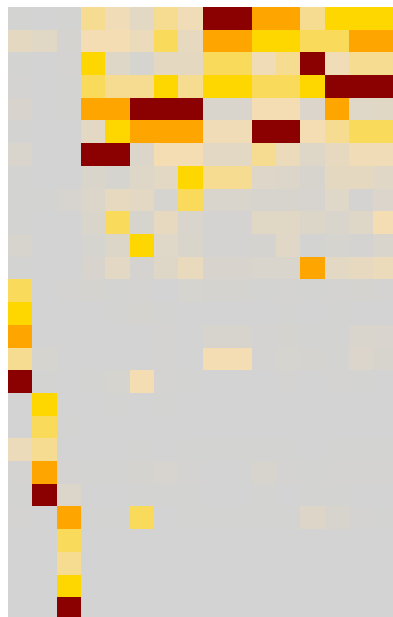
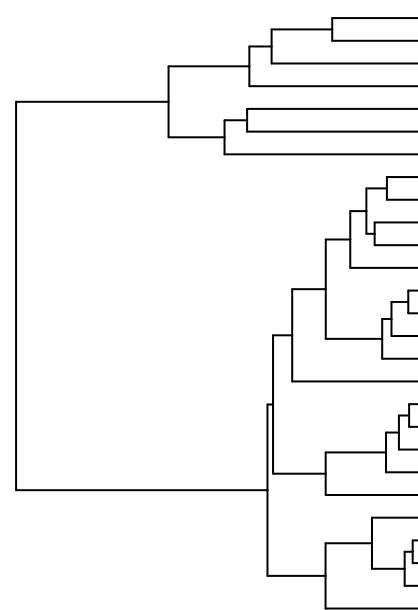
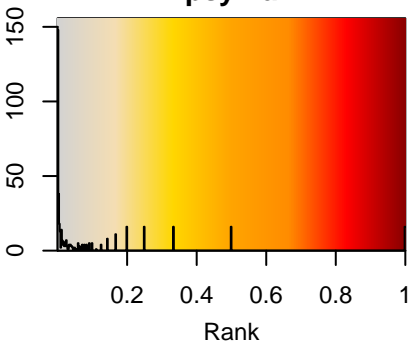


CD030_RS16270:ABC transporter ATP-binding protein/permease; protein_id=WP_010968430.1
 CD030_RS07580:purU, formyltetrahydrofolate deformylase; protein_id=WP_010968430.1
 CD030_RS03630:GGDEF domain-containing phosphodiesterase; protein_id=WP_010968430.1
 CD030_RS05195:mscL, large conductance mechanosensitive channel protein; protein_id=WP_010968430.1
 CD030_RS04135:MBL fold metallo-hydrolase; protein_id=WP_015445556
 CD030_RS15555:cobN, cobaltochelate subunit CobN; protein_id=WP_010968430.1
 CD030_RS06970:TonB-dependent receptor; protein_id=WP_010968430.1
 CD030_RS06960:MFS transporter; protein_id=WP_010968432.1
 CD030_RS04545:flhA, flagellar biosynthesis protein FlhA; protein_id=WP_010968430.1
 CD030_RS05080:SDR family NAD(P)-dependent oxidoreductase (pseudogen); protein_id=WP_010968430.1
 CD030_RS00270:ABC family ABC transporter permease; protein_id=WP_010968430.1
 CD030_RS02435:rkpK, UDP-glucose 6-dehydrogenase; protein_id=WP_010968430.1
 CD030_RS08485:autoinducer binding domain-containing protein (pseudogen); protein_id=WP_010968430.1
 CD030_RS04400:XRE family transcriptional regulator; protein_id=WP_010968430.1
 CD030_RS01280:dprA, DNA-processing protein DprA; protein_id=WP_010968430.1
 CD030_RS03085:EAL domain-containing protein; protein_id=WP_010968430.1
 CD030_RS06075:sppA, signal peptide peptidase SppA; protein_id=WP_010968430.1
 CD030_RS04360:PAS domain S-box protein; protein_id=WP_010968771.1
 CD030_RS17535:winged helix-turn-helix domain-containing tetratricopeptide repeat domain-containing protein; protein_id=WP_010968771.1
 CD030_RS00140:exbD, TonB system transport protein ExbD; protein_id=WP_010968430.1
 CD030_RS02865:HAMP domain-containing histidine kinase; protein_id=WP_010968430.1
 CD030_RS16895:BCCT family protein transporter; protein_id=WP_010968412.1
 CD030_RS05255:Rrf2 family transcriptional regulator; protein_id=WP_010968430.1
 CD028_RS01640:hypothetical protein; protein_id=WP_088195496.1
 CD030_RS16855:hypothetical protein; protein_id=WP_015445609.1
 CD030_RS16125:LTA synthase family protein; protein_id=WP_003534093
 CD030_RS01435:NADH ubiquinone oxidoreductase; protein_id=WP_010968430.1
 CD030_RS07610:hypothetical protein; protein_id=WP_013844967.1
 CD030_RS07580:purU, formyltetrahydrofolate deformylase; protein_id=WP_010968430.1
 CD030_RS07660:sarcosine oxidase subunit gamma; protein_id=WP_010968430.1
 CD030_RS07655:sarcosine oxidase subunit alpha; protein_id=WP_010968430.1
 CD030_RS04655:flagellar basal body P-ring protein FlgI; protein_id=WP_010968430.1
 CD030_RS10040:translocation/assembly module TamB; protein_id=WP_010968430.1
 CD030_RS16285:cytochrome c1; protein_id=WP_010969491.1
 CD030_RS11905:electron transfer flavoprotein subunit beta/FixA family protein; protein_id=WP_010968430.1
 CD030_RS16025:OmpA family protein; protein_id=WP_041170153.1
 CD030_RS06705:GIY-YIG nuclease family protein; protein_id=WP_010968430.1
 CD030_RS17140:molybdopter molybdoxotransferase MoeA; protein_id=WP_010968430.1
 CD030_RS02085:pdxA, 4-hydroxythreonine-4-phosphate dehydrogenase; protein_id=WP_010968430.1
 CD030_RS05200:hybrid sensor histidine kinase/response regulator; protein_id=WP_010968430.1
 CD030_RS16380:recA, recombinase RecA; protein_id=WP_010969478.1
 CD030_RS02735:PAS-domain containing protein; protein_id=WP_013844967.1
 CD030_RS12270:glutamine synthetase family protein; protein_id=WP_010968430.1

