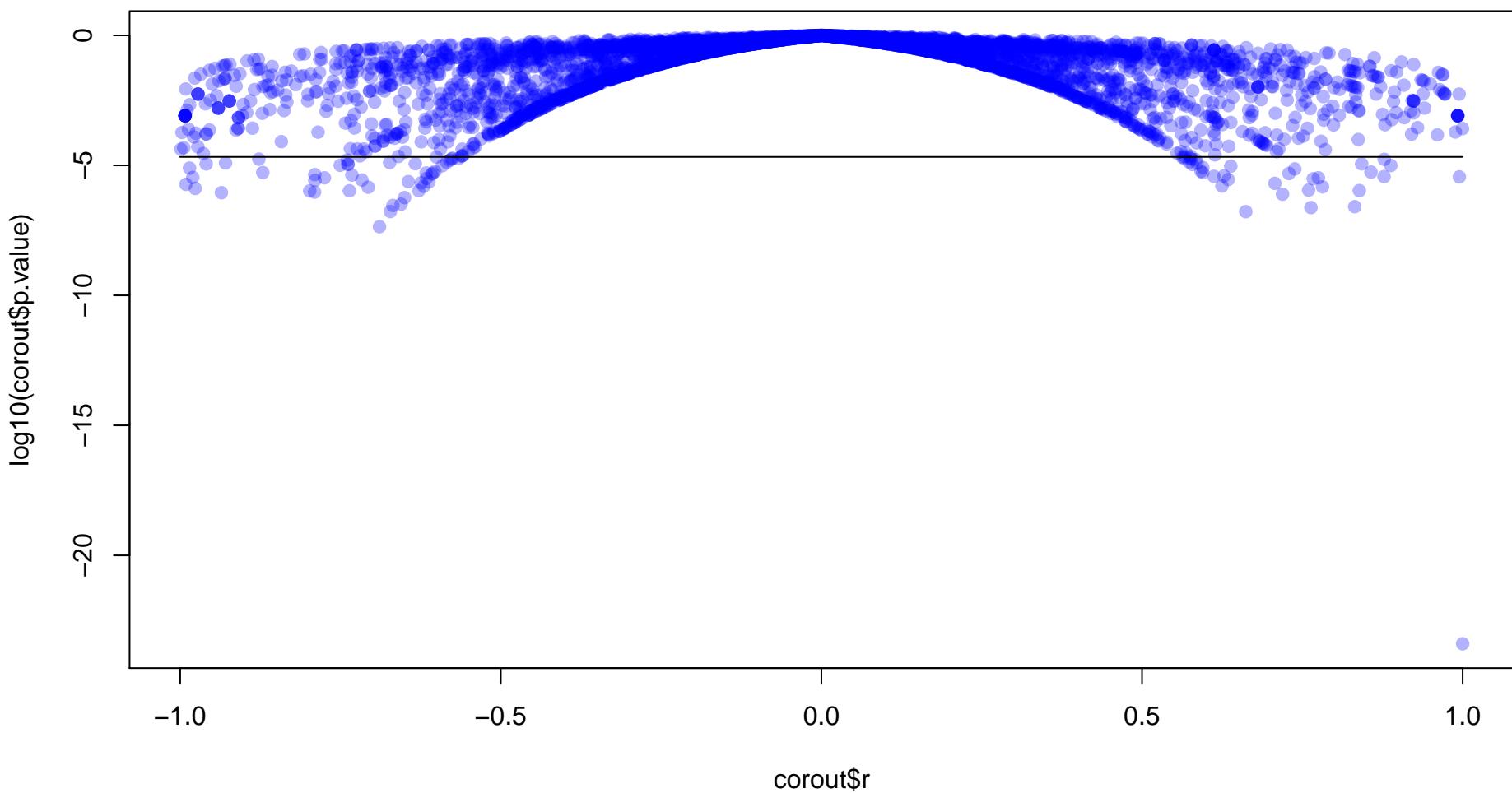
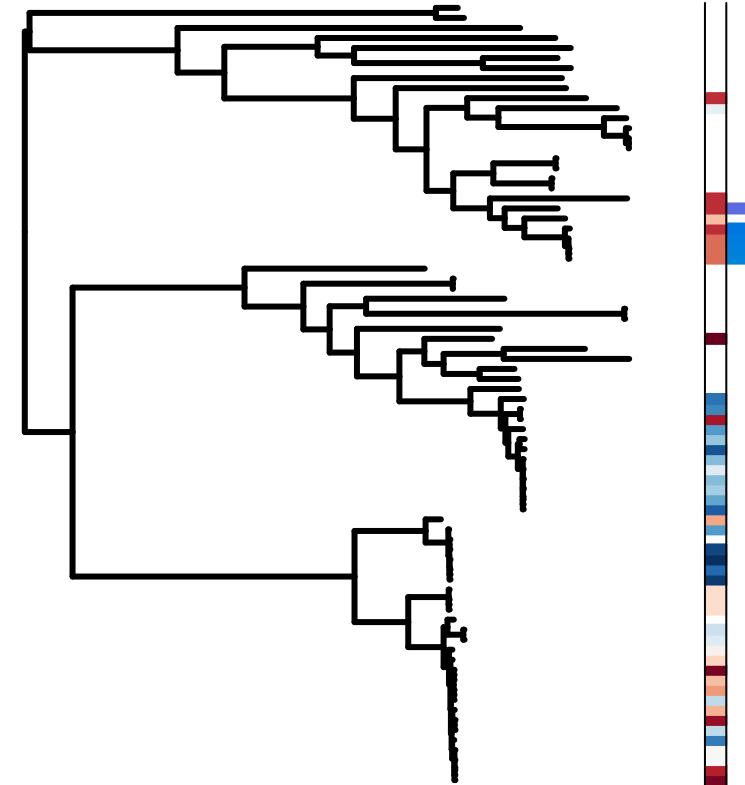
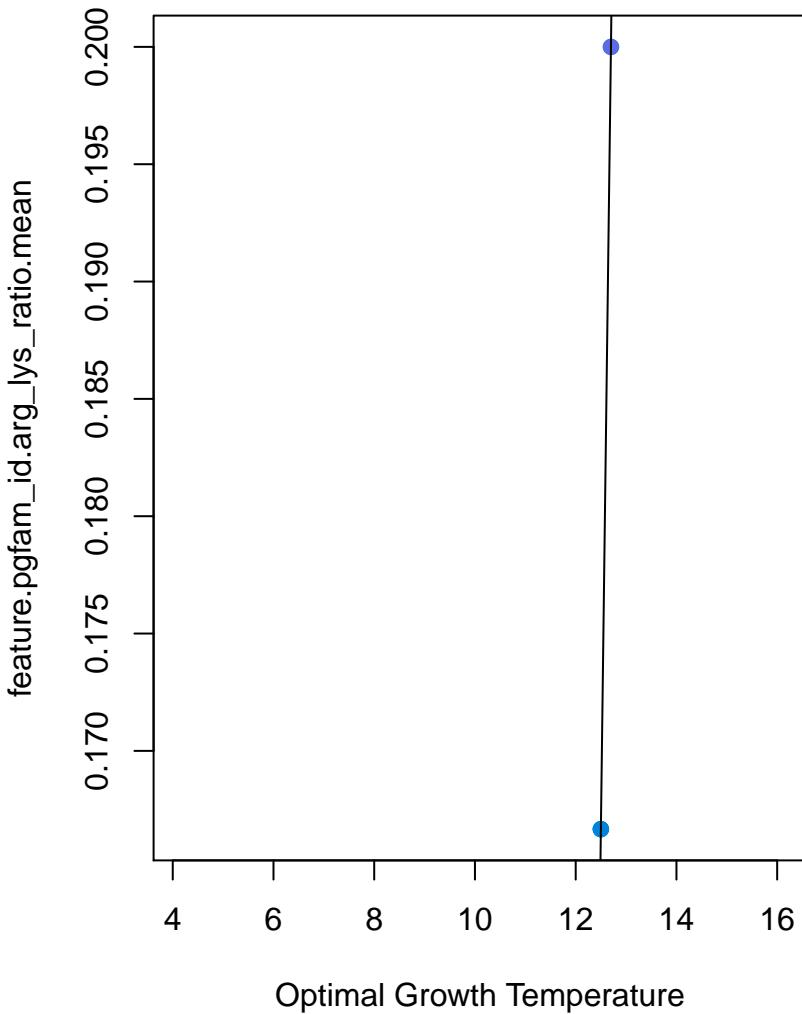


feature.pgfam_id.arg_lys_ratio.mean

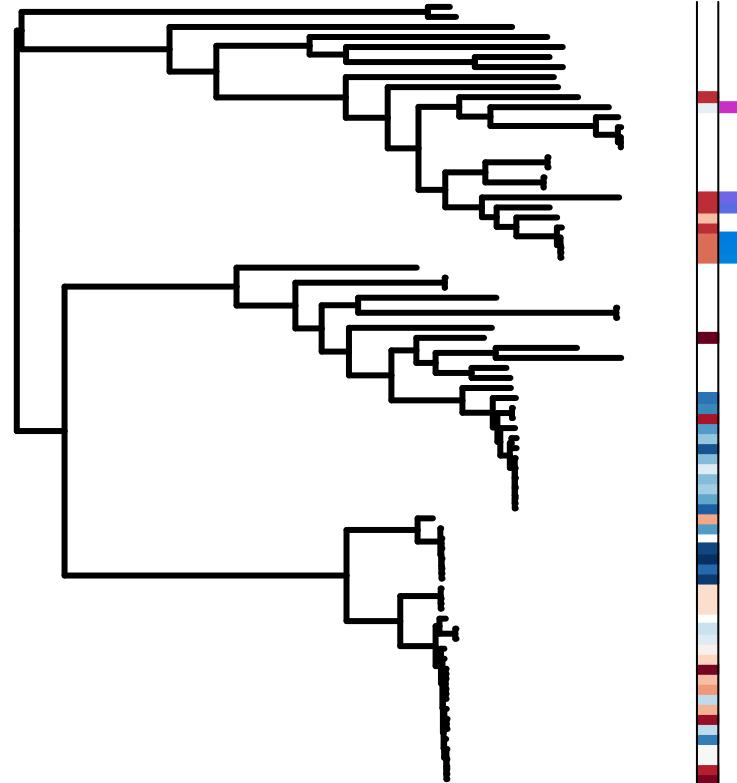
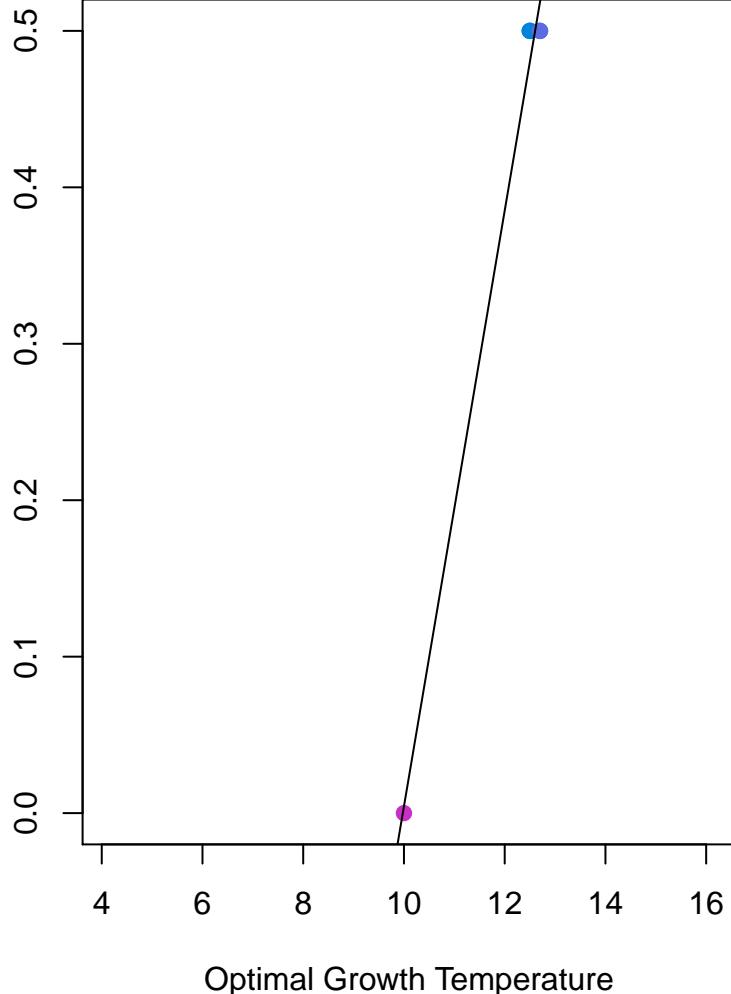


feature.pgfam_id.arg_lys_ratio.mean
PGF_01338035
hypothetical protein
 $r = 1, p = 10^{-23.401}$

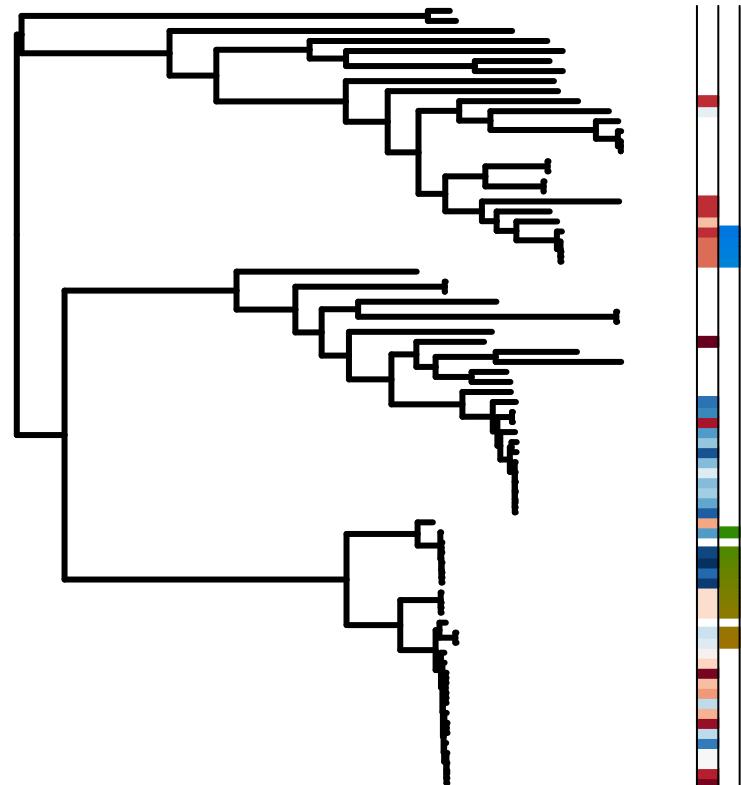
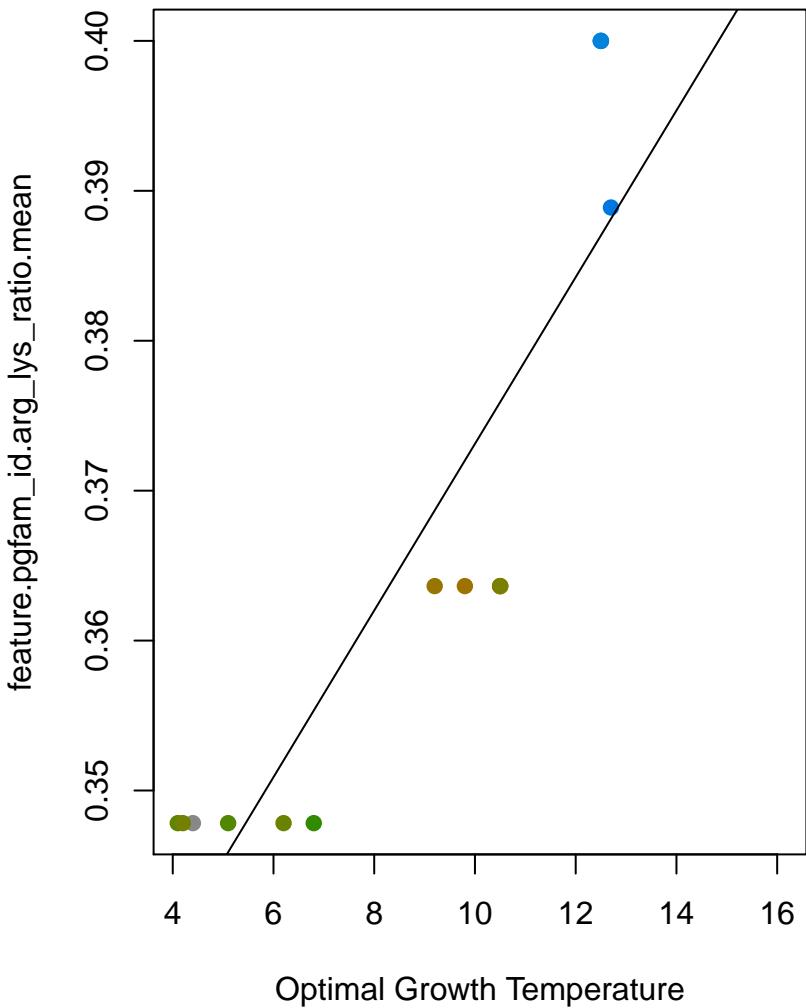


feature.pgfam_id.arg_lys_ratio.mean
PGF_01337096
hypothetical protein
 $r = 0.995, p = 10^{-5.441}$

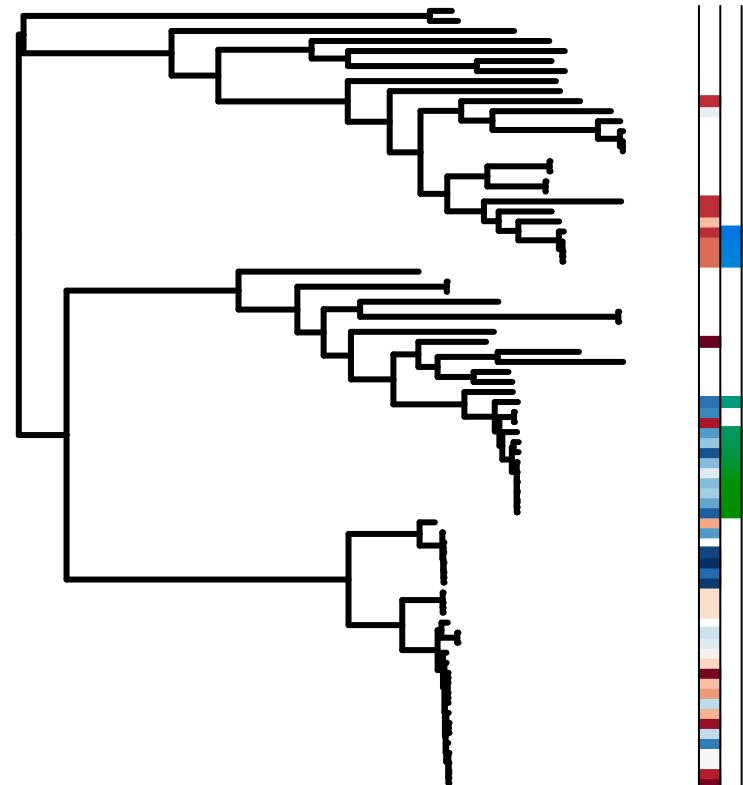
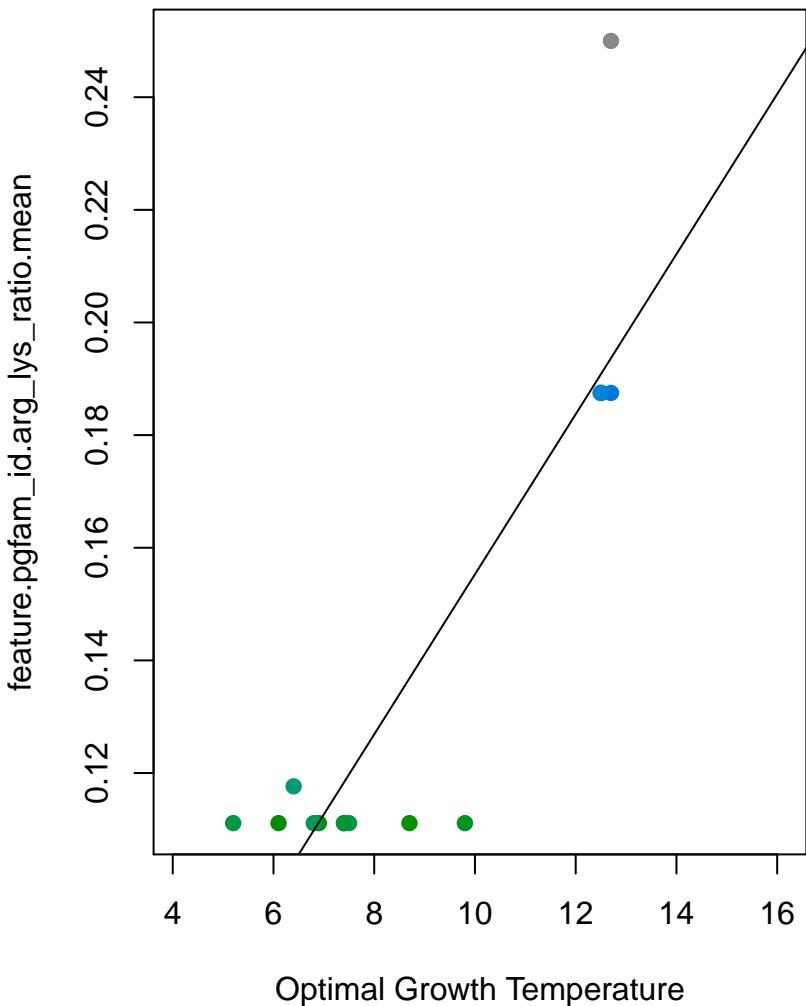
feature.pgfam_id.arg_lys_ratio.mean



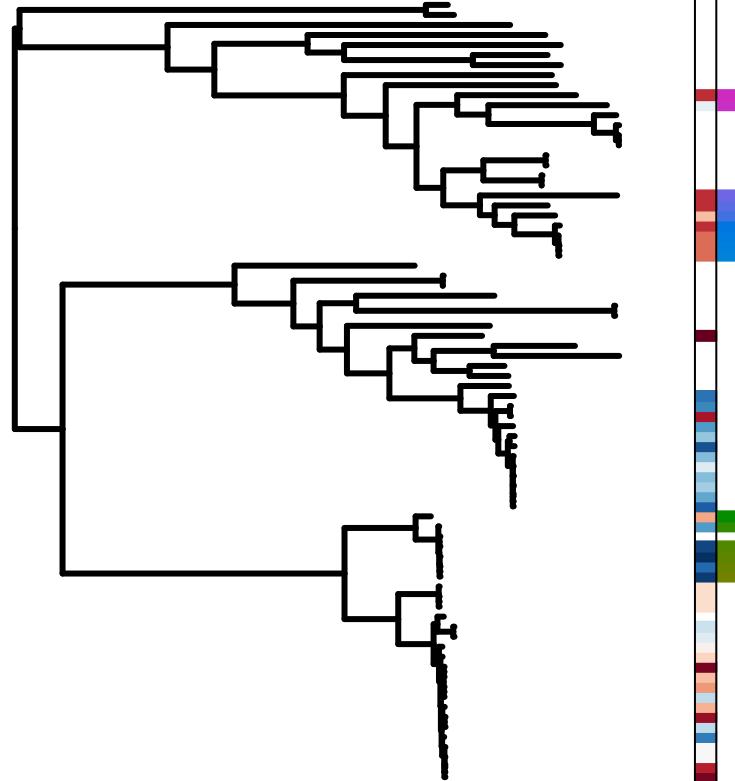
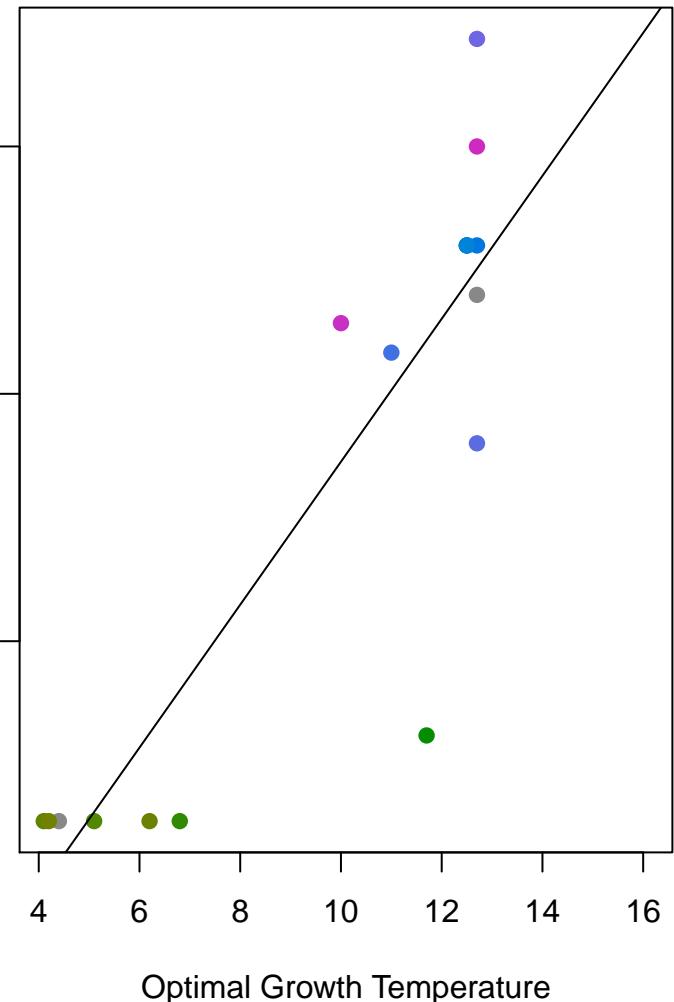
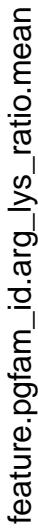
feature.pgfam_id.arg_lys_ratio.mean
PGF_01338042
hypothetical protein
 $r = 0.888$, $p = 10^{-5.005}$

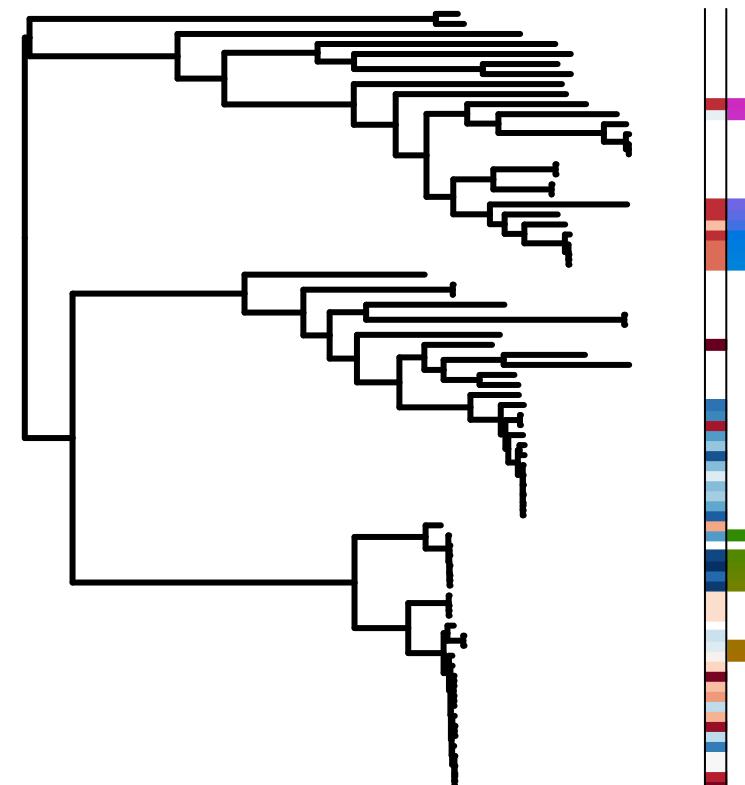
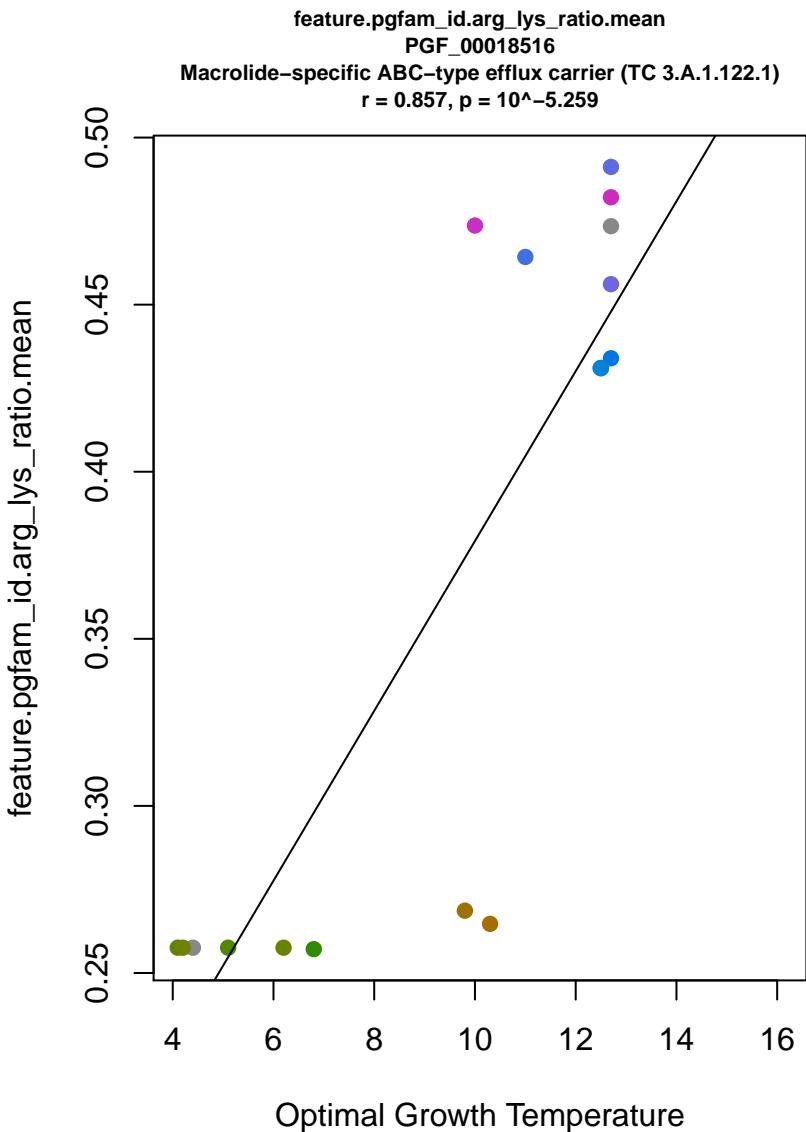


feature.pgfam_id.arg_lys_ratio.mean
PGF_06830555
SapC-like S-layer protein
 $r = 0.878, p = 10^{-4.77}$



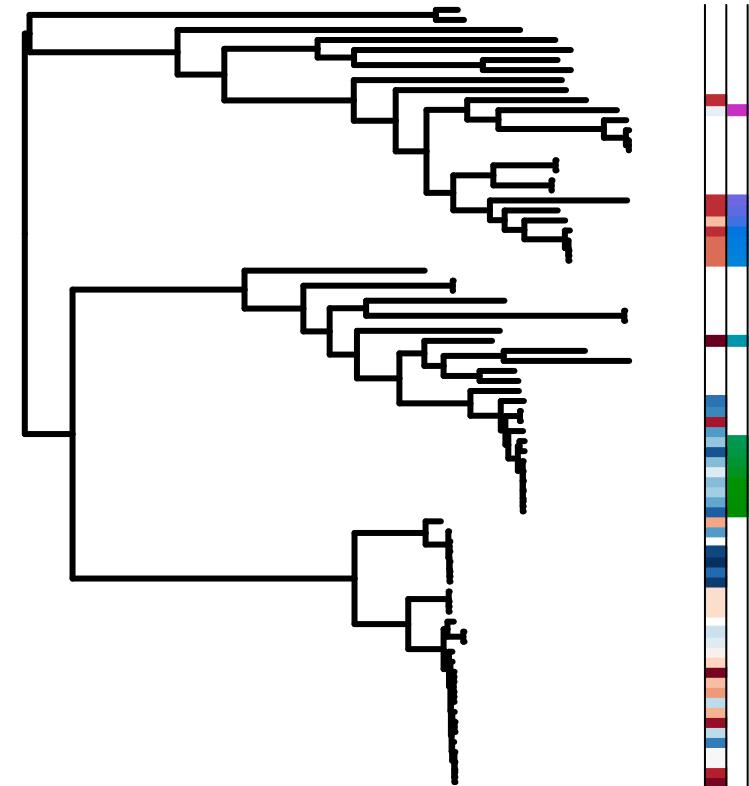
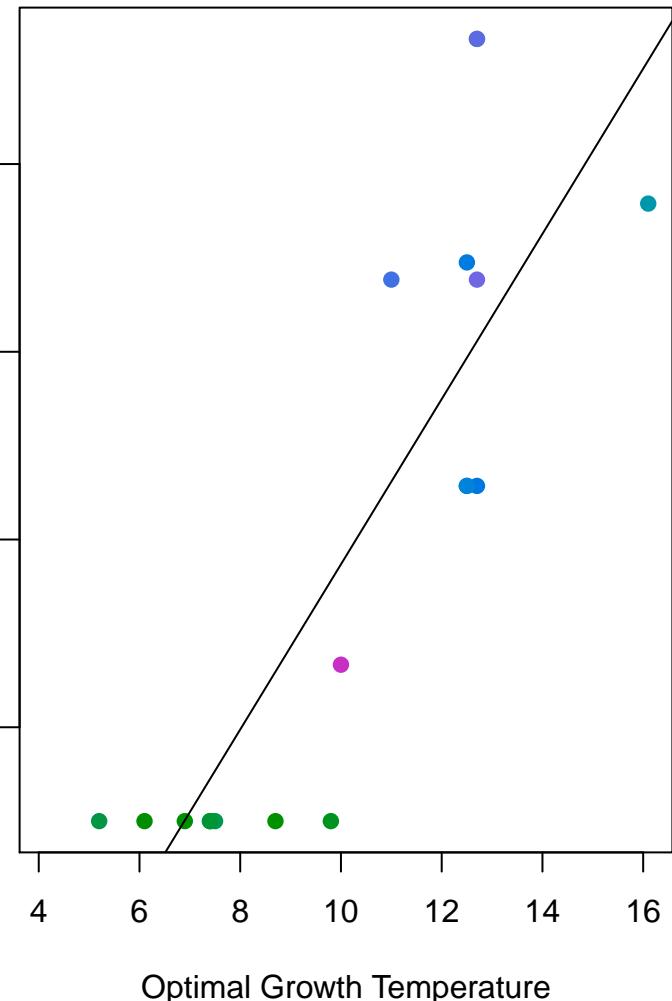
feature.pgfam_id.arg_lys_ratio.mean
PGF_00425647
FHA domain protein
 $r = 0.878, p = 10^{-5.431}$



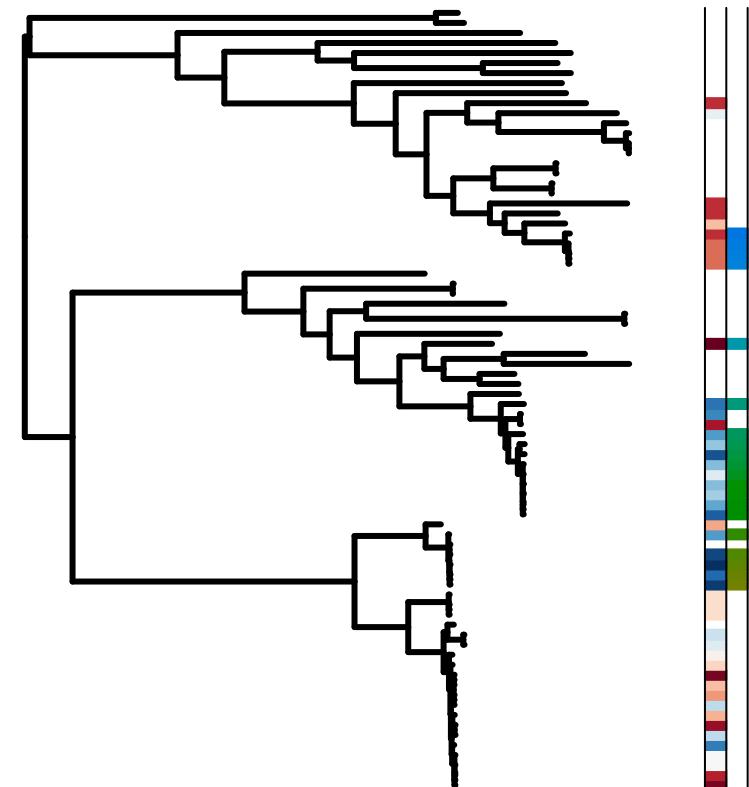
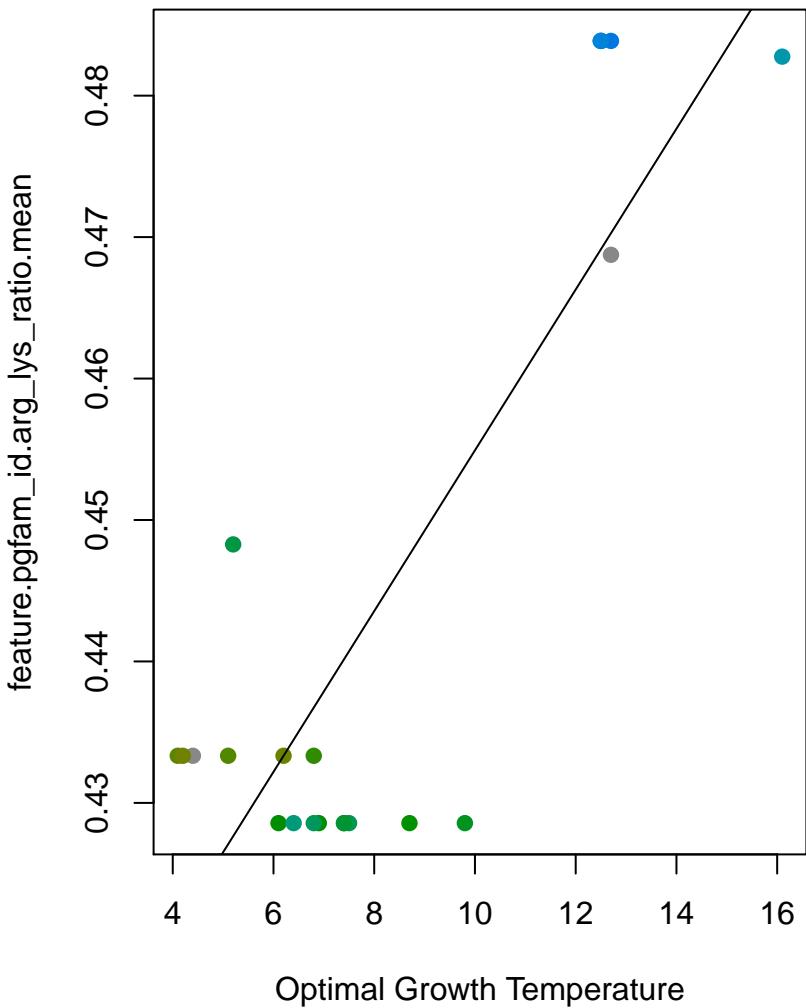


feature.pgfam_id.arg_lys_ratio.mean
PGF_01336587
hypothetical protein
 $r = 0.842, p = 10^{-4.94}$

feature.pgfam_id.arg_lys_ratio.mean

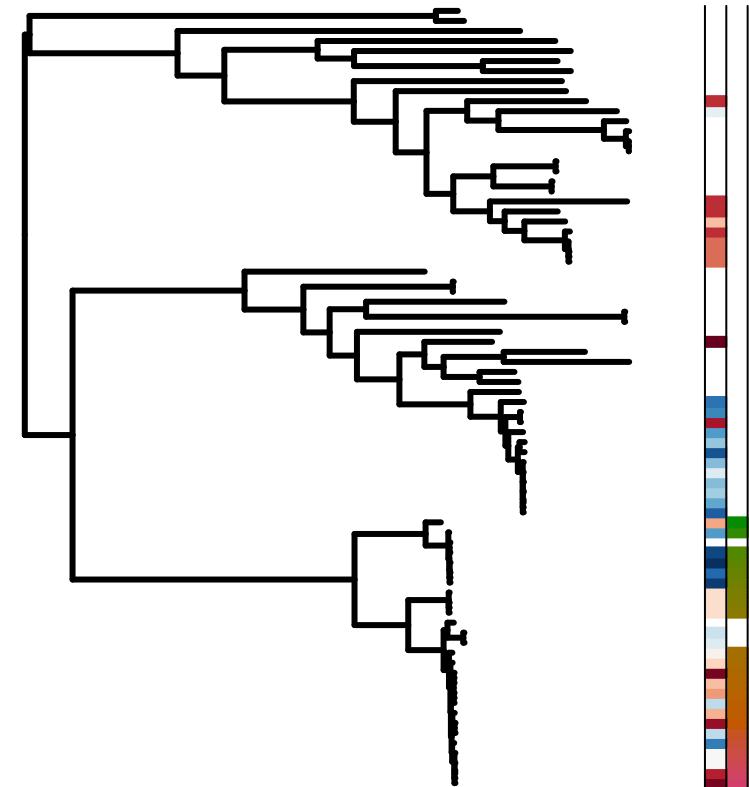
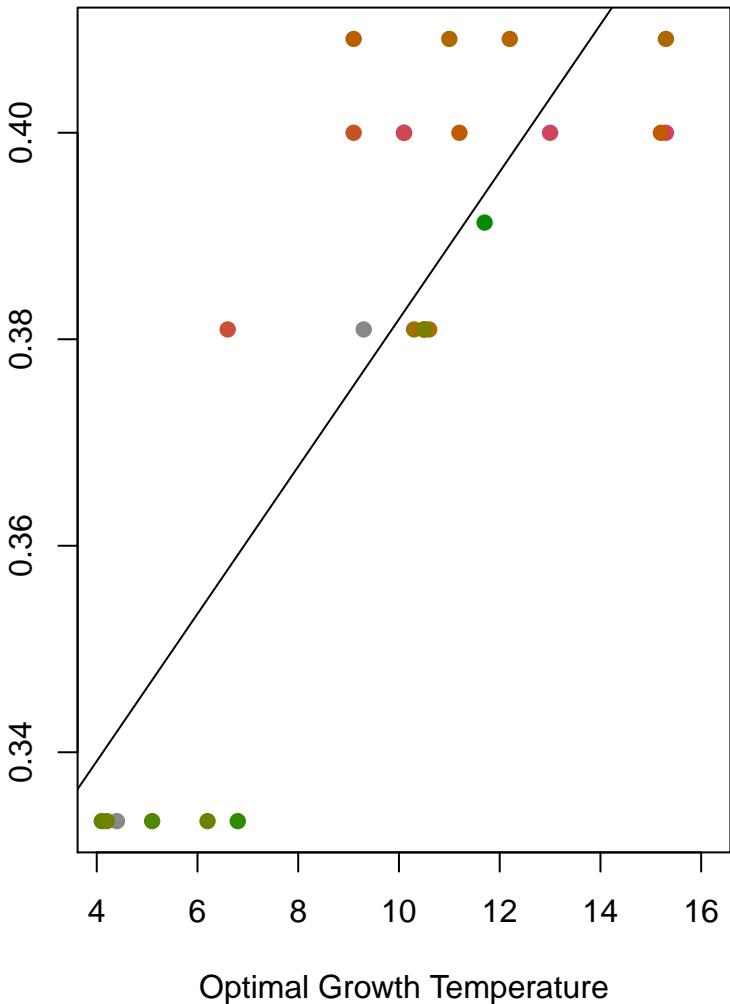


feature.pgfam_id.arg_lys_ratio.mean
PGF_02732386
Glucose/mannose:H⁺ symporter GlcP
 $r = 0.839$, $p = 10^{-5.969}$



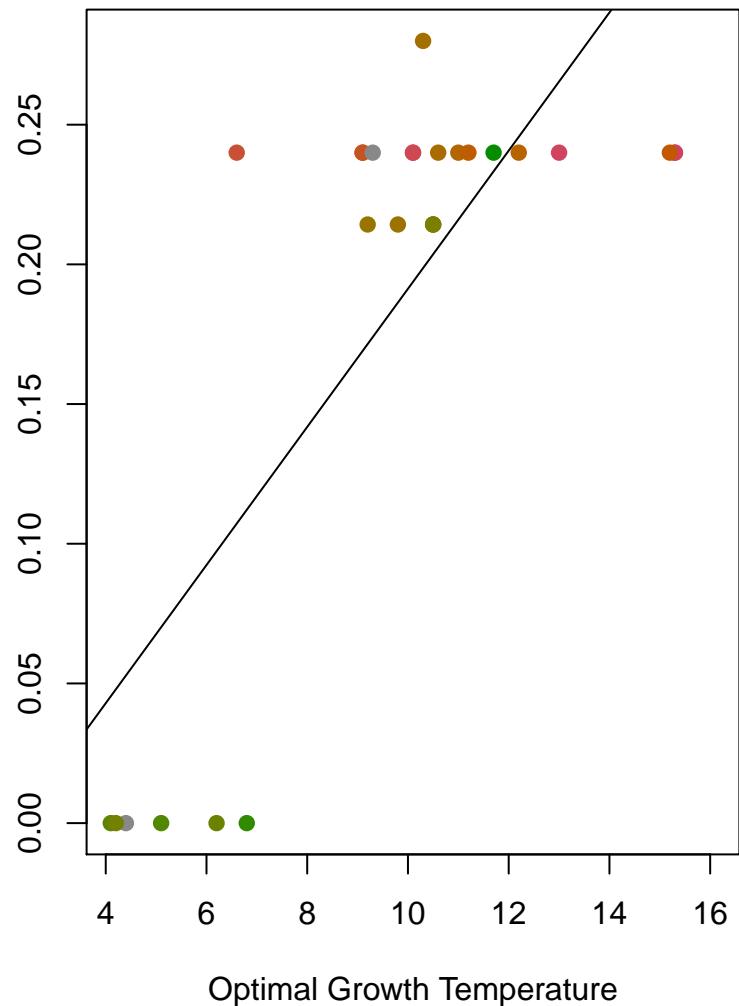
feature.pgfam_id.arg_lys_ratio.mean
PGF_08025863
hypothetical protein
 $r = 0.832, p = 10^{-6.589}$

feature.pgfam_id.arg_lys_ratio.mean

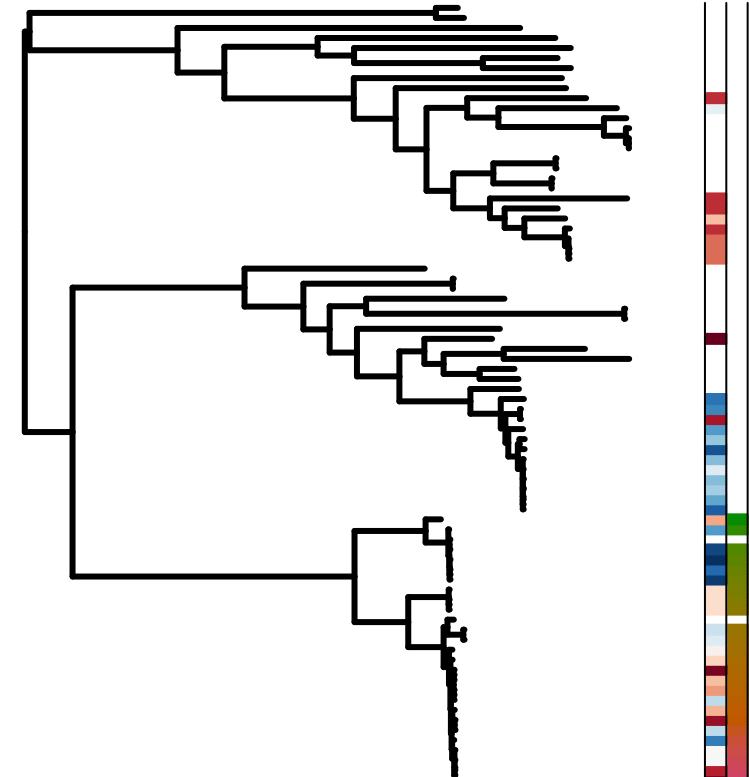


feature.pgfam_id.arg_lys_ratio.mean
PGF_11018774
hypothetical protein
 $r = 0.781, p = 10^{-5.826}$

feature.pgfam_id.arg_lys_ratio.mean

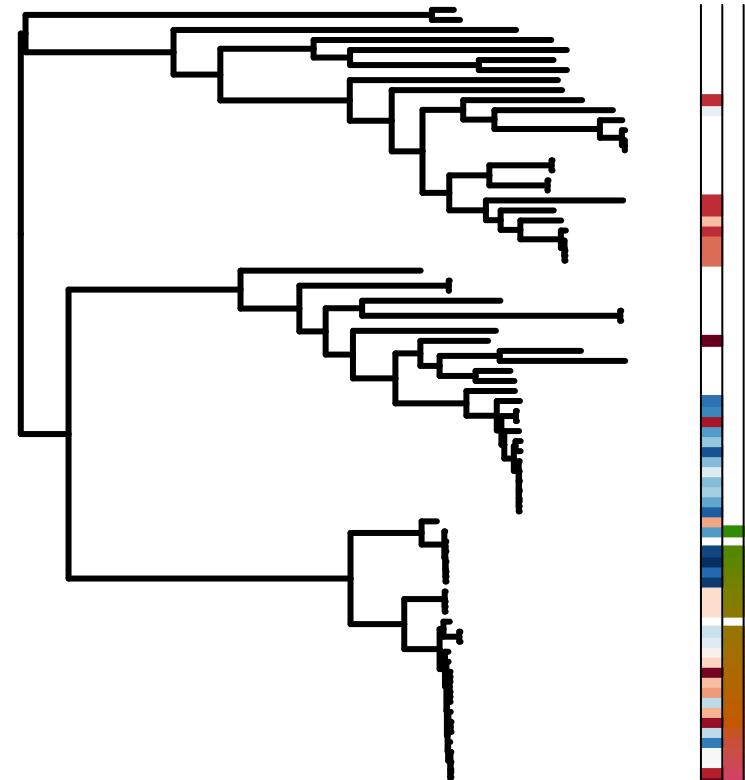
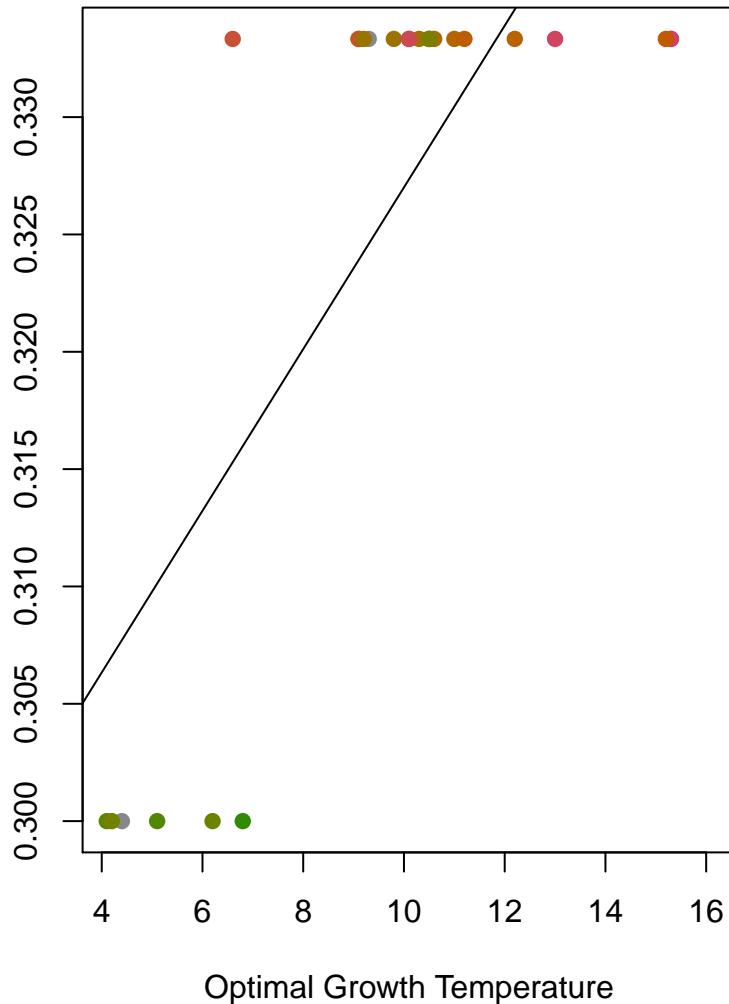


Optimal Growth Temperature



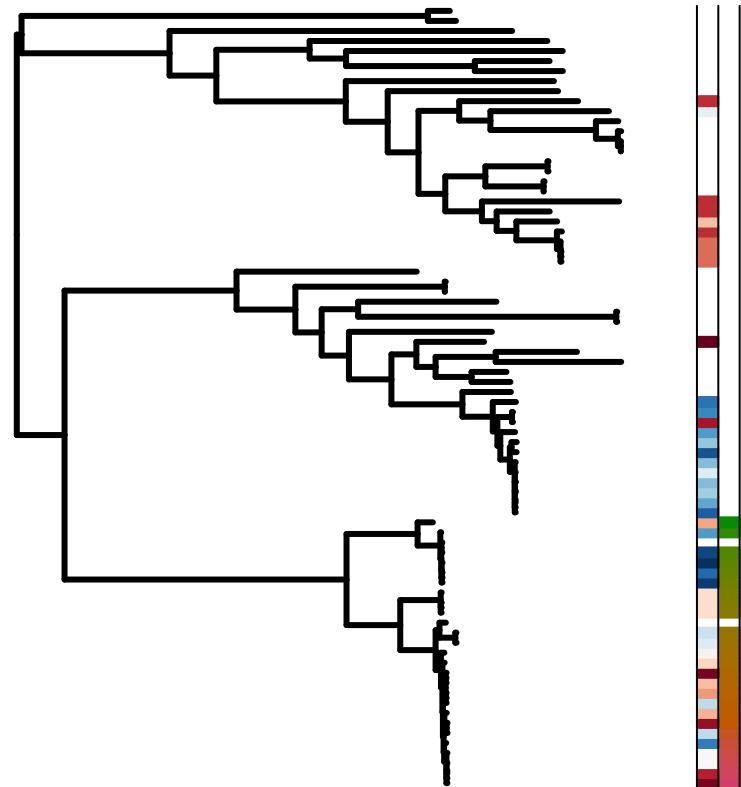
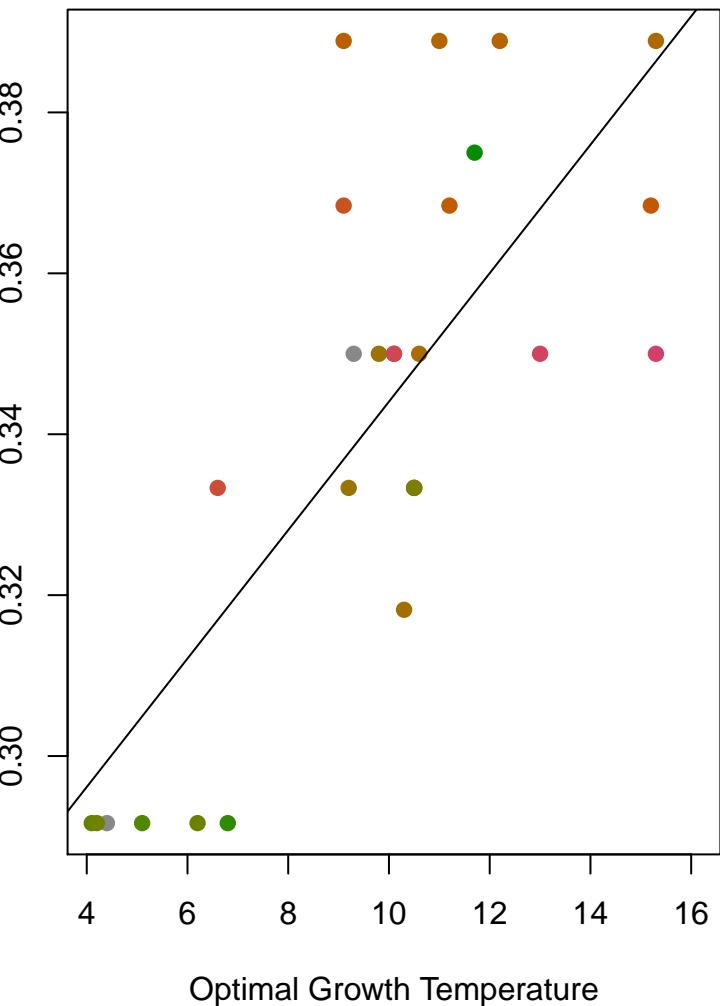
feature.pgfam_id.arg_lys_ratio.mean
PGF_12237460
hypothetical protein
 $r = 0.775, p = 10^{-5.478}$

feature.pgfam_id.arg_lys_ratio.mean



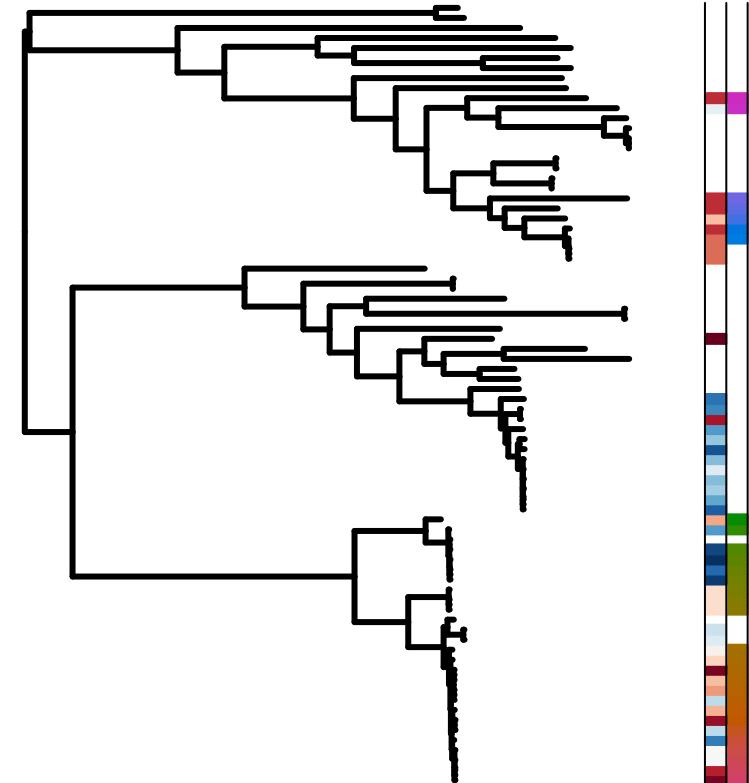
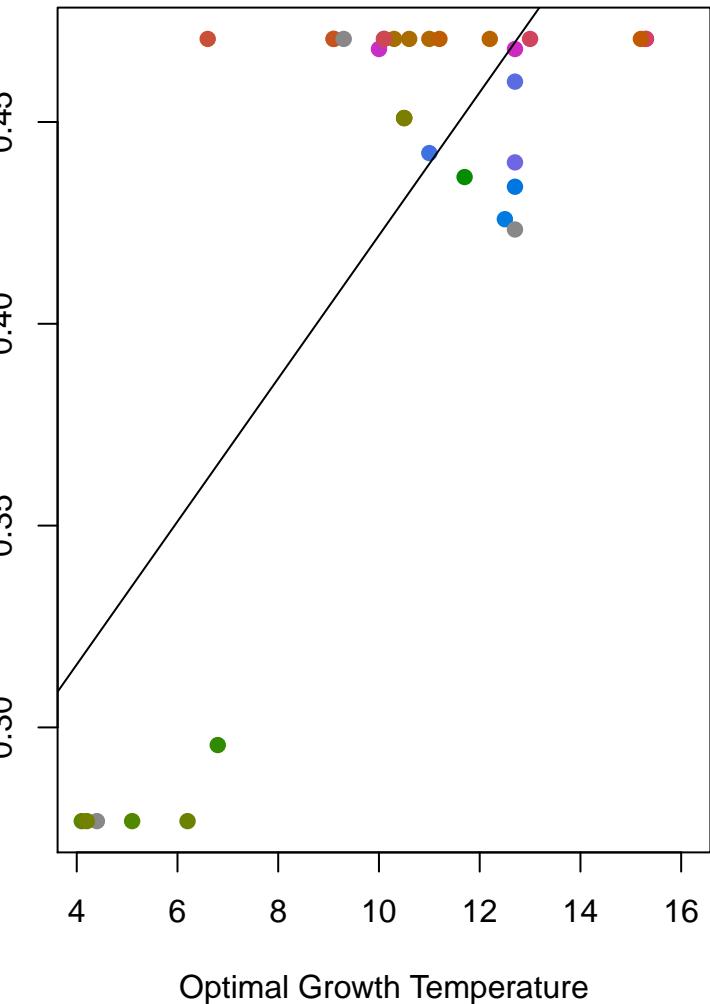
feature.pgfam_id.arg_lys_ratio.mean
PGF_11569208
hypothetical protein
 $r = 0.767, p = 10^{-5.515}$

feature.pgfam_id.arg_lys_ratio.mean



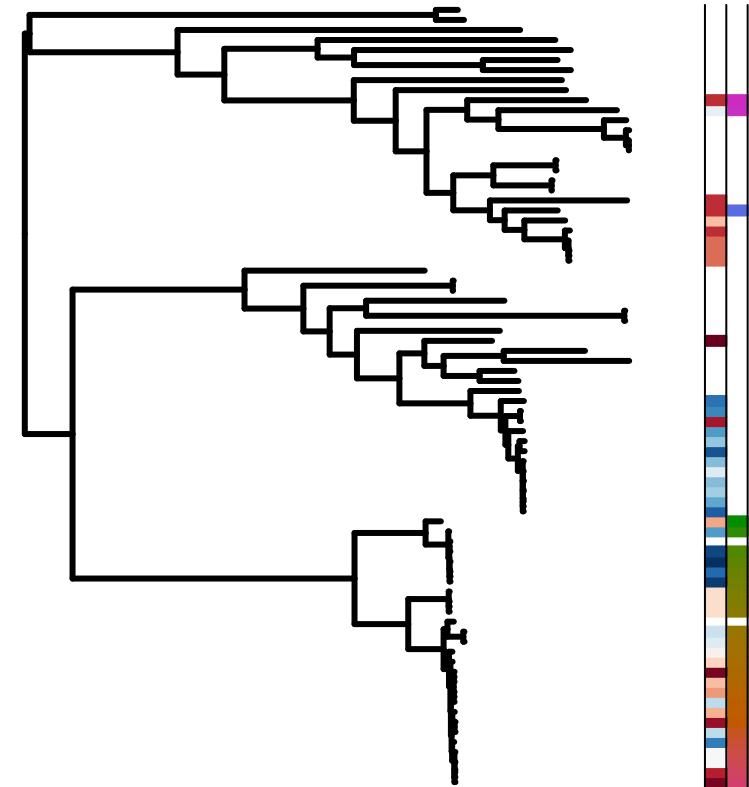
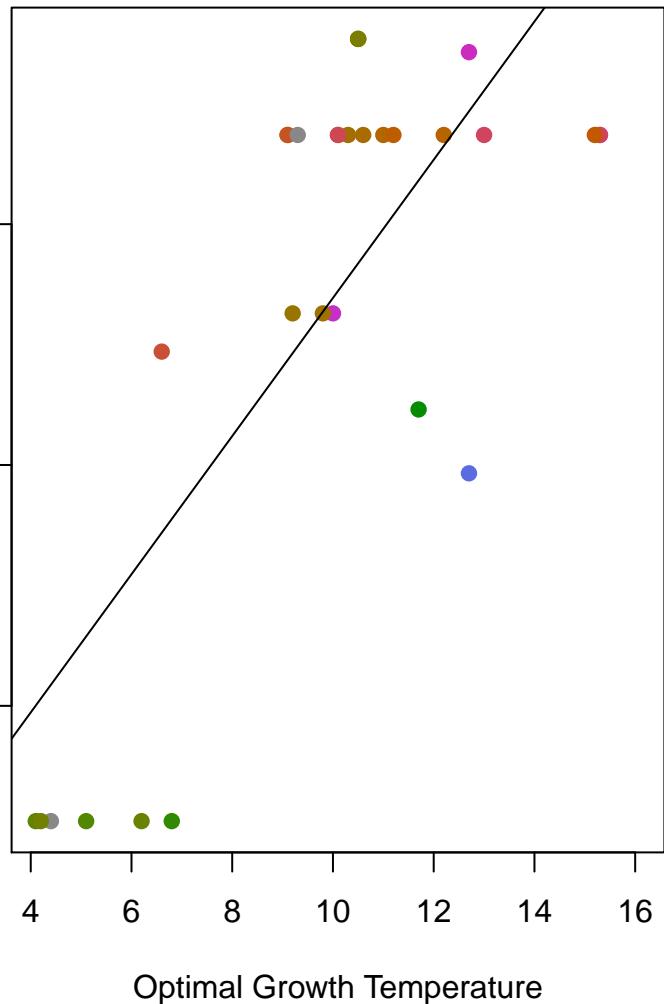
feature.pgfam_id.arg_lys_ratio.mean
PGF_02105064
Uncharacterized protease YegQ
 $r = 0.763$, $p = 10^{-6.624}$

feature.pgfam_id.arg_lys_ratio.mean



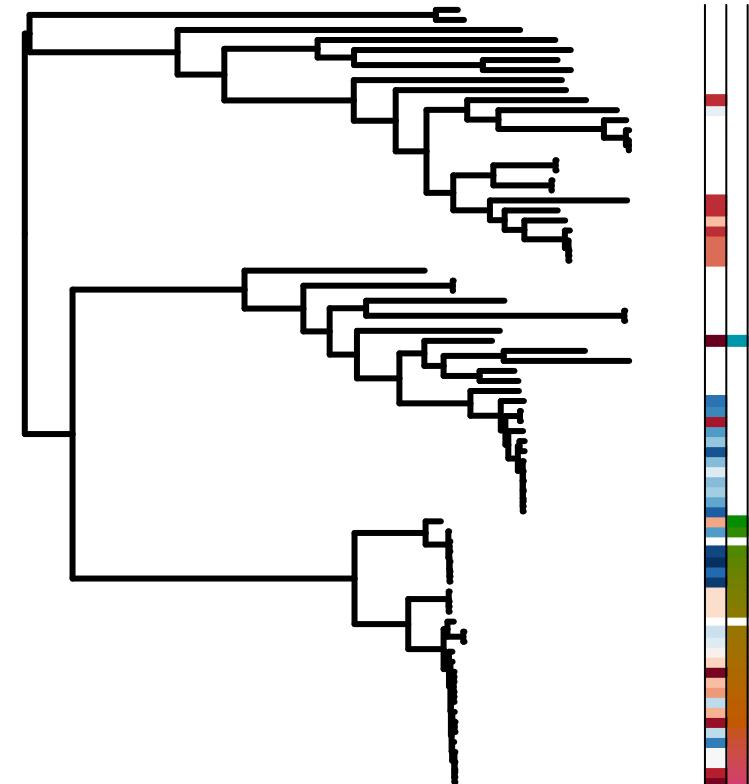
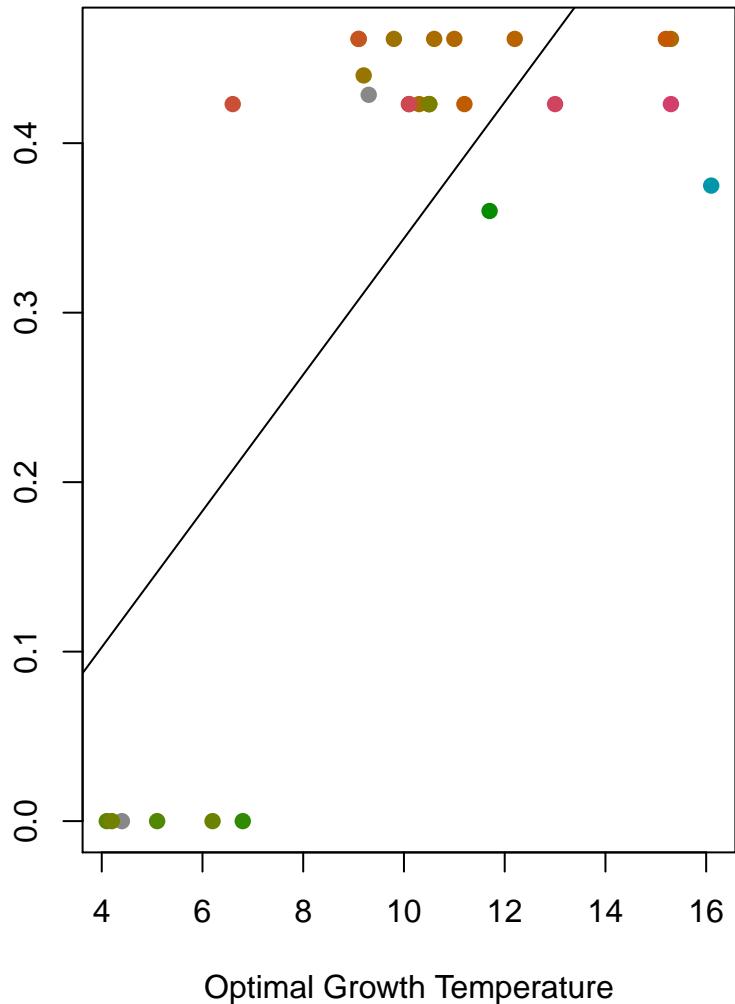
feature.pgfam_id.arg_lys_ratio.mean
PGF_01481272
Chemotaxis protein CheD
 $r = 0.76$, $p = 10^{-5.951}$

feature.pgfam_id.arg_lys_ratio.mean



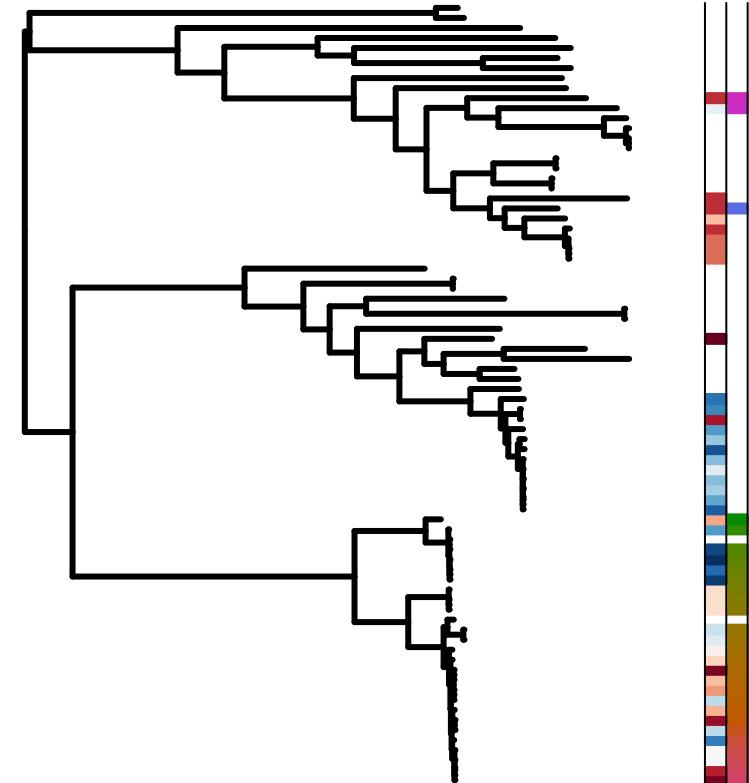
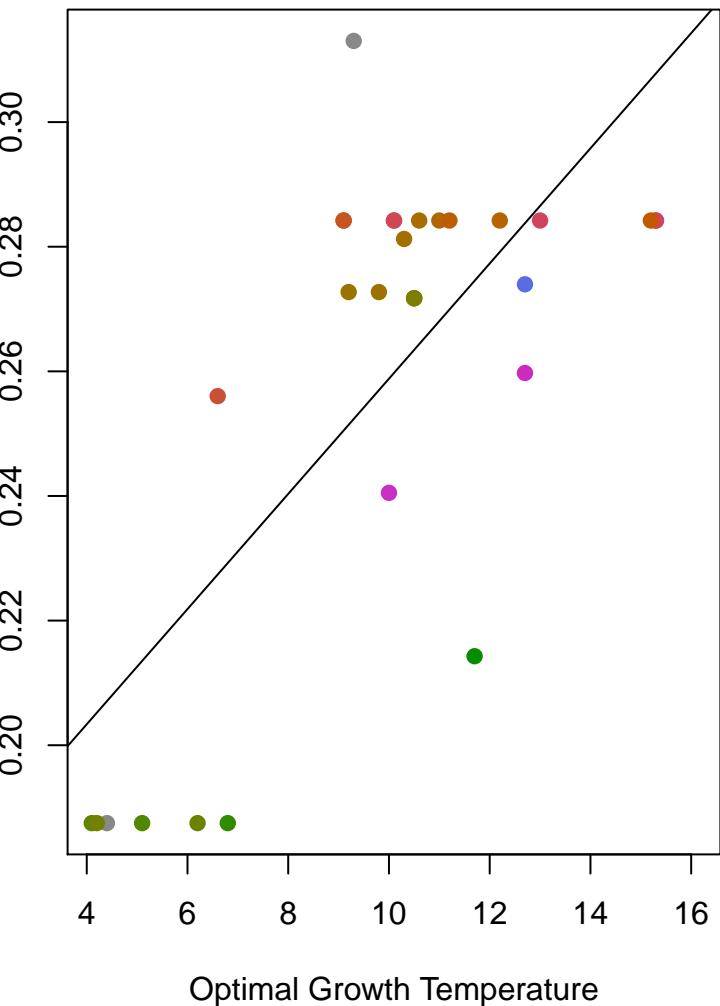
feature.pgfam_id.arg_lys_ratio.mean
PGF_06202619
hypothetical protein
 $r = 0.738, p = 10^{-5.136}$

feature.pgfam_id.arg_lys_ratio.mean



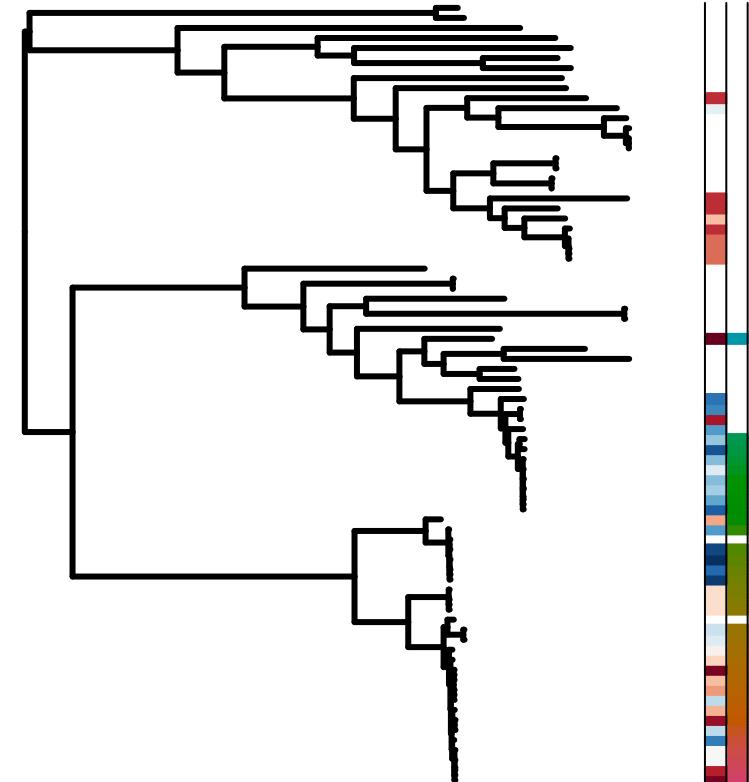
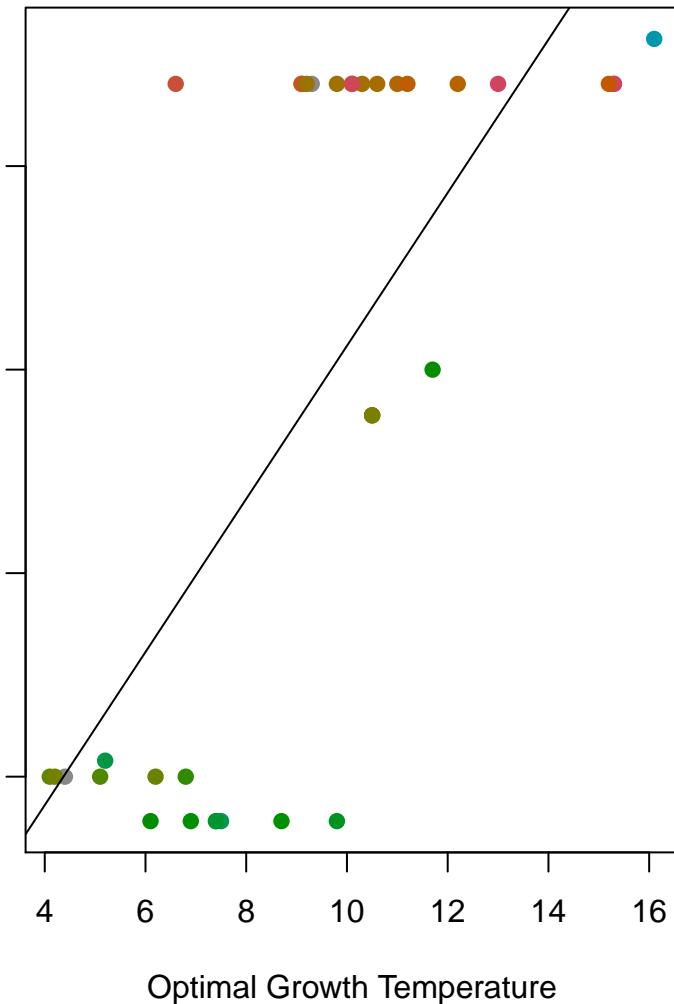
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336773
hypothetical protein
 $r = 0.729$, $p = 10^{-5.311}$

feature.pgfam_id.arg_lys_ratio.mean



feature.pgfam_id.arg_lys_ratio.mean
PGF_10437481
hypothetical protein
 $r = 0.719, p = 10^{-6.111}$

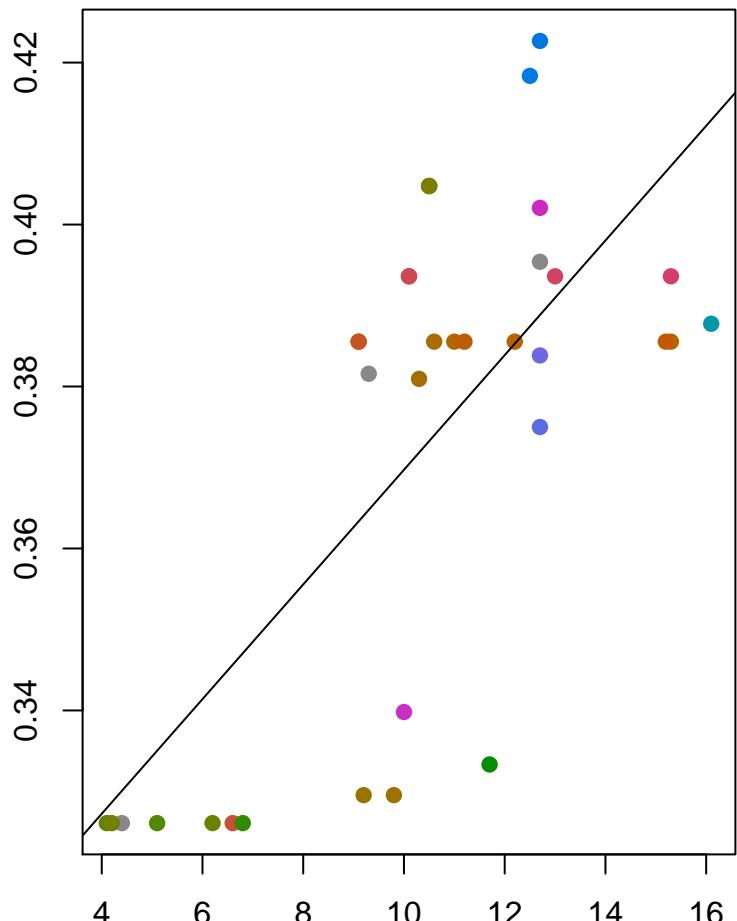
feature.pgfam_id.arg_lys_ratio.mean



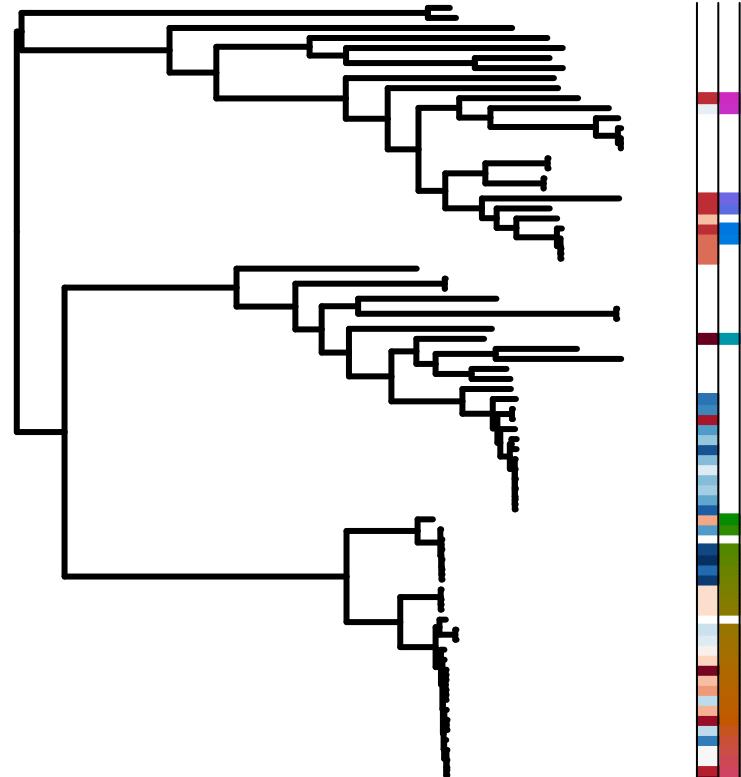
feature.pgfam_id.arg_lys_ratio.mean
PGF_12728693

Two-component system sensor histidine kinase/response regulator hybrid
 $r = 0.707, p = 10^{-5.692}$

feature.pgfam_id.arg_lys_ratio.mean

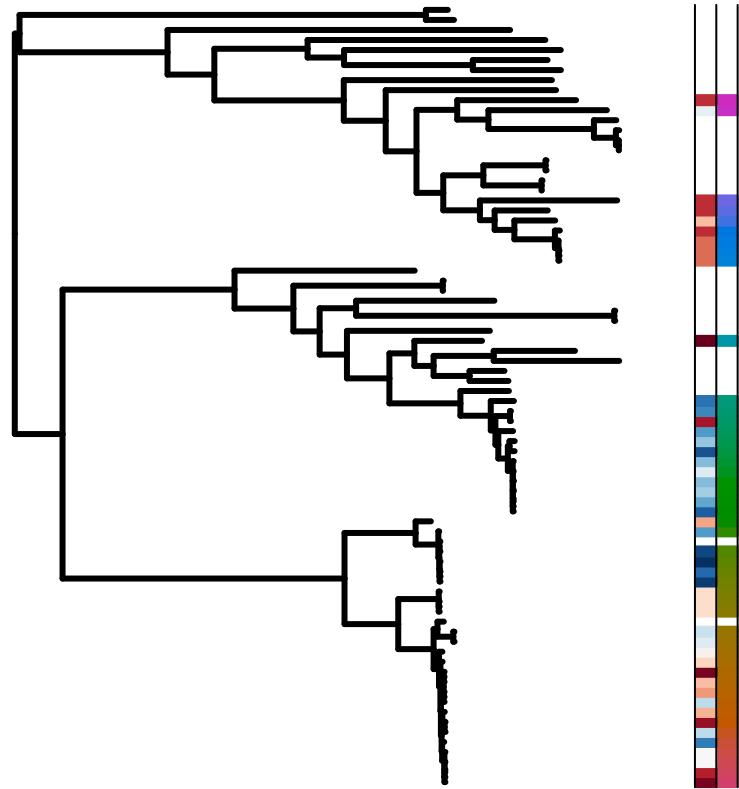
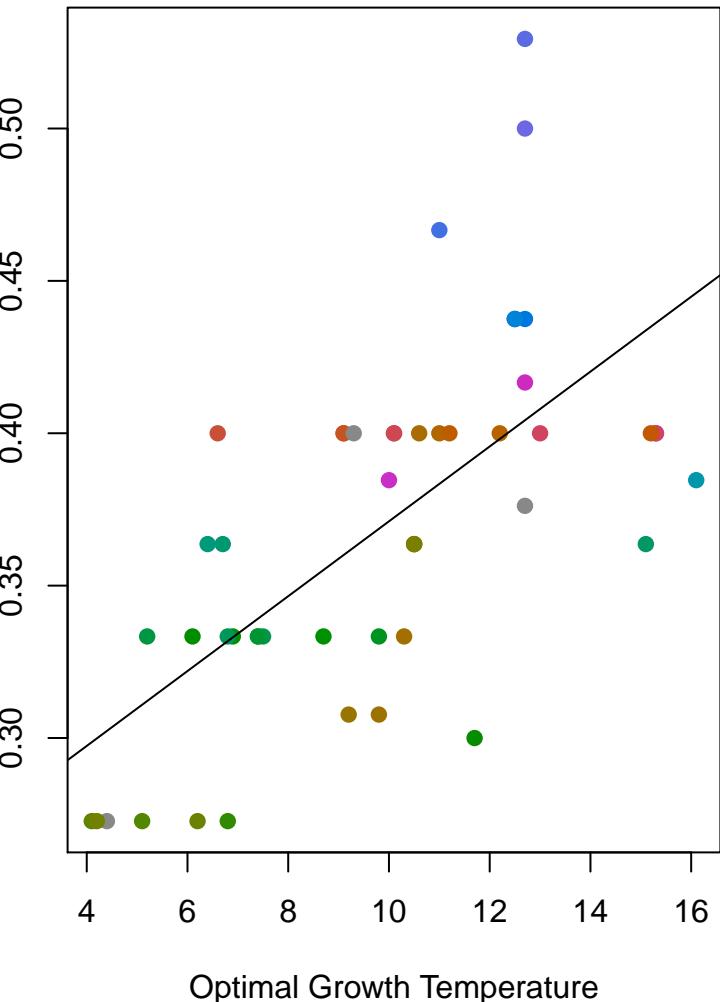


Optimal Growth Temperature



feature.pgfam_id.arg_lys_ratio.mean
PGF_00018430
MSHA pilin protein MshB
 $r = 0.662$, $p = 10^{-6.78}$

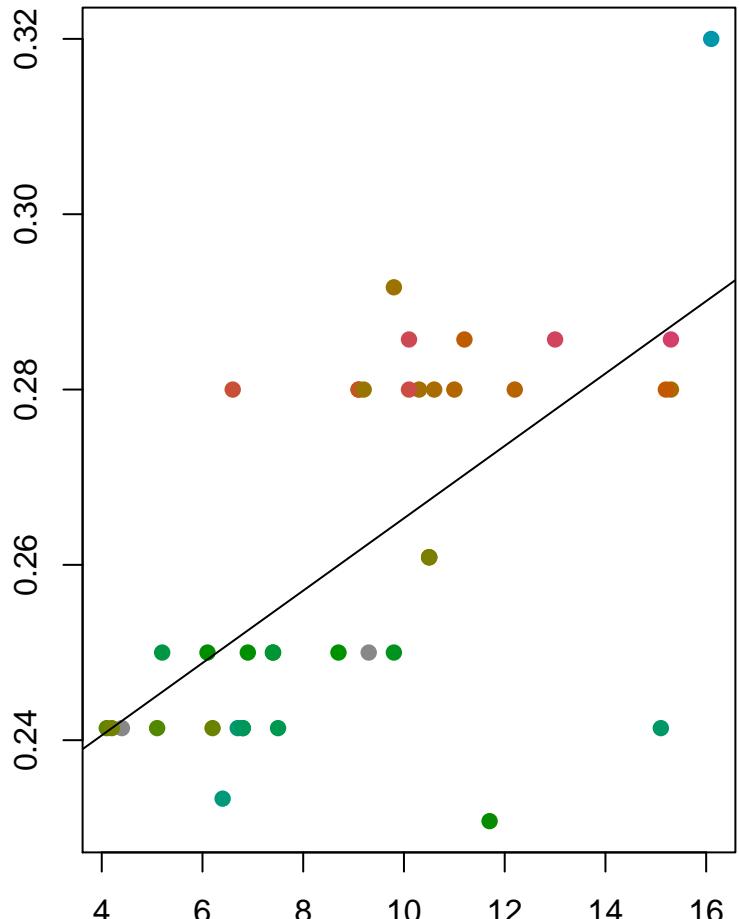
feature.pgfam_id.arg_lys_ratio.mean



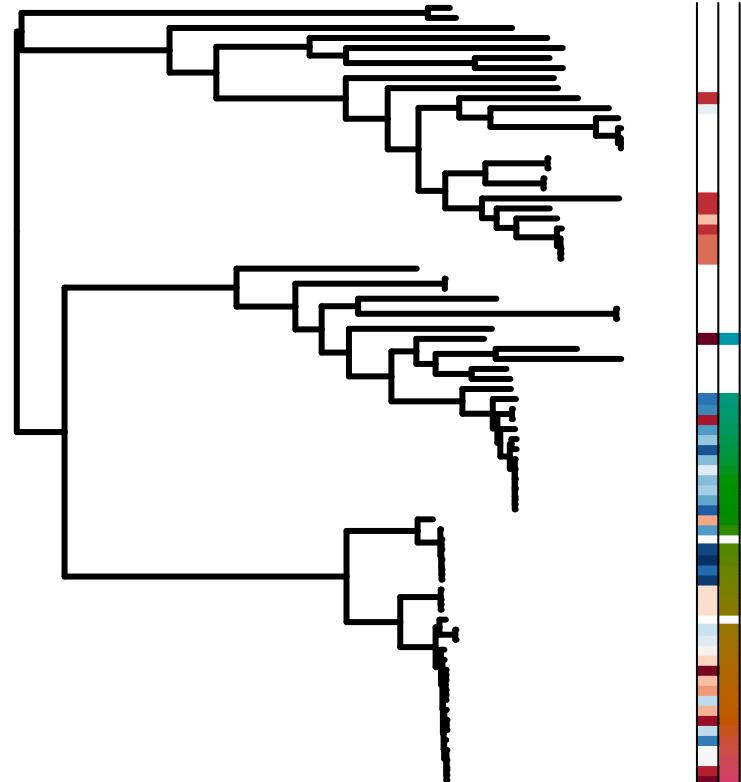
feature.pgfam_id.arg_lys_ratio.mean
PGF_00049322

S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), eukaryotic
 $r = 0.638, p = 10^{-5.032}$

feature.pgfam_id.arg_lys_ratio.mean



Optimal Growth Temperature



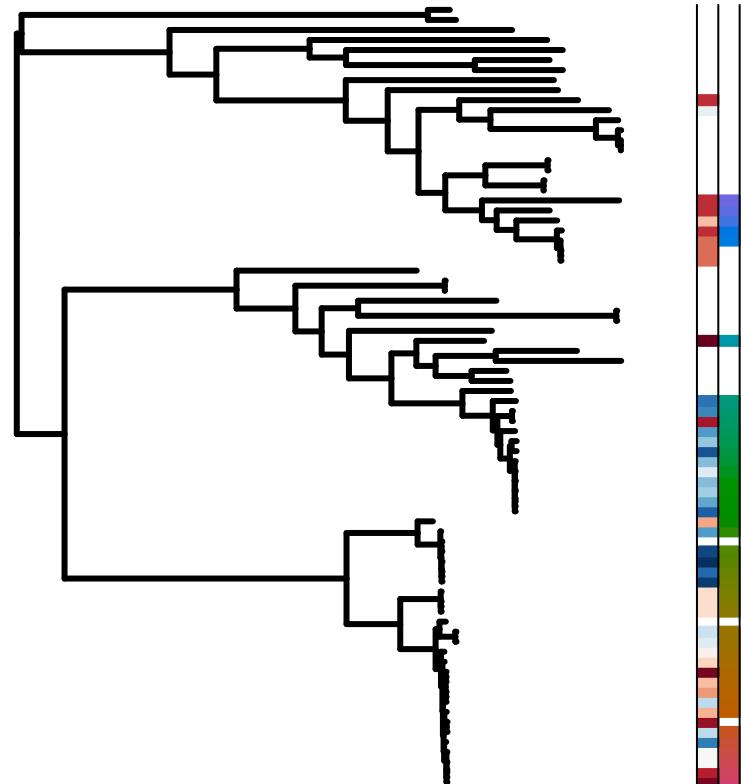
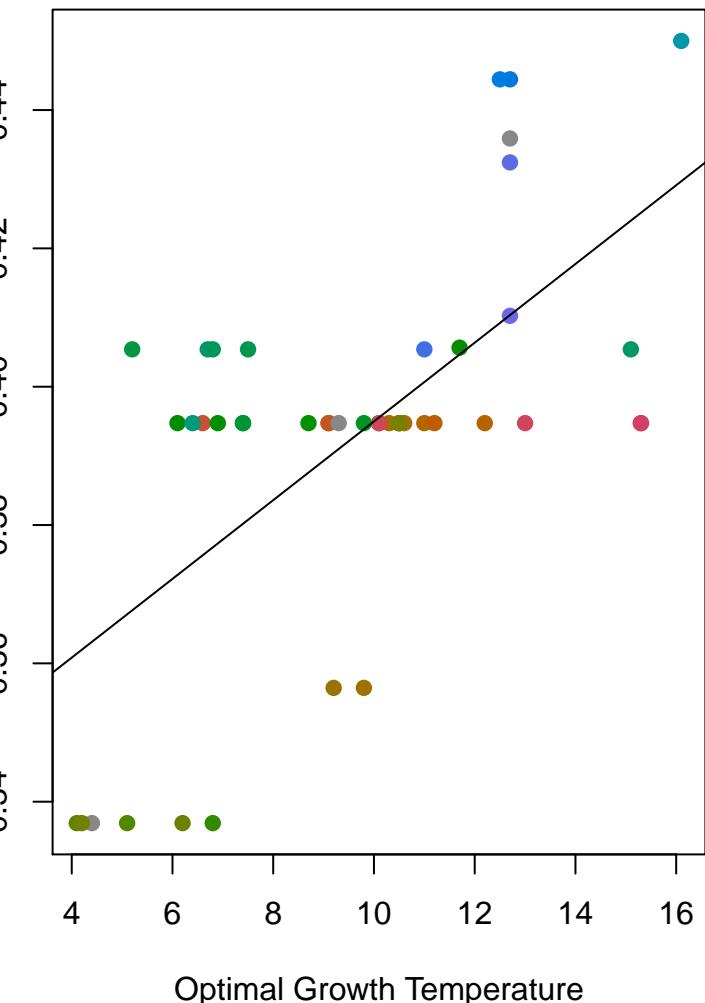
feature.pgfam_id.arg_lys_ratio.mean

PGF_02820072

aminotransferase, Class III pyridoxal–phosphate dependent

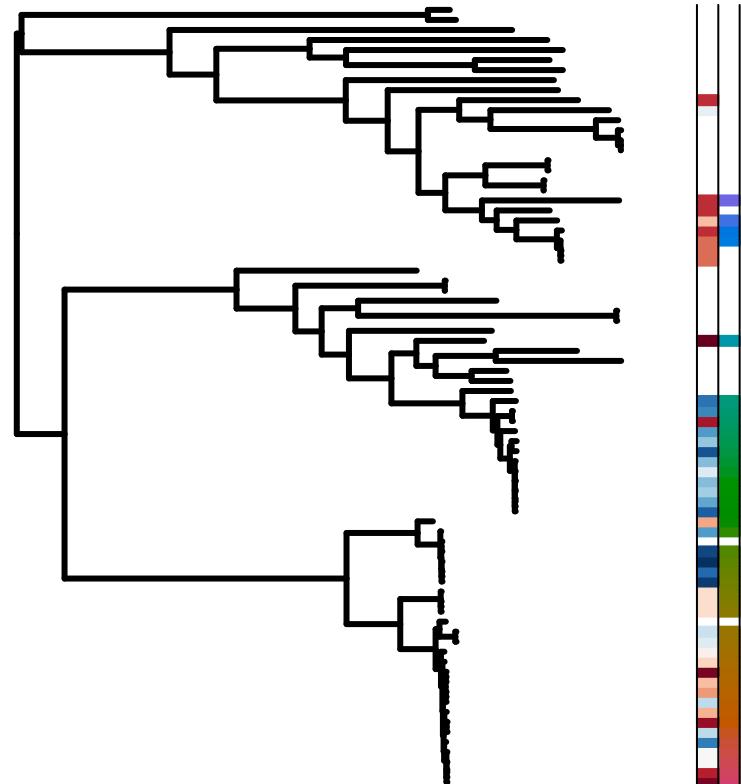
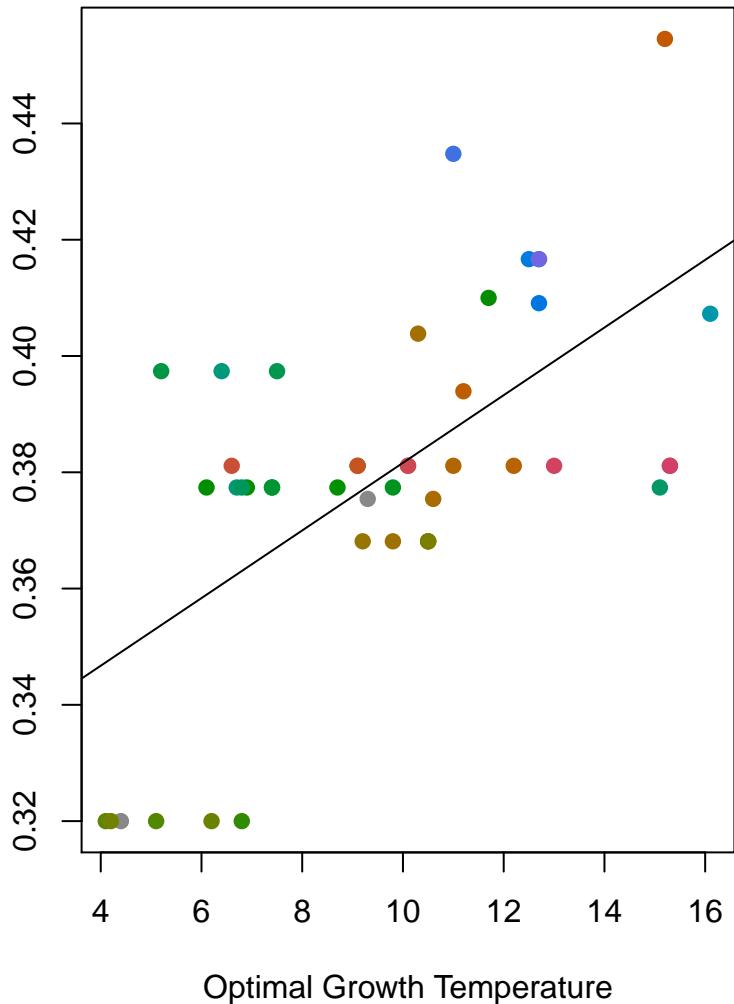
$r = 0.634, p = 10^{-5.543}$

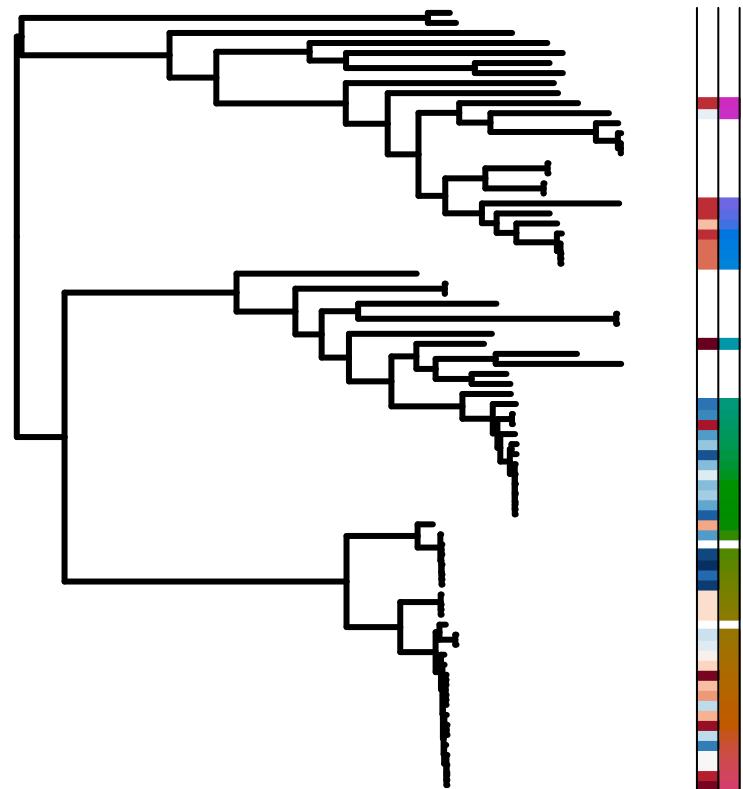
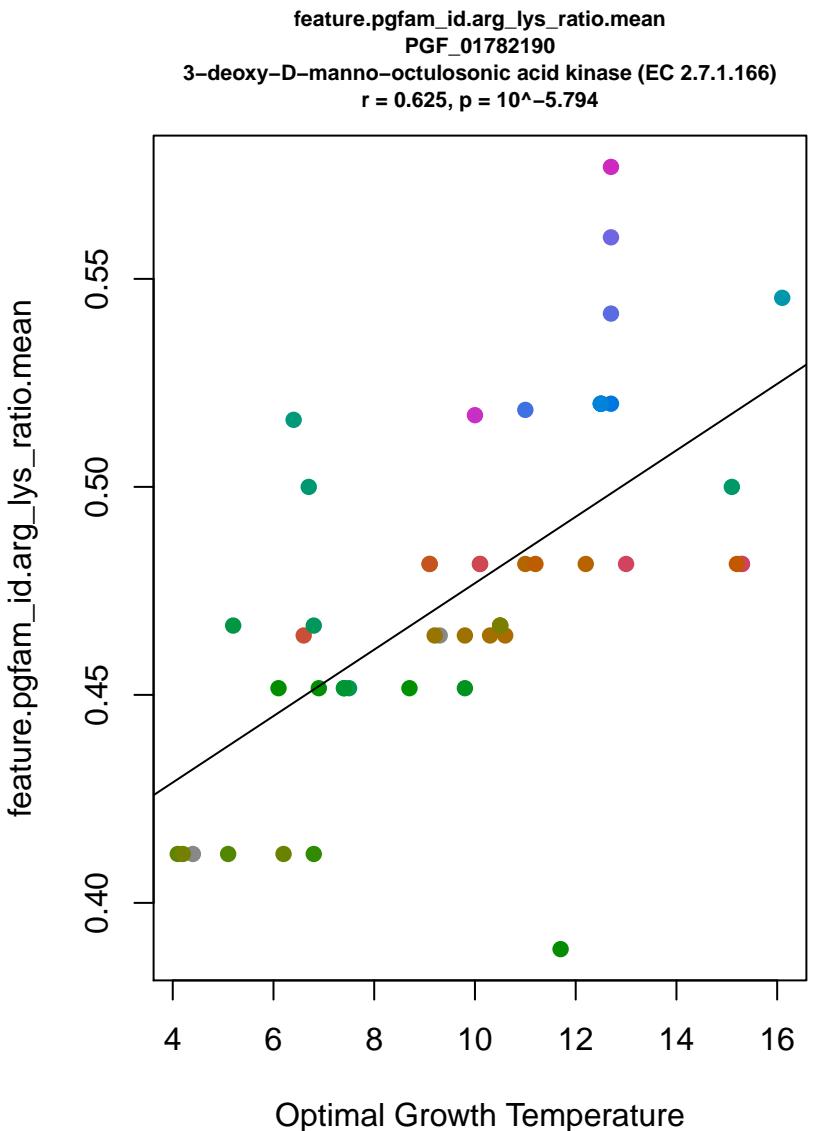
feature.pgfam_id.arg_lys_ratio.mean

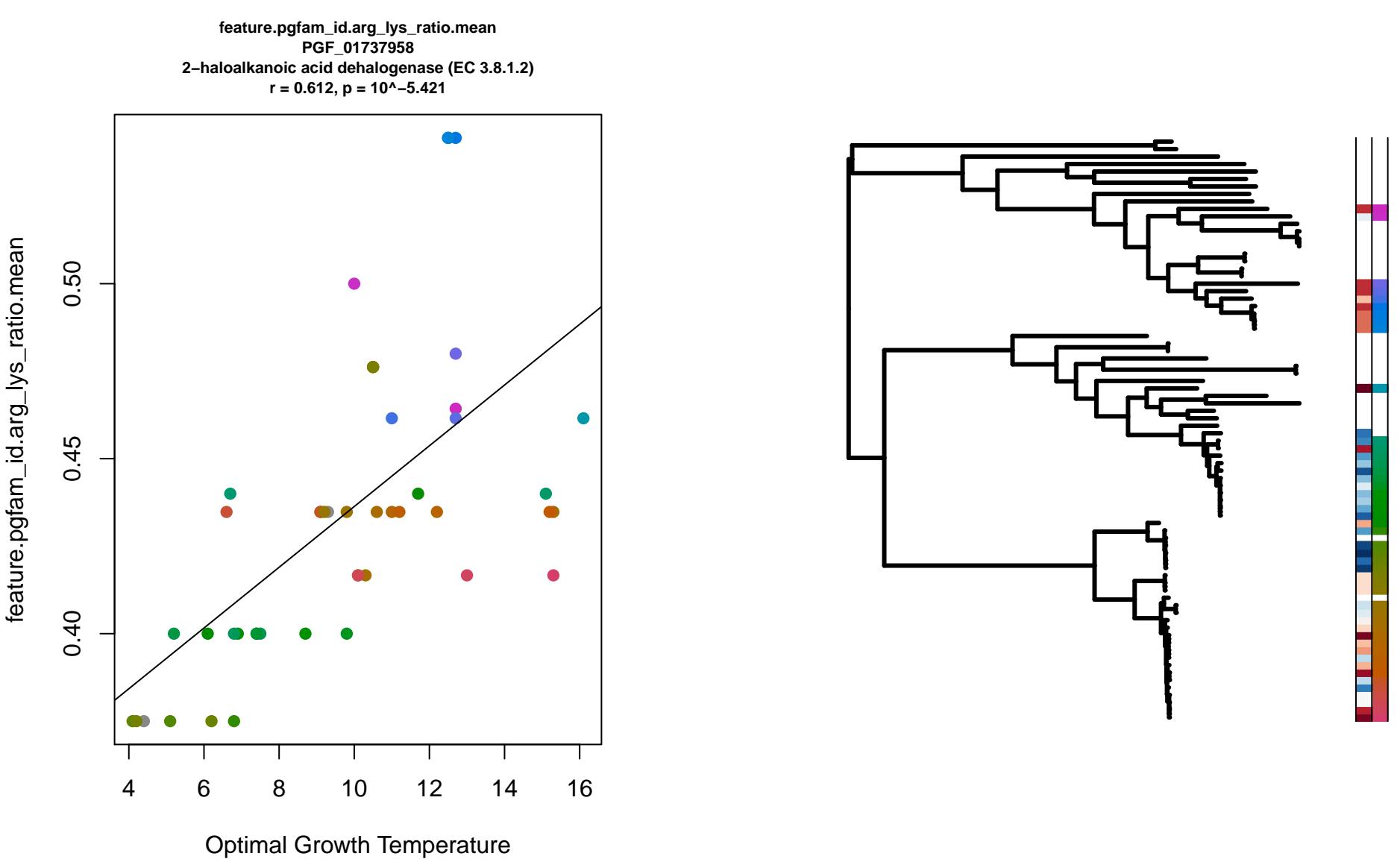


feature.pgfam_id.arg_lys_ratio.mean
PGF_07370053
RNA polymerase sigma-70 factor
 $r = 0.628$, $p = 10^{-5.405}$

feature.pgfam_id.arg_lys_ratio.mean





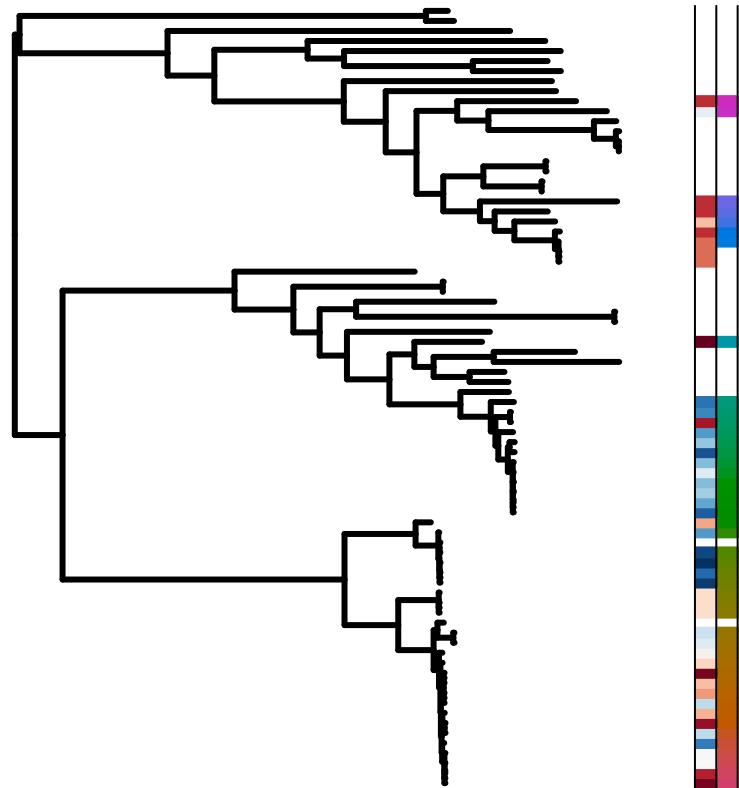
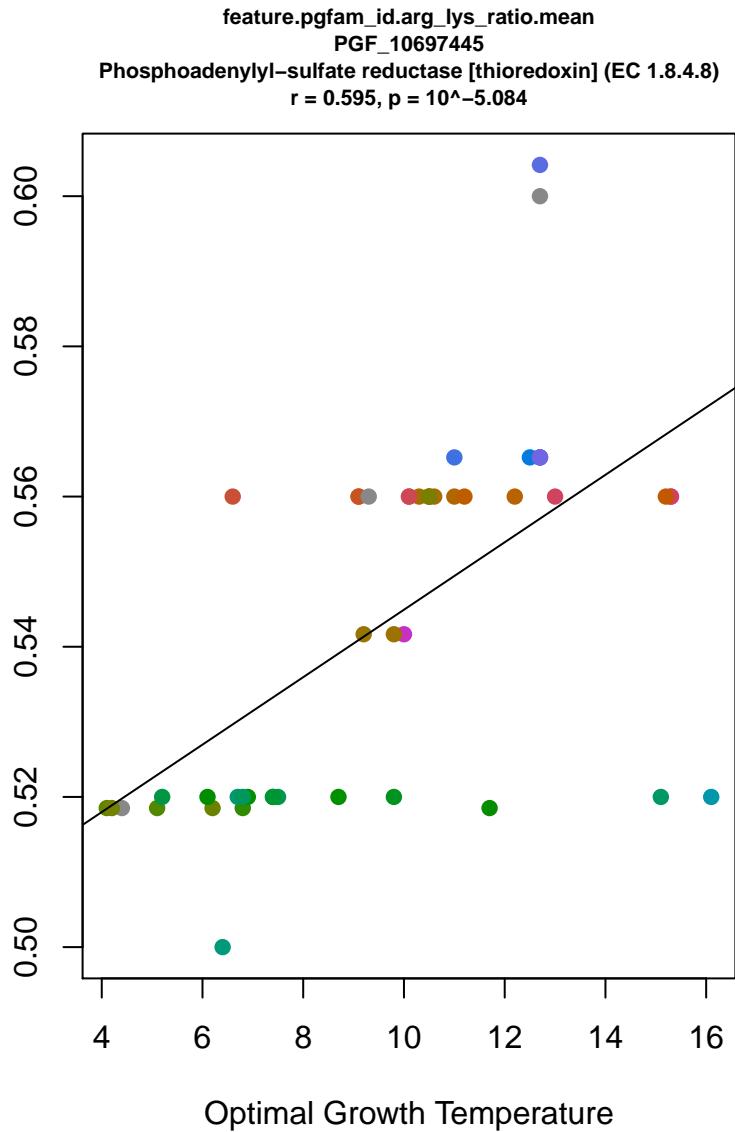
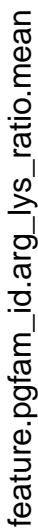


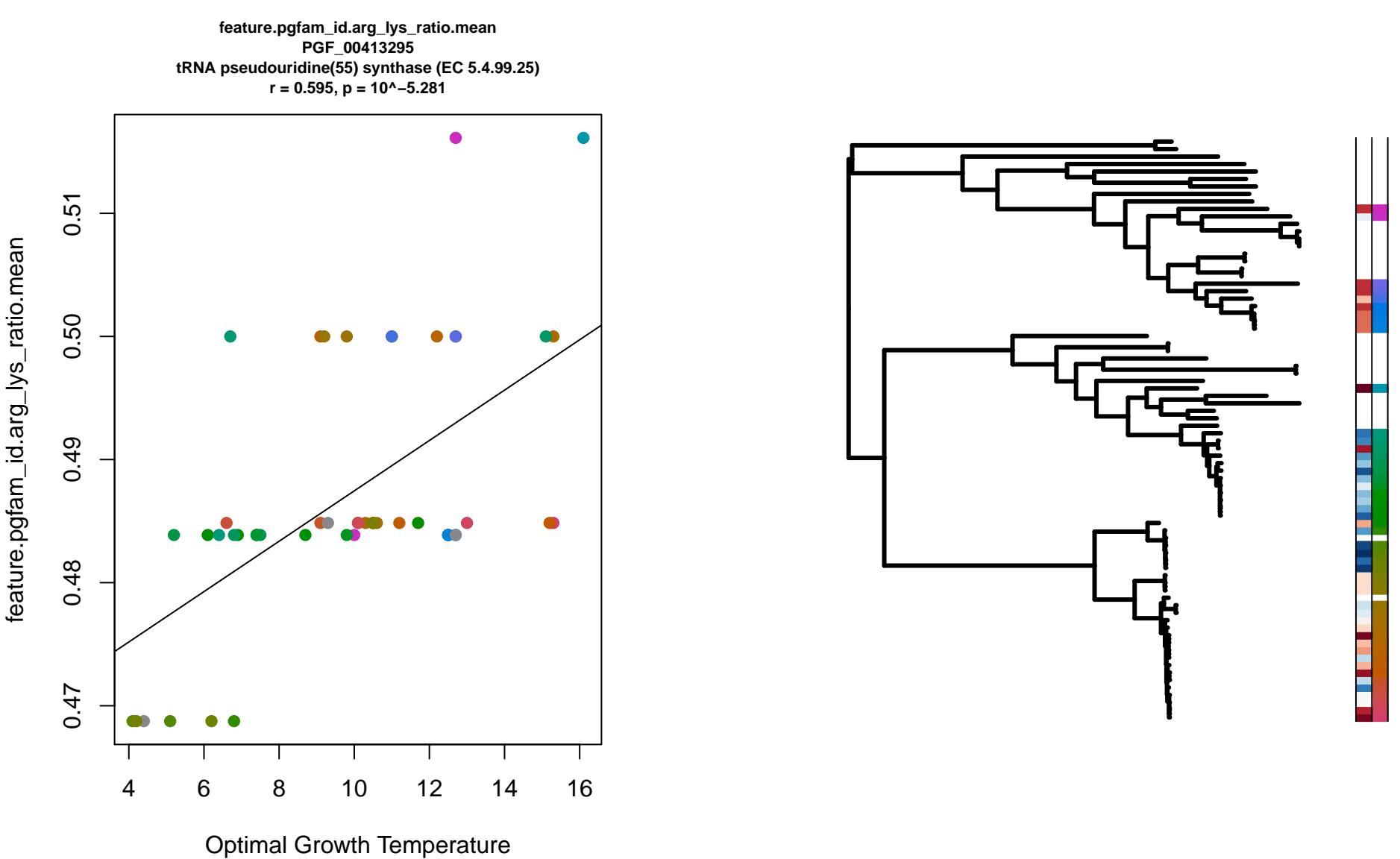
feature.pgfam_id.arg_lyc_ratio.mean

PGF_10697445

Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)

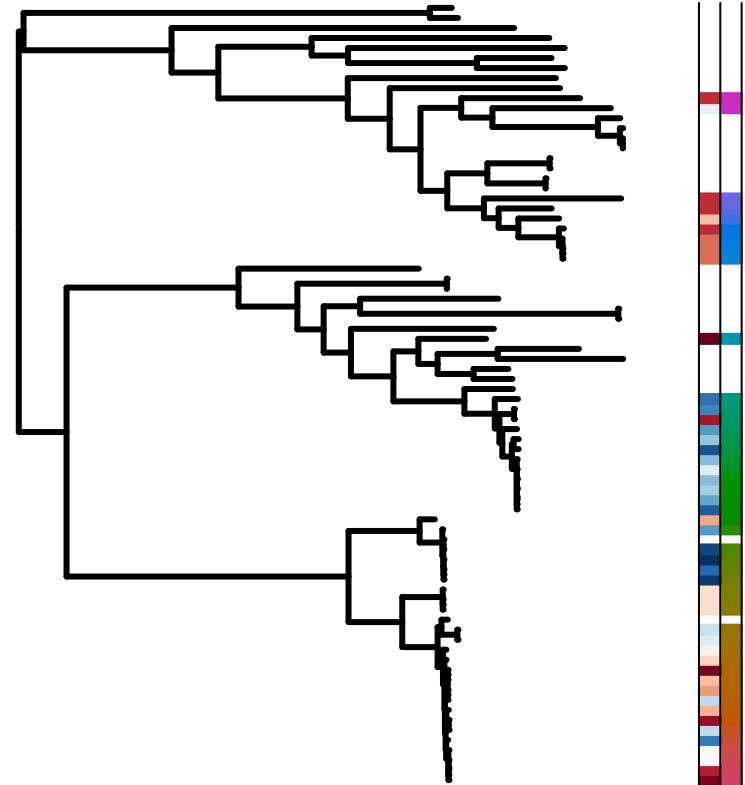
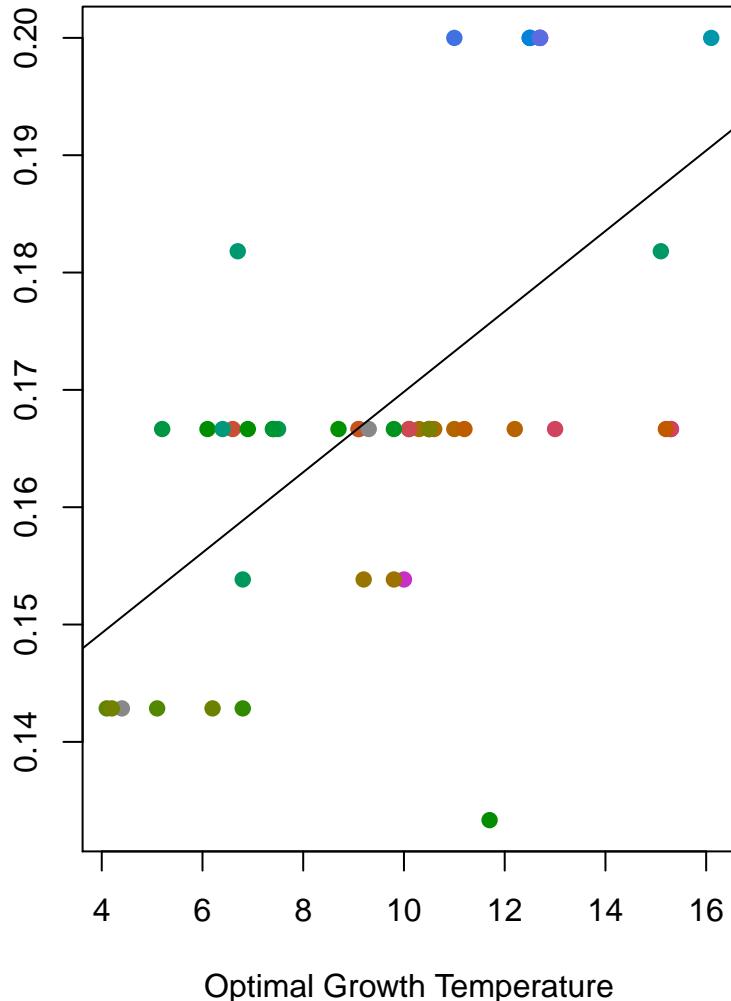
$r = 0.595$, $p = 10^{-5.084}$





feature.pgfam_id.arg_lys_ratio.mean
PGF_00059675
Antioxidant, AhpC/Tsa family
 $r = 0.592$, $p = 10^{-5.226}$

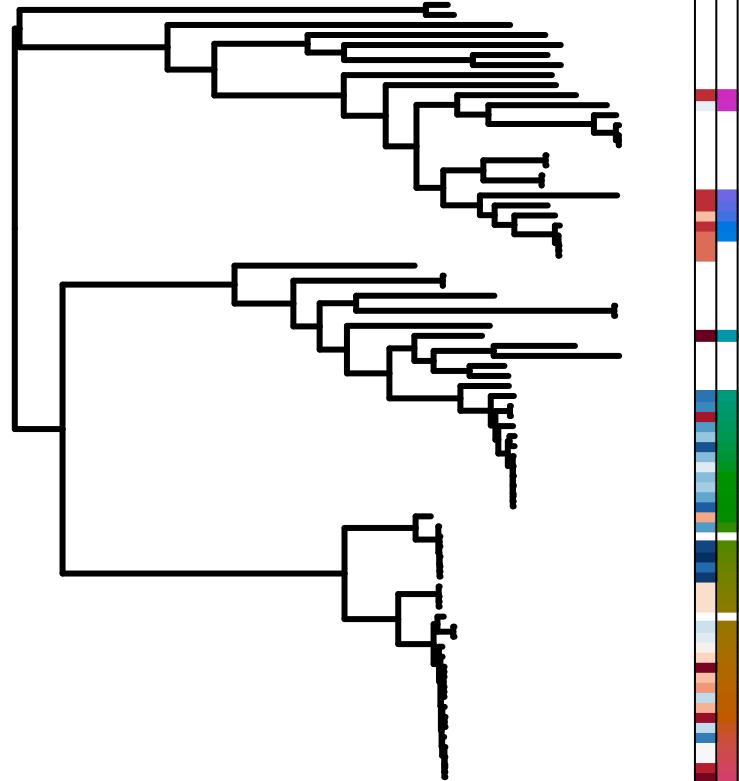
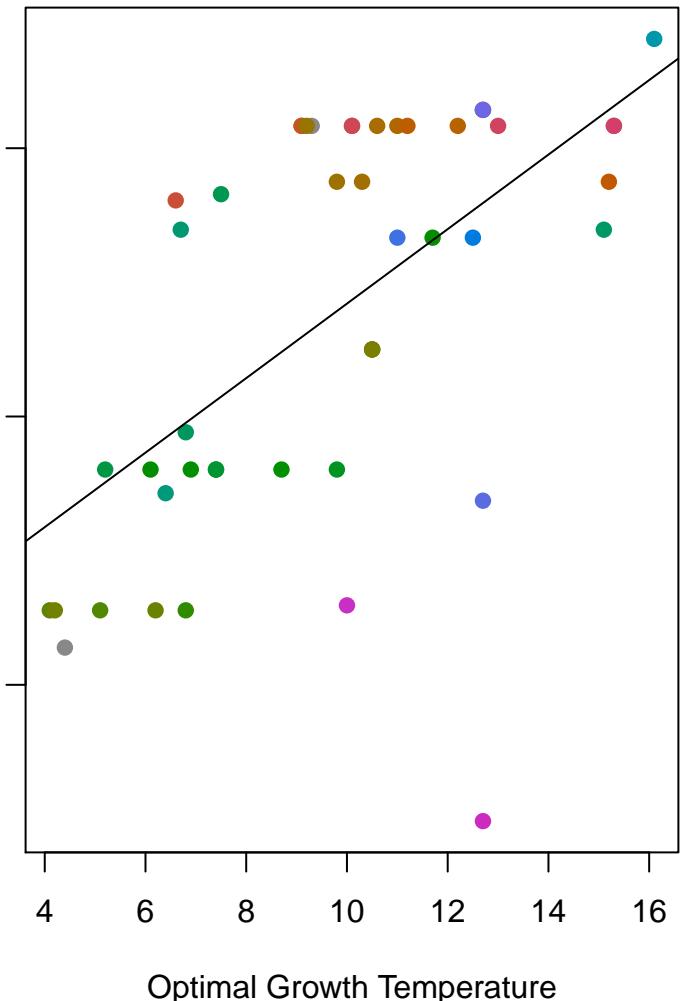
feature.pgfam_id.arg_lys_ratio.mean



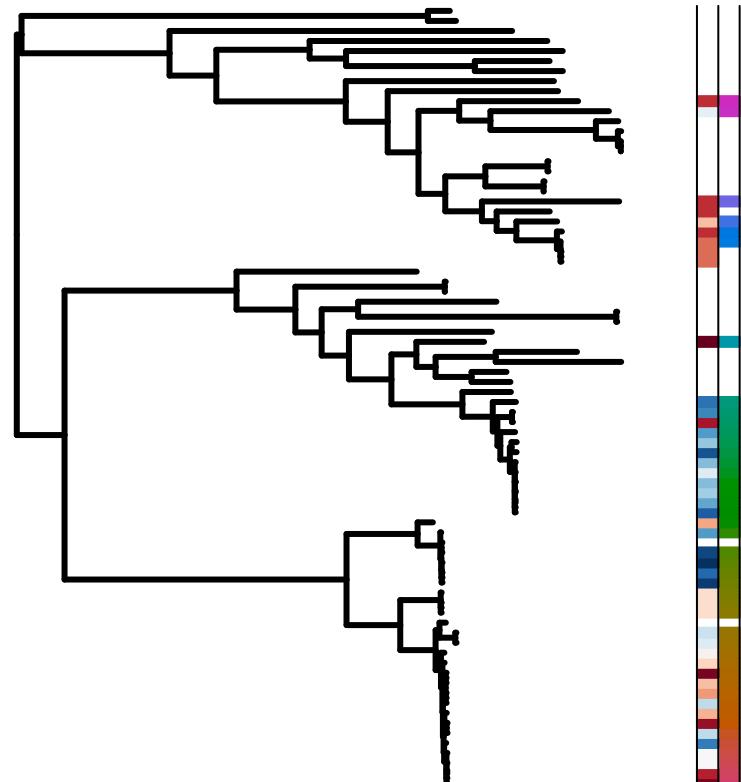
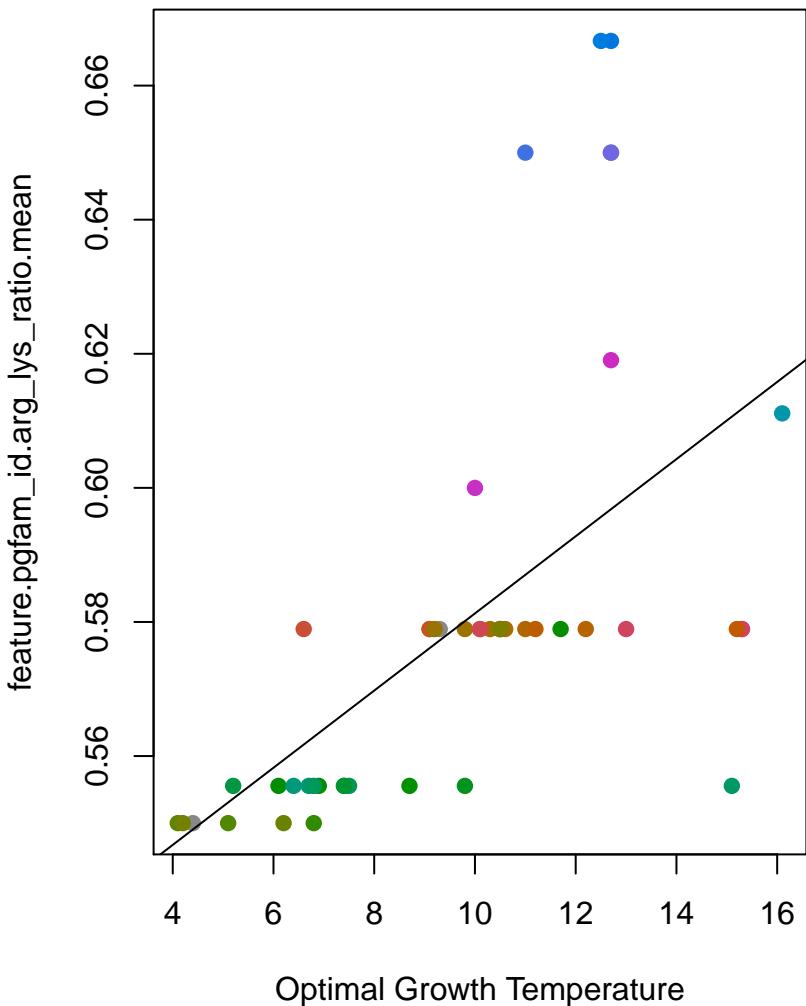
feature.pgfam_id.arg_lys_ratio.mean
PGF_10238627

Chemotaxis regulator – transmits chemoreceptor signals to flagellar motor components CheY
 $r = 0.586, p = 10^{-4.912}$

feature.pgfam_id.arg_lys_ratio.mean

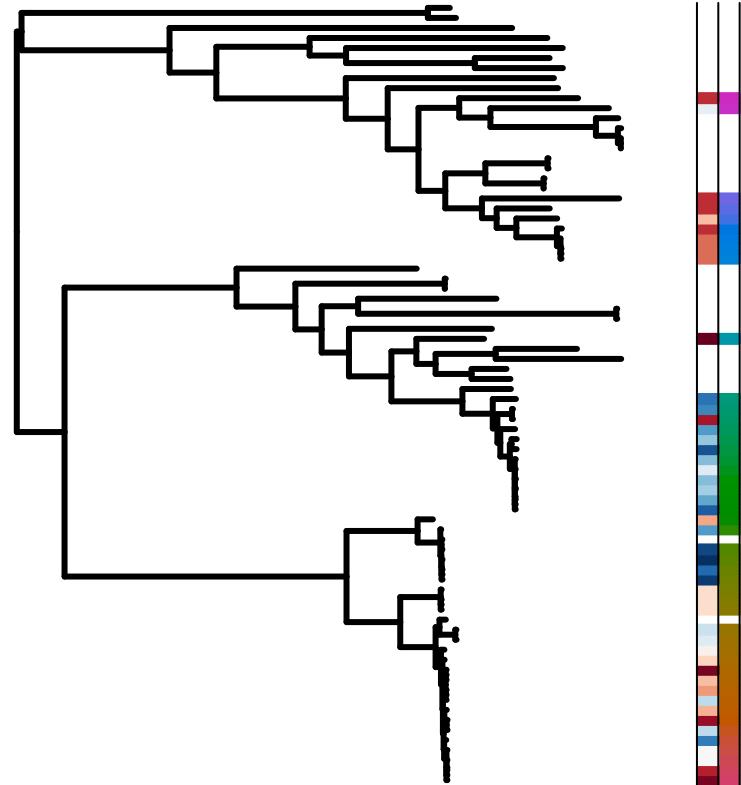
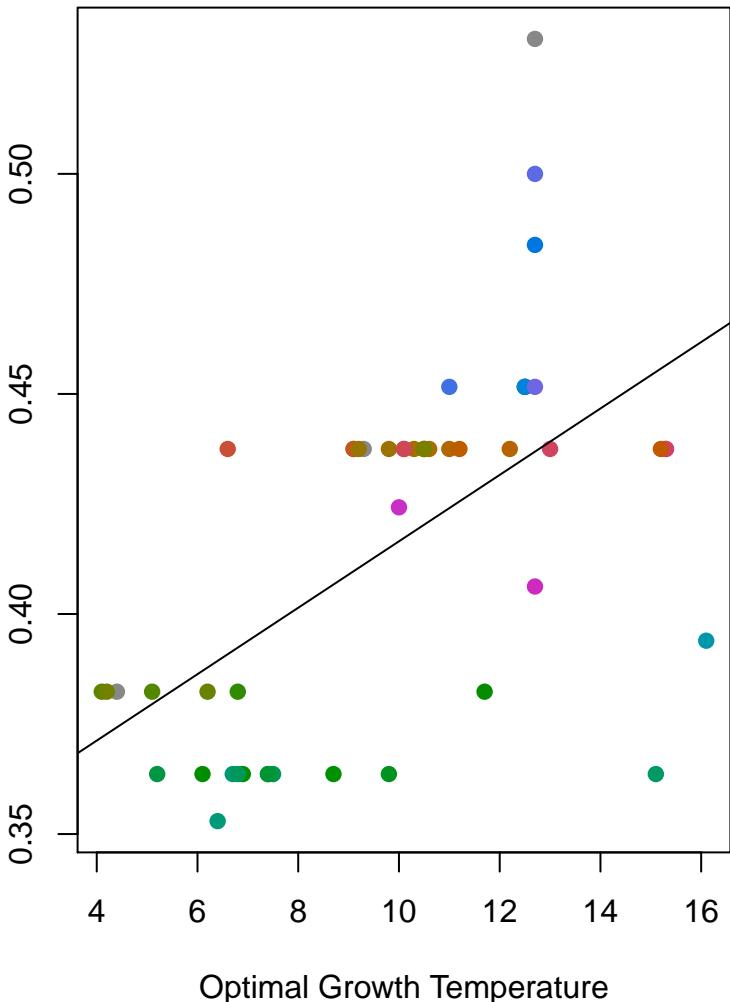


feature.pgfam_id.arg_lys_ratio.mean
PGF_03073036
hypothetical protein
 $r = 0.584$, $p = 10^{-4.782}$



feature.pgfam_id.arg_lys_ratio.mean
PGF_01496598
Chemotaxis protein CheV (EC 2.7.3.-)
 $r = 0.579$, $p = 10^{-4.967}$

feature.pgfam_id.arg_lys_ratio.mean



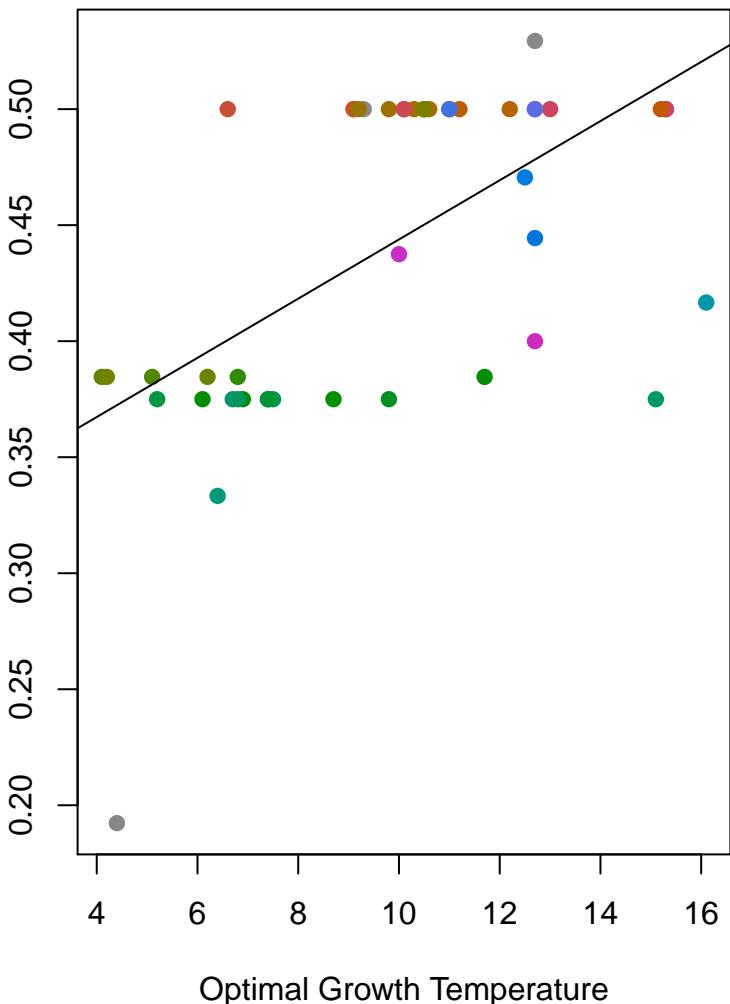
feature.pgfam_id.arg_lys_ratio.mean

PGF_02031353

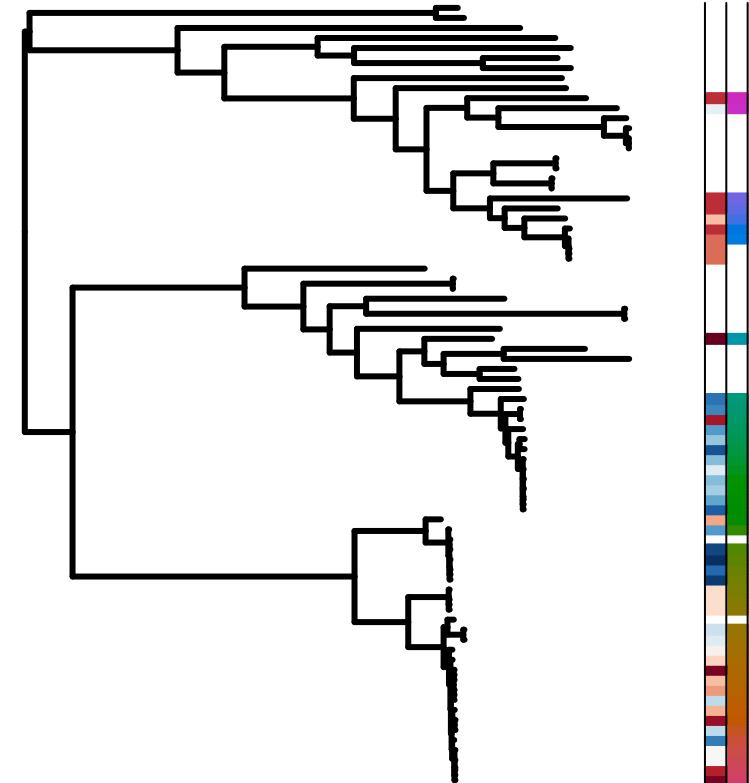
FIG01269488: protein, clustered with ribosomal protein L32p

$r = 0.577, p = 10^{-4.757}$

feature.pgfam_id.arg_lys_ratio.mean

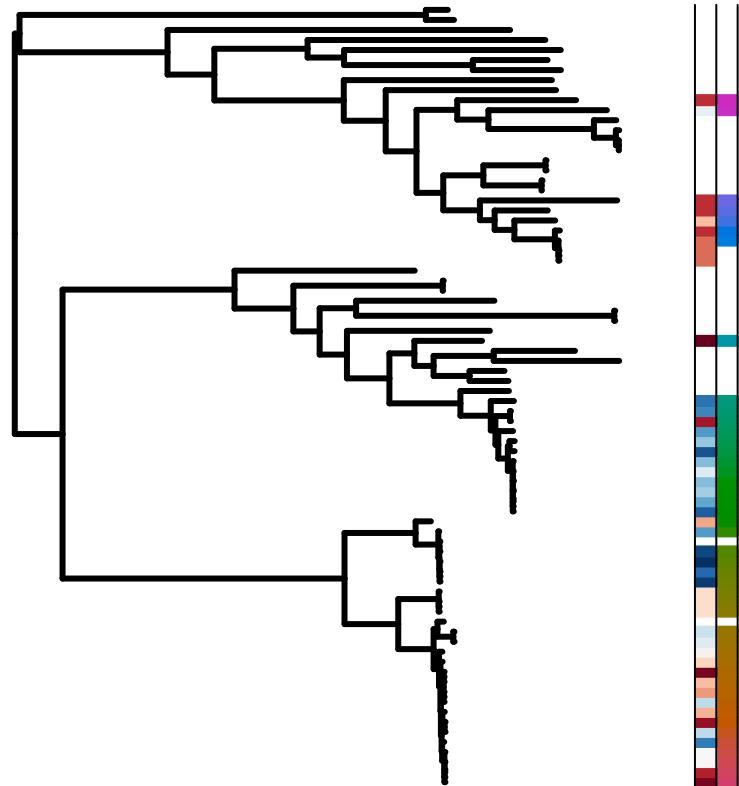
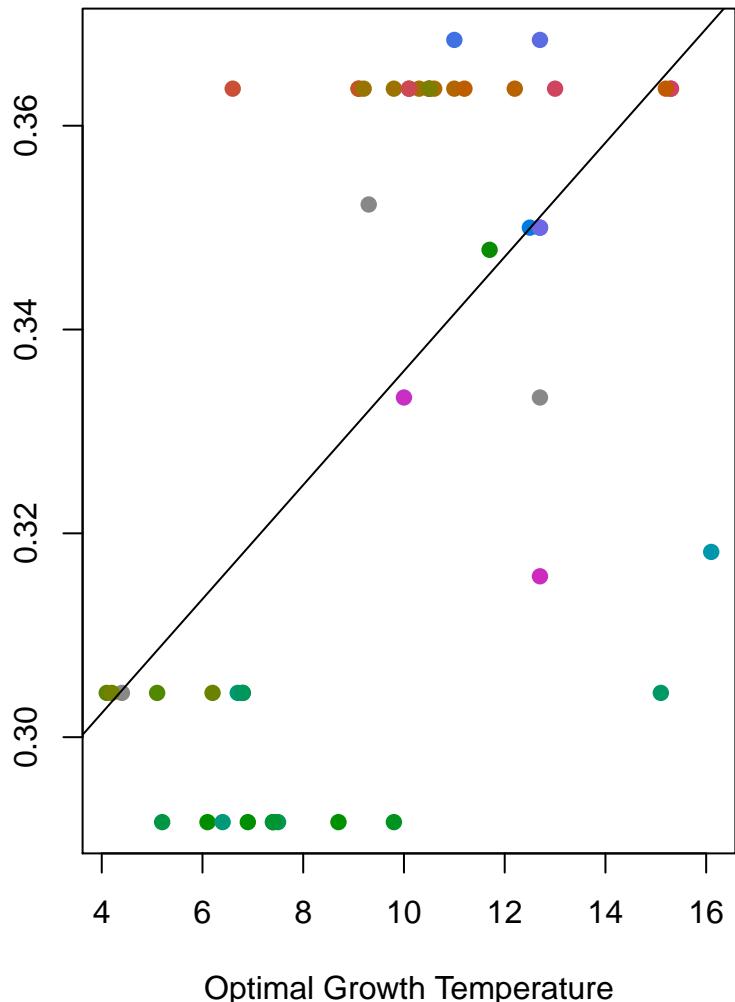


Optimal Growth Temperature

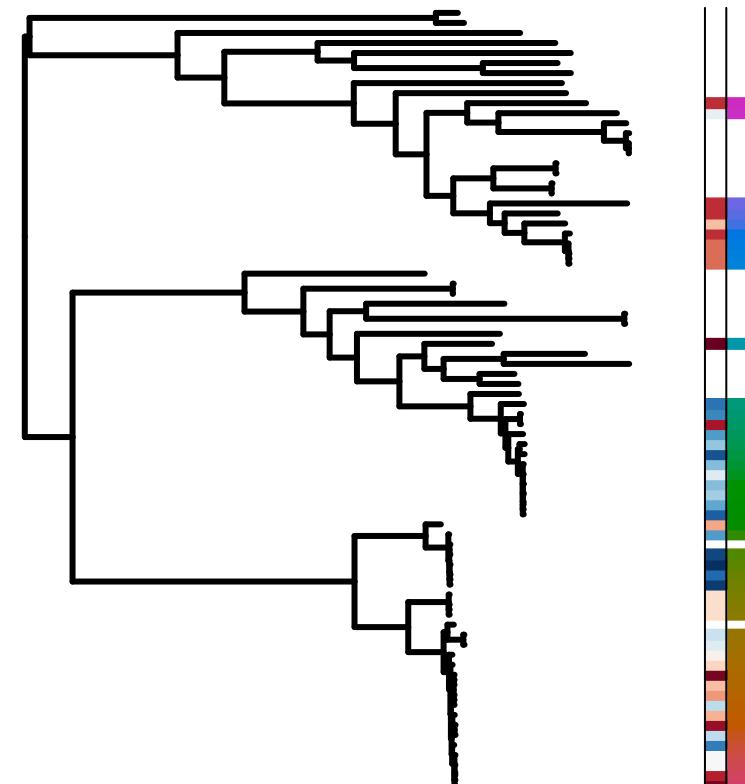
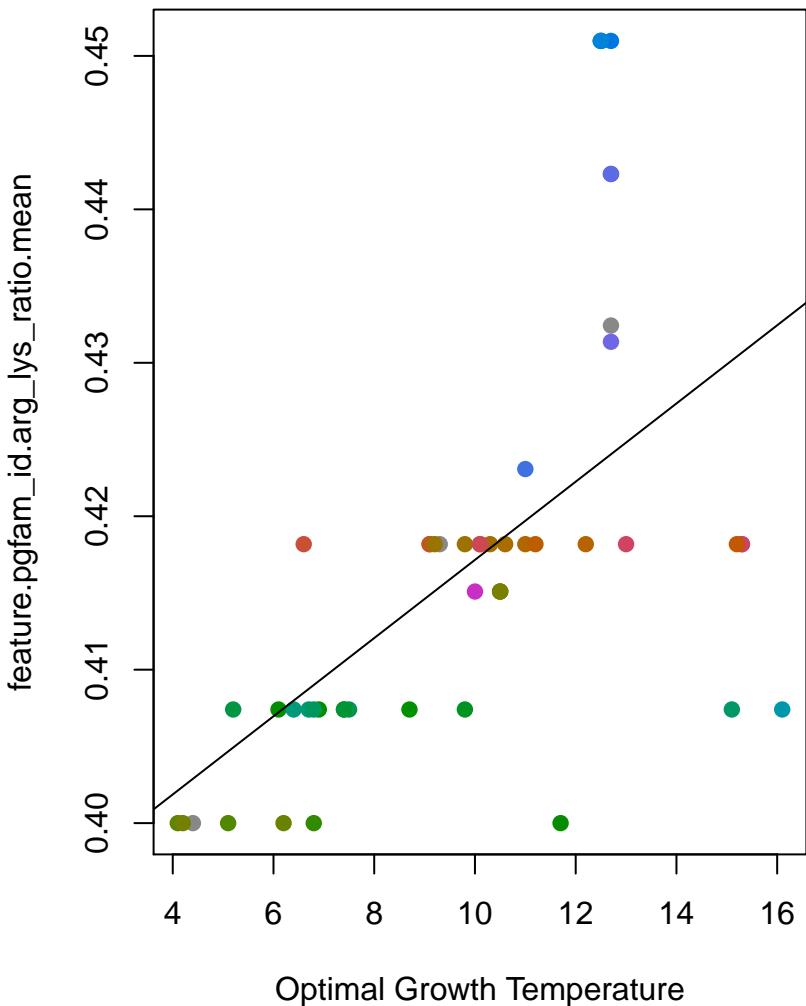


feature.pgfam_id.arg_lys_ratio.mean
PGF_12783000
hypothetical protein
 $r = 0.575, p = 10^{-4.714}$

feature.pgfam_id.arg_lys_ratio.mean

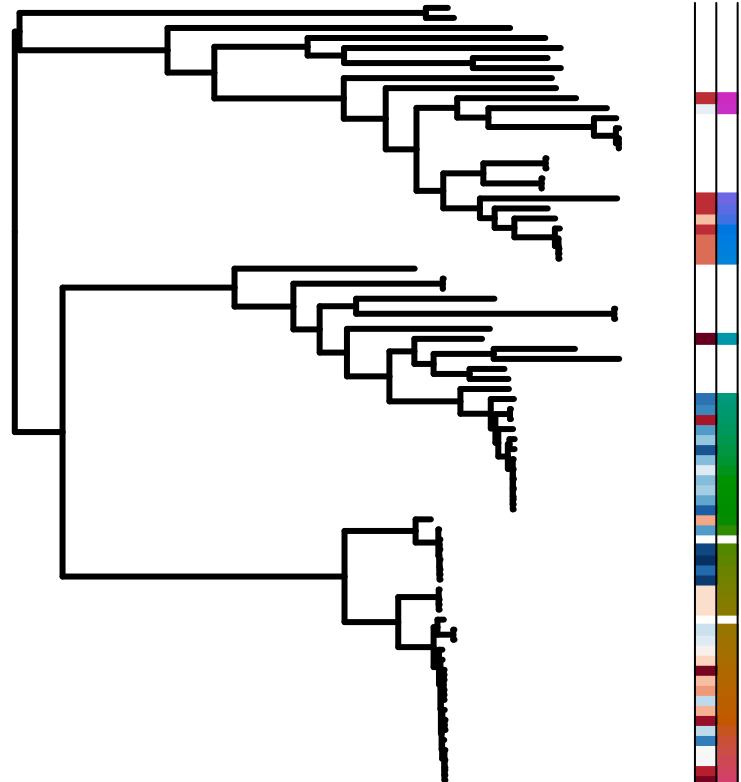
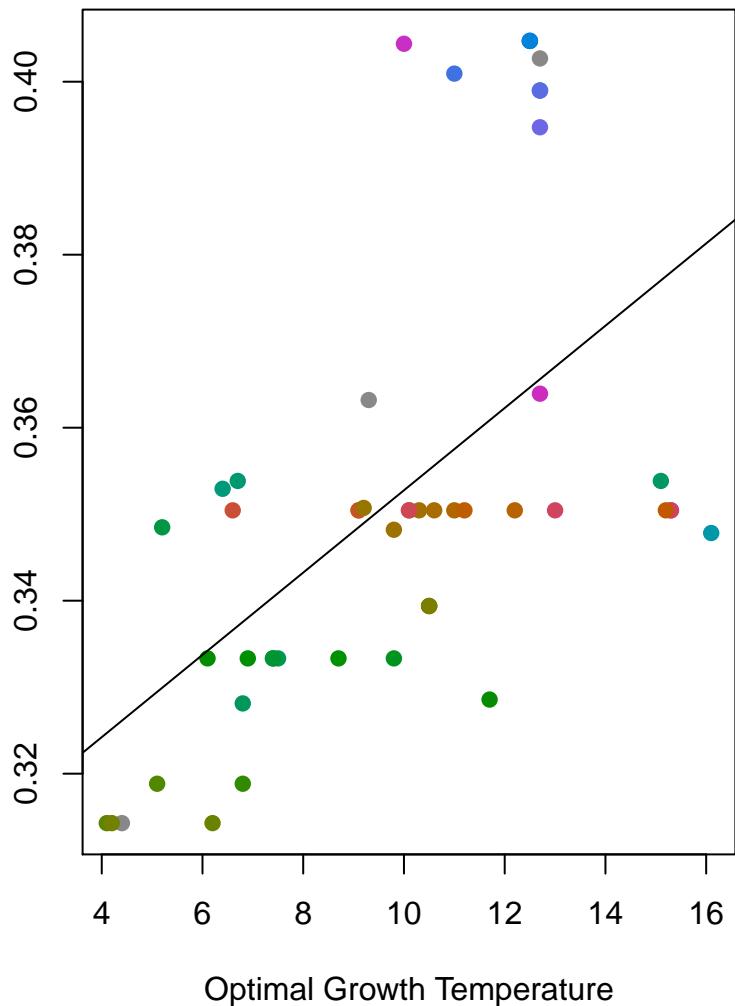


feature.pgfam_id.arg_lys_ratio.mean
PGF_00005384
Flagellar biosynthesis protein FlhA
 $r = 0.574$, $p = 10^{-4.877}$



feature.pgfam_id.arg_lys_ratio.mean
PGF_00018965
Malate synthase G (EC 2.3.3.9)
 $r = 0.565$, $p = 10^{-4.726}$

feature.pgfam_id.arg_lys_ratio.mean

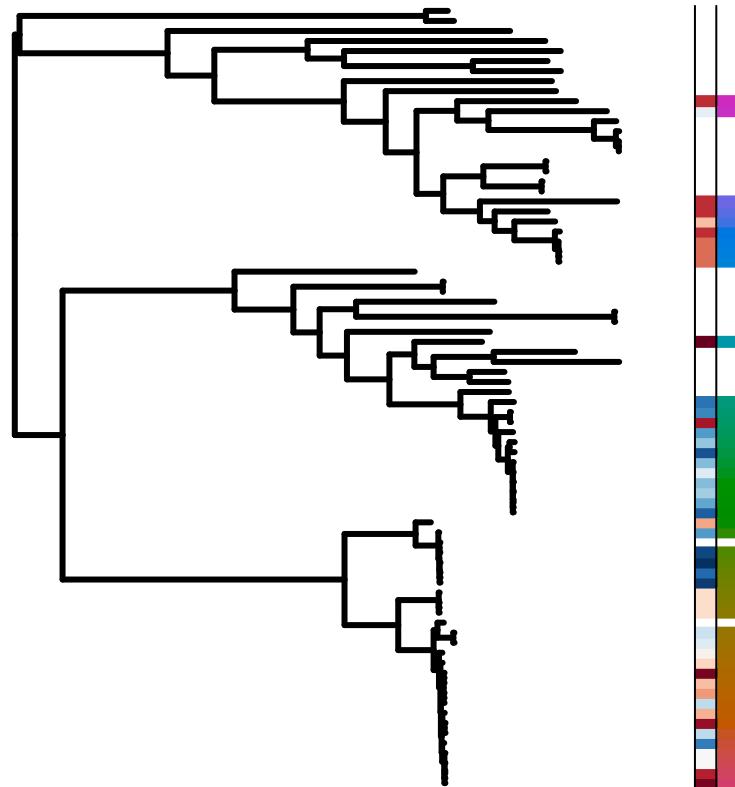
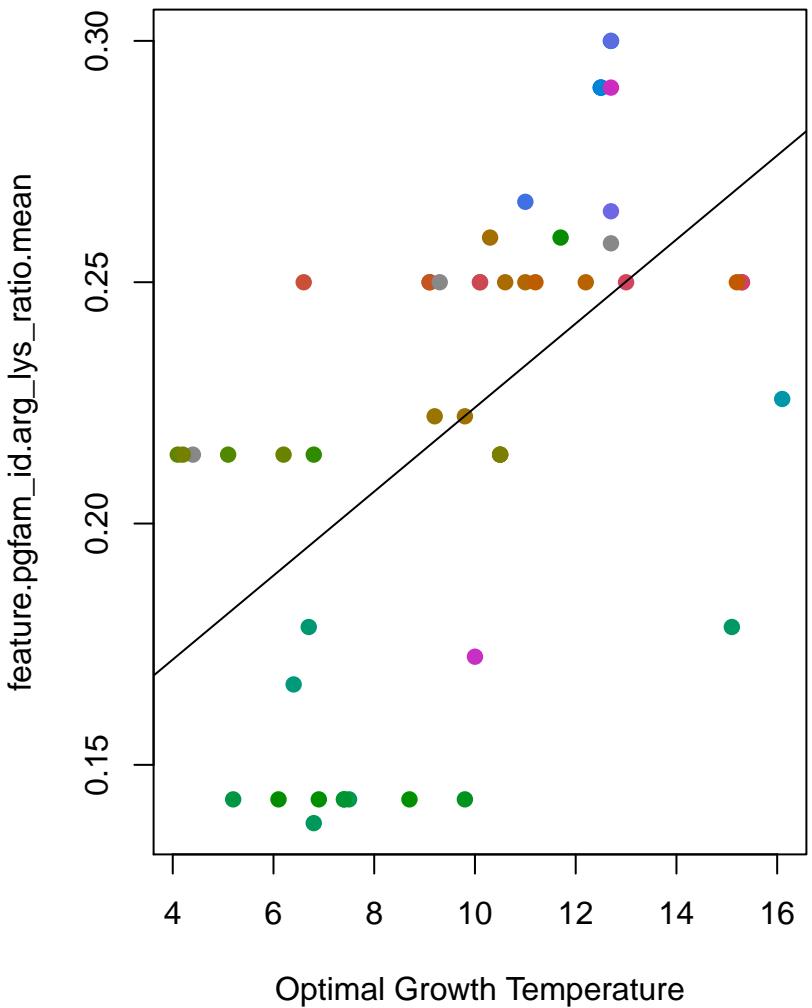


feature.pgfam_id.arg_lyc_ratio.mean

PGF_00025187

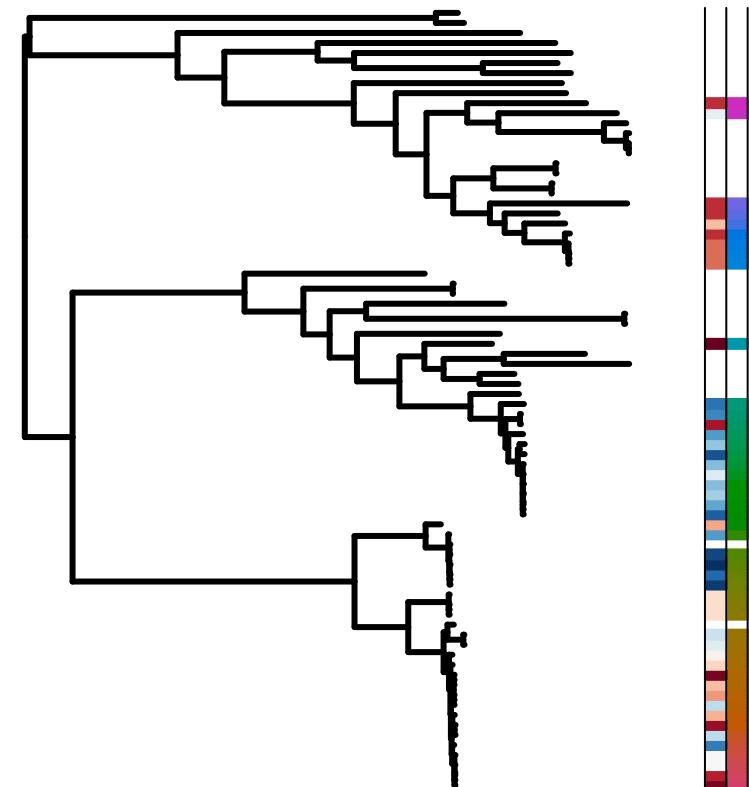
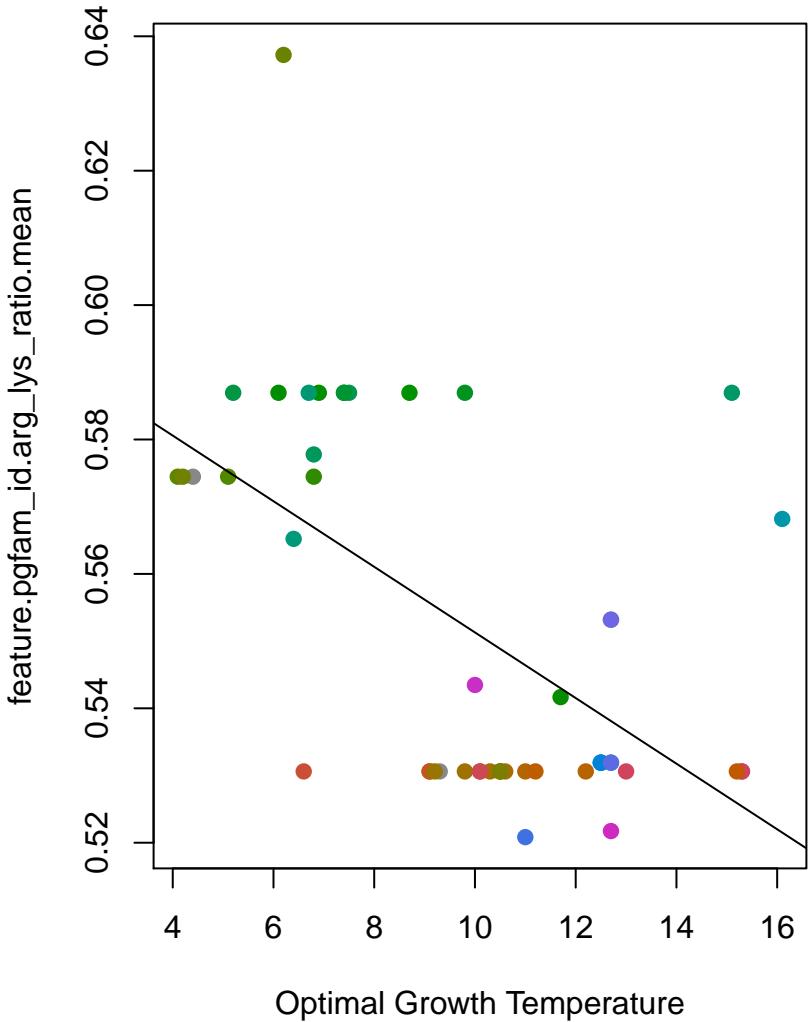
Na⁽⁺⁾-translocating NADH-quinone reductase subunit C (EC 1.6.5.8)

$r = 0.563, p = 10^{-4.684}$



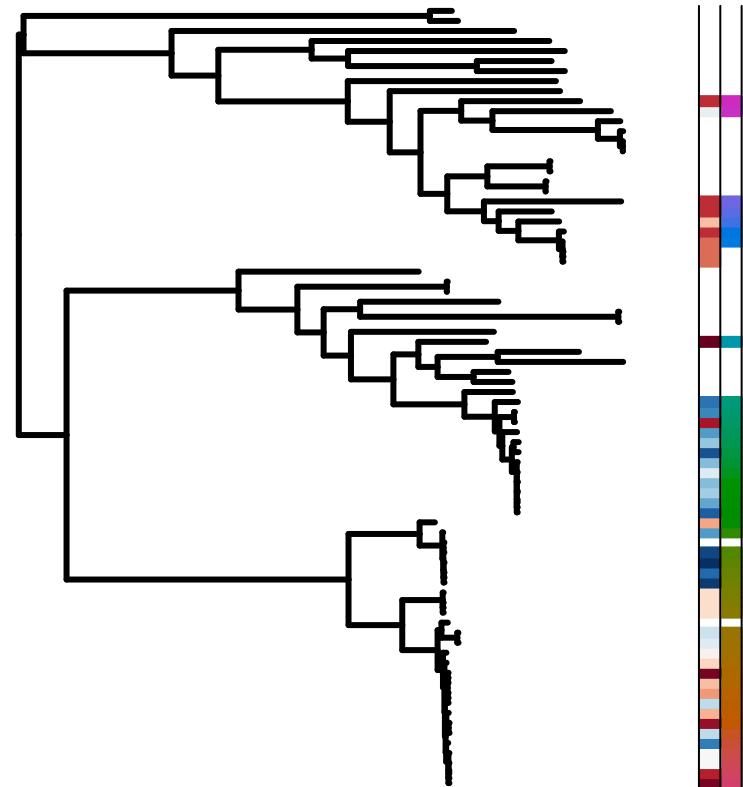
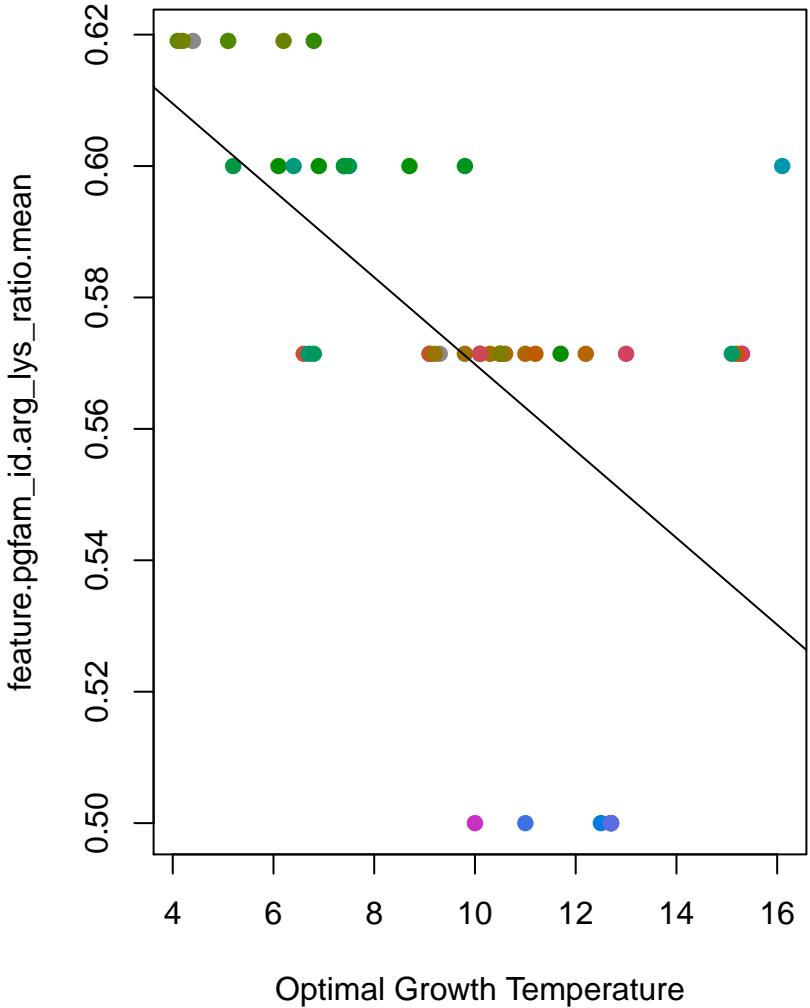
feature.pgfam_id.arg_lys_ratio.mean
PGF_00426236

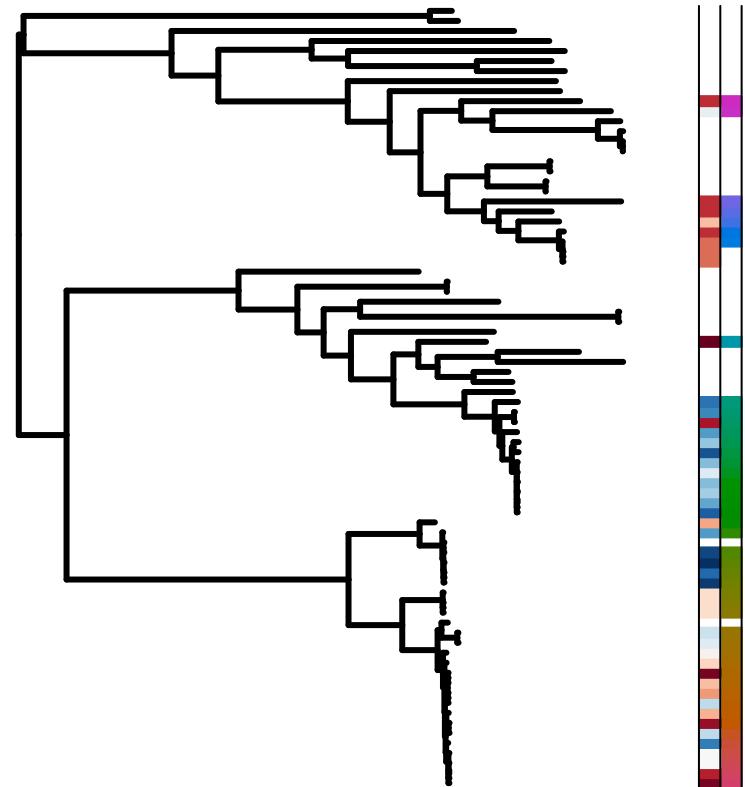
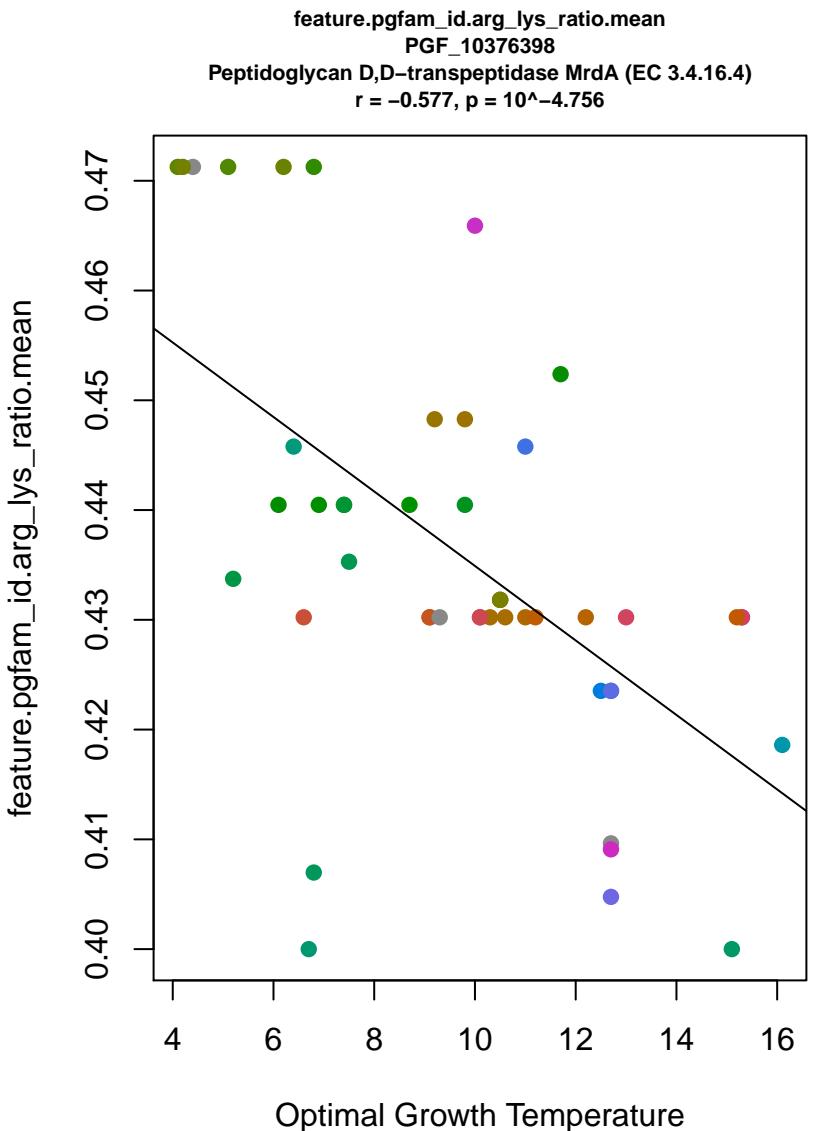
(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase (flavodoxin) (EC 1.17.7.3)
 $r = -0.566, p = 10^{-4.736}$

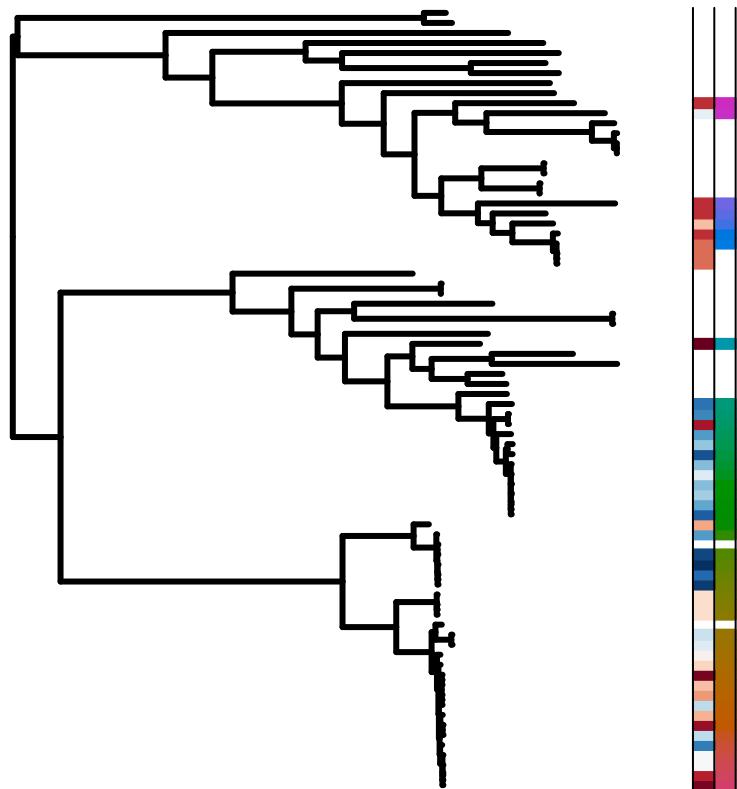
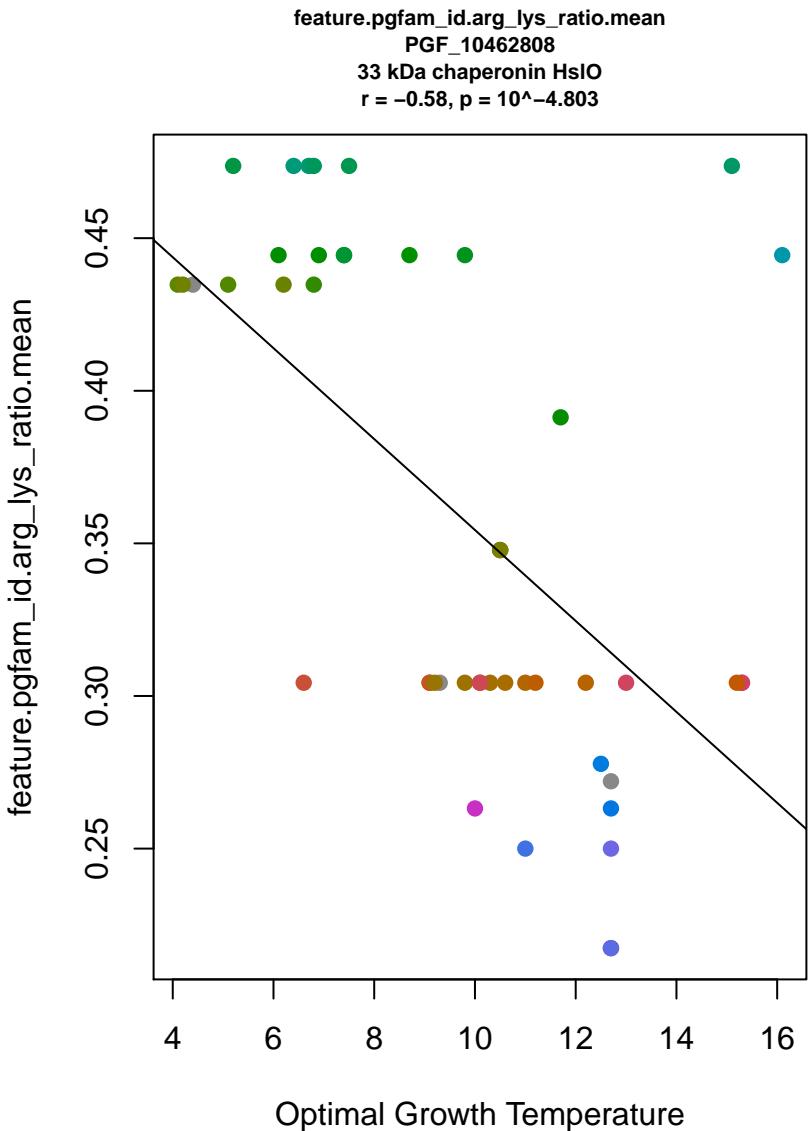


feature.pgfam_id.arg_lys_ratio.mean
PGF_07480521

23S rRNA (pseudouridine(1915)-N(3))-methyltransferase (EC 2.1.1.177)
 $r = -0.575, p = 10^{-4.722}$

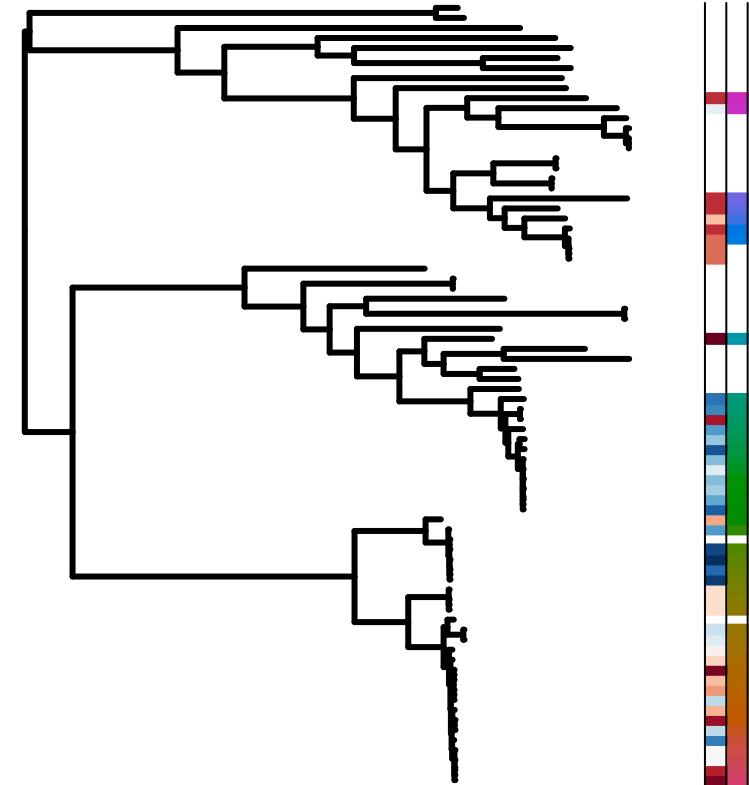
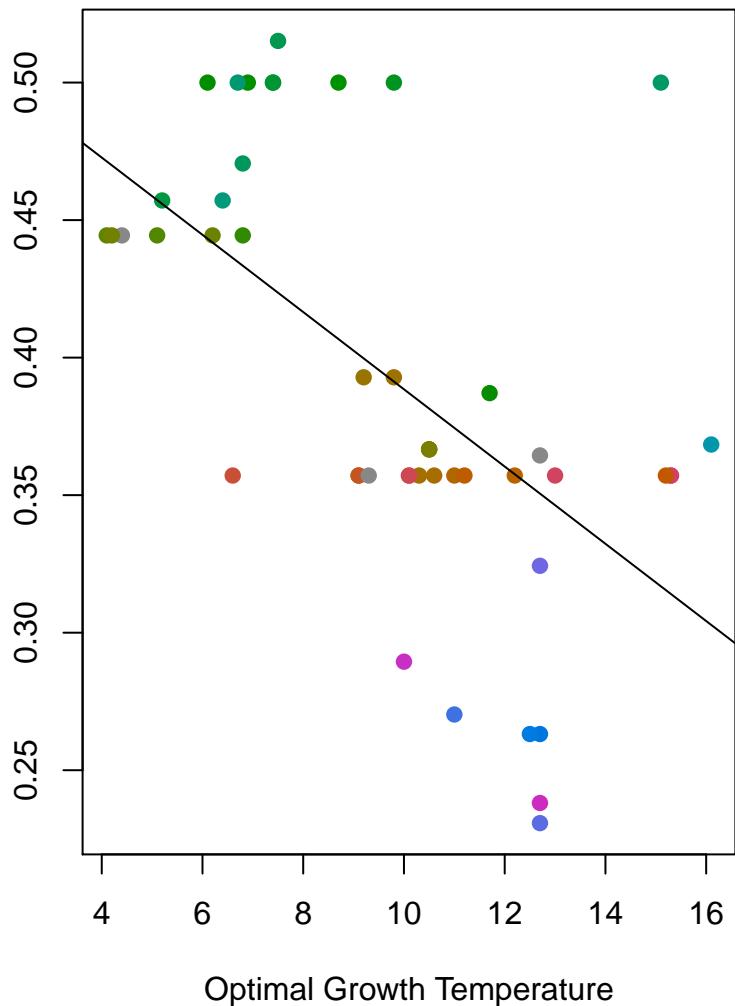


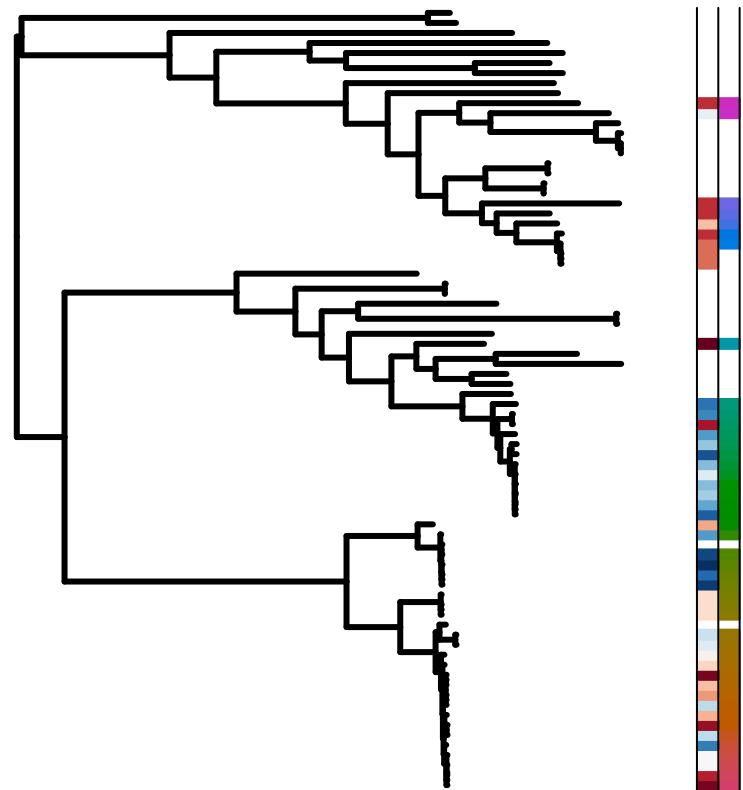
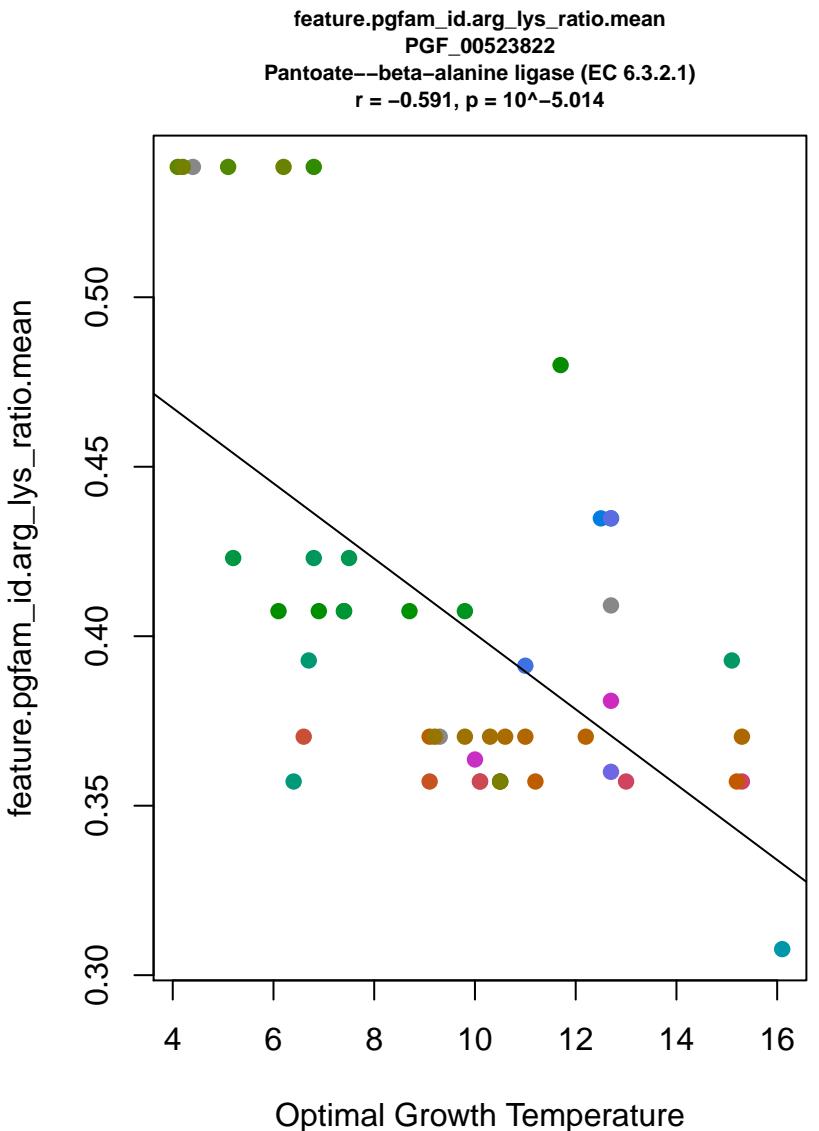




feature.pgfam_id.arg_lys_ratio.mean
PGF_09566238
Septum-associated rare lipoprotein A
 $r = -0.584$, $p = 10^{-4.884}$

feature.pgfam_id.arg_lys_ratio.mean





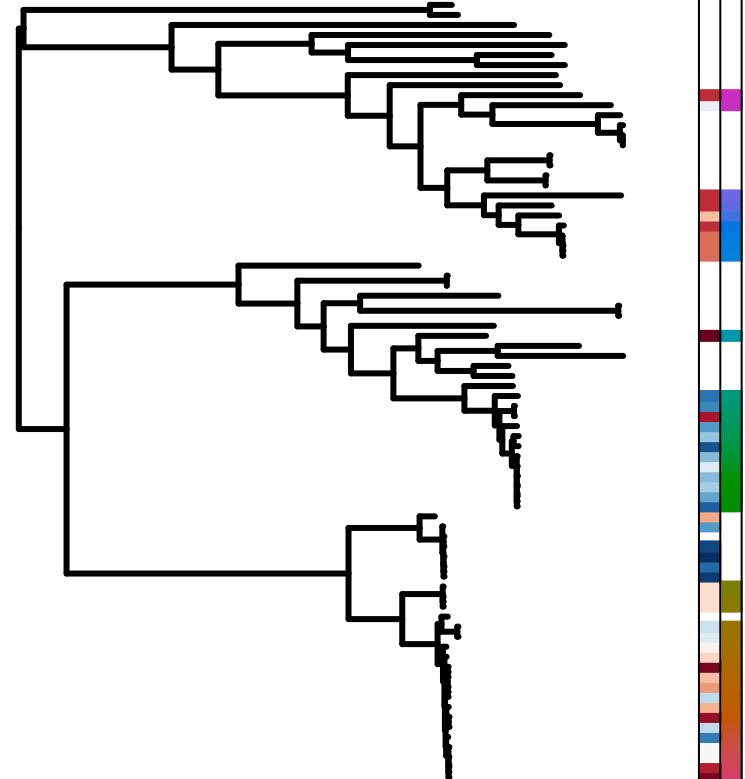
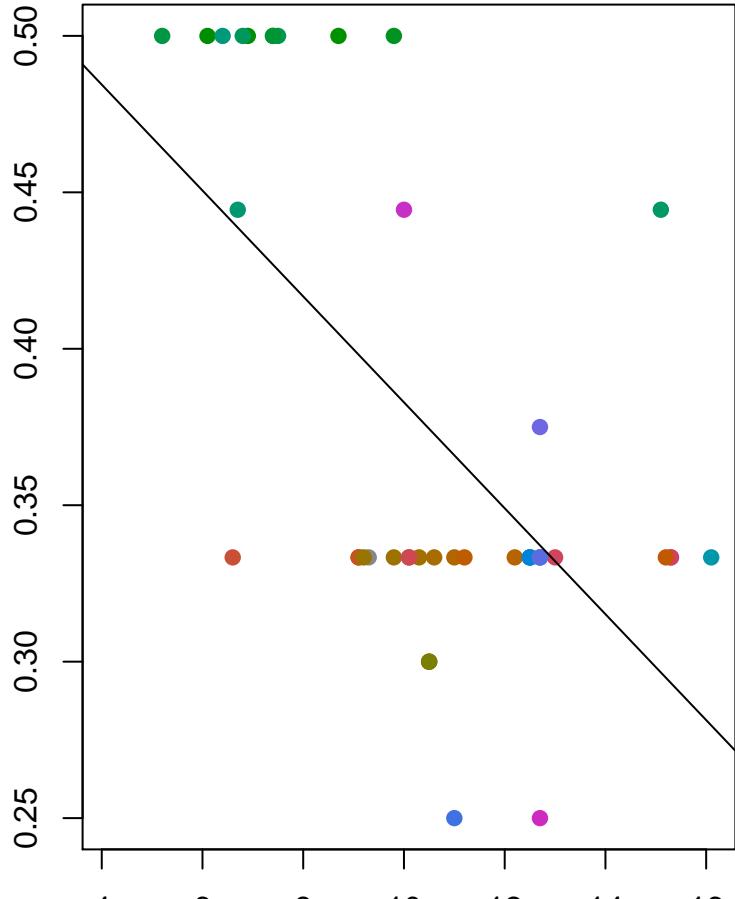
feature.pgfam_id.arg_lys_ratio.mean

PGF_00413243

tRNA 5-methylaminomethyl-2-thiouridine synthase subunit TusC

$r = -0.6, p = 10^{-4.68}$

feature.pgfam_id.arg_lys_ratio.mean



Optimal Growth Temperature

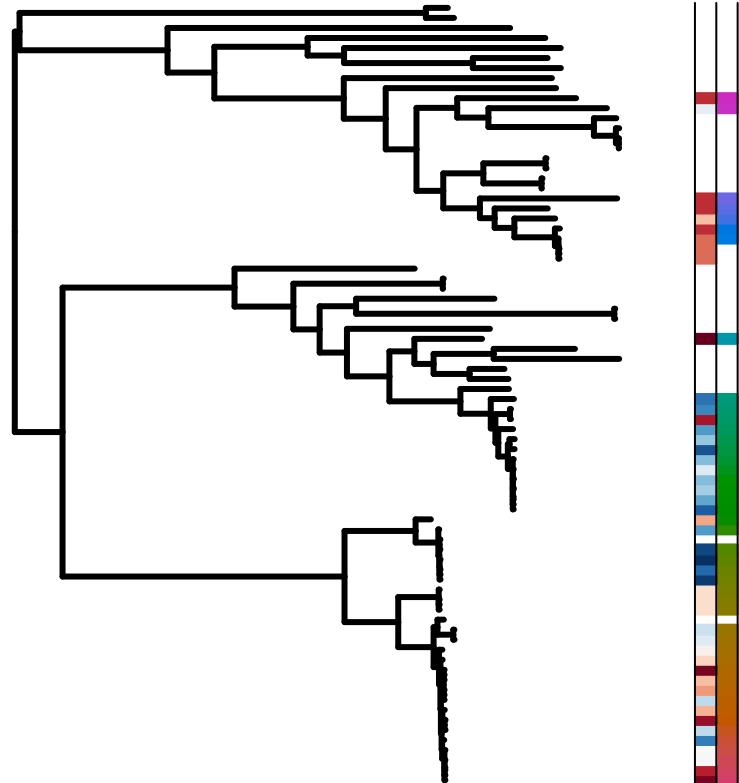
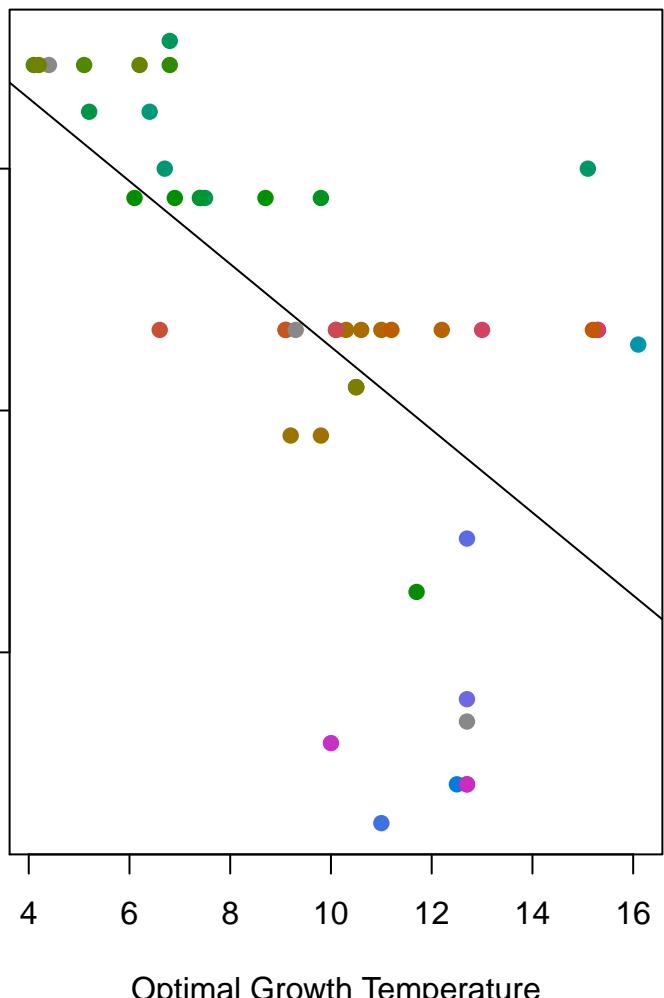
feature.pgfam_id.arg_lys_ratio.mean

PGF_10414515

Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)

$r = -0.603, p = 10^{-5.236}$

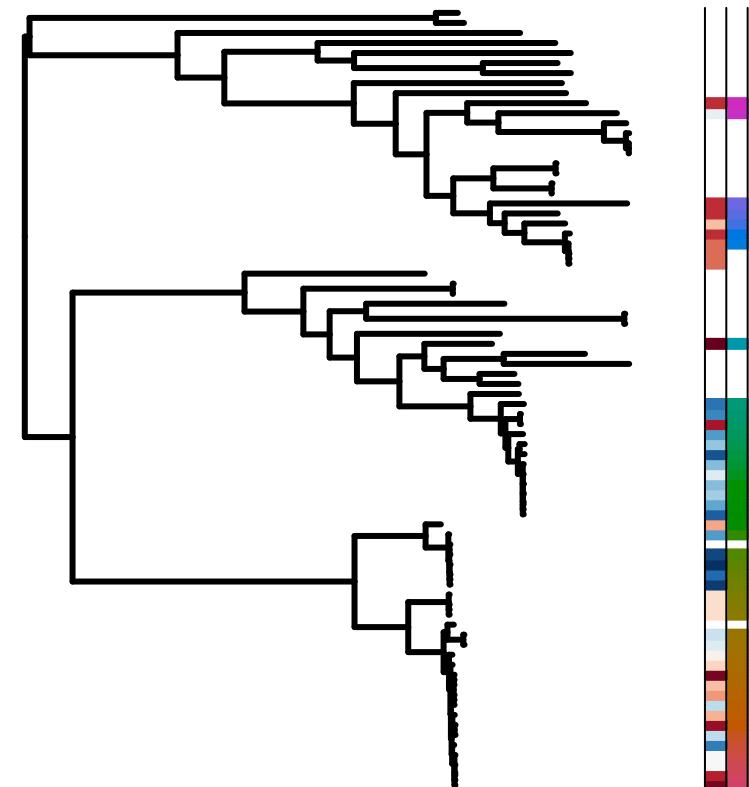
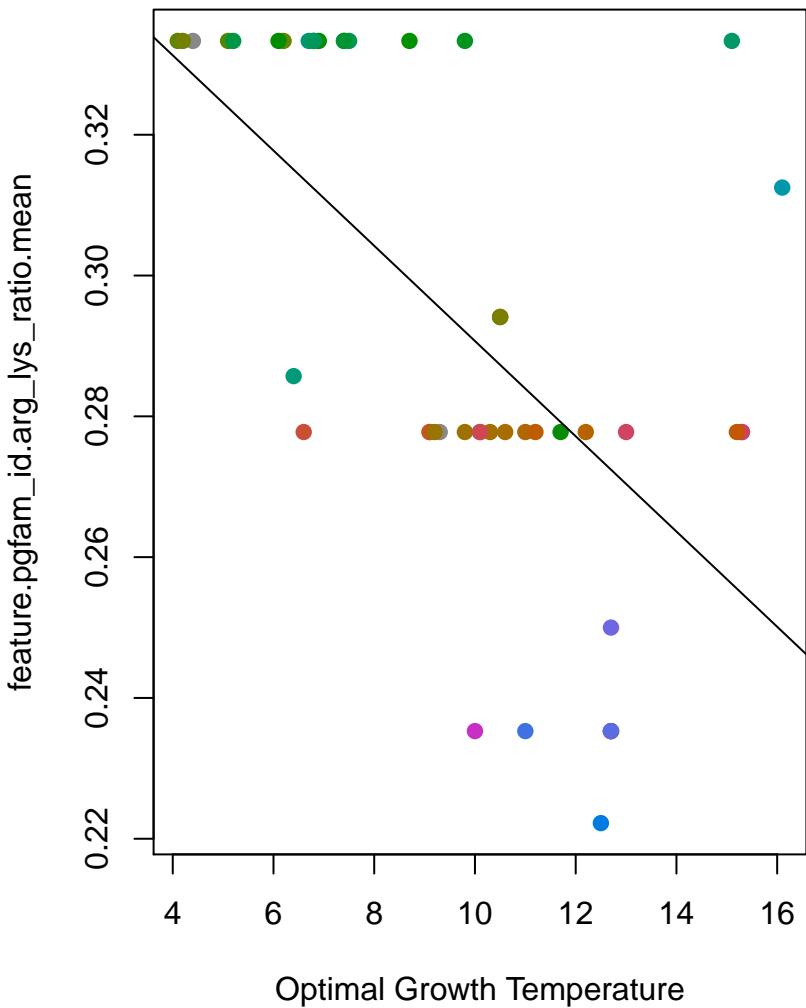
feature.pgfam_id.arg_lys_ratio.mean

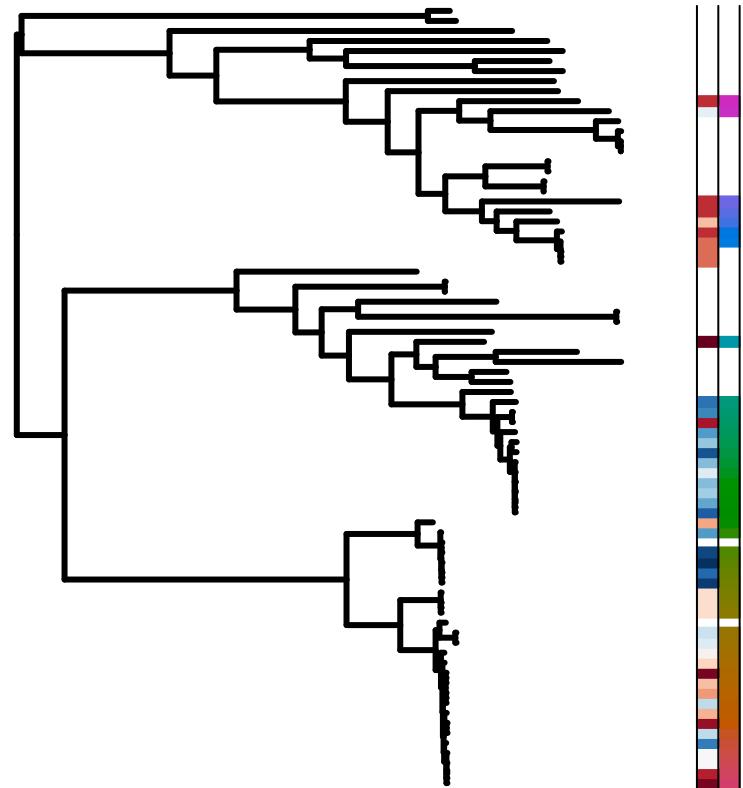
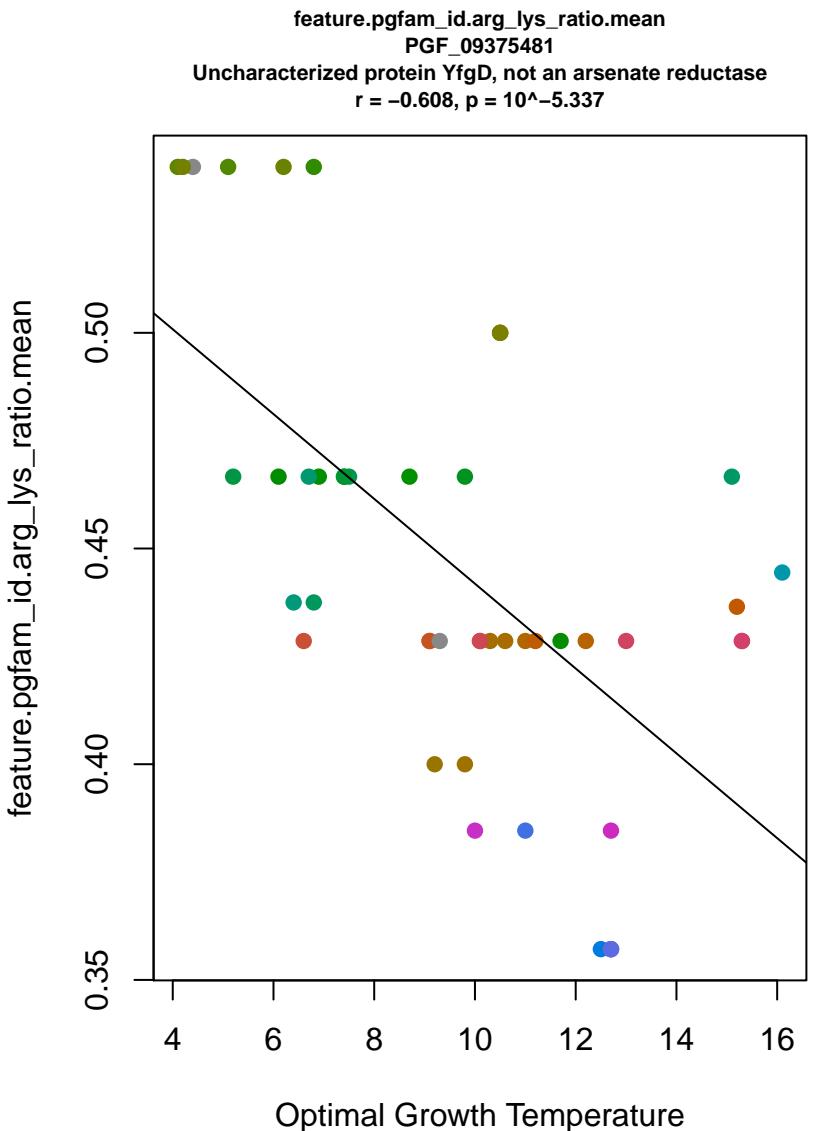


feature.pgfam_id.arg_lys_ratio.mean

PGF_02658061

phoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.
 $r = -0.606, p = 10^{-5.299}$





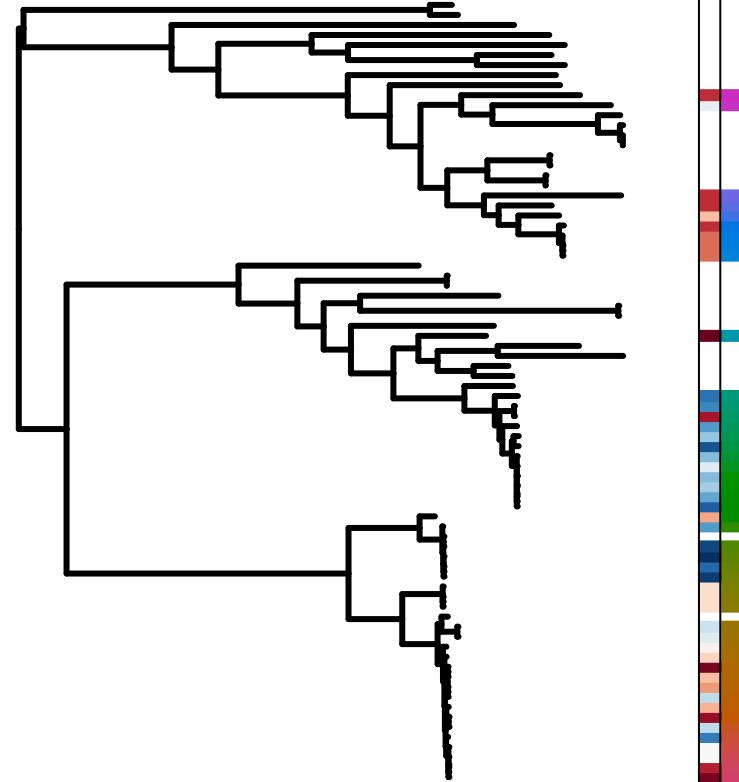
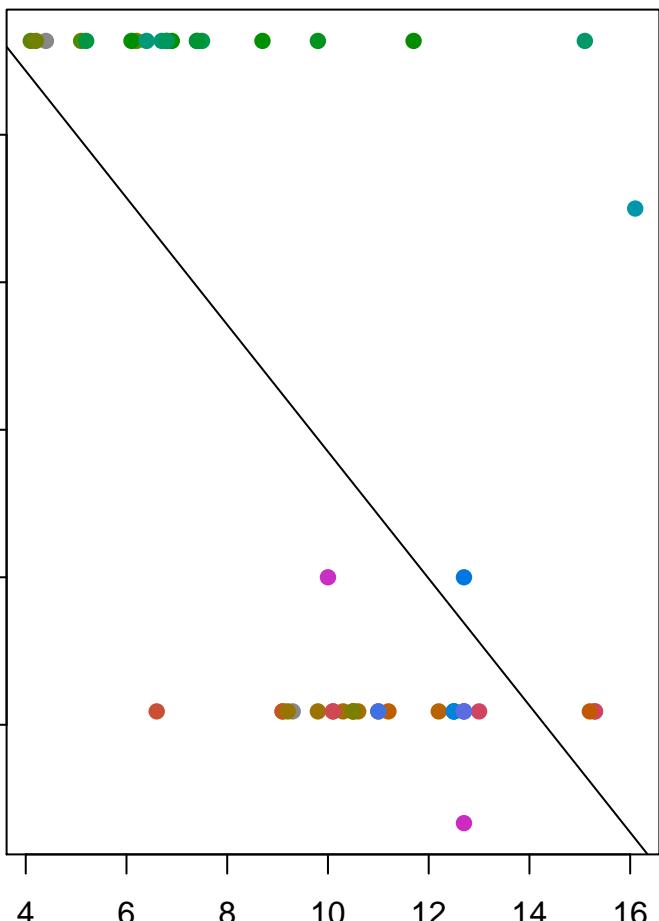
feature.pgfam_id.arg_lys_ratio.mean

PGF_02744871

Flagellar hook–basal body complex protein FliE

$r = -0.612$, $p = 10^{-5.633}$

feature.pgfam_id.arg_lys_ratio.mean



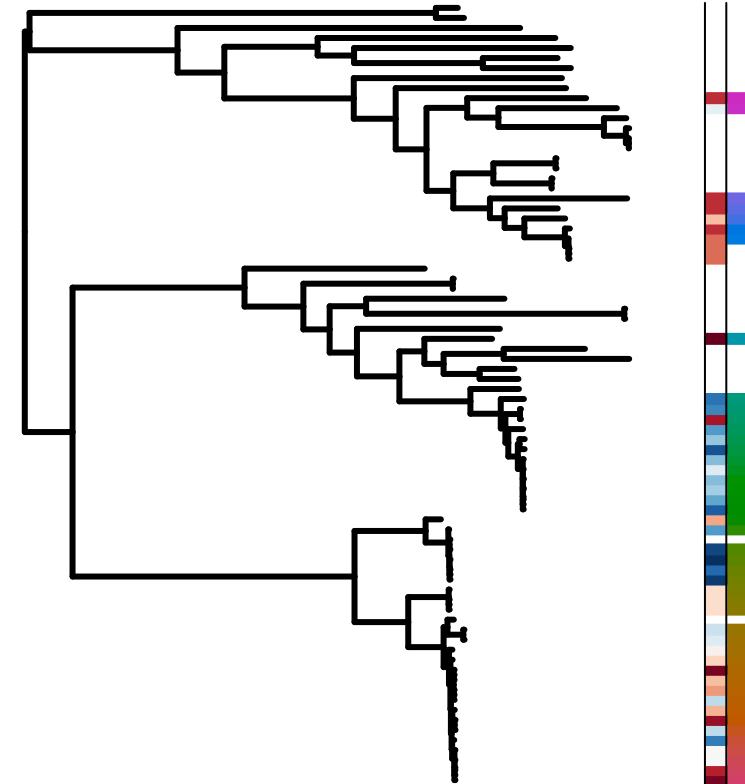
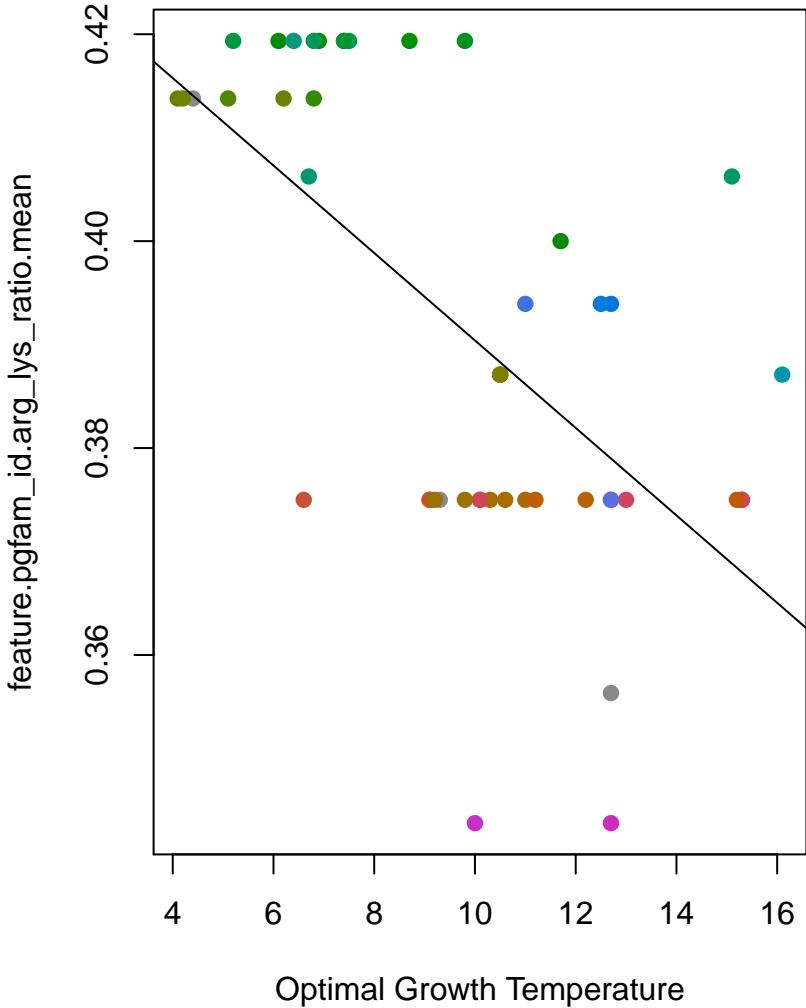
Optimal Growth Temperature

feature.pgfam_id.arg_lyc_ratio.mean

PGF_03237586

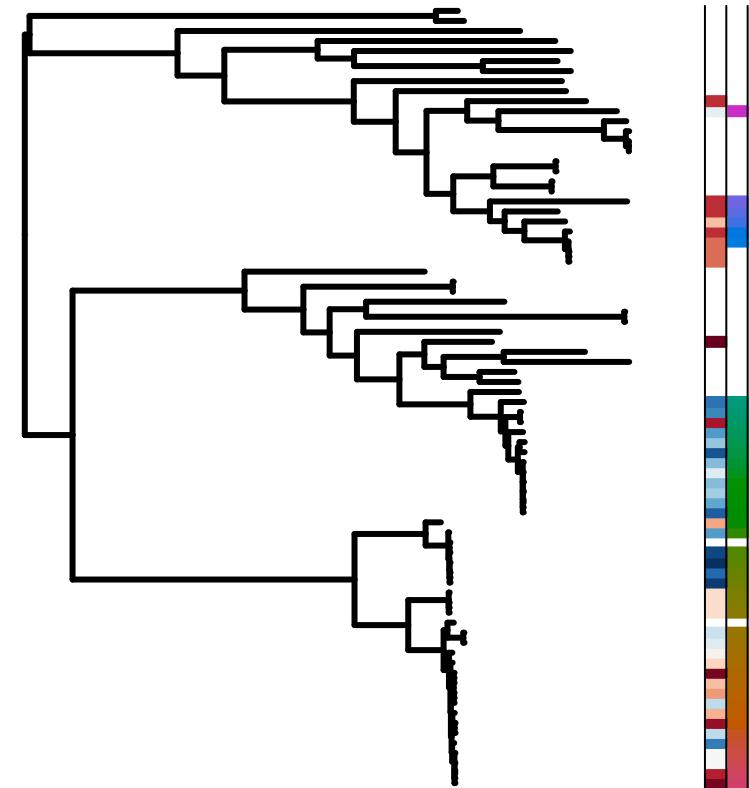
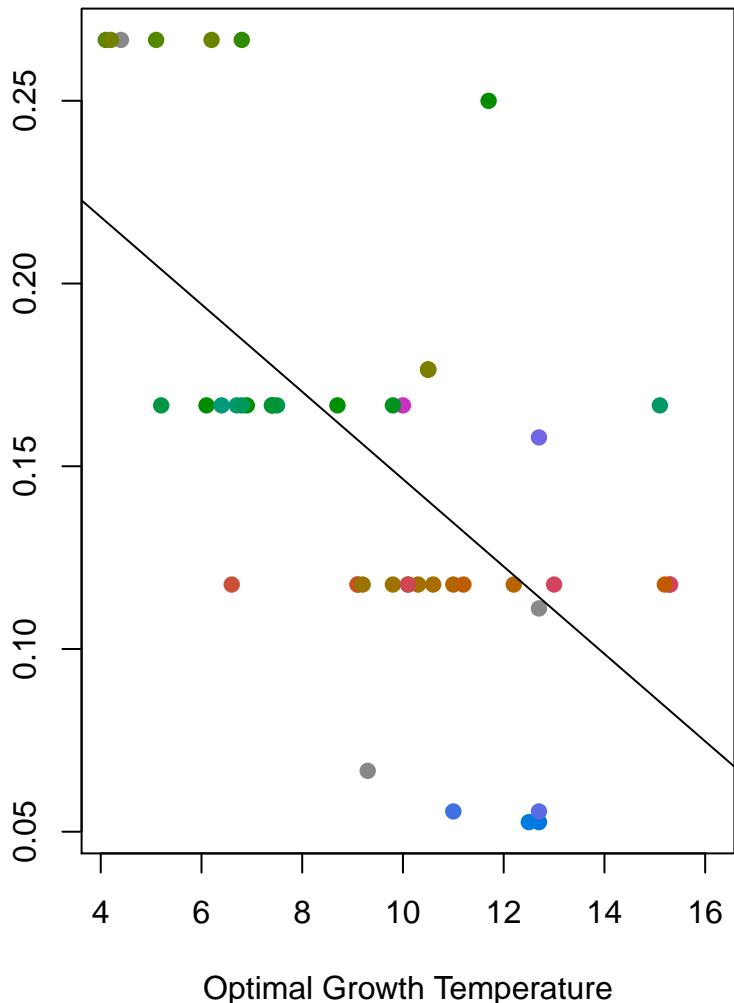
L-threonine 3-dehydrogenase (EC 1.1.1.103)

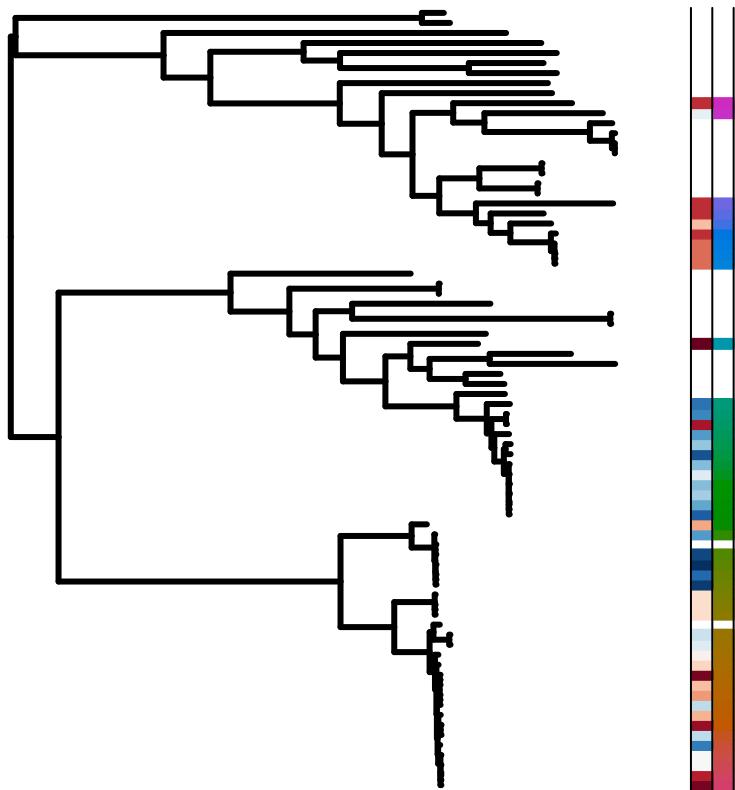
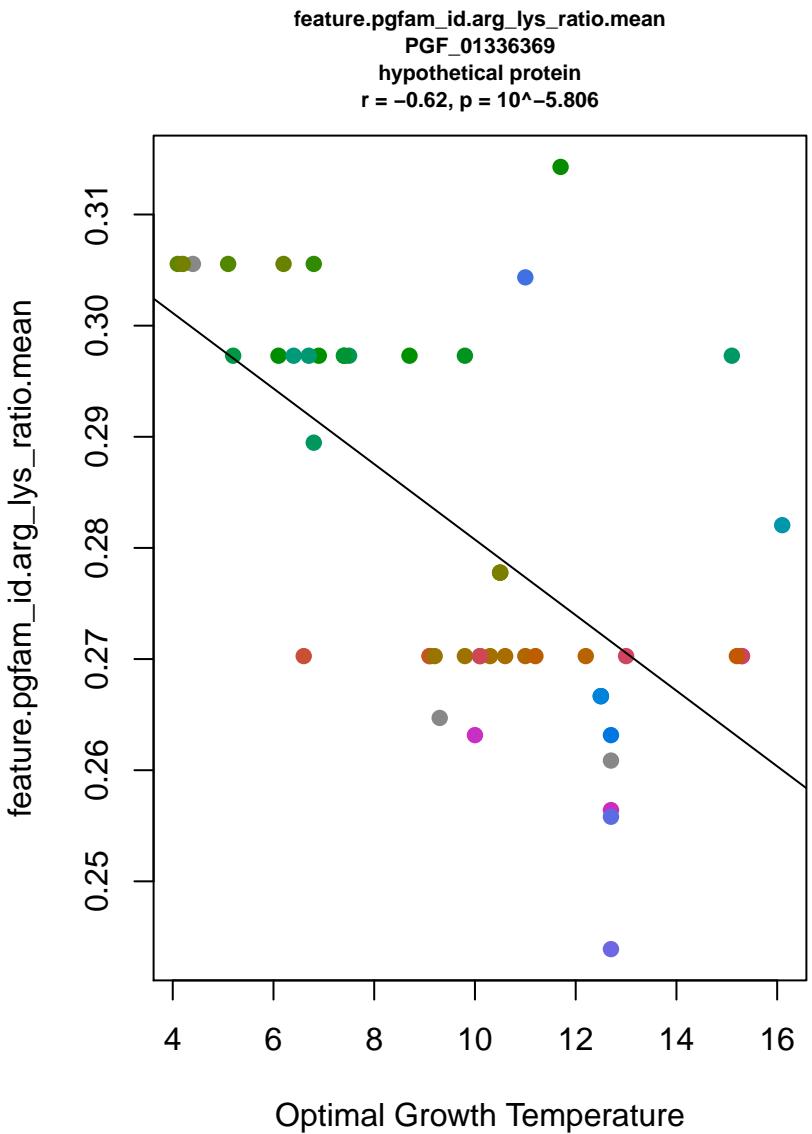
$r = -0.616$, $p = 10^{-5.503}$



feature.pgfam_id.arg_lys_ratio.mean
PGF_08252890
hypothetical protein
 $r = -0.616$, $p = 10^{-5.291}$

feature.pgfam_id.arg_lys_ratio.mean



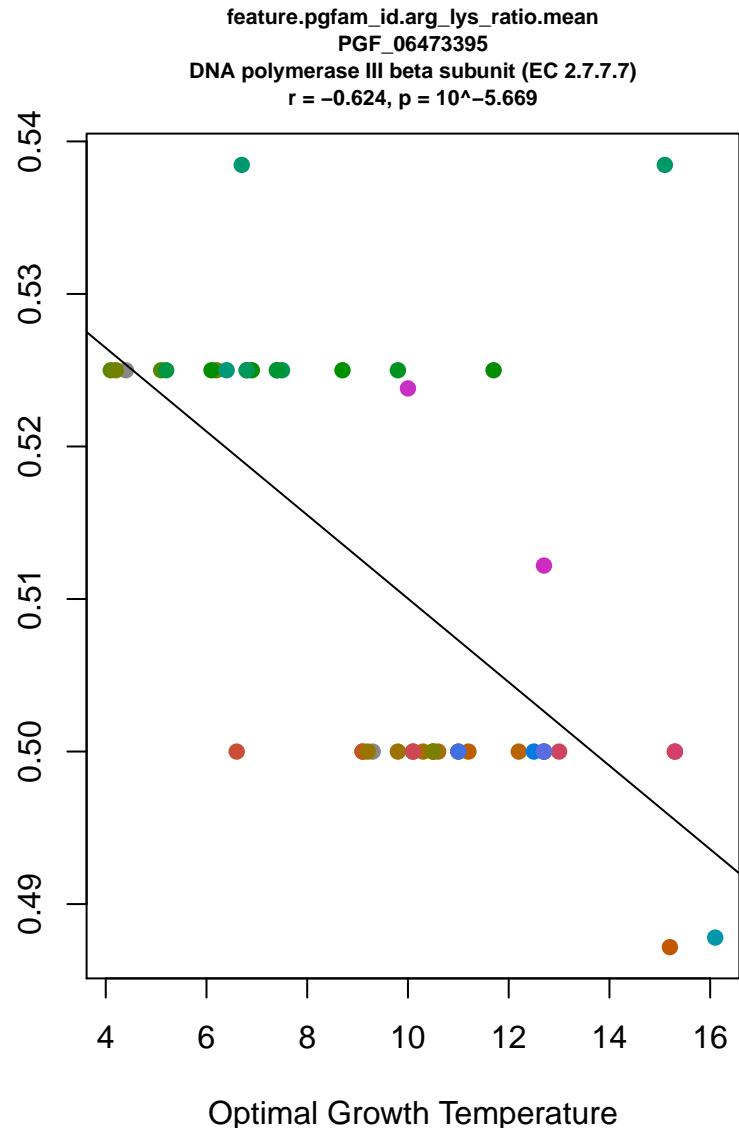
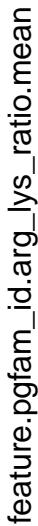


feature.pgfam_id.arg_lyc_ratio.mean

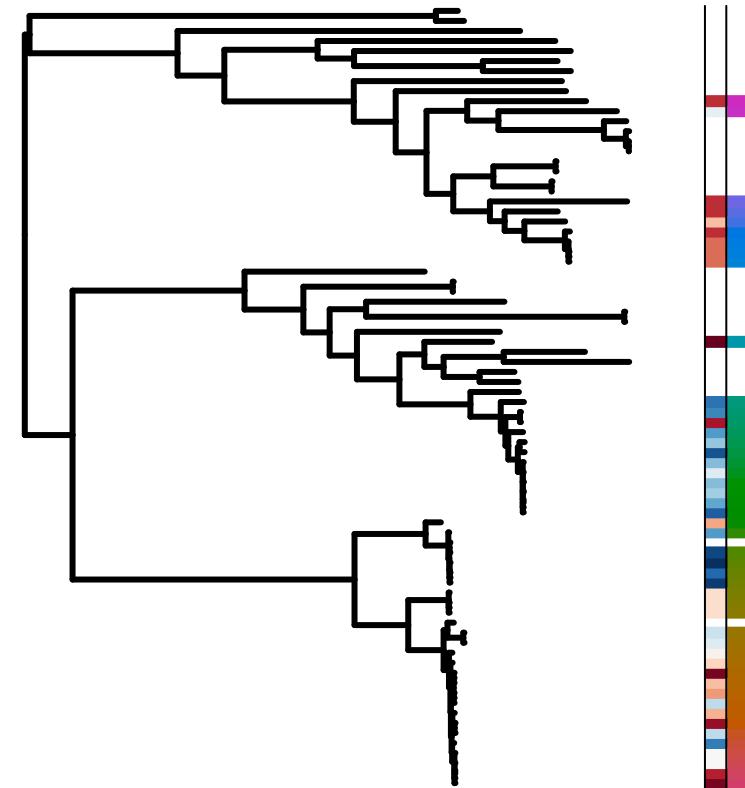
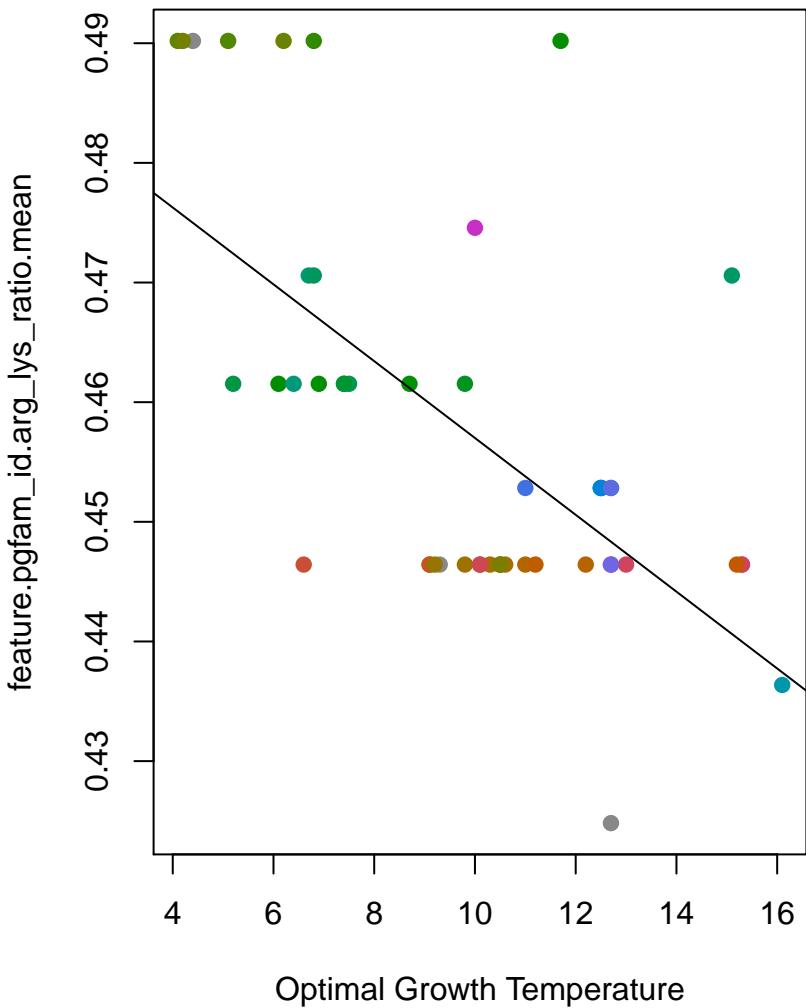
PGF_06473395

DNA polymerase III beta subunit (EC 2.7.7.7)

$r = -0.624$, $p = 10^{-5.669}$

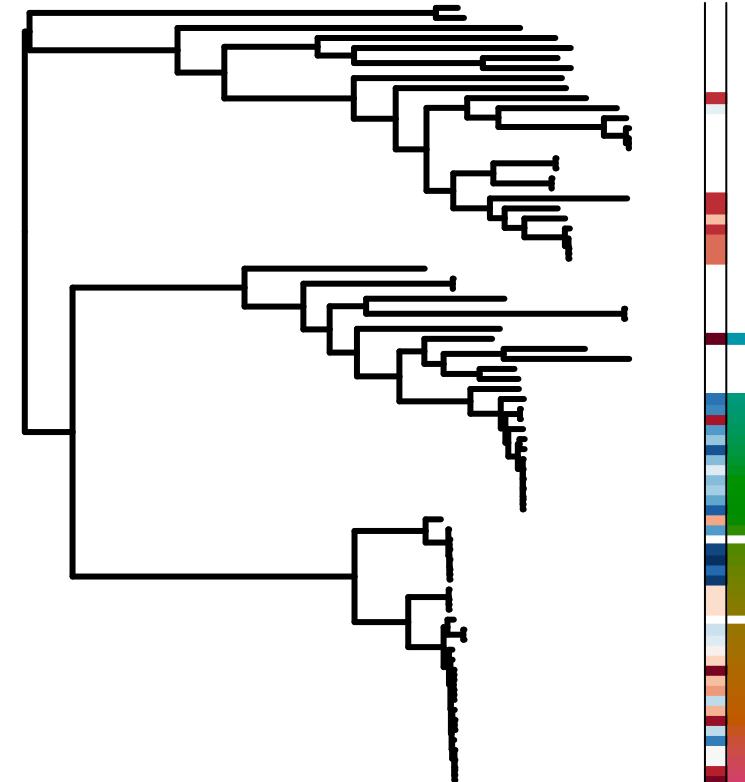
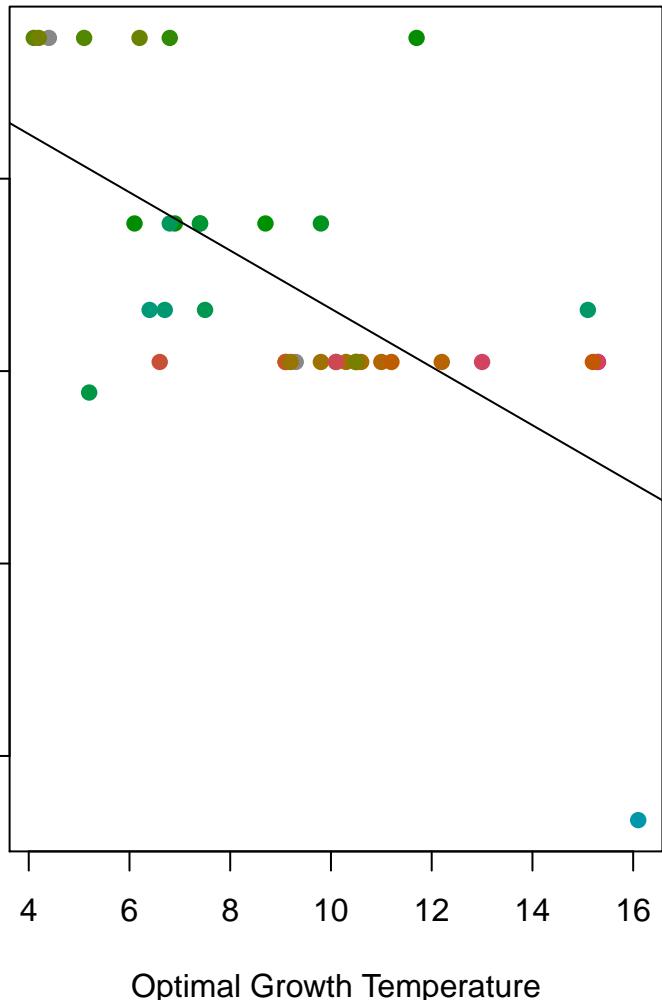


feature.pgfam_id.arg_lys_ratio.mean
PGF_00015709
Isocitrate lyase (EC 4.1.3.1)
 $r = -0.628$, $p = 10^{-5.974}$



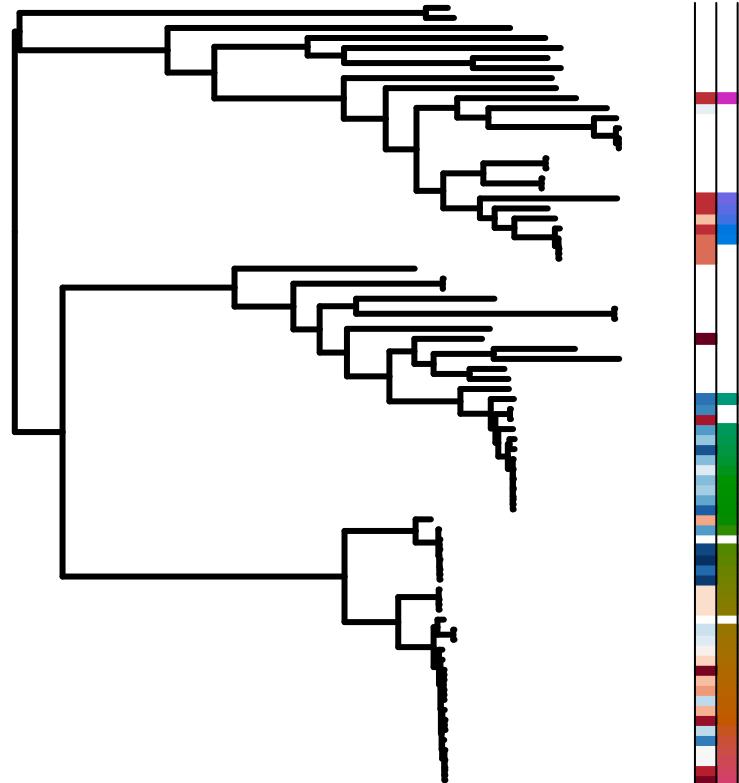
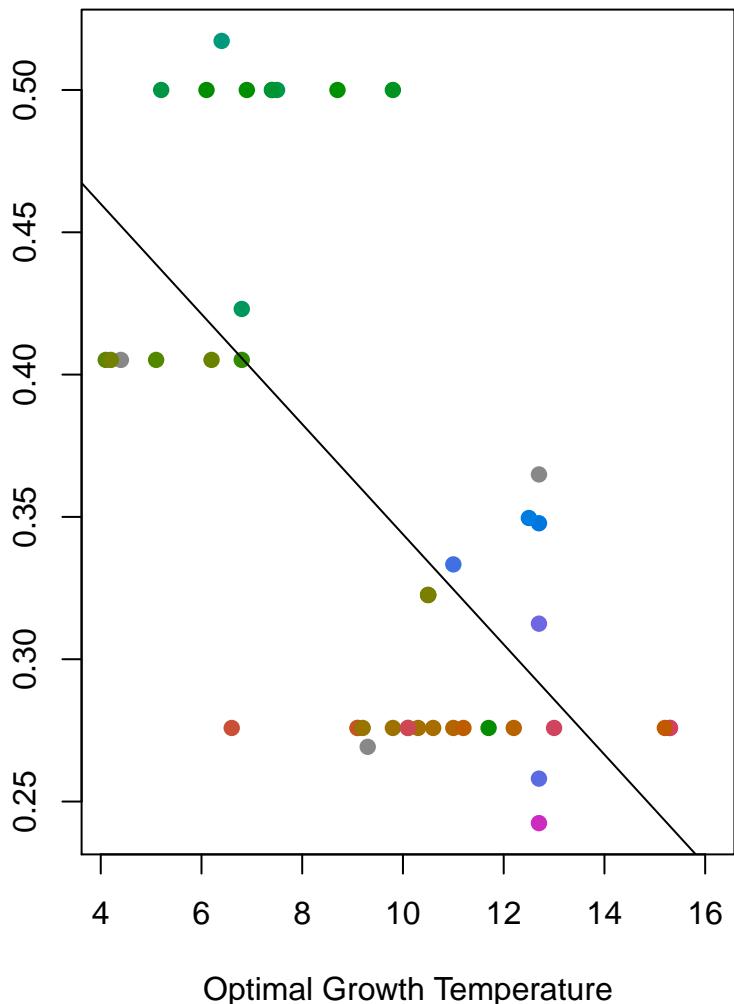
feature.pgfam_id.arg_lys_ratio.mean
PGF_12012739
hypothetical protein
 $r = -0.633, p = 10^{-4.936}$

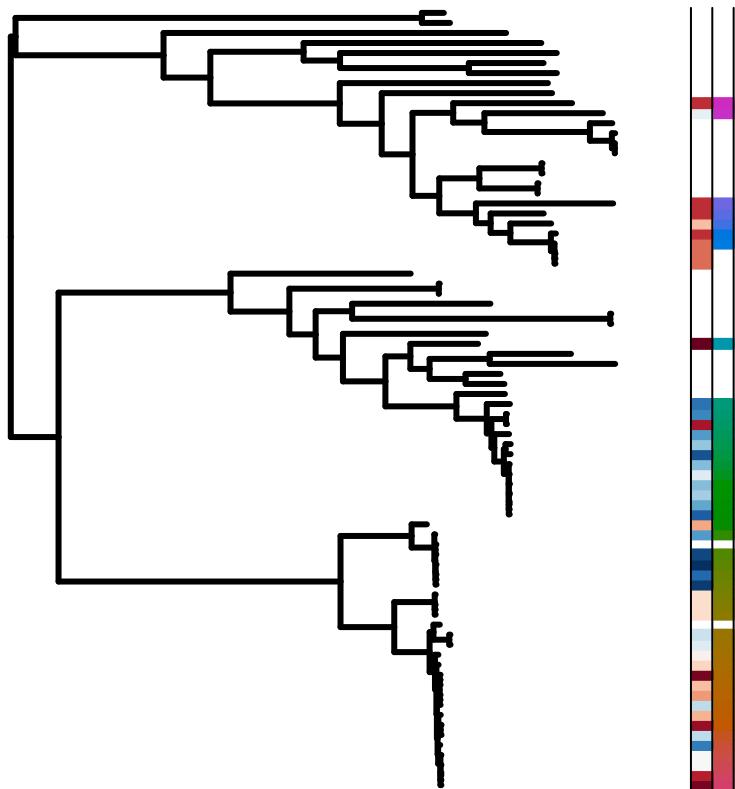
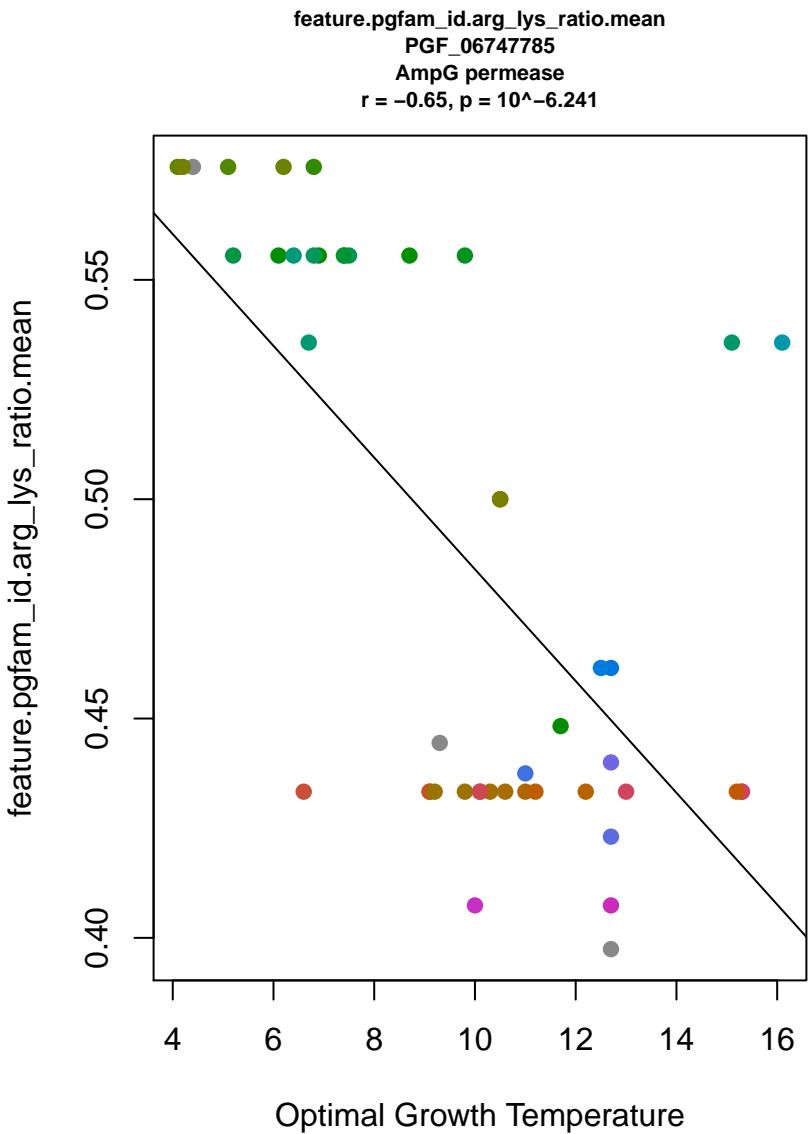
feature.pgfam_id.arg_lys_ratio.mean



feature.pgfam_id.arg_lys_ratio.mean
PGF_12669666
FIG006045: Sigma factor, ECF subfamily
 $r = -0.644$, $p = 10^{-5.624}$

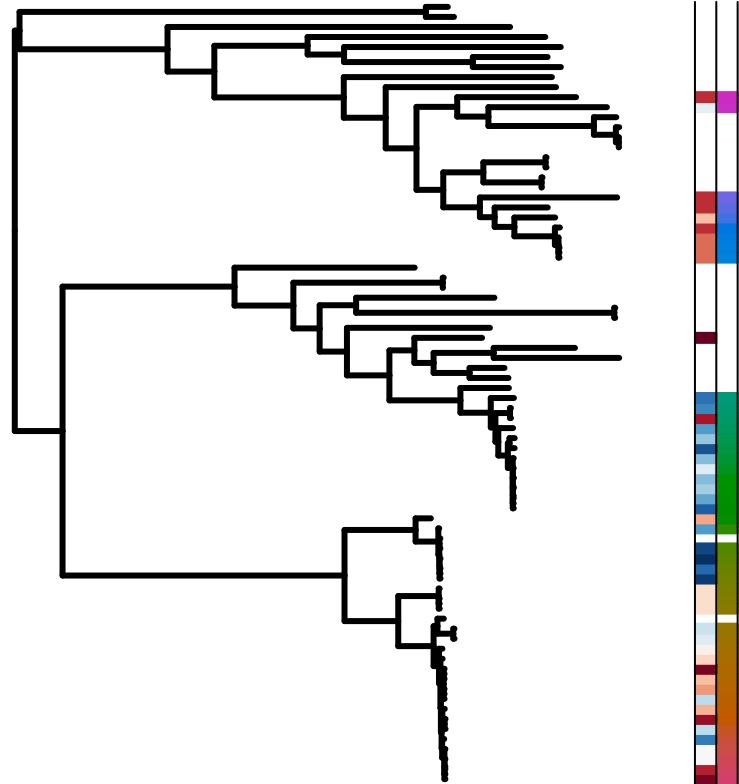
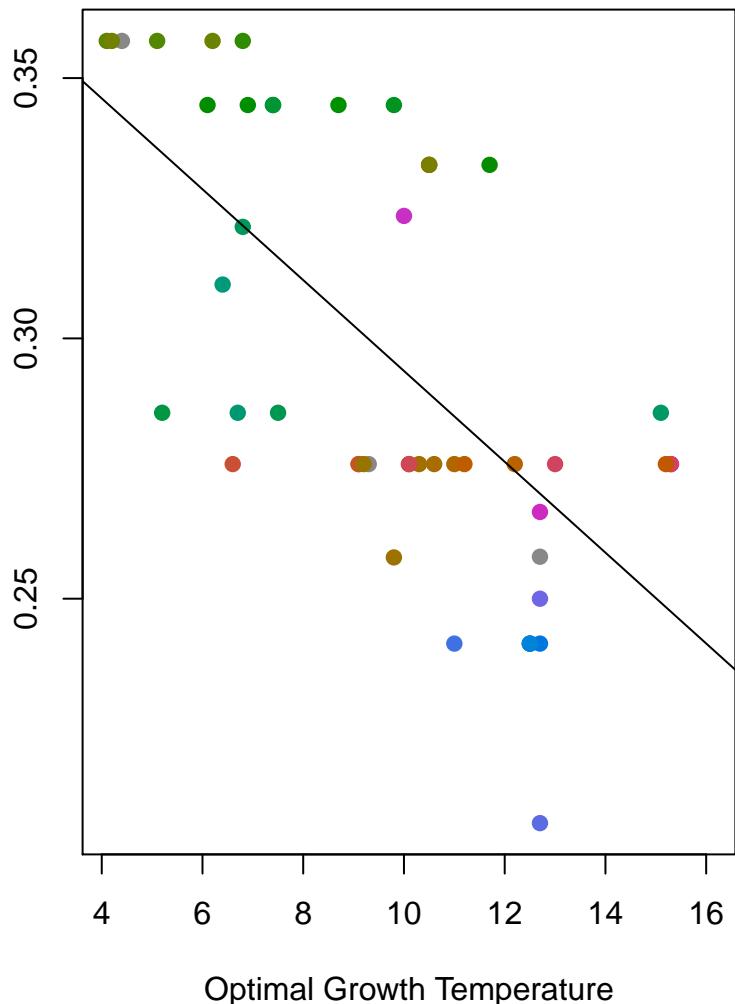
feature.pgfam_id.arg_lys_ratio.mean





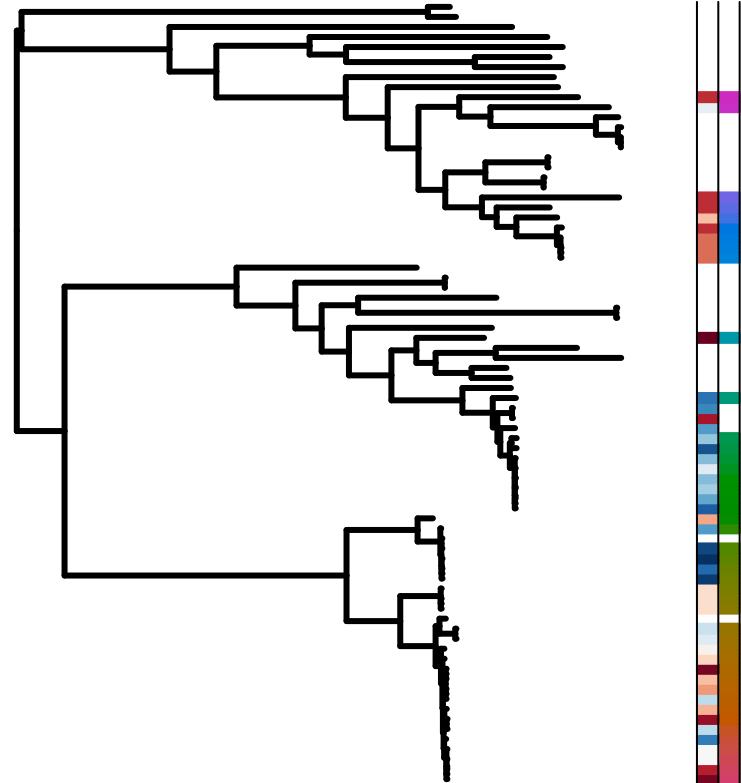
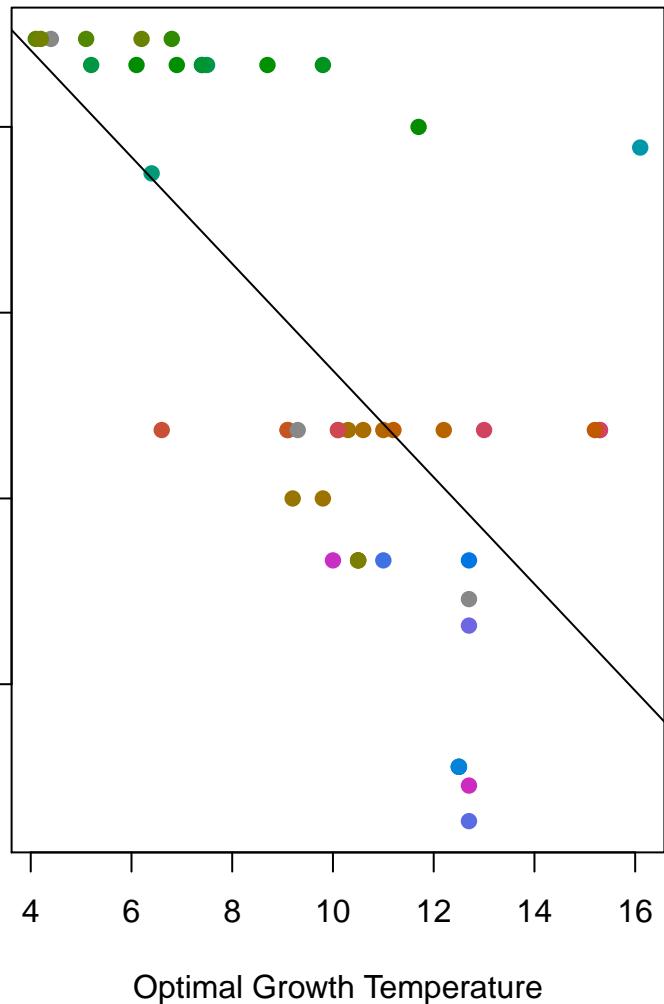
feature.pgfam_id.arg_lys_ratio.mean
PGF_00343871
hypothetical protein
 $r = -0.655, p = 10^{-6.492}$

feature.pgfam_id.arg_lys_ratio.mean



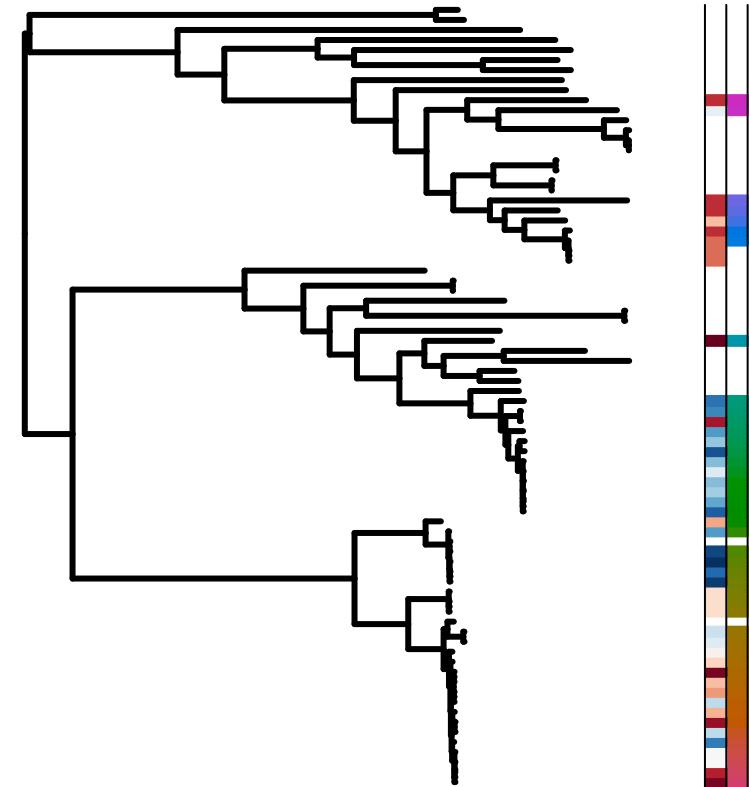
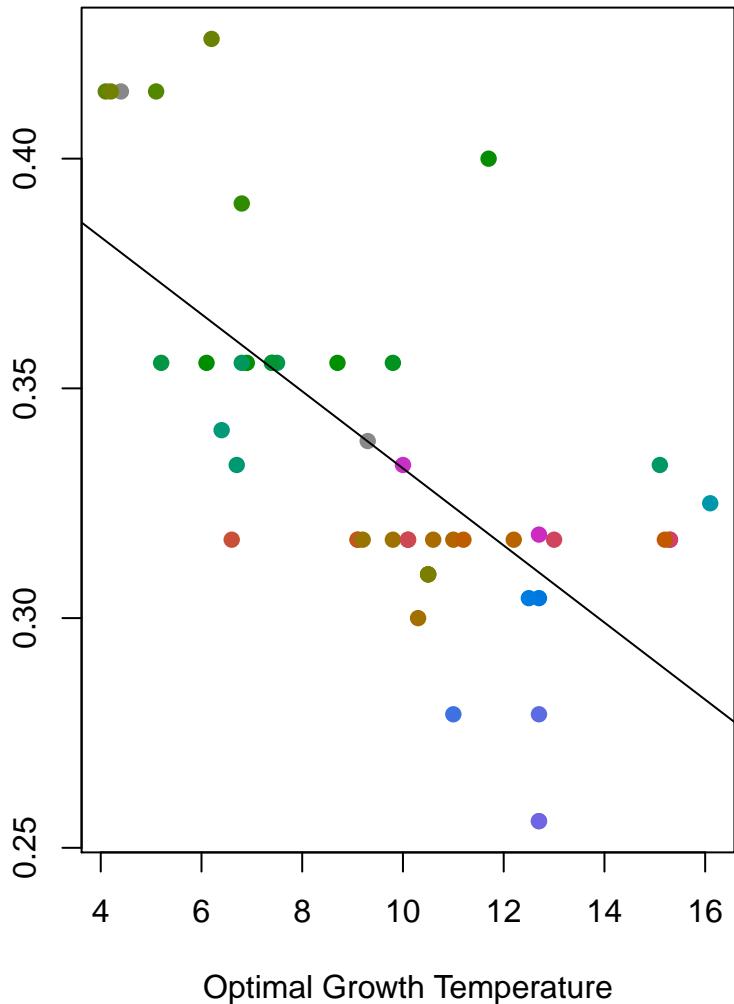
feature.pgfam_id.arg_lys_ratio.mean
PGF_00035421
Potential queD like 2
 $r = -0.668$, $p = 10^{-6.541}$

feature.pgfam_id.arg_lys_ratio.mean



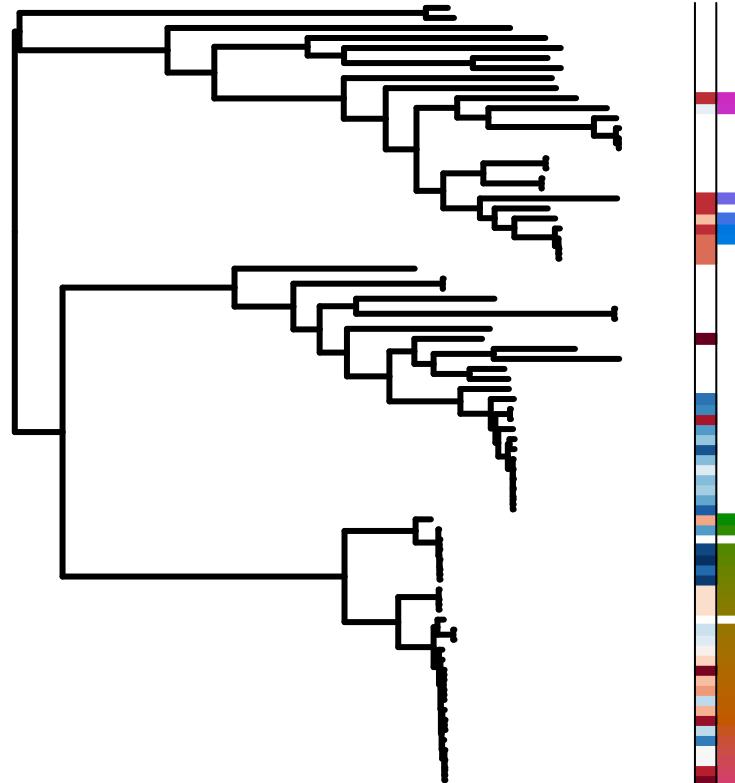
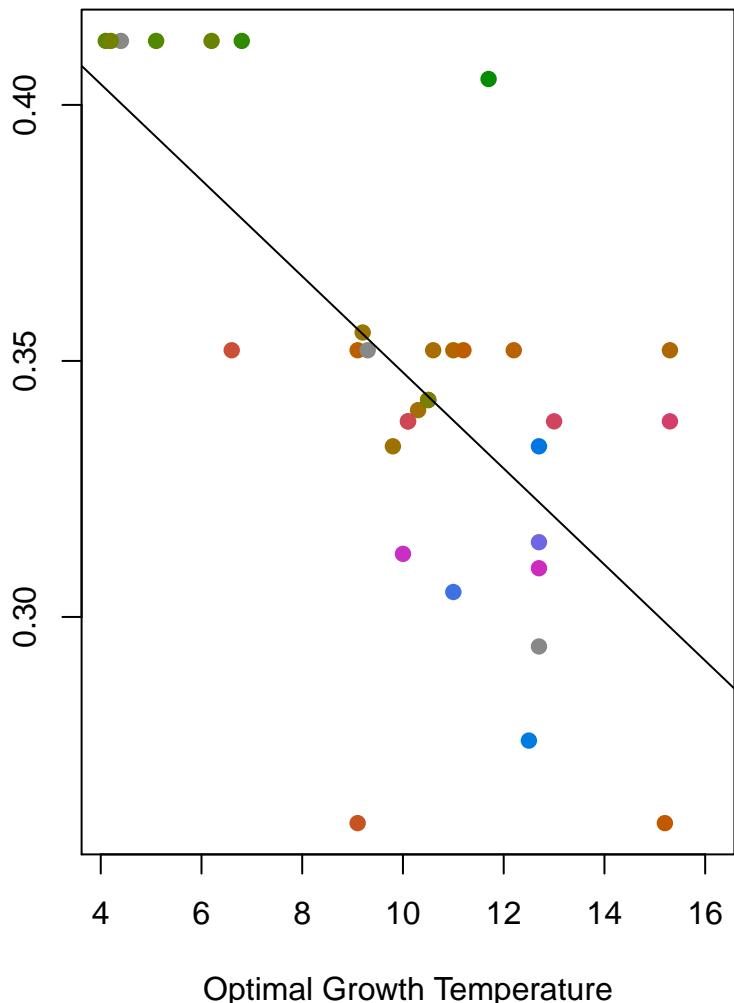
feature.pgfam_id.arg_lys_ratio.mean
PGF_06606669
Alanine transaminase (EC 2.6.1.2)
 $r = -0.672$, $p = 10^{-6.776}$

feature.pgfam_id.arg_lys_ratio.mean



feature.pgfam_id.arg_lys_ratio.mean
PGF_07356637
Prolyl oligopeptidase family protein
 $r = -0.673$, $p = 10^{-4.891}$

feature.pgfam_id.arg_lys_ratio.mean



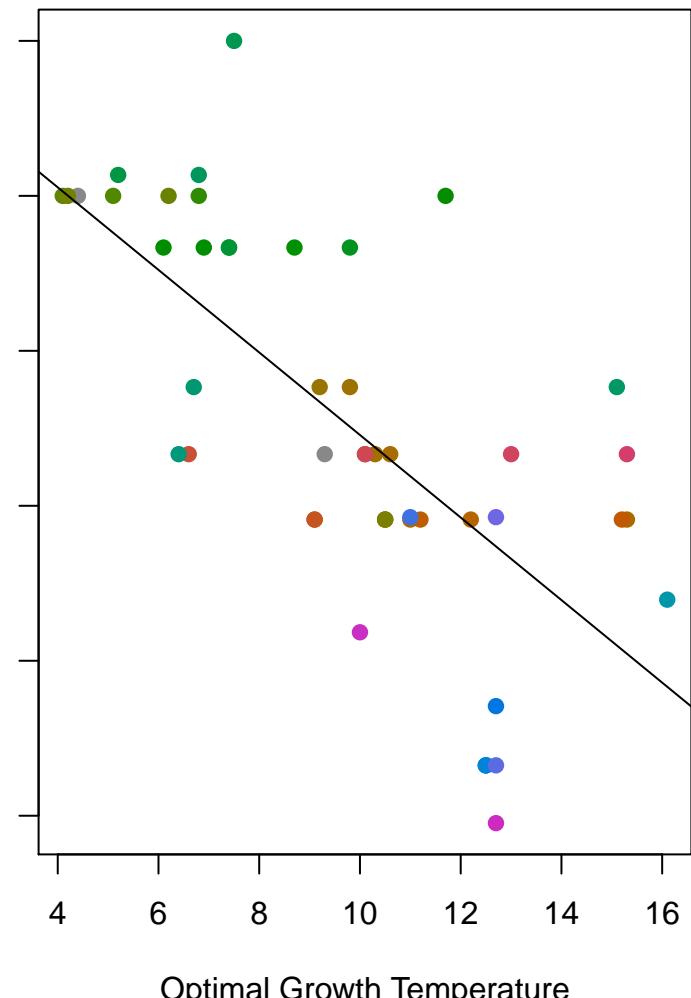
feature.pgfam_id.arg_lys_ratio.mean

PGF_00047484

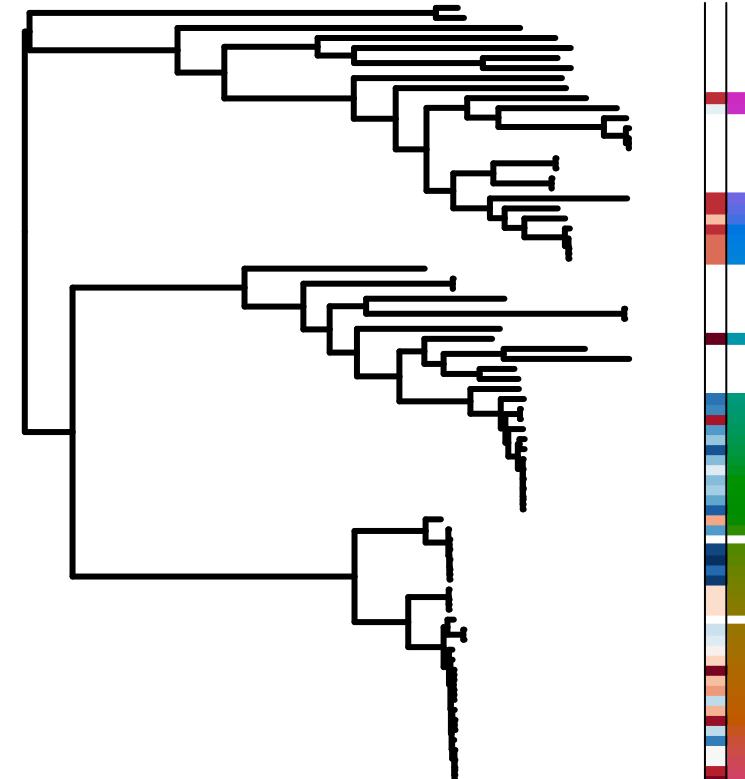
Related to collagenase

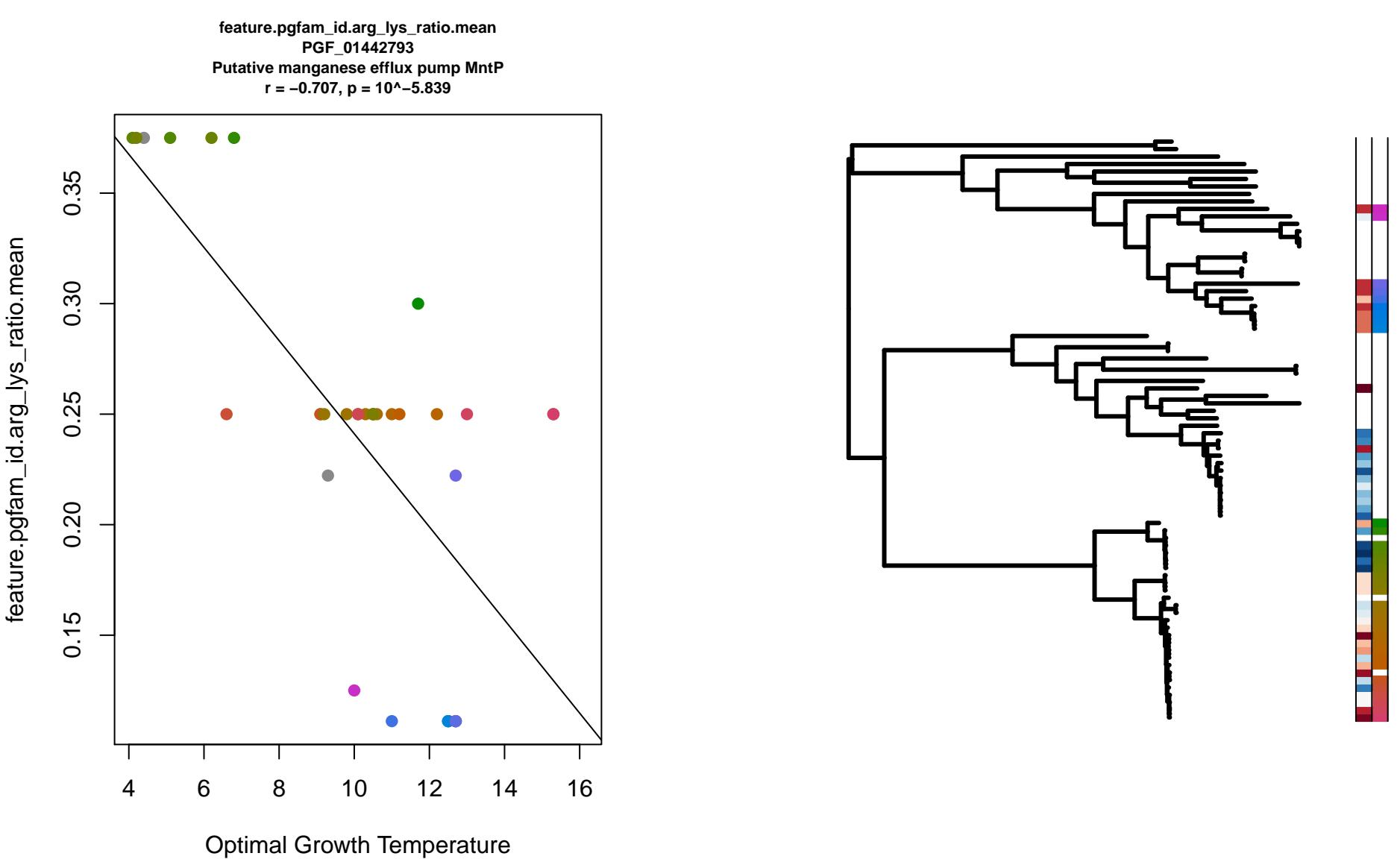
r = -0.689, p = 10^-7.359

feature.pgfam_id.arg_lys_ratio.mean



Optimal Growth Temperature





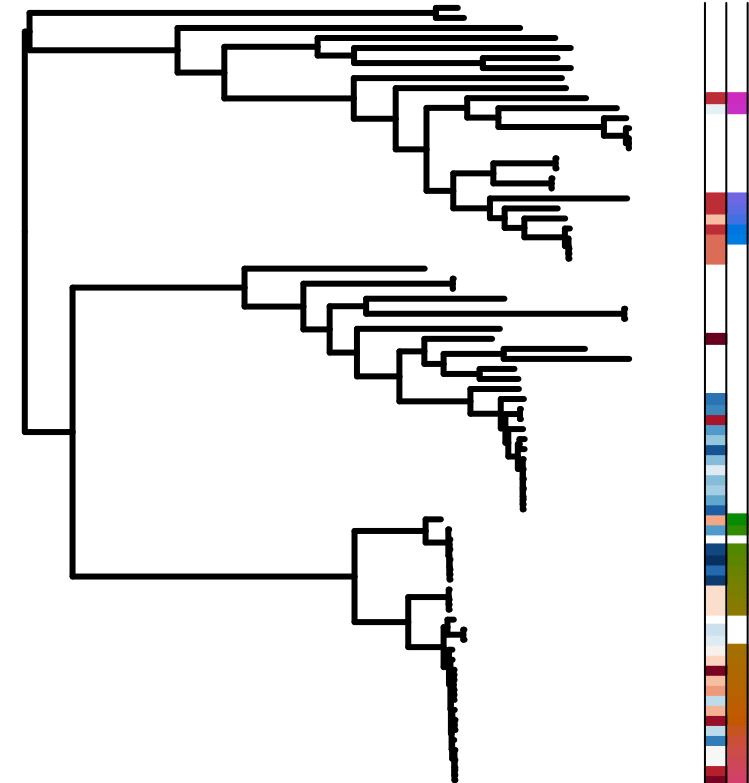
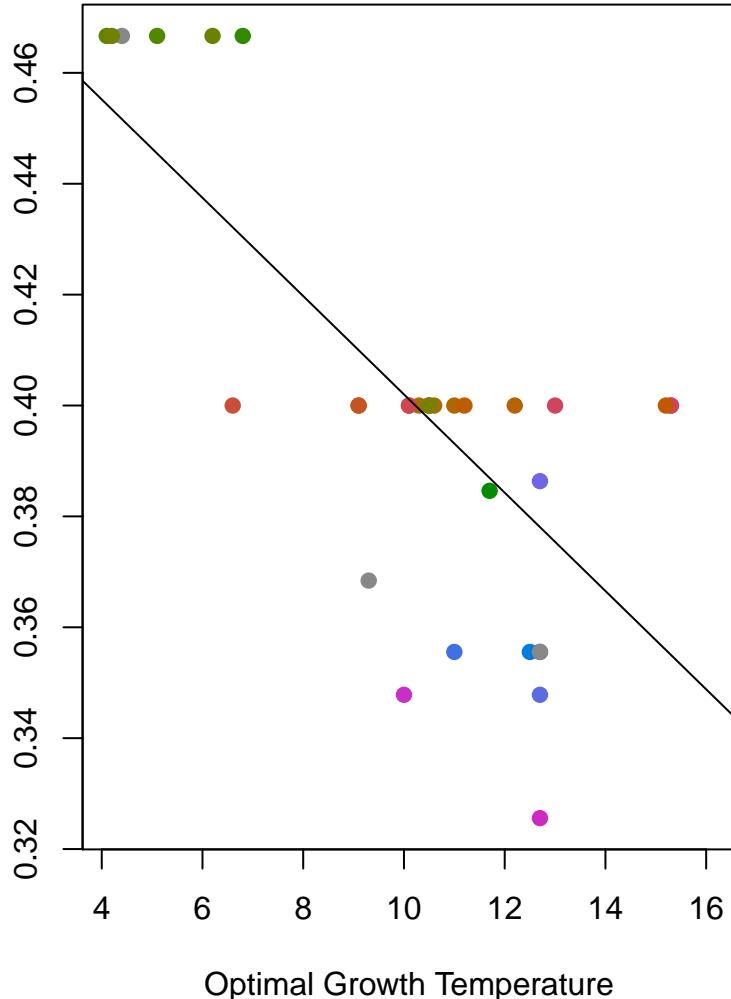
feature.pgfam_id.arg_lys_ratio.mean

PGF_12765299

Two-component system sensor histidine kinase

$r = -0.717, p = 10^{-5.564}$

feature.pgfam_id.arg_lys_ratio.mean

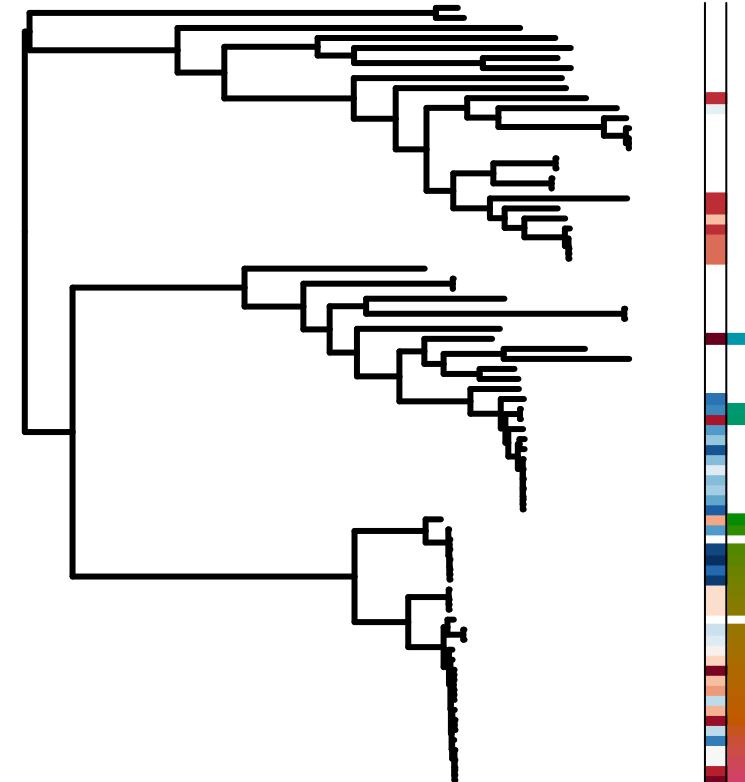
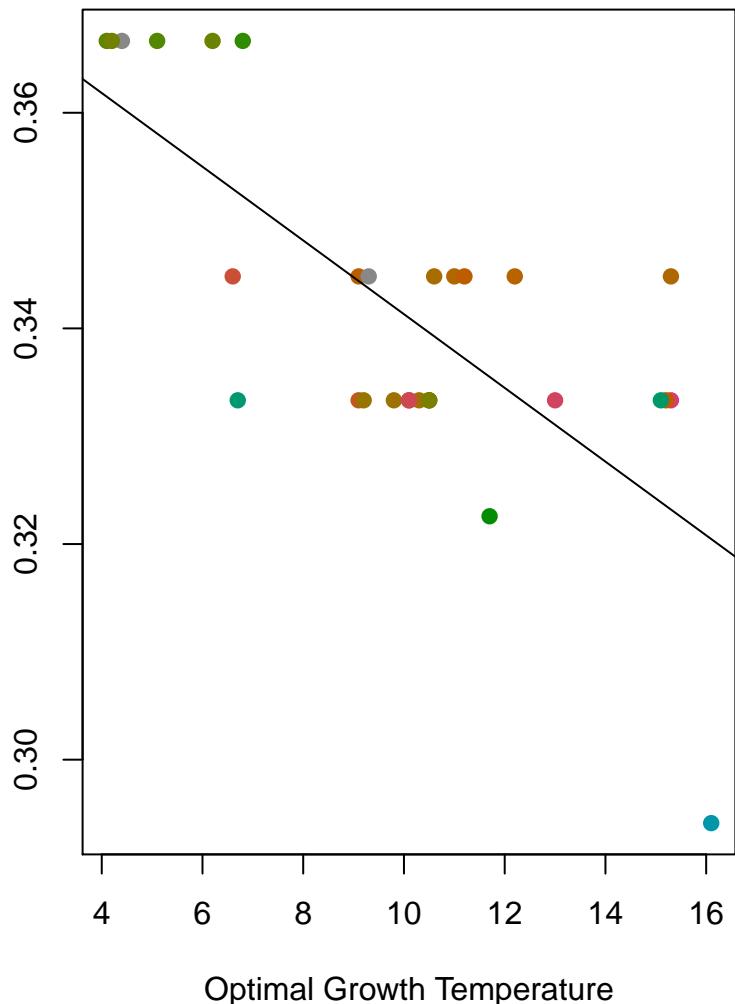
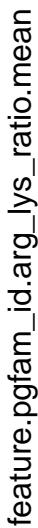


feature.pgfam_id.arg_lyc_ratio.mean

PGF_00062002

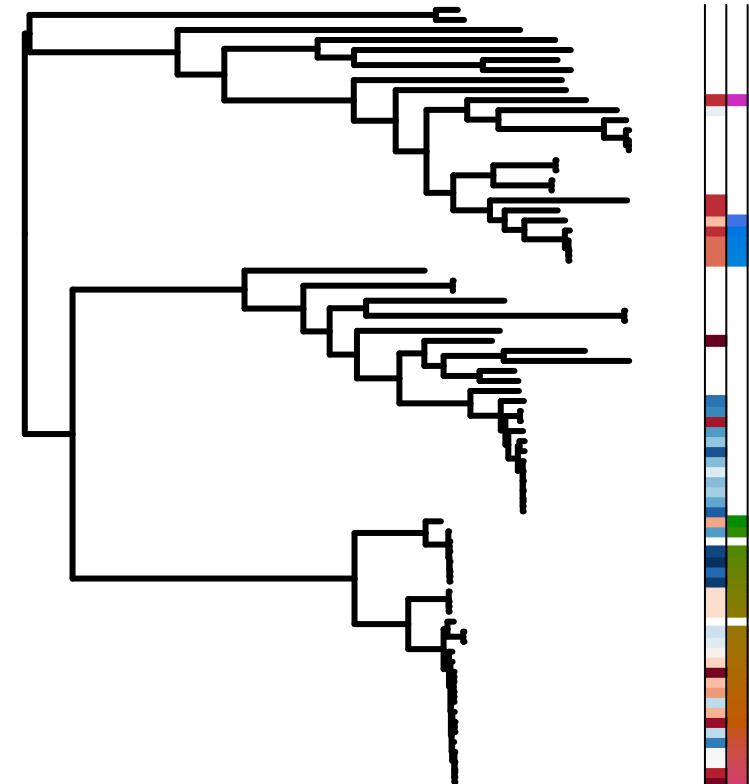
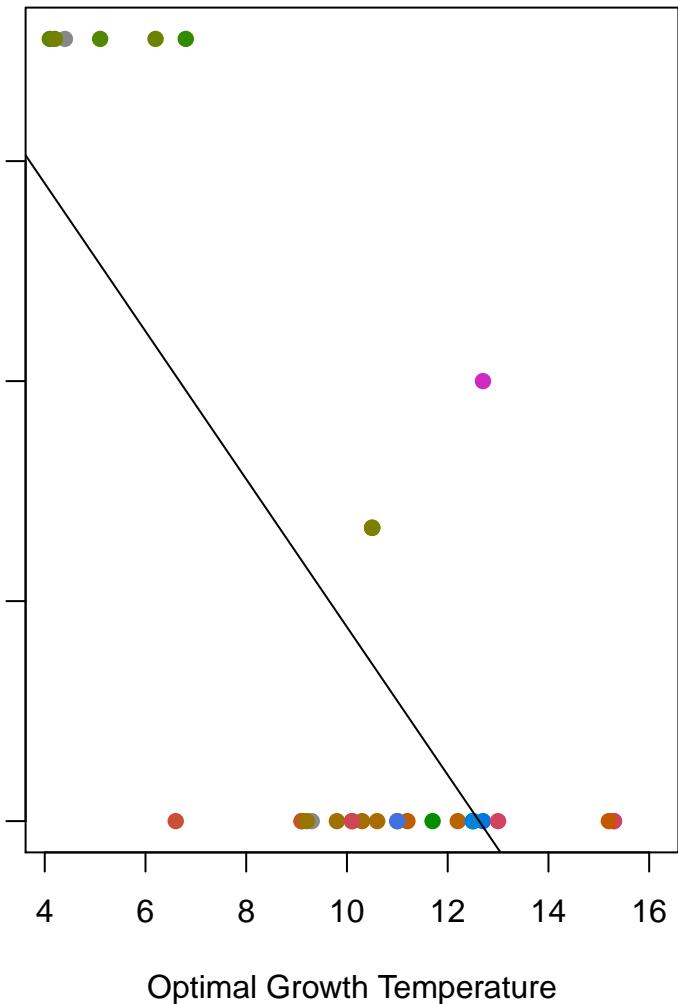
Tryptophan 2,3-dioxygenase (EC 1.13.11.11)

$r = -0.732, p = 10^{-5.371}$

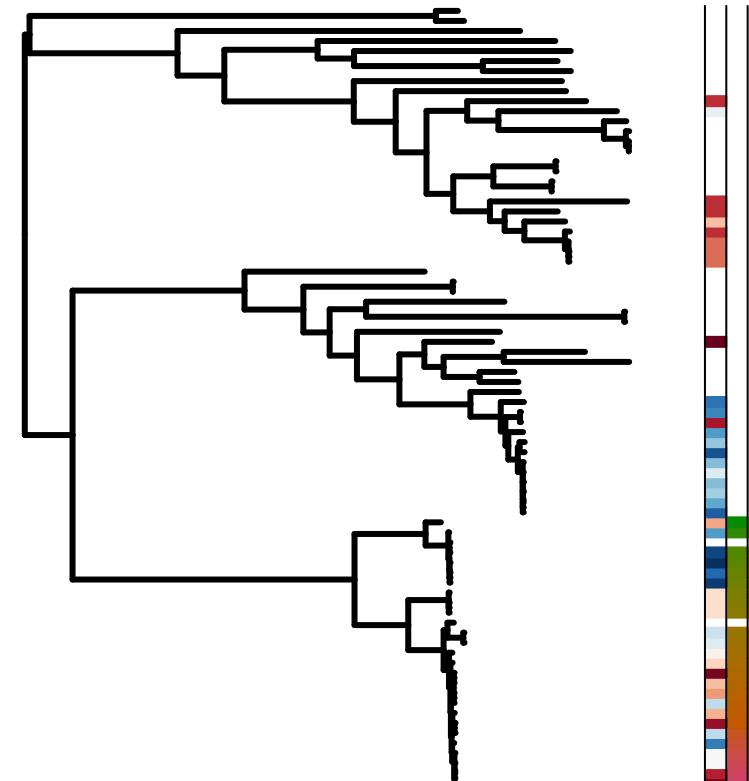
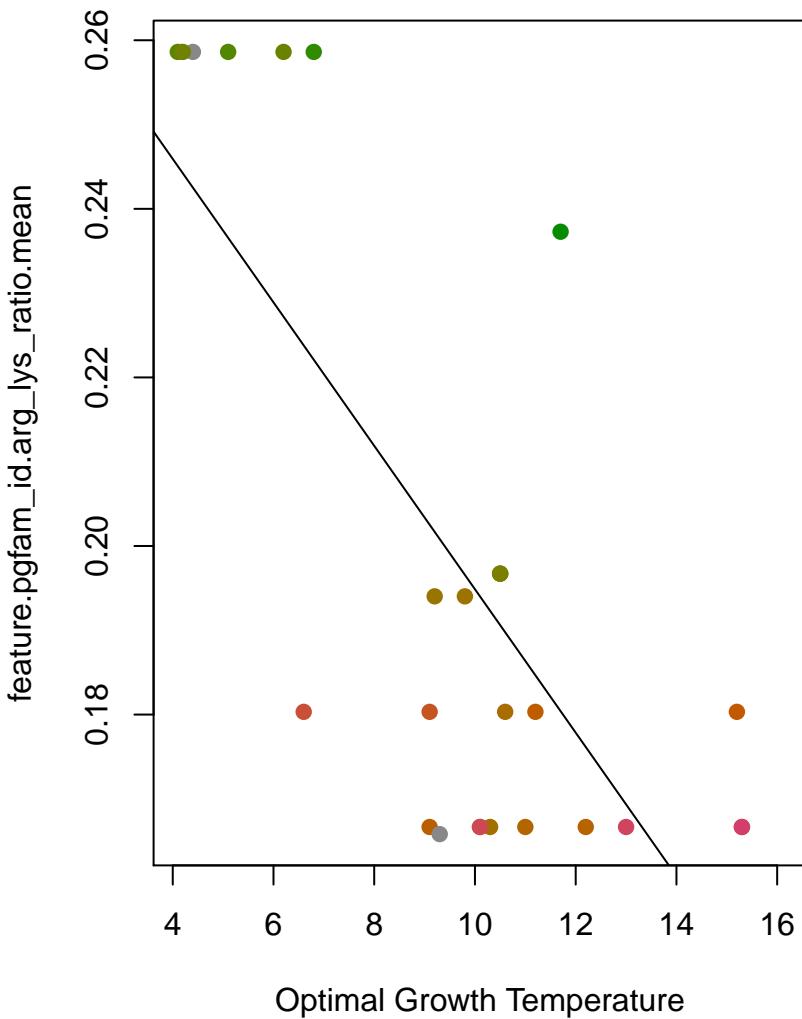


feature.pgfam_id.arg_lys_ratio.mean
PGF_00044582
Putative transmembrane protein
 $r = -0.736$, $p = 10^{-5.978}$

feature.pgfam_id.arg_lys_ratio.mean

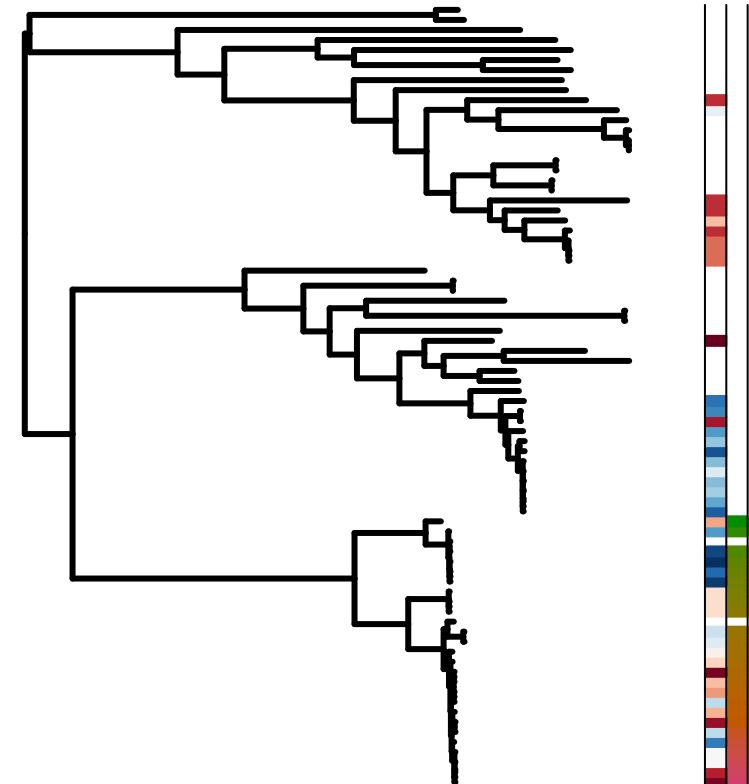
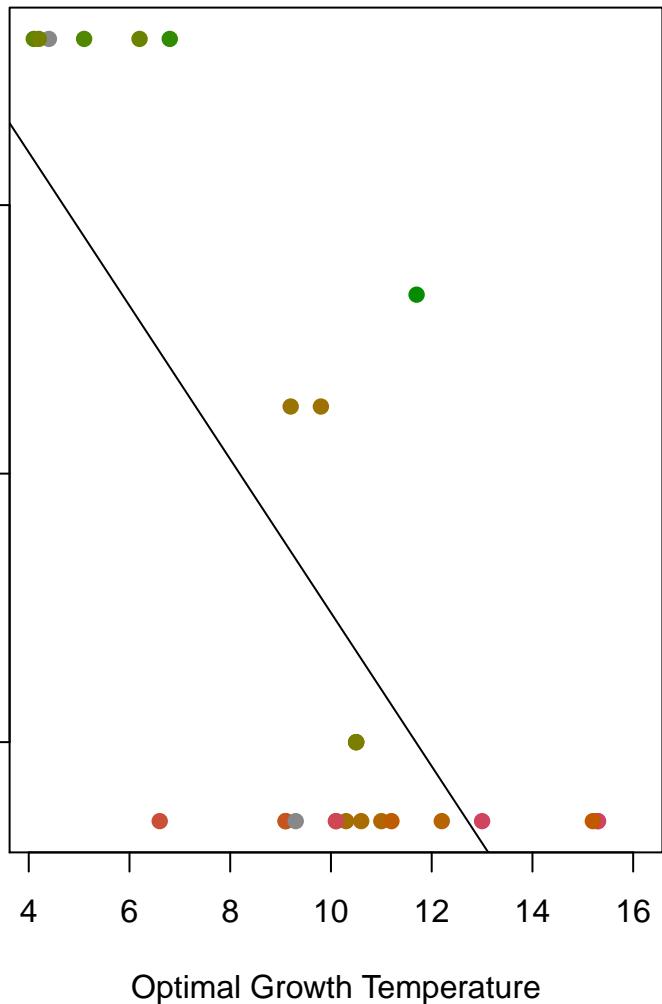


feature.pgfam_id.arg_lys_ratio.mean
PGF_07171270
hypothetical protein
 $r = -0.738$, $p = 10^{-4.952}$



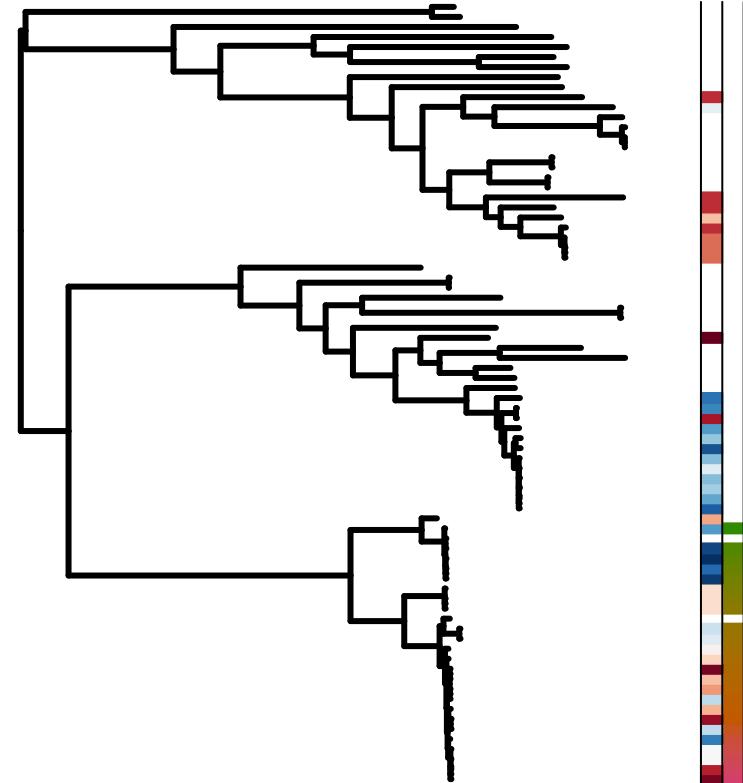
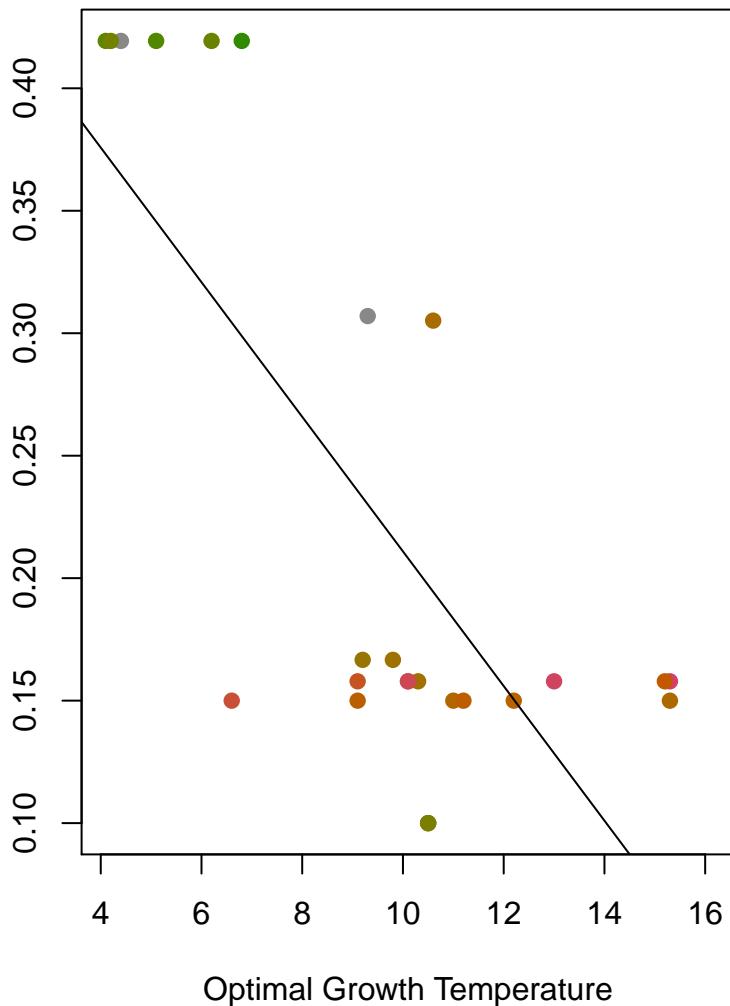
feature.pgfam_id.arg_lys_ratio.mean
PGF_11506828
hypothetical protein
 $r = -0.739$, $p = 10^{-4.963}$

feature.pgfam_id.arg_lys_ratio.mean



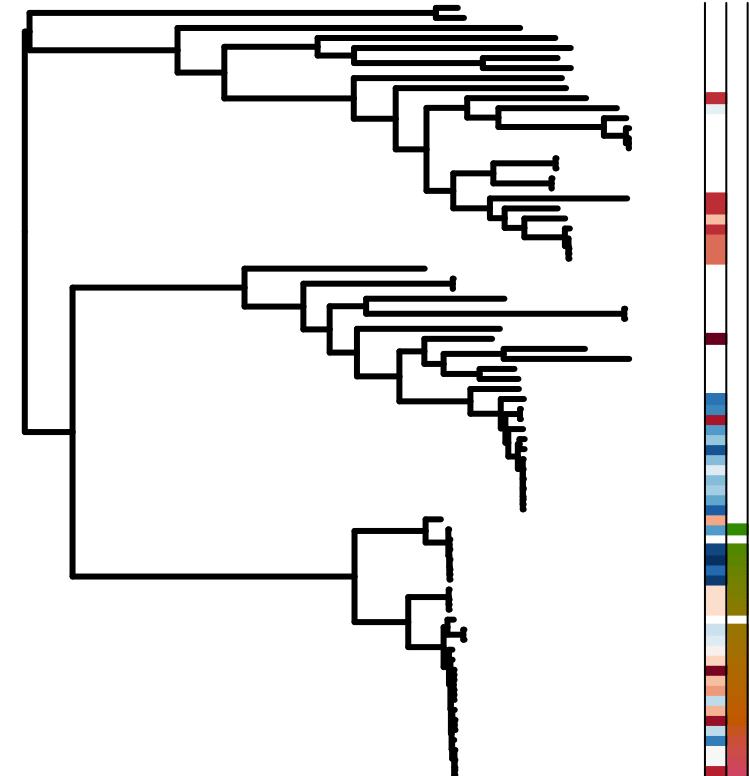
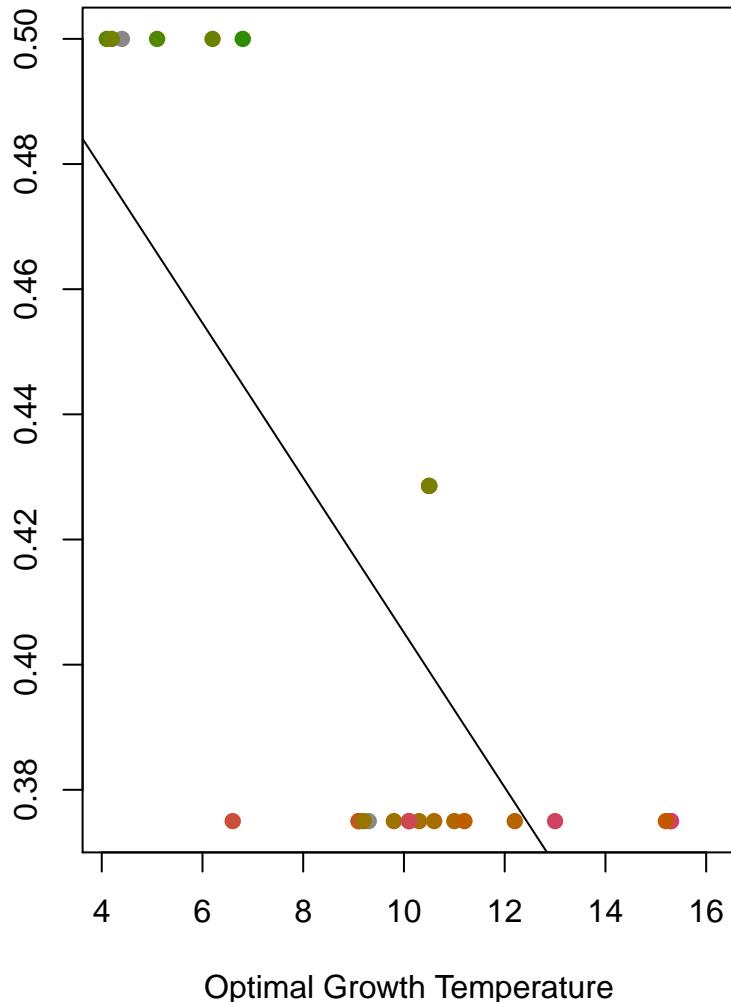
feature.pgfam_id.arg_lys_ratio.mean
PGF_07132870
hypothetical protein
 $r = -0.739$, $p = 10^{-4.797}$

feature.pgfam_id.arg_lys_ratio.mean



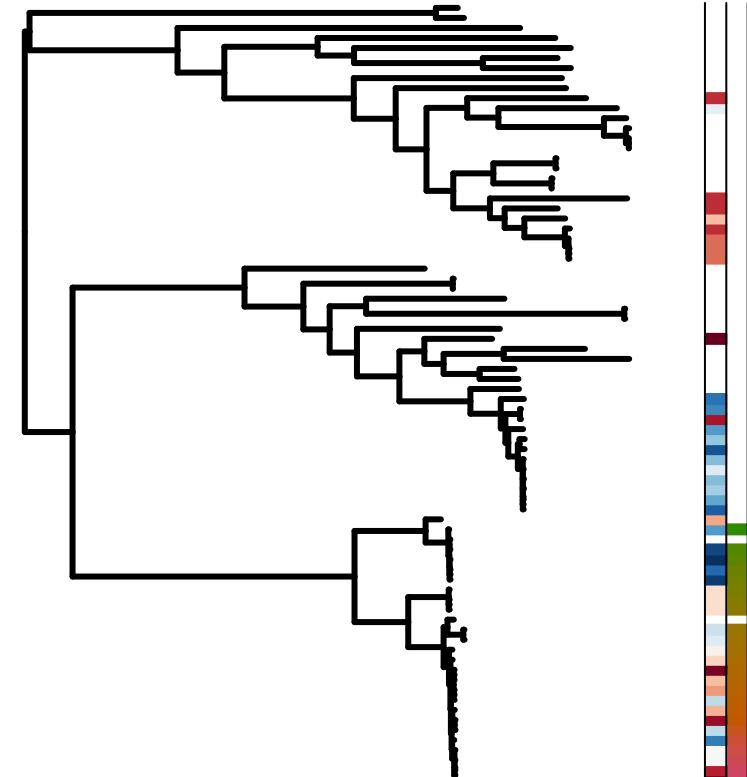
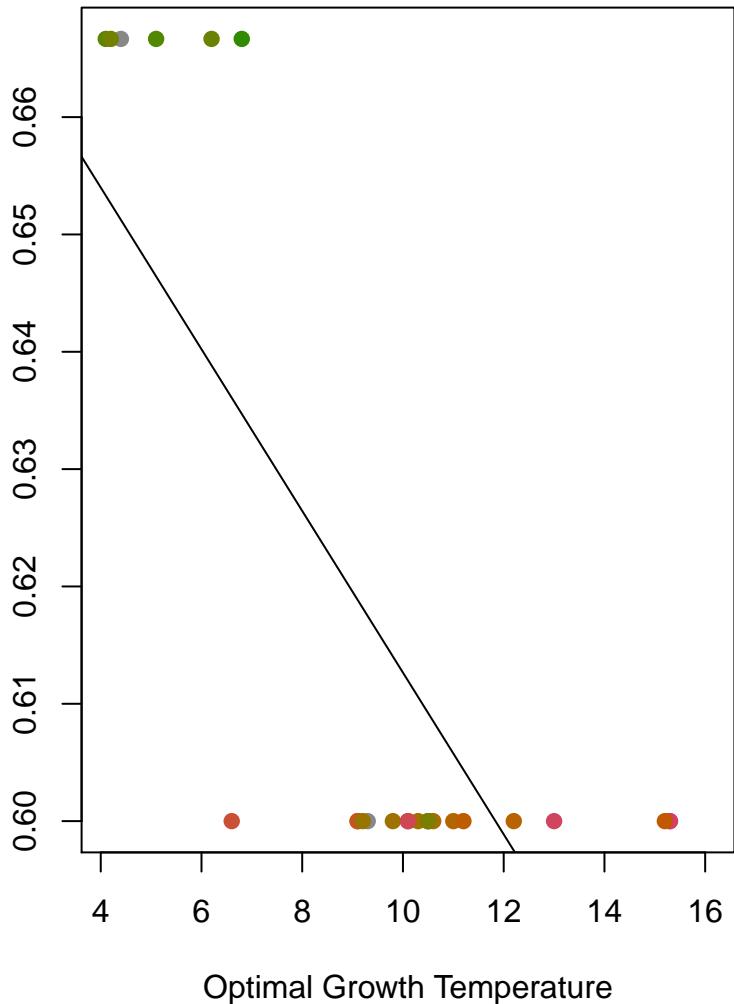
feature.pgfam_id.arg_lys_ratio.mean
PGF_11600935
hypothetical protein
 $r = -0.75, p = 10^{-4.996}$

feature.pgfam_id.arg_lys_ratio.mean



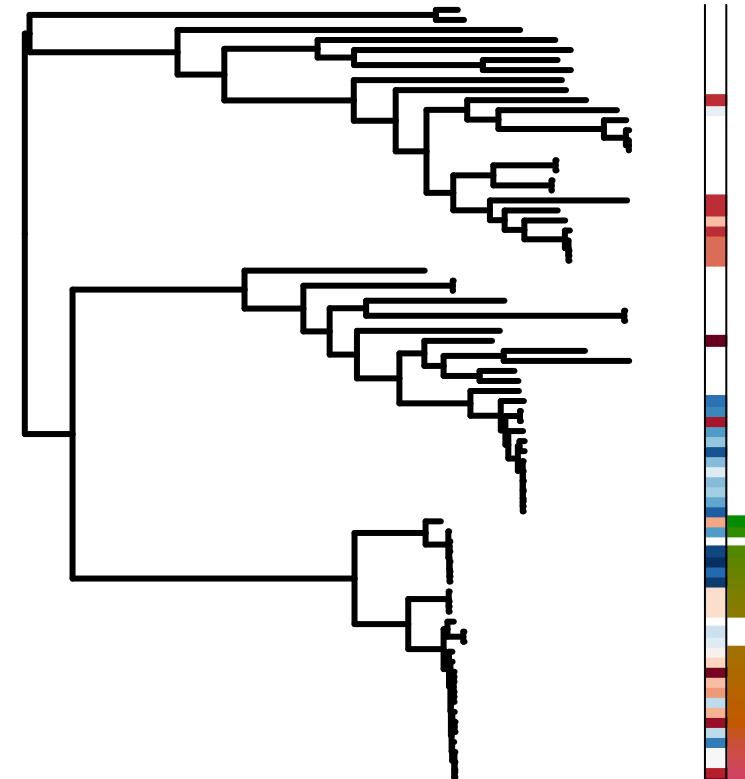
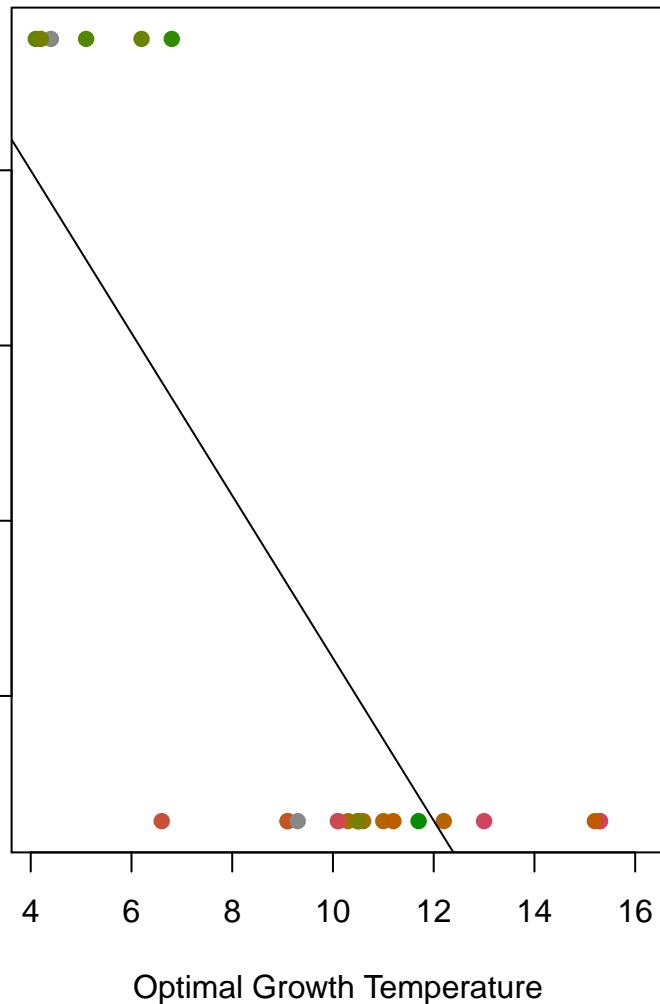
feature.pgfam_id.arg_lys_ratio.mean
PGF_12071964
hypothetical protein
 $r = -0.775$, $p = 10^{-5.478}$

feature.pgfam_id.arg_lys_ratio.mean

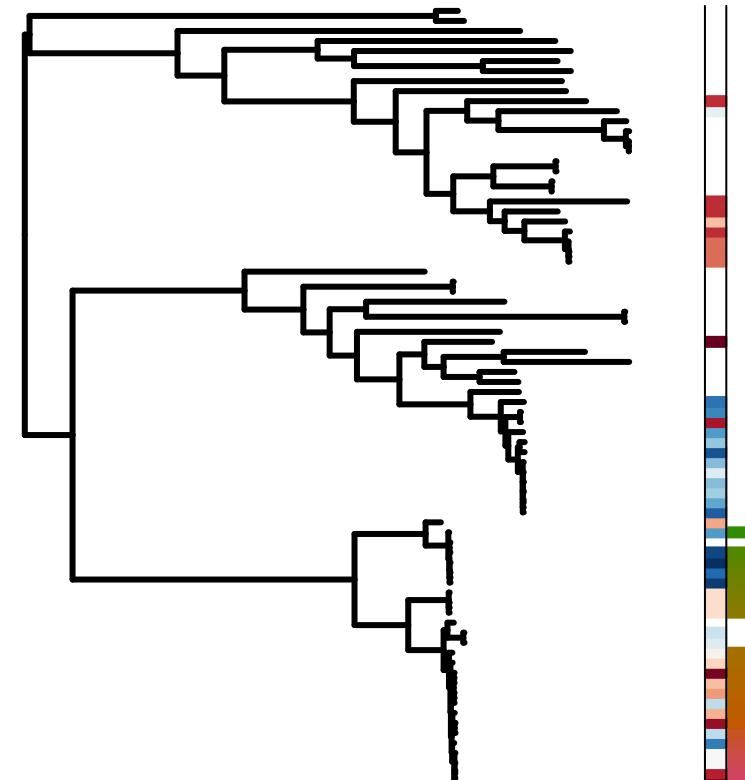
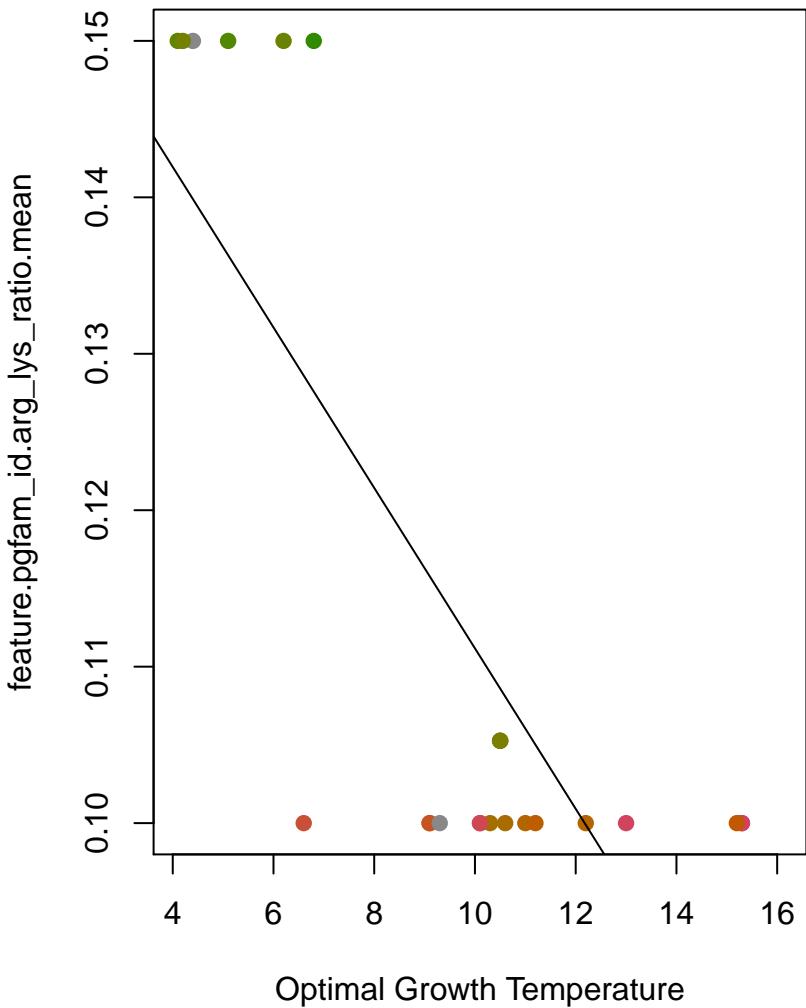


feature.pgfam_id.arg_lys_ratio.mean
PGF_10906072
hypothetical protein
 $r = -0.79$, $p = 10^{-5.574}$

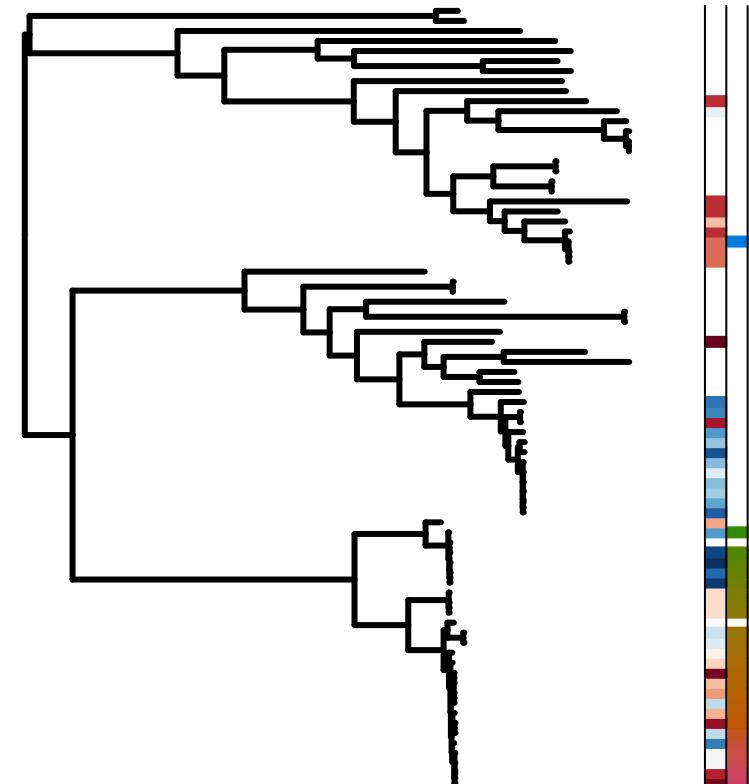
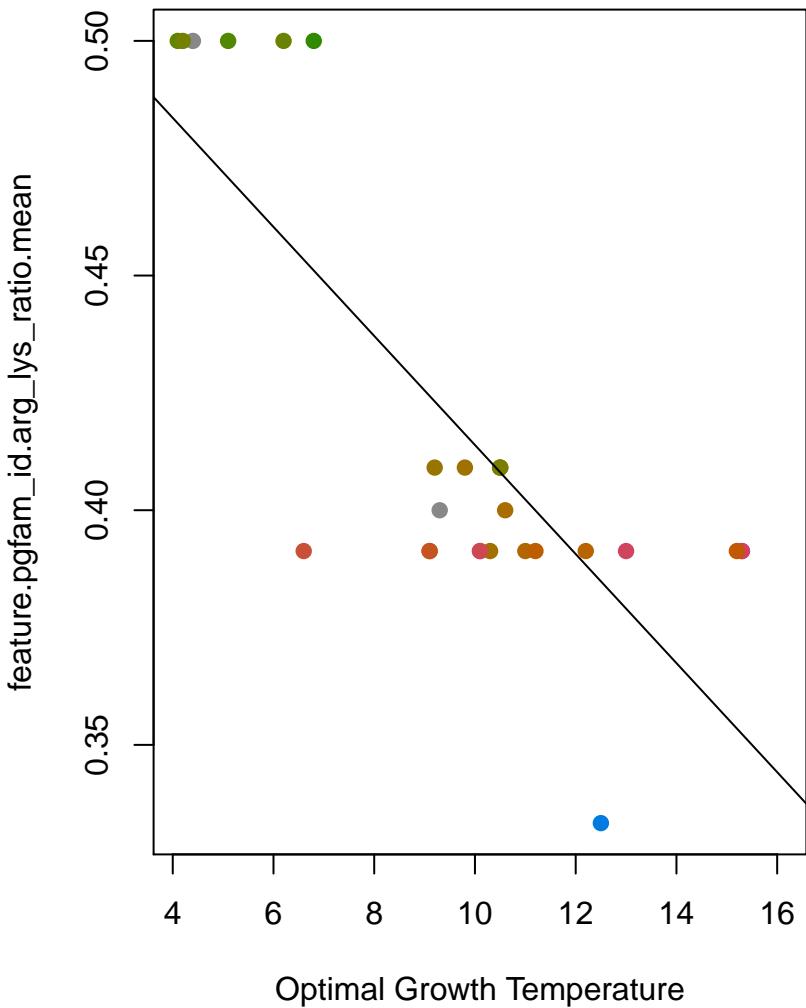
feature.pgfam_id.arg_lys_ratio.mean

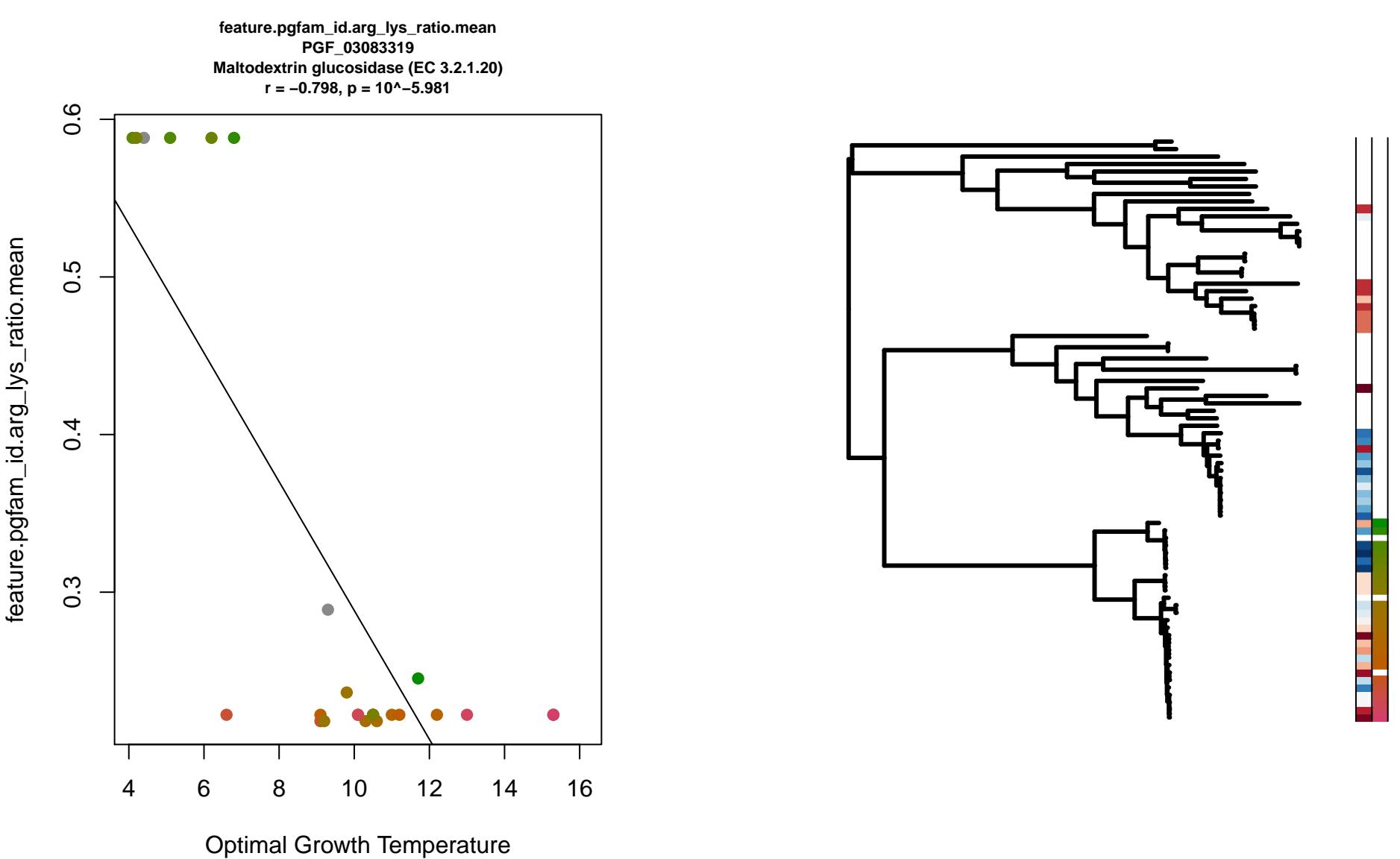


feature.pgfam_id.arg_lys_ratio.mean
PGF_10751741
Redoxin domain protein
 $r = -0.79$, $p = 10^{-5.356}$



feature.pgfam_id.arg_lys_ratio.mean
PGF_06792096
hypothetical protein
 $r = -0.79, p = 10^{-6.029}$

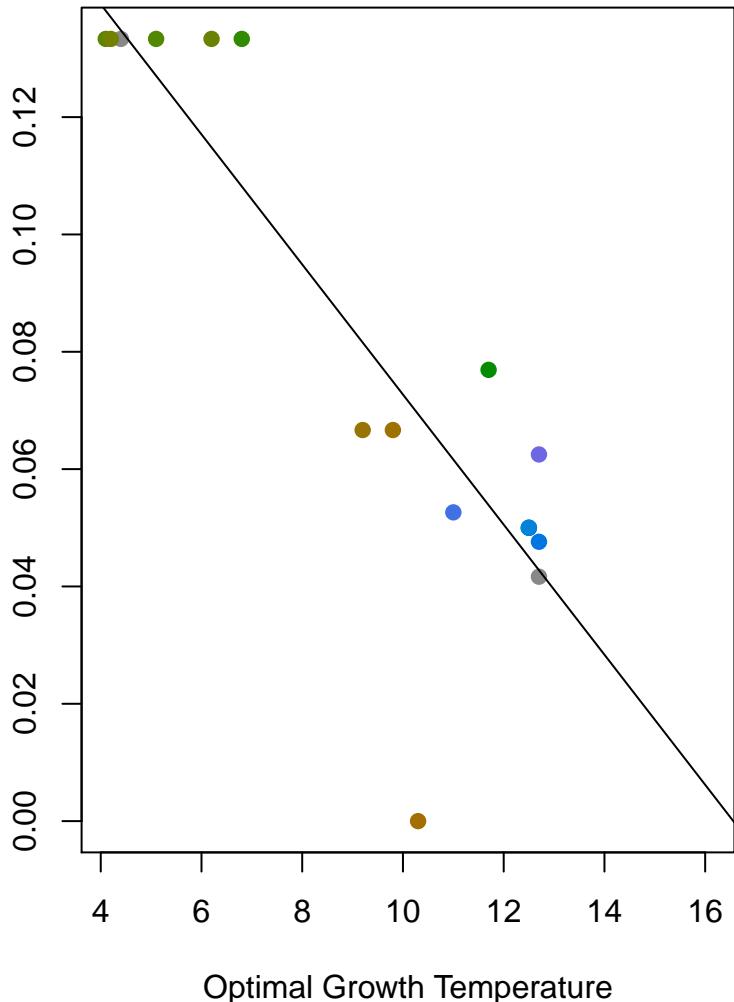




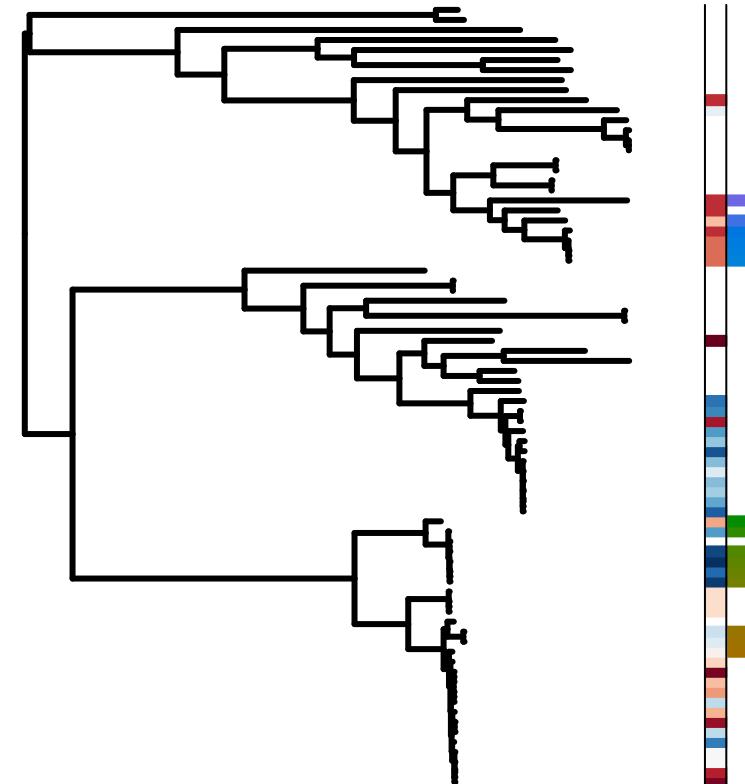
feature.pgfam_id.arg_lys_ratio.mean
PGF_00060323

Transforming growth factor-beta induced protein IG-H3 precursor
 $r = -0.871, p = 10^{-5.274}$

feature.pgfam_id.arg_lys_ratio.mean

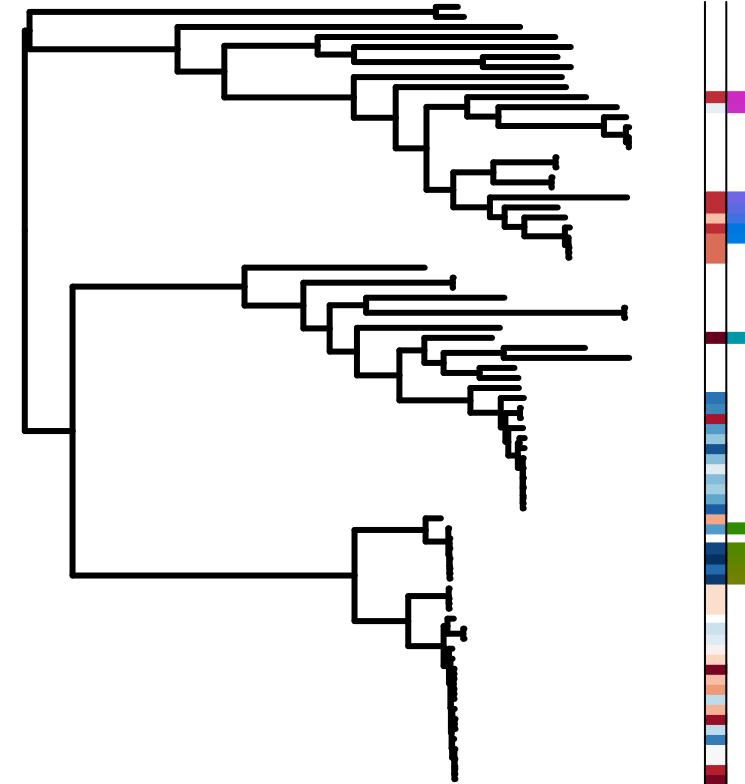
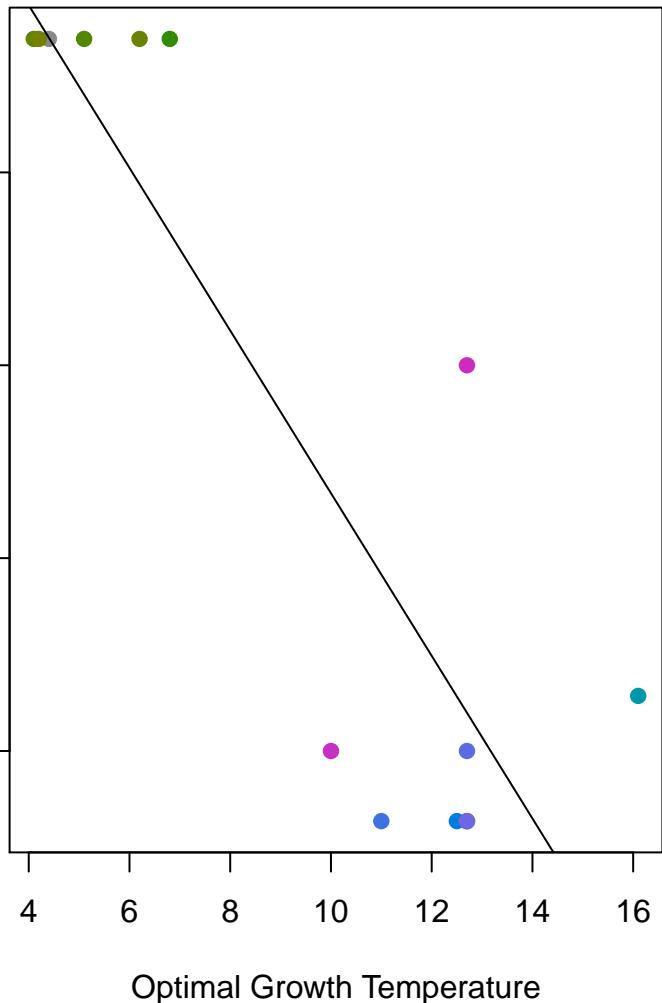


Optimal Growth Temperature



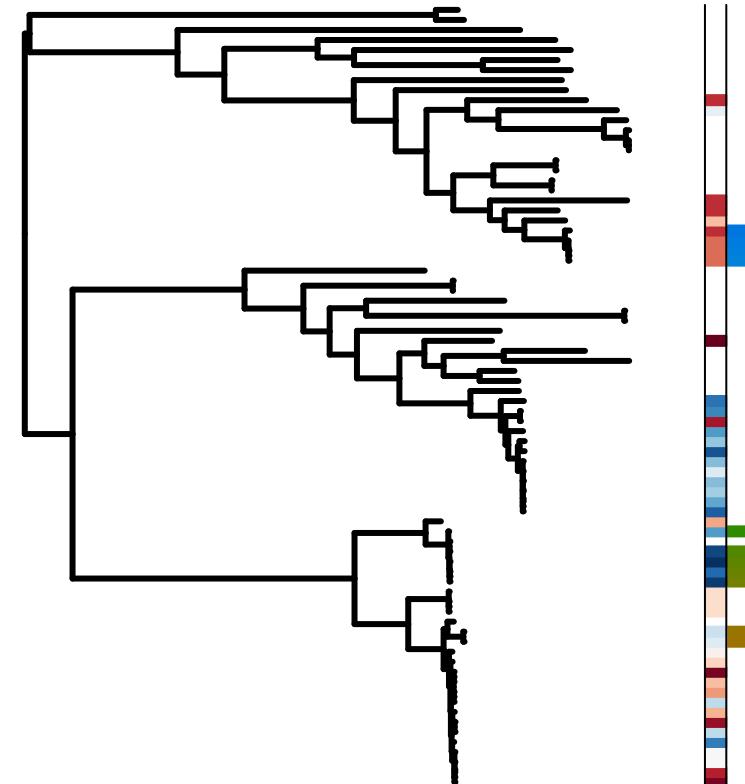
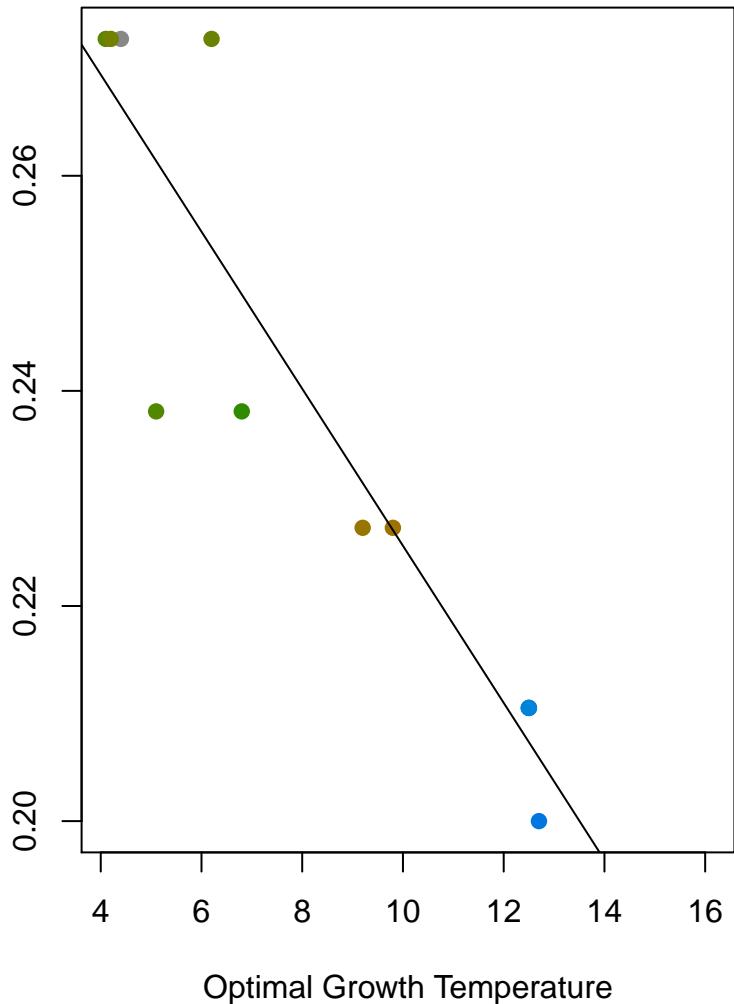
feature.pgfam_id.arg_lys_ratio.mean
PGF_03063421
GcvR-like protein
 $r = -0.877$, $p = 10^{-4.76}$

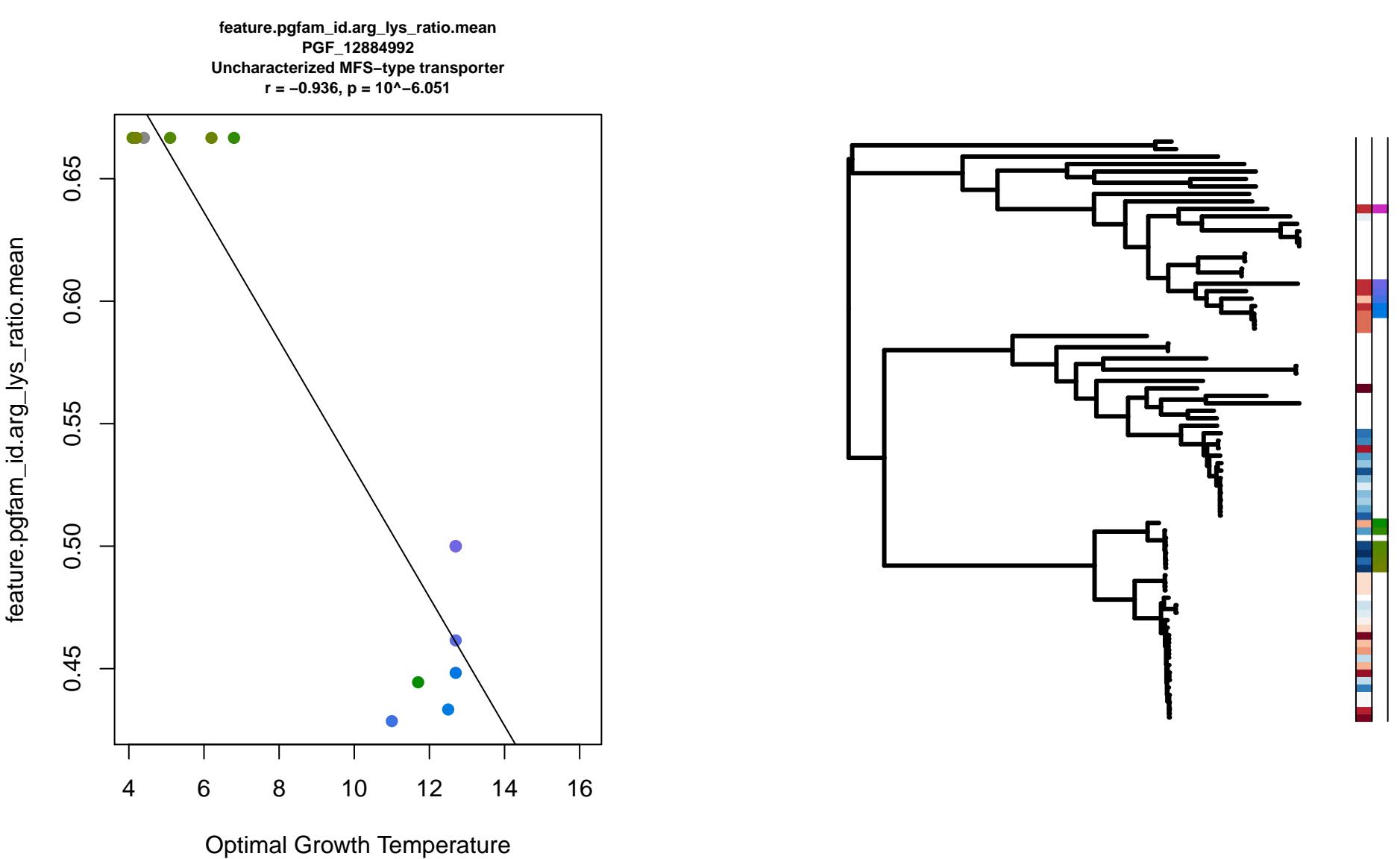
feature.pgfam_id.arg_lys_ratio.mean



feature.pgfam_id.arg_lys_ratio.mean
PGF_01337912
Predicted zinc-binding protein
 $r = -0.929$, $p = 10^{-4.906}$

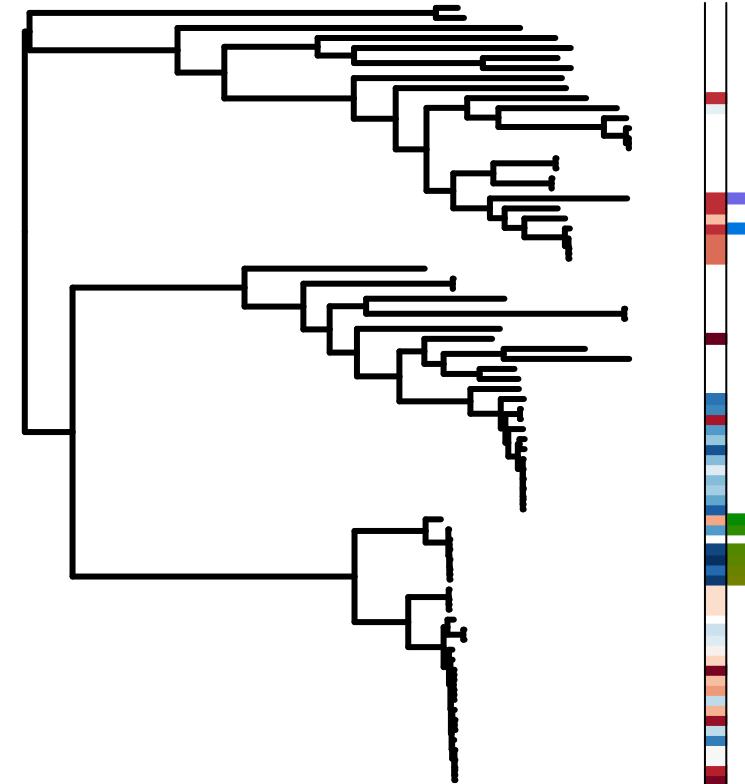
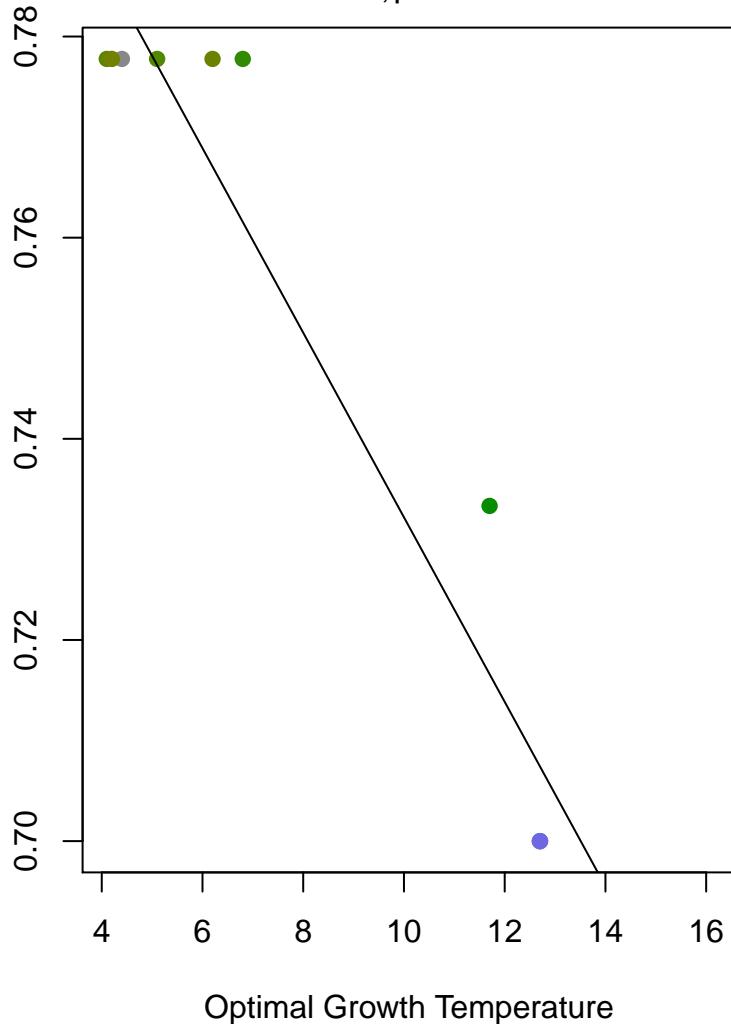
feature.pgfam_id.arg_lys_ratio.mean





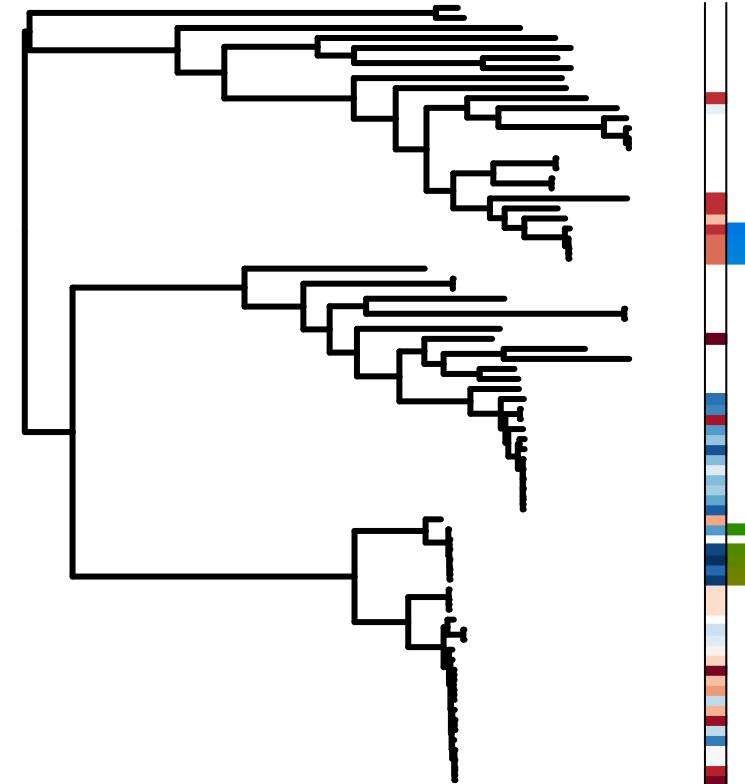
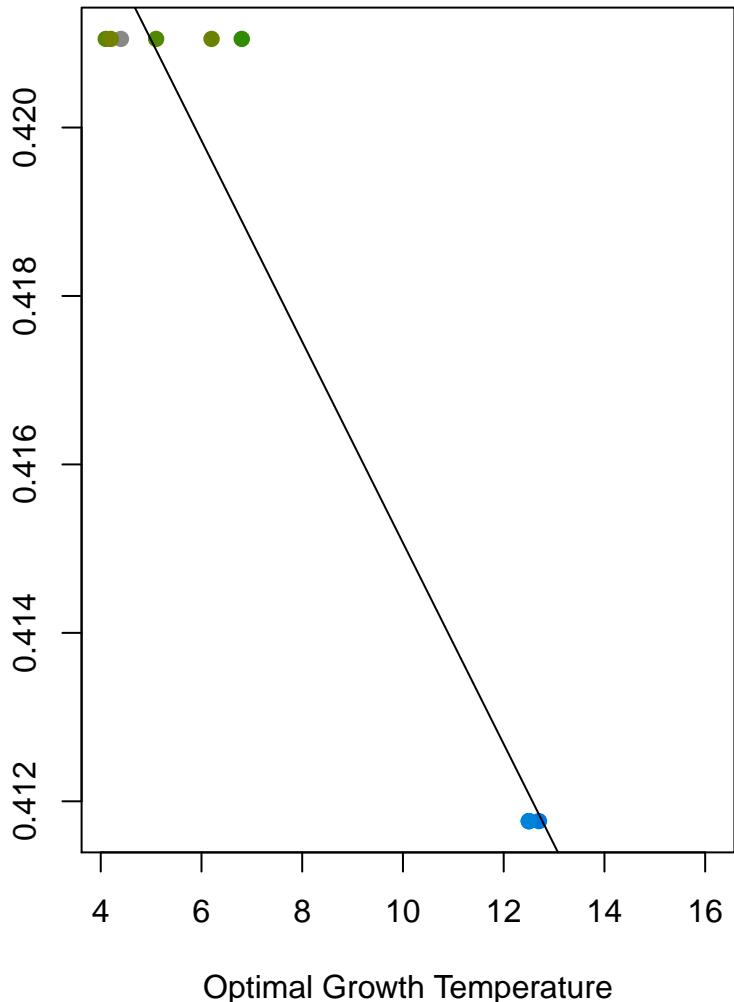
feature.pgfam_id.arg_lys_ratio.mean
PGF_03221663
Phage tail collar domain
 $r = -0.959$, $p = 10^{-4.943}$

feature.pgfam_id.arg_lys_ratio.mean

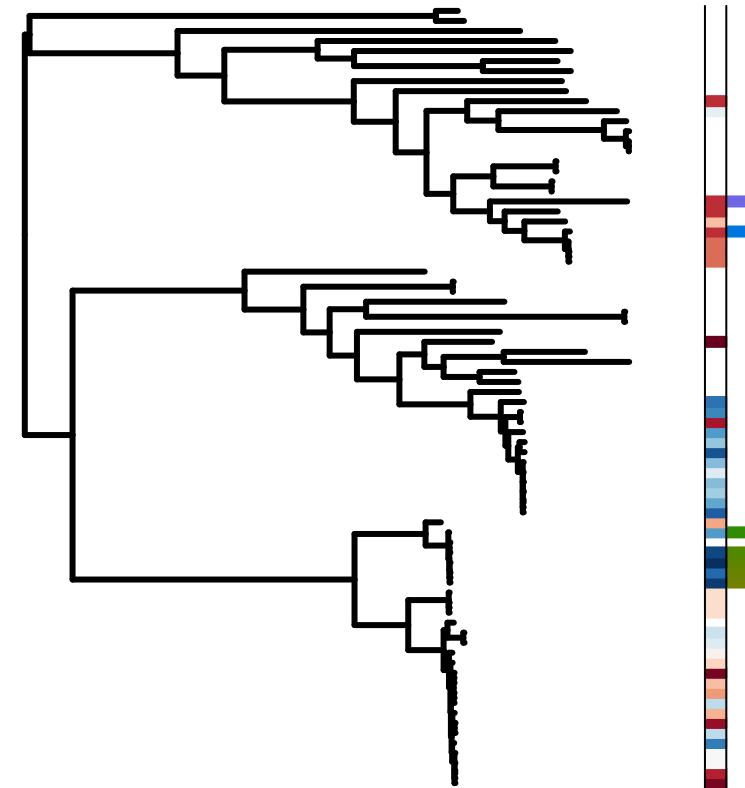
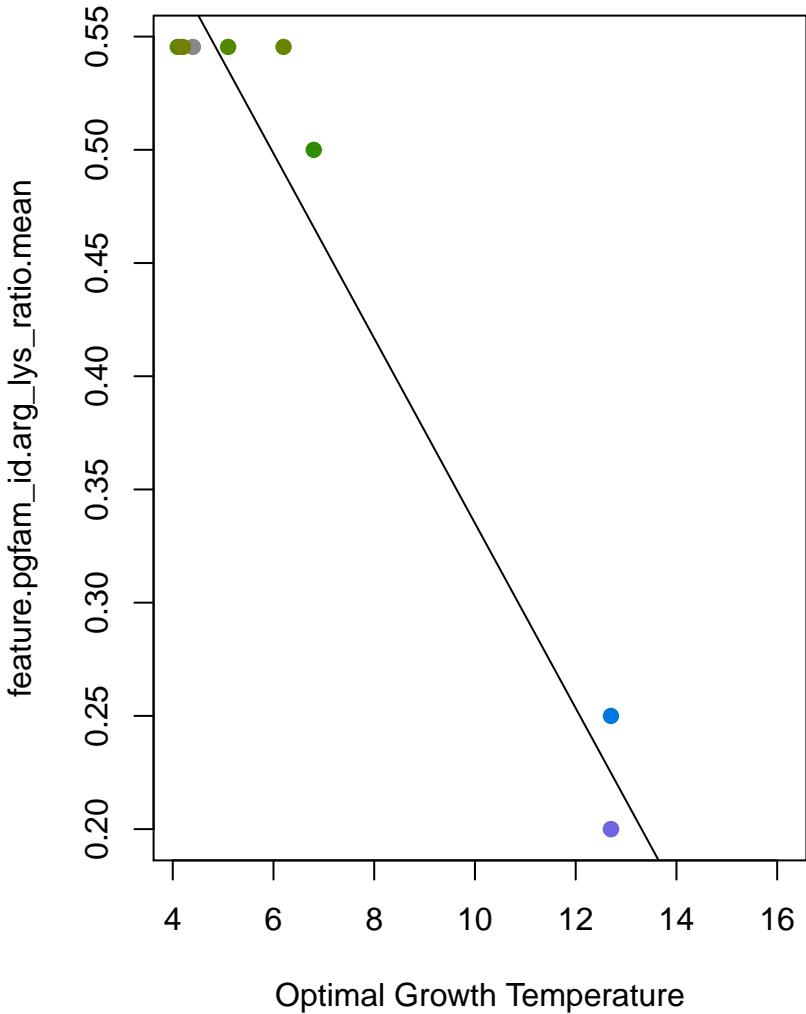


feature.pgfam_id.arg_lys_ratio.mean
PGF_01338043
hypothetical protein
 $r = -0.977$, $p = 10^{-5.889}$

feature.pgfam_id.arg_lys_ratio.mean



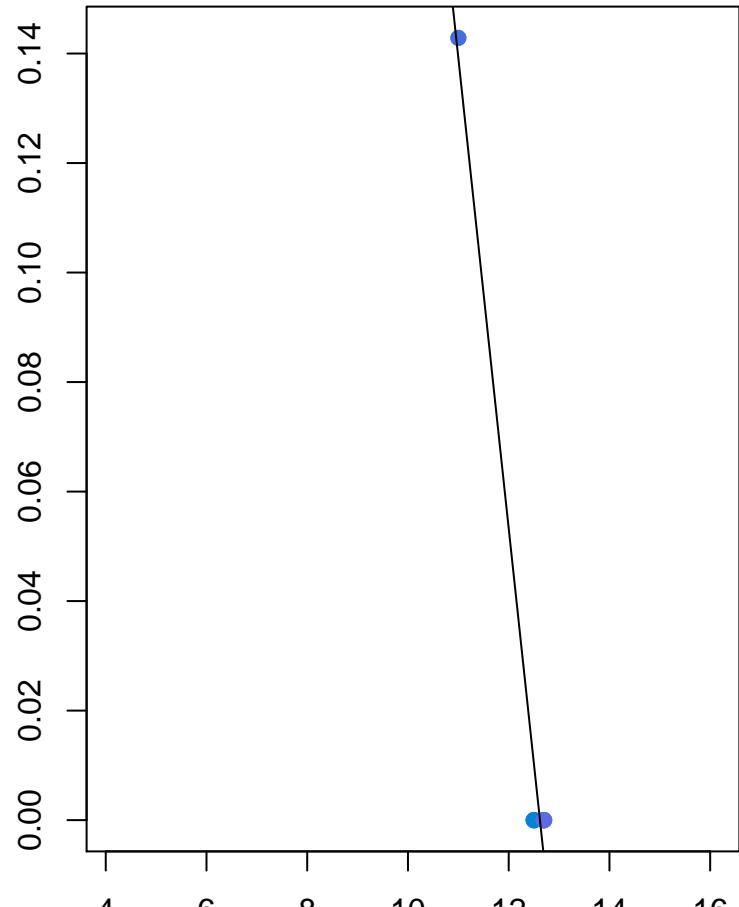
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336811
hypothetical protein
 $r = -0.98$, $p = 10^{-5.464}$



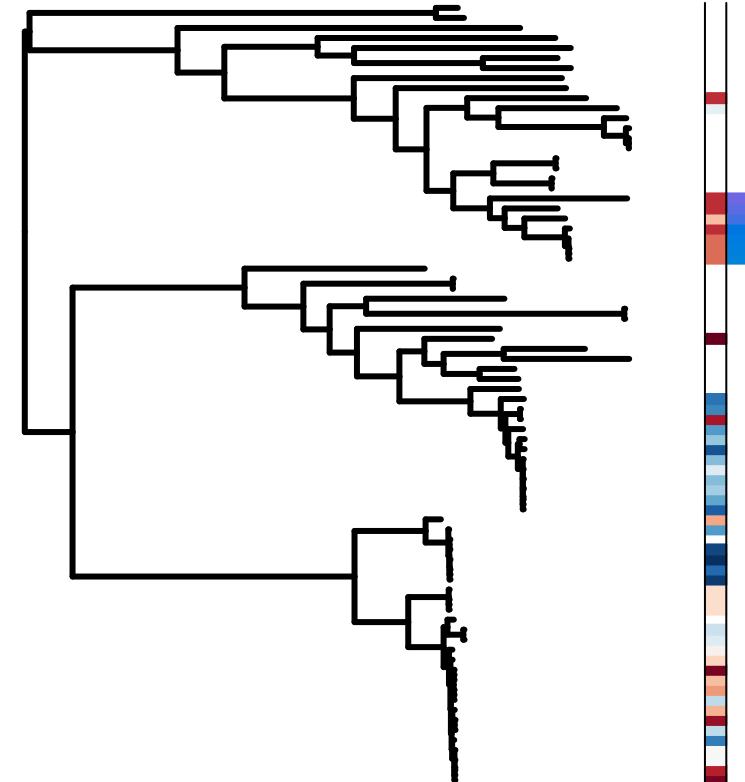
feature.pgfam_id.arg_lys_ratio.mean
PGF_00414476

uncharacterized conserved protein containing predicted Zn–ribbon like domain
 $r = -0.985, p = 10^{-5.104}$

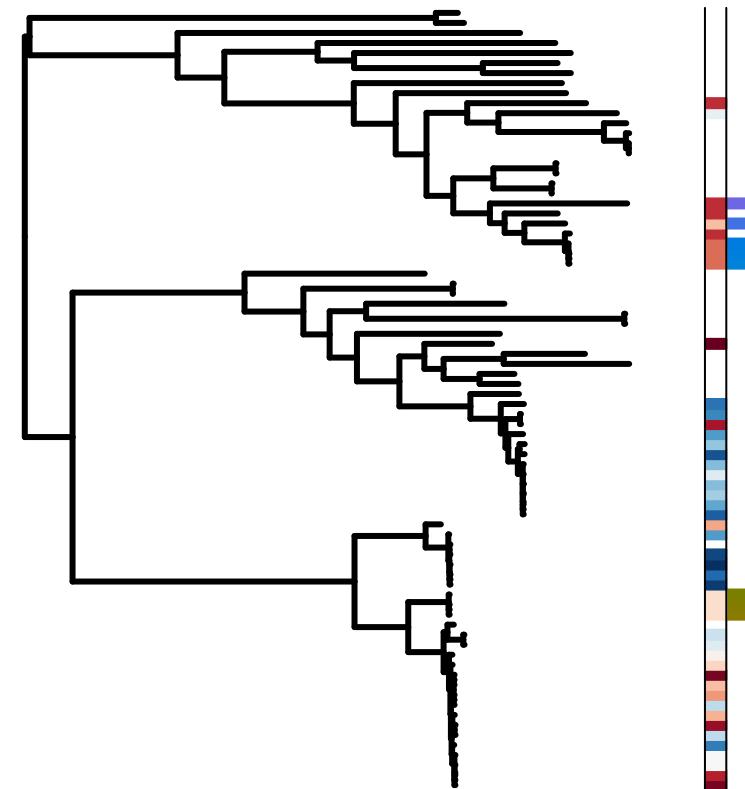
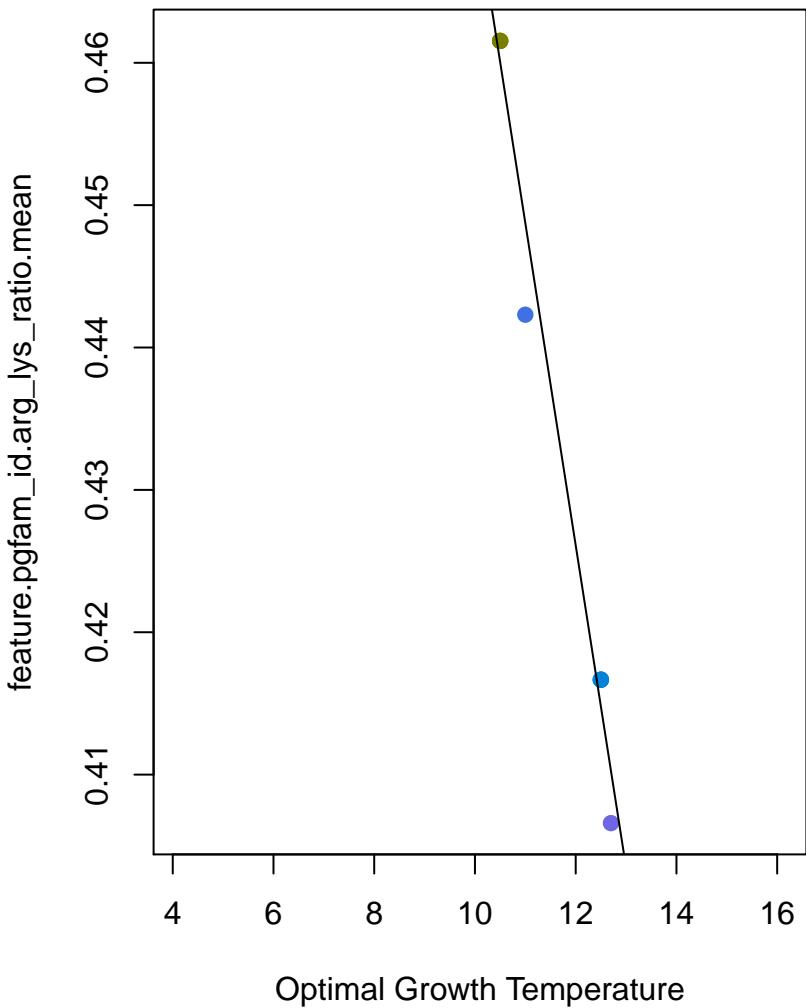
feature.pgfam_id.arg_lys_ratio.mean



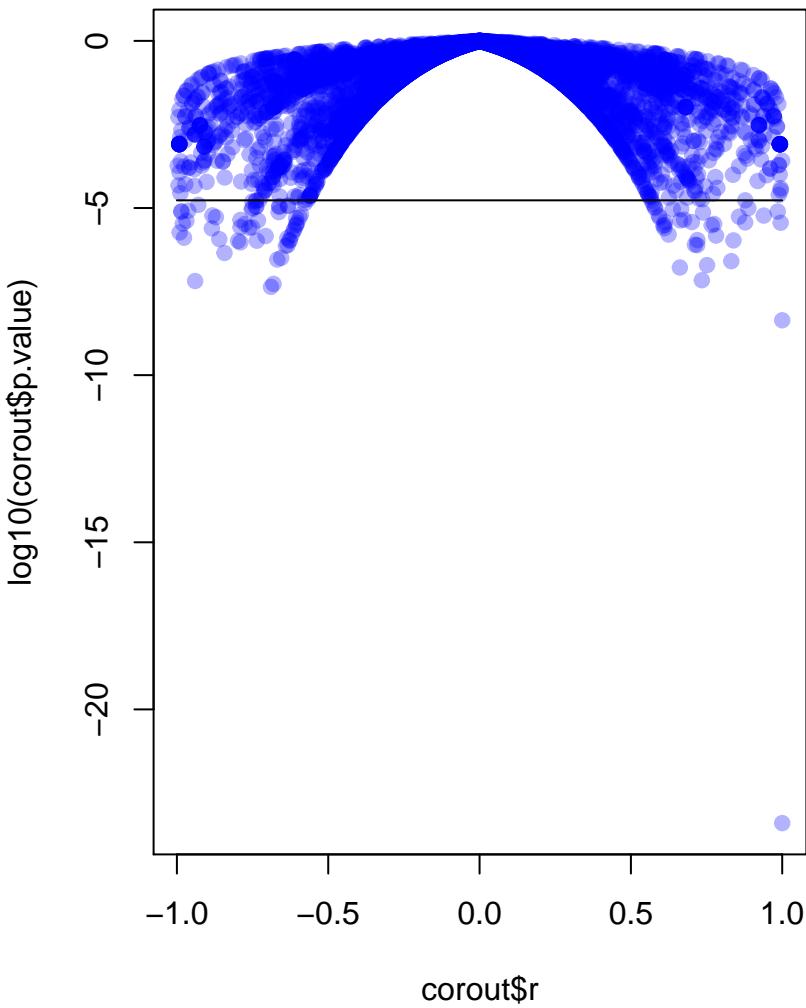
Optimal Growth Temperature



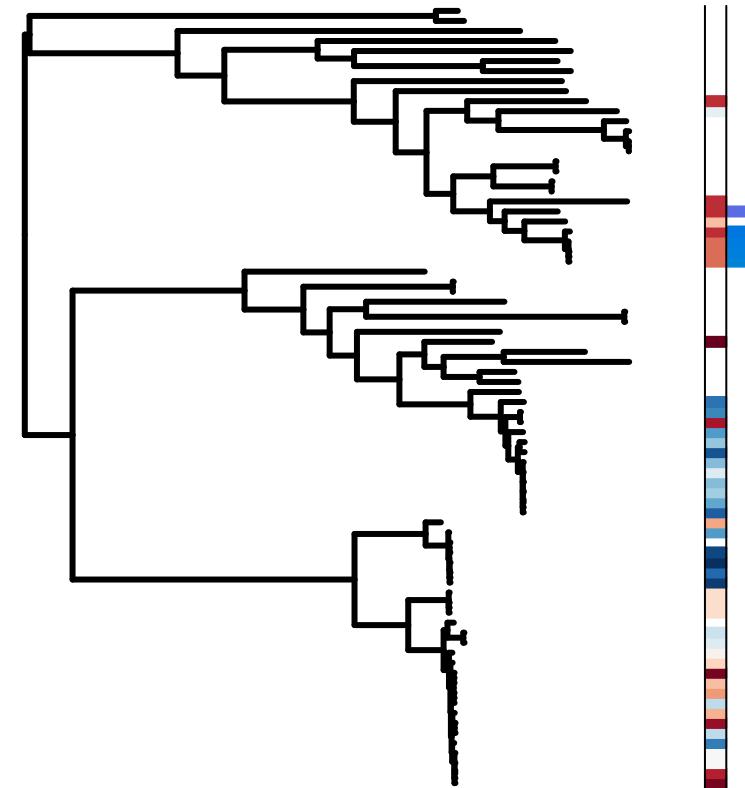
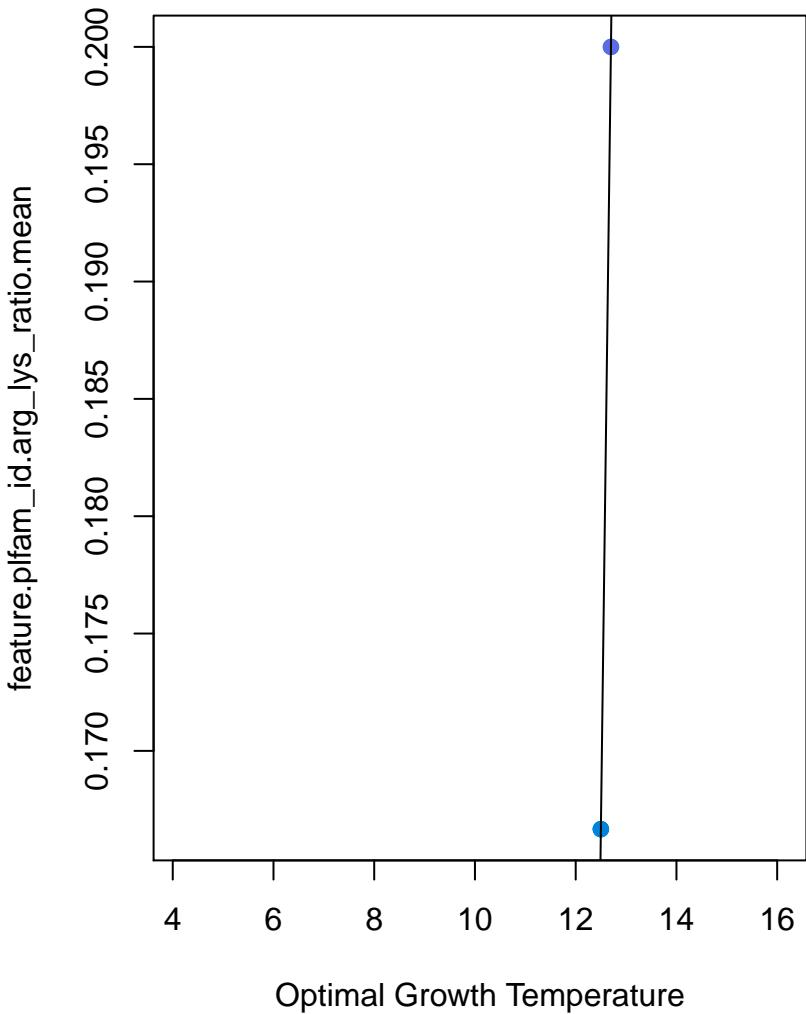
feature.pgfam_id.arg_lys_ratio.mean
PGF_01339224
hypothetical protein
 $r = -0.991$, $p = 10^{-5.73}$



feature.plfam_id.arg_lyc_ratio.mean

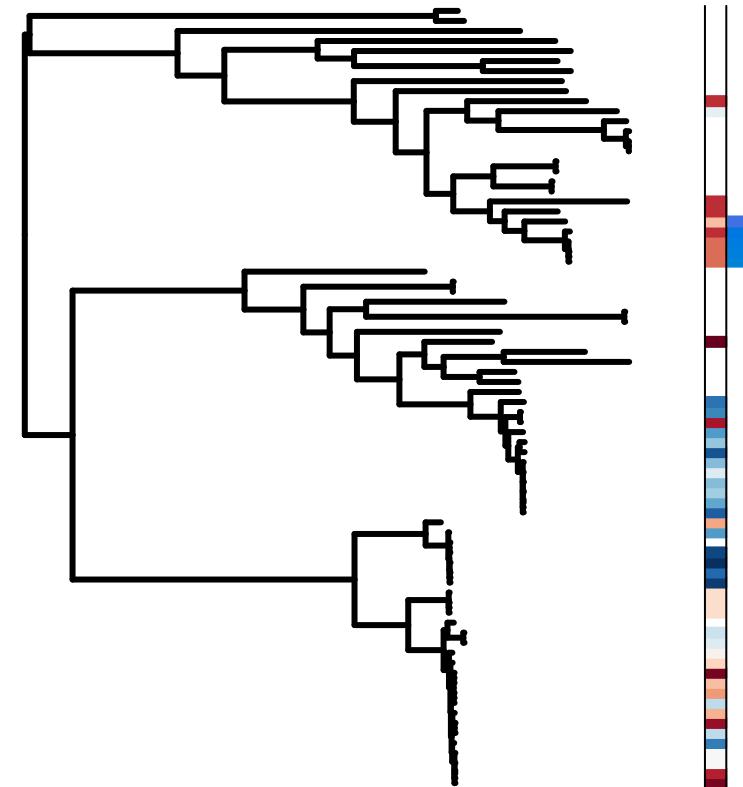
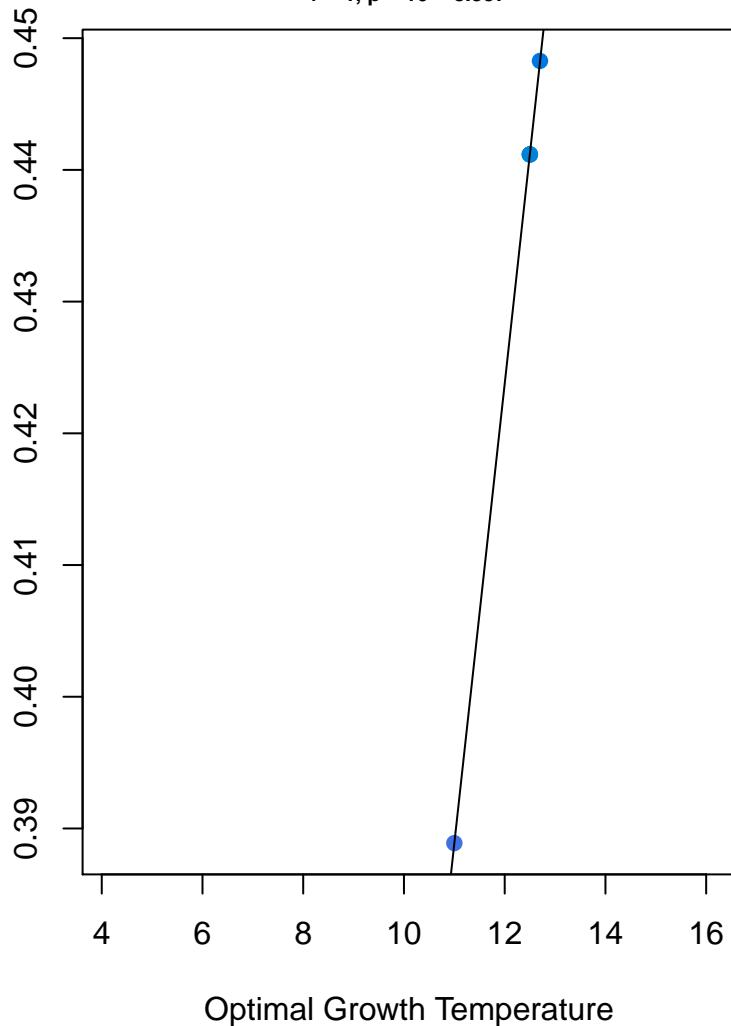


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007816
hypothetical protein
 $r = 1$, $p = 10^{-23.401}$



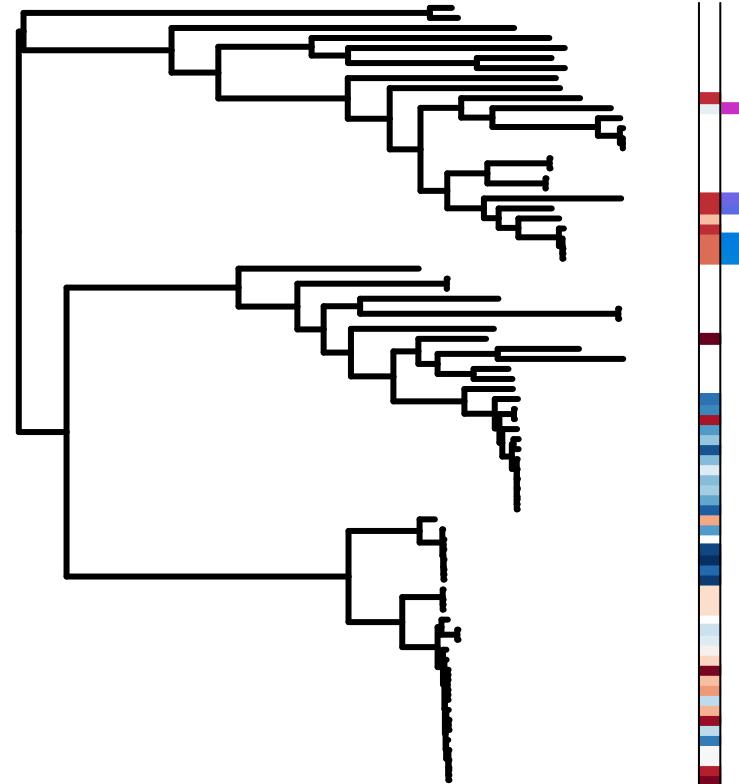
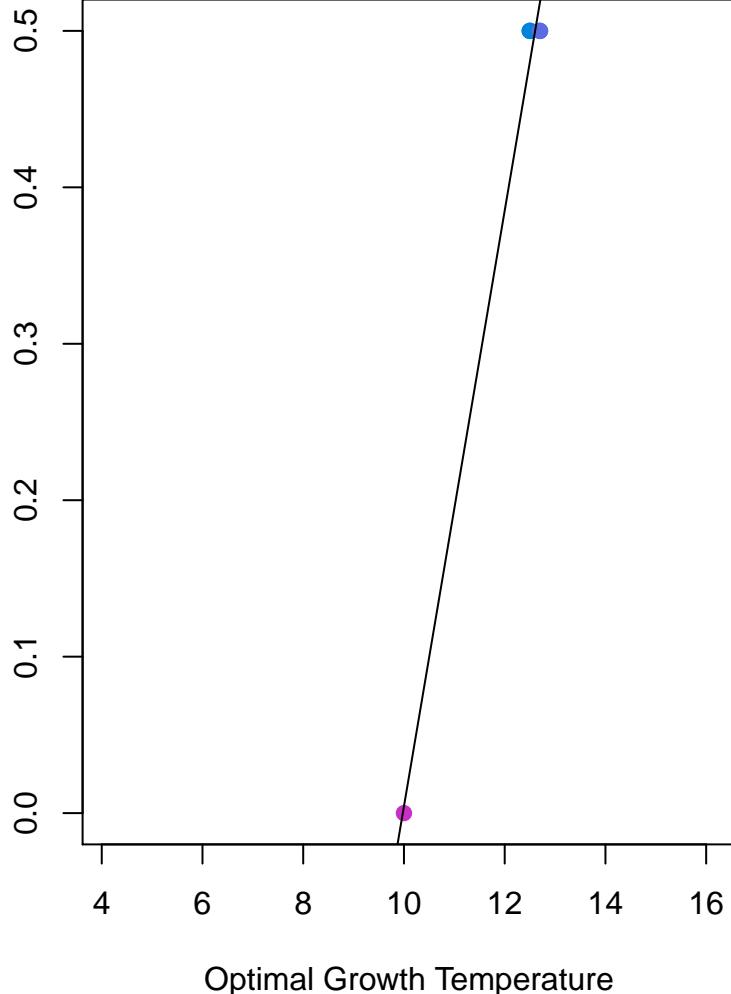
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007529
GGDEF domain protein
 $r = 1$, $p = 10^{-8.357}$

feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00004382
hypothetical protein
 $r = 0.995, p = 10^{-5.441}$

feature.plfam_id.arg_lys_ratio.mean

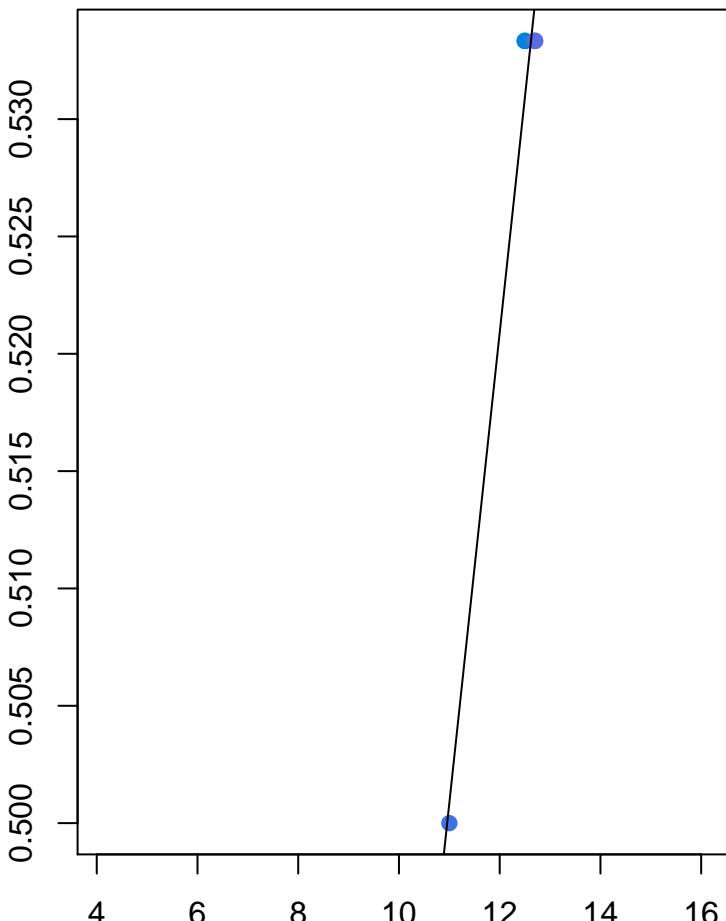


feature.plfam_id.arg_lys_ratio.mean

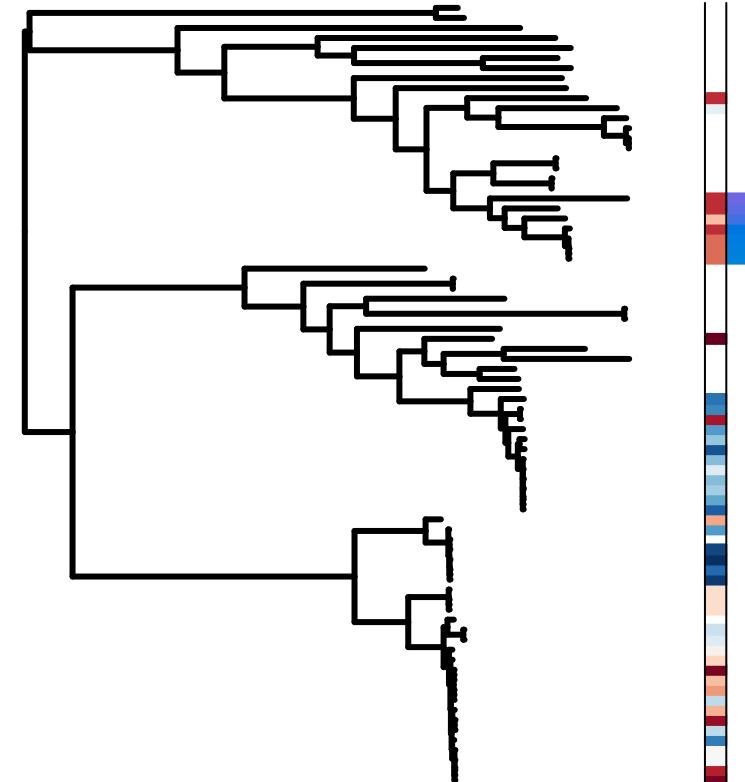
PLF_28228_00003991

serine dehydratase, beta subunit (EC 4.3.1.17) / L-serine dehydratase, alpha subunit (EC 4.3.1.1)
 $r = 0.985, p = 10^{-5.104}$

feature.plfam_id.arg_lys_ratio.mean

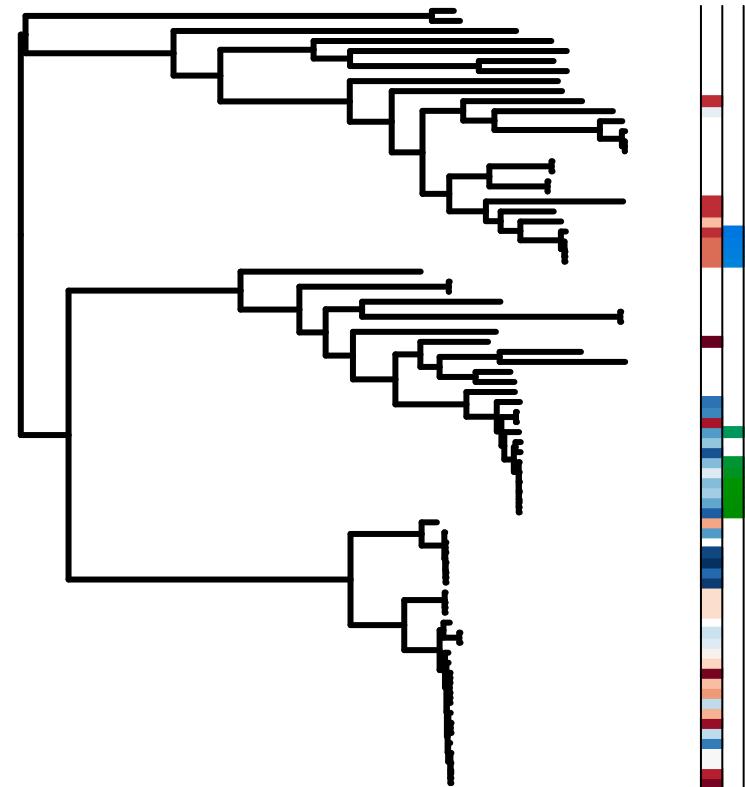
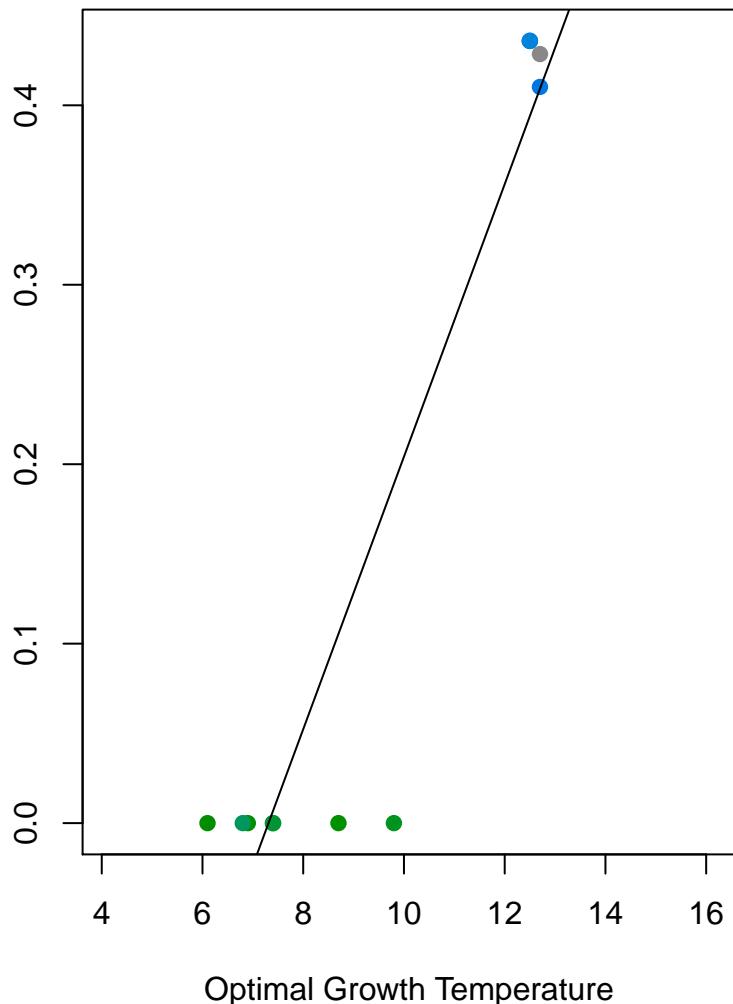


Optimal Growth Temperature



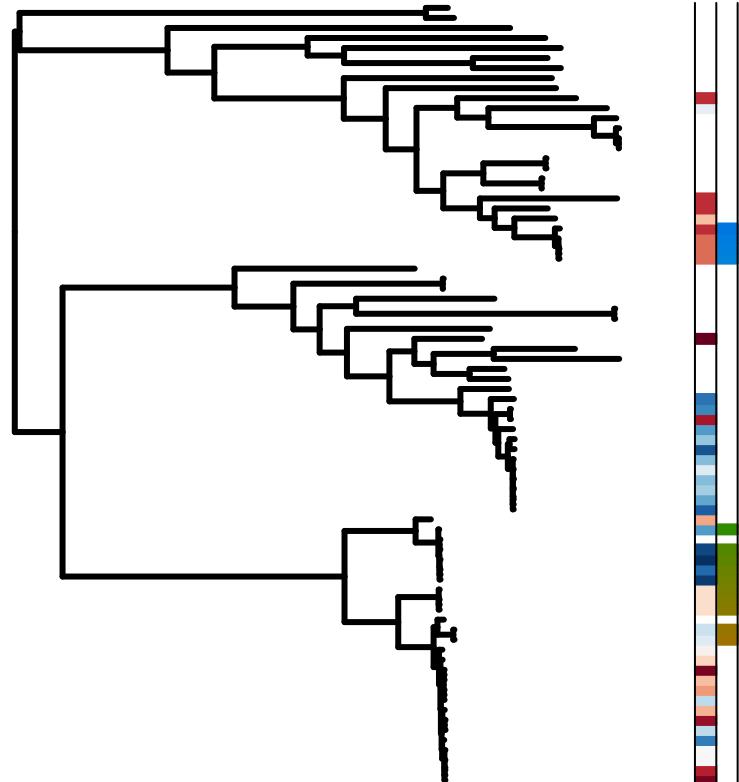
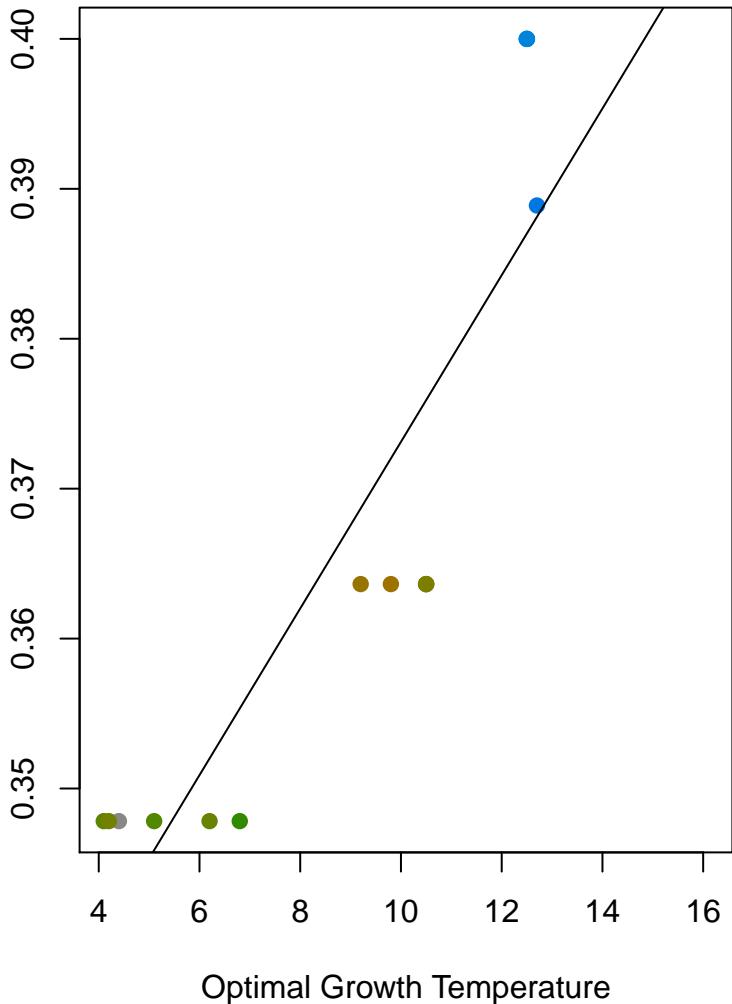
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007748
EAL domain protein
 $r = 0.939$, $p = 10^{-5.226}$

feature.plfam_id.arg_lys_ratio.mean



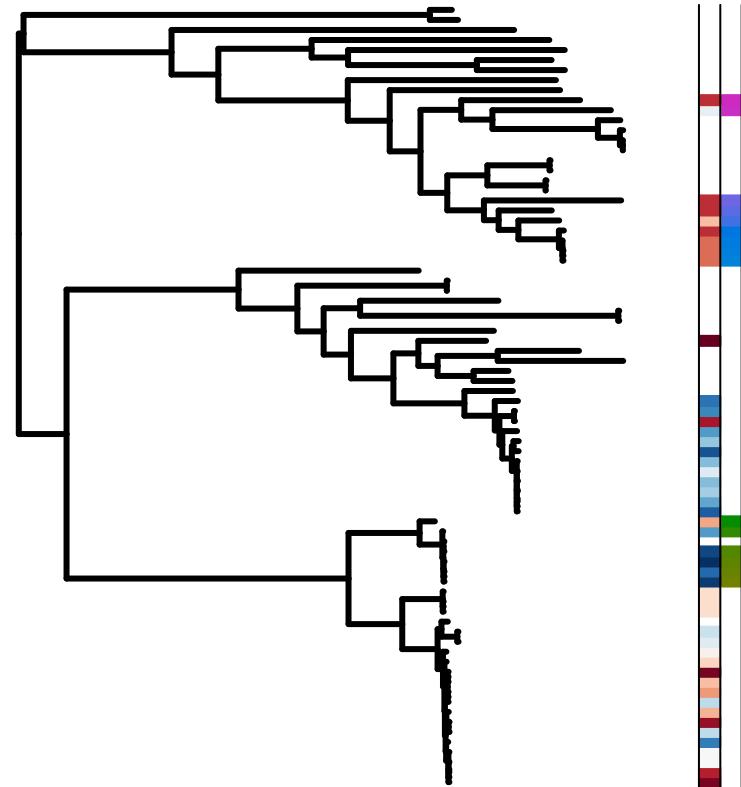
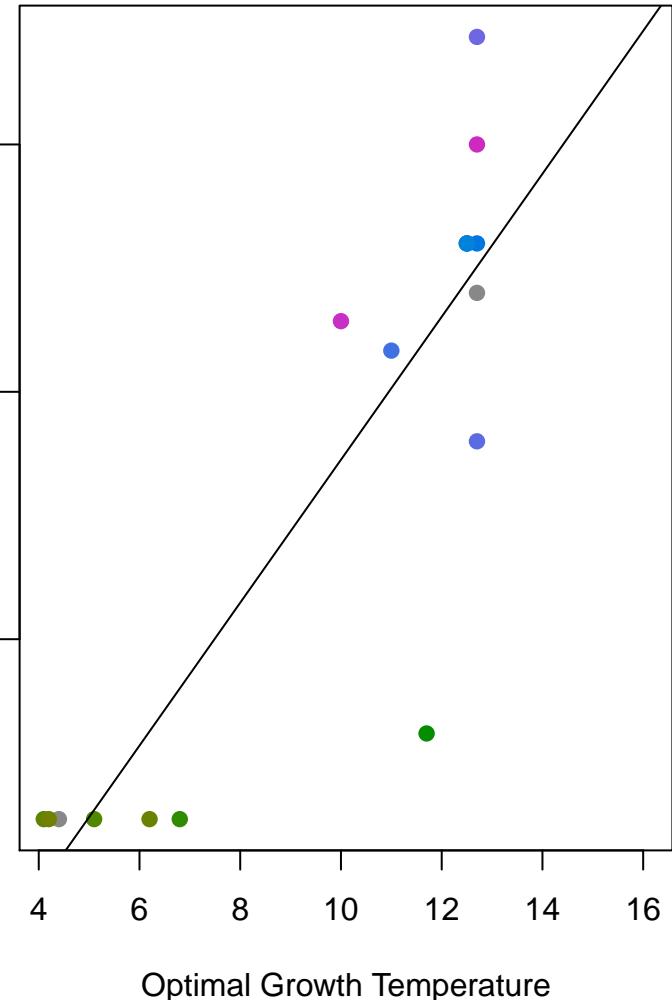
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007835
hypothetical protein
 $r = 0.888$, $p = 10^{-5.005}$

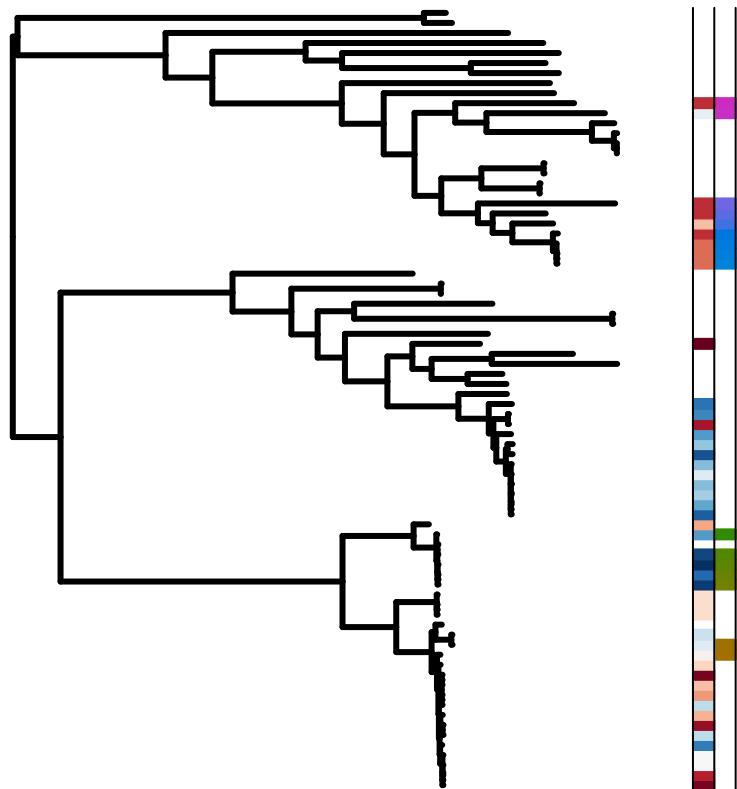
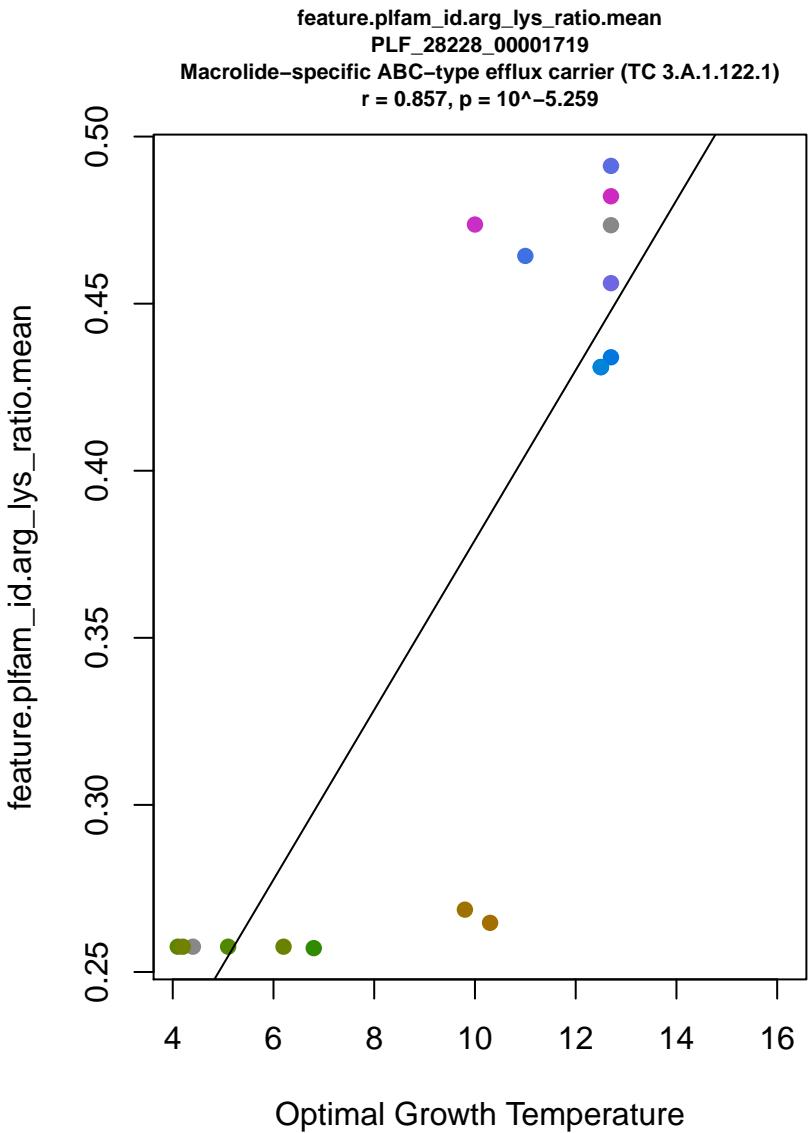
feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001528
FHA domain protein
 $r = 0.878$, $p = 10^{-5.431}$

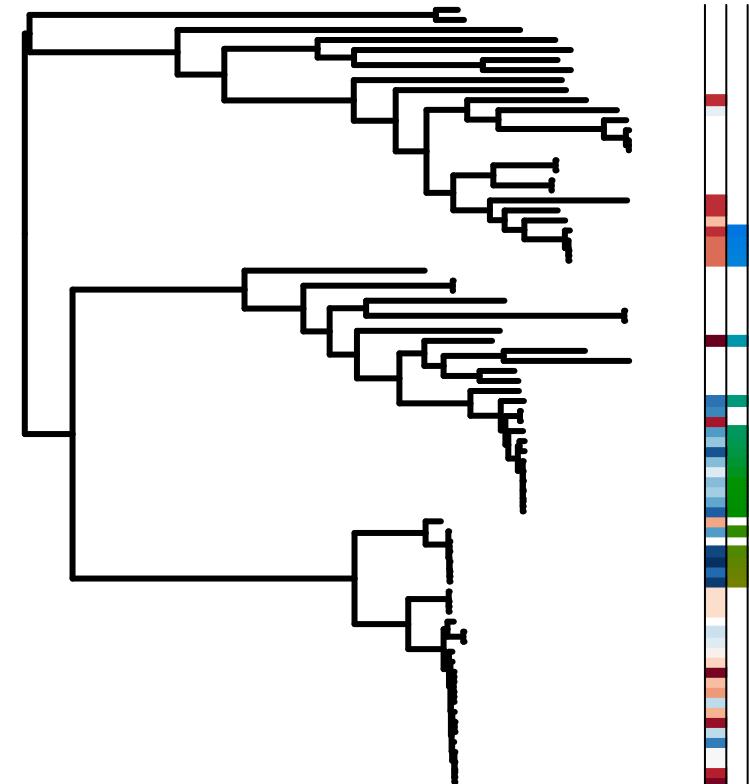
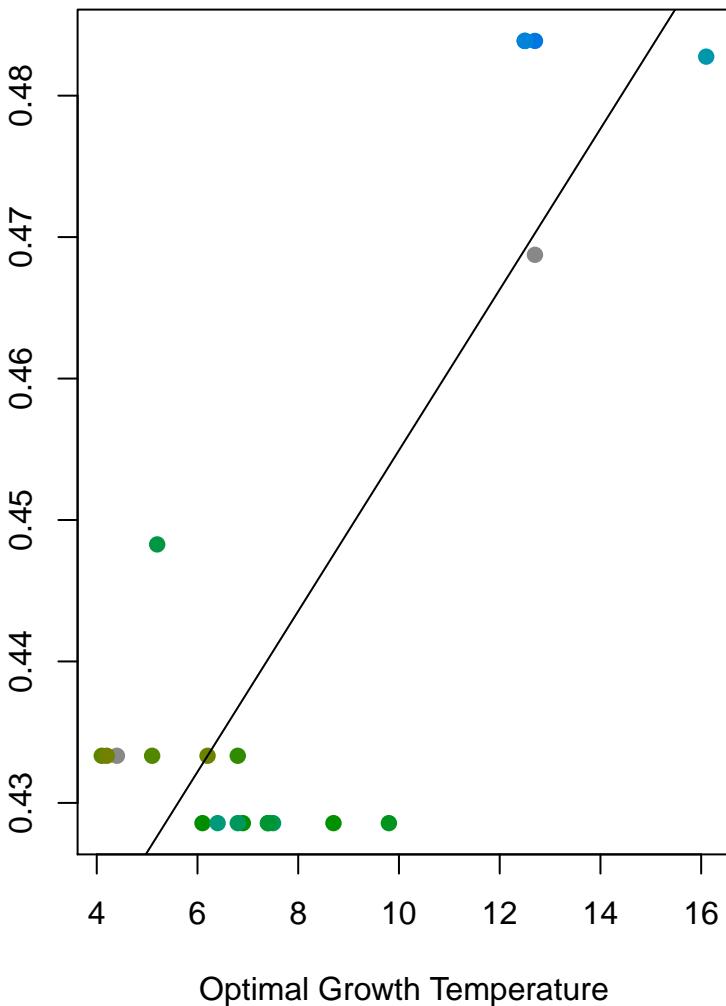
feature.plfam_id.arg_lys_ratio.mean





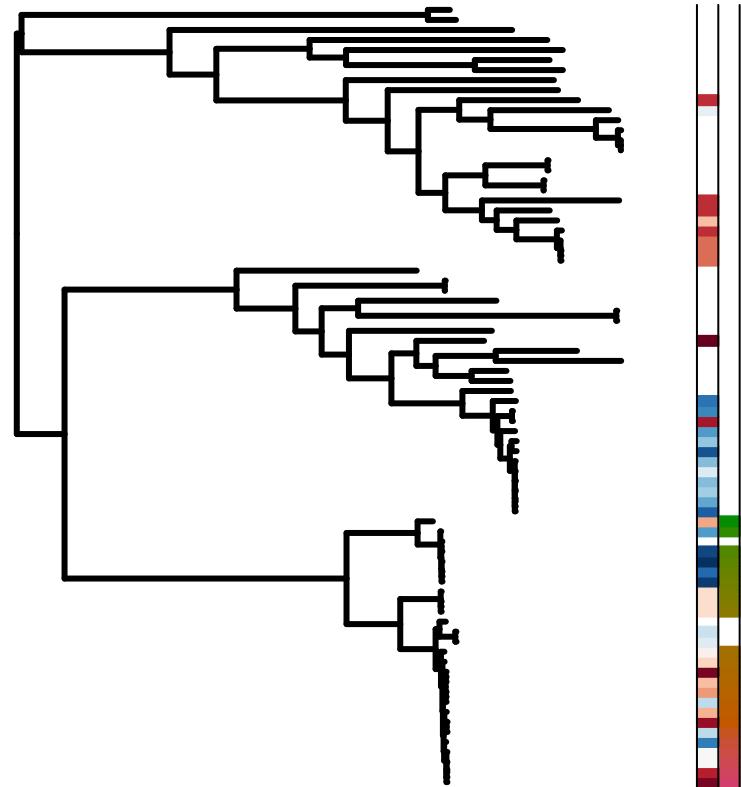
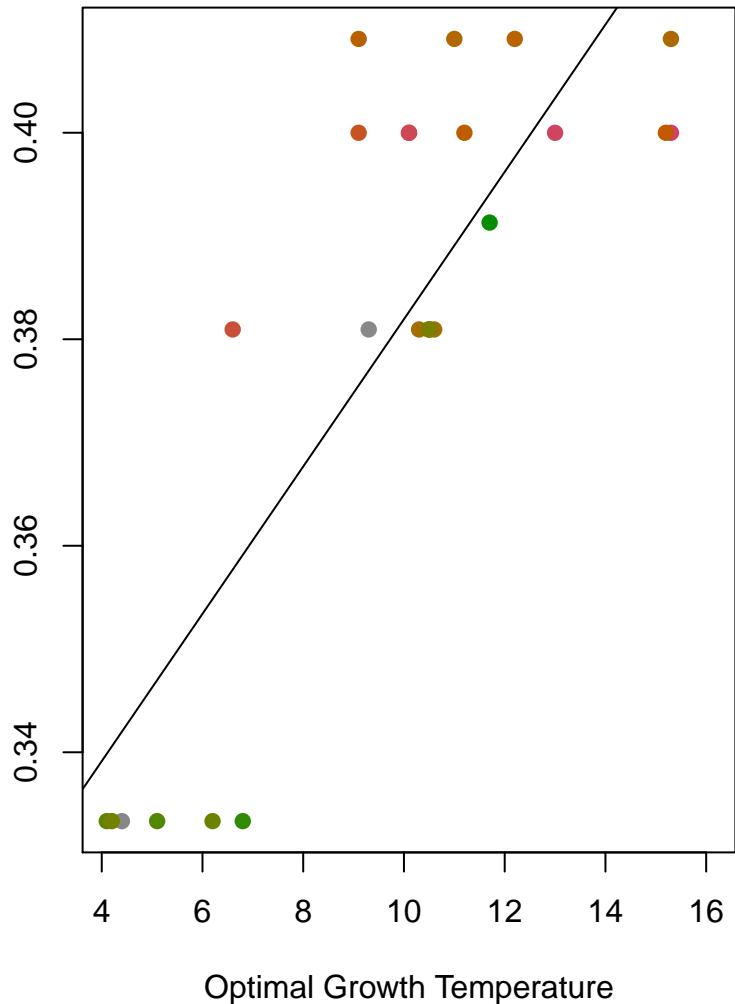
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003471
Glucose/mannose:H⁺ symporter GlcP
 $r = 0.839$, $p = 10^{-5.969}$

feature.plfam_id.arg_lys_ratio.mean



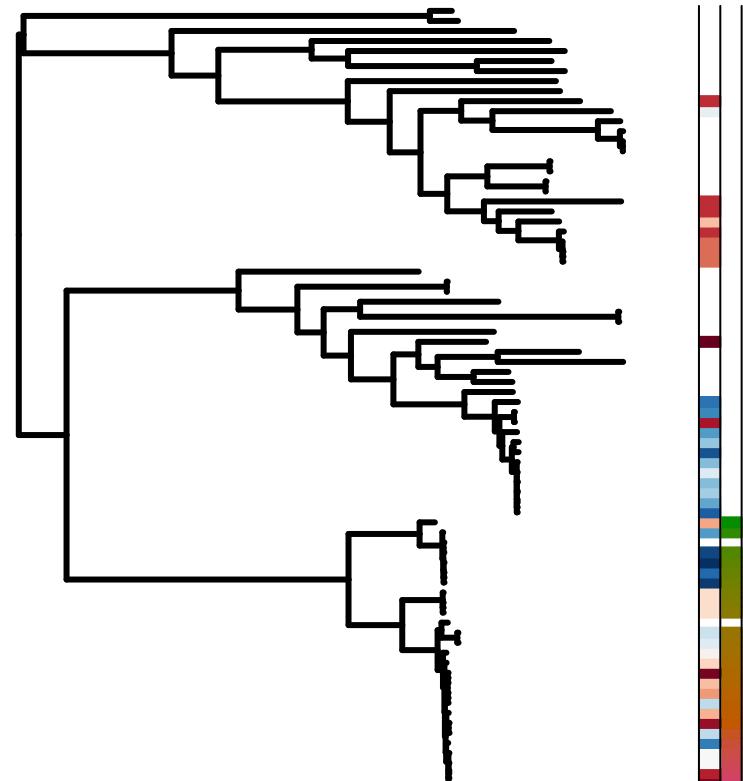
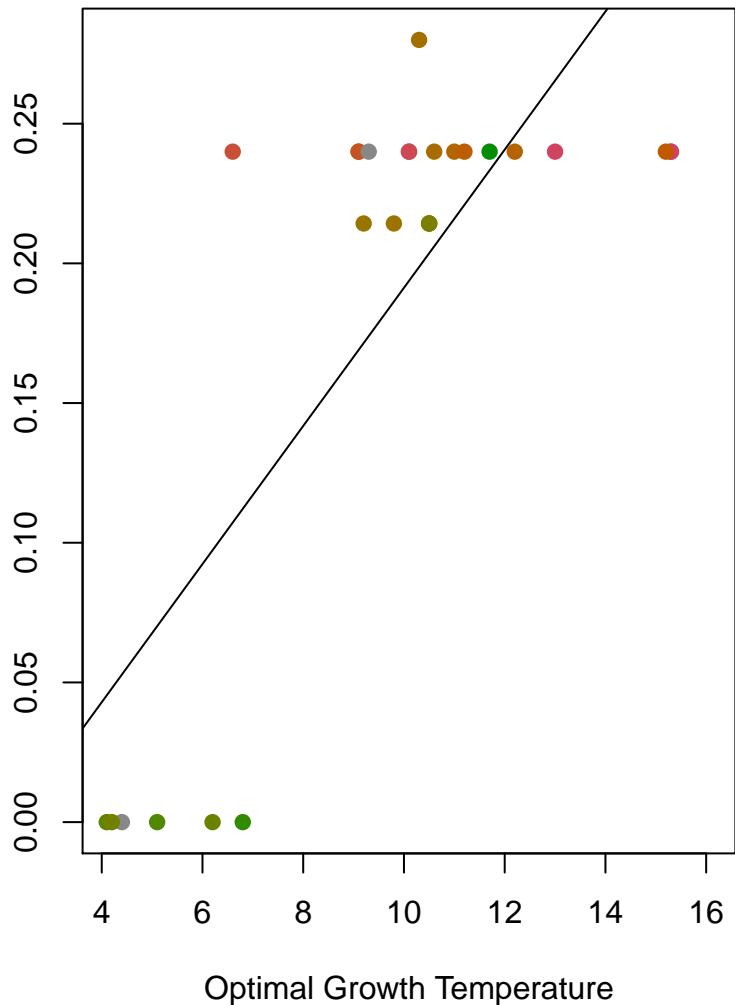
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00020926
hypothetical protein
 $r = 0.832, p = 10^{-6.589}$

feature.plfam_id.arg_lys_ratio.mean



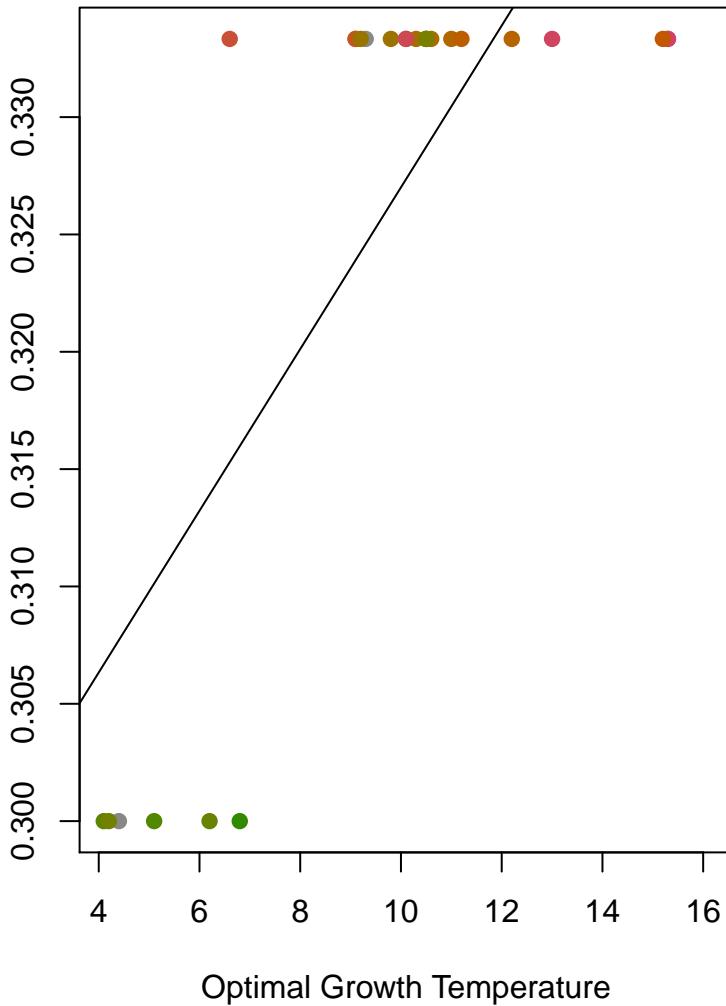
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00031426
hypothetical protein
 $r = 0.781$, $p = 10^{-5.826}$

feature.plfam_id.arg_lys_ratio.mean

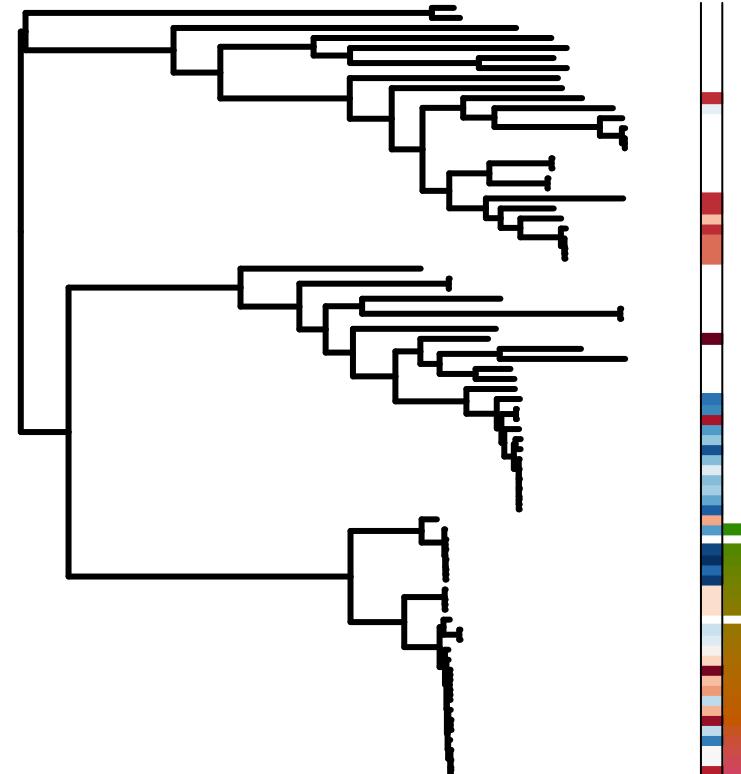


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00032018
hypothetical protein
 $r = 0.775, p = 10^{-5.478}$

feature.plfam_id.arg_lys_ratio.mean

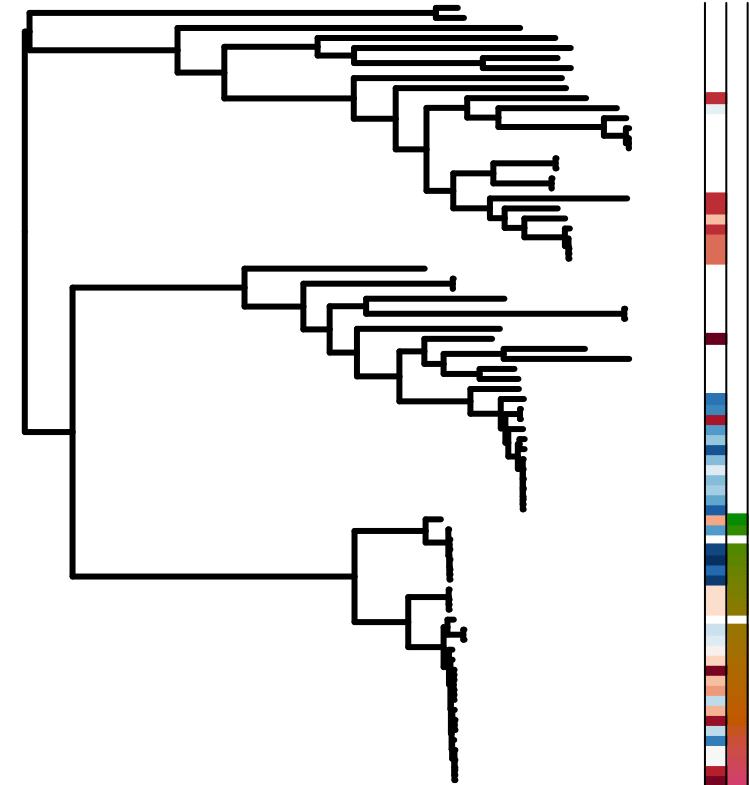
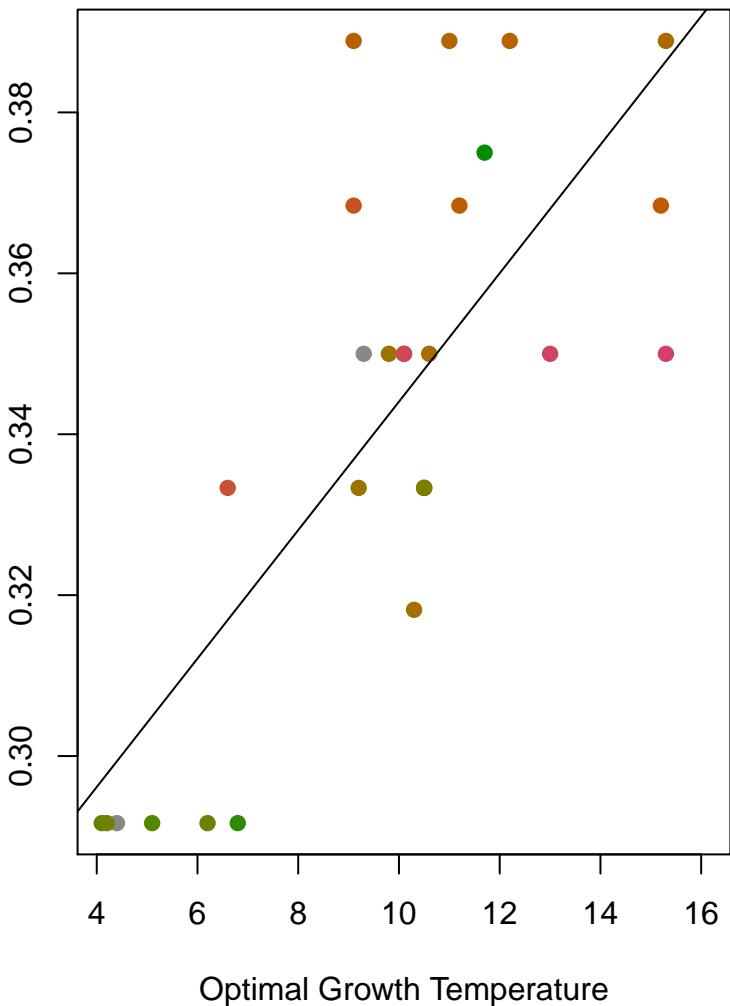


