Suplementary figures for significantly altered pathways

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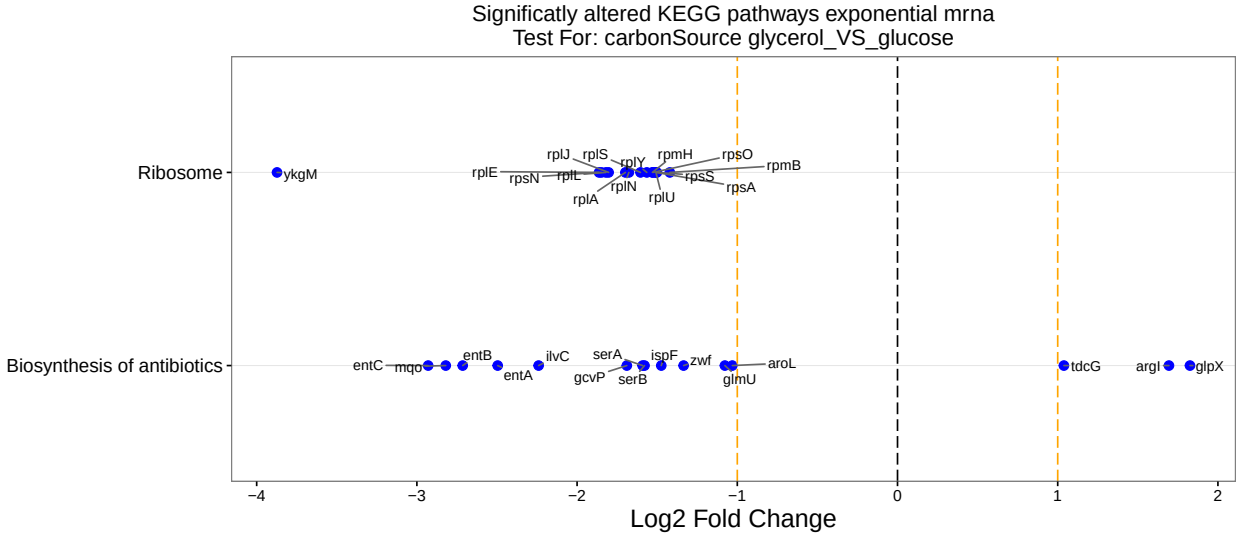
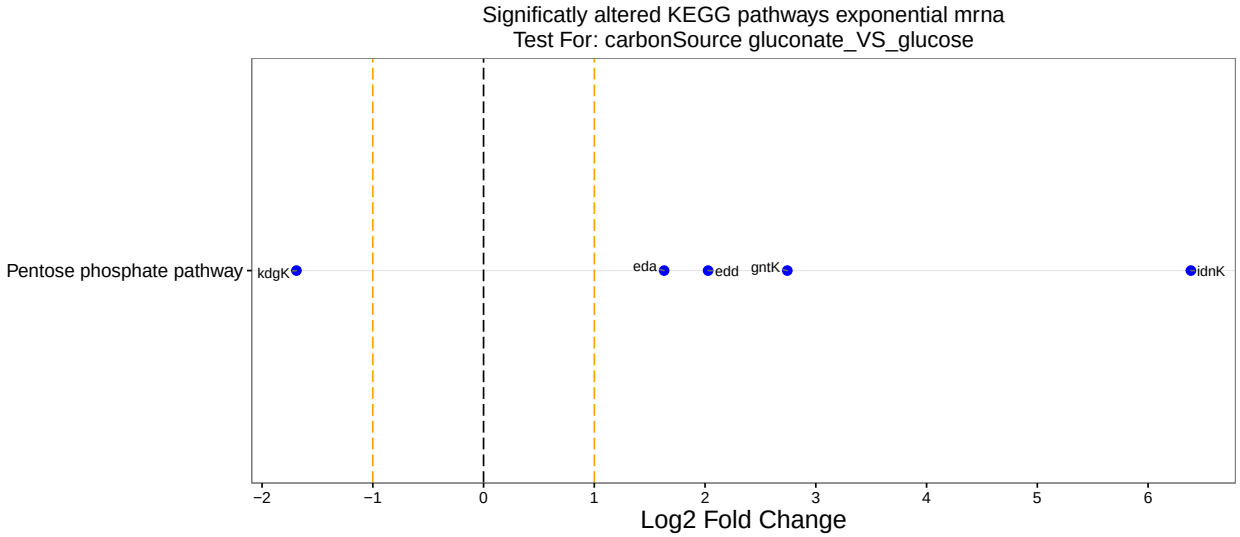
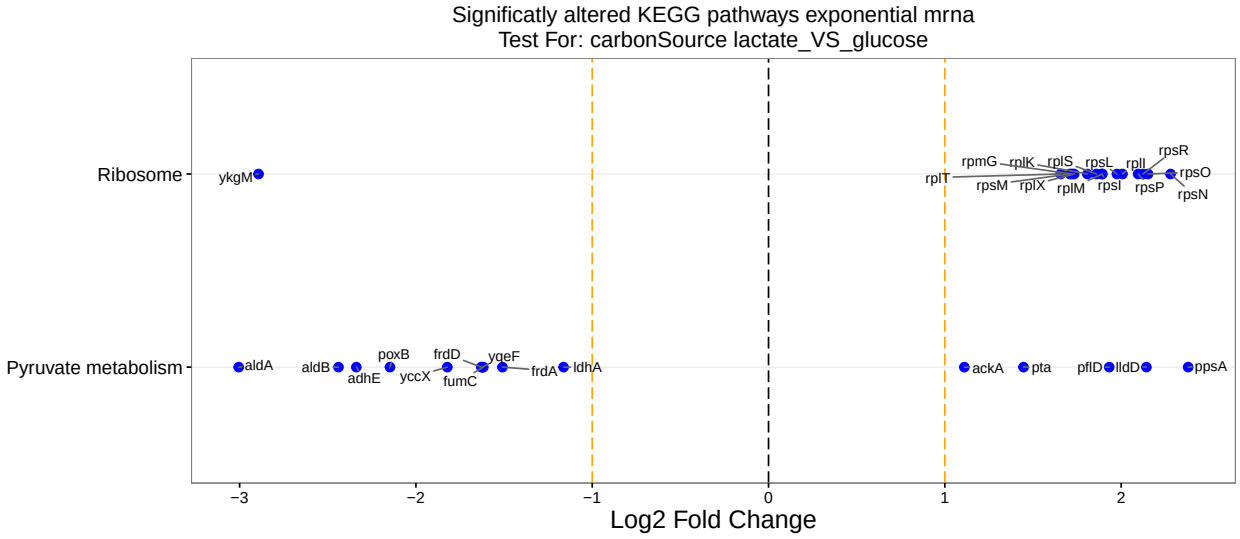
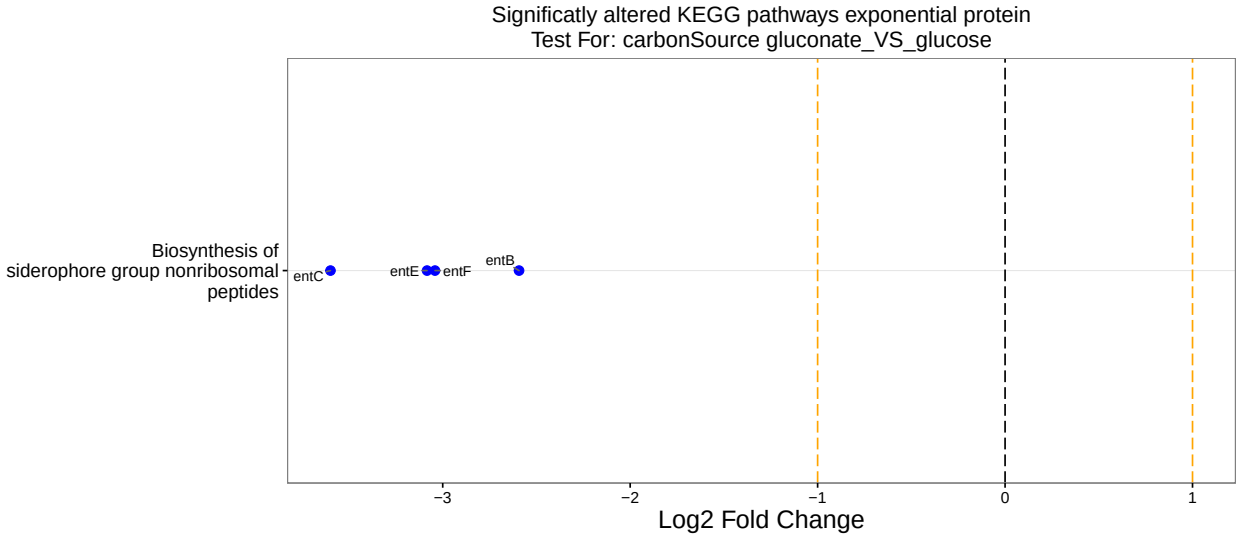
Significantly altered pathways and significantly altered genes within the pathways with respect to different external conditions are shown. Gene alterations are ordered with repect to change in expression levels and filtered by log change and adjusted P values. Only (1) The genes that change more than 2 fold and with an adjusted p value less than 0.05 are shown. (2) The patways that change with an ajusted p value less than 0.05 are shown (3) If the number of genes that satisfy the property "1" is more than 15 only 15 of them are shown. (4) If the number of pathways that satisfy property "2" is more than 10 only 10 of them are shown

