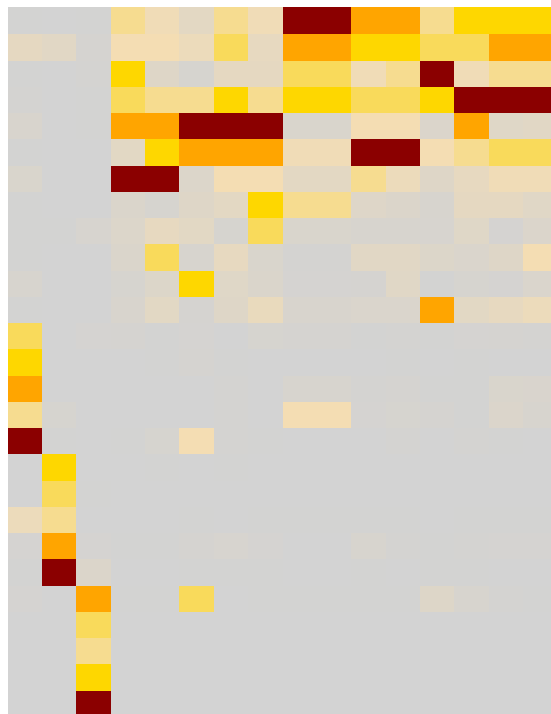
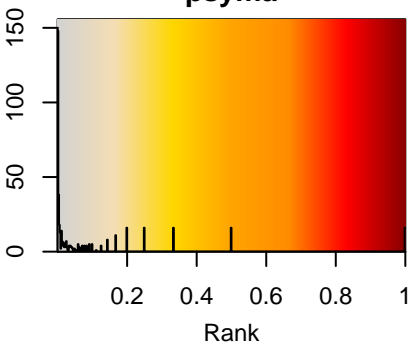


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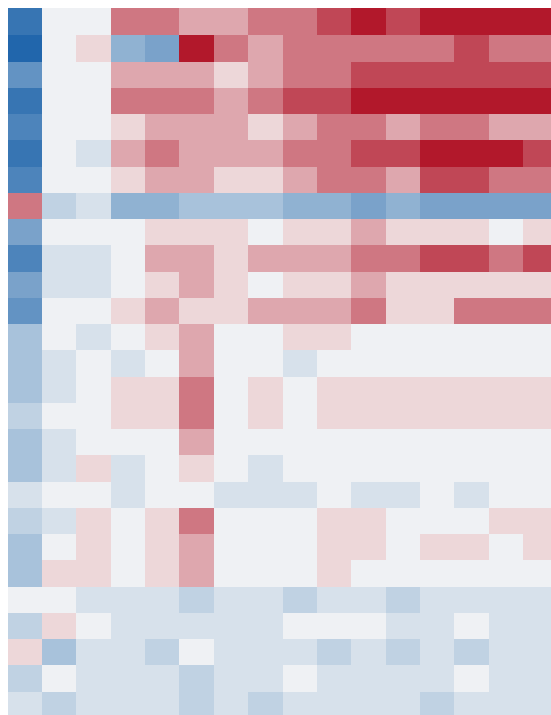
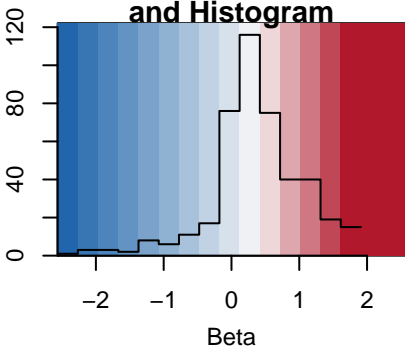


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dnf1 dnf2
dnf5 dnf2
rdn1
sunn1
dnf4
dnf2
dnf7
ipd3

