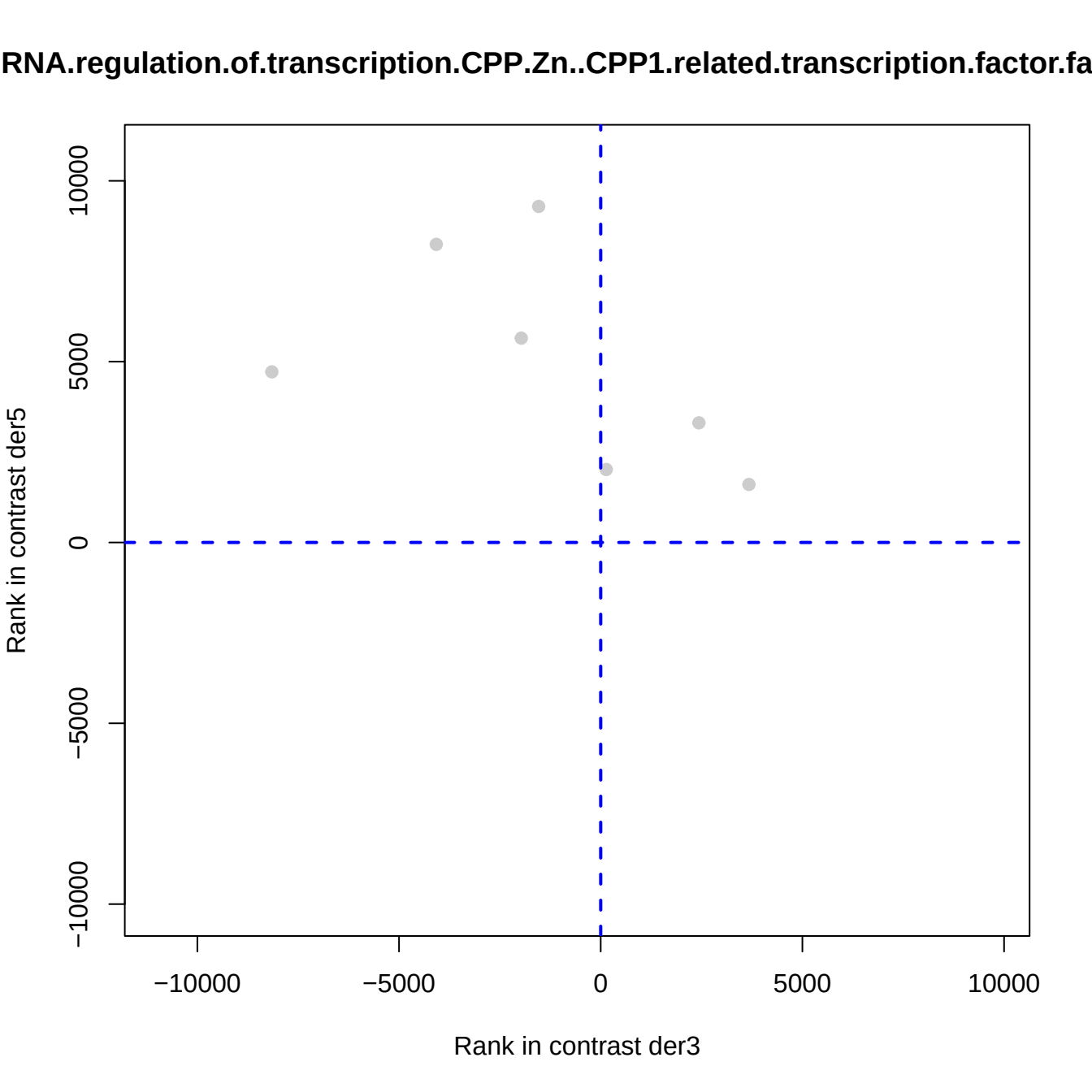
8e−09
6e−09
4e−09
2e−09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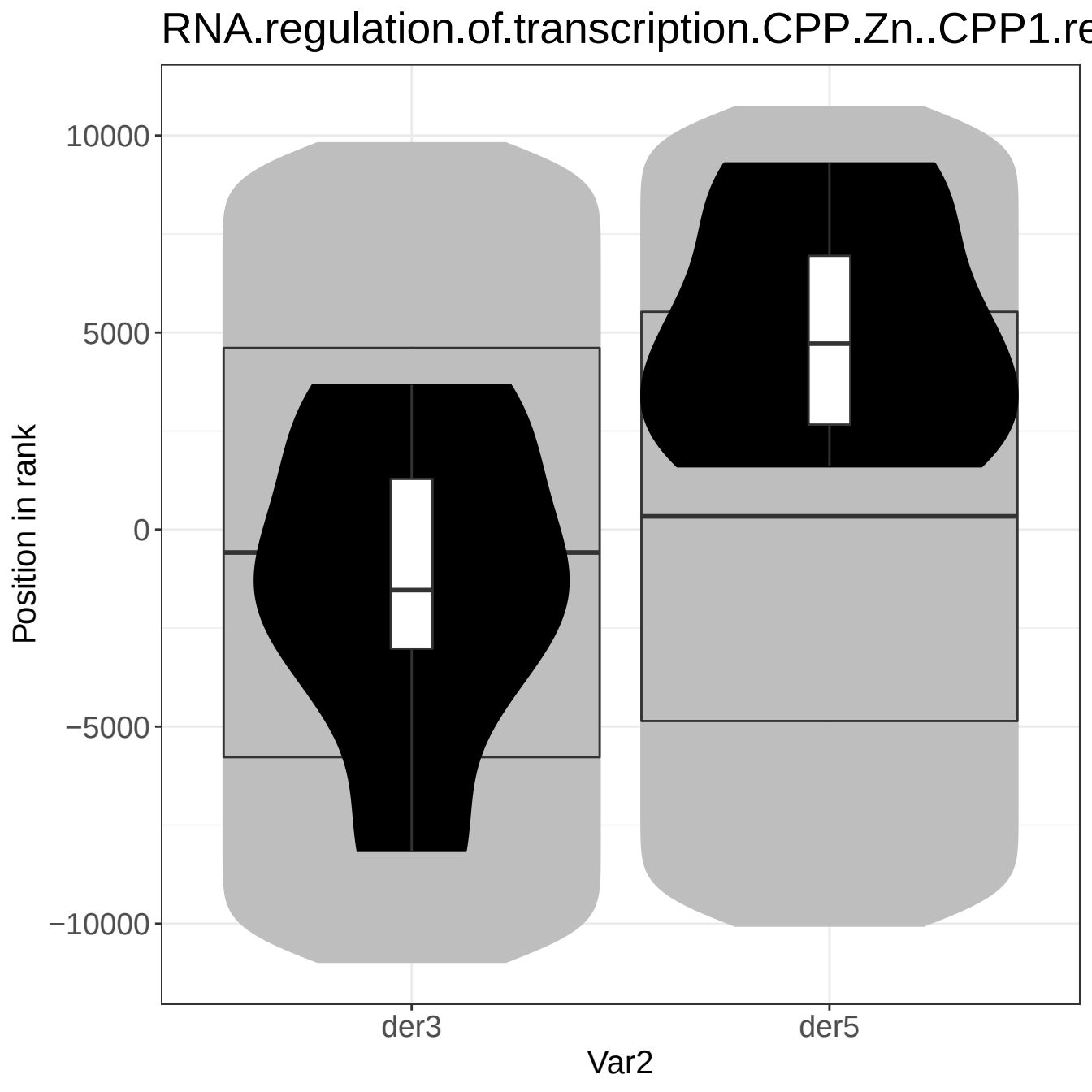
Rank in contrast der3


RNA.regulation.of.transcription.CPP.Zn..CPP1.re
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Position in rank
der3
der5
Var2