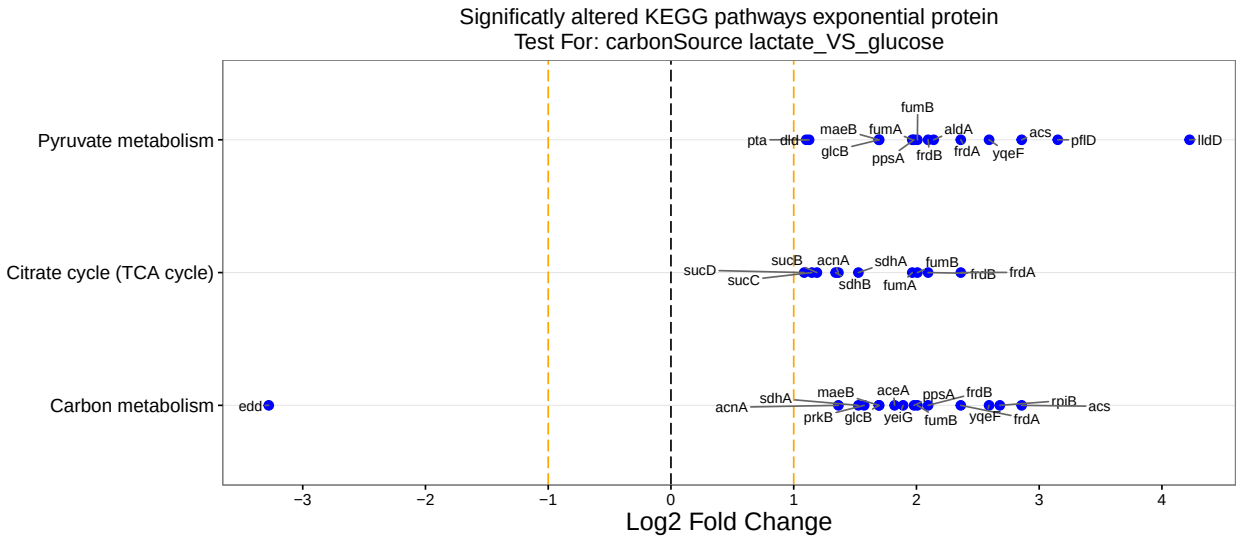
Figures related with KEGG Pathway

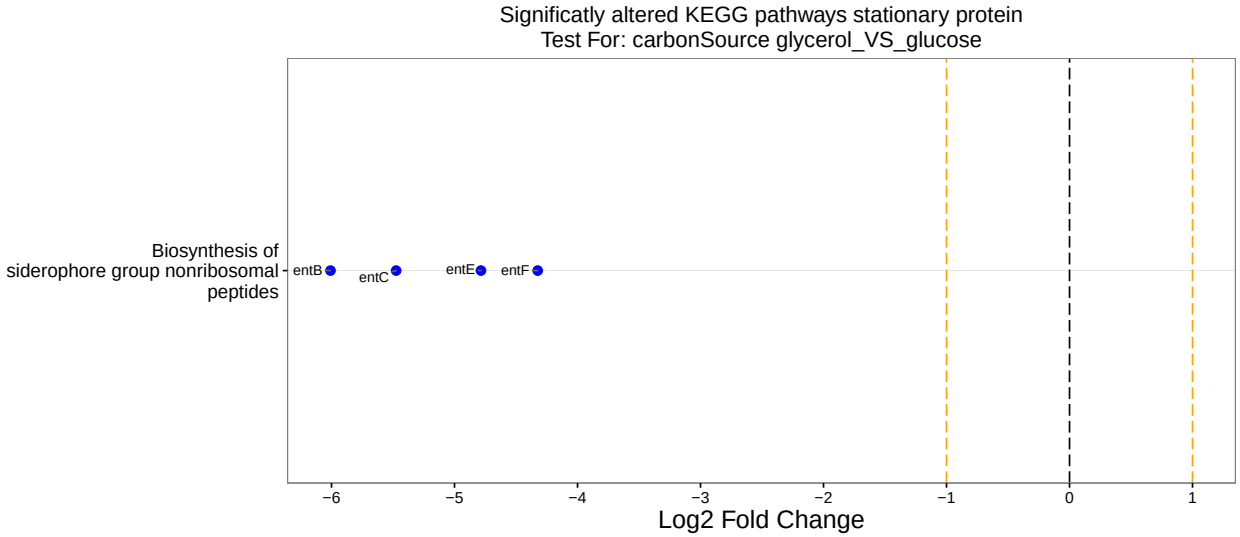


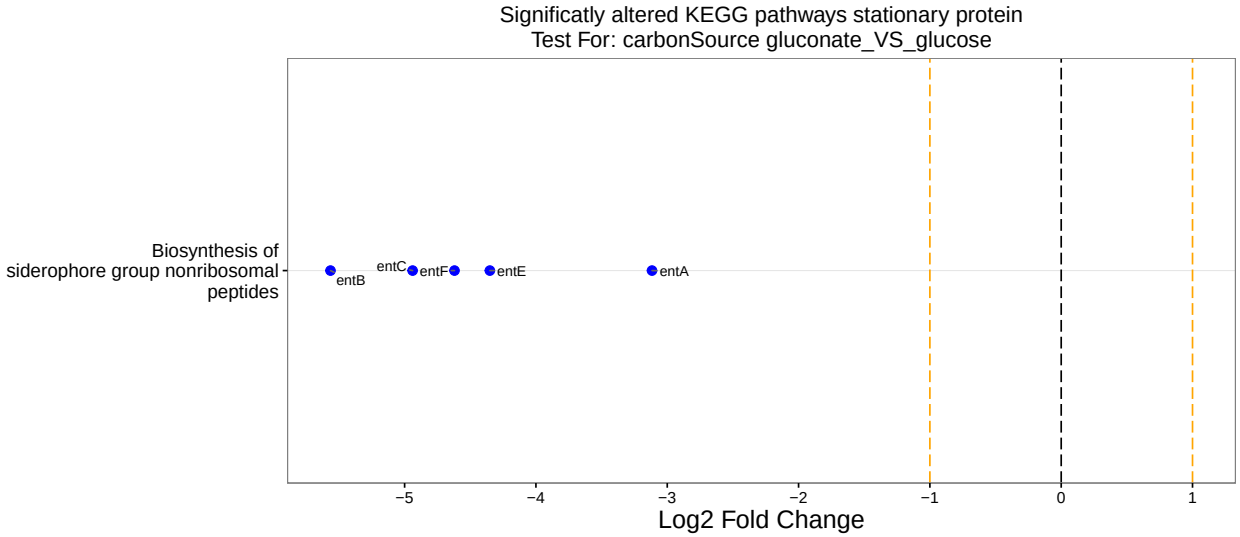

Significatly altered KEGG pathways exponential mrna
Test For: carbonSource gluconate_VS_glucose
Pentose phosphate pathway
kdgK
eda
edd
gntK
idnK
−2
−1
0
1
2
3
4
5
6
Log2 Fold Change

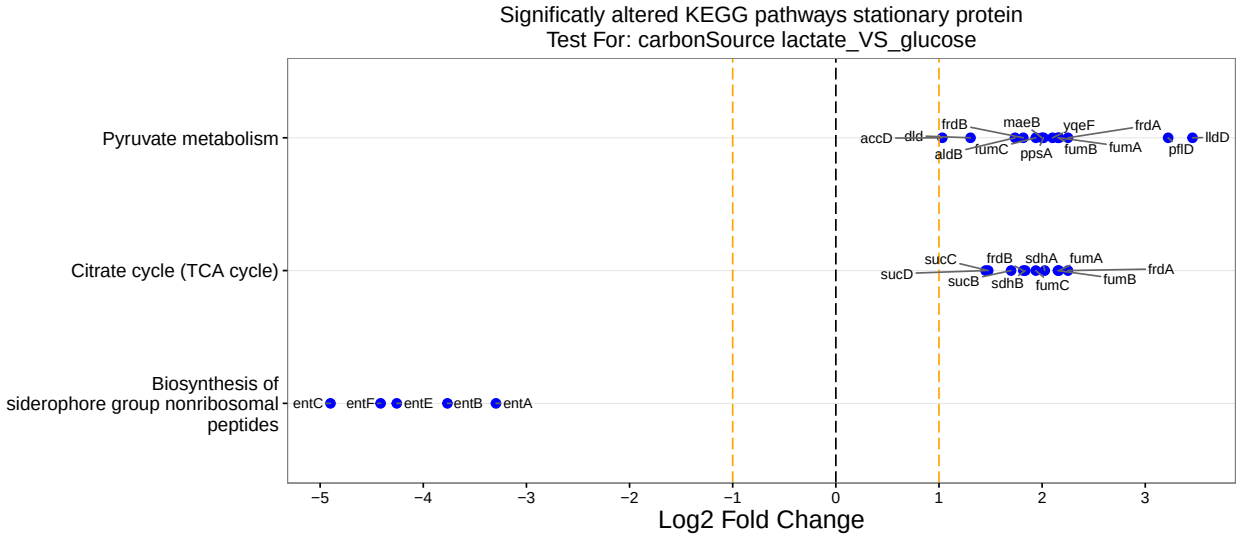

Significatly altered KEGG pathways exponential mrna
Test For: carbonSource lactate_VS_glucose