CDO30_RS23155:MFS transporter; protein_id=V
CDO30_RS23125:SDR family oxidoreductase (p
CDO30_RS23065:SGNH/GDSL hydrolase family
CDO30_RS22325:hypothetical protein; protein_i
CDO30_RS21460:malonyl-CoA synthase; prote
CDO30_RS18080:fixL, oxygen sensor histidine k
CDO30_RS22055:class I SAM-dependent methy
CDO30_RS22005:amidase; protein_id=WP_010
CDO30_RS21460:malonyl-CoA synthase; prote
CDO30_RS19190:nodQ, bifunctional sulfate ade
CDO30_RS19605:stc4, stachydrine N-demethyl
CDO30_RS22335:site-specific integrase; protei
CDO30_RS20200:type II toxin-antitoxin system
CDO30_RS21100:DUF2200 domain-containing
CDO30_RS21085:class I SAM-dependent methy
CDO30_RS20205:type II toxin-antitoxin system
CDO30_RS21175:TRAP transporter small perme
CDO30_RS18965:traA, Ti-type conjugative trans
CDO30_RS21490:S8 family serine peptidase; pr
CDO30_RS21375:PhzF family phenazine biosyn
CDO30_RS21370:cold-shock protein; protein_id
CDO30_RS19120:glmS, glutamine-fructose-6-
CDO30_RS24215:CopG family transcriptional re
CDO30_RS19555:ccoN, cytochrome-c oxidase?
CDO30_RS24970:type II toxin-antitoxin system
CDO30_RS22190:aldo/keto reductase; protein_i

Color Key

and Histogram



A17
hcl
dnf3
dnf5dnf2
nad1
latd
dnf6
dnf4
sunn4
dnf2
dnf1dnf2
sunn1
rdn1
dnf1
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ipd3