psyma



latd
dnf3
hcl
sunn4
WT
dnf6
dnf1
nad1
dnf1dnf2
dnf5dnf2
rdn1
sunn1
dnf4
dnf2
dnf7
ipd3

CDO30_RS23155:MFS transporter; protein_id=WP_010968029.1

CDO30_RS23125:SDR family oxidoreductase (pseudogene)

CDO30_RS23065:SGNH/GDSL hydrolase family protein; protein_id=WP_010968029.1

CDO30_RS22325:hypothetical protein; protein_id=WP_041170015.1

CDO30_RS21460:malonyl-CoA synthase; protein_id=WP_010967081.1

CDO30_RS18080:fixL, oxygen sensor histidine kinase FixL; protein_id=WP_010967081.1

CDO30_RS22055:class I SAM-dependent methyltransferase; protein_id=WP_010967081.1

CDO30_RS22005:amidase; protein_id=WP_010968222.1

CDO30_RS21460:malonyl-CoA synthase; protein_id=WP_010967081.1

CDO30_RS19190:nodQ, bifunctional sulfate adenylyltransferase/adenylyl-sulfate lyase; protein_id=WP_010967081.1

CDO30_RS19605:stc4, stachydrine N-demethylase reductase subunit Stc4; protein_id=WP_010967081.1

CDO30_RS22335:site-specific integrase; protein_id=WP_010968163.1

CDO30_RS20200:type II toxin-antitoxin system RelE/ParE family toxin; protein_id=WP_010967081.1

CDO30_RS21100:DUF2200 domain-containing protein; protein_id=WP_010967081.1

CDO30_RS21085:class I SAM-dependent methyltransferase; protein_id=WP_010967081.1

CDO30_RS20205:type II toxin-antitoxin system ParD family antitoxin; protein_id=WP_010967081.1

CDO30_RS21175:TRAP transporter small permease; protein_id=WP_010967081.1

CDO30_RS18965:traA, Ti-type conjugative transfer relaxase TraA; protein_id=WP_010967081.1

CDO30_RS21490:S8 family serine peptidase; protein_id=WP_010967075.1

CDO30_RS21375:PhzF family phenazine biosynthesis protein; protein_id=WP_010967081.1

CDO30_RS21370:cold-shock protein; protein_id=WP_010967097.1

CDO30_RS19120:glmS, glutamine--fructose-6-phosphate transaminase (pseudogene); protein_id=WP_010967081.1