Ribosome
Pyruvate metabolism
ykgM
rplT
rpmG
rplK
rplS
rpsL
rplI
rpsR
rpsO
rpsN
rpsM
rplX
rplM
rpsI
rpsP
aldA
aldB
adhE
poxB
yccX
frdD
fumC
yqeF
frdA
ldhA
ackA
pta
pflD
lldD
ppsA
−3
−2
−1
0
1
2
Log2 Fold Change

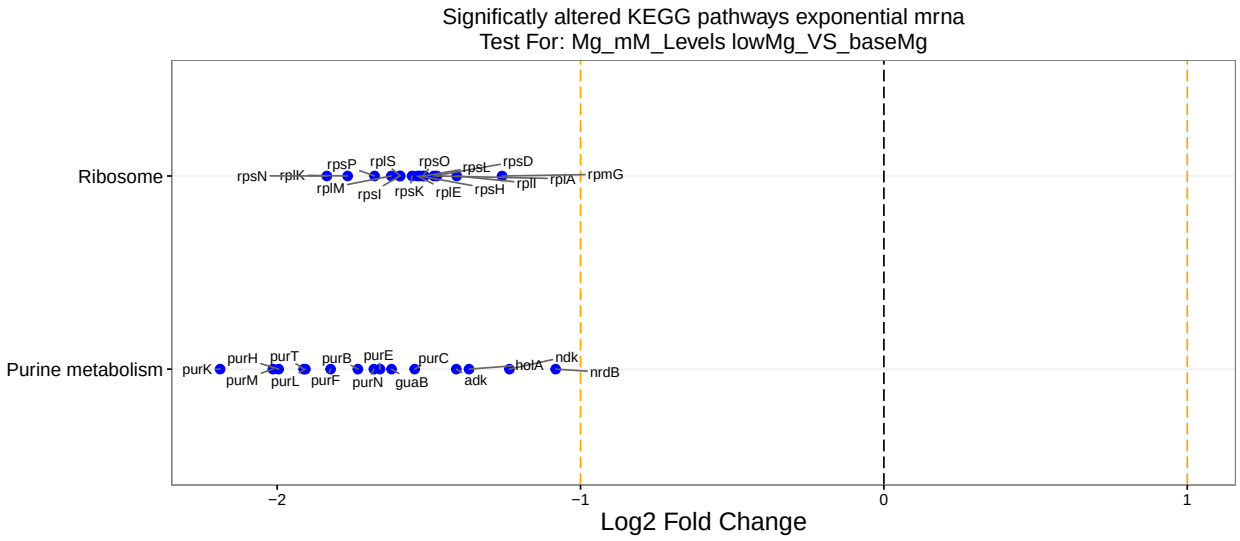

Significatly altered KEGG pathways exponential protein
Test For: carbonSource gluconate_VS_glucose
Biosynthesis of siderophore group nonribosomal peptides
entC
entE
entF
entB
−3
−2
−1
0
1
Log2 Fold Change