Optimal Growth Temperature



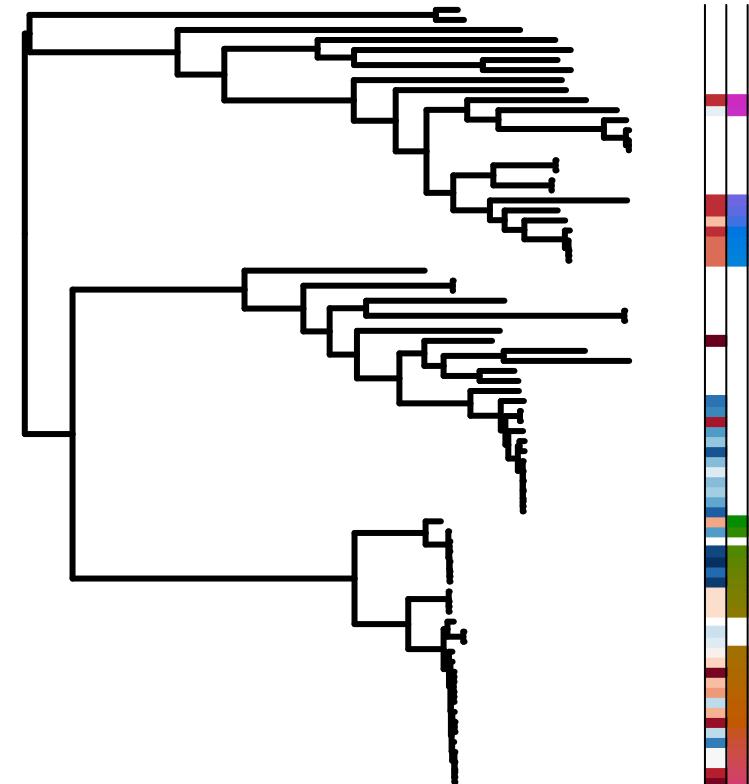
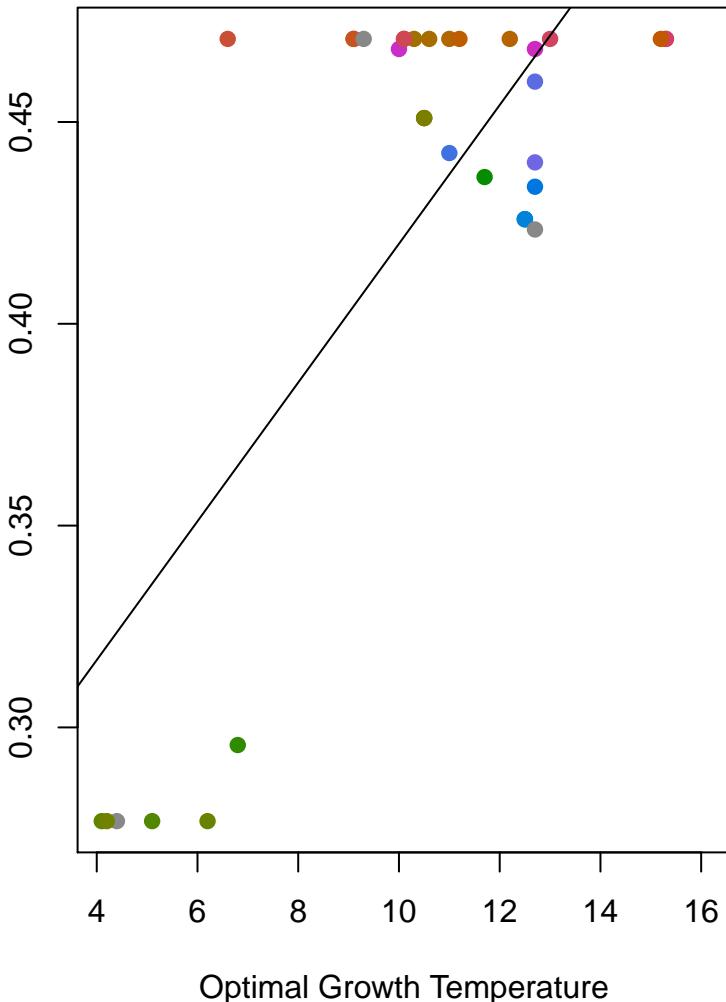
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00030698
hypothetical protein
 $r = 0.767, p = 10^{-5.515}$

feature.plfam_id.arg_lys_ratio.mean



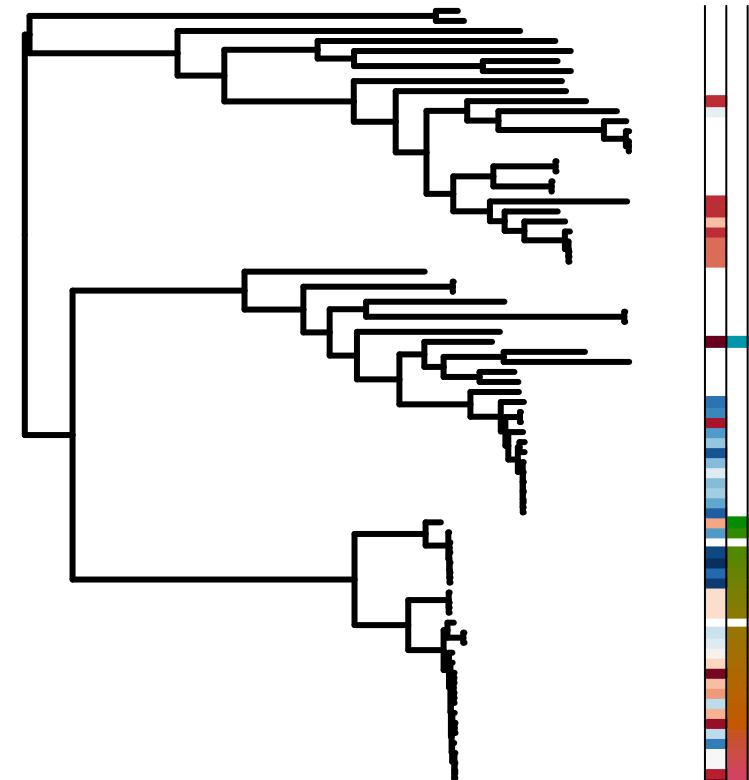
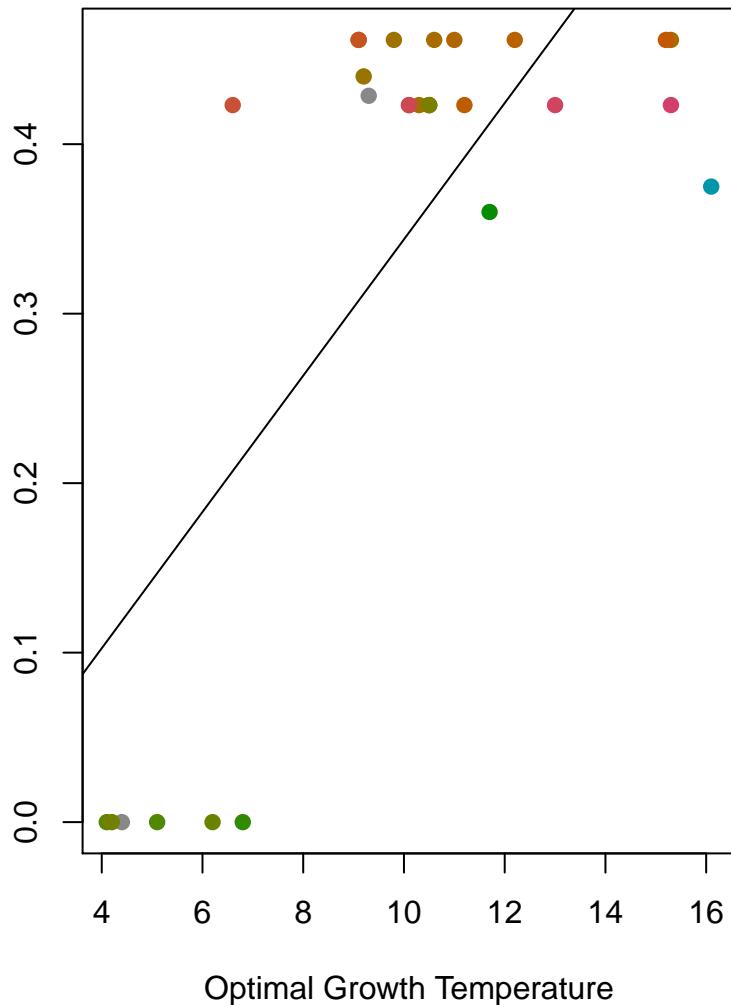
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001289
Uncharacterized protease YegQ
 $r = 0.752$, $p = 10^{-6.708}$

feature.plfam_id.arg_lys_ratio.mean

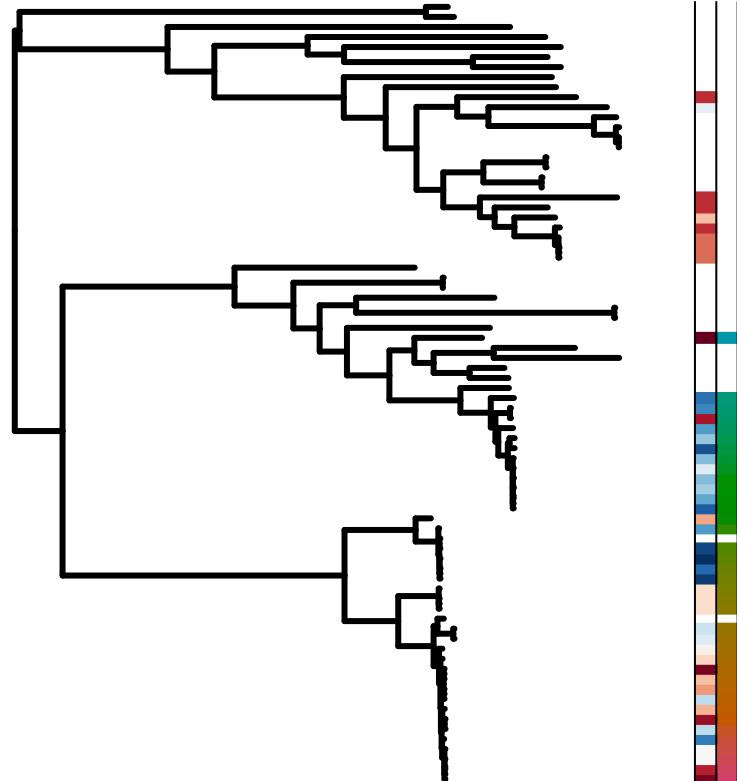
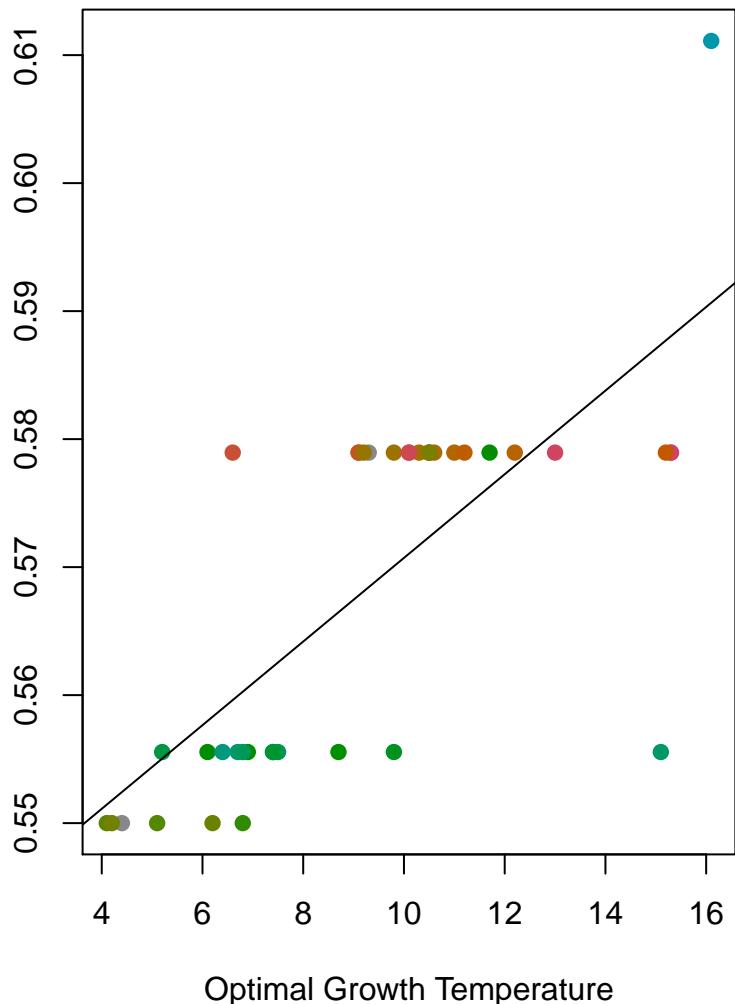


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00021389
hypothetical protein
 $r = 0.738, p = 10^{-5.136}$

feature.plfam_id.arg_lys_ratio.mean

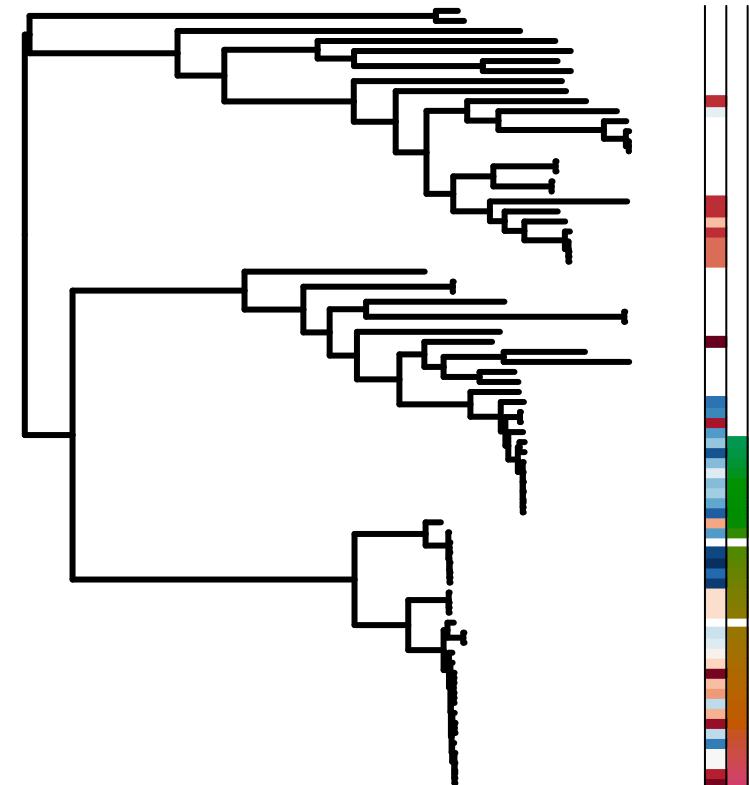
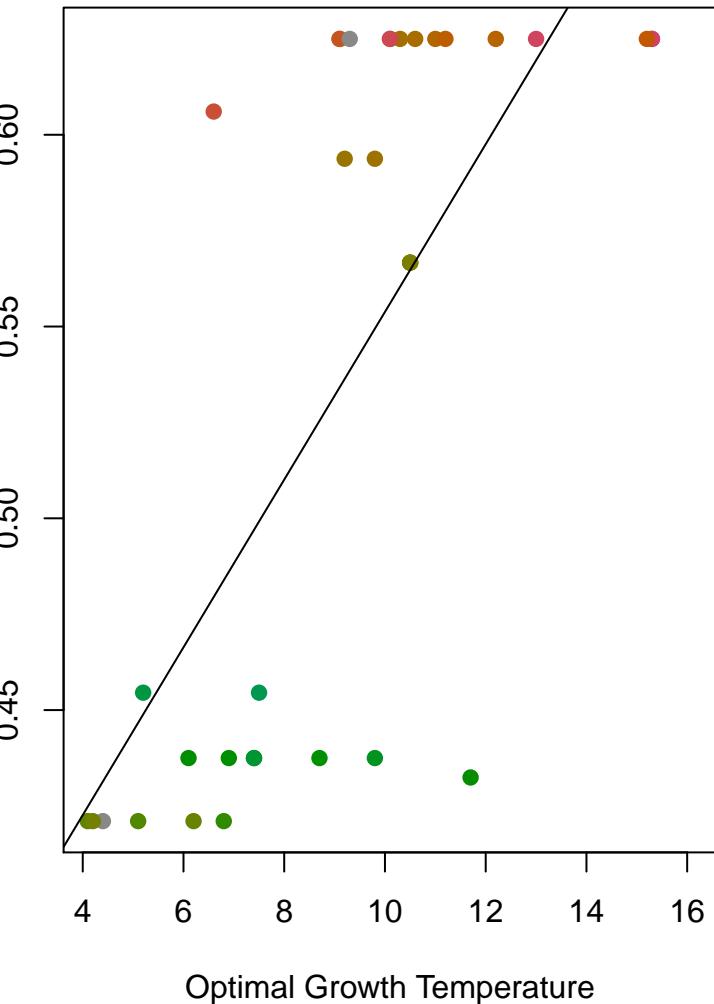


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00014664
hypothetical protein
 $r = 0.734$, $p = 10^{-7.161}$

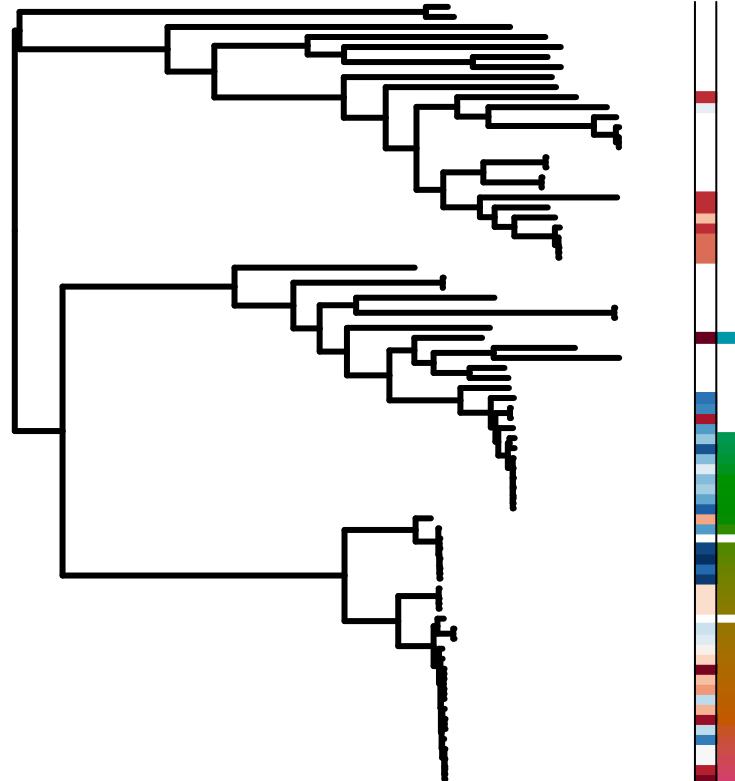
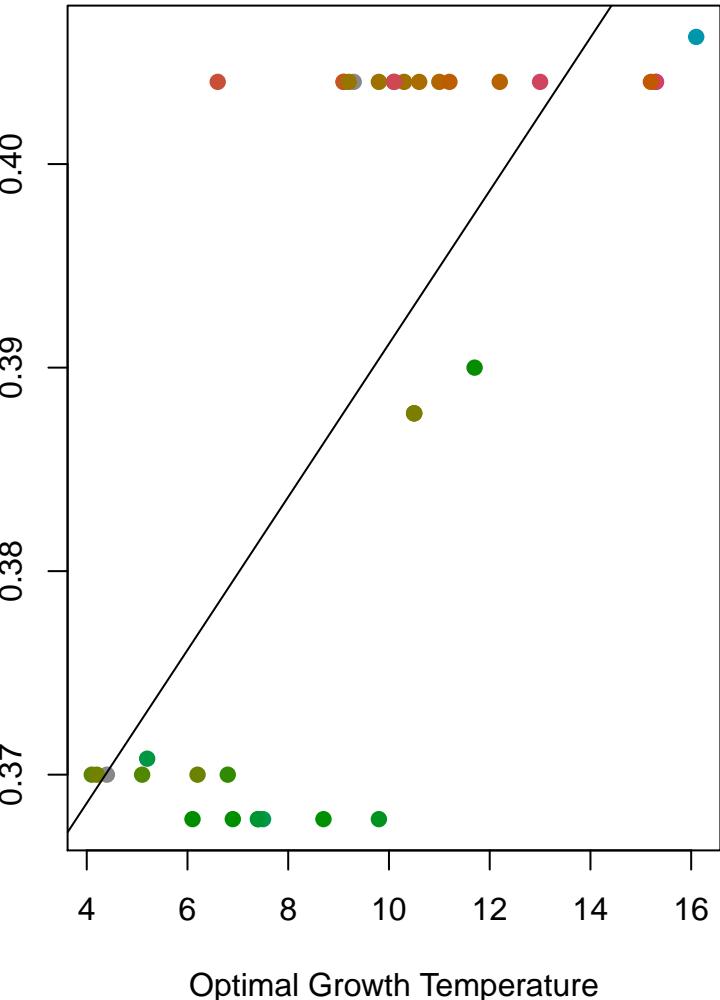


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00013738
hypothetical protein
 $r = 0.72$, $p = 10^{-5.959}$

feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00018174
hypothetical protein
 $r = 0.719, p = 10^{-6.111}$

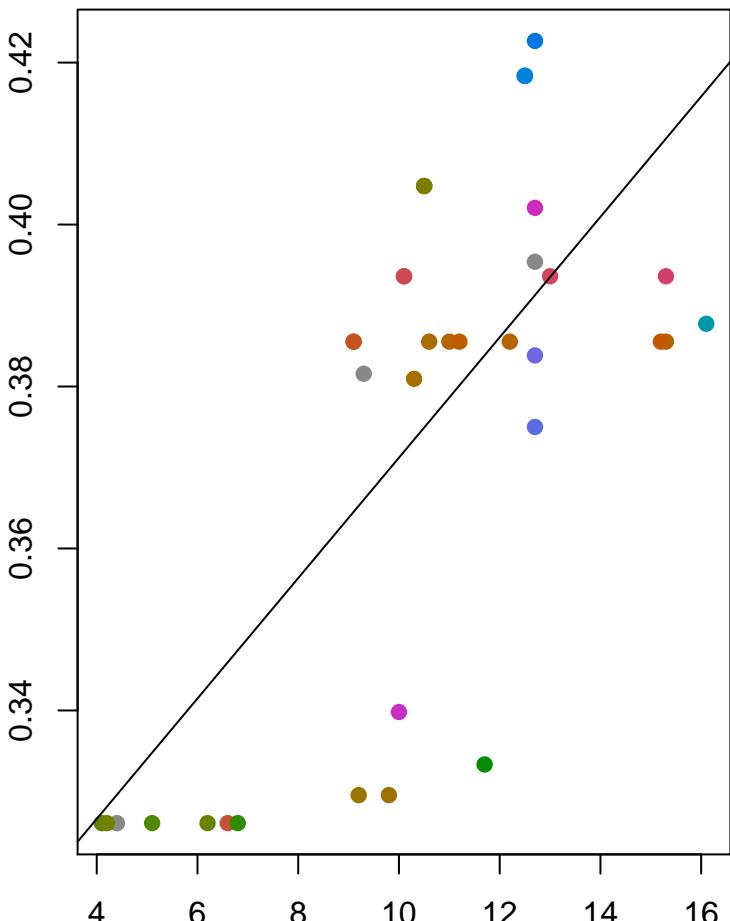


feature.plfam_id.arg_lys_ratio.mean

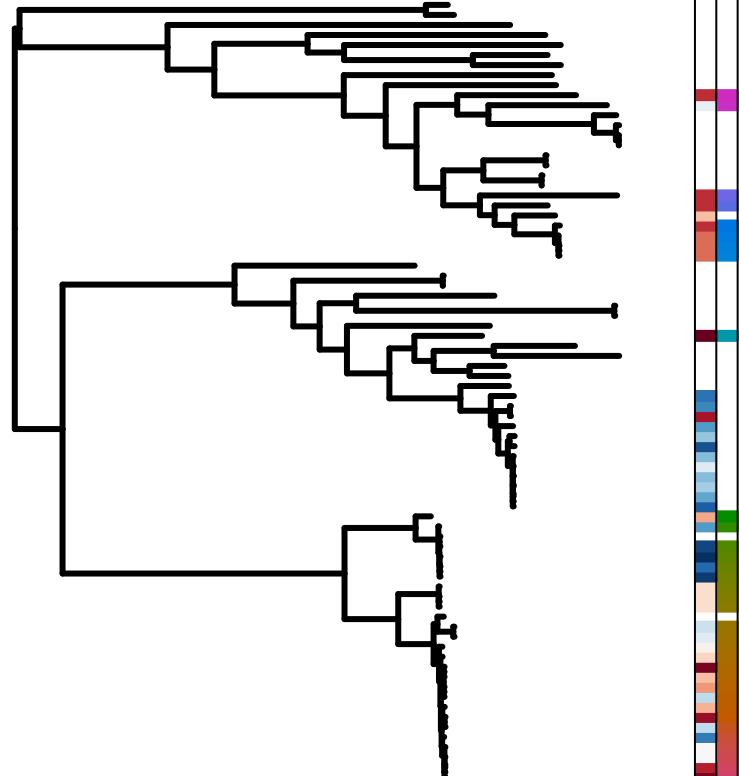
PLF_28228_00002160

Two-component system sensor histidine kinase/response regulator hybrid
 $r = 0.711, p = 10^{-6.097}$

feature.plfam_id.arg_lys_ratio.mean



Optimal Growth Temperature



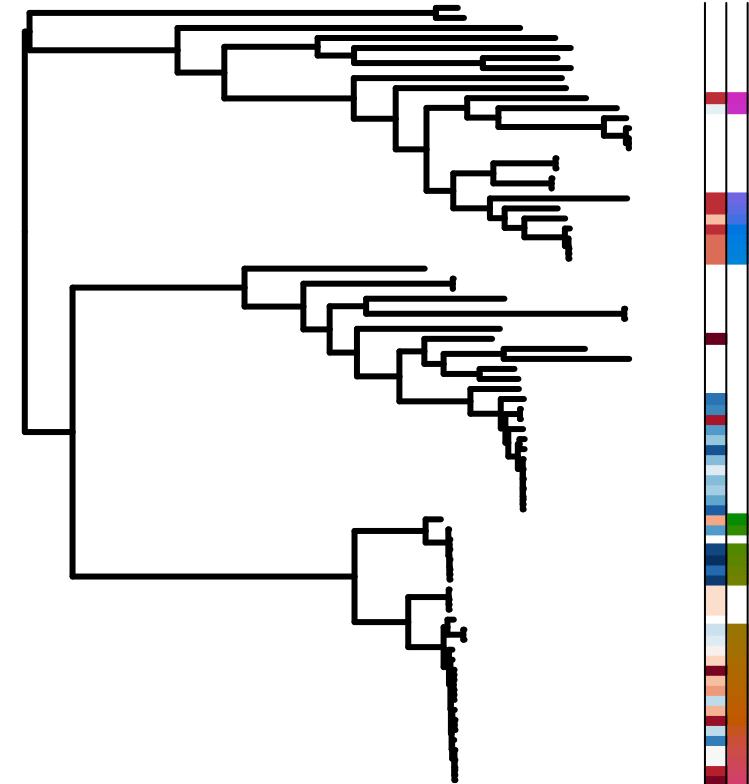
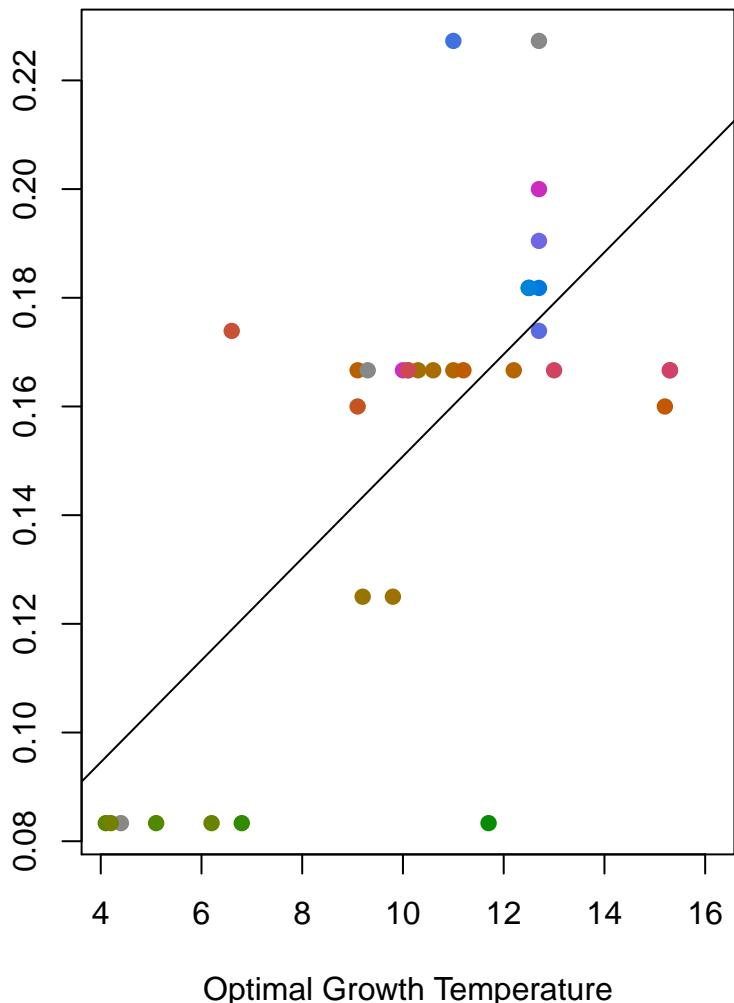
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000629

N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)

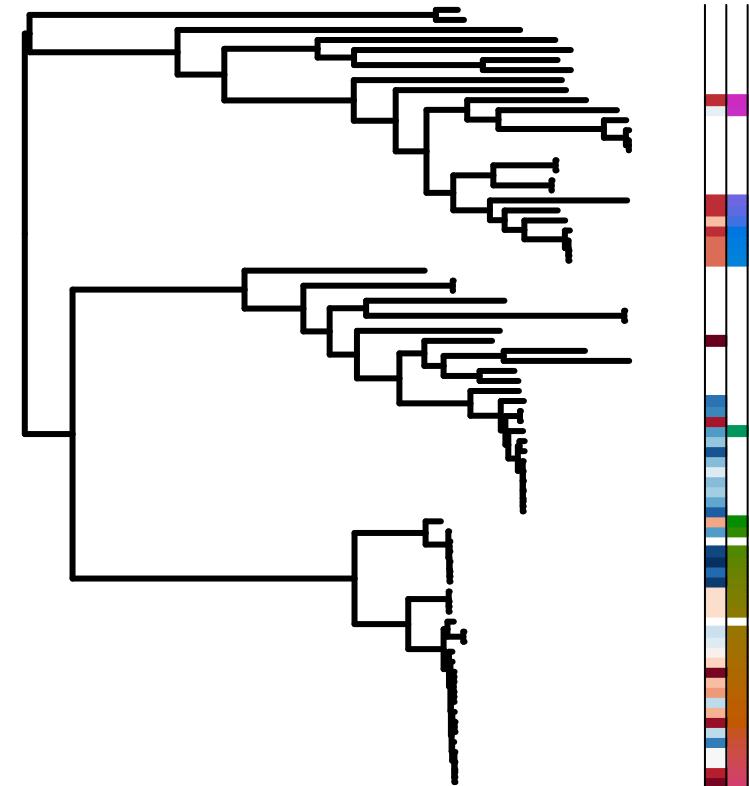
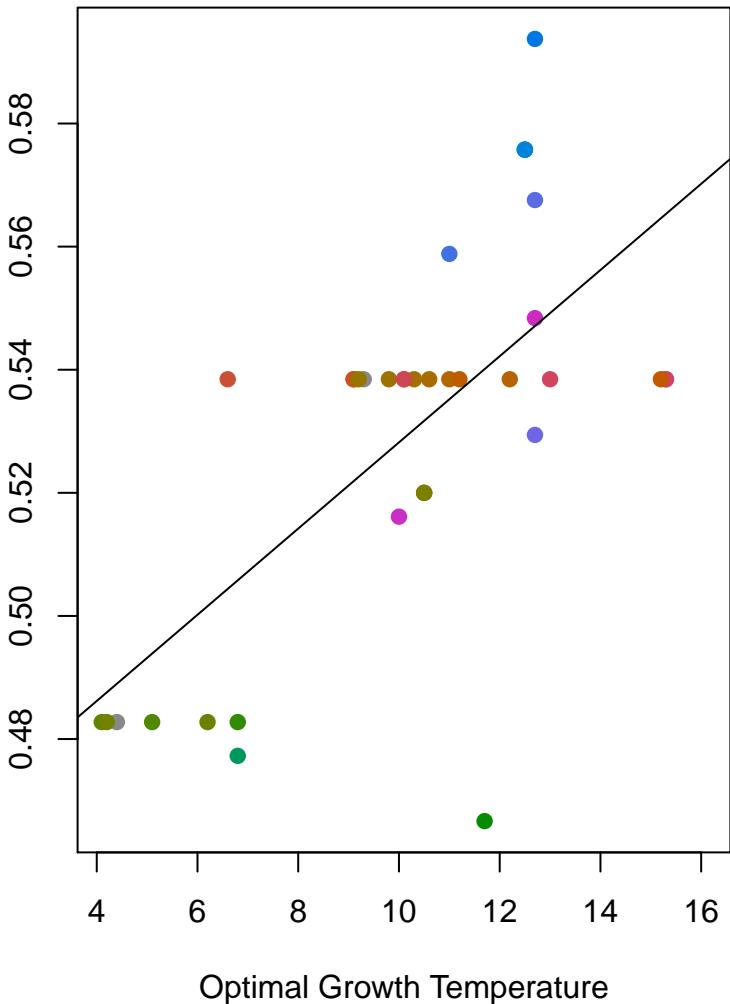
$r = 0.701, p = 10^{-5.42}$

feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001857
GGDEF domain protein
 $r = 0.676$, $p = 10^{-5.349}$

feature.plfam_id.arg_lys_ratio.mean

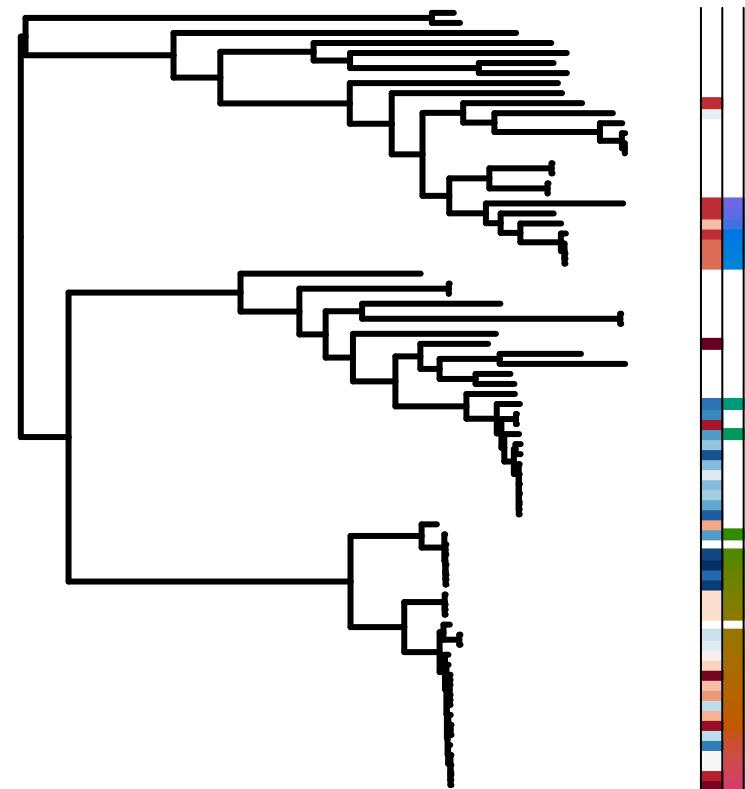
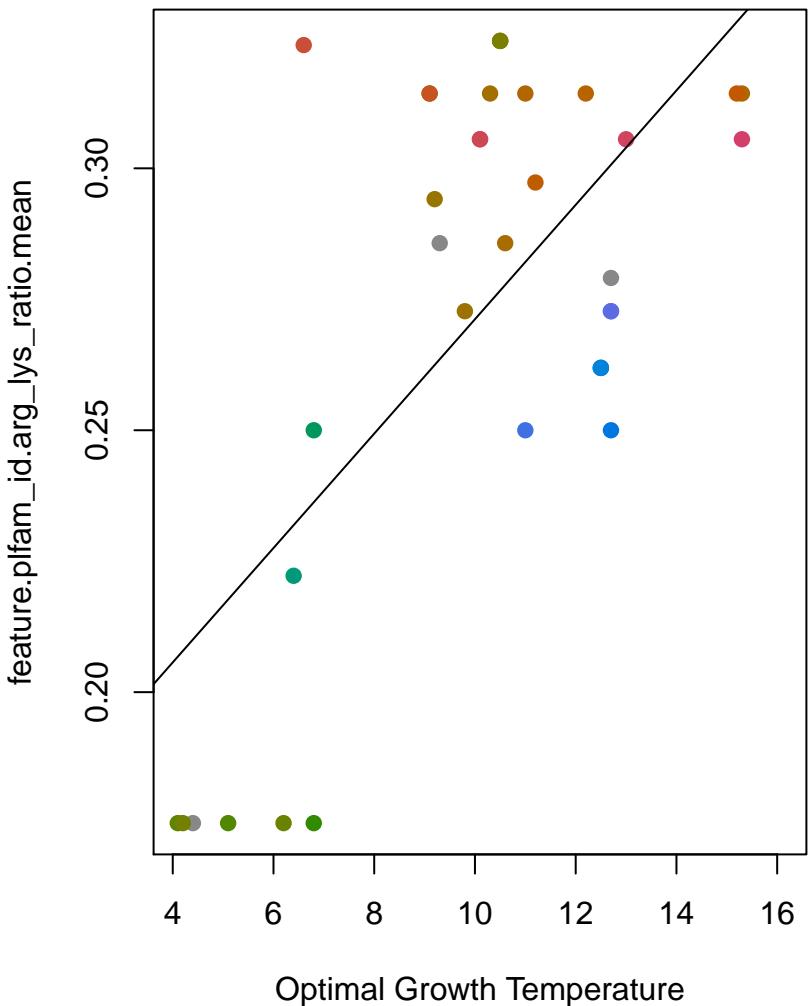


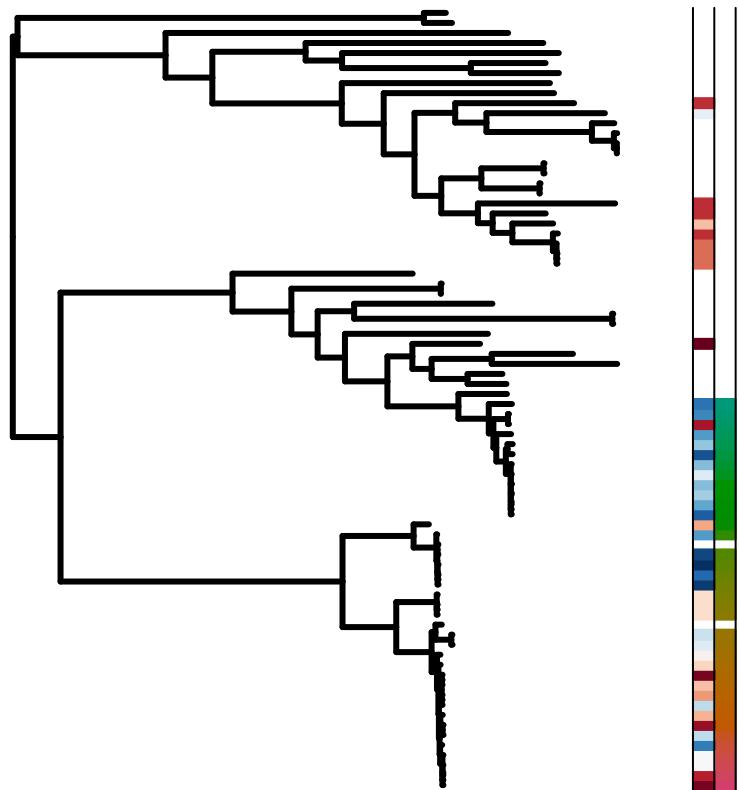
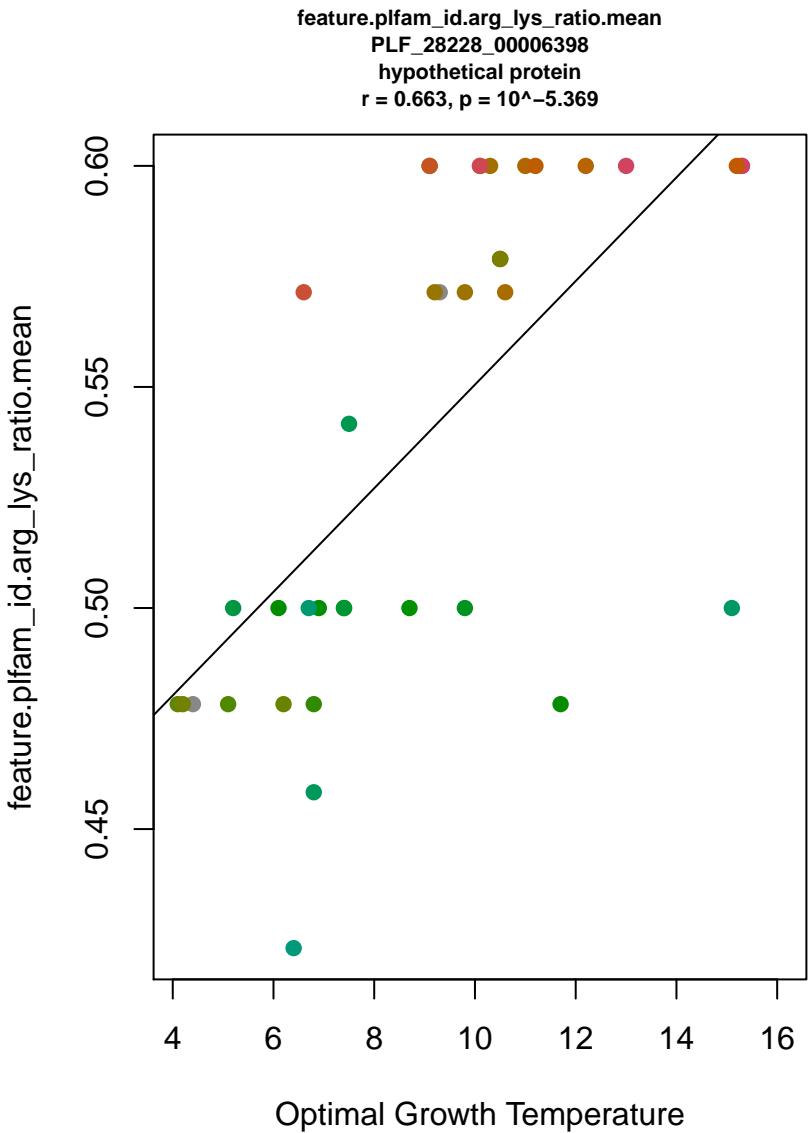
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00003411

r = 0.666, p = 10^-5.036

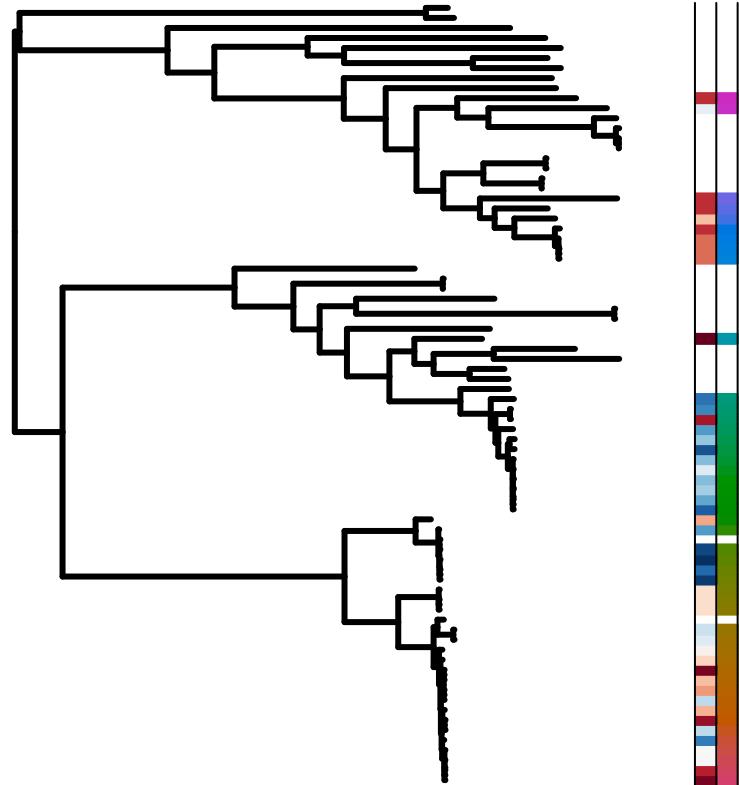
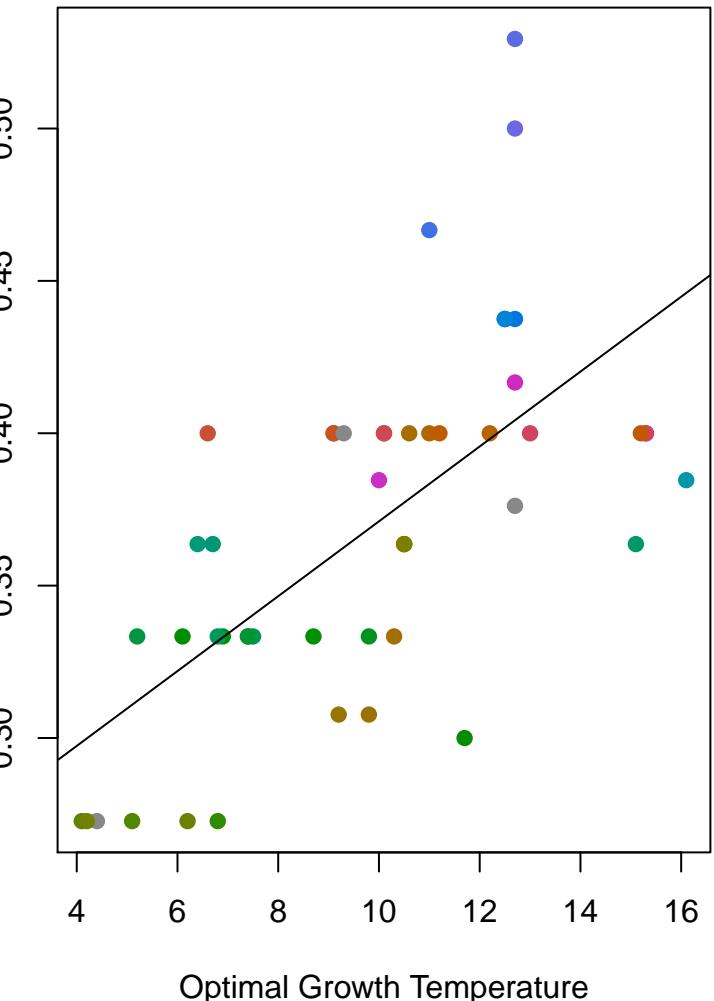
acetyl-beta-D-mannosaminyl-1,4-N-acetyl-D-glucosaminylidiphosphoundecaprenyl glycerol





feature.pifam_id.arg_lys_ratio.mean
PLF_28228_00001718
MSHA pilin protein MshB
 $r = 0.662, p = 10^{-6.78}$

feature.pifam_id.arg_lys_ratio.mean

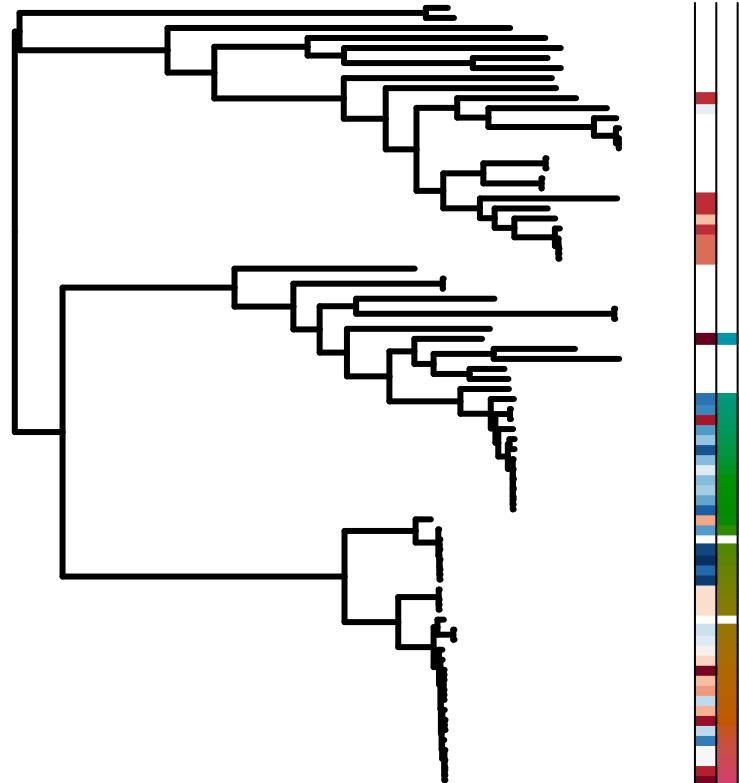
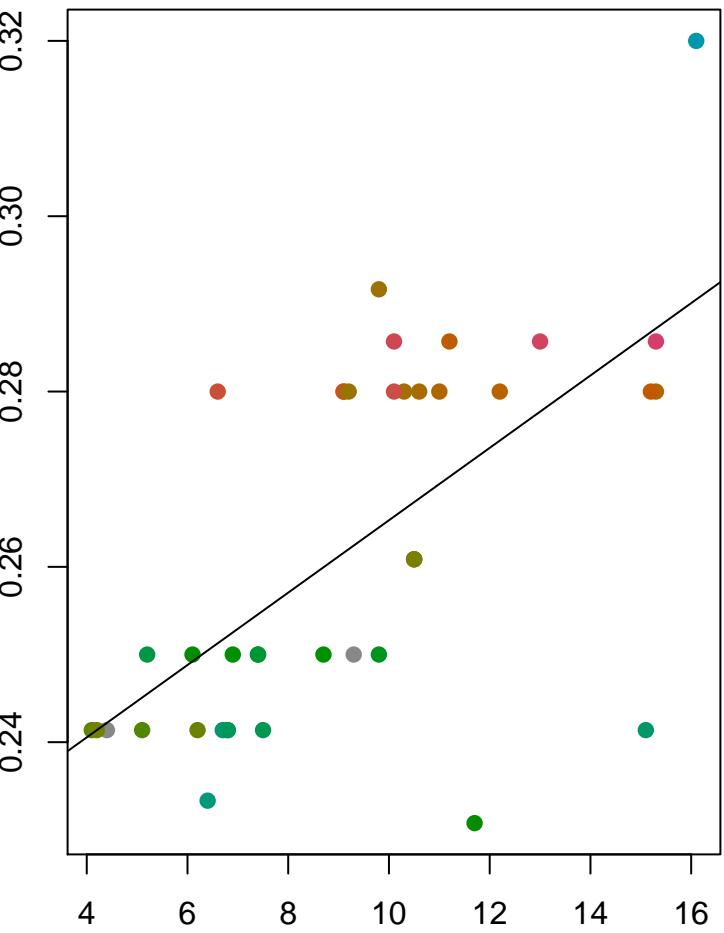


feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00012901

S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), eukaryotic
 $r = 0.638, p = 10^{-5.032}$

feature.plfam_id.arg_lys_ratio.mean



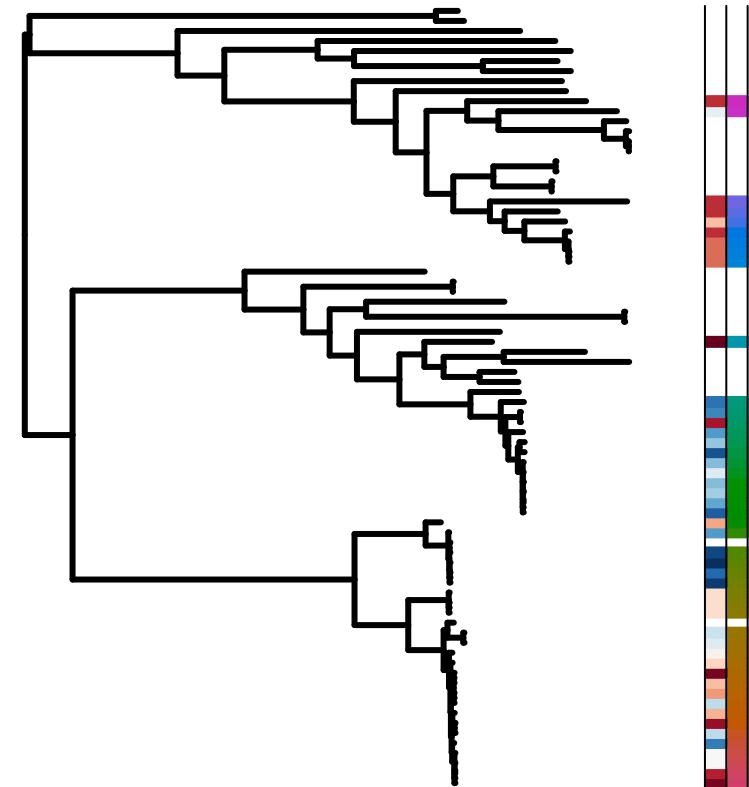
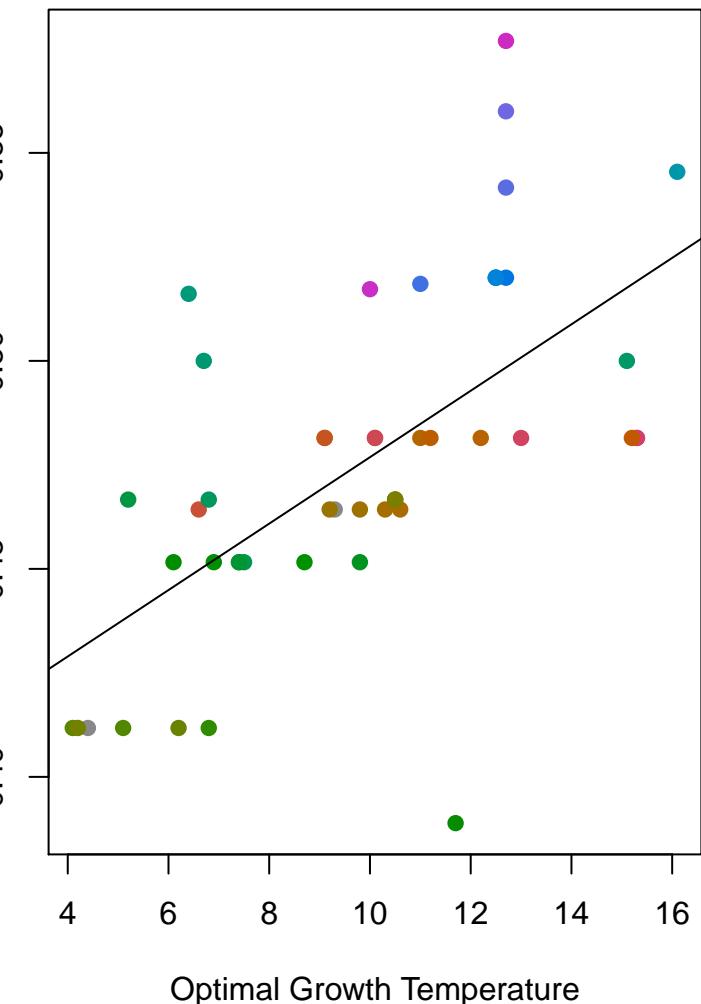
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000268

3-deoxy-D-manno-octulonic acid kinase (EC 2.7.1.166)

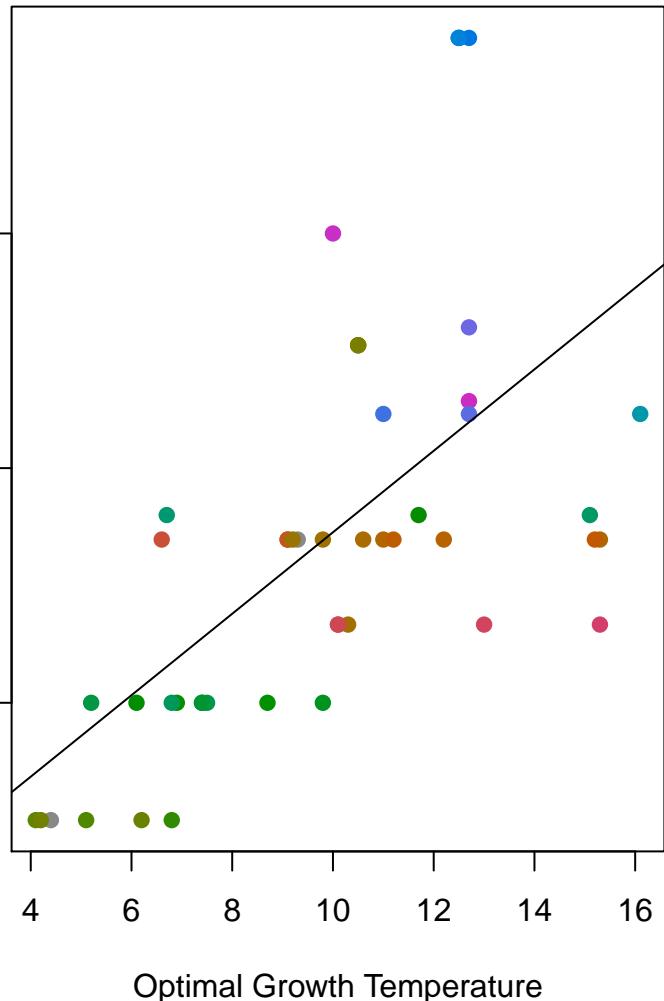
$r = 0.625, p = 10^{-5.794}$

feature.plfam_id.arg_lys_ratio.mean

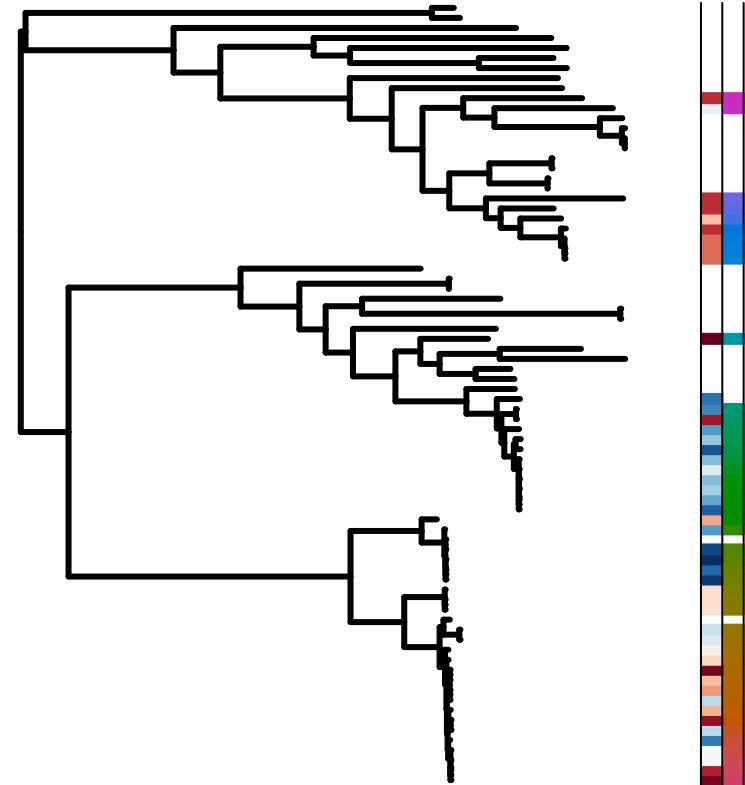


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000242
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)
 $r = 0.612$, $p = 10^{-5.421}$

feature.plfam_id.arg_lys_ratio.mean



Optimal Growth Temperature

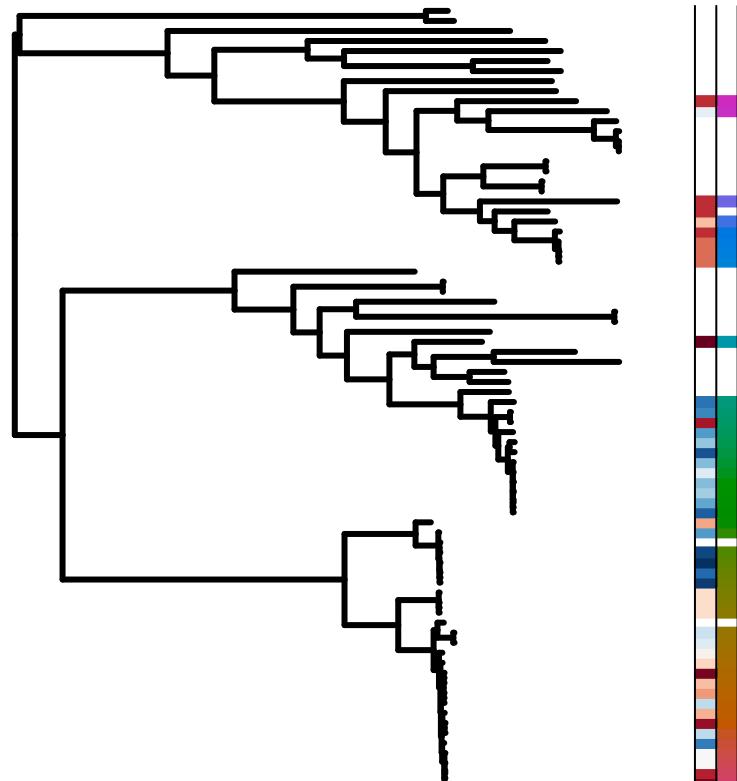
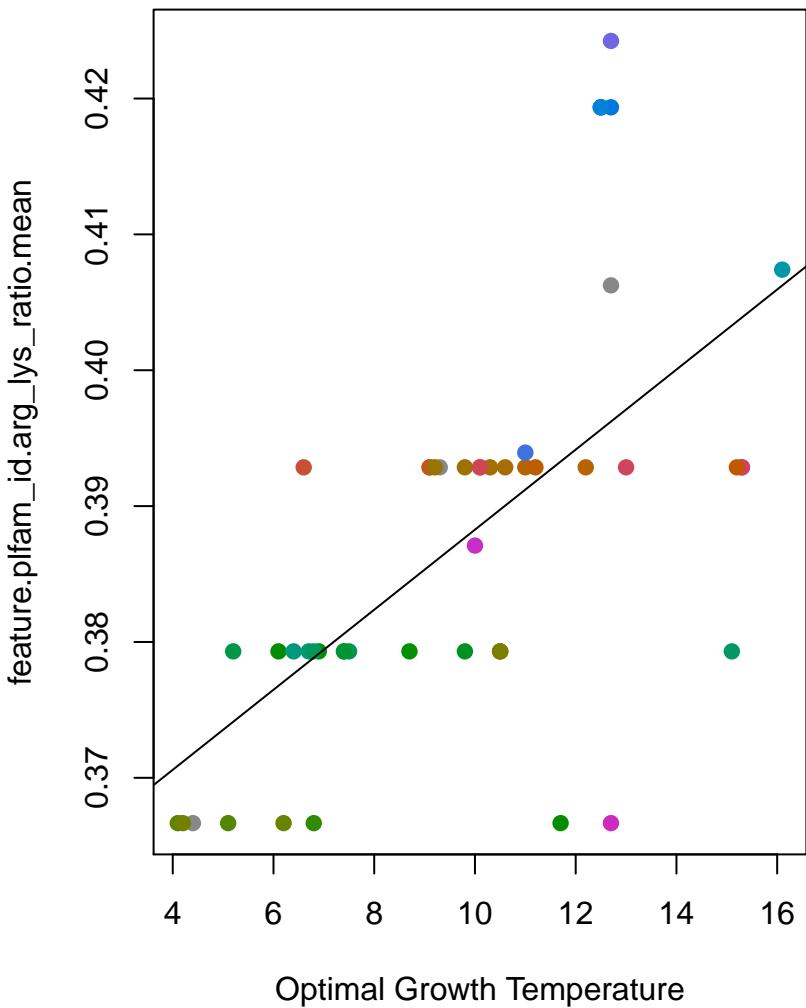


feature.plfam_id.arg_lys_ratio.mean

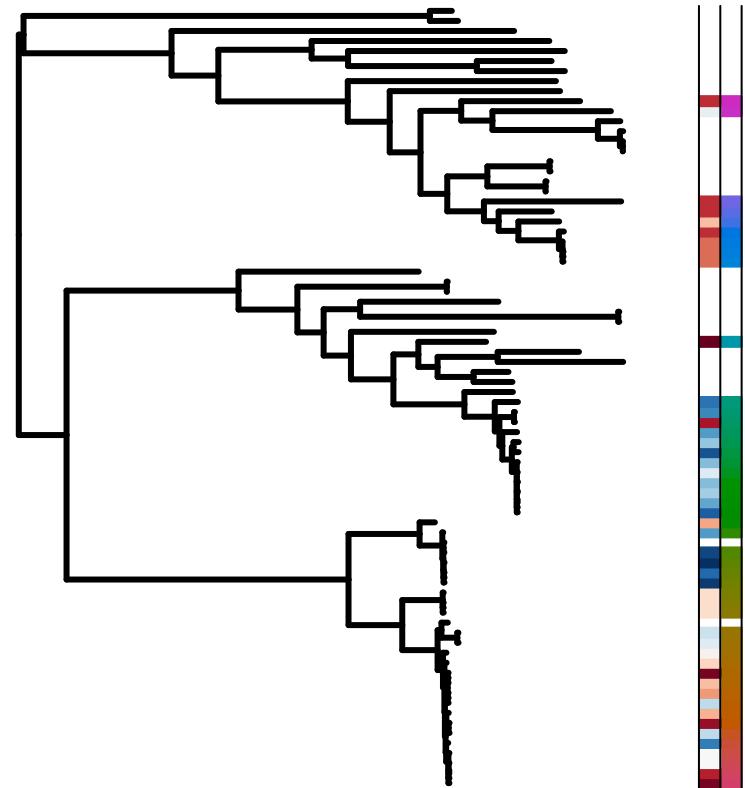
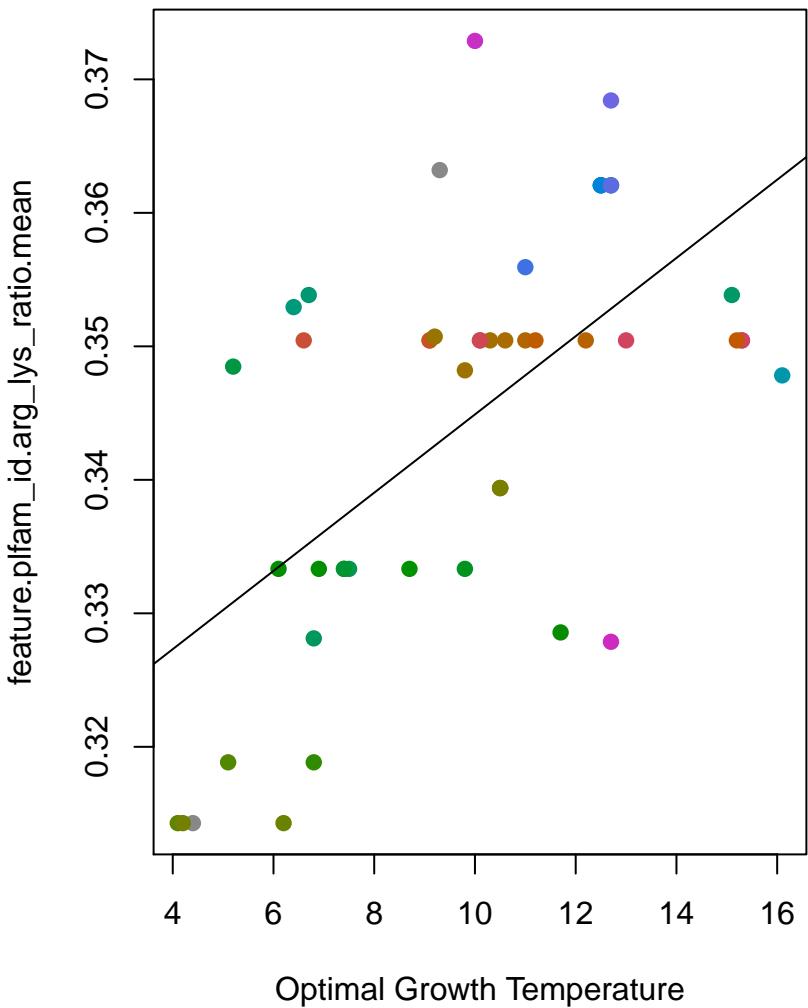
PLF_28228_00000103

5-methyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / Methylenetetrahydrofolate dehydrogenase (NADP+)

r = 0.611, p = 10^-5.509



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000597
Malate synthase G (EC 2.3.3.9)
 $r = 0.611$, $p = 10^{-5.606}$



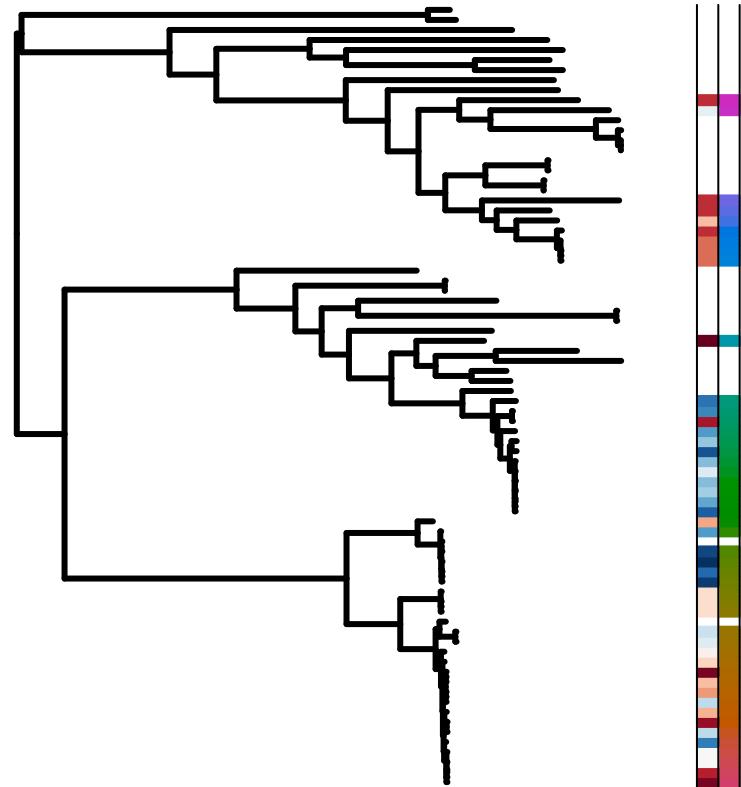
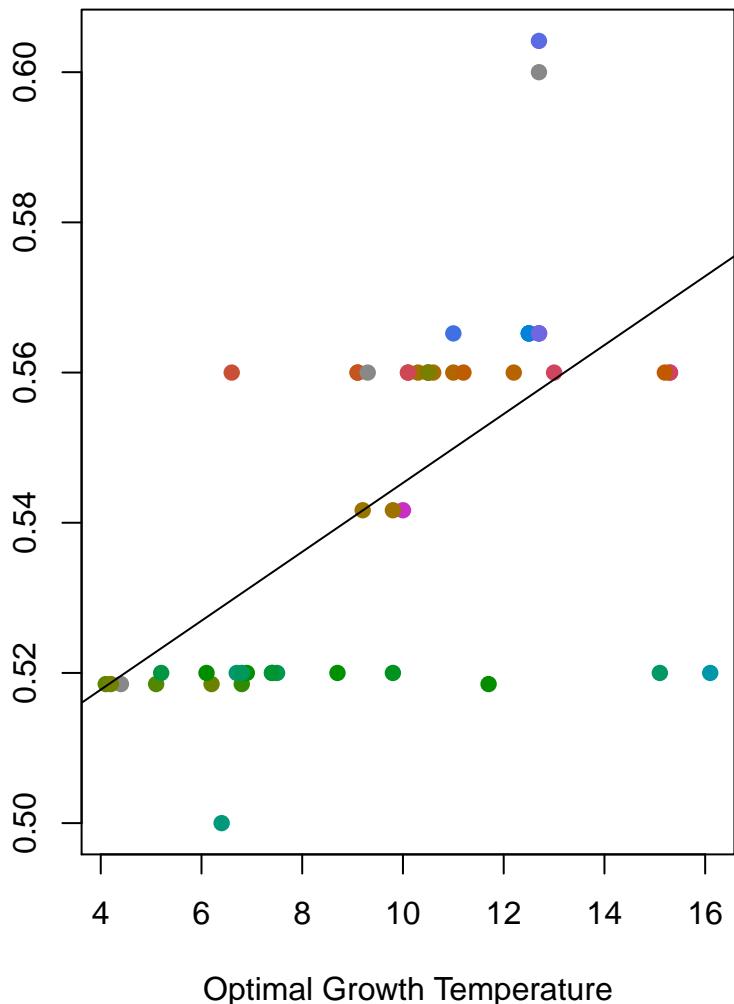
feature.plfam_id.arg_lys_ratio.mean

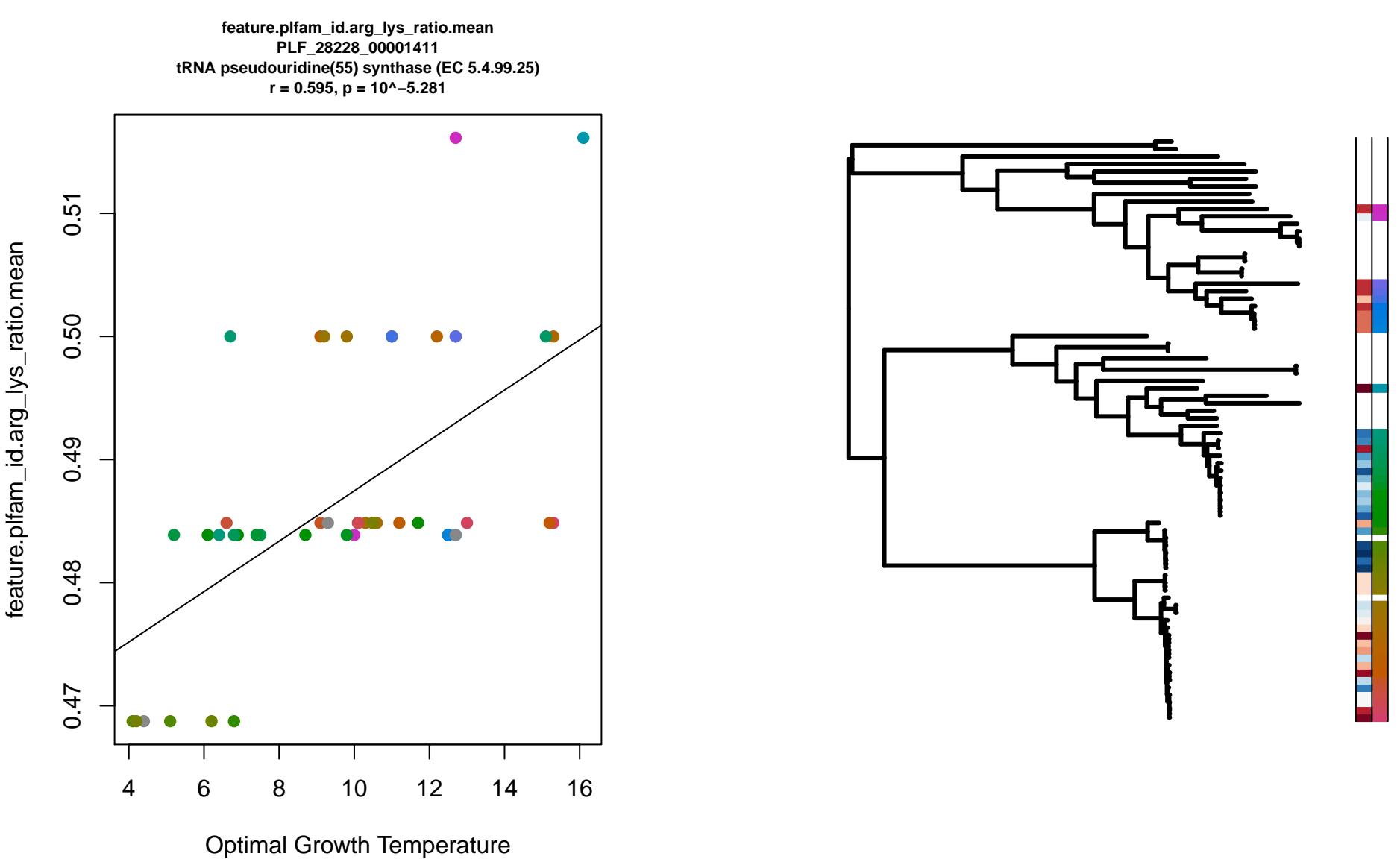
PLF_28228_00000955

Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)

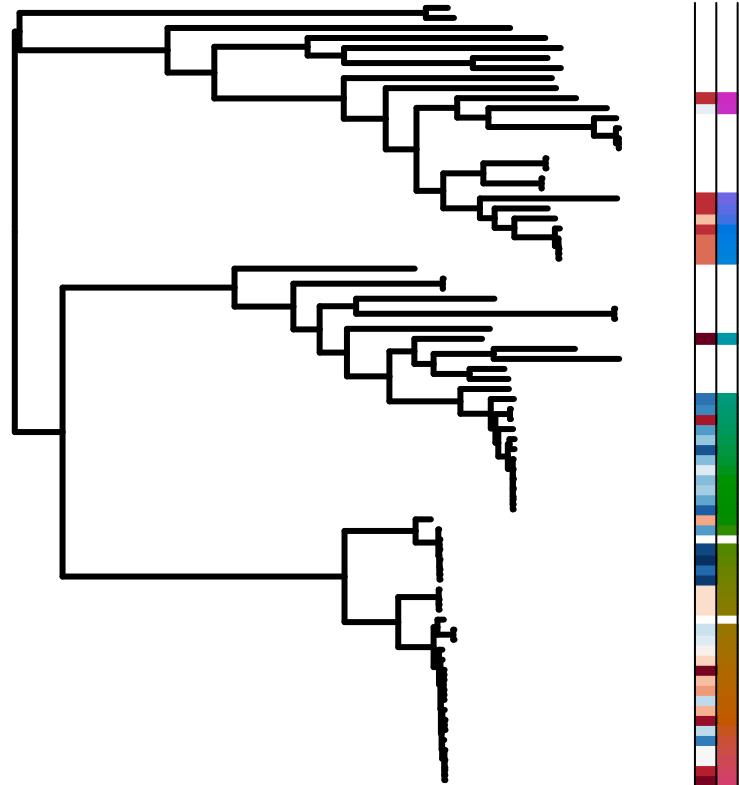
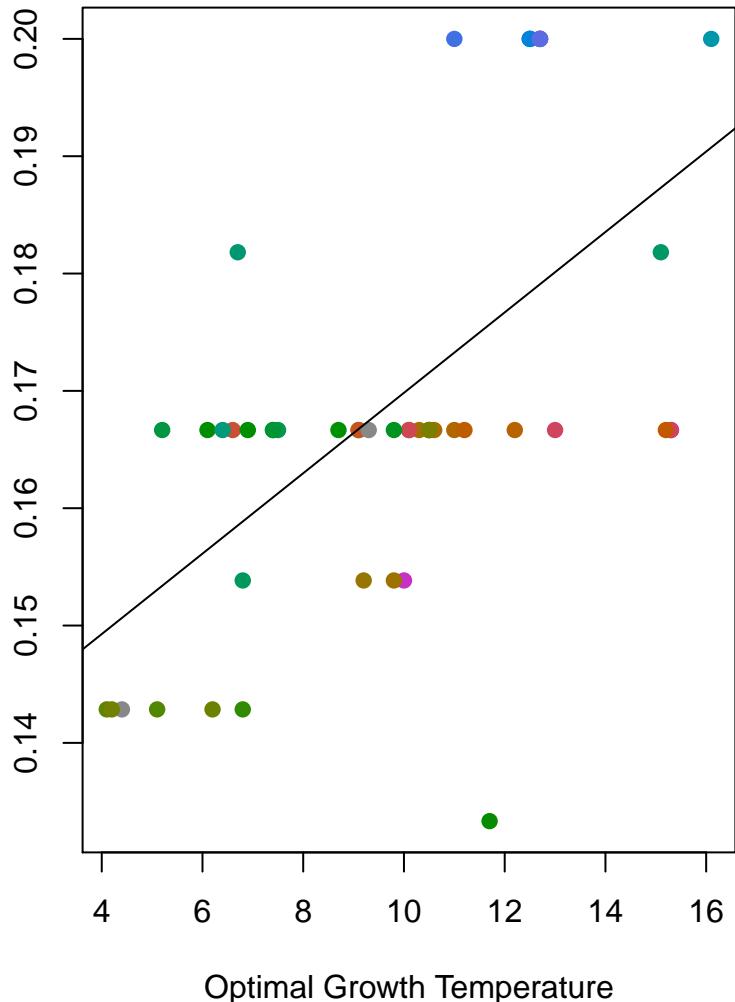
$r = 0.607$, $p = 10^{-5.532}$

feature.plfam_id.arg_lys_ratio.mean



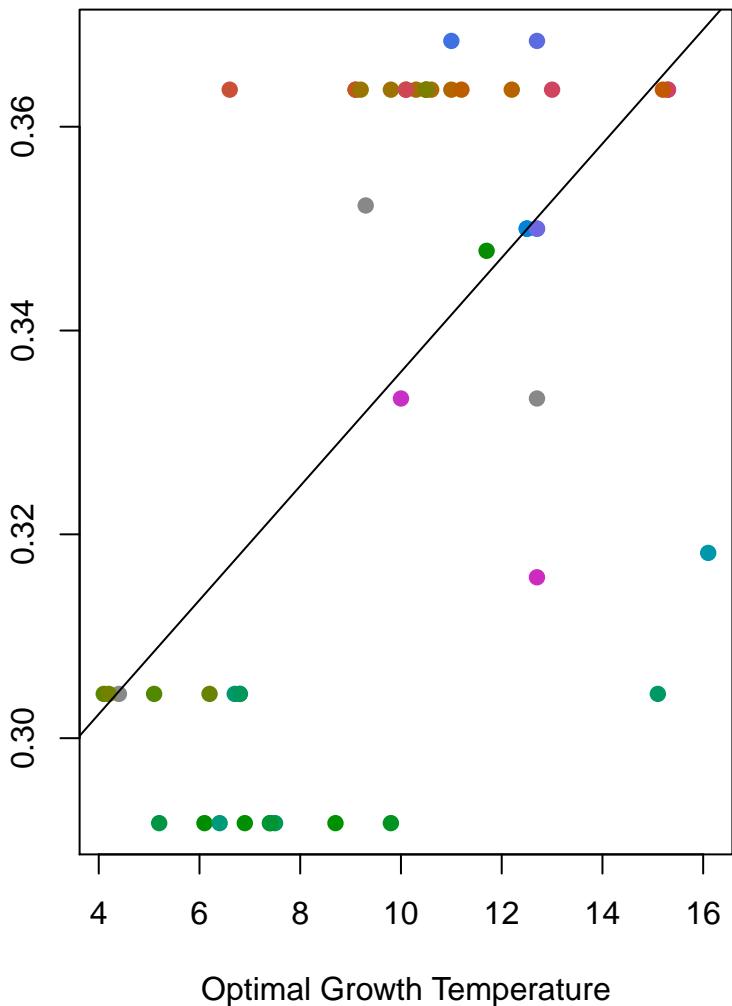


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000115
Antioxidant, AhpC/Tsa family
 $r = 0.592$, $p = 10^{-5.226}$

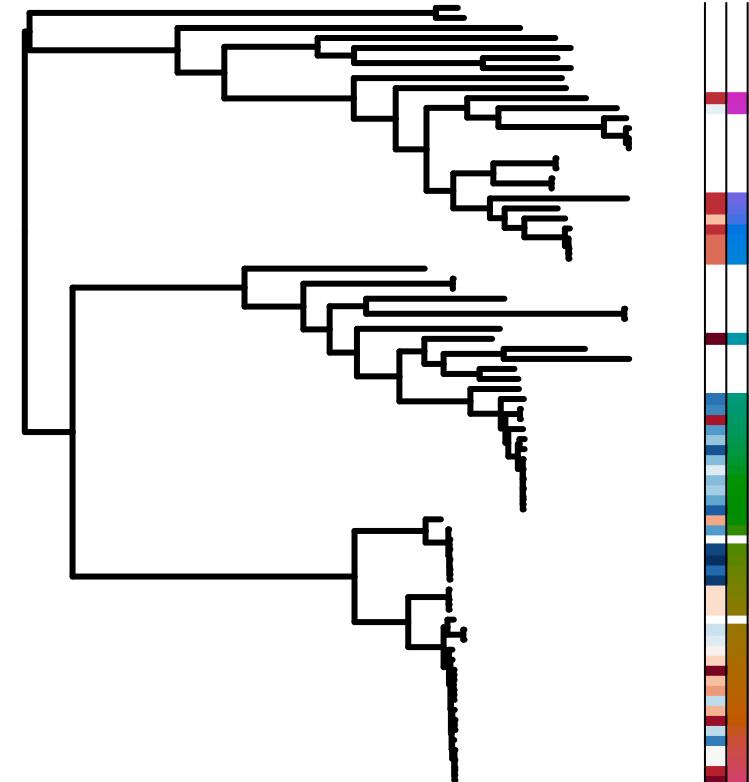


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002304
hypothetical protein
 $r = 0.581, p = 10^{-5.005}$

feature.plfam_id.arg_lys_ratio.mean

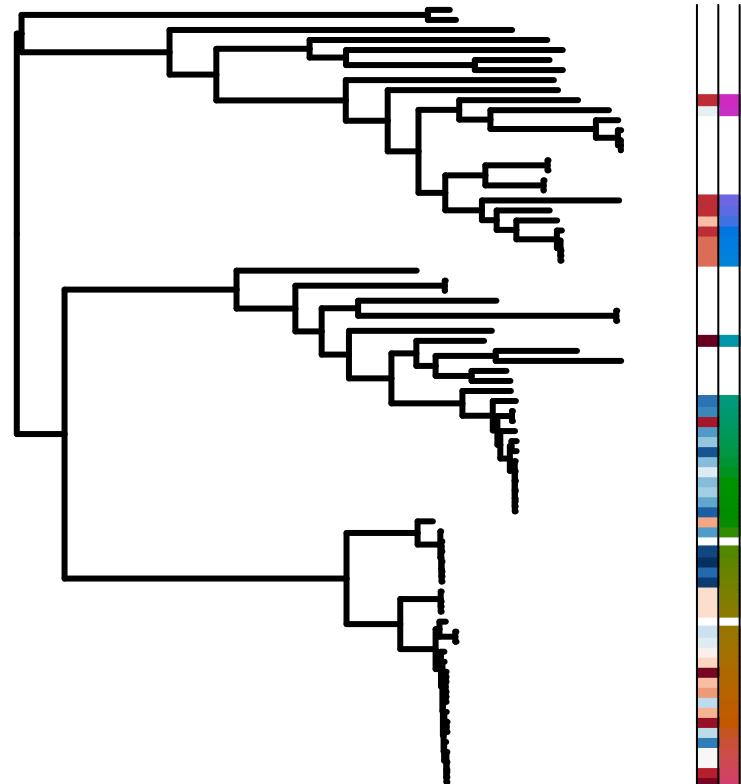
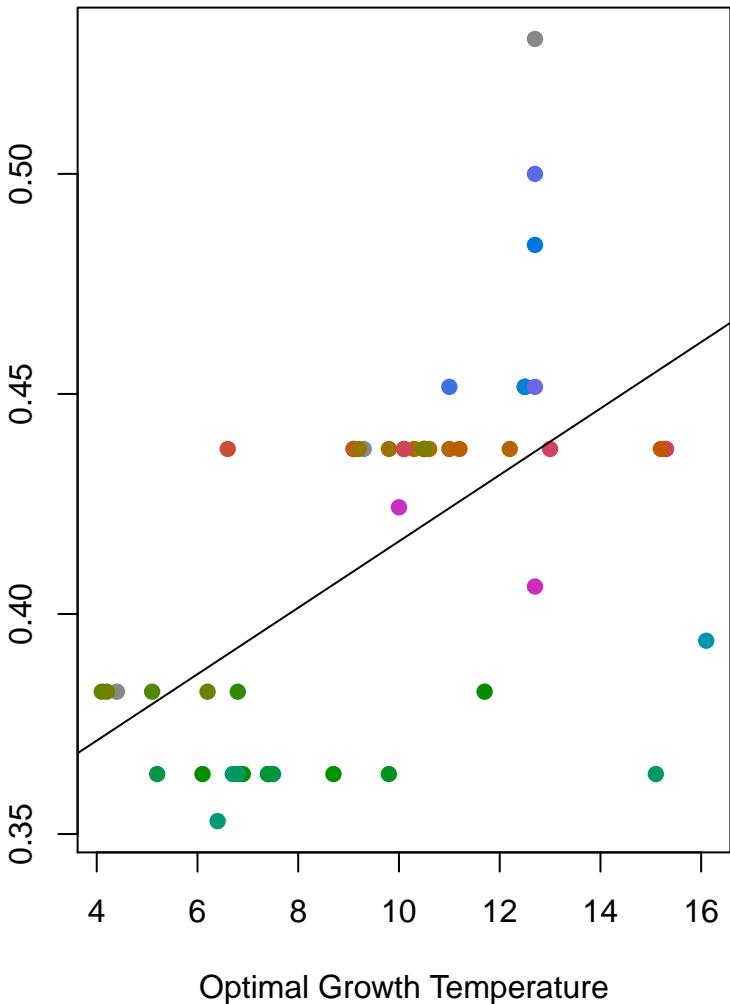


Optimal Growth Temperature



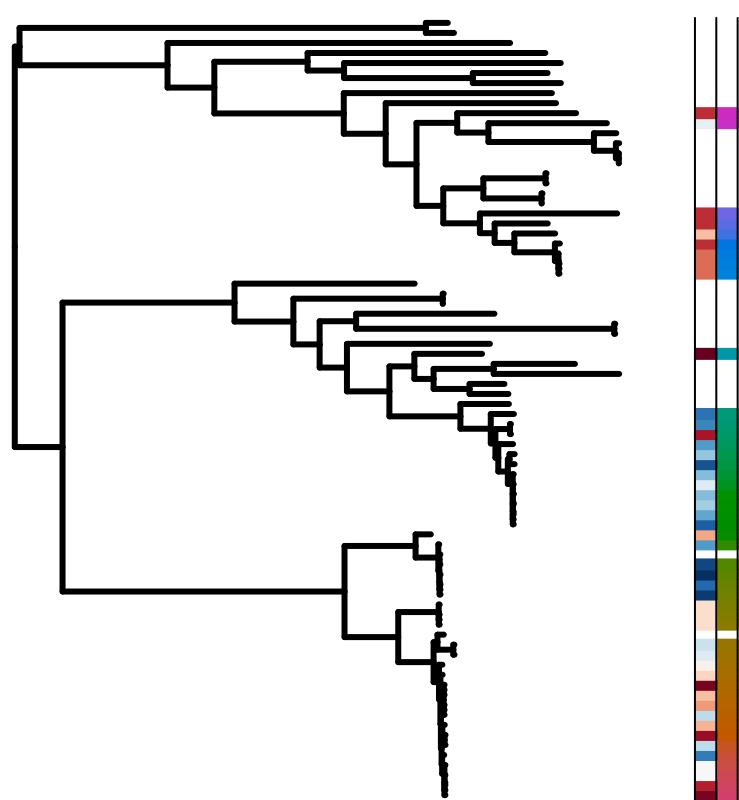
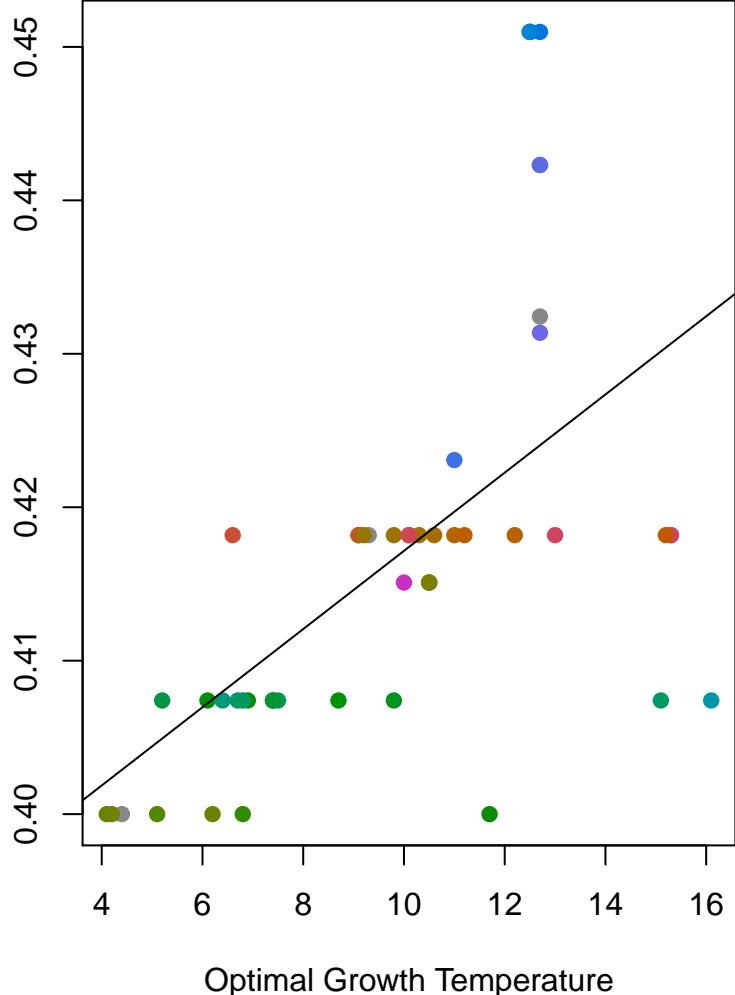
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000099
Chemotaxis protein CheV (EC 2.7.3.-)
 $r = 0.579$, $p = 10^{-4.967}$

feature.plfam_id.arg_lys_ratio.mean

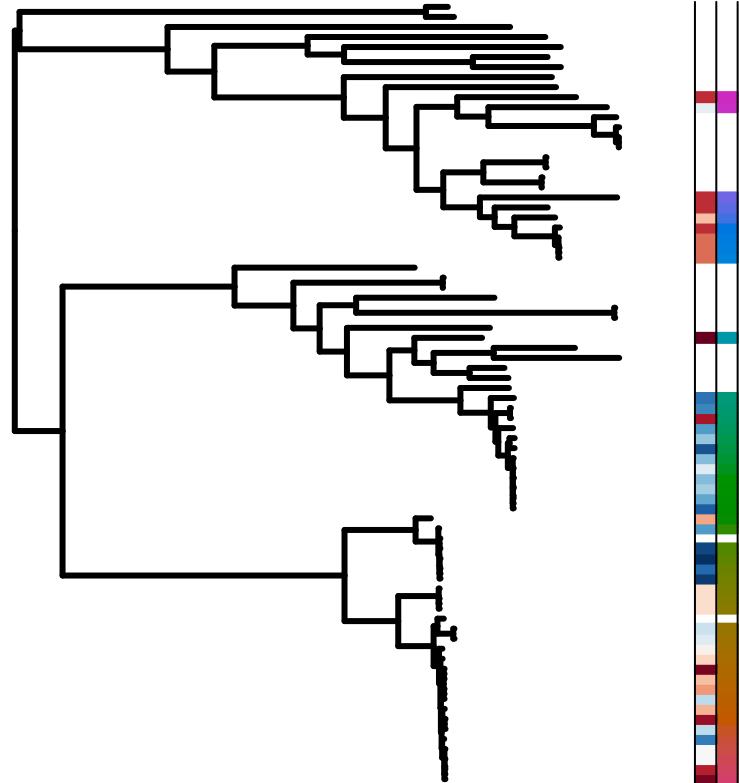
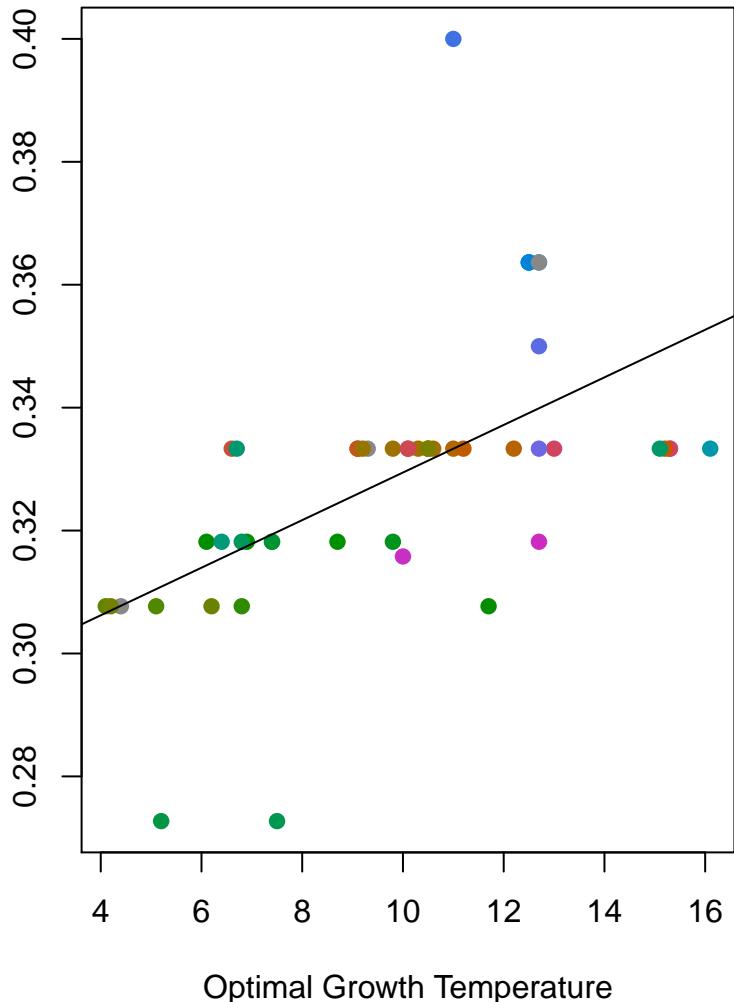


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000484
Flagellar biosynthesis protein FlhA
 $r = 0.574$, $p = 10^{-4.877}$

feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001638
HD domain protein
 $r = 0.568$, $p = 10^{-4.778}$



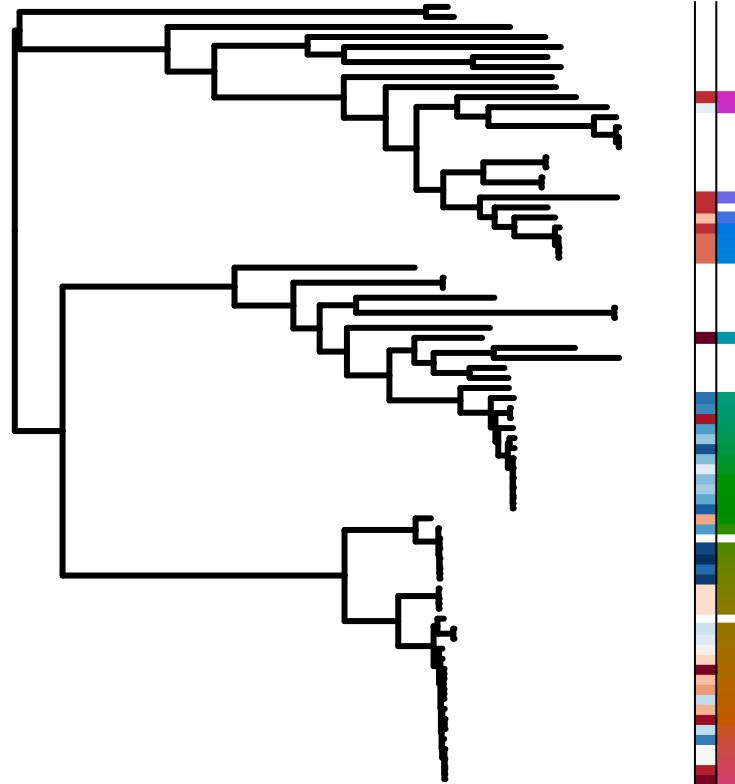
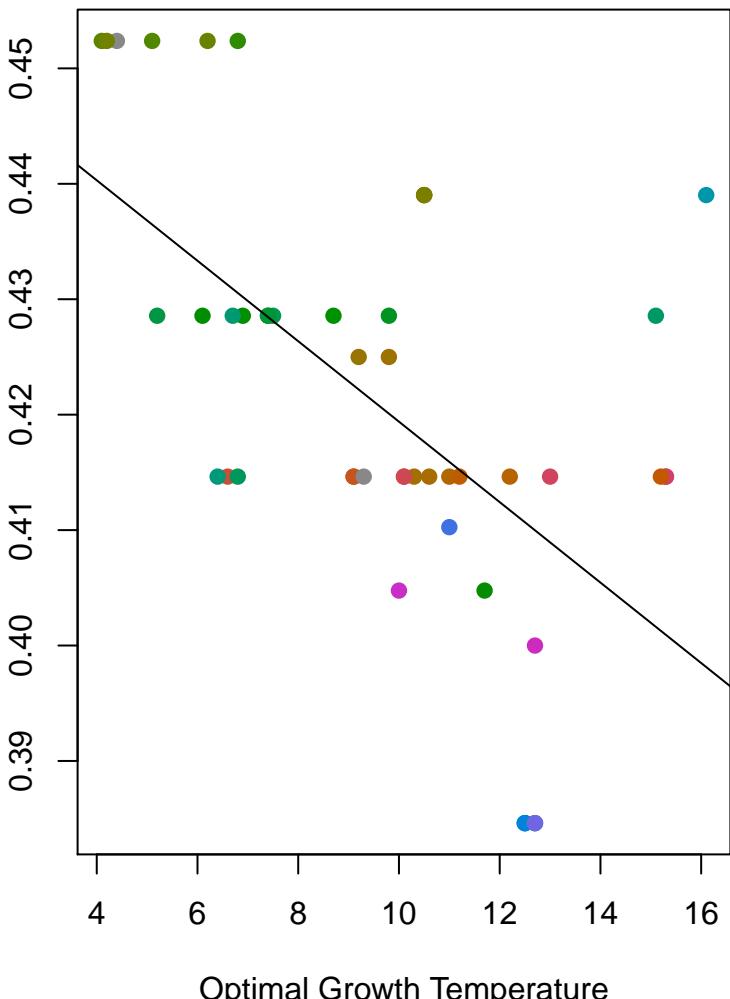
feature.plfam_id.arg_lyc_ratio.mean

PLF_28228_00000375

Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)

$r = -0.578, p = 10^{-4.858}$

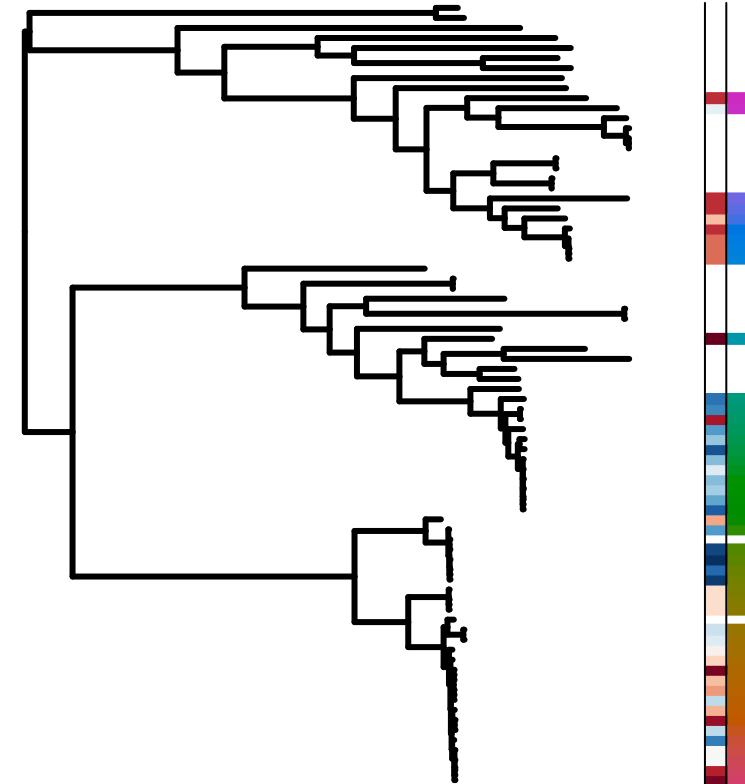
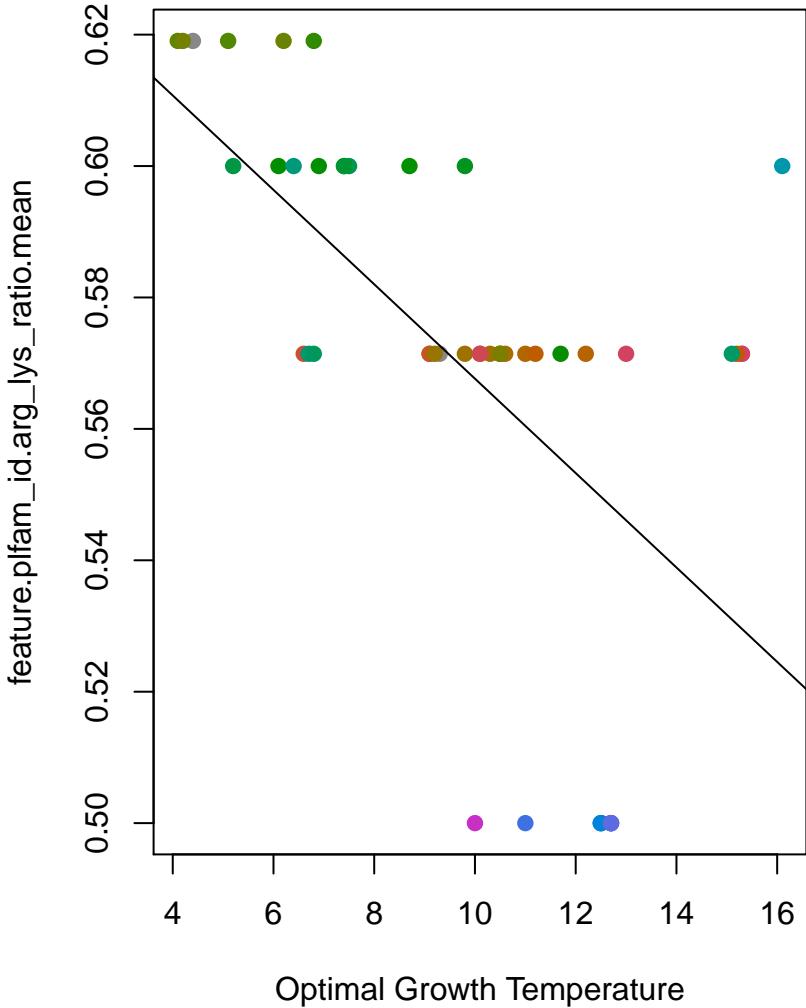
feature.plfam_id.arg_lyc_ratio.mean



feature.plfam_id.arg_lys_ratio.mean

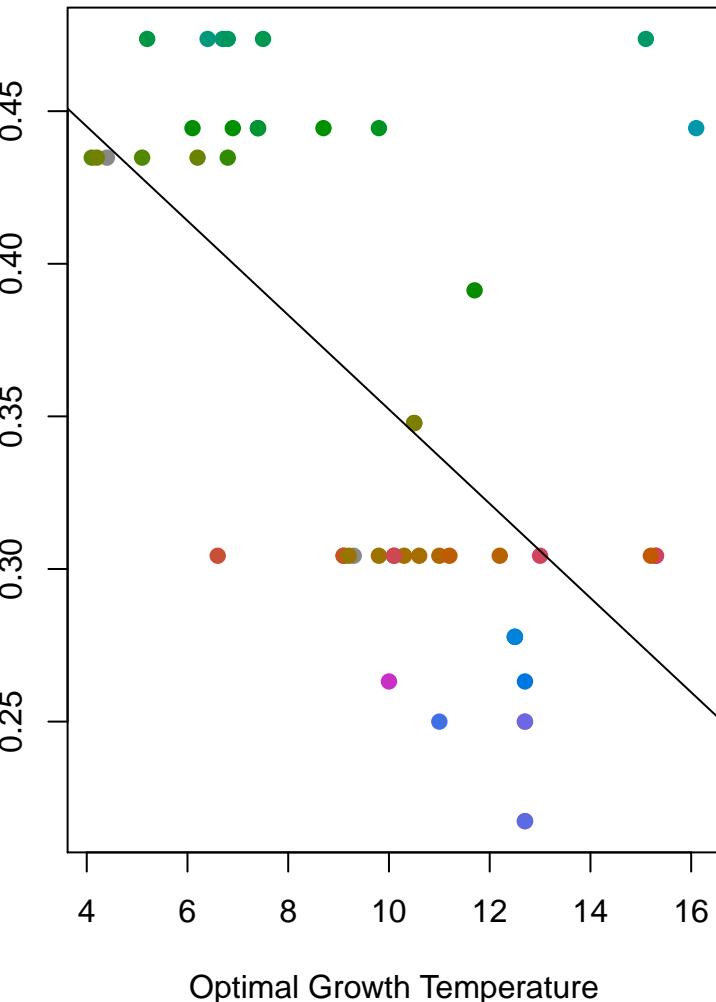
PLF_28228_00000260

23S rRNA (pseudouridine(1915)-N(3))-methyltransferase (EC 2.1.1.177)
 $r = -0.59$, $p = 10^{-5.189}$

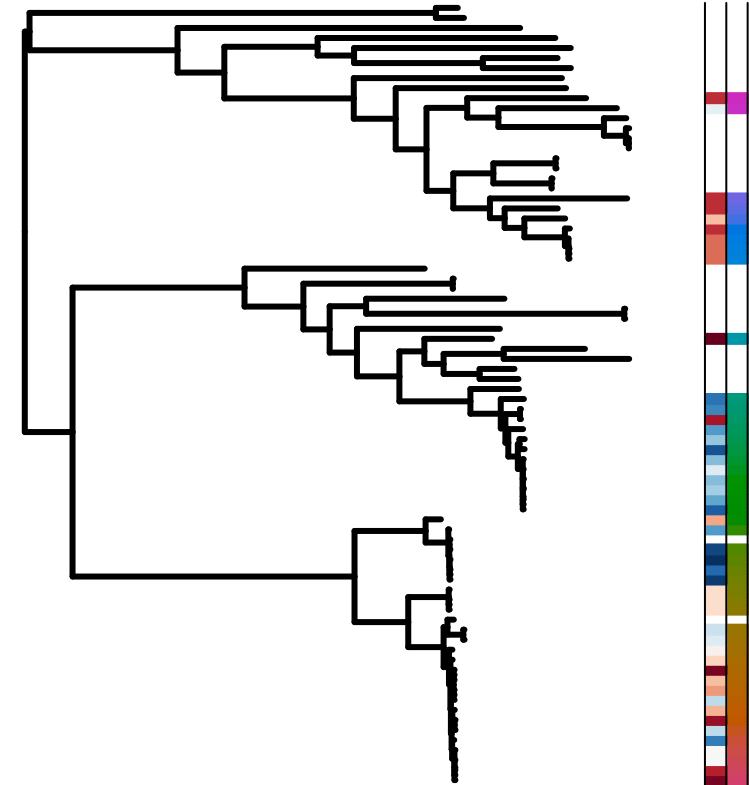


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000224
33 kDa chaperonin HsI0
 $r = -0.595$, $p = 10^{-5.282}$

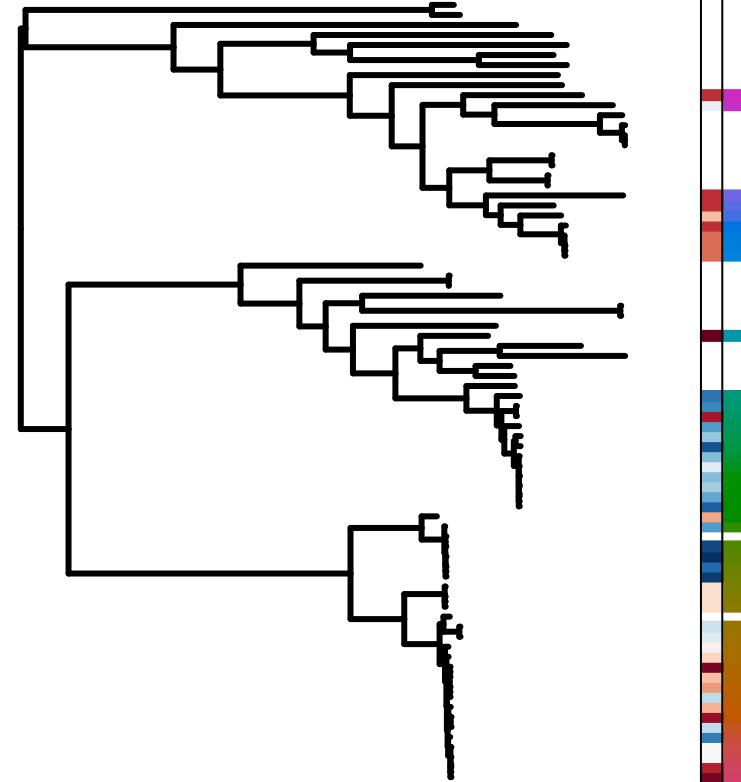
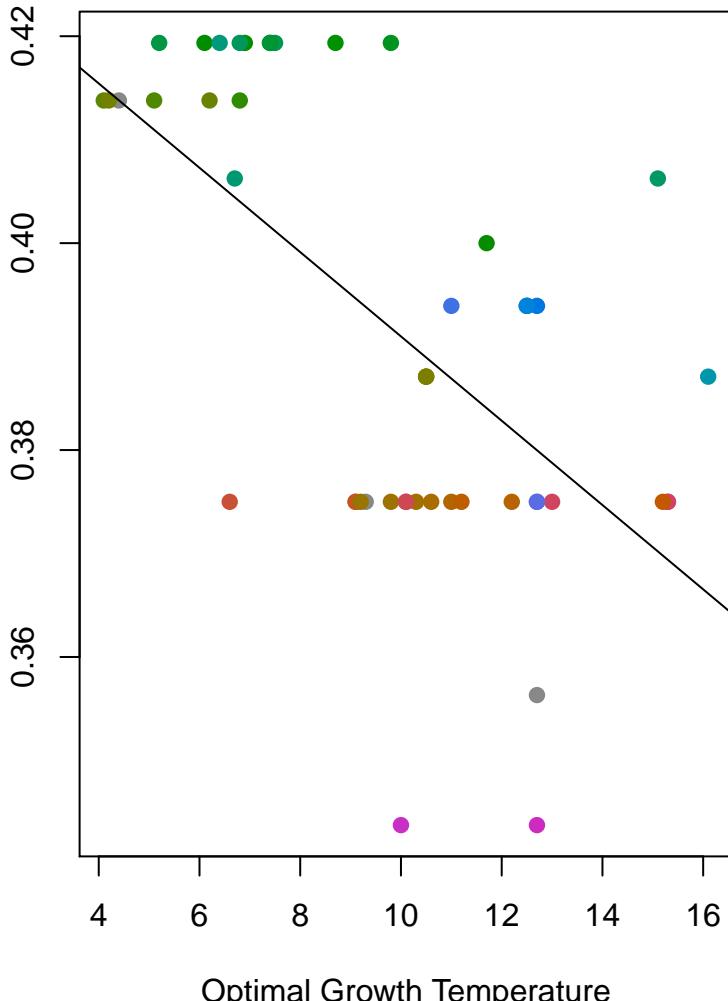
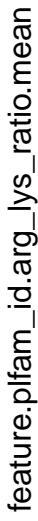
feature.plfam_id.arg_lys_ratio.mean



Optimal Growth Temperature



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000809
L-threonine 3-dehydrogenase (EC 1.1.1.103)
 $r = -0.603, p = 10^{-5.441}$



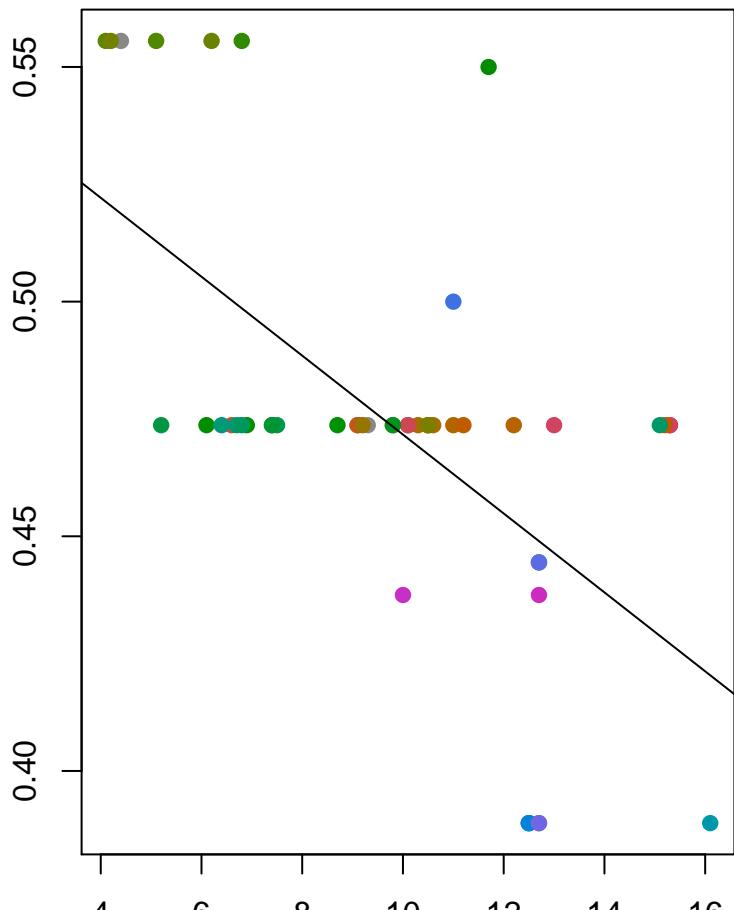
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000522

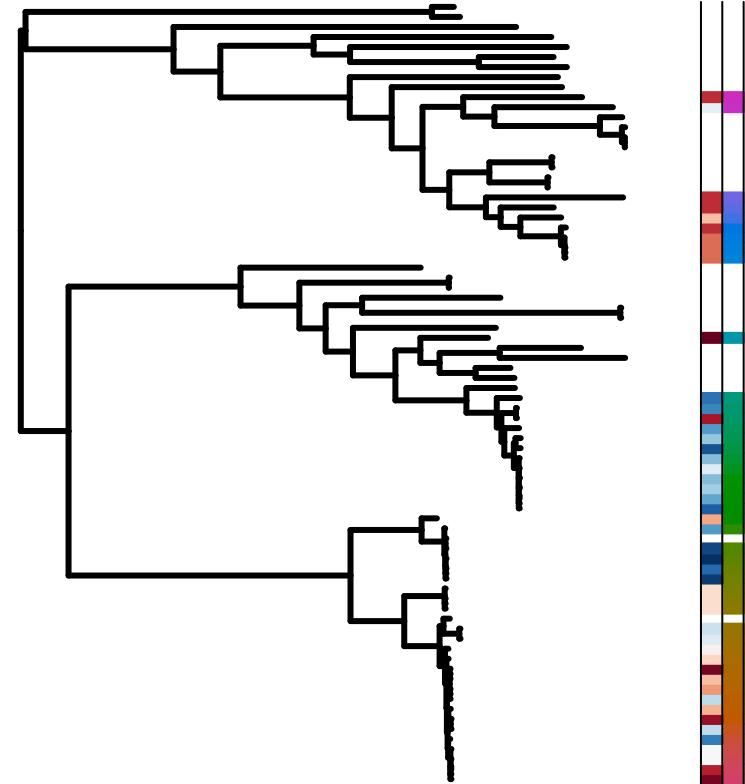
Inner membrane protein YrbG, predicted calcium/sodium:proton antiporter

$r = -0.606, p = 10^{-5.499}$

feature.plfam_id.arg_lys_ratio.mean



Optimal Growth Temperature

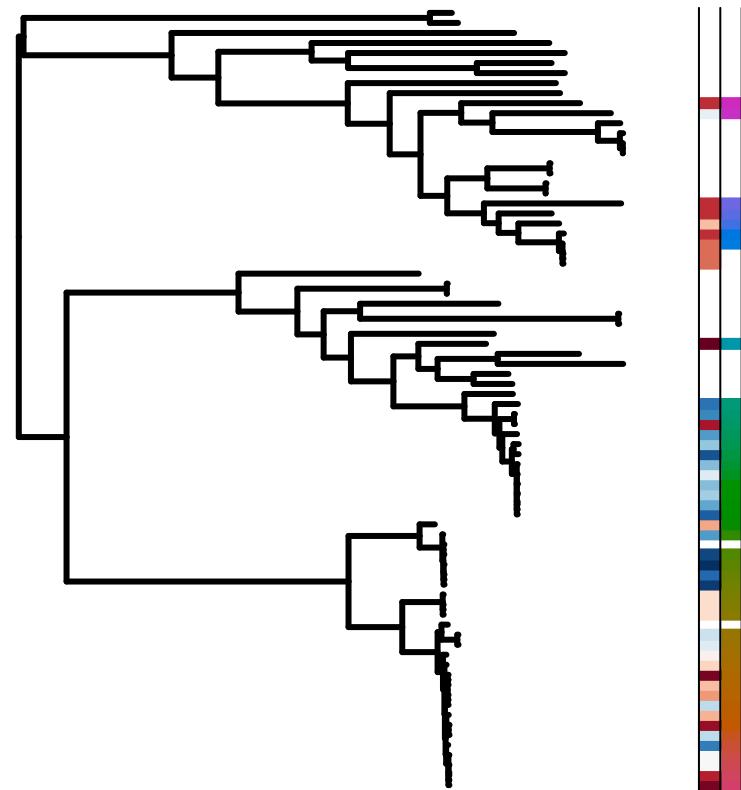
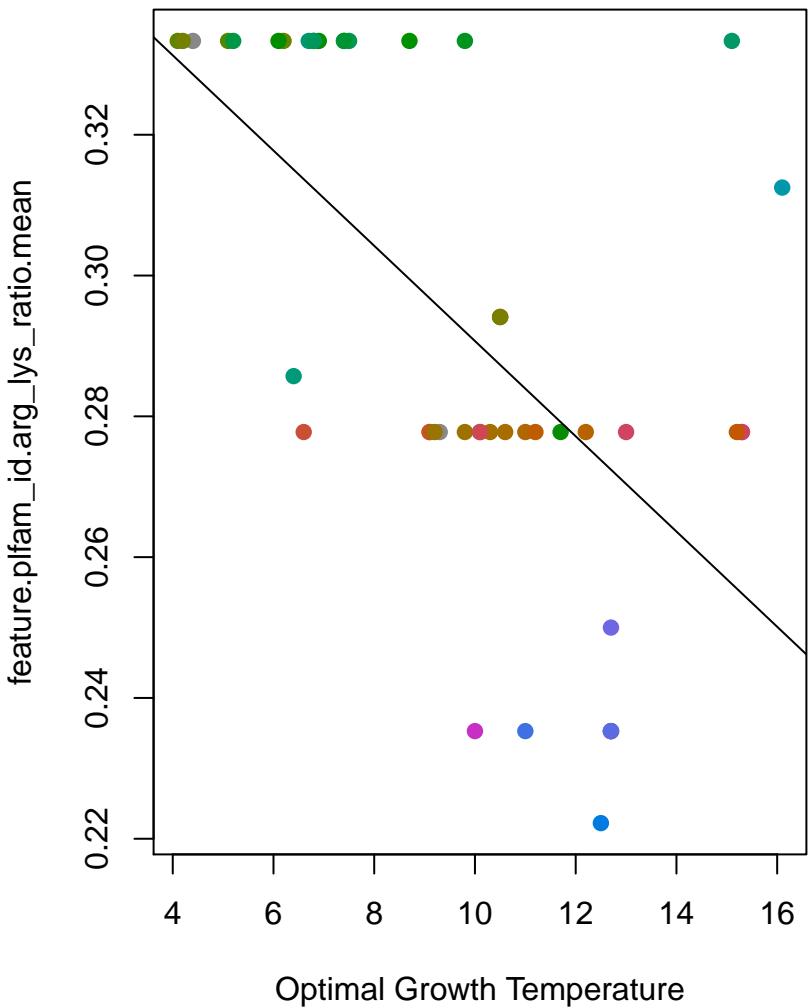


feature.plfam_id.arg_lyc_ratio.mean

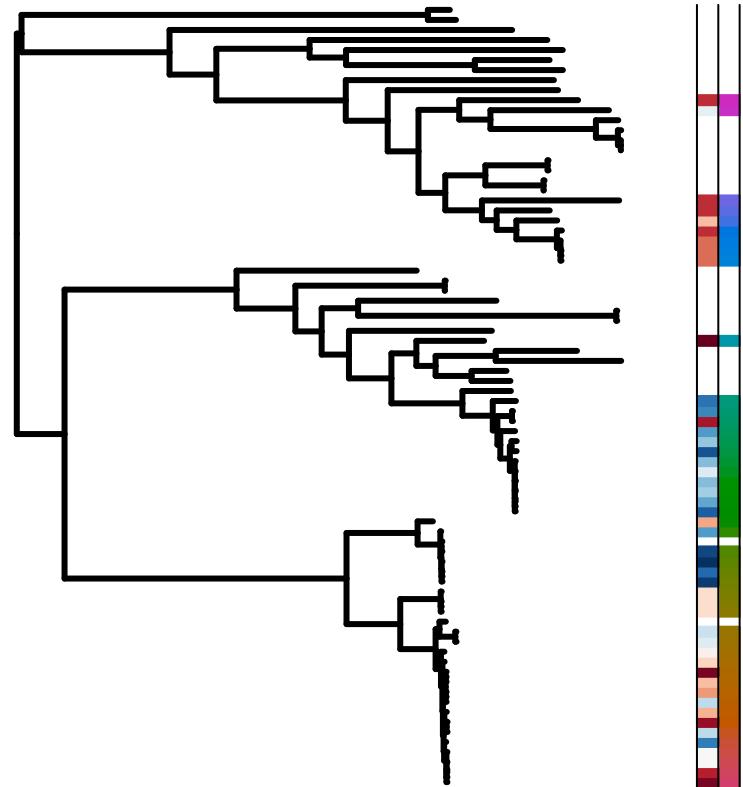
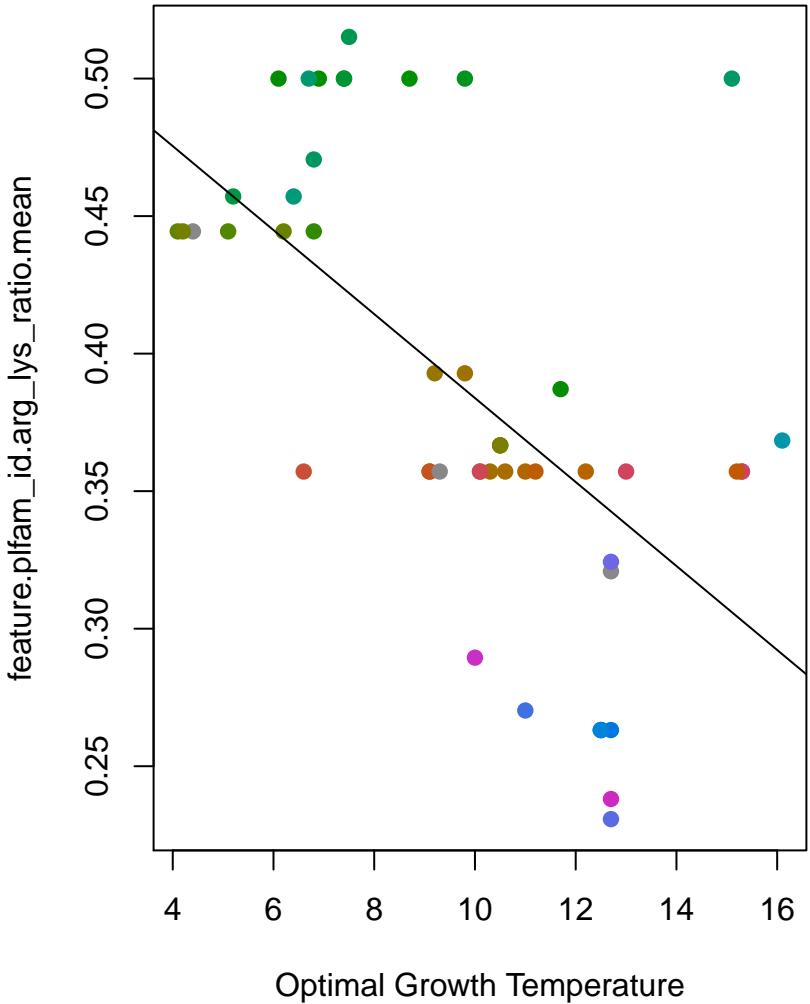
PLF_28228_00028265

phoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.

$r = -0.606$, $p = 10^{-5.299}$



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001134
Septum-associated rare lipoprotein A
 $r = -0.606$, $p = 10^{-5.517}$



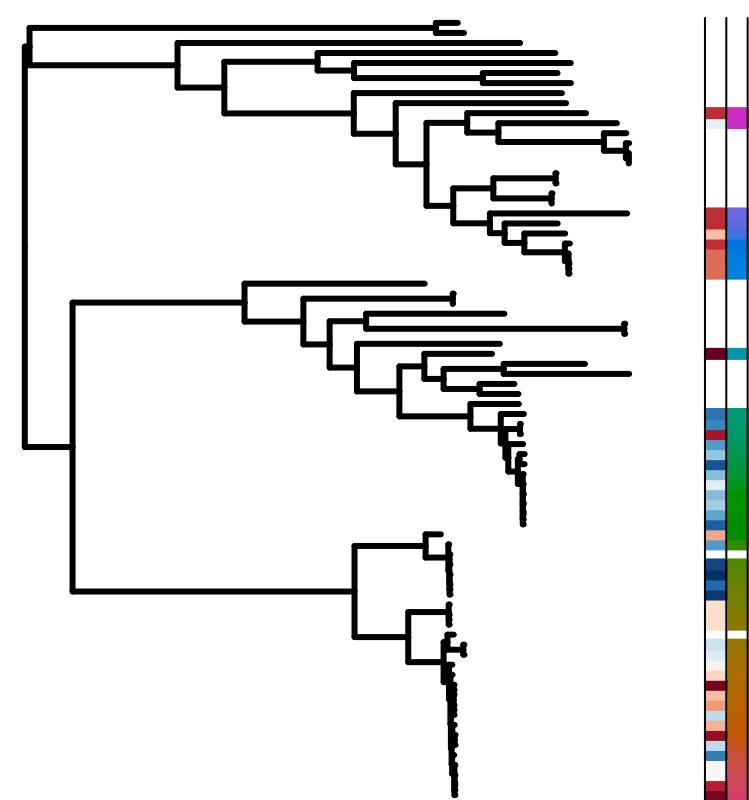
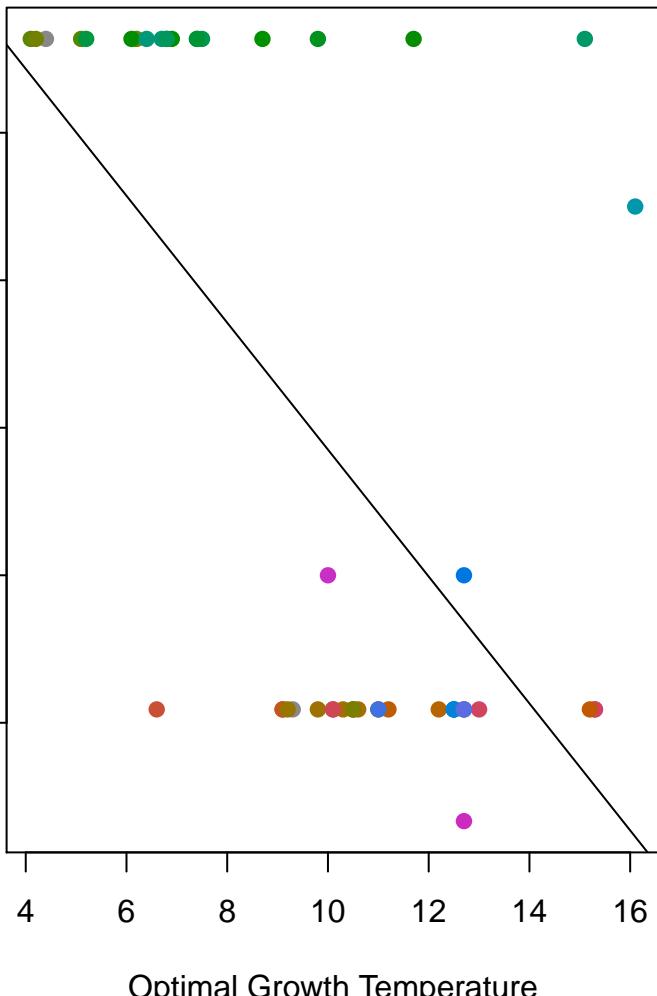
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00001841

Flagellar hook-basal body complex protein FliE

$r = -0.612, p = 10^{-5.633}$

feature.plfam_id.arg_lys_ratio.mean



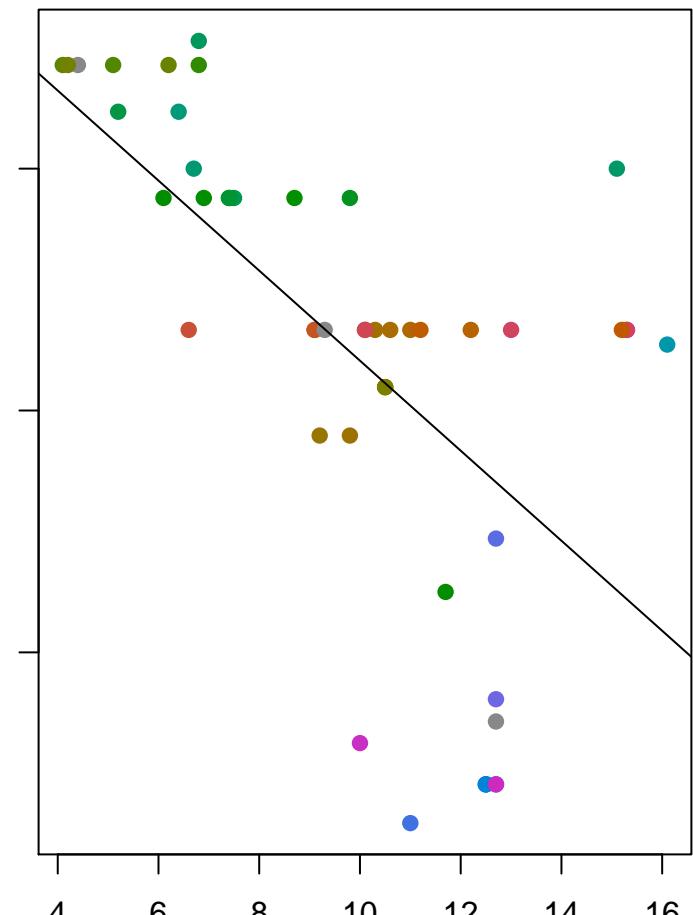
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000670

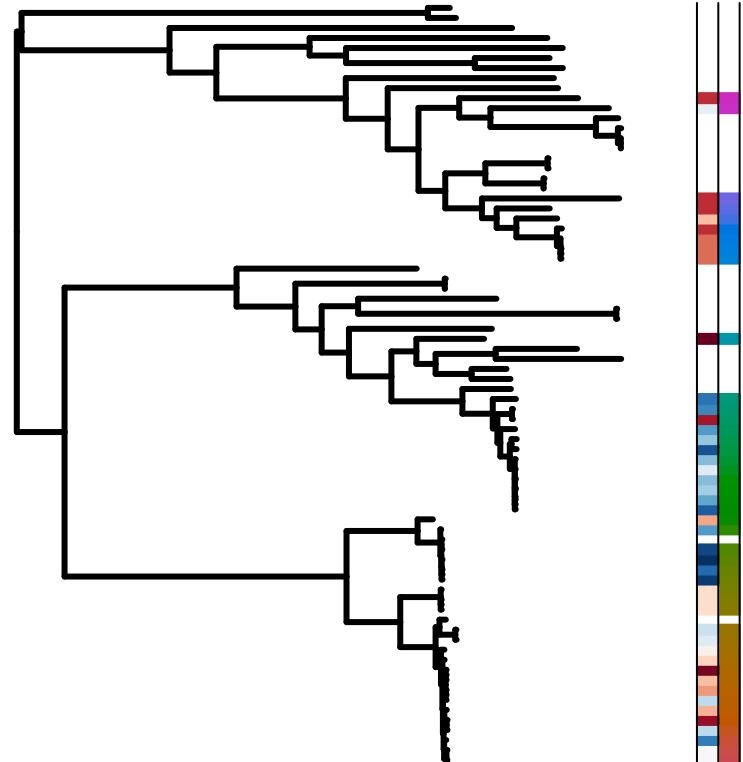
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)

$r = -0.614, p = 10^{-5.681}$

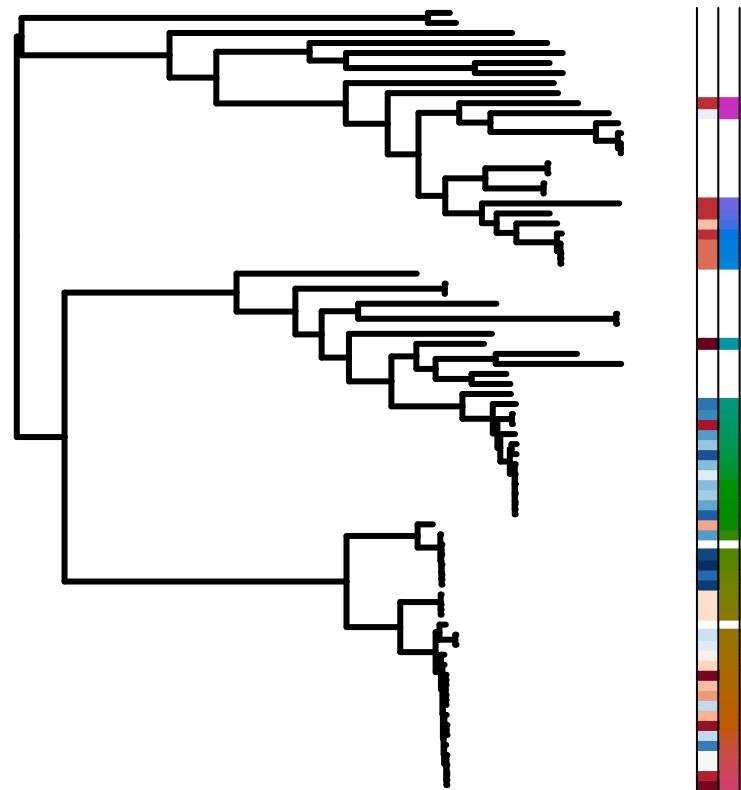
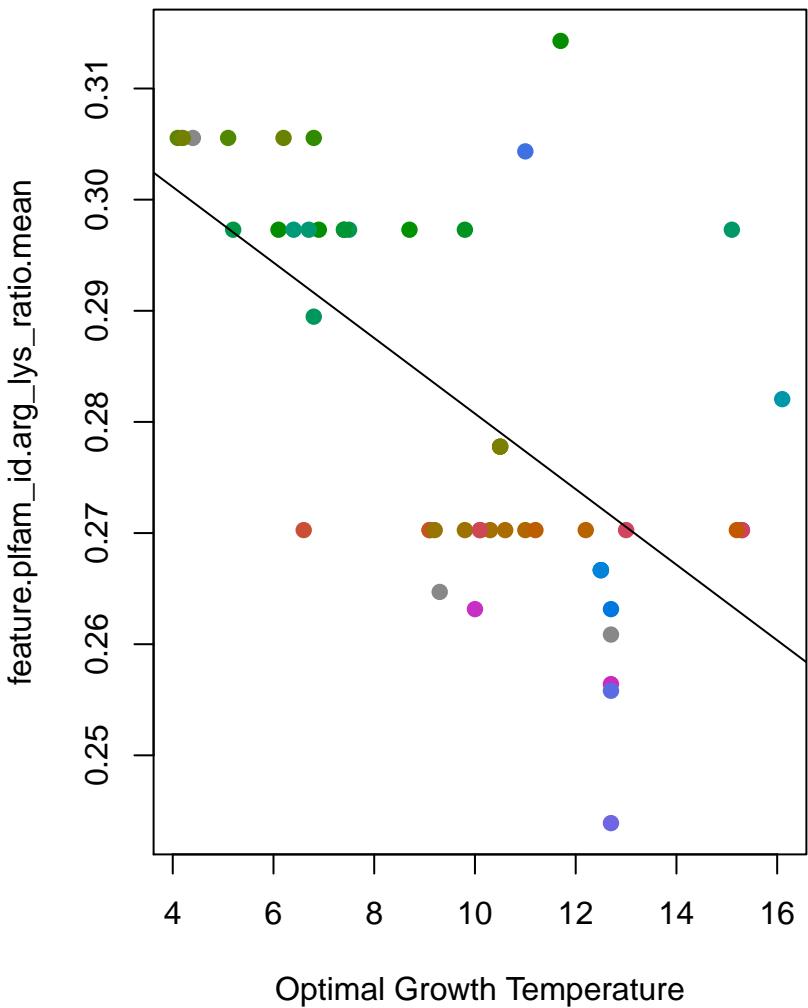
feature.plfam_id.arg_lys_ratio.mean



Optimal Growth Temperature



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002251
hypothetical protein
 $r = -0.62, p = 10^{-5.806}$



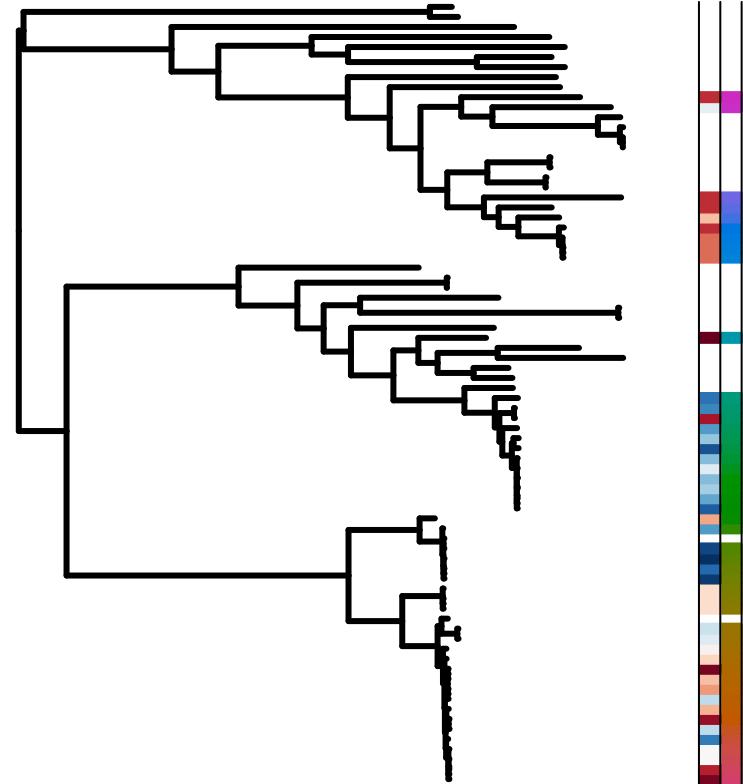
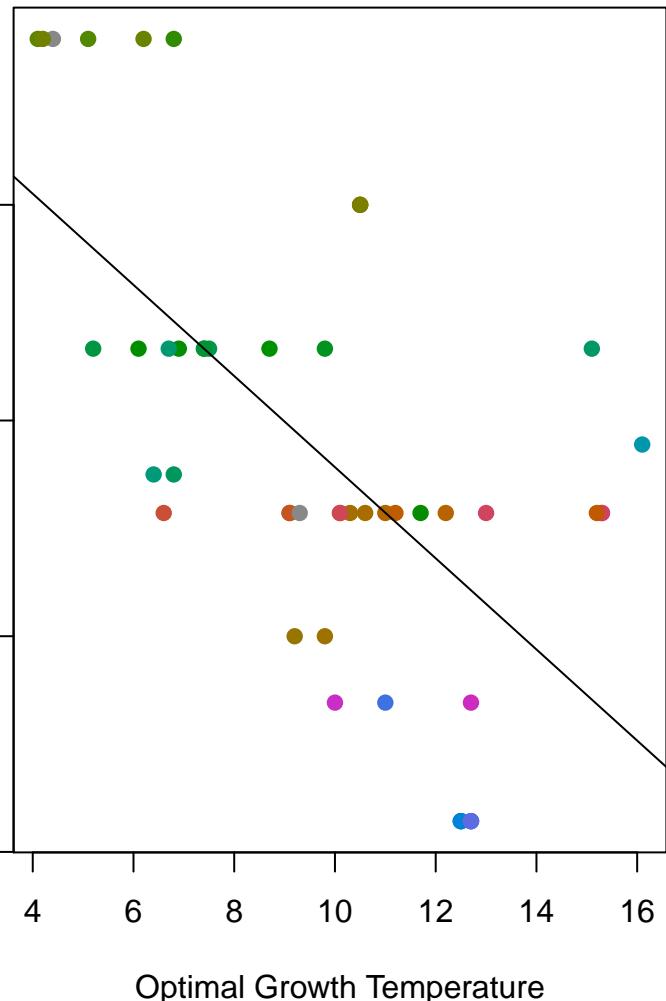
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00002875

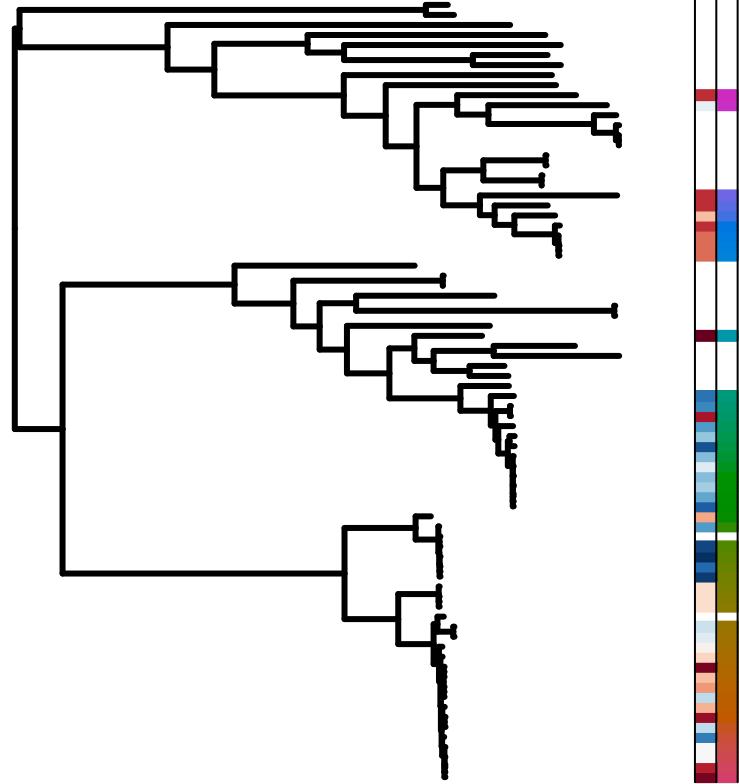
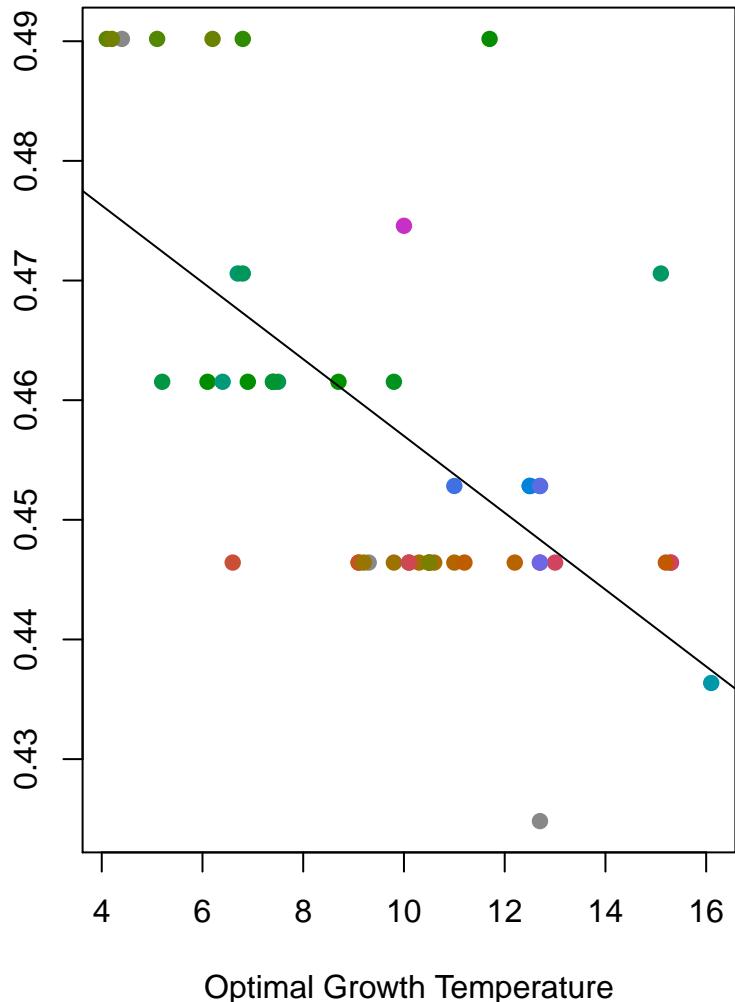
Uncharacterized protein YfgD, not an arsenate reductase

$r = -0.627, p = 10^{-5.957}$

feature.plfam_id.arg_lys_ratio.mean

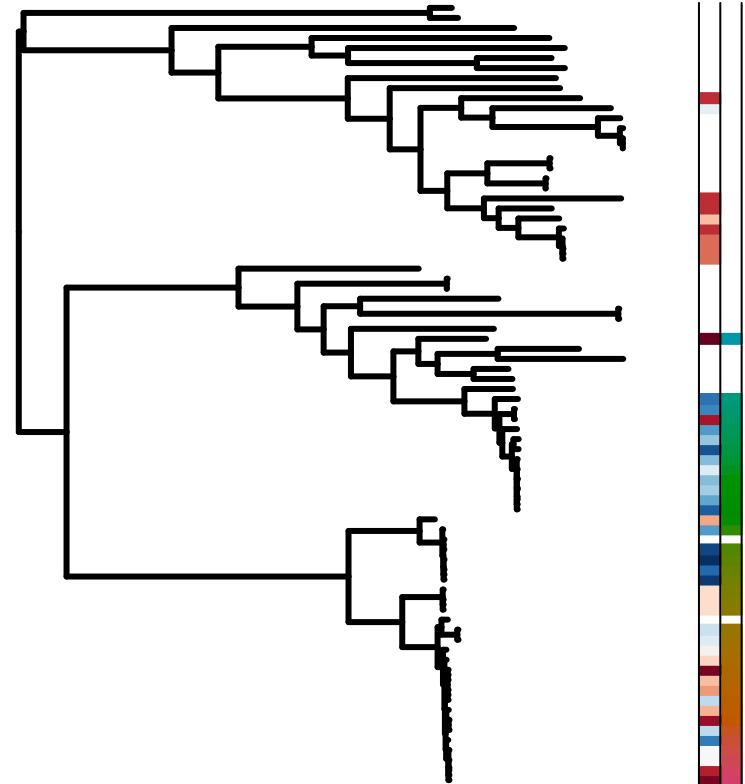
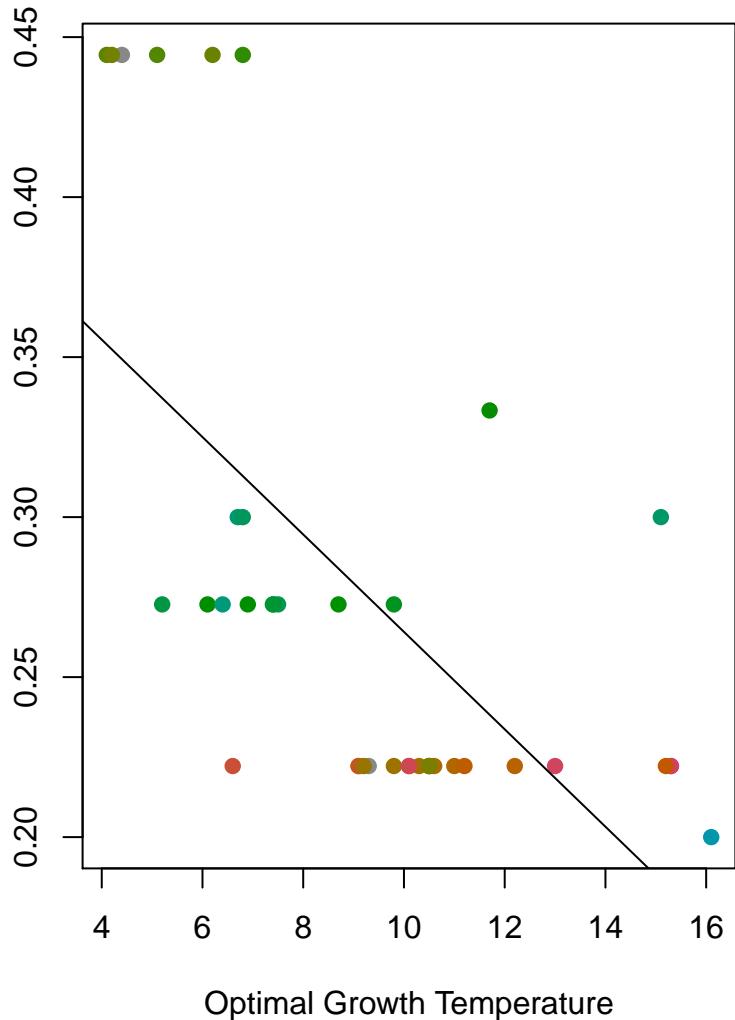


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000537
Isocitrate lyase (EC 4.1.3.1)
 $r = -0.628, p = 10^{-5.974}$



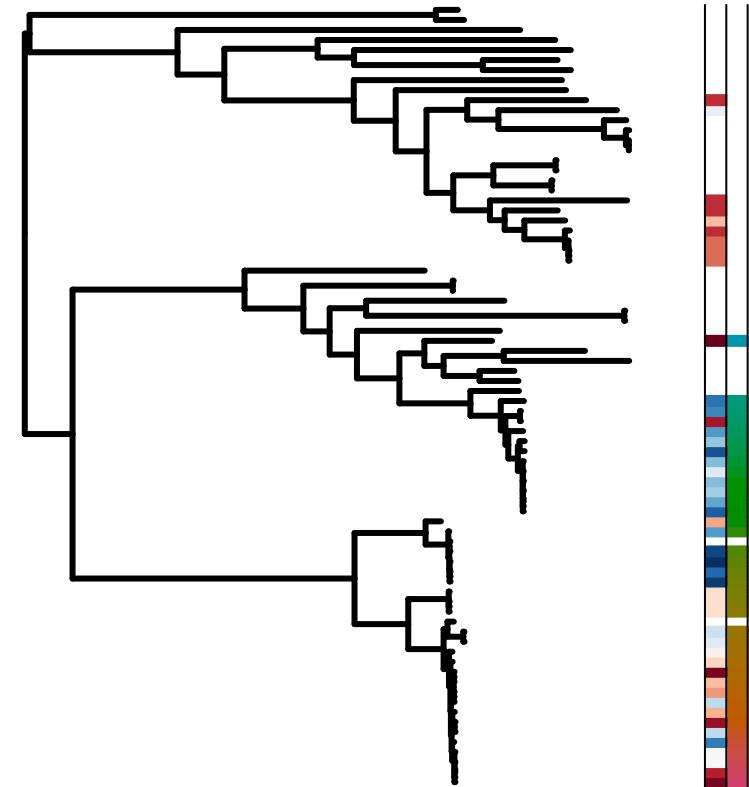
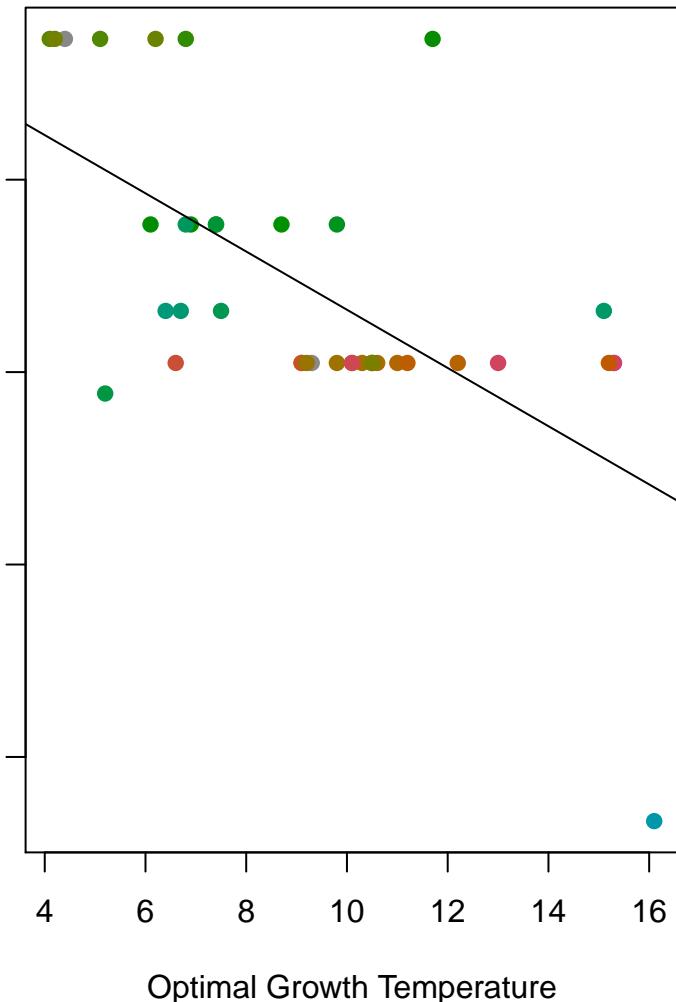
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00012099
Acid stress protein IbaG
 $r = -0.633$, $p = 10^{-4.926}$

feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00031798
hypothetical protein
 $r = -0.633, p = 10^{-4.936}$

feature.plfam_id.arg_lys_ratio.mean

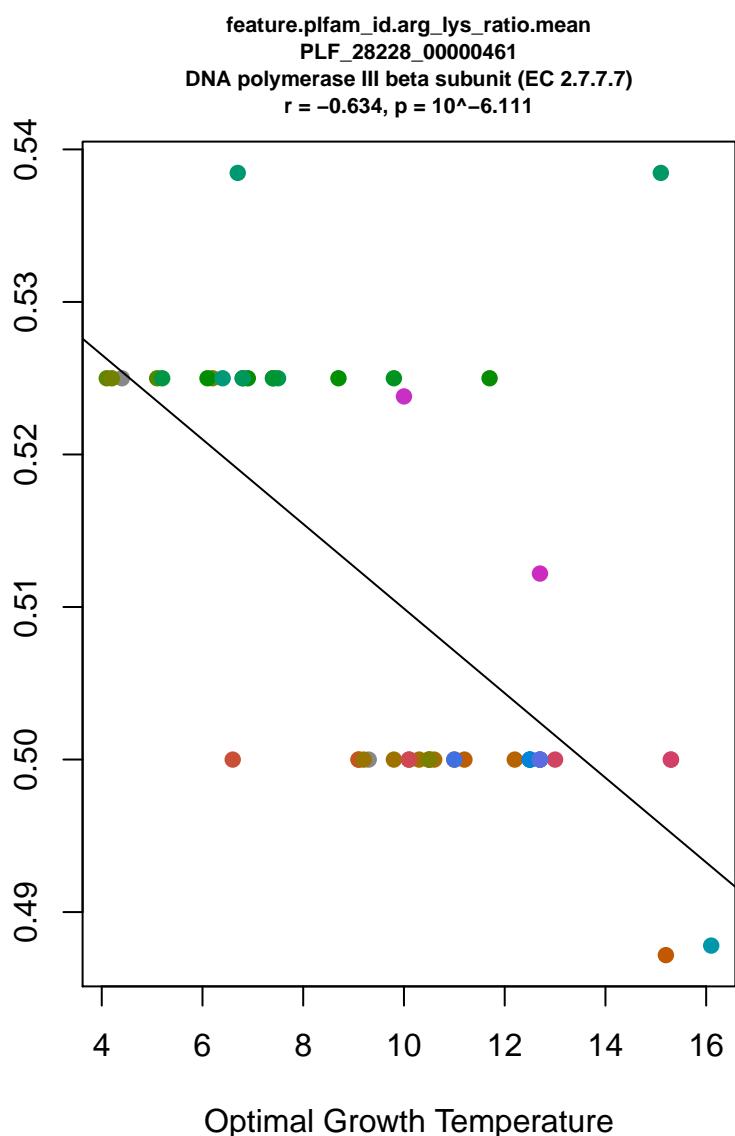
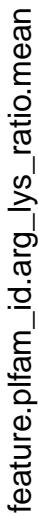


feature.plfam_id.arg_lyc_ratio.mean

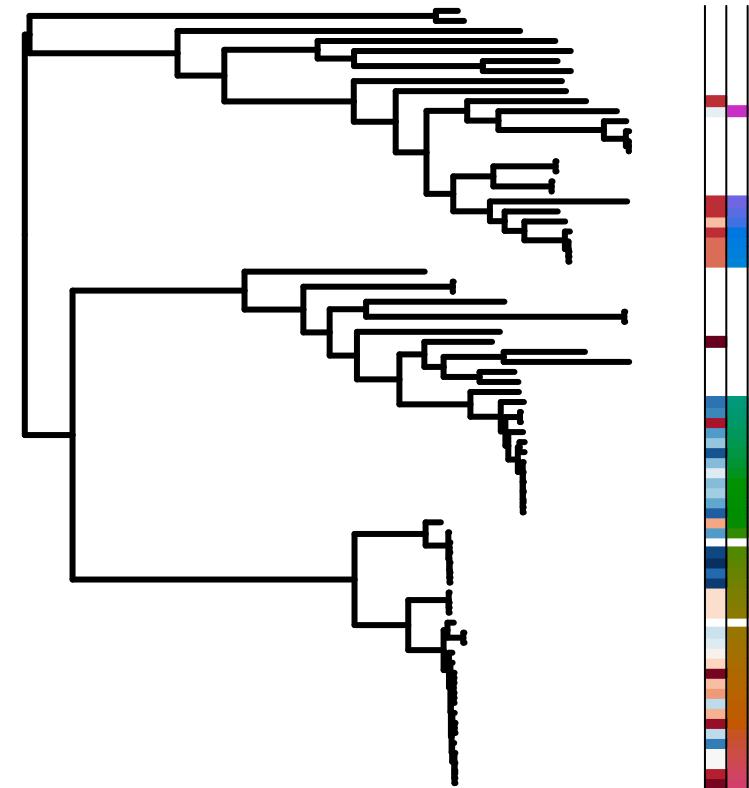
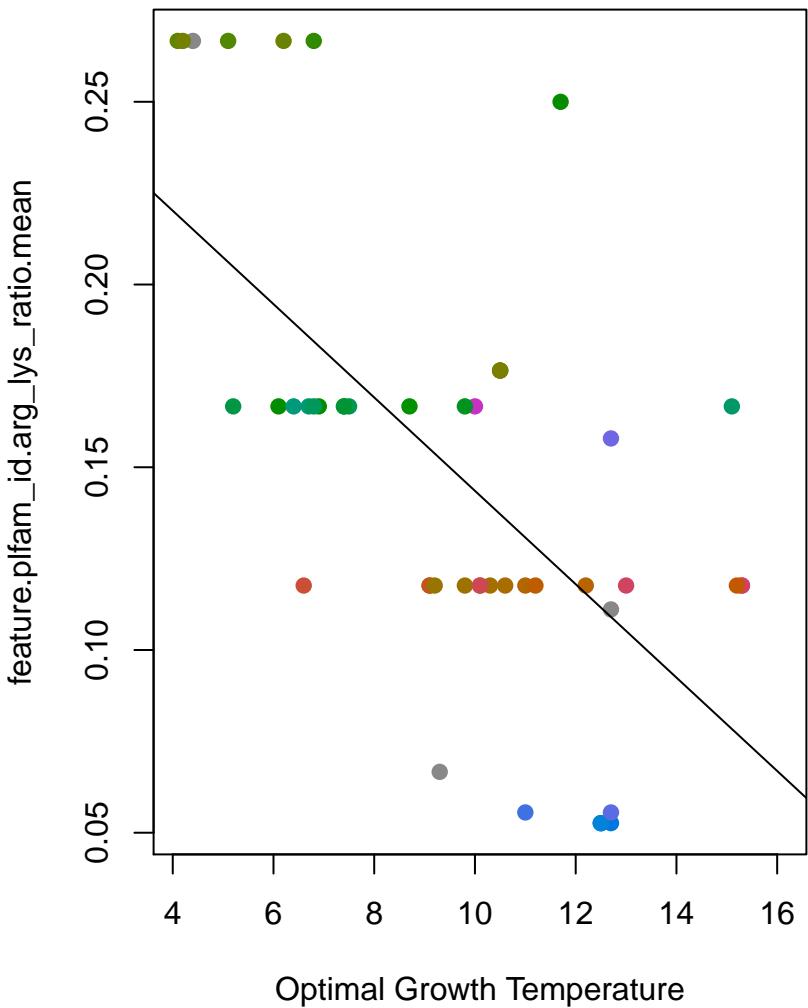
PLF_28228_00000461

DNA polymerase III beta subunit (EC 2.7.7.7)

$r = -0.634$, $p = 10^{-6.111}$



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002406
hypothetical protein
 $r = -0.635$, $p = 10^{-5.9}$



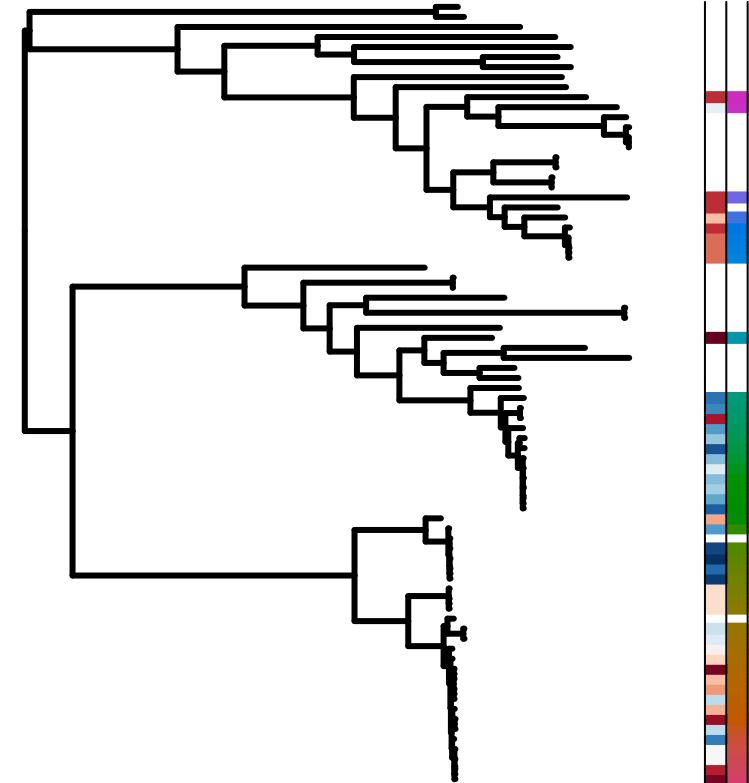
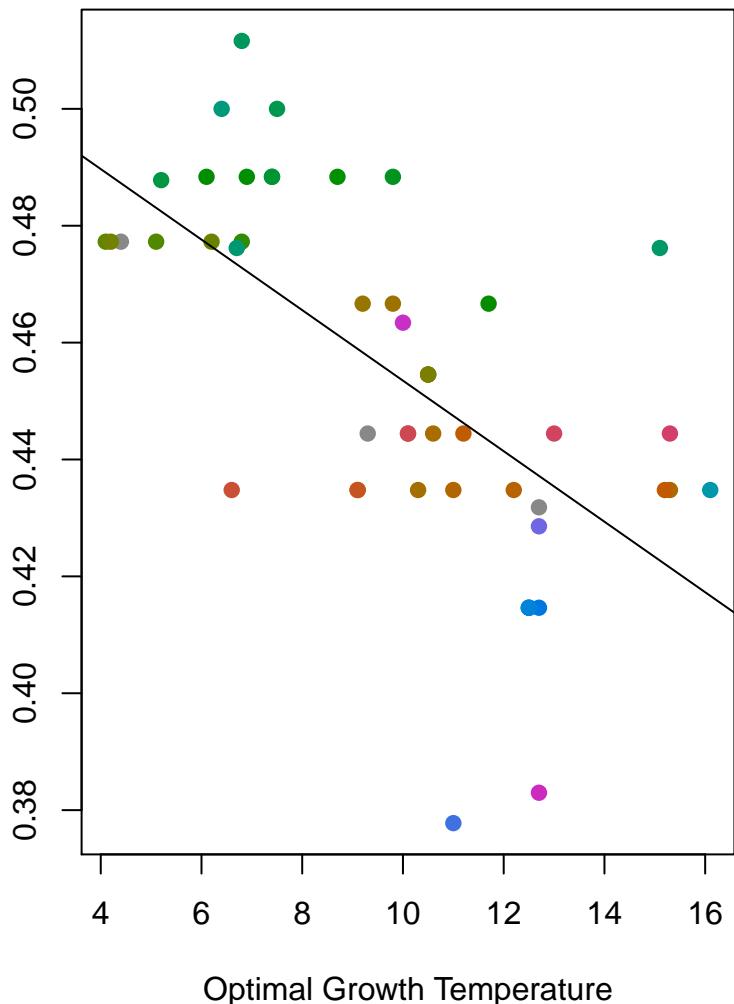
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000141

RND efflux system, membrane fusion protein

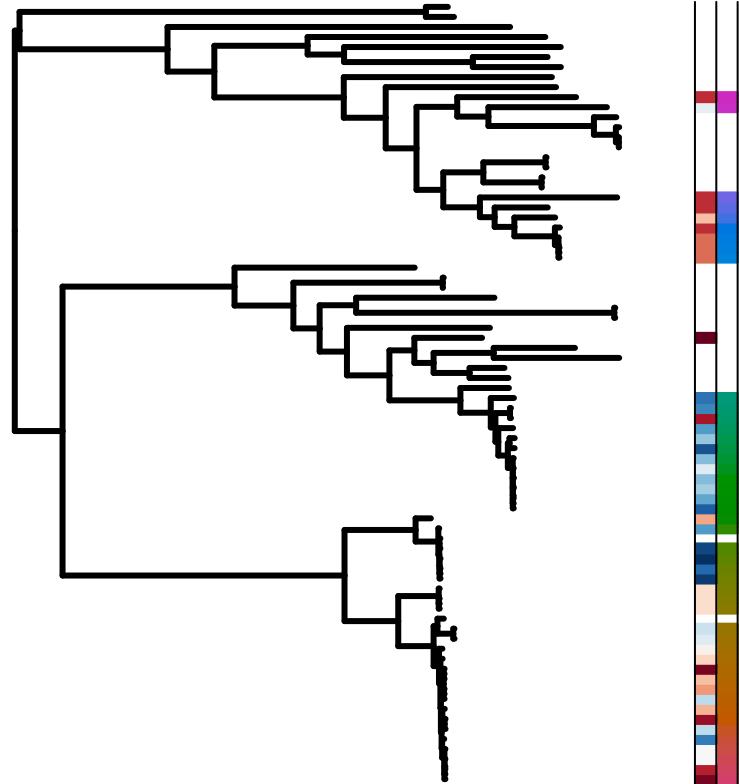
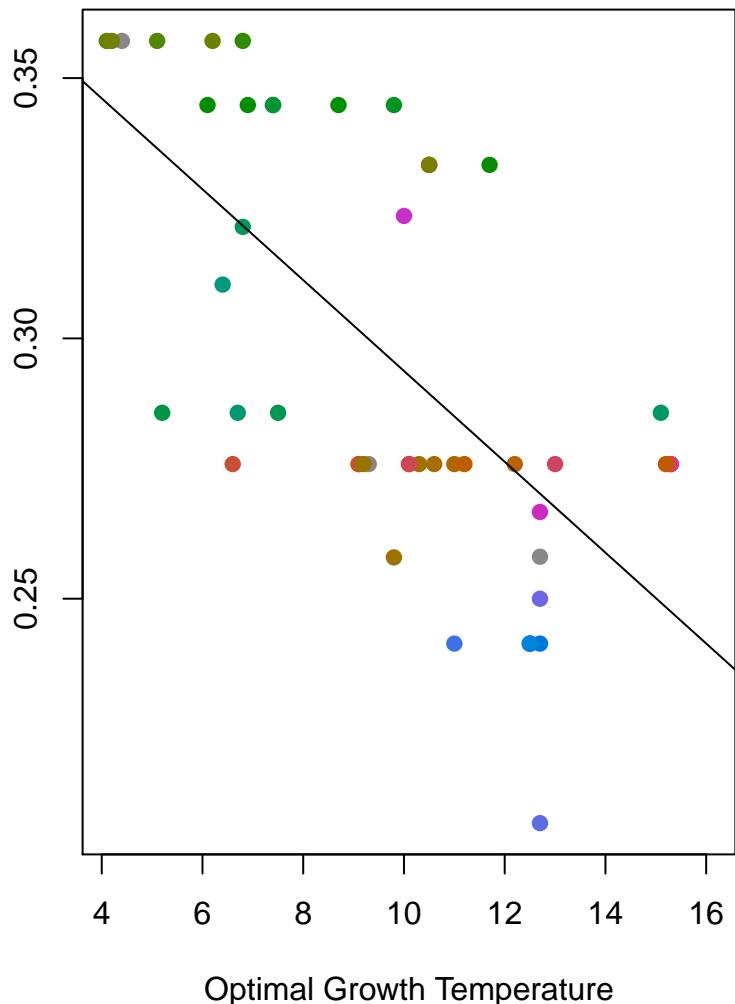
$r = -0.64, p = 10^{-6.129}$

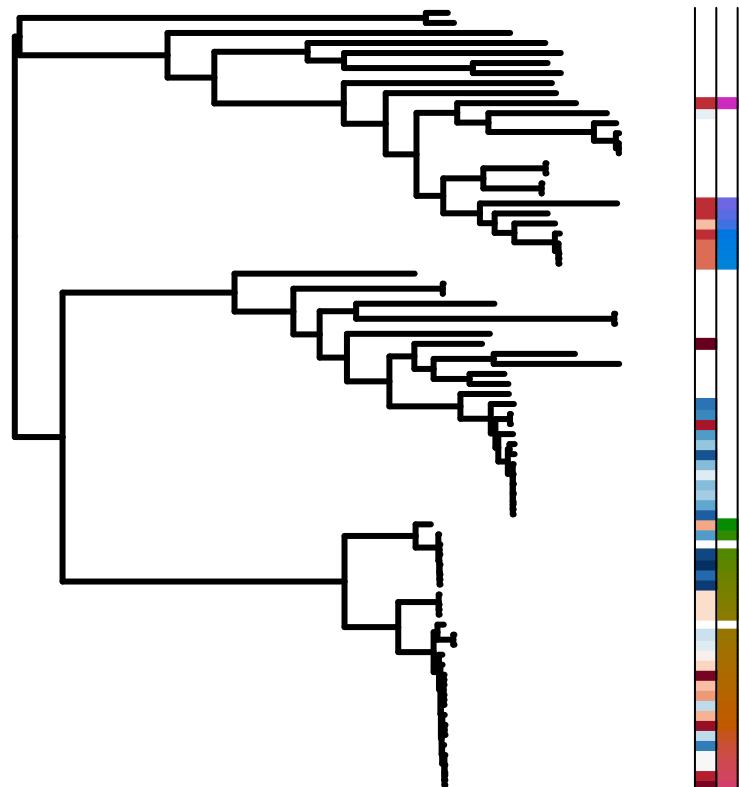
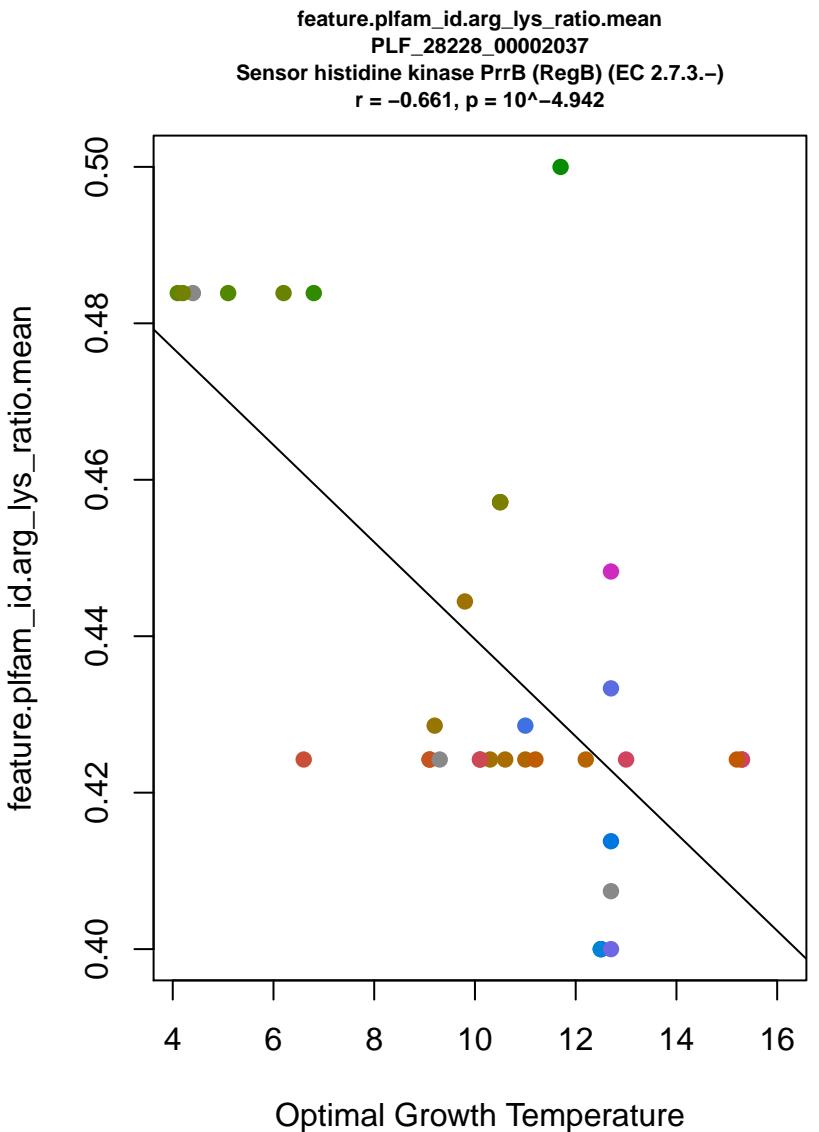
feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001366
hypothetical protein
 $r = -0.655, p = 10^{-6.492}$

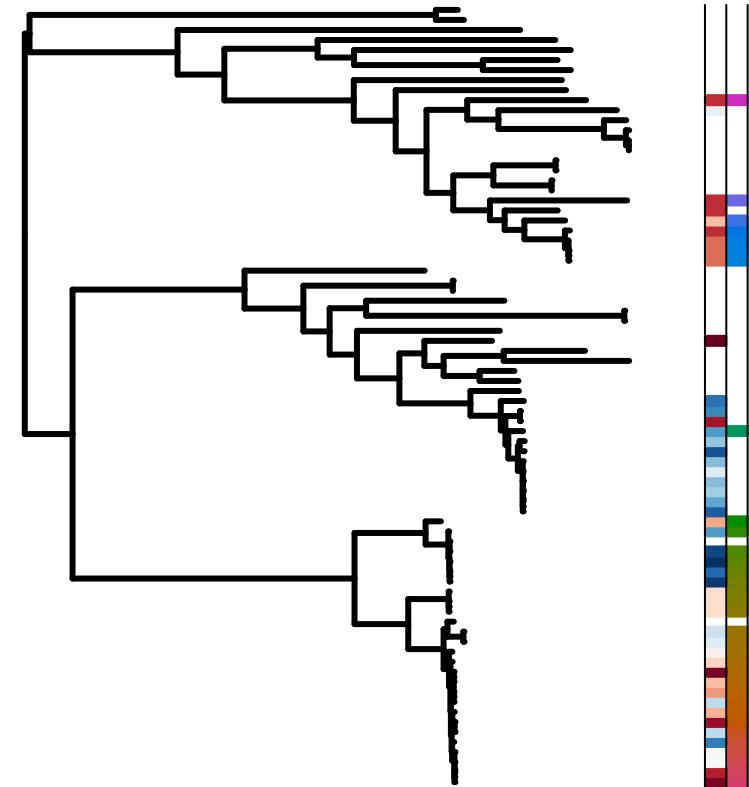
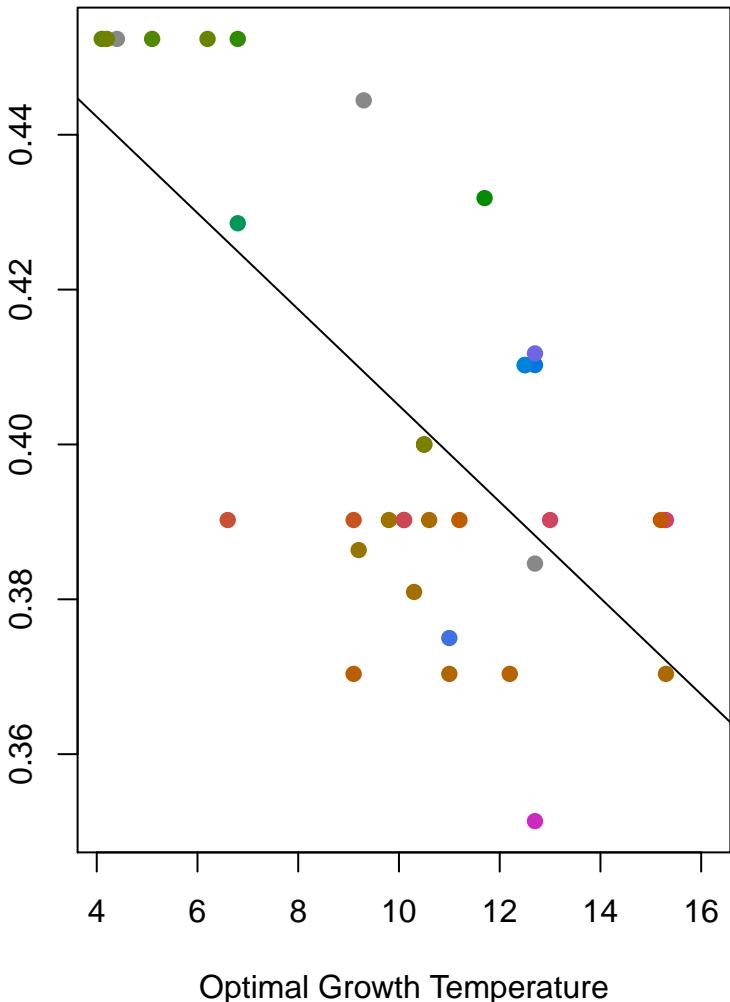
feature.plfam_id.arg_lys_ratio.mean





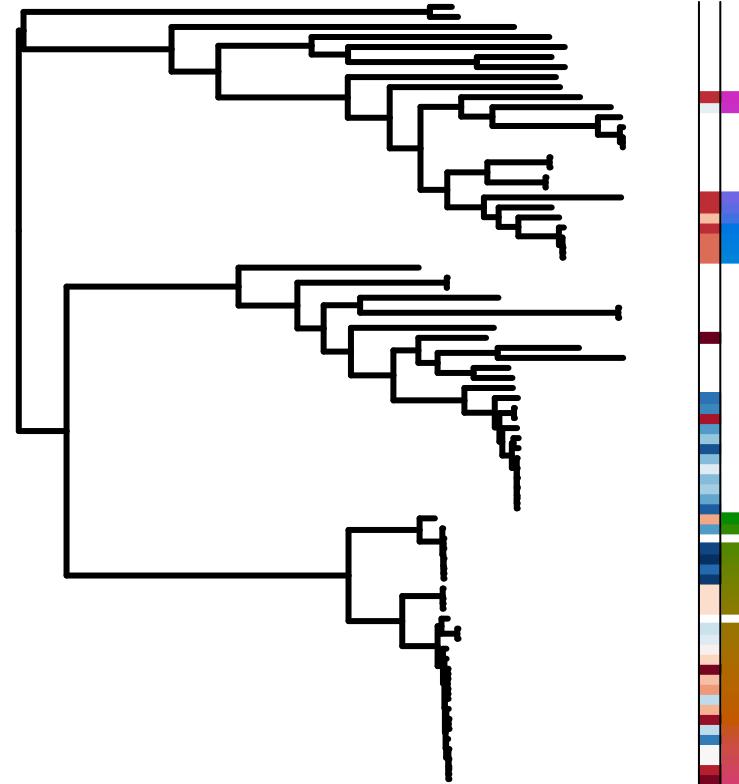
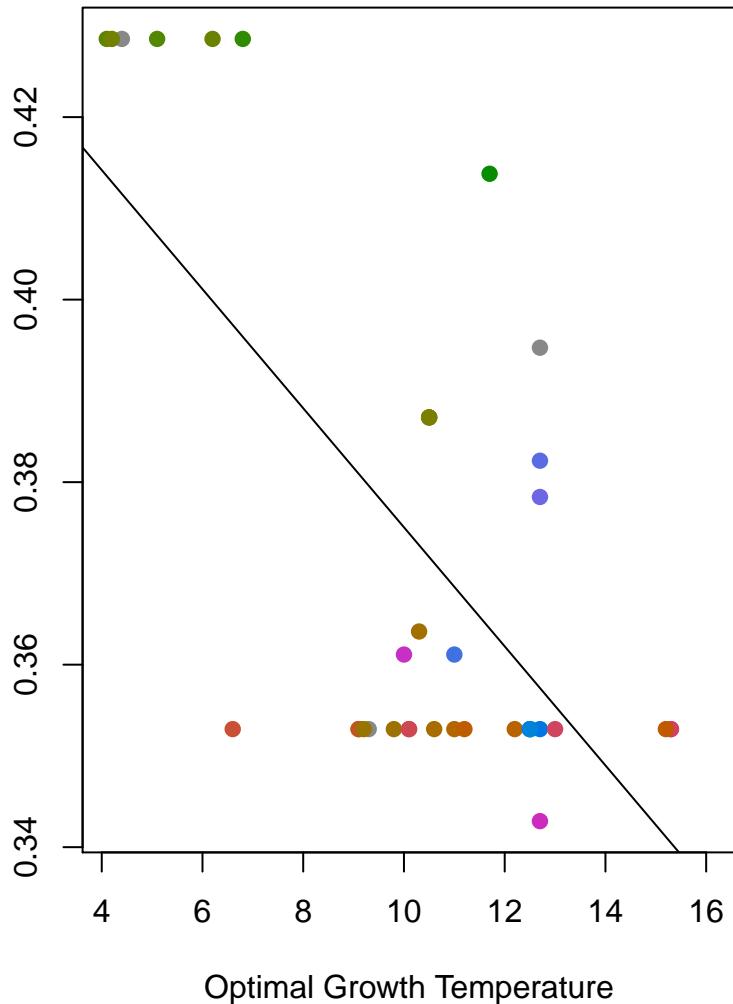
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002334
hypothetical protein
 $r = -0.662$, $p = 10^{-4.963}$

feature.plfam_id.arg_lys_ratio.mean



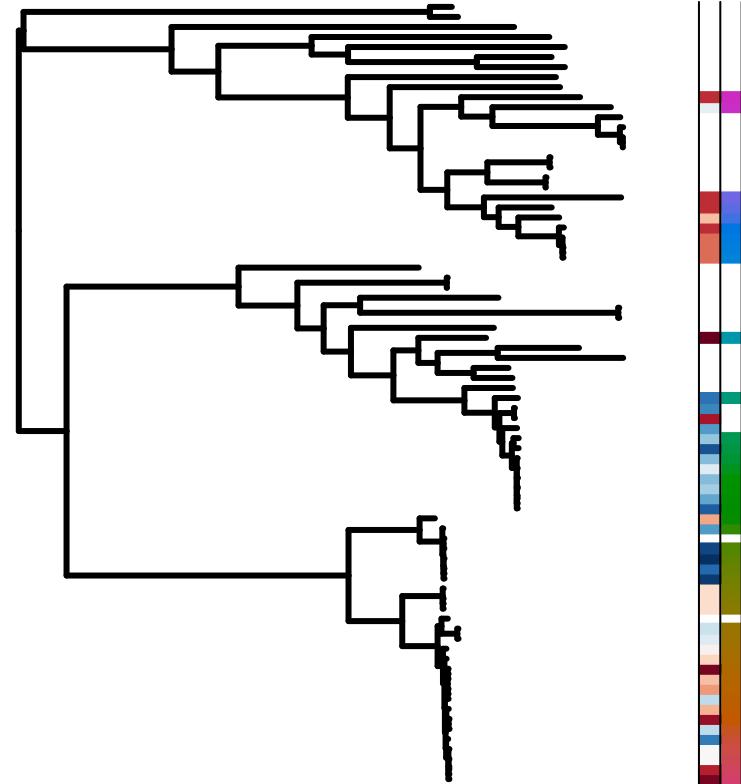
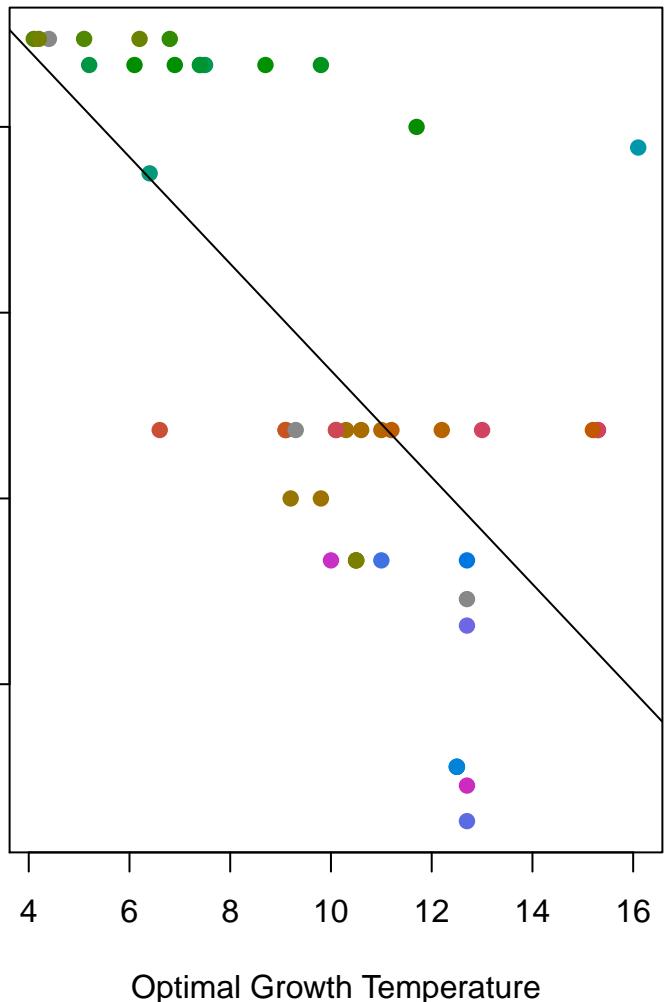
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001203
Cell division coordinator CpoB
 $r = -0.664$, $p = 10^{-5.123}$

feature.plfam_id.arg_lys_ratio.mean



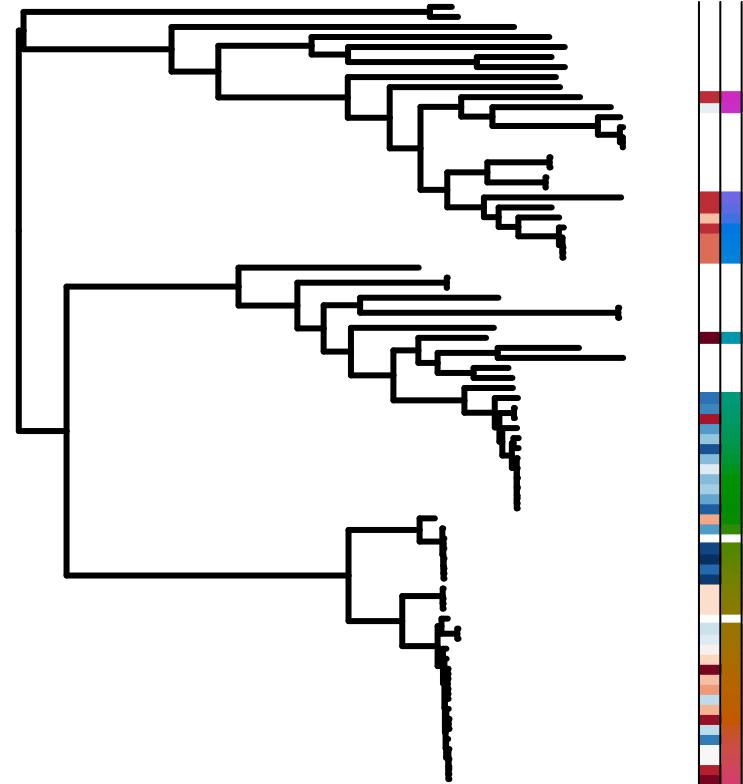
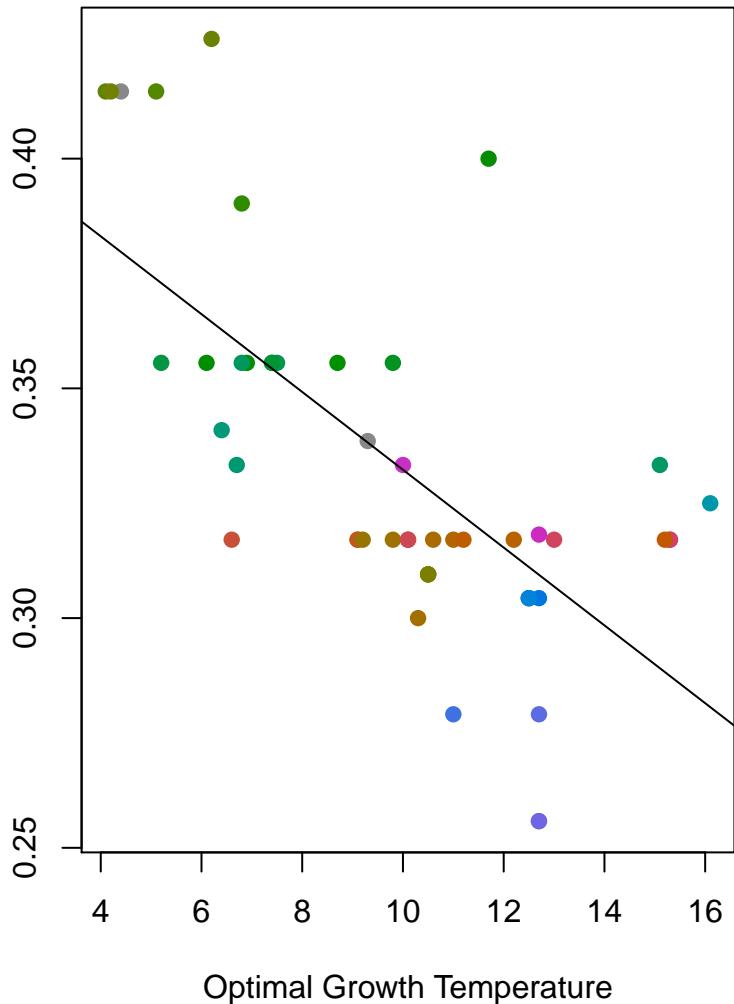
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001927
Potential queD like 2
 $r = -0.668$, $p = 10^{-6.541}$

feature.plfam_id.arg_lys_ratio.mean

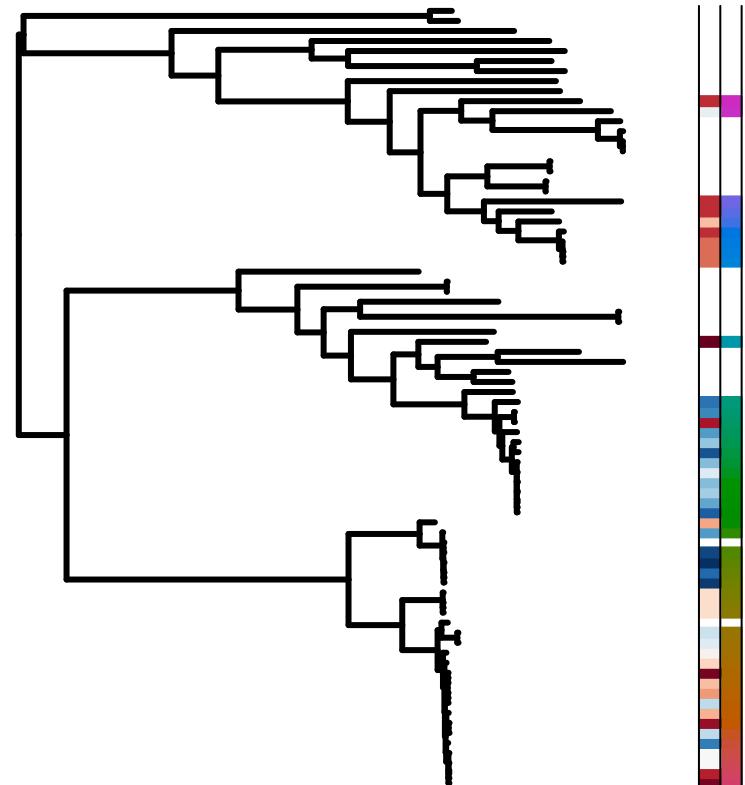
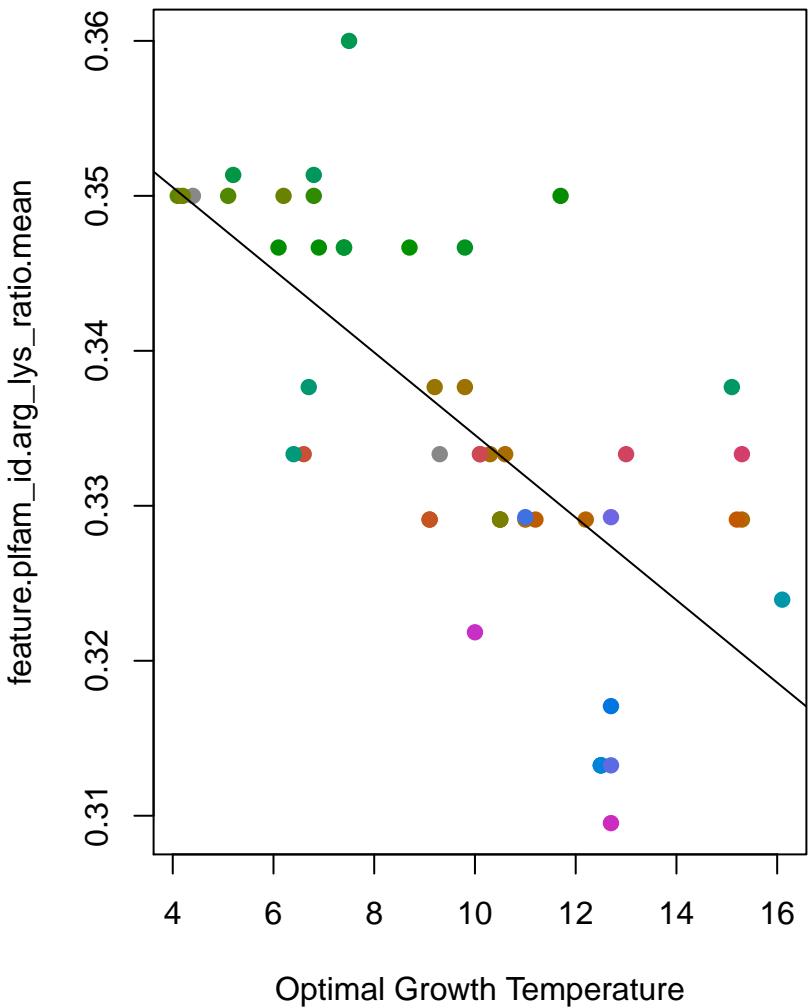


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000740
Alanine transaminase (EC 2.6.1.2)
 $r = -0.681$, $p = 10^{-7.27}$

feature.plfam_id.arg_lys_ratio.mean

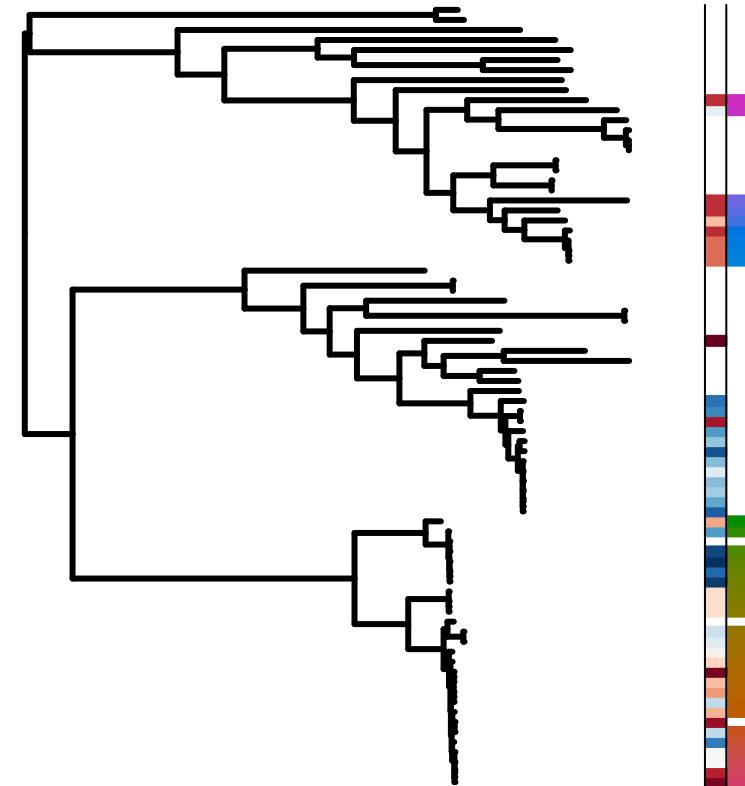
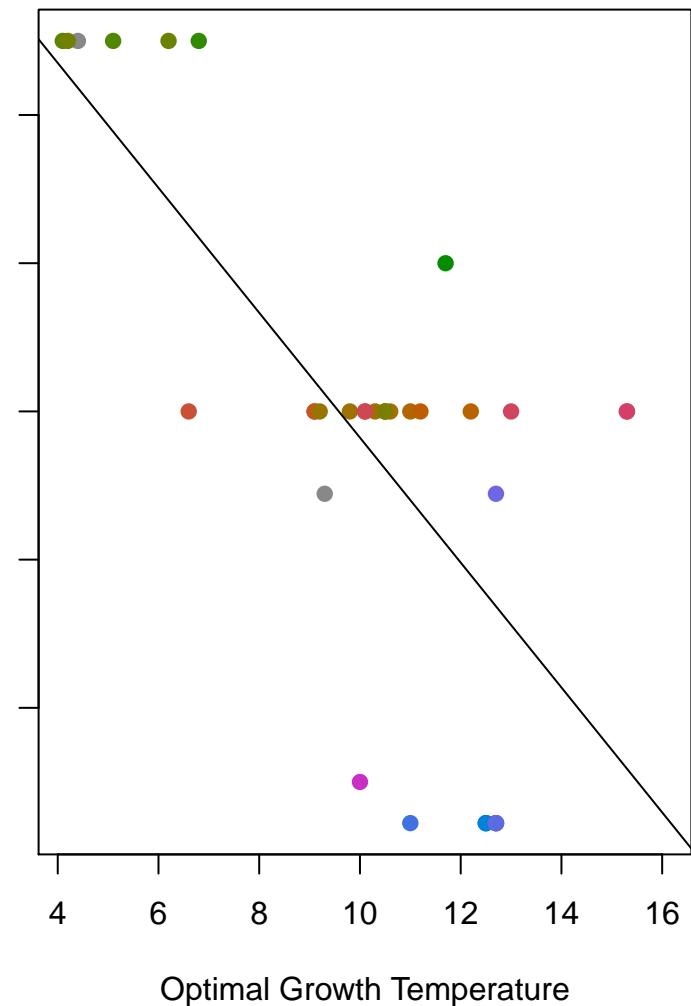


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002008
Related to collagenase
 $r = -0.689$, $p = 10^{-7.359}$

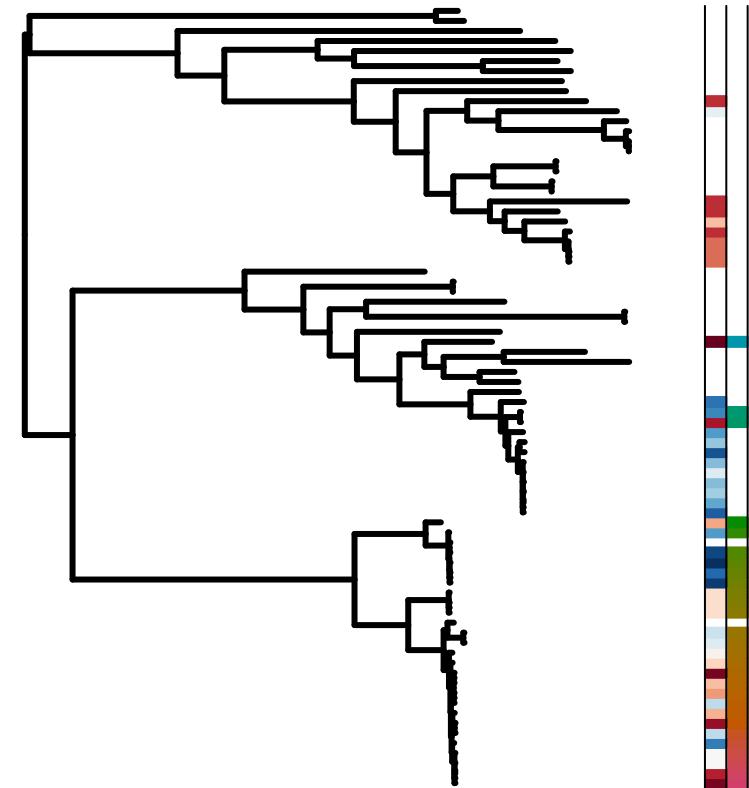
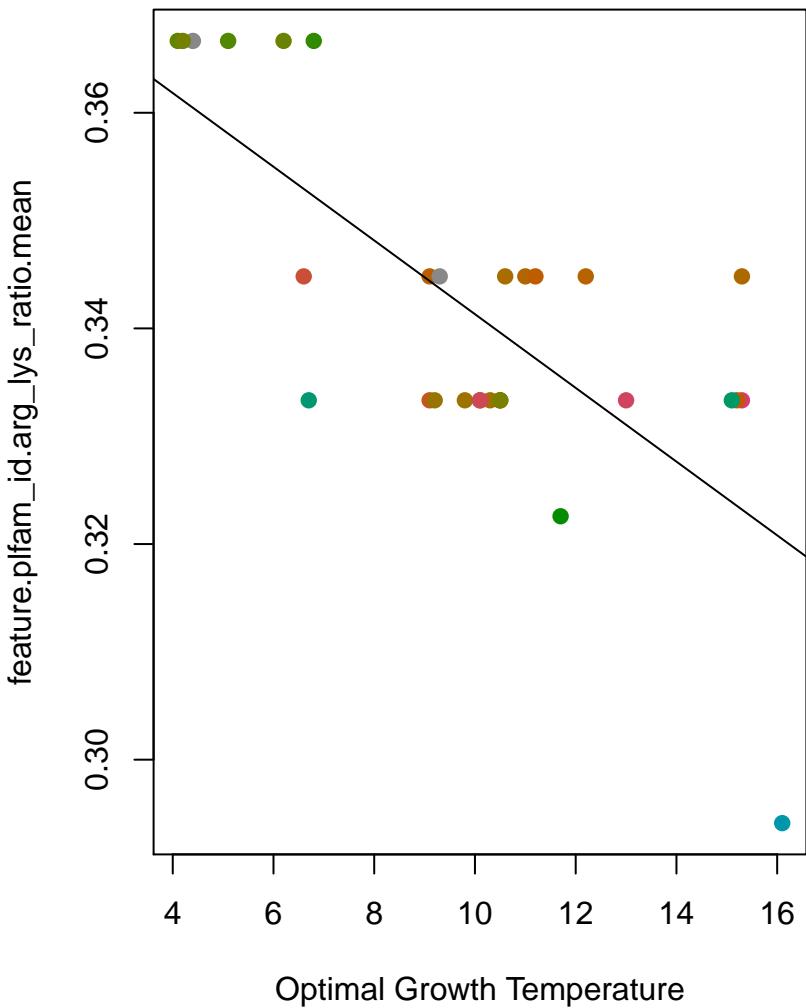


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000991
Putative manganese efflux pump MntP
 $r = -0.707$, $p = 10^{-5.839}$

feature.plfam_id.arg_lys_ratio.mean

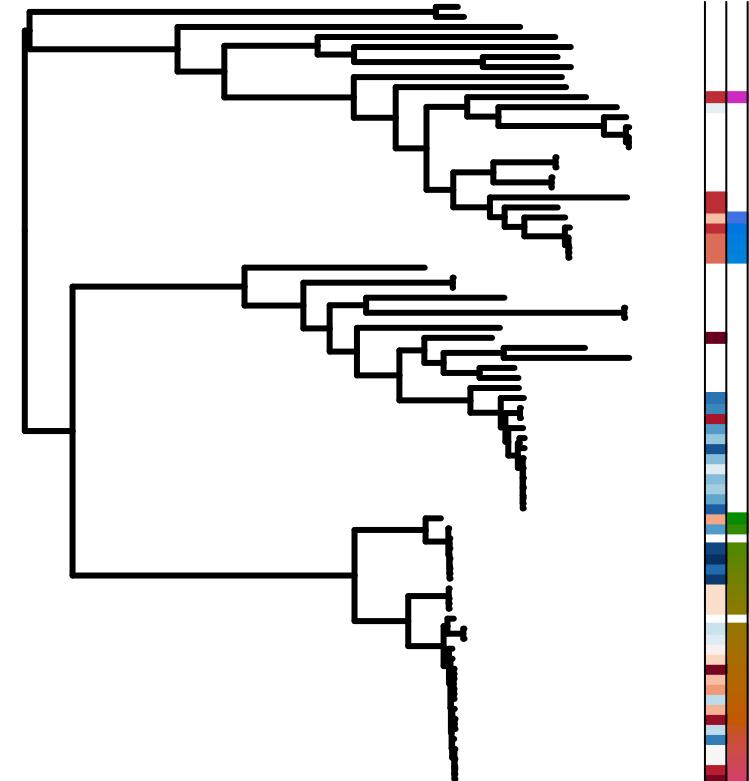
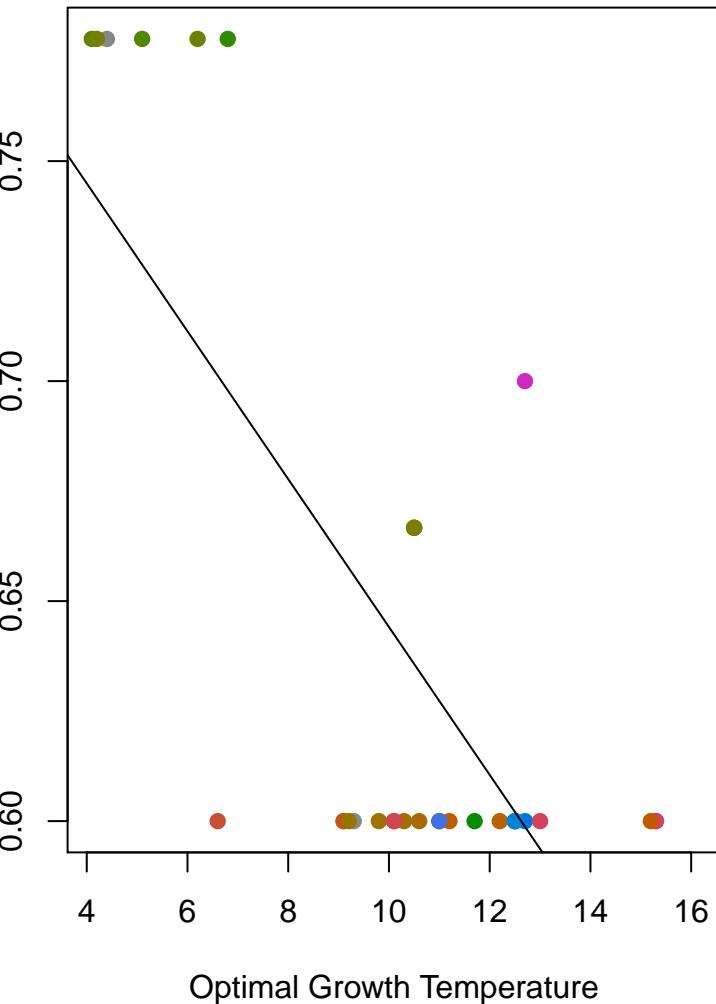


feature.pifam_id.arg_lys_ratio.mean
PLF_28228_00016853
Tryptophan 2,3-dioxygenase (EC 1.13.11.11)
 $r = -0.732$, $p = 10^{-5.371}$



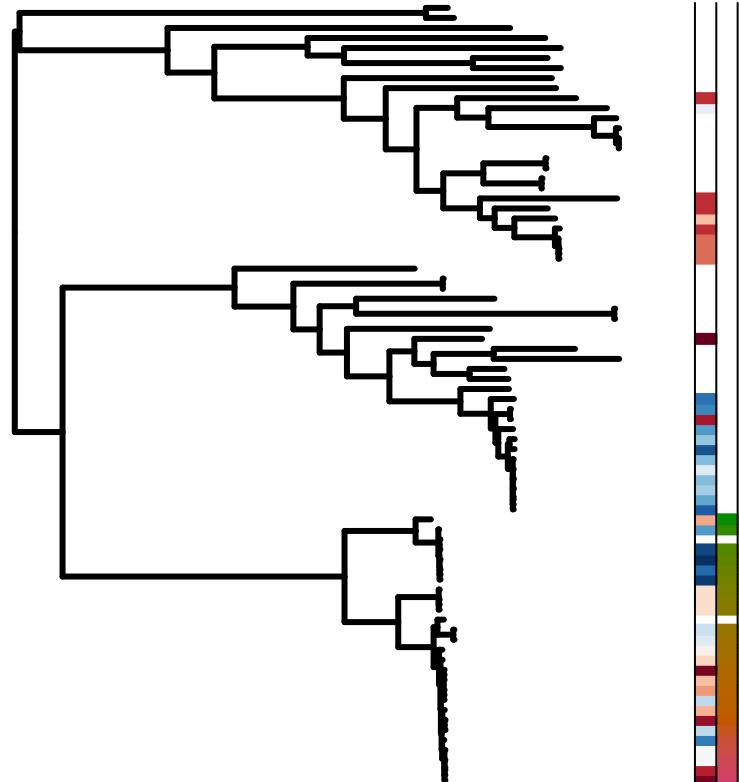
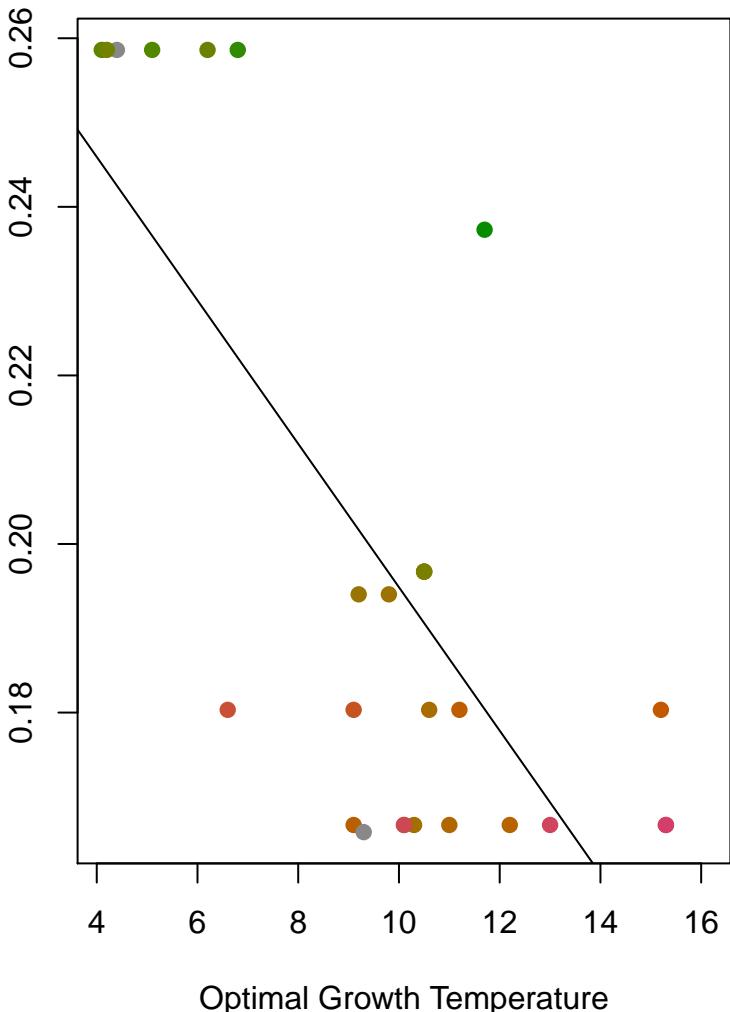
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003600
Putative transmembrane protein
 $r = -0.736$, $p = 10^{-5.978}$

feature.plfam_id.arg_lys_ratio.mean



feature.pifam_id.arg_lys_ratio.mean
PLF_28228_00014674
hypothetical protein
 $r = -0.738$, $p = 10^{-4.952}$

feature.pifam_id.arg_lys_ratio.mean



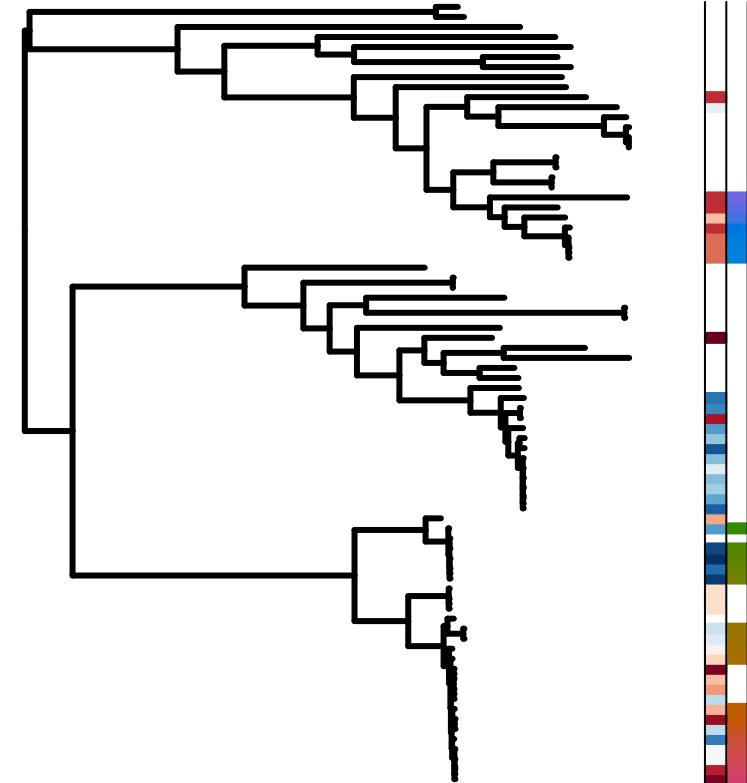
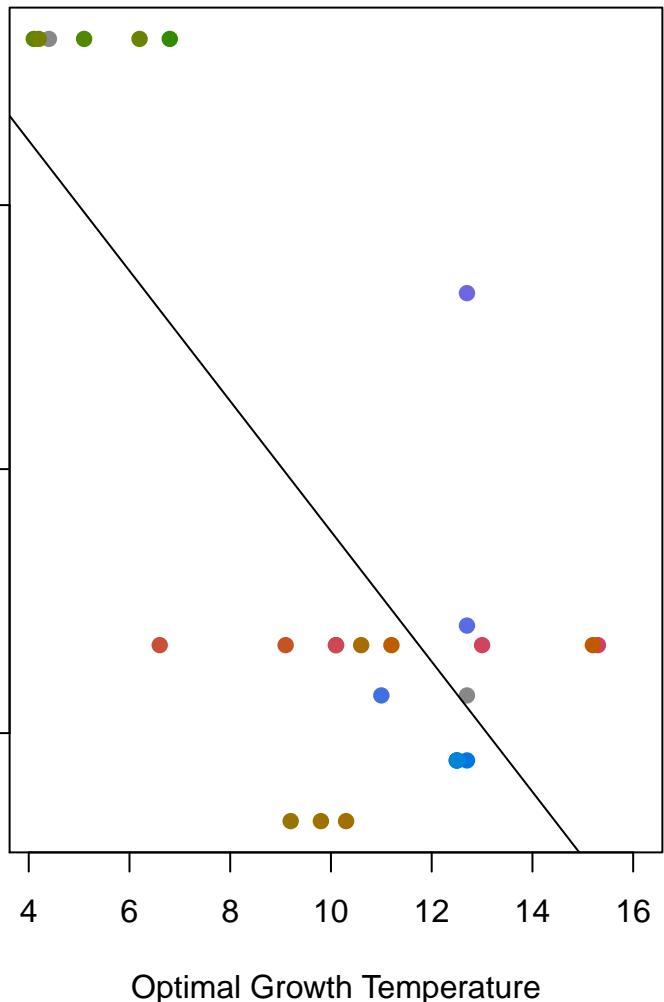
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00003793

Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)

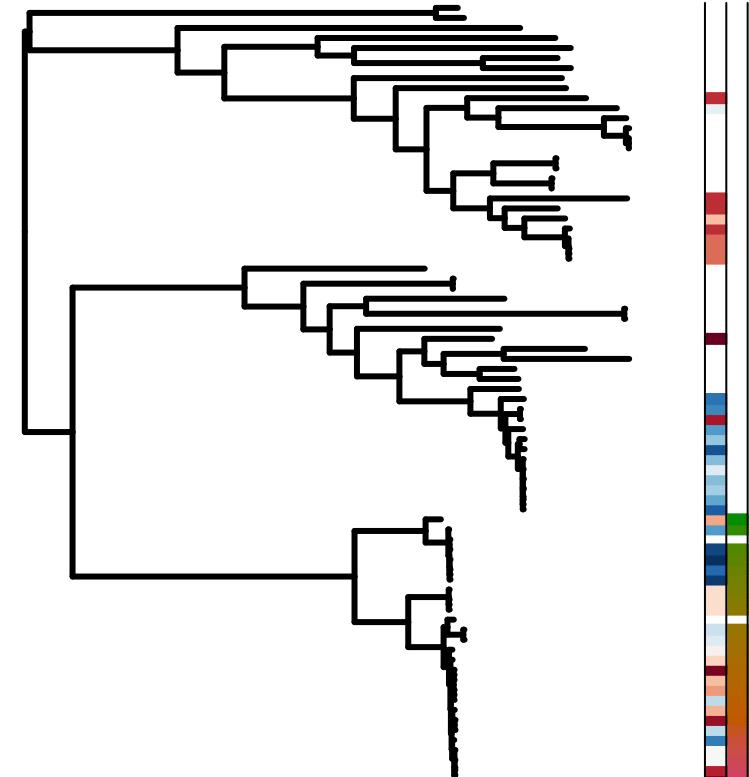
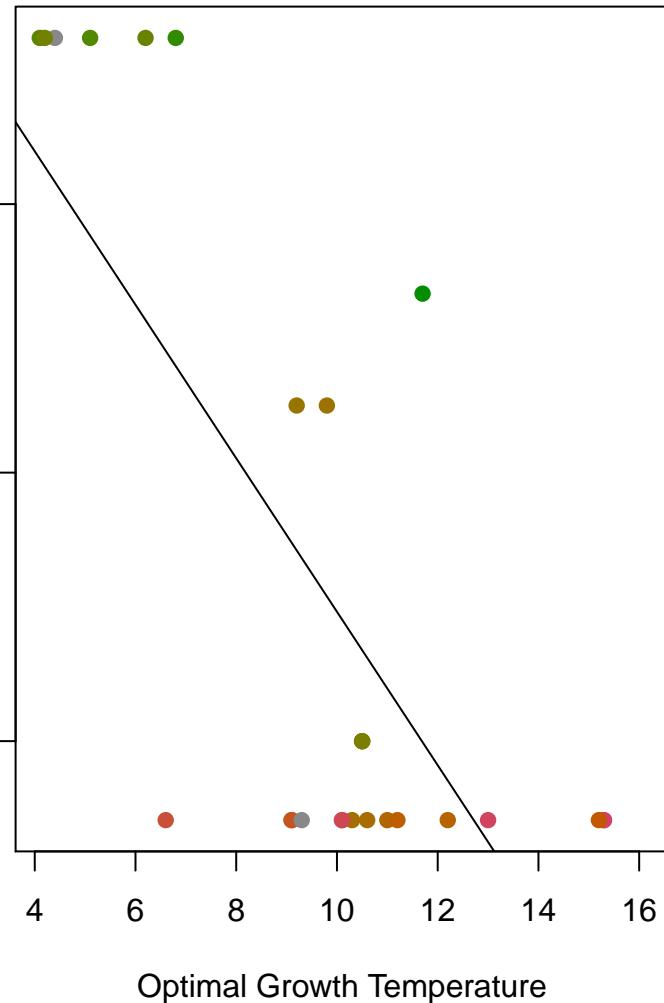
$r = -0.738, p = 10^{-4.774}$

feature.plfam_id.arg_lys_ratio.mean



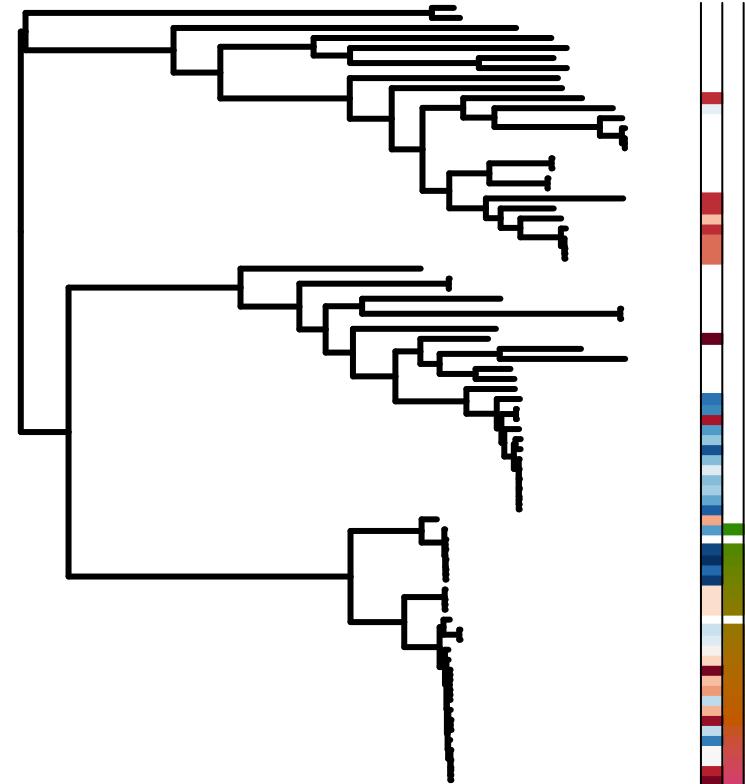
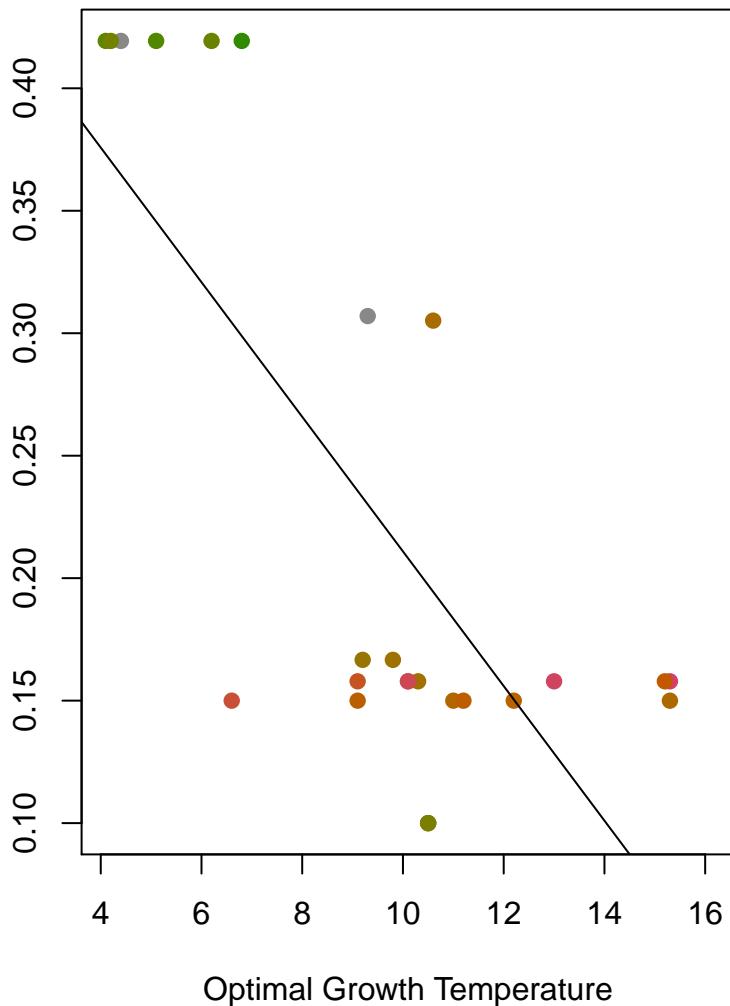
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00031009
hypothetical protein
 $r = -0.739$, $p = 10^{-4.963}$

feature.plfam_id.arg_lys_ratio.mean

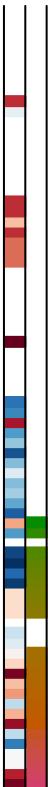
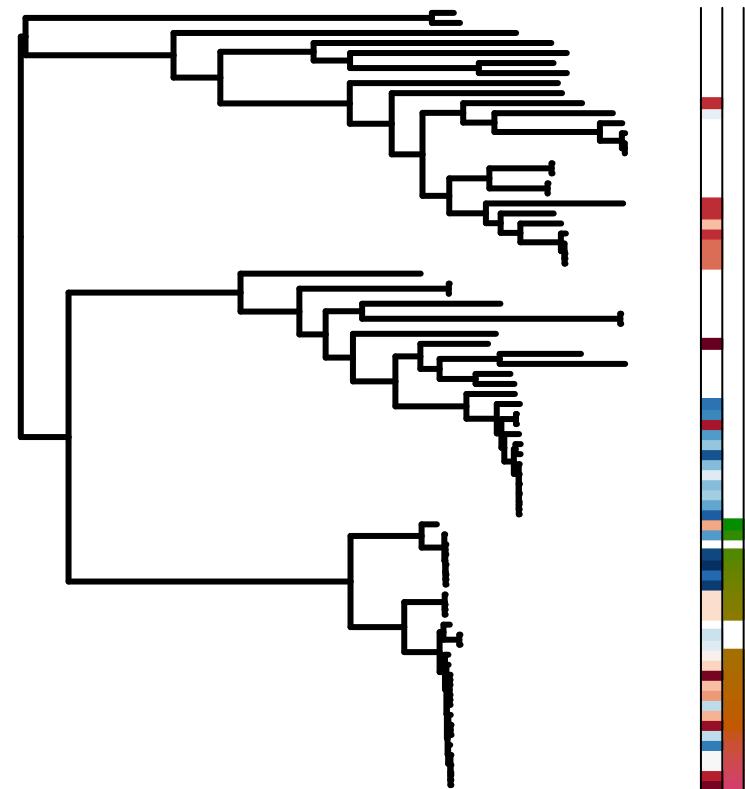
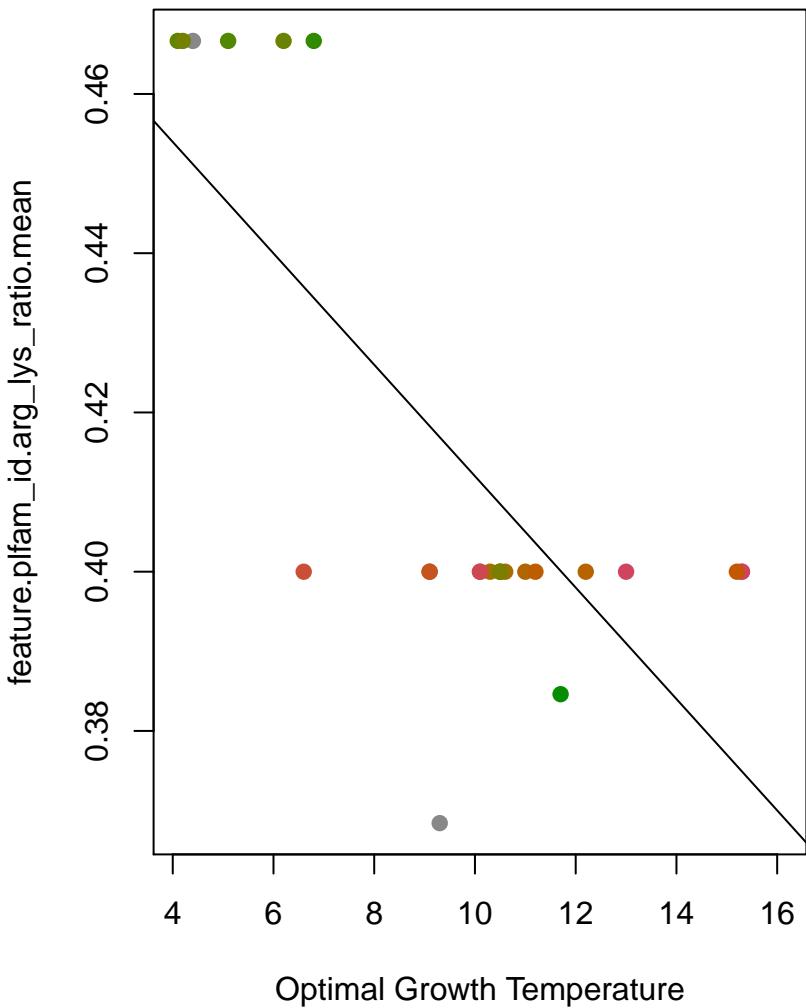


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00015307
hypothetical protein
 $r = -0.739$, $p = 10^{-4.797}$

feature.plfam_id.arg_lys_ratio.mean

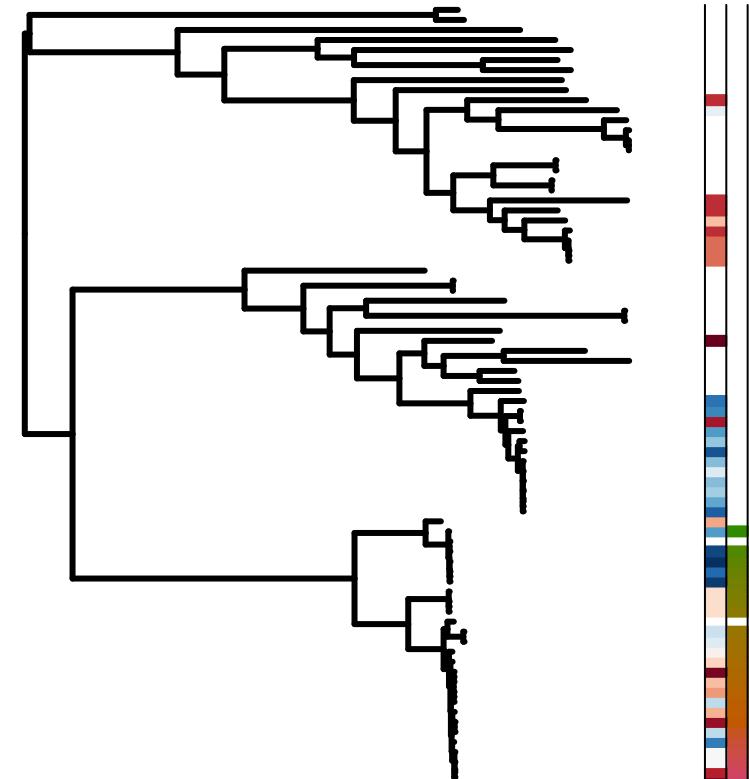
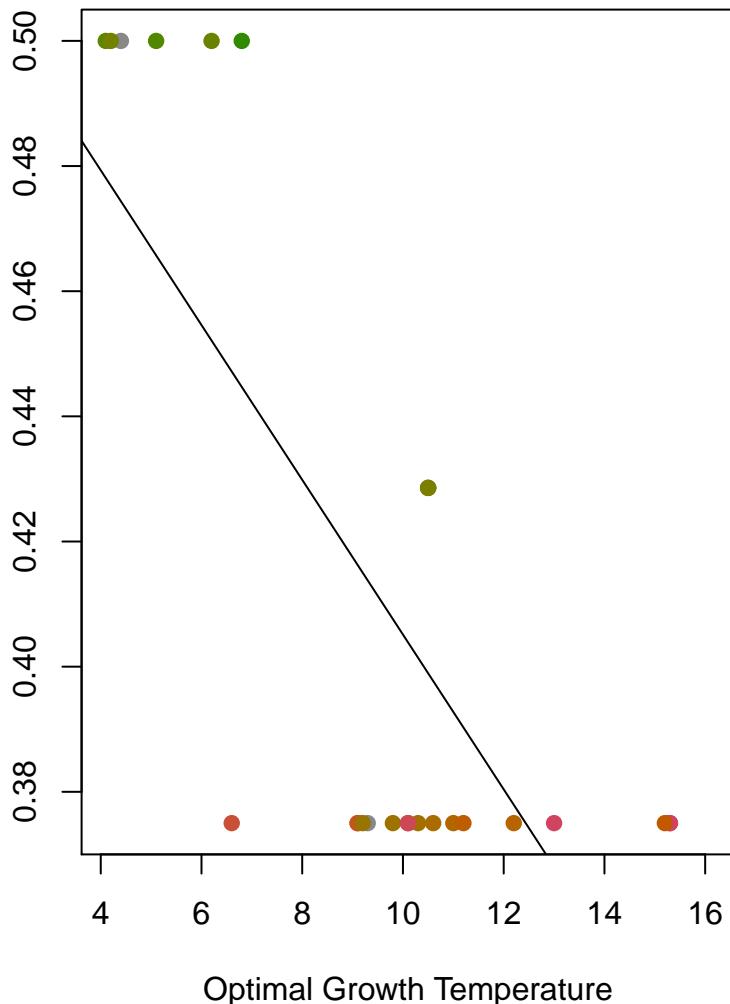


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00022096
Two-component system sensor histidine kinase
 $r = -0.75$, $p = 10^{-4.804}$

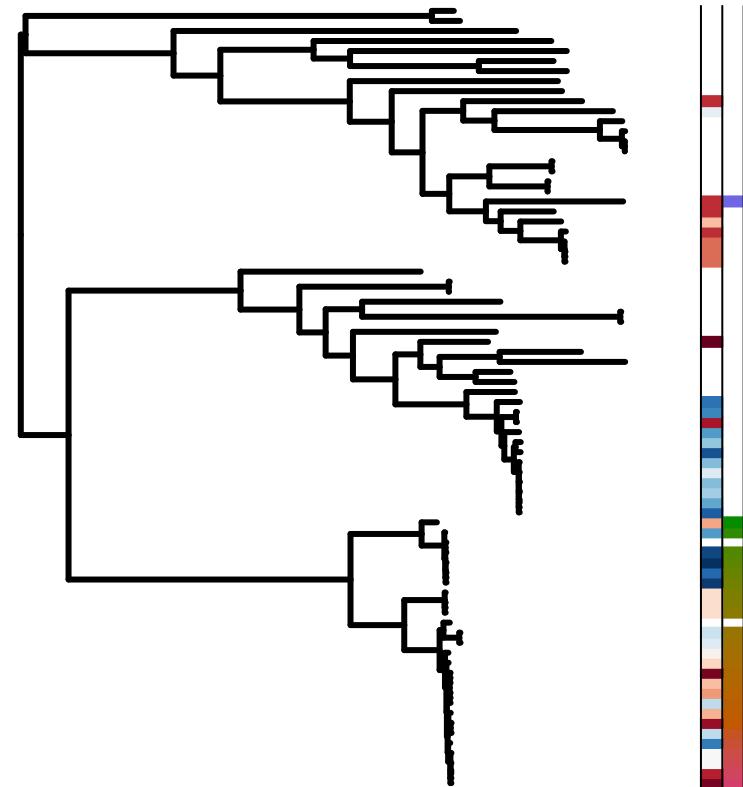
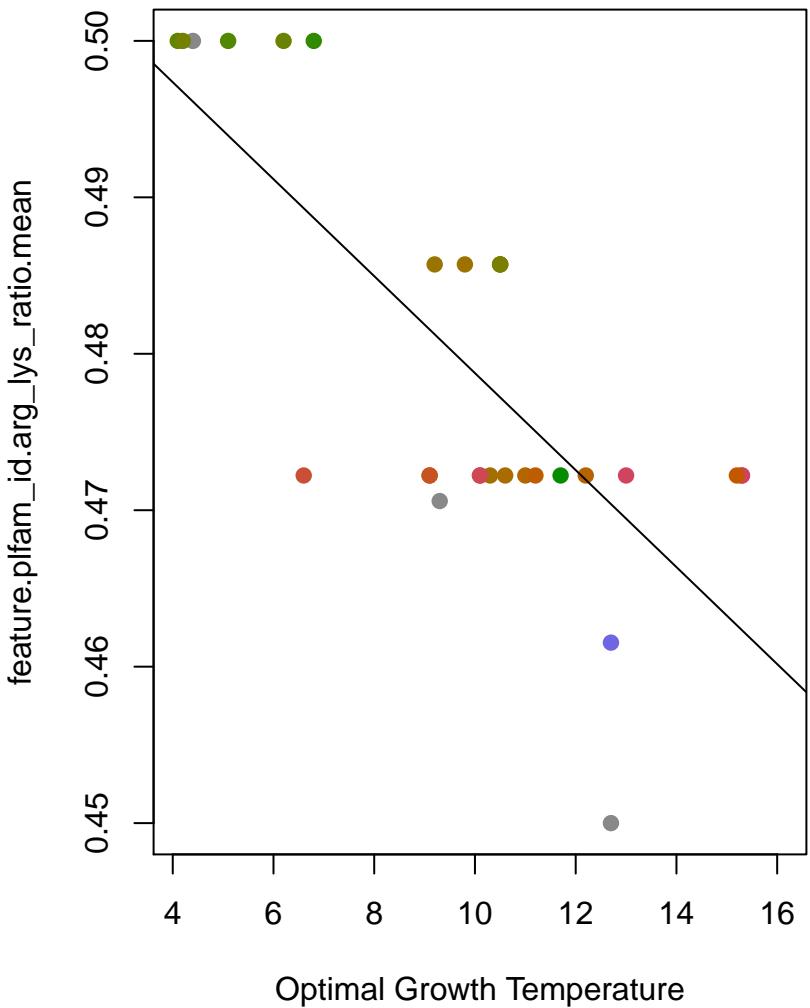


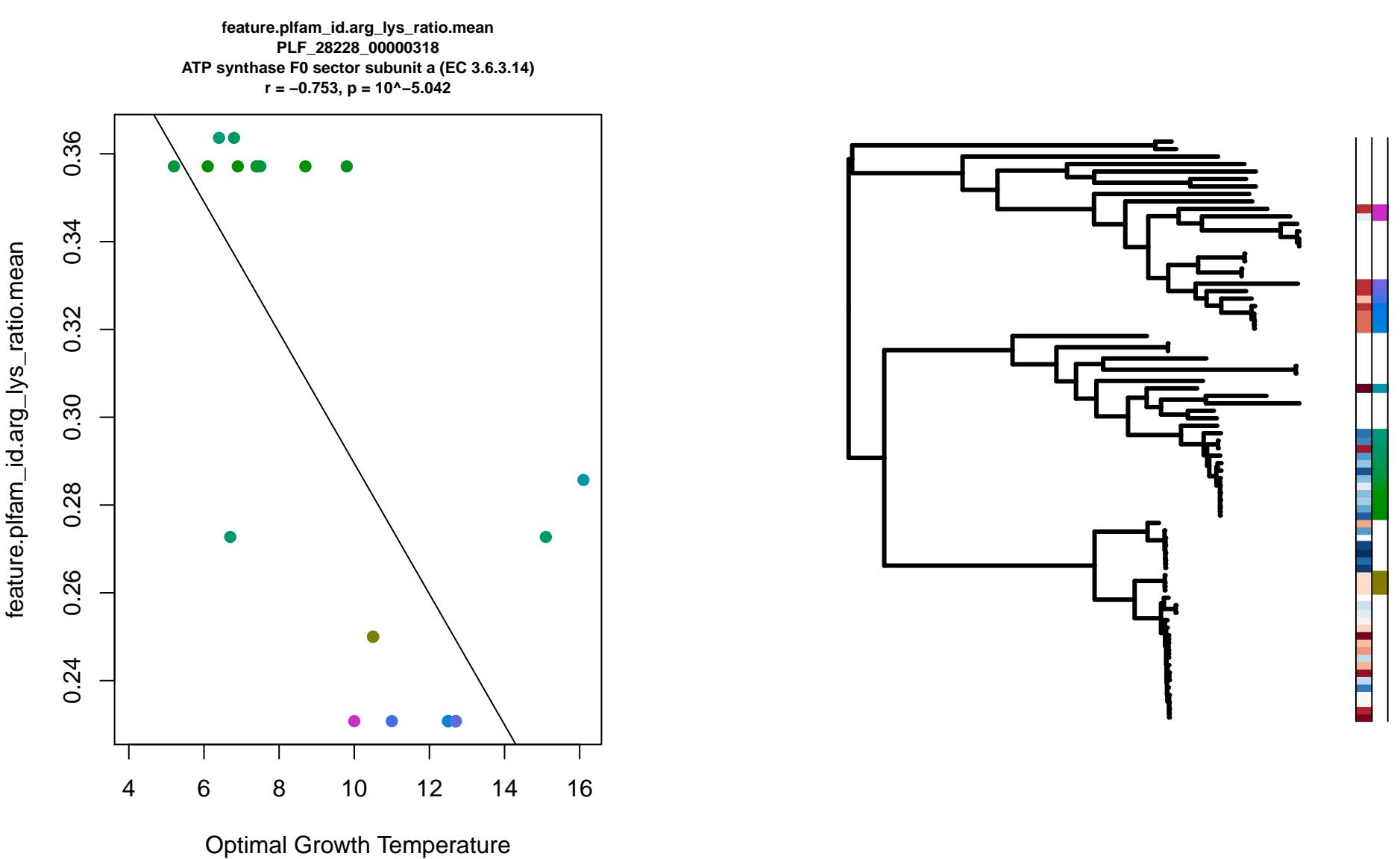
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00030864
hypothetical protein
 $r = -0.75$, $p = 10^{-4.996}$

feature.plfam_id.arg_lys_ratio.mean



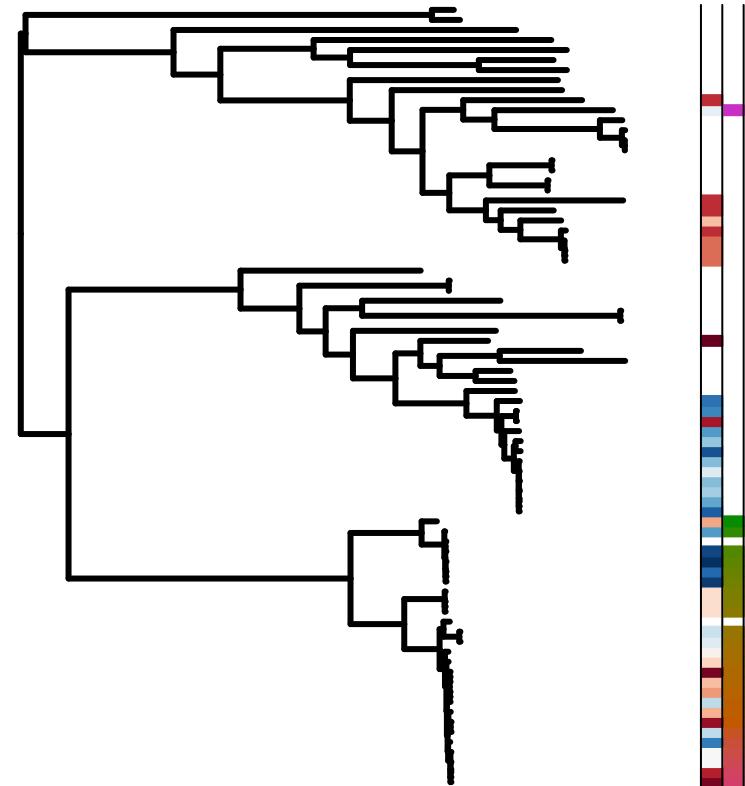
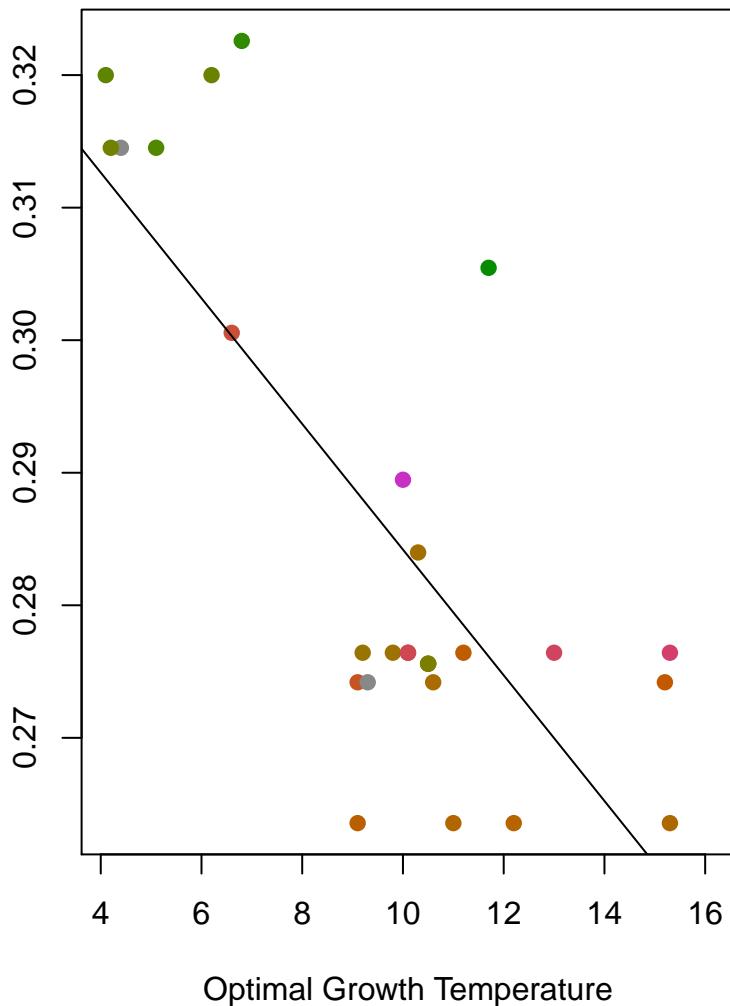
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00005643
hypothetical protein
 $r = -0.751, p = 10^{-5.579}$





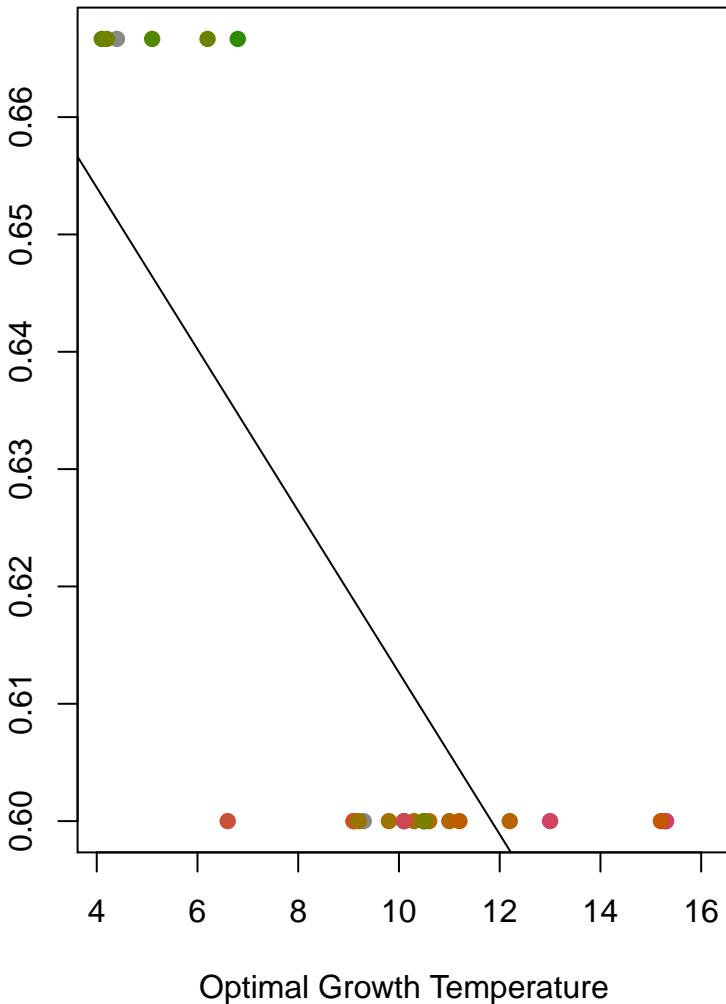
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00015154
hypothetical protein
 $r = -0.761$, $p = 10^{-5.593}$

feature.plfam_id.arg_lys_ratio.mean

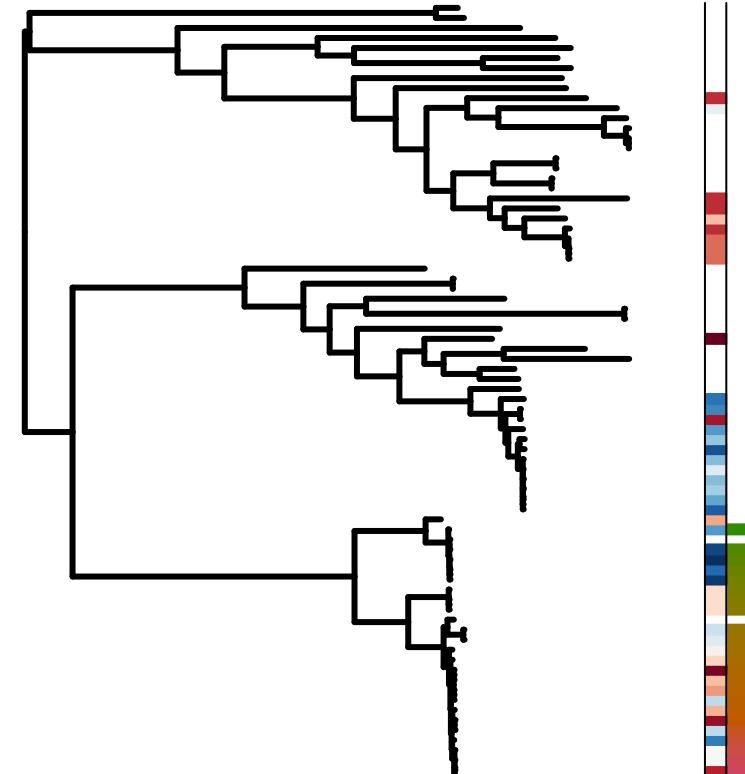


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00029369
hypothetical protein
 $r = -0.775$, $p = 10^{-5.478}$

feature.plfam_id.arg_lys_ratio.mean

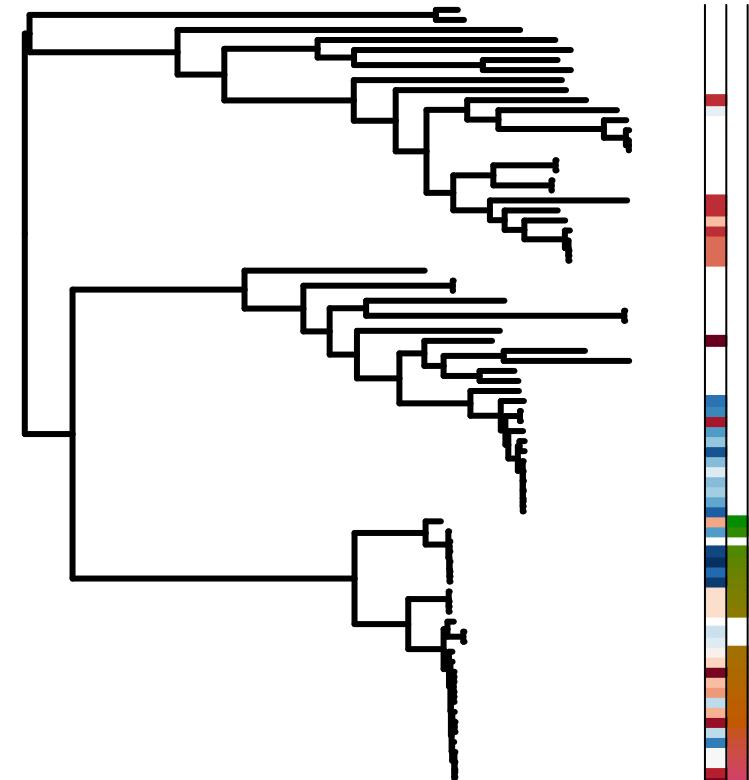
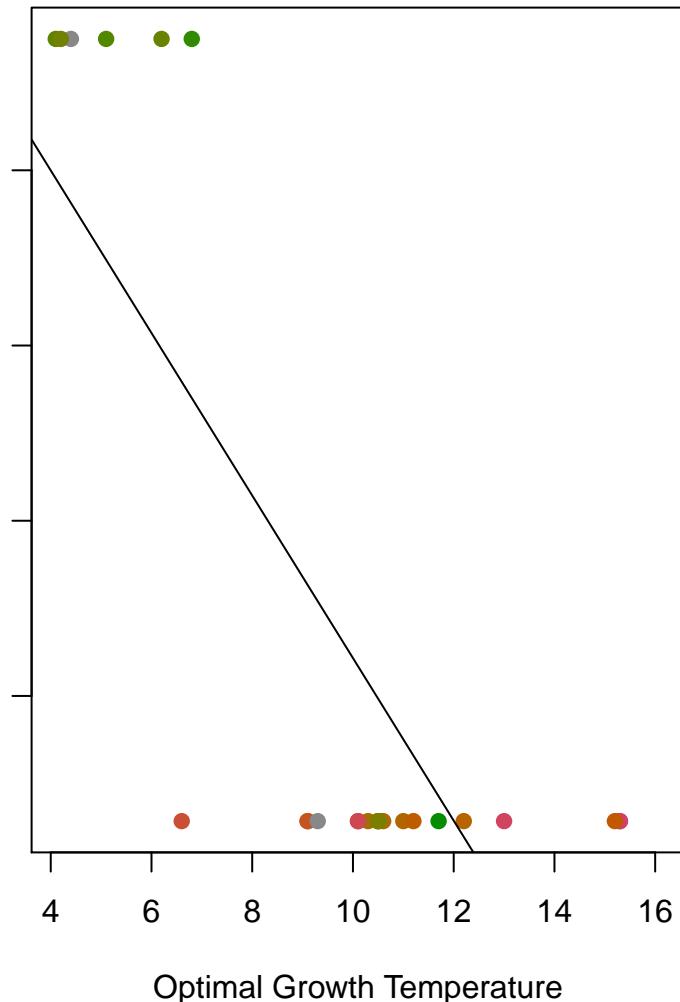


Optimal Growth Temperature



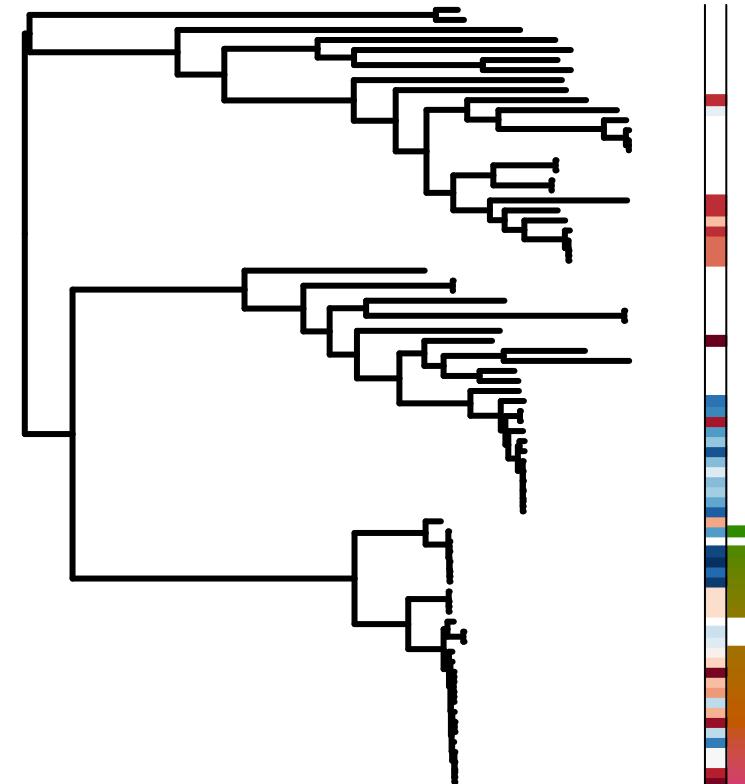
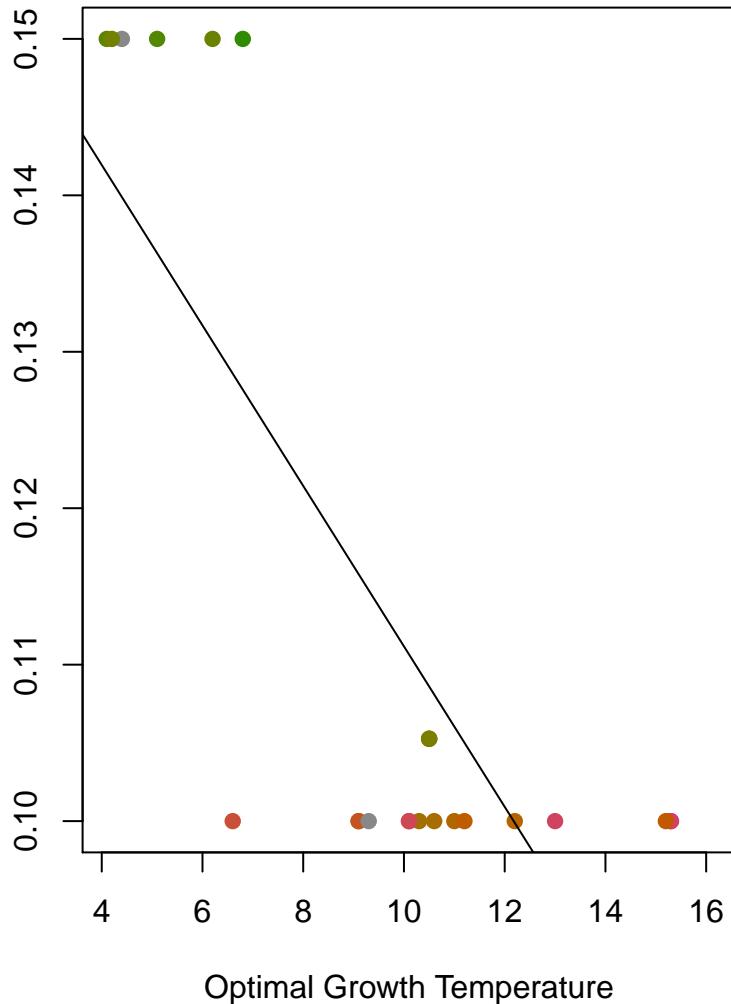
feature.pifam_id.arg_lys_ratio.mean
PLF_28228_00029549
hypothetical protein
 $r = -0.79$, $p = 10^{-5.574}$

feature.pifam_id.arg_lys_ratio.mean



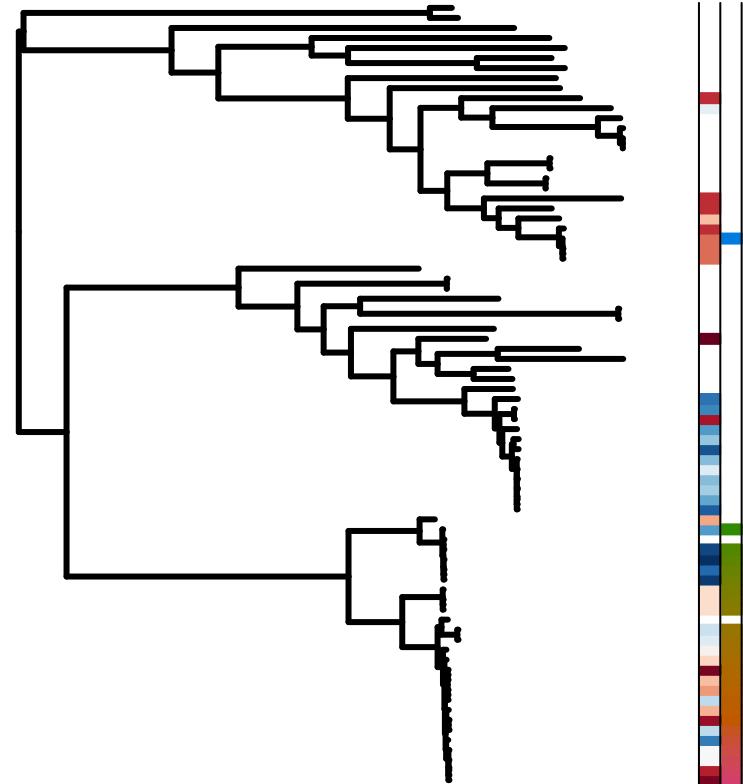
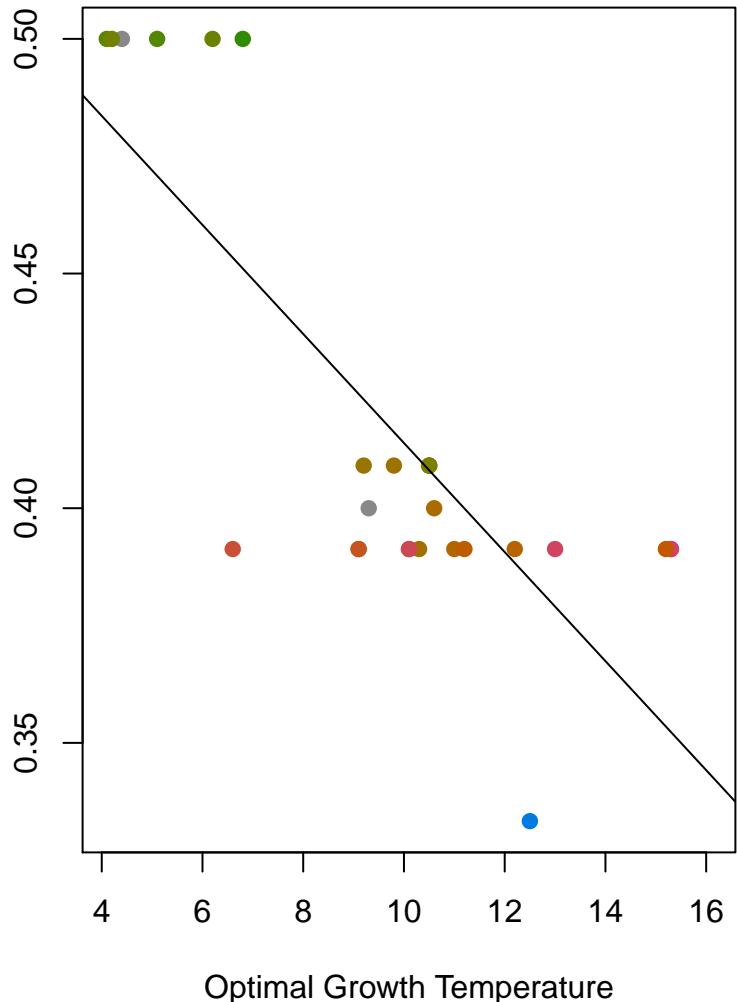
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00030467
Redoxin domain protein
 $r = -0.79$, $p = 10^{-5.356}$

feature.plfam_id.arg_lys_ratio.mean



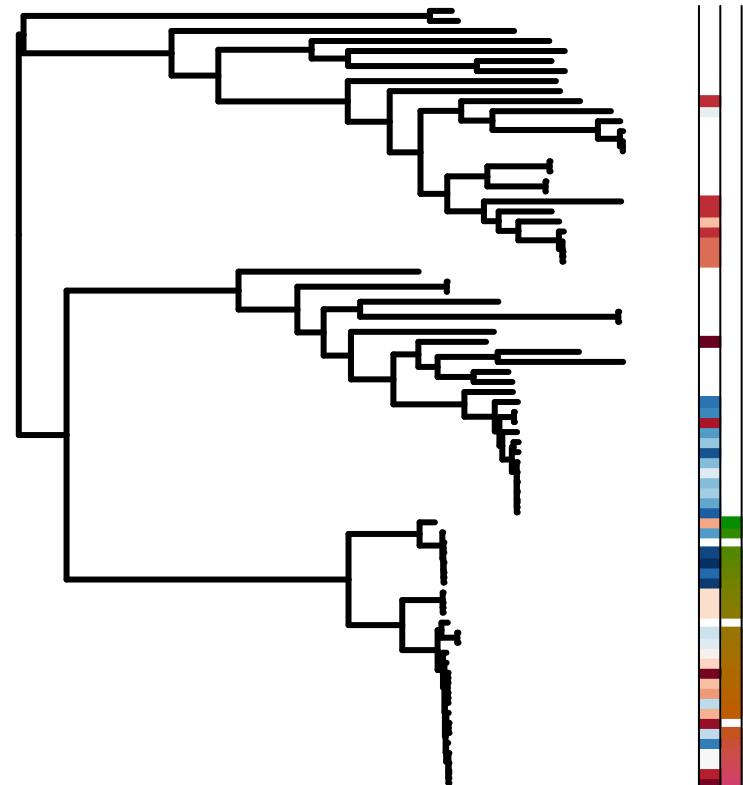
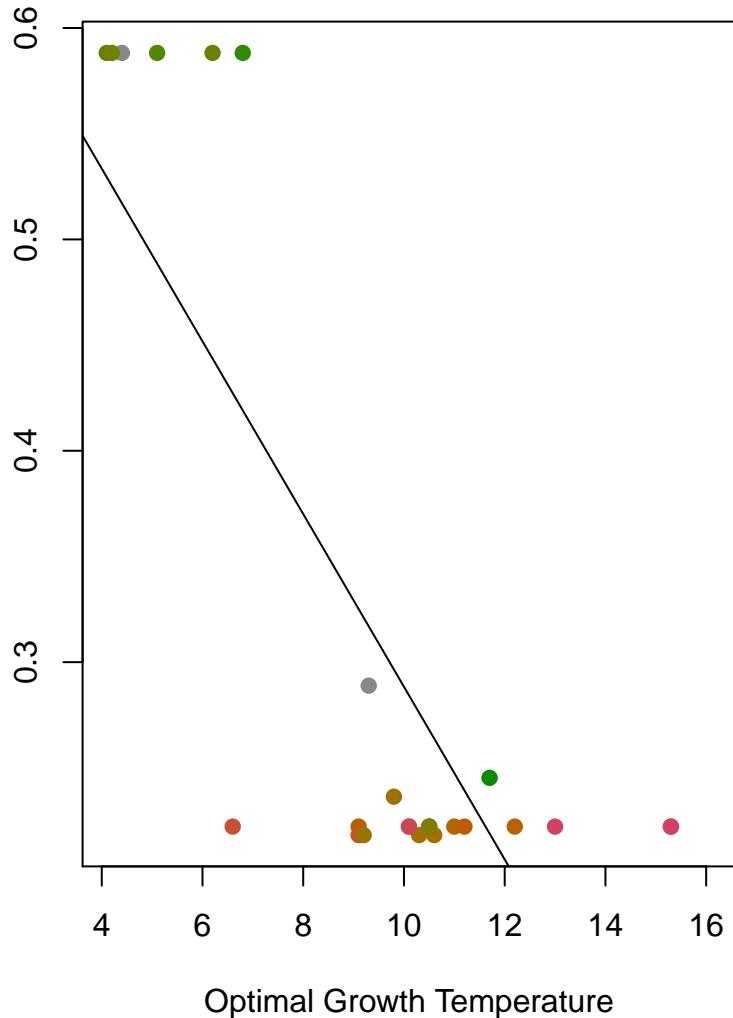
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00014070
hypothetical protein
 $r = -0.79$, $p = 10^{-6.029}$

feature.plfam_id.arg_lys_ratio.mean



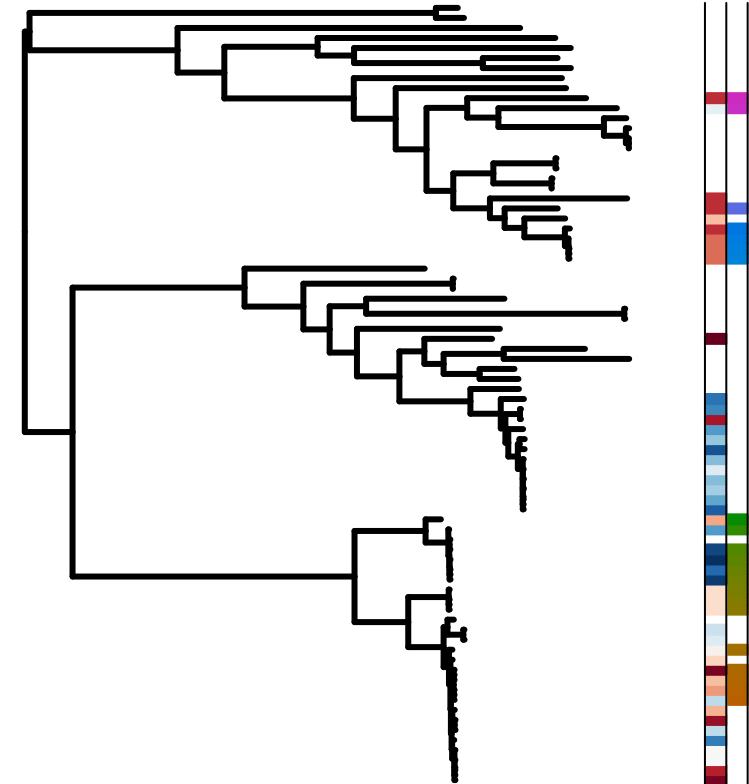
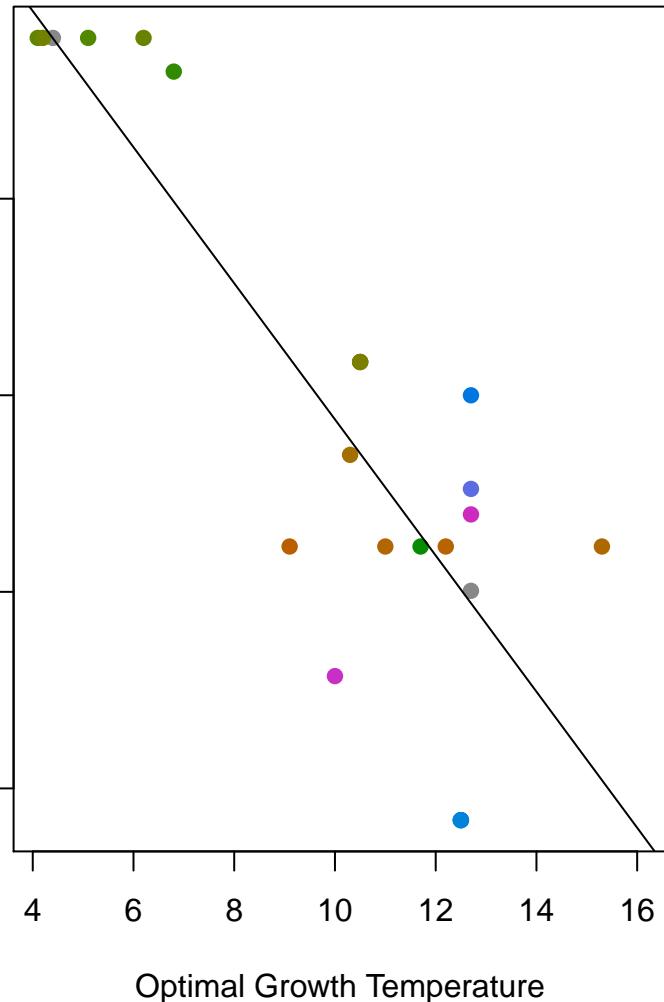
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00017455
Maltodextrin glucosidase (EC 3.2.1.20)
 $r = -0.798$, $p = 10^{-5.981}$

feature.plfam_id.arg_lys_ratio.mean



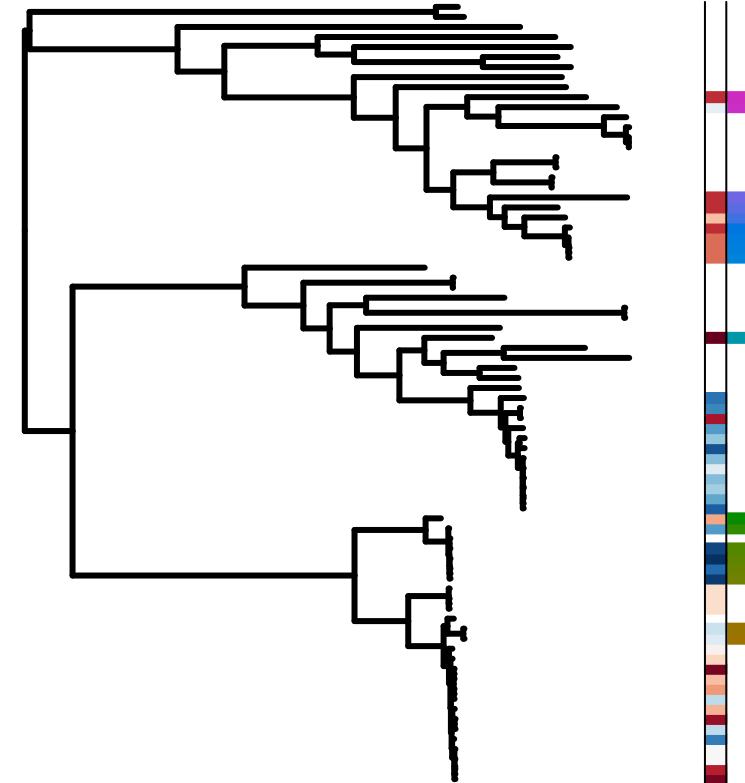
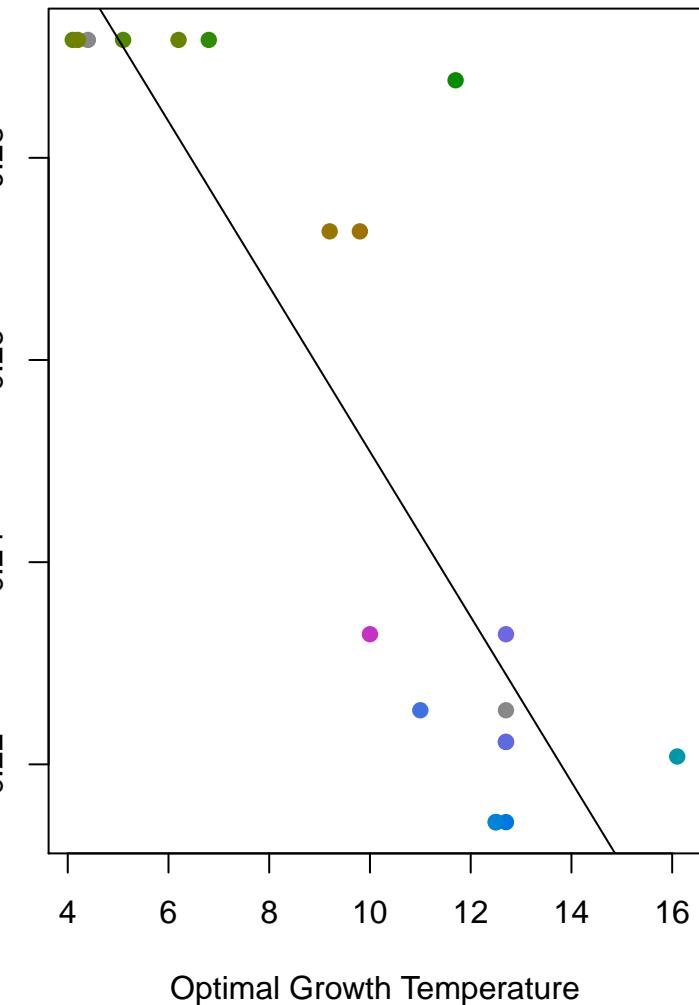
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001912
Phage integrase
 $r = -0.843$, $p = 10^{-6.345}$

feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001859
GGDEF domain protein
 $r = -0.86$, $p = 10^{-5.93}$

feature.plfam_id.arg_lys_ratio.mean



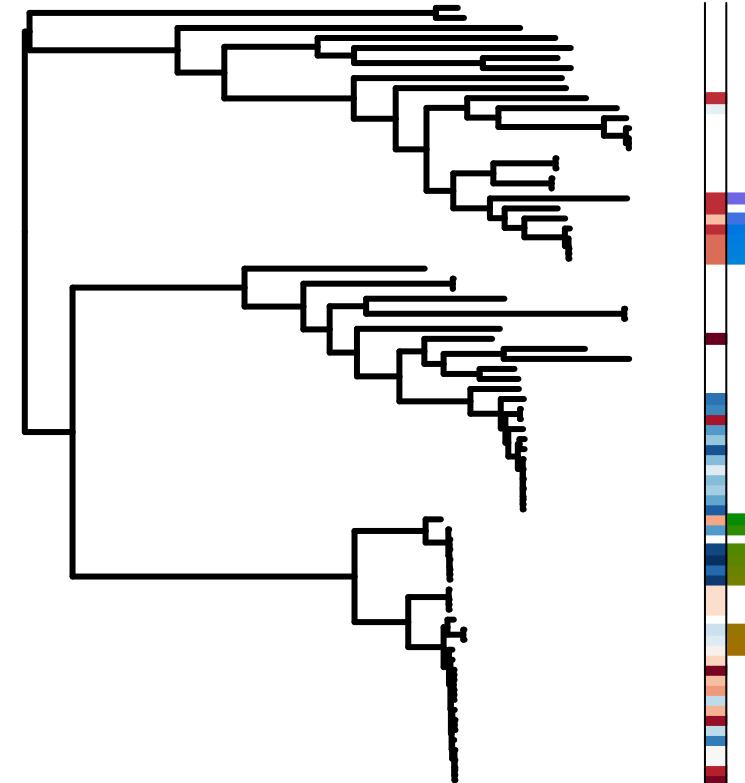
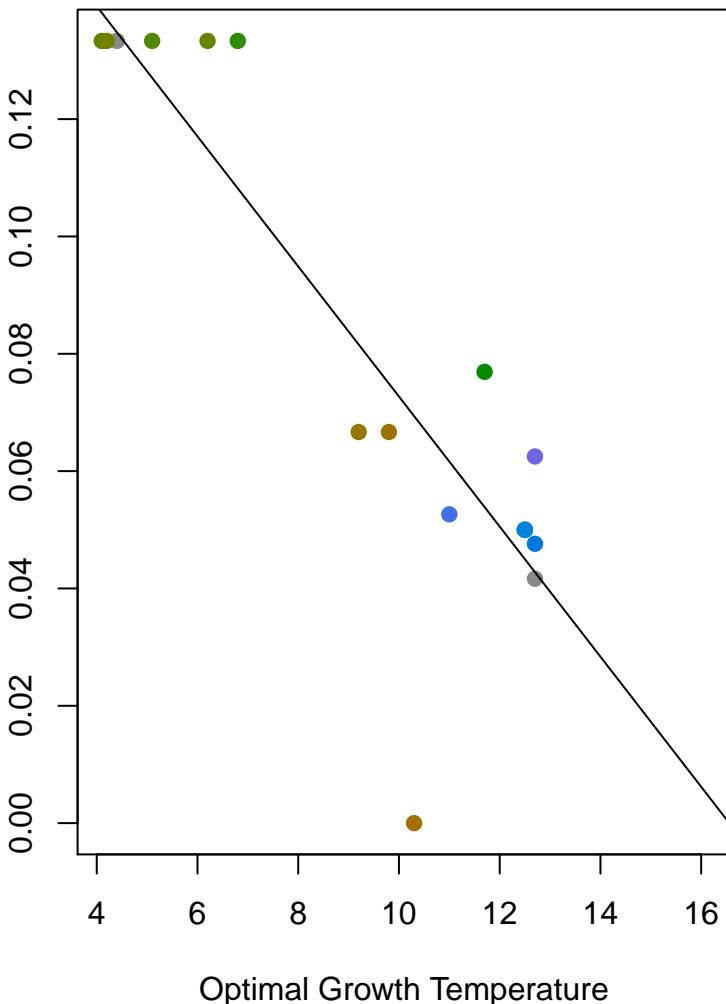
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00002857

Transforming growth factor-beta induced protein IG-H3 precursor

$r = -0.871, p = 10^{-5.274}$

feature.plfam_id.arg_lys_ratio.mean



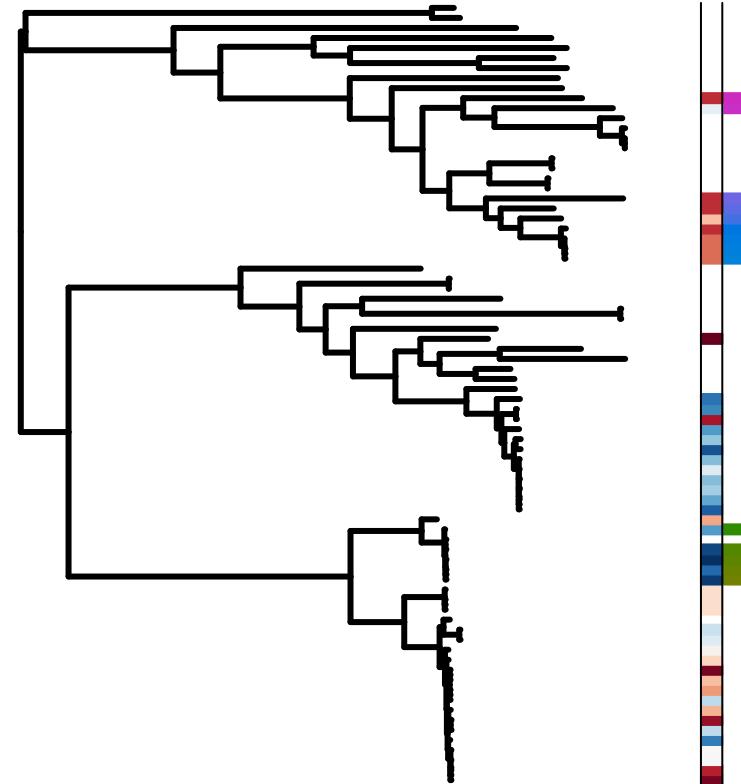
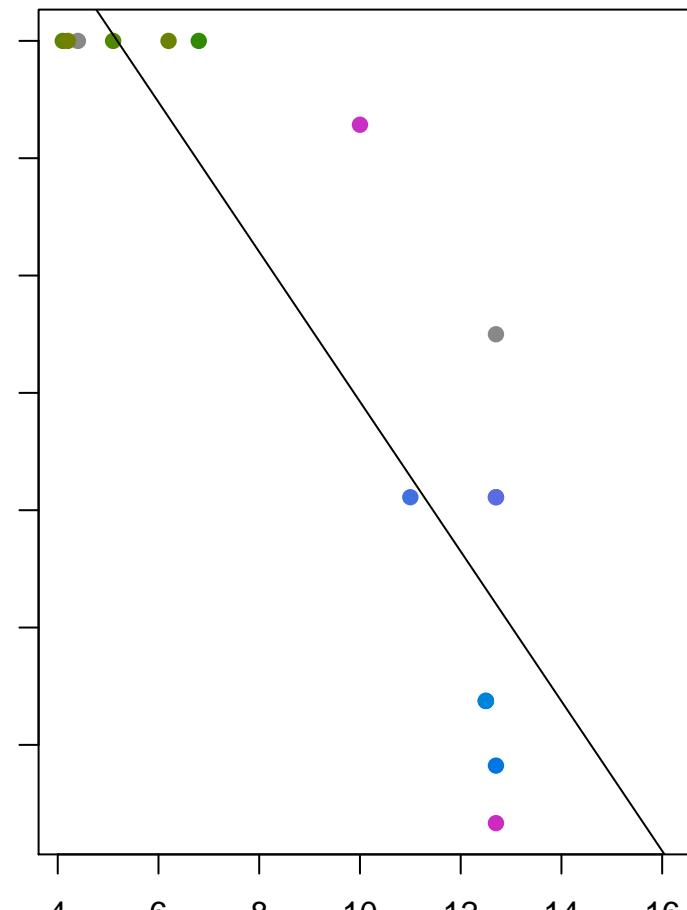
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00001794

Outer membrane beta-barrel assembly protein BamE

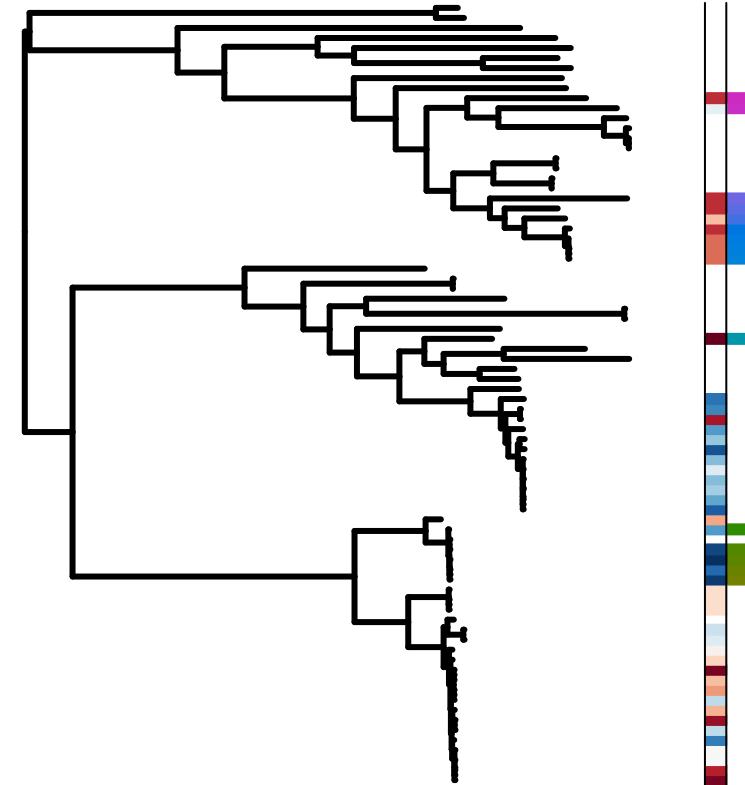
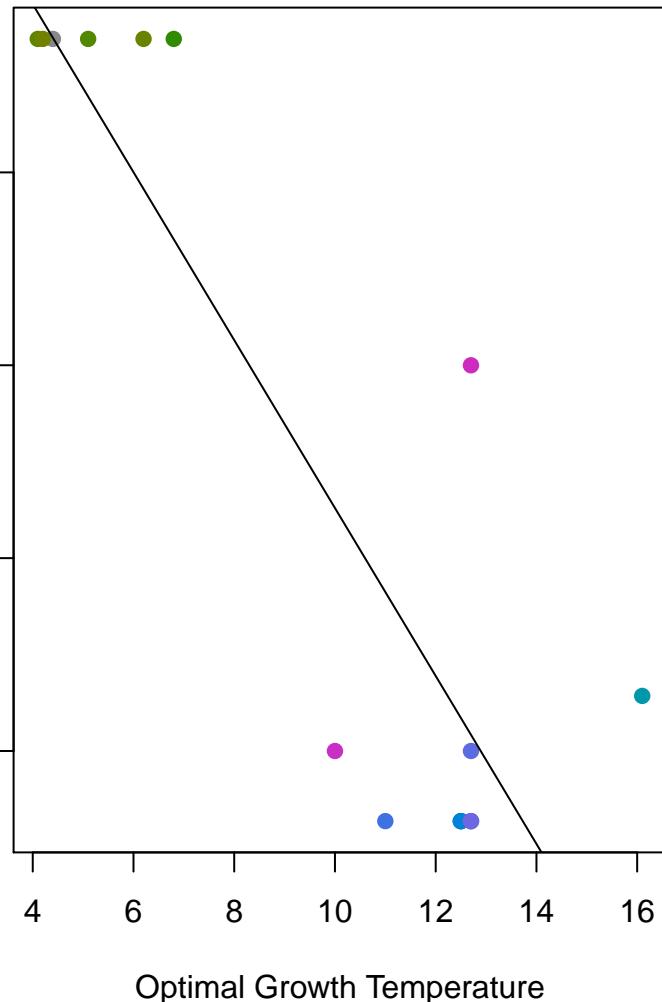
$r = -0.883, p = 10^{-5.222}$

feature.plfam_id.arg_lys_ratio.mean



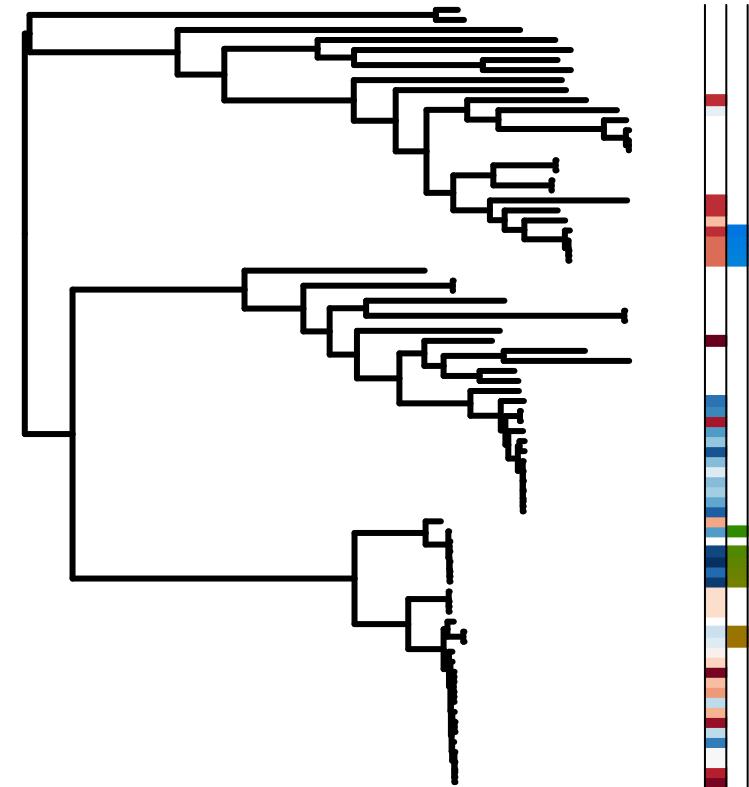
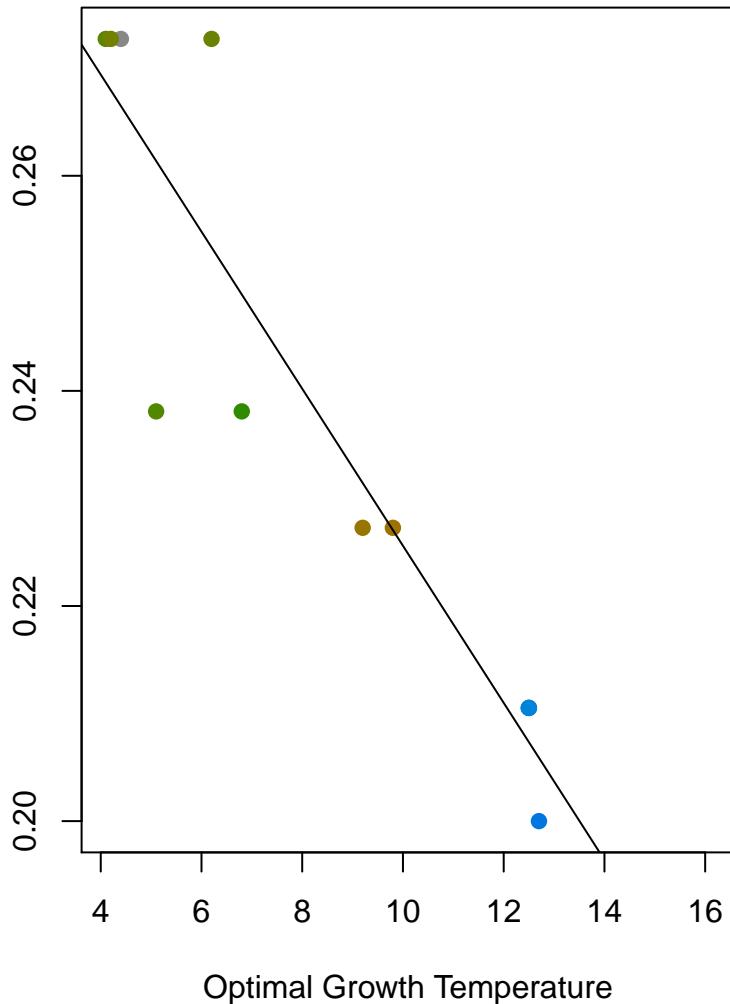
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001519
GcvR-like protein
 $r = -0.884$, $p = 10^{-5.611}$

feature.plfam_id.arg_lys_ratio.mean



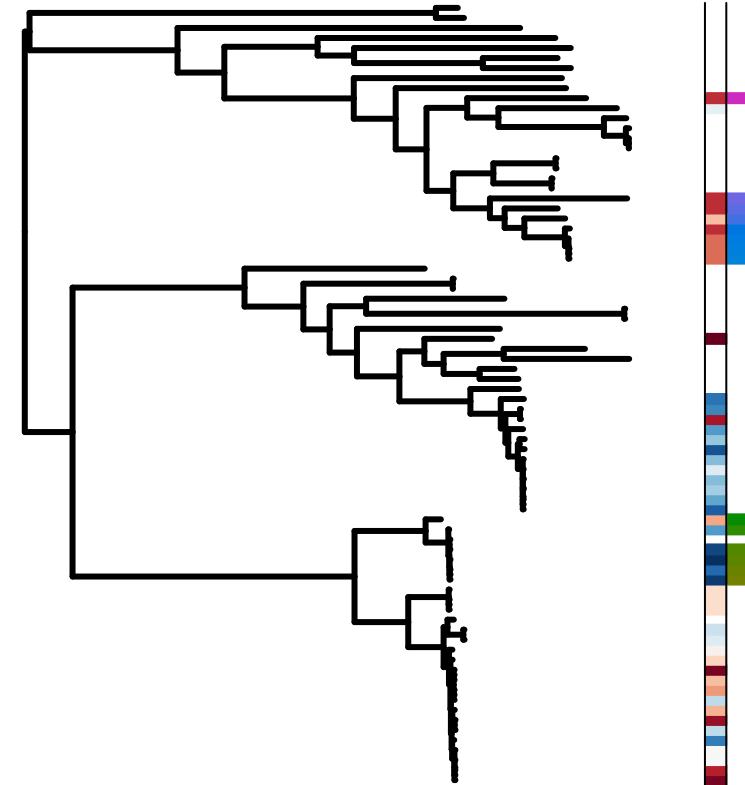
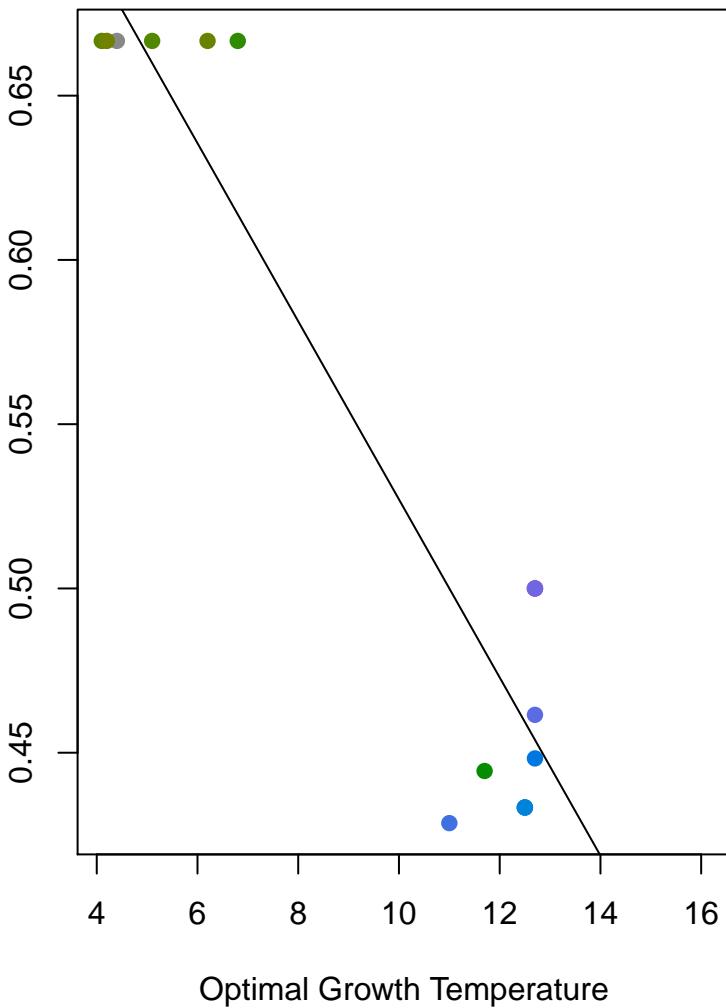
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007547
Predicted zinc-binding protein
 $r = -0.929$, $p = 10^{-4.906}$

feature.plfam_id.arg_lys_ratio.mean



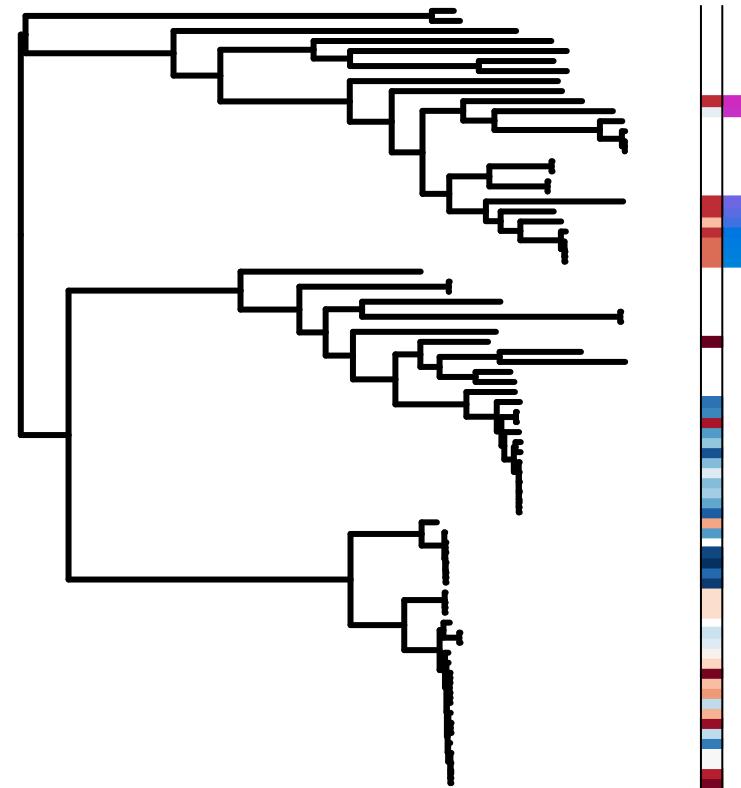
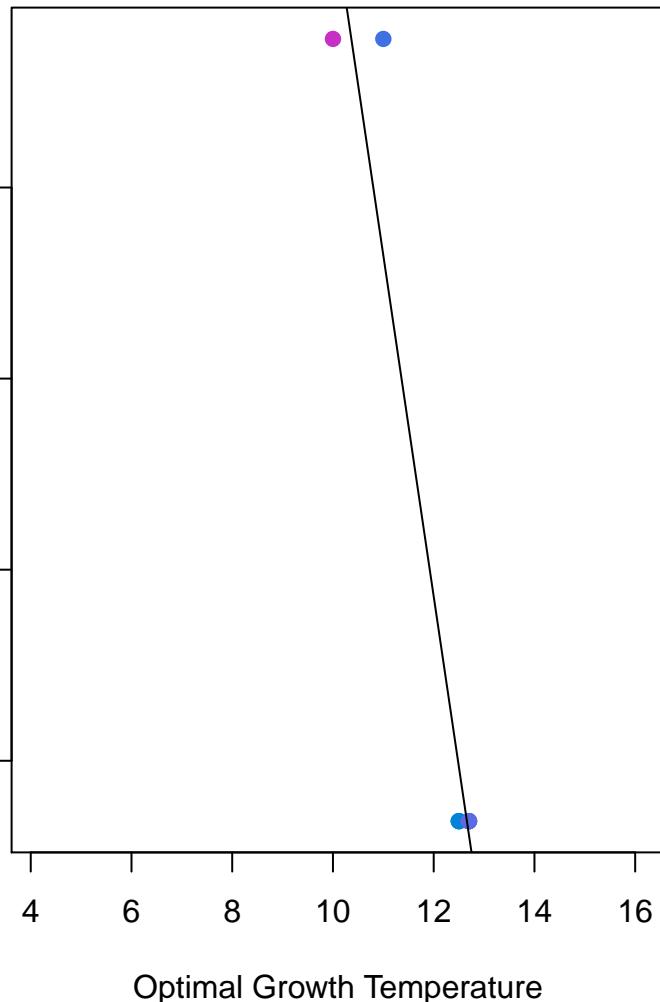
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002761
Uncharacterized MFS-type transporter
 $r = -0.94$, $p = 10^{-7.185}$

feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001345
hypothetical protein
 $r = -0.962$, $p = 10^{-5.08}$

feature.plfam_id.arg_lys_ratio.mean



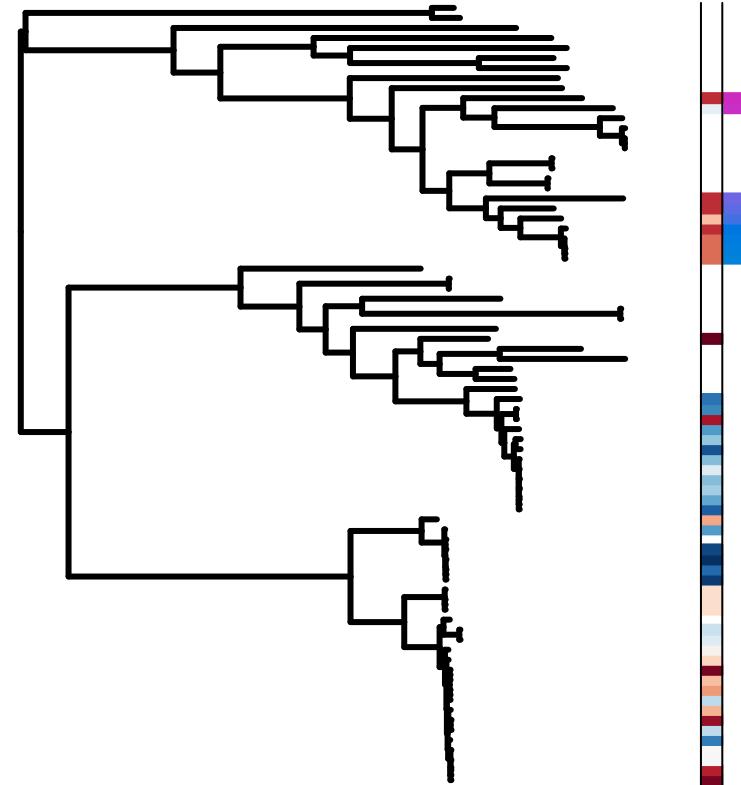
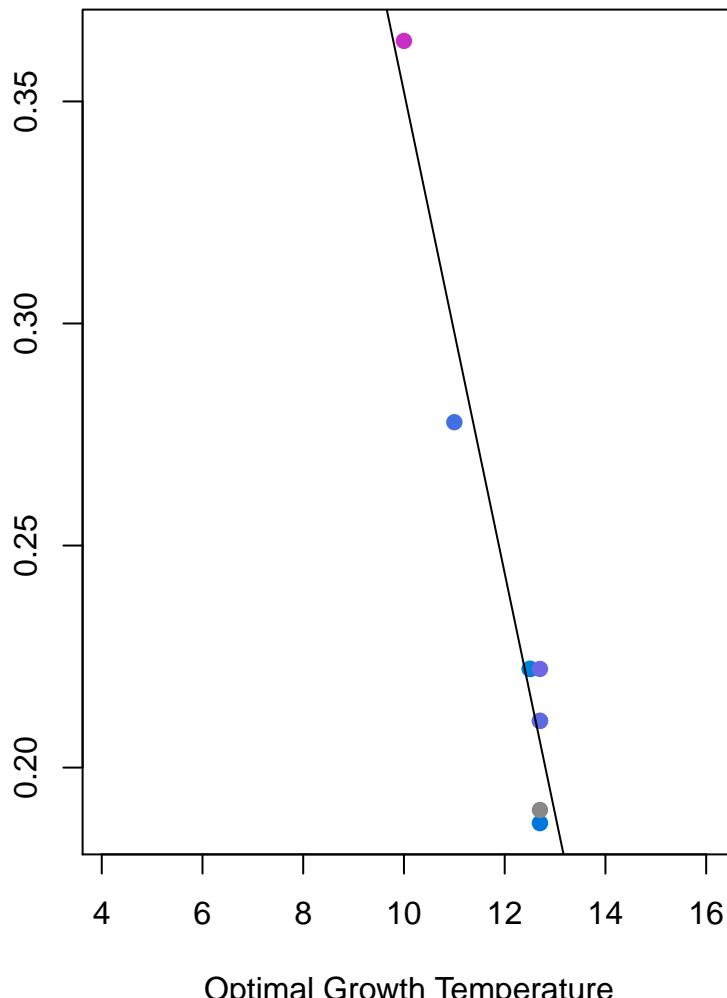
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00001877

Outer membrane lipoprotein carrier protein LoA

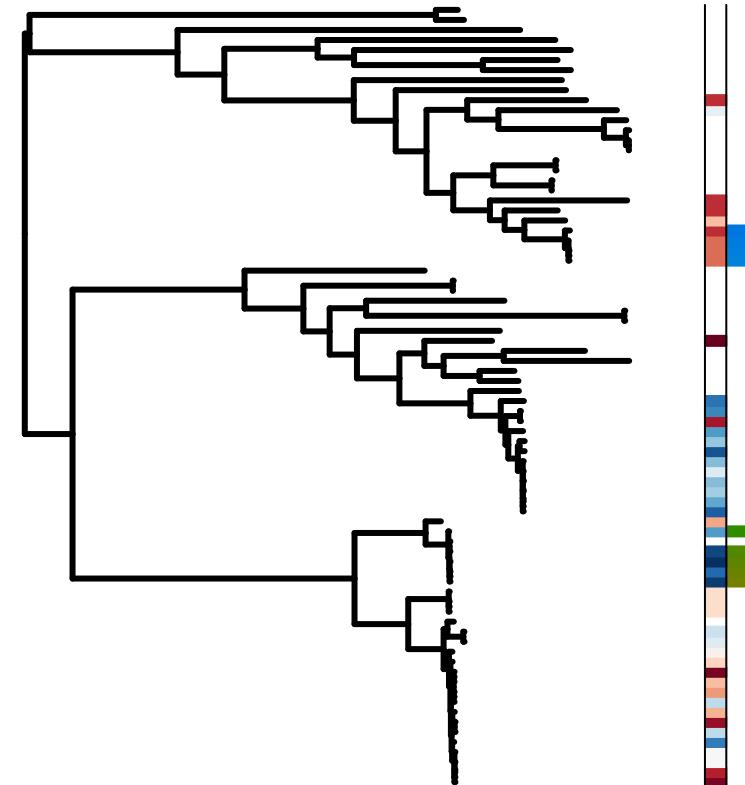
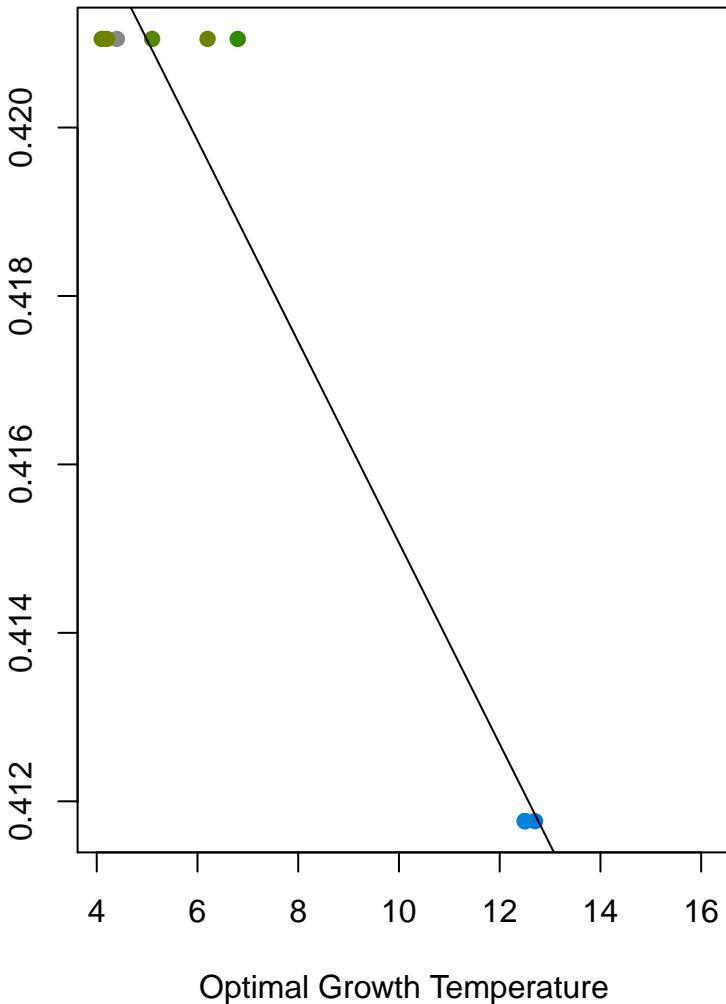
$r = -0.968, p = 10^{-5.38}$

feature.plfam_id.arg_lys_ratio.mean



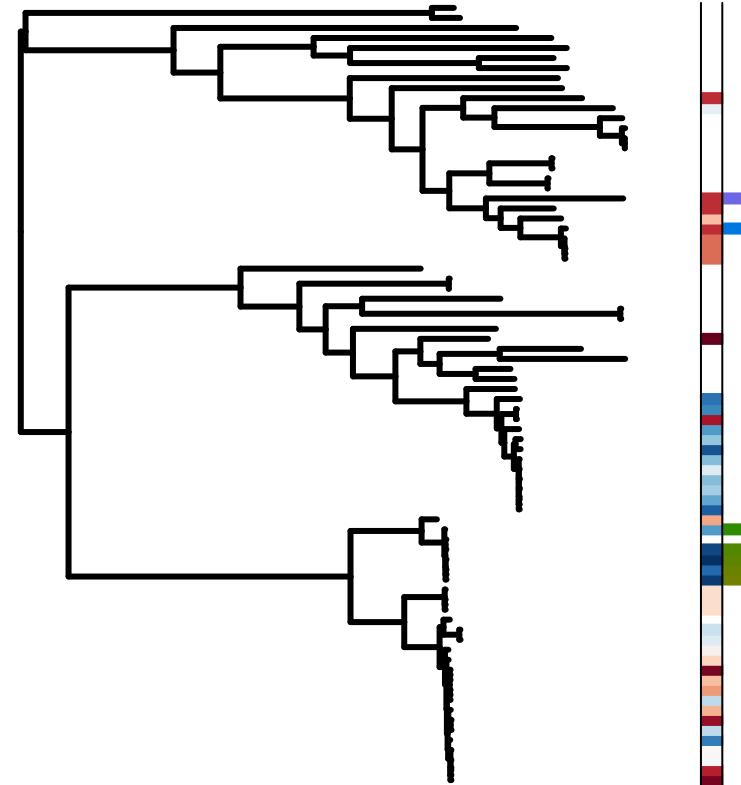
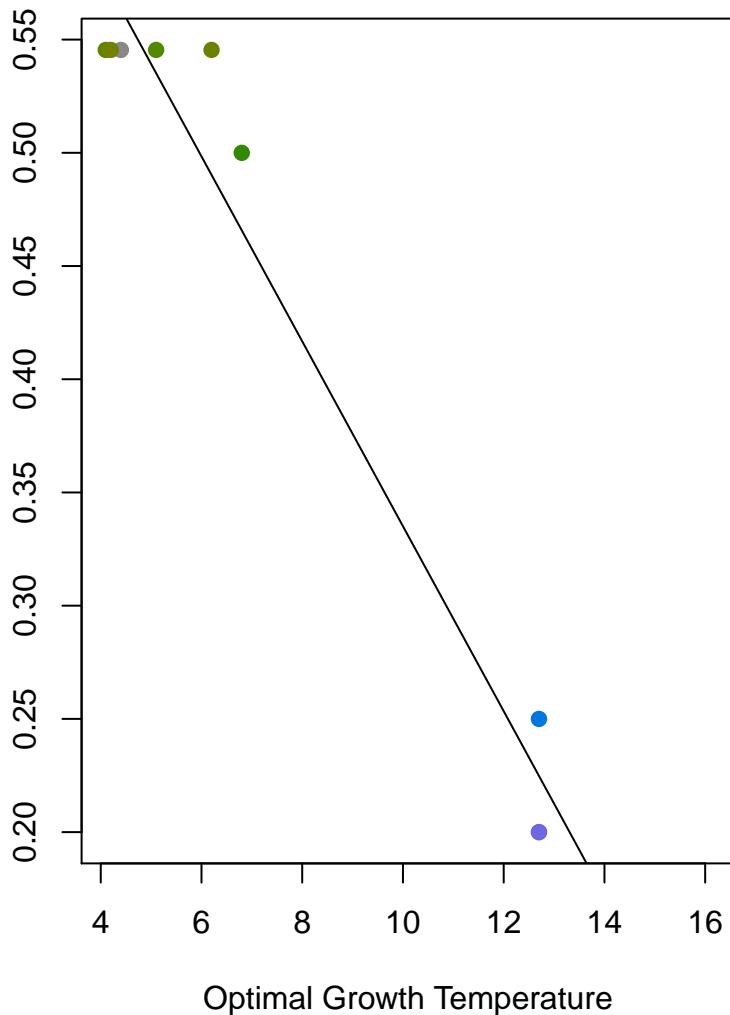
feature.pifam_id.arg_lys_ratio.mean
PLF_28228_00007839
hypothetical protein
 $r = -0.977$, $p = 10^{-5.889}$

feature.pifam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003941
hypothetical protein
 $r = -0.98$, $p = 10^{-5.464}$

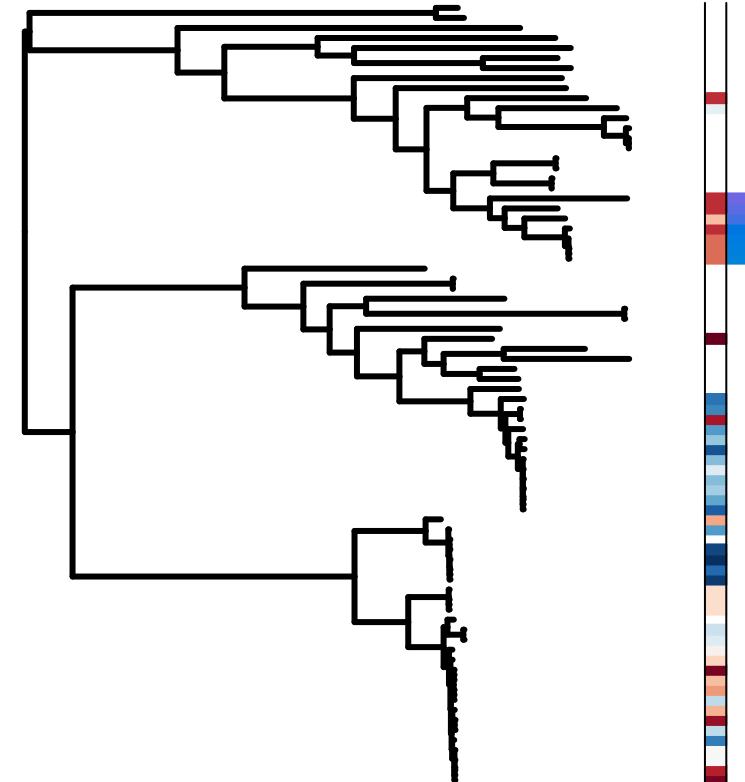
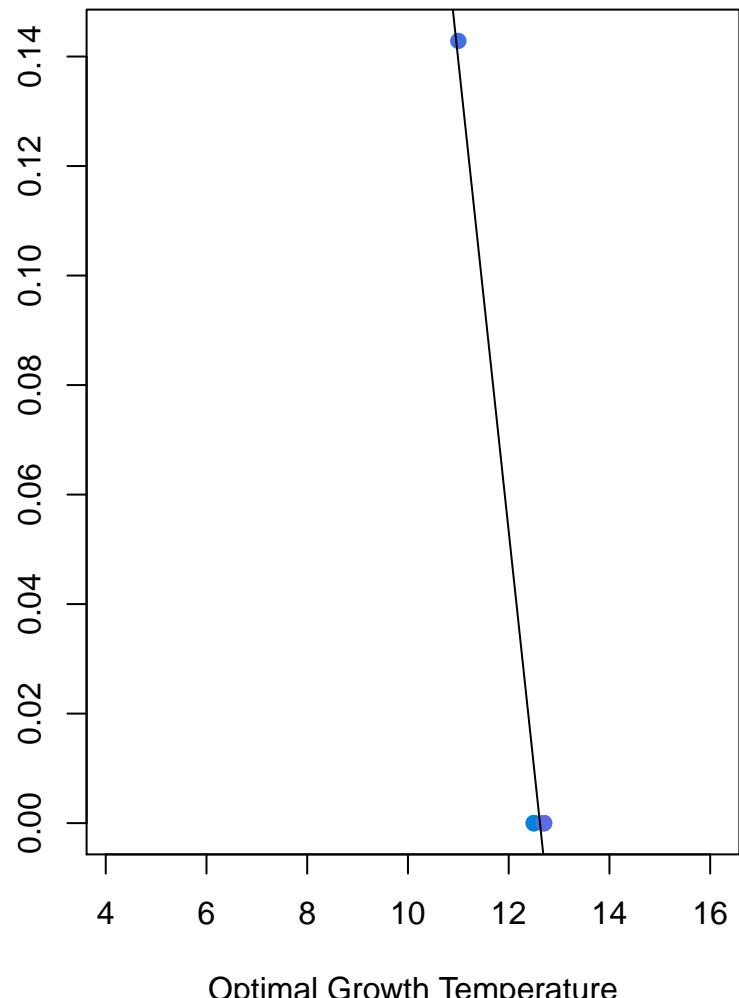
feature.plfam_id.arg_lys_ratio.mean



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00004147

uncharacterized conserved protein containing predicted Zn–ribbon like domain
 $r = -0.985, p = 10^{-5.104}$

feature.plfam_id.arg_lys_ratio.mean



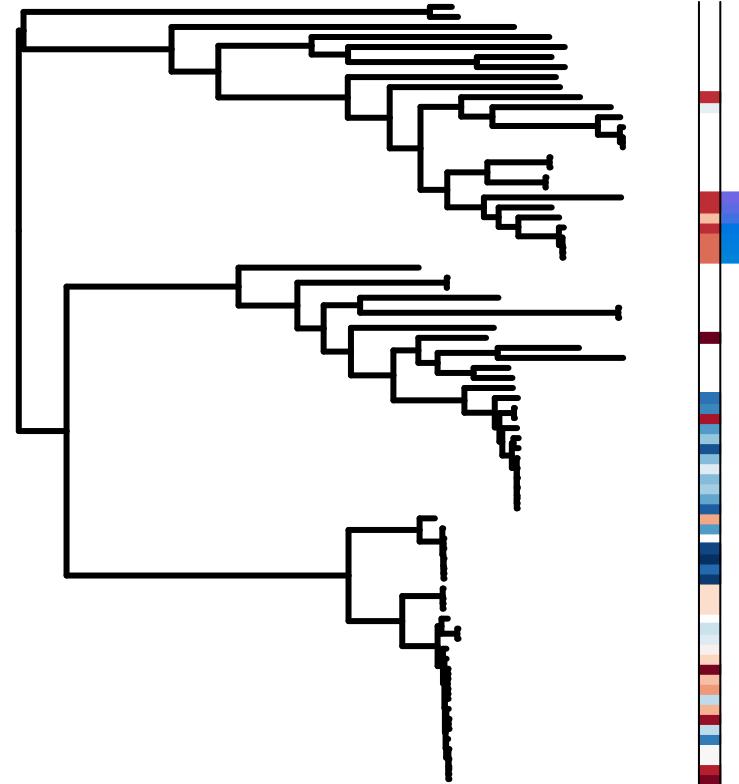
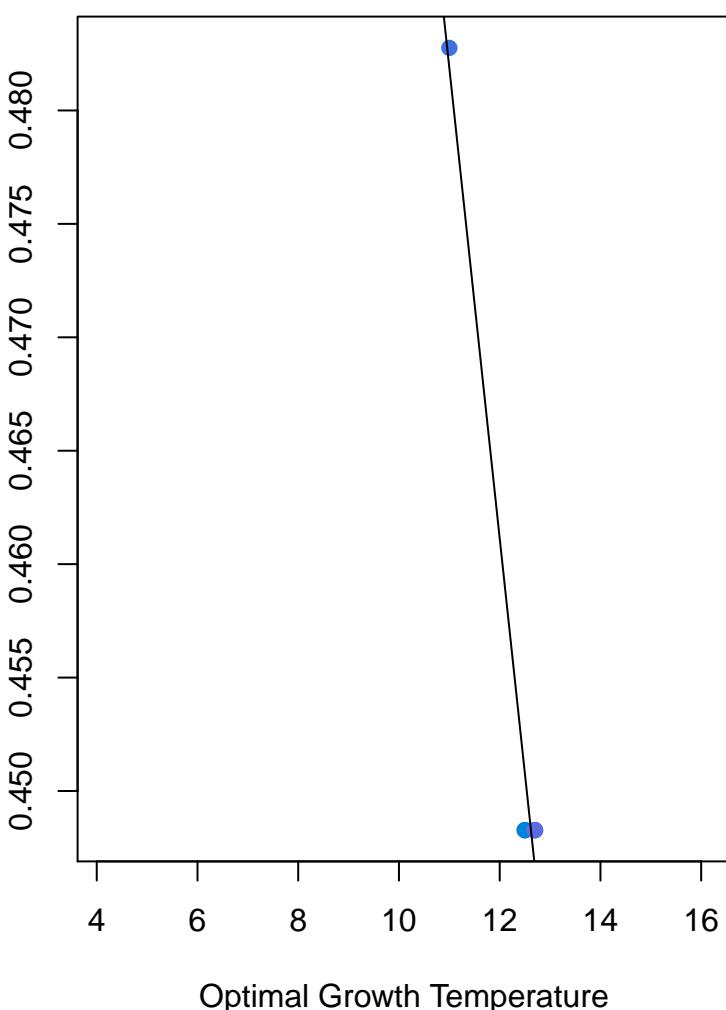
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00003137

Two-component transcriptional response regulator, LuxR family

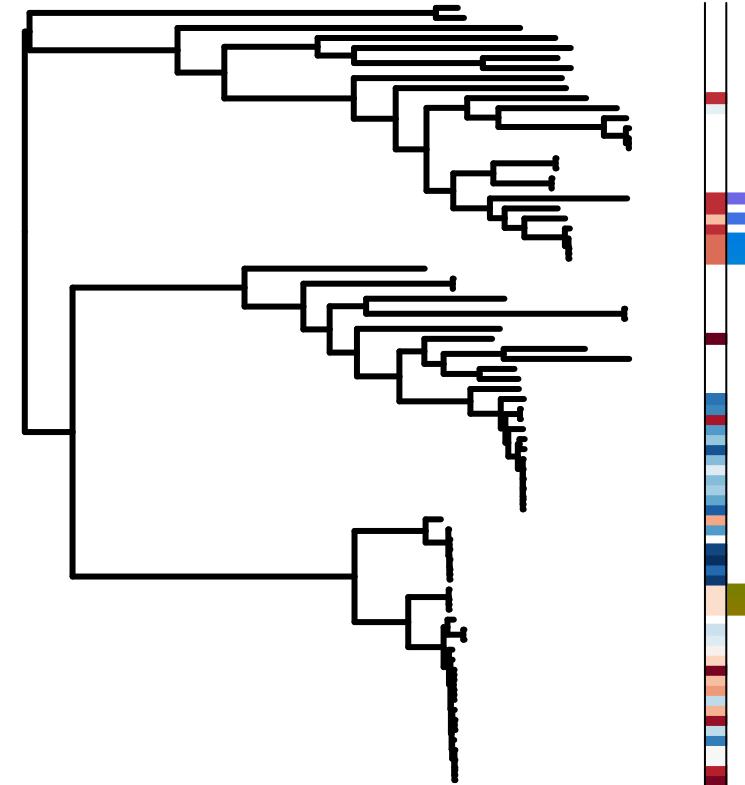
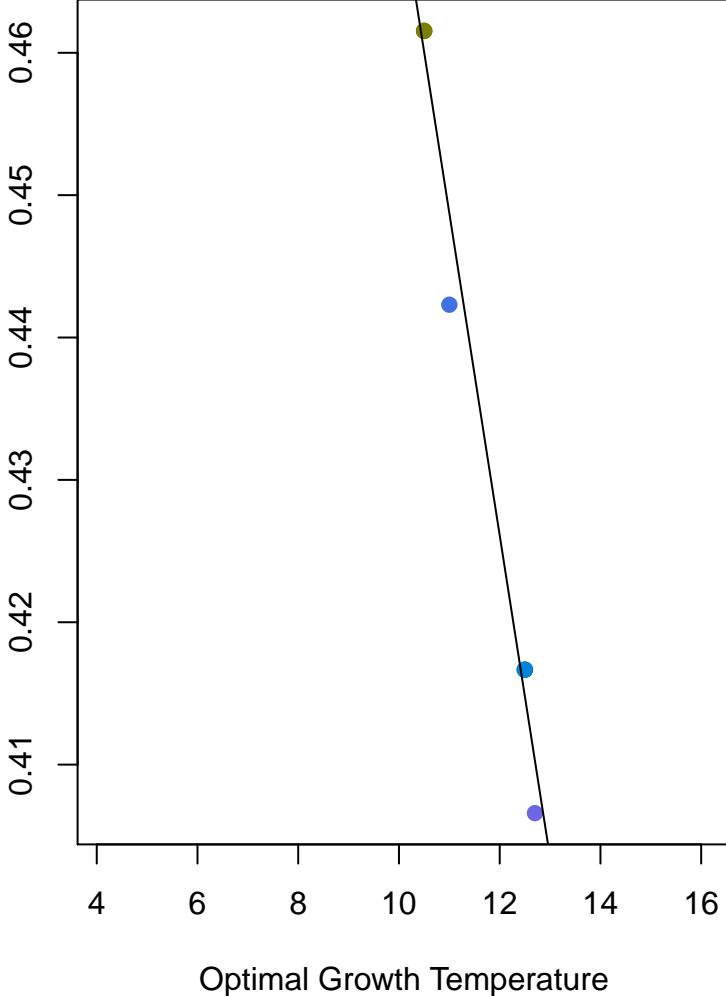
$r = -0.985$, $p = 10^{-5.104}$

feature.plfam_id.arg_lys_ratio.mean

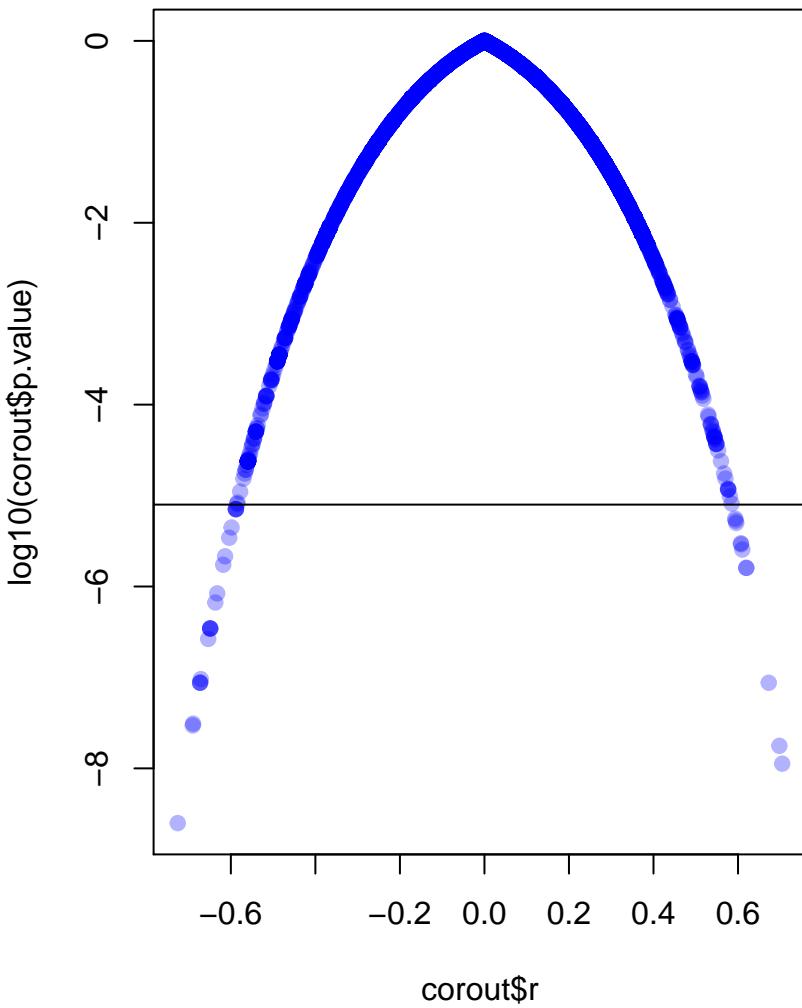


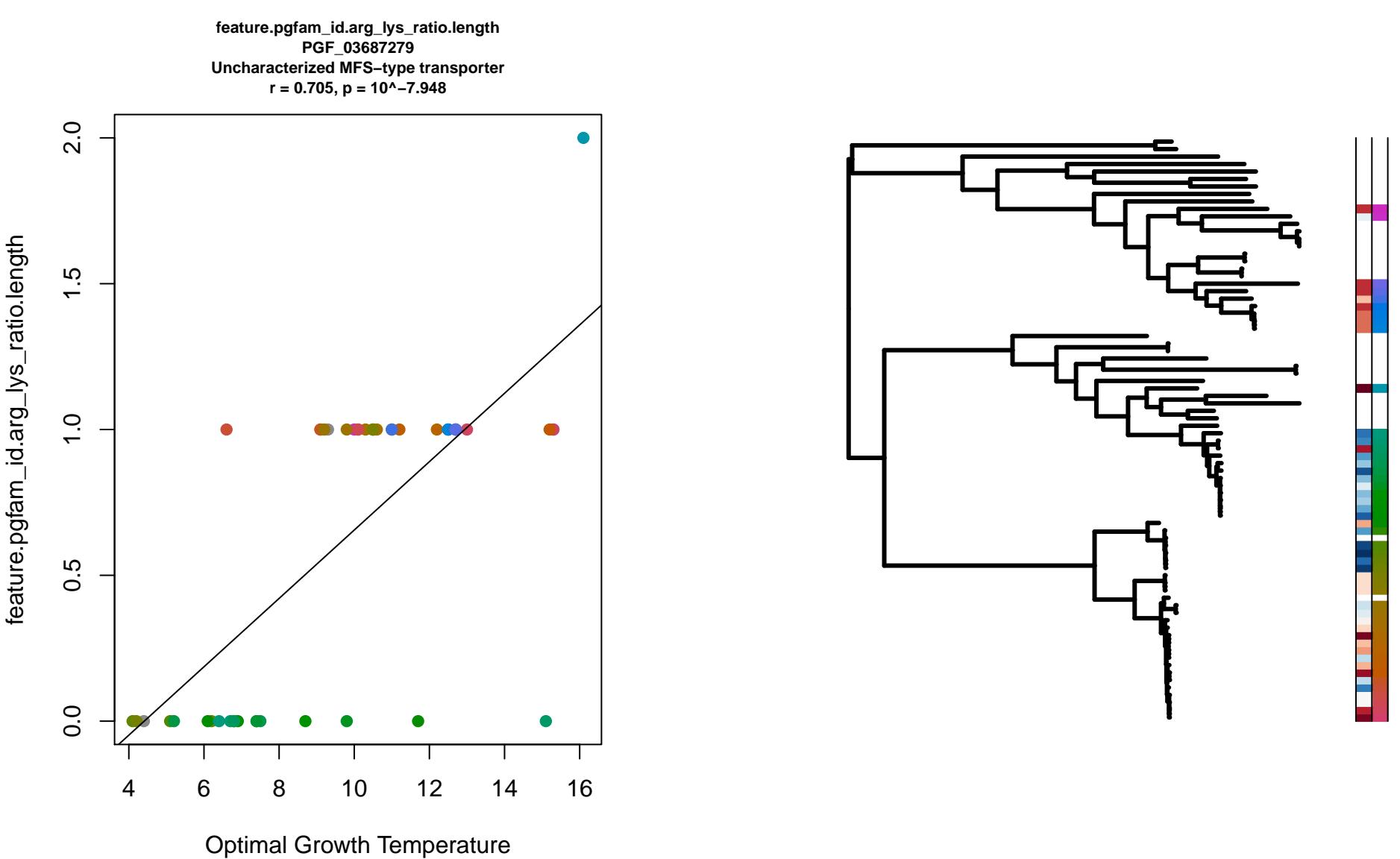
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00009489
hypothetical protein
 $r = -0.991$, $p = 10^{-5.73}$

feature.plfam_id.arg_lys_ratio.mean

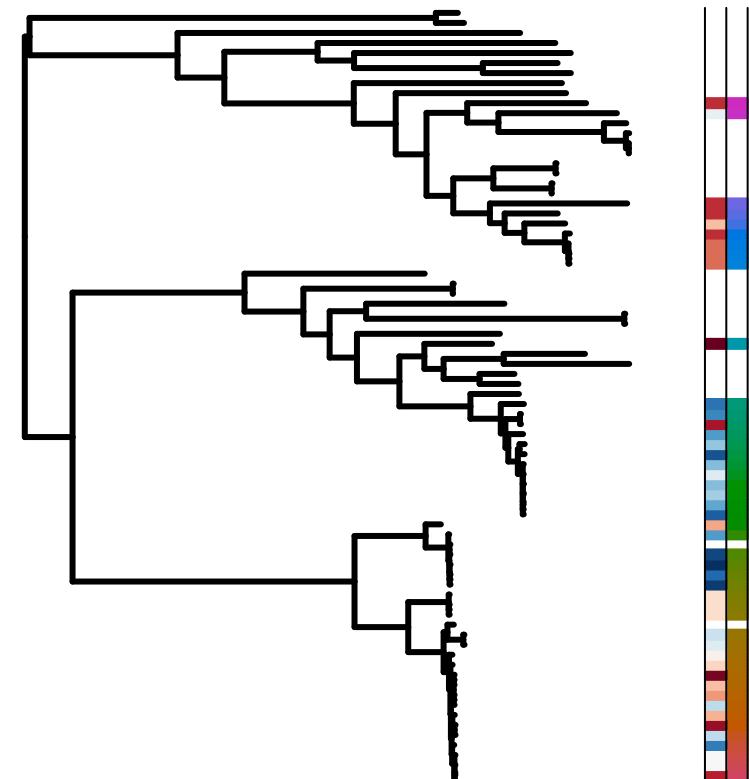
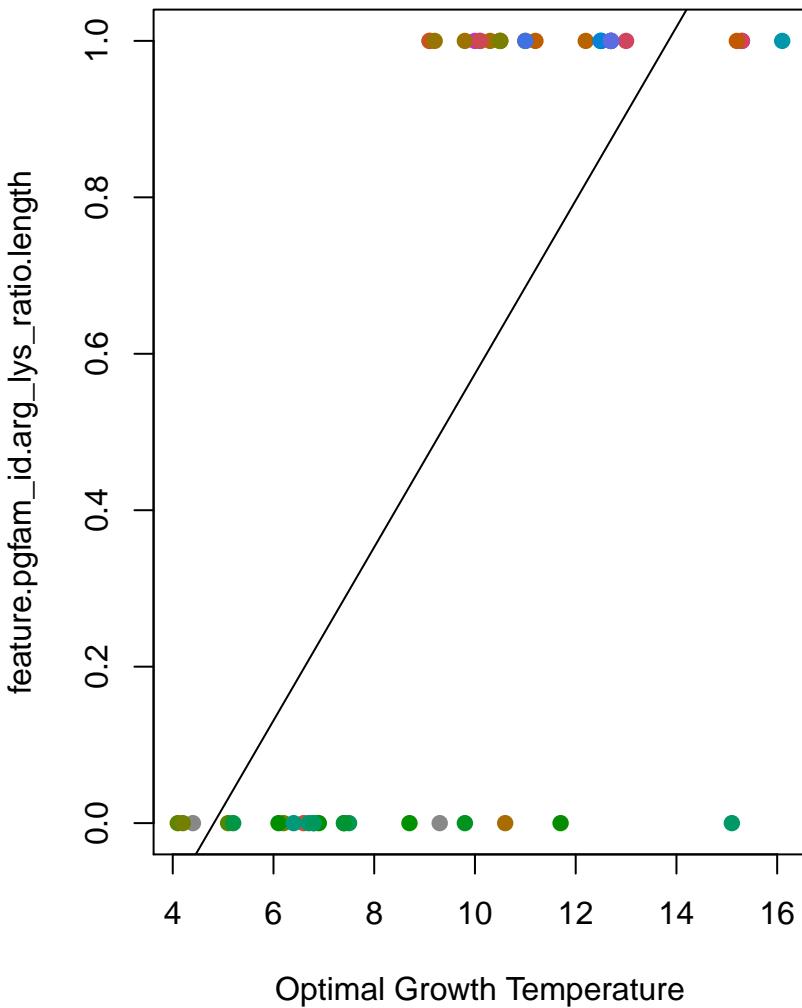


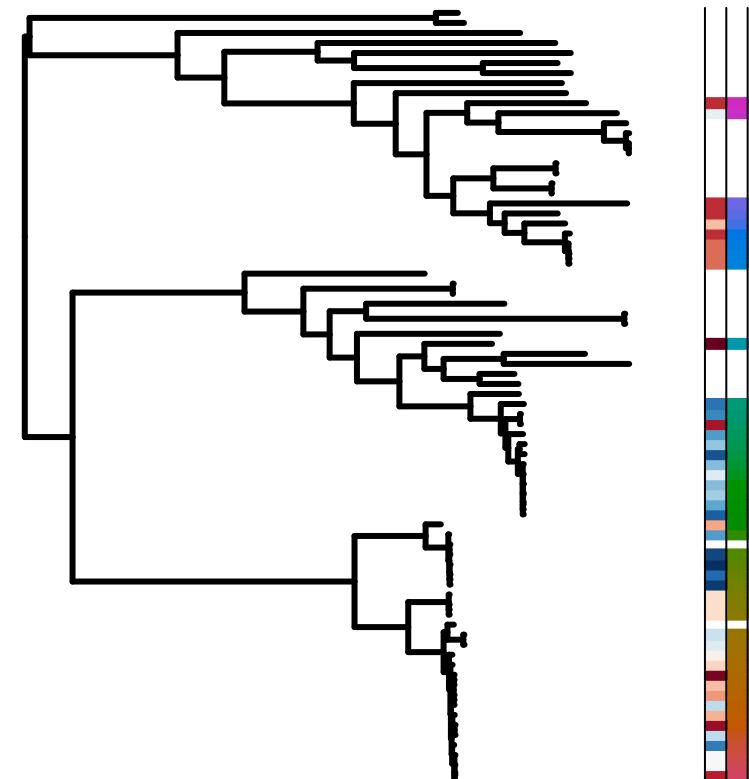
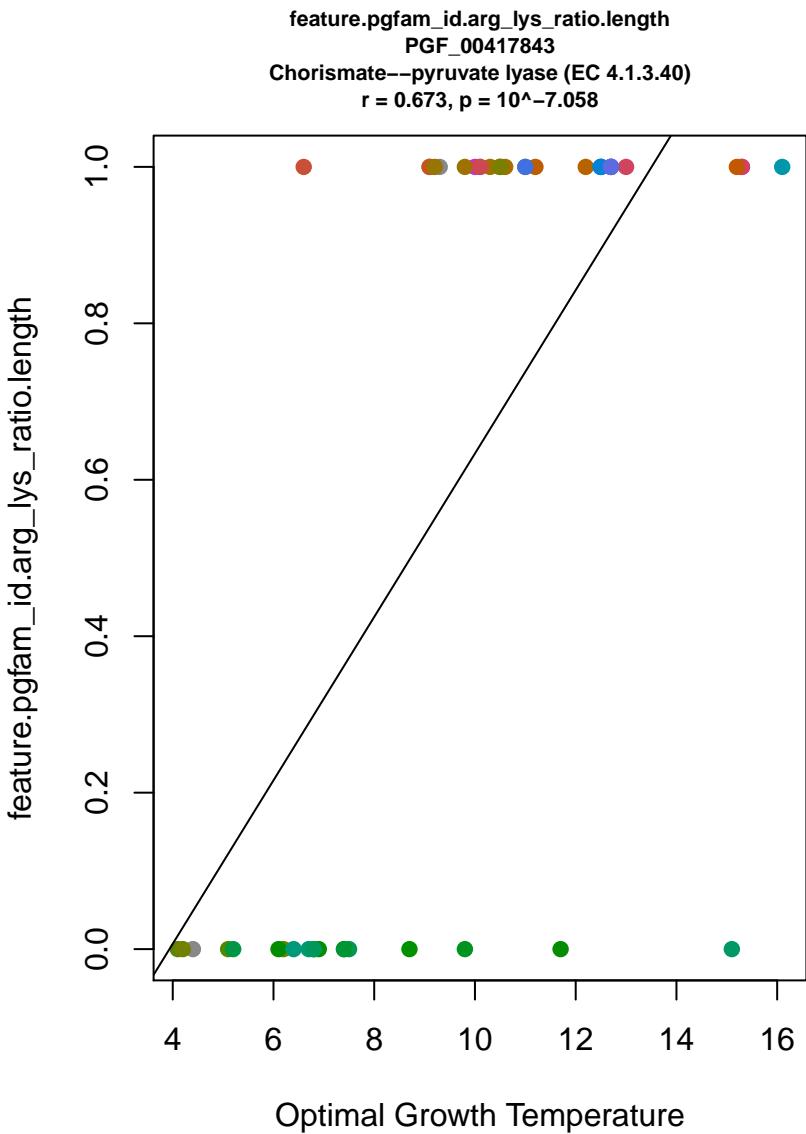
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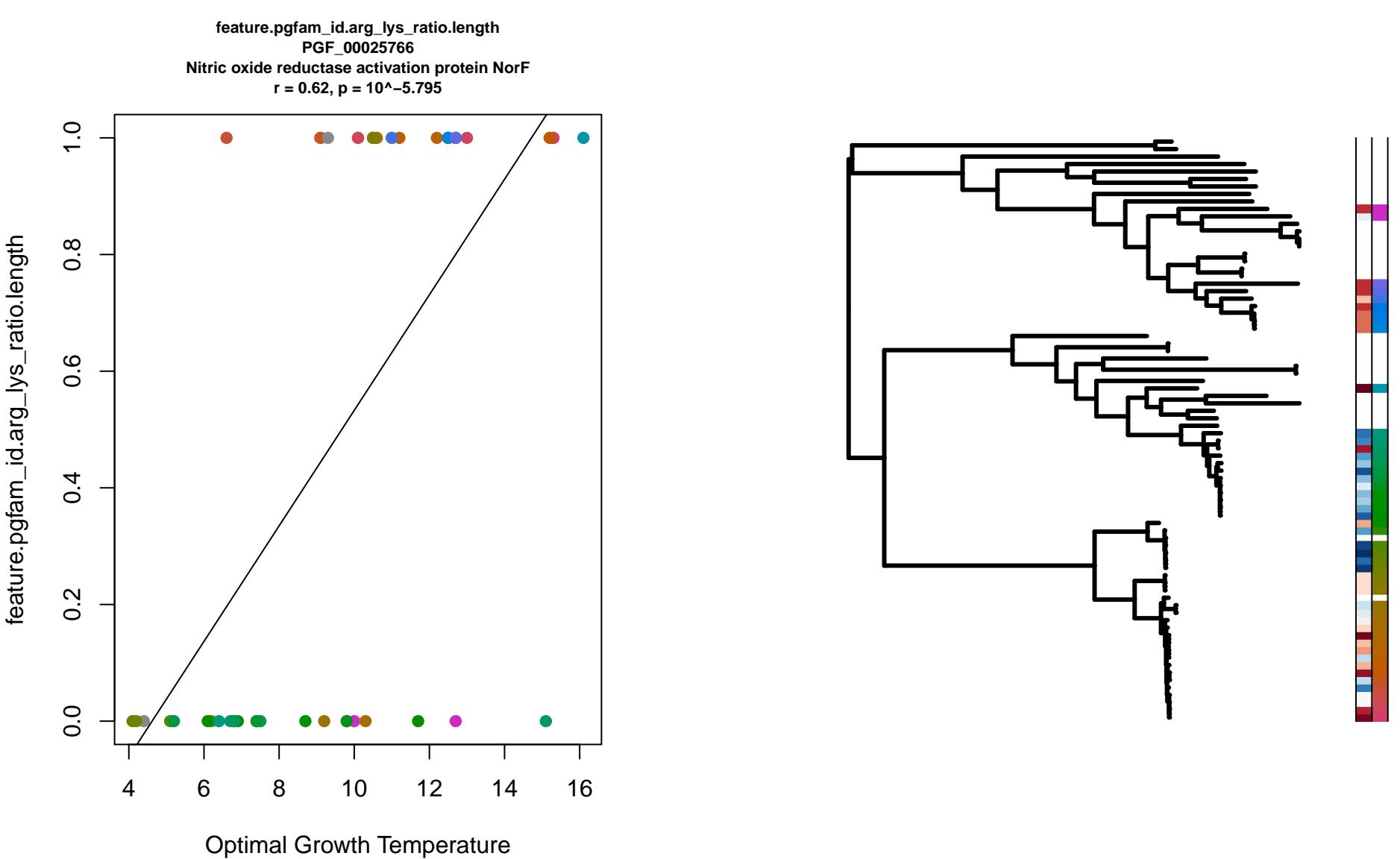


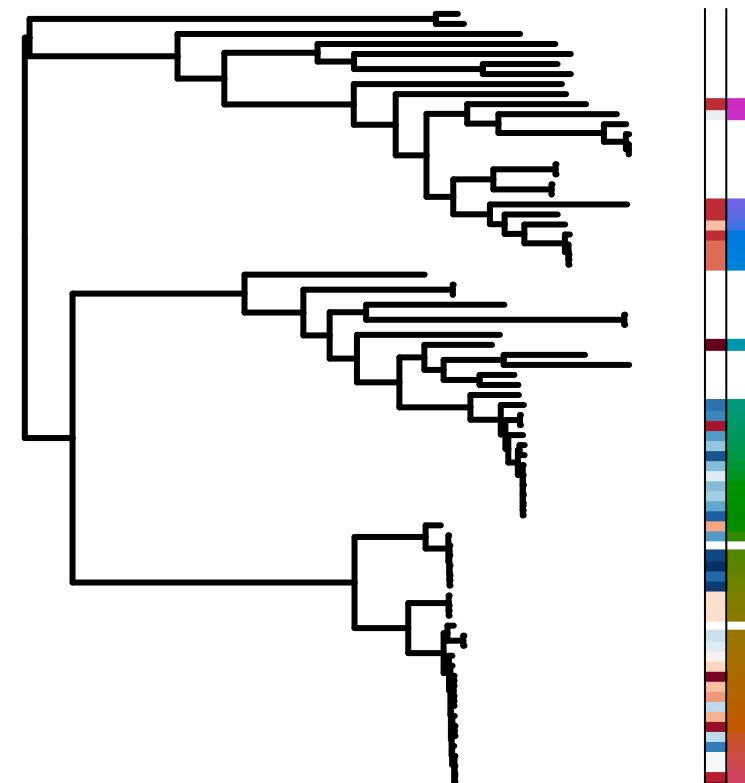
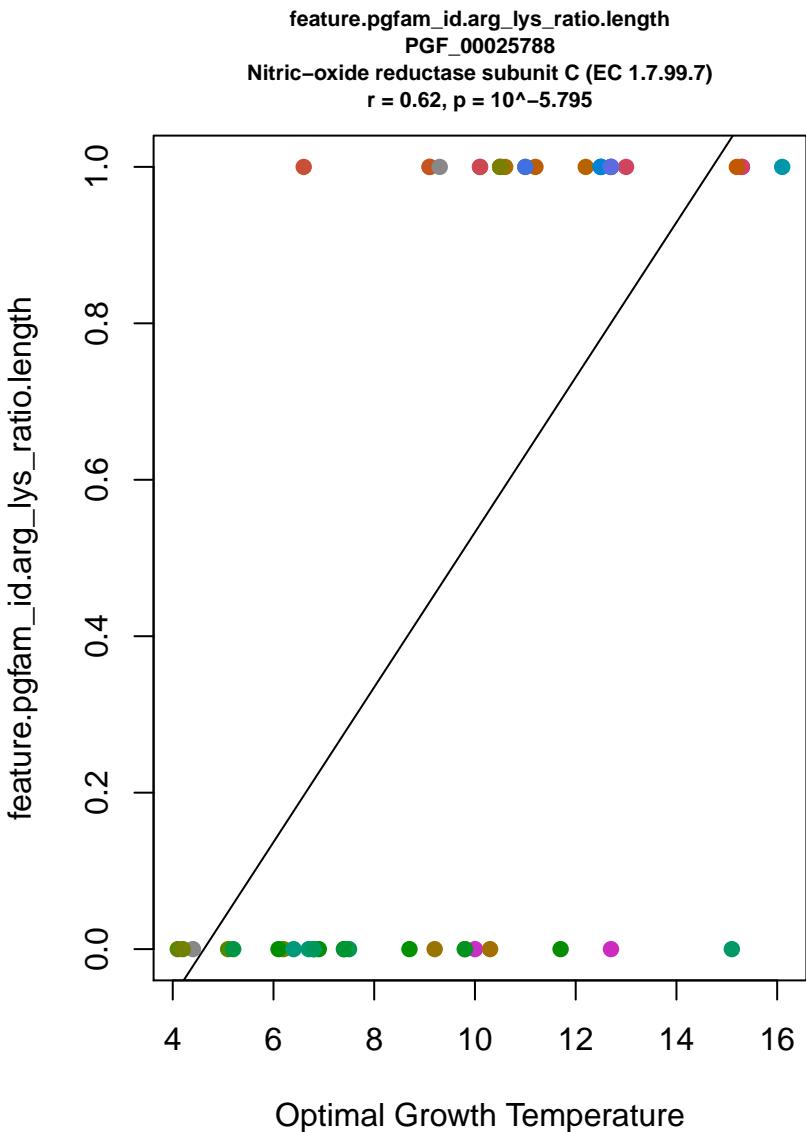


feature.pgfam_id.arg_lys_ratio.length
PGF_01917480
General secretion pathway protein L
 $r = 0.698$, $p = 10^{-7.752}$







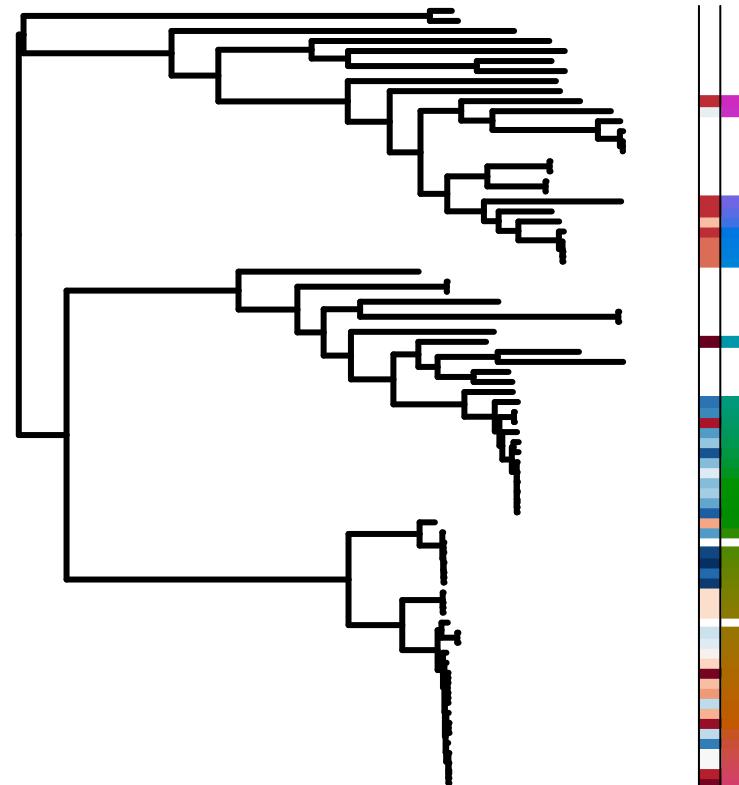
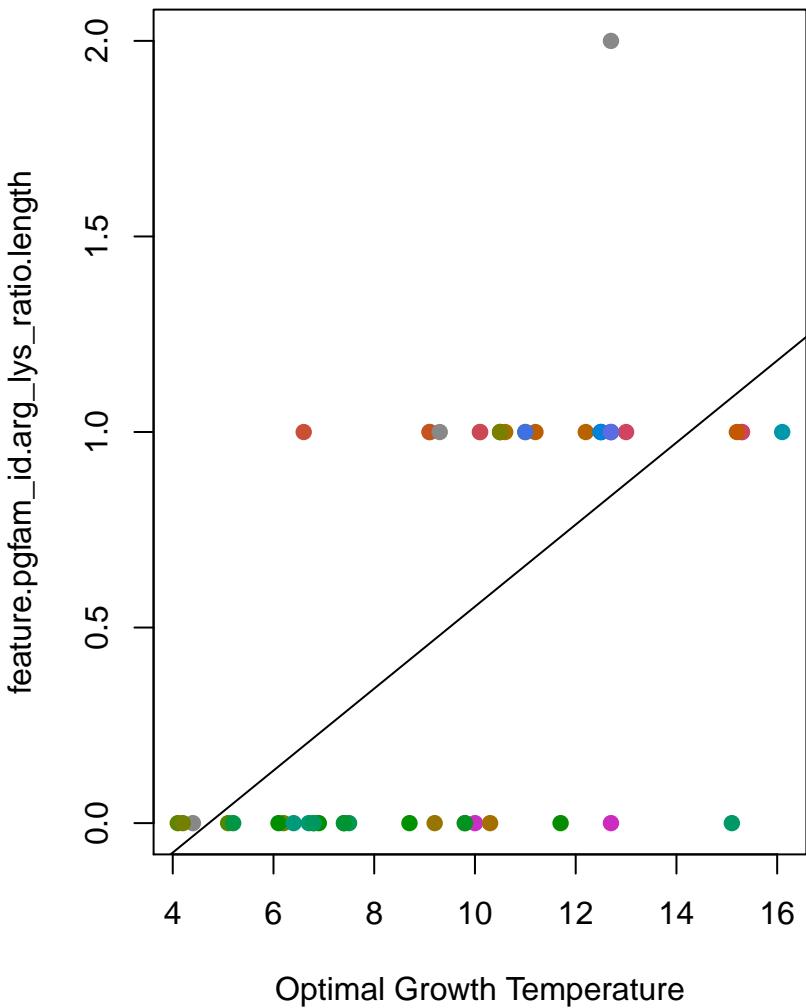


feature.pgfam_id.arg_lyc_ratio.length

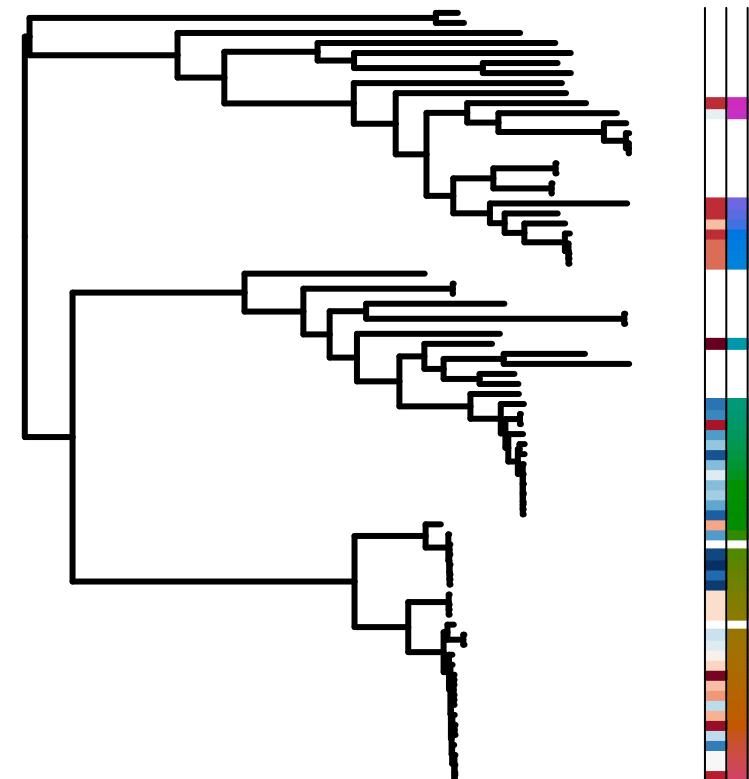
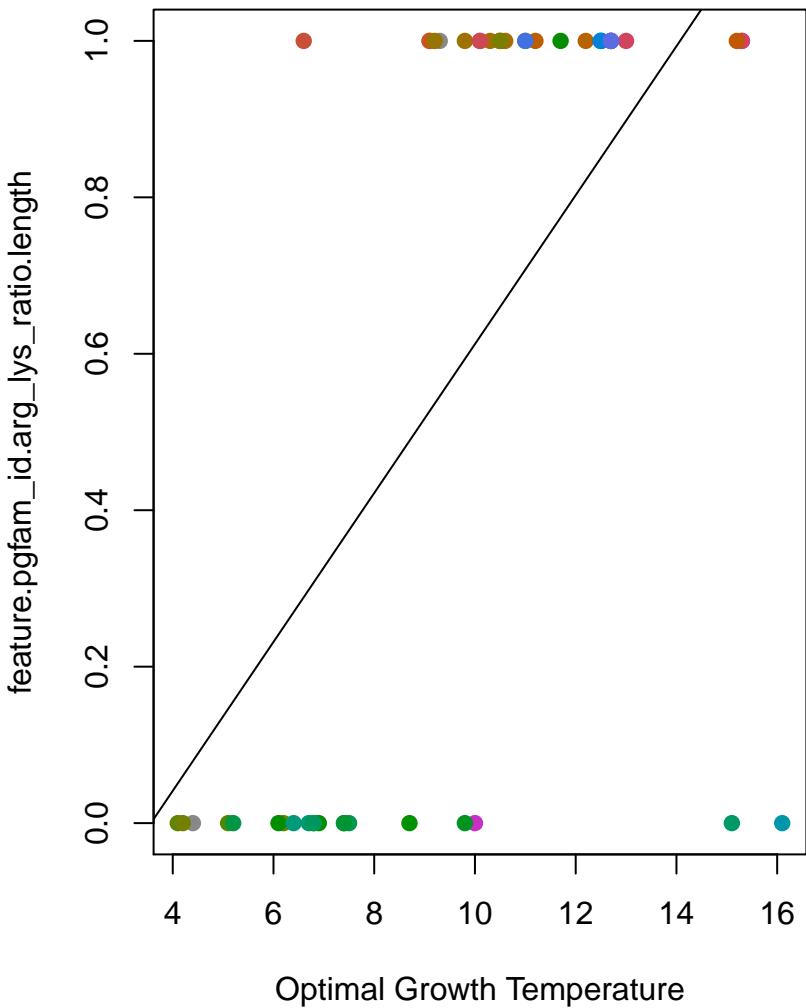
PGF_04886077

Nitric oxide reductase activation protein NorQ

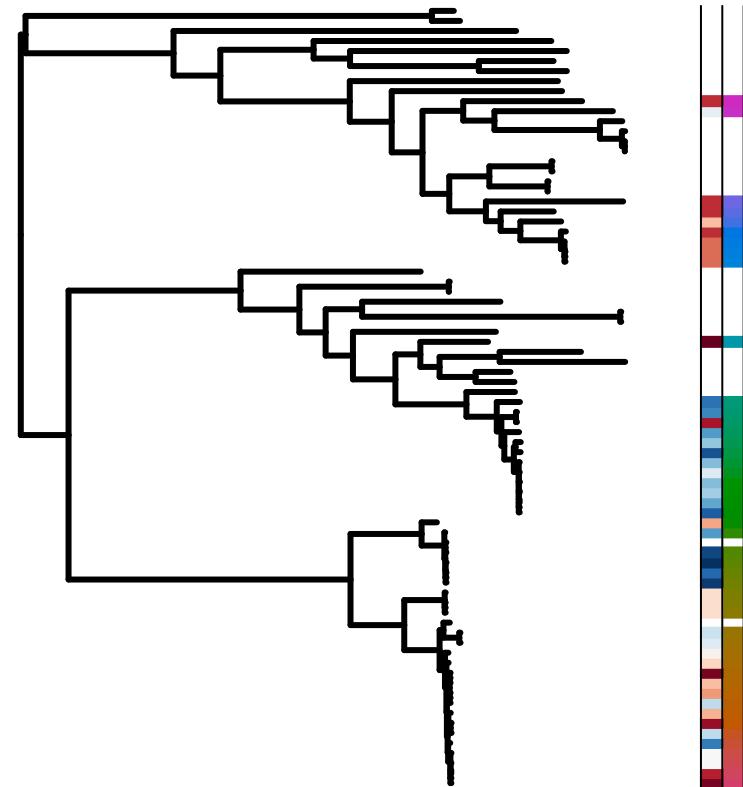
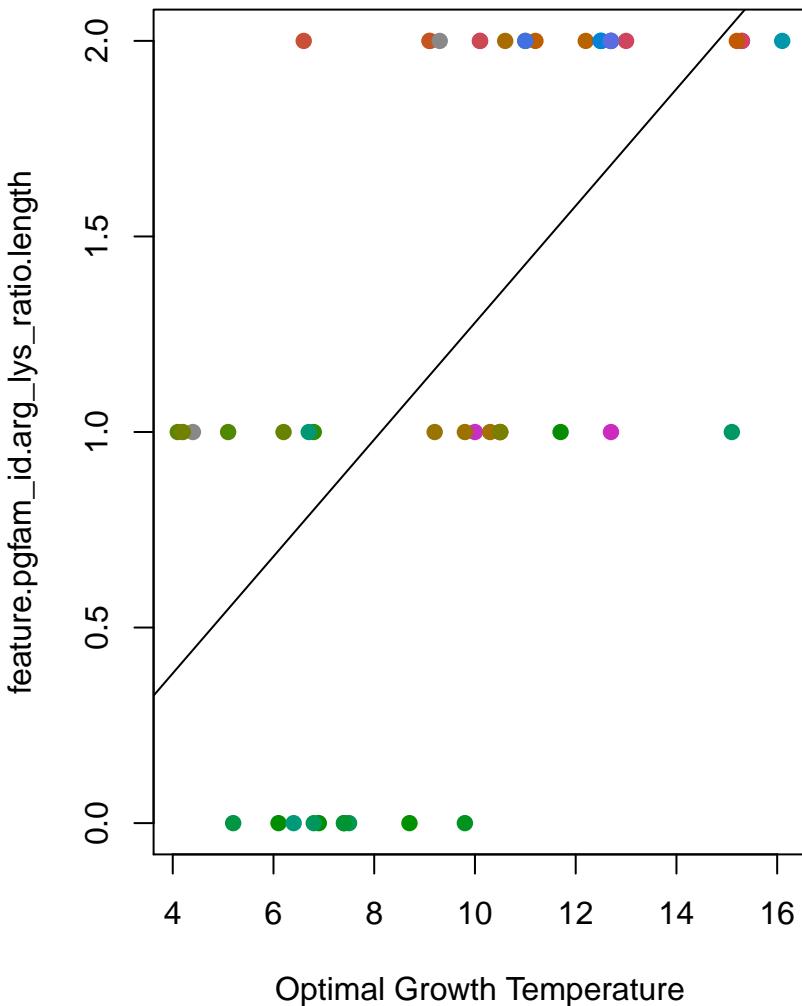
$r = 0.61, p = 10^{-5.594}$

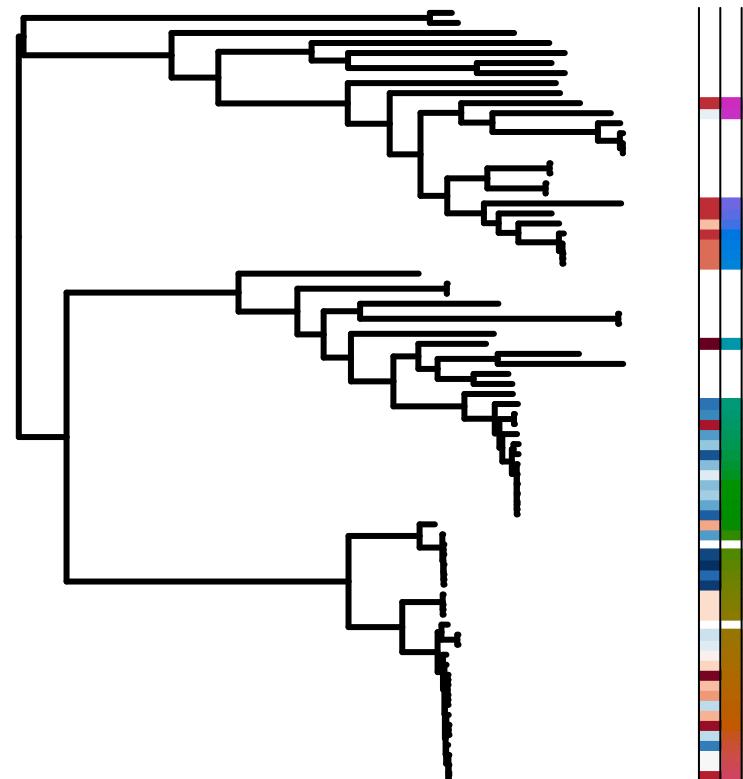
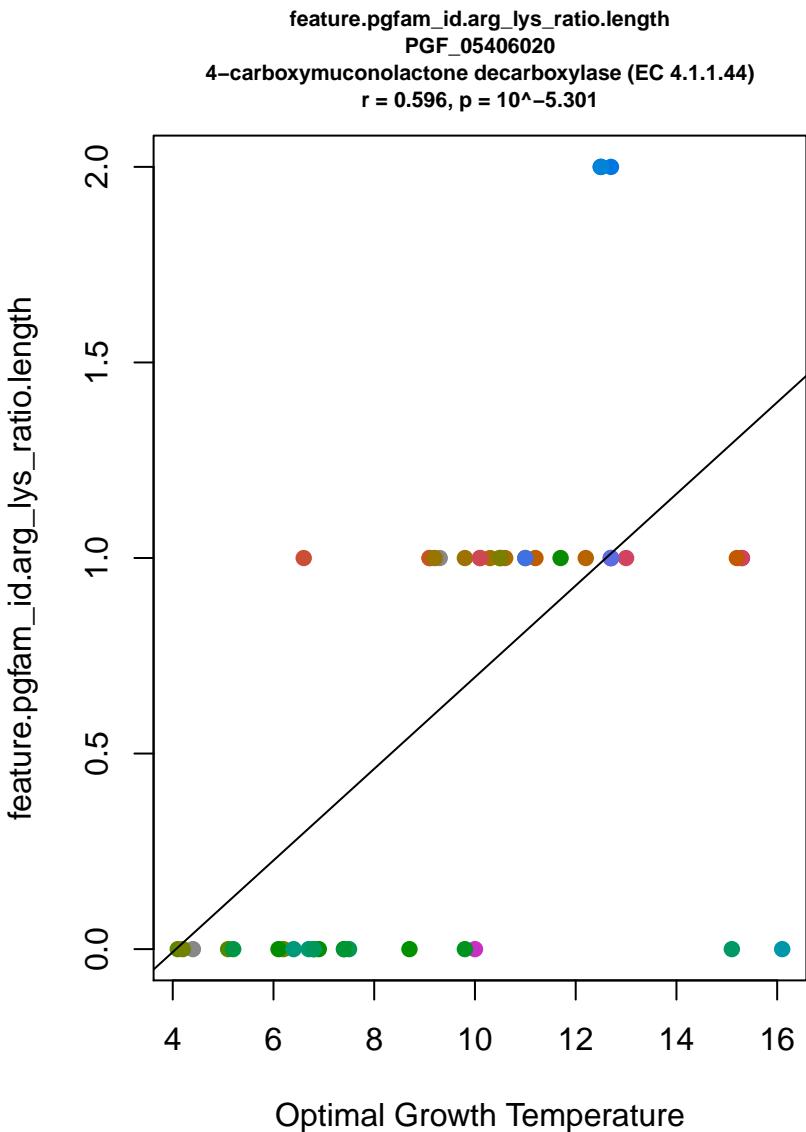


feature.pgfam_id.arg_lys_ratio.length
PGF_01336627
hypothetical protein
 $r = 0.607$, $p = 10^{-5.535}$

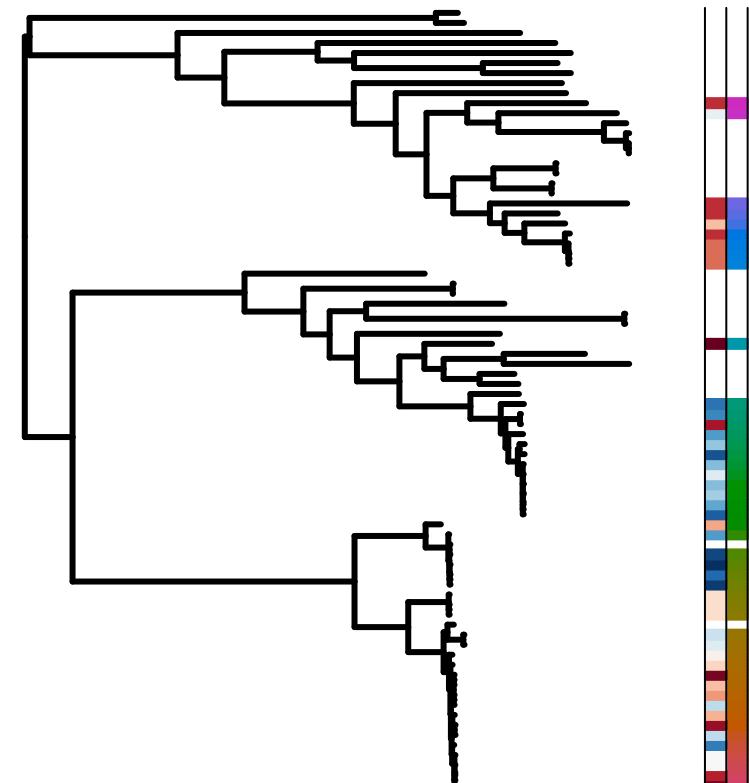
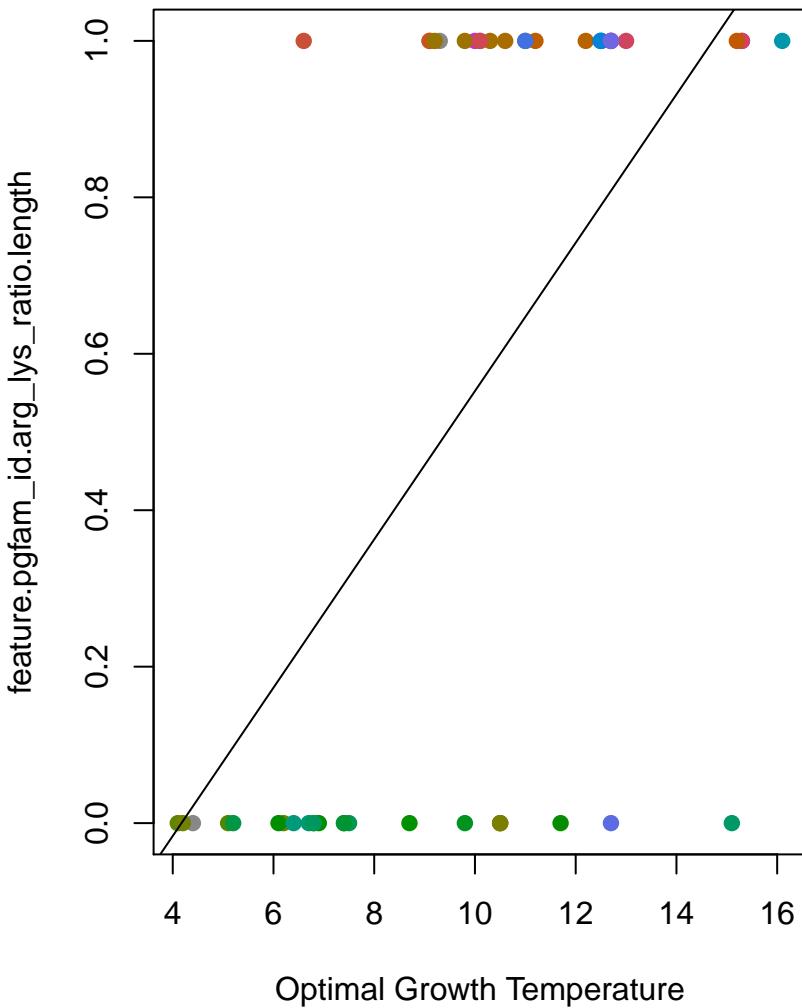


feature.pgfam_id.arg_lys_ratio.length
PGF_00420526
Cytochrome c-type protein NapC
r = 0.607, p = 10^-5.524

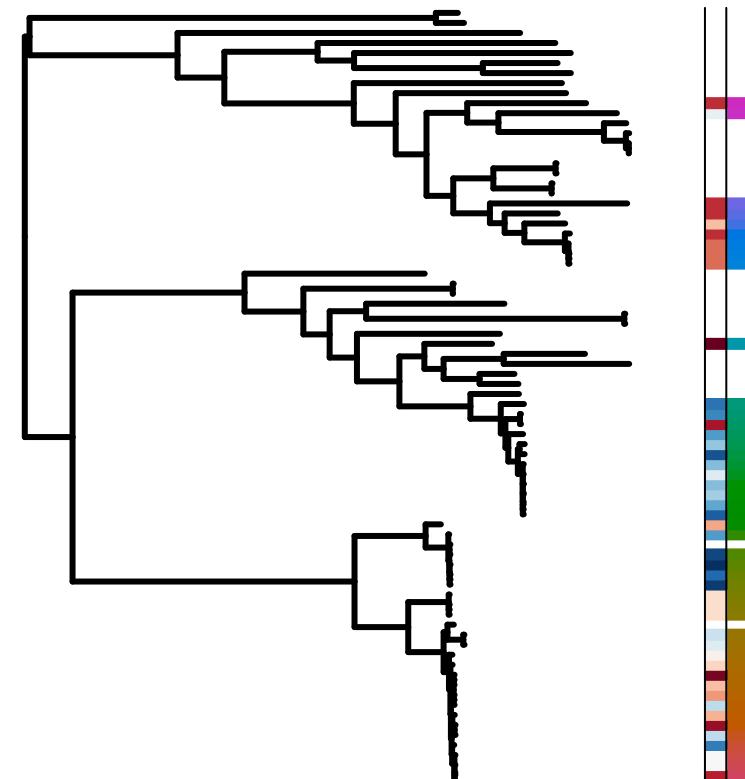
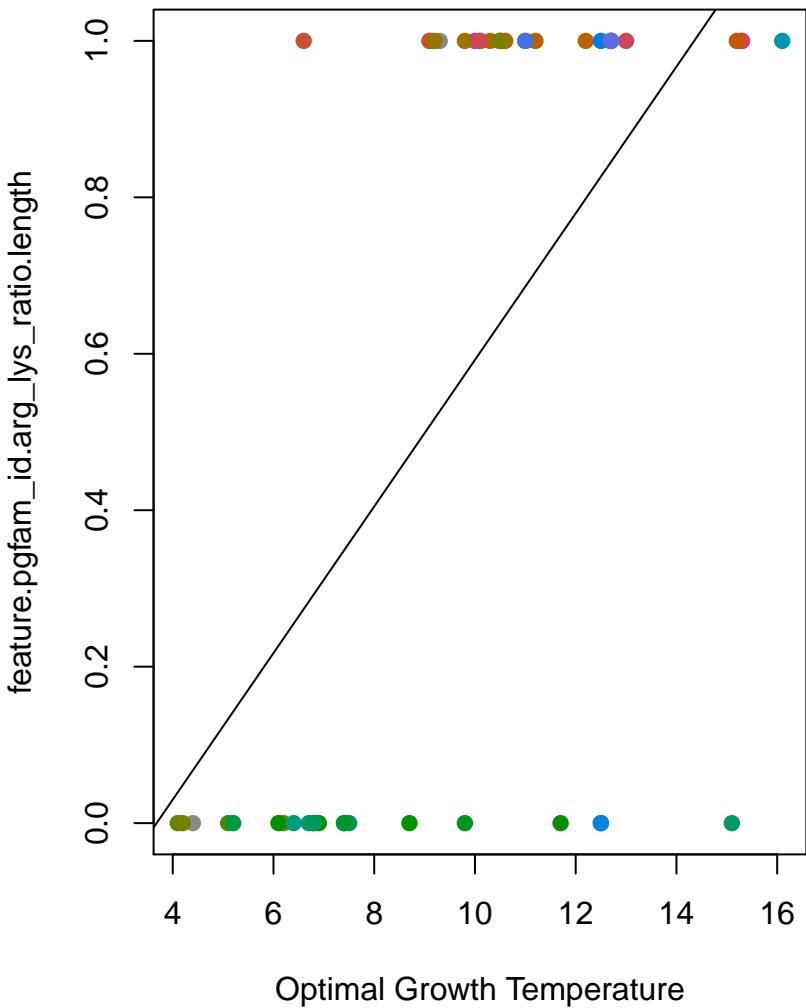


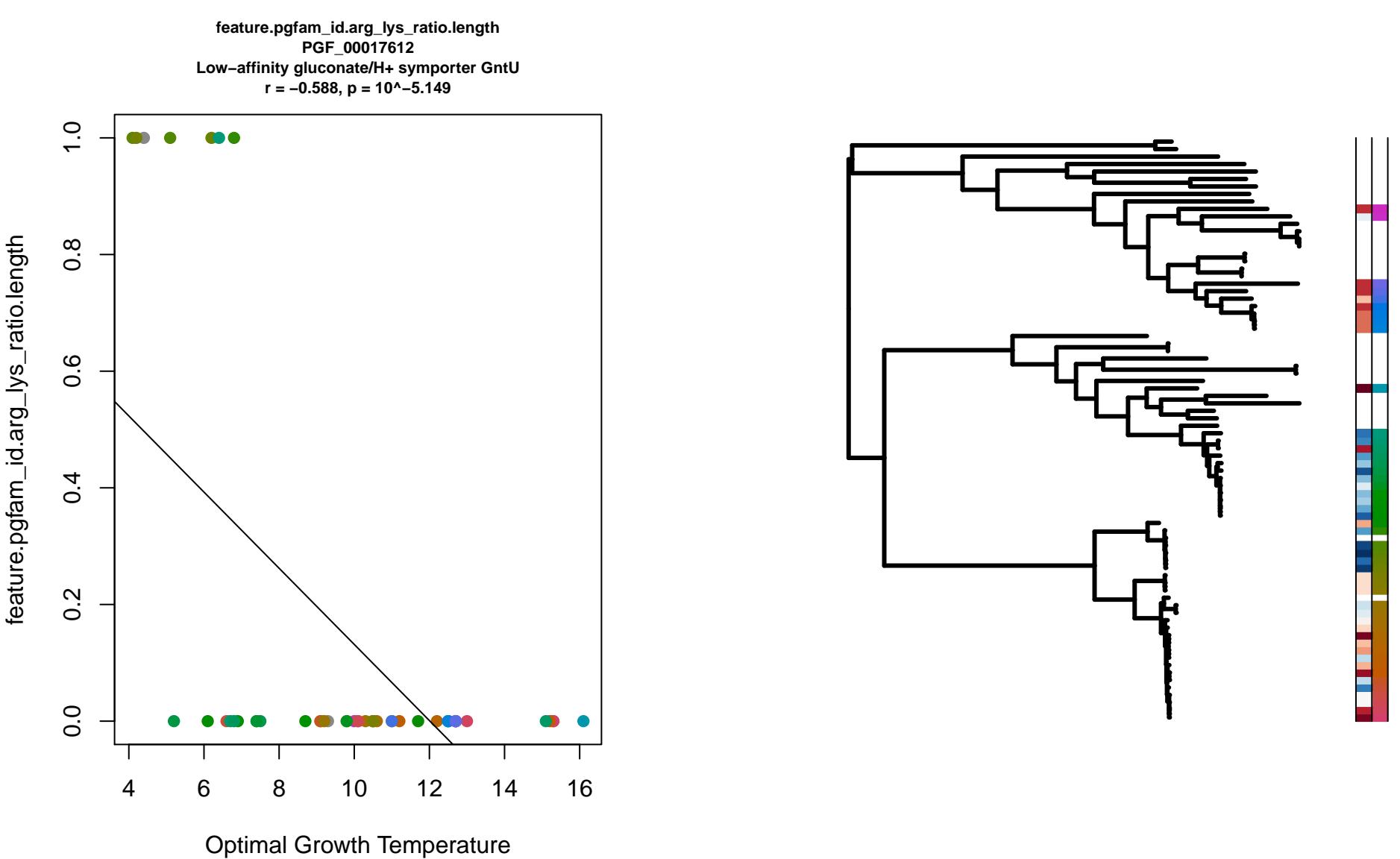


feature.pgfam_id.arg_lys_ratio.length
PGF_00142125
hypothetical protein
 $r = 0.595$, $p = 10^{-5.276}$



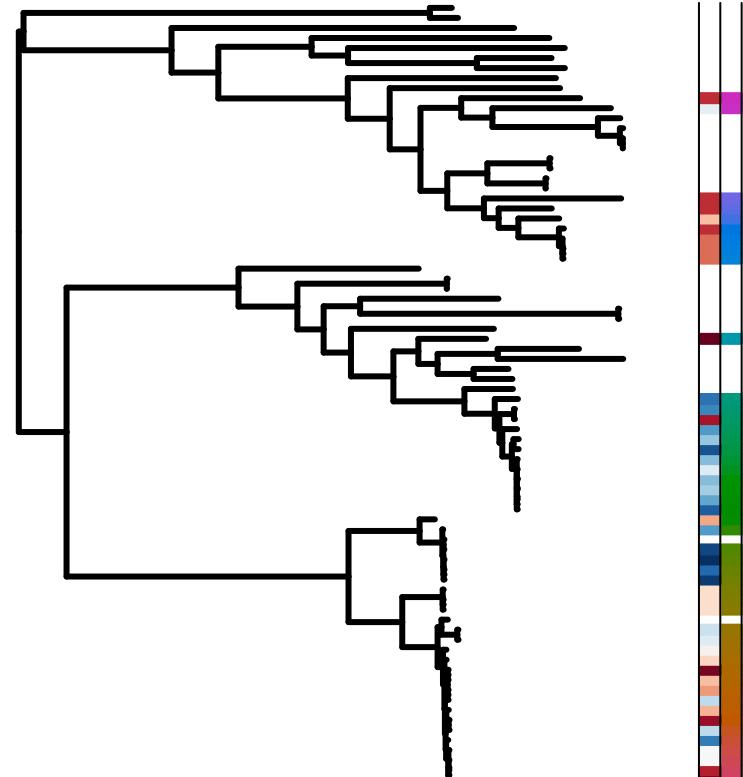
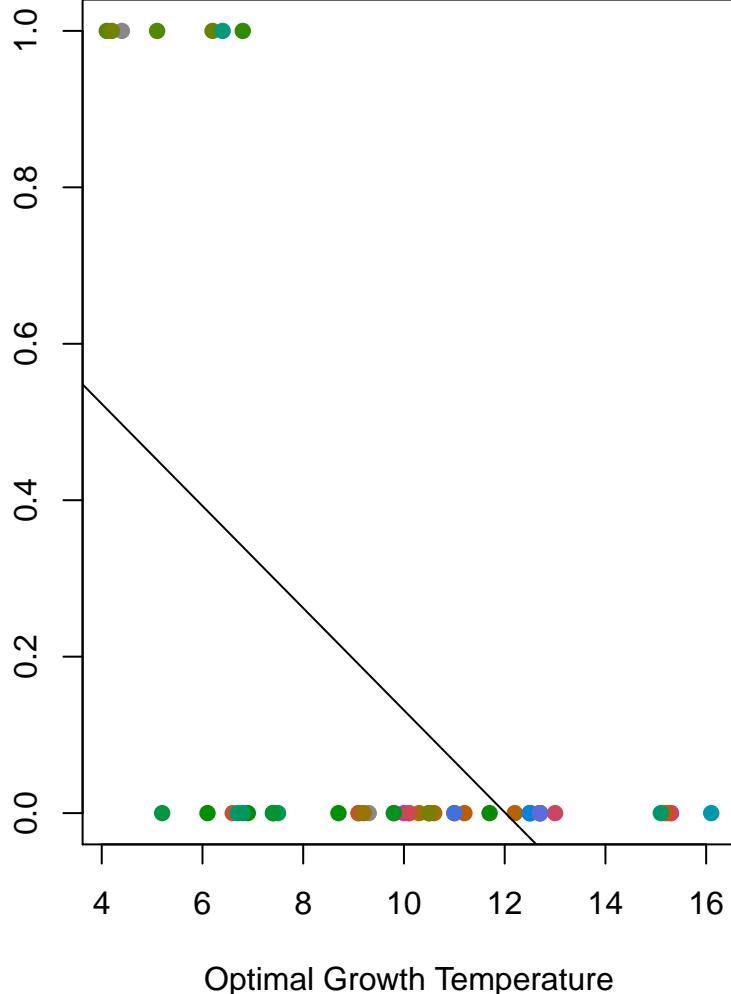
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PGF_10314609
Acyltransferase
 $r = 0.593$, $p = 10^{-5.253}$



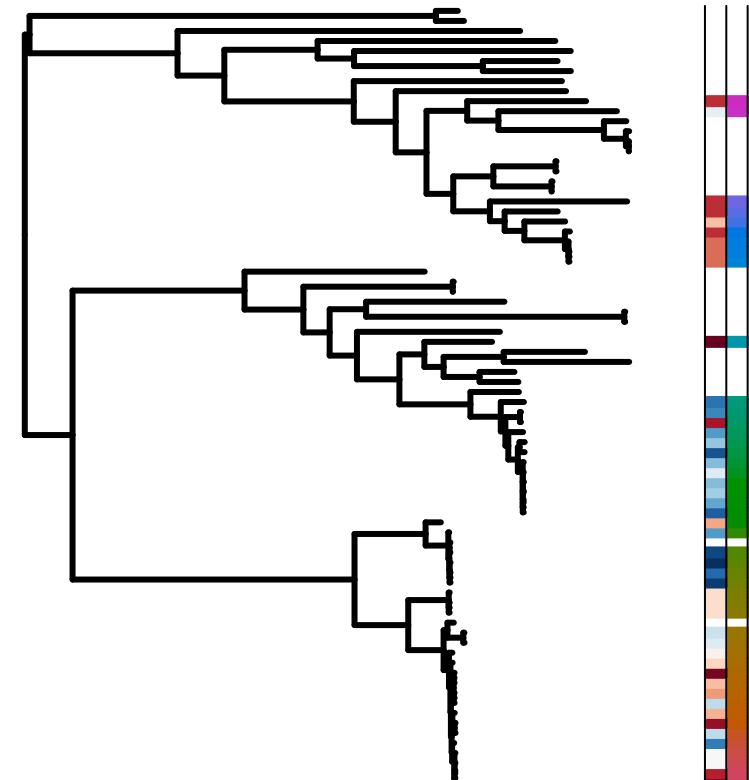
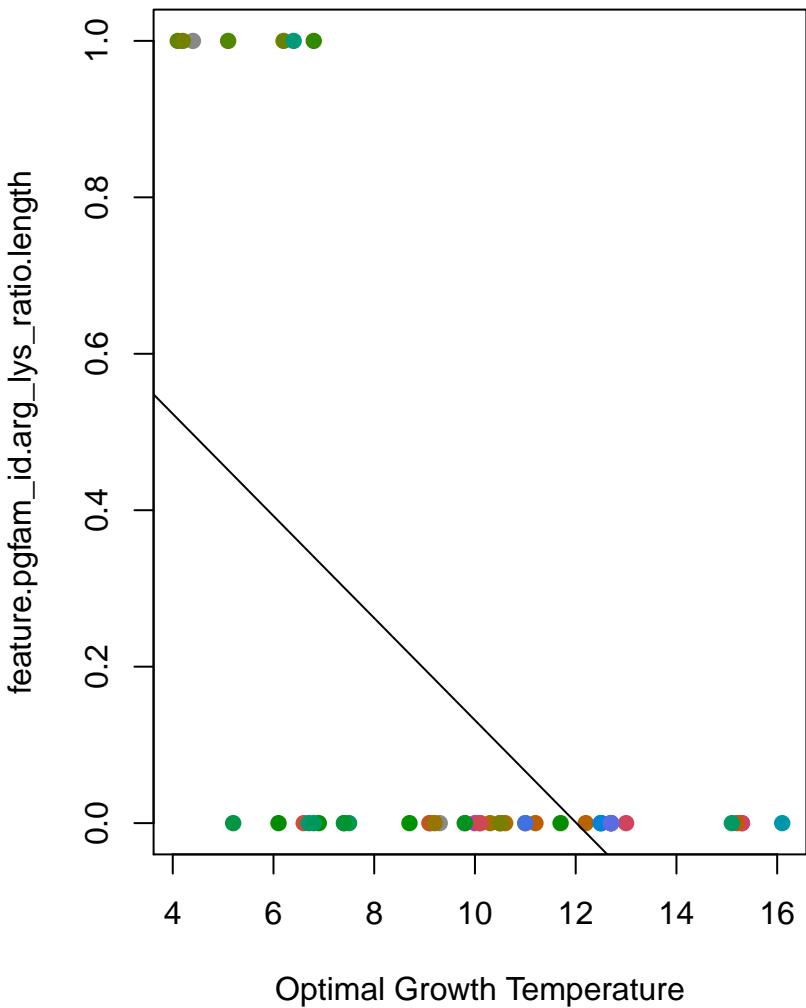


feature.pgfam_id.arg_lys_ratio.length
PGF_00033768
Phospholipid methyltransferase
 $r = -0.588$, $p = 10^{-5.149}$

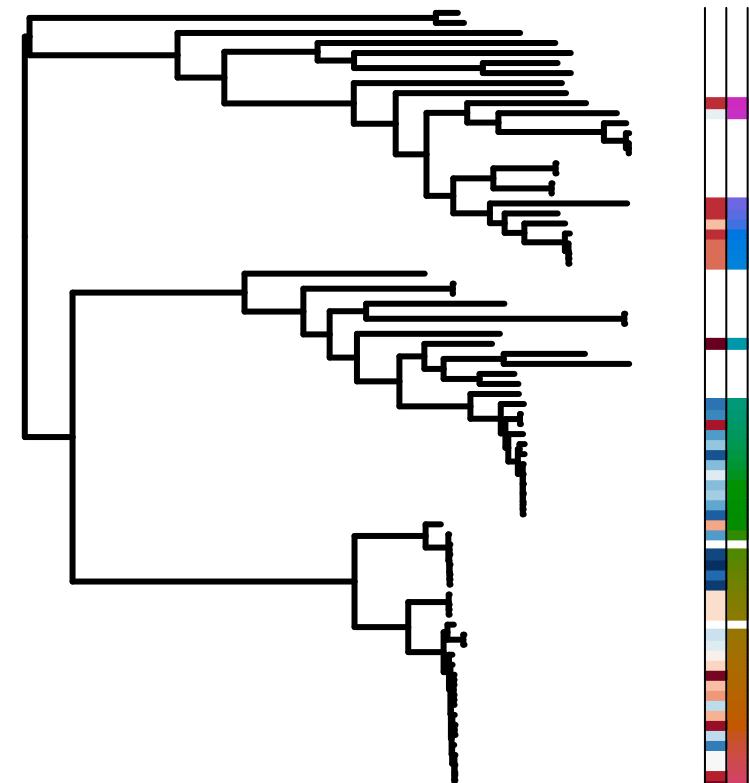
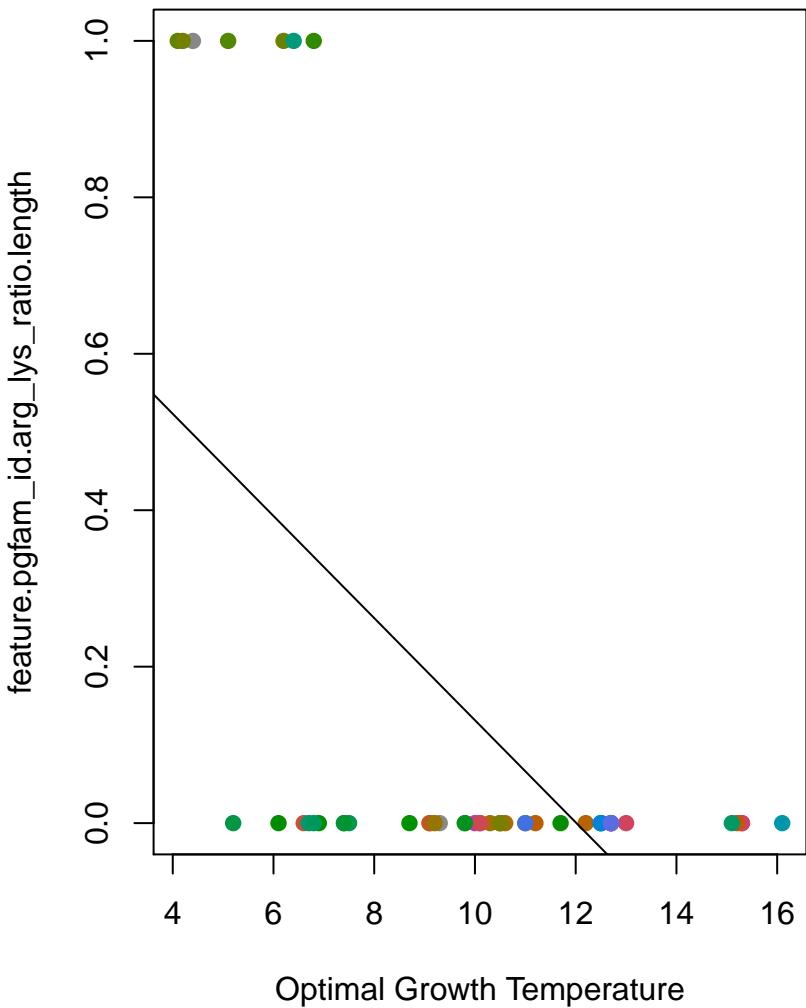
feature.pgfam_id.arg_lys_ratio.length



feature.pgfam_id.arg_lys_ratio.length
PGF_00099967
hypothetical protein
 $r = -0.588$, $p = 10^{-5.149}$

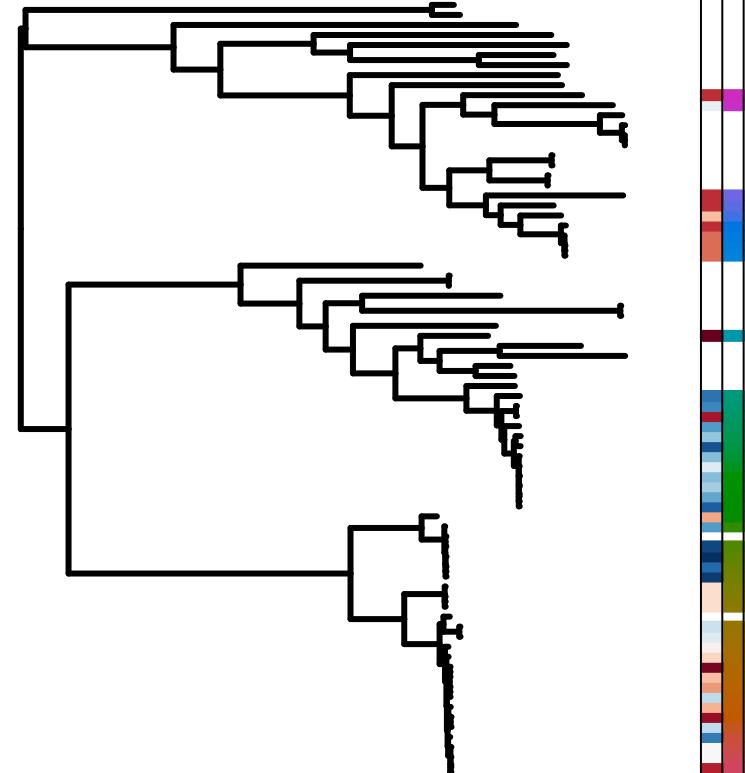
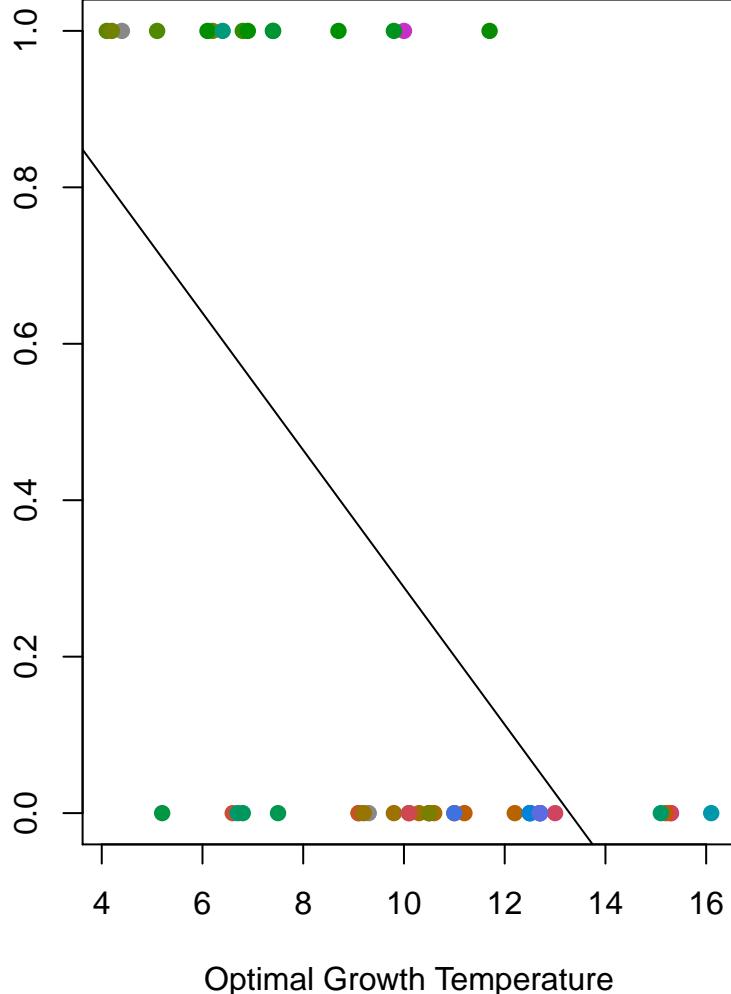


feature.pgfam_id.arg_lys_ratio.length
PGF_04413368
Gluconolactonase (EC 3.1.1.17)
 $r = -0.588$, $p = 10^{-5.149}$



feature.pgfam_id.arg_lys_ratio.length
PGF_04762212
Uncharacterized MFS-type transporter
 $r = -0.598$, $p = 10^{-5.351}$

feature.pgfam_id.arg_lys_ratio.length

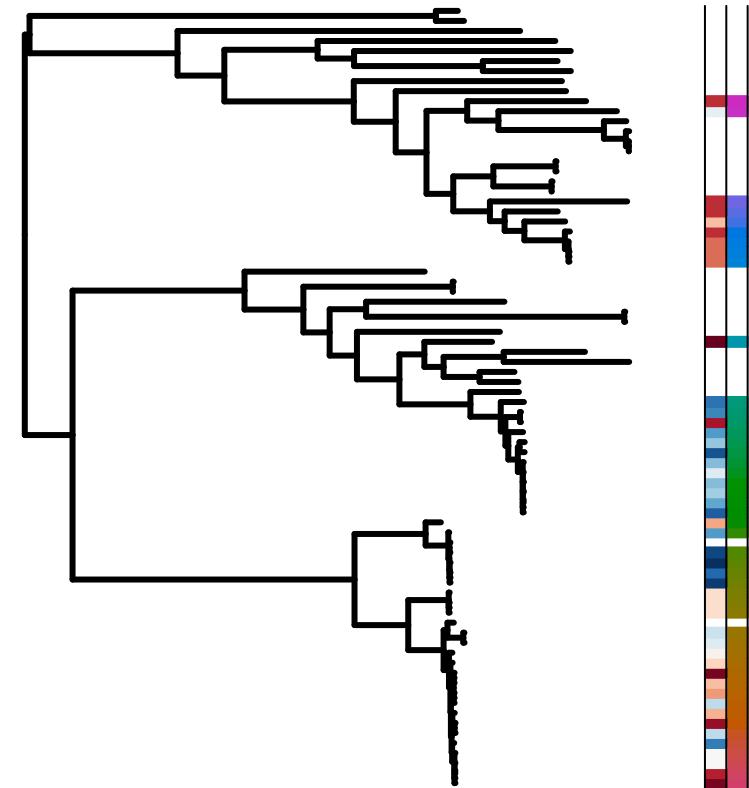
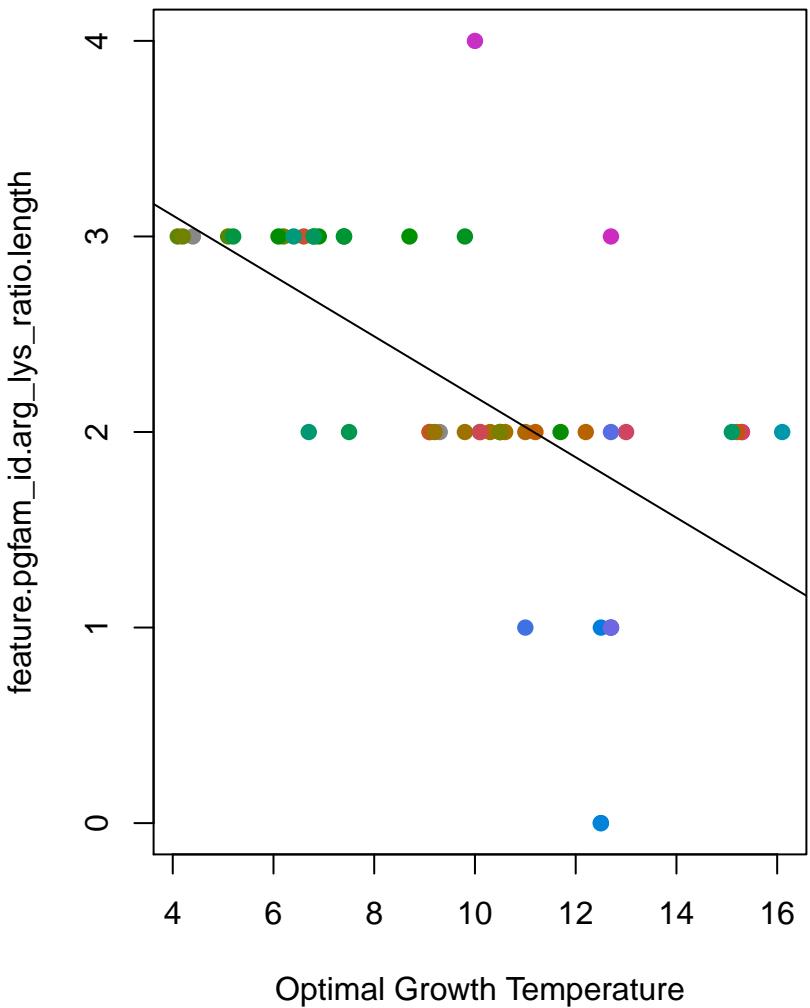


feature.pgfam_id.arg_lys_ratio.length

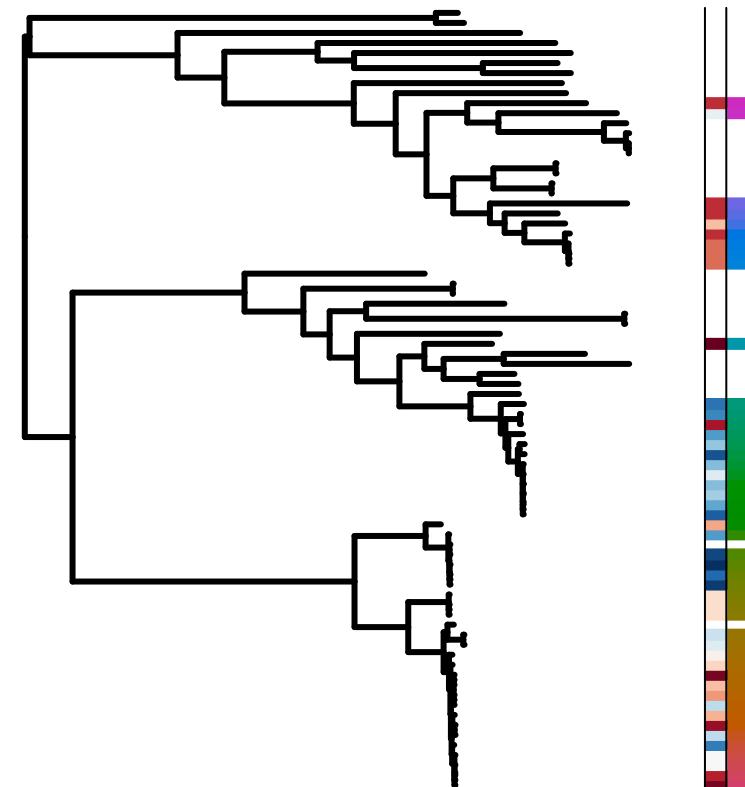
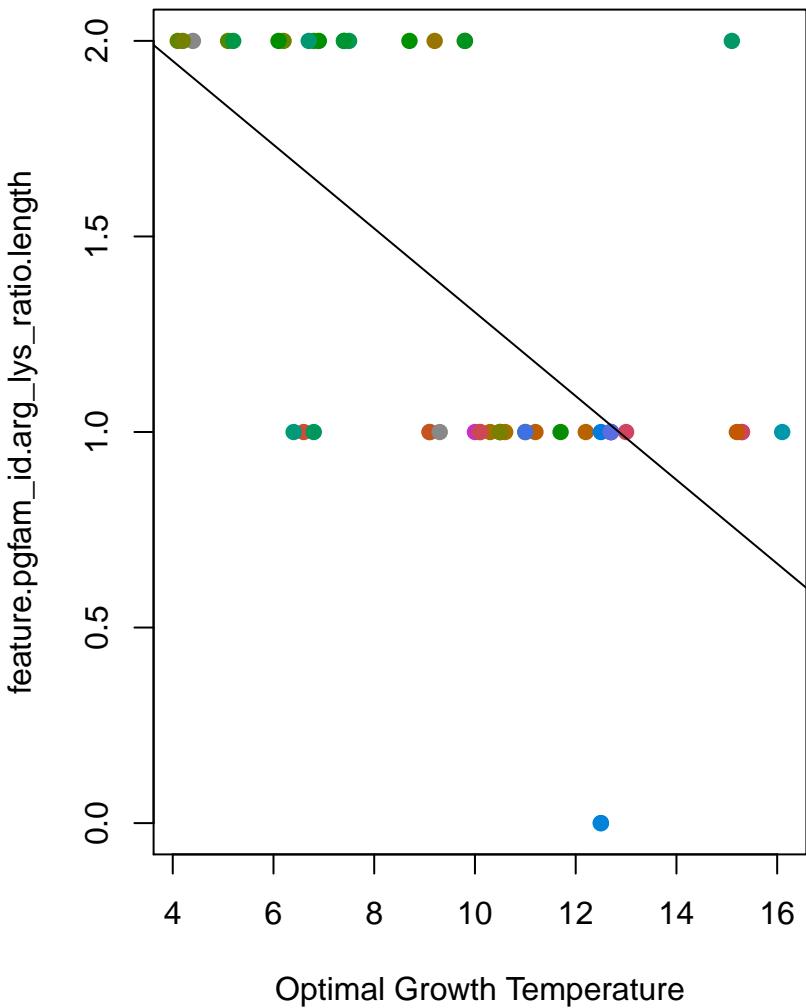
PGF_10238627

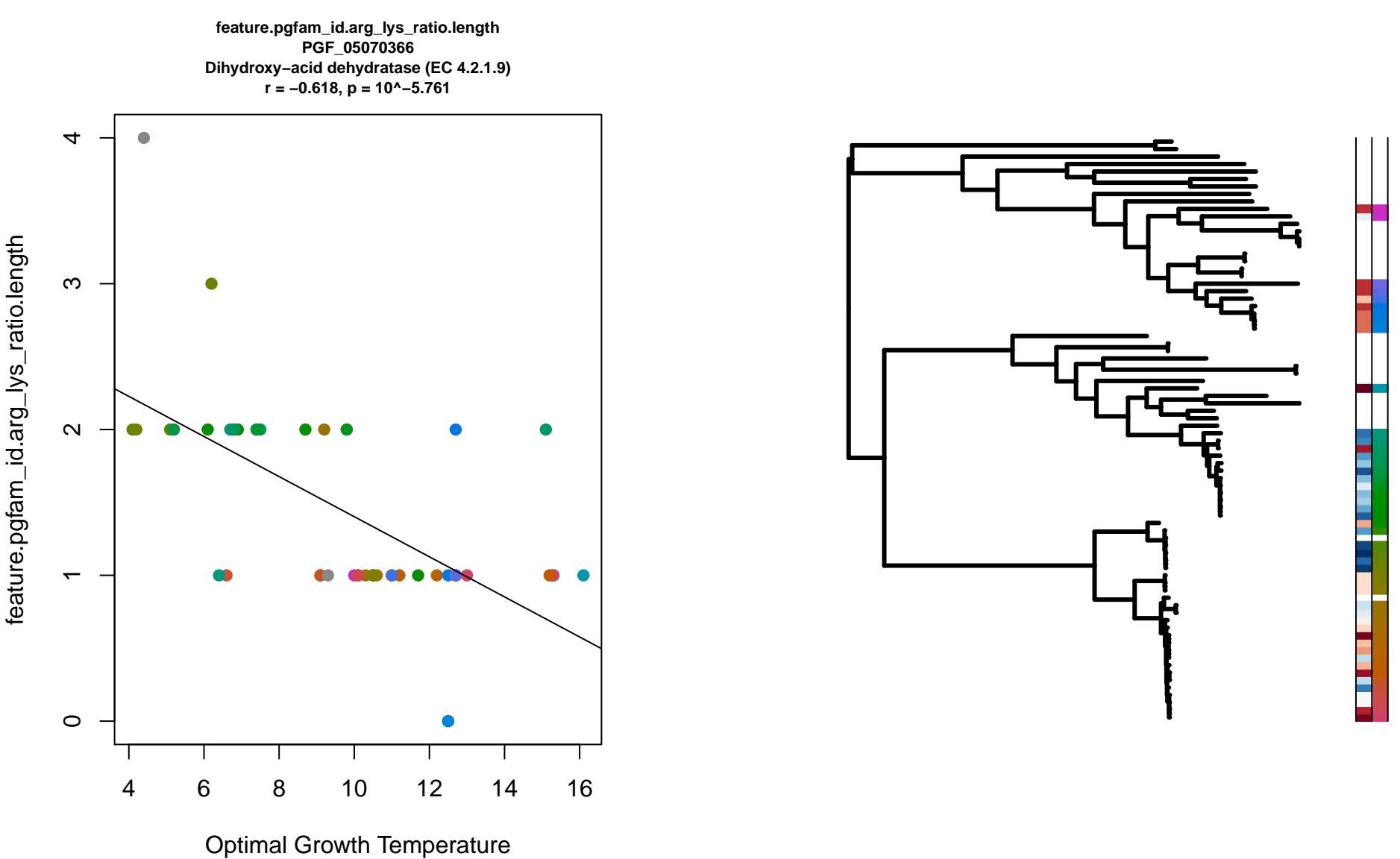
Chemotaxis regulator – transmits chemoreceptor signals to flagellar motor components CheY