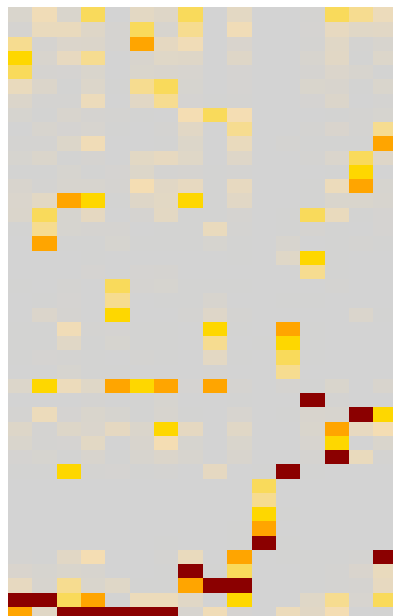
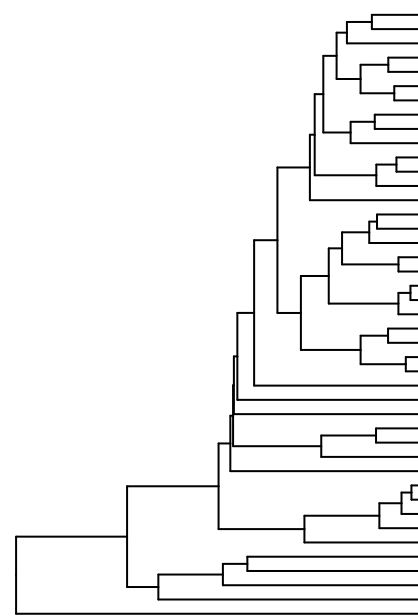
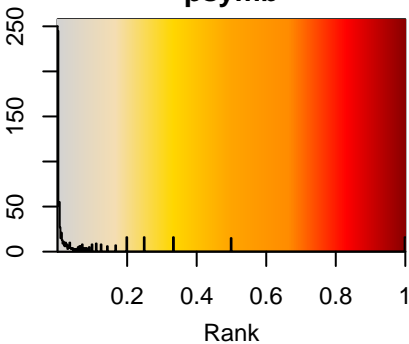
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CDO30_RS19555:ccoN, cytochrome-c oxidase%2C cbb3-type subunit I; protein_id=WP_010967081.1

CDO30_RS24970:type II toxin-antitoxin system RelE/ParE family toxin; protein_id=WP_010967081.1

CDO30_RS22190:aldo/keto reductase; protein_id=WP_010968188.1

psymb



sunn1
 nad1
 dnf2
 dnf1
 dnf6
 WT
 dnf1
 ipd3
 latd
 dnf7
 hcl
 dnf3
 sunn4
 rdn1
 dnf4
 dnf5
 dnf2

CDO30_RS32685:four-carbon acid sugar kinase family protein; protein_id=WP_010975138.1
 CDO30_RS27930:LysR family transcriptional regulator; protein_id=WP_010975138.1
 CDO30_RS28005:araG, L-arabinose ABC transporter ATP-binding protein; protein_id=WP_010975138.1
 CDO30_RS28530:ABC transporter ATP-binding protein; protein_id=WP_010975138.1
 CDO30_RS27355:aspartate aminotransferase family protein; protein_id=WP_010975138.1
 CDO30_RS31870:hypothetical protein (pseudogene)
 CDO30_RS32205:sugar ABC transporter permease; protein_id=WP_010975138.1
 CDO30_RS28760:ligD, DNA ligase D; protein_id=WP_041170090.1
 CDO30_RS26680:zinc-binding dehydrogenase; protein_id=WP_010975138.1
 CDO30_RS32445:hypothetical protein; protein_id=WP_088239368.1
 CDO30_RS25985:NAD(P)/FAD-dependent oxidoreductase; protein_id=WP_010975138.1
 CDO30_RS32015:sugar ABC transporter substrate-binding protein; protein_id=WP_010975138.1
 CDO30_RS28760:ligD, DNA ligase D; protein_id=WP_041170090.1
 CDO30_RS28675:hypothetical protein; protein_id=WP_010975138.1
 CDO30_RS31425:xdhA, xanthine dehydrogenase small subunit; protein_id=WP_010975138.1
 CDO30_RS26675:NAD-dependent epimerase/dehydratase family protein; protein_id=WP_010975138.1
 CDO30_RS29535:ABC transporter substrate-binding protein; protein_id=WP_010975138.1
 CDO30_RS31845:glycoside hydrolase family 19 protein (pseudogene)
 CDO30_RS28095:flavodoxin family protein; protein_id=WP_010975138.1
 CDO30_RS27870:Lacl family DNA-binding transcriptional regulator; protein_id=WP_010975138.1
 CDO30_RS27095:sulfatase (pseudogene)
 CDO30_RS34595:helix-turn-helix transcriptional regulator (pseudogene)
 CDO30_RS27435:four-carbon acid sugar kinase family protein; protein_id=WP_010975138.1
 CDO30_RS27440:xanthine dehydrogenase family protein molybdopterin-binding protein; protein_id=WP_010975138.1
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 CDO30_RS26745:dihydropicolinate synthase family protein; protein_id=WP_010975138.1
 CDO30_RS28095:flavodoxin family protein; protein_id=WP_010975138.1
 CDO30_RS30150:glycosyltransferase; protein_id=WP_010975138.1
 CDO30_RS25485:pyridoxamine 5'-phosphate oxidase family protein; protein_id=WP_010975138.1
 CDO30_RS31555:MASE1 domain-containing protein; protein_id=WP_010975138.1
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 CDO30_RS27440:xanthine dehydrogenase family protein molybdopterin-binding protein; protein_id=WP_010975138.1
 CDO30_RS27015:ABC transporter permease; protein_id=WP_010975138.1
 CDO30_RS29305:amino acid ABC transporter ATP-binding protein; protein_id=WP_010975138.1
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 CDO30_RS29490:mechanosensitive ion channel family protein; protein_id=WP_010975138.1
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