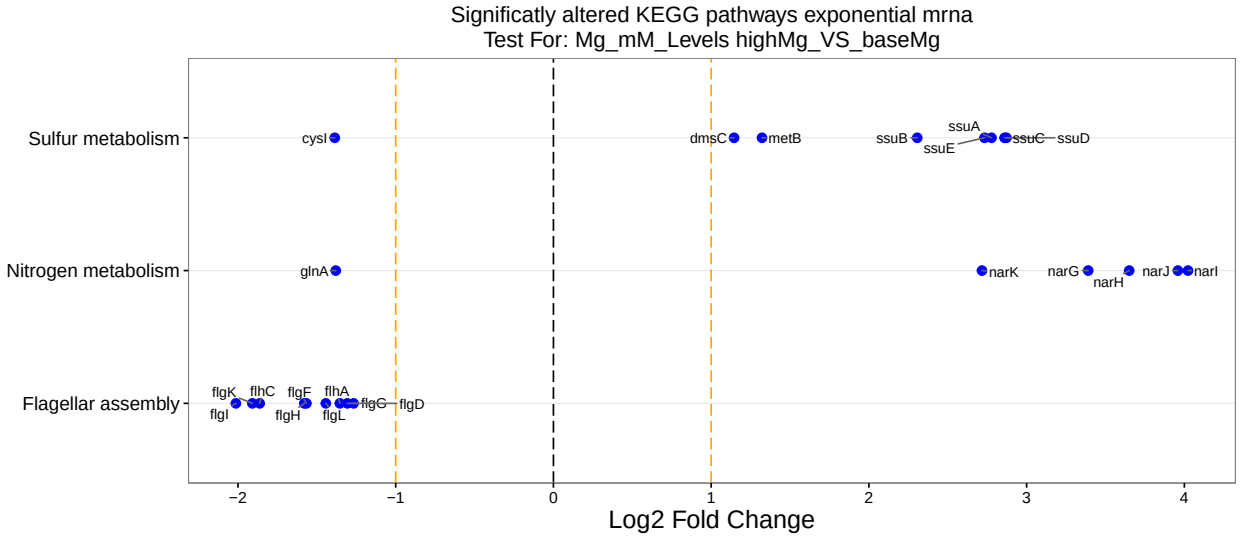

Significatly altered KEGG pathways exponential protein
Test For: carbonSource lactate_VS_glucose
Pyruvate metabolism
Citrate cycle (TCA cycle)
Carbon metabolism
pta
dld
maeB
fumA
fumB
glcB
ppsA
frdB
aldA
frdA
yqeF
acs
pflD
lldD
sucD
sucC
sucB
acnA
sdhB
sdhA
fumA
fumB
frdB
frdA
edd
acnA
sdhA
maeB
prkB
glcB
aceA
yeiG
ppsA
fumB
frdB
yqeF
frdA
rpiB
acs
−3
−2
−1
0
1
2
3
4
Log2 Fold Change

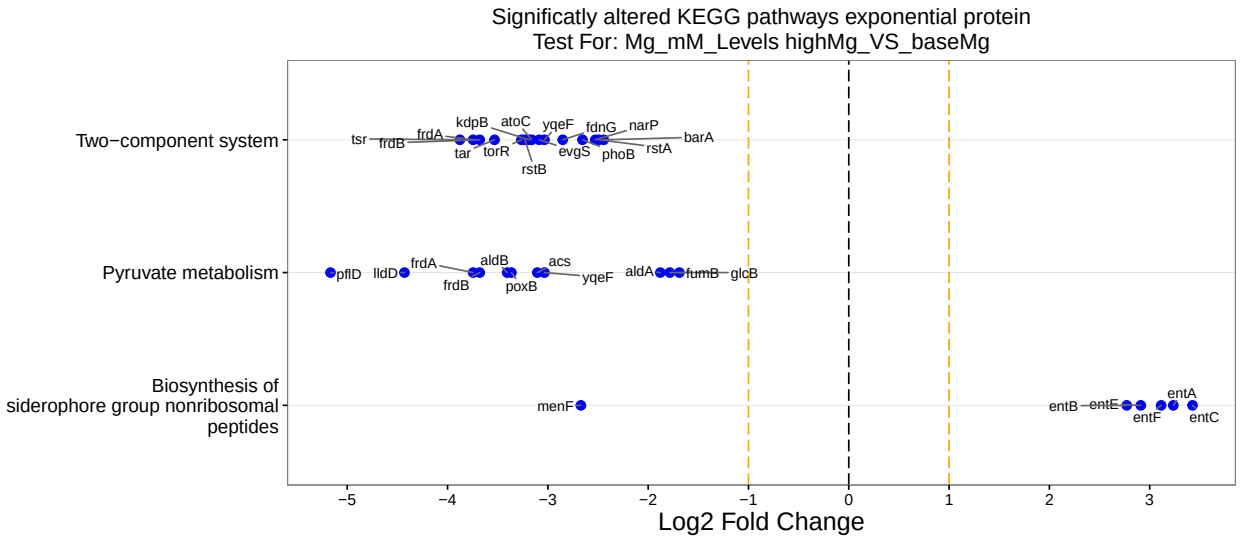

Significatly altered KEGG pathways stationary protein
Test For: carbonSource glycerol_VS_glucose
Biosynthesis of siderophore group nonribosomal peptides
entB
entC
entE
entF
−6
−5
−4
−3
−2
−1
0
1
Log2 Fold Change

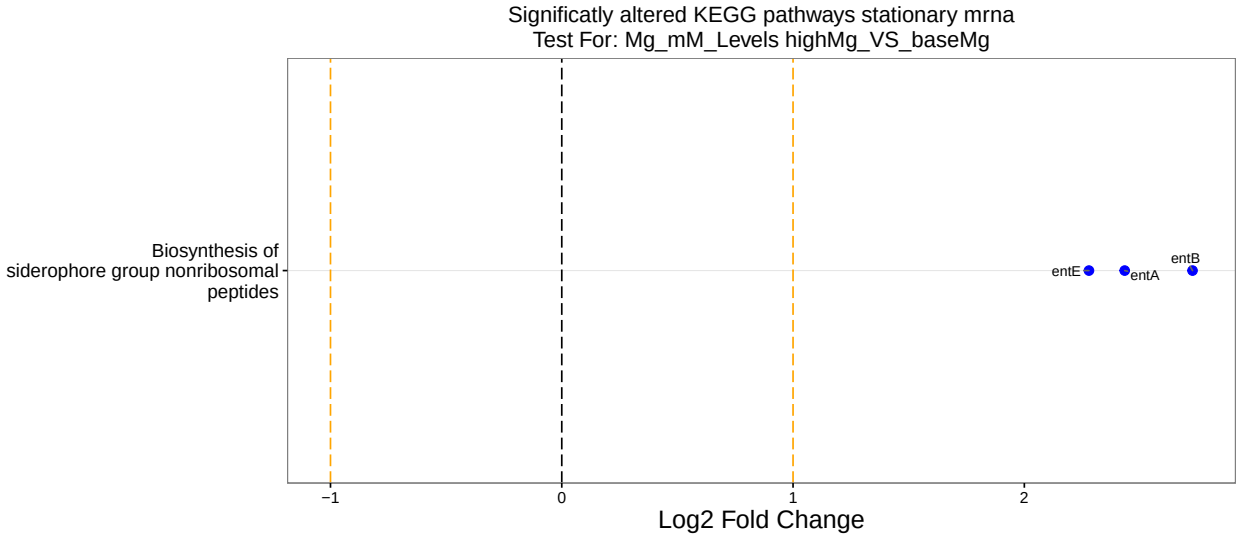

Significatly altered KEGG pathways stationary protein
Test For: carbonSource gluconate_VS_glucose
Biosynthesis of siderophore group nonribosomal peptides
entB
entC
entF
entE
entA
−5
−4
−3
−2
−1
0
1
Log2 Fold Change