$r = -0.604, p = 10^{-5.464}$



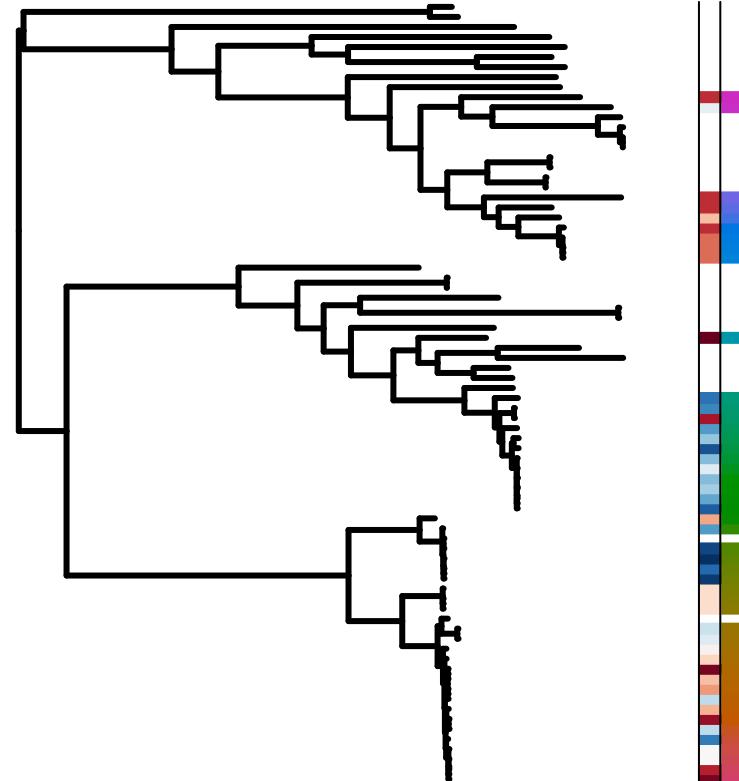
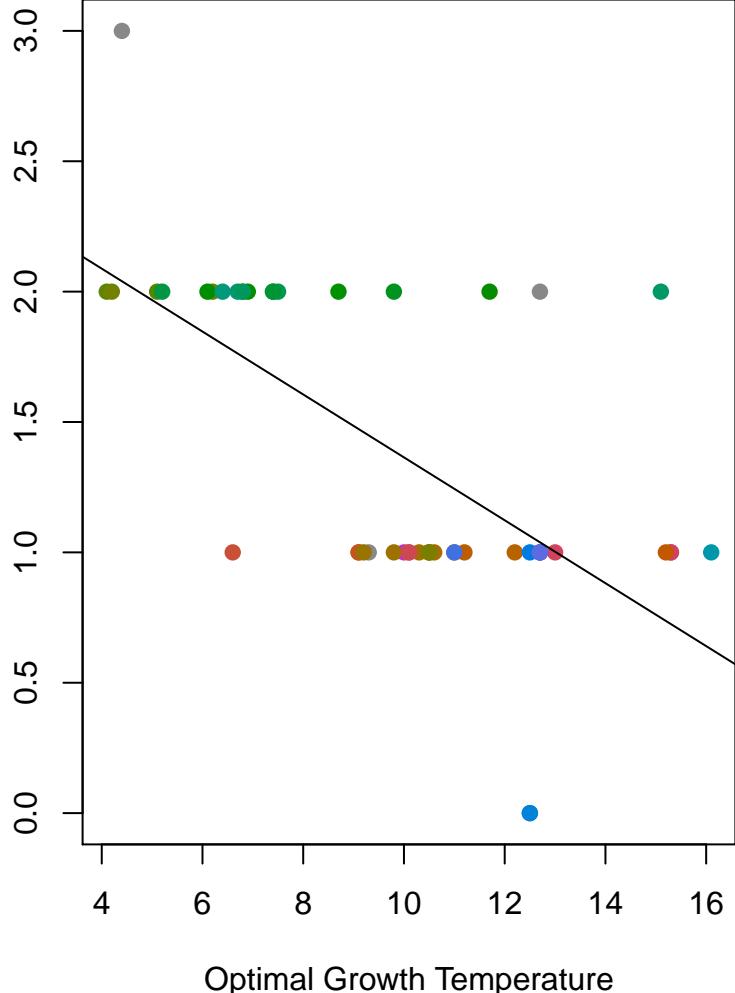
feature.pgfam_id.arg_lys_ratio.length
PGF_00751789
hypothetical protein
 $r = -0.614$, $p = 10^{-5.668}$



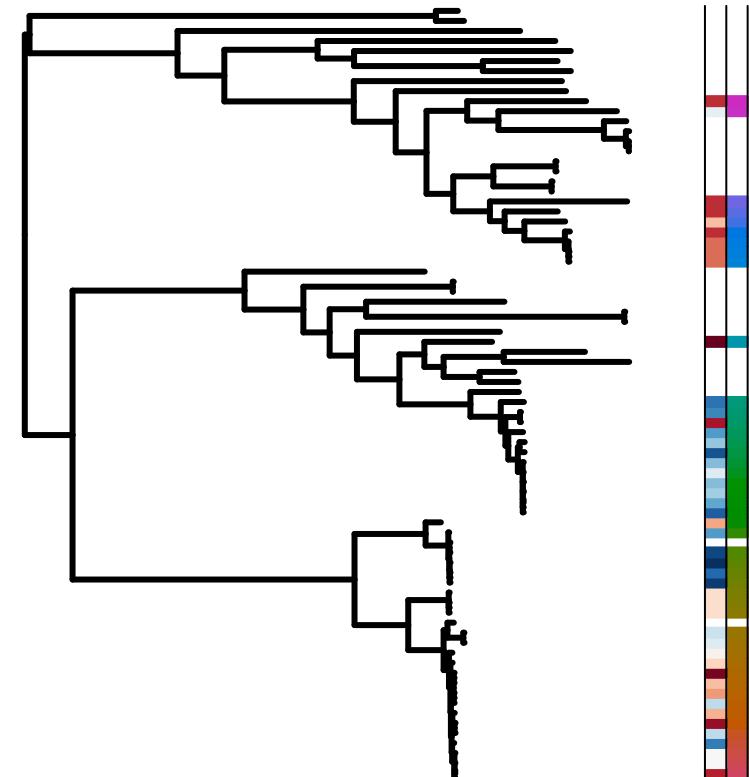
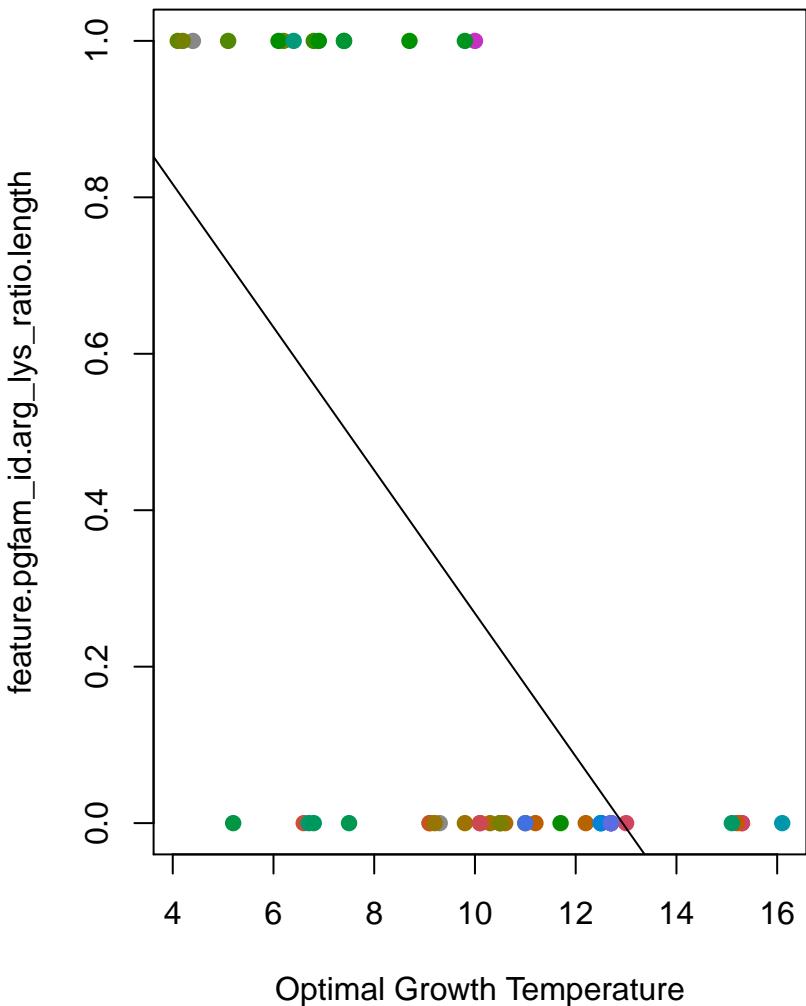


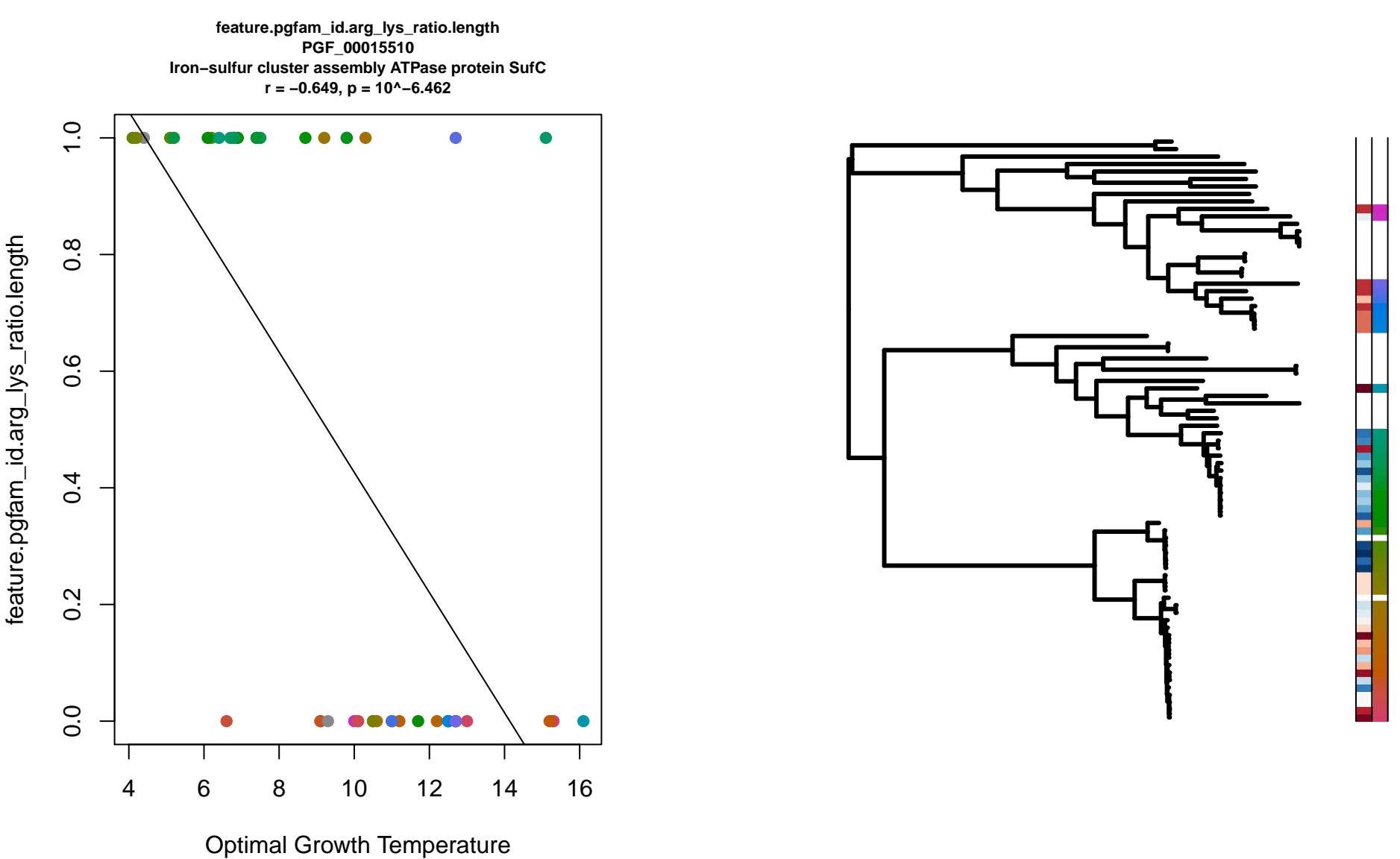
feature.pgfam_id.arg_lys_ratio.length
PGF_10523783
Acetyl-CoA synthetase (EC 6.2.1.1)
 $r = -0.632$, $p = 10^{-6.076}$

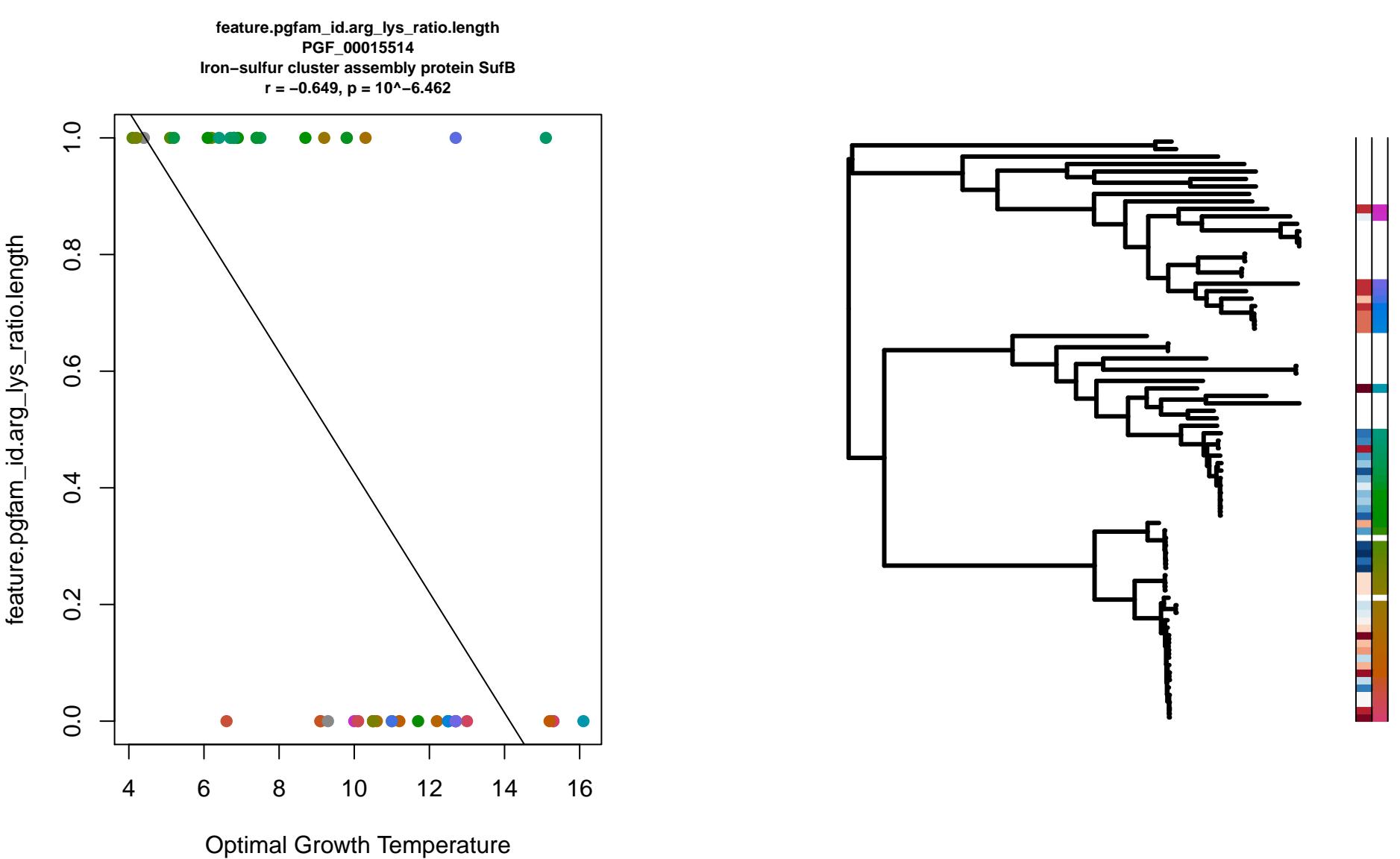
feature.pgfam_id.arg_lys_ratio.length

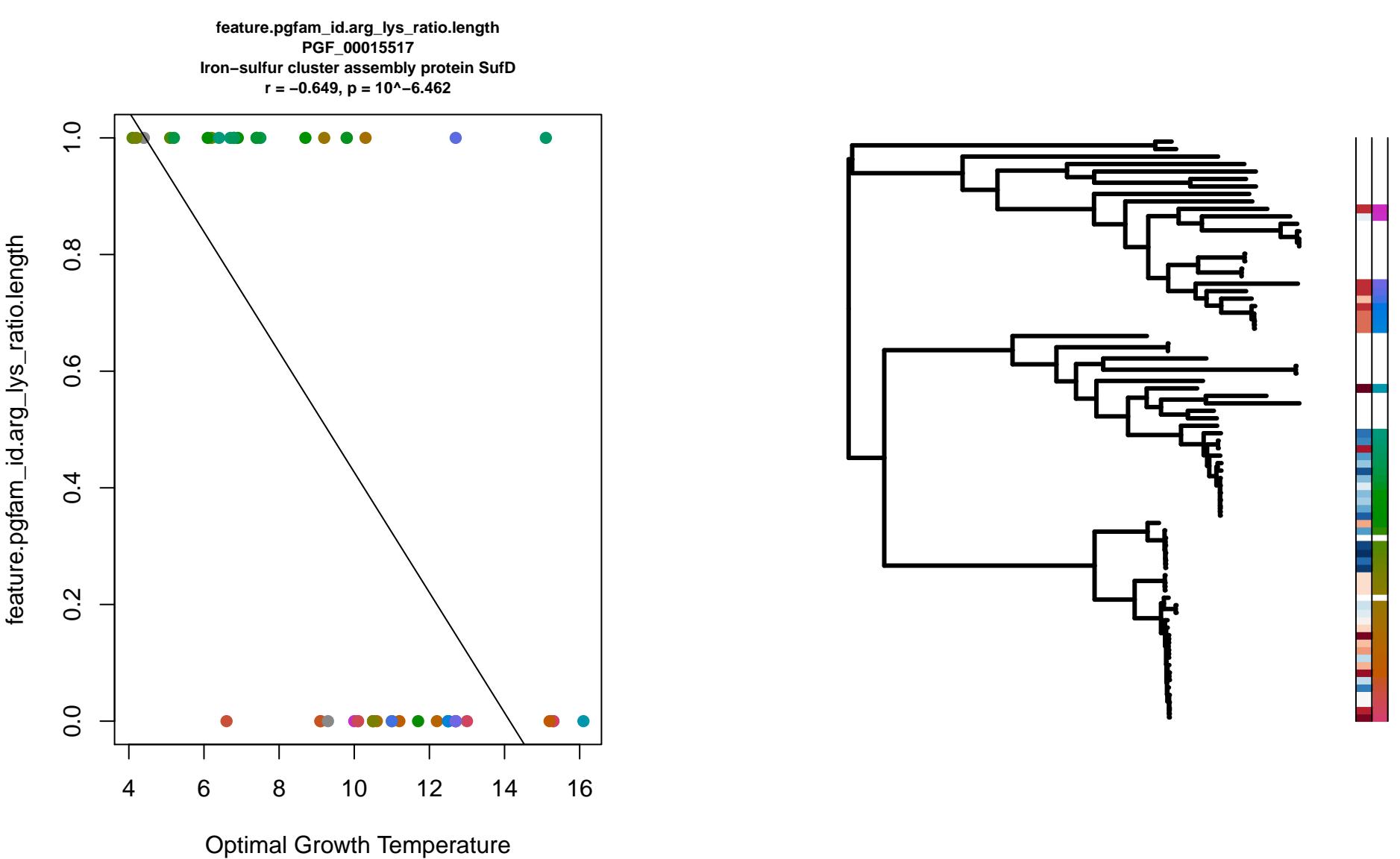


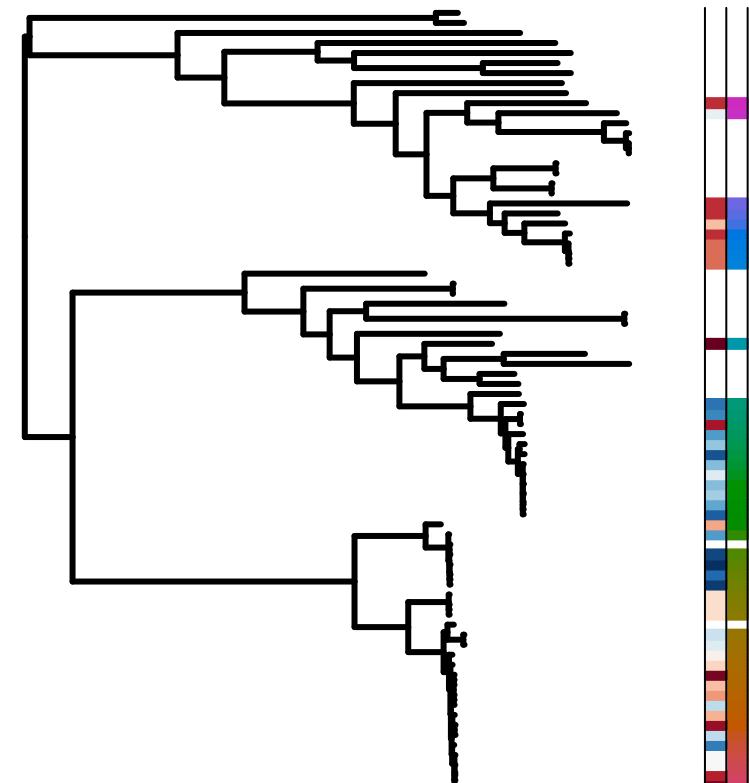
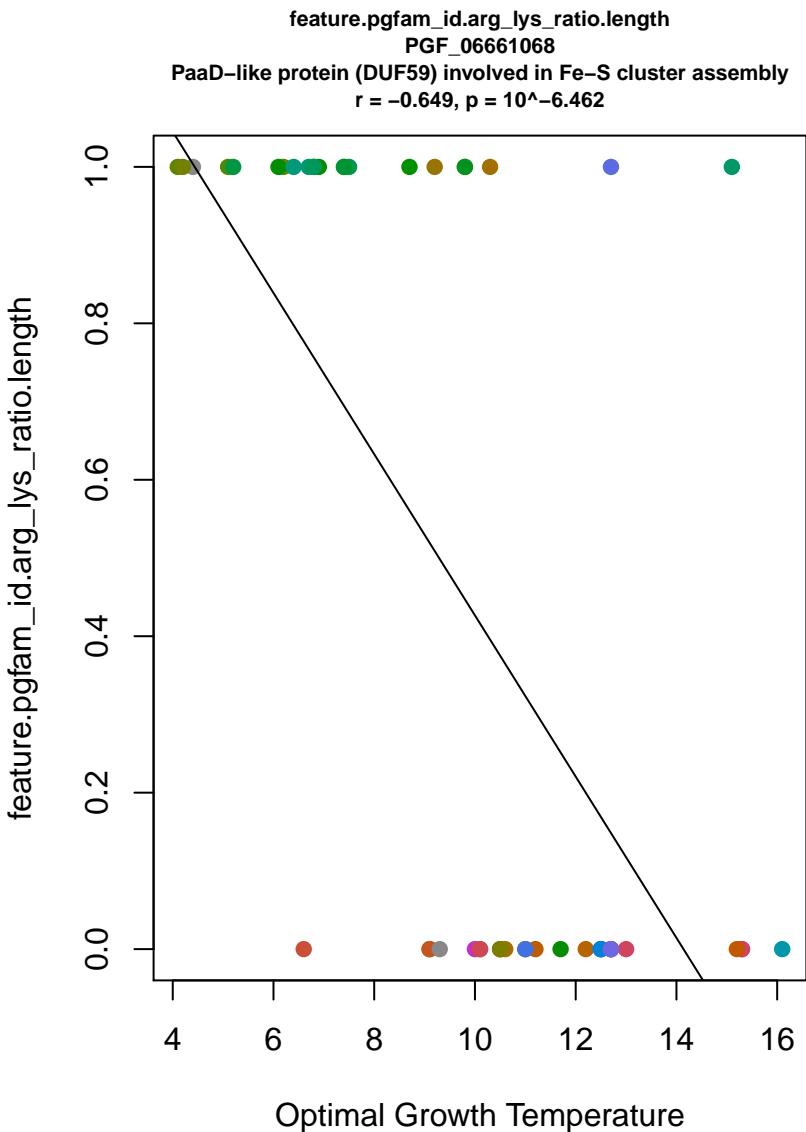
feature.pgfam_id.arg_lys_ratio.length
PGF_03775681
YoeB toxin protein
 $r = -0.637$, $p = 10^{-6.176}$

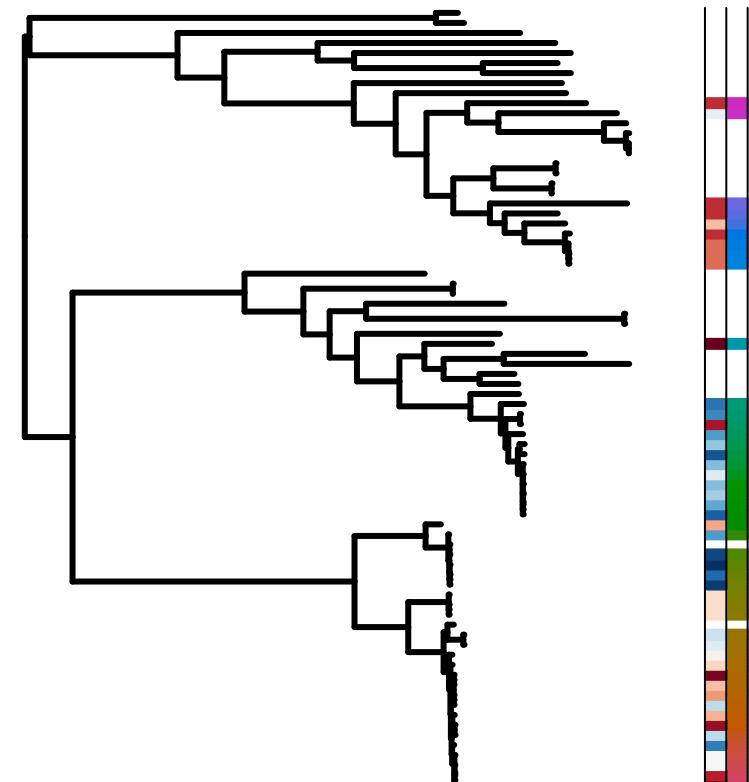
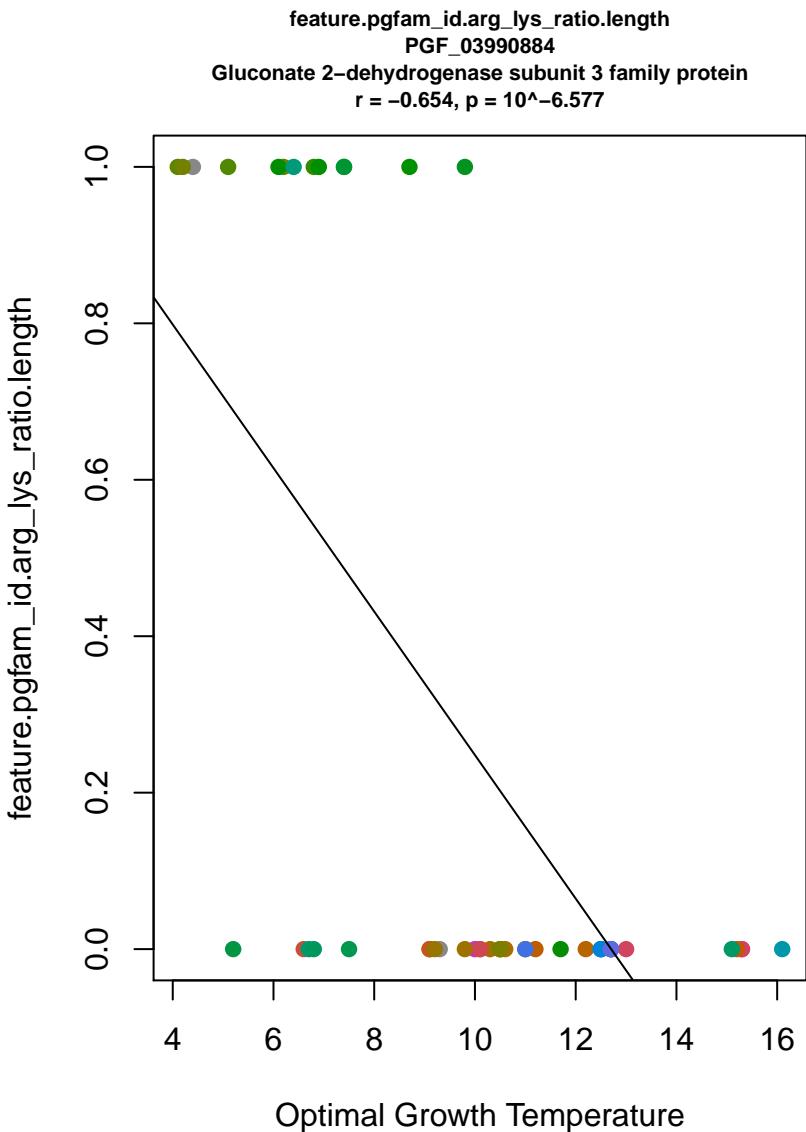




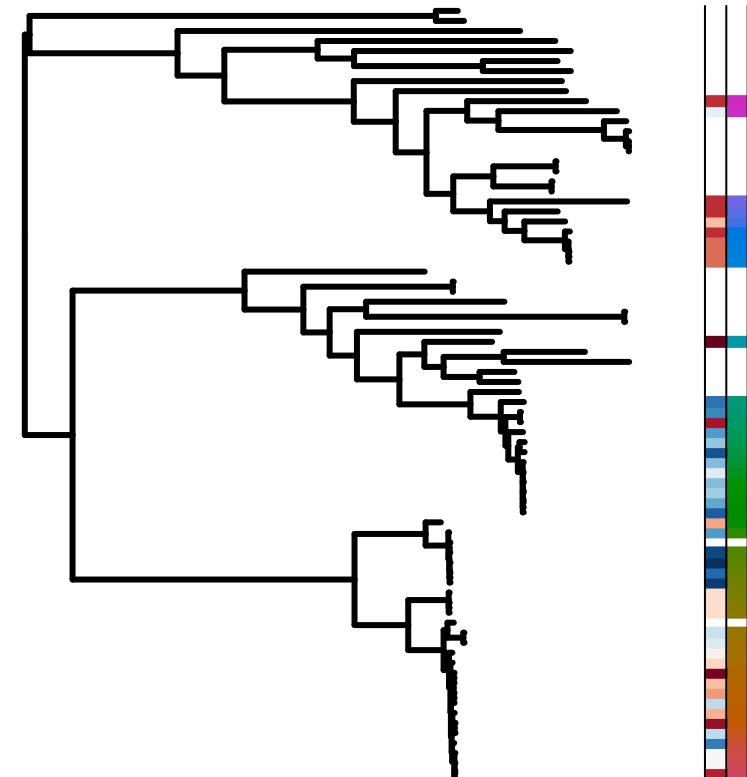
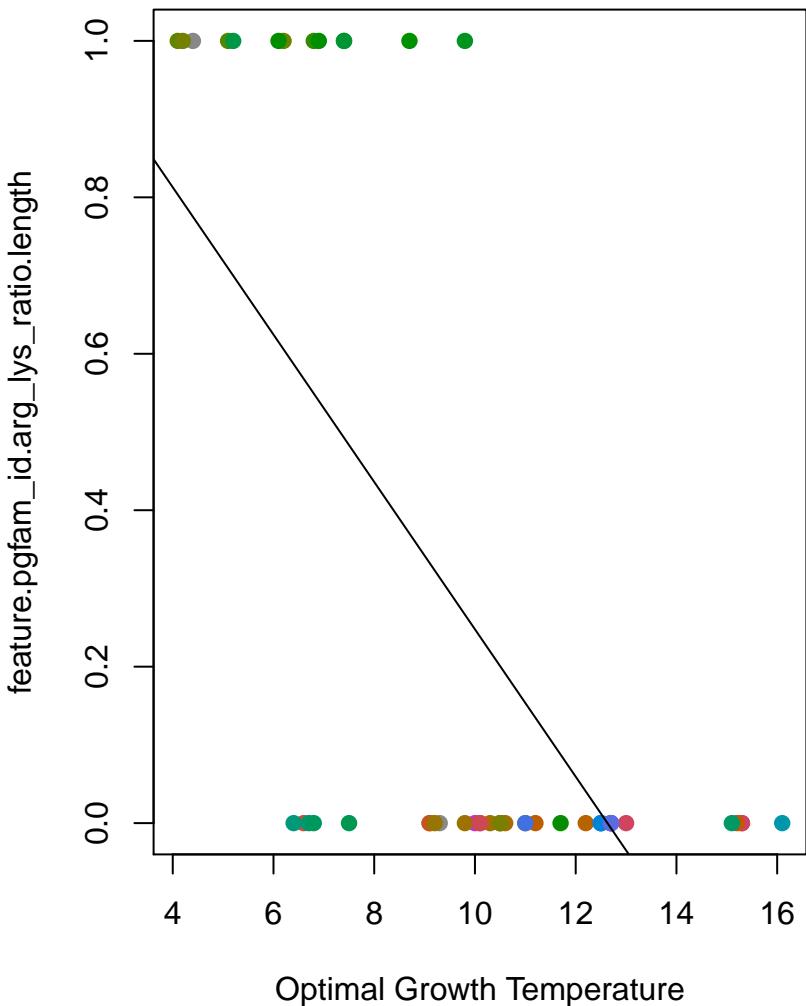




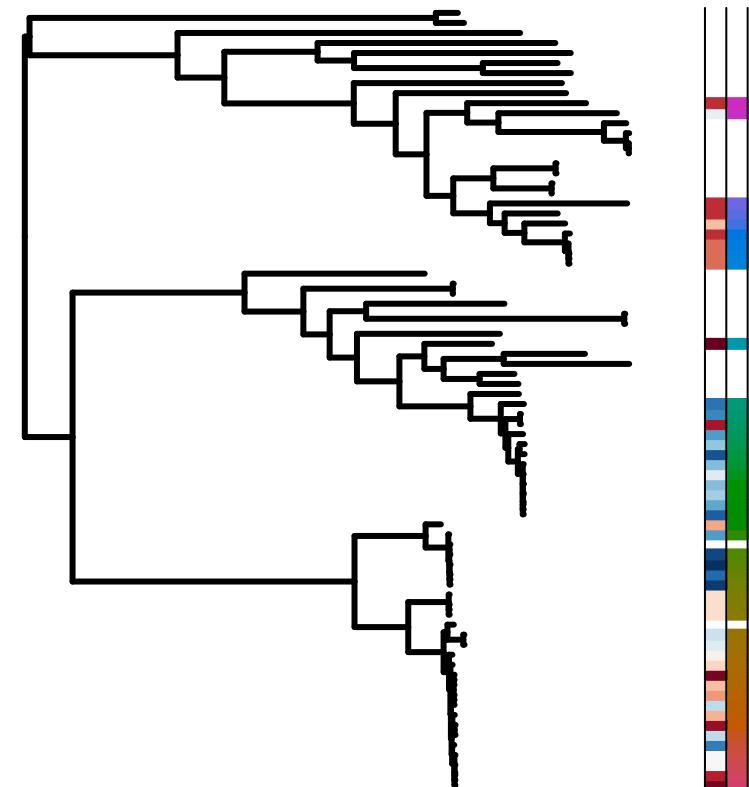
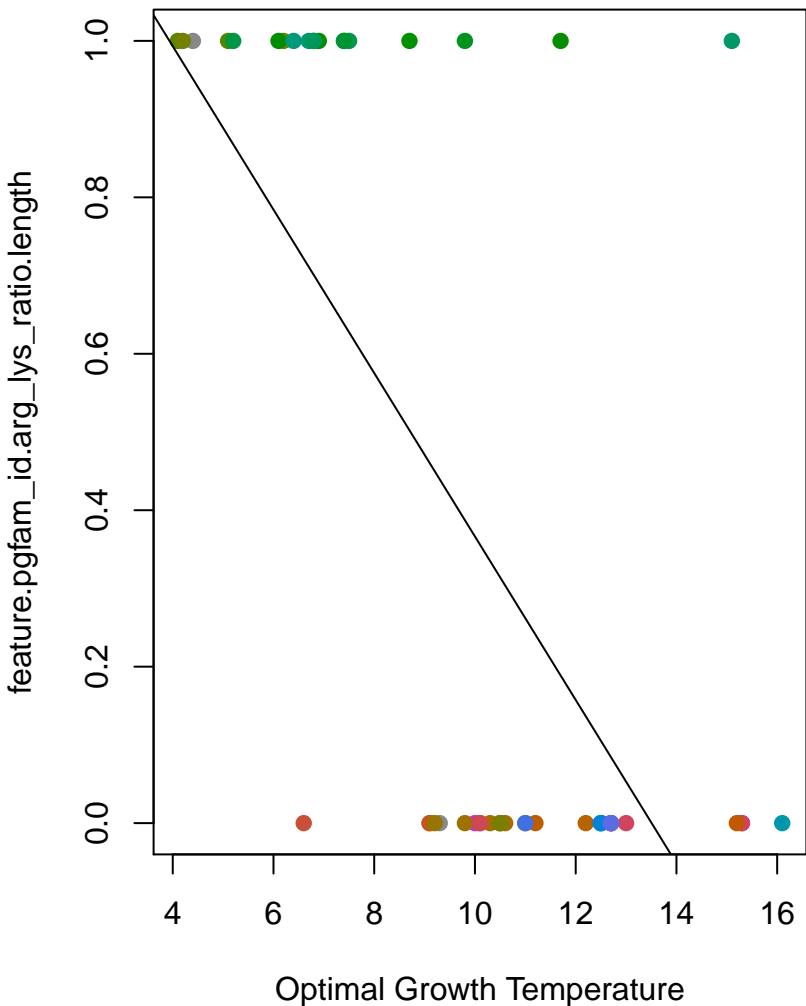


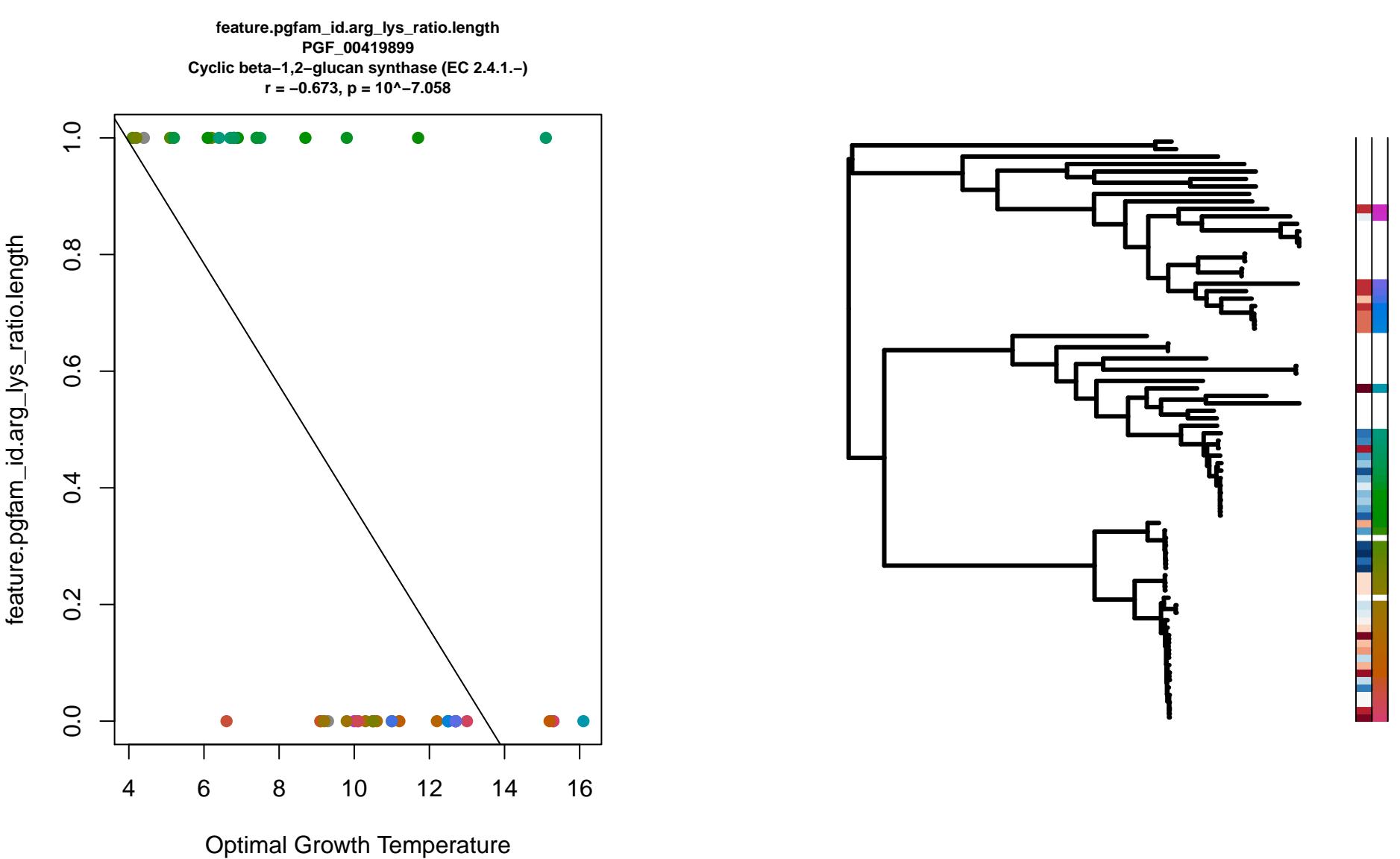


feature.pgfam_id.arg_lys_ratio.length
PGF_05722284
hypothetical protein
 $r = -0.671$, $p = 10^{-7.018}$



feature.pgfam_id.arg_lys_ratio.length
PGF_00006186
Formate efflux transporter FocA
 $r = -0.673$, $p = 10^{-7.058}$





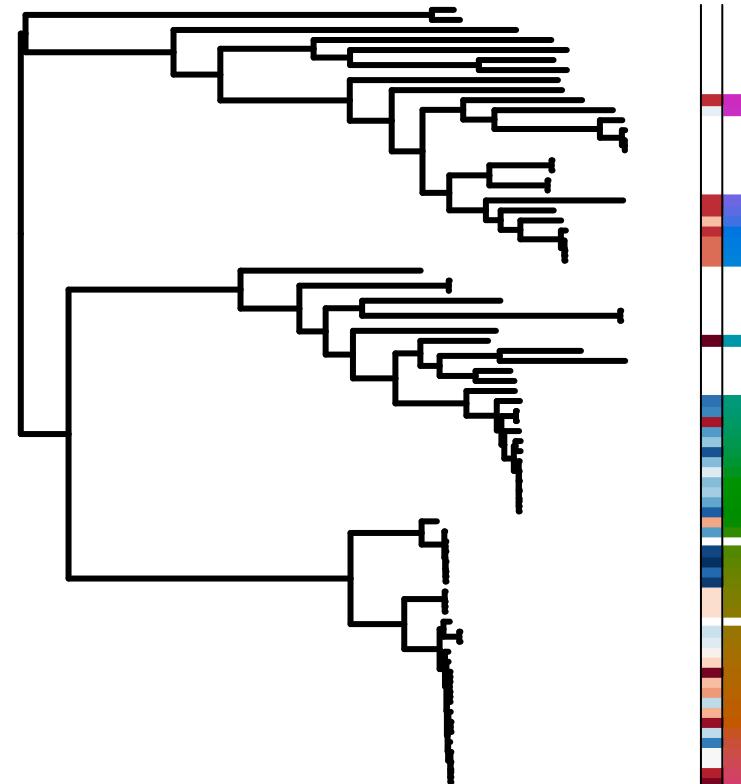
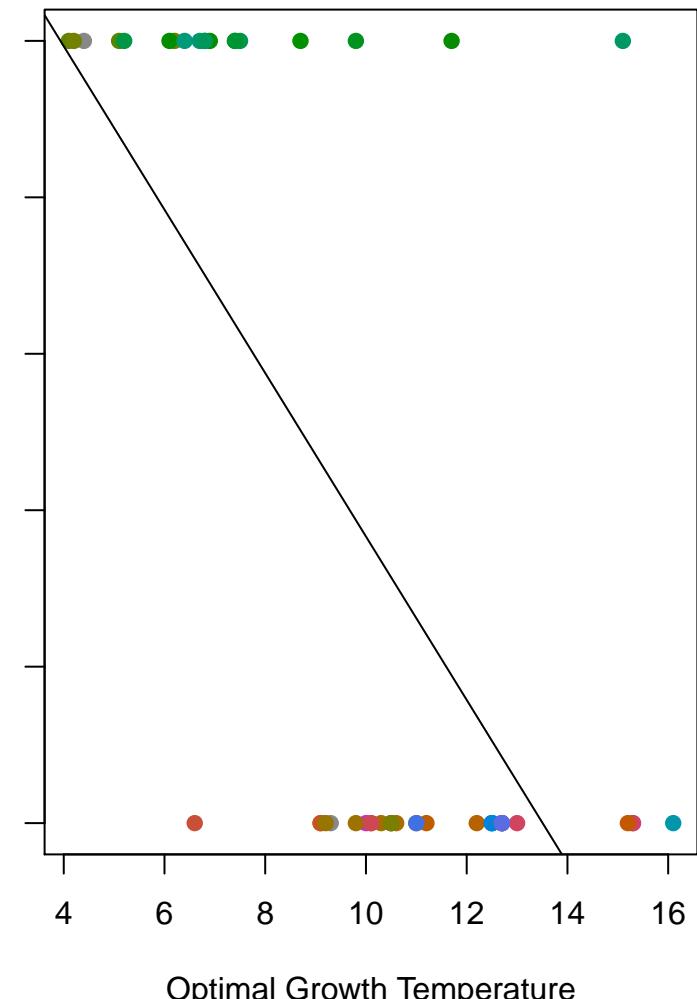
feature.pgfam_id.arg_lys_ratio.length

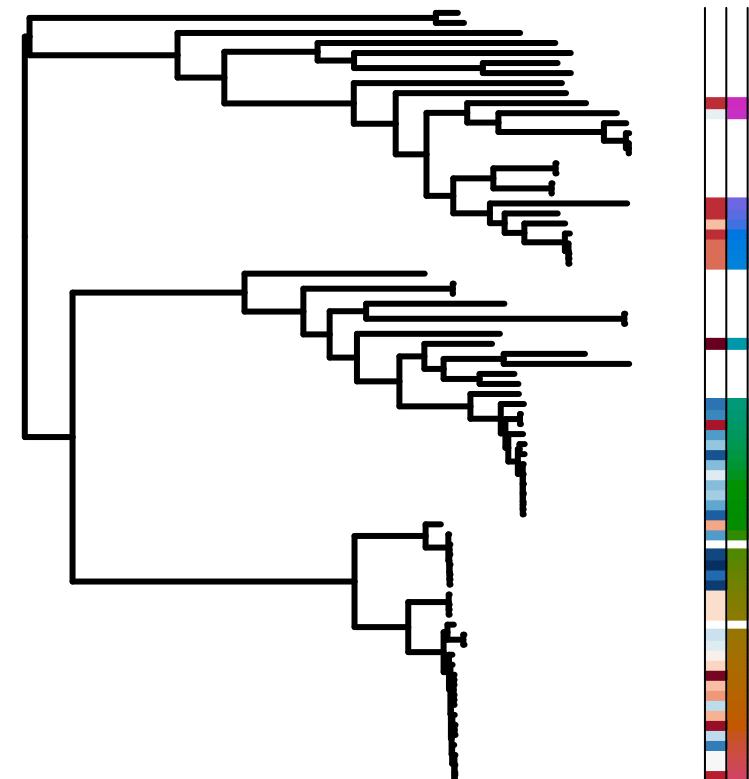
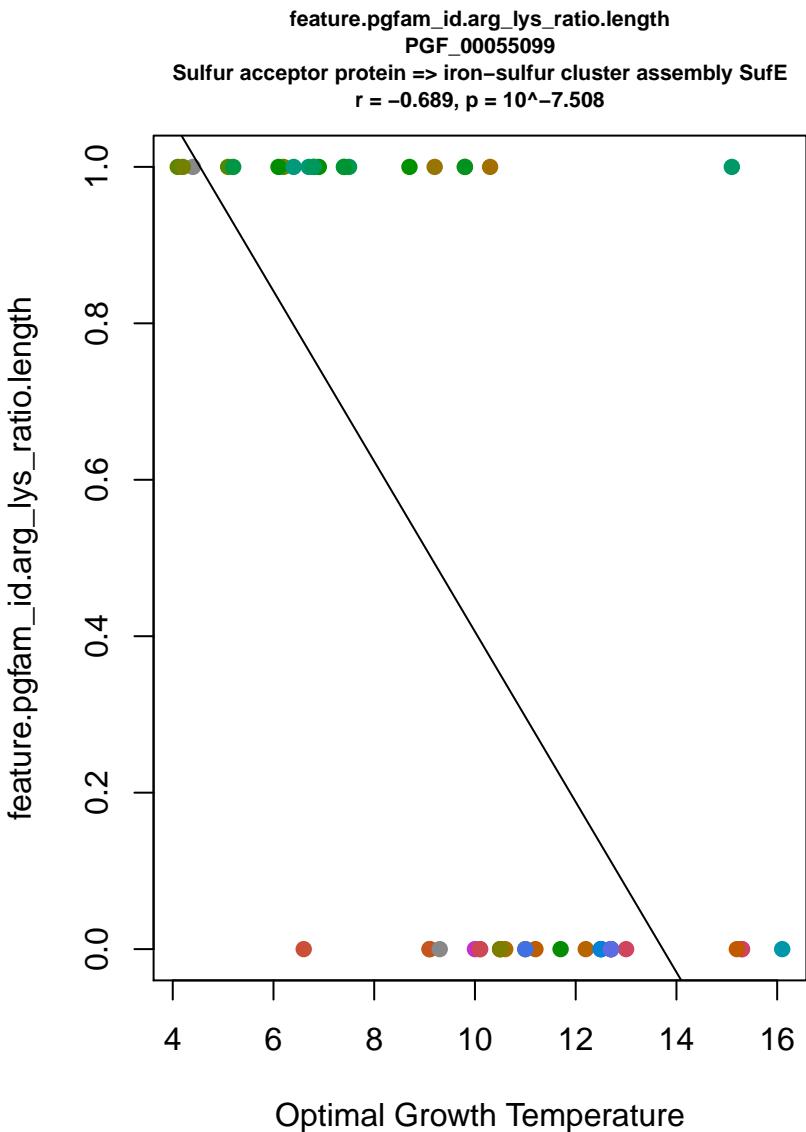
PGF_01679161

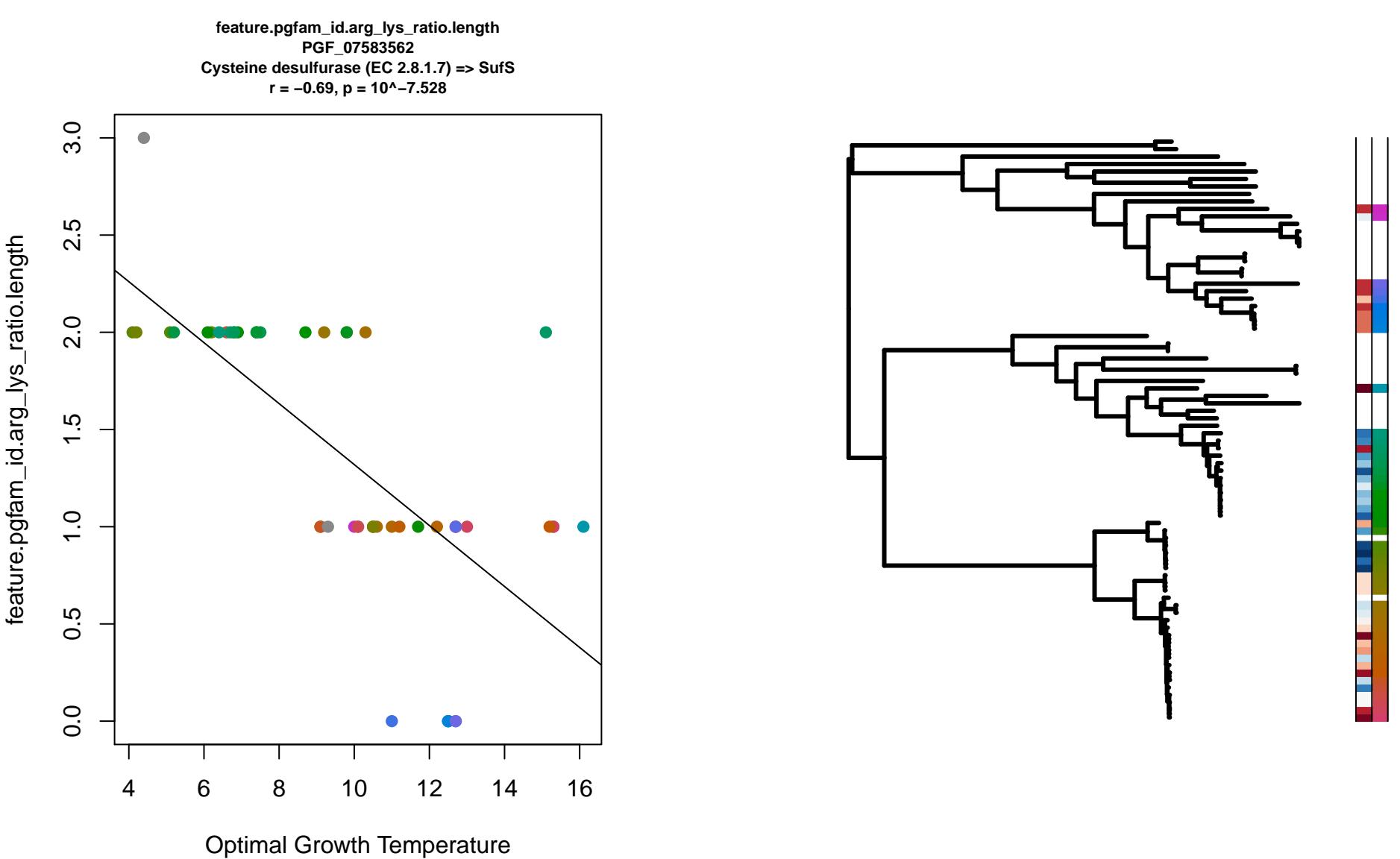
hypothetical protein

$r = -0.673, p = 10^{-7.058}$

feature.pgfam_id.arg_lys_ratio.length







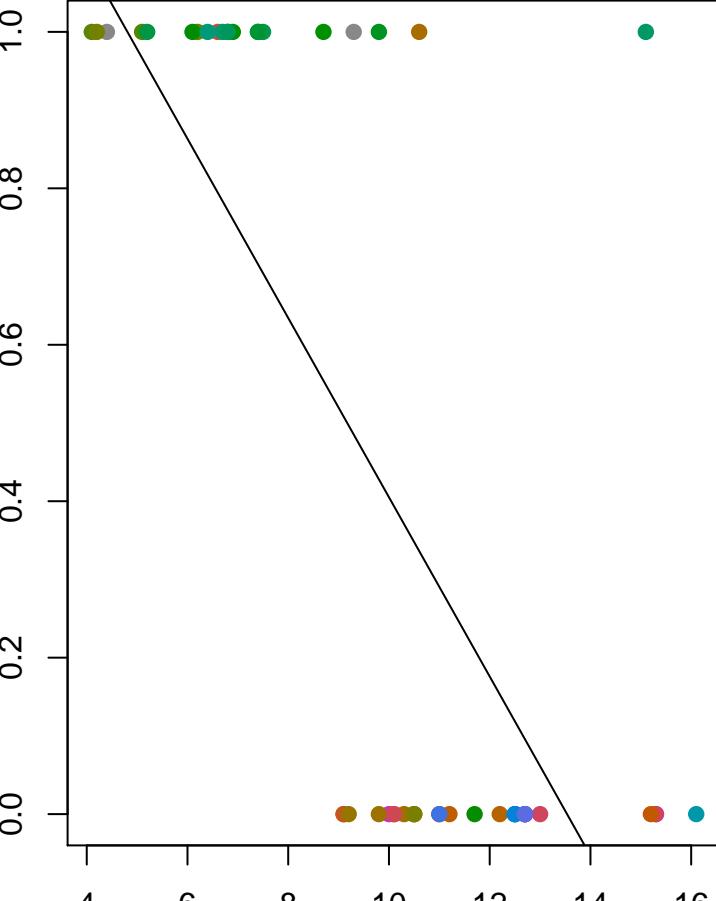
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PGF_07383941

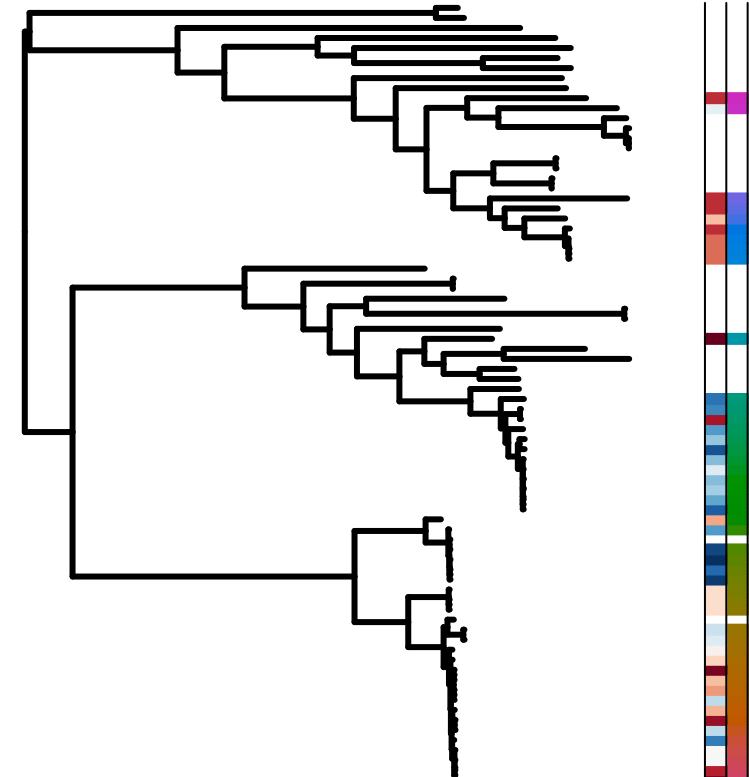
hypothetical protein

$r = -0.726, p = 10^{-8.602}$

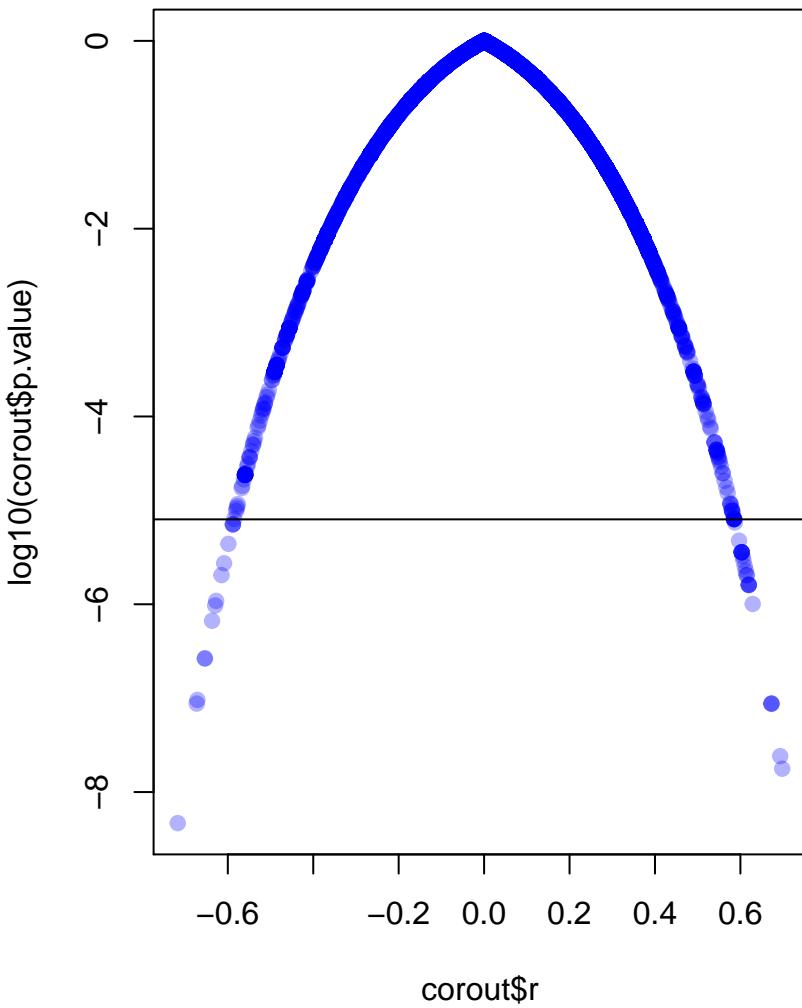
feature.pgfam_id.arg_lys_ratio.length



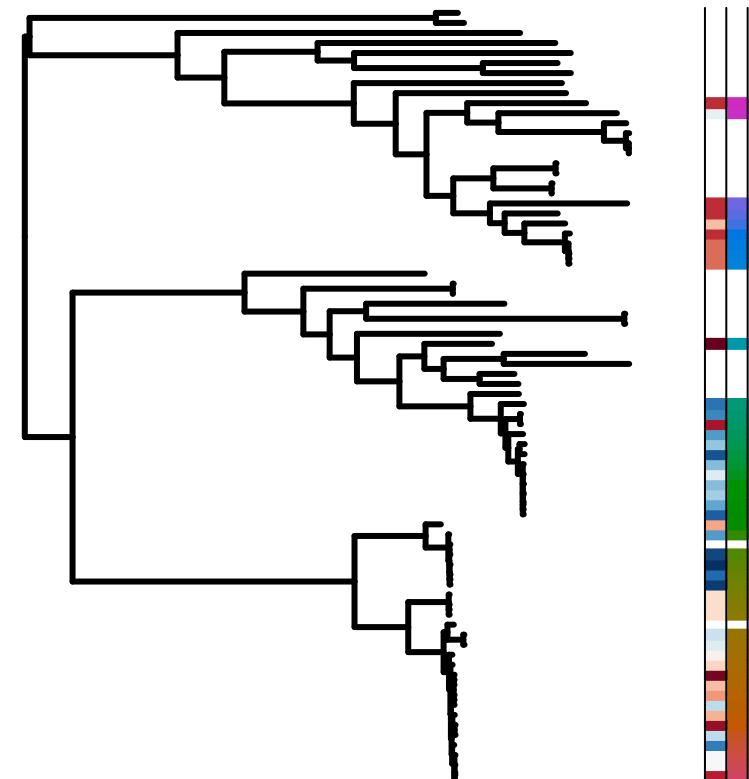
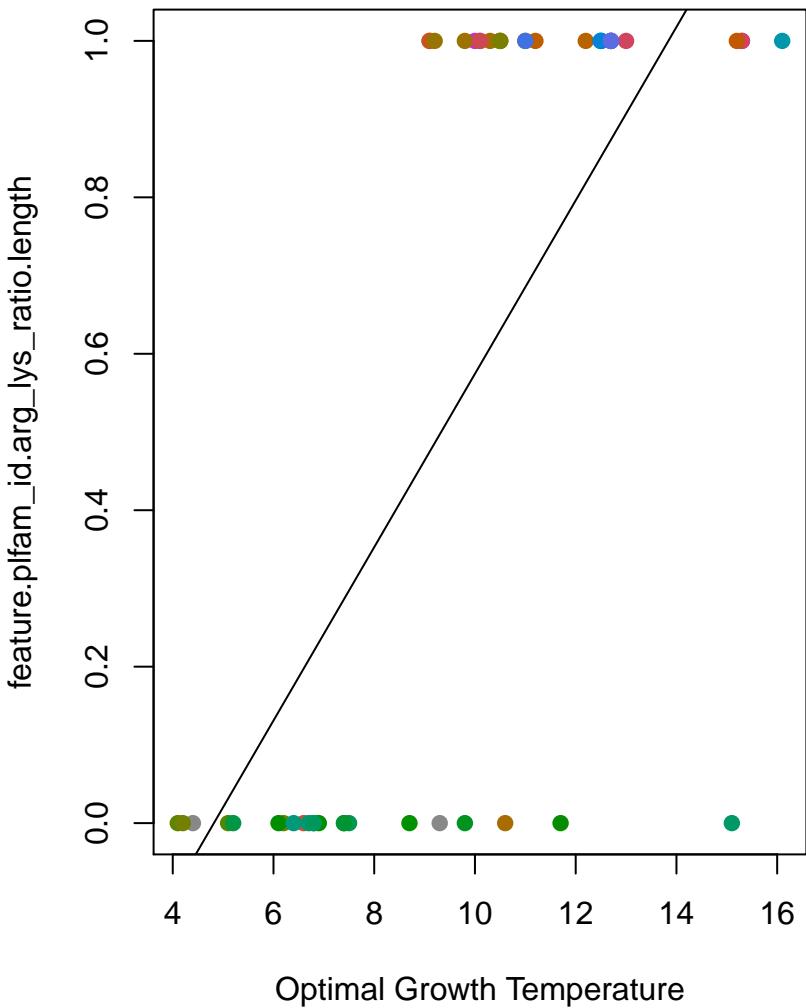
Optimal Growth Temperature

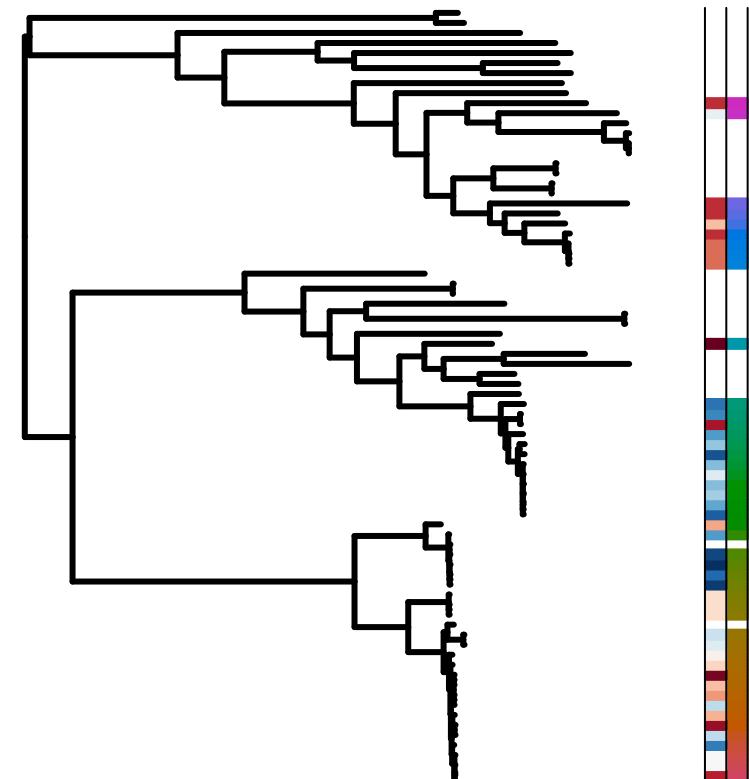
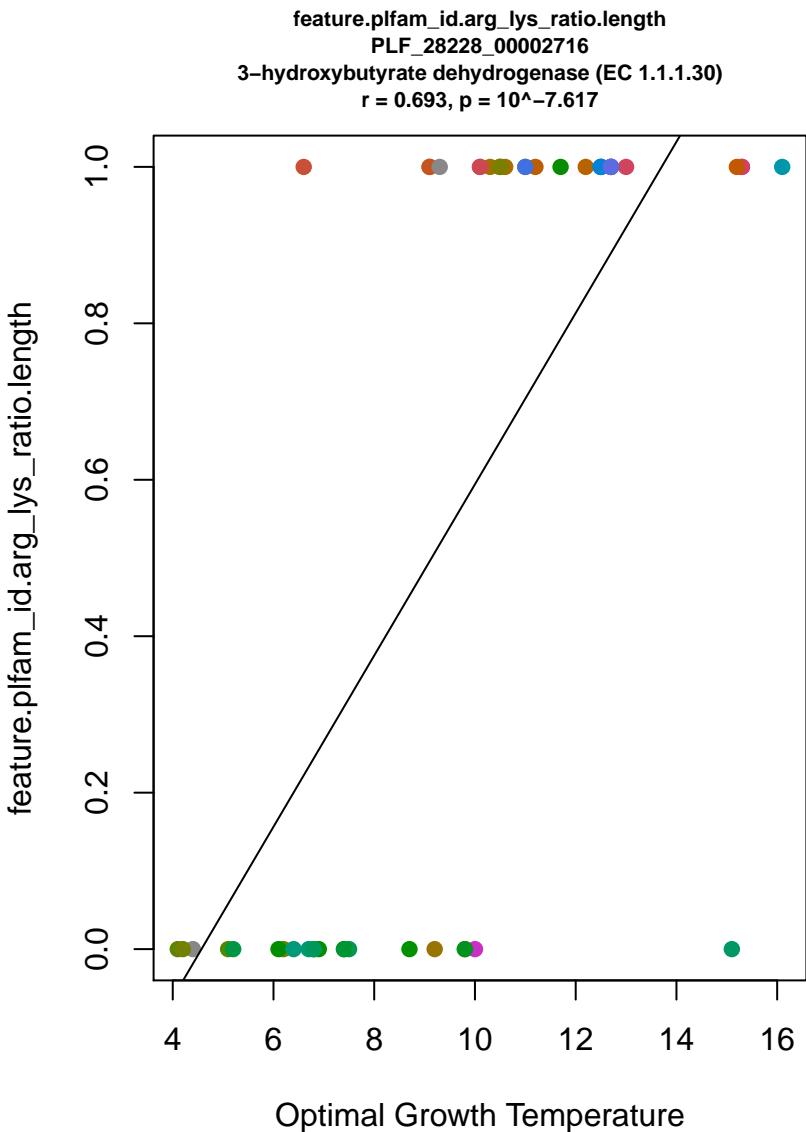


feature.plfam_id.arg_lyc_ratio.length



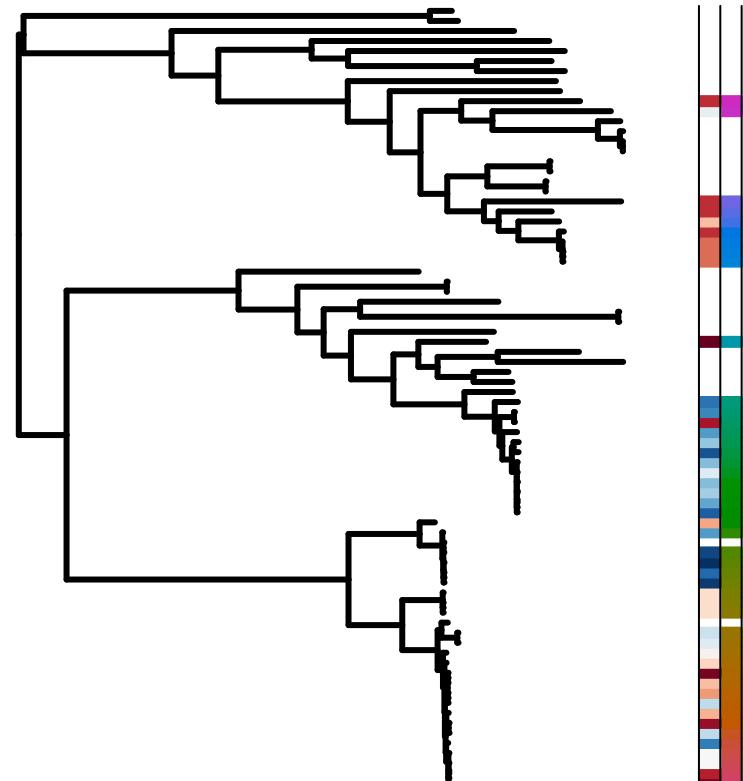
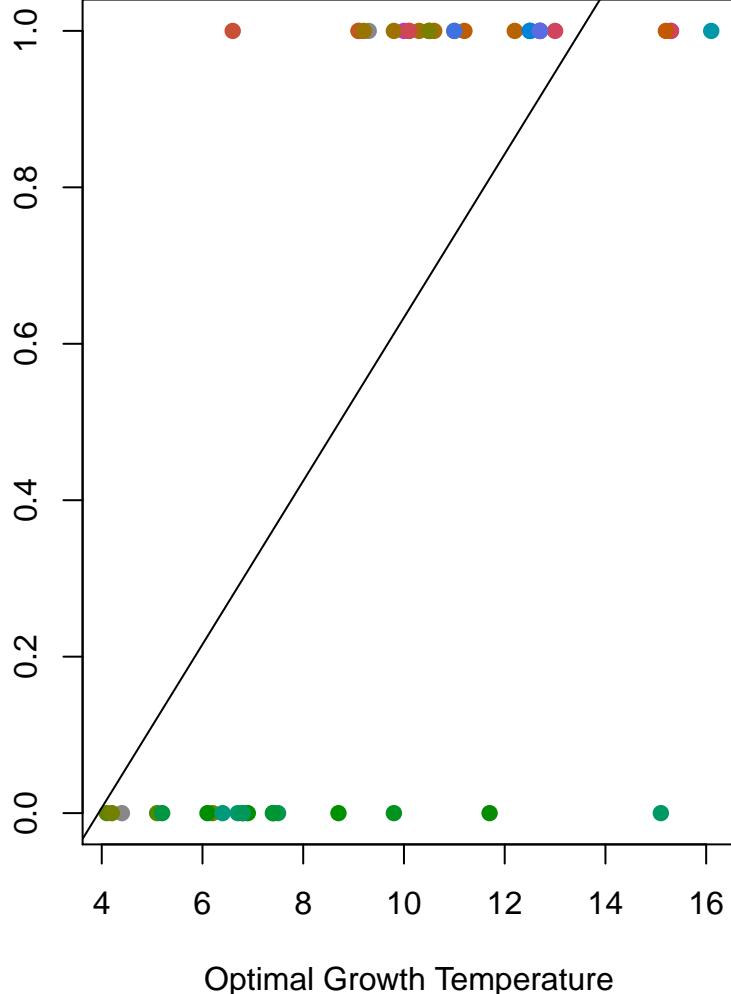
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00000882
General secretion pathway protein L
 $r = 0.698$, $p = 10^{-7.752}$



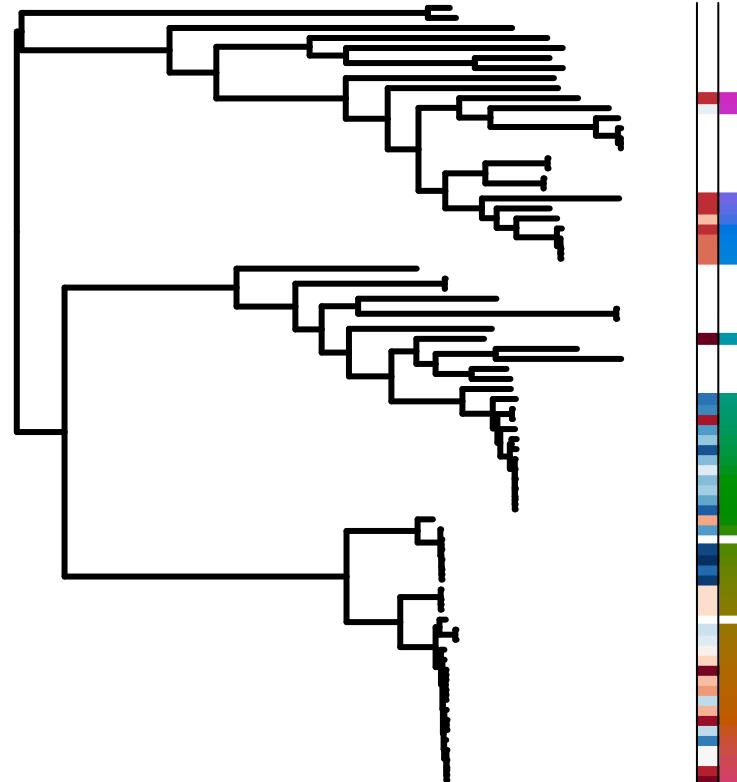
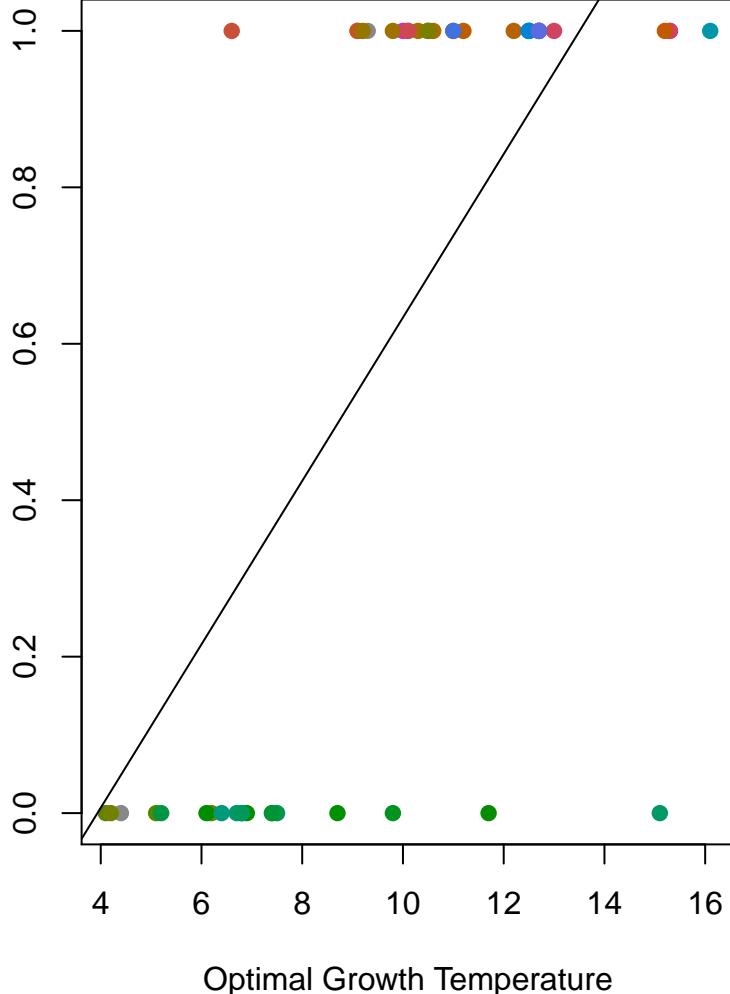


feature.plfam_id.arg_lys_ratio.length
PLF_28228_00001431
Acyltransferase
 $r = 0.673$, $p = 10^{-7.058}$

feature.plfam_id.arg_lys_ratio.length

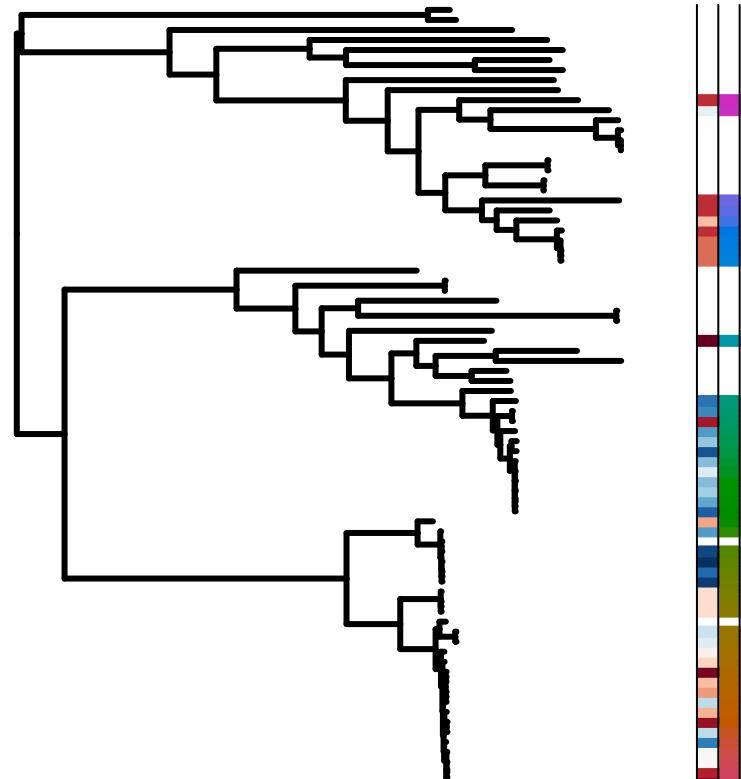
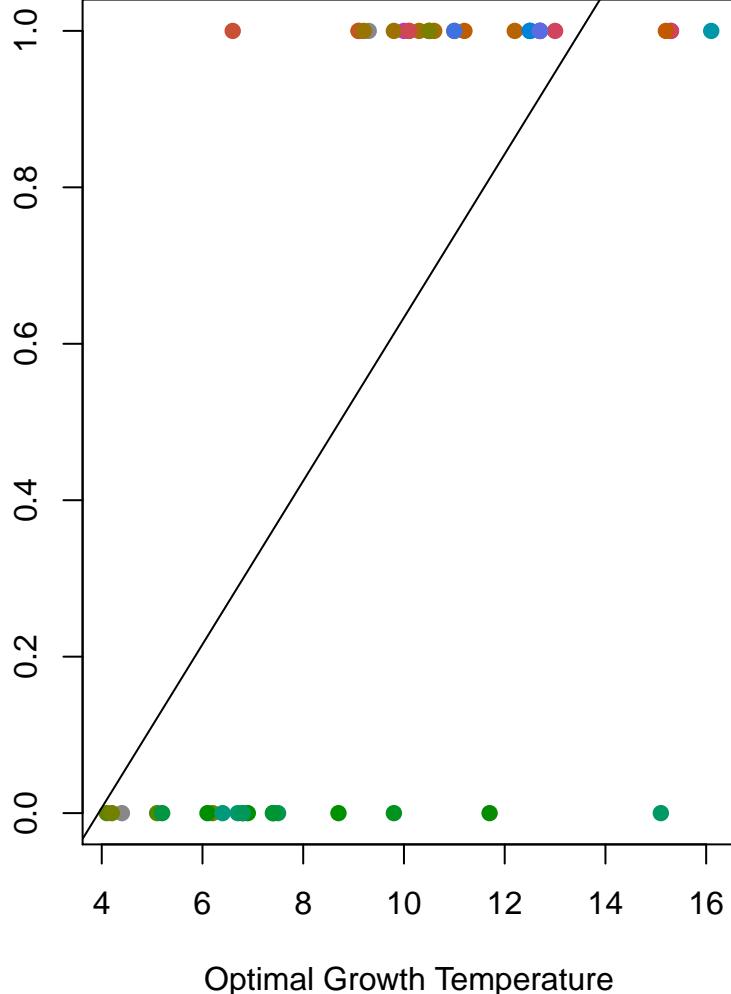


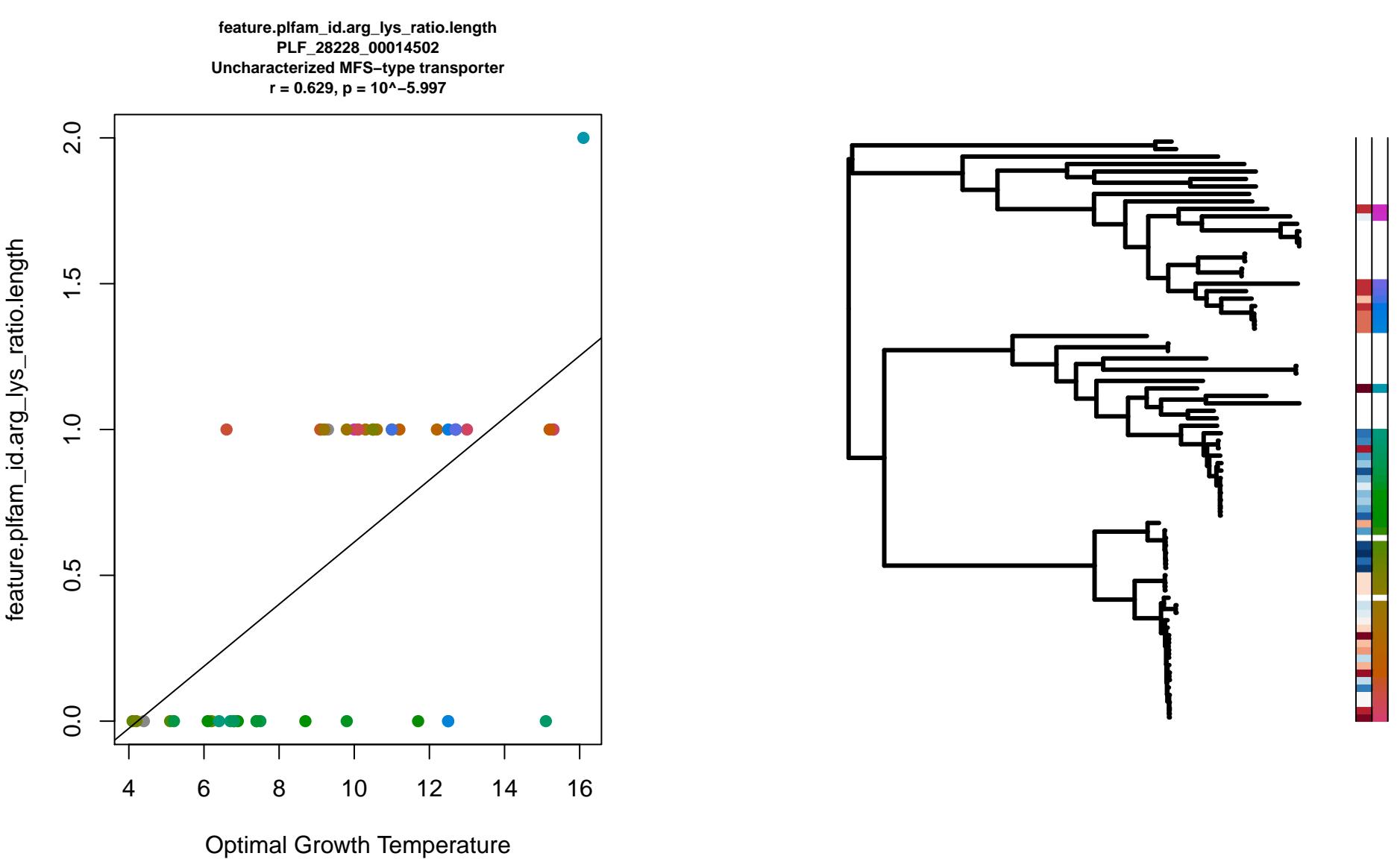
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00001492
Enoyl-CoA hydratase (EC 4.2.1.17)
 $r = 0.673$, $p = 10^{-7.058}$



feature.plfam_id.arg_lys_ratio.length
PLF_28228_00001694
Chorismate--pyruvate lyase (EC 4.1.3.40)
 $r = 0.673$, $p = 10^{-7.058}$

feature.plfam_id.arg_lys_ratio.length





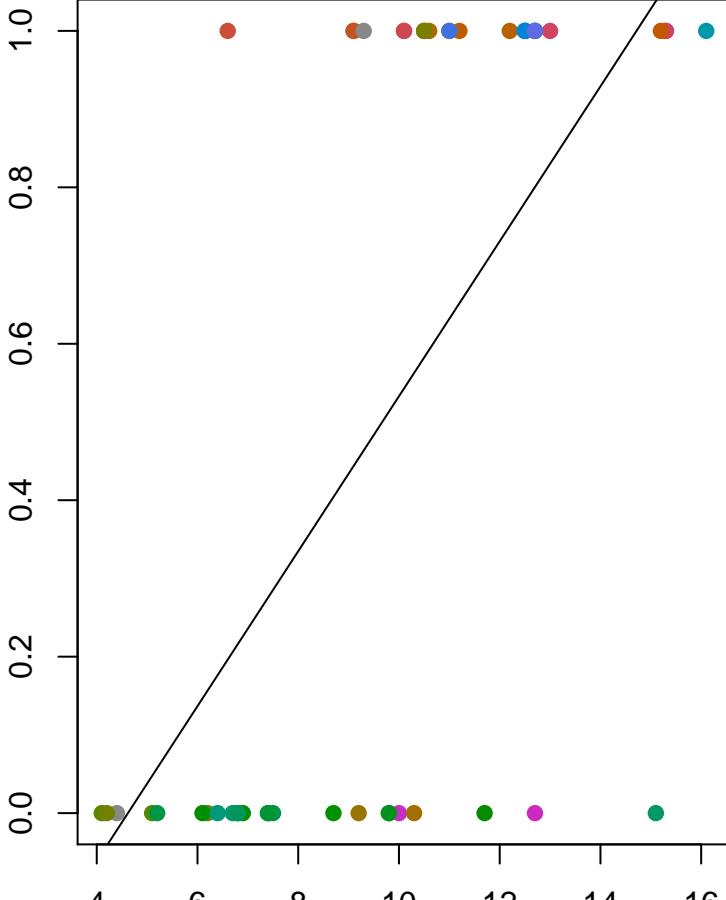
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PLF_28228_00003362

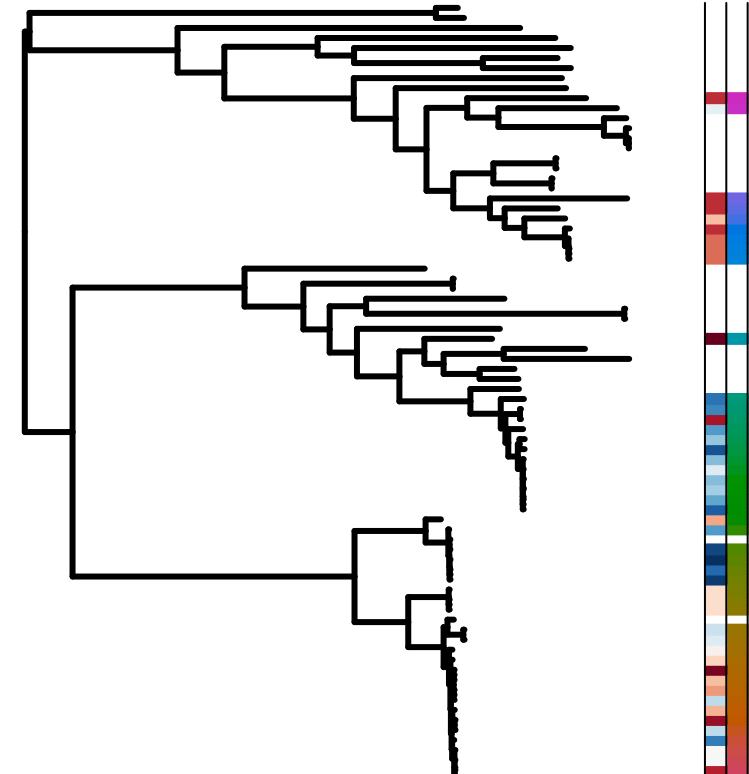
Nitric oxide reductase activation protein NorE

$r = 0.62, p = 10^{-5.795}$

feature.plfam_id.arg_lys_ratio.length



Optimal Growth Temperature



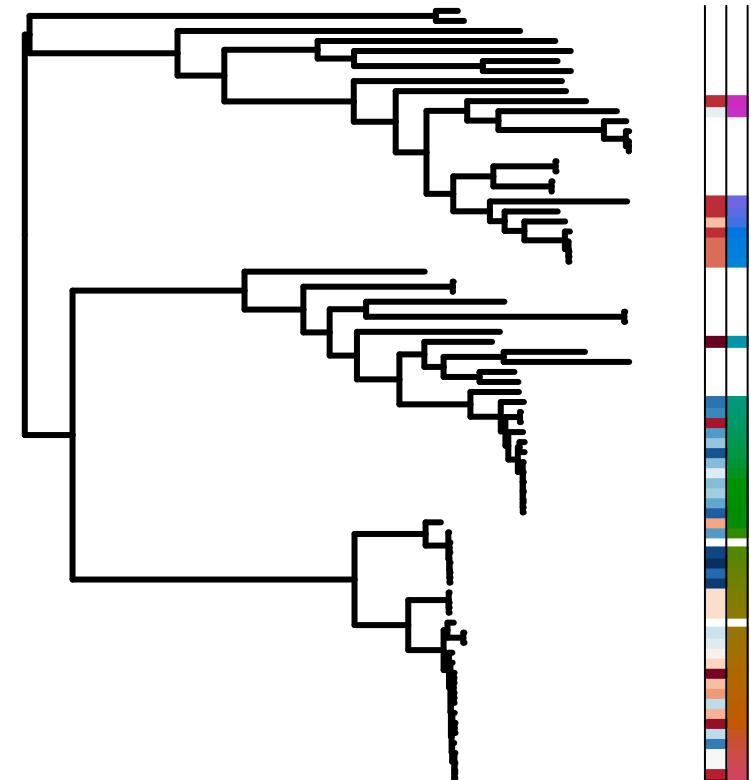
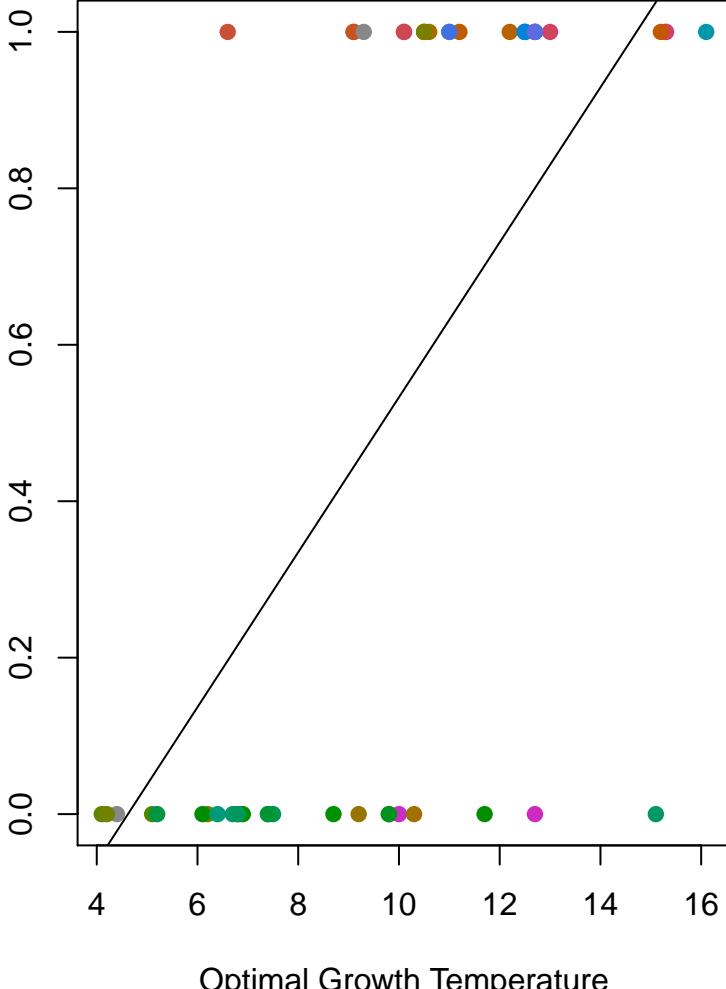
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PLF_28228_00003364

Nitric oxide reductase activation protein NorF

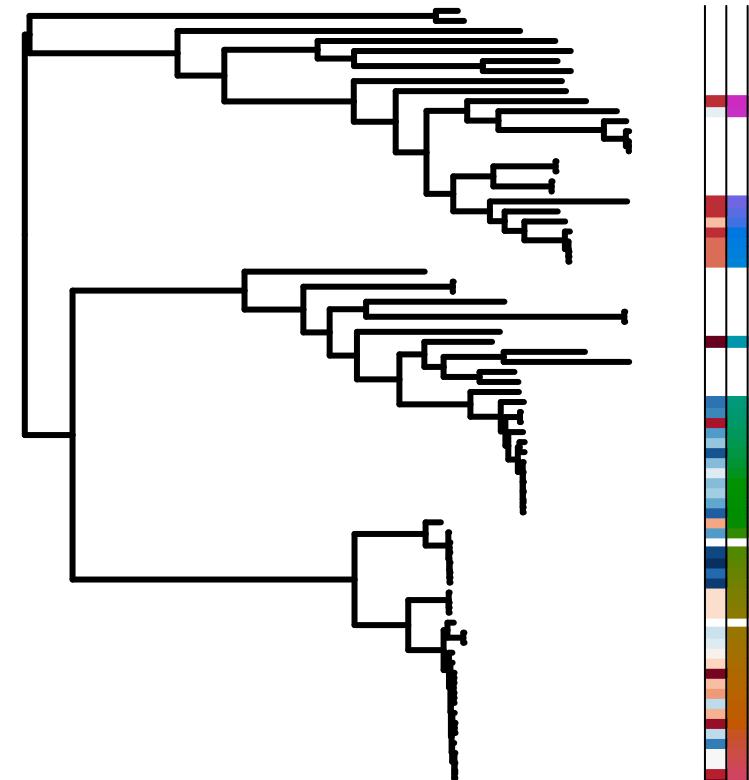
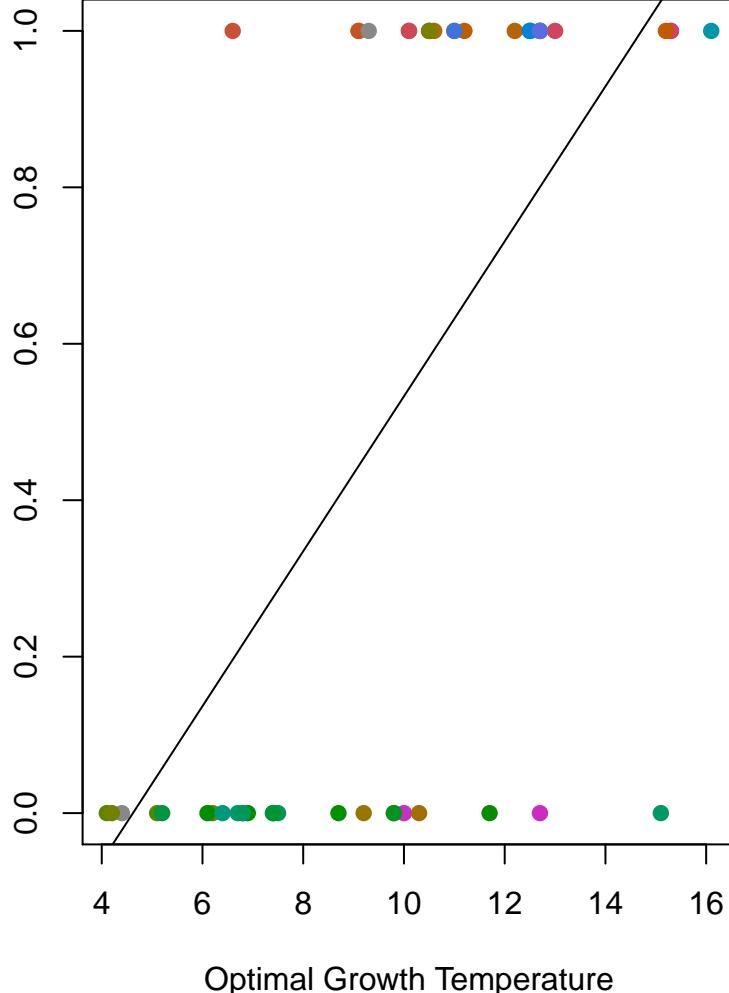
$r = 0.62, p = 10^{-5.795}$

feature.plfam_id.arg_lys_ratio.length



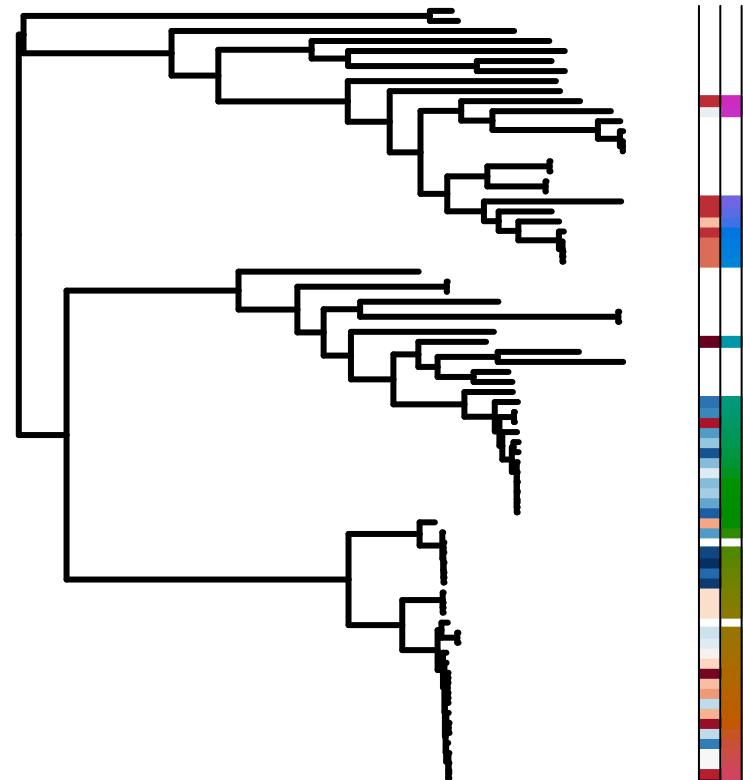
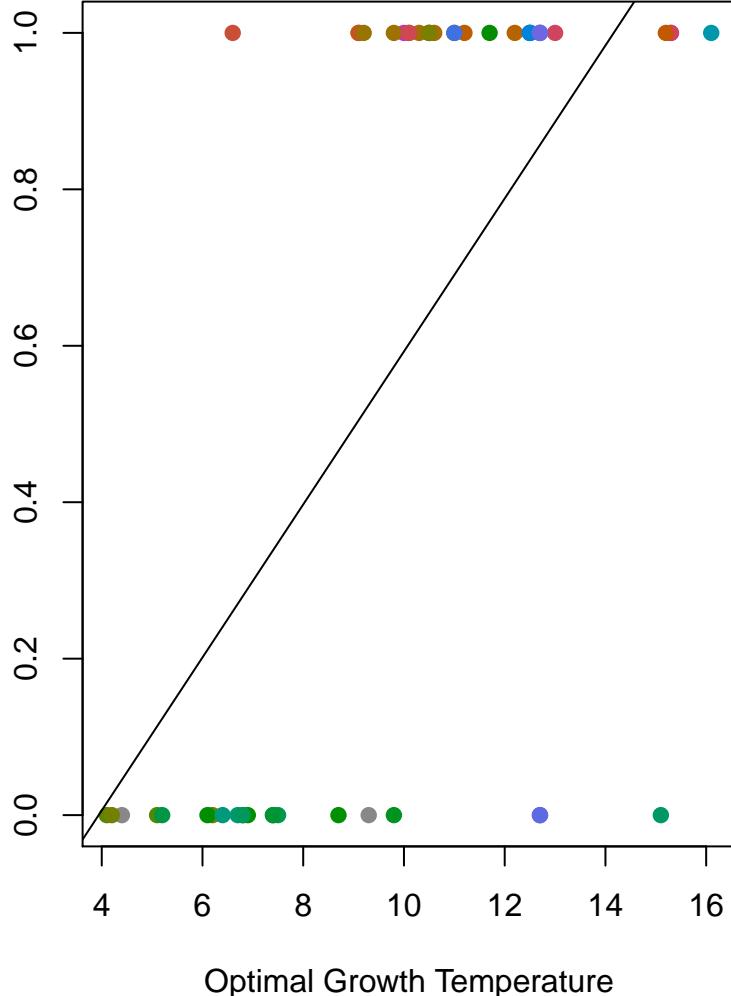
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00003367
Nitric-oxide reductase subunit C (EC 1.7.99.7)
 $r = 0.62, p = 10^{-5.795}$

feature.plfam_id.arg_lys_ratio.length

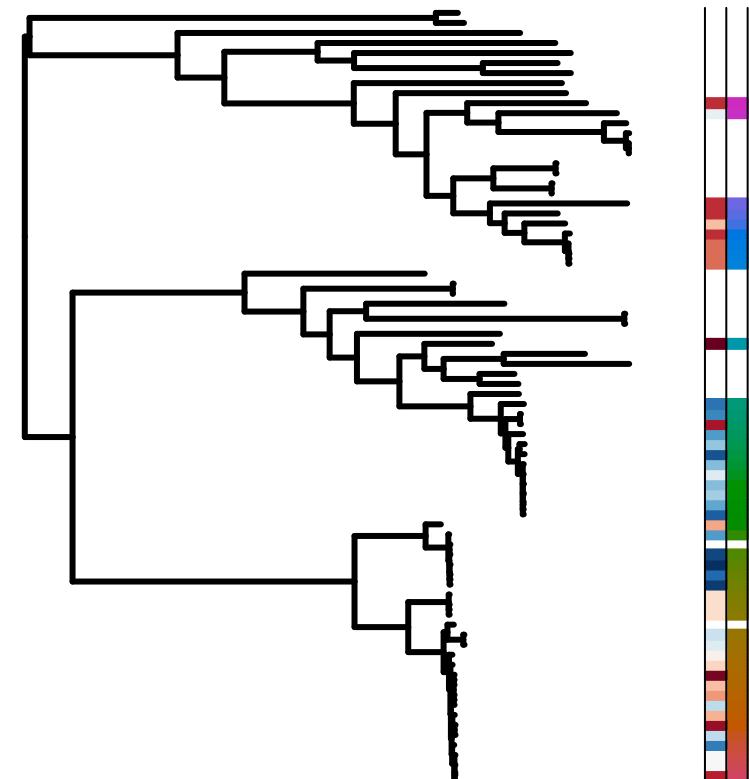
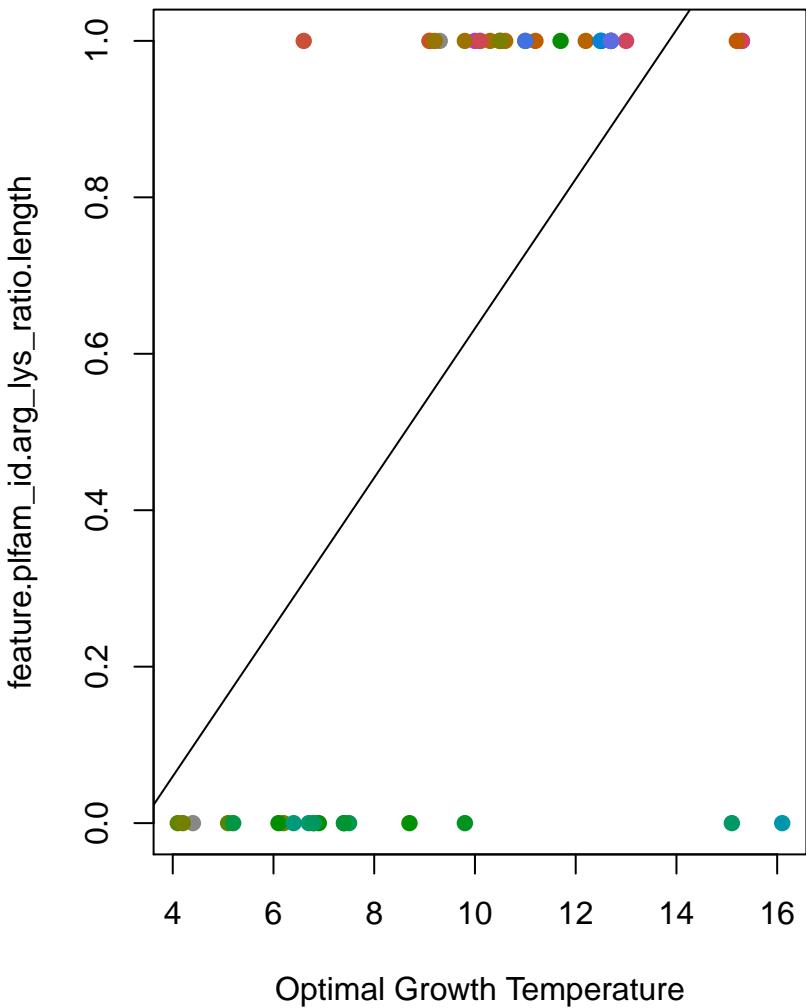


feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002988
hypothetical protein
 $r = 0.619, p = 10^{-5.788}$

feature.plfam_id.arg_lys_ratio.length



feature.plfam_id.arg_lys_ratio.length
PLF_28228_00000912
Paraquat-inducible protein A
 $r = 0.615, p = 10^{-5.69}$



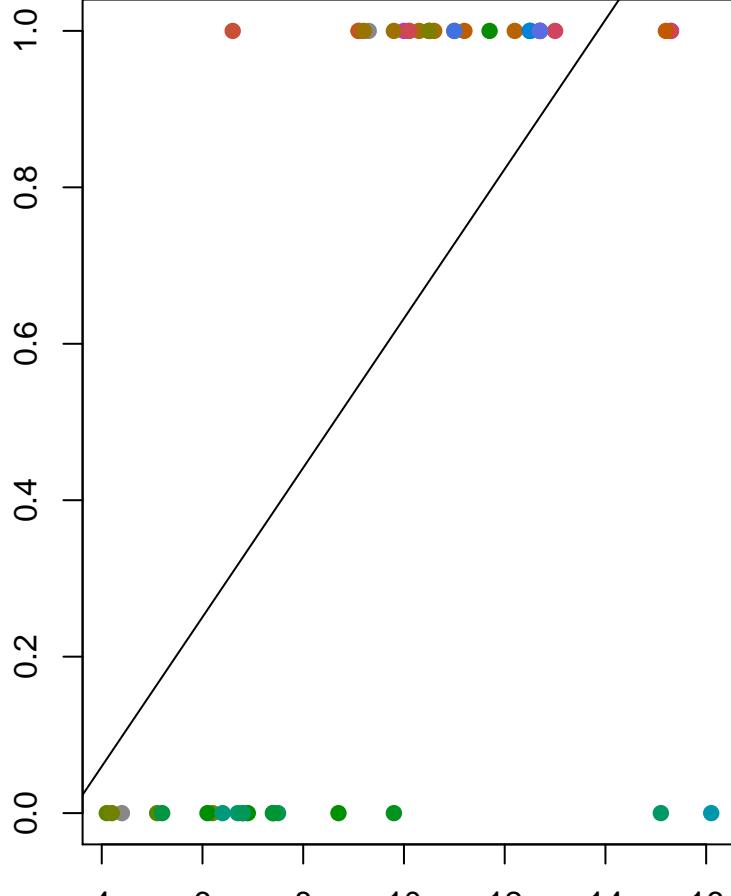
feature.plfam_id.arg_lys_ratio.length

PLF_28228_00000956

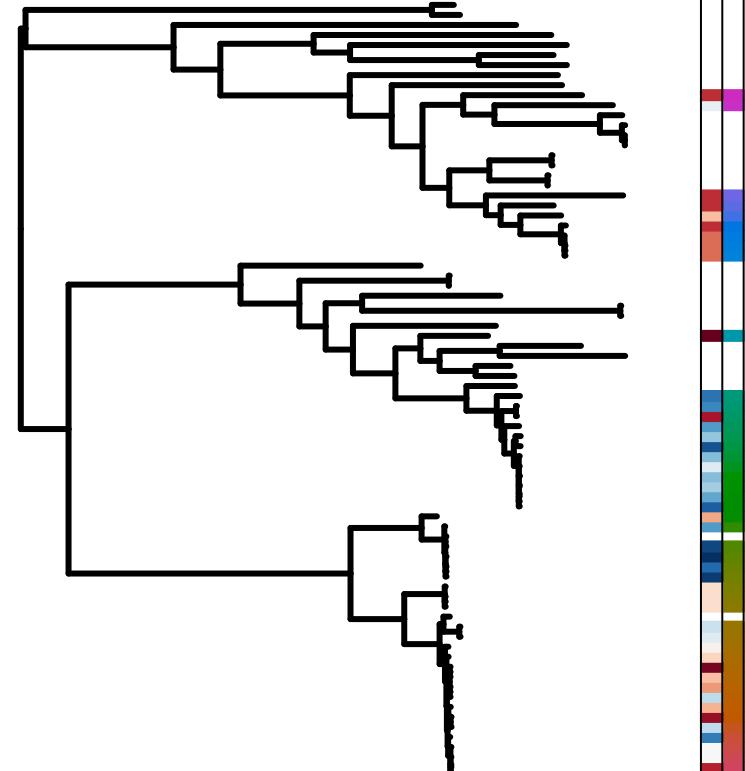
Phosphocarrier protein, nitrogen regulation associated

$r = 0.615, p = 10^{-5.69}$

feature.plfam_id.arg_lys_ratio.length



Optimal Growth Temperature



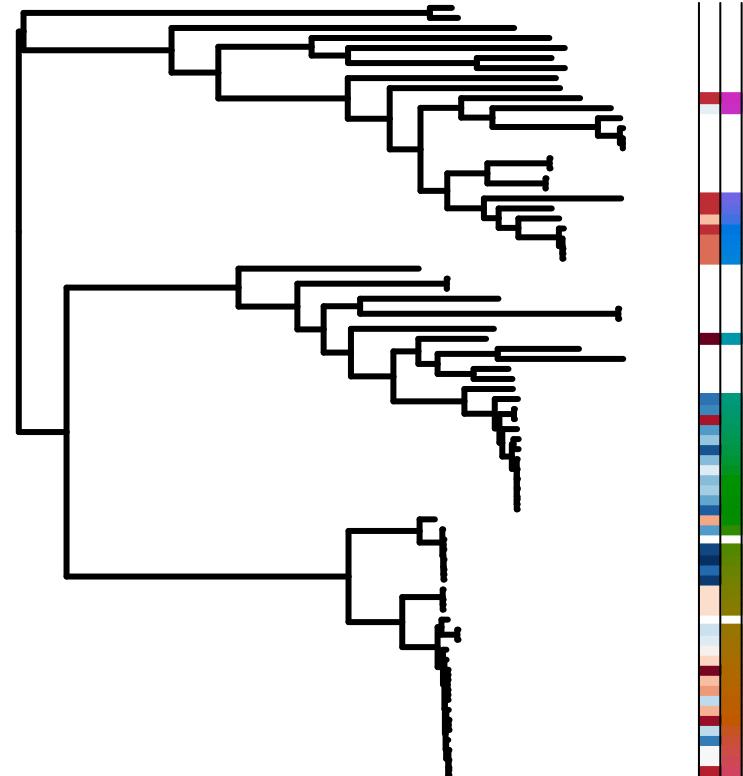
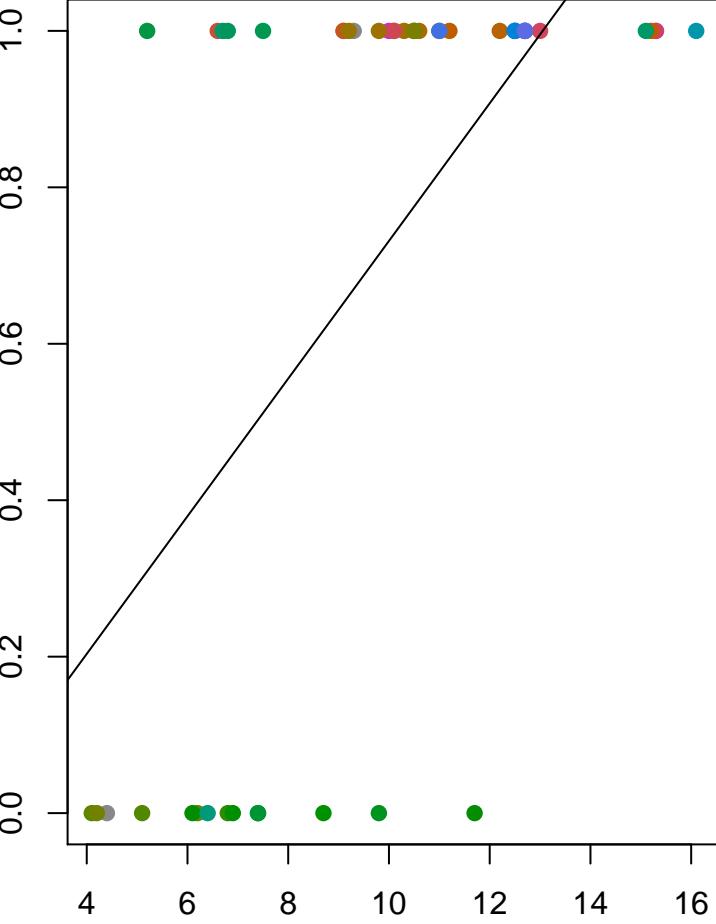
feature.plfam_id.arg_lys_ratio.length

PLF_28228_00001742

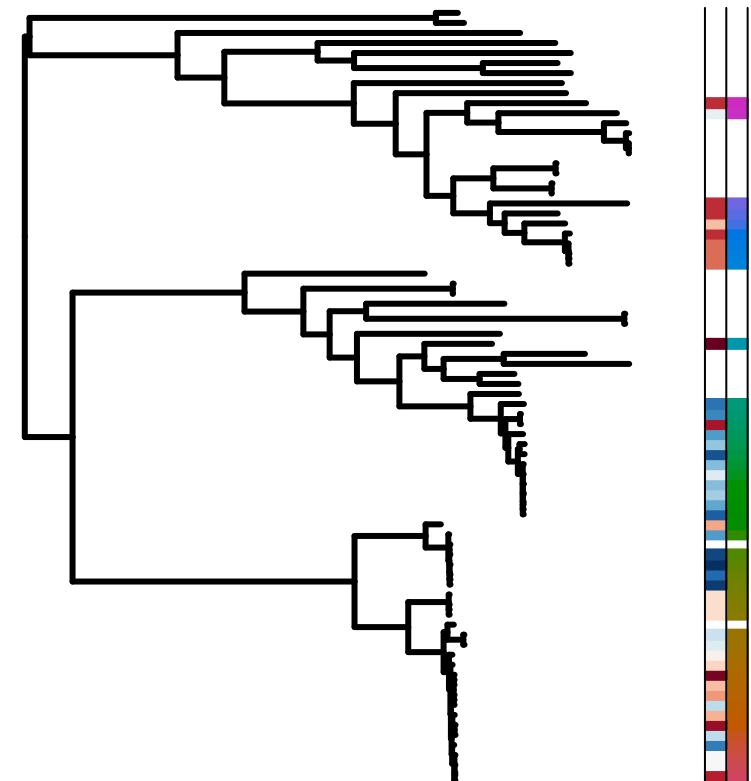
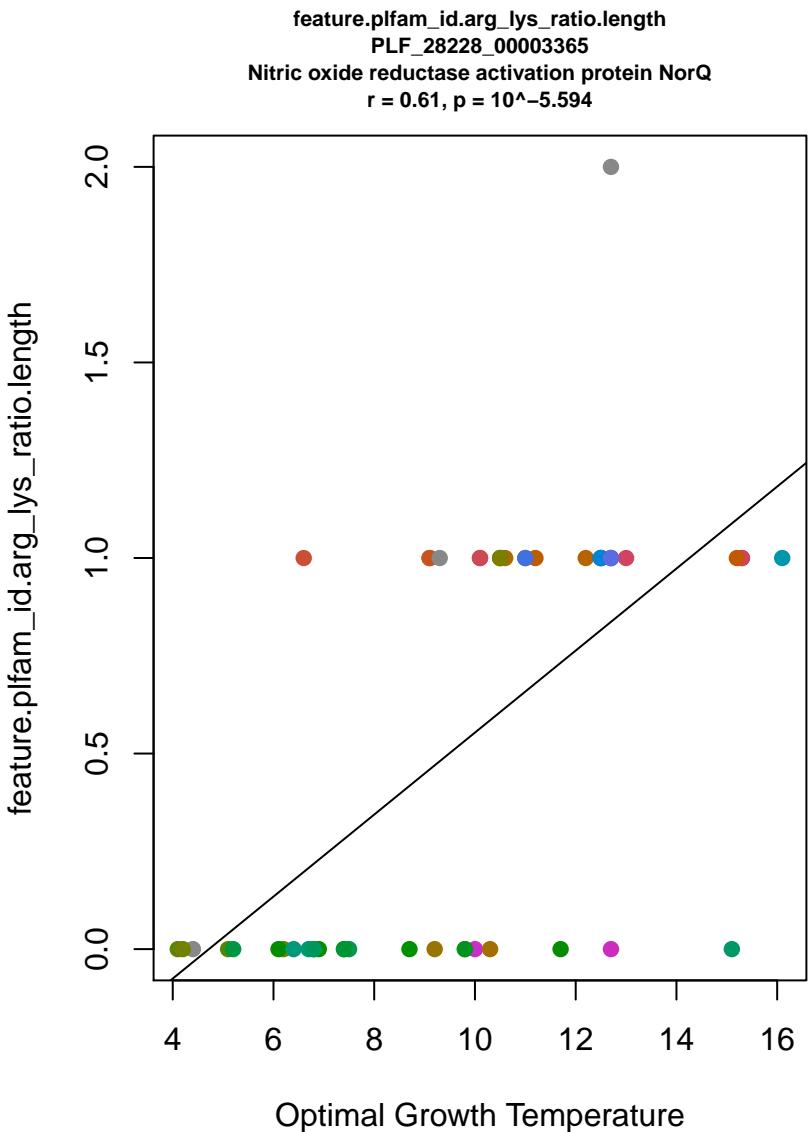
Molybdenum ABC transporter, substrate-binding protein ModA

$r = 0.613, p = 10^{-5.643}$

feature.plfam_id.arg_lys_ratio.length

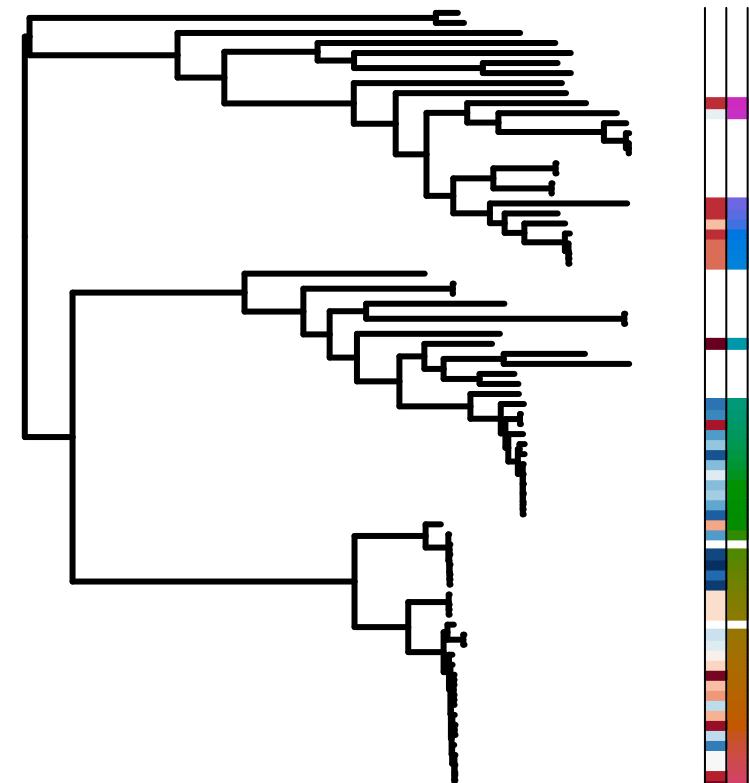
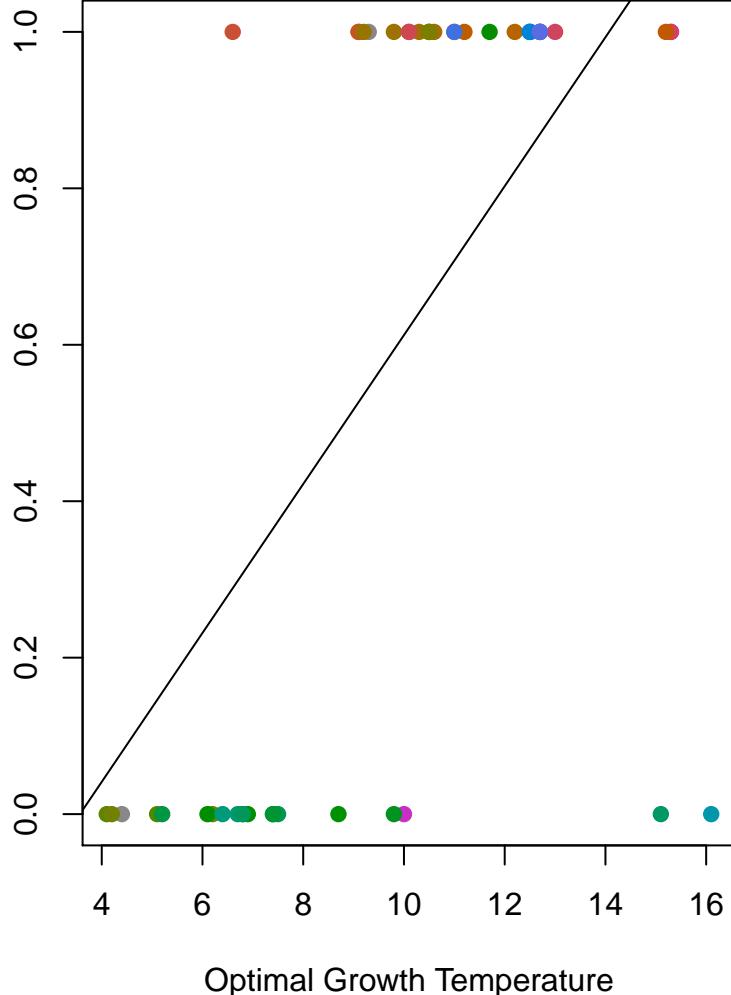


Optimal Growth Temperature



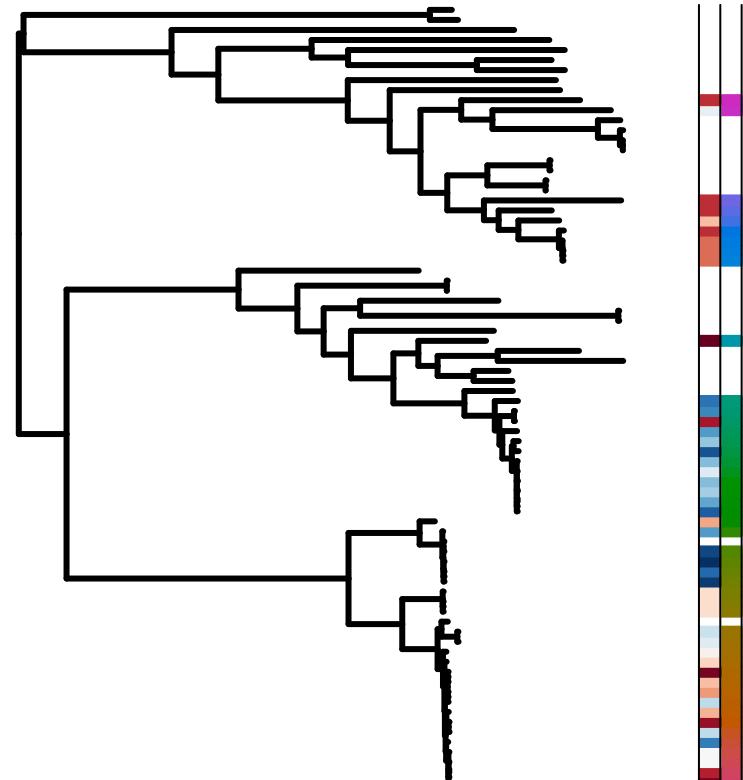
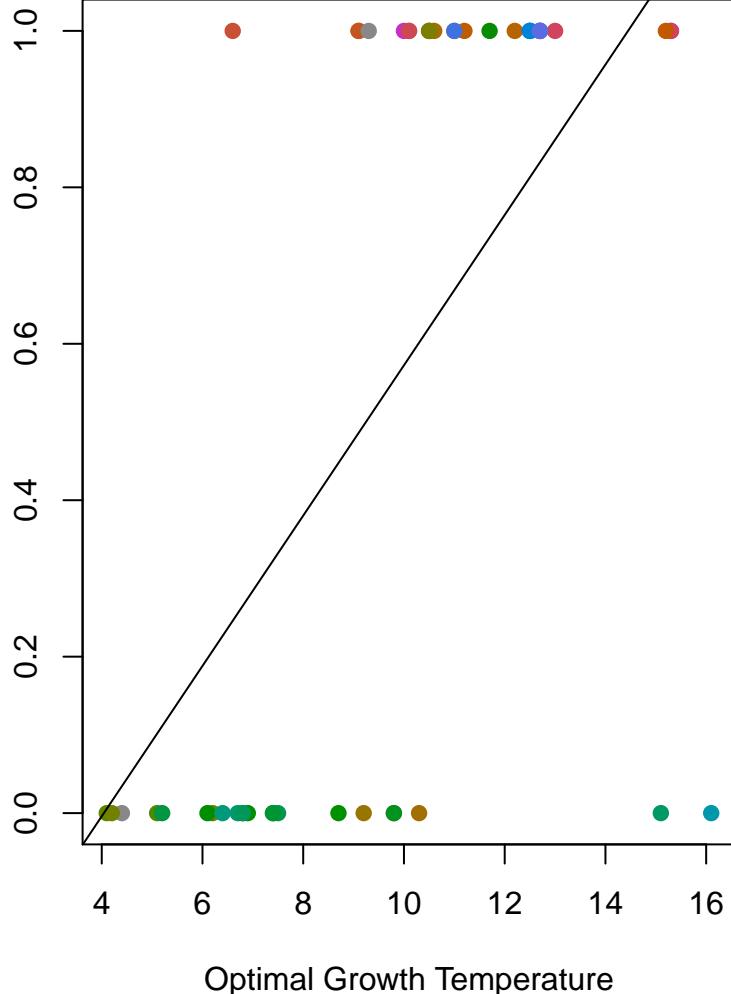
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002982
hypothetical protein
 $r = 0.607$, $p = 10^{-5.535}$

feature.plfam_id.arg_lys_ratio.length

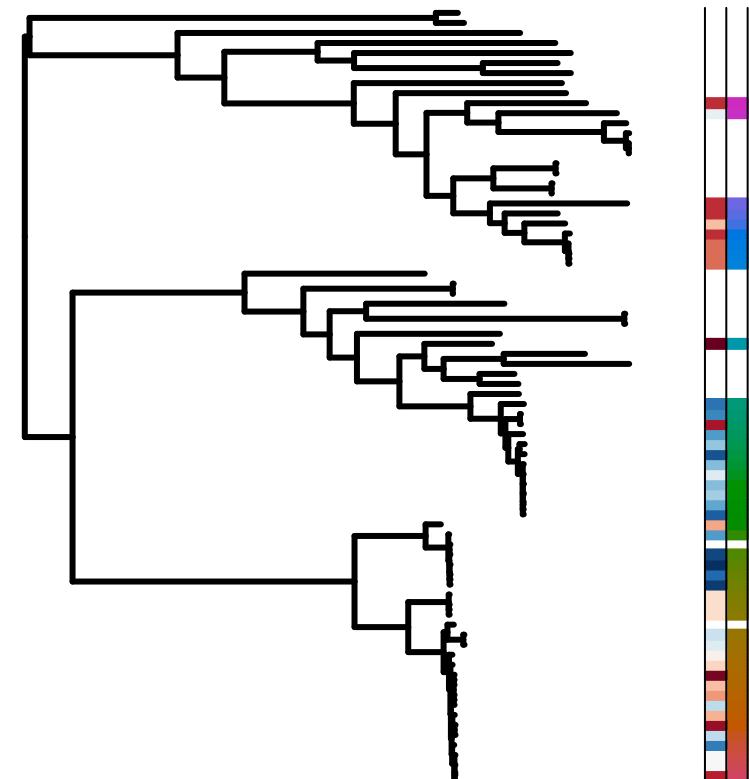
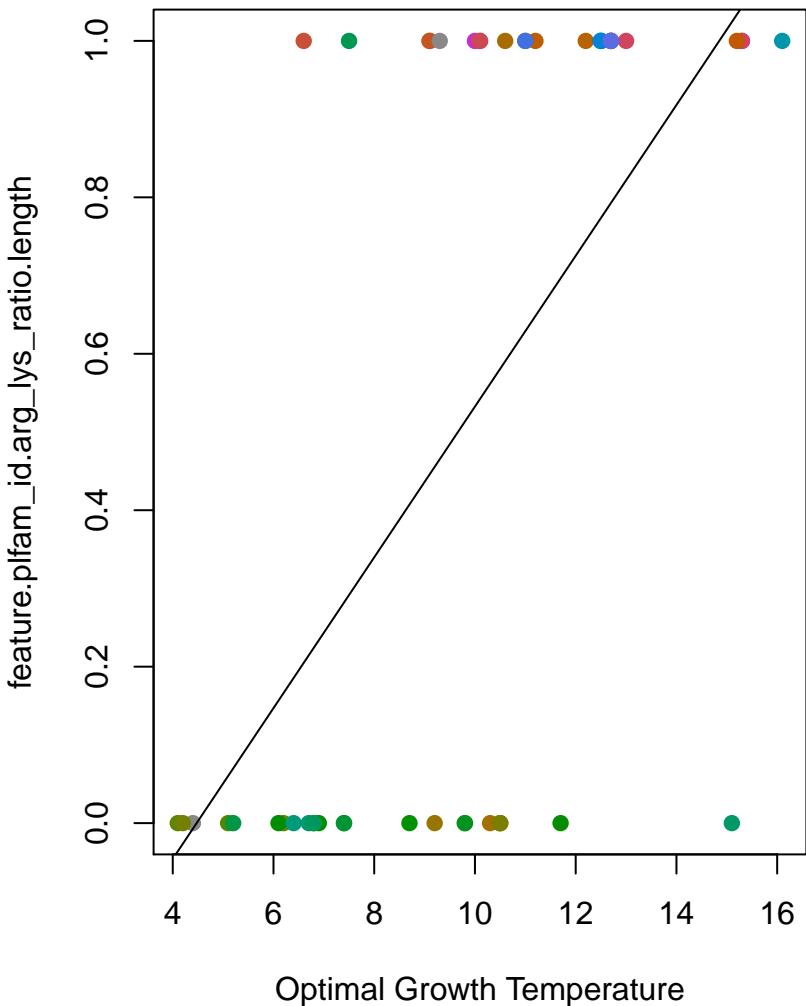


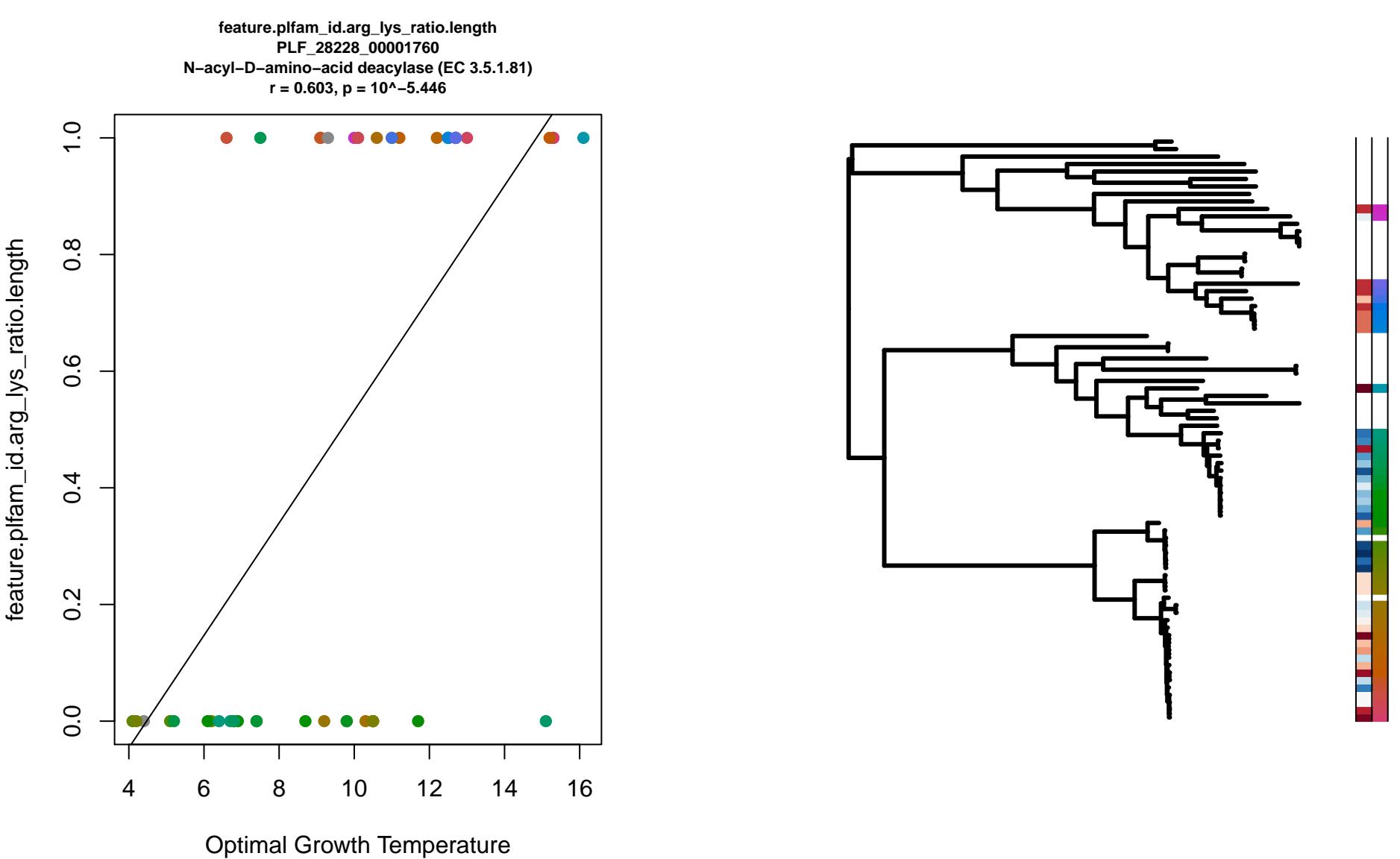
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00000171
hypothetical protein
 $r = 0.605, p = 10^{-5.489}$

feature.plfam_id.arg_lys_ratio.length



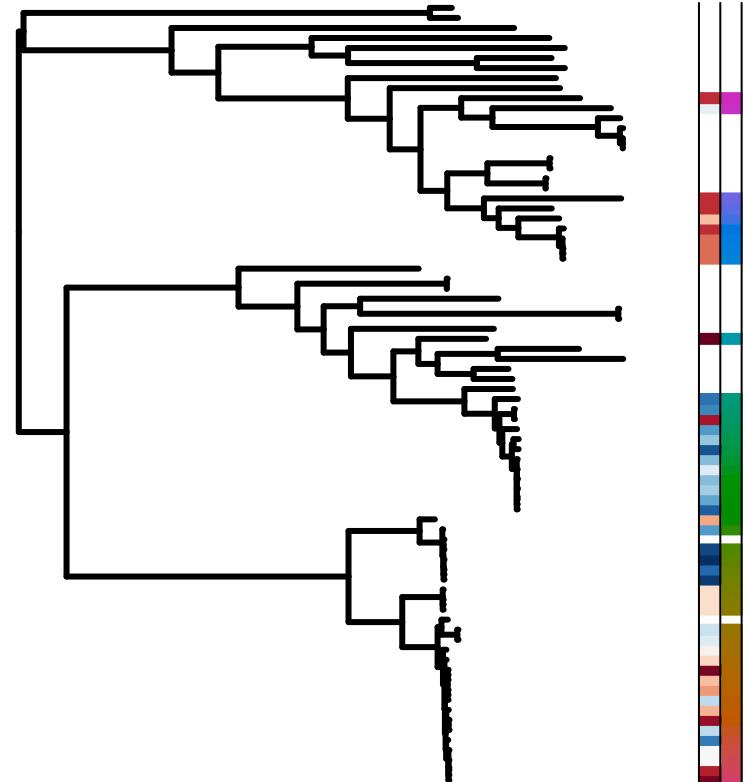
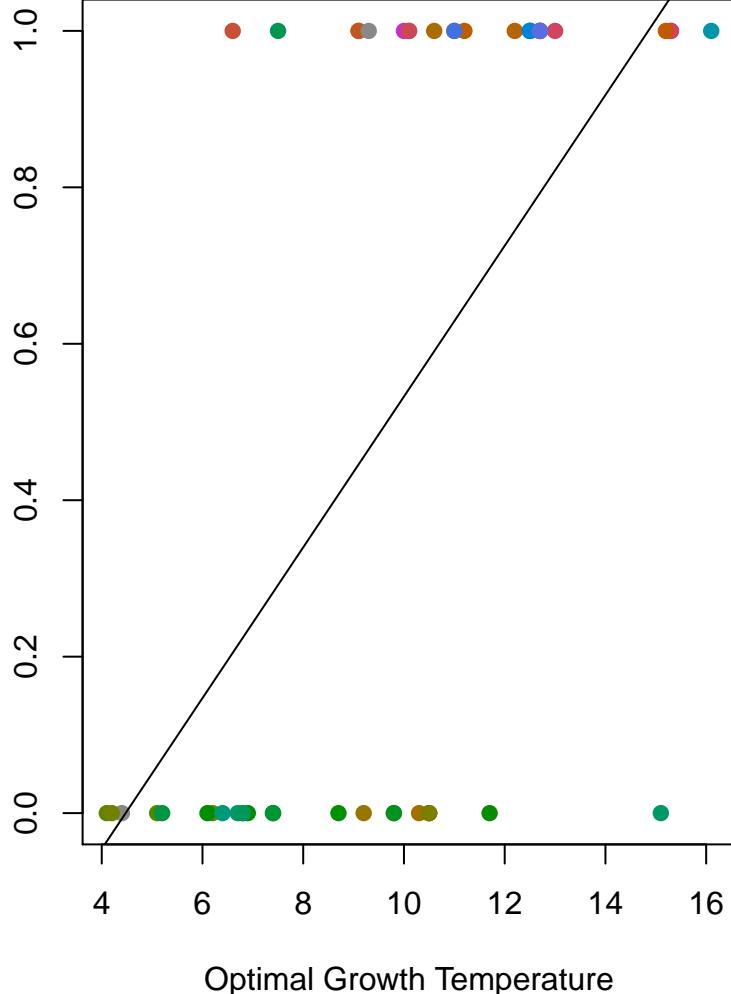
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00001673
Capsule biosynthesis protein capA
 $r = 0.603$, $p = 10^{-5.446}$



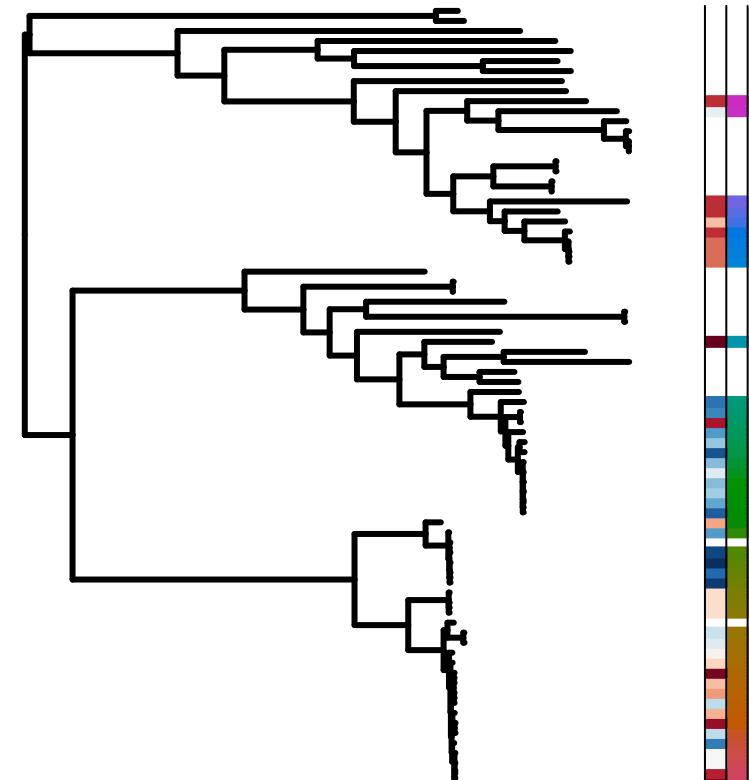
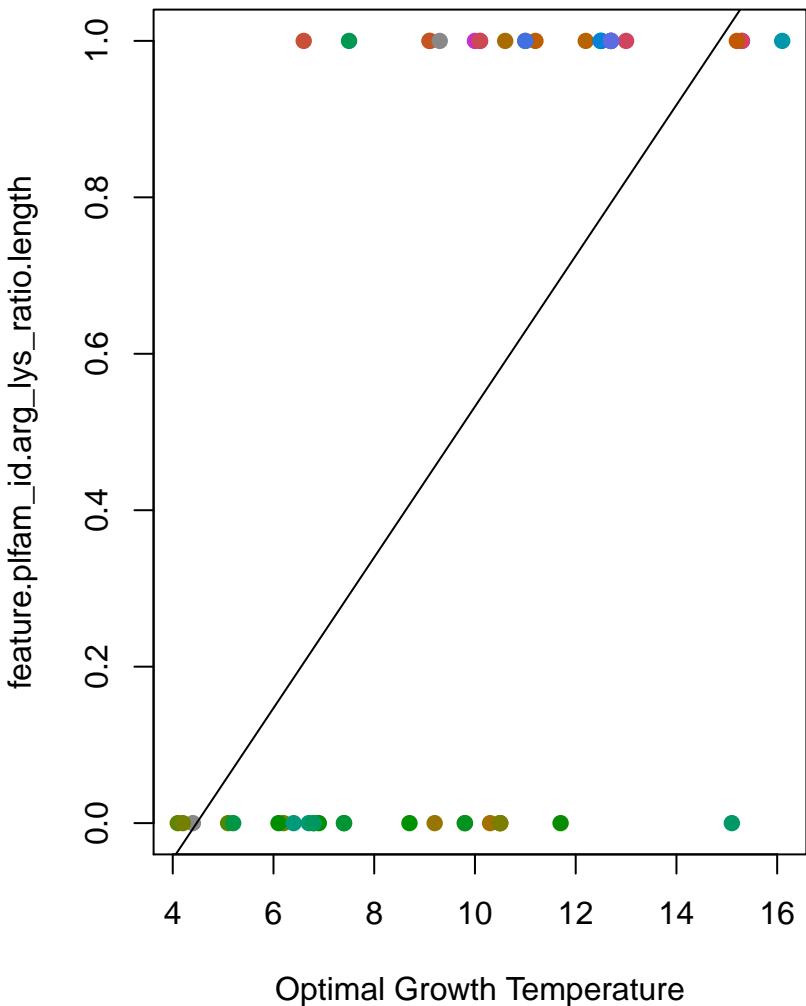


feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002077
Sodium/glutamate symporter
 $r = 0.603$, $p = 10^{-5.446}$

feature.plfam_id.arg_lys_ratio.length

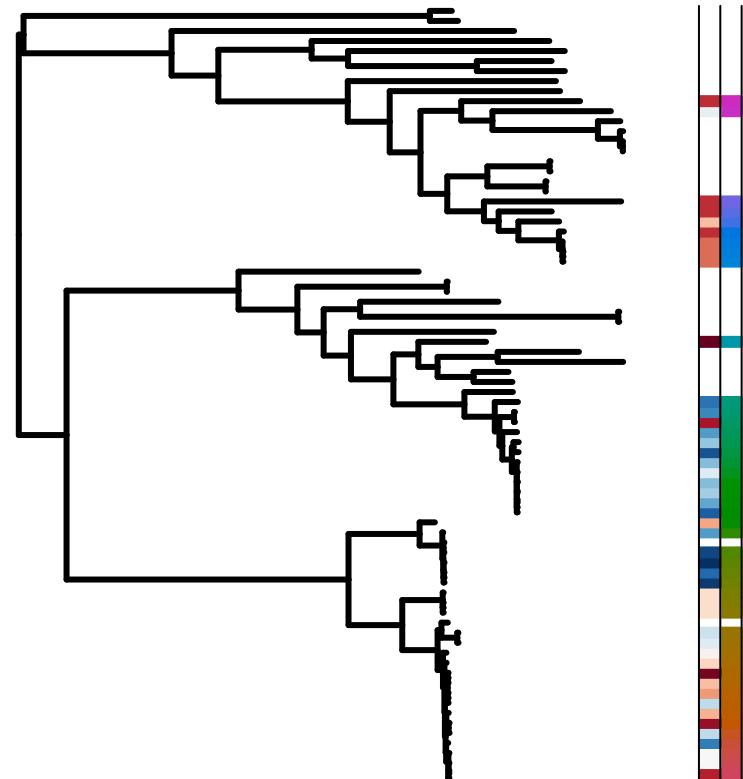
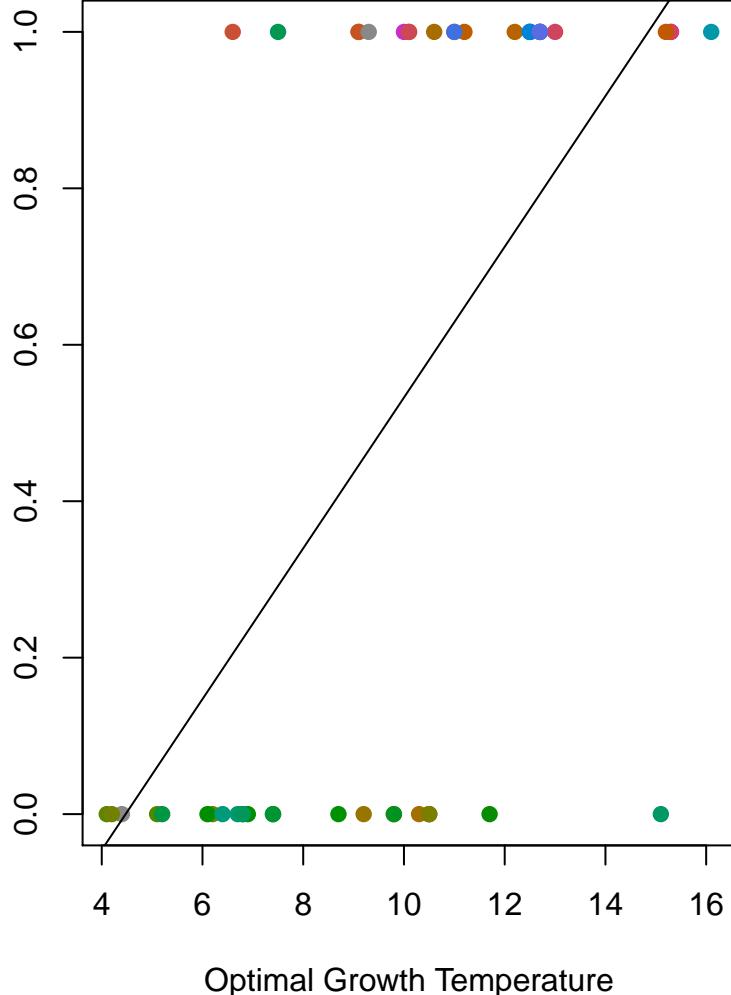


feature.plfam_id.arg_lyc_ratio.length
PLF_28228_00002147
Transcriptional regulator, LysR family
 $r = 0.603$, $p = 10^{-5.446}$

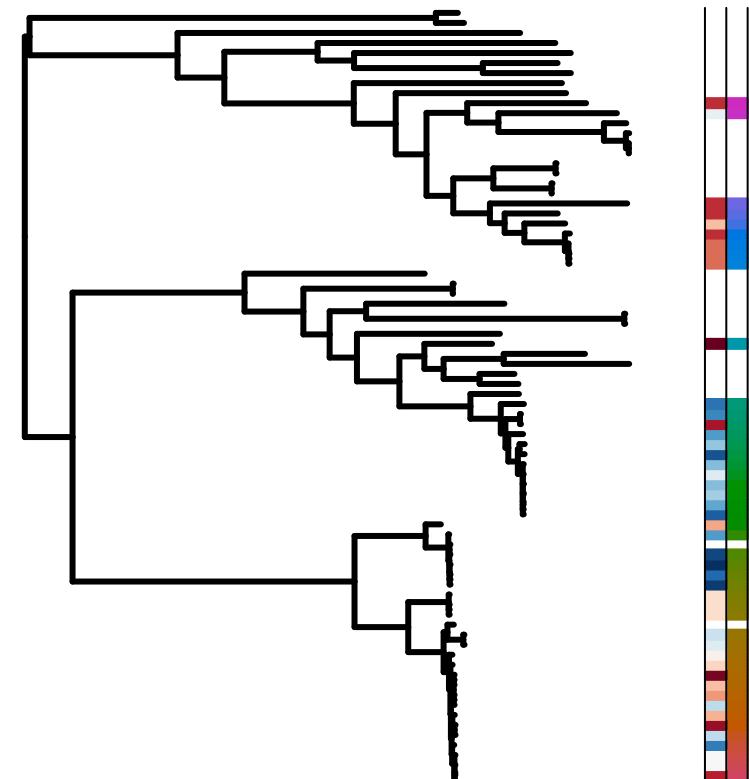
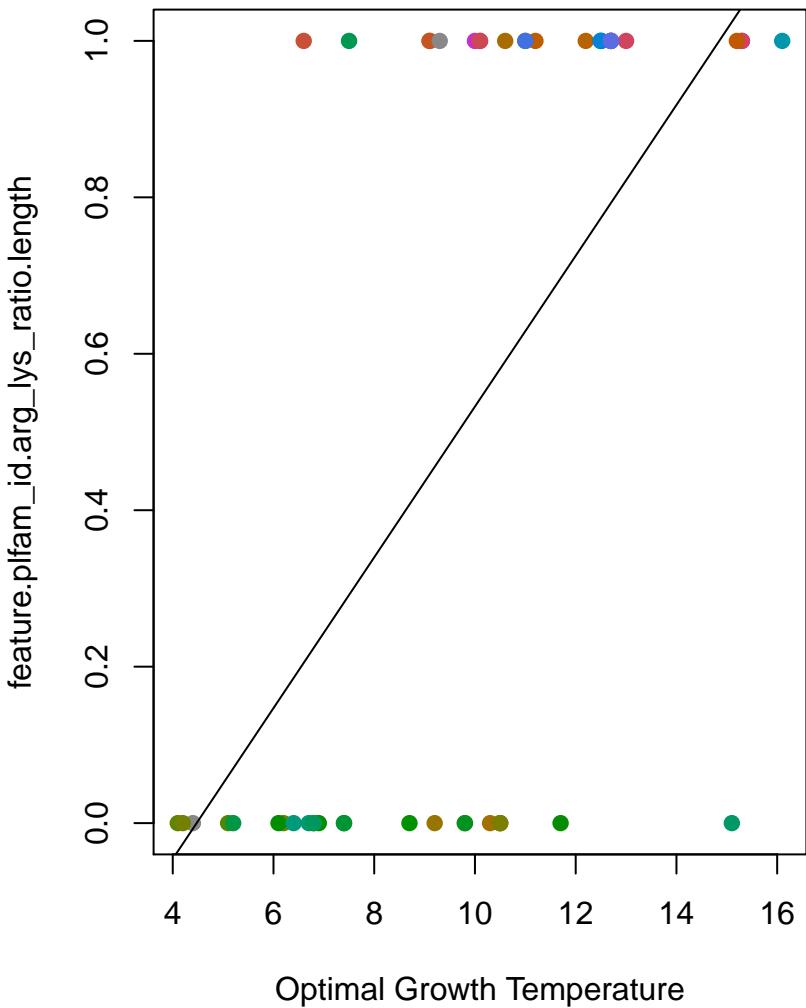


feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002319
hypothetical protein
 $r = 0.603$, $p = 10^{-5.446}$

feature.plfam_id.arg_lys_ratio.length

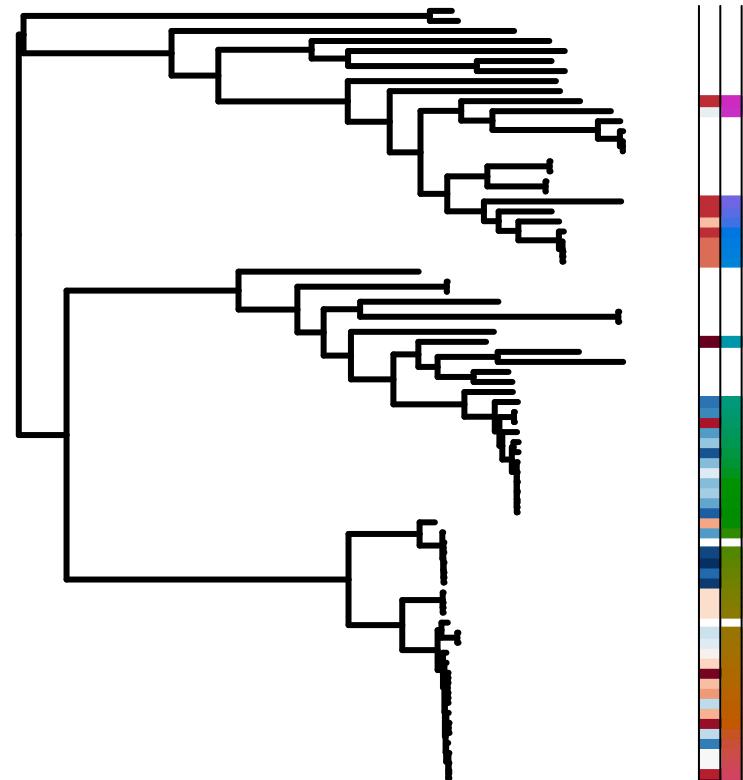
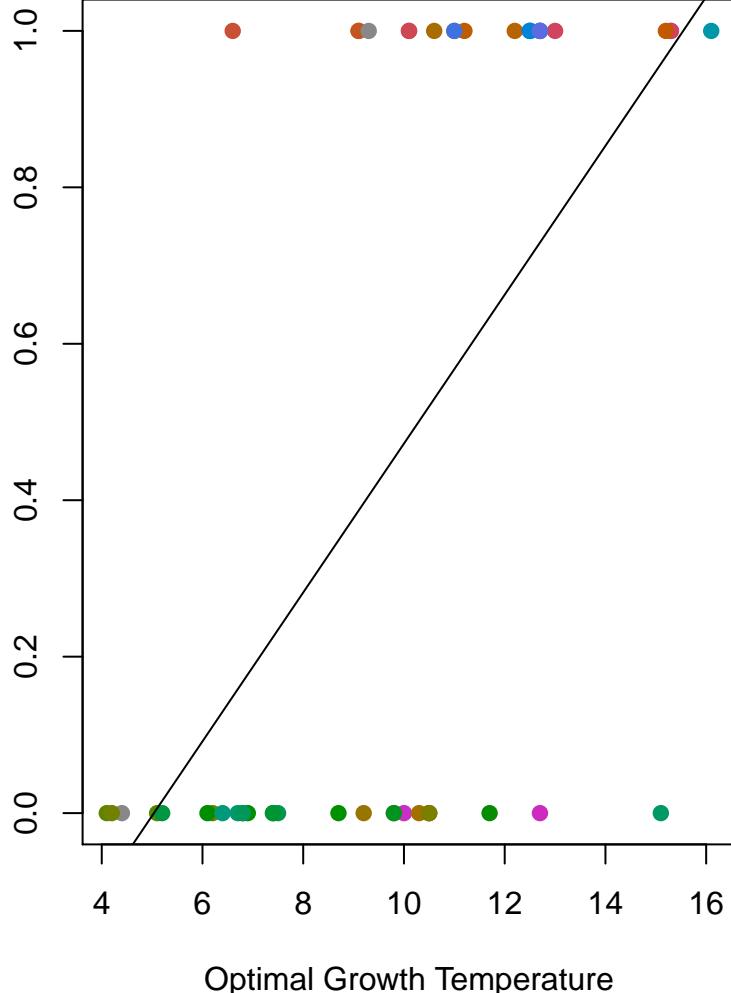


feature.plfam_id.arg_lys_ratio.length
PLF_28228_00003696
TonB-dependent receptor
 $r = 0.603$, $p = 10^{-5.446}$



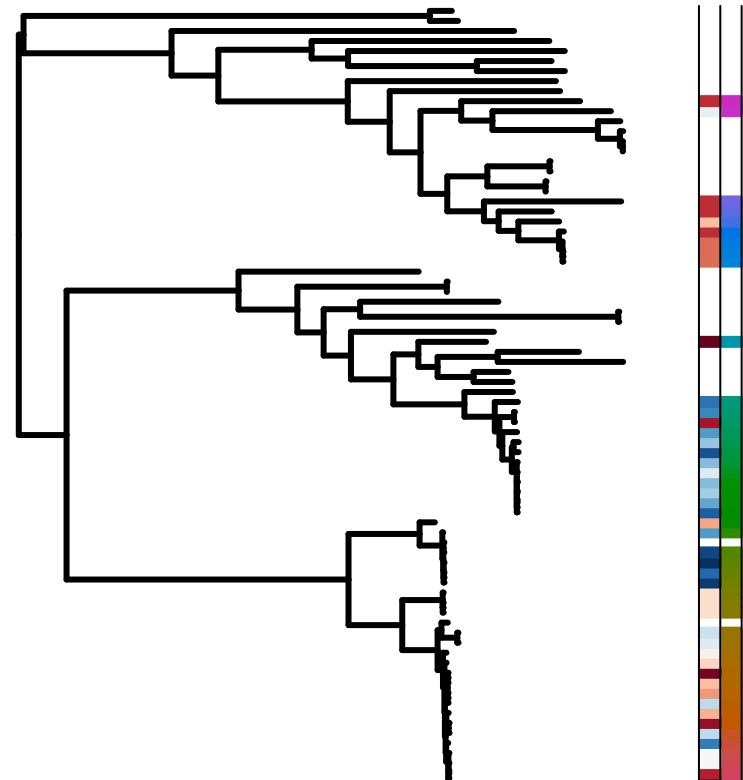
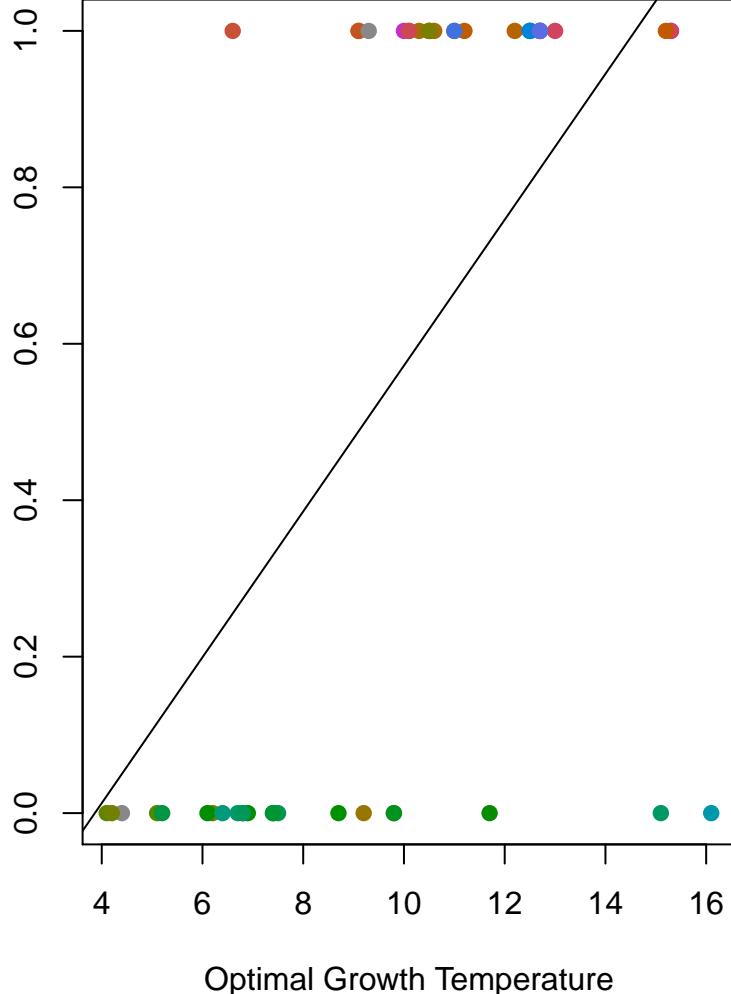
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00003208
Cytochrome c-type protein NapC
 $r = 0.597$, $p = 10^{-5.322}$

feature.plfam_id.arg_lys_ratio.length



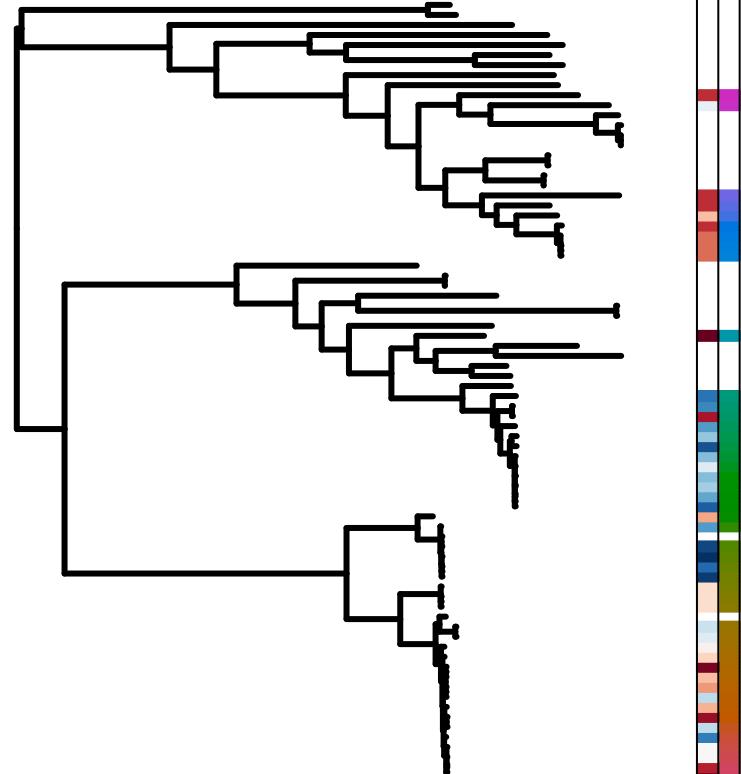
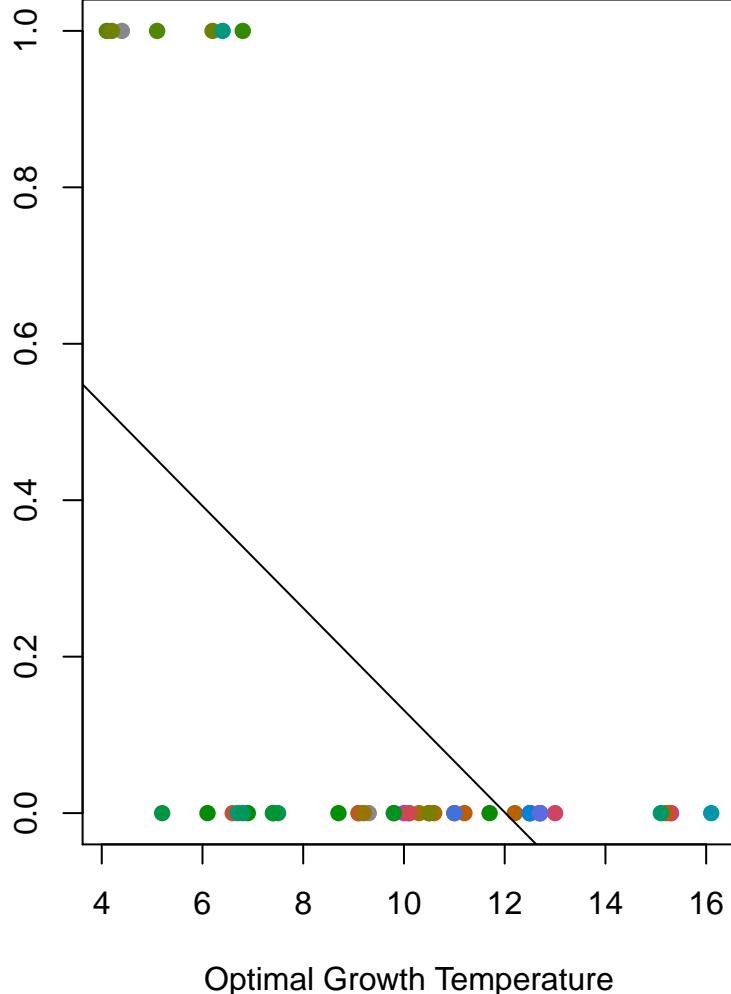
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002221
cytochrome c554
 $r = 0.587$, $p = 10^{-5.129}$

feature.plfam_id.arg_lys_ratio.length



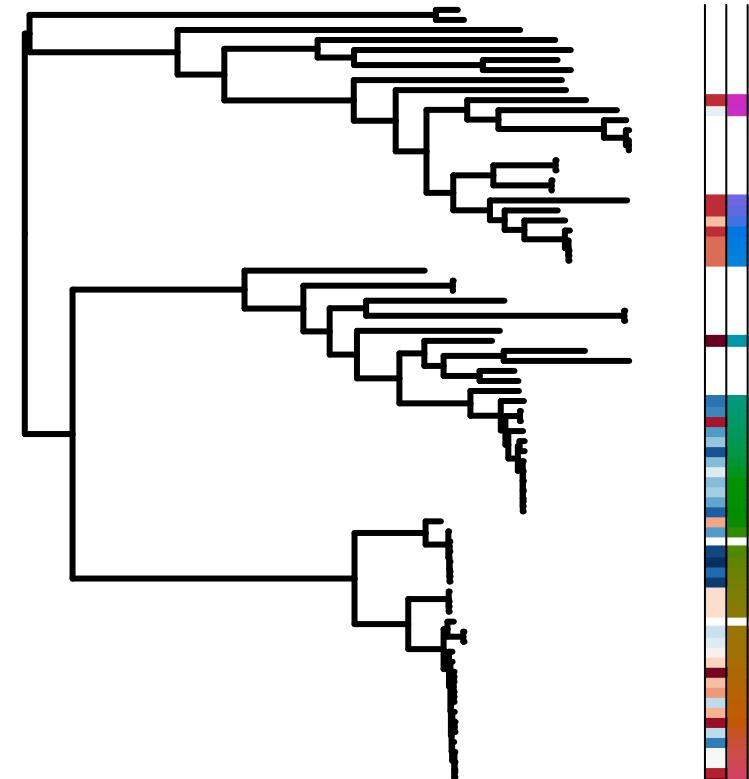
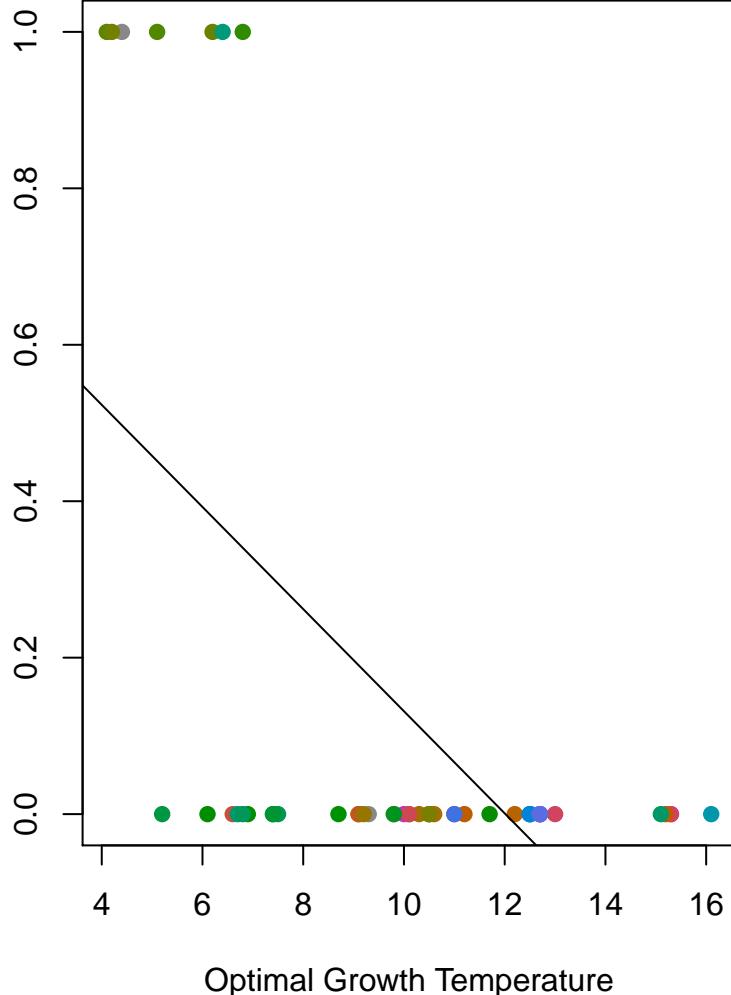
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00026068
Gluconolactonase (EC 3.1.1.17)
 $r = -0.588$, $p = 10^{-5.149}$

feature.plfam_id.arg_lys_ratio.length



feature.plfam_id.arg_lys_ratio.length
PLF_28228_00026635
hypothetical protein
 $r = -0.588$, $p = 10^{-5.149}$

feature.plfam_id.arg_lys_ratio.length



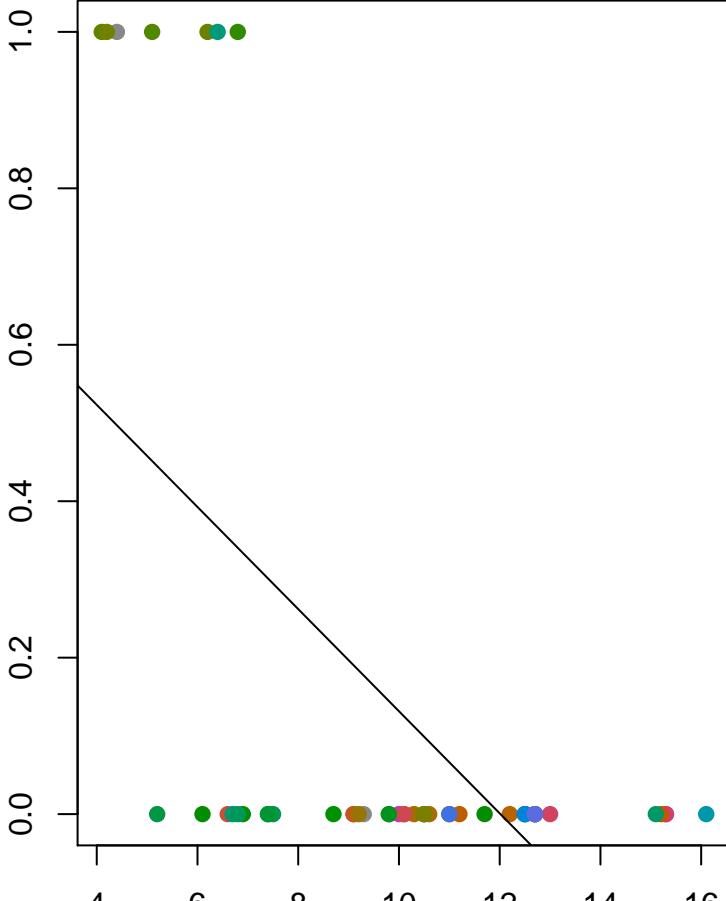
feature.plfam_id.arg_lys_ratio.length

PLF_28228_00026926

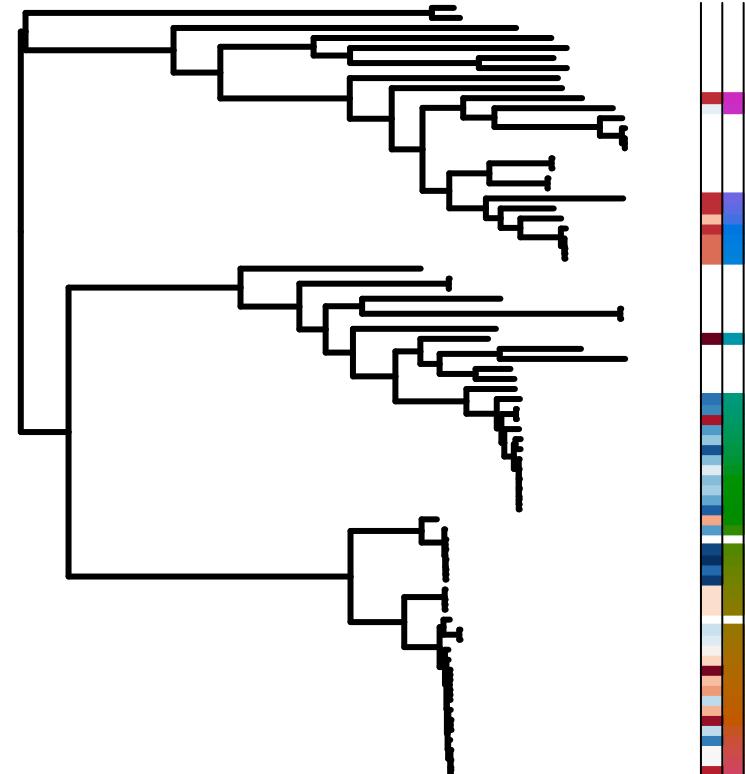
Gluconate 2-dehydrogenase subunit 3 family protein

$r = -0.588, p = 10^{-5.149}$

feature.plfam_id.arg_lys_ratio.length

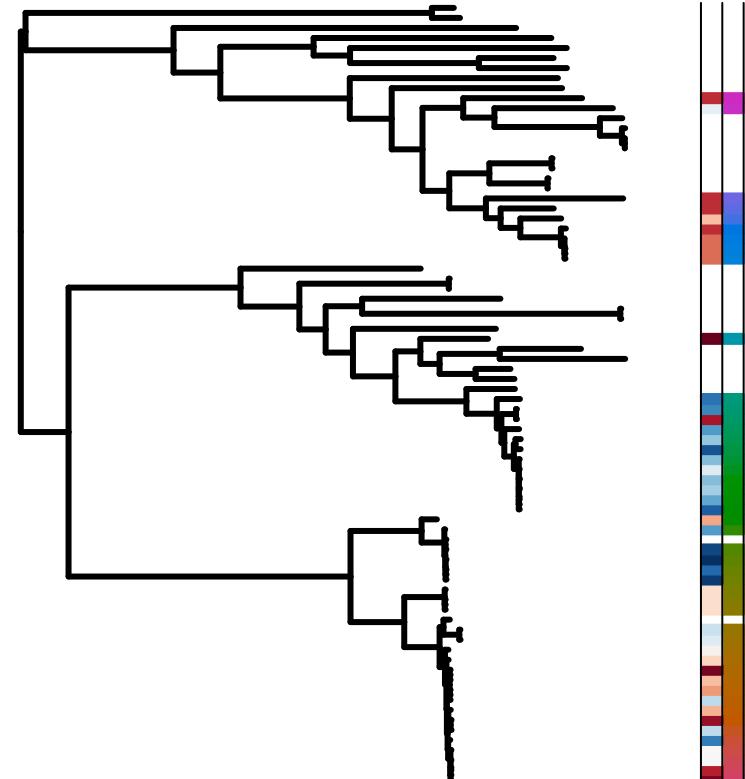
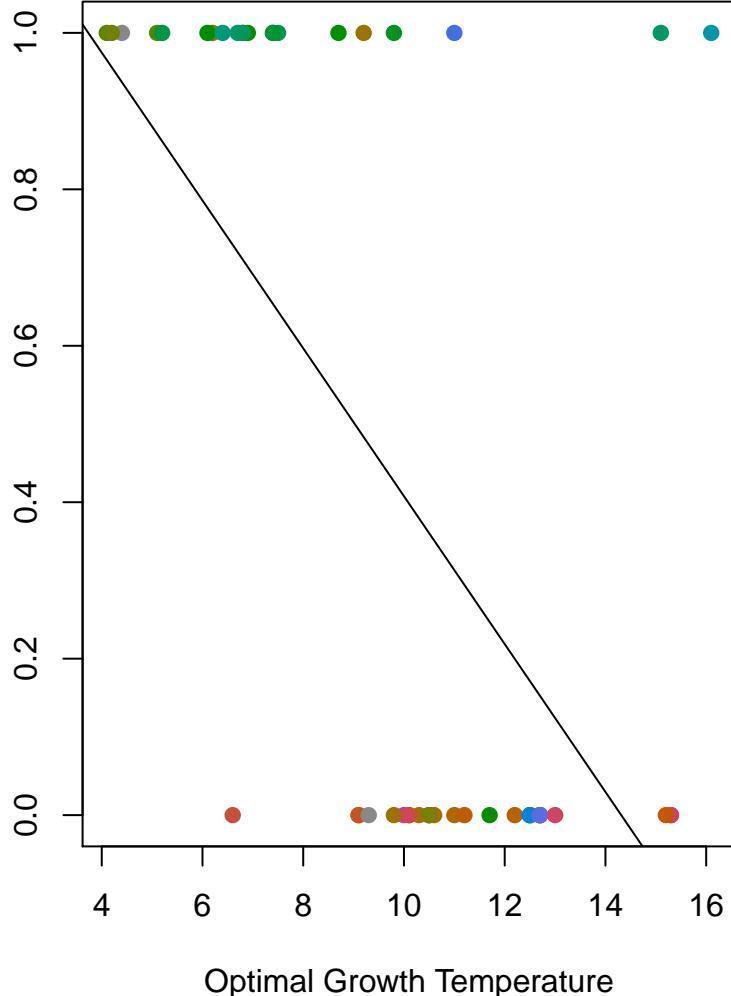


Optimal Growth Temperature



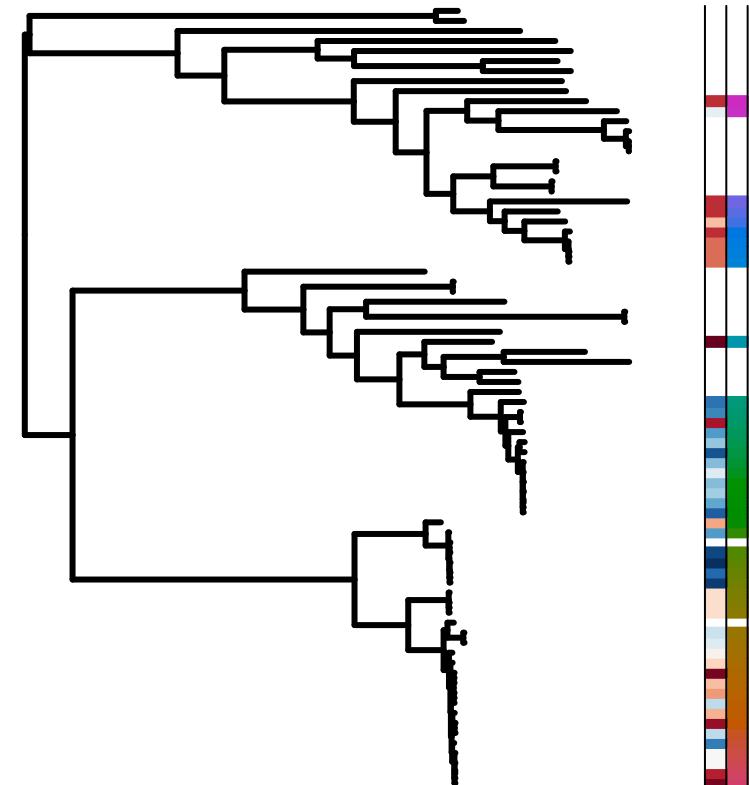
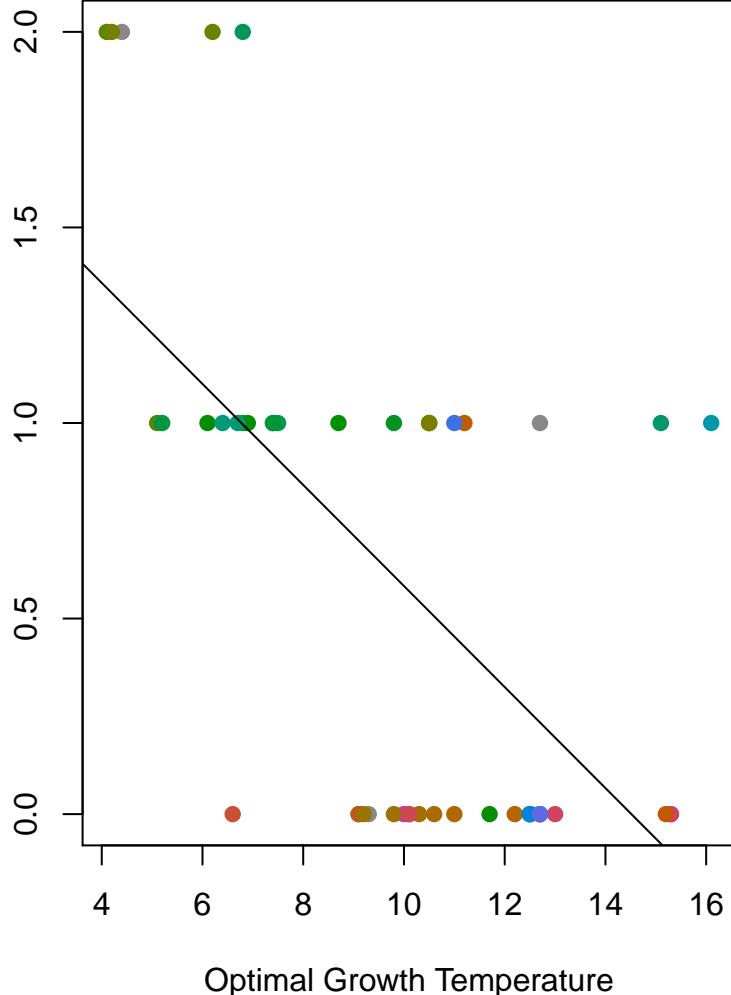
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00012978
hypothetical protein
 $r = -0.599$, $p = 10^{-5.356}$

feature.plfam_id.arg_lys_ratio.length



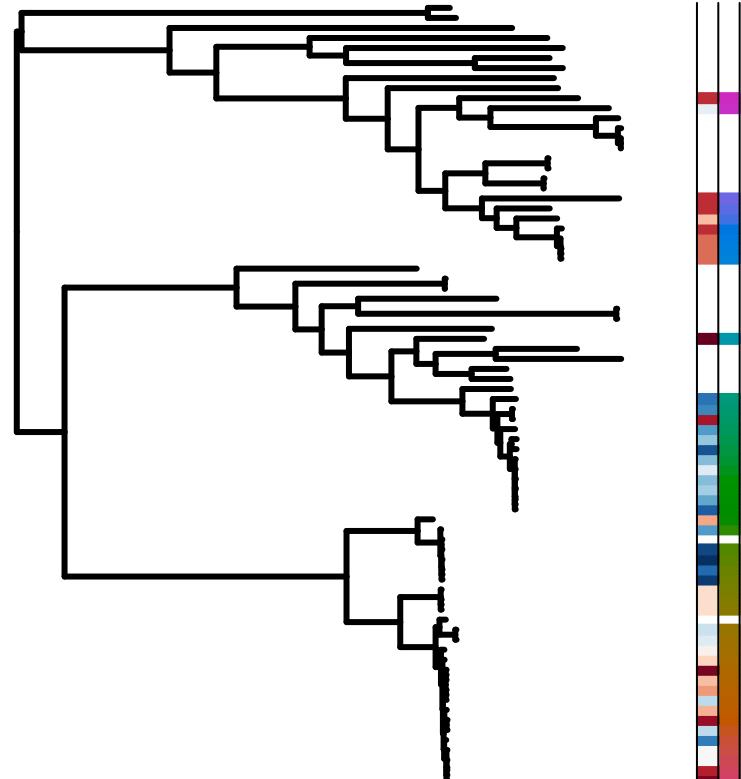
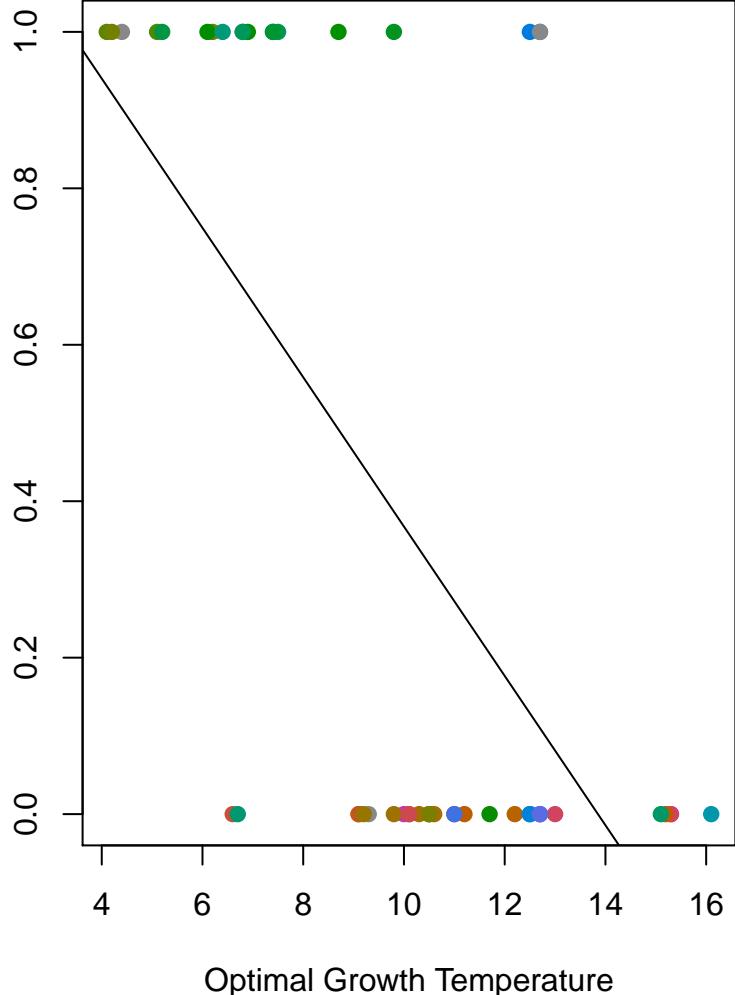
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00013710
hypothetical protein
 $r = -0.609$, $p = 10^{-5.563}$

feature.plfam_id.arg_lys_ratio.length



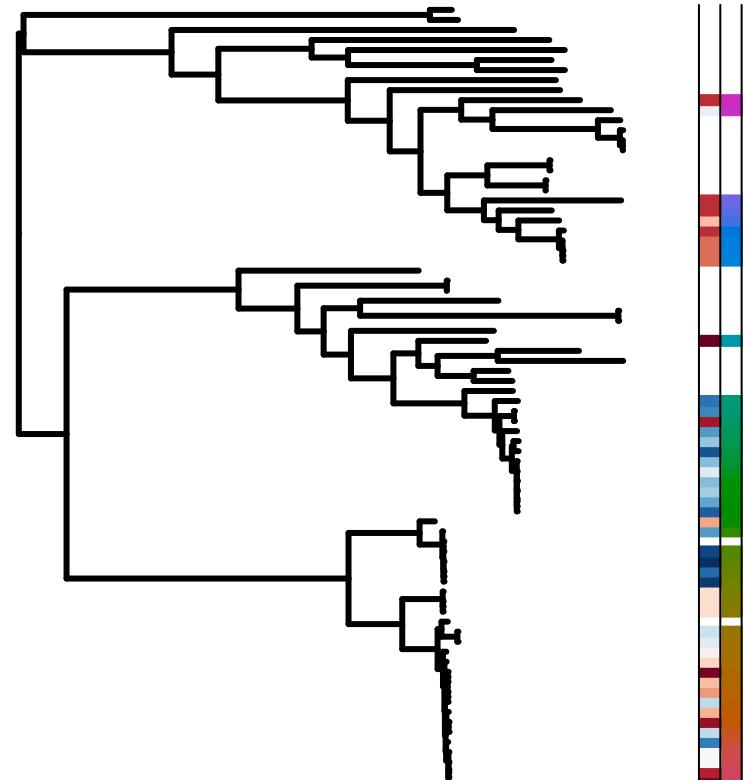
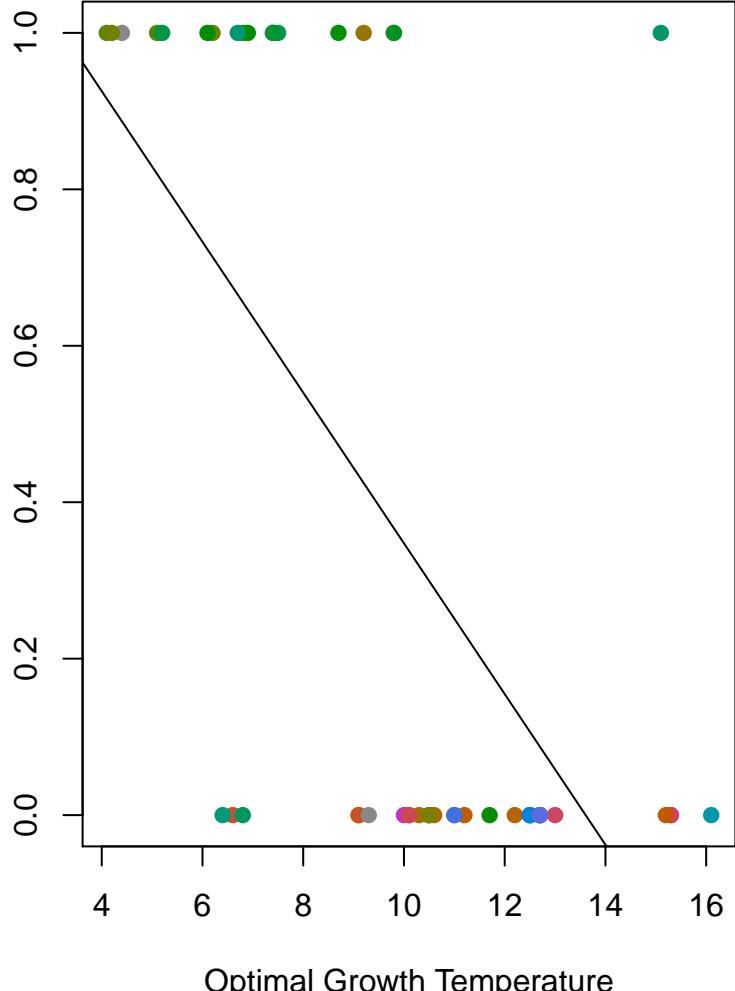
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00028262
Iron siderophore sensor protein
 $r = -0.615$, $p = 10^{-5.69}$

feature.plfam_id.arg_lys_ratio.length



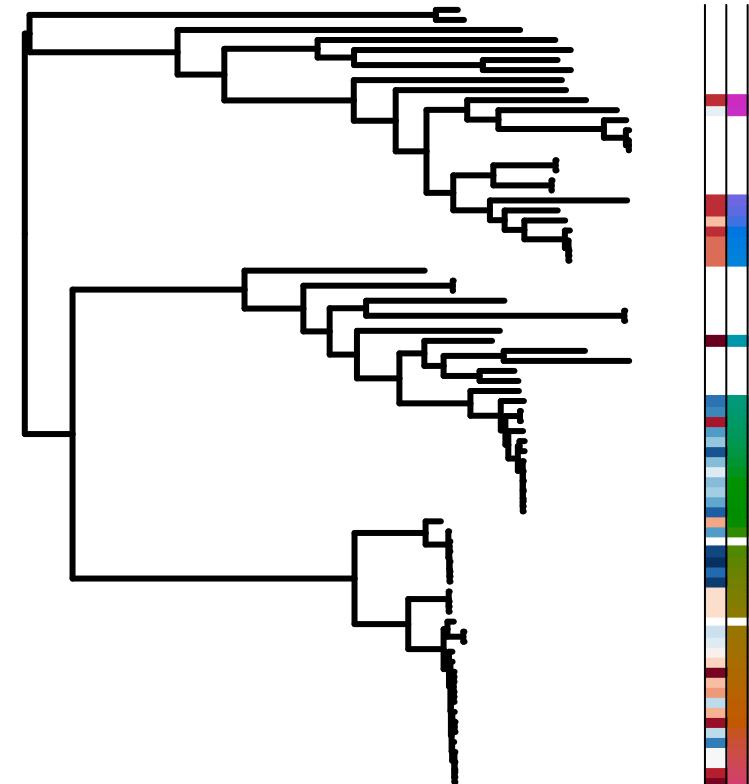
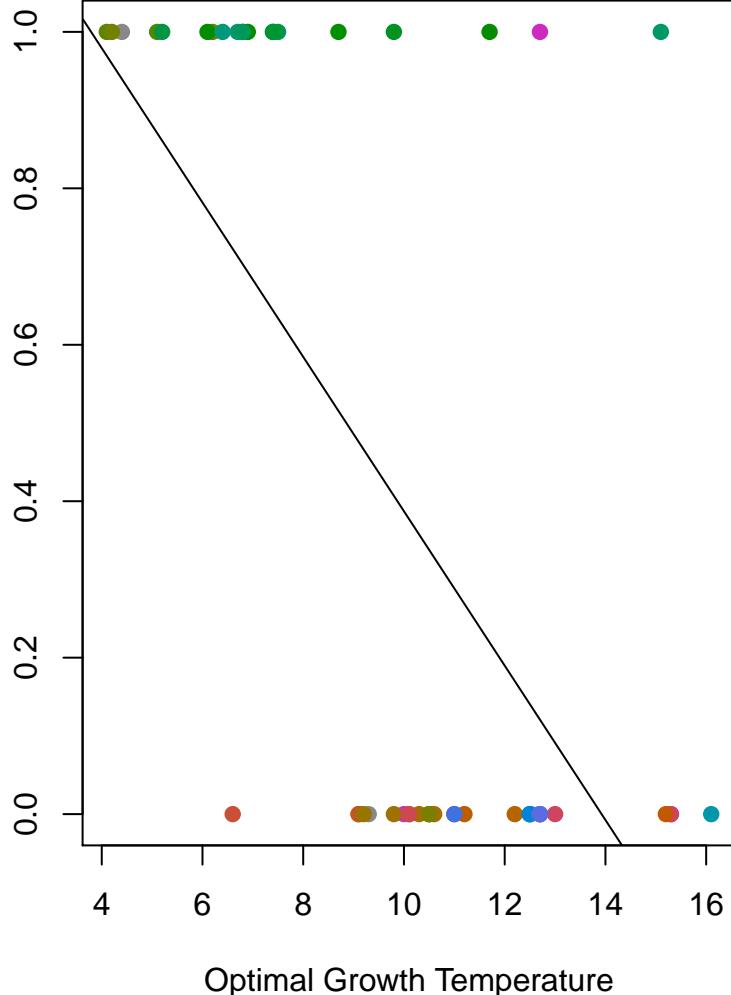
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00028105
hypothetical protein
 $r = -0.627$, $p = 10^{-5.964}$

feature.plfam_id.arg_lys_ratio.length



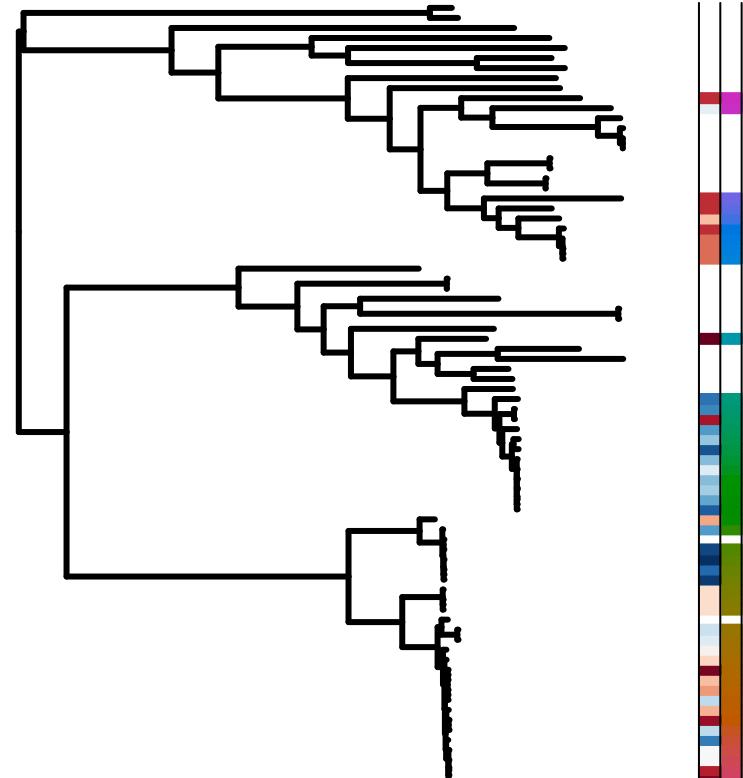
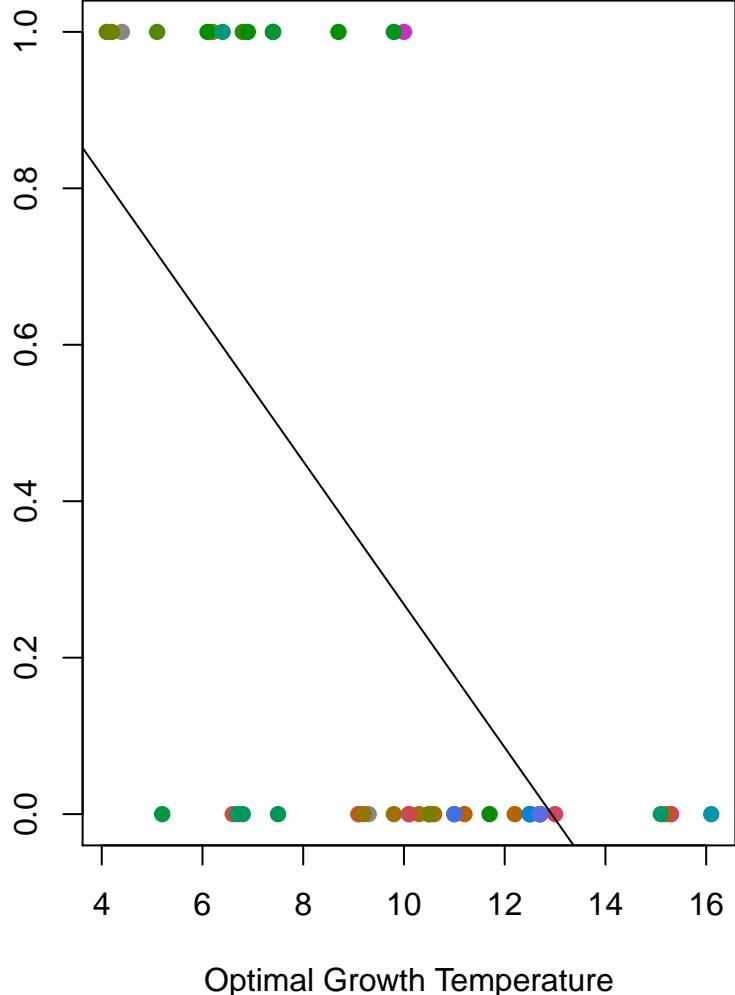
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00008182
hypothetical protein
 $r = -0.63$, $p = 10^{-6.013}$

feature.plfam_id.arg_lys_ratio.length



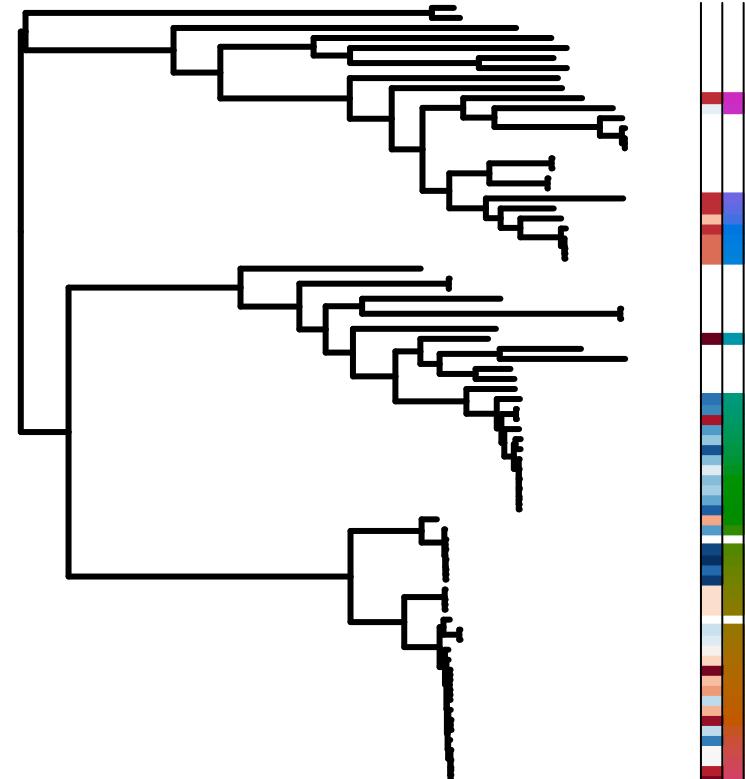
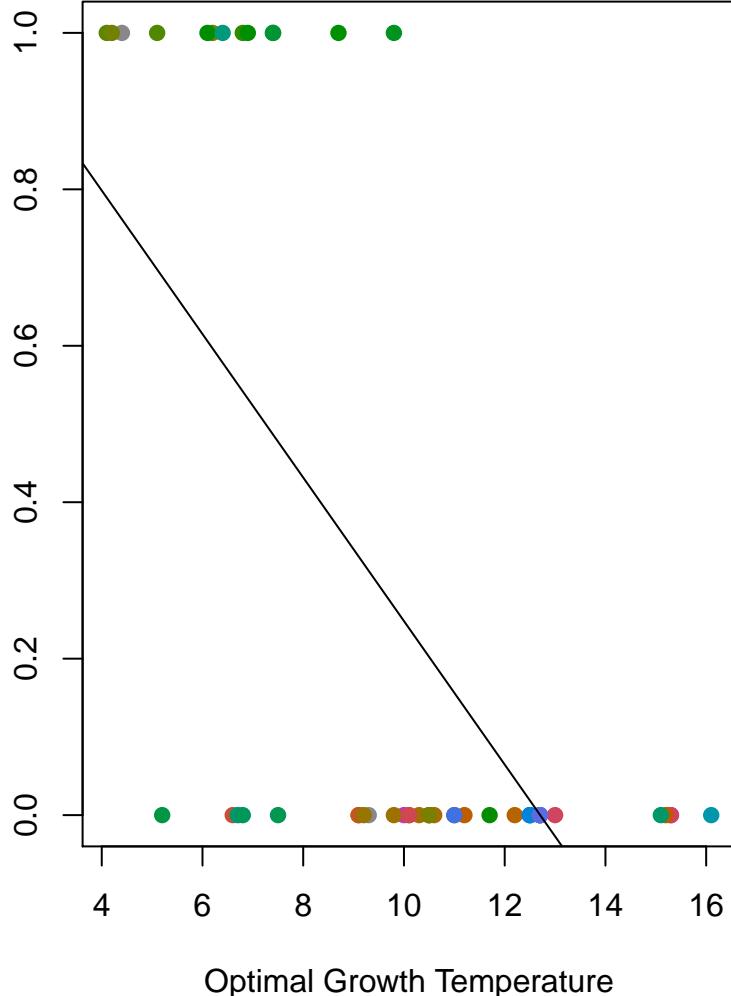
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00023136
YoeB toxin protein
 $r = -0.637$, $p = 10^{-6.176}$

feature.plfam_id.arg_lys_ratio.length



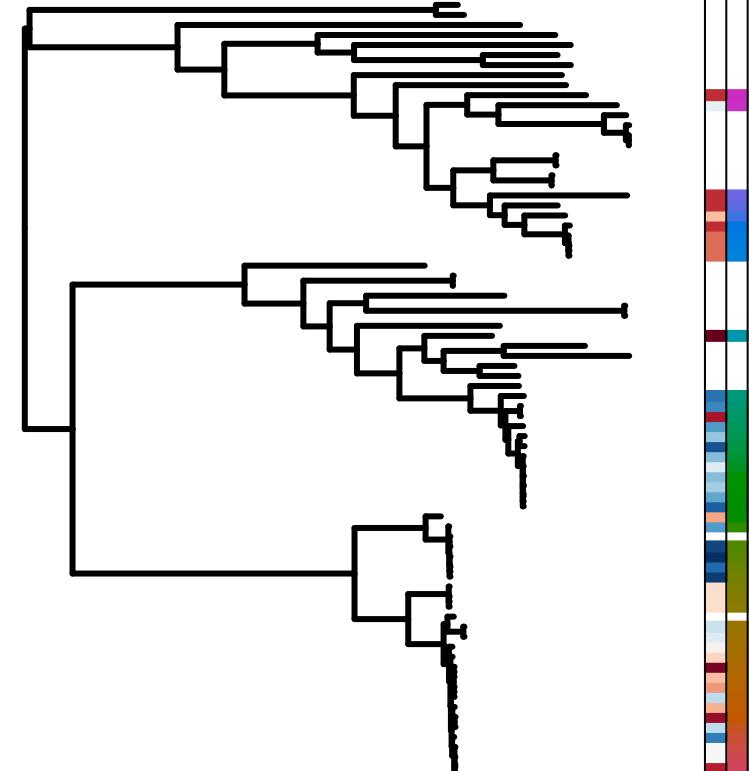
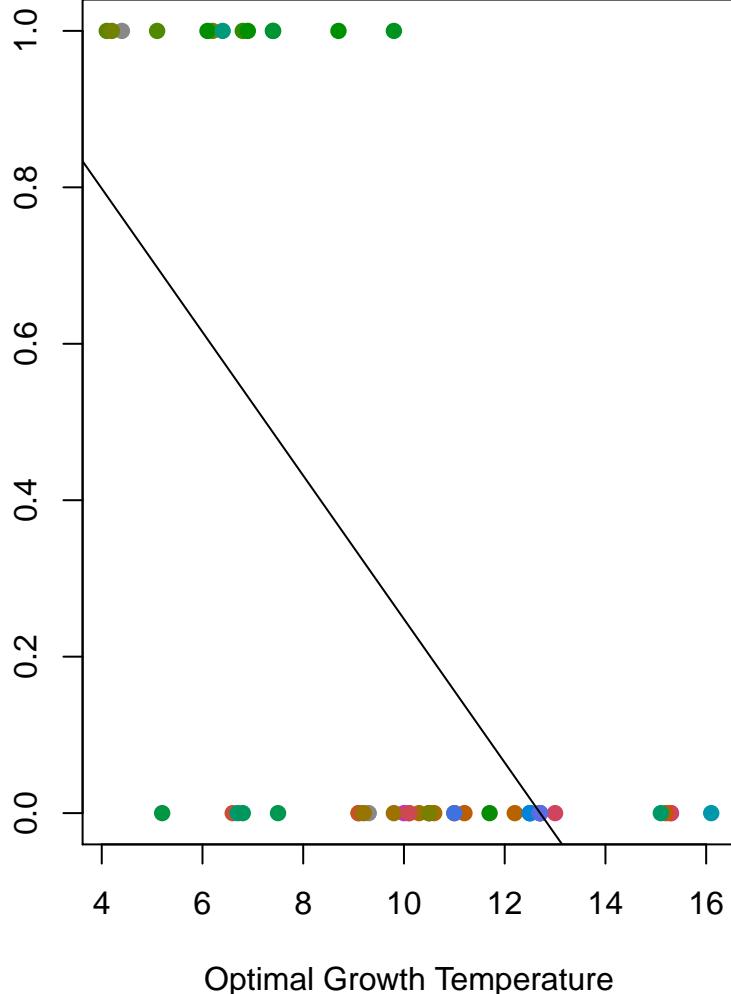
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00028678
Uncharacterized MFS-type transporter
 $r = -0.654$, $p = 10^{-6.577}$

feature.plfam_id.arg_lys_ratio.length



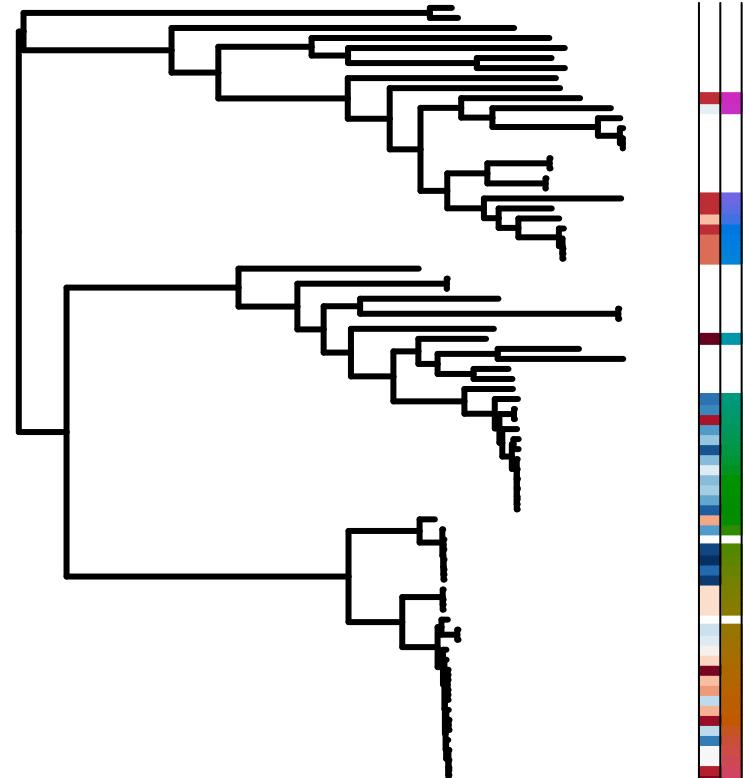
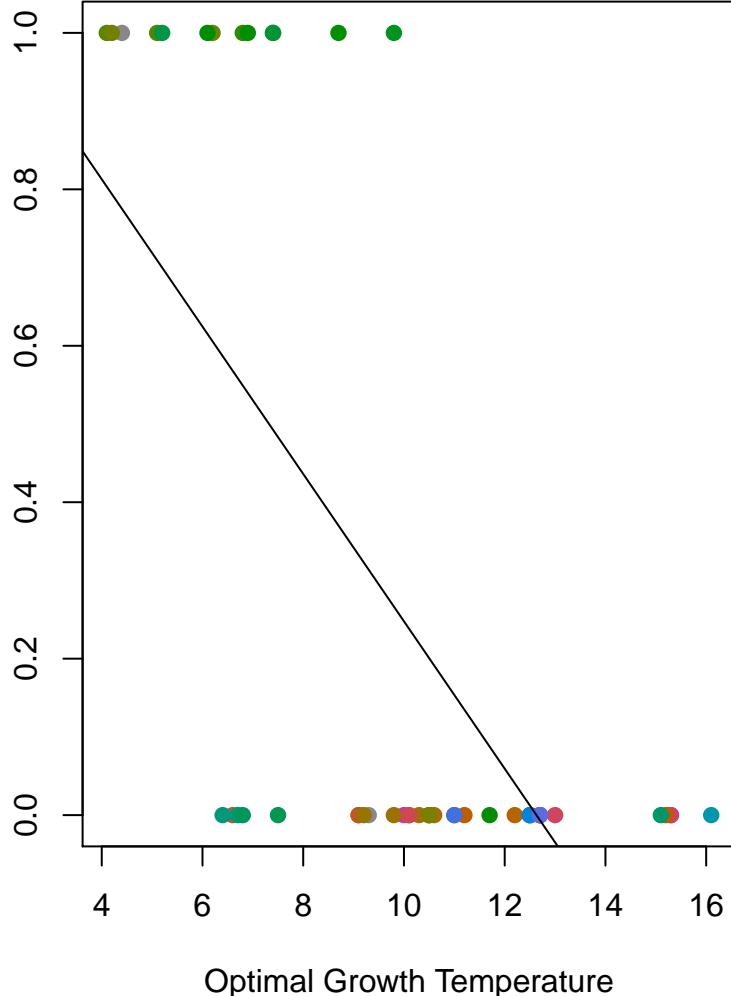
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00028766
Transcriptional regulator, AraC family
 $r = -0.654$, $p = 10^{-6.577}$

feature.plfam_id.arg_lys_ratio.length



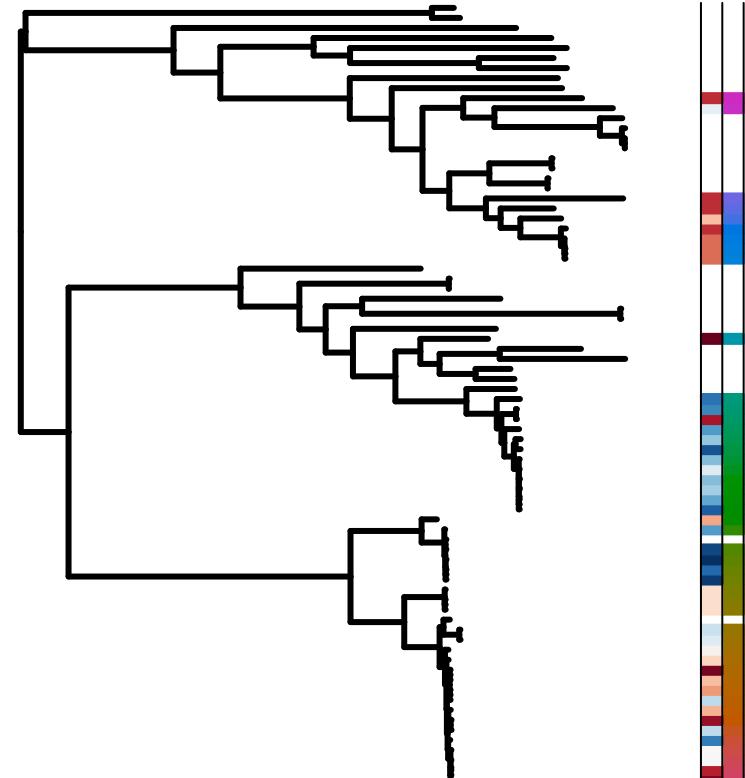
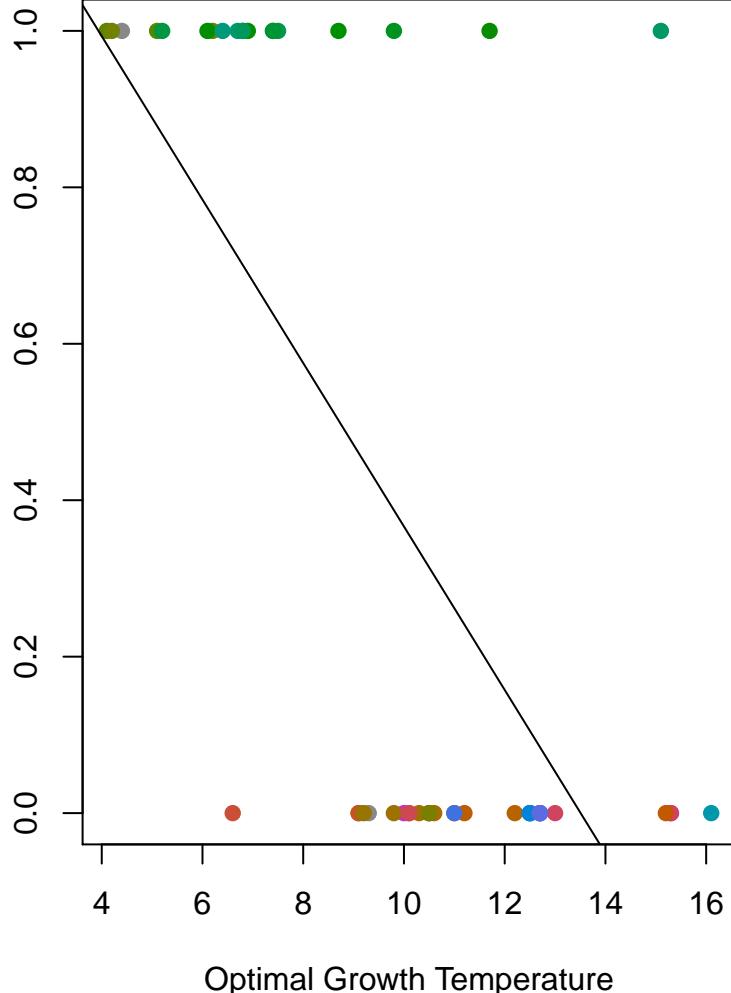
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00026393
hypothetical protein
 $r = -0.671$, $p = 10^{-7.018}$

feature.plfam_id.arg_lys_ratio.length



feature.plfam_id.arg_lys_ratio.length
PLF_28228_00016260
hypothetical protein
 $r = -0.673$, $p = 10^{-7.058}$

feature.plfam_id.arg_lys_ratio.length



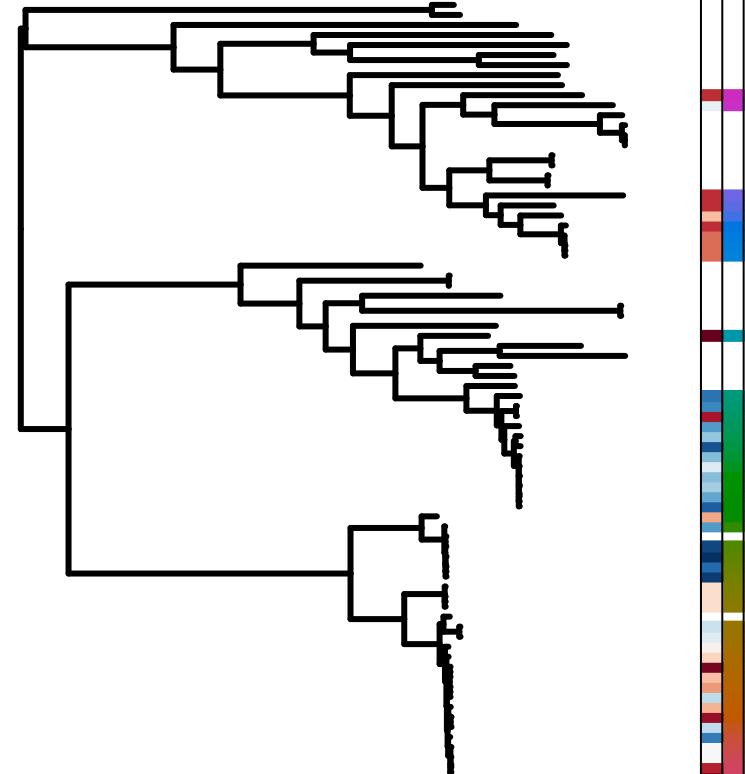
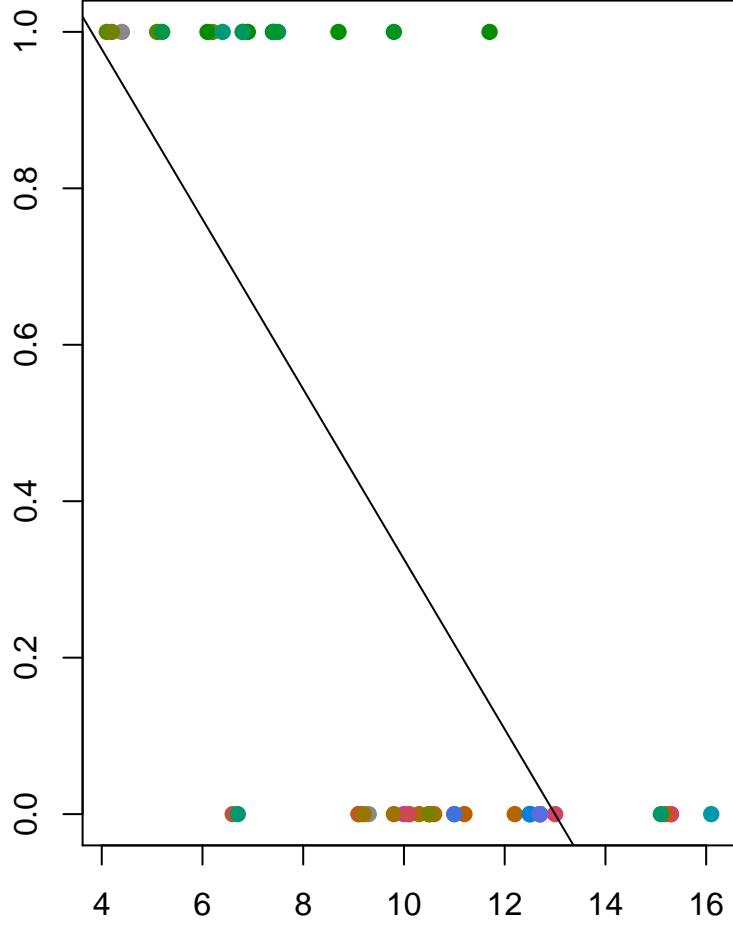
feature.plfam_id.arg_lys_ratio.length

PLF_28228_00011707

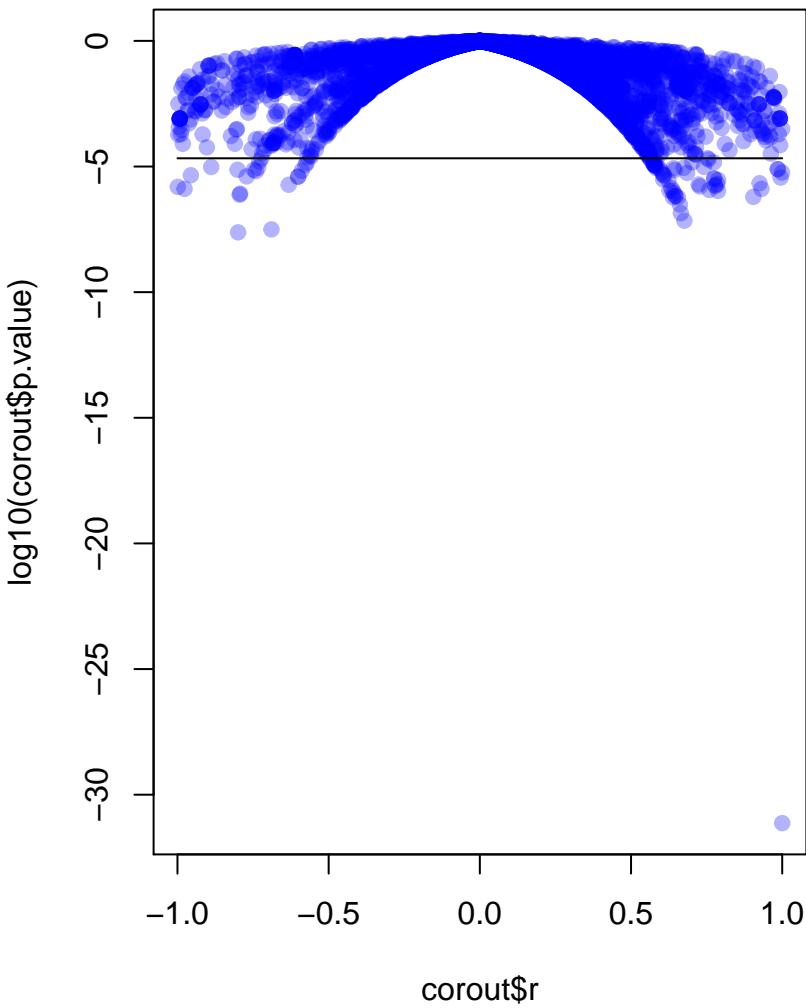
Membrane-bound lytic murein transglycosylase C (EC 3.2.1.n1)

$r = -0.717, p = 10^{-8.331}$

feature.plfam_id.arg_lys_ratio.length



`feature.pgfam_id.acidic_residue.mean`



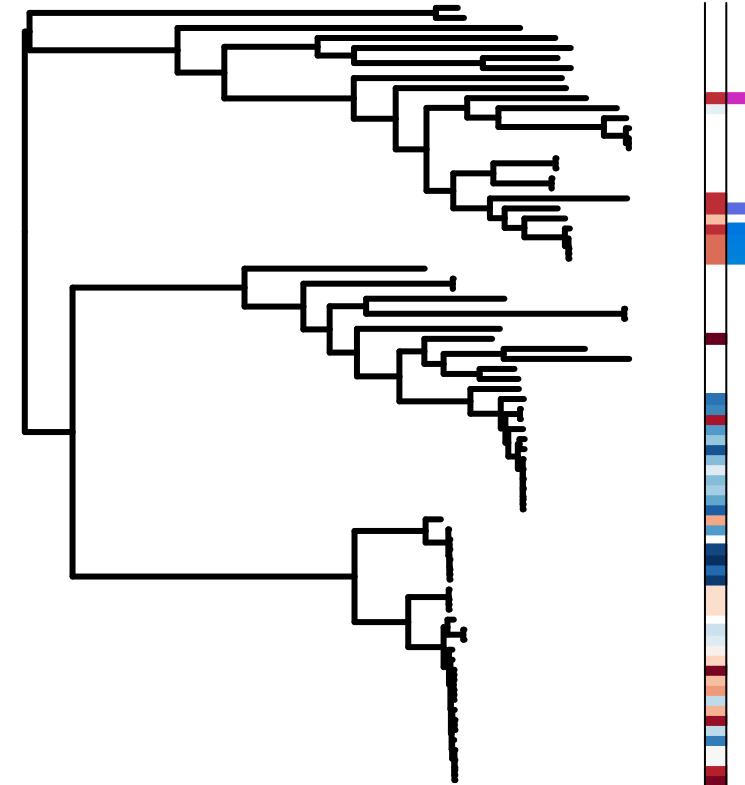
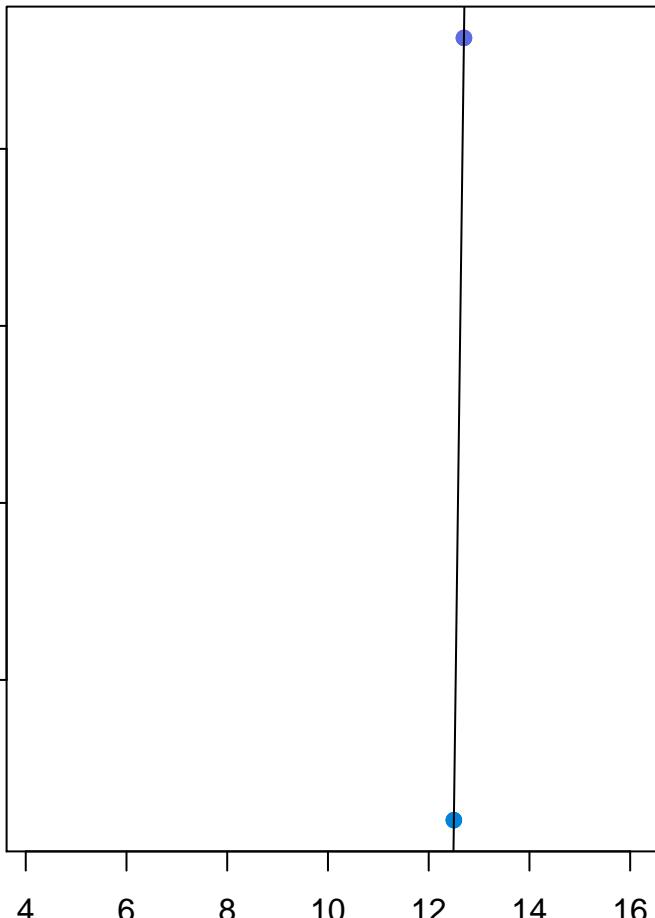
feature.pgfam_id.acidic_residue.mean

PGF_01336638

hypothetical protein

r = 1, p = 10^-31.131

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature

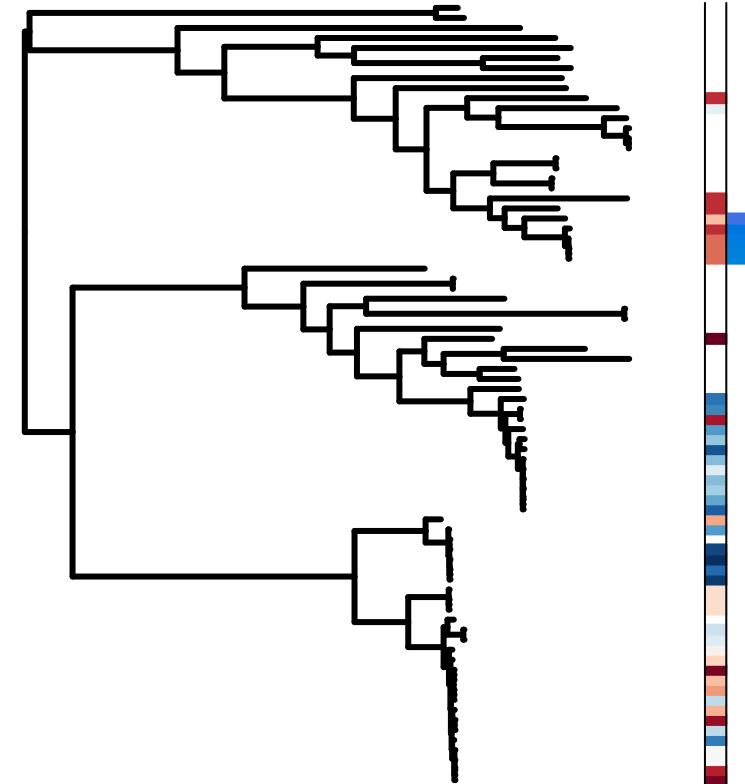
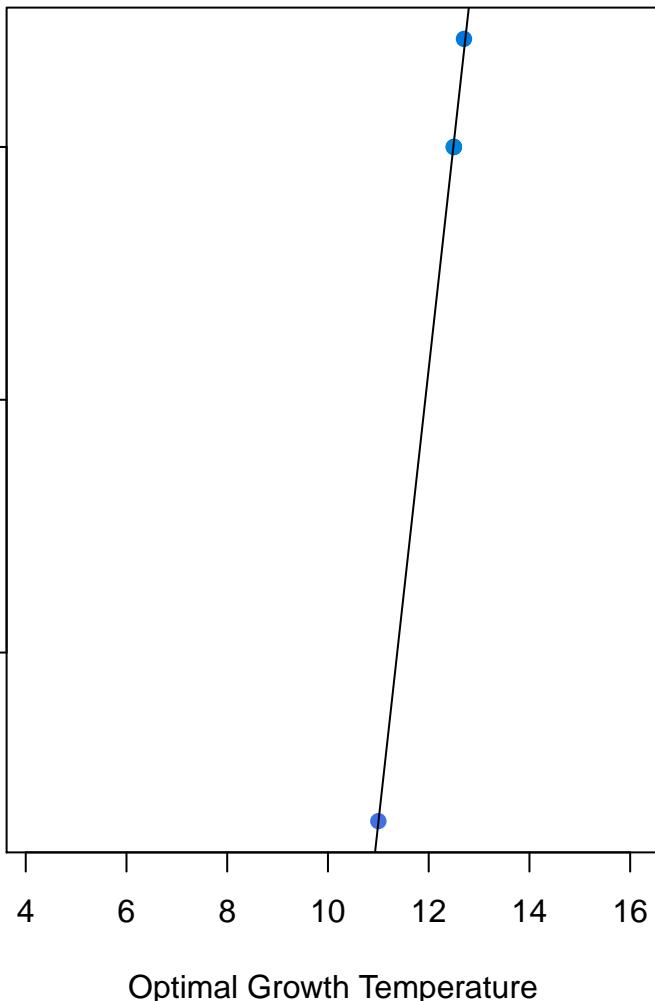
feature.pgfam_id.acidic_residue.mean

PGF_00038084

Fluoride ion transporter CrcB

$r = 1, p = 10^{-5.24}$

feature.pgfam_id.acidic_residue.mean



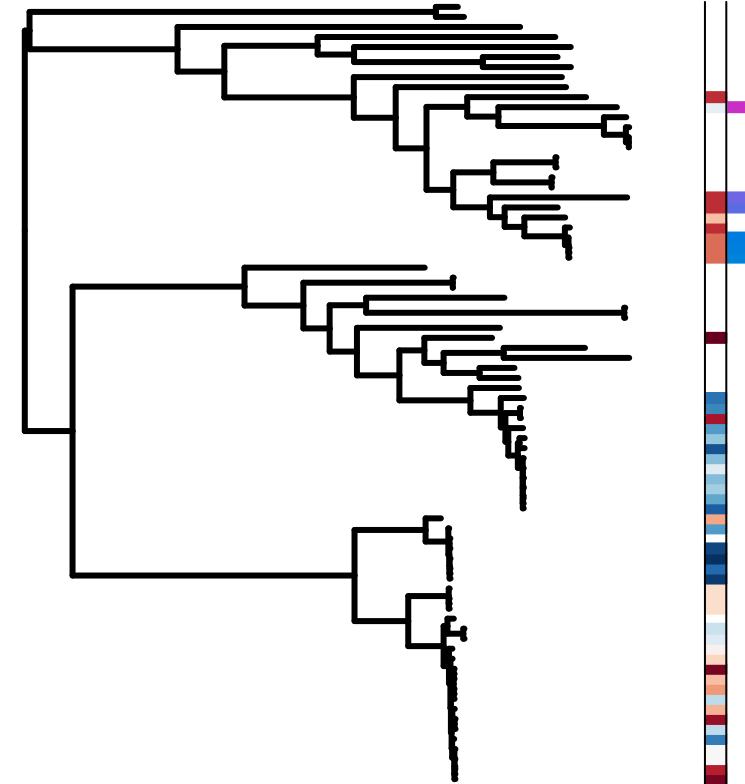
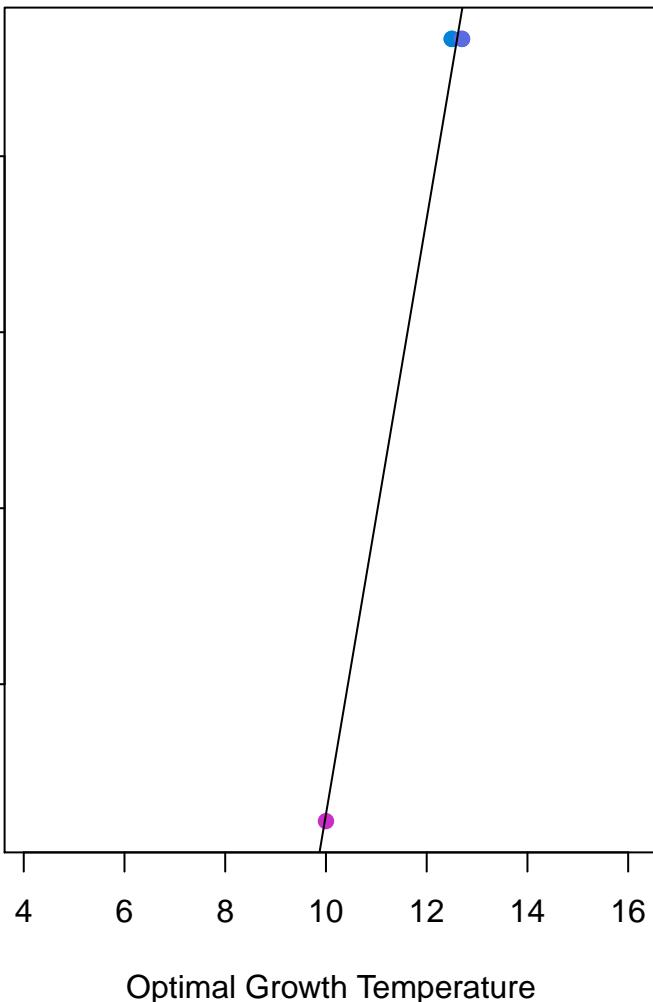
feature.pgfam_id.acidic_residue.mean

PGF_01337096

hypothetical protein

$r = 0.995, p = 10^{-5.441}$

feature.pgfam_id.acidic_residue.mean



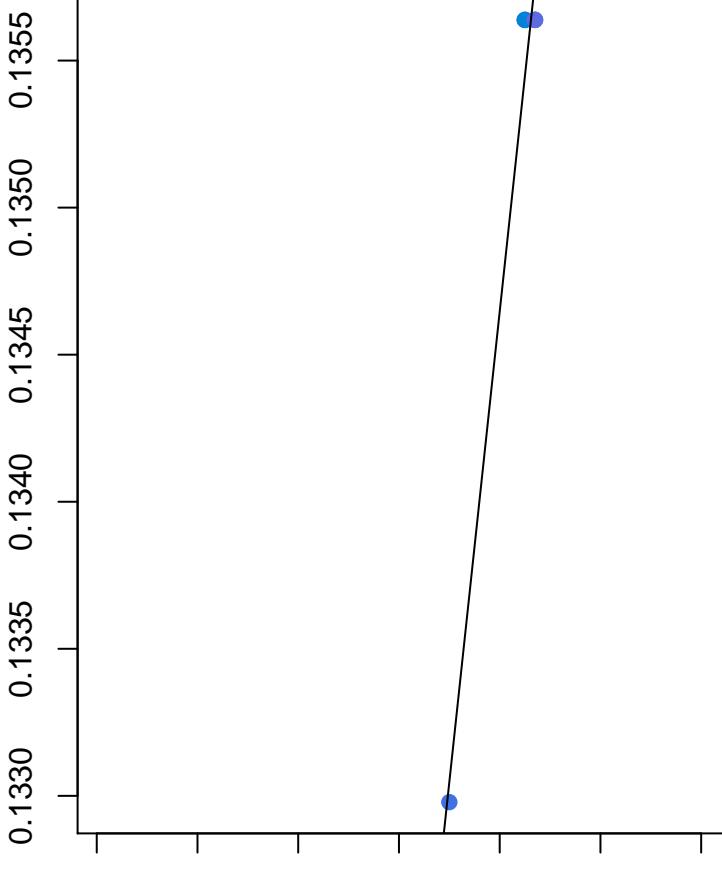
feature.pgfam_id.acidic_residue.mean

PGF_04965976

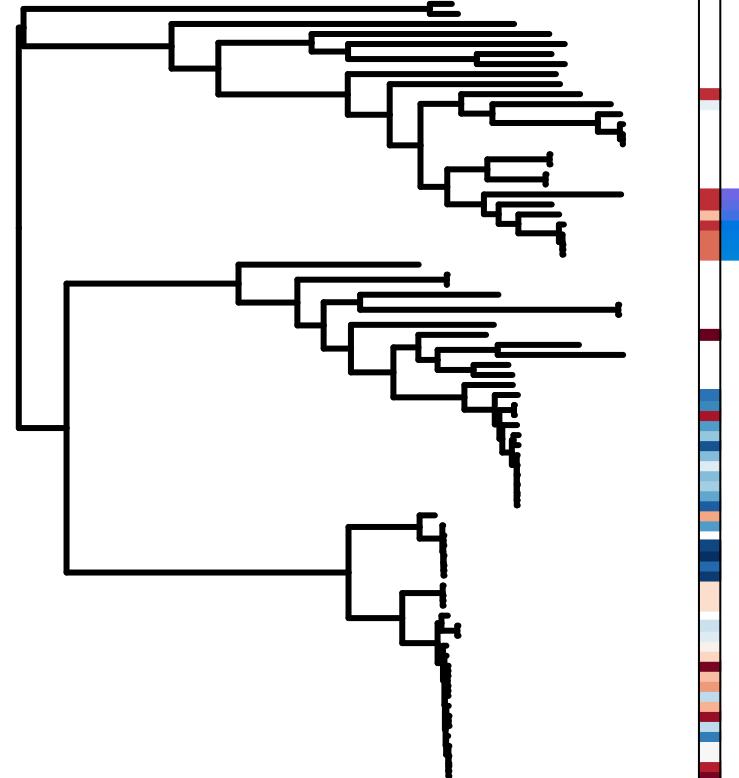
Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2)

r = 0.985, p = 10^-5.104

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature



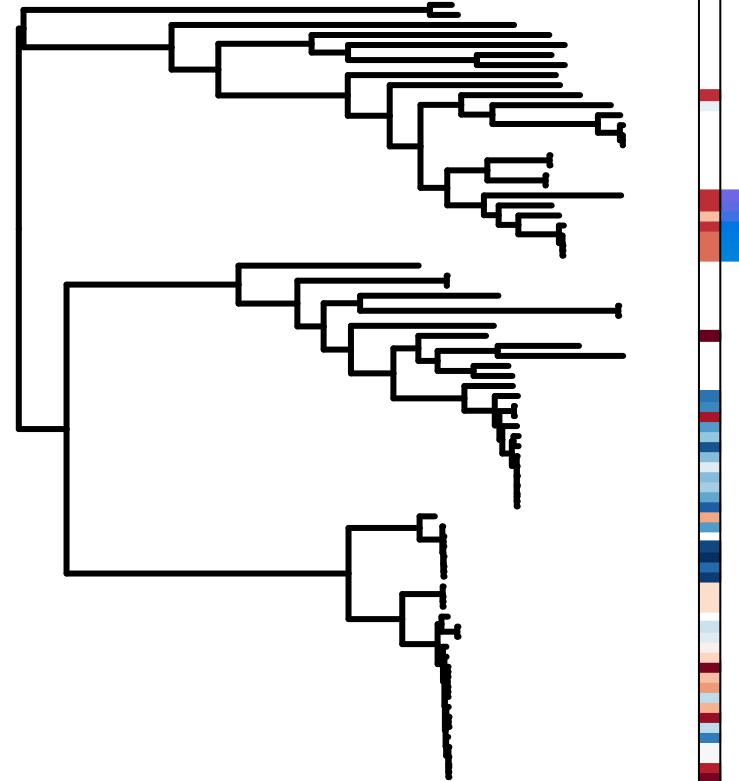
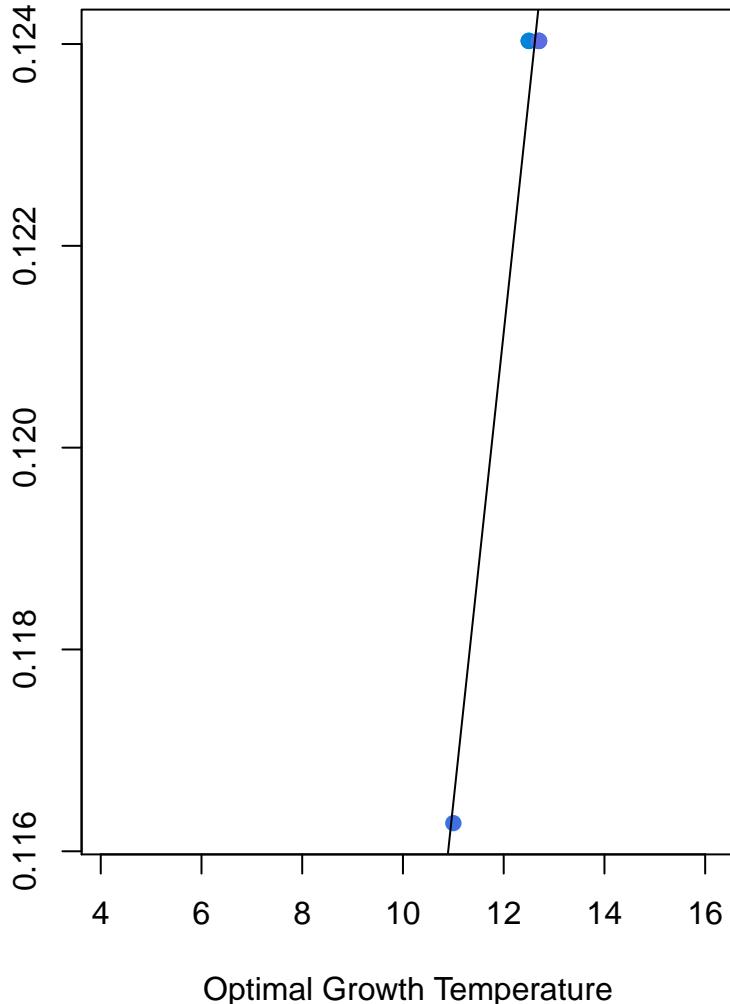
feature.pgfam_id.acidic_residue.mean

PGF_01336845

hypothetical protein

$r = 0.985, p = 10^{-5.104}$

feature.pgfam_id.acidic_residue.mean



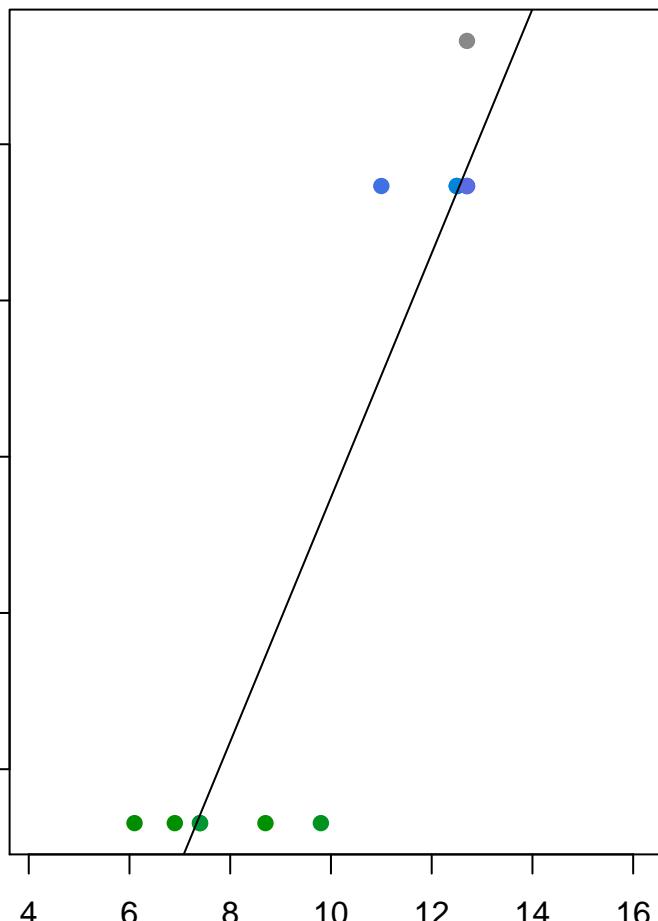
feature.pgfam_id.acidic_residue.mean

PGF_04463652

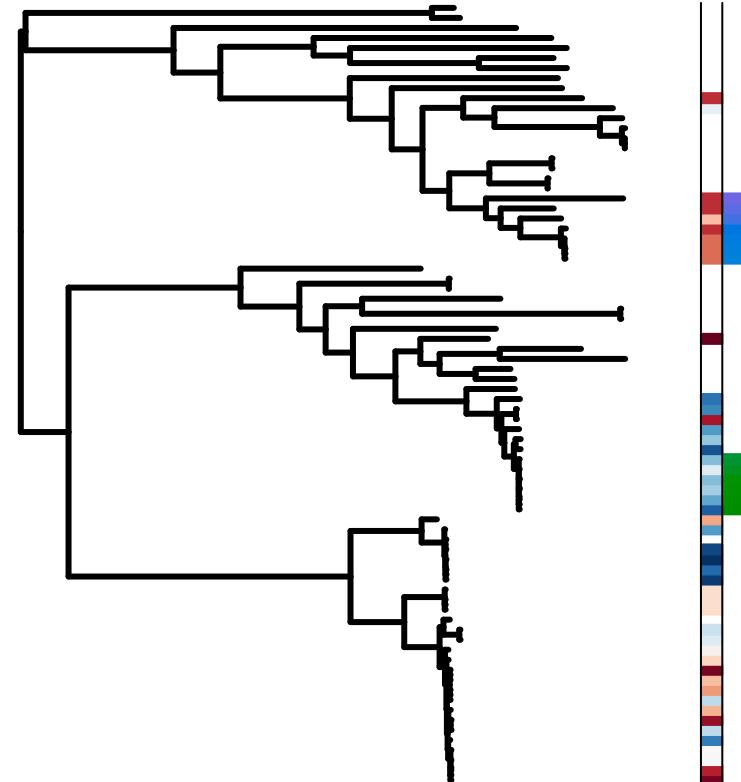
C4-dicarboxylate transport transcriptional regulatory protein

$r = 0.931, p = 10^{-5.89}$

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature



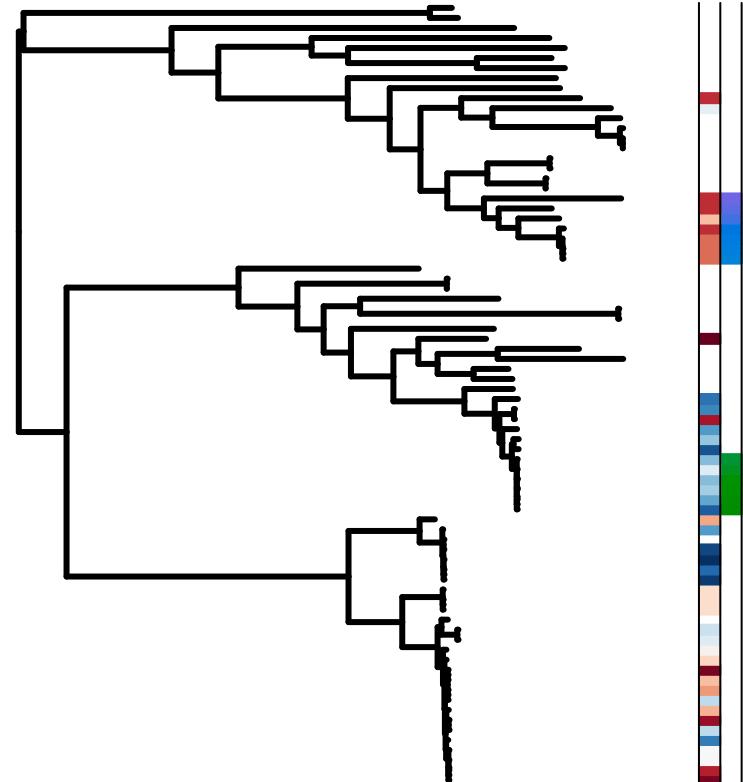
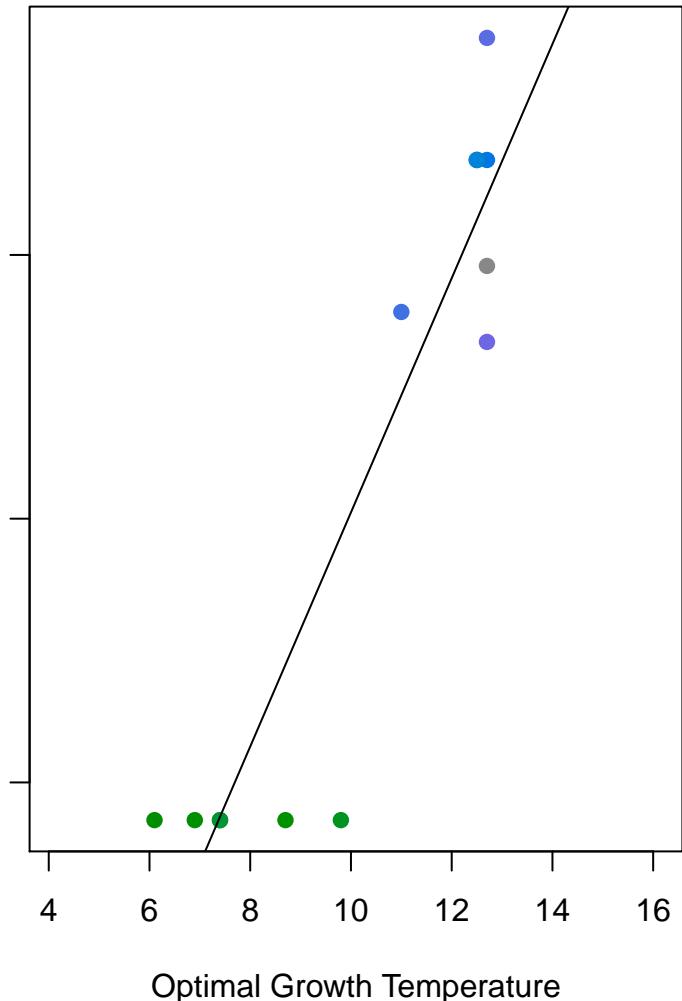
feature.pgfam_id.acidic_residue.mean

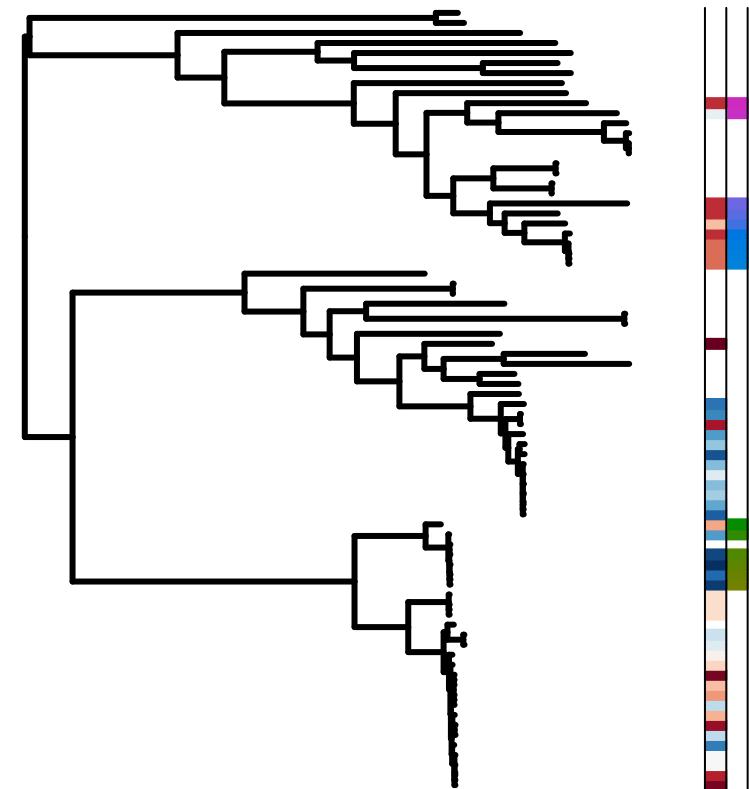
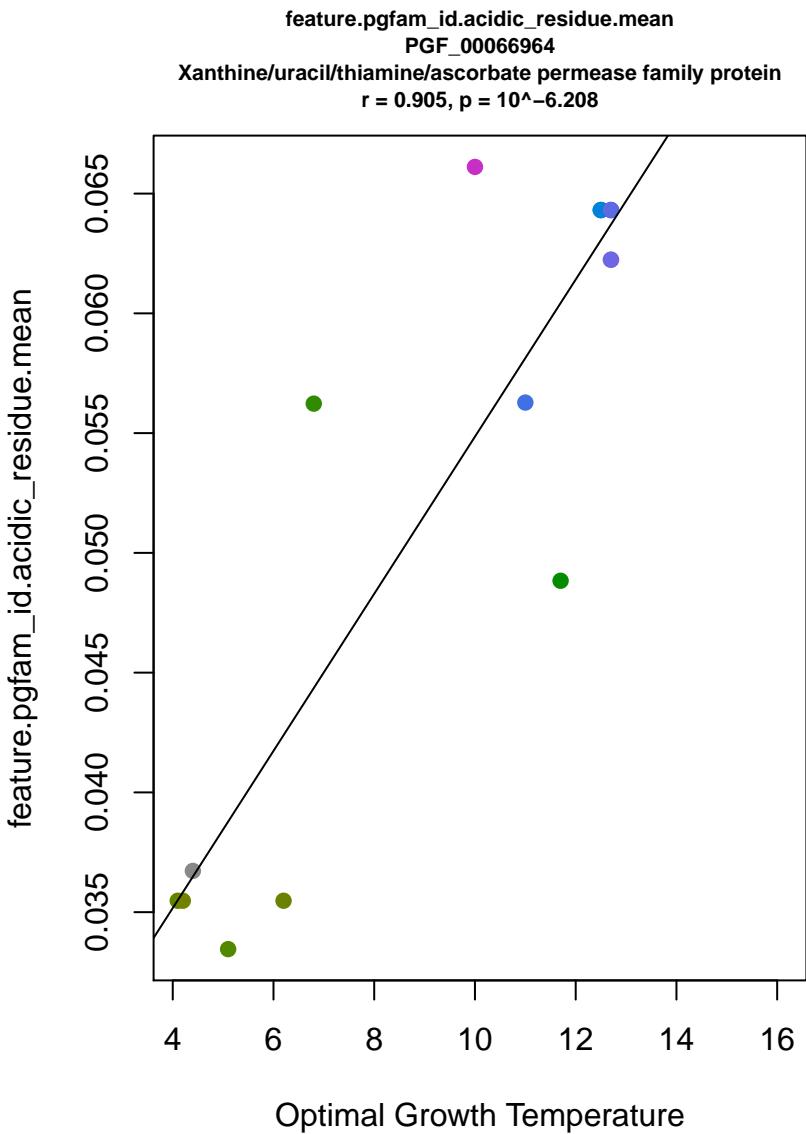
PGF_01336575

Porin

$r = 0.925, p = 10^{-5.664}$

feature.pgfam_id.acidic_residue.mean





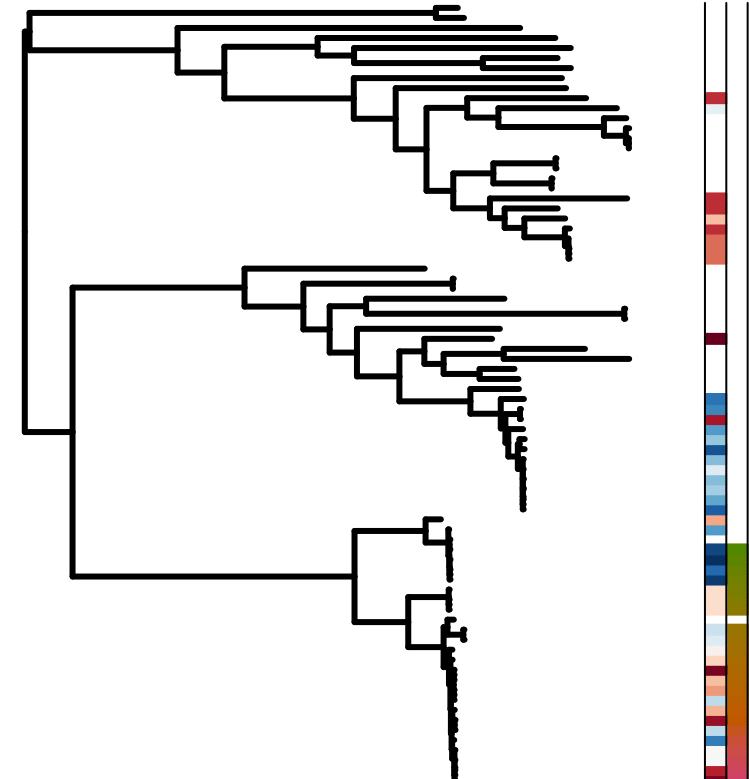
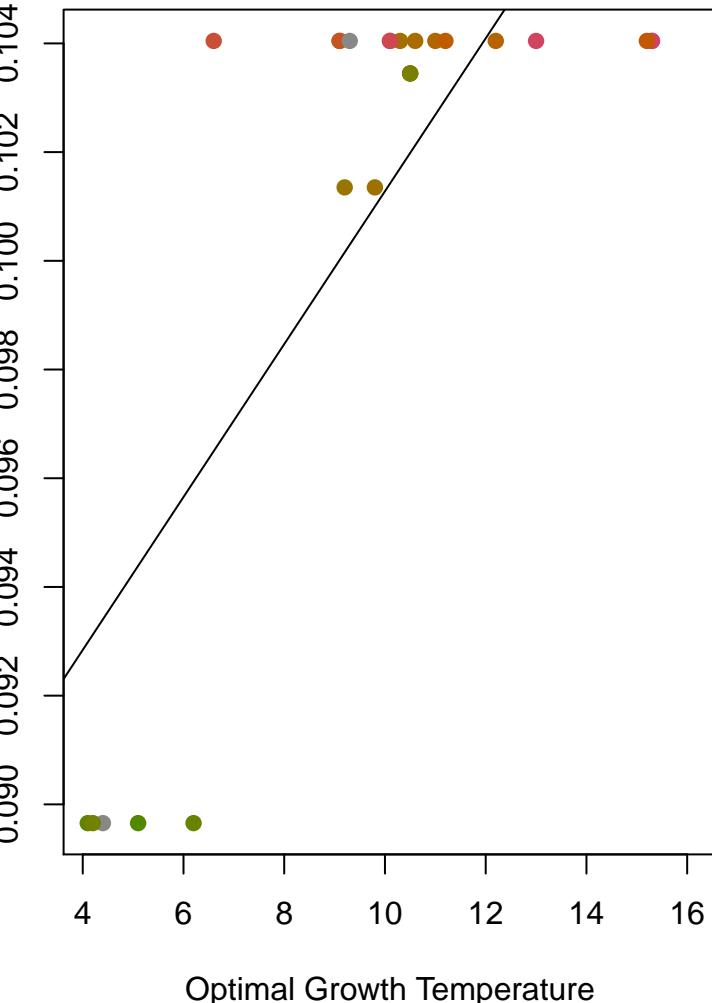
feature.pgfam_id.acidic_residue.mean

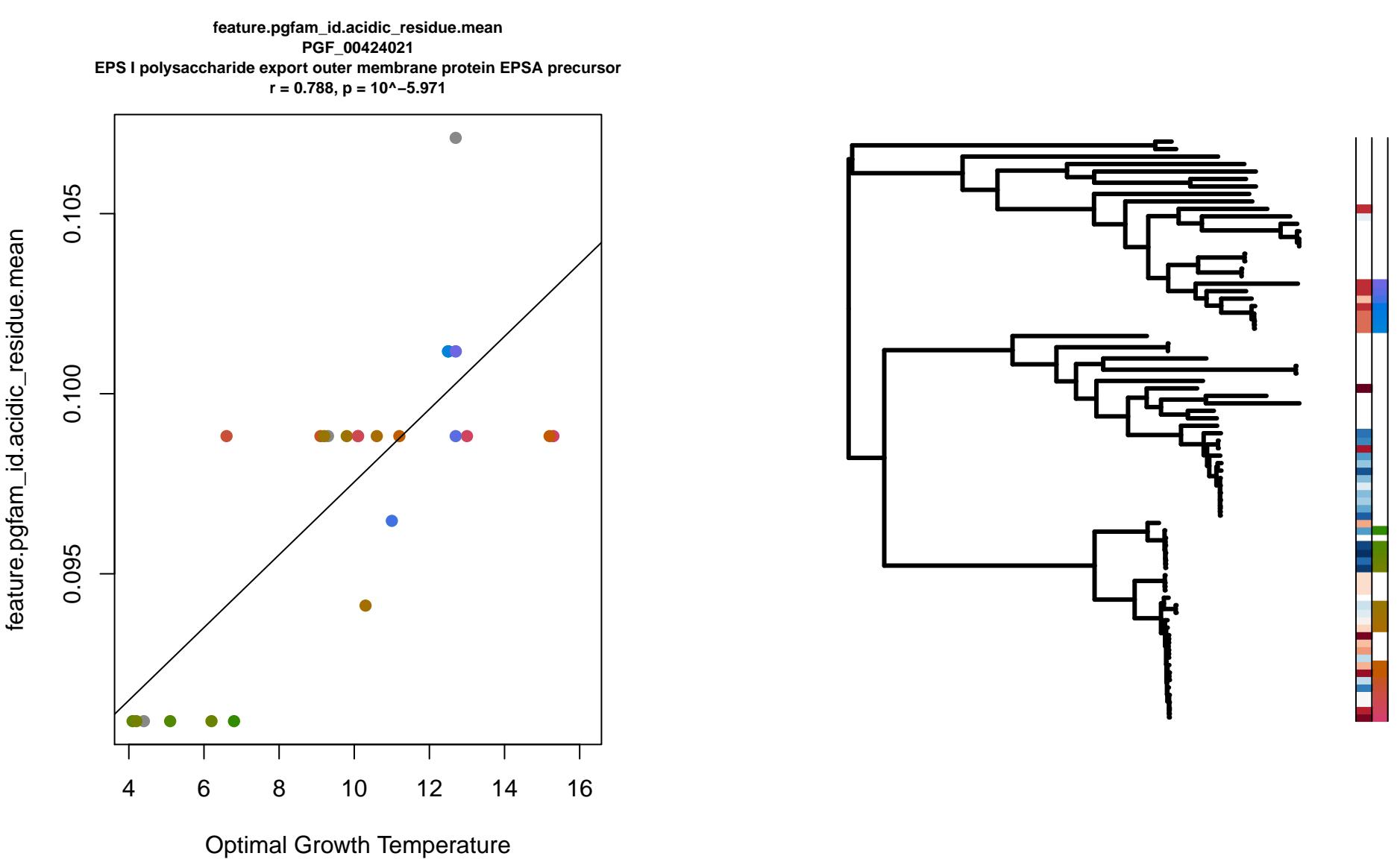
PGF_07418929

hypothetical protein

$r = 0.788, p = 10^{-5.537}$

feature.pgfam_id.acidic_residue.mean





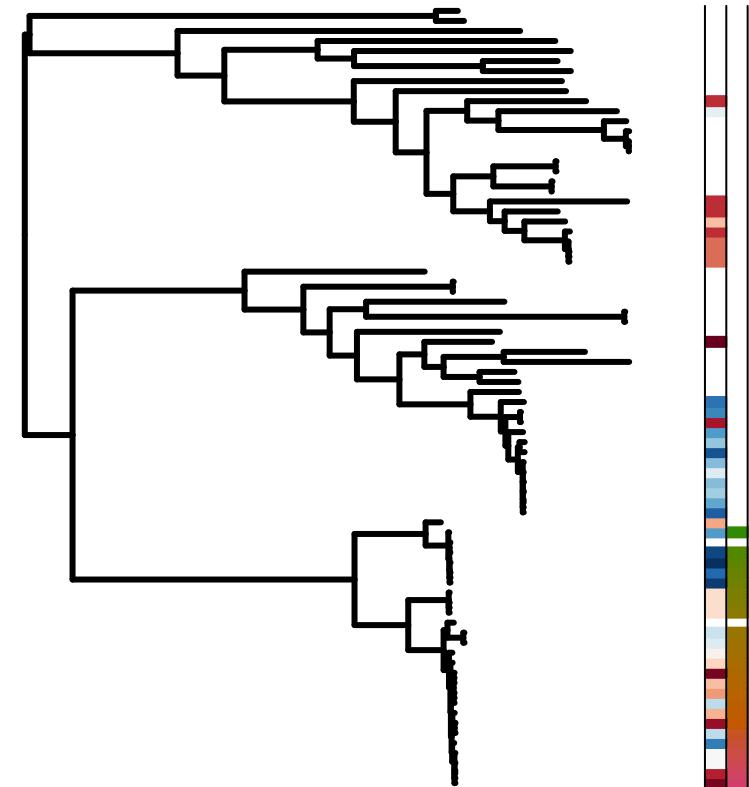
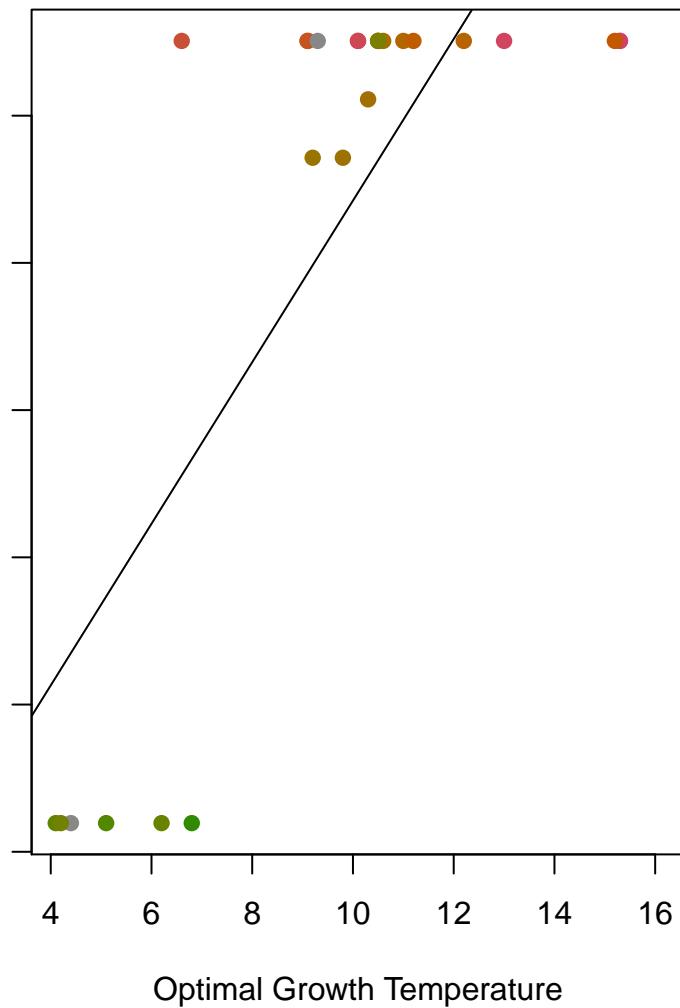
feature.pgfam_id.acidic_residue.mean

PGF_12049070

hypothetical protein

$r = 0.785, p = 10^{-5.697}$

feature.pgfam_id.acidic_residue.mean



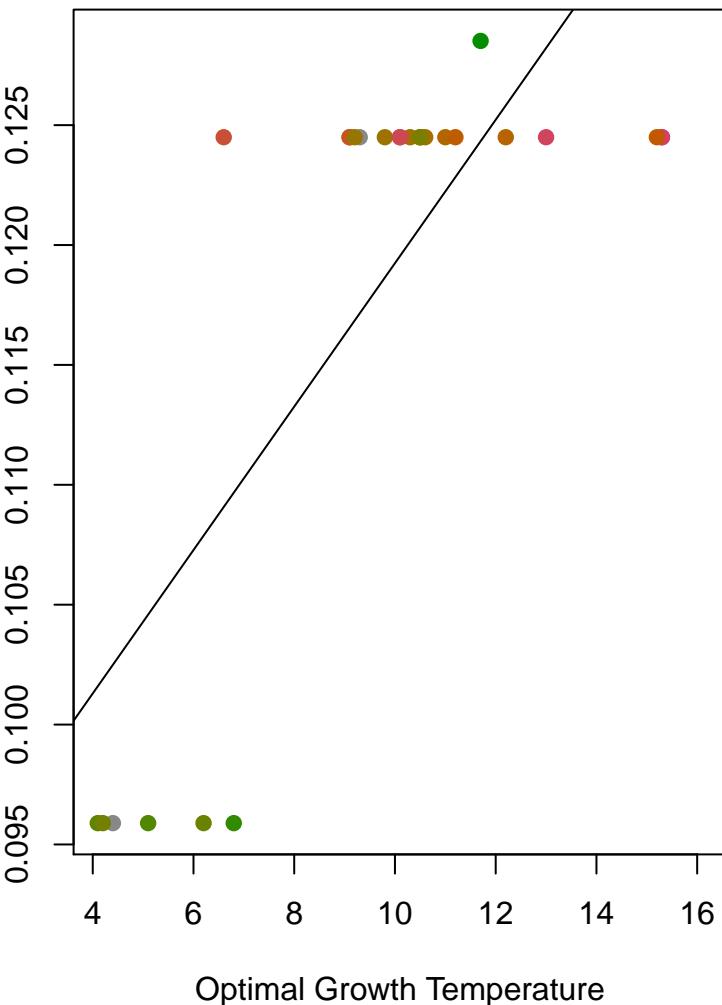
feature.pgfam_id.acidic_residue.mean

PGF_11018774

hypothetical protein

$r = 0.779, p = 10^{-5.775}$

feature.pgfam_id.acidic_residue.mean



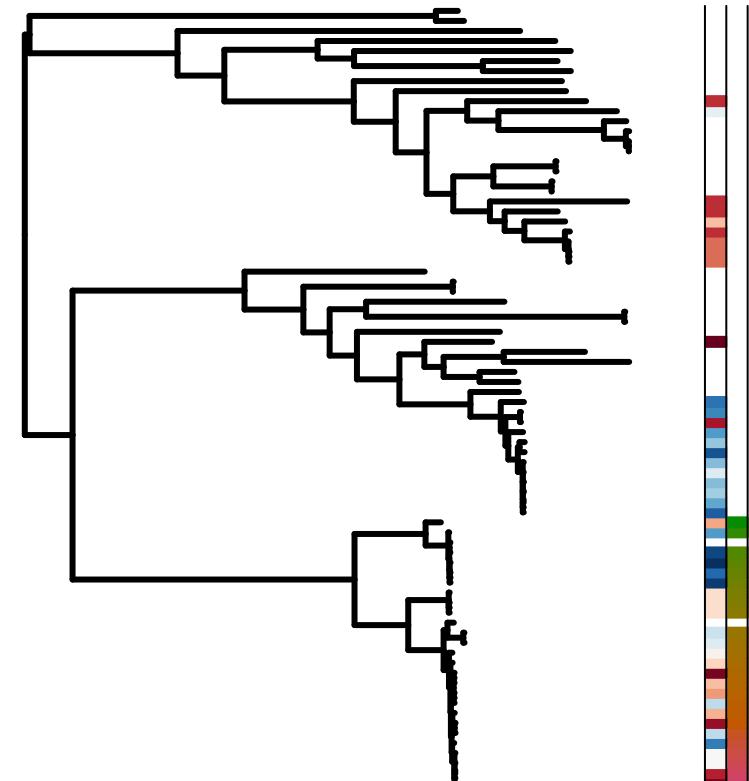
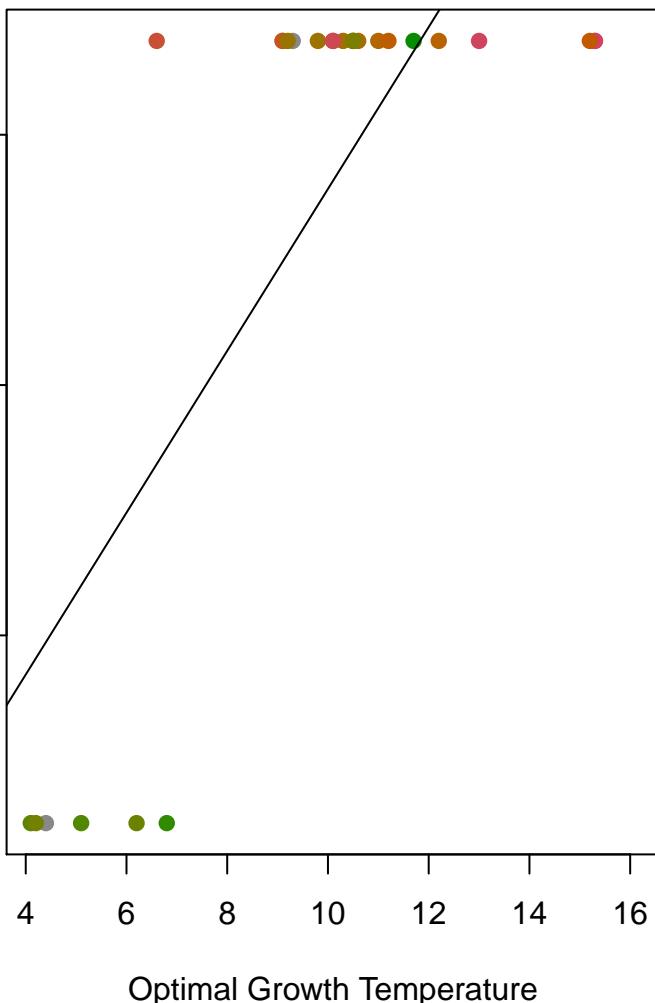
feature.pgfam_id.acidic_residue.mean

PGF_07004481

hypothetical protein

$r = 0.778, p = 10^{-5.746}$

feature.pgfam_id.acidic_residue.mean



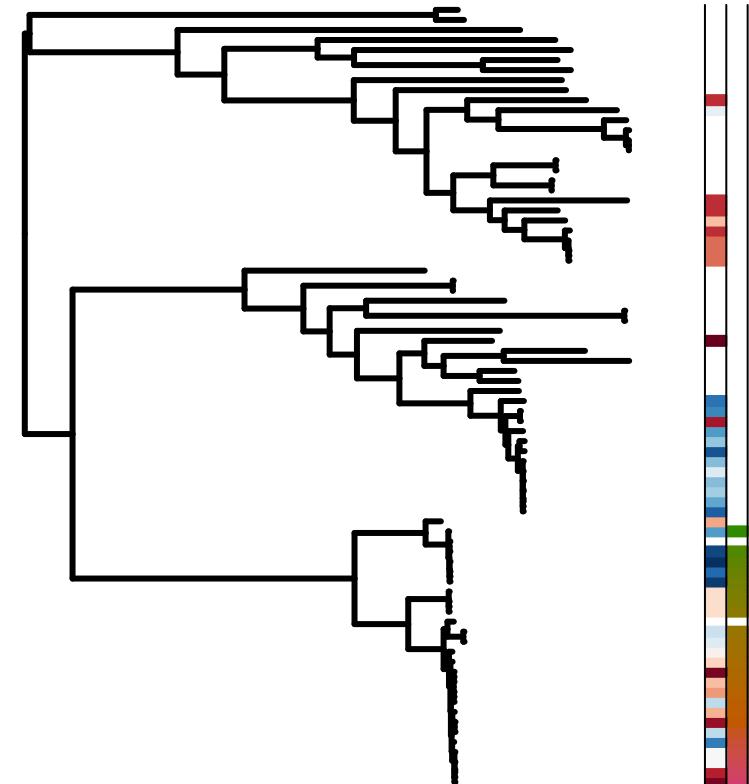
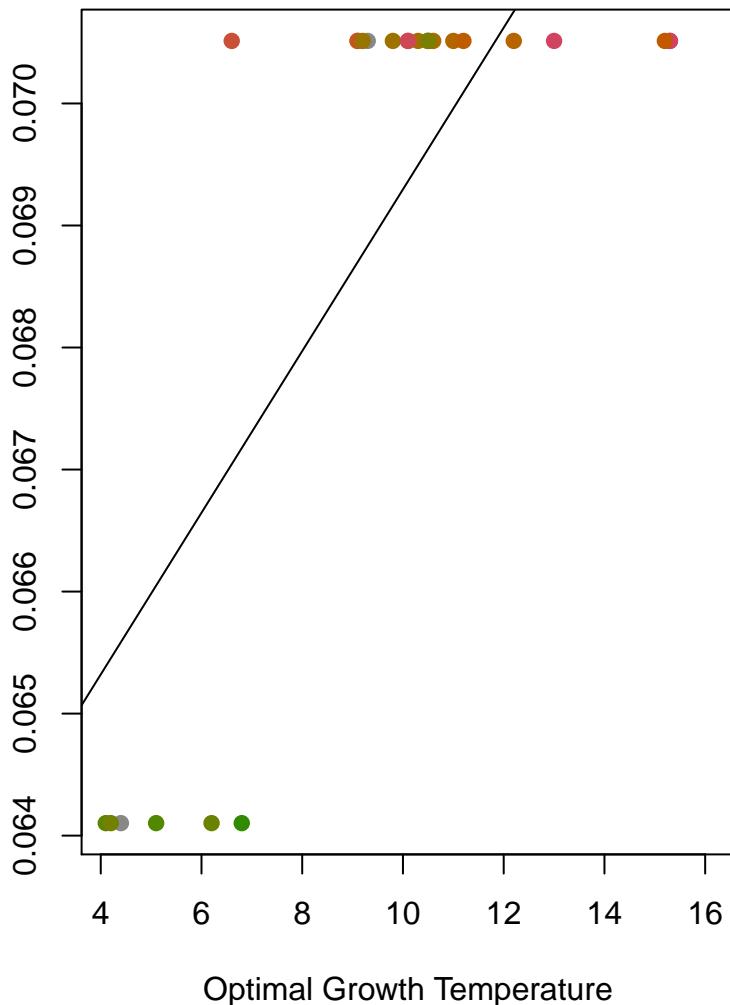
feature.pgfam_id.acidic_residue.mean

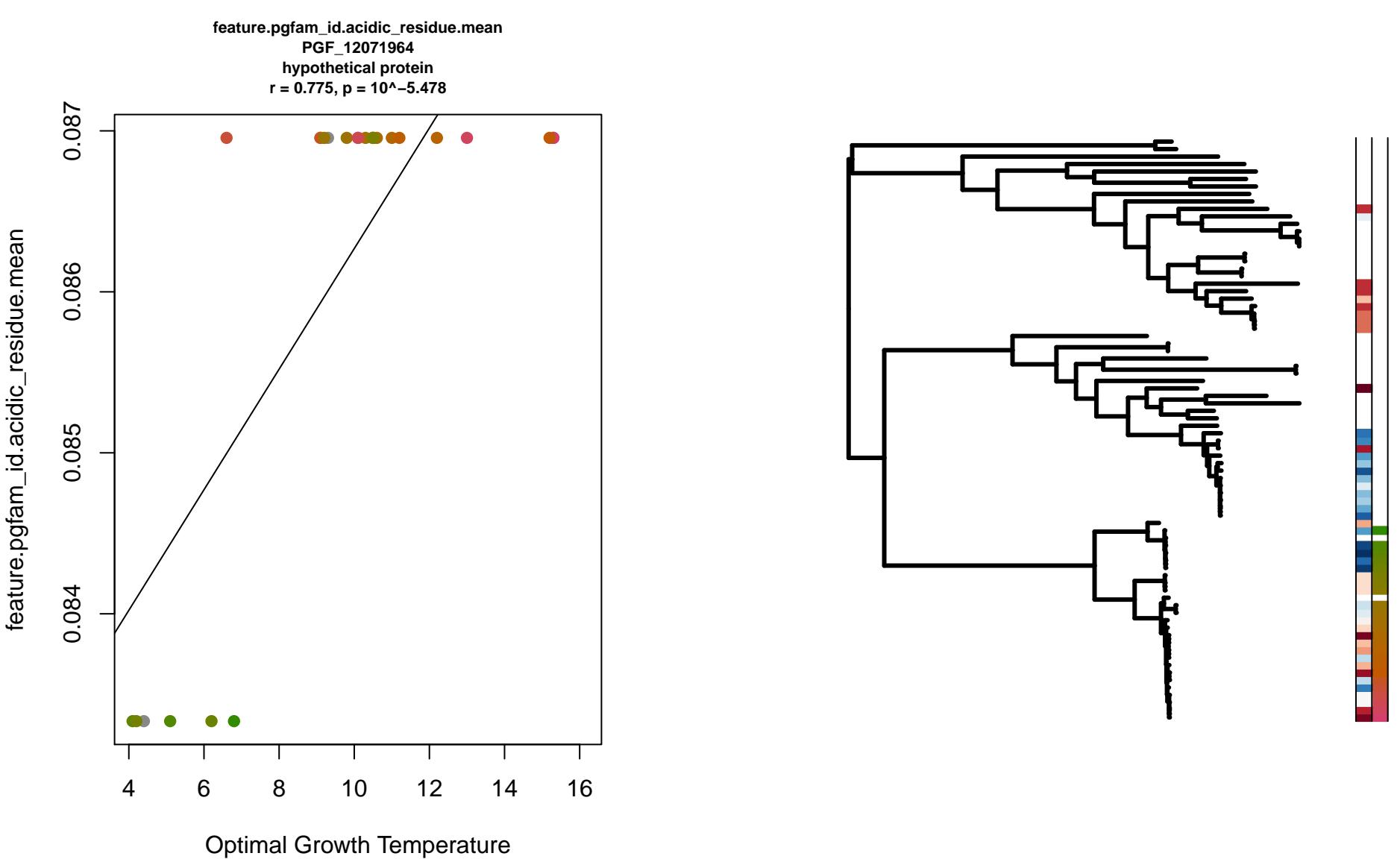
PGF_04213500

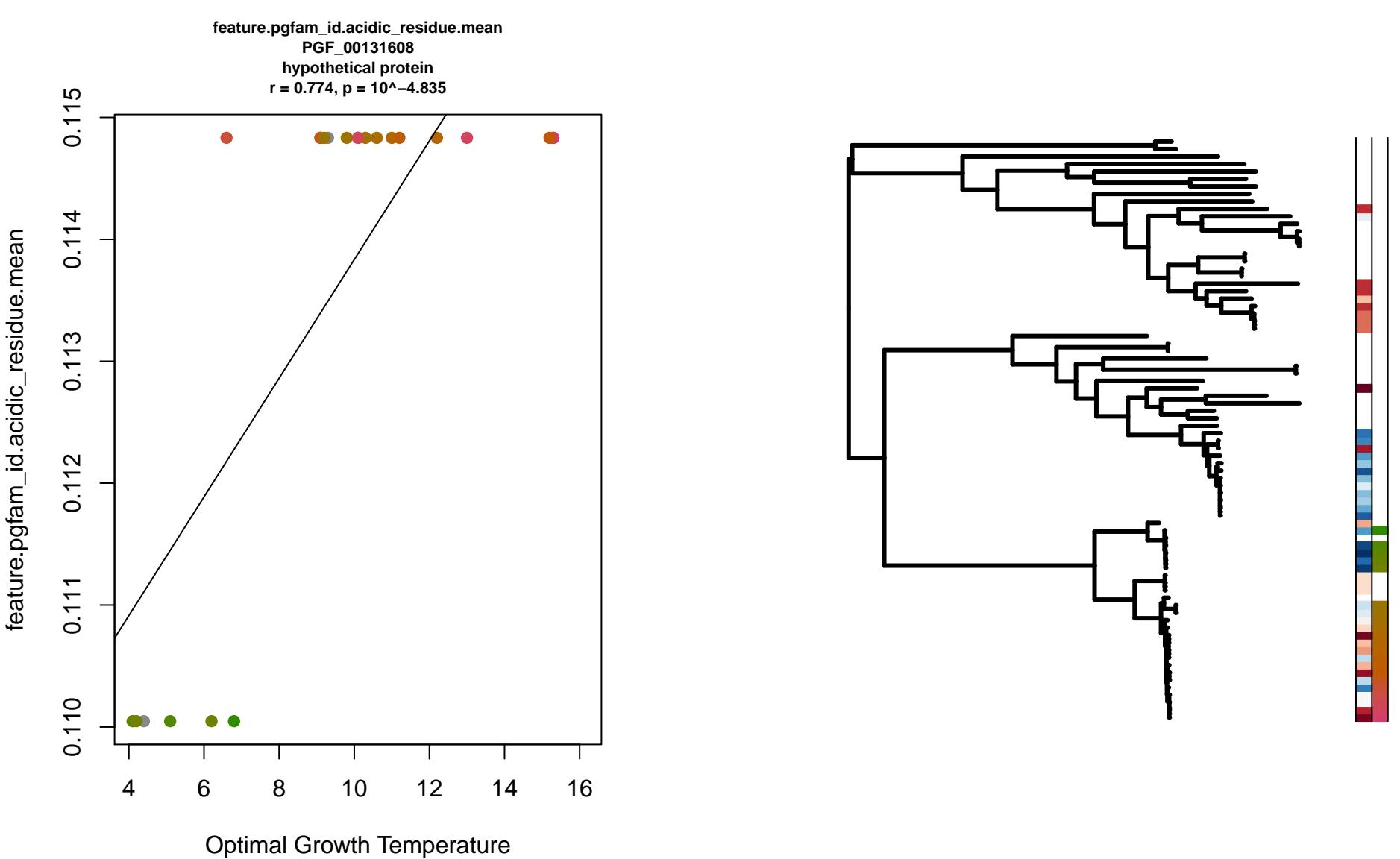
hypothetical protein

$r = 0.775, p = 10^{-5.478}$

feature.pgfam_id.acidic_residue.mean







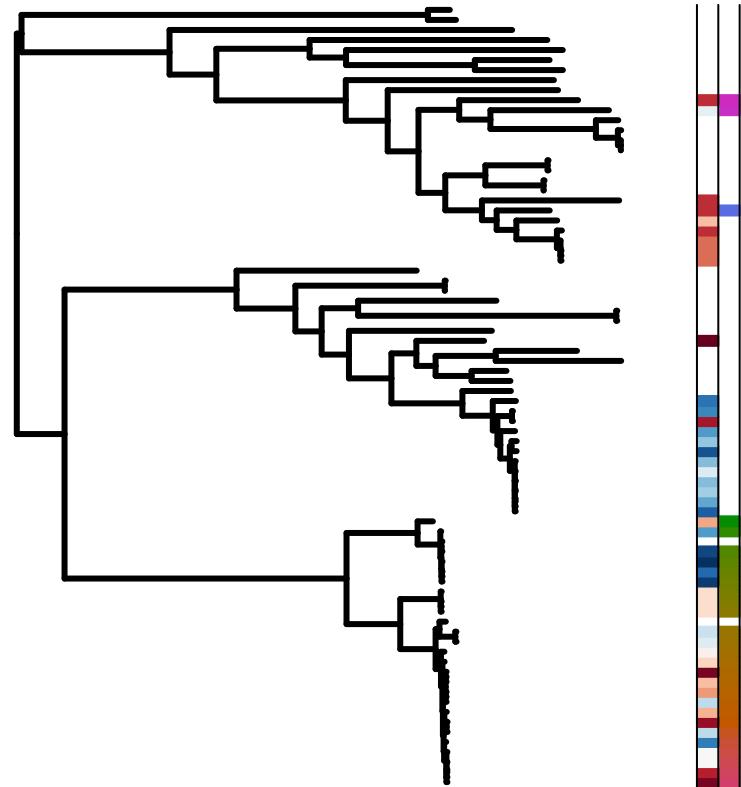
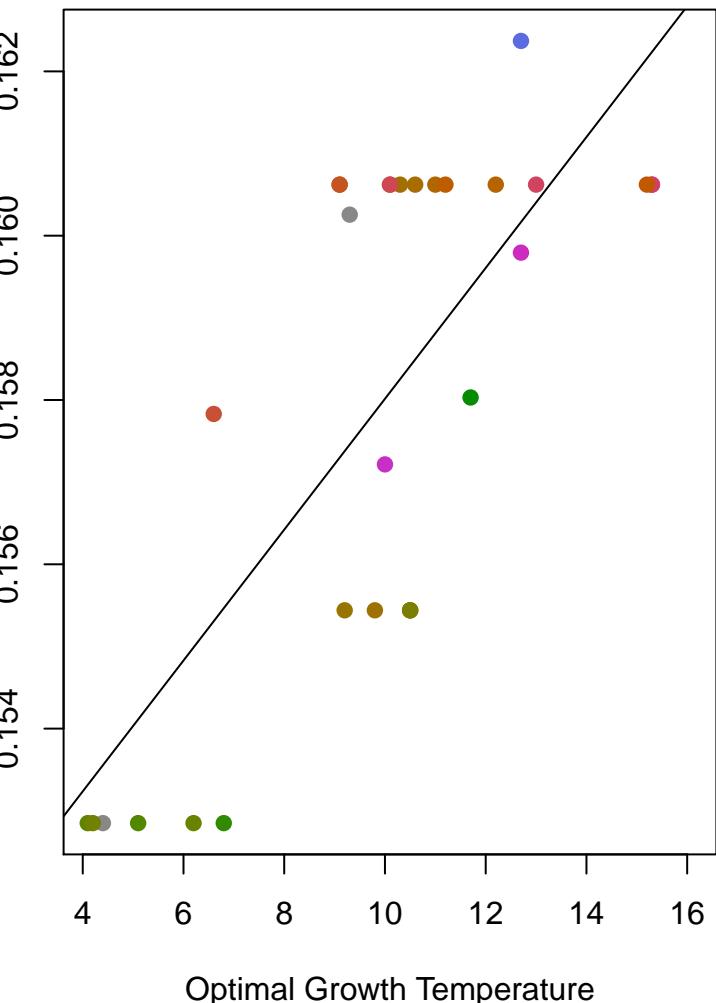
feature.pgfam_id.acidic_residue.mean

PGF_01336977

hypothetical protein

$r = 0.759, p = 10^{-5.932}$

feature.pgfam_id.acidic_residue.mean



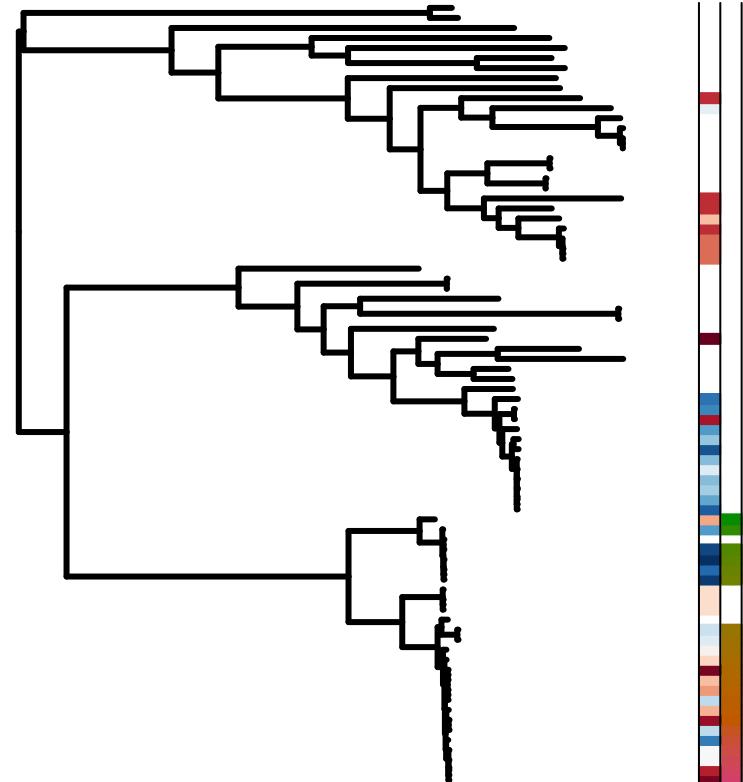
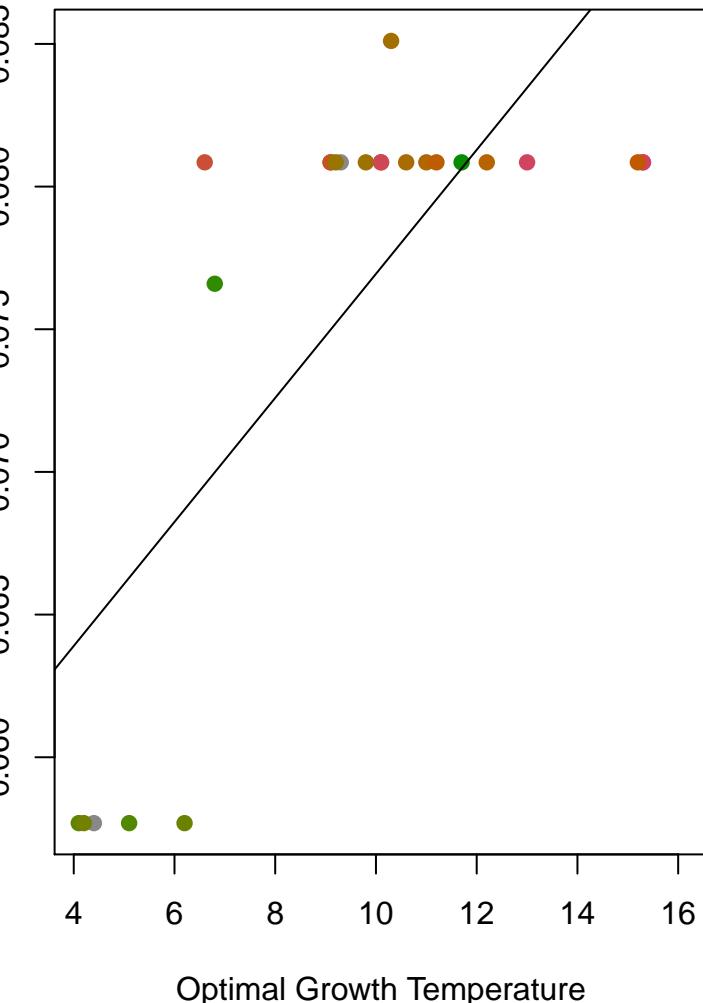
feature.pgfam_id.acidic_residue.mean

PGF_11855093

hypothetical protein

$r = 0.756, p = 10^{-4.721}$

feature.pgfam_id.acidic_residue.mean



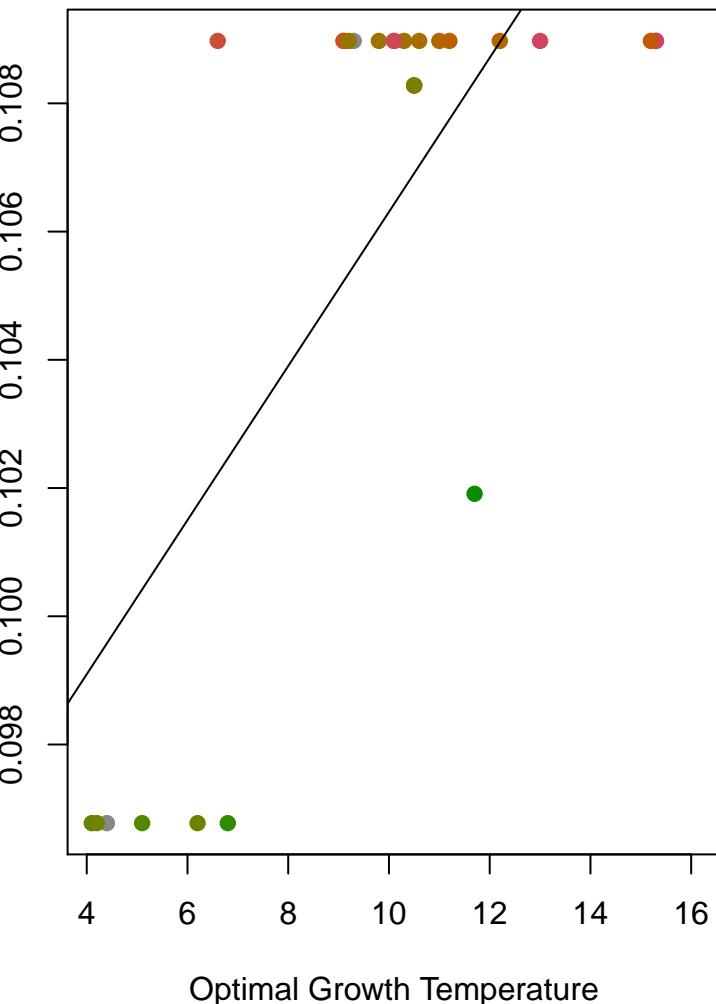
feature.pgfam_id.acidic_residue.mean

PGF_07813500

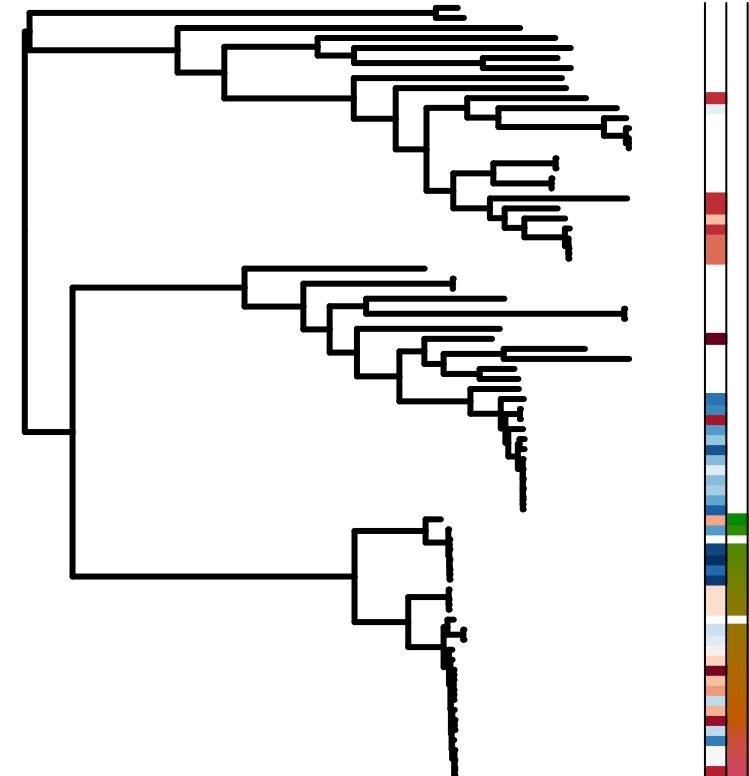
hypothetical protein

$r = 0.741, p = 10^{-5.013}$

feature.pgfam_id.acidic_residue.mean

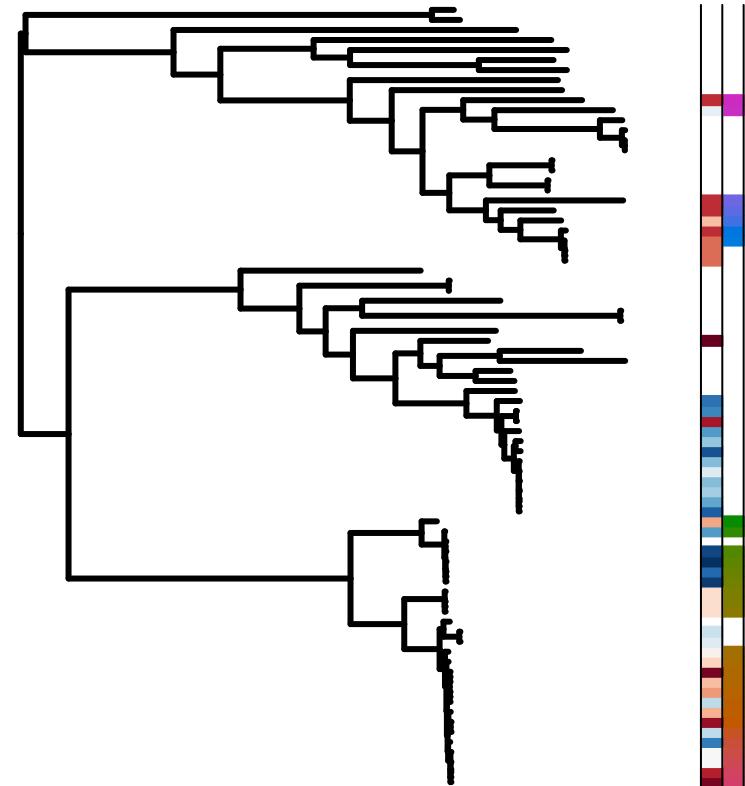
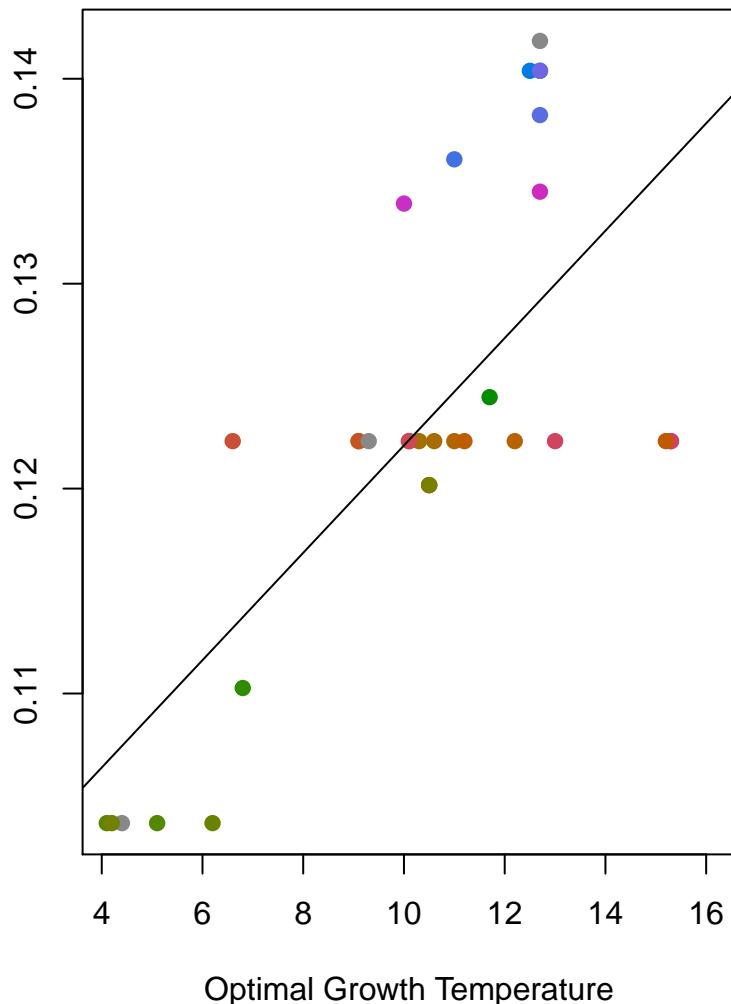


Optimal Growth Temperature



feature.pgfam_id.acidic_residue.mean
PGF_02105064
Uncharacterized protease YegQ
 $r = 0.728$, $p = 10^{-5.793}$

feature.pgfam_id.acidic_residue.mean



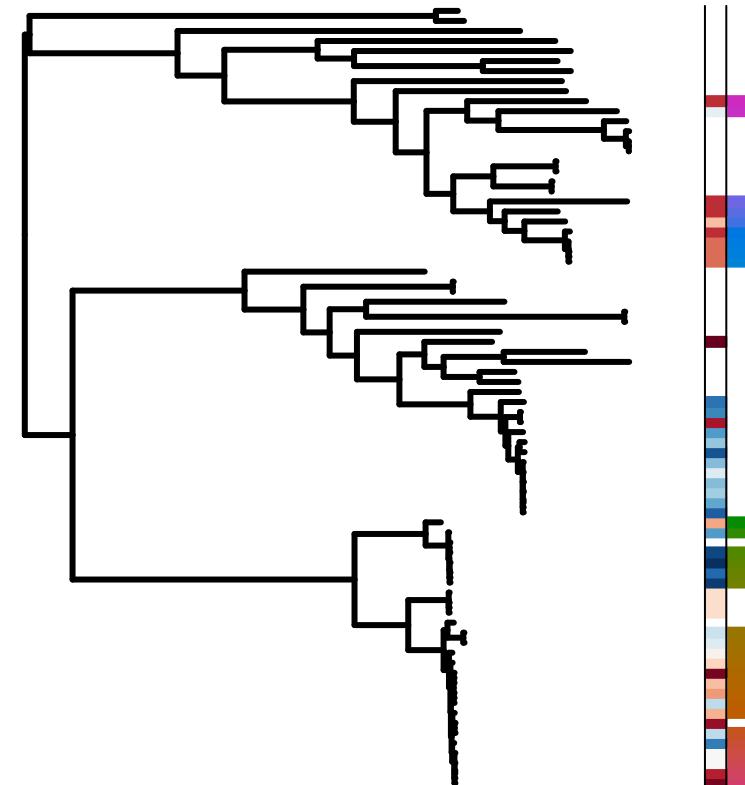
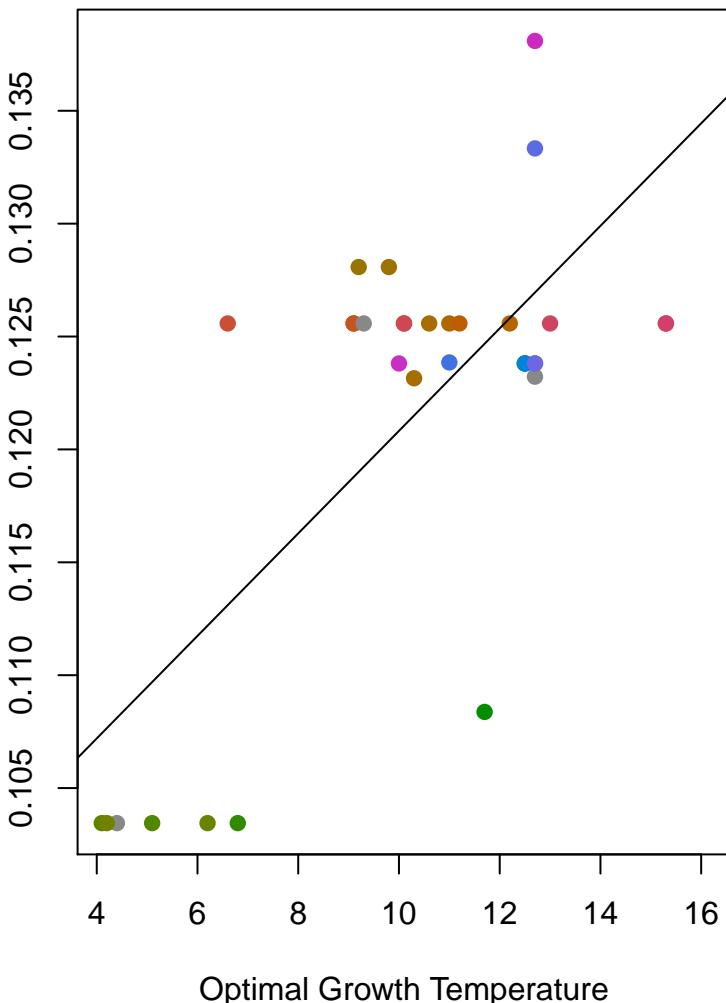
feature.pgfam_id.acidic_residue.mean

PGF_03940803

Alkylated DNA repair protein

$r = 0.724, p = 10^{-5.714}$

feature.pgfam_id.acidic_residue.mean



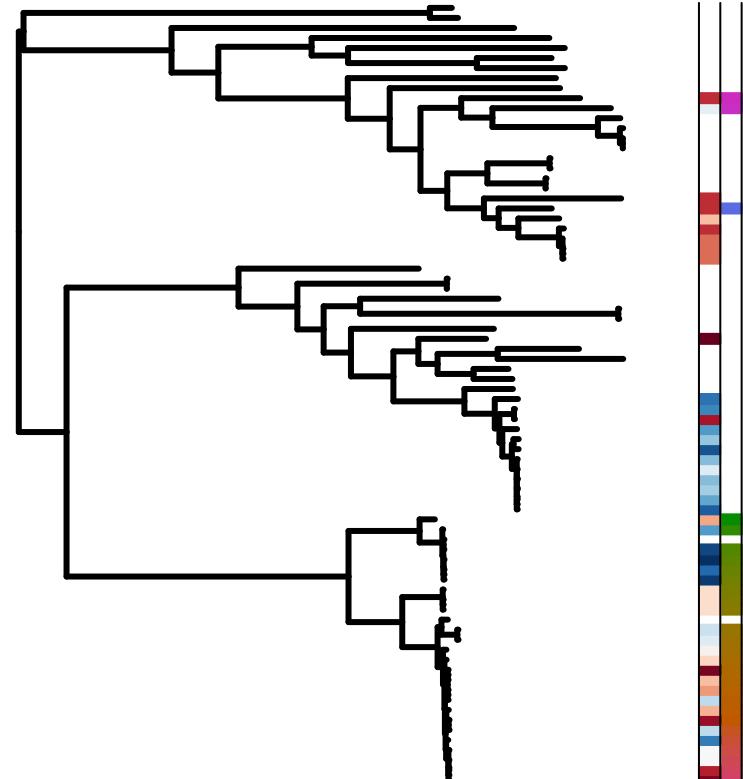
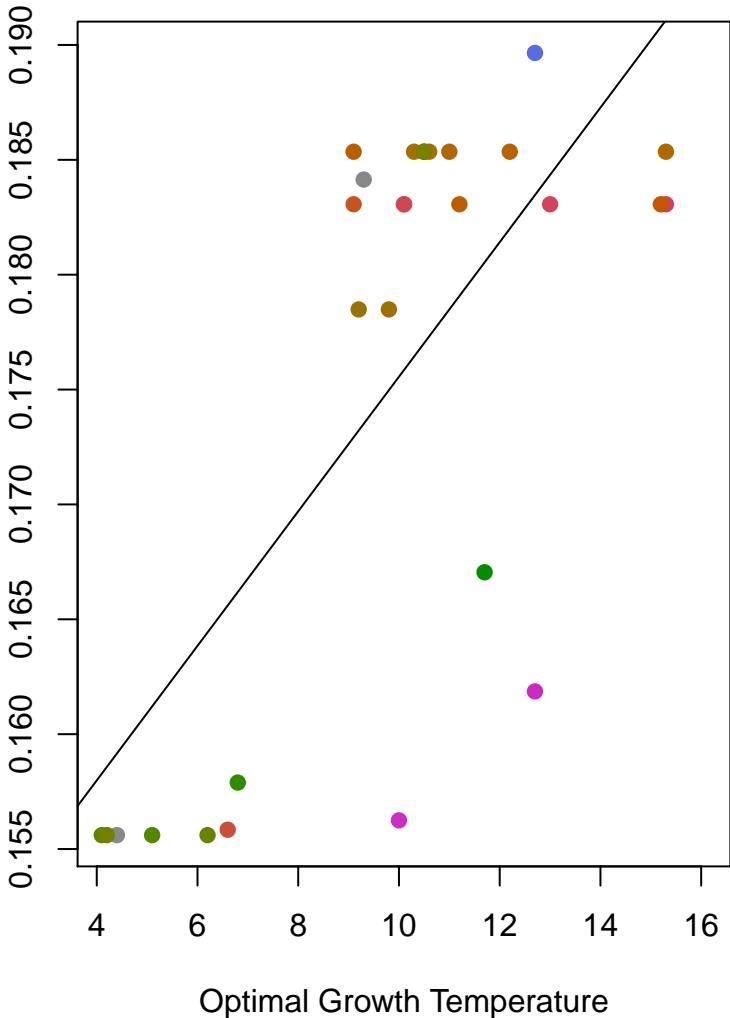
feature.pgfam_id.acidic_residue.mean

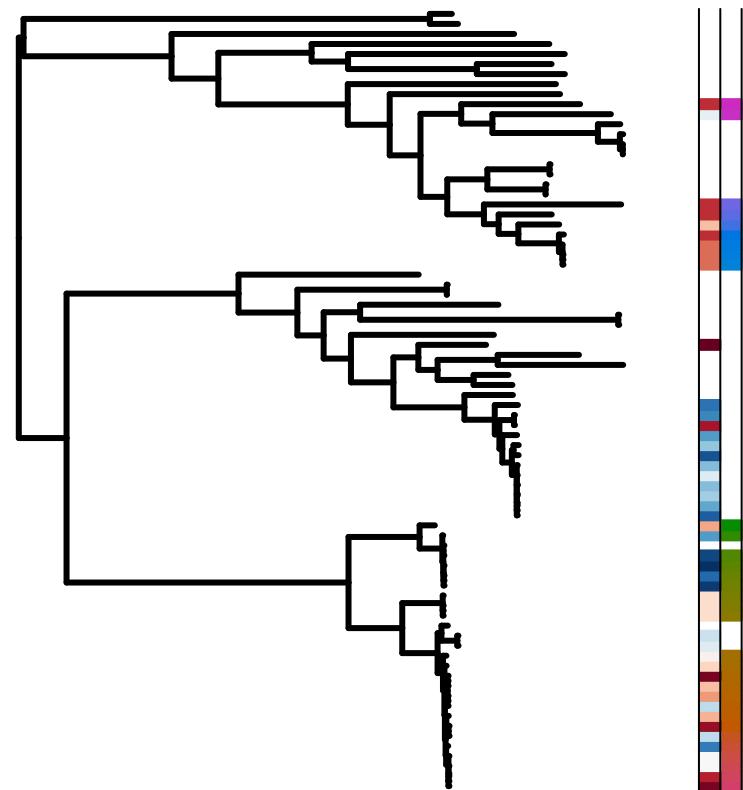
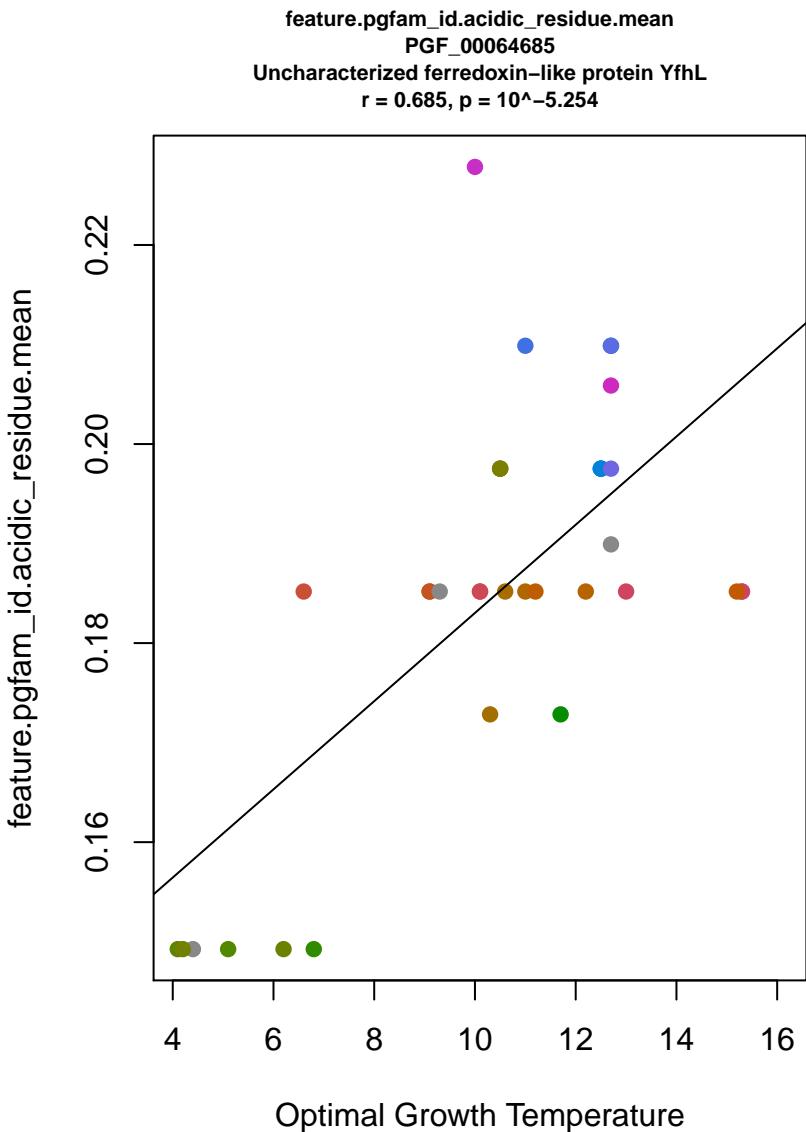
PGF_01336976

hypothetical protein

$r = 0.703, p = 10^{-4.834}$

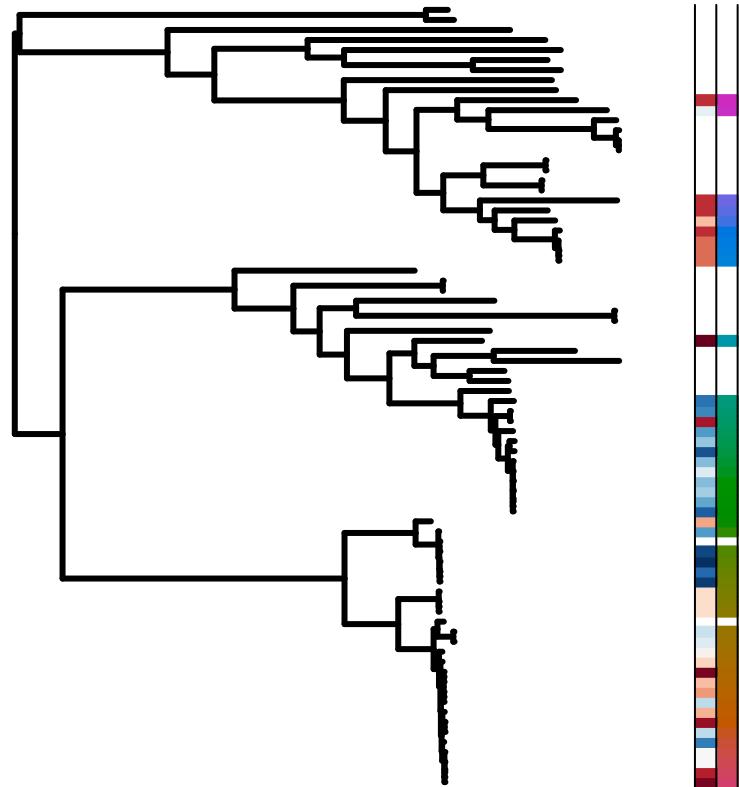
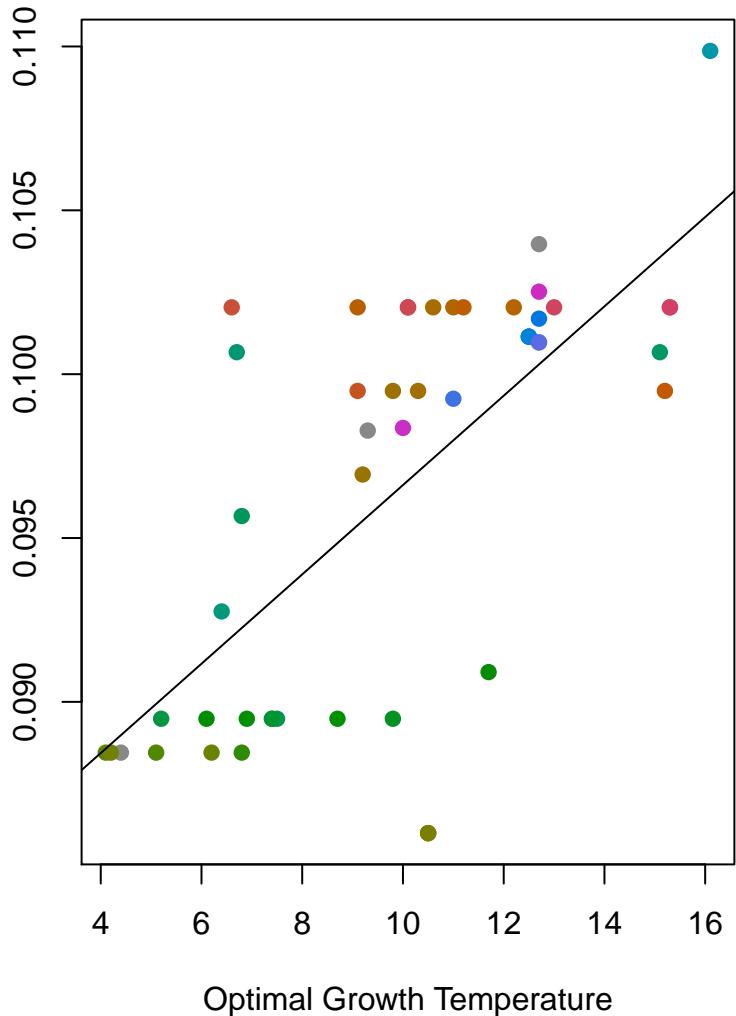
feature.pgfam_id.acidic_residue.mean





feature.pgfam_id.acidic_residue.mean
PGF_02328856
Type IV pilus biogenesis protein PilF
 $r = 0.676$, $p = 10^{-7.155}$

feature.pgfam_id.acidic_residue.mean



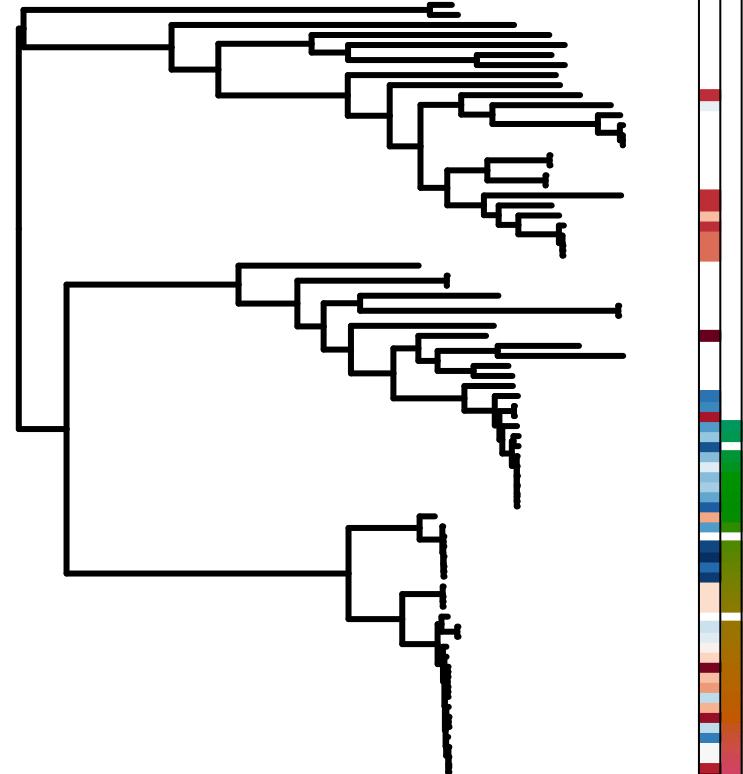
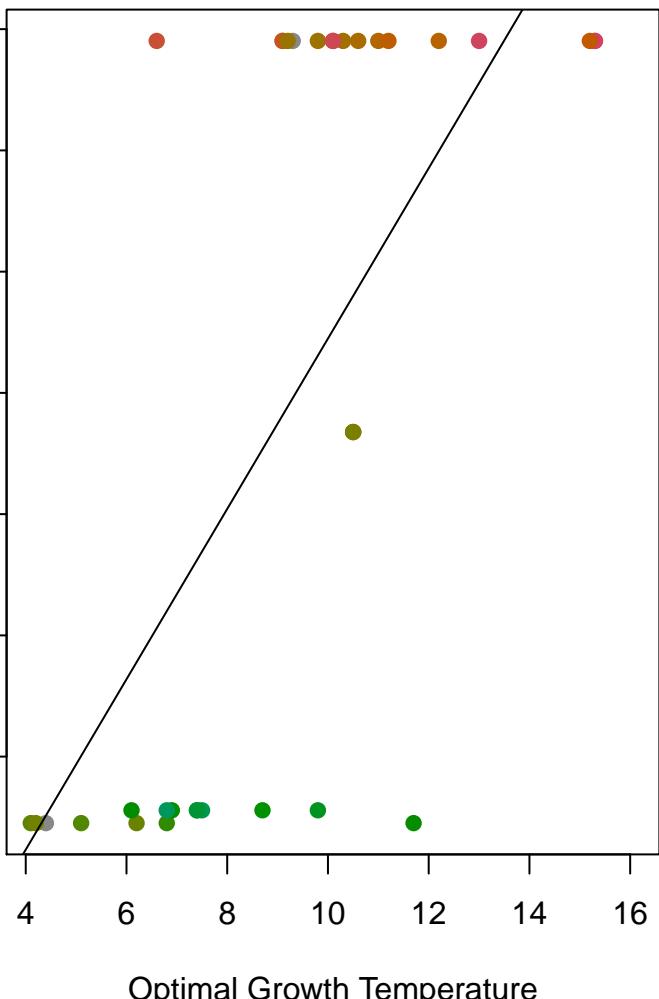
feature.pgfam_id.acidic_residue.mean

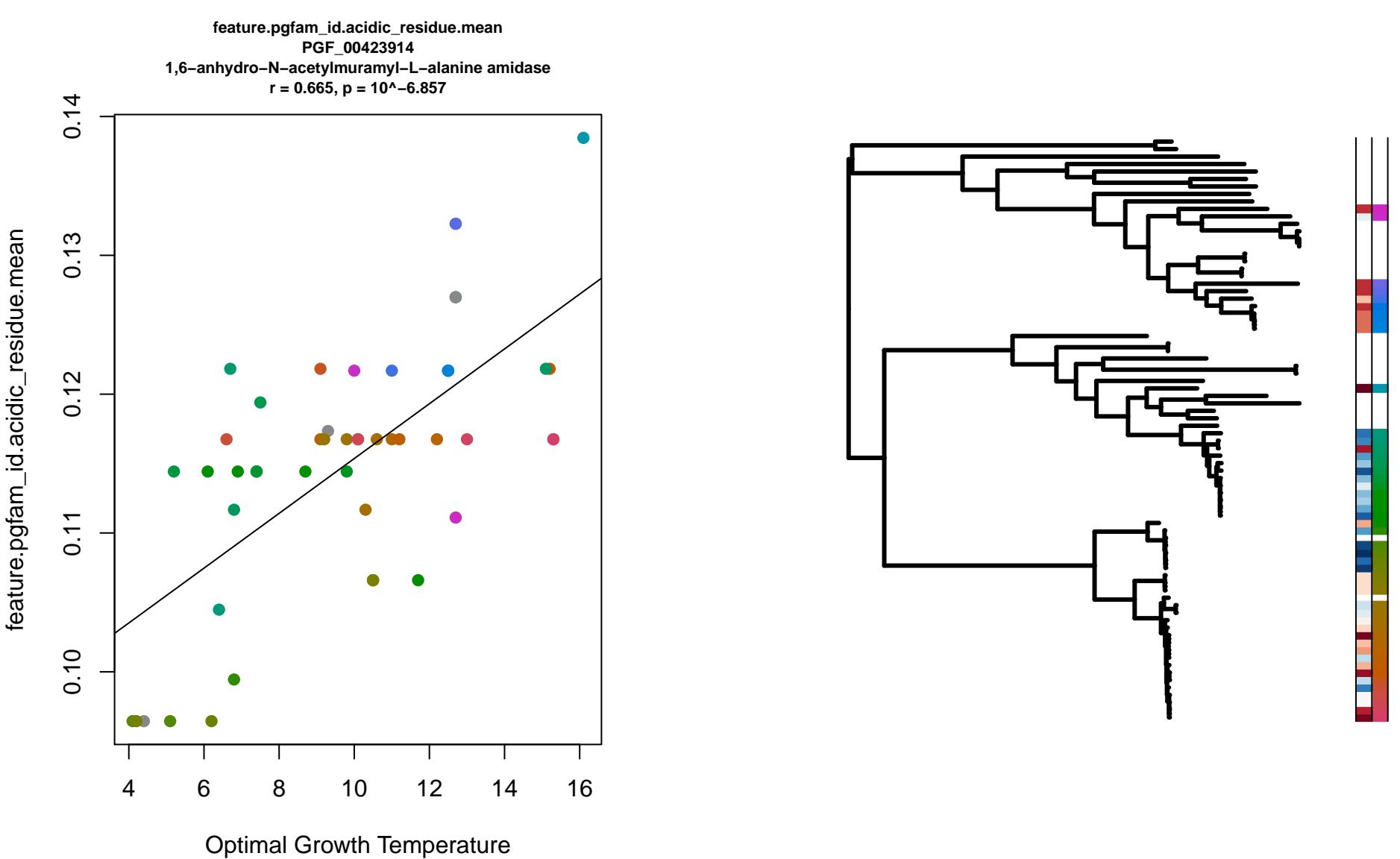
PGF_07991944

hypothetical protein

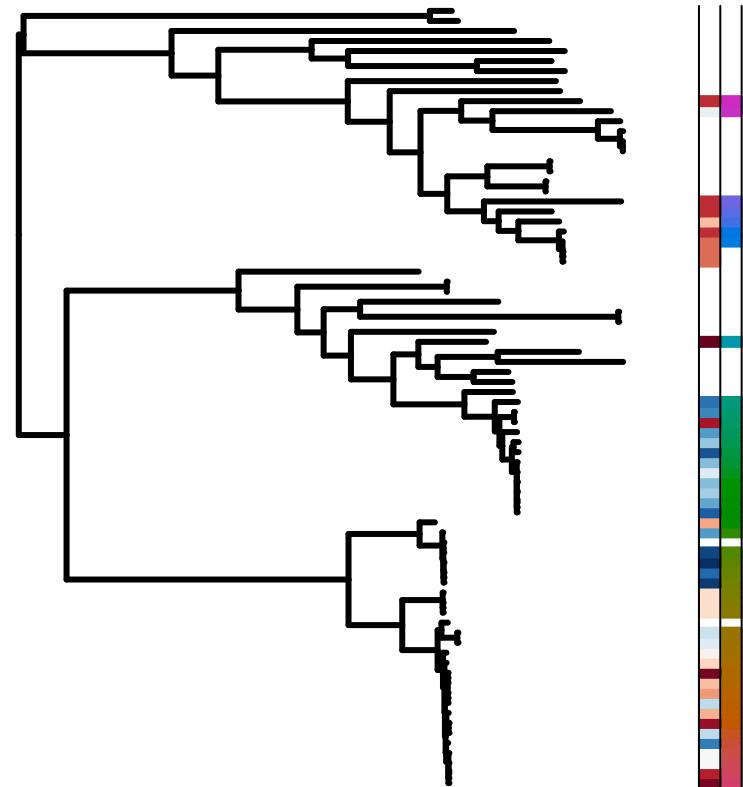
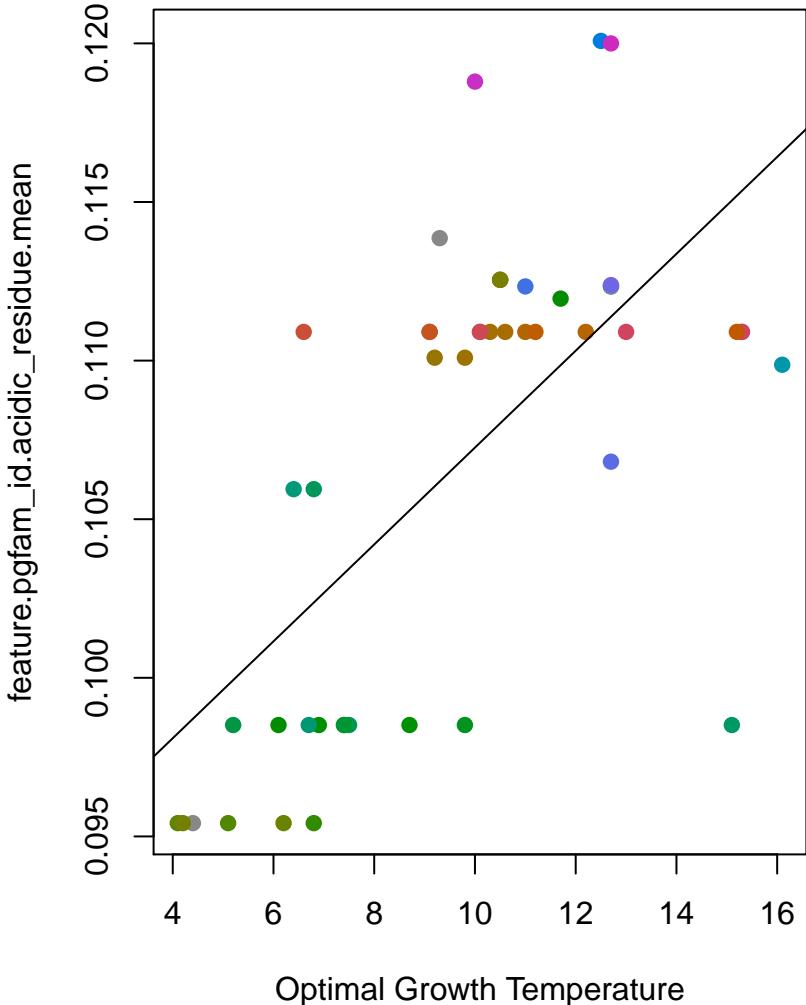
$r = 0.675, p = 10^{-5.053}$

feature.pgfam_id.acidic_residue.mean

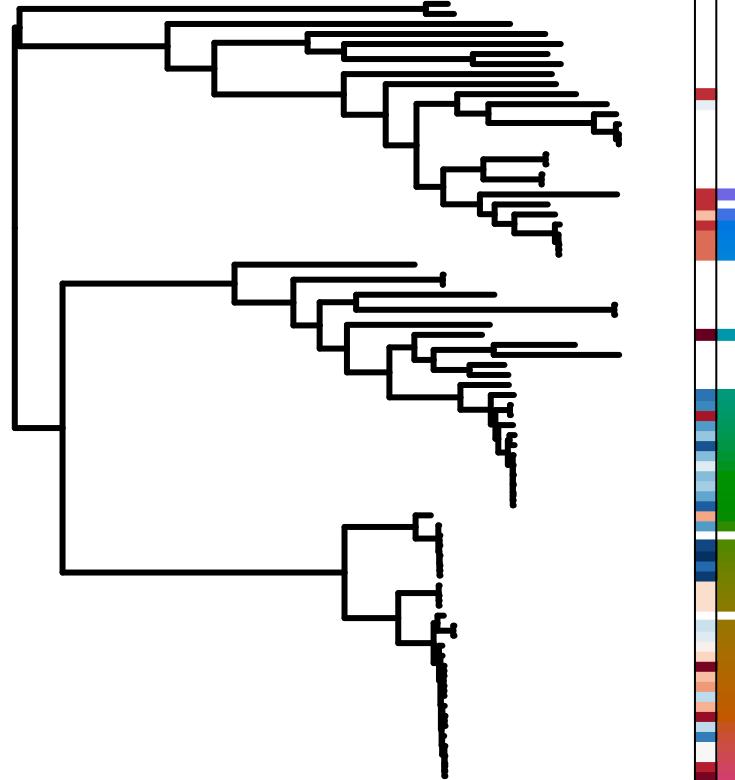
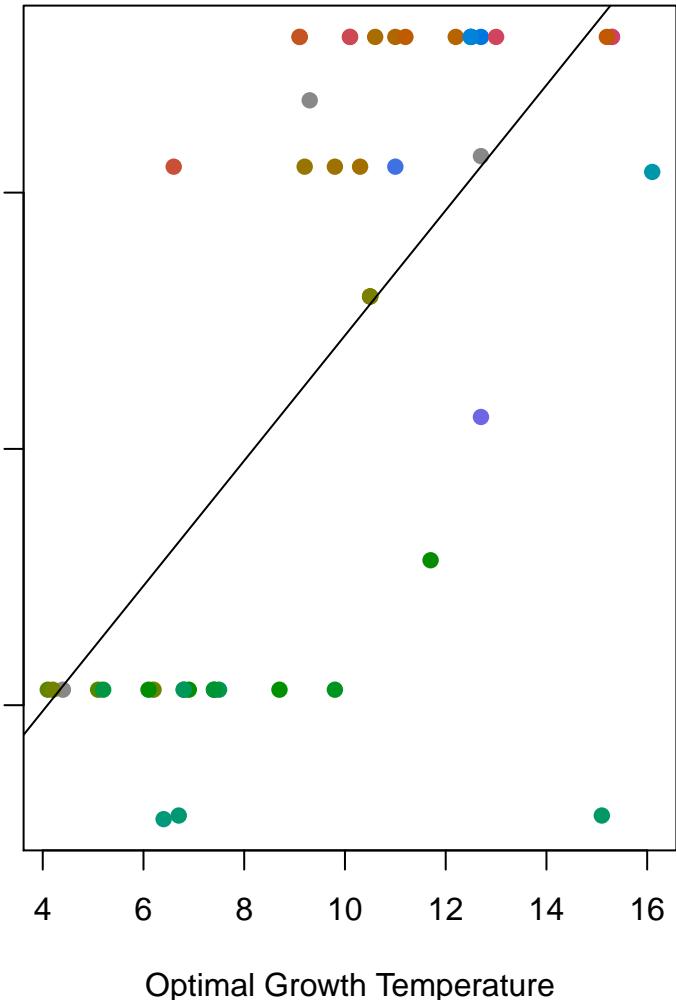


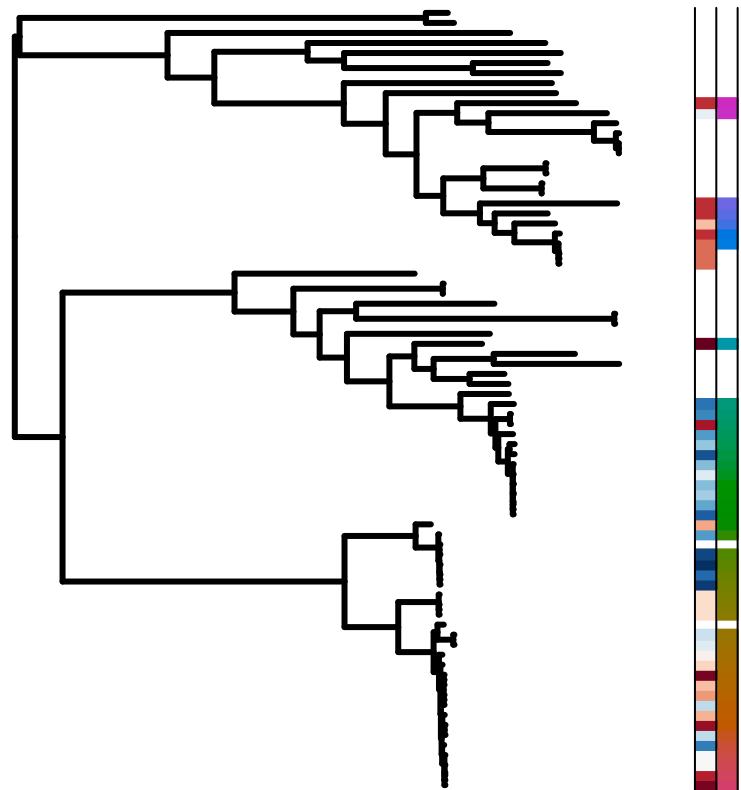
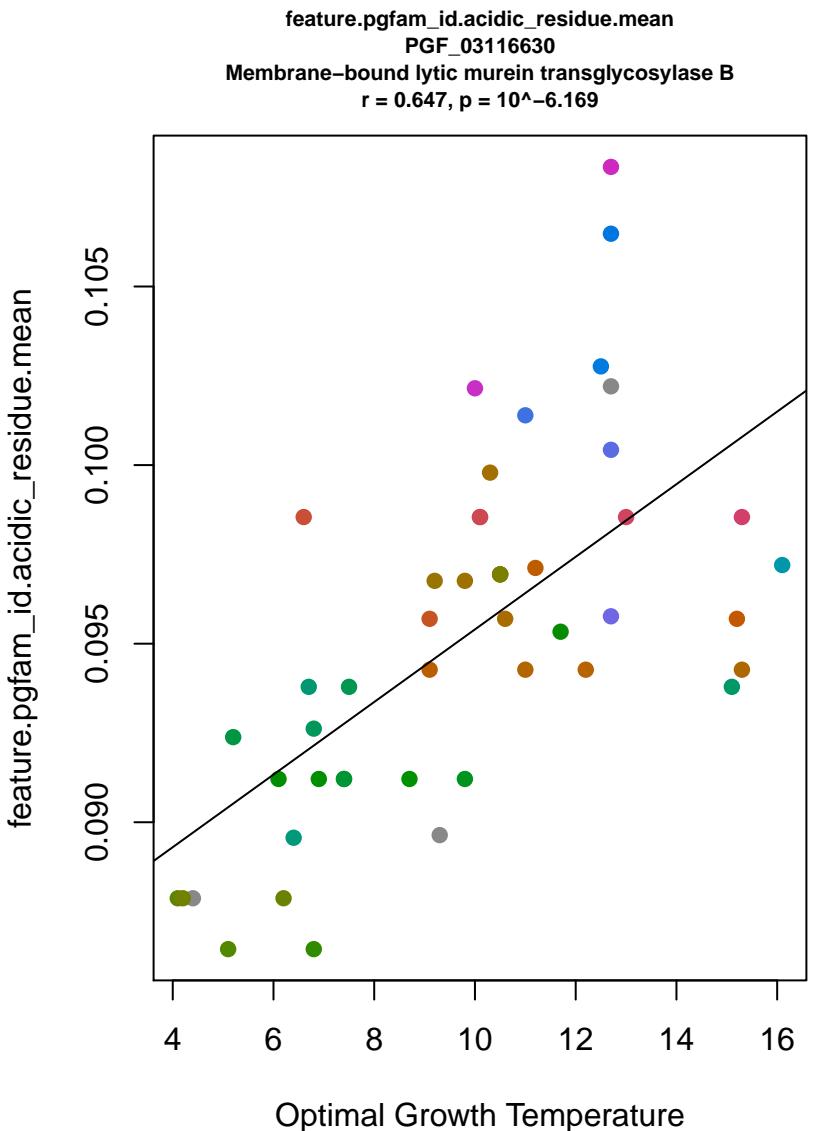


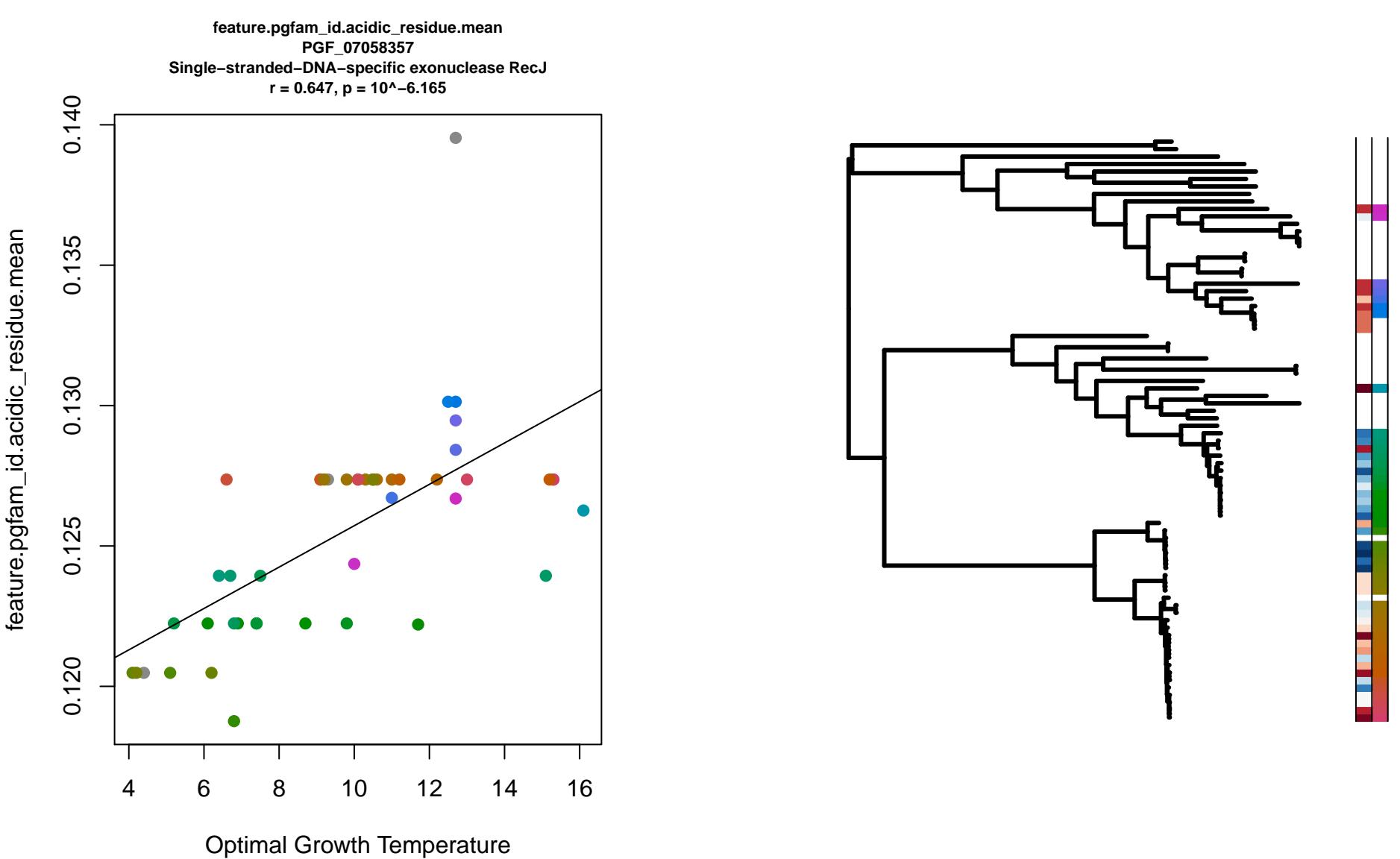
feature.pgfam_id.acidic_residue.mean
PGF_01763633
Sensory box histidine kinase
 $r = 0.662$, $p = 10^{-6.516}$



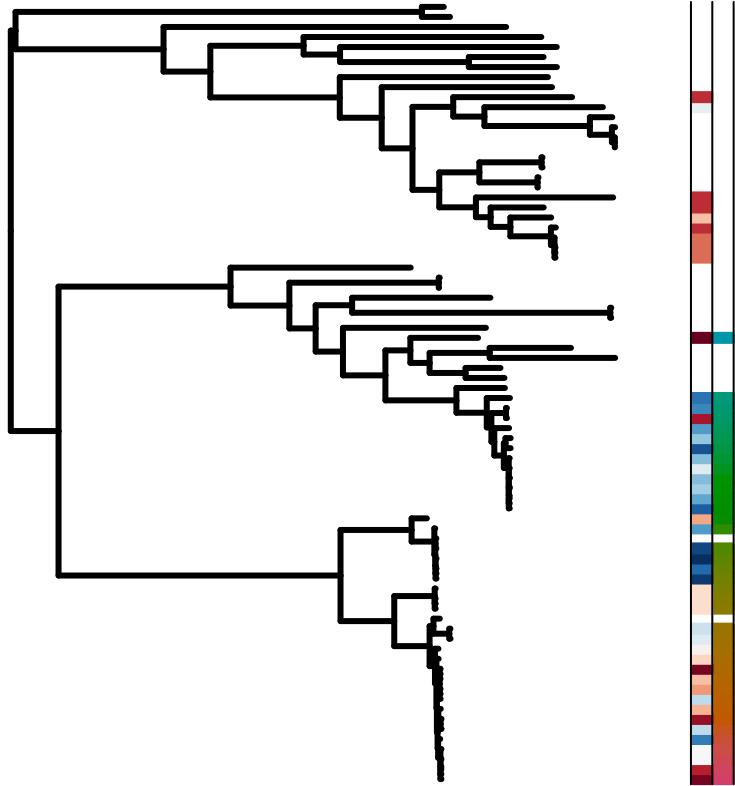
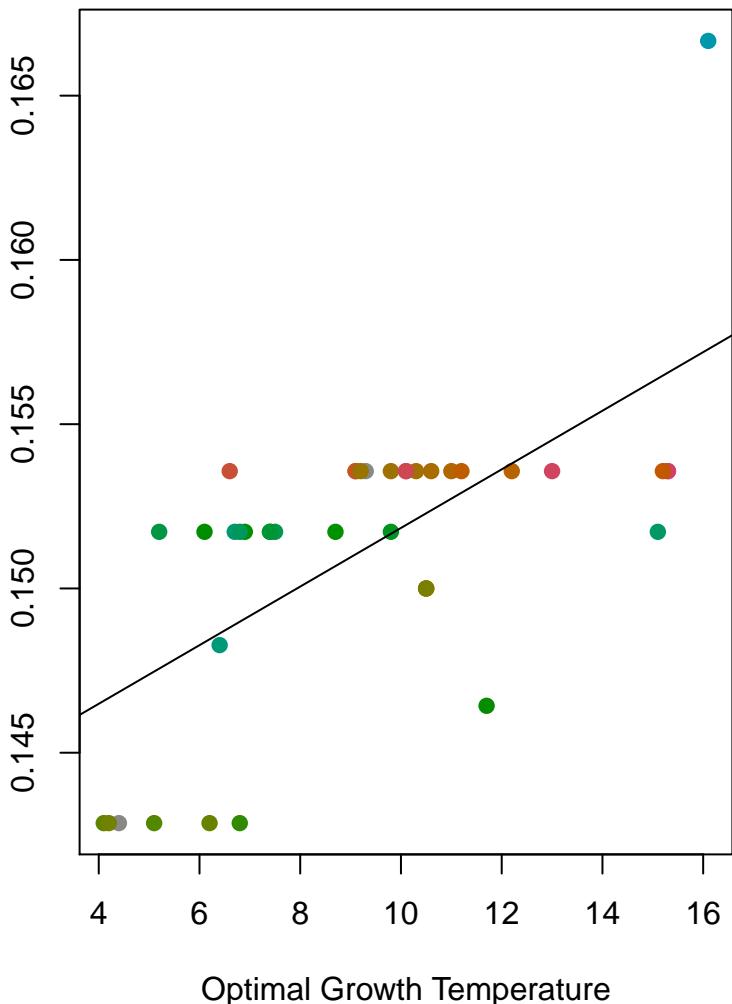
feature.pgfam_id.acidic_residue.mean
PGF_00755593
Uncharacterized MFS-type transporter
 $r = 0.655, p = 10^{-6.228}$



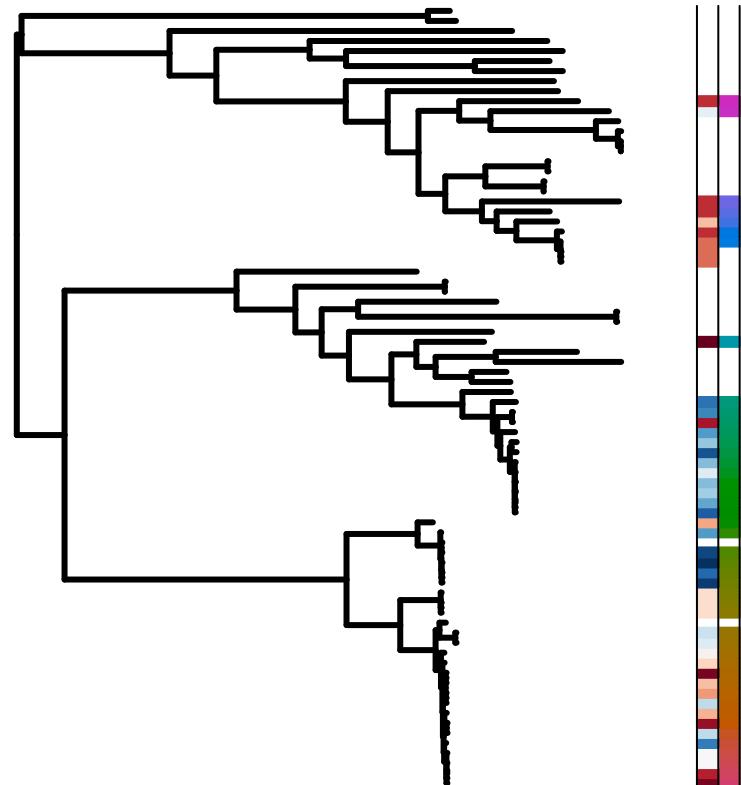
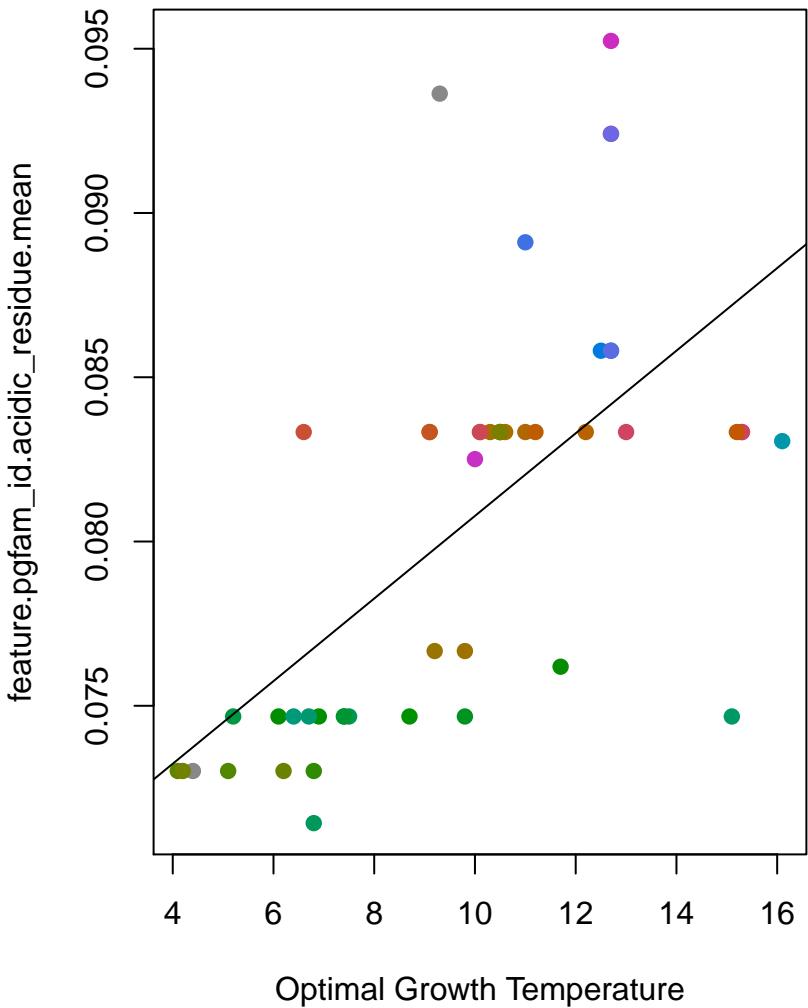




feature.pgfam_id.acidic_residue.mean
PGF_02517283
Segregation and condensation protein A
 $r = 0.644$, $p = 10^{-5.141}$



feature.pgfam_id.acidic_residue.mean
PGF_05546469
Probable acyltransferase PA0834
 $r = 0.642$, $p = 10^{-6.057}$



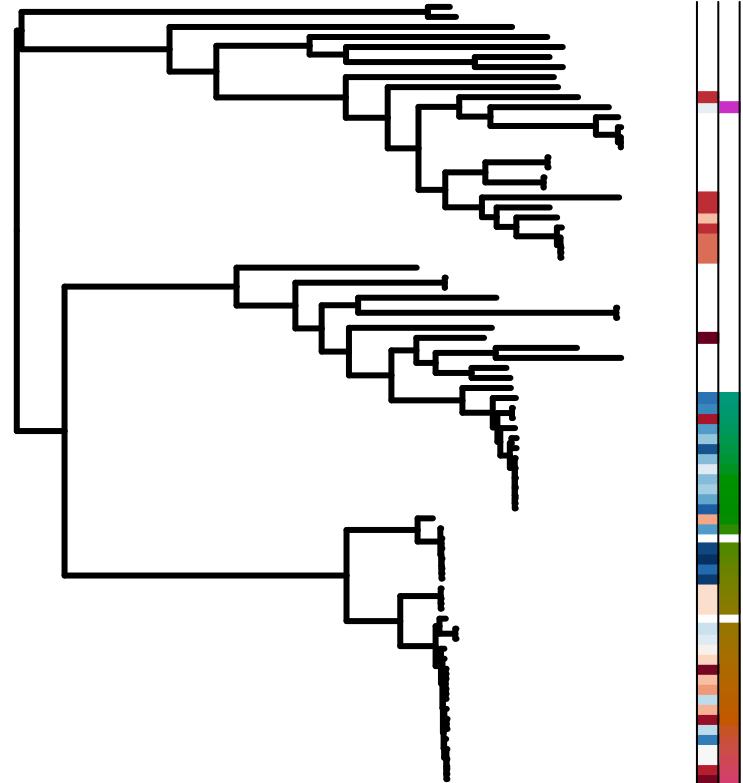
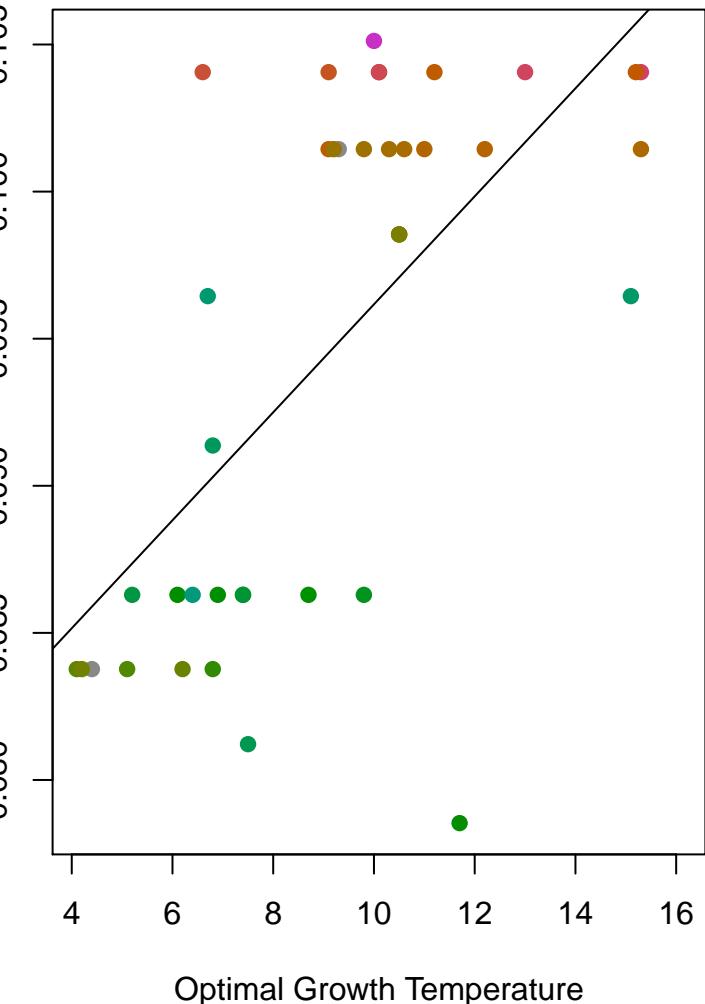
feature.pgfam_id.acidic_residue.mean

PGF_01338555

hypothetical protein

$r = 0.64, p = 10^{-5.068}$

feature.pgfam_id.acidic_residue.mean

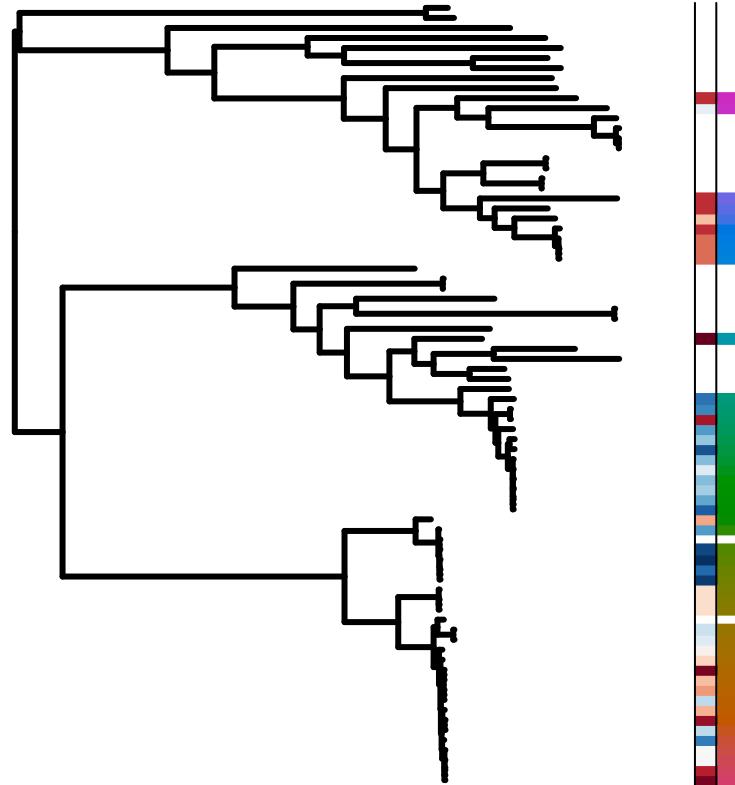
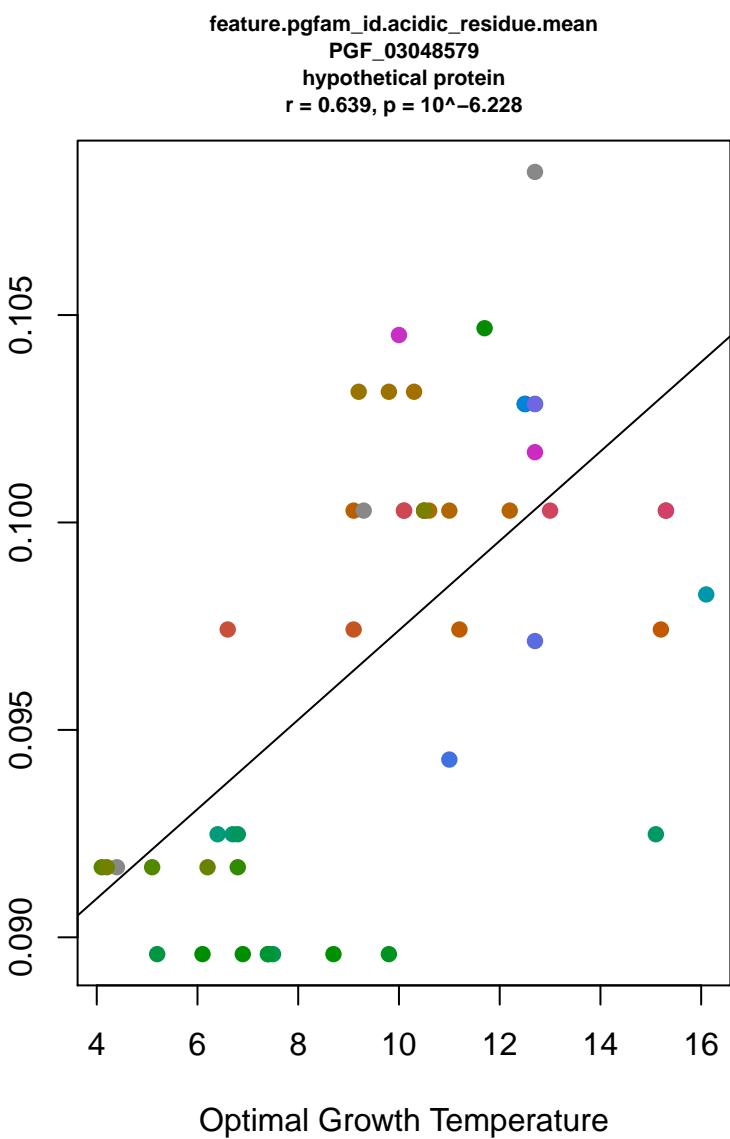


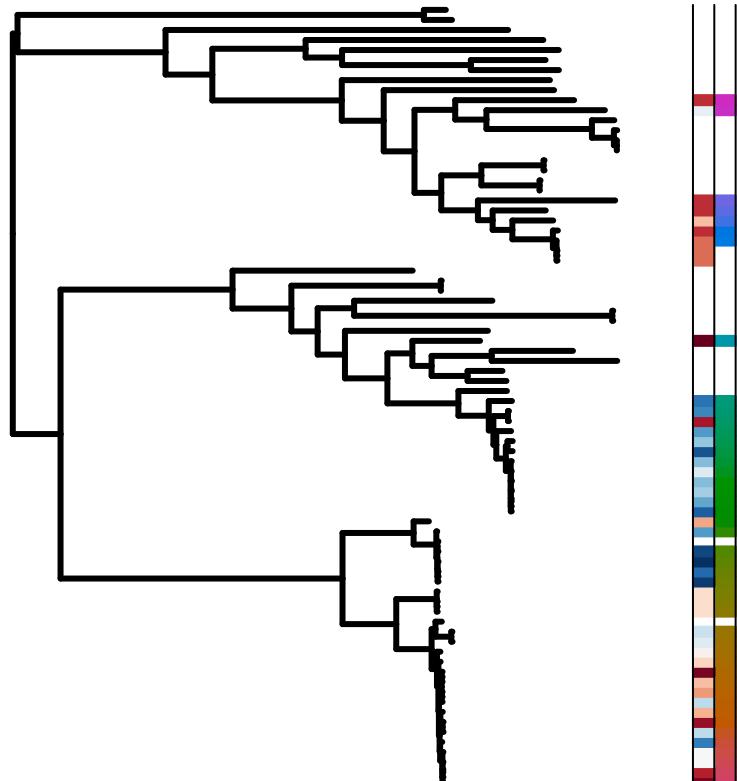
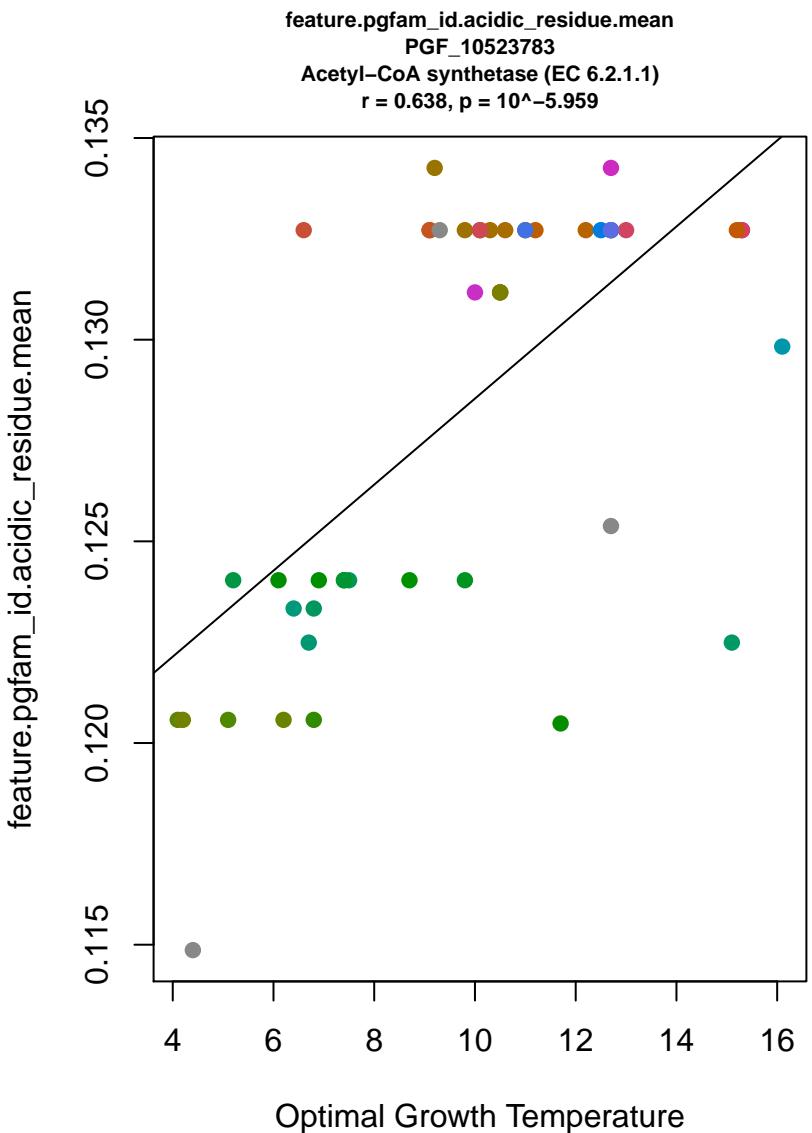
feature.pgfam_id.acidic_residue.mean

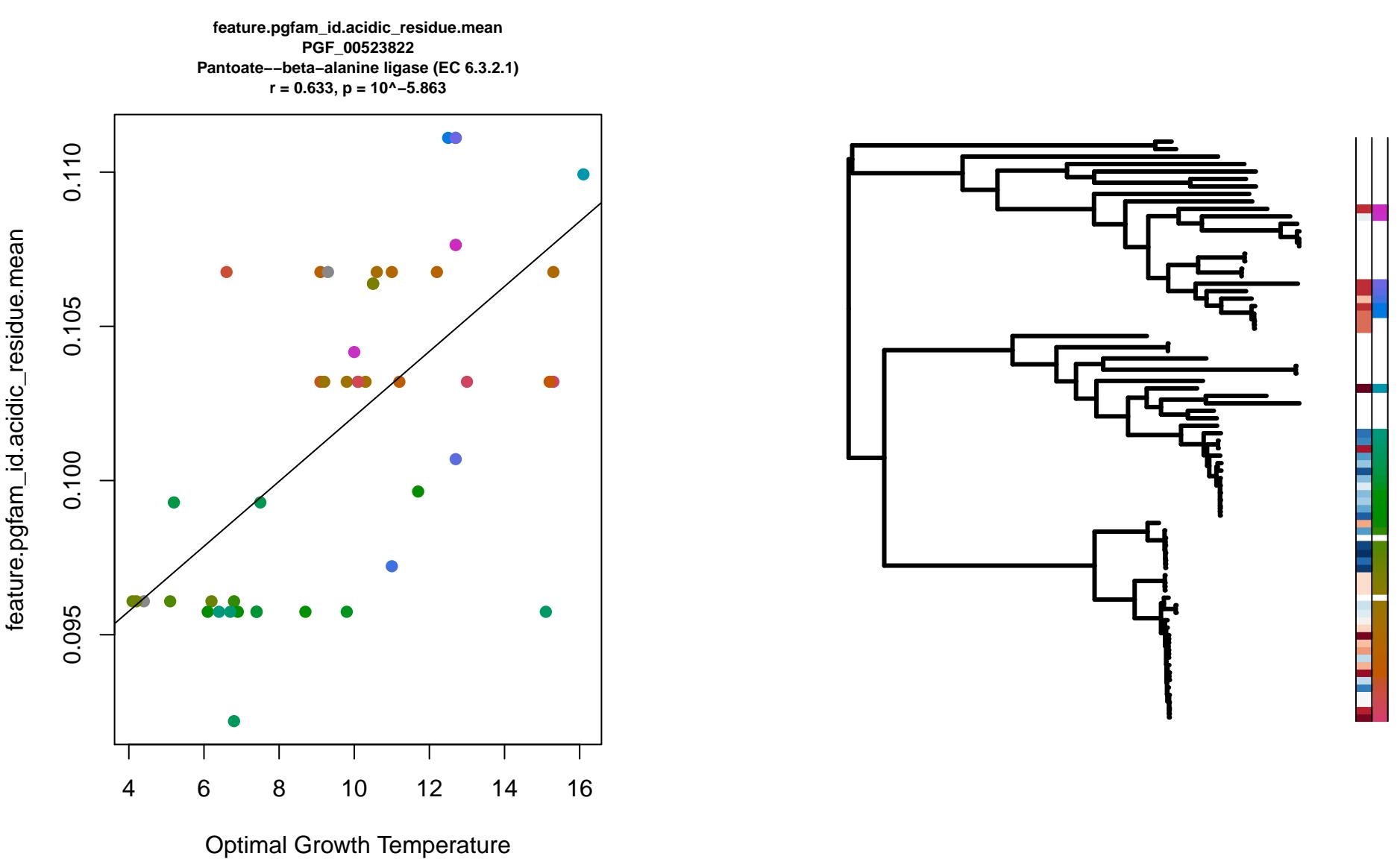
PGF_03048579

hypothetical protein

$r = 0.639$, $p = 10^{-6.228}$



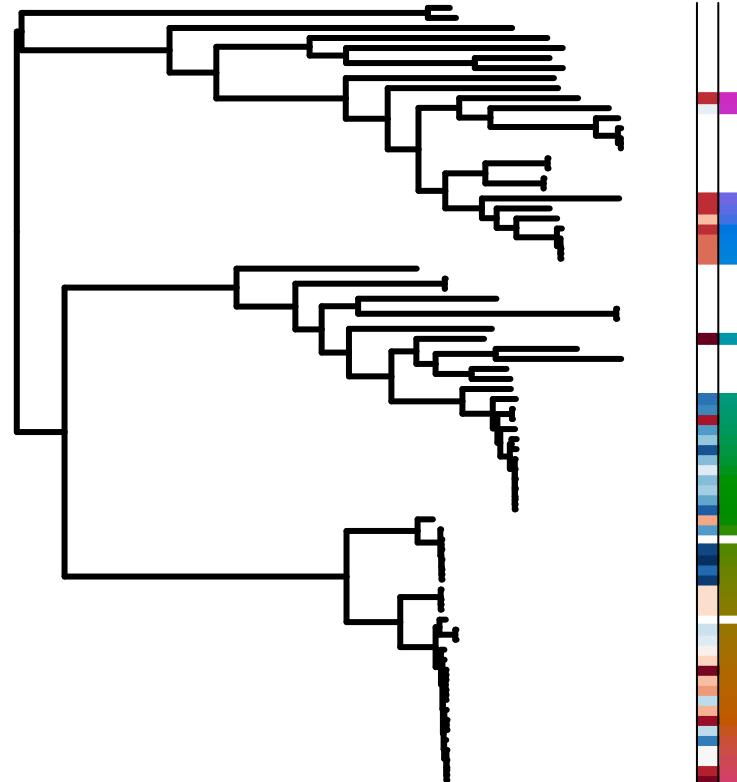
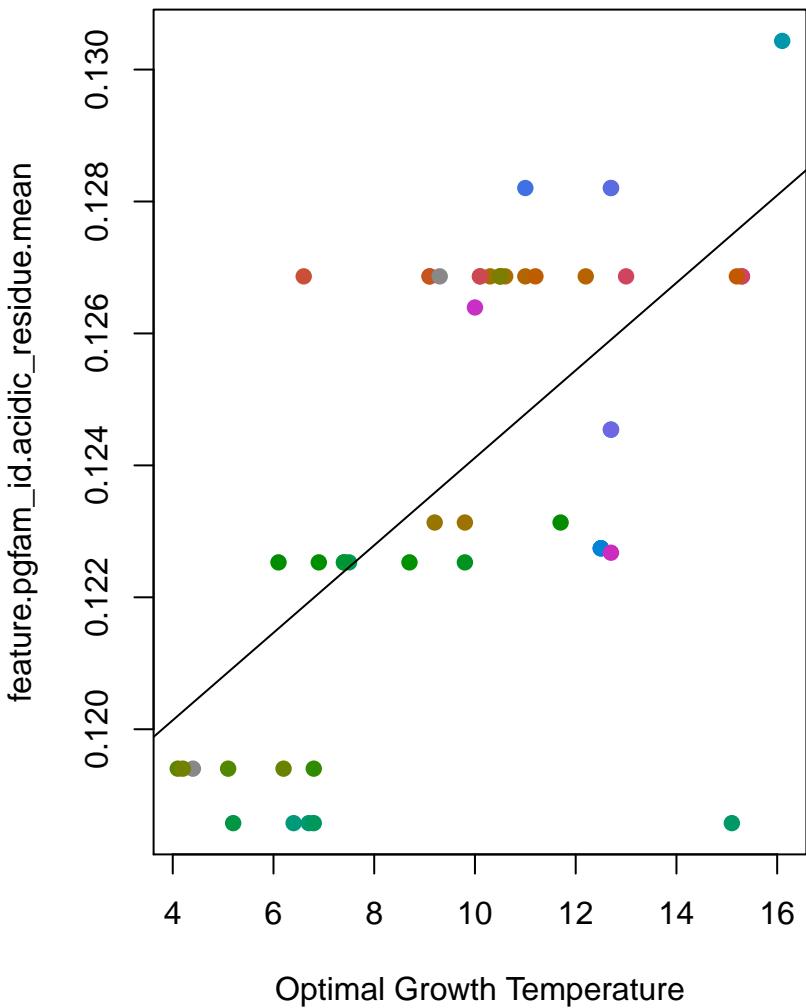




feature.pgfam_id.acidic_residue.mean

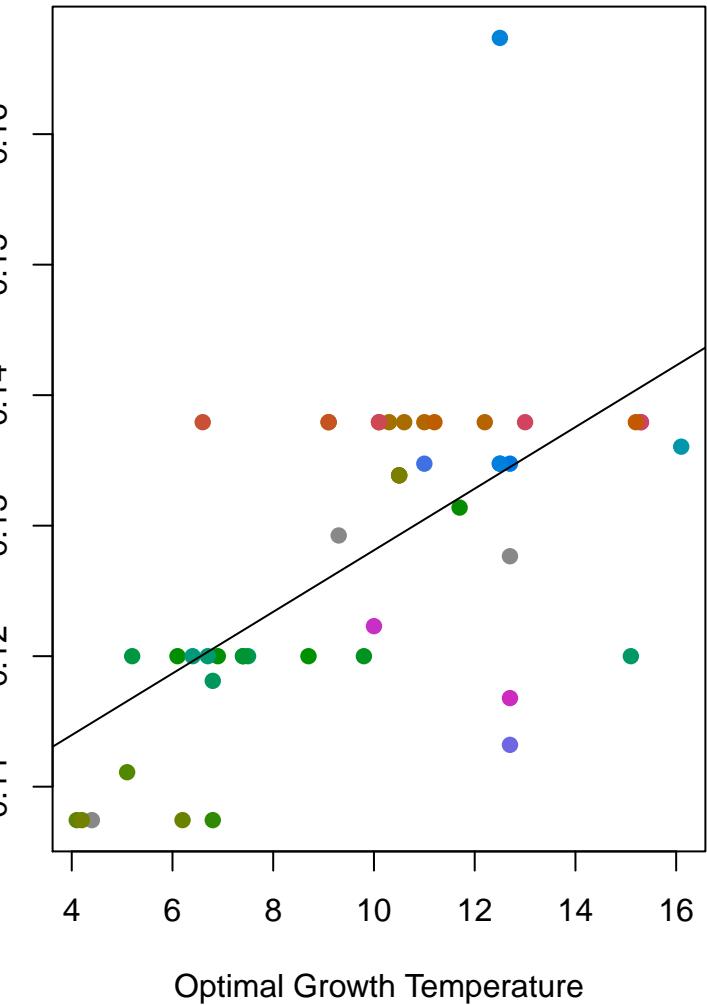
PGF_02473279

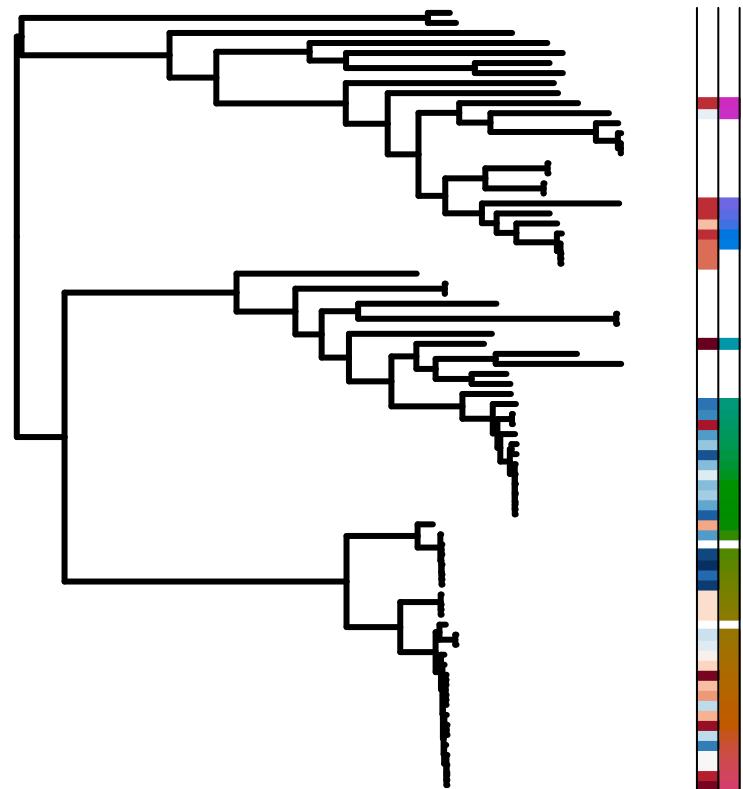
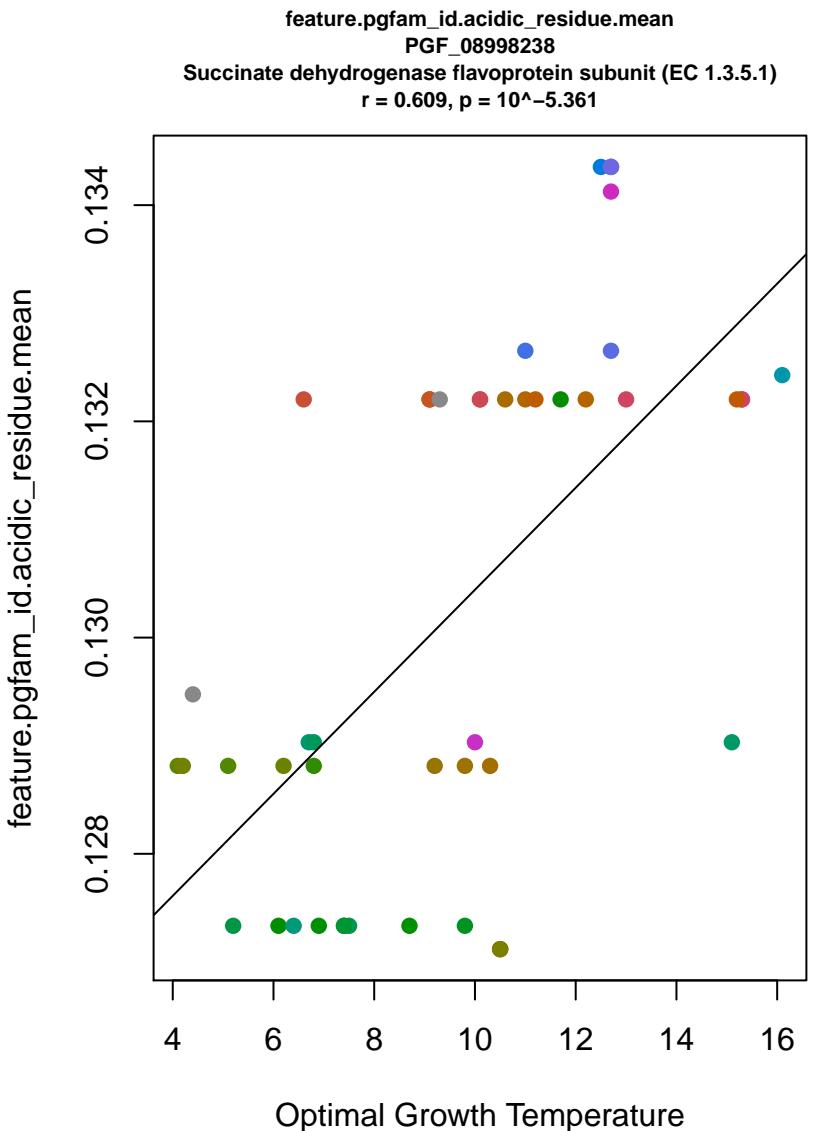
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)
 $r = 0.627$, $p = 10^{-5.957}$



feature.pgfam_id.acidic_residue.mean
PGF_00002863
FIG024746: hypothetical protein
 $r = 0.624, p = 10^{-5.552}$

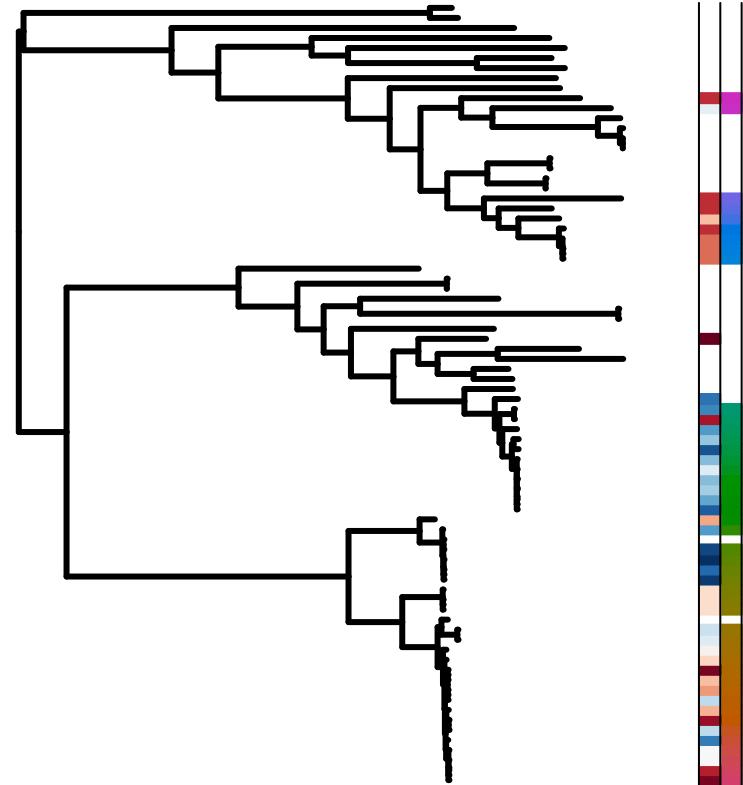
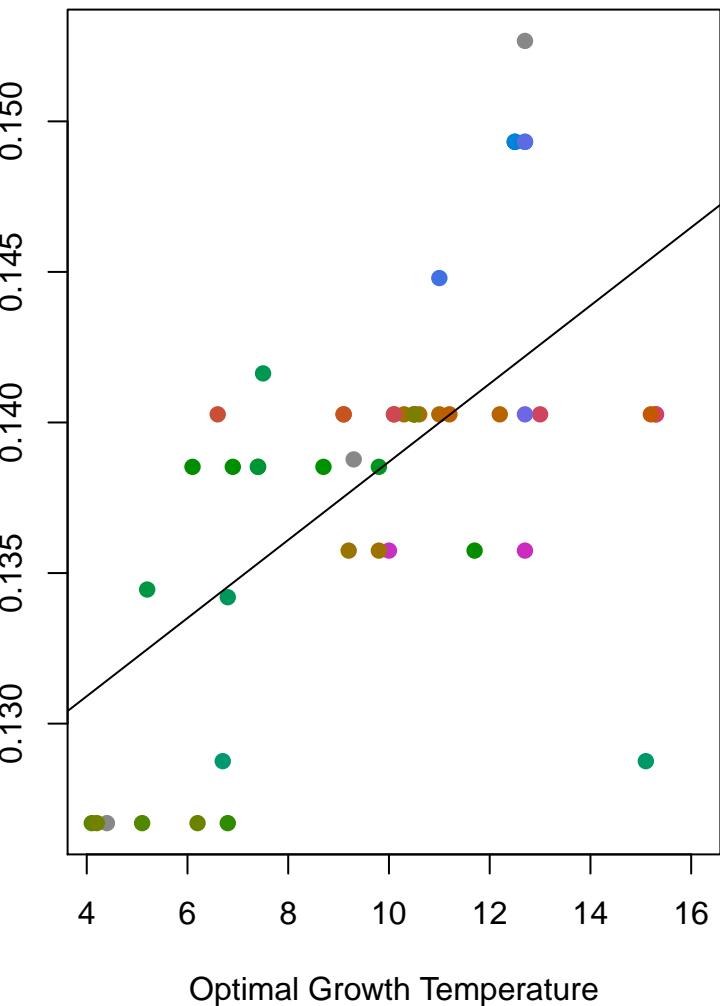
feature.pgfam_id.acidic_residue.mean

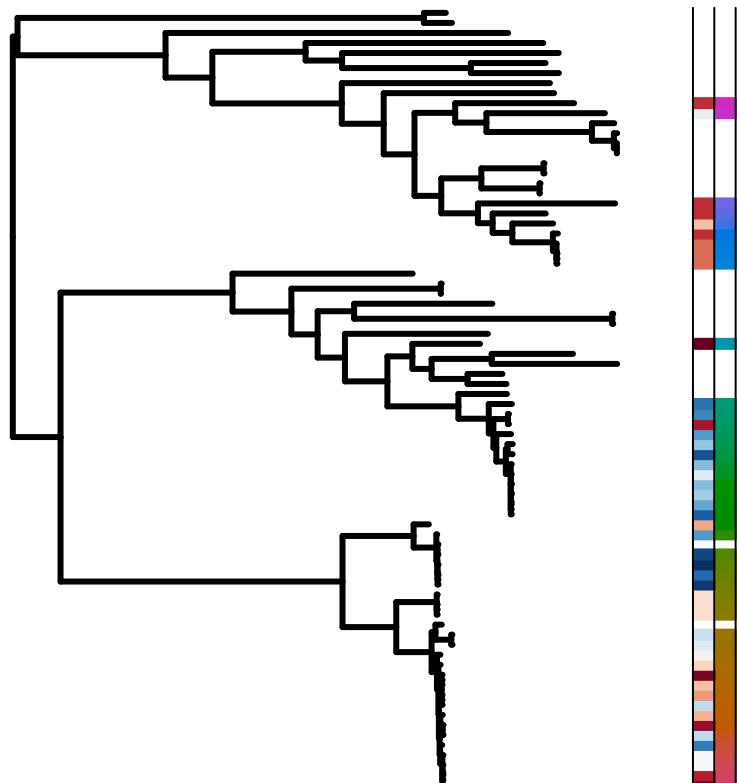
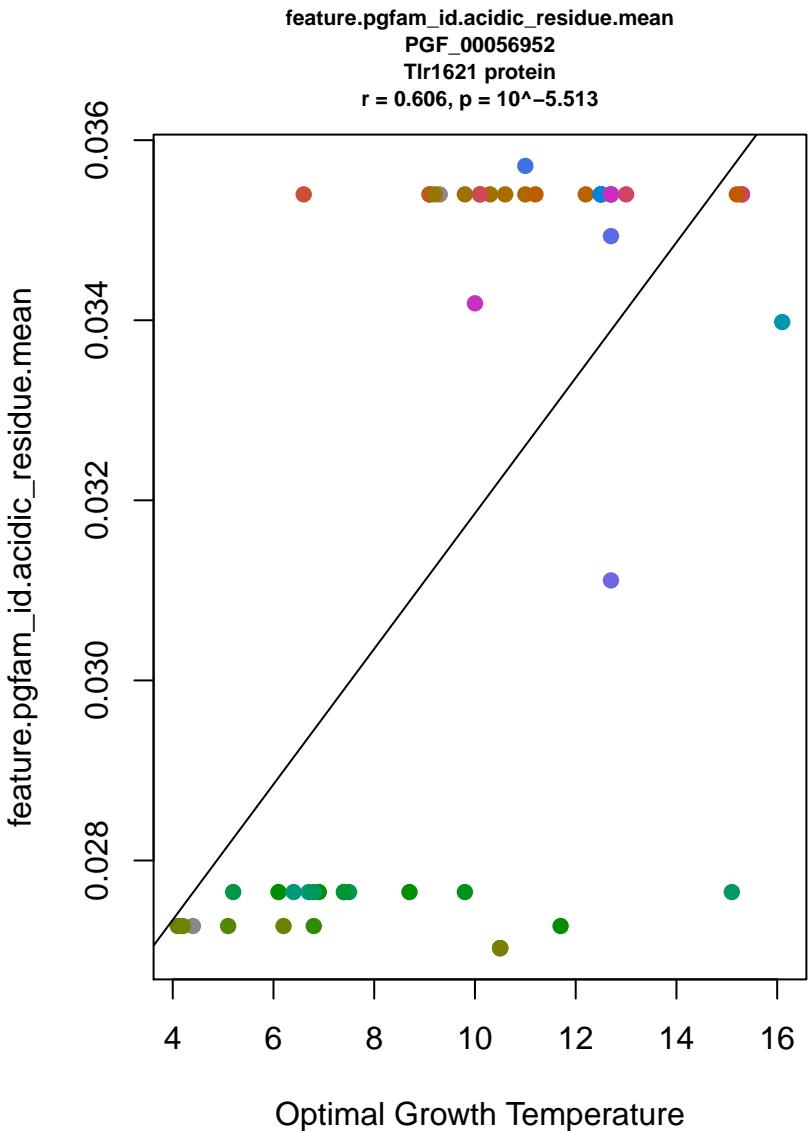




feature.pgfam_id.acidic_residue.mean
PGF_00038573
Protein of unknown function YceH
 $r = 0.608$, $p = 10^{-5.342}$

feature.pgfam_id.acidic_residue.mean



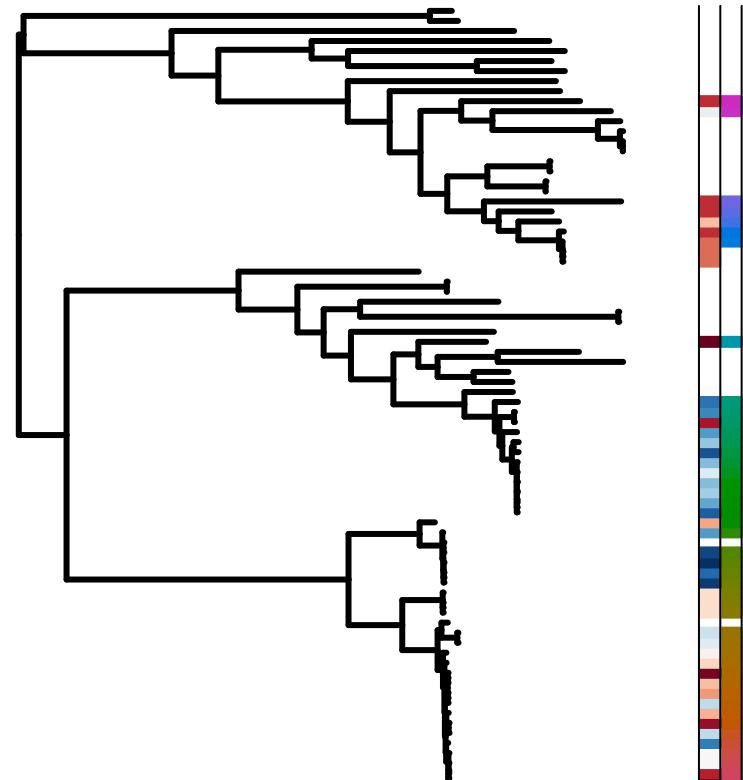
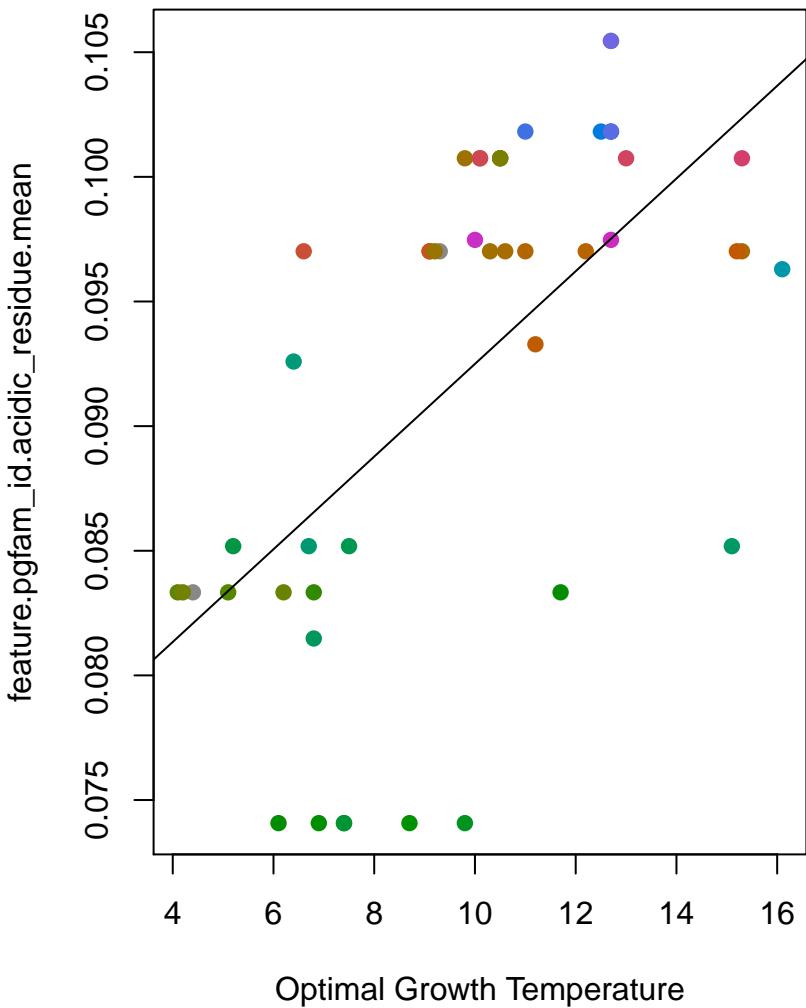


feature.pgfam_id.acidic_residue.mean

PGF_08181546

Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)

$r = 0.606$, $p = 10^{-5.294}$

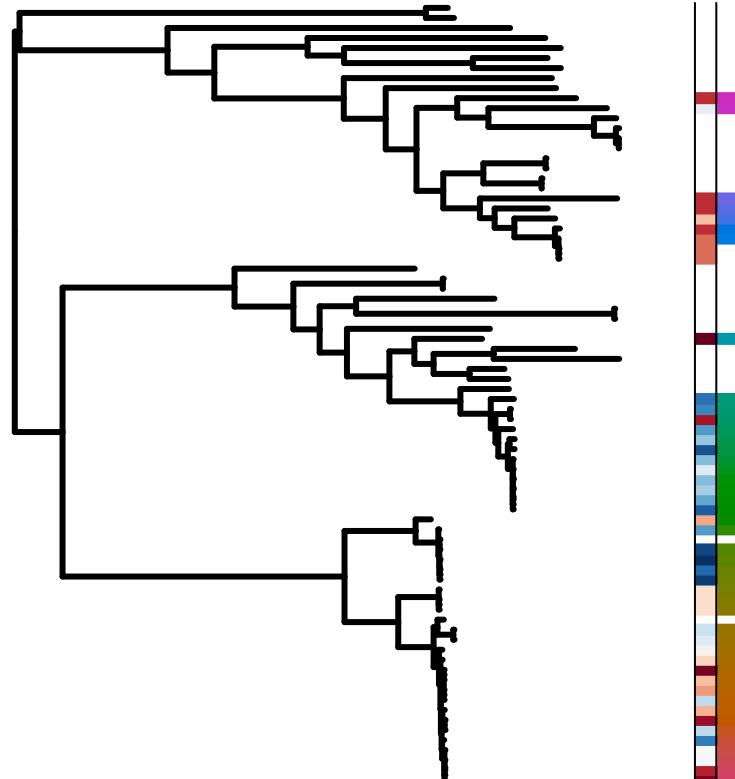
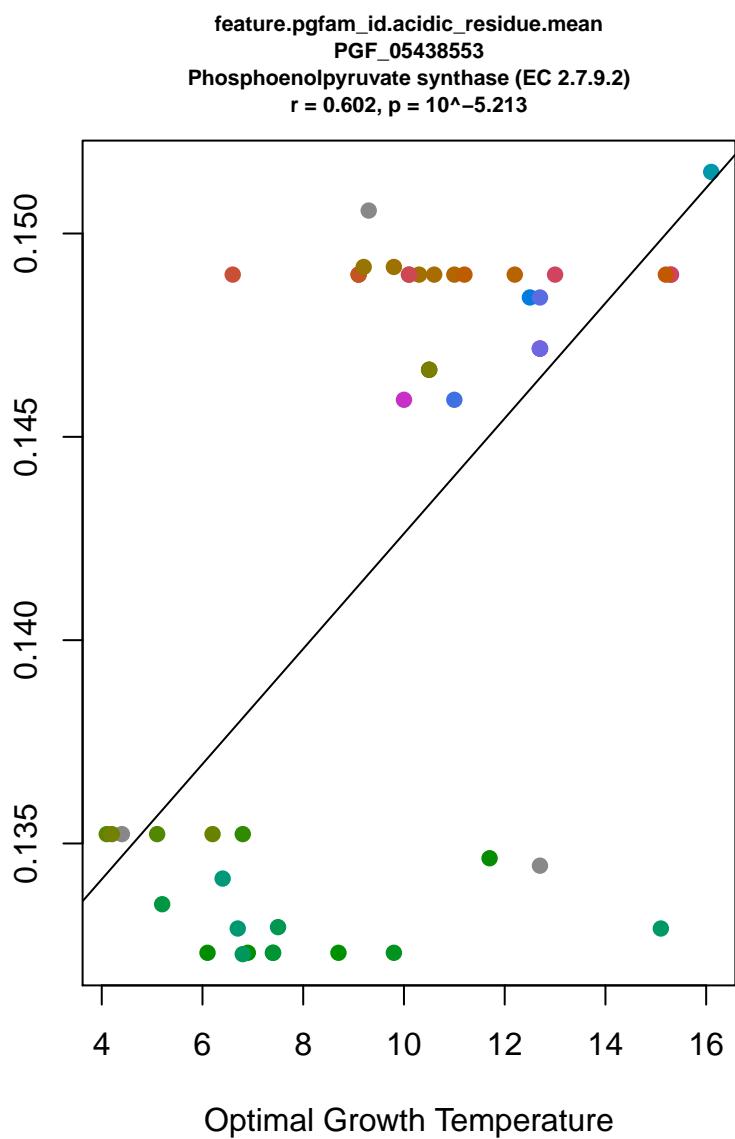


feature.pgfam_id.acidic_residue.mean

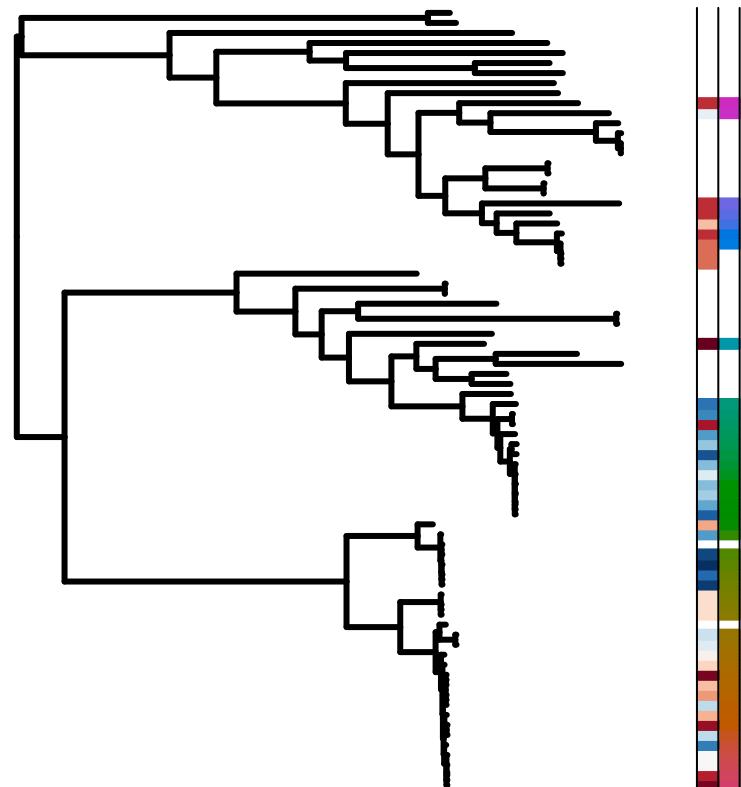
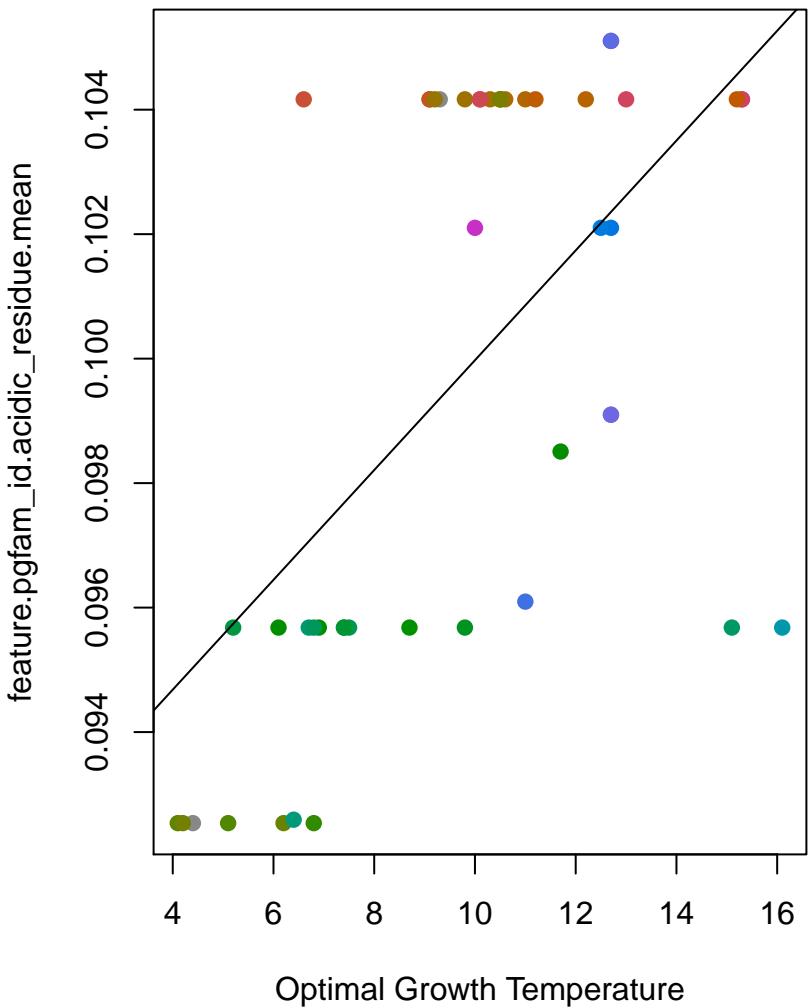
PGF_05438553

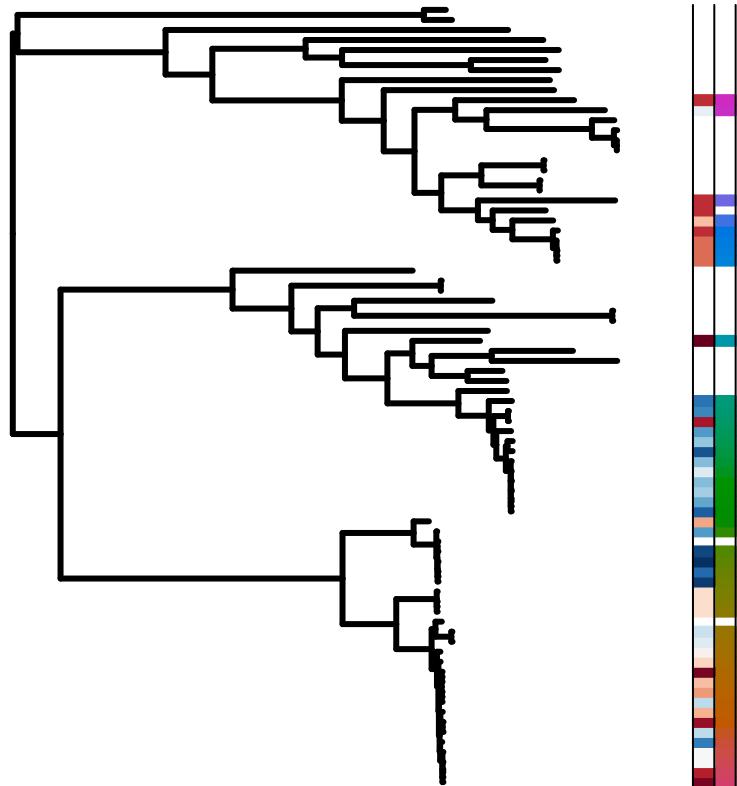
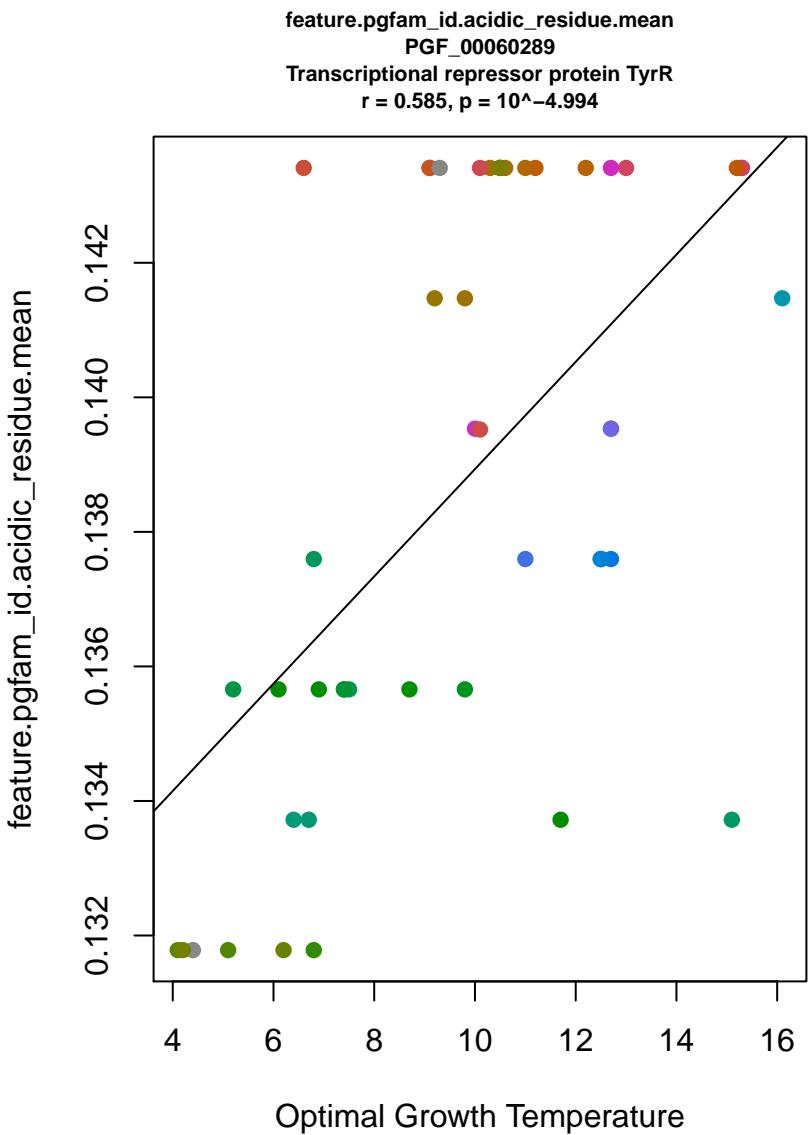
Phosphoenolpyruvate synthase (EC 2.7.9.2)