CDO30_RS23155:MFS transporter; protein_id=

CDO30_RS23125:SDR family oxidoreductase (p

CDO30_RS23065:SGNH/GDSL hydrolase family

CDO30_RS22325:hypothetical protein; protein_i

CDO30_RS21460:malonyl-CoA synthase; prote

CDO30_RS18080:fixL, oxygen sensor histidine k

CDO30_RS22055:class I SAM-dependent meth

CDO30_RS22005:amidase; protein_id=WP_010

CDO30_RS21460:malonyl-CoA synthase; prote

CDO30_RS19190:nodQ, bifunctional sulfate ade

CDO30_RS19605:stc4, stachydrine N-demethyl

CDO30_RS22335:site-specific integrase; protei

CDO30_RS20200:type II toxin-antitoxin system

CDO30_RS21100:DUF2200 domain-containing

CDO30_RS21085:class I SAM-dependent meth

CDO30_RS20205:type II toxin-antitoxin system

CDO30_RS21175:TRAP transporter small perme

CDO30_RS18965:traA, Ti-type conjugative trans

CDO30_RS21490:S8 family serine peptidase; pr

CDO30_RS21375:PhzF family phenazine biosyn

CDO30_RS21370:cold-shock protein; protein_ic

CDO30_RS19120:glmS, glutamine-fructose-6

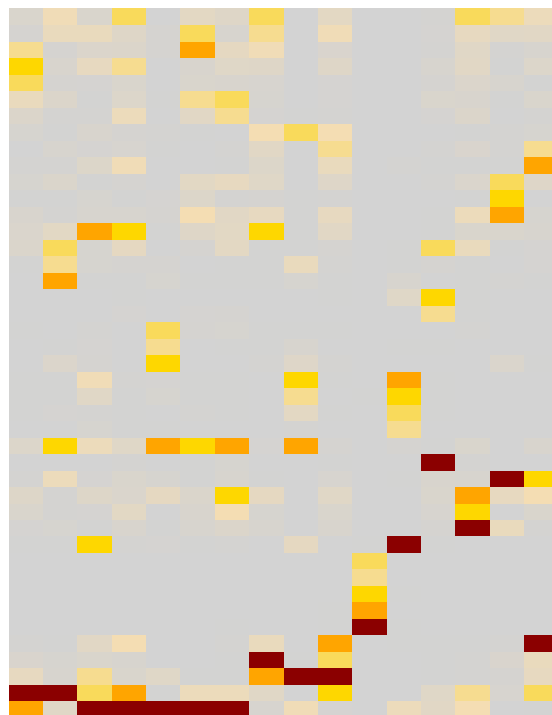
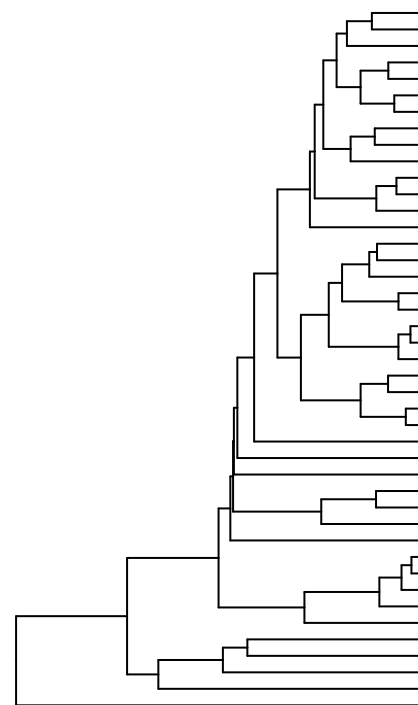
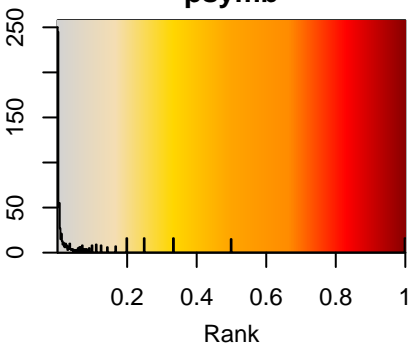
CDO30_RS24215:CopG family transcriptional re

CDO30_RS19555:ccoN, cytochrome-c oxidase9

CDO30_RS24970:type II toxin-antitoxin system

CDO30_RS22190:aldo/keto reductase; protein_i

psymb

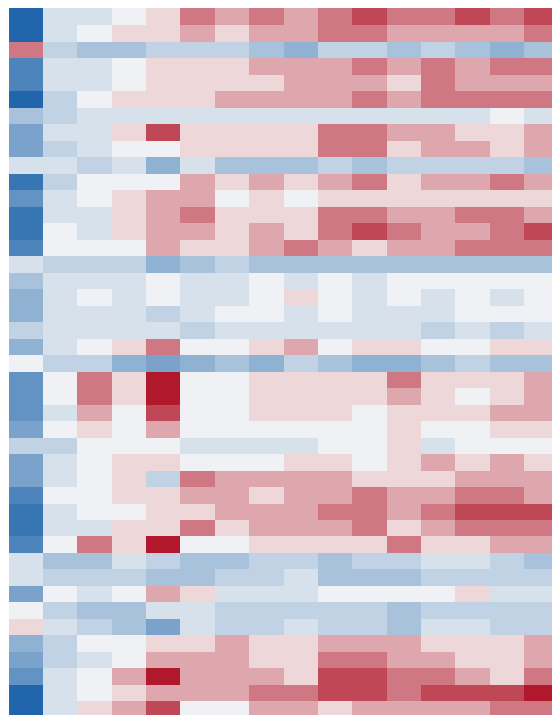
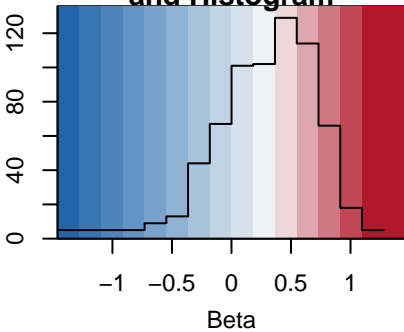


sunn1
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latd
dnf7
hcl
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sunn4
rdn1
dnf4
dnf5dnf2