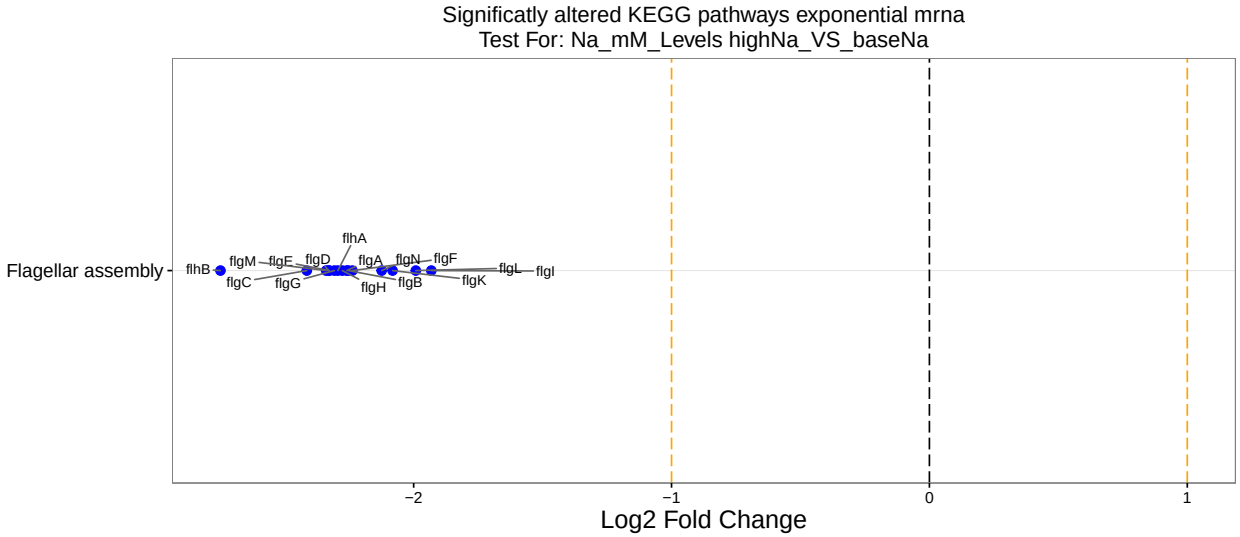

Significatly altered KEGG pathways stationary protein
Test For: carbonSource lactate_VS_glucose
Pyruvate metabolism
Citrate cycle (TCA cycle)
Biosynthesis of siderophore group nonribosomal peptides
accD
dld
frdB
aldB
fumC
maeB
ppsA
yqeF
fumB
frdA
fumA
pflD
lldD
sucC
sucD
frdB
sucB
sdhA
sdhB
fumA
fumC
frdA
fumB
entC
entF
entE
entB
entA
−5
−4
−3
−2
−1
0
1
2
3
Log2 Fold Change

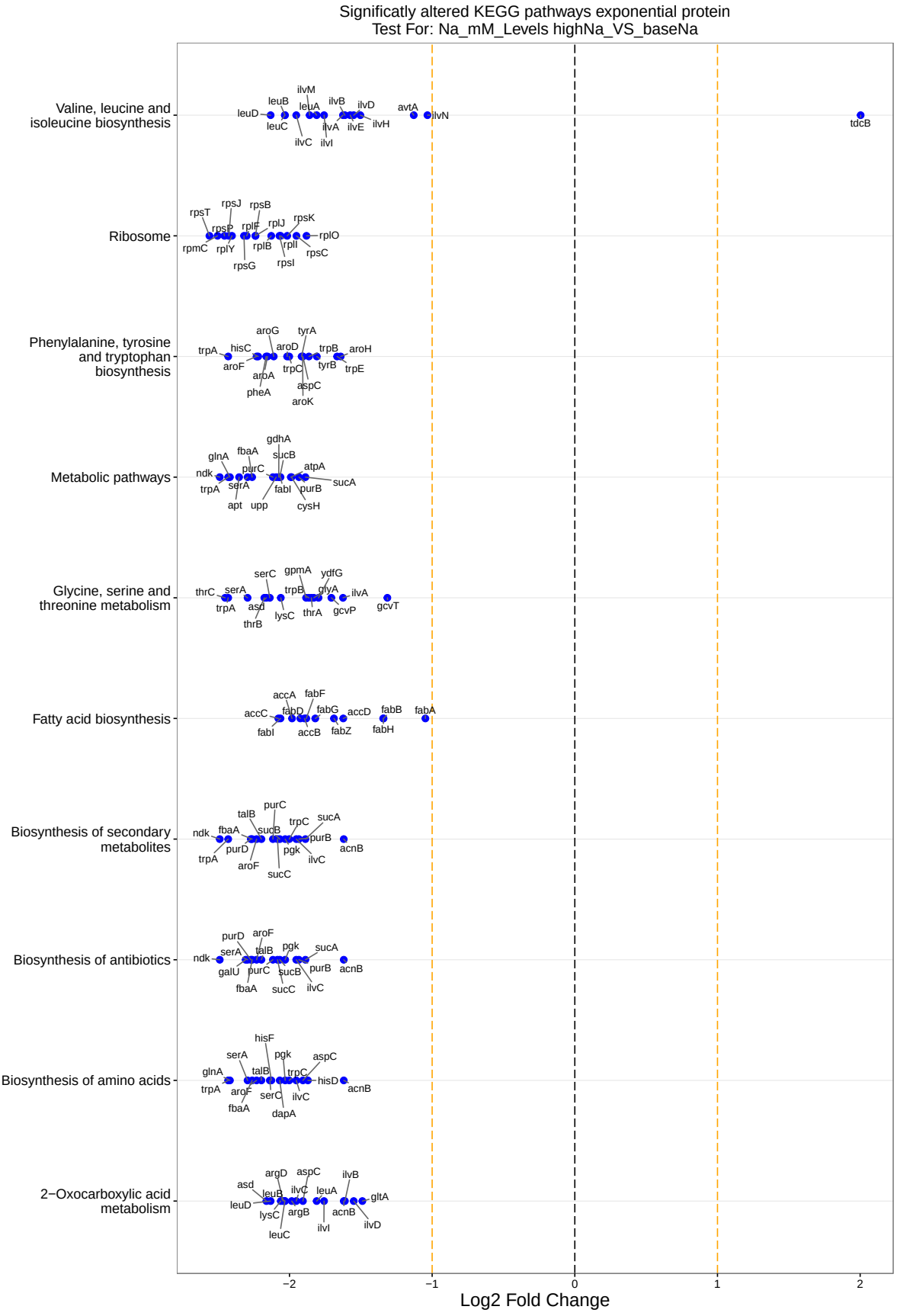

Significatly altered KEGG pathways exponential mrna
Test For: Mg_mM_Levels lowMg_VS_baseMg
Ribosome
Purine metabolism
rpsN
rplK
rpsP
rplS
rpsO
rpsL
rpsD
rpmG
rplM
rpsI
rpsK
rplE
rpsH
rplI
rplA
purK
purH
purT
purB
purE
purC
hotA
ndk
nrdB
purM
purL
purF
purN
guaB
adk
−2
−1
0
1
Log2 Fold Change