$r = 0.602$, $p = 10^{-5.213}$



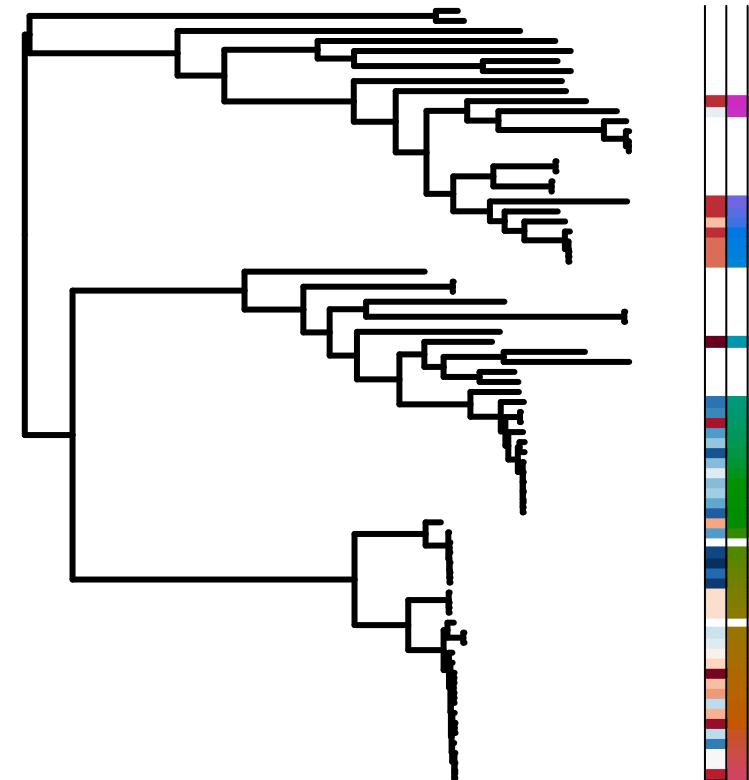
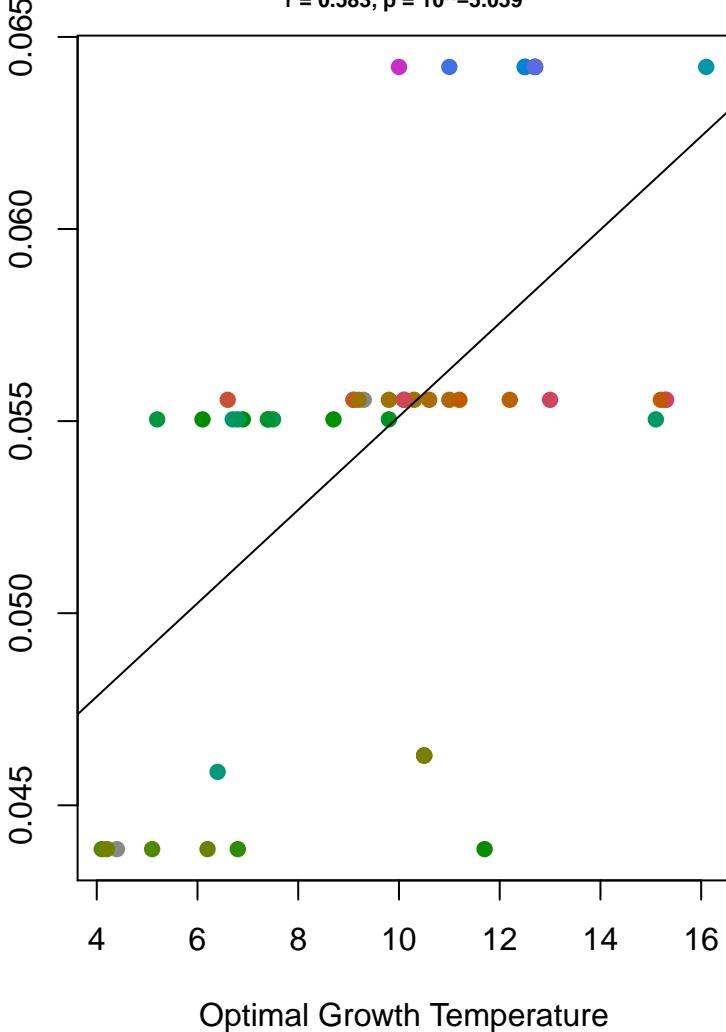
feature.pgfam_id.acidic_residue.mean
PGF_04486278
Biotin operon repressor / Biotin--protein ligase (EC 6.3.4.9)(EC 6.3.4.10)(EC 6.3.4.11)(EC 6.3.4.15)
 $r = 0.595$, $p = 10^{-5.087}$





feature.pgfam_id.acidic_residue.mean
PGF_03074033
FIG020302: hypothetical protein
 $r = 0.583$, $p = 10^{-5.059}$

feature.pgfam_id.acidic_residue.mean

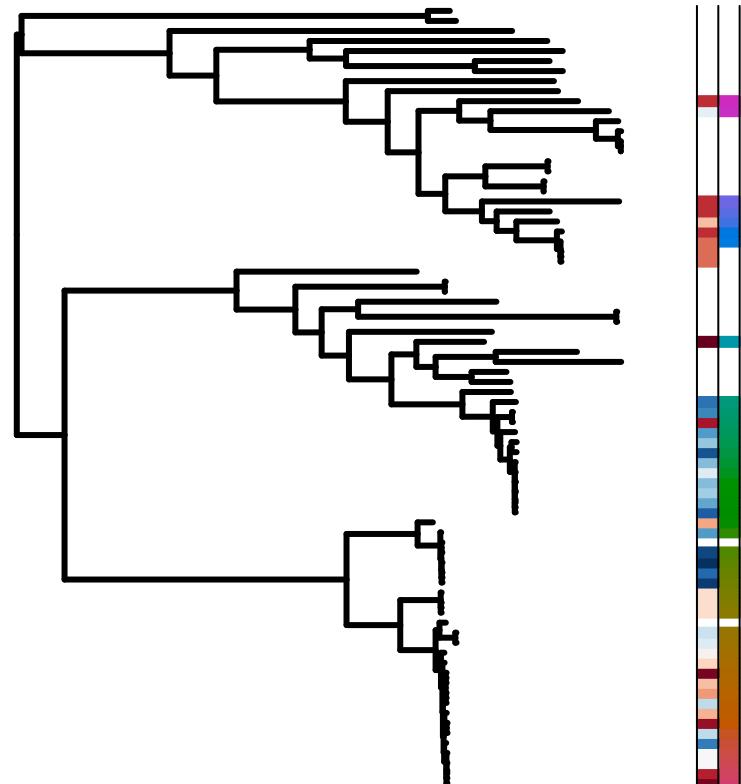
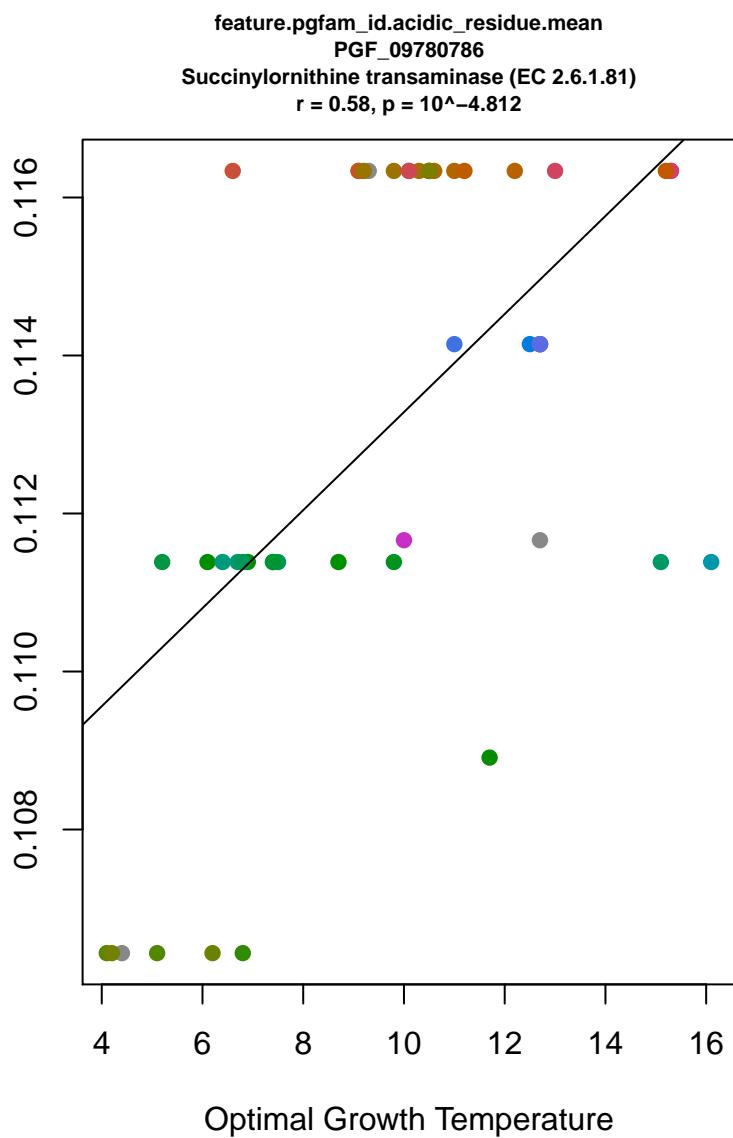


feature.pgfam_id.acidic_residue.mean

PGF_09780786

Succinylornithine transaminase (EC 2.6.1.81)

$r = 0.58, p = 10^{-4.812}$



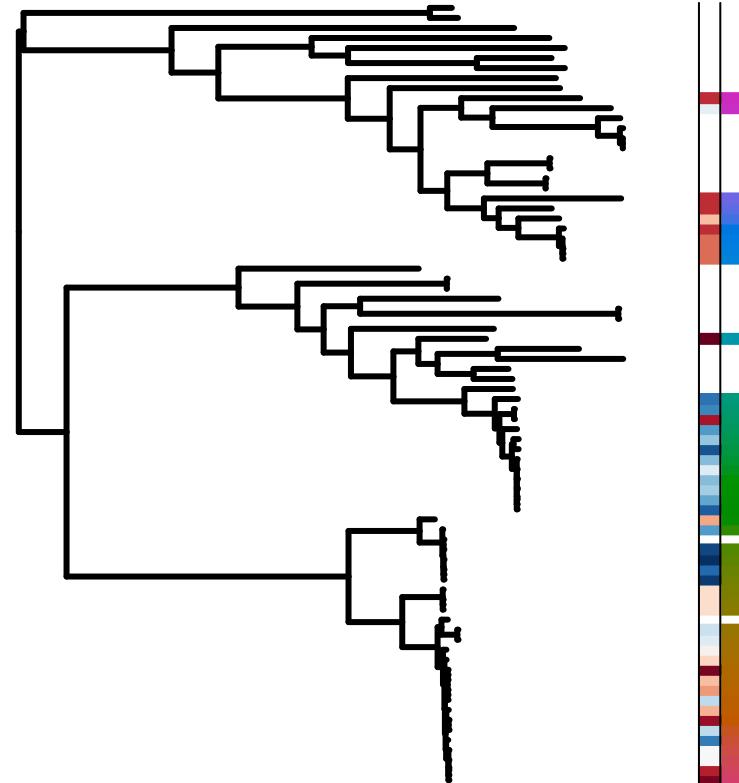
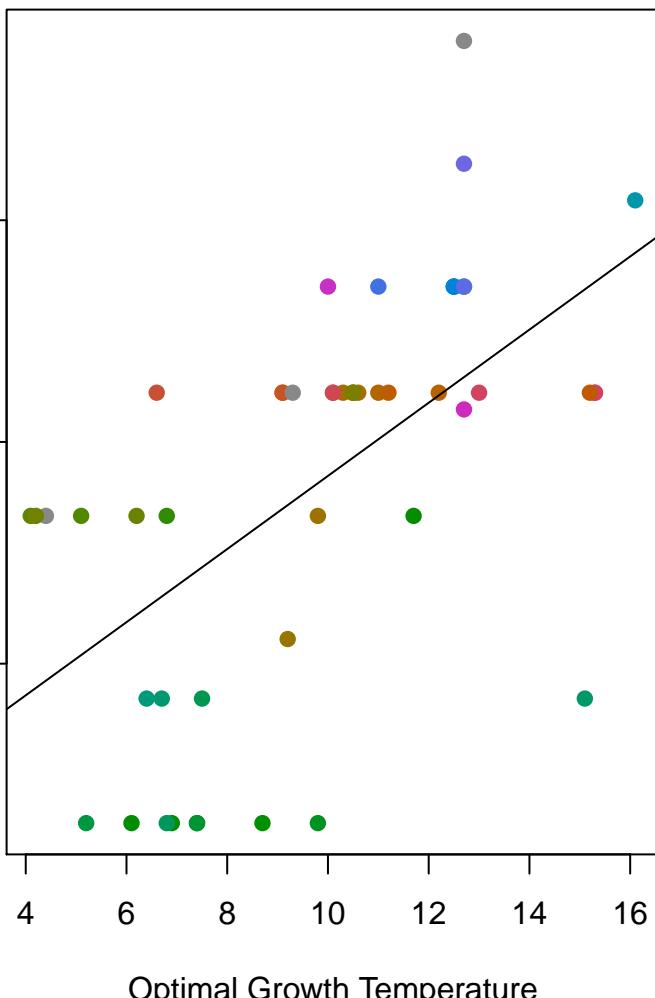
feature.pgfam_id.acidic_residue.mean

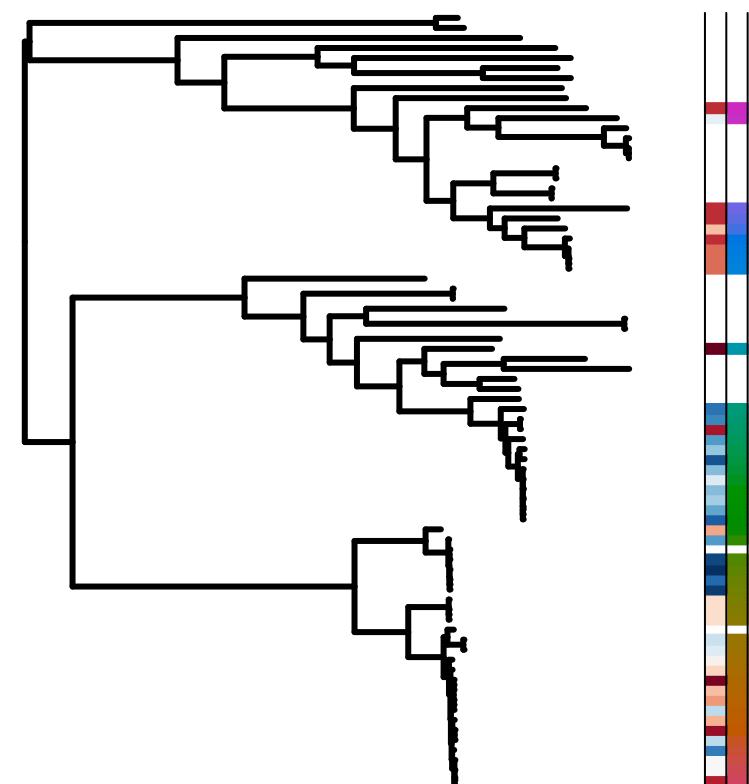
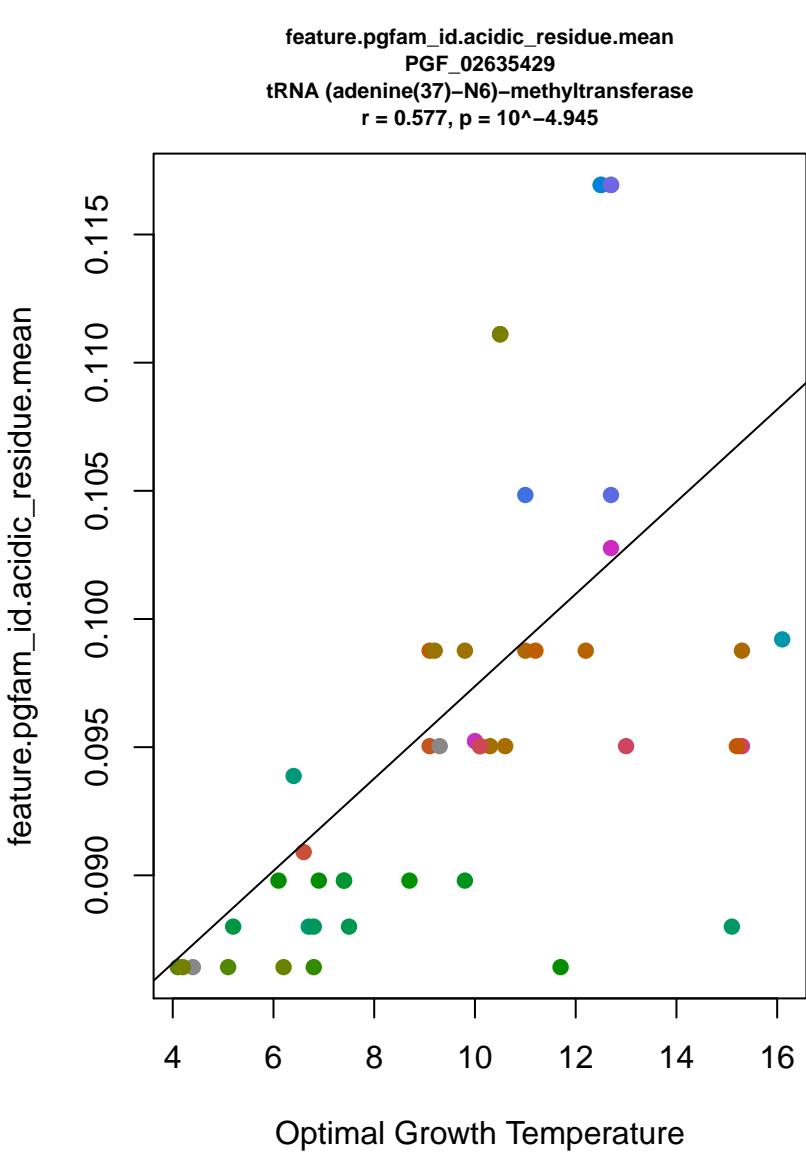
PGF_00011990

Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)

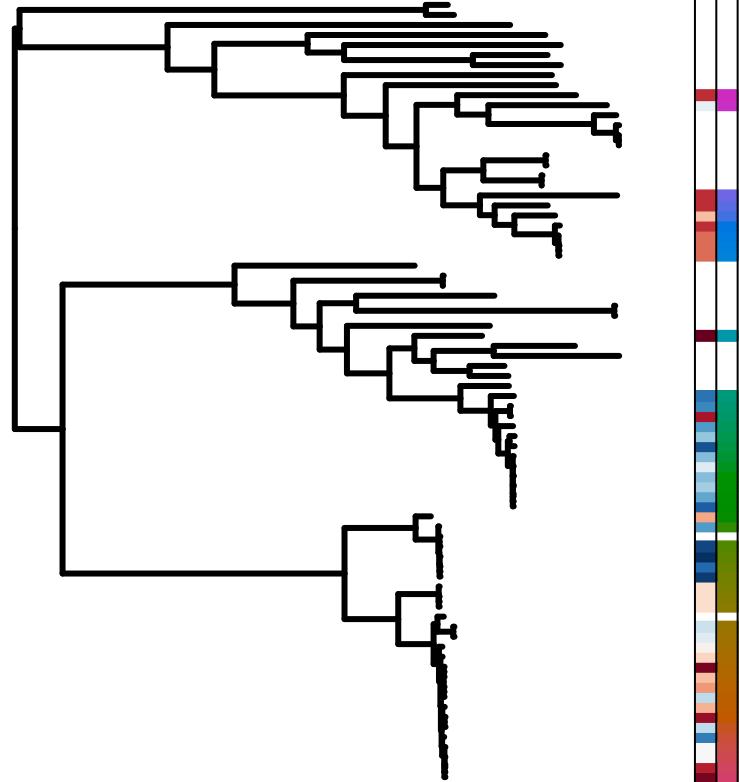
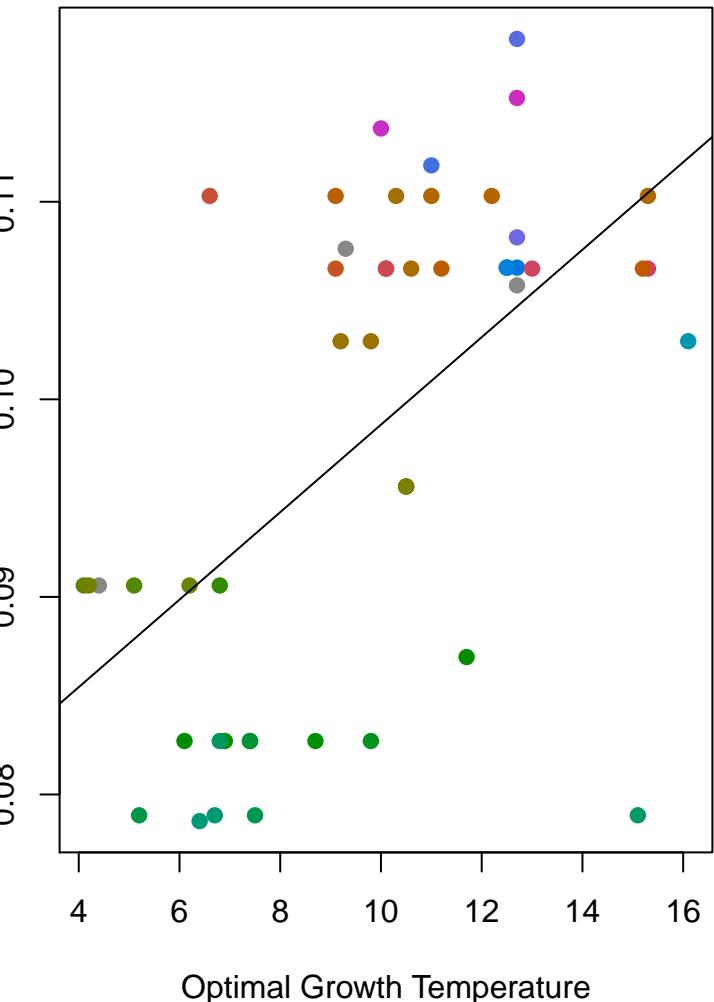
$r = 0.58, p = 10^{-4.99}$

feature.pgfam_id.acidic_residue.mean



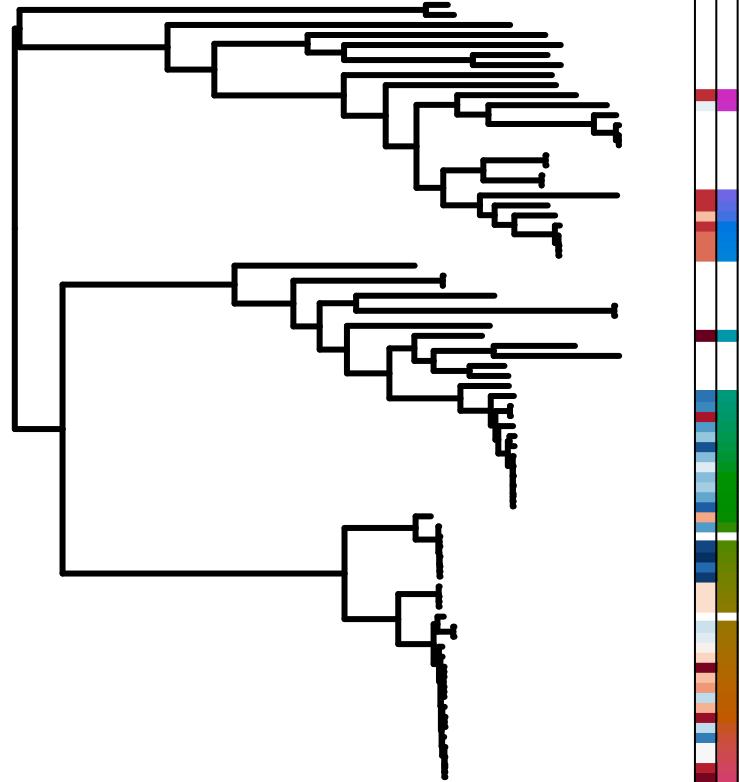
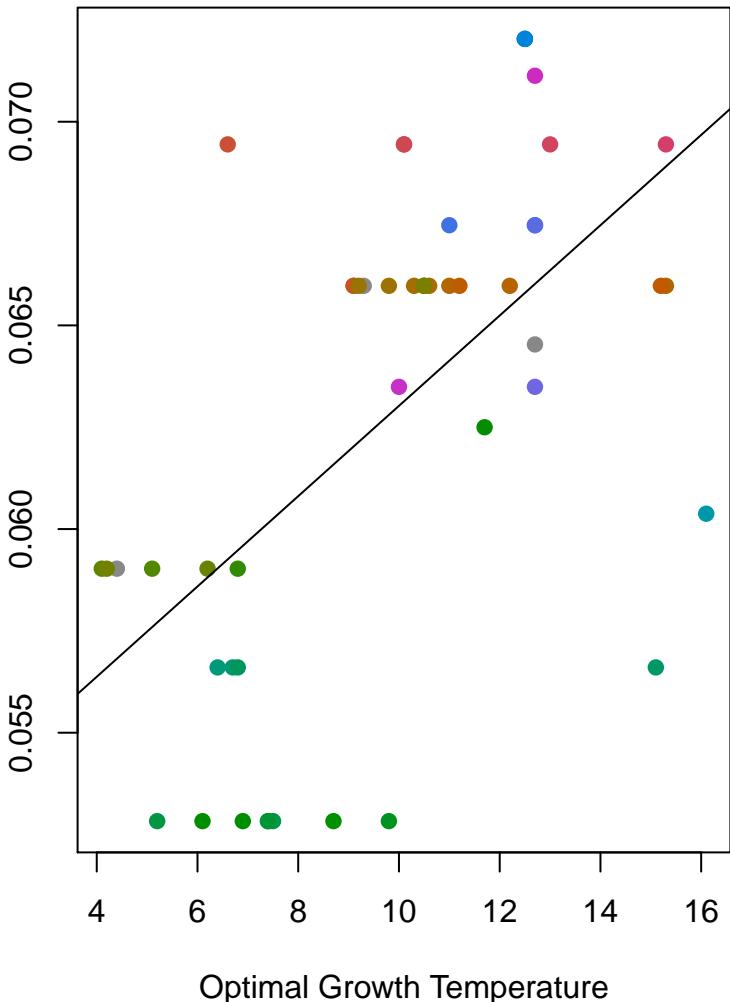


feature.pgfam_id.acidic_residue.mean
PGF_00040580
Putative deoxyribonuclease YjjV
 $r = 0.577$, $p = 10^{-4.931}$



feature.pgfam_id.acidic_residue.mean
PGF_06326847
Flagellar biosynthesis protein FliP
 $r = 0.577$, $p = 10^{-4.93}$

feature.pgfam_id.acidic_residue.mean



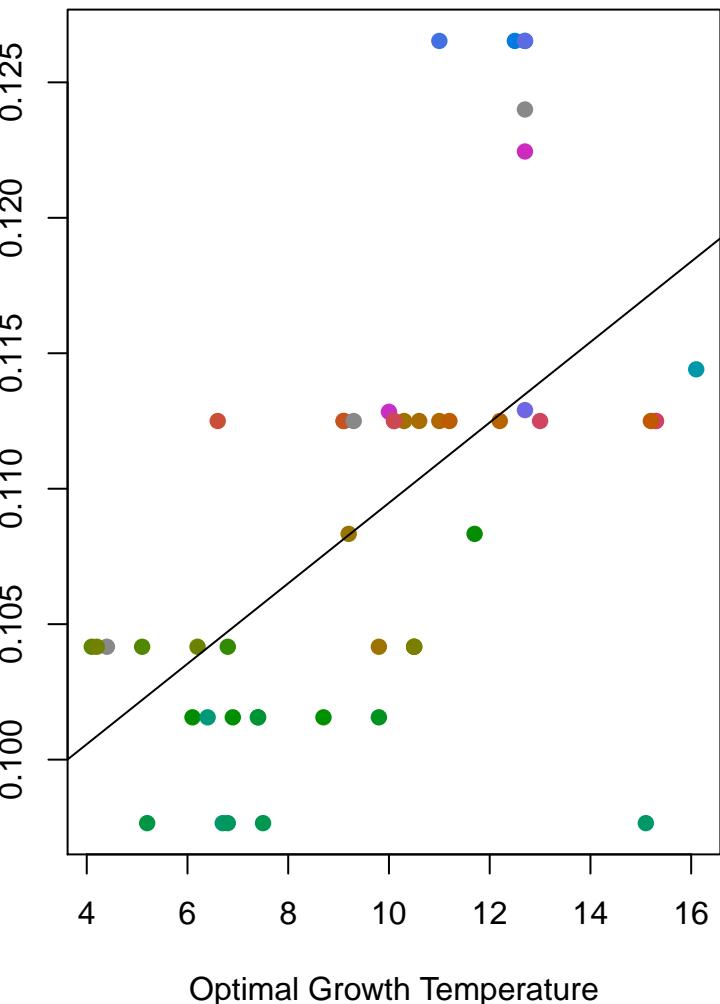
feature.pgfam_id.acidic_residue.mean

PGF_07711219

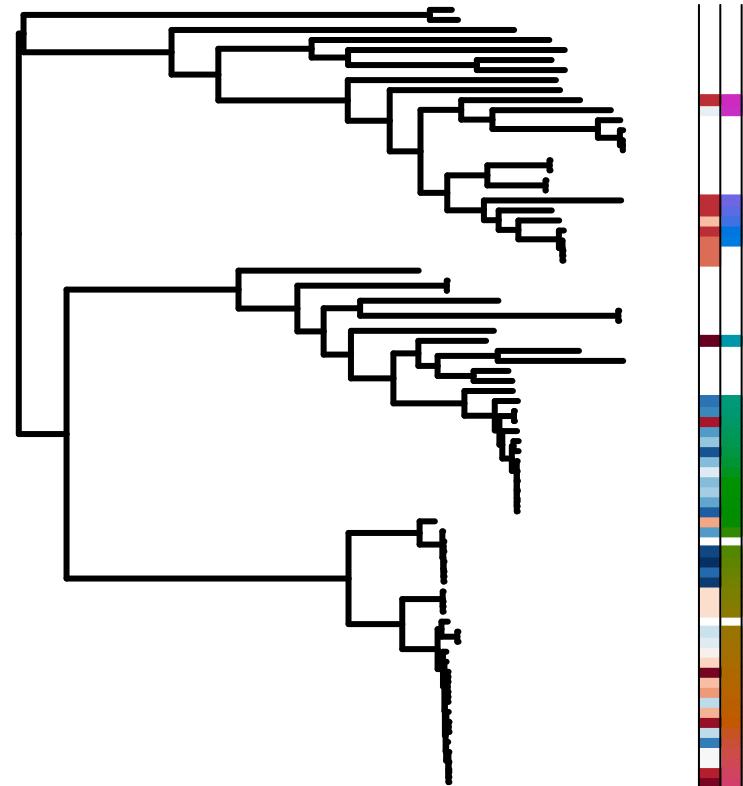
Histidine utilization repressor

$r = 0.577, p = 10^{-4.746}$

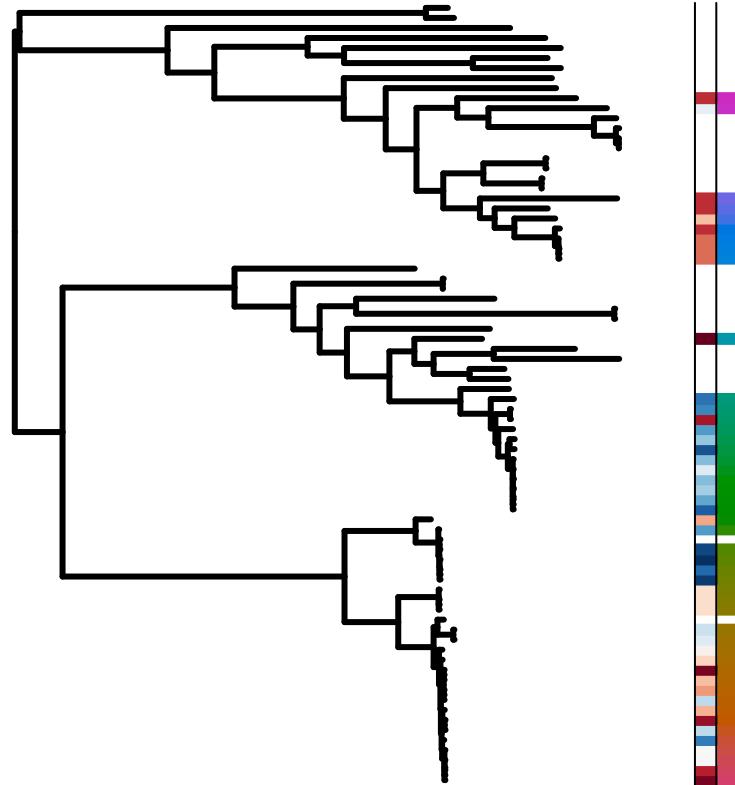
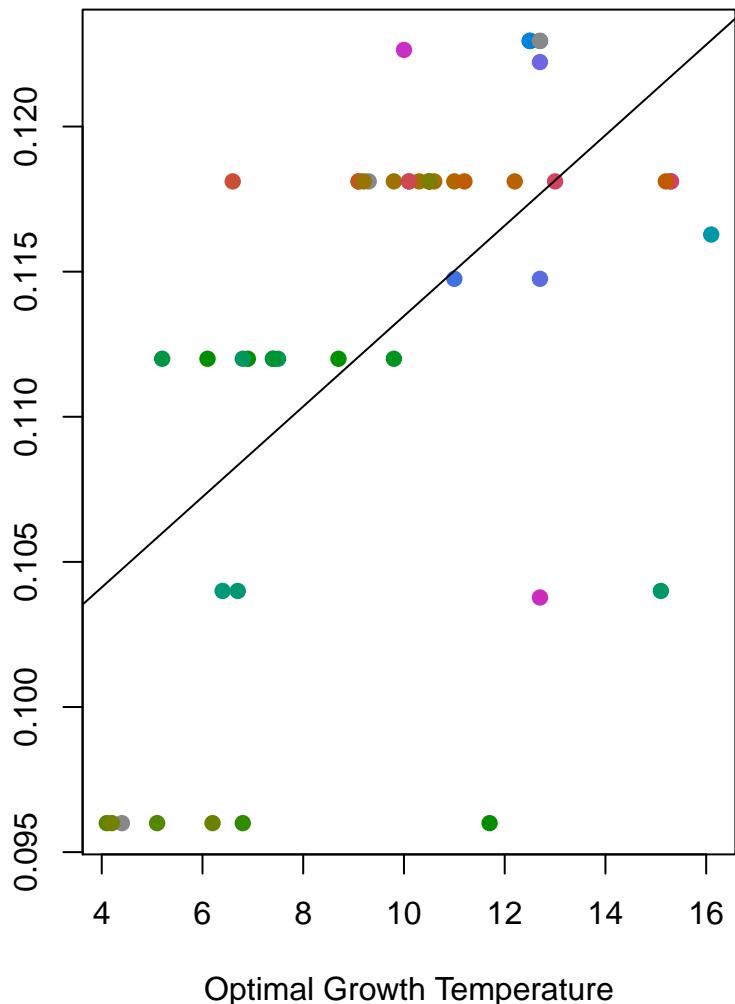
feature.pgfam_id.acidic_residue.mean



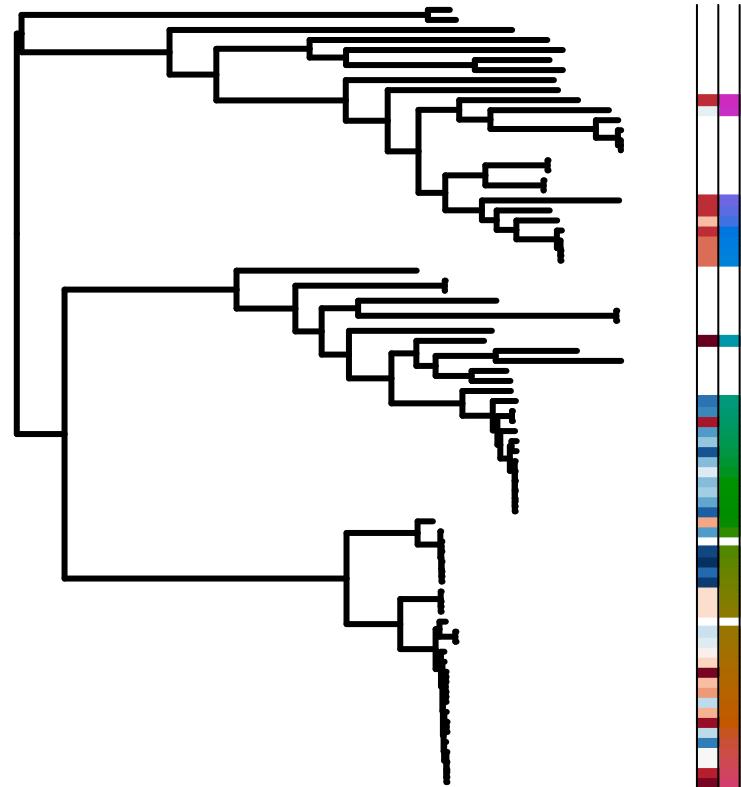
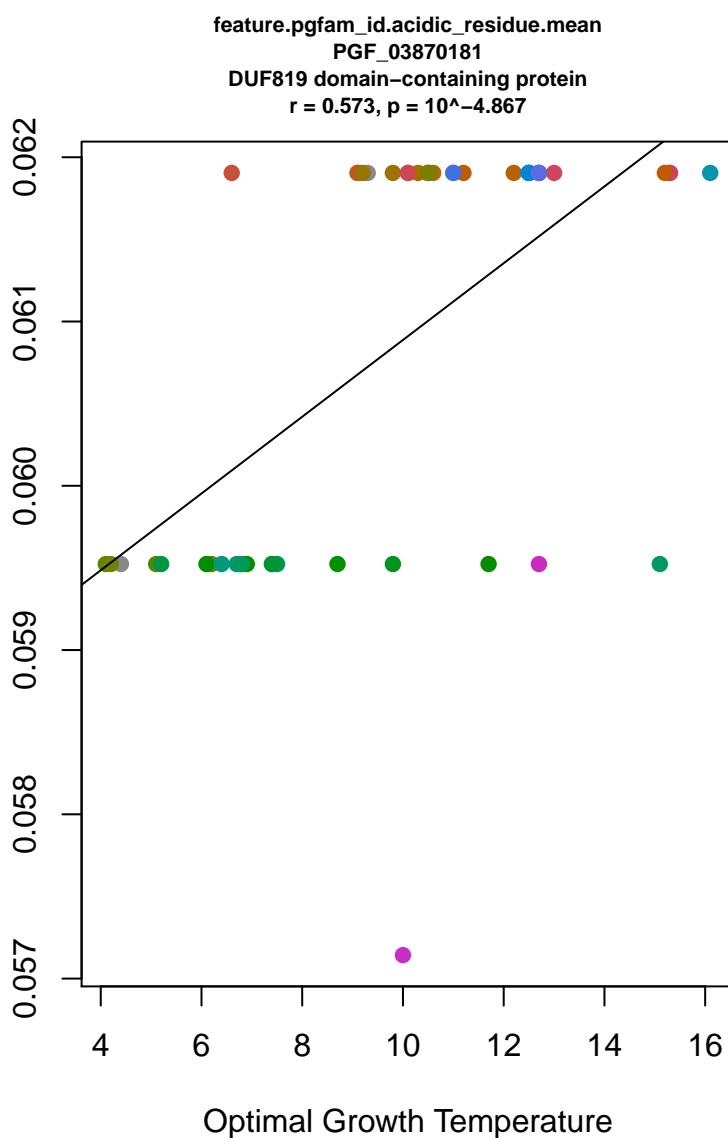
Optimal Growth Temperature



feature.pgfam_id.acidic_residue.mean
PGF_01336380
hypothetical protein
 $r = 0.576, p = 10^{-4.927}$



feature.pgfam_id.acidic_residue.mean
PGF_03870181
DUF819 domain-containing protein
 $r = 0.573, p = 10^{-4.867}$



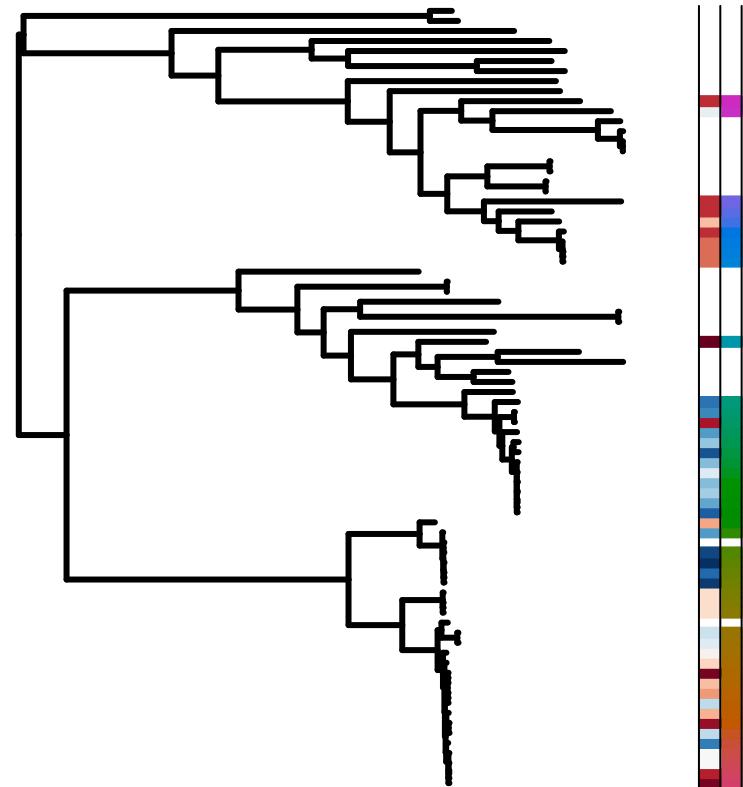
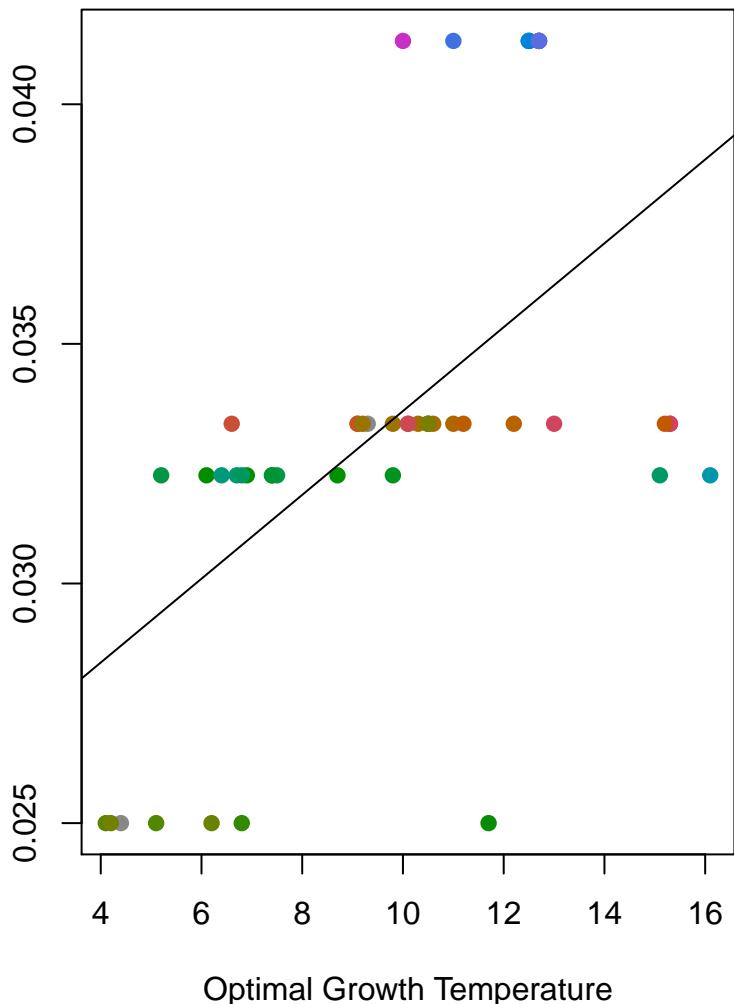
feature.pgfam_id.acidic_residue.mean

PGF_00425763

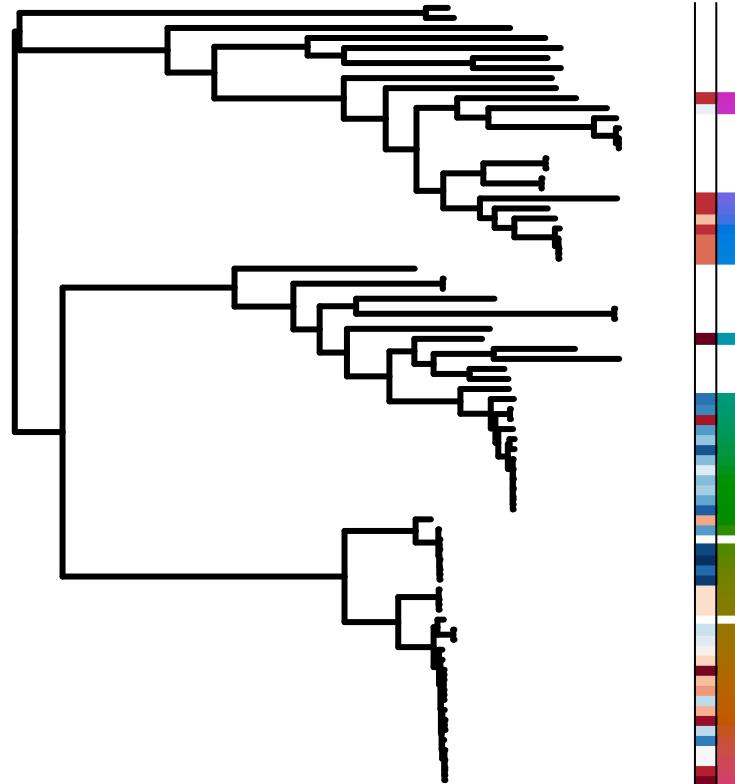
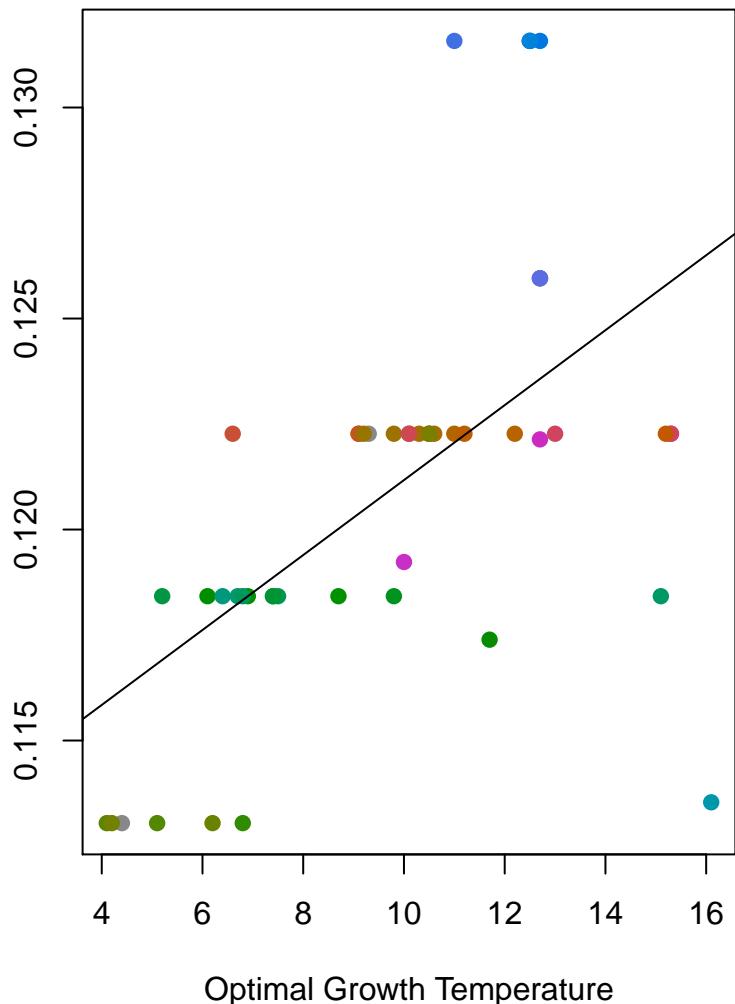
FIG002082: Protein SirB2

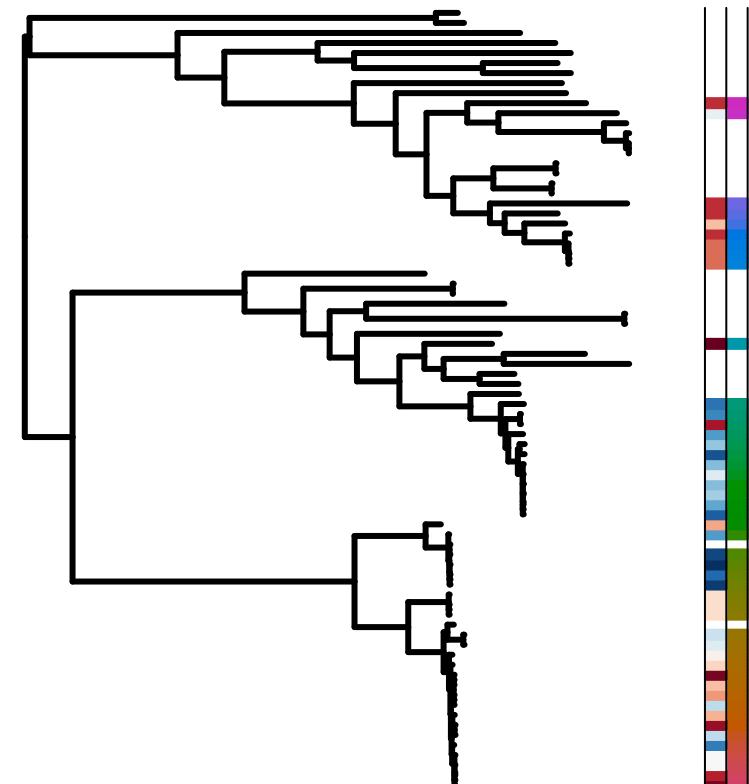
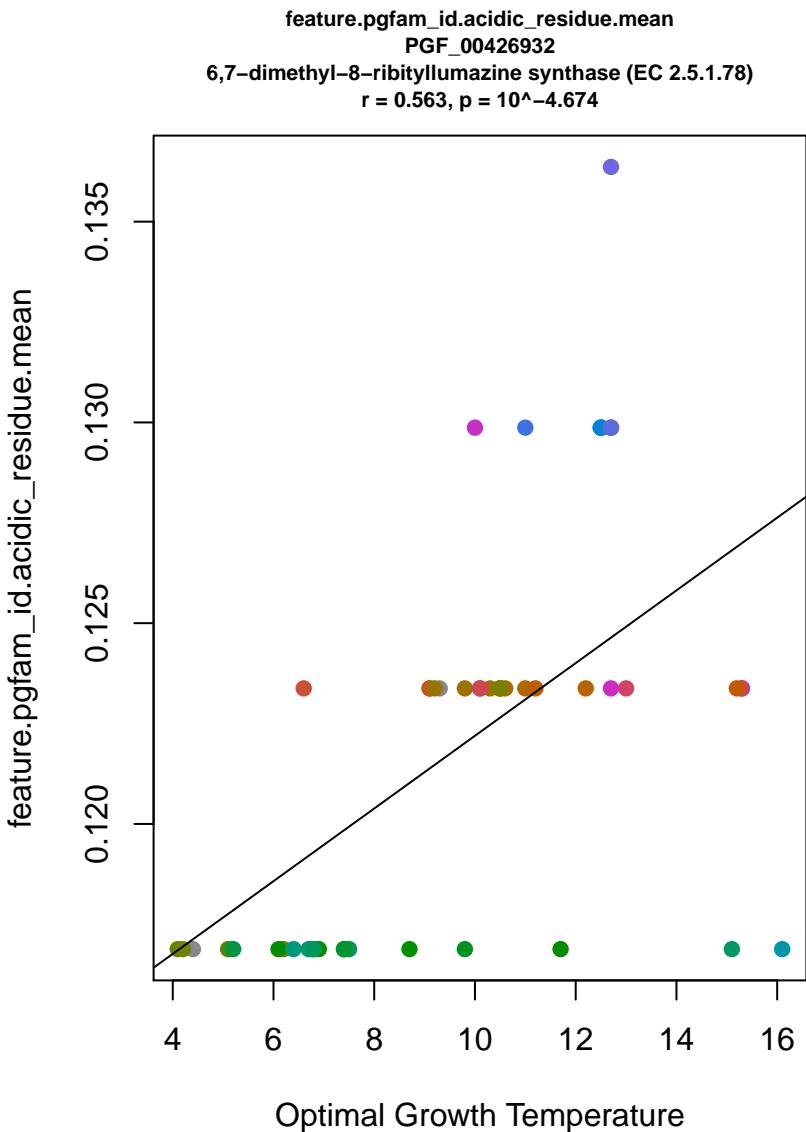
$r = 0.573, p = 10^{-4.865}$

feature.pgfam_id.acidic_residue.mean



feature.pgfam_id.acidic_residue.mean
PGF_03790040
Ribonuclease III (EC 3.1.26.3)
 $r = 0.567$, $p = 10^{-4.754}$





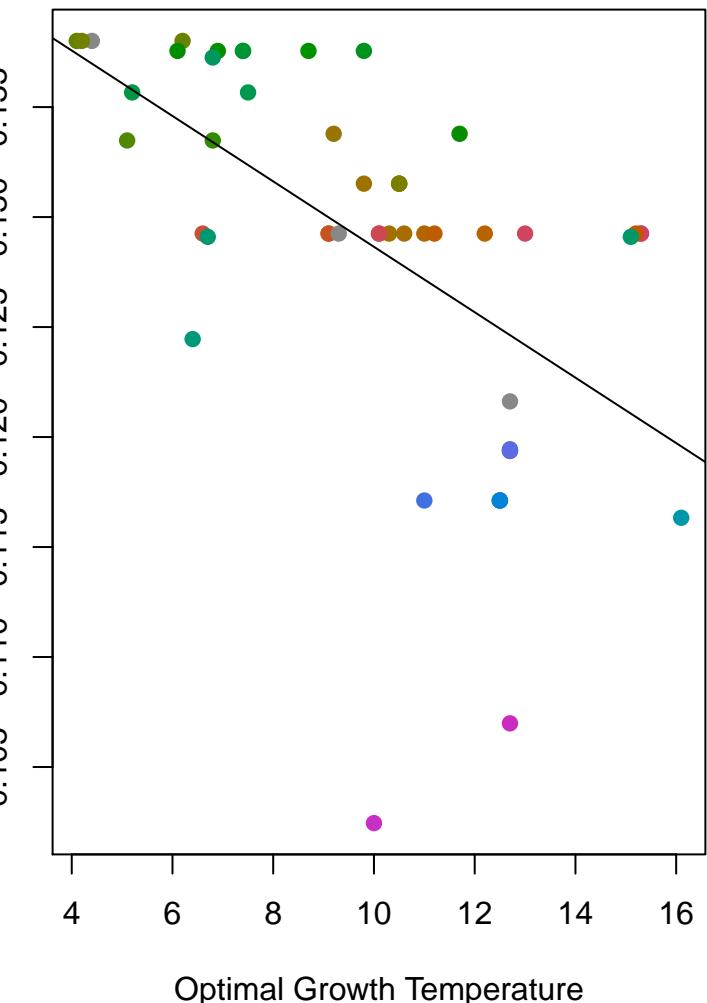
feature.pgfam_id.acidic_residue.mean

PGF_03336368

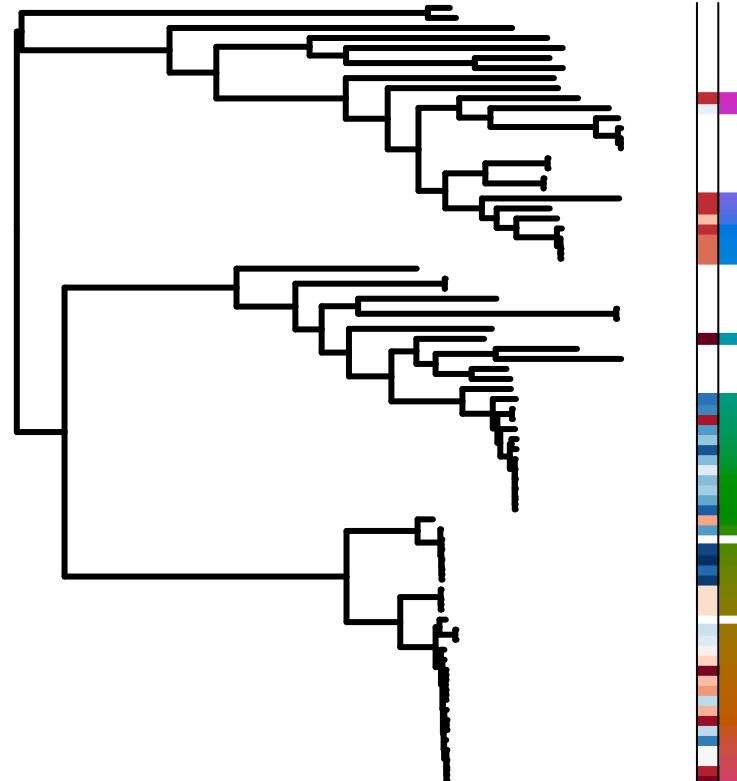
hypothetical protein

$r = -0.572, p = 10^{-4.85}$

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature



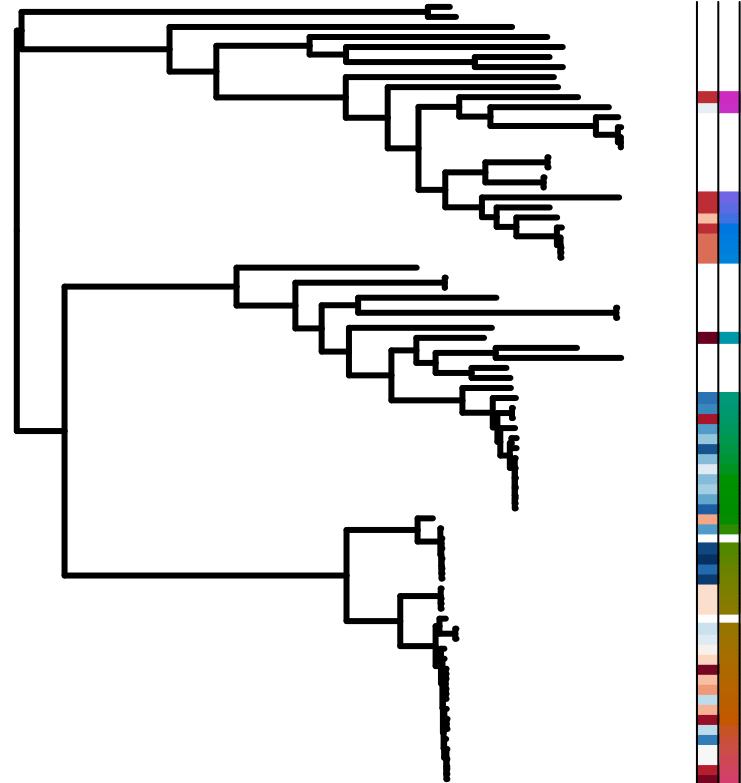
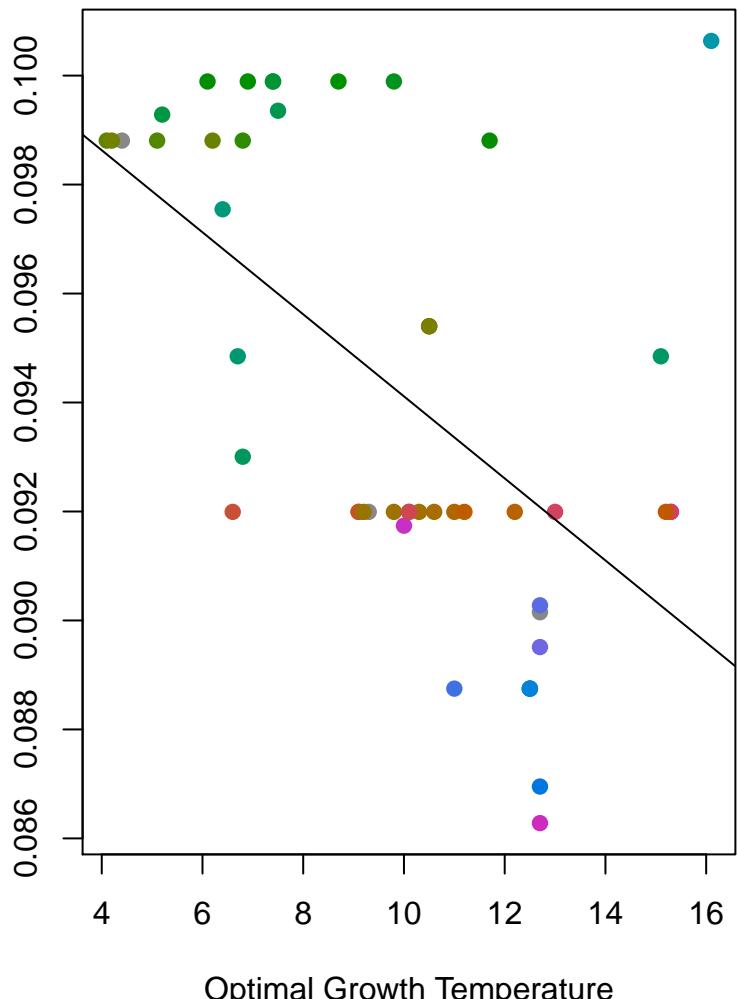
feature.pgfam_id.acidic_residue.mean

PGF_02890229

Gamma-glutamyltranspeptidase (EC 2.3.2.2) @ Glutathione hydrolase (EC 3.4.19.13)

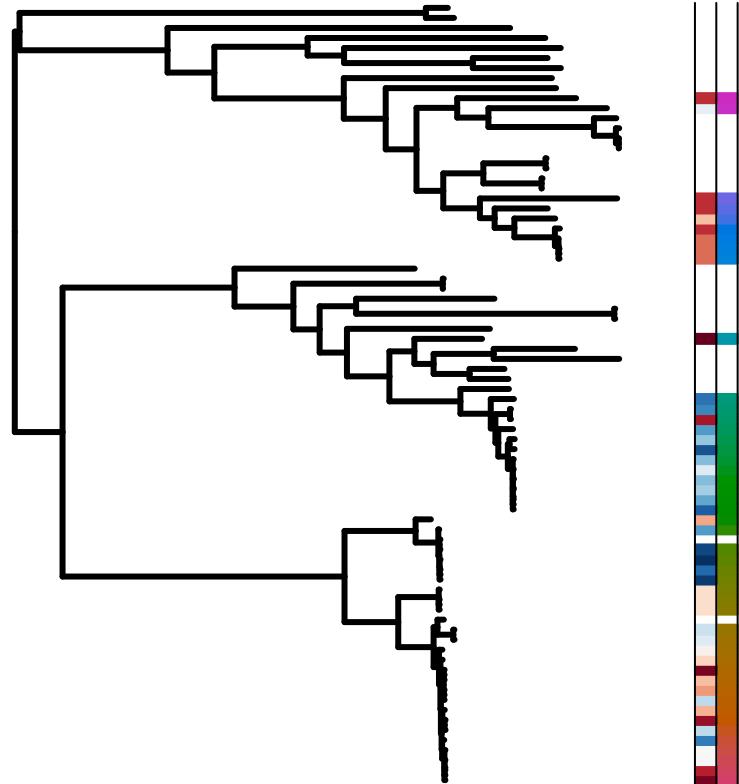
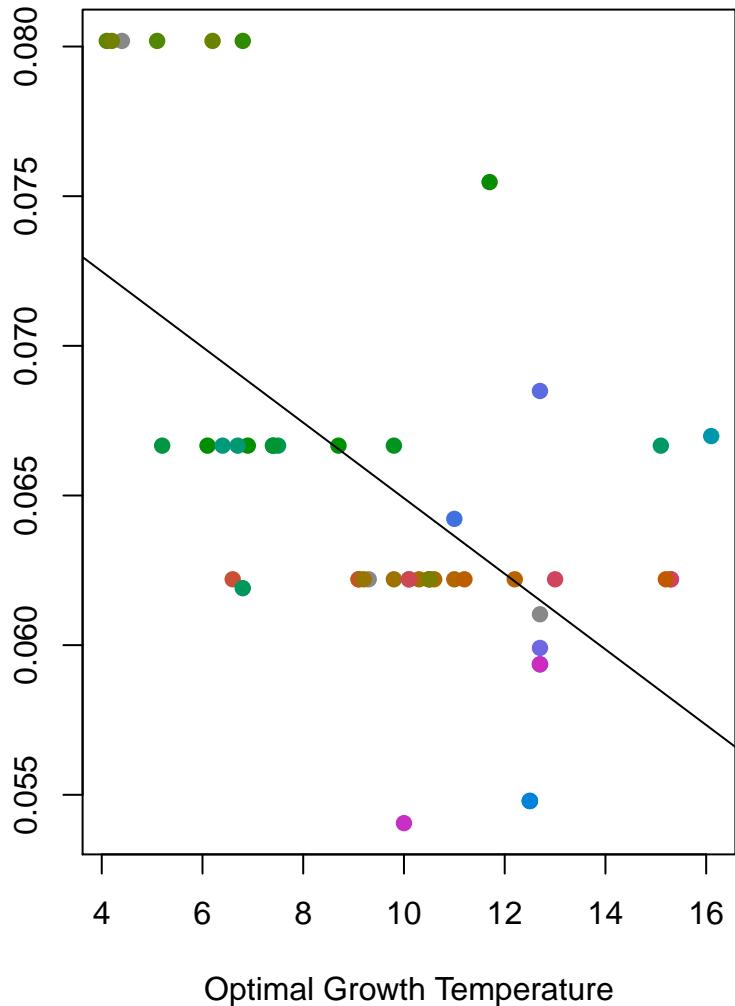
$r = -0.577$, $p = 10^{-4.94}$

feature.pgfam_id.acidic_residue.mean



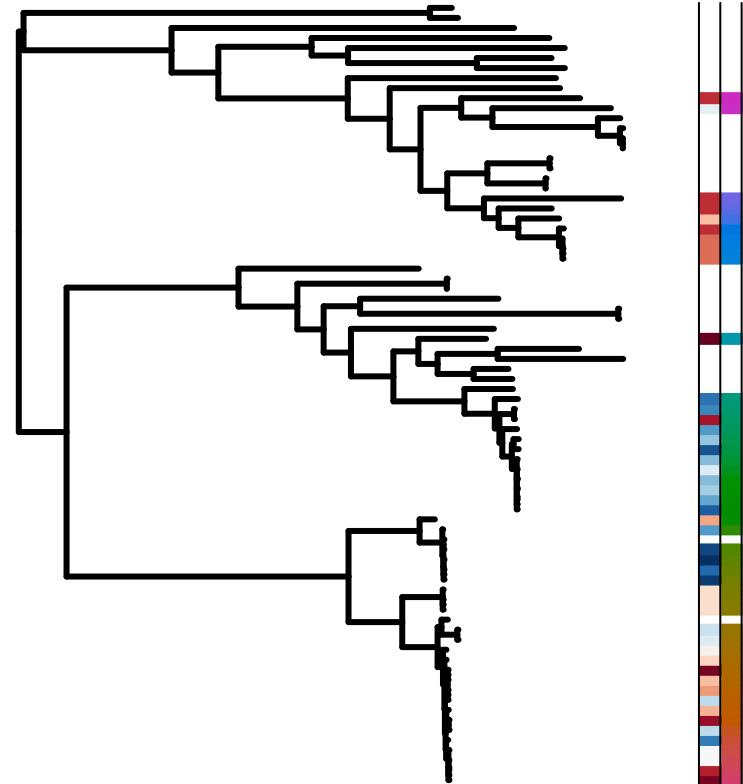
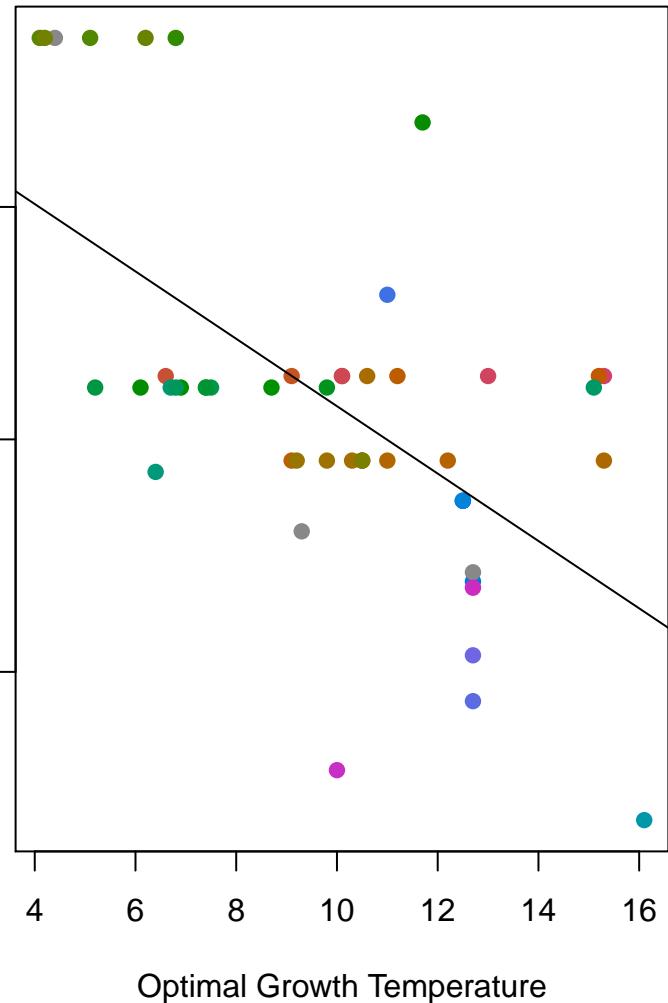
feature.pgfam_id.acidic_residue.mean
PGF_00612013
UPF0126 inner membrane protein YadS
 $r = -0.589$, $p = 10^{-5.17}$

feature.pgfam_id.acidic_residue.mean



feature.pgfam_id.acidic_residue.mean
PGF_00026525
Nudix hydrolase 3 (EC 3.6.1.-)
 $r = -0.6$, $p = 10^{-5.394}$

feature.pgfam_id.acidic_residue.mean



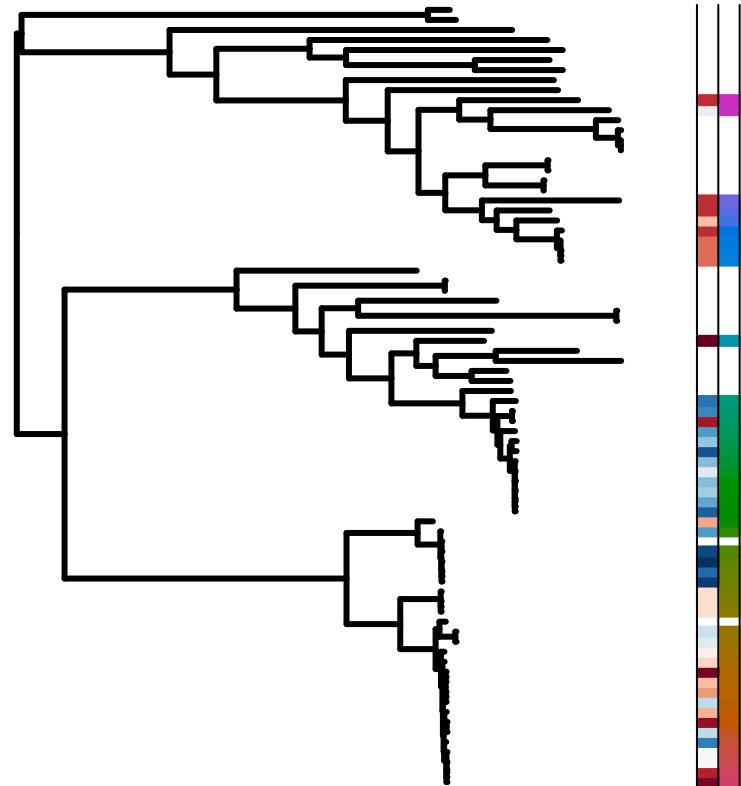
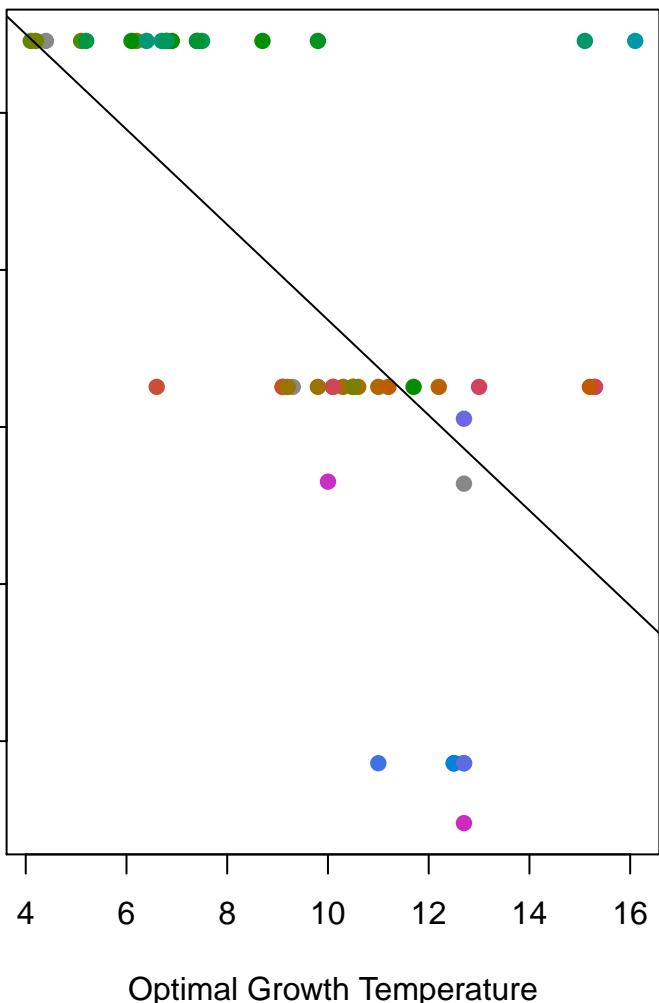
feature.pgfam_id.acidic_residue.mean

PGF_00648054

Tol-Pal system protein TolQ

$r = -0.601, p = 10^{-5.41}$

feature.pgfam_id.acidic_residue.mean



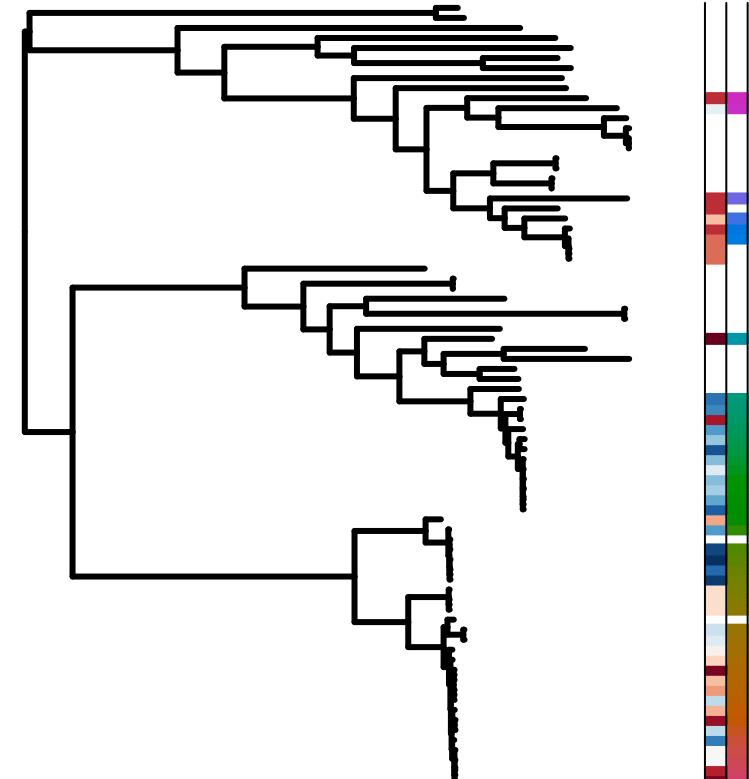
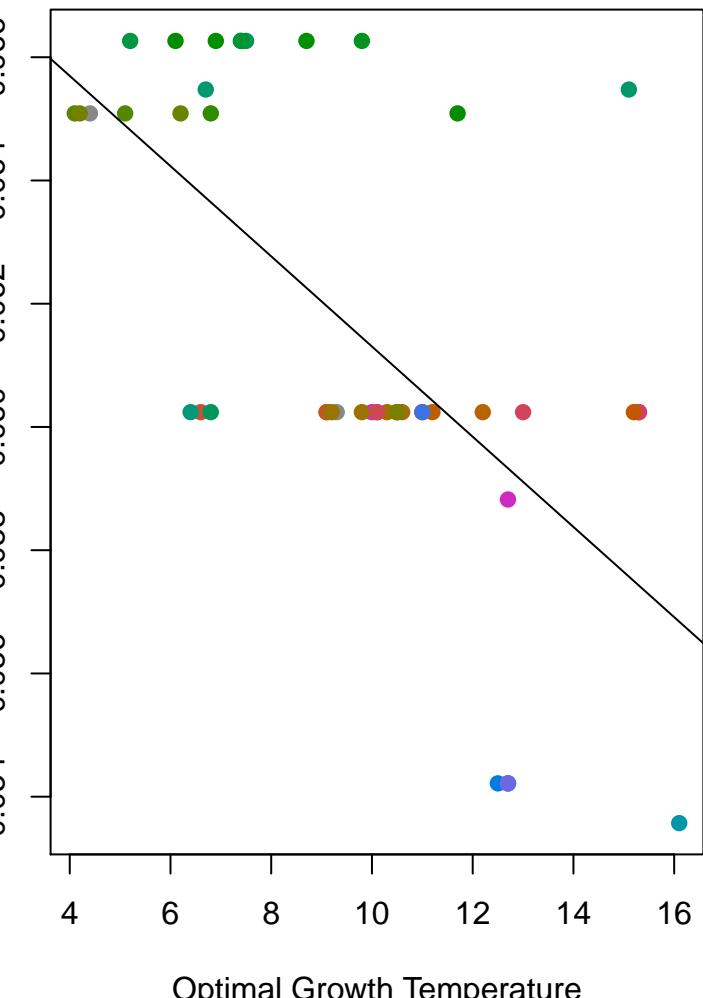
feature.pgfam_id.acidic_residue.mean

PGF_03073036

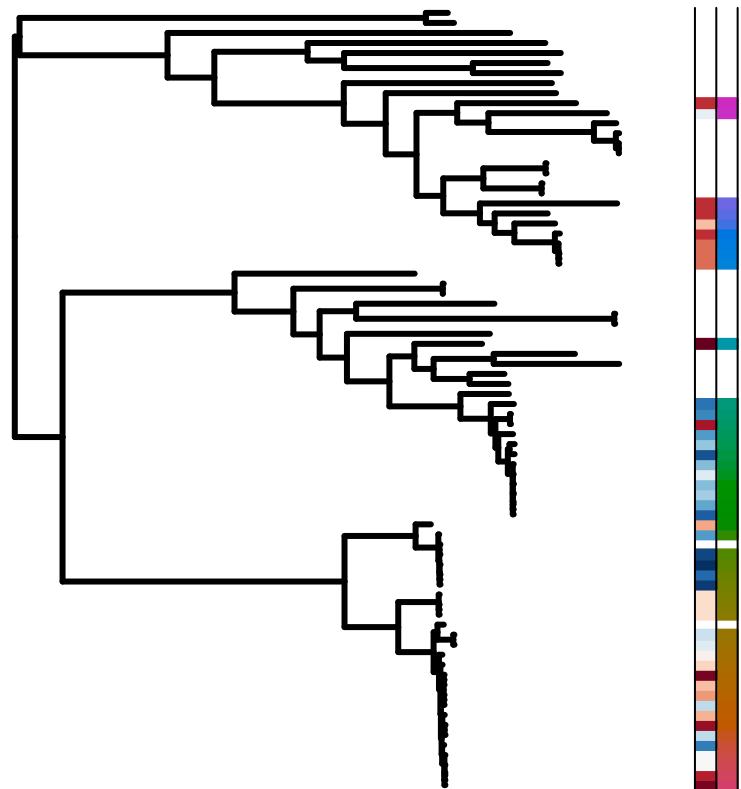
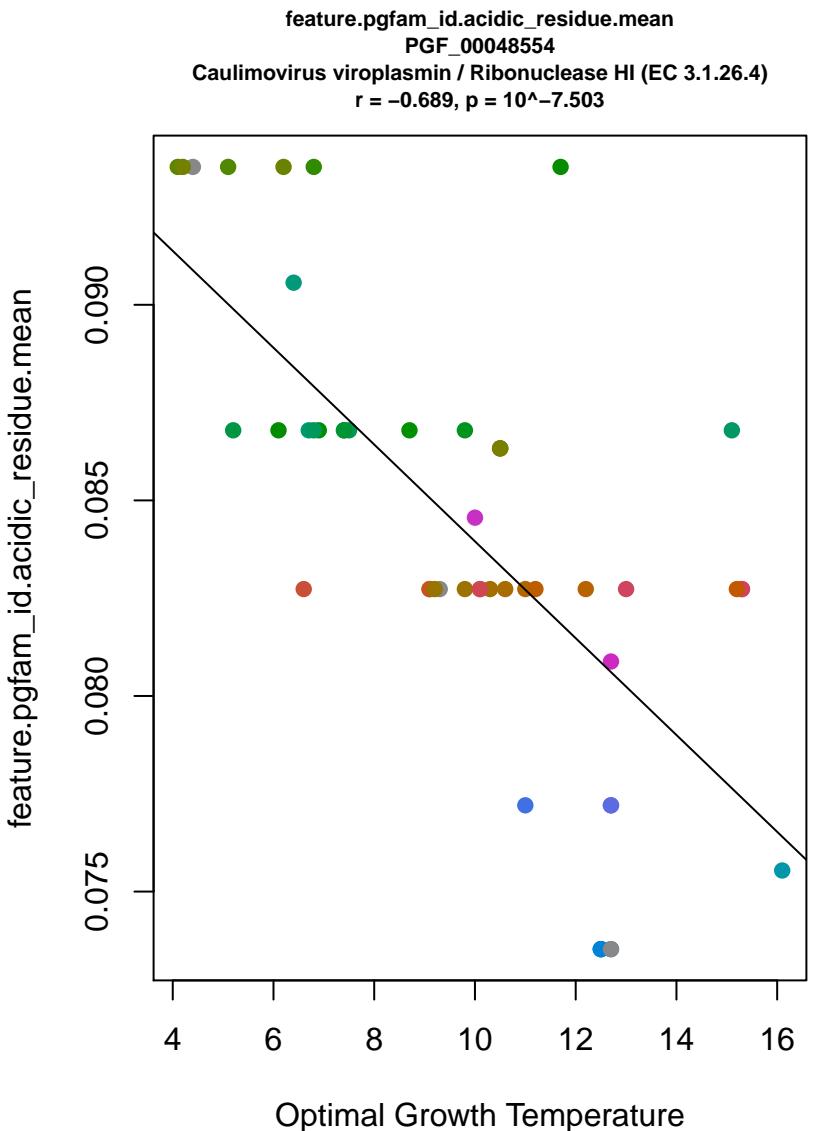
hypothetical protein

$r = -0.632, p = 10^{-5.726}$

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature



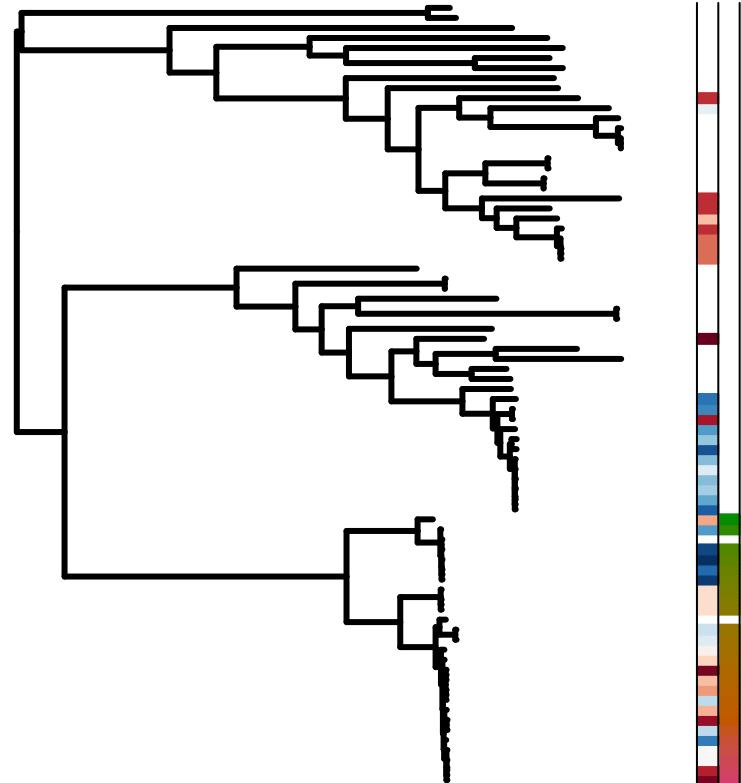
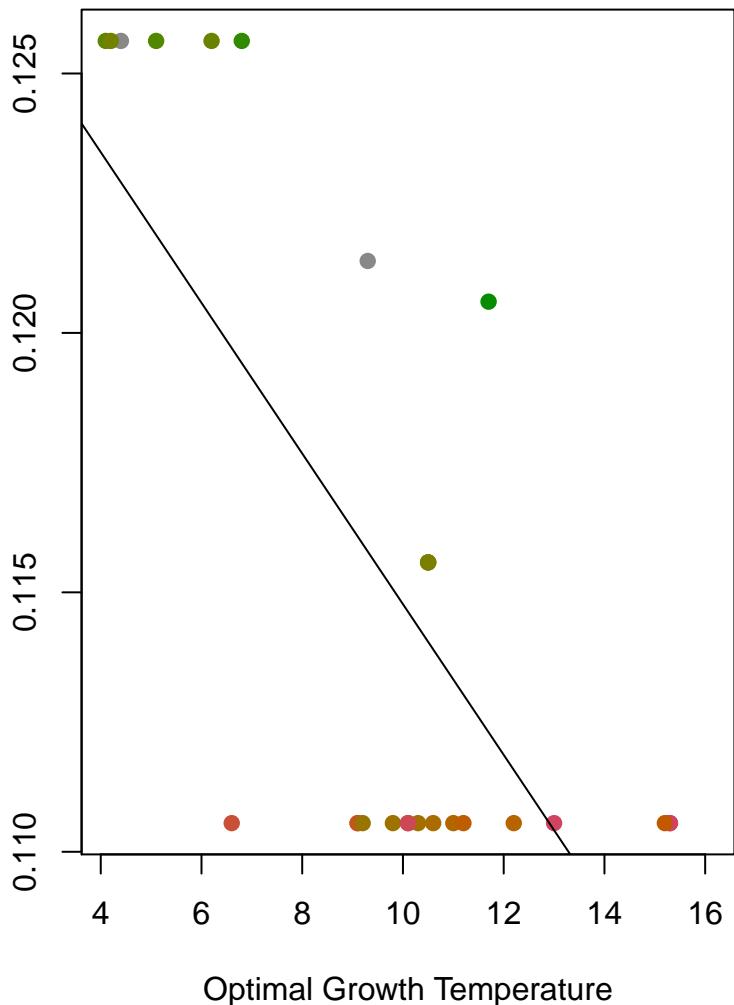
feature.pgfam_id.acidic_residue.mean

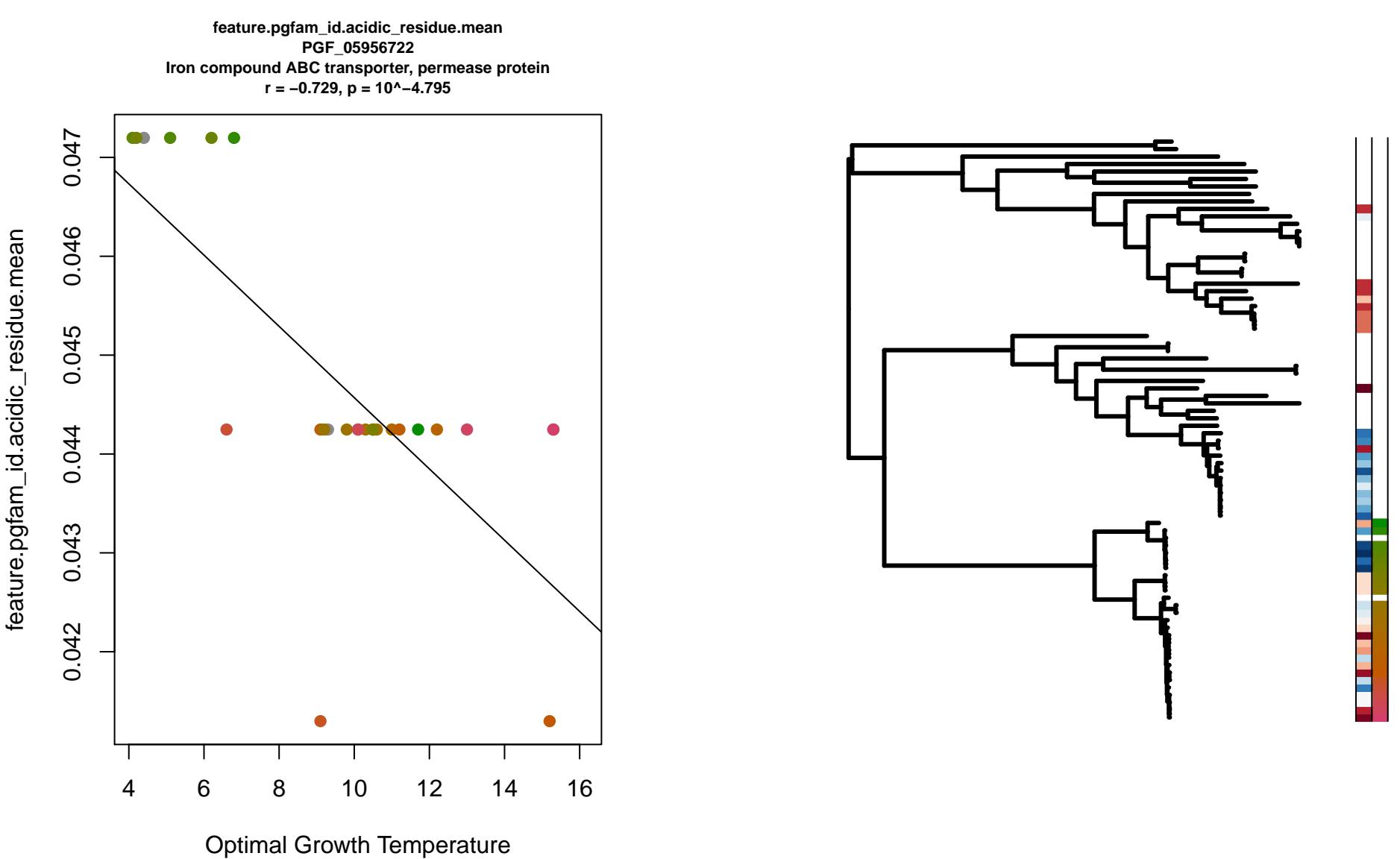
PGF_07373398

hypothetical protein

$r = -0.722, p = 10^{-4.676}$

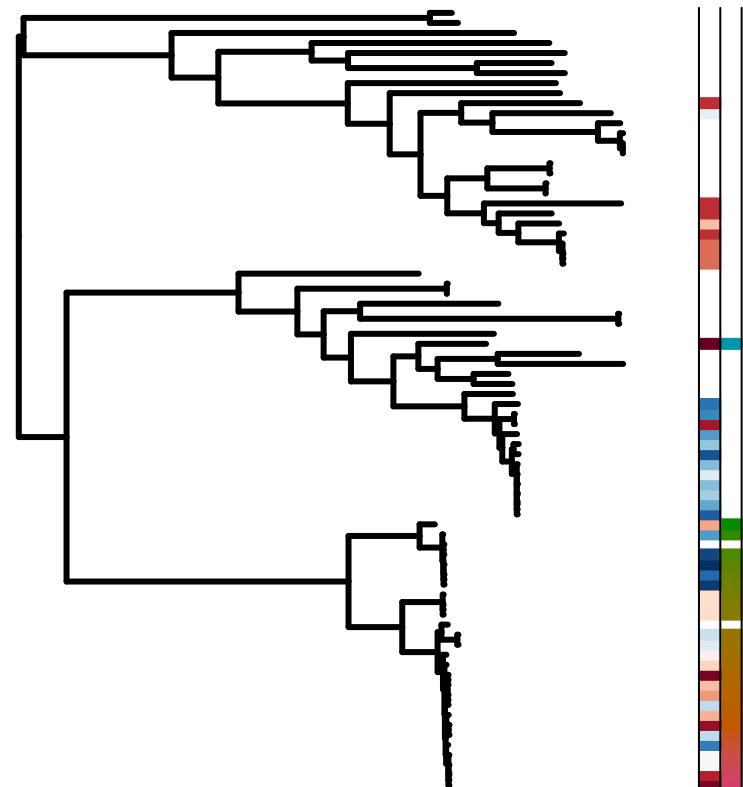
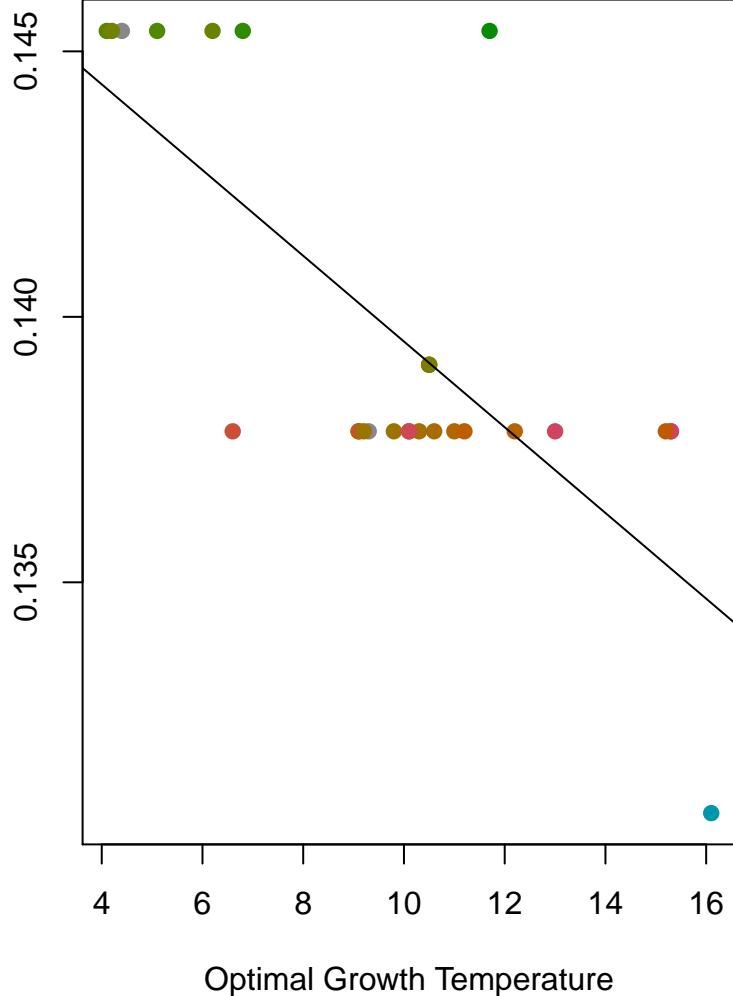
feature.pgfam_id.acidic_residue.mean





feature.pgfam_id.acidic_residue.mean
PGF_00001616
FIG01056734: hypothetical protein
 $r = -0.734$, $p = 10^{-5.048}$

feature.pgfam_id.acidic_residue.mean

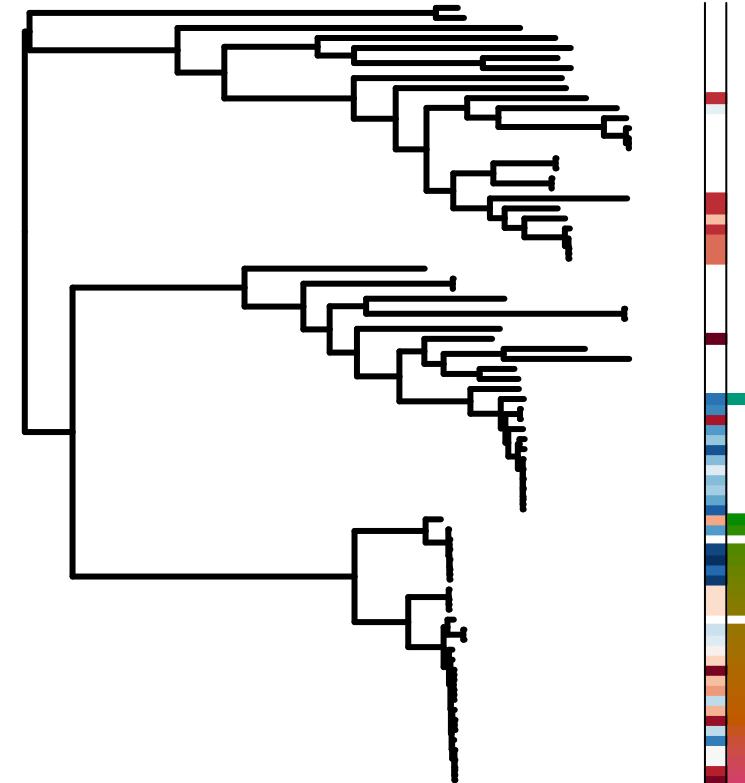
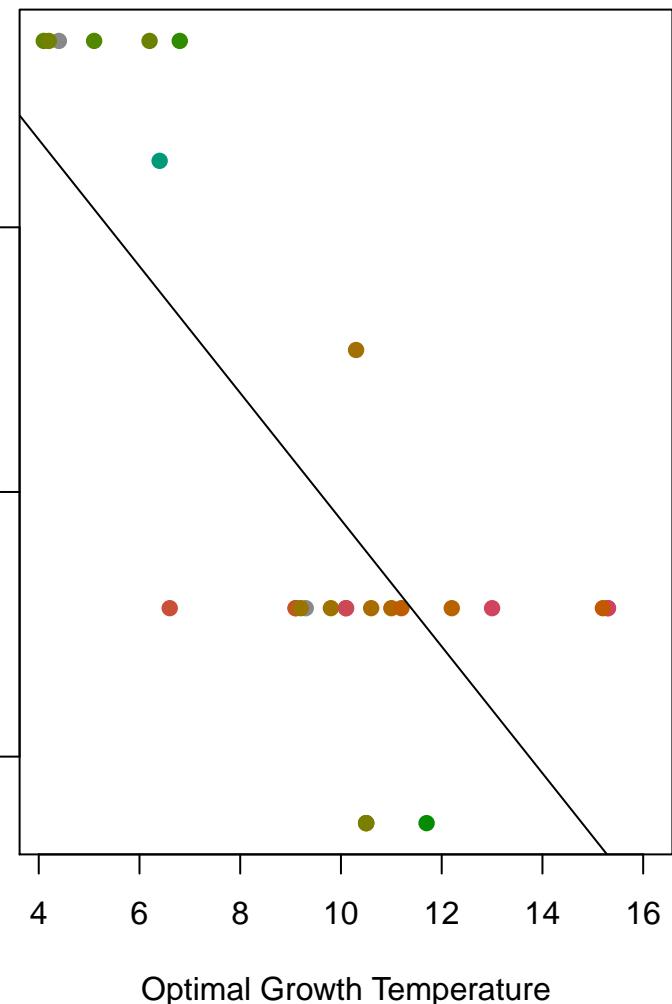


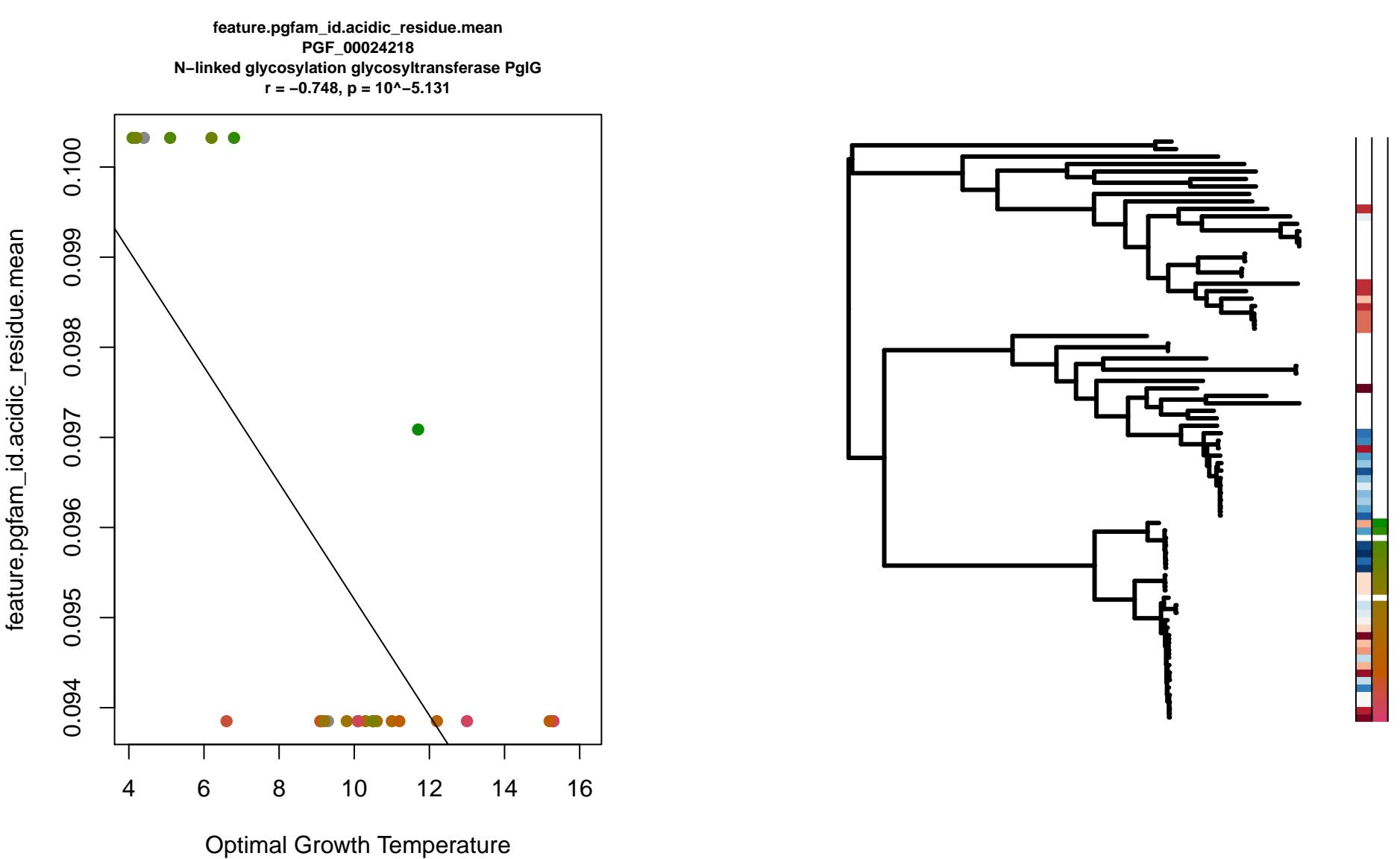
feature.pgfam_id.acidic_residue.mean

PGF_12826297

hypothetical protein

$r = -0.741, p = 10^{-5.186}$





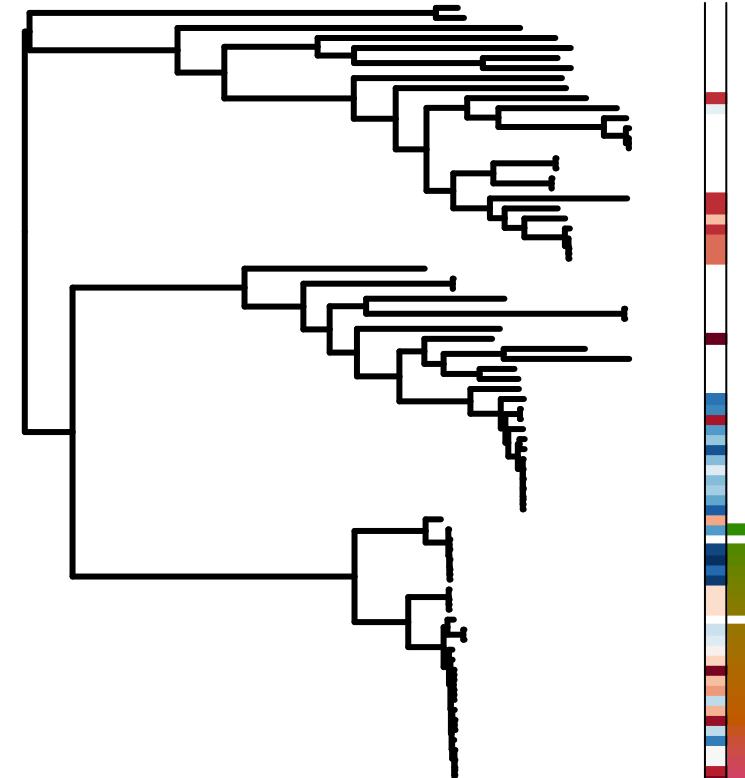
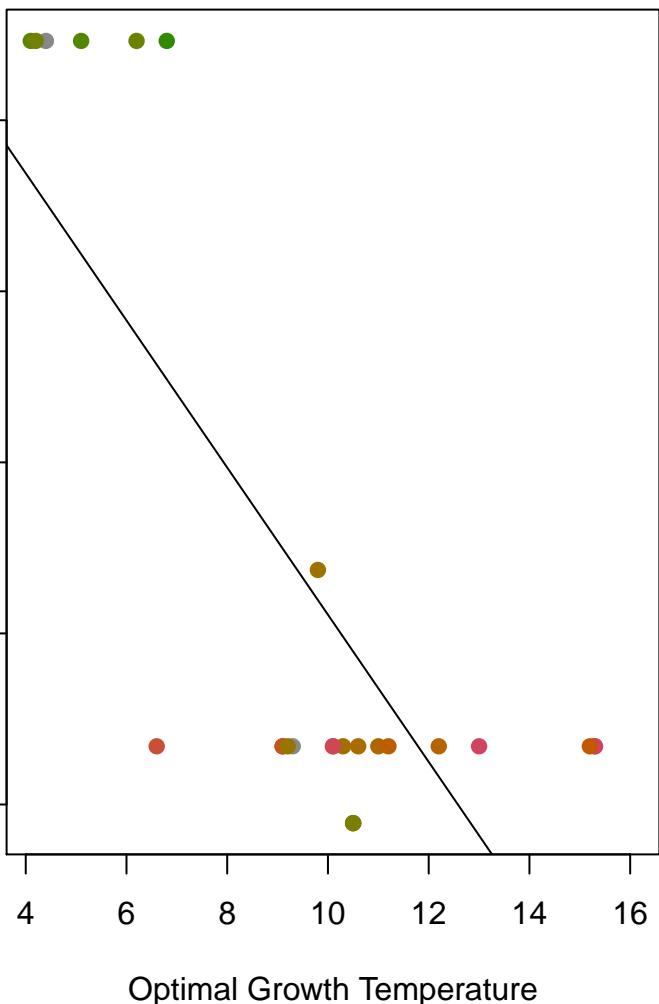
feature.pgfam_id.acidic_residue.mean

PGF_11915740

hypothetical protein

$r = -0.771, p = 10^{-5.395}$

feature.pgfam_id.acidic_residue.mean



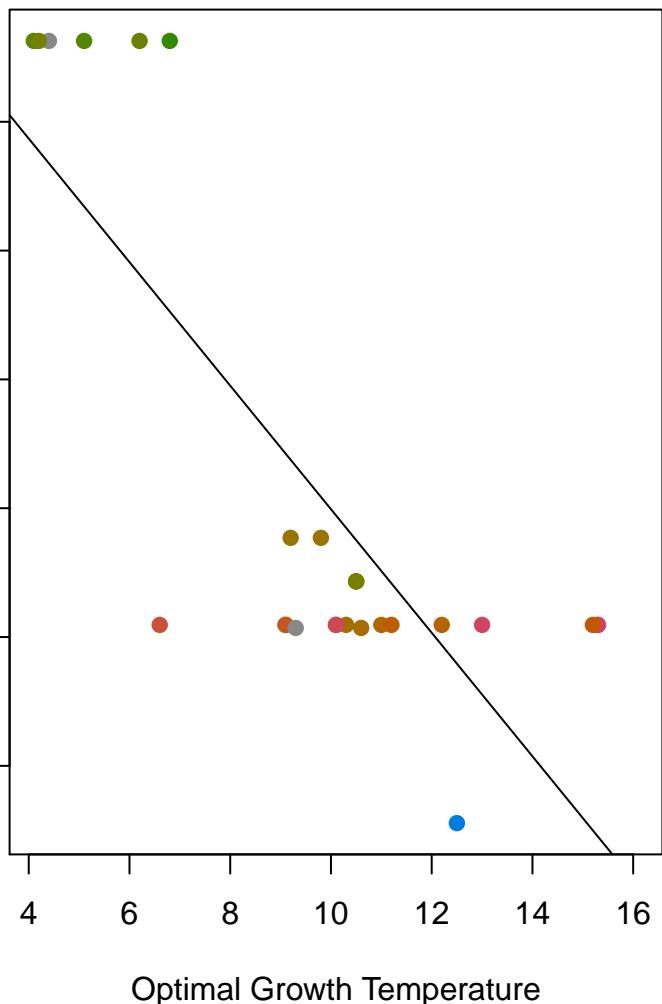
feature.pgfam_id.acidic_residue.mean

PGF_06792096

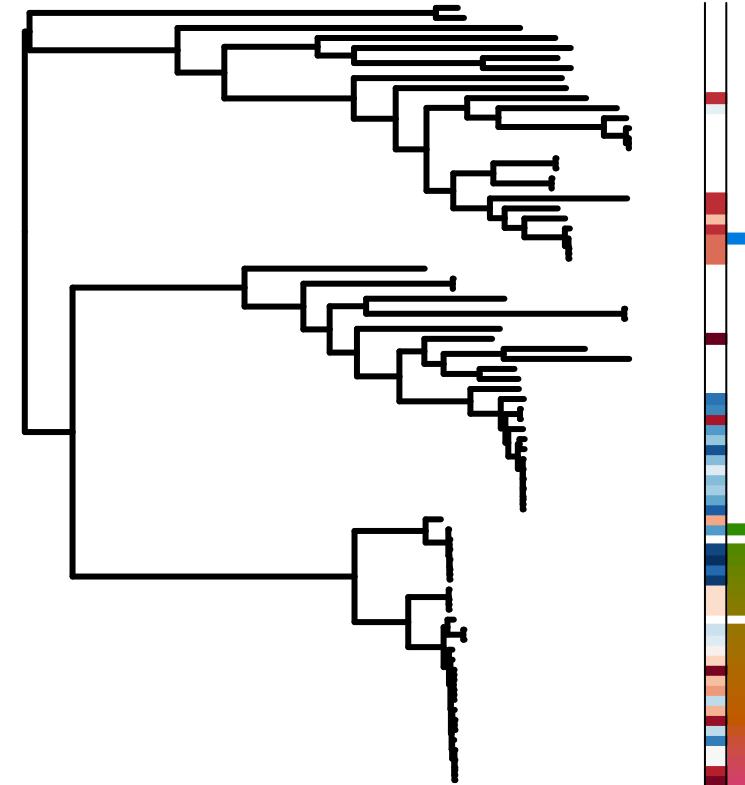
hypothetical protein

$r = -0.793, p = 10^{-6.081}$

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature



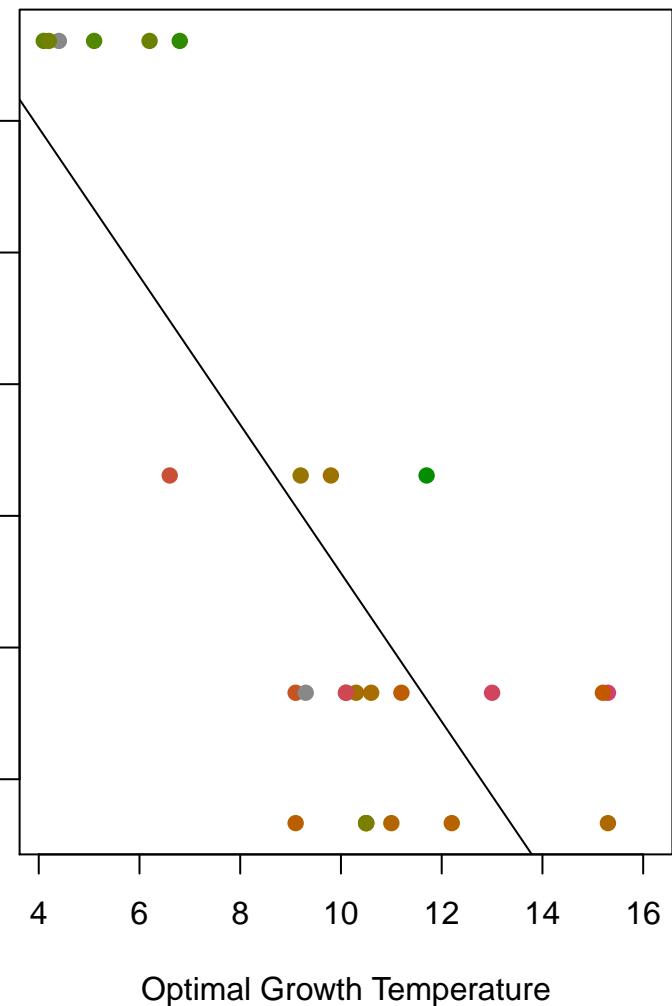
feature.pgfam_id.acidic_residue.mean

PGF_12817314

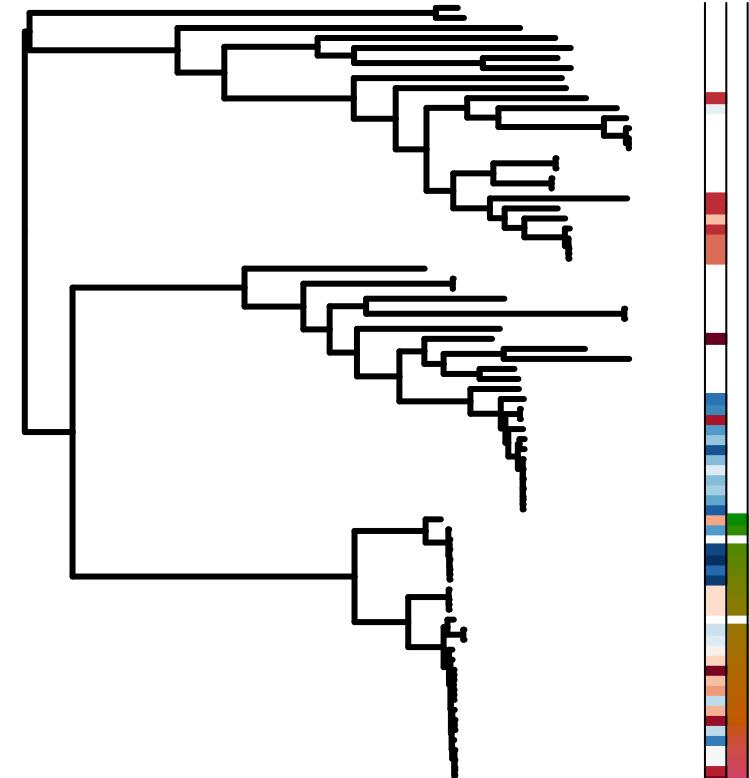
hypothetical protein

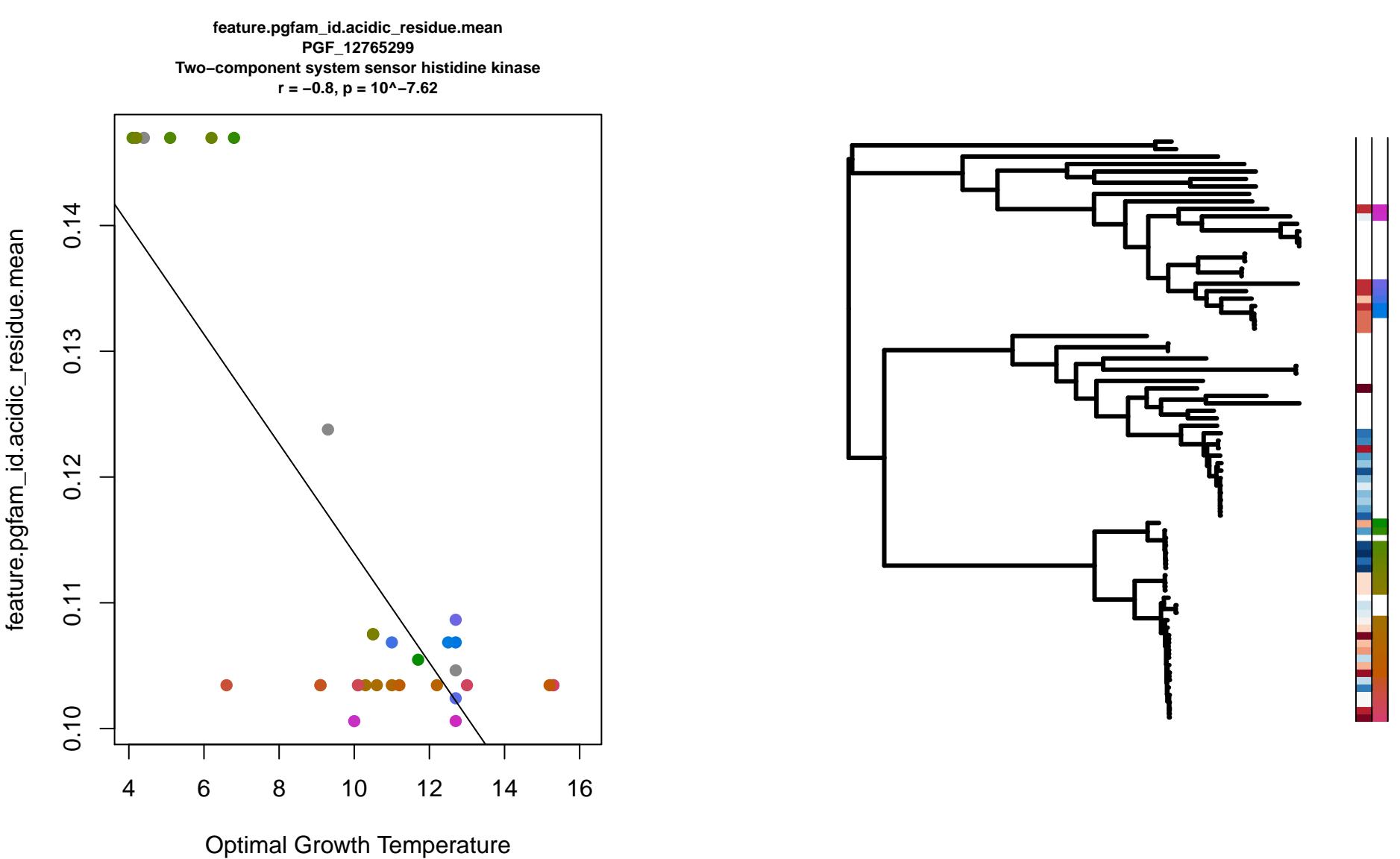
$r = -0.794, p = 10^{-6.12}$

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature





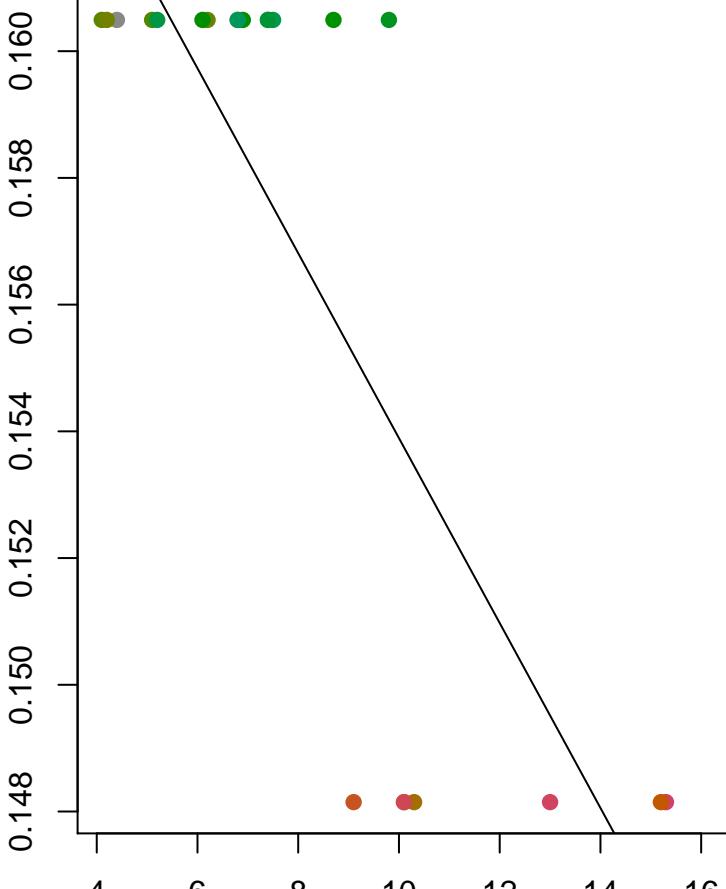
feature.pgfam_id.acidic_residue.mean

PGF_00393434

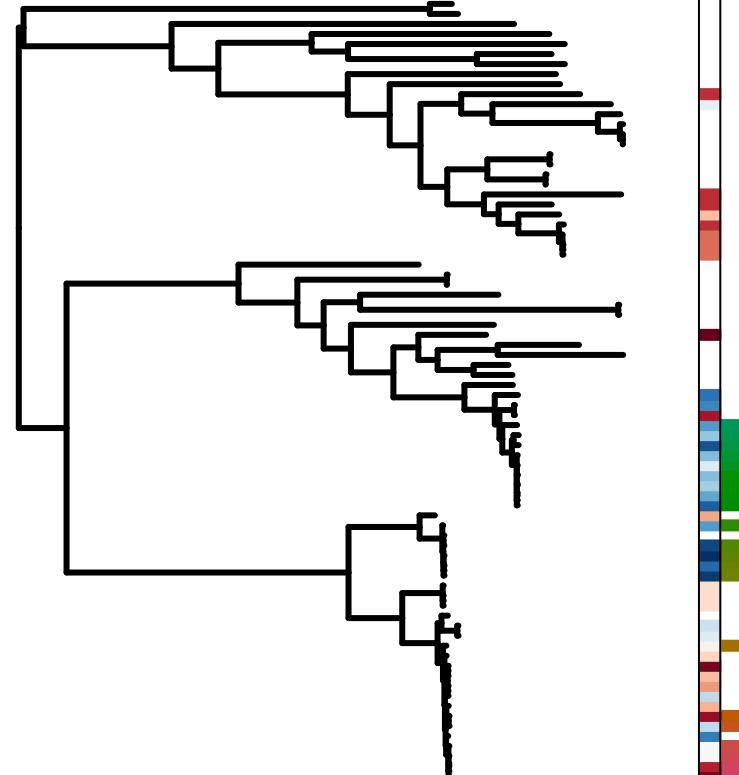
hypothetical protein

$r = -0.801, p = 10^{-5.129}$

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature



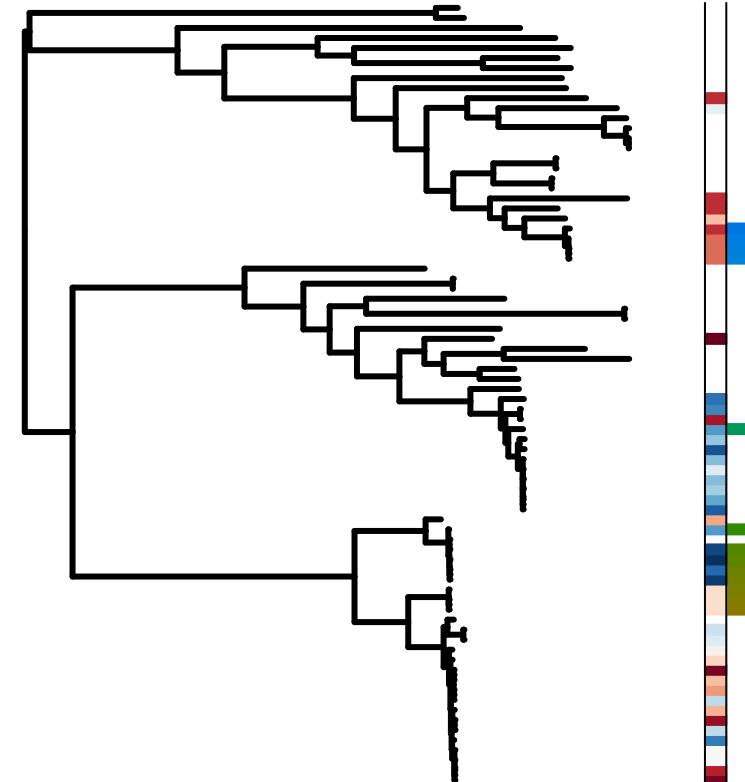
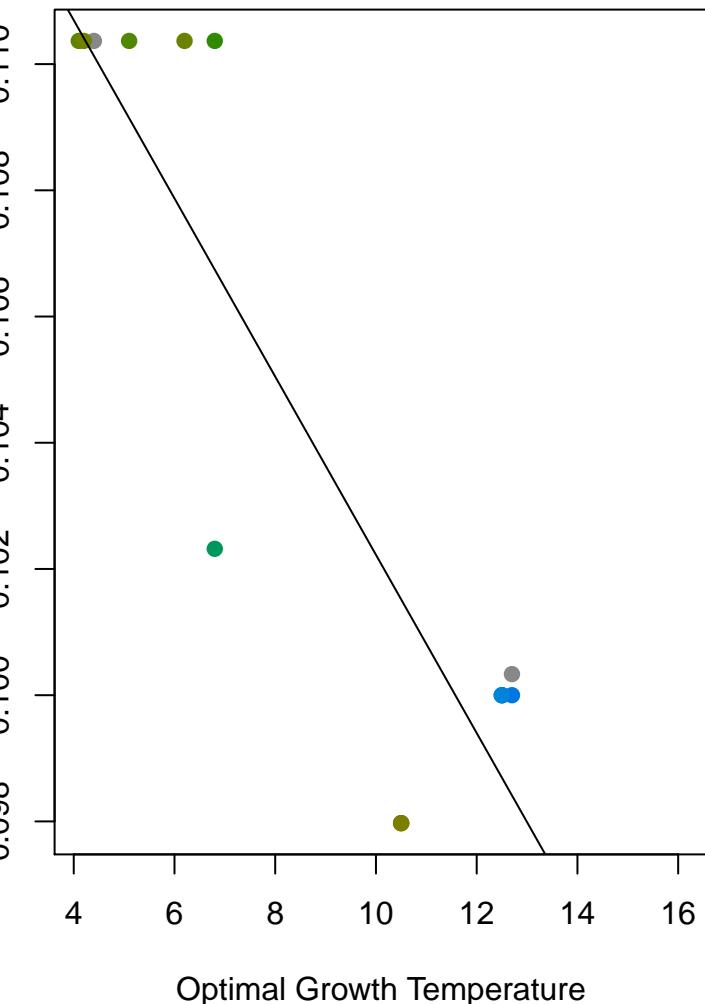
feature.pgfam_id.acidic_residue.mean

PGF_01338001

hypothetical protein

$r = -0.889, p = 10^{-5.017}$

feature.pgfam_id.acidic_residue.mean



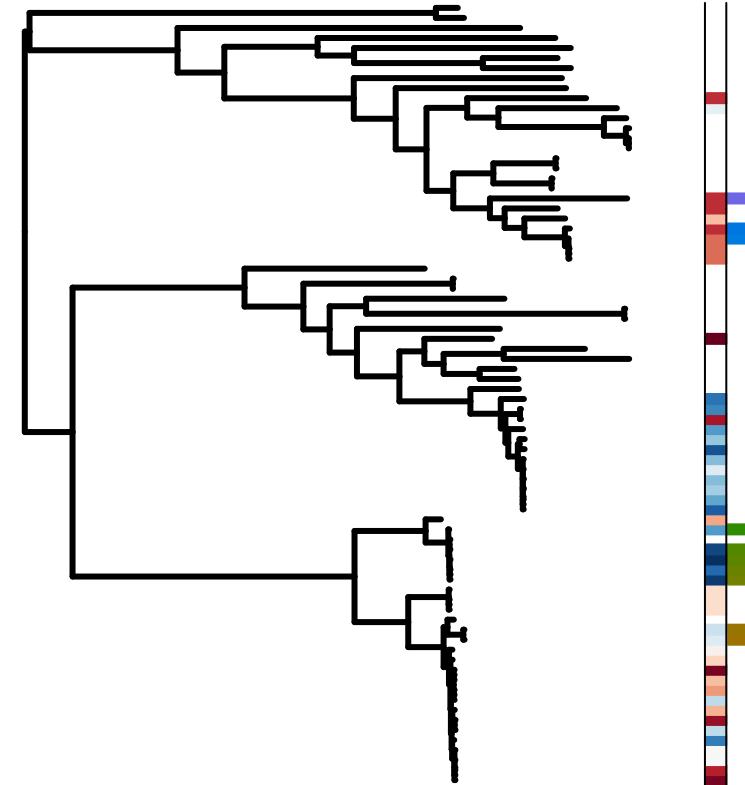
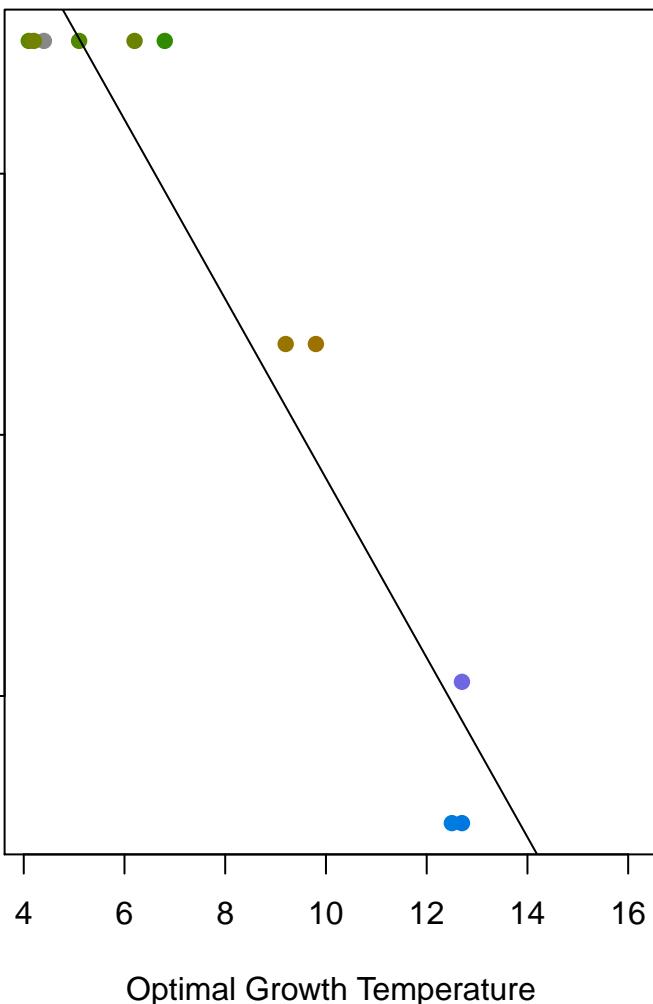
feature.pgfam_id.acidic_residue.mean

PGF_09542755

putative lipoprotein

$r = -0.956, p = 10^{-5.348}$

feature.pgfam_id.acidic_residue.mean



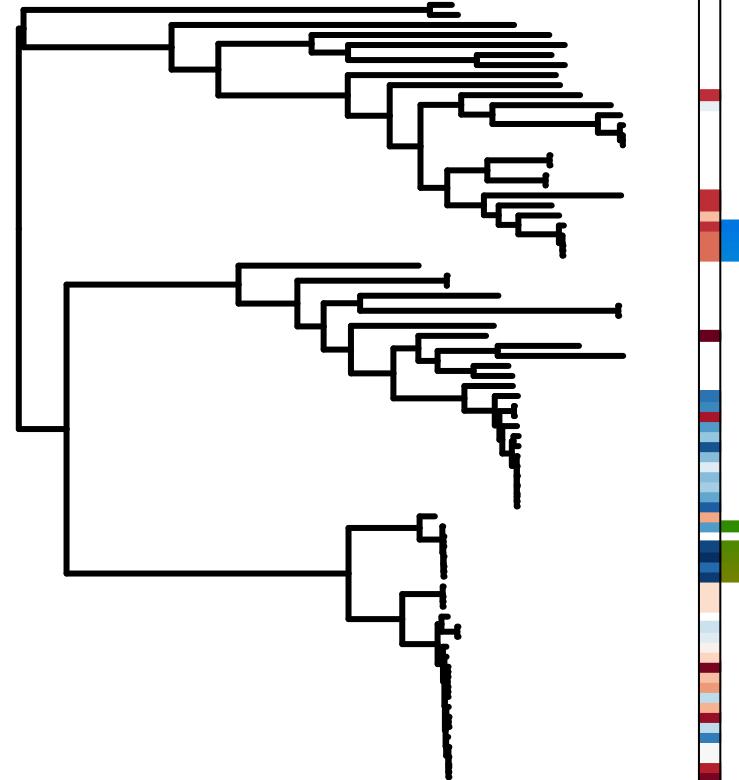
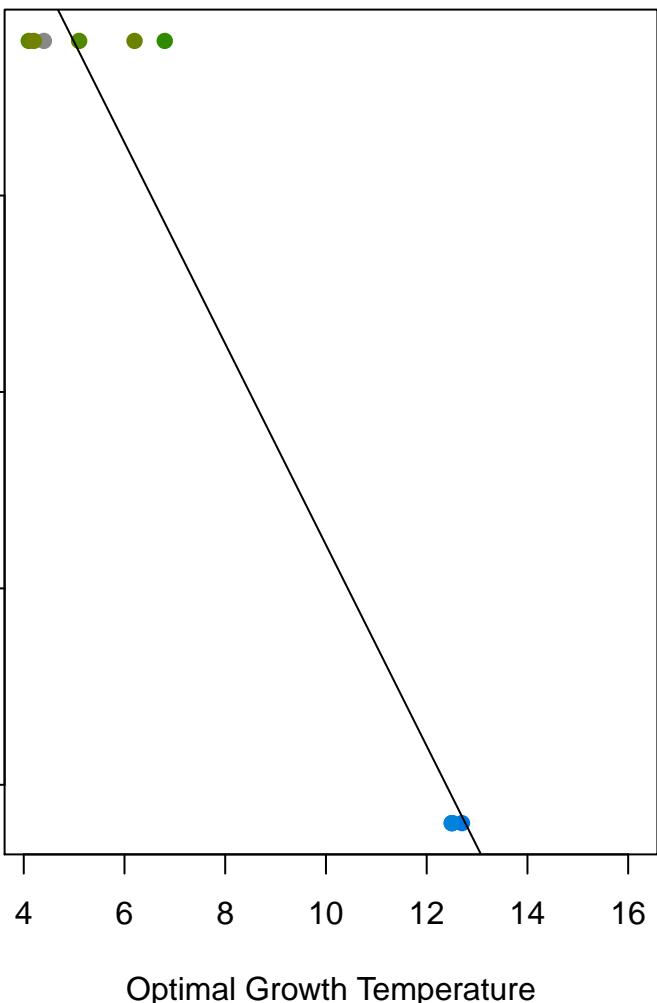
feature.pgfam_id.acidic_residue.mean

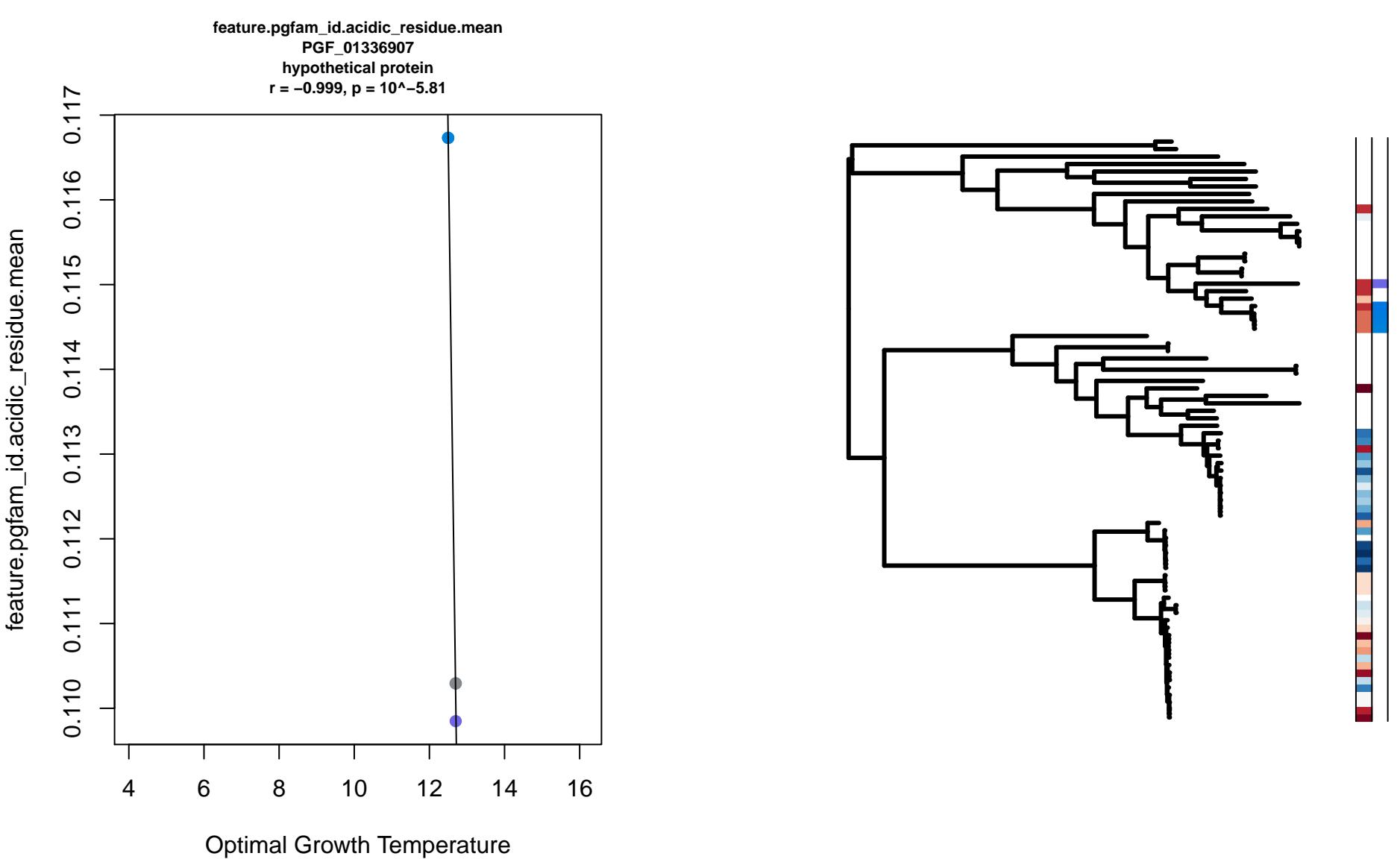
PGF_01338043

hypothetical protein

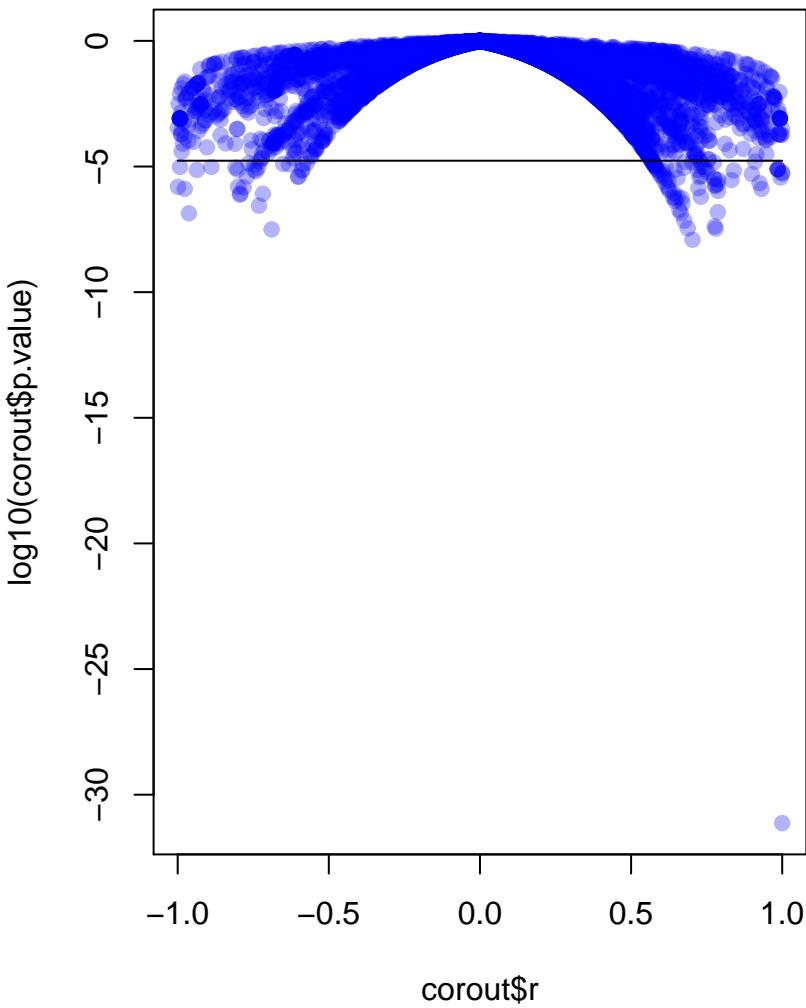
$r = -0.977, p = 10^{-5.889}$

feature.pgfam_id.acidic_residue.mean



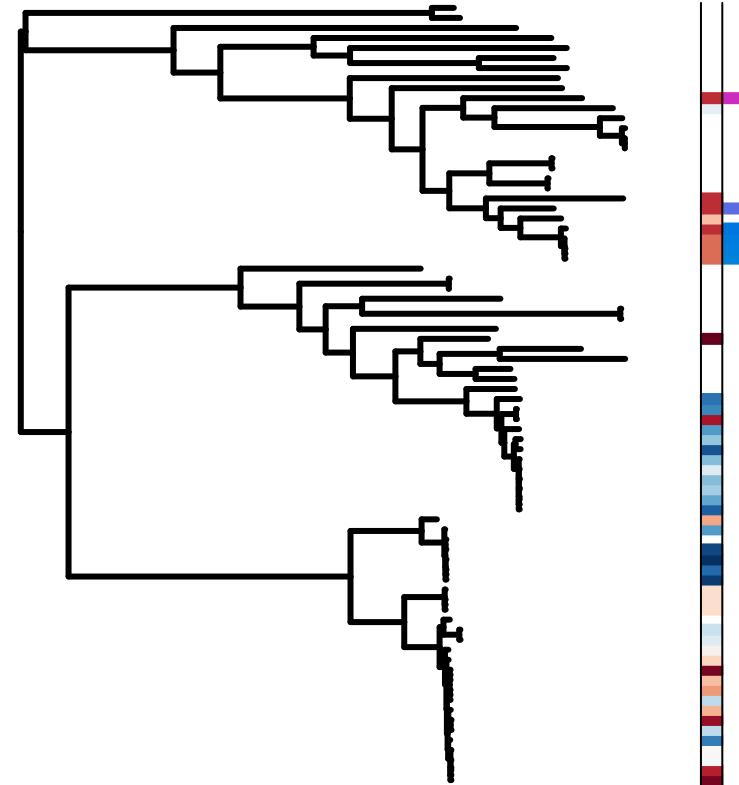
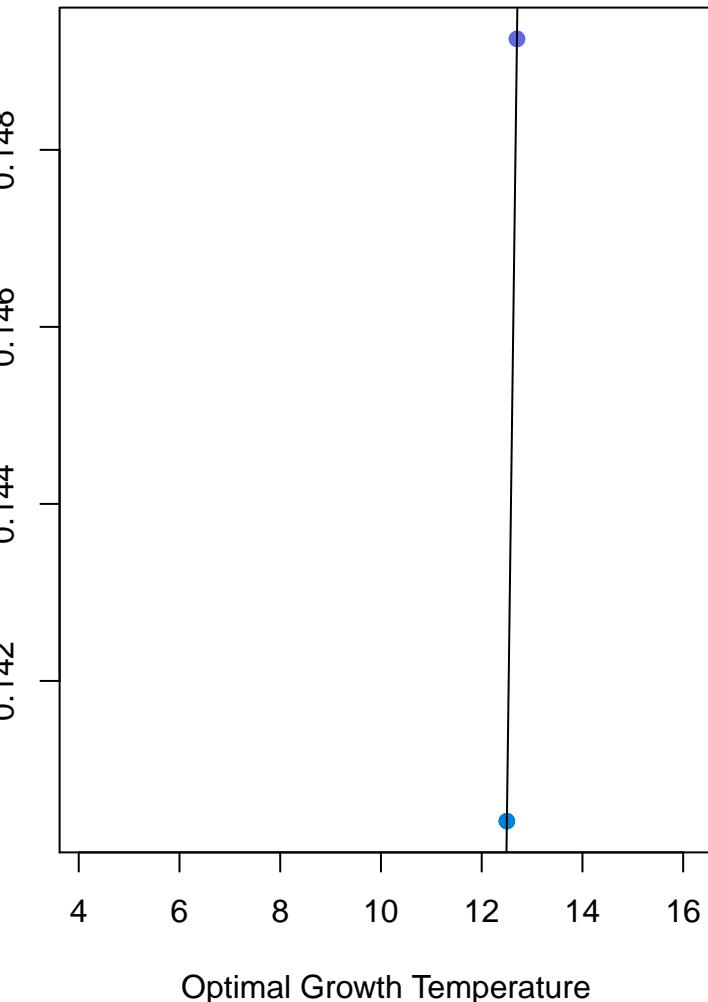


feature.plfam_id.acidic_residue.mean



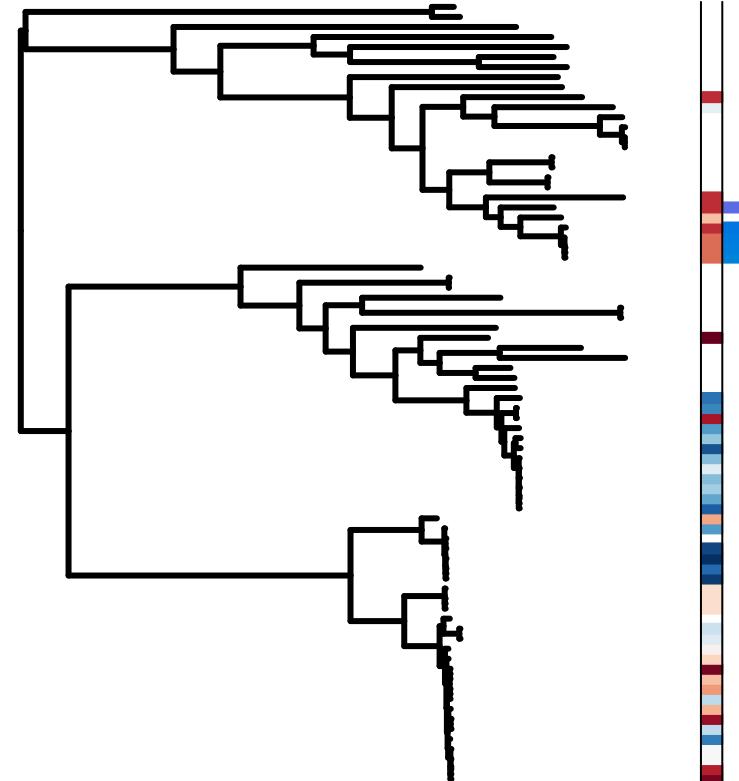
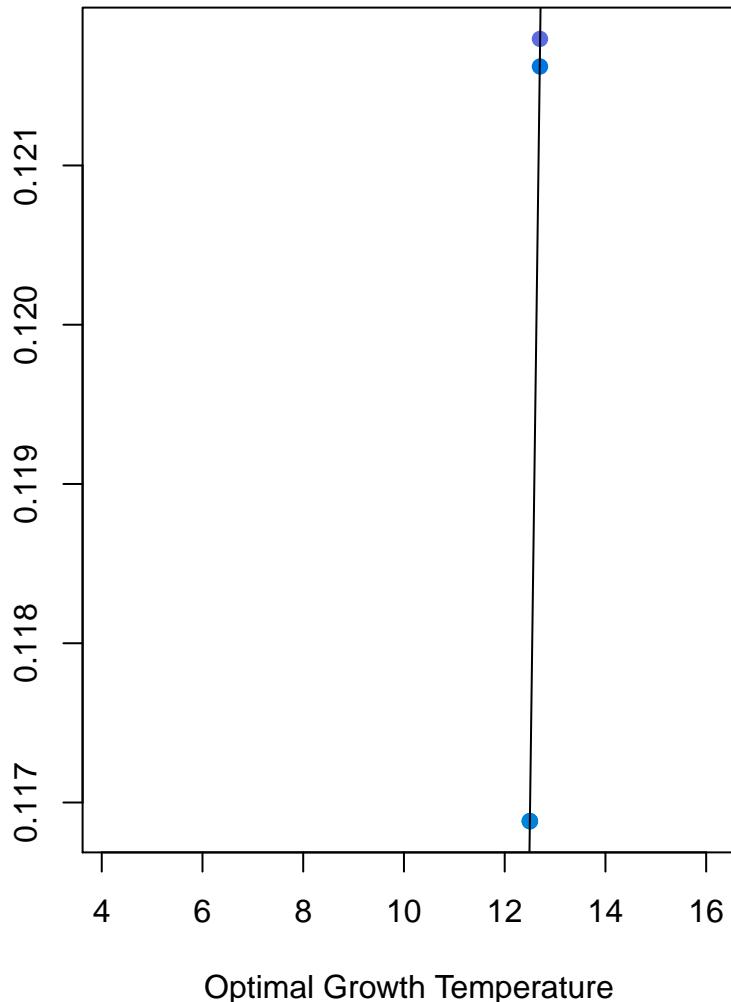
feature.plfam_id.acidic_residue.mean
PLF_28228_00003006
hypothetical protein
 $r = 1$, $p = 10^{-31.131}$

feature.plfam_id.acidic_residue.mean



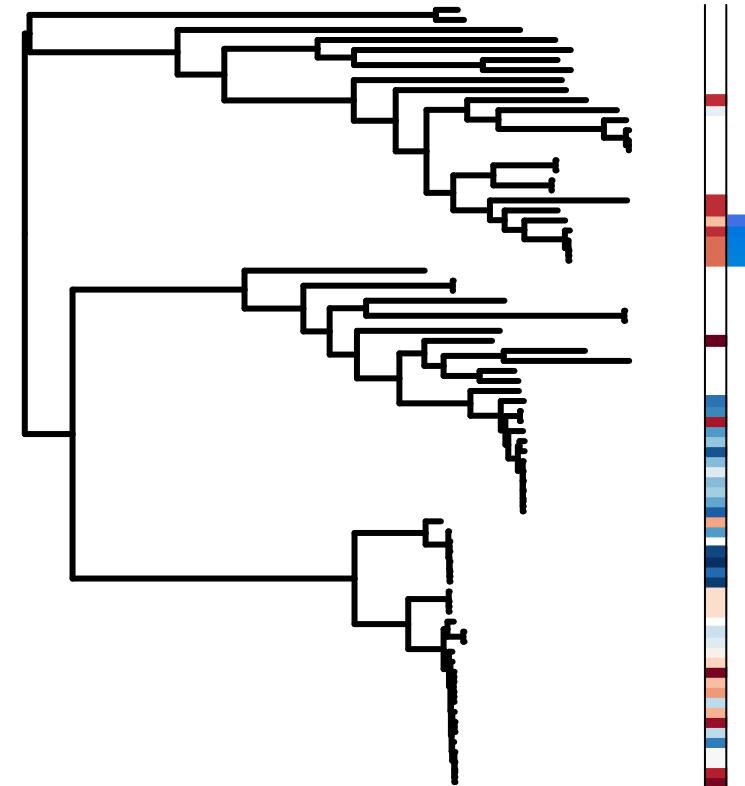
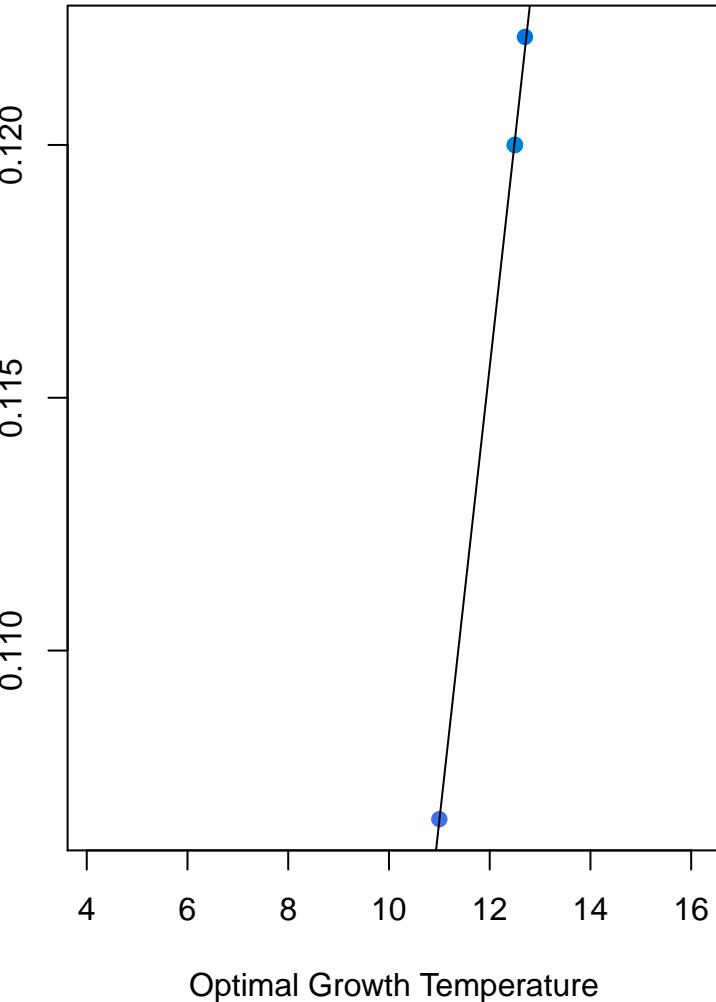
feature.plfam_id.acidic_residue.mean
PLF_28228_00007900
Regulatory protein LuxR
 $r = 1$, $p = 10^{-5.277}$

feature.plfam_id.acidic_residue.mean



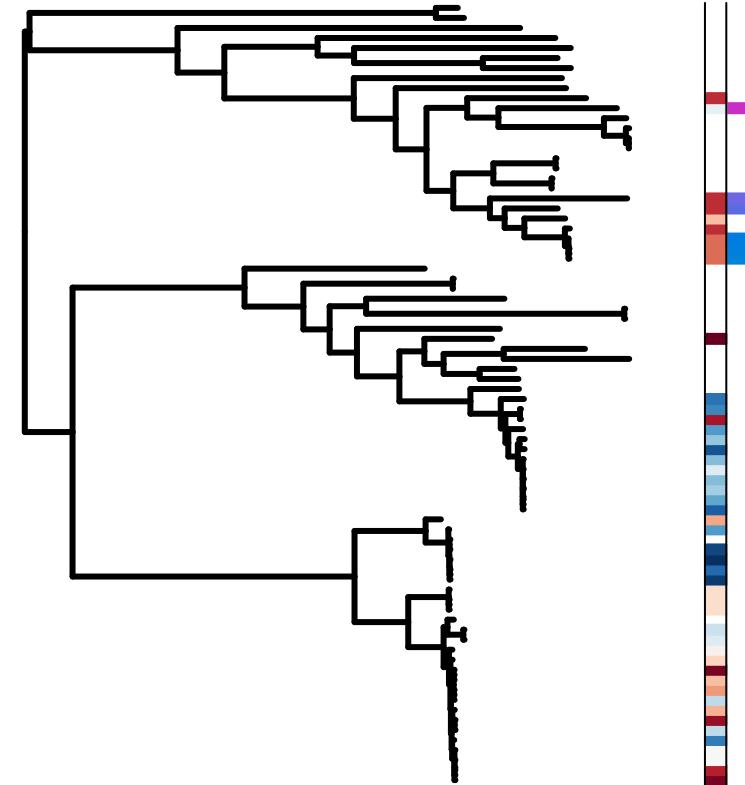
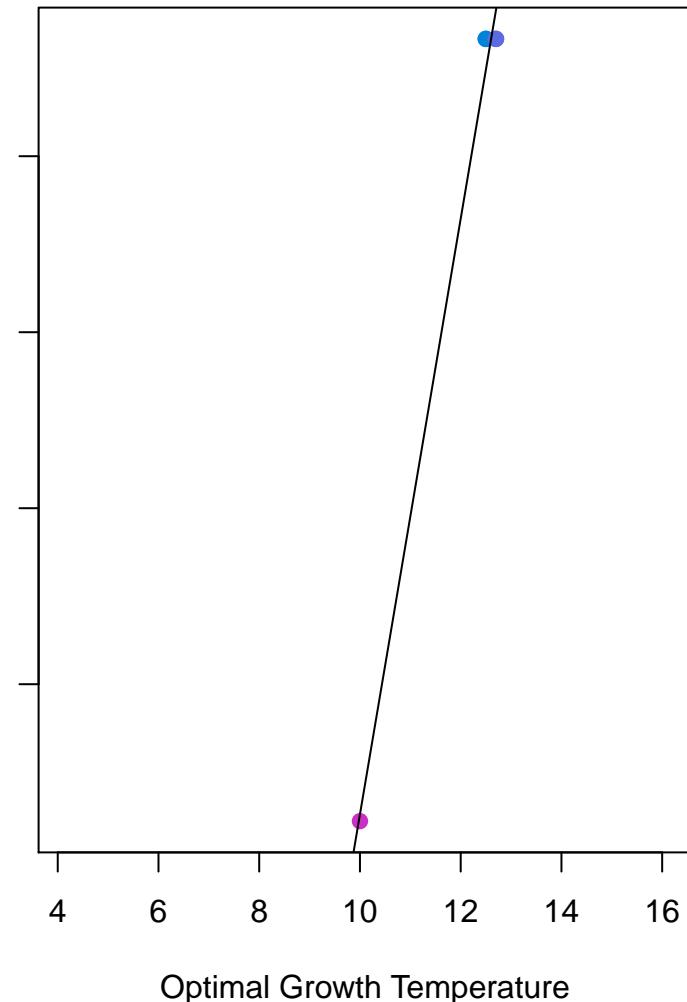
feature.plfam_id.acidic_residue.mean
PLF_28228_00007757
Fluoride ion transporter CrcB
 $r = 1, p = 10^{-5.24}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00004382
hypothetical protein
 $r = 0.995, p = 10^{-5.441}$

feature.plfam_id.acidic_residue.mean



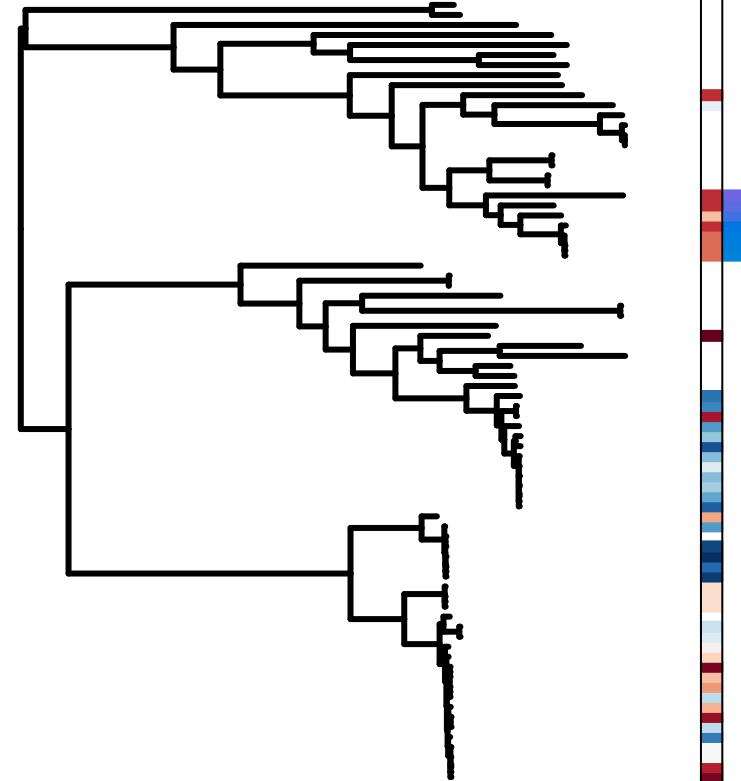
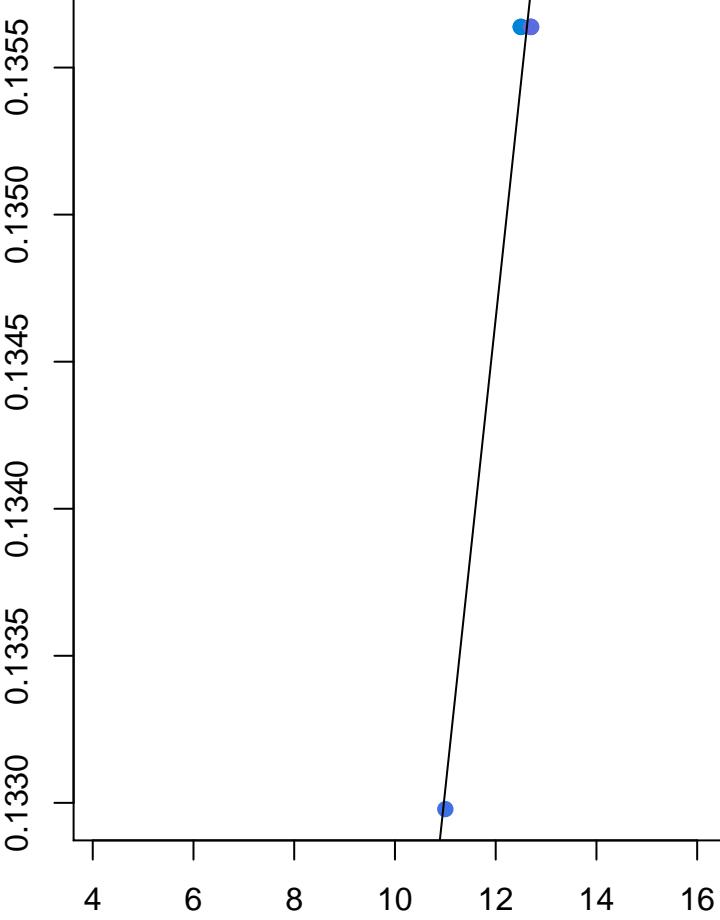
feature.plfam_id.acidic_residue.mean

PLF_28228_00003607

Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2)

r = 0.985, p = 10^-5.104

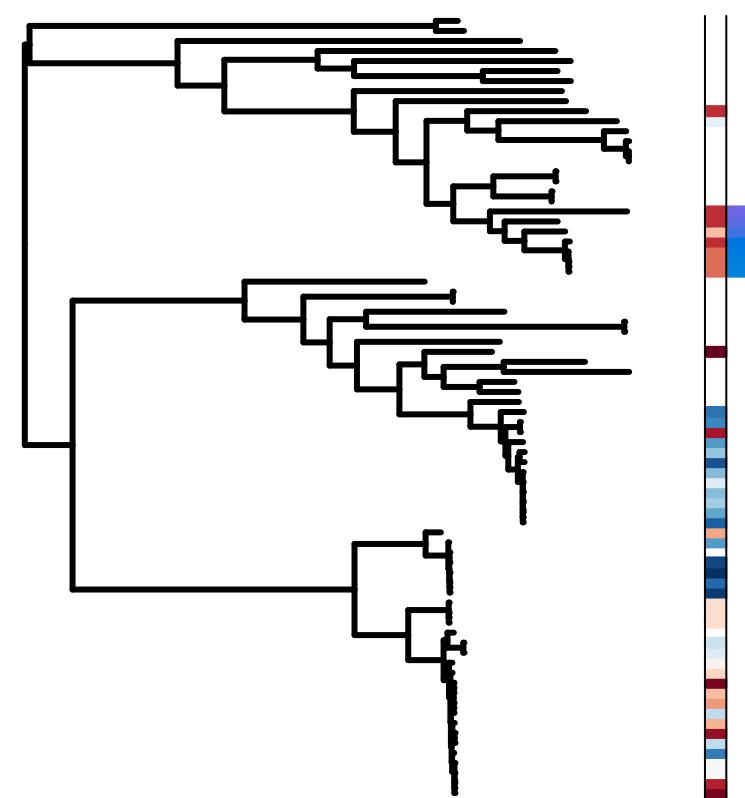
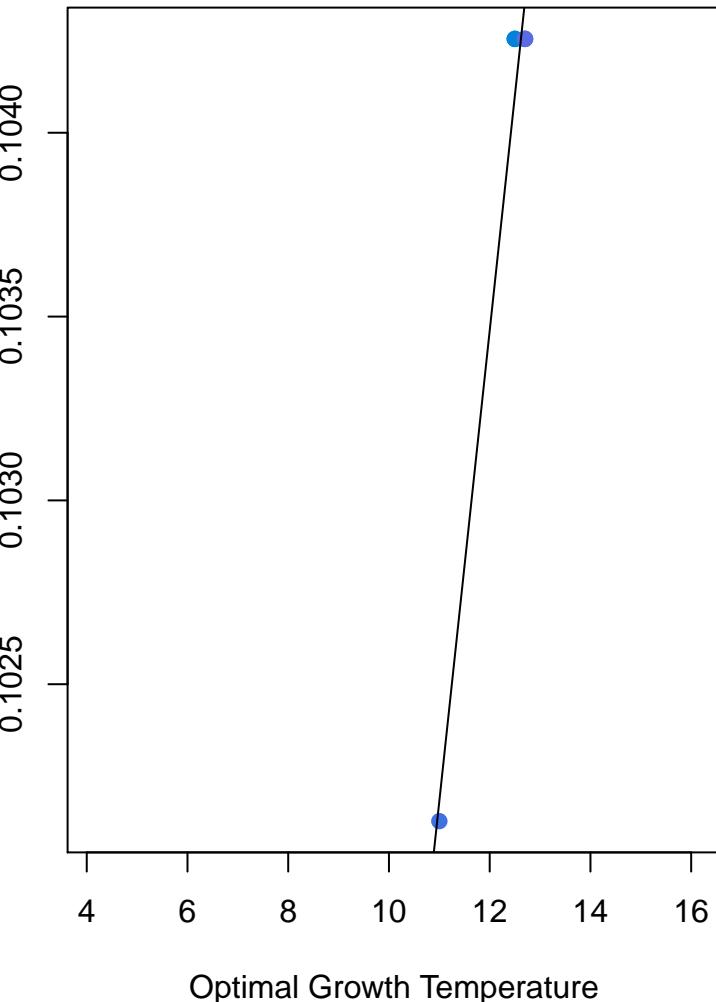
feature.plfam_id.acidic_residue.mean



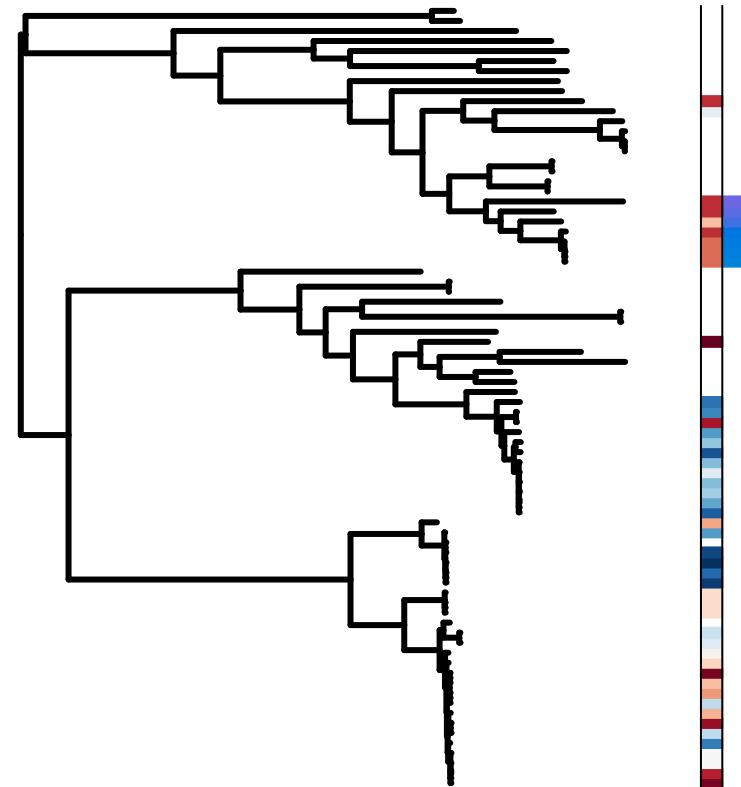
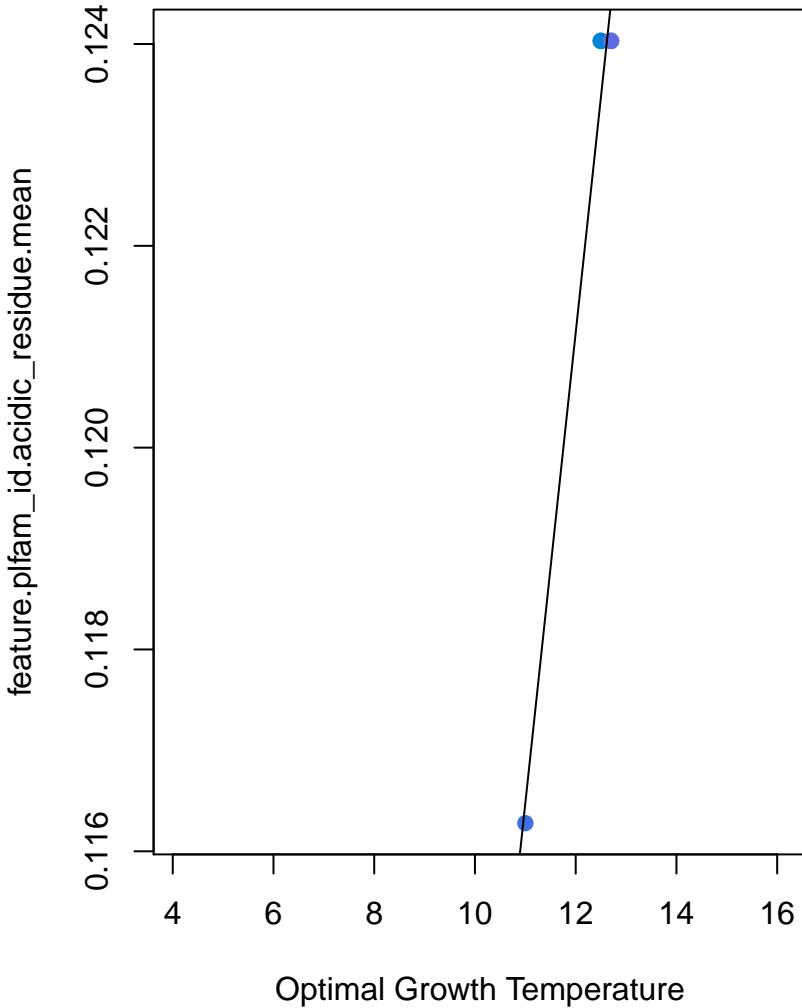
Optimal Growth Temperature

feature.plfam_id.acidic_residue.mean
PLF_28228_00003399
Alpha-amylase precursor (EC 3.2.1.1)
 $r = 0.985$, $p = 10^{-5.104}$

feature.plfam_id.acidic_residue.mean

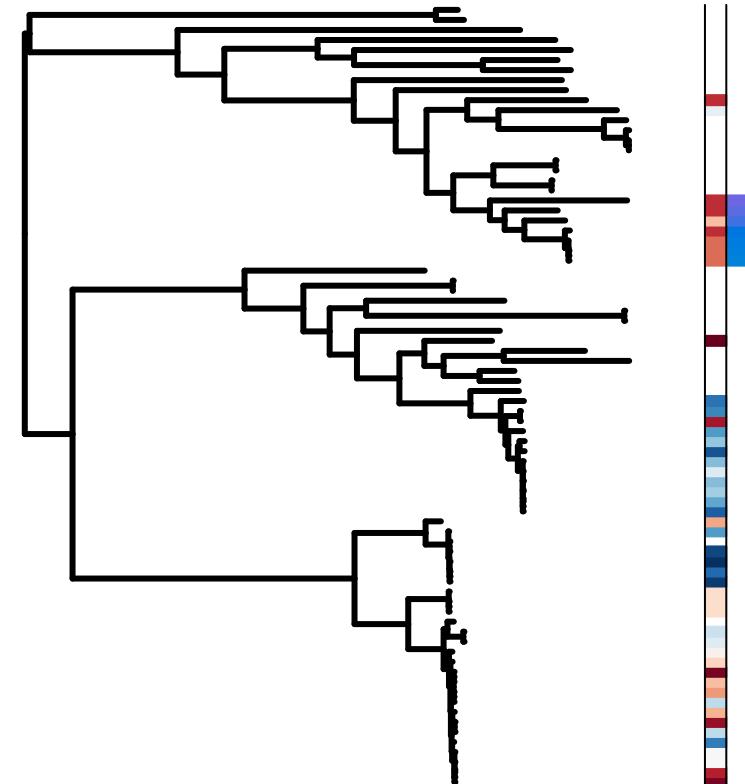
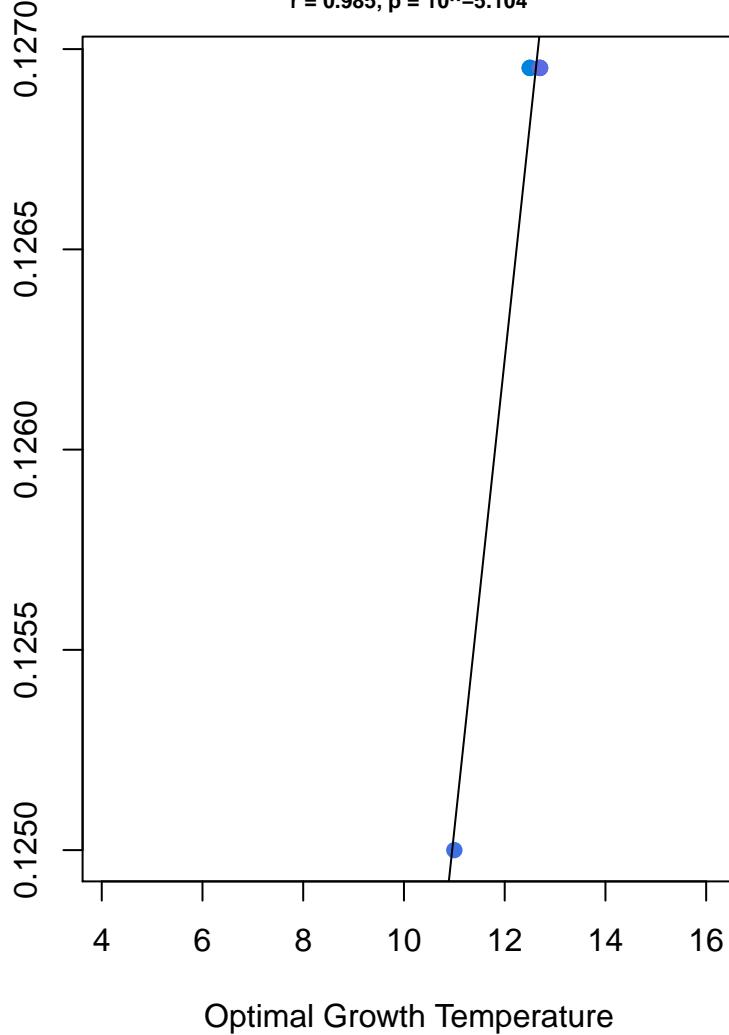


feature.plfam_id.acidic_residue.mean
PLF_28228_00004001
hypothetical protein
 $r = 0.985, p = 10^{-5.104}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00003079
Arylsulfatase (EC 3.1.6.1)
 $r = 0.985$, $p = 10^{-5.104}$

feature.plfam_id.acidic_residue.mean



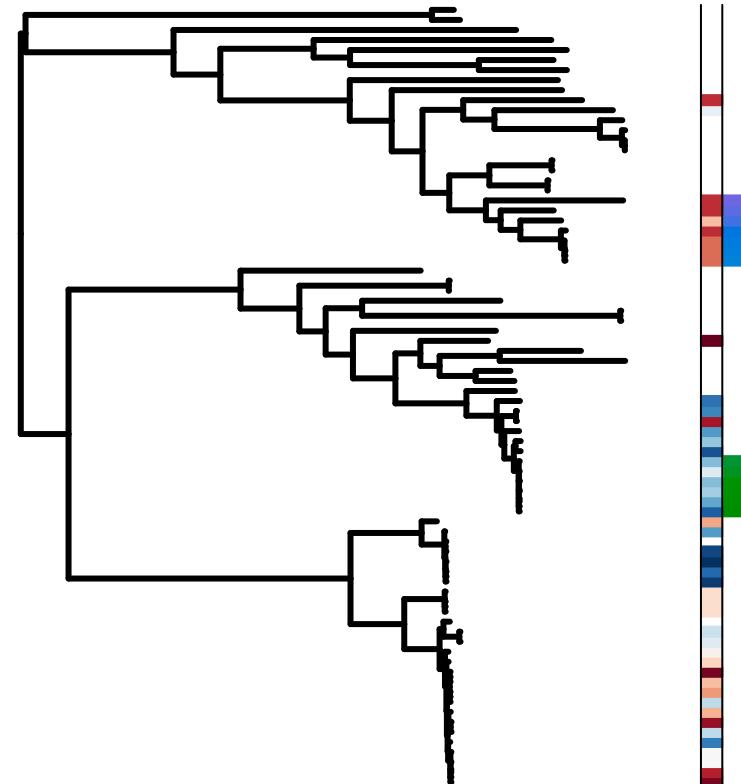
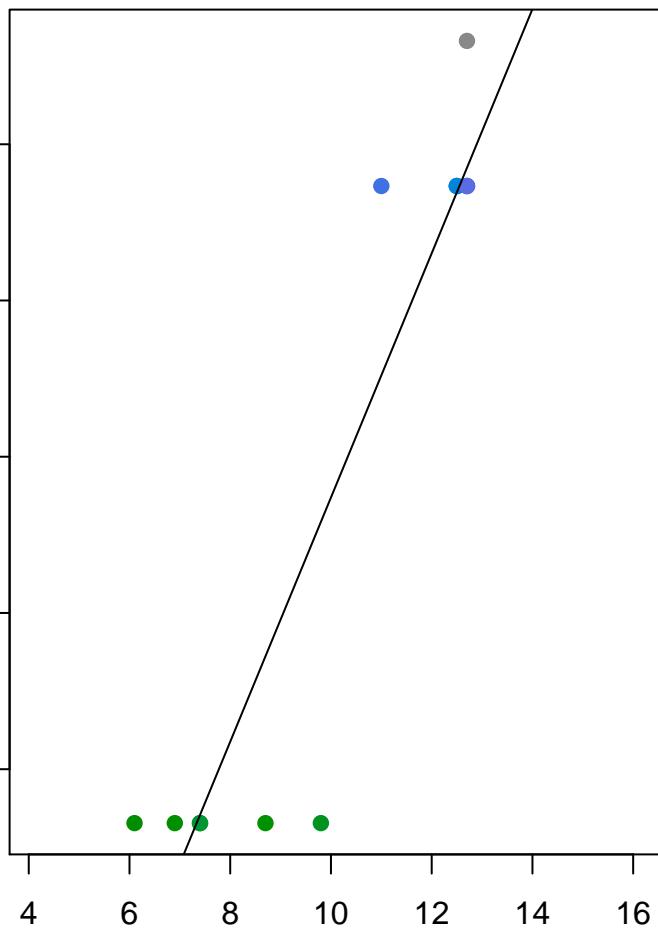
feature.plfam_id.acidic_residue.mean

PLF_28228_00003260

C4-dicarboxylate transport transcriptional regulatory protein

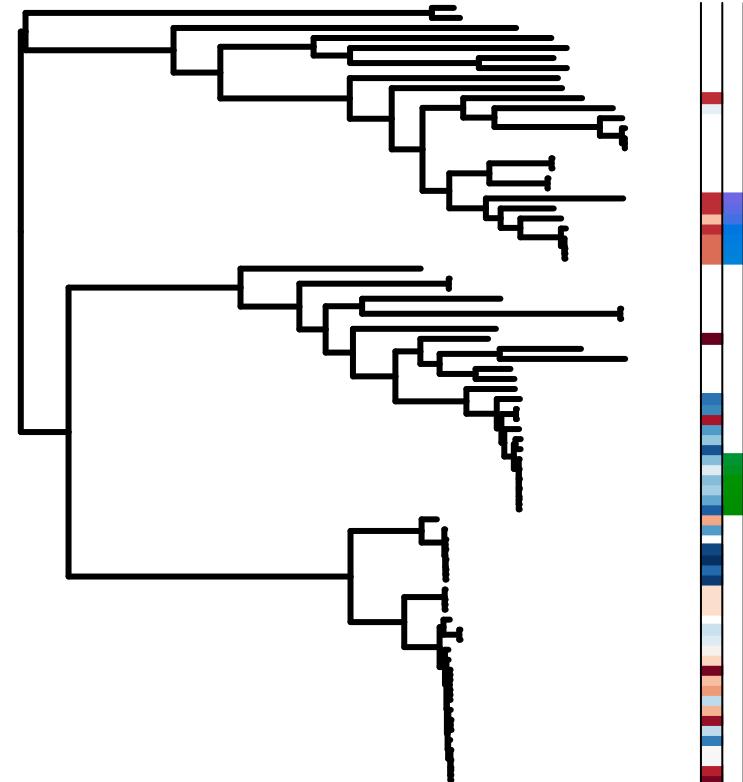
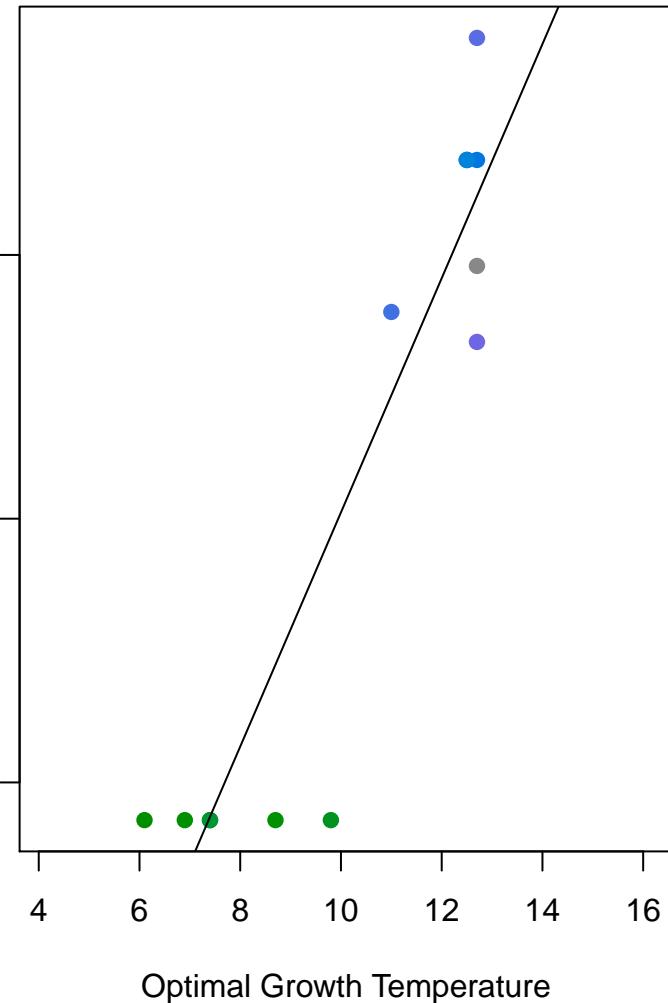
$r = 0.931, p = 10^{-5.89}$

feature.plfam_id.acidic_residue.mean



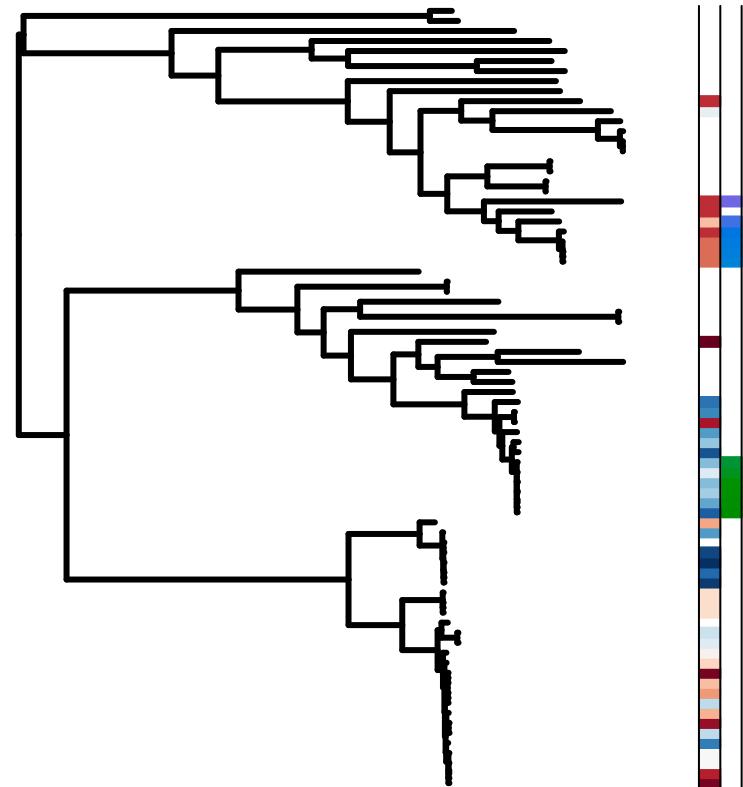
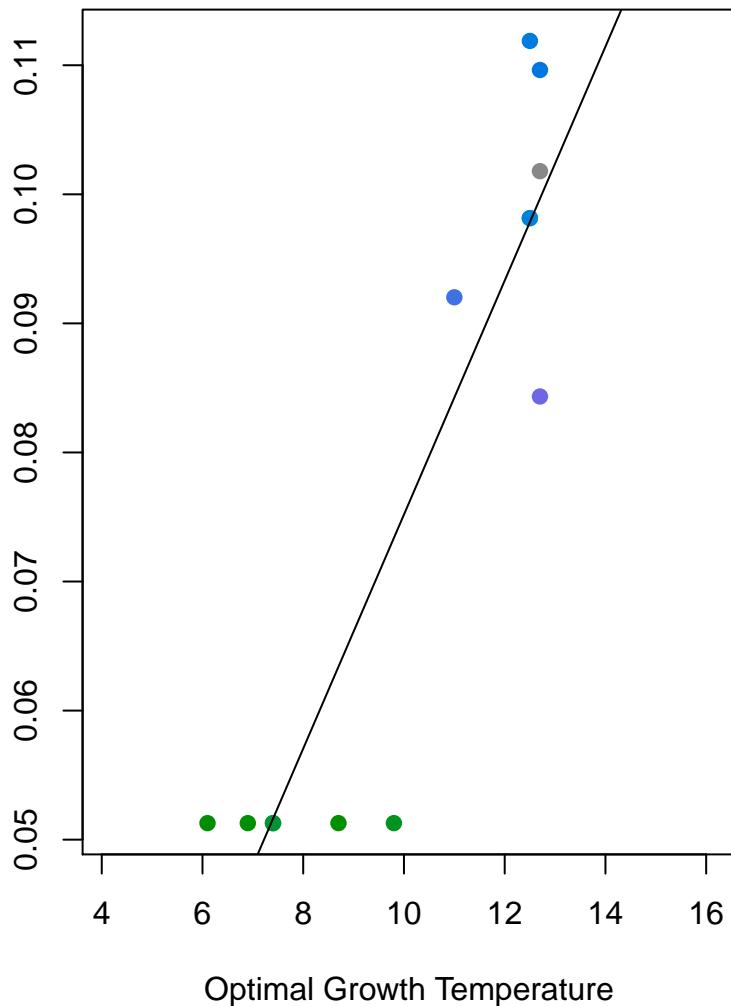
feature.plfam_id.acidic_residue.mean
PLF_28228_00002766
Porin
 $r = 0.925, p = 10^{-5.664}$

feature.plfam_id.acidic_residue.mean



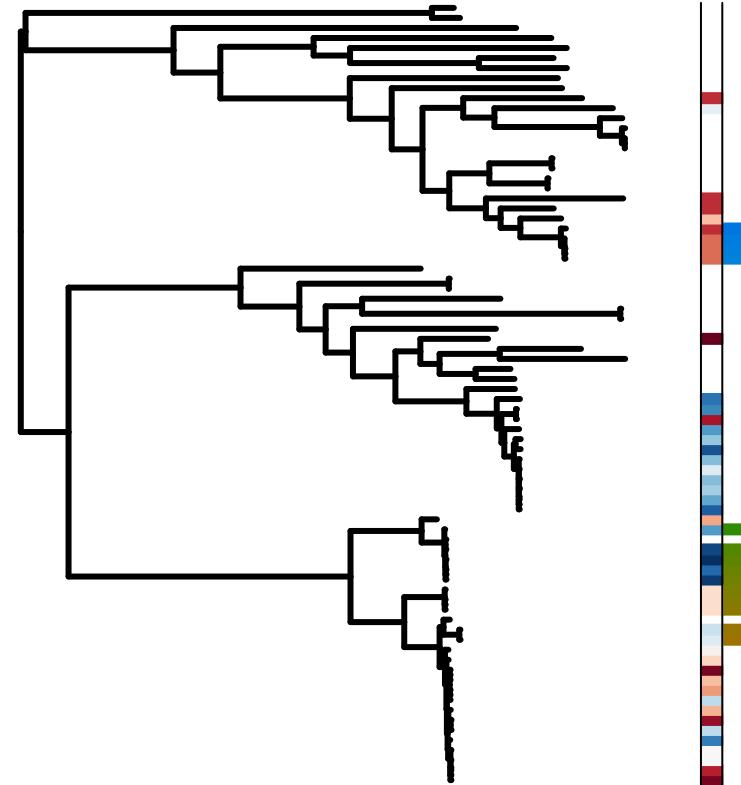
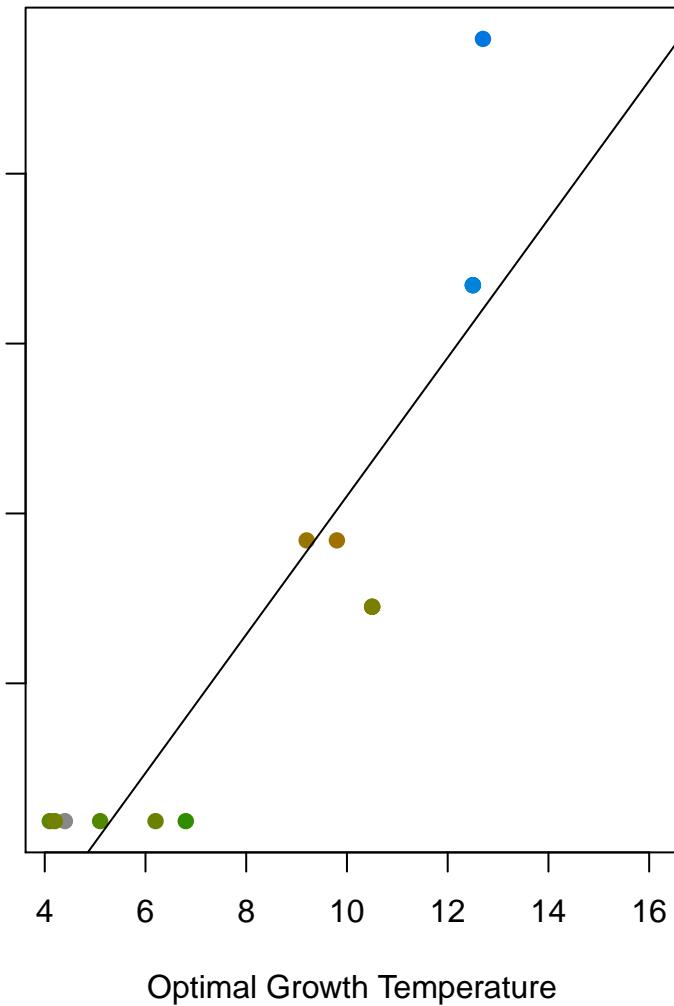
feature.plfam_id.acidic_residue.mean
PLF_28228_00002635
Glyoxalase family protein
 $r = 0.91, p = 10^{-4.803}$

feature.plfam_id.acidic_residue.mean



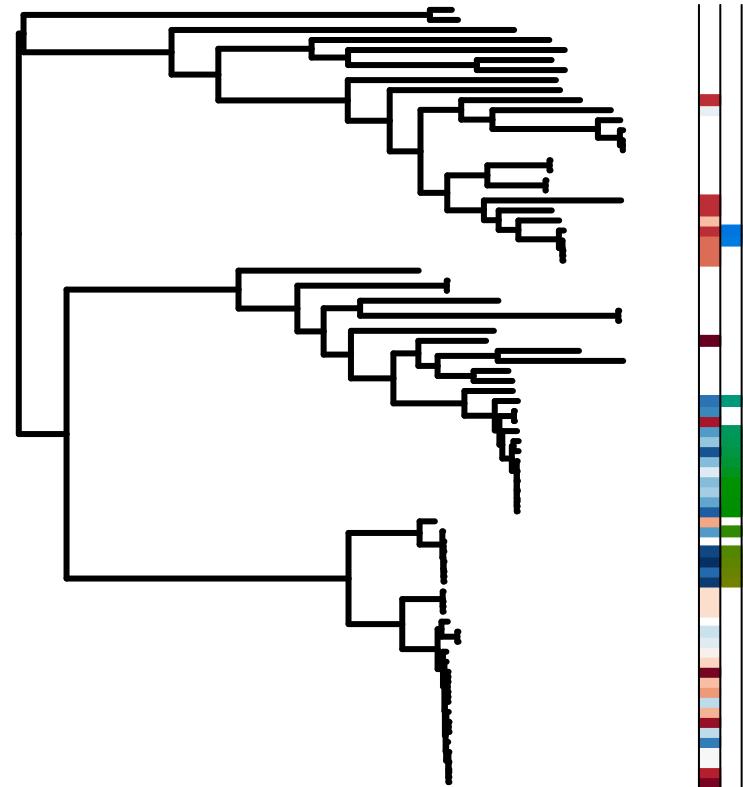
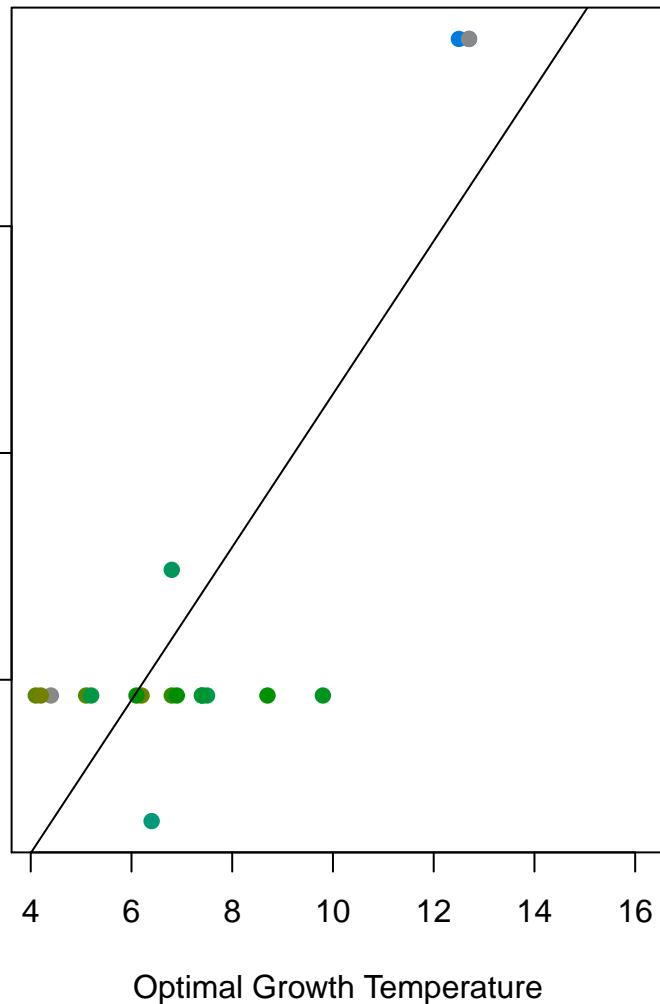
feature.plfam_id.acidic_residue.mean
PLF_28228_00007837
Transcriptional regulator, AraC family
 $r = 0.9$, $p = 10^{-5.3}$

feature.plfam_id.acidic_residue.mean



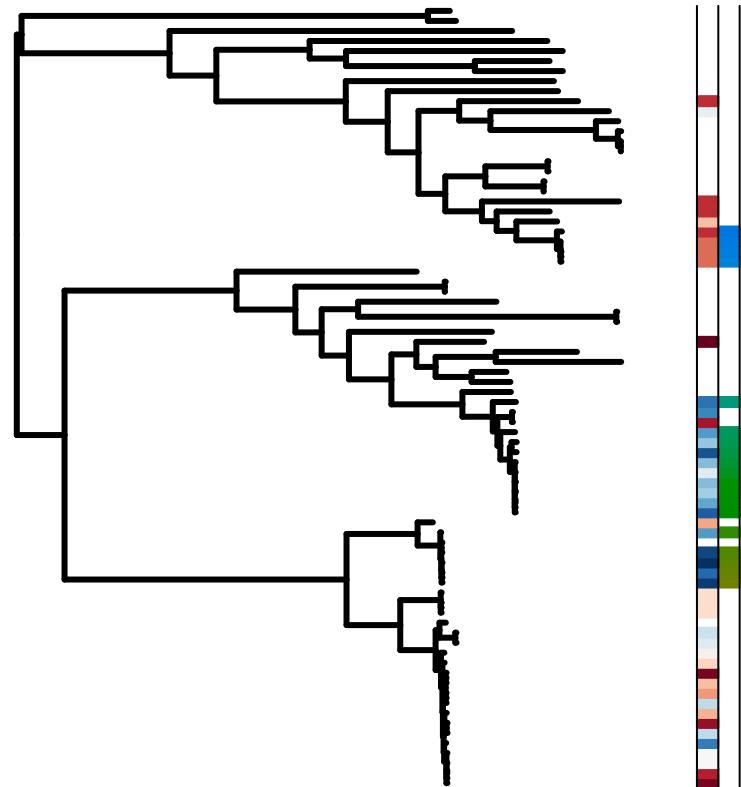
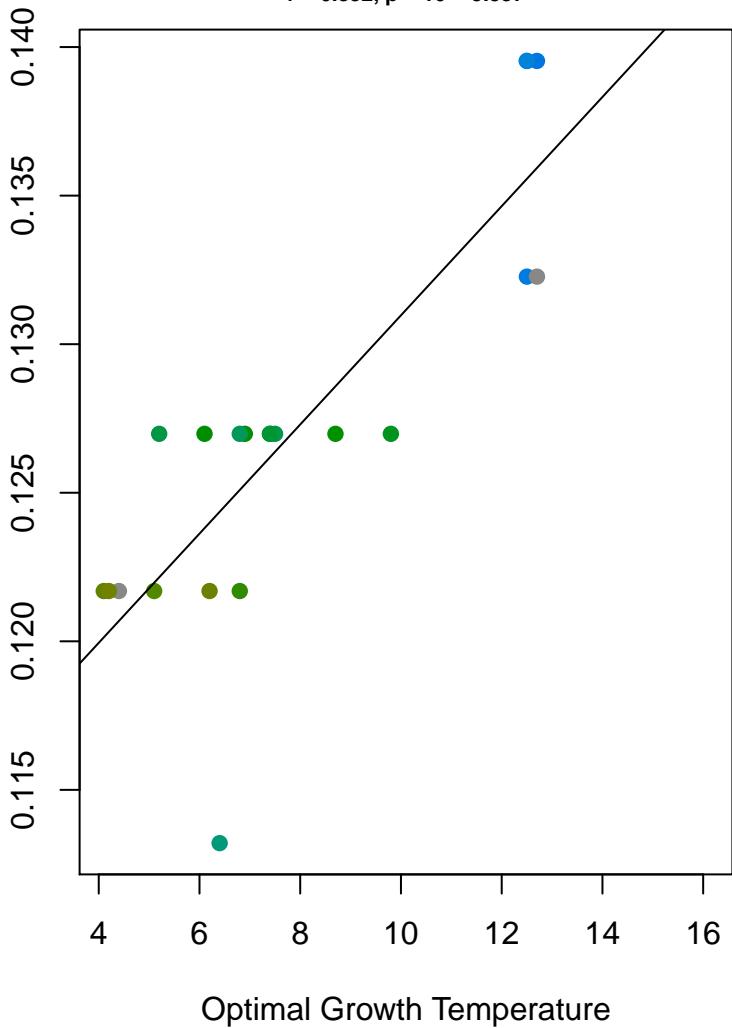
feature.plfam_id.acidic_residue.mean
PLF_28228_00028262
Iron siderophore sensor protein
 $r = 0.84, p = 10^{-5.159}$

feature.plfam_id.acidic_residue.mean

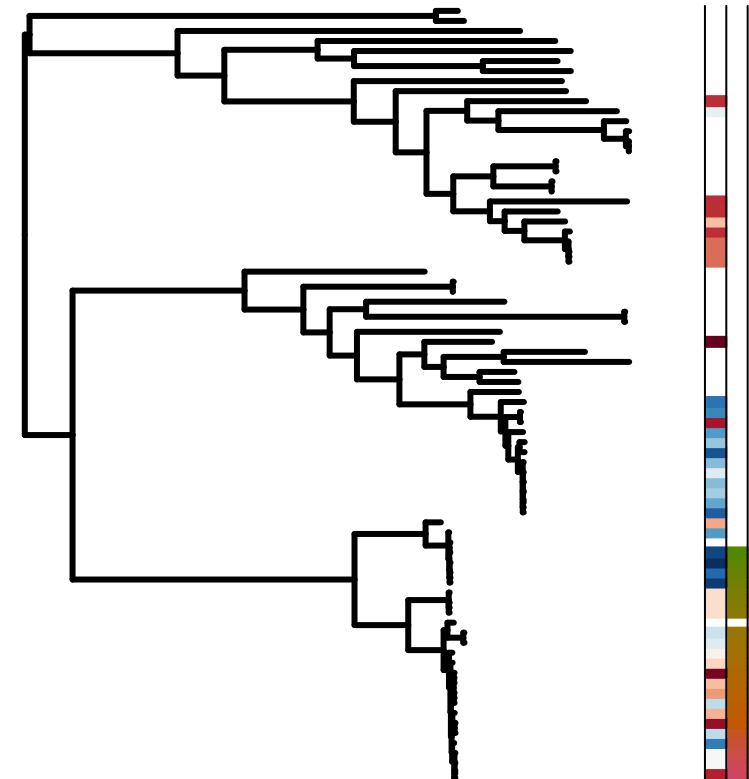
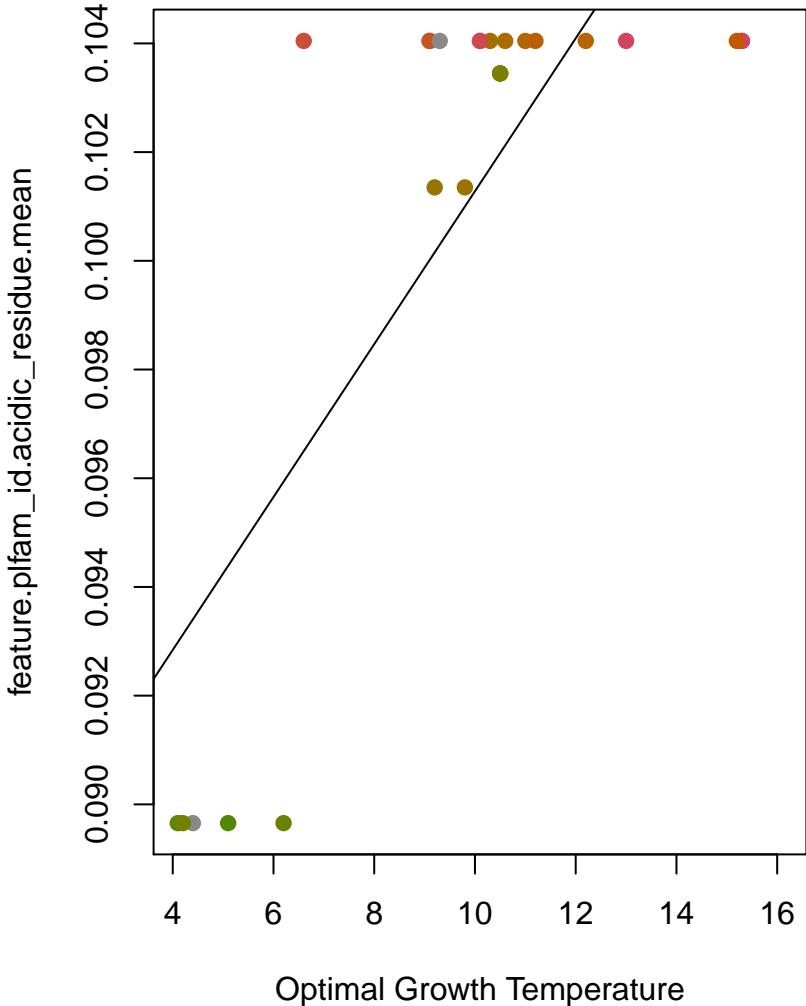


feature.plfam_id.acidic_residue.mean
PLF_28228_00014224
FIG006045: Sigma factor, ECF subfamily
 $r = 0.832$, $p = 10^{-5.537}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00015220
hypothetical protein
 $r = 0.788, p = 10^{-5.537}$



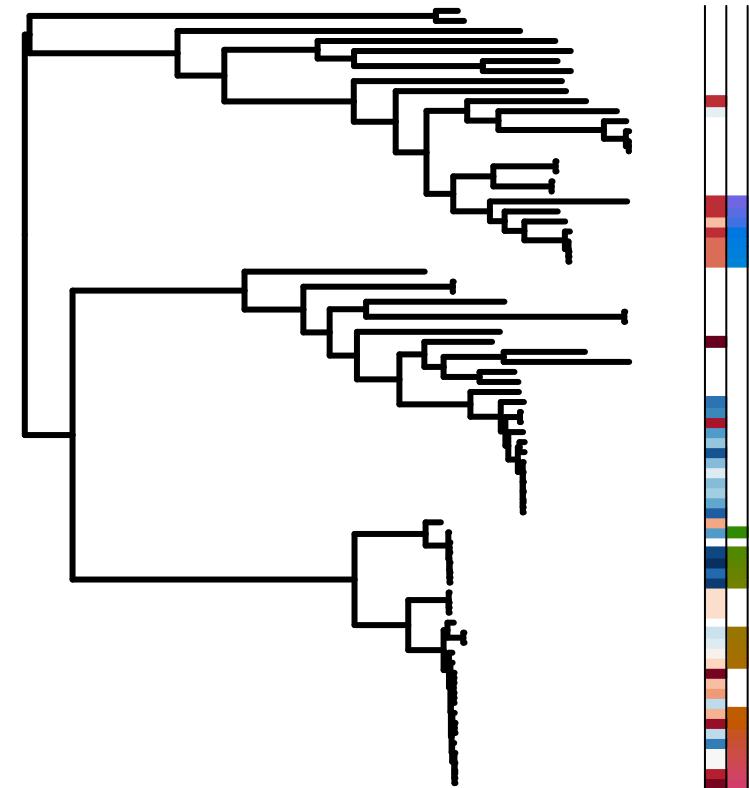
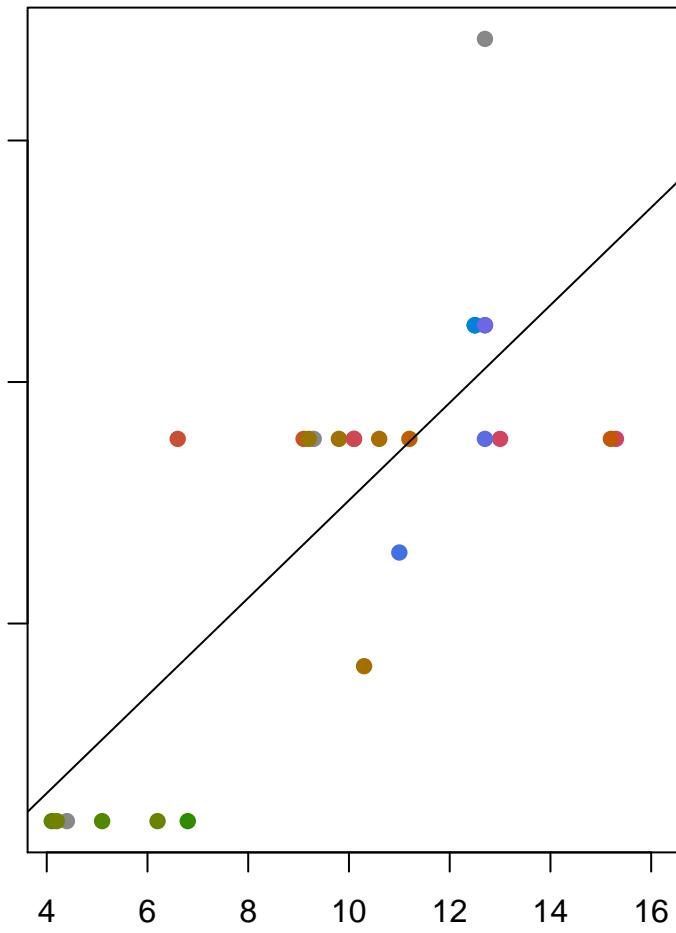
feature.plfam_id.acidic_residue.mean

PLF_28228_00003089

EPS I polysaccharide export outer membrane protein EPSA precursor

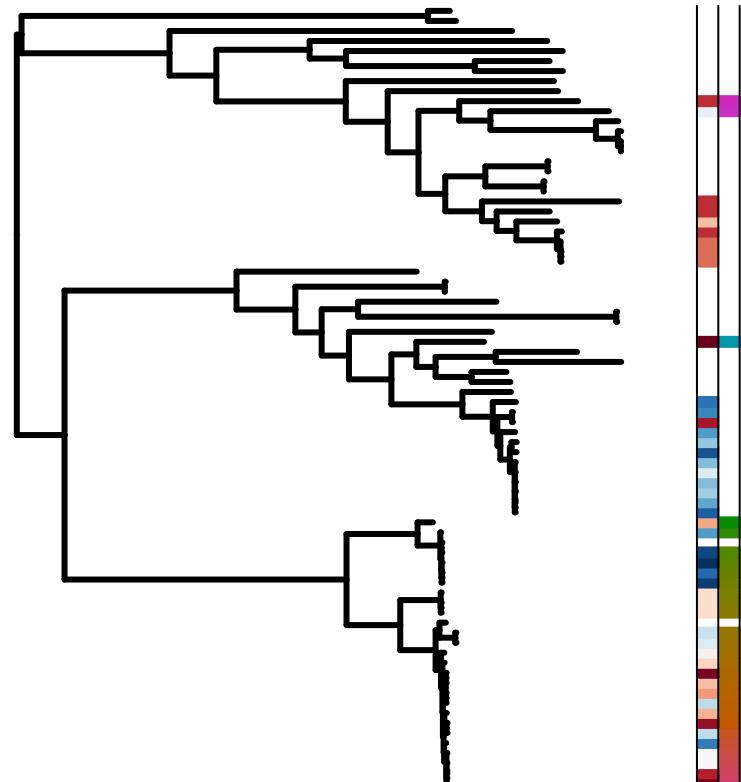
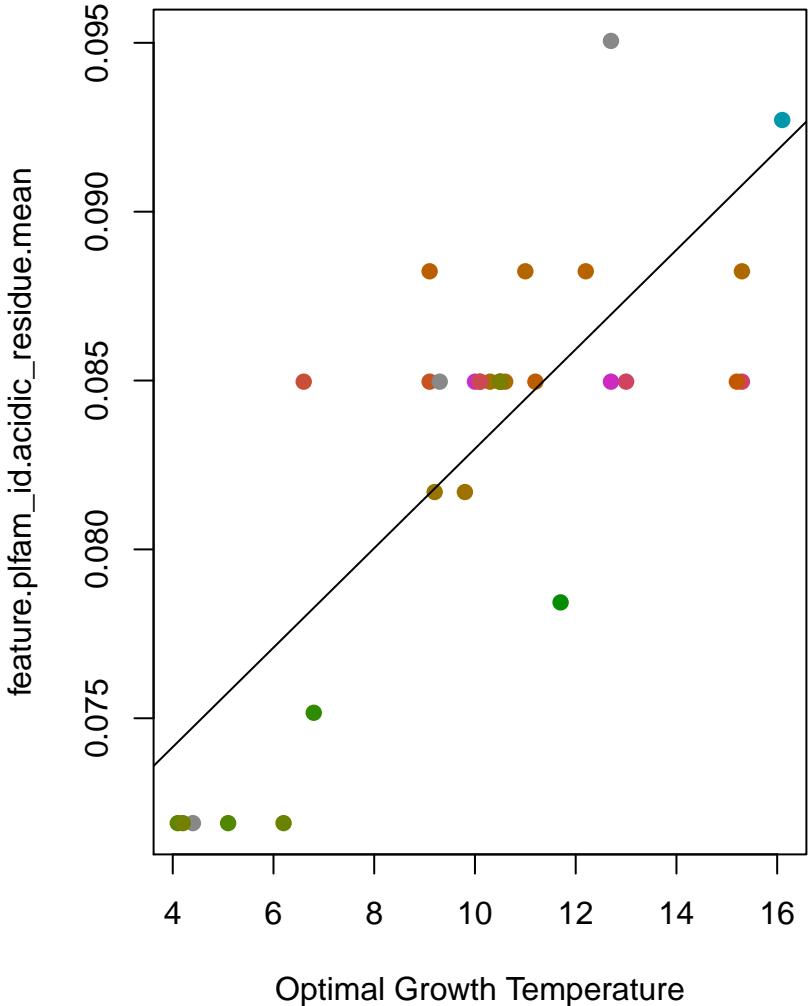
$r = 0.788, p = 10^{-5.971}$

feature.plfam_id.acidic_residue.mean



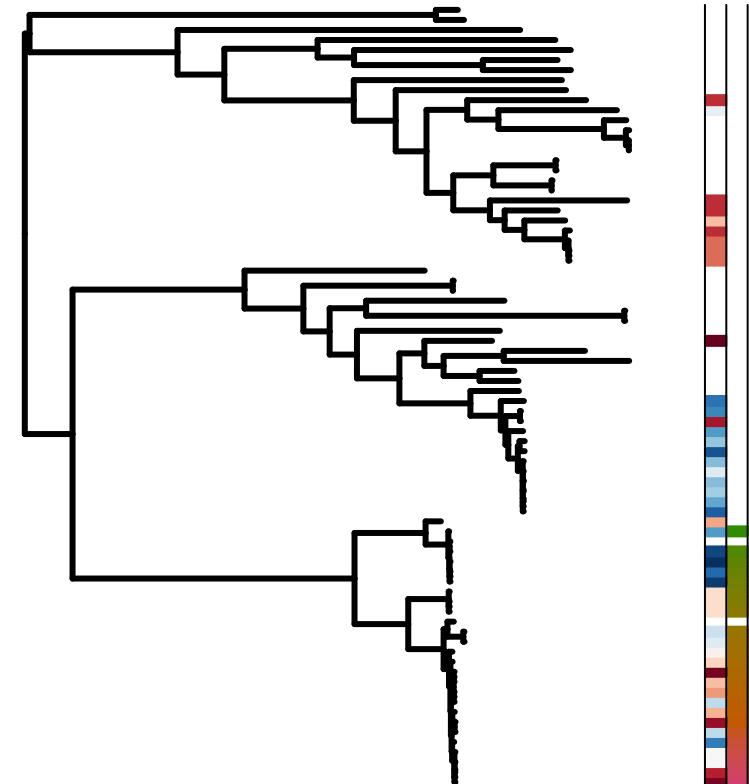
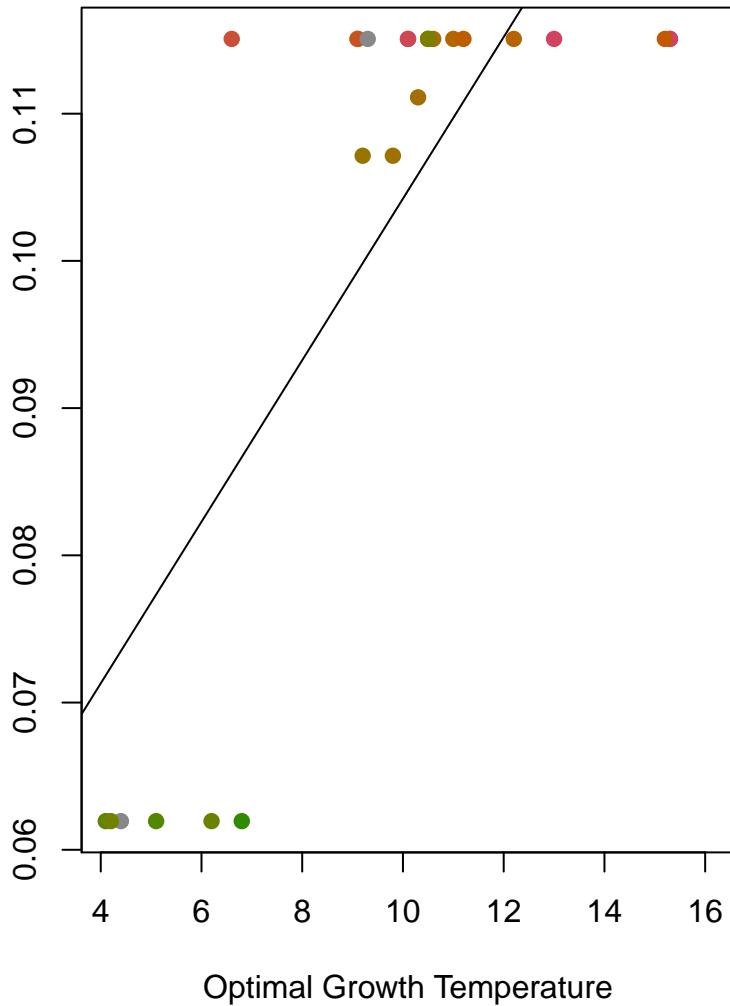
Optimal Growth Temperature

feature.plfam_id.acidic_residue.mean
PLF_28228_00002780
Protein translocase subunit SecF
 $r = 0.787$, $p = 10^{-6.815}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00030076
hypothetical protein
 $r = 0.785, p = 10^{-5.697}$

feature.plfam_id.acidic_residue.mean



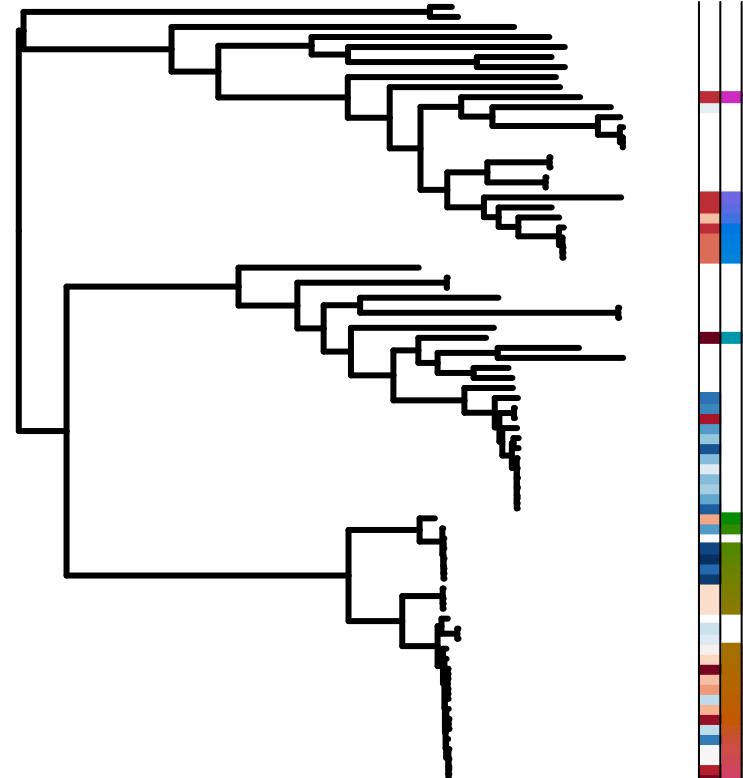
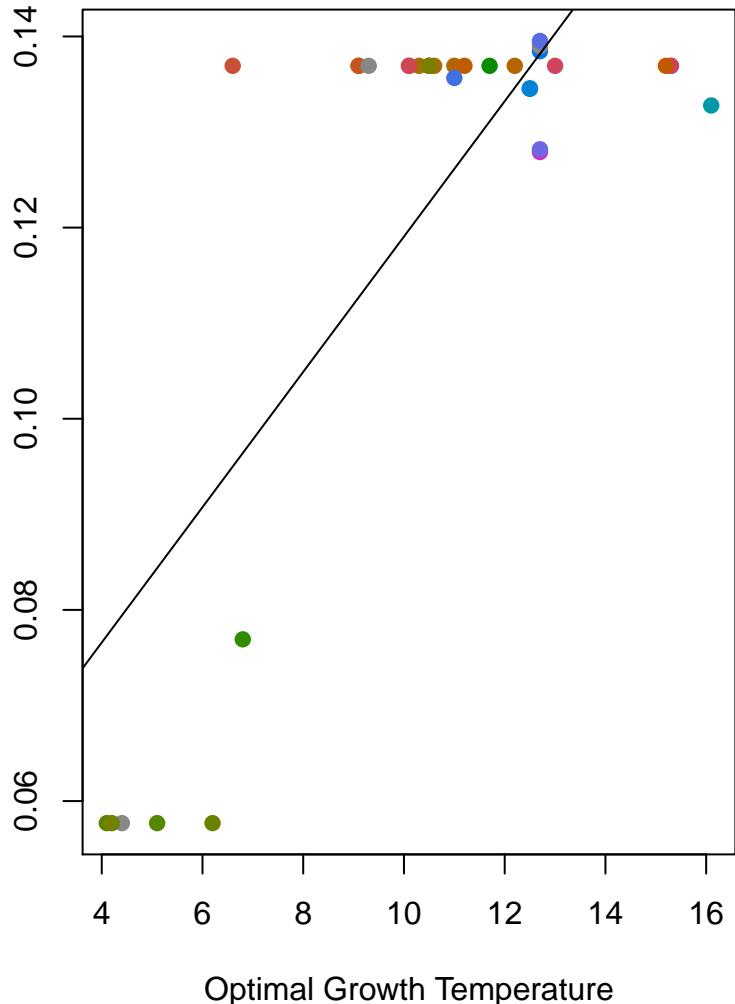
feature.plfam_id.acidic_residue.mean

PLF_28228_00002798

Two-component transcriptional response regulator, OmpR family

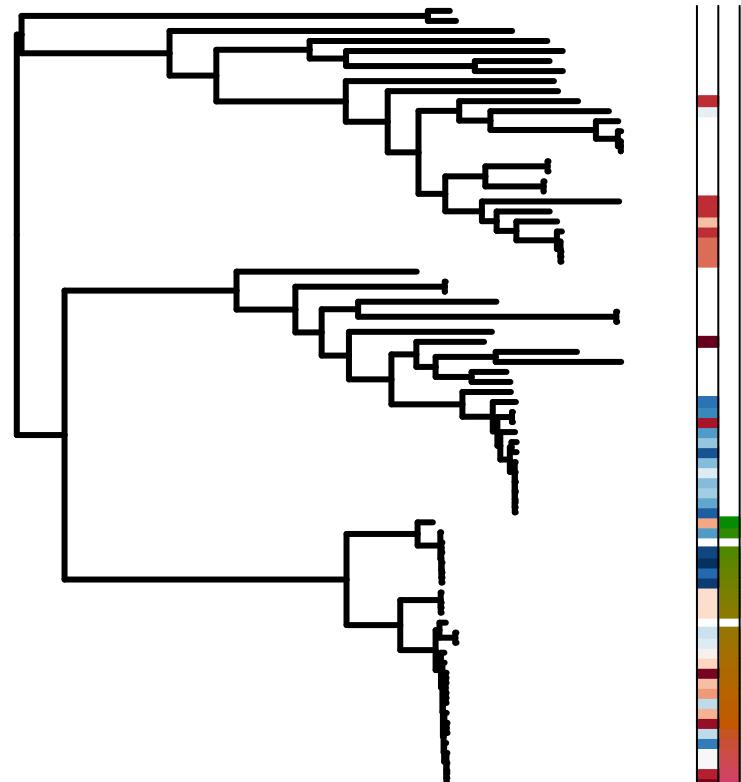
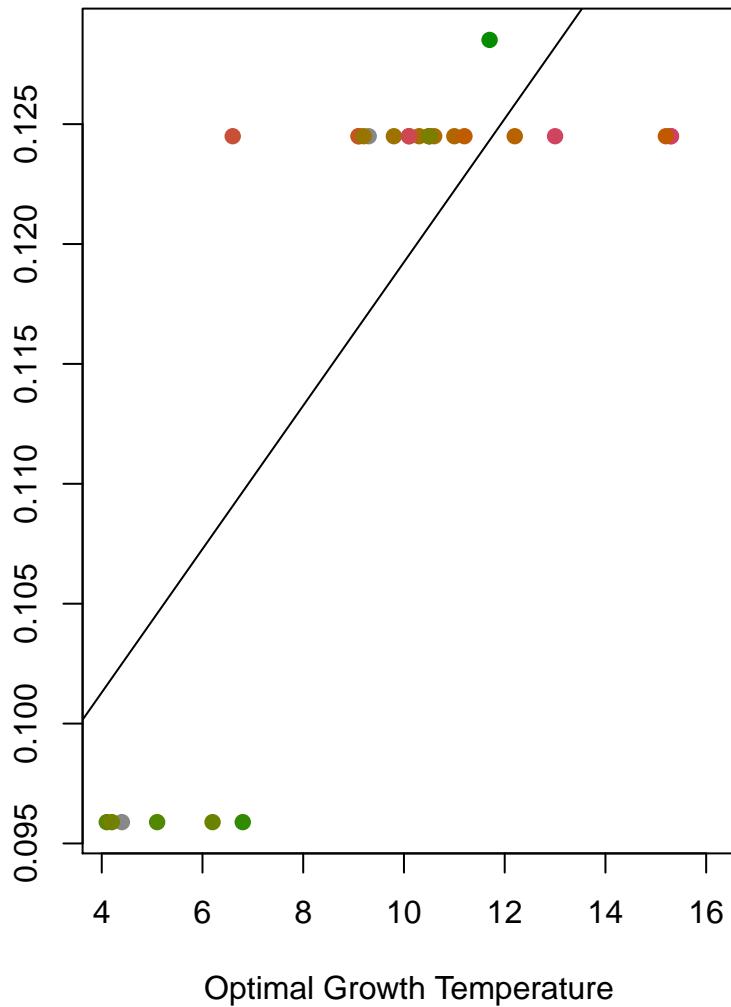
$r = 0.78, p = 10^{-7.475}$

feature.plfam_id.acidic_residue.mean



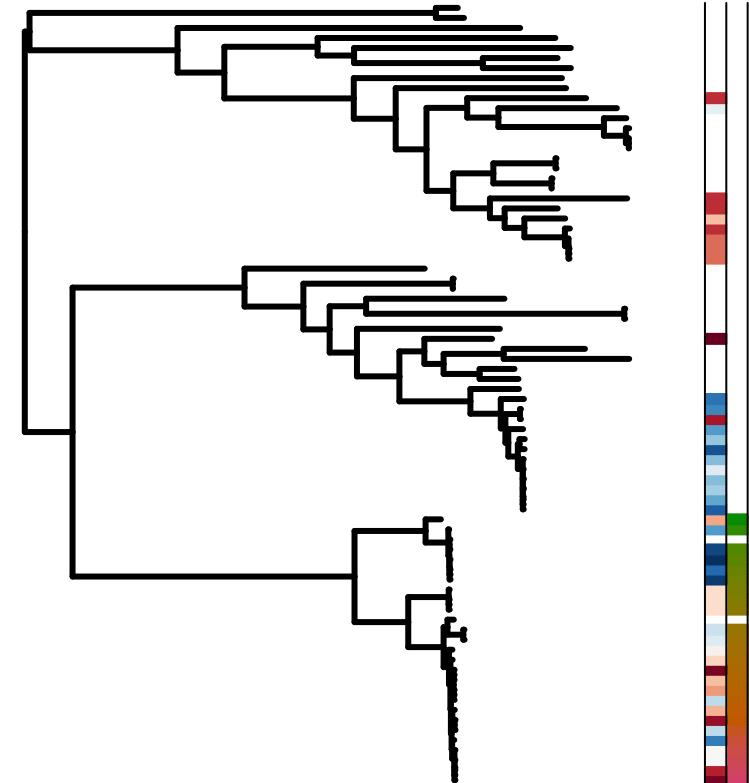
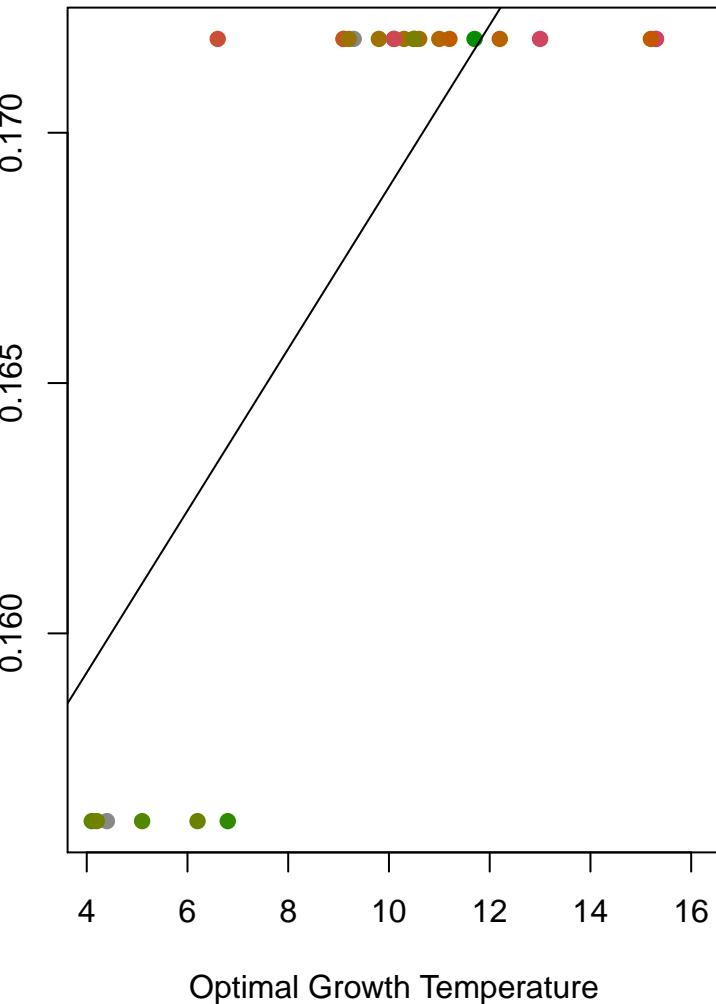
feature.plfam_id.acidic_residue.mean
PLF_28228_00031426
hypothetical protein
 $r = 0.779, p = 10^{-5.775}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00016786
hypothetical protein
 $r = 0.778, p = 10^{-5.746}$

feature.plfam_id.acidic_residue.mean



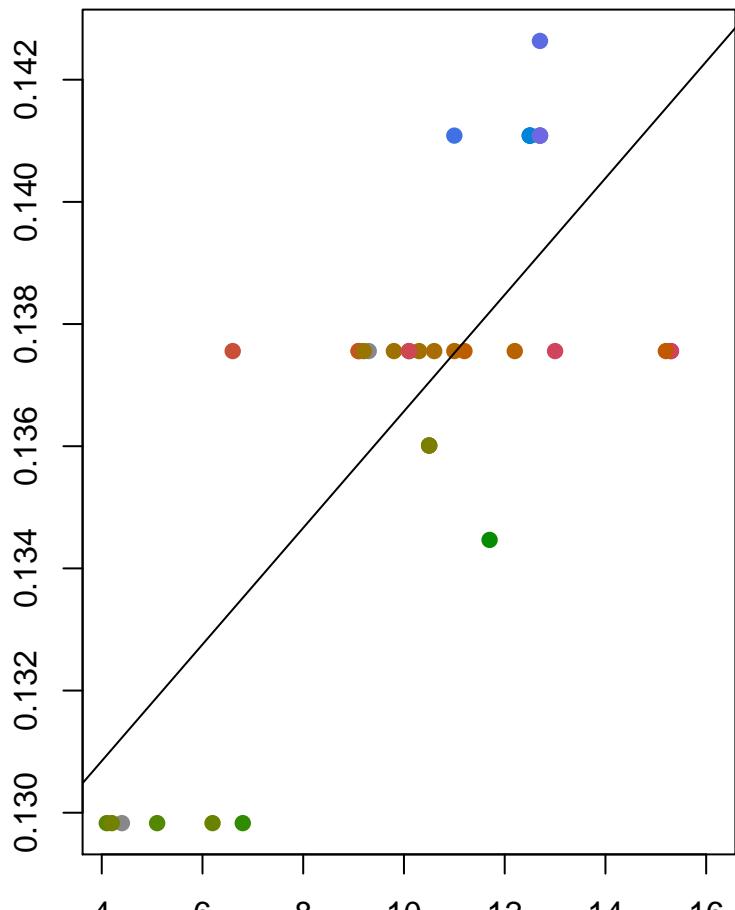
feature.plfam_id.acidic_residue.mean

PLF_28228_00007395

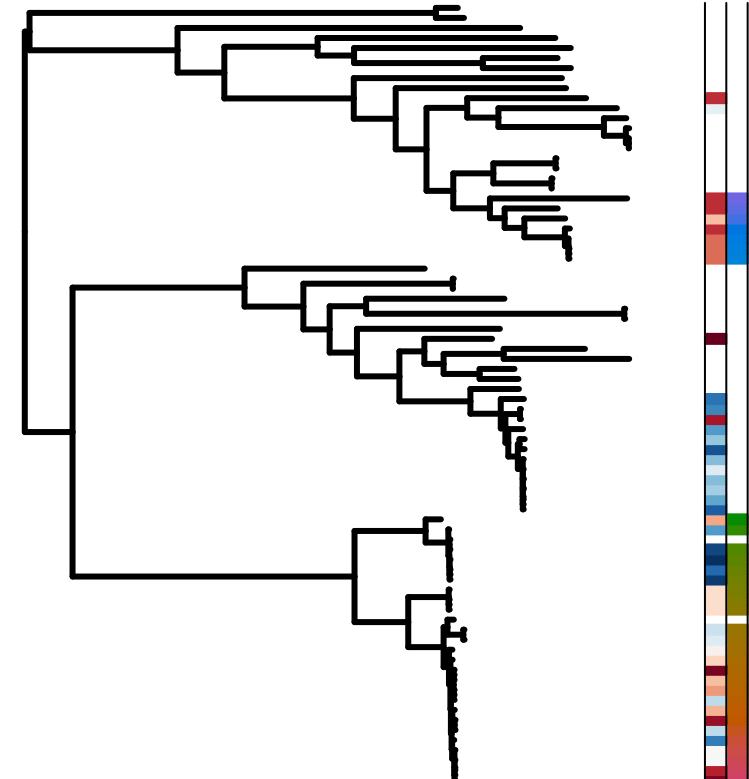
Argininosuccinate lyase (EC 4.3.2.1) / N-acetylglutamate synthase (EC 2.3.1.1)

$r = 0.777$, $p = 10^{-7.382}$

feature.plfam_id.acidic_residue.mean

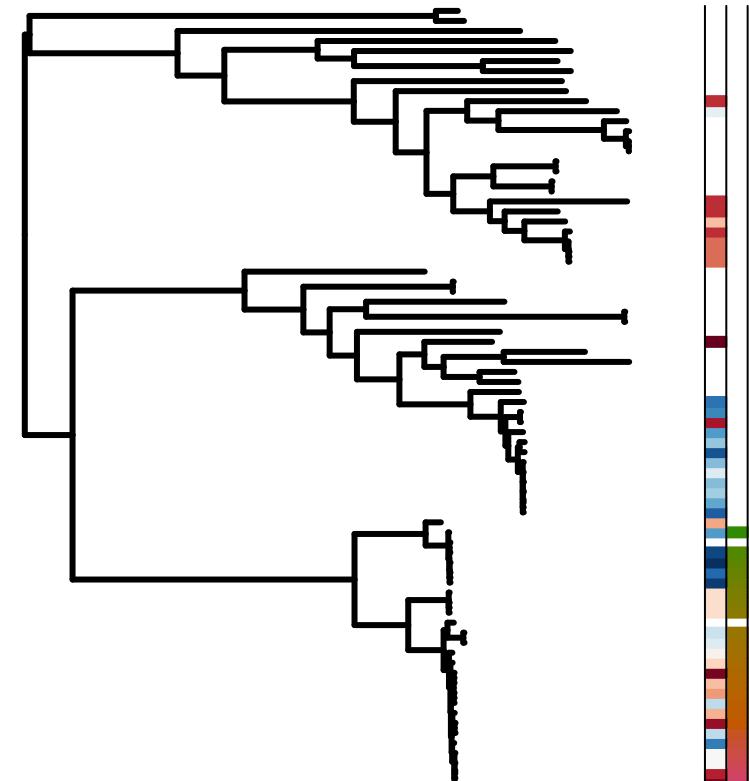
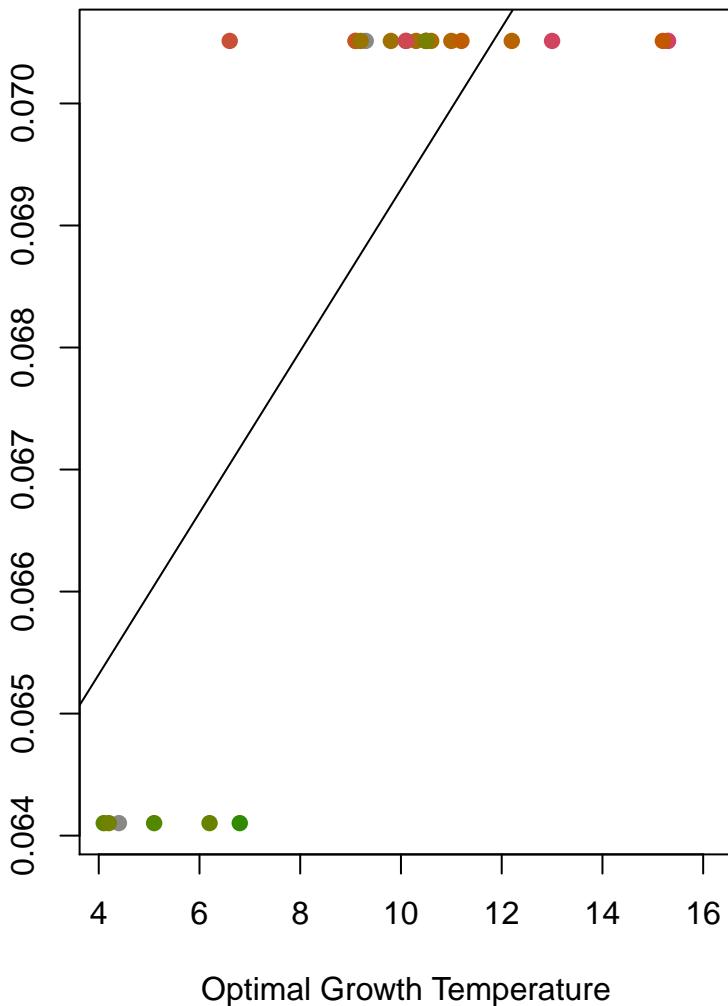


Optimal Growth Temperature

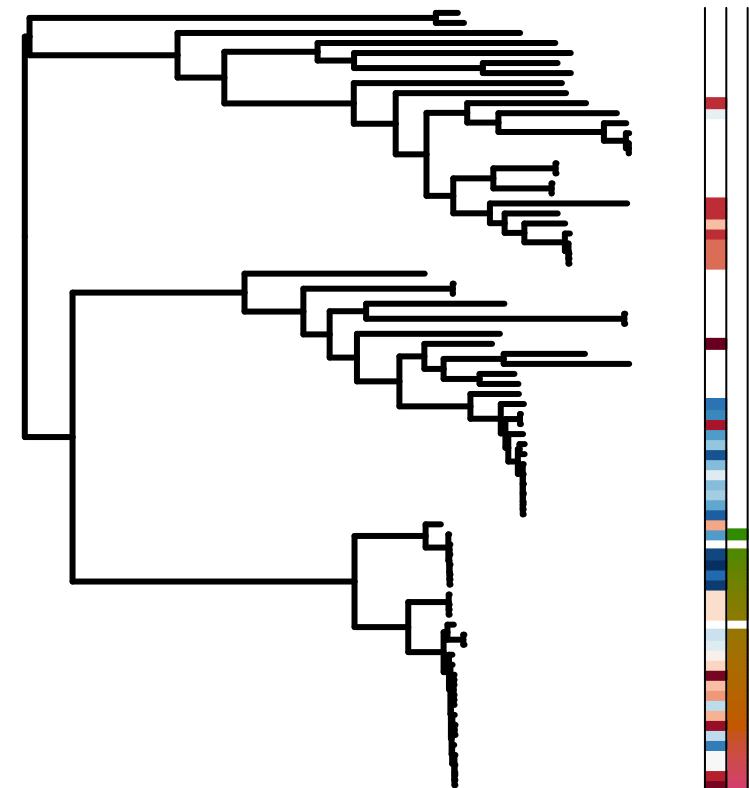
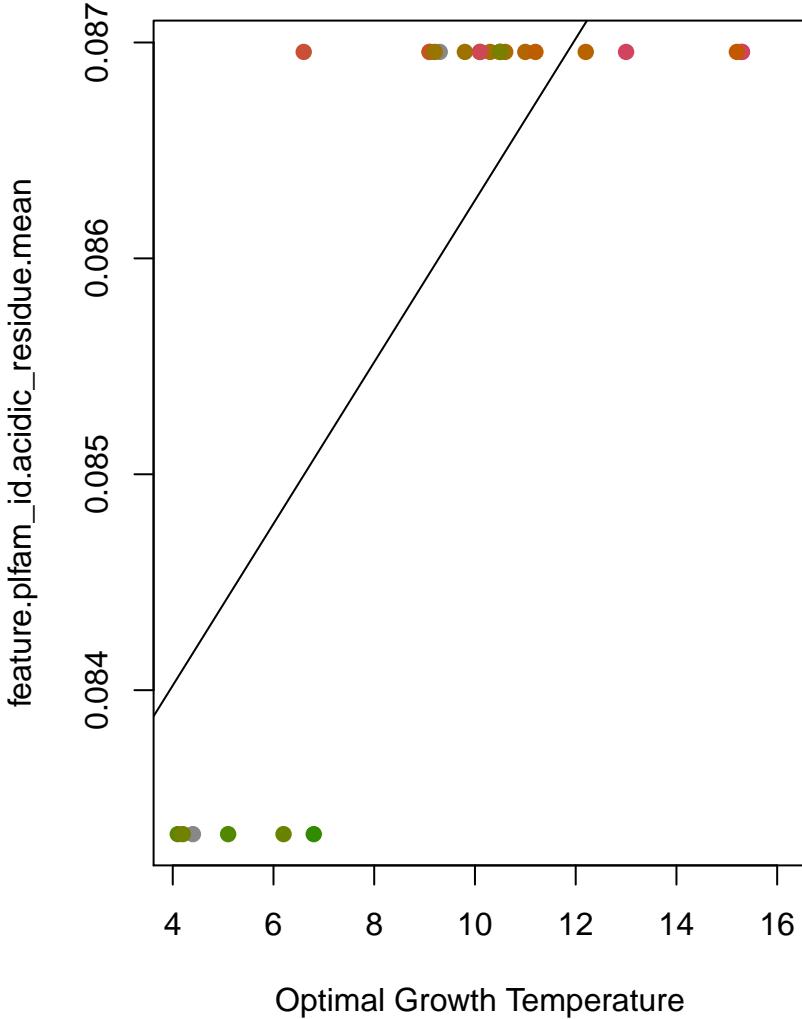


feature.plfam_id.acidic_residue.mean
PLF_28228_00015077
hypothetical protein
 $r = 0.775, p = 10^{-5.478}$

feature.plfam_id.acidic_residue.mean

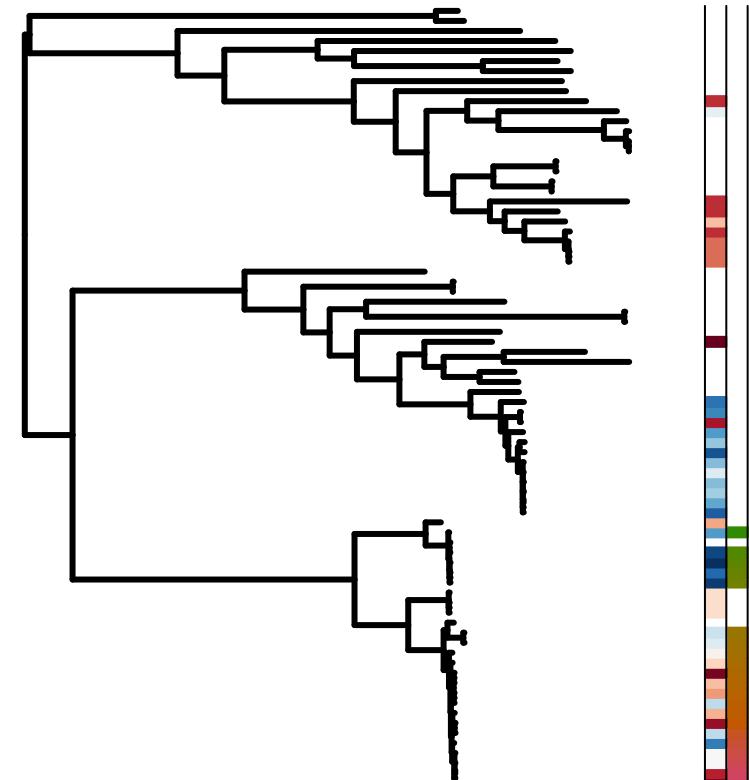
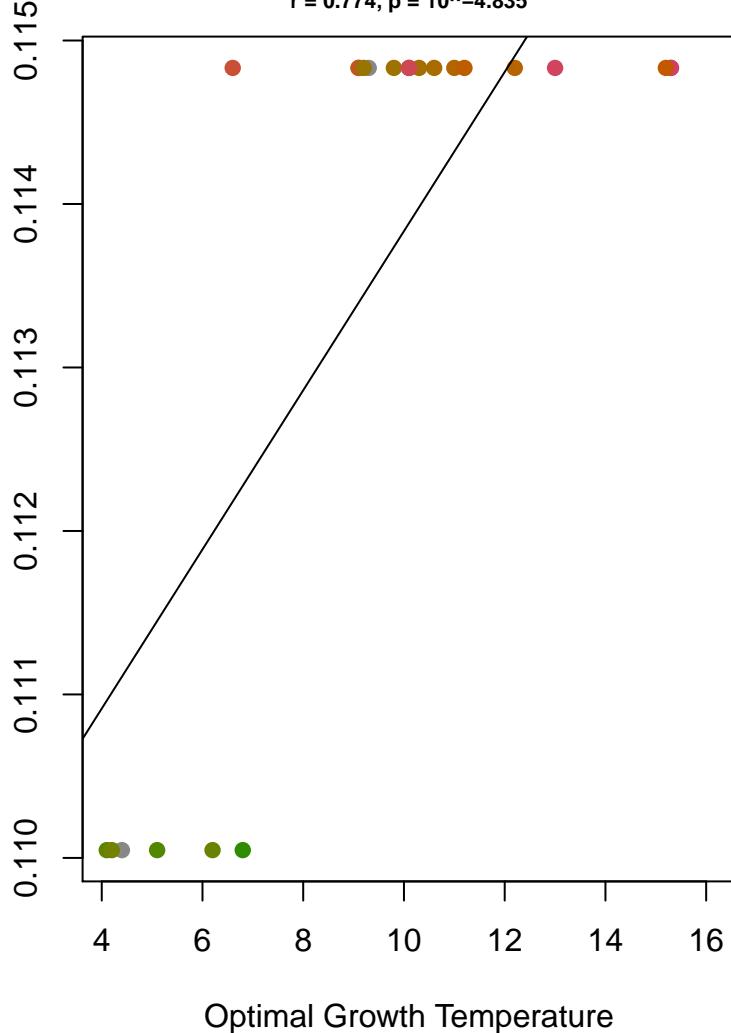


feature.plfam_id.acidic_residue.mean
PLF_28228_00029369
hypothetical protein
 $r = 0.775, p = 10^{-5.478}$



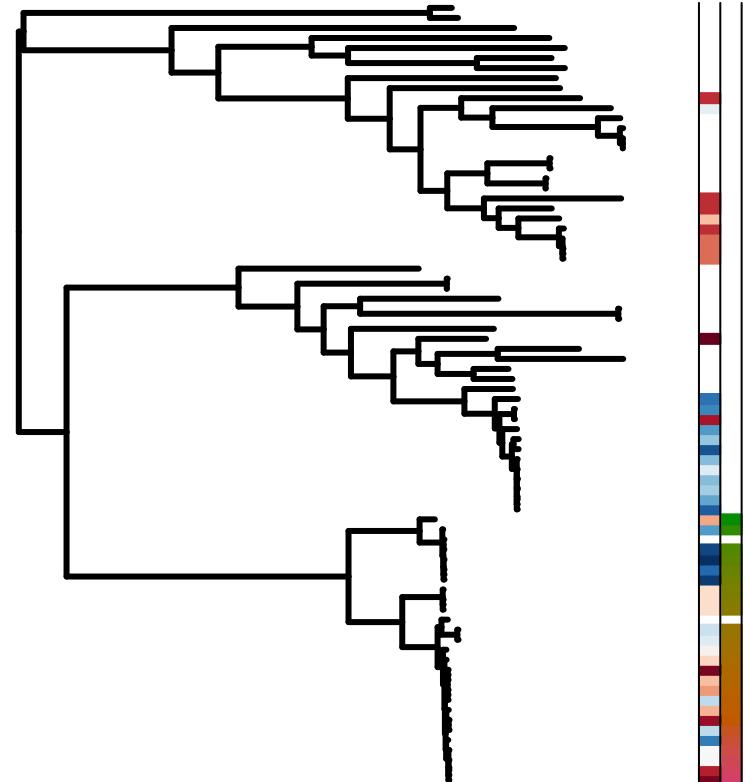
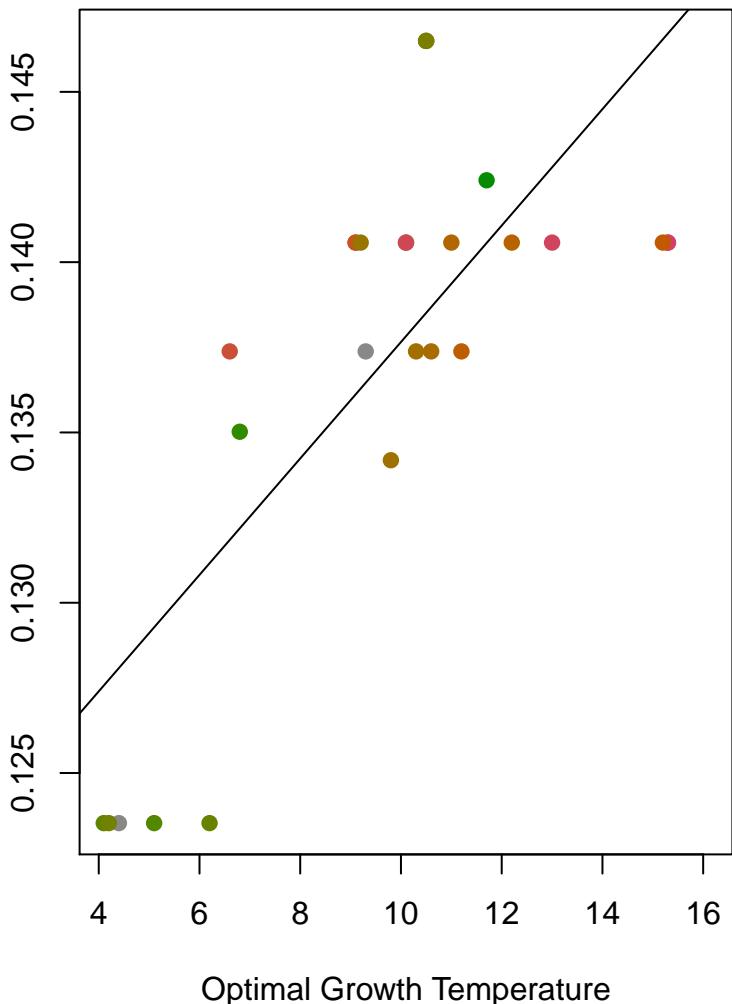
feature.plfam_id.acidic_residue.mean
PLF_28228_00014776
hypothetical protein
 $r = 0.774$, $p = 10^{-4.835}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00011660
Agmatinase (EC 3.5.3.11)
 $r = 0.753$, $p = 10^{-5.23}$

feature.plfam_id.acidic_residue.mean

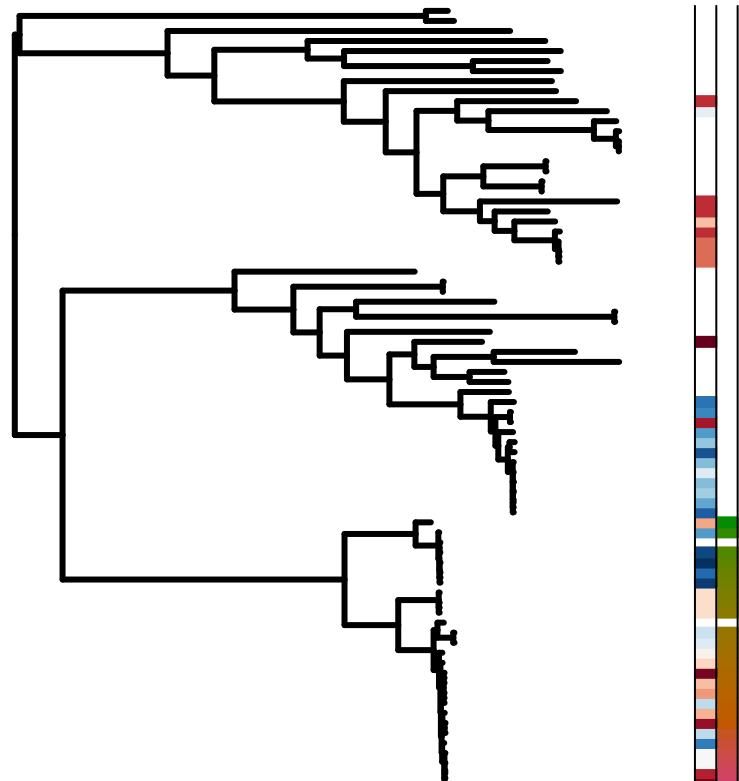
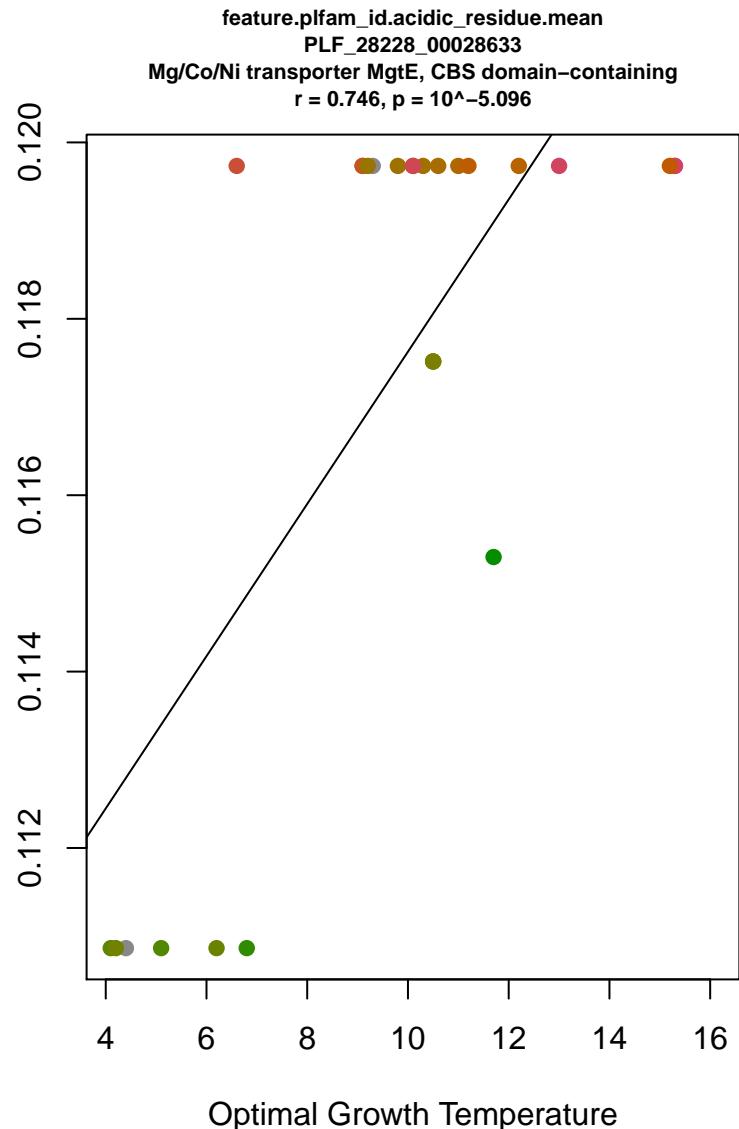


feature.plfam_id.acidic_residue.mean

PLF_28228_00028633

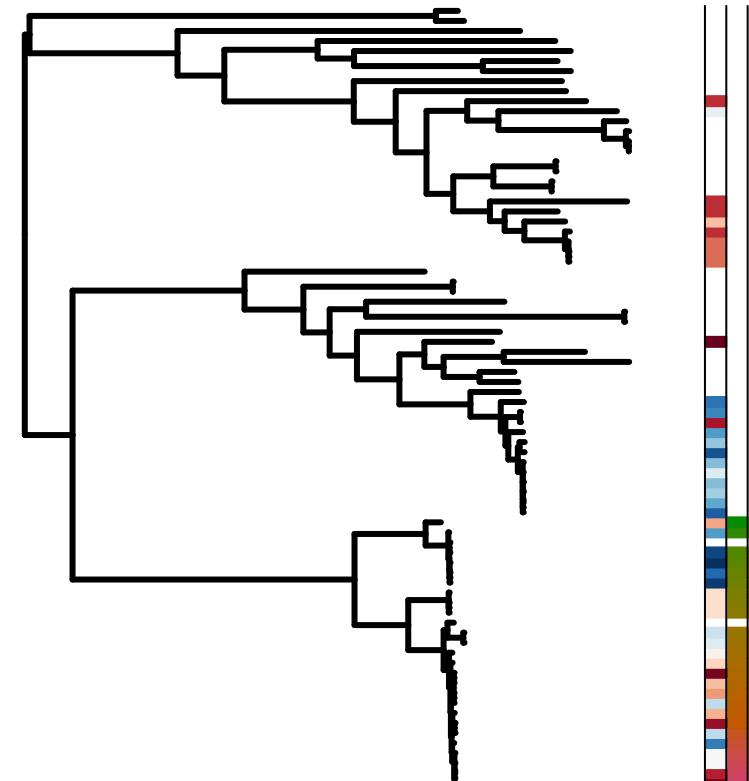
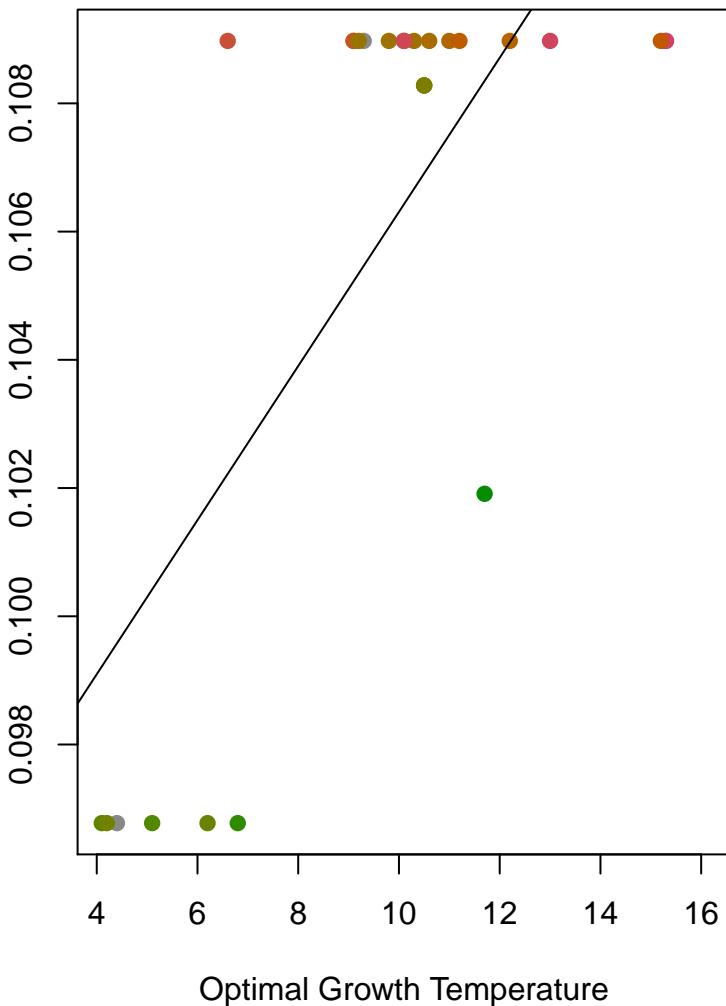
Mg/Co/Ni transporter MgtE, CBS domain-containing

$r = 0.746$, $p = 10^{-5.096}$



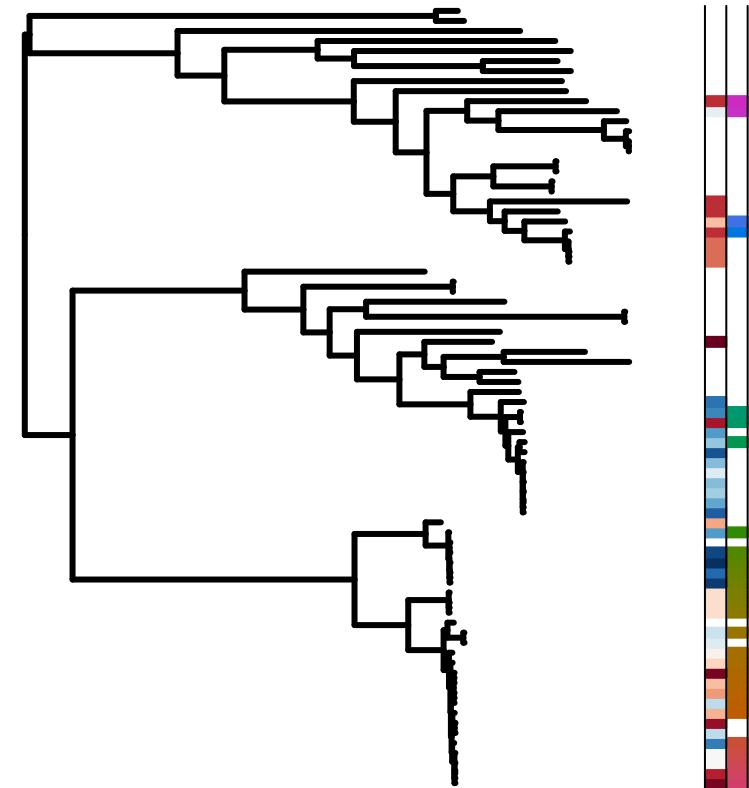
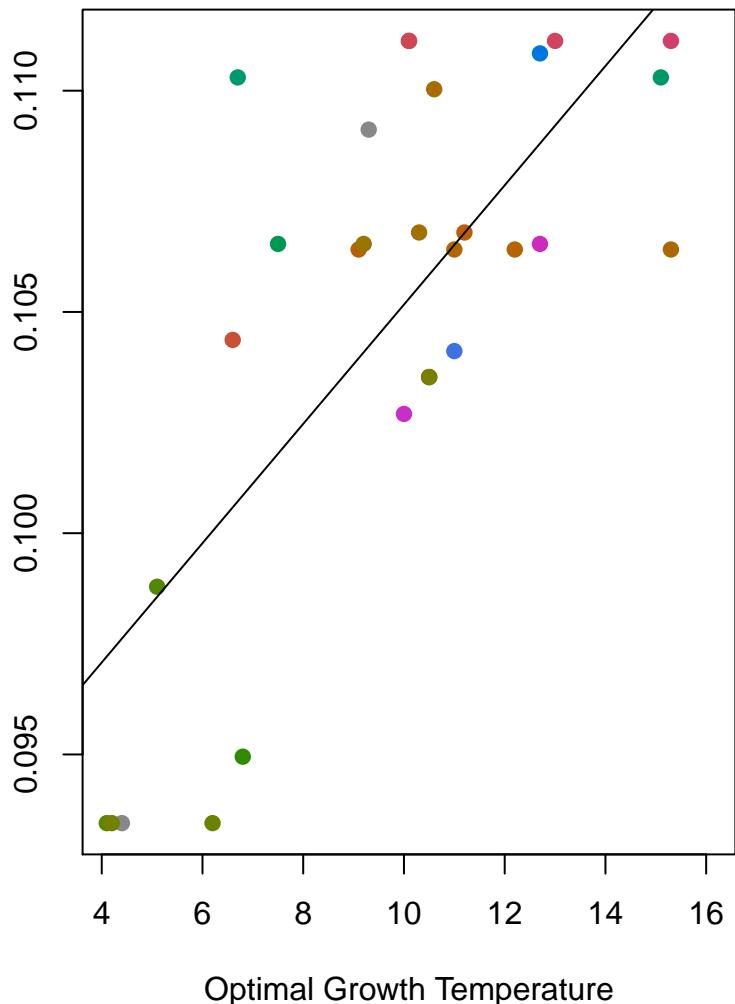
feature.plfam_id.acidic_residue.mean
PLF_28228_00019543
hypothetical protein
 $r = 0.741, p = 10^{-5.013}$

feature.plfam_id.acidic_residue.mean



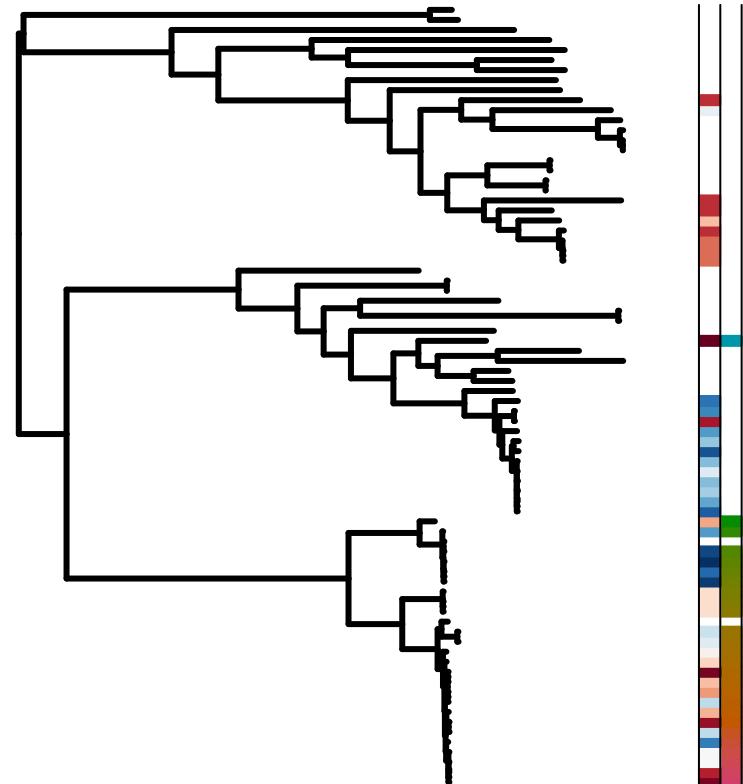
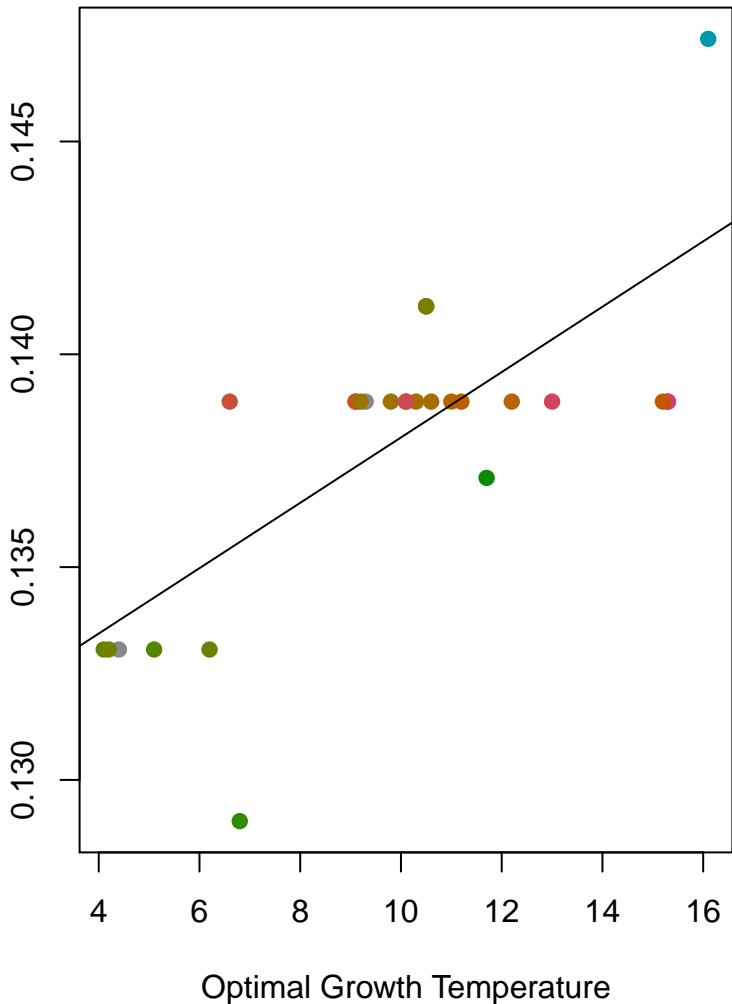
feature.plfam_id.acidic_residue.mean
PLF_28228_00022189
Phage integrase
 $r = 0.732$, $p = 10^{-5.374}$

feature.plfam_id.acidic_residue.mean



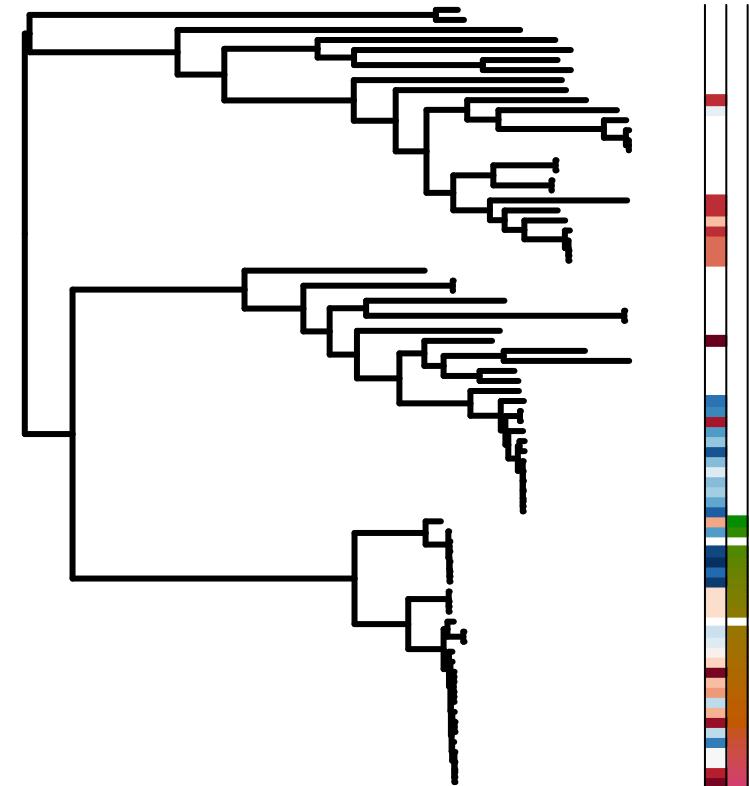
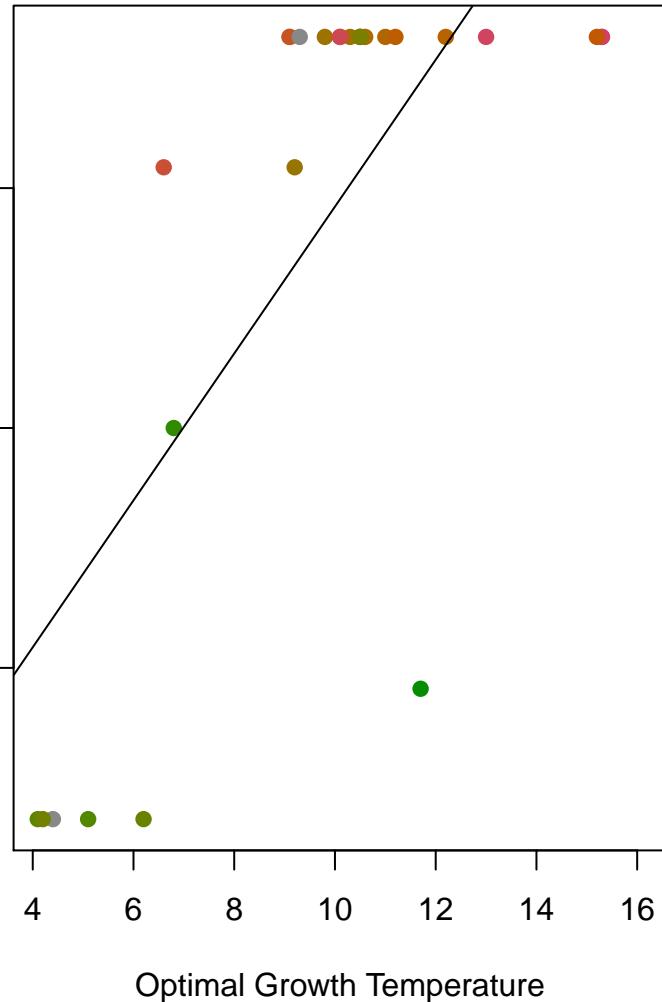
feature.plfam_id.acidic_residue.mean
PLF_28228_00021085
hypothetical protein
 $r = 0.731, p = 10^{-5.01}$

feature.plfam_id.acidic_residue.mean



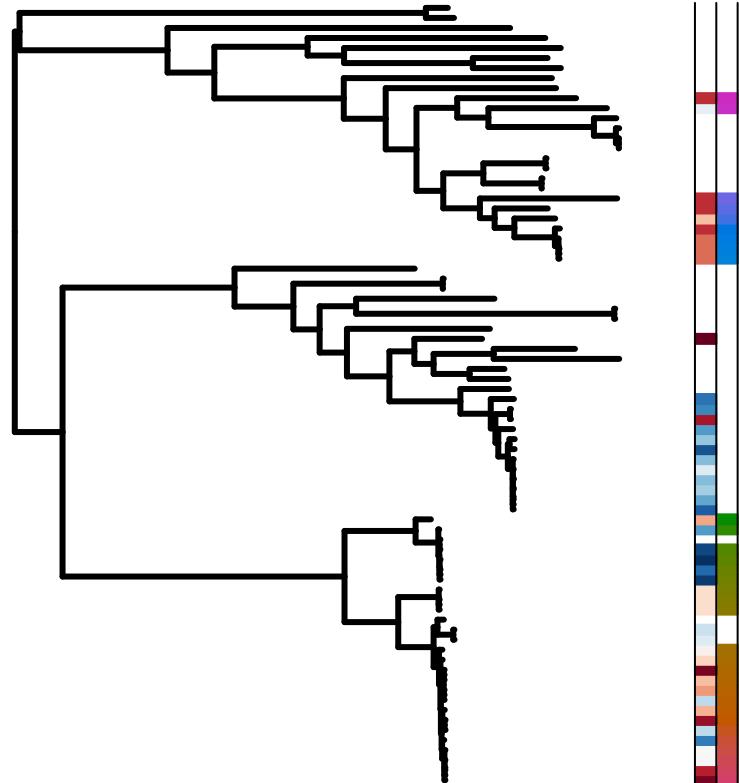
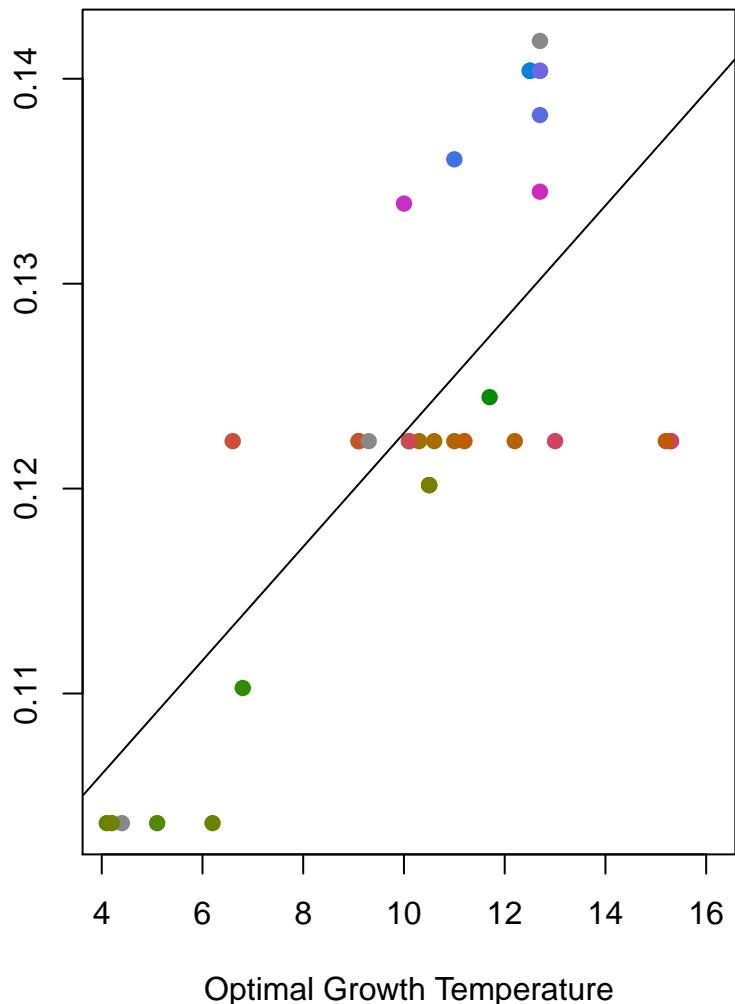
feature.plfam_id.acidic_residue.mean
PLF_28228_00032200
hypothetical protein
 $r = 0.731, p = 10^{-4.822}$

feature.plfam_id.acidic_residue.mean

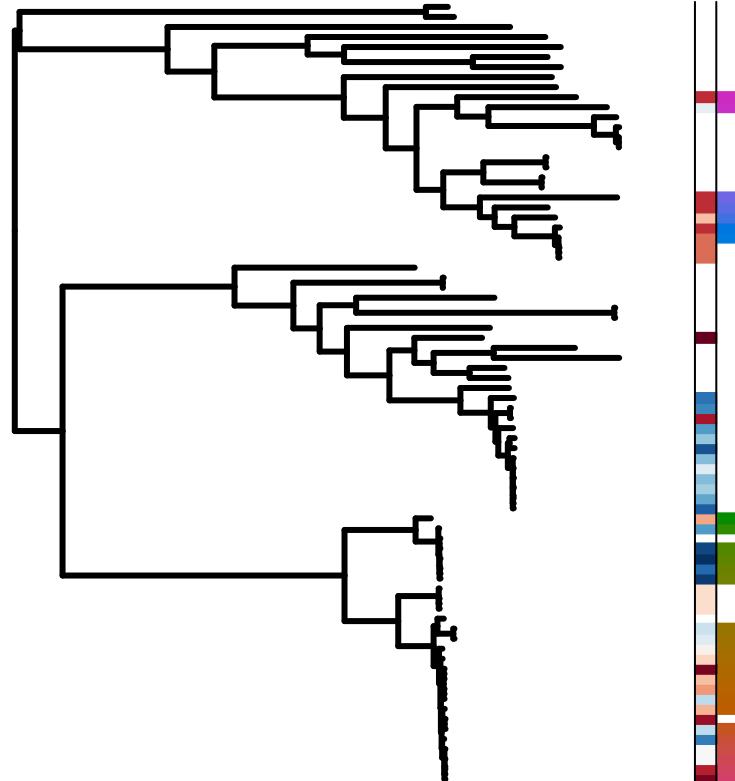
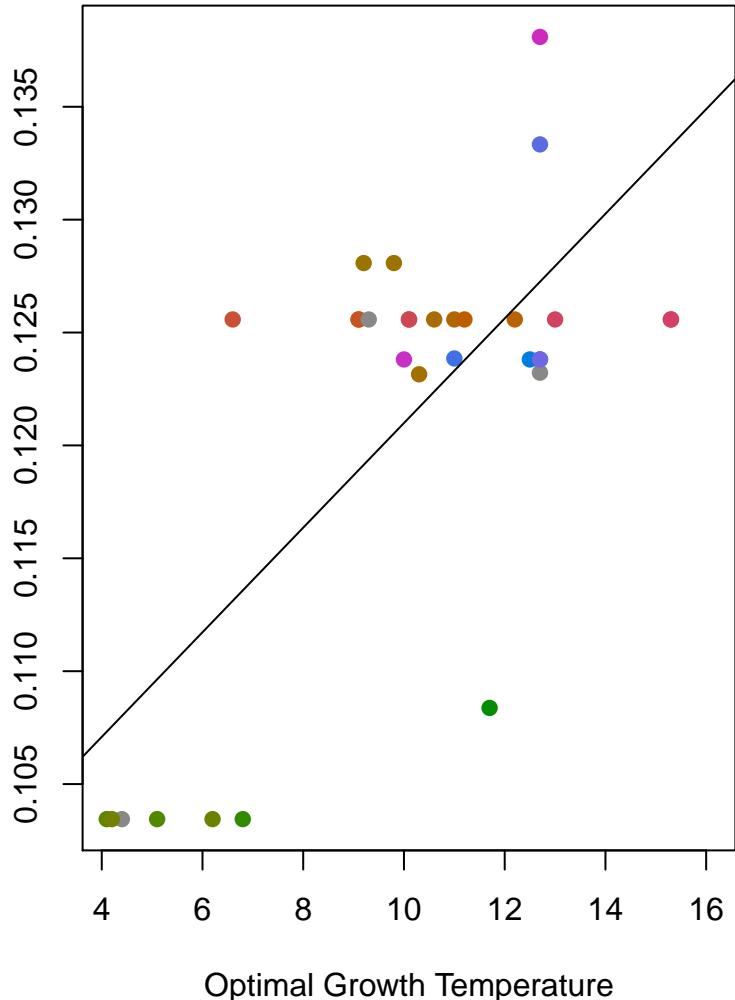


feature.plfam_id.acidic_residue.mean
PLF_28228_00001289
Uncharacterized protease YegQ
 $r = 0.731$, $p = 10^{-6.205}$

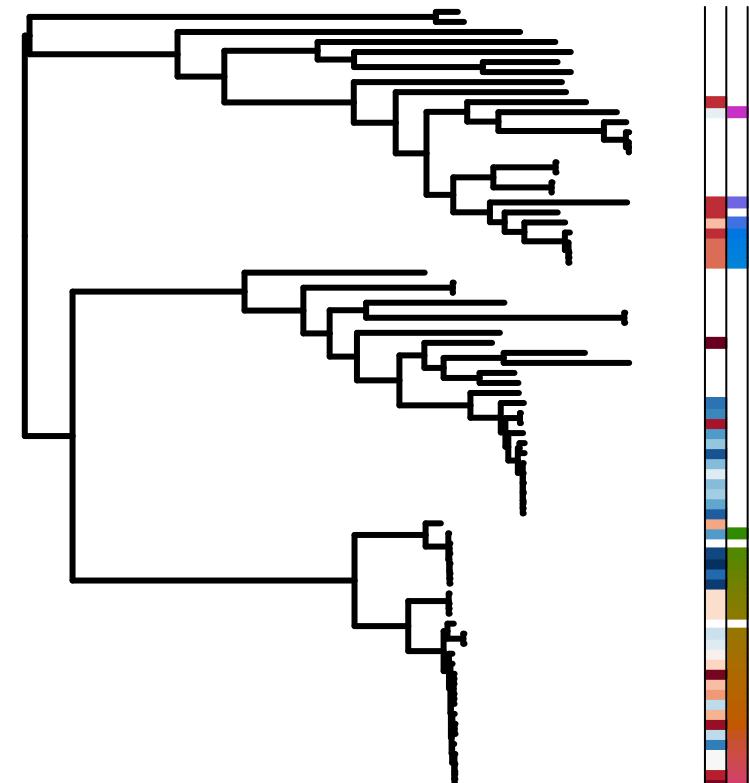
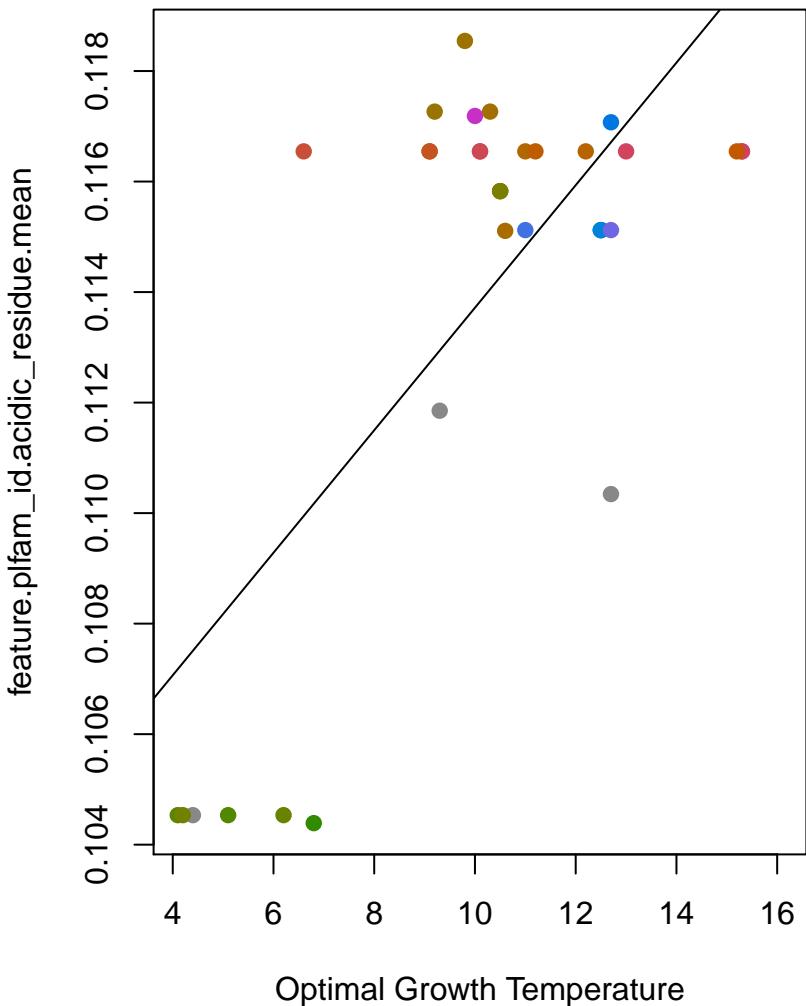
feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00017084
Alkylated DNA repair protein
 $r = 0.726$, $p = 10^{-5.424}$

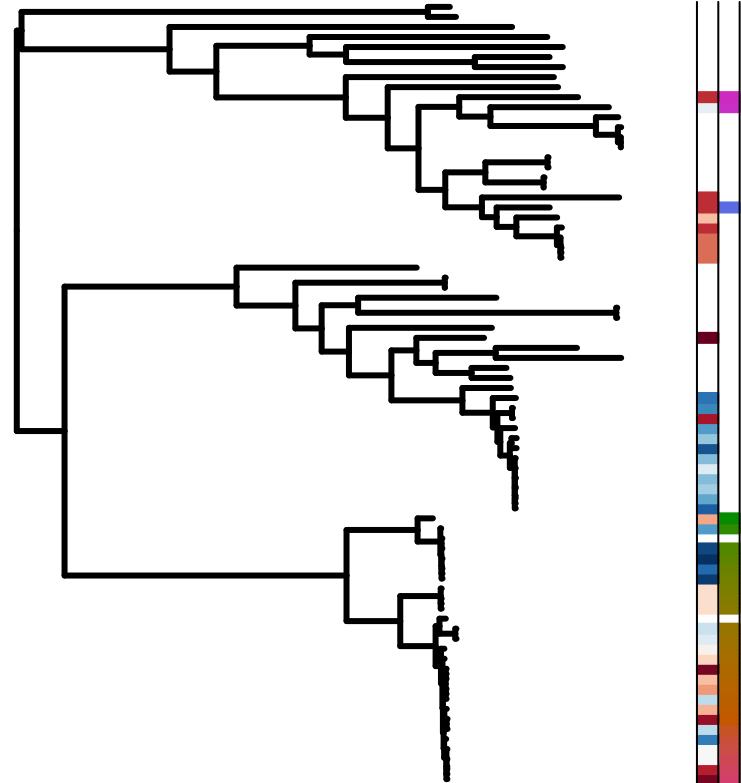
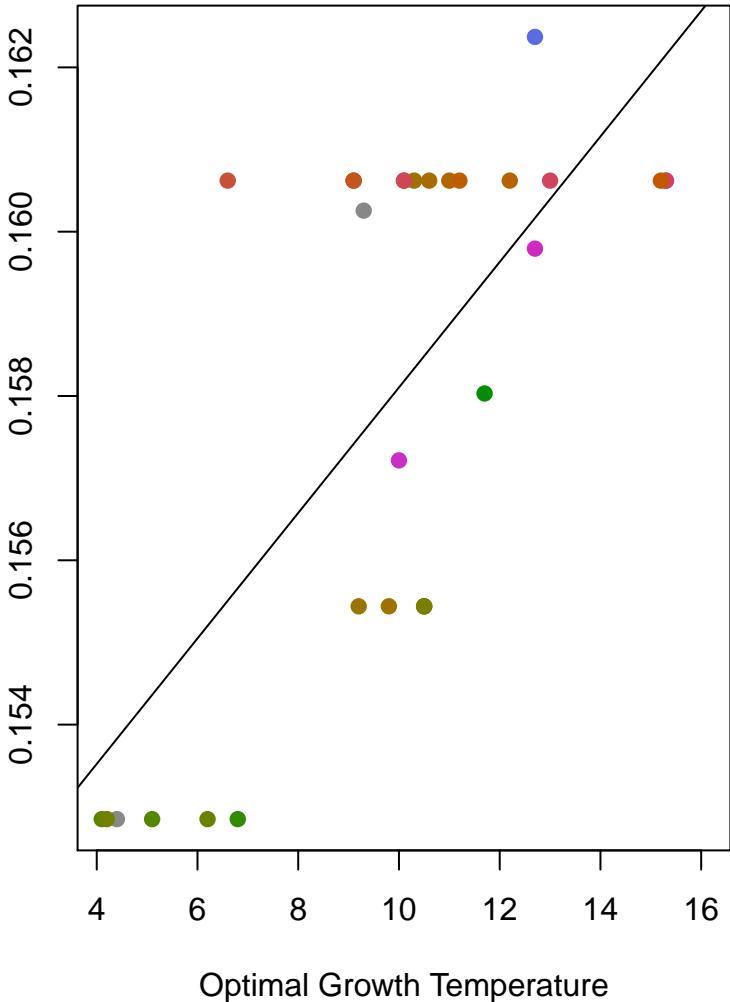


feature.plfam_id.acidic_residue.mean
PLF_28228_00002732
GGDEF domain protein
 $r = 0.723, p = 10^{-5.862}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00004222
hypothetical protein
 $r = 0.72, p = 10^{-5.131}$

feature.plfam_id.acidic_residue.mean

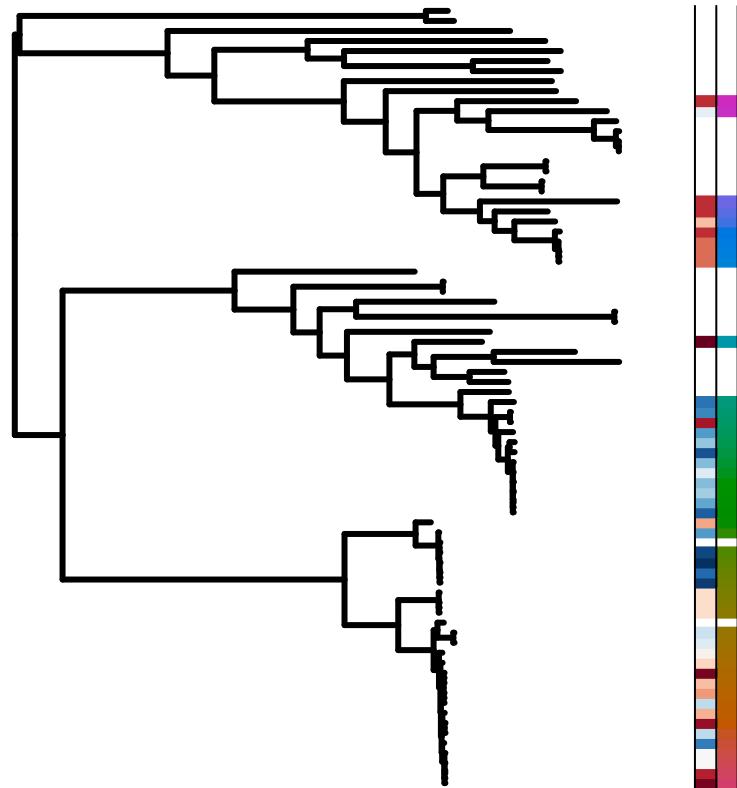
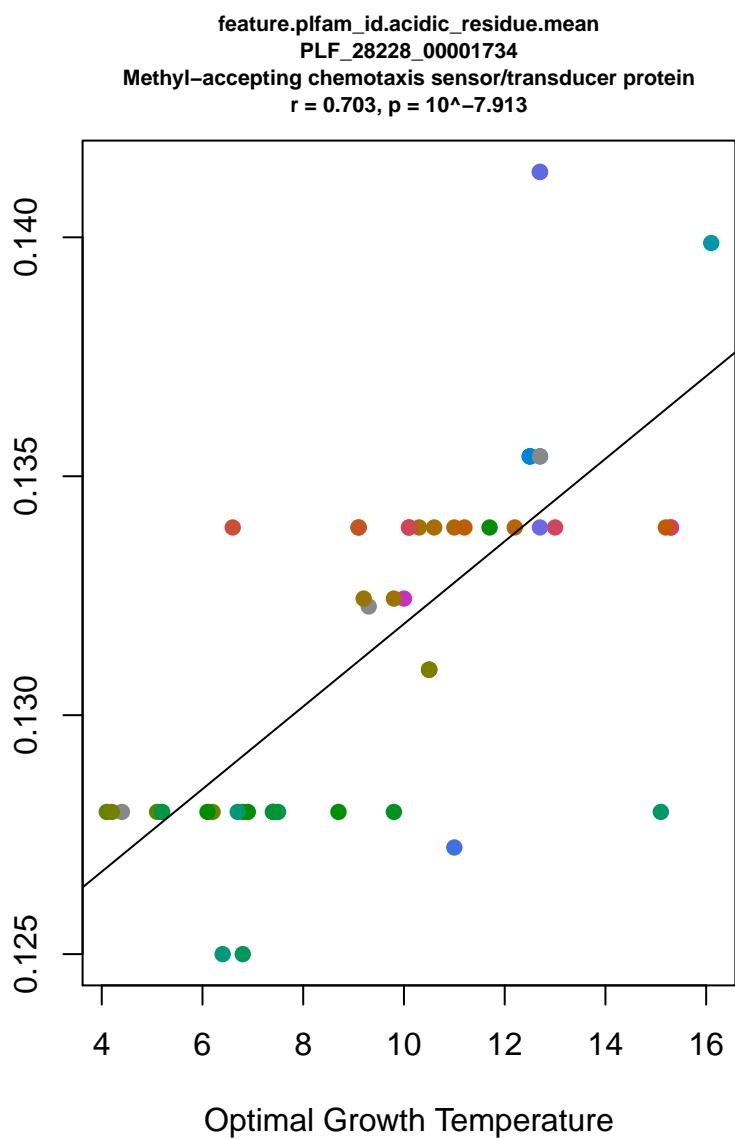


feature.plfam_id.acidic_residue.mean

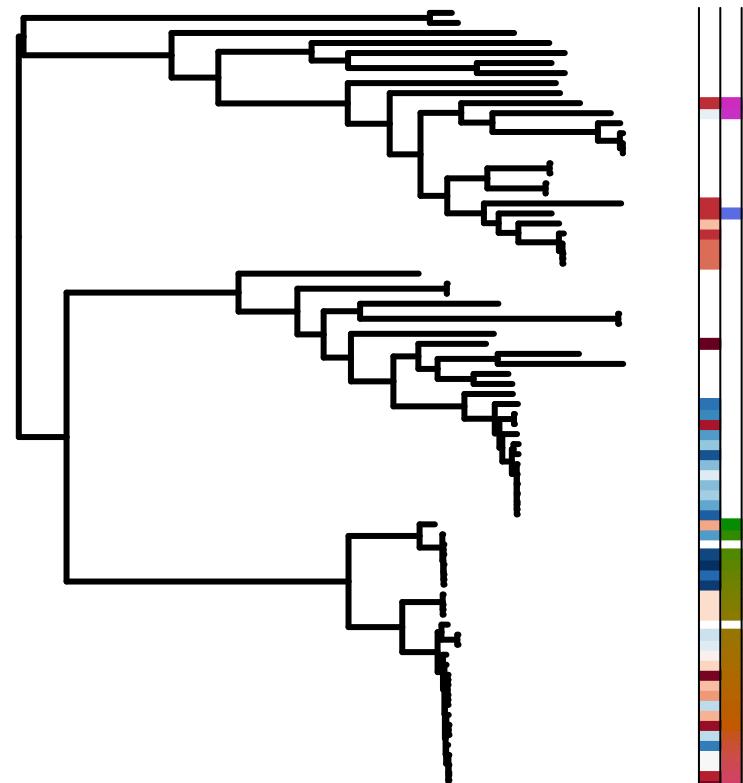
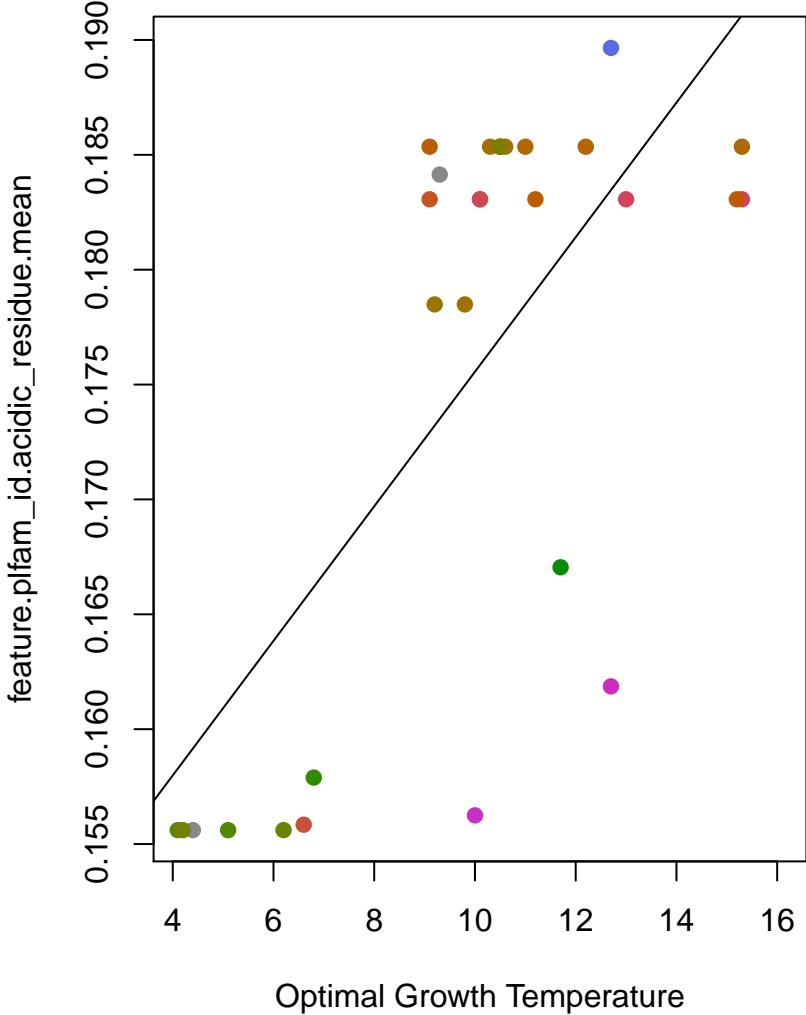
PLF_28228_00001734

Methyl-accepting chemotaxis sensor/transducer protein

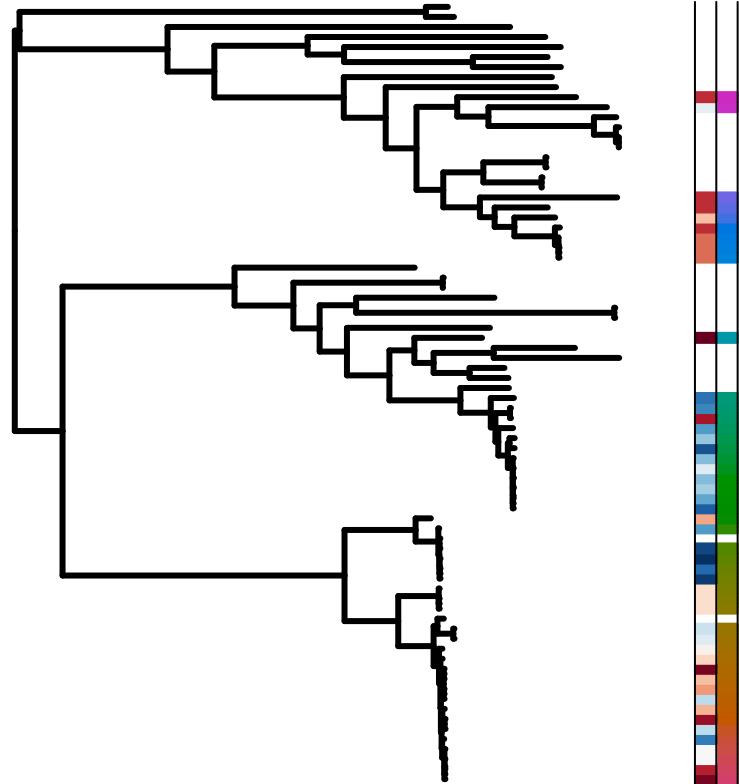
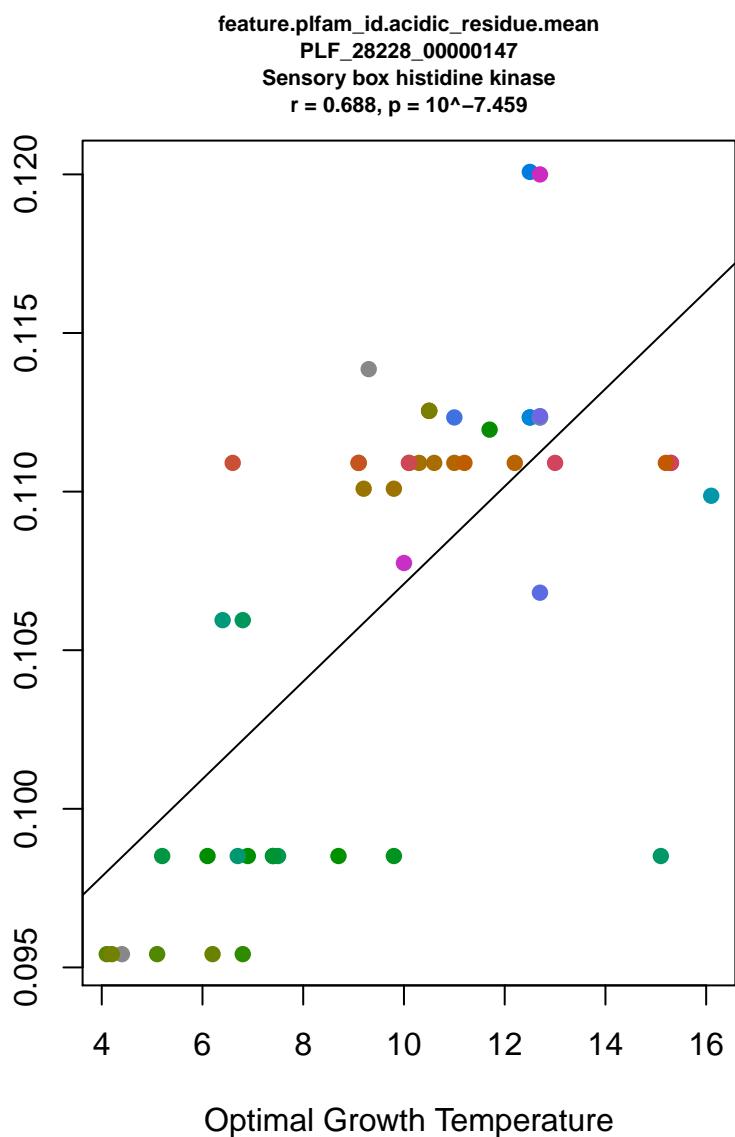
$r = 0.703$, $p = 10^{-7.913}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00004221
hypothetical protein
 $r = 0.703, p = 10^{-4.834}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00000147
Sensory box histidine kinase
 $r = 0.688, p = 10^{-7.459}$

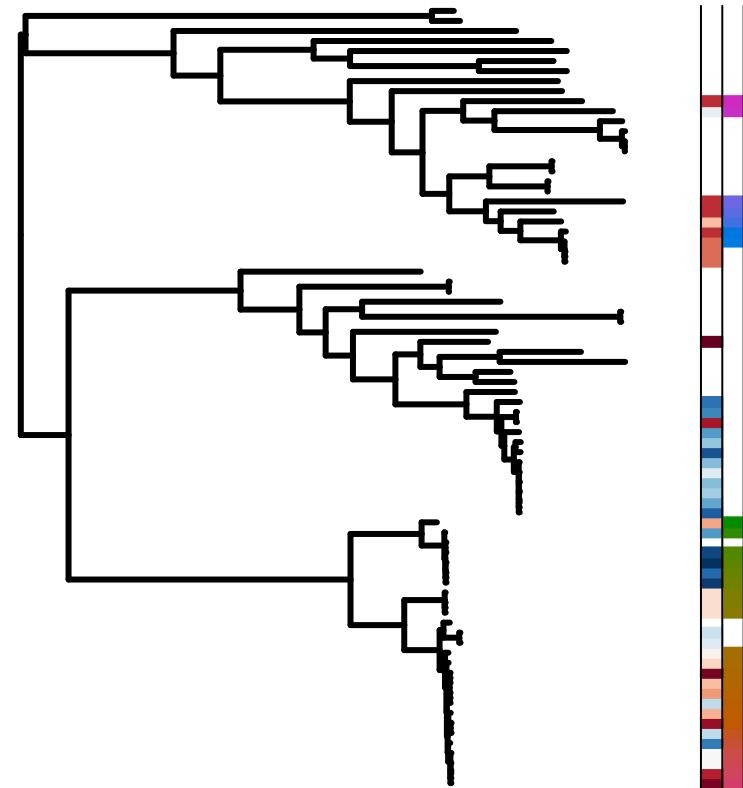
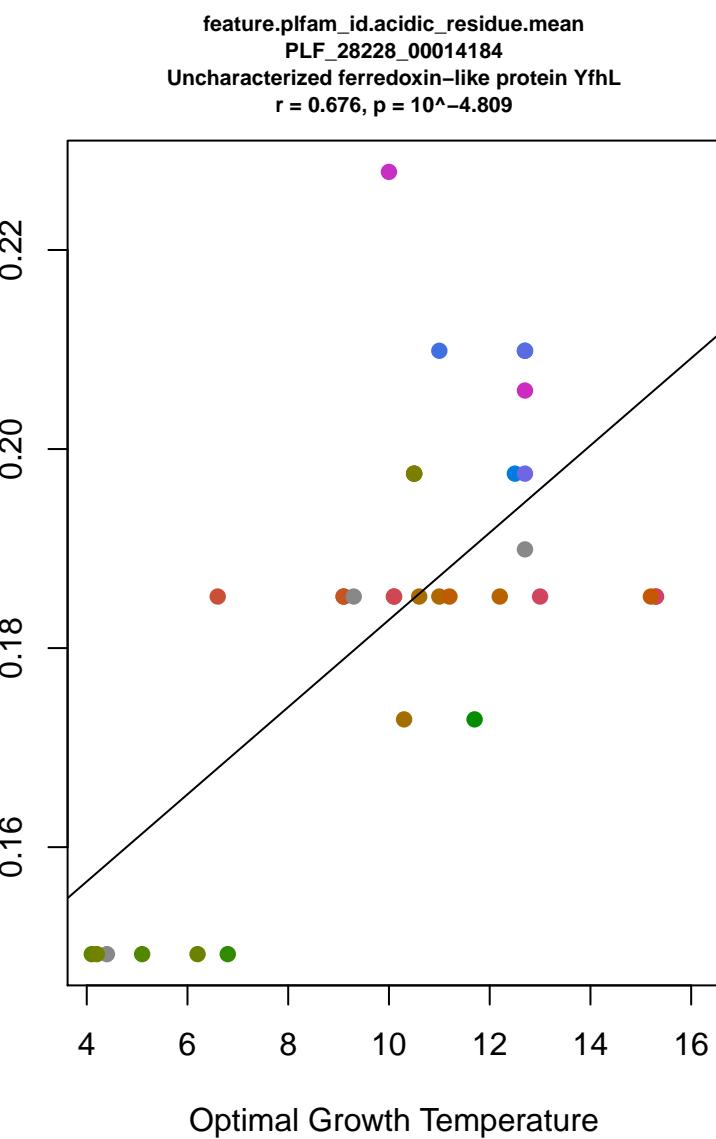


feature.plfam_id.acidic_residue.mean

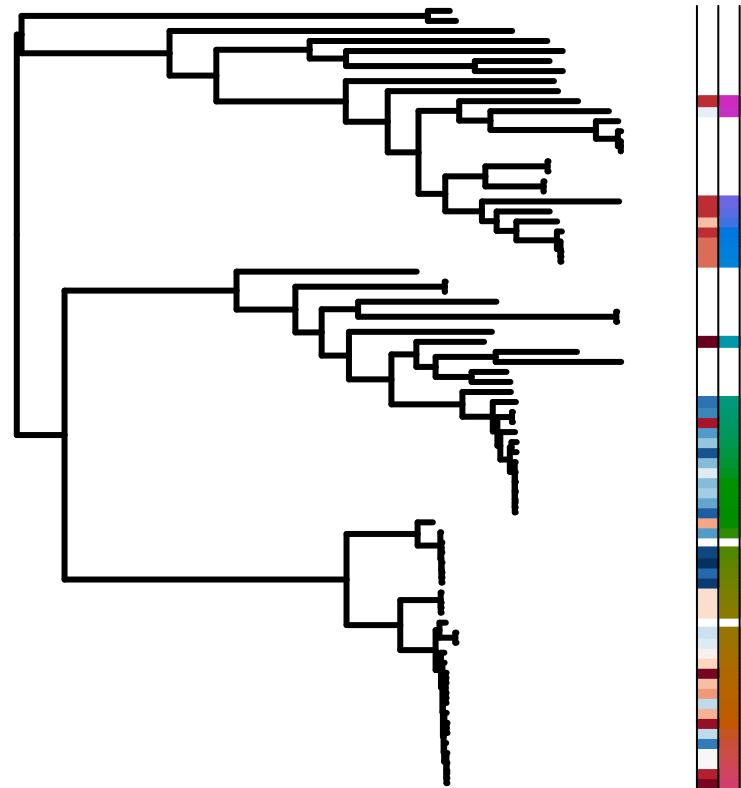
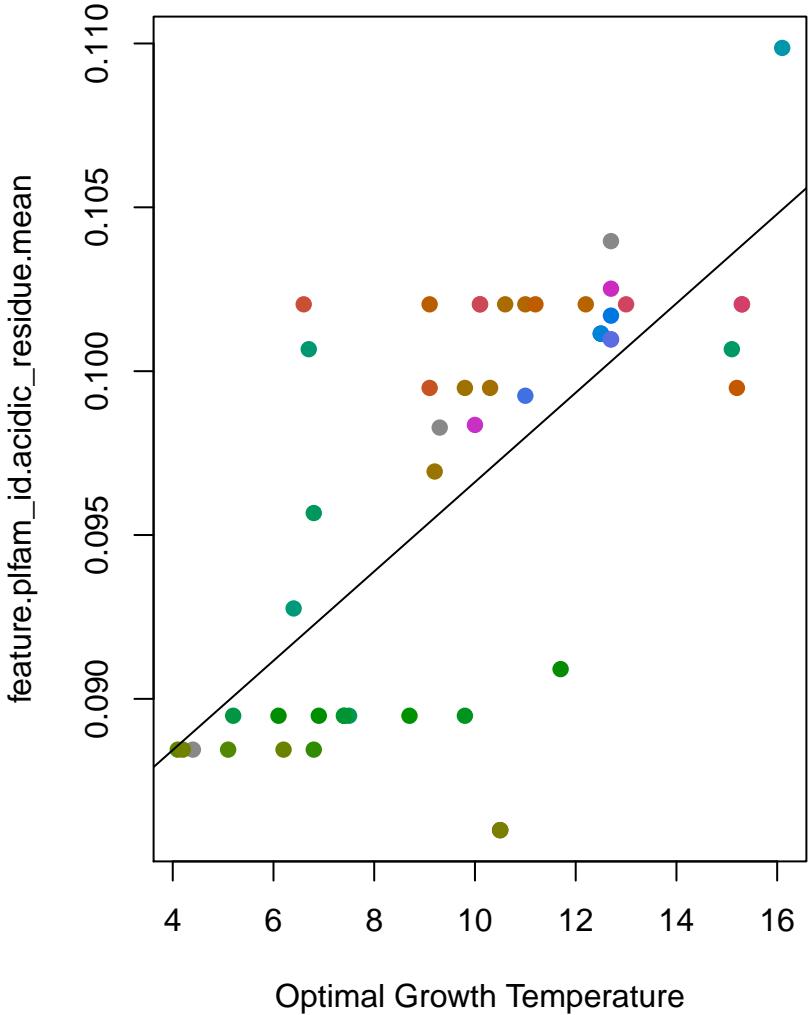
PLF_28228_00014184

Uncharacterized ferredoxin-like protein YfhL

$r = 0.676, p = 10^{-4.809}$

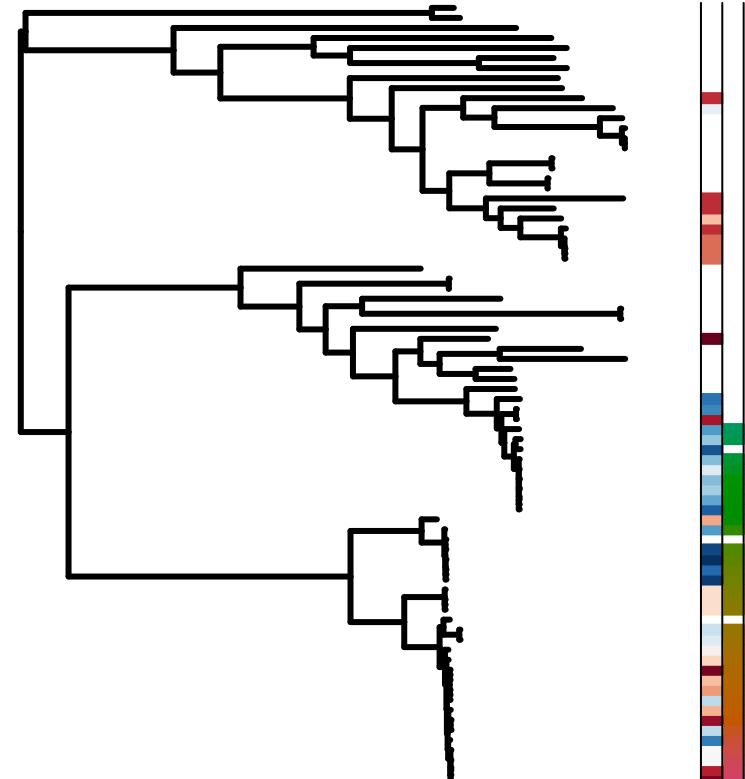
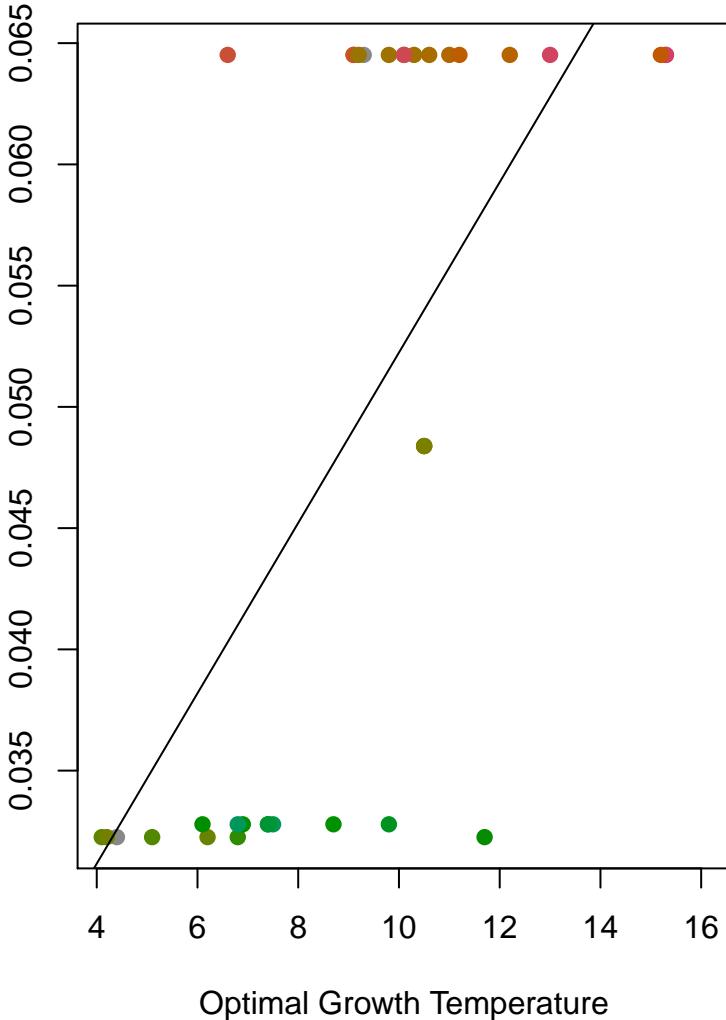


feature.plfam_id.acidic_residue.mean
PLF_28228_00002173
Type IV pilus biogenesis protein PilF
 $r = 0.676$, $p = 10^{-7.155}$



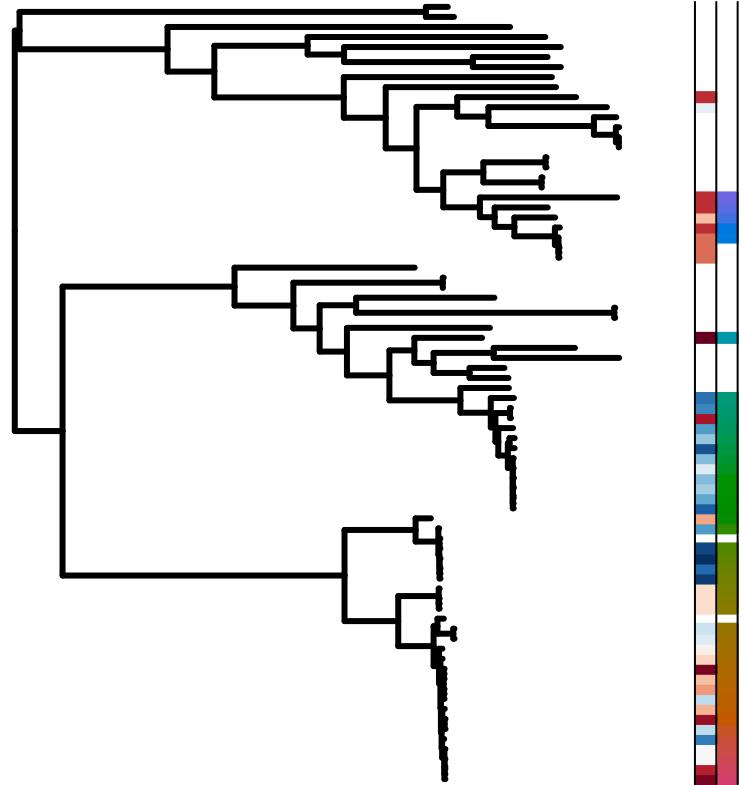
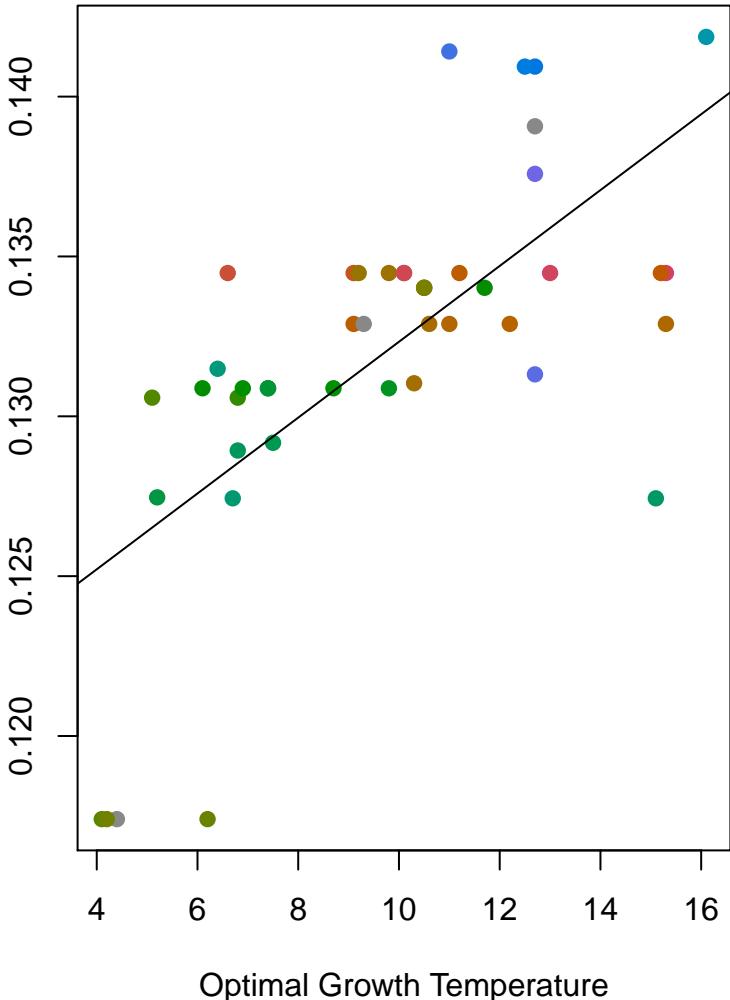
feature.plfam_id.acidic_residue.mean
PLF_28228_00019712
hypothetical protein
 $r = 0.675, p = 10^{-5.053}$

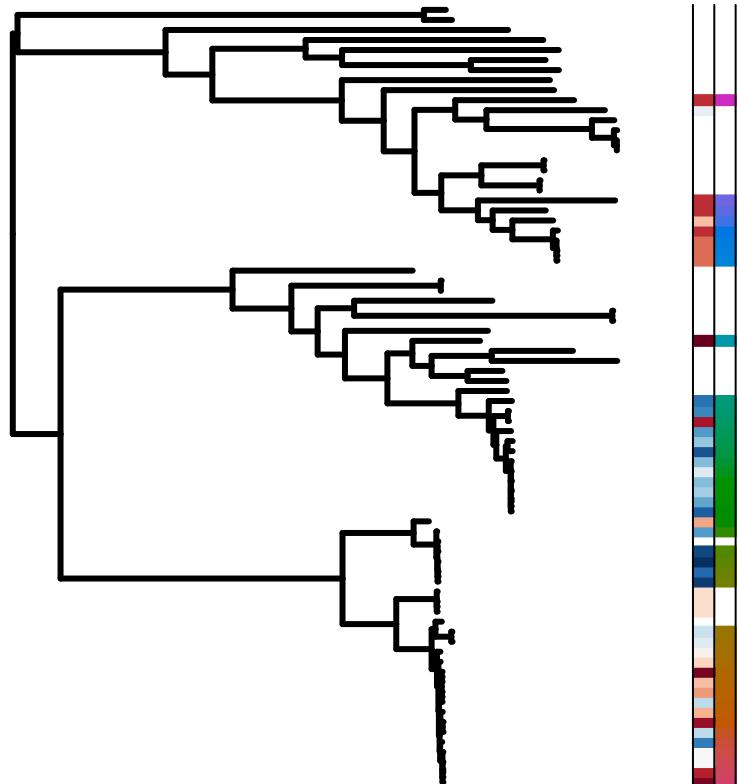
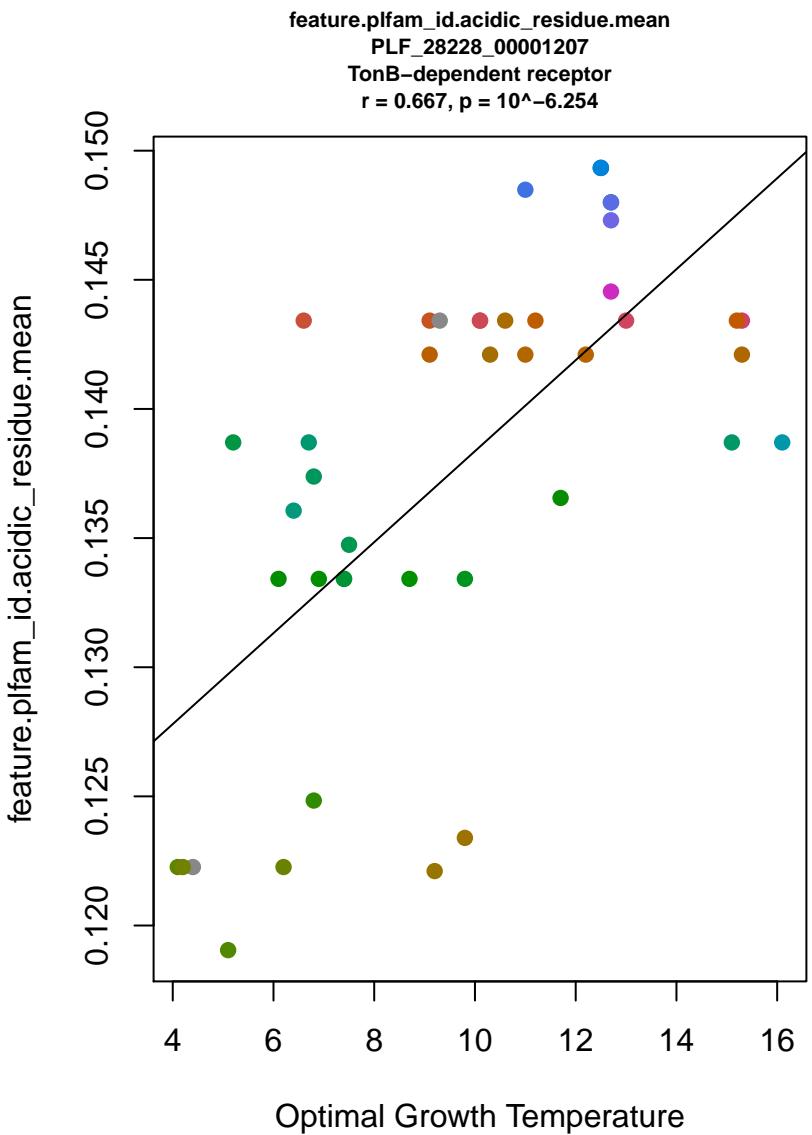
feature.plfam_id.acidic_residue.mean

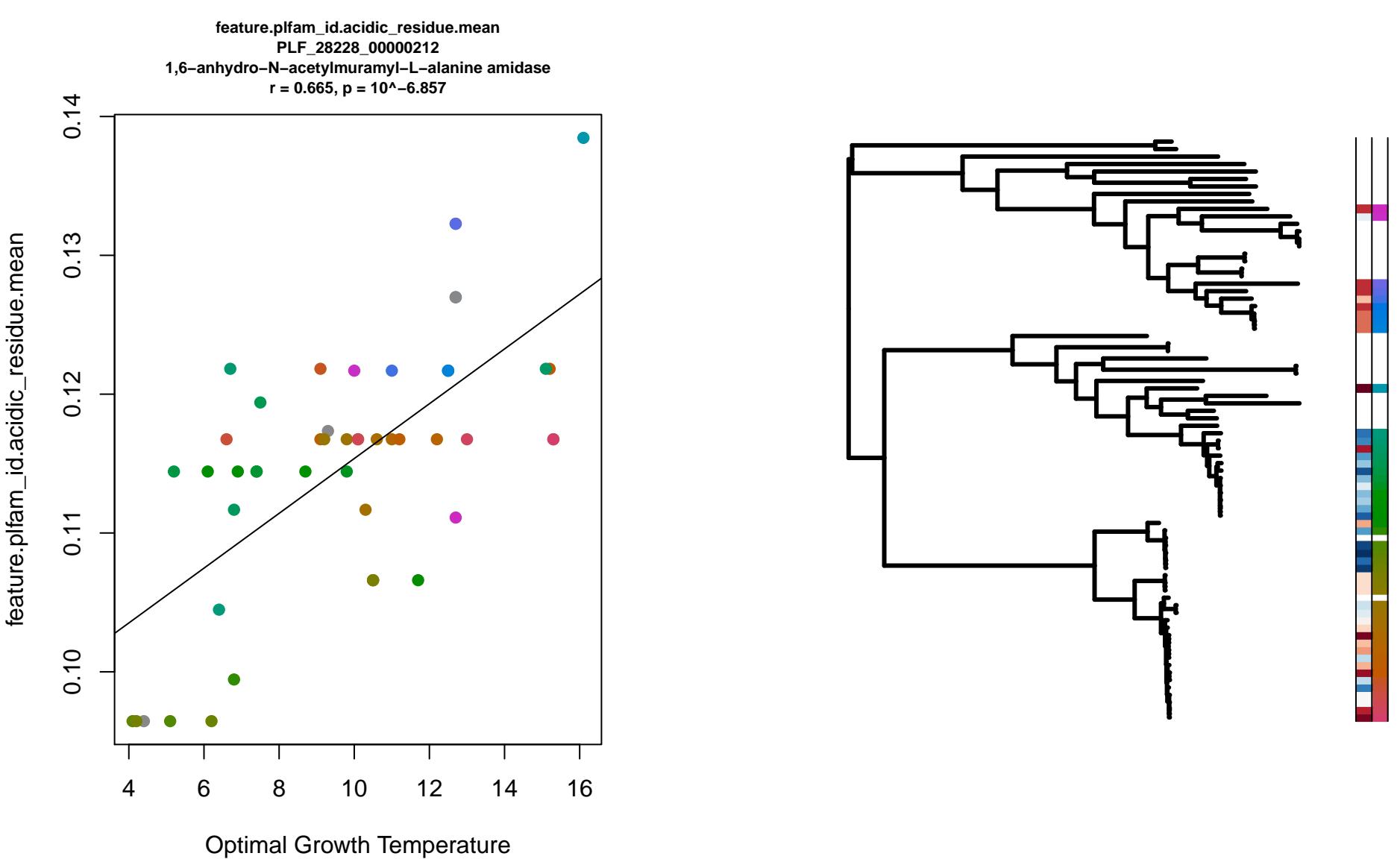


feature.plfam_id.acidic_residue.mean
PLF_28228_00028215
Glutathione S-transferase (EC 2.5.1.18)
 $r = 0.671$, $p = 10^{-6.468}$

feature.plfam_id.acidic_residue.mean





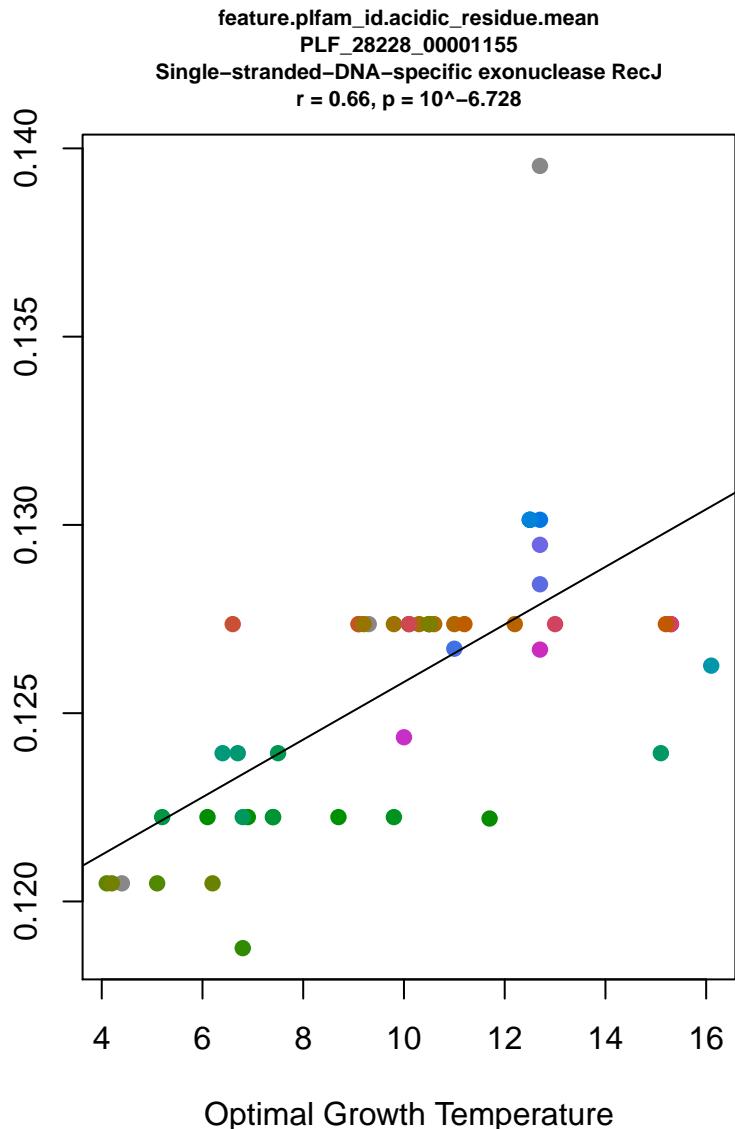


feature.plfam_id.acidic_residue.mean

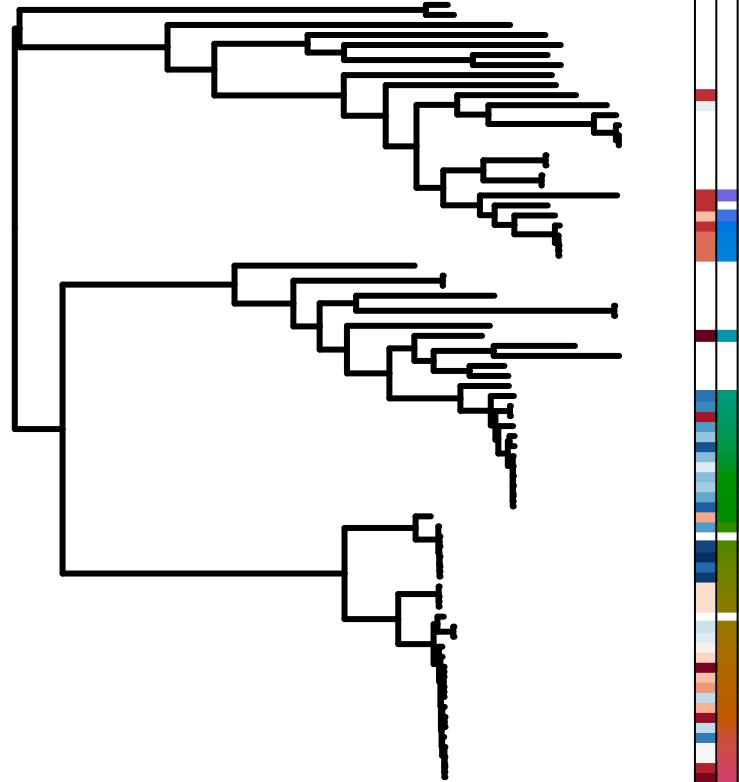
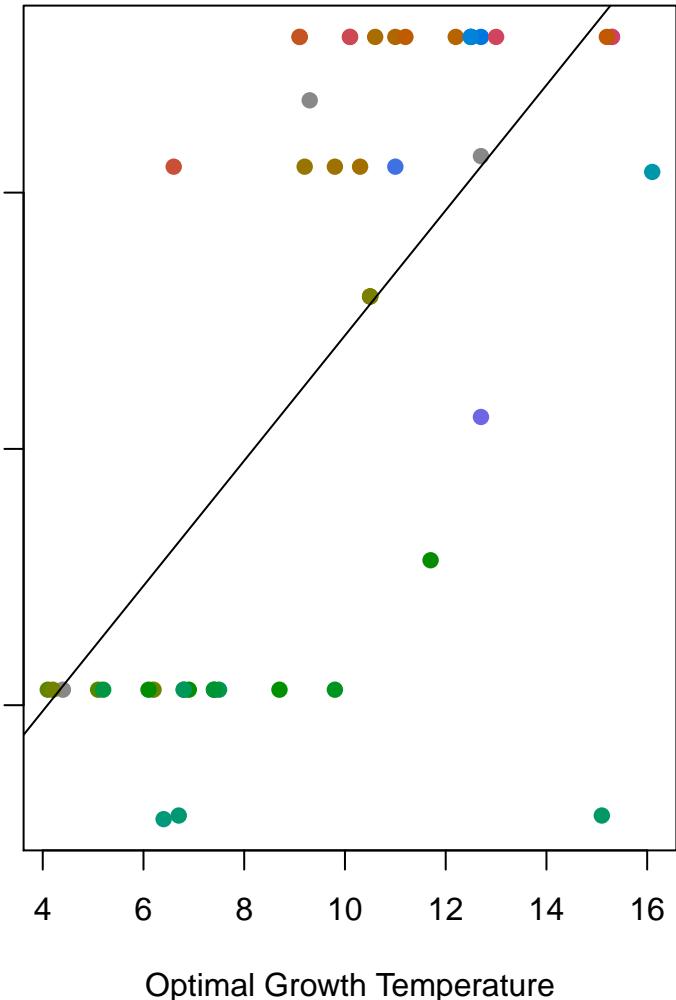
PLF_28228_00001155

Single-stranded-DNA-specific exonuclease RecJ

$r = 0.66$, $p = 10^{-6.728}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00003765
Uncharacterized MFS-type transporter
 $r = 0.655$, $p = 10^{-6.228}$

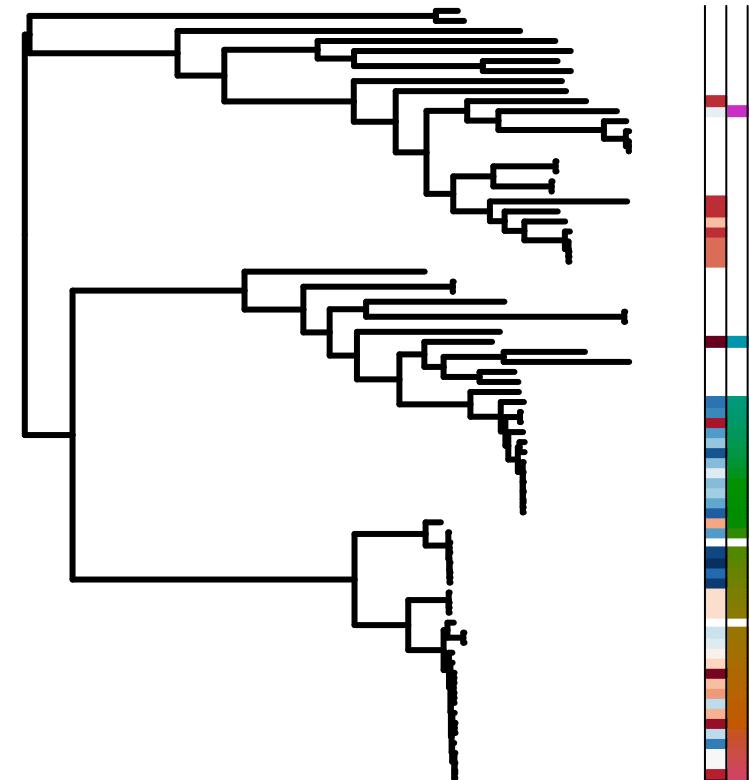
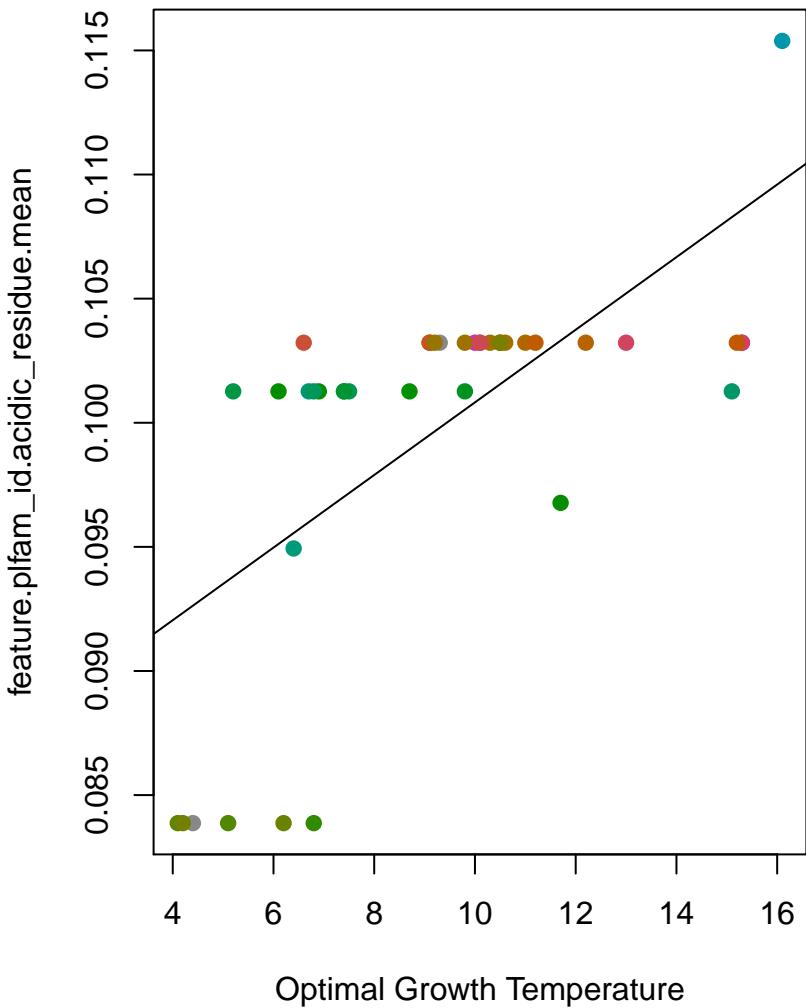


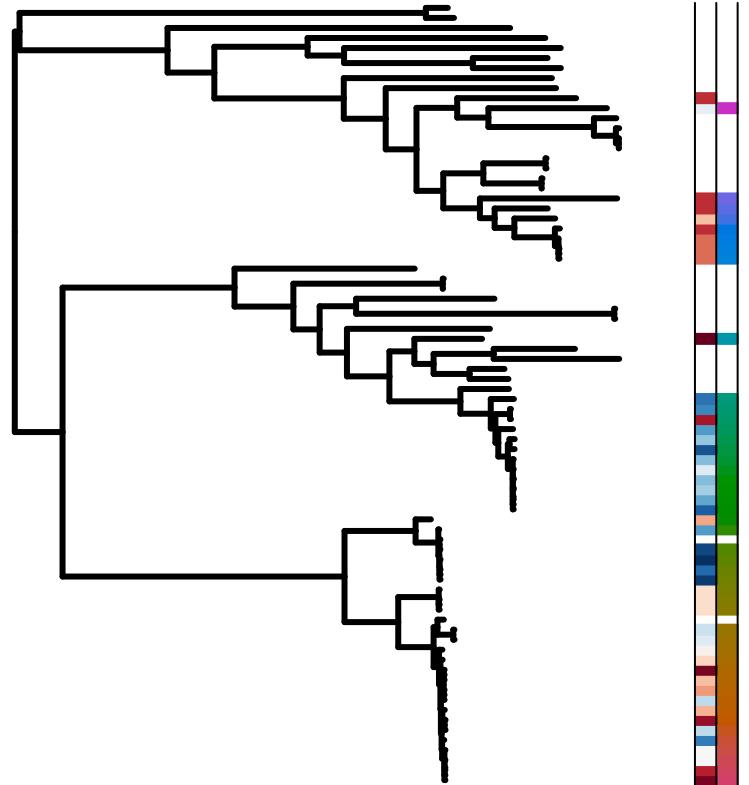
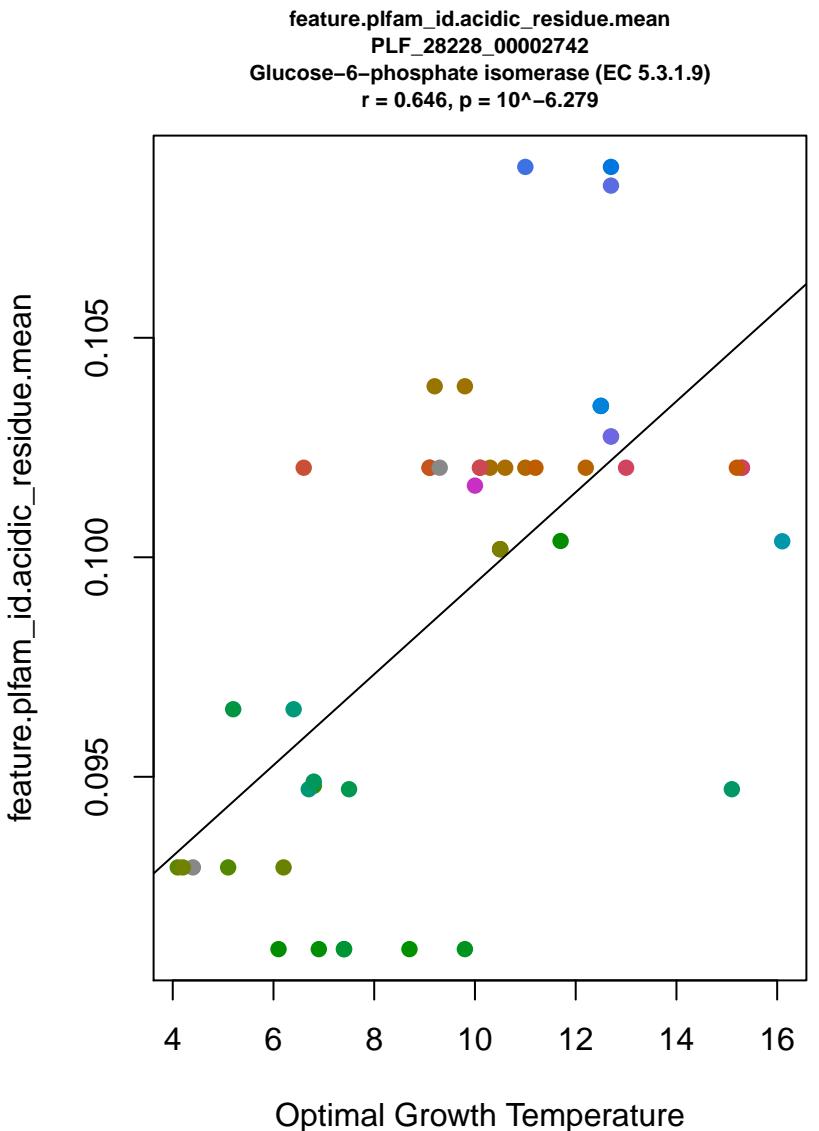
feature.plfam_id.acidic_residue.mean

PLF_28228_00015721

Uncharacterized aldehyde oxidase, 2Fe–2S subunit

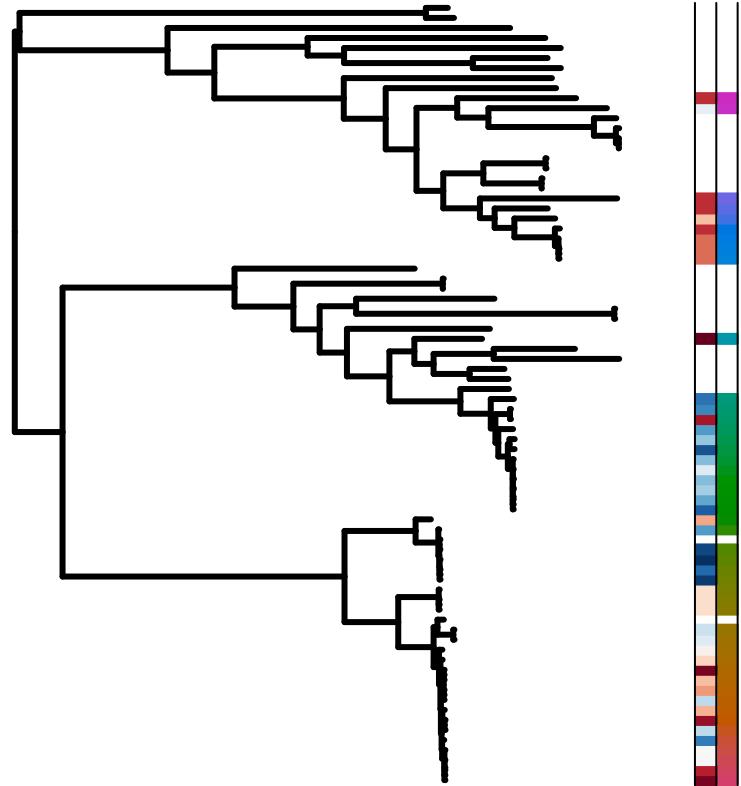
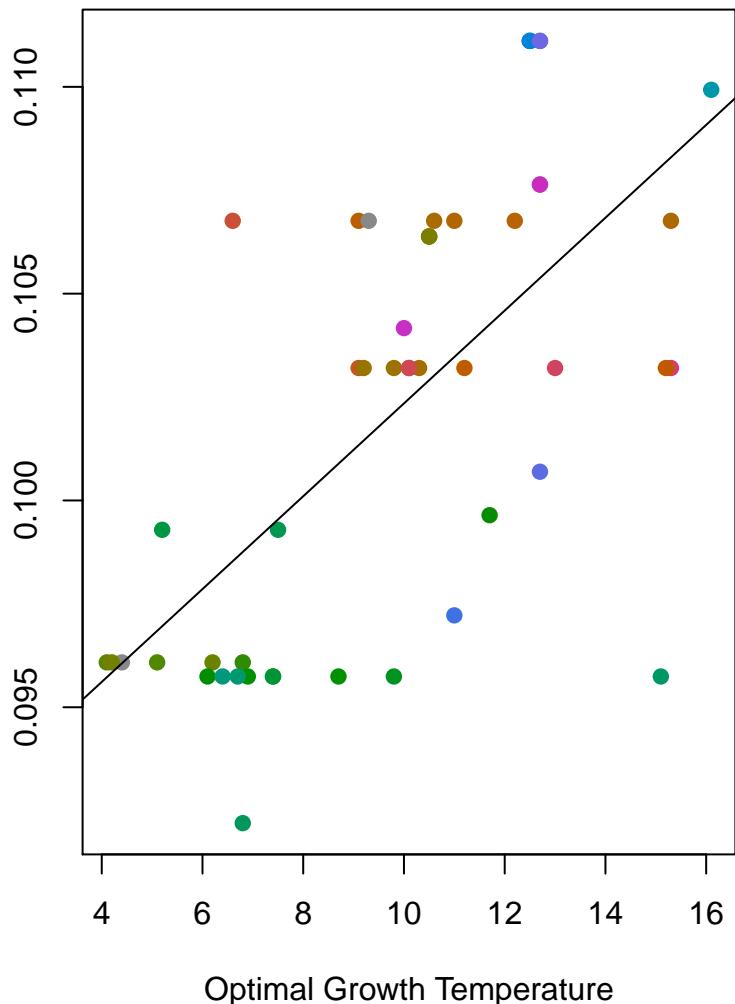
$r = 0.654, p = 10^{-5.45}$



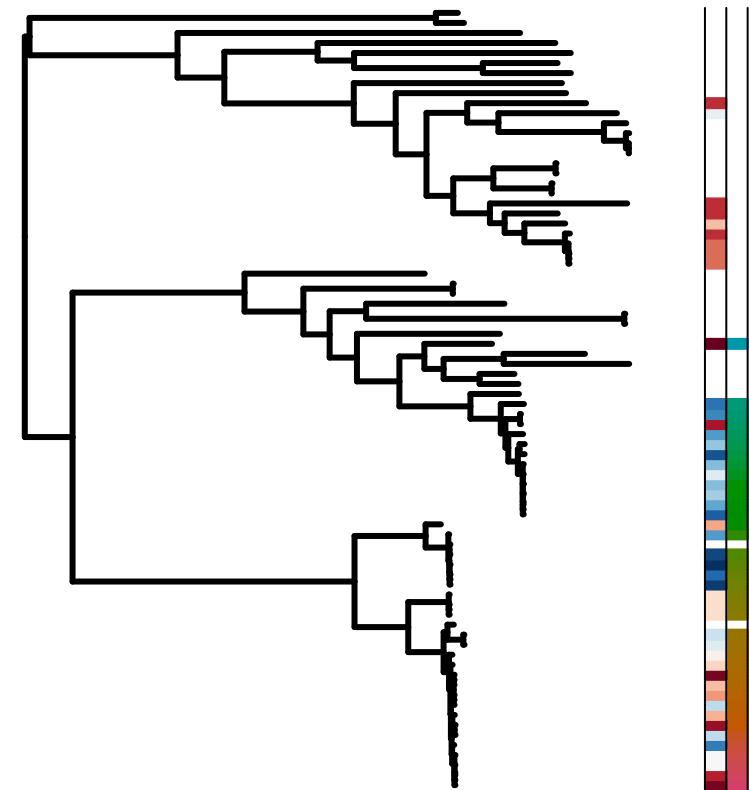
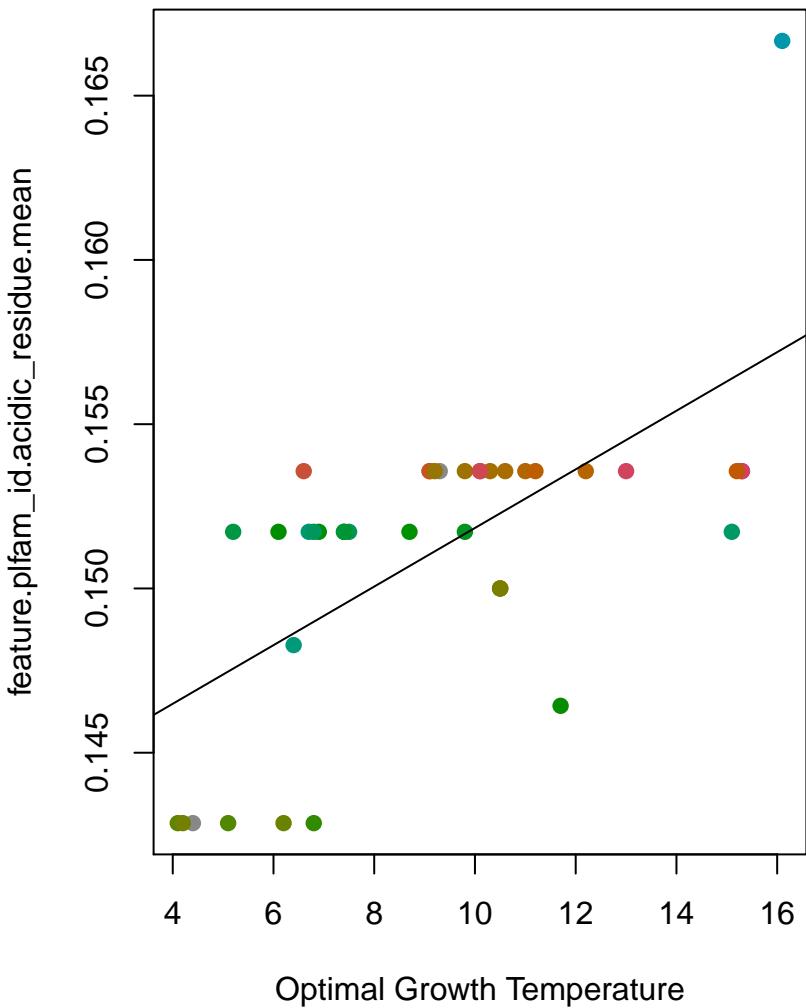


feature.plfam_id.acidic_residue.mean
PLF_28228_00000908
Pantoate--beta-alanine ligase (EC 6.3.2.1)
 $r = 0.645$, $p = 10^{-6.374}$

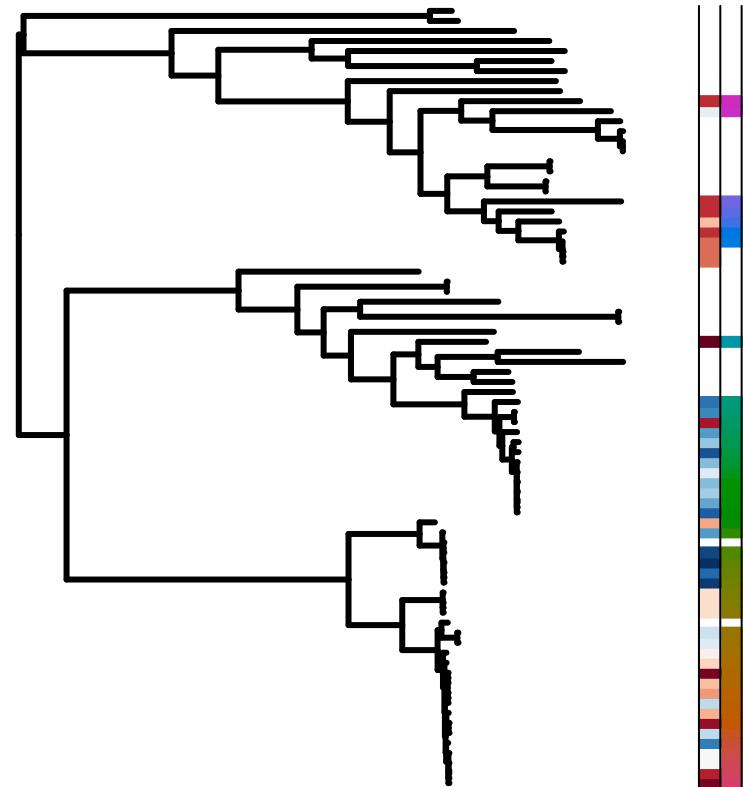
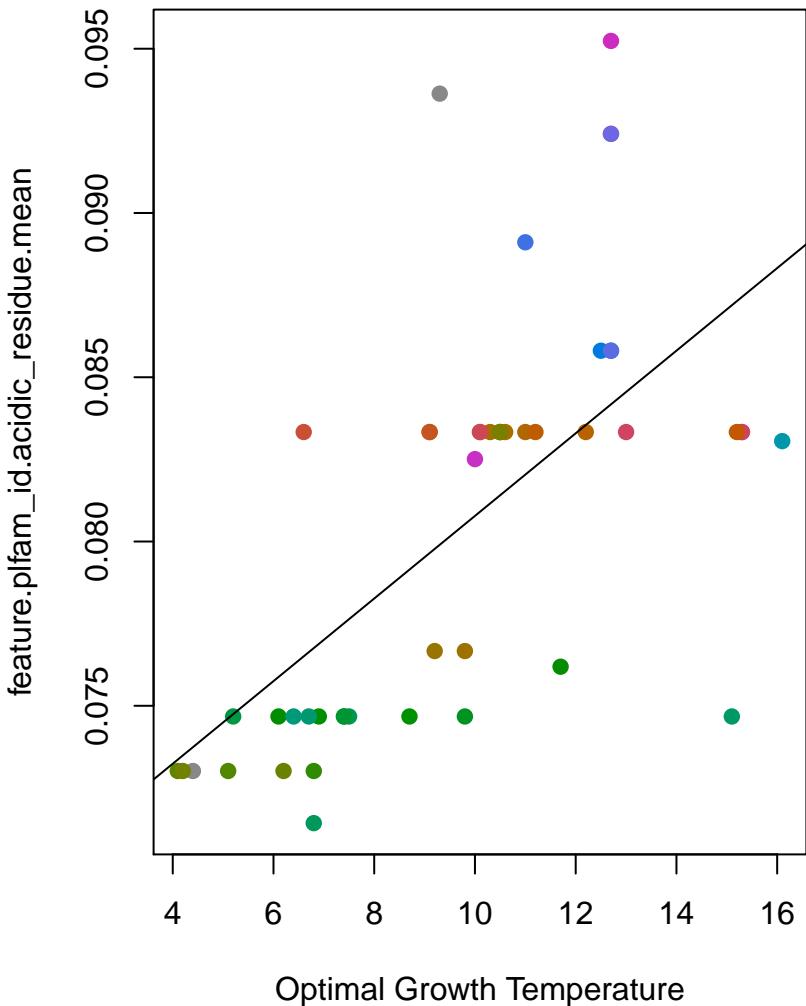
feature.plfam_id.acidic_residue.mean



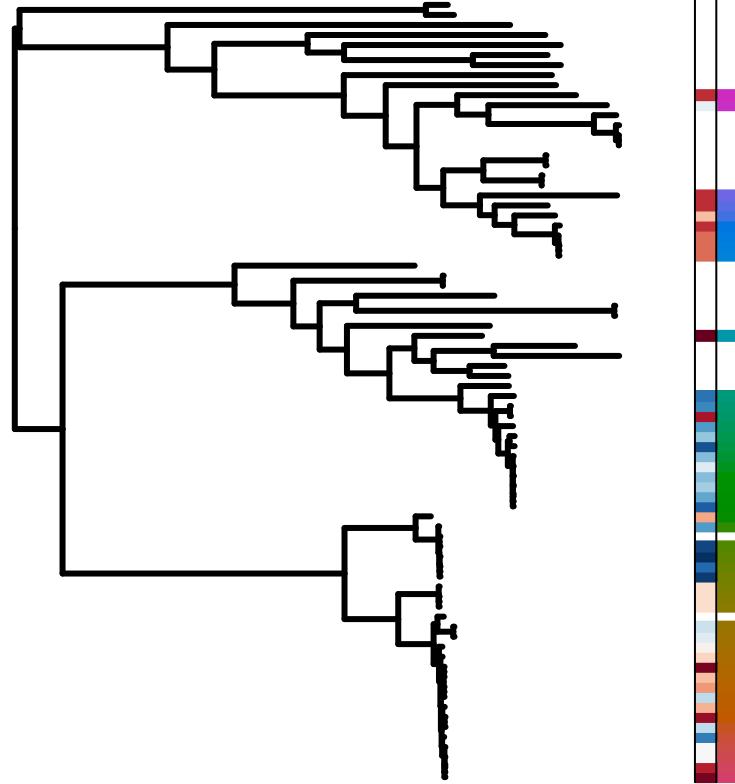
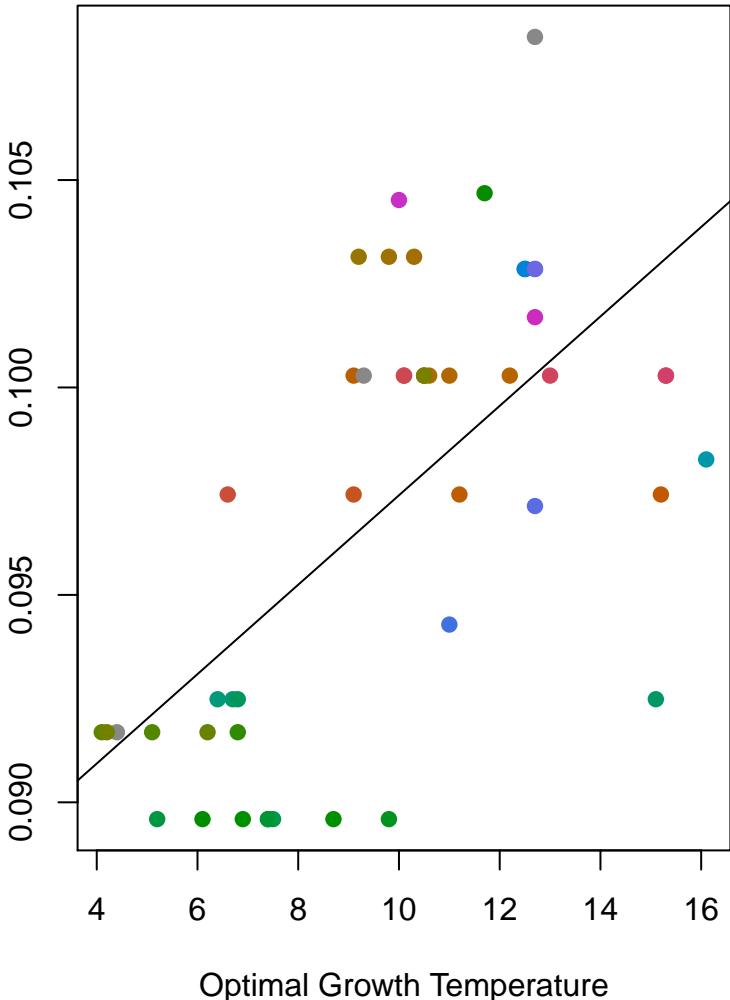
feature.plfam_id.acidic_residue.mean
PLF_28228_00005964
Segregation and condensation protein A
 $r = 0.644$, $p = 10^{-5.141}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00016541
Probable acyltransferase PA0834
 $r = 0.642$, $p = 10^{-6.057}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00002415
hypothetical protein
 $r = 0.639, p = 10^{-6.228}$

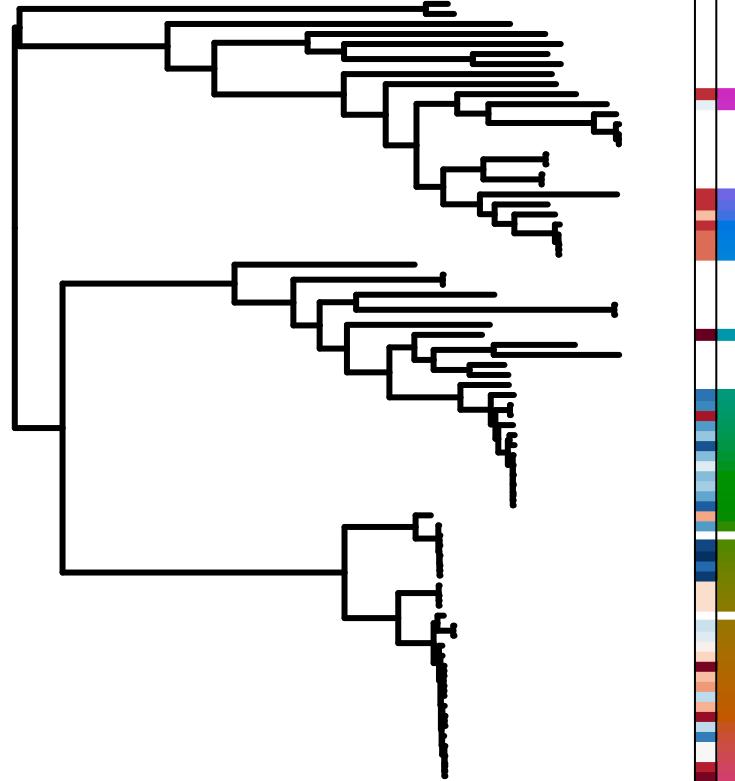
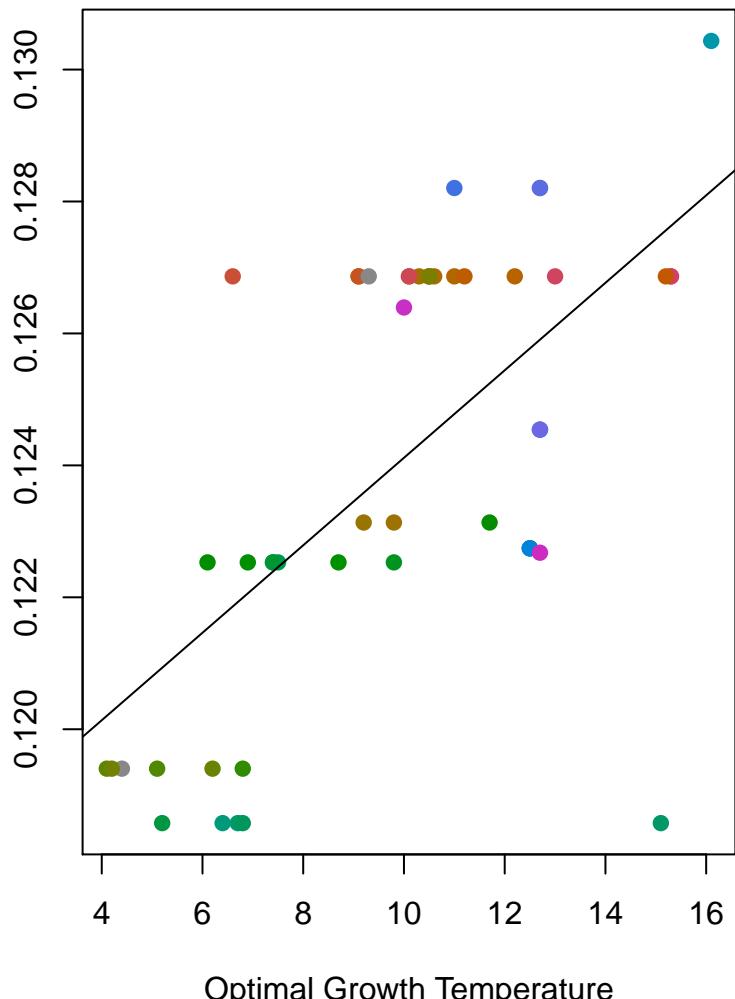


feature.plfam_id.acidic_residue.mean

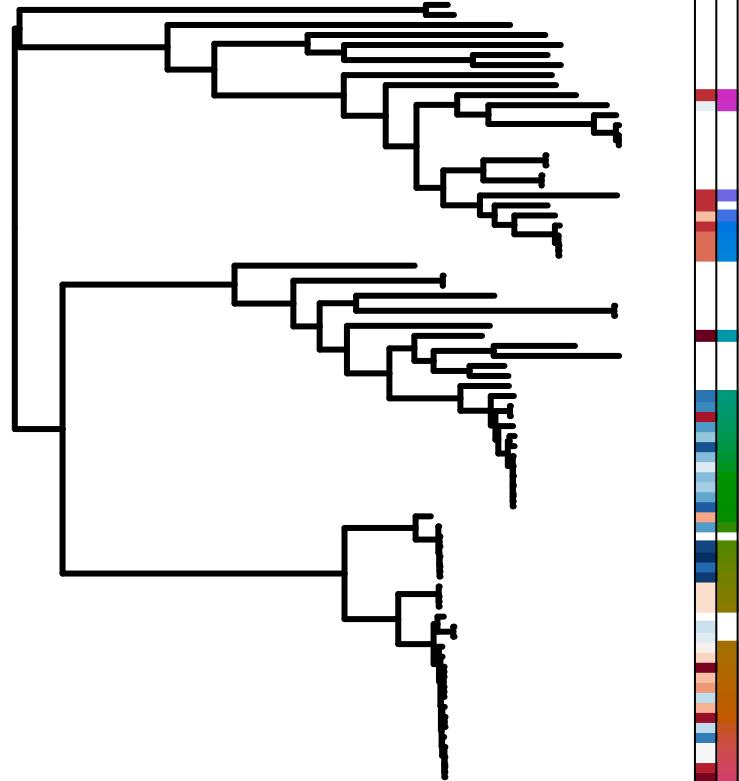
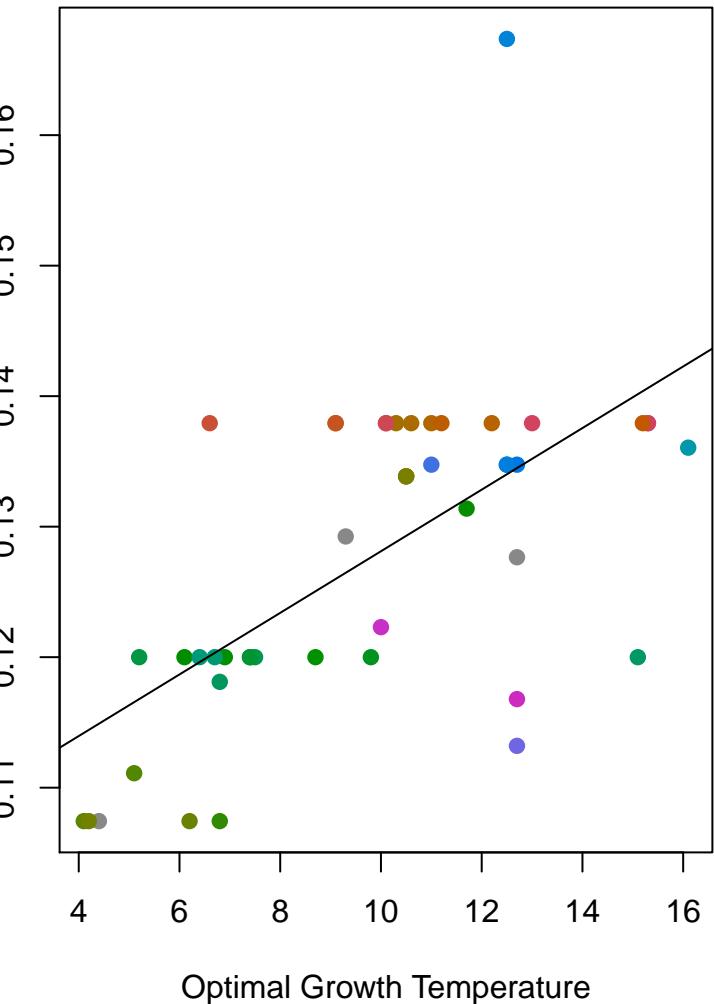
PLF_28228_00001395

tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)

$r = 0.627$, $p = 10^{-5.957}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00000407
FIG024746: hypothetical protein
 $r = 0.624, p = 10^{-5.552}$

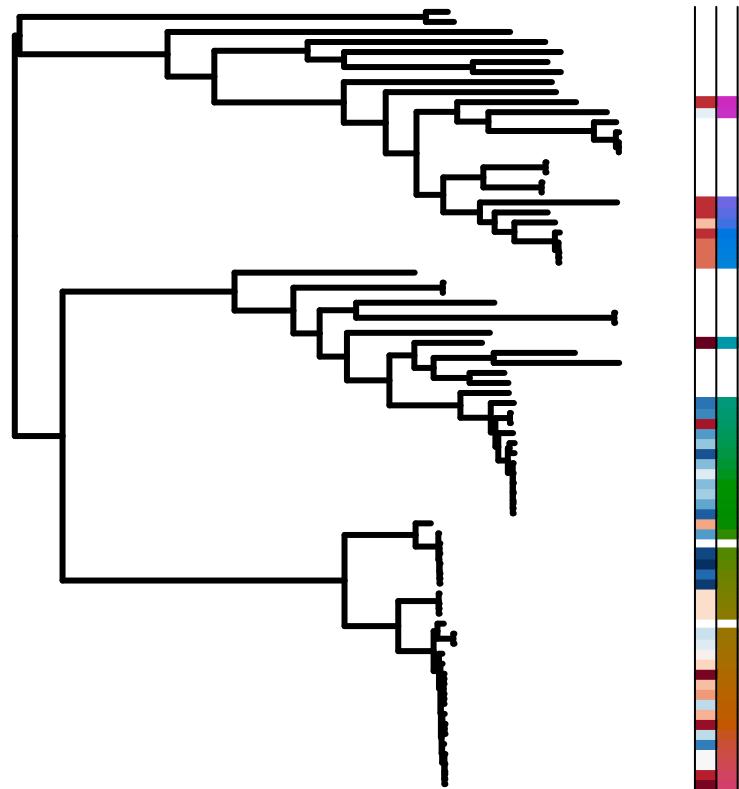
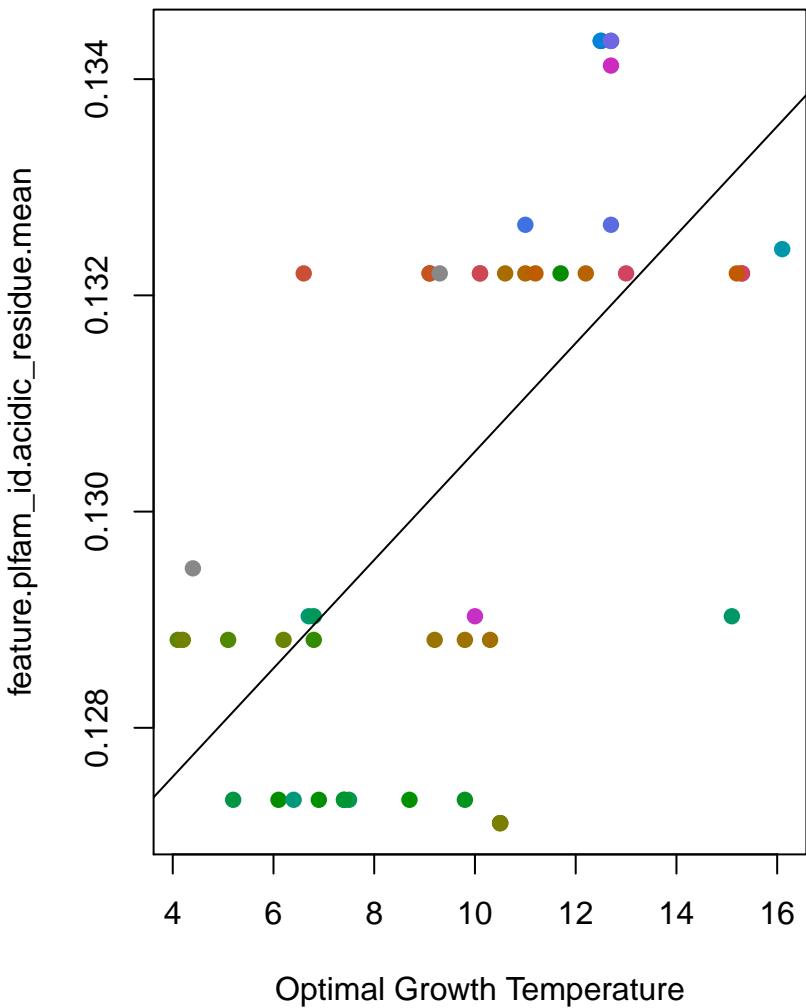


feature.plfam_id.acidic_residue.mean

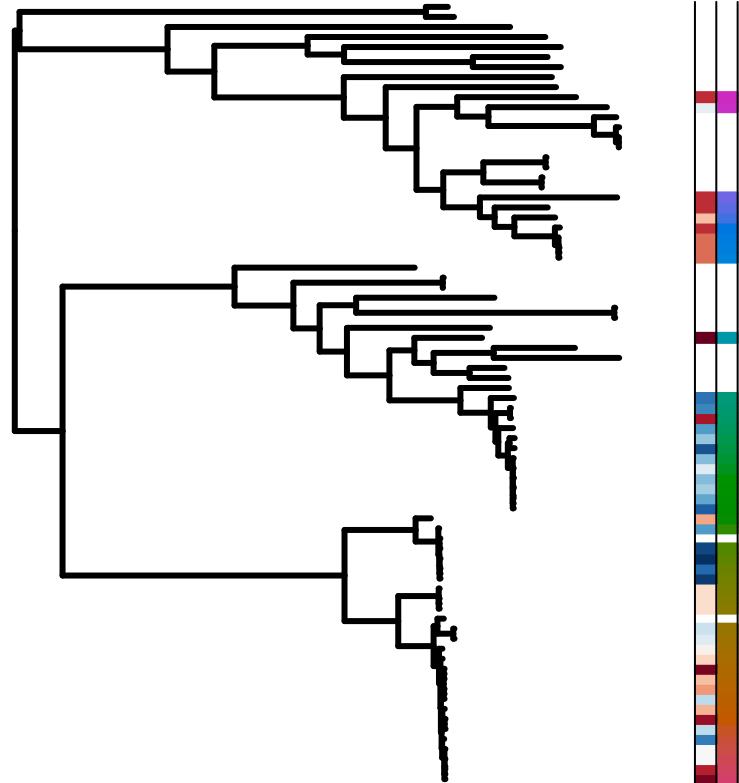
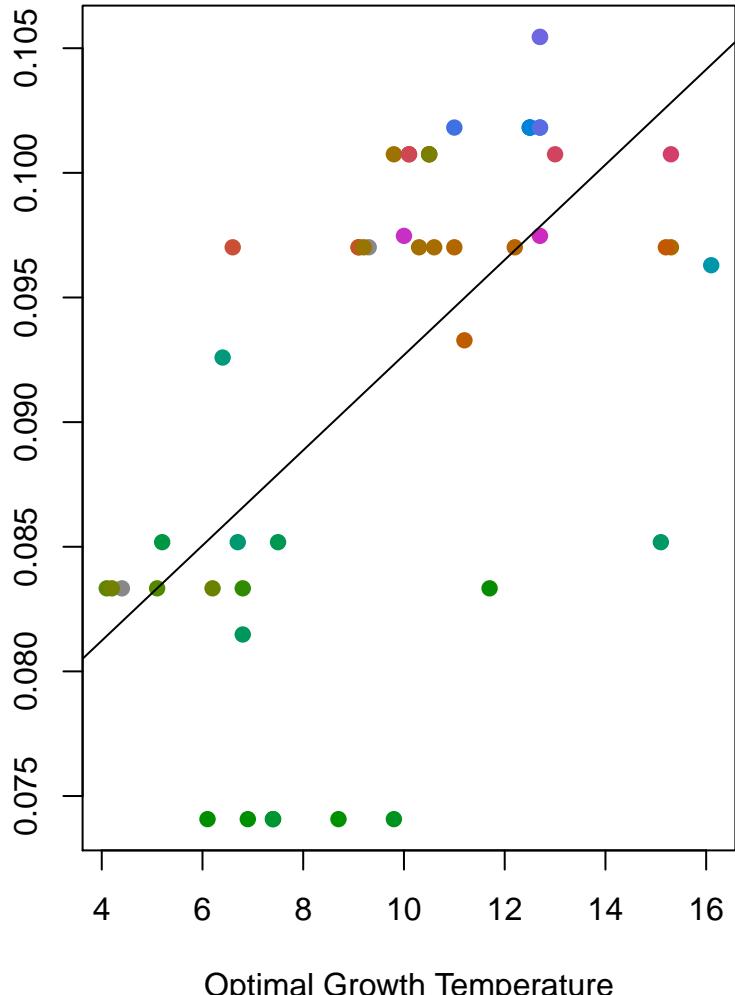
PLF_28228_00001165

Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)

$r = 0.624$, $p = 10^{-5.881}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00001140
Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)
 $r = 0.619$, $p = 10^{-5.78}$



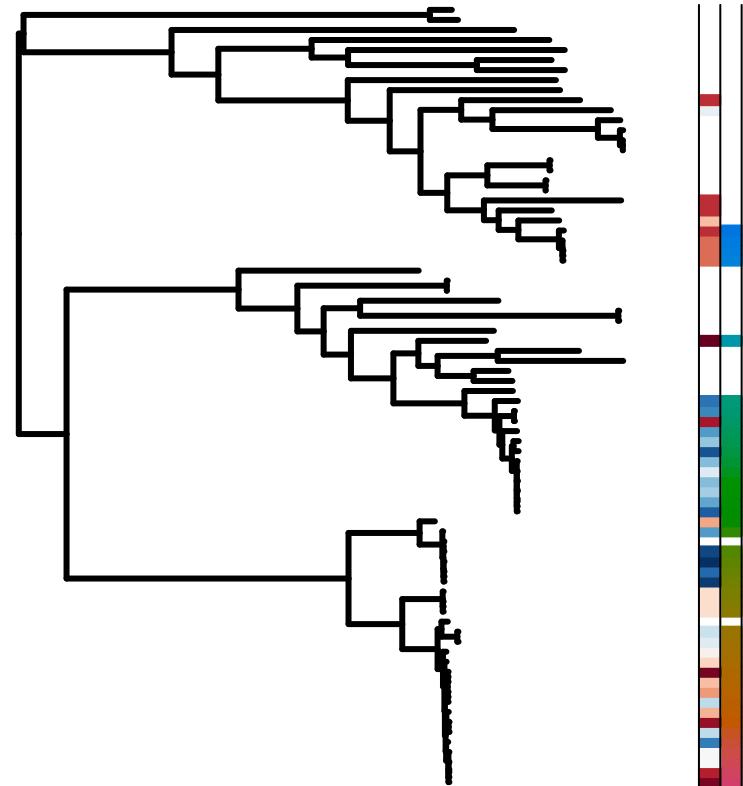
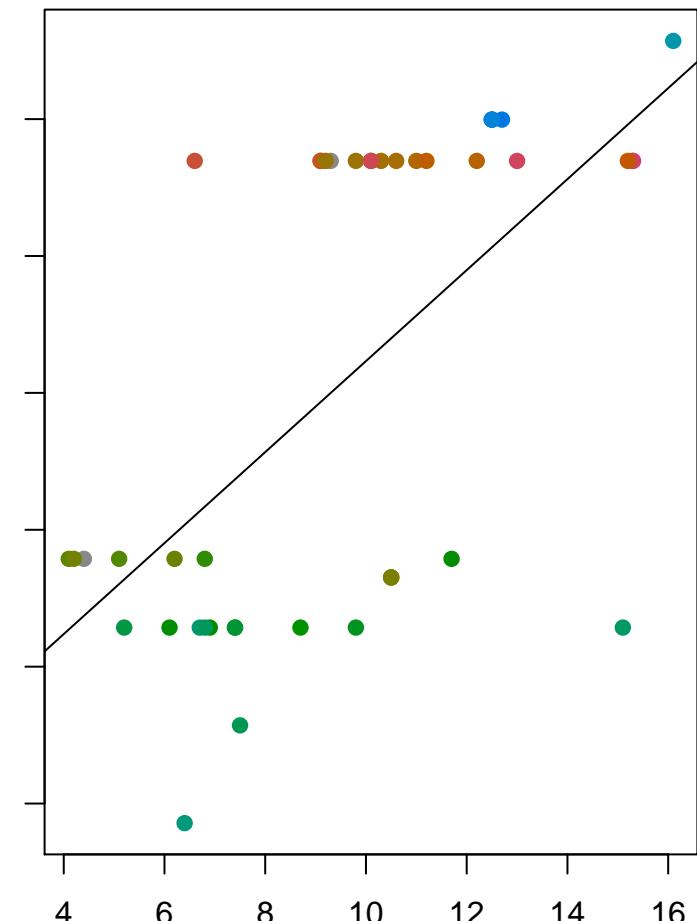
feature.plfam_id.acidic_residue.mean

PLF_28228_00007407

Putative mannosyl-3-phosphoglycerate phosphatase (EC 3.1.3.70)

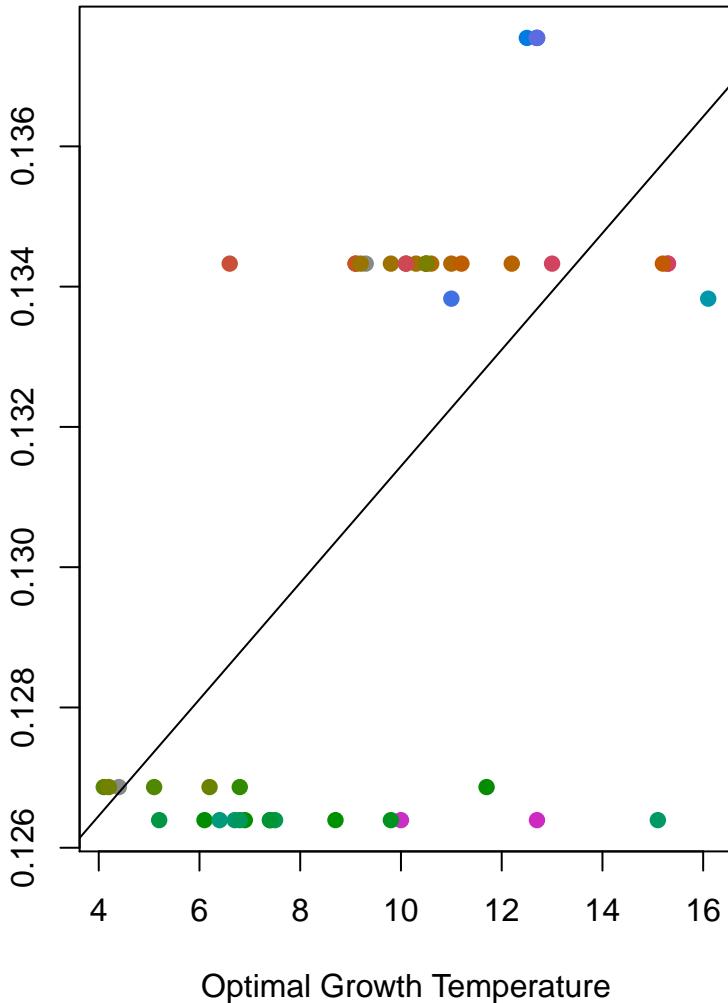
$r = 0.615, p = 10^{-5.048}$

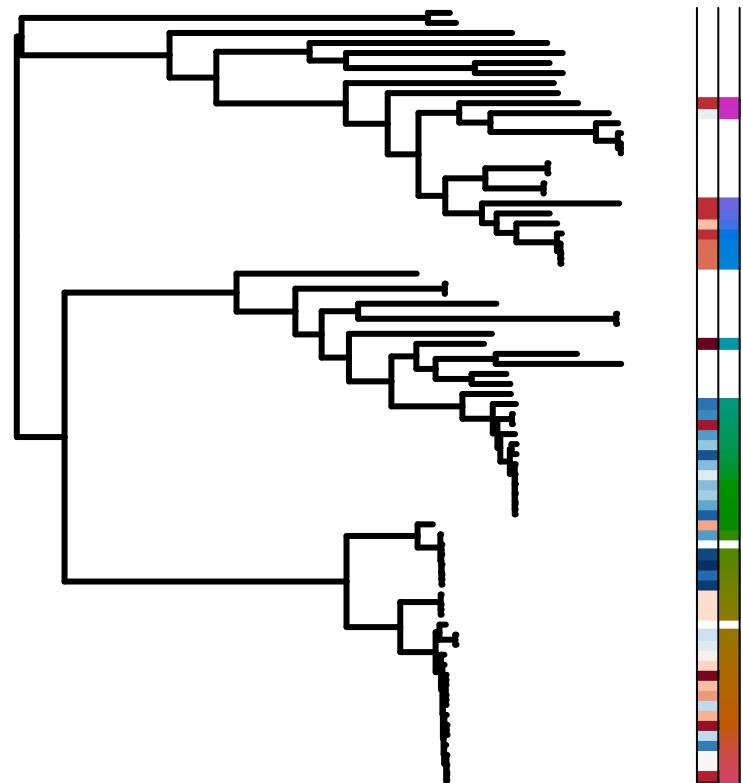
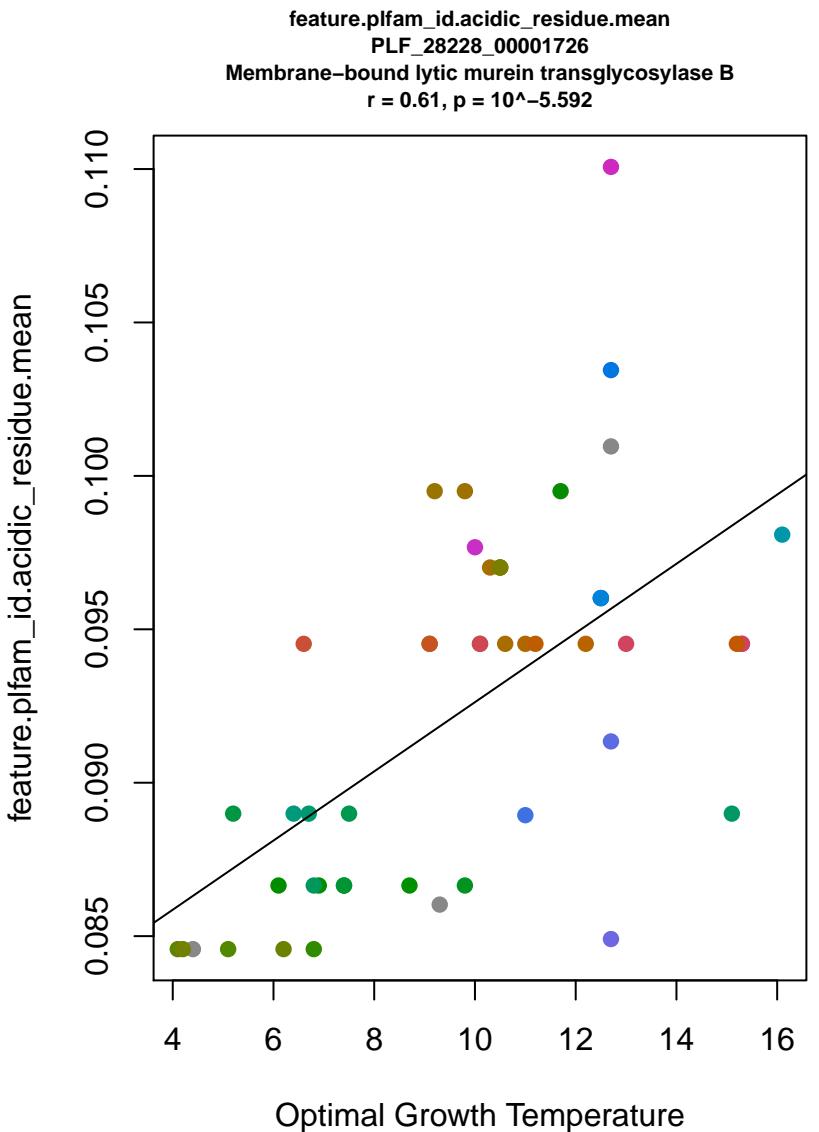
feature.plfam_id.acidic_residue.mean



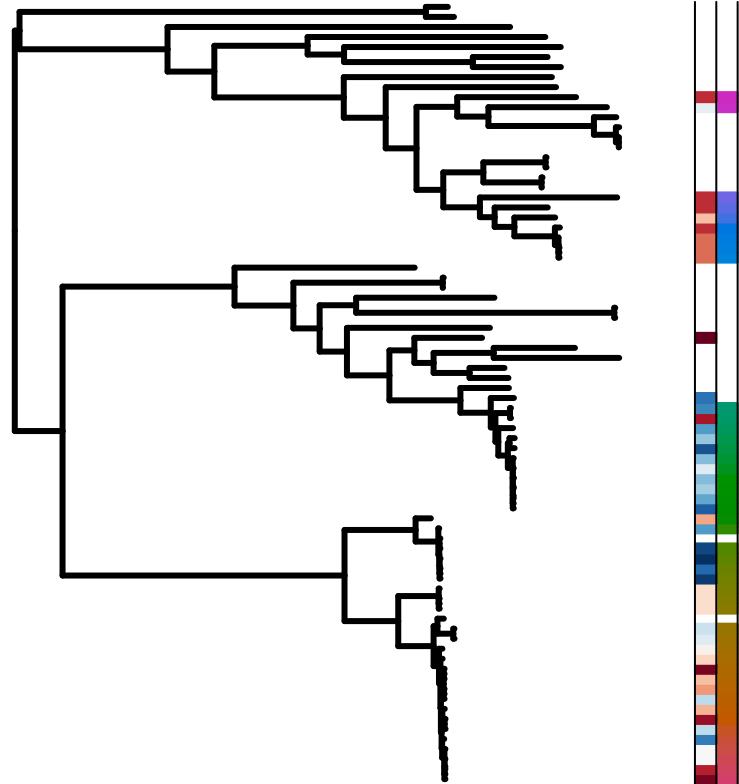
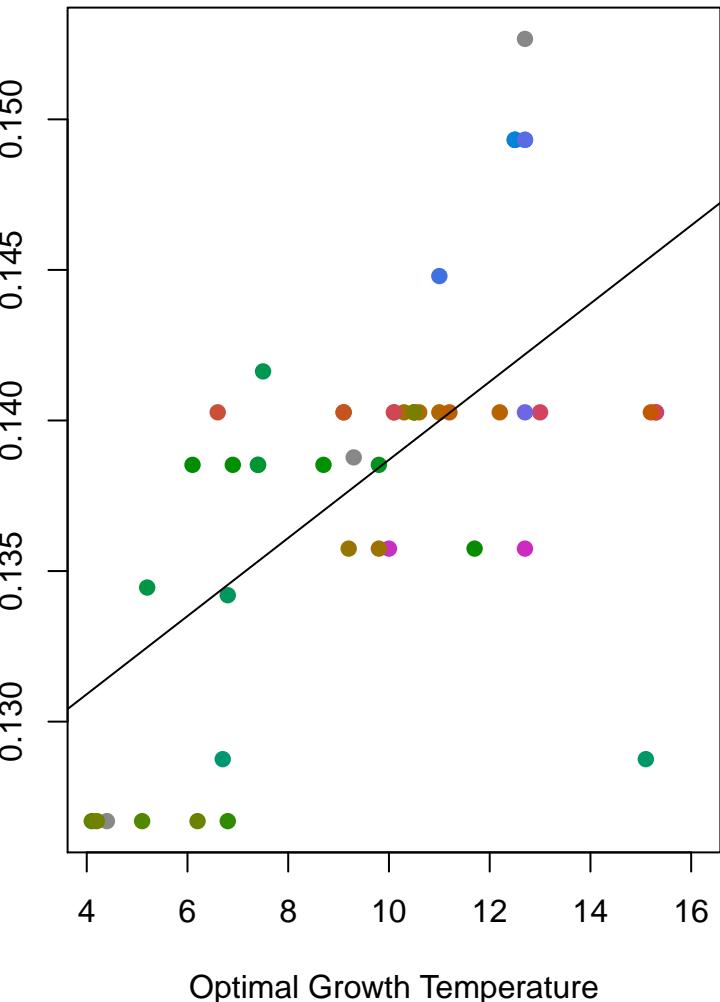
feature.plfam_id.acidic_residue.mean
PLF_28228_00022237
Serine acetyltransferase (EC 2.3.1.30)
 $r = 0.615, p = 10^{-5.476}$

feature.plfam_id.acidic_residue.mean

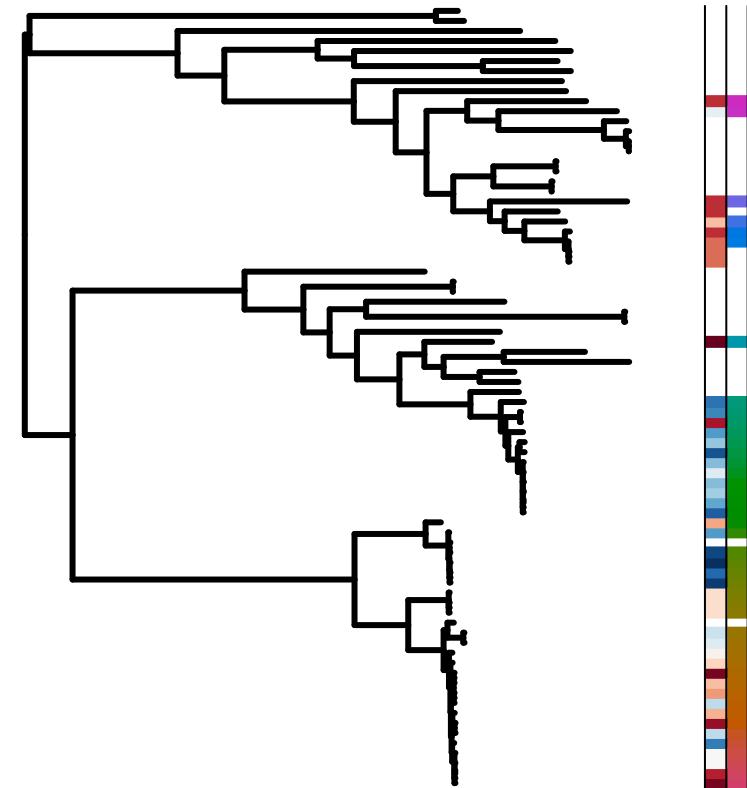
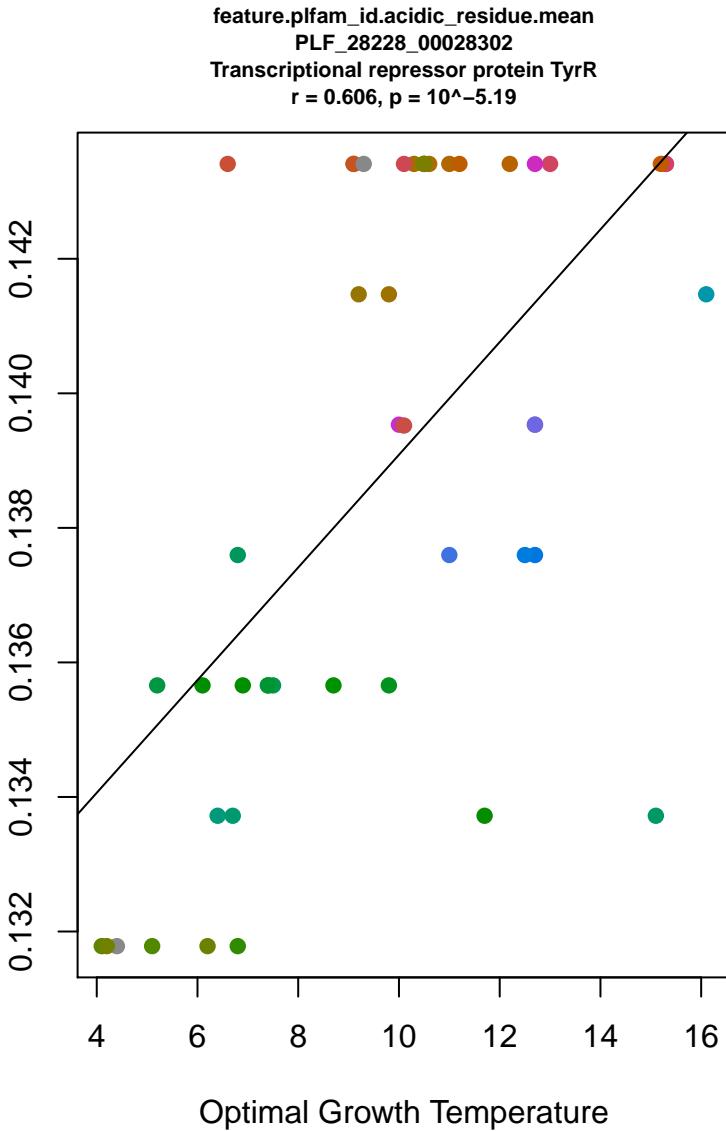




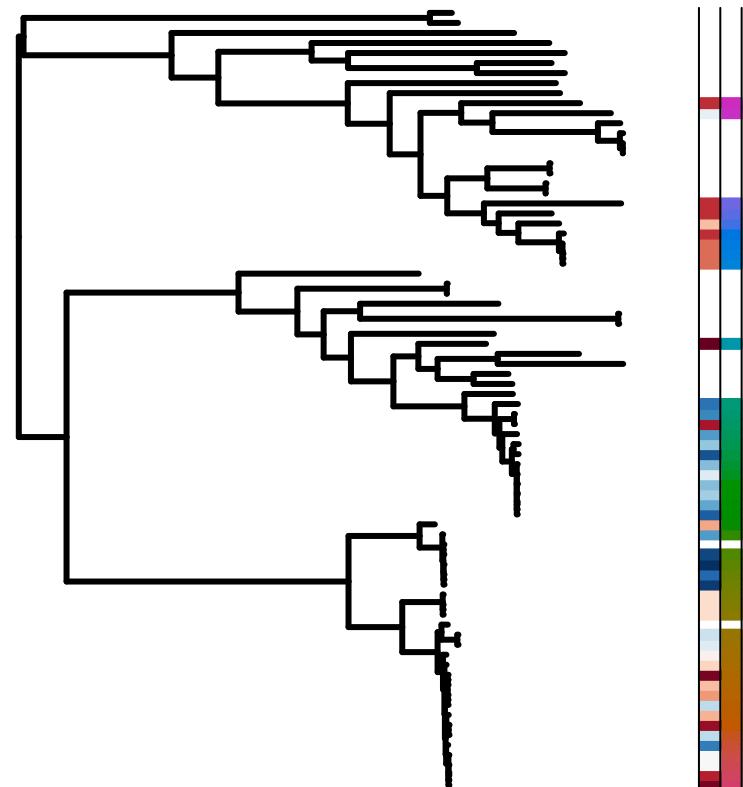
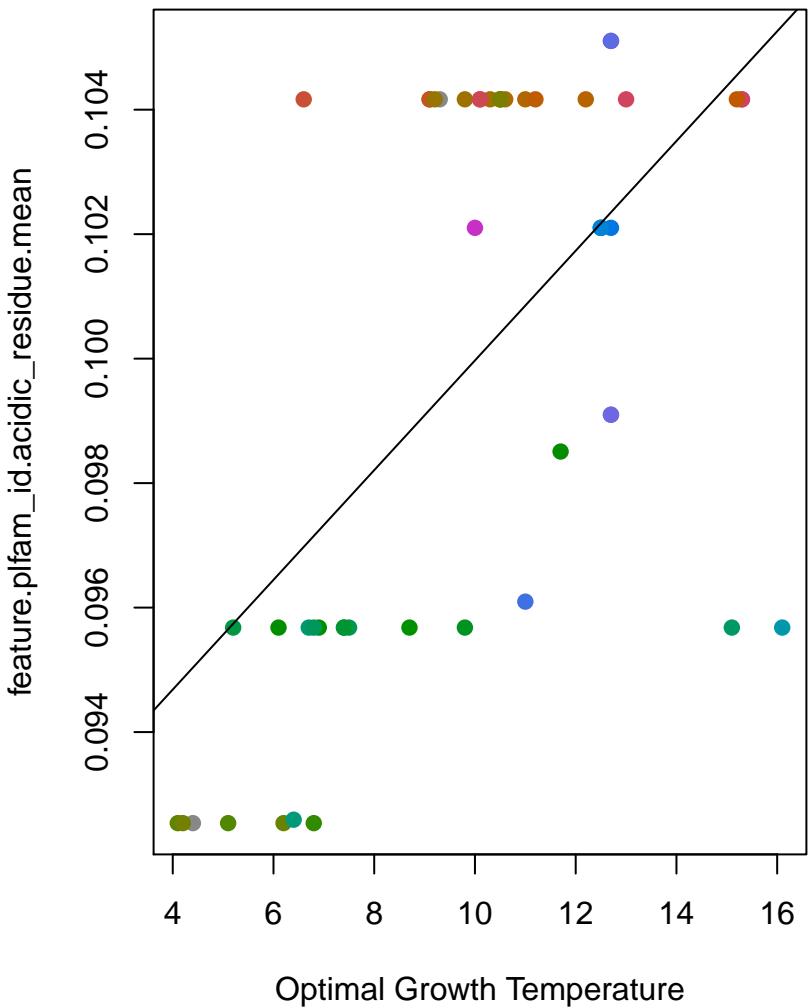
feature.plfam_id.acidic_residue.mean
PLF_28228_00001009
Protein of unknown function YceH
 $r = 0.608, p = 10^{-5.342}$



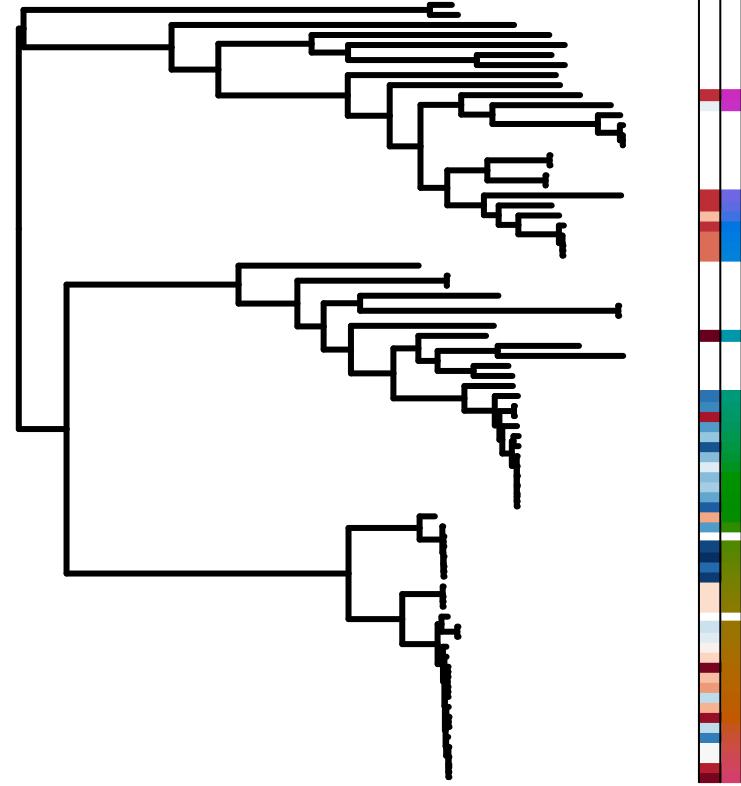
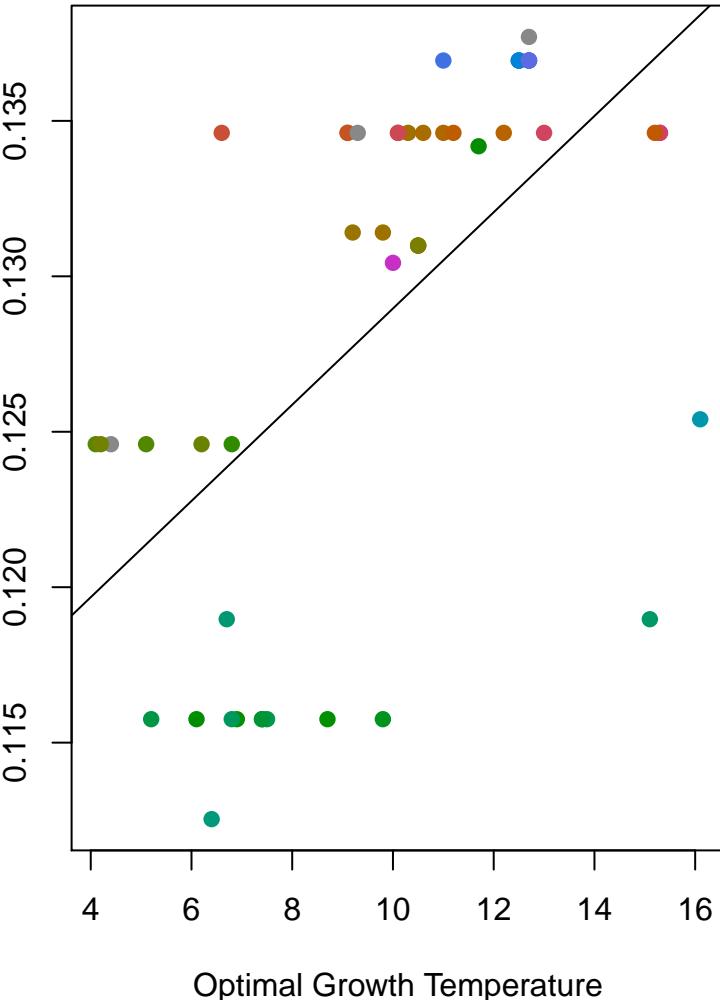
feature_pfam_id.acidic_residue.mean
PLF_28228_00028302
Transcriptional repressor protein TyrR
 $r = 0.606$, $p = 10^{-5.19}$



feature.plfam_id.acidic_residue.mean
PLF_28228_00000392
Biotin operon repressor / Biotin--protein ligase (EC 6.3.4.9)(EC 6.3.4.10)(EC 6.3.4.11)(EC 6.3.4.15)
 $r = 0.6$, $p = 10^{-5.393}$