CD030_RS32685:four-carbon acid sugar kinase
CD030_RS27930:LysR family transcriptional reg
CD030_RS28005:araG, L-arabinose ABC trans
CD030_RS28530:ABC transporter ATP-binding
CD030_RS27355:aspartate aminotransferase fa
CD030_RS31870:hypothetical protein (pseudog
CD030_RS32205:sugar ABC transporter perme
CD030_RS28760:ligD, DNA ligase D; protein_id
CD030_RS26680:zinc-binding dehydrogenase;
CD030_RS32445:hypothetical protein; protein_id
CD030_RS25985:NAD(P)/FAD-dependent oxid
CD030_RS32015:sugar ABC transporter substr
CD030_RS28760:ligD, DNA ligase D; protein_id
CD030_RS28675:hypothetical protein; protein_id
CD030_RS31425:xdhA, xanthine dehydrogenas
CD030_RS26675:NAD-dependent epimerase/d
CD030_RS29535:ABC transporter substrate-bi
CD030_RS31845:glycoside hydrolase family 19
CD030_RS28095:flavodoxin family protein; prote
CD030_RS27870:LacI family DNA-binding trans
CD030_RS27095:sulfatase (pseudogene)
CD030_RS34595:helix-turn-helix transcription
CD030_RS27435:four-carbon acid sugar kinase
CD030_RS27440:xanthine dehydrogenase fami
CD030_RS27435:four-carbon acid sugar kinase
CD030_RS27440:xanthine dehydrogenase fami
CD030_RS26745:dihydrodipicolinate synthase f
CD030_RS28095:flavodoxin family protein; prote
CD030_RS30150:glycosyltransferase; protein_id
CD030_RS25485:pyridoxamine 5'-phosphate ox
CD030_RS31555:MASE1 domain-containing pro
CD030_RS32910:LysR family transcriptional reg
CD030_RS27440:xanthine dehydrogenase fami
CD030_RS27015:ABC transporter permease; p
CD030_RS29305:amino acid ABC transporter A
CD030_RS27010:sugar ABC transporter ATP-b
CD030_RS29490:mechanosensitive ion channe
CD030_RS29490:mechanosensitive ion channe
CD030_RS32445:hypothetical protein; protein_id
CD030_RS27310:ABC transporter ATP-binding
CD030_RS28740:pepT, peptidase T; protein_id
CD030_RS28530:ABC transporter ATP-binding
CD030_RS27255:hypothetical protein; protein_id

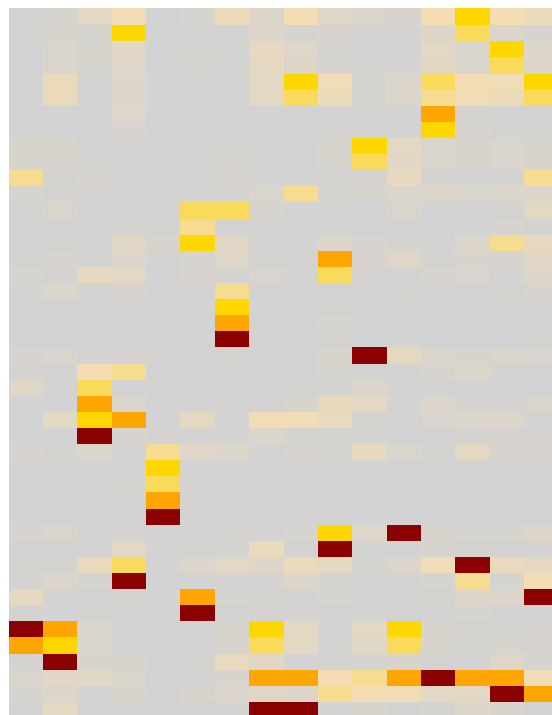
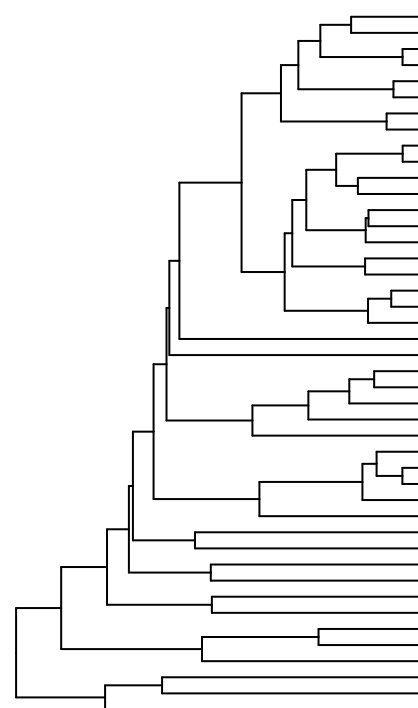
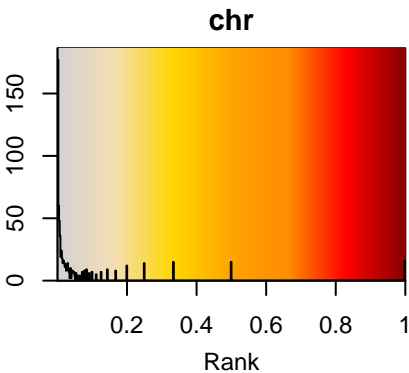
Color Key