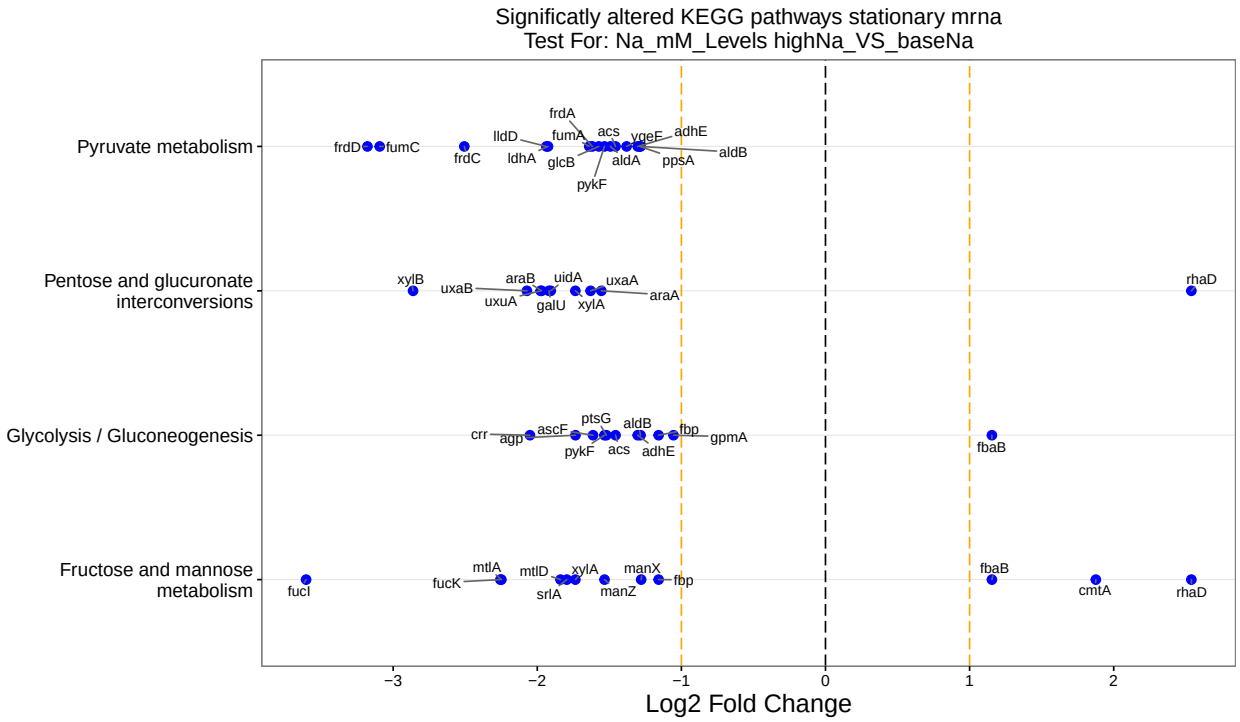

Significatly altered KEGG pathways exponential mrna
Test For: Mg_mM_Levels highMg_VS_baseMg
Sulfur metabolism
Nitrogen metabolism
Flagellar assembly
cysI
dmsC
metB
ssuB
ssuA
ssuE
ssuC
ssuD
glnA
narK
narG
narH
narJ
narI
flgK
flhC
flgI
flgE
flgH
flhA
flgL
flgG
flgD
−2
−1
0
1
2
3
4
Log2 Fold Change

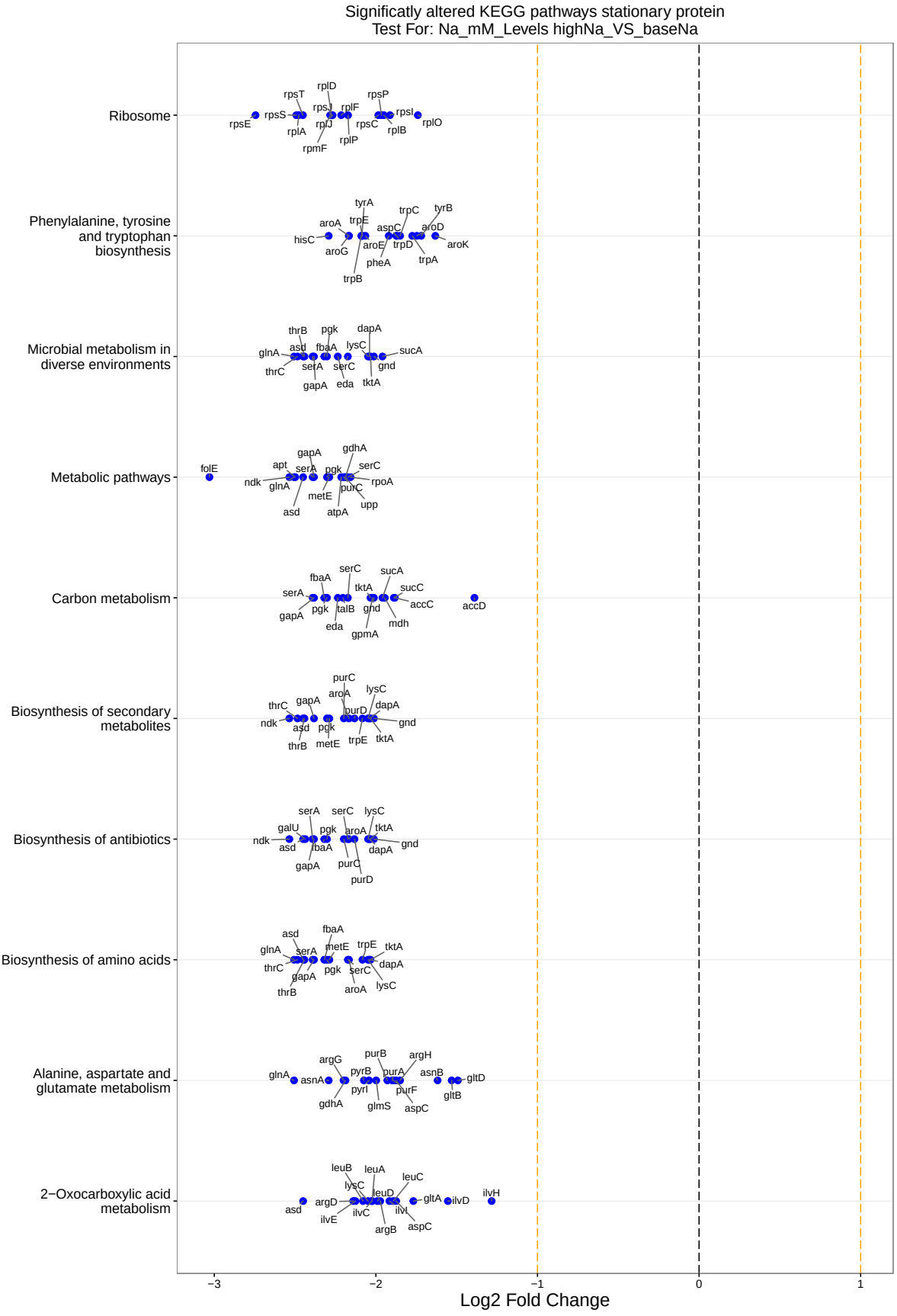

Significatly altered KEGG pathways exponential protein
Test For: Mg_mM_Levels highMg_VS_baseMg
Two−component system
Pyruvate metabolism
Biosynthesis of siderophore group nonribosomal peptides
tsr
frdB
frdA
kdpB
tar
torR
atoC
rstB
yqeF
evgS
fdnG
phoB
narP
rstA
barA
pflD
lldD
frdA
frdB
aldB
poxB
acs
yqeF
aldA
fumB
glcB
menF
entB
entE
entF
entA
entC
−5
−4
−3
−2
−1
0
1
2
3
Log2 Fold Change


Significatly altered KEGG pathways stationary mrna
Test For: Mg_mM_Levels highMg_VS_baseMg
Biosynthesis of siderophore group nonribosomal peptides
entE
entA
entB
−1
0
1
2
Log2 Fold Change