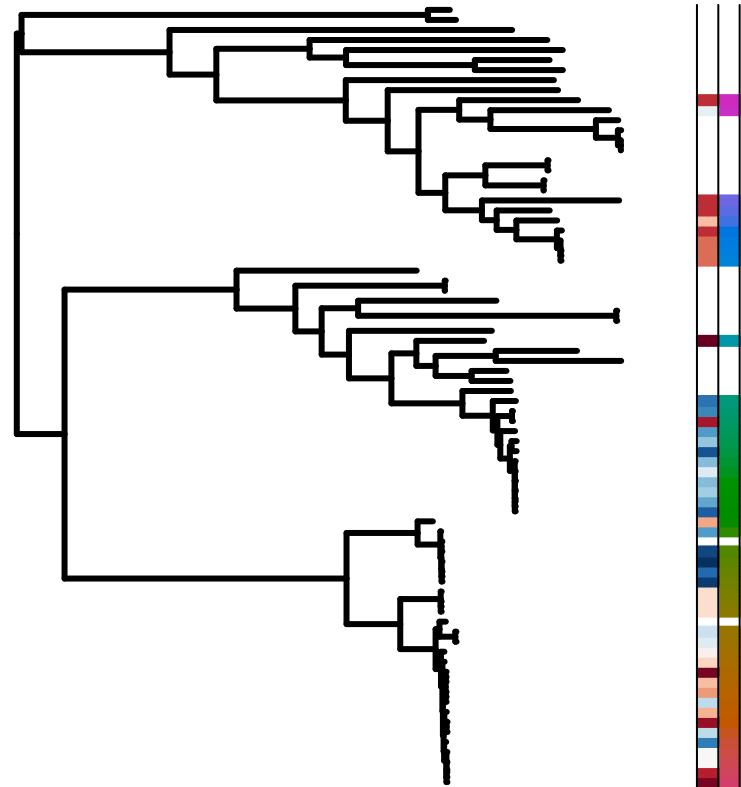
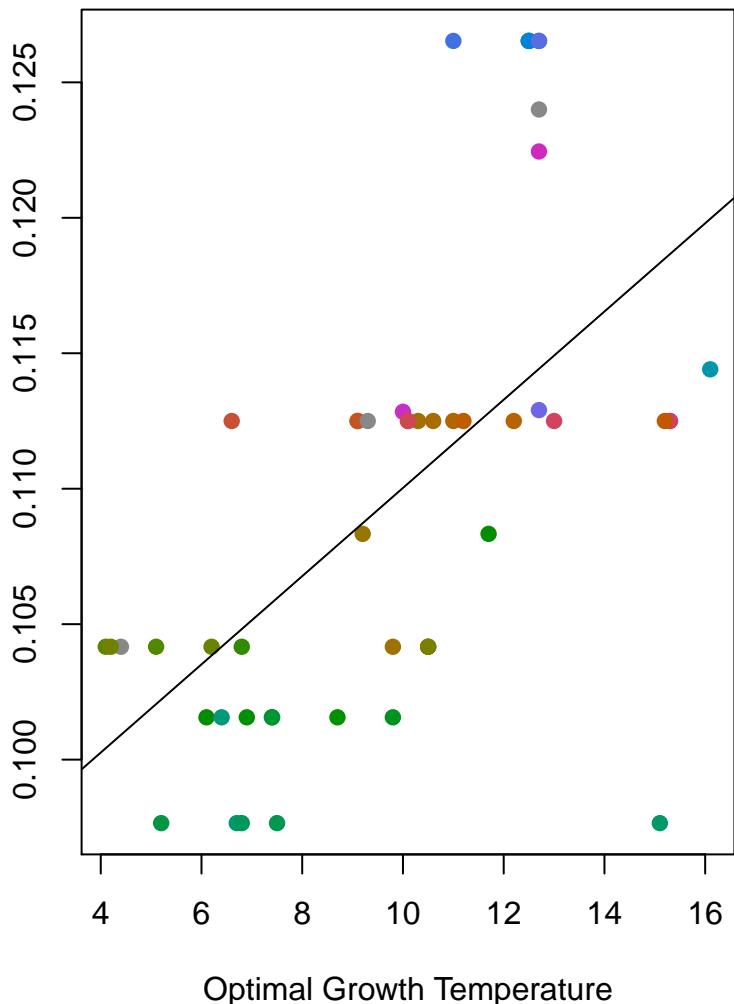


feature.plfam_id.acidic_residue.mean
PLF_28228_00000841
Flagellar motor rotation protein MotB
 $r = 0.597$, $p = 10^{-5.328}$



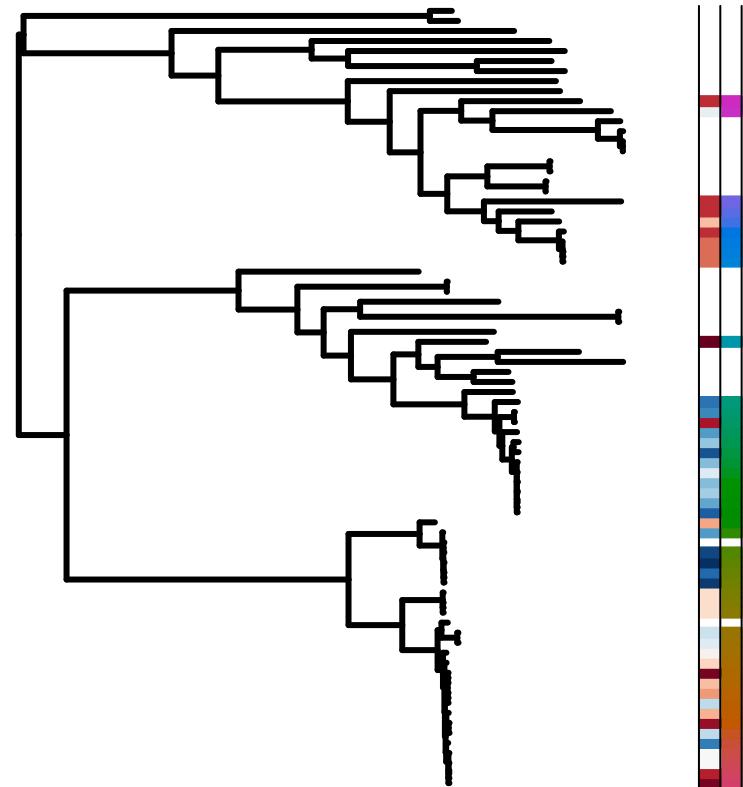
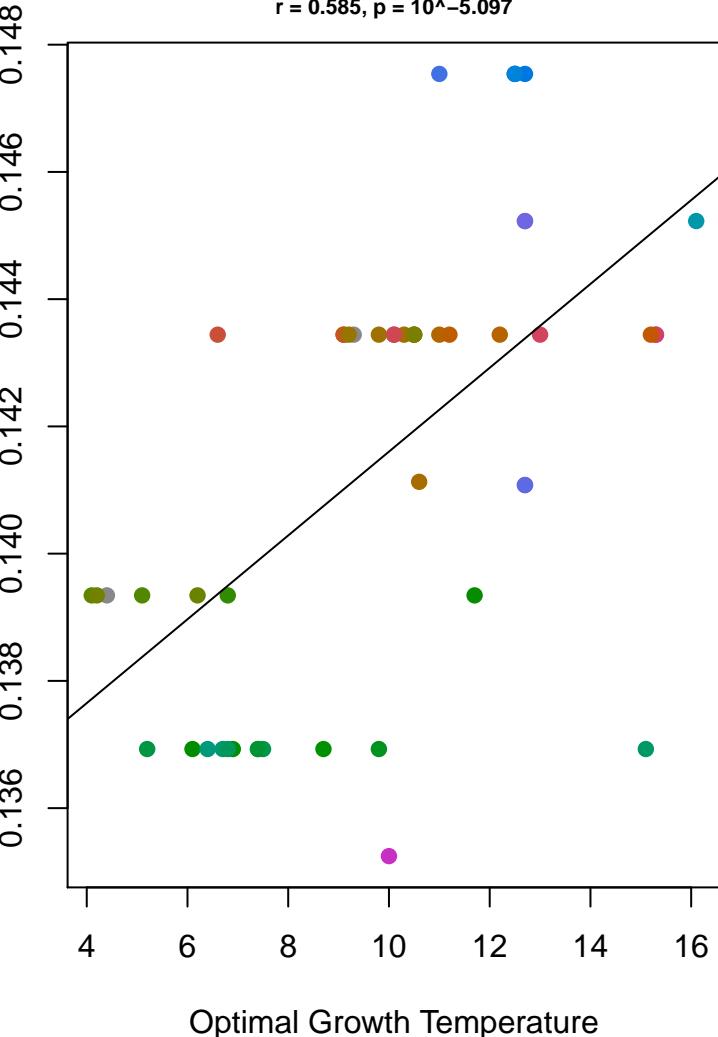
feature.plfam_id.acidic_residue.mean
PLF_28228_00000498
Histidine utilization repressor
 $r = 0.59$, $p = 10^{-5.179}$

feature.plfam_id.acidic_residue.mean



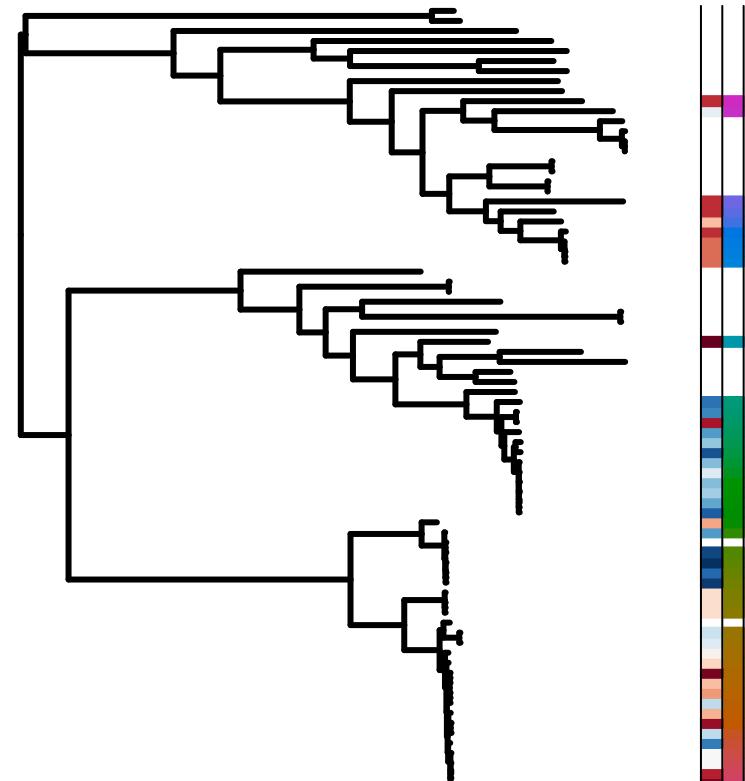
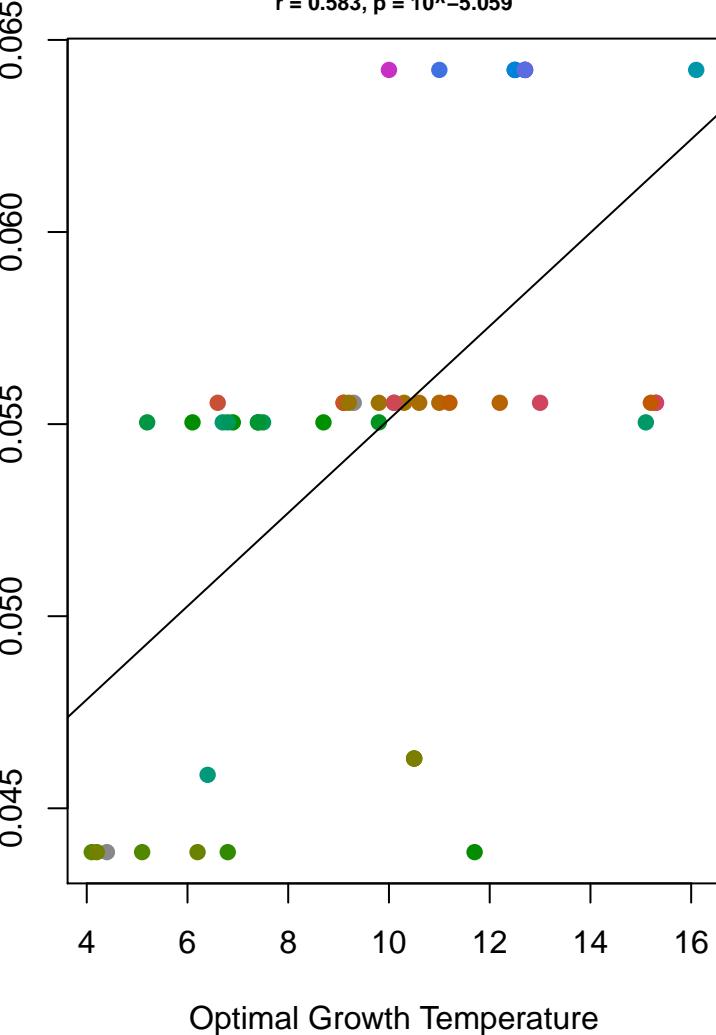
feature.plfam_id.acidic_residue.mean
PLF_28228_00001398
tRNA (guanine(46)-N(7))-methyltransferase (EC 2.1.1.33)
 $r = 0.585$, $p = 10^{-5.097}$

feature.plfam_id.acidic_residue.mean

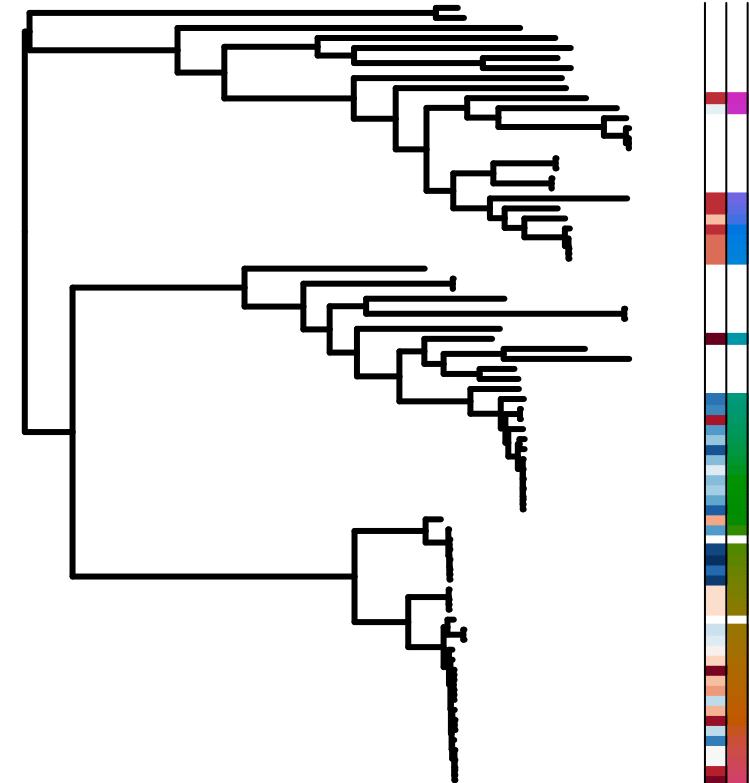
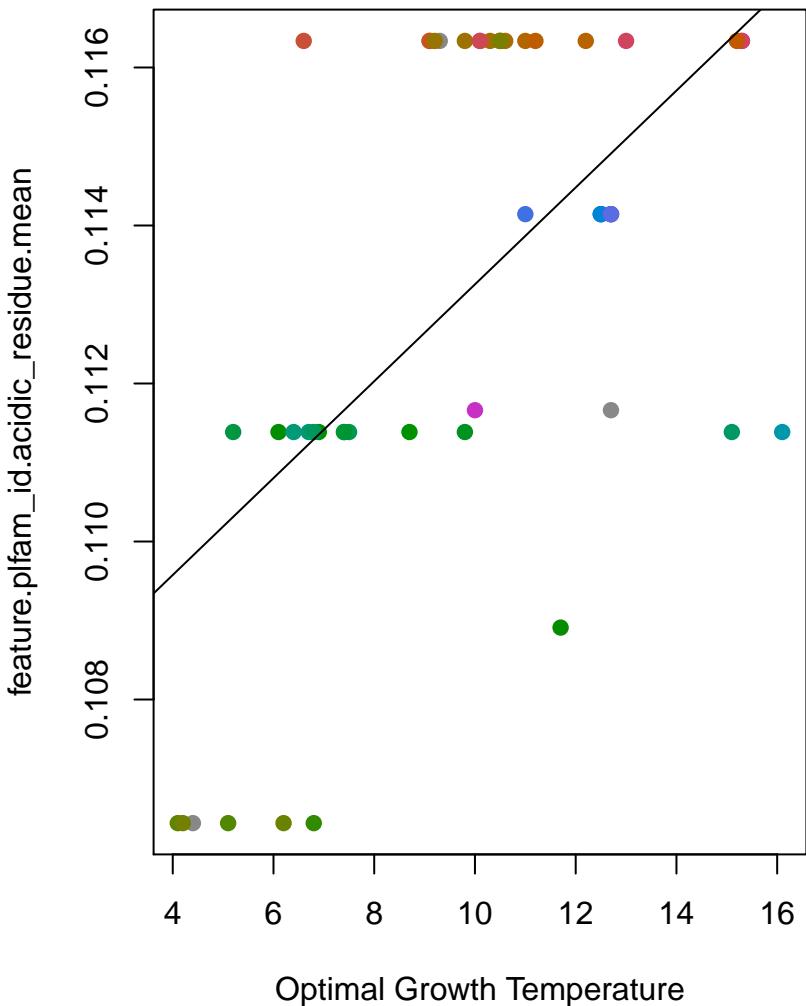


feature.plfam_id.acidic_residue.mean
PLF_28228_00001687
FIG020302: hypothetical protein
 $r = 0.583$, $p = 10^{-5.059}$

feature.plfam_id.acidic_residue.mean



feature.pfam_id.acidic_residue.mean
PLF_28228_00000083
Succinylornithine transaminase (EC 2.6.1.81)
 $r = 0.581, p = 10^{-5.011}$



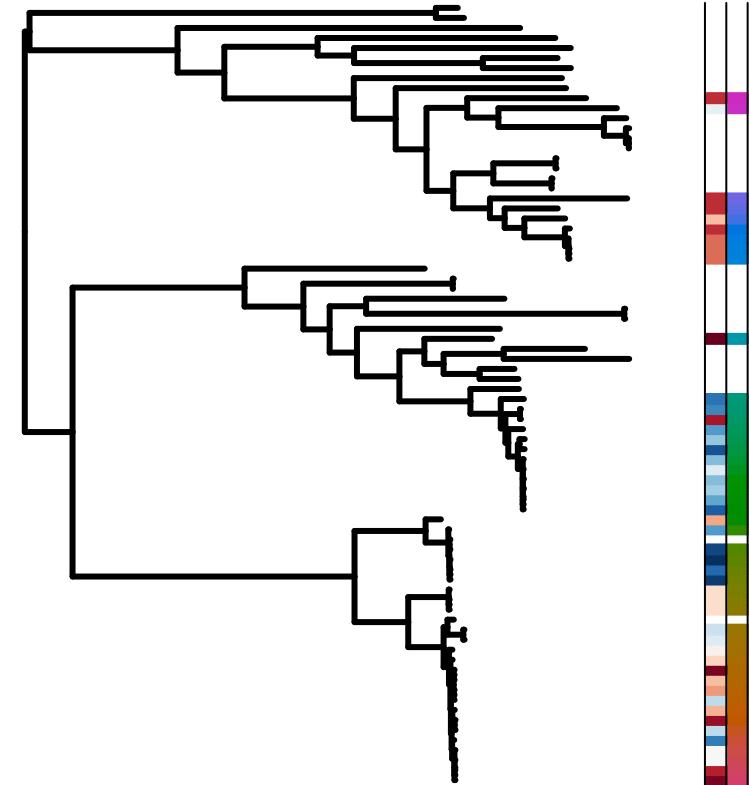
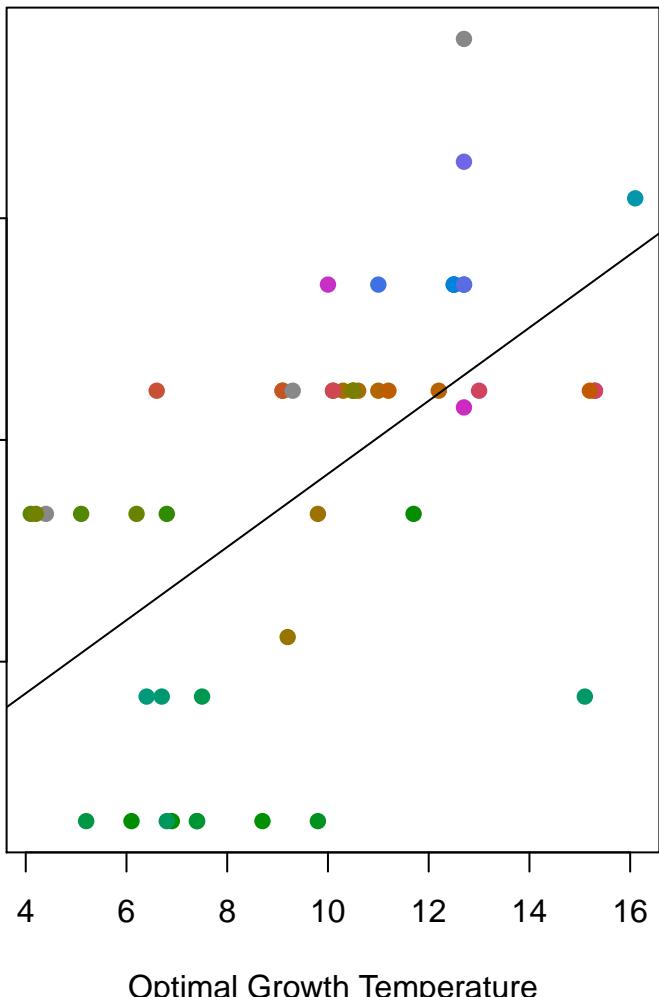
feature.plfam_id.acidic_residue.mean

PLF_28228_00000500

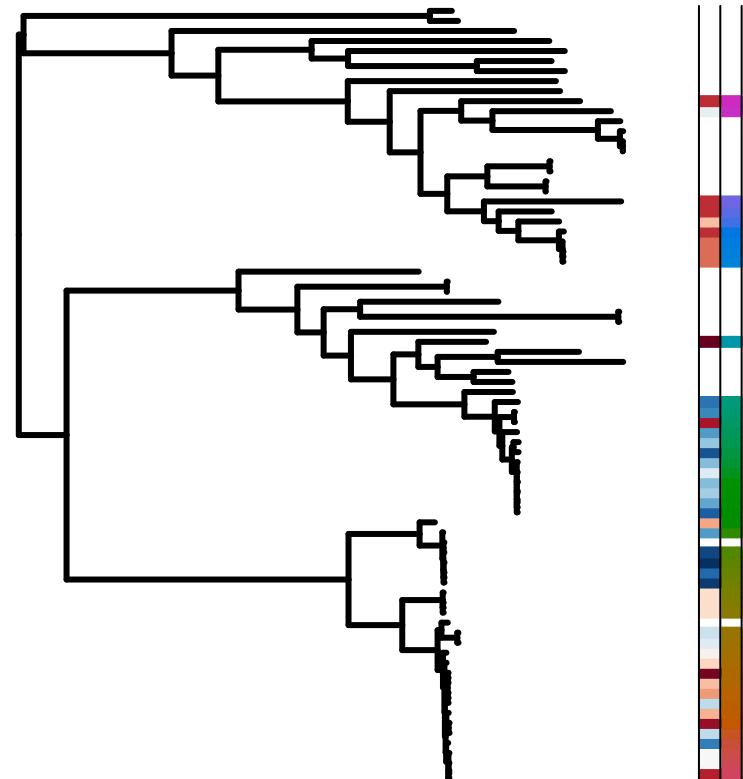
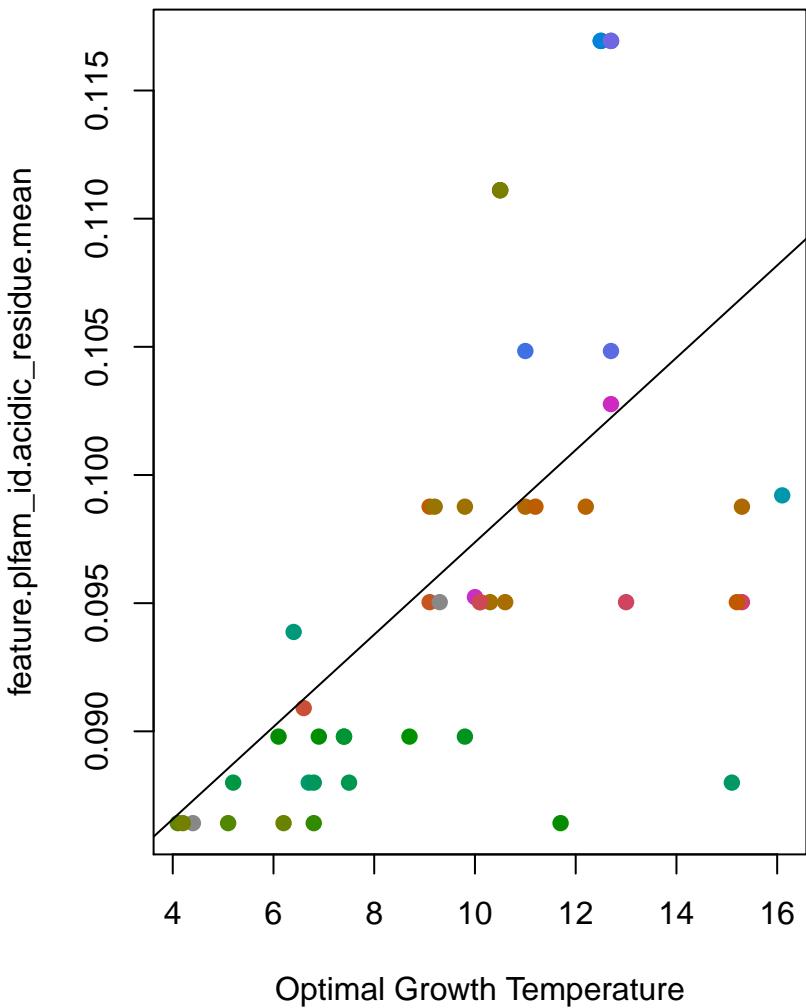
Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)

$r = 0.58, p = 10^{-4.99}$

feature.plfam_id.acidic_residue.mean

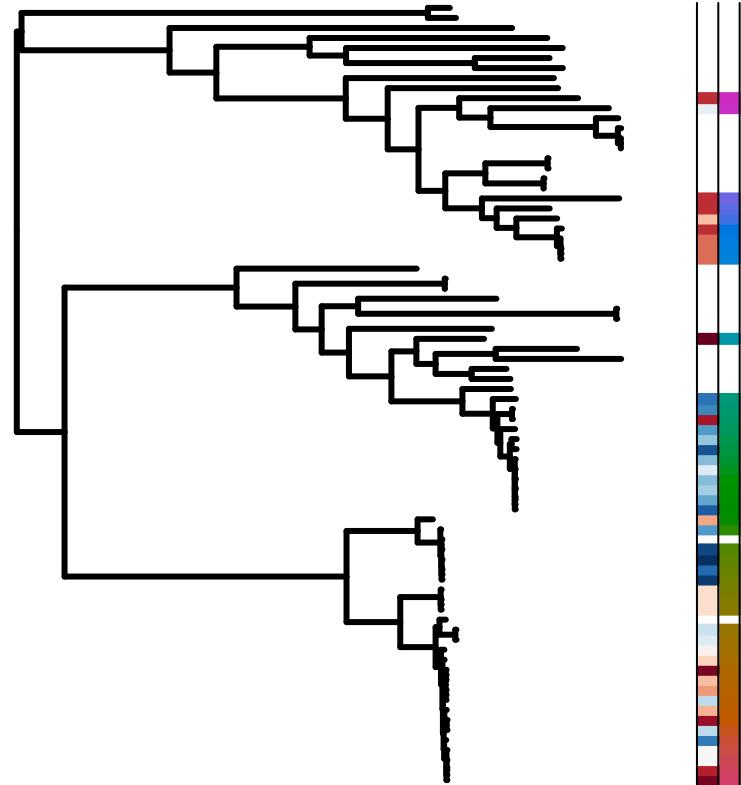
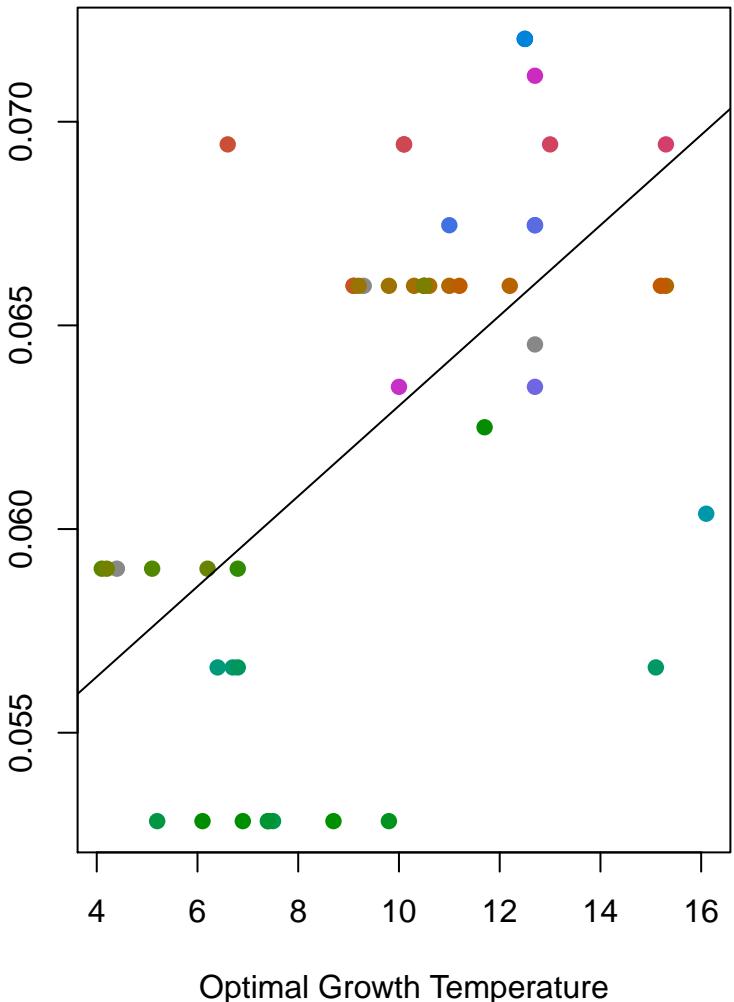


feature.plfam_id.acidic_residue.mean
PLF_28228_00001104
tRNA (adenine(37)-N6)-methyltransferase
 $r = 0.577$, $p = 10^{-4.945}$



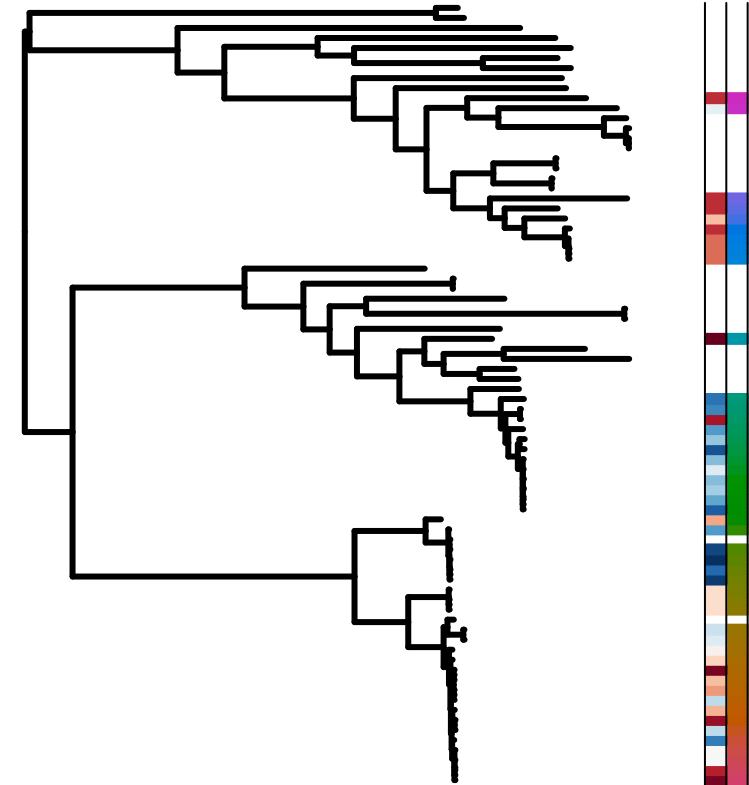
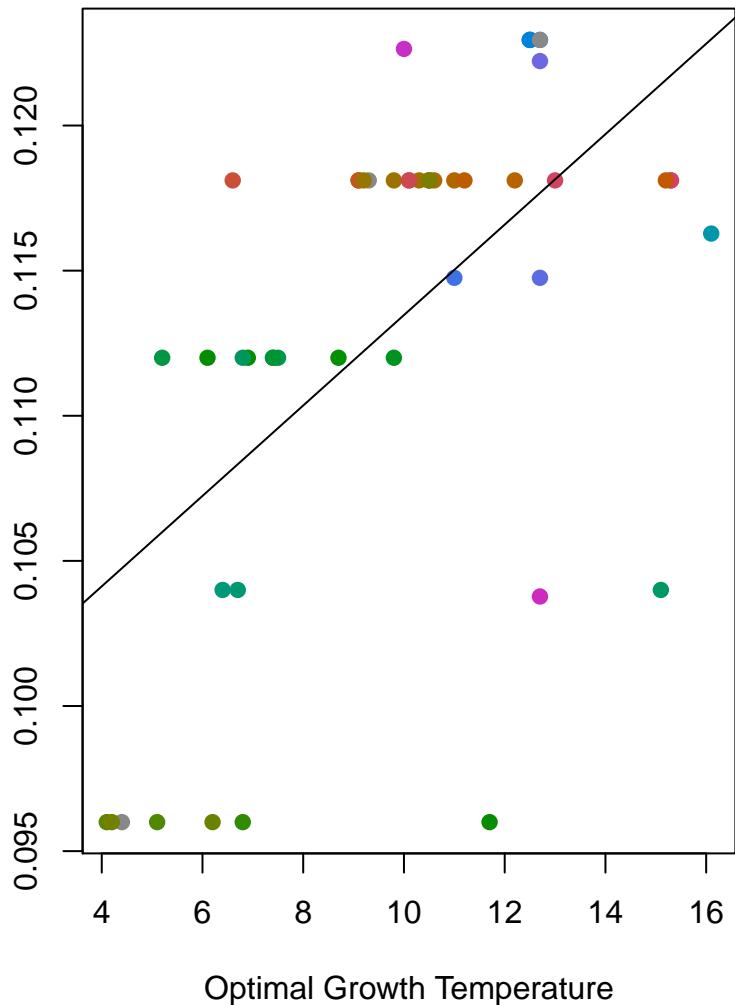
feature.plfam_id.acidic_residue.mean
PLF_28228_00000831
Flagellar biosynthesis protein FliP
 $r = 0.577, p = 10^{-4.93}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00002263
hypothetical protein
 $r = 0.576, p = 10^{-4.927}$

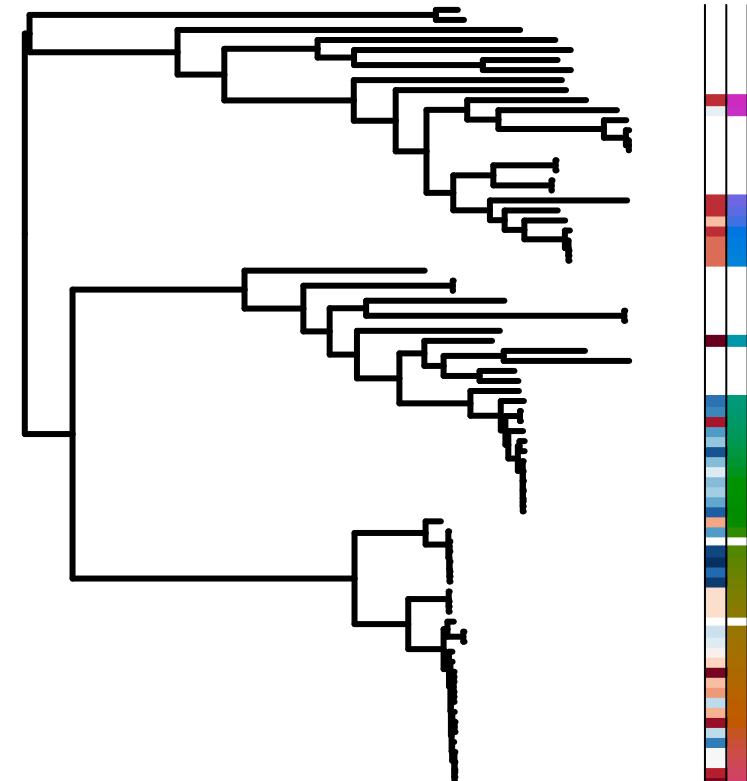
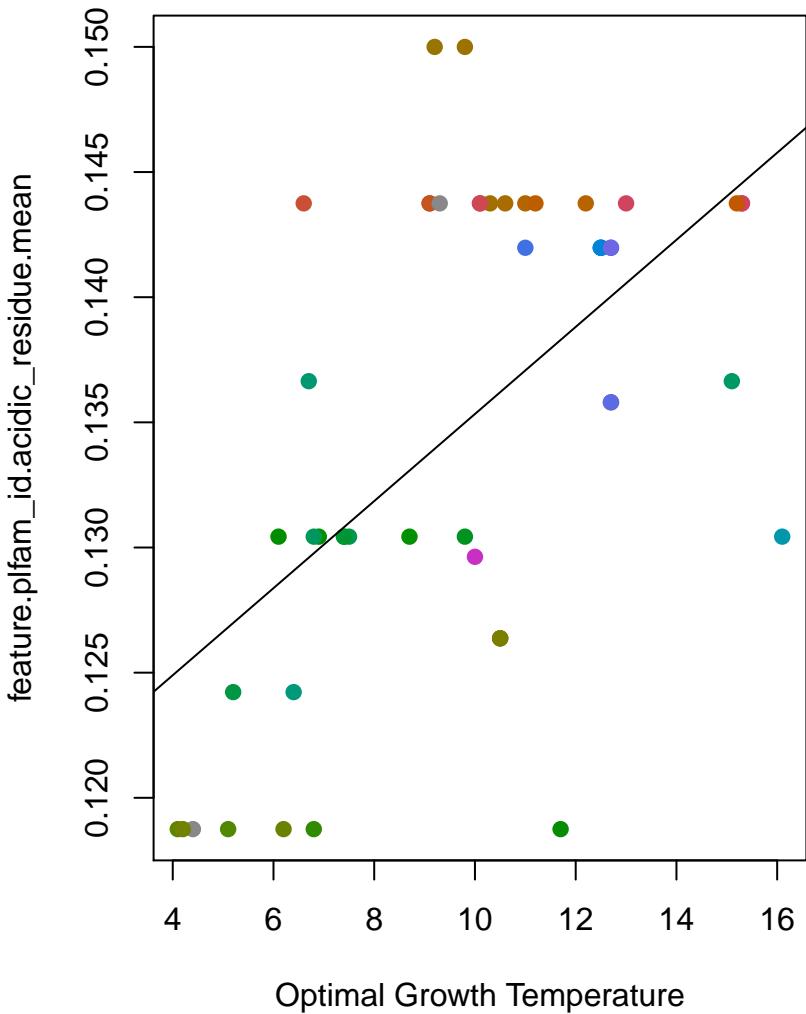
feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean

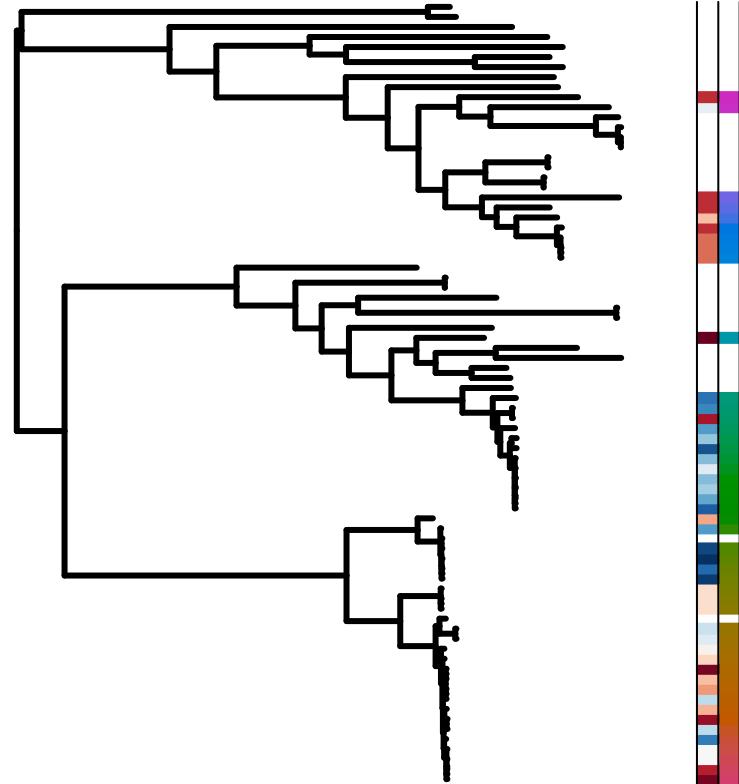
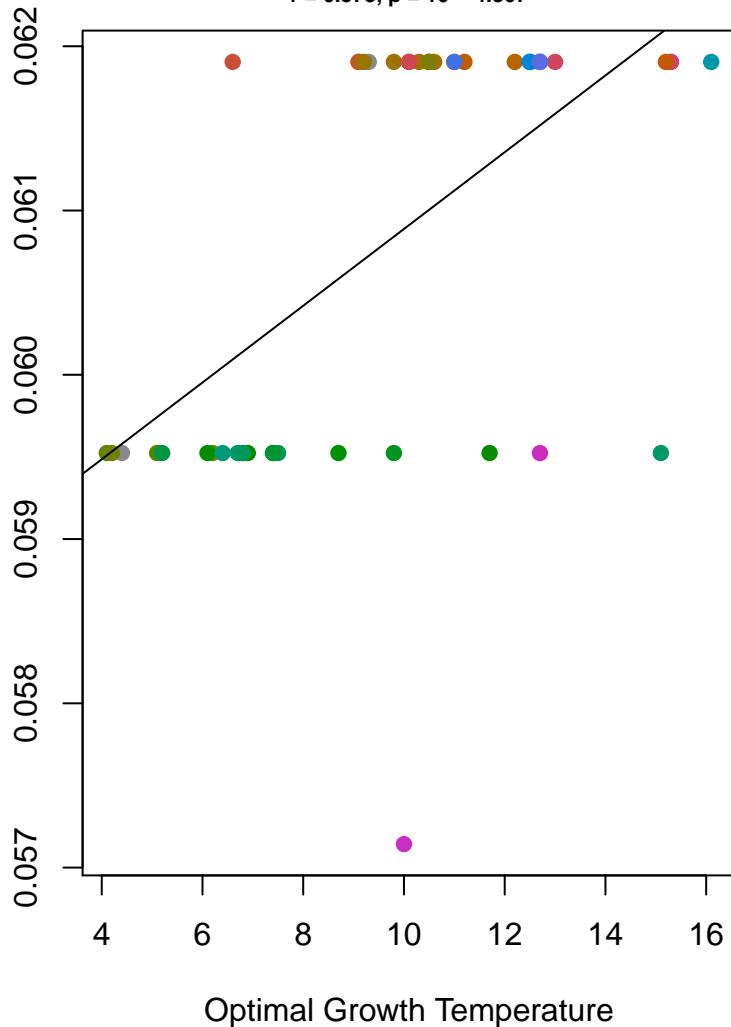
PLF_28228_00001249

tRNA threonylcarbamoyladenosine biosynthesis protein TsaE
 $r = 0.574, p = 10^{-4.784}$



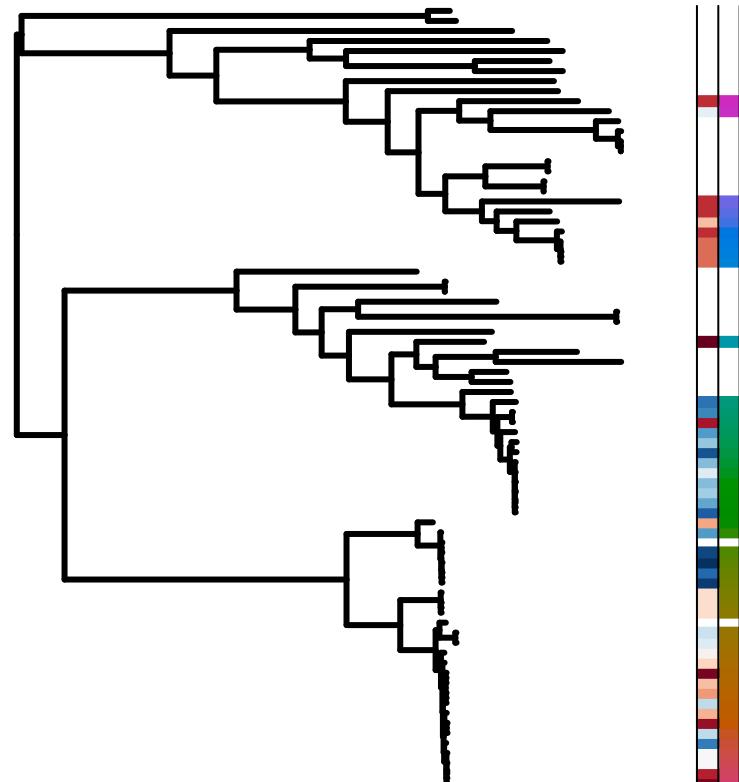
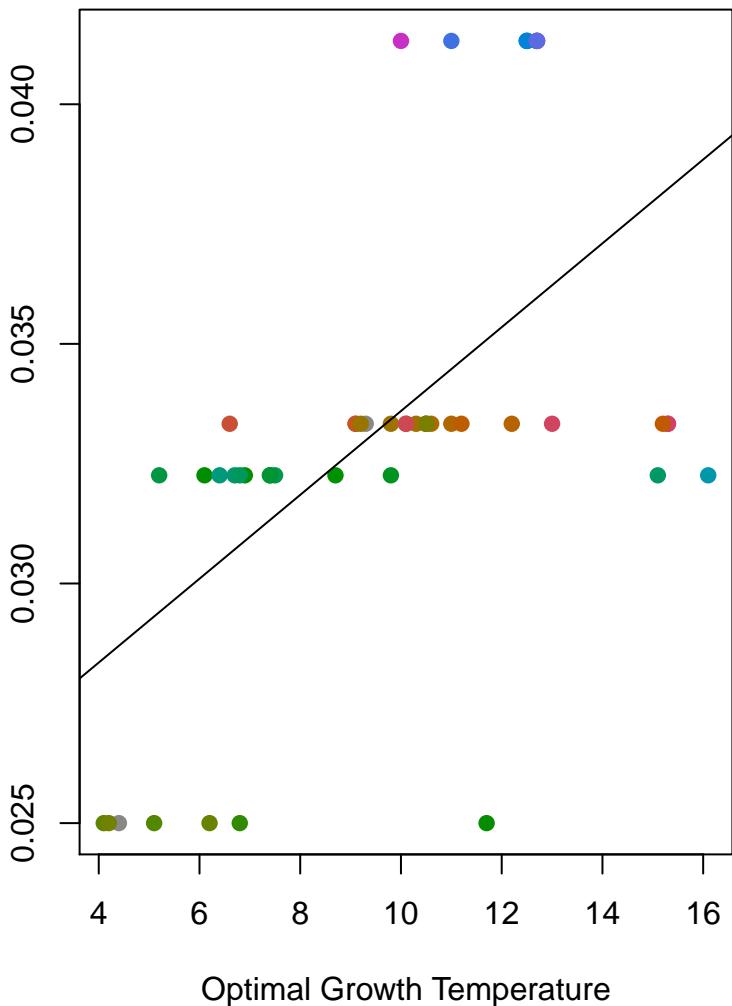
feature.plfam_id.acidic_residue.mean
PLF_28228_00000359
DUF819 domain-containing protein
 $r = 0.573$, $p = 10^{-4.867}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00001535
FIG002082: Protein SirB2
 $r = 0.573$, $p = 10^{-4.865}$

feature.plfam_id.acidic_residue.mean



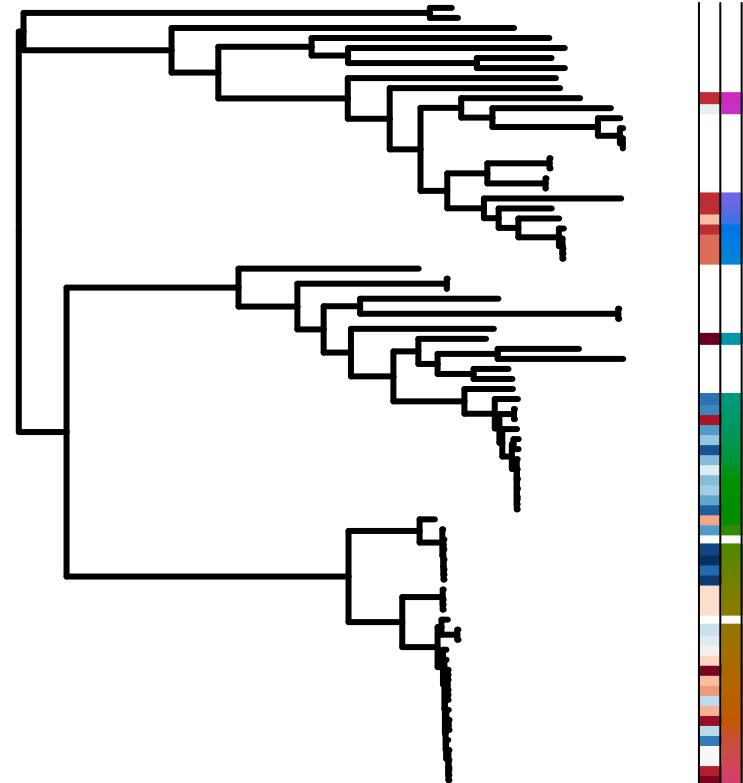
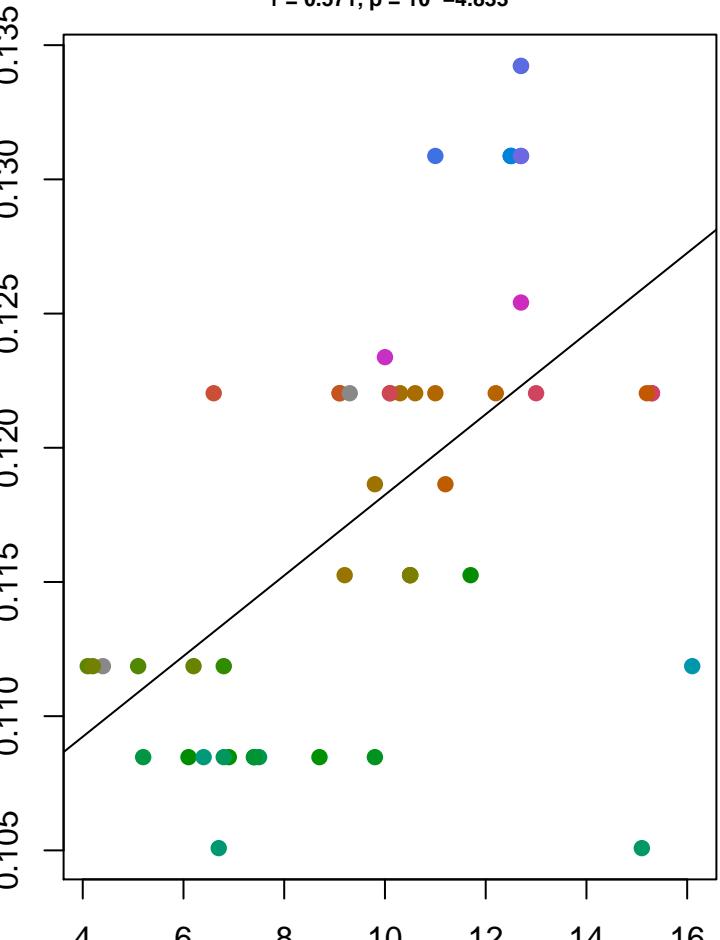
feature.plfam_id.acidic_residue.mean

PLF_28228_00001035

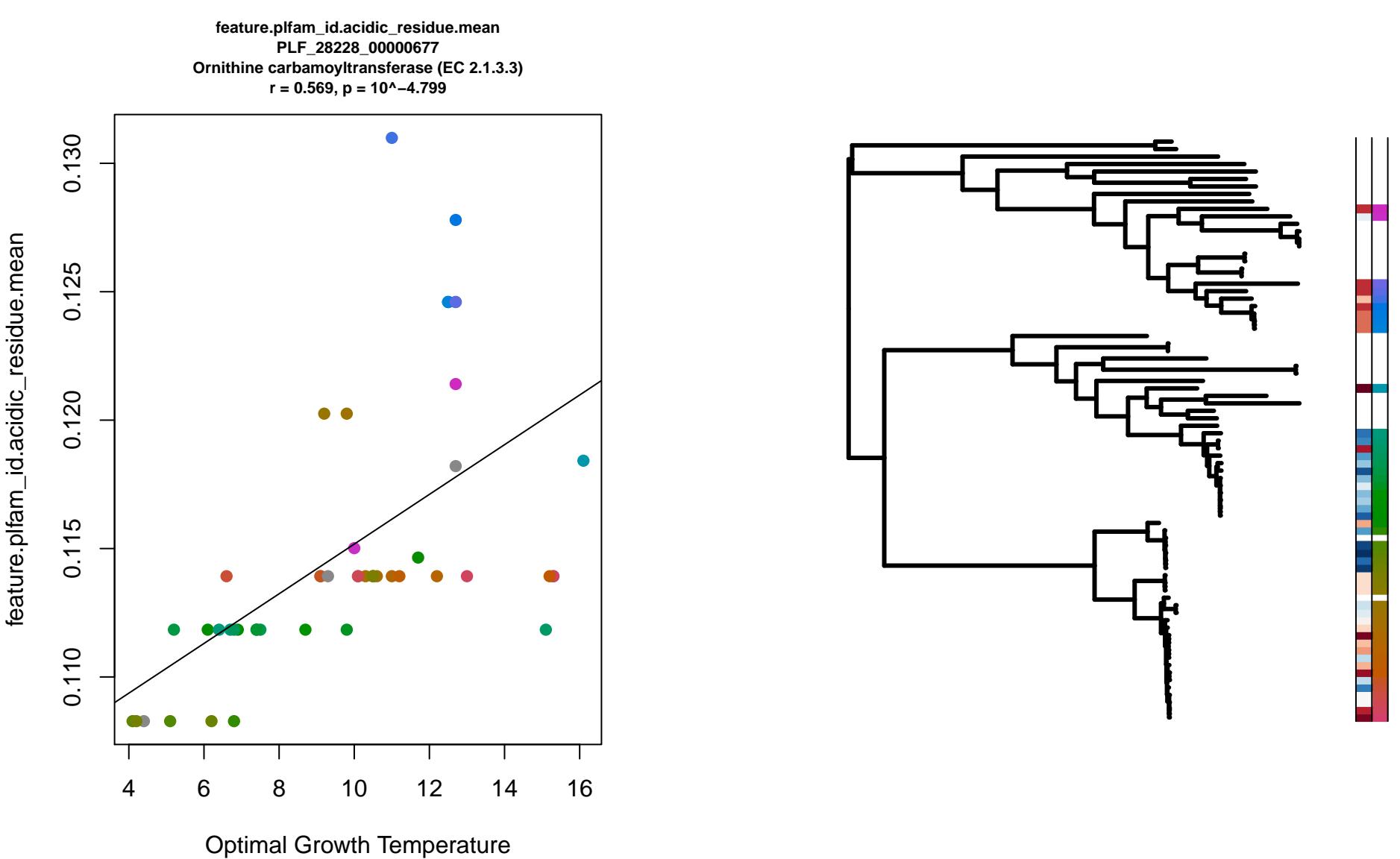
Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)

$r = 0.571$, $p = 10^{-4.833}$

feature.plfam_id.acidic_residue.mean

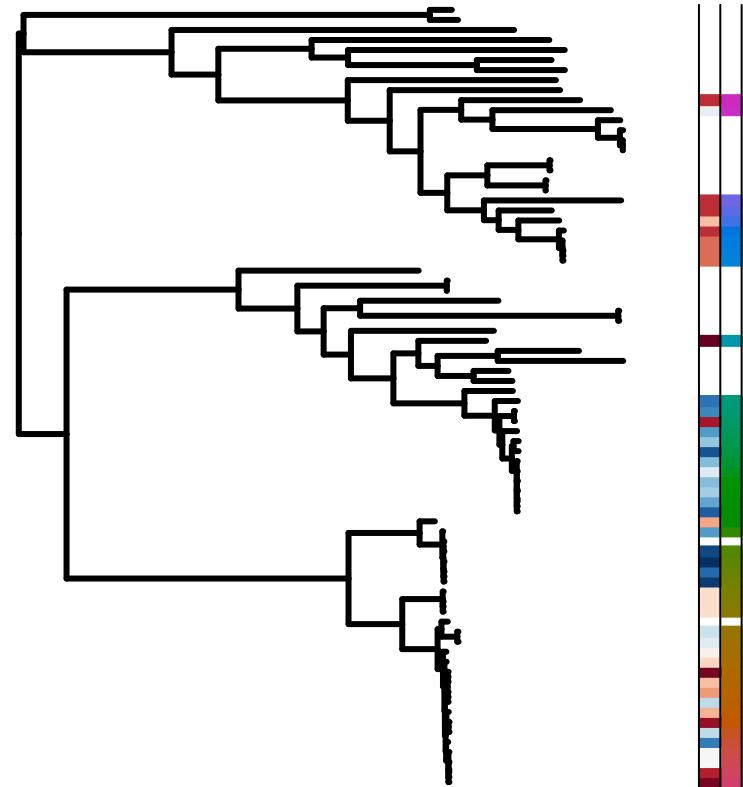
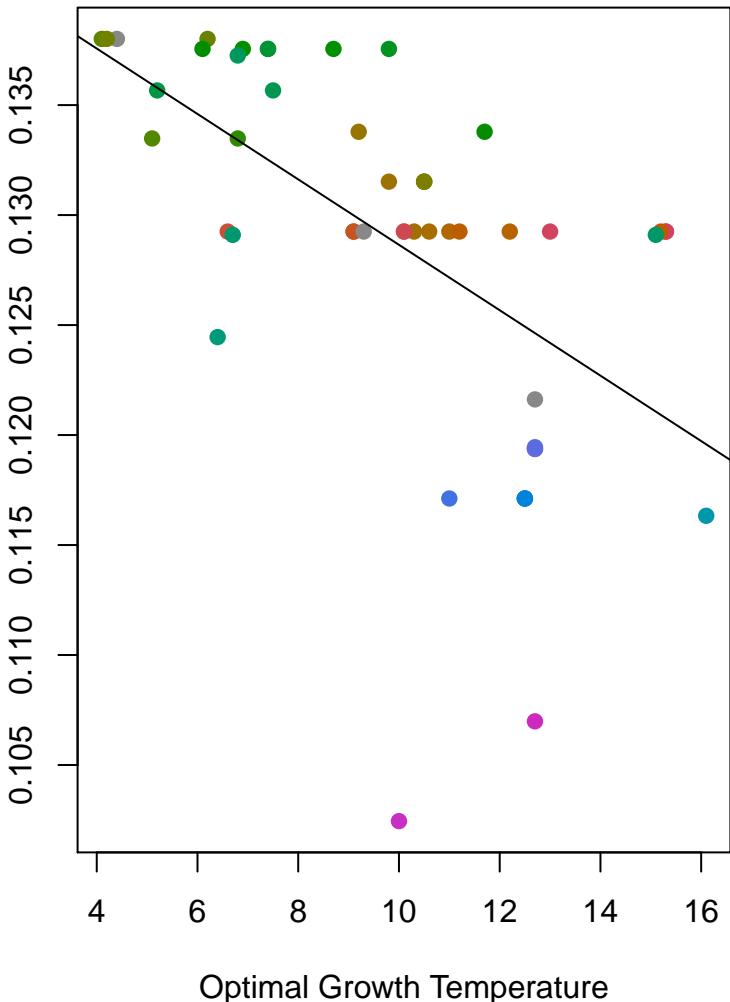


Optimal Growth Temperature



feature.plfam_id.acidic_residue.mean
PLF_28228_00002282
hypothetical protein
 $r = -0.572$, $p = 10^{-4.85}$

feature.plfam_id.acidic_residue.mean

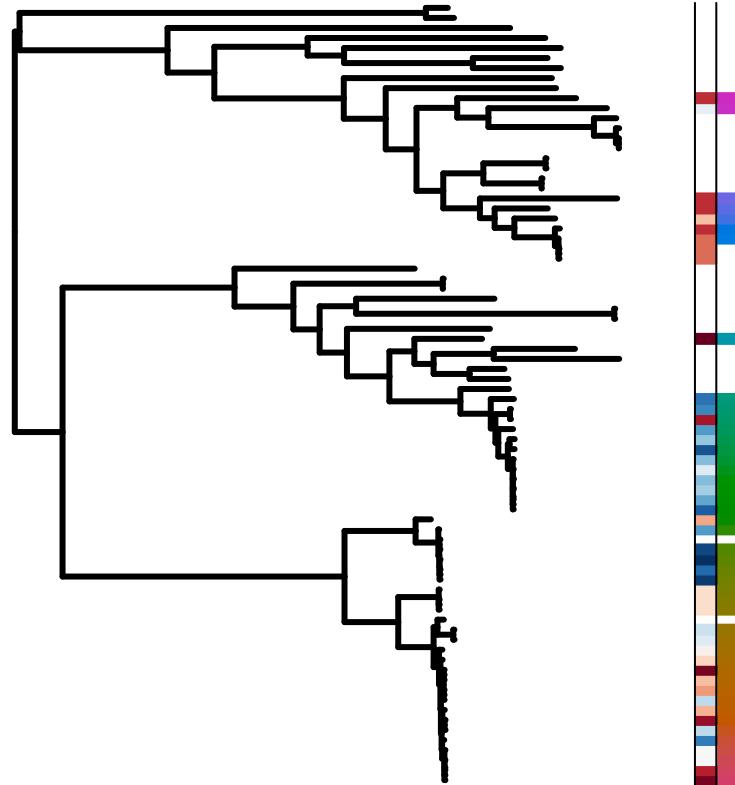
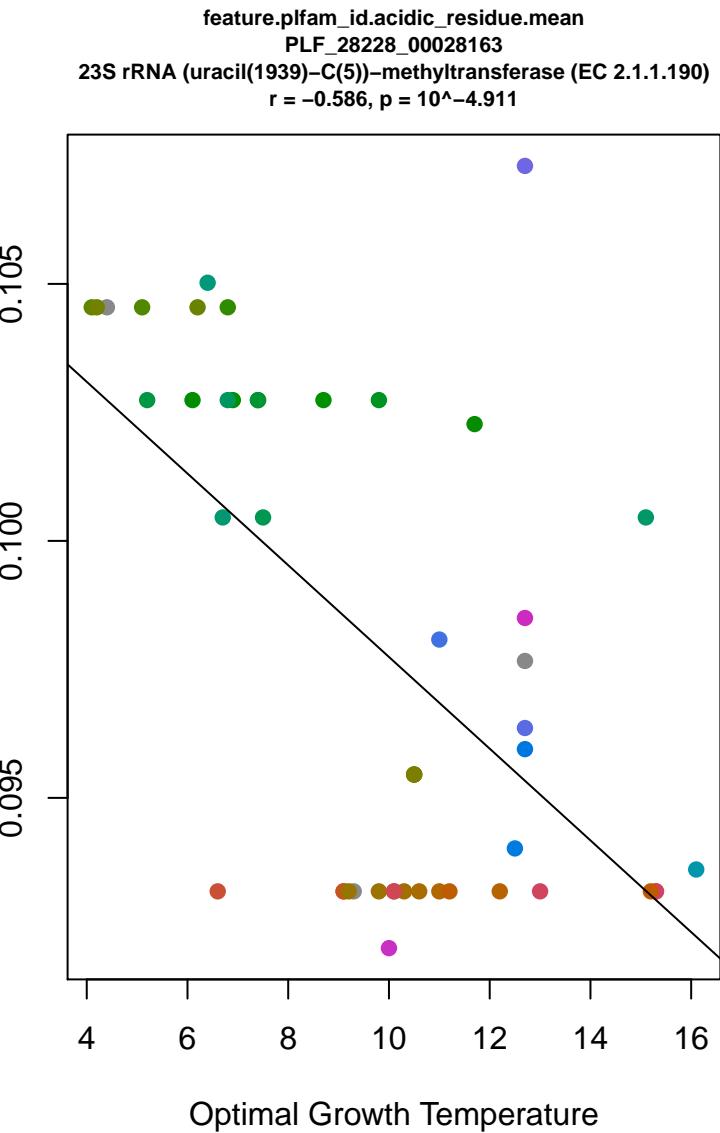


feature.plfam_id.acidic_residue.mean

PLF_28228_00028163

23S rRNA (uracil(1939)-C(5))-methyltransferase (EC 2.1.1.190)

$r = -0.586, p = 10^{-4.911}$

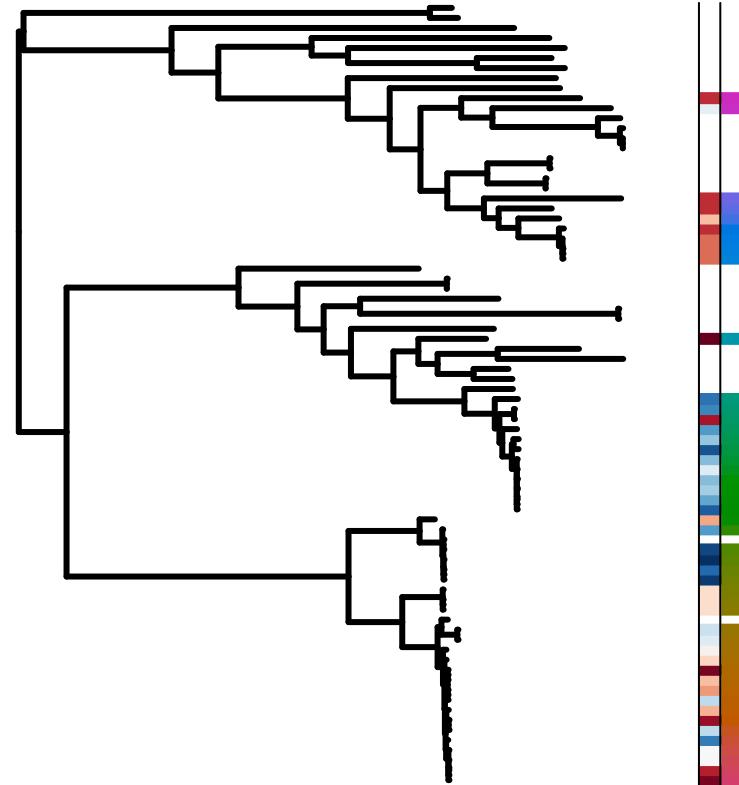
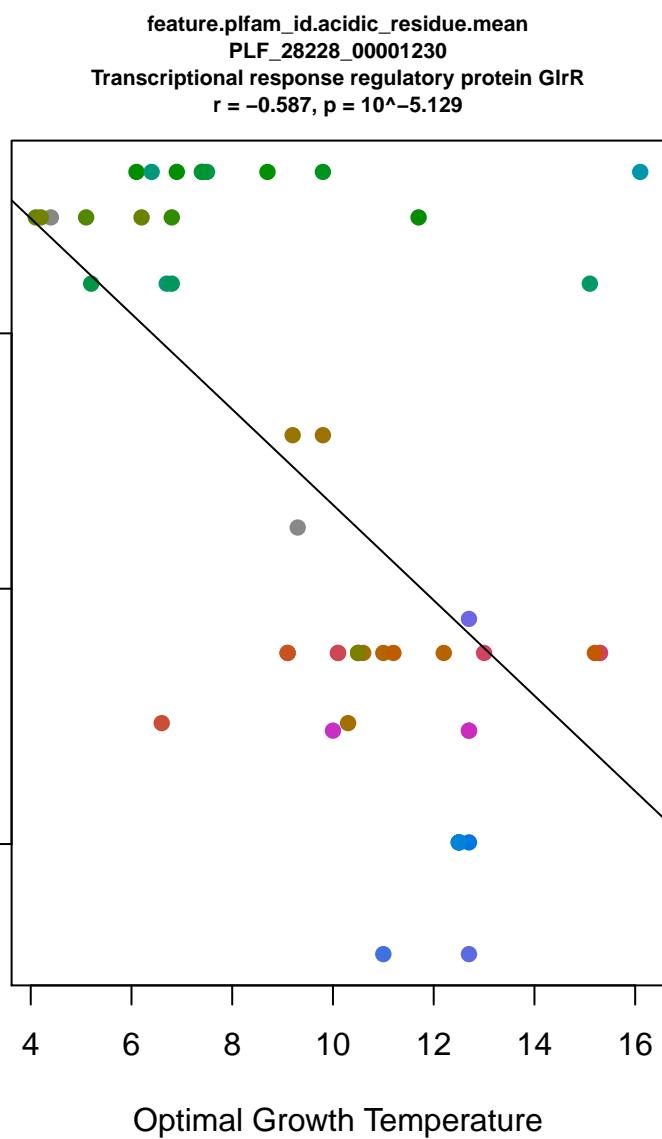


feature.plfam_id.acidic_residue.mean

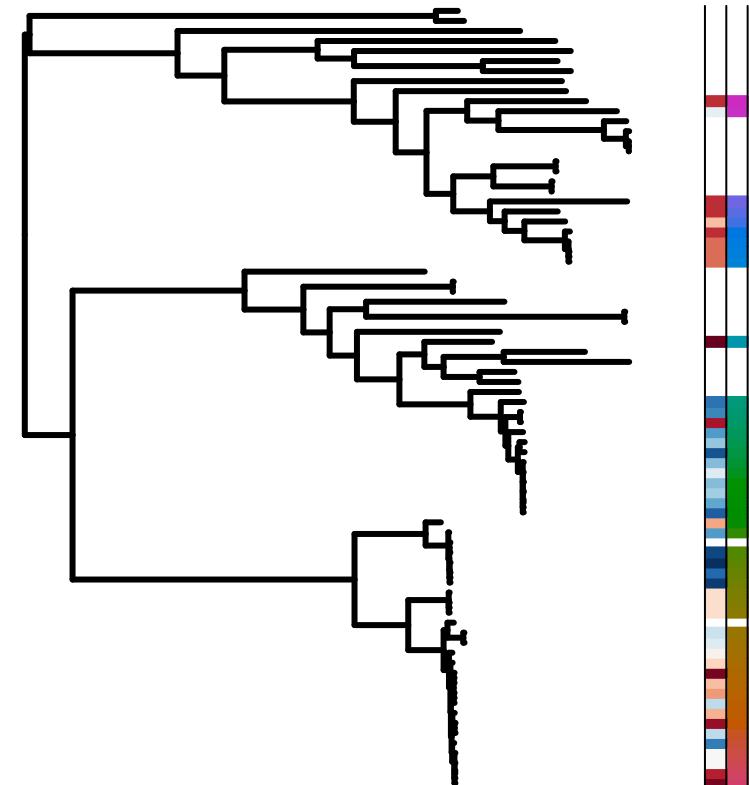
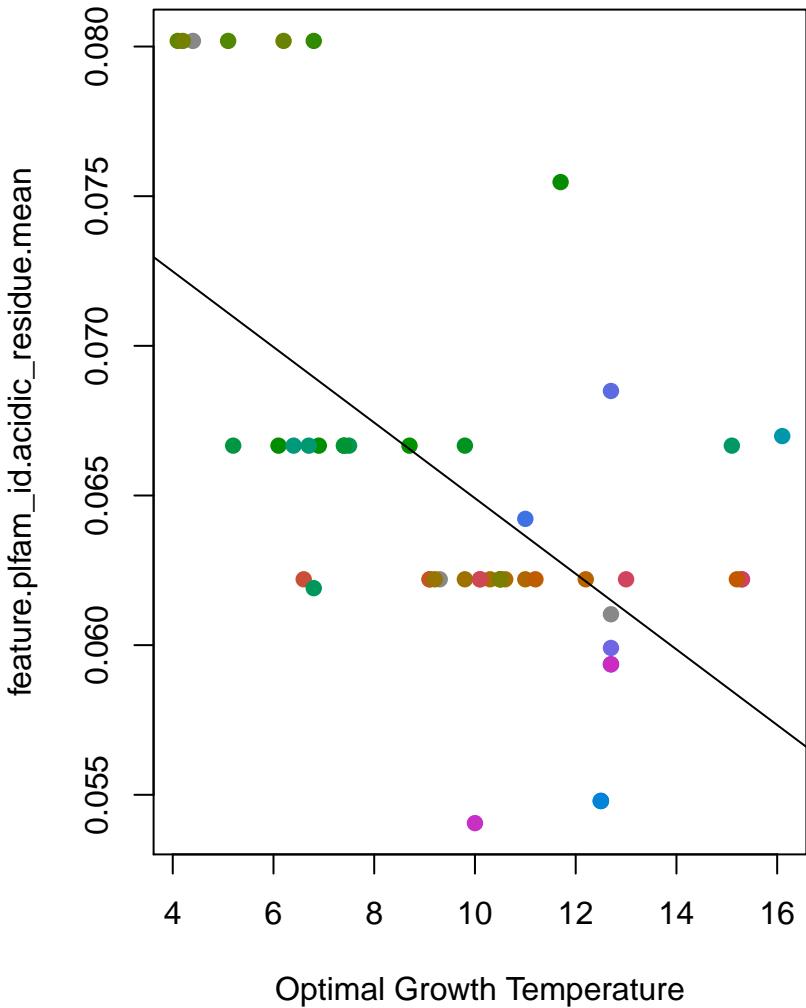
PLF_28228_00001230

Transcriptional response regulatory protein GlrR

$r = -0.587$, $p = 10^{-5.129}$

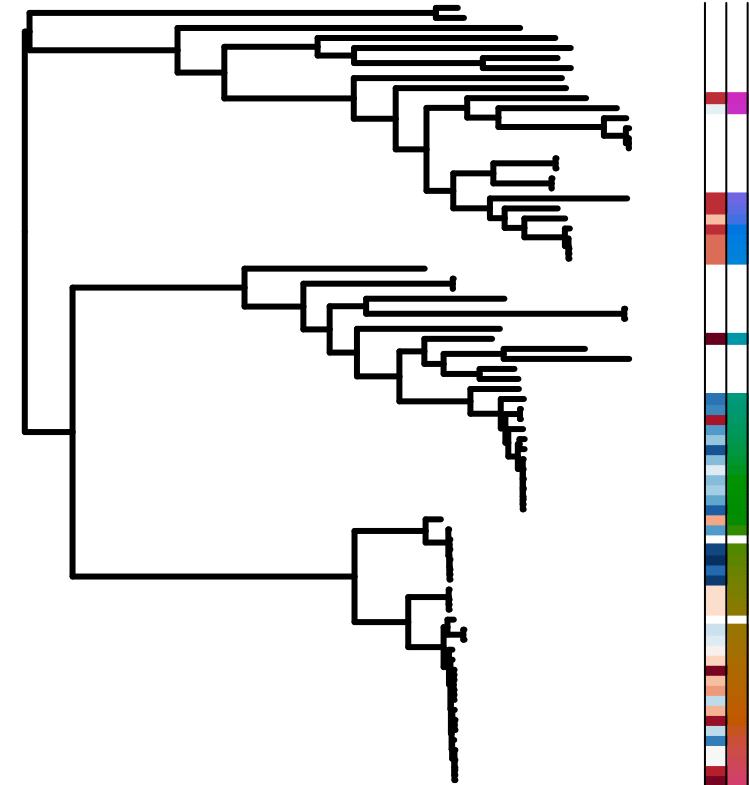
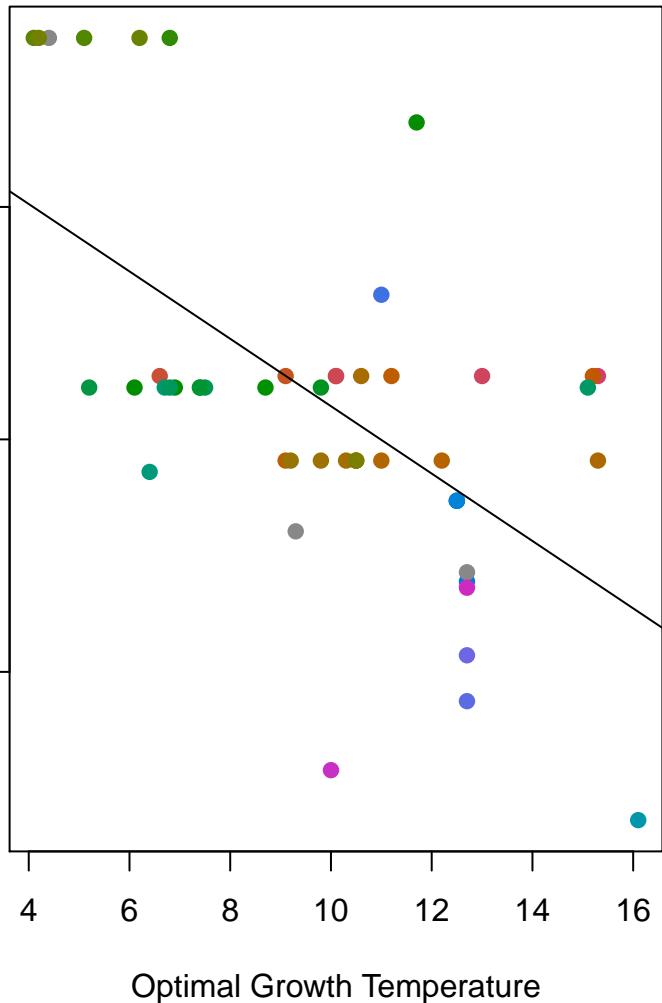


feature.plfam_id.acidic_residue.mean
PLF_28228_00001986
UPF0126 inner membrane protein YadS
 $r = -0.589$, $p = 10^{-5.17}$



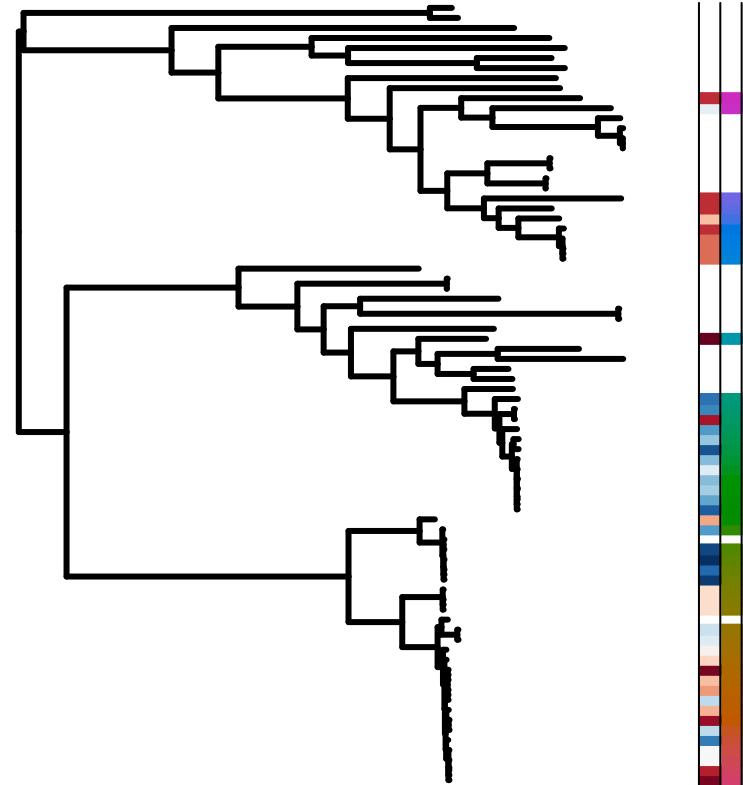
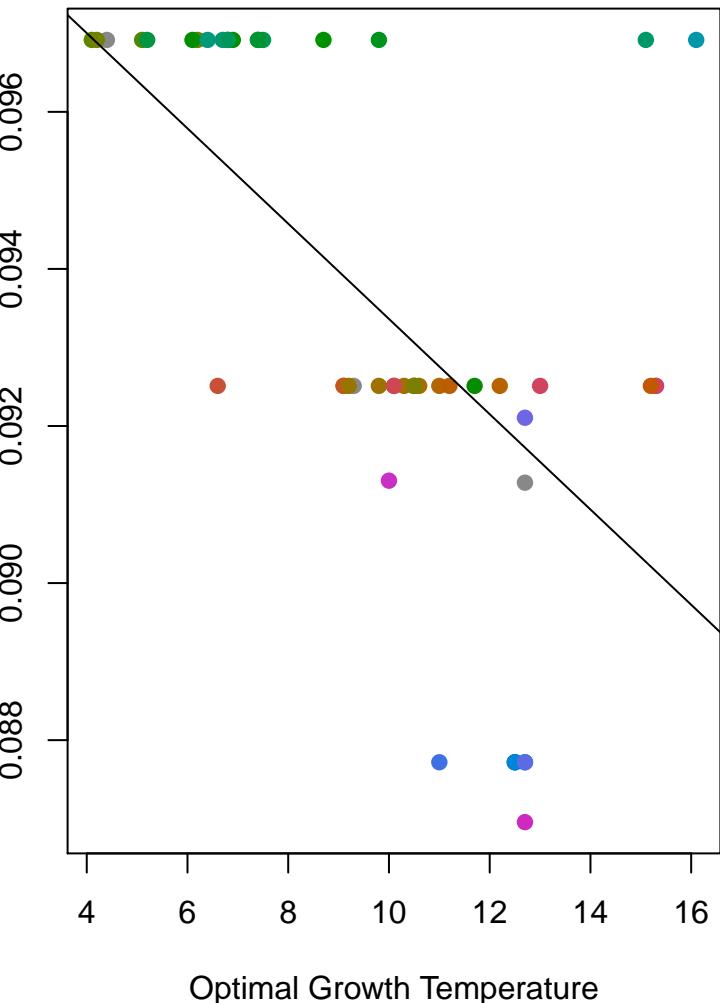
feature.plfam_id.acidic_residue.mean
PLF_28228_00000671
Nudix hydrolase 3 (EC 3.6.1.-)
 $r = -0.6$, $p = 10^{-5.394}$

feature.plfam_id.acidic_residue.mean



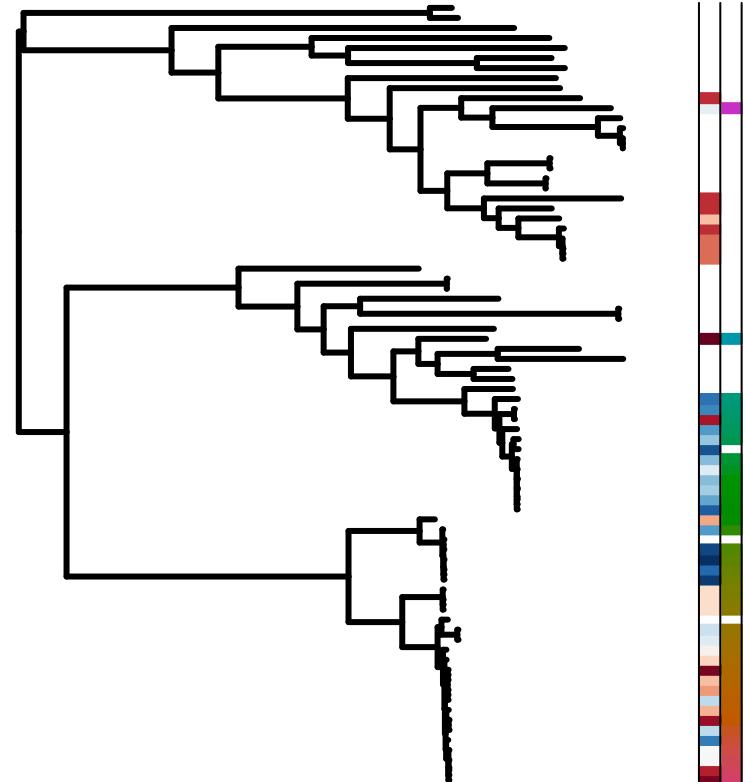
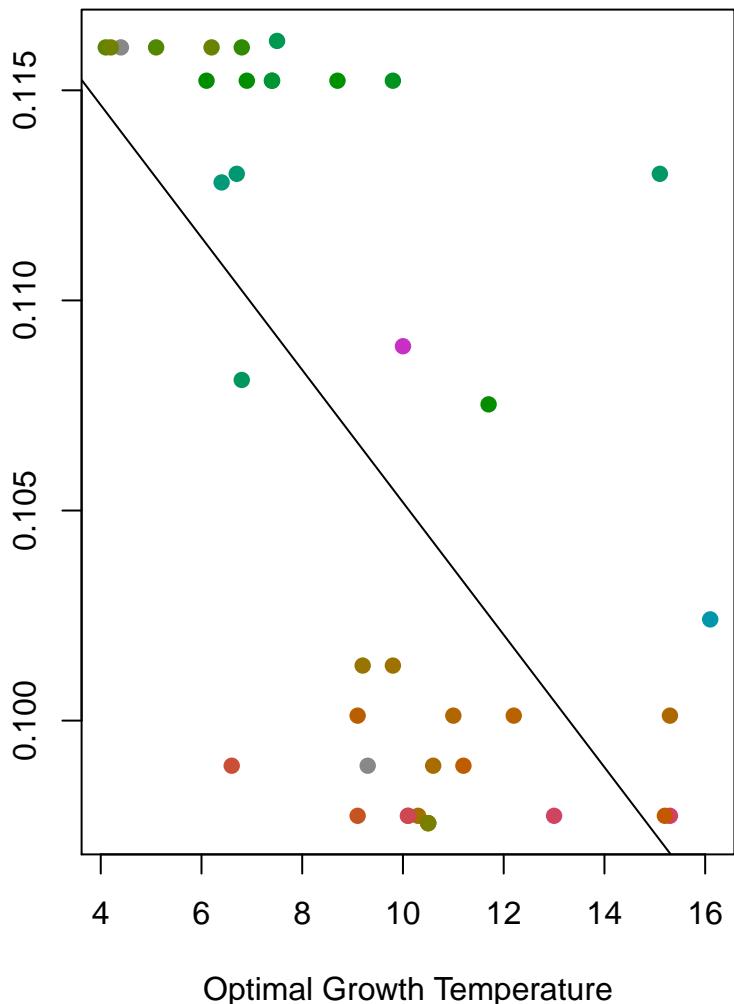
feature.plfam_id.acidic_residue.mean
PLF_28228_00001206
Tol-Pal system protein TolQ
 $r = -0.601$, $p = 10^{-5.41}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00022897
Invasin domain protein
 $r = -0.632$, $p = 10^{-4.91}$

feature.plfam_id.acidic_residue.mean

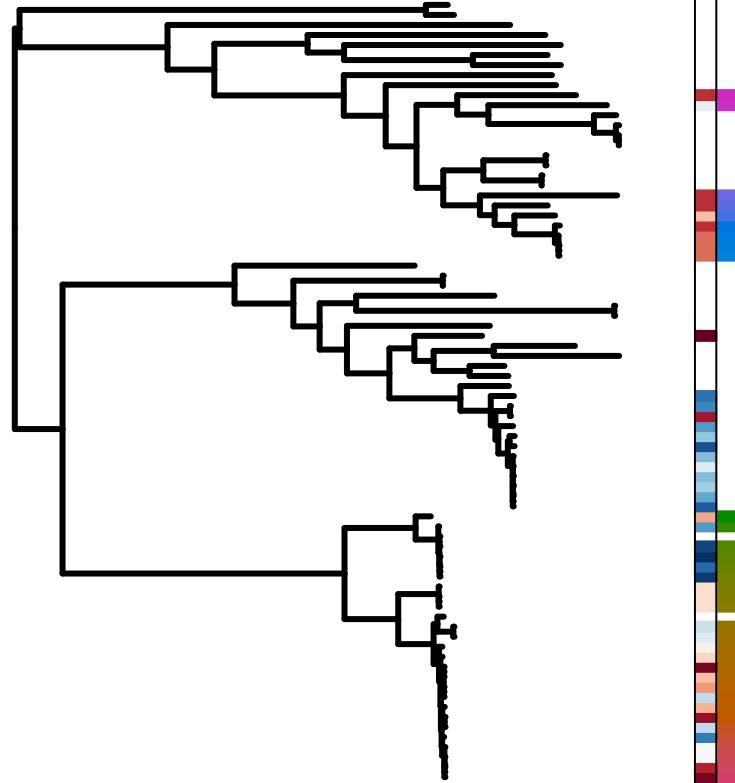
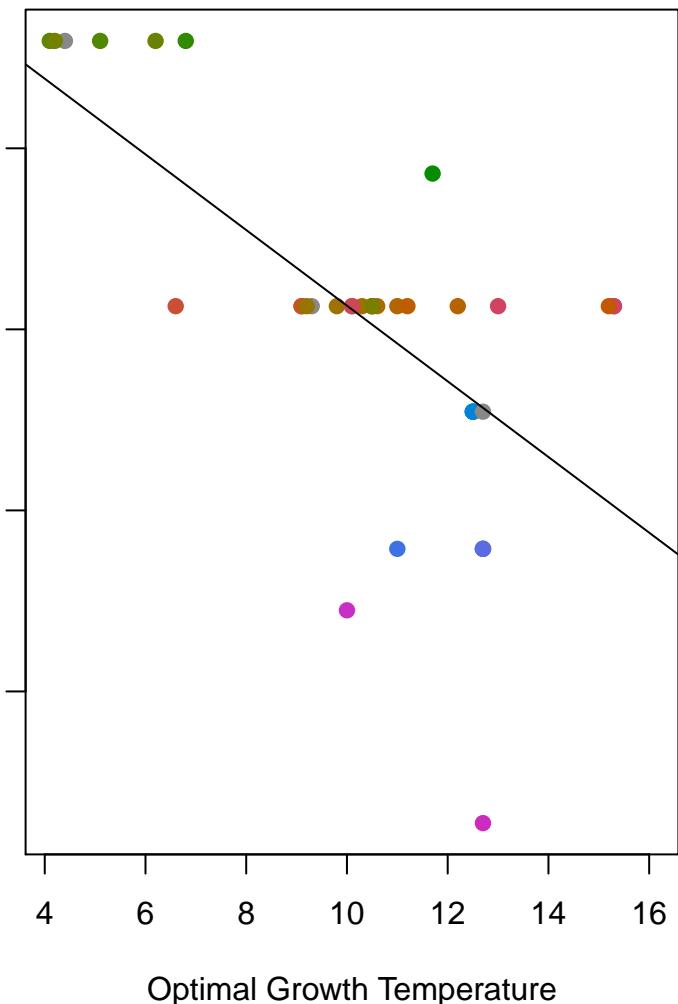


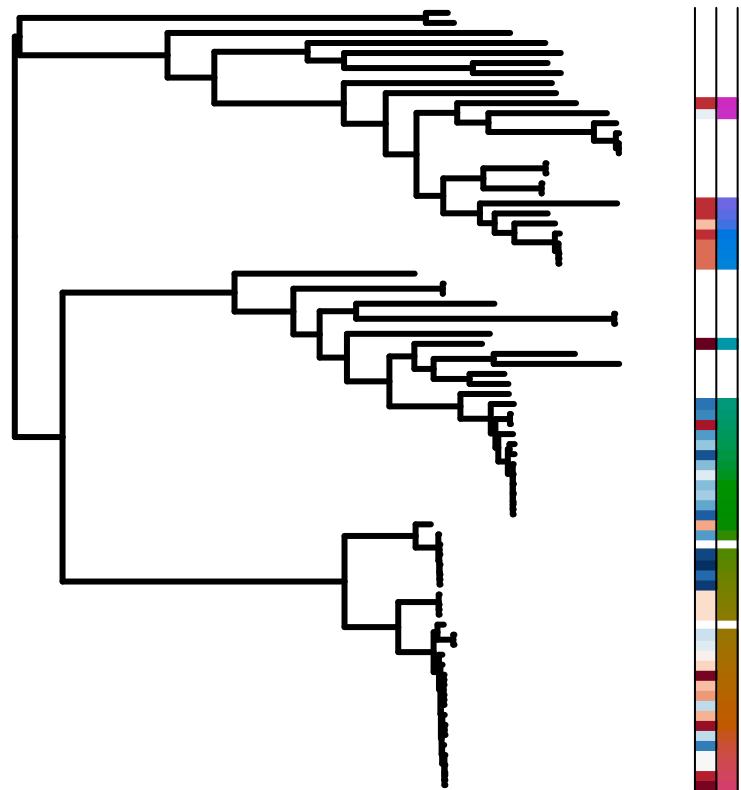
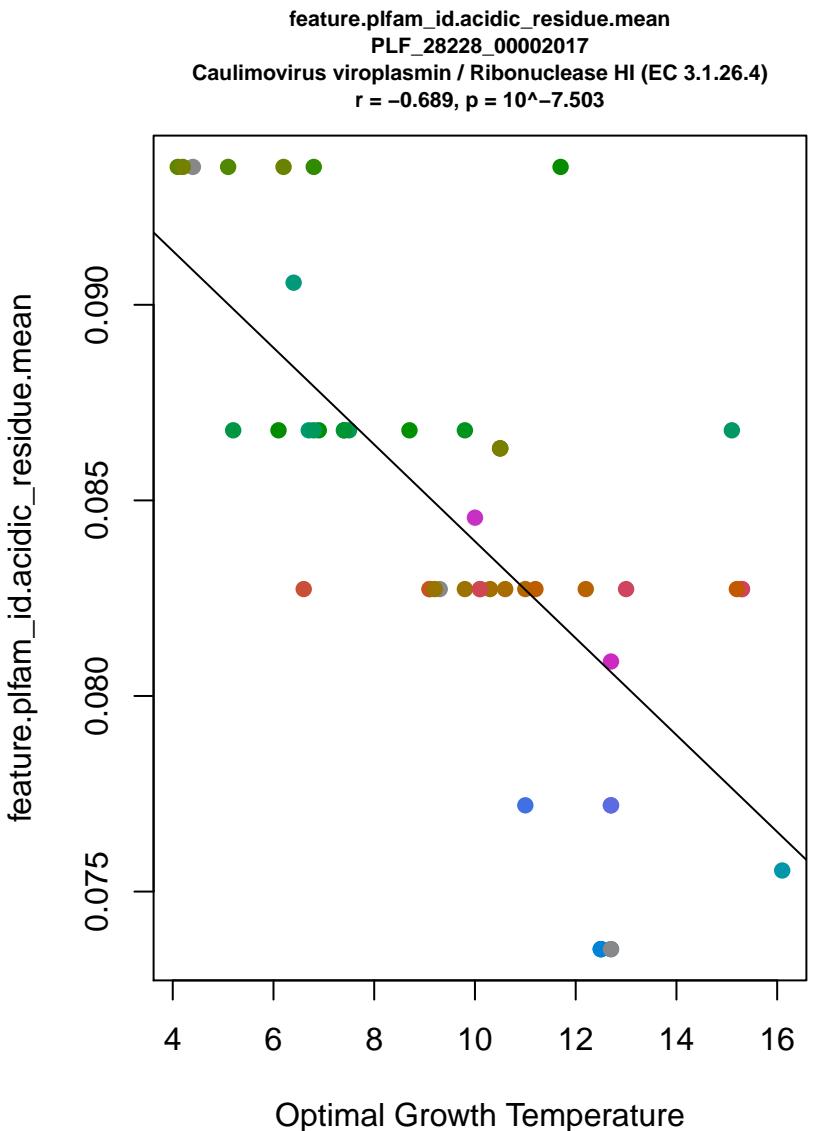
feature.plfam_id.acidic_residue.mean

PLF_28228_00001007

Uncharacterized UPF0721 integral membrane protein

$r = -0.651, p = 10^{-4.892}$





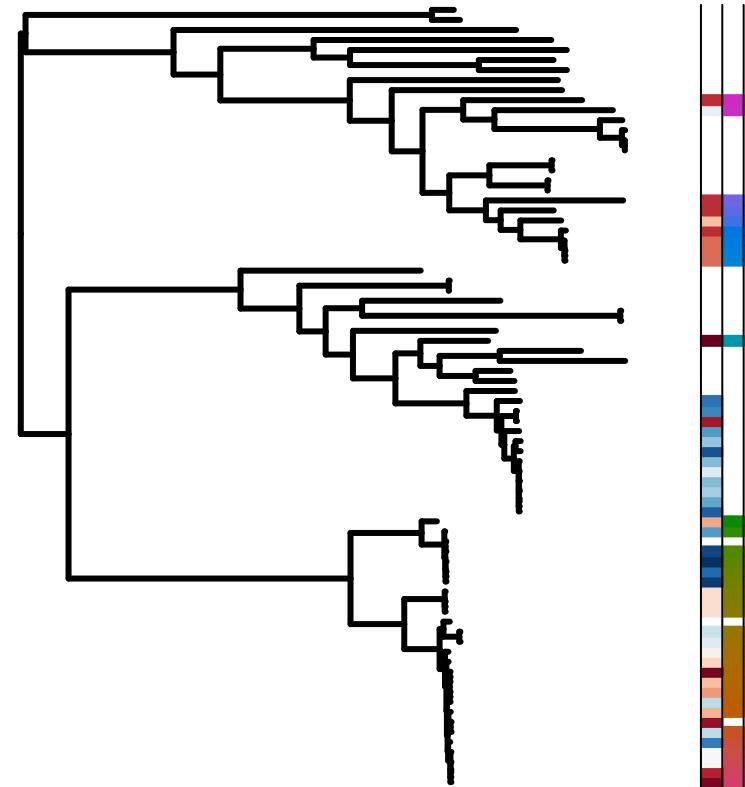
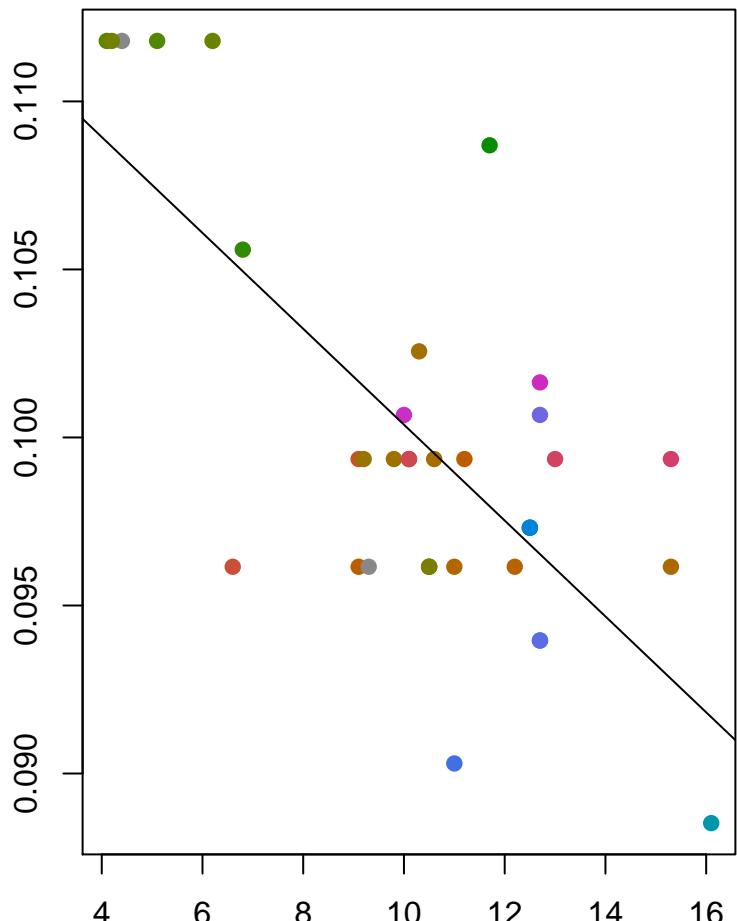
feature.plfam_id.acidic_residue.mean

PLF_28228_00002202

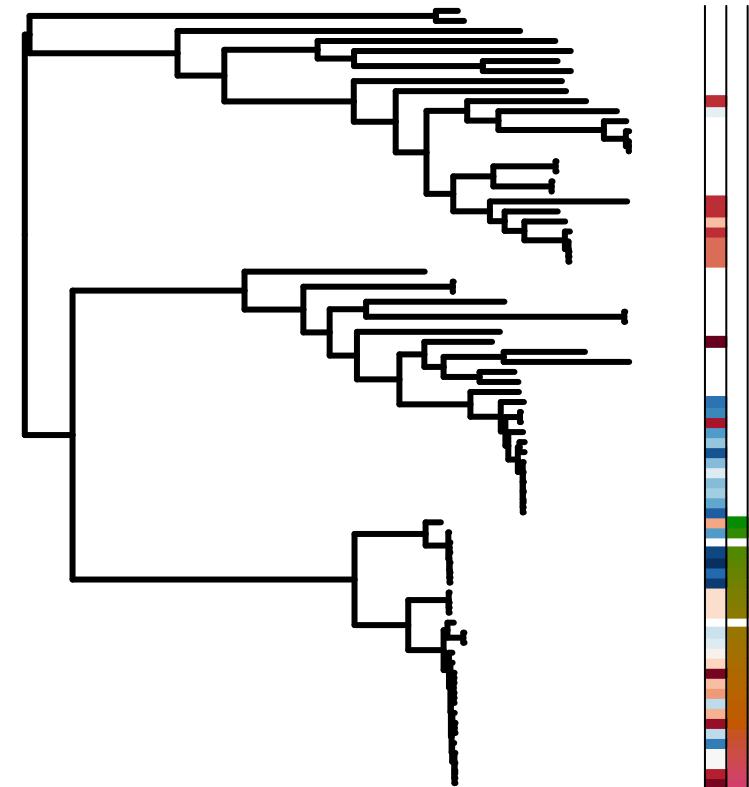
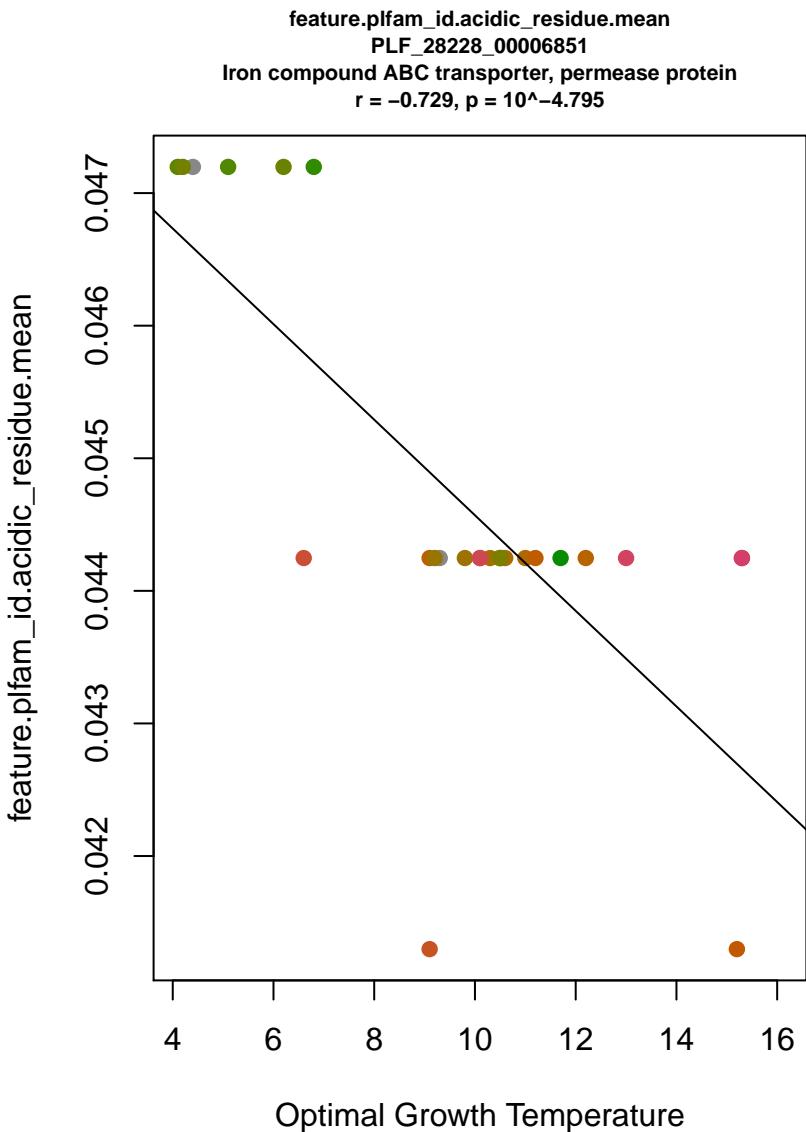
Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family

$r = -0.718$, $p = 10^{-6.085}$

feature.plfam_id.acidic_residue.mean



Optimal Growth Temperature

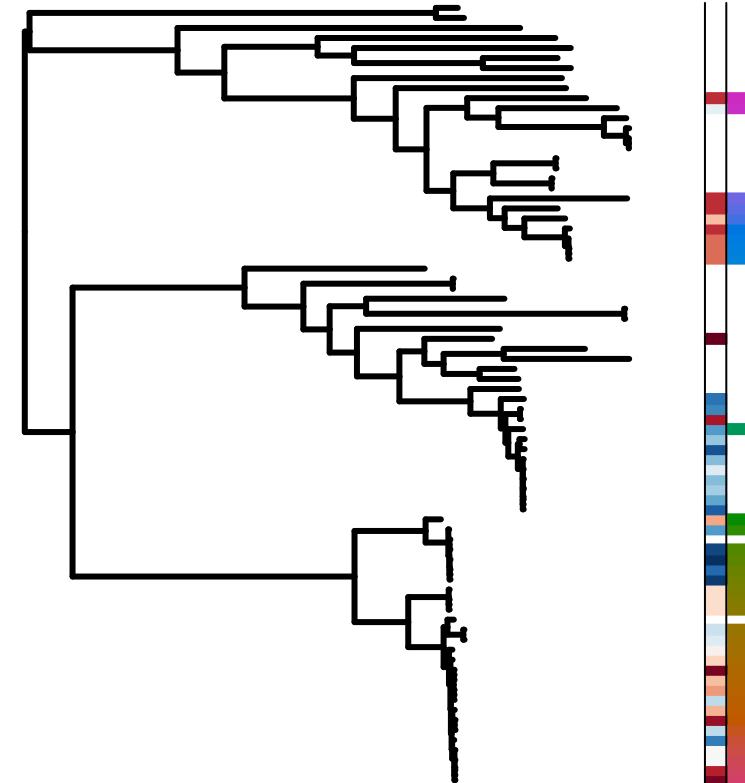
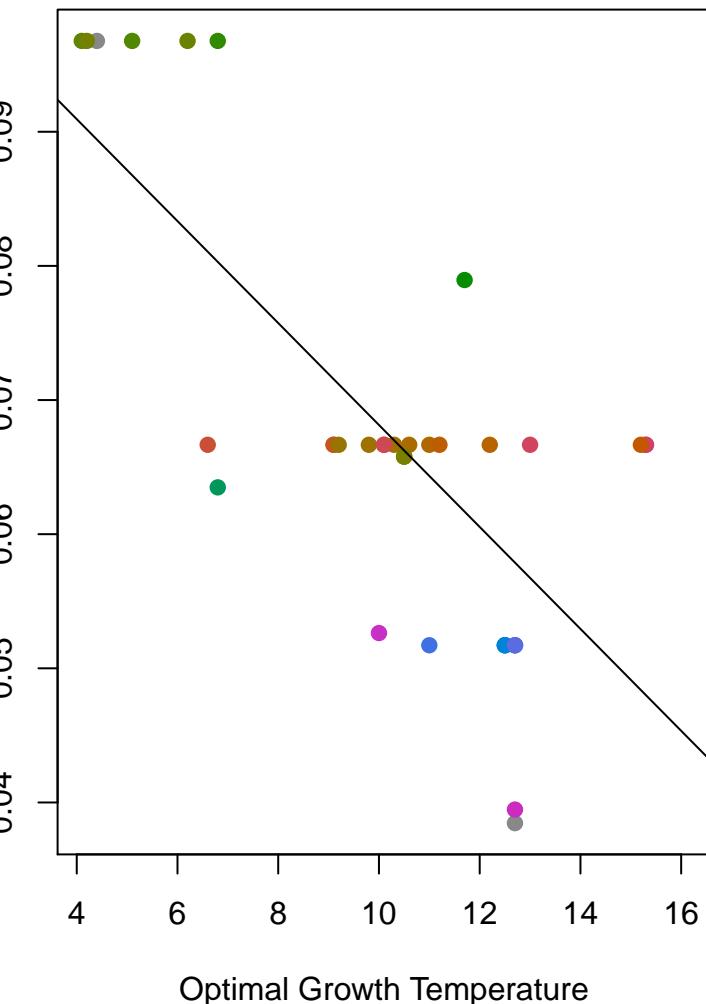


feature.plfam_id.acidic_residue.mean

PLF_28228_00001333

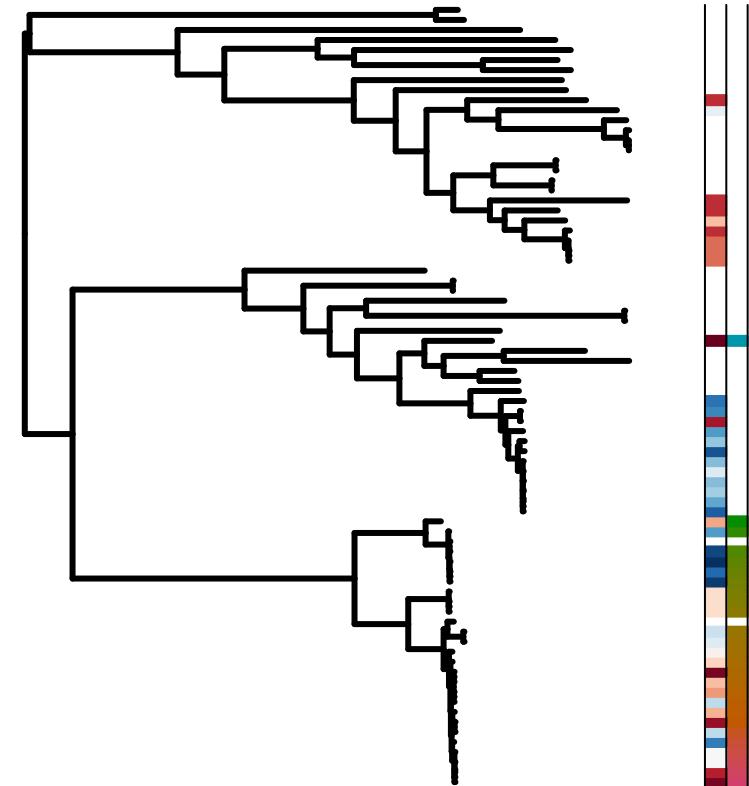
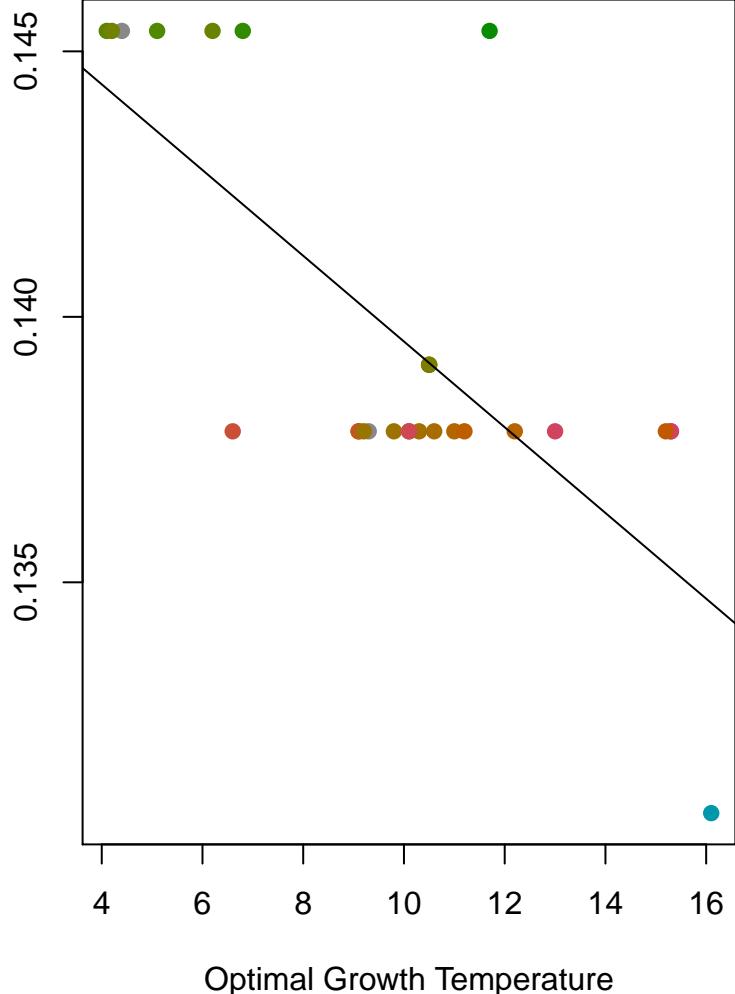
Uncharacterized membrane protein SO_0290

$r = -0.731, p = 10^{-6.559}$



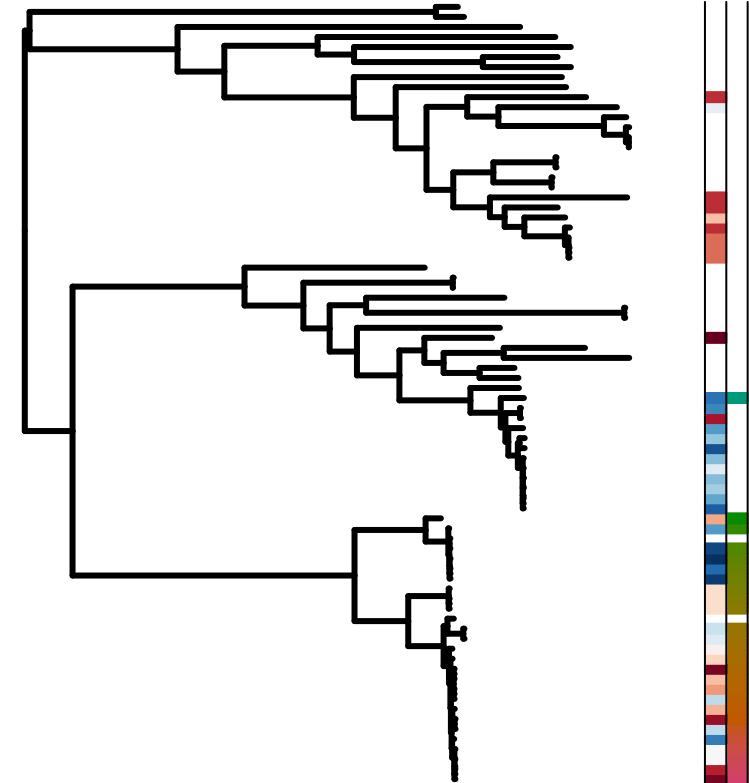
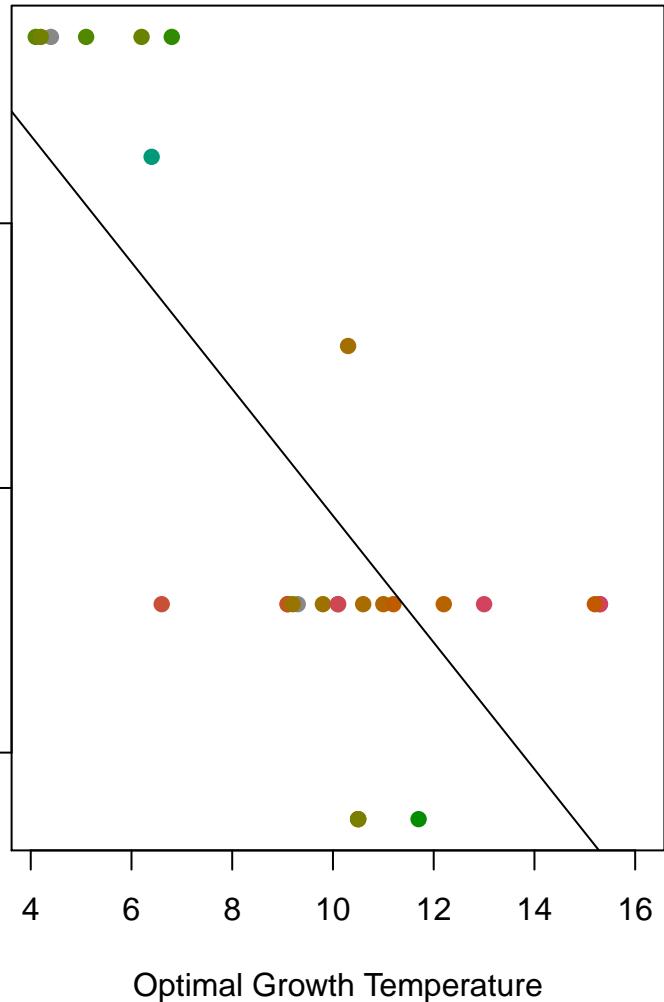
feature.plfam_id.acidic_residue.mean
PLF_28228_00027807
FIG01056734: hypothetical protein
 $r = -0.734$, $p = 10^{-5.048}$

feature.plfam_id.acidic_residue.mean



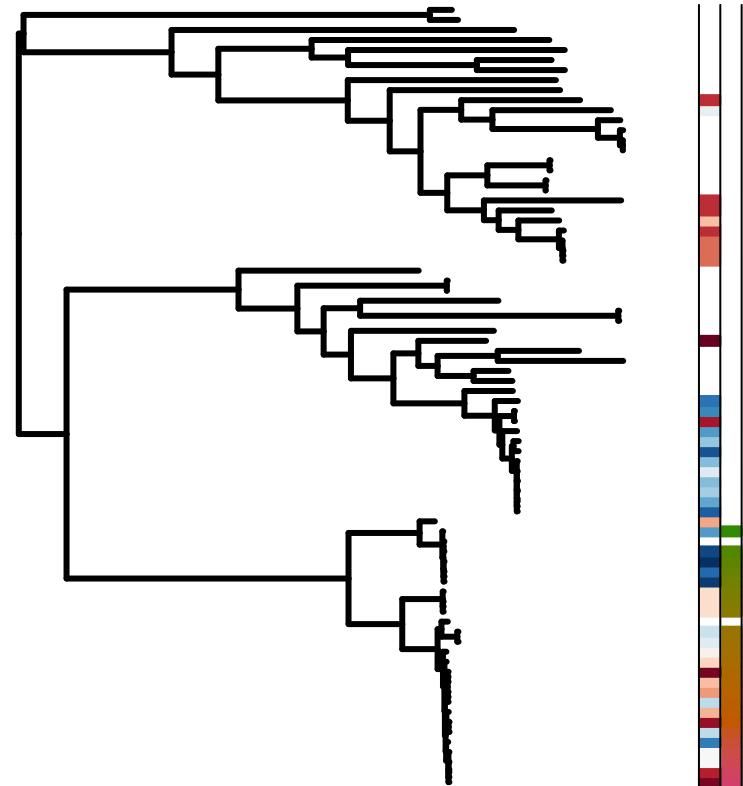
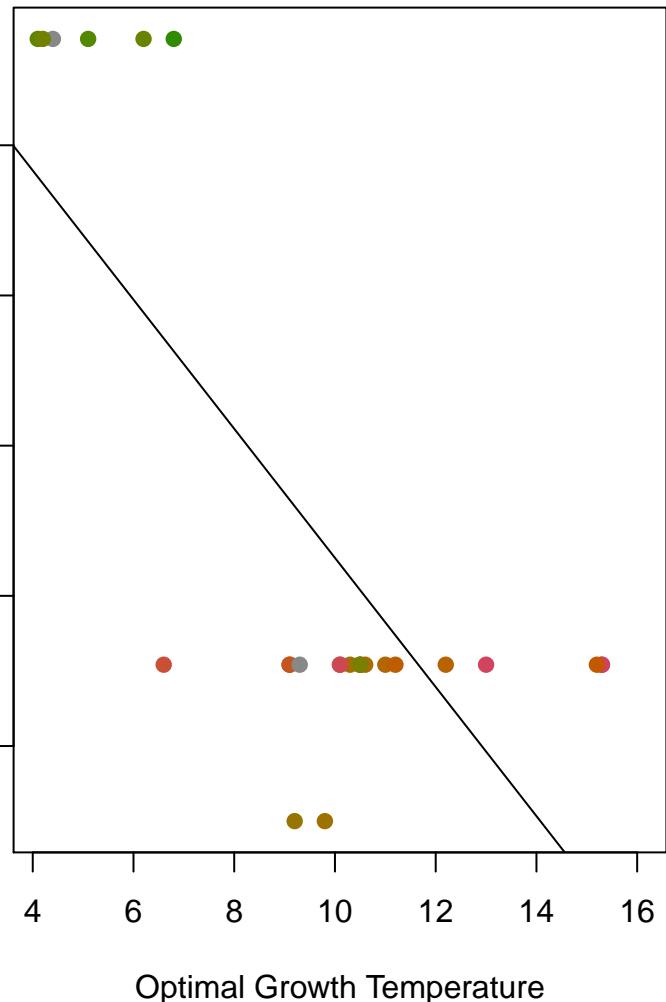
feature.plfam_id.acidic_residue.mean
PLF_28228_00015281
hypothetical protein
 $r = -0.741$, $p = 10^{-5.186}$

feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00020960
hypothetical protein
 $r = -0.746$, $p = 10^{-4.917}$

feature.plfam_id.acidic_residue.mean

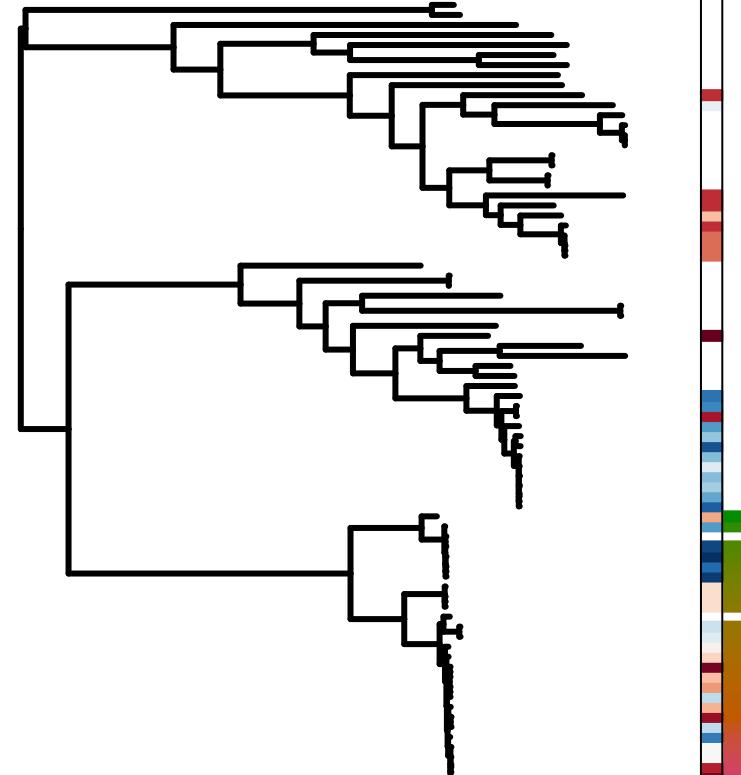
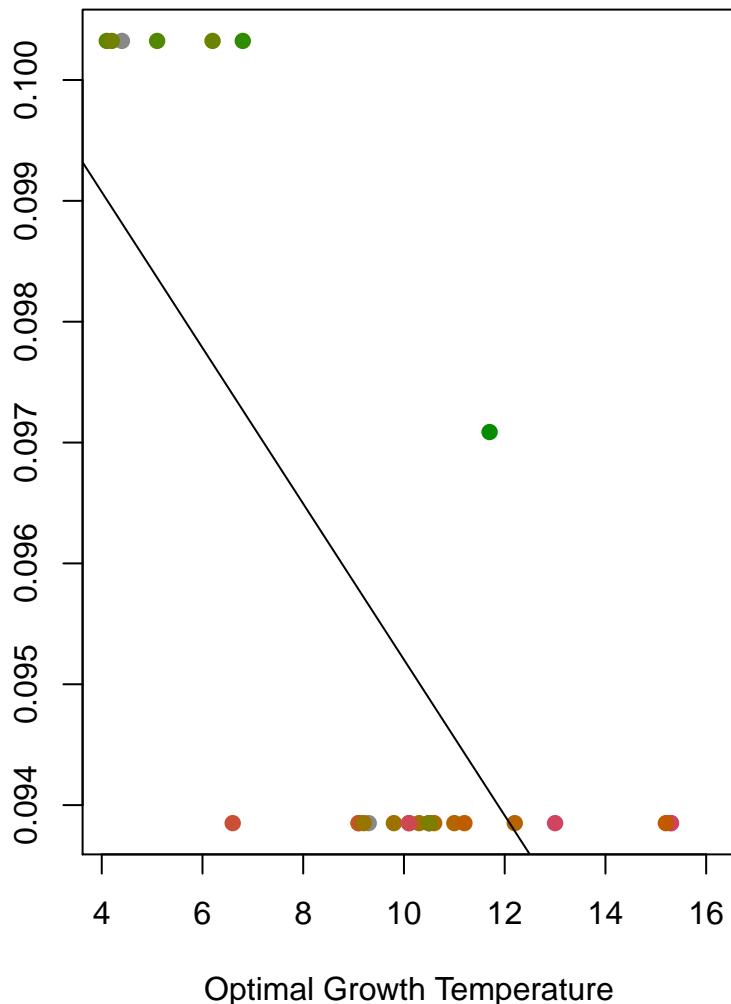


feature.plfam_id.acidic_residue.mean

PLF_28228_00006015

N-linked glycosylation glycosyltransferase PgIG

$r = -0.748, p = 10^{-5.131}$

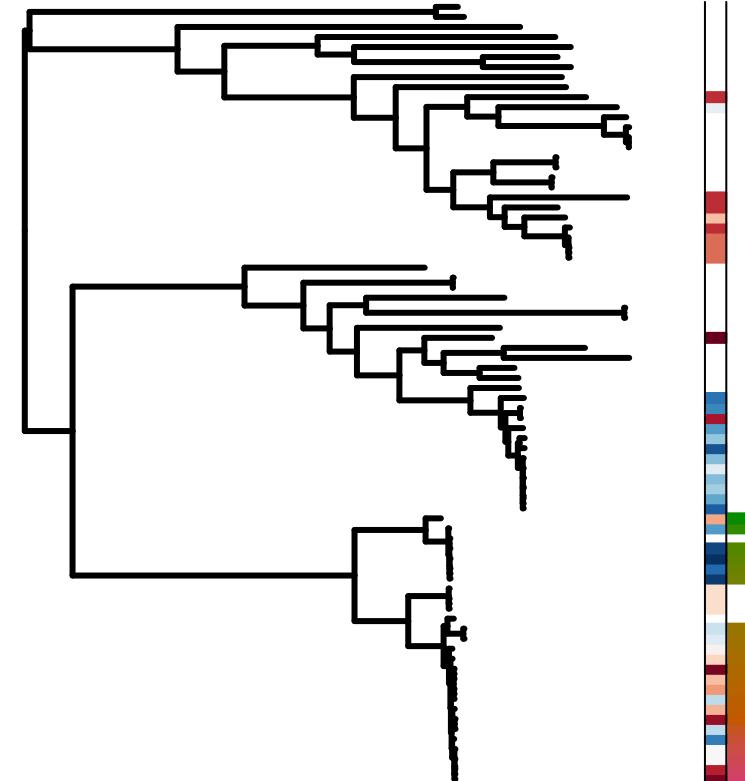
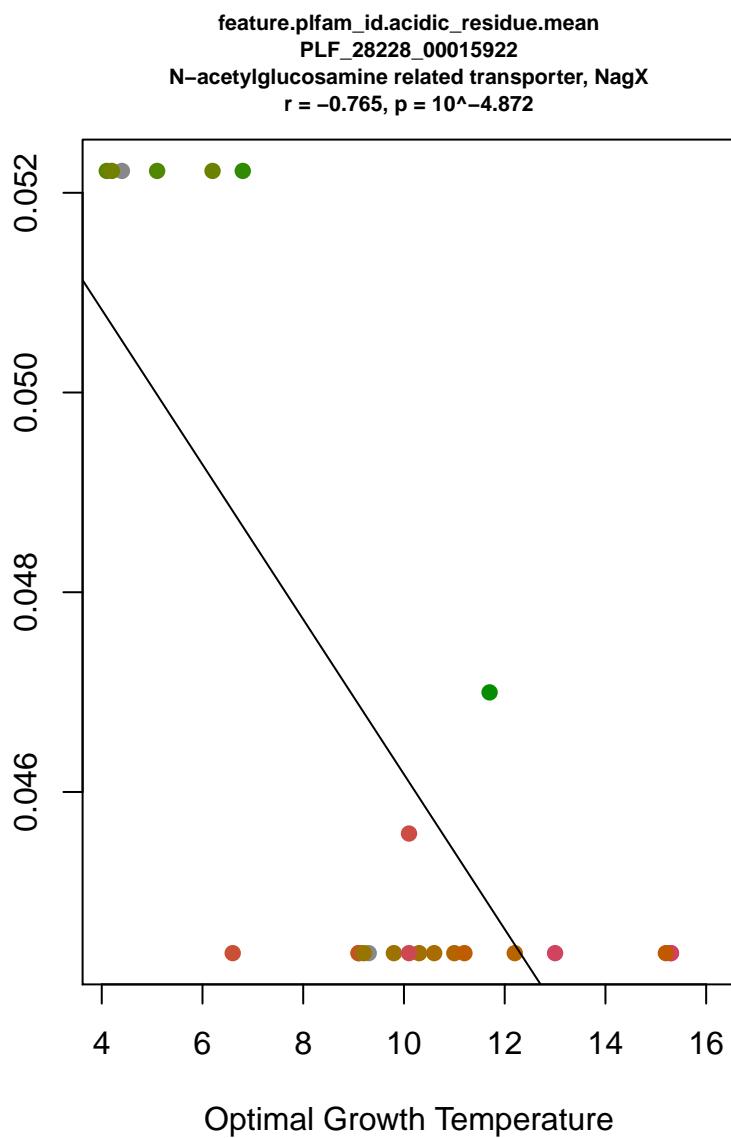


feature.plfam_id.acidic_residue.mean

PLF_28228_00015922

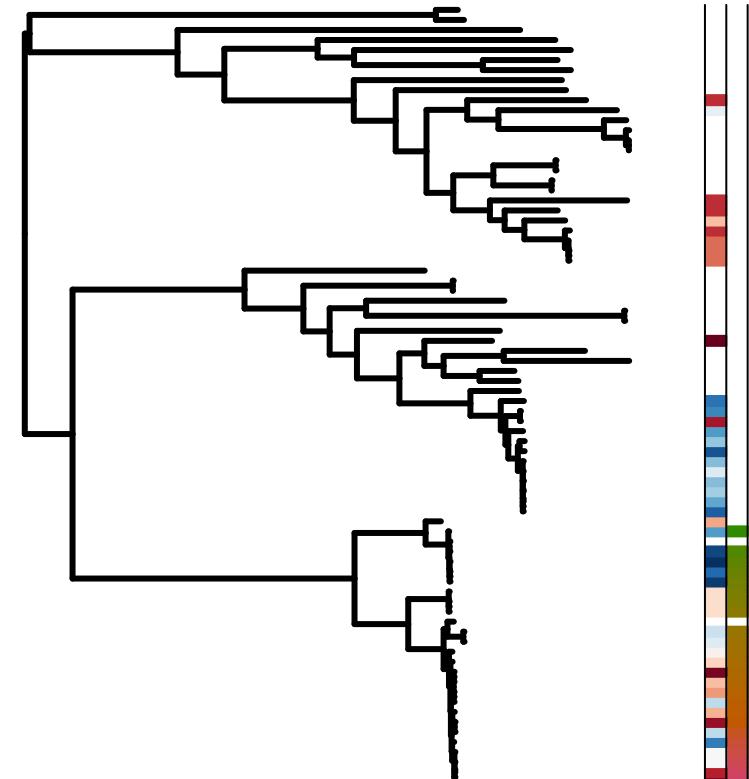
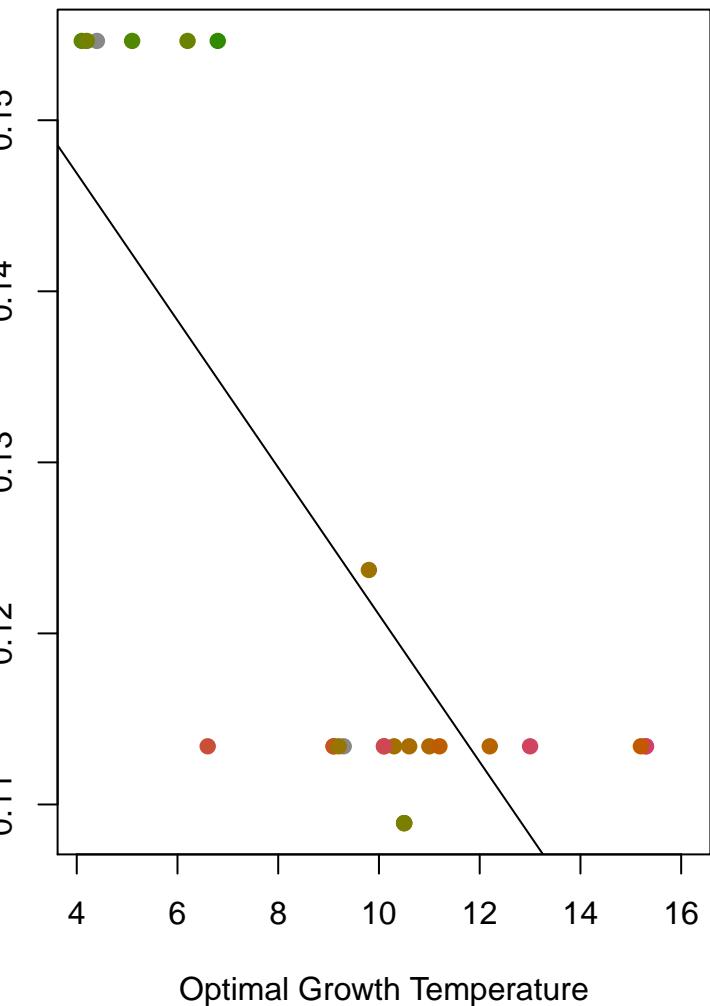
N-acetylglucosamine related transporter, NagX

$r = -0.765, p = 10^{-4.872}$



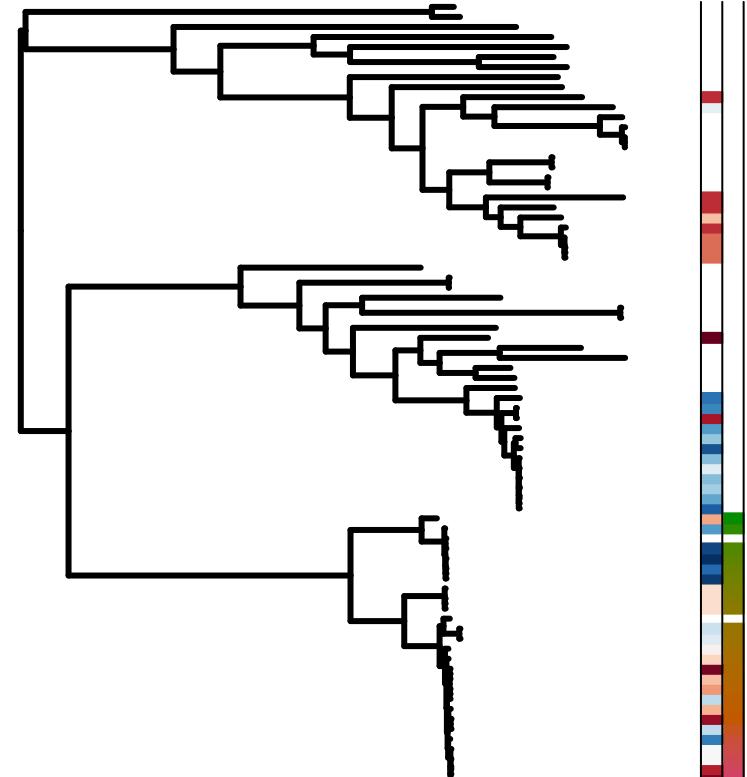
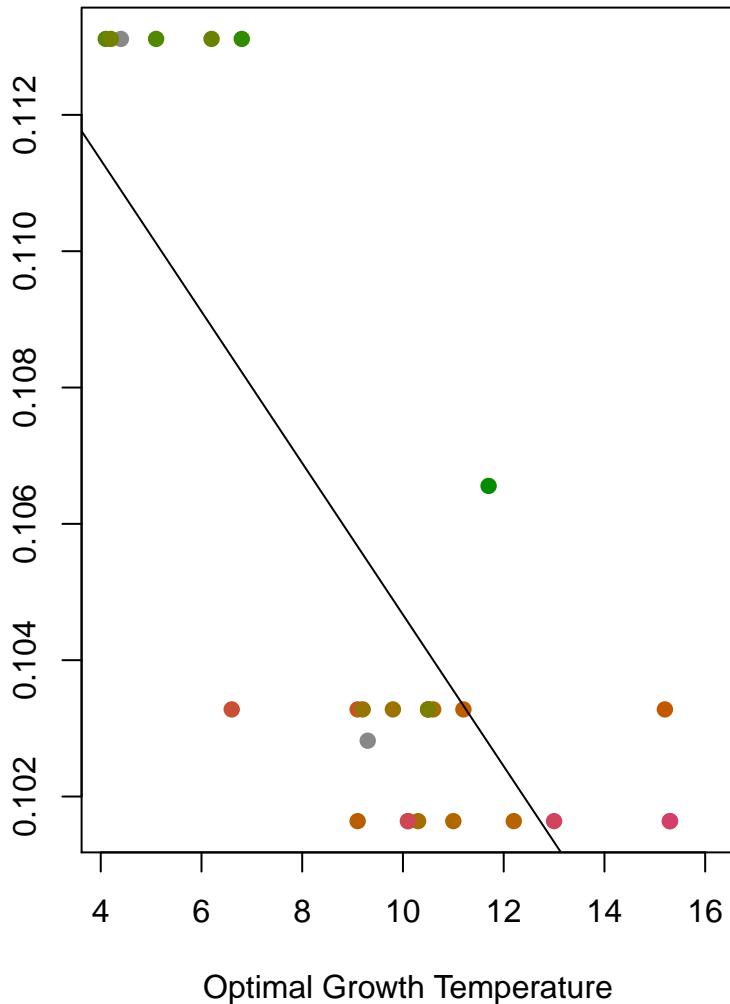
feature.plfam_id.acidic_residue.mean
PLF_28228_00030961
hypothetical protein
 $r = -0.771$, $p = 10^{-5.395}$

feature.plfam_id.acidic_residue.mean



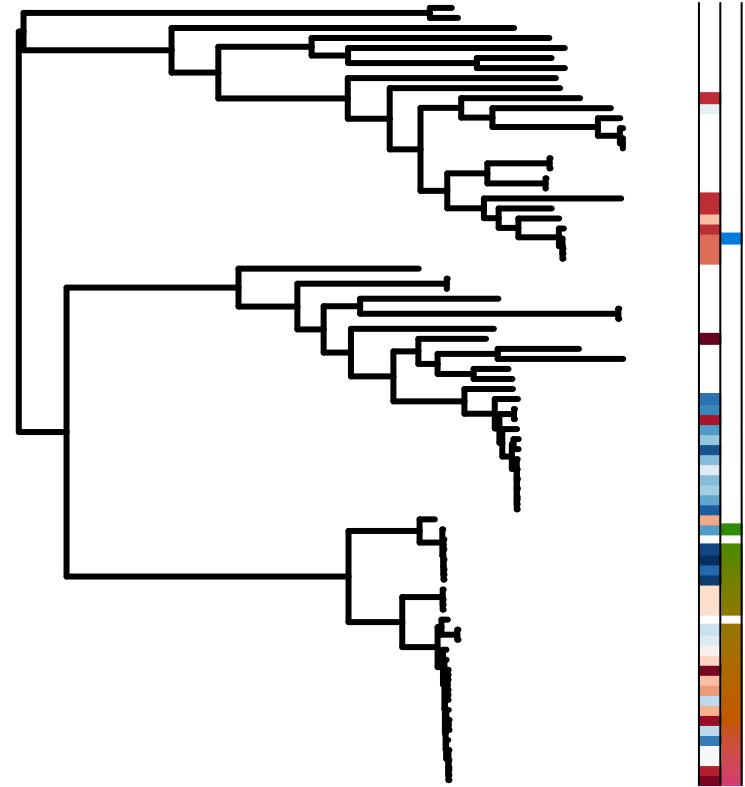
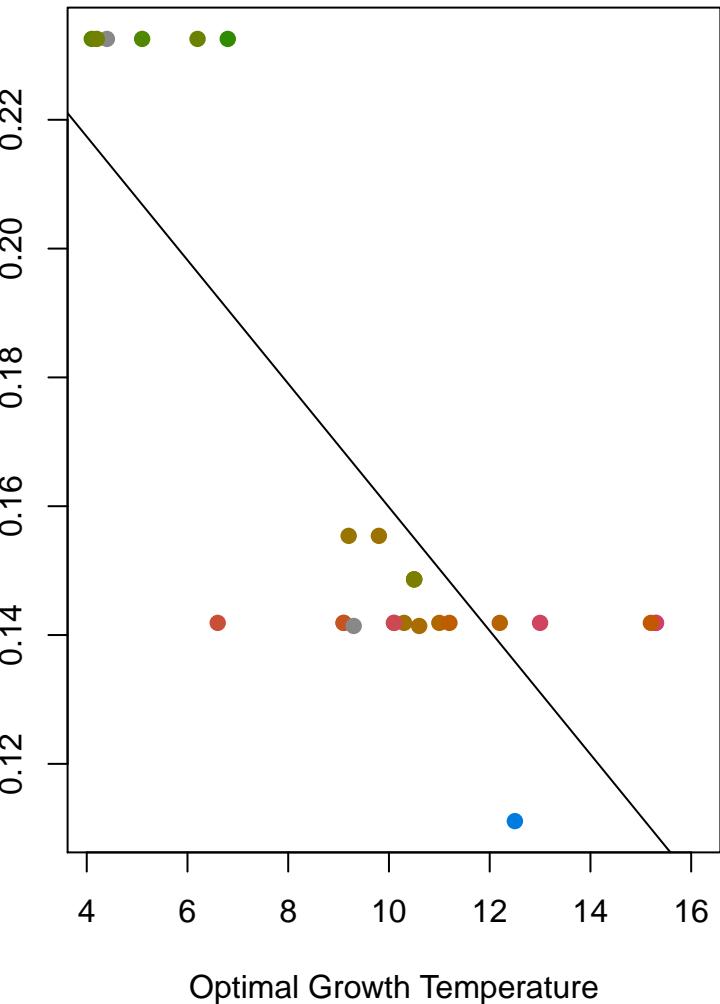
feature.plfam_id.acidic_residue.mean
PLF_28228_00028646
hypothetical protein
 $r = -0.782$, $p = 10^{-5.83}$

feature.plfam_id.acidic_residue.mean



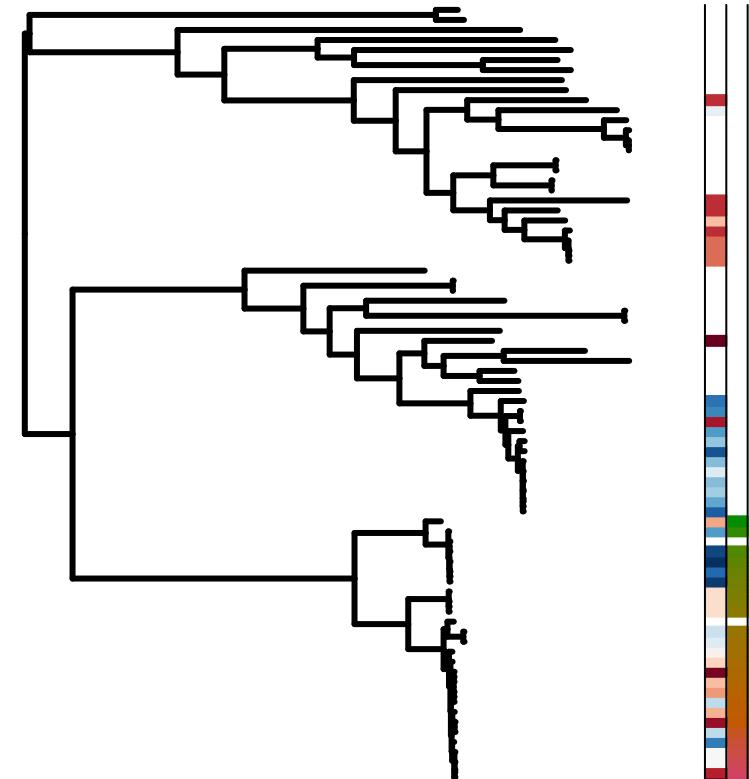
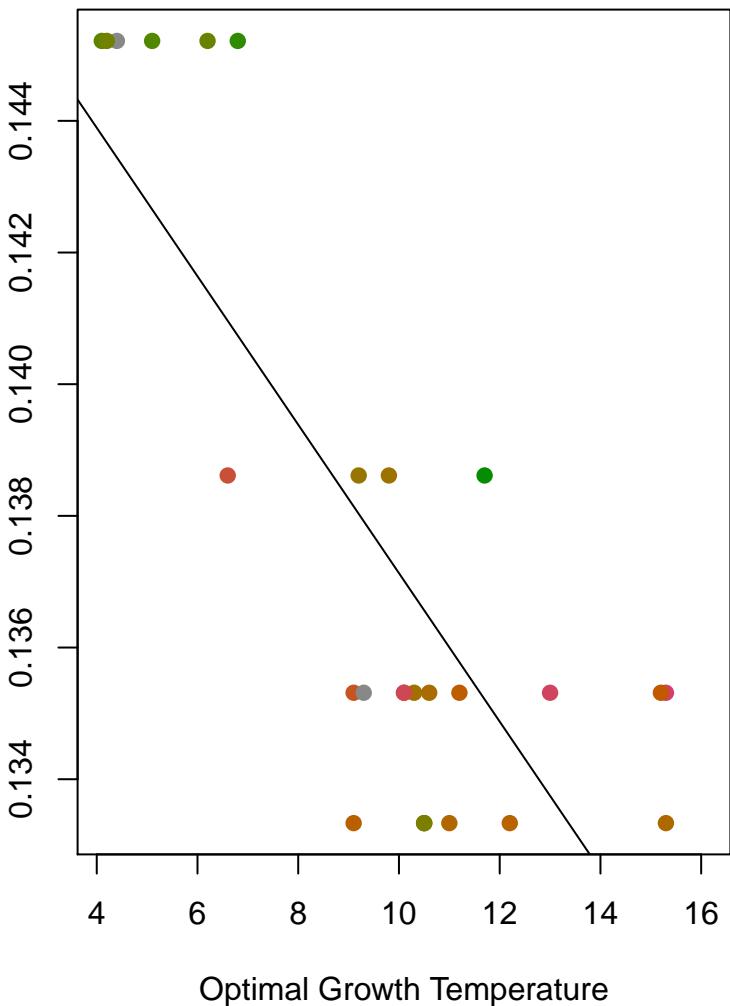
feature.plfam_id.acidic_residue.mean
PLF_28228_00014070
hypothetical protein
 $r = -0.793, p = 10^{-6.081}$

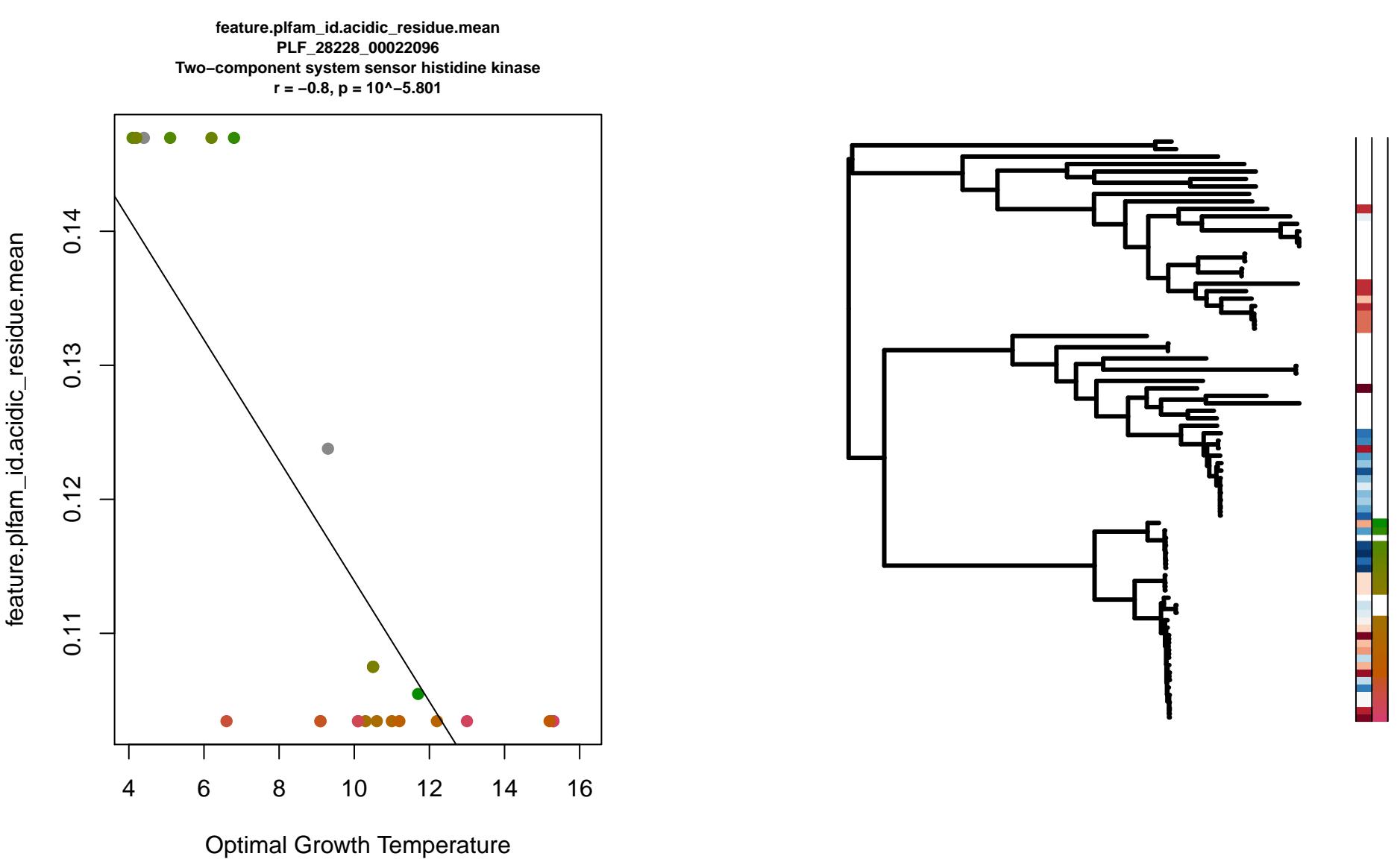
feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00014238
hypothetical protein
 $r = -0.794$, $p = 10^{-6.12}$

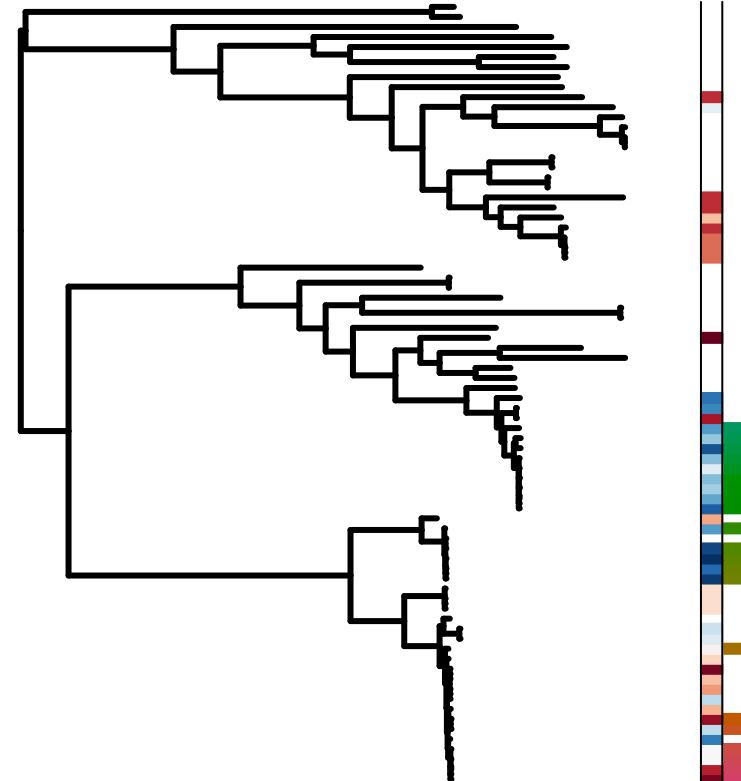
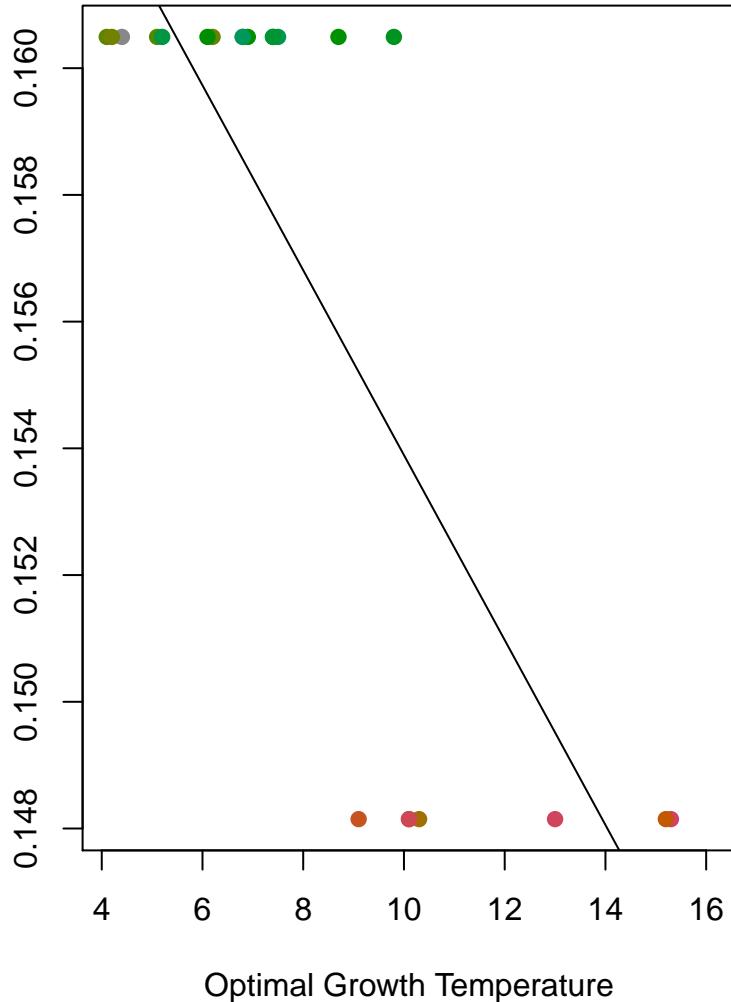
feature.plfam_id.acidic_residue.mean



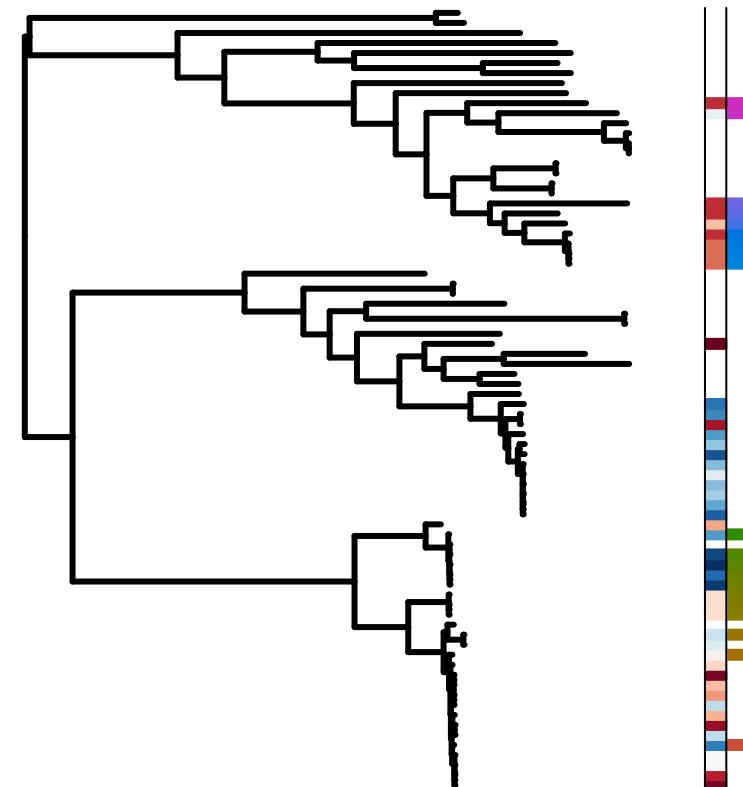
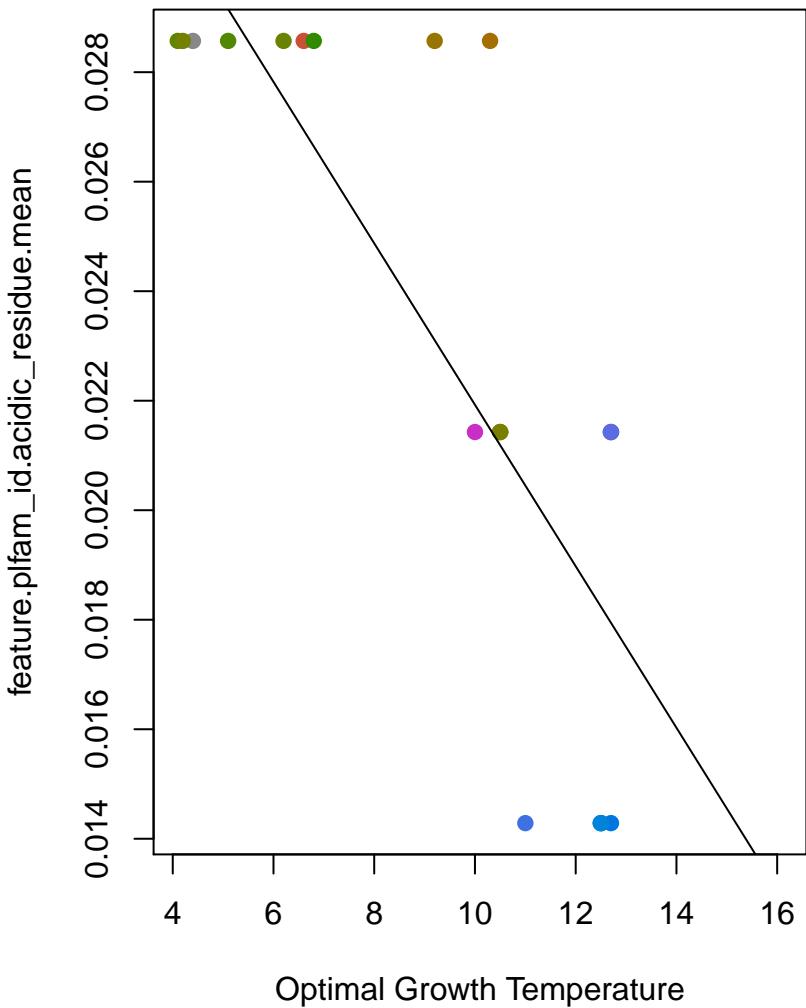


feature.plfam_id.acidic_residue.mean
PLF_28228_00016087
hypothetical protein
 $r = -0.801$, $p = 10^{-5.129}$

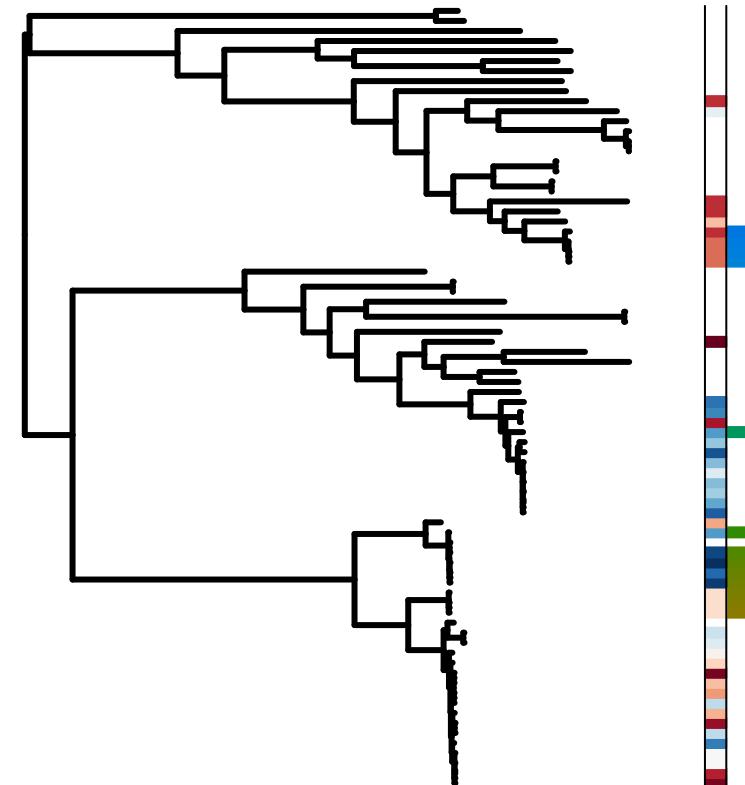
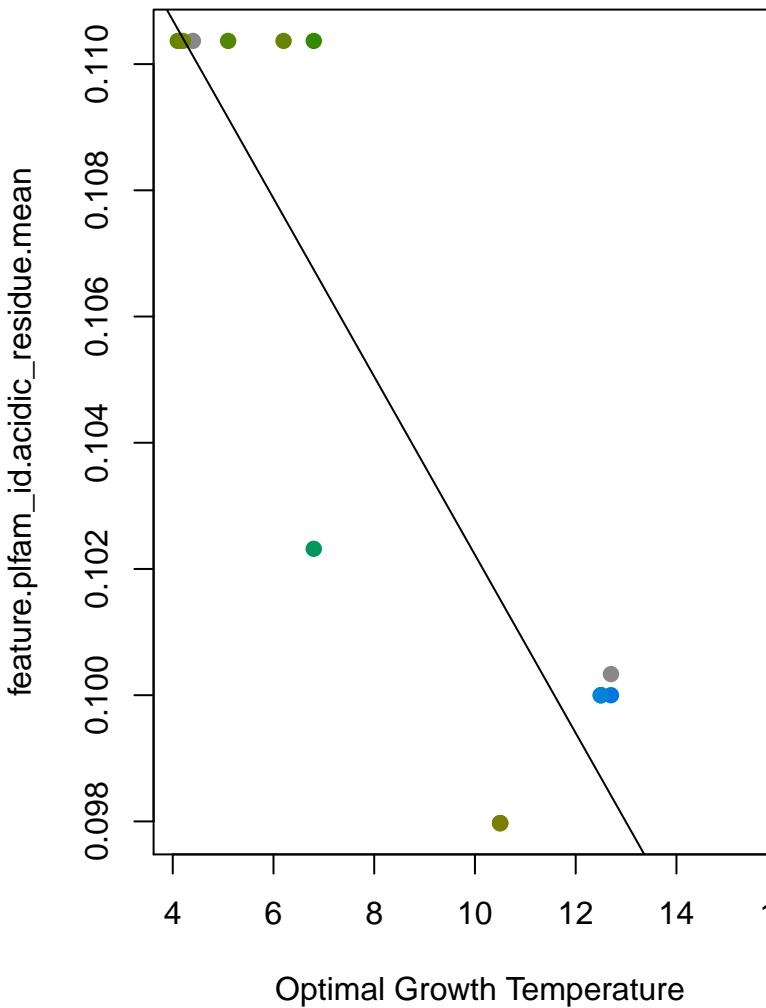
feature.plfam_id.acidic_residue.mean



feature.plfam_id.acidic_residue.mean
PLF_28228_00002238
hypothetical protein
 $r = -0.809$, $p = 10^{-5.044}$

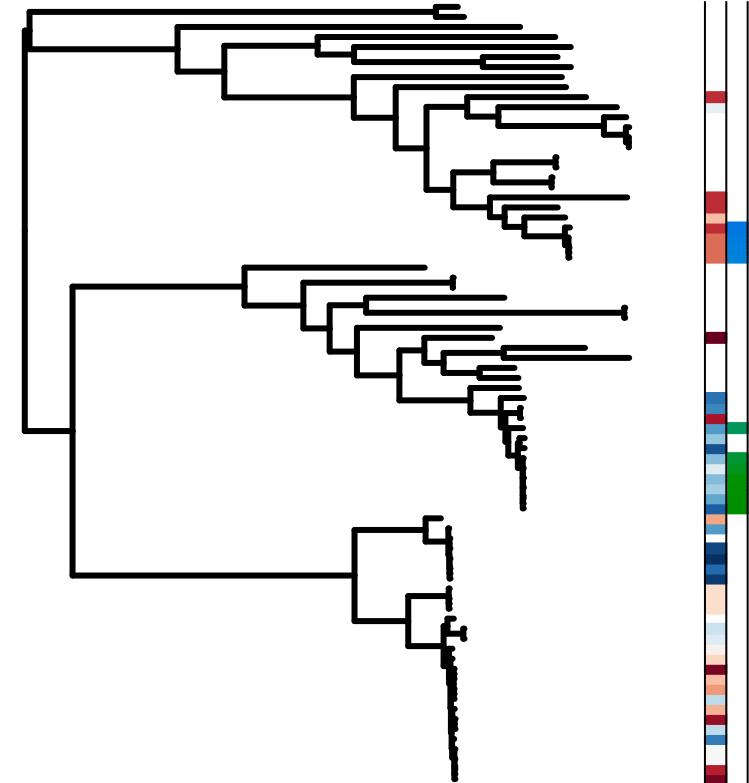
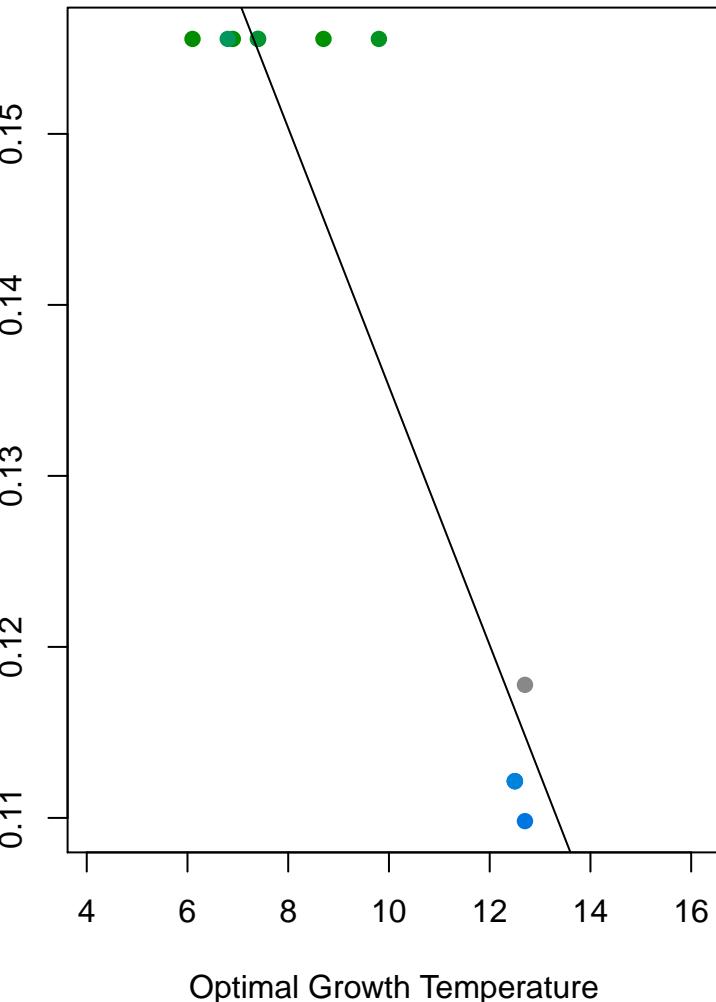


feature.plfam_id.acidic_residue.mean
PLF_28228_00007744
hypothetical protein
 $r = -0.889$, $p = 10^{-5.017}$



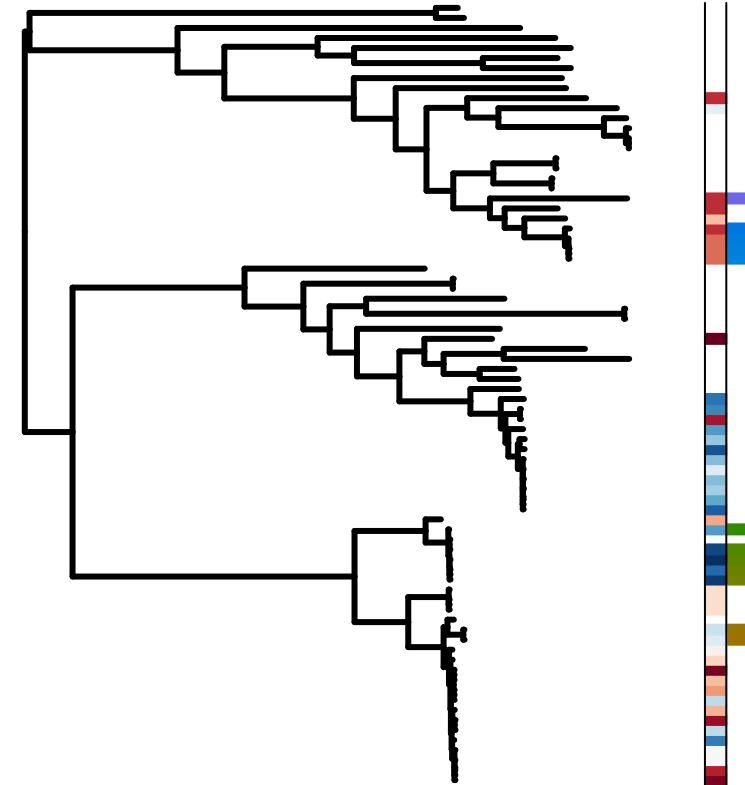
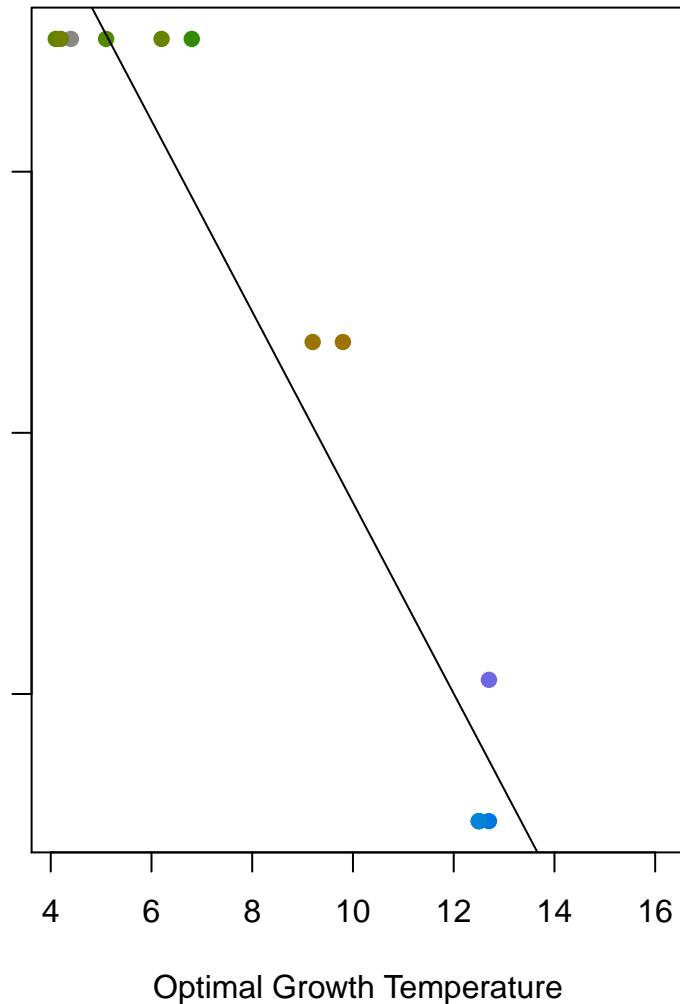
feature.plfam_id.acidic_residue.mean
PLF_28228_00007748
EAL domain protein
 $r = -0.936$, $p = 10^{-5.136}$

feature.plfam_id.acidic_residue.mean



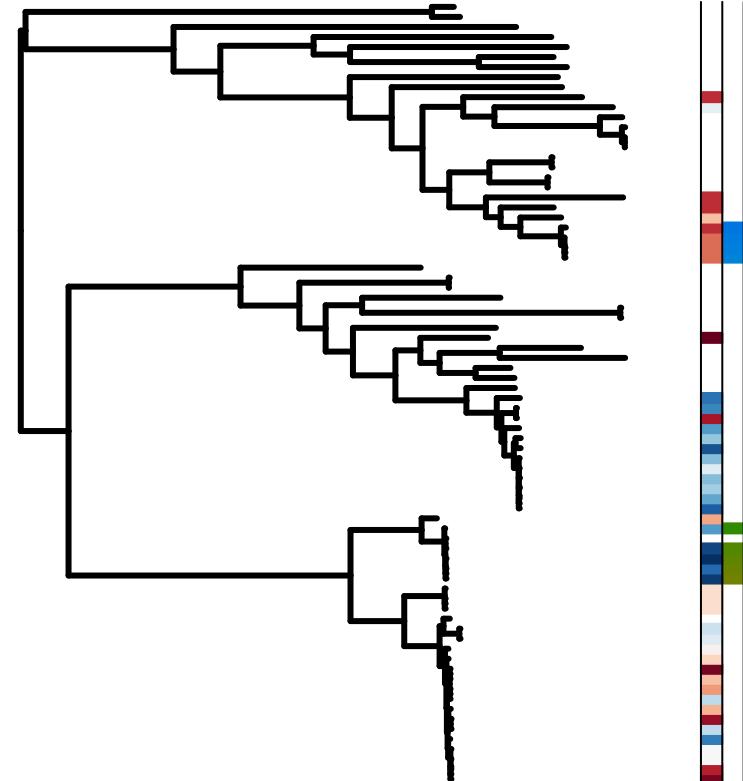
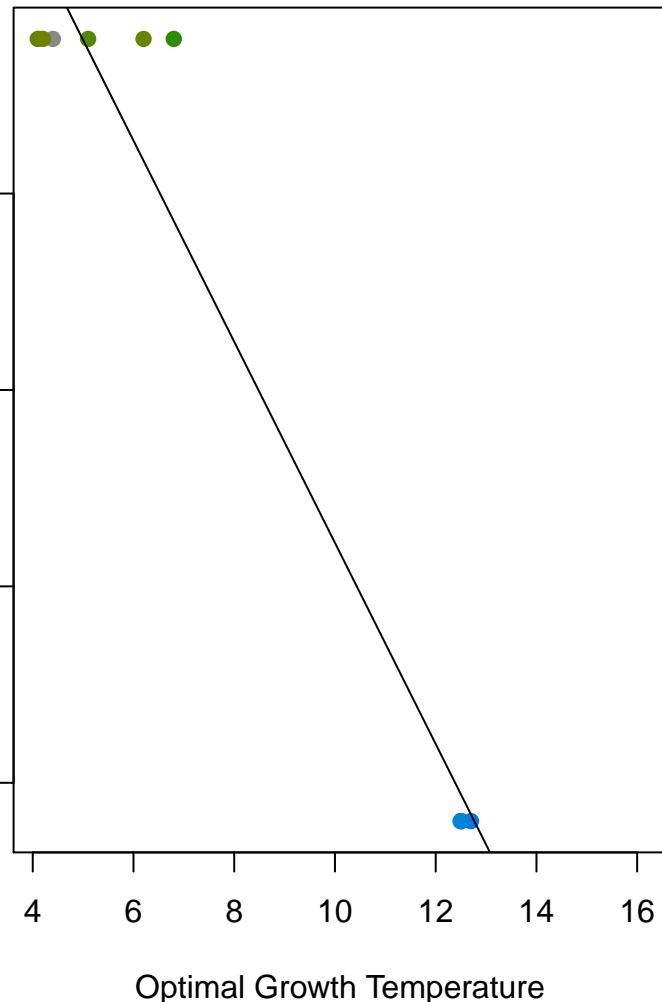
feature.plfam_id.acidic_residue.mean
PLF_28228_00018284
putative lipoprotein
 $r = -0.963$, $p = 10^{-6.863}$

feature.plfam_id.acidic_residue.mean



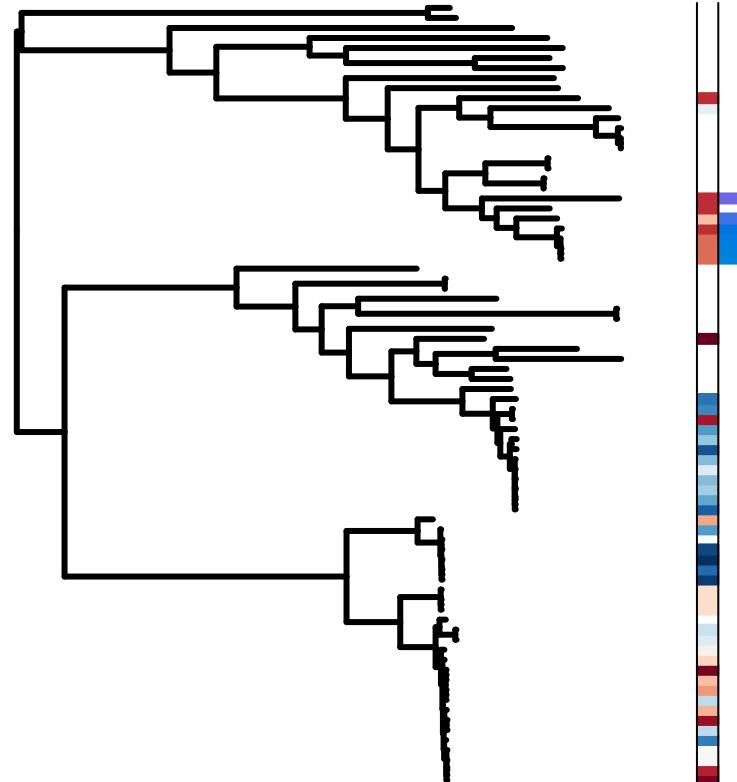
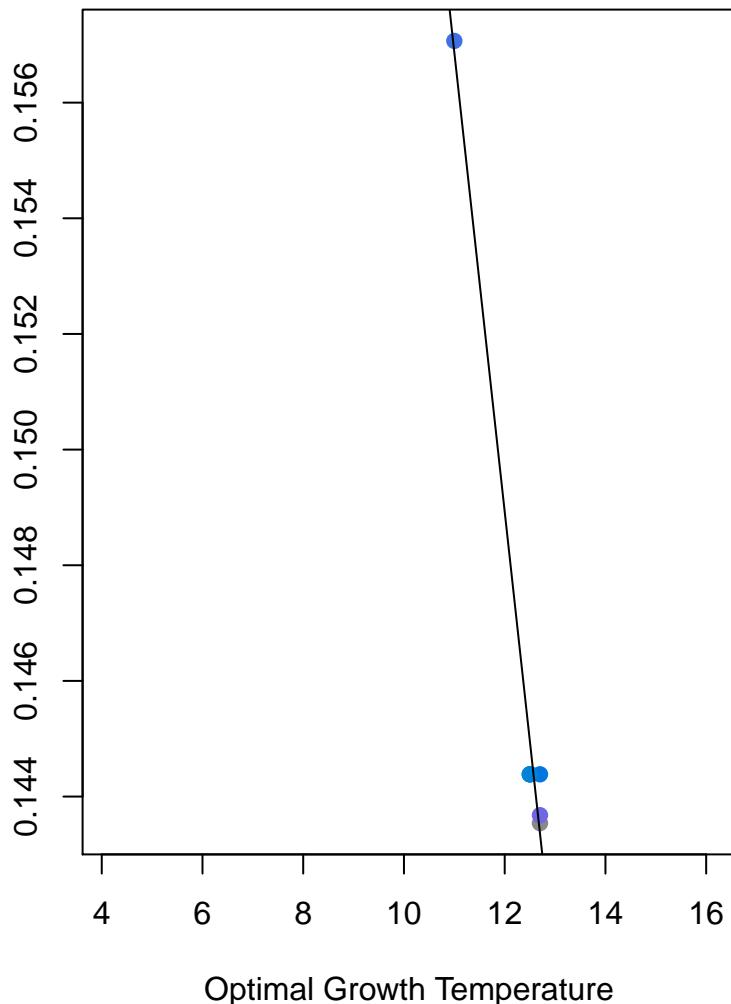
feature.plfam_id.acidic_residue.mean
PLF_28228_00007839
hypothetical protein
 $r = -0.977$, $p = 10^{-5.889}$

feature.plfam_id.acidic_residue.mean



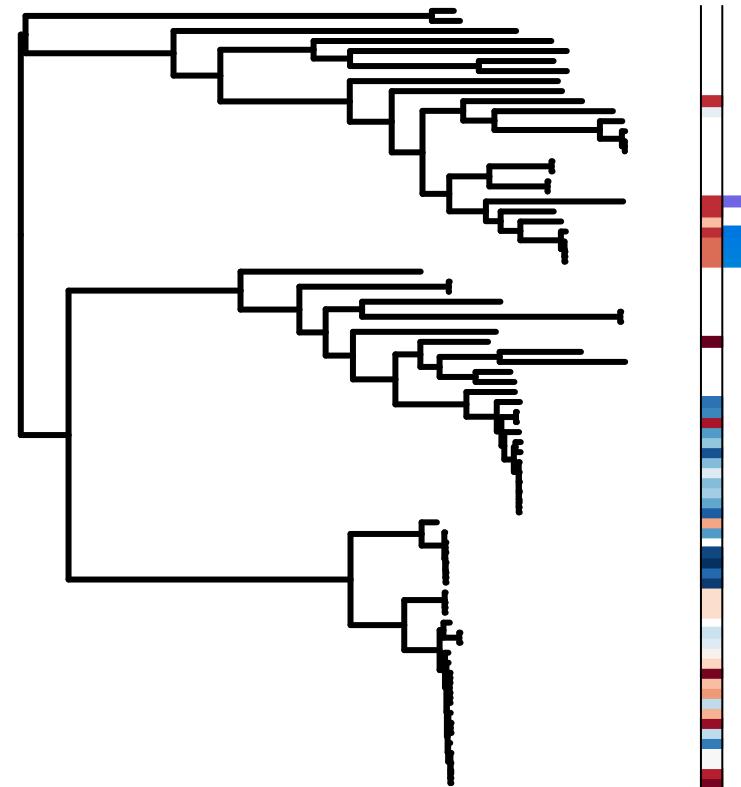
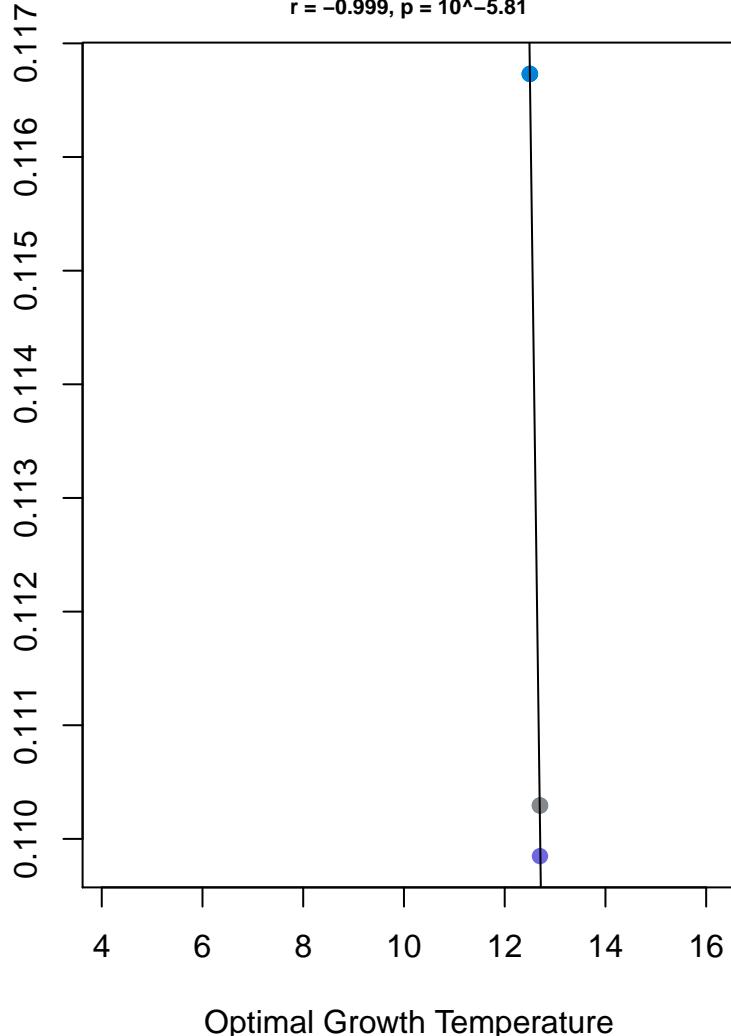
feature.plfam_id.acidic_residue.mean
PLF_28228_00003960
hypothetical protein
 $r = -0.992$, $p = 10^{-5.02}$

feature.plfam_id.acidic_residue.mean

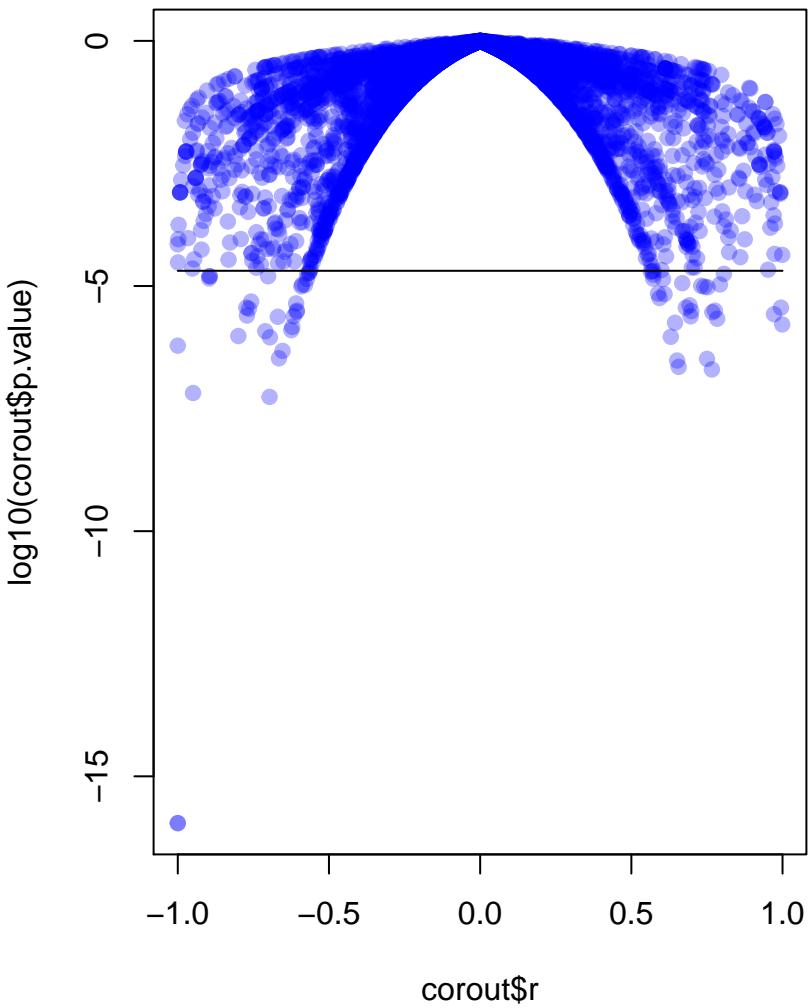


feature.plfam_id.acidic_residue.mean
PLF_28228_00018366
hypothetical protein
 $r = -0.999$, $p = 10^{-5.81}$

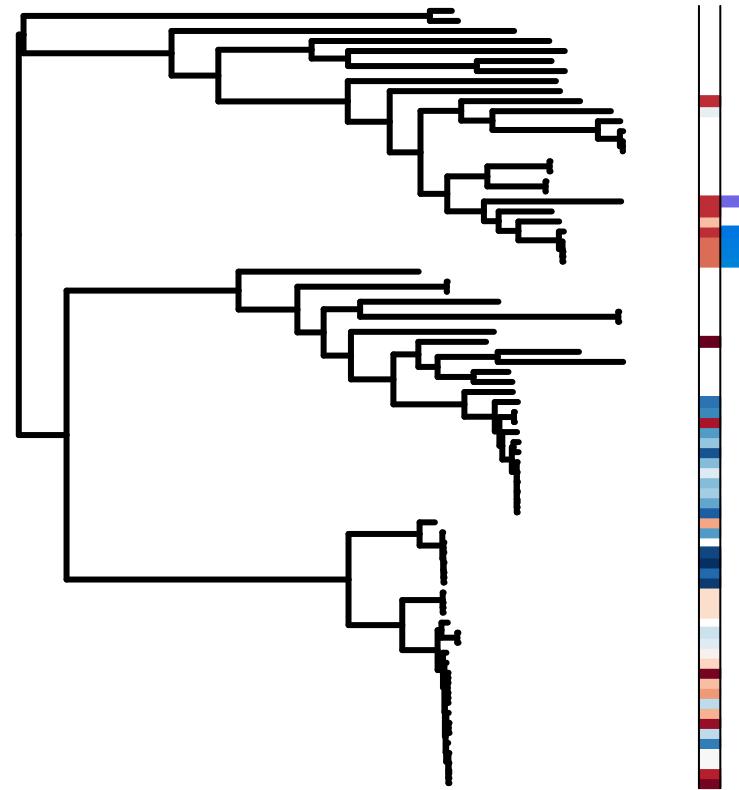
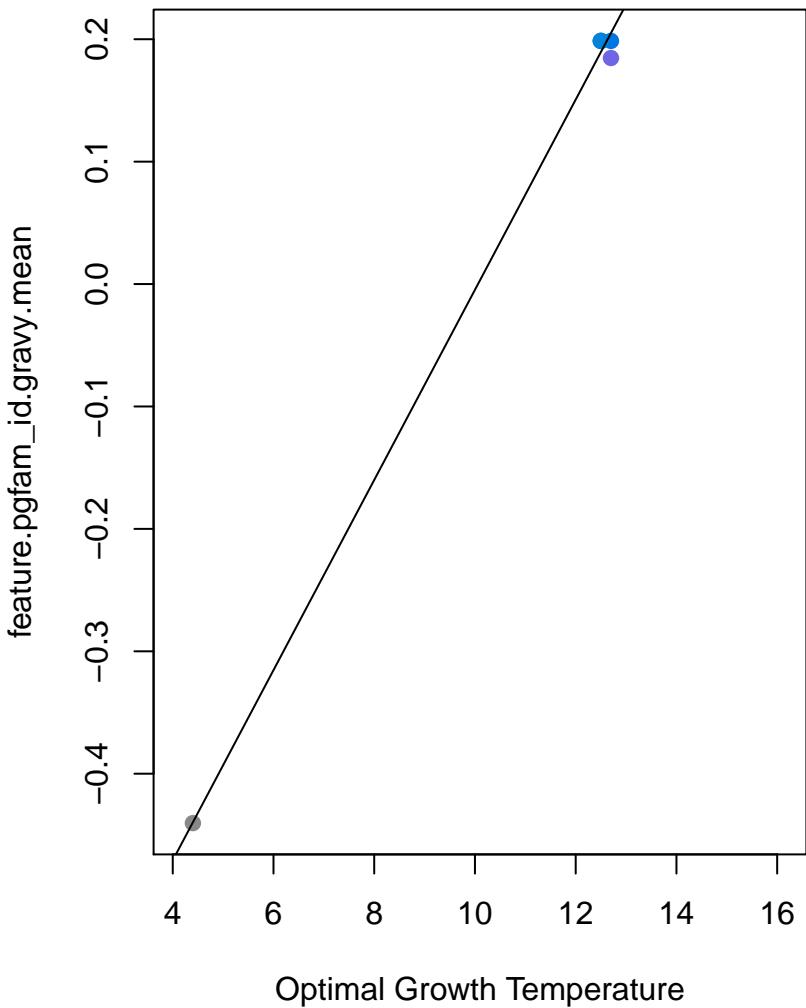
feature.plfam_id.acidic_residue.mean



`feature.pgfam_id.gravy.mean`

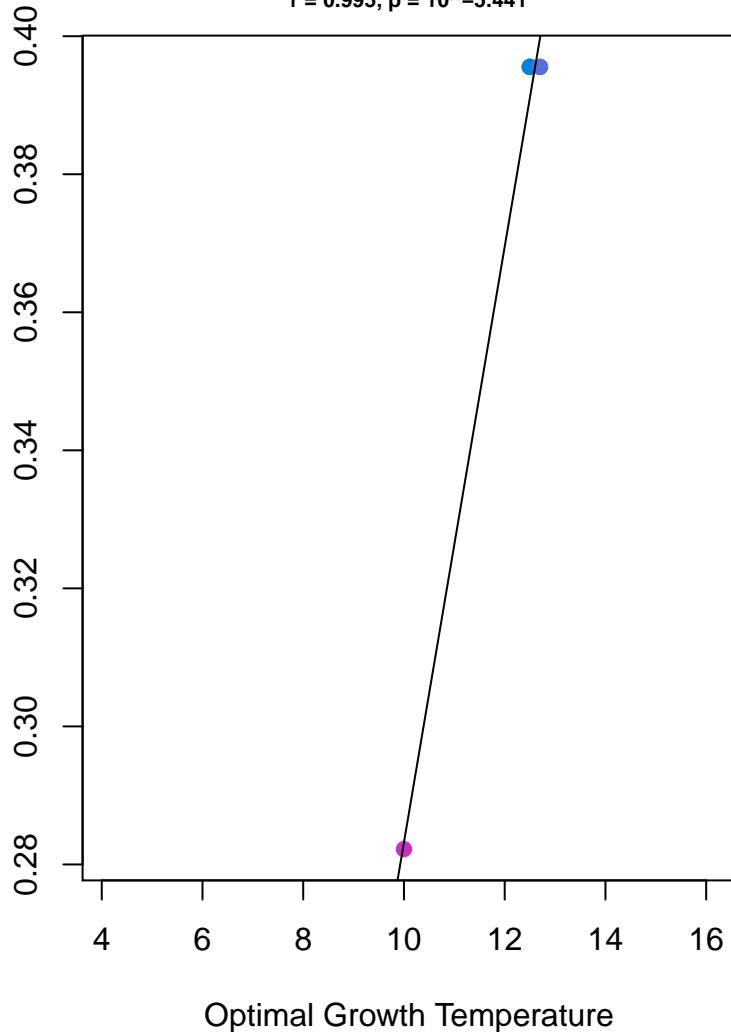


feature.pgfam_id.gravy.mean
PGF_06863675
Beta-phosphoglucomutase (EC 5.4.2.6)
 $r = 0.999$, $p = 10^{-5.784}$

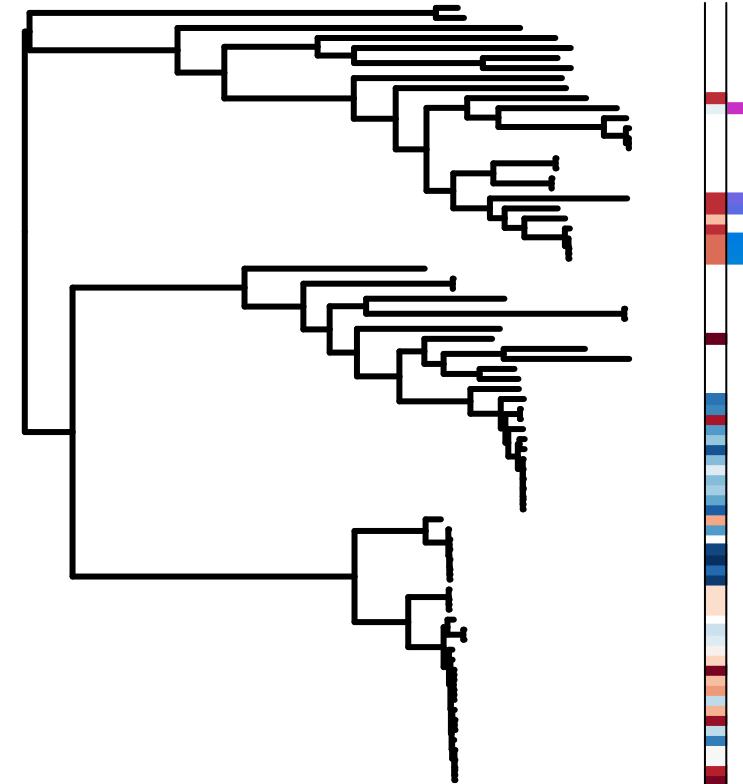


feature.pgfam_id.gravy.mean
PGF_01337096
hypothetical protein
 $r = 0.995, p = 10^{-5.441}$

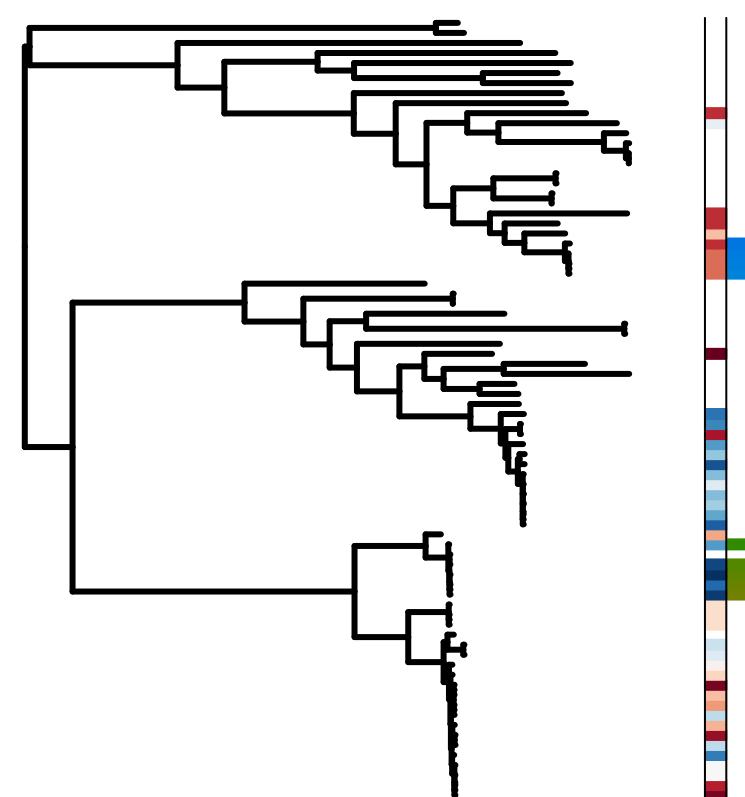
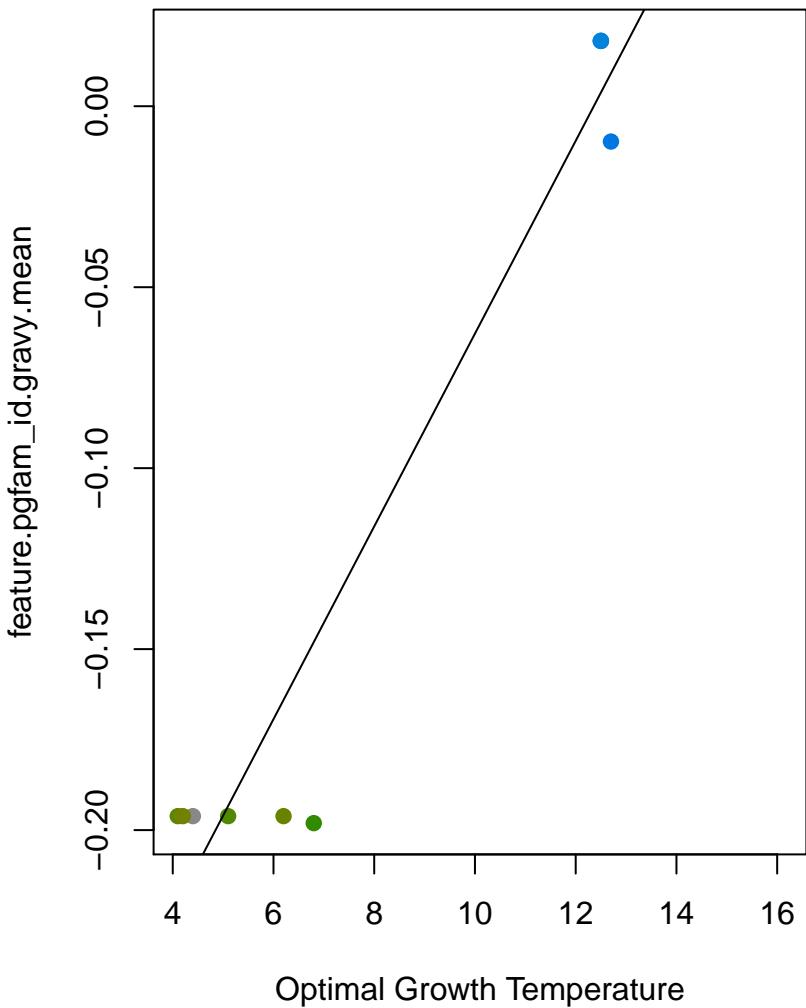
feature.pgfam_id.gravy.mean



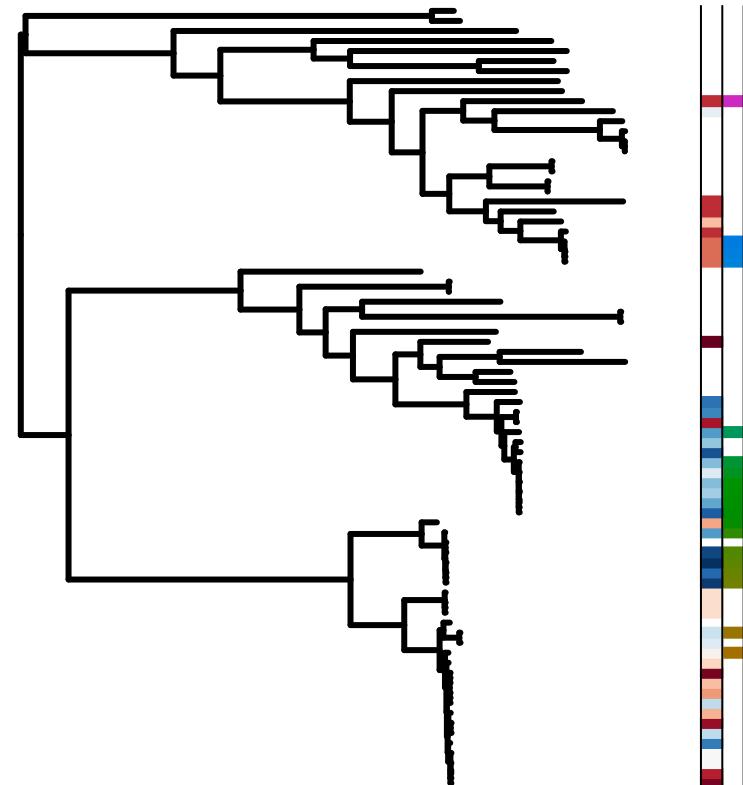
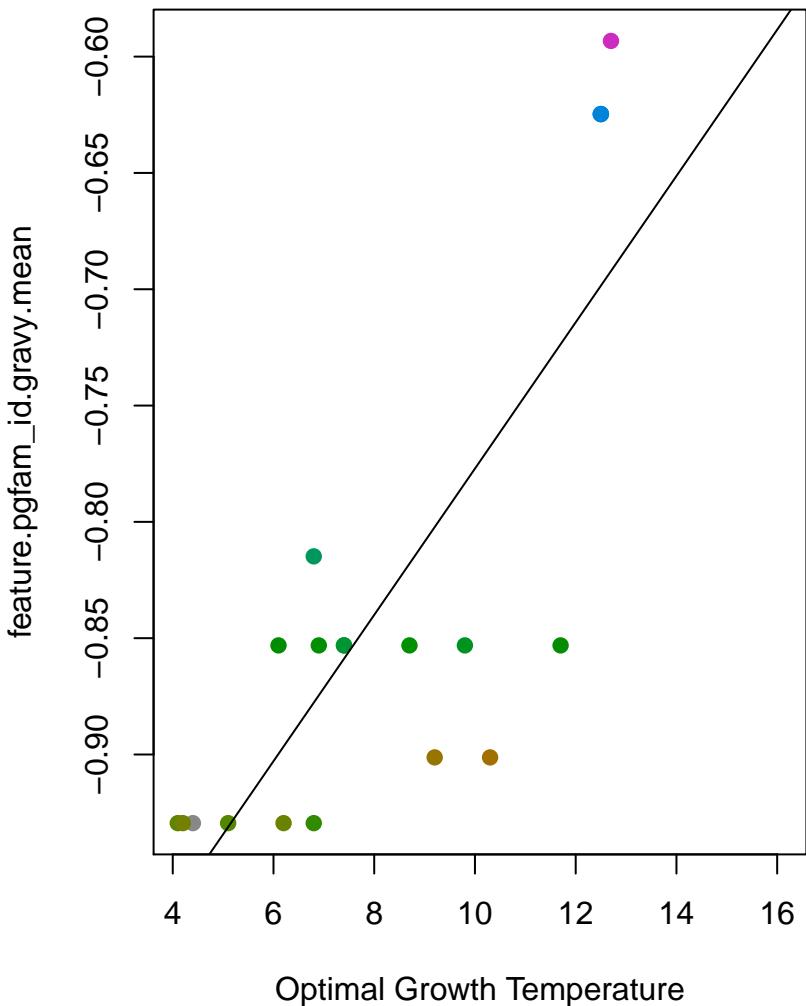
Optimal Growth Temperature



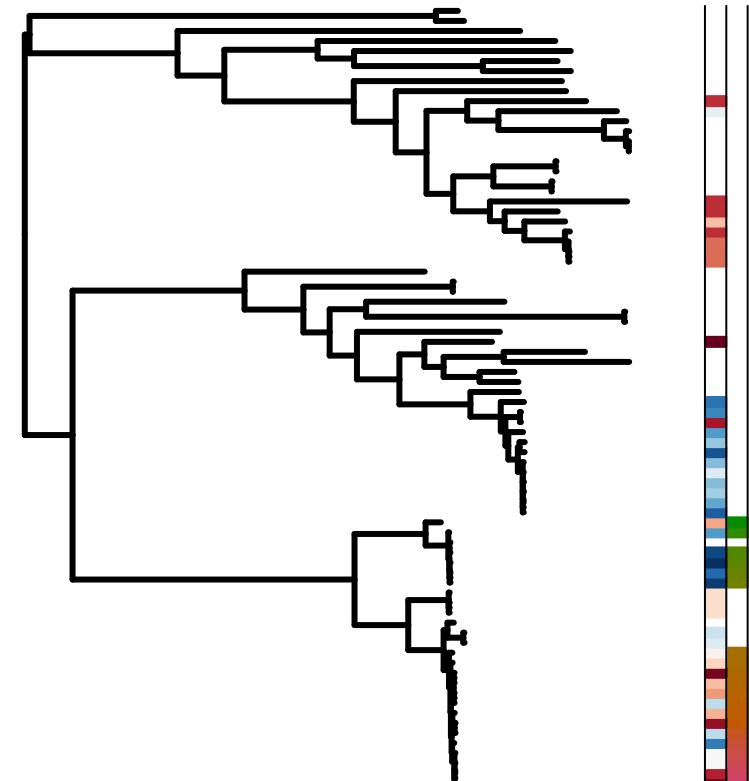
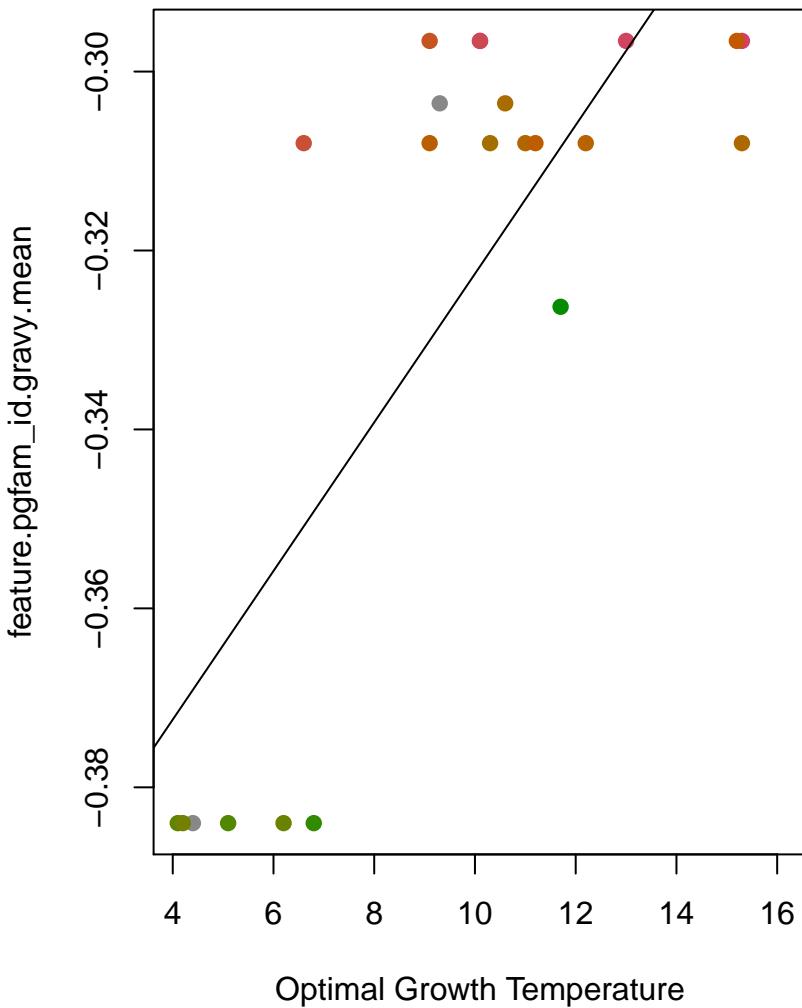
feature.pgfam_id.gravy.mean
PGF_01338043
hypothetical protein
 $r = 0.972$, $p = 10^{-5.575}$



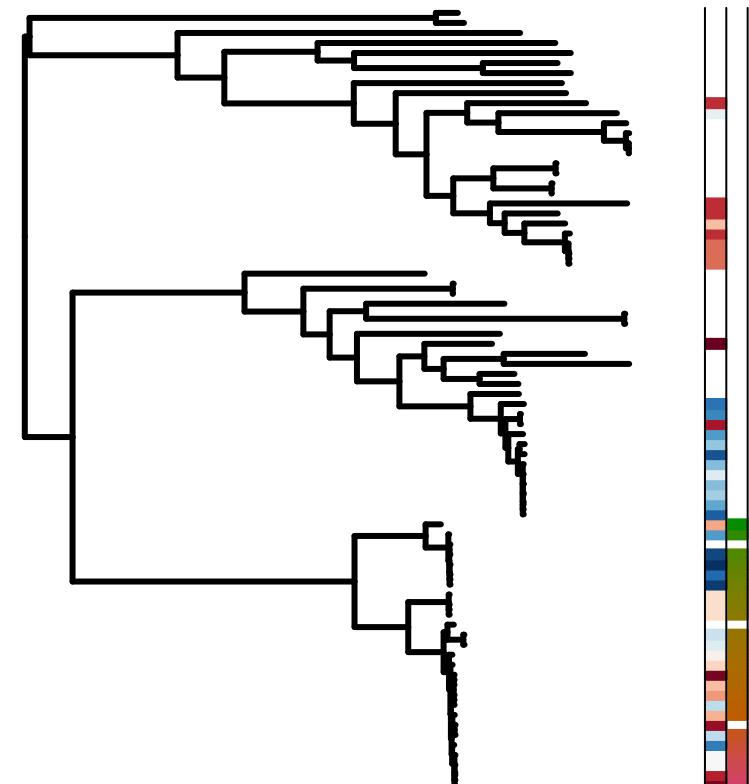
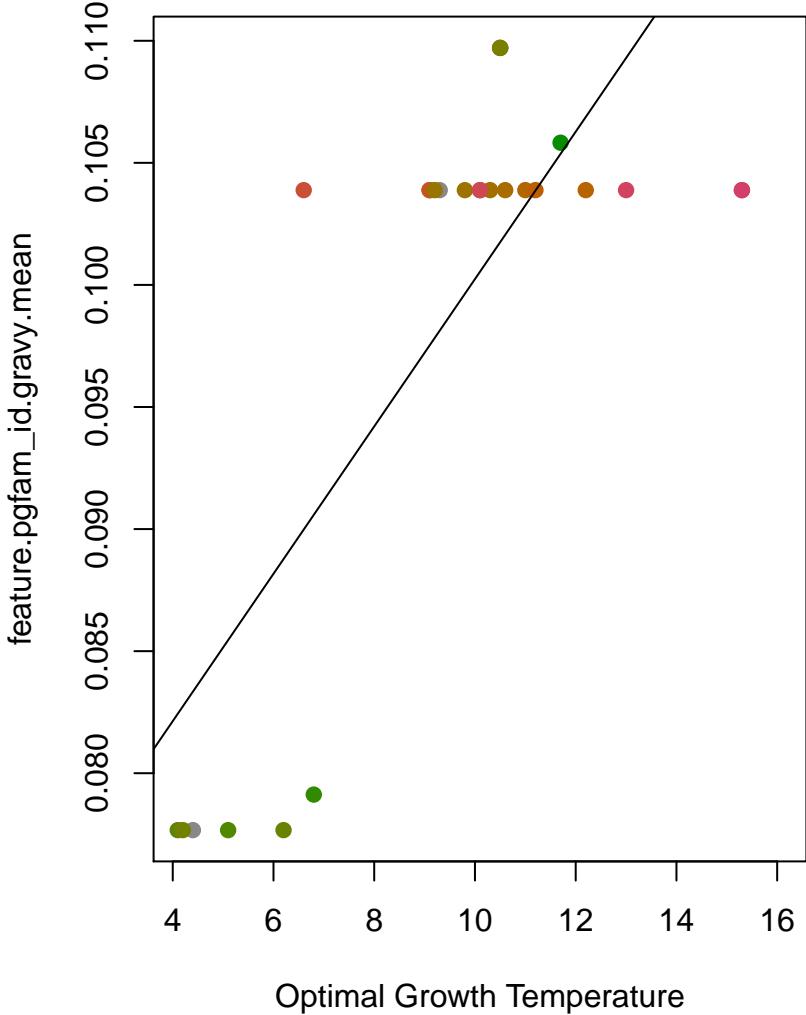
feature.pgfam_id.gravy.mean
PGF_00257343
hypothetical protein
 $r = 0.806$, $p = 10^{-4.752}$



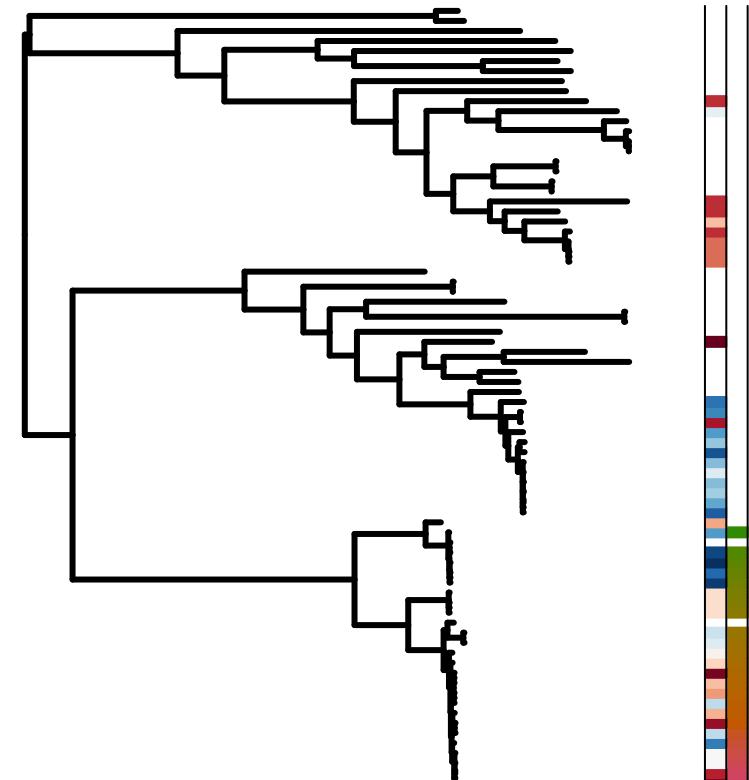
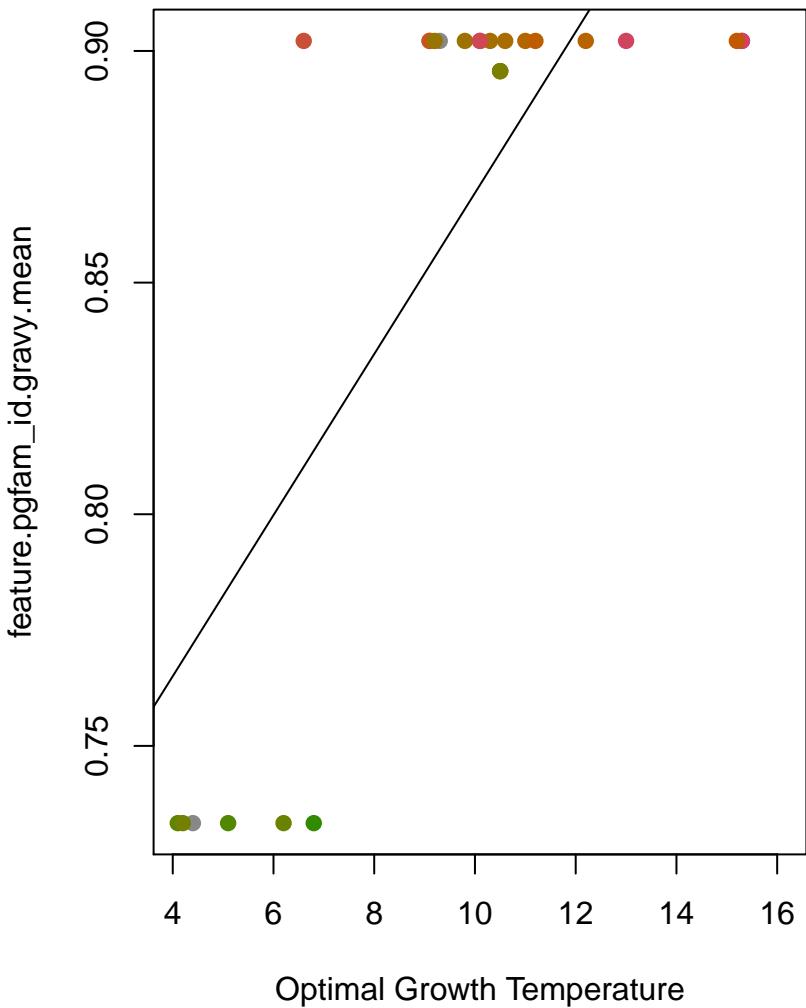
feature.pgfam_id.gravy.mean
PGF_10918576
hypothetical protein
 $r = 0.793, p = 10^{-4.969}$



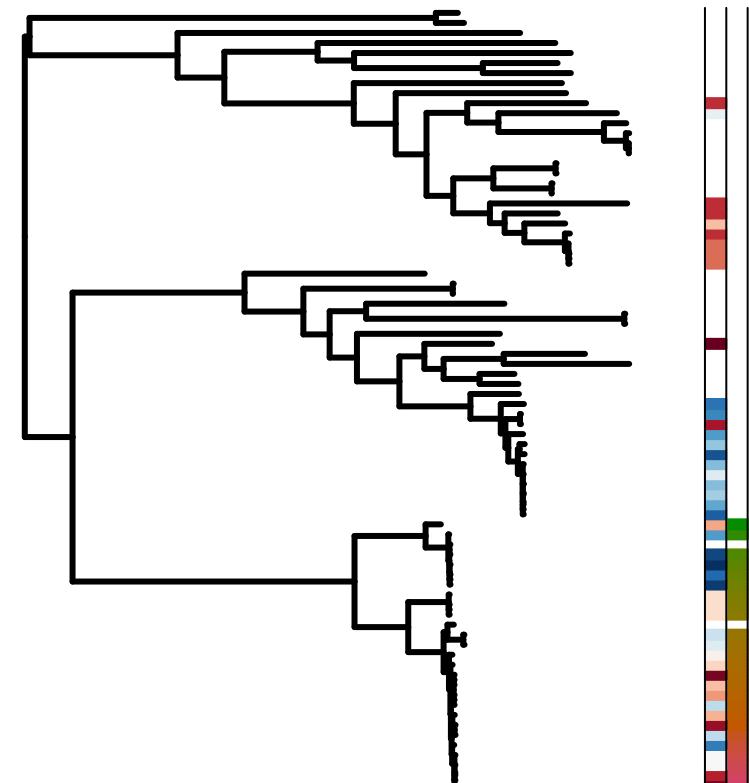
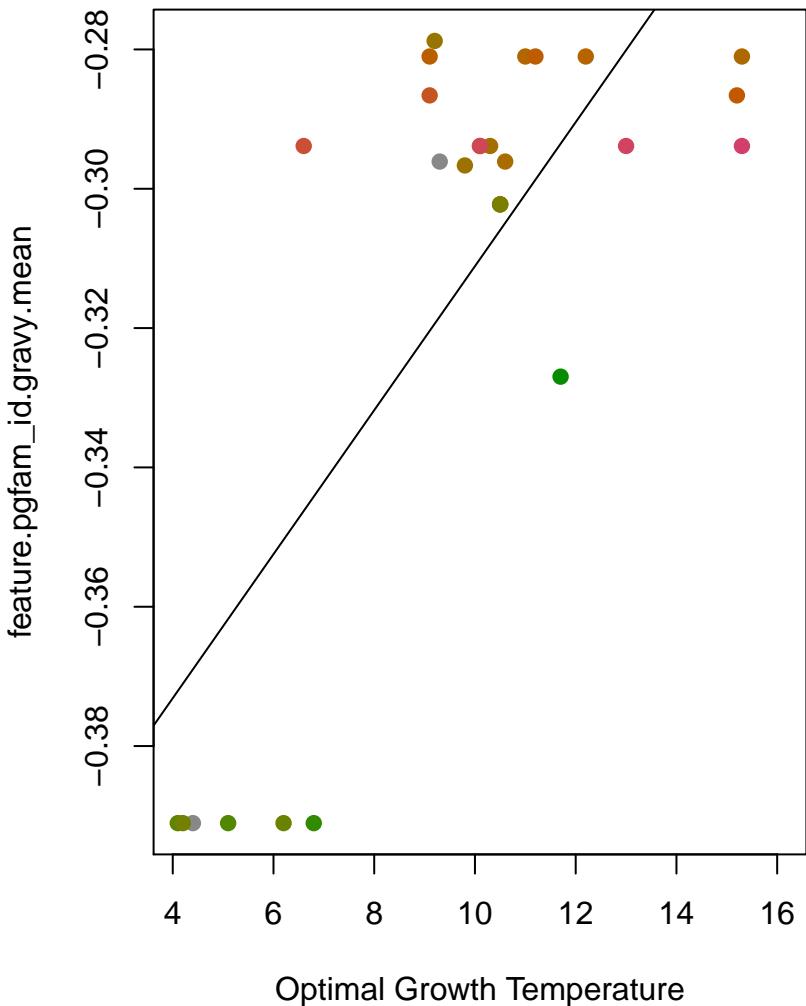
feature.pgfam_id.gravy.mean
PGF_07210740
hypothetical protein
 $r = 0.784$, $p = 10^{-5.667}$

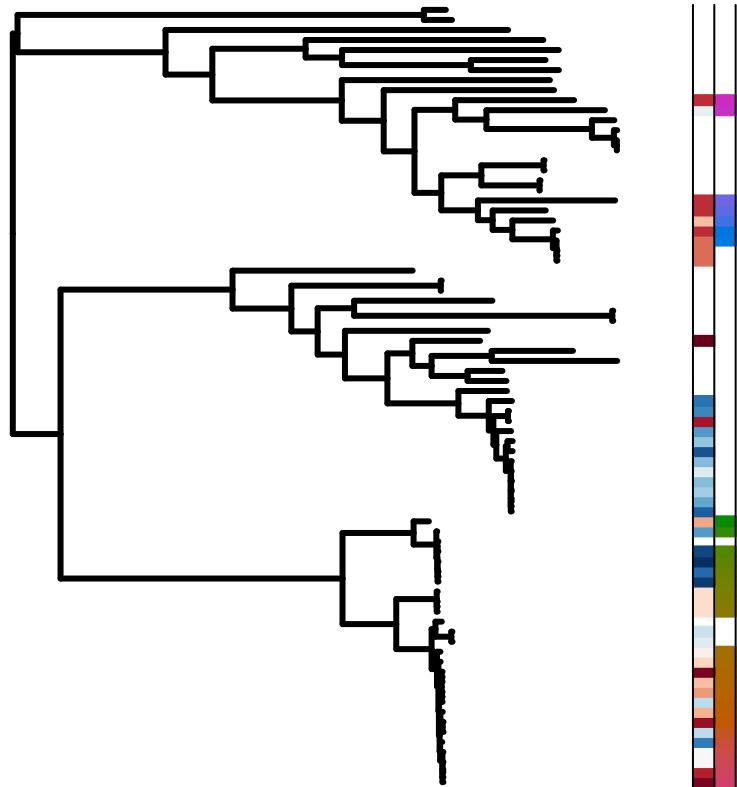
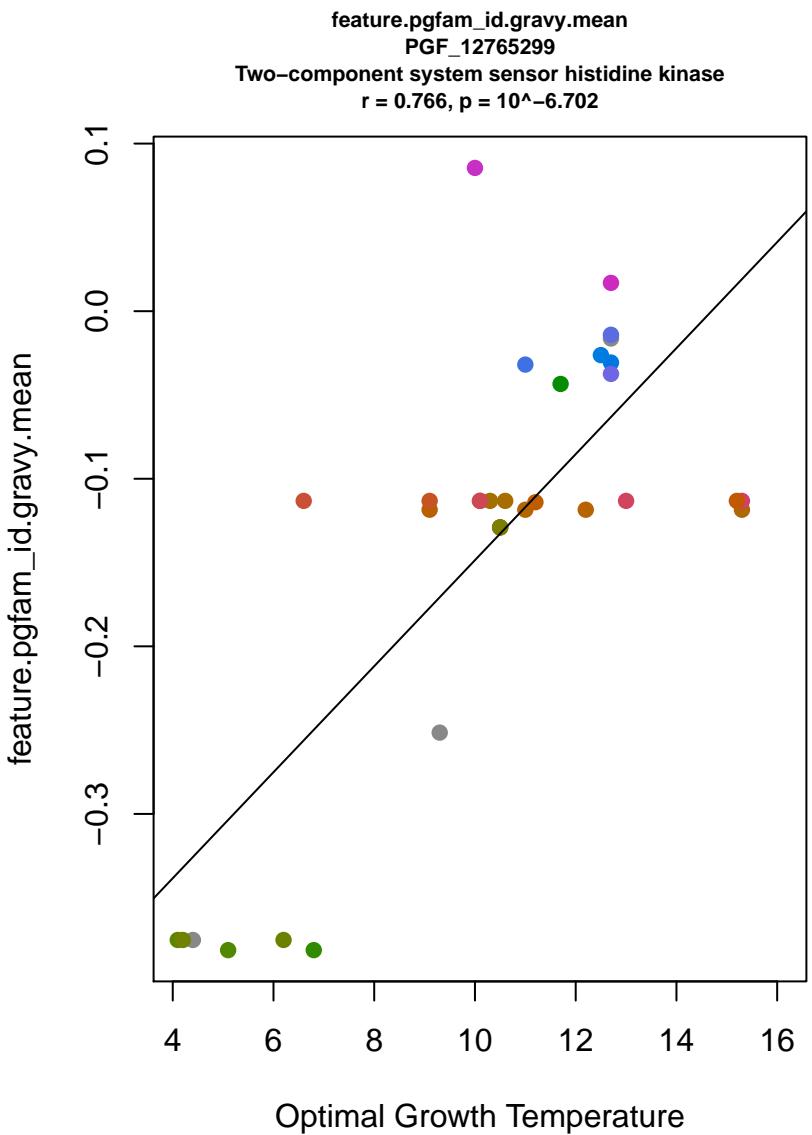


feature.pgfam_id.gravy.mean
PGF_12071964
hypothetical protein
 $r = 0.776$, $p = 10^{-5.502}$

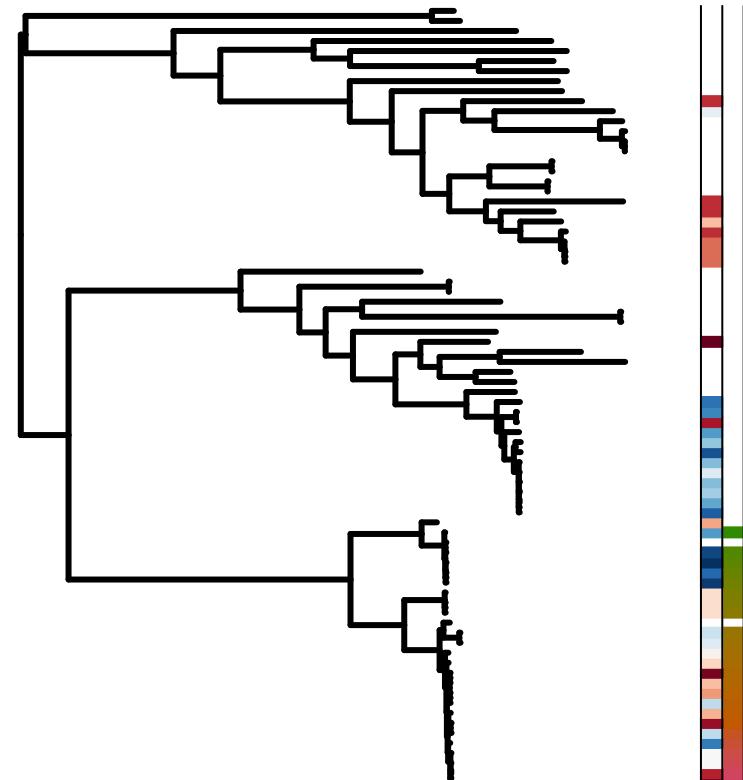
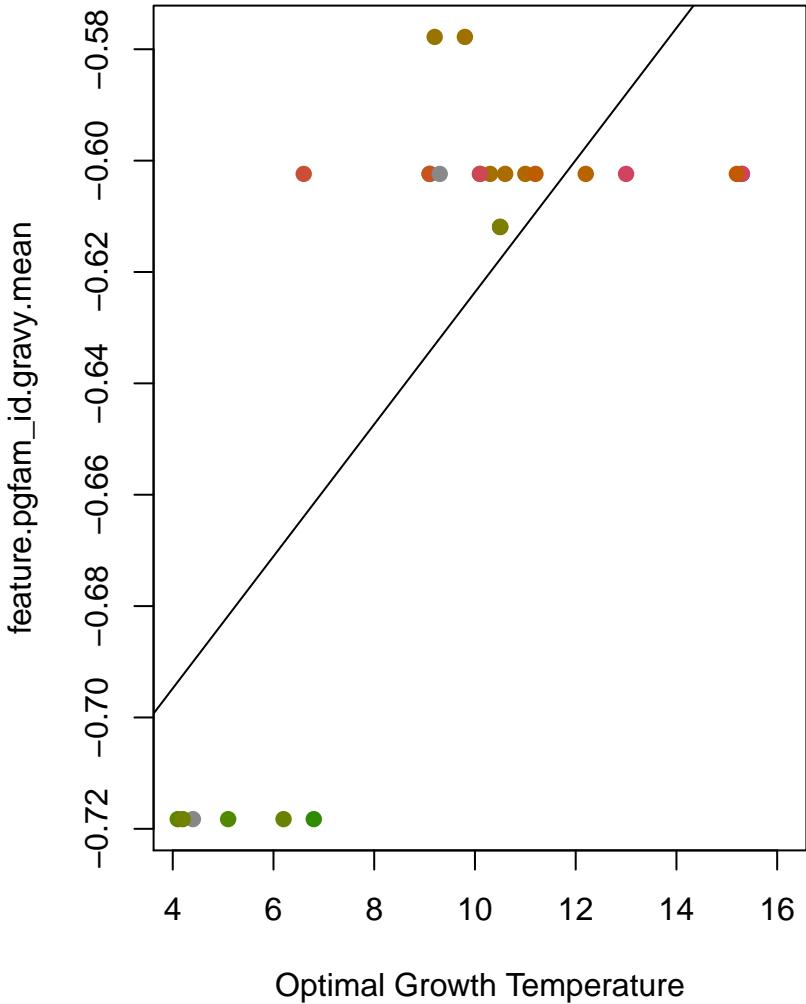


feature.pgfam_id.gravy.mean
PGF_07250446
hypothetical protein
 $r = 0.768$, $p = 10^{-5.534}$

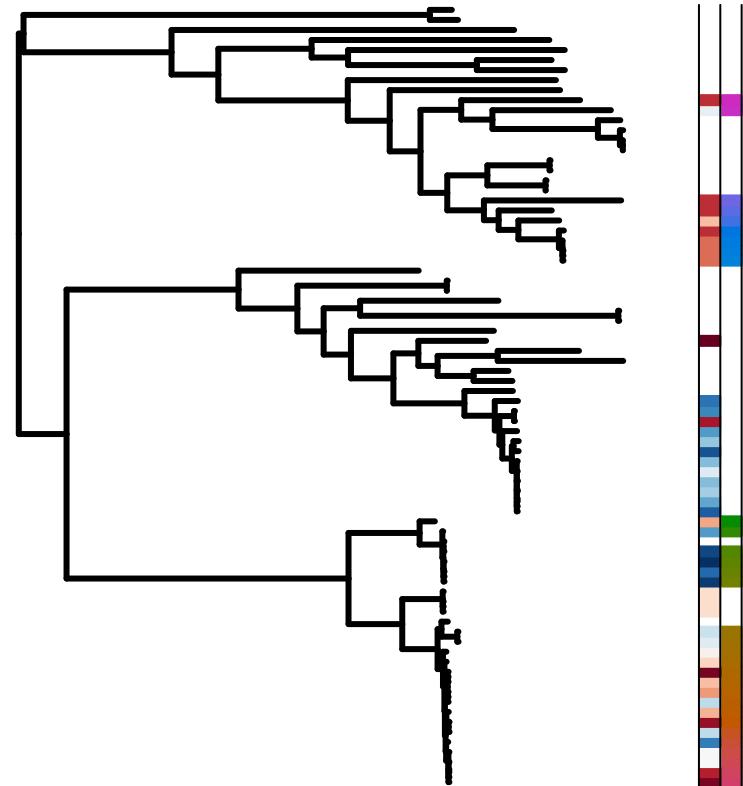
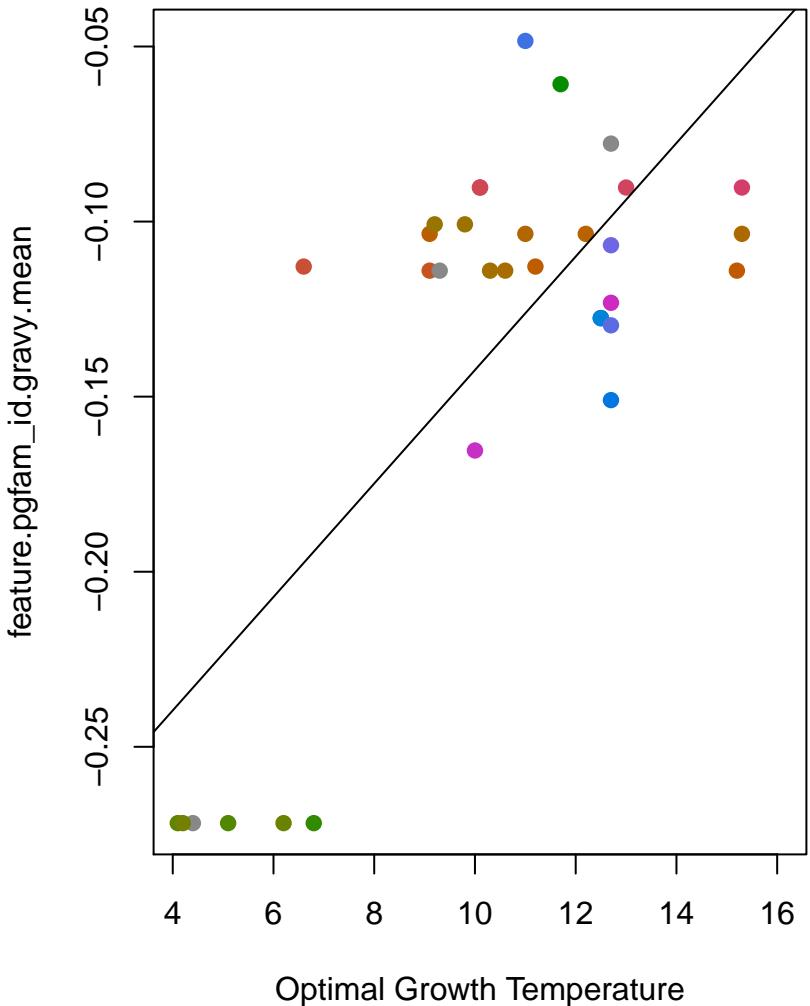




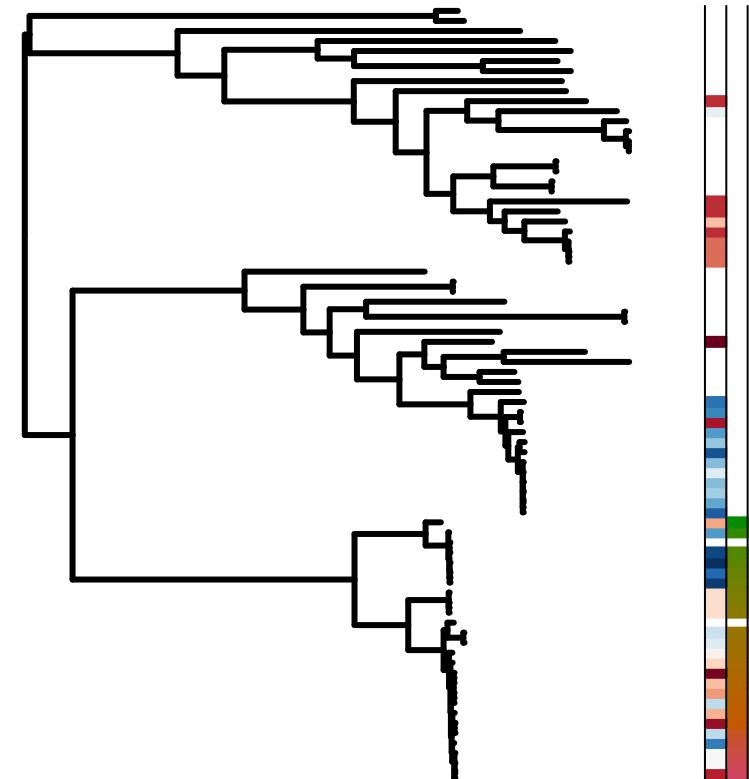
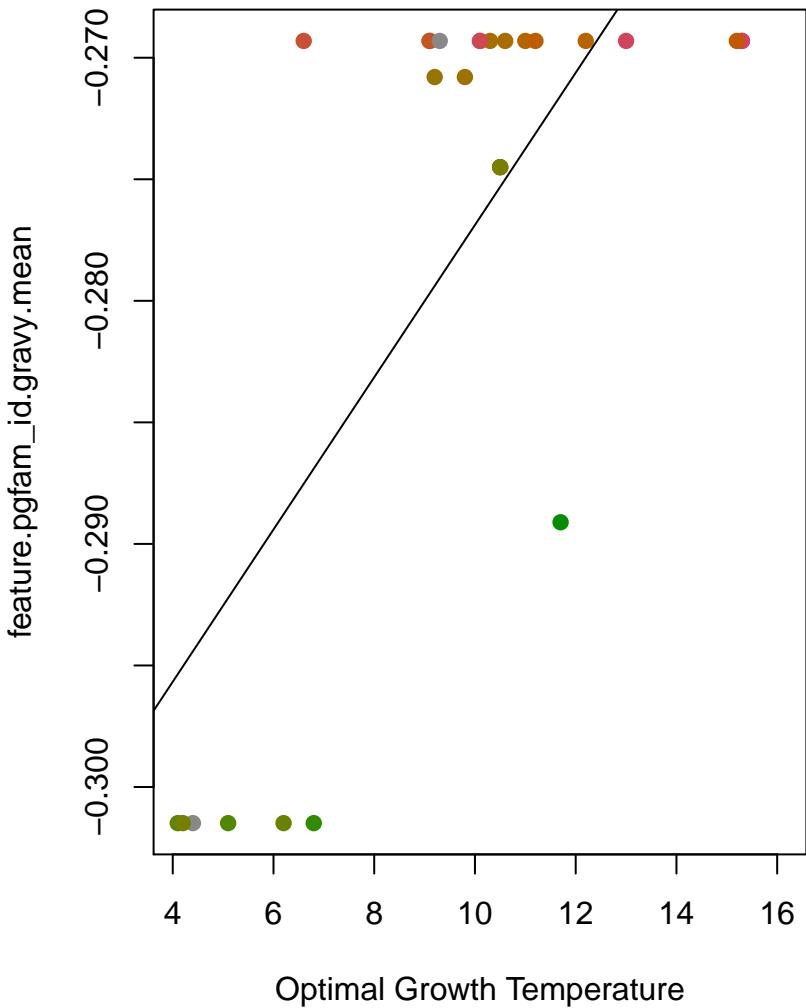
feature.pgfam_id.gravy.mean
PGF_12288710
hypothetical protein
 $r = 0.752$, $p = 10^{-5.025}$



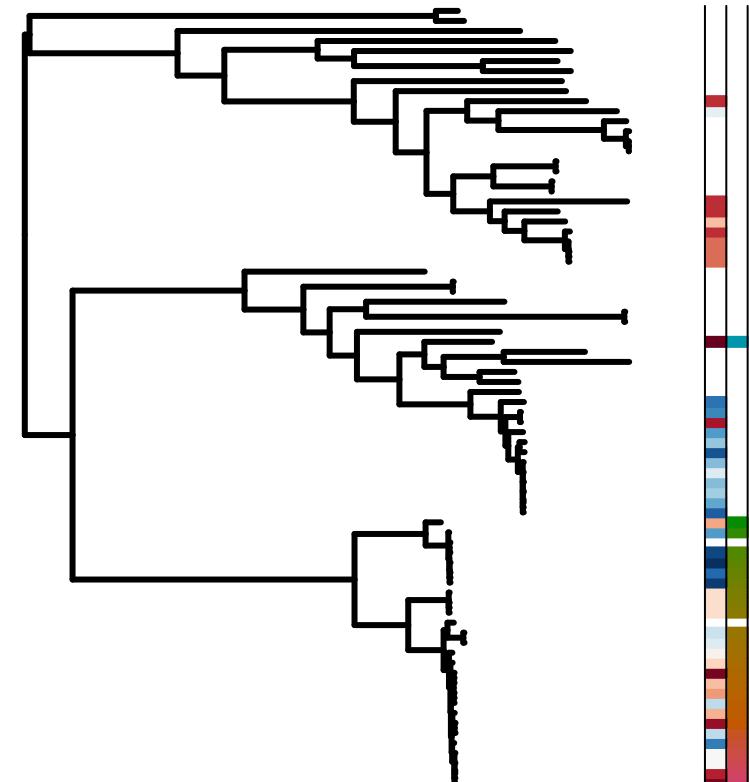
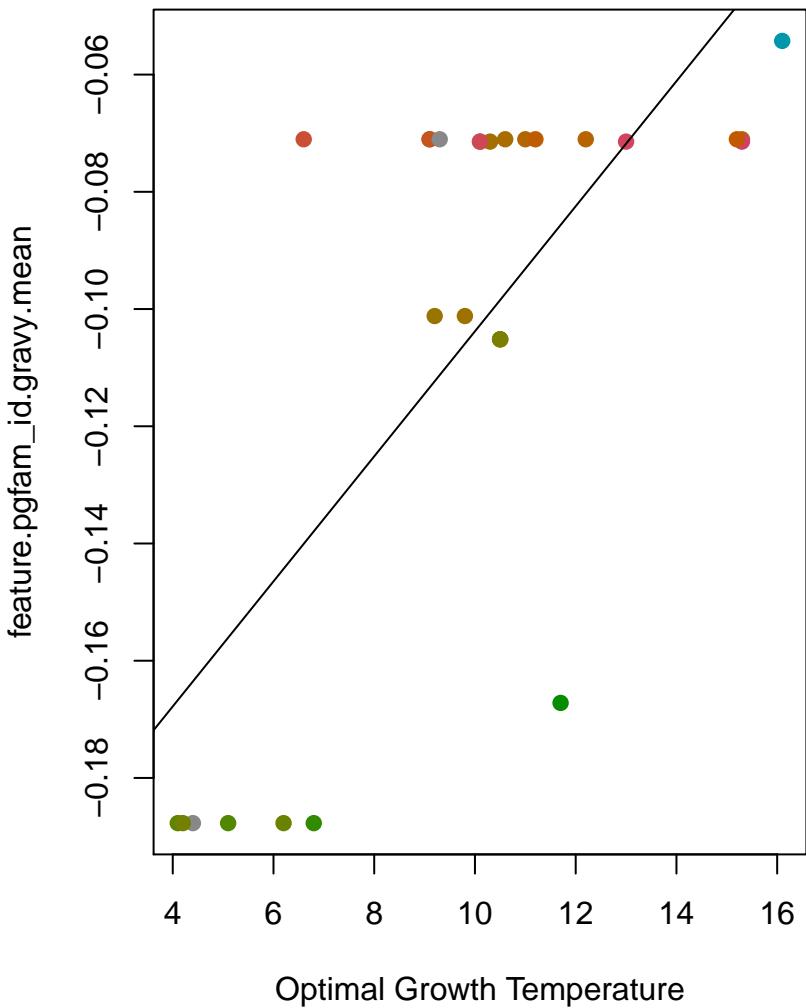
feature.pgfam_id.gravy.mean
PGF_01336501
hypothetical protein
 $r = 0.75$, $p = 10^{-6.486}$



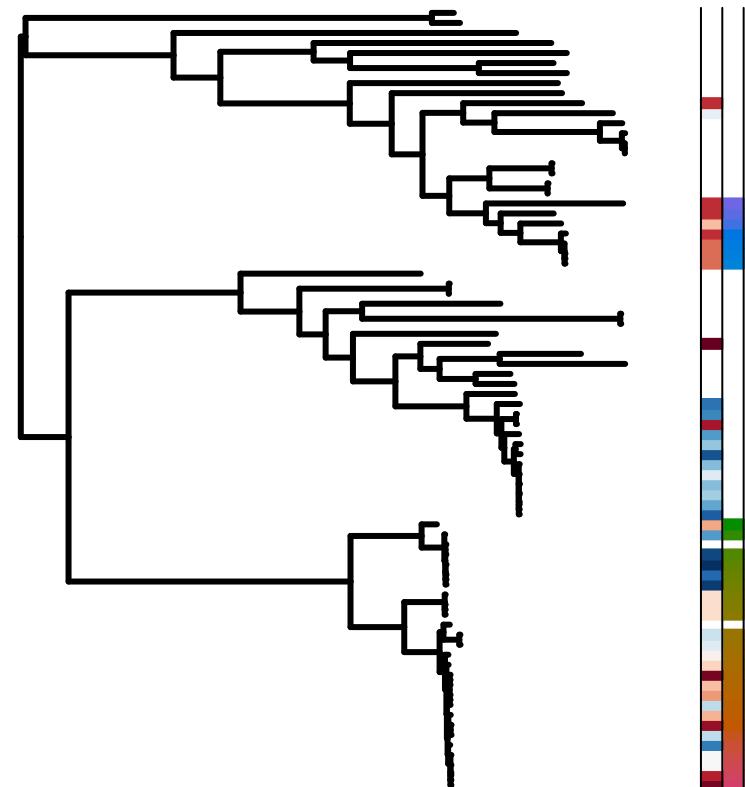
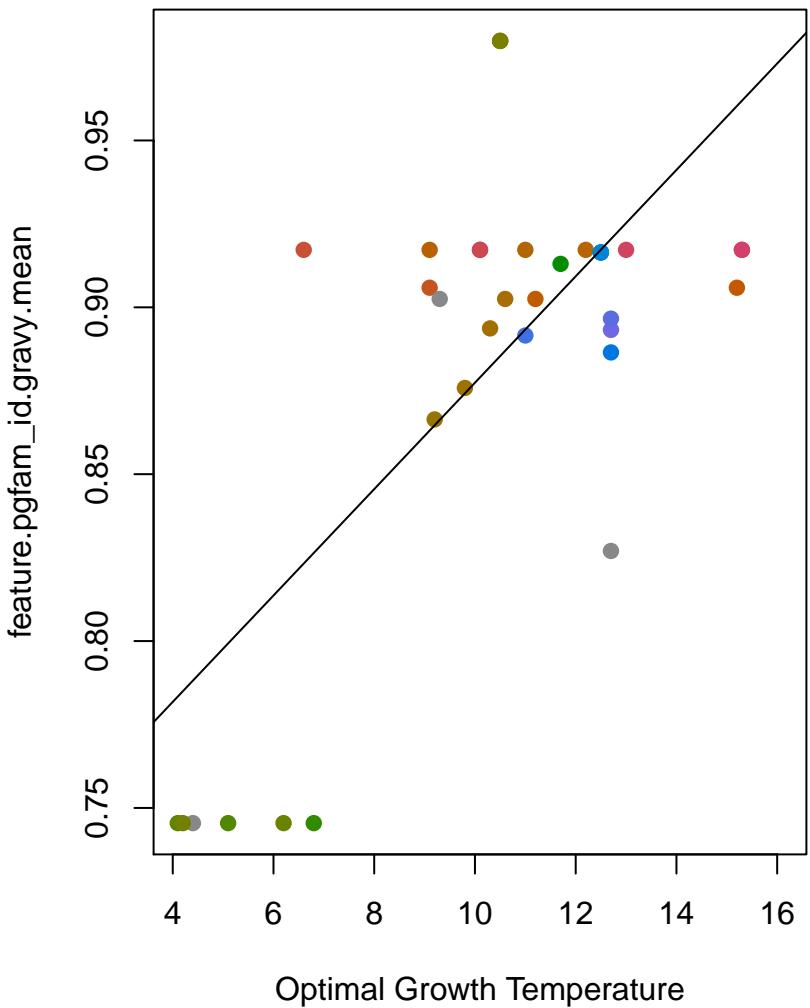
feature.pgfam_id.gravy.mean
PGF_11979758
hypothetical protein
 $r = 0.741, p = 10^{-5.014}$



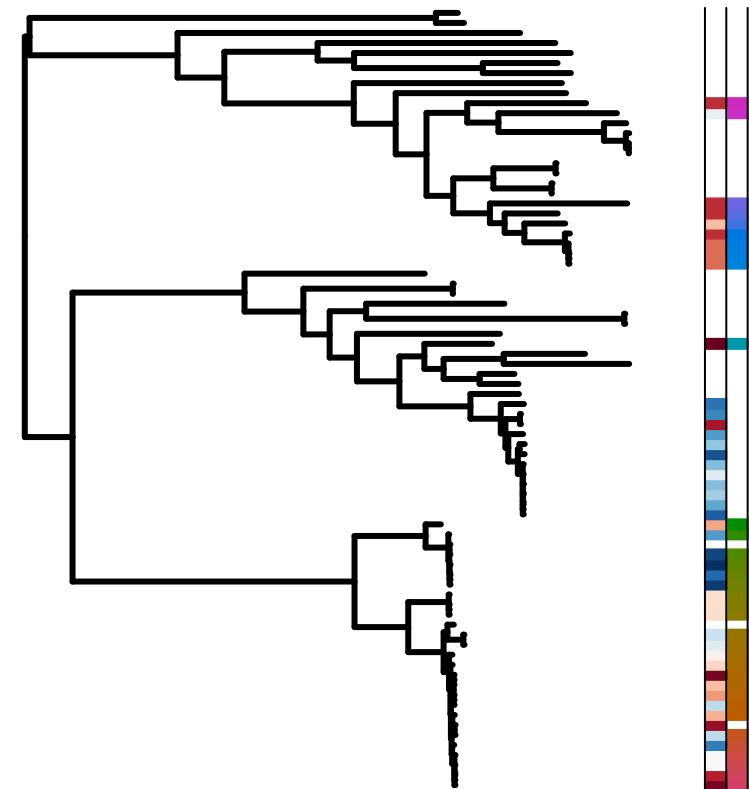
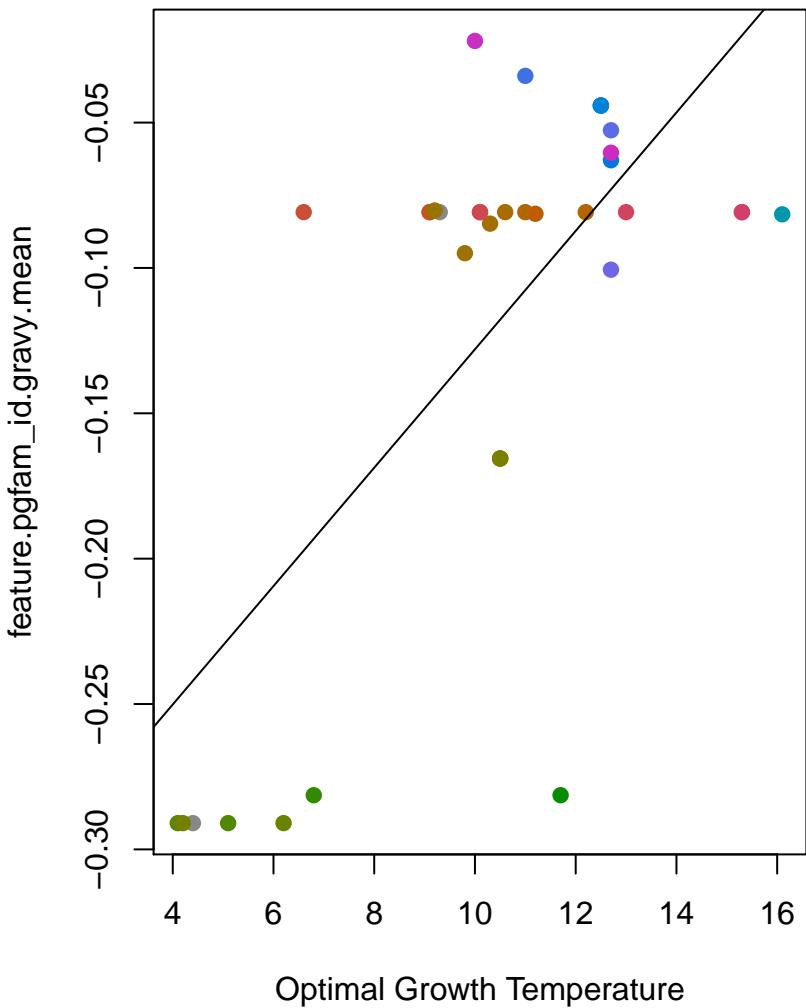
feature.pgfam_id.gravy.mean
PGF_07824917
hypothetical protein
 $r = 0.731, p = 10^{-4.995}$



feature.pgfam_id.gravy.mean
PGF_00067426
ZIP zinc transporter family protein
 $r = 0.698$, $p = 10^{-5.511}$



feature.pgfam_id.gravy.mean
PGF_03021302
Ureidoglycolate lyase (EC 4.3.2.3)
 $r = 0.696$, $p = 10^{-5.618}$

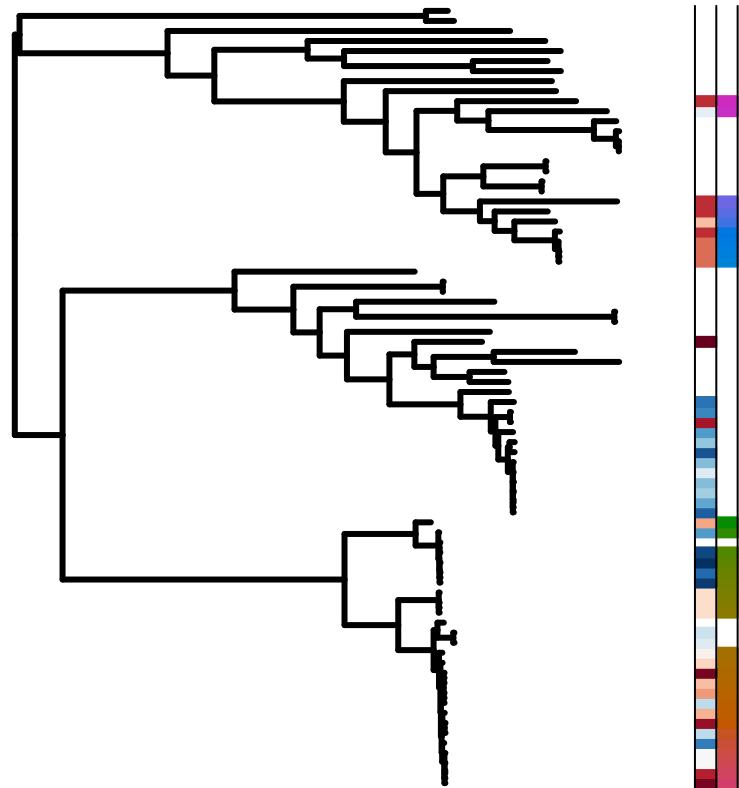
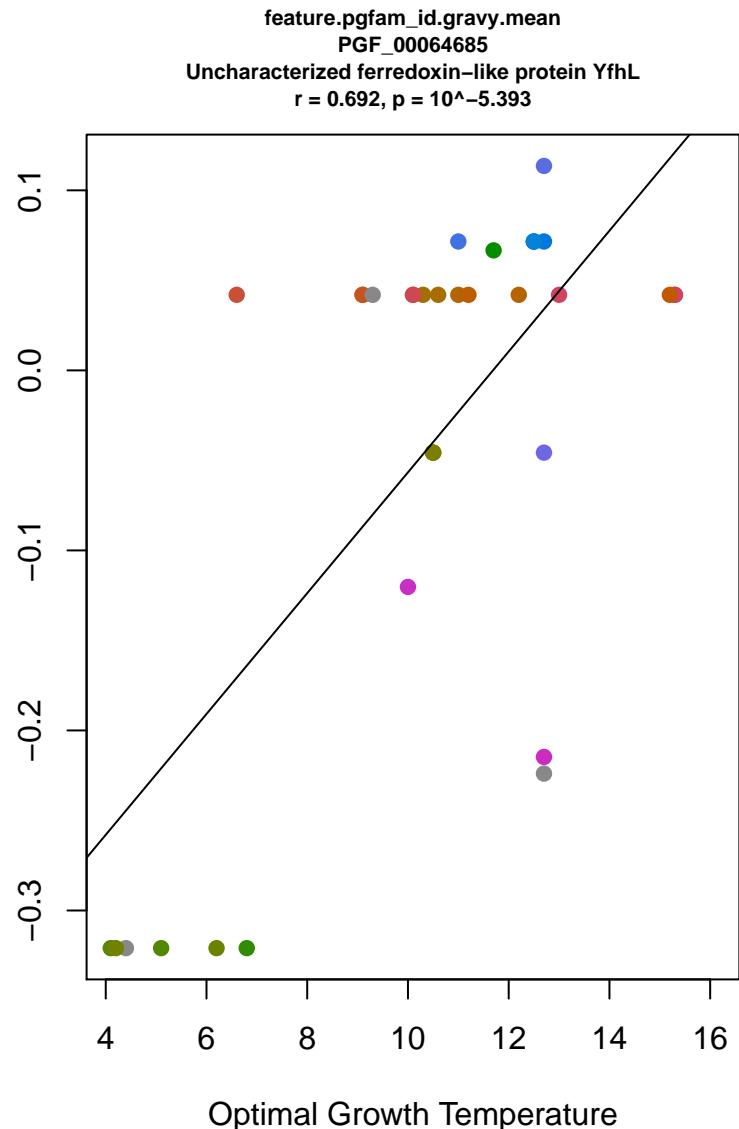


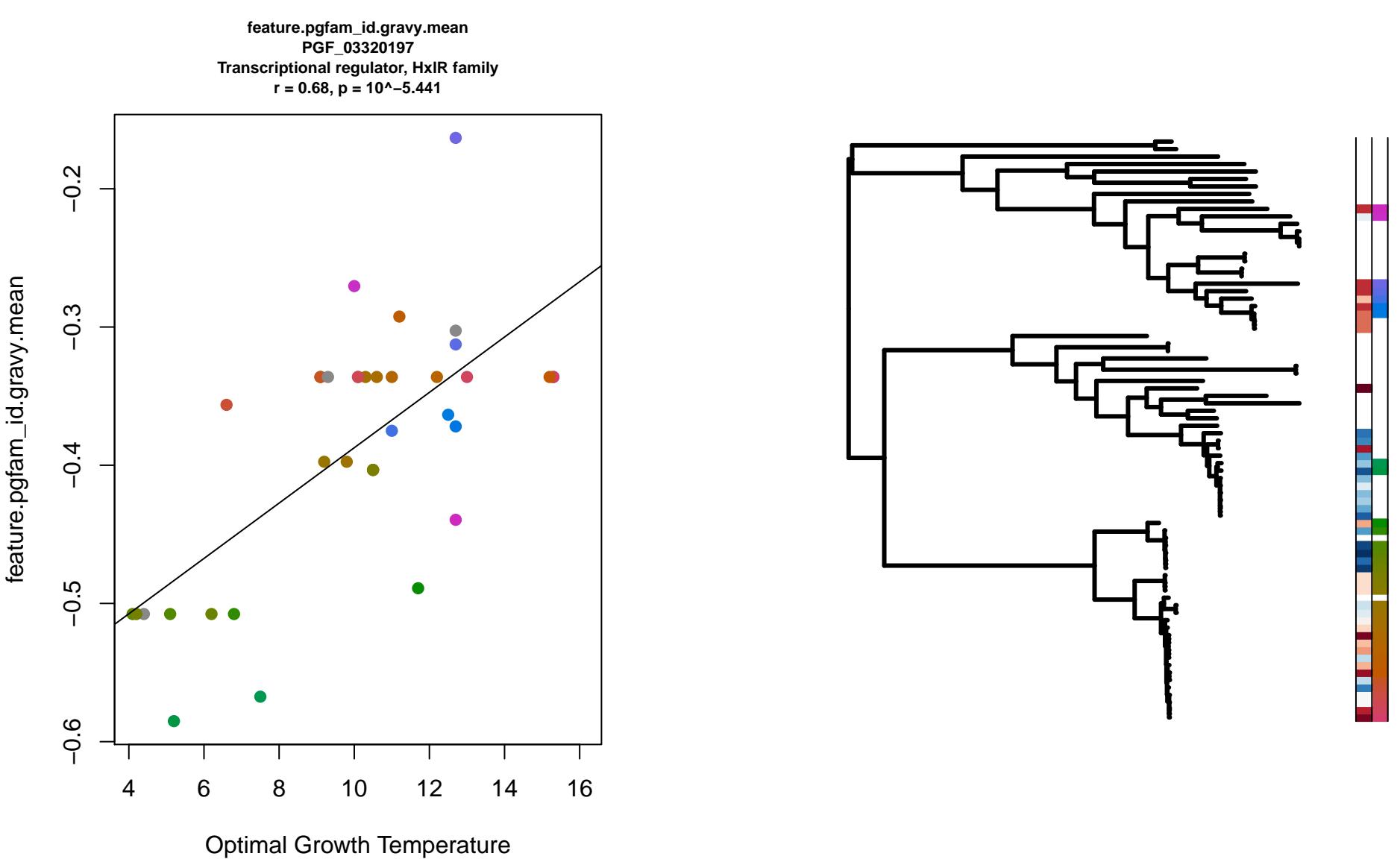
feature.pgfam_id.gravy.mean

PGF_00064685

Uncharacterized ferredoxin-like protein YfhL

$r = 0.692, p = 10^{-5.393}$



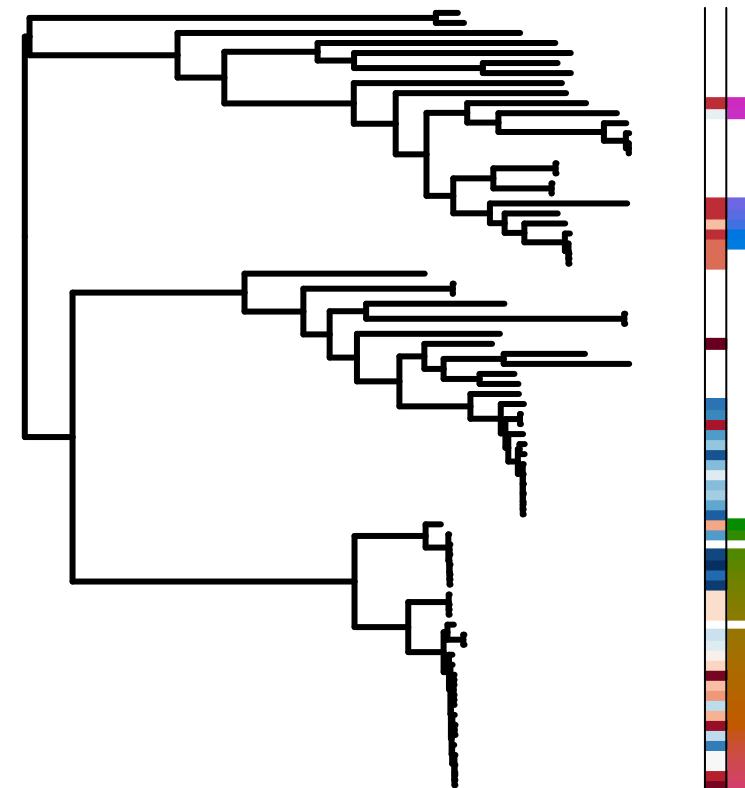
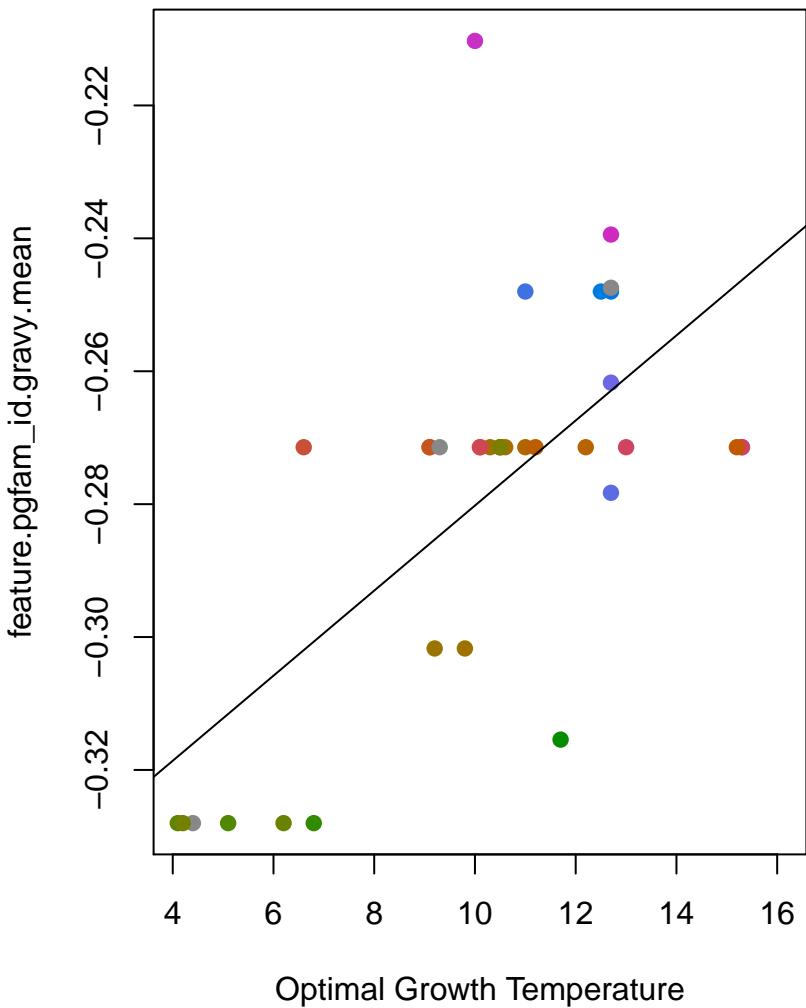


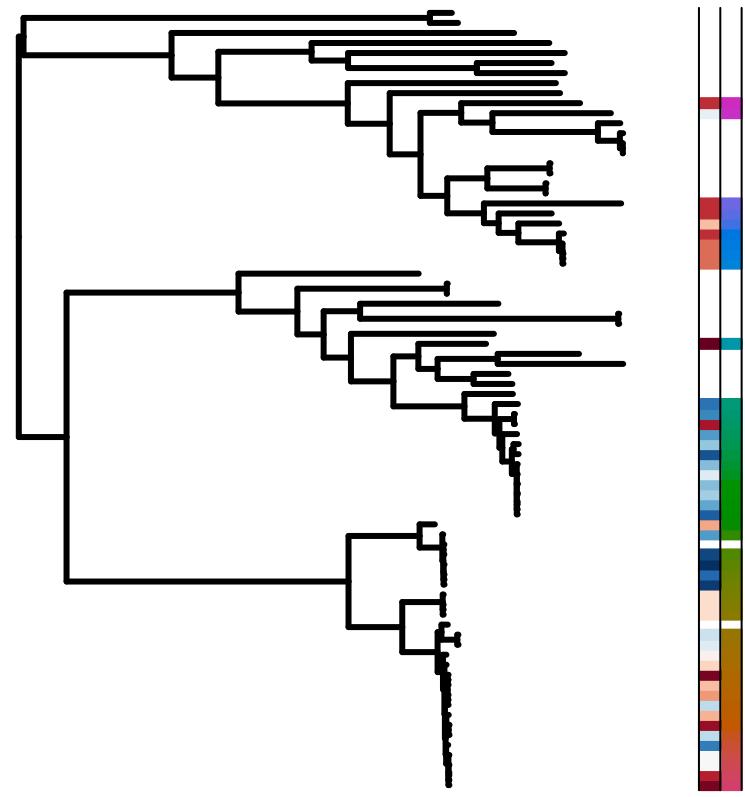
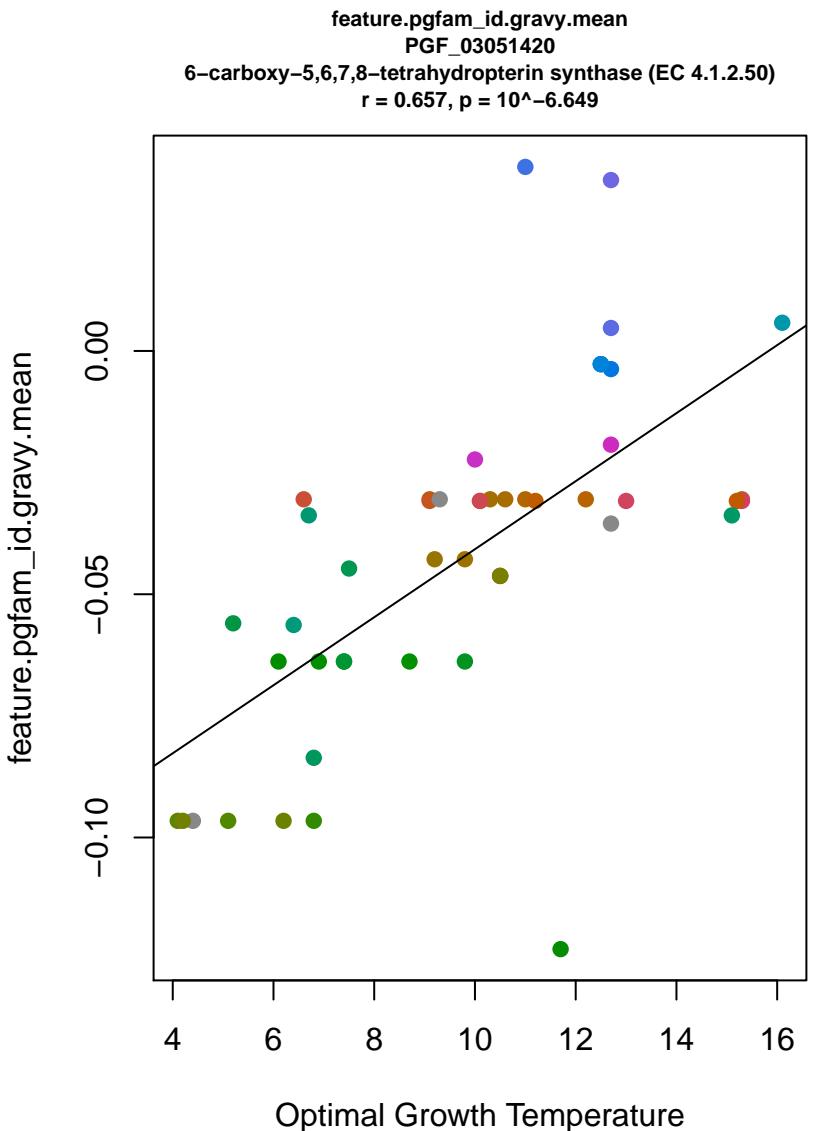
feature.pgfam_id.gravy.mean

PGF_06077968

Bacterial non-heme ferritin (EC 1.16.3.2)

$r = 0.668, p = 10^{-4.942}$



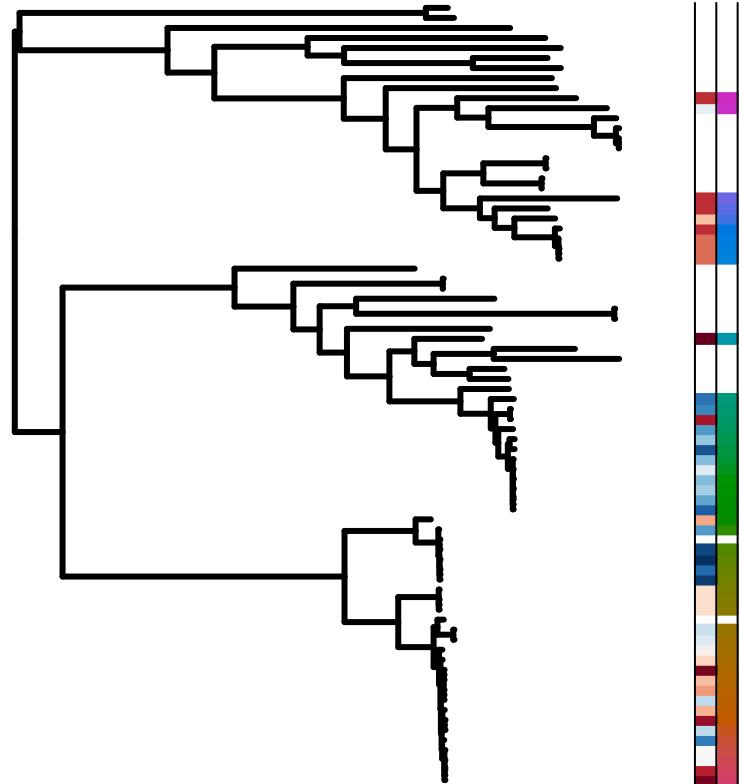
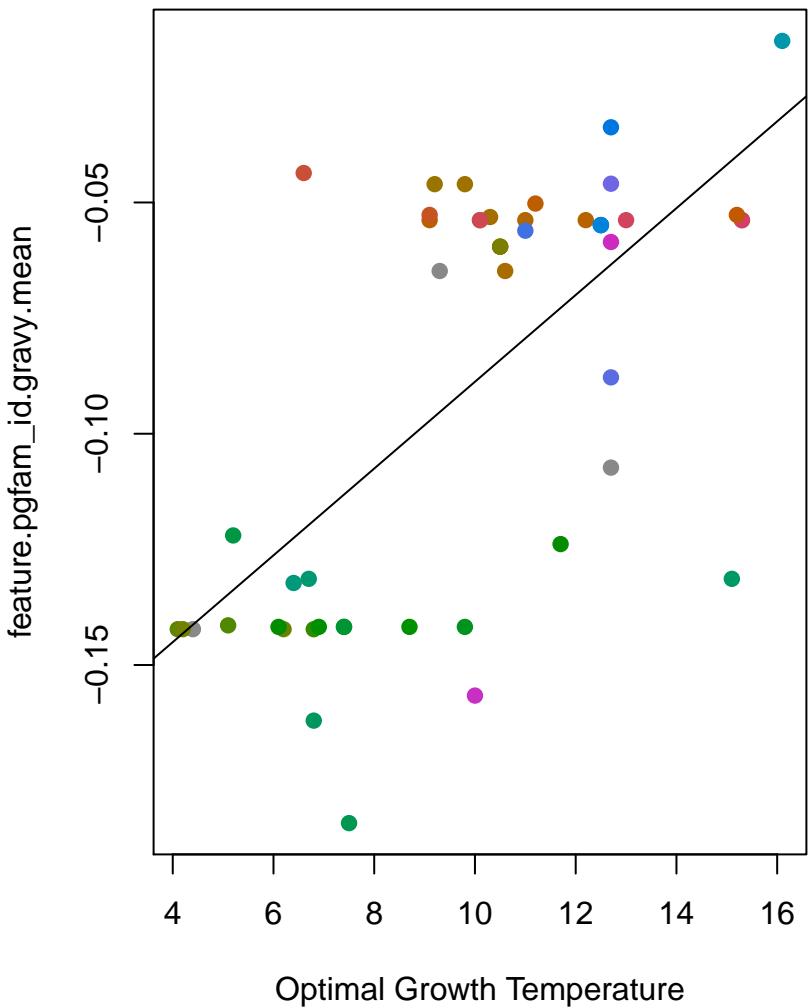


feature.pgfam_id.gravy.mean

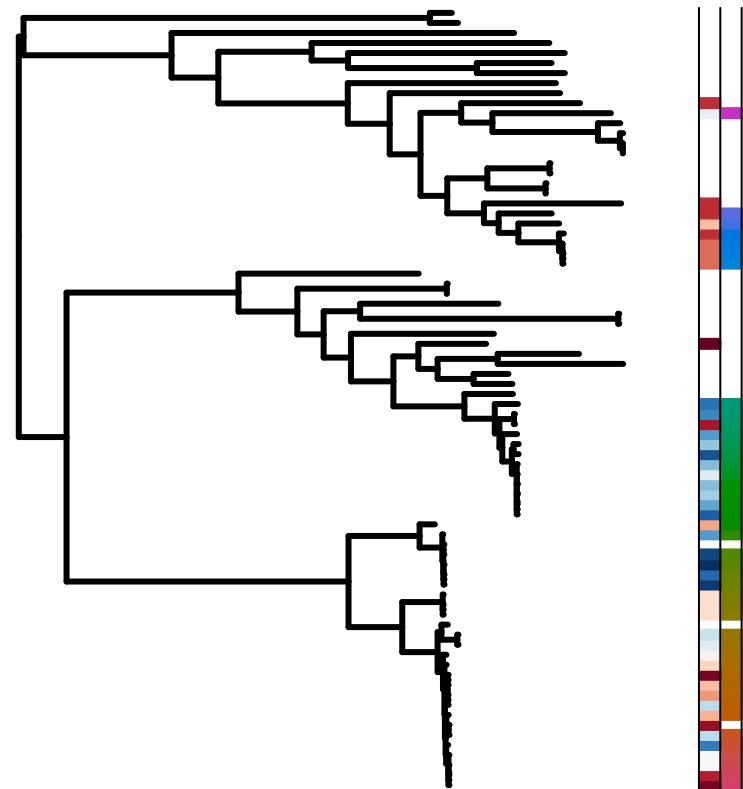
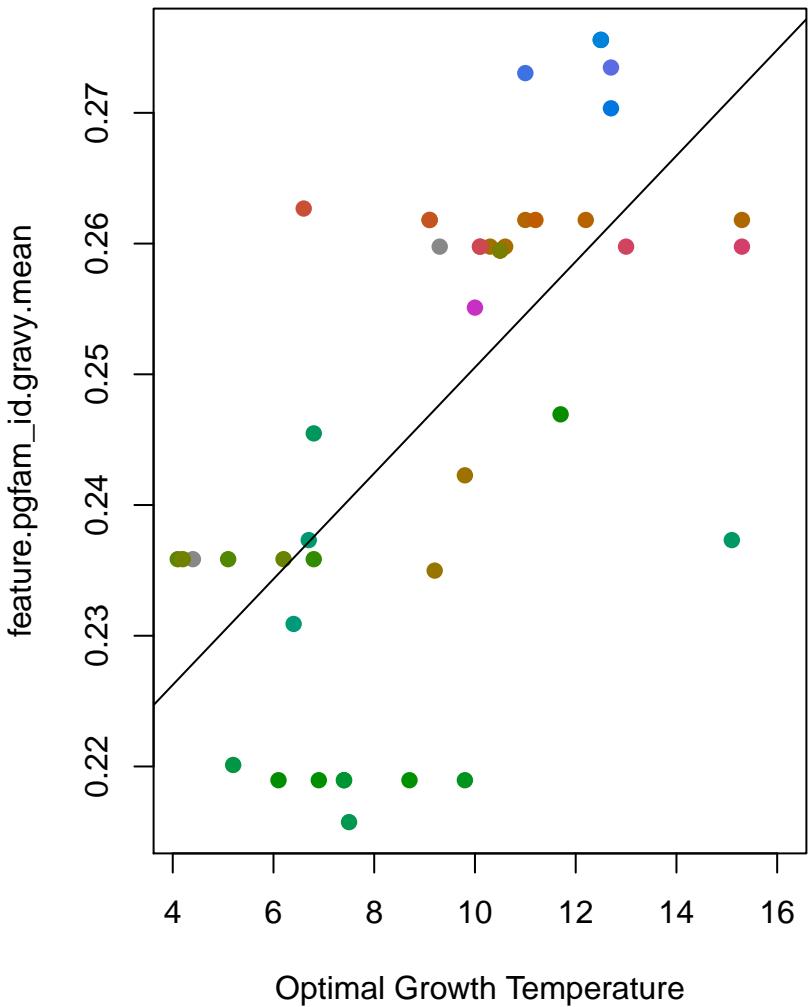
PGF_00417755

ubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6-hydroxyphenyl methylase (E

$r = 0.651, p = 10^{-6.519}$



feature.pgfam_id.gravy.mean
PGF_05770898
Selenide,water dikinase (EC 2.7.9.3)
 $r = 0.644$, $p = 10^{-5.749}$



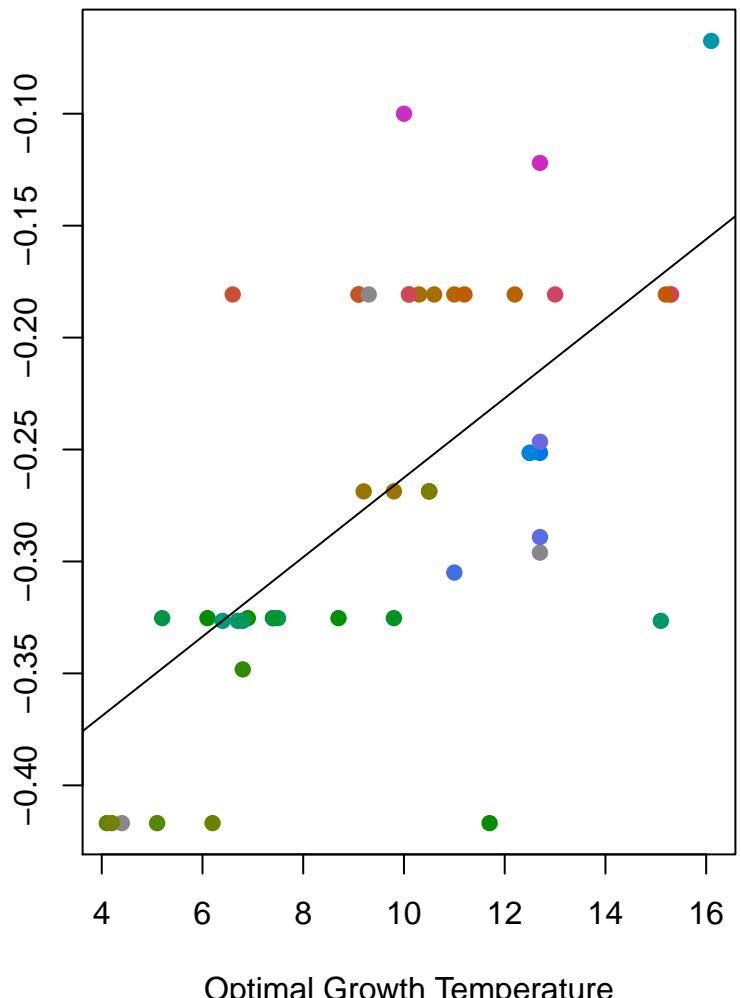
feature.pgfam_id.gravy.mean

PGF_02069837

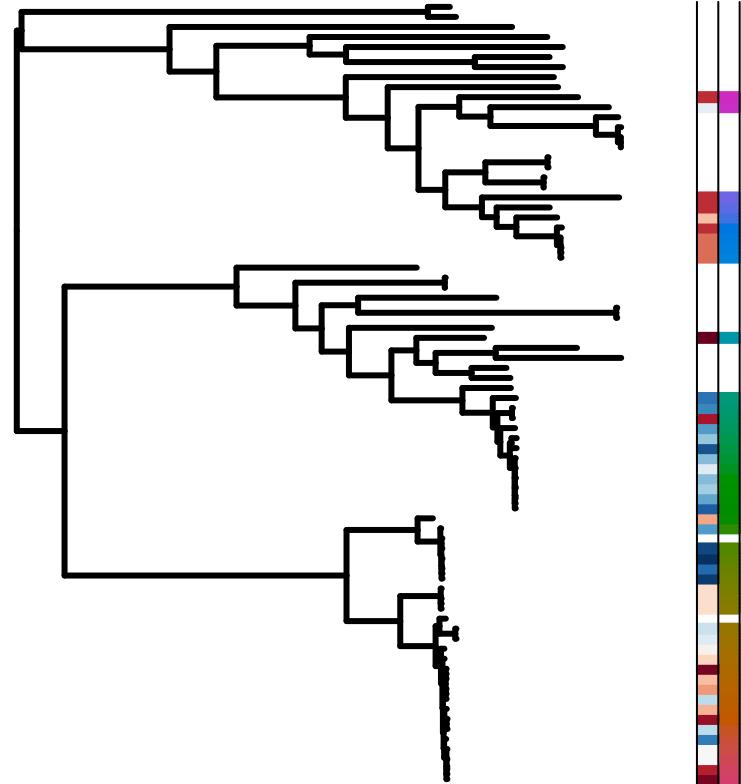
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin

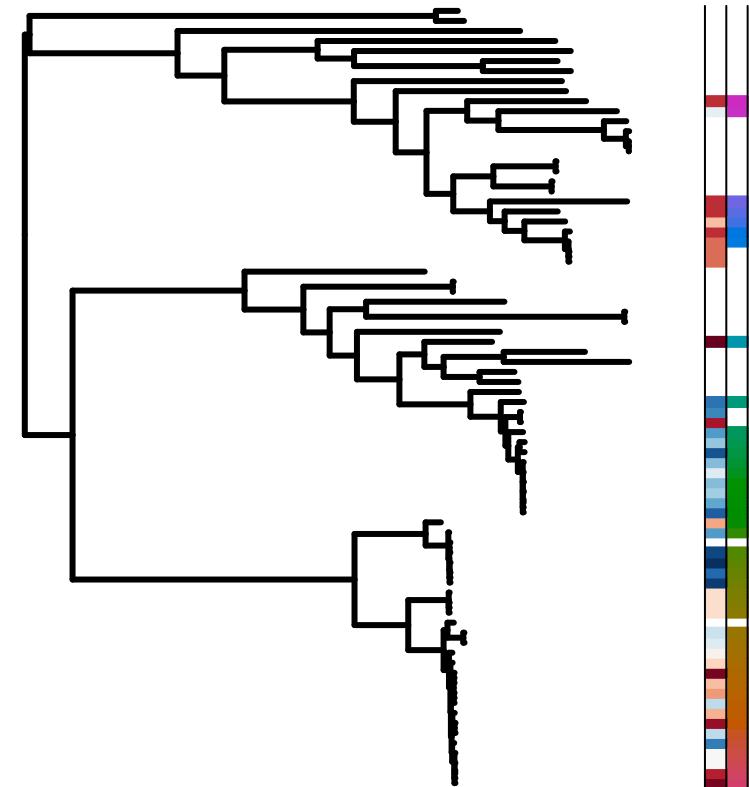
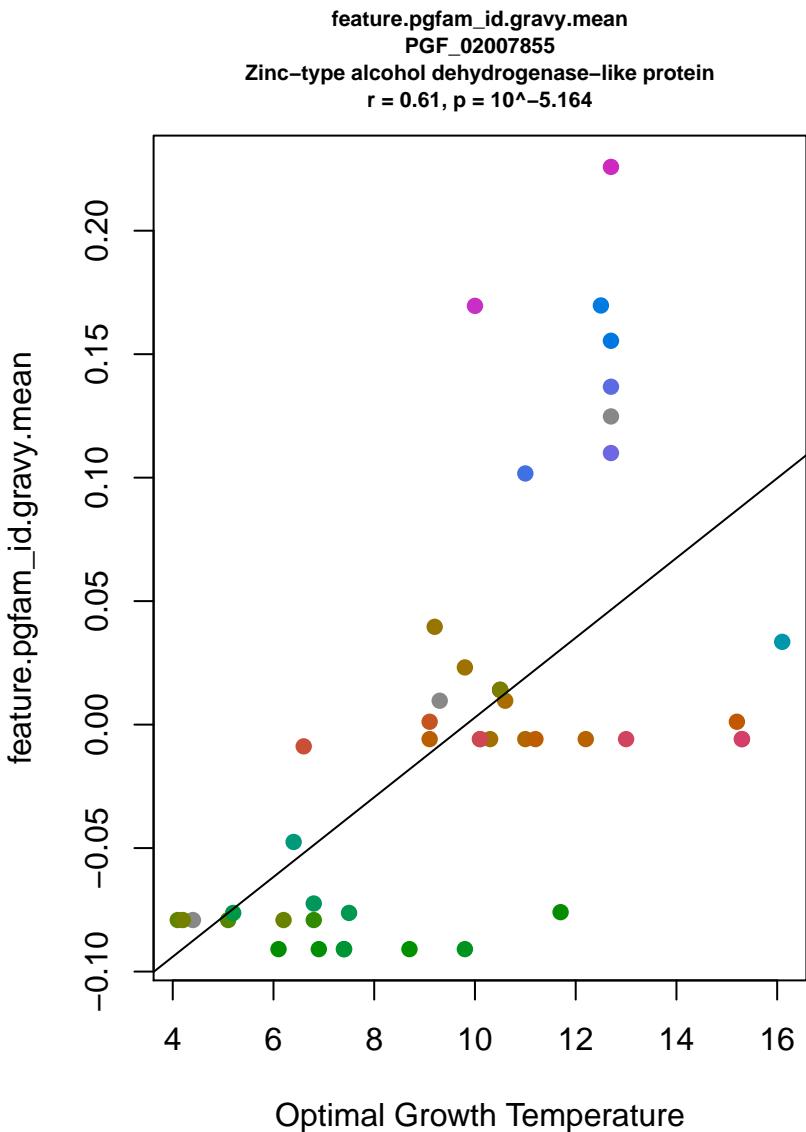
$r = 0.631, p = 10^{-6.036}$

feature.pgfam_id.gravy.mean



Optimal Growth Temperature





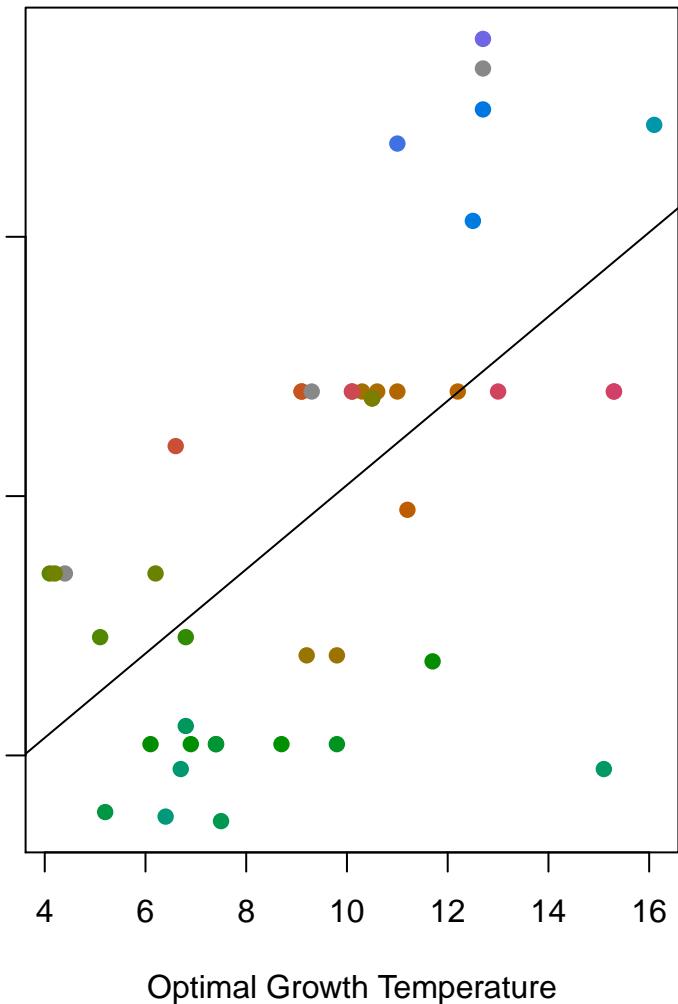
feature.pgfam_id.gravy.mean

PGF_03832998

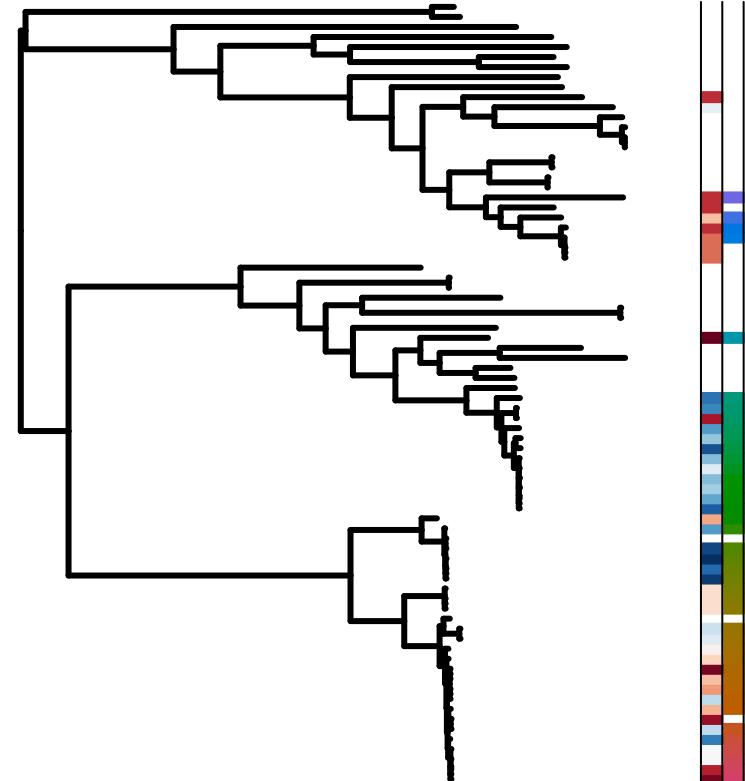
FIG111991: hypothetical protein

$r = 0.605, p = 10^{-4.86}$

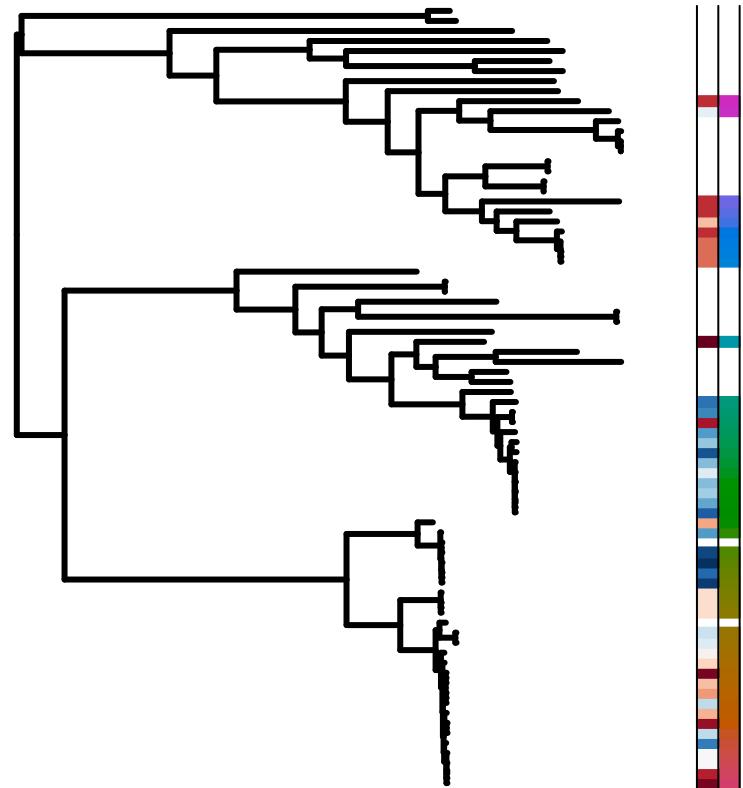
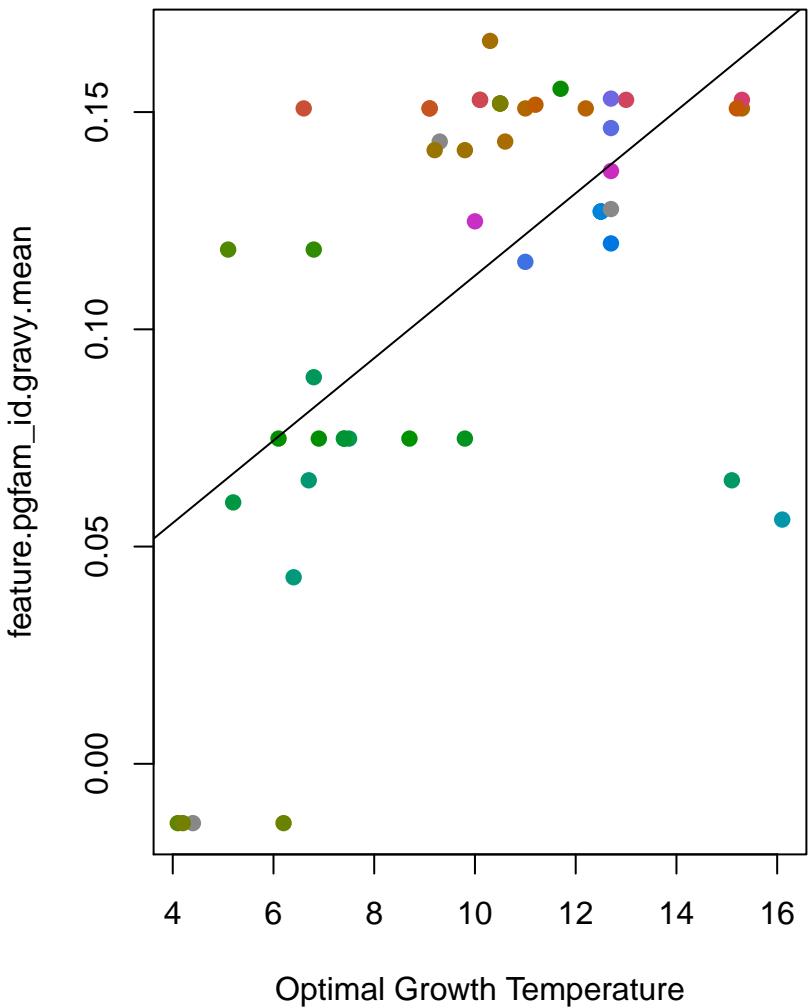
feature.pgfam_id.gravy.mean



Optimal Growth Temperature



feature.pgfam_id.gravy.mean
PGF_00417658
3-dehydroquinate synthase (EC 4.2.3.4)
 $r = 0.593$, $p = 10^{-5.245}$

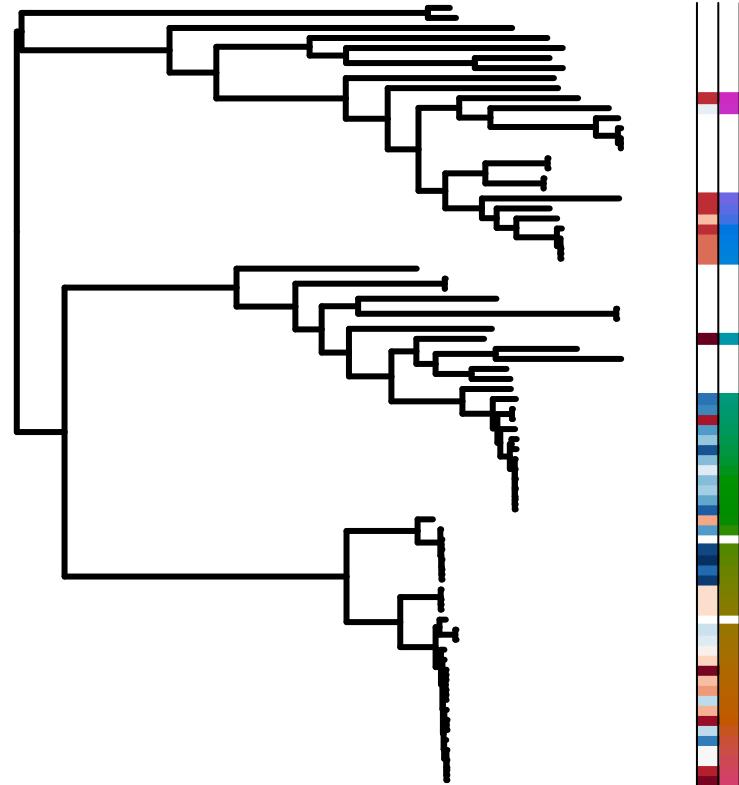
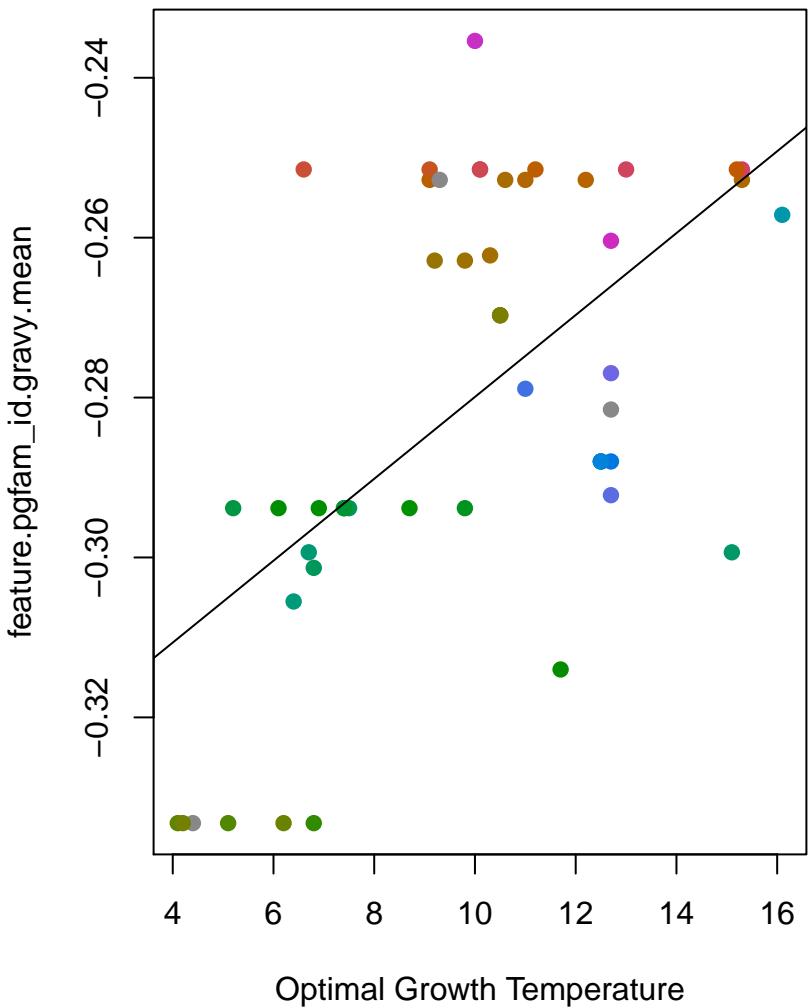


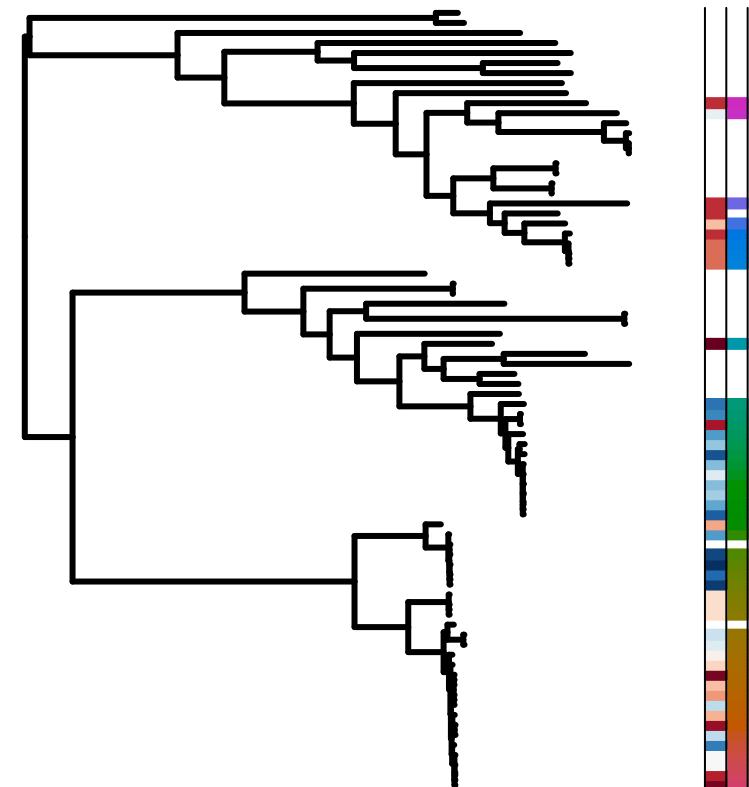
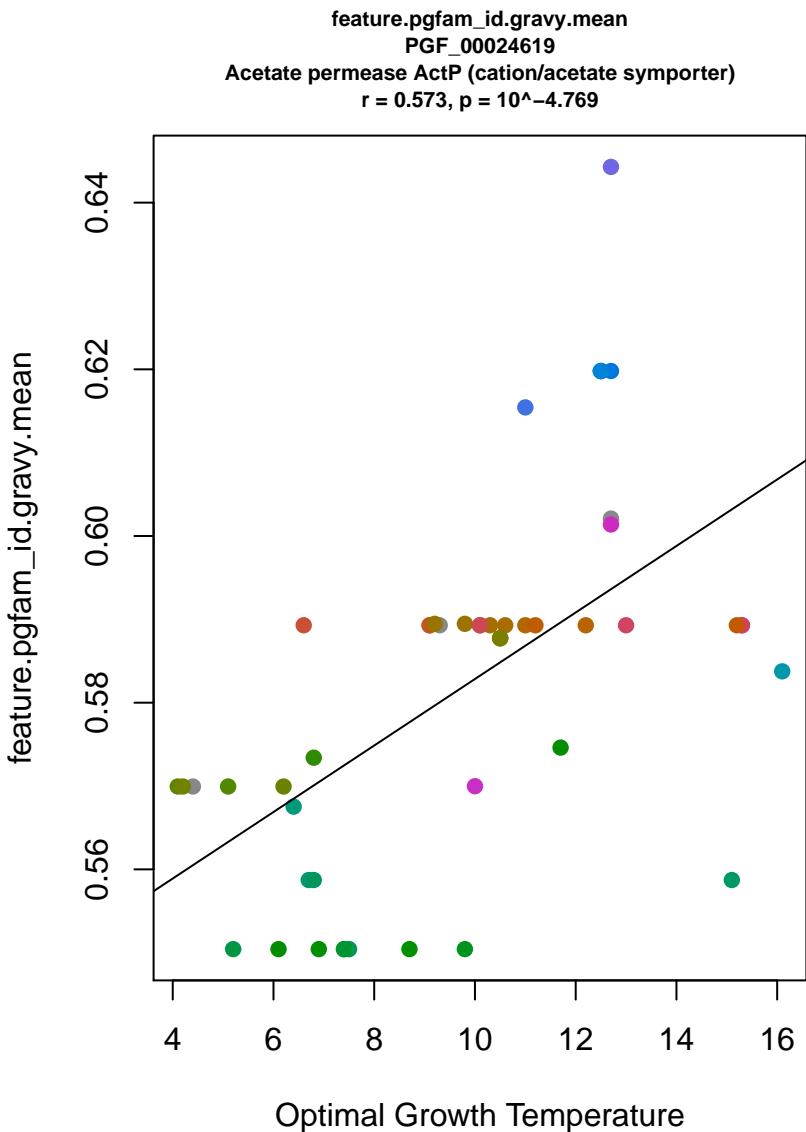
feature.pgfam_id.gravy.mean

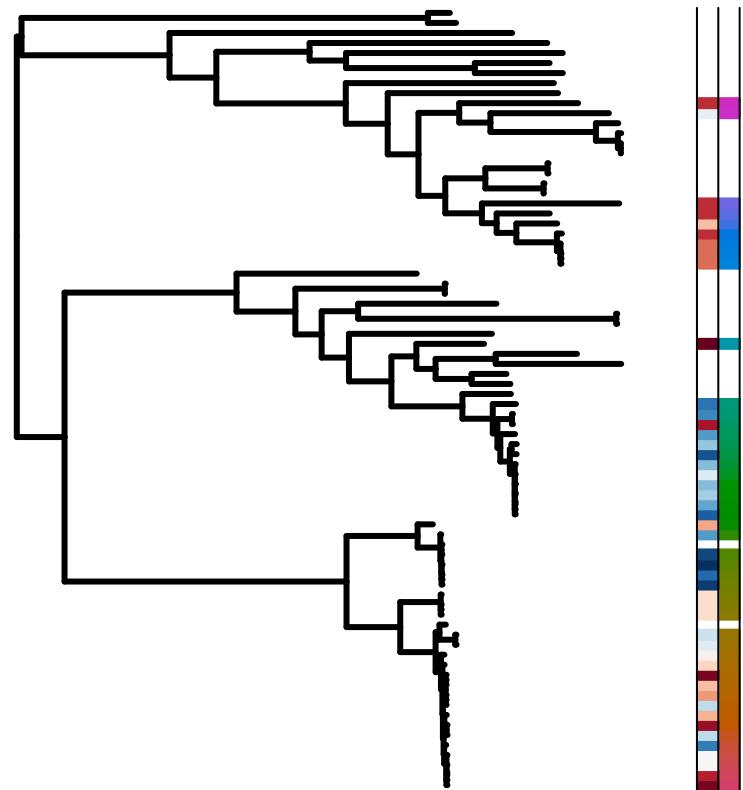
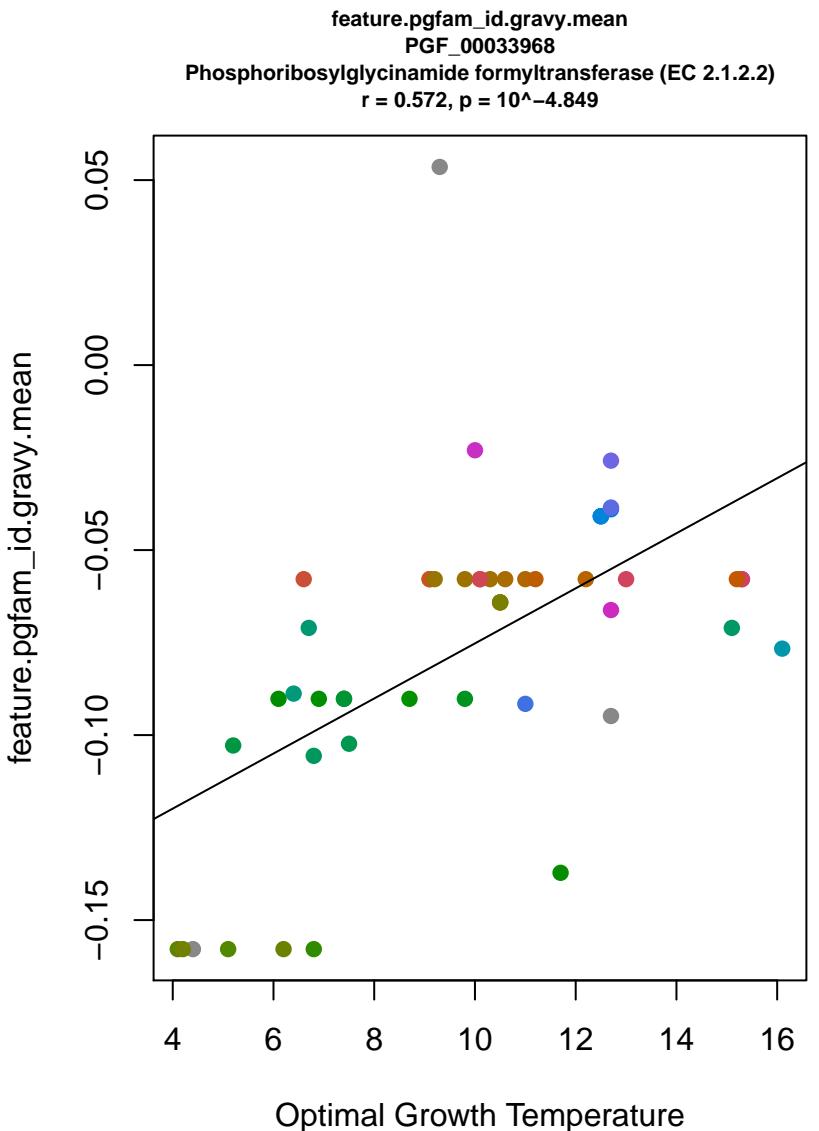
PGF_00006983

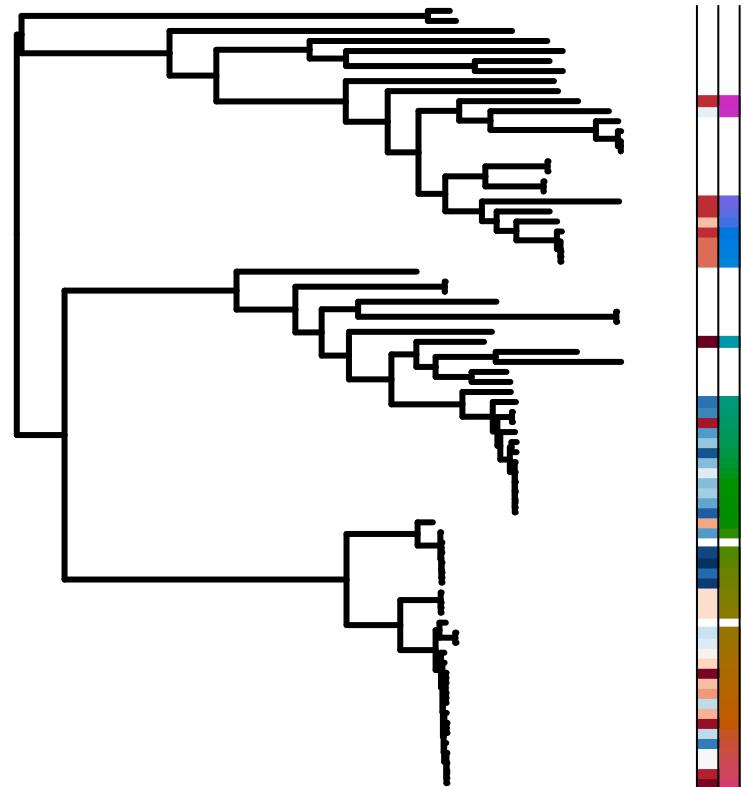
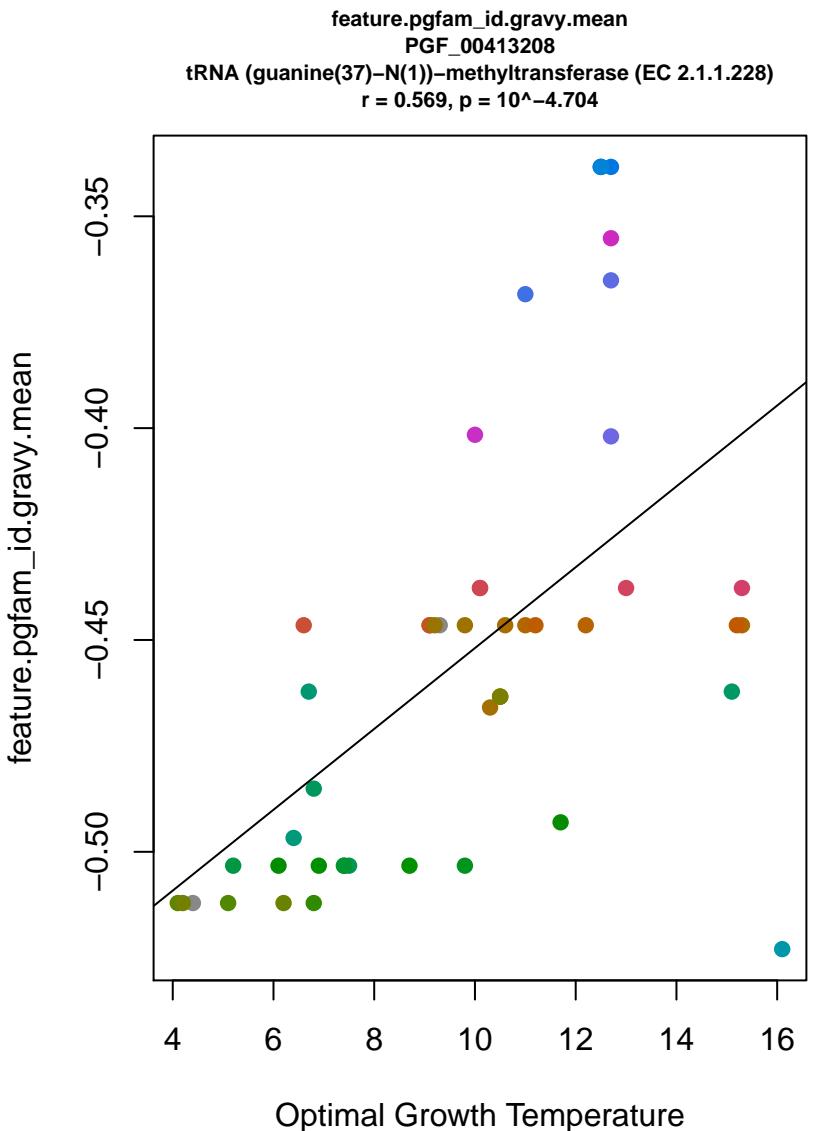
GTP cyclohydrolase I (EC 3.5.4.16) type 2

$r = 0.588, p = 10^{-5.154}$







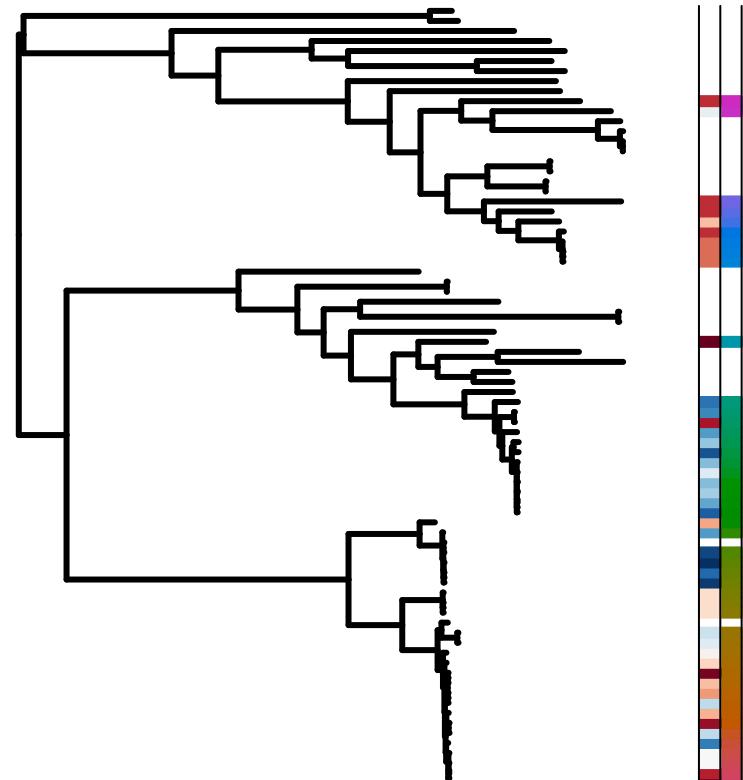
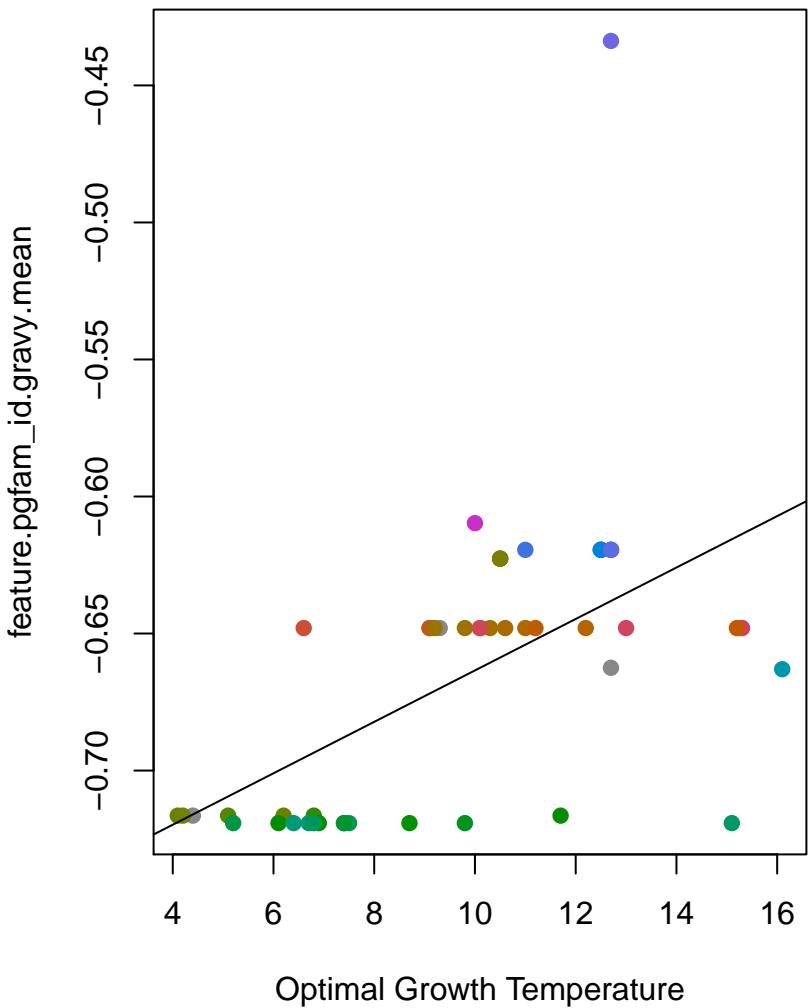


feature.pgfam_id.gravy.mean

PGF_00502502

Cold shock protein of CSP family => CspD (naming convention as in E.coli)

r = 0.564, p = 10^-4.705



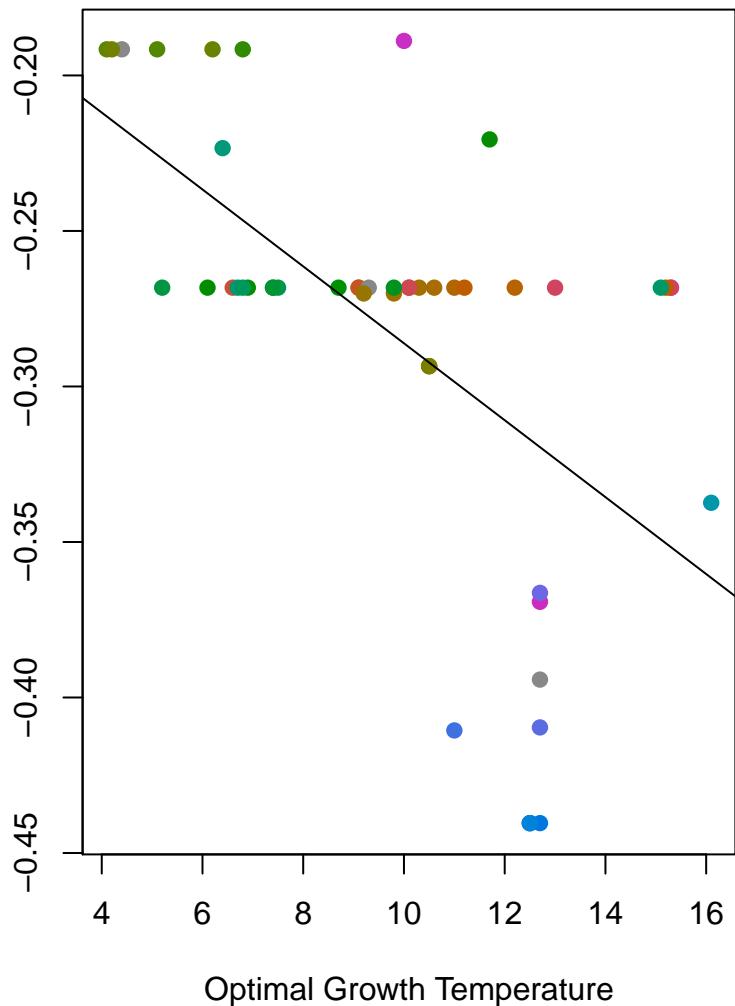
feature.pgfam_id.gravy.mean

PGF_00649271

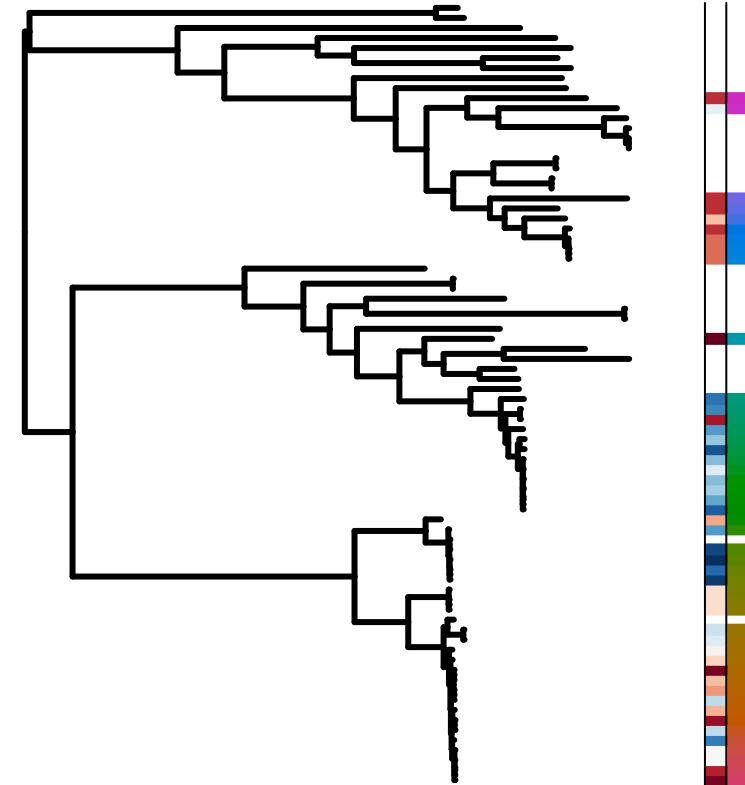
Cell division protein BolA

$r = -0.565$, $p = 10^{-4.722}$

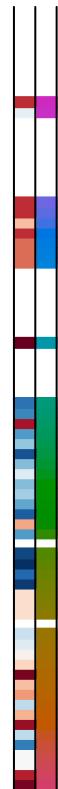
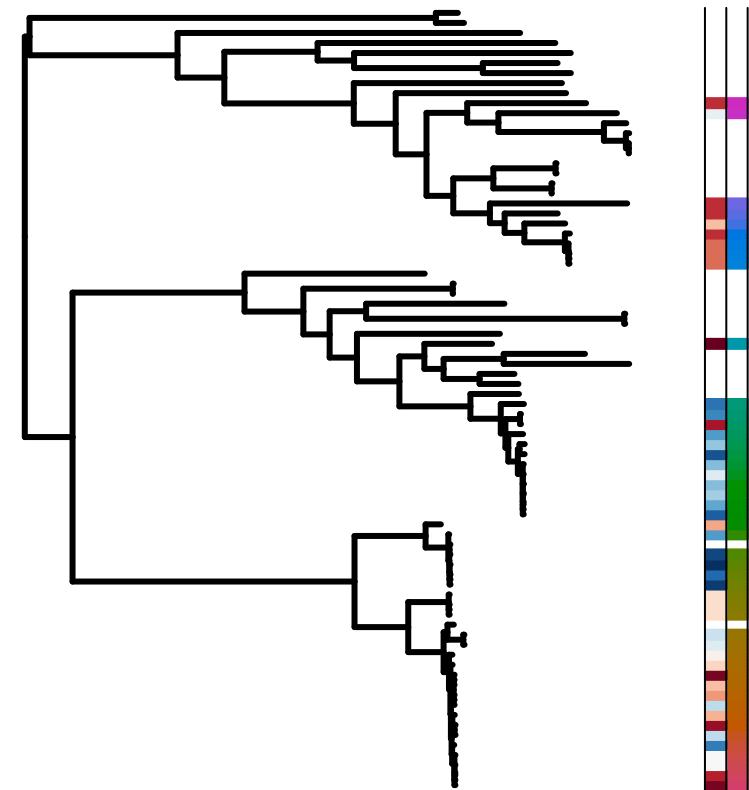
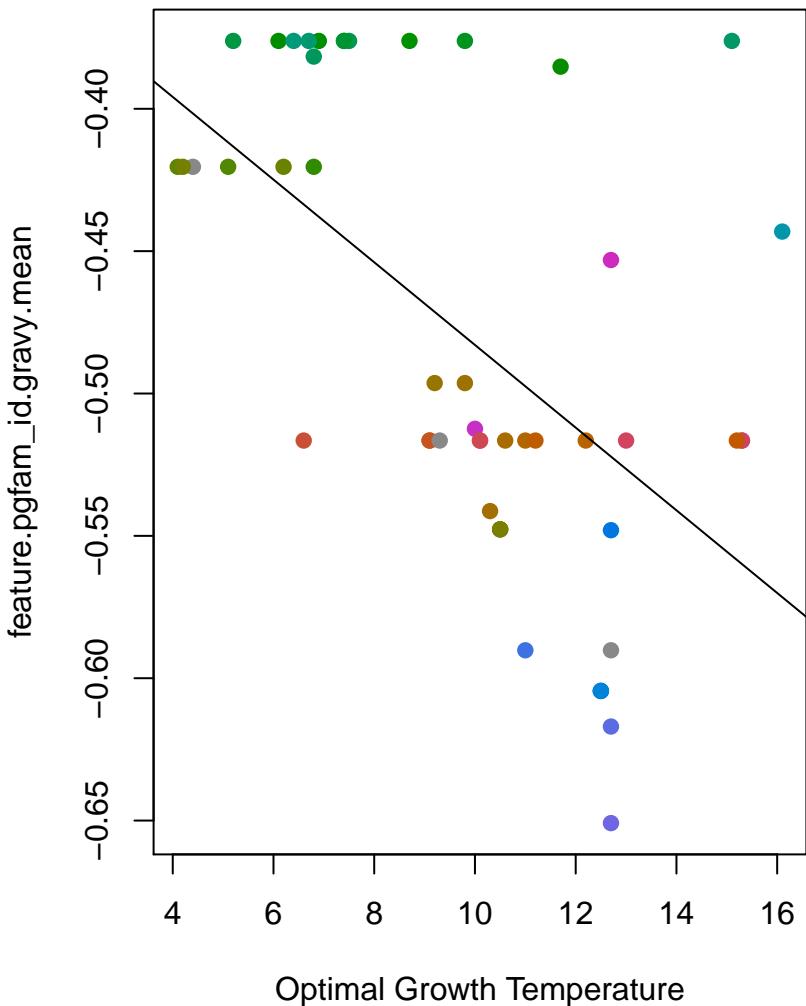
feature.pgfam_id.gravy.mean

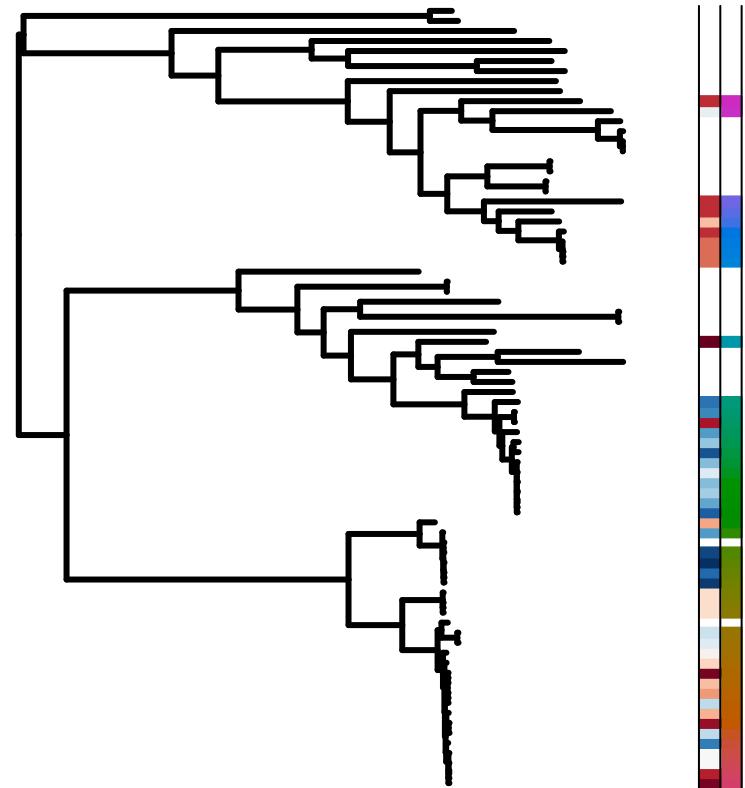
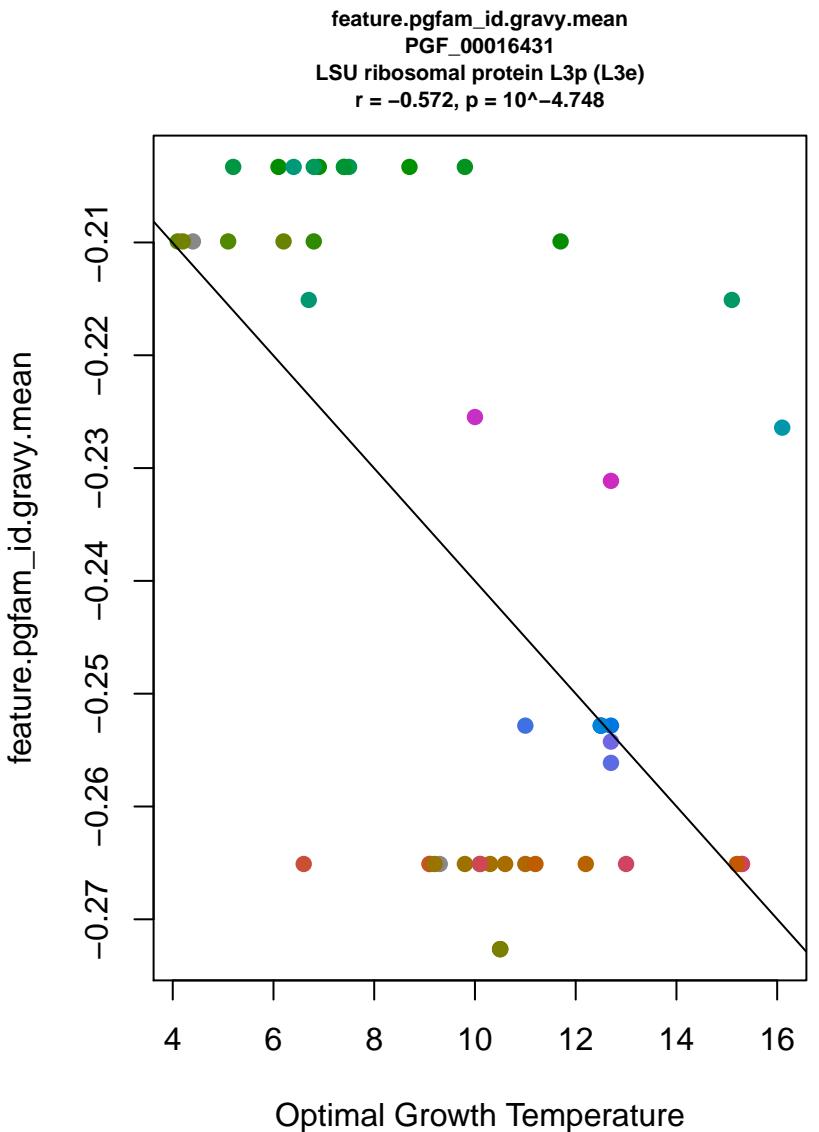


Optimal Growth Temperature

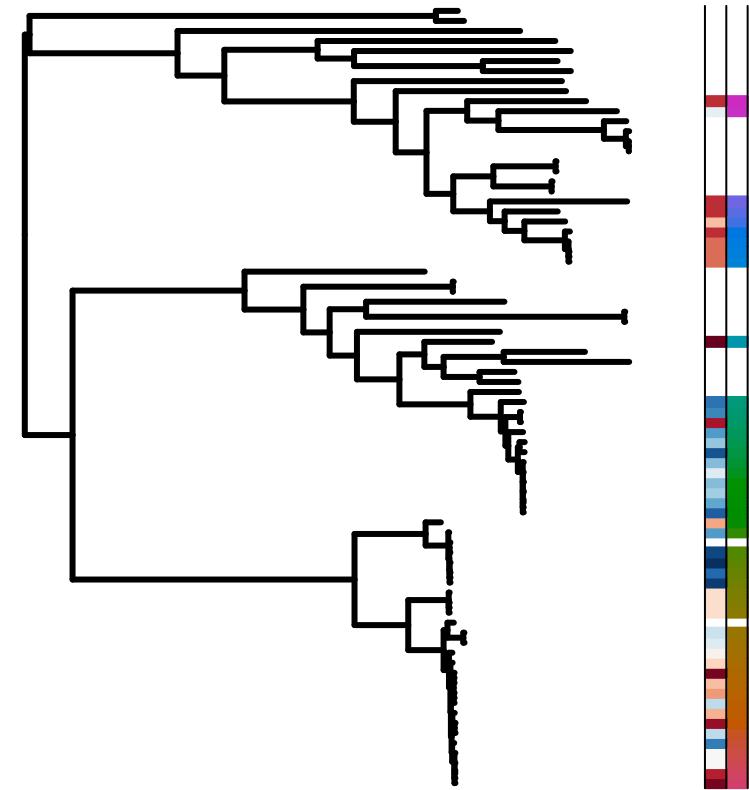
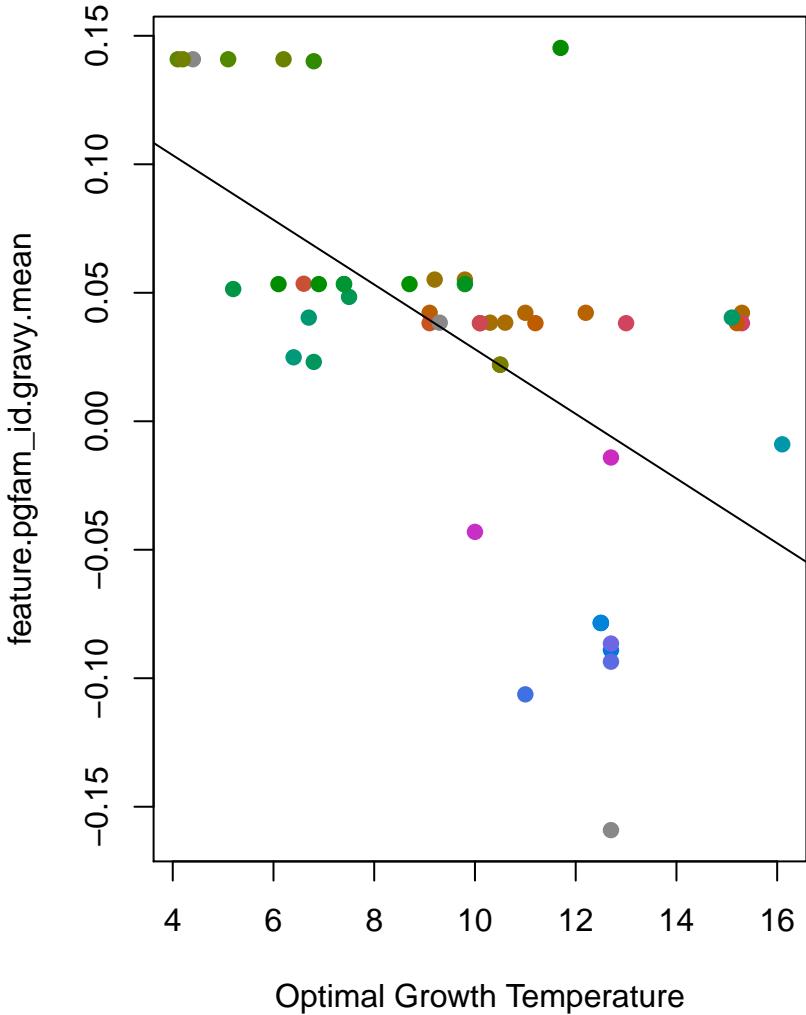


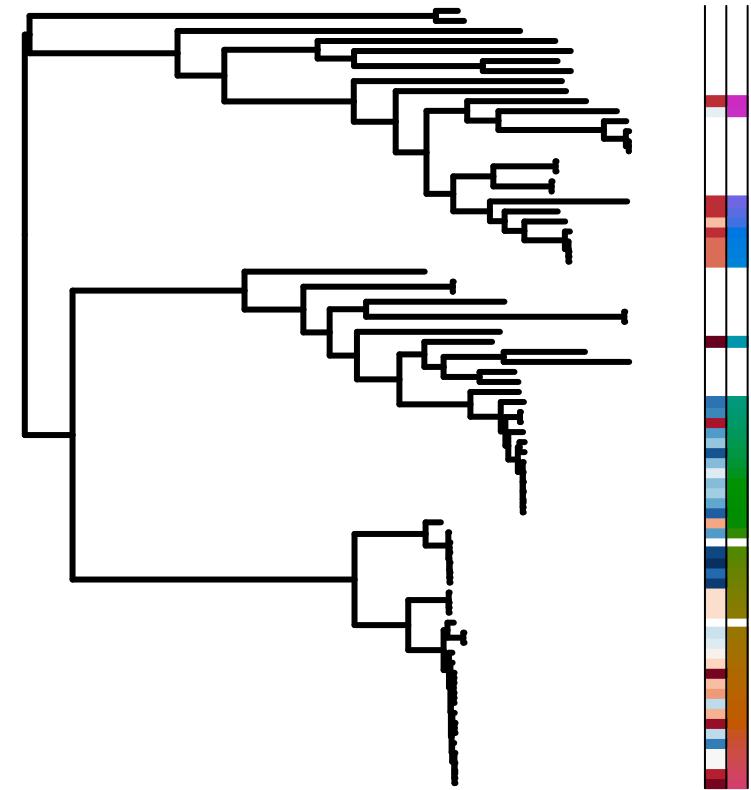
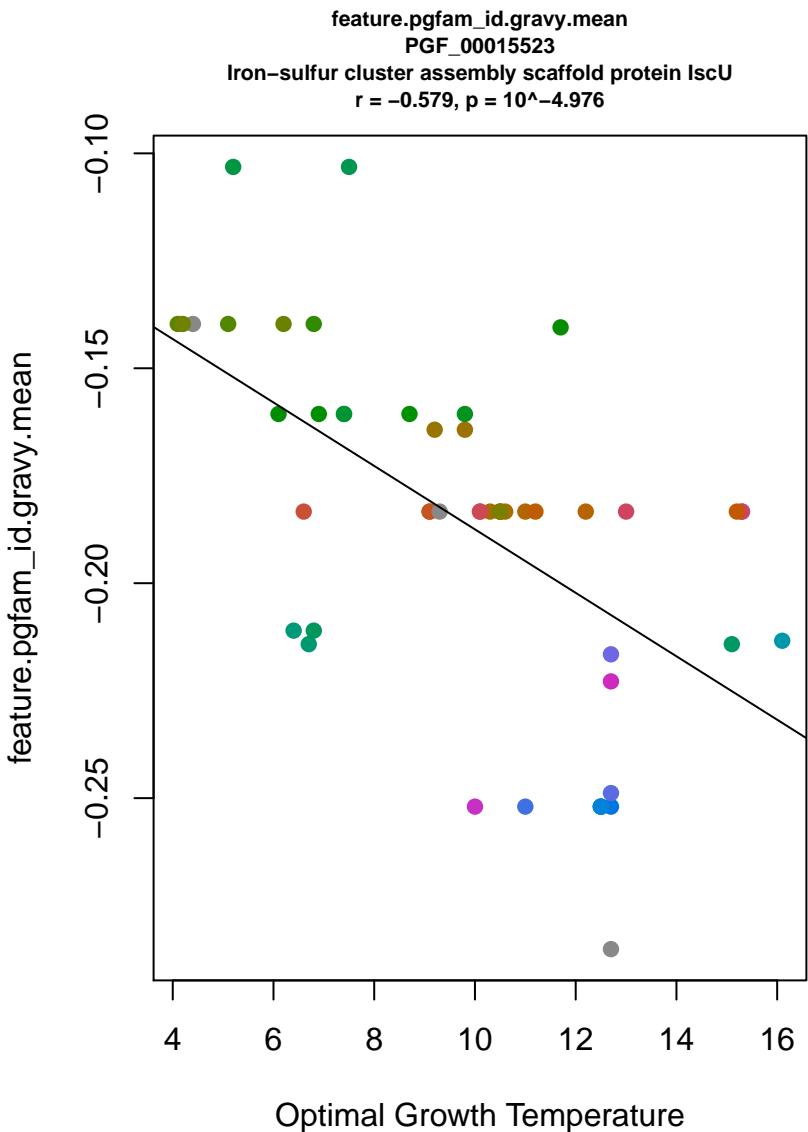
feature.pgfam_id.gravy.mean
PGF_00101847
hypothetical protein
 $r = -0.566$, $p = 10^{-4.731}$





feature.pgfam_id.gravy.mean
PGF_03772086
Sensor histidine kinase GirK
 $r = -0.572$, $p = 10^{-4.854}$



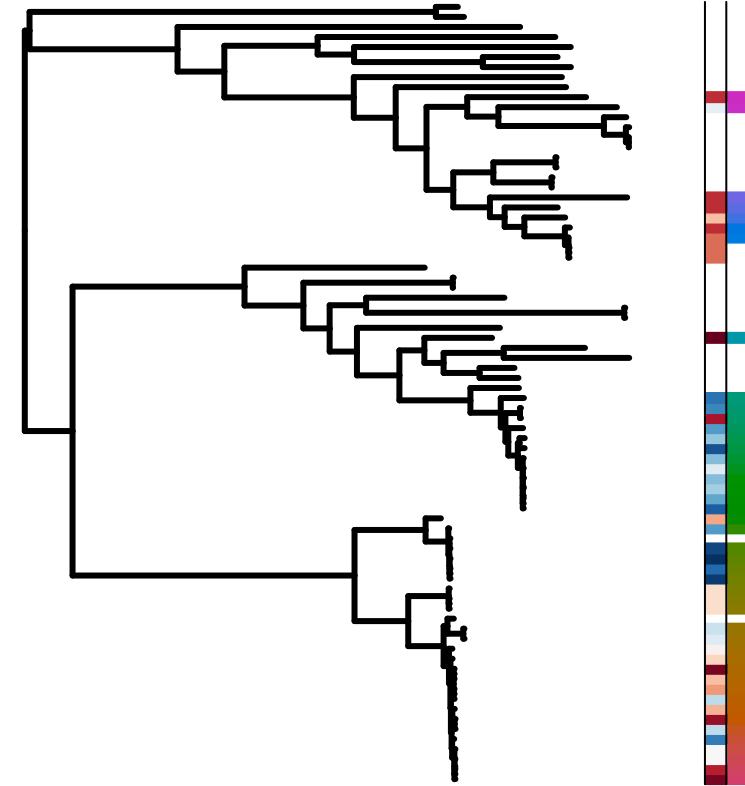
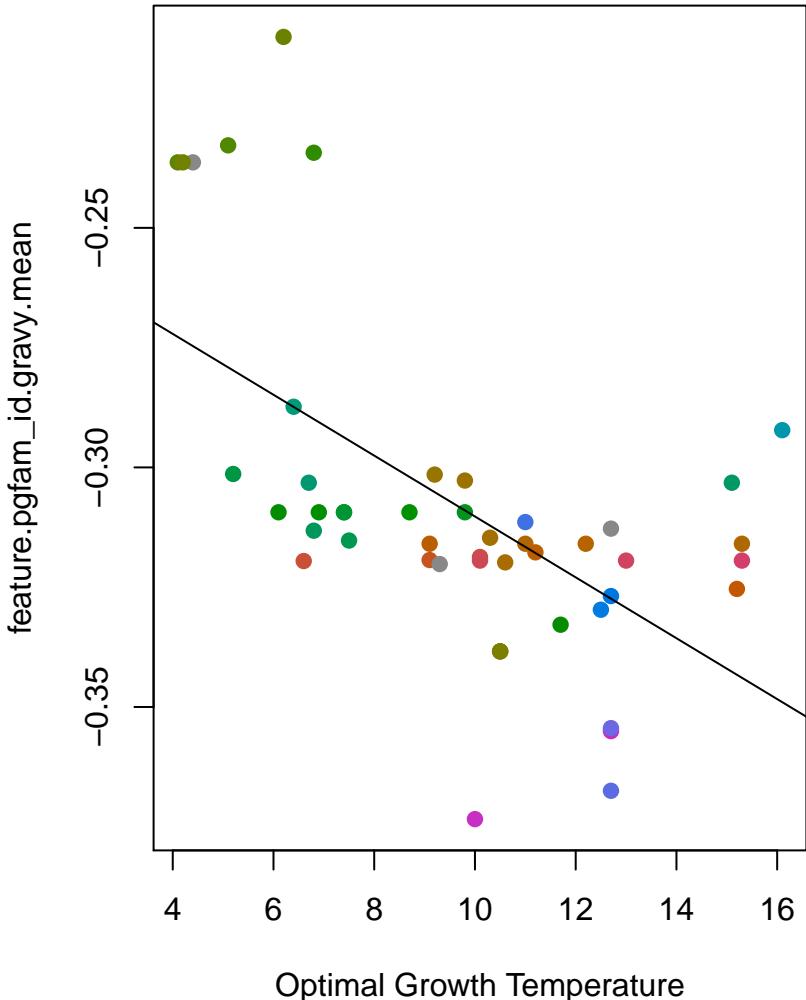


feature.pgfam_id.gravy.mean

PGF_10537966

TonB-dependent receptor

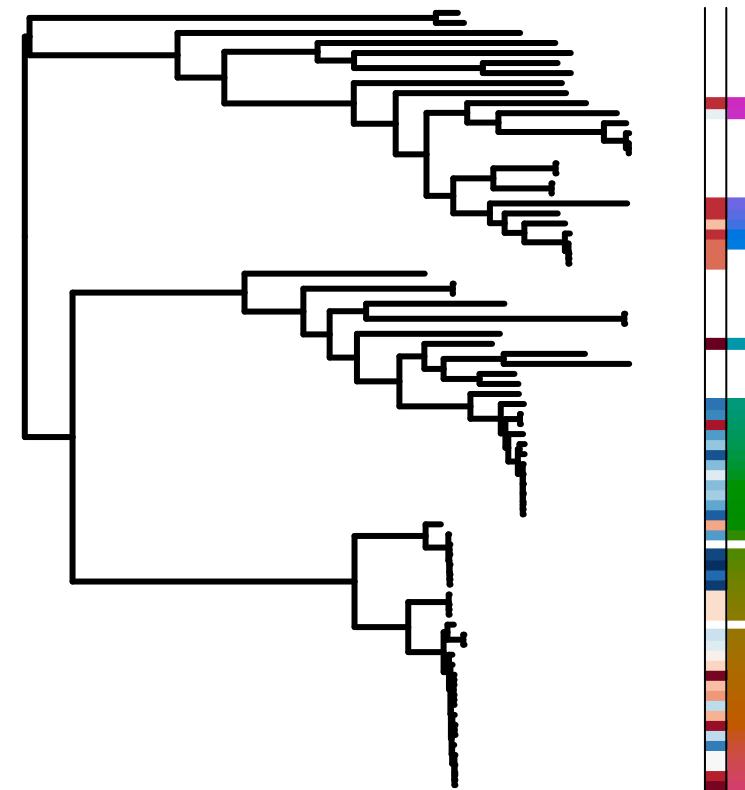
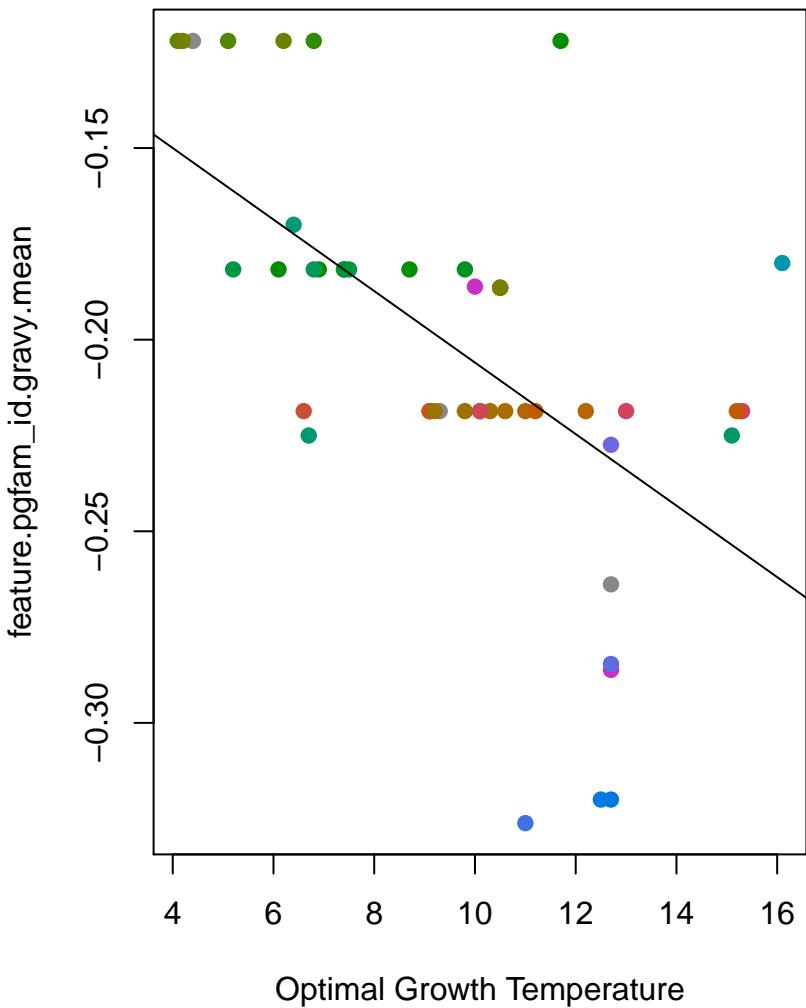
$r = -0.589$, $p = 10^{-4.972}$



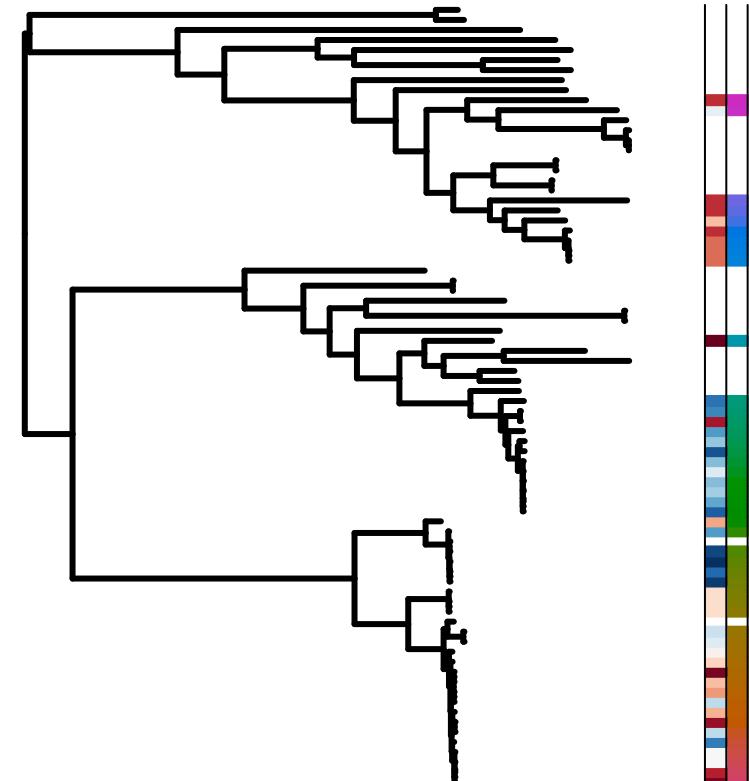
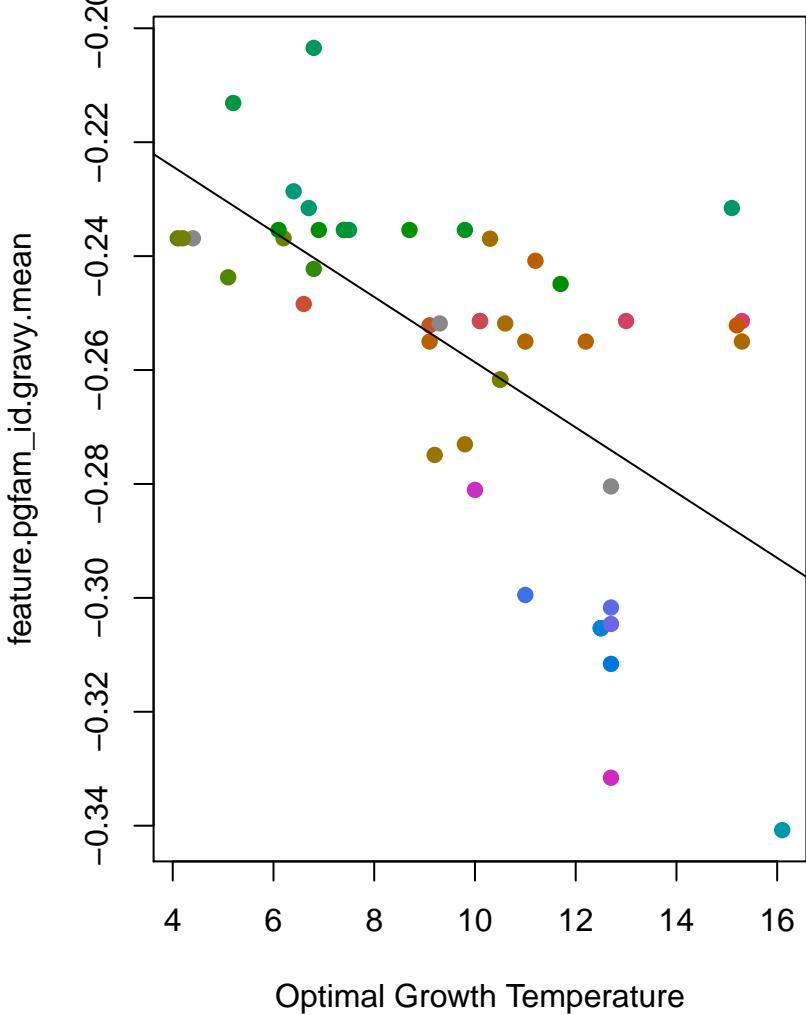
feature.pgfam_id.gravy.mean

PGF_07550057

FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster
 $r = -0.591, p = 10^{-5.008}$



feature.pgfam_id.gravy.mean
PGF_02315316
Peptidase, M23/M37 family
 $r = -0.606$, $p = 10^{-5.502}$

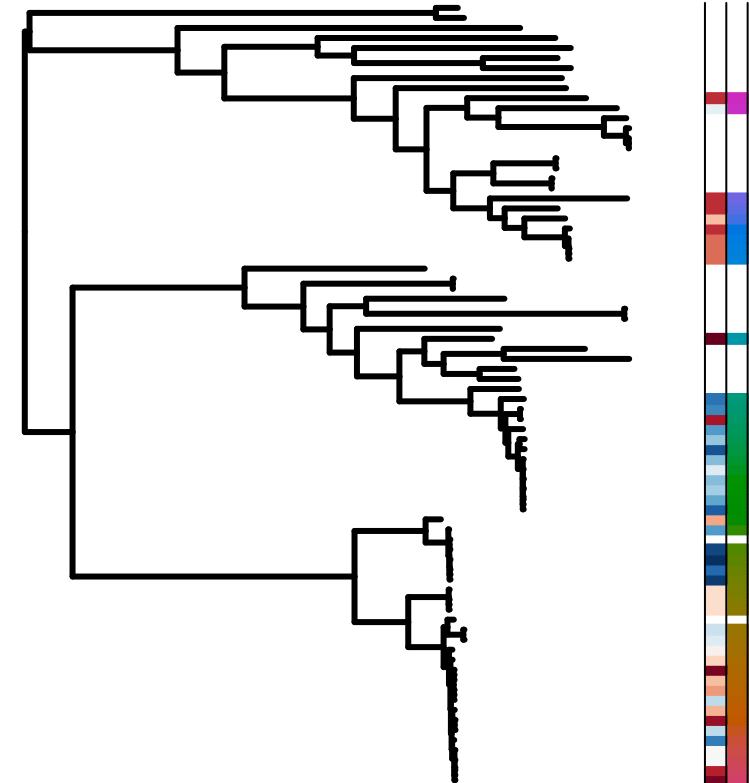
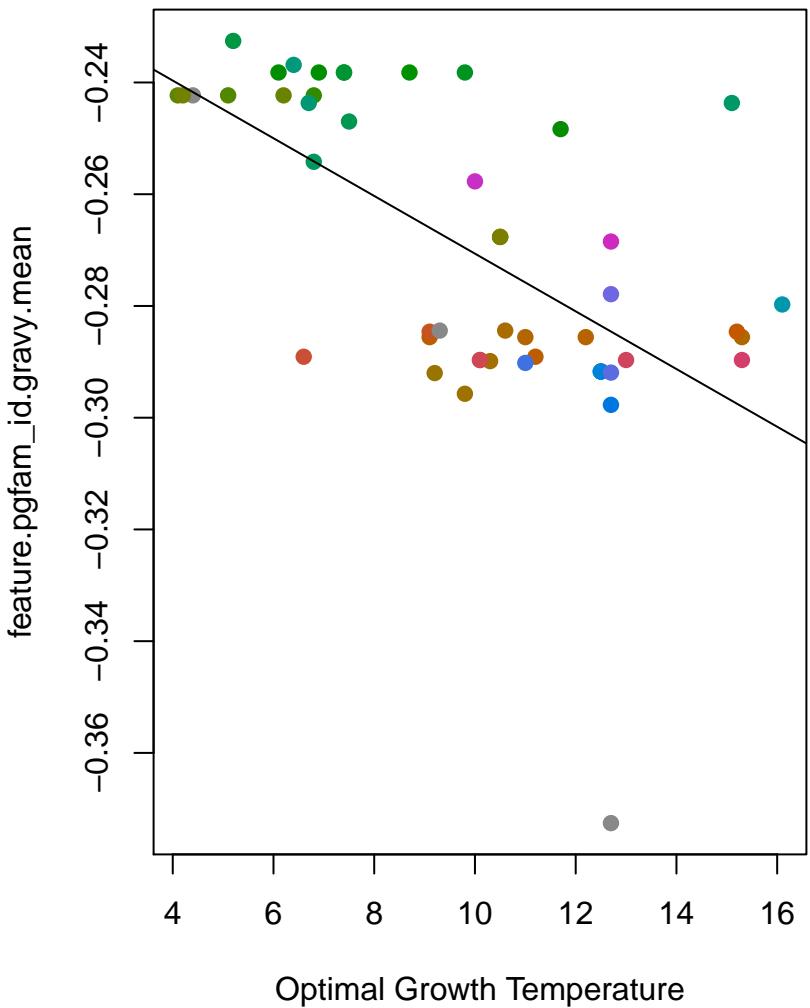


feature.pgfam_id.gravy.mean

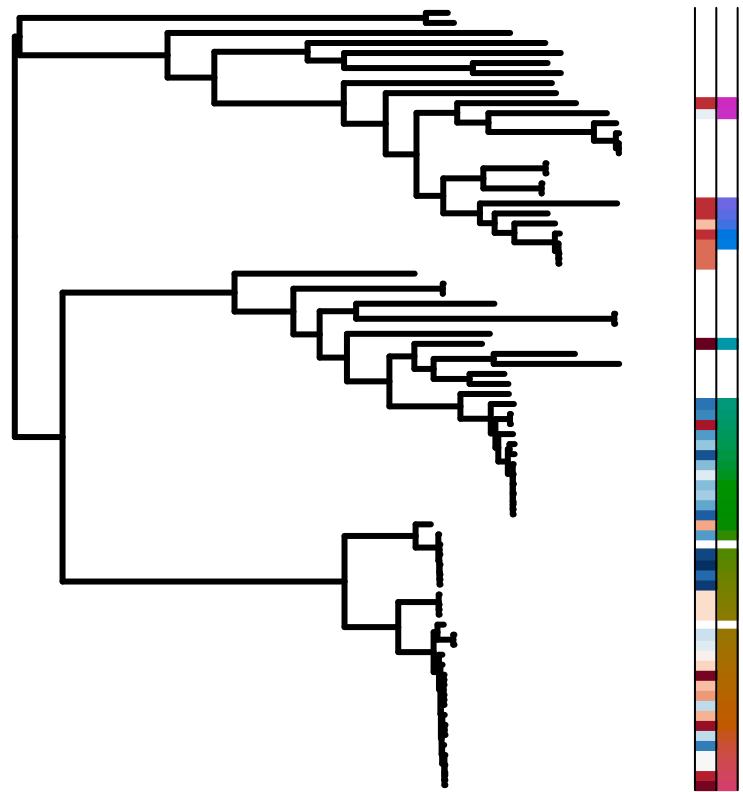
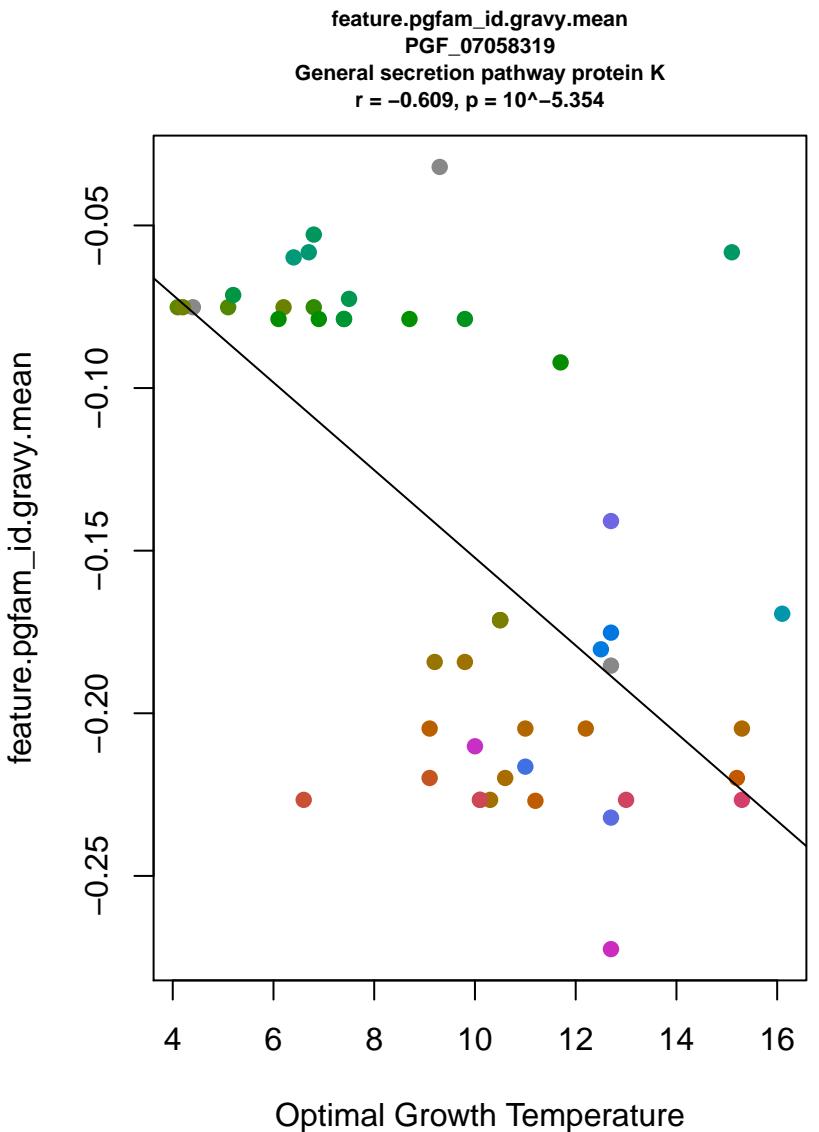
PGF_00021217

2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)

$r = -0.607$, $p = 10^{-5.527}$



Optimal Growth Temperature

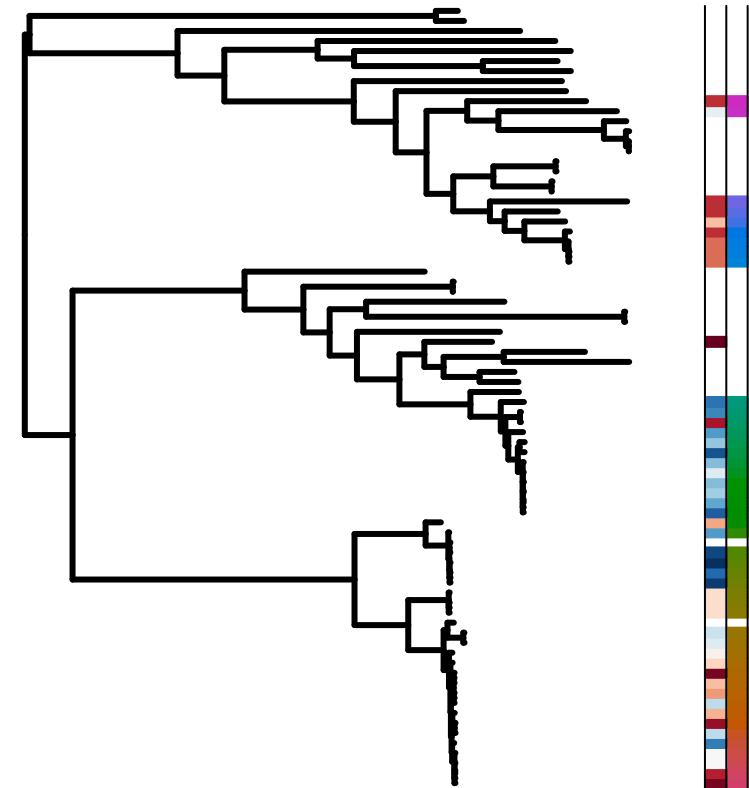
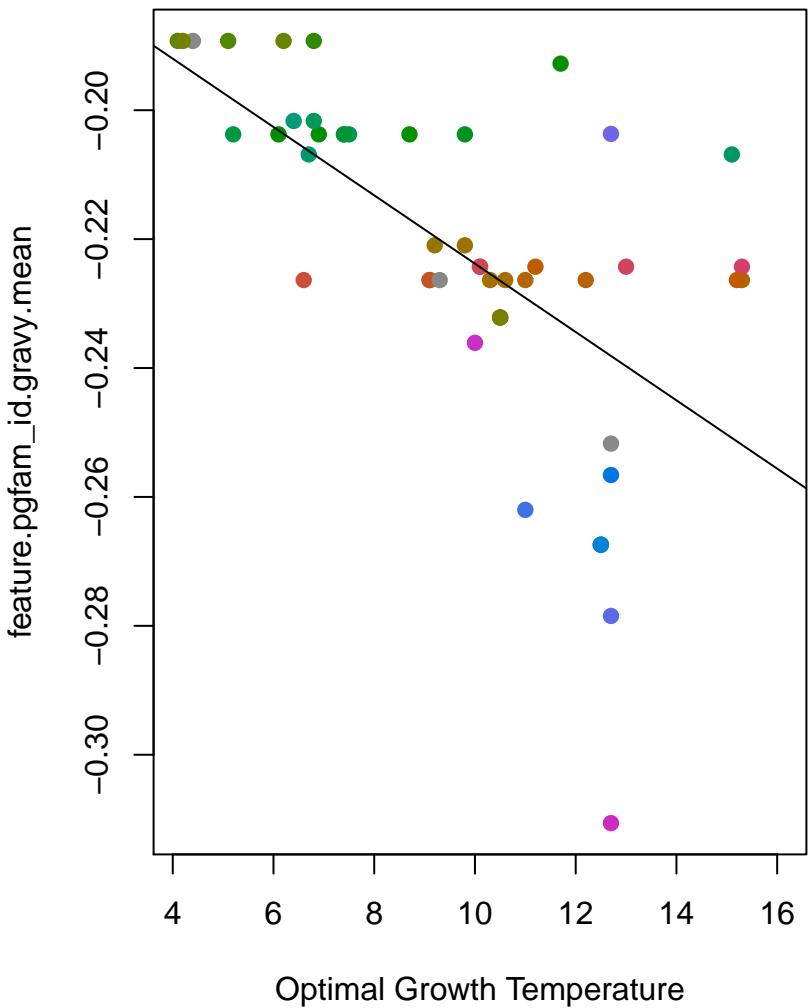


feature.pgfam_id.gravy.mean

PGF_06775354

DNA-binding transcriptional regulator, MocR family / aminotransferase domain

$r = -0.616, p = 10^{-5.617}$

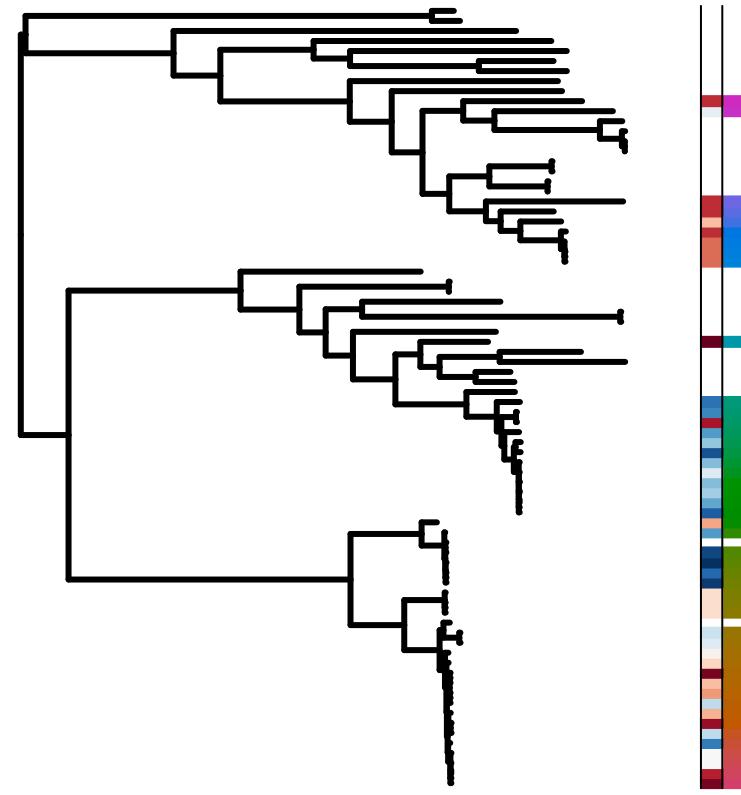
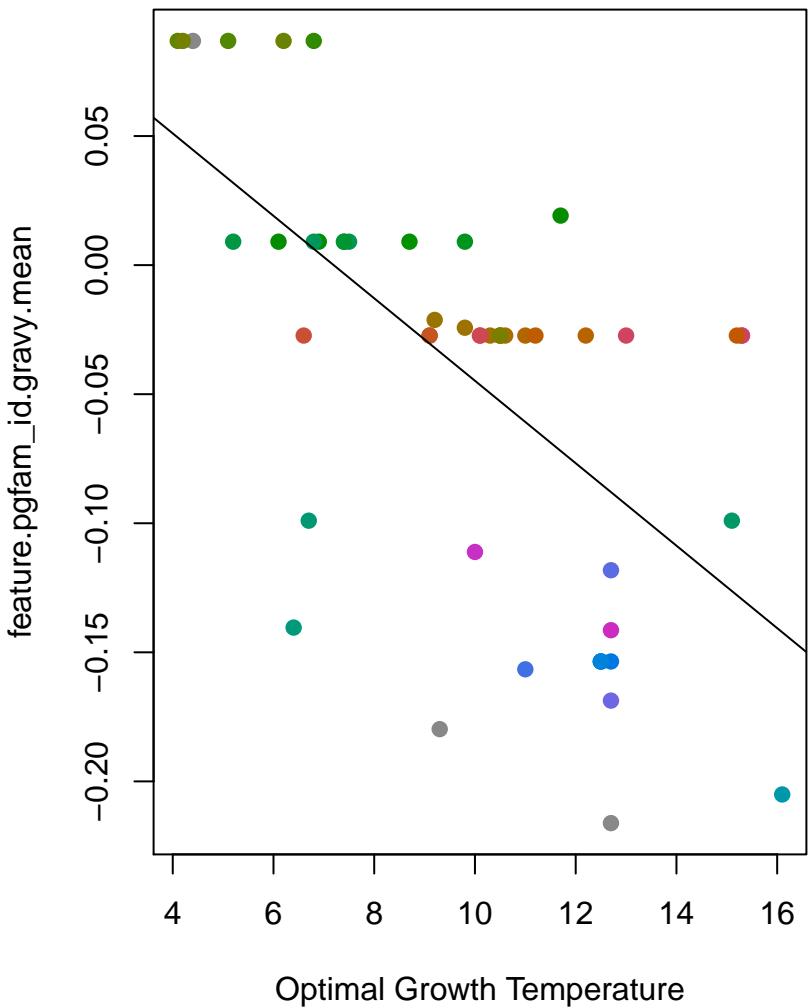


feature.pgfam_id.gravy.mean

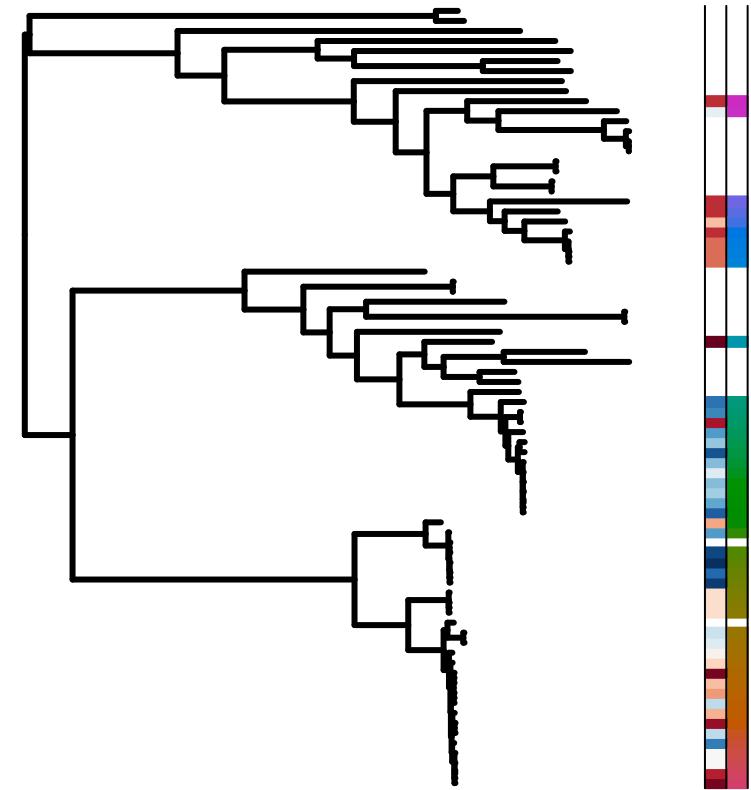
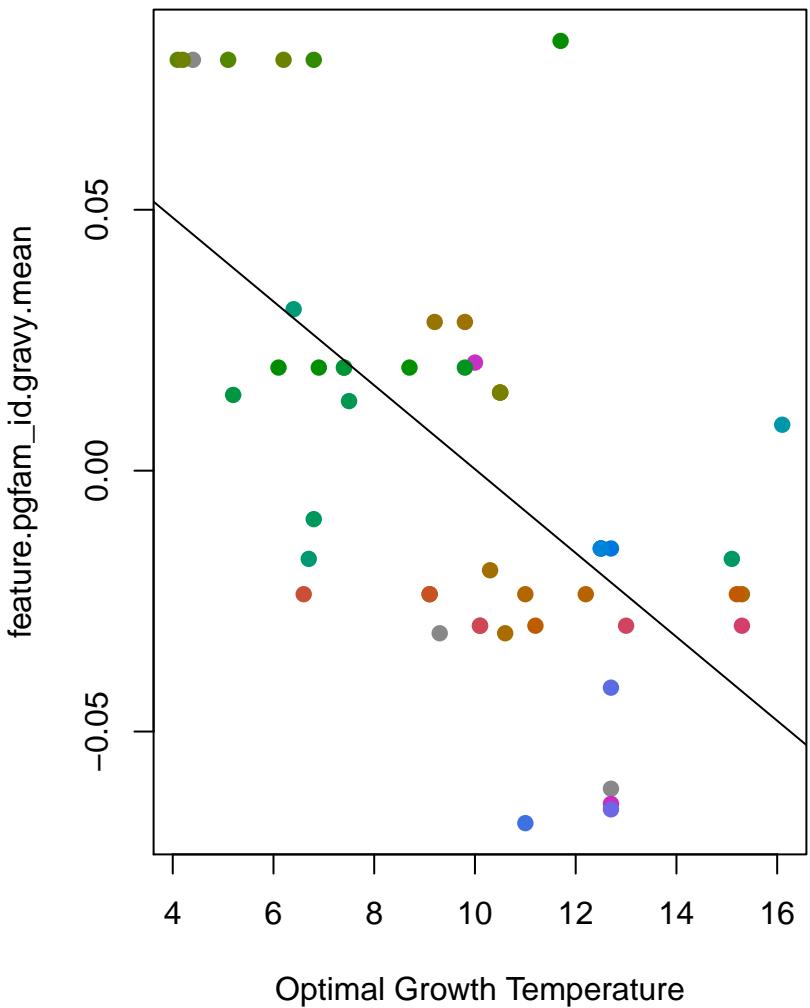
PGF_01336539

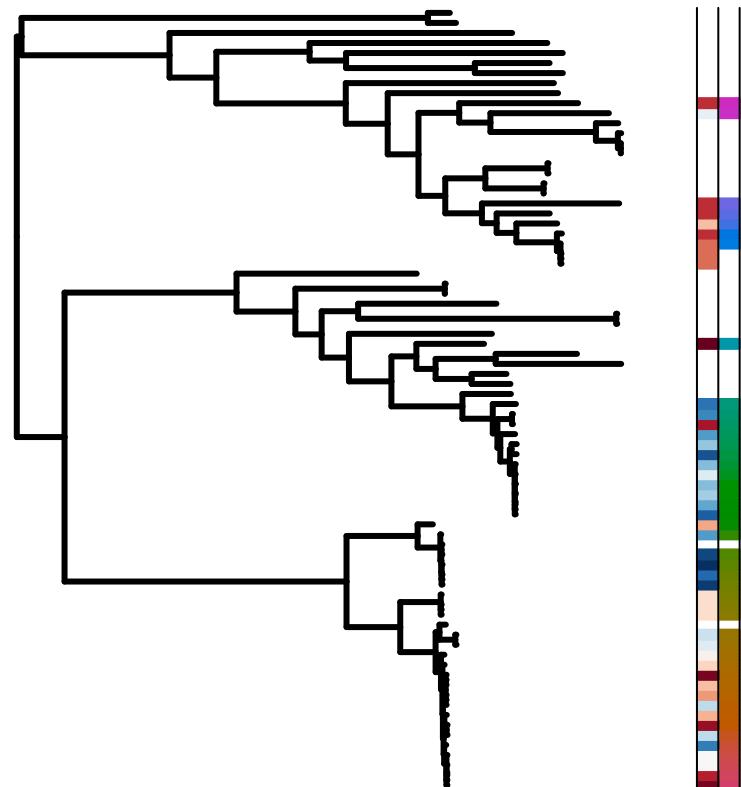
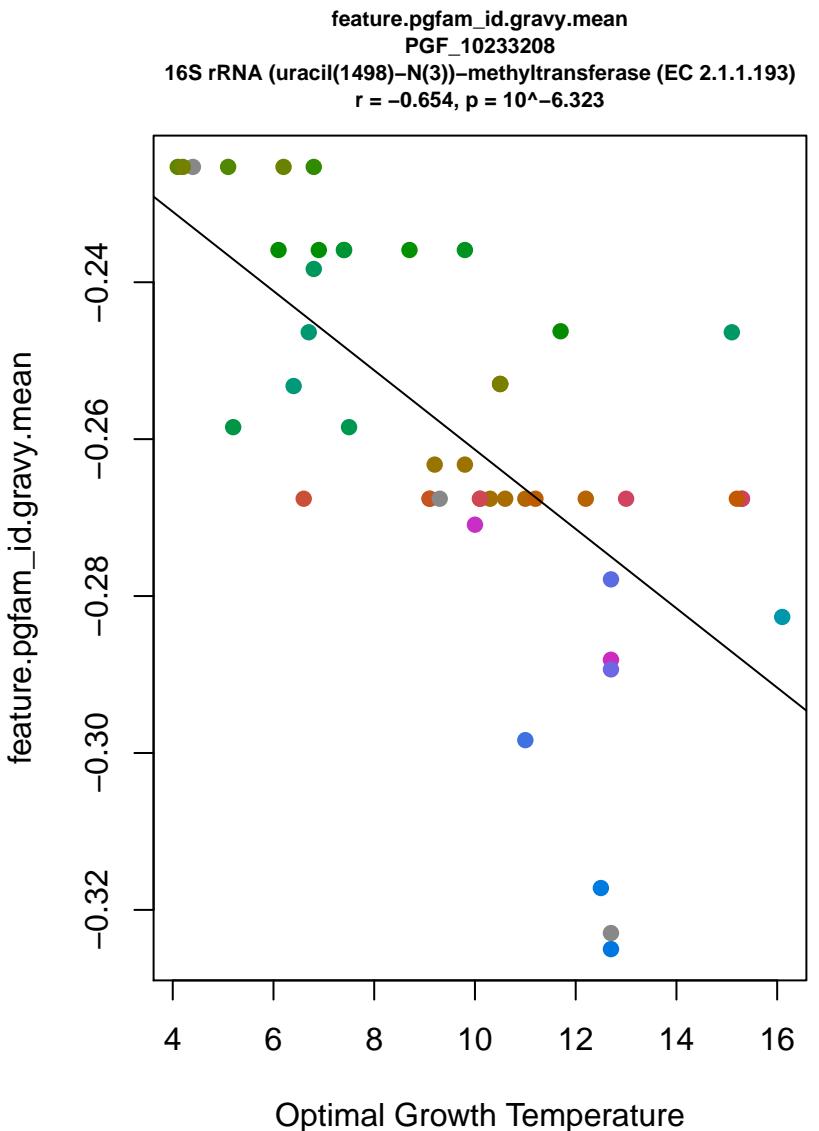
hypothetical protein

$r = -0.621$, $p = 10^{-5.833}$

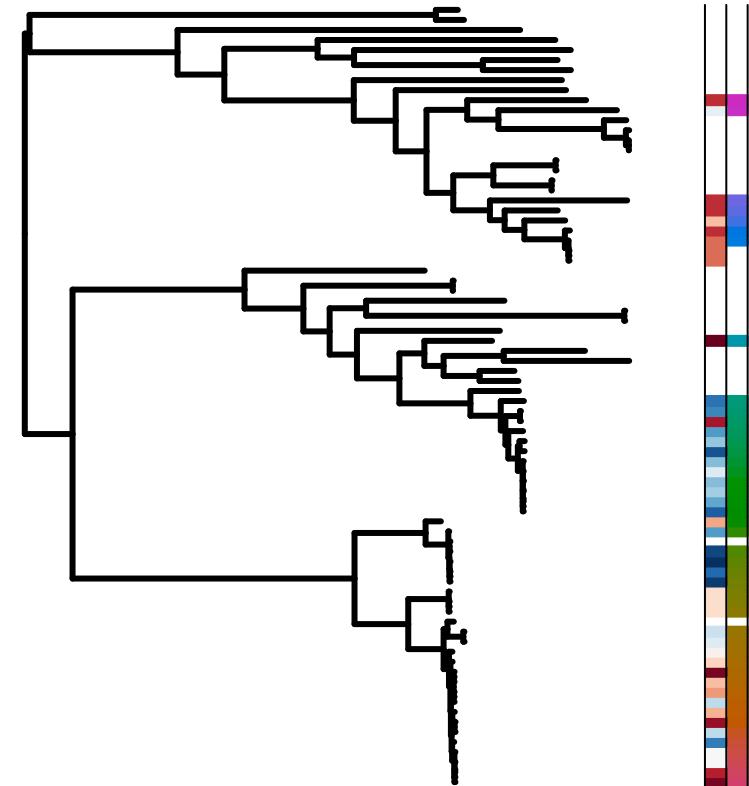
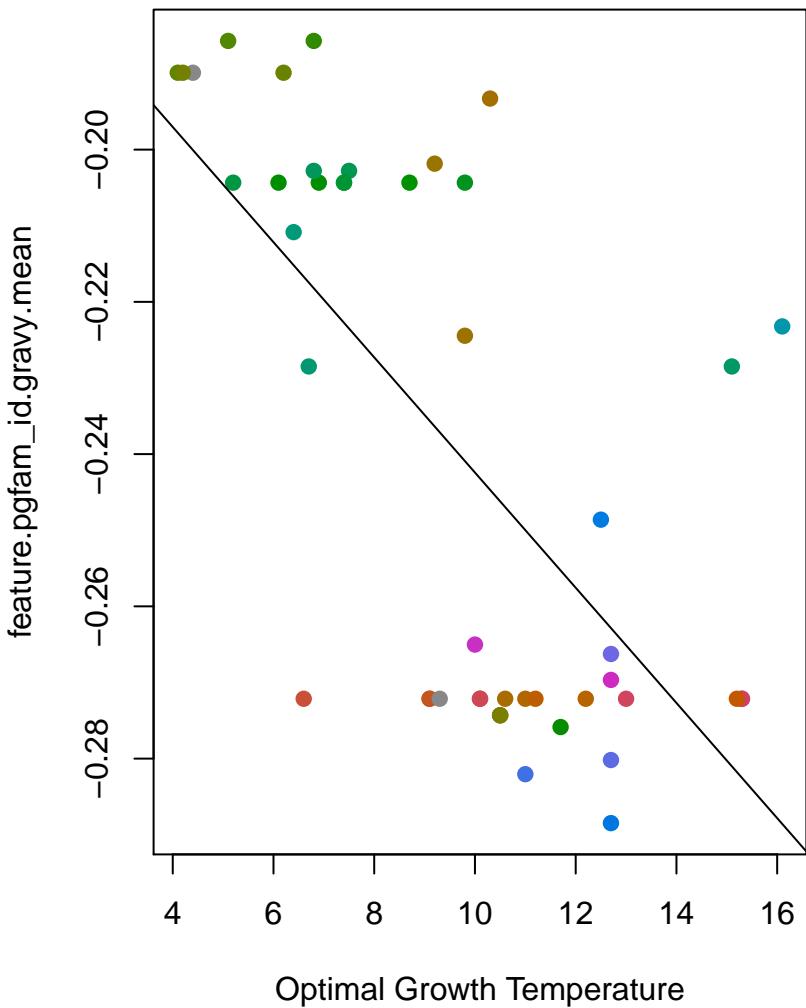


feature.pgfam_id.gravy.mean
PGF_00846740
Orn/DAP/Arg family decarboxylase
 $r = -0.624$, $p = 10^{-5.9}$

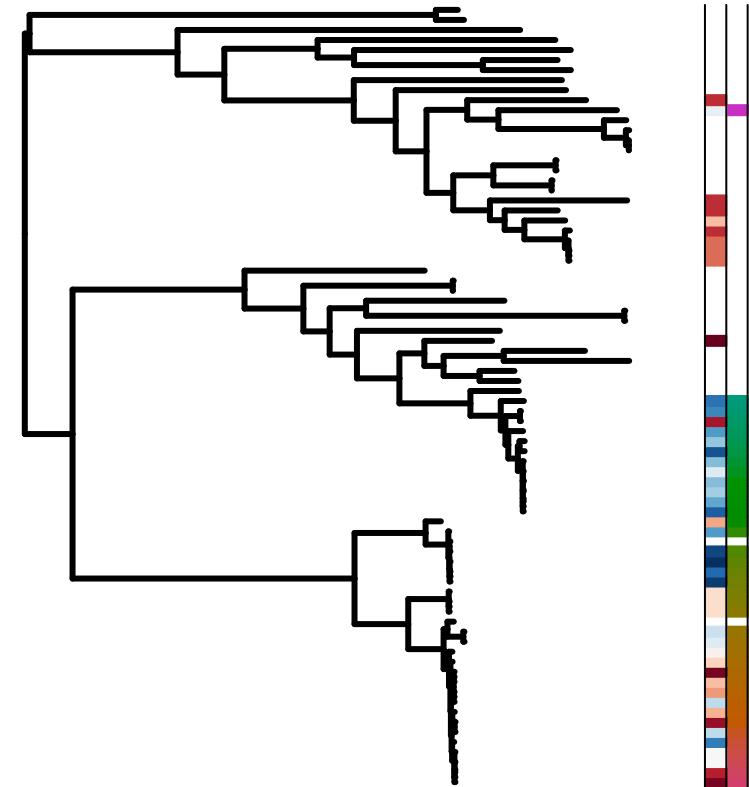
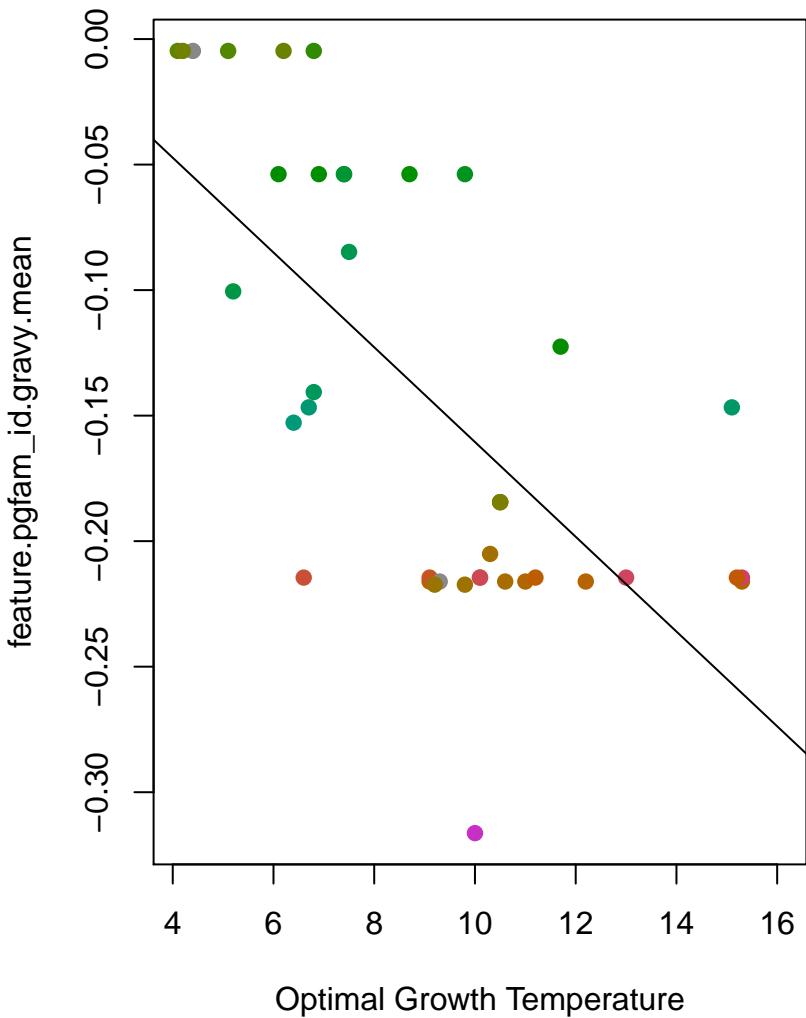




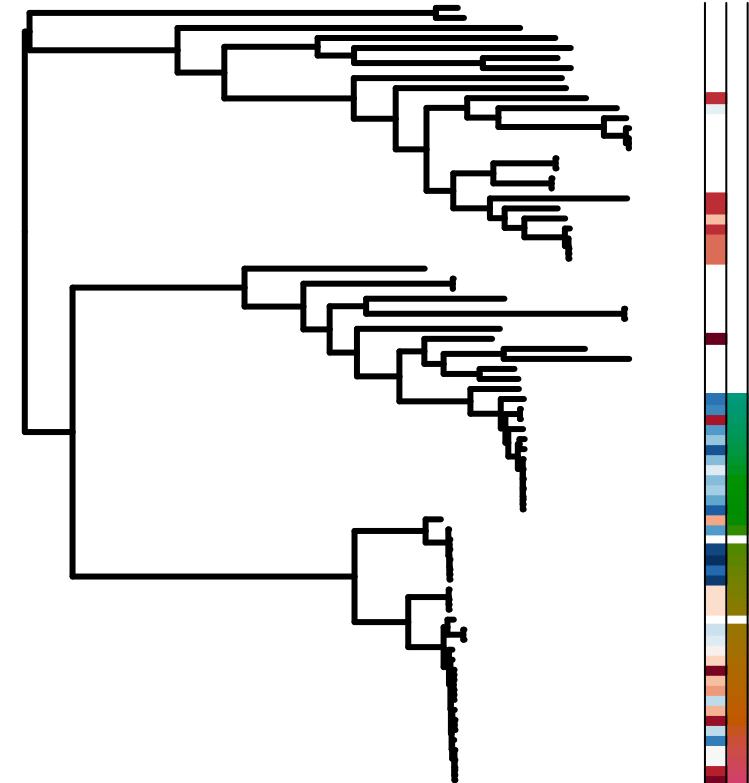
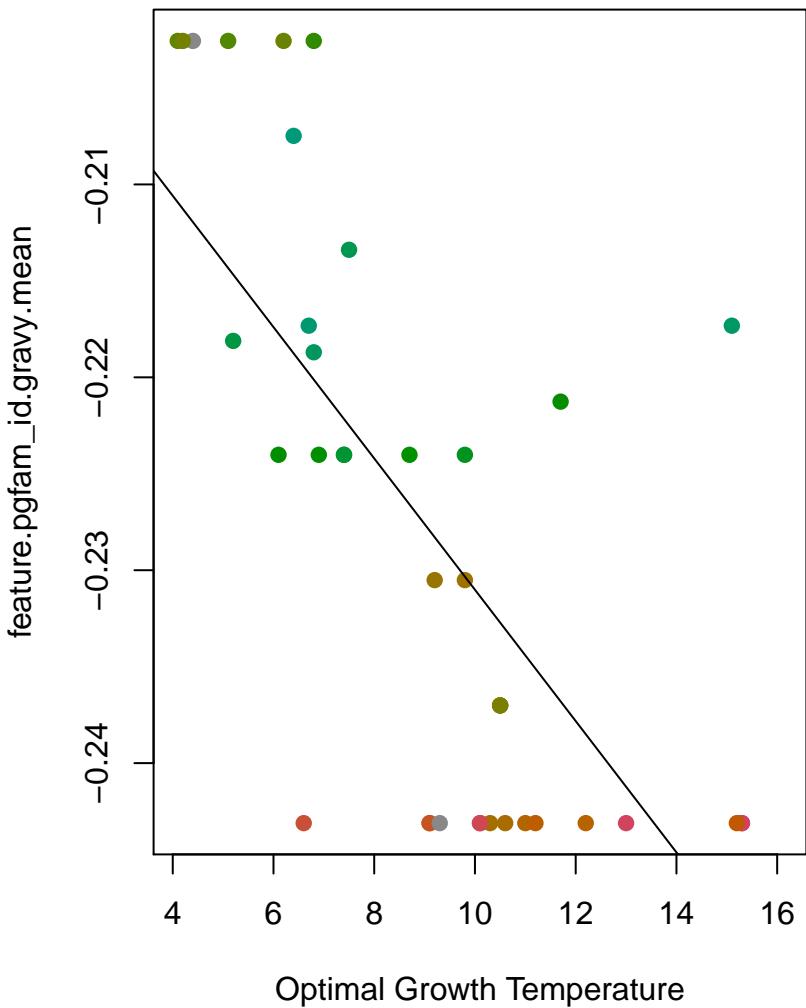
feature.pgfam_id.gravy.mean
PGF_10244701
GTP 3',8-cyclase (EC 4.1.99.22)
 $r = -0.665$, $p = 10^{-6.475}$



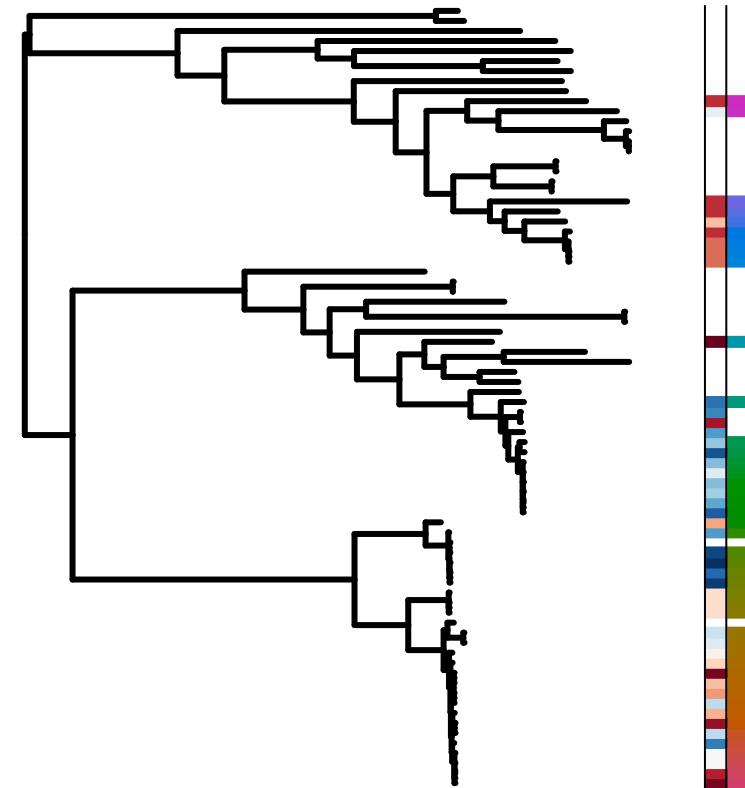
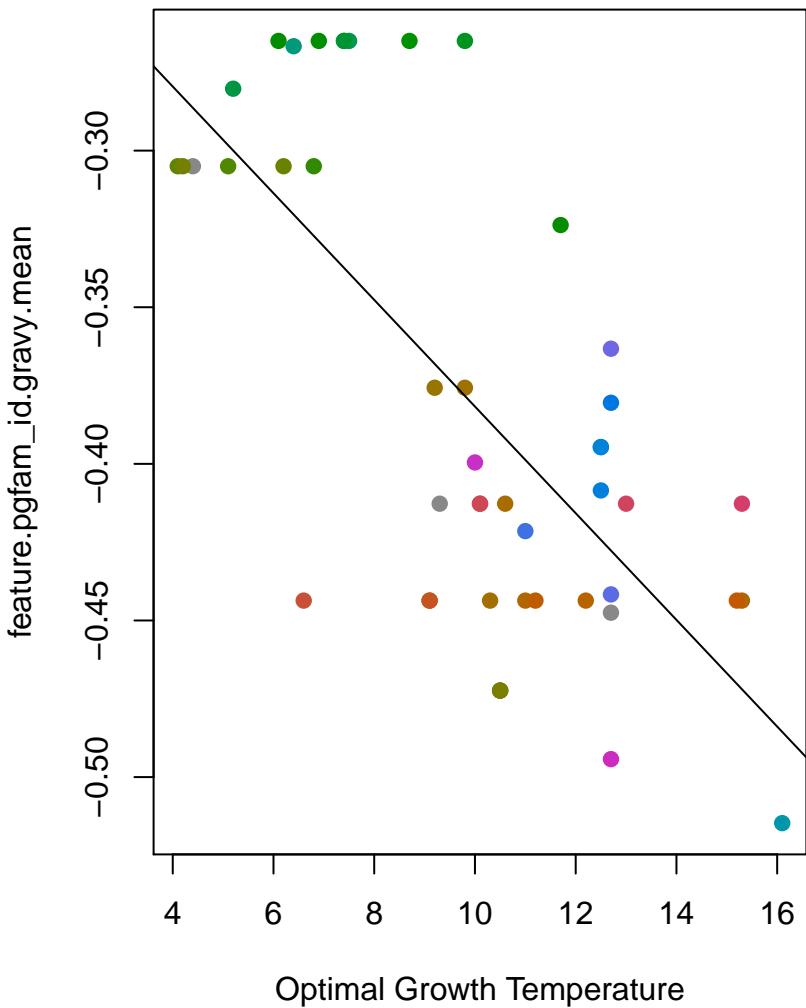
feature.pgfam_id.gravy.mean
PGF_01338555
hypothetical protein
 $r = -0.669$, $p = 10^{-5.627}$

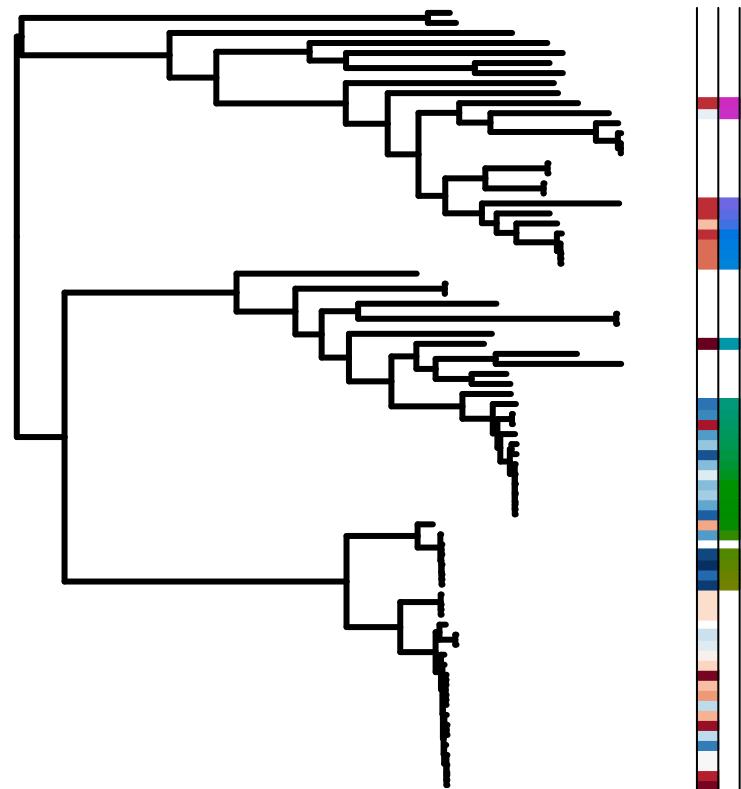
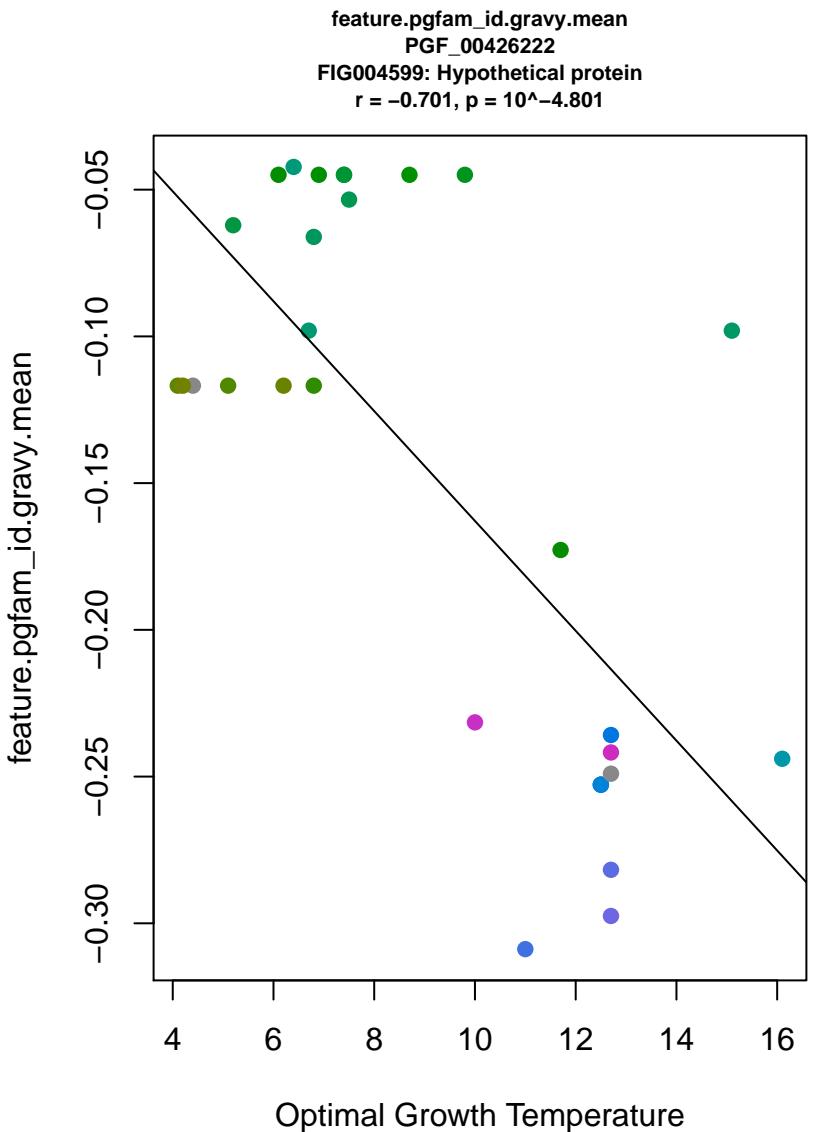


feature.pgfam_id.gravy.mean
PGF_00416513
Carbon–nitrogen hydrolase
 $r = -0.695$, $p = 10^{-6.047}$

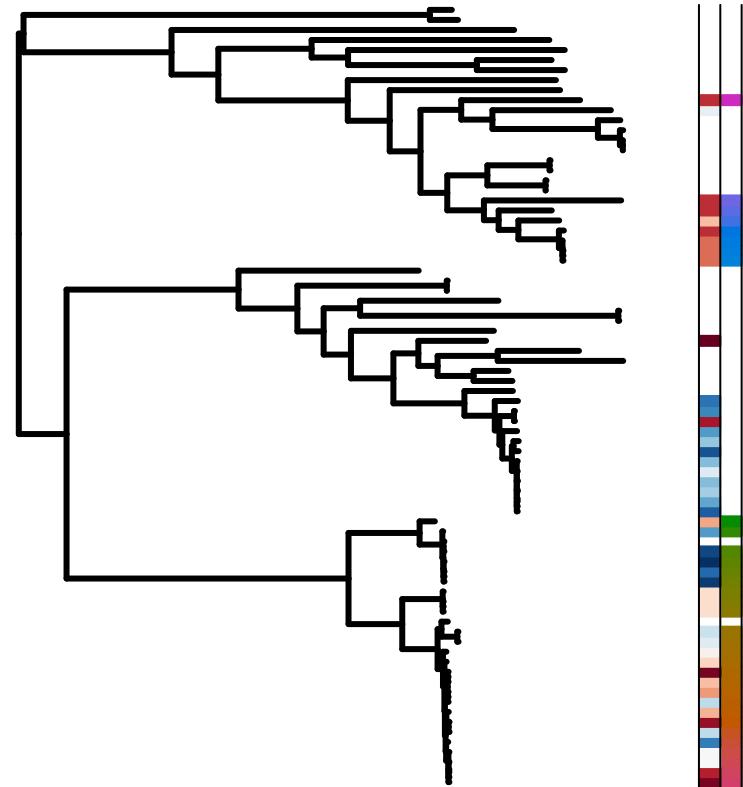
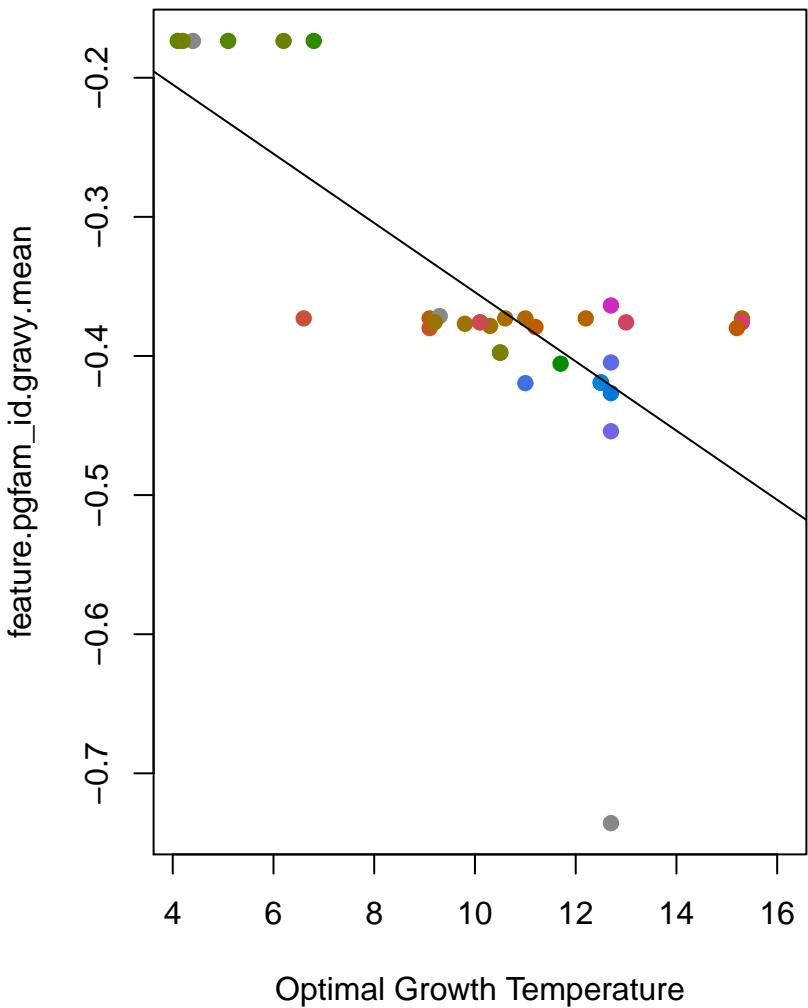


feature.pgfam_id.gravy.mean
PGF_00035421
Potential queD like 2
 $r = -0.696$, $p = 10^{-7.262}$