and Histogram



A17
hcl
dnf3
dnf6
latd
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dnf5dnf2
nad1
sunn4
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ipd3
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dnf1
dnf1dnf2

CD030_RS32685:four-carbon acid sugar kinase
CD030_RS27930:LysR family transcriptional reg
CD030_RS28005:araG, L-arabinose ABC trans
CD030_RS28530:ABC transporter ATP-binding
CD030_RS27355:aspartate aminotransferase fa
CD030_RS31870:hypothetical protein (pseudog
CD030_RS32205:sugar ABC transporter perme
CD030_RS28760:ligD, DNA ligase D; protein_id
CD030_RS26680:zinc-binding dehydrogenase;
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CD030_RS25985:NAD(P)/FAD-dependent oxid
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CD030_RS29490:mechanosensitive ion channe
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CD030_RS32445:hypothetical protein; protein_id
CD030_RS27310:ABC transporter ATP-binding
CD030_RS28740:pepT, peptidase T; protein_id
CD030_RS28530:ABC transporter ATP-binding
CD030_RS27255:hypothetical protein; protein_id

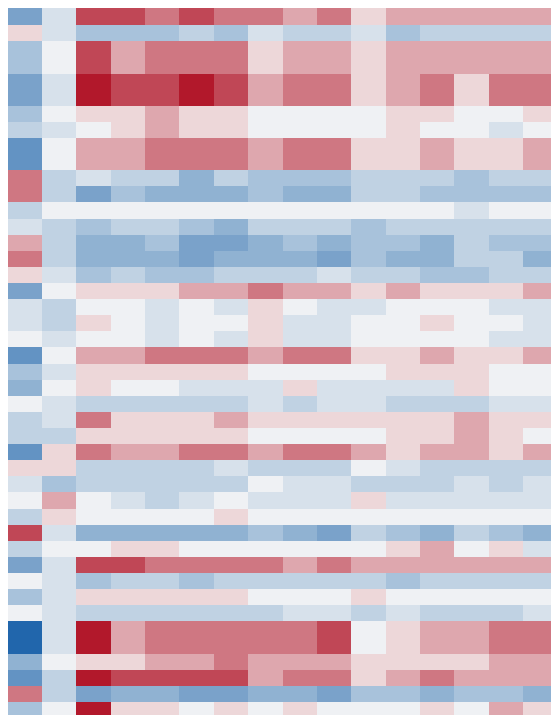
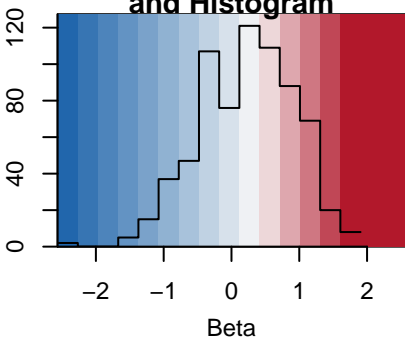


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sunn4
dnf6
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nad1
rdn1
dnf1
ipd3
dnf7
dnf2
dnf1dnf2