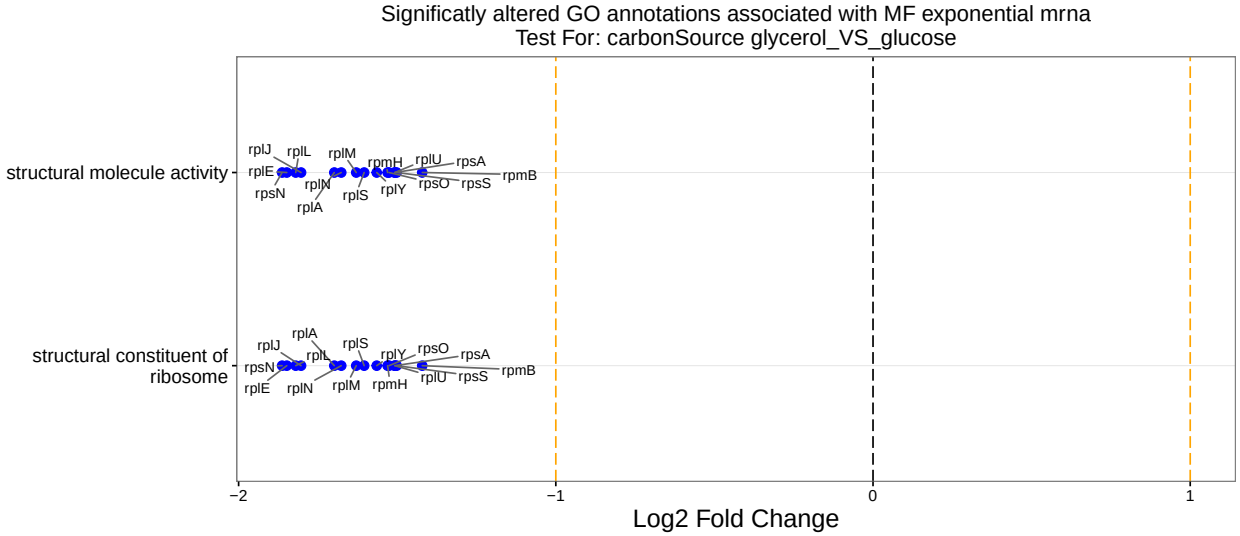

Significatly altered KEGG pathways exponential mrna
Test For: Na_mM_Levels highNa_VS_baseNa
Flagellar assembly
flhB
flgM
flgE
flgD
flhA
flgA
flgN
flgF
flgL
flgI
flgC
flgG
flgH
flgB
flgK
−2
−1
0
1
Log2 Fold Change

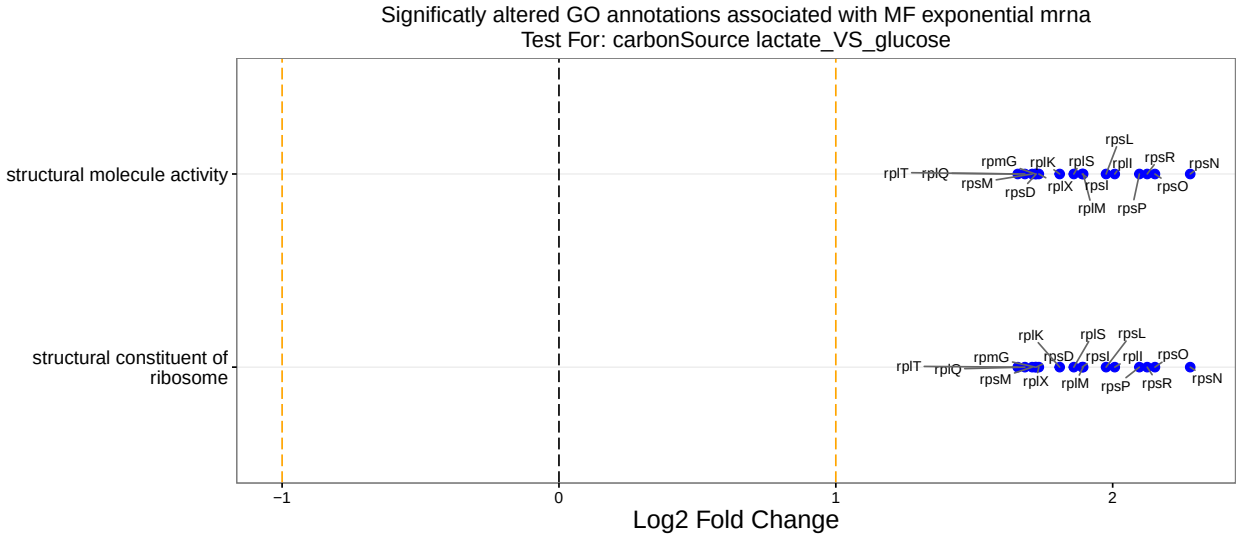

Significatly altered KEGG pathways exponential protein
Test For: Na_mM_Levels highNa_VS_baseNa
Valine, leucine and isoleucine biosynthesis
Ribosome
Phenylalanine, tyrosine and tryptophan biosynthesis
Metabolic pathways
Glycine, serine and threonine metabolism
Fatty acid biosynthesis
Biosynthesis of secondary metabolites
Biosynthesis of antibiotics
Biosynthesis of amino acids
2−Oxocarboxylic acid metabolism
ilvM
leuB
leuA
ilvB
ilvD
avtA
leuD
ilvN
tdcB
leuC
ilvA
ilvE
ilvH
ilvC
ilvI
rpsJ
rpsB
rpsT
rpsK
rplF
rplJ
rplO
rpsP
rplI
rpmC
rplY
rplB
rpsC
rpsG
rpsI
aroG
tyrA
trpA
hisC
aroD
trpB
aroH
aroF
trpC
tyrB
trpE
aroA
aspC
pheA
aroK
gdhA
glnA
fbaA
sucB
ndk
purC
atpA
sucA
trpA
serA
fabI
purB
apt
upp
cysH
serC
gpmA
ydfG
thrC
serA
trpB
glyA
ilvA
trpA
asd
thrA
gcvP
gcvT
lysC
thrB
accA
fabF
accC
fabD
fabG
accD
fabB
fabA
fabI
accB
fabZ
fabH
talB
purC
ndk
fbaA
sucB
trpC
sucA
purB
acnB
purD
pgk
trpA
ilvC
aroF
sucC
purD
aroF
ndk
serA
talB
pgk
sucA
galU
purC
sucB
purB
acnB
fbaA
sucC
ilvC
hisF
serA
pgk
aspC
glnA
talB
trpC
hisD
acnB
trpA
argF
serC
ilvC
fbaA
dapA
argD
aspC
ilvB
asd
ilvC
leuA
leuB
gltA
leuD
argB
acnB
lysC
ilvI
ilvD
leuC
−2
−1
0
1
2
Log2 Fold Change

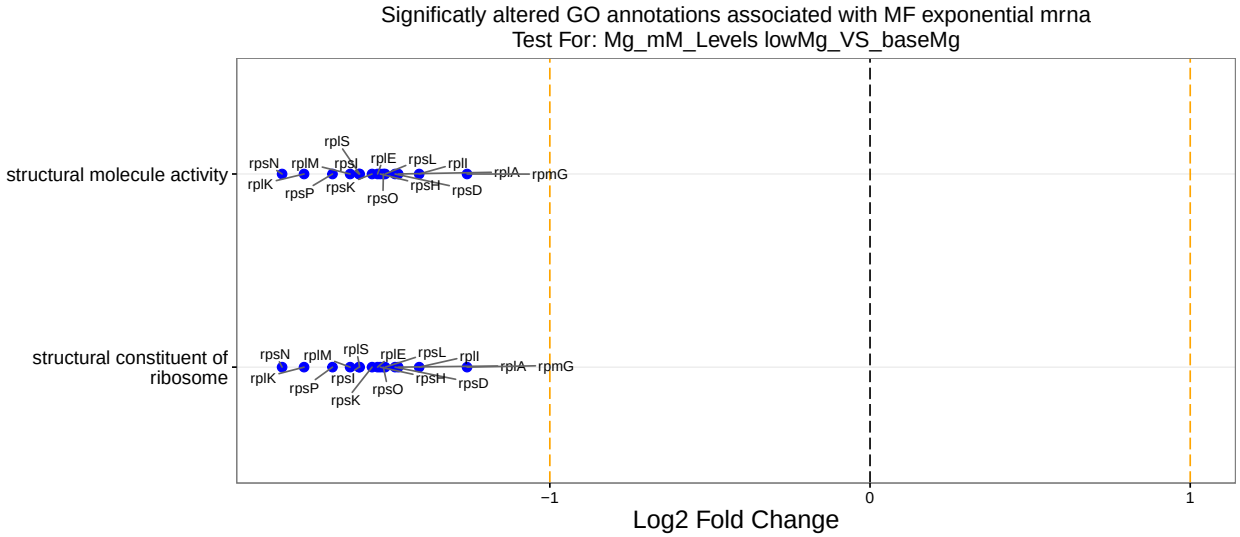

Significatly altered KEGG pathways stationary mrna
Test For: Na_mM_Levels highNa_VS_baseNa
Pyruvate metabolism
Pentose and glucuronate interconversions
Glycolysis / Gluconeogenesis
Fructose and mannose metabolism
frdA
frdD
fumC
frdC
lldD
fumA
acs
vgeF
adhE
aldB
ldhA
glcB
aldA
ppsA
pykF
xylB
uxaB
araB
uidA
uxaA
rhaD
uxuA
galU
xylA
araA
crr
agp
ascF
ptsG
aldB
fbp
gpmA
pykF
acs
adhE
fbaB
fucI
fucK
mtlA
mtlD
xylA
manX
fbp
srlA
manZ
fbaB
cmtA
rhaD
−3
−2
−1
0
1
2
Log2 Fold Change

