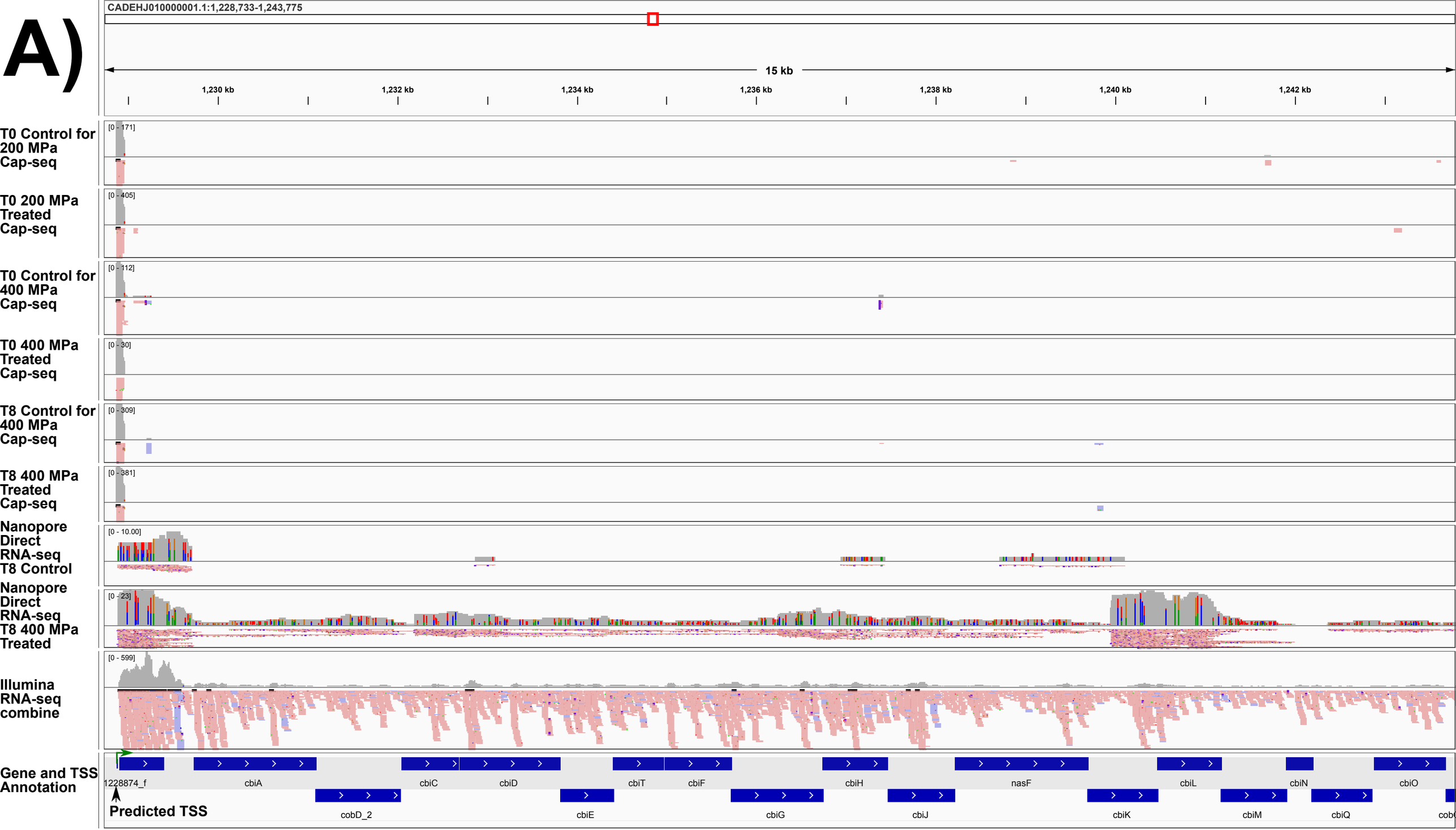
Figure S9. Visualization of A) cobalamin biosynthesis and B) ethanolamine utilization genes on *L. monocytogenes* RO15 region 543550 bp - 545050 Mbp. Nine rows of data, in descending order: 0 min control sample for 200 MPa cap-seq reads, 0 min 200 MPa treated samples cap-seq reads, 0 min control sample for 400 MPa cap-seq reads, 0 min 400 MPa treated samples cap-seq reads, 24 h control sample for 400 MPa cap-seq reads, 24 h 400 MPa treated sample cap-seq reads, 24 h control sample for 400 MPa direct RNA-seq reads, 24 h 400 MPa treated sample direct RNA-seq reads, and Illumina short RNA-seq reads. Red lines are forward reads, and blue lines are reverse reads. Grey bars are coverage bar plots.