CD030_RS16270:ABC transporter ATP-binding
CD030_RS07580:purU, formyltetrahydrofolate d
CD030_RS03630:GGDEF domain-containing p
CD030_RS05195:mscl, large conductance mec
CD030_RS04135:MBL fold metallo-hydrolase; p
CD030_RS15555:cobN, cobaltochelate subun
CD030_RS06970:TonB-dependent receptor; pr
CD030_RS06960:MFS transporter; protein_id=V
CD030_RS04545:flhA, flagellar biosynthesis pr
CD030_RS05080:SDR family NAD(P)-depende
CD030_RS0270:AzC family ABC transporter p
CD030_RS02435:rpK, UDP-glucose 6-dehydr
CD030_RS08485:autoinducer binding domain-c
CD030_RS04400:XRE family transcriptional reg
CD030_RS01280:dpA, DNA-processing protei
CD030_RS03085:EAL domain-containing prote
CD030_RS06075:spA, signal peptide peptidase
CD030_RS04360:PAS domain S-box protein; p
CD030_RS17535:winged helix-turn-helix doma
CD030_RS17200:mfd, transcription-repair coup
CD030_RS00140:exbD, TonB system transport
CD030_RS02865:HAMP domain-containing his
CD030_RS16895:BCCT family transporter; prot
CD030_RS05255:Rrf2 family transcriptional reg
CD028_RS01640:hypothetical protein; protein_i
CD030_RS16855:hypothetical protein; protein_i
CD030_RS16125:LTA synthase family protein; p
CD030_RS01435:NADH ubiquinone oxidoreduc
CD030_RS07610:hypothetical protein; protein_i
CD030_RS07580:purU, formyltetrahydrofolate d
CD030_RS07660:sarcosine oxidase subunit gar
CD030_RS07655:sarcosine oxidase subunit alp
CD030_RS04655:flagellar basal body P-ring pr
CD030_RS10040:translocation/assembly modul
CD030_RS16285:cytochrome c1; protein_id=W
CD030_RS11905:electron transfer flavoprotein s
CD030_RS16025:OmpA family protein; protein_i
CD030_RS06705:GIY-YIG nuclease family prot
CD030_RS17140:molybdopterin molybdotransfe
CD030_RS02085:pdxA, 4-hydroxythreonine-4-
CD030_RS05200:hybrid sensor histidine kinase
CD030_RS16380:recA, recombinase RecA; prot
CD030_RS02735:PAS-domain containing prote
CD030_RS12270:glutamine synthetase family p

Color Key

and Histogram



A17
 hcl
 latd
 dnf7
 ipd3
 dnf1dnf2
 dnf2
 sunn4
 rdh1
 dnf1
 dnf3
 dnf5dnf2
 nad1
 dnf4
 dnf6
 sunn1

CDO30_RS16270:ABC transporter ATP-binding
 CDO30_RS07580:purU, formyltetrahydrofolate d
 CDO30_RS03630:GGDEF domain-containing p
 CDO30_RS05195:mscL, large conductance mec
 CDO30_RS04135:MBL fold metallo-hydrolase; p
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 CDO30_RS05080:SDR family NAD(P)-depende
 CDO30_RS00270:AzIC family ABC transporter p
 CDO30_RS02435:kpK, UDP-glucose 6-dehydr
 CDO30_RS08485:autoinducer binding domain-c
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 CDO30_RS06075:spA, signal peptide peptidas
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 CDO30_RS17535:winged helix-turn-helix doma
 CDO30_RS17200:mfd, transcription-repair coup
 CDO30_RS00140:exbD, TonB system transport
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 CDO28_RS01640:hypothetical protein; protein_i
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 CDO30_RS01435:NADH ubiquinone oxidoreduc
 CDO30_RS07610:hypothetical protein; protein_i
 CDO30_RS07580:purU, formyltetrahydrofolate d
 CDO30_RS07660:sarcosine oxidase subunit gar
 CDO30_RS07655:sarcosine oxidase subunit alp
 CDO30_RS04655:flagellar basal body P-ring pr
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 CDO30_RS16285:cytochrome c1; protein_id=WI
 CDO30_RS11905:electron transfer flavoprotein
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