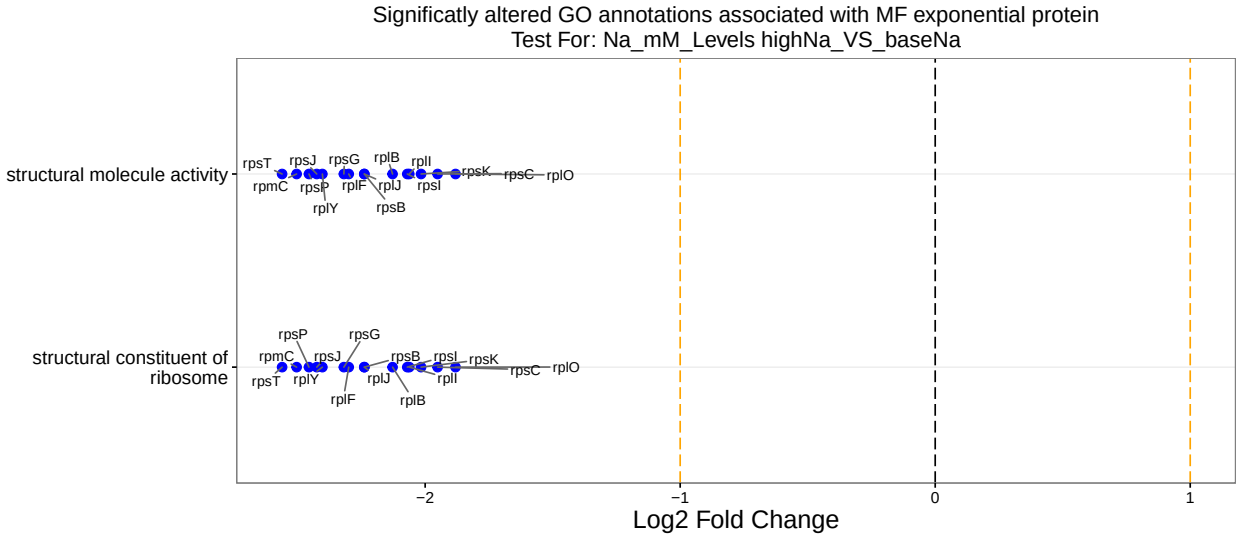

Significatly altered KEGG pathways stationary protein
Test For: Na_mM_Levels highNa_VS_baseNa
Ribosome
Phenylalanine, tyrosine and tryptophan biosynthesis
Microbial metabolism in diverse environments
Metabolic pathways
Carbon metabolism
Biosynthesis of secondary metabolites
Biosynthesis of antibiotics
Biosynthesis of amino acids
Alanine, aspartate and glutamate metabolism
2−Oxocarboxylic acid metabolism
−3
−2
−1
0
1
Log2 Fold Change

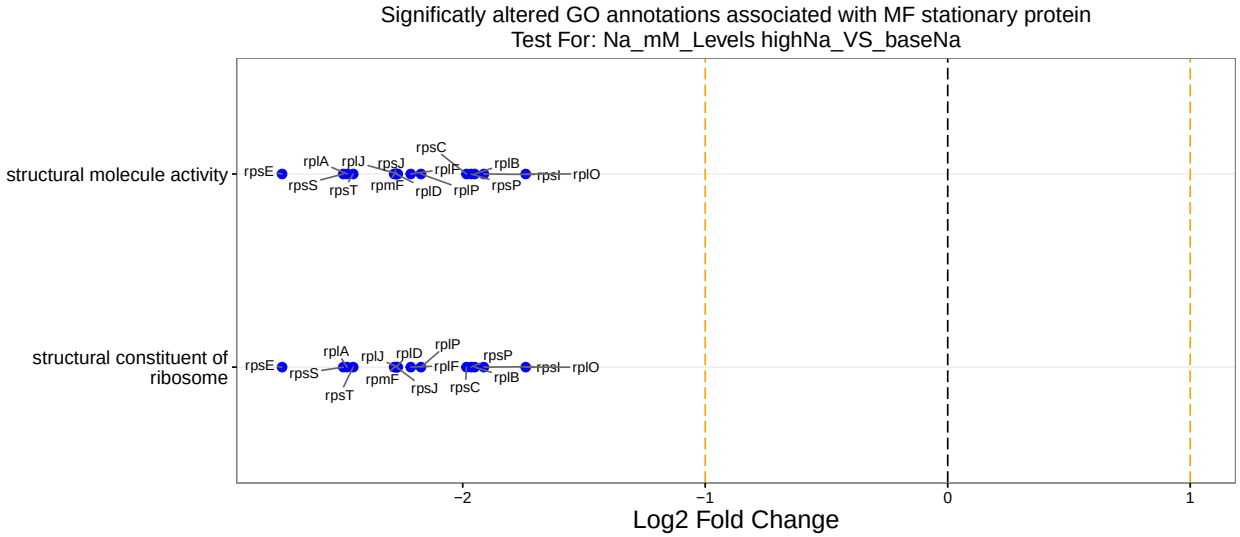
Figures related with GO Annotations associated with Molecular Function




Significatly altered GO annotations associated with MF exponential mrna
Test For: carbonSource lactate_VS_glucose
structural molecule activity
structural constituent of ribosome
rplT
rplQ
rpmG
rplK
rplS
rpsL
rplI
rpsR
rpsN
rpsM
rpsD
rplX
rpsI
rplM
rpsP
rpsO
−1
0
1
2
Log2 Fold Change


Significatly altered GO annotations associated with MF exponential mrna
Test For: Mg_mM_Levels lowMg_VS_baseMg
structural molecule activity
structural constituent of ribosome
rpsN
rplM
rplS
rplE
rpsL
rplI
rplA
rpmG
rplK
rpsP
rpsK
rpsO
rpsH
rpsD
rpsI
−1
0
1
Log2 Fold Change


Significatly altered GO annotations associated with MF exponential protein
Test For: Na_mM_Levels highNa_VS_baseNa
structural molecule activity
structural constituent of ribosome
rpsT
rpsJ
rpsG
rplB
rplI
rpsK
rpsC
rplO
rpmC
rpsP
rplF
rplJ
rpsI
rplY
rpsB
−2
−1
0
1
Log2 Fold Change


Significatly altered GO annotations associated with MF stationary protein
Test For: Na_mM_Levels highNa_VS_baseNa
structural molecule activity
structural constituent of ribosome
rpsE
rplA
rplJ
rpsJ
rpsC
rplF
rplB
rpsS
rpsT
rpmF
rplD
rplP
rpsP
rpsI
rplO
−2
−1
0
1
Log2 Fold Change