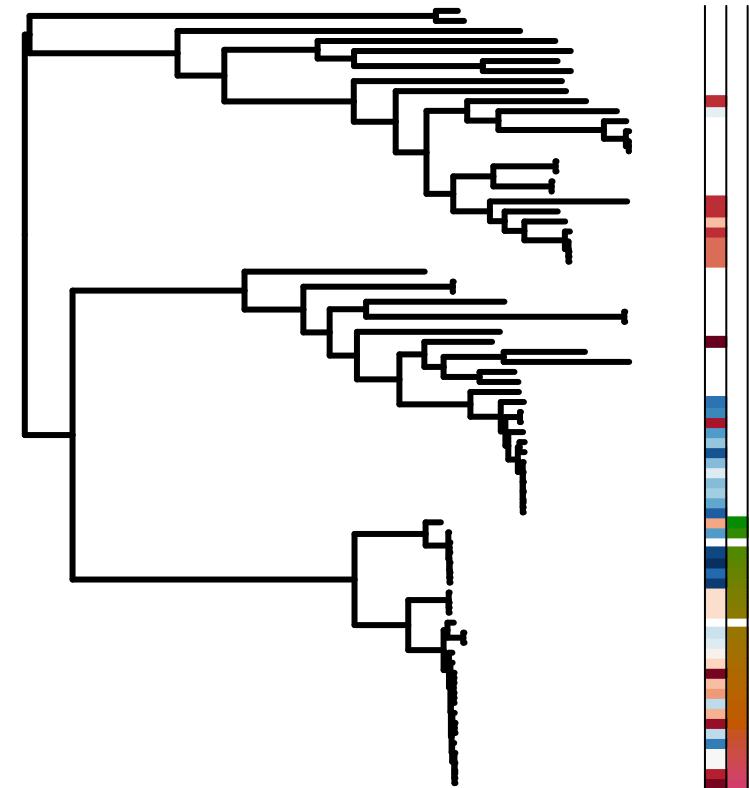
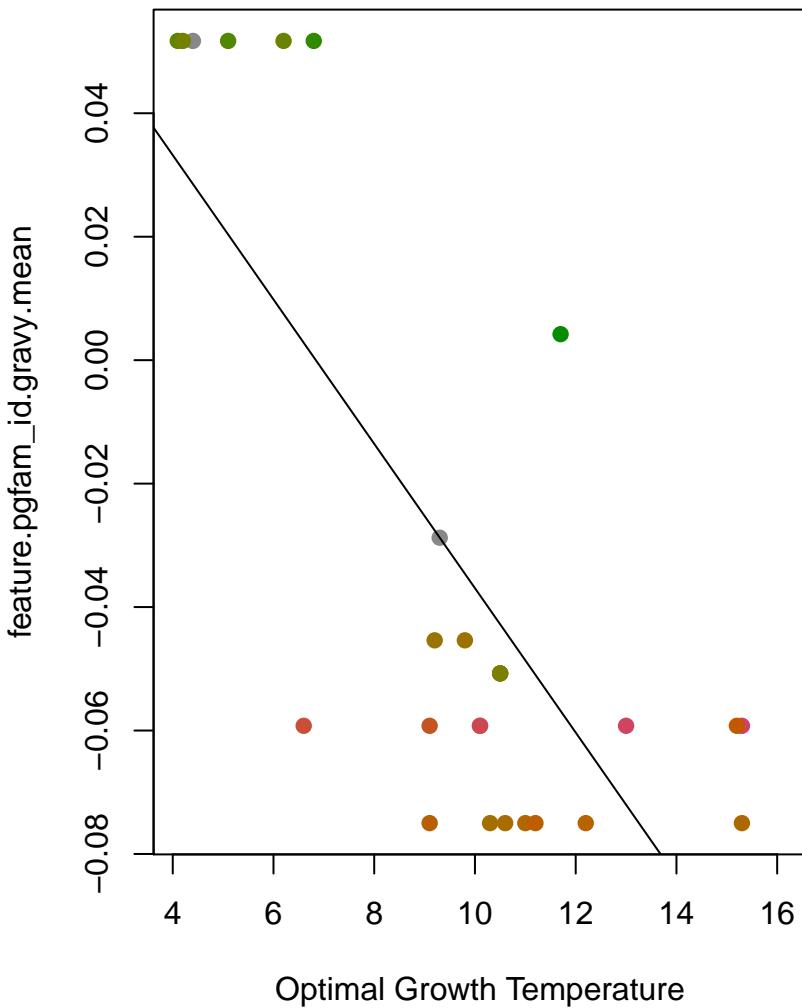




feature.pgfam_id.gravy.mean
PGF_00004056
Fatty acid cis/trans isomerase
 $r = -0.711$, $p = 10^{-5.922}$



feature.pgfam_id.gravy.mean
PGF_07319198
hypothetical protein
 $r = -0.757$, $p = 10^{-5.316}$



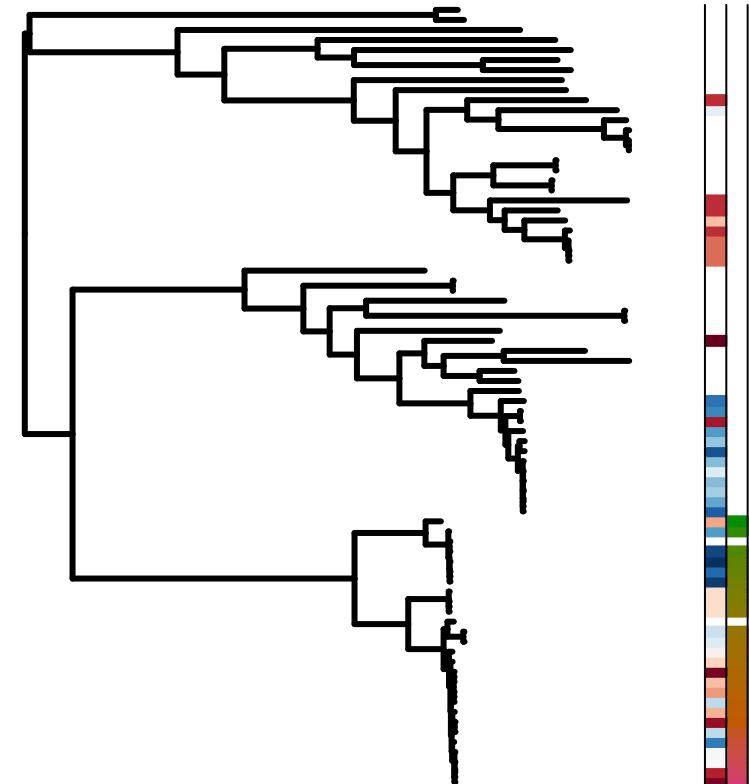
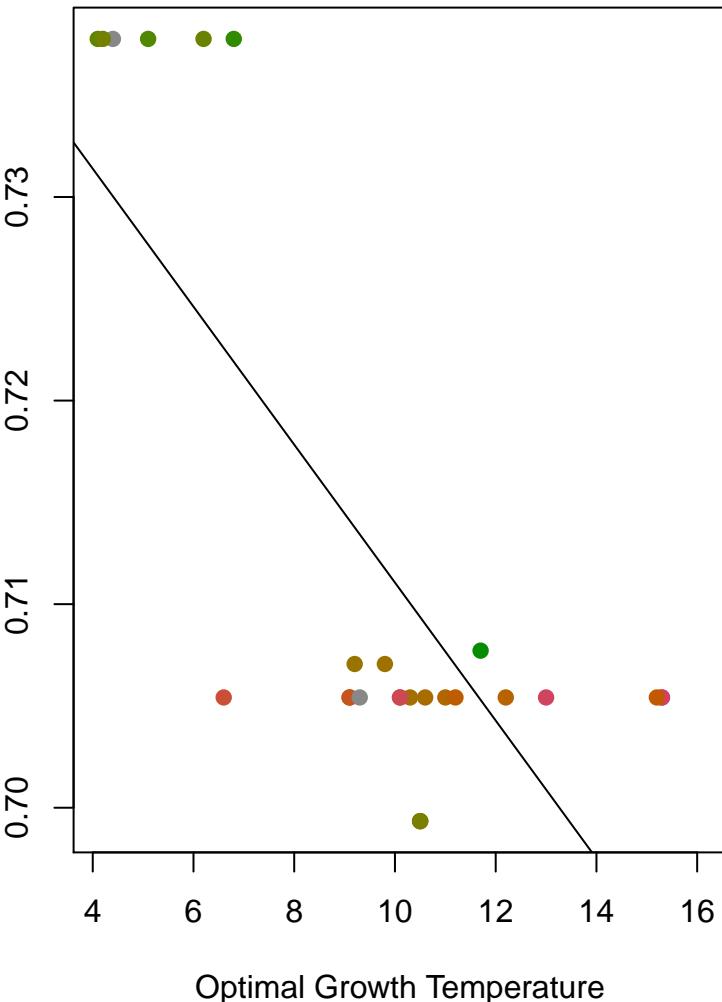
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PGF_00061953

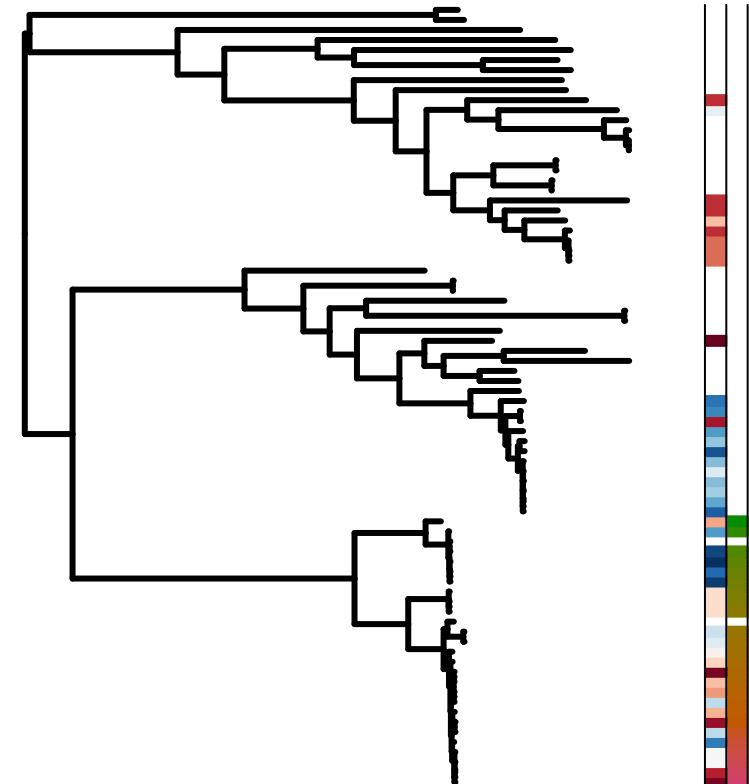
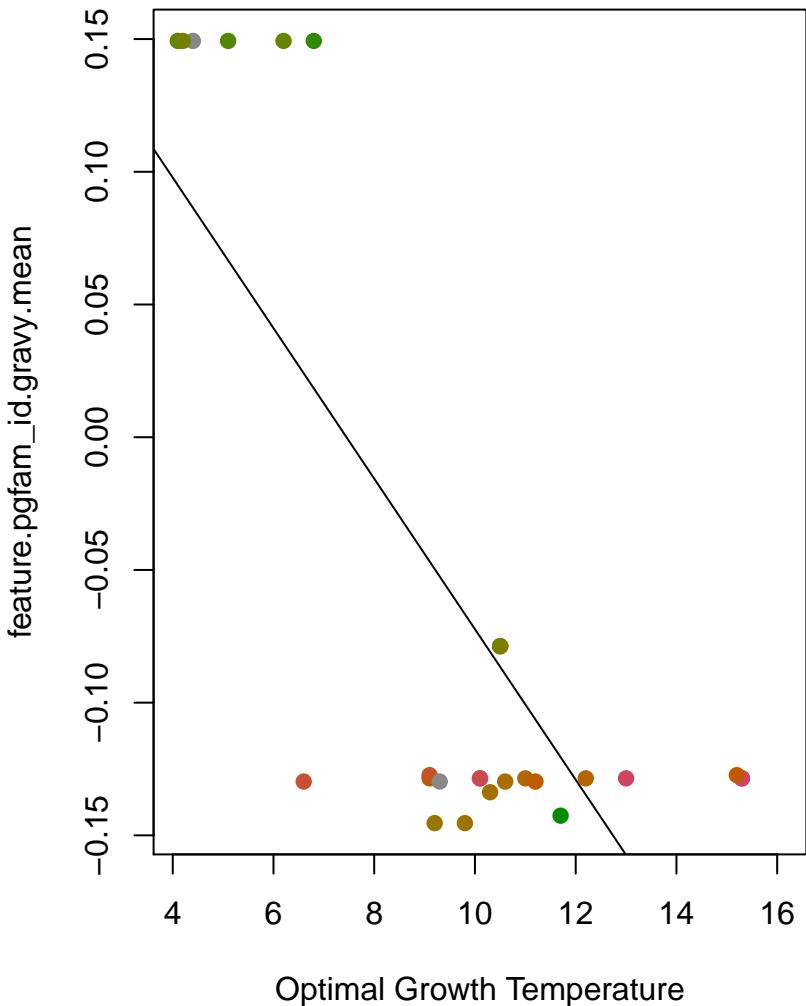
TrkA-C domain protein

r = -0.765, p = 10^-5.464

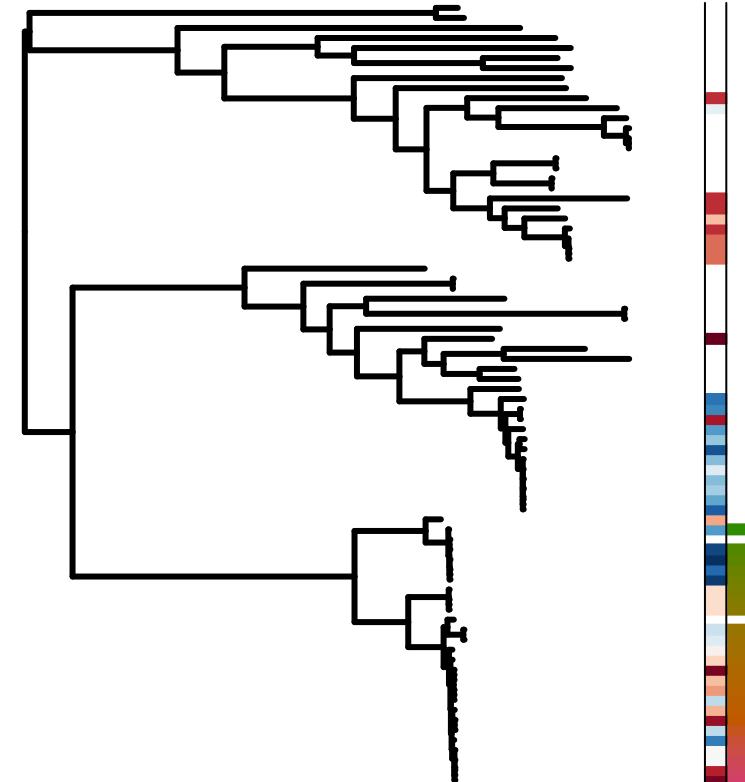
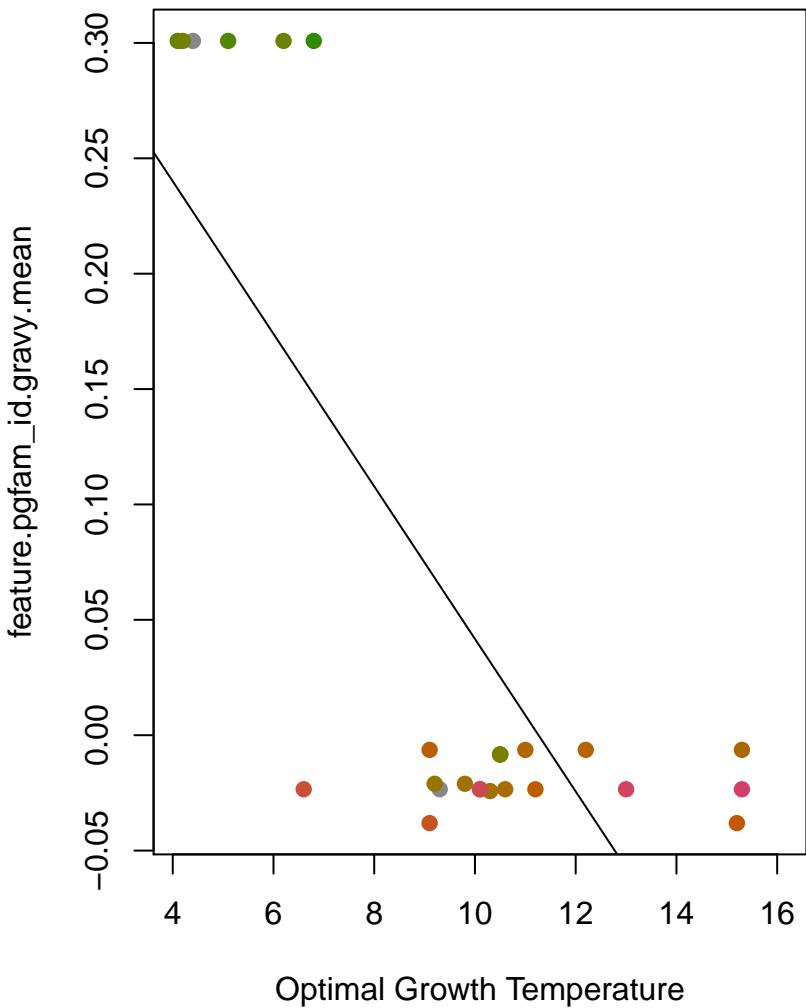
feature.pgfam_id.gravy.mean



feature.pgfam_id.gravy.mean
PGF_11018774
hypothetical protein
 $r = -0.771$, $p = 10^{-5.602}$



feature.pgfam_id.gravy.mean
PGF_12049070
hypothetical protein
 $r = -0.773$, $p = 10^{-5.439}$

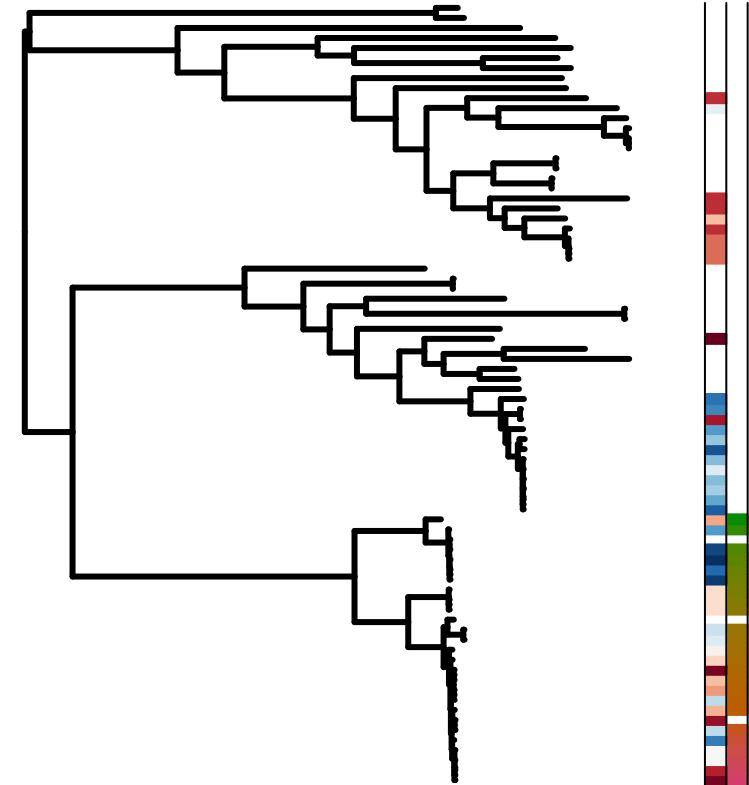
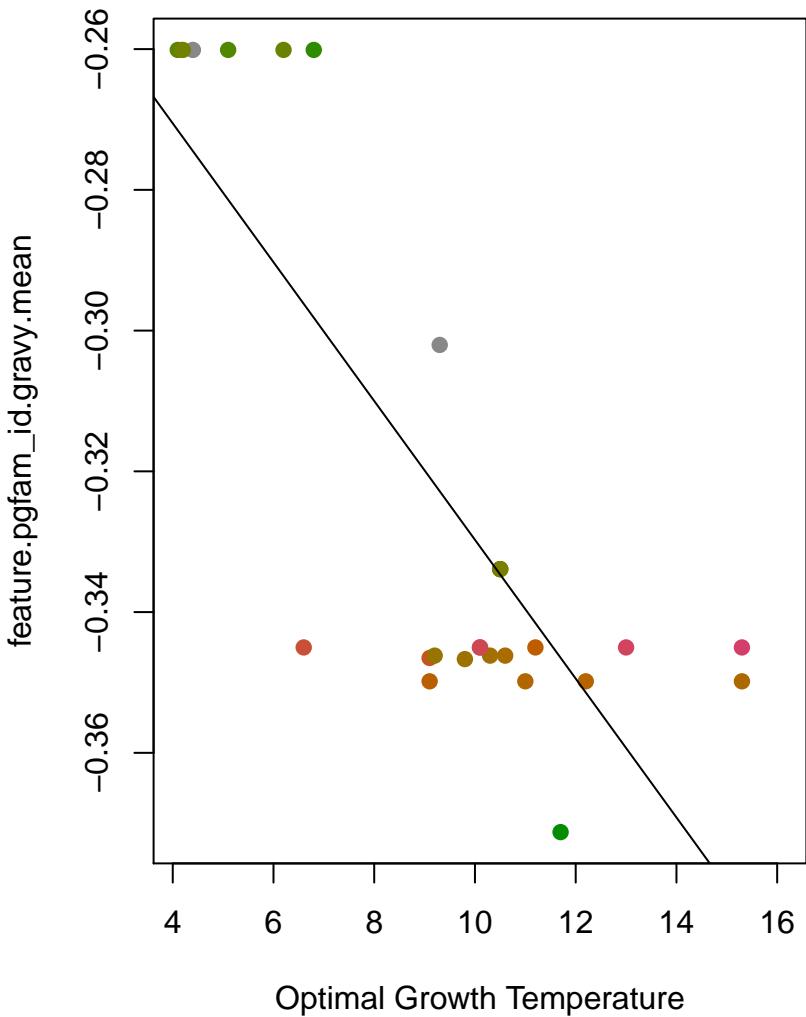


feature.pgfam_id.gravy.mean

PGF_03083319

Maltodextrin glucosidase (EC 3.2.1.20)

$r = -0.8, p = 10^{-6.02}$

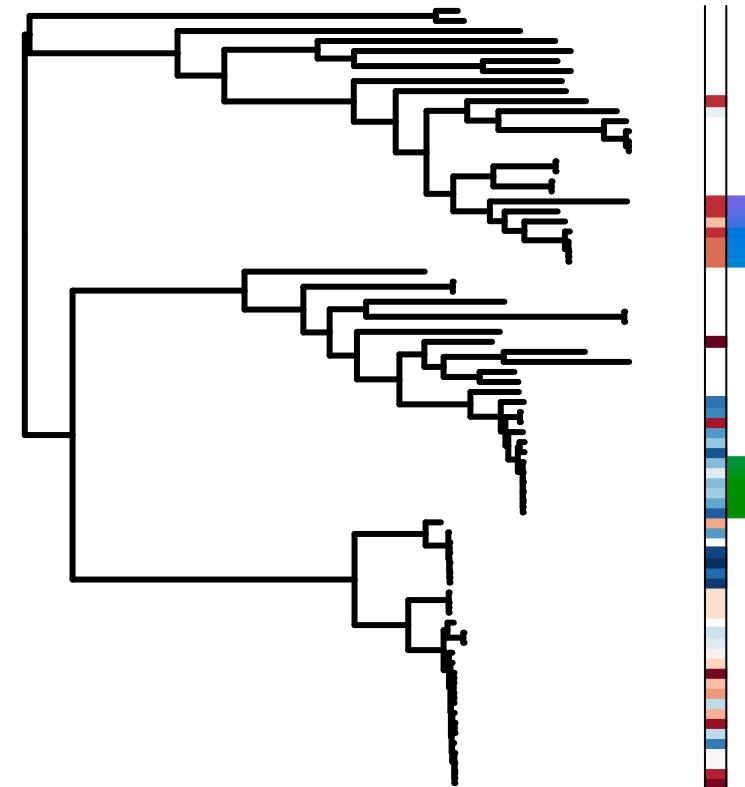
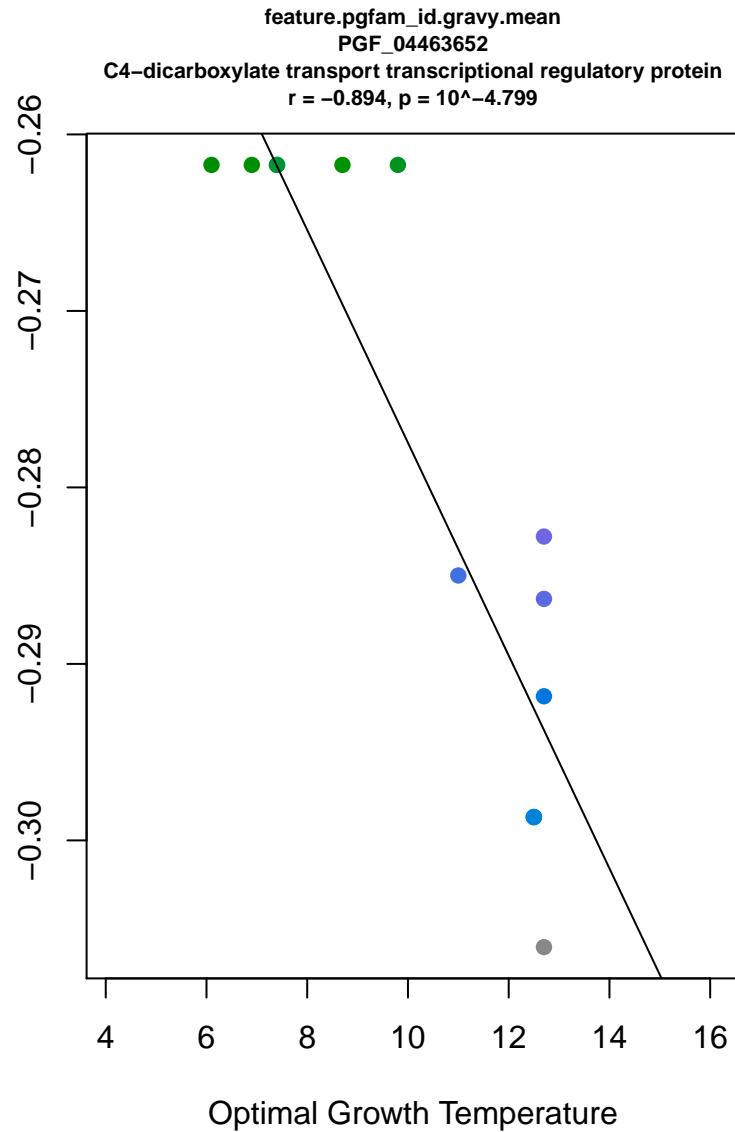


feature.pgfam_id.gravy.mean

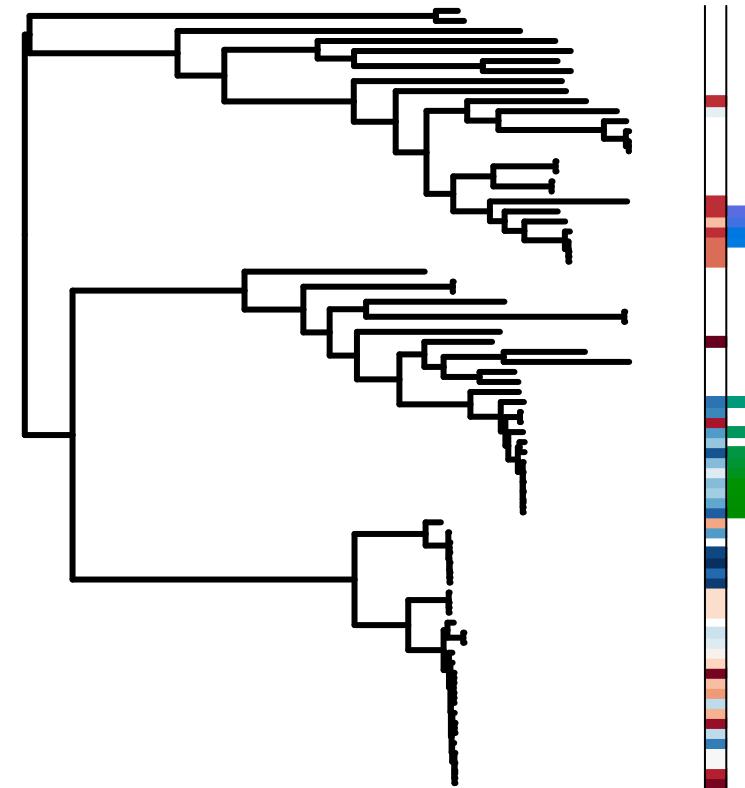
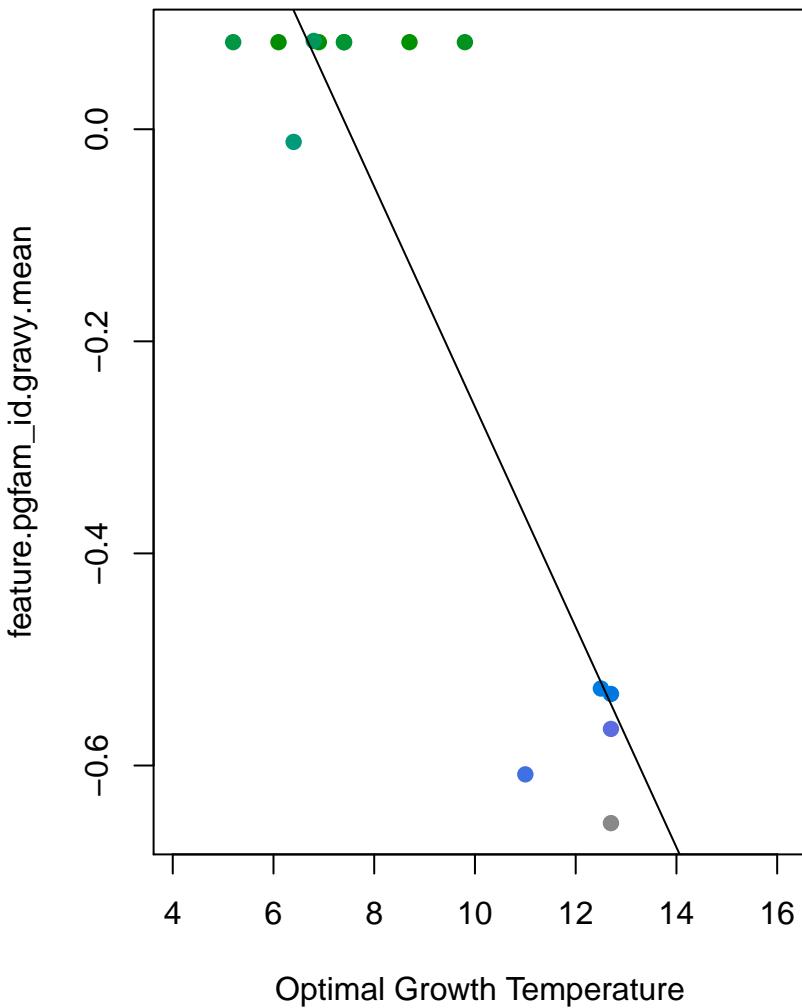
PGF_04463652

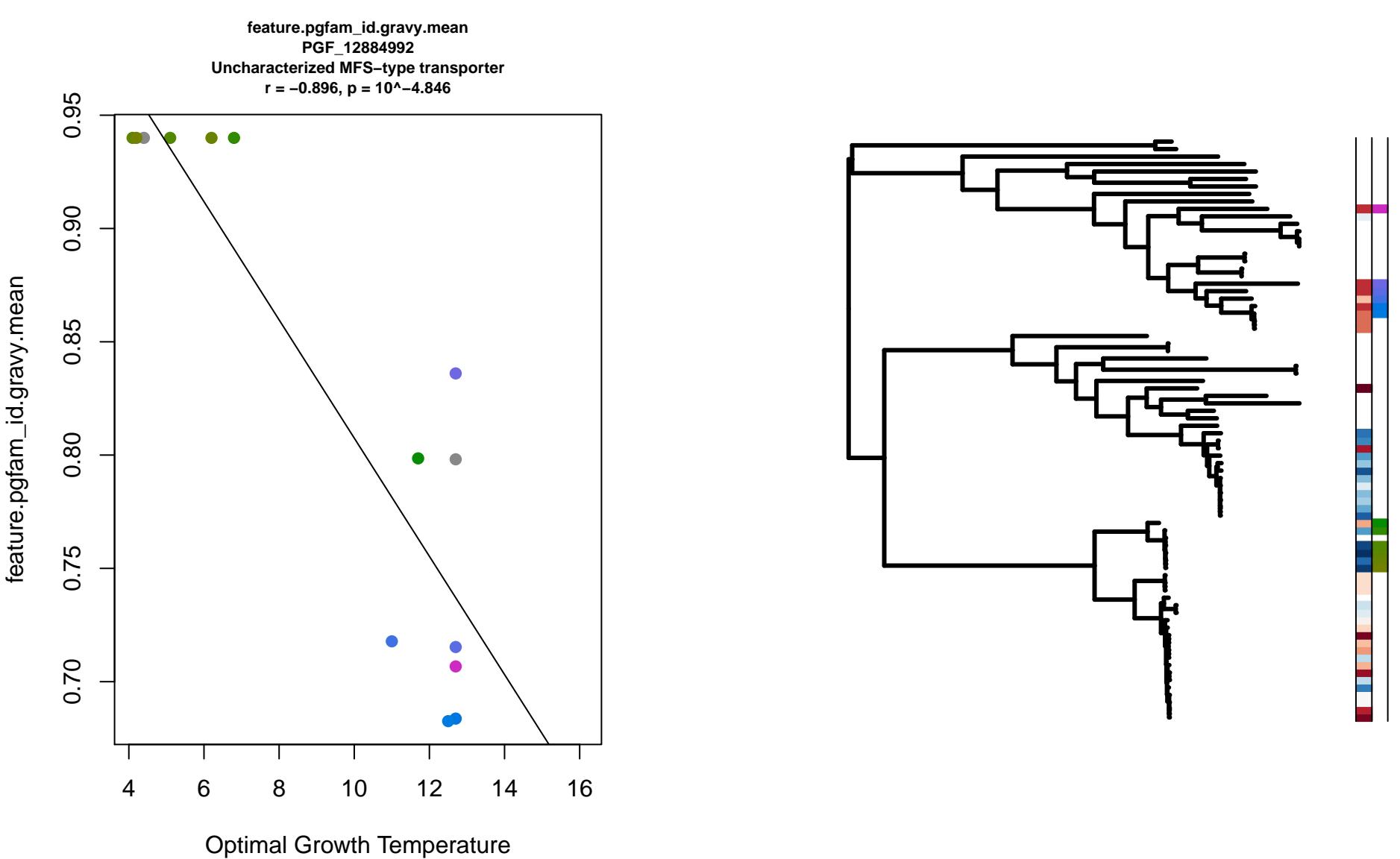
C4-dicarboxylate transport transcriptional regulatory protein

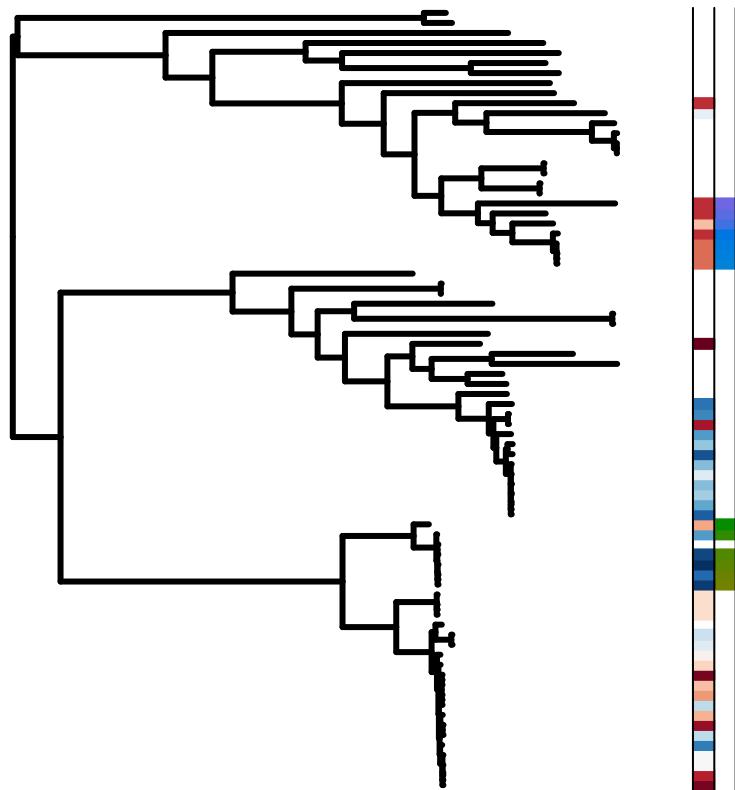
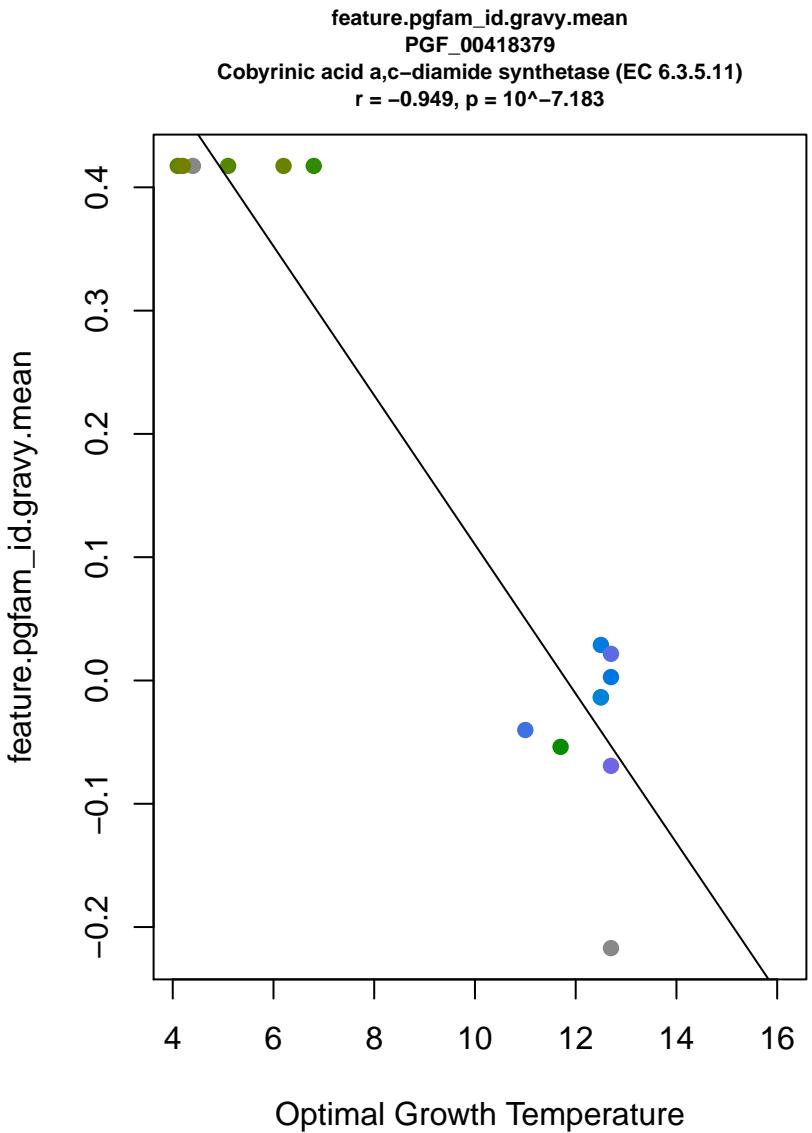
$r = -0.894$, $p = 10^{-4.799}$

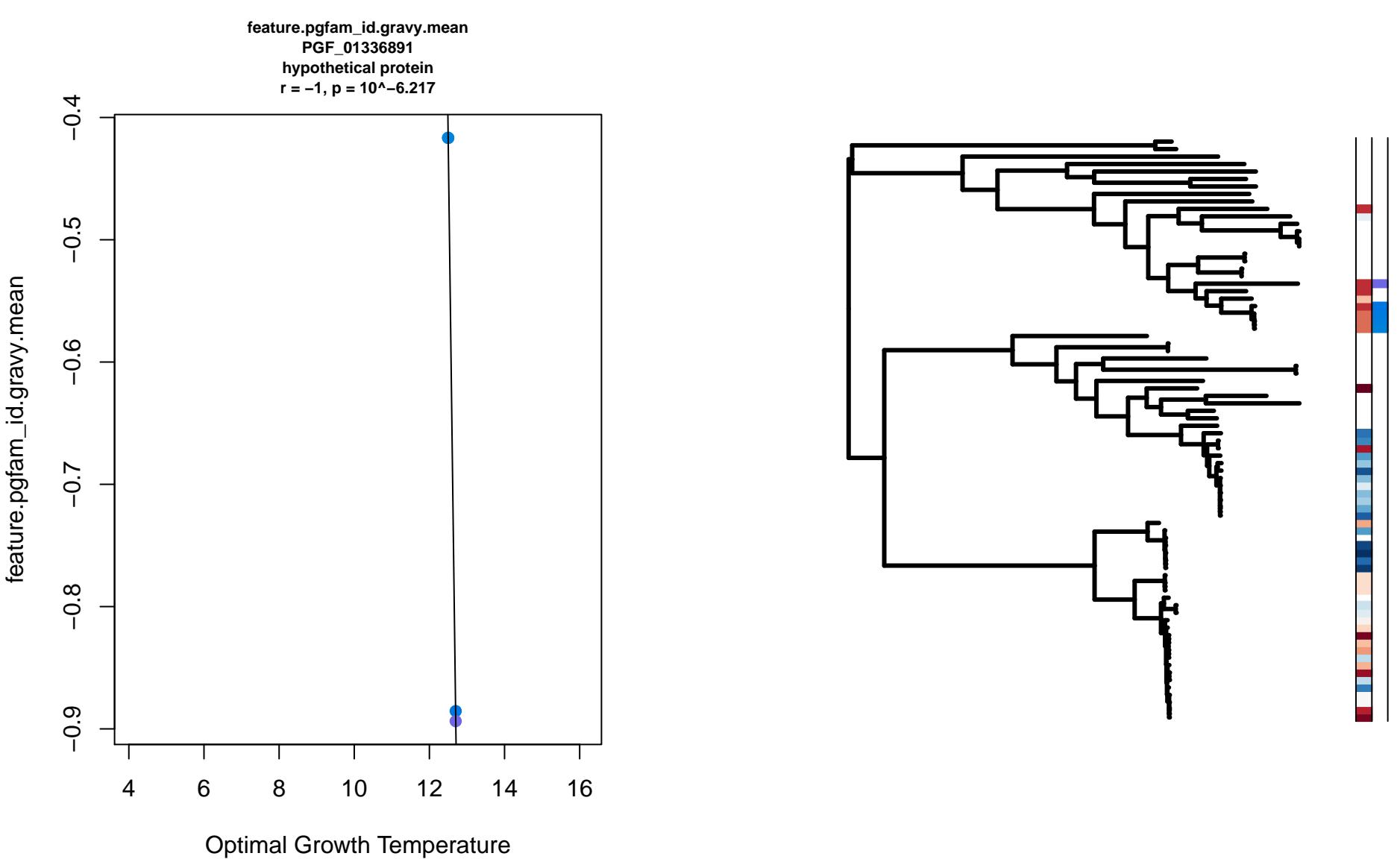


feature.pgfam_id.gravy.mean
PGF_01668026
Glutaredoxin 3
 $r = -0.895$, $p = 10^{-4.802}$

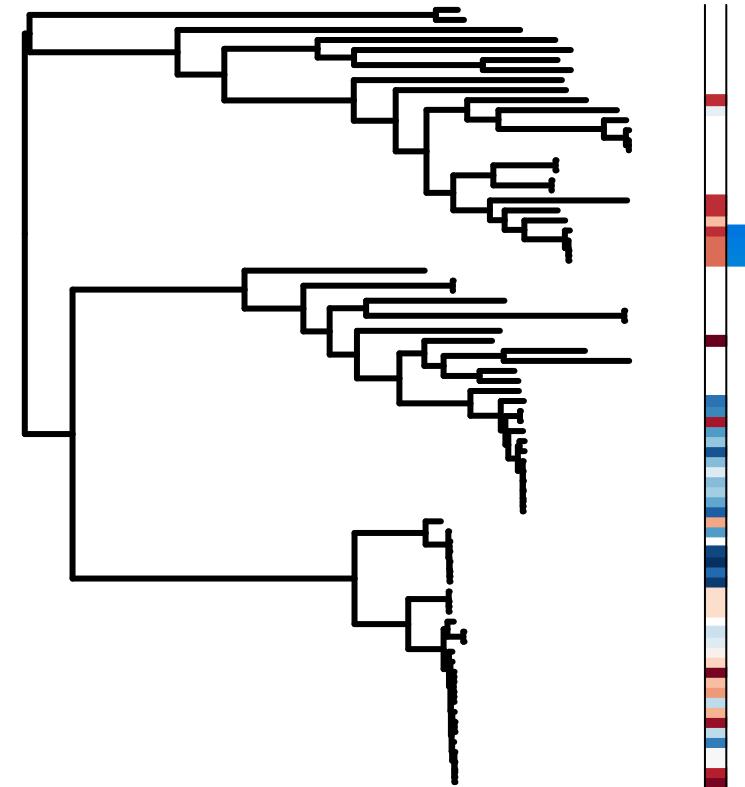
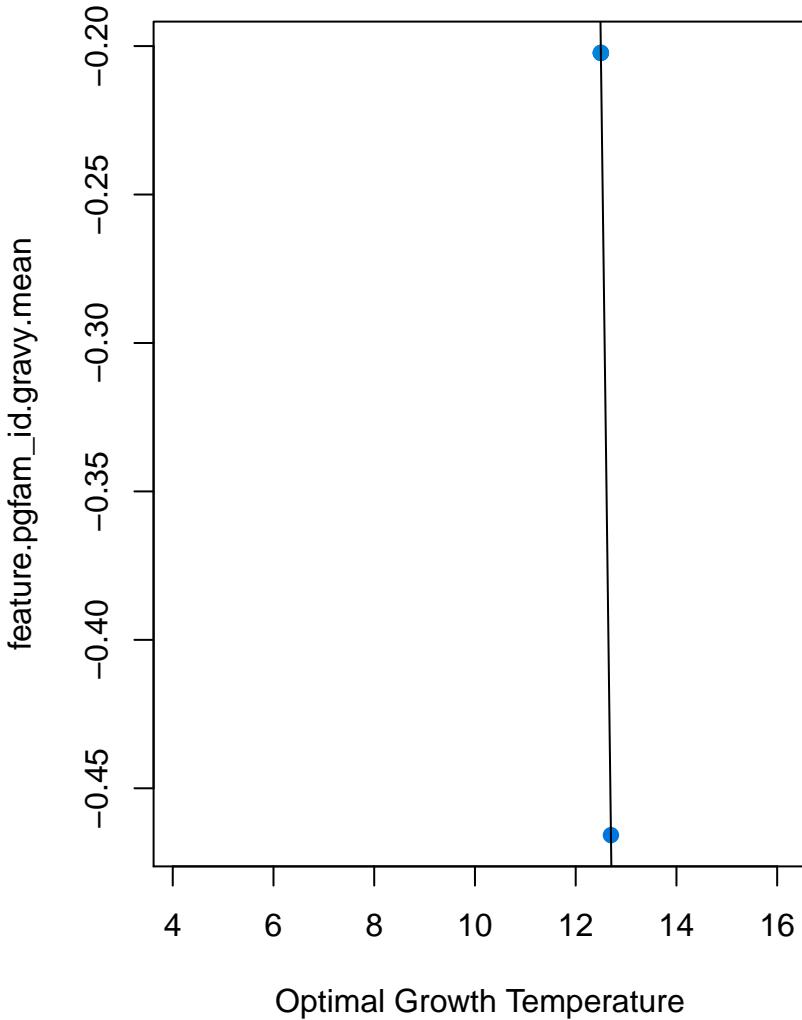




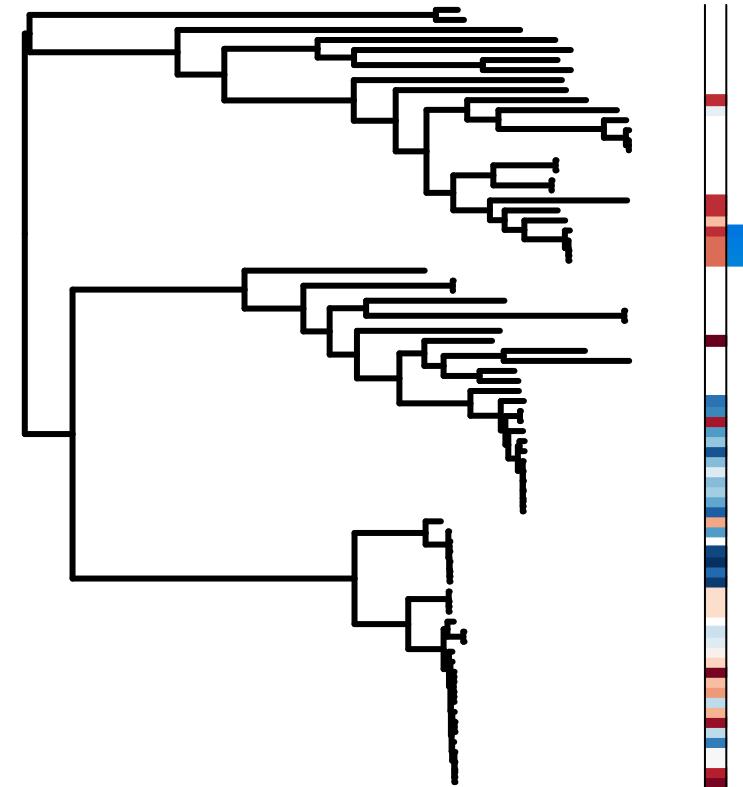
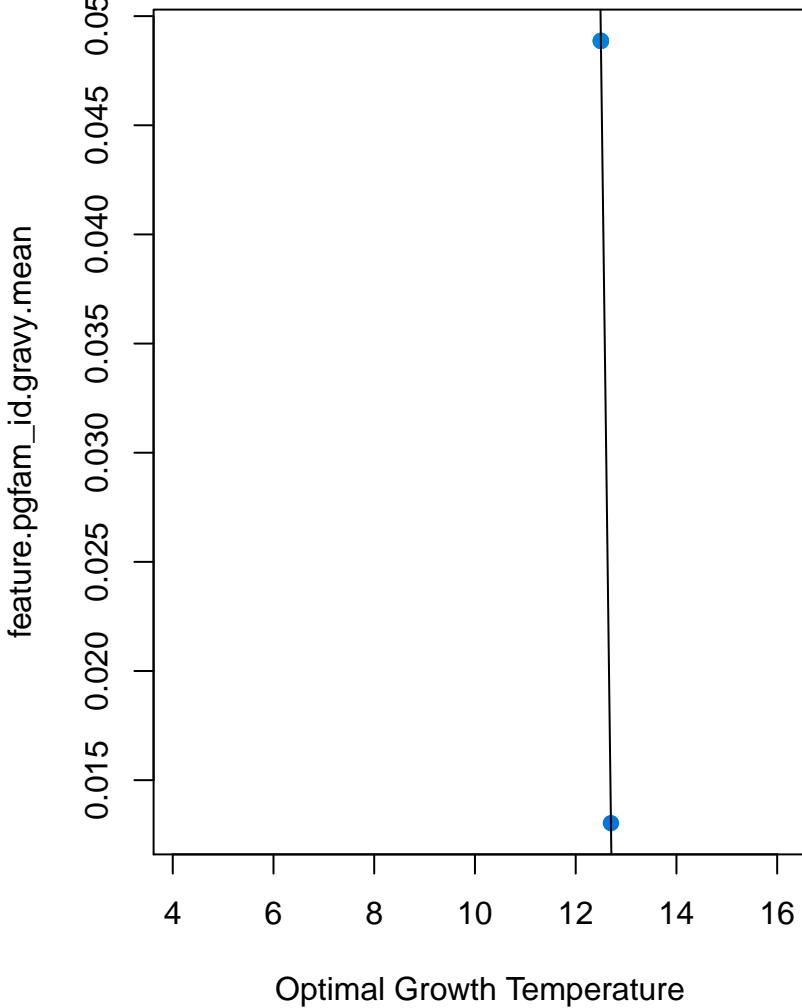




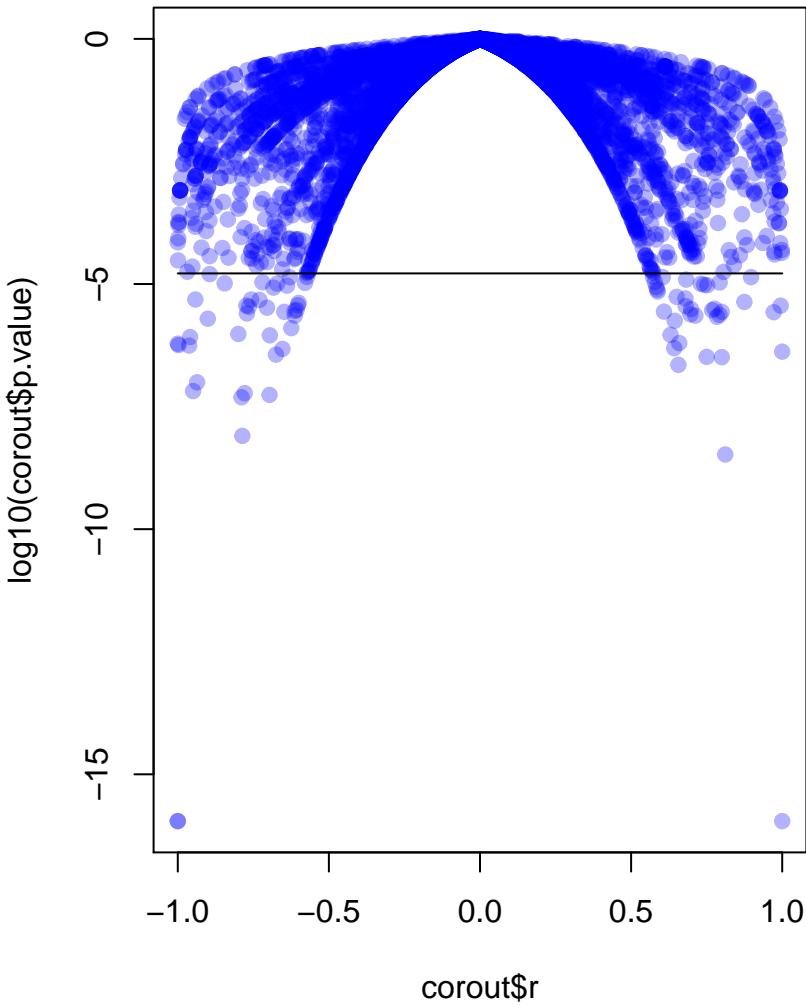
feature.pgfam_id.gravy.mean
PGF_00211286
hypothetical protein
 $r = -1$, $p = 10^{-15.955}$



feature.pgfam_id.gravy.mean
PGF_00336673
hypothetical protein
 $r = -1$, $p = 10^{-15.955}$



feature.plfam_id.gravy.mean

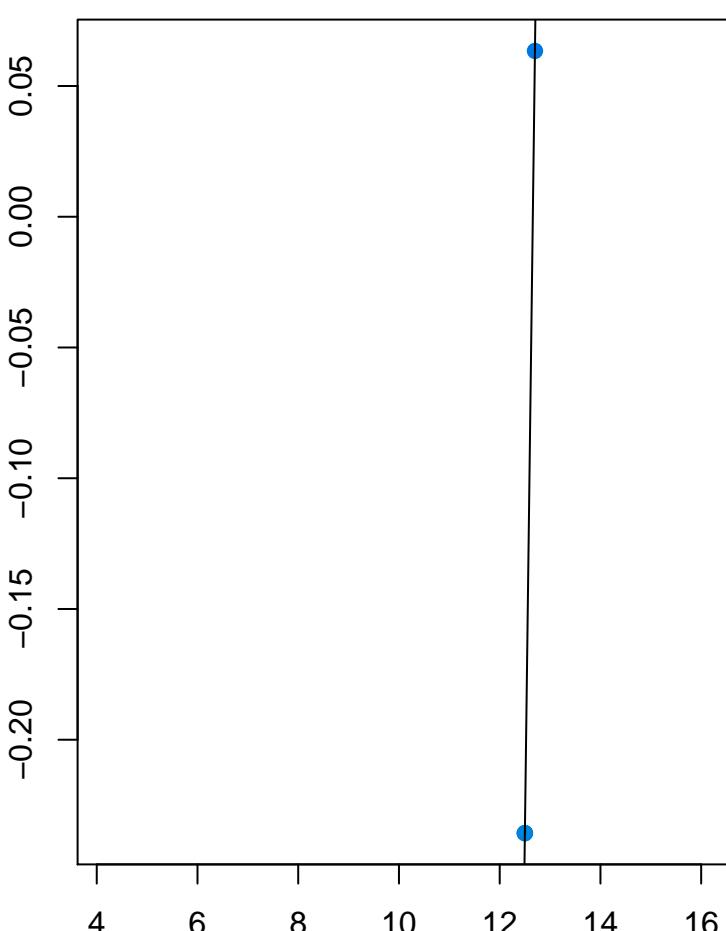


feature.plfam_id.gravy.mean

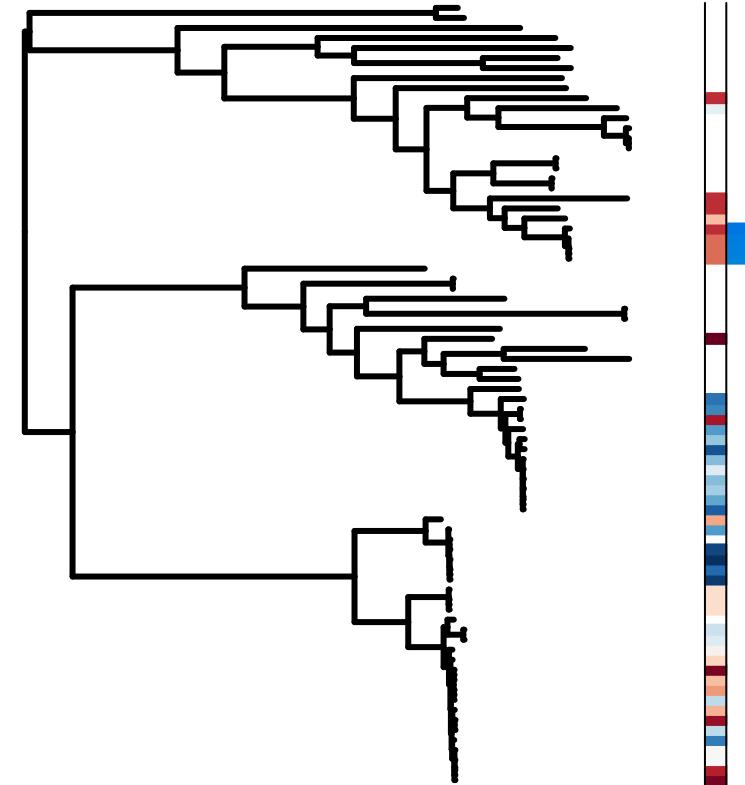
PLF_28228_00007754

Lipid A phosphoethanolamine transferase, putative
 $r = 1, p = 10^{-15.955}$

feature.plfam_id.gravy.mean



Optimal Growth Temperature



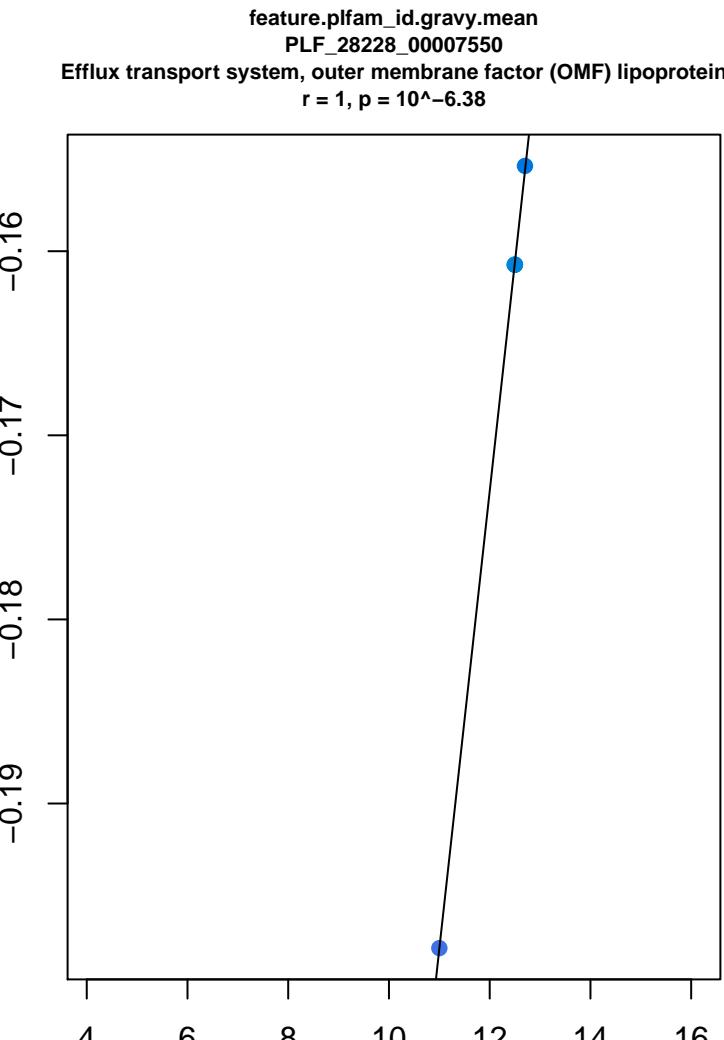
feature.plfam_id.gravy.mean

PLF_28228_00007550

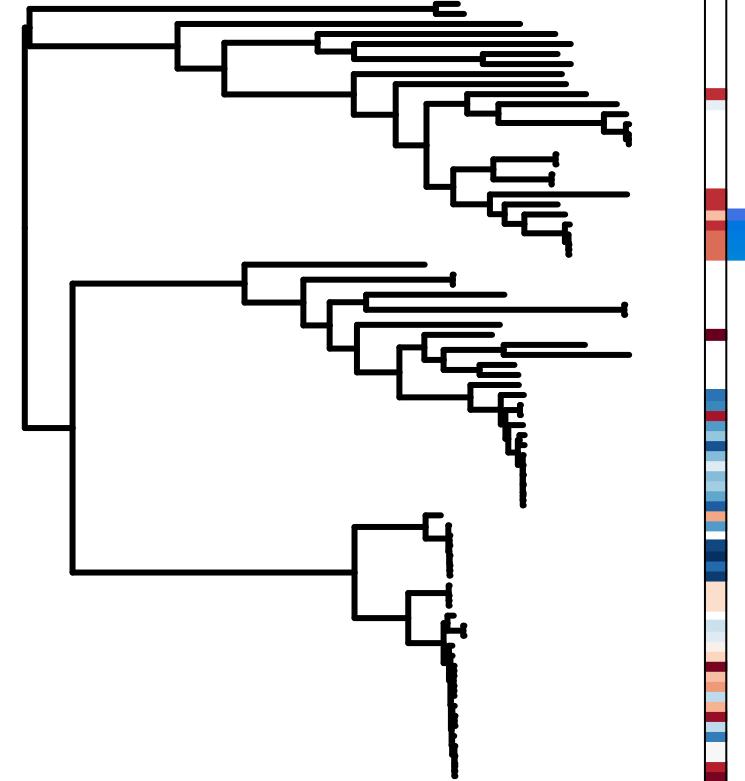
Efflux transport system, outer membrane factor (OMF) lipoprotein

$r = 1, p = 10^{-6.38}$

feature.plfam_id.gravy.mean

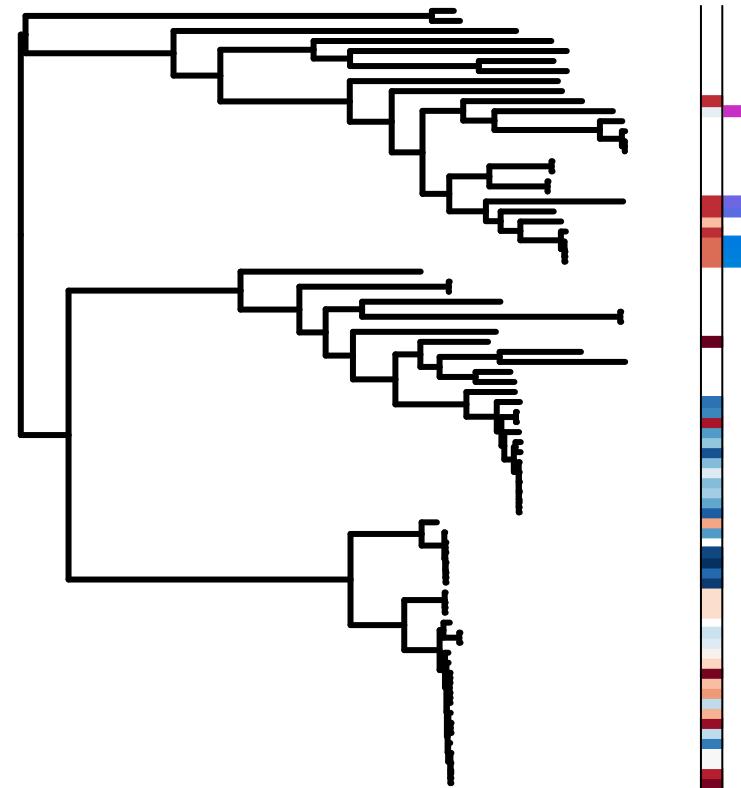
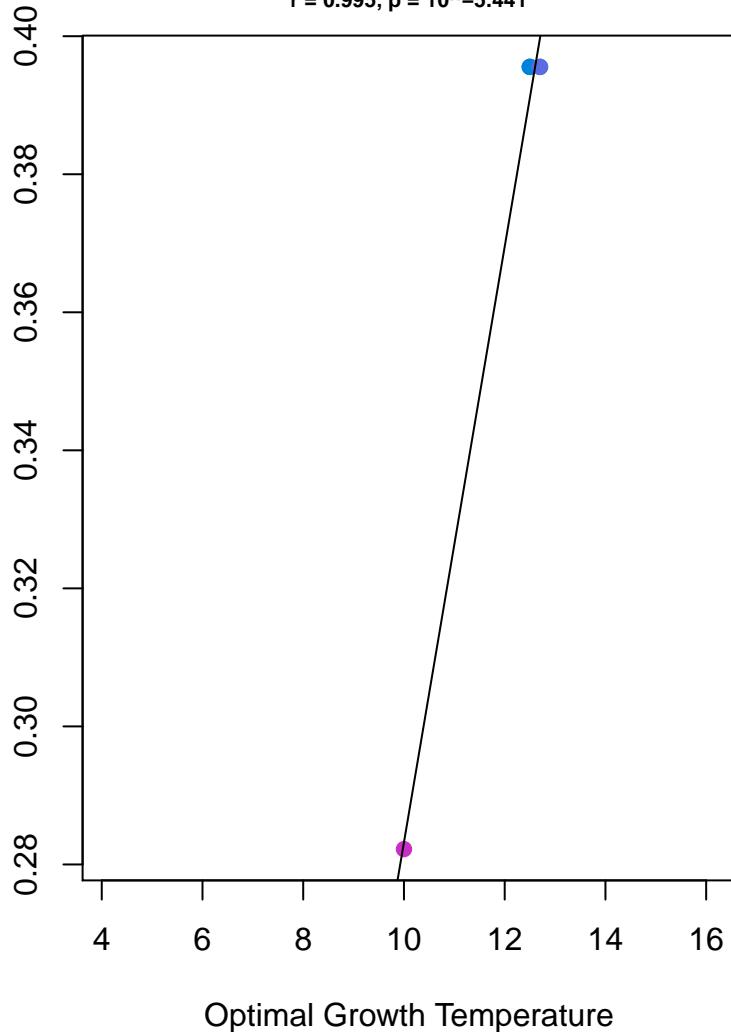


Optimal Growth Temperature

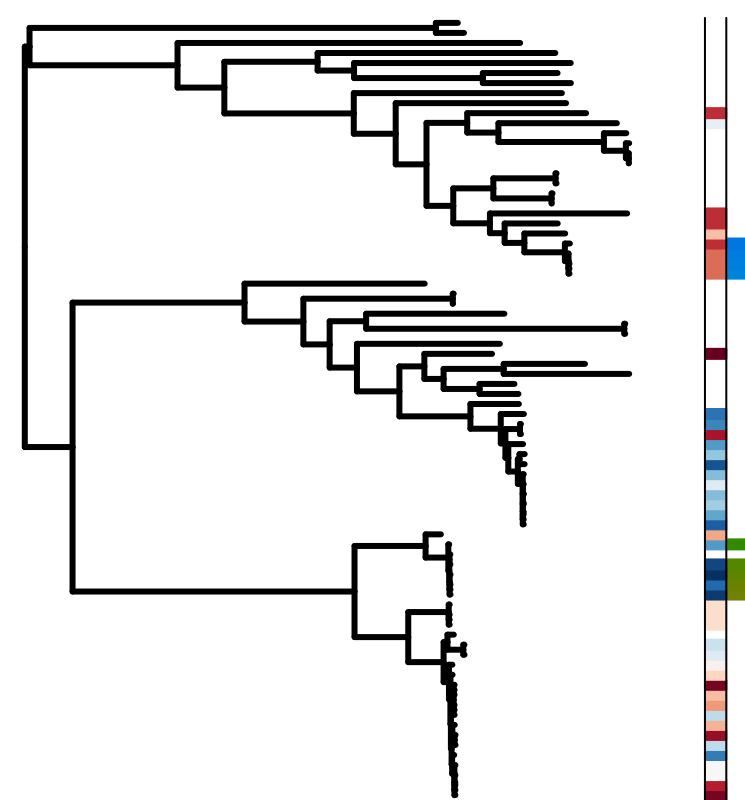
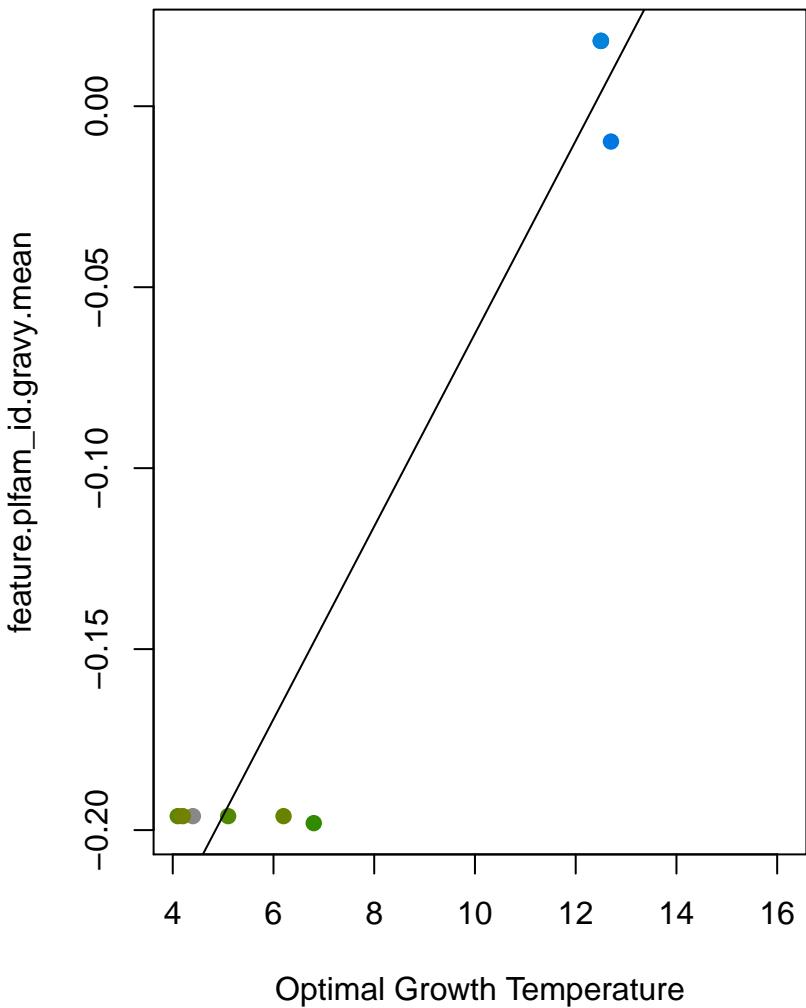


feature.plfam_id.gravy.mean
PLF_28228_00004382
hypothetical protein
 $r = 0.995, p = 10^{-5.441}$

feature.plfam_id.gravy.mean

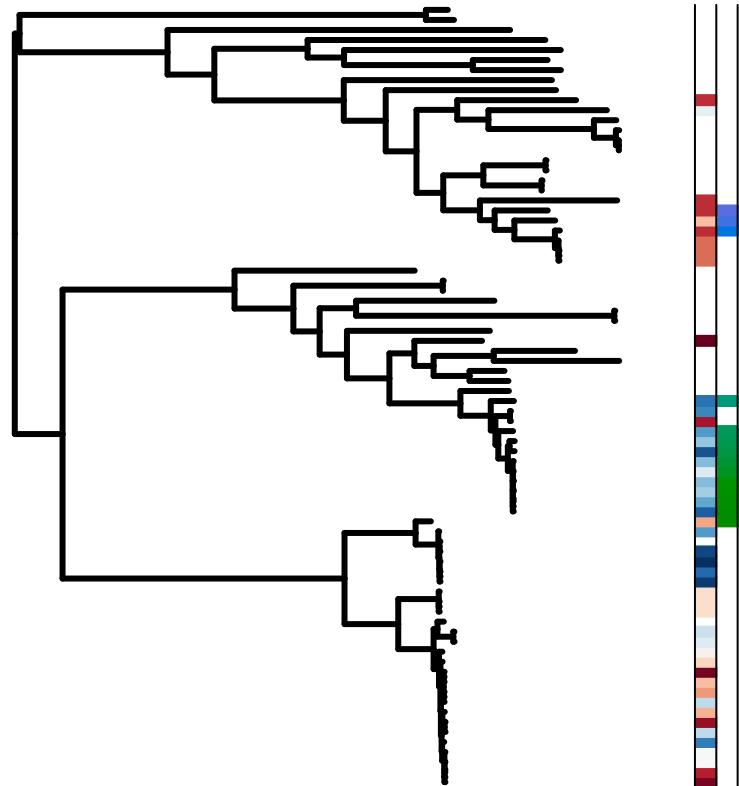
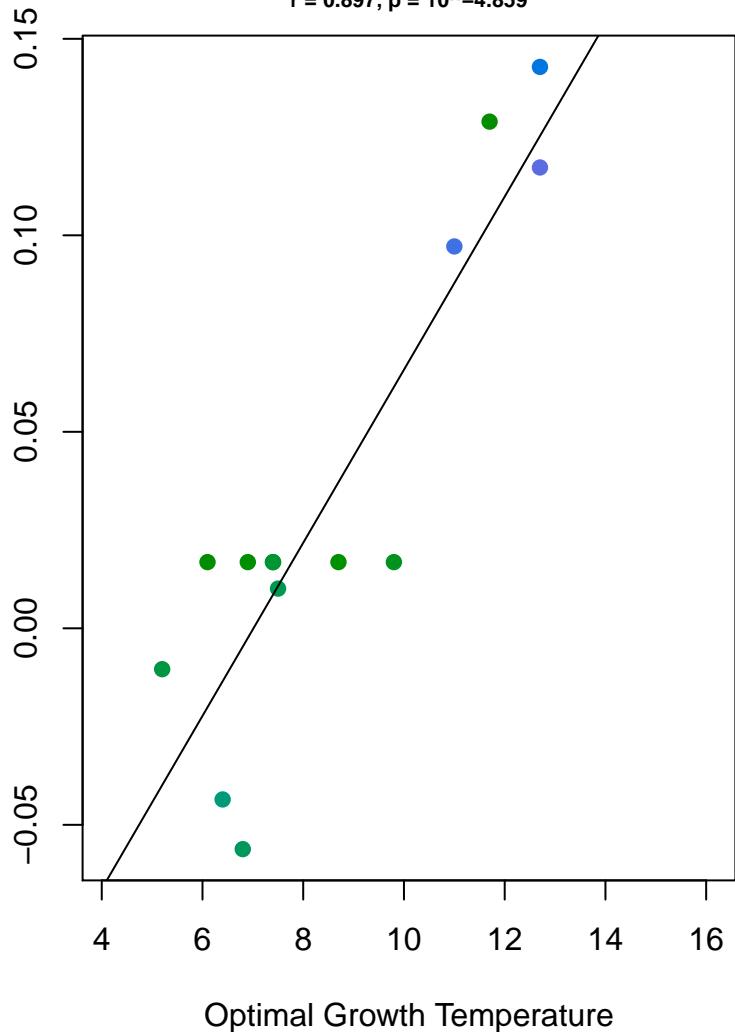


feature.plfam_id.gravy.mean
PLF_28228_00007839
hypothetical protein
 $r = 0.972, p = 10^{-5.575}$

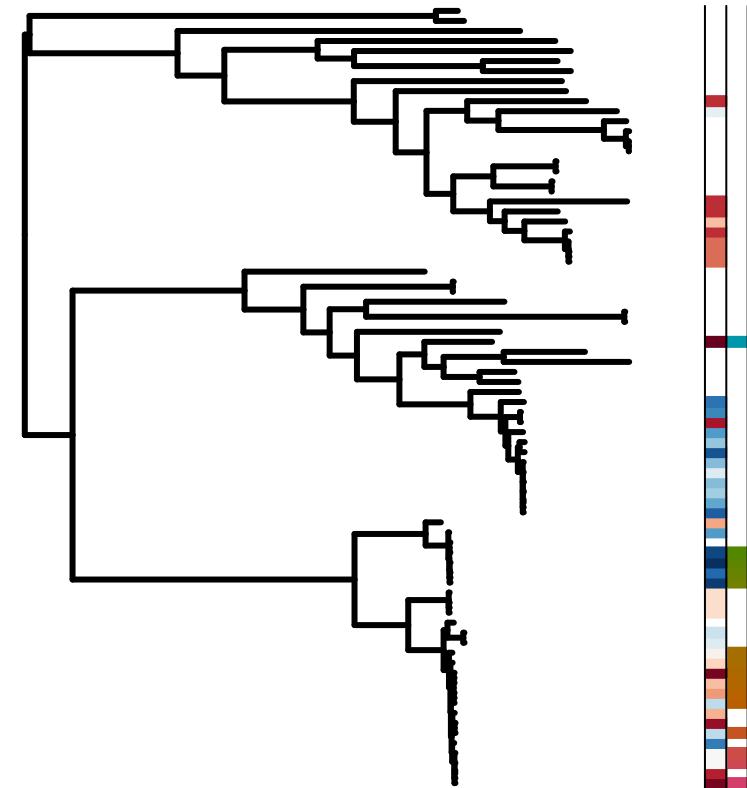
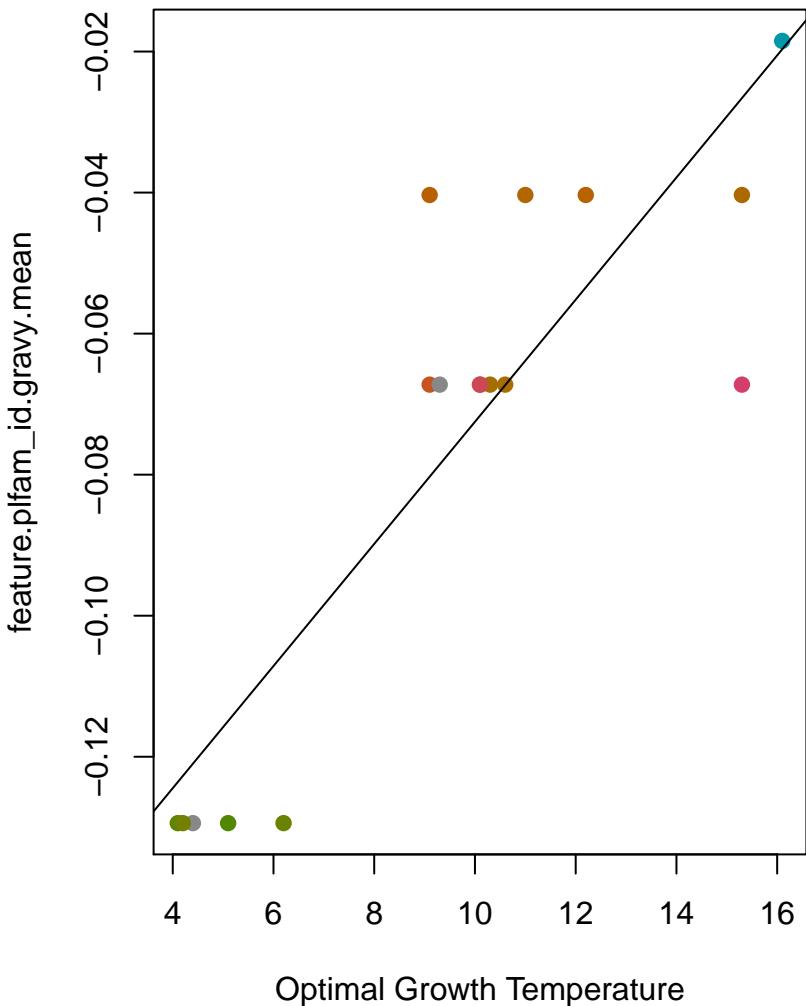


feature.plfam_id.gravy.mean
PLF_28228_00008026
hypothetical protein
 $r = 0.897, p = 10^{-4.859}$

feature.plfam_id.gravy.mean



feature.plfam_id.gravy.mean
PLF_28228_00018861
Glyoxalase family protein
 $r = 0.875, p = 10^{-5.365}$

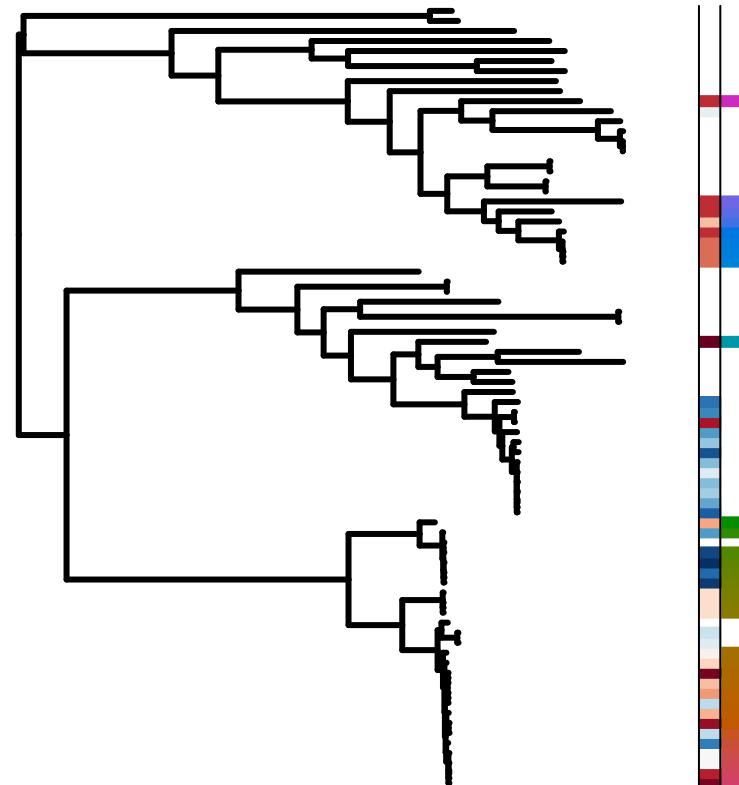
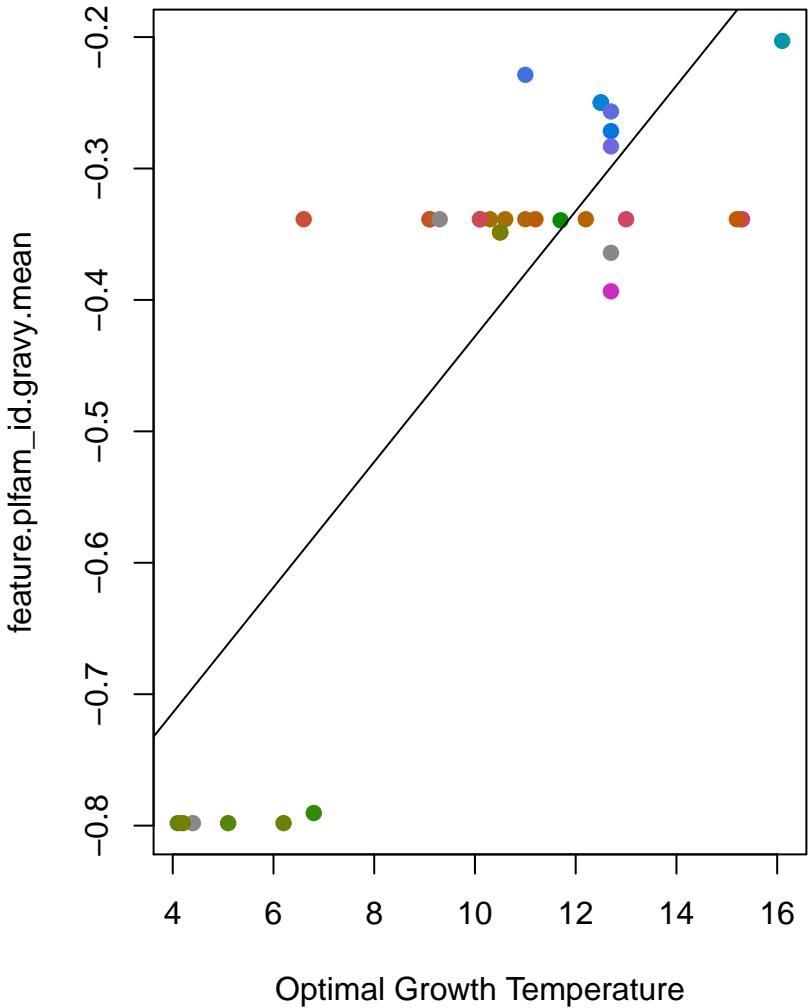


feature.plfam_id.gravy.mean

PLF_28228_00002798

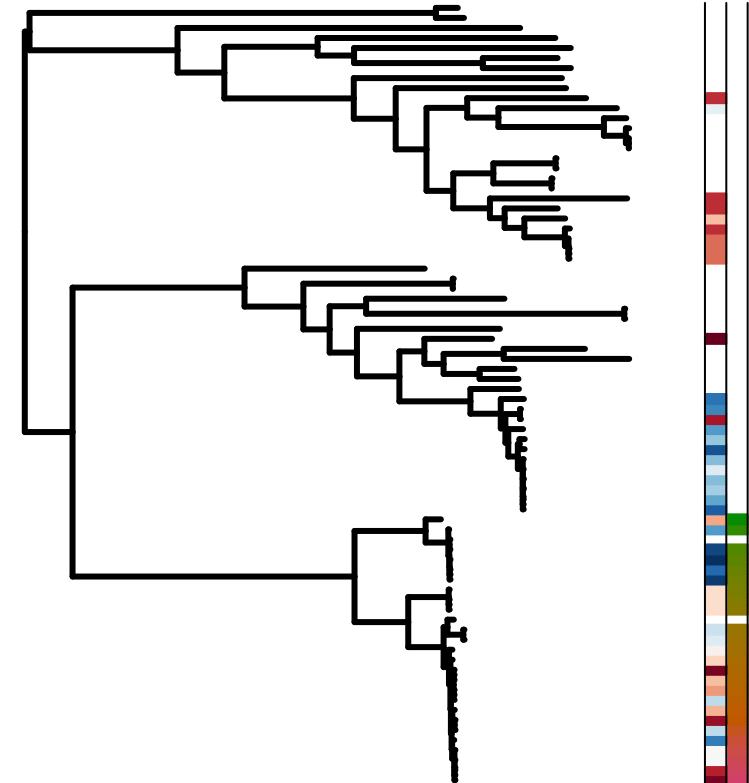
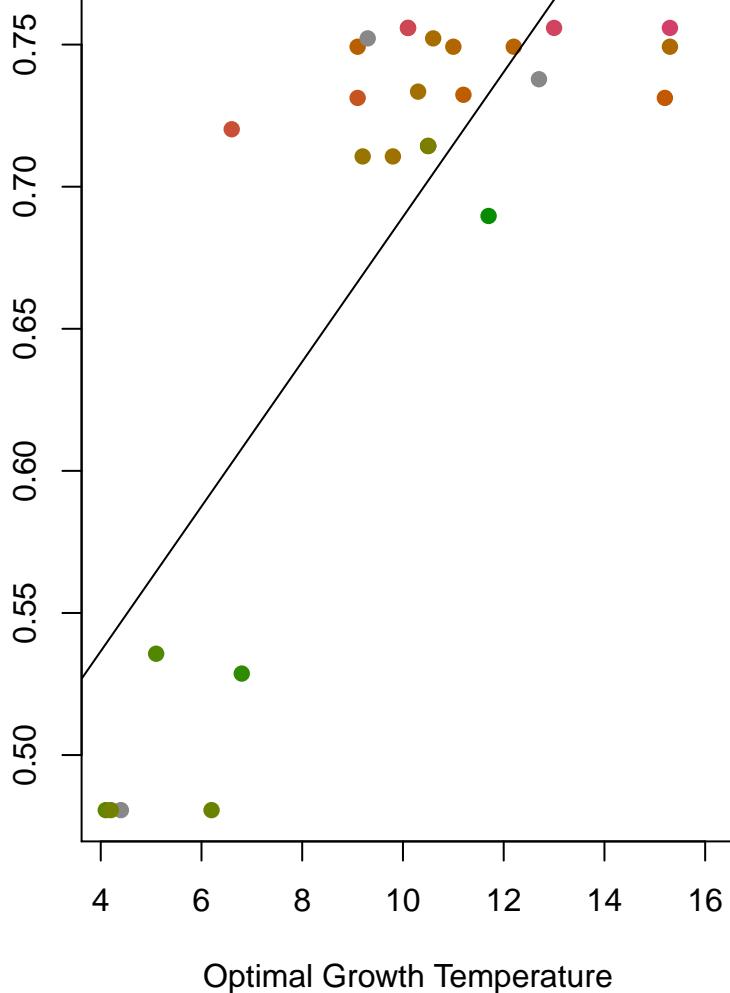
Two-component transcriptional response regulator, OmpR family

$r = 0.812, p = 10^{-8.477}$



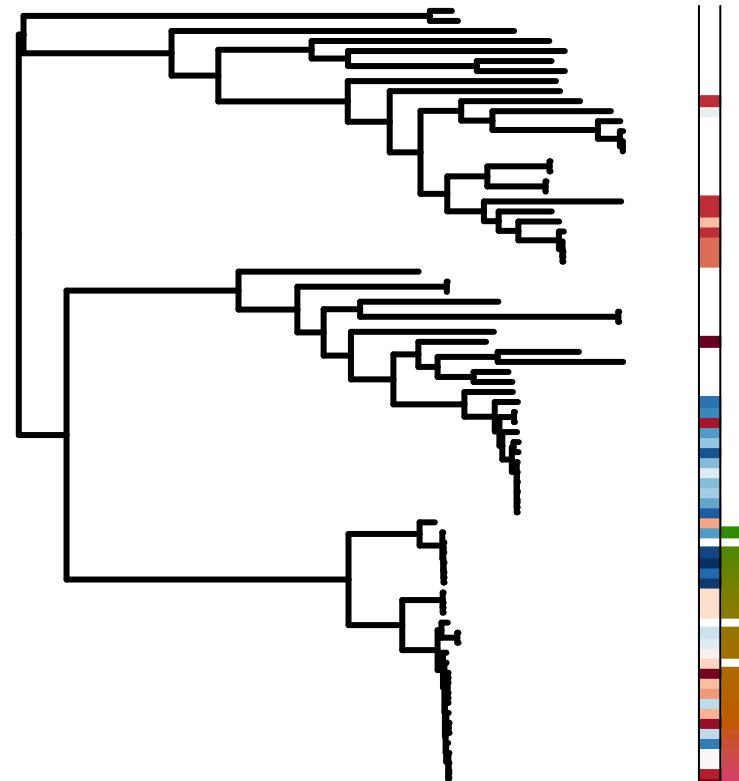
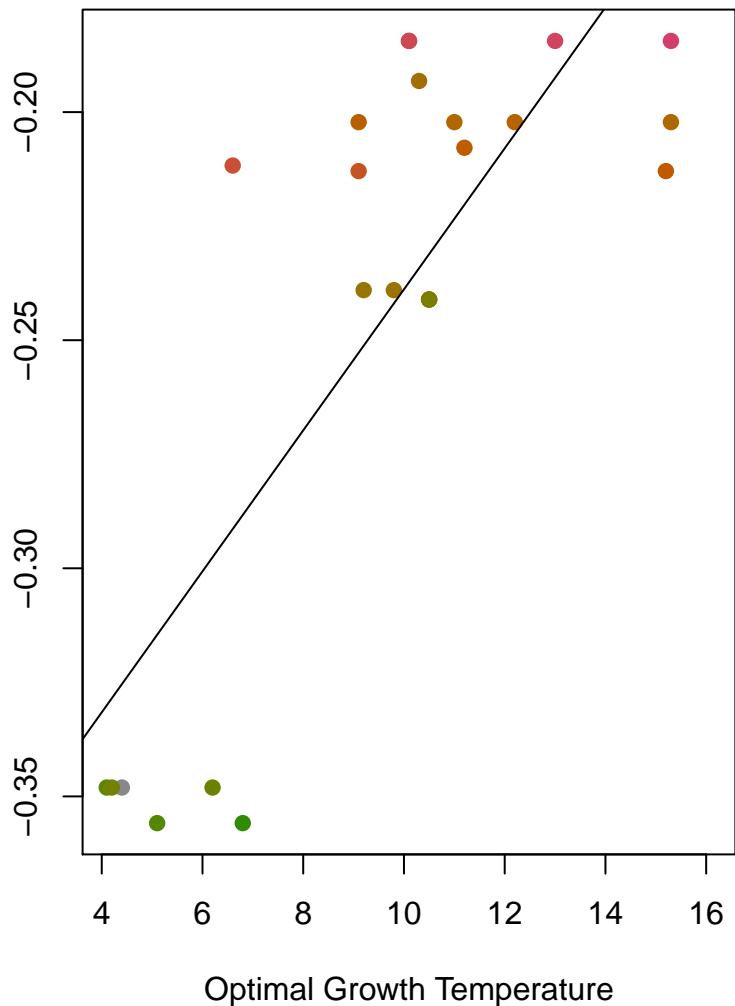
feature.plfam_id.gravy.mean
PLF_28228_00016648
hypothetical protein
 $r = 0.8, p = 10^{-6.492}$

feature.plfam_id.gravy.mean



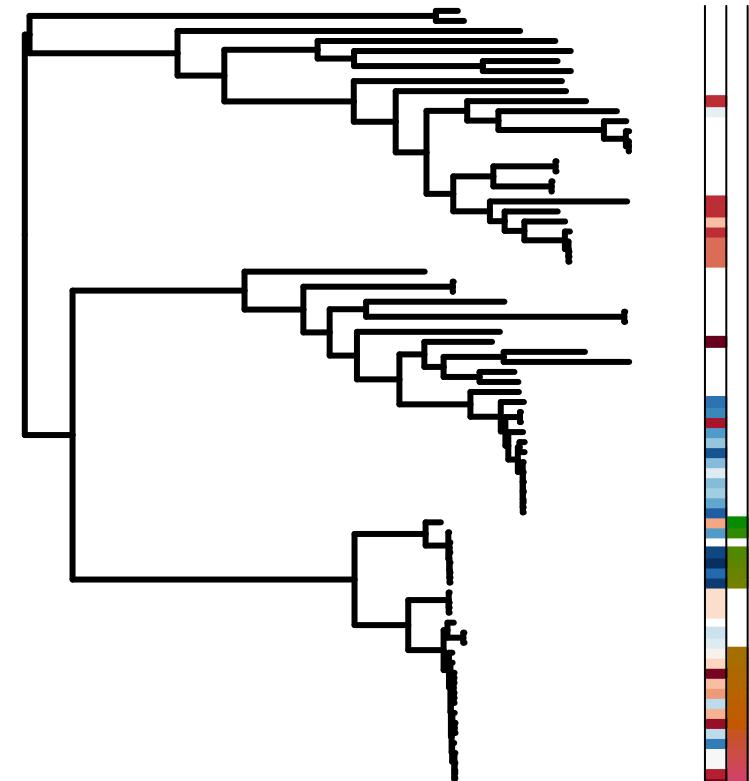
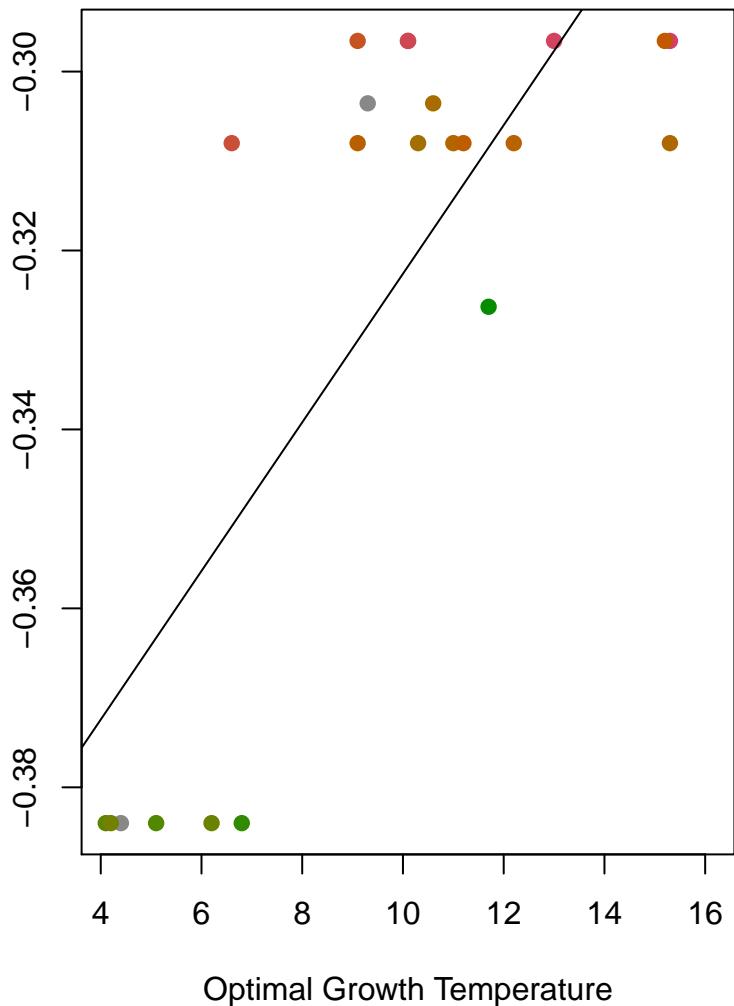
feature.plfam_id.gravy.mean
PLF_28228_00017800
HD domain protein
 $r = 0.8$, $p = 10^{-5.568}$

feature.plfam_id.gravy.mean



feature.plfam_id.gravy.mean
PLF_28228_00031192
hypothetical protein
 $r = 0.793, p = 10^{-4.969}$

feature.plfam_id.gravy.mean

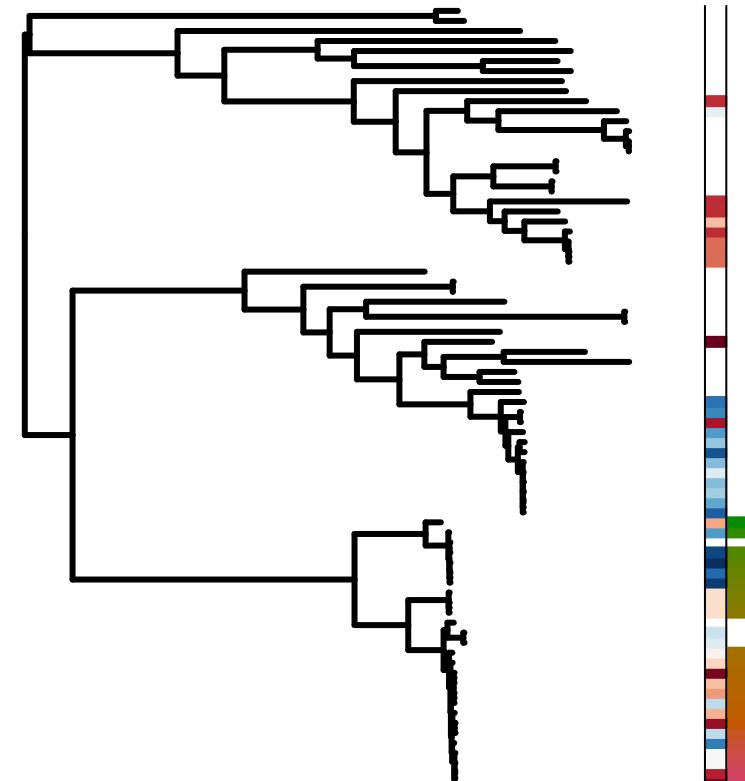
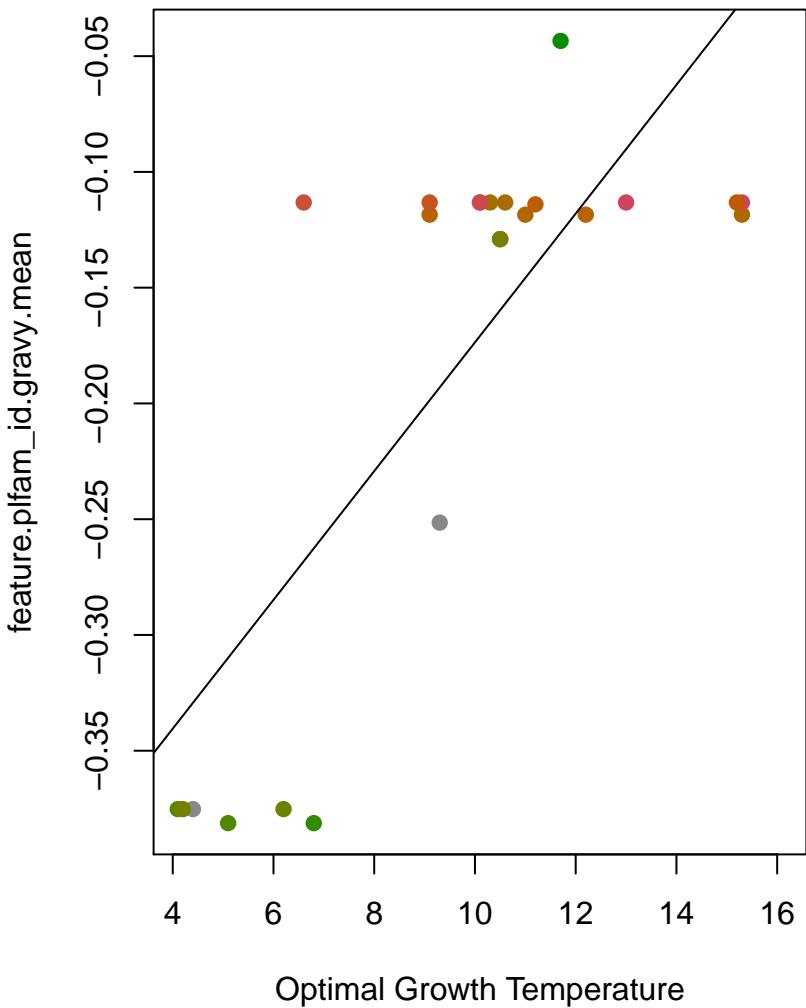


feature.plfam_id.gravy.mean

PLF_28228_00022096

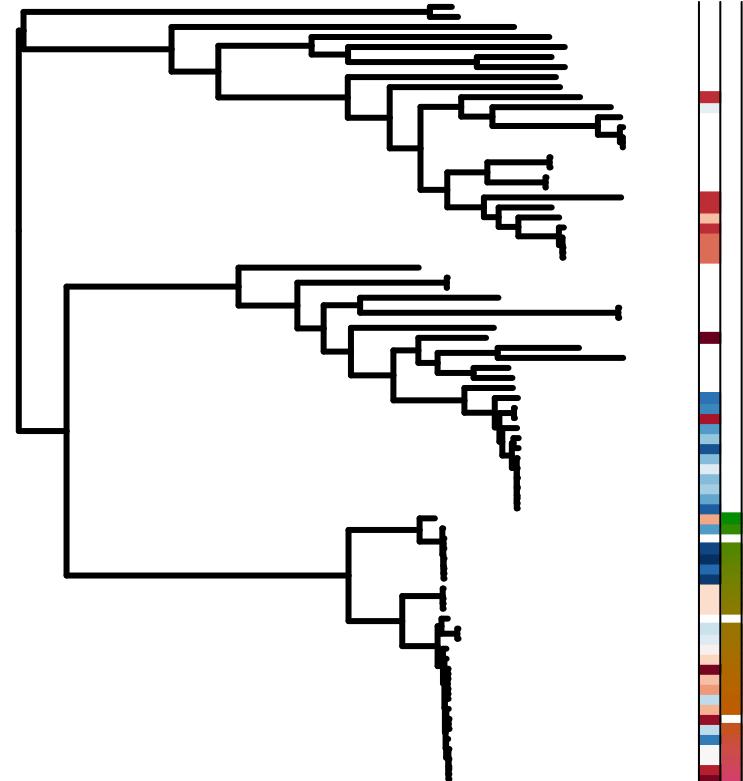
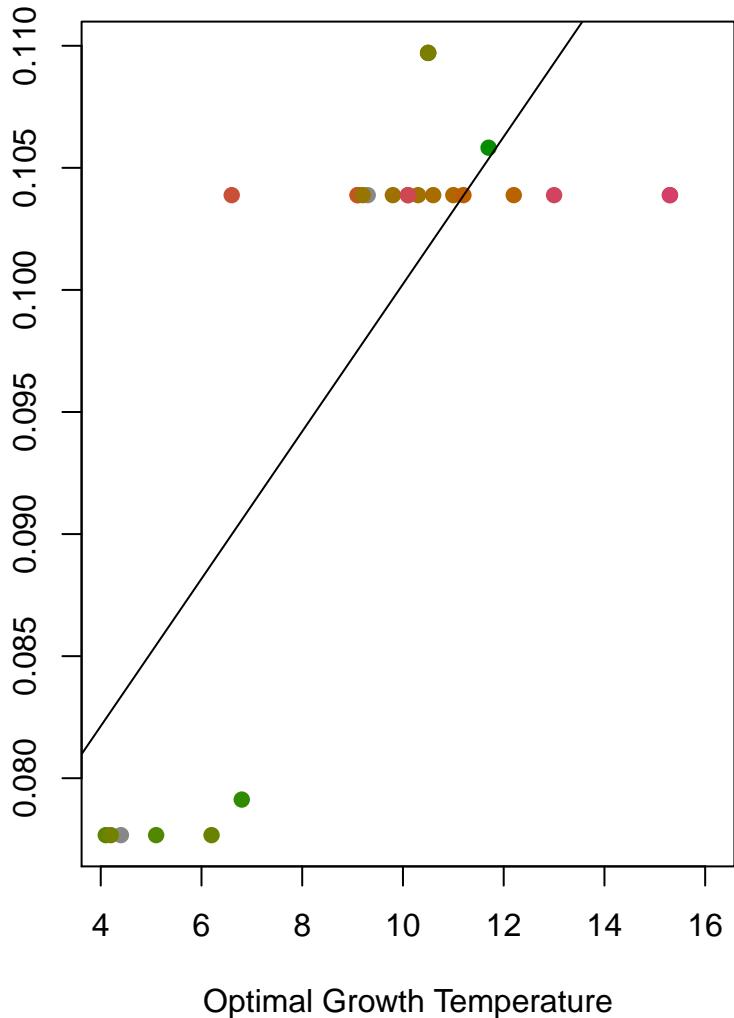
Two-component system sensor histidine kinase

$r = 0.792, p = 10^{-5.628}$



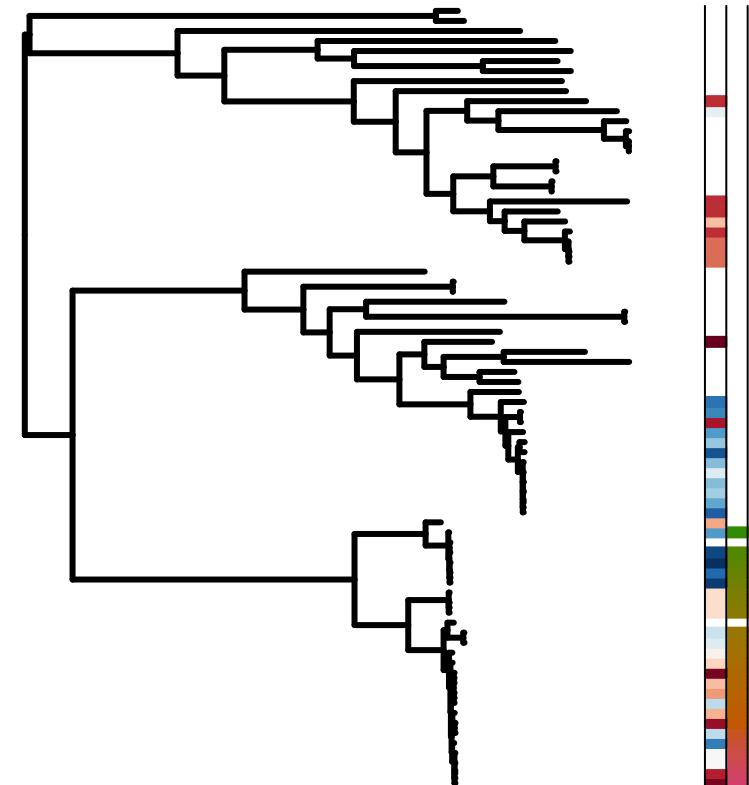
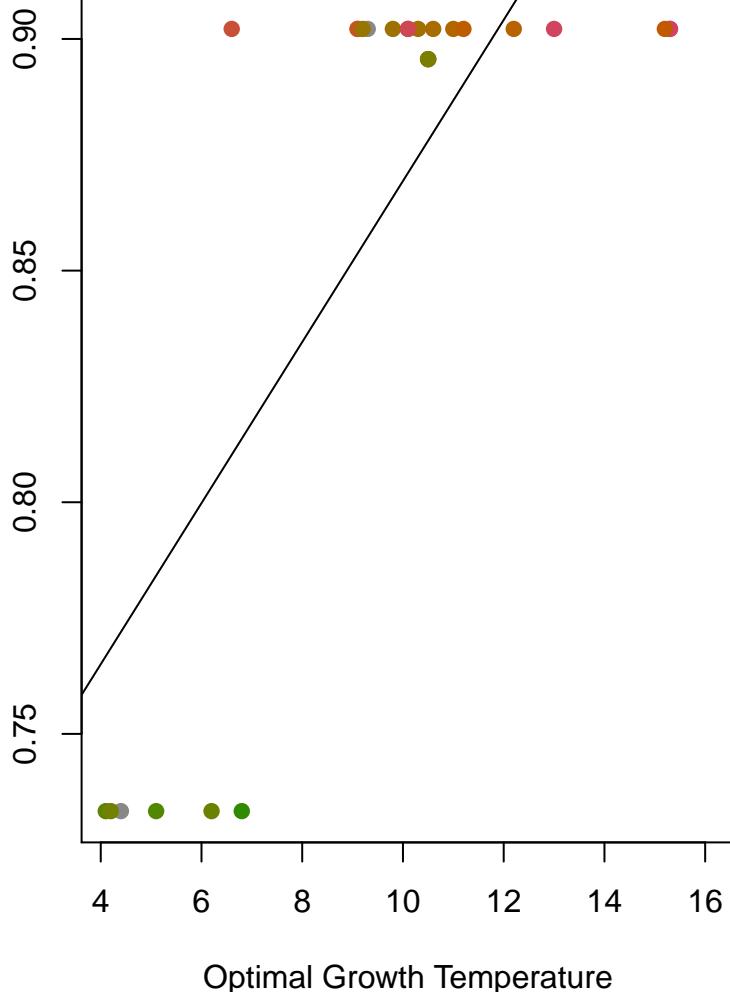
feature.plfam_id.gravy.mean
PLF_28228_00015263
hypothetical protein
 $r = 0.784, p = 10^{-5.667}$

feature.plfam_id.gravy.mean

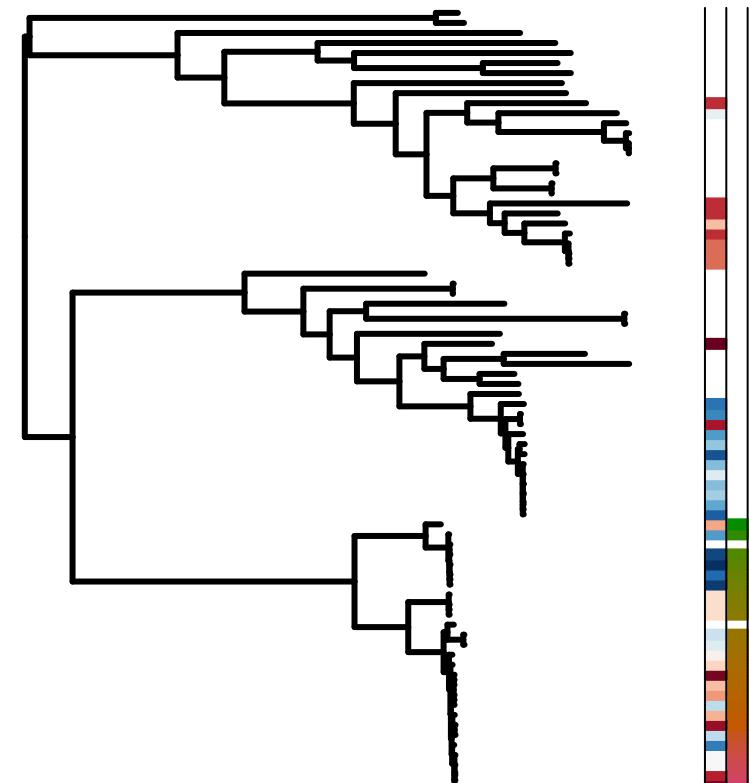
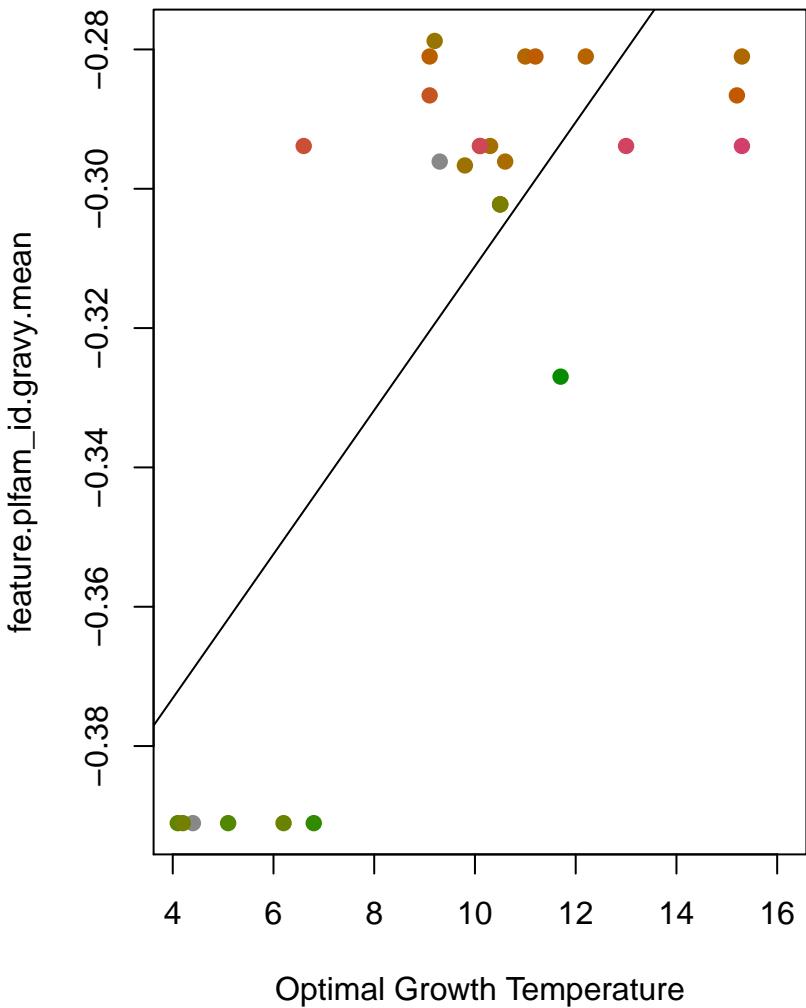


feature.plfam_id.gravy.mean
PLF_28228_00029369
hypothetical protein
 $r = 0.776$, $p = 10^{-5.502}$

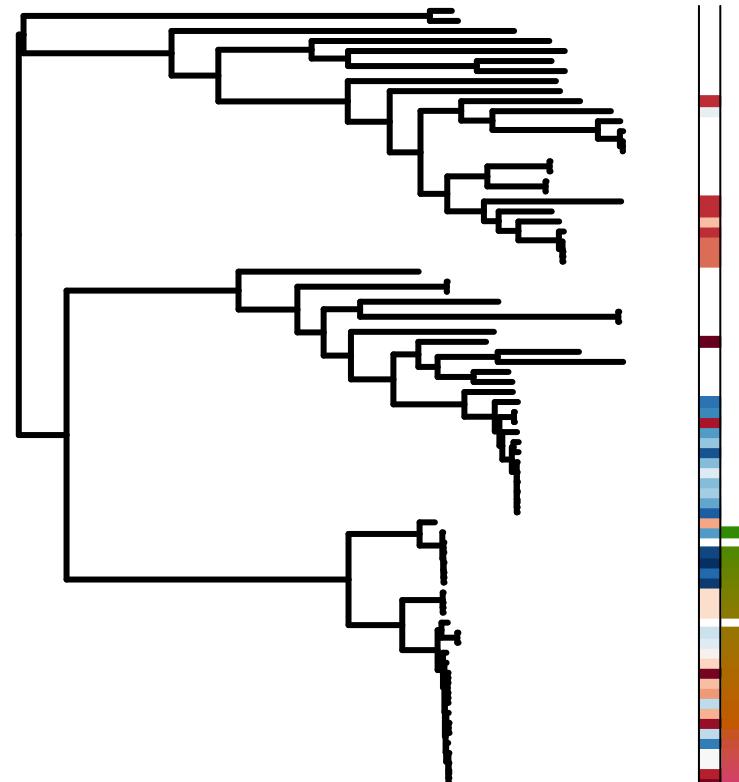
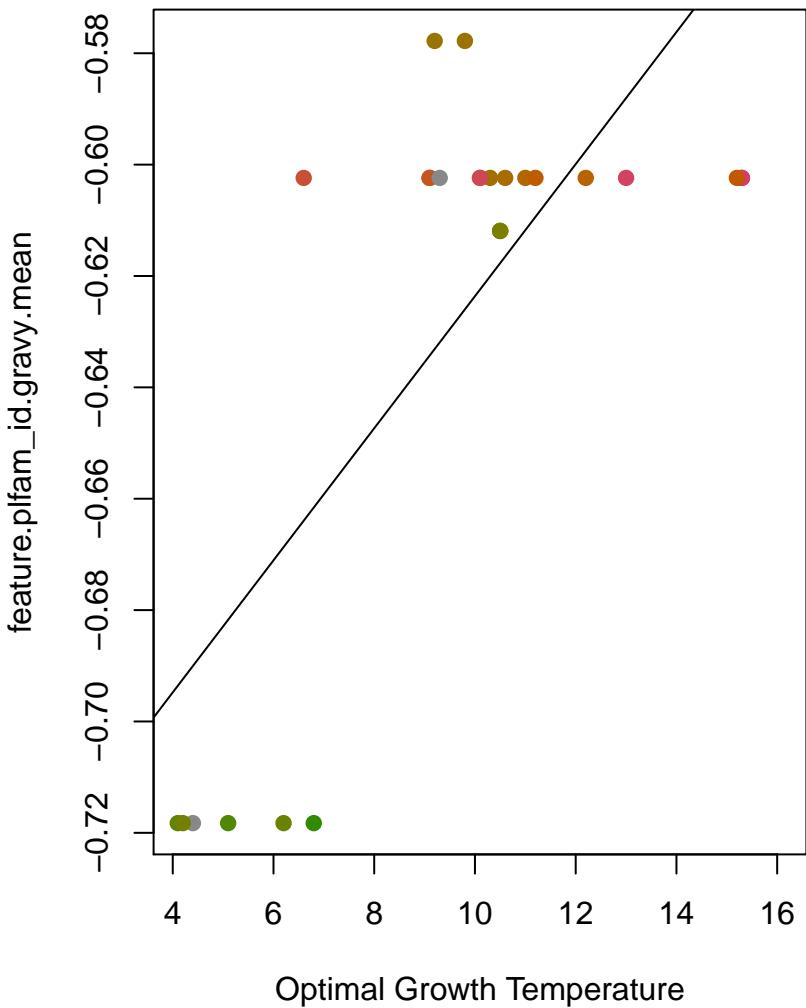
feature.plfam_id.gravy.mean



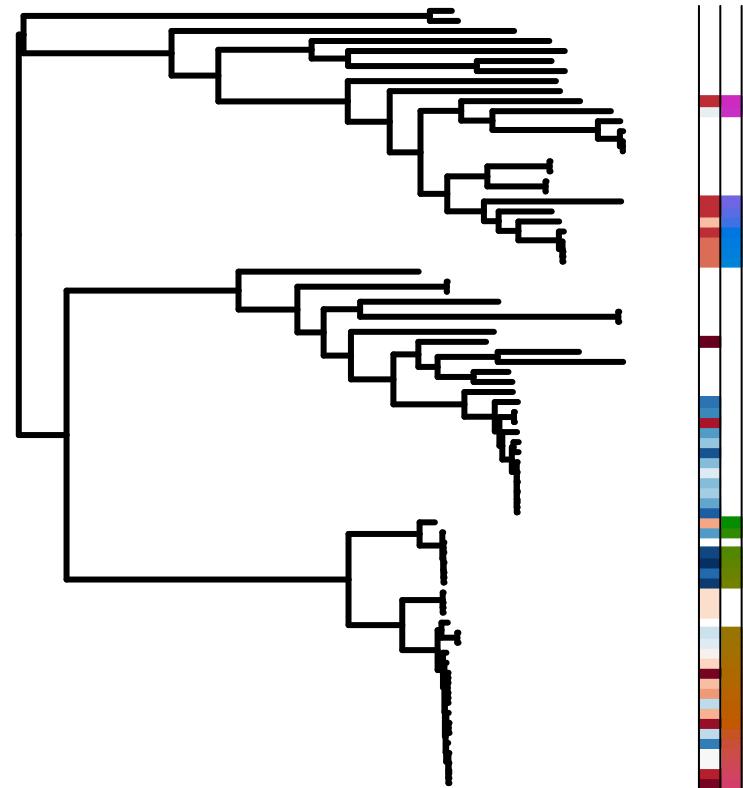
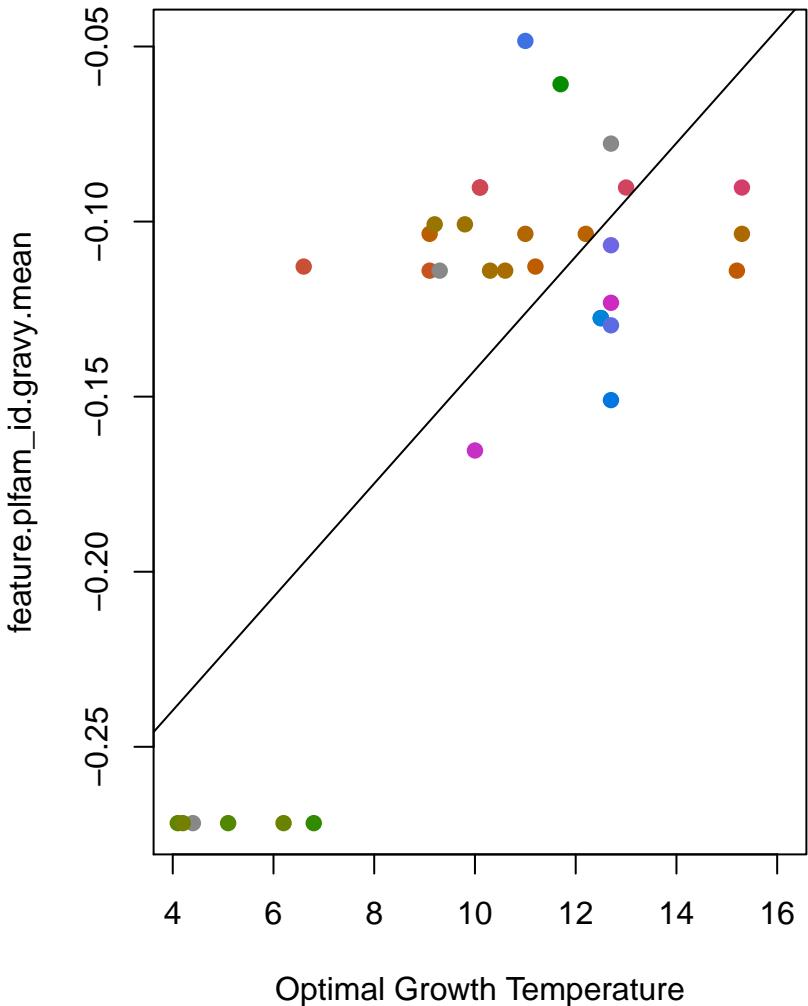
feature.plfam_id.gravy.mean
PLF_28228_00014896
hypothetical protein
 $r = 0.768, p = 10^{-5.534}$



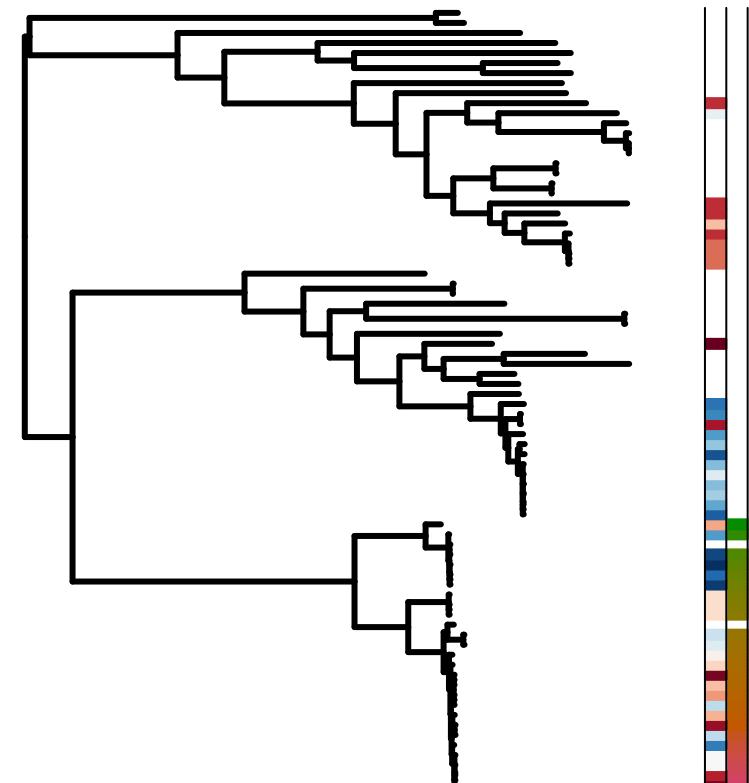
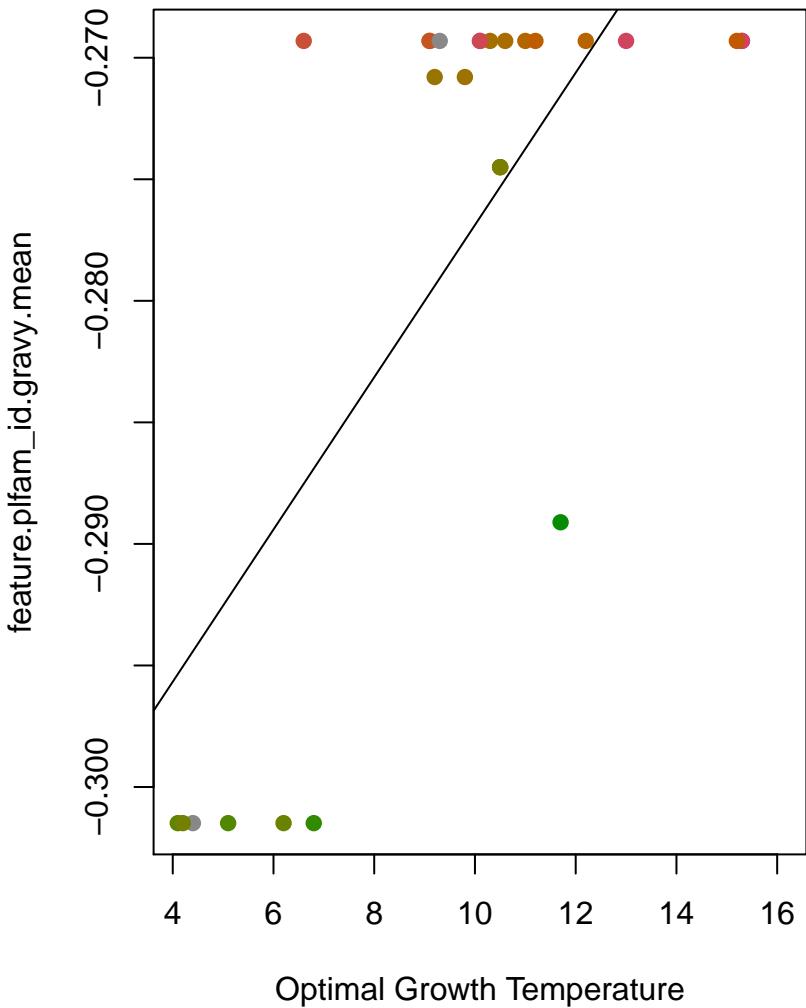
feature_pfam_id.gravy.mean
PLF_28228_00030463
hypothetical protein
 $r = 0.752$, $p = 10^{-5.025}$



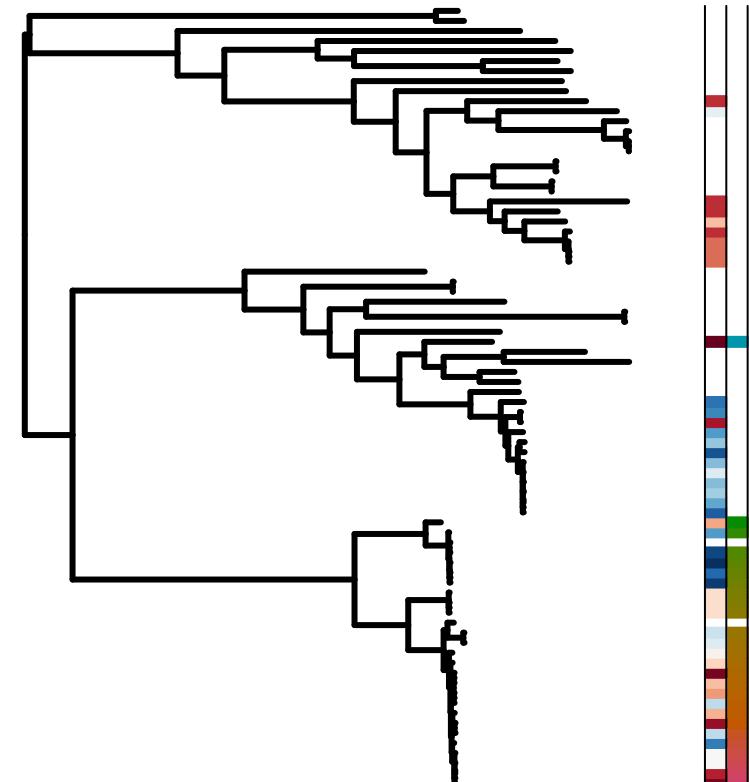
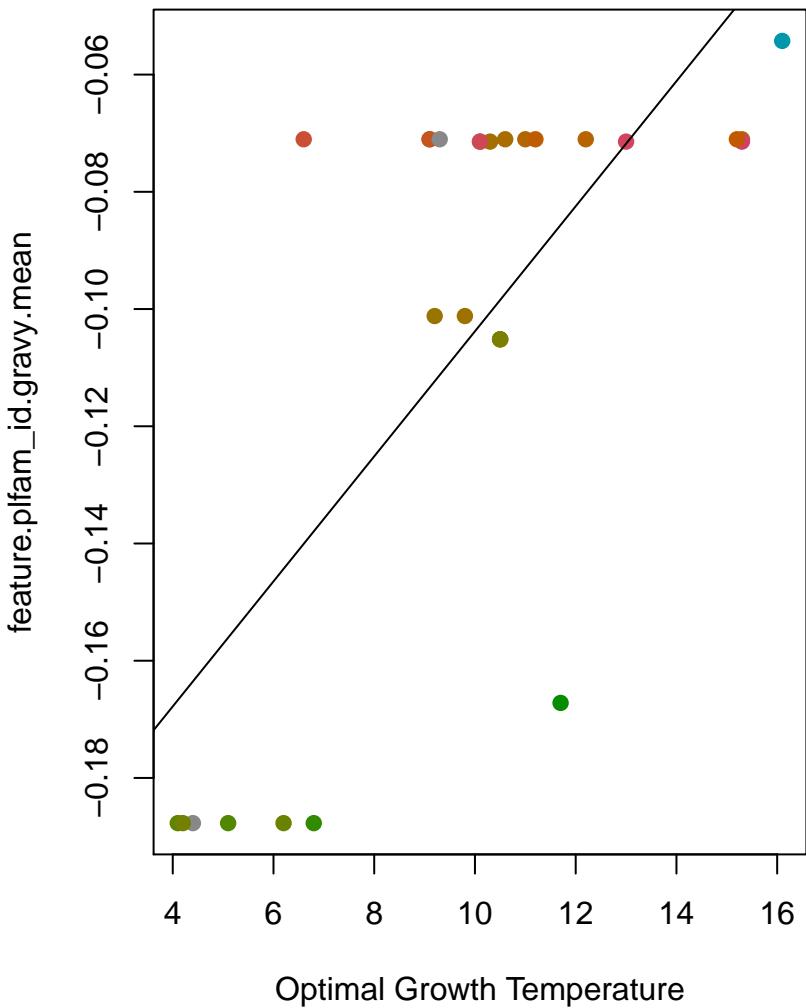
feature.plfam_id.gravy.mean
PLF_28228_00002434
hypothetical protein
 $r = 0.75, p = 10^{-6.486}$

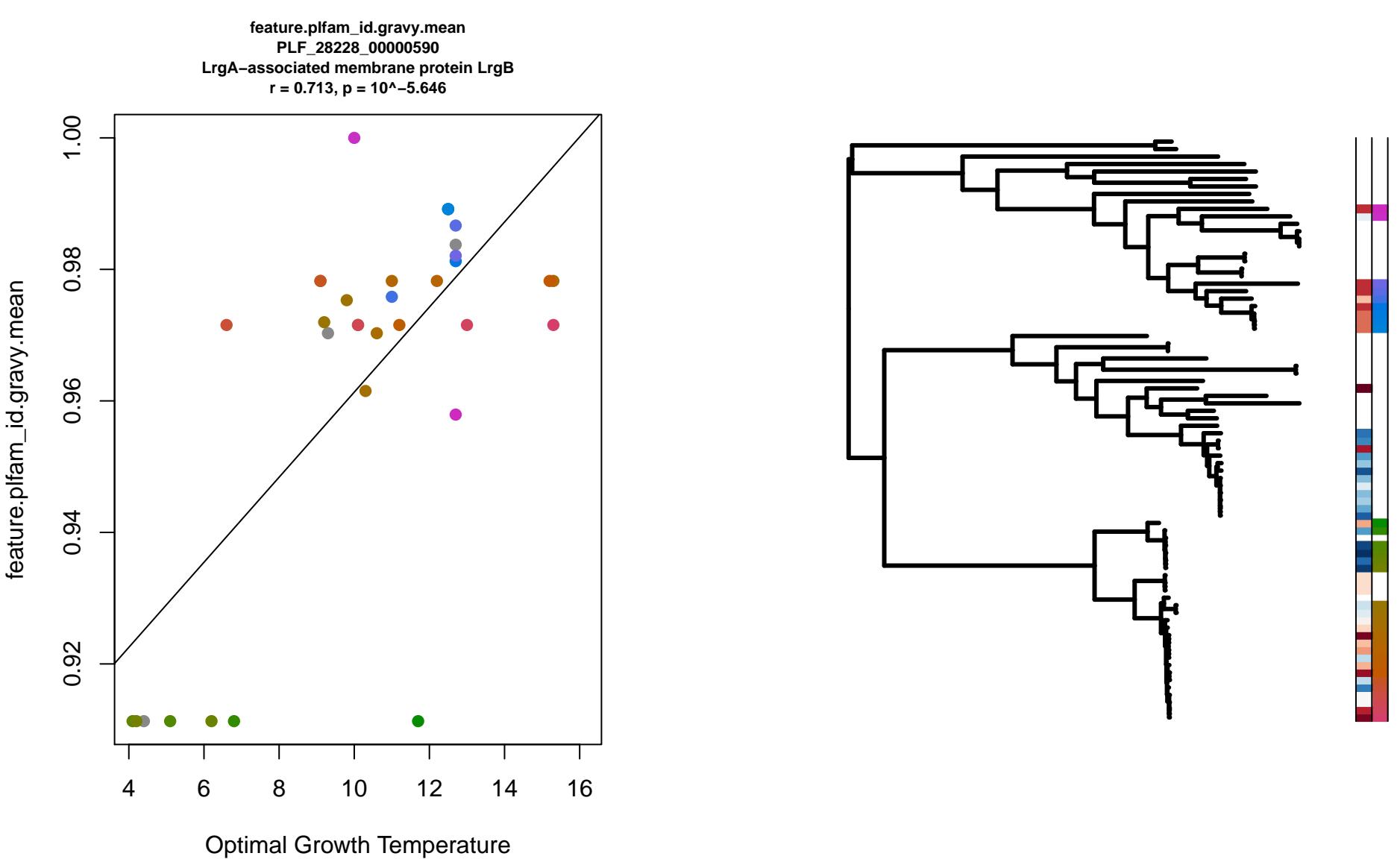


feature.plfam_id.gravy.mean
PLF_28228_00029998
hypothetical protein
 $r = 0.741, p = 10^{-5.014}$



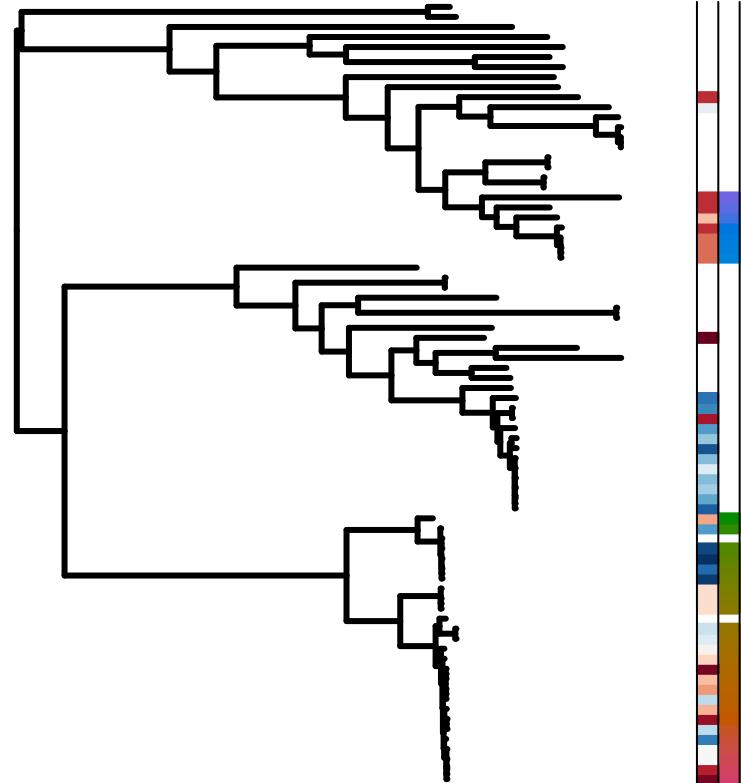
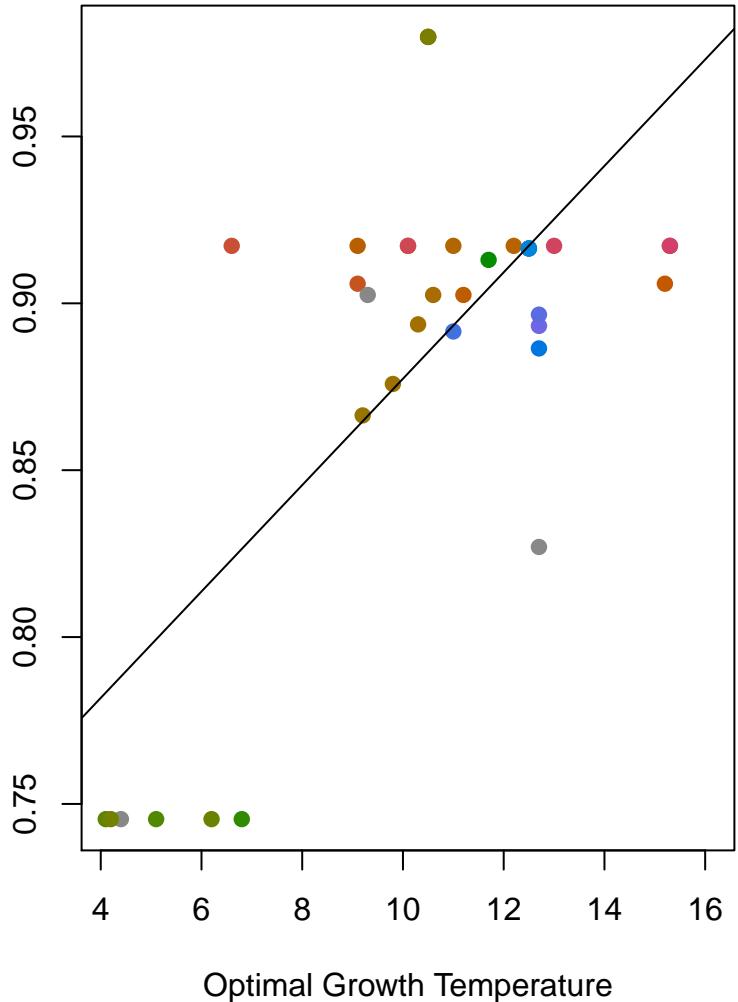
feature.plfam_id.gravy.mean
PLF_28228_00015428
hypothetical protein
 $r = 0.731, p = 10^{-4.995}$



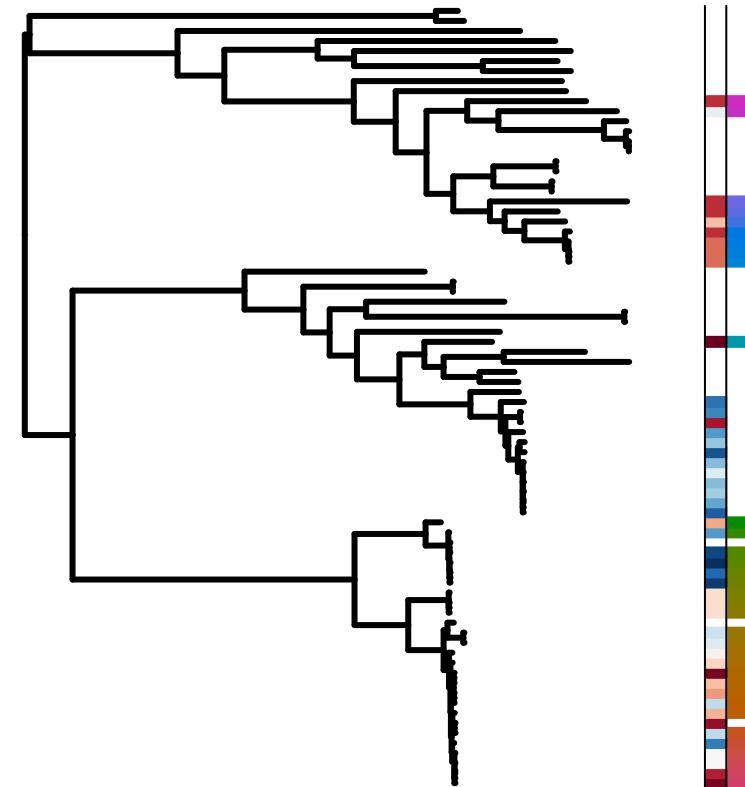
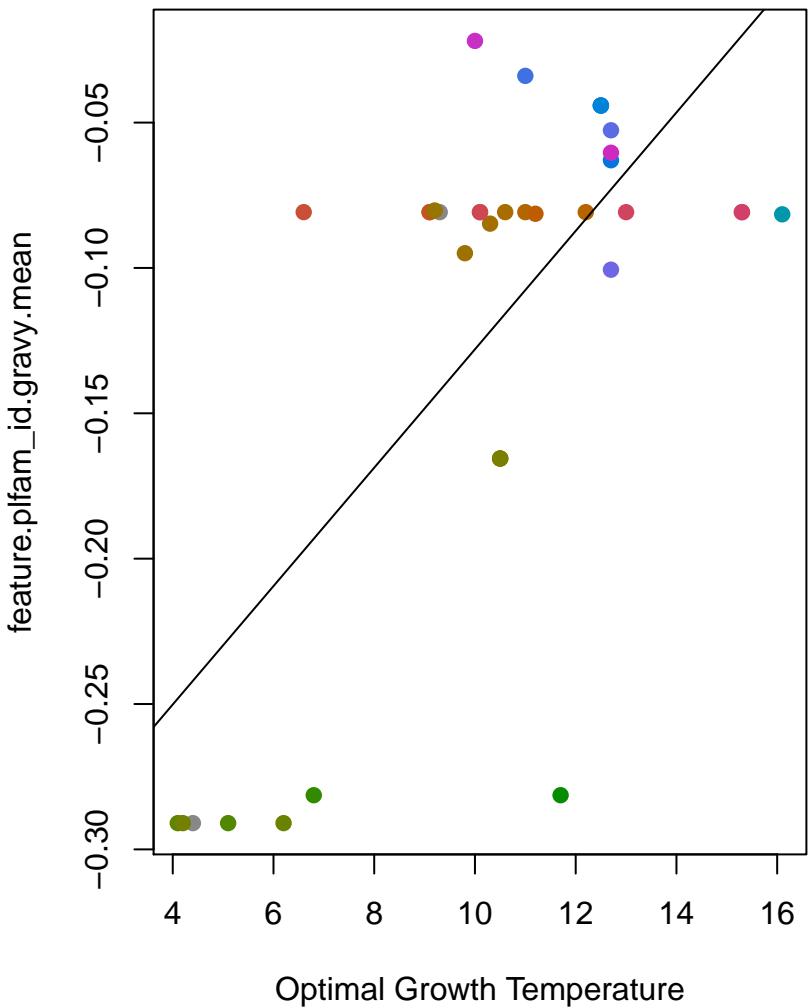


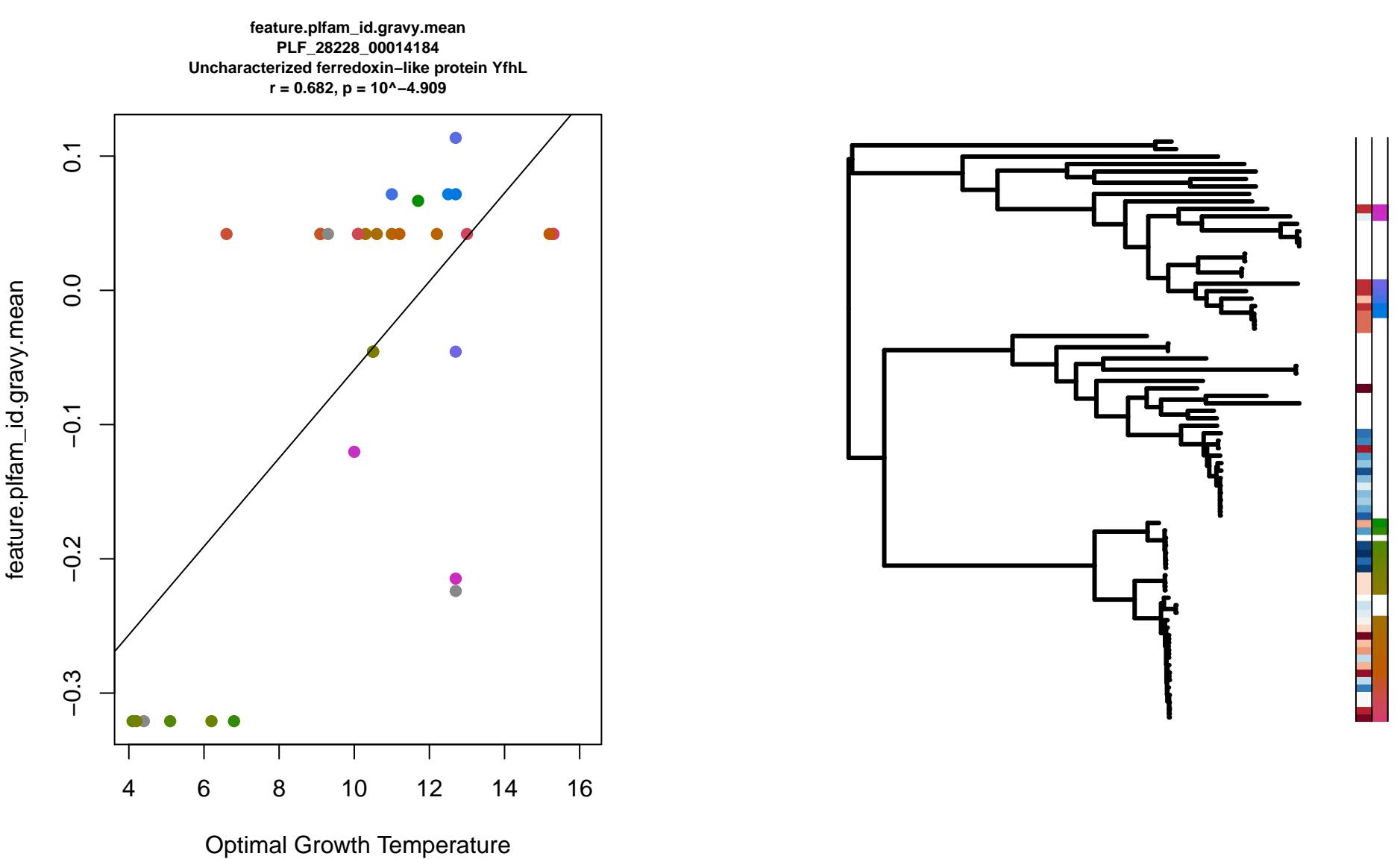
feature.plfam_id.gravy.mean
PLF_28228_00003803
ZIP zinc transporter family protein
 $r = 0.698$, $p = 10^{-5.511}$

feature.plfam_id.gravy.mean

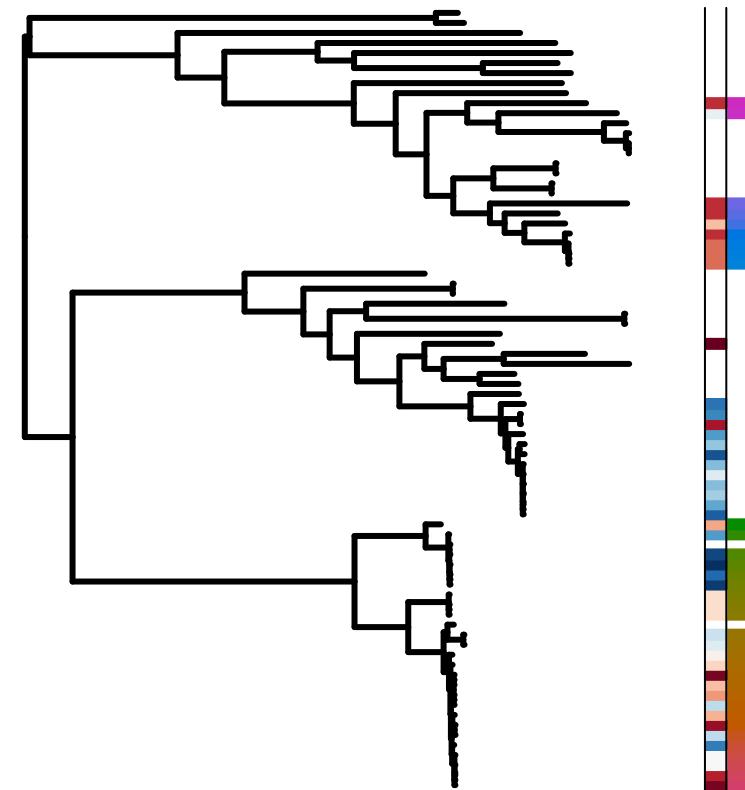
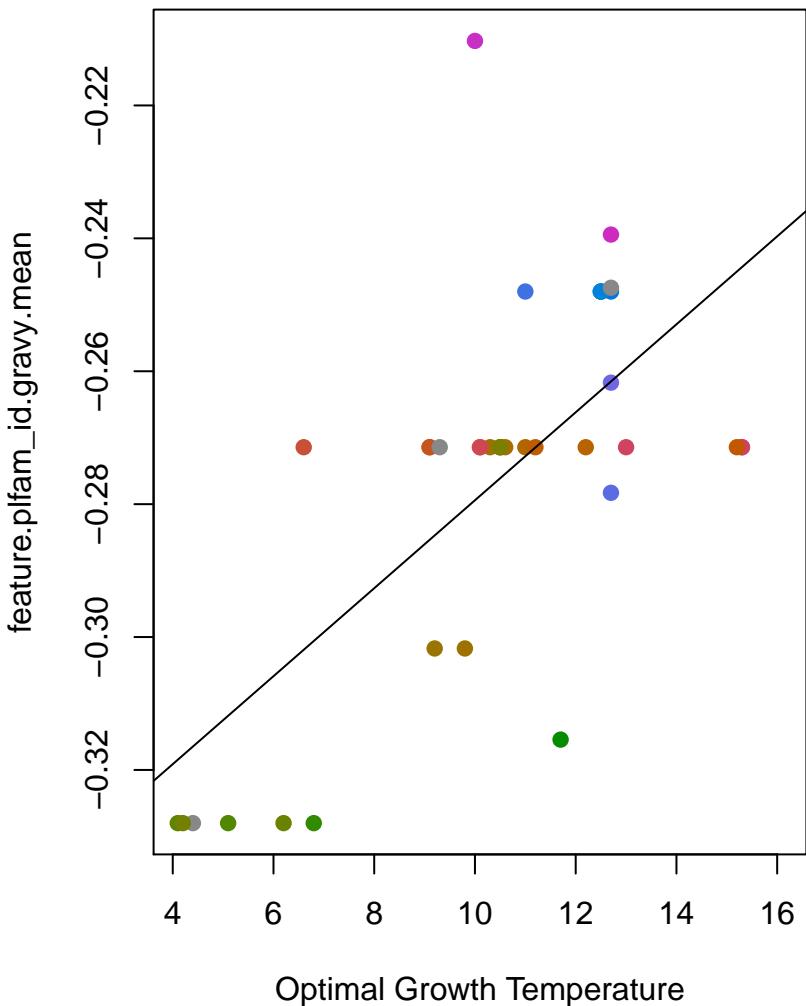


feature.plfam_id.gravy.mean
PLF_28228_00002195
Ureidoglycolate lyase (EC 4.3.2.3)
 $r = 0.696$, $p = 10^{-5.618}$



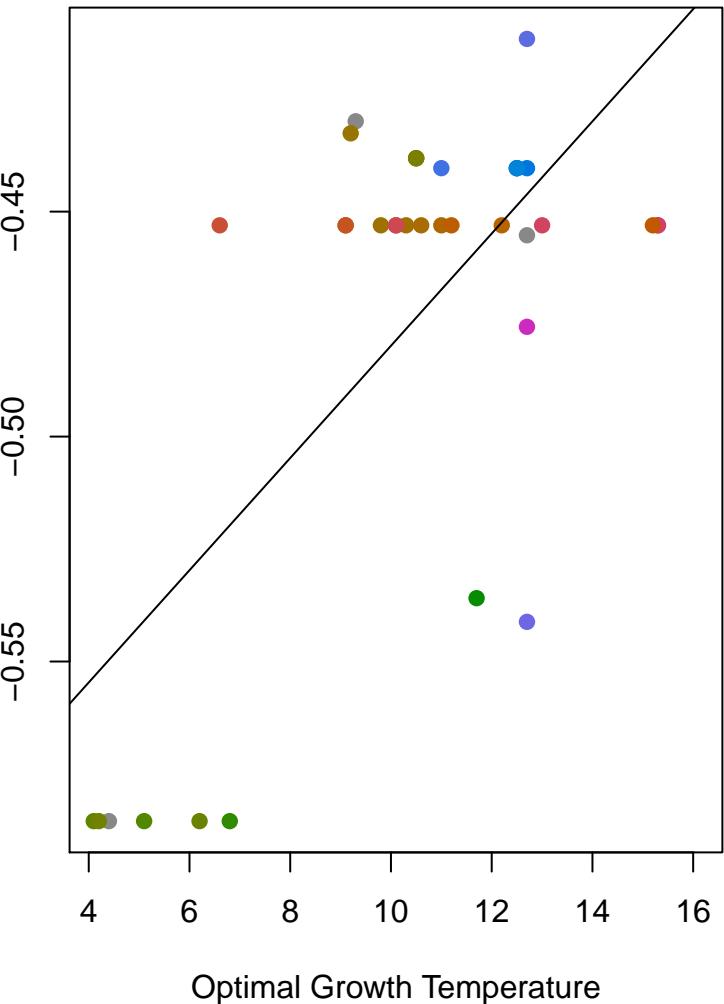


feature.plfam_id.gravy.mean
PLF_28228_00001835
Bacterial non-heme ferritin (EC 1.16.3.2)
 $r = 0.681$, $p = 10^{-5.452}$

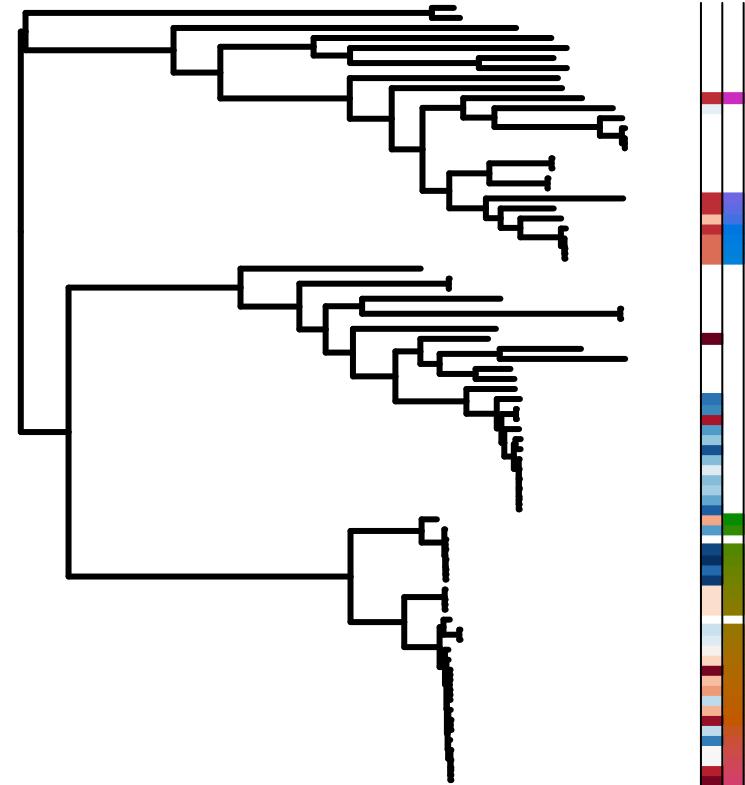


feature.plfam_id.gravy.mean
PLF_28228_00002946
hypothetical protein
 $r = 0.68$, $p = 10^{-5.294}$

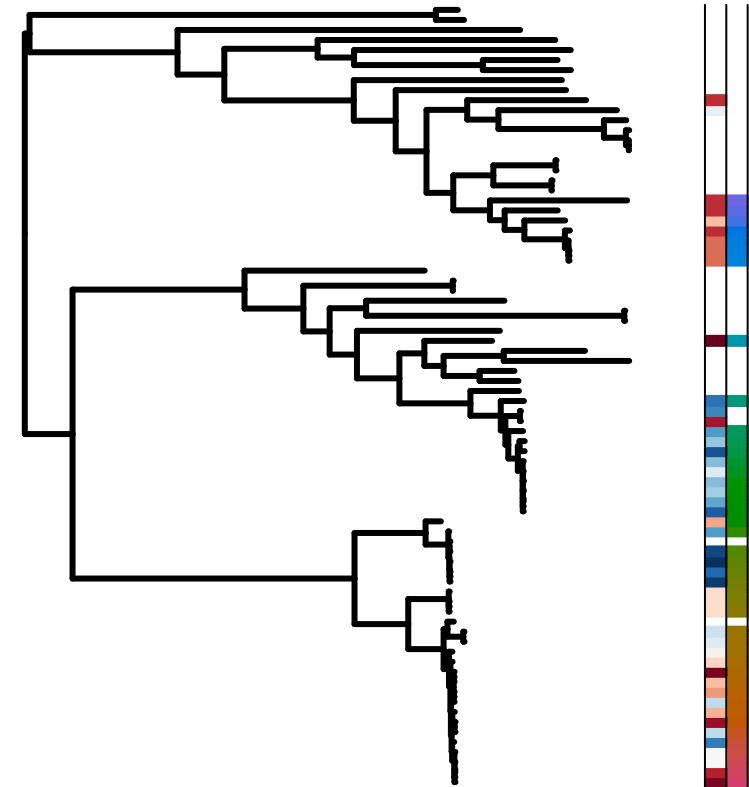
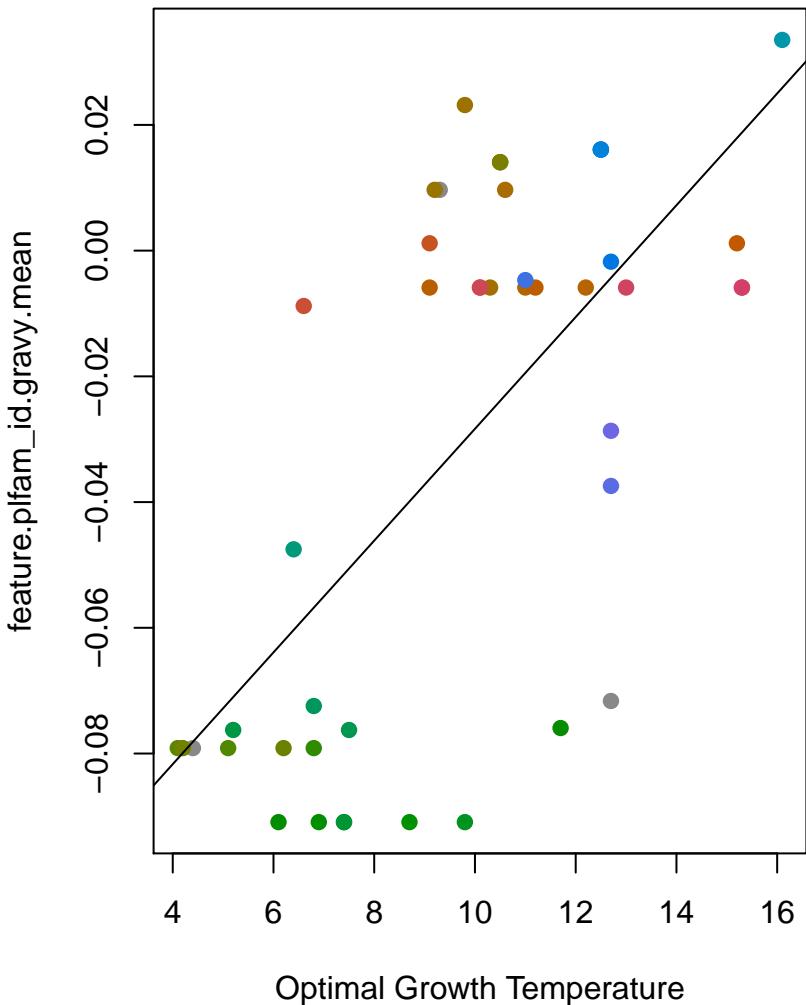
feature.plfam_id.gravy.mean



Optimal Growth Temperature

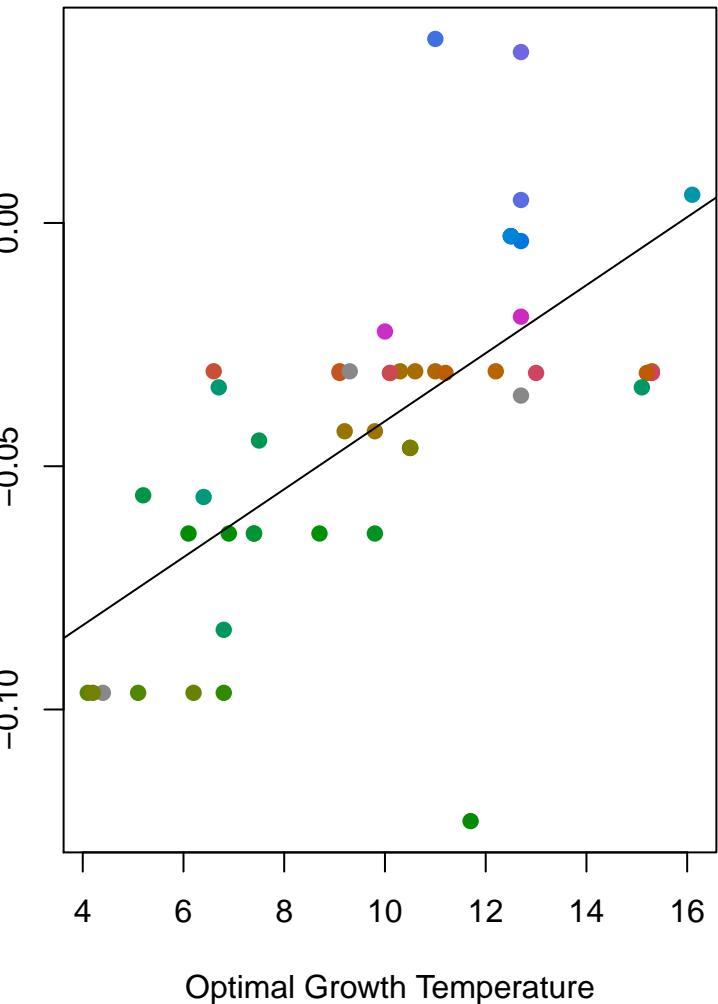


feature.plfam_id.gravy.mean
 PLF_28228_00003170
 Zinc-type alcohol dehydrogenase-like protein
 $r = 0.659$, $p = 10^{-6.205}$

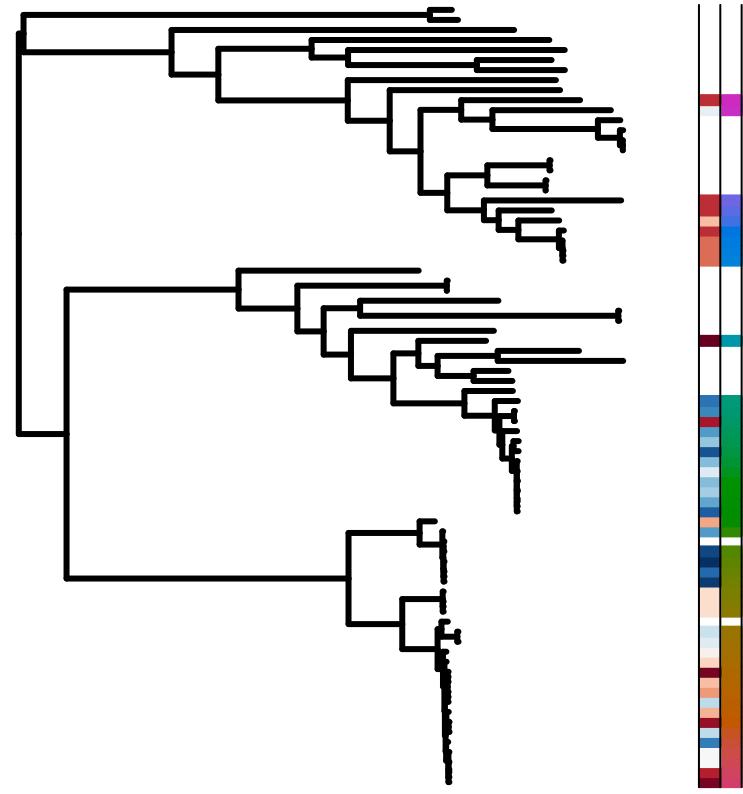


feature.plfam_id.gravy.mean
PLF_28228_00002316
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)
 $r = 0.657$, $p = 10^{-6.649}$

feature.plfam_id.gravy.mean

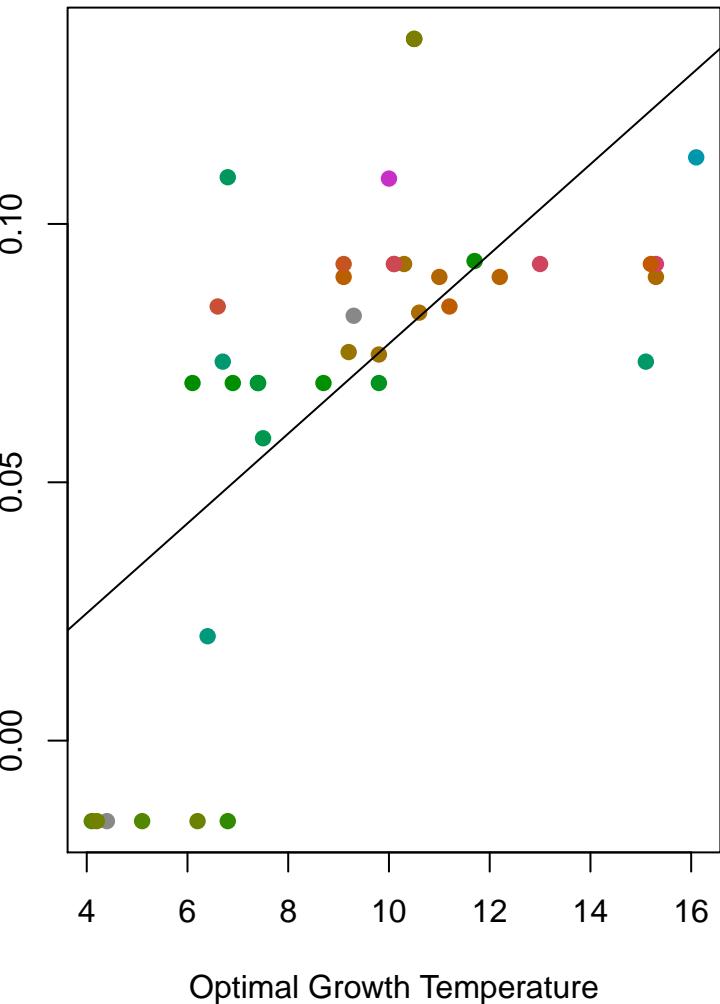


Optimal Growth Temperature

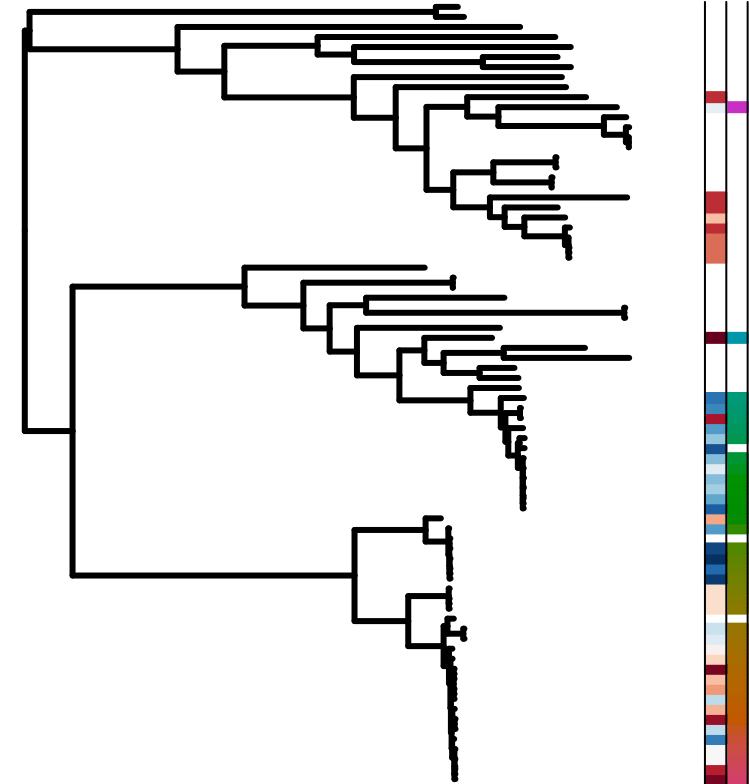


feature.plfam_id.gravy.mean
PLF_28228_00022897
Invasin domain protein
 $r = 0.651$, $p = 10^{-5.261}$

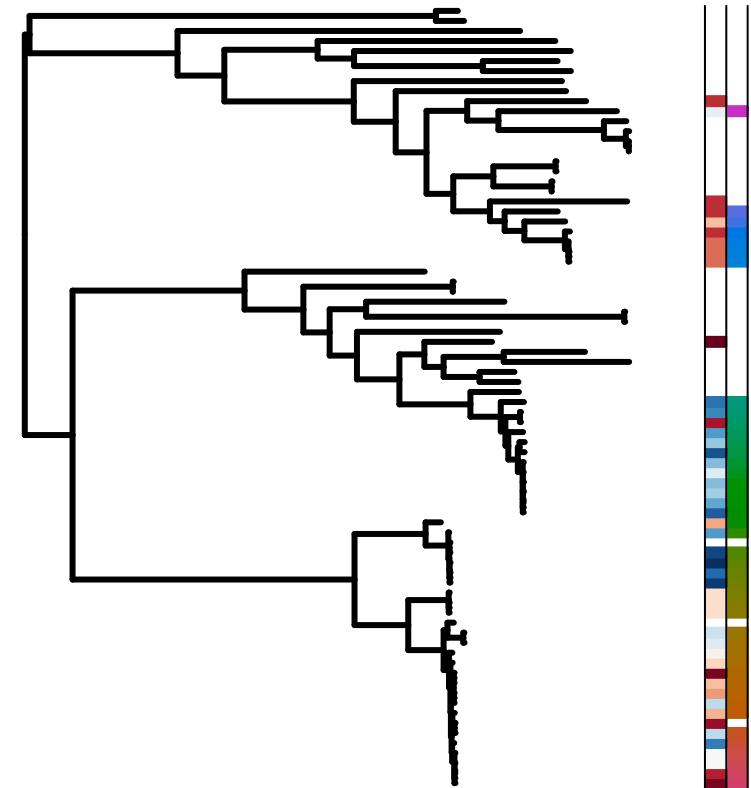
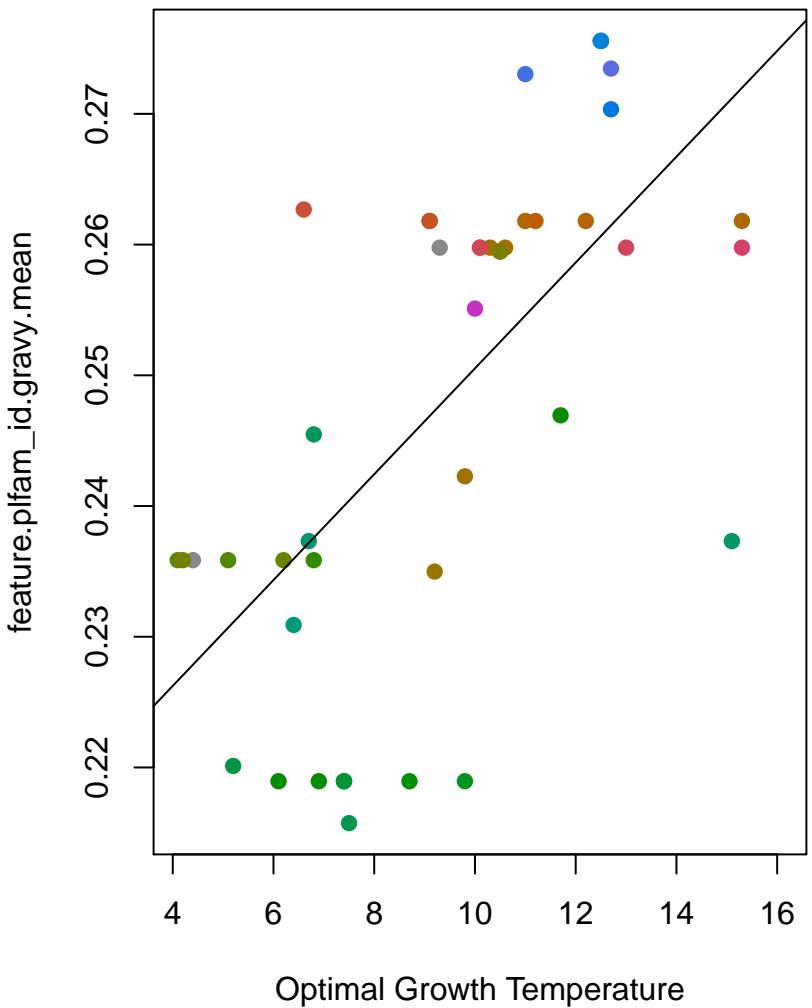
feature.plfam_id.gravy.mean



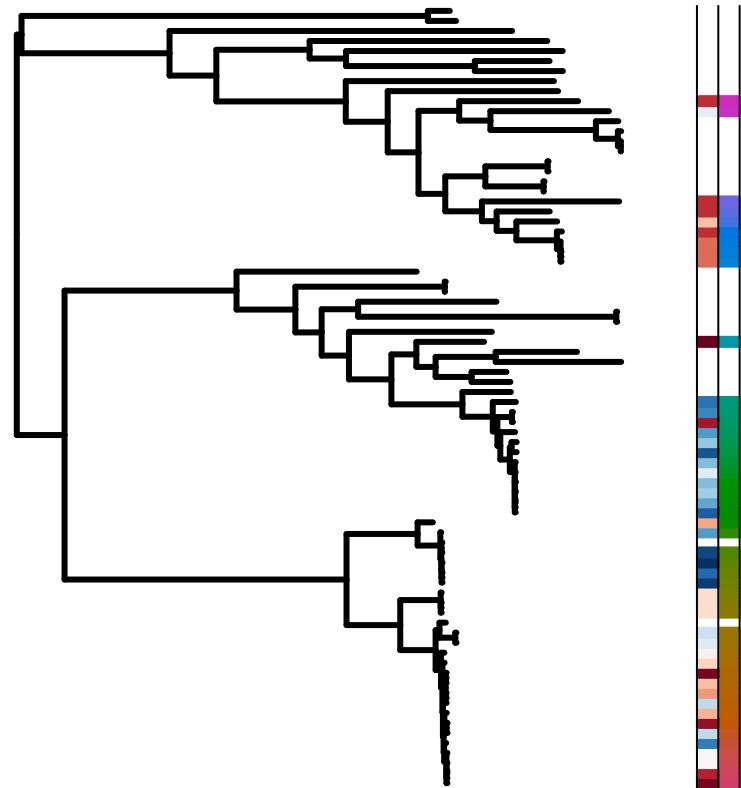
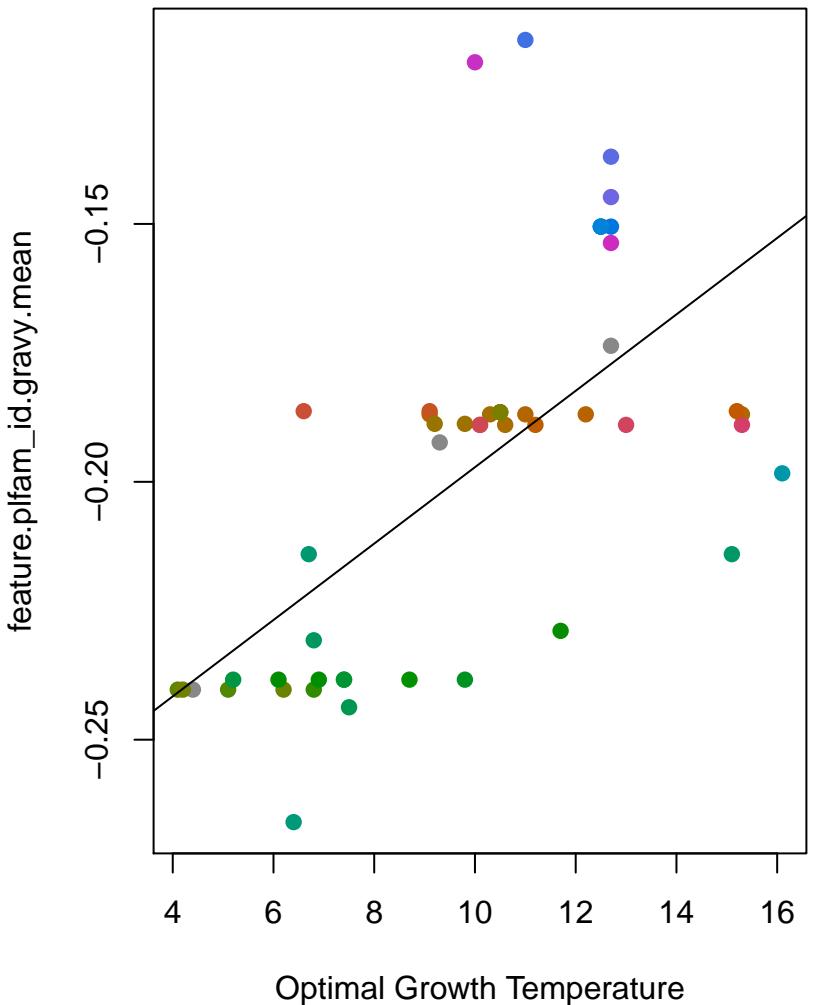
Optimal Growth Temperature



feature.plfam_id.gravy.mean
PLF_28228_00003639
Selenide,water dikinase (EC 2.7.9.3)
 $r = 0.644$, $p = 10^{-5.749}$



feature.plfam_id.gravy.mean
PLF_28228_00000790
Exported zinc metalloprotease YfgC precursor
r = 0.642, p = 10^-6.308

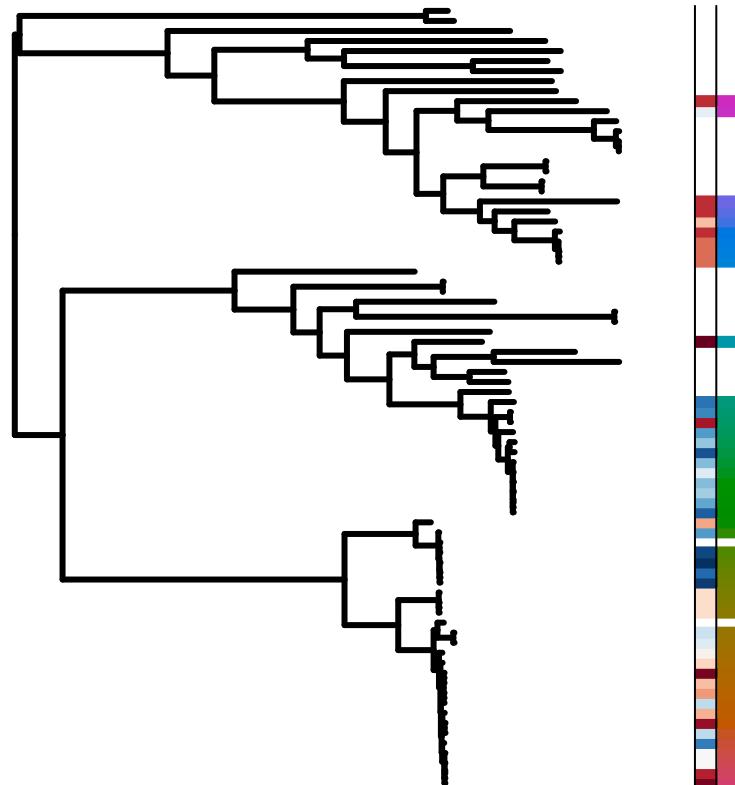
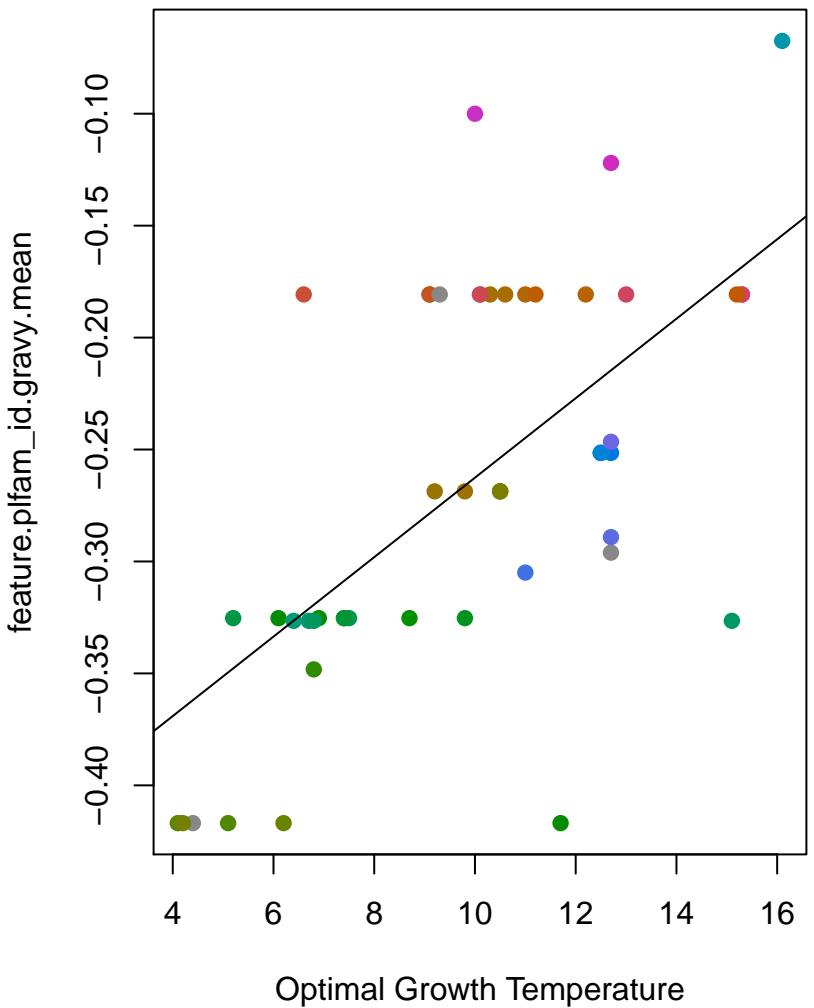


feature.plfam_id.gravy.mean

PLF_28228_00001310

Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin

$r = 0.631, p = 10^{-6.036}$



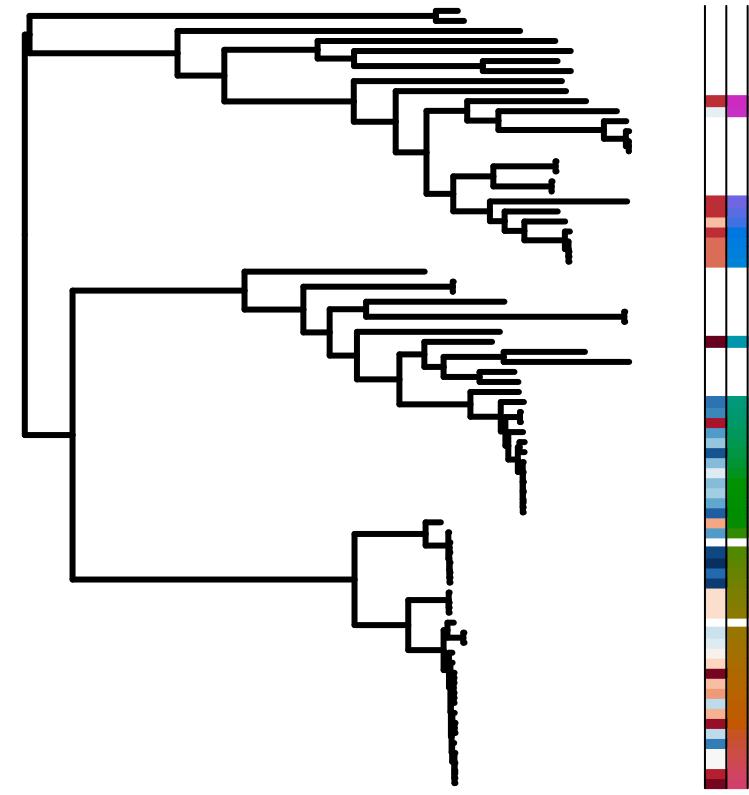
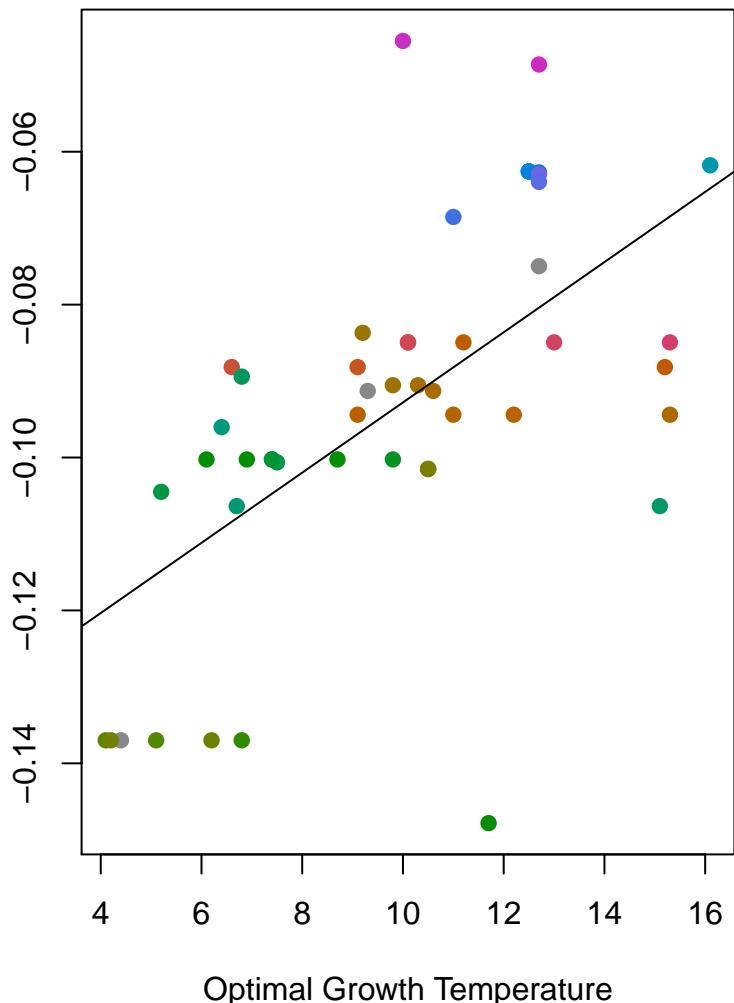
feature.plfam_id.gravy.mean

PLF_28228_00000941

Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)

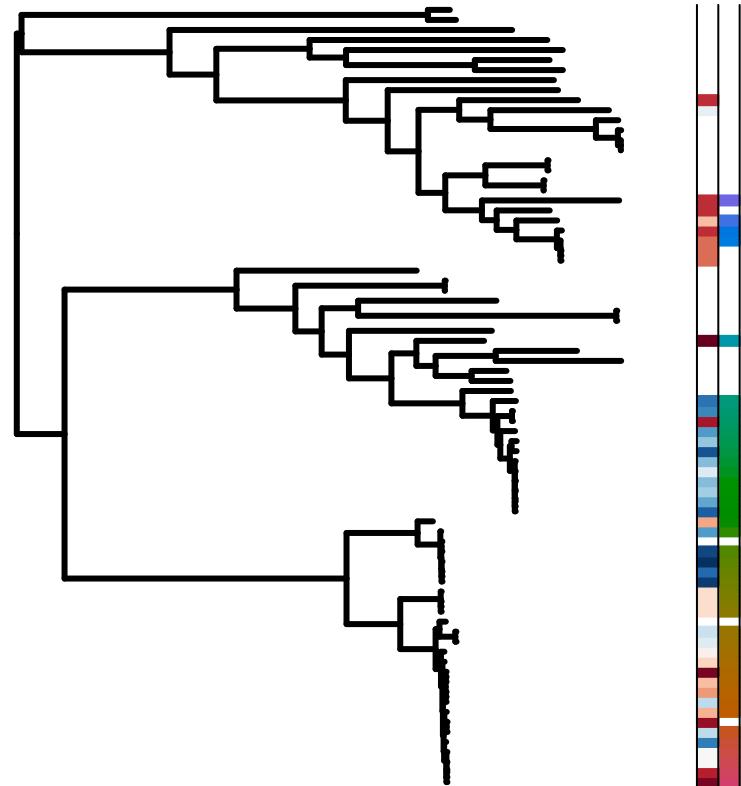
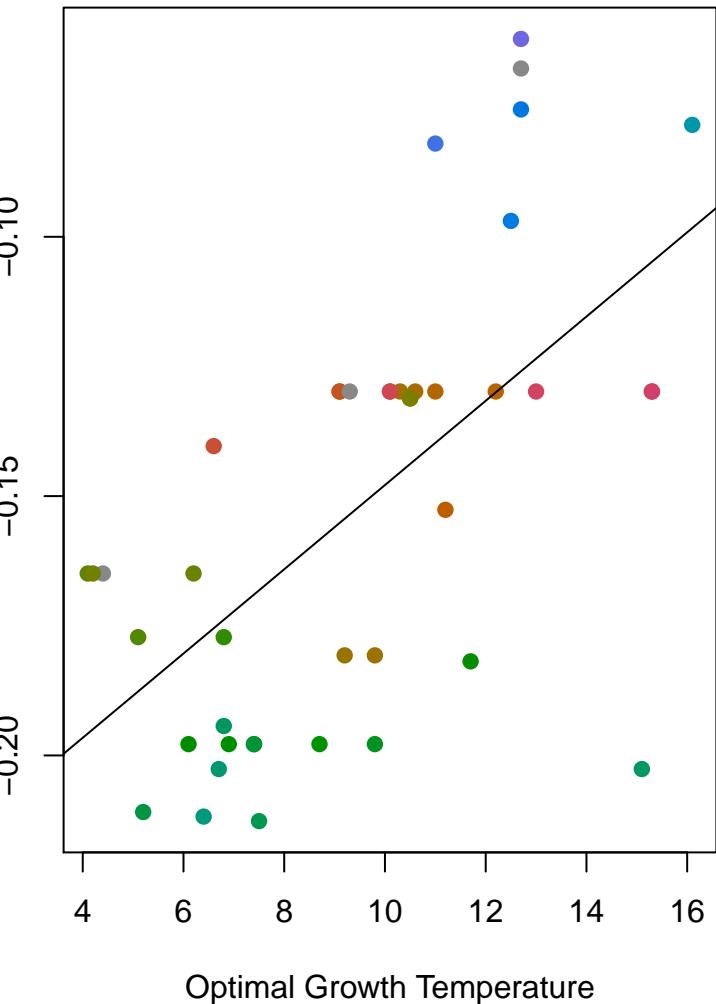
$r = 0.609, p = 10^{-5.563}$

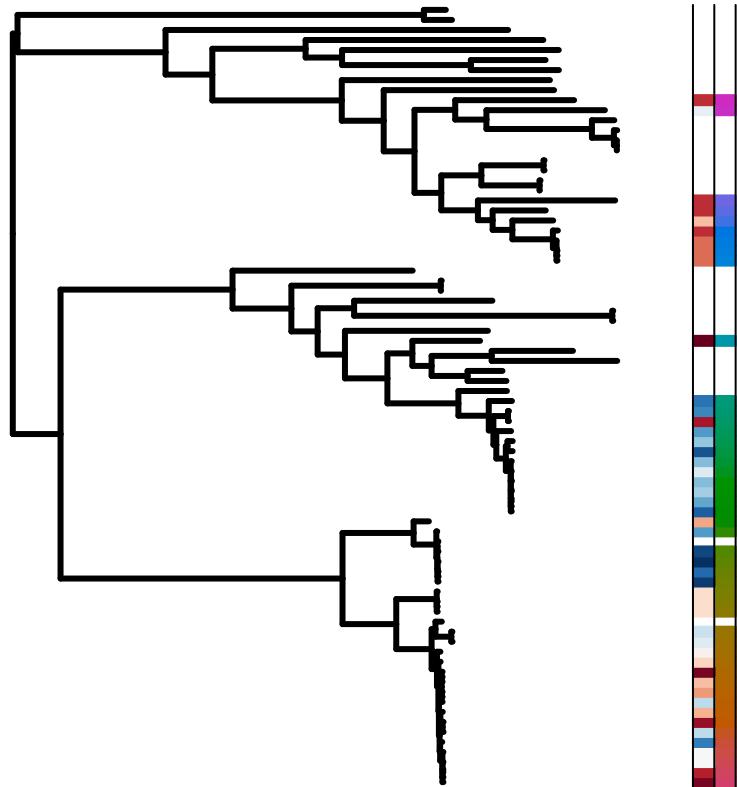
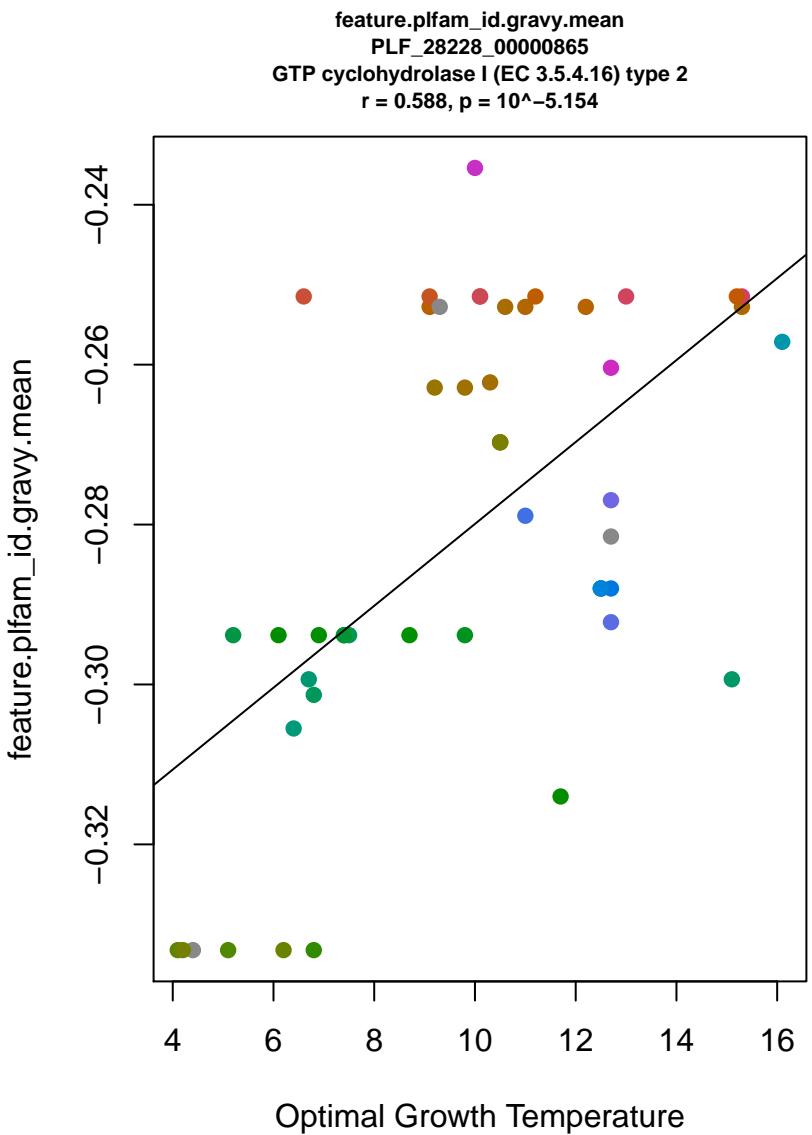
feature.plfam_id.gravy.mean



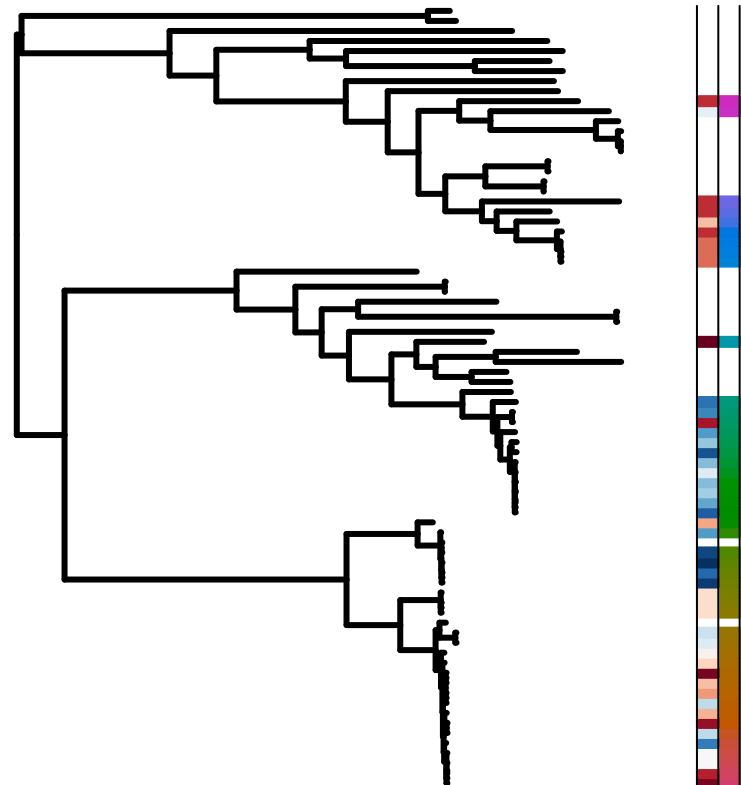
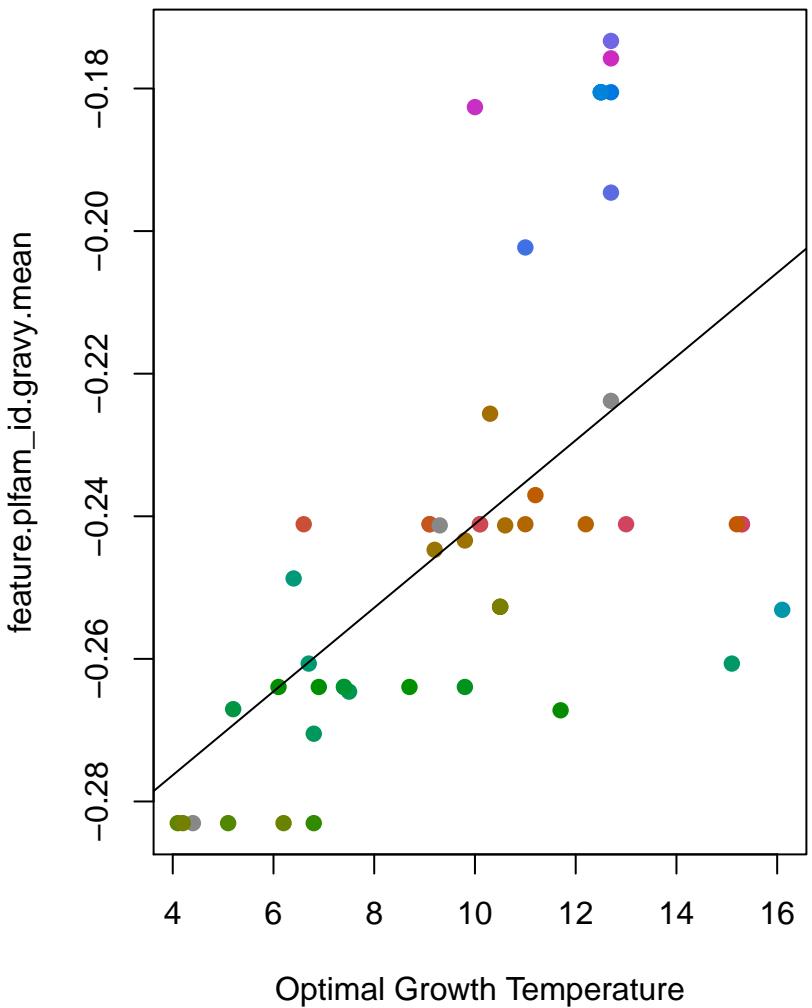
feature.plfam_id.gravy.mean
PLF_28228_00028198
FIG111991: hypothetical protein
 $r = 0.605, p = 10^{-4.86}$

feature.plfam_id.gravy.mean

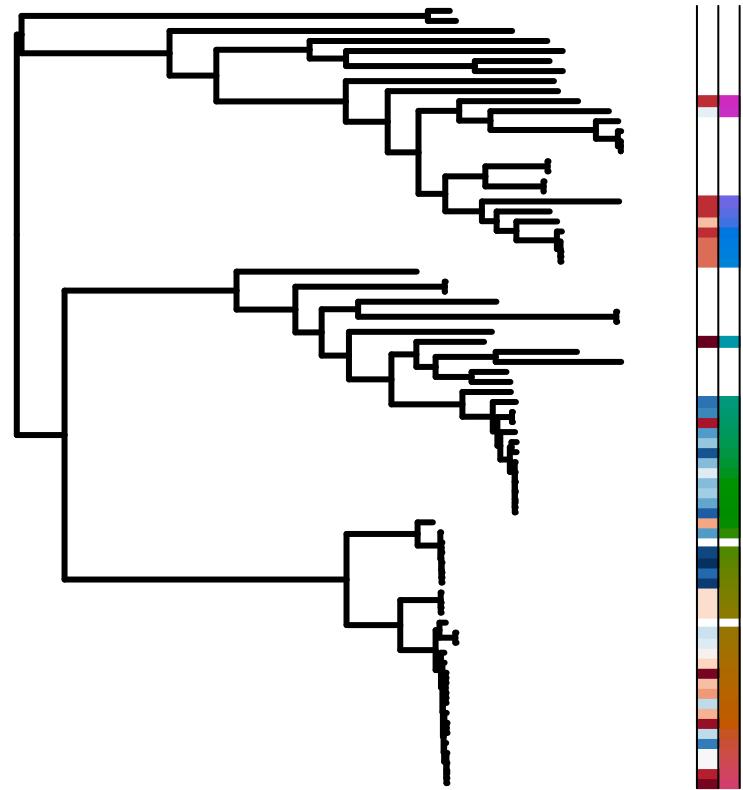
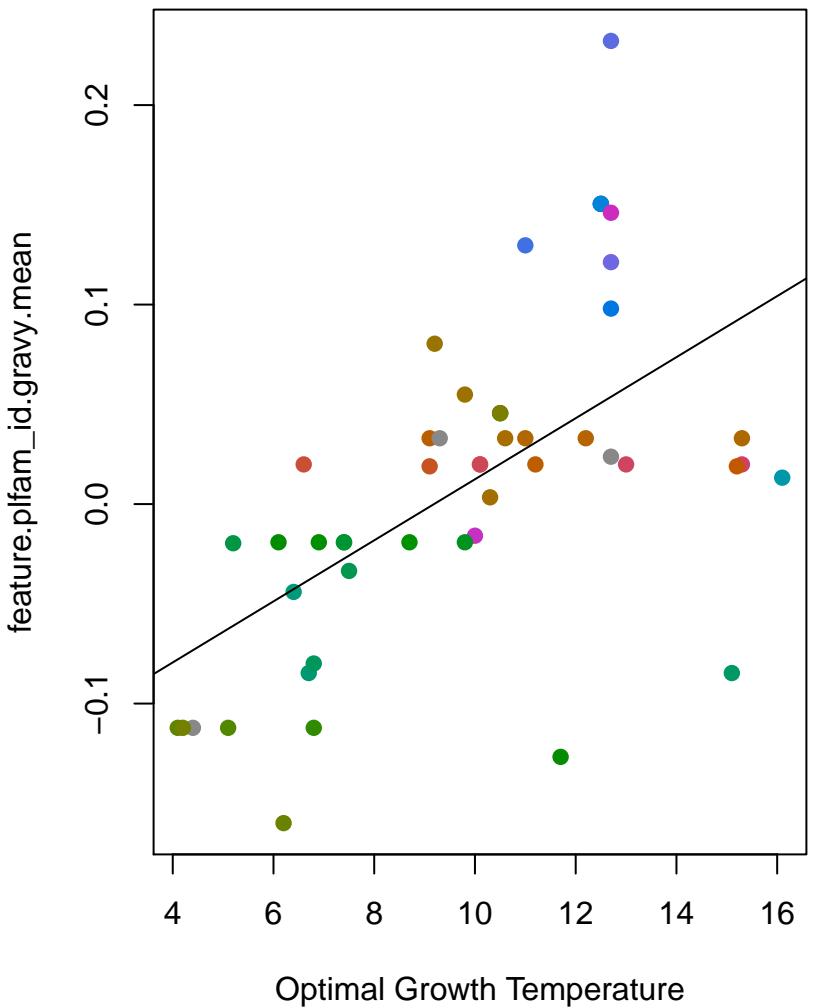




feature.plfam_id.gravy.mean
PLF_28228_00001960
Protein kinase
 $r = 0.586$, $p = 10^{-5.113}$



feature.plfam_id.gravy.mean
PLF_28228_00000361
Dephospho-CoA kinase (EC 2.7.1.24)
 $r = 0.583$, $p = 10^{-5.059}$

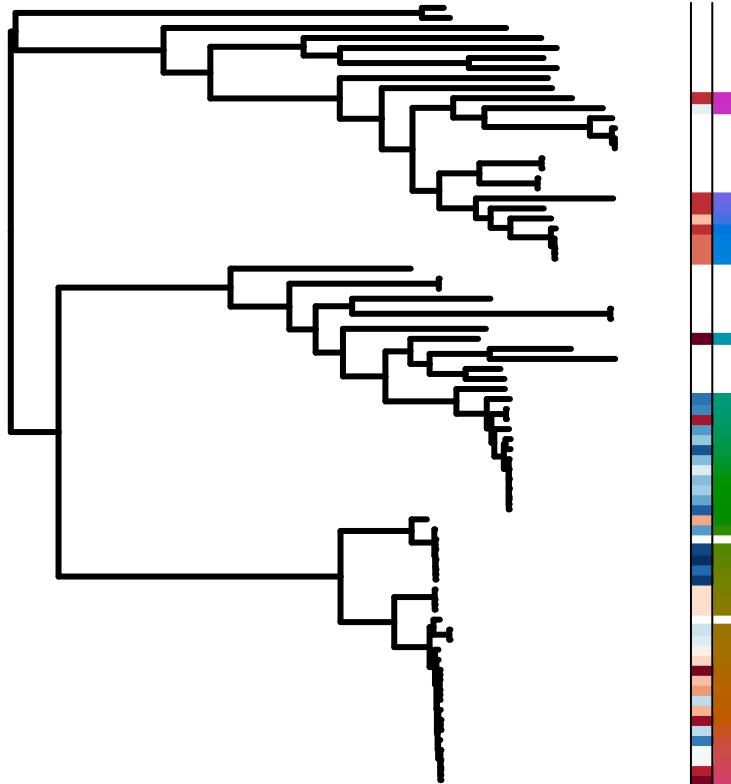
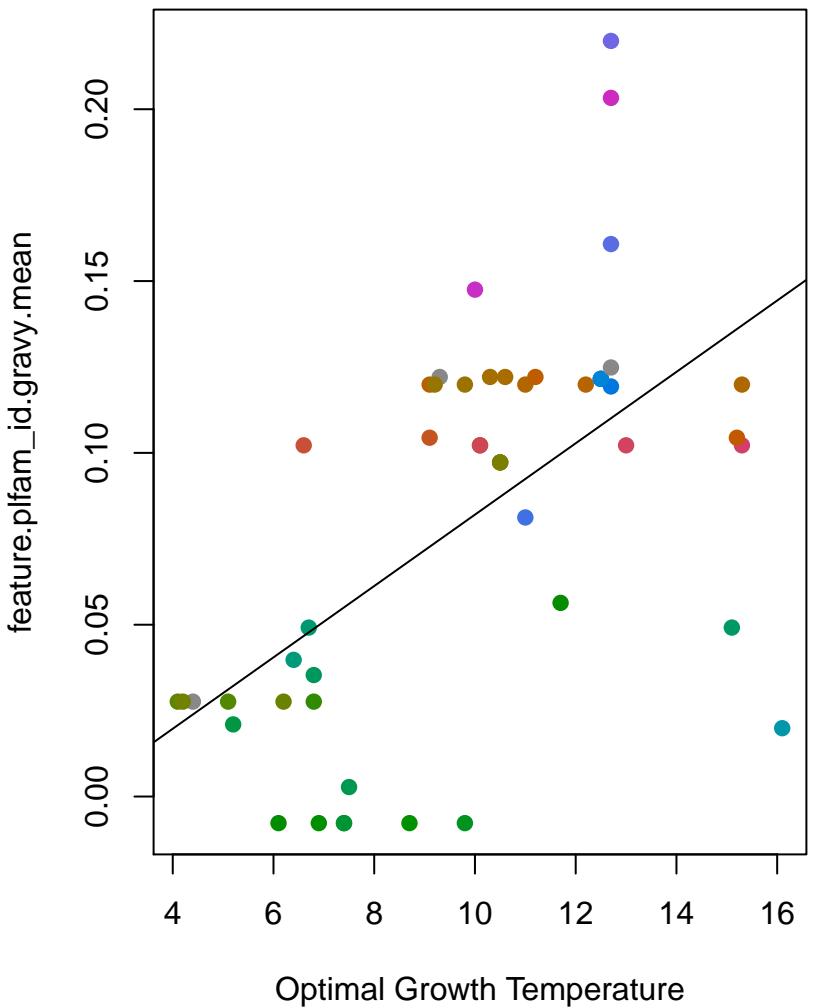


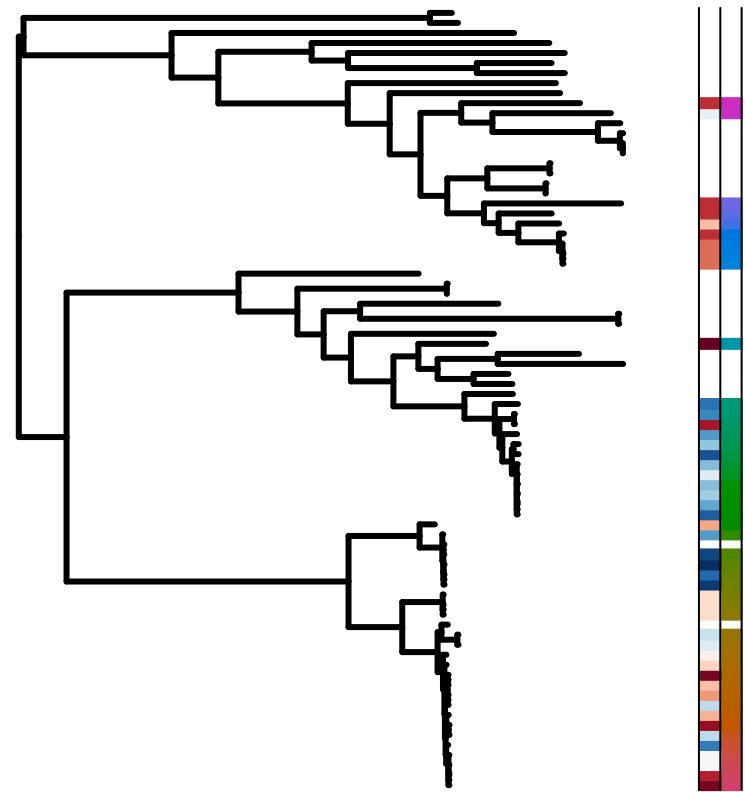
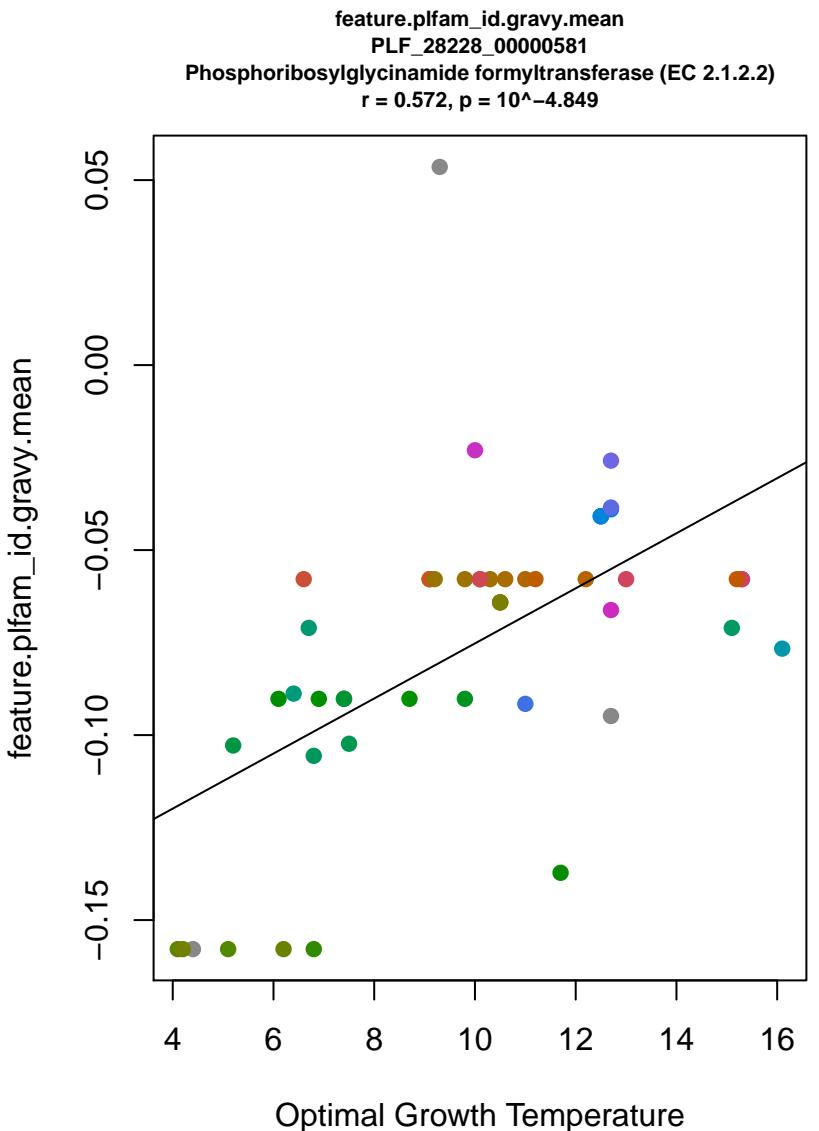
feature.plfam_id.gravy.mean

PLF_28228_00000267

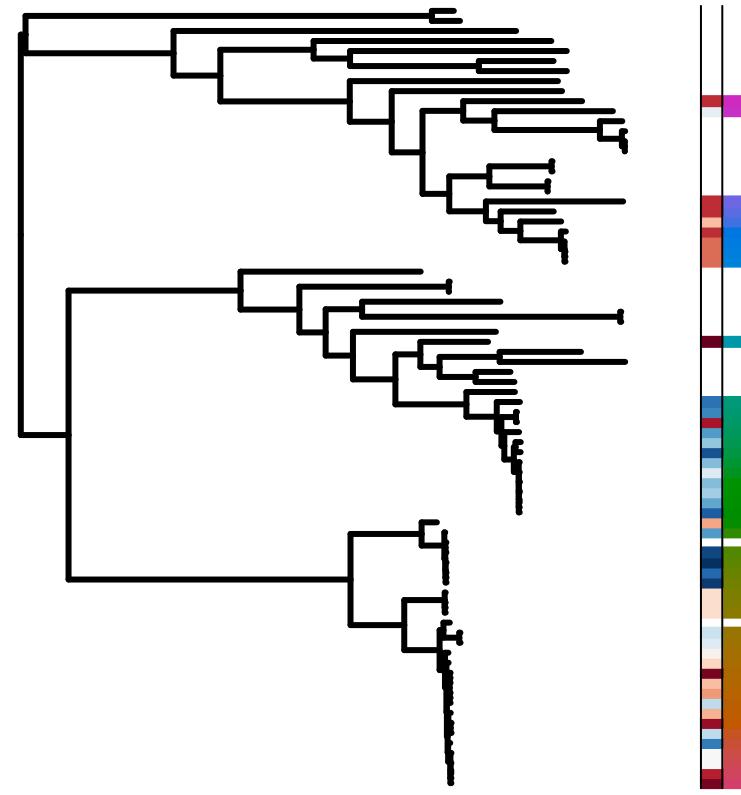
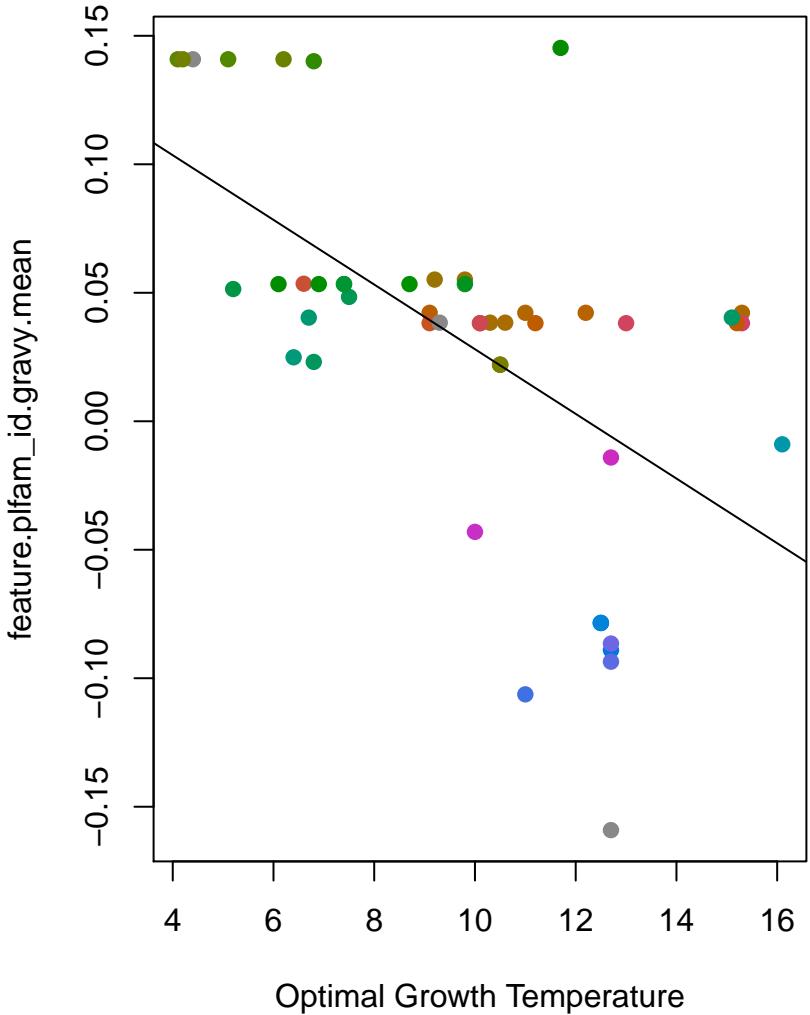
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)

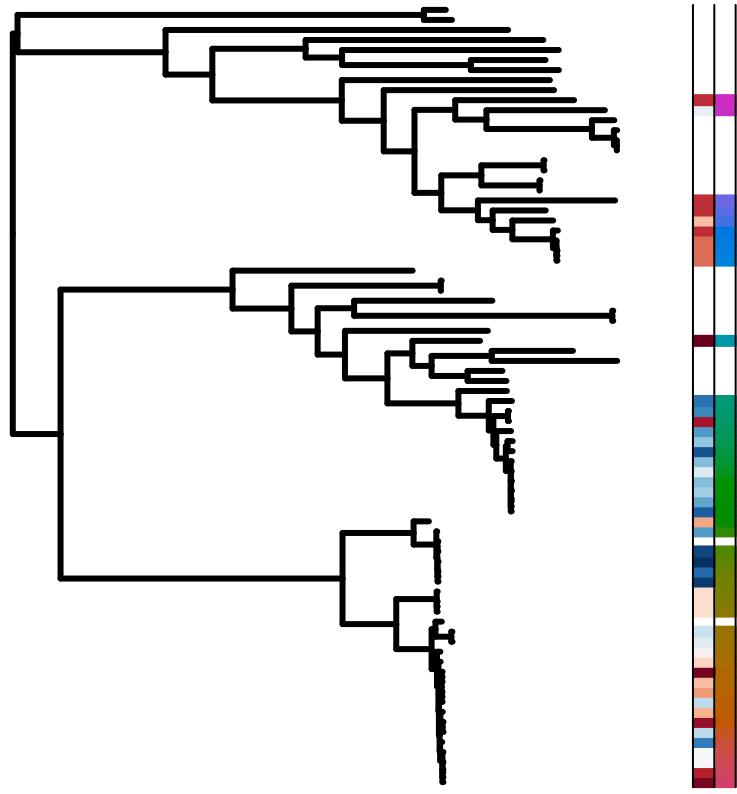
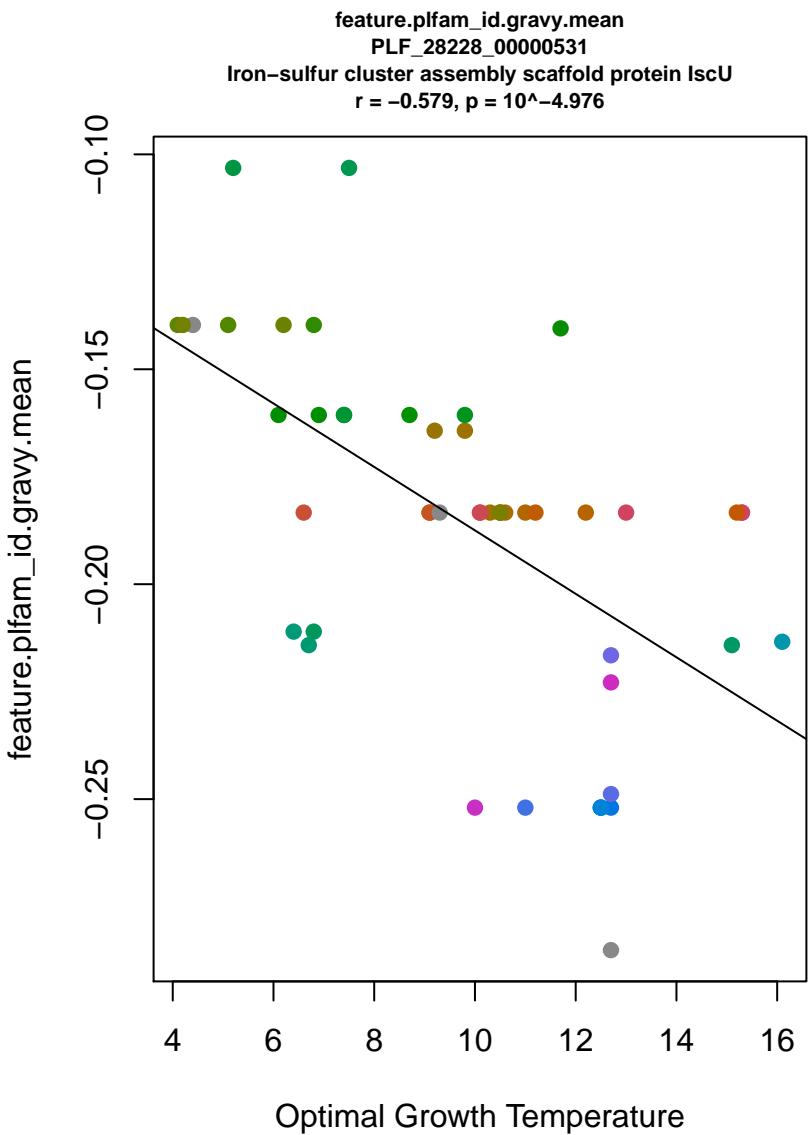
$r = 0.578, p = 10^{-4.961}$





feature.plfam_id.gravy.mean
PLF_28228_00002036
Sensor histidine kinase GlnK
 $r = -0.572$, $p = 10^{-4.854}$



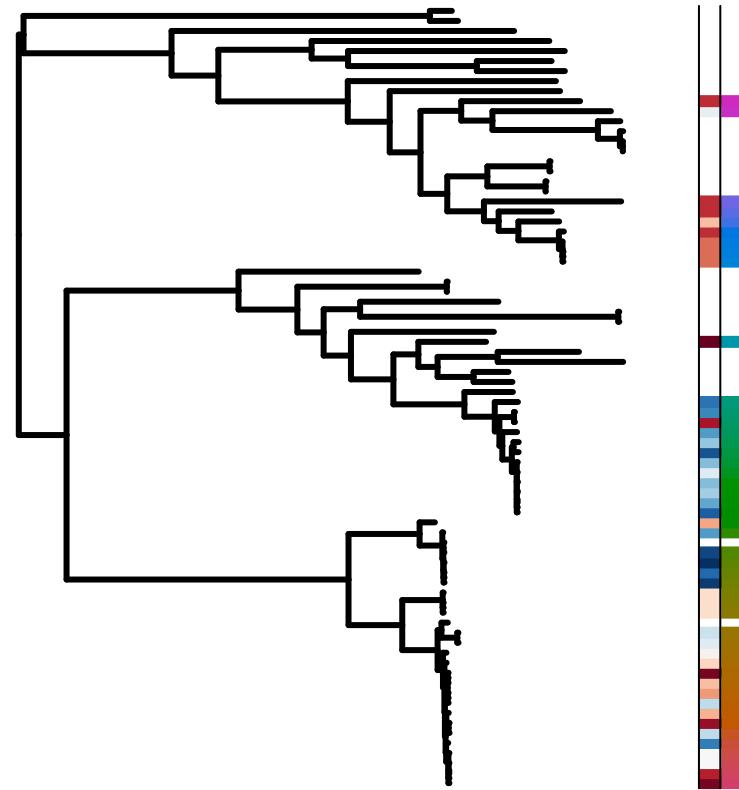
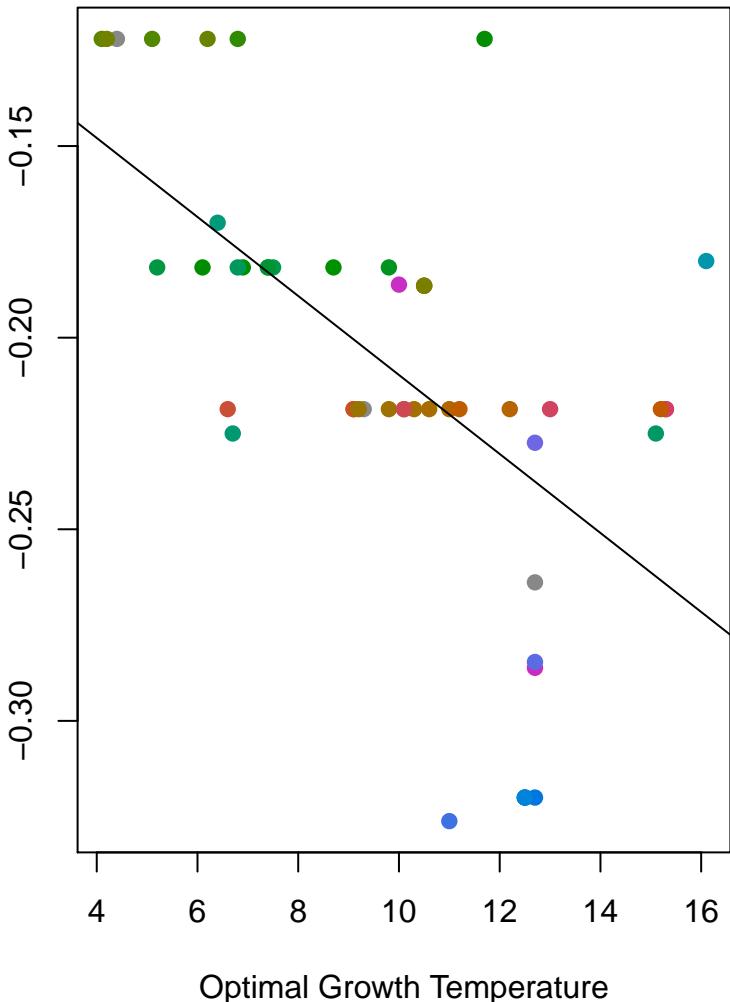


feature.plfam_id.gravy.mean

PLF_28228_00000348

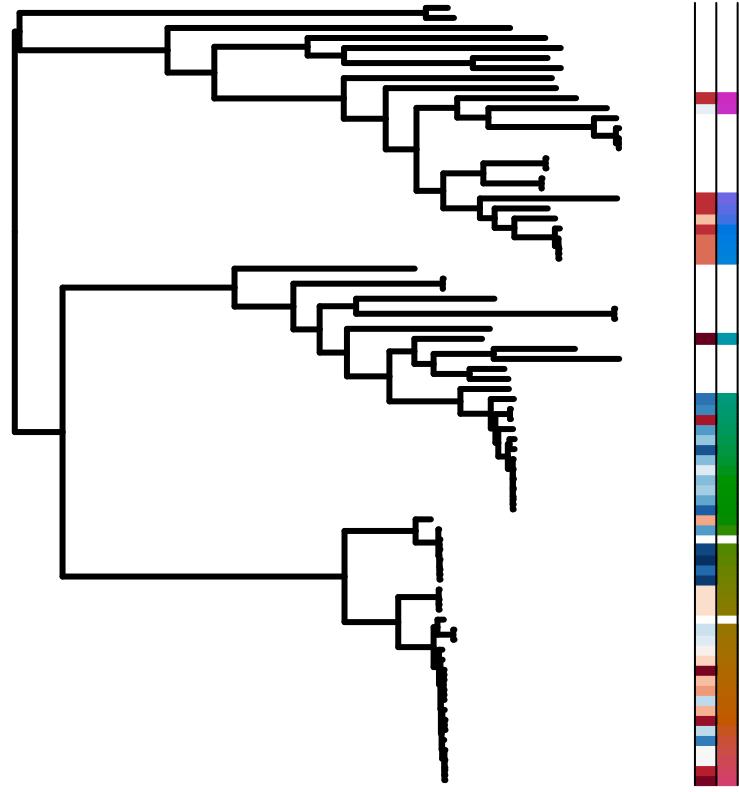
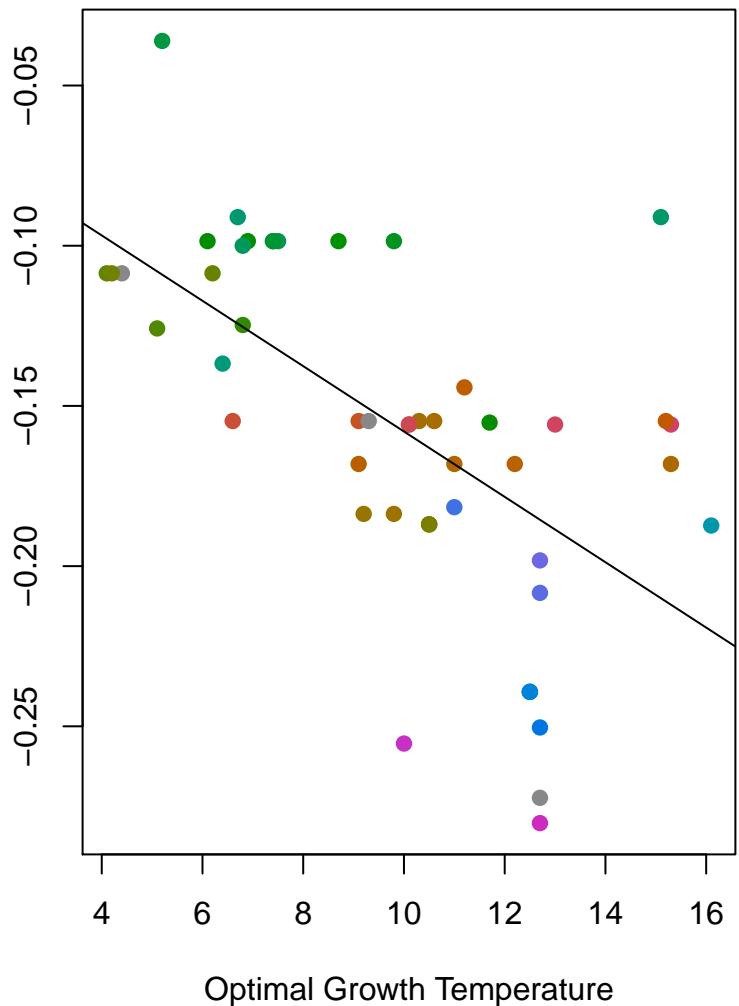
FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster
 $r = -0.6, p = 10^{-5.384}$

feature.plfam_id.gravy.mean



feature.plfam_id.gravy.mean
PLF_28228_00000917
Peptidase, M23/M37 family
 $r = -0.602$, $p = 10^{-5.432}$

feature.plfam_id.gravy.mean



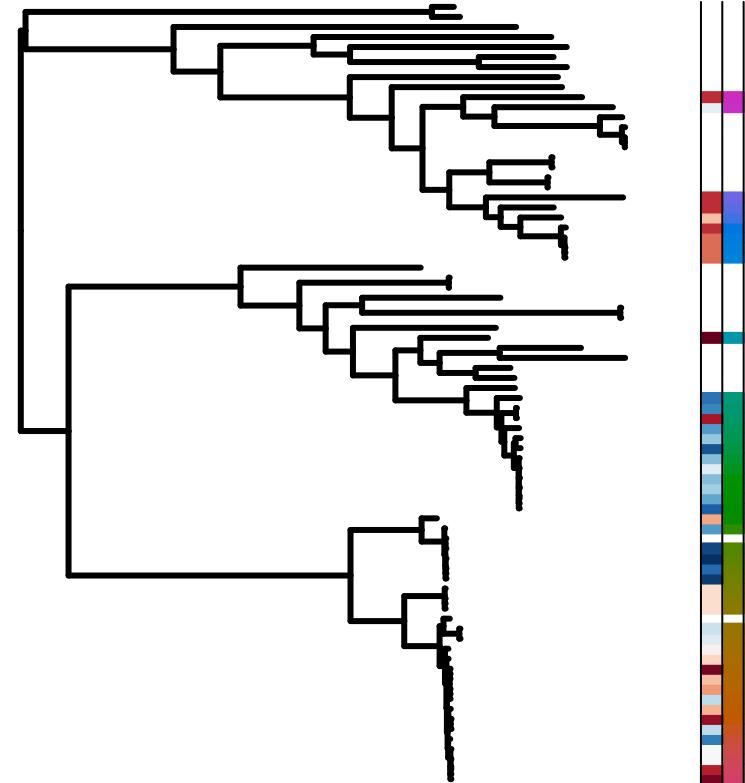
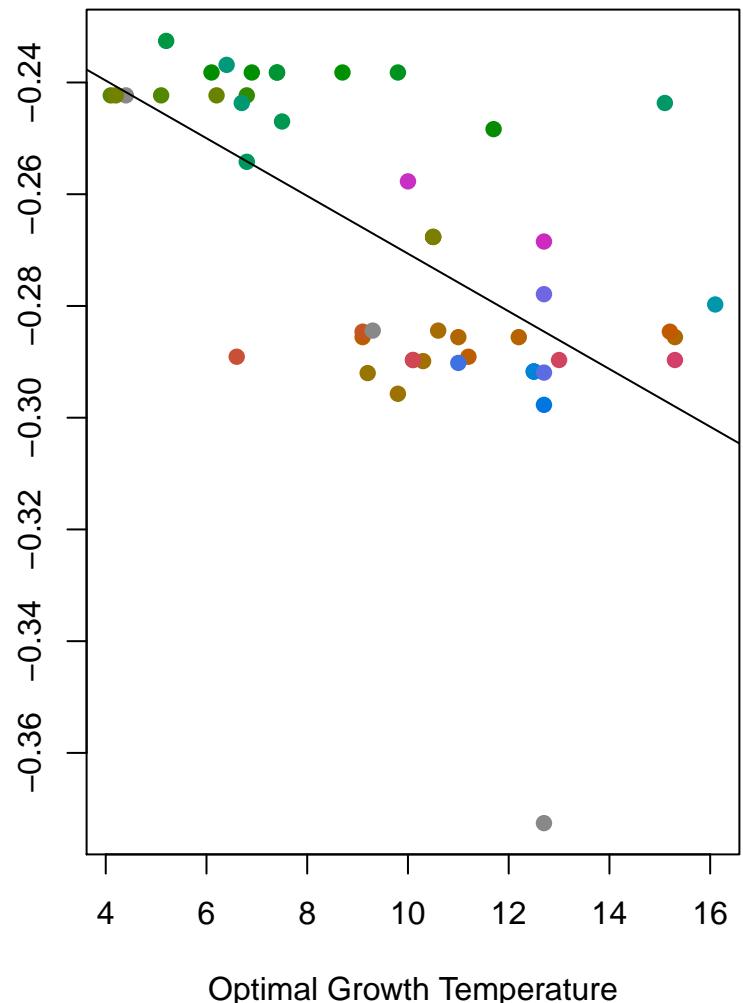
feature.plfam_id.gravy.mean

PLF_28228_00000235

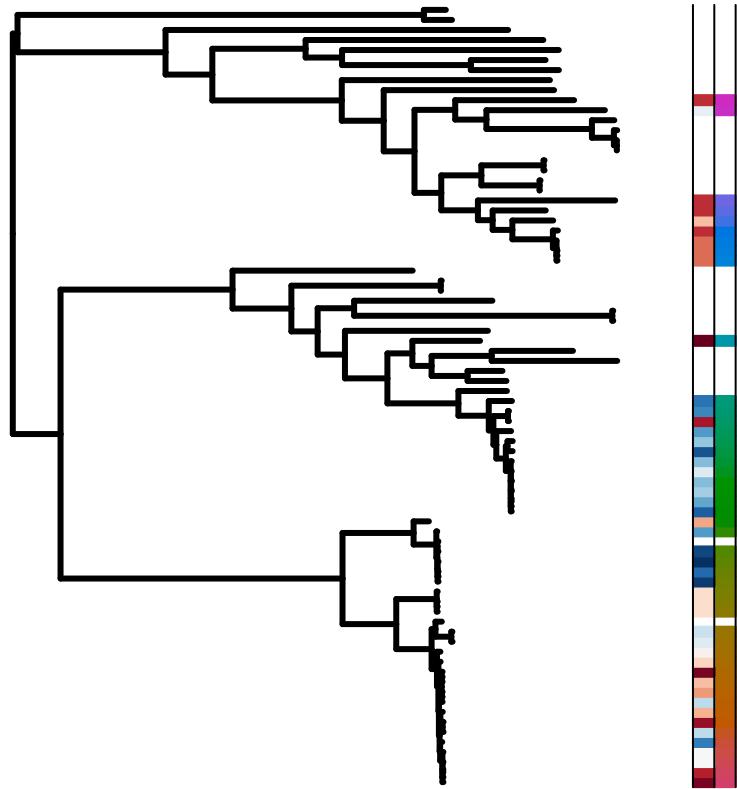
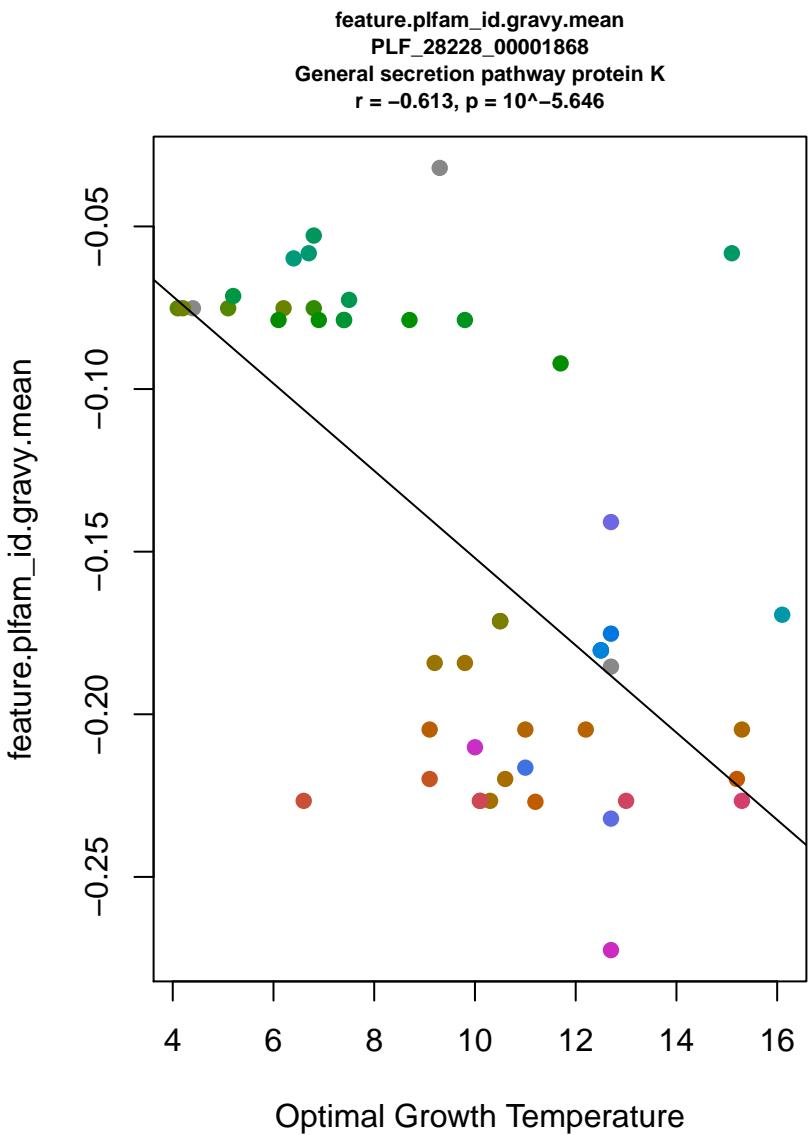
2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)

$r = -0.607$, $p = 10^{-5.527}$

feature.plfam_id.gravy.mean



Optimal Growth Temperature



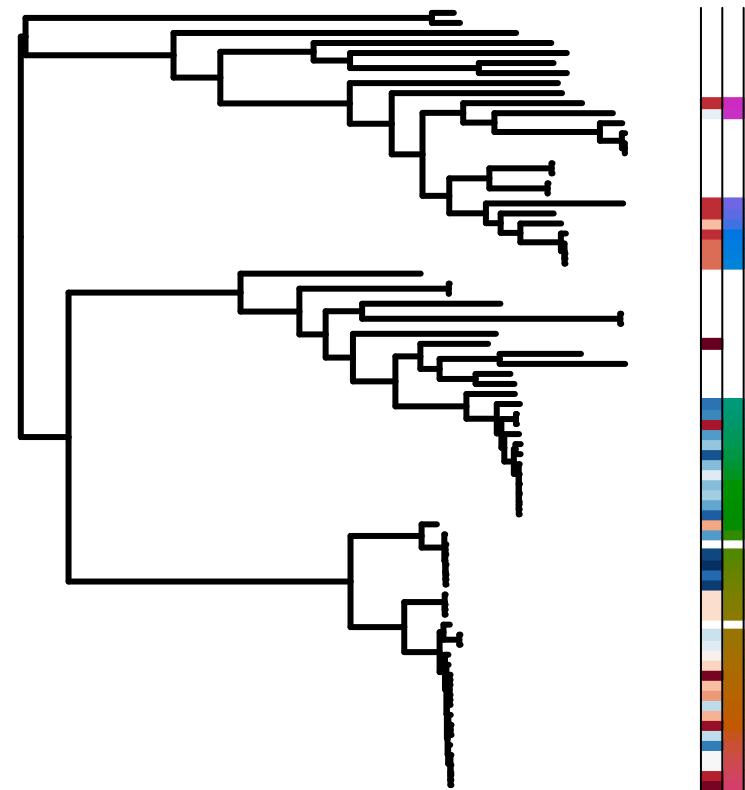
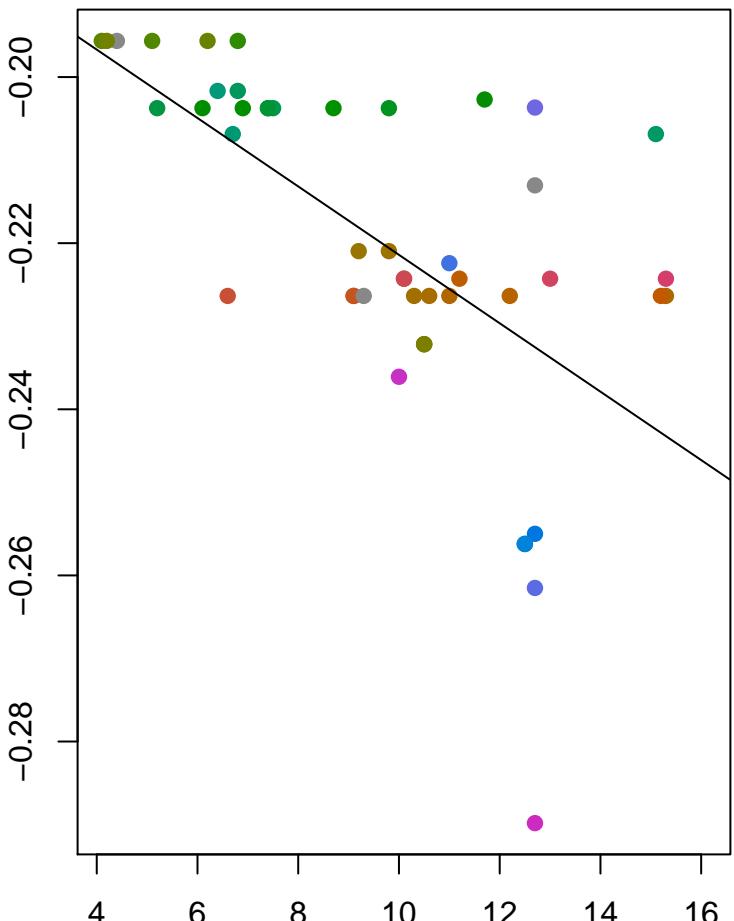
feature.plfam_id.gravy.mean

PLF_28228_00001635

DNA-binding transcriptional regulator, MocR family / aminotransferase domain

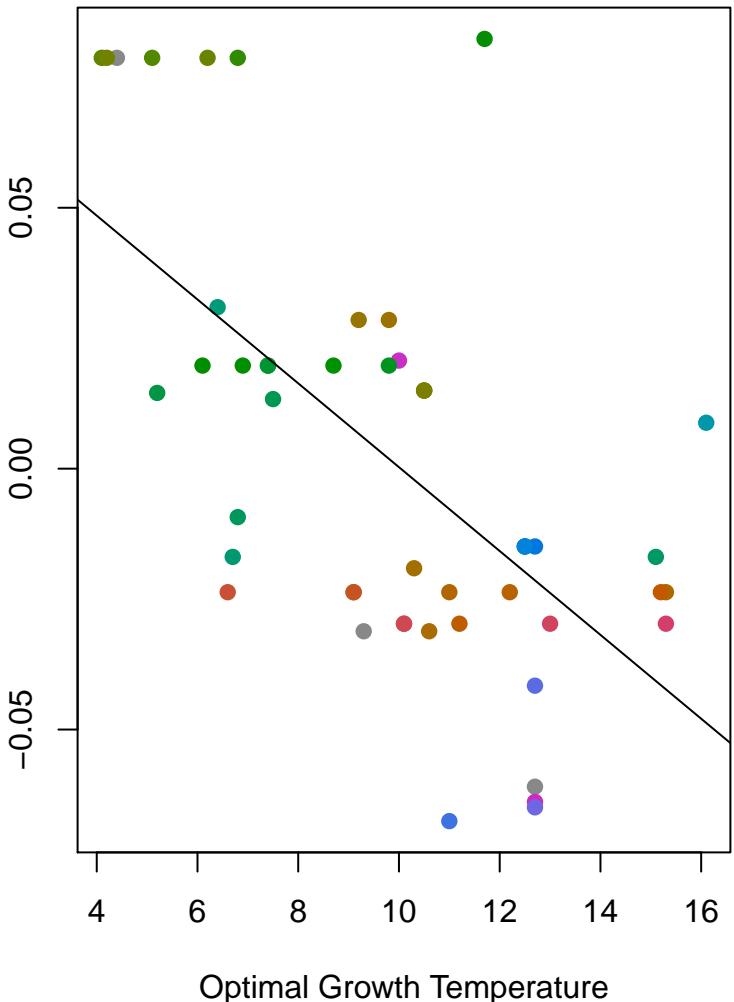
$r = -0.613, p = 10^{-5.547}$

feature.plfam_id.gravy.mean

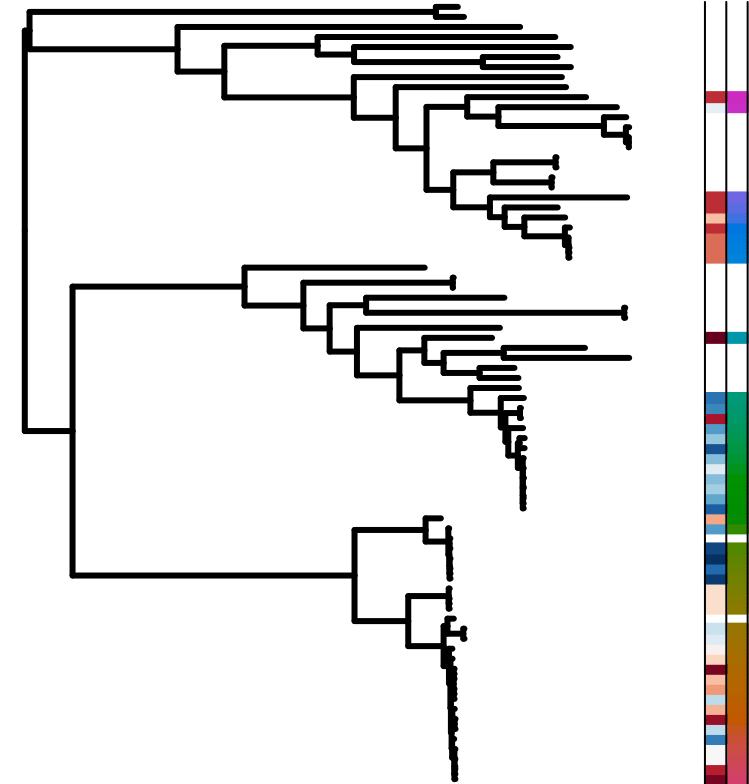


feature.plfam_id.gravy.mean
PLF_28228_00001790
Orn/DAP/Arg family decarboxylase
 $r = -0.624$, $p = 10^{-5.9}$

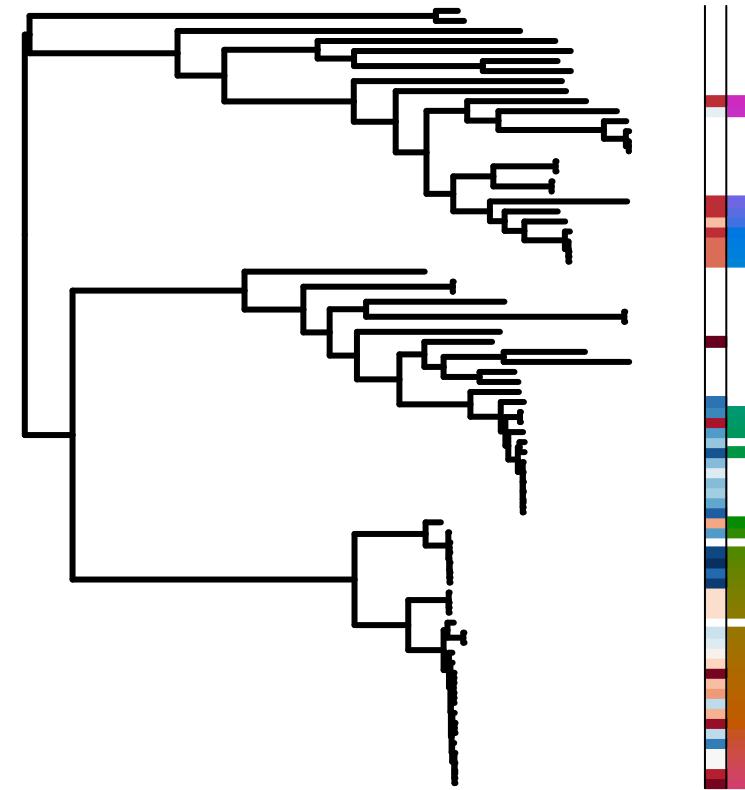
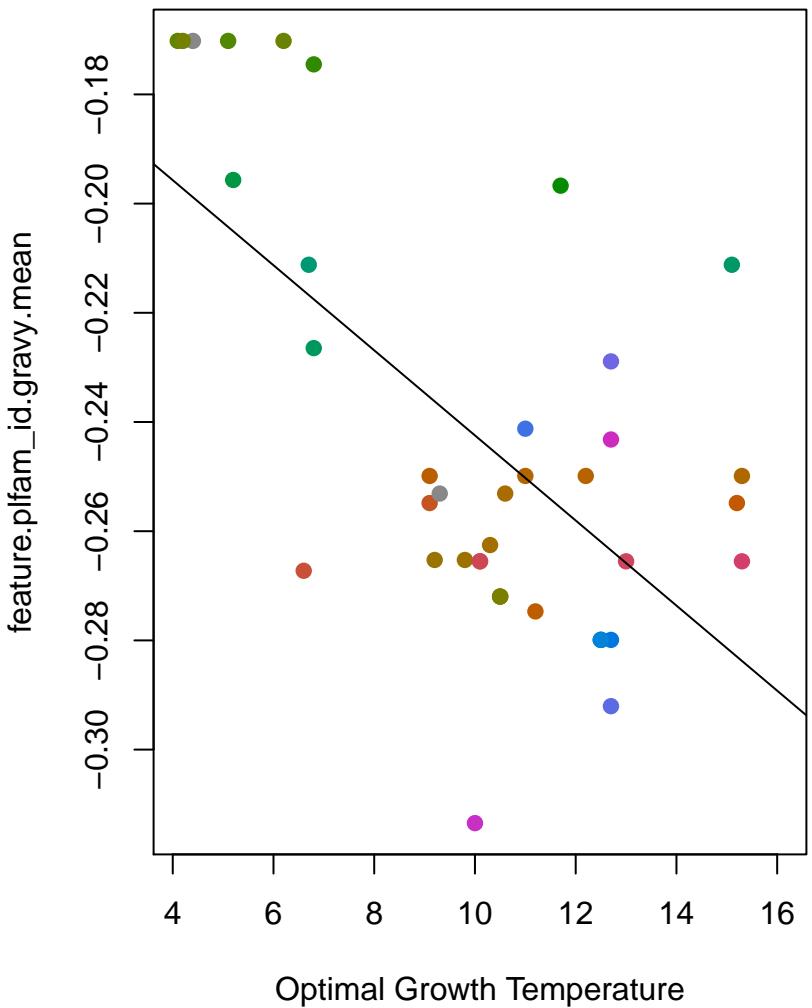
feature.plfam_id.gravy.mean

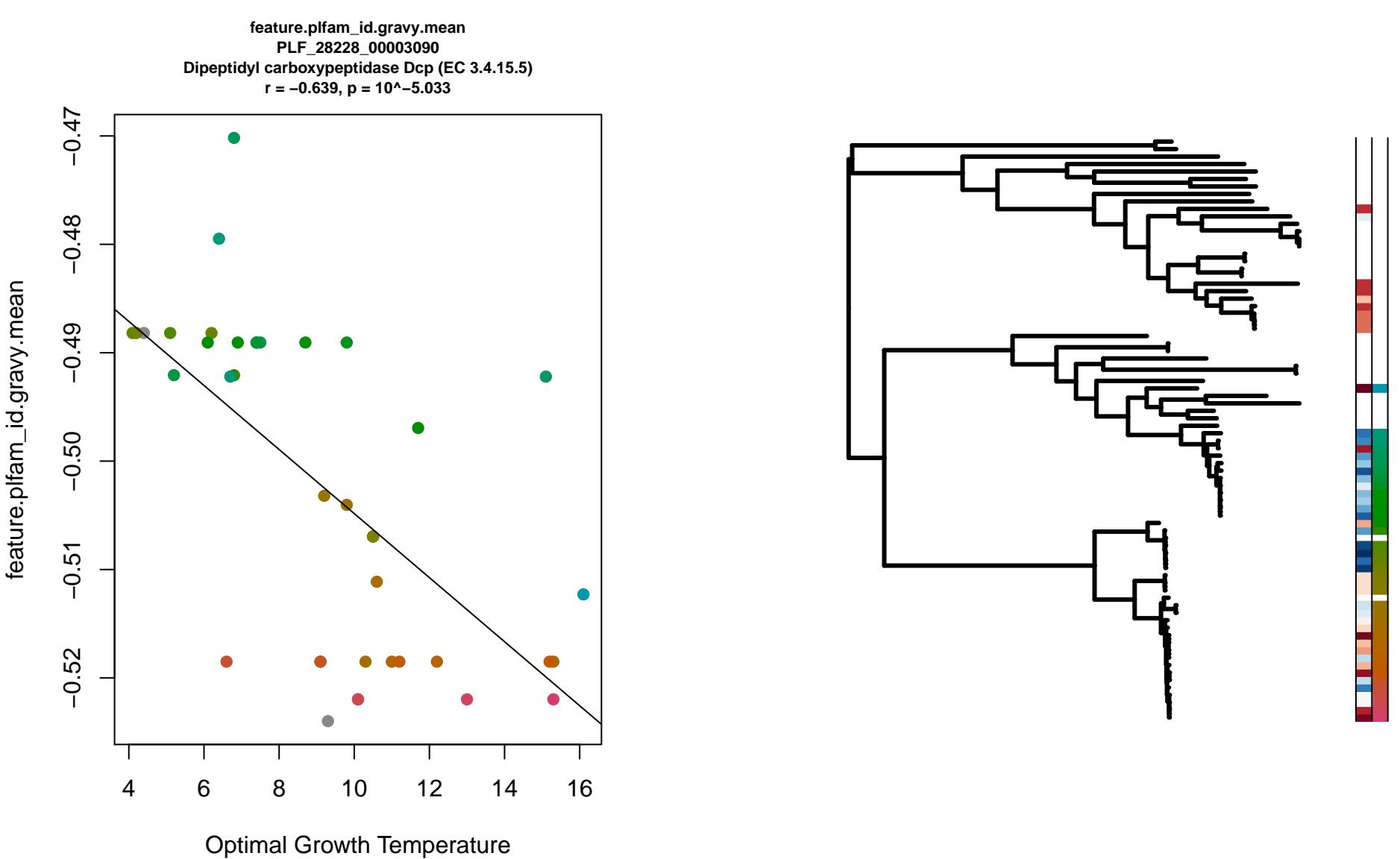


Optimal Growth Temperature



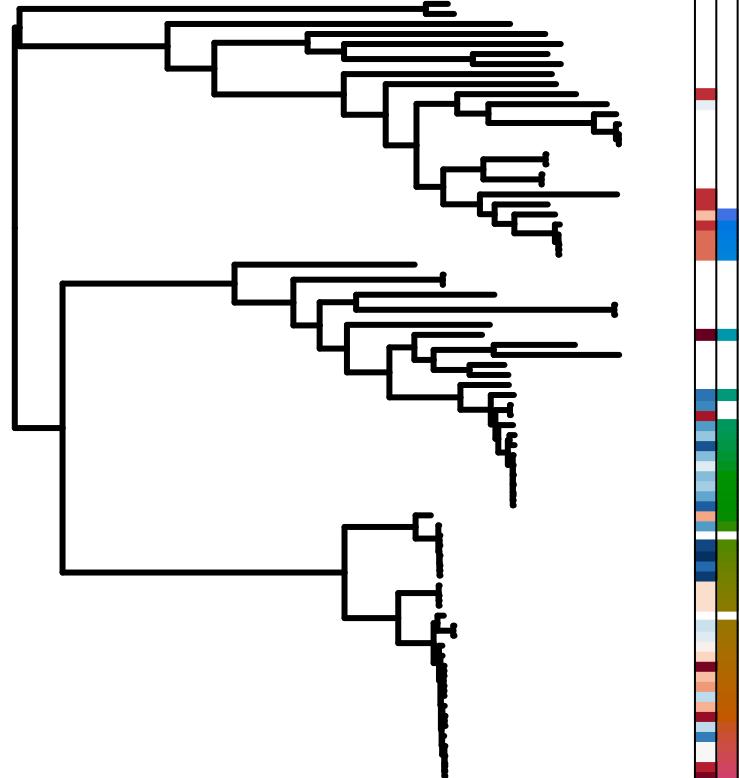
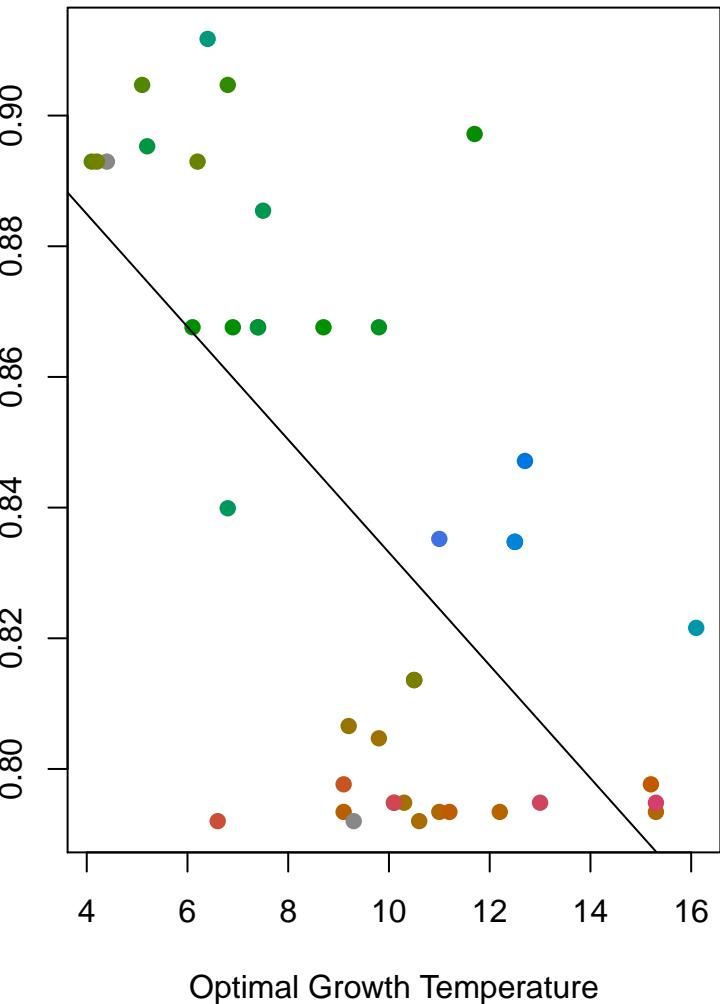
feature.plfam_id.gravy.mean
PLF_28228_00000419
Glycine oxidase ThiO (EC 1.4.3.19)
 $r = -0.629$, $p = 10^{-4.862}$





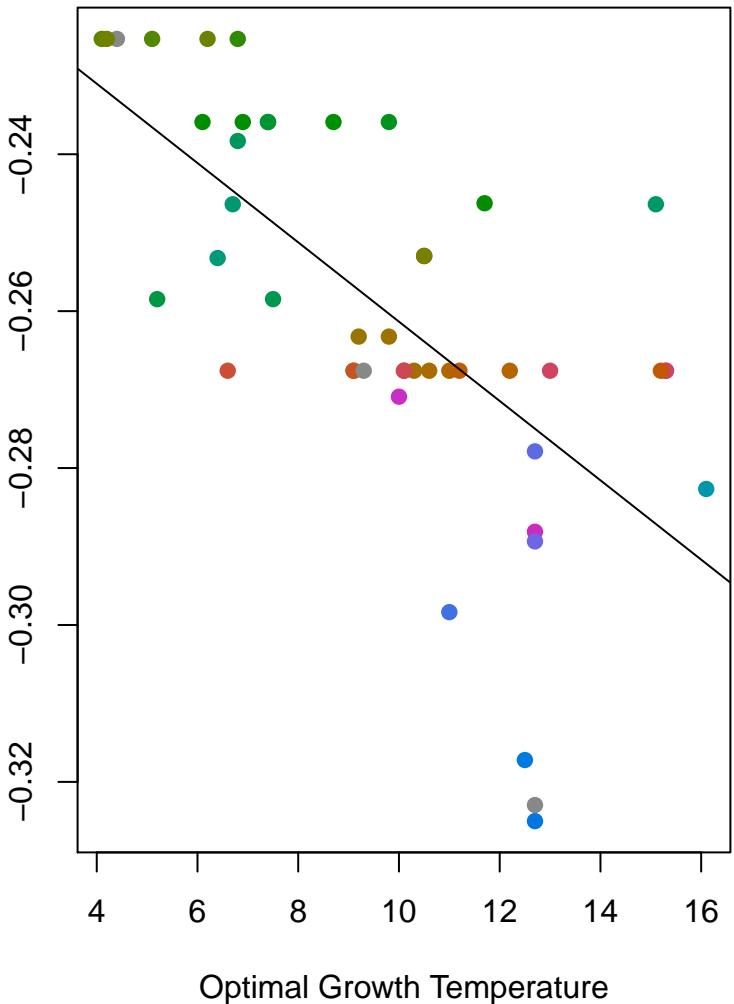
feature.plfam_id.gravy.mean
PLF_28228_00007491
Threonine efflux protein
 $r = -0.647$, $p = 10^{-5.568}$

feature.plfam_id.gravy.mean

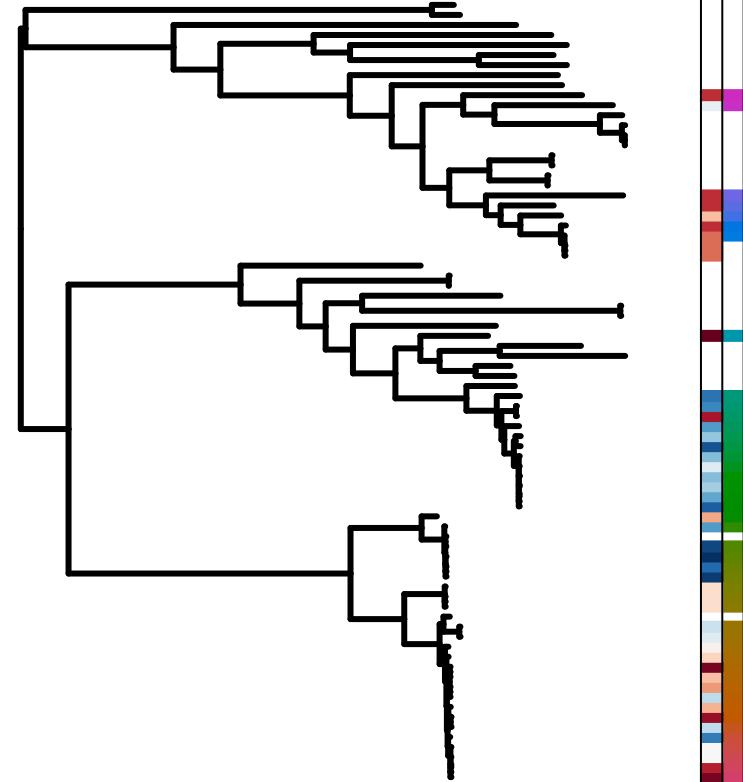


feature.plfam_id.gravy.mean
PLF_28228_00027836
16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)
 $r = -0.654$, $p = 10^{-6.323}$

feature.plfam_id.gravy.mean



Optimal Growth Temperature



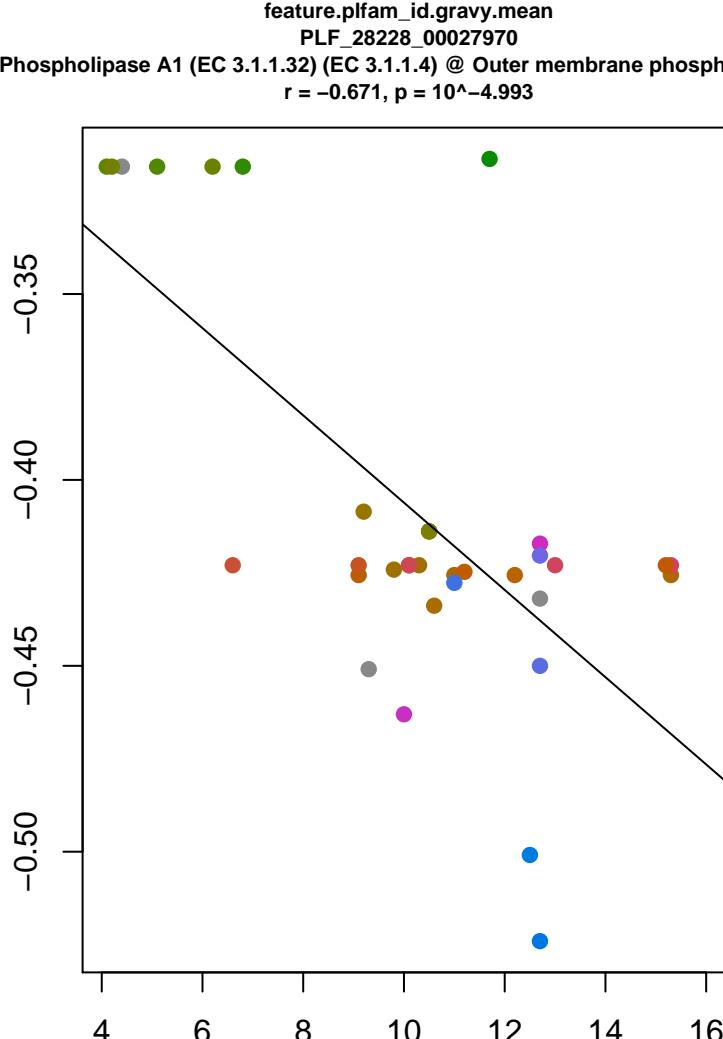
feature.plfam_id.gravy.mean

PLF_28228_00027970

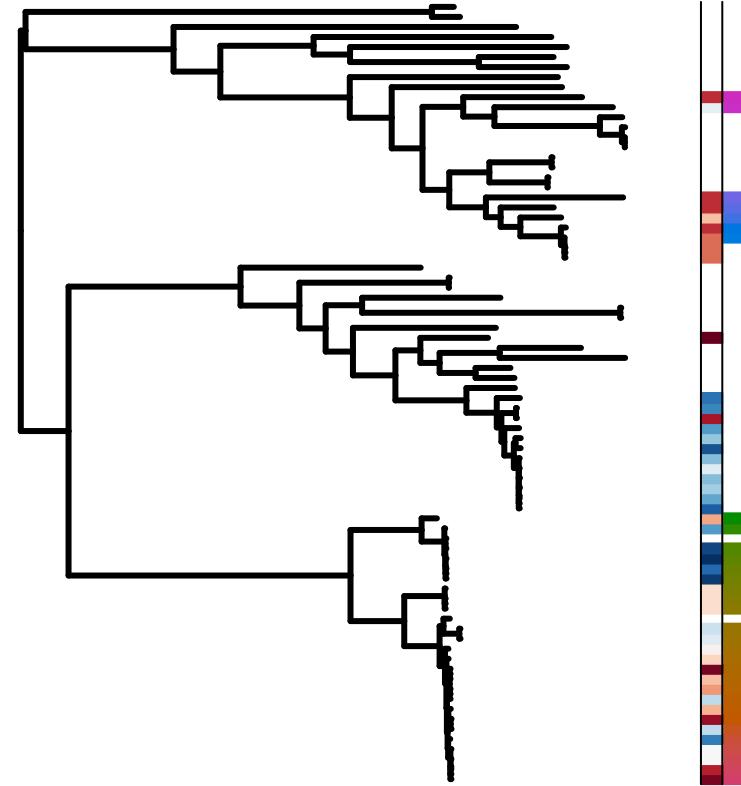
Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) @ Outer membrane phospholipase A

$r = -0.671$, $p = 10^{-4.993}$

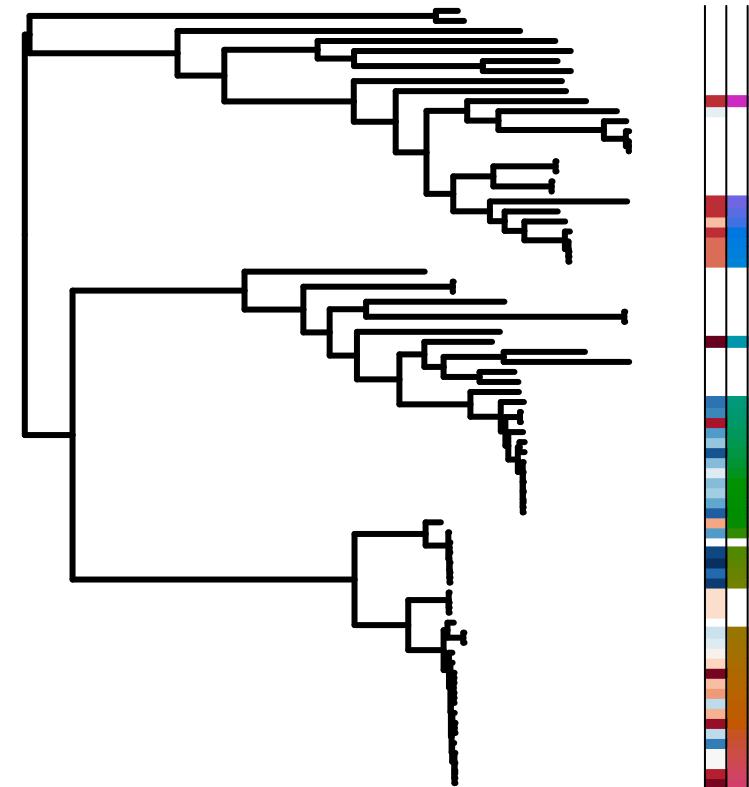
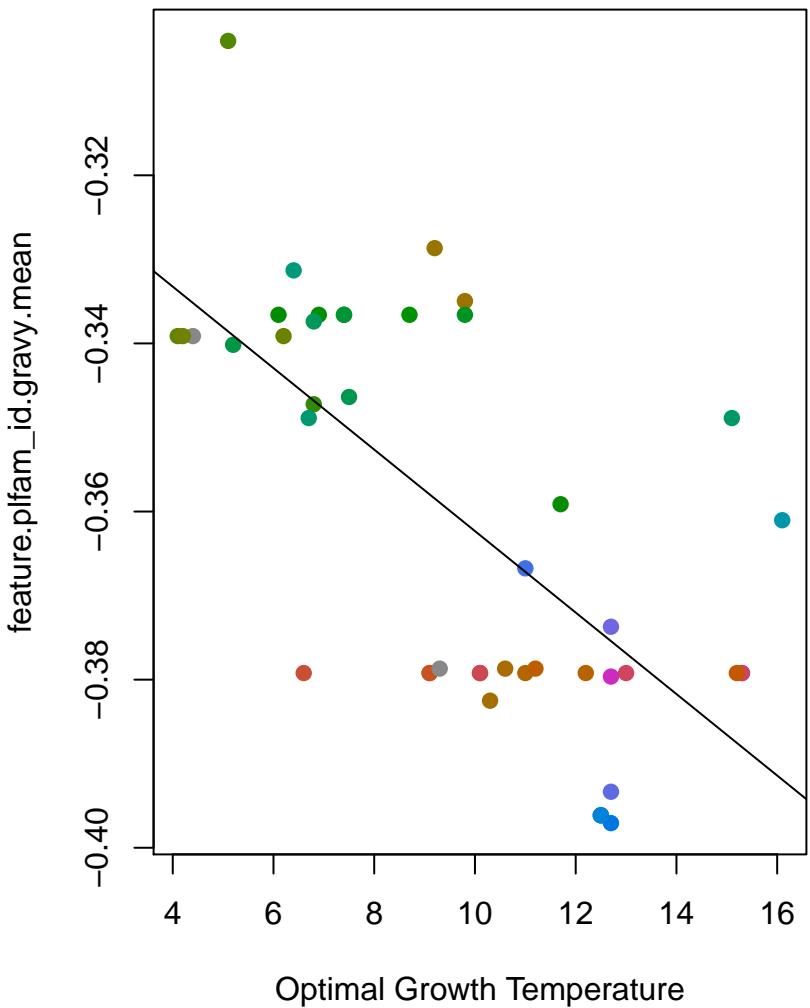
feature.plfam_id.gravy.mean



Optimal Growth Temperature



feature.plfam_id.gravy.mean
PLF_28228_00001207
TonB-dependent receptor
 $r = -0.675$, $p = 10^{-6.44}$



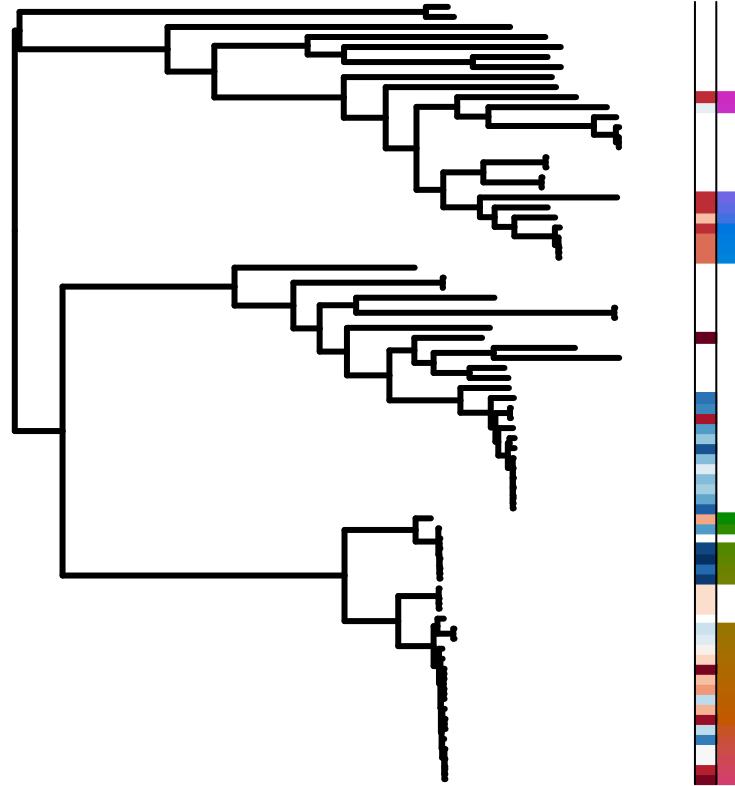
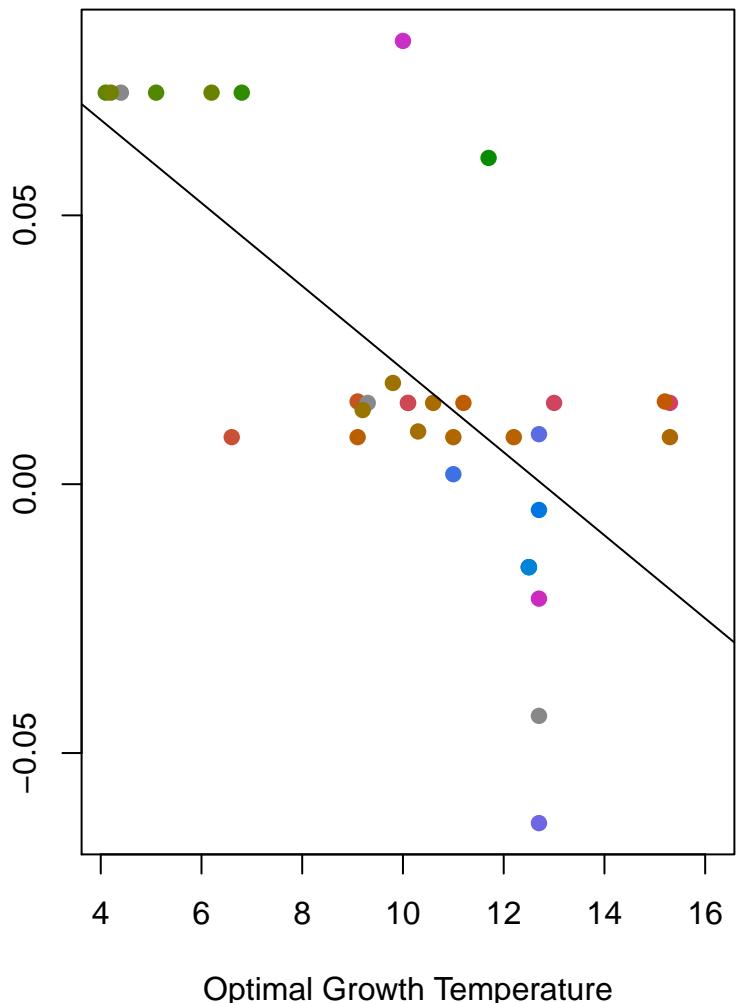
feature.plfam_id.gravy.mean

PLF_28228_00000108

N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)

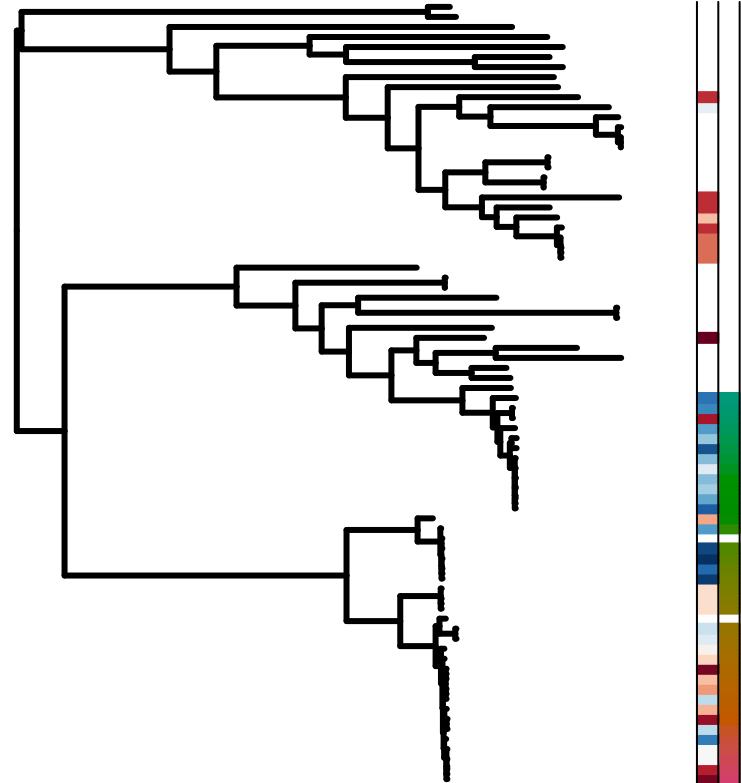
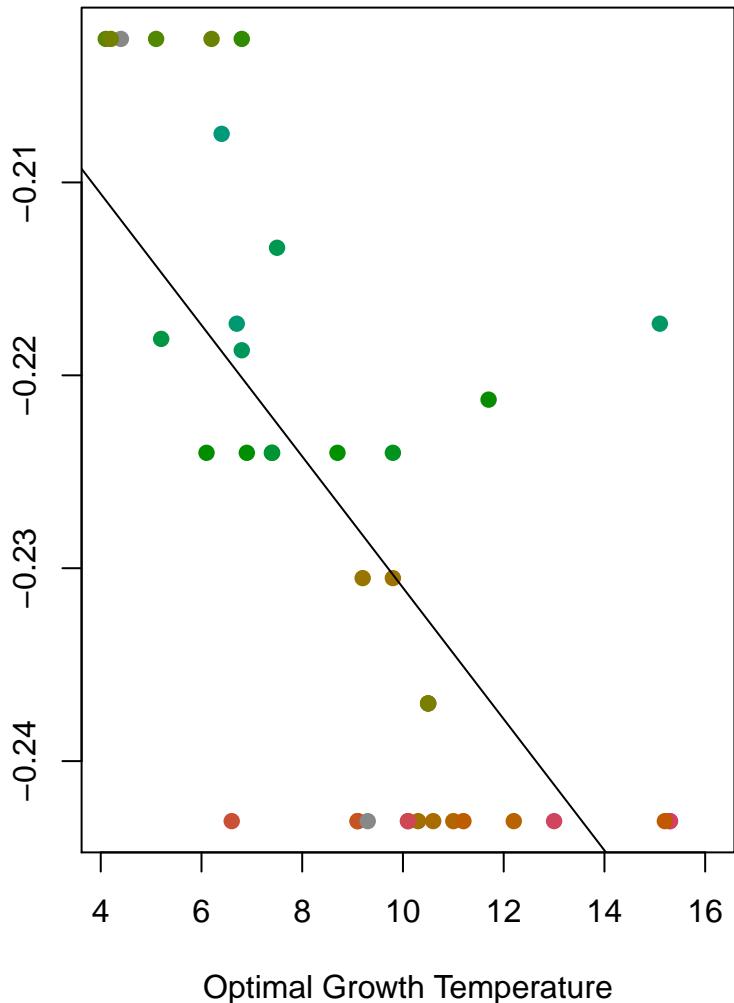
$r = -0.683, p = 10^{-5.074}$

feature.plfam_id.gravy.mean



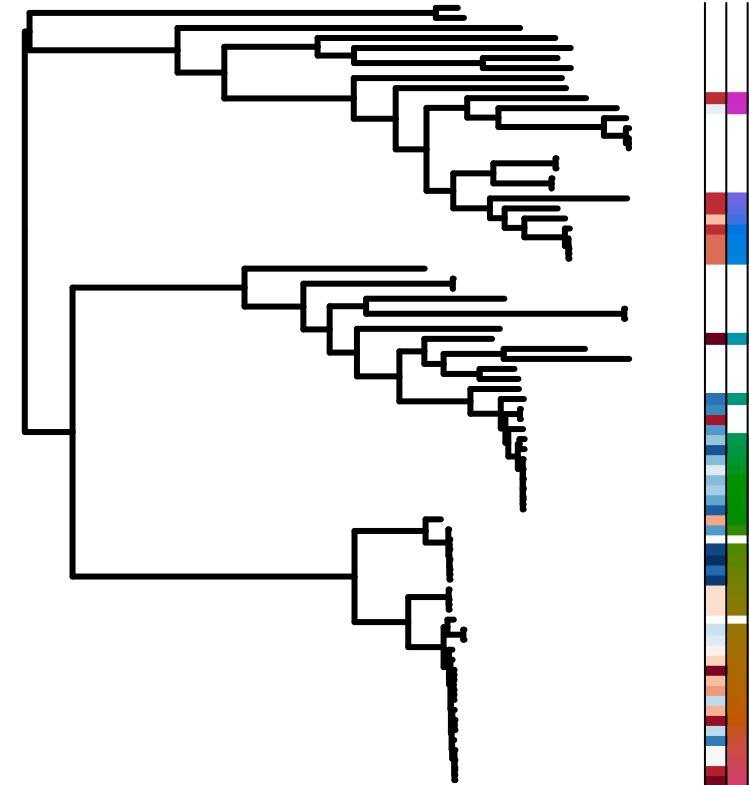
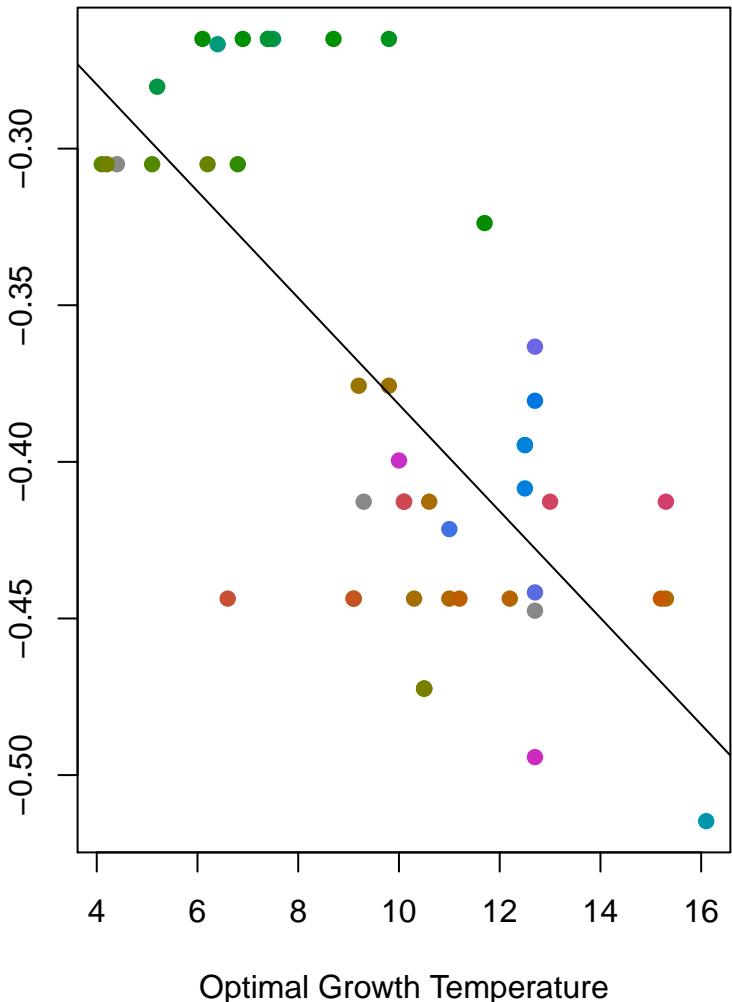
feature.plfam_id.gravy.mean
PLF_28228_00006965
Carbon–nitrogen hydrolase
 $r = -0.695$, $p = 10^{-6.047}$

feature.plfam_id.gravy.mean

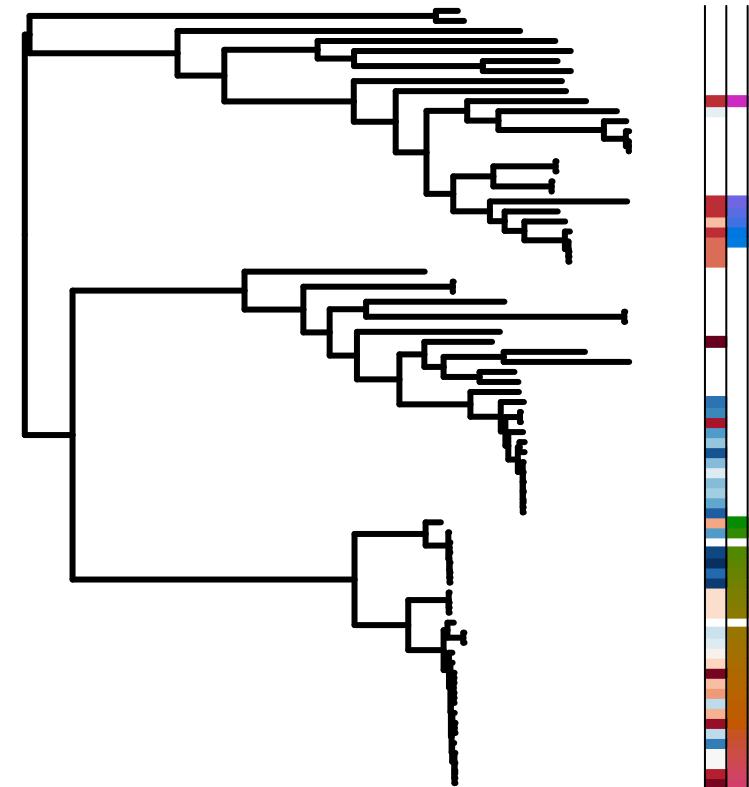
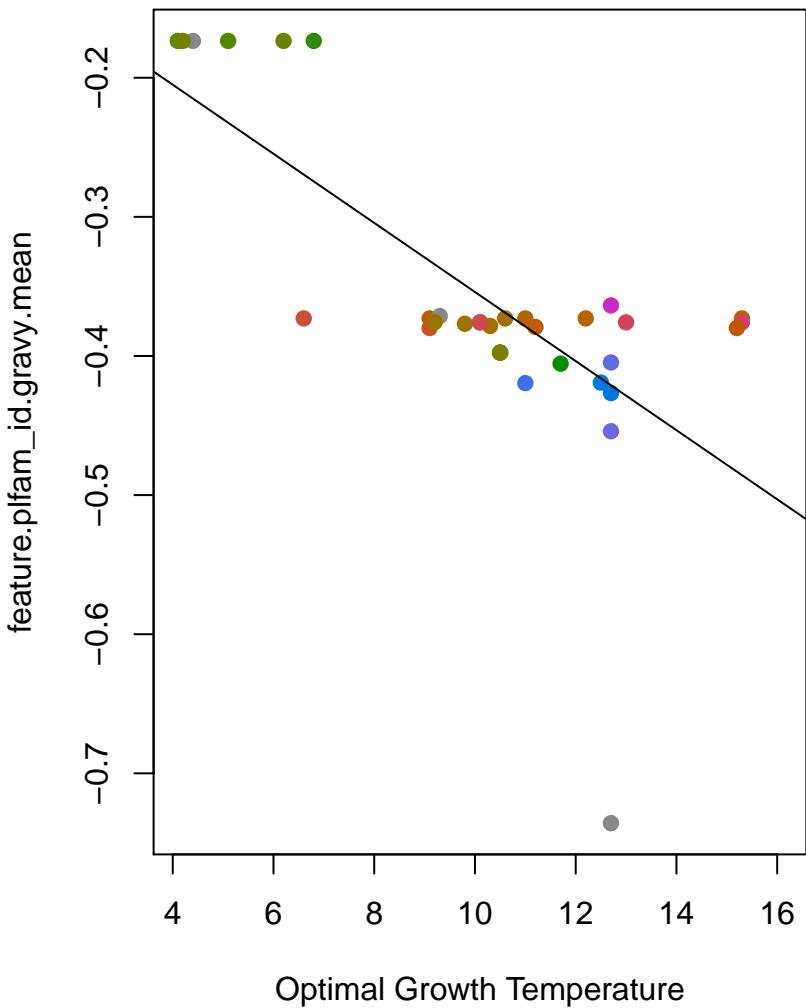


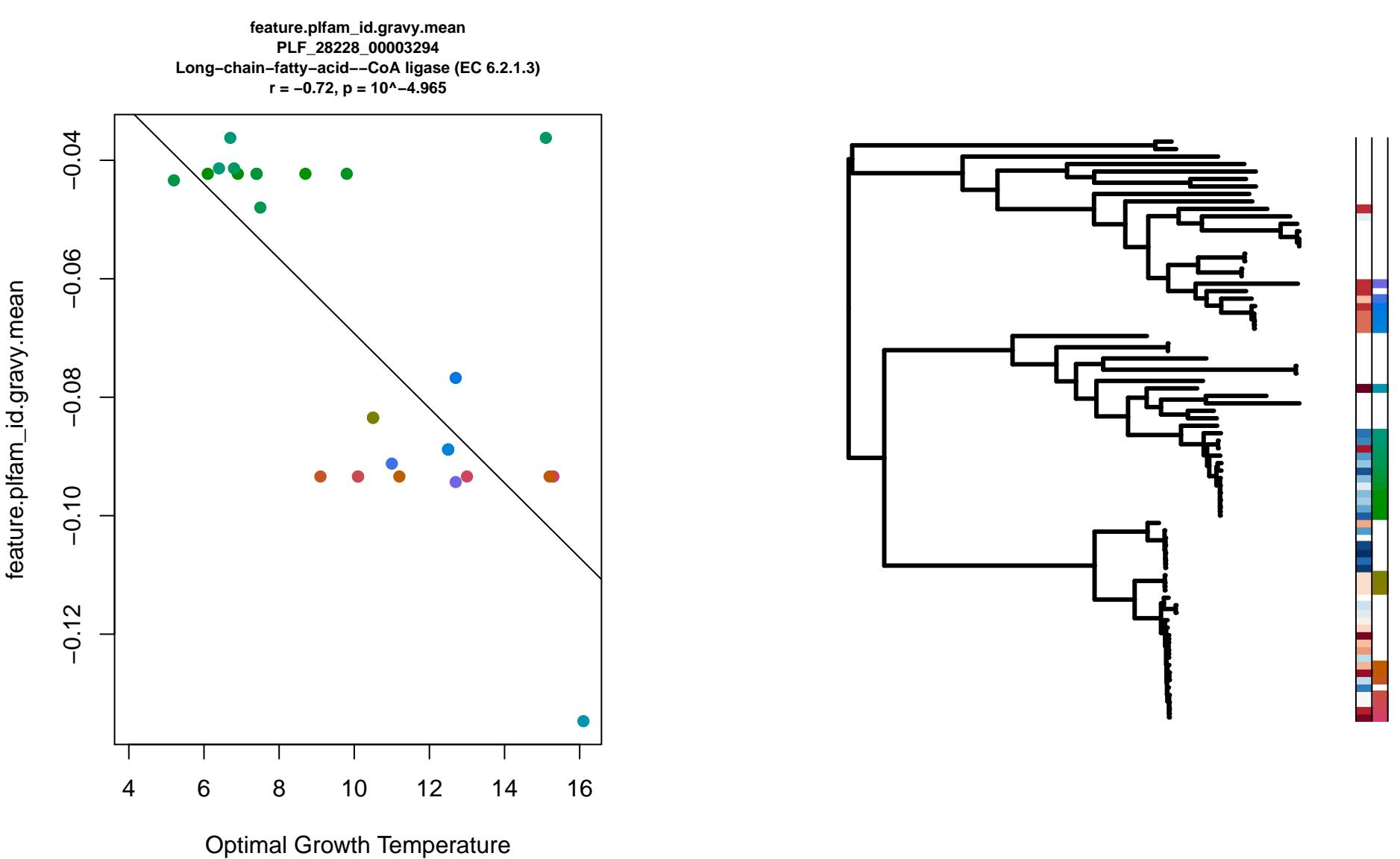
feature.plfam_id.gravy.mean
PLF_28228_00001927
Potential queD like 2
 $r = -0.696$, $p = 10^{-7.262}$

feature.plfam_id.gravy.mean

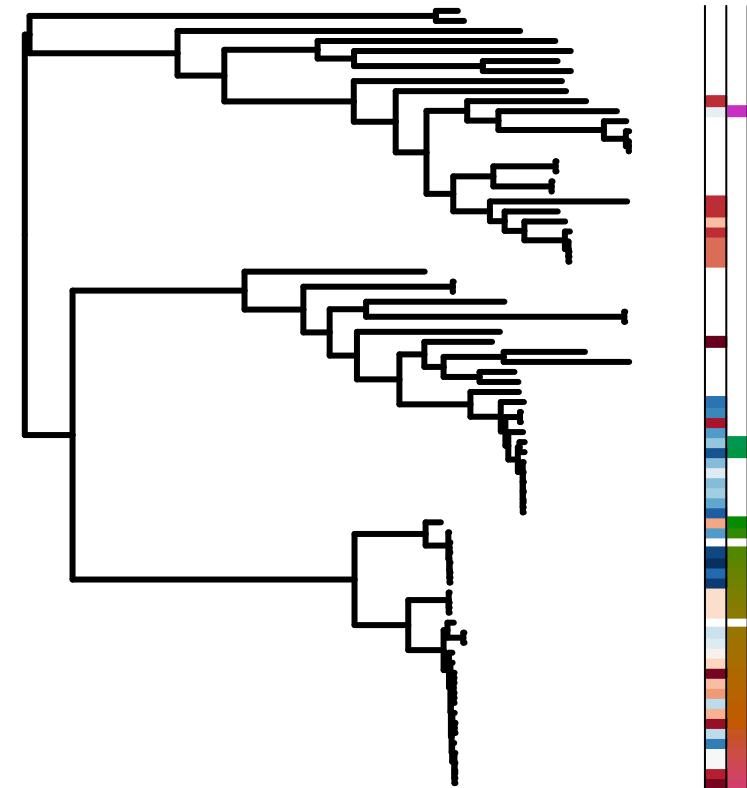
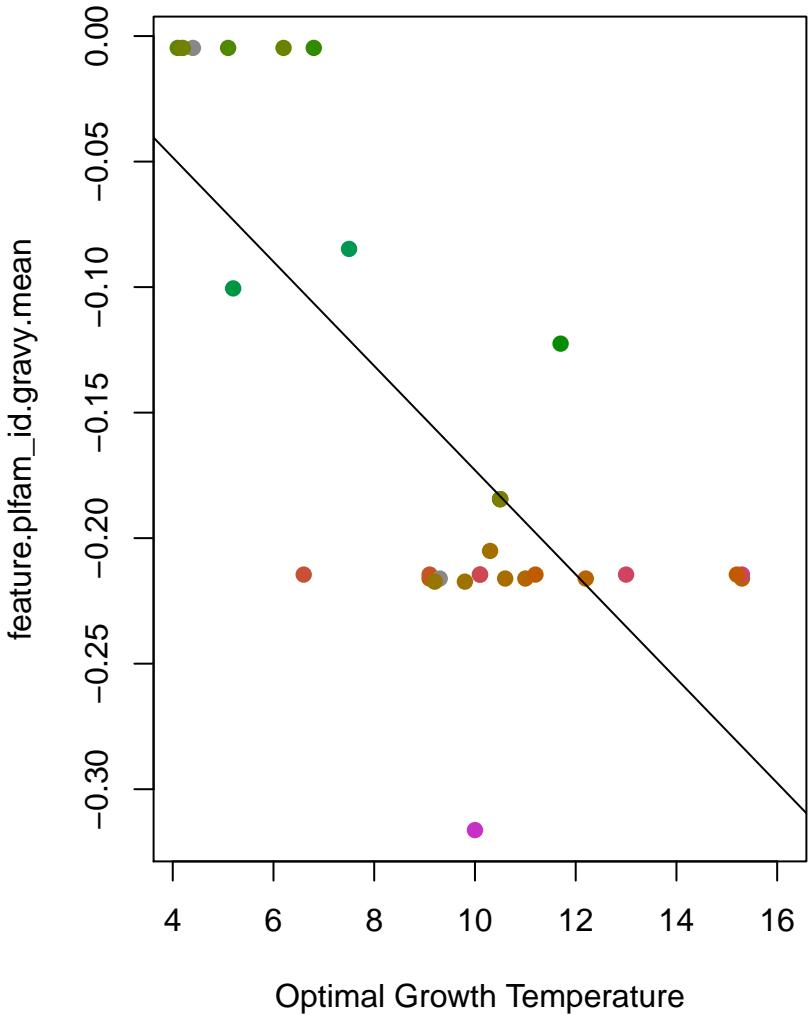


feature.plfam_id.gravy.mean
PLF_28228_00028047
Fatty acid cis/trans isomerase
 $r = -0.705$, $p = 10^{-5.483}$



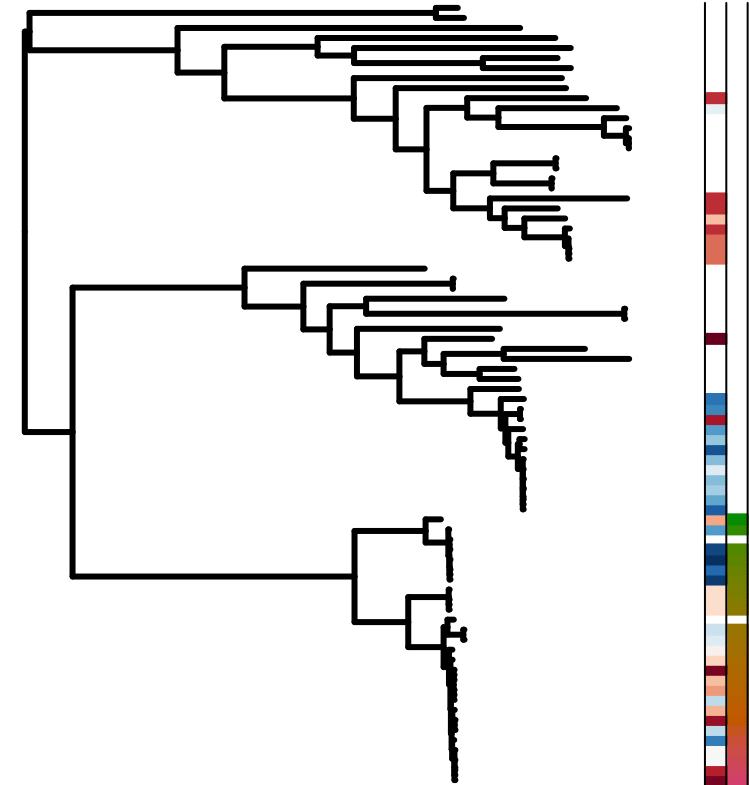
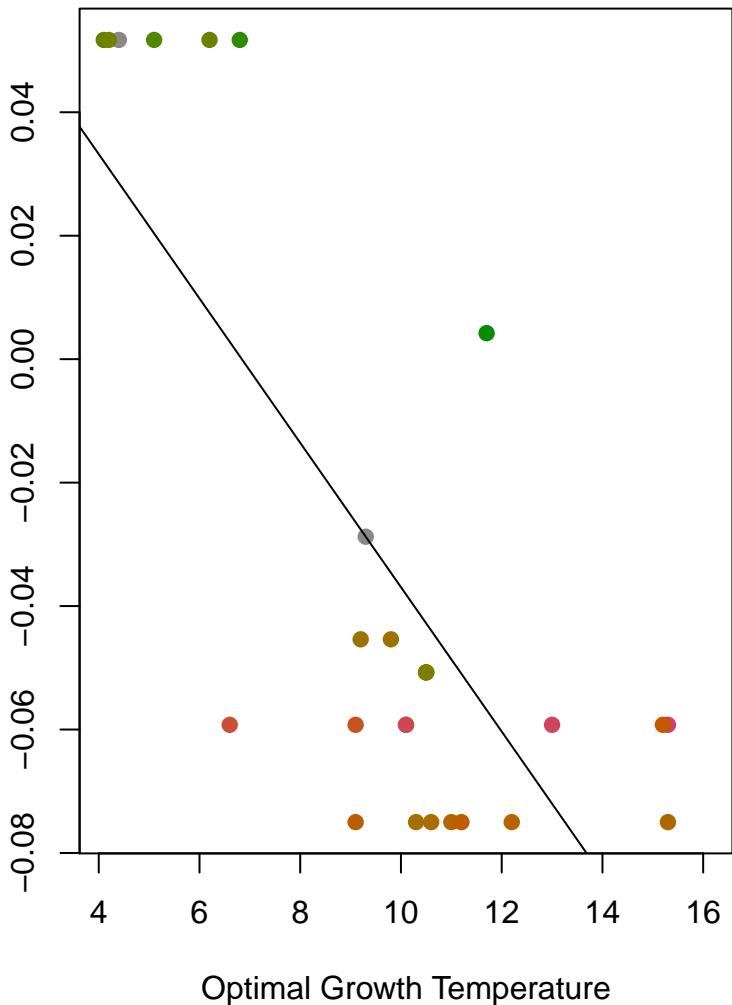


feature.plfam_id.gravy.mean
PLF_28228_00008631
hypothetical protein
 $r = -0.73, p = 10^{-5.324}$



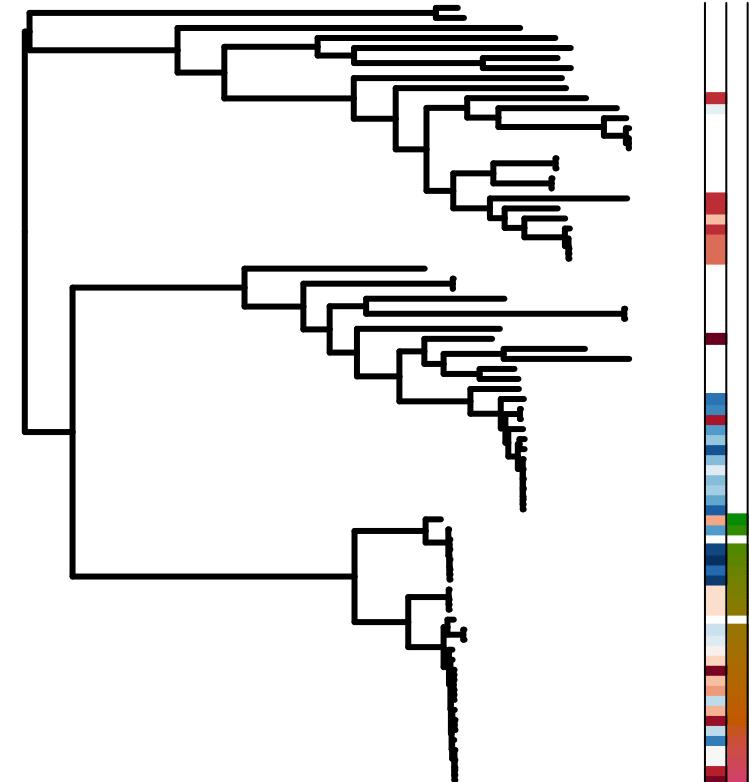
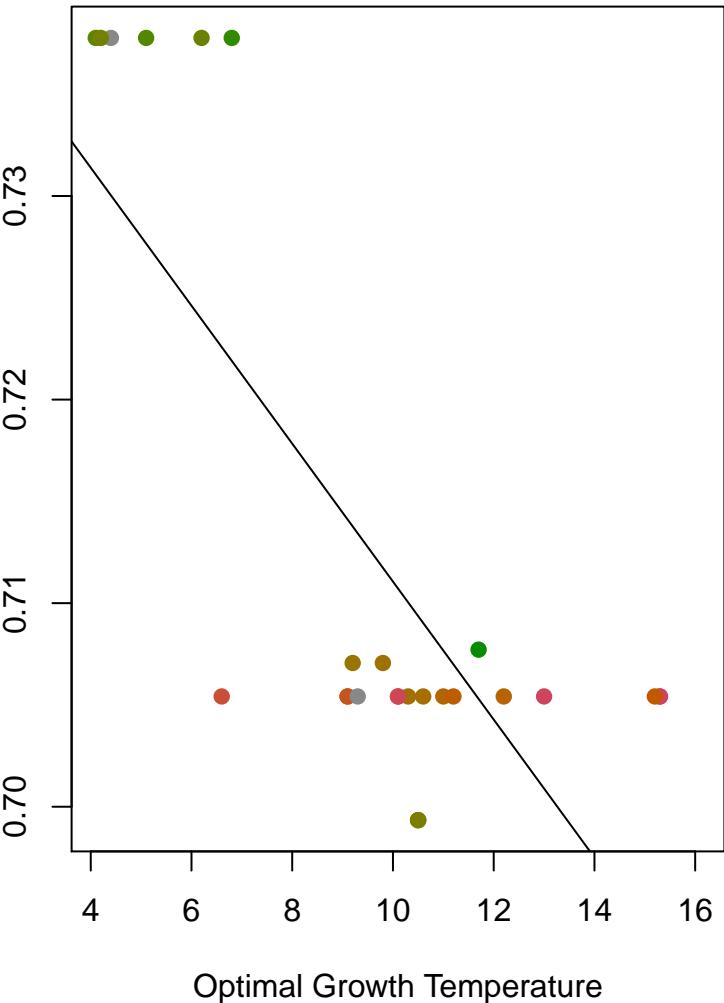
feature.plfam_id.gravy.mean
PLF_28228_00016362
hypothetical protein
 $r = -0.757$, $p = 10^{-5.316}$

feature.plfam_id.gravy.mean

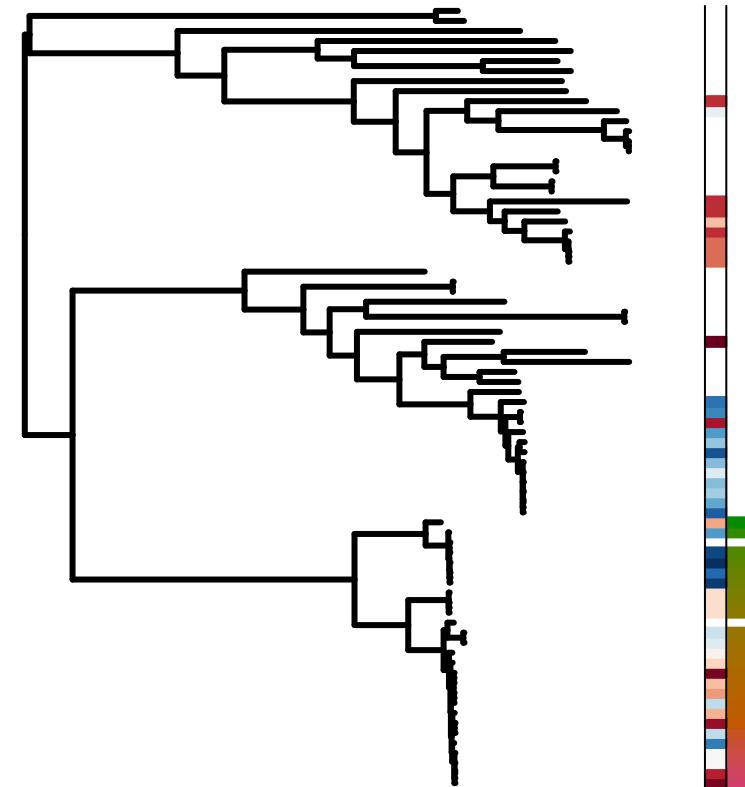
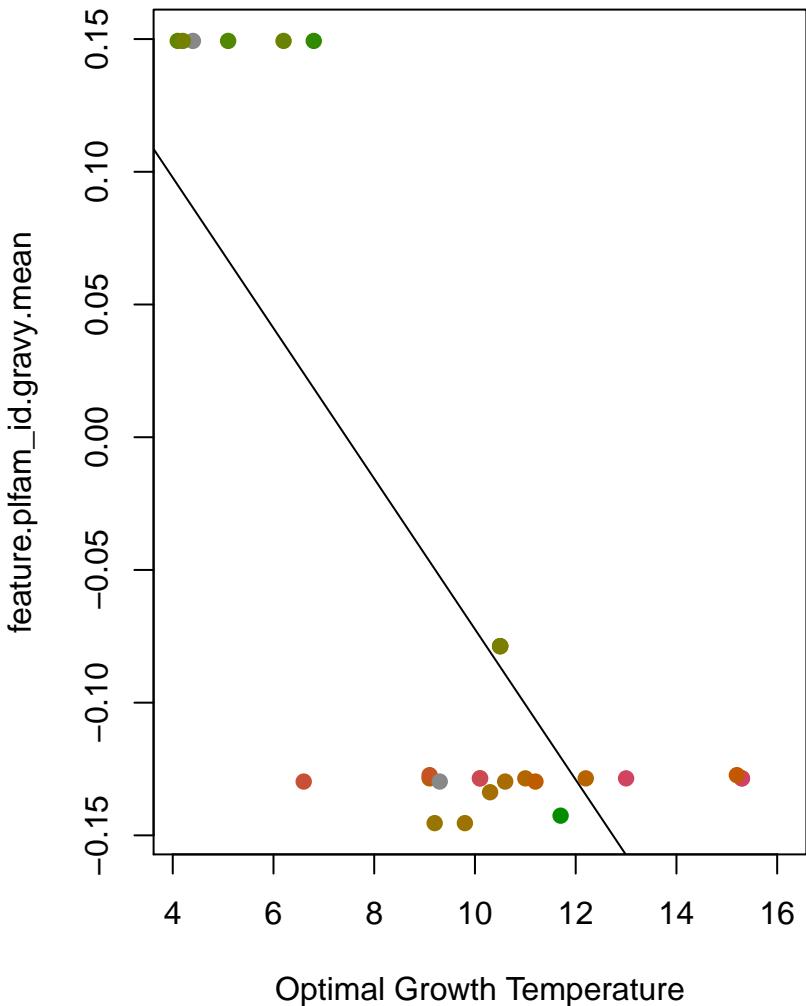


feature.plfam_id.gravy.mean
PLF_28228_00016373
TrkA-C domain protein
 $r = -0.765$, $p = 10^{-5.464}$

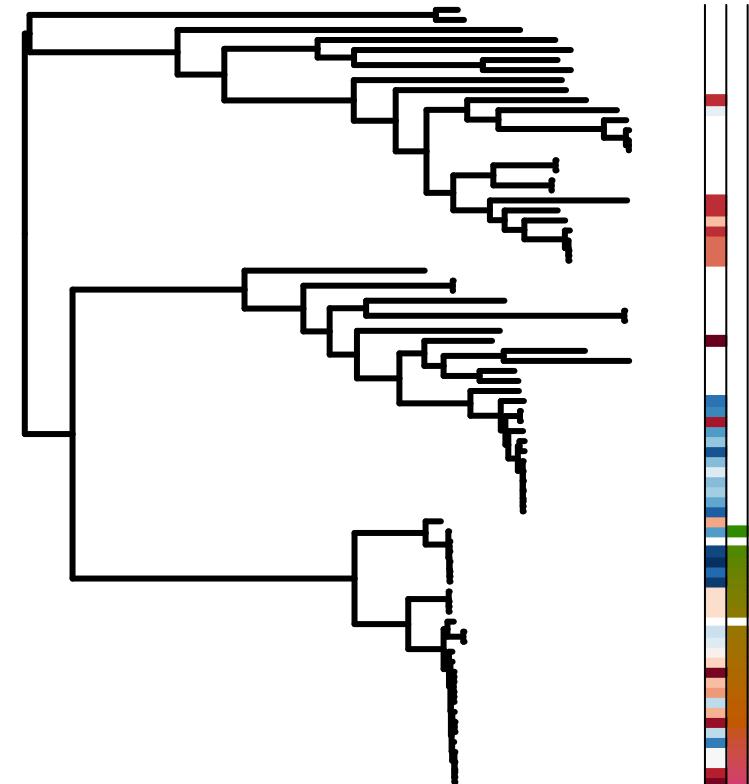
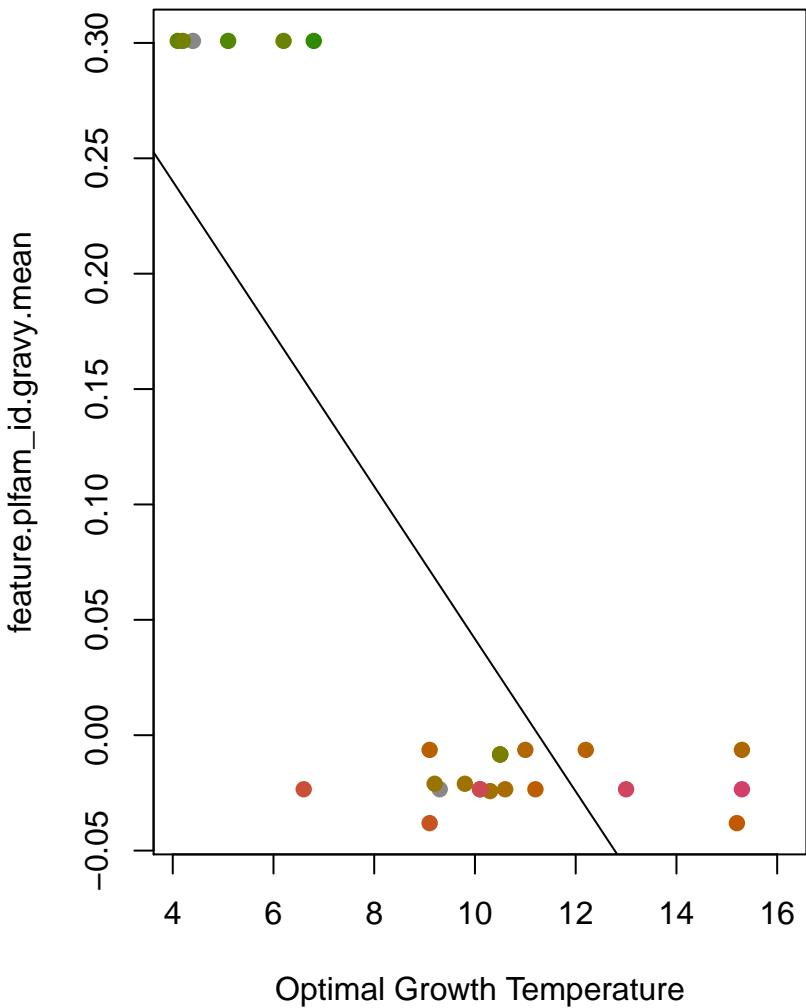
feature.plfam_id.gravy.mean



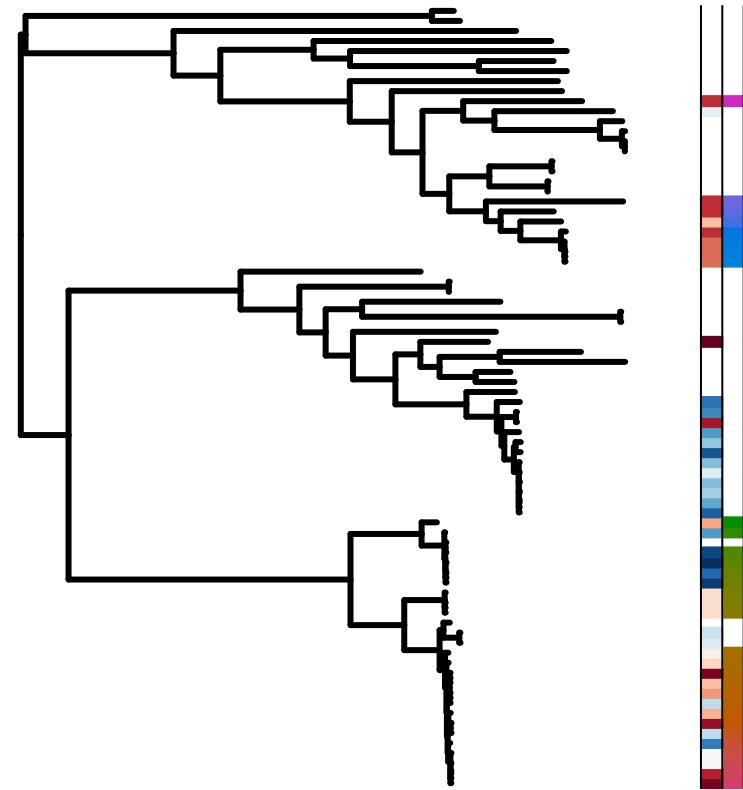
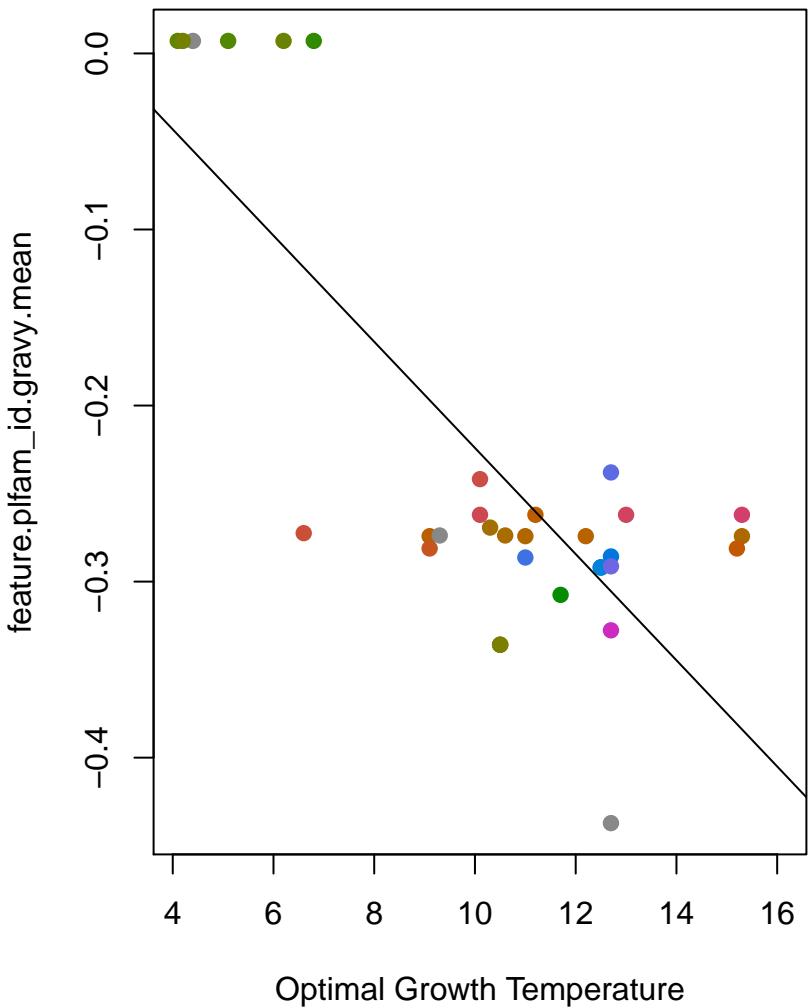
feature.plfam_id.gravy.mean
PLF_28228_00031426
hypothetical protein
 $r = -0.771$, $p = 10^{-5.602}$



feature.plfam_id.gravy.mean
PLF_28228_00030076
hypothetical protein
 $r = -0.773$, $p = 10^{-5.439}$

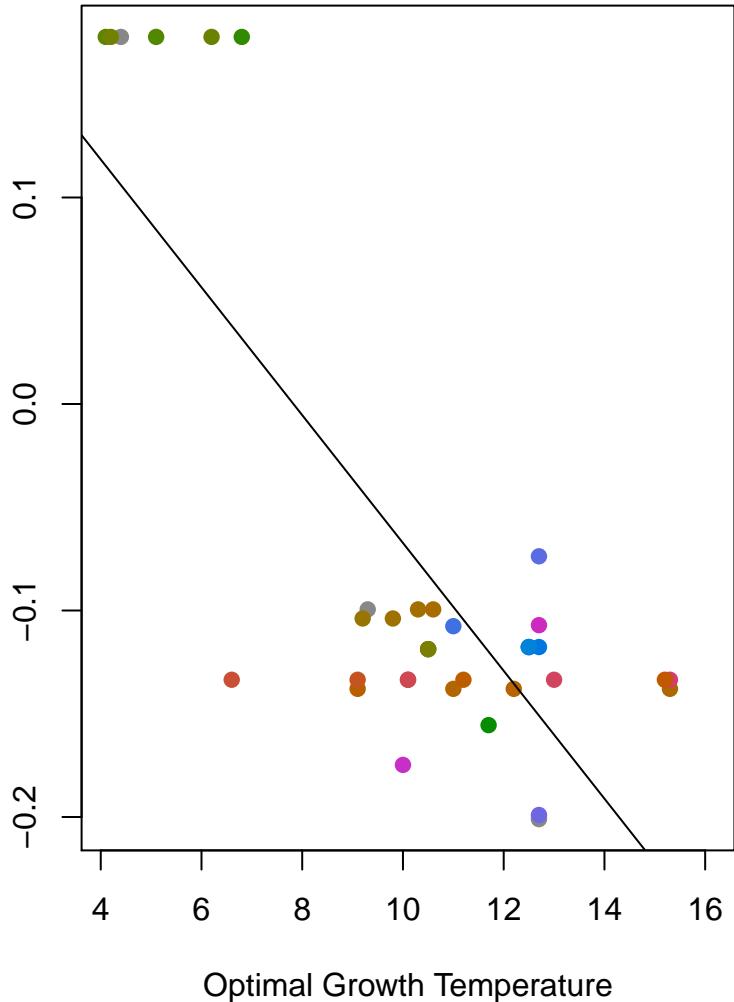


feature.plfam_id.gravy.mean
PLF_28228_00002829
TonB-dependent receptor
 $r = -0.778$, $p = 10^{-7.226}$

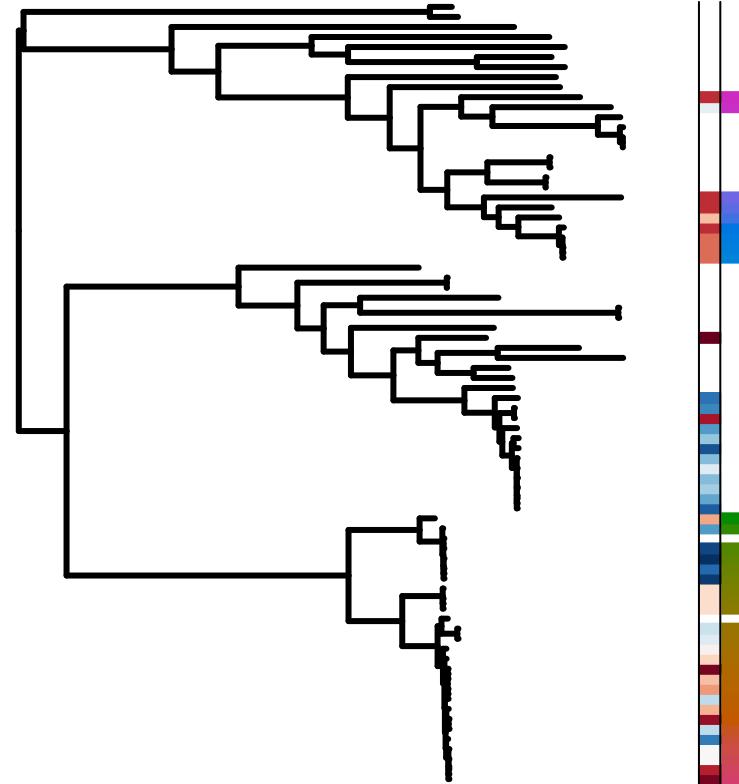


feature.plfam_id.gravy.mean
PLF_28228_00001024
Putative NAD(P)H nitroreductase YdjA
 $r = -0.786$, $p = 10^{-8.097}$

feature.plfam_id.gravy.mean

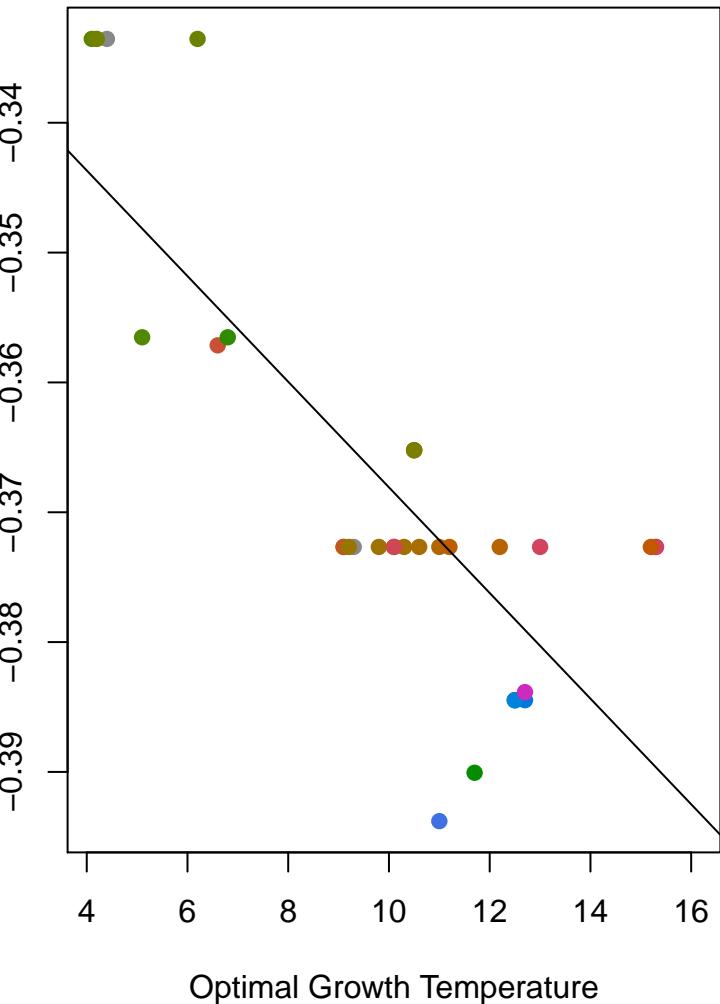


Optimal Growth Temperature

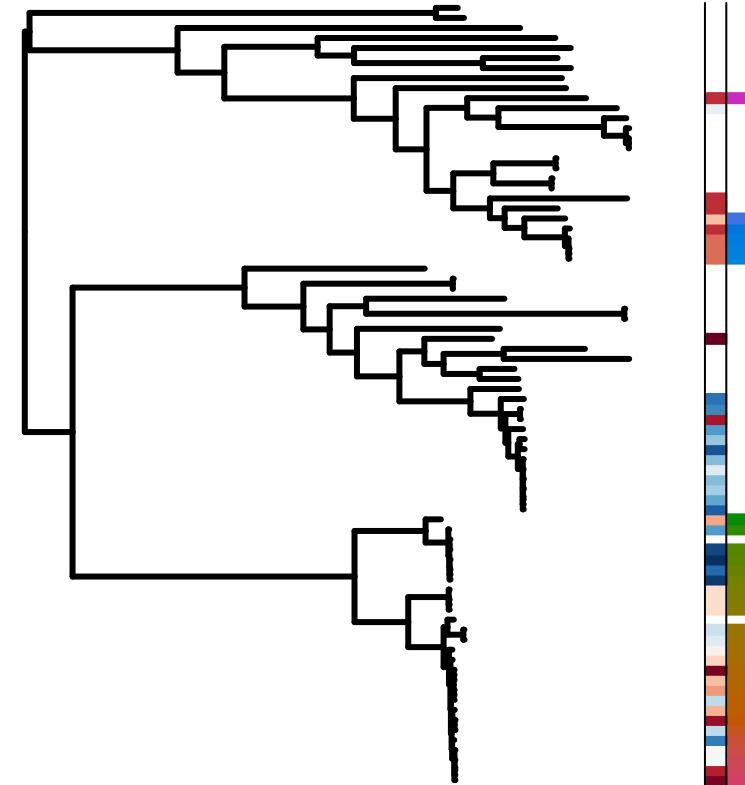


feature.plfam_id.gravy.mean
PLF_28228_00003922
hypothetical protein
 $r = -0.789$, $p = 10^{-7.31}$

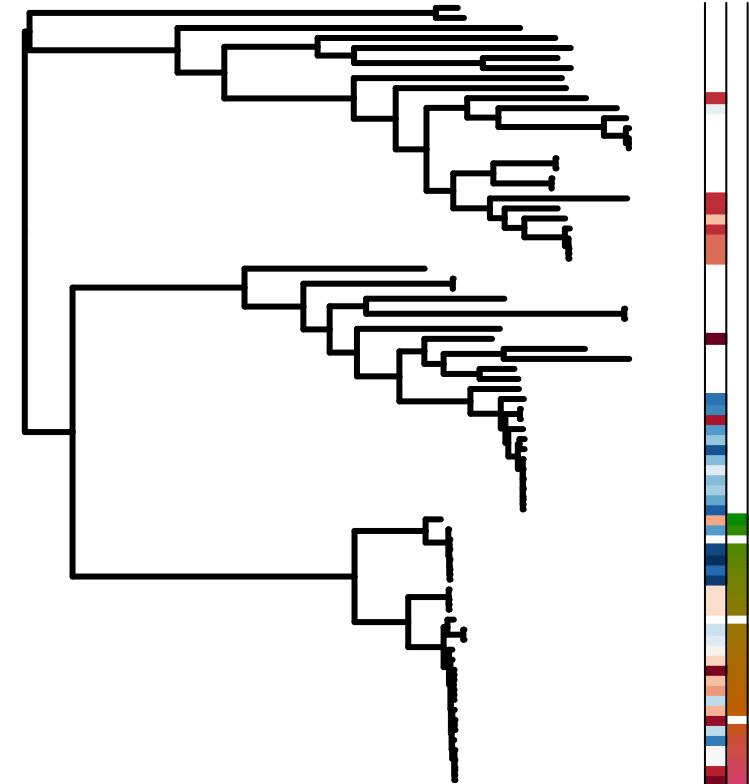
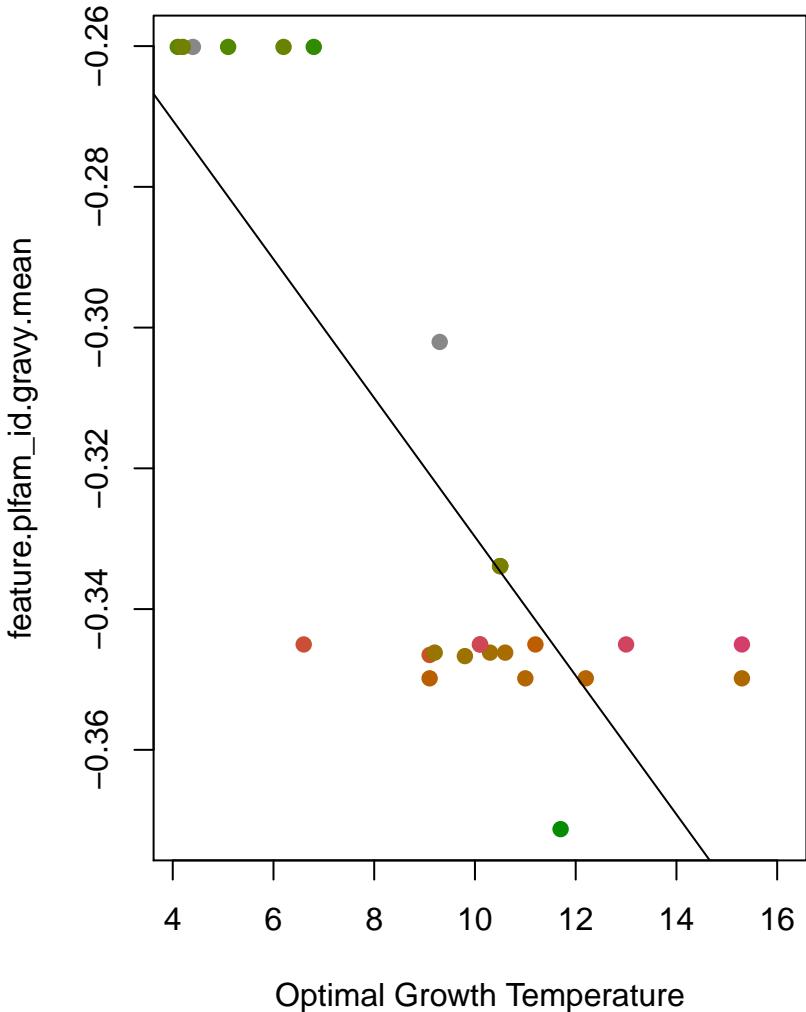
feature.plfam_id.gravy.mean



Optimal Growth Temperature



feature.plfam_id.gravy.mean
PLF_28228_00017455
Maltodextrin glucosidase (EC 3.2.1.20)
 $r = -0.8$, $p = 10^{-6.02}$



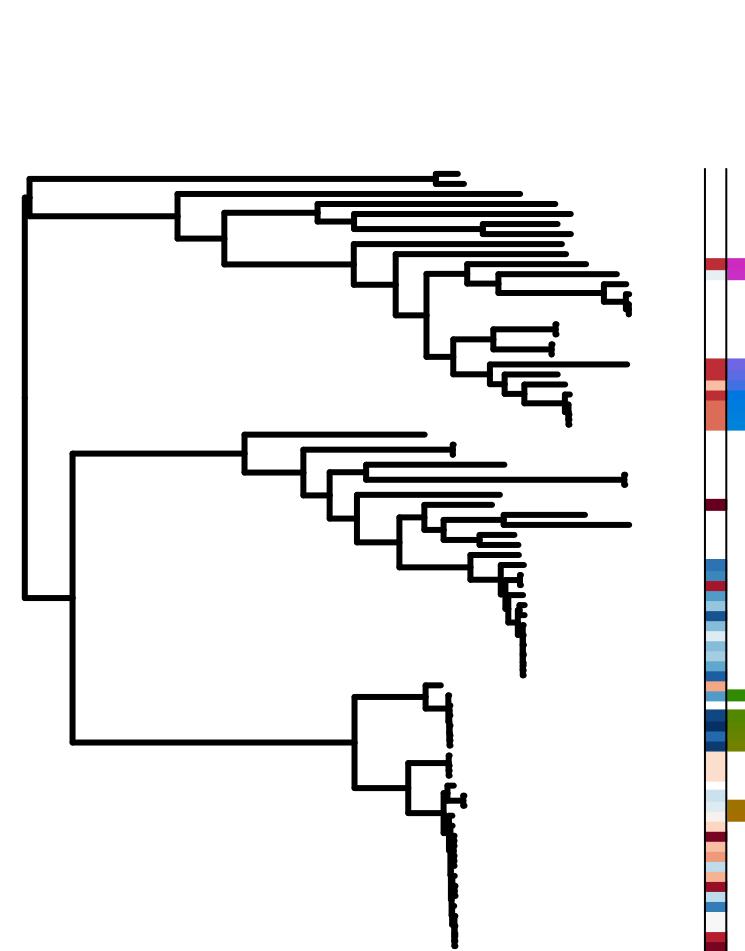
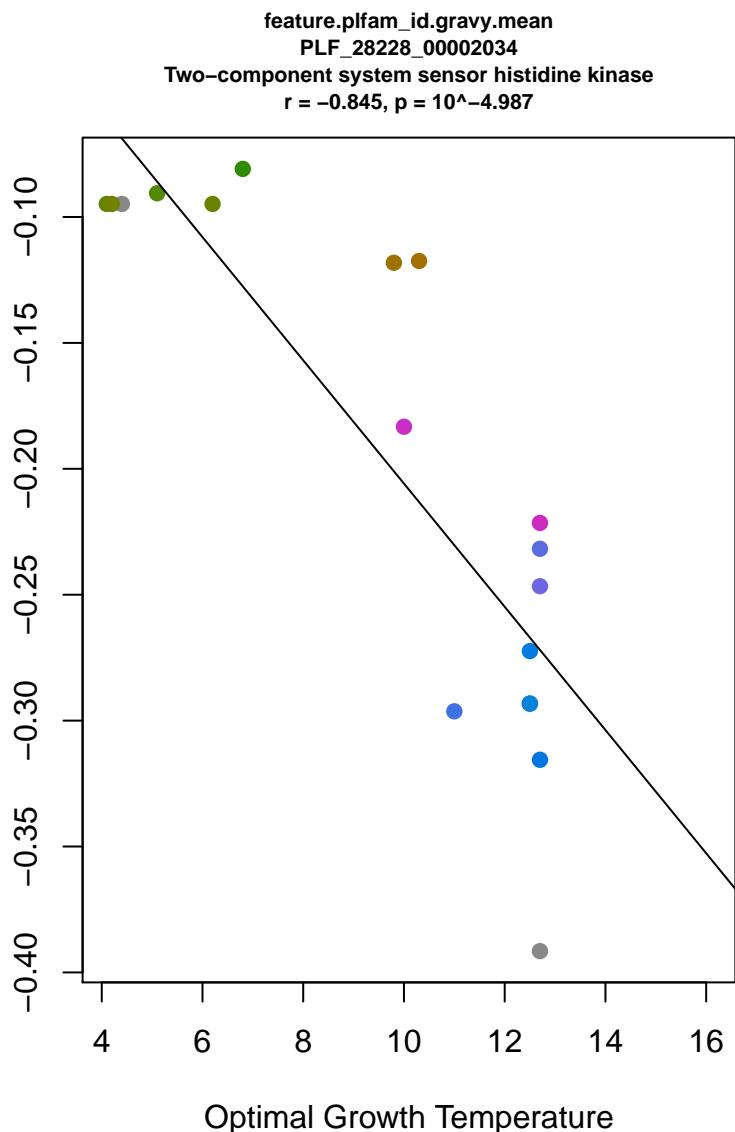
feature.plfam_id.gravy.mean

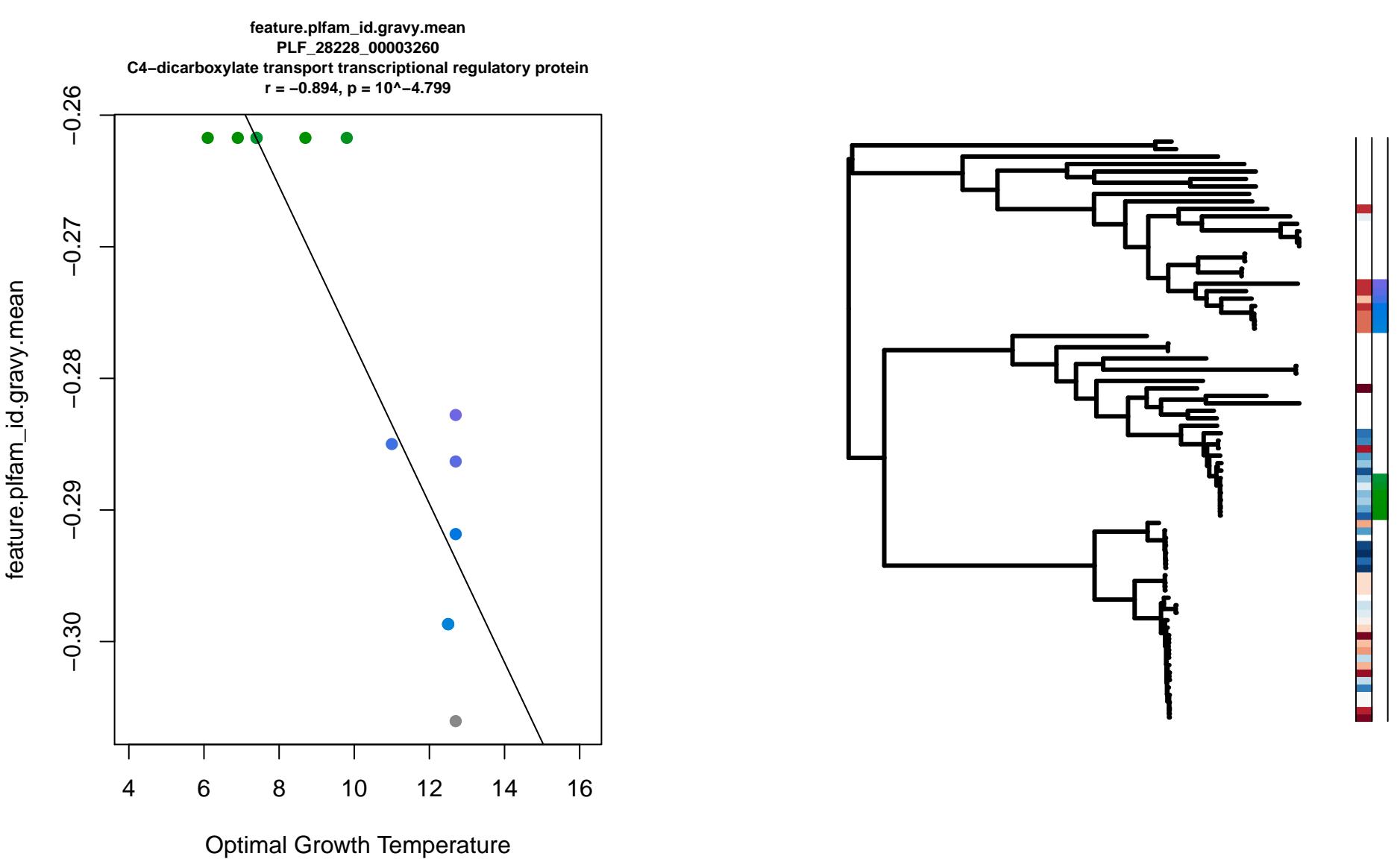
PLF_28228_00002034

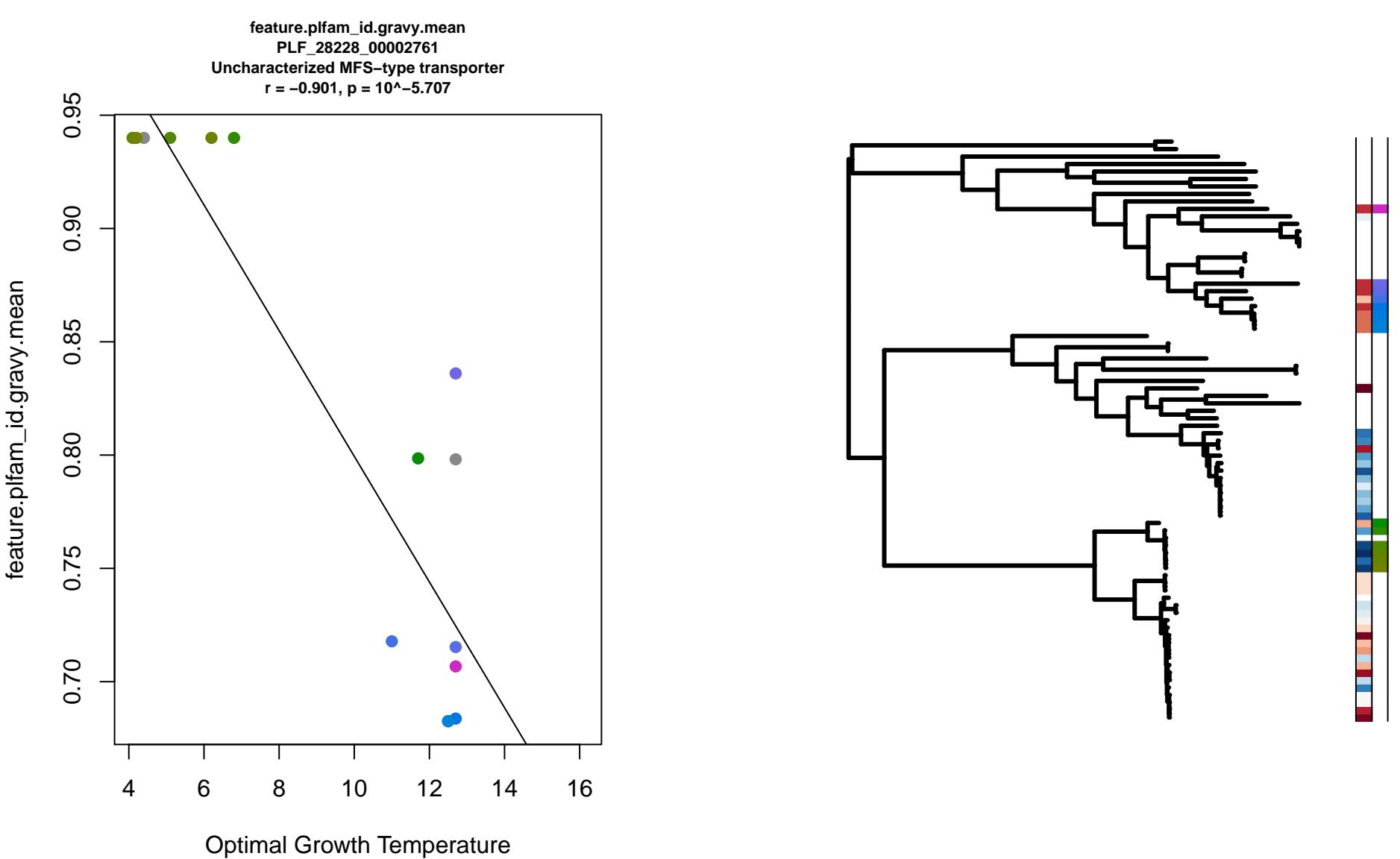
Two-component system sensor histidine kinase

$r = -0.845, p = 10^{-4.987}$

feature.plfam_id.gravy.mean







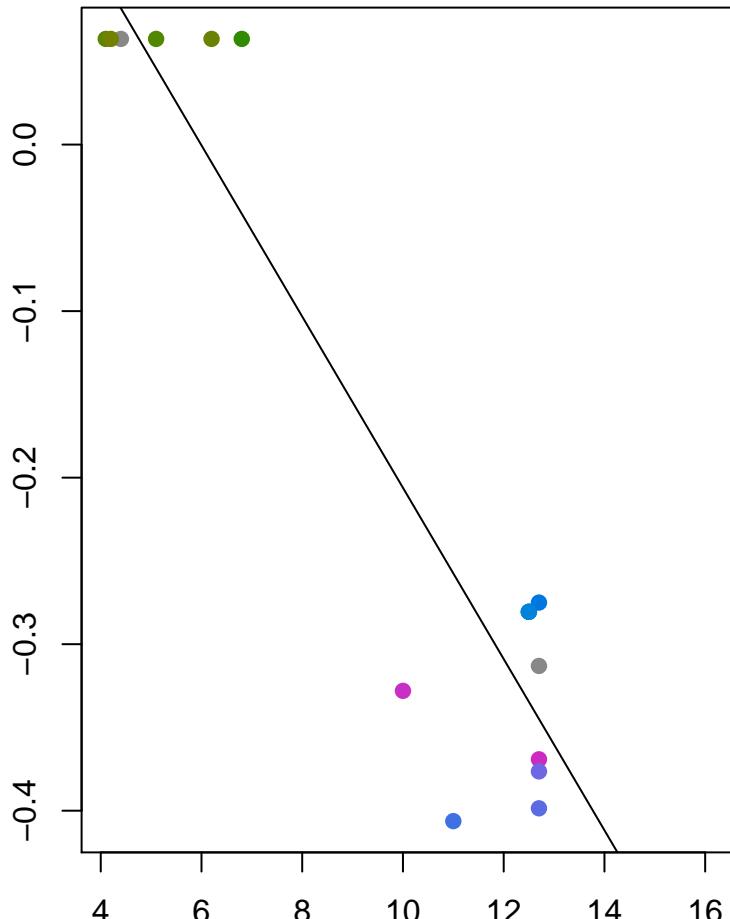
feature.plfam_id.gravy.mean

PLF_28228_00001794

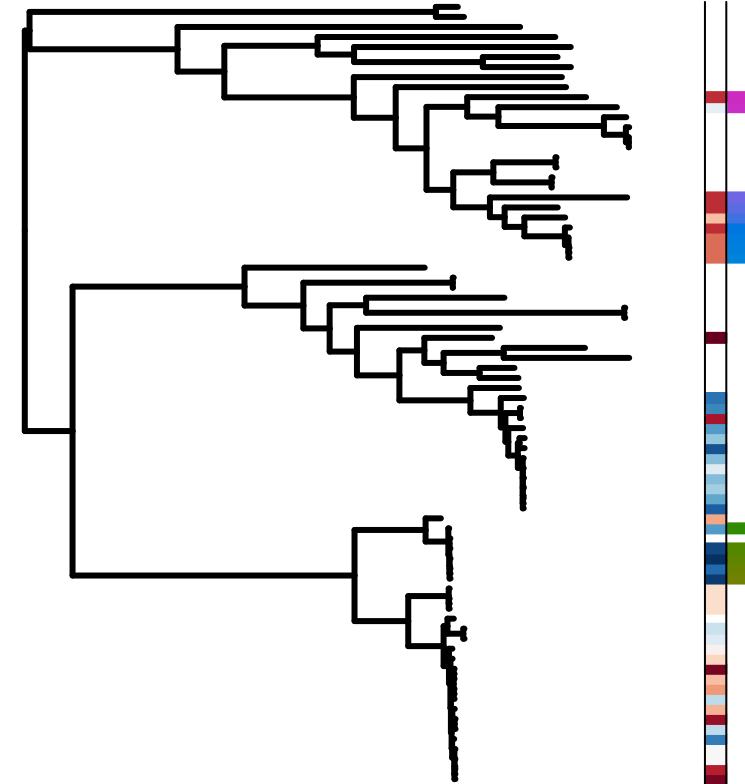
Outer membrane beta-barrel assembly protein BamE

$r = -0.936$, $p = 10^{-7.004}$

feature.plfam_id.gravy.mean

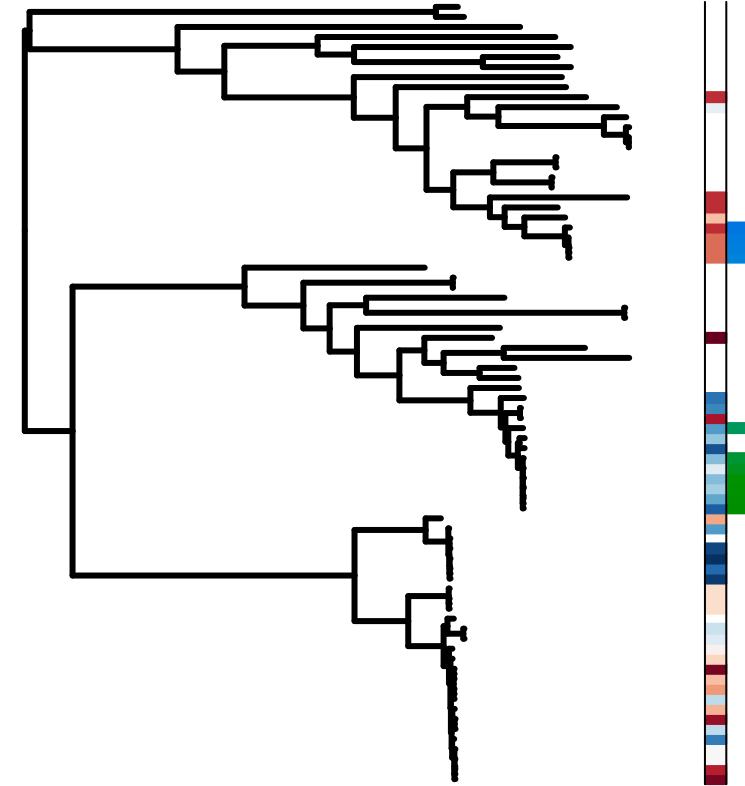
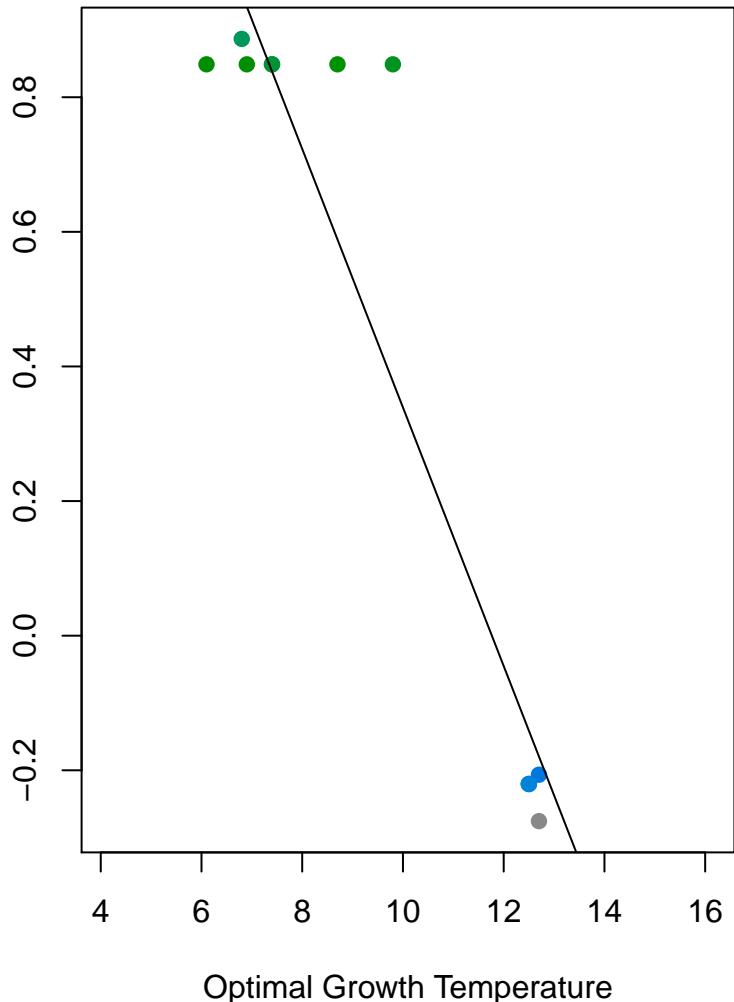


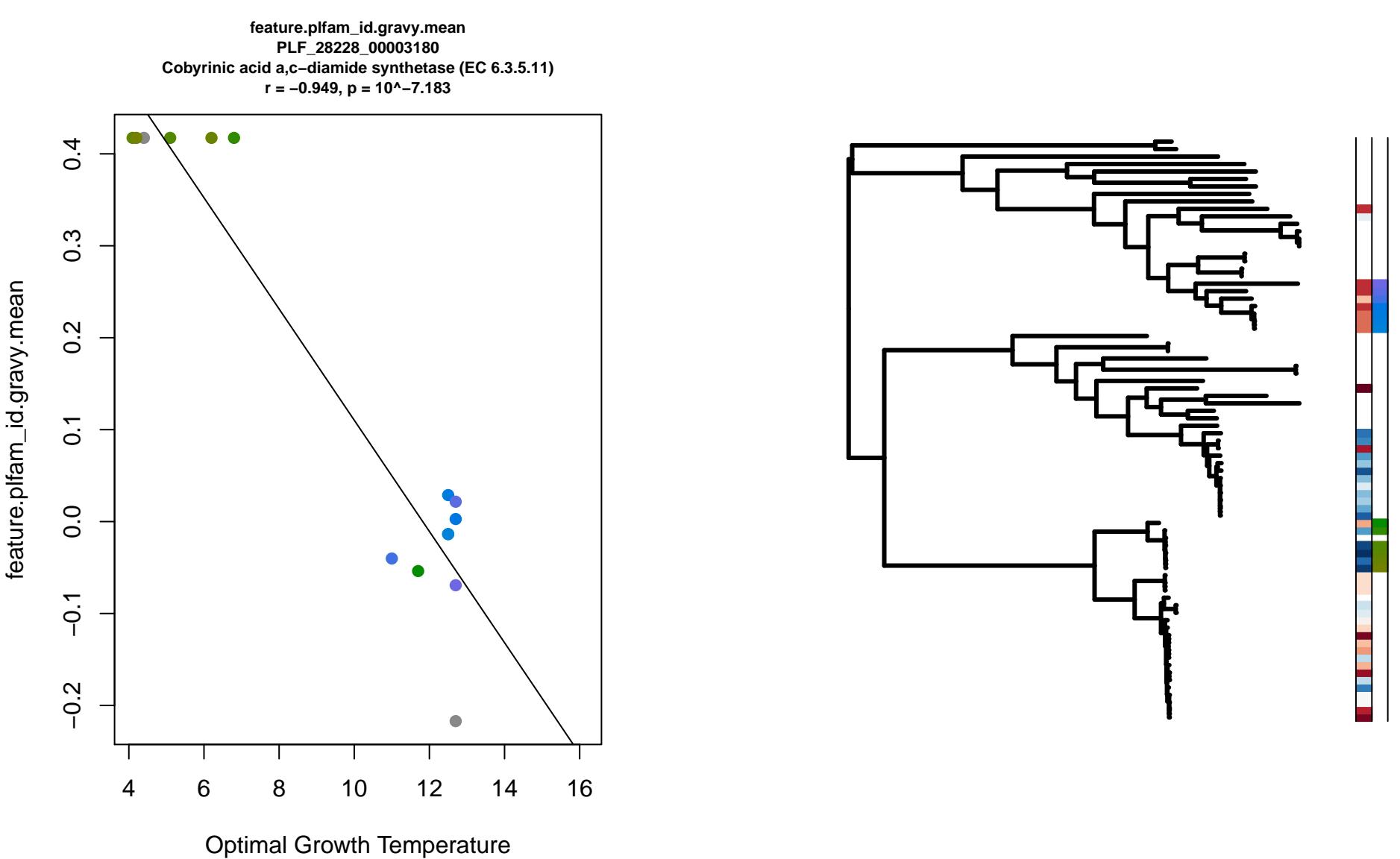
Optimal Growth Temperature



feature.plfam_id.gravy.mean
PLF_28228_00007748
EAL domain protein
 $r = -0.942$, $p = 10^{-5.316}$

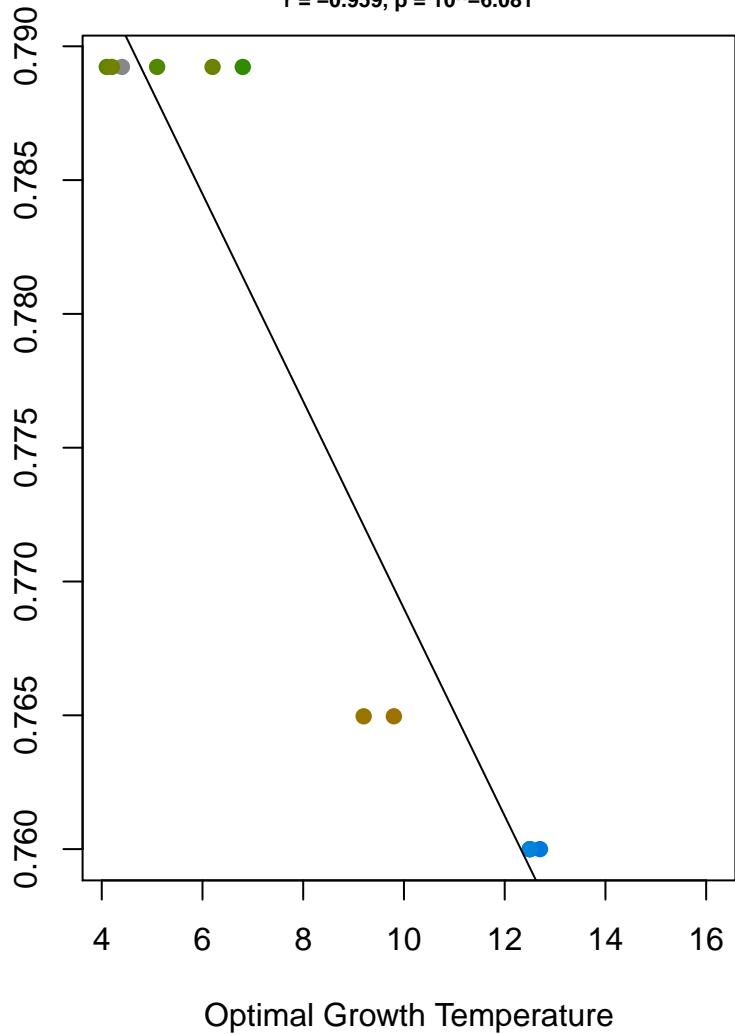
feature.plfam_id.gravy.mean



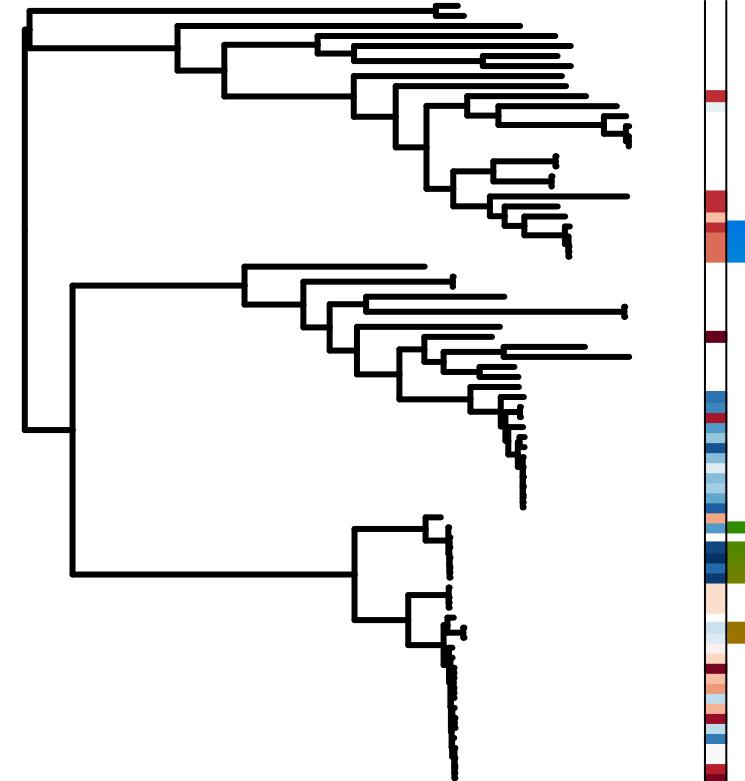


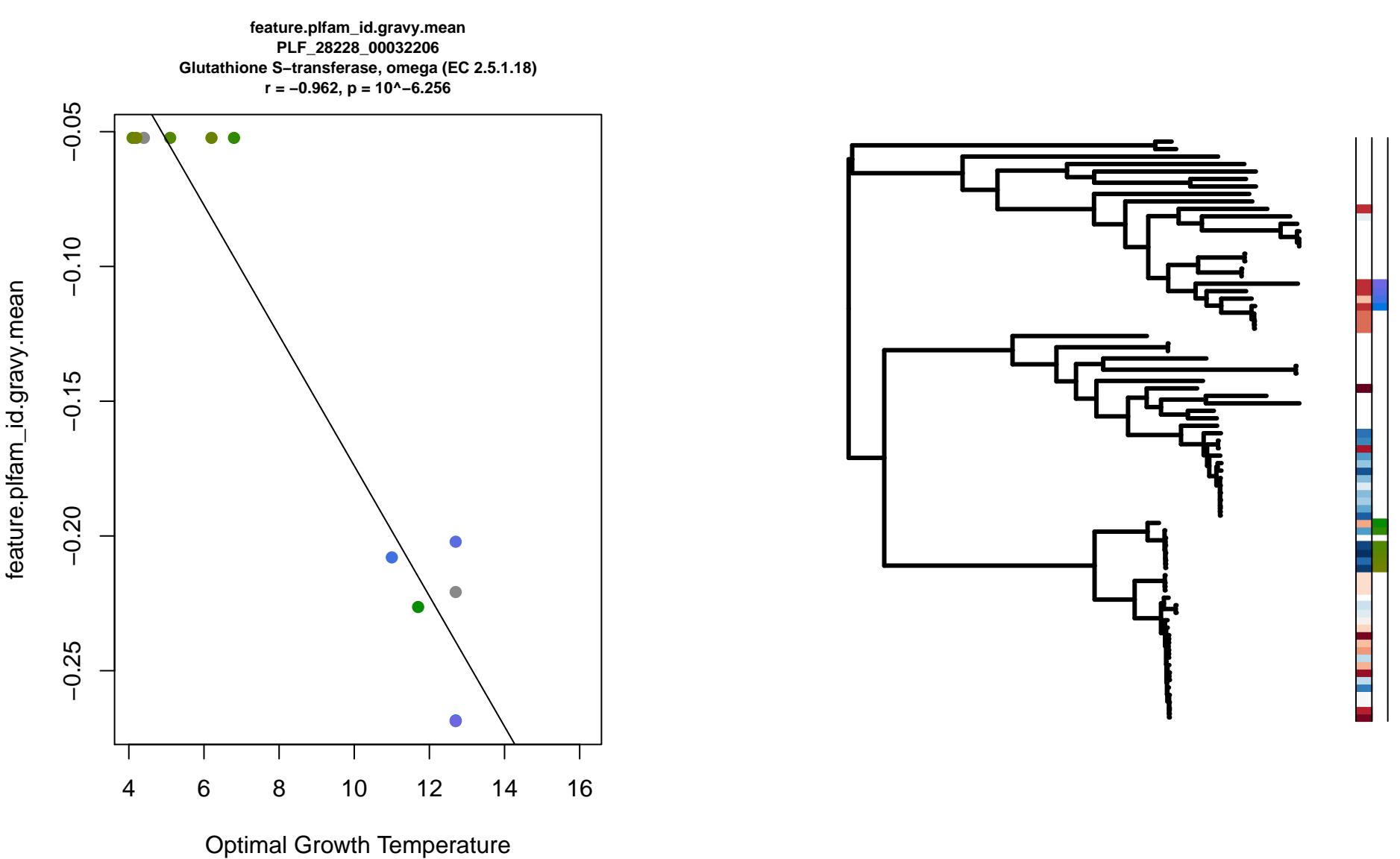
feature.plfam_id.gravy.mean
PLF_28228_00004005
hypothetical protein
 $r = -0.959$, $p = 10^{-6.081}$

feature.plfam_id.gravy.mean



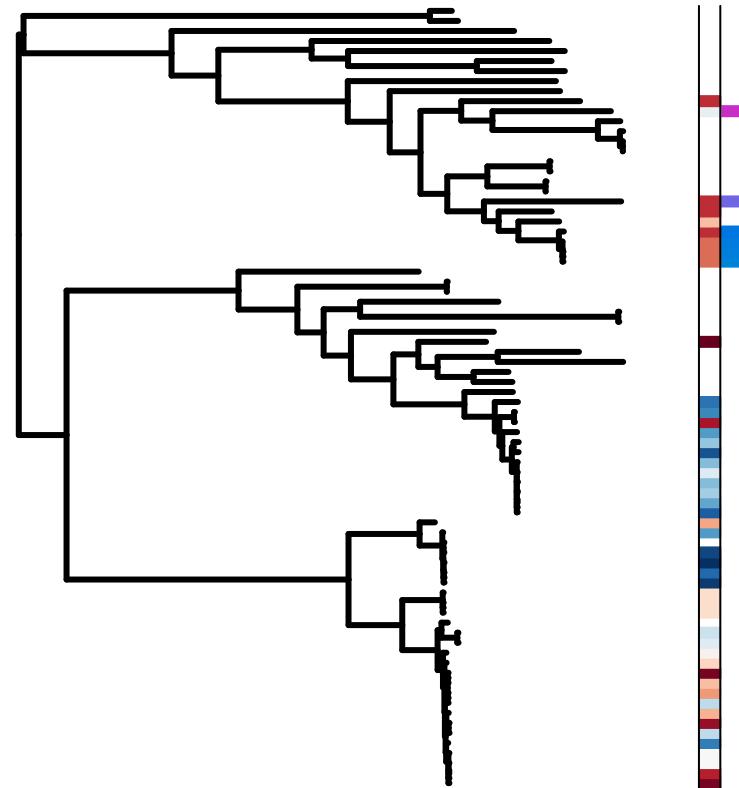
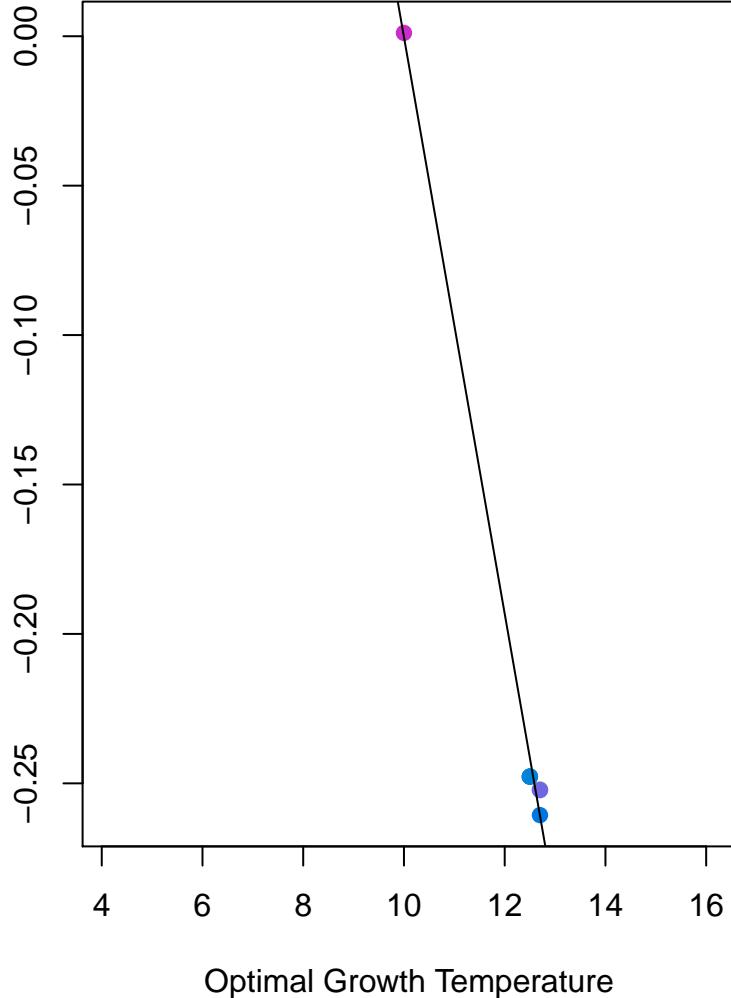
Optimal Growth Temperature

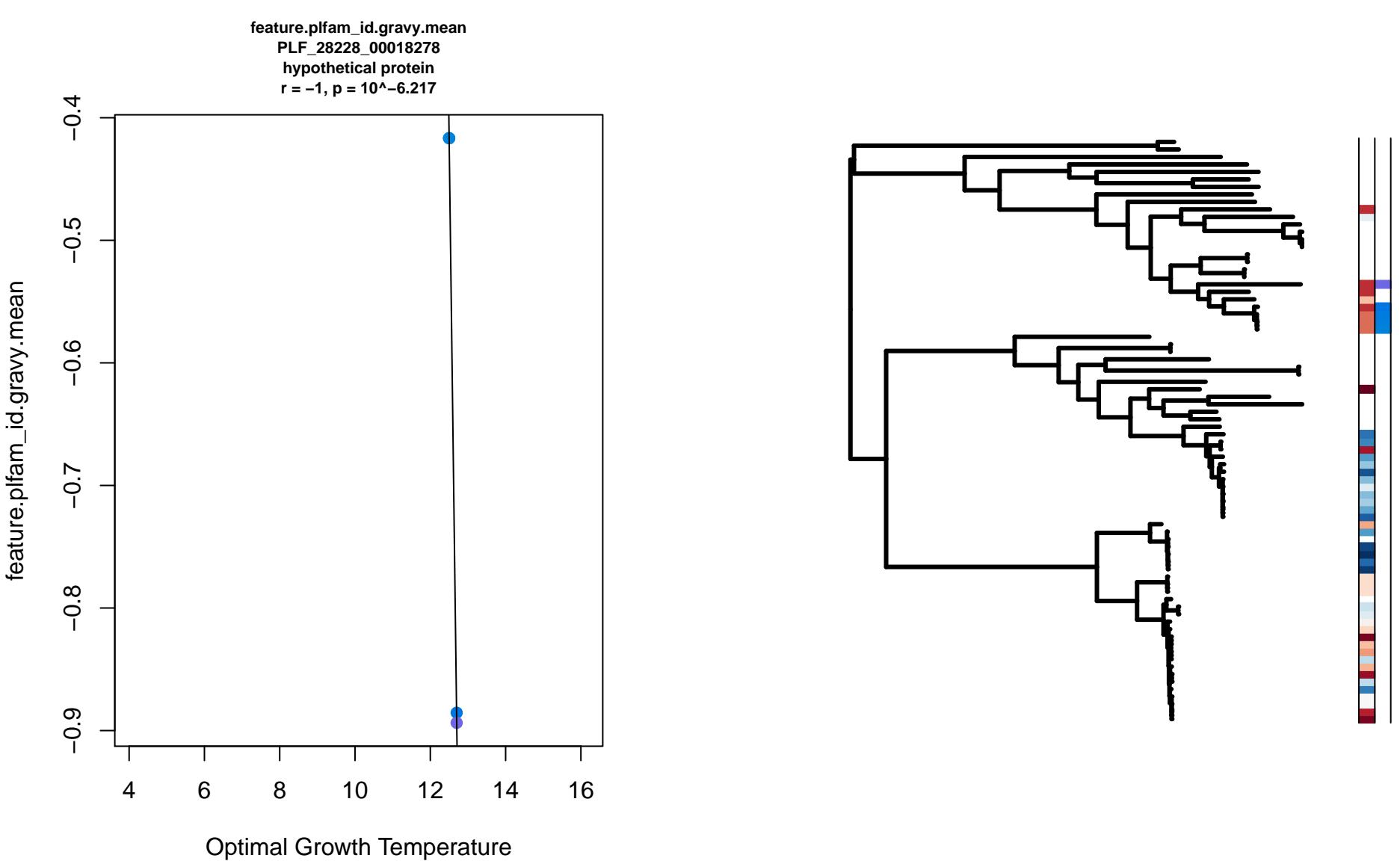




feature.plfam_id.gravy.mean
PLF_28228_00003946
hypothetical protein
 $r = -0.998$, $p = 10^{-6.246}$

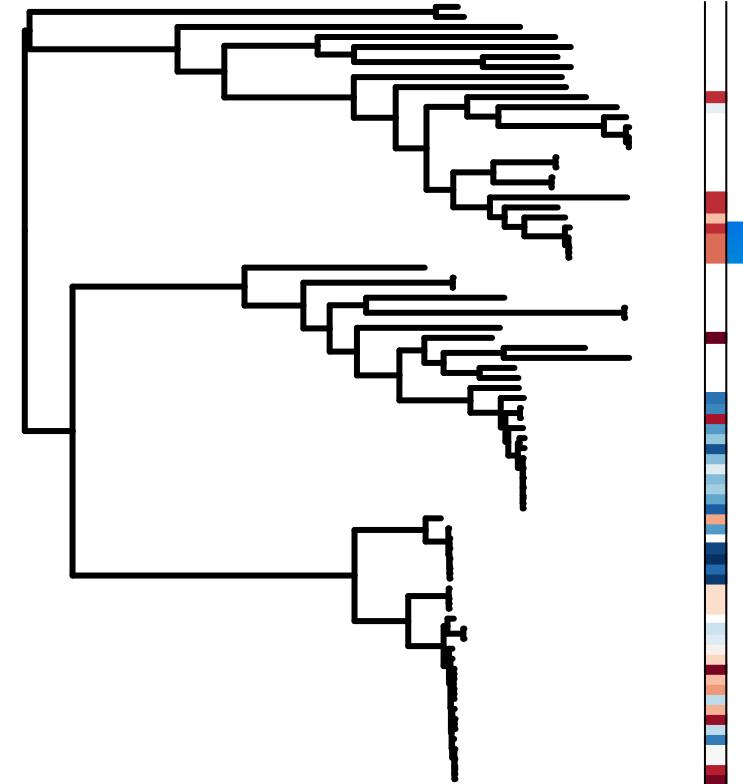
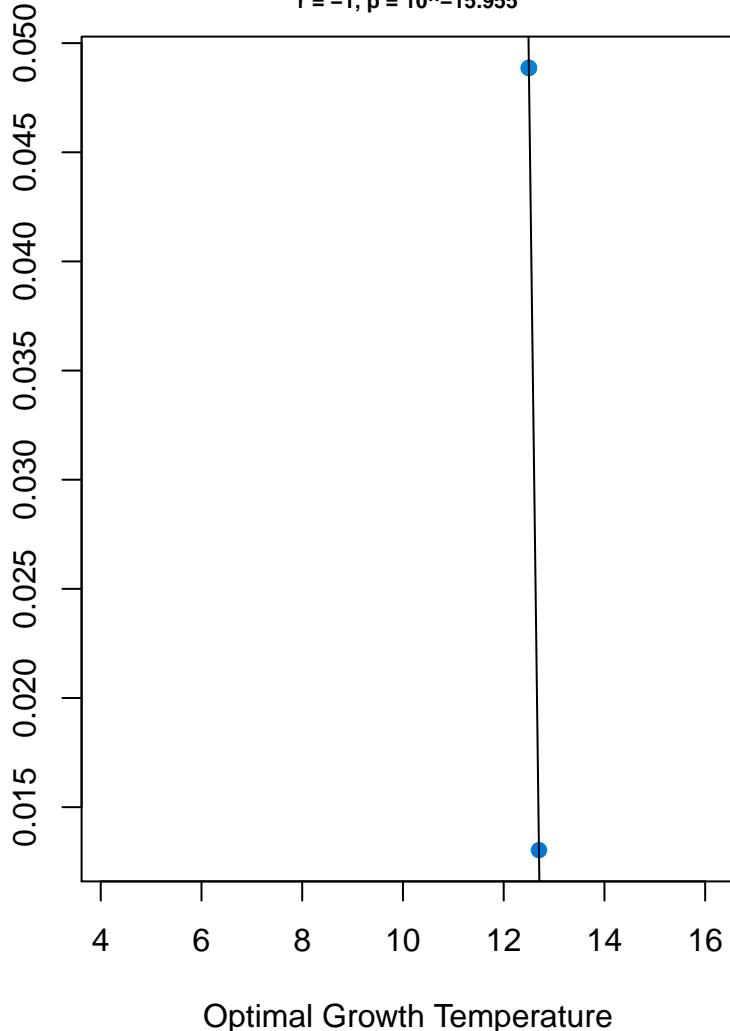
feature.plfam_id.gravy.mean





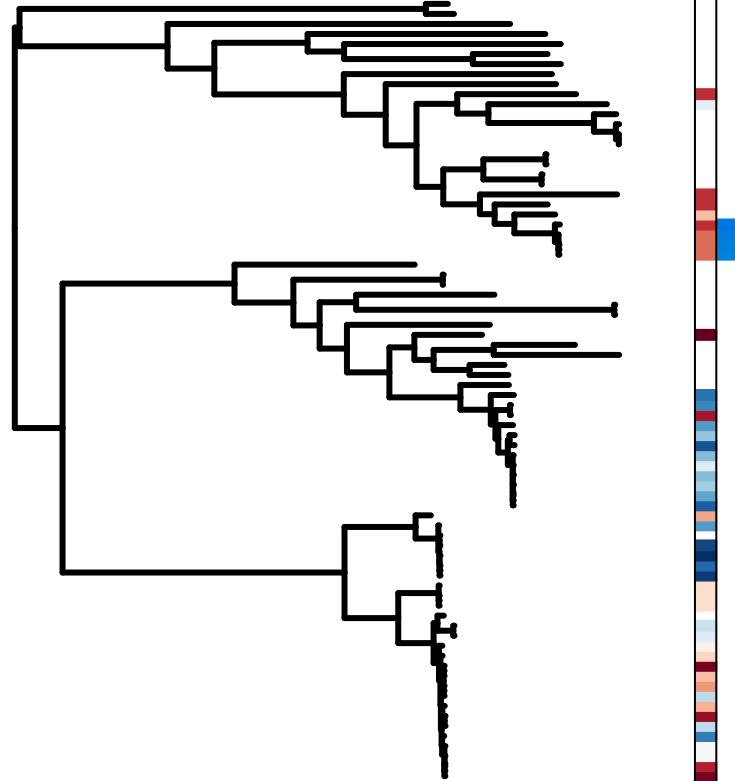
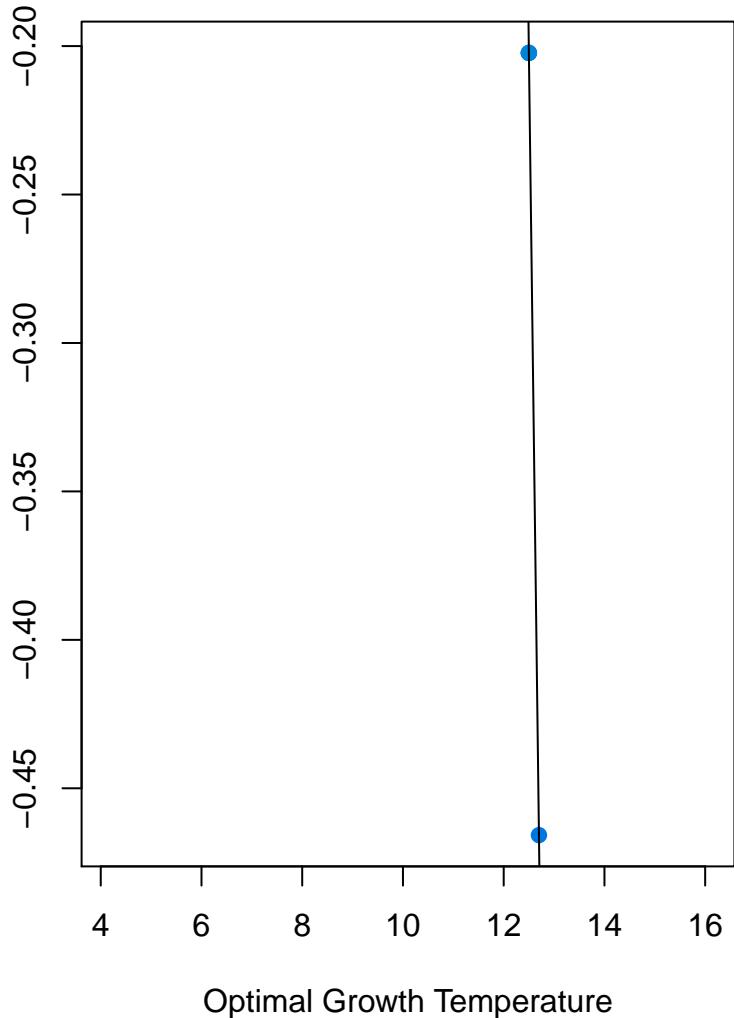
feature.plfam_id.gravy.mean
PLF_28228_00007819
hypothetical protein
 $r = -1$, $p = 10^{-15.955}$

feature.plfam_id.gravy.mean

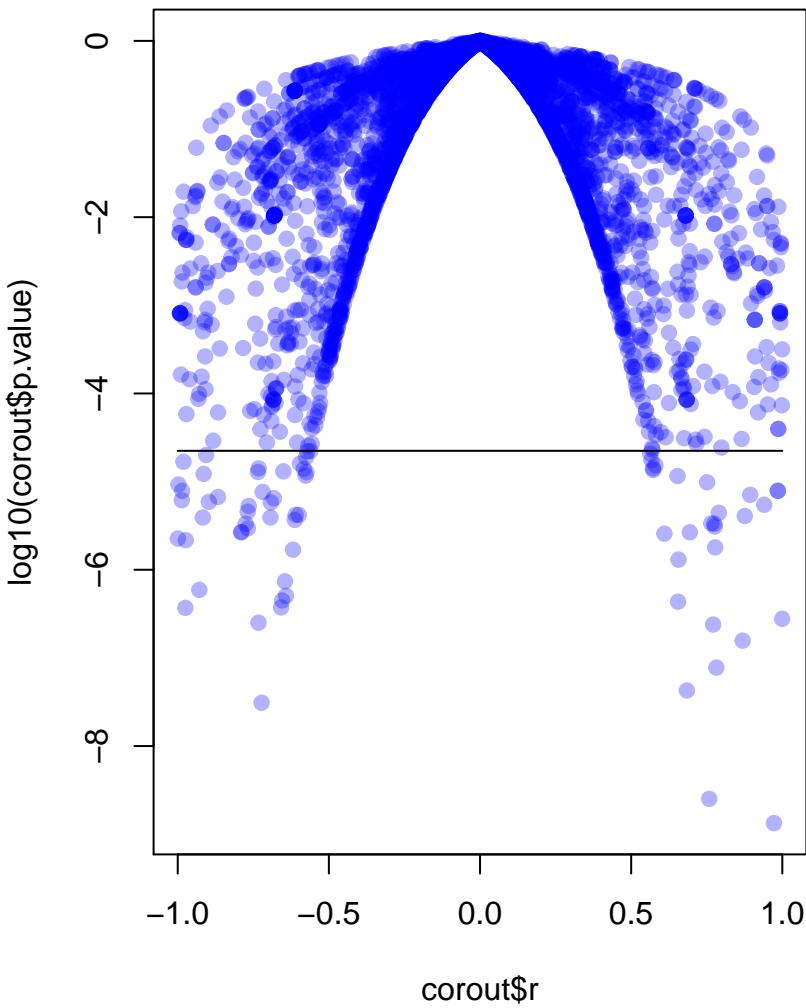


feature.plfam_id.gravy.mean
PLF_28228_00022141
hypothetical protein
 $r = -1$, $p = 10^{-15.955}$

feature.plfam_id.gravy.mean

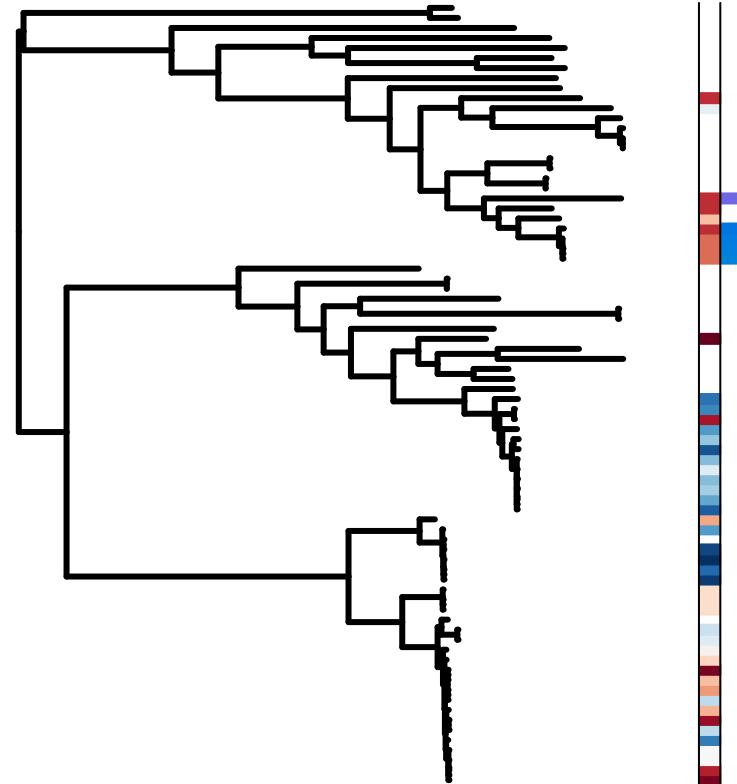
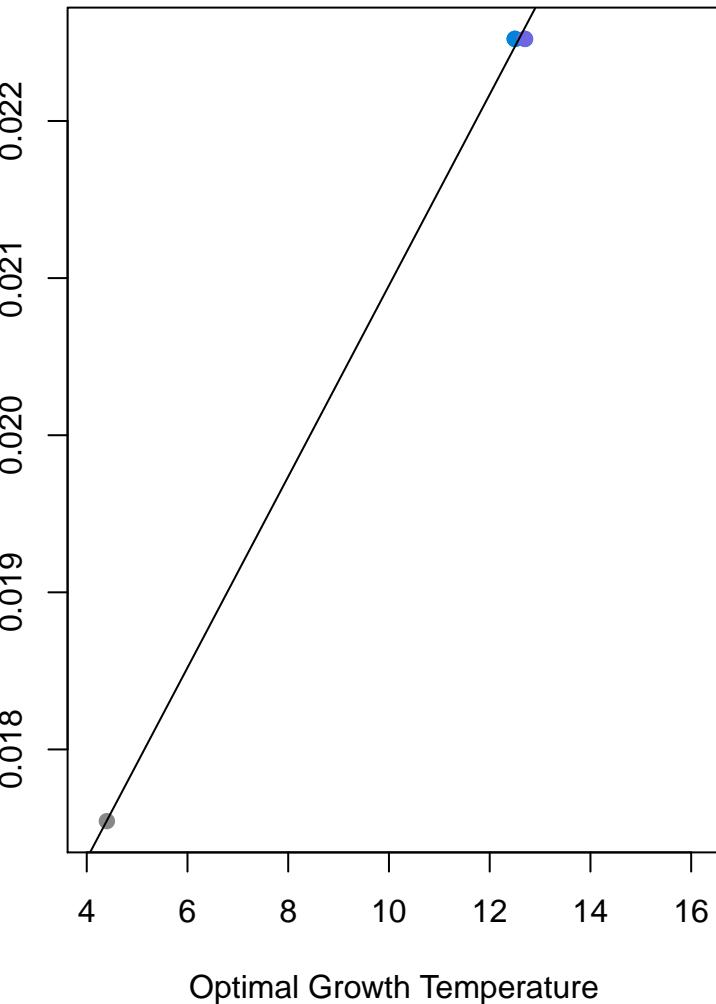


`feature.pgfam_id.proline_residue.mean`



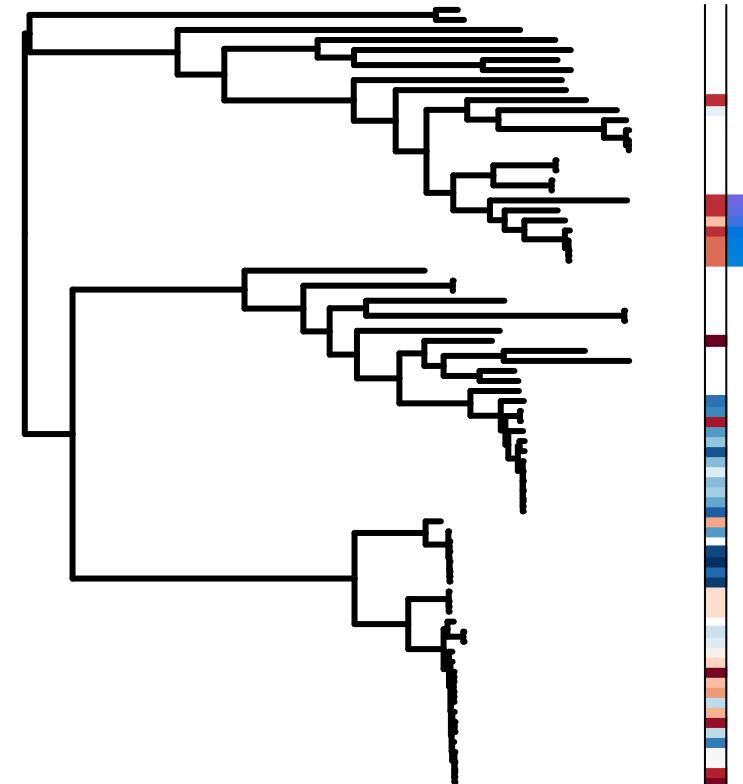
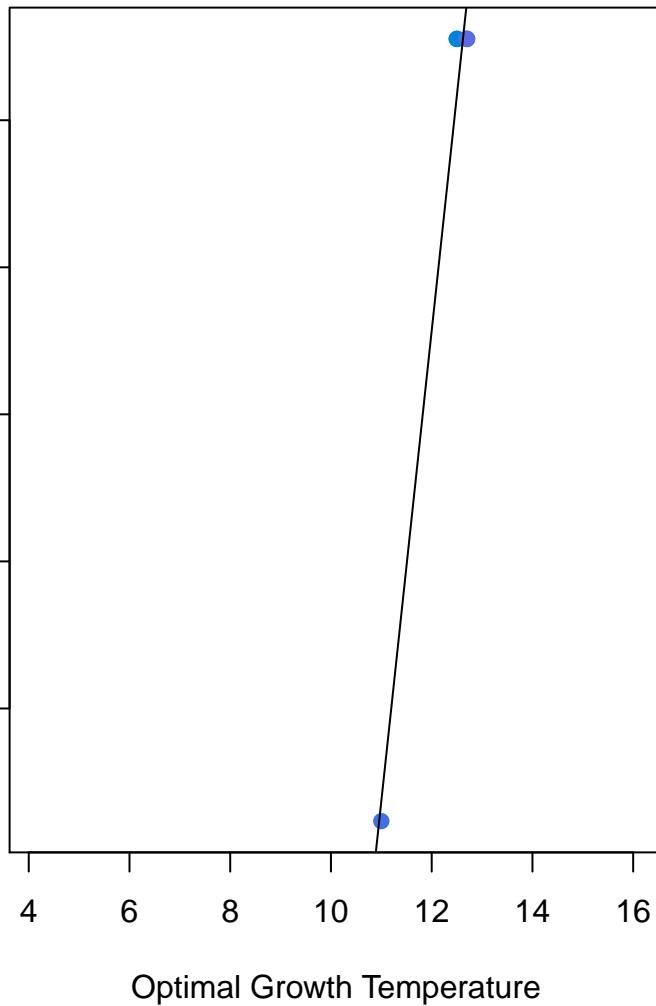
feature.pgfam_id.proline_residue.mean
PGF_06863675
Beta-phosphoglucomutase (EC 5.4.2.6)
 $r = 1$, $p = 10^{-6.557}$

feature.pgfam_id.proline_residue.mean



feature.pgfam_id.proline_residue.mean
PGF_00056170
Tellurite methyltransferase (EC 2.1.1.265)
 $r = 0.985$, $p = 10^{-5.104}$

feature.pgfam_id.proline_residue.mean



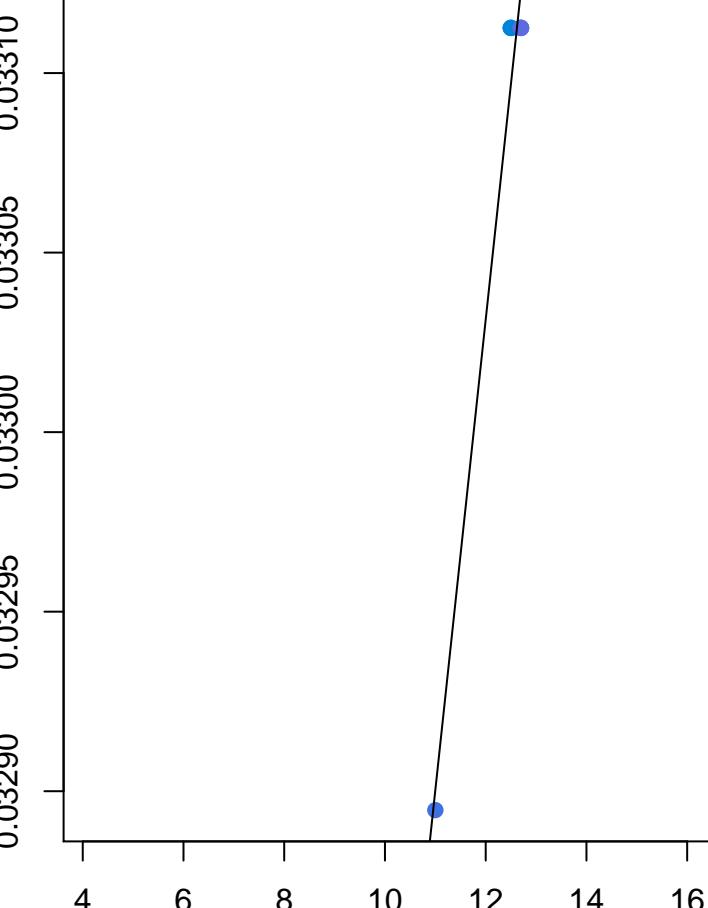
feature.pgfam_id.proline_residue.mean

PGF_01336833

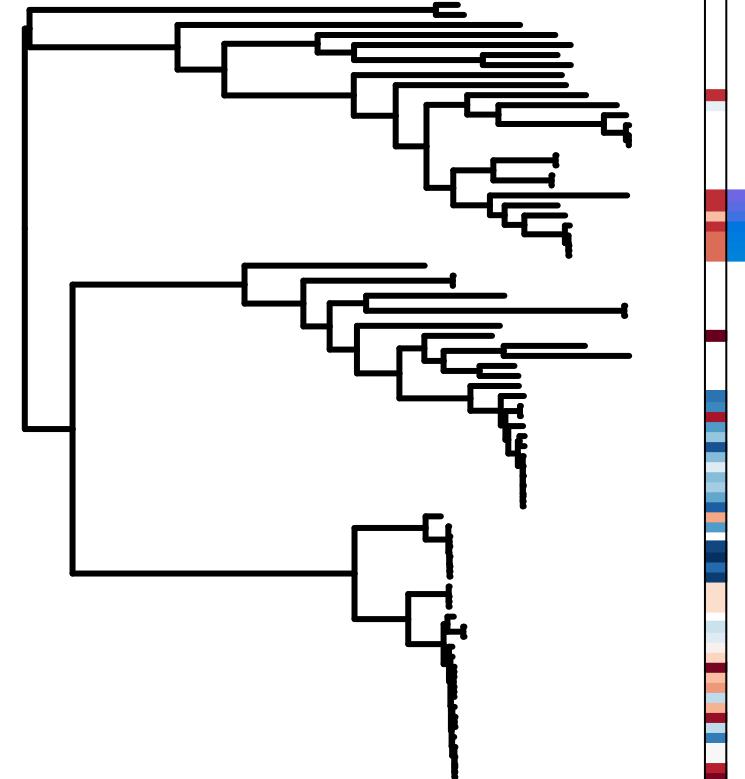
hypothetical protein

$r = 0.985, p = 10^{-5.104}$

feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature

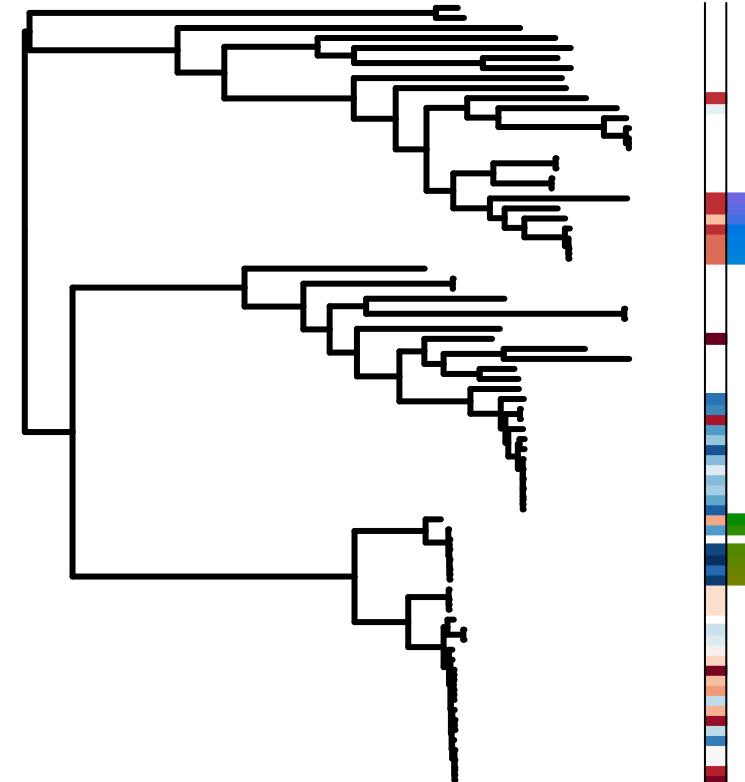
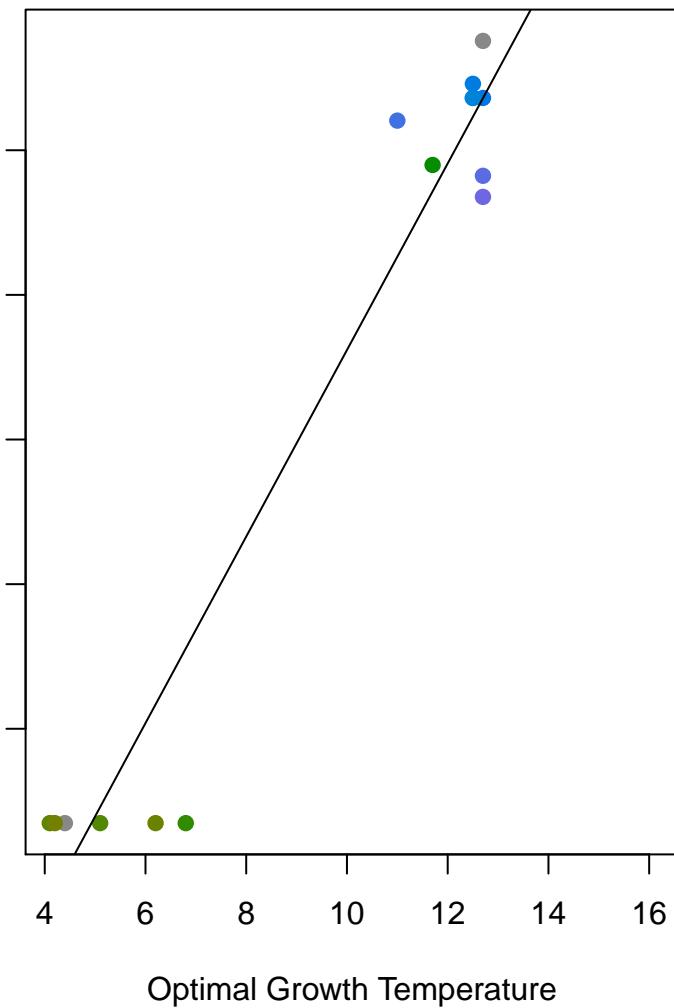


feature.pgfam_id.proline_residue.mean

PGF_00418379

Cobyrinic acid a,c-diamide synthetase (EC 6.3.5.11)

$r = 0.972$, $p = 10^{-8.874}$



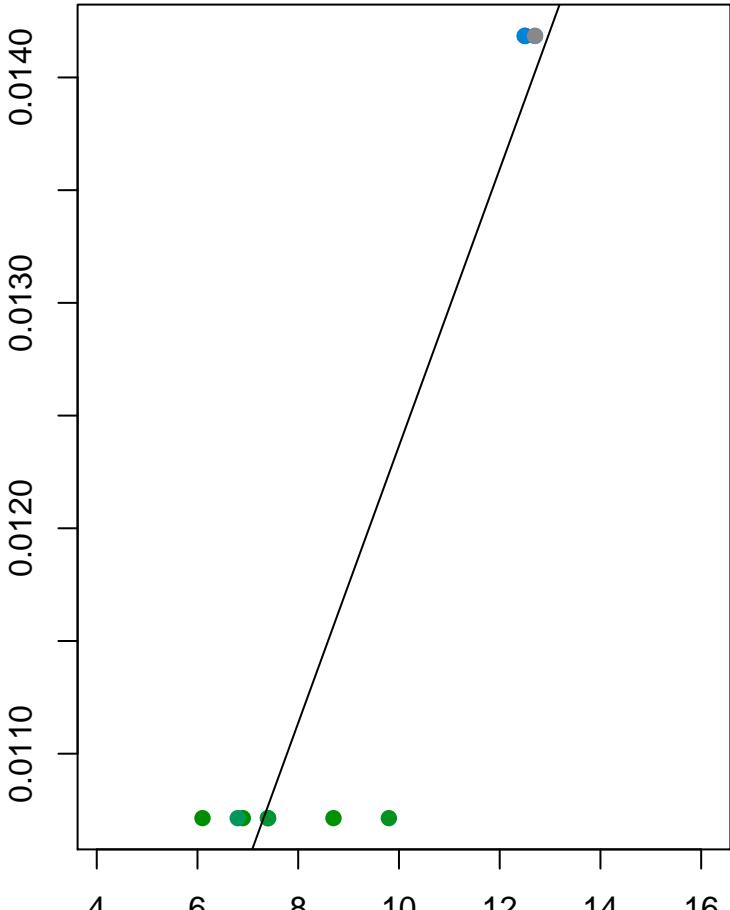
feature.pgfam_id.proline_residue.mean

PGF_01338003

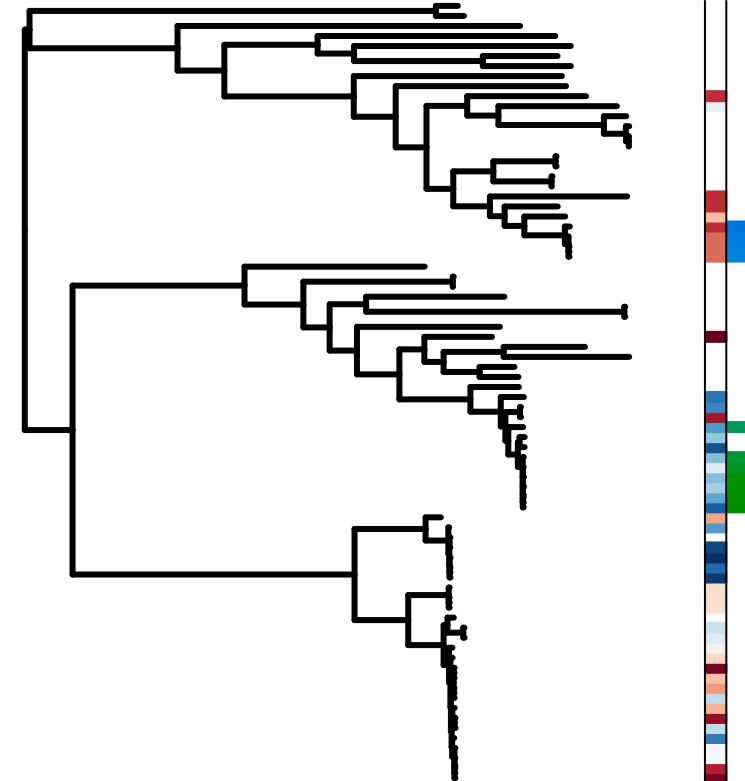
Membrane-associated methyl-accepting chemotaxis protein with HAMP domain