A)
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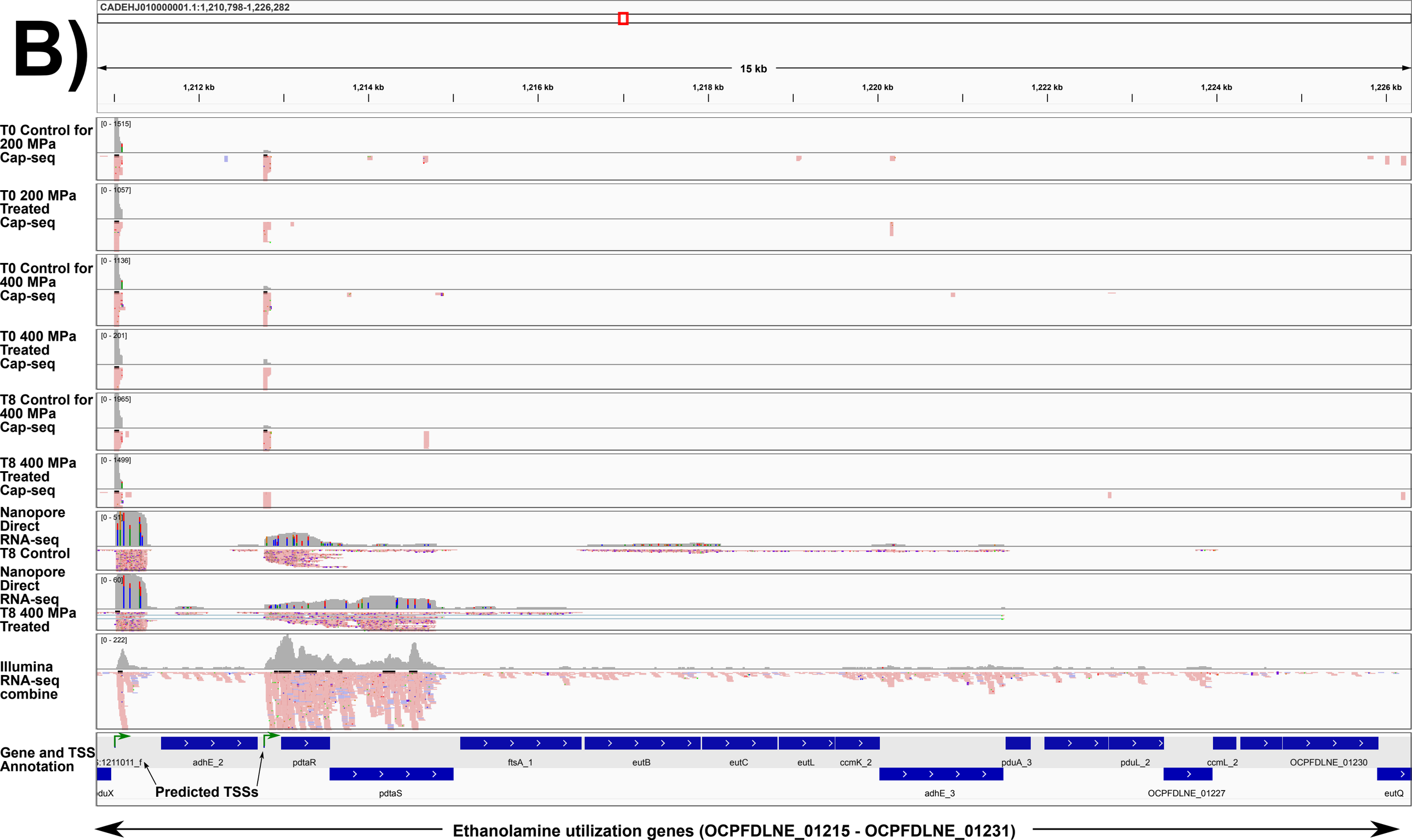
1,230 kb
1,232 kb
1,234 kb
1,236 kb
1,238 kb
1,240 kb
1,242 kb
T0 Control for 200 MPa Cap-seq
[0 - 171]
T0 200 MPa Treated Cap-seq
[0 - 405]
T0 Control for 400 MPa Cap-seq
[0 - 112]
T0 400 MPa Treated Cap-seq
[0 - 30]
T8 Control for 400 MPa Cap-seq
[0 - 309]
T8 400 MPa Treated Cap-seq
[0 - 381]
Nanopore Direct RNA-seq T8 Control
[0 - 10.00]
Nanopore Direct RNA-seq T8 400 MPa Treated
[0 - 23]
Illumina RNA-seq combine
[0 - 599]
Gene and TSS Annotation
1228874_f
cbiA
cbiC
cbiD
cbiT
cbiF
cbiH
nasF
cbiL
cbiN
cbiO
Predicted TSS
cobD_2
cbiE
cbiG
cbiJ
cbiK
cbiM
cbiQ
Cobalamin biosynthesis operon (OCPFDLNE_01234 - OCPFDLNE_01251)


B)
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1,214 kb
1,216 kb
1,218 kb
1,220 kb
1,222 kb
1,224 kb
1,226 kb
T0 Control for 200 MPa Cap-seq
[0 - 1515]
T0 200 MPa Treated Cap-seq
[0 - 1057]
T0 Control for 400 MPa Cap-seq
[0 - 1136]
T0 400 MPa Treated Cap-seq
[0 - 201]
T8 Control for 400 MPa Cap-seq
[0 - 1965]
T8 400 MPa Treated Cap-seq
[0 - 1499]
Nanopore Direct RNA-seq T8 Control
[0 - 51]
Nanopore Direct RNA-seq T8 400 MPa Treated
[0 - 60]
Illumina RNA-seq combine
[0 - 222]
Gene and TSS Annotation
:1211011_f
adhE_2
pdtaR
ftsA_1
eutB
eutC
eutL
ccmK_2
pduA_3
pduL_2
ccmL_2
OCPFDLNE_01230
duX
Predicted TSSs
pdtaS
adhE_3
OCPFDLNE_01227
eutQ
Ethanolamine utilization genes (OCPFDLNE_01215 - OCPFDLNE_01231)