$r = 0.94, p = 10^{-5.262}$

feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature



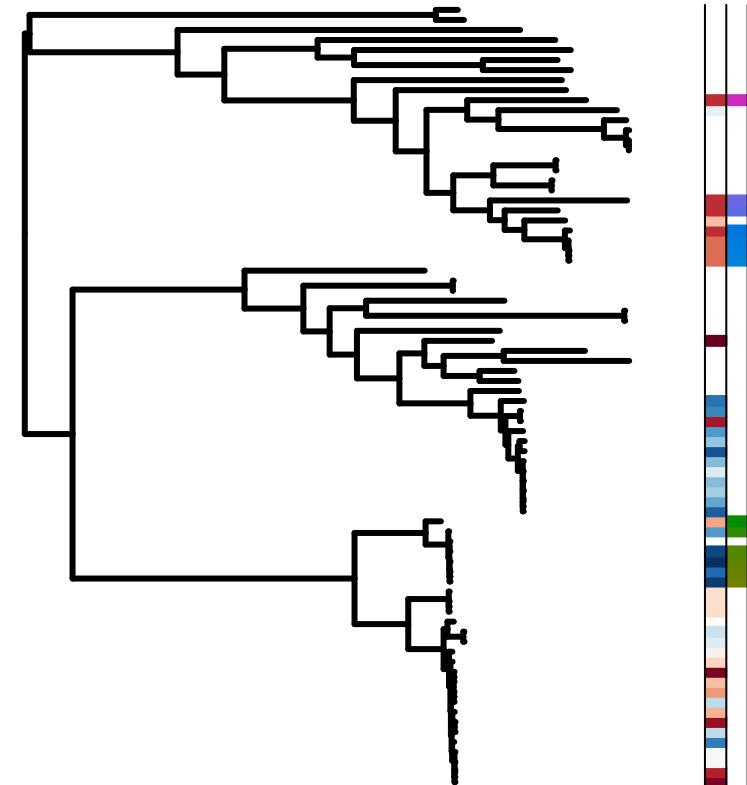
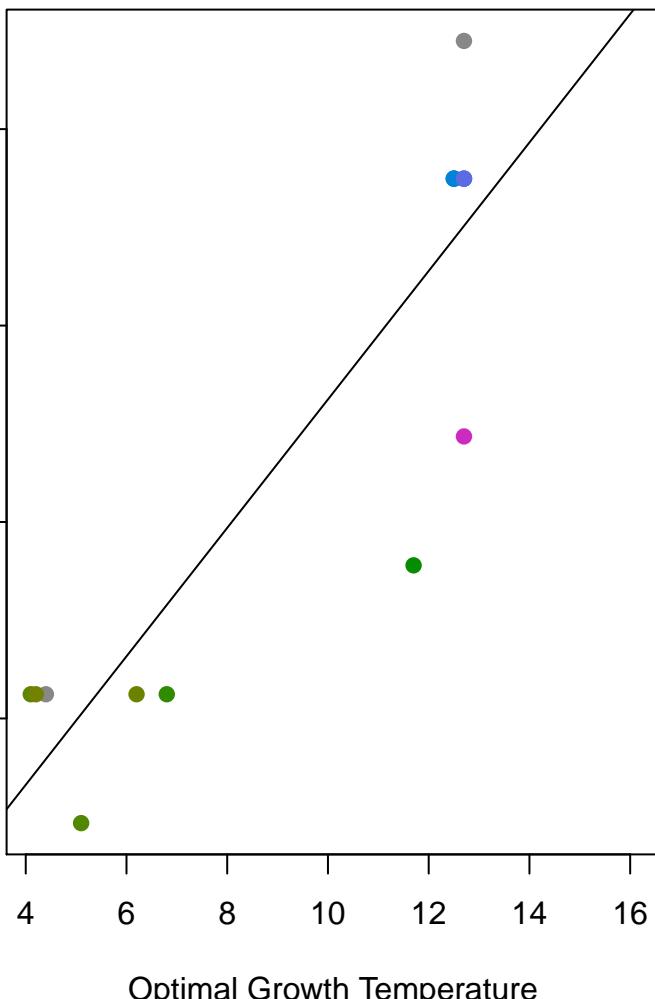
feature.pgfam_id.proline_residue.mean

PGF_00658019

TonB-dependent receptor

$r = 0.894, p = 10^{-5.15}$

feature.pgfam_id.proline_residue.mean

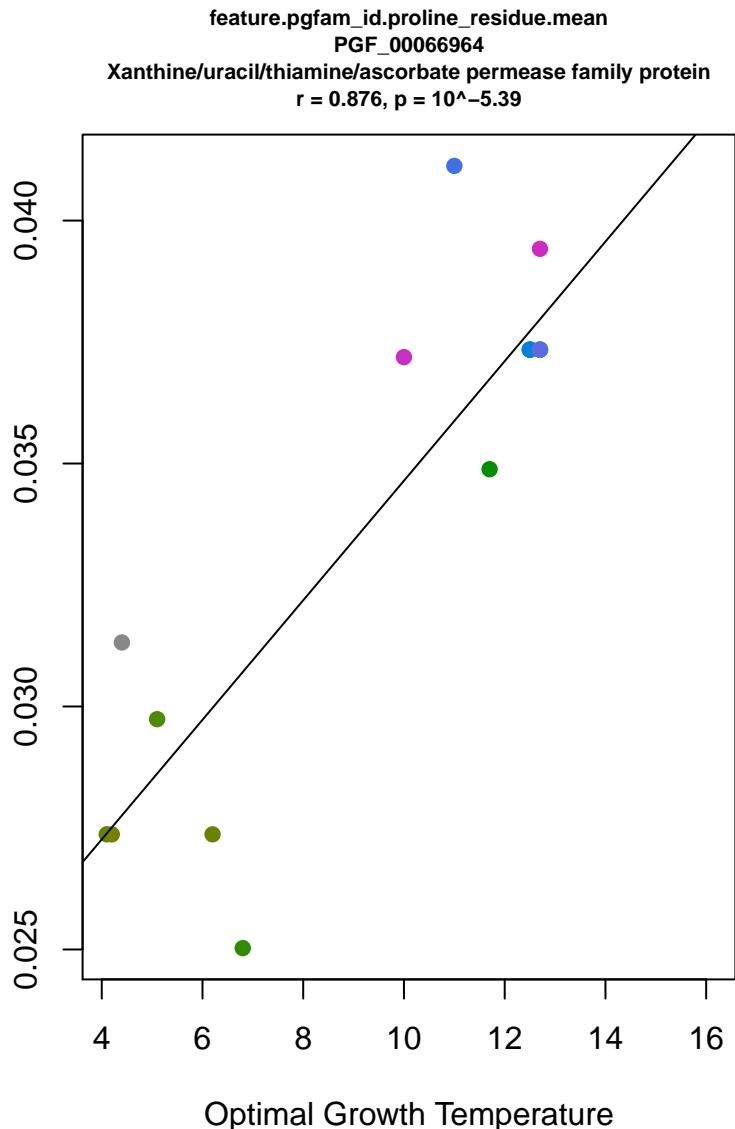


feature.pgfam_id.proline_residue.mean

PGF_00066964

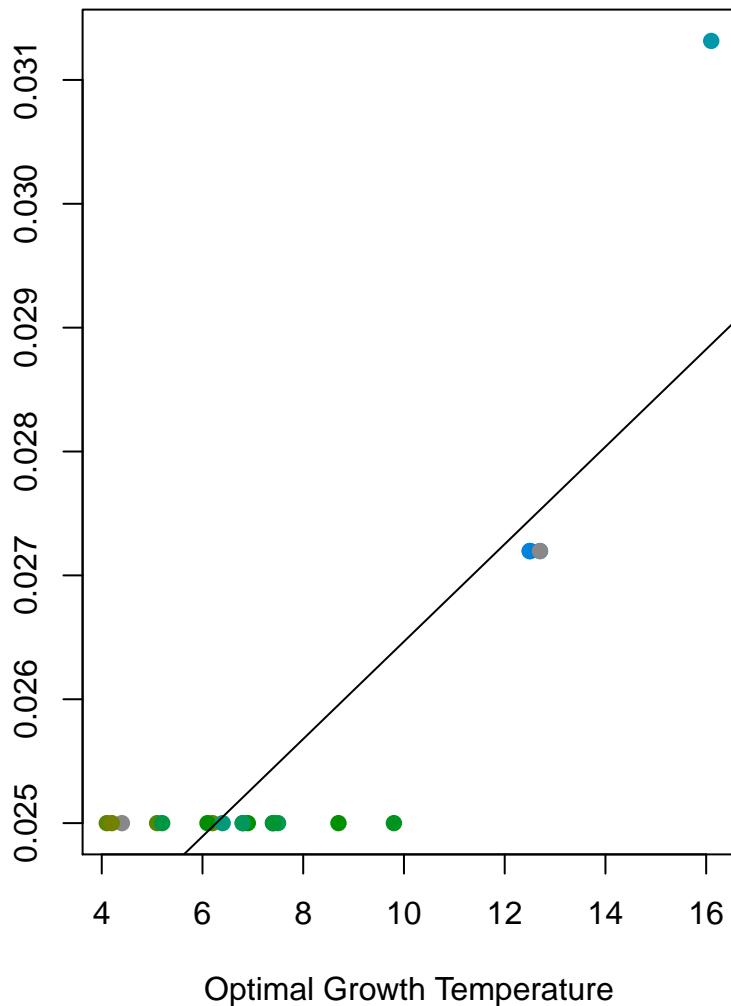
Xanthine/uracil/thiamine/ascorbate permease family protein

$r = 0.876, p = 10^{-5.39}$

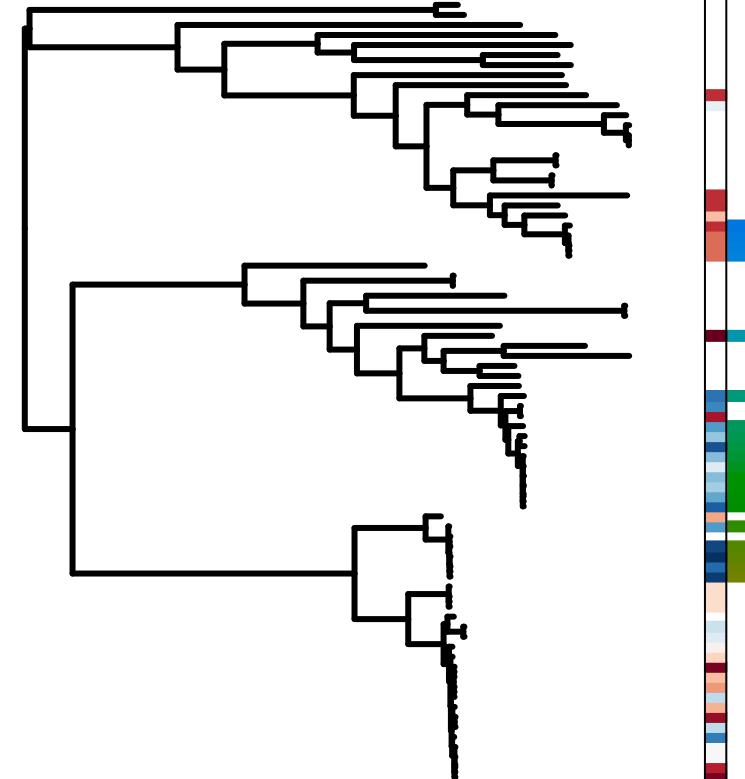


feature.pgfam_id.proline_residue.mean
PGF_02732386
Glucose/mannose:H⁺ symporter GlcP
 $r = 0.869$, $p = 10^{-6.804}$

feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature



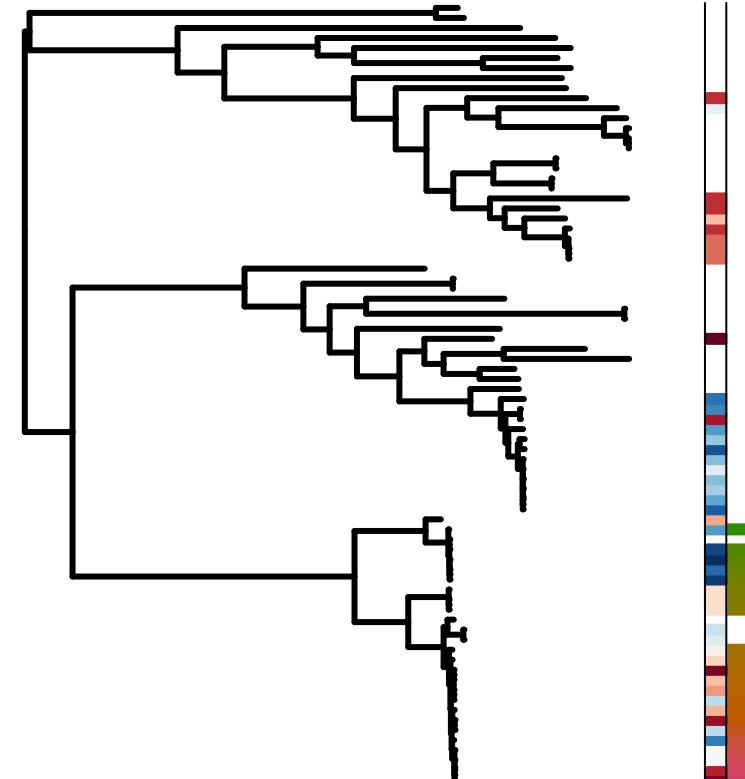
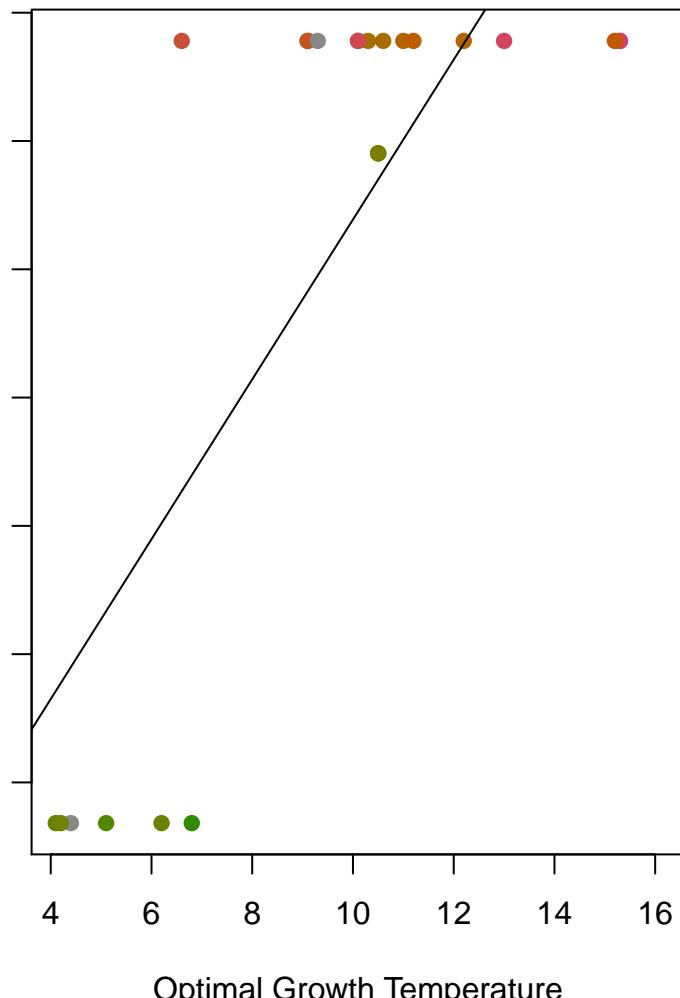
feature.pgfam_id.proline_residue.mean

PGF_10751741

Redoxin domain protein

$r = 0.79, p = 10^{-5.354}$

feature.pgfam_id.proline_residue.mean

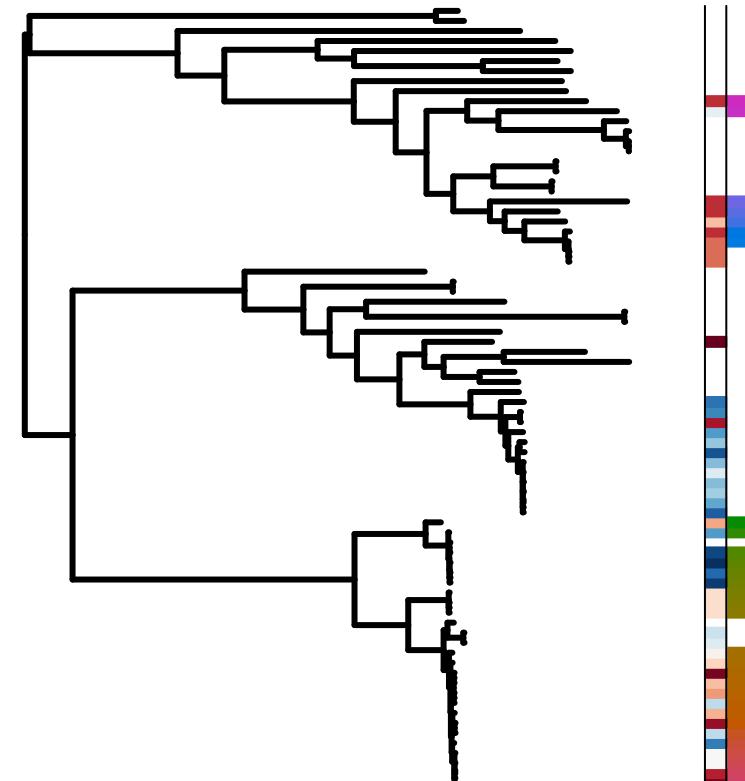
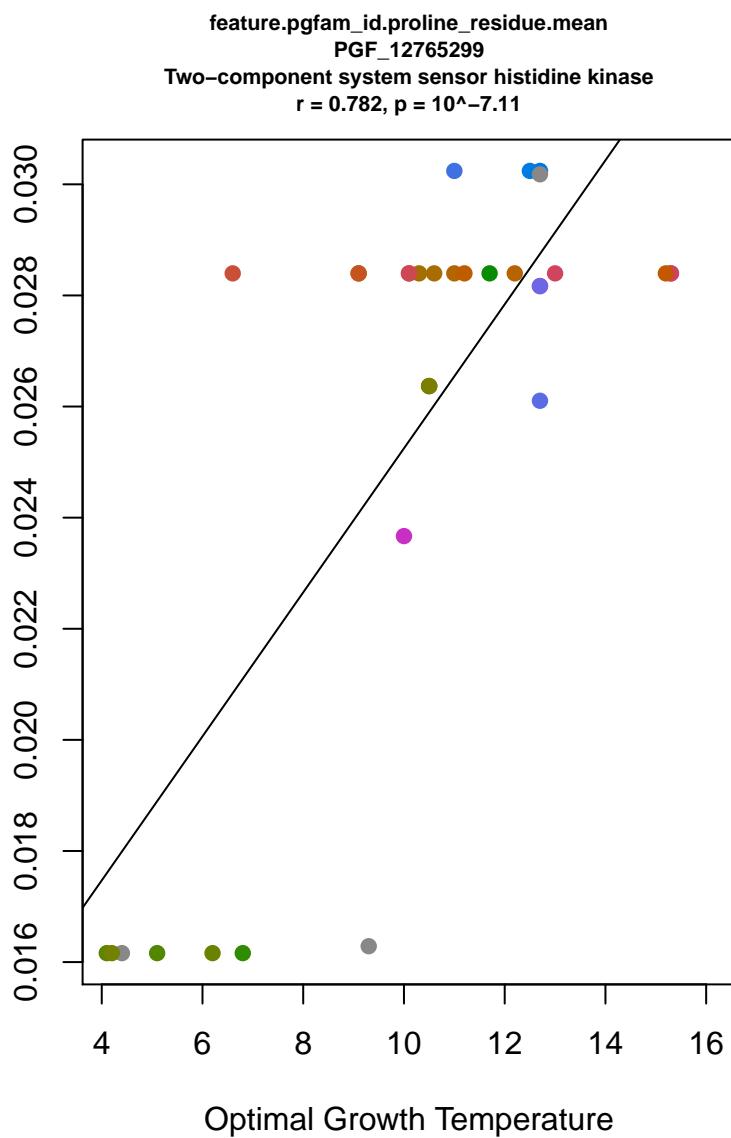


feature.pgfam_id.proline_residue.mean

PGF_12765299

Two-component system sensor histidine kinase

$r = 0.782, p = 10^{-7.11}$



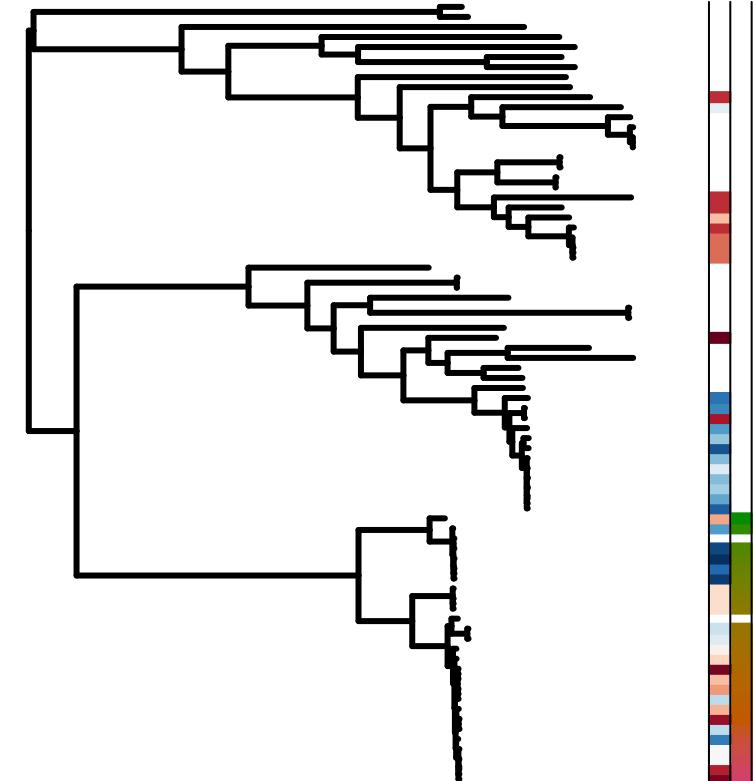
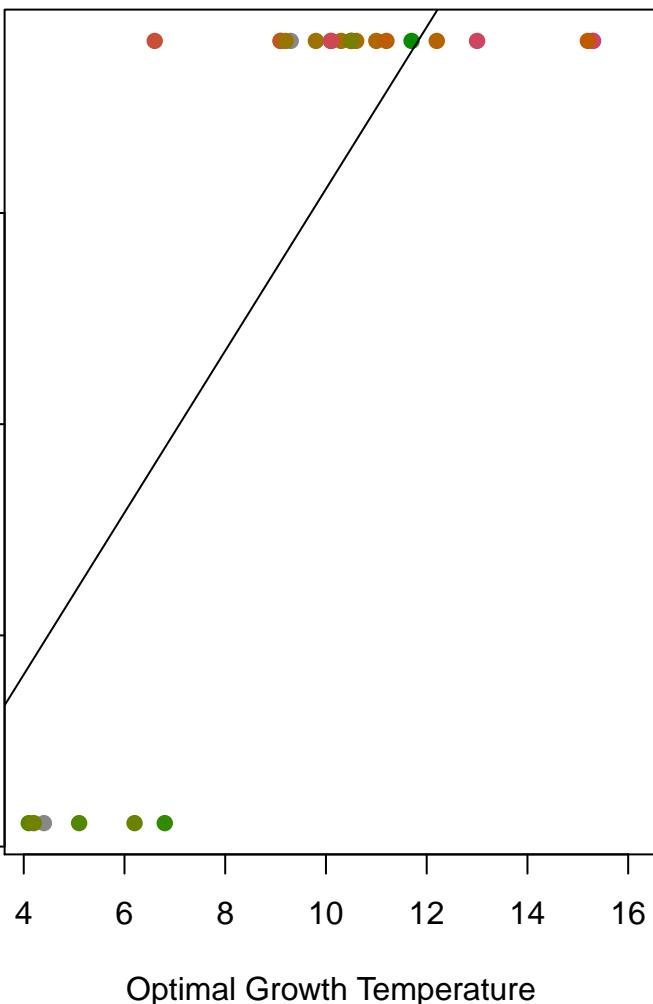
feature.pgfam_id.proline_residue.mean

PGF_10494566

hypothetical protein

$r = 0.778, p = 10^{-5.746}$

feature.pgfam_id.proline_residue.mean



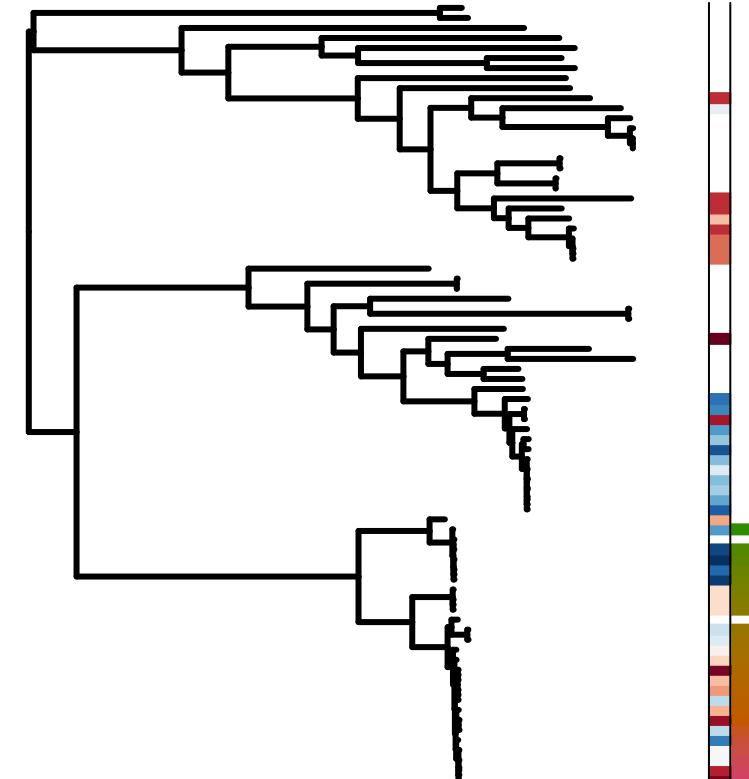
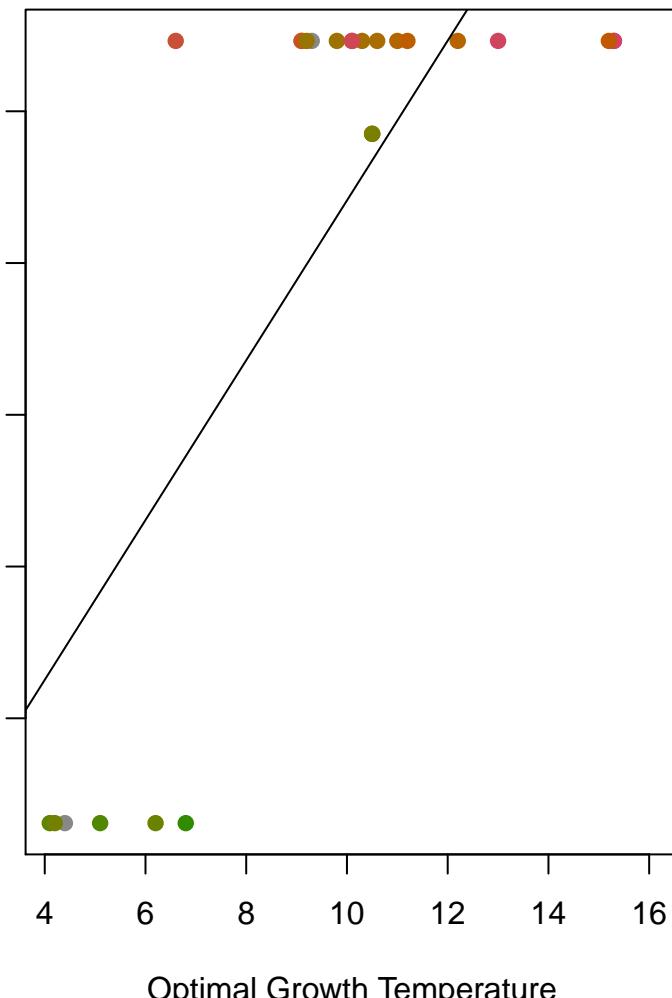
feature.pgfam_id.proline_residue.mean

PGF_11915740

hypothetical protein

$r = 0.777, p = 10^{-5.509}$

feature.pgfam_id.proline_residue.mean



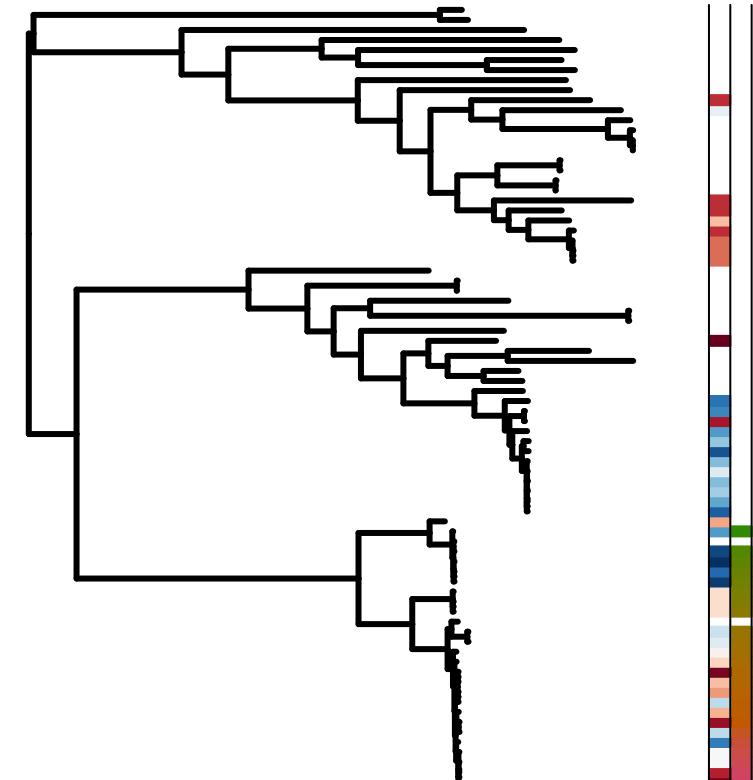
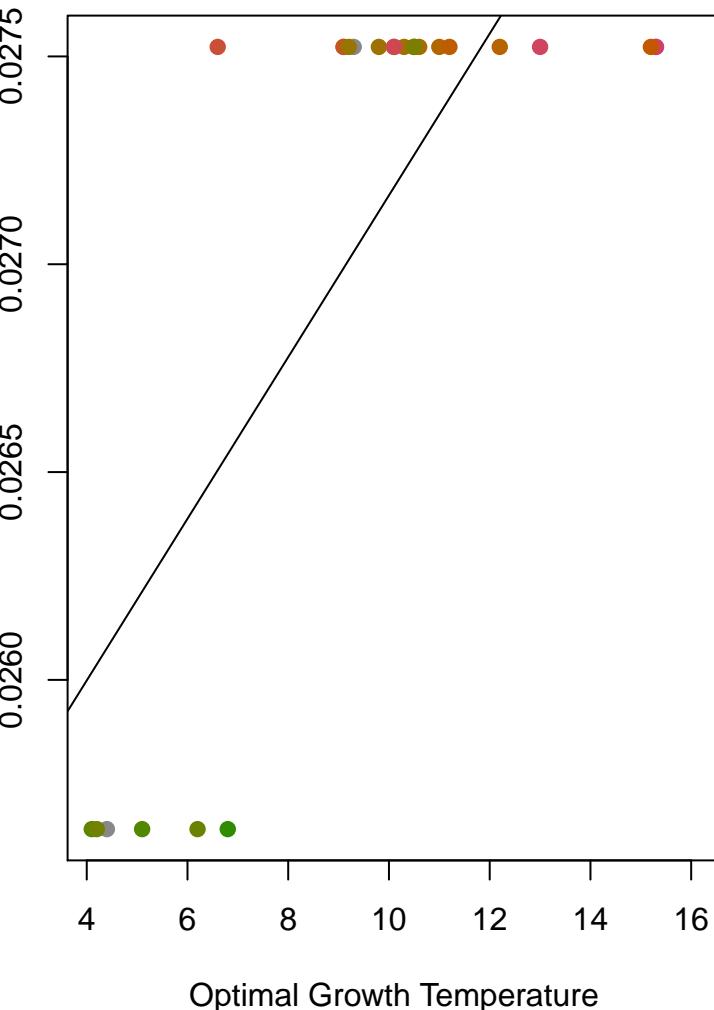
feature.pgfam_id.proline_residue.mean

PGF_11025496

hypothetical protein

$r = 0.775, p = 10^{-5.478}$

feature.pgfam_id.proline_residue.mean



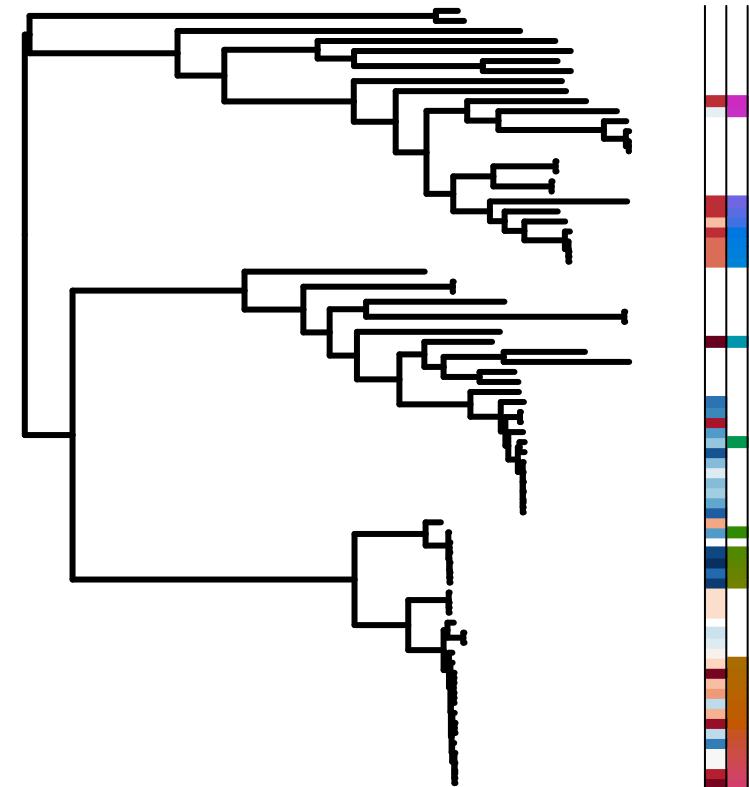
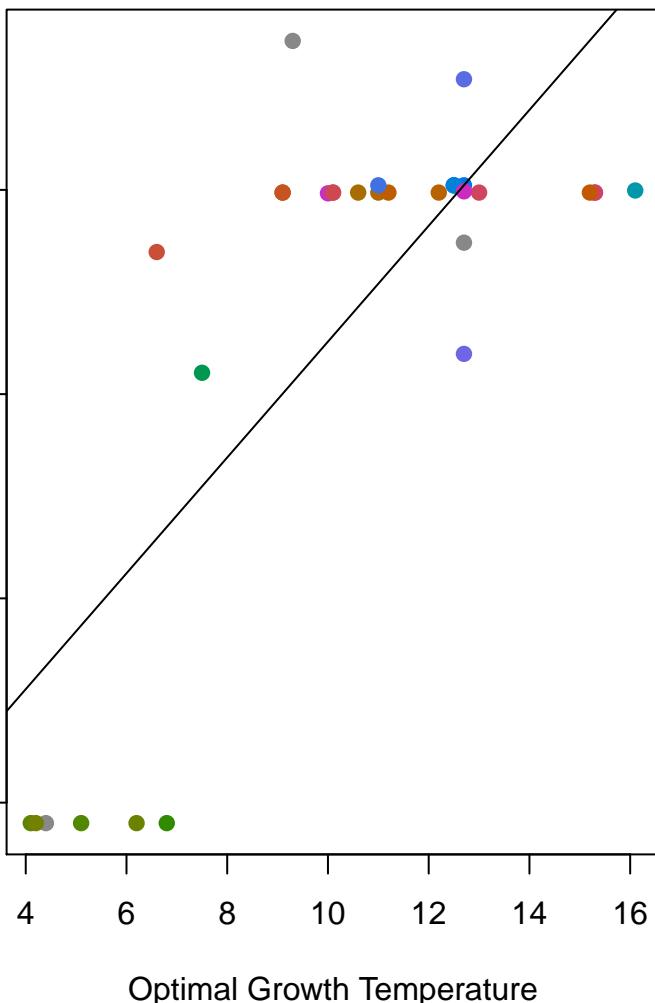
feature.pgfam_id.proline_residue.mean

PGF_06641194

Capsule biosynthesis protein capA

$r = 0.771$, $p = 10^{-6.621}$

feature.pgfam_id.proline_residue.mean



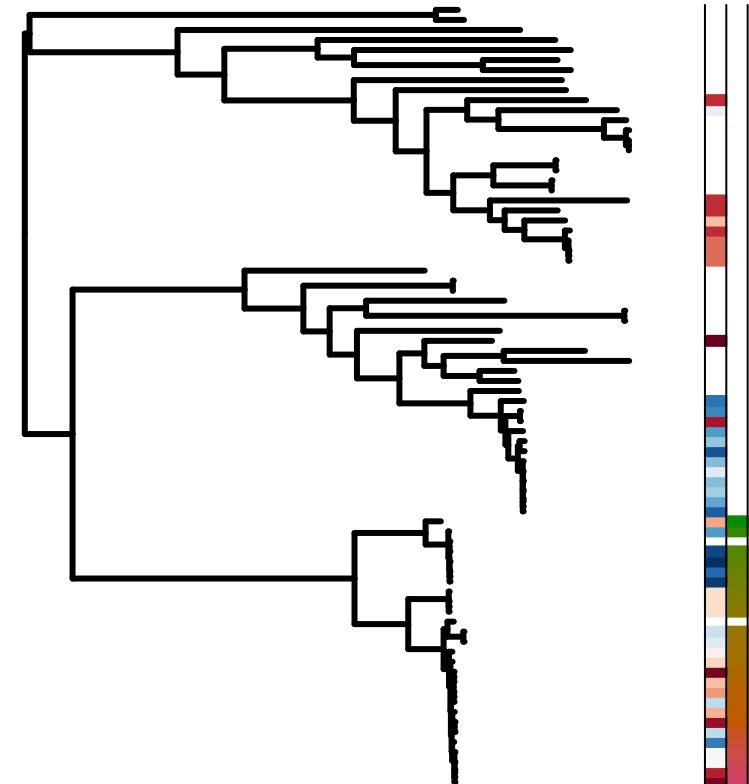
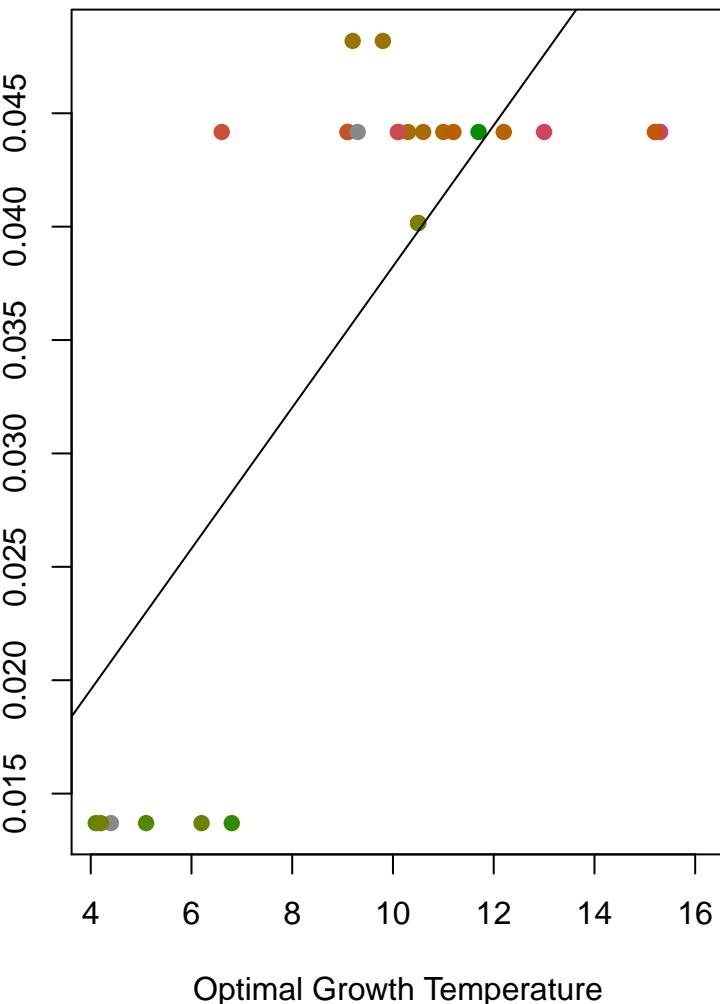
feature.pgfam_id.proline_residue.mean

PGF_11018774

hypothetical protein

$r = 0.765, p = 10^{-5.474}$

feature.pgfam_id.proline_residue.mean



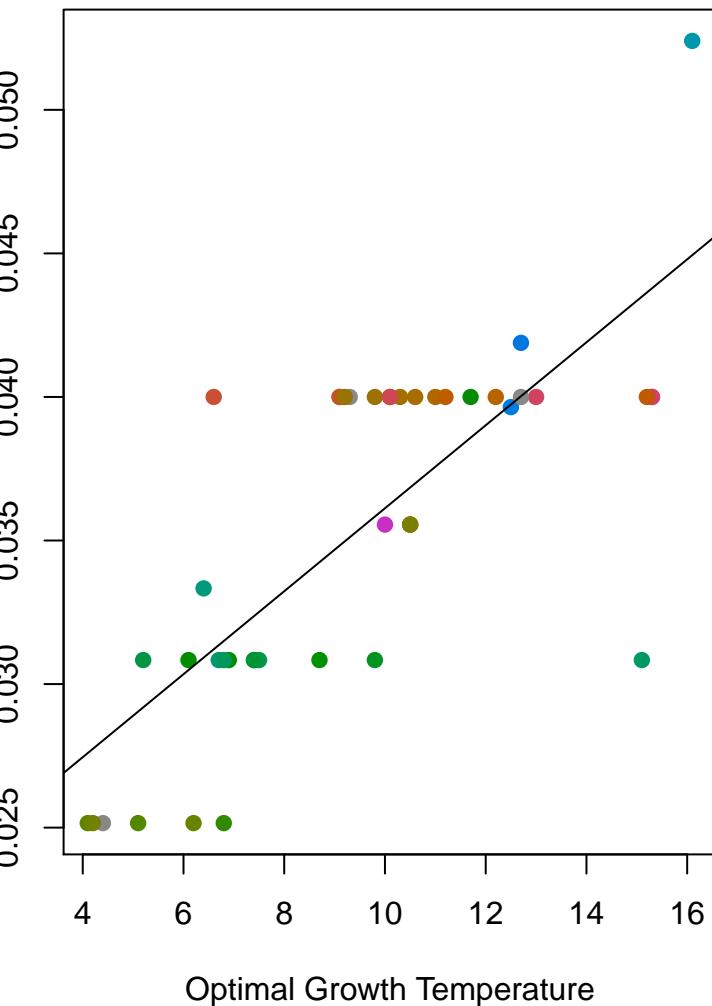
feature.pgfam_id.proline_residue.mean

PGF_02911177

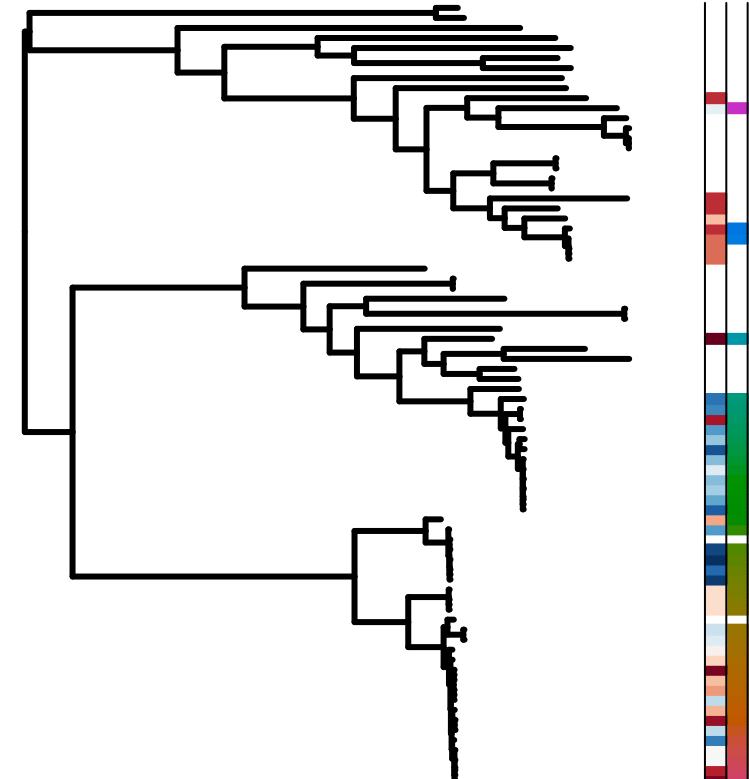
SM-20-related protein

$r = 0.758, p = 10^{-8.599}$

feature.pgfam_id.proline_residue.mean

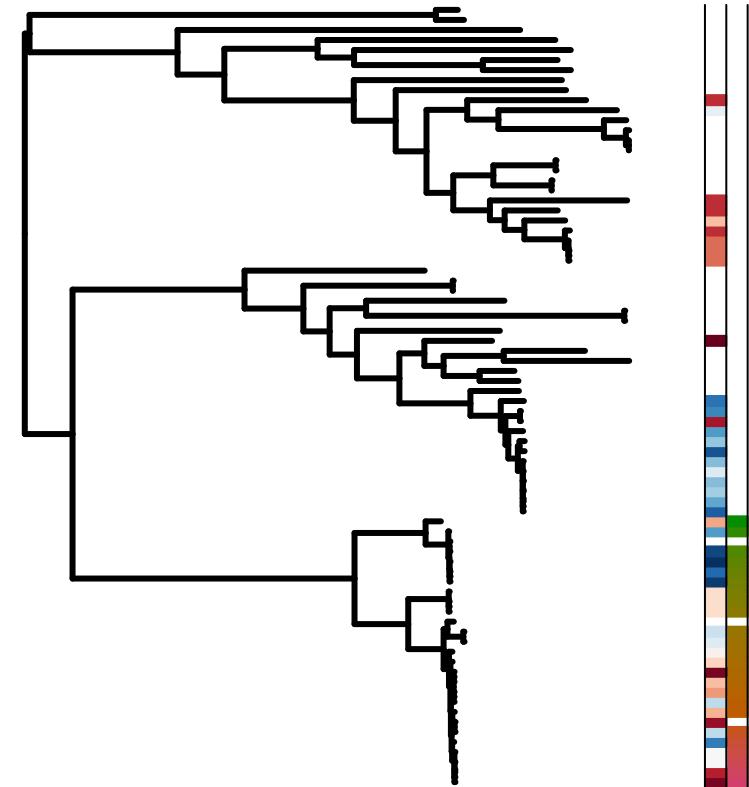
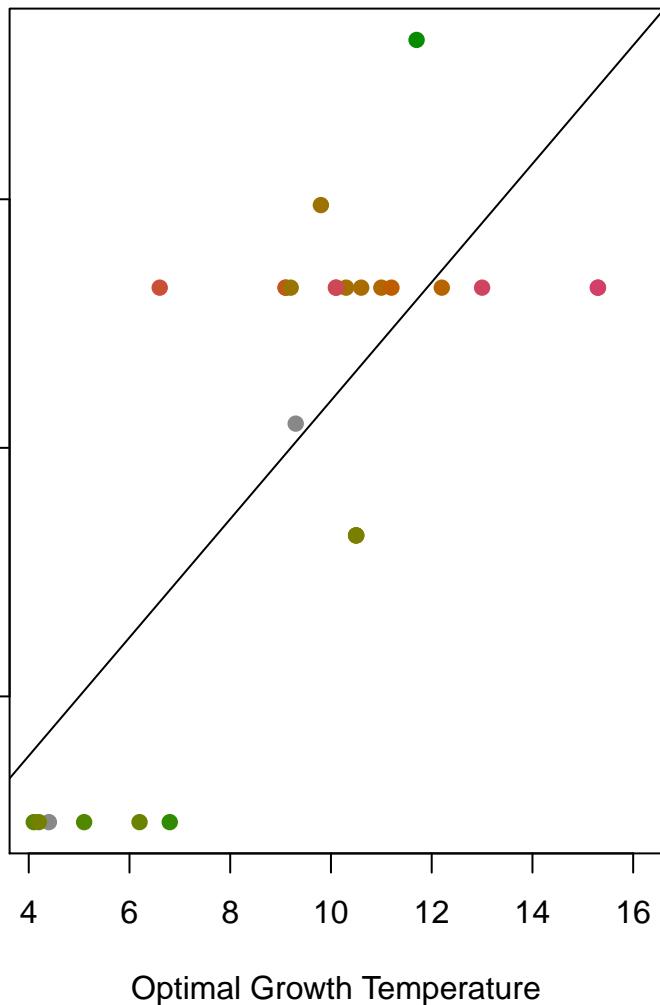


Optimal Growth Temperature



feature.pgfam_id.proline_residue.mean
PGF_03083319
Maltodextrin glucosidase (EC 3.2.1.20)
 $r = 0.751$, $p = 10^{-5.008}$

feature.pgfam_id.proline_residue.mean

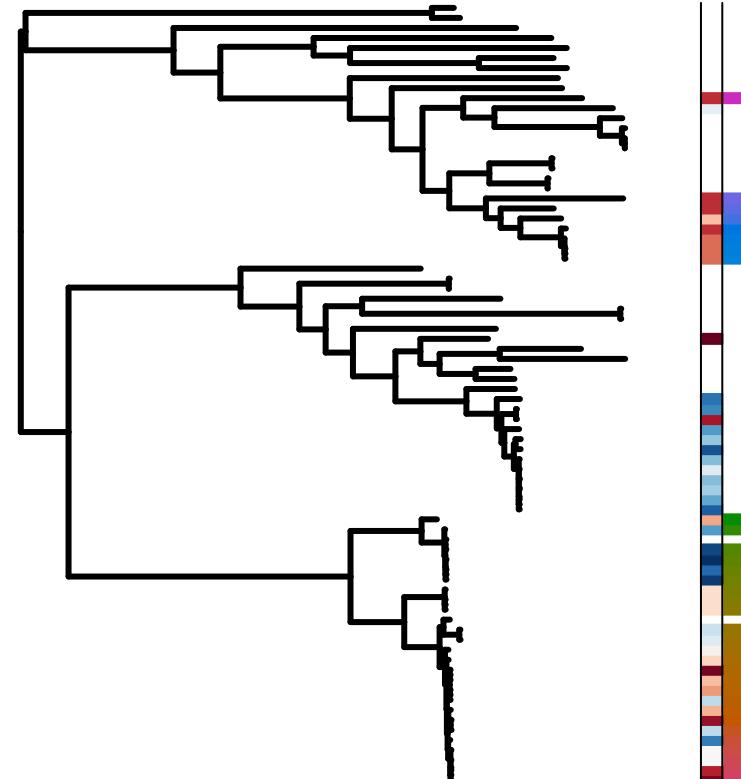
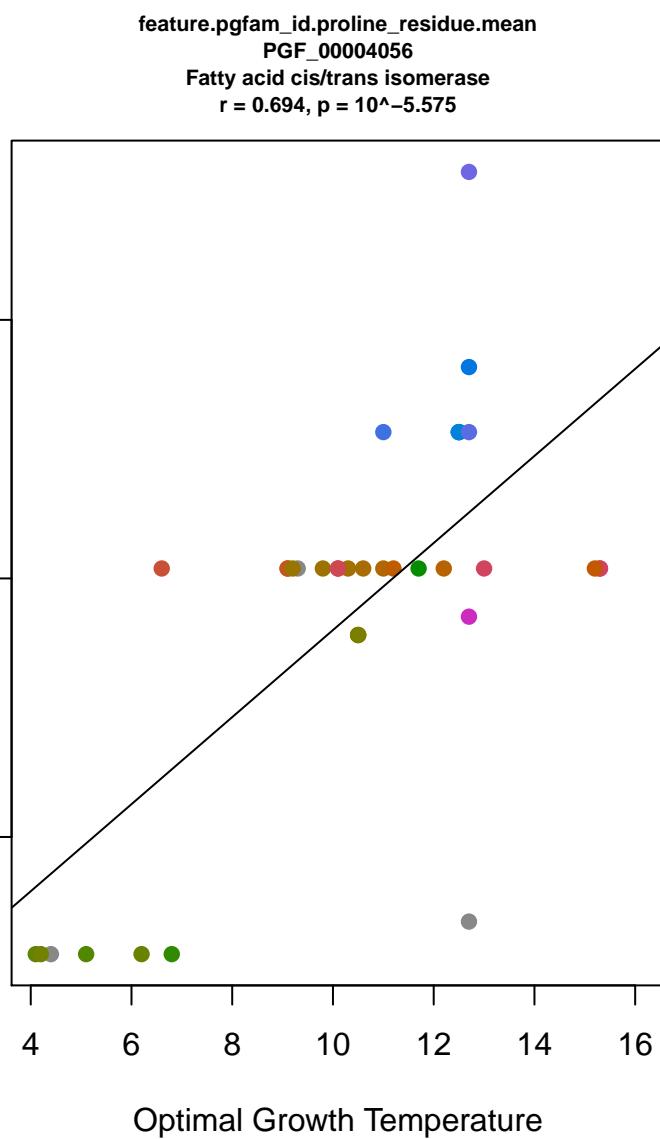


feature.pgfam_id.proline_residue.mean

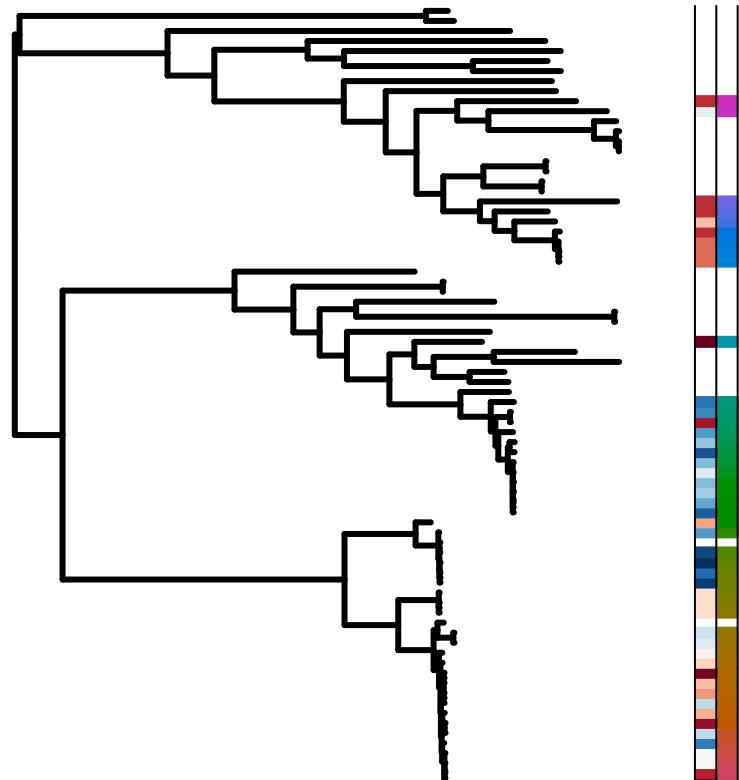
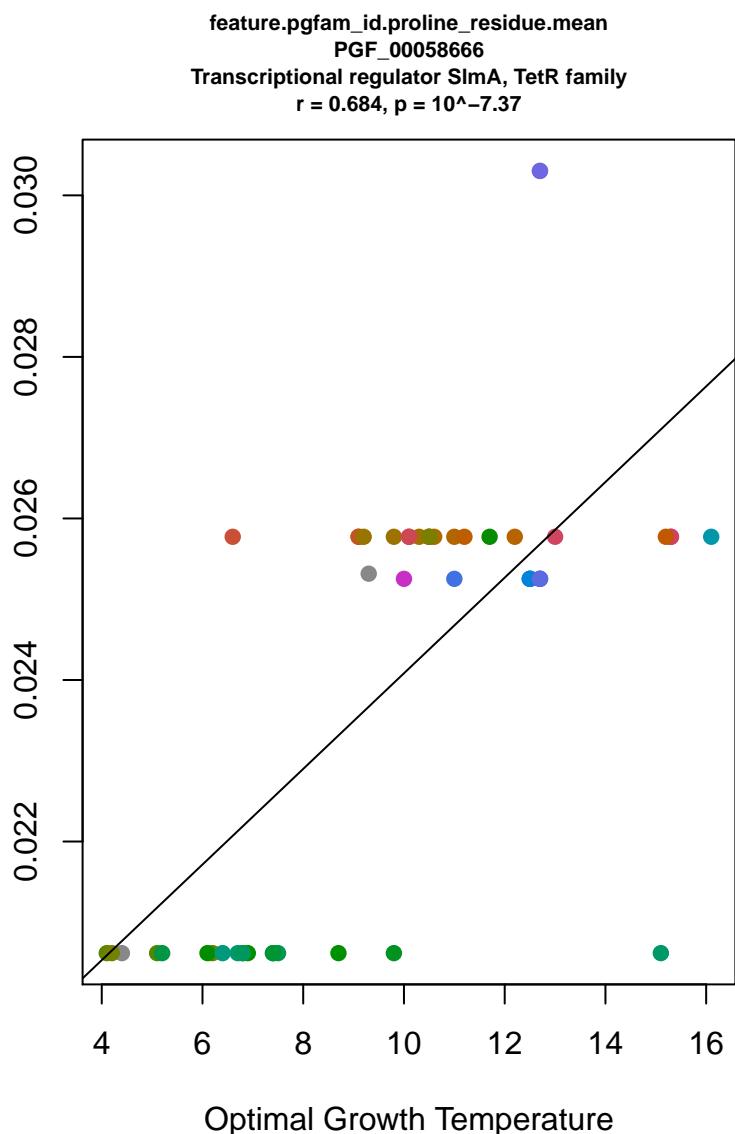
PGF_00004056

Fatty acid cis/trans isomerase

$r = 0.694$, $p = 10^{-5.575}$



feature.pgfam_id.proline_residue.mean
PGF_00058666
Transcriptional regulator SlmA, TetR family
 $r = 0.684$, $p = 10^{-7.37}$

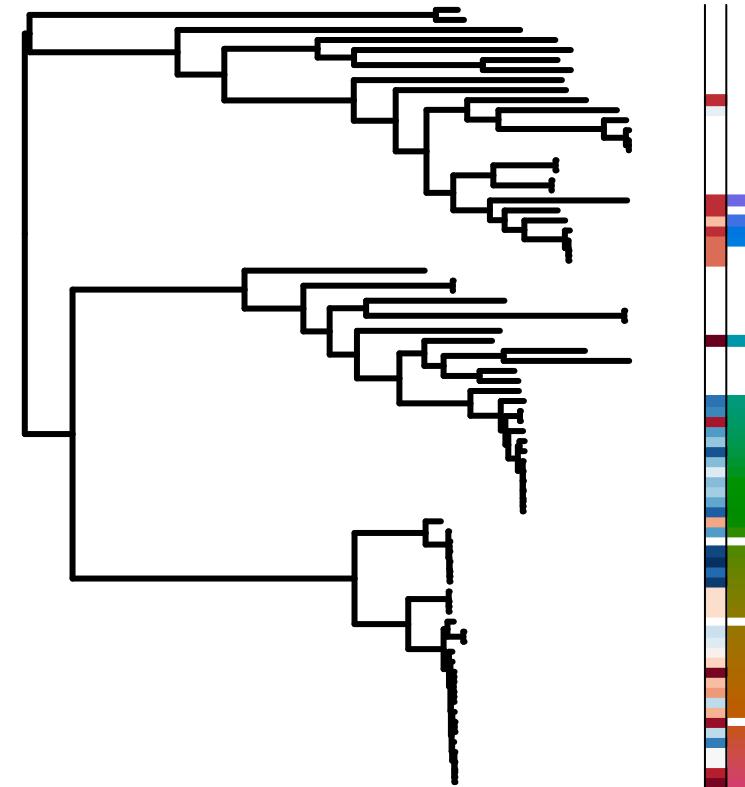
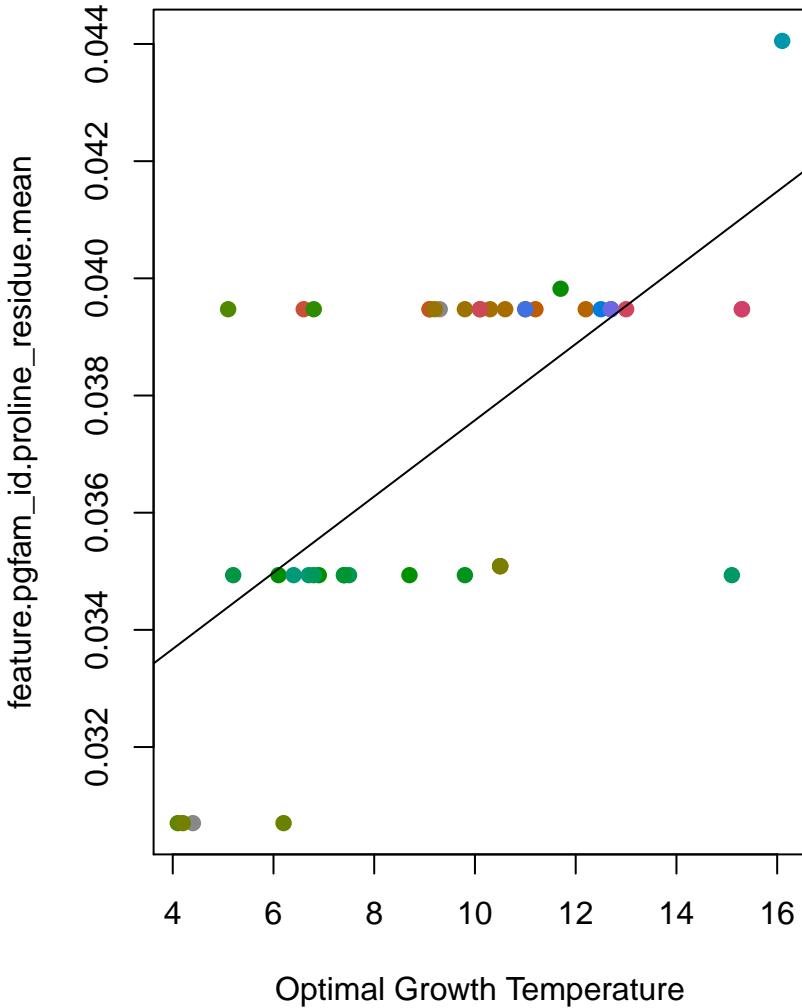


feature.pgfam_id.proline_residue.mean

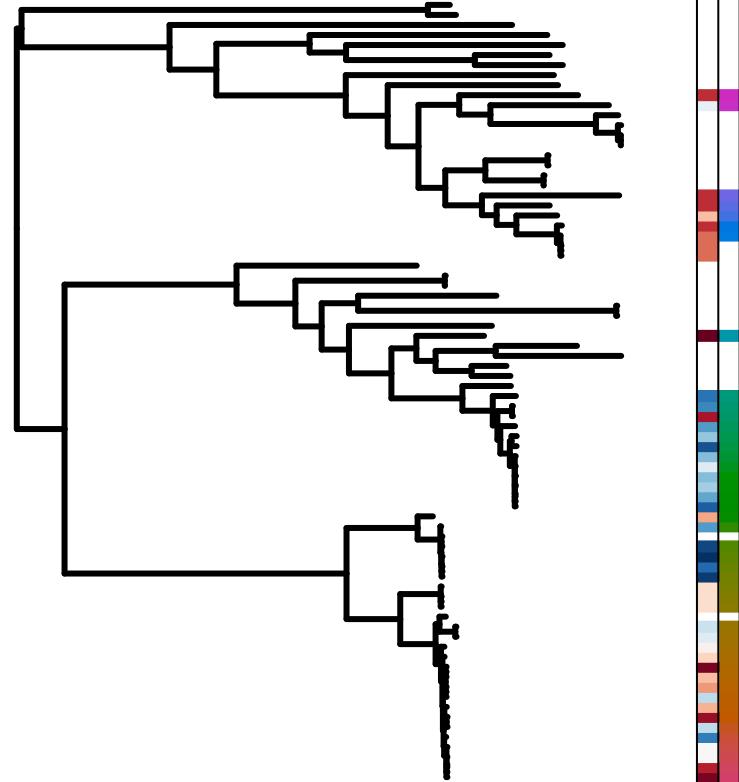
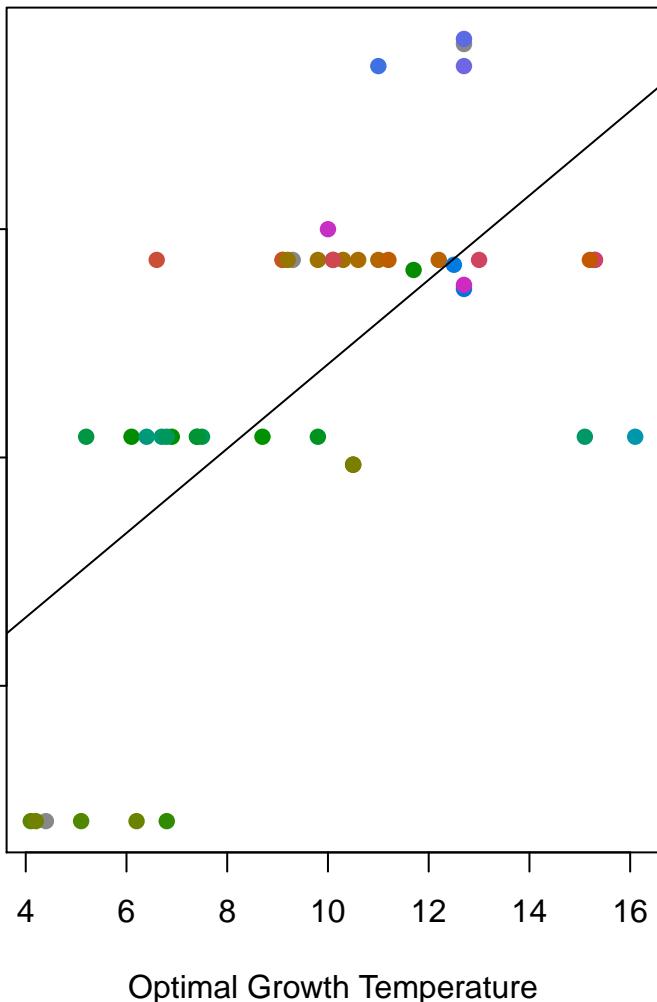
PGF_03832998

FIG111991: hypothetical protein

$r = 0.657$, $p = 10^{-5.885}$



feature.pgfam_id.proline_residue.mean
PGF_04602939
Paraquat-inducible protein A
 $r = 0.655, p = 10^{-6.362}$



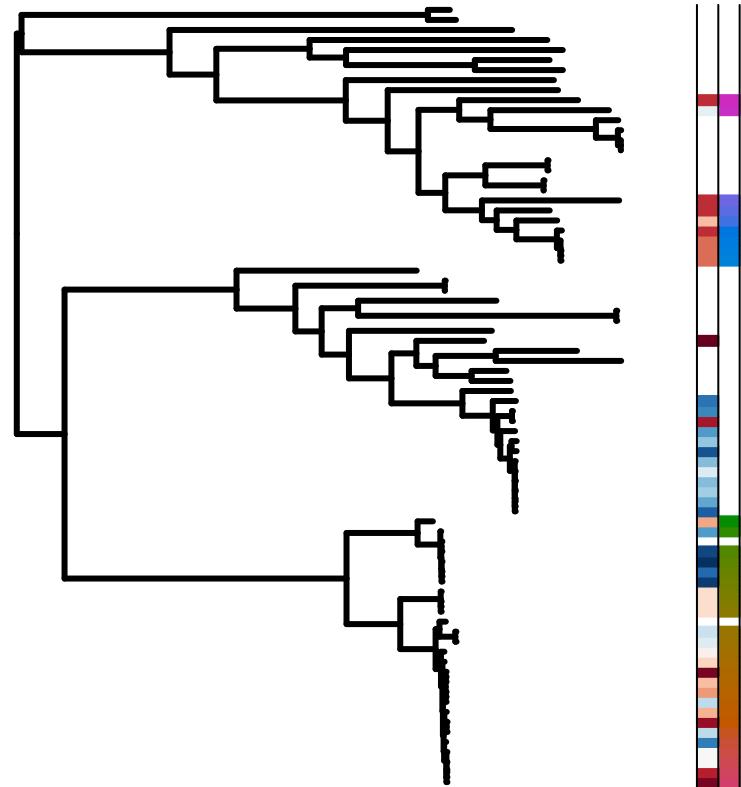
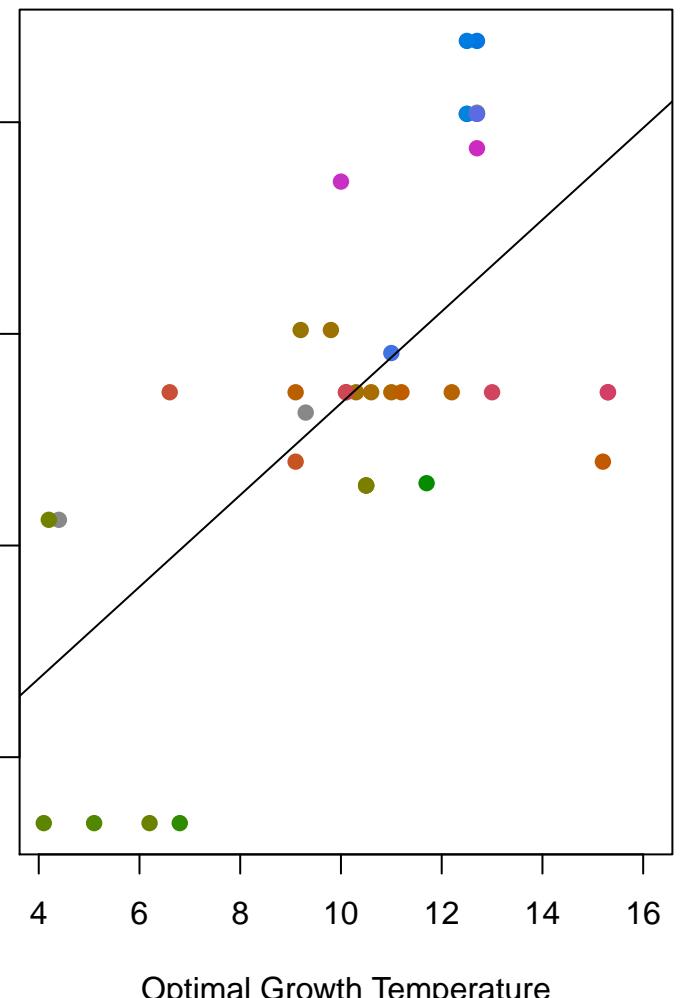
feature.pgfam_id.proline_residue.mean

PGF_00300187

Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) @ Outer membrane phospholipase A

$r = 0.654$, $p = 10^{-4.937}$

feature.pgfam_id.proline_residue.mean

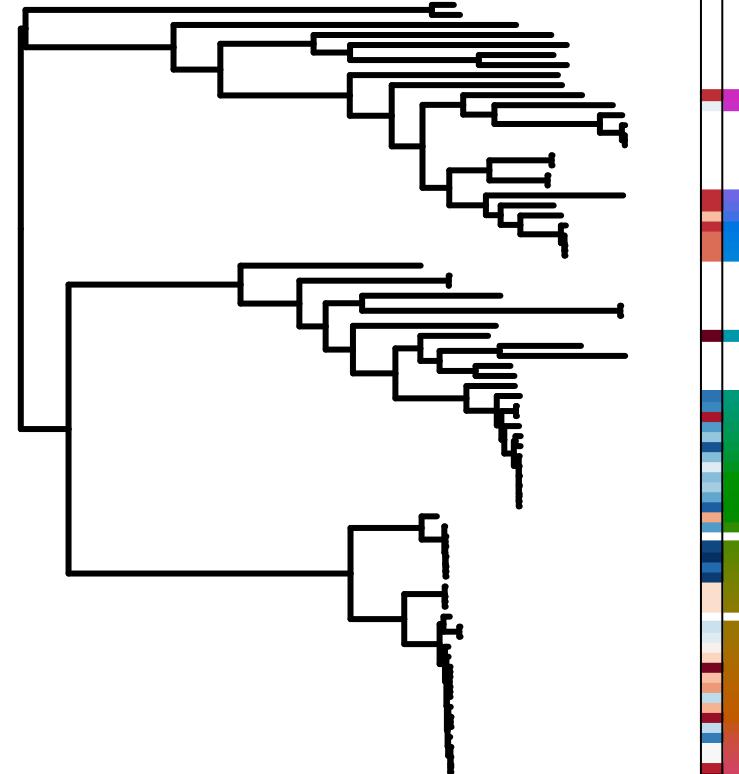
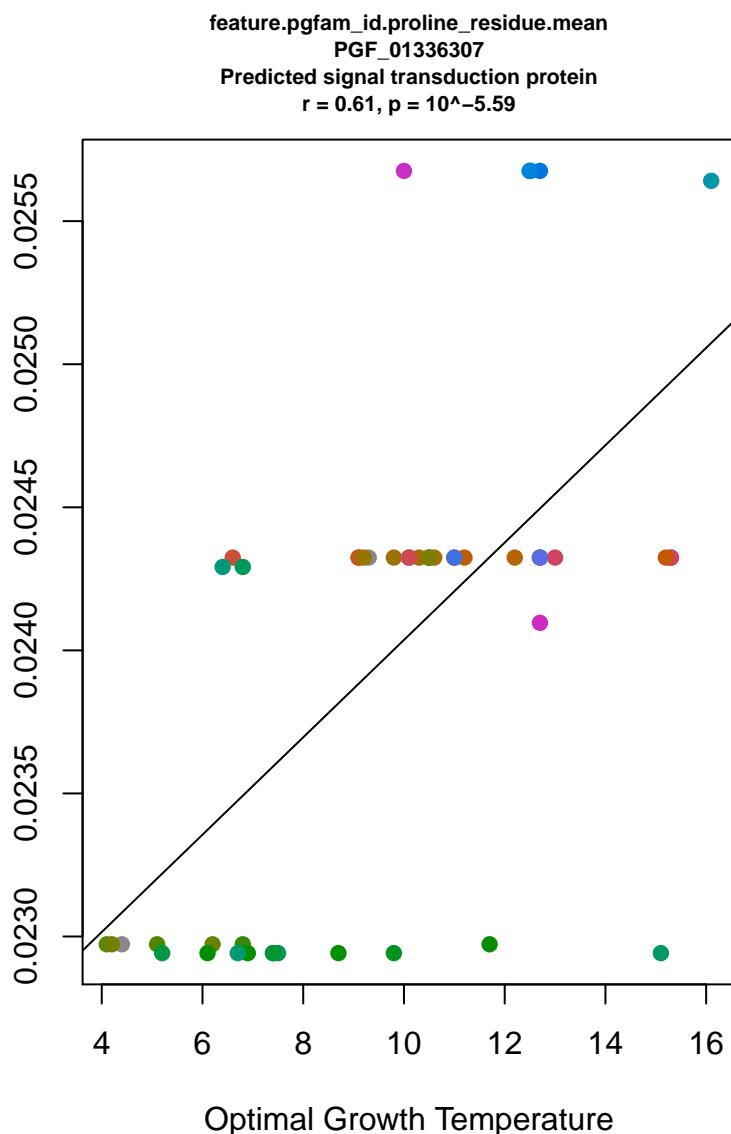


feature.pgfam_id.proline_residue.mean

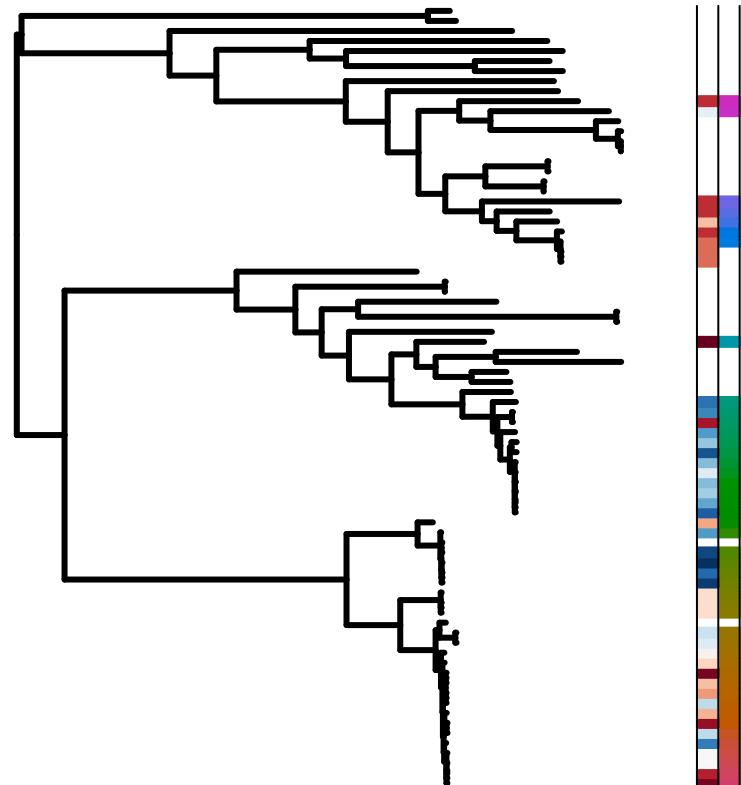
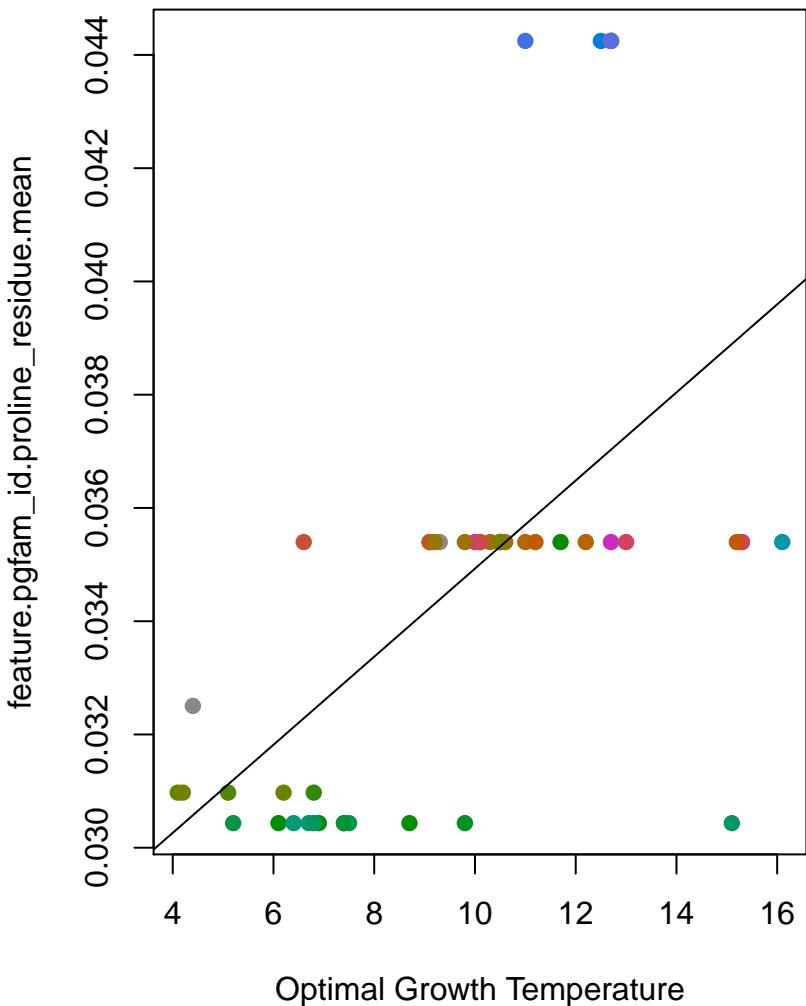
PGF_01336307

Predicted signal transduction protein

$r = 0.61, p = 10^{-5.59}$



feature.pgfam_id.proline_residue.mean
PGF_02455692
Cytidylate kinase (EC 2.7.4.25)
 $r = 0.58, p = 10^{-4.815}$

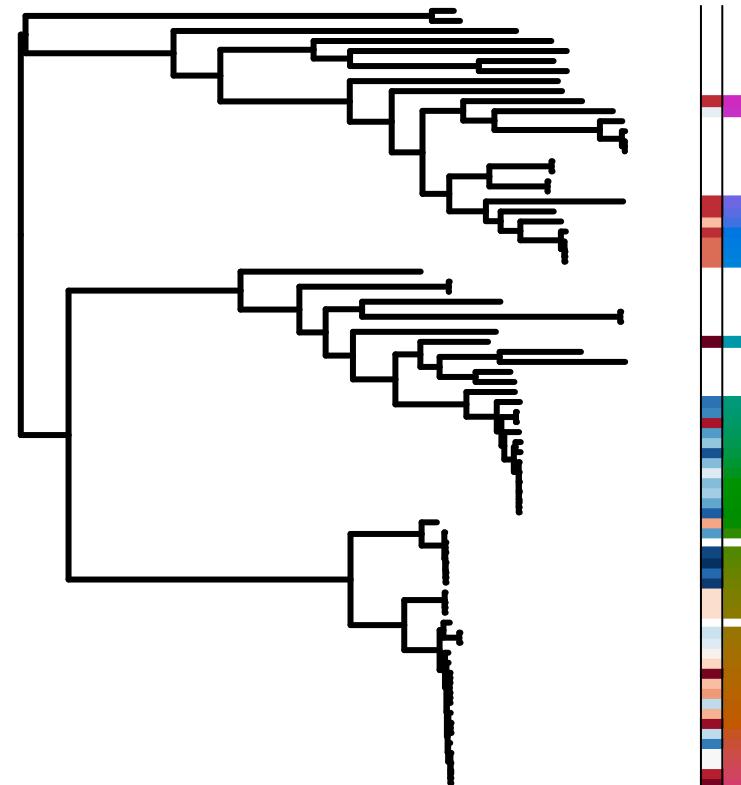
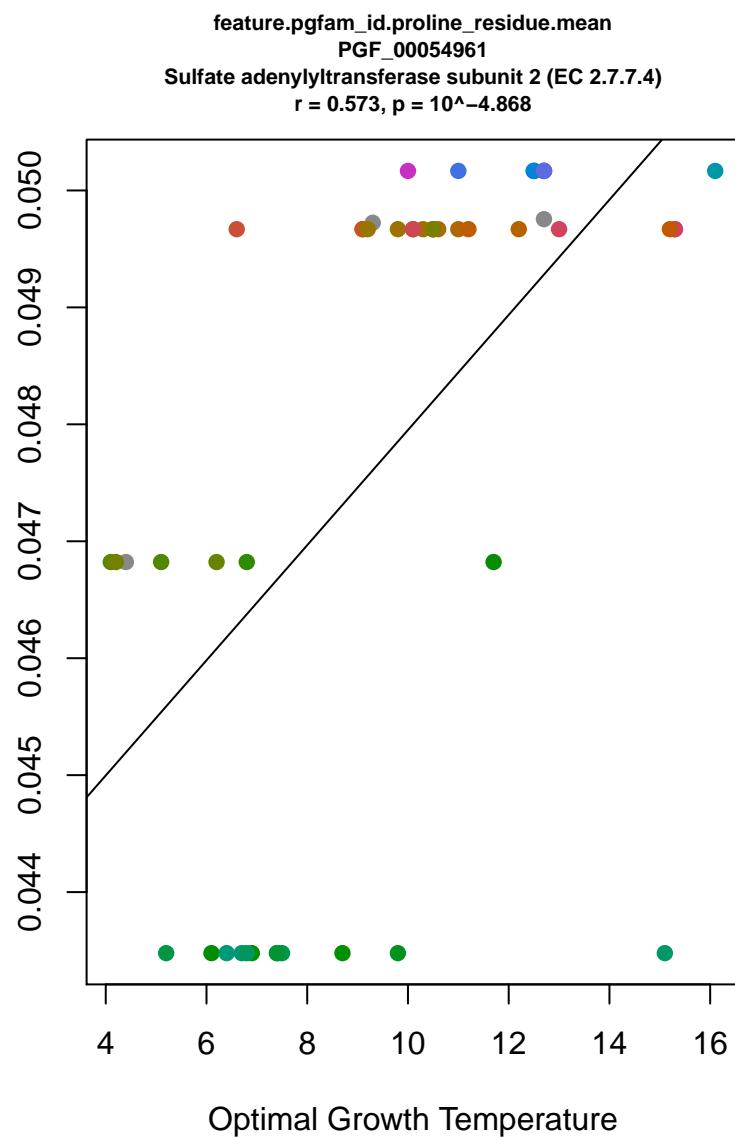


feature.pgfam_id.proline_residue.mean

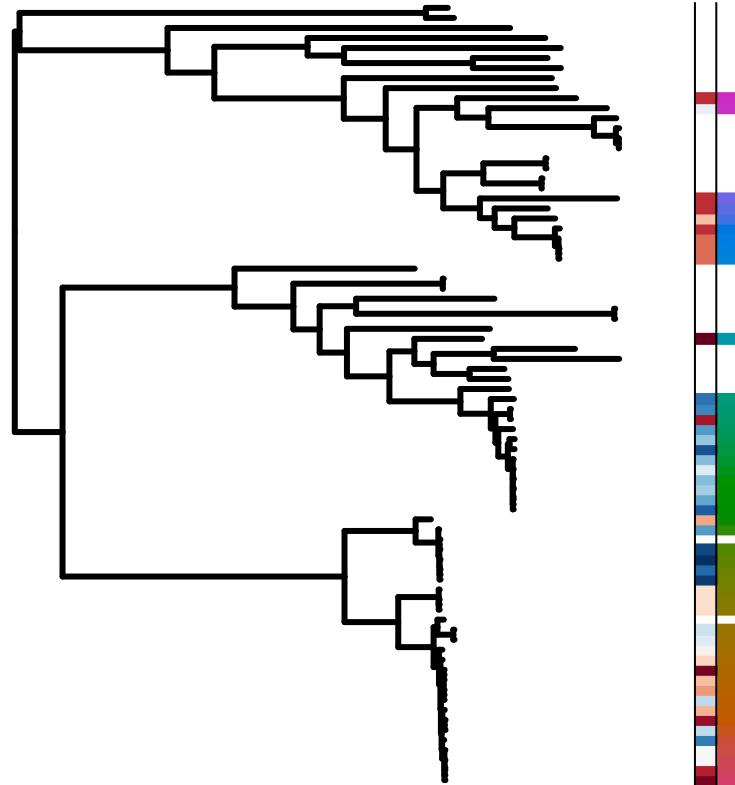
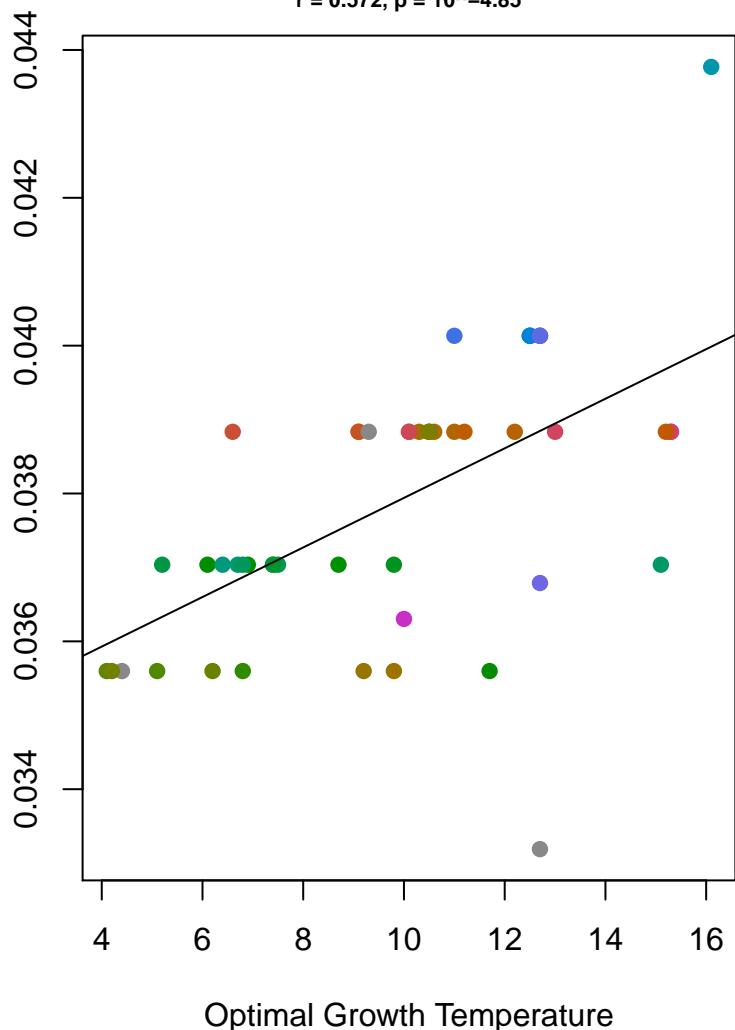
PGF_00054961

Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)

$r = 0.573, p = 10^{-4.868}$



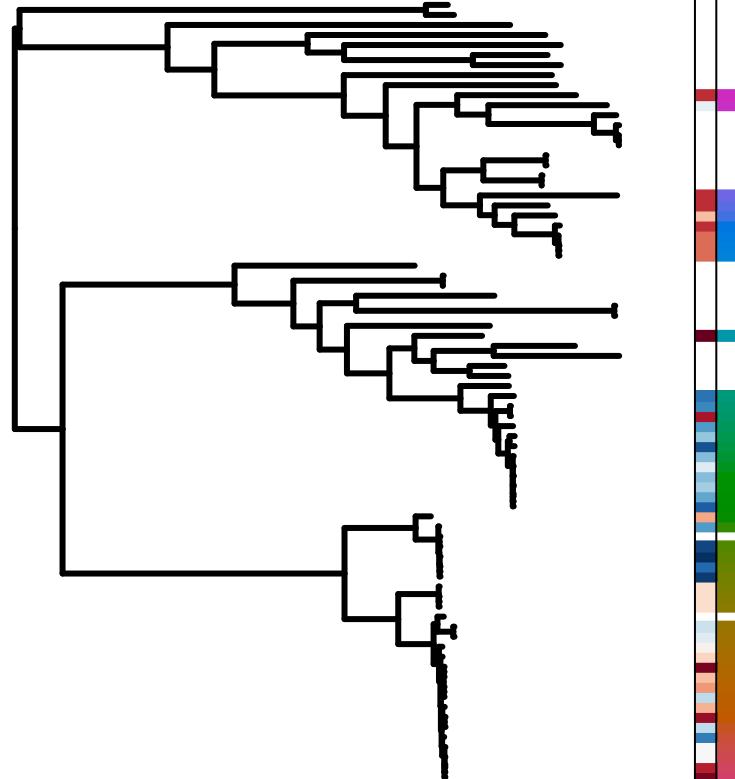
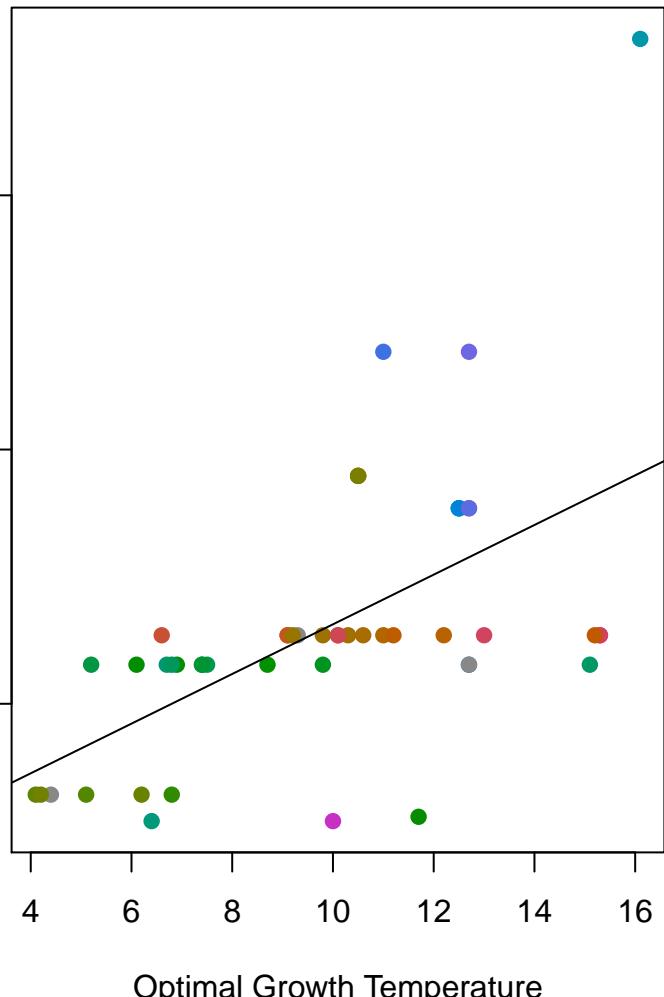
feature.pgfam_id.proline_residue.mean
PGF_00064827
Uncharacterized methyltransferase PA1407
 $r = 0.572$, $p = 10^{-4.85}$



feature.pgfam_id.proline_residue.mean

PGF_00060424

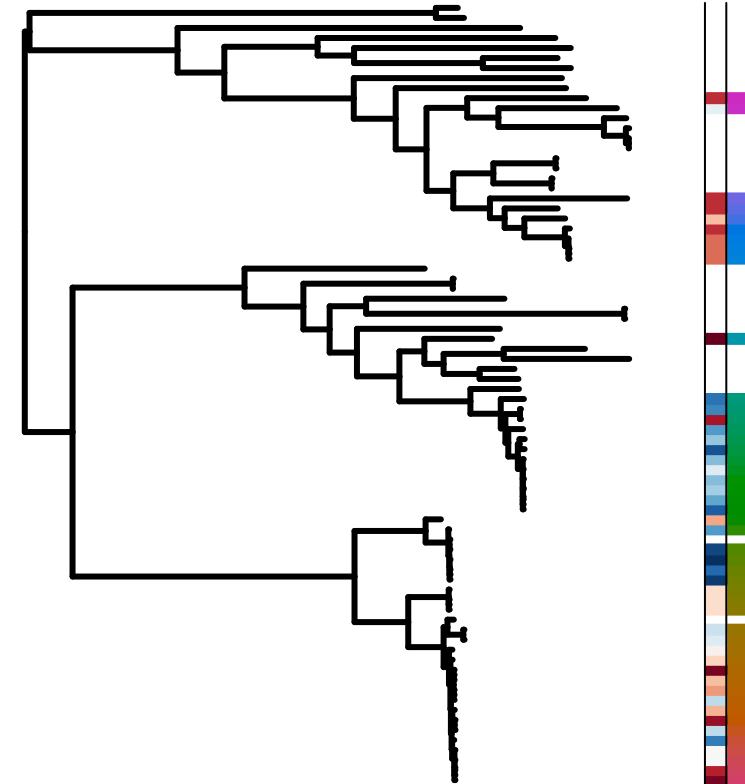
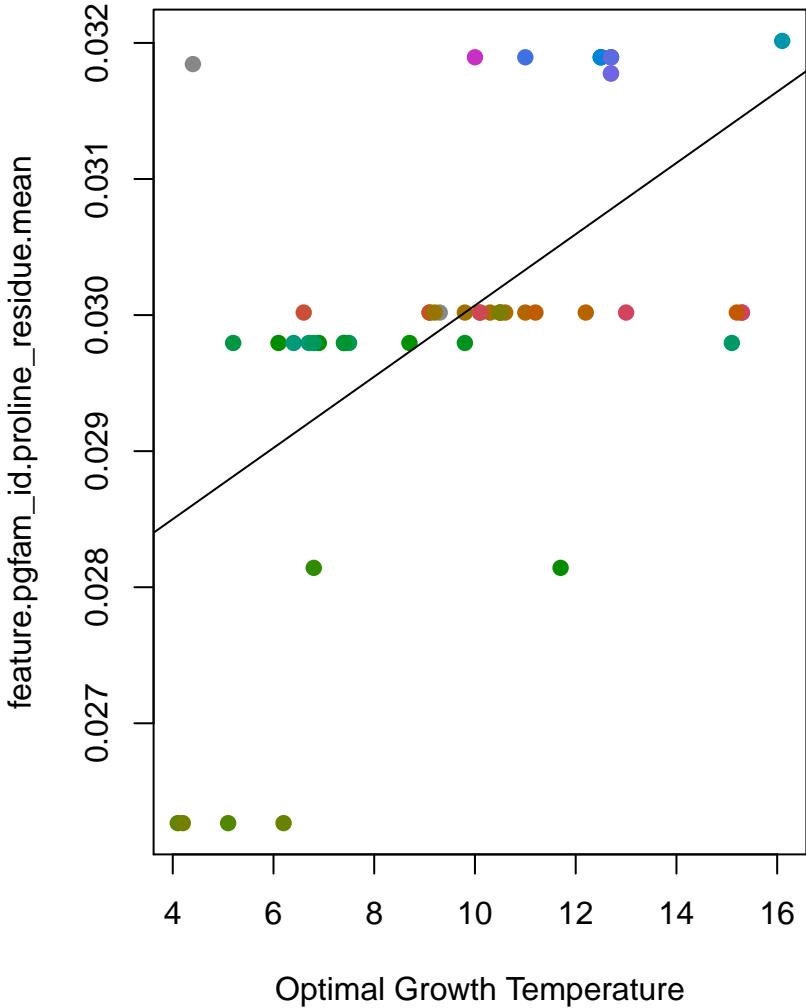
Translation elongation factor P Lys34--(R)-beta-lysine ligase
 $r = 0.567, p = 10^{-4.758}$

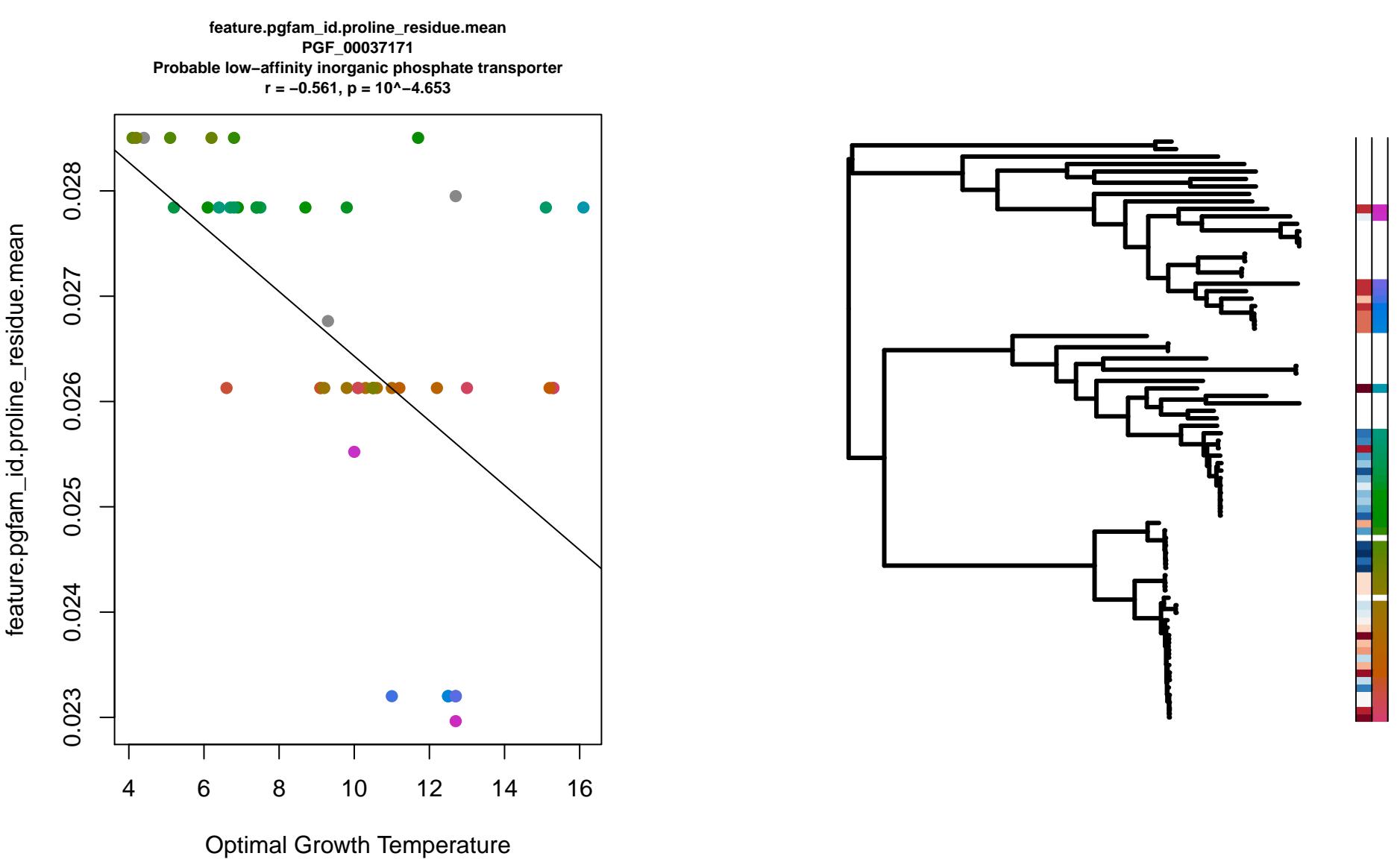


feature.pgfam_id.proline_residue.mean

PGF_00013509

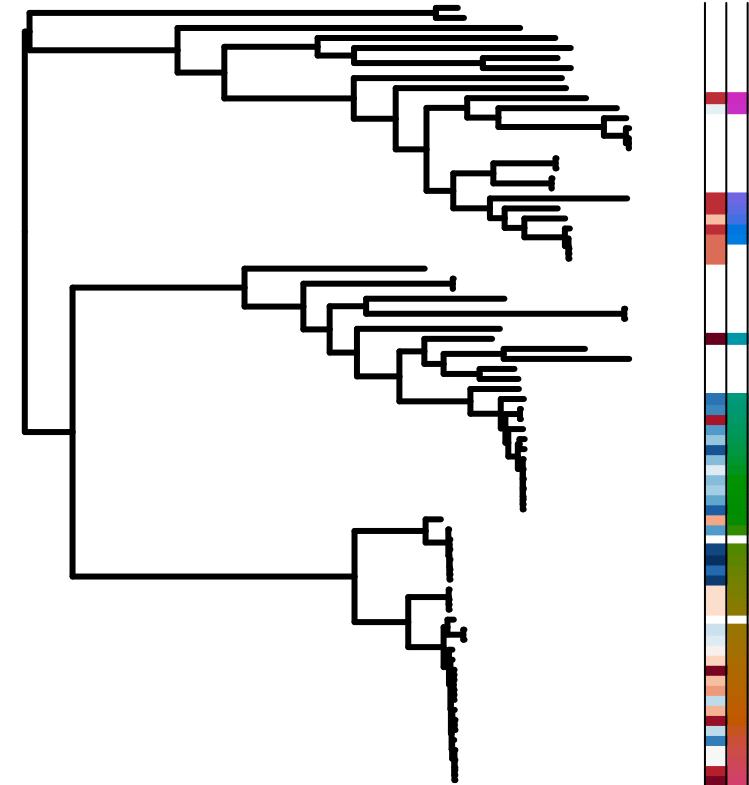
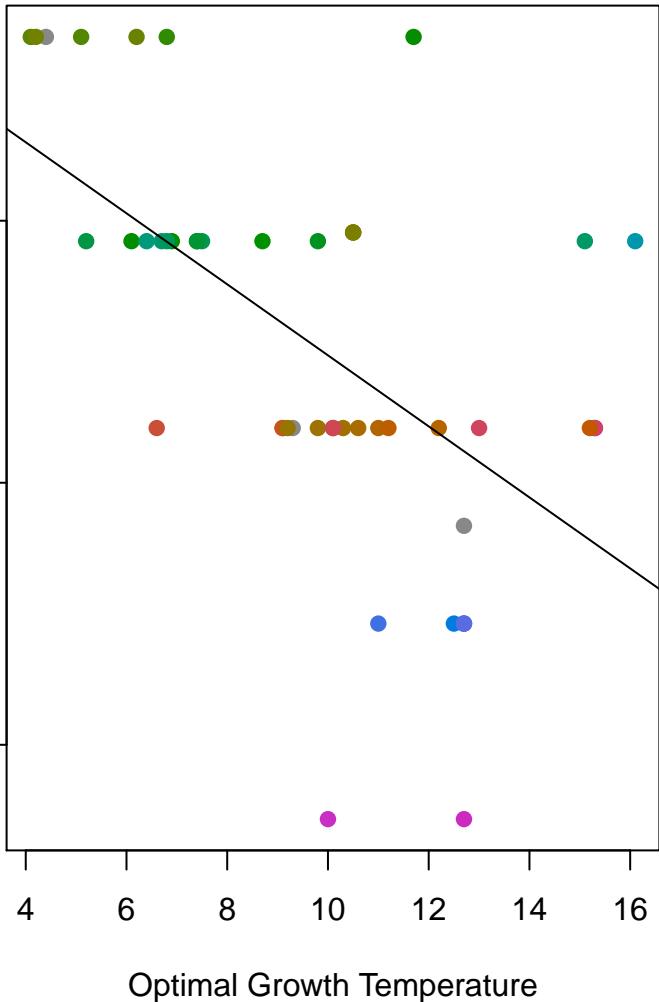
clohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC
 $r = 0.563$, $p = 10^{-4.683}$





feature.pgfam_id.proline_residue.mean
PGF_07420523
Exodeoxyribonuclease III (EC 3.1.11.2)
 $r = -0.572$, $p = 10^{-4.657}$

feature.pgfam_id.proline_residue.mean



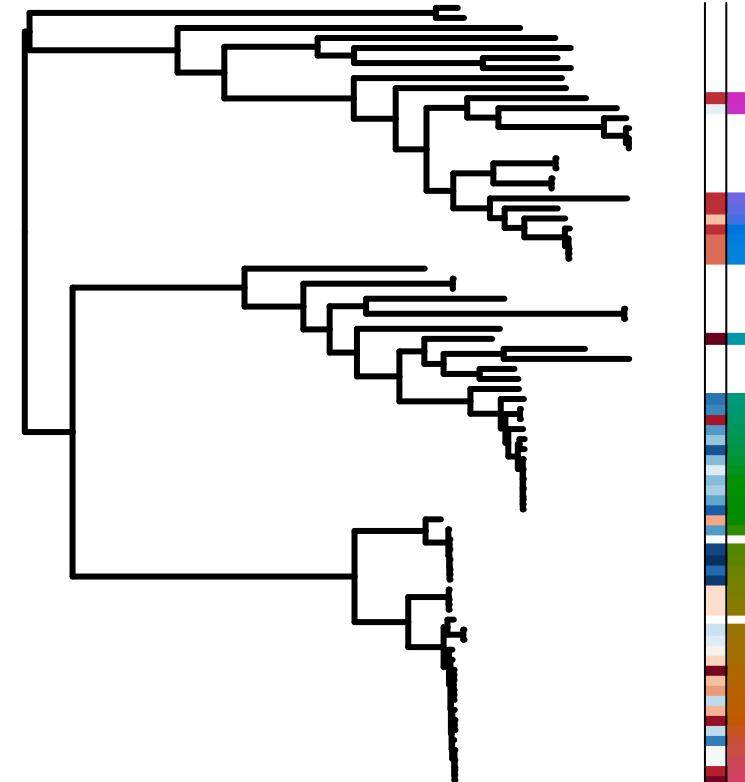
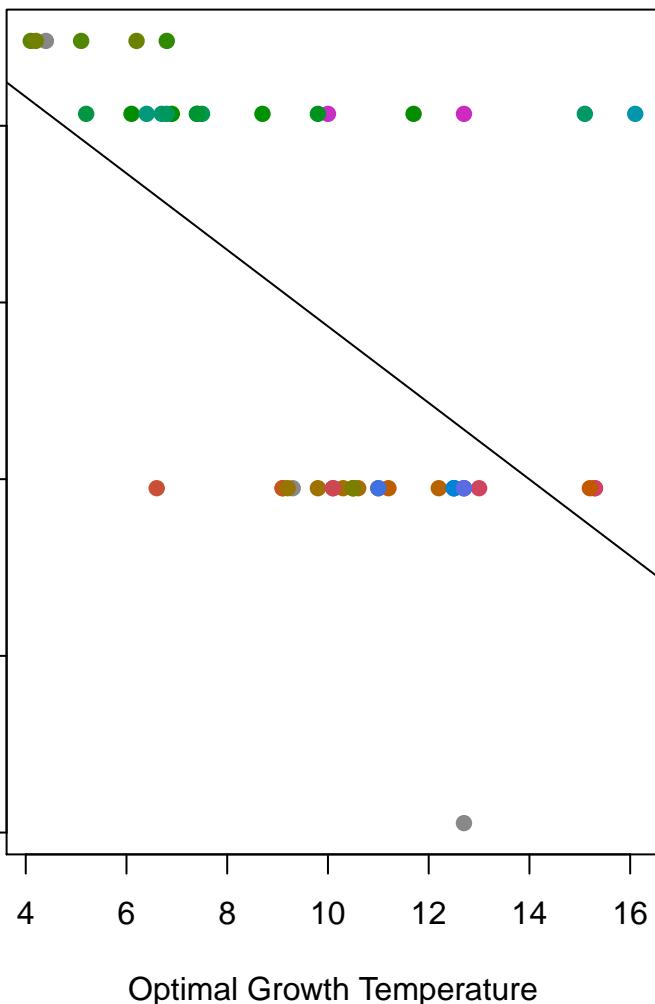
feature.pgfam_id.proline_residue.mean

PGF_00194856

hypothetical protein

$r = -0.575, p = 10^{-4.894}$

feature.pgfam_id.proline_residue.mean



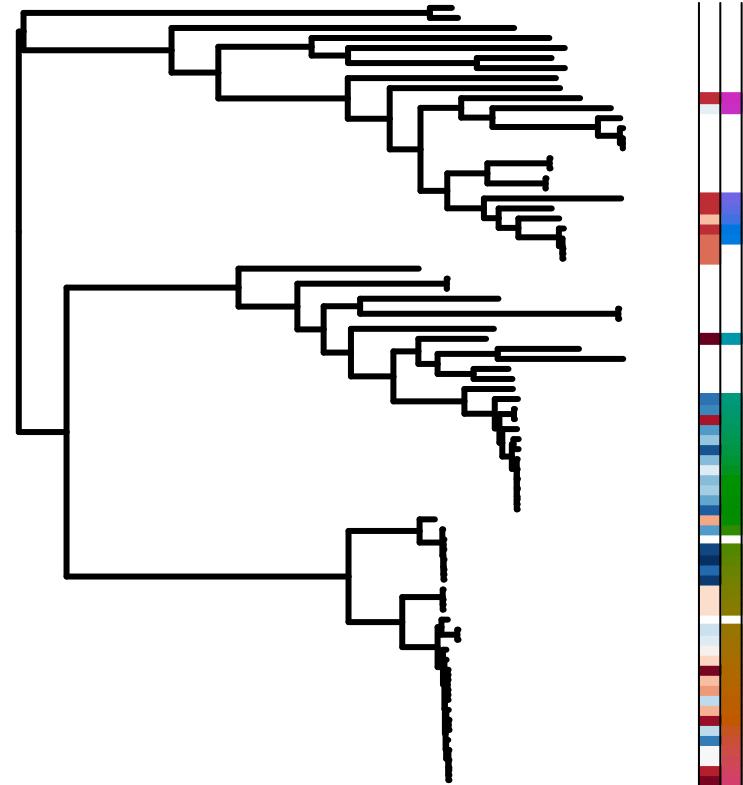
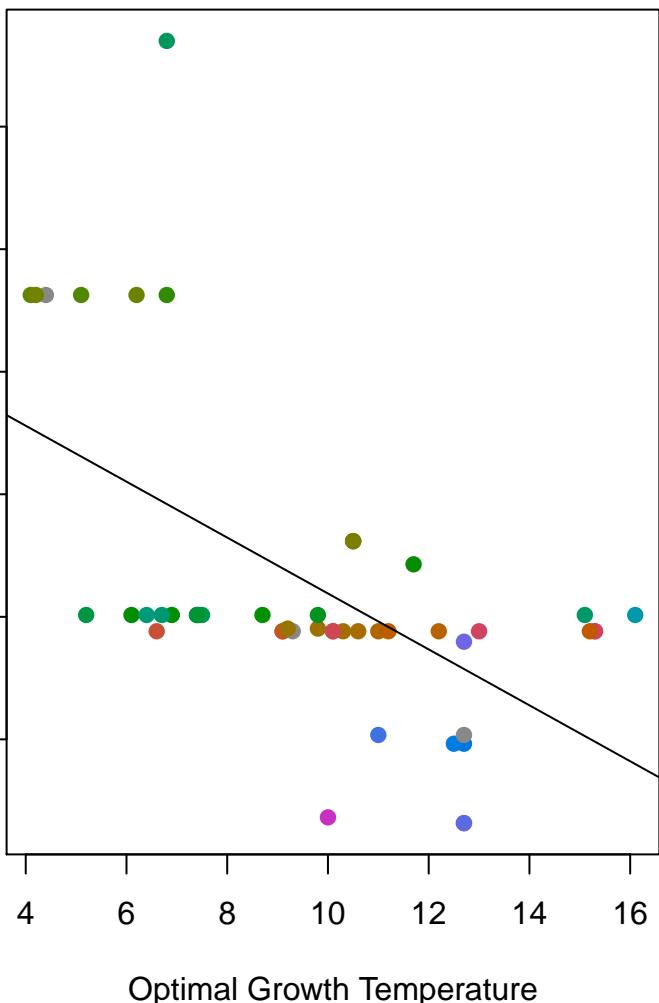
feature.pgfam_id.proline_residue.mean

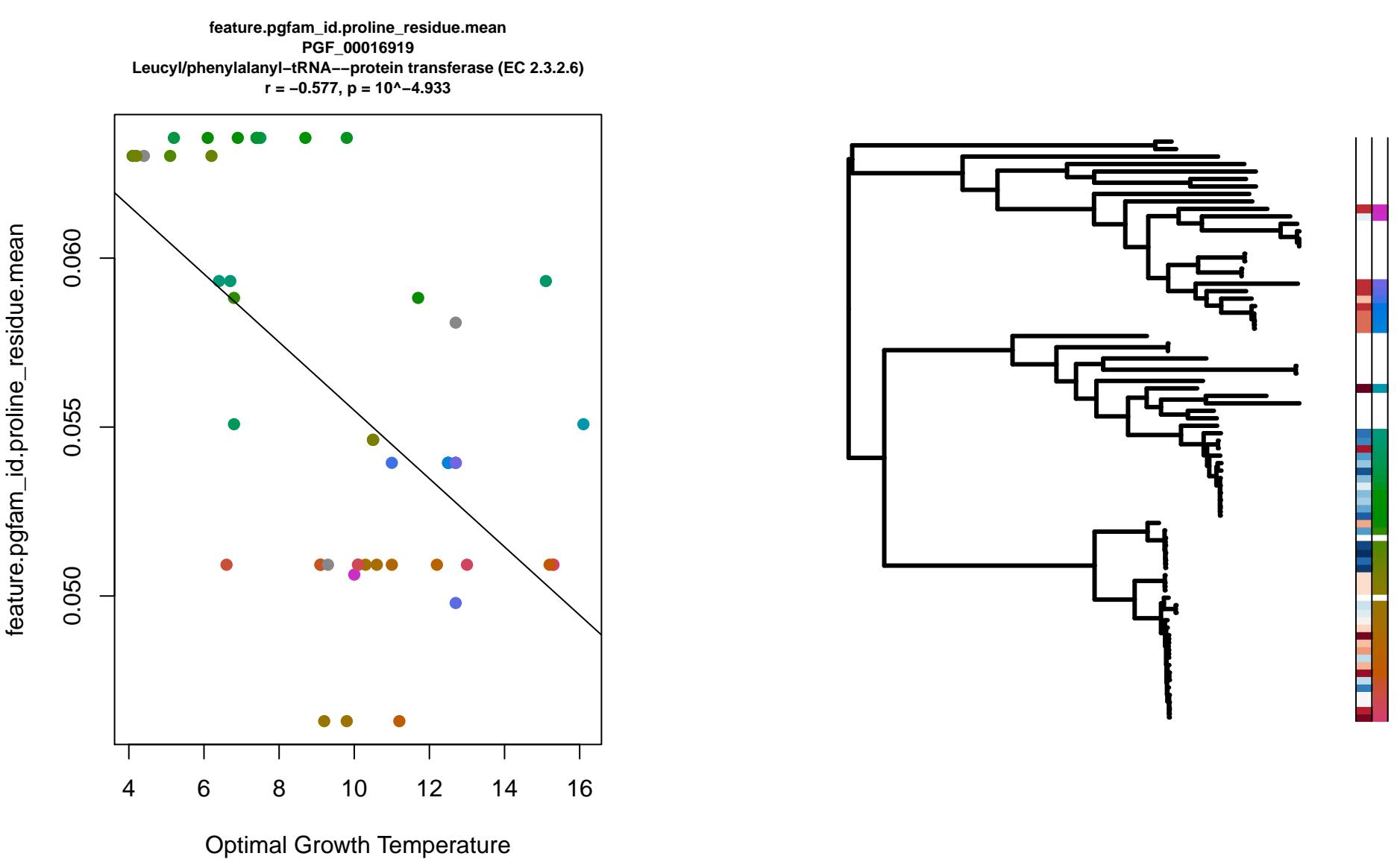
PGF_10414515

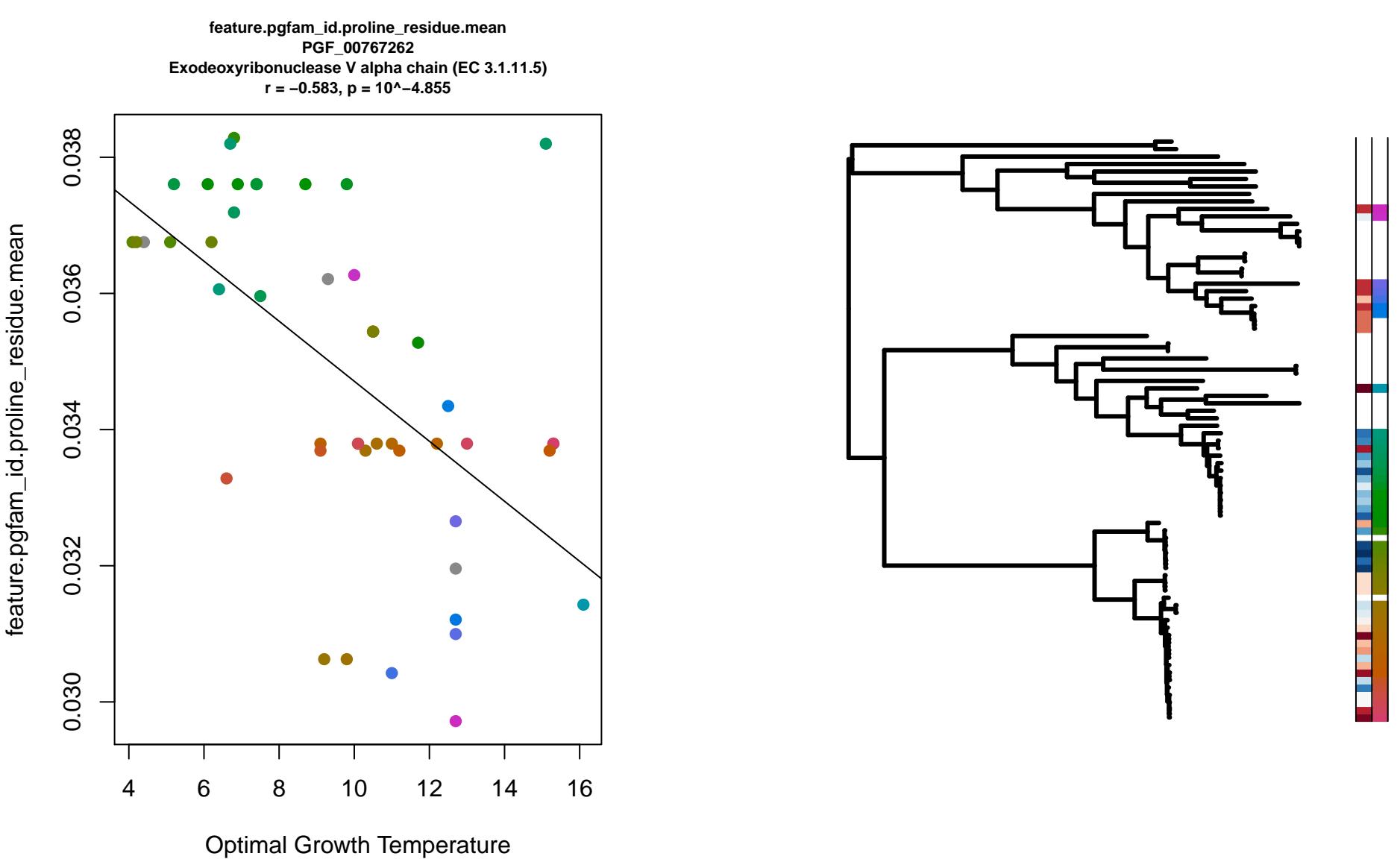
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)

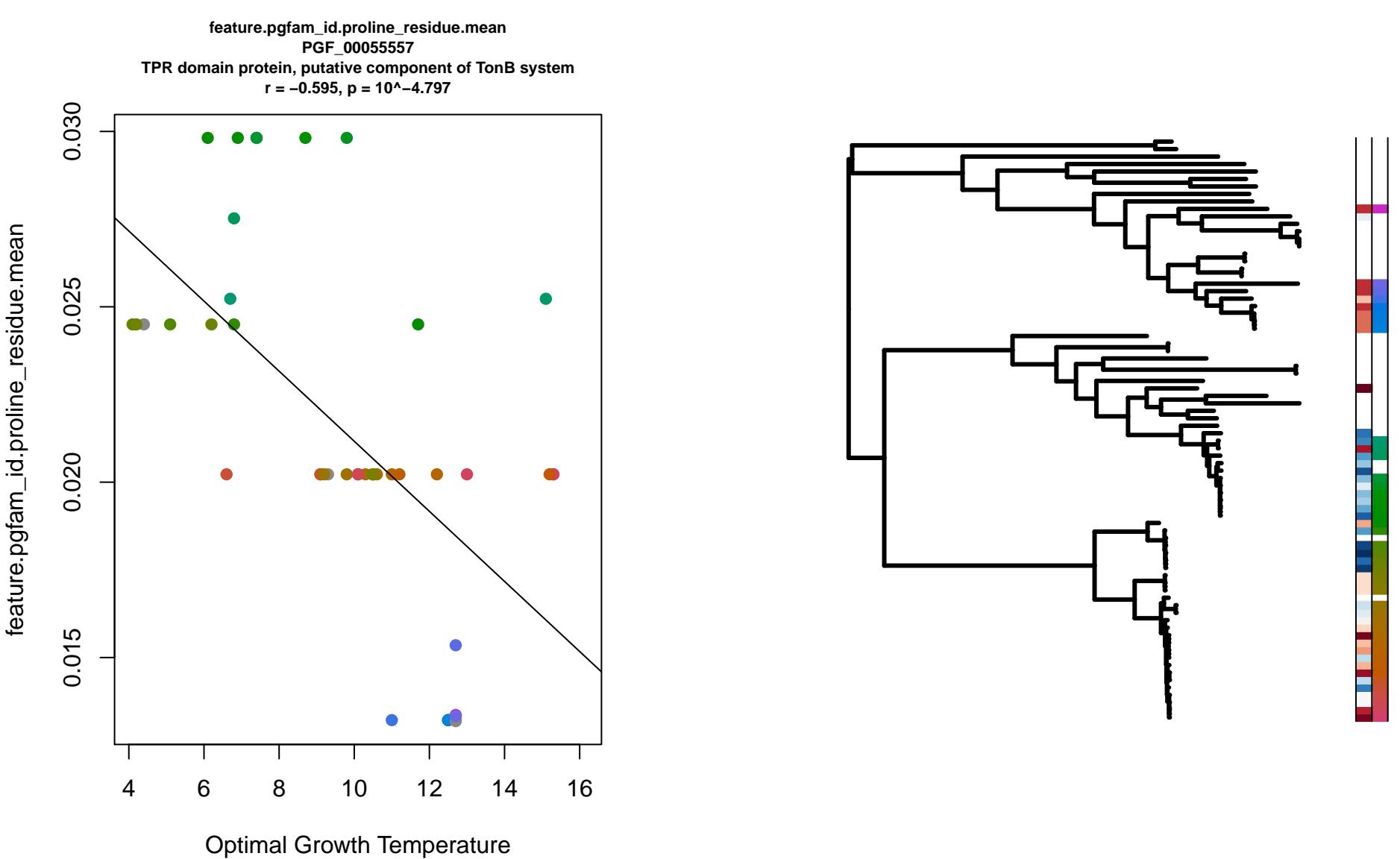
$r = -0.575$, $p = 10^{-4.725}$

feature.pgfam_id.proline_residue.mean



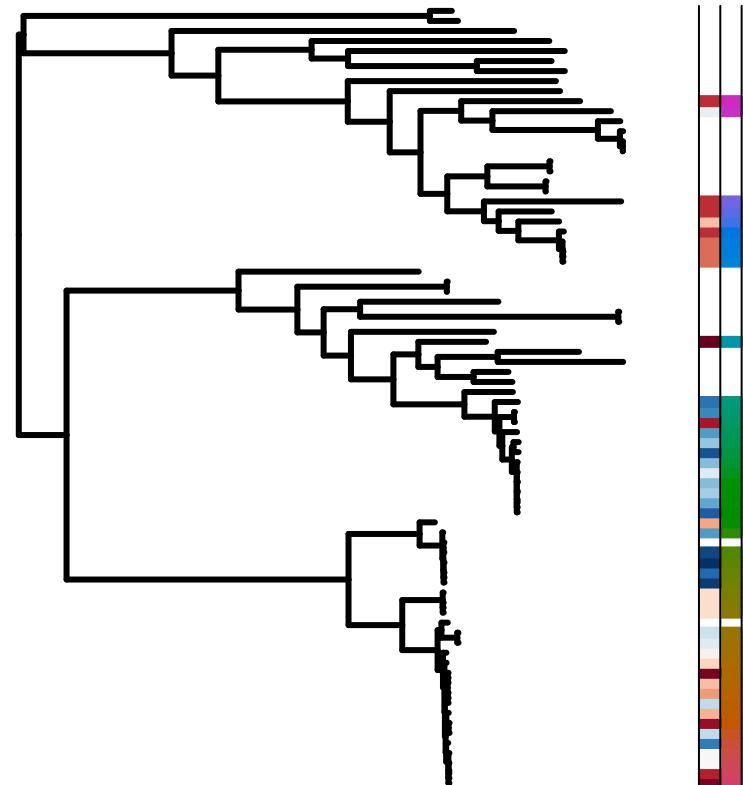
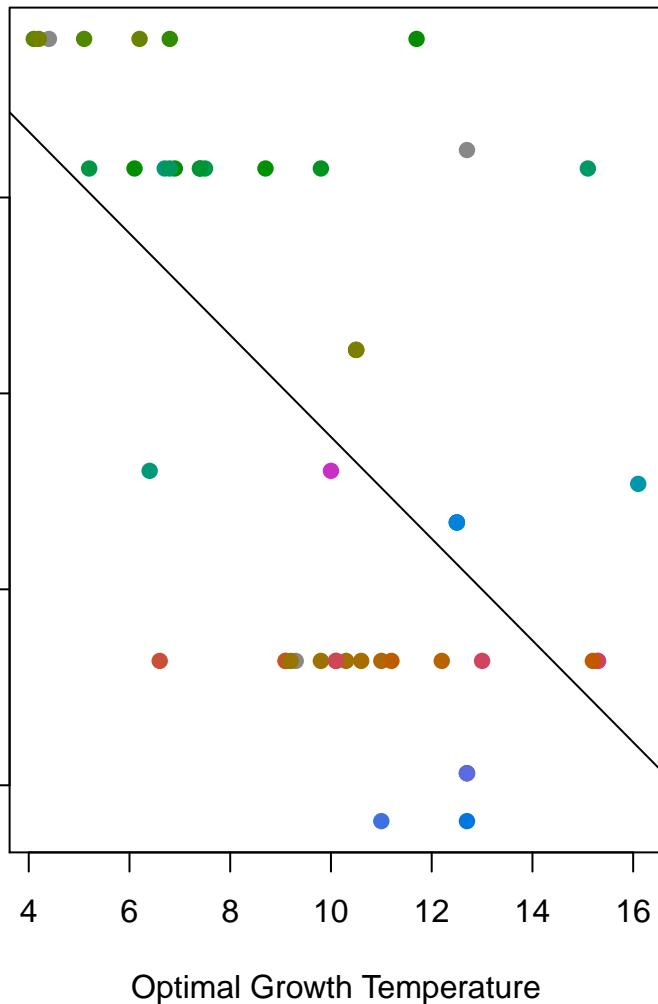






feature.pgfam_id.proline_residue.mean
PGF_00012356
Homoserine kinase (EC 2.7.1.39)
 $r = -0.6$, $p = 10^{-5.378}$

feature.pgfam_id.proline_residue.mean

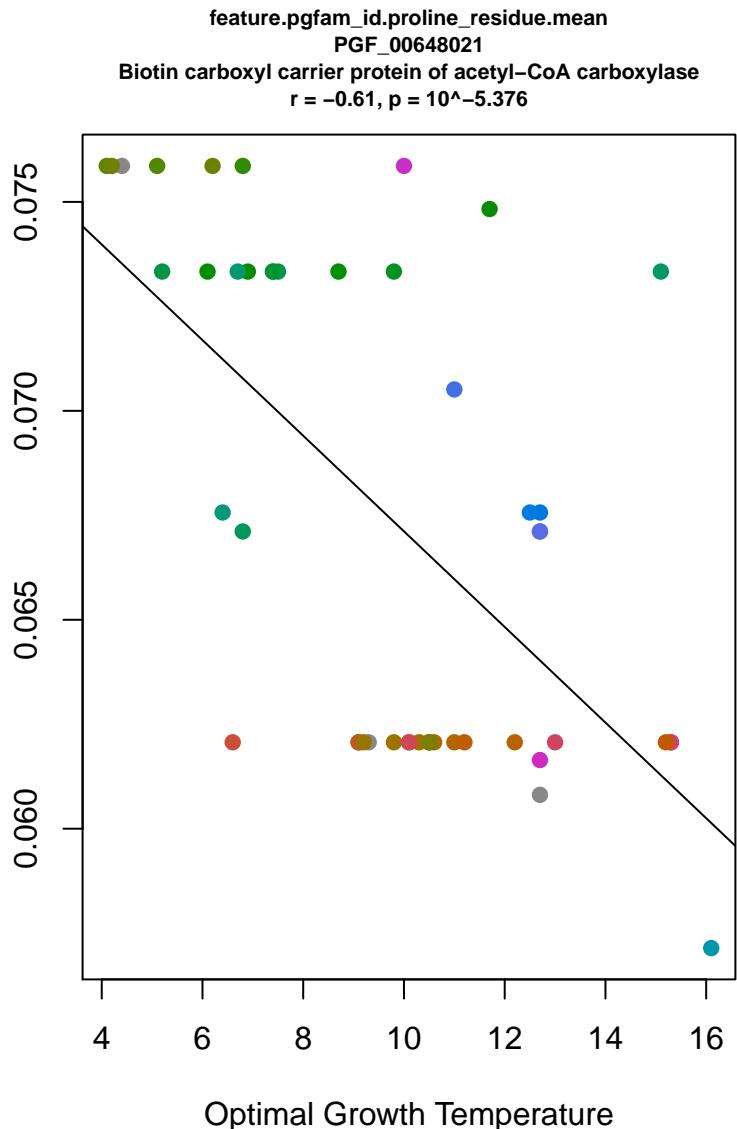


feature.pgfam_id.proline_residue.mean

PGF_00648021

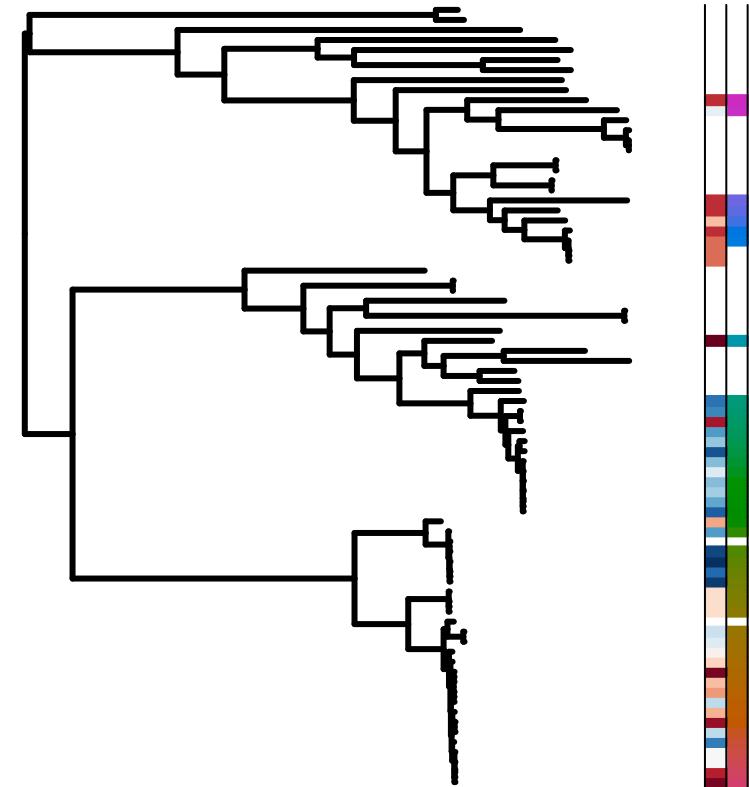
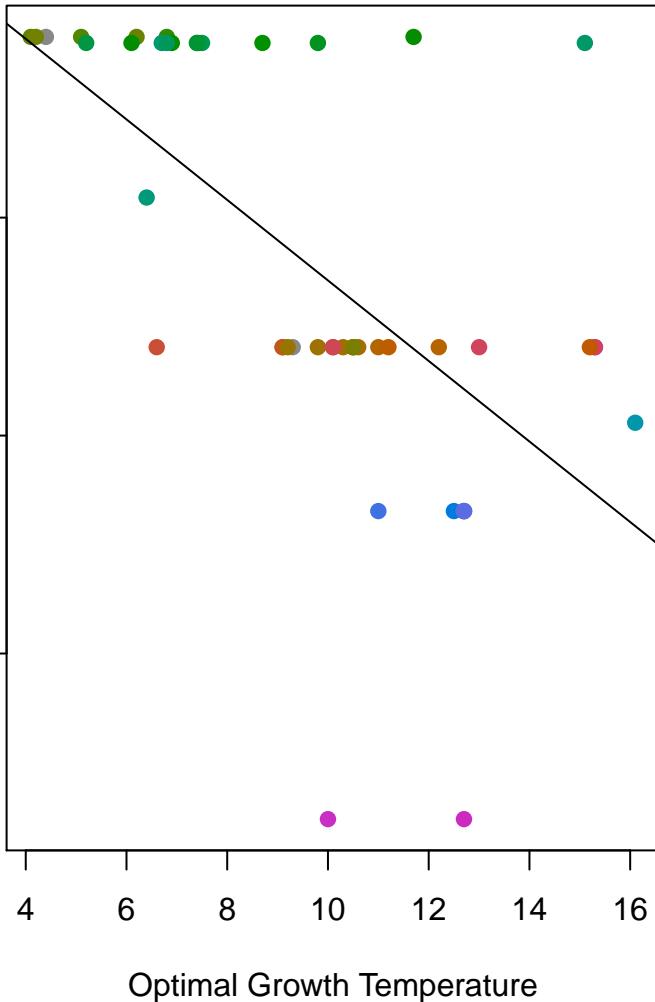
Biotin carboxyl carrier protein of acetyl-CoA carboxylase

$r = -0.61$, $p = 10^{-5.376}$



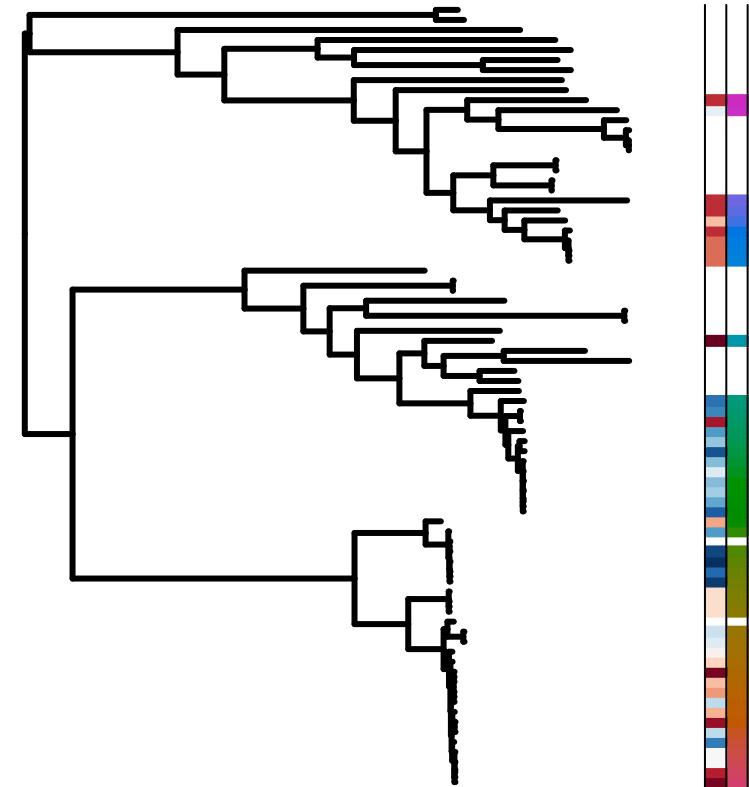
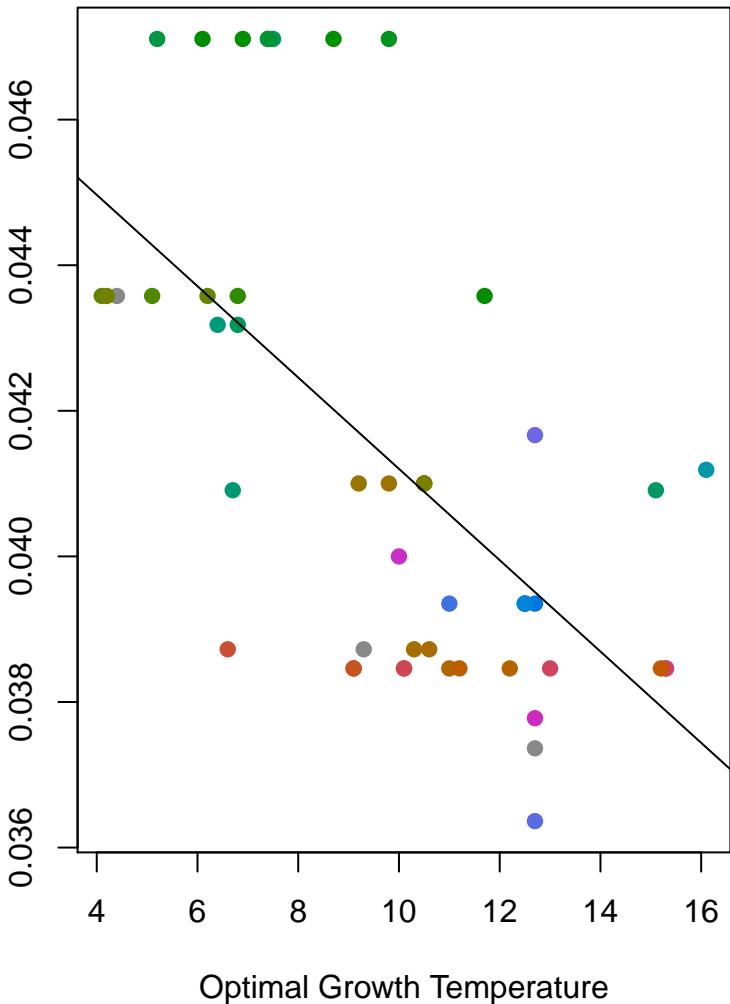
feature.pgfam_id.proline_residue.mean
PGF_00010518
HD domain protein
 $r = -0.613$, $p = 10^{-5.435}$

feature.pgfam_id.proline_residue.mean



feature.pgfam_id.proline_residue.mean
PGF_00017737
ATP-dependent RNA helicase VF1437
 $r = -0.619$, $p = 10^{-5.772}$

feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature

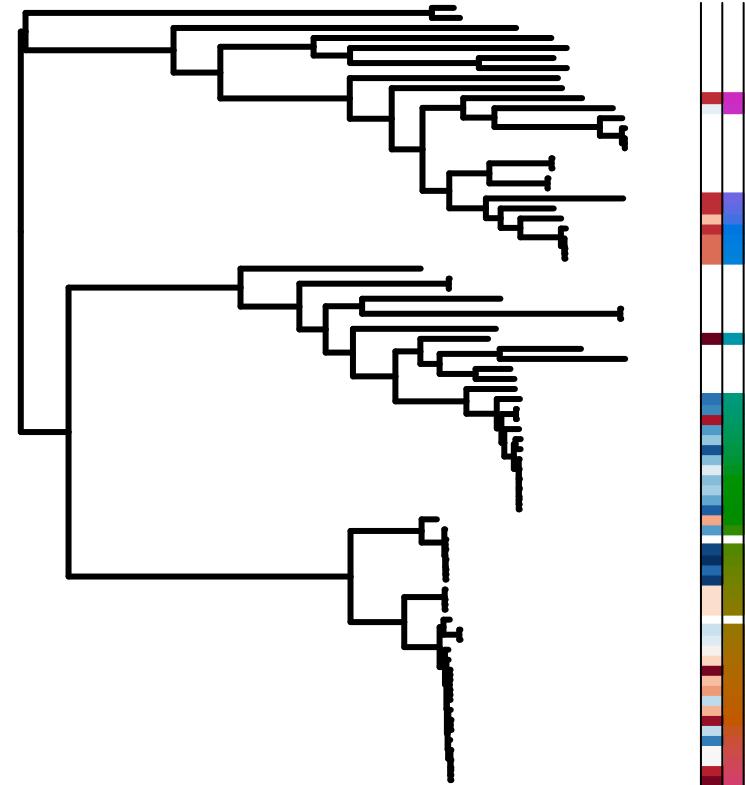
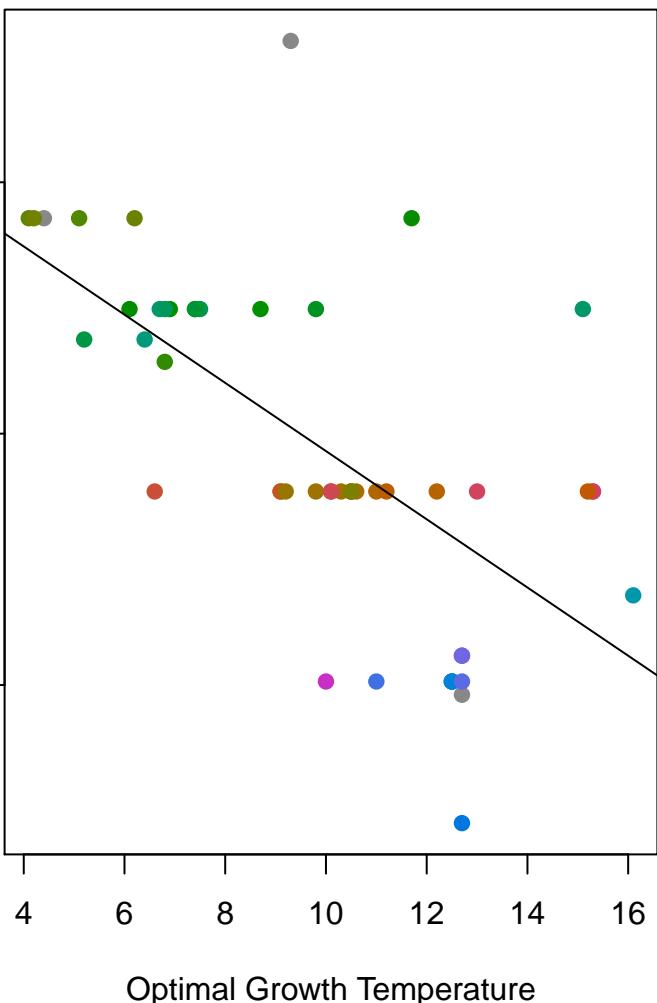
feature.pgfam_id.proline_residue.mean

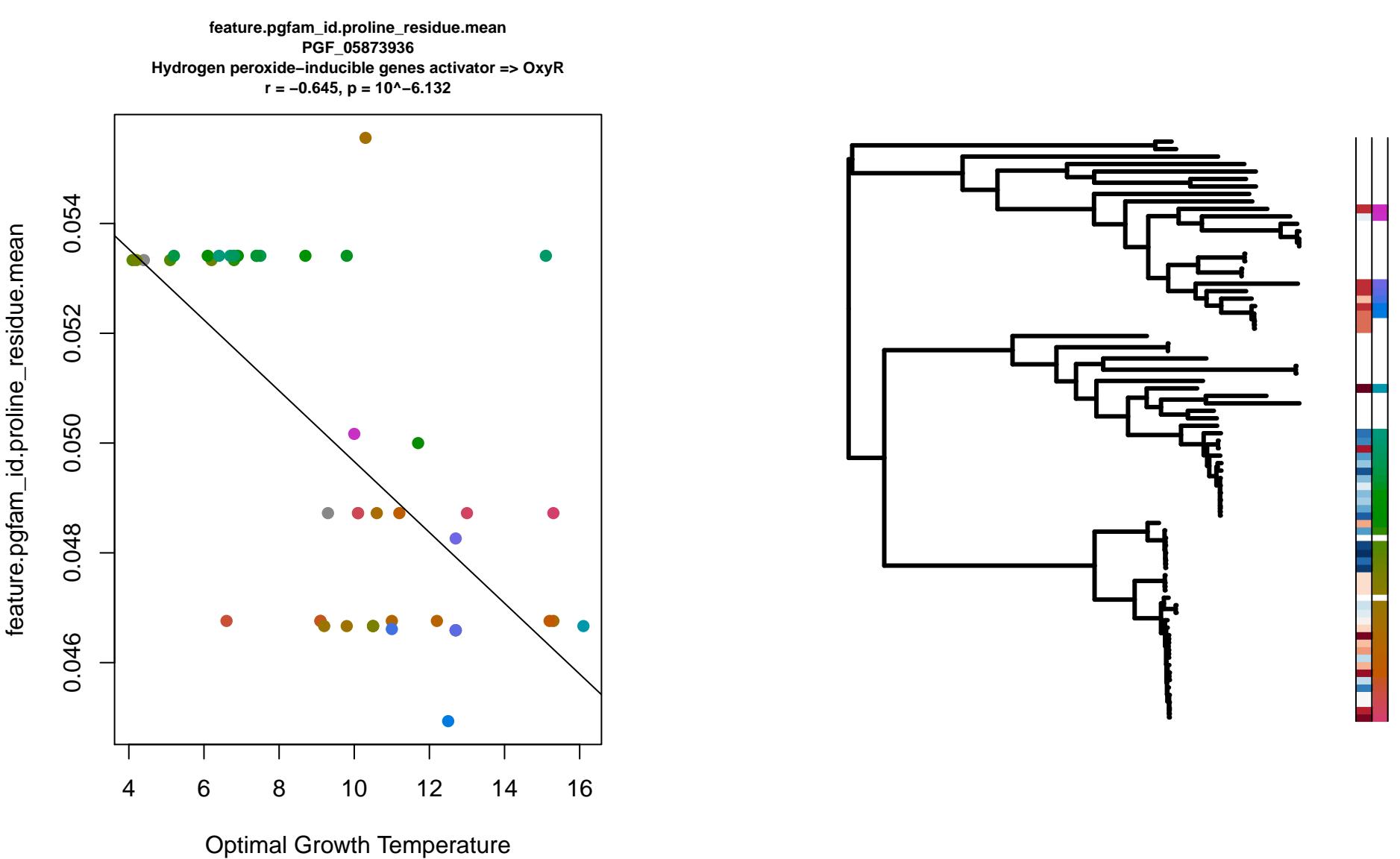
PGF_00423382

Dihydroorotate (EC 3.5.2.3)

$r = -0.642, p = 10^{-6.294}$

feature.pgfam_id.proline_residue.mean



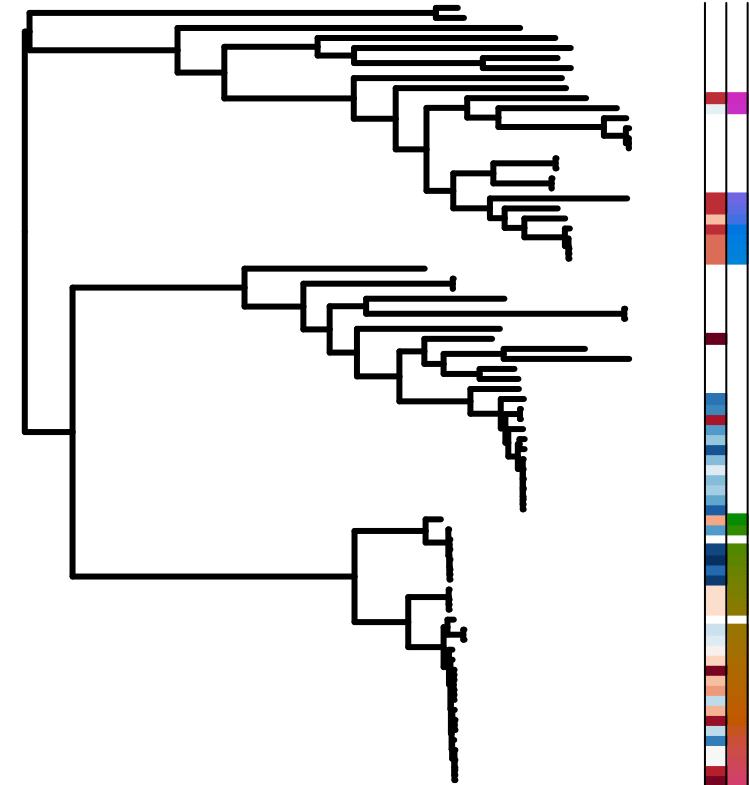
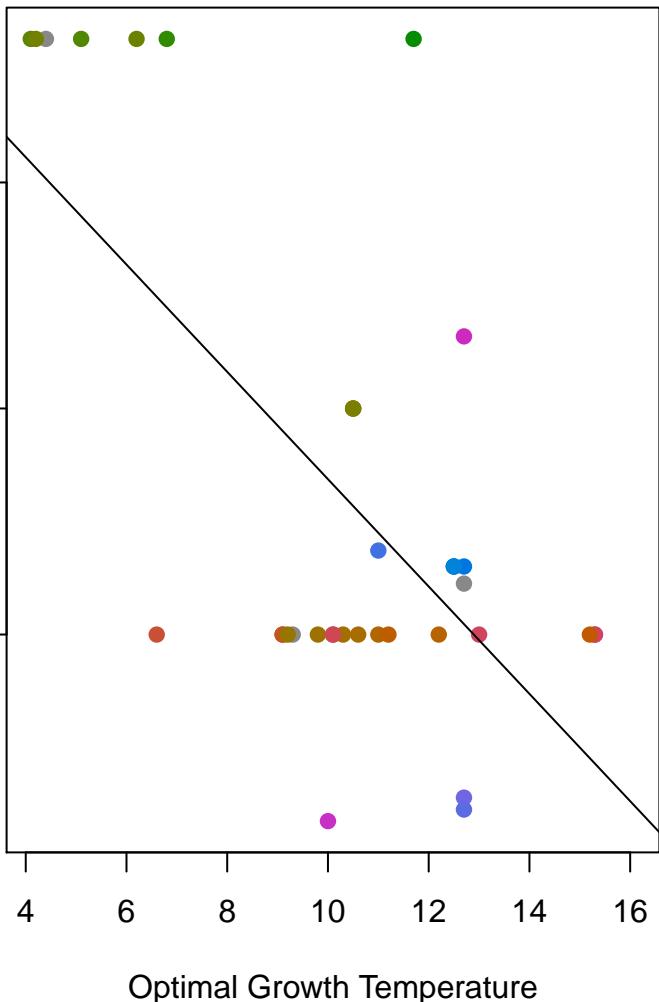


feature.pgfam_id.proline_residue.mean

PGF_02790700

ylcobinamide kinase (EC 2.7.1.156) / Adenosylcobinamide-phosphate guanylyltransferase (EC :
 $r = -0.651, p = 10^{-4.883}$

feature.pgfam_id.proline_residue.mean

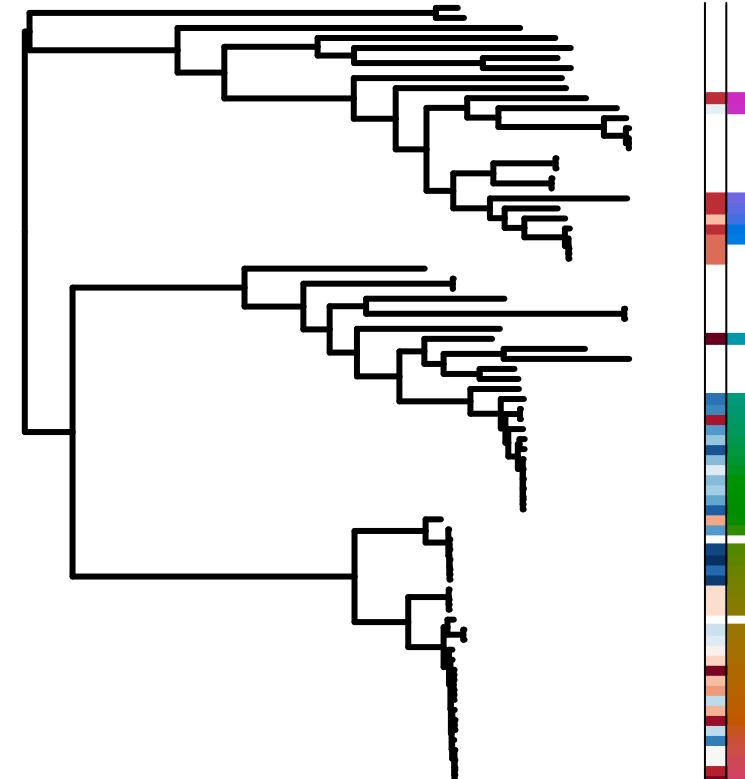
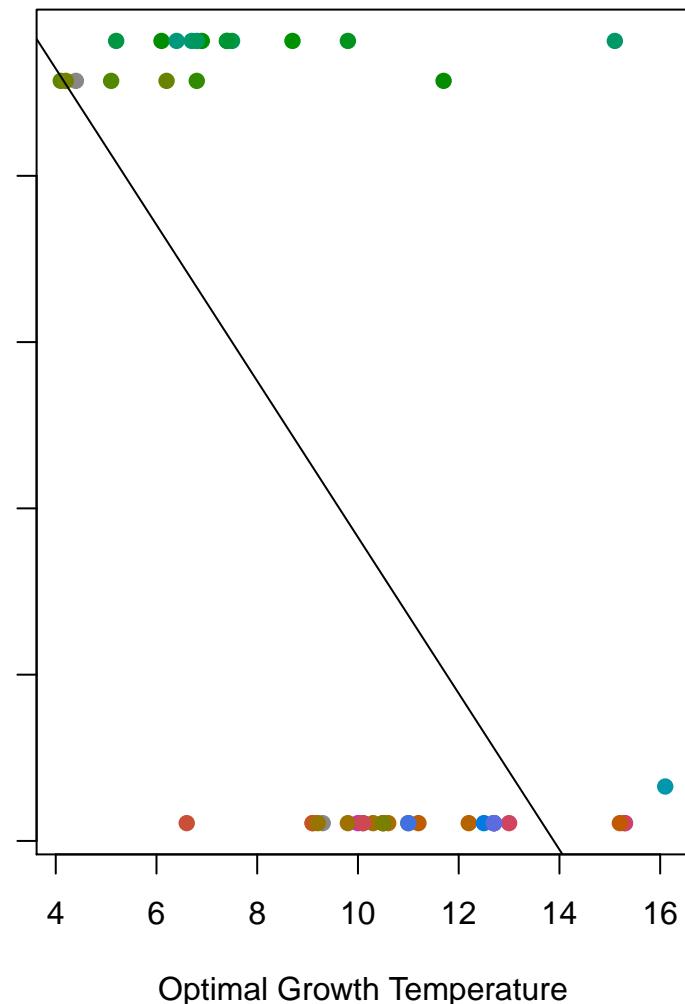


feature.pgfam_id.proline_residue.mean

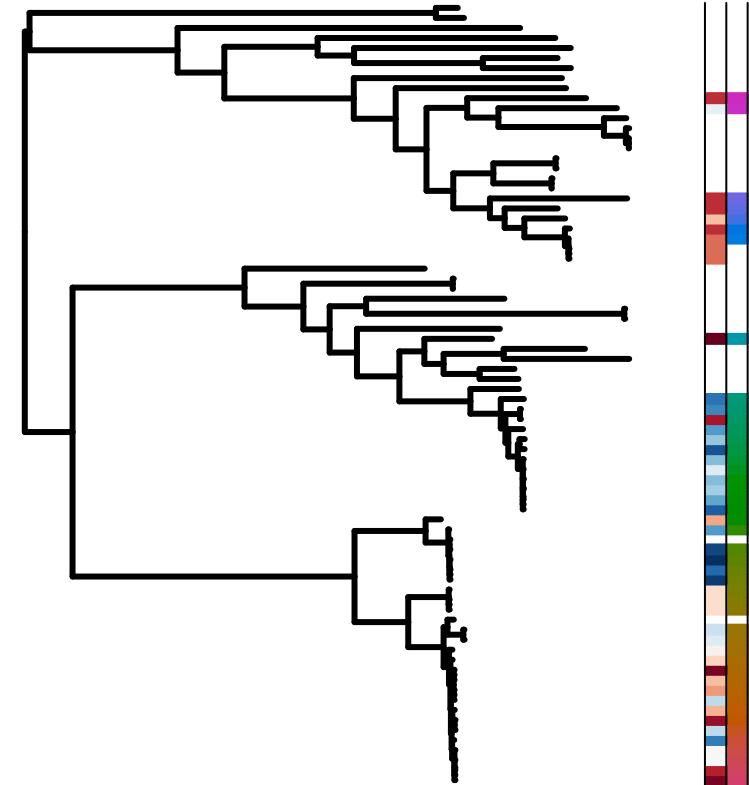
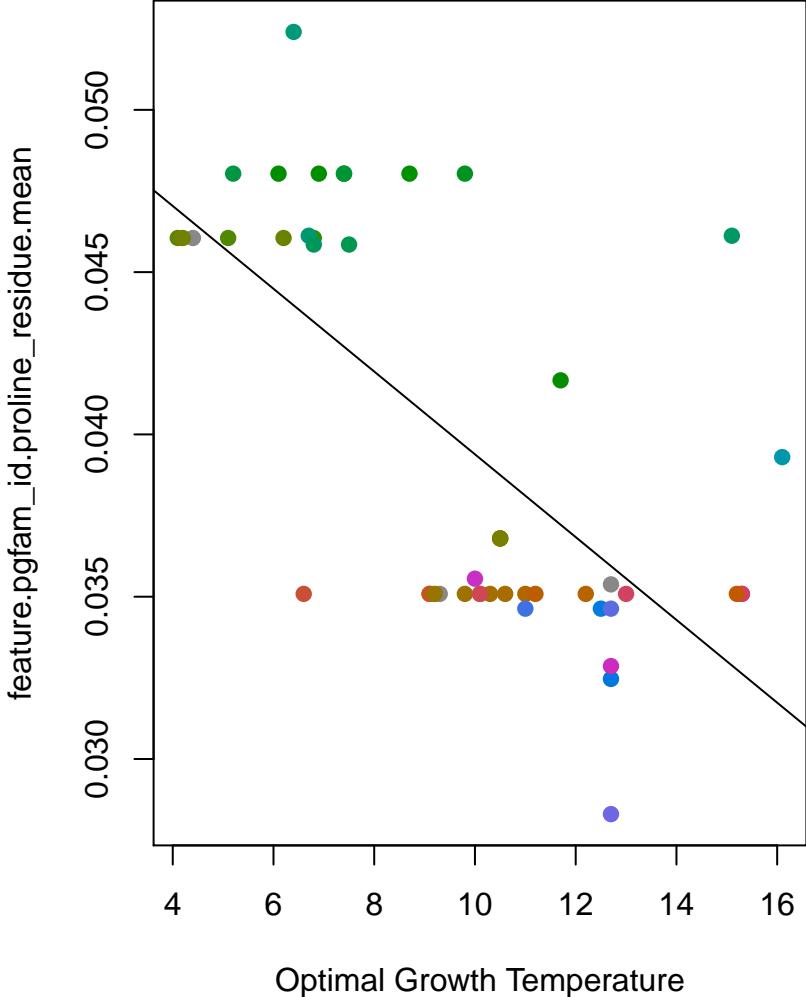
PGF_10245672

Ribulose-phosphate 3-epimerase (EC 5.1.3.1)

$r = -0.655$, $p = 10^{-6.348}$



feature.pgfam_id.proline_residue.mean
PGF_09087715
tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)
 $r = -0.658$, $p = 10^{-6.428}$



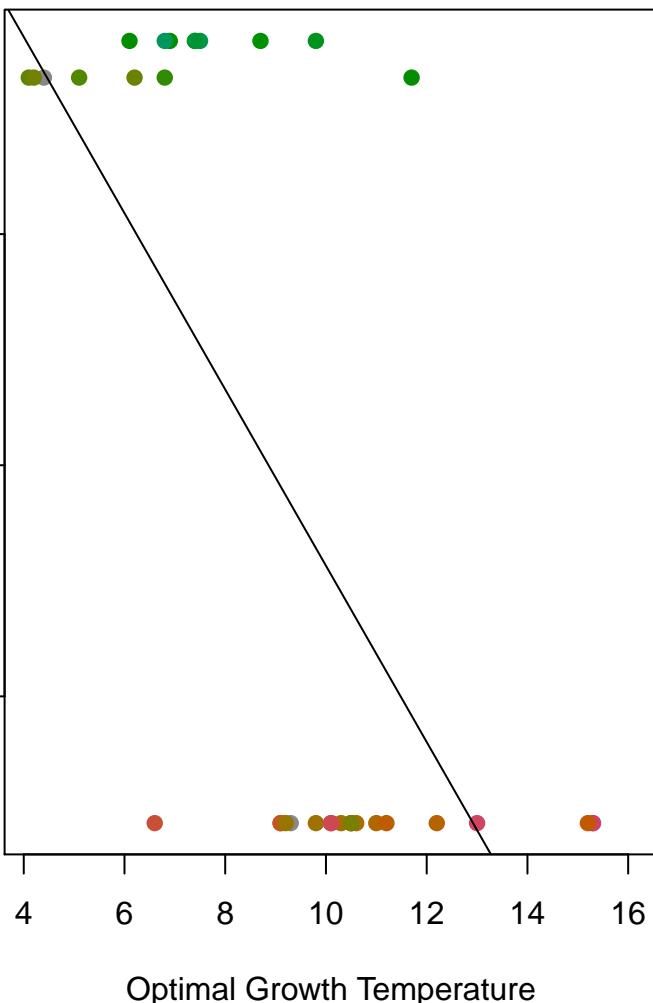
feature.pgfam_id.proline_residue.mean

PGF_07991944

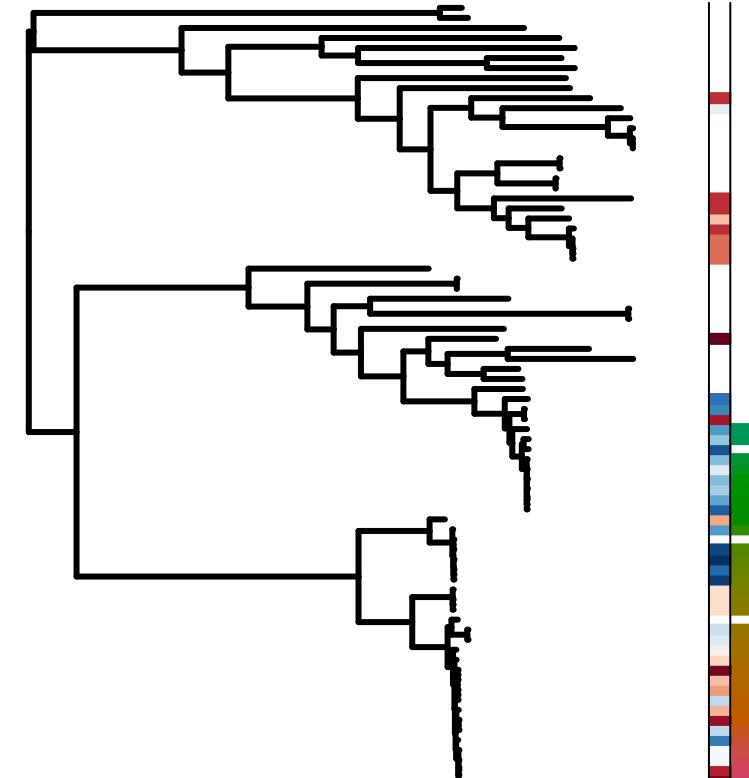
hypothetical protein

$r = -0.682, p = 10^{-5.189}$

feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature

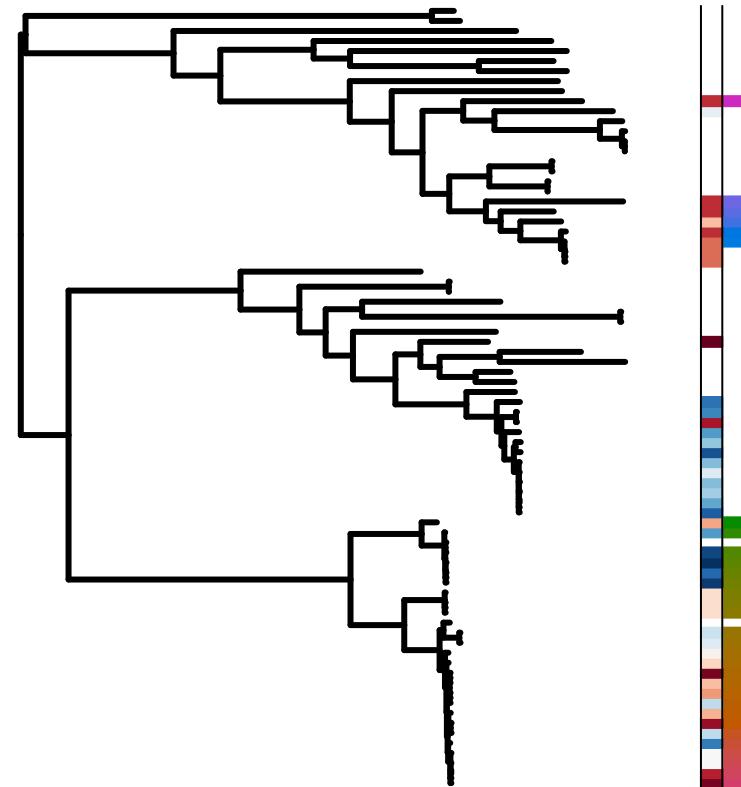
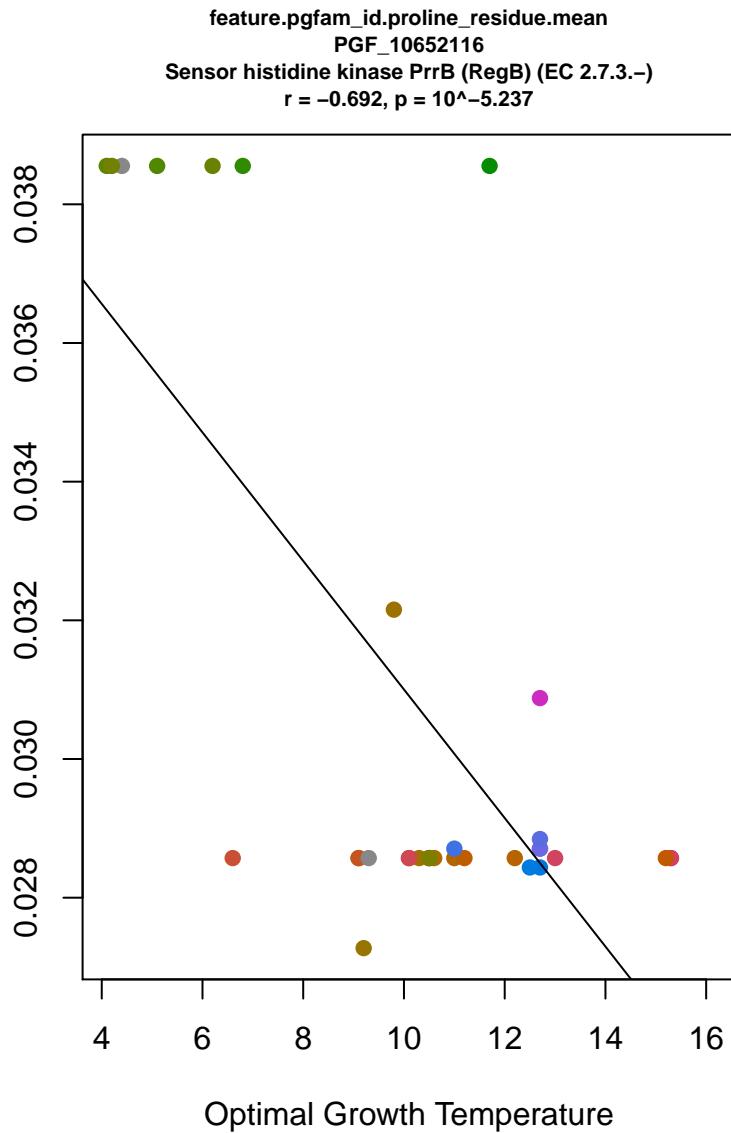


feature.pgfam_id.proline_residue.mean

PGF_10652116

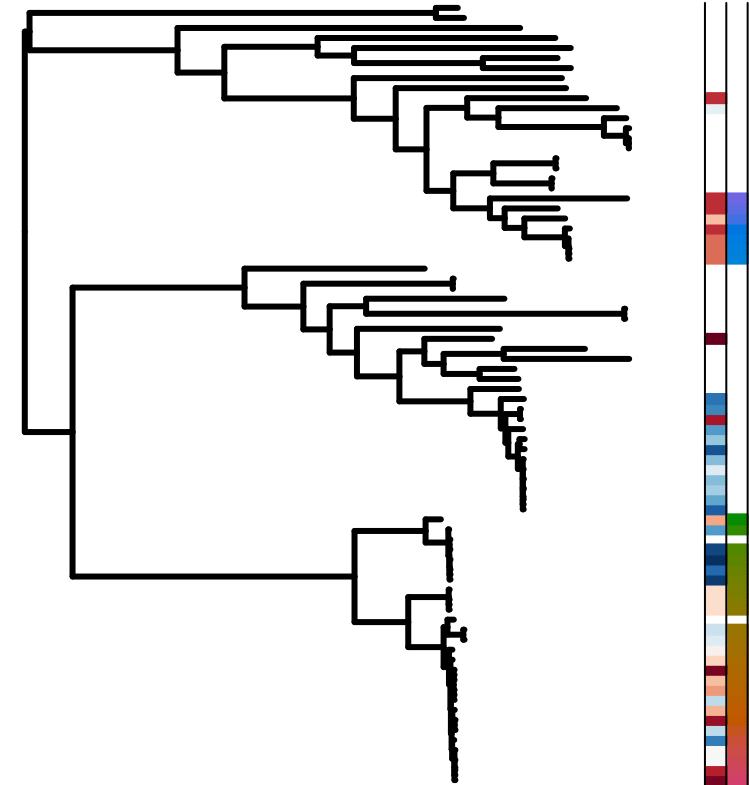
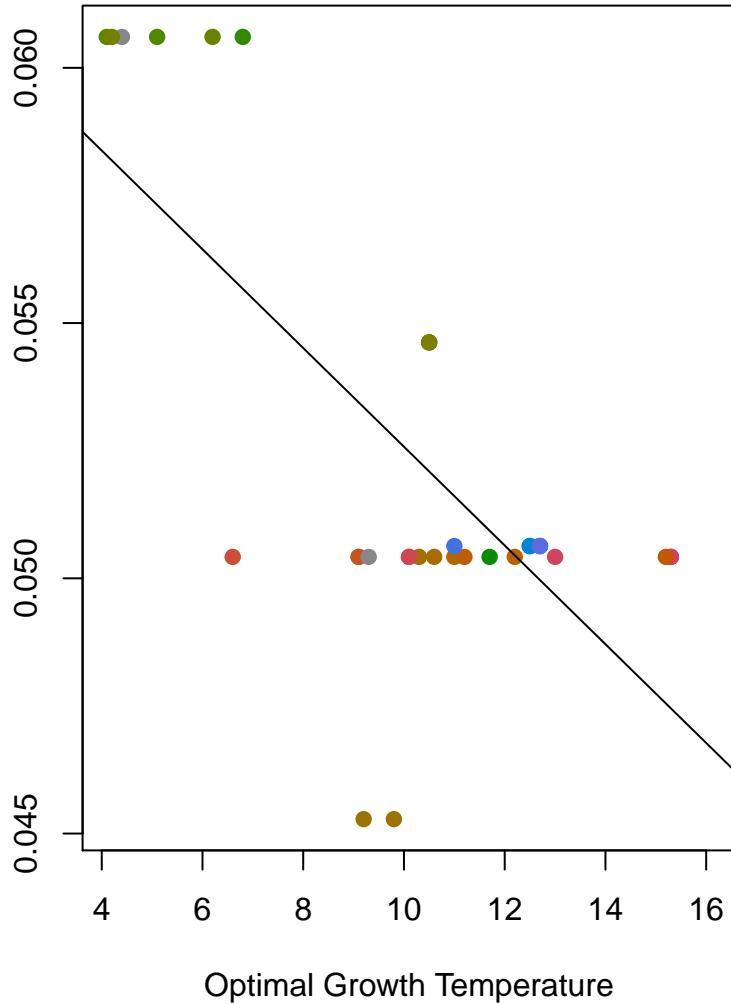
Sensor histidine kinase PrrB (RegB) (EC 2.7.3.-)

$r = -0.692, p = 10^{-5.237}$



feature.pgfam_id.proline_residue.mean
PGF_00067426
ZIP zinc transporter family protein
 $r = -0.693$, $p = 10^{-5.407}$

feature.pgfam_id.proline_residue.mean



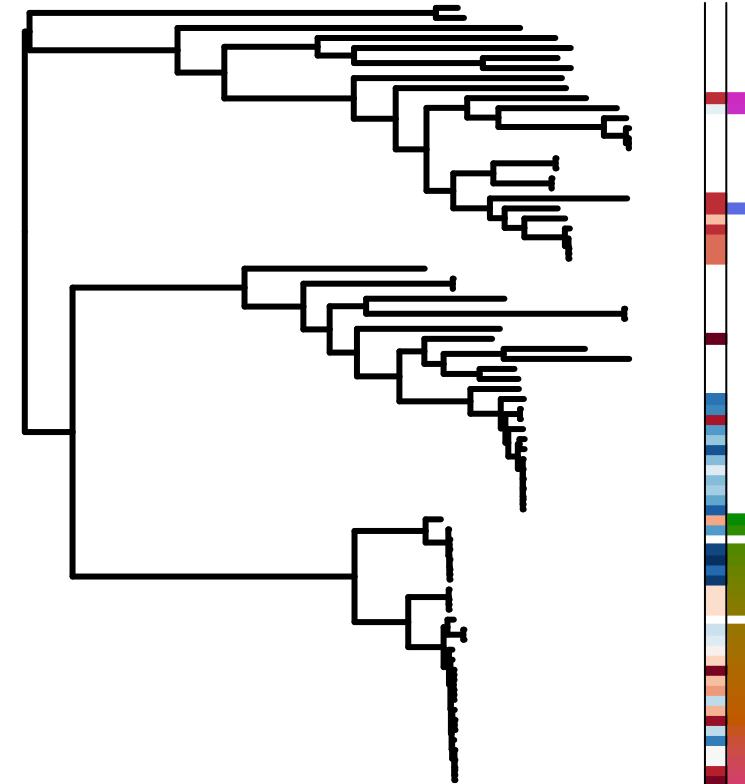
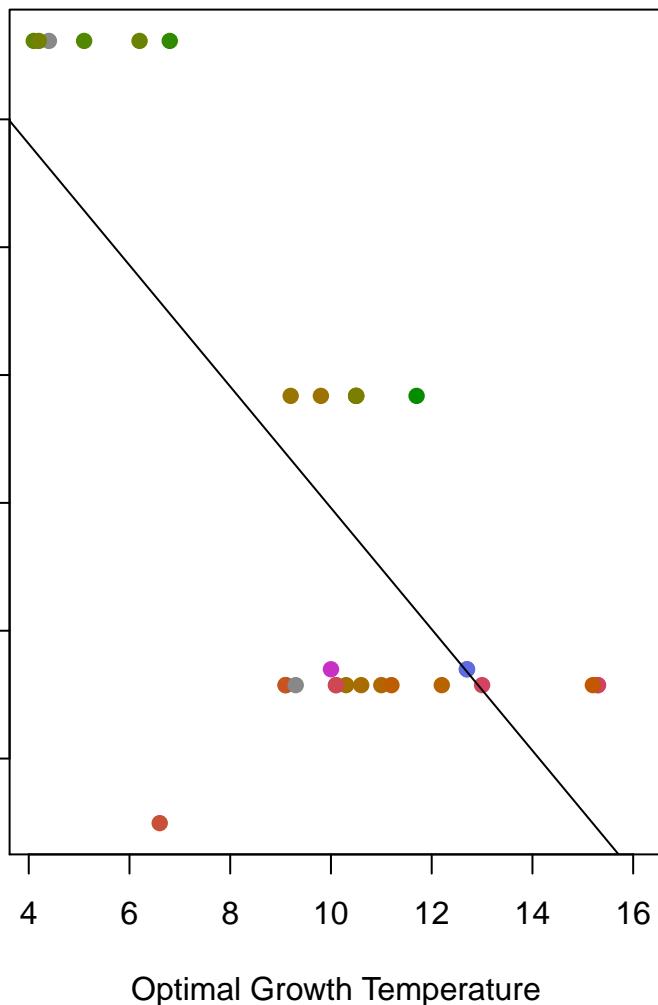
feature.pgfam_id.proline_residue.mean

PGF_01481272

Chemotaxis protein CheD

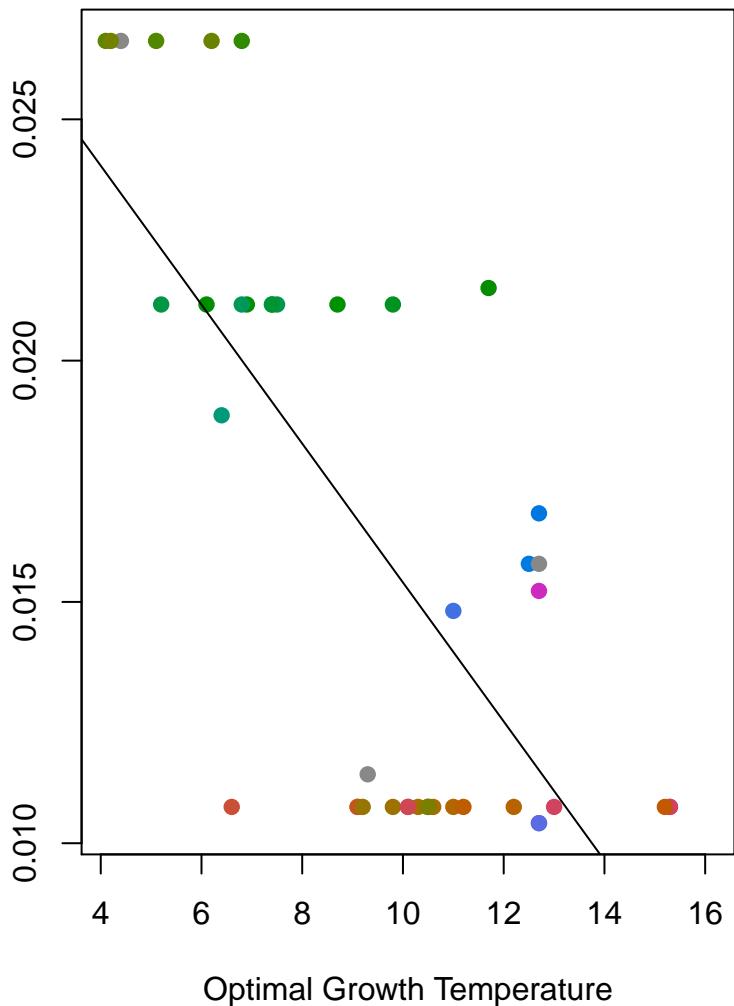
$r = -0.719, p = 10^{-5.117}$

feature.pgfam_id.proline_residue.mean

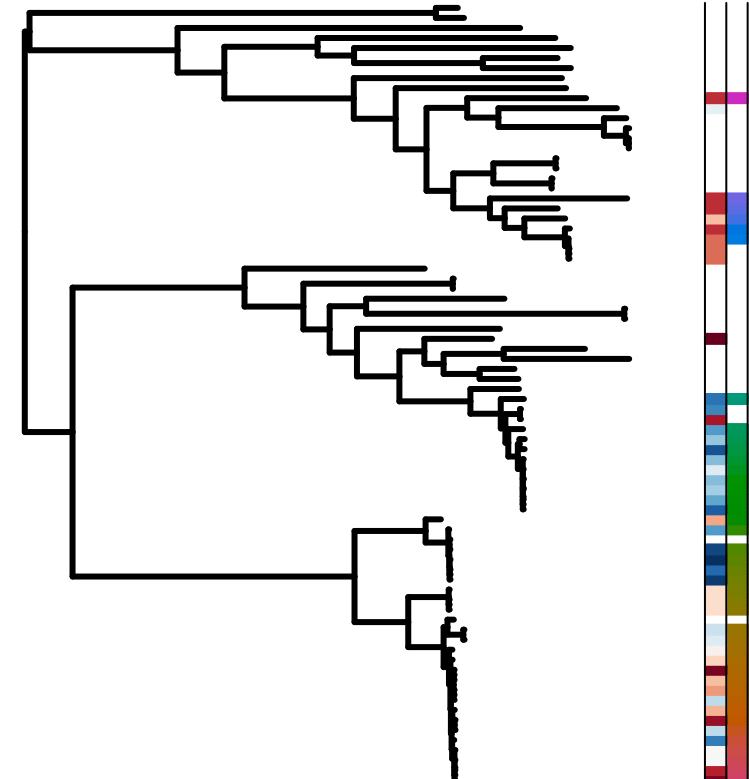


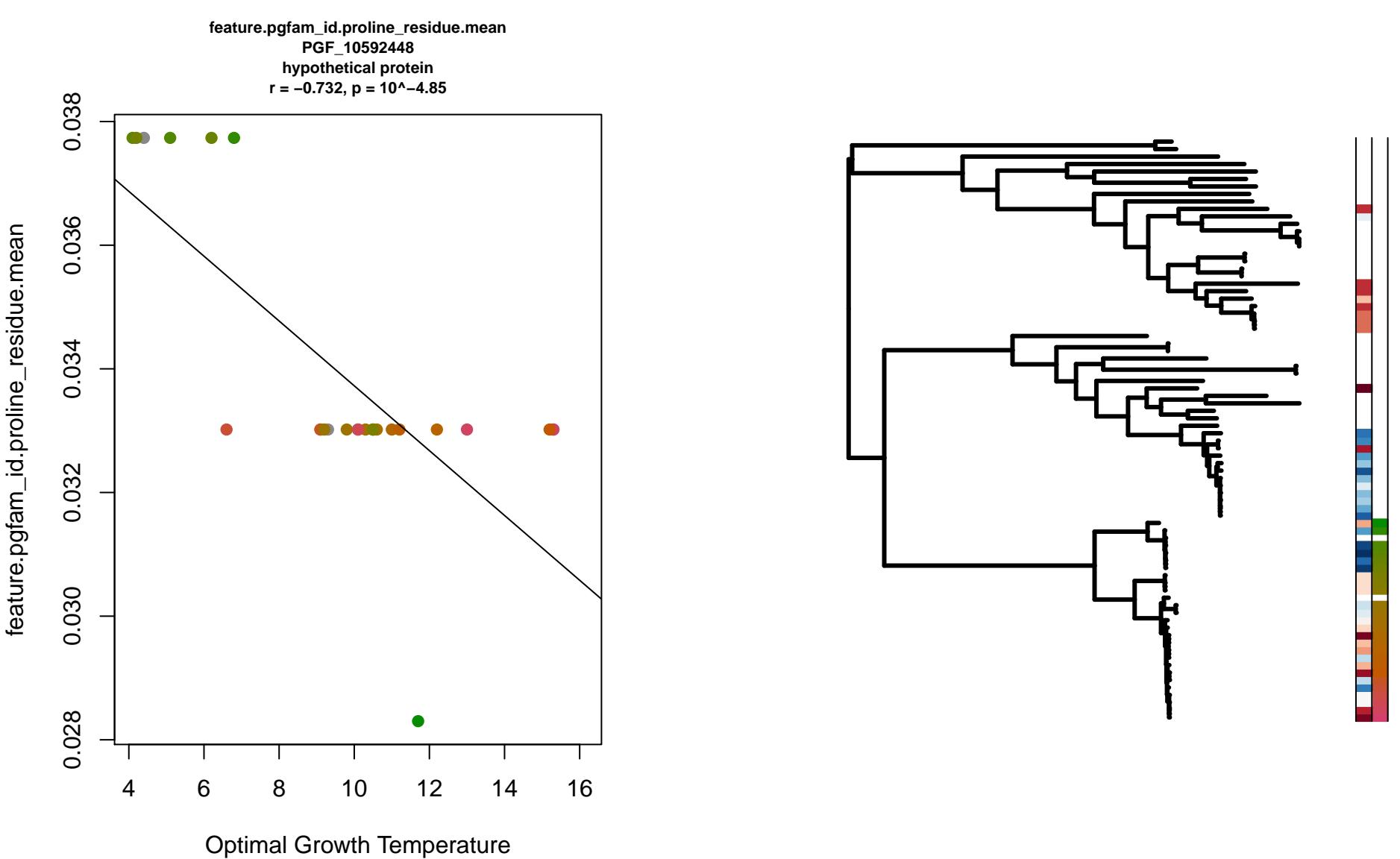
feature.pgfam_id.proline_residue.mean
PGF_12669666
FIG006045: Sigma factor, ECF subfamily
 $r = -0.722$, $p = 10^{-7.509}$

feature.pgfam_id.proline_residue.mean

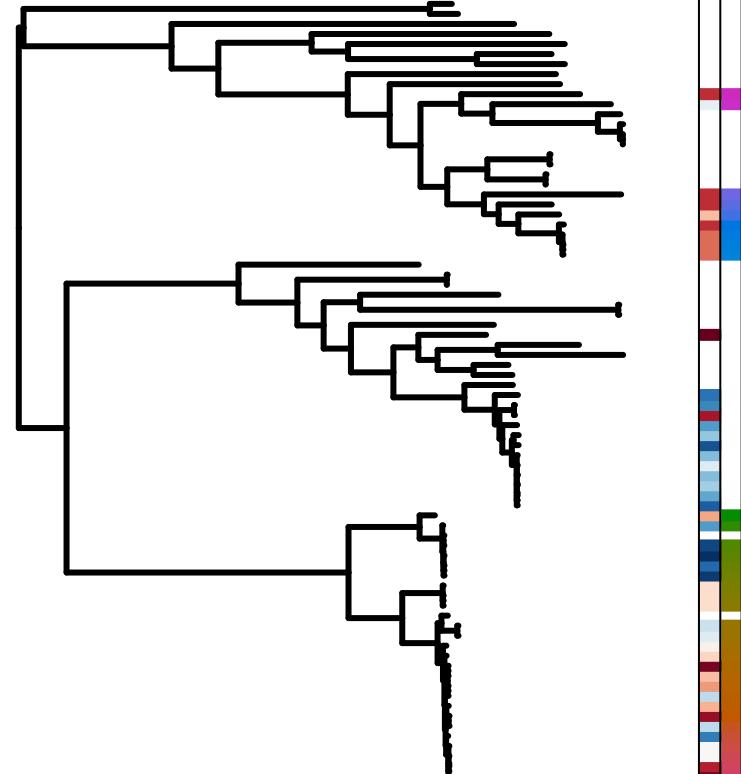
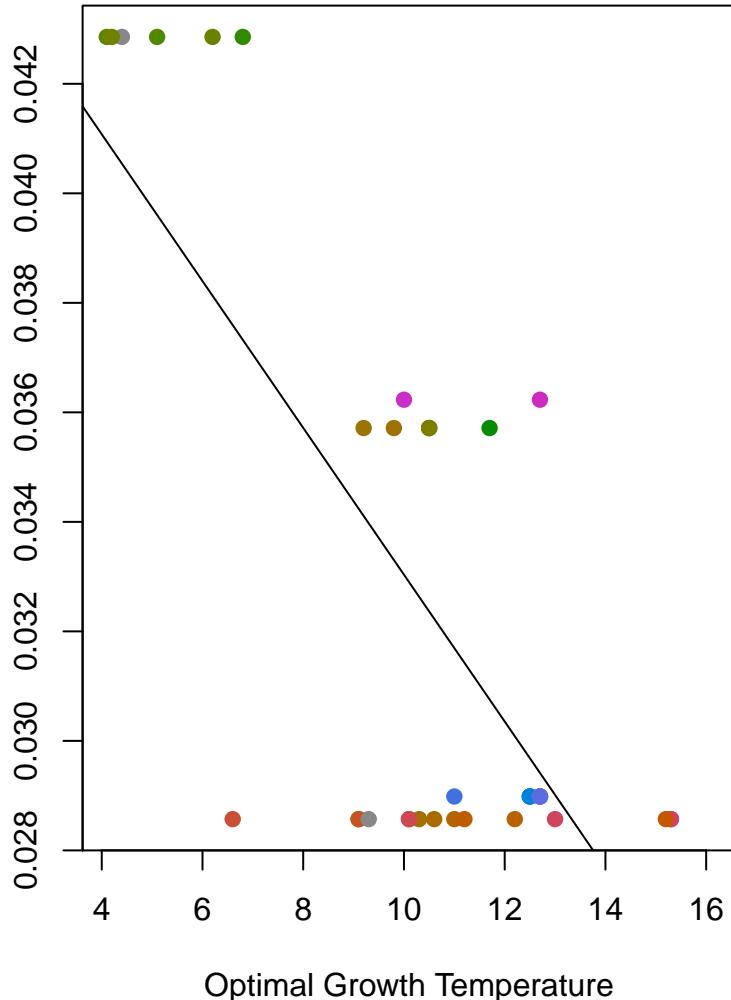


Optimal Growth Temperature





feature.pgfam_id.proline_residue.mean
PGF_01009507
Glyoxalase family protein
 $r = -0.733, p = 10^{-6.6}$



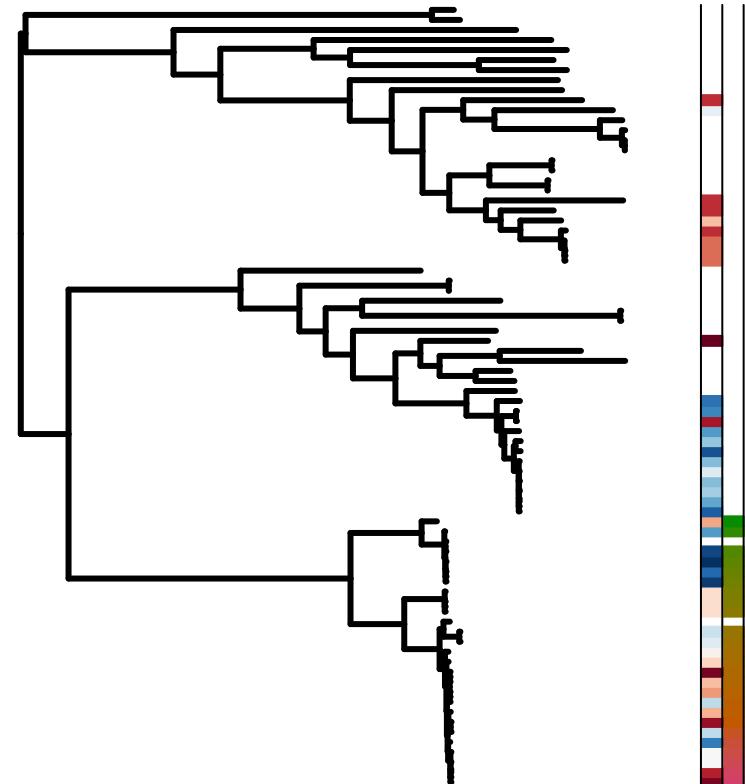
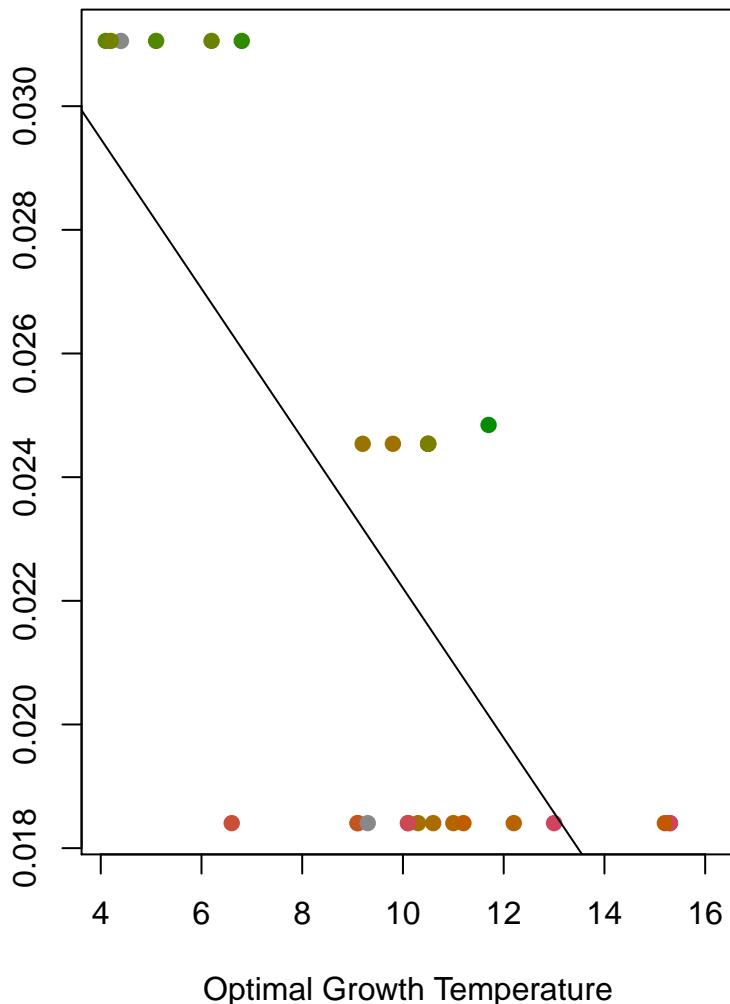
feature.pgfam_id.proline_residue.mean

PGF_10497182

hypothetical protein

$r = -0.735, p = 10^{-4.891}$

feature.pgfam_id.proline_residue.mean



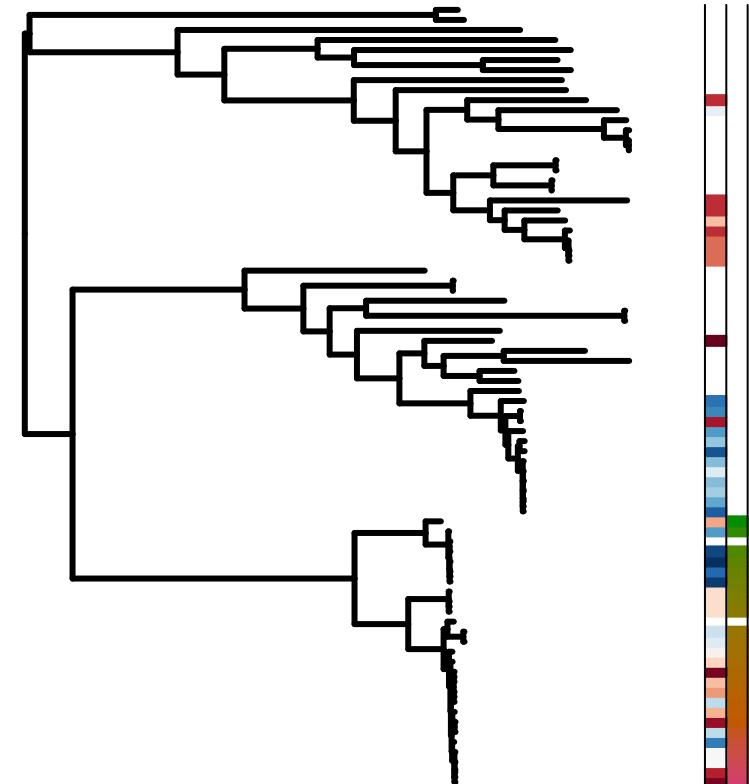
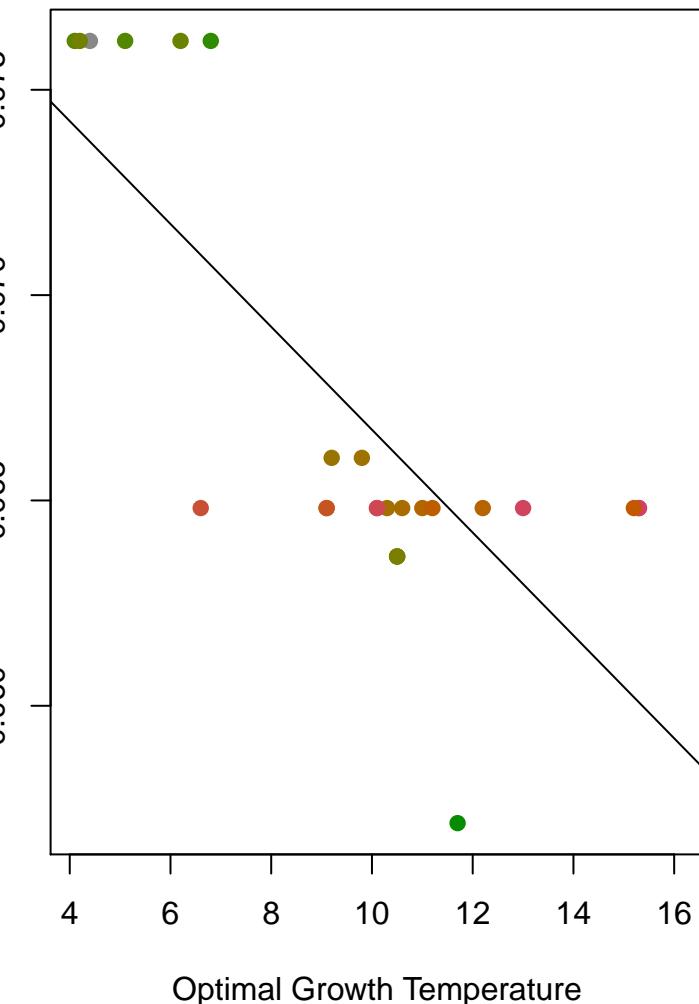
feature.pgfam_id.proline_residue.mean

PGF_07363283

hypothetical protein

$r = -0.765, p = 10^{-5.276}$

feature.pgfam_id.proline_residue.mean



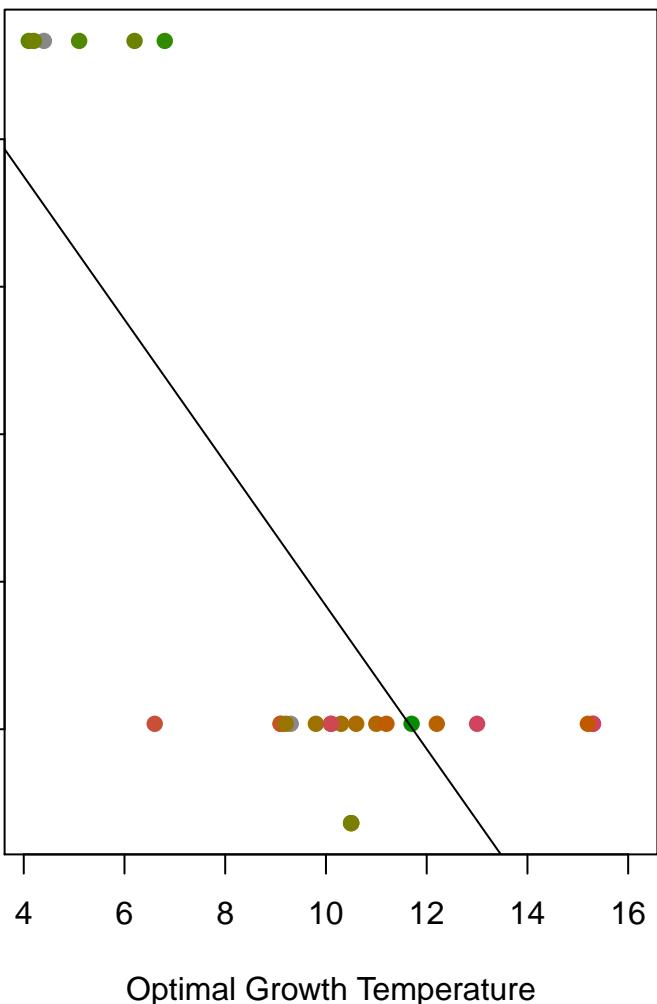
feature.pgfam_id.proline_residue.mean

PGF_11247394

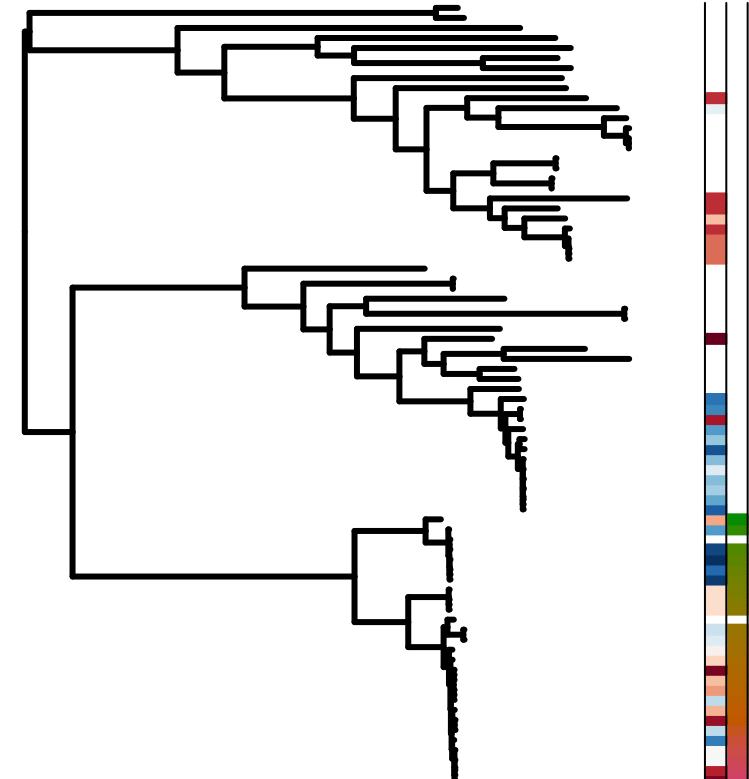
hypothetical protein

$r = -0.768, p = 10^{-5.53}$

feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature



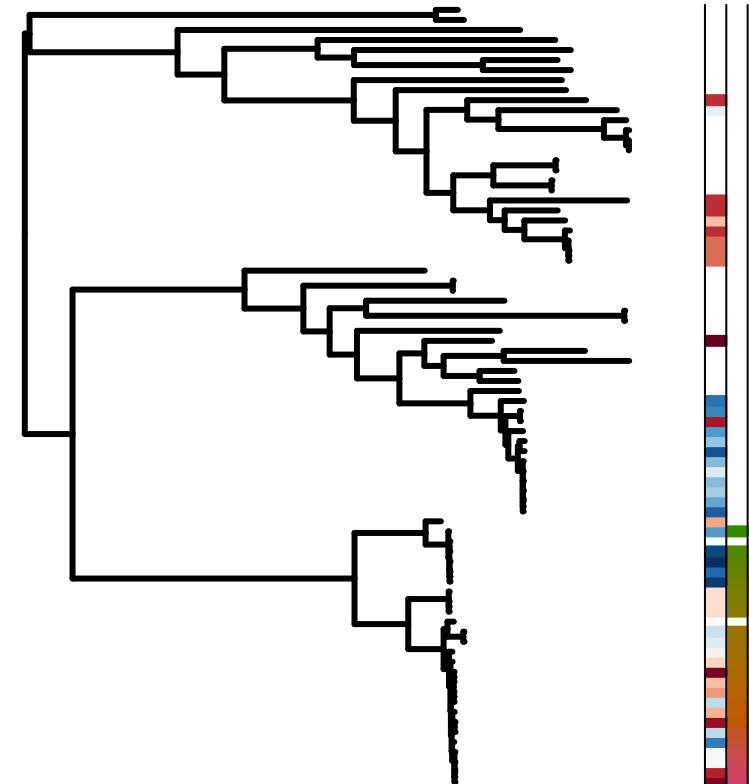
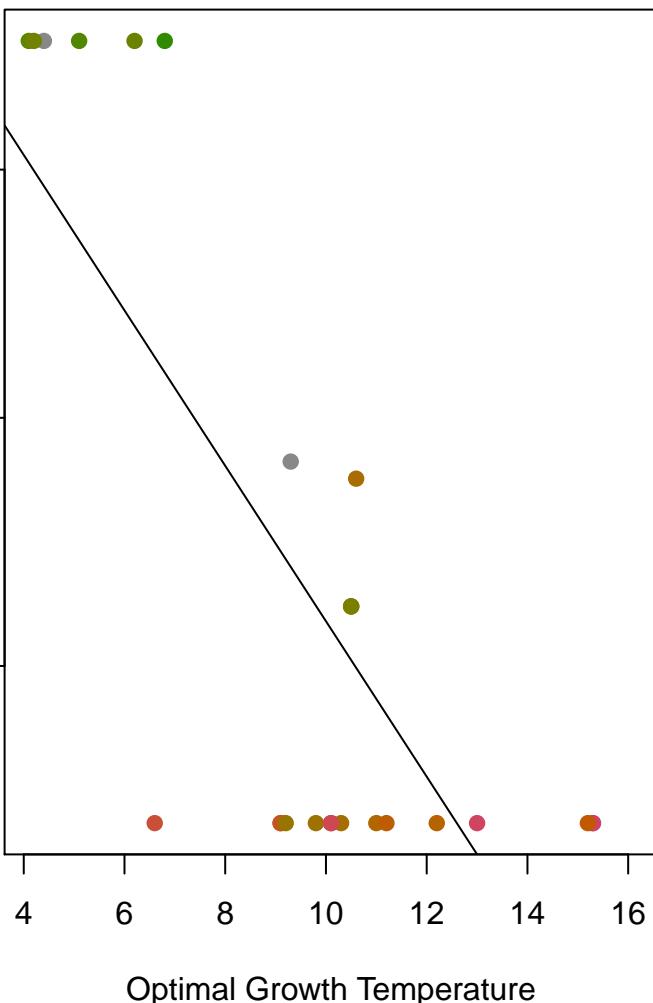
feature.pgfam_id.proline_residue.mean

PGF_07132870

hypothetical protein

$r = -0.768, p = 10^{-5.342}$

feature.pgfam_id.proline_residue.mean



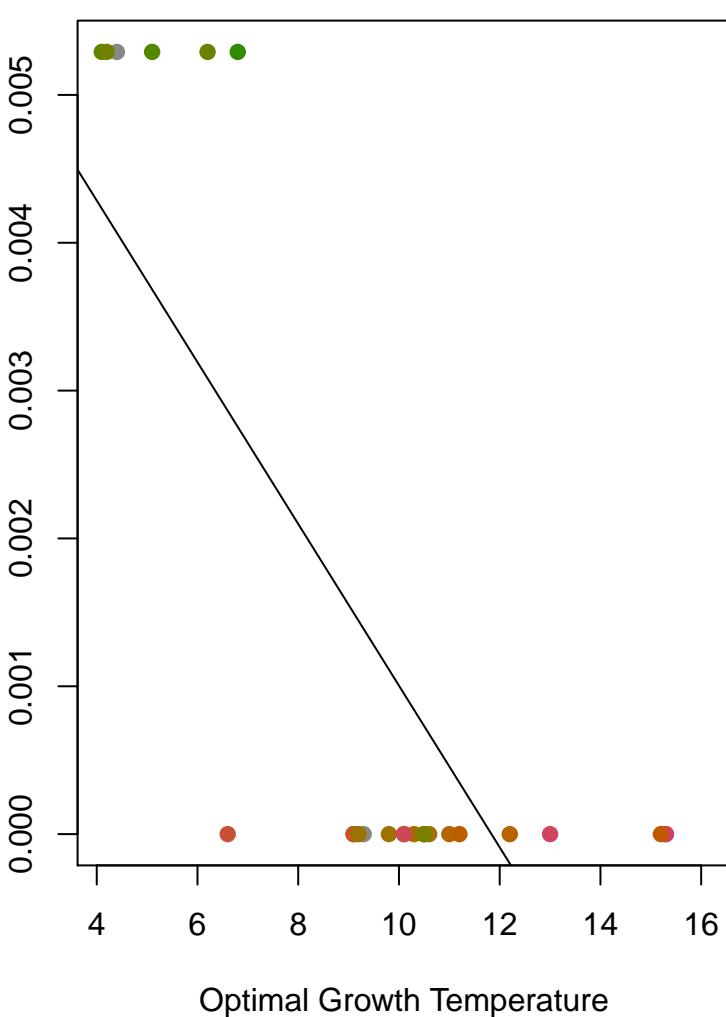
feature.pgfam_id.proline_residue.mean

PGF_12159935

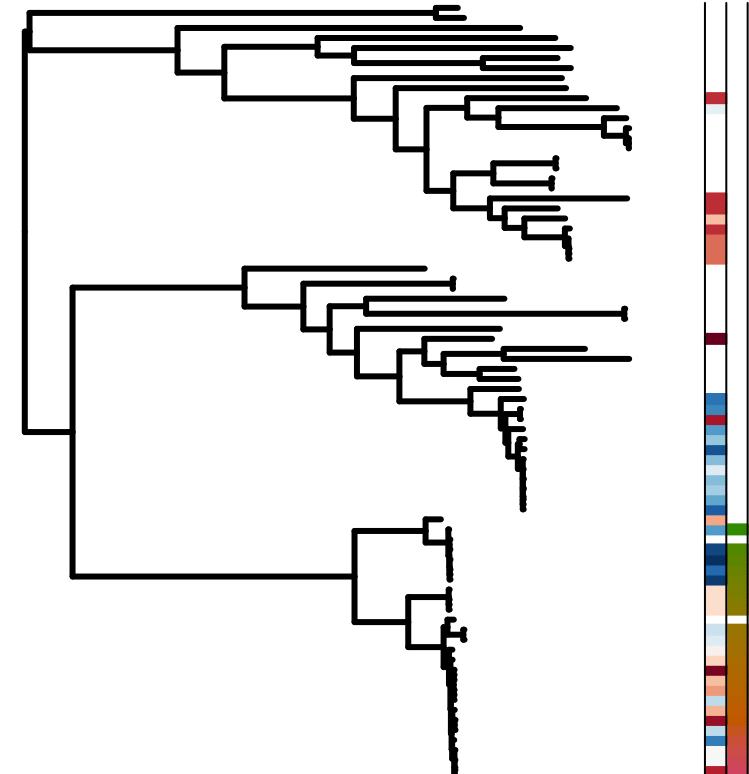
hypothetical protein

$r = -0.775, p = 10^{-5.478}$

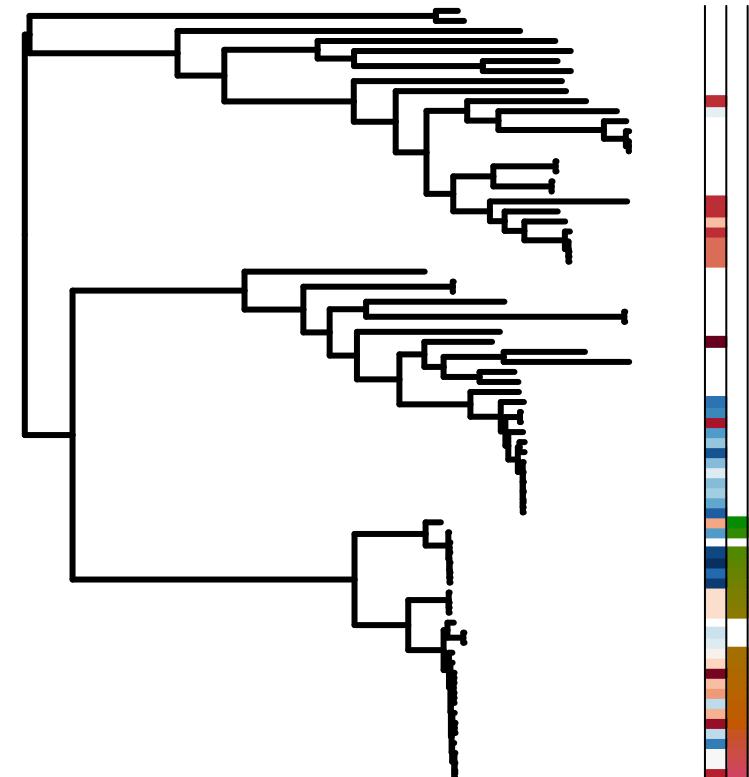
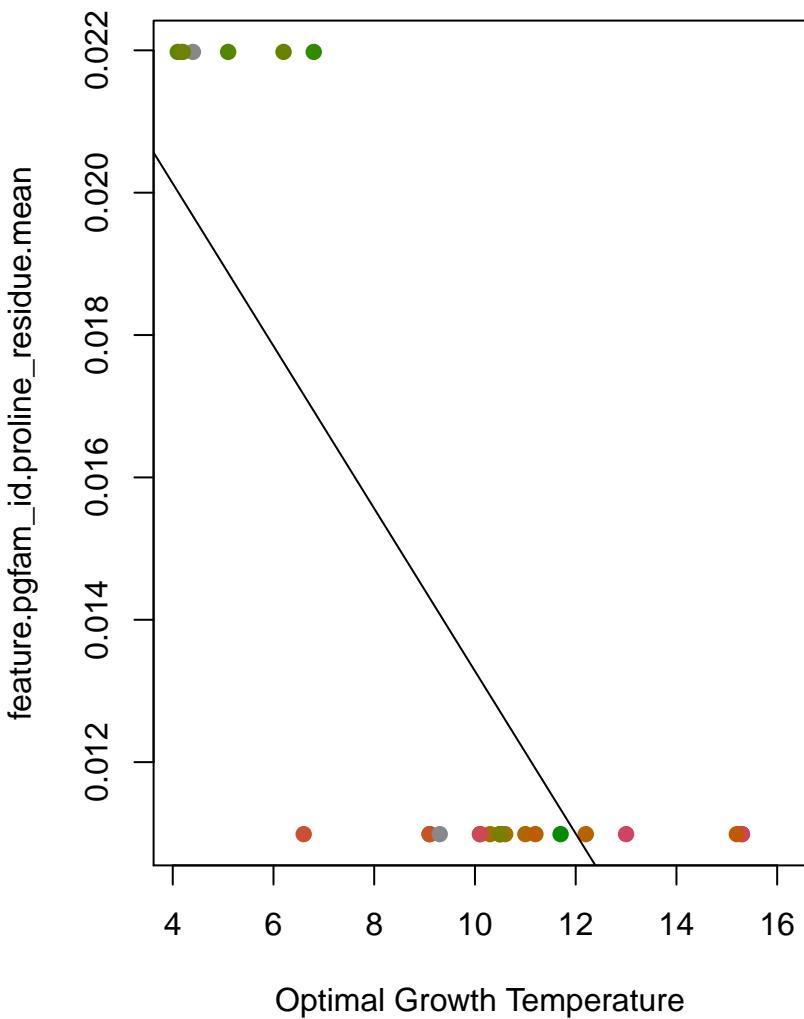
feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature



feature.pgfam_id.proline_residue.mean
PGF_10906072
hypothetical protein
 $r = -0.79$, $p = 10^{-5.574}$

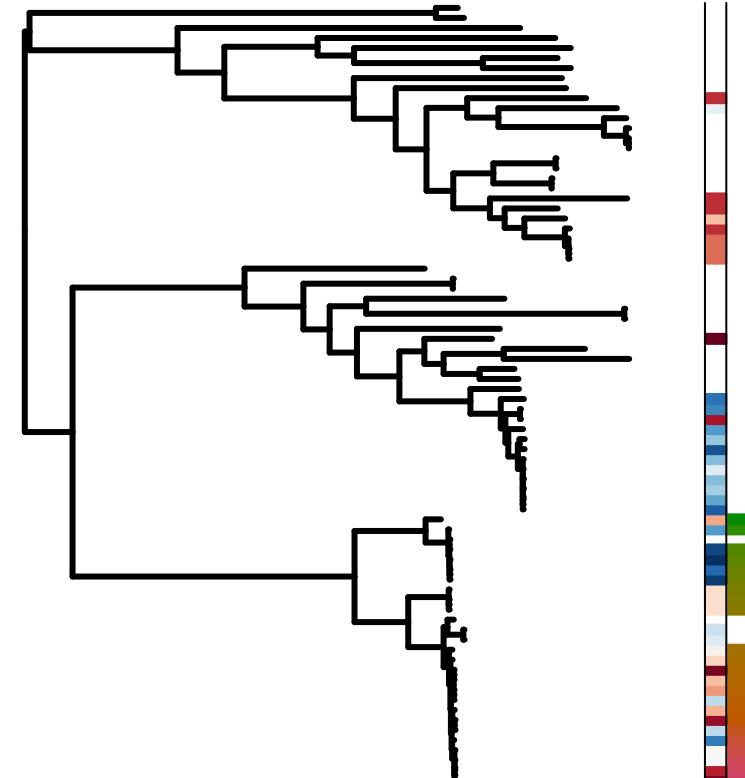
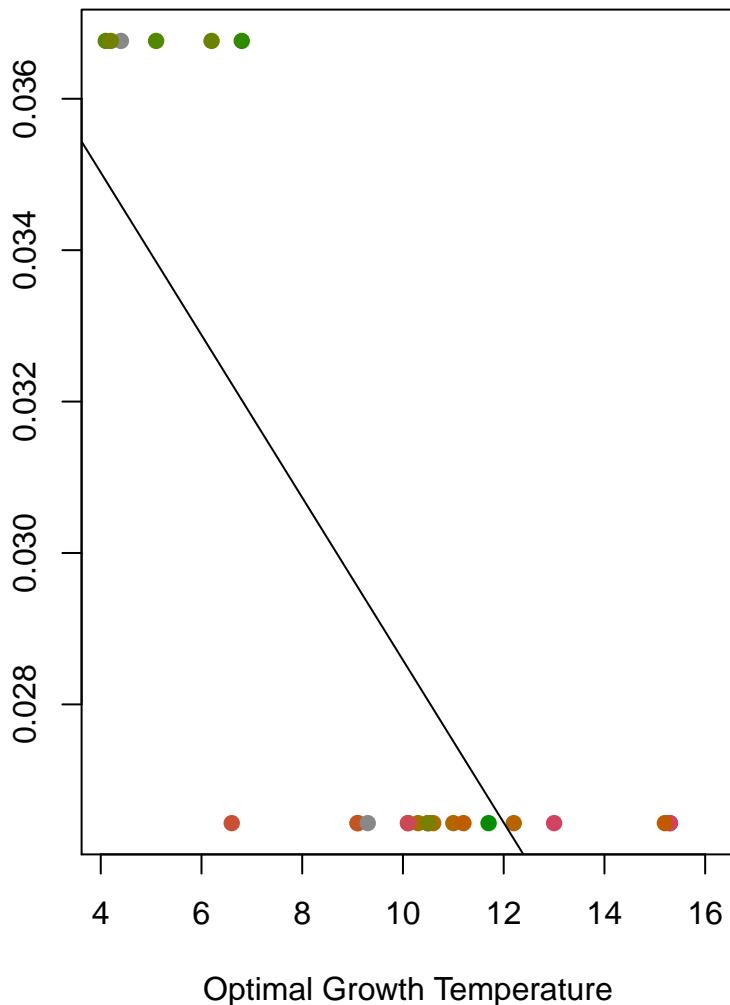


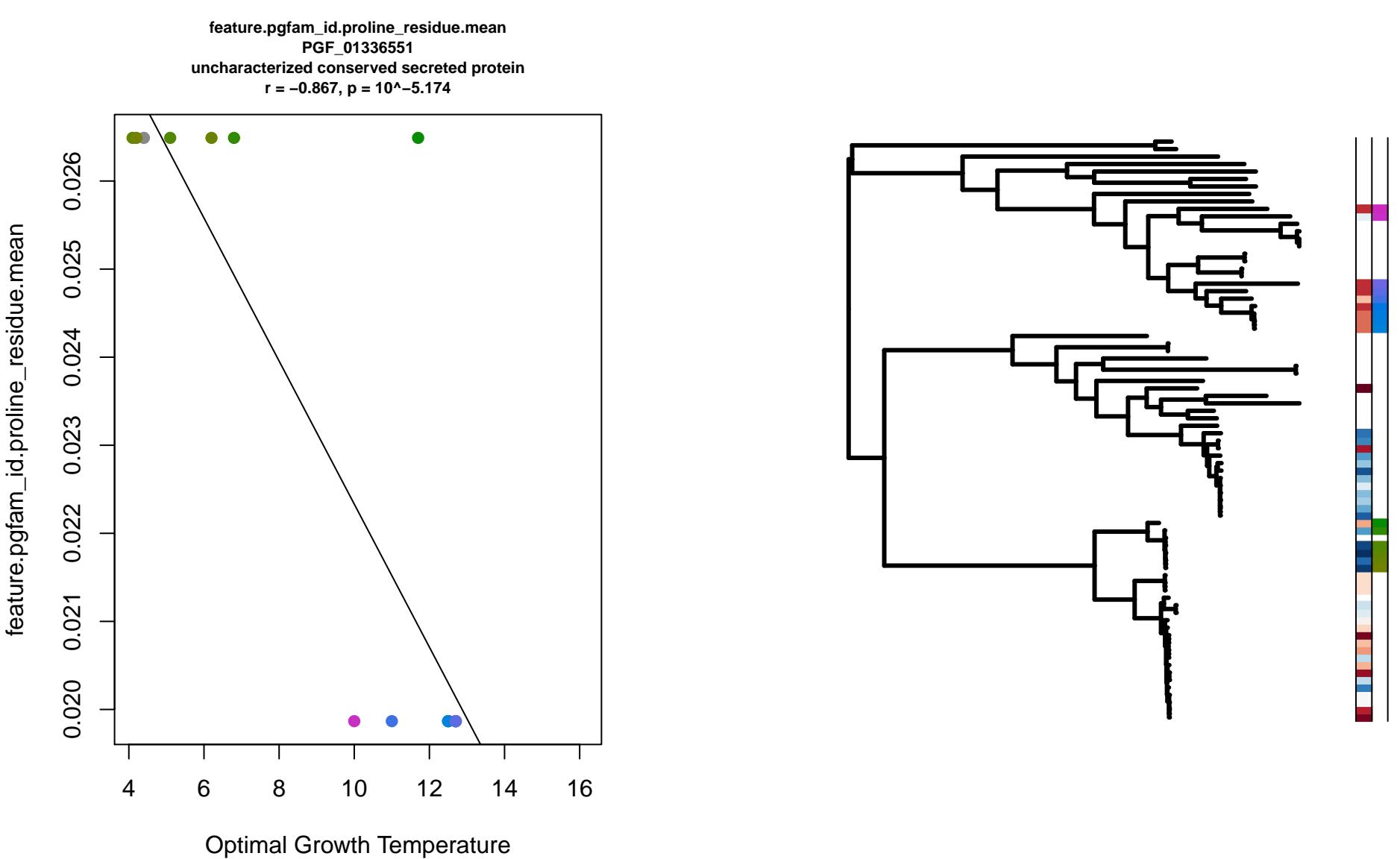
feature.pgfam_id.proline_residue.mean

PGF_11620197

hypothetical protein

$r = -0.79$, $p = 10^{-5.574}$





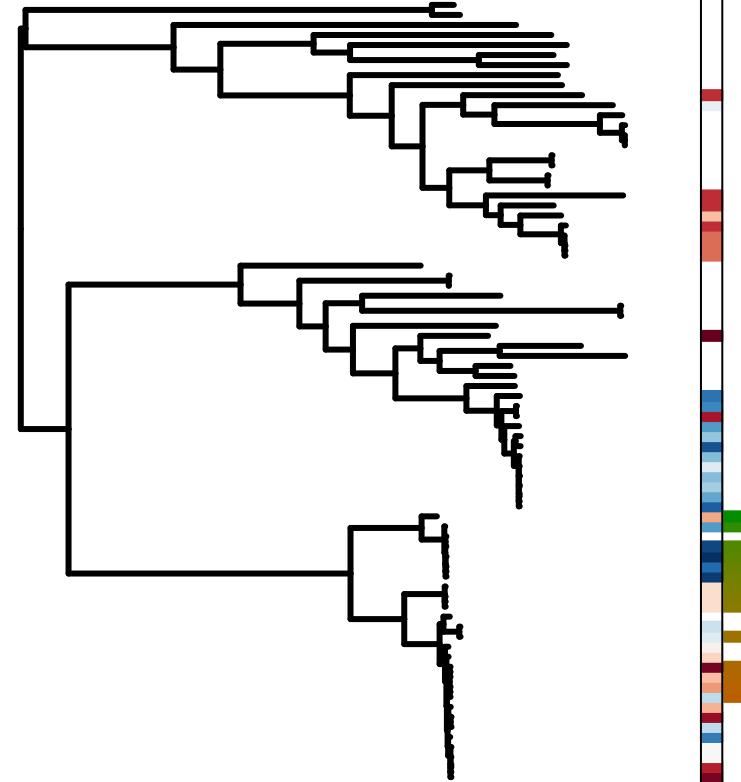
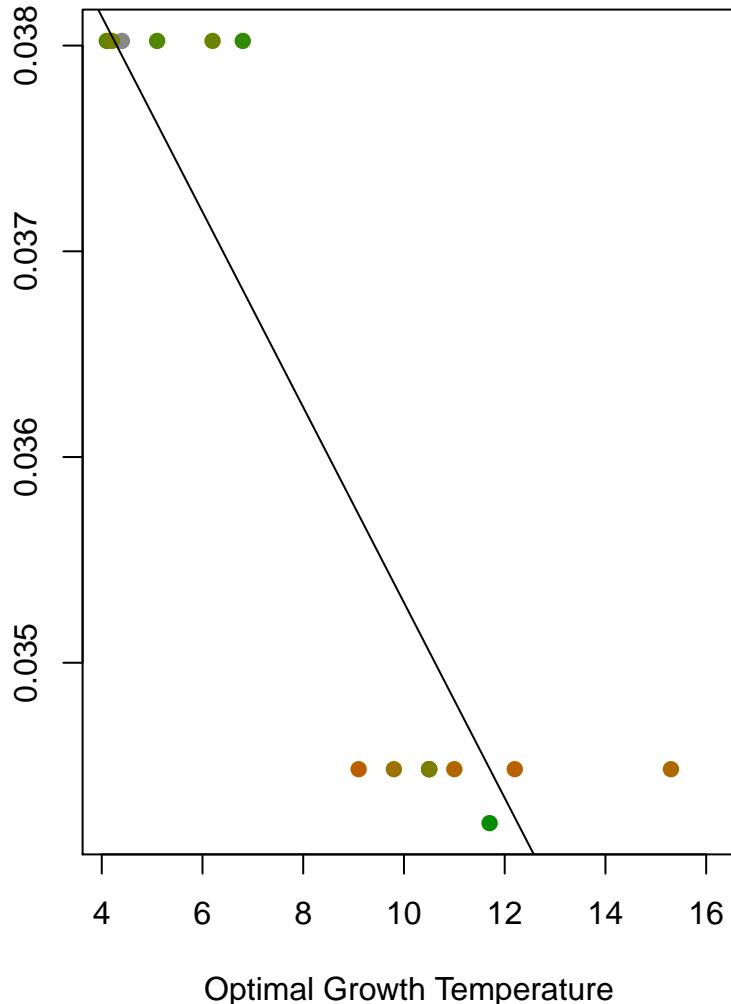


feature.pgfam_id.proline_residue.mean

PGF_10029046

hypothetical protein

$r = -0.897$, $p = 10^{-5.23}$



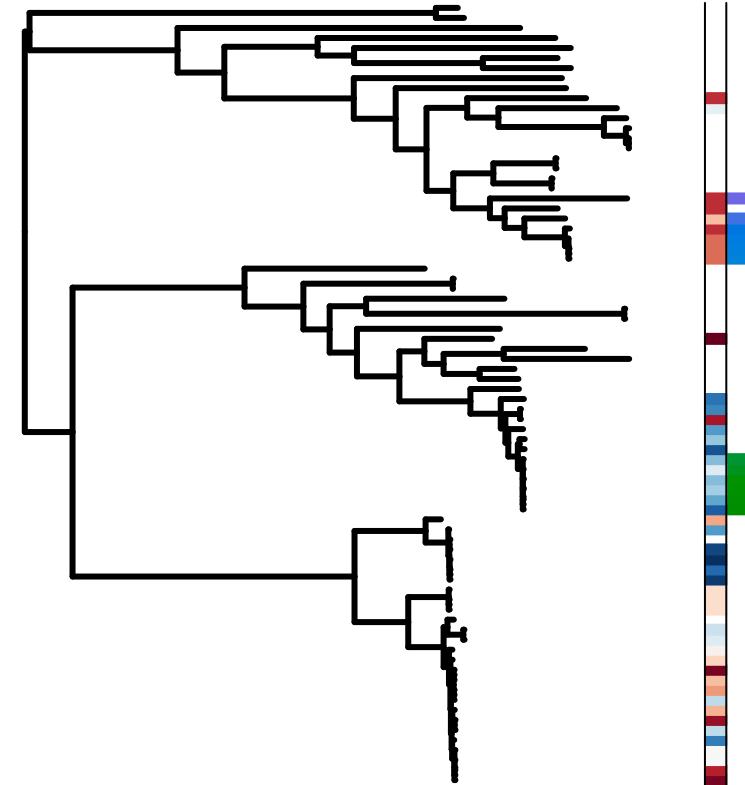
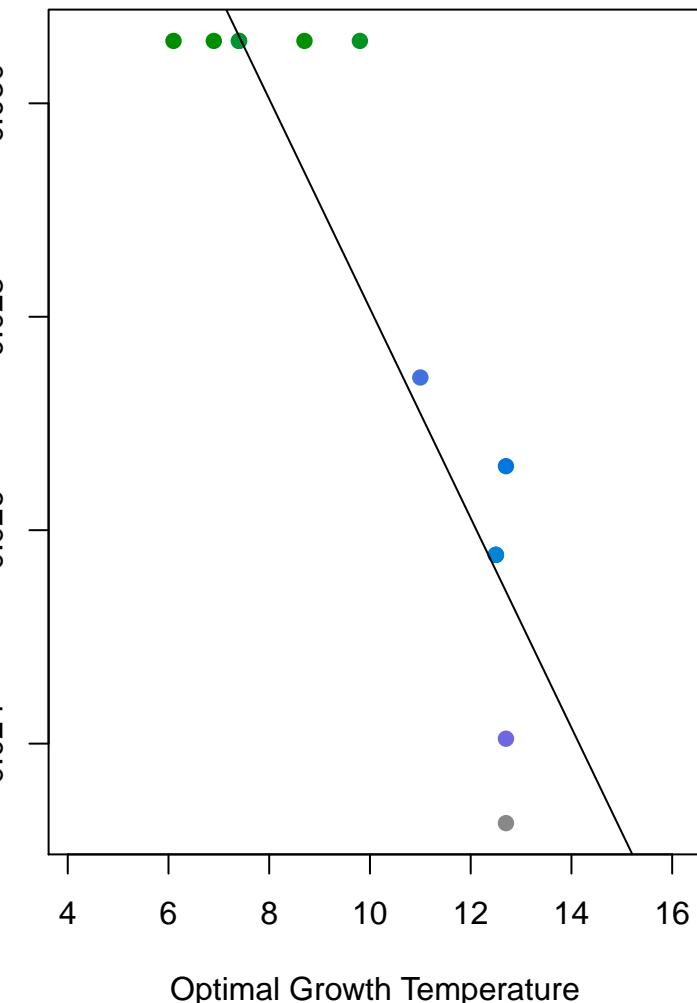
feature.pgfam_id.proline_residue.mean

PGF_00050846

Sensory box protein

$r = -0.906$, $p = 10^{-4.698}$

feature.pgfam_id.proline_residue.mean



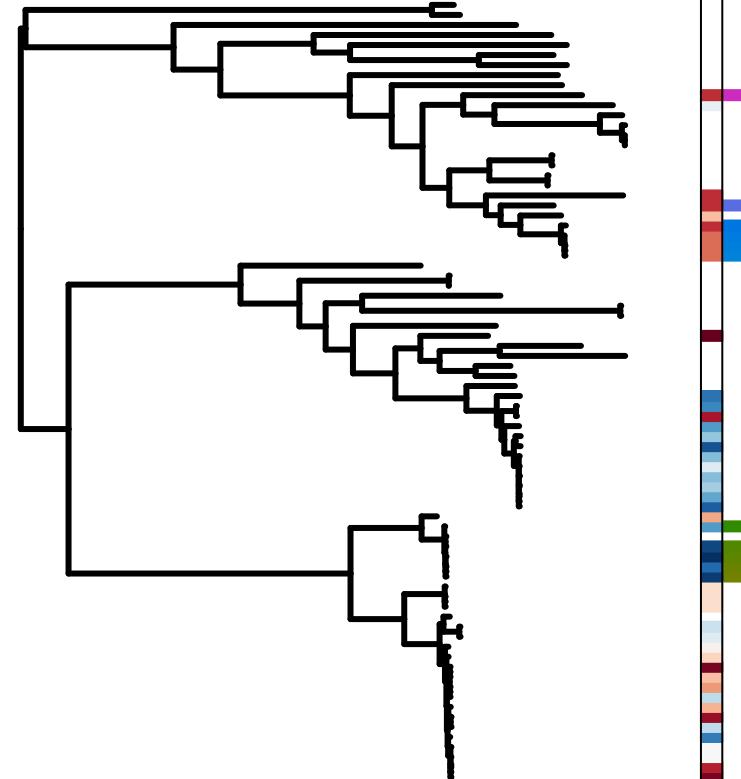
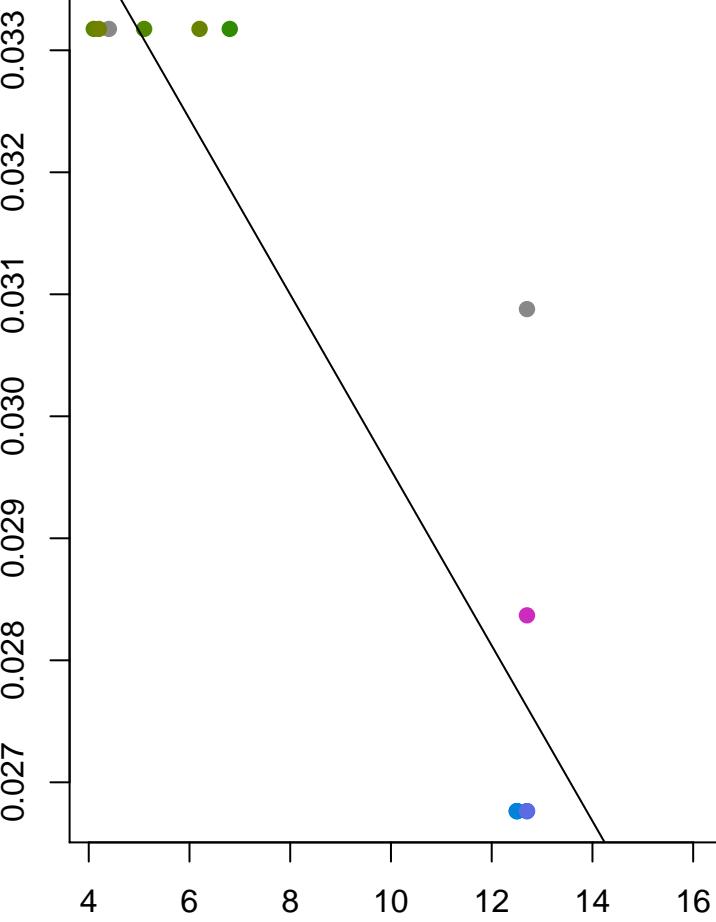
feature.pgfam_id.proline_residue.mean

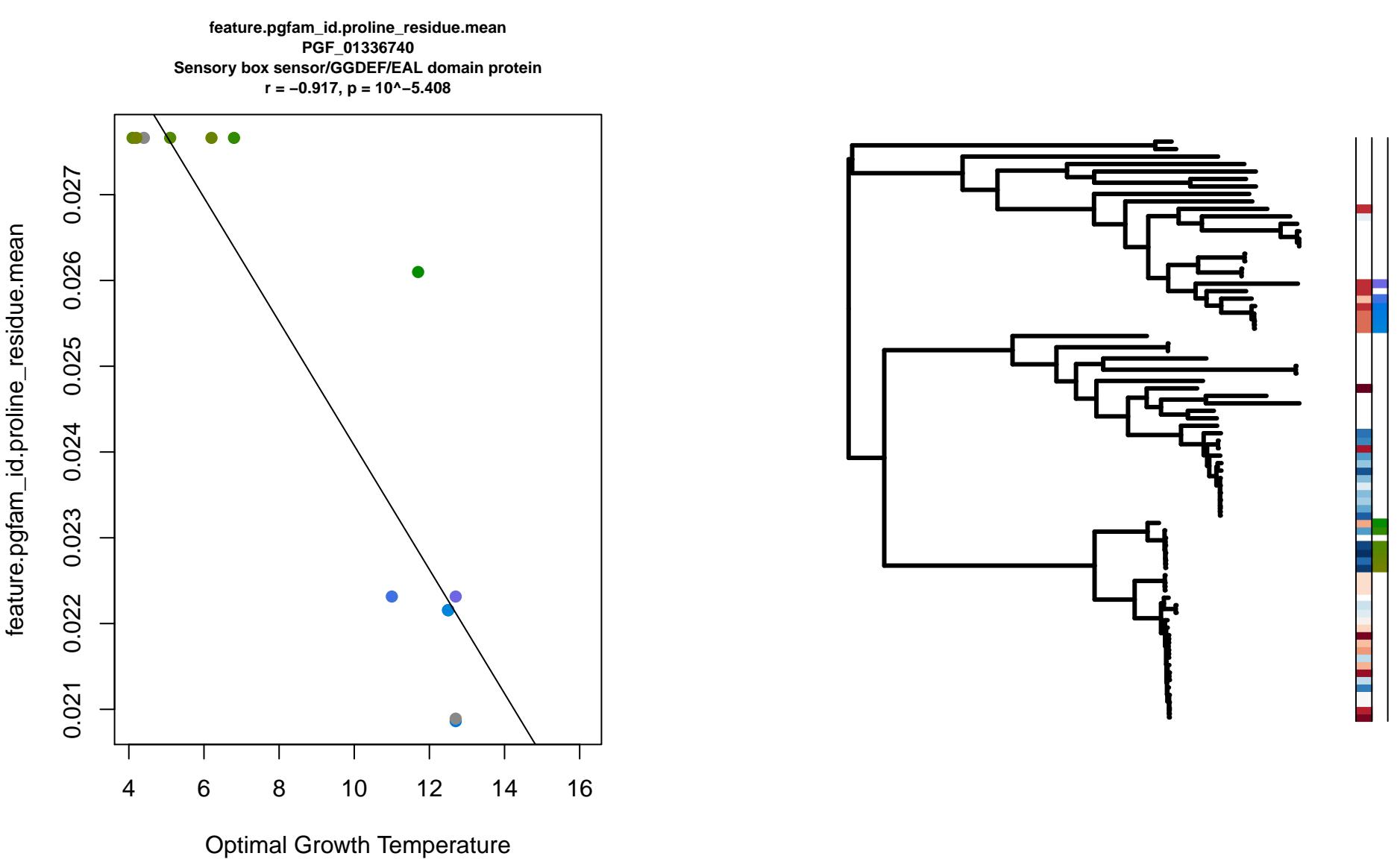
PGF_07481765

hypothetical protein

$r = -0.914, p = 10^{-4.913}$

feature.pgfam_id.proline_residue.mean





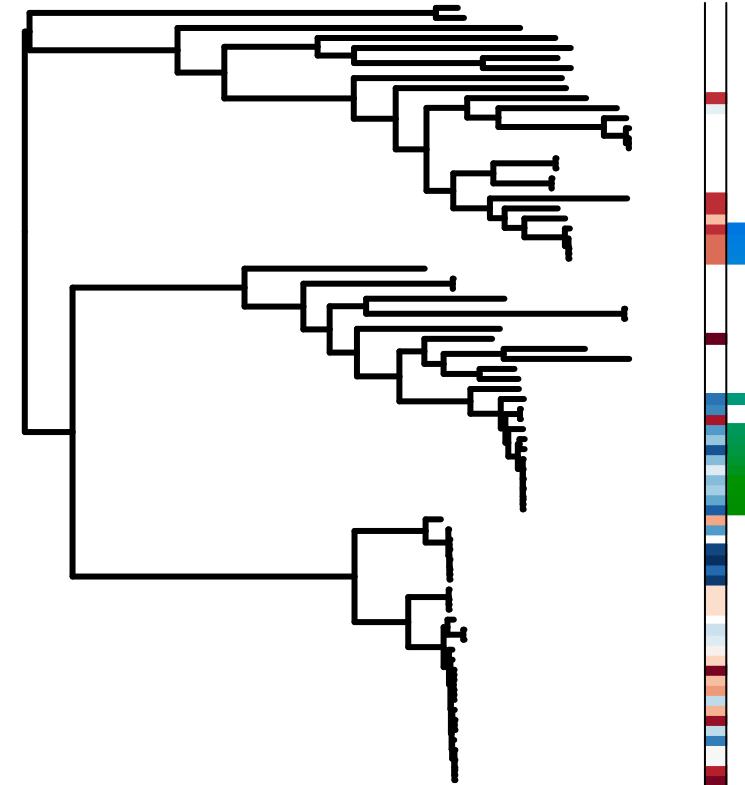
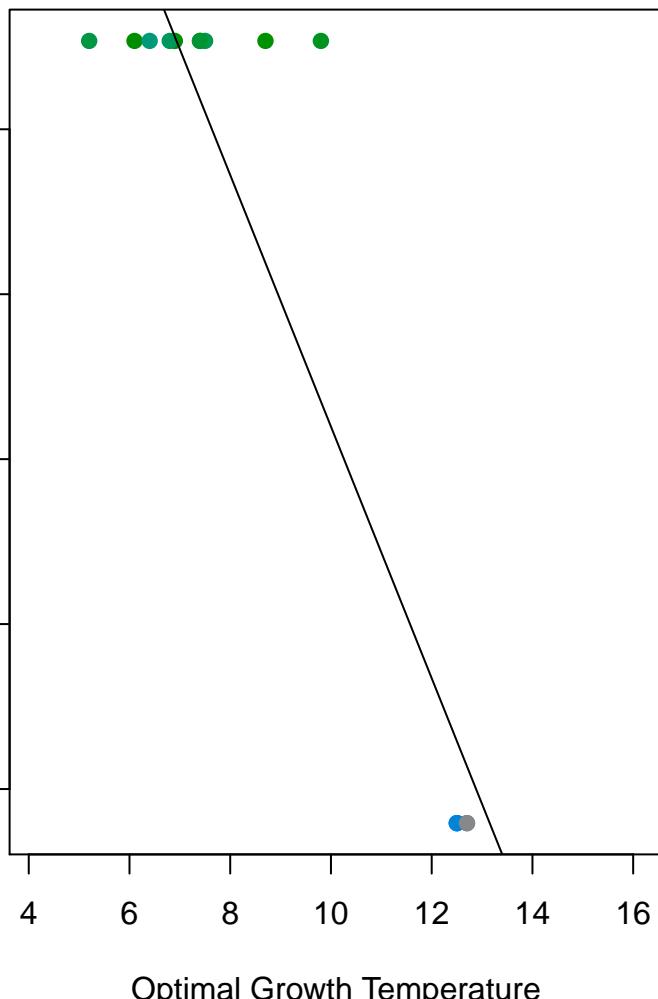
feature.pgfam_id.proline_residue.mean

PGF_06830555

SapC-like S-layer protein

$r = -0.928$, $p = 10^{-6.228}$

feature.pgfam_id.proline_residue.mean



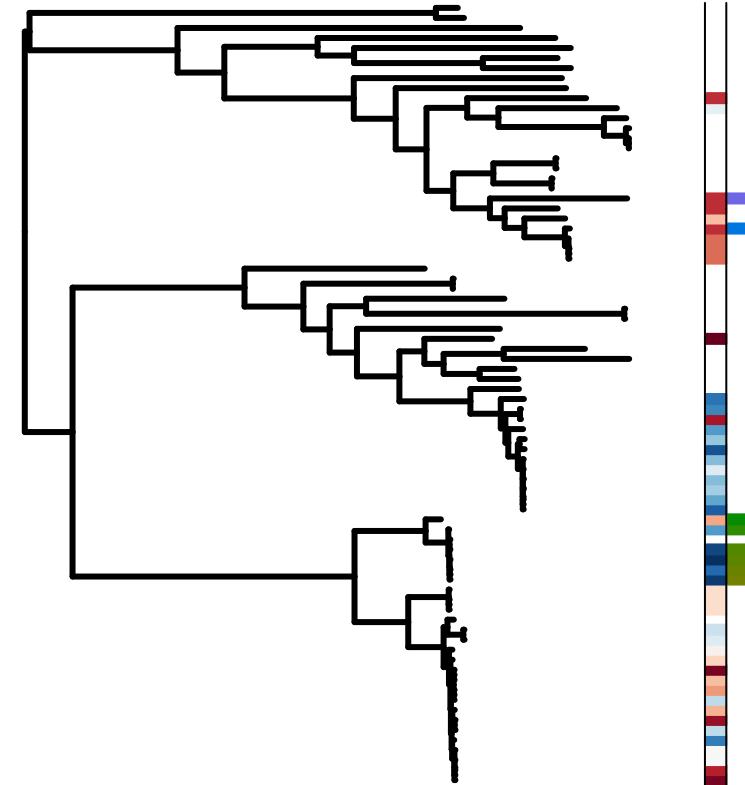
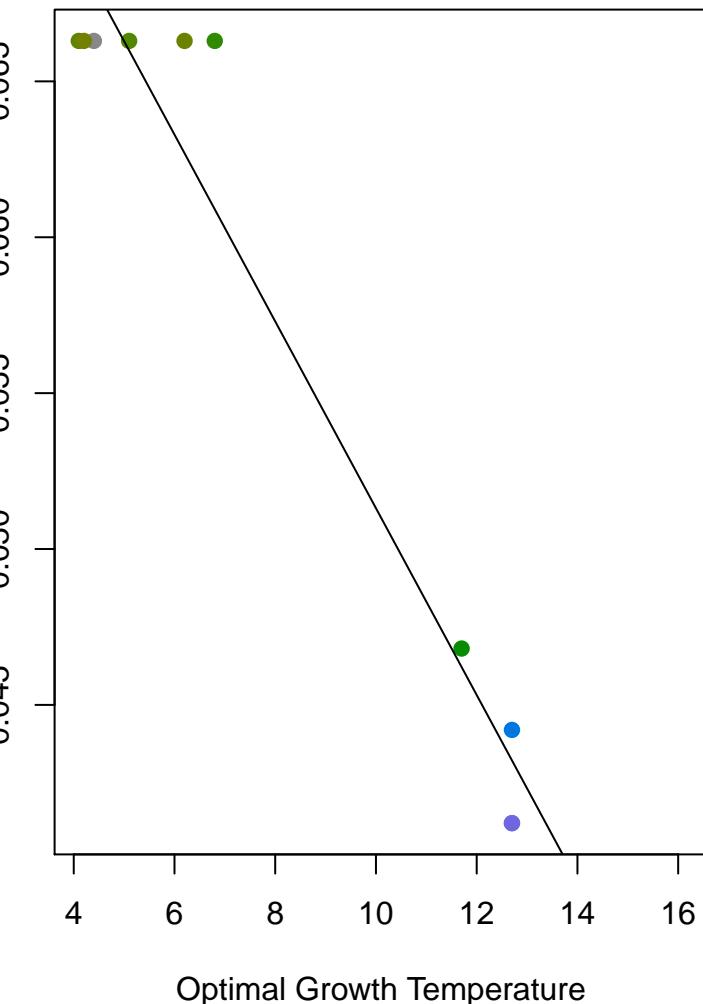
feature.pgfam_id.proline_residue.mean

PGF_03221663

Phage tail collar domain

$r = -0.973$, $p = 10^{-5.665}$

feature.pgfam_id.proline_residue.mean

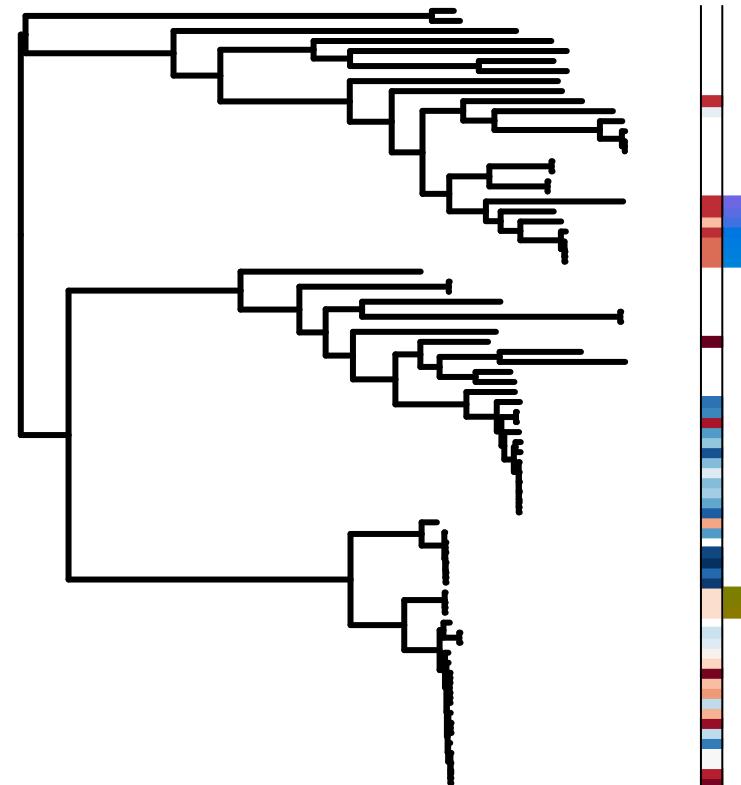
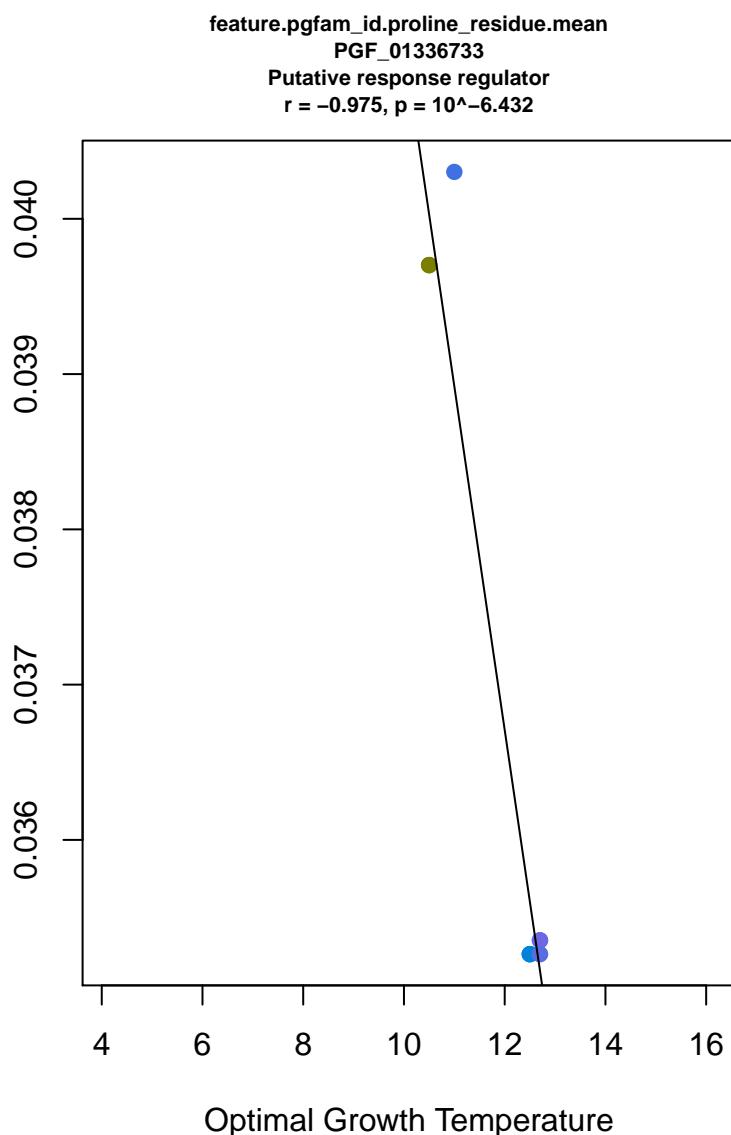


feature.pgfam_id.proline_residue.mean

PGF_01336733

Putative response regulator

$r = -0.975, p = 10^{-6.432}$



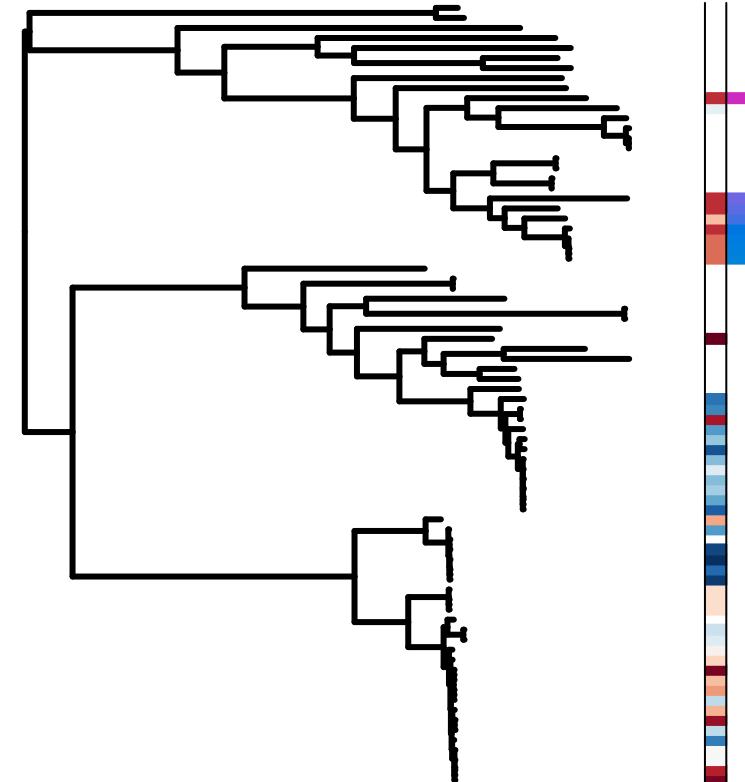
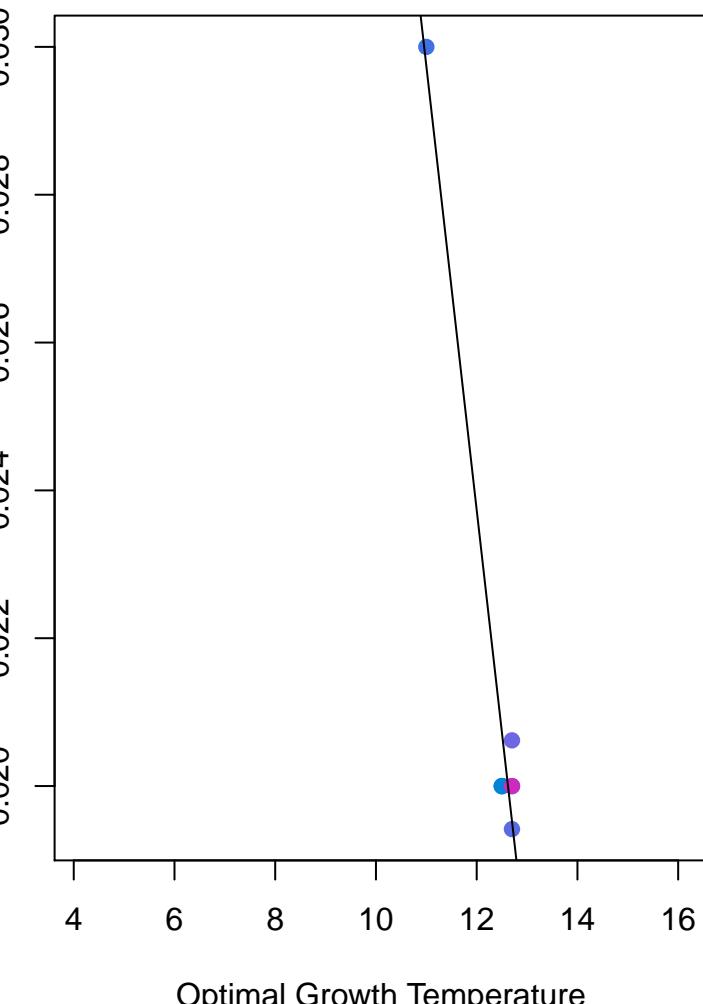
feature.pgfam_id.proline_residue.mean

PGF_01336600

hypothetical protein

$r = -0.981, p = 10^{-4.775}$

feature.pgfam_id.proline_residue.mean



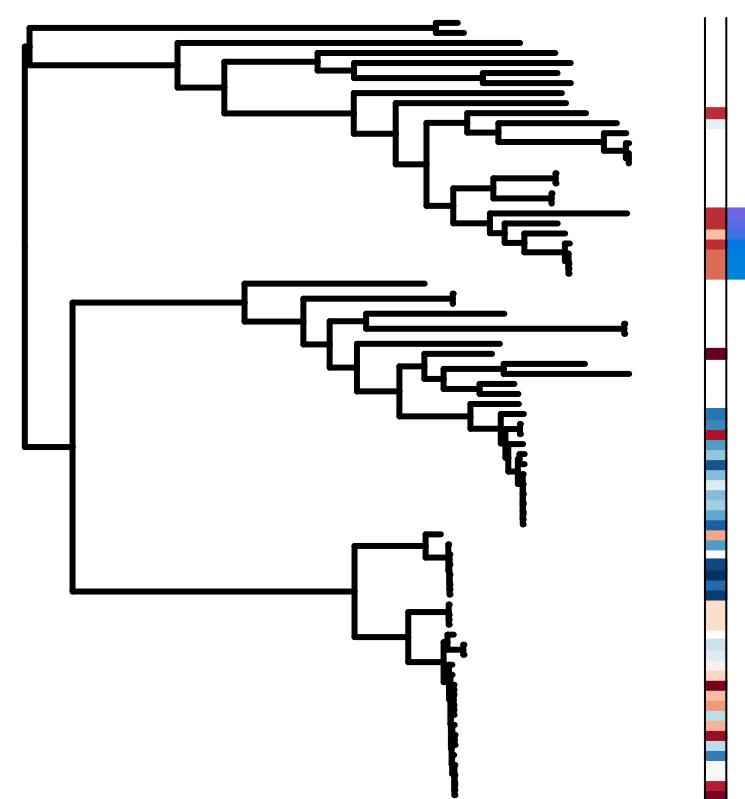
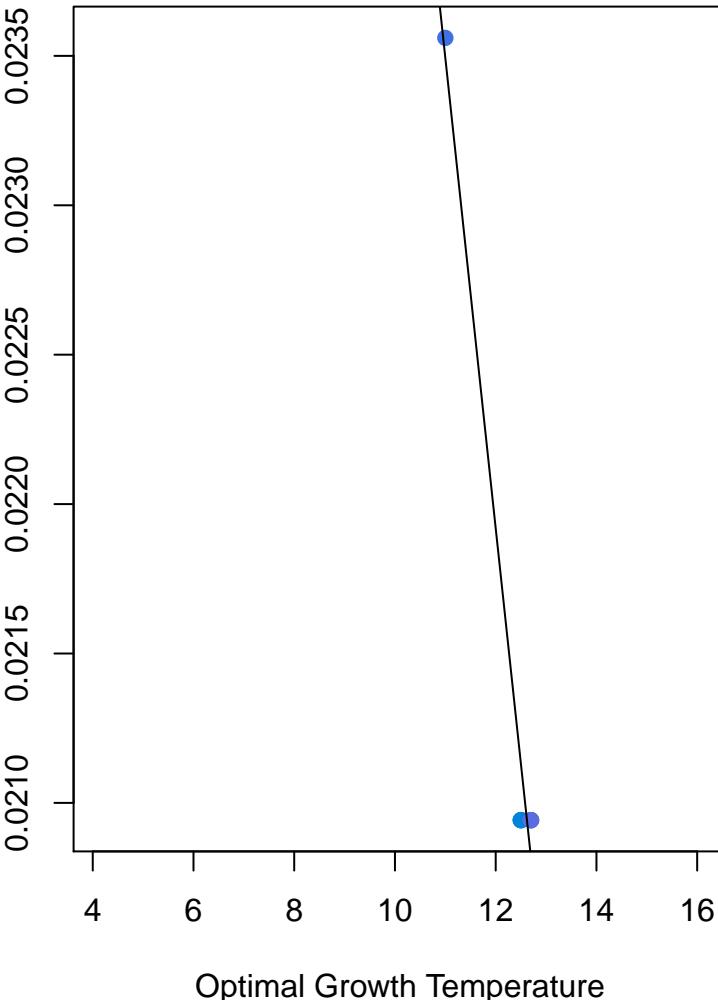
feature.pgfam_id.proline_residue.mean

PGF_00007576

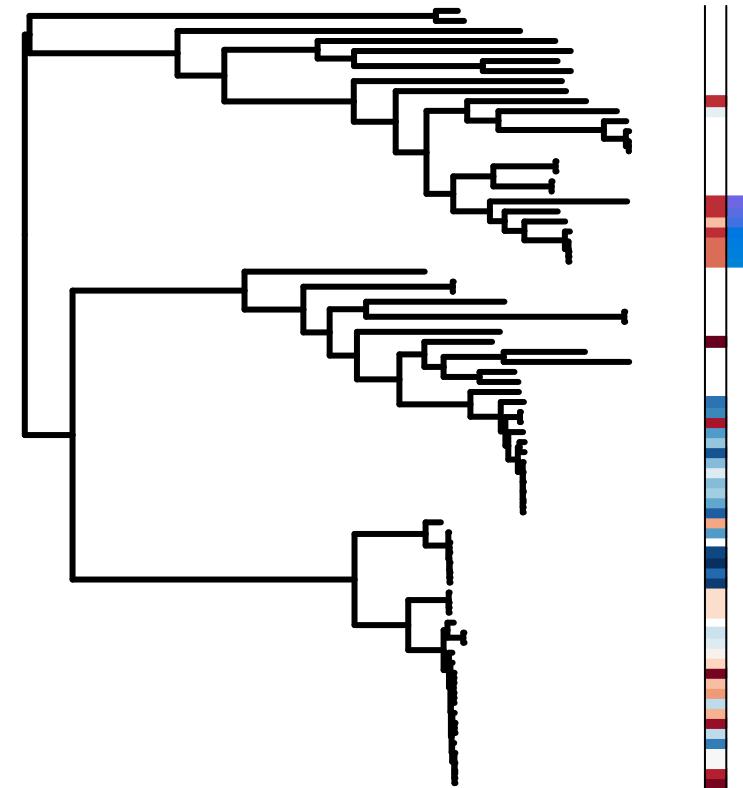
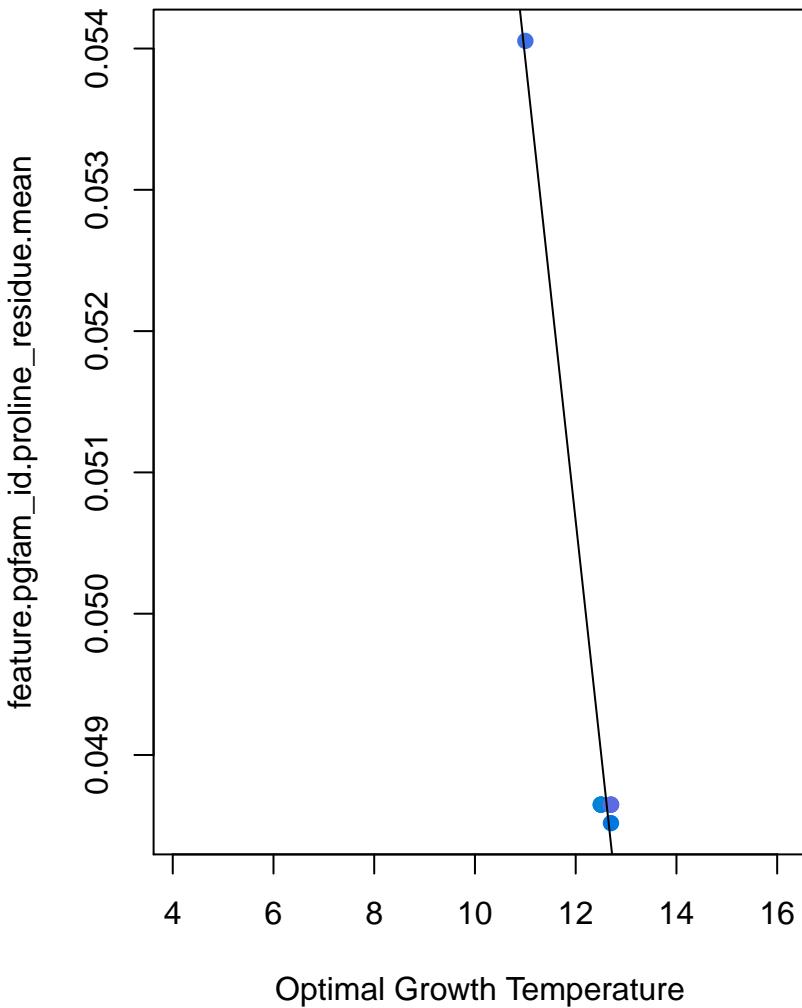
GfdT

$r = -0.985, p = 10^{-5.104}$

feature.pgfam_id.proline_residue.mean



feature.pgfam_id.proline_residue.mean
PGF_04249868
UPF0098 protein ybcL precursor
 $r = -0.986$, $p = 10^{-5.211}$



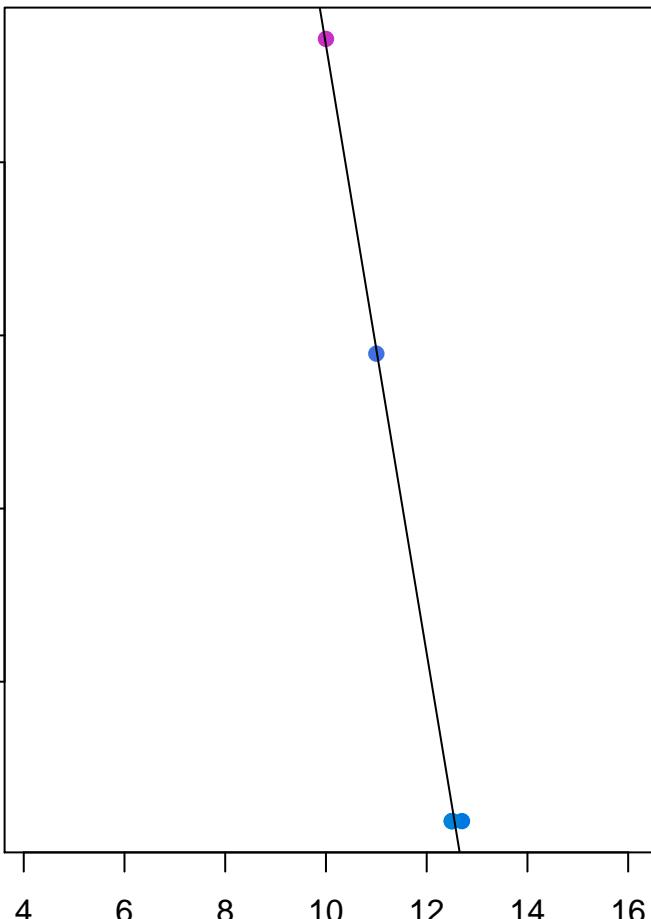
feature.pgfam_id.proline_residue.mean

PGF_08076270

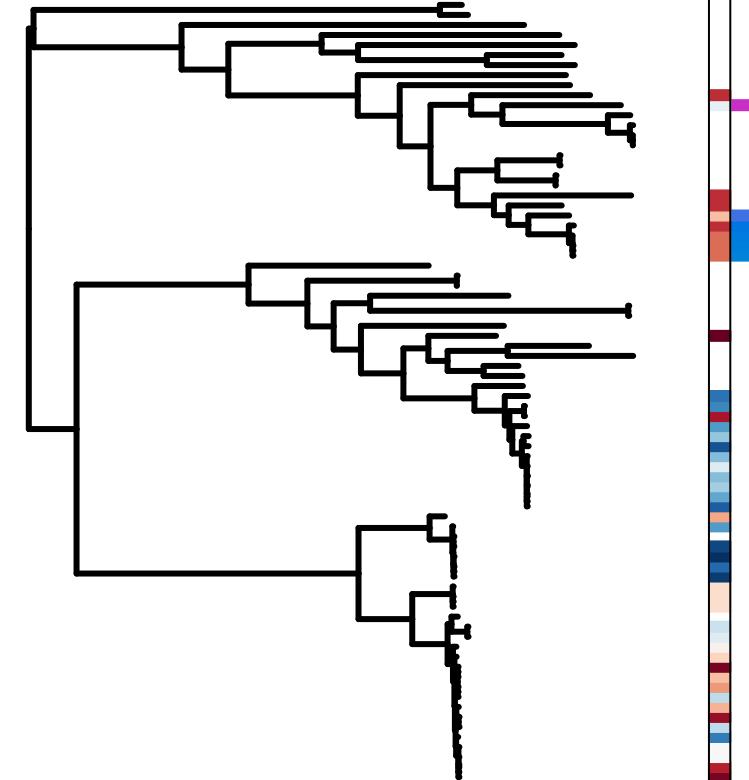
hypothetical protein

$r = -0.998, p = 10^{-5.032}$

feature.pgfam_id.proline_residue.mean



Optimal Growth Temperature



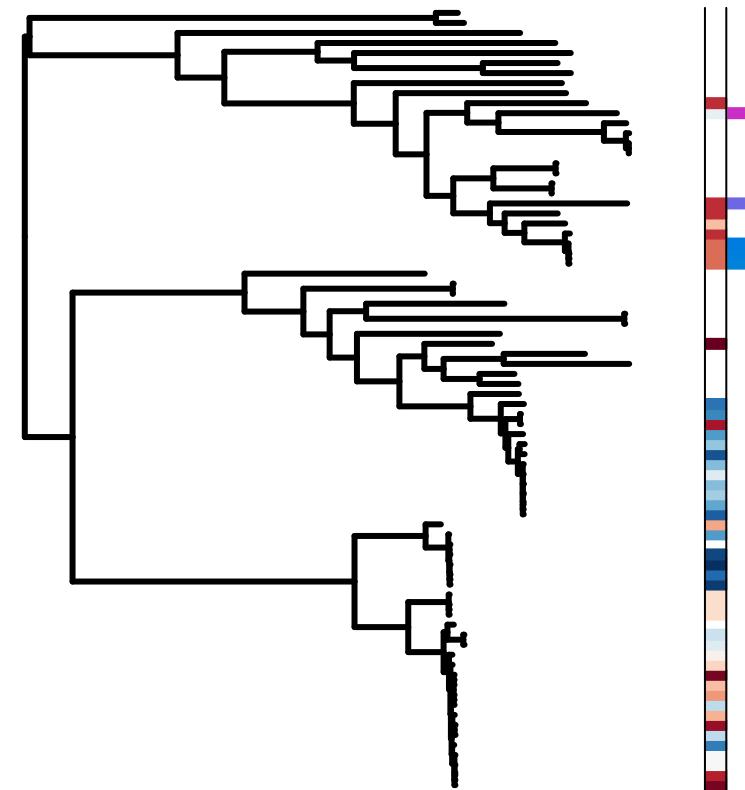
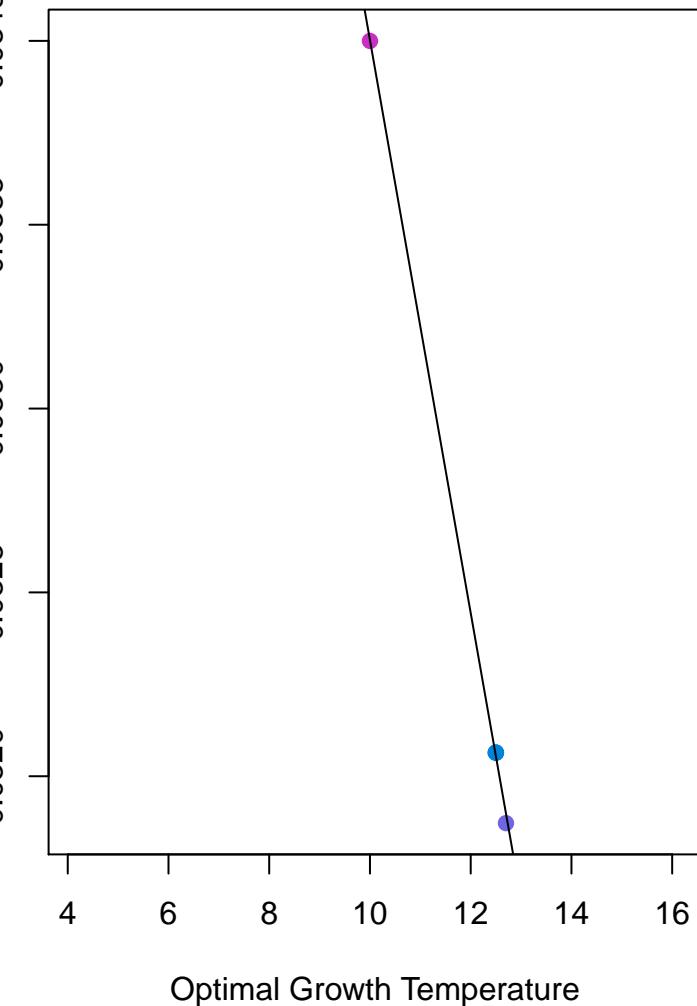
feature.pgfam_id.proline_residue.mean

PGF_01336815

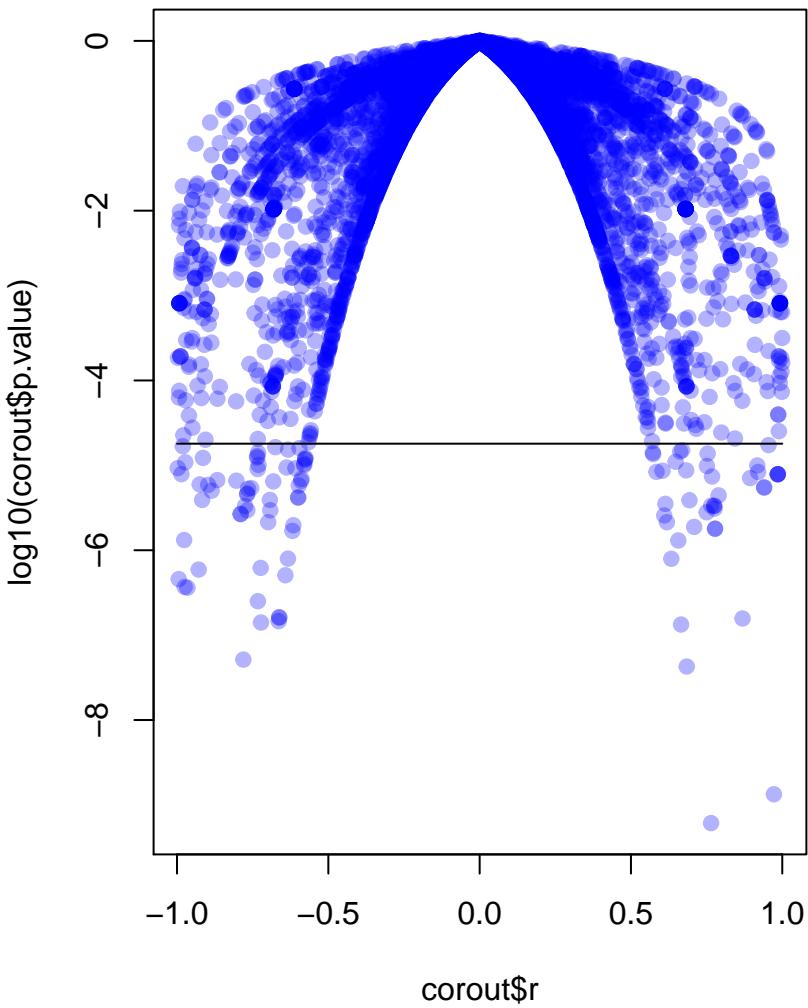
hypothetical protein

$r = -1, p = 10^{-5.646}$

feature.pgfam_id.proline_residue.mean

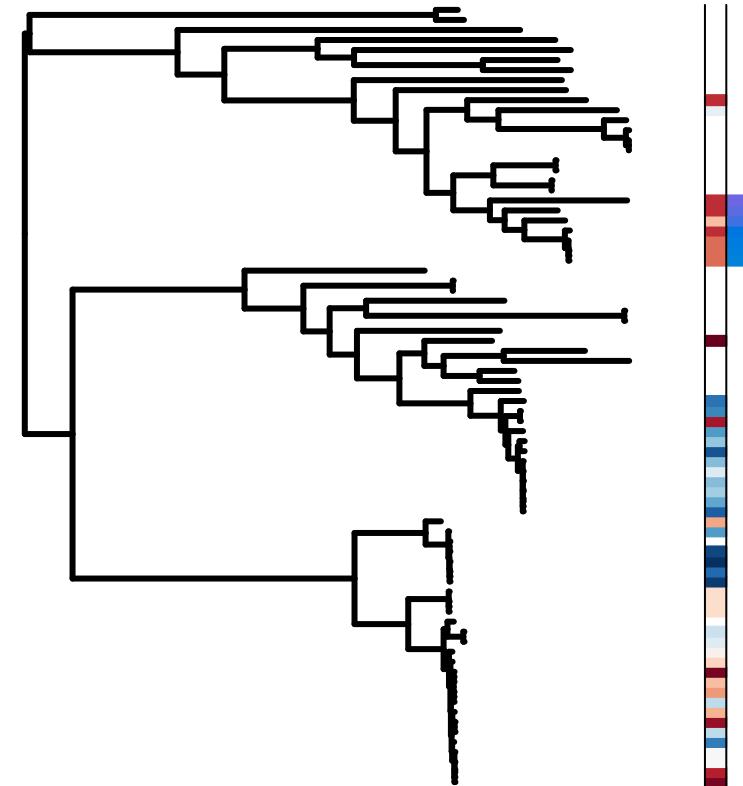
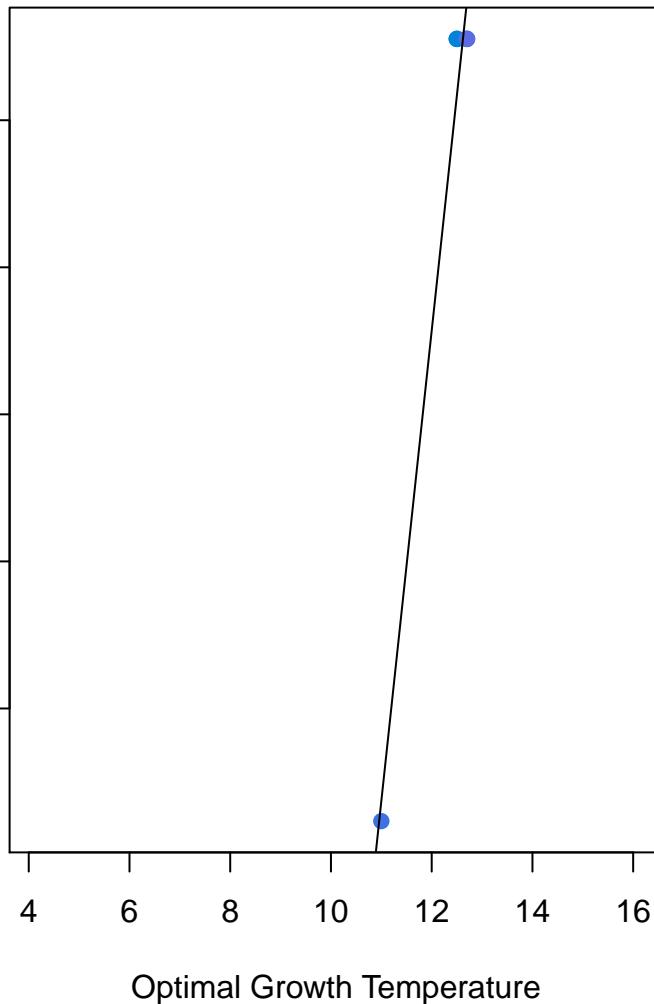


feature.plfam_id.proline_residue.mean



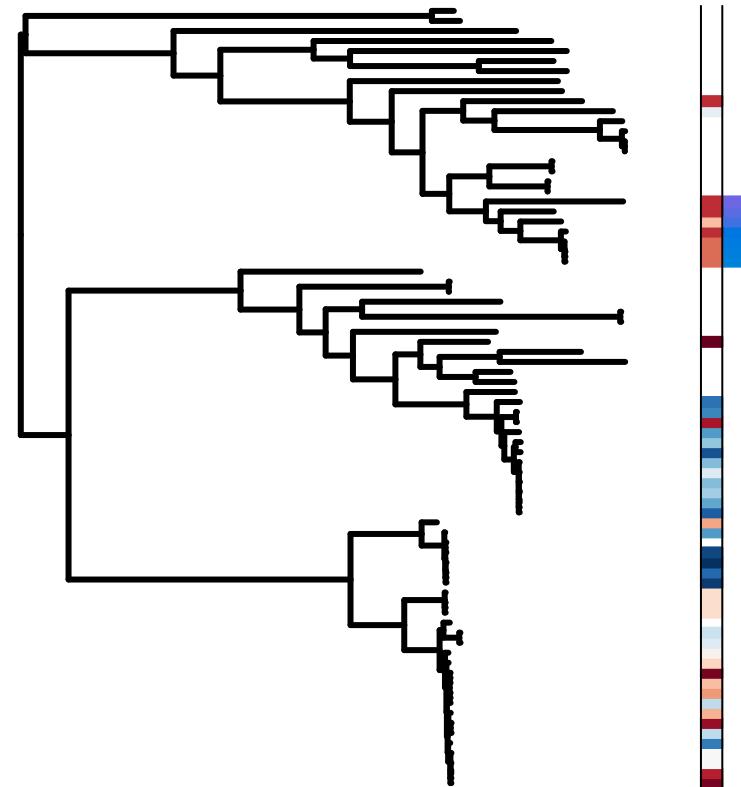
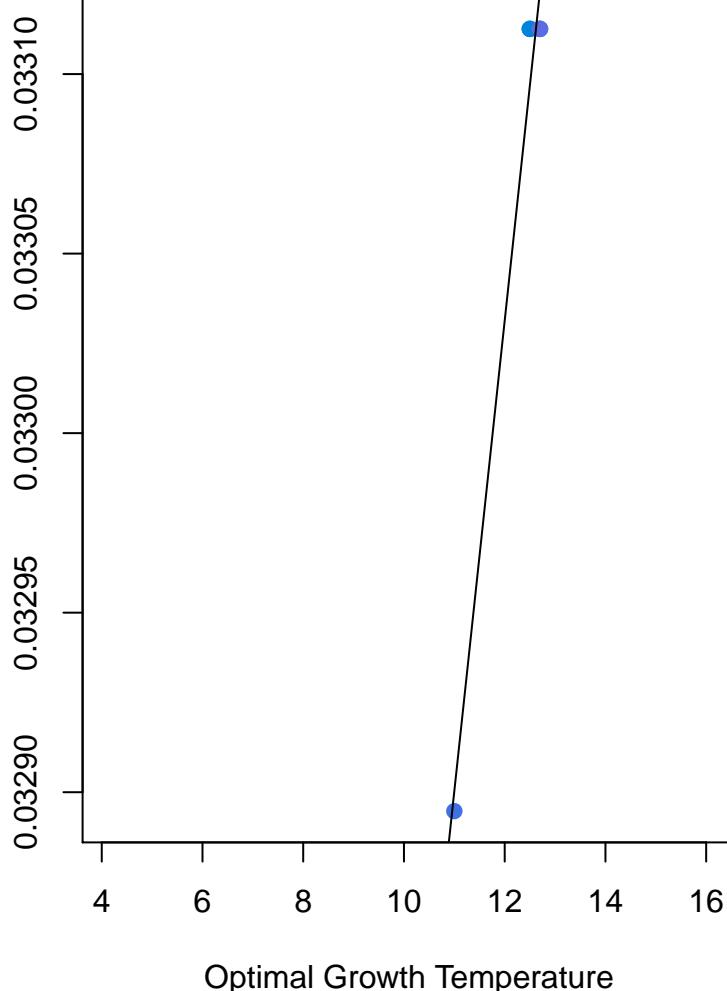
feature.plfam_id.proline_residue.mean
PLF_28228_00003688
Tellurite methyltransferase (EC 2.1.1.265)
 $r = 0.985$, $p = 10^{-5.104}$

feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00003980
hypothetical protein
 $r = 0.985, p = 10^{-5.104}$

feature.plfam_id.proline_residue.mean



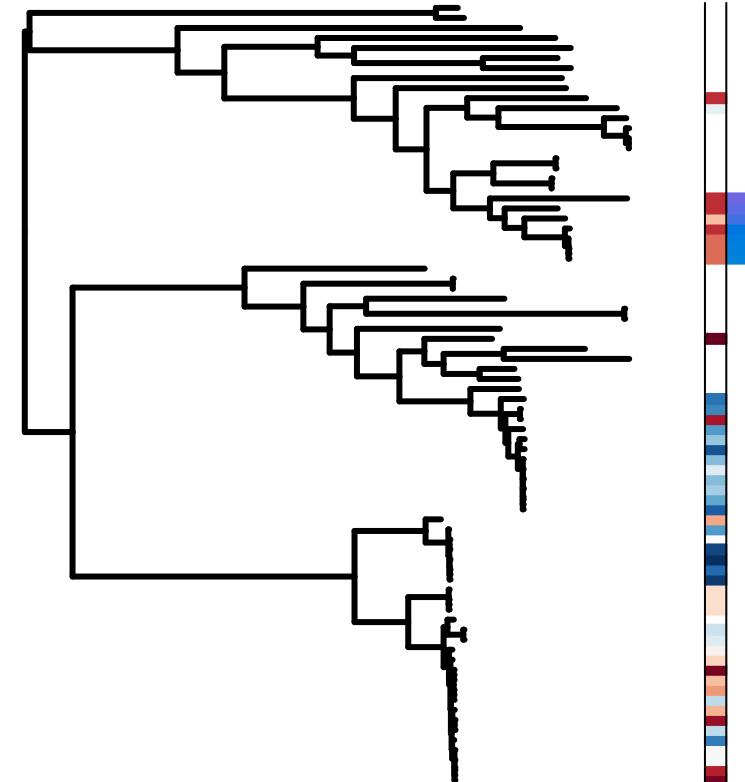
feature.plfam_id.proline_residue.mean

PLF_28228_00014485

RND efflux system, inner membrane transporter

$r = 0.985, p = 10^{-5.104}$

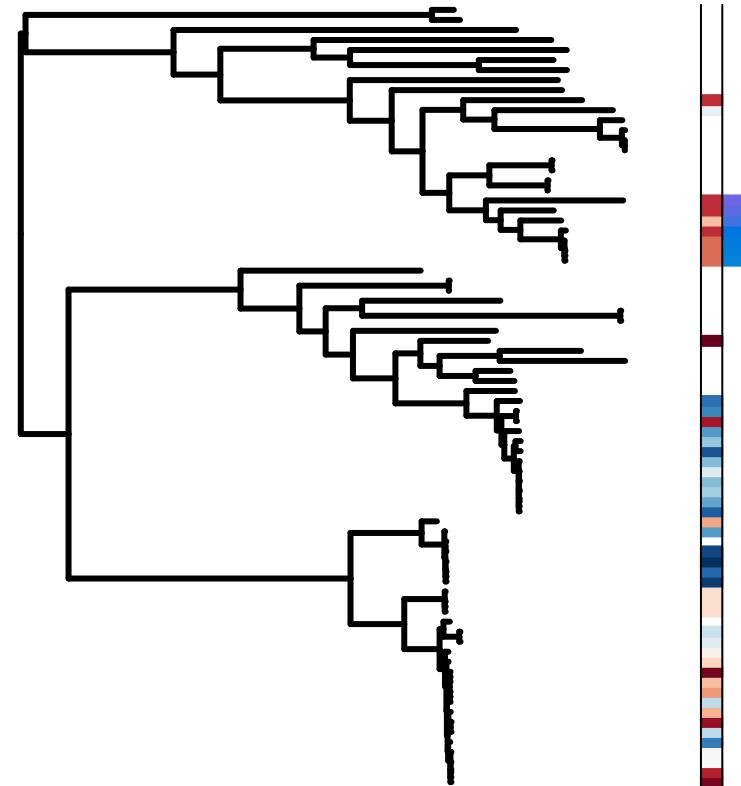
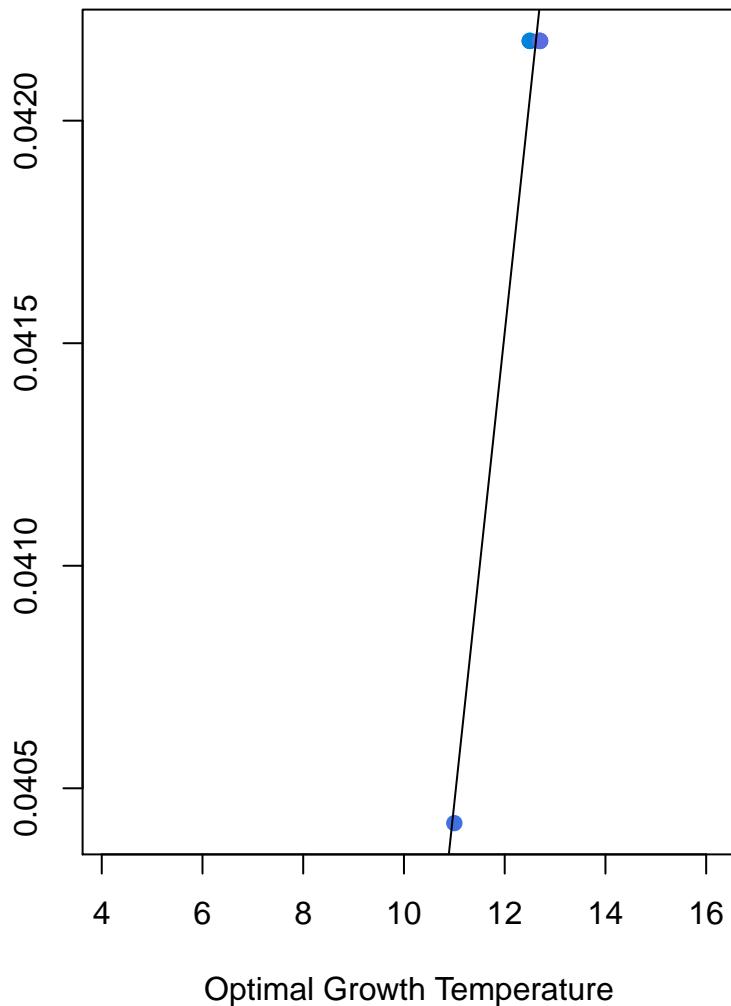
feature.plfam_id.proline_residue.mean

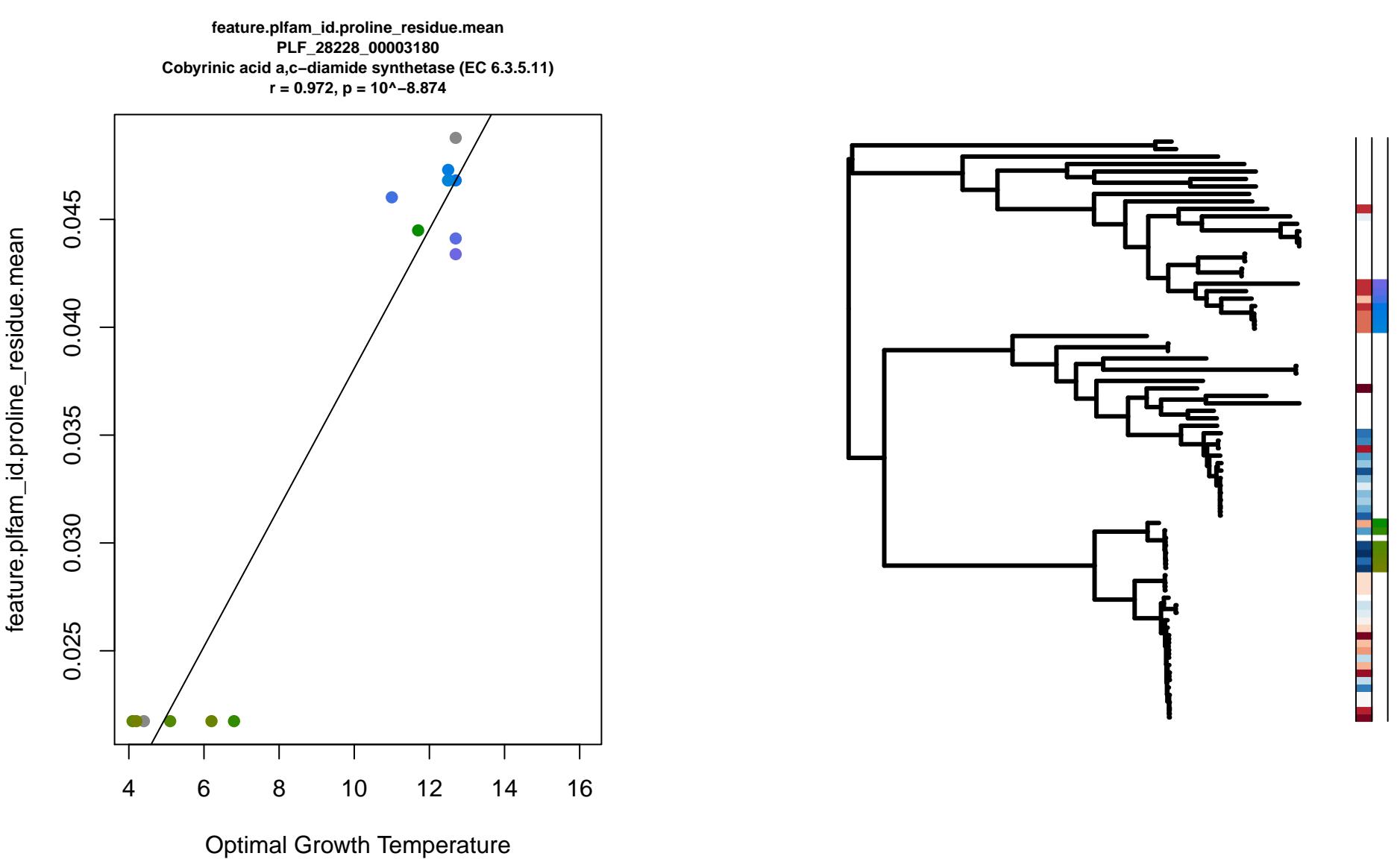


Optimal Growth Temperature

feature.plfam_id.proline_residue.mean
PLF_28228_00018479
hypothetical protein
 $r = 0.985, p = 10^{-5.104}$

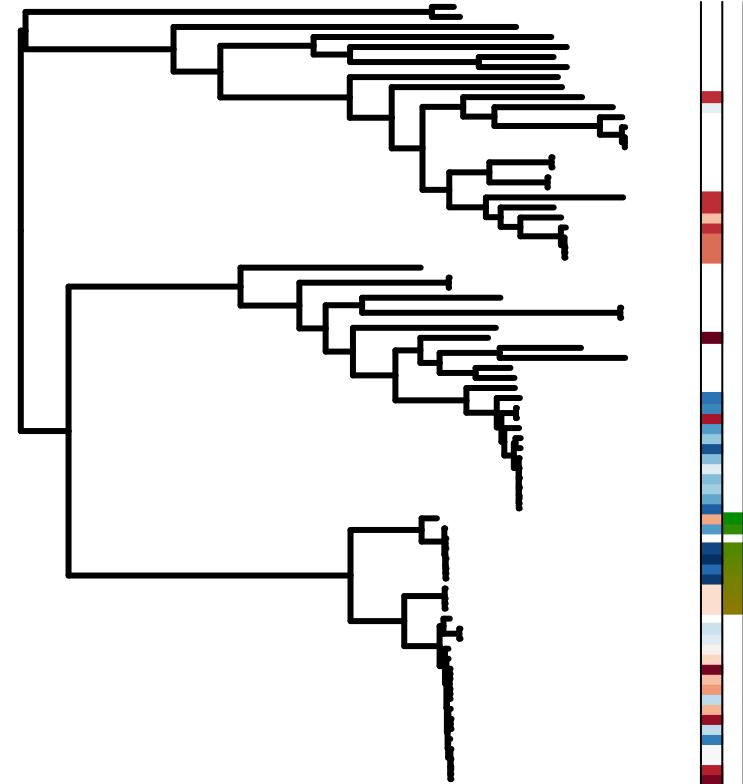
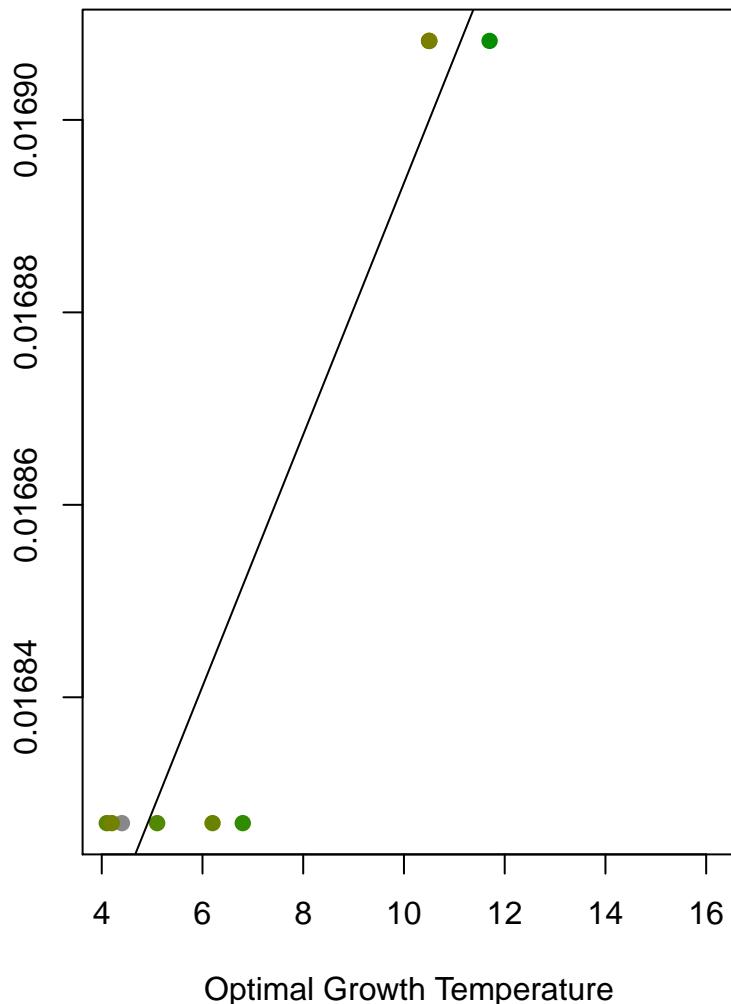
feature.plfam_id.proline_residue.mean





feature.plfam_id.proline_residue.mean
PLF_28228_00011513
hypothetical protein
 $r = 0.955, p = 10^{-4.761}$

feature.plfam_id.proline_residue.mean



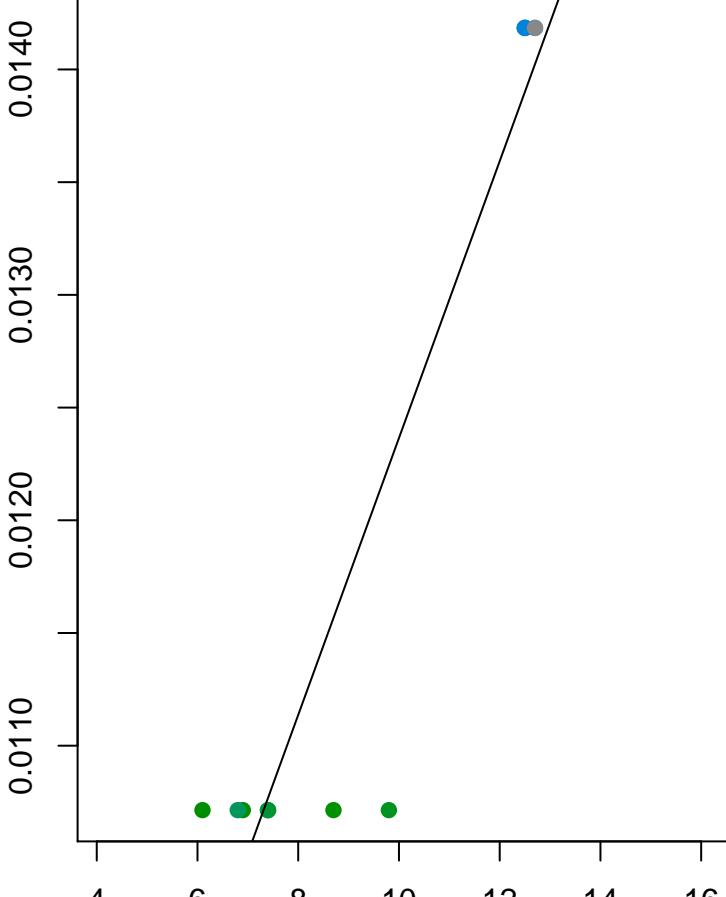
feature.plfam_id.proline_residue.mean

PLF_28228_00007747

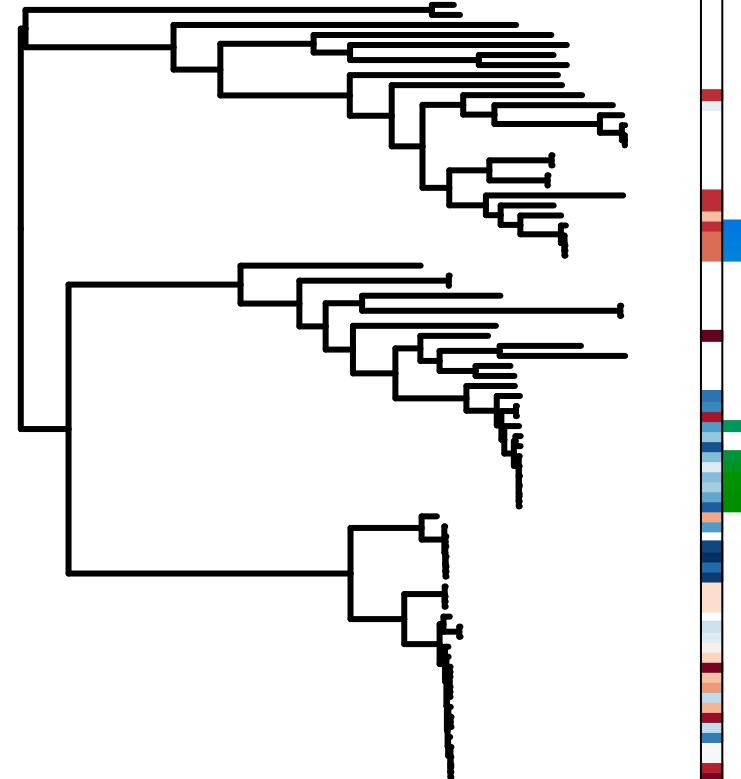
Membrane-associated methyl-accepting chemotaxis protein with HAMP domain

$r = 0.94, p = 10^{-5.262}$

feature.plfam_id.proline_residue.mean

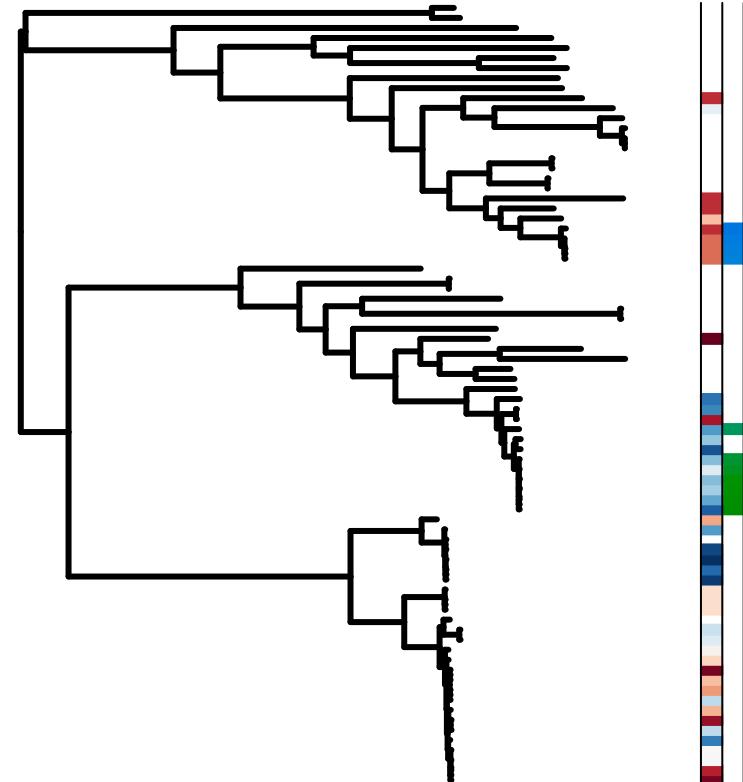
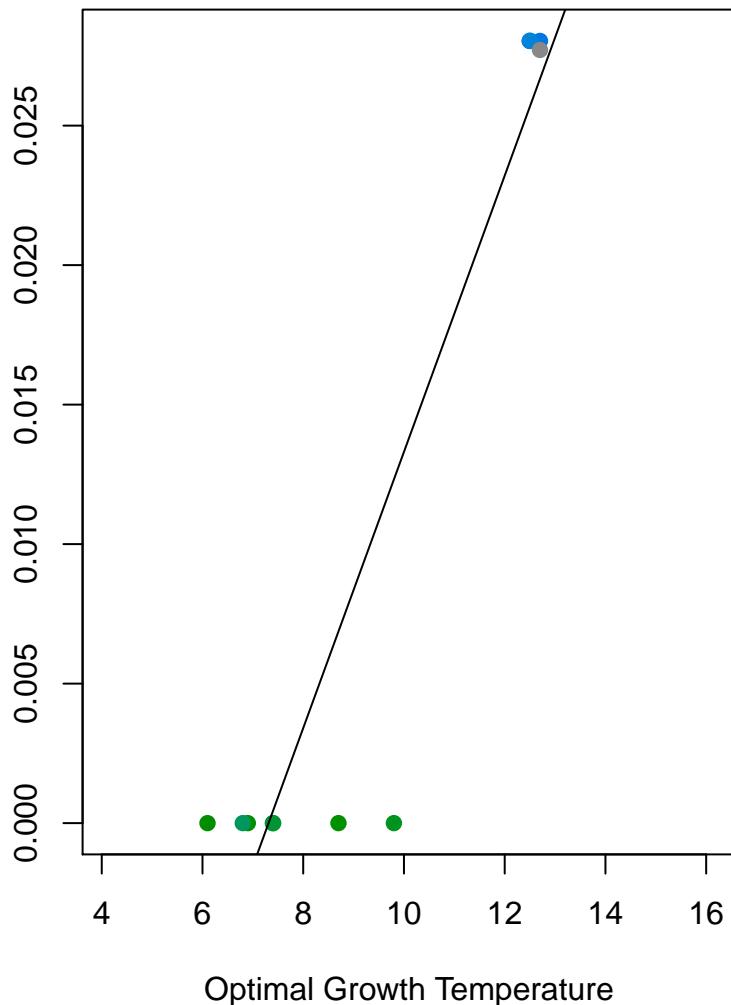


Optimal Growth Temperature



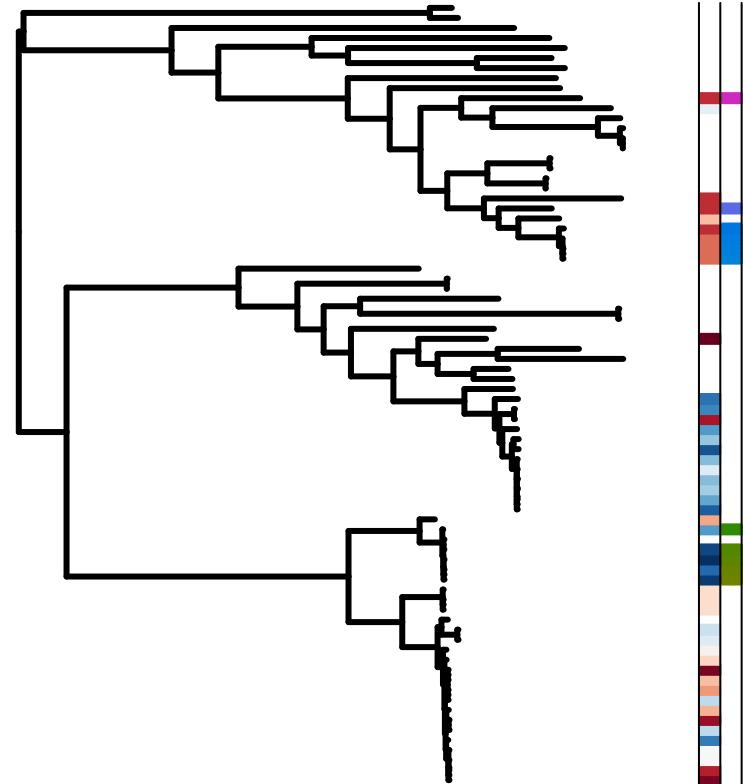
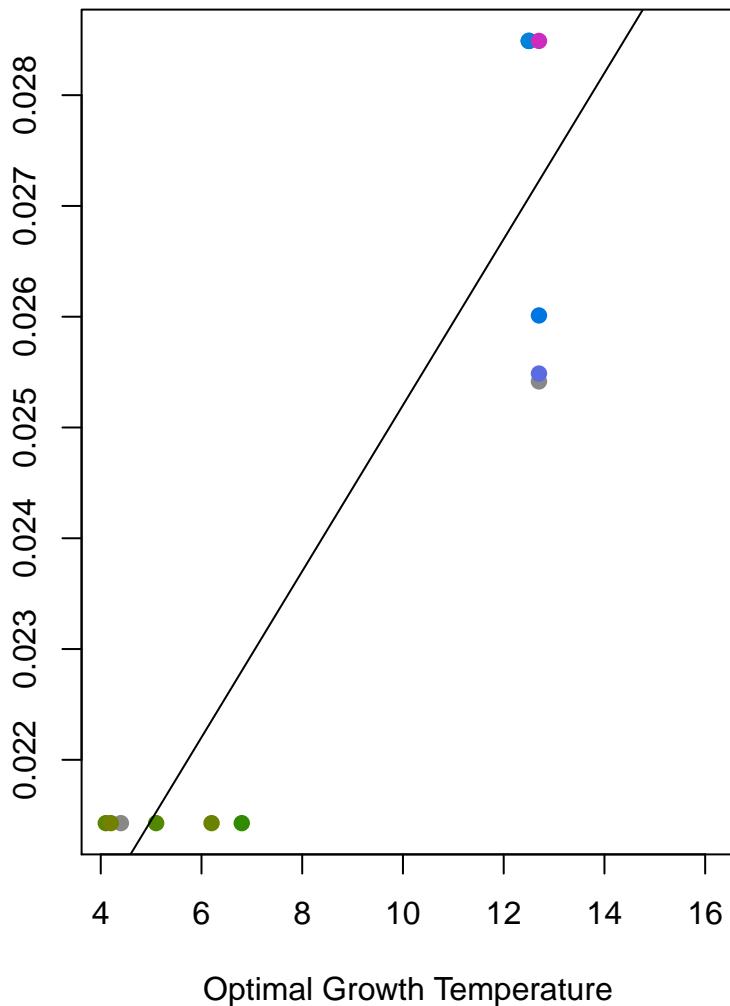
feature.plfam_id.proline_residue.mean
PLF_28228_00007748
EAL domain protein
 $r = 0.94$, $p = 10^{-5.259}$

feature.plfam_id.proline_residue.mean

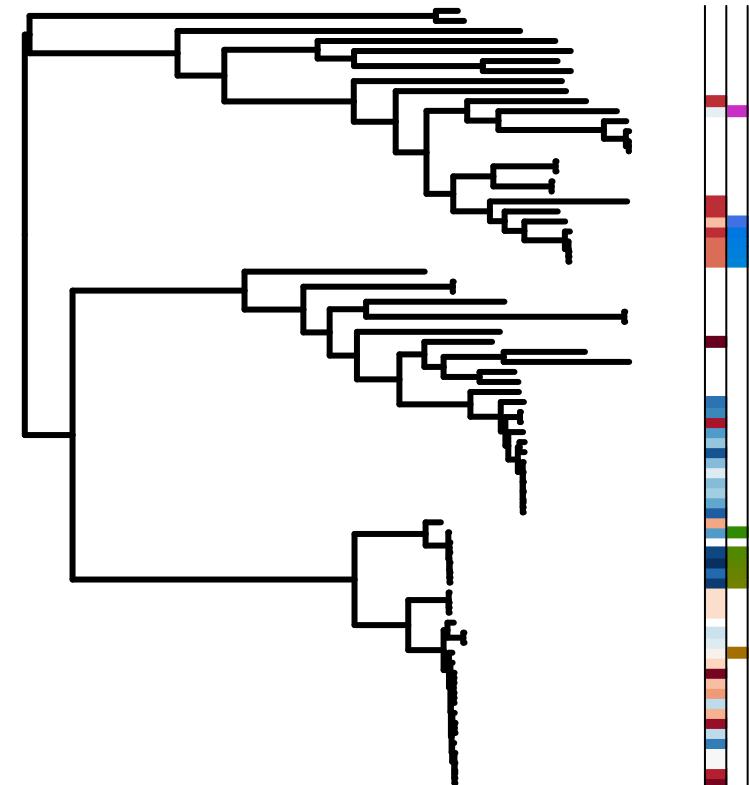
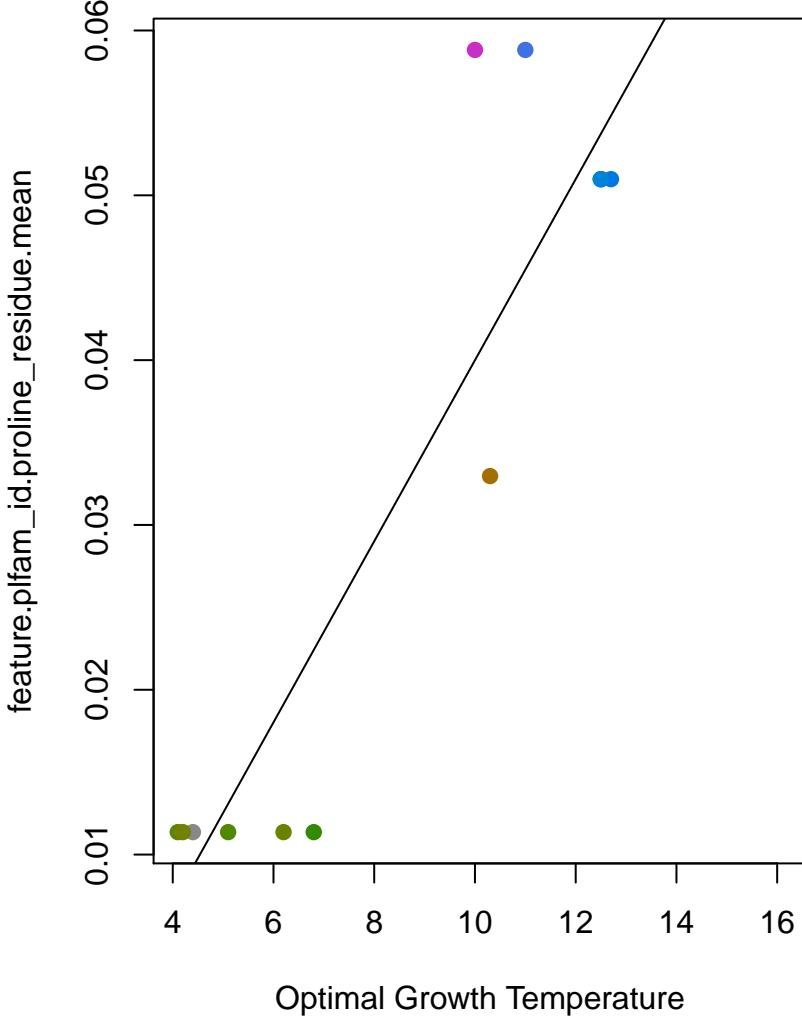


feature.plfam_id.proline_residue.mean
PLF_28228_00003700
TonB-dependent receptor
 $r = 0.92$, $p = 10^{-5.078}$

feature.plfam_id.proline_residue.mean

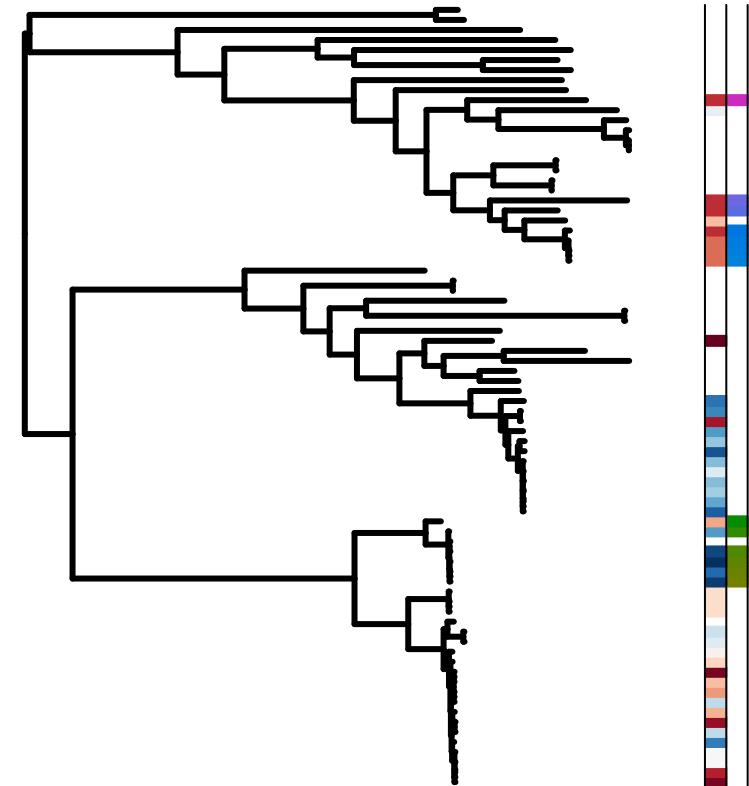
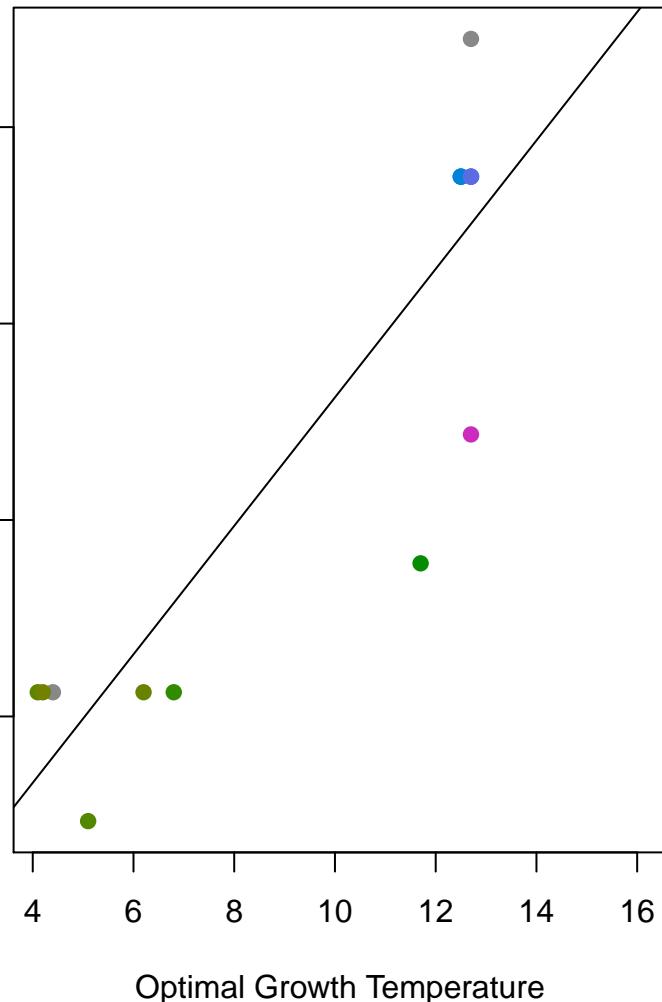


feature.pfam_id.proline_residue.mean
PLF_28228_00003739
Transcriptional regulator, IclR family
 $r = 0.917$, $p = 10^{-5.001}$



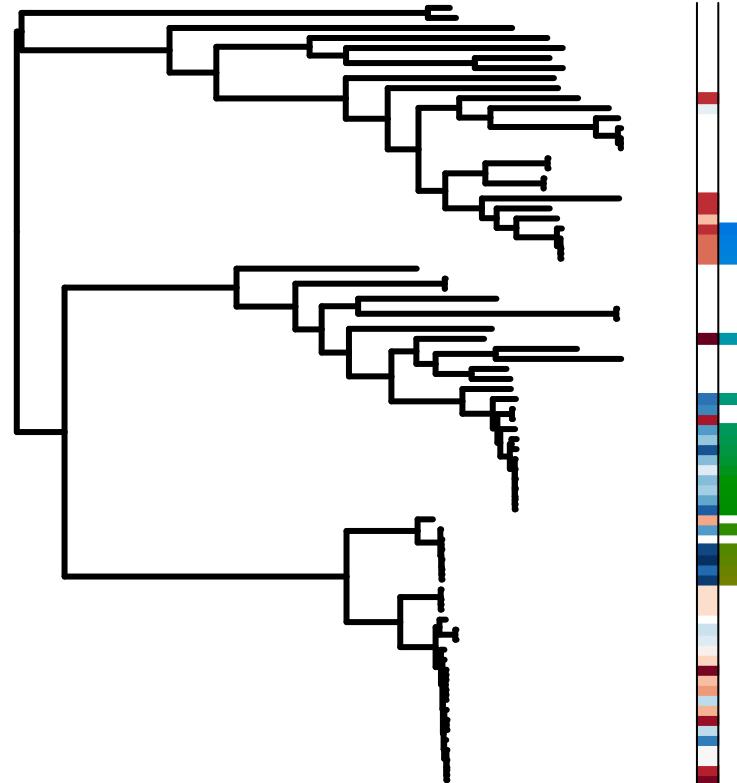
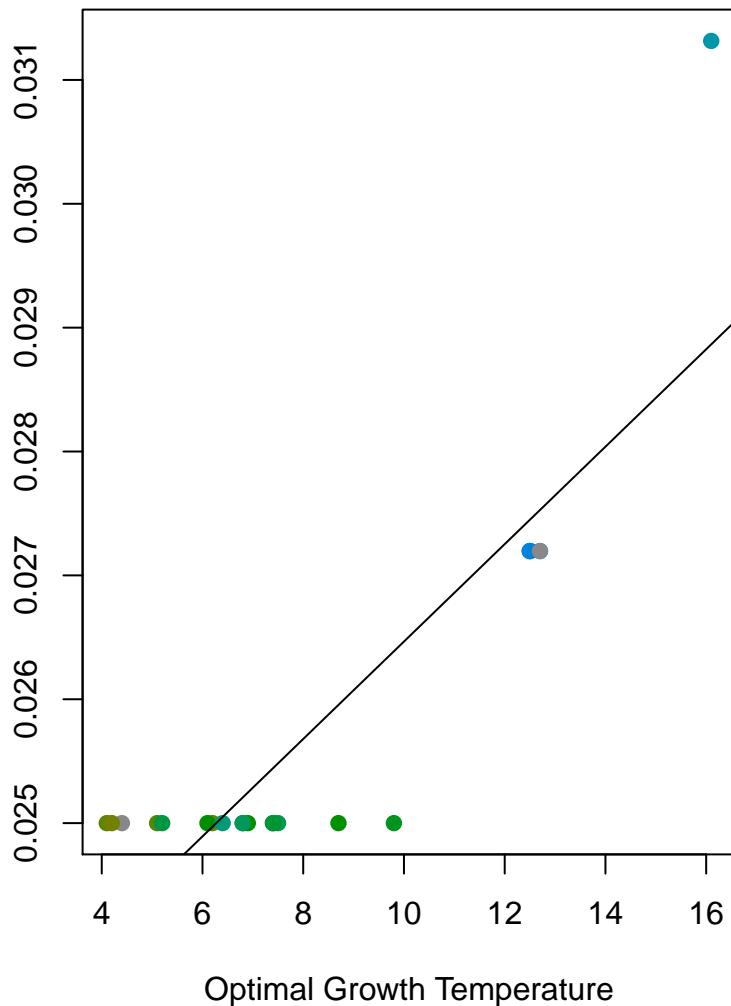
feature.plfam_id.proline_residue.mean
PLF_28228_00002110
TonB-dependent receptor
 $r = 0.894$, $p = 10^{-5.15}$

feature.plfam_id.proline_residue.mean



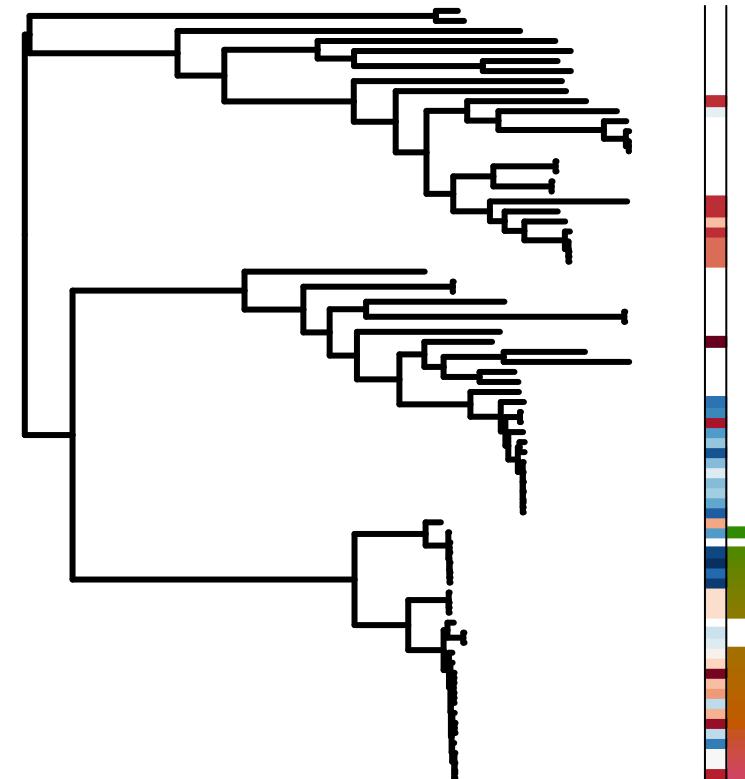
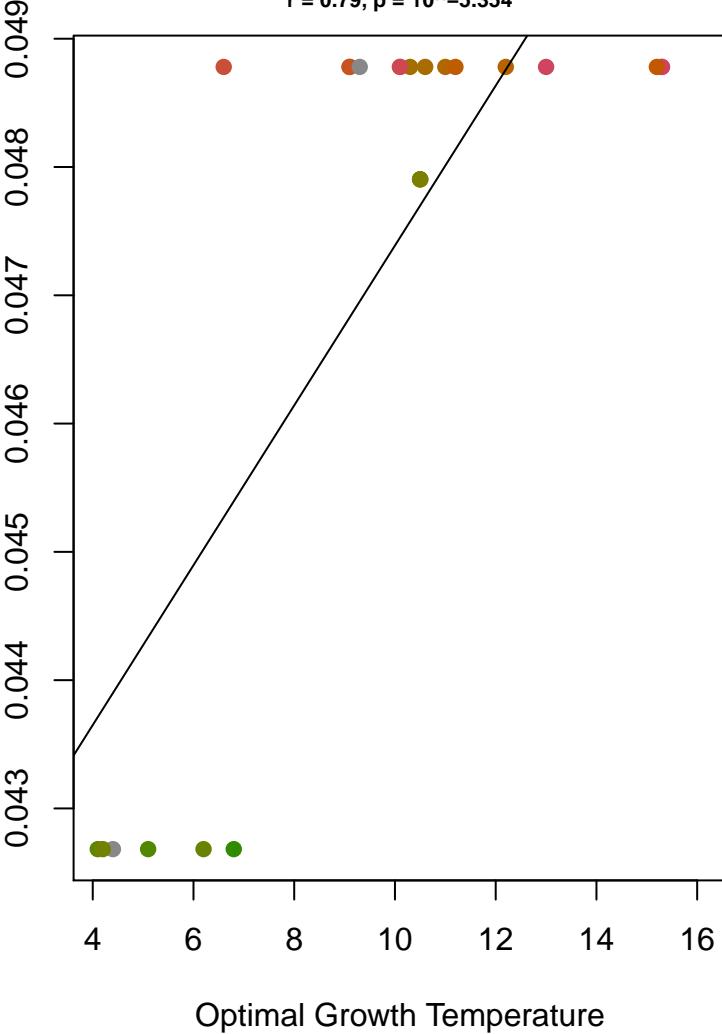
feature.plfam_id.proline_residue.mean
PLF_28228_00003471
Glucose/mannose:H⁺ symporter GlcP
 $r = 0.869$, $p = 10^{-6.804}$

feature.plfam_id.proline_residue.mean



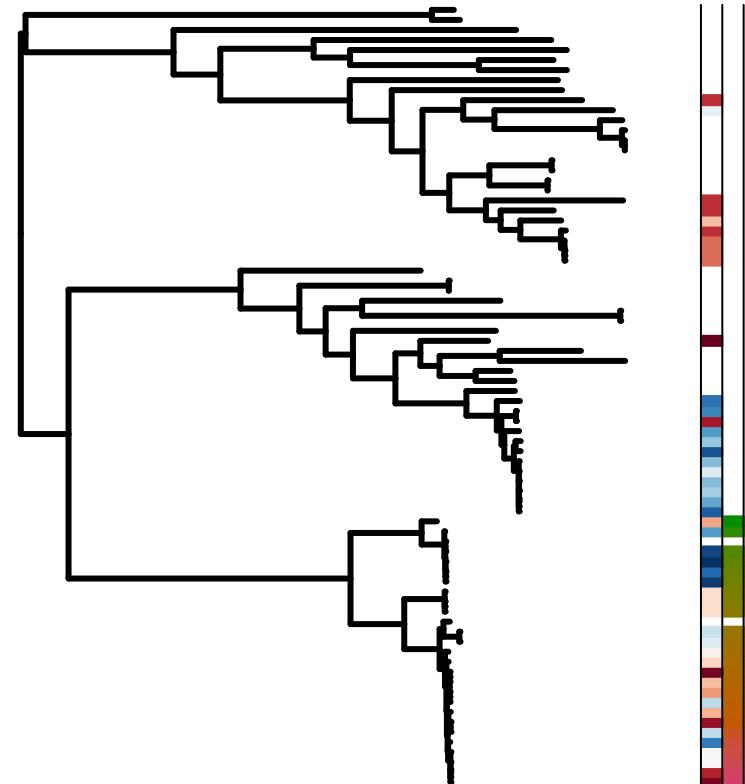
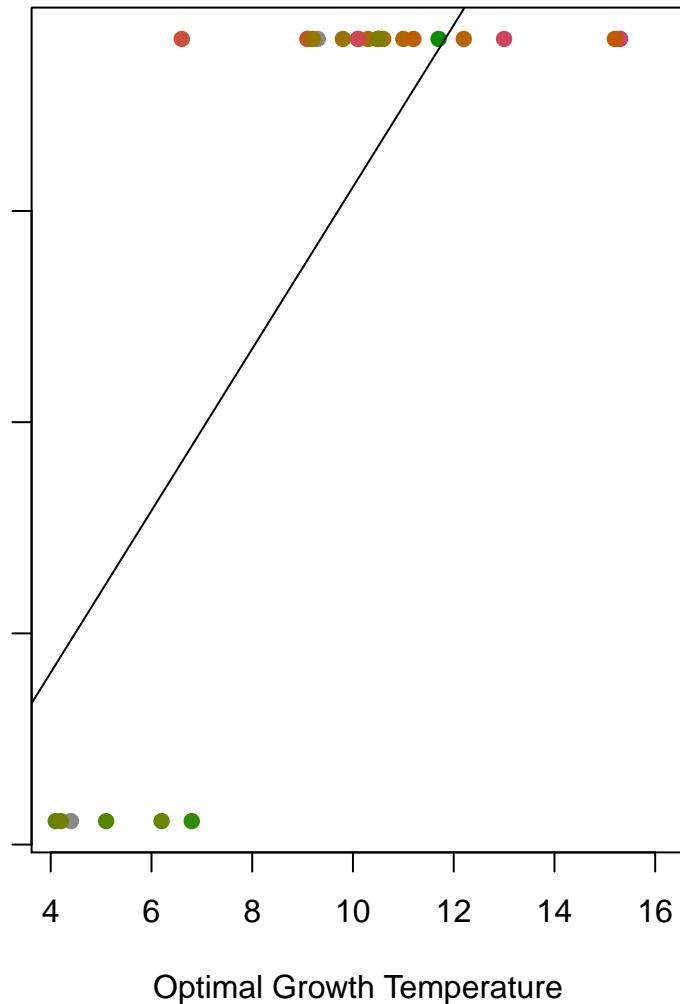
feature.pfam_id.proline_residue.mean
PLF_28228_00030467
Redoxin domain protein
 $r = 0.79$, $p = 10^{-5.354}$

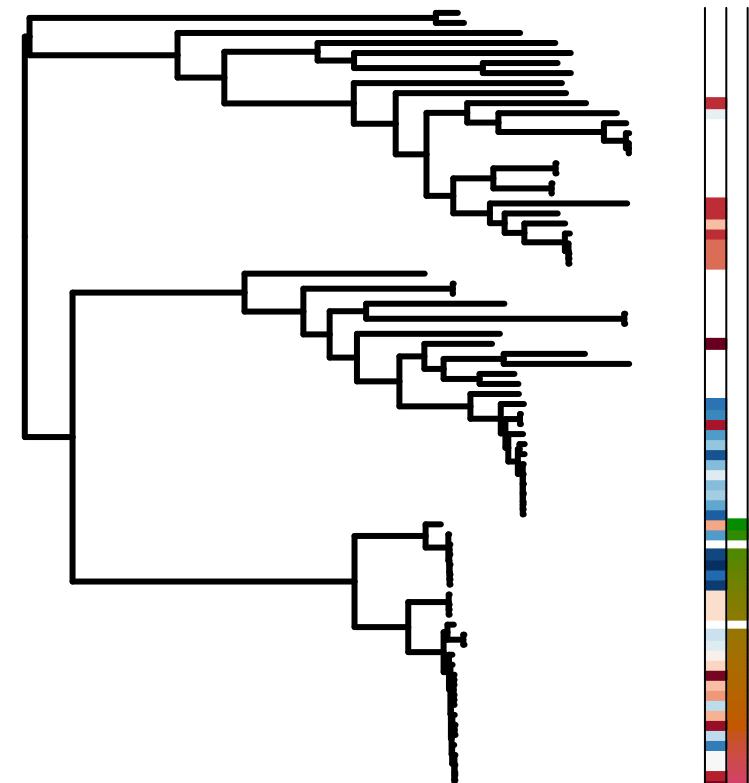
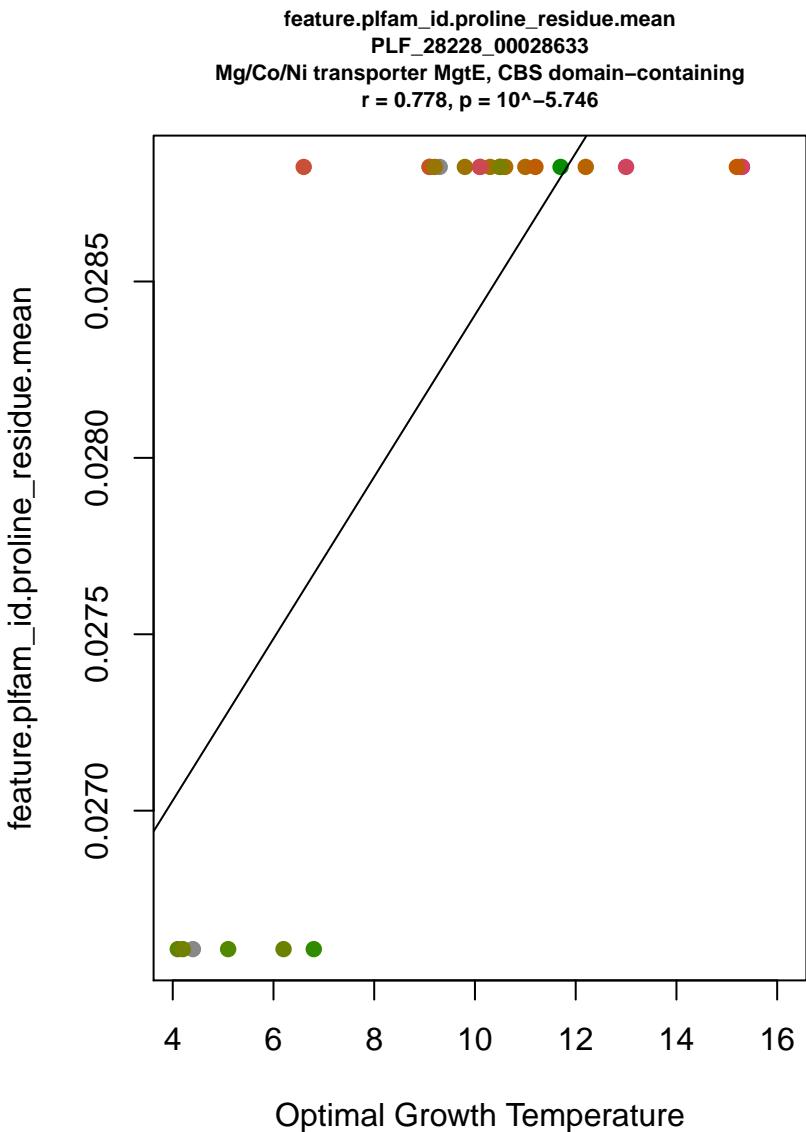
feature.pfam_id.proline_residue.mean



feature.pfam_id.proline_residue.mean
PLF_28228_00028208
hypothetical protein
 $r = 0.778, p = 10^{-5.746}$

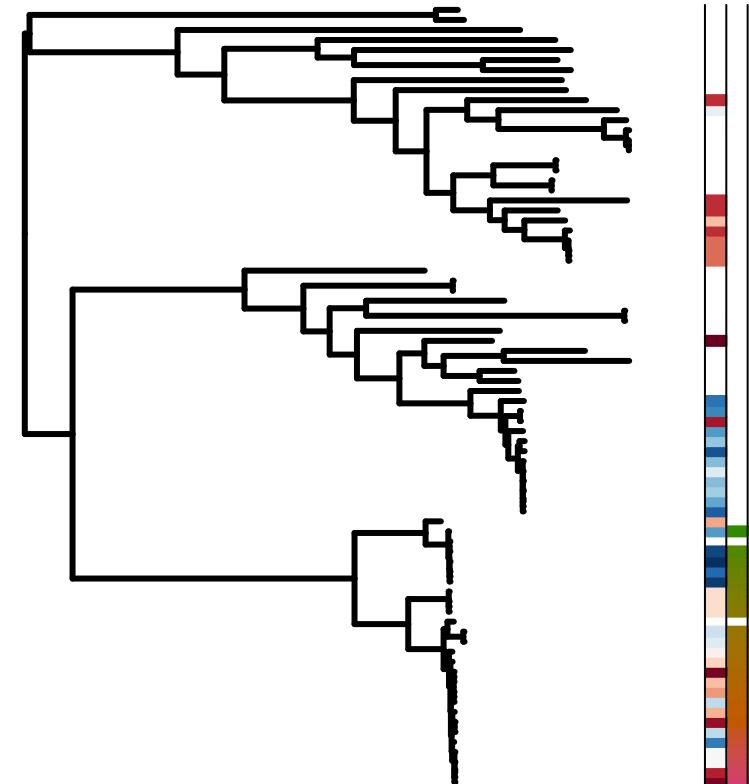
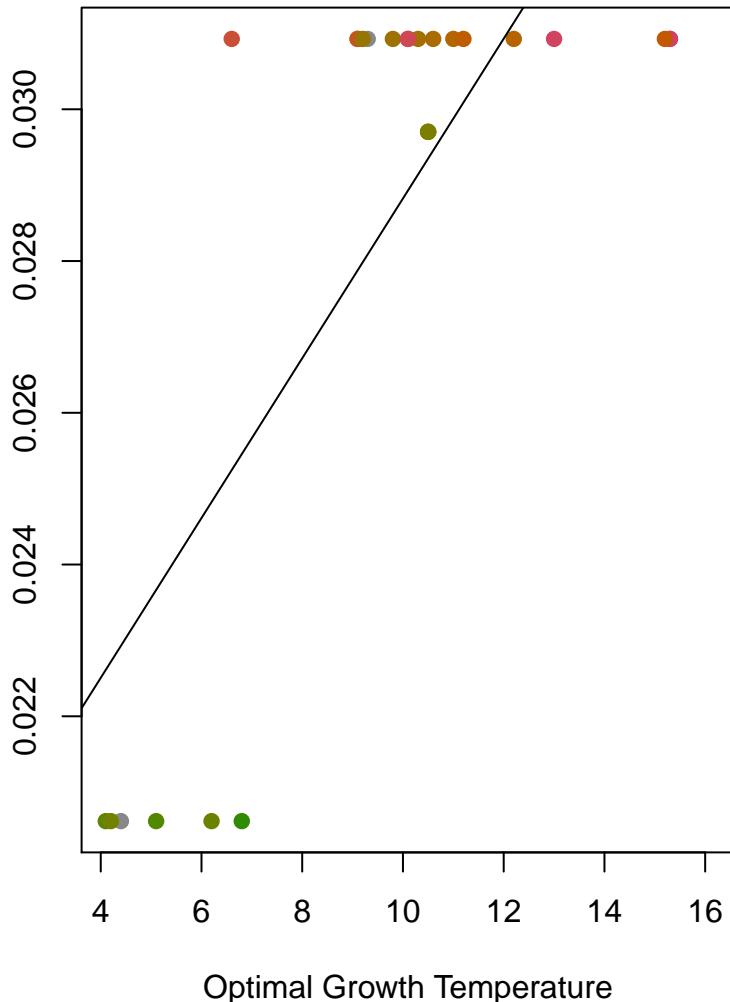
feature.pfam_id.proline_residue.mean

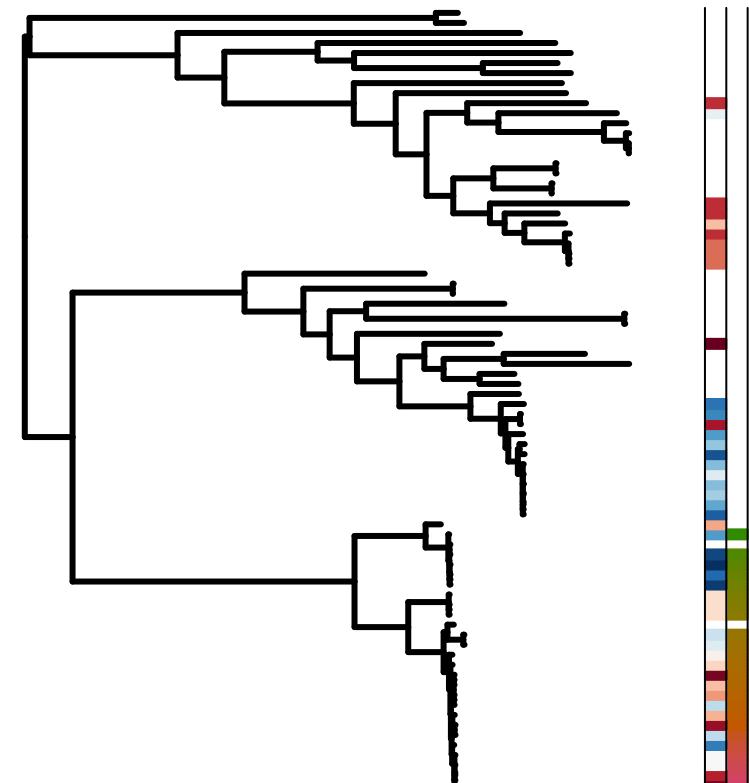
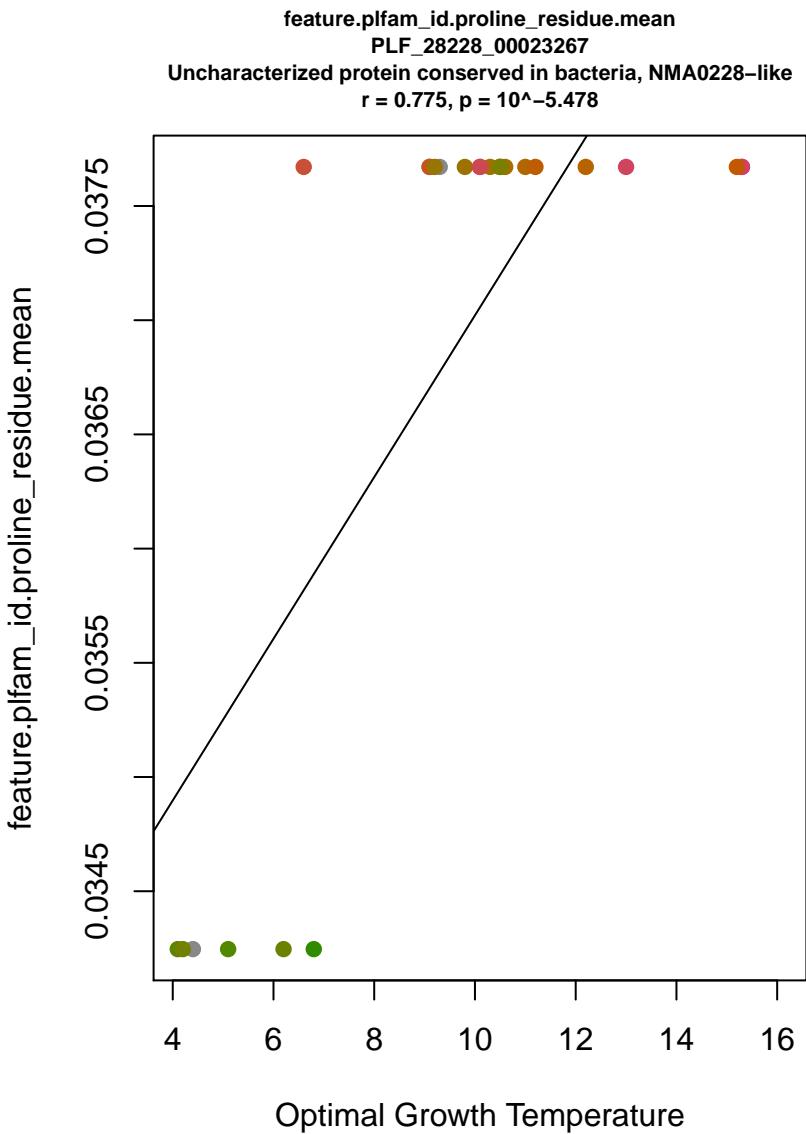




feature.plfam_id.proline_residue.mean
PLF_28228_00030961
hypothetical protein
 $r = 0.777$, $p = 10^{-5.509}$

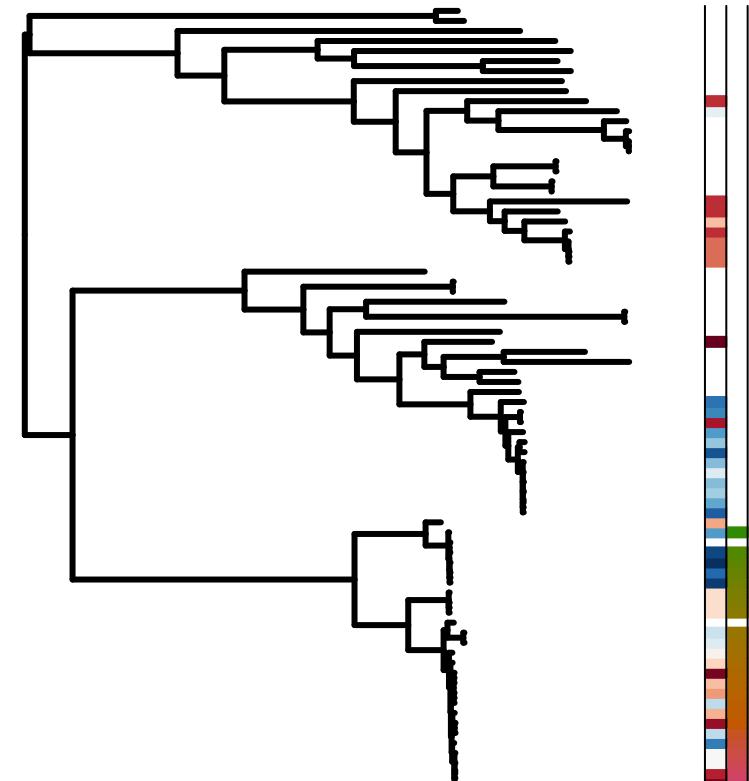
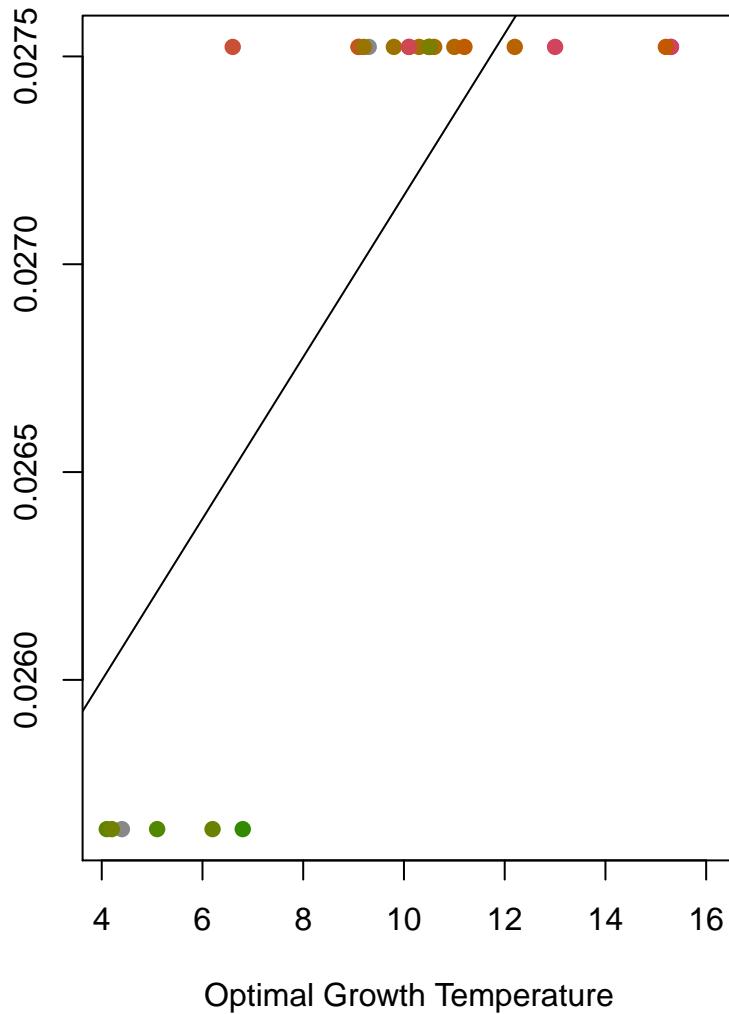
feature.plfam_id.proline_residue.mean





feature.plfam_id.proline_residue.mean
PLF_28228_00031492
hypothetical protein
 $r = 0.775, p = 10^{-5.478}$

feature.plfam_id.proline_residue.mean



Optimal Growth Temperature

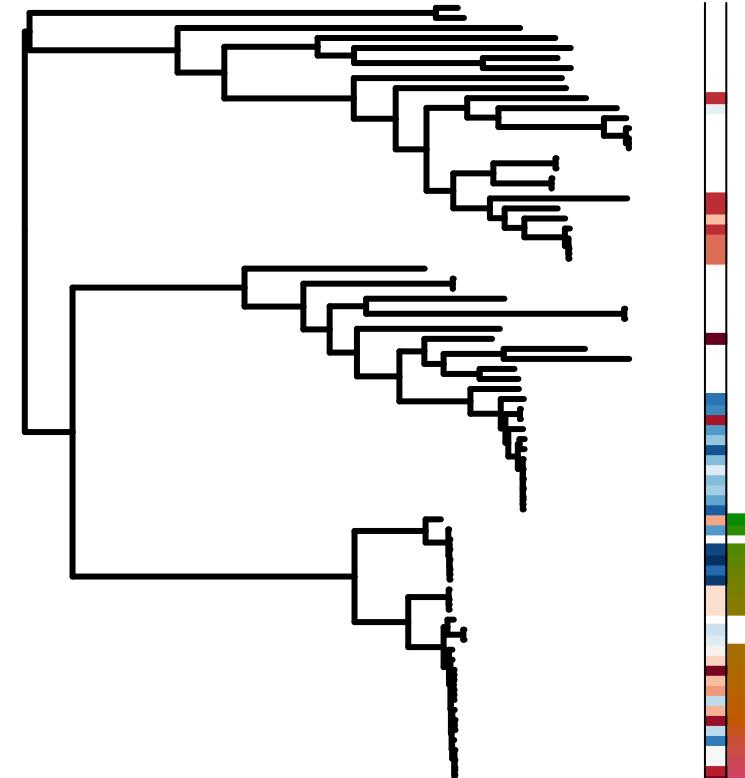
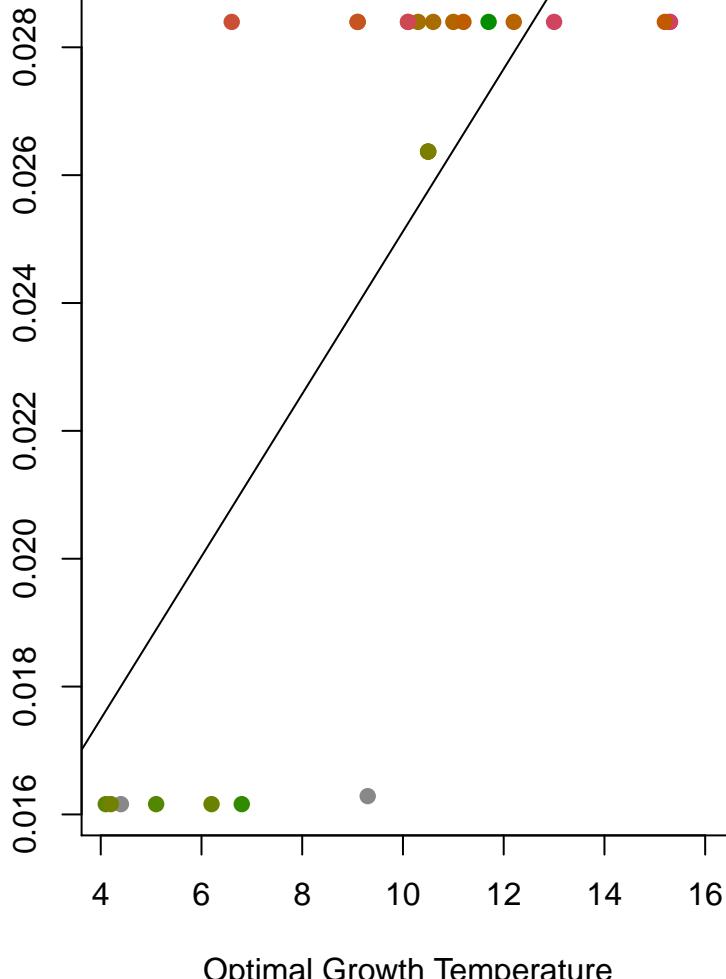
feature.pfam_id.proline_residue.mean

PLF_28228_00022096

Two-component system sensor histidine kinase

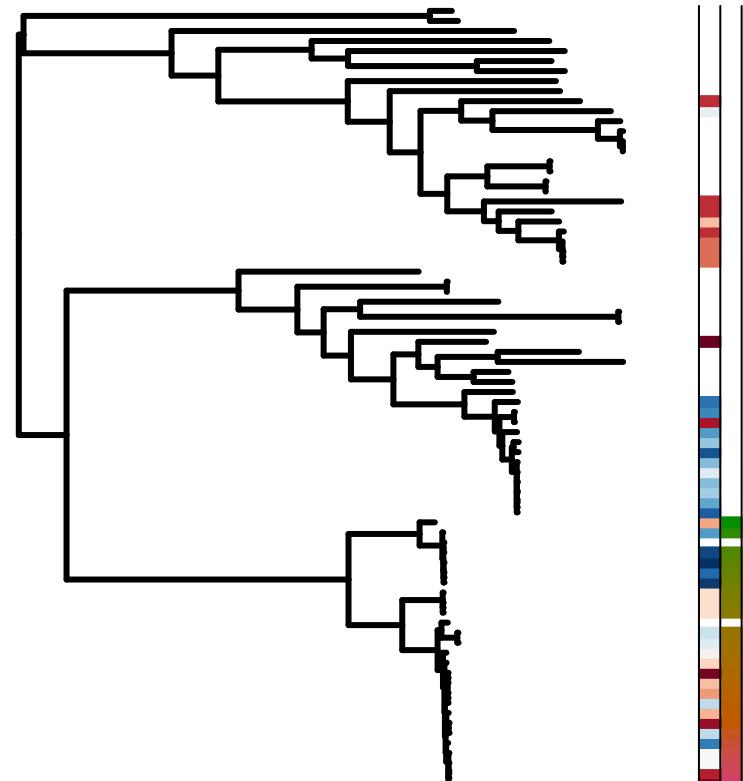
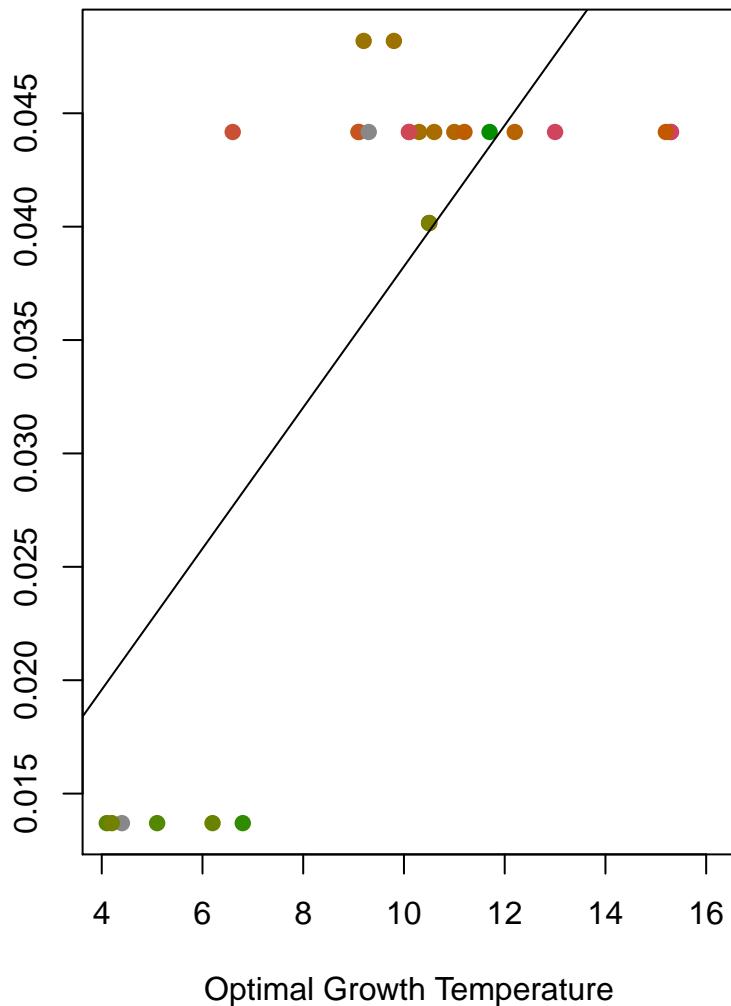
$r = 0.768$, $p = 10^{-5.131}$

feature.pfam_id.proline_residue.mean



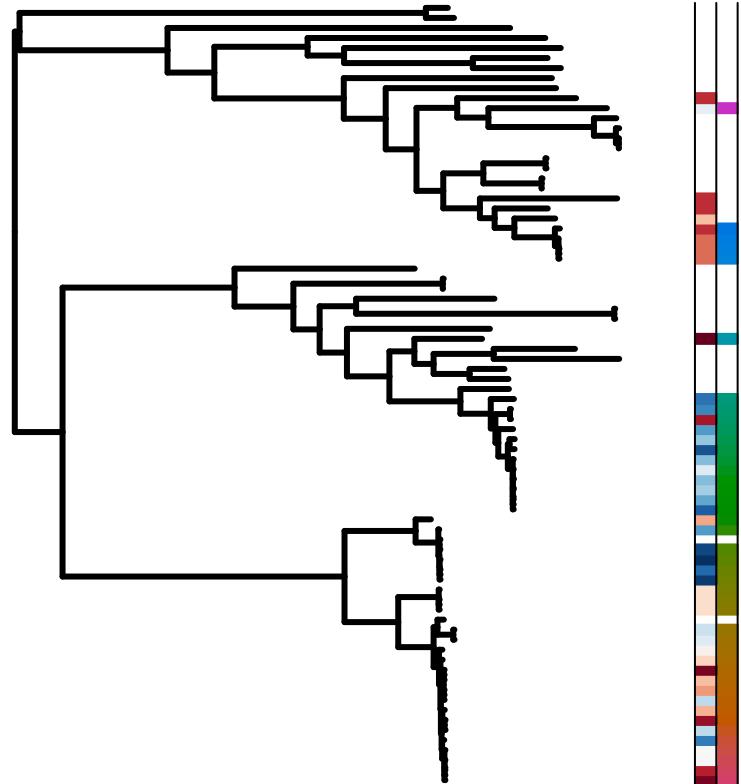
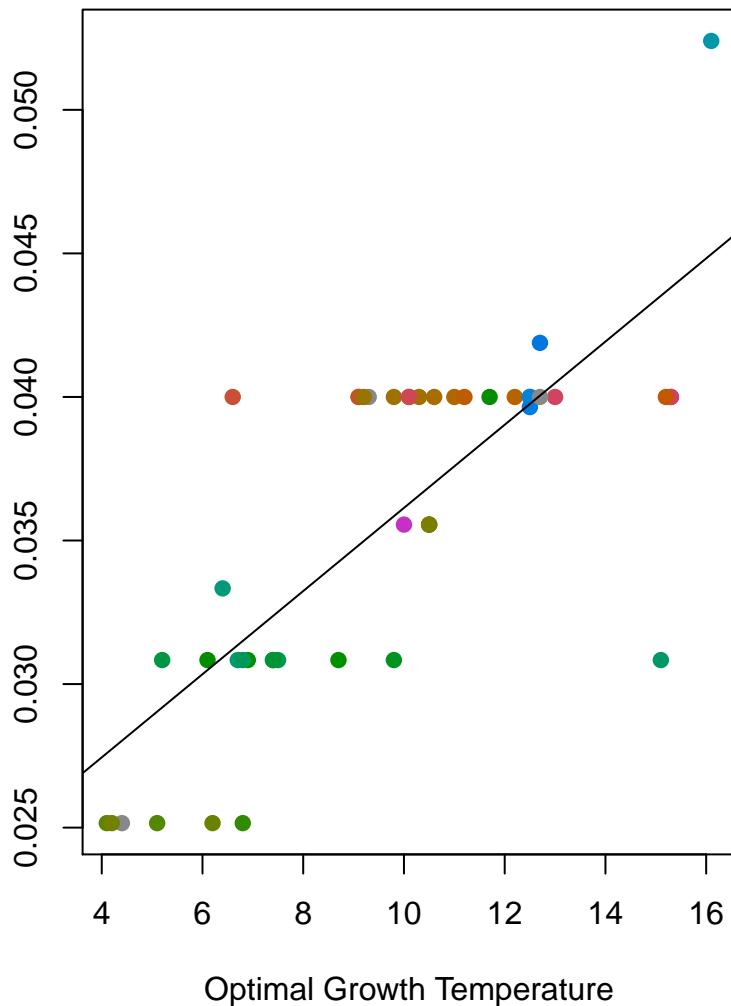
feature.plfam_id.proline_residue.mean
PLF_28228_00031426
hypothetical protein
 $r = 0.765, p = 10^{-5.474}$

feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00002803
SM-20-related protein
 $r = 0.765, p = 10^{-9.214}$

feature.plfam_id.proline_residue.mean



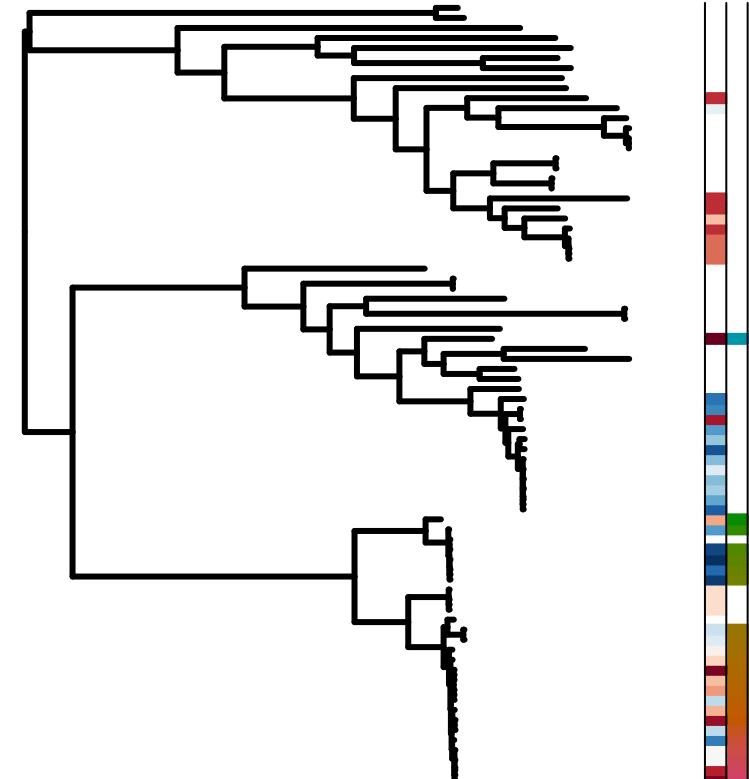
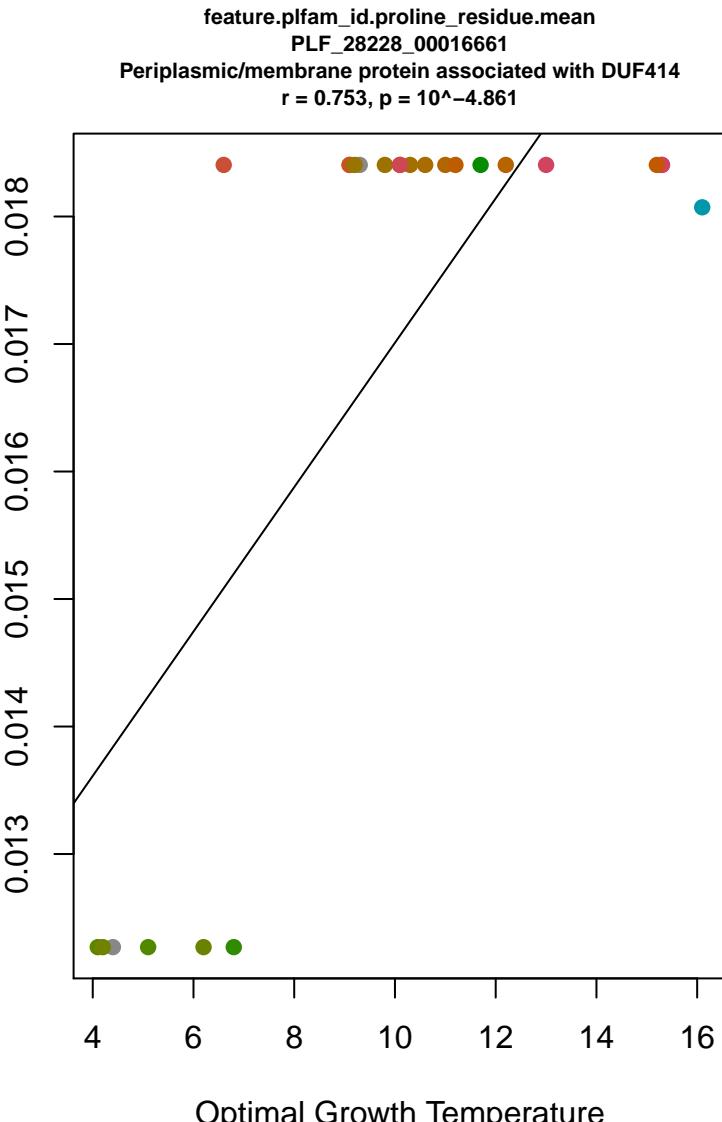
feature.plfam_id.proline_residue.mean

PLF_28228_00016661

Periplasmic/membrane protein associated with DUF414

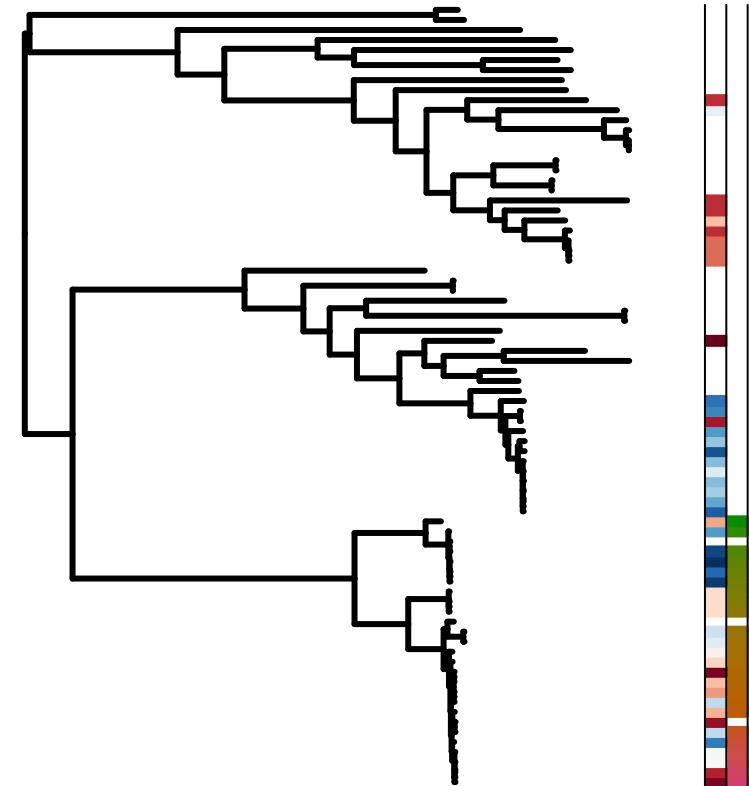
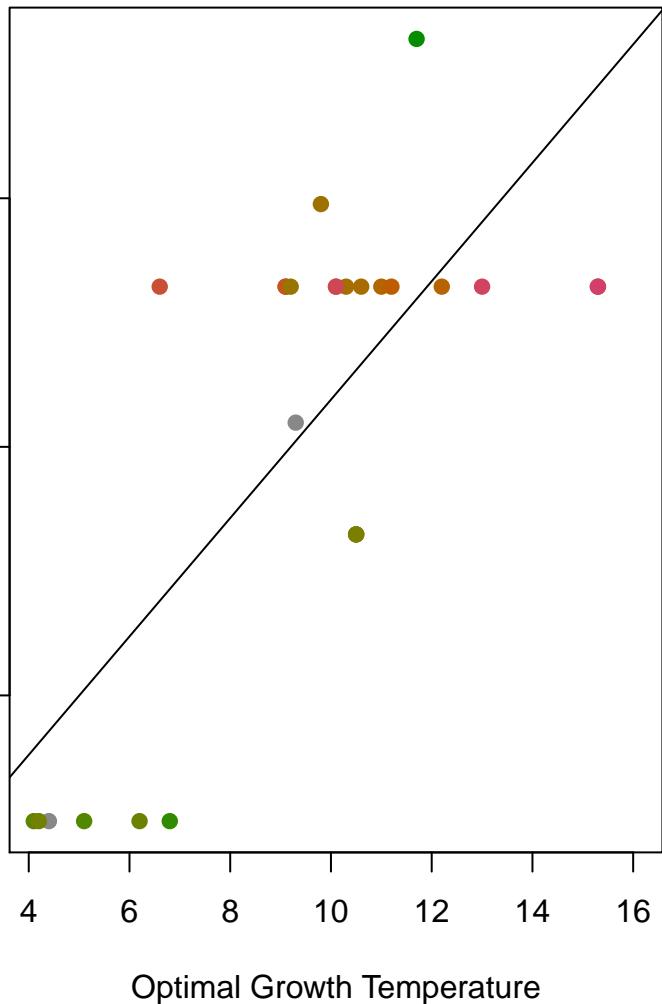
$r = 0.753, p = 10^{-4.861}$

feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00017455
Maltodextrin glucosidase (EC 3.2.1.20)
 $r = 0.751$, $p = 10^{-5.008}$

feature.plfam_id.proline_residue.mean



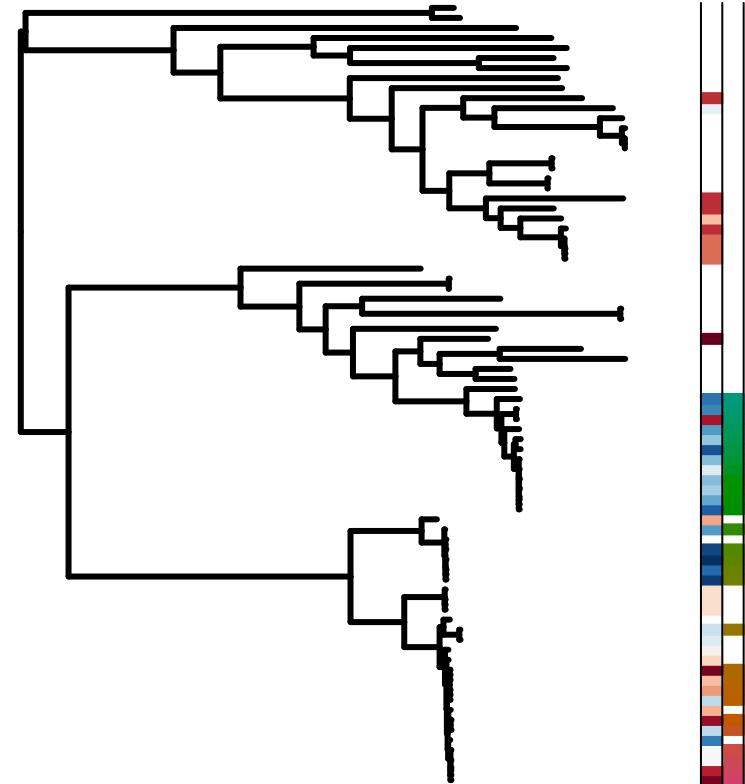
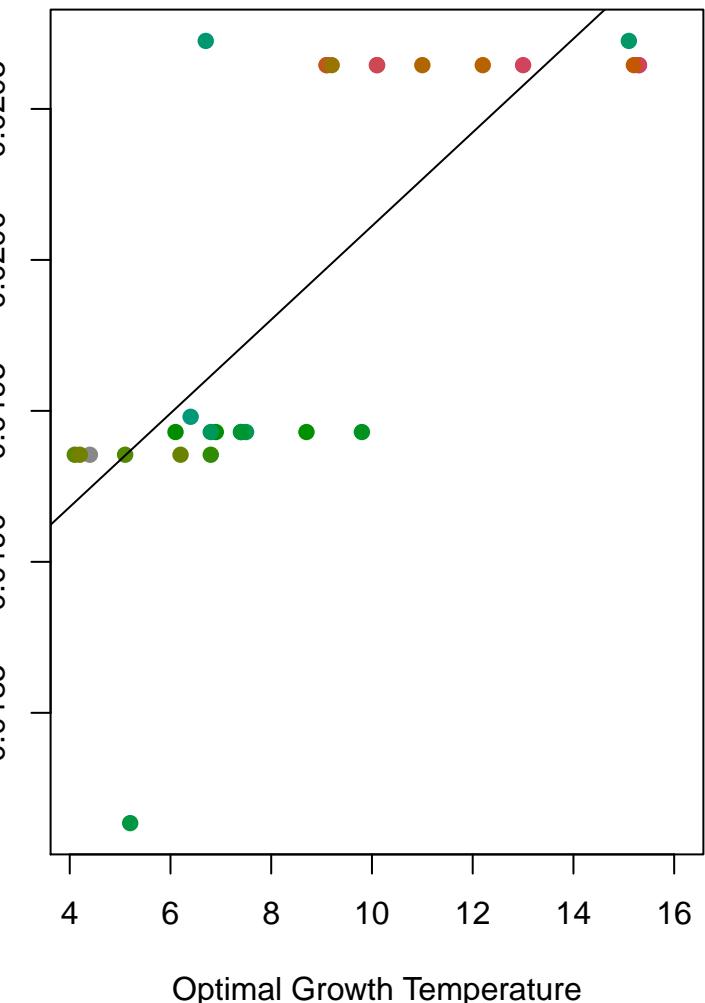
feature.plfam_id.proline_residue.mean

PLF_28228_00021199

diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)

$r = 0.75, p = 10^{-5.553}$

feature.plfam_id.proline_residue.mean



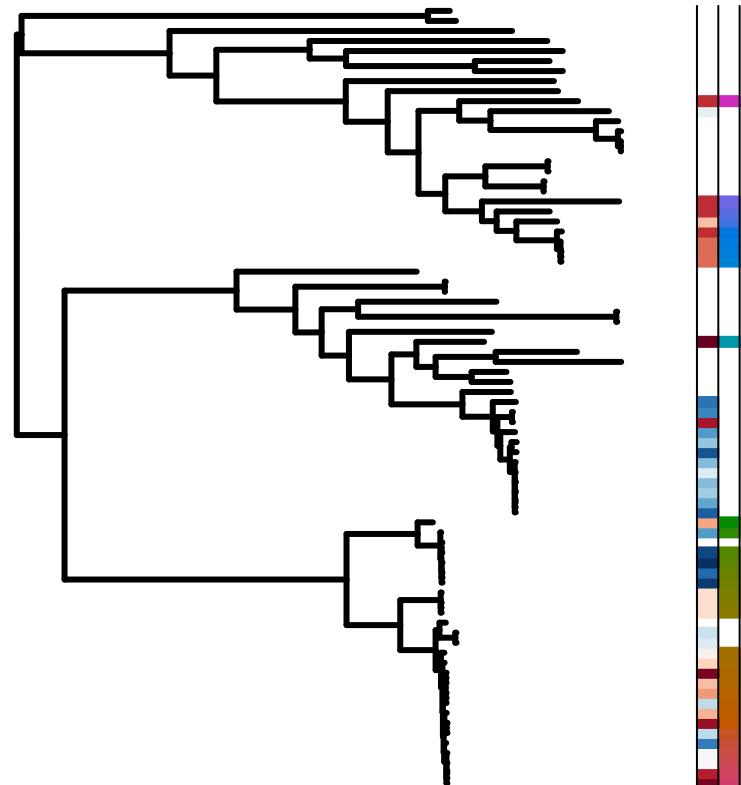
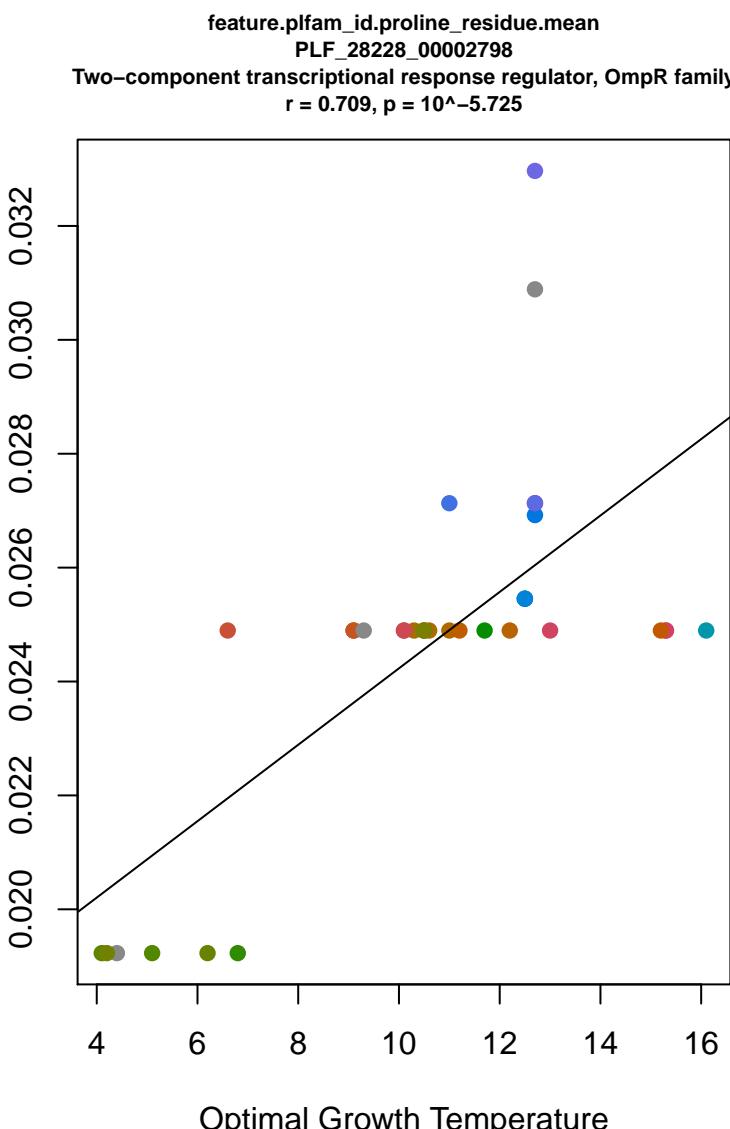
feature.pfam_id.proline_residue.mean

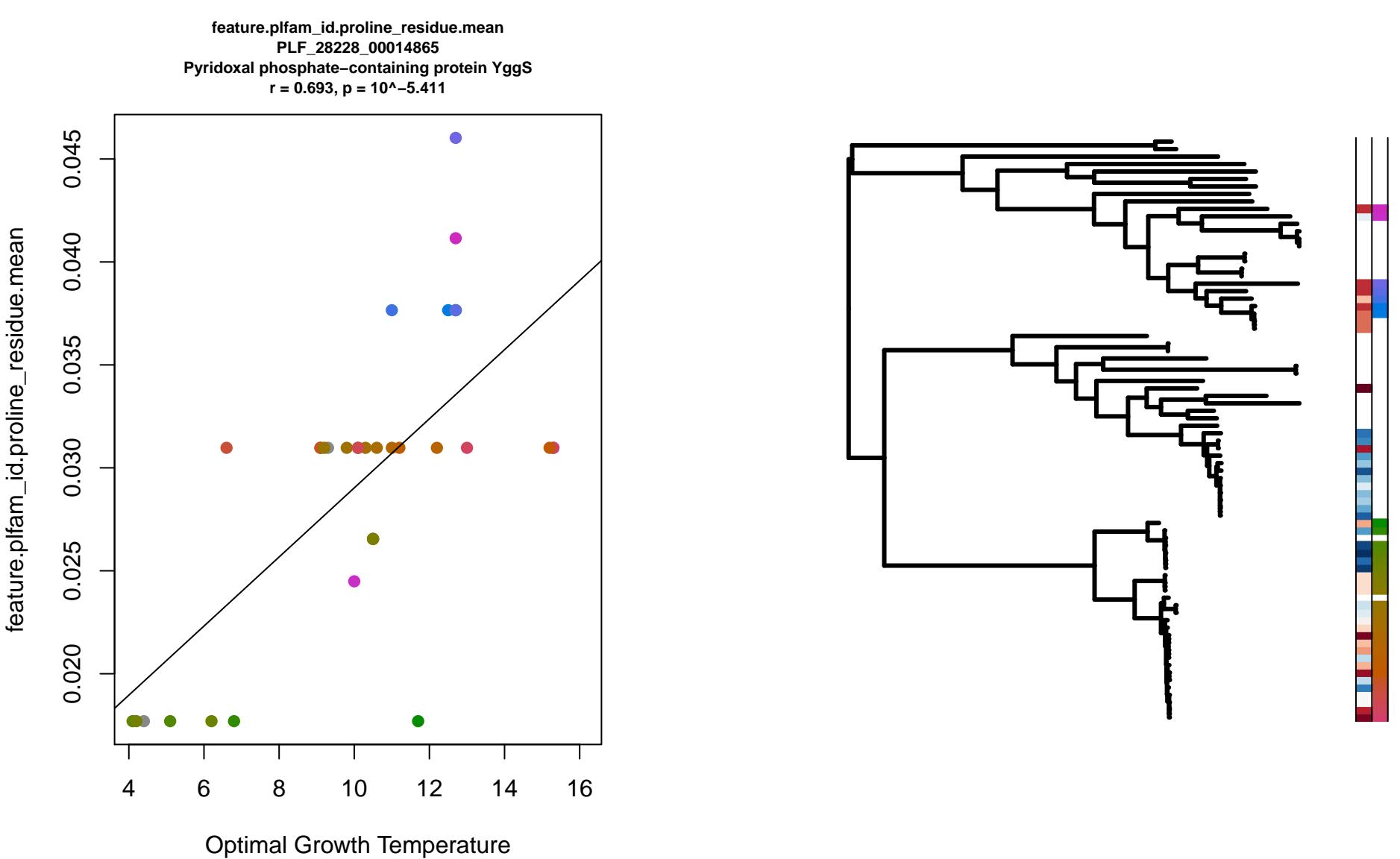
PLF_28228_00002798

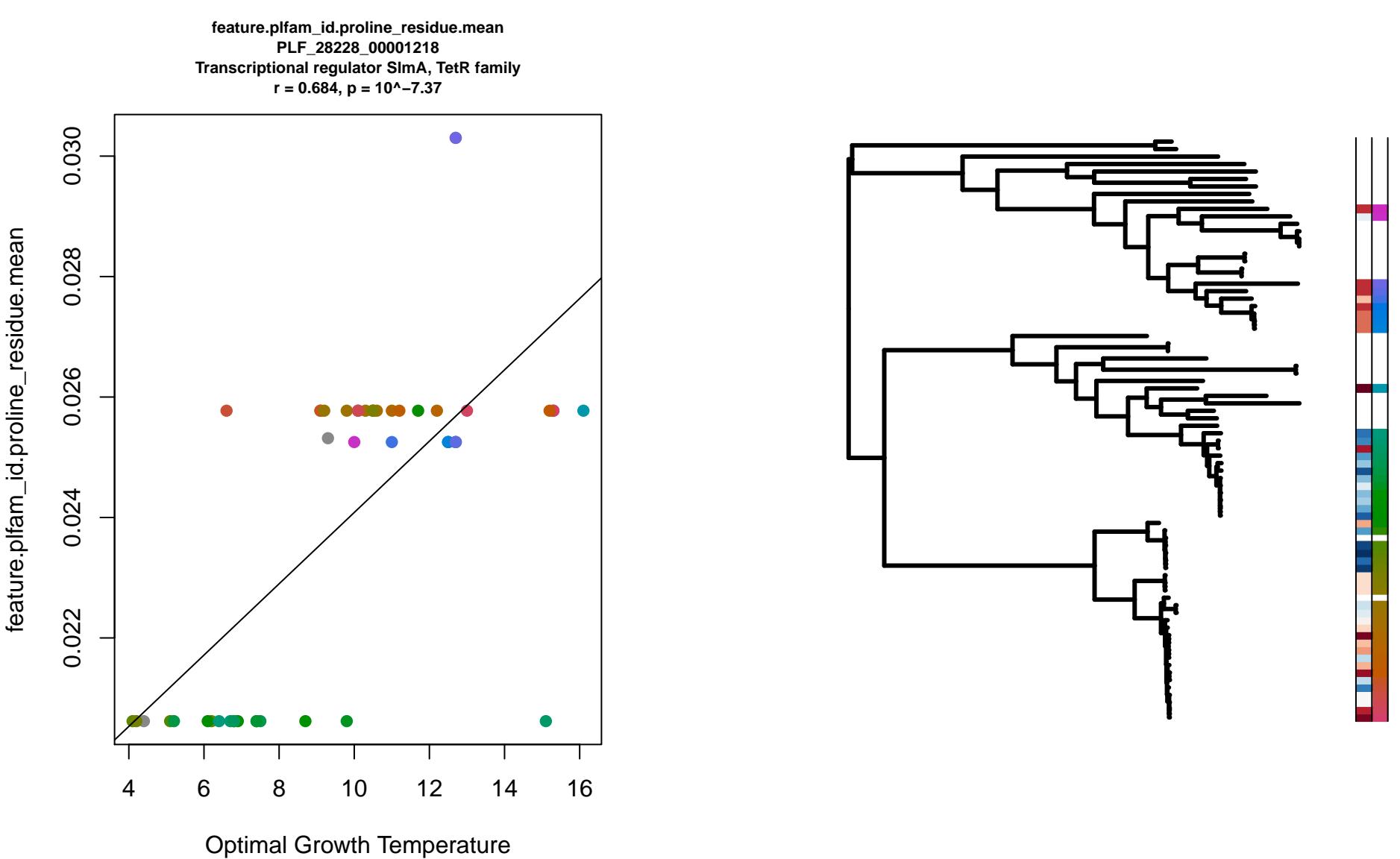
Two-component transcriptional response regulator, OmpR family

$r = 0.709, p = 10^{-5.725}$

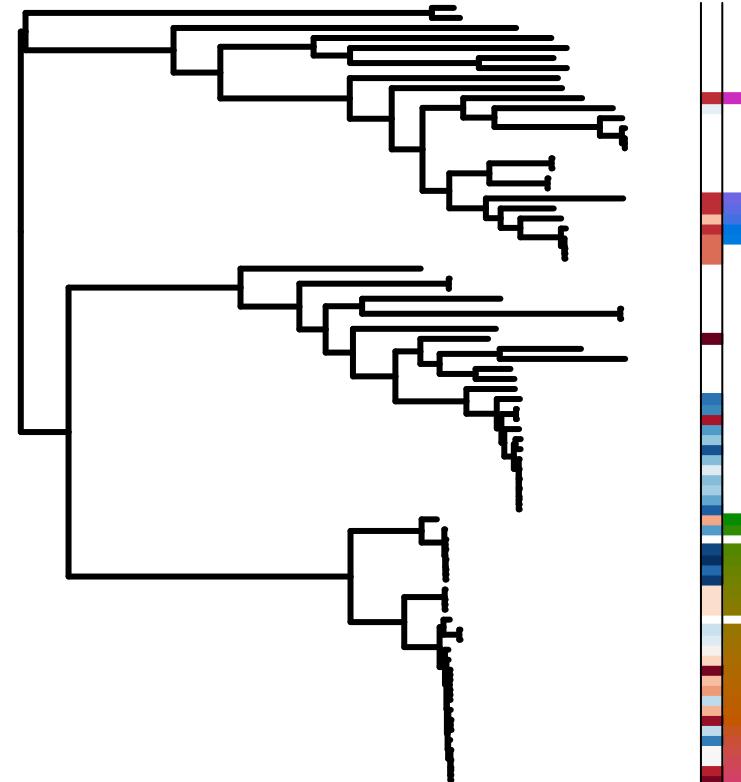
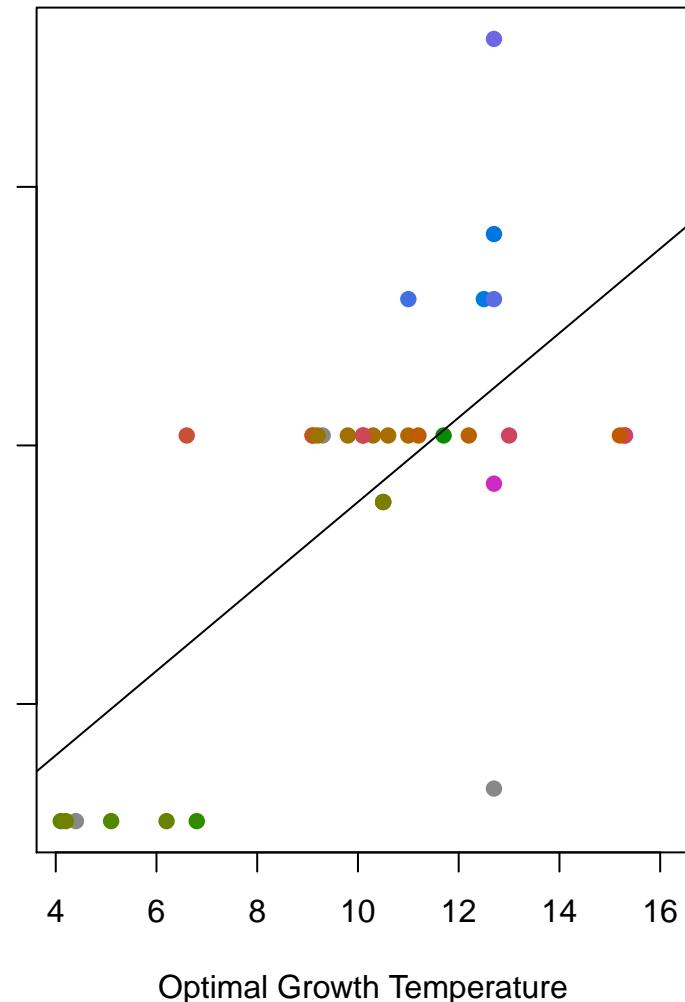
feature.pfam_id.proline_residue.mean







feature.plfam_id.proline_residue.mean
PLF_28228_00028047
Fatty acid cis/trans isomerase
 $r = 0.683$, $p = 10^{-5.059}$



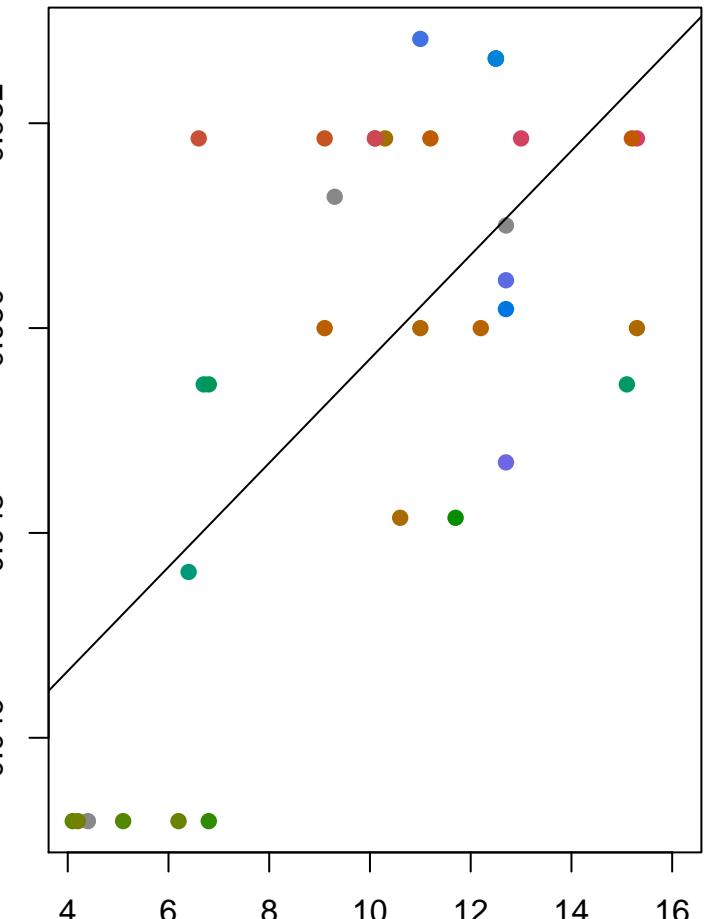
feature.plfam_id.proline_residue.mean

PLF_28228_00010728

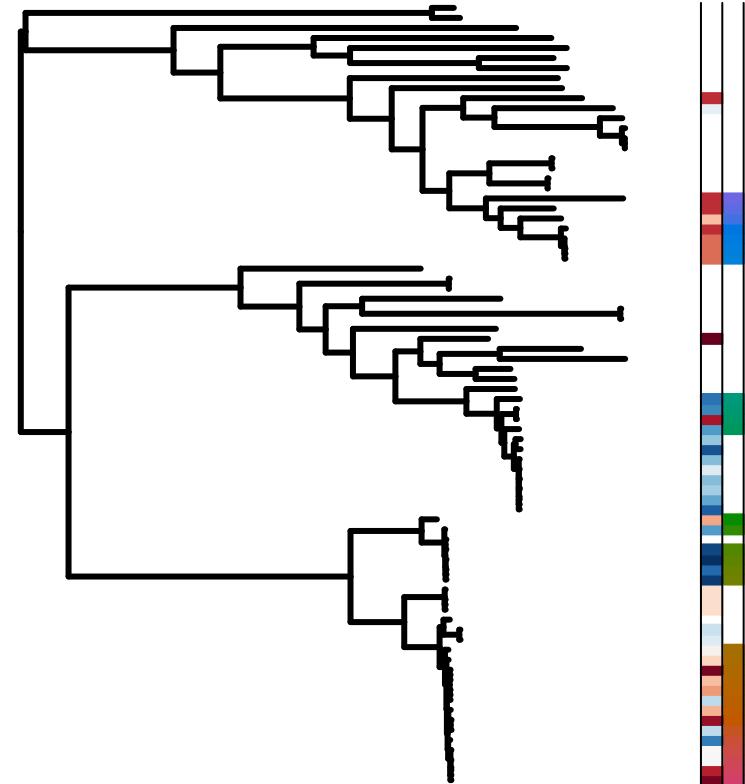
Probable thiol oxidoreductase with 2 cytochrome c heme-binding sites

$r = 0.669, p = 10^{-4.822}$

feature.plfam_id.proline_residue.mean



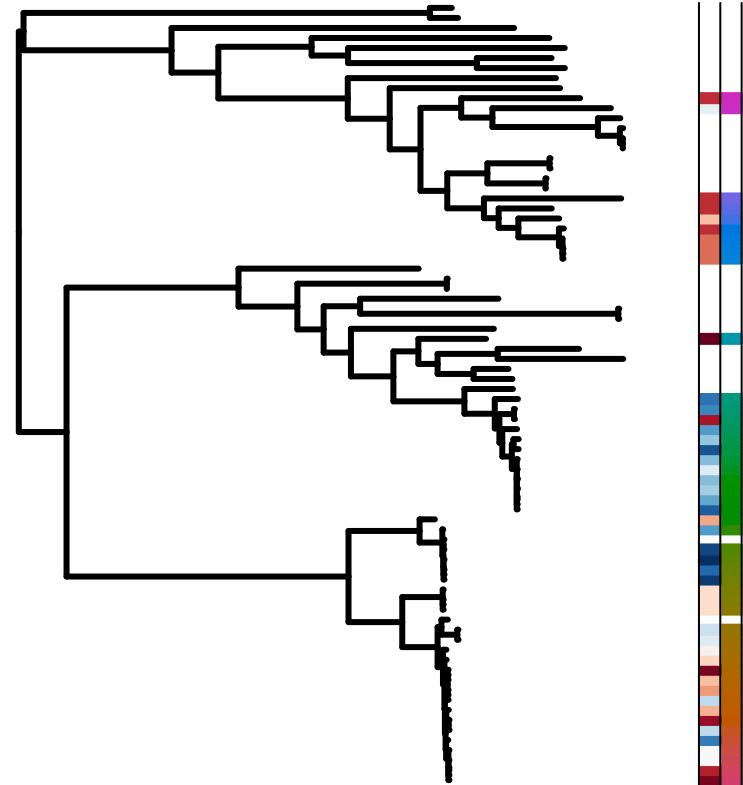
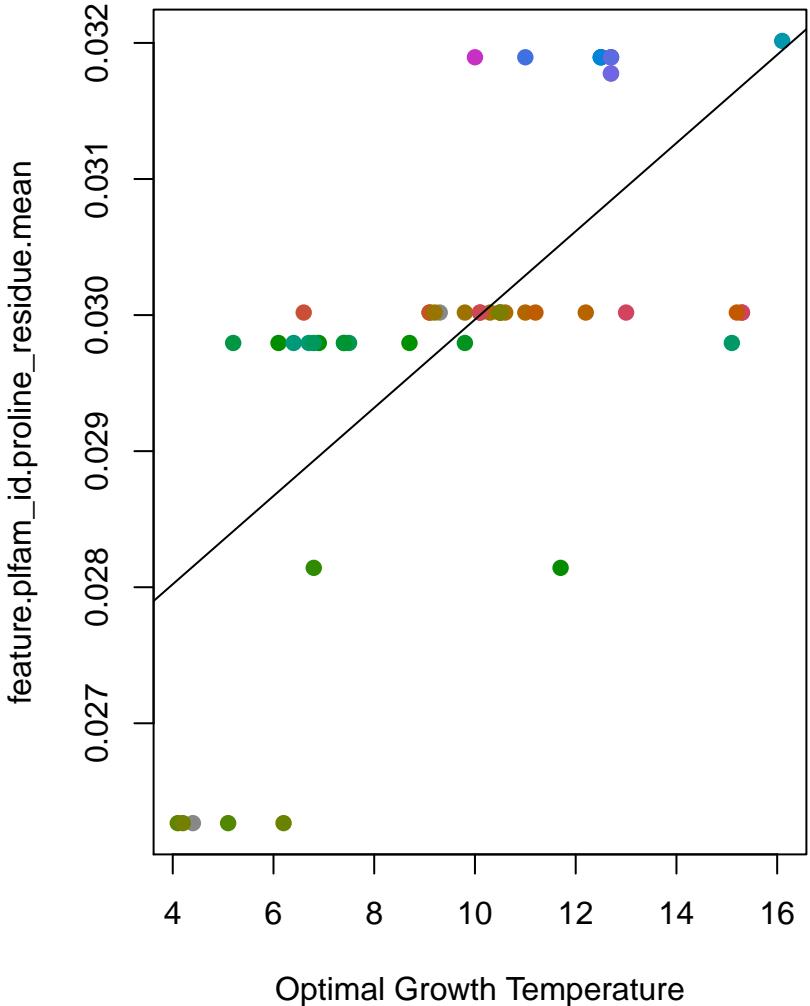
Optimal Growth Temperature



feature.plfam_id.proline_residue.mean

PLF_28228_00000516

Clohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC
 $r = 0.666, p = 10^{-6.875}$



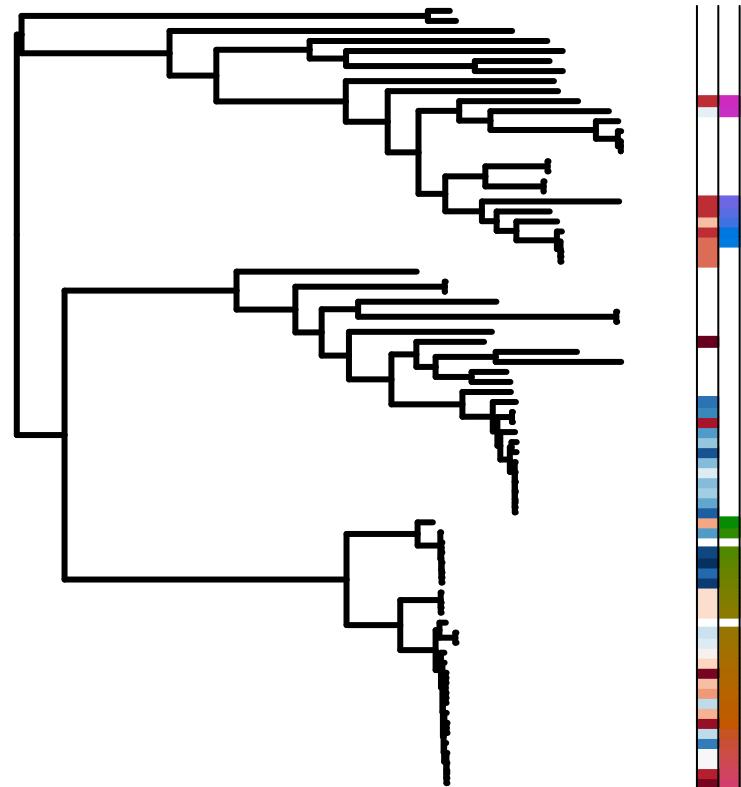
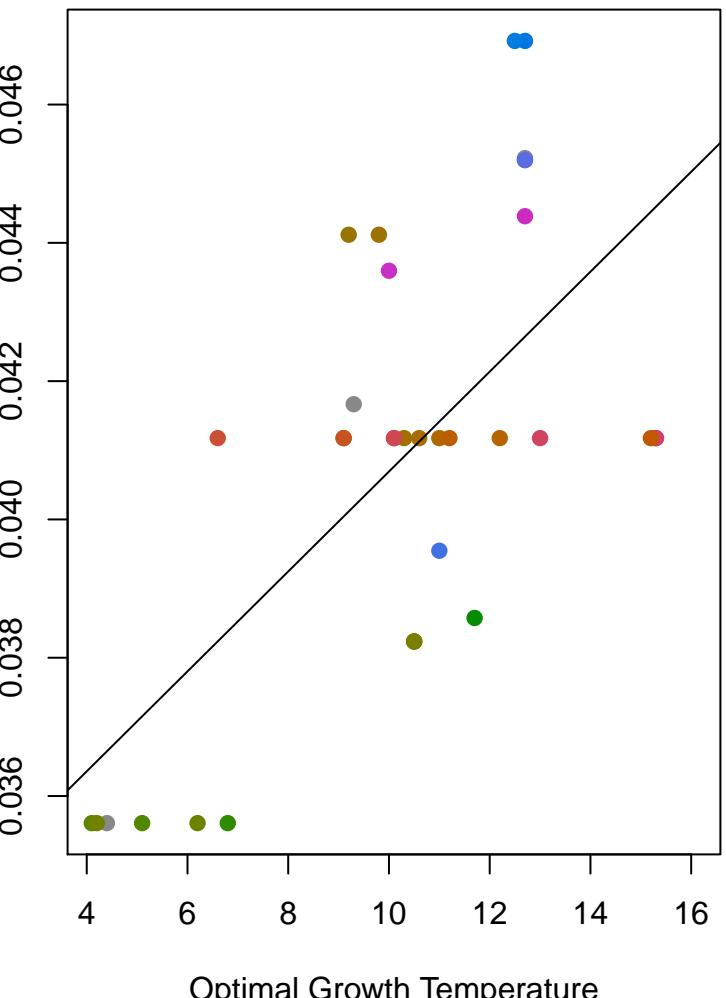
feature.plfam_id.proline_residue.mean

PLF_28228_00027970

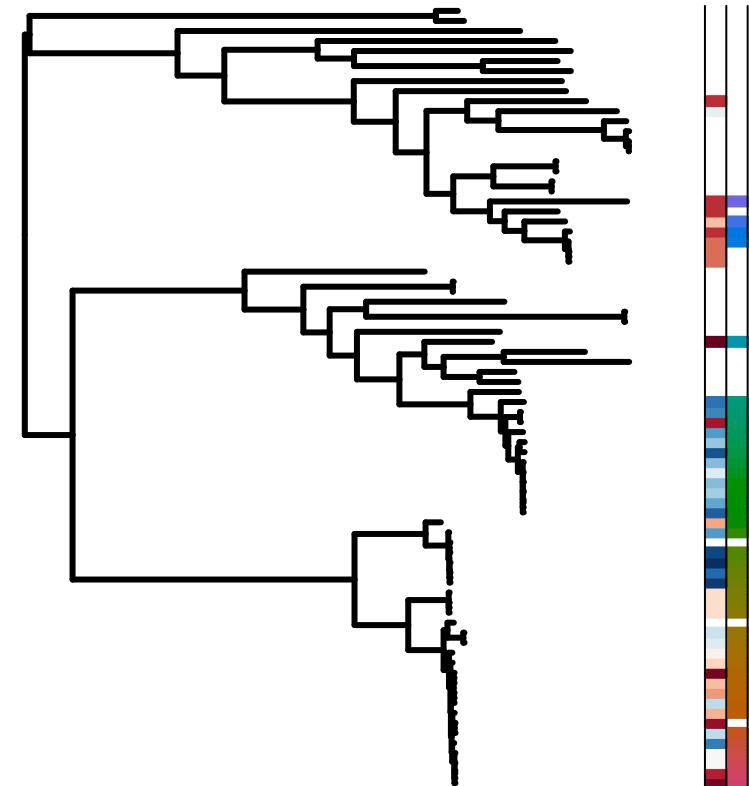
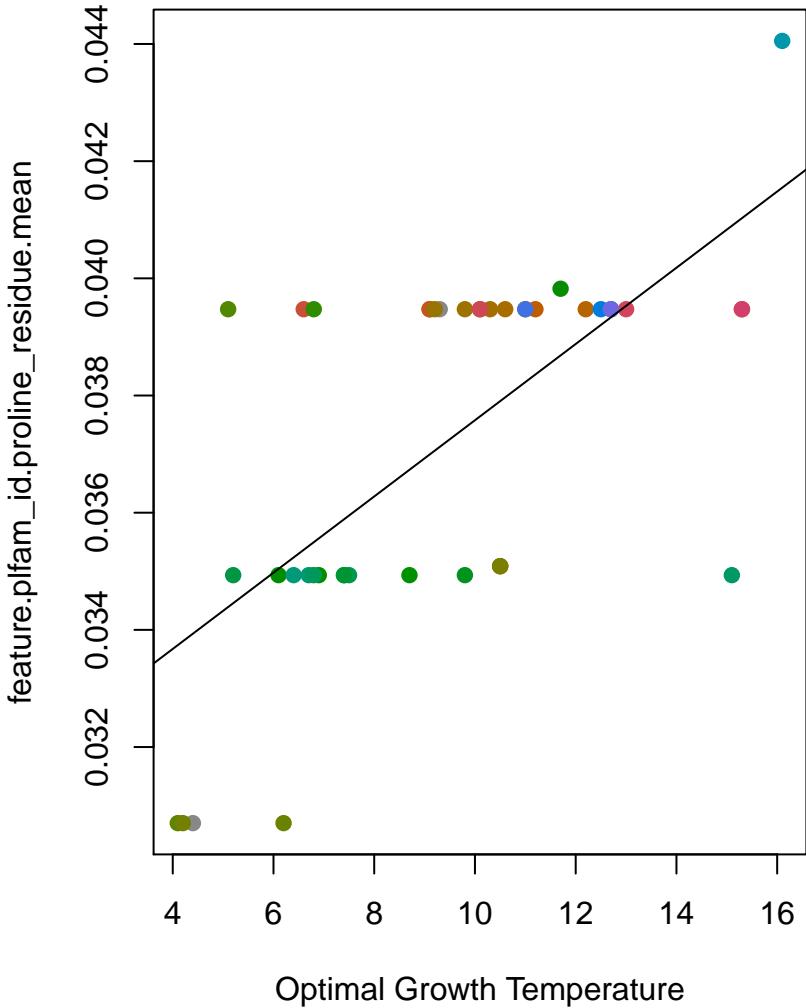
Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) @ Outer membrane phospholipase A

$r = 0.663$, $p = 10^{-4.838}$

feature.plfam_id.proline_residue.mean

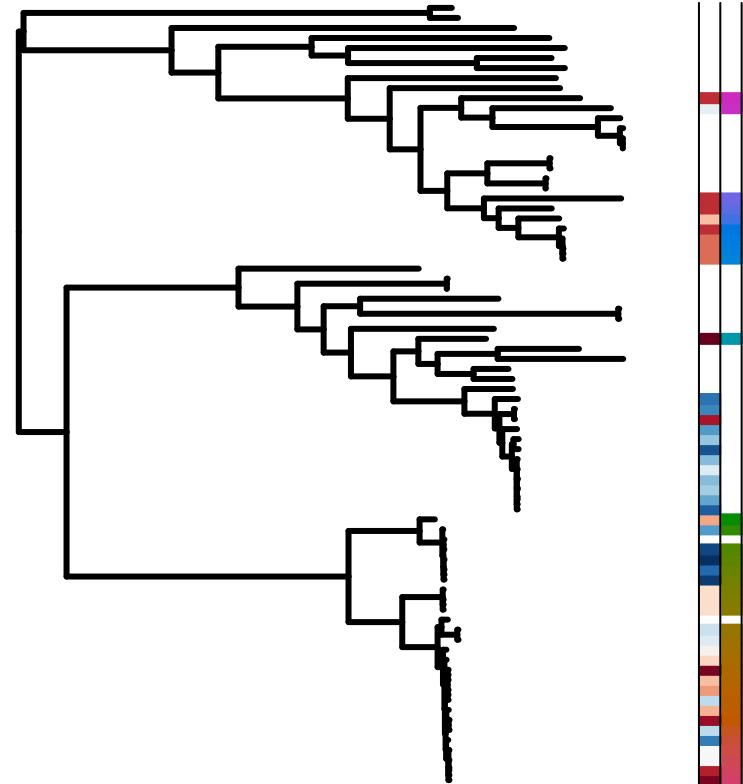
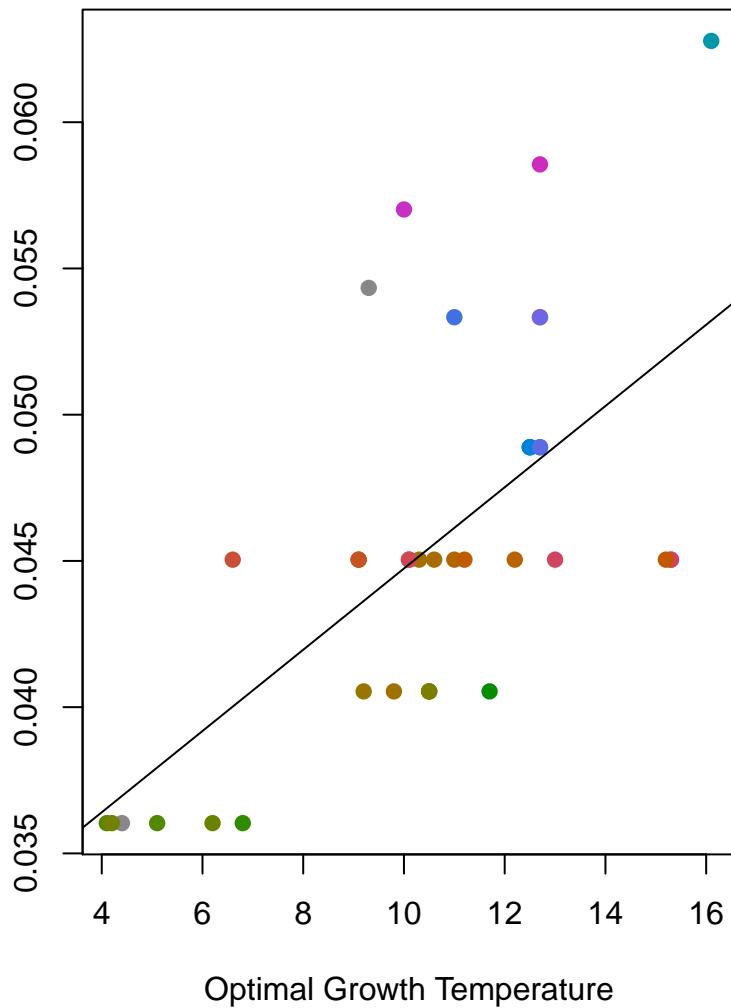


feature.plfam_id.proline_residue.mean
PLF_28228_00028198
FIG111991: hypothetical protein
 $r = 0.657, p = 10^{-5.885}$



feature.plfam_id.proline_residue.mean
PLF_28228_00001354
hypothetical protein
 $r = 0.648, p = 10^{-4.957}$

feature.plfam_id.proline_residue.mean



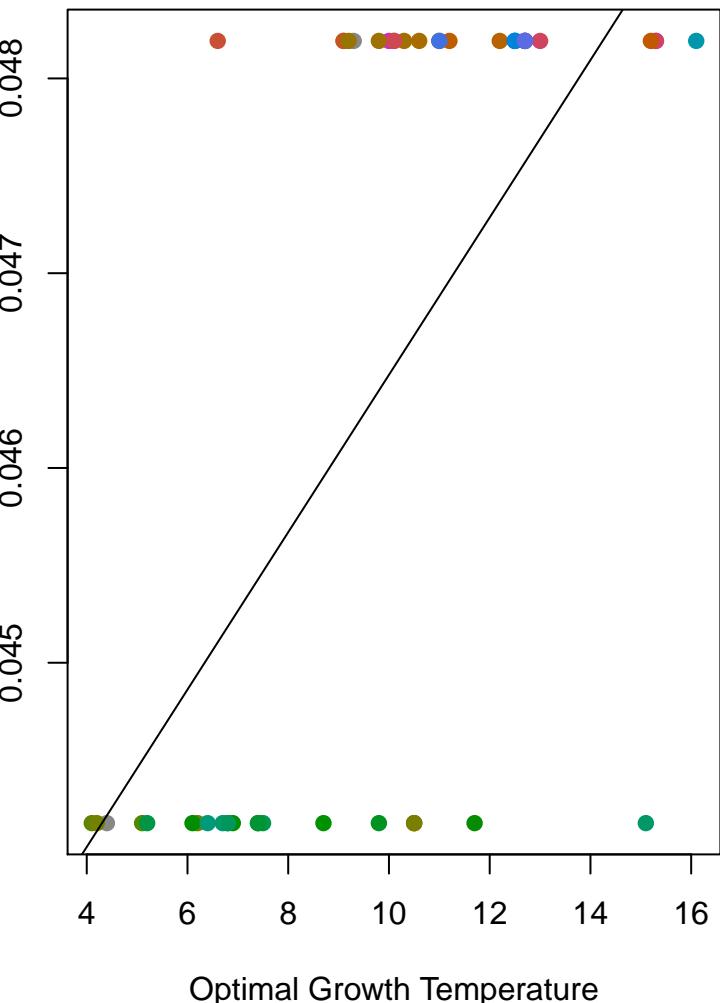
feature.plfam_id.proline_residue.mean

PLF_28228_00000234

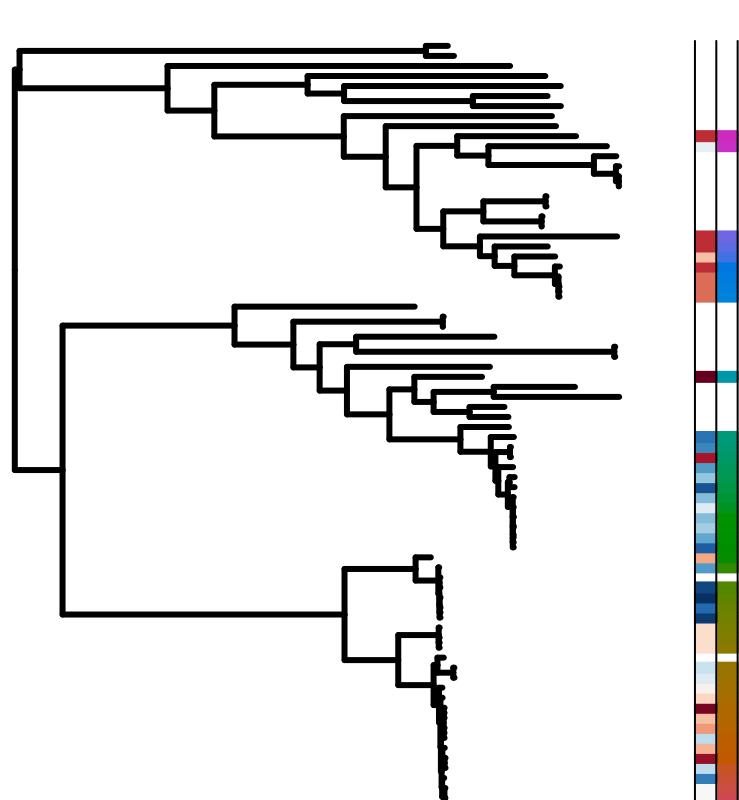
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117)

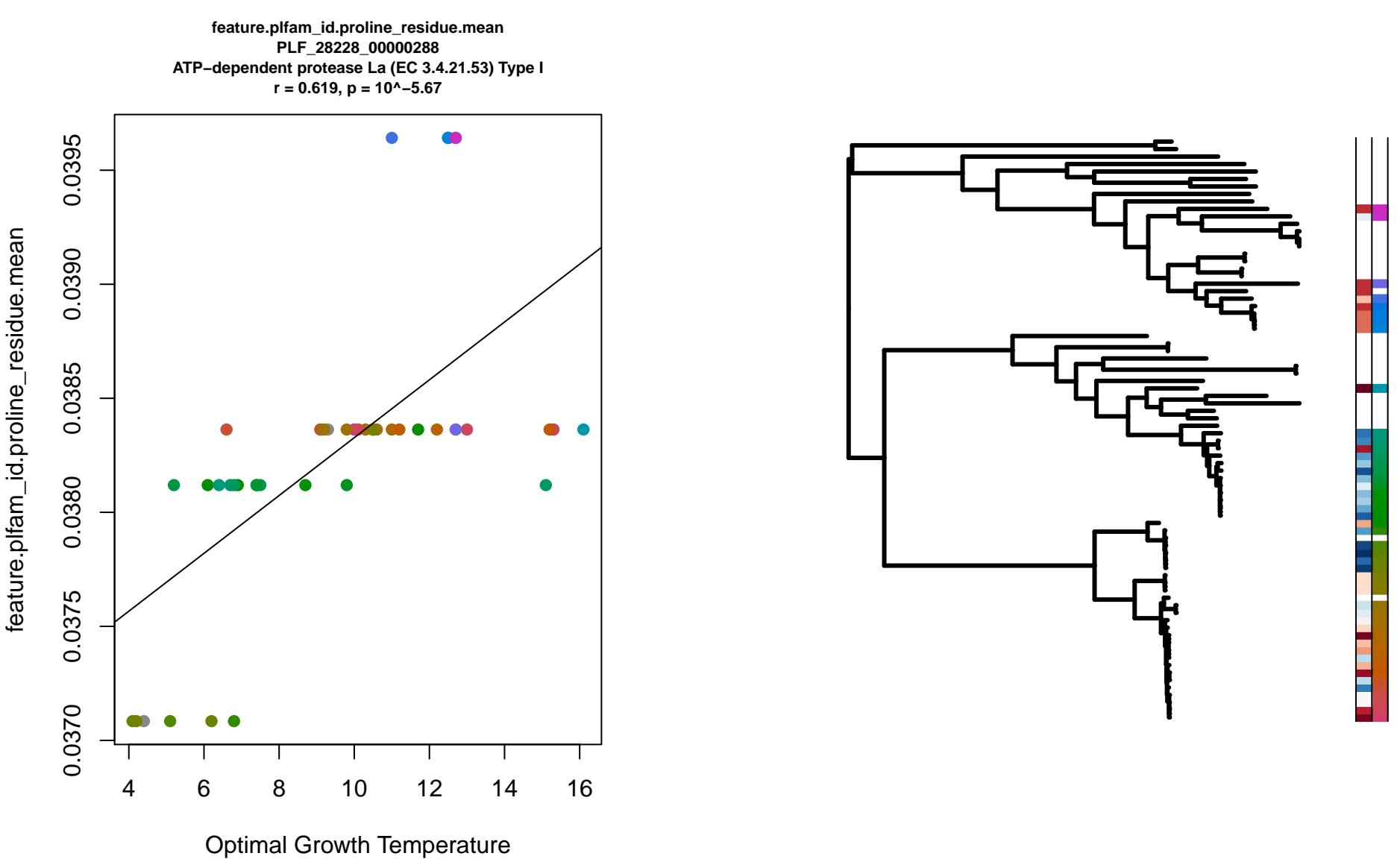
$r = 0.633$, $p = 10^{-6.101}$

feature.plfam_id.proline_residue.mean



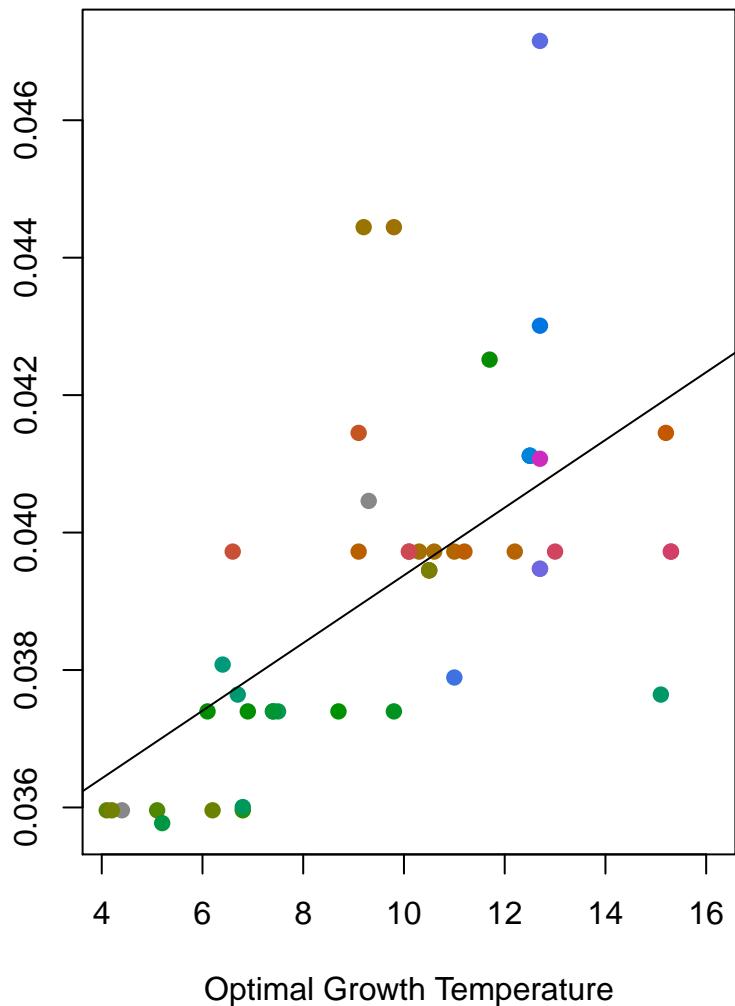
Optimal Growth Temperature



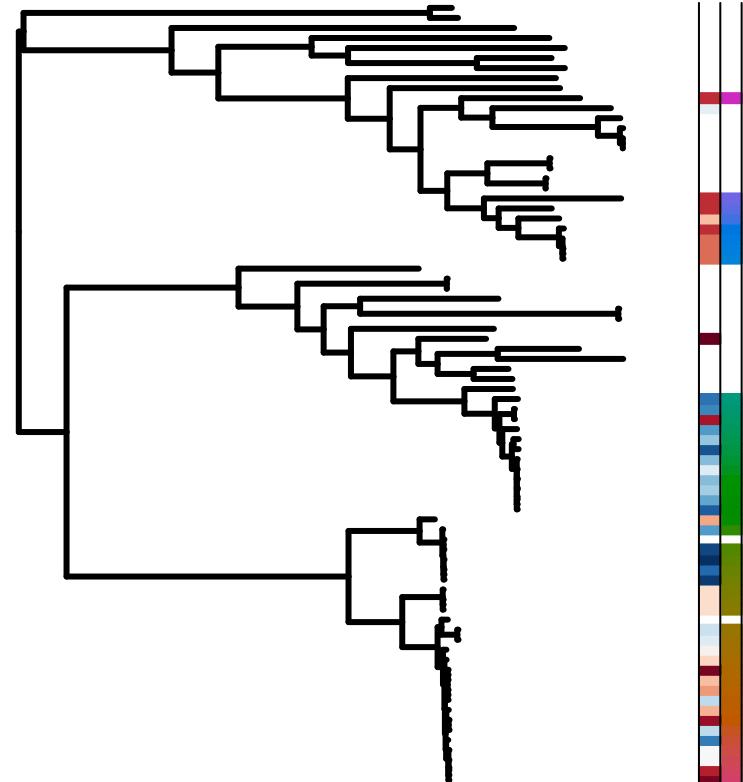


feature.pfam_id.proline_residue.mean
PLF_28228_00002320
hypothetical protein
 $r = 0.614, p = 10^{-5.453}$

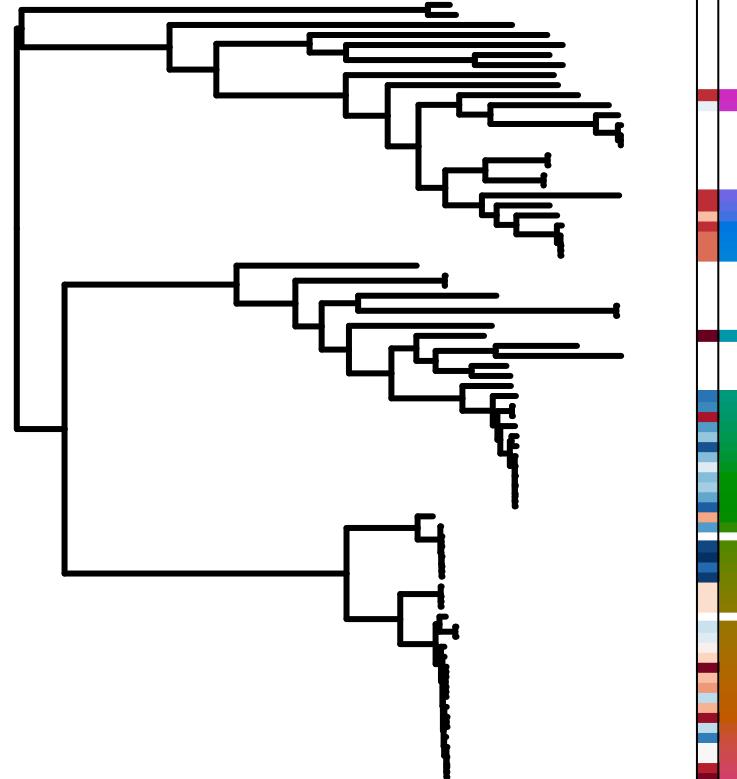
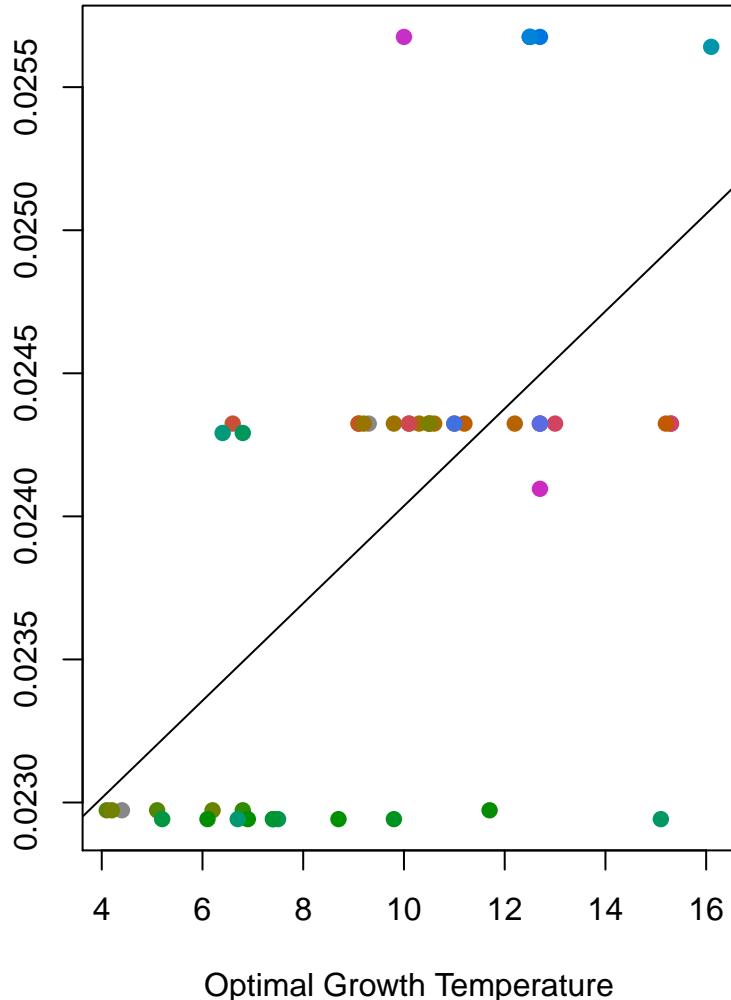
feature.pfam_id.proline_residue.mean



Optimal Growth Temperature



feature.plfam_id.proline_residue.mean
PLF_28228_00001936
Predicted signal transduction protein
 $r = 0.61, p = 10^{-5.59}$



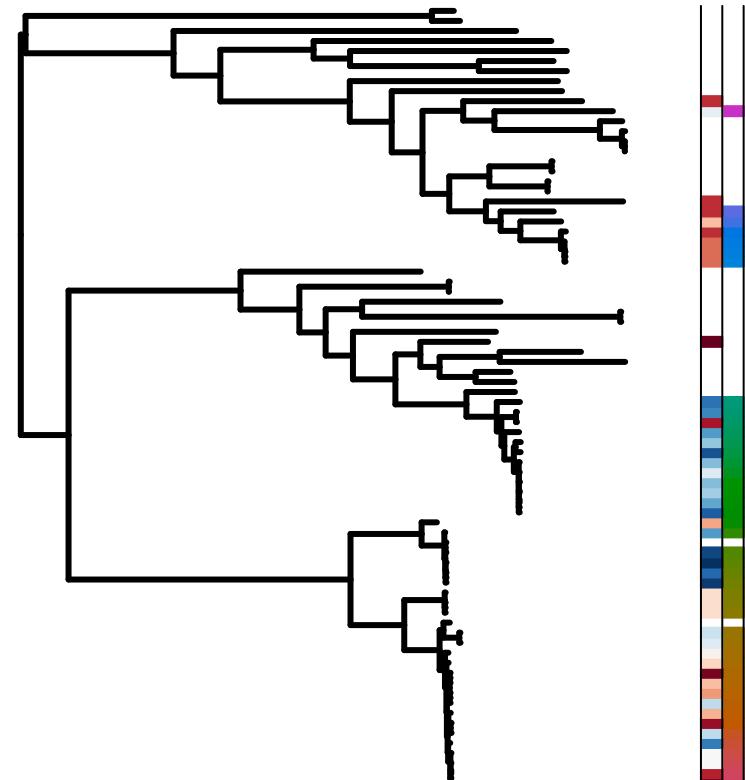
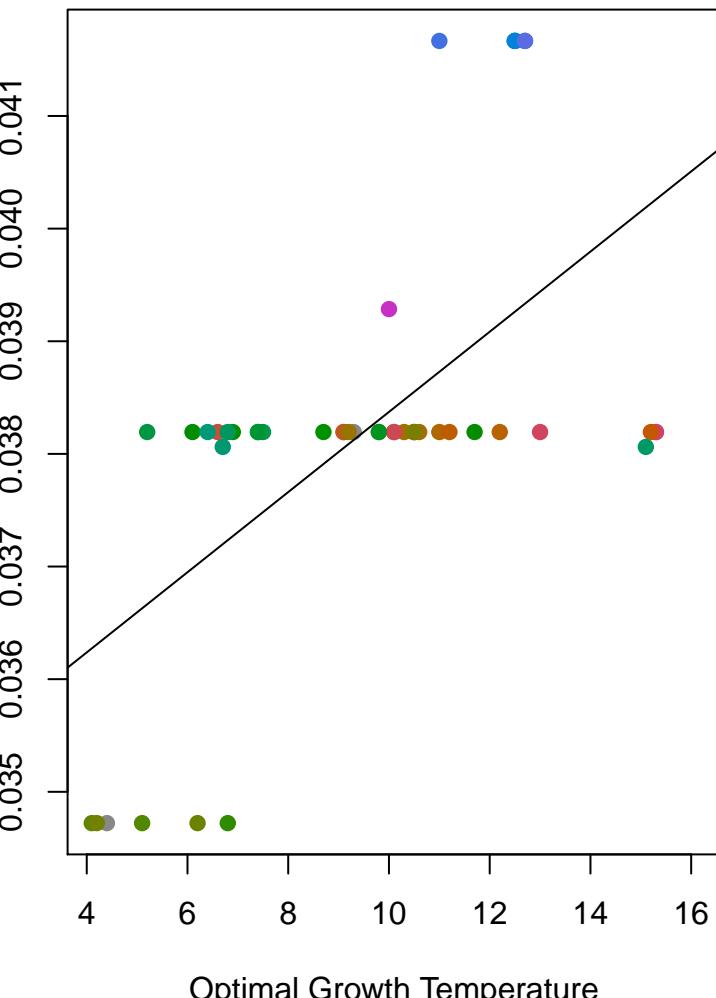
feature.plfam_id.proline_residue.mean

PLF_28228_00003394

ABC transporter, substrate-binding protein (cluster 12, methionine/phosphonates)

$r = 0.604$, $p = 10^{-5.063}$

feature.plfam_id.proline_residue.mean

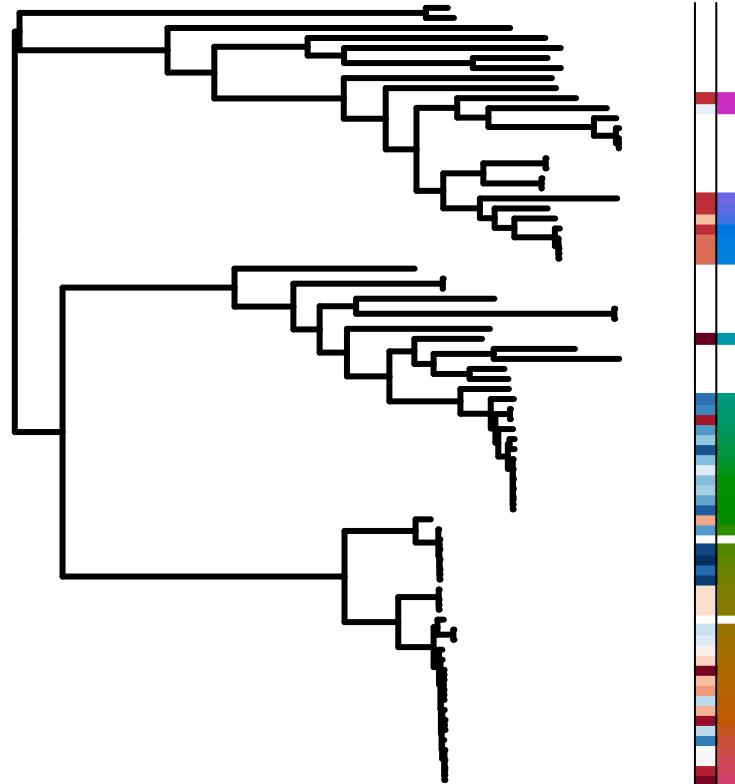
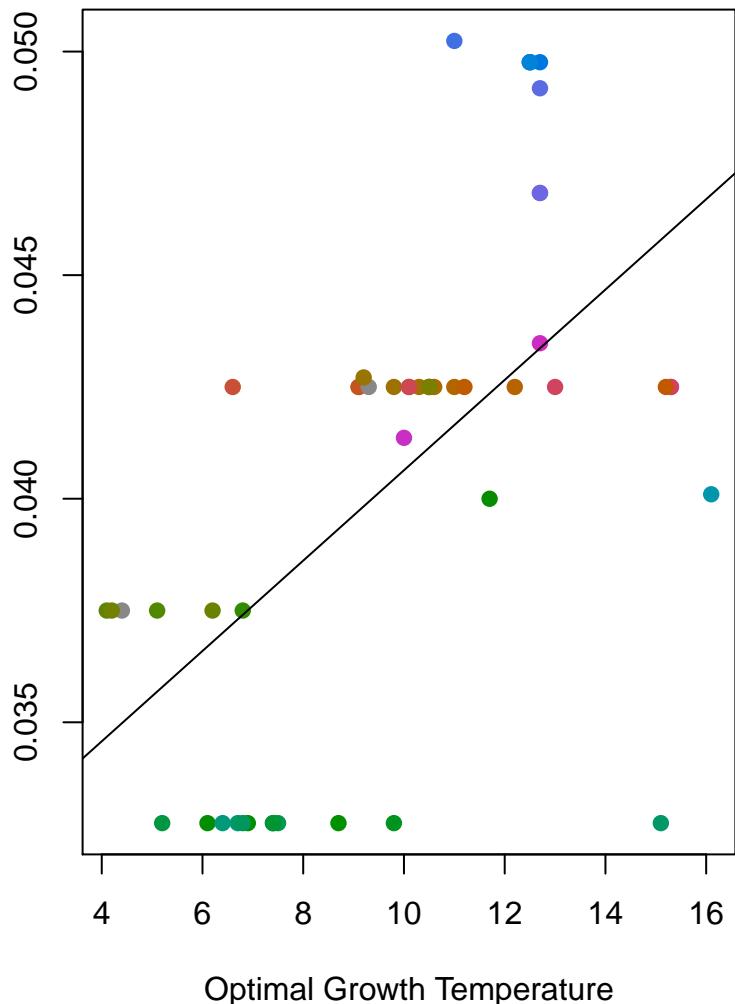


feature.plfam_id.proline_residue.mean

PLF_28228_00001909

Multidrug resistance transporter, Bcr/CfIA family

$r = 0.584$, $p = 10^{-5.077}$

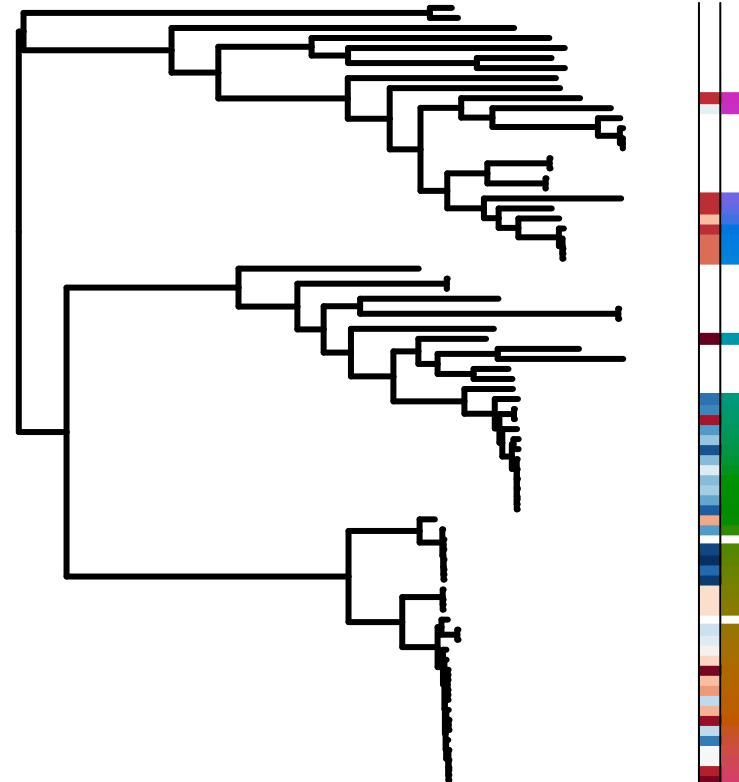
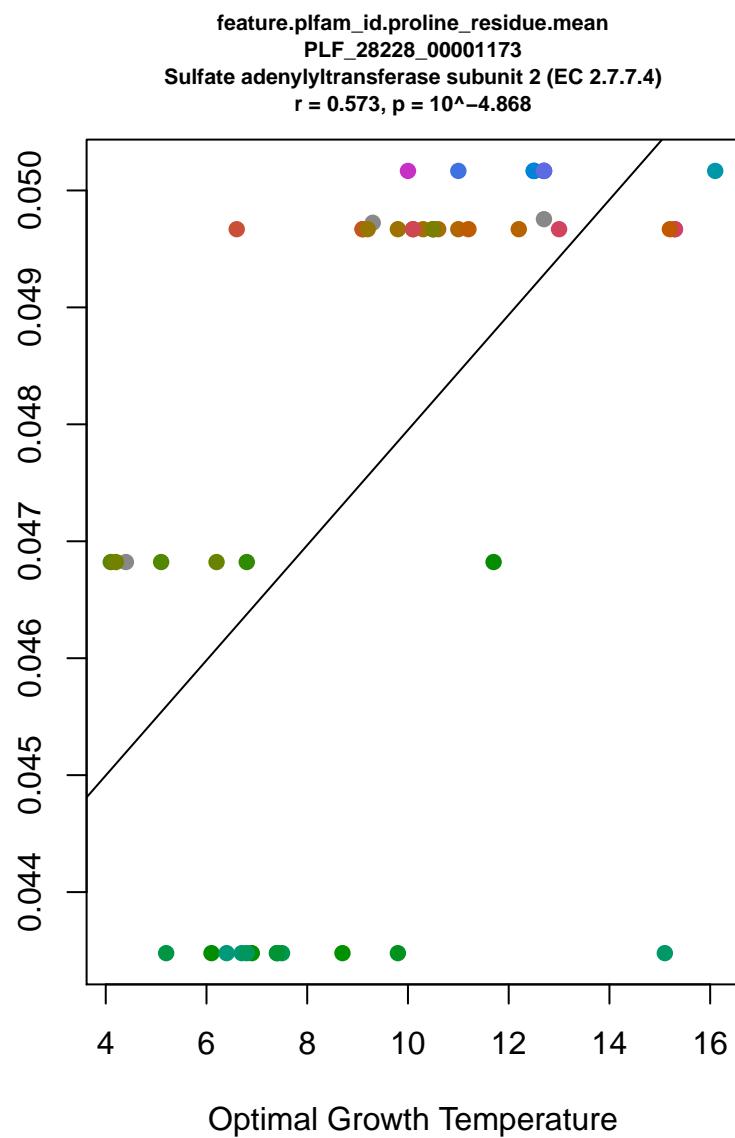


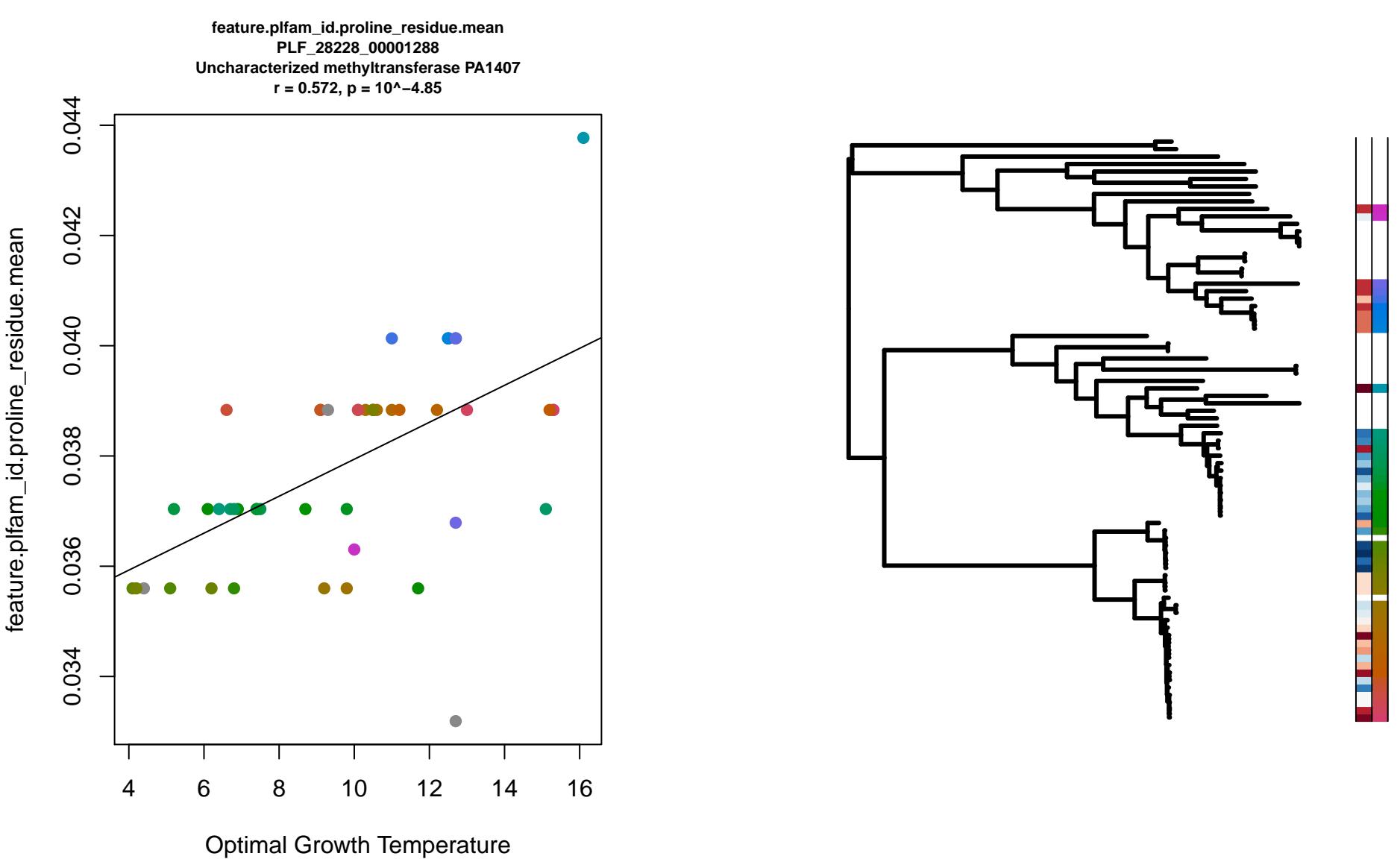
feature.plfam_id.proline_residue.mean

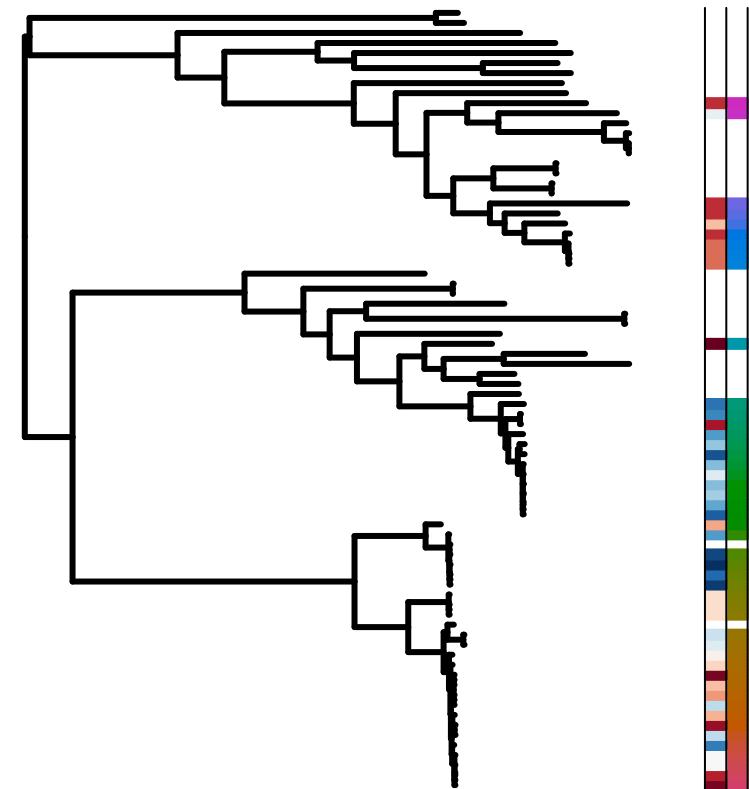
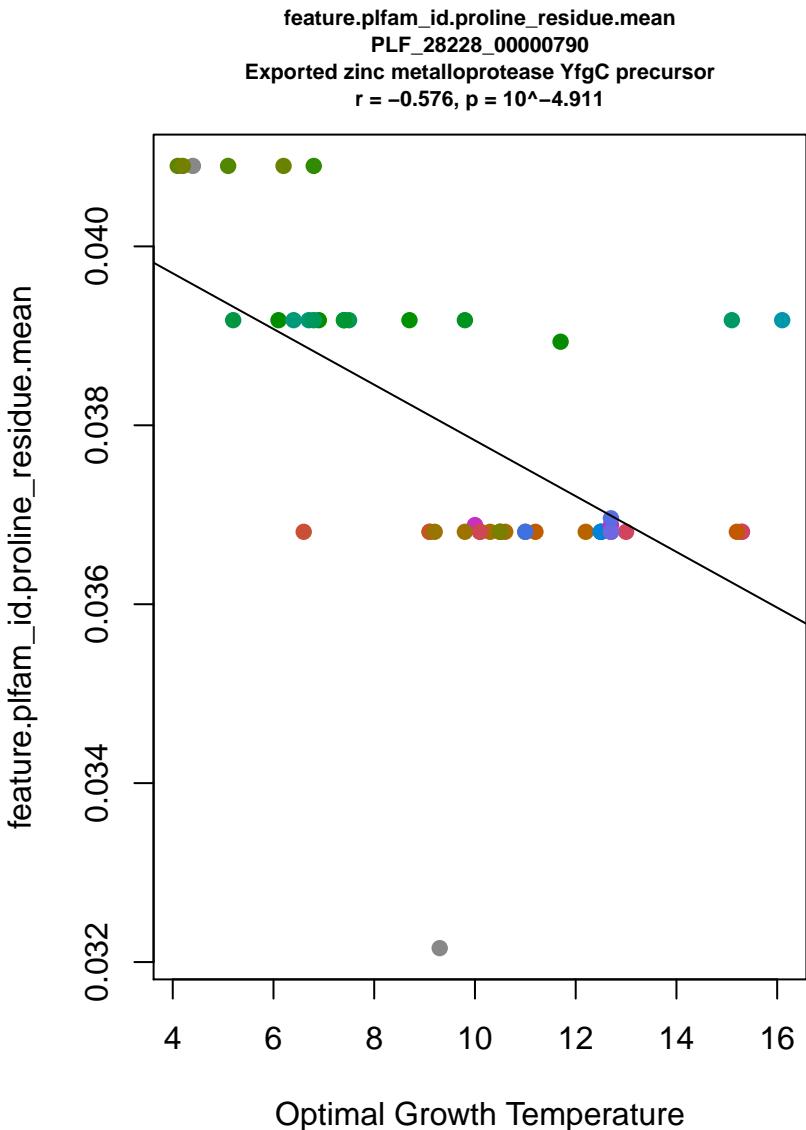
PLF_28228_00001173

Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)

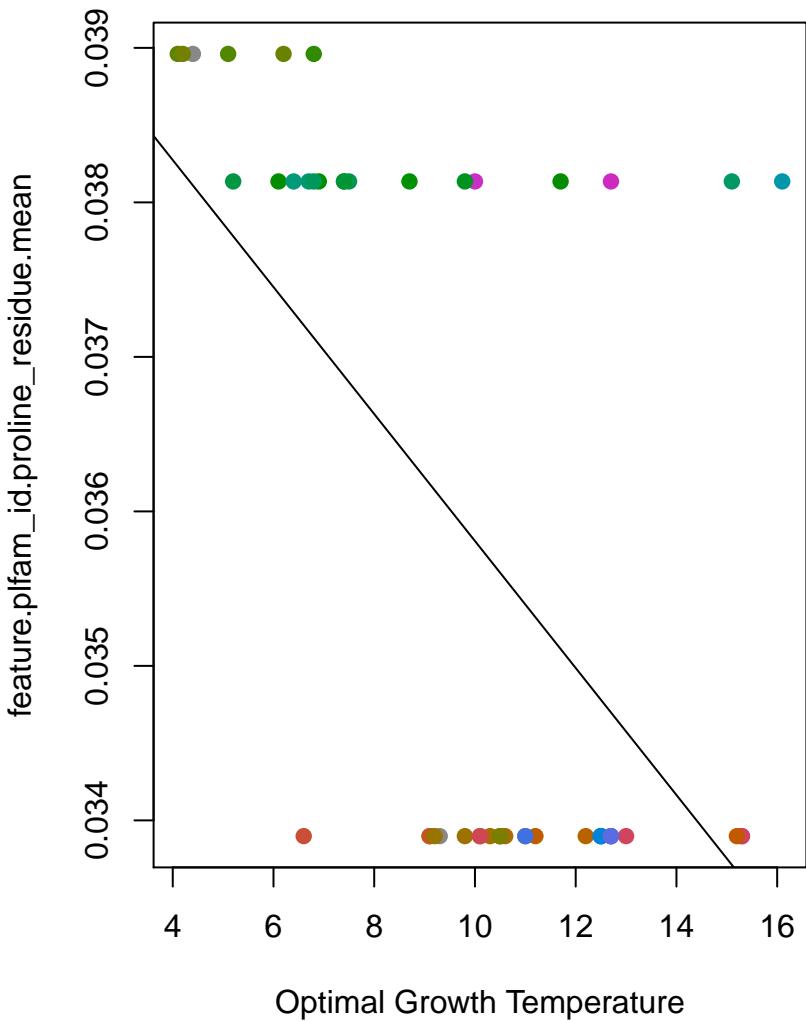
$r = 0.573, p = 10^{-4.868}$

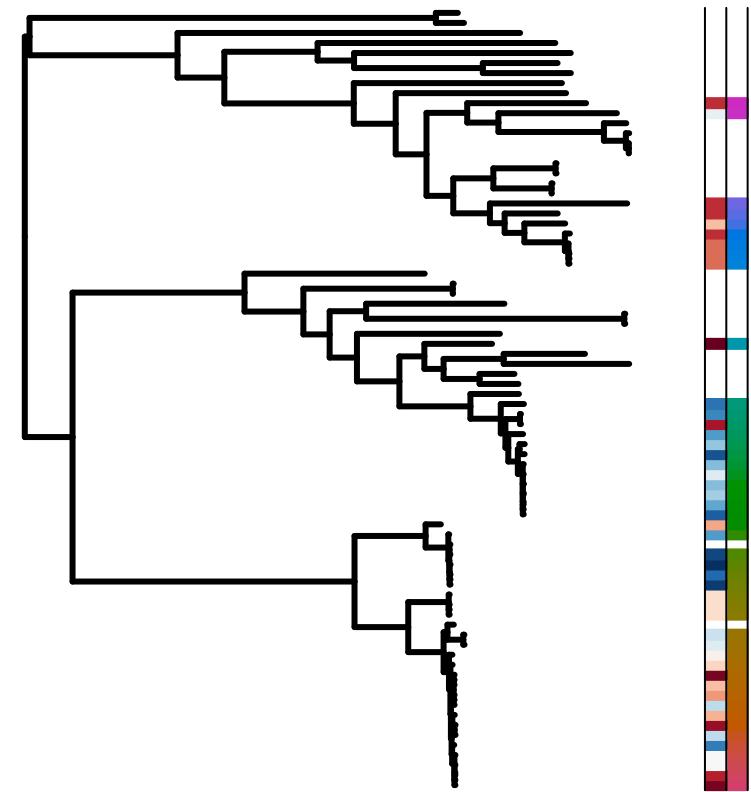
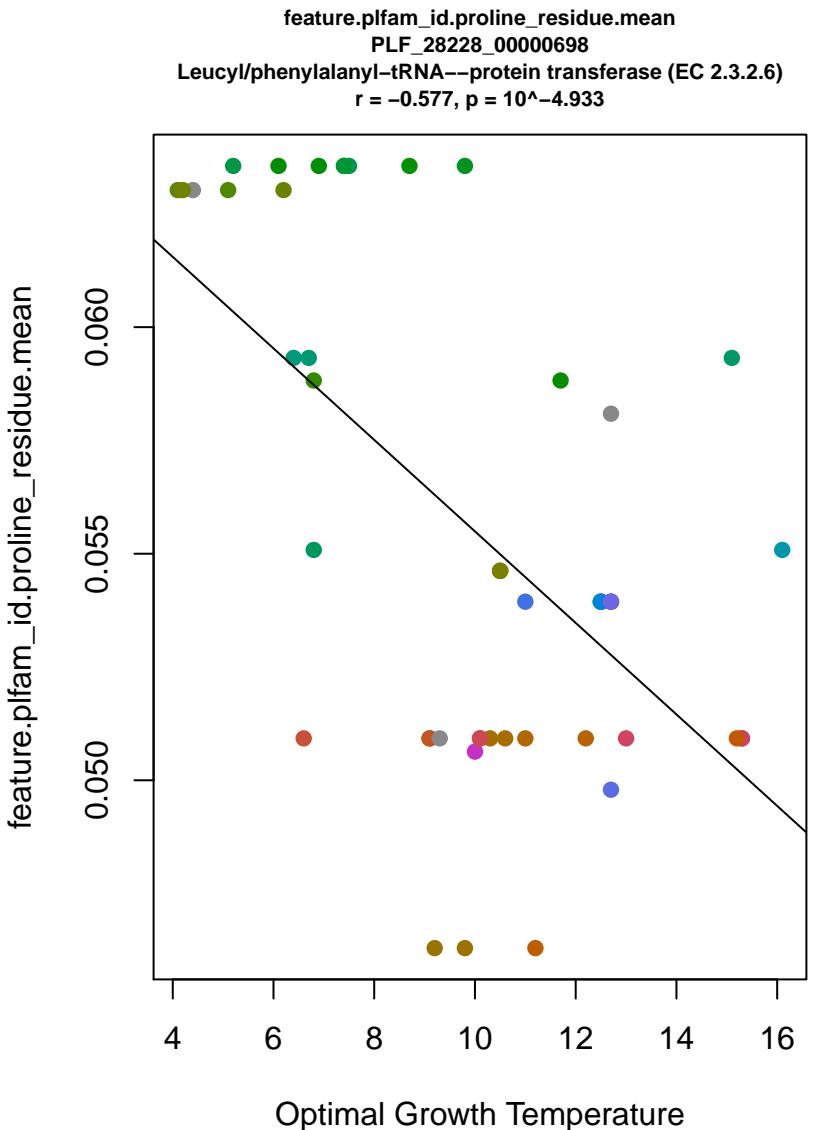






feature.plfam_id.proline_residue.mean
PLF_28228_00001342
hypothetical protein
 $r = -0.576$, $p = 10^{-4.927}$



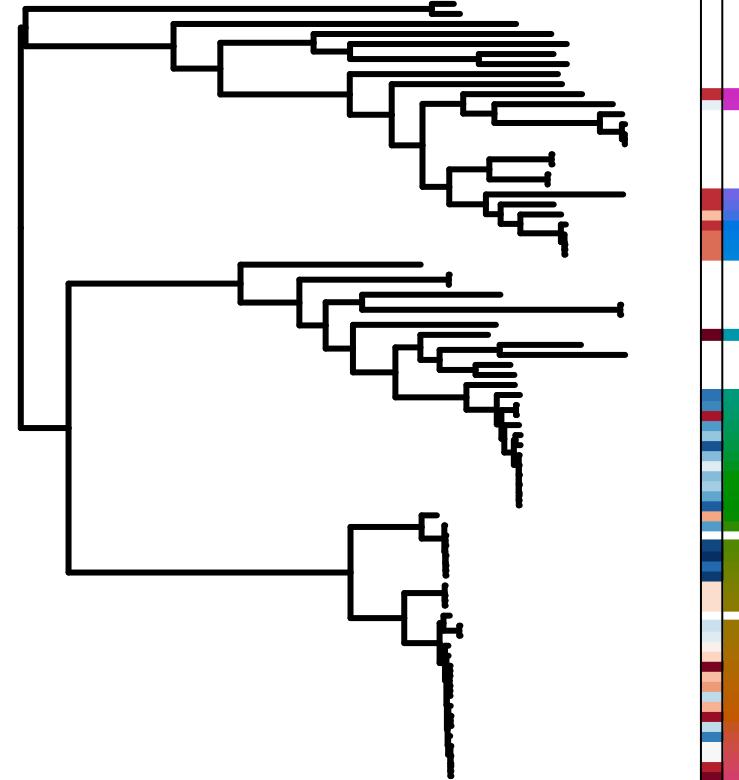
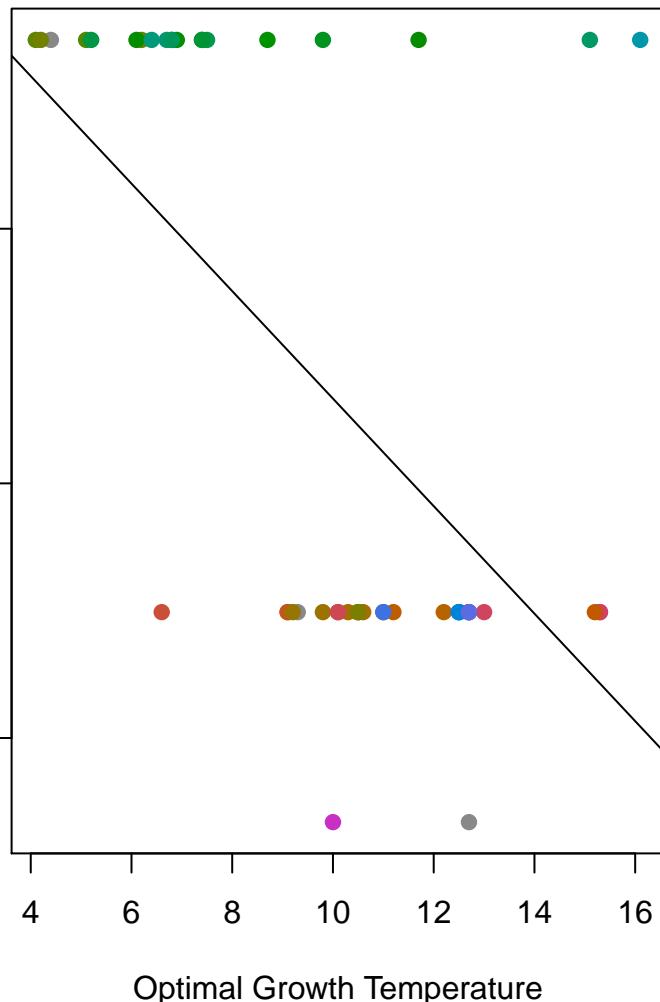


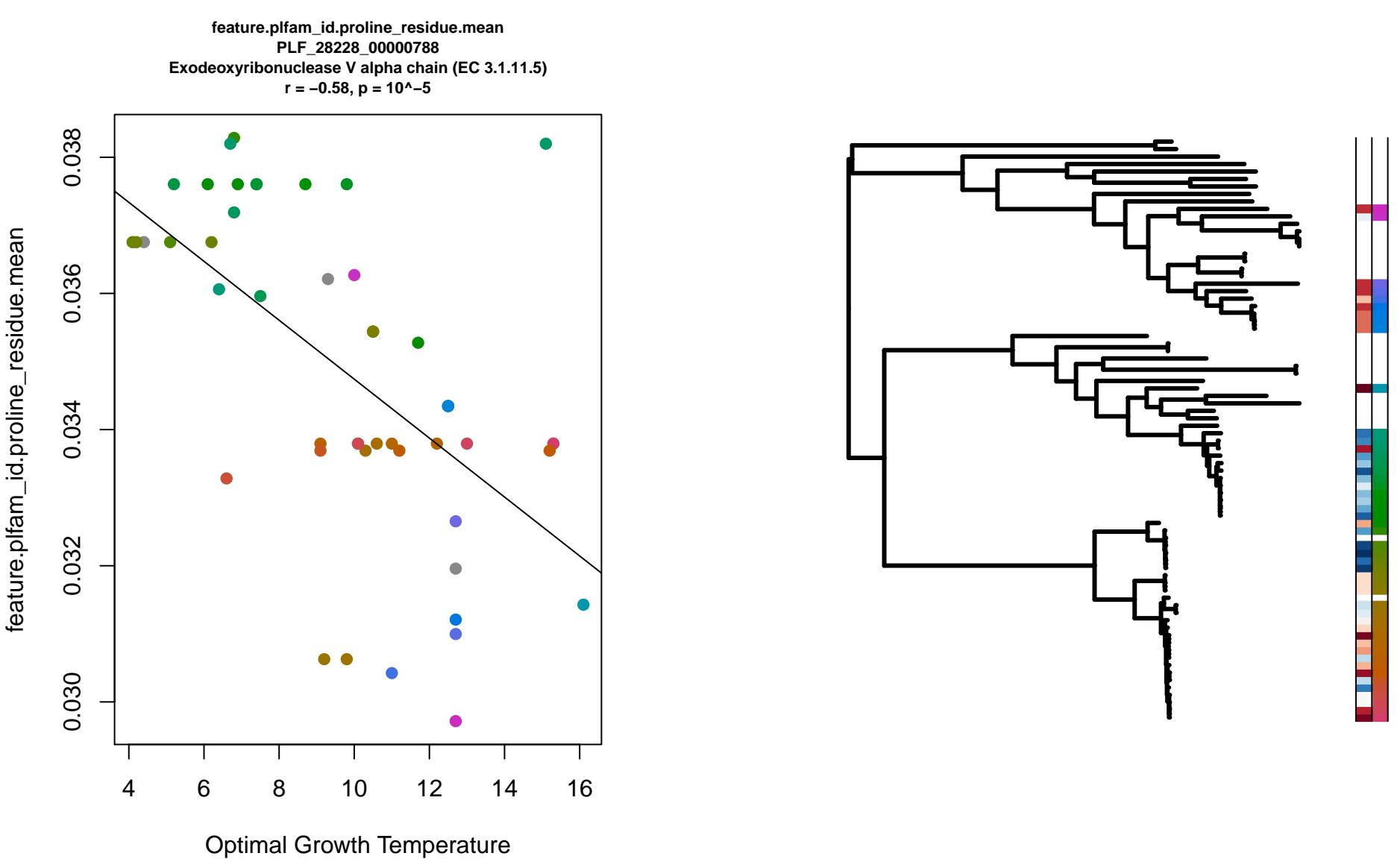
feature.plfam_id.proline_residue.mean

PLF_28228_00001430

Acylphosphate phosphohydrolase (EC 3.6.1.7)

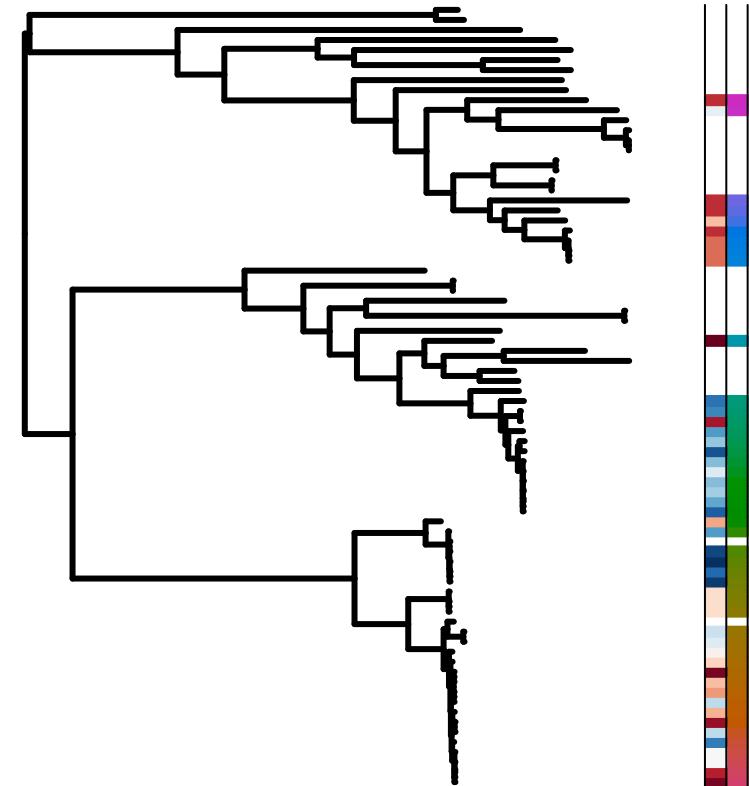
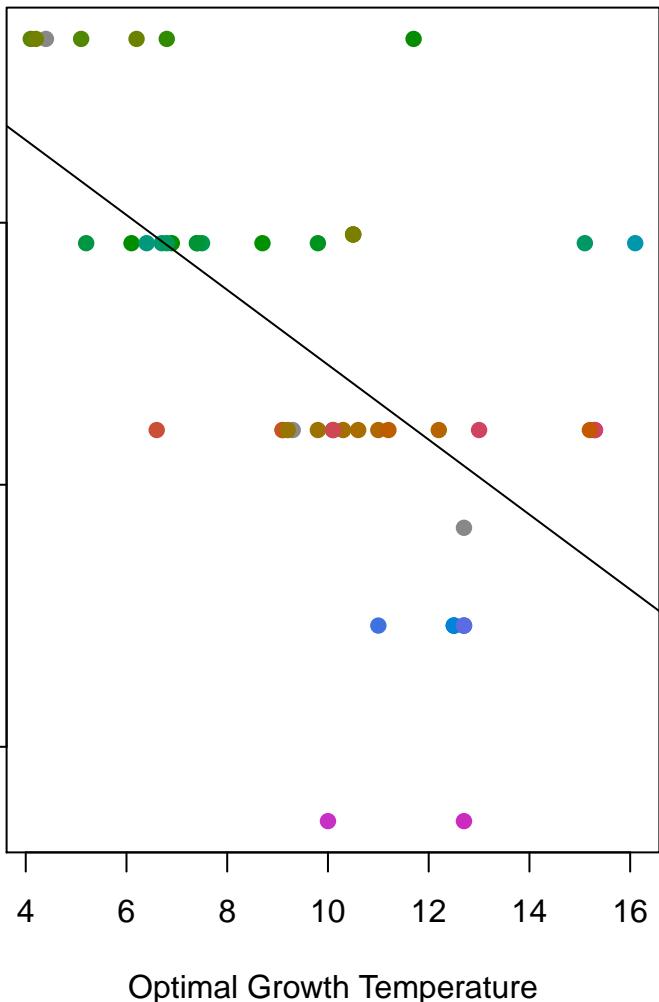
$r = -0.579, p = 10^{-4.981}$





feature.plfam_id.proline_residue.mean
PLF_28228_00000381
Exodeoxyribonuclease III (EC 3.1.11.2)
 $r = -0.589$, $p = 10^{-5.159}$

feature.plfam_id.proline_residue.mean



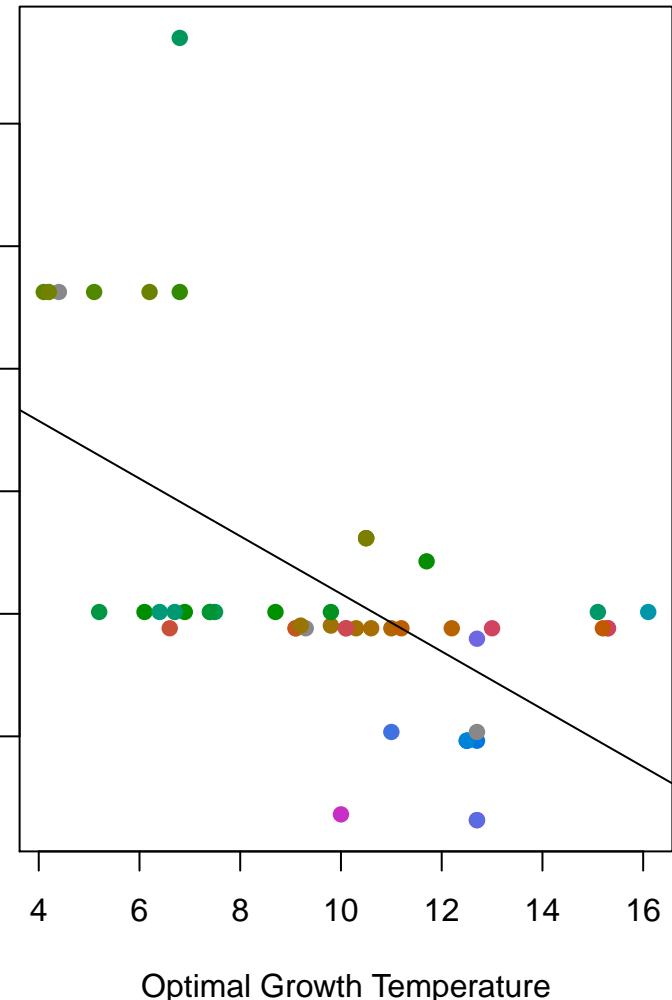
feature.pfam_id.proline_residue.mean

PLF_28228_00000670

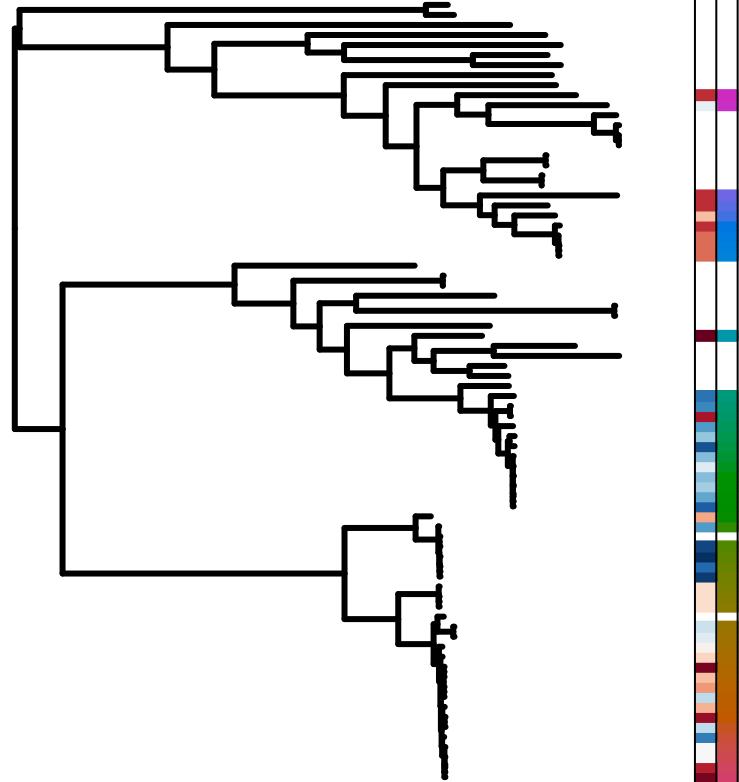
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)

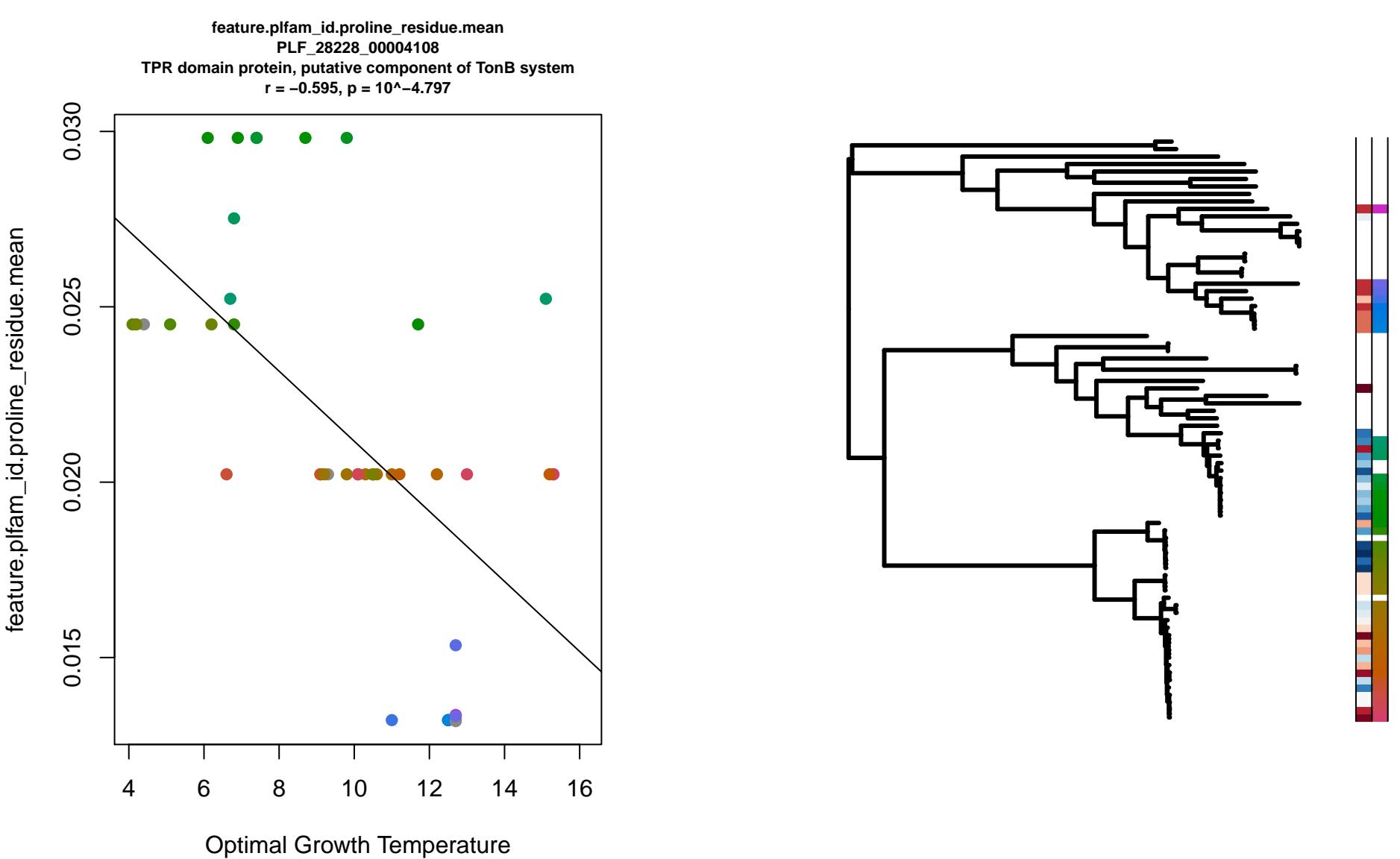
$r = -0.59$, $p = 10^{-5.183}$

feature.pfam_id.proline_residue.mean



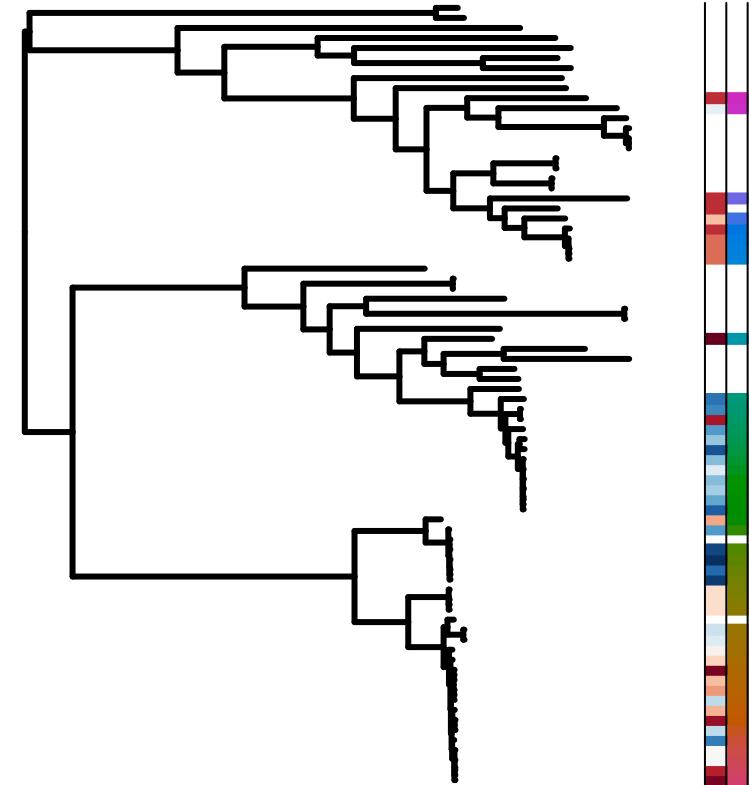
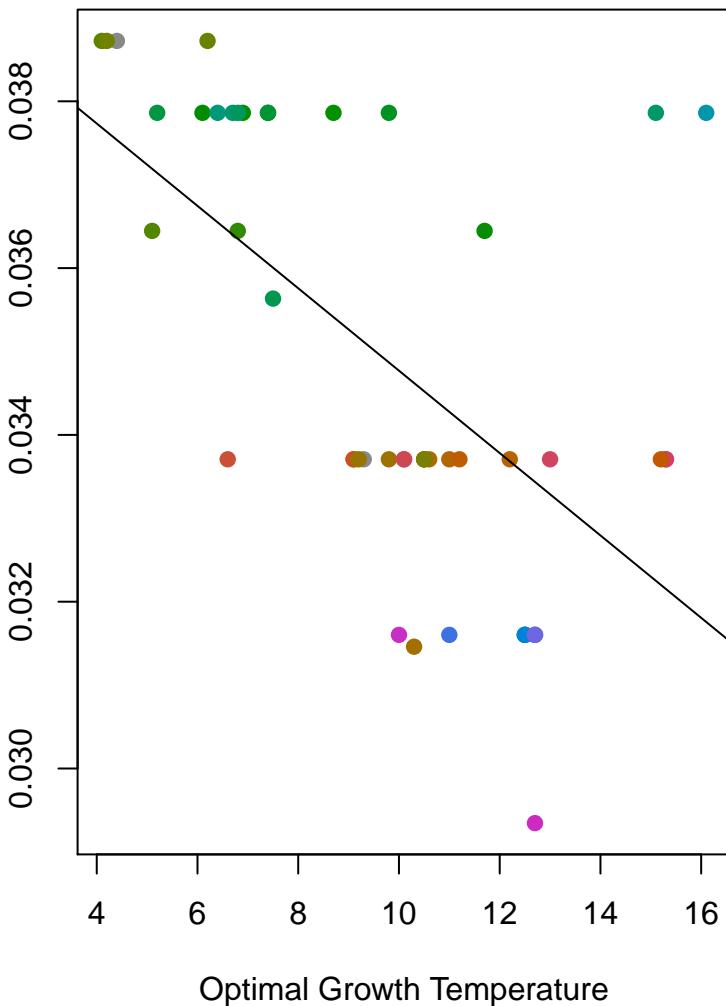
Optimal Growth Temperature



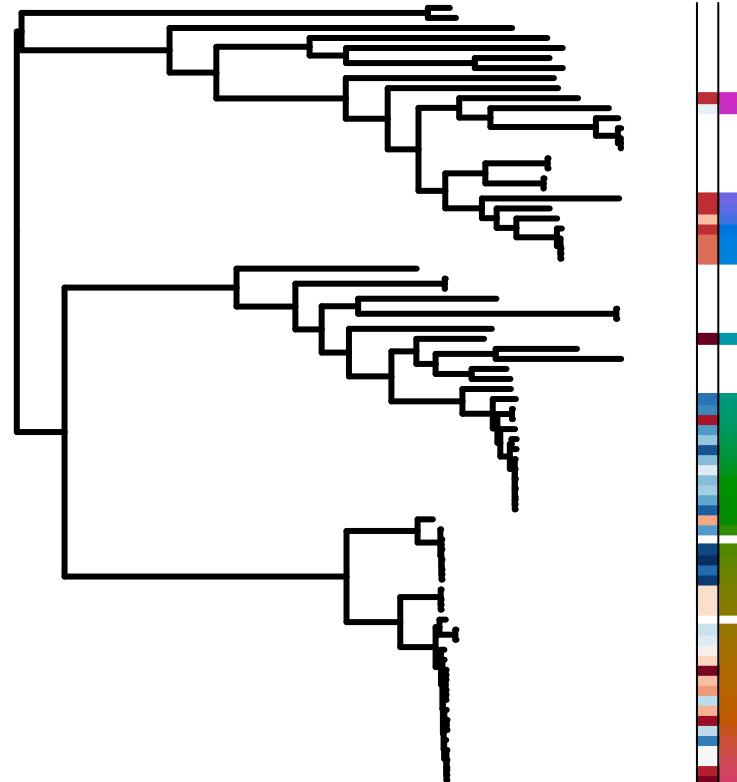
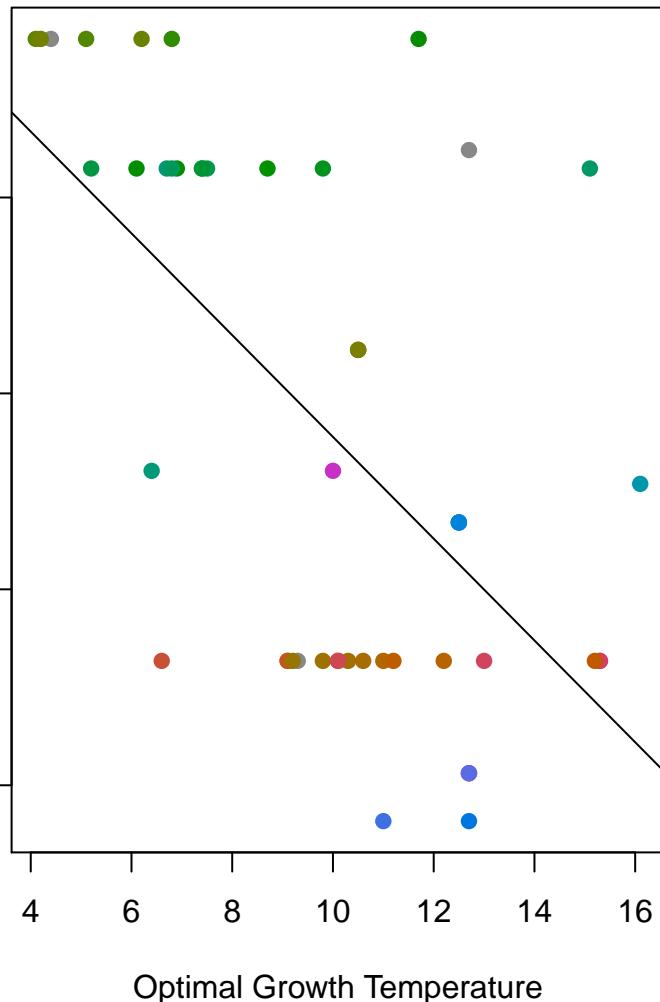


feature.plfam_id.proline_residue.mean
PLF_28228_00000608
Methionine transporter MetT
 $r = -0.598, p = 10^{-5.237}$

feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00000506
Homoserine kinase (EC 2.7.1.39)
 $r = -0.6$, $p = 10^{-5.378}$

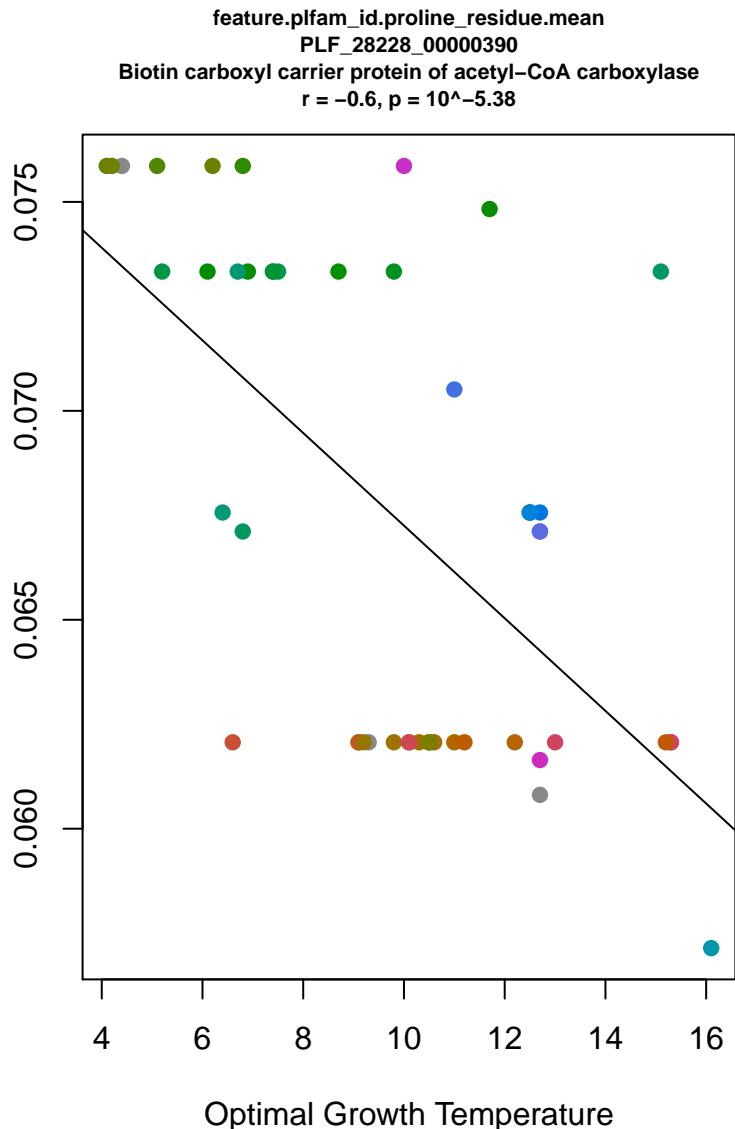


feature_pfam_id.proline_residue.mean

PLF_28228_00000390

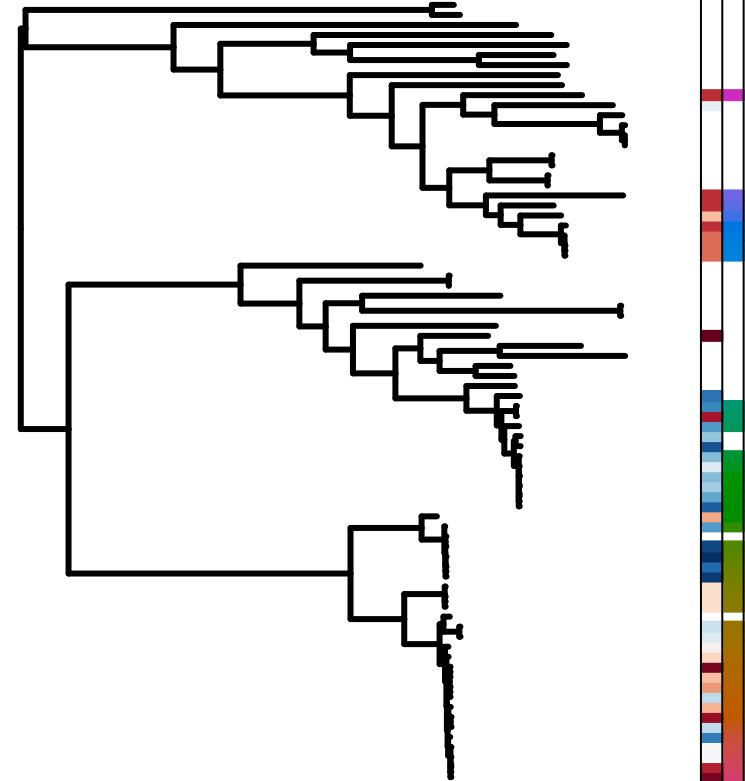
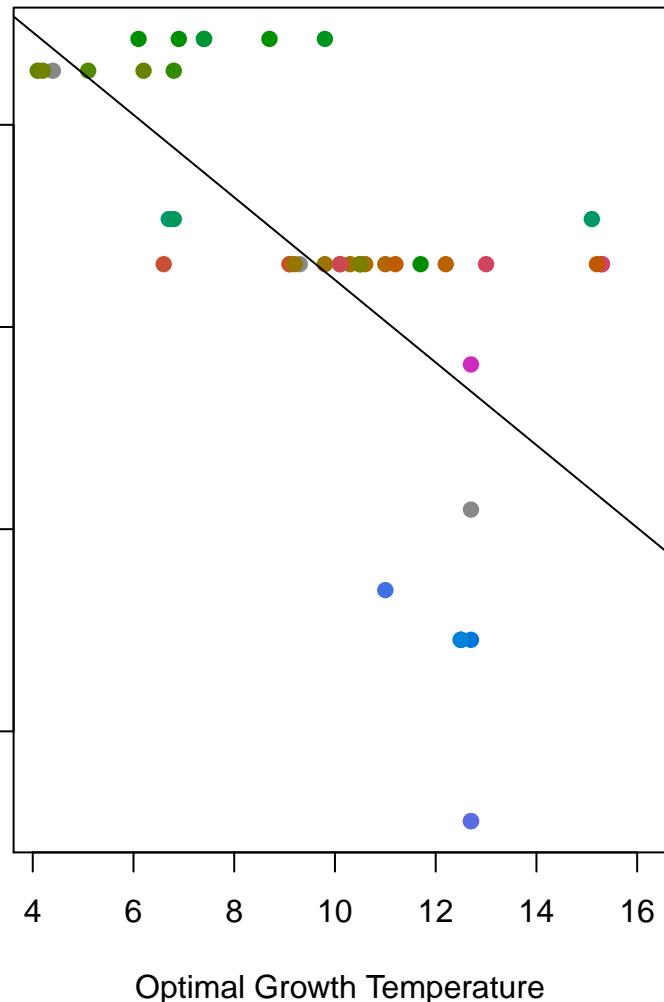
Biotin carboxyl carrier protein of acetyl-CoA carboxylase

$r = -0.6, p = 10^{-5.38}$



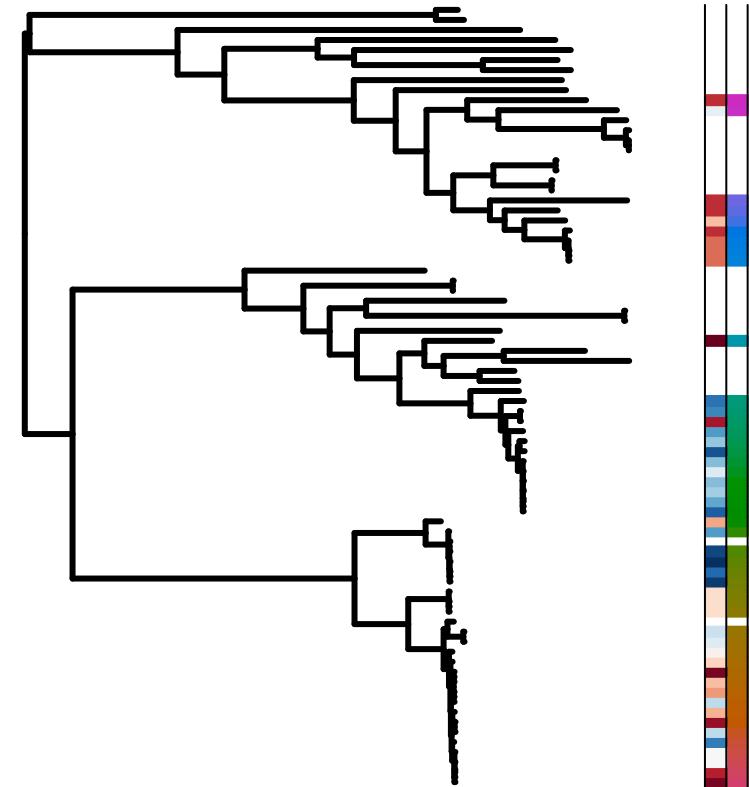
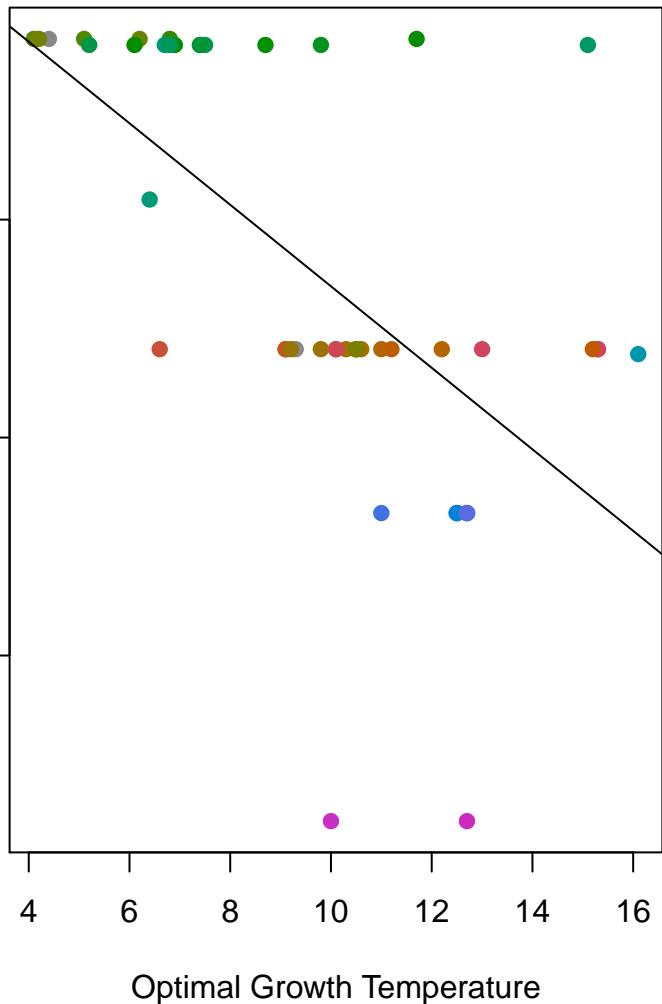
feature.plfam_id.proline_residue.mean
PLF_28228_00001698
putative TonB-dependent receptor
 $r = -0.608$, $p = 10^{-5.034}$

feature.plfam_id.proline_residue.mean



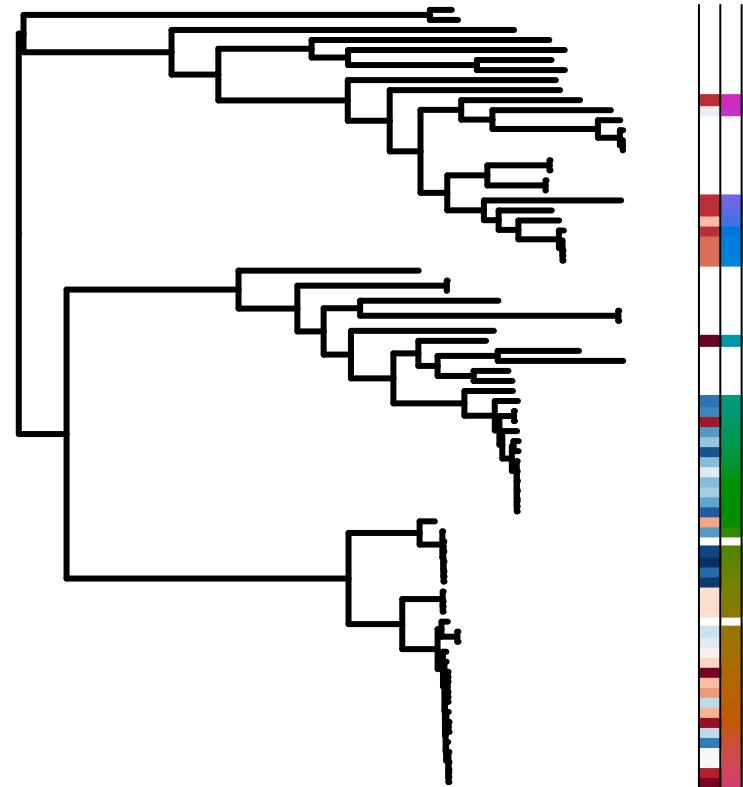
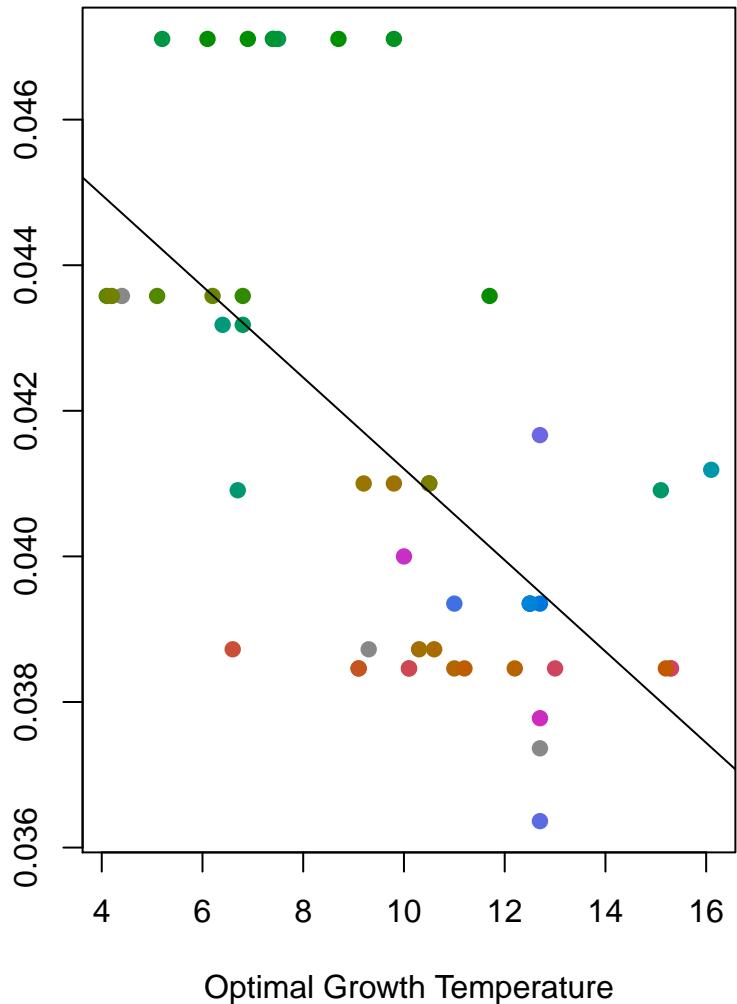
feature.plfam_id.proline_residue.mean
PLF_28228_00001638
HD domain protein
 $r = -0.615, p = 10^{-5.706}$

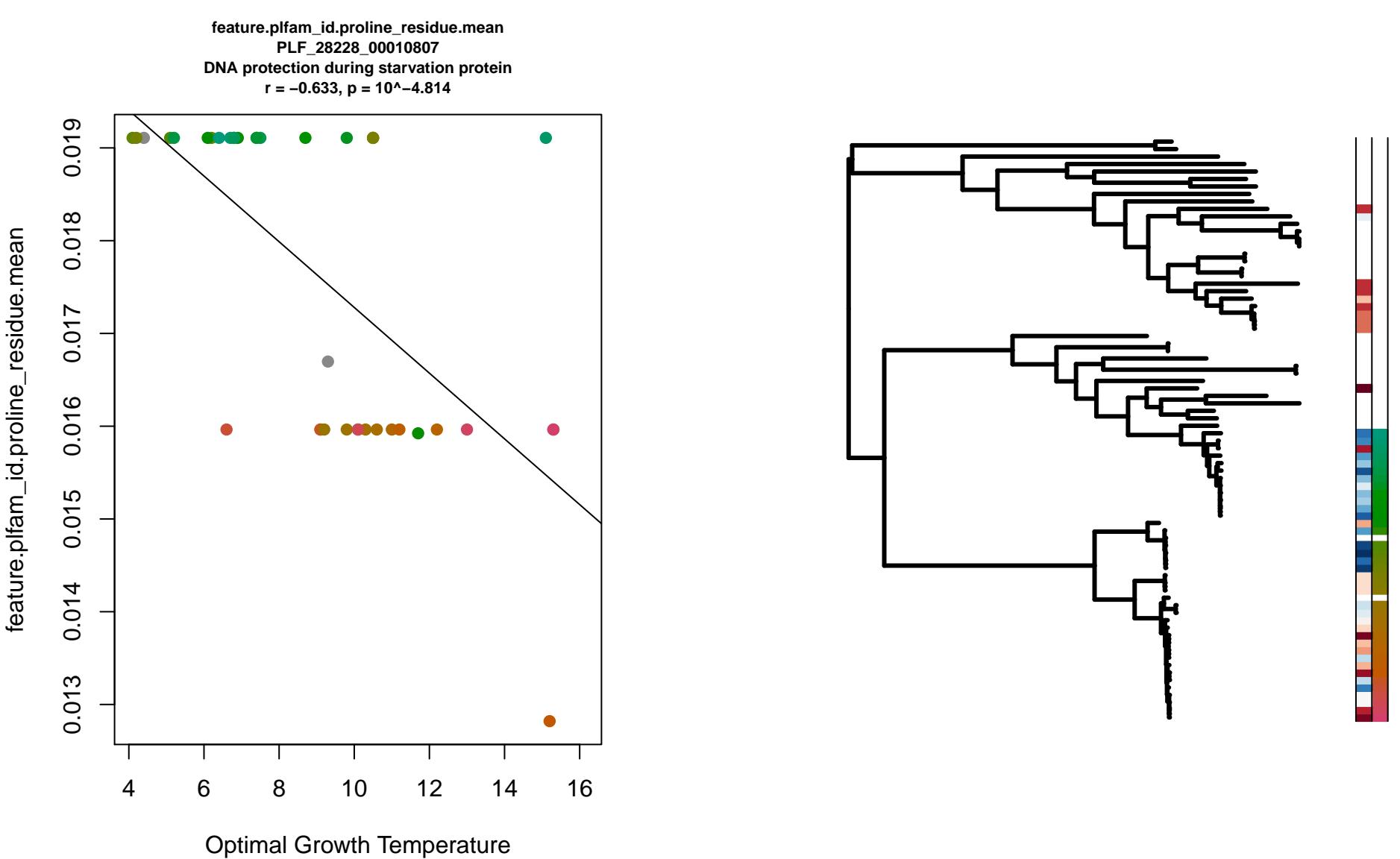
feature.plfam_id.proline_residue.mean



feature.pfam_id.proline_residue.mean
PLF_28228_00000283
ATP-dependent RNA helicase VF1437
 $r = -0.619$, $p = 10^{-5.772}$

feature.pfam_id.proline_residue.mean





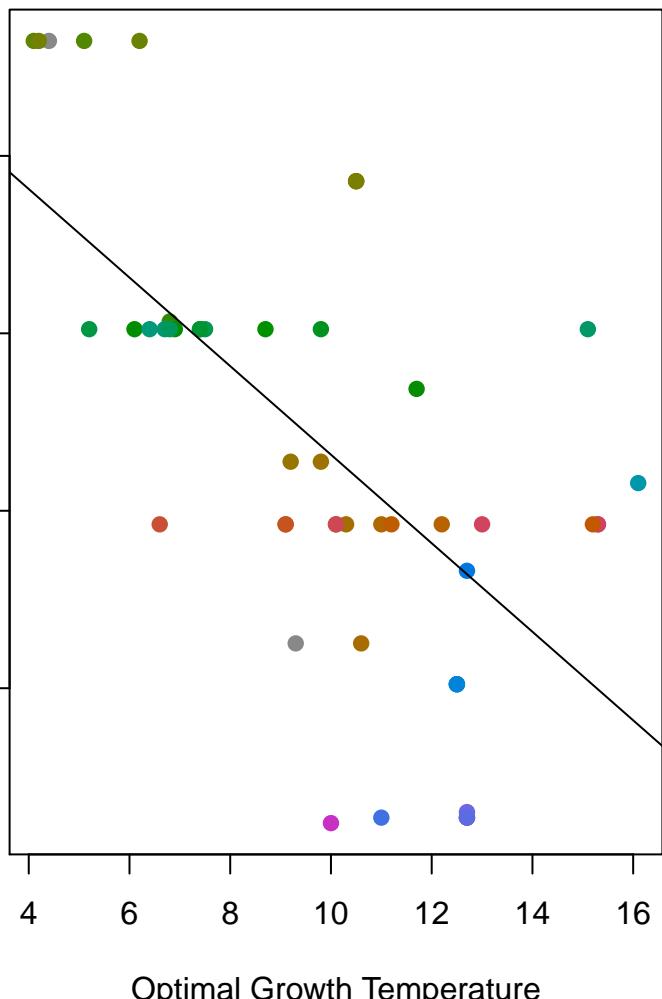
feature.plfam_id.proline_residue.mean

PLF_28228_00001825

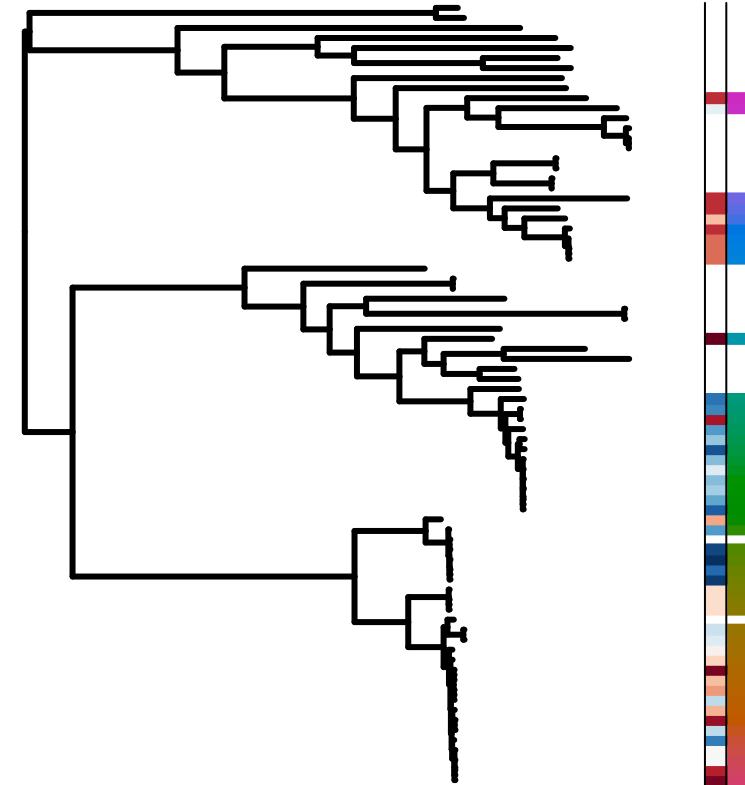
Uncharacterized conserved protein YfiP, contains DTW domain

$r = -0.633, p = 10^{-6.099}$

feature.plfam_id.proline_residue.mean

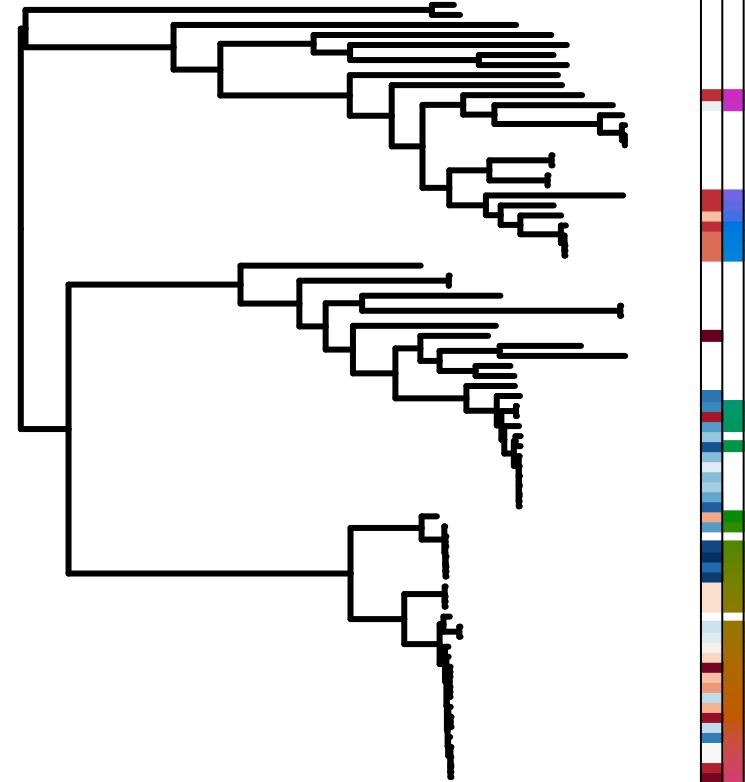
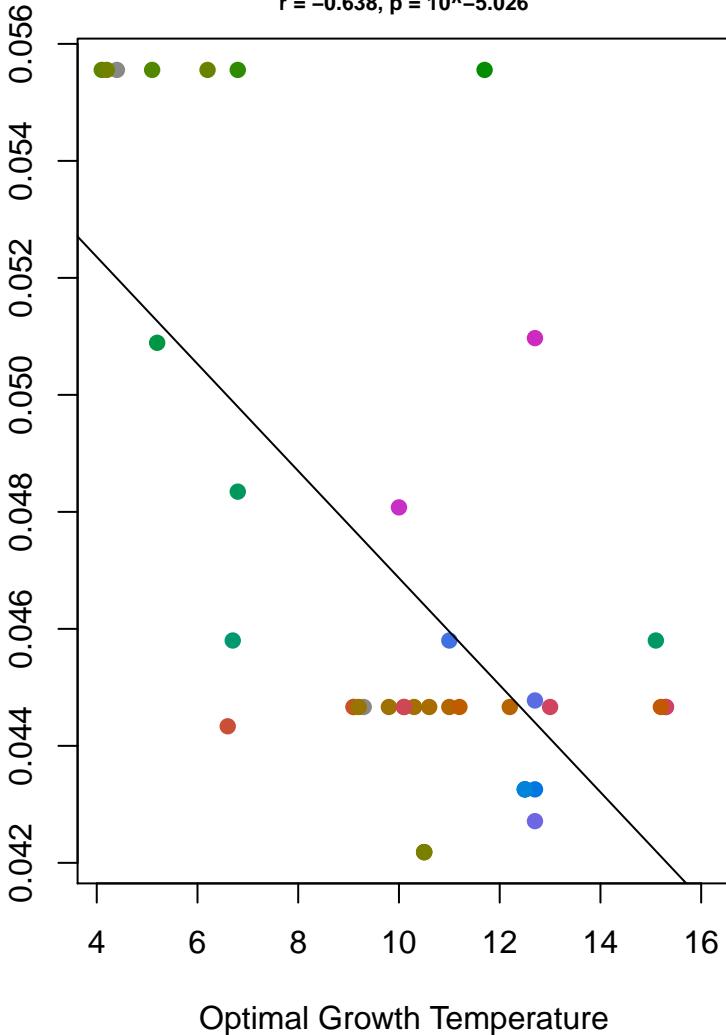


Optimal Growth Temperature



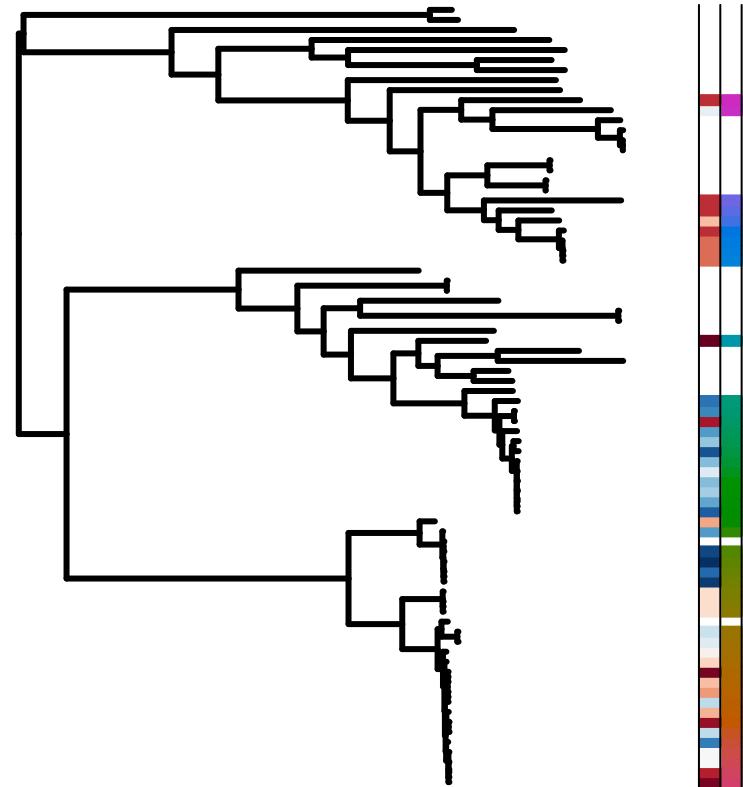
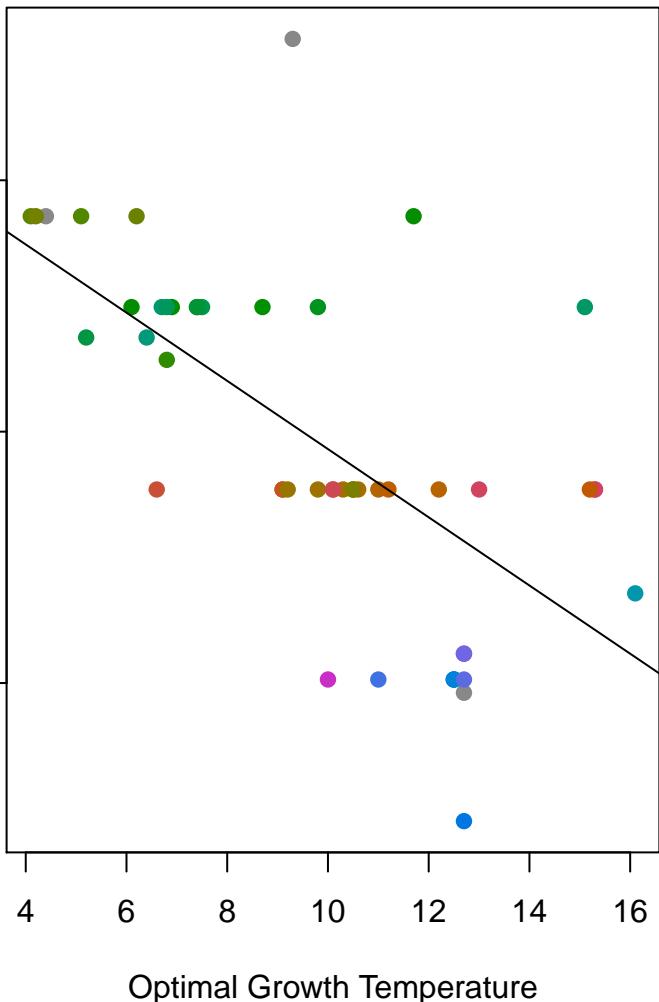
feature.plfam_id.proline_residue.mean
PLF_28228_00000419
Glycine oxidase ThiO (EC 1.4.3.19)
 $r = -0.638, p = 10^{-5.026}$

feature.plfam_id.proline_residue.mean

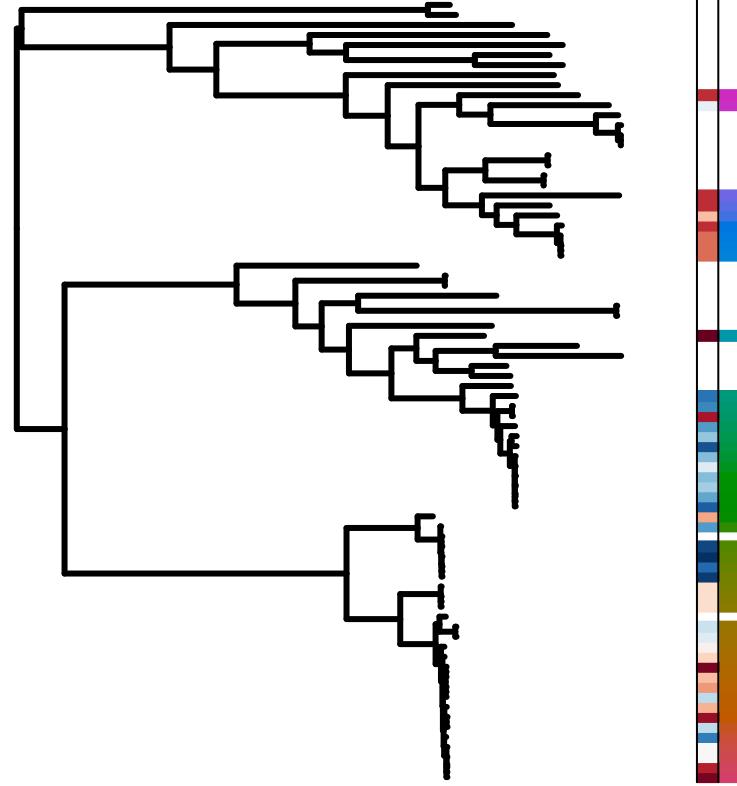
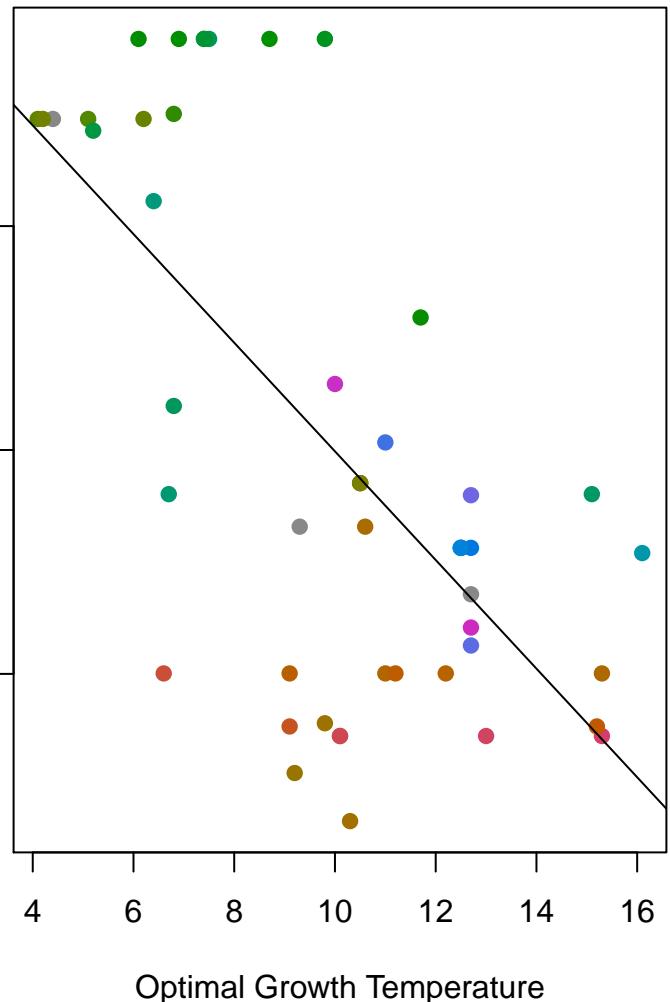


feature.pfam_id.proline_residue.mean
PLF_28228_00000216
Dihydroorotate (EC 3.5.2.3)
 $r = -0.642$, $p = 10^{-6.294}$

feature.pfam_id.proline_residue.mean

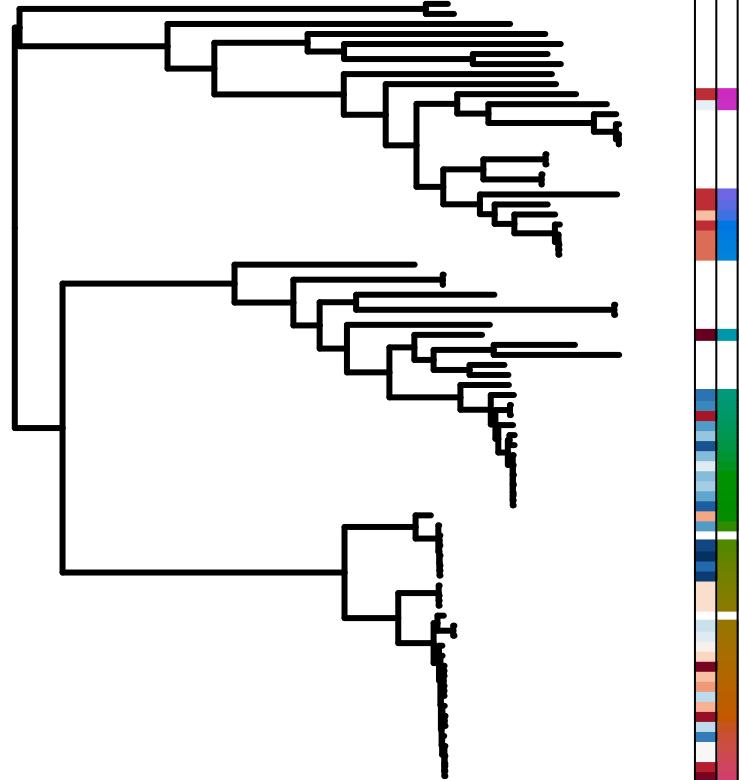
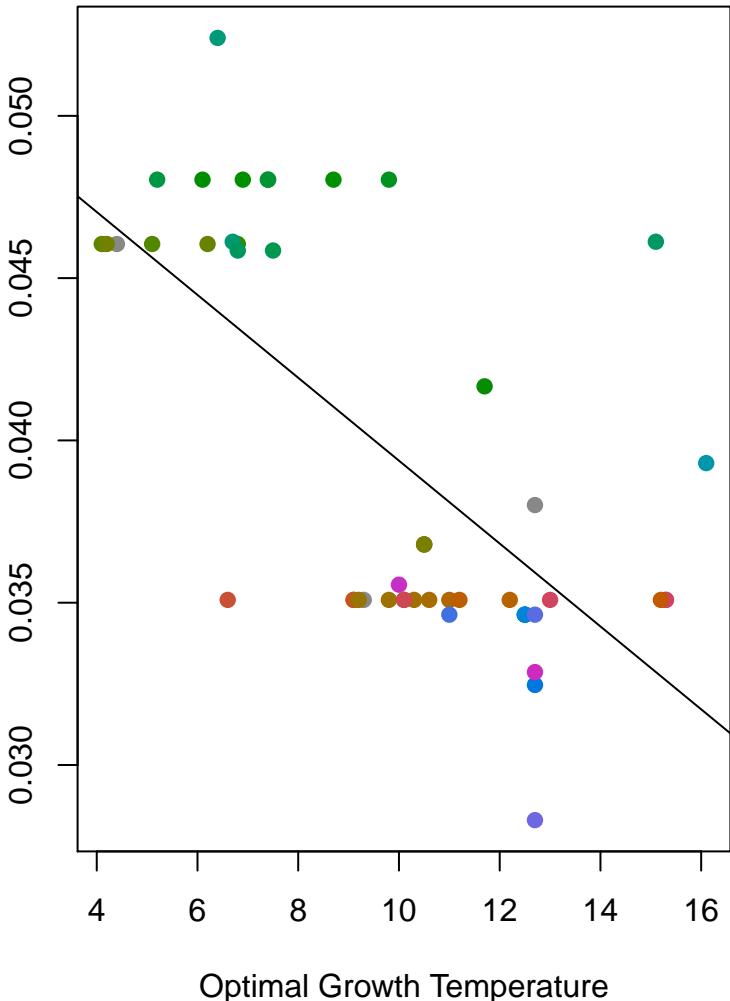


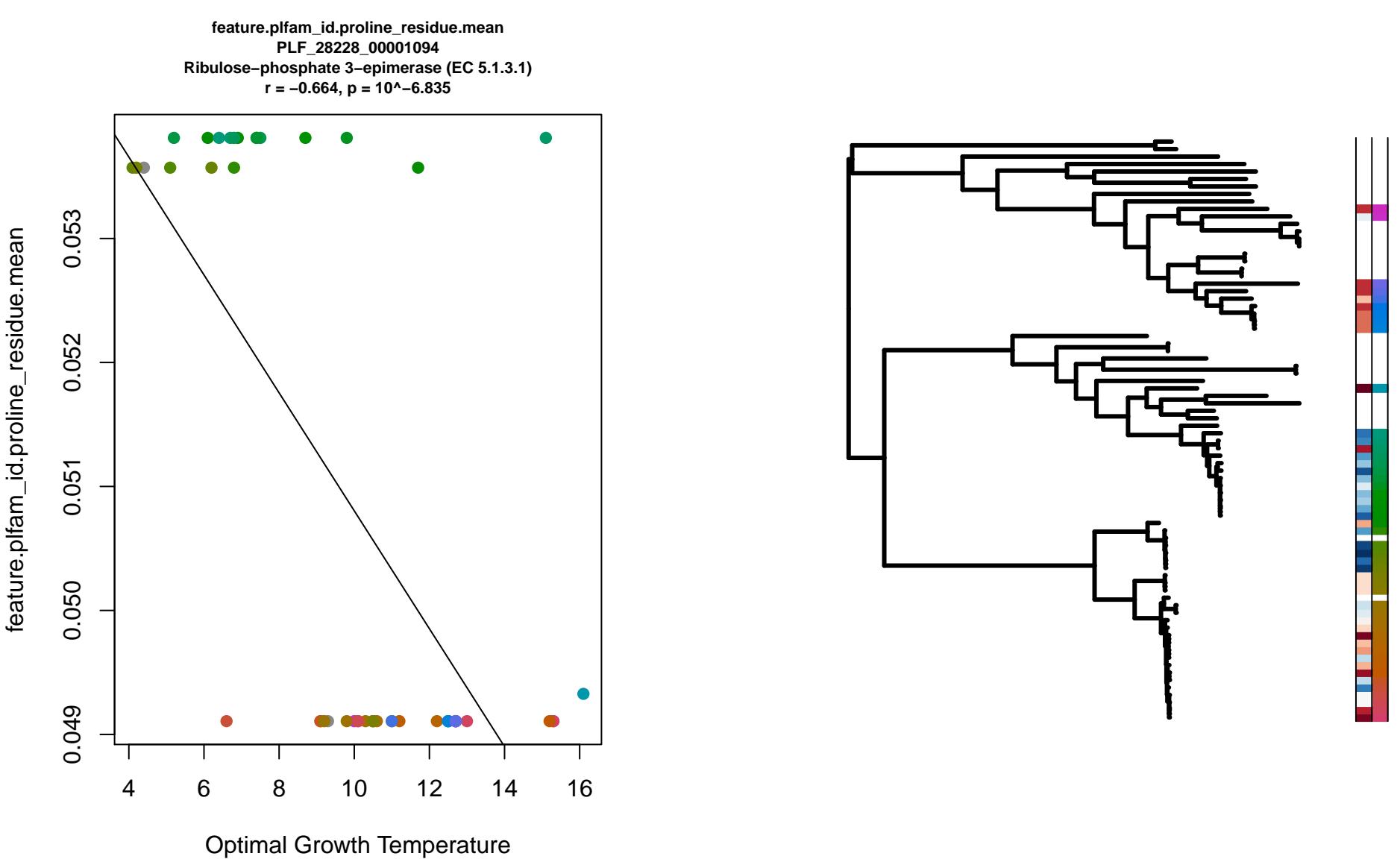
feature.plfam_id.proline_residue.mean
PLF_28228_00002525
hypothetical protein
 $r = -0.662$, $p = 10^{-6.788}$



feature.plfam_id.proline_residue.mean
PLF_28228_00001414
tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)
 $r = -0.662$, $p = 10^{-6.794}$

feature.plfam_id.proline_residue.mean





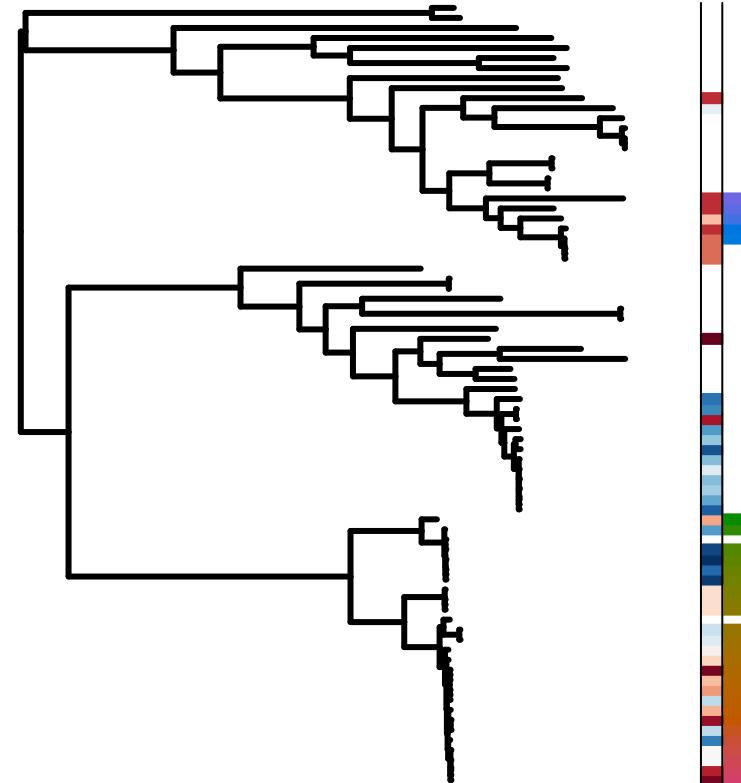
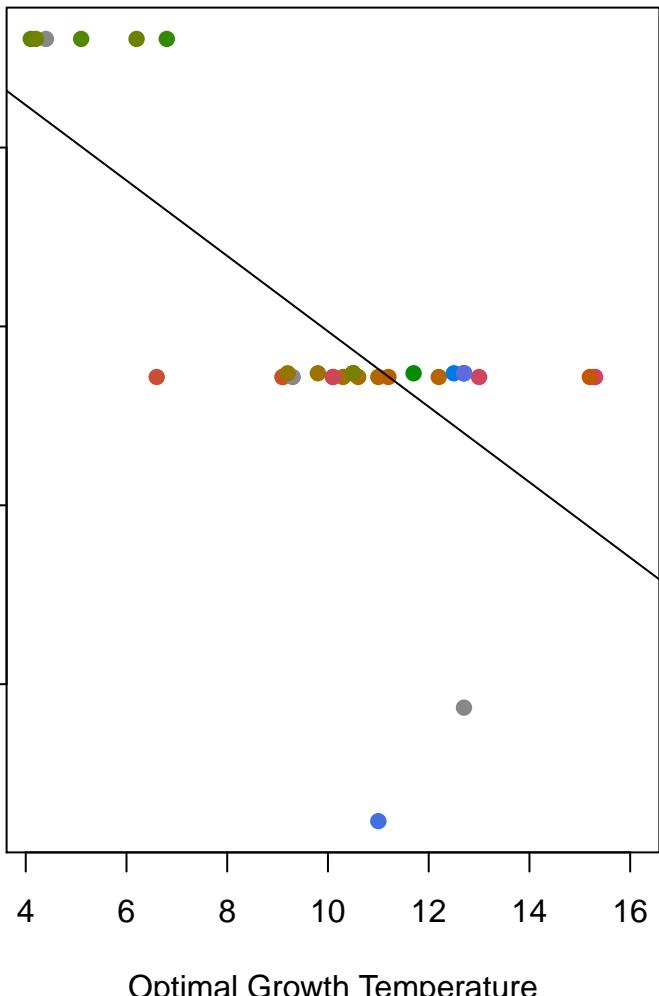
feature.pfam_id.proline_residue.mean

PLF_28228_00028320

Methyl-accepting chemotaxis sensor/transducer protein

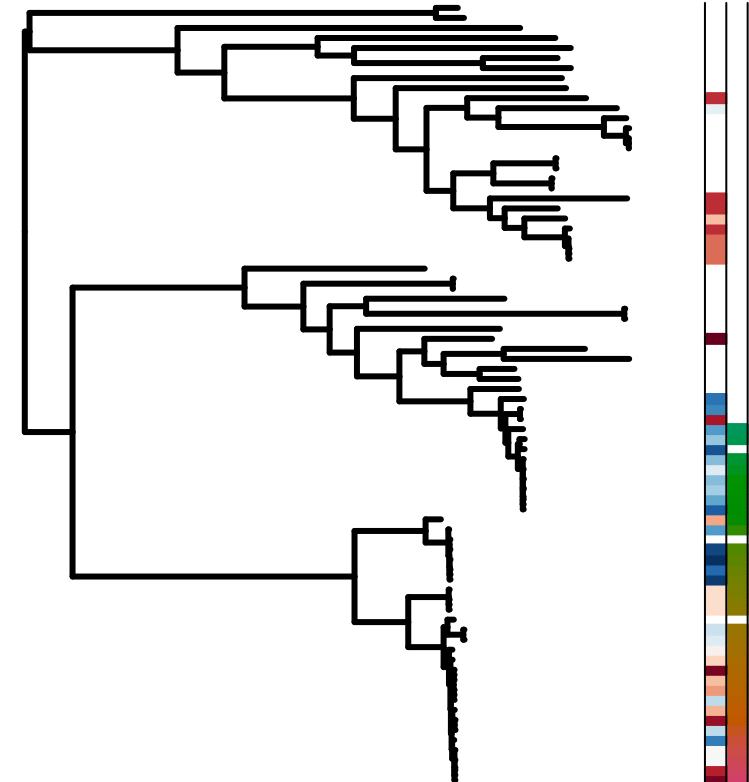
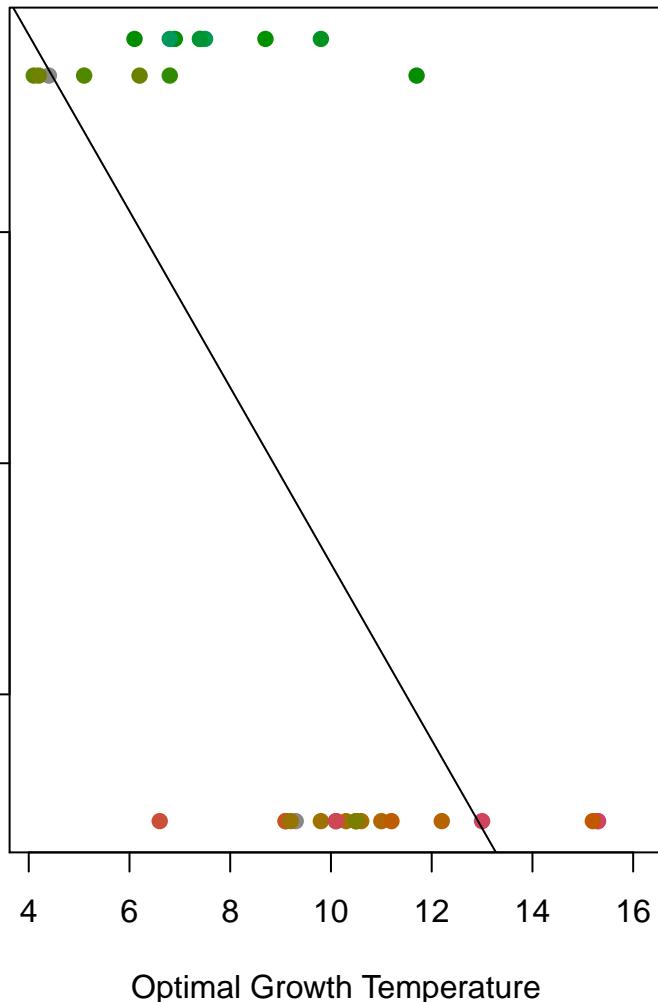
$r = -0.675, p = 10^{-4.786}$

feature.pfam_id.proline_residue.mean

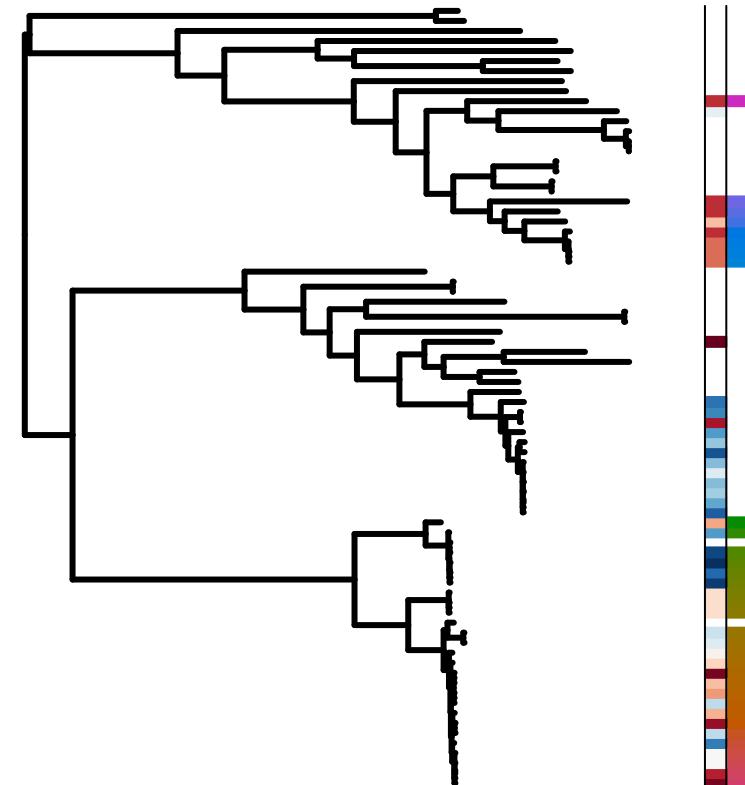
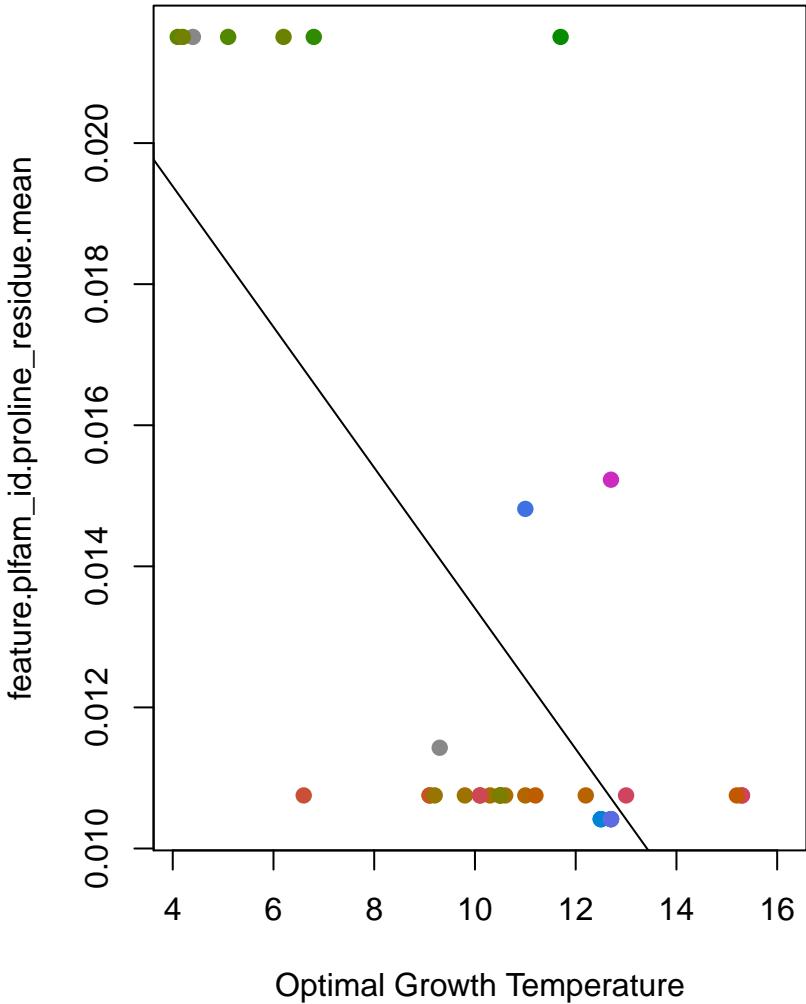


feature.plfam_id.proline_residue.mean
PLF_28228_00019712
hypothetical protein
 $r = -0.682$, $p = 10^{-5.189}$

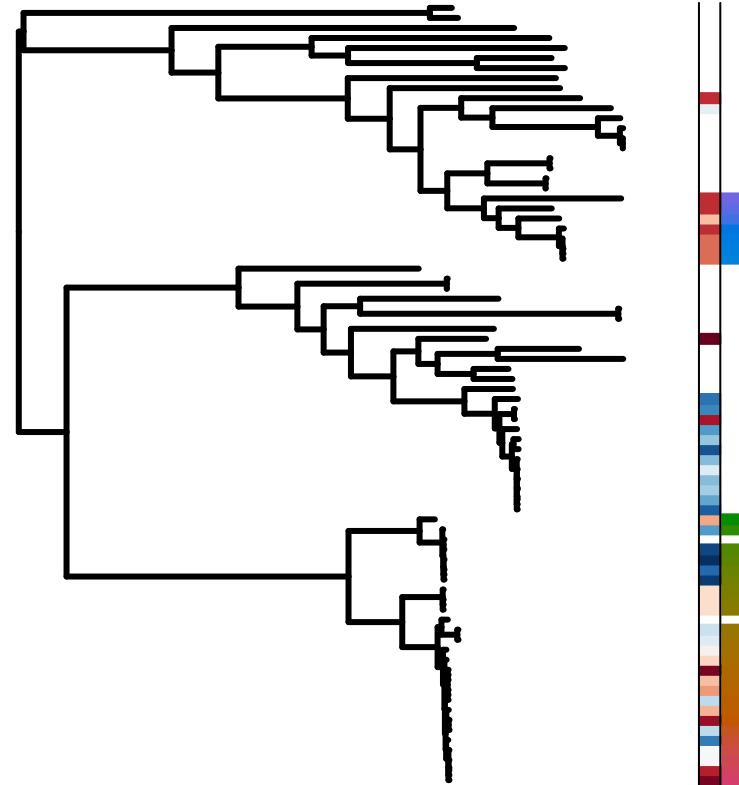
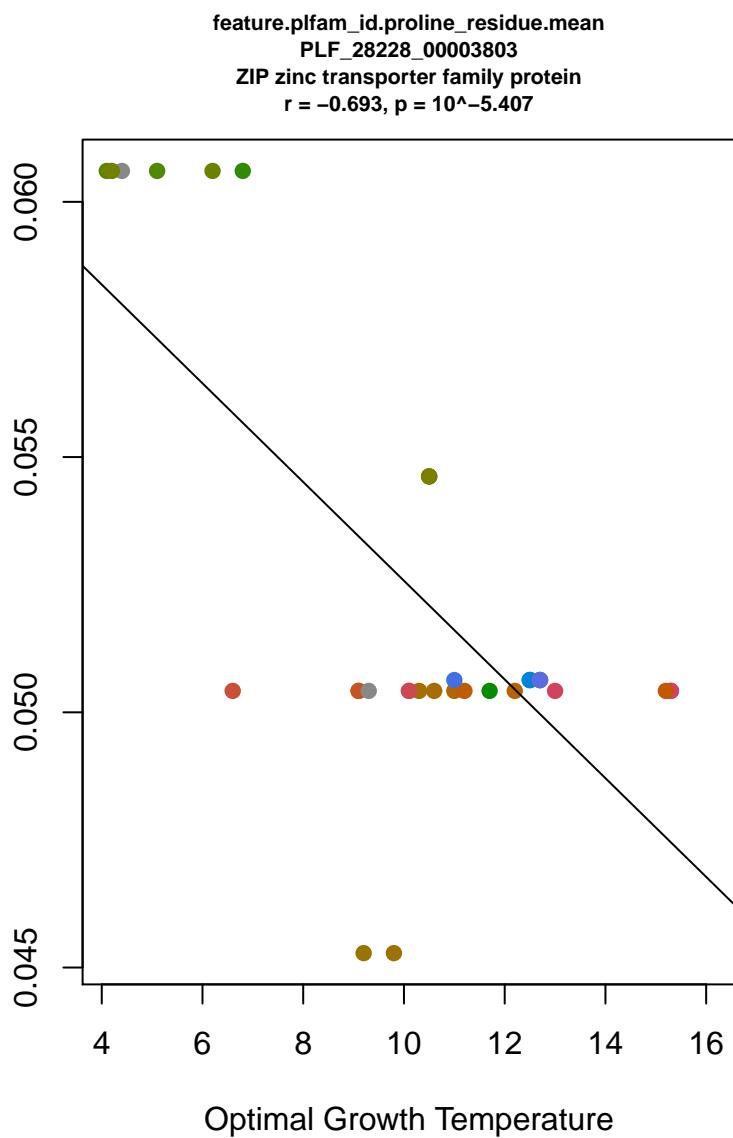
feature.plfam_id.proline_residue.mean

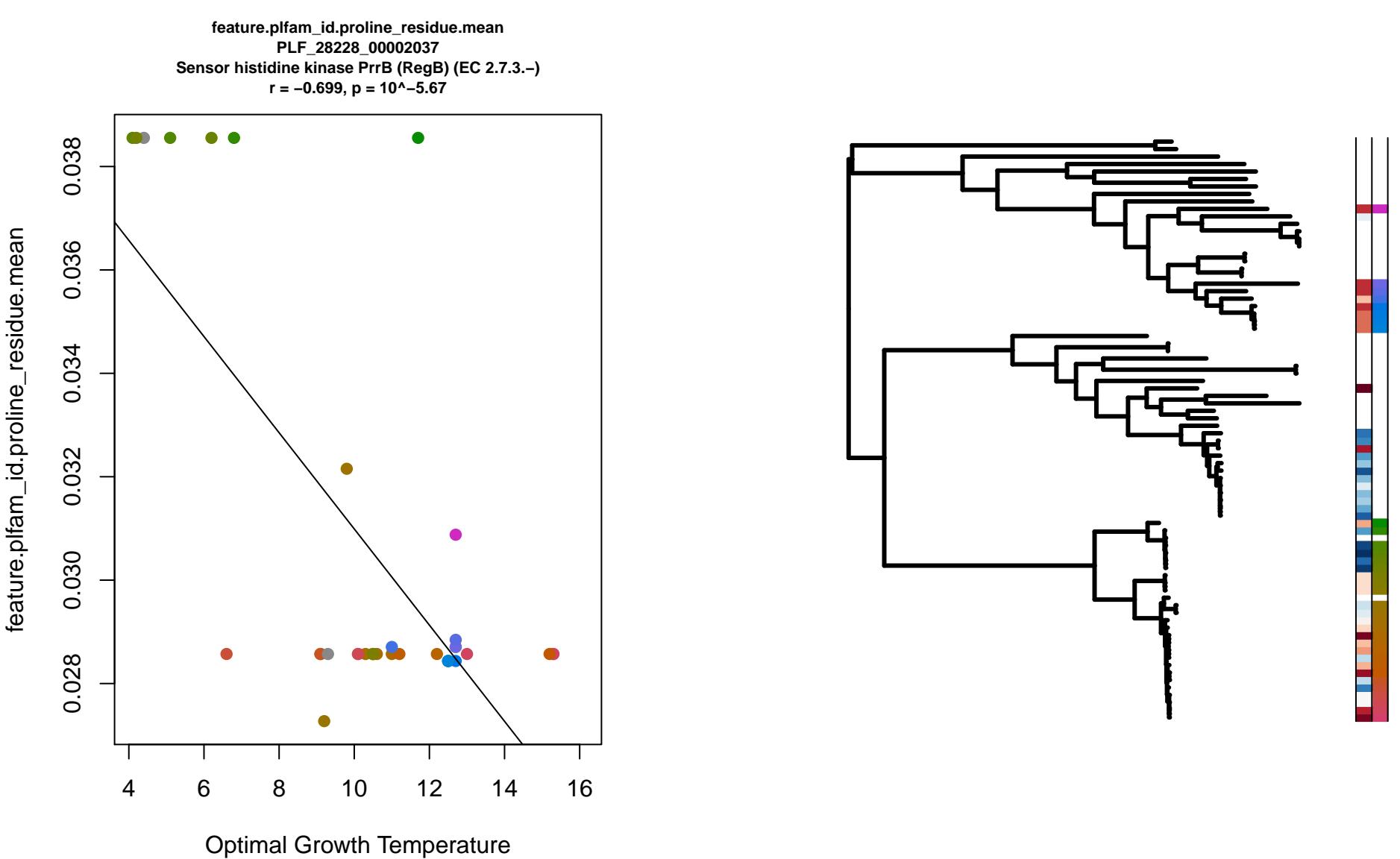


feature_pfam_id.proline_residue.mean
PLF_28228_00000396
FIG006045: Sigma factor, ECF subfamily
 $r = -0.692$, $p = 10^{-5.529}$



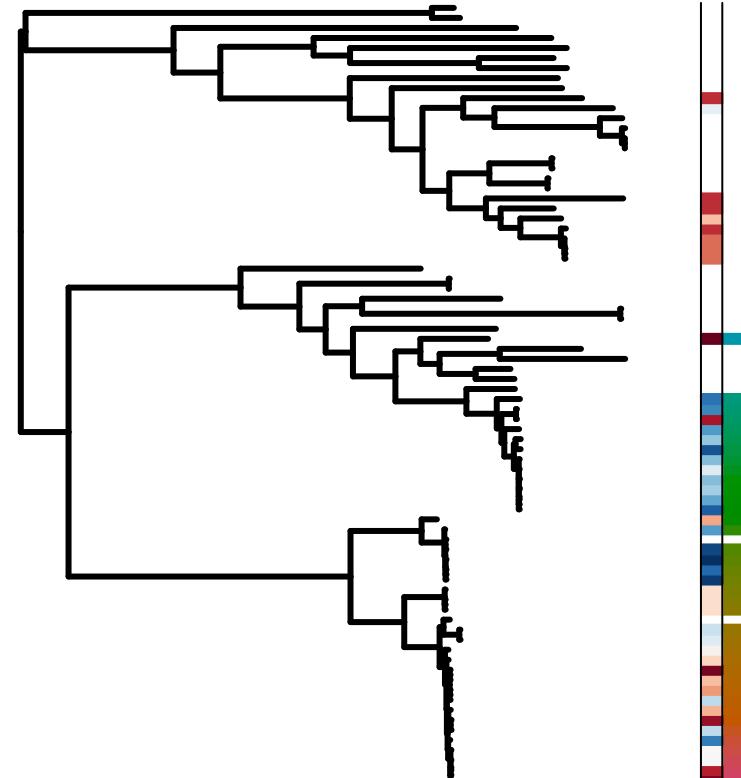
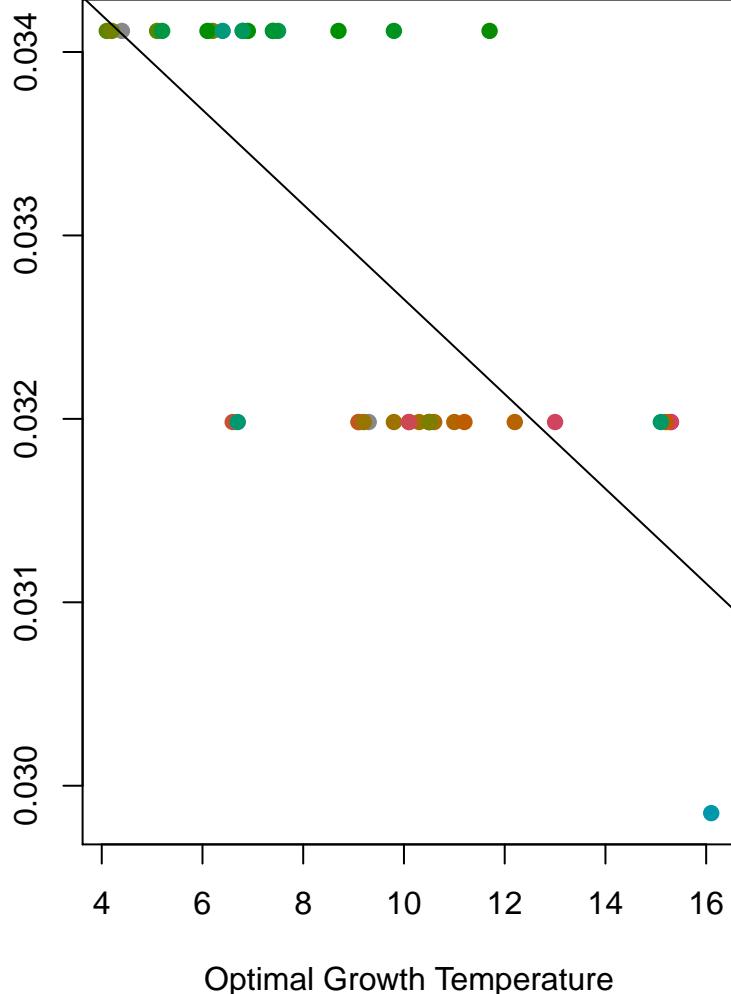
feature.plfam_id.proline_residue.mean
PLF_28228_00003803
ZIP zinc transporter family protein
 $r = -0.693, p = 10^{-5.407}$





feature.plfam_id.proline_residue.mean
PLF_28228_00014301
Aminopeptidase CC_2544
 $r = -0.723$, $p = 10^{-6.851}$

feature.plfam_id.proline_residue.mean

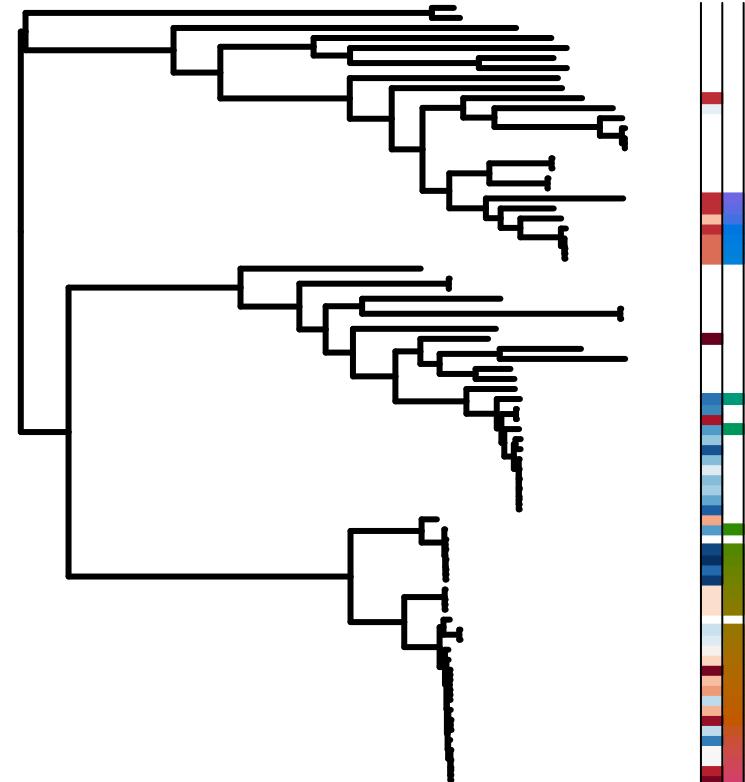
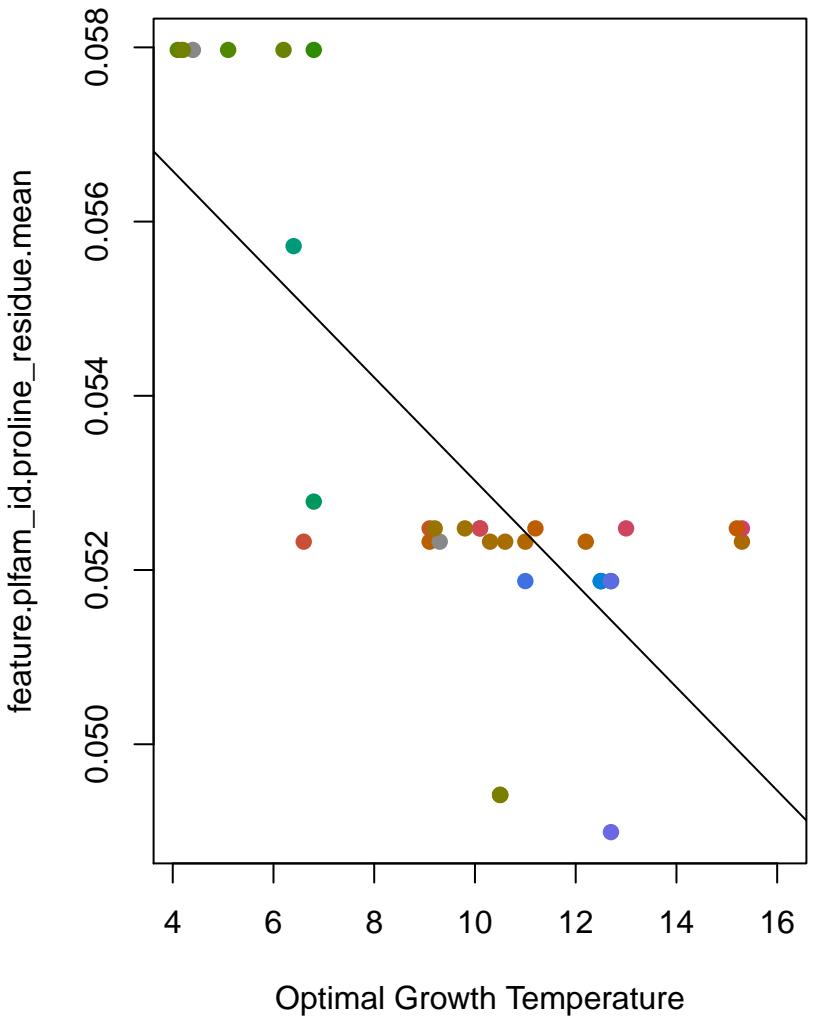


feature.plfam_id.proline_residue.mean

PLF_28228_00003411

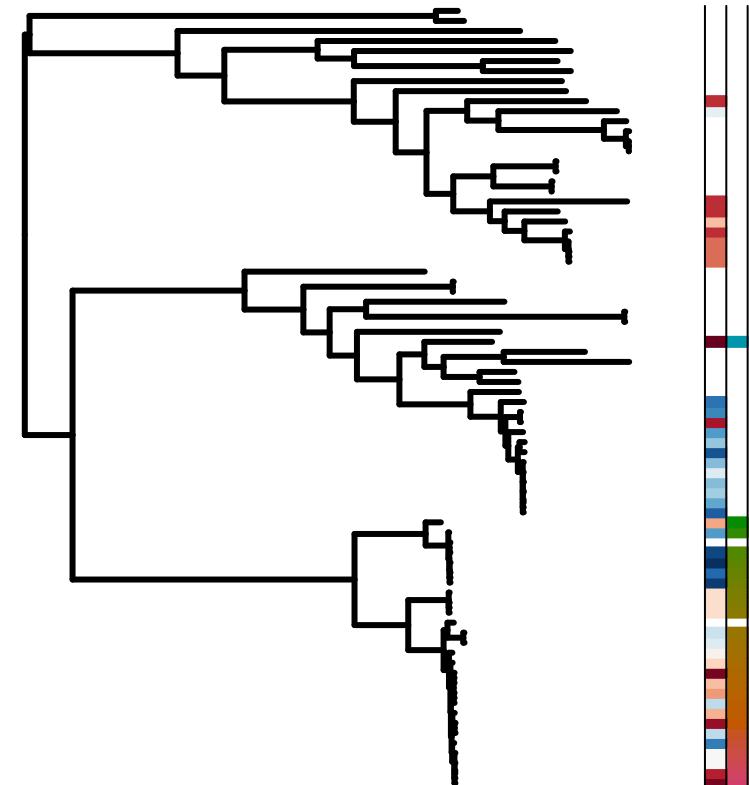
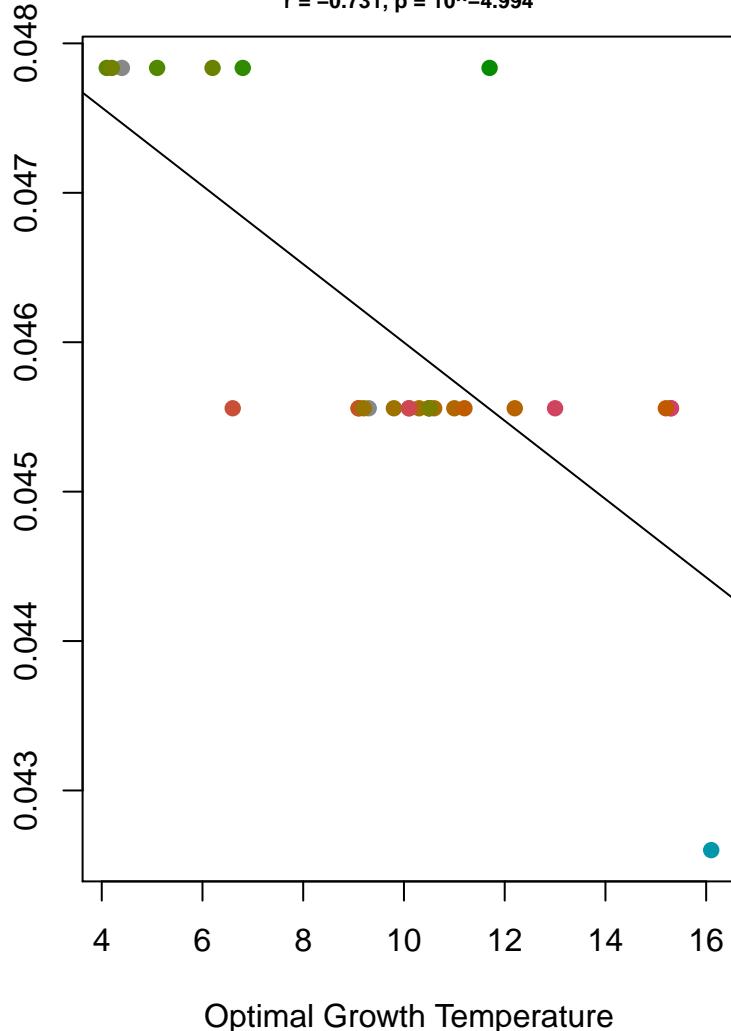
$r = -0.723, p = 10^{-6.208}$

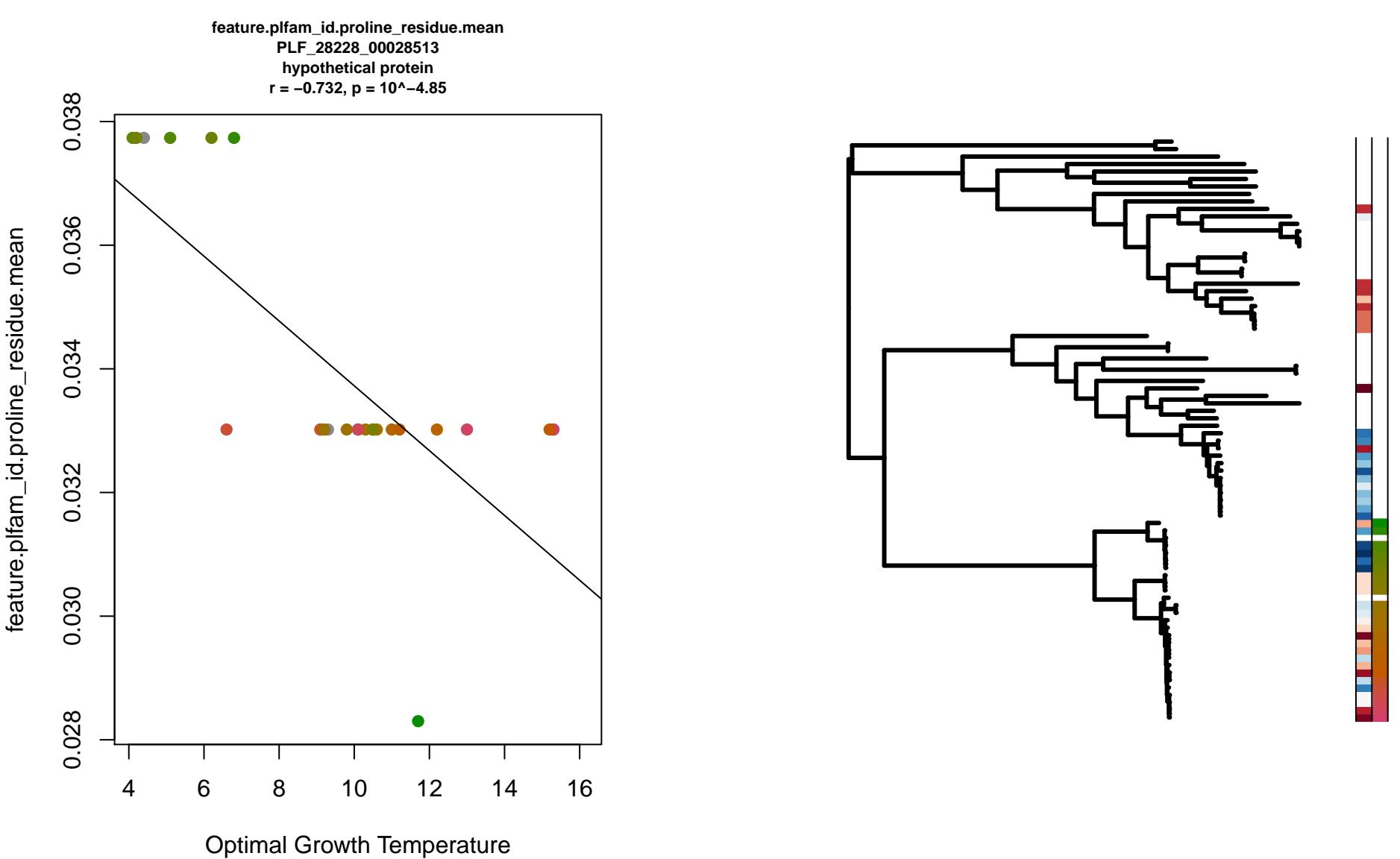
acetyl-beta-D-mannosaminyl-1,4-N-acetyl-D-glucosaminylidiphosphoundecaprenyl glycerol



feature.plfam_id.proline_residue.mean
PLF_28228_00006263
ATP-dependent RNA helicase VVA0939
 $r = -0.731$, $p = 10^{-4.994}$

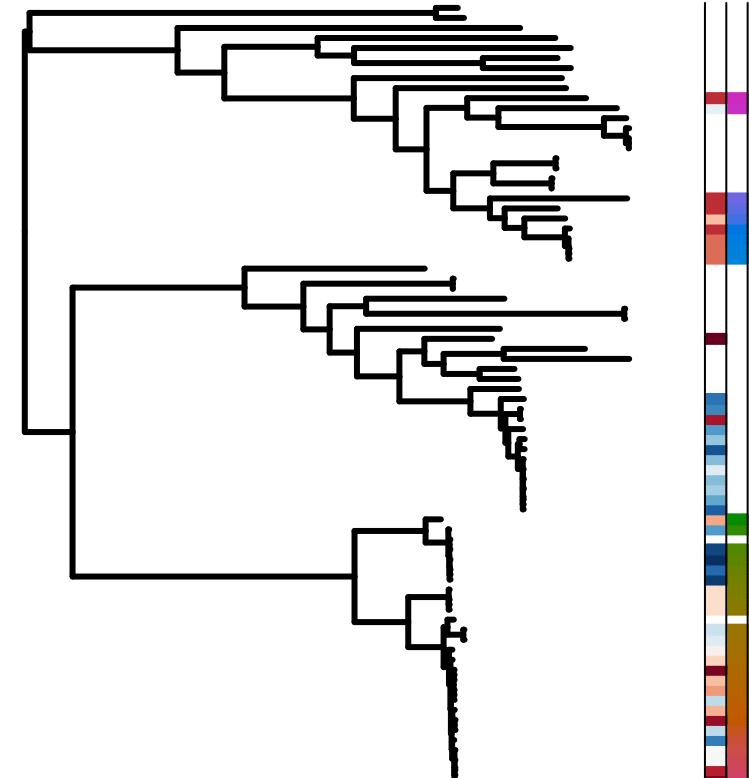
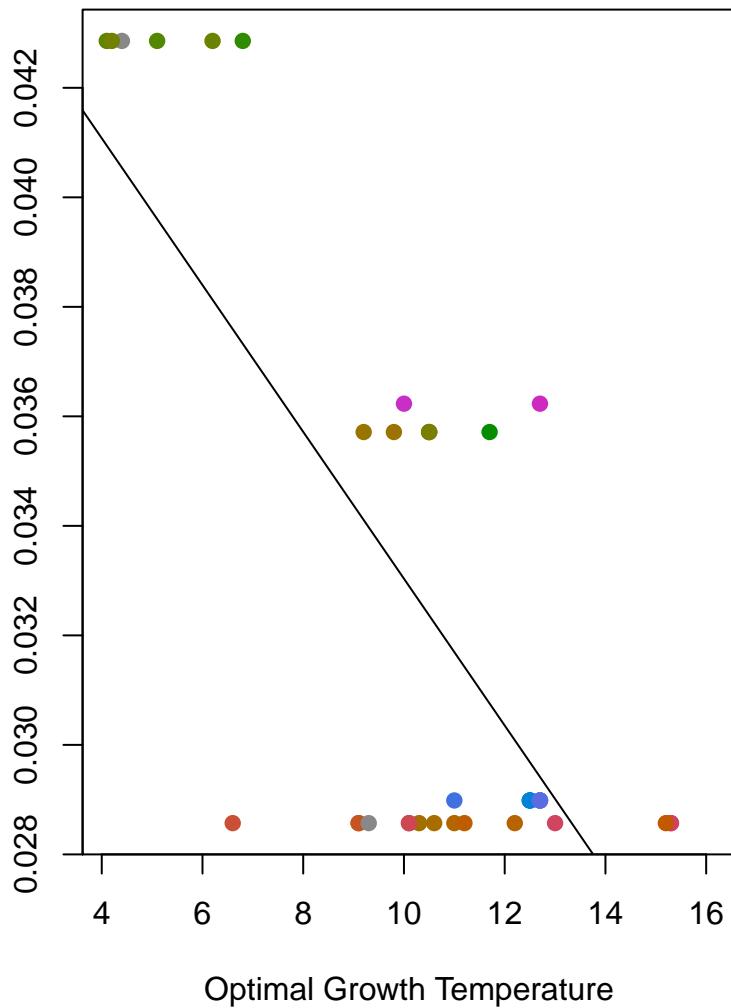
feature.plfam_id.proline_residue.mean





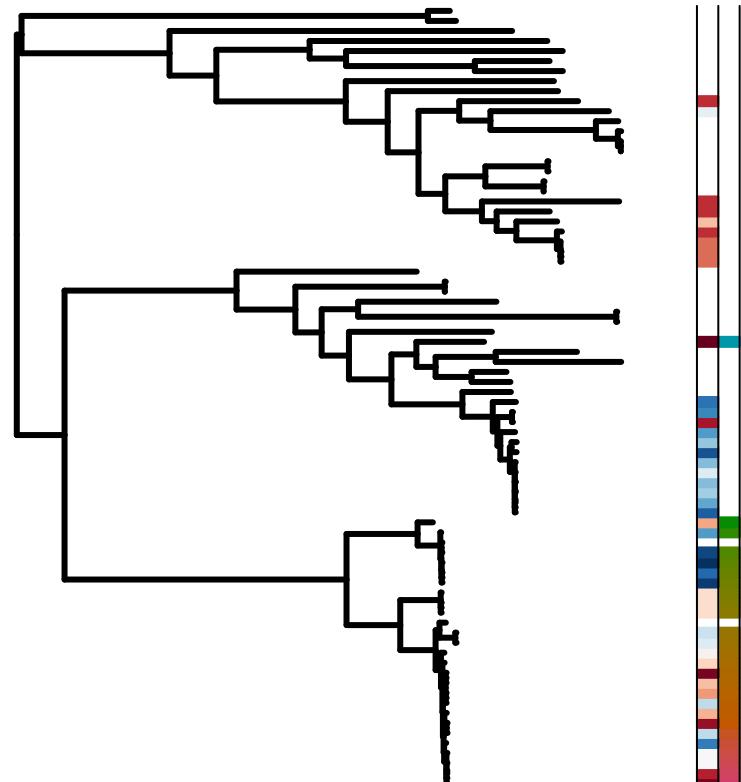
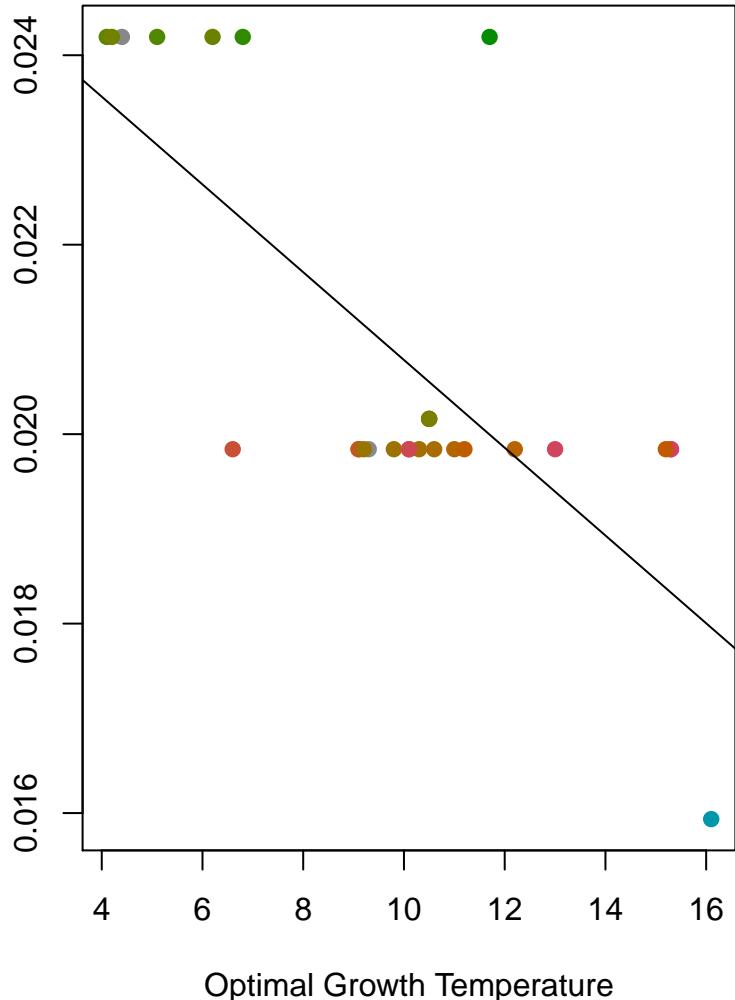
feature.plfam_id.proline_residue.mean
PLF_28228_00000478
Glyoxalase family protein
 $r = -0.733$, $p = 10^{-6.6}$

feature.plfam_id.proline_residue.mean



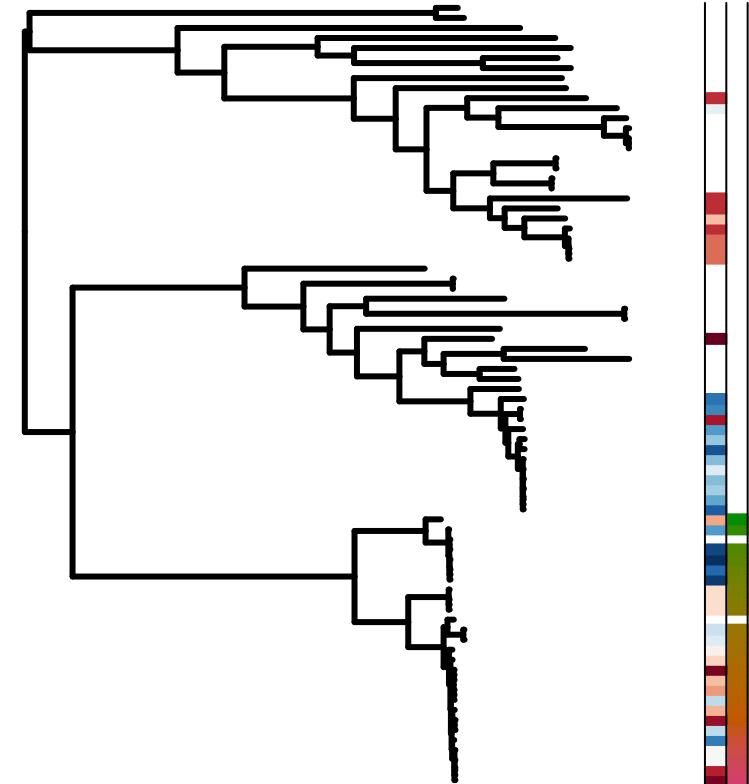
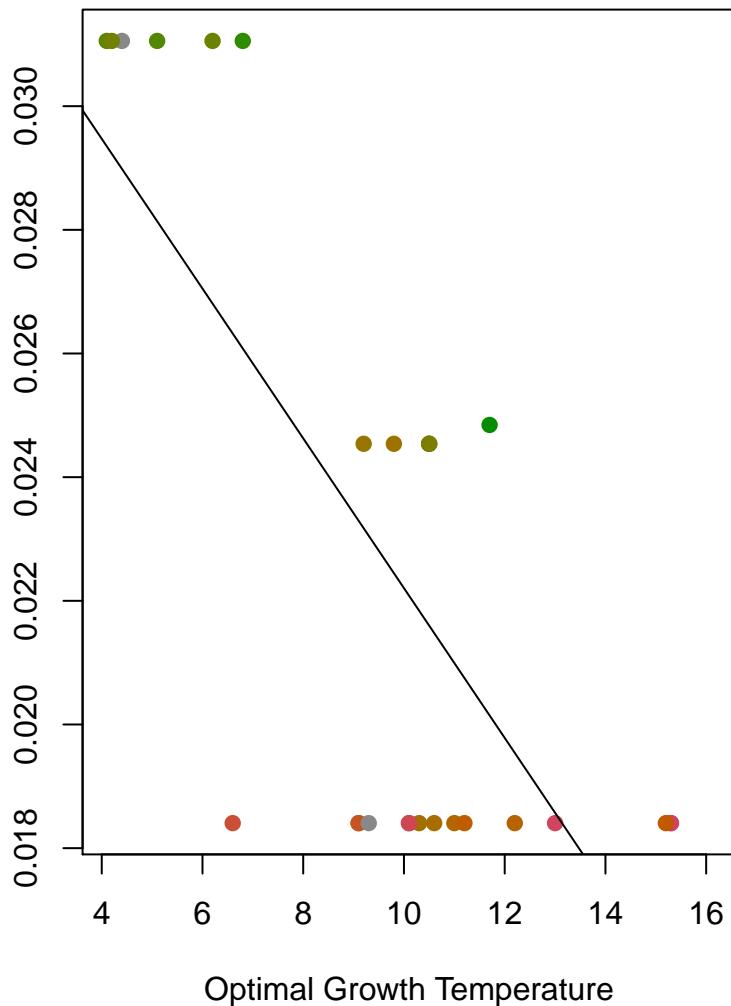
feature.plfam_id.proline_residue.mean
PLF_28228_00021085
hypothetical protein
 $r = -0.733, p = 10^{-5.044}$

feature.plfam_id.proline_residue.mean



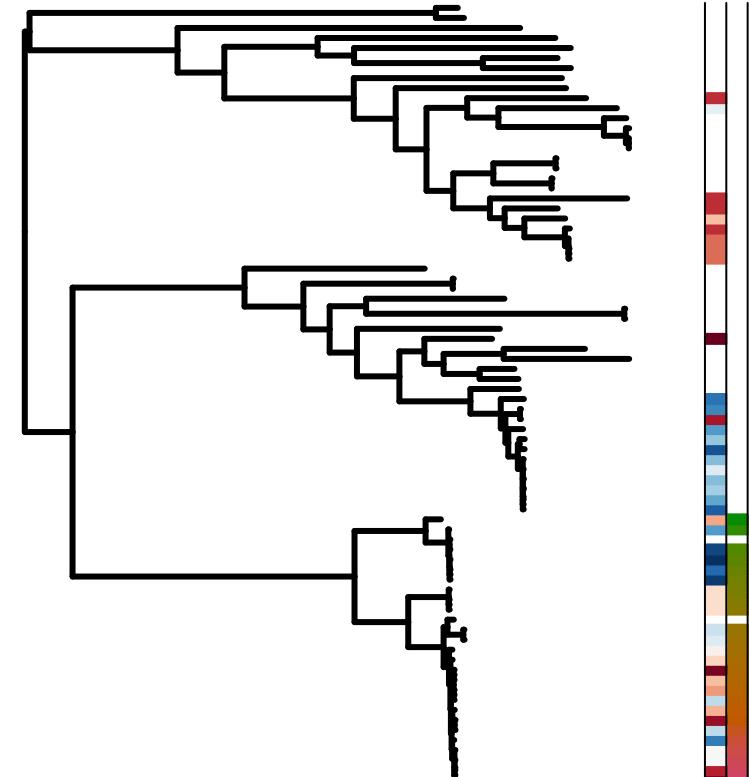
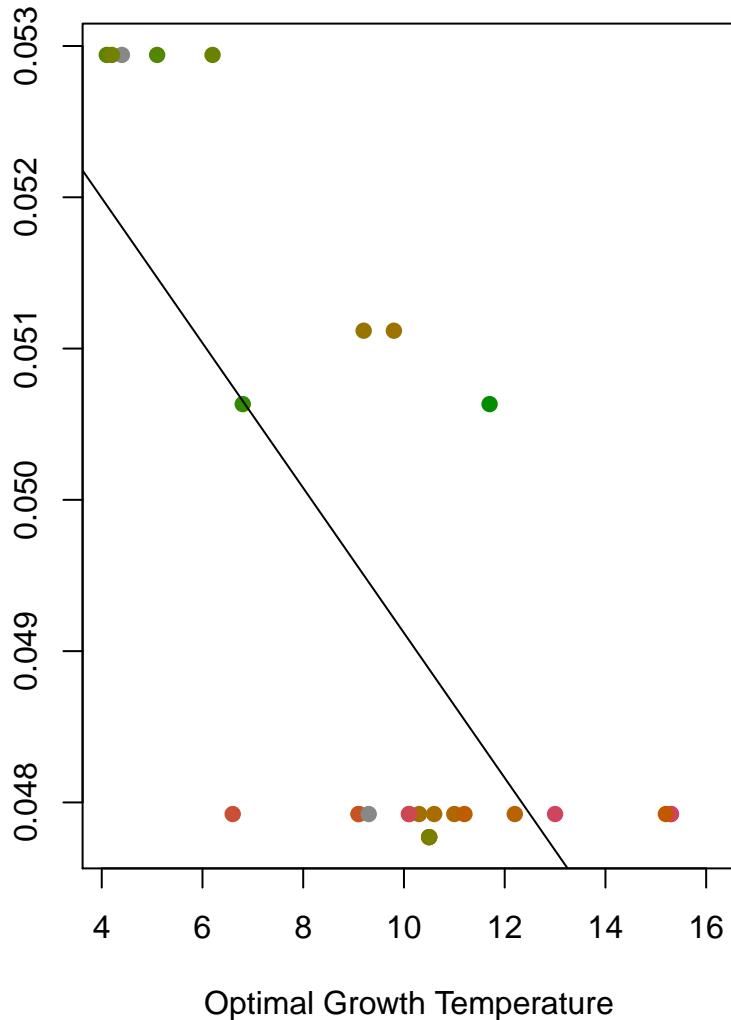
feature.plfam_id.proline_residue.mean
PLF_28228_00027872
hypothetical protein
 $r = -0.735$, $p = 10^{-4.891}$

feature.plfam_id.proline_residue.mean

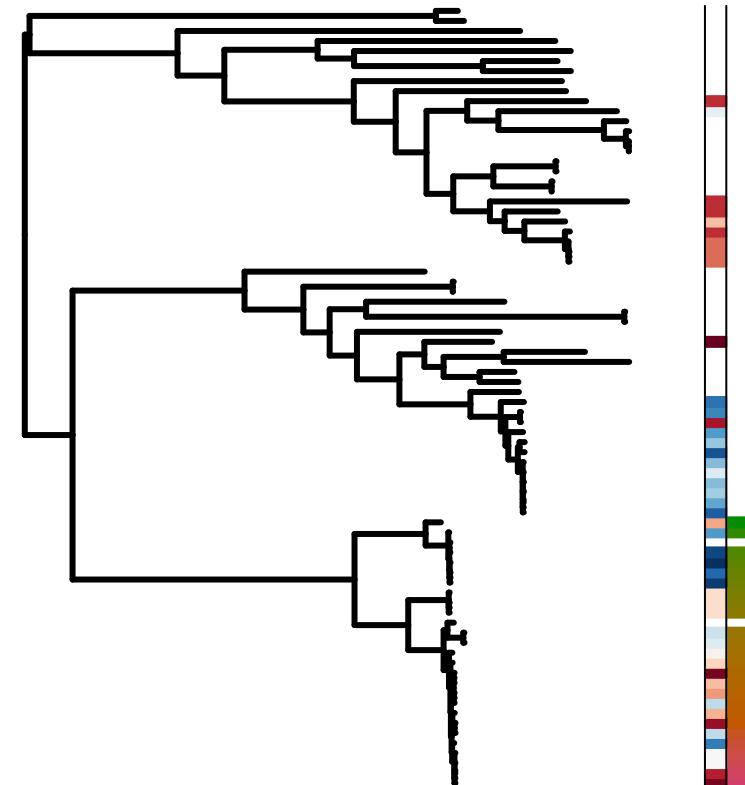
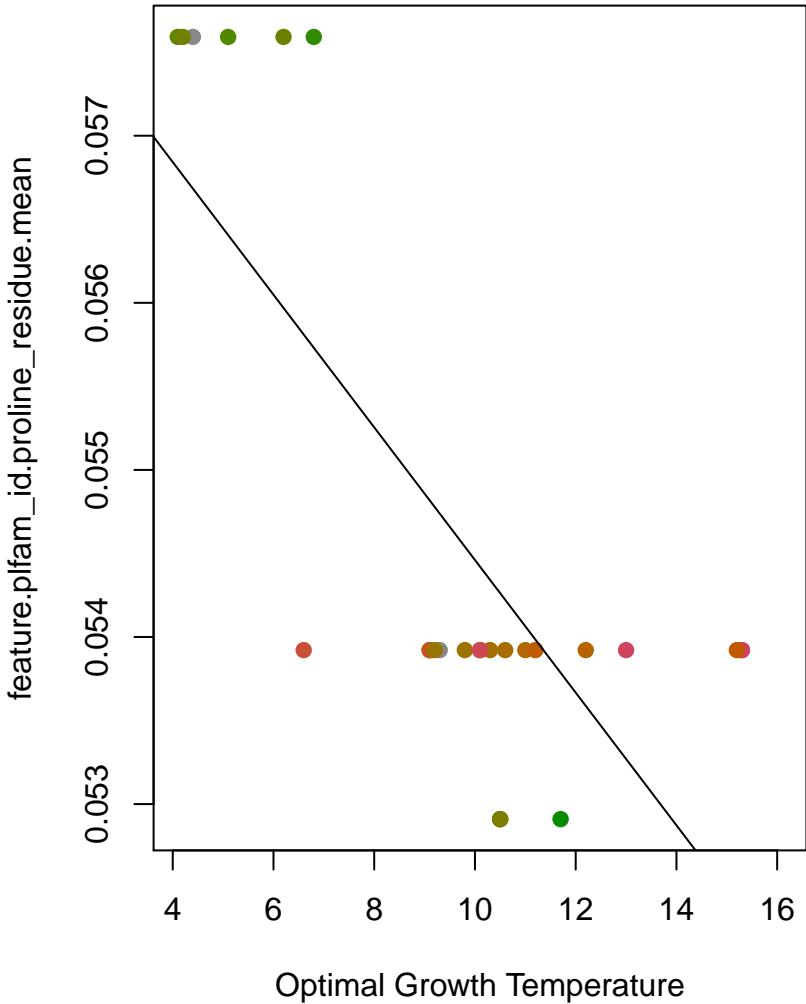


feature.plfam_id.proline_residue.mean
PLF_28228_00011660
Agmatinase (EC 3.5.3.11)
 $r = -0.736$, $p = 10^{-4.908}$

feature.plfam_id.proline_residue.mean

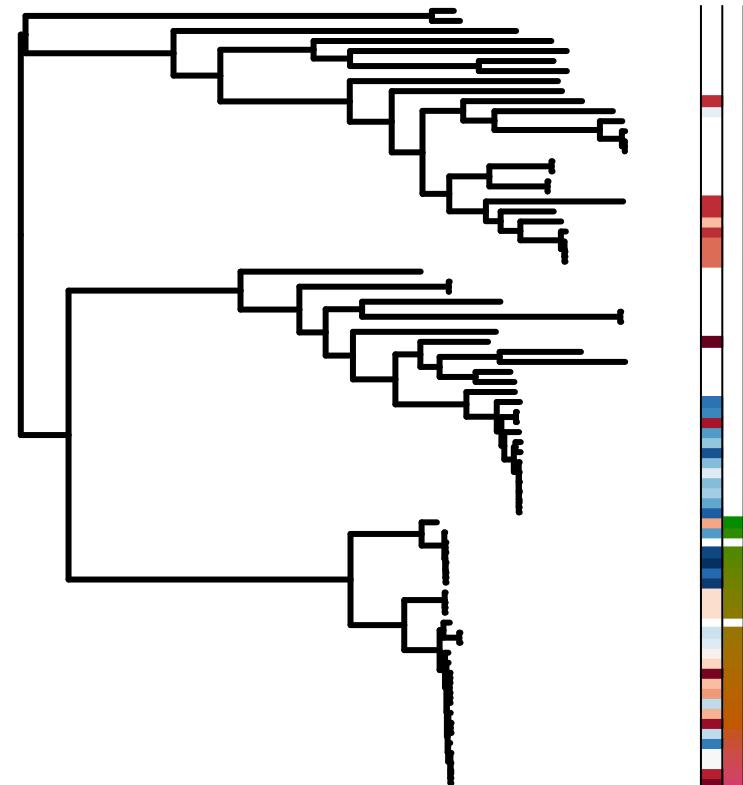
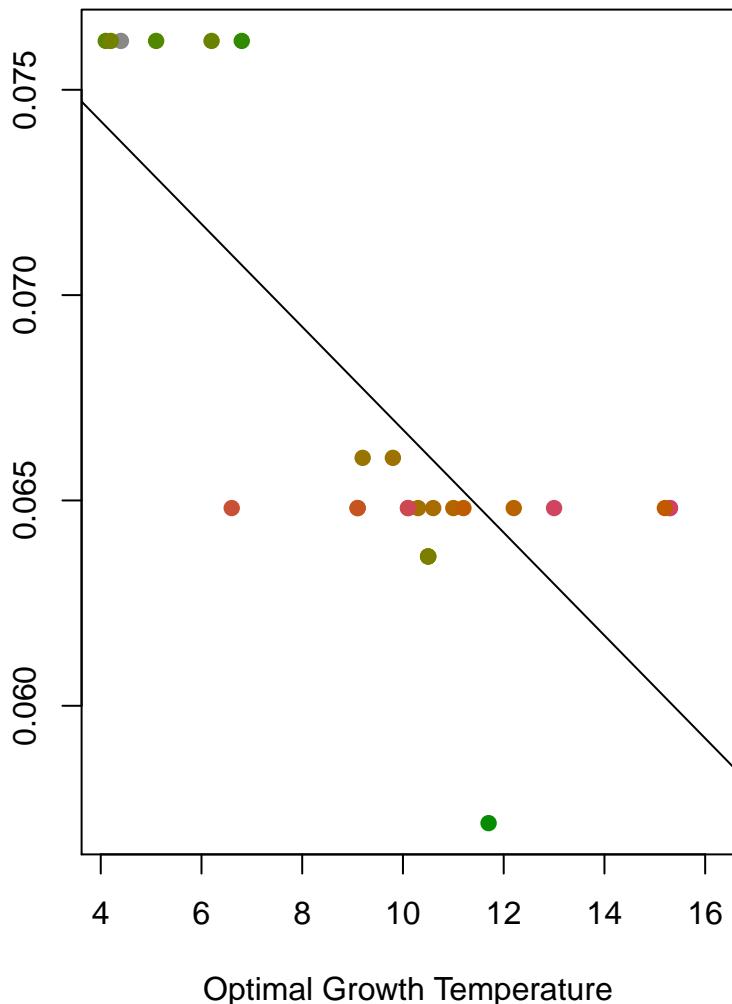


feature.plfam_id.proline_residue.mean
PLF_28228_00007320
Arylesterase precursor (EC 3.1.1.2)
 $r = -0.755, p = 10^{-5.267}$



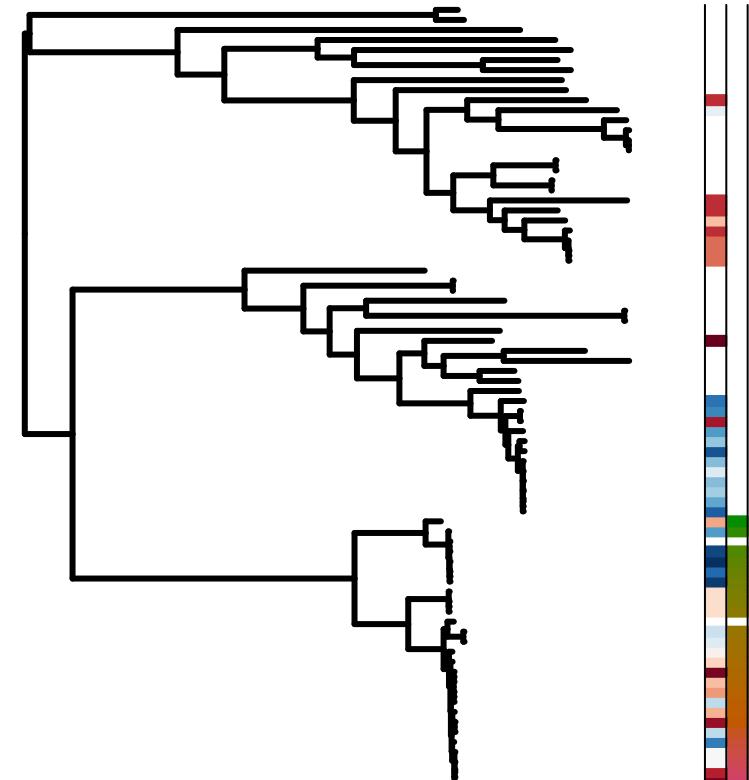
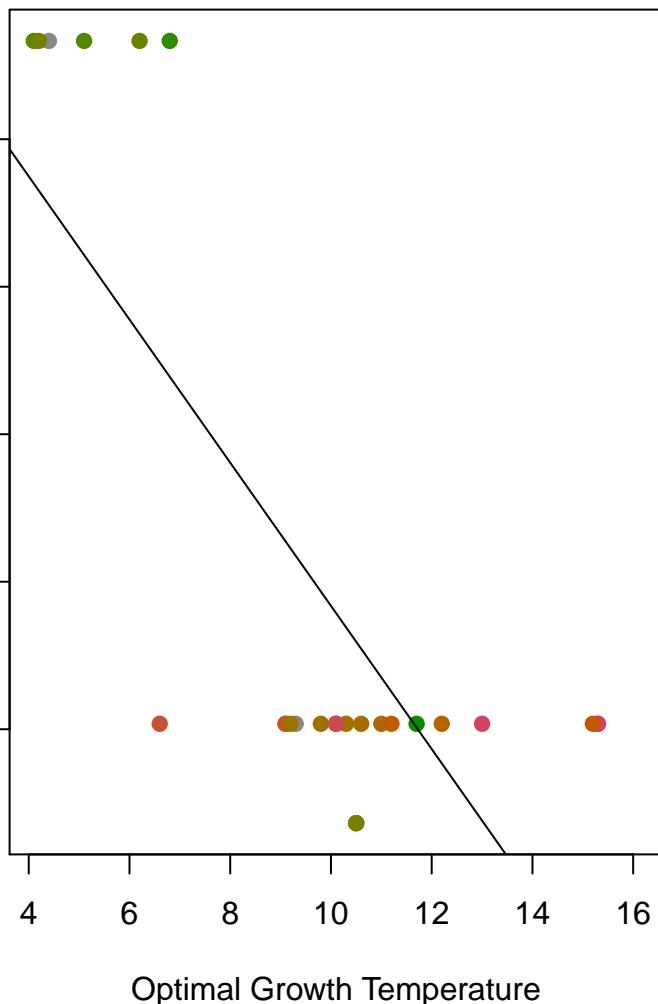
feature.plfam_id.proline_residue.mean
PLF_28228_00016690
hypothetical protein
 $r = -0.765$, $p = 10^{-5.276}$

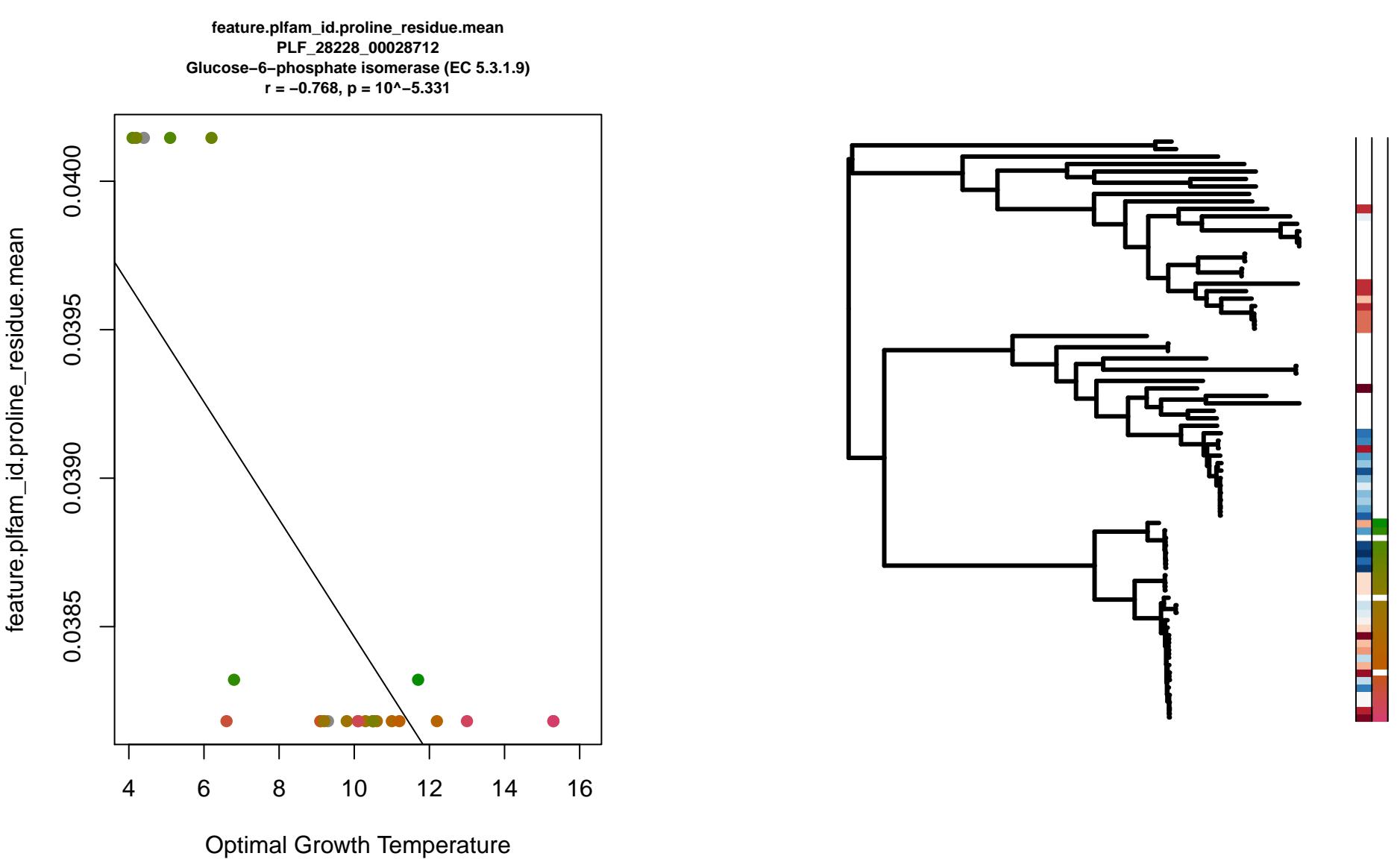
feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00031893
hypothetical protein
 $r = -0.768$, $p = 10^{-5.53}$

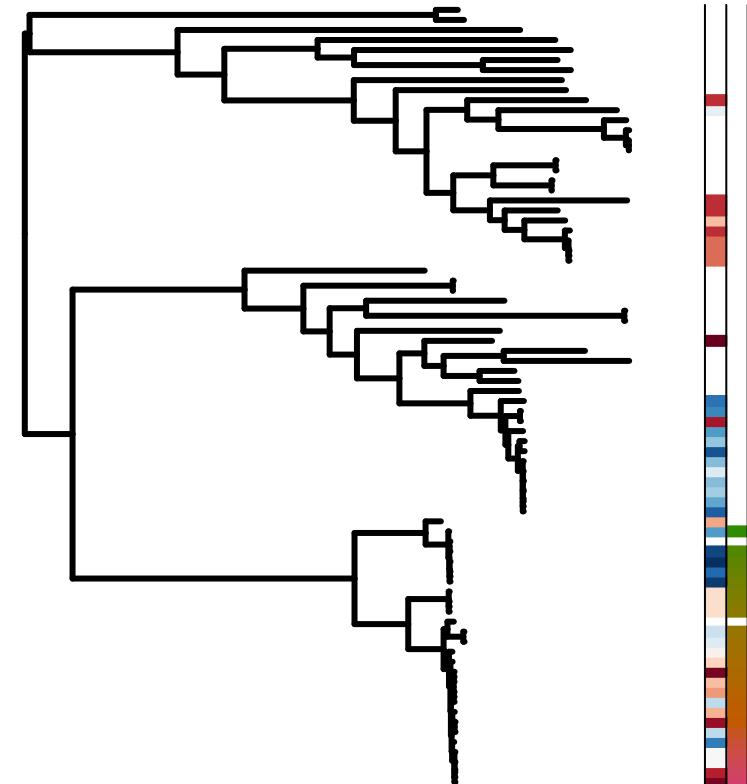
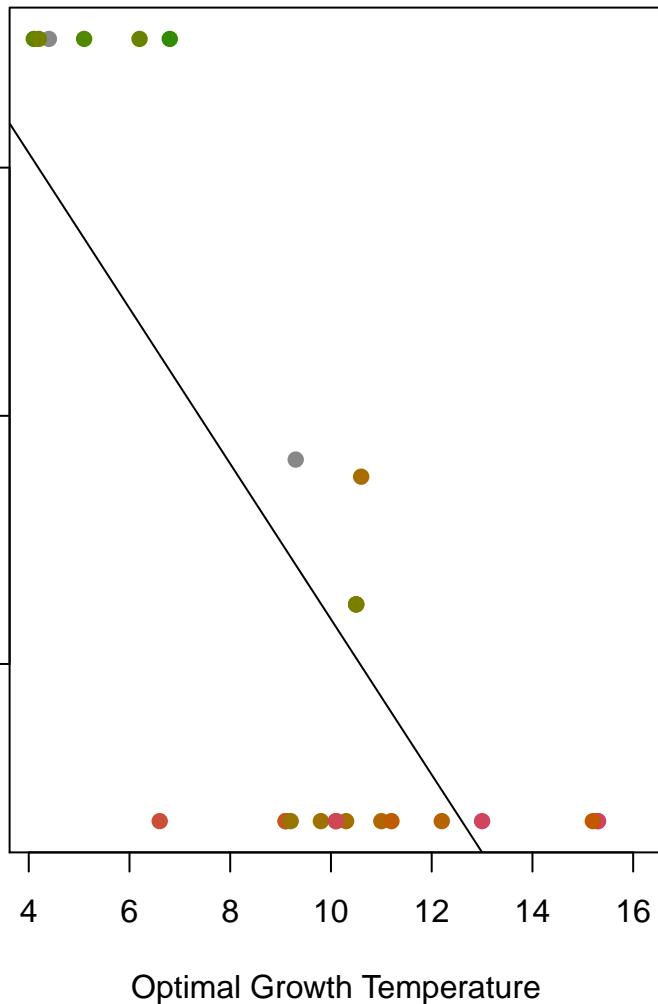
feature.plfam_id.proline_residue.mean





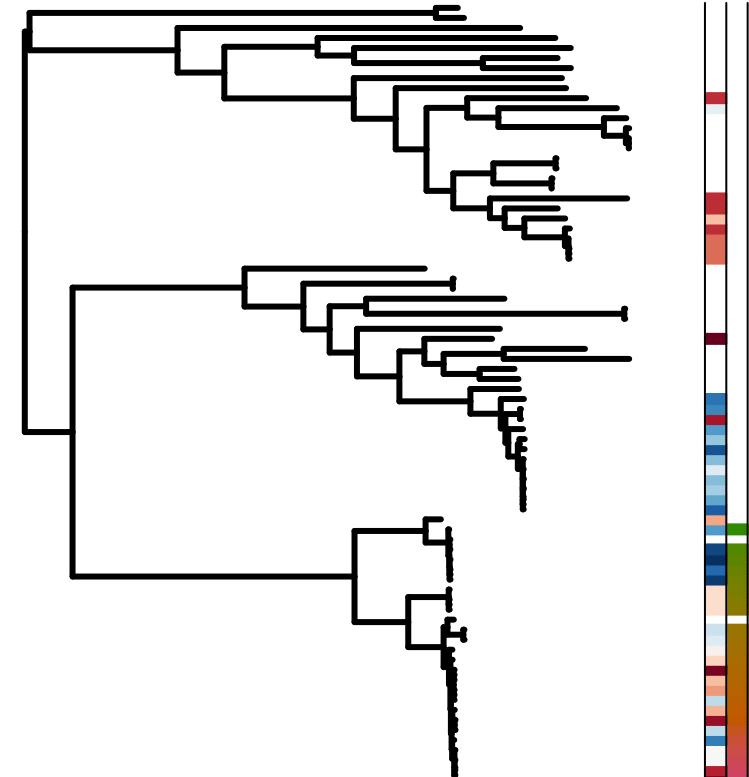
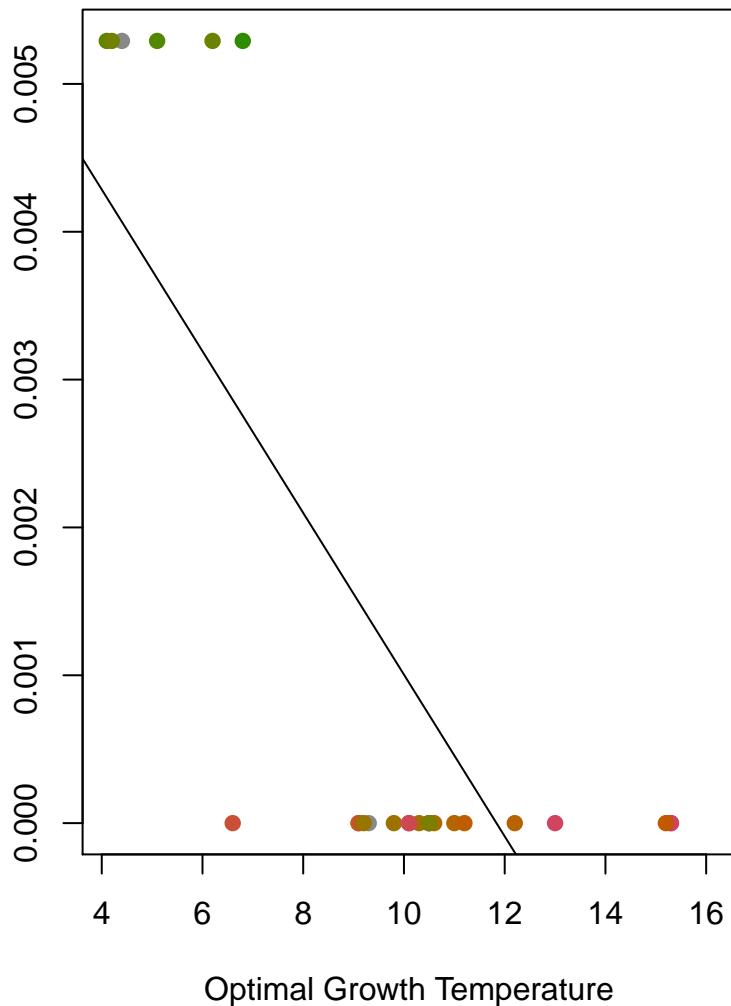
feature.pfam_id.proline_residue.mean
PLF_28228_00015307
hypothetical protein
 $r = -0.768$, $p = 10^{-5.342}$

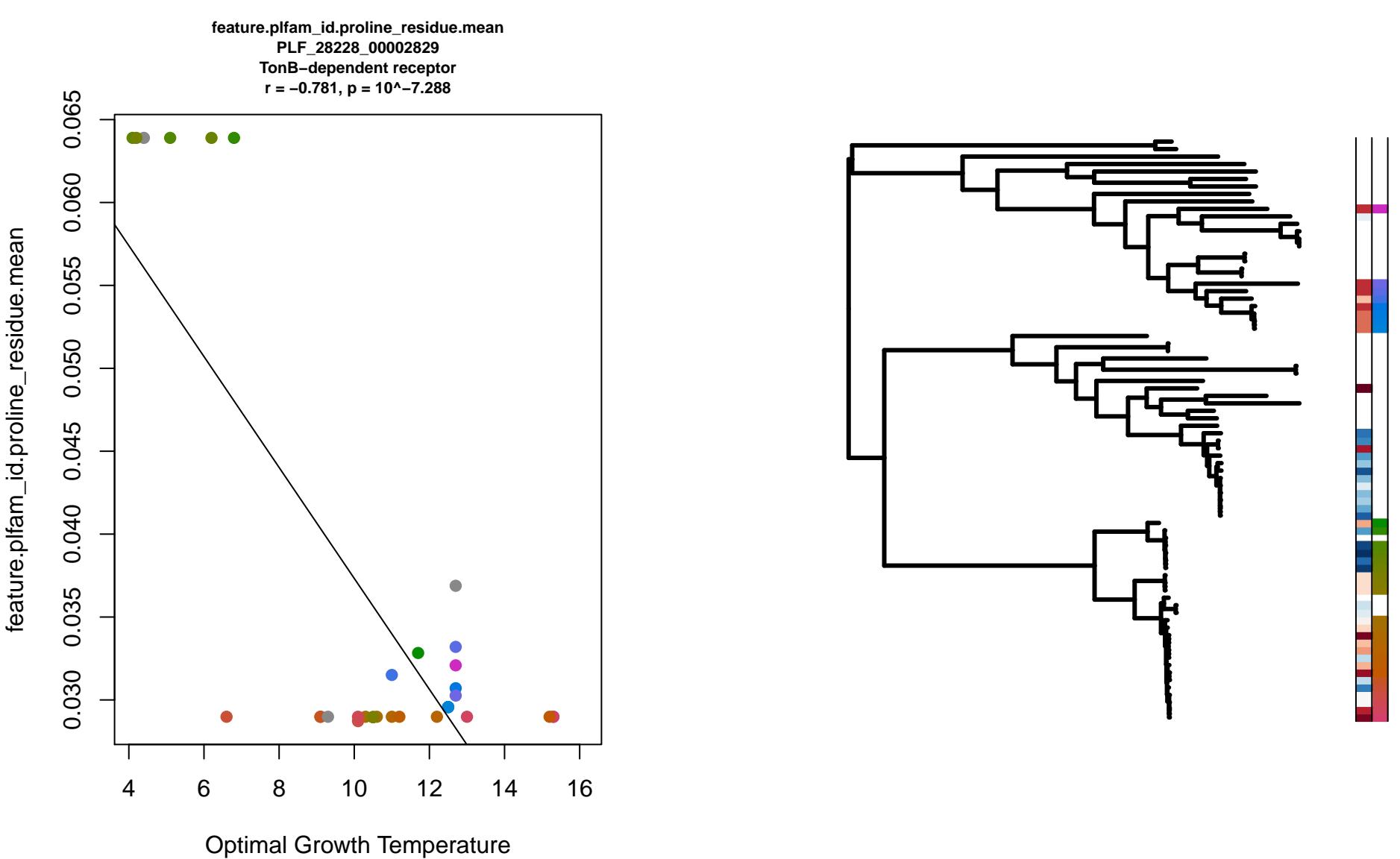
feature.pfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00031666
hypothetical protein
 $r = -0.775$, $p = 10^{-5.478}$

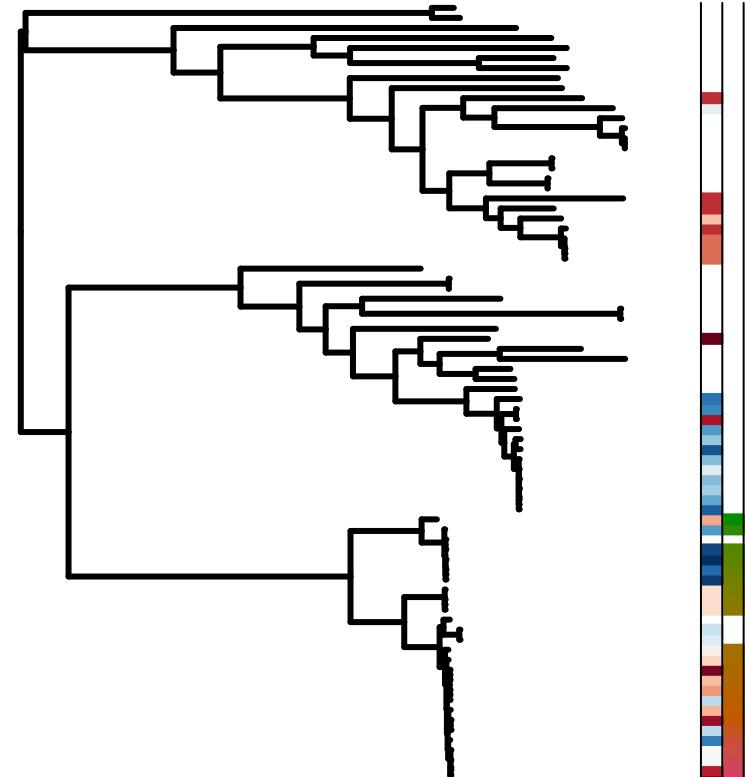
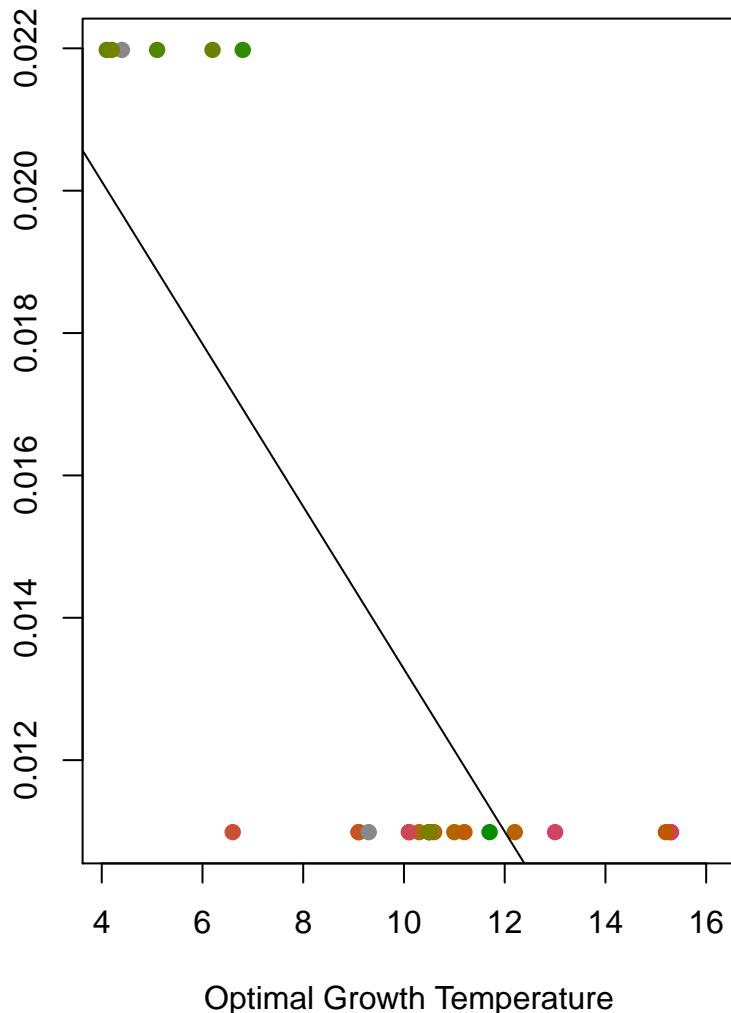
feature.plfam_id.proline_residue.mean





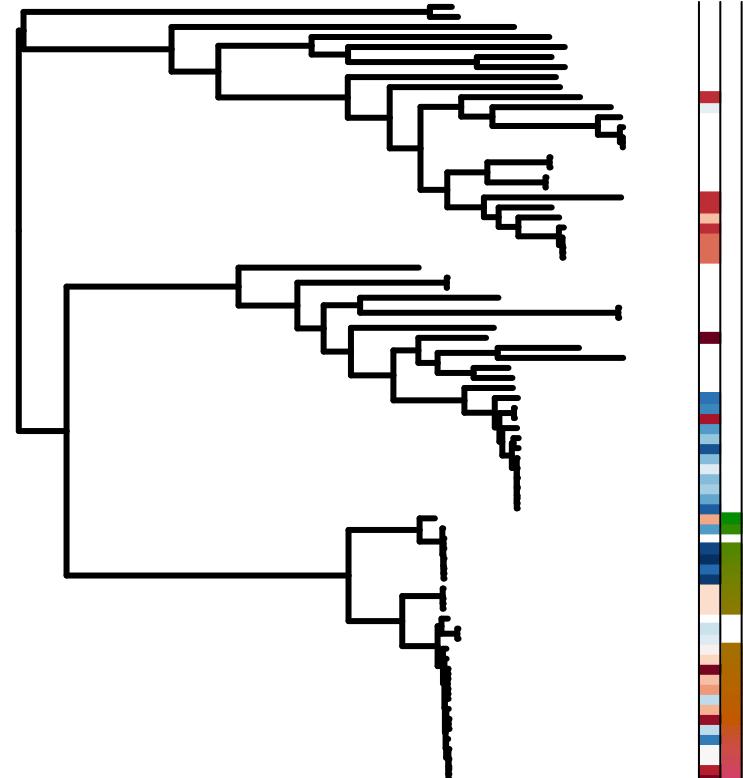
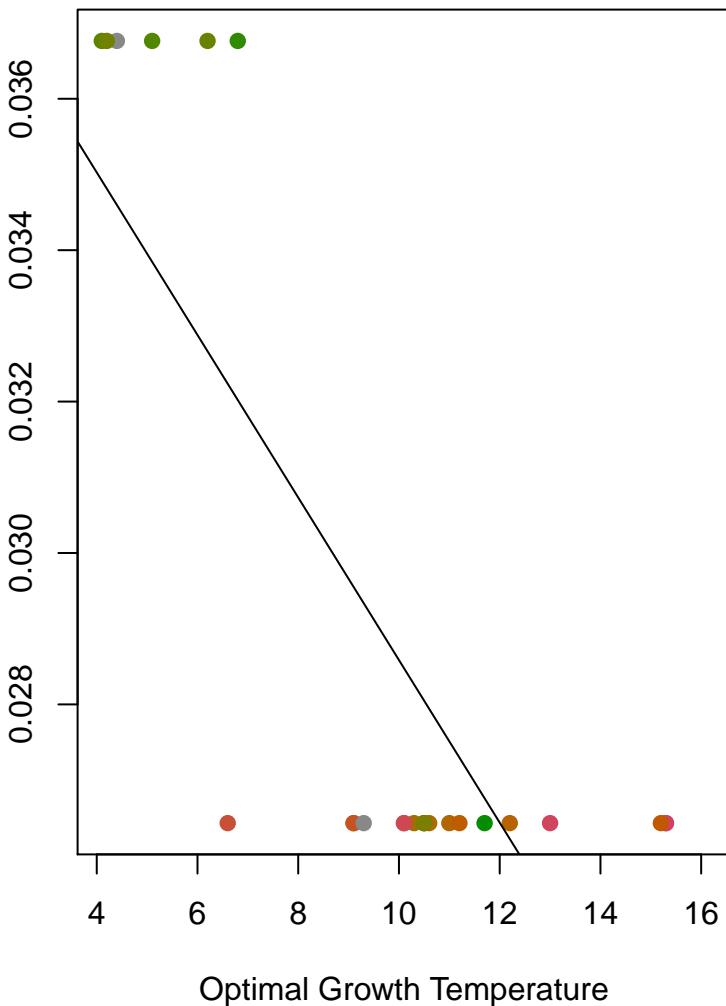
feature.plfam_id.proline_residue.mean
PLF_28228_00029549
hypothetical protein
 $r = -0.79$, $p = 10^{-5.574}$

feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00031467
hypothetical protein
 $r = -0.79$, $p = 10^{-5.574}$

feature.plfam_id.proline_residue.mean



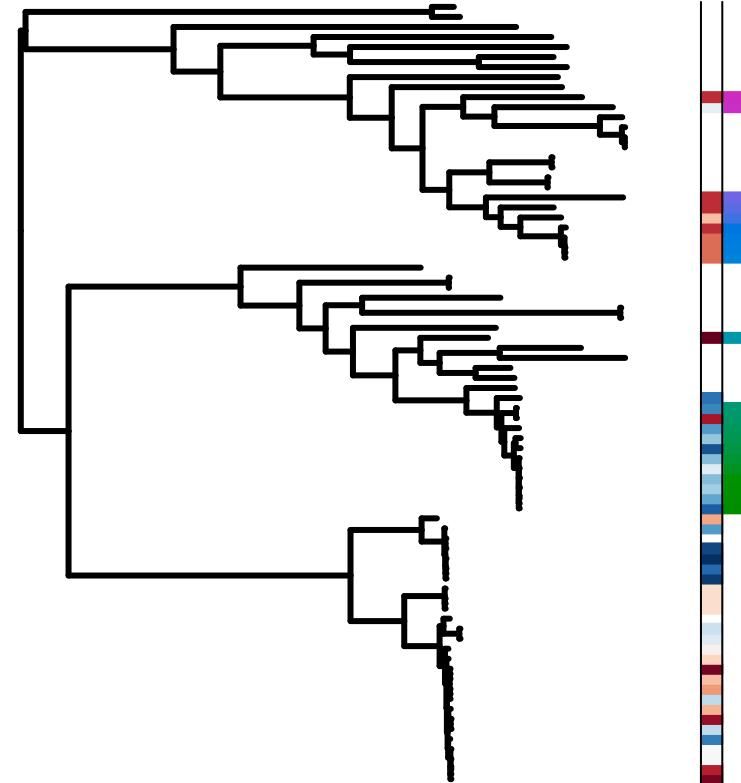
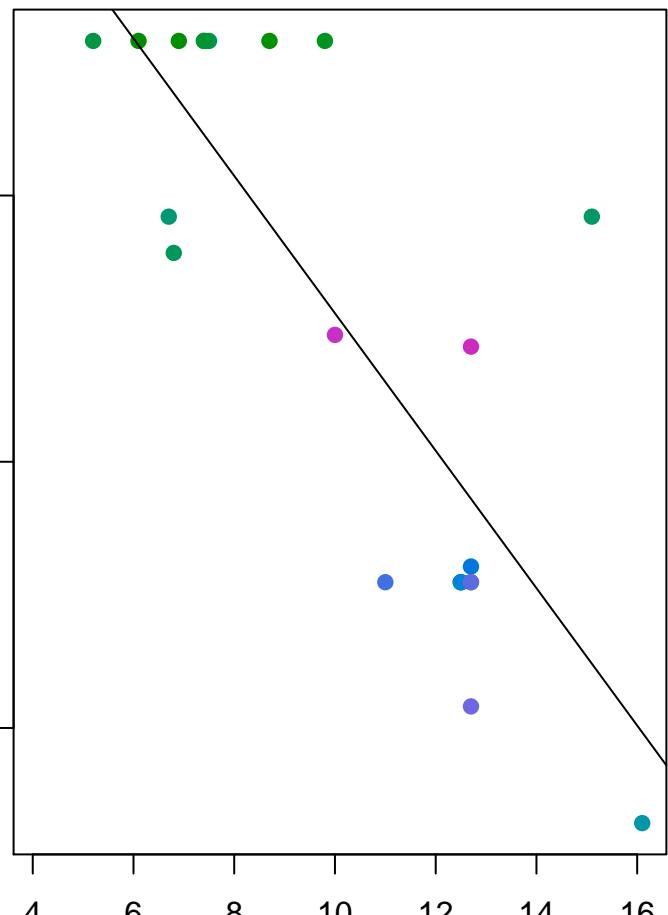
feature.plfam_id.proline_residue.mean

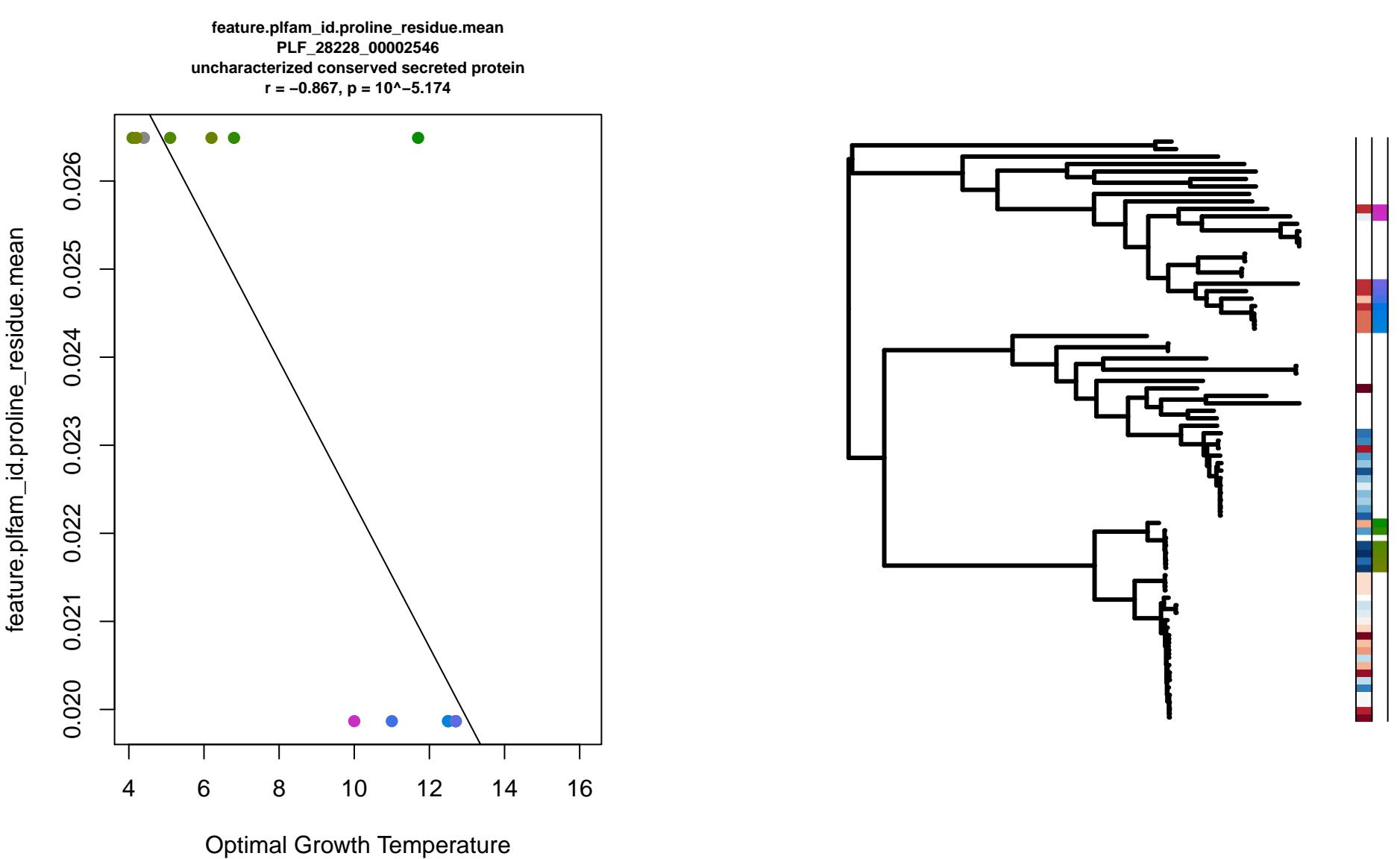
PLF_28228_00002402

ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)

$r = -0.804, p = 10^{-5.18}$

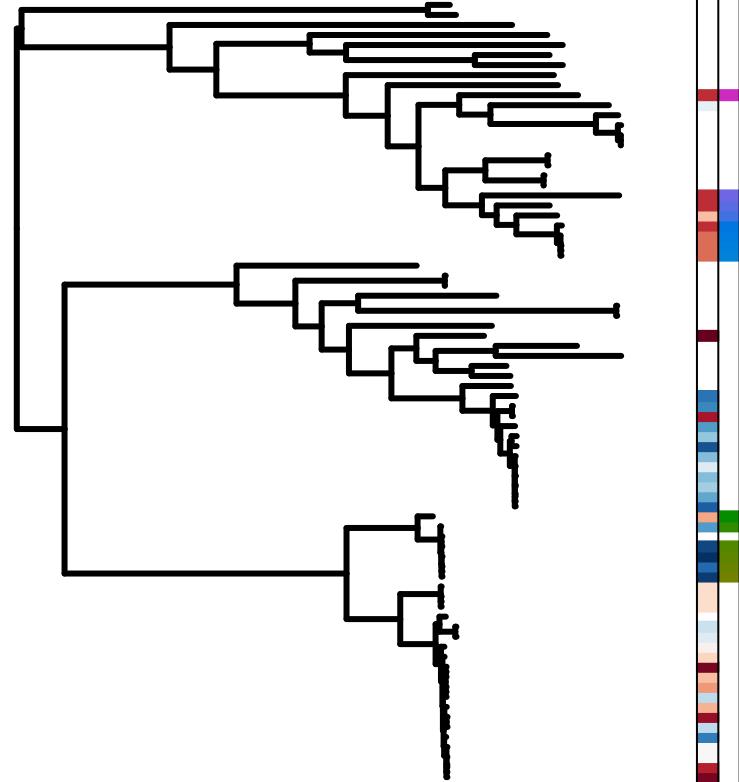
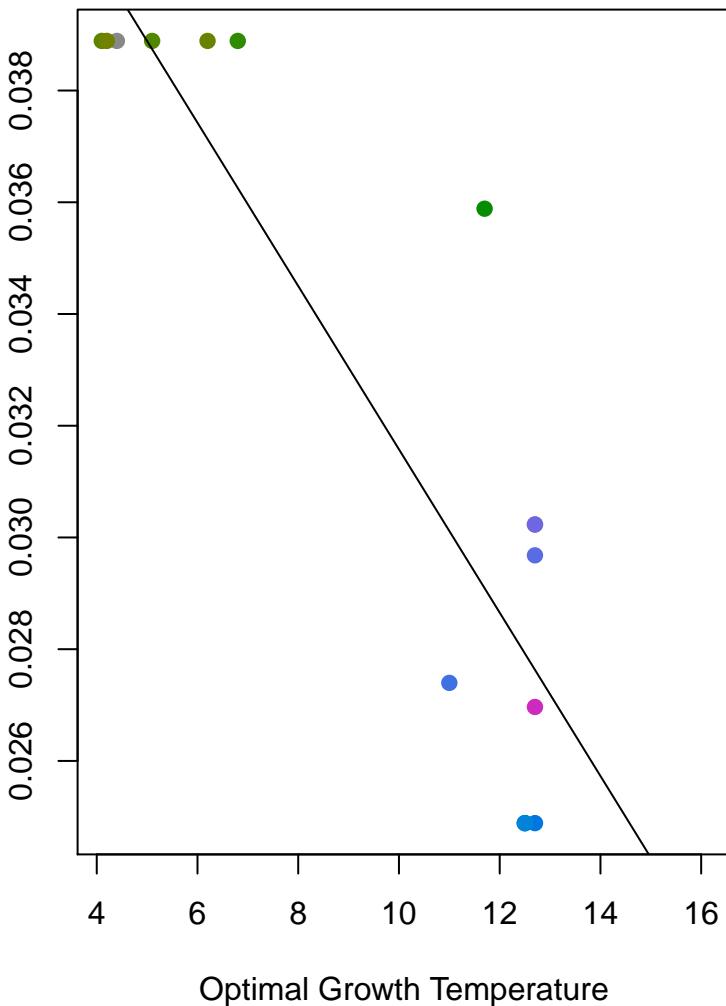
feature.plfam_id.proline_residue.mean





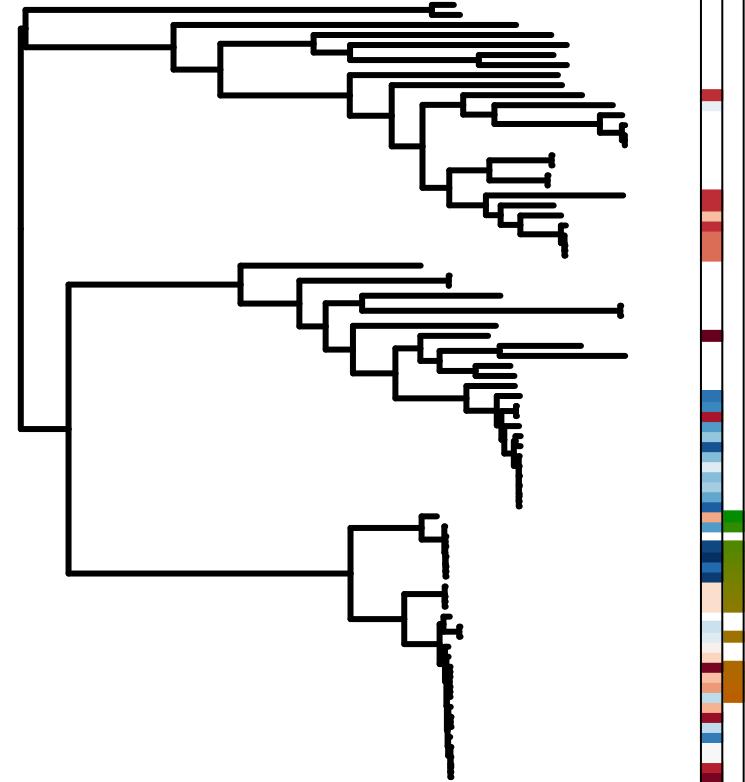
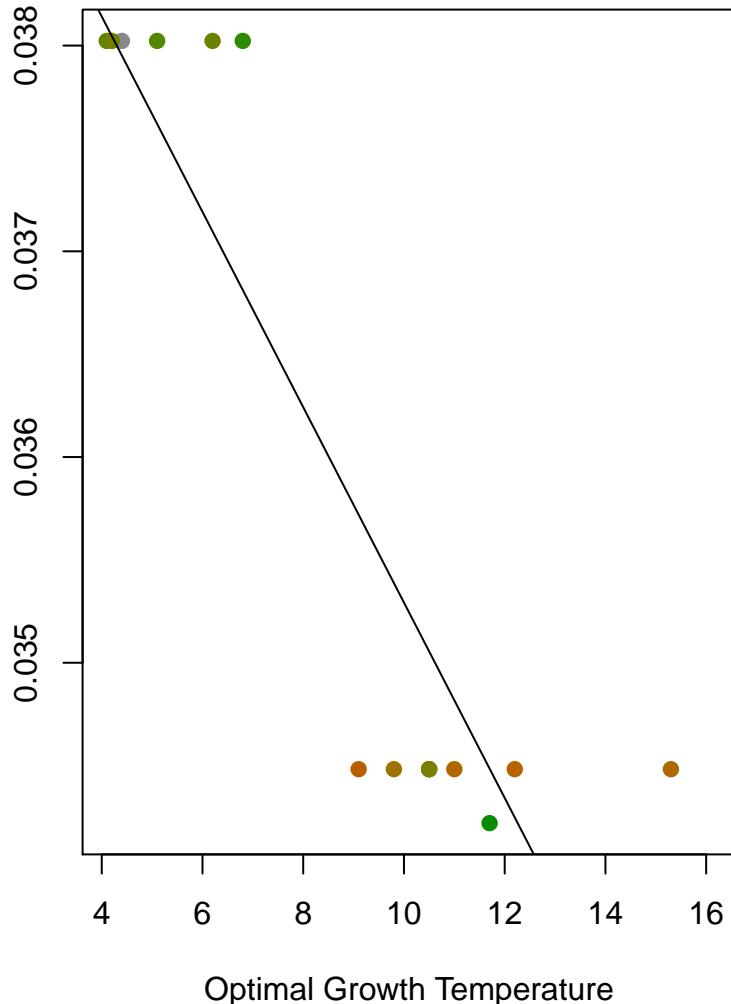
feature.plfam_id.proline_residue.mean
PLF_28228_00002761
Uncharacterized MFS-type transporter
 $r = -0.886$, $p = 10^{-5.298}$

feature.plfam_id.proline_residue.mean



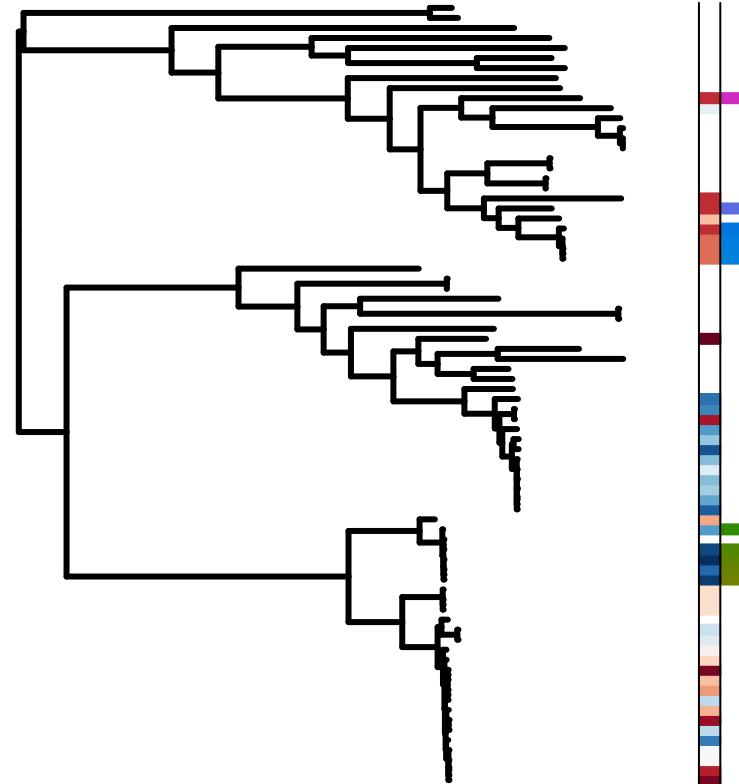
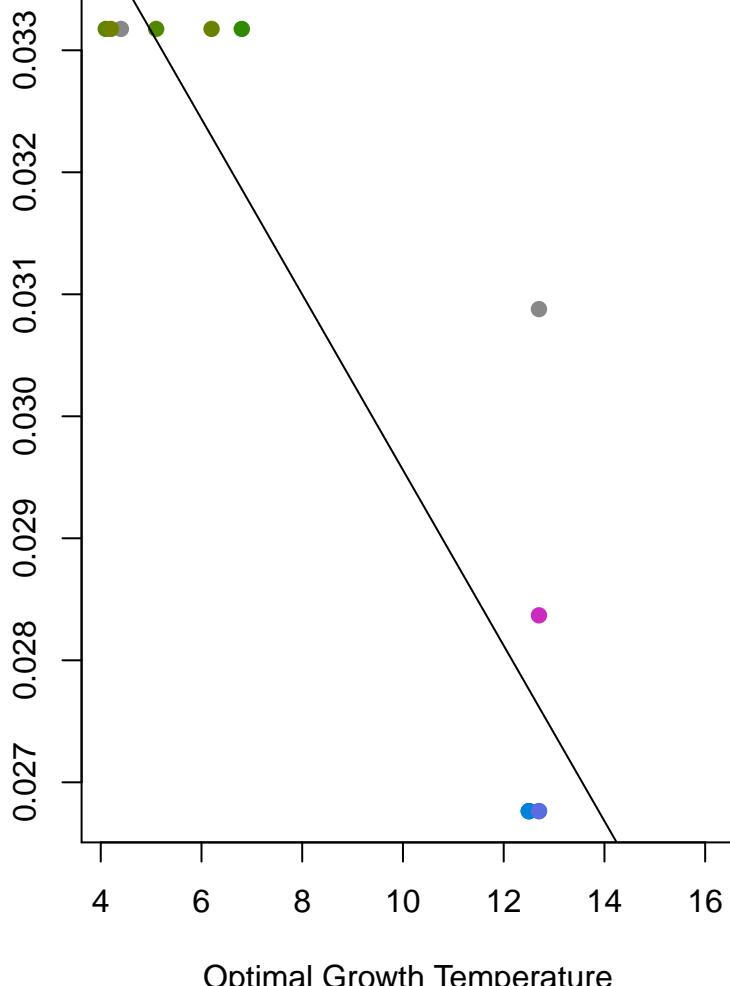
feature.plfam_id.proline_residue.mean
PLF_28228_00024614
hypothetical protein
 $r = -0.897$, $p = 10^{-5.23}$

feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00003595
hypothetical protein
 $r = -0.914$, $p = 10^{-4.913}$

feature.plfam_id.proline_residue.mean

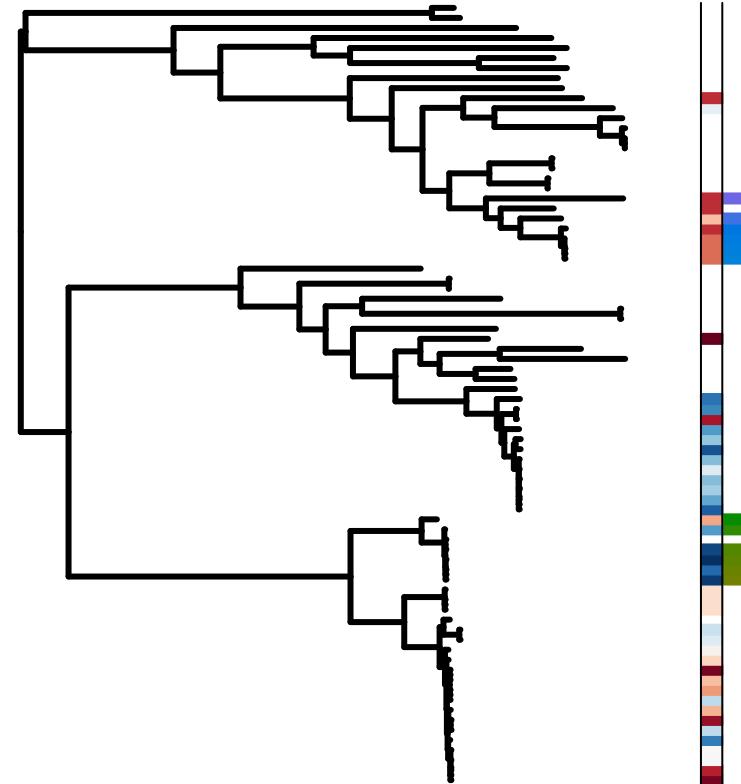
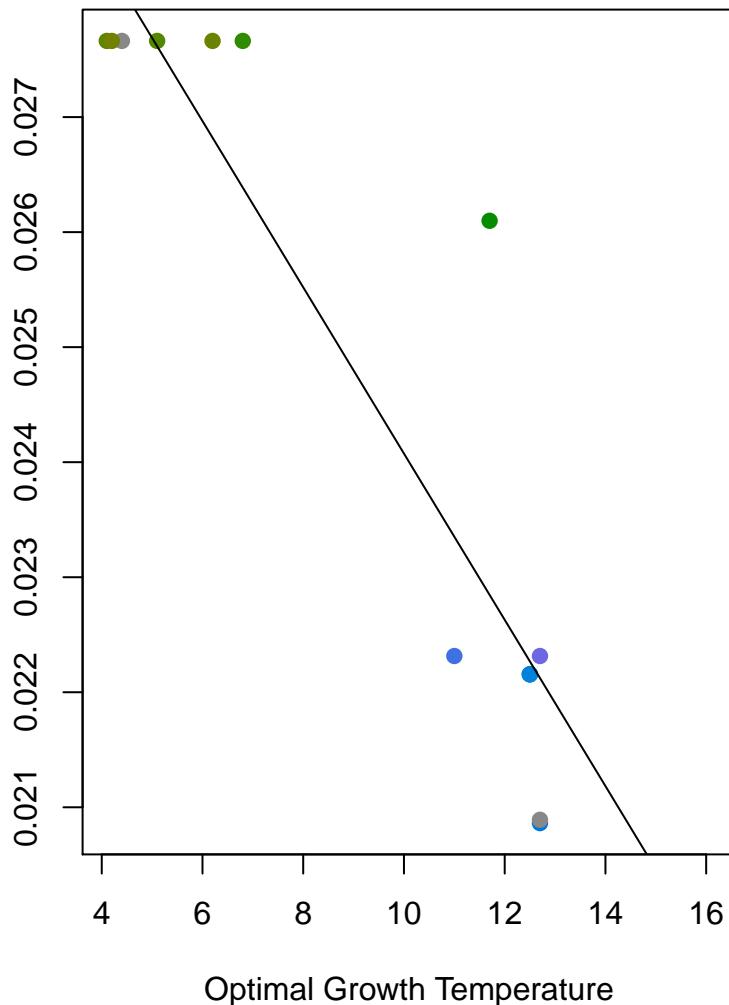


feature.plfam_id.proline_residue.mean

PLF_28228_00003654

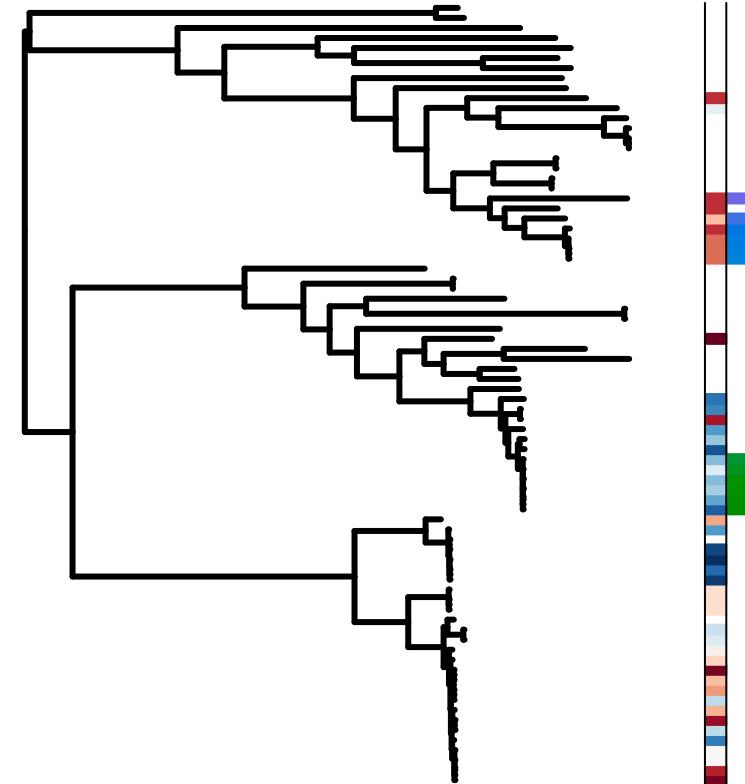
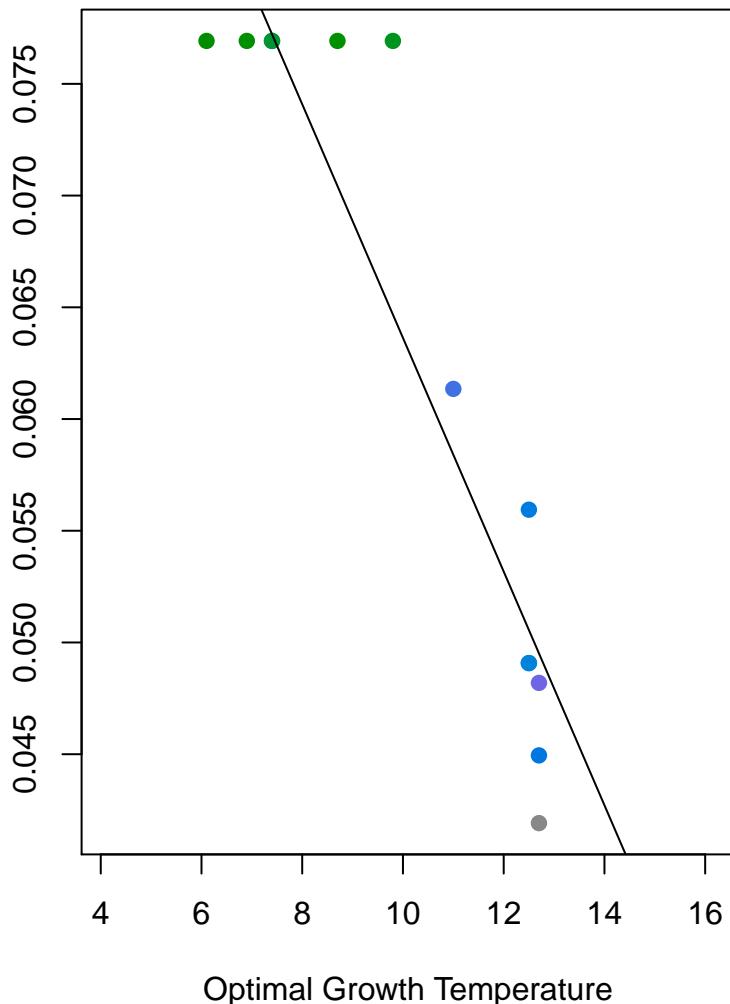
Sensory box sensor/GGDEF/EAL domain protein

$r = -0.917, p = 10^{-5.408}$



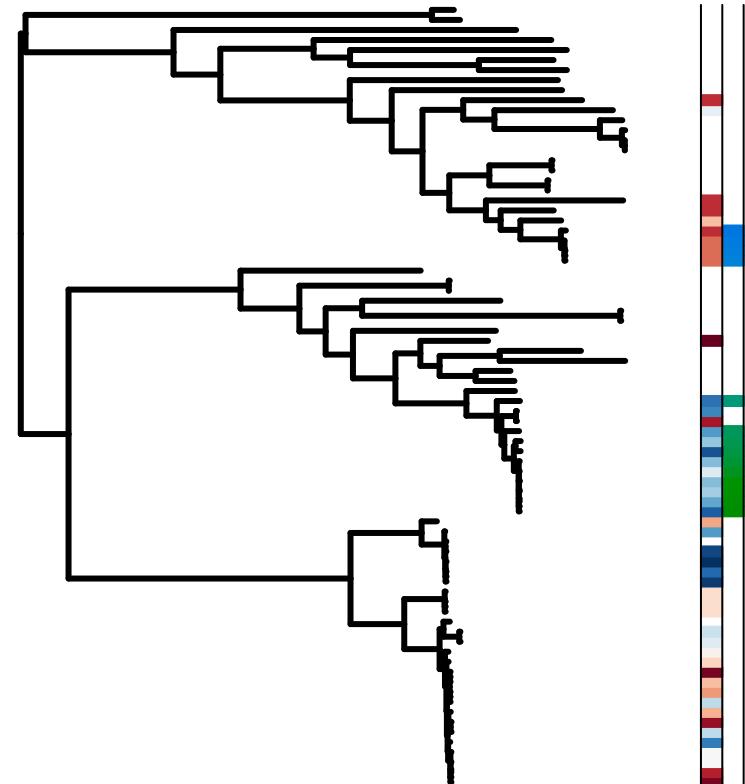
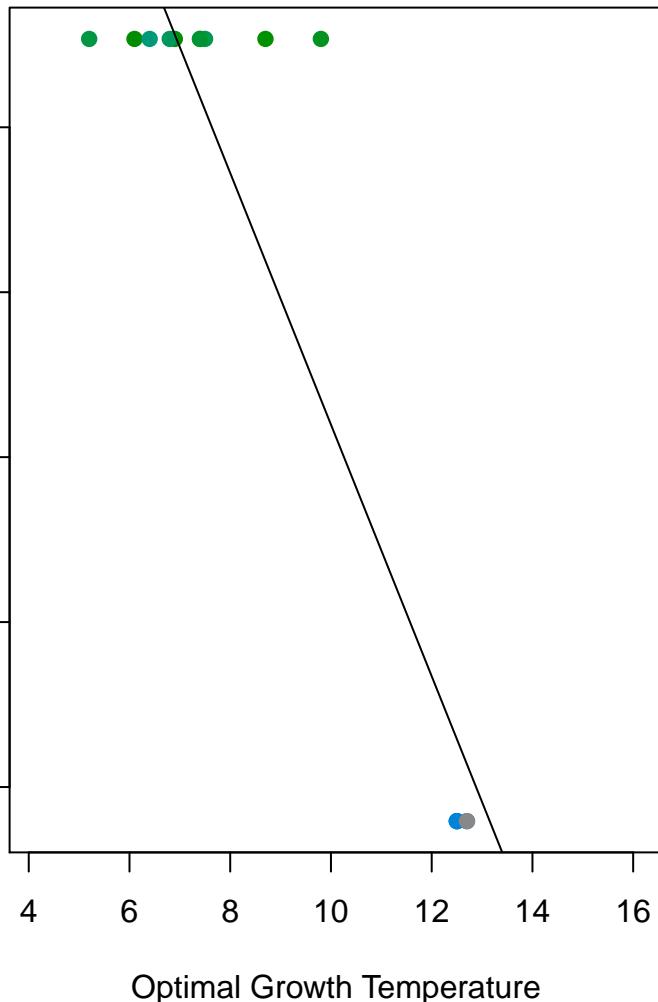
feature.plfam_id.proline_residue.mean
PLF_28228_00002635
Glyoxalase family protein
 $r = -0.925$, $p = 10^{-5.224}$

feature.plfam_id.proline_residue.mean



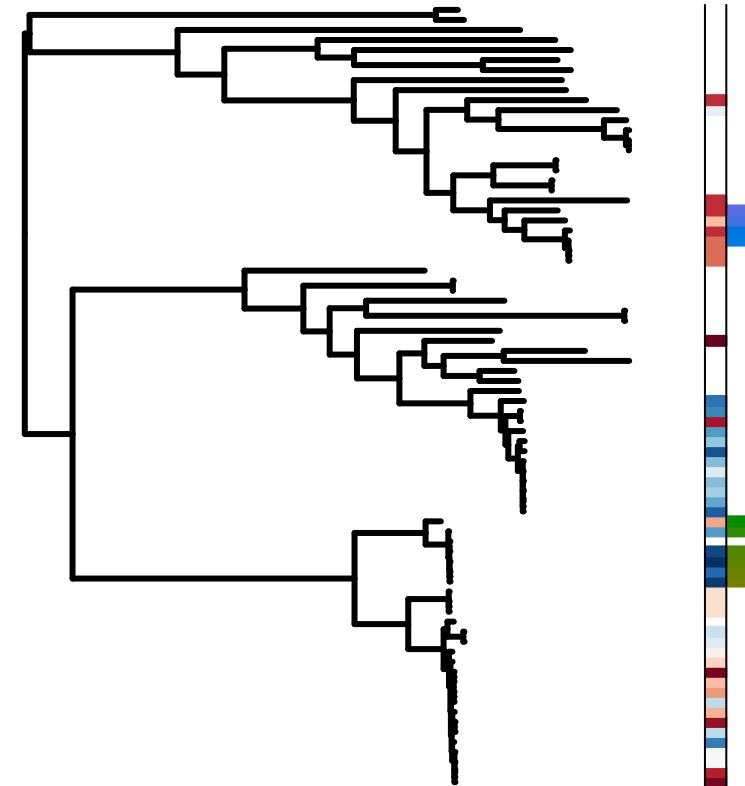
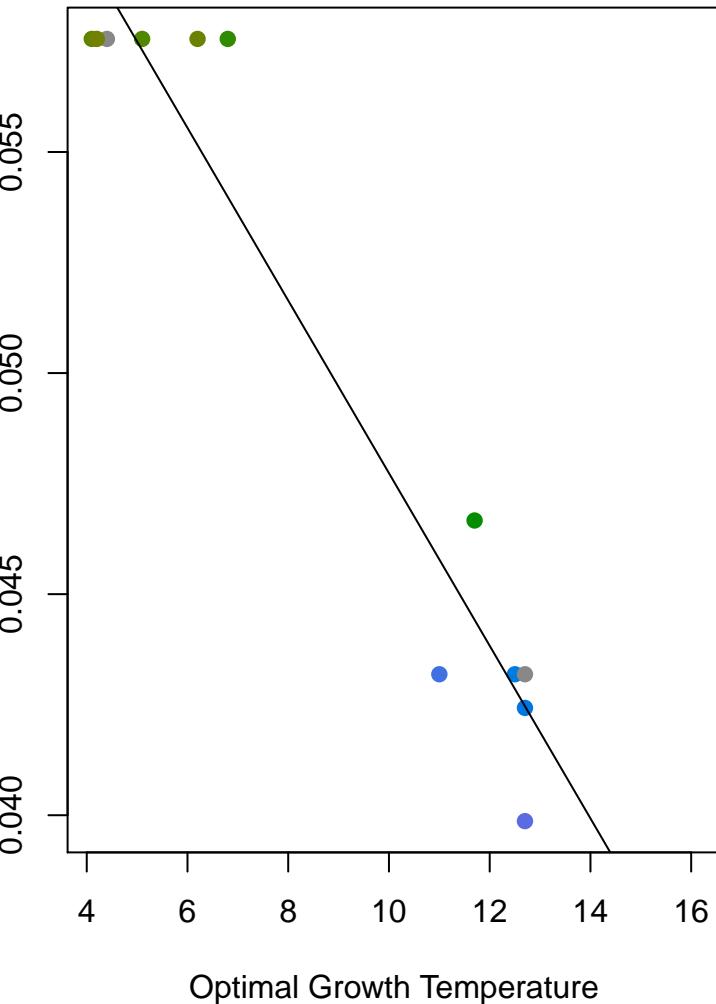
feature.plfam_id.proline_residue.mean
PLF_28228_00007378
SapC-like S-layer protein
 $r = -0.928$, $p = 10^{-6.228}$

feature.plfam_id.proline_residue.mean

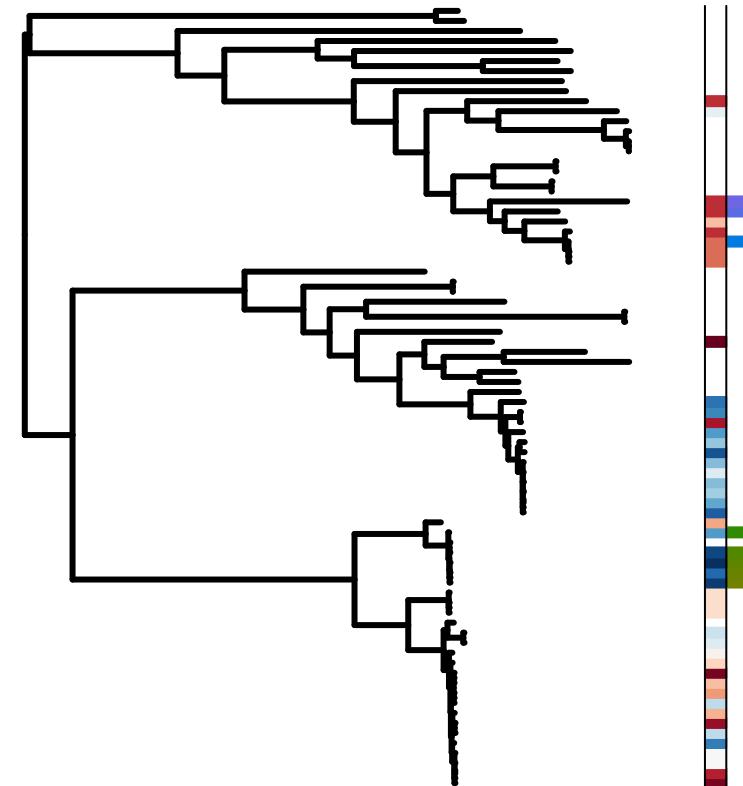
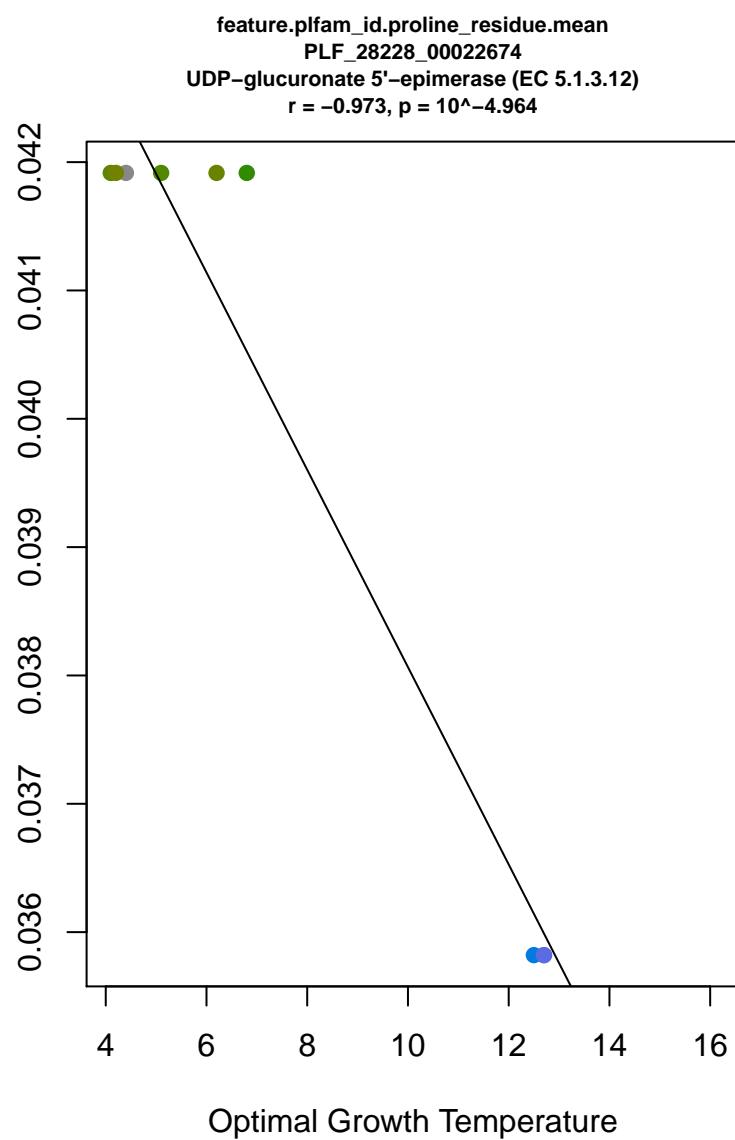


feature.pfam_id.proline_residue.mean
PLF_28228_00028314
Transcriptional regulator, LysR family
 $r = -0.966$, $p = 10^{-6.441}$

feature.pfam_id.proline_residue.mean

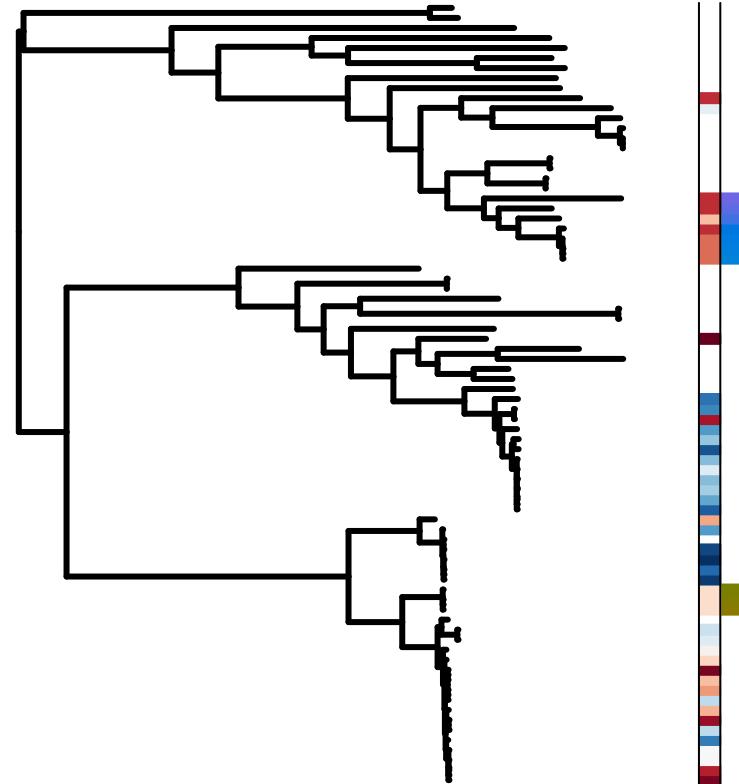
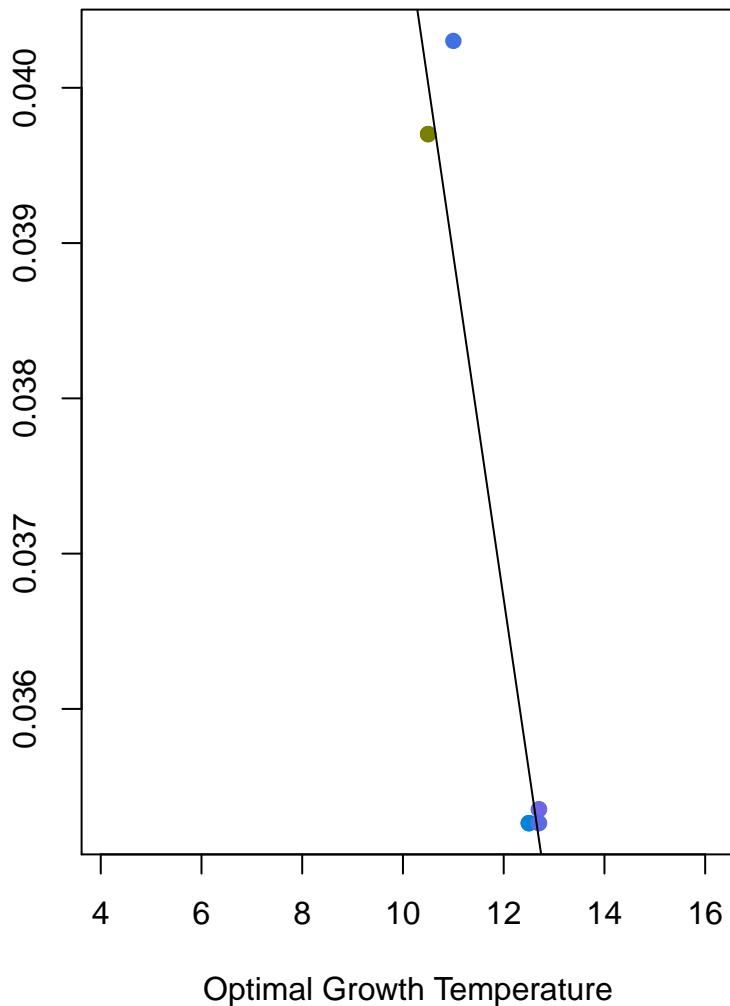


feature.plfam_id.proline_residue.mean
 PLF_28228_00022674
 DP-glucuronate 5'-epimerase (EC 5.1.3.12)
 $r = -0.973$, $p = 10^{-4.964}$



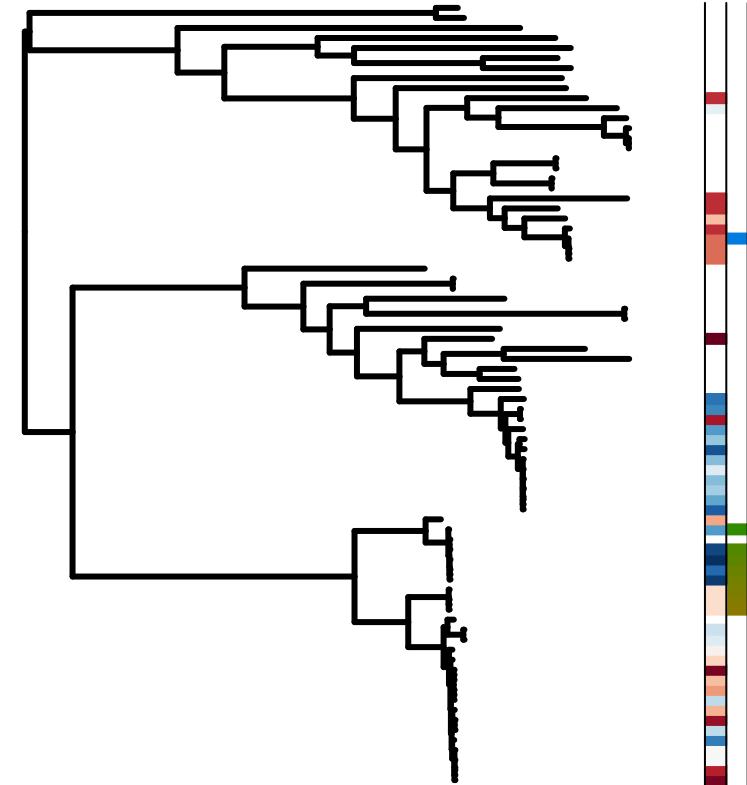
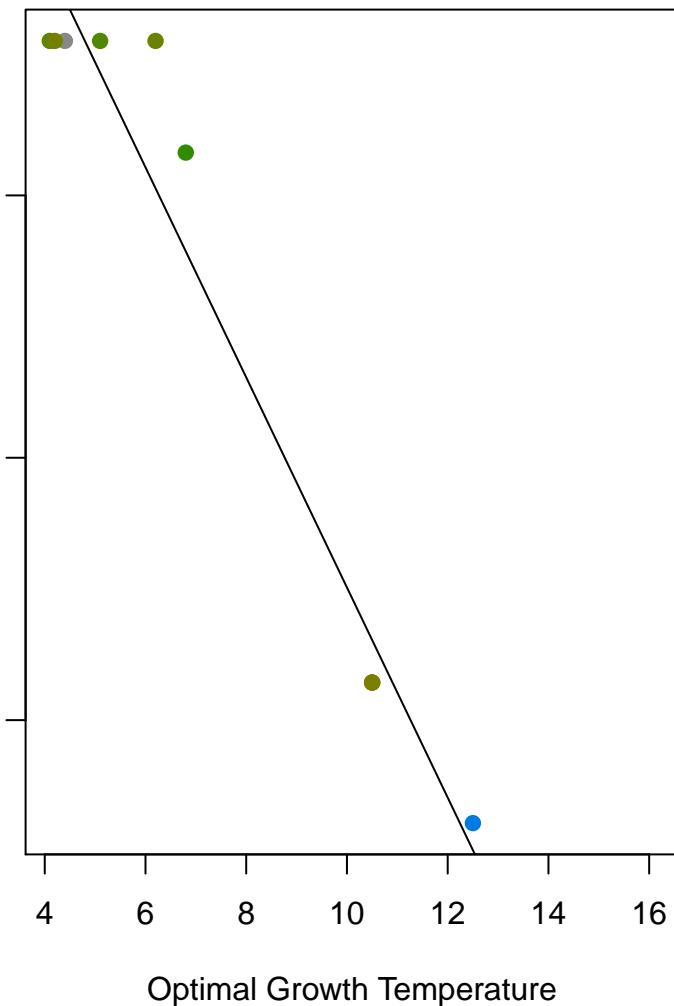
feature.plfam_id.proline_residue.mean
PLF_28228_00003591
Putative response regulator
 $r = -0.975$, $p = 10^{-6.432}$

feature.plfam_id.proline_residue.mean

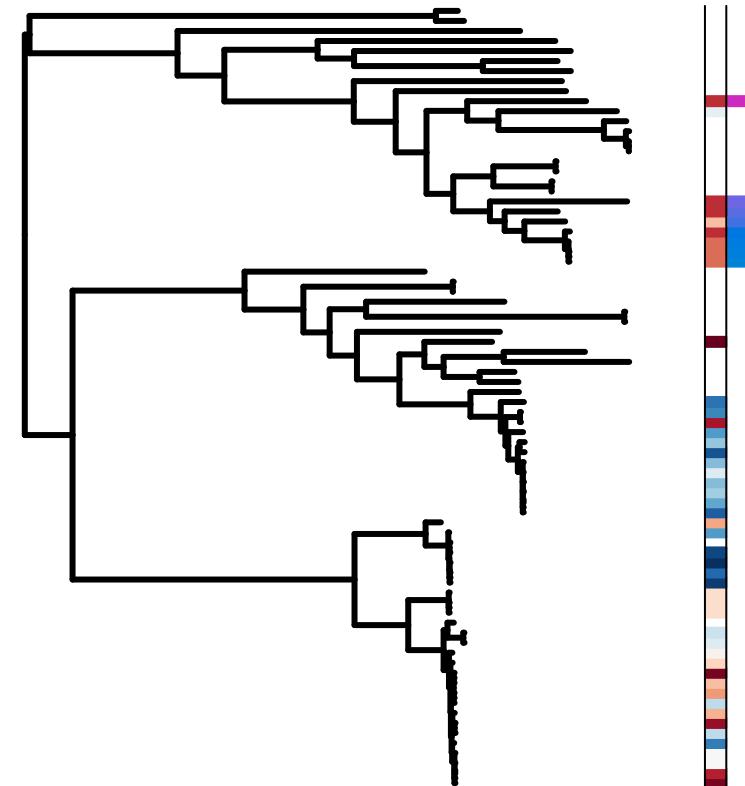
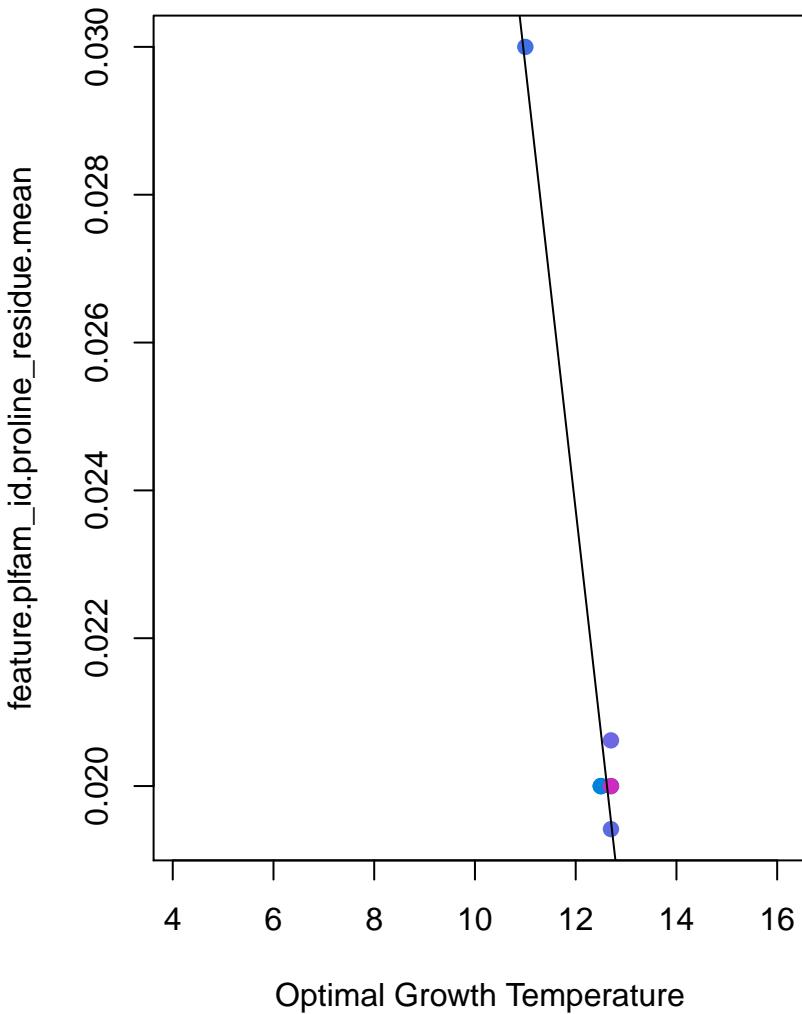


feature.plfam_id.proline_residue.mean
PLF_28228_00023076
Mobile element protein
 $r = -0.976$, $p = 10^{-5.88}$

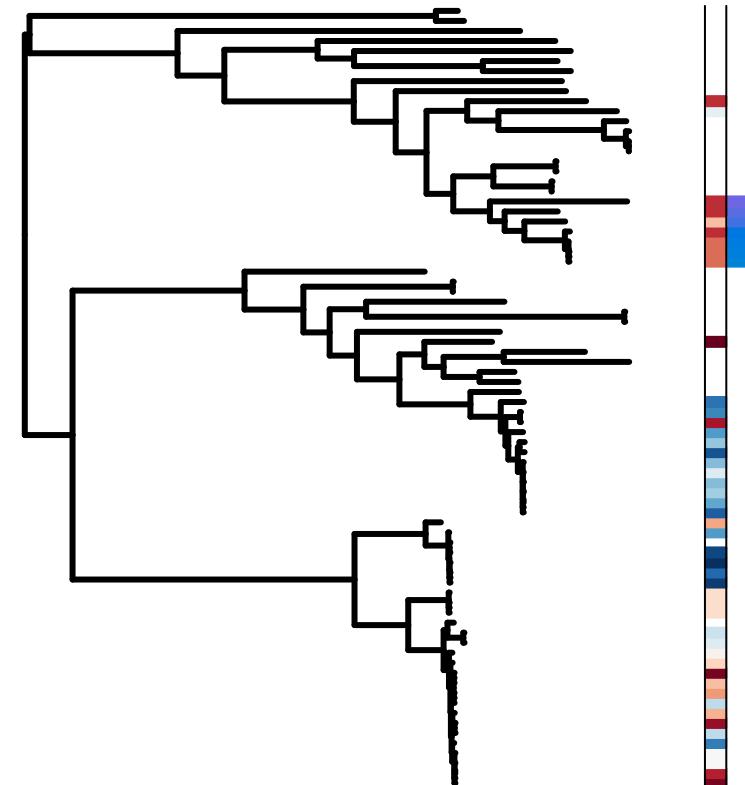
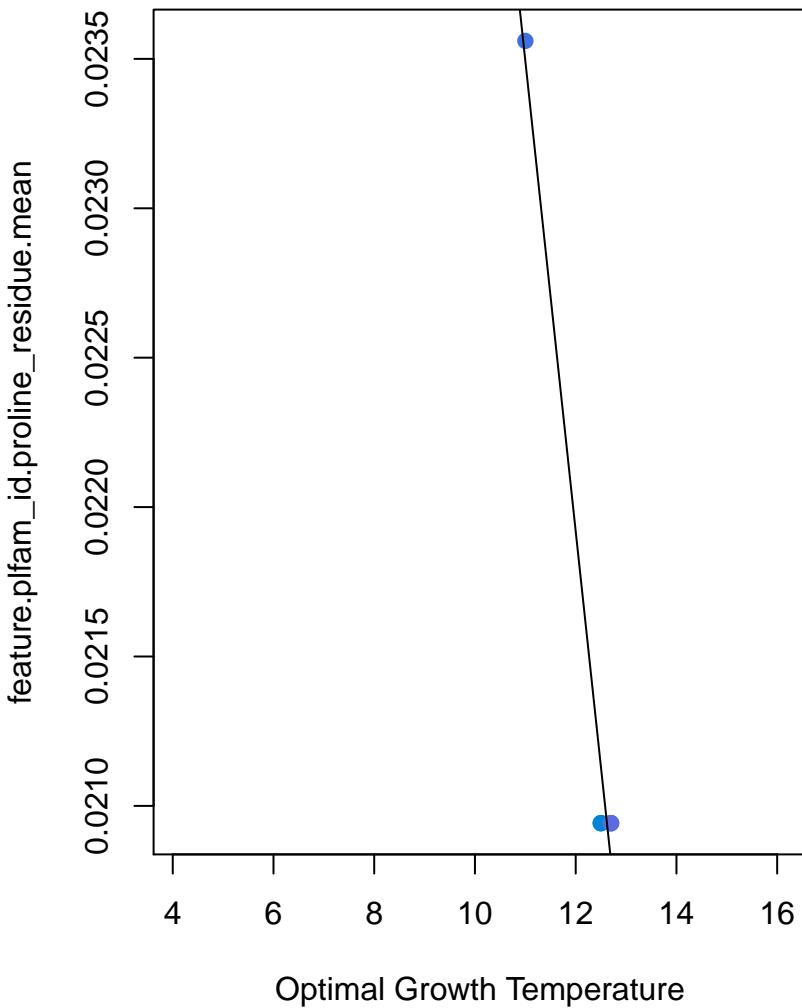
feature.plfam_id.proline_residue.mean



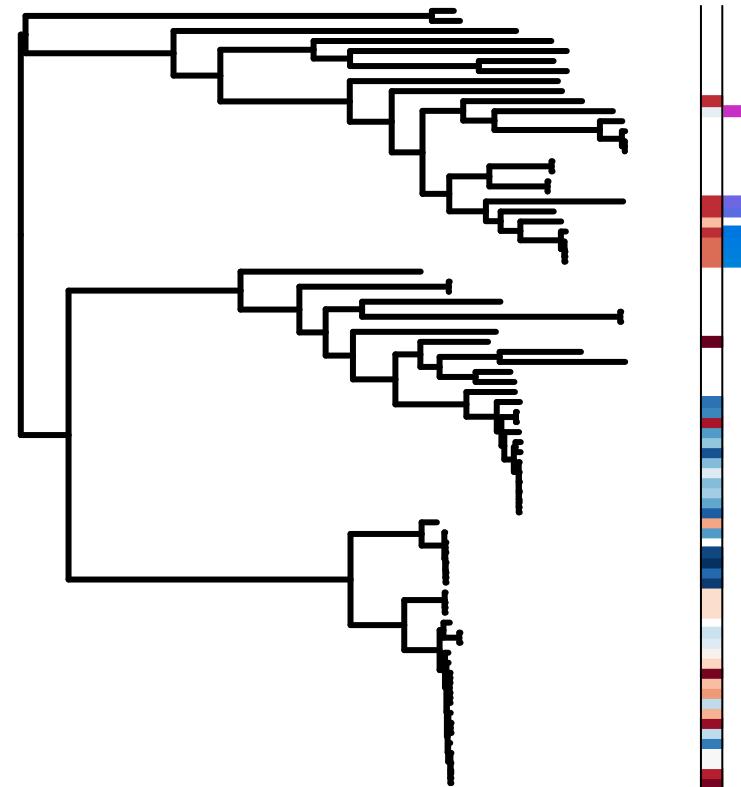
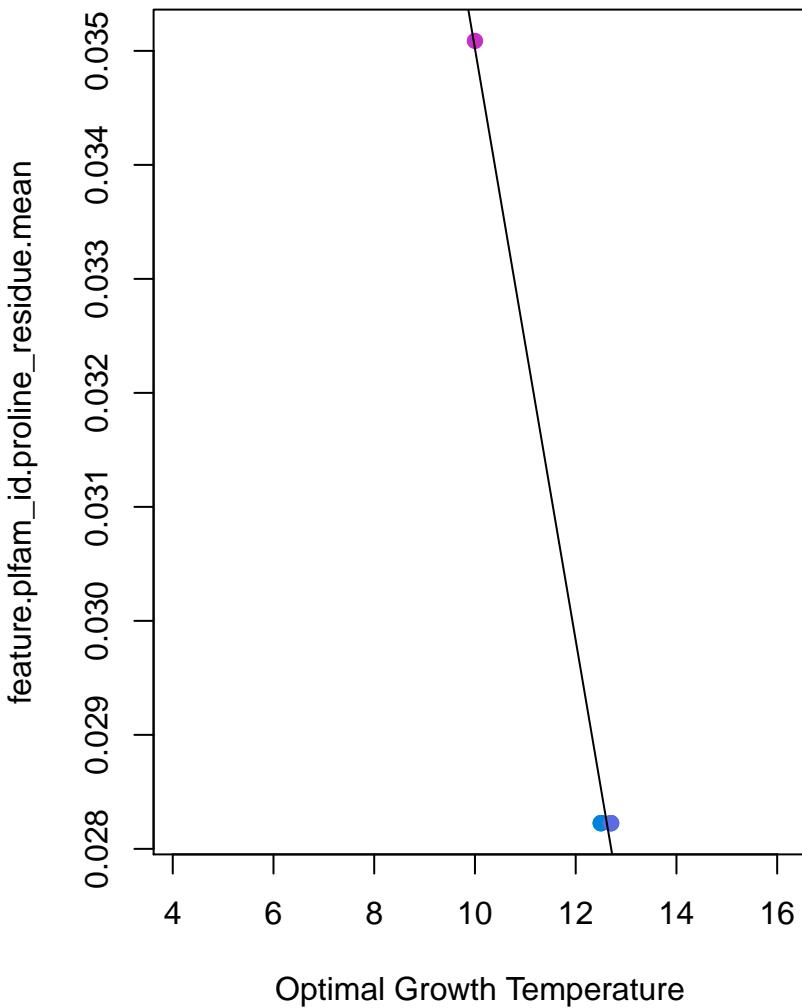
feature.plfam_id.proline_residue.mean
PLF_28228_00002933
hypothetical protein
 $r = -0.981$, $p = 10^{-4.775}$



feature.plfam_id.proline_residue.mean
PLF_28228_00003466
GfdT
 $r = -0.985, p = 10^{-5.104}$

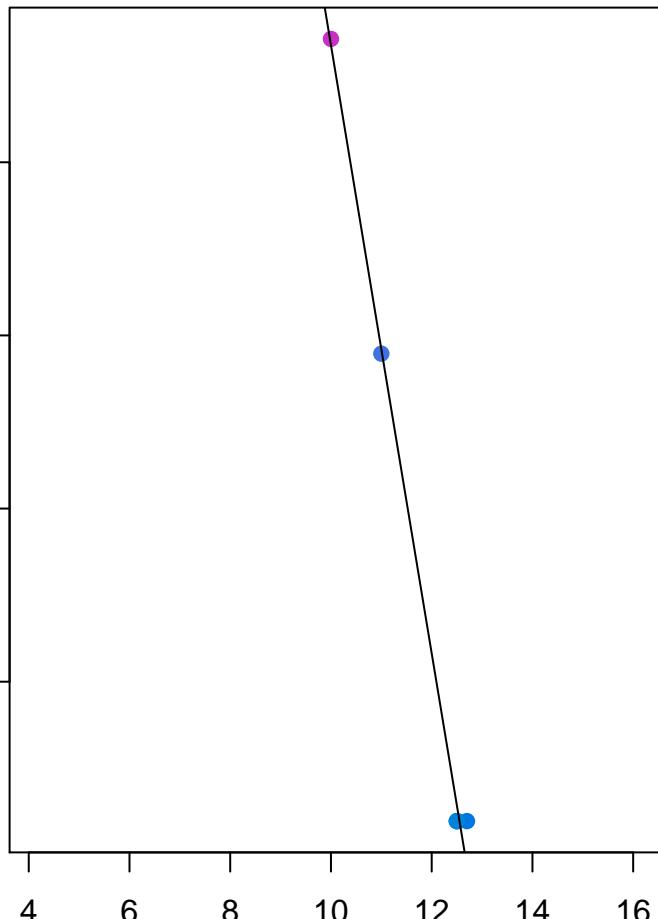


feature.plfam_id.proline_residue.mean
PLF_28228_00002578
Acetoacetyl-CoA reductase (EC 1.1.1.36)
 $r = -0.994$, $p = 10^{-6.34}$

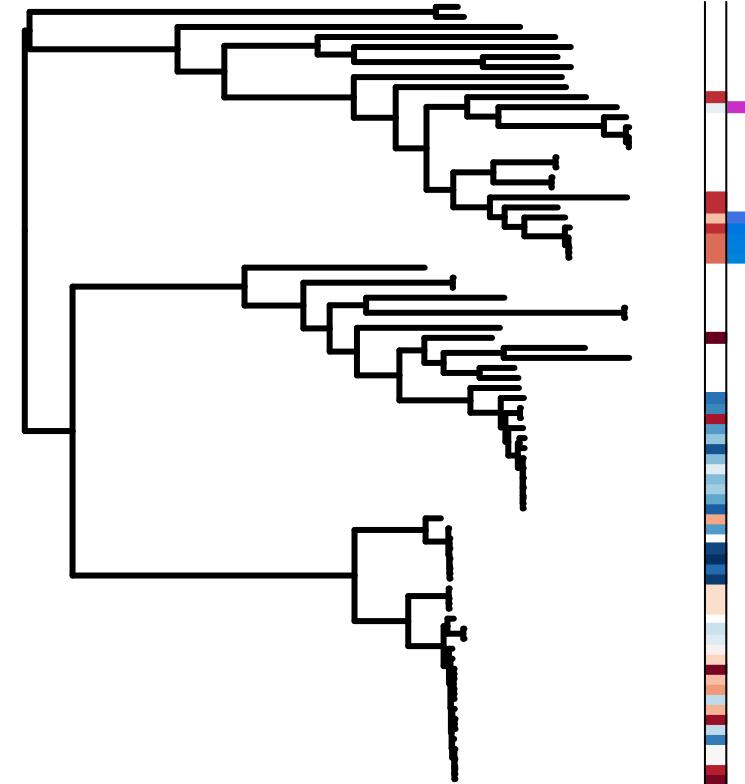


feature.plfam_id.proline_residue.mean
PLF_28228_00002926
hypothetical protein
 $r = -0.998$, $p = 10^{-5.032}$

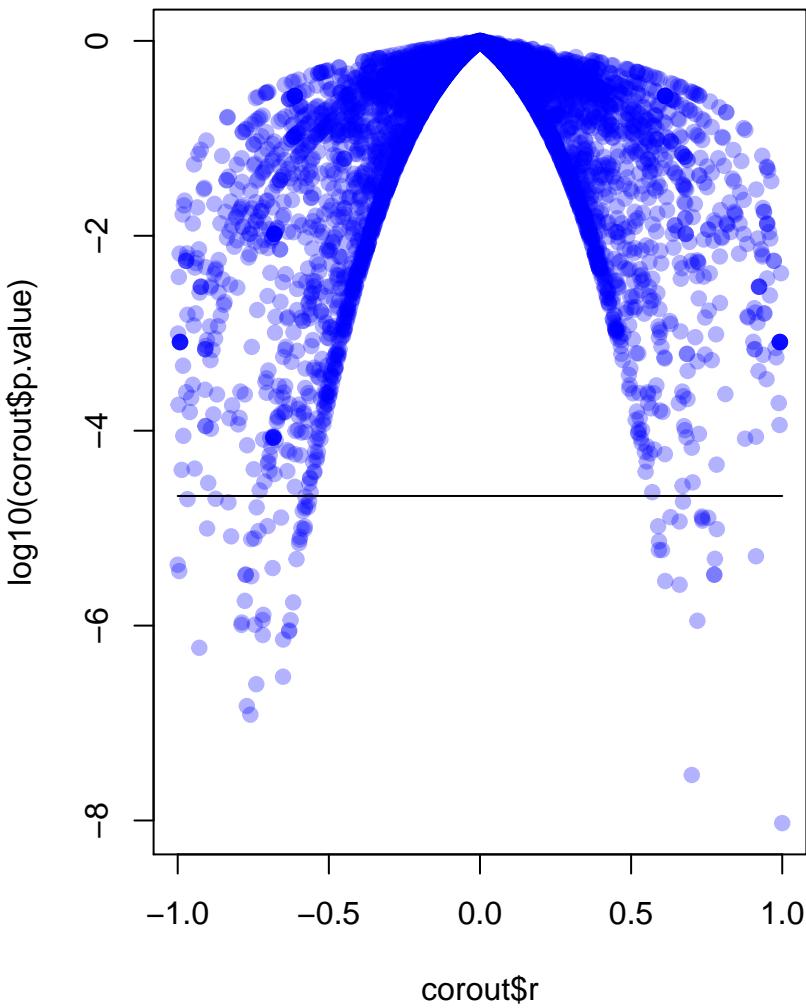
feature.plfam_id.proline_residue.mean



Optimal Growth Temperature



feature.pgfam_id.aromaticity.mean



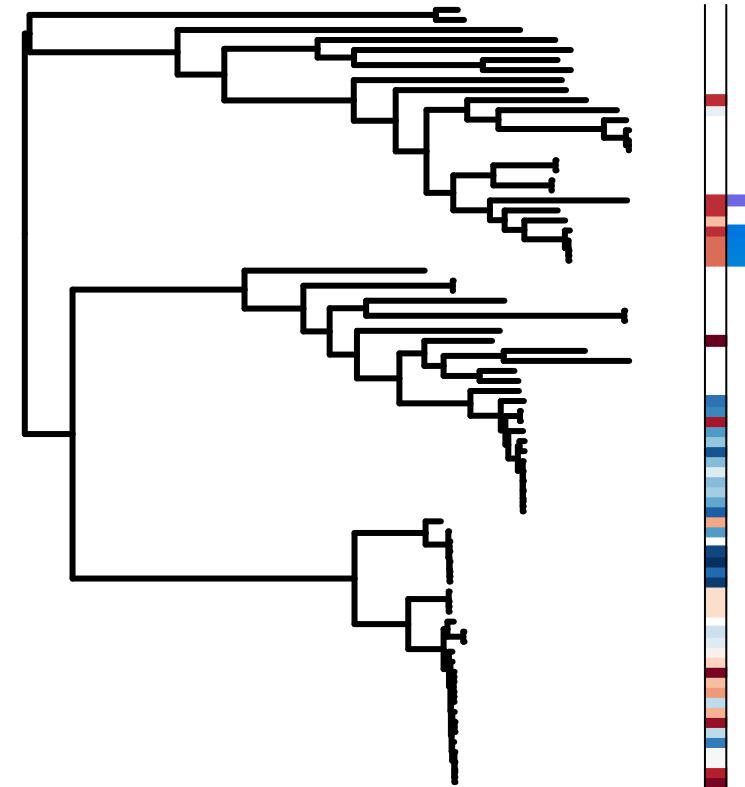
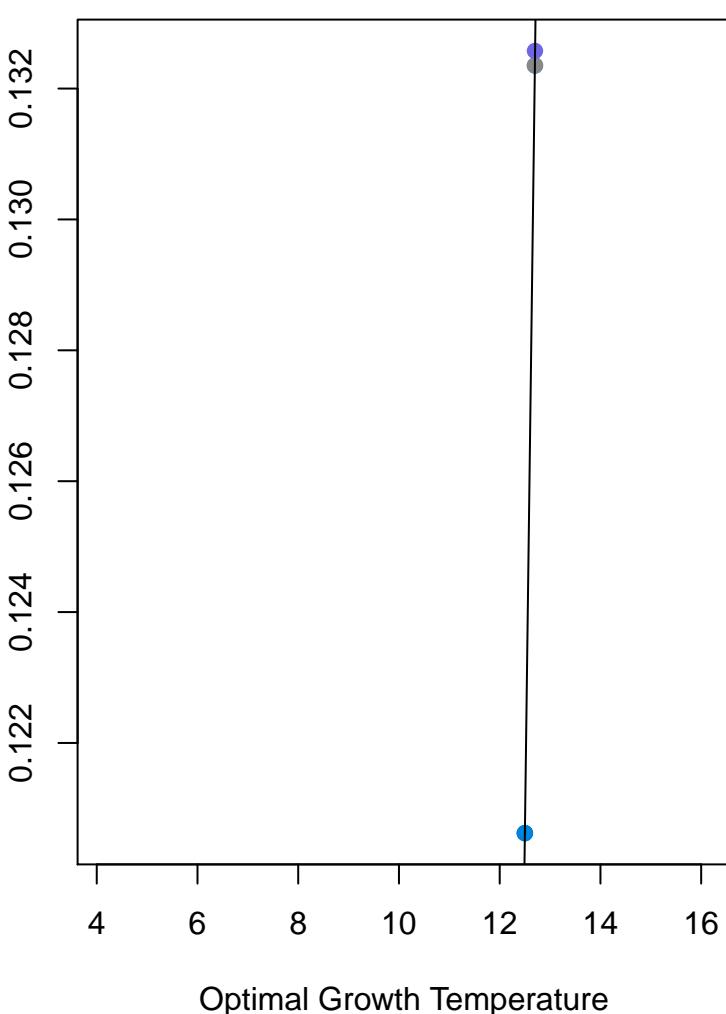
feature.pgfam_id.aromaticity.mean

PGF_01336907

hypothetical protein

r = 1, p = $10^{-8.027}$

feature.pgfam_id.aromaticity.mean



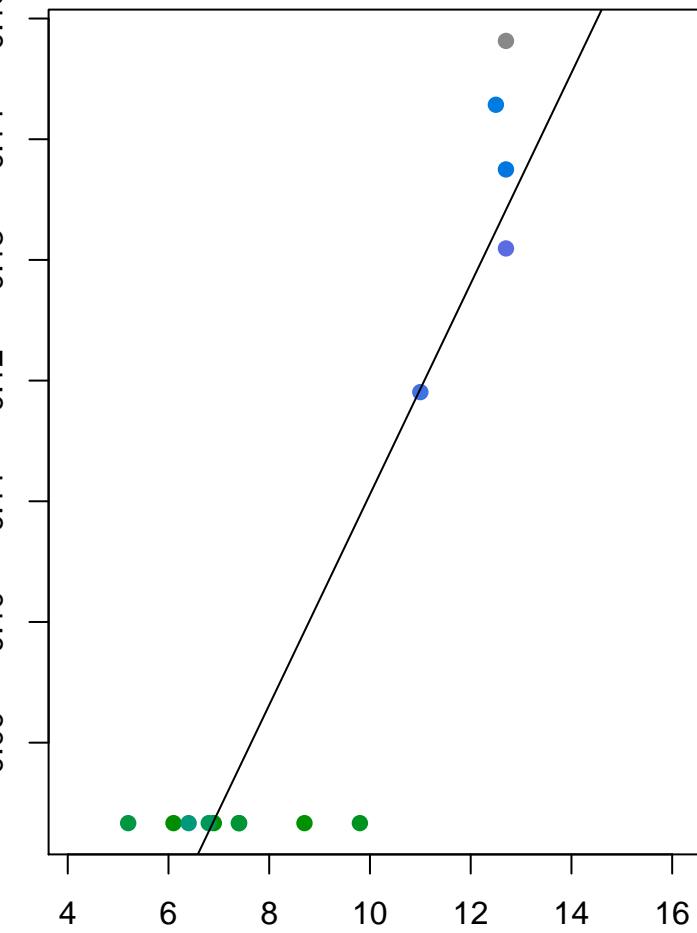
feature.pgfam_id.aromaticity.mean

PGF_01668026

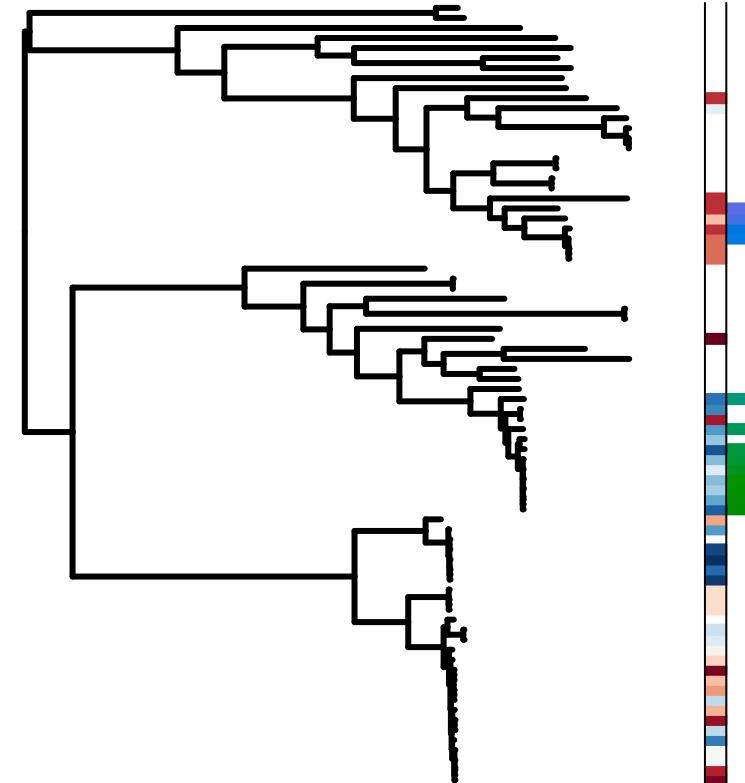
Glutaredoxin 3

$r = 0.913, p = 10^{-5.289}$

feature.pgfam_id.aromaticity.mean



Optimal Growth Temperature



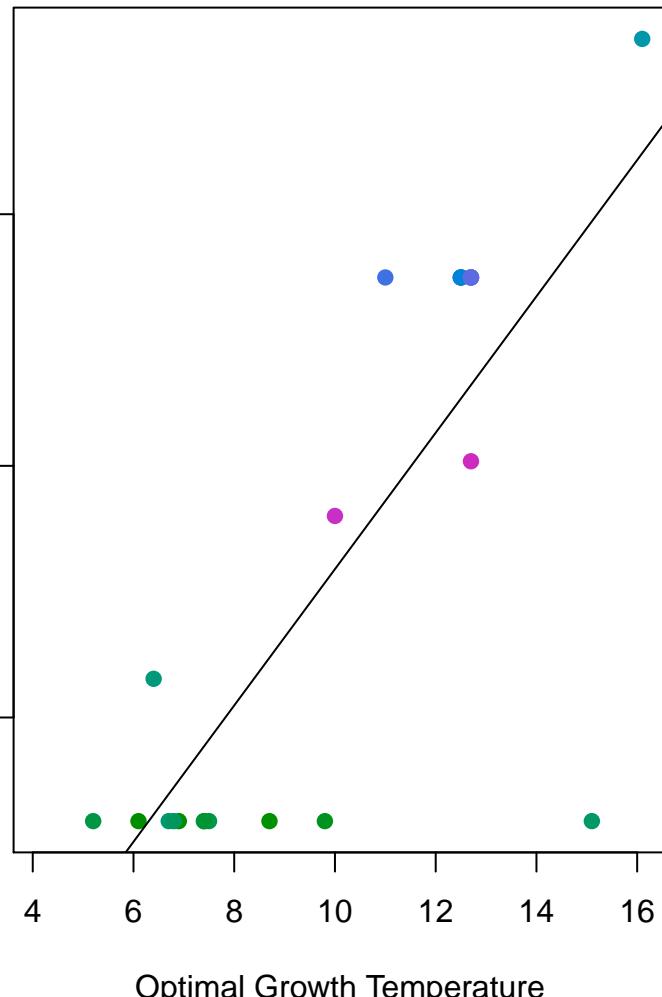
feature.pgfam_id.aromaticity.mean

PGF_02880814

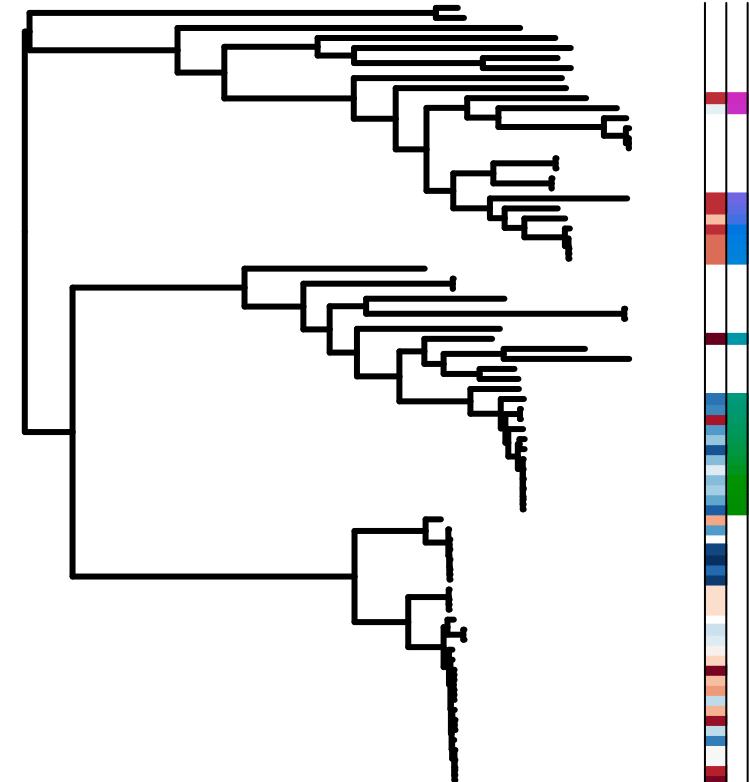
hypothetical protein

r = 0.784, p = 10^{-5.01}

feature.pgfam_id.aromaticity.mean



Optimal Growth Temperature



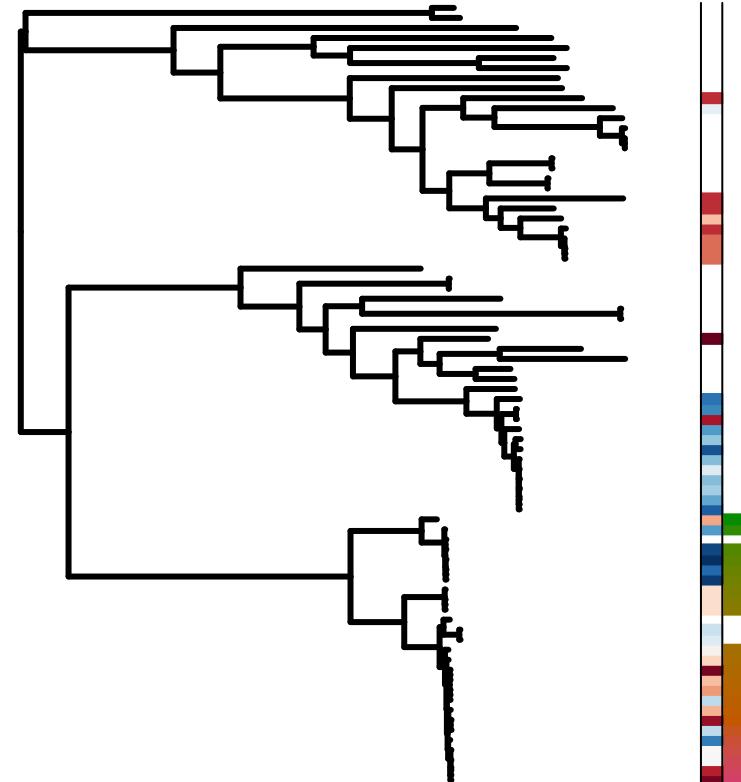
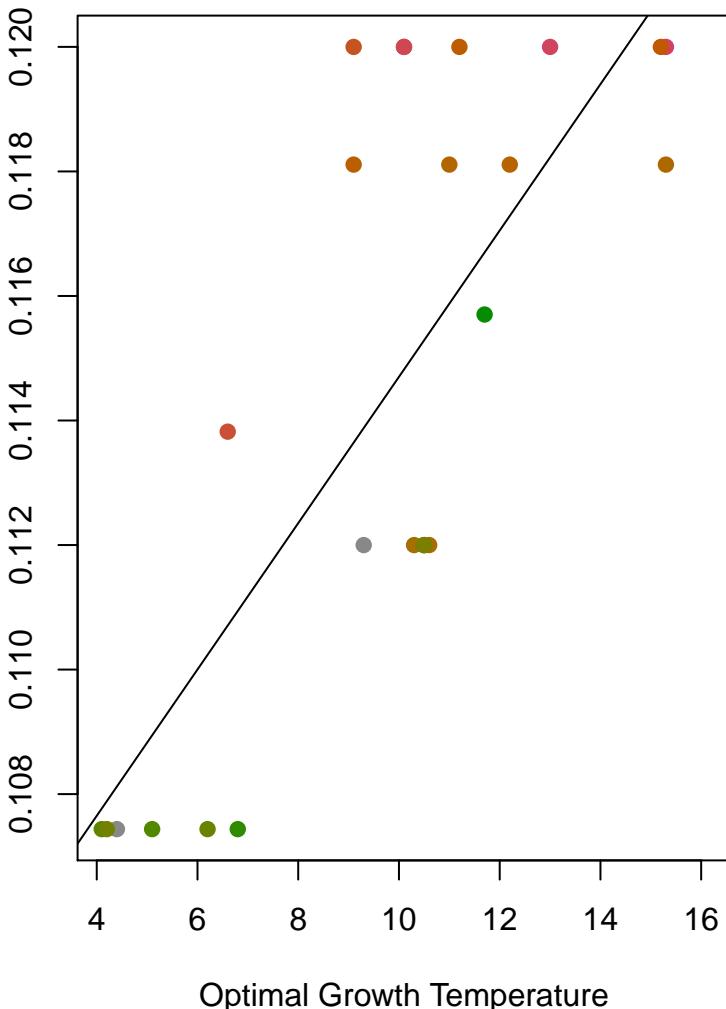
feature.pgfam_id.aromaticity.mean

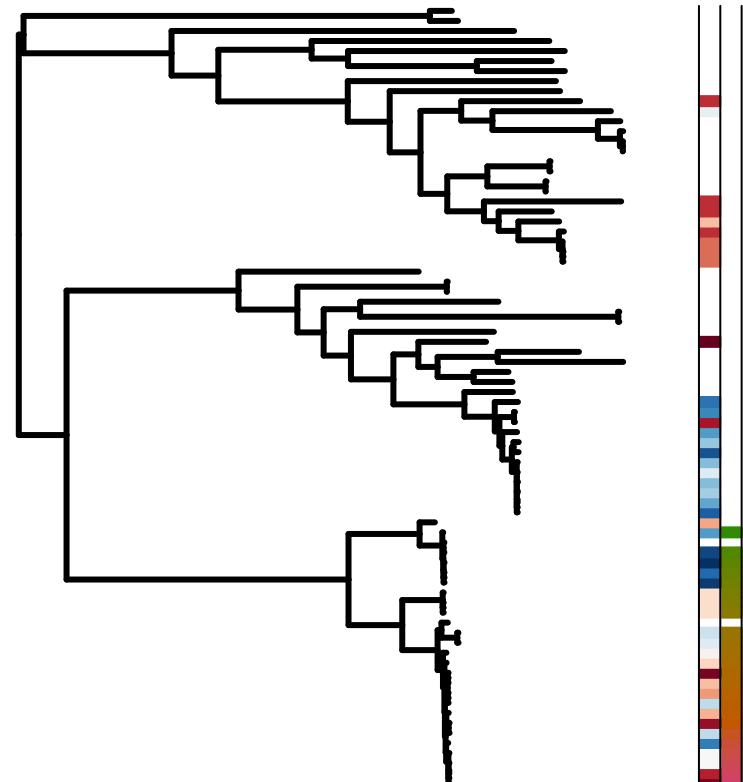
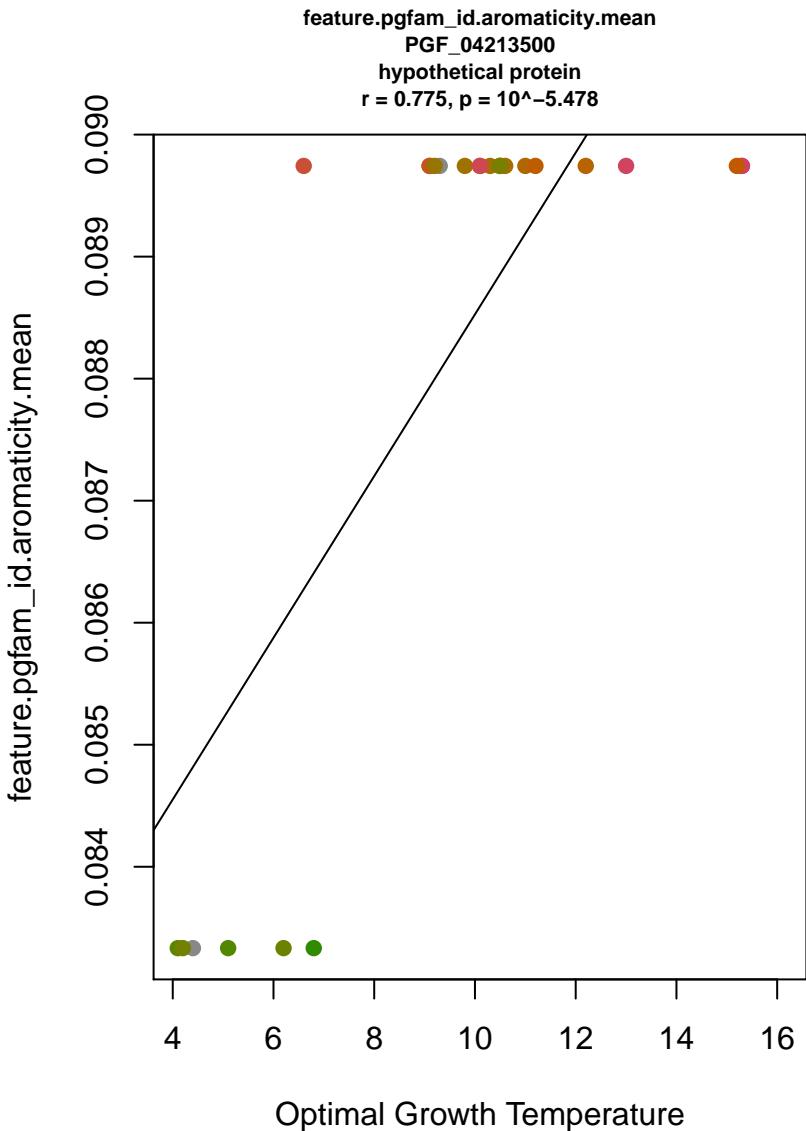
PGF_08025863

hypothetical protein

$r = 0.777, p = 10^{-5.315}$

feature.pgfam_id.aromaticity.mean





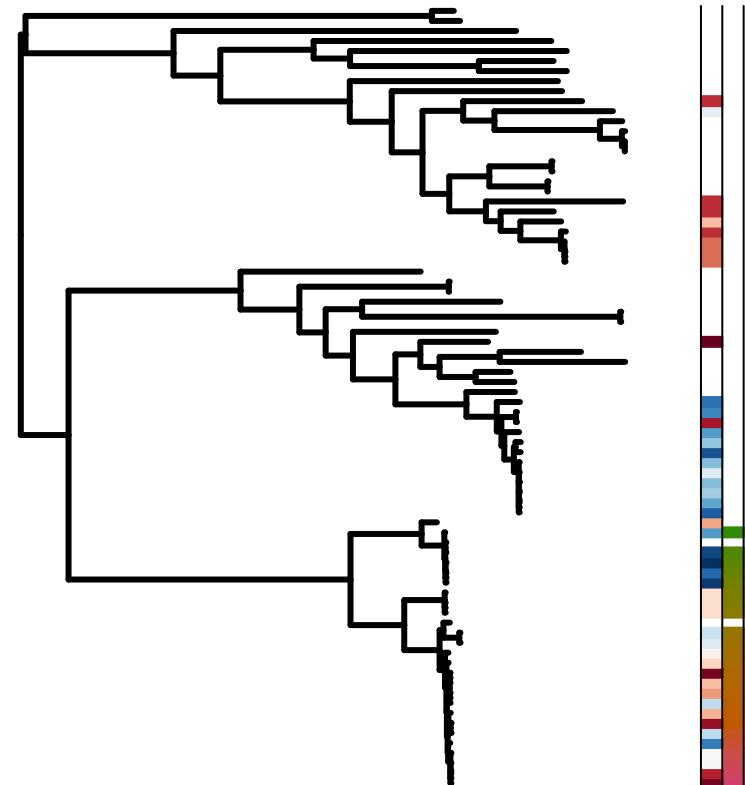
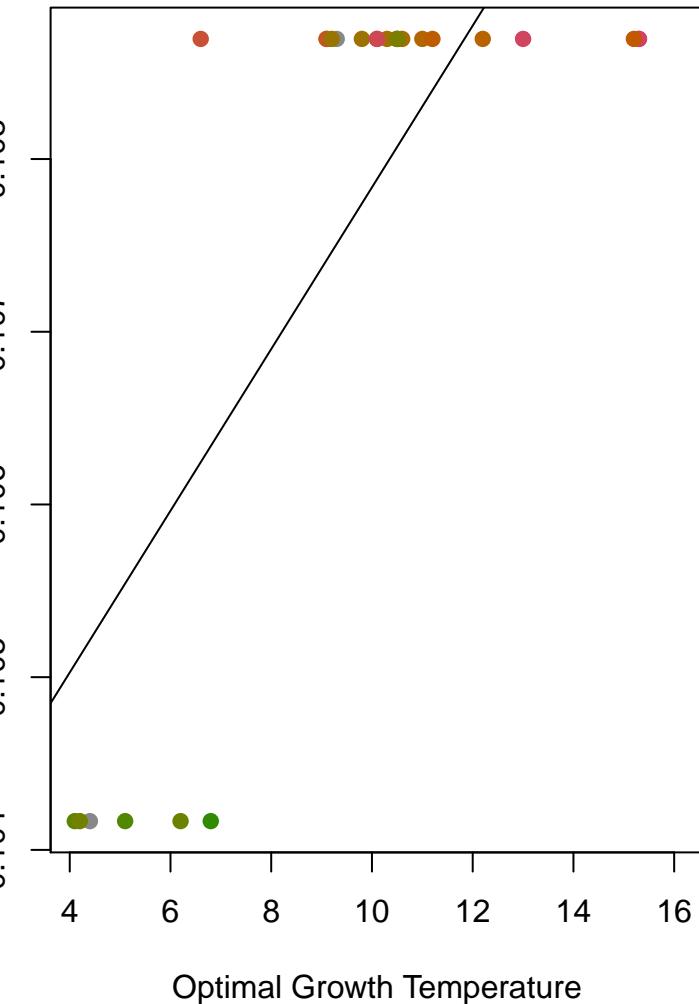
feature.pgfam_id.aromaticity.mean

PGF_12071964

hypothetical protein

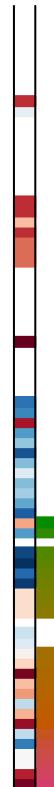
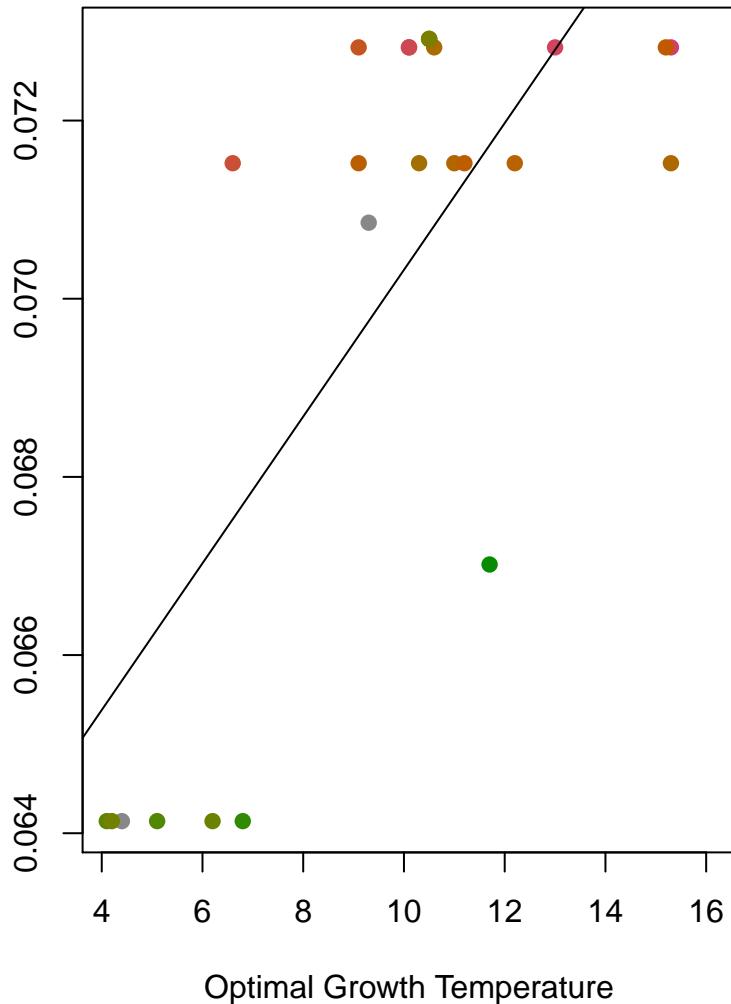
$r = 0.775, p = 10^{-5.478}$

feature.pgfam_id.aromaticity.mean



feature.pgfam_id.aromaticity.mean
PGF_00001178
FIG00951615: hypothetical protein
 $r = 0.755, p = 10^{-4.894}$

feature.pgfam_id.aromaticity.mean



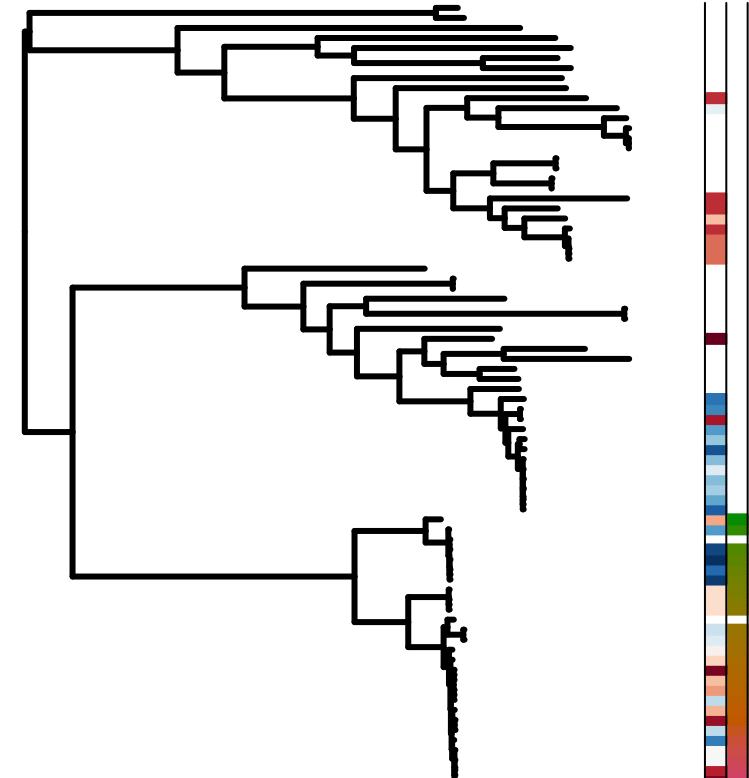
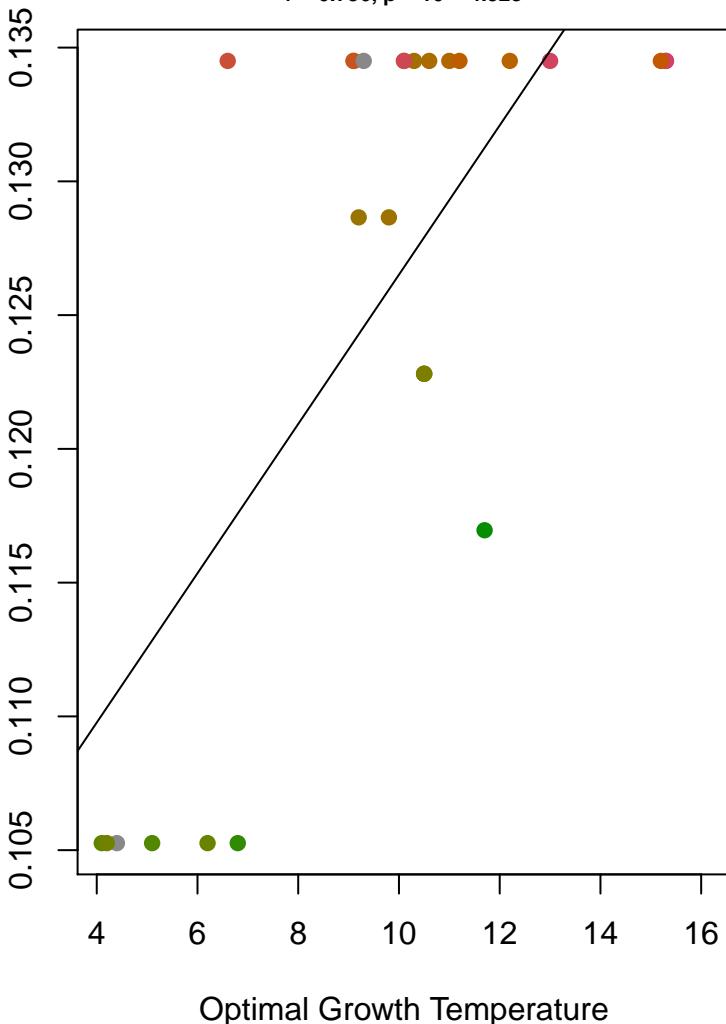
feature.pgfam_id.aromaticity.mean

PGF_11552181

hypothetical protein

$r = 0.736, p = 10^{-4.923}$

feature.pgfam_id.aromaticity.mean



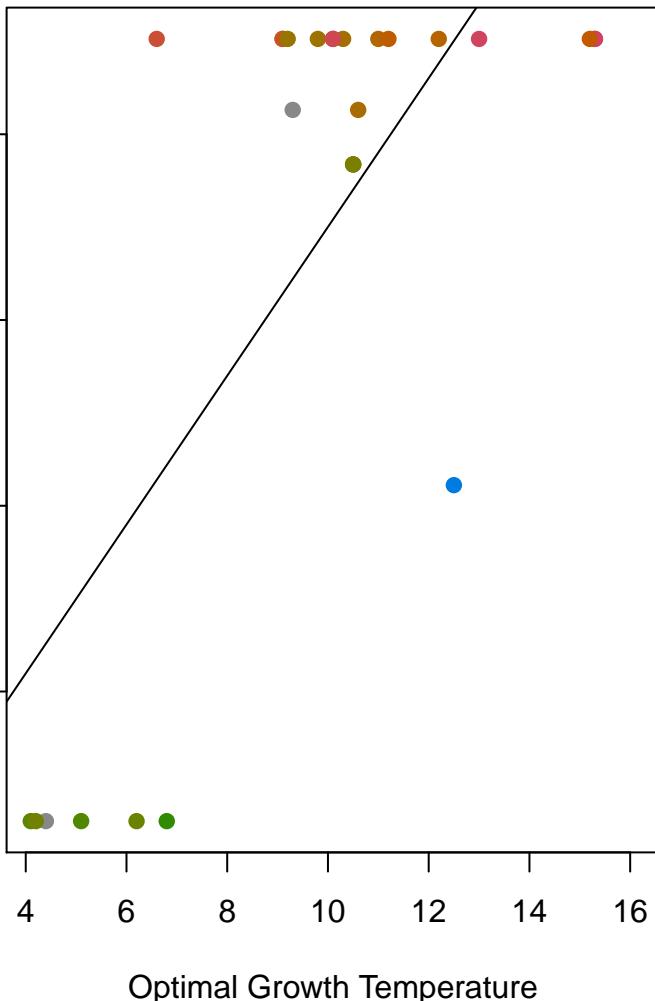
feature.pgfam_id.aromaticity.mean

PGF_06792096

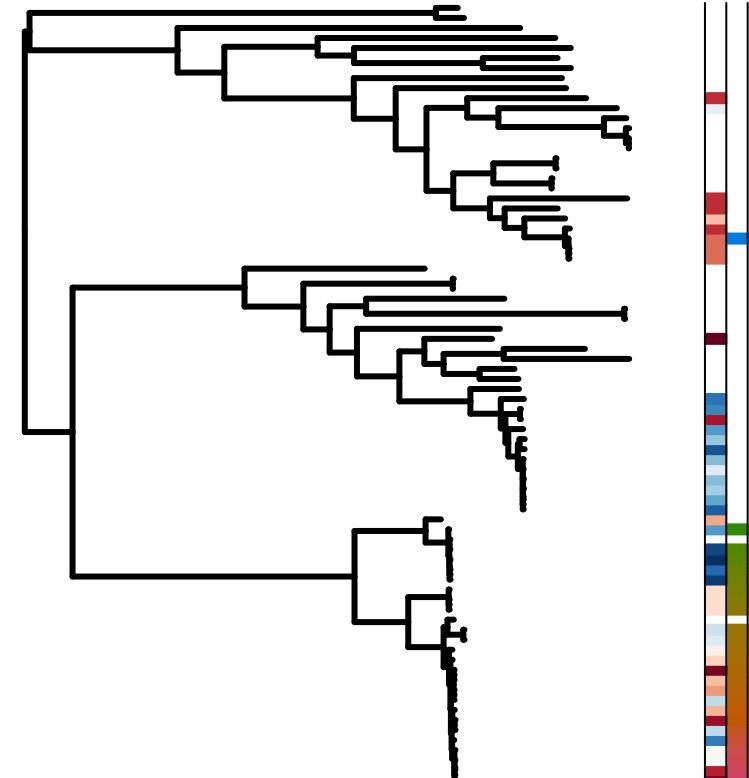
hypothetical protein

$r = 0.735, p = 10^{-4.899}$

feature.pgfam_id.aromaticity.mean



Optimal Growth Temperature



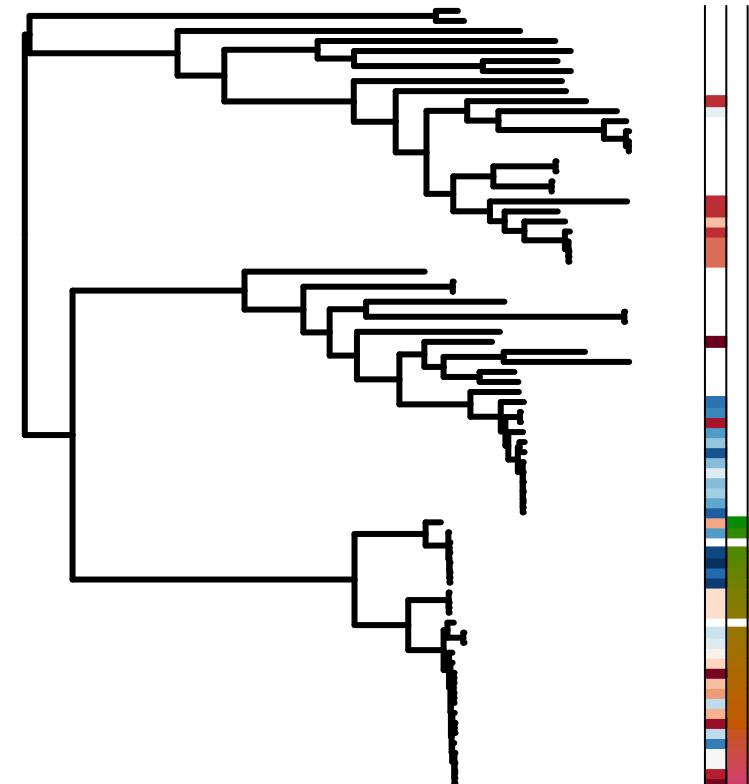
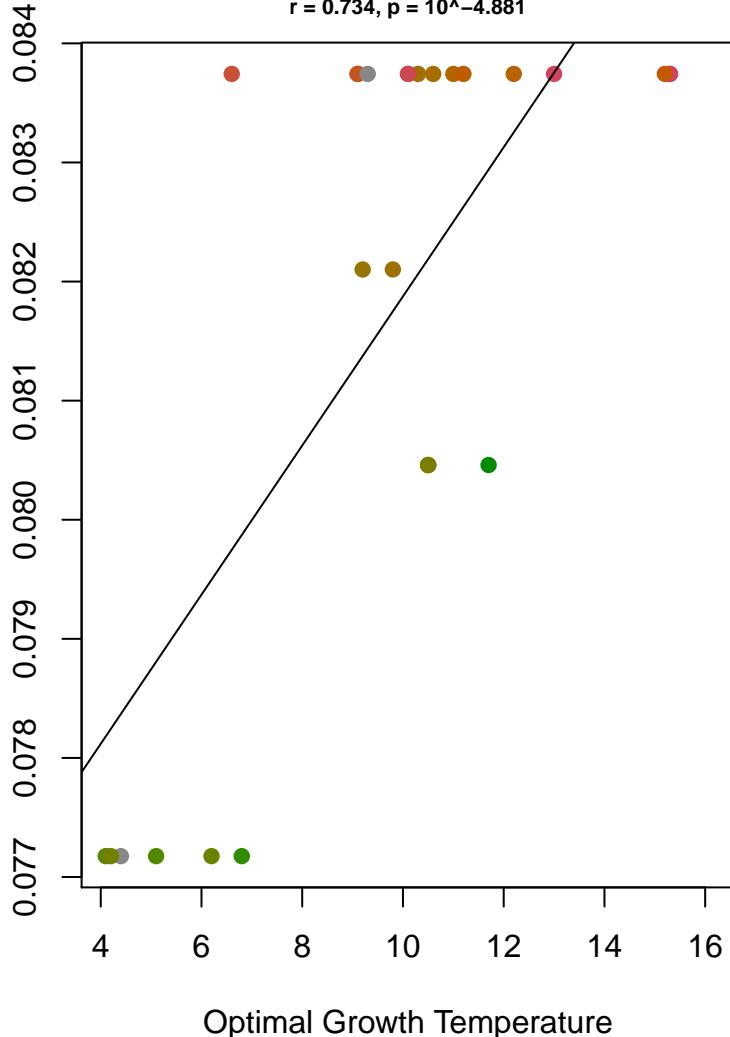
feature.pgfam_id.aromaticity.mean

PGF_00061953

TrkA-C domain protein

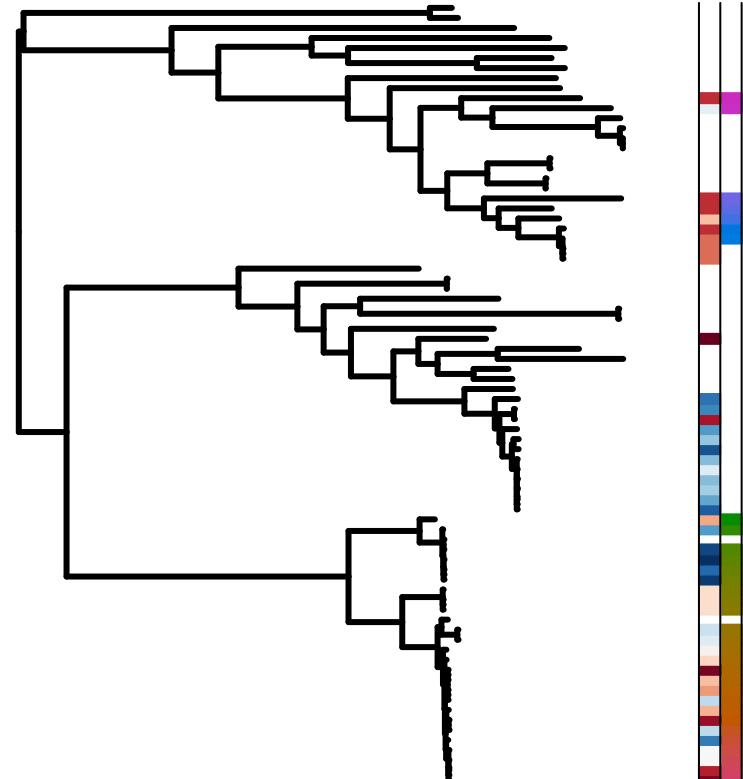
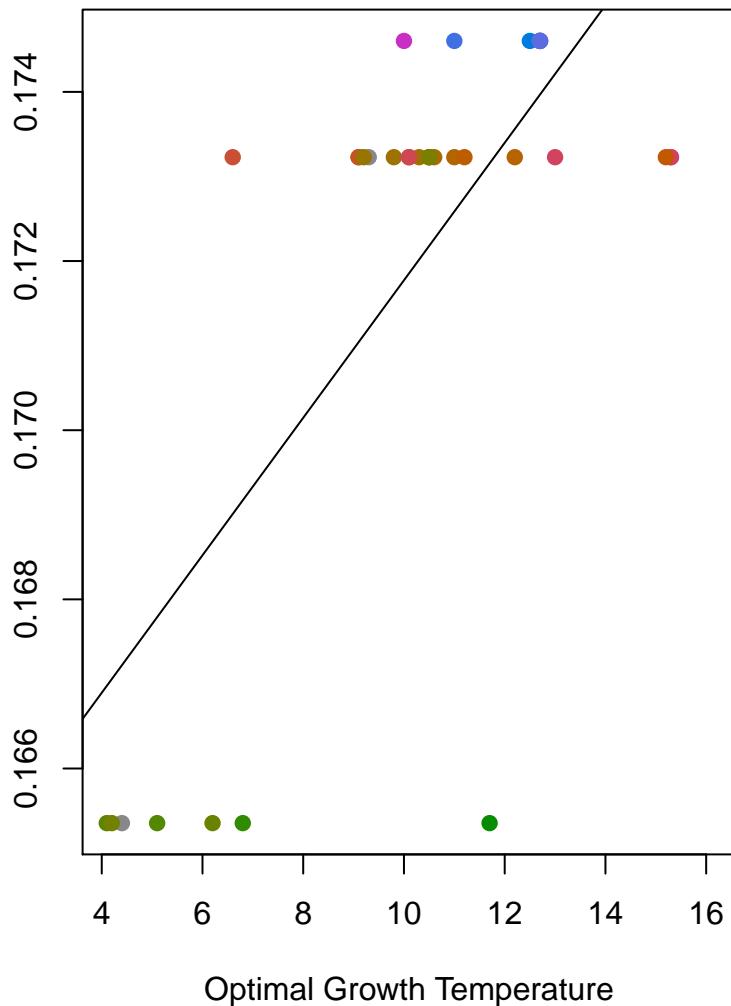
$r = 0.734, p = 10^{-4.881}$

feature.pgfam_id.aromaticity.mean



feature.pgfam_id.aromaticity.mean
PGF_03072985
hypothetical protein
 $r = 0.719$, $p = 10^{-5.951}$

feature.pgfam_id.aromaticity.mean

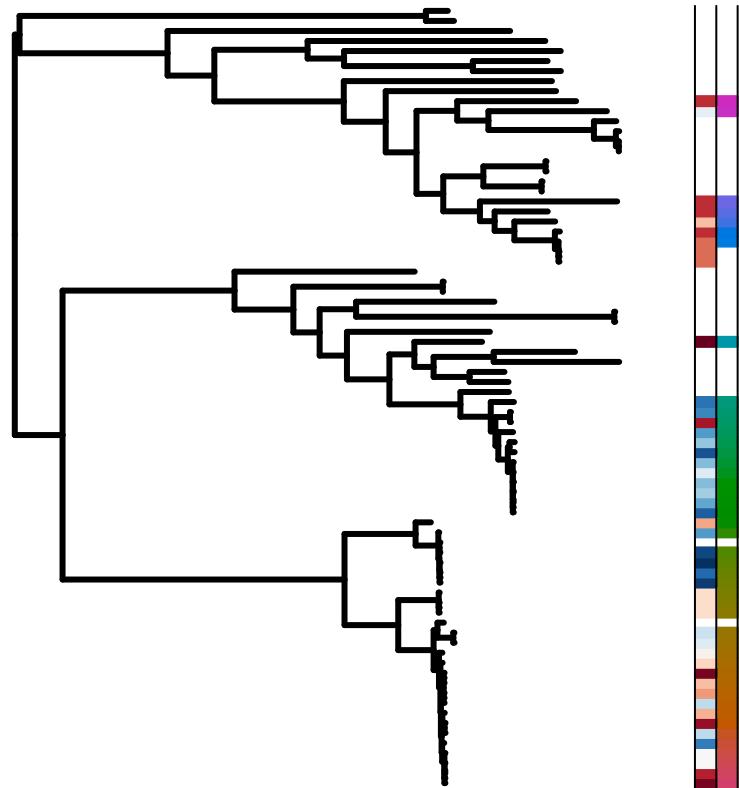
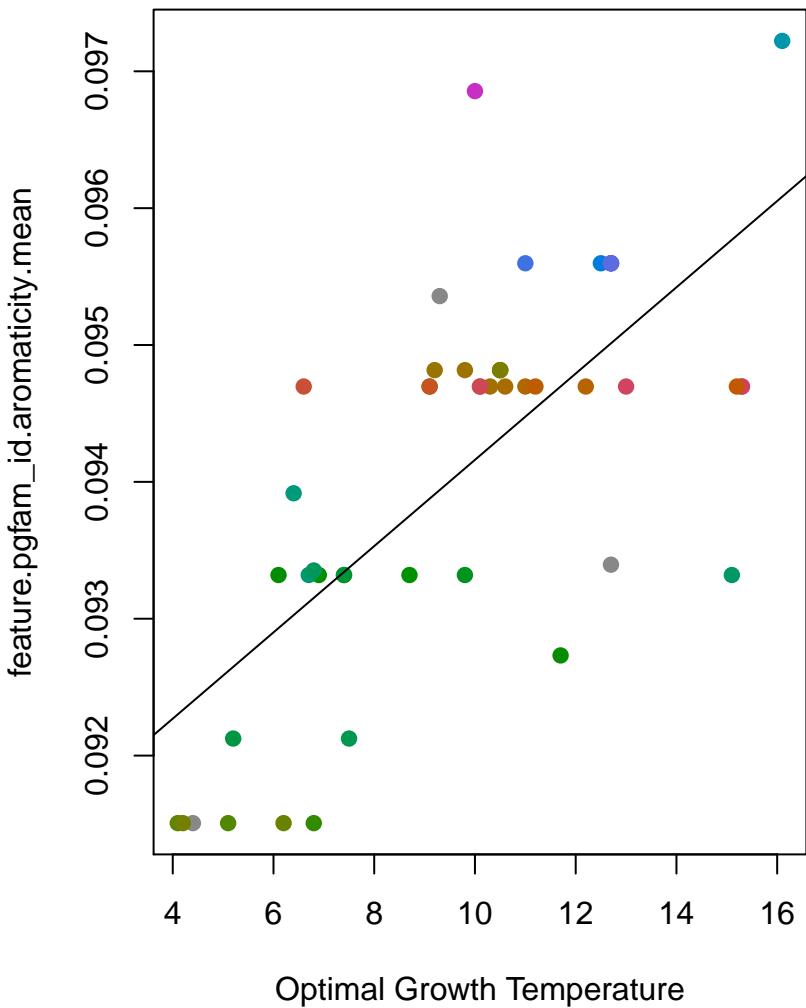


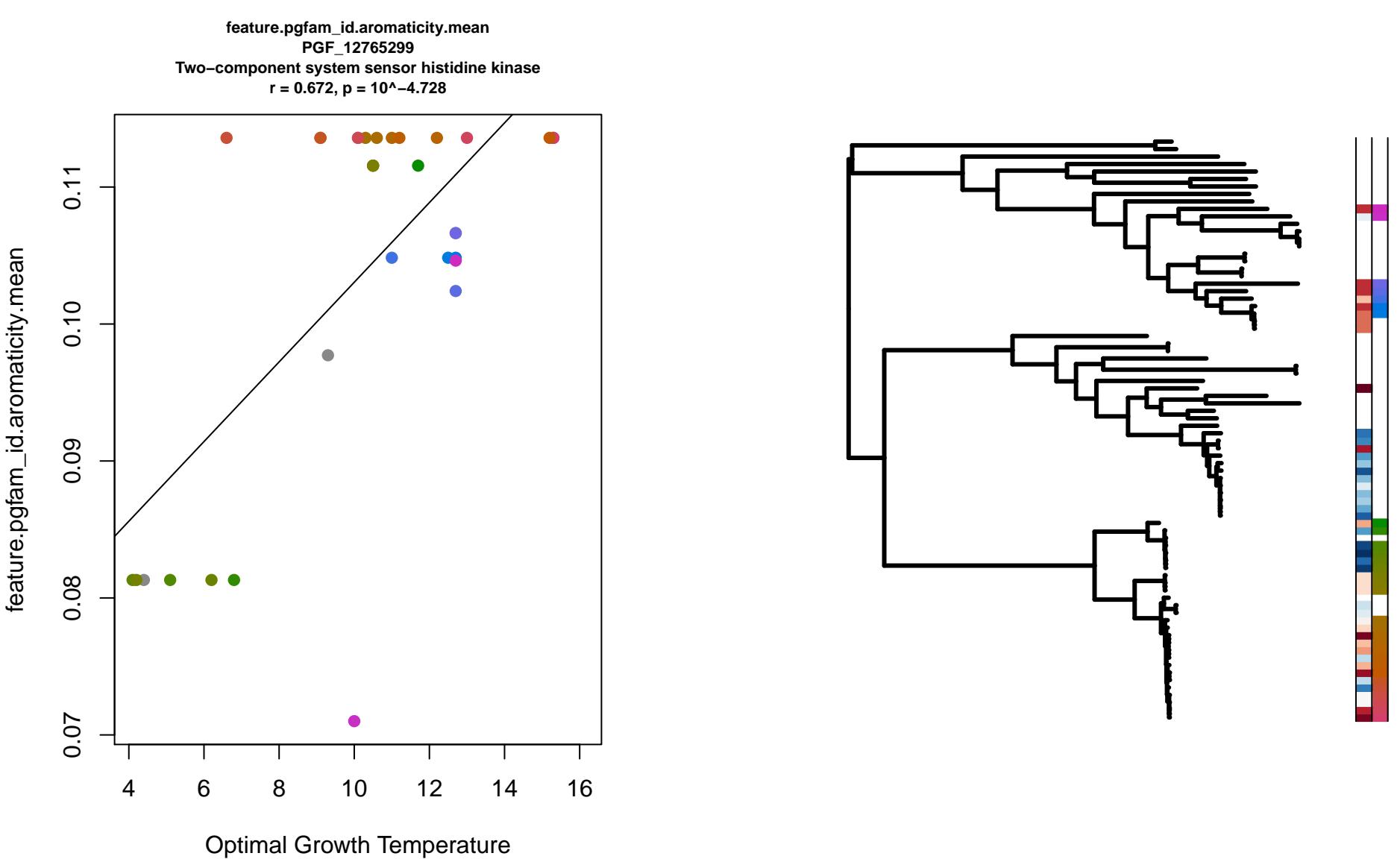
feature.pgfam_id.aromaticity.mean

PGF_05438553

Phosphoenolpyruvate synthase (EC 2.7.9.2)

r = 0.701, p = 10^-7.533





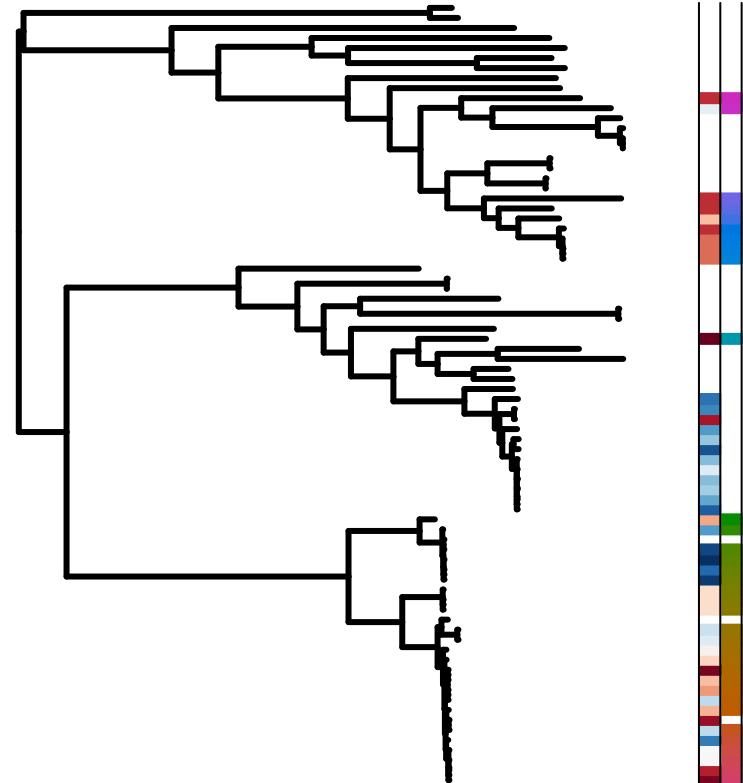
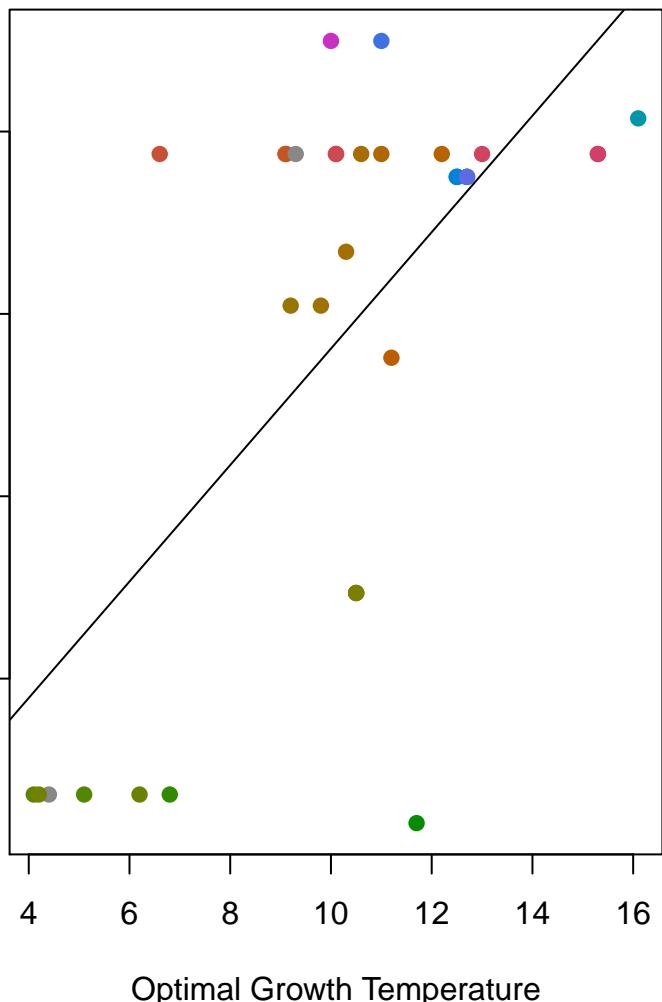
feature.pgfam_id.aromaticity.mean

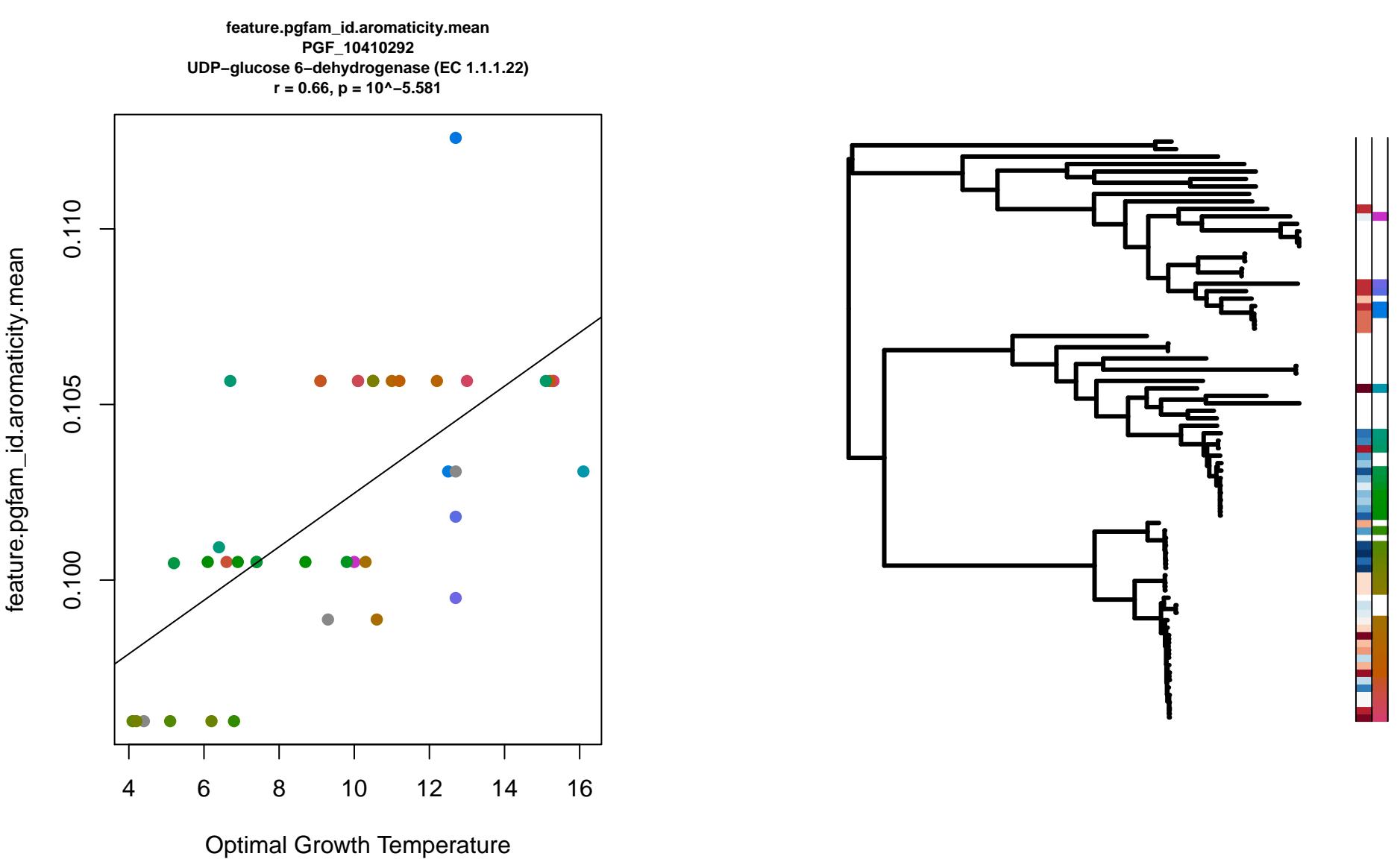
PGF_00405416

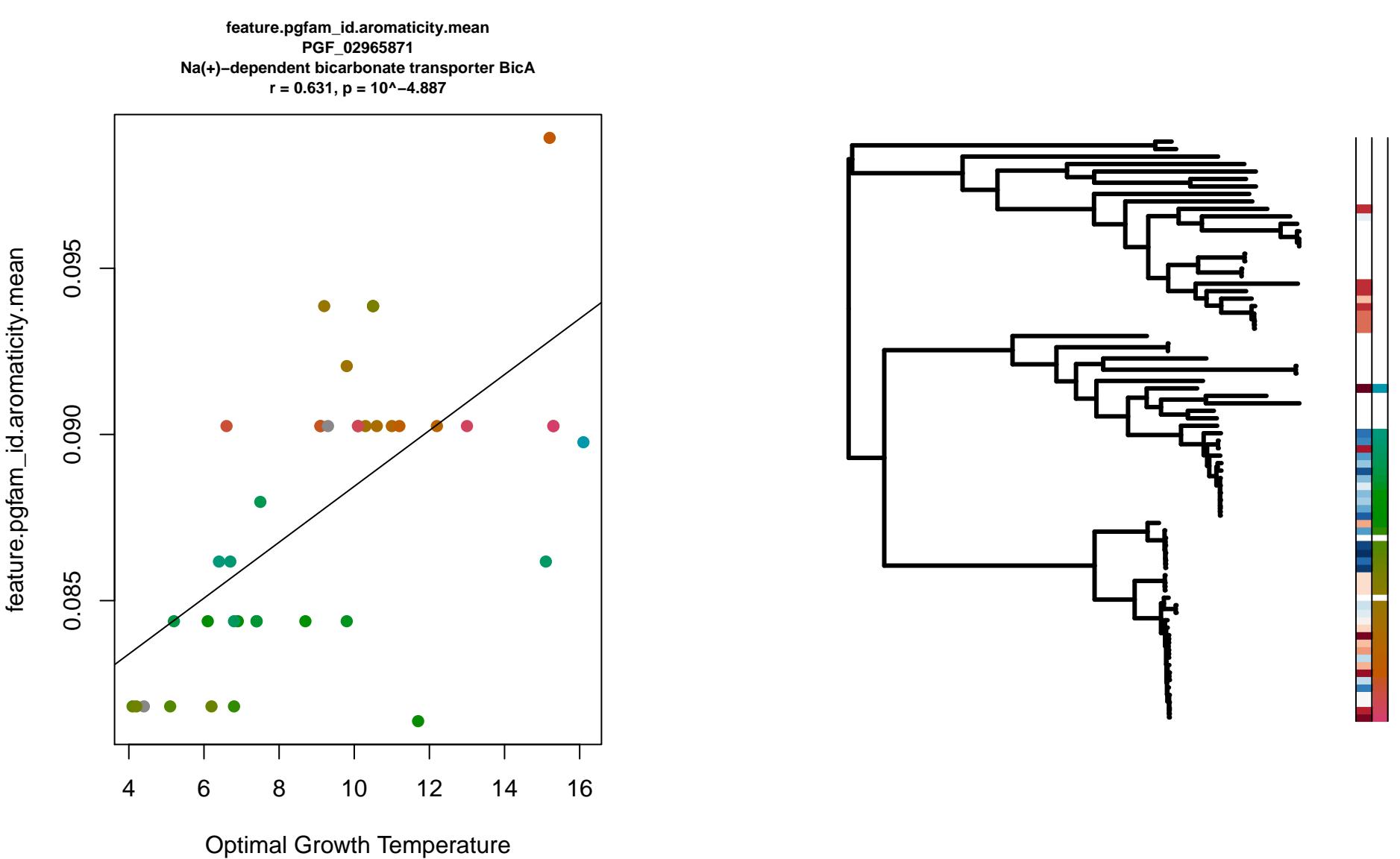
2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline (OHCU) decarboxylase (EC 4.1.1.97)

$r = 0.66, p = 10^{-4.932}$

feature.pgfam_id.aromaticity.mean







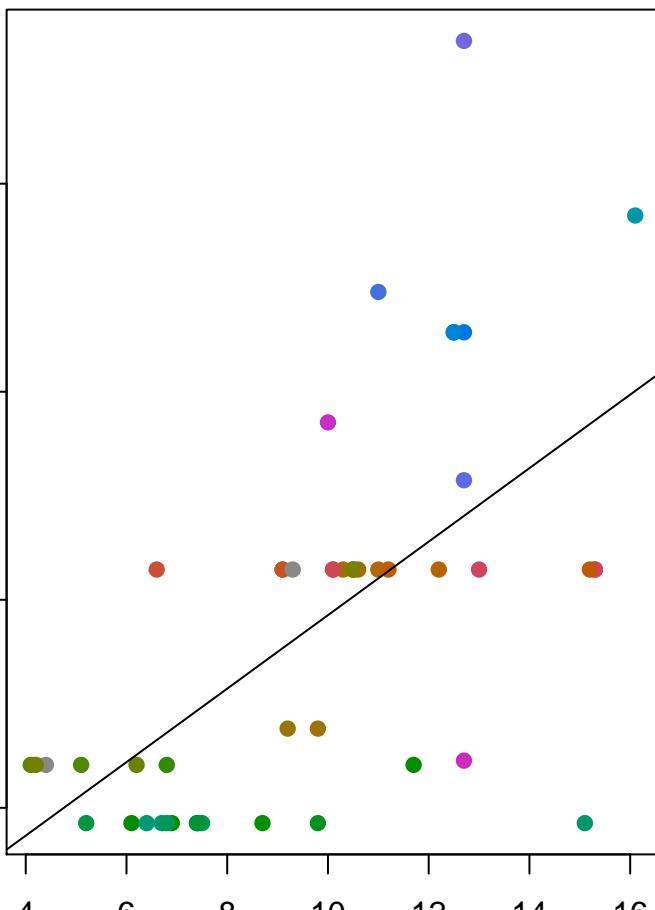
feature.pgfam_id.aromaticity.mean

PGF_00007026

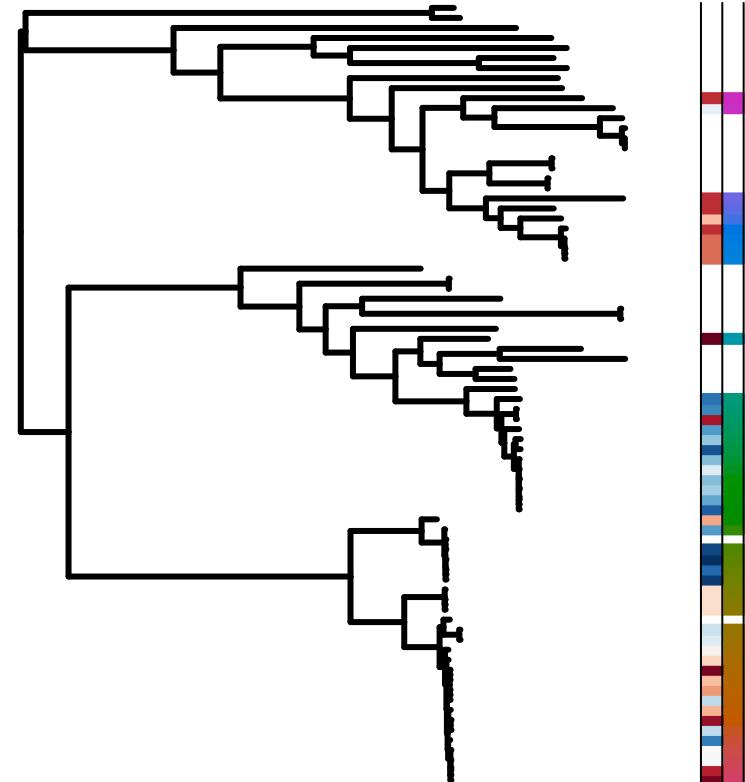
GTP-binding protein EngB

$r = 0.613, p = 10^{-5.543}$

feature.pgfam_id.aromaticity.mean

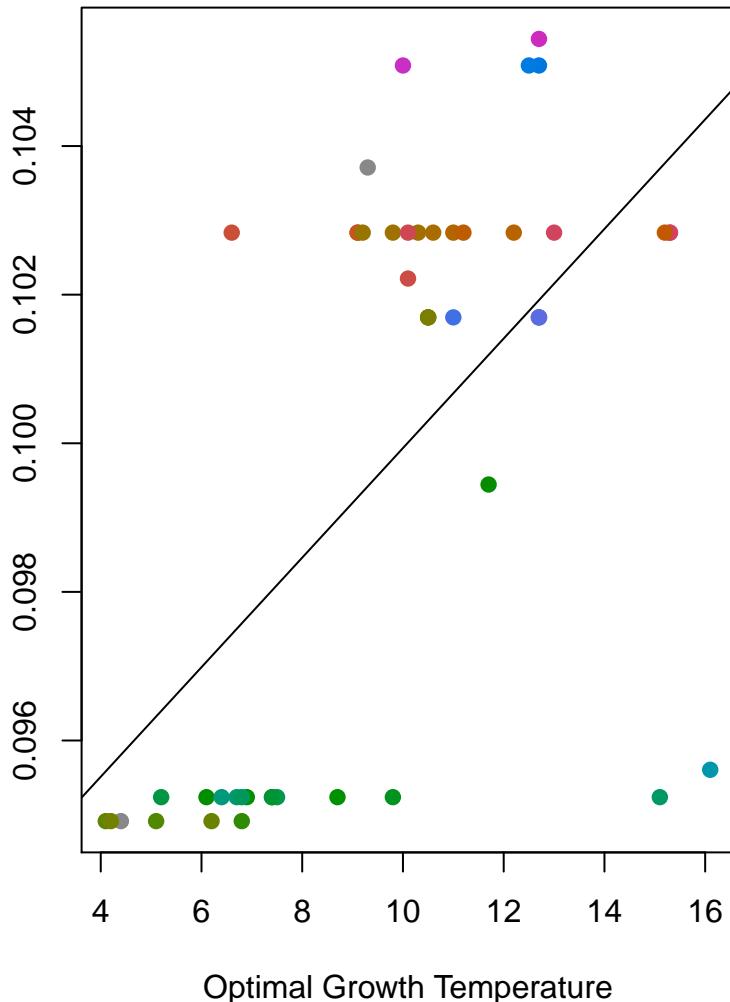


Optimal Growth Temperature

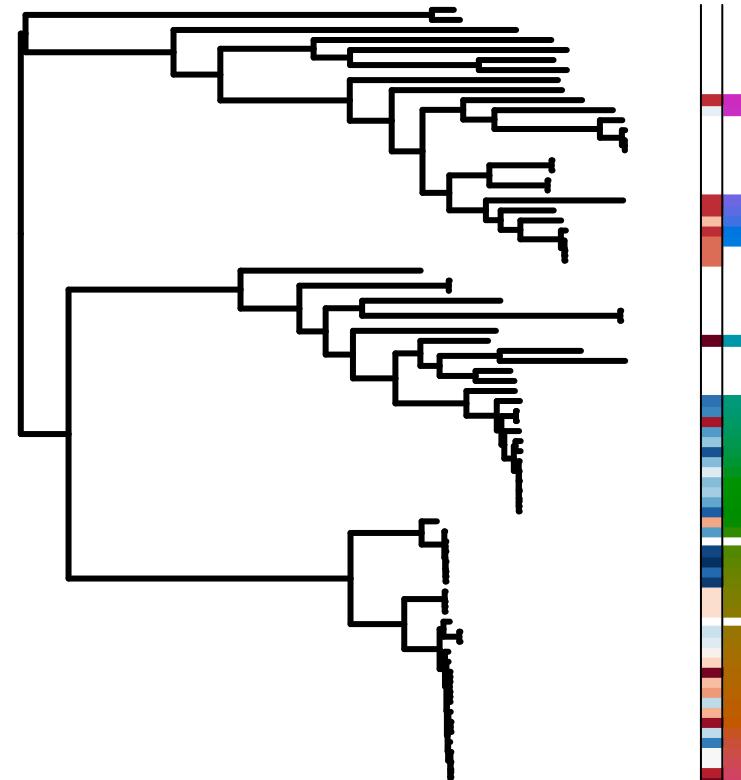


feature.pgfam_id.aromaticity.mean
PGF_00902417
HfIC protein
 $r = 0.602$, $p = 10^{-5.225}$

feature.pgfam_id.aromaticity.mean

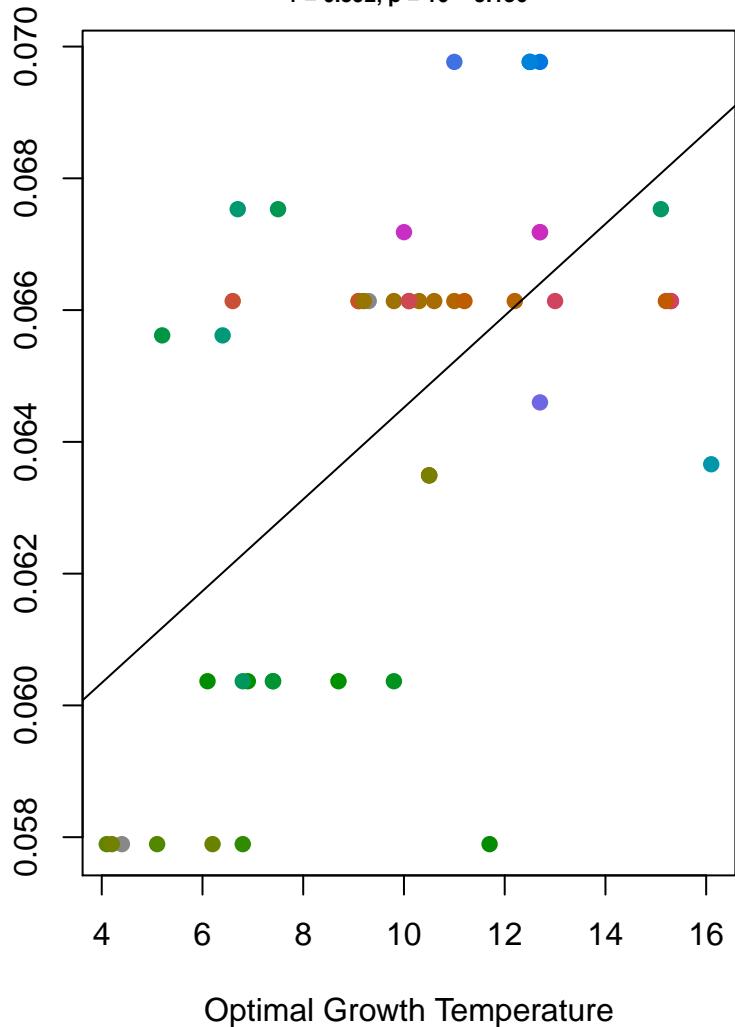


Optimal Growth Temperature

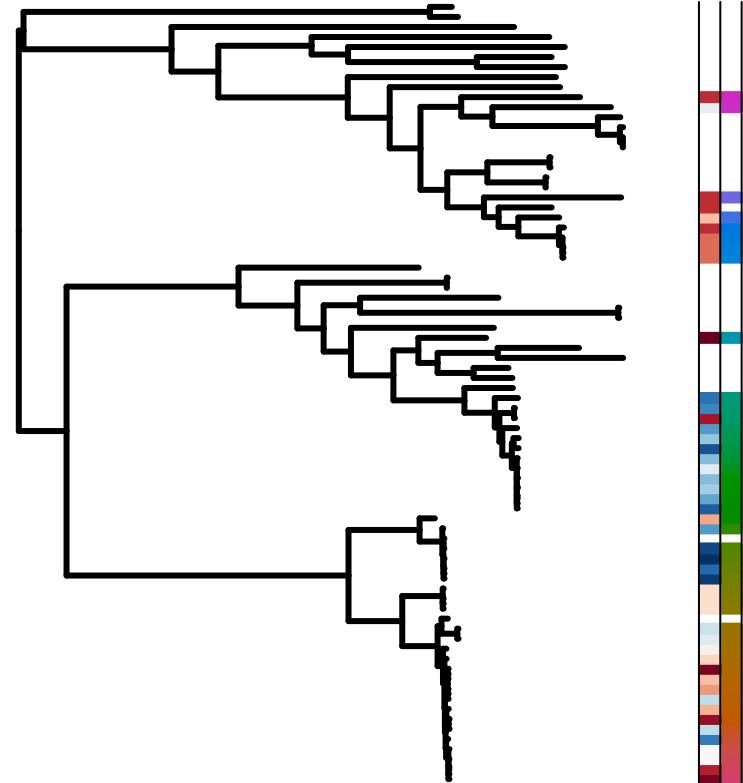


feature.pgfam_id.aromaticity.mean
PGF_00065334
Uncharacterized protein SO_3077
 $r = 0.592$, $p = 10^{-5.136}$

feature.pgfam_id.aromaticity.mean

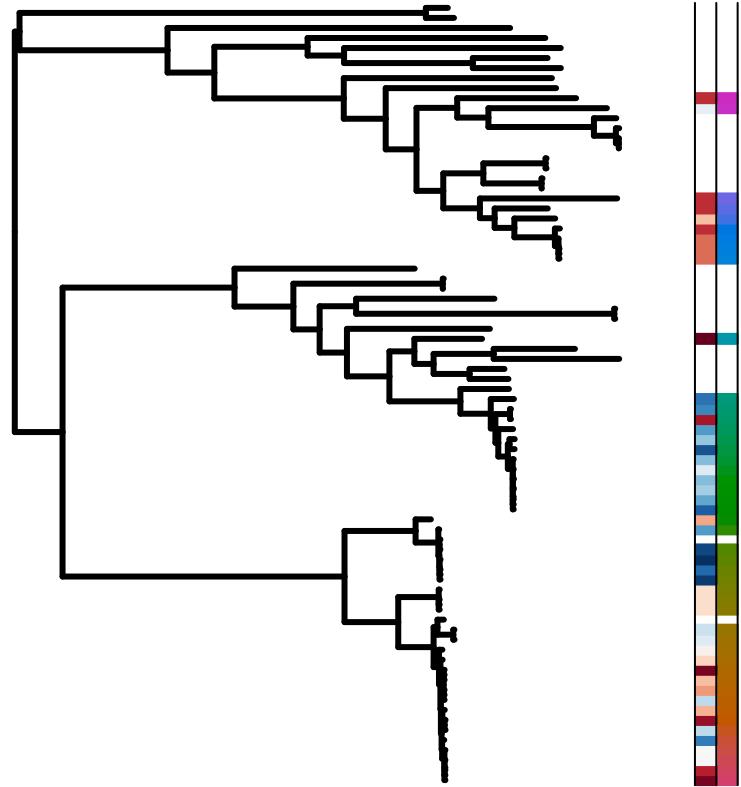
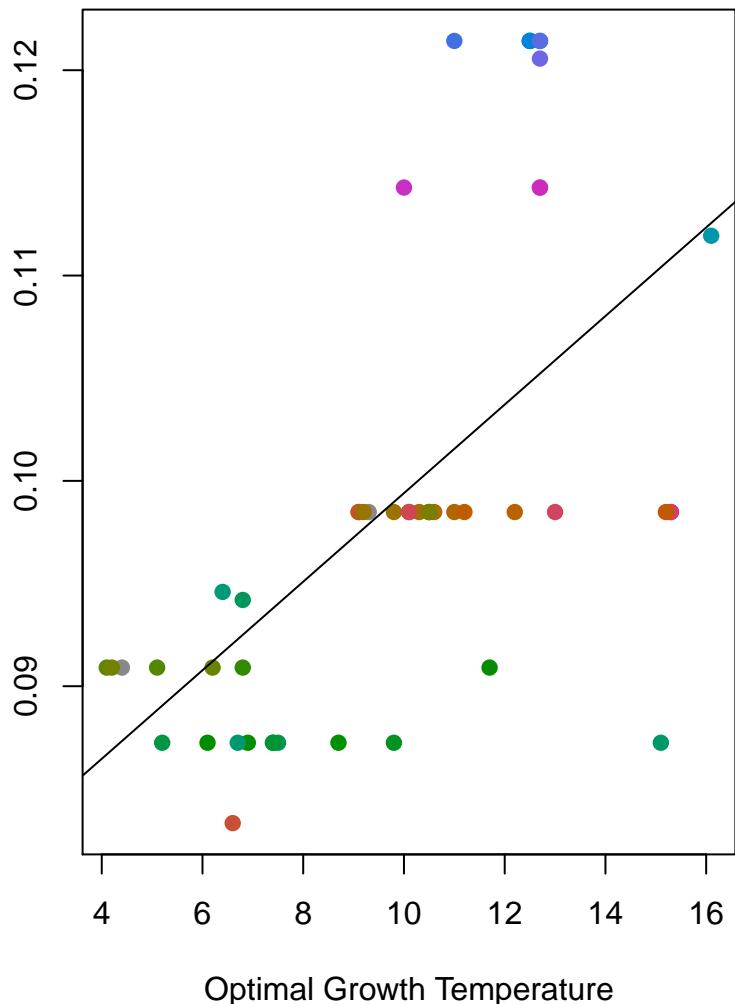


Optimal Growth Temperature



feature.pgfam_id.aromaticity.mean
PGF_00422096
DNA-binding protein, CopG family
 $r = 0.592$, $p = 10^{-5.224}$

feature.pgfam_id.aromaticity.mean



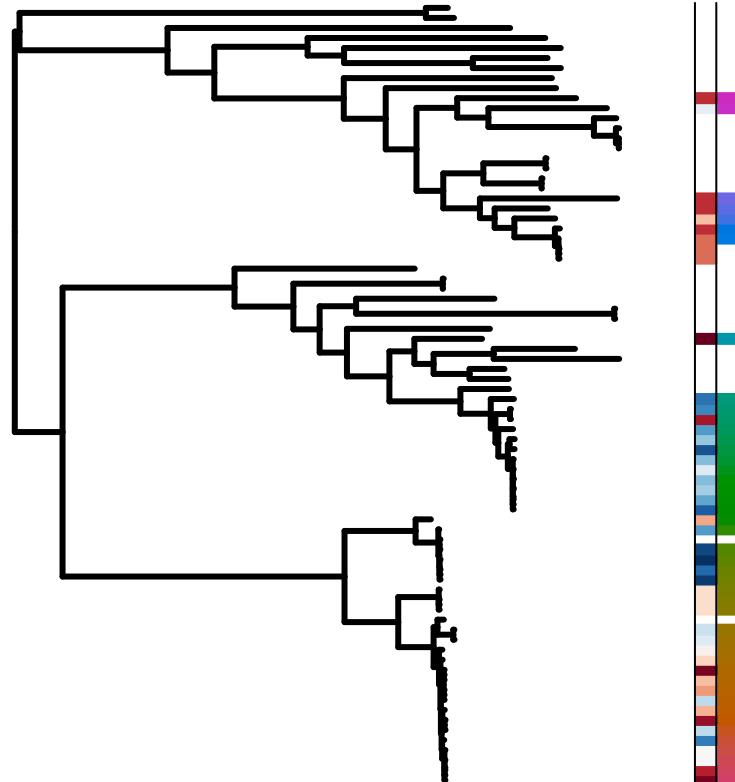
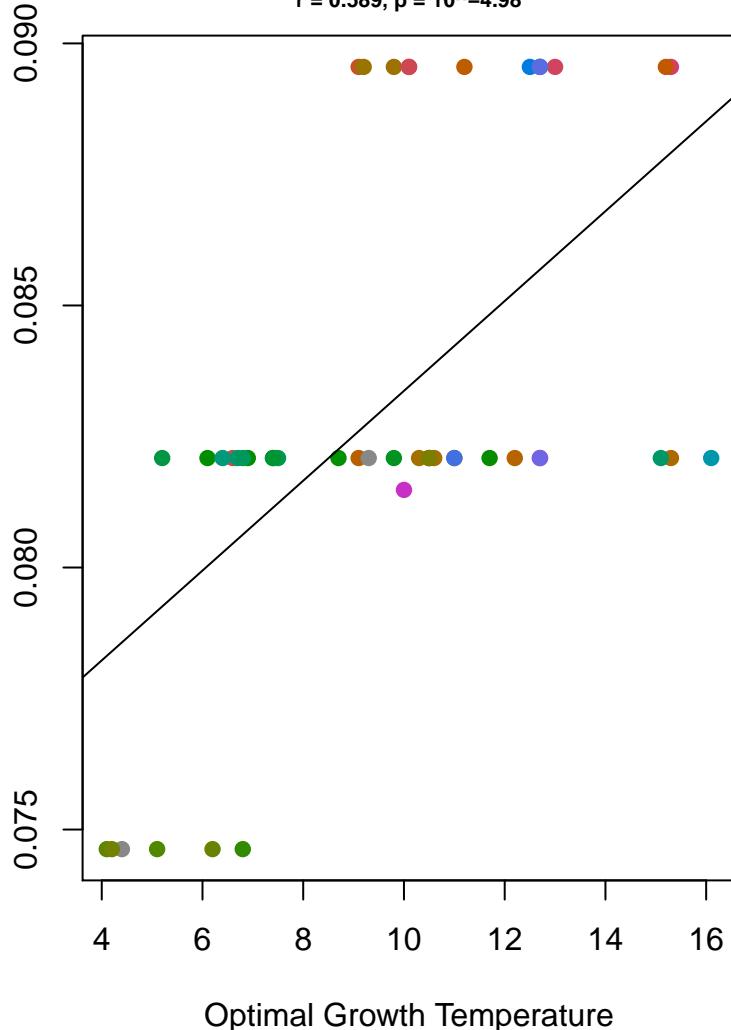


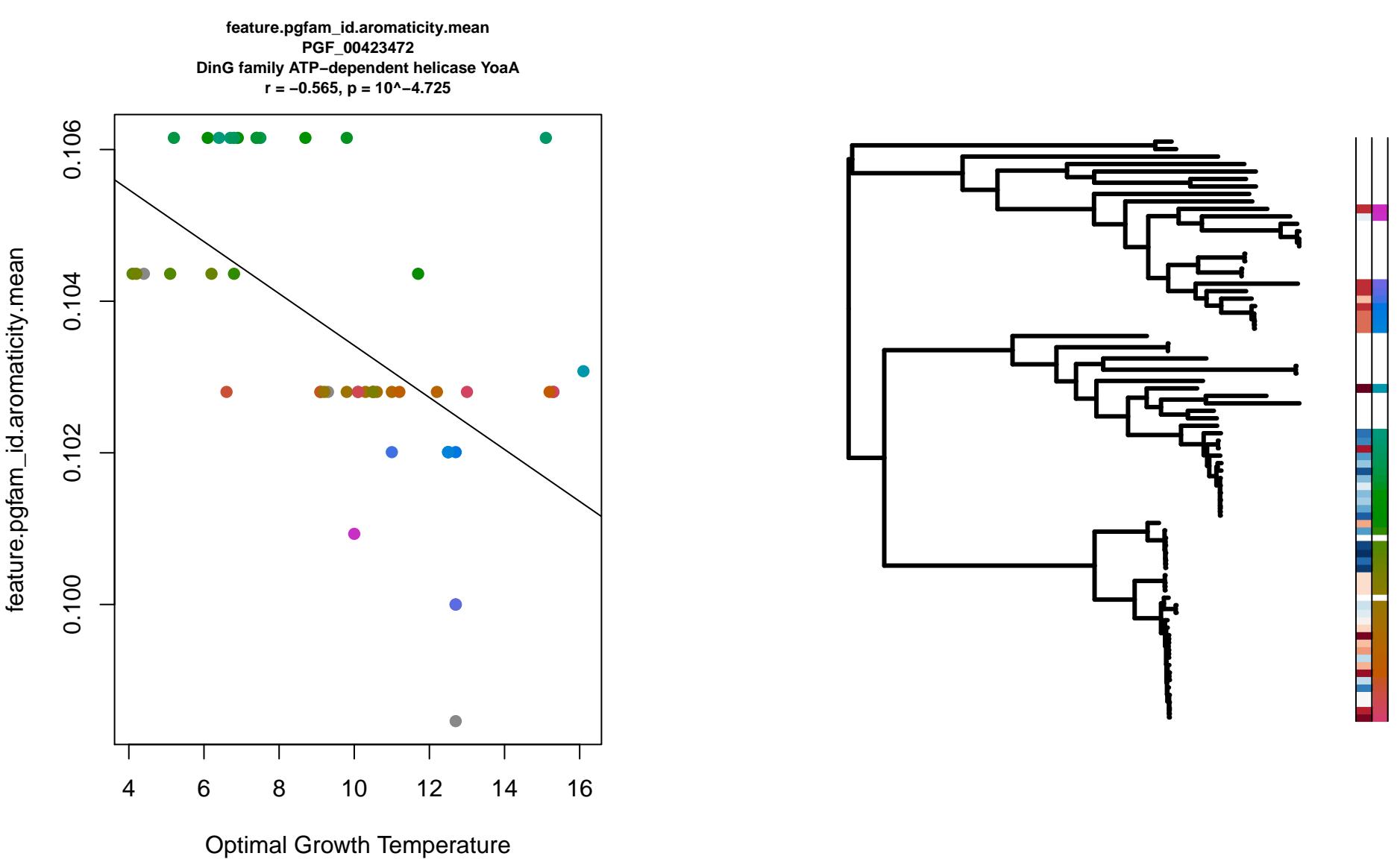
feature.pgfam_id.aromaticity.mean

PGF_03837024

Protein YhfA

$r = 0.589$, $p = 10^{-4.98}$



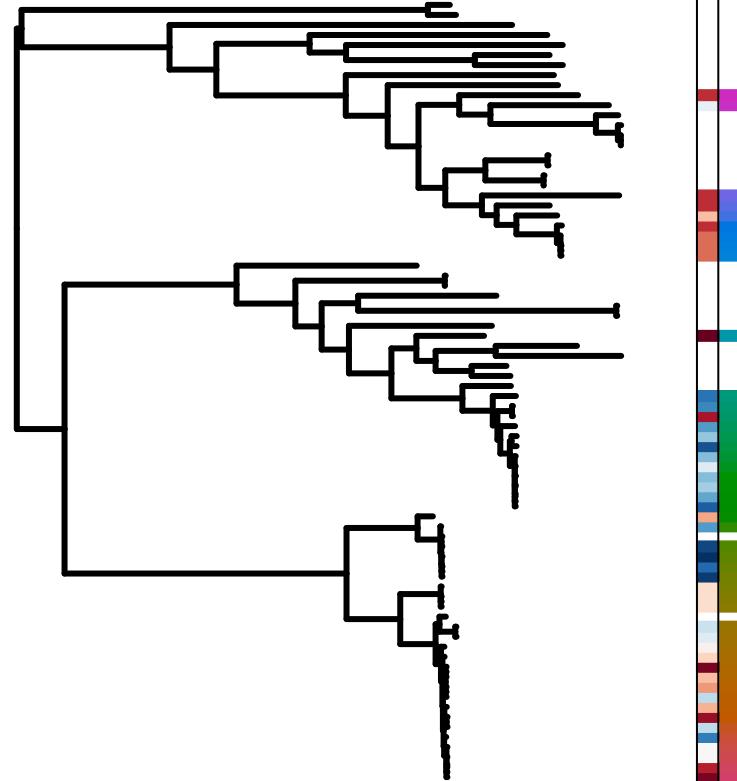
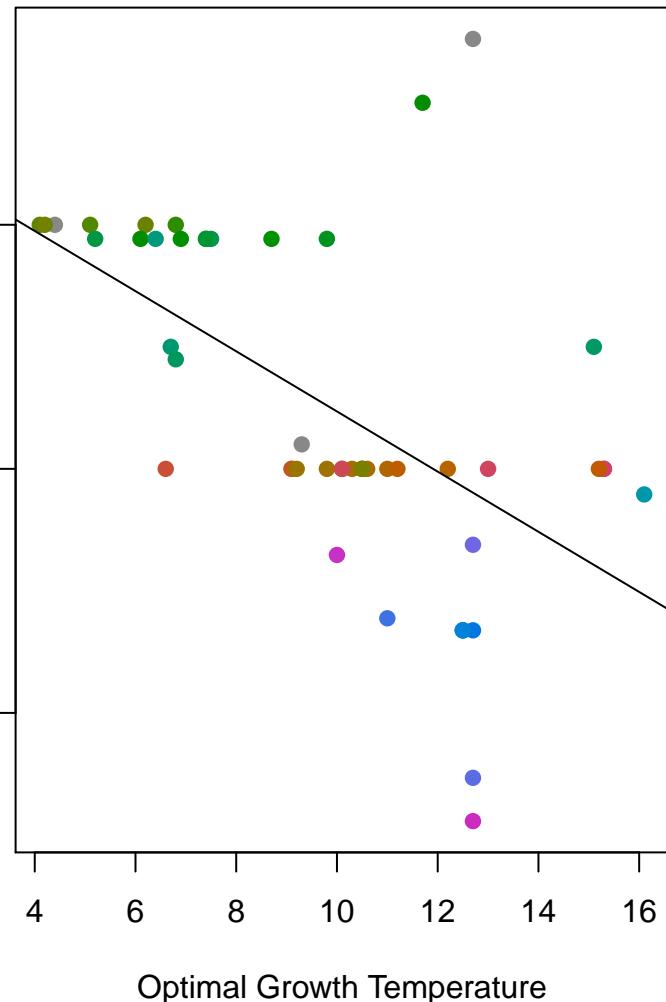


feature.pgfam_id.aromaticity.mean

PGF_00017109

Lipid-A-disaccharide synthase (EC 2.4.1.182)

$r = -0.569$, $p = 10^{-4.784}$

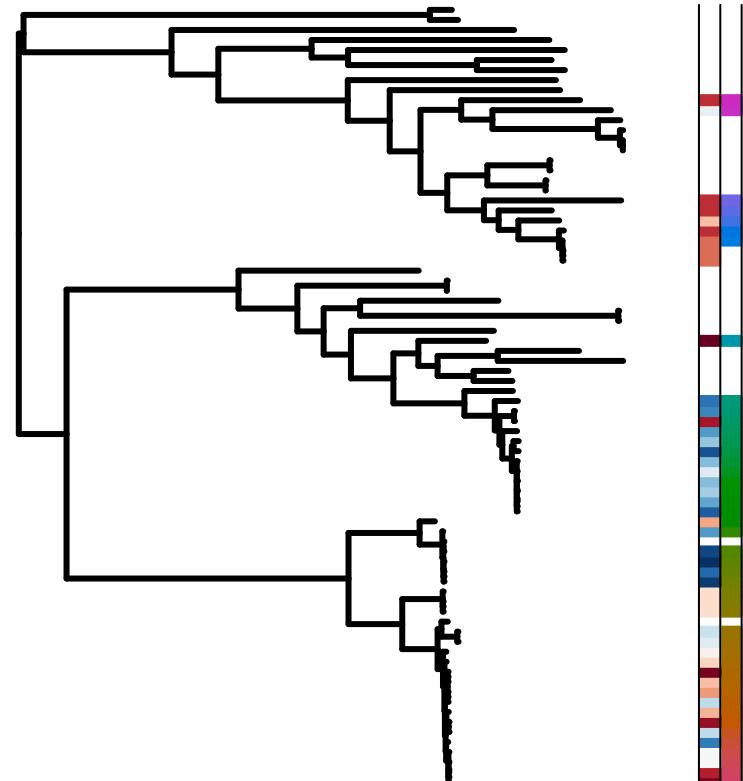
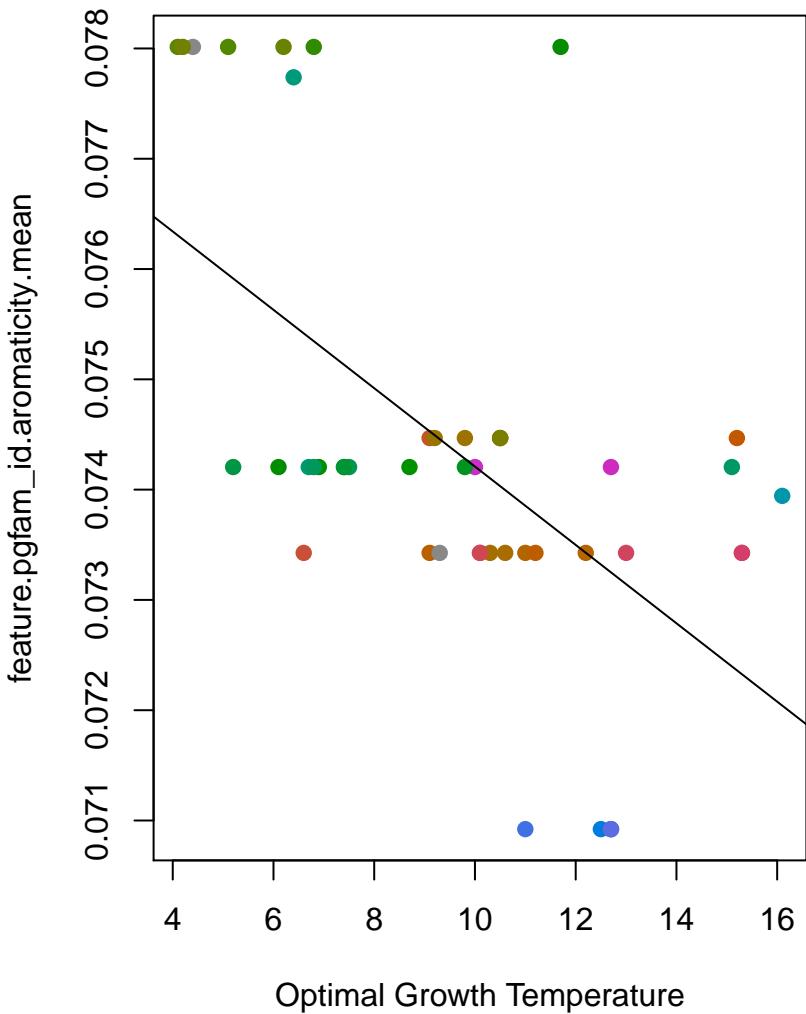


feature.pgfam_id.aromaticity.mean

PGF_03215471

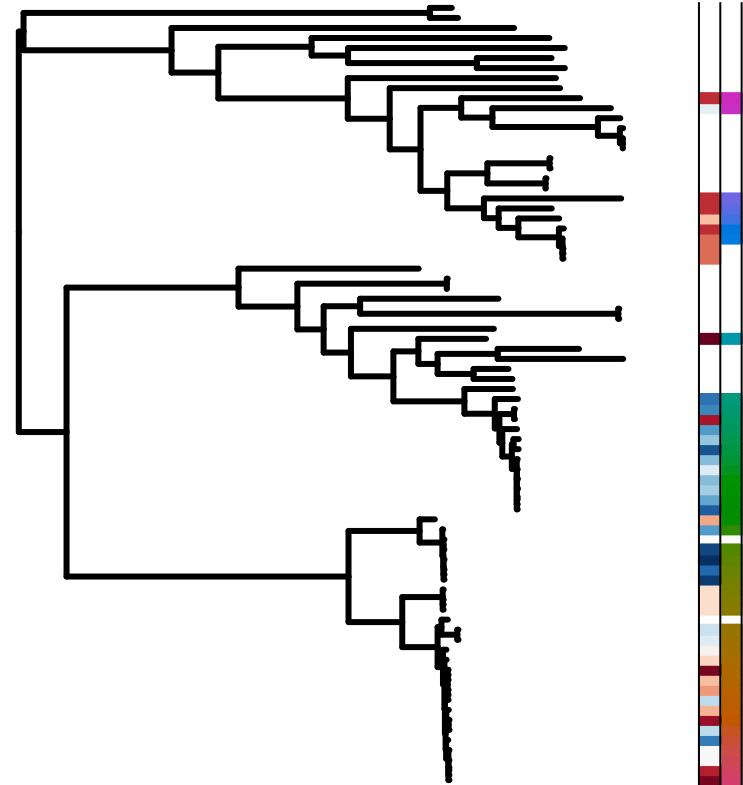
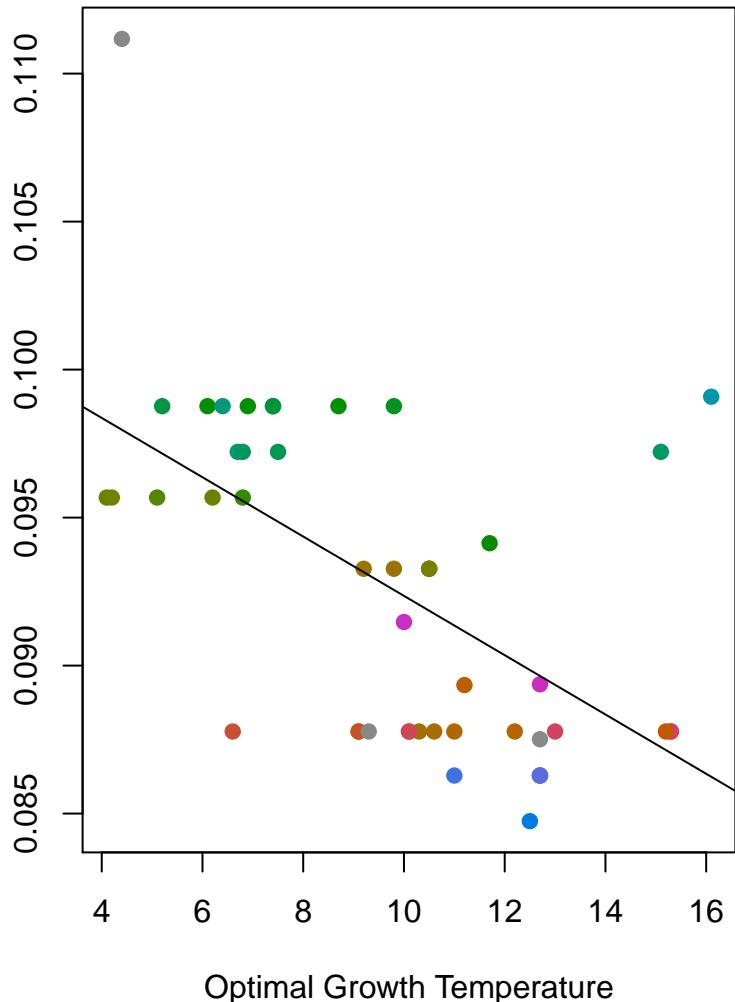
16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)

$r = -0.578$, $p = 10^{-4.678}$

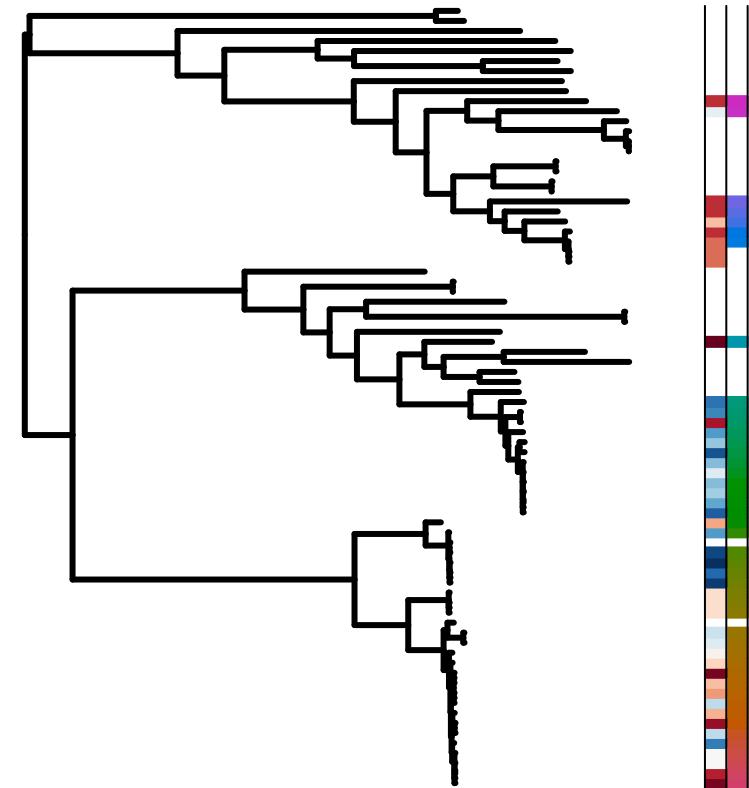
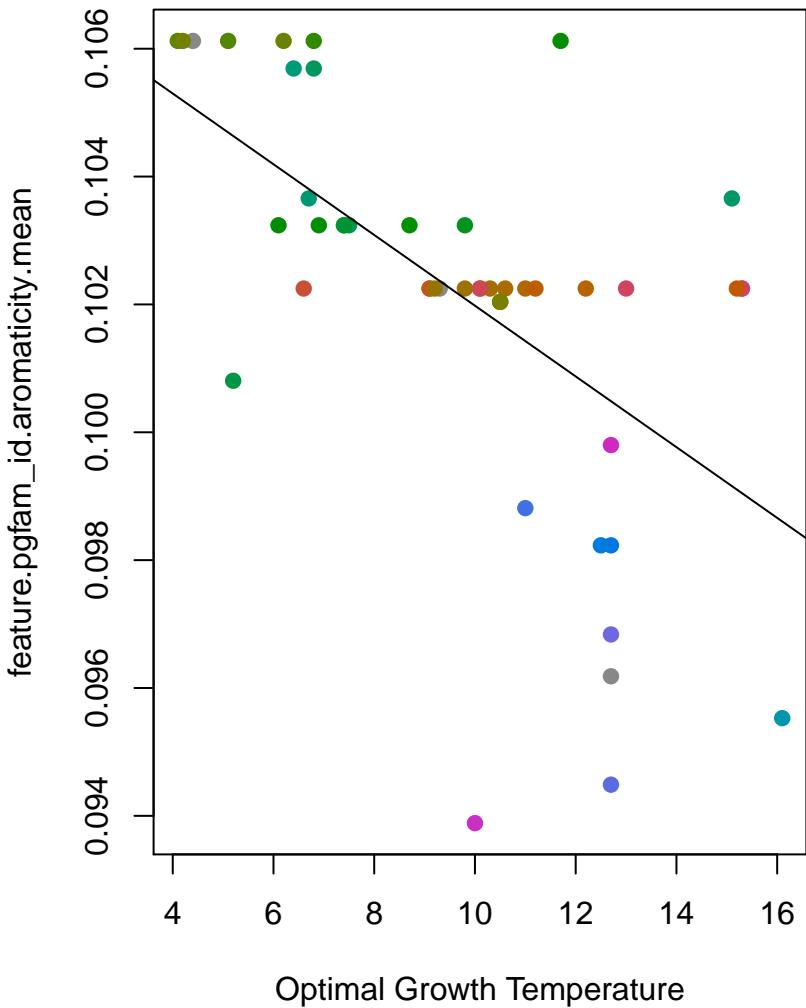


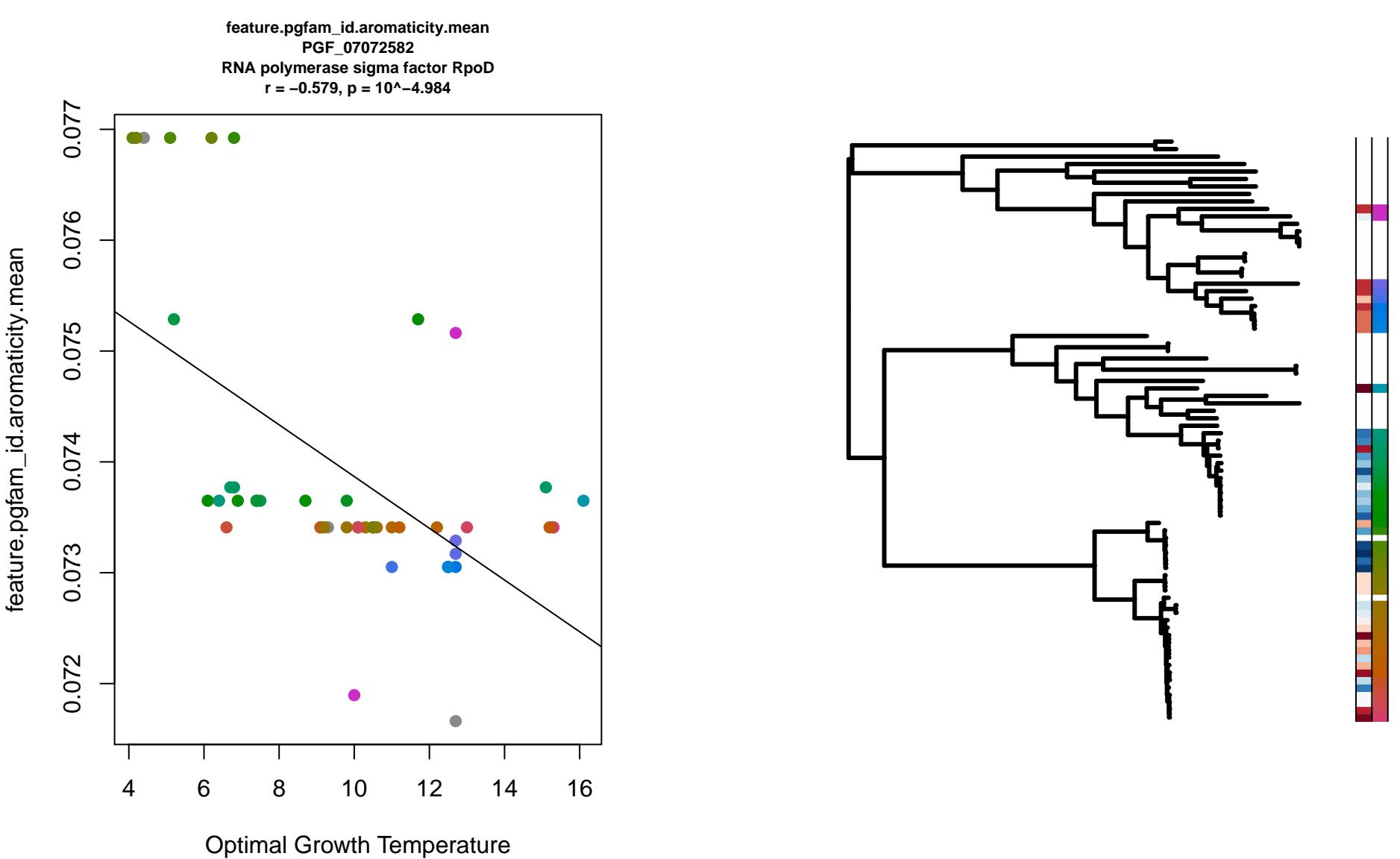
feature.pgfam_id.aromaticity.mean
PGF_10013075
DNA topoisomerase III (EC 5.99.1.2)
 $r = -0.578$, $p = 10^{-4.773}$

feature.pgfam_id.aromaticity.mean



feature.pgfam_id.aromaticity.mean
PGF_06261512
Flagellar regulatory protein FleQ
 $r = -0.579$, $p = 10^{-4.794}$



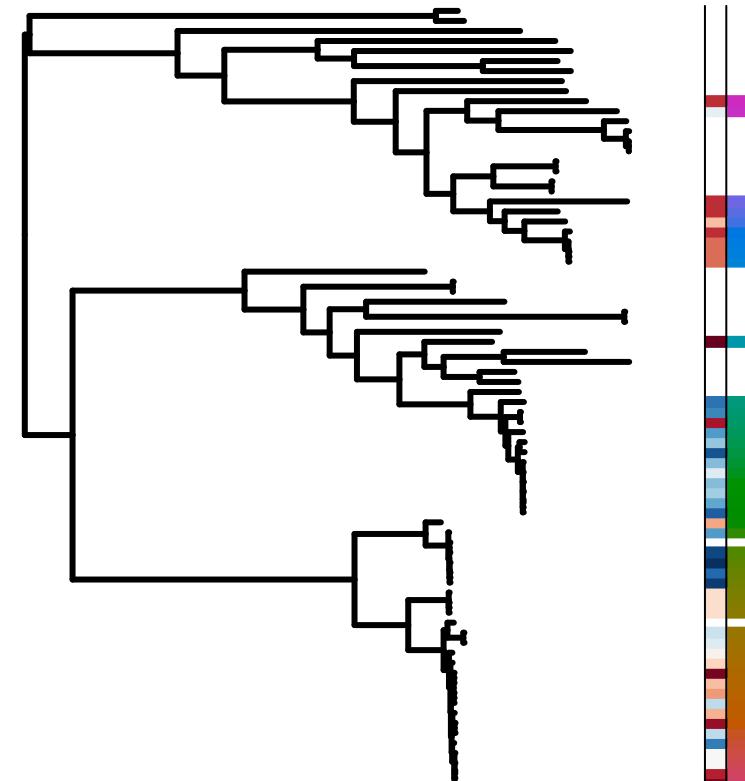
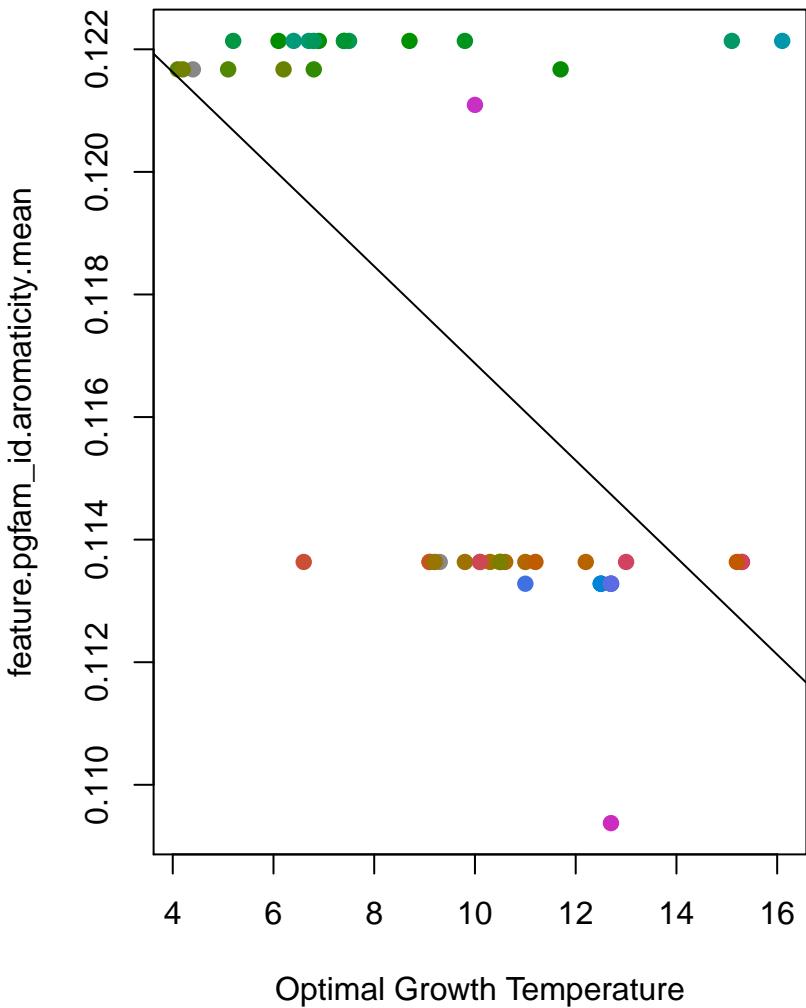


feature.pgfam_id.aromaticity.mean

PGF_00033729

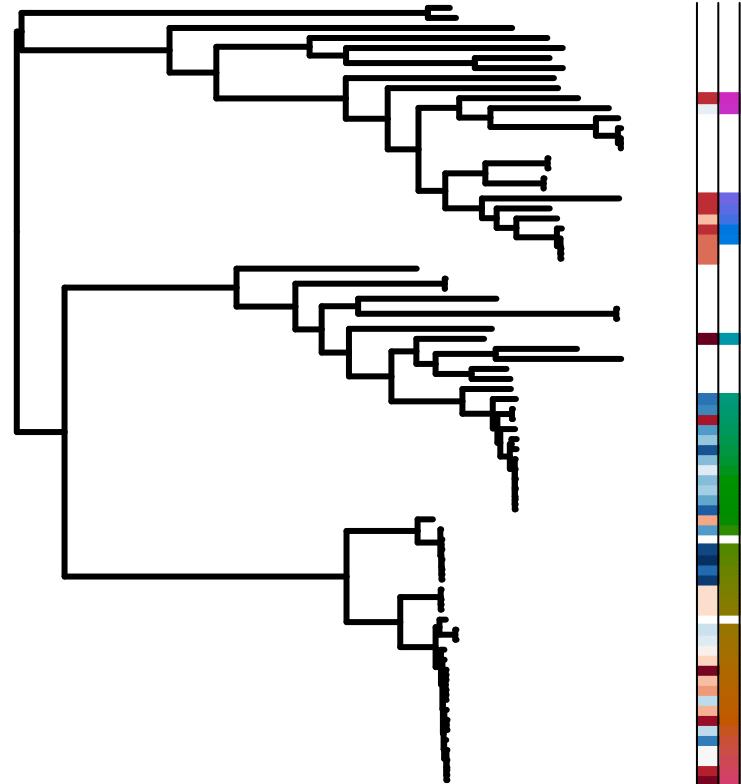
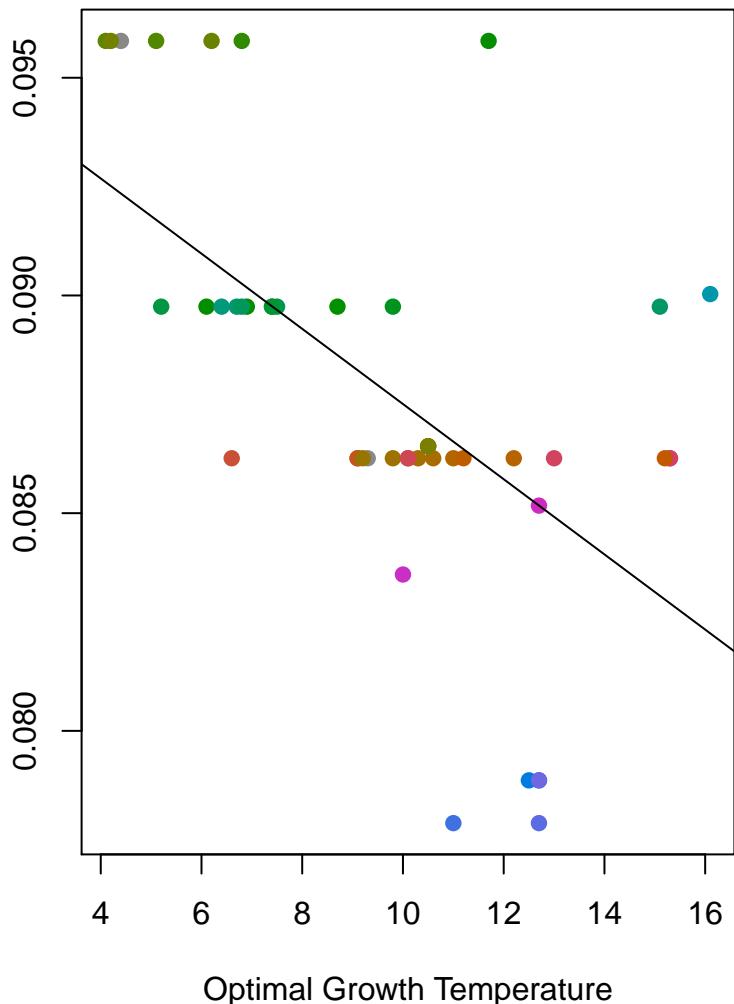
Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129)

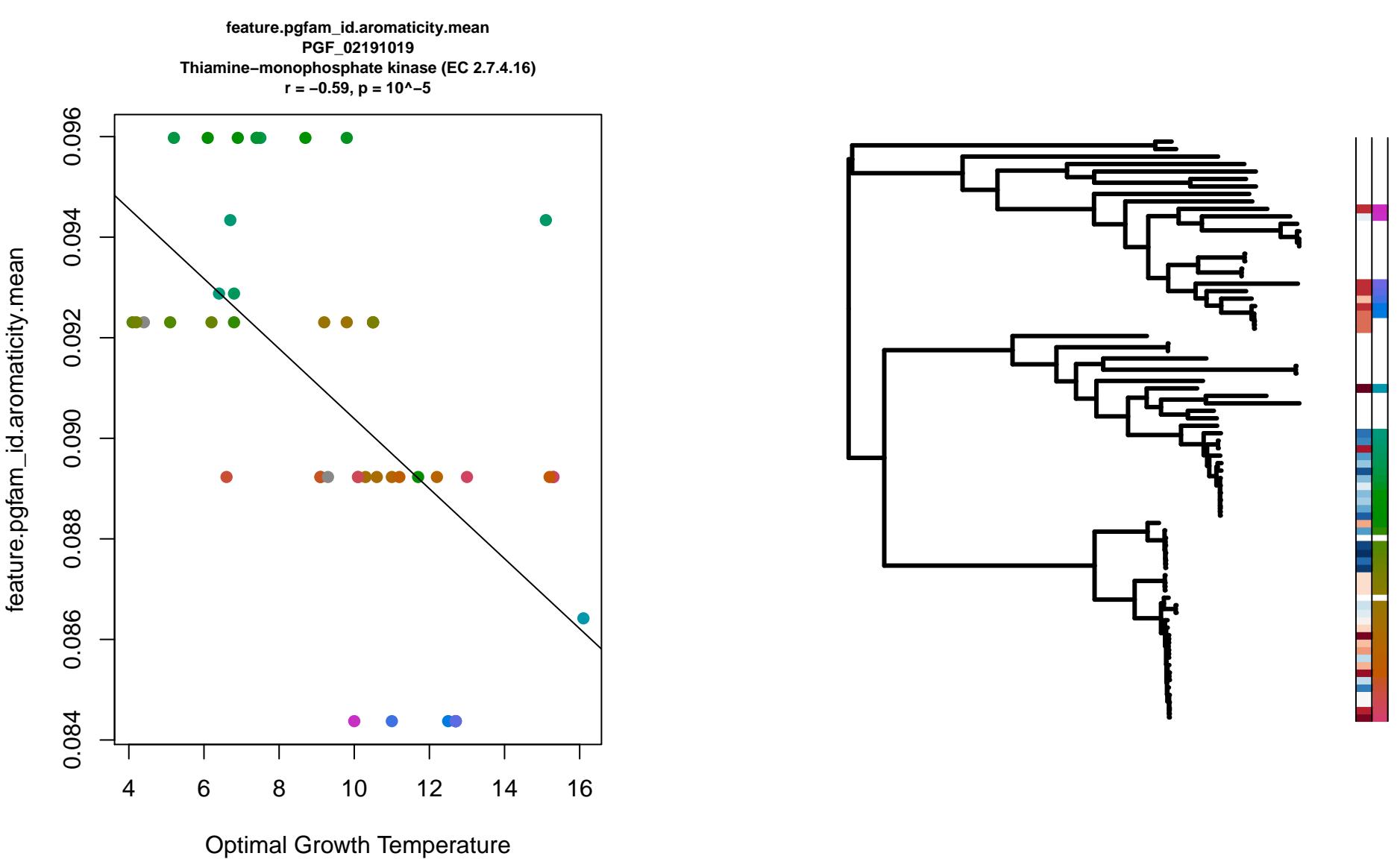
$r = -0.581$, $p = 10^{-5.011}$



feature.pgfam_id.aromaticity.mean
PGF_10518532
D-alanine--D-alanine ligase (EC 6.3.2.4)
 $r = -0.586$, $p = 10^{-4.825}$

feature.pgfam_id.aromaticity.mean





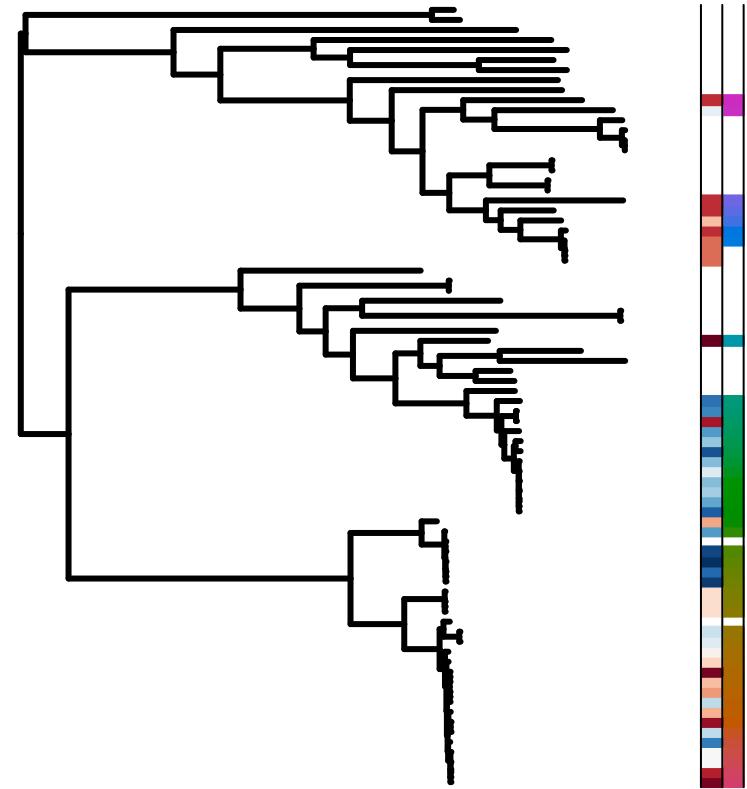
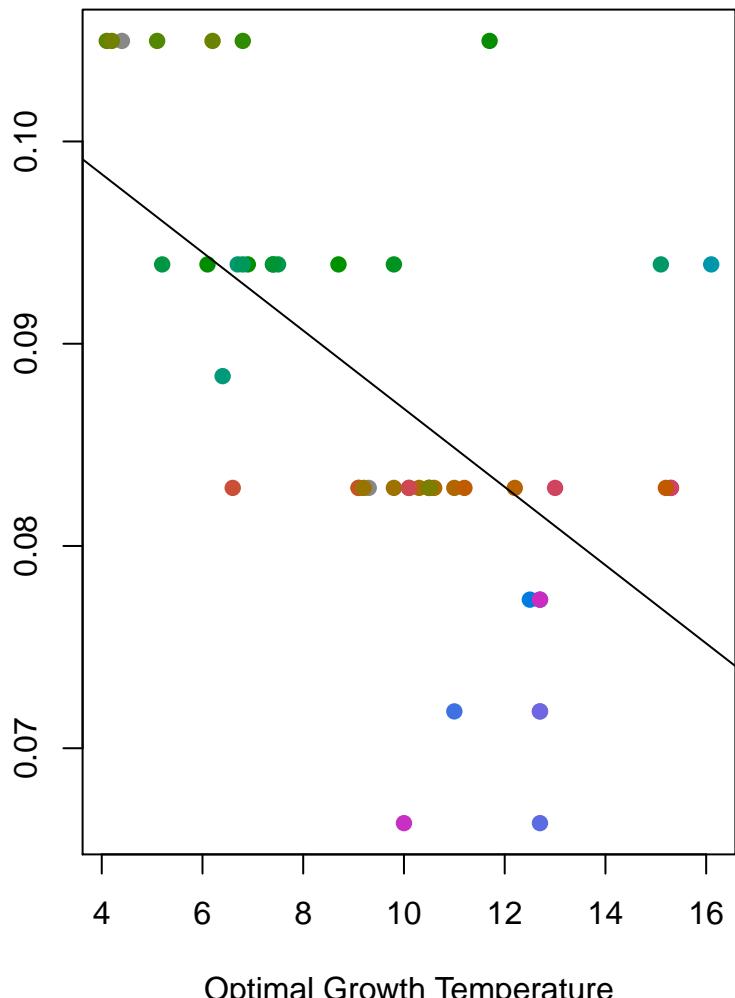
feature.pgfam_id.aromaticity.mean

PGF_06894101

3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)

$r = -0.595, p = 10^{-5.089}$

feature.pgfam_id.aromaticity.mean

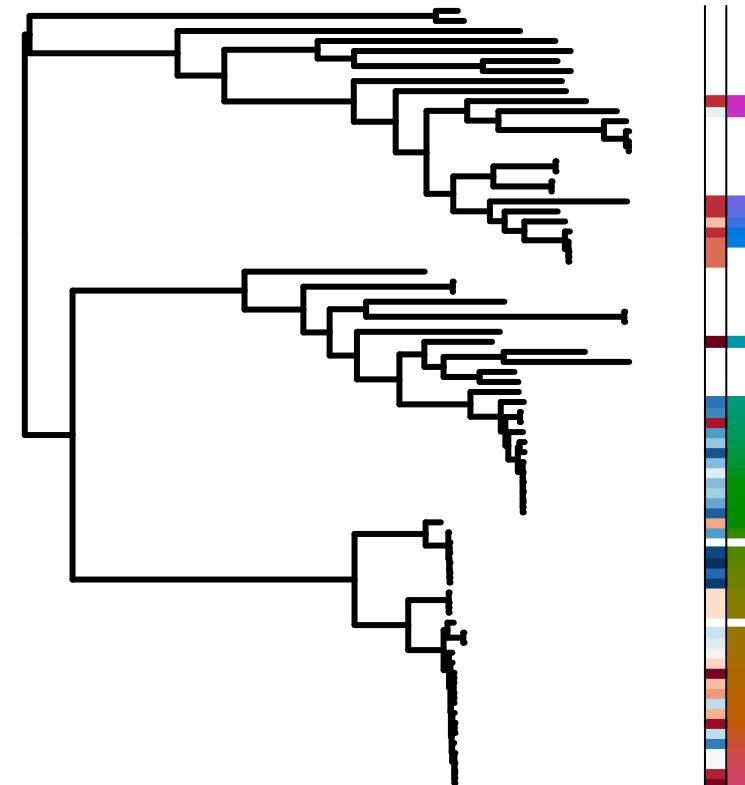
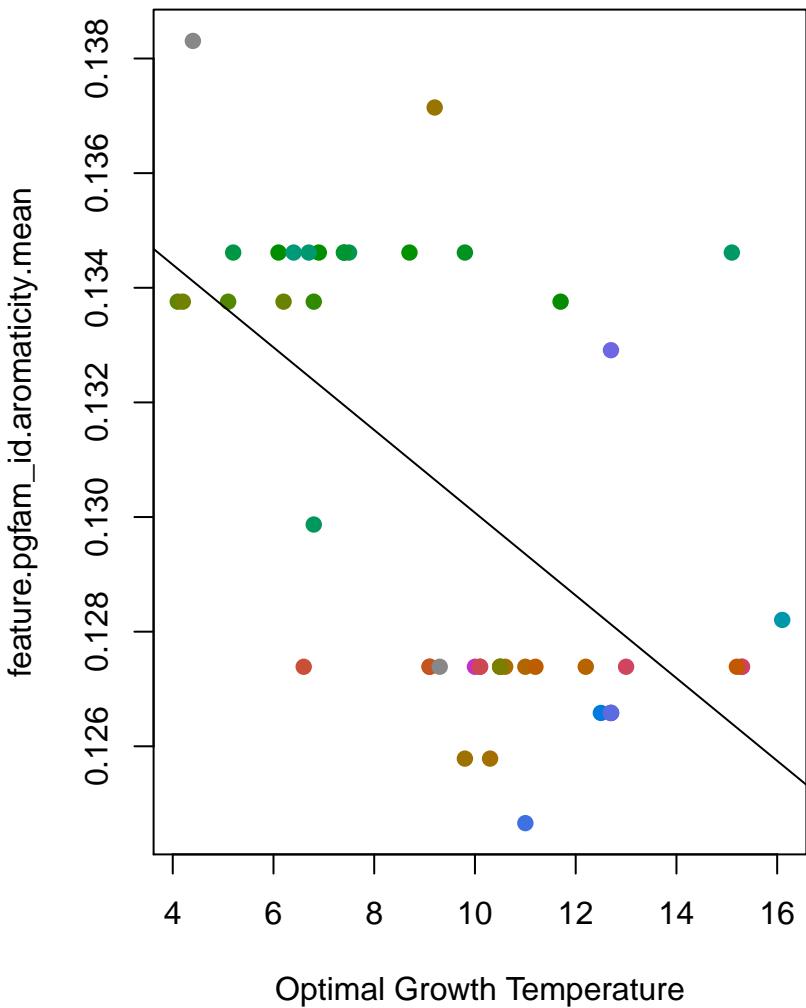


feature.pgfam_id.aromaticity.mean

PGF_00220548

Thiol peroxidase, Bcp-type (EC 1.11.1.15)

$r = -0.597, p = 10^{-5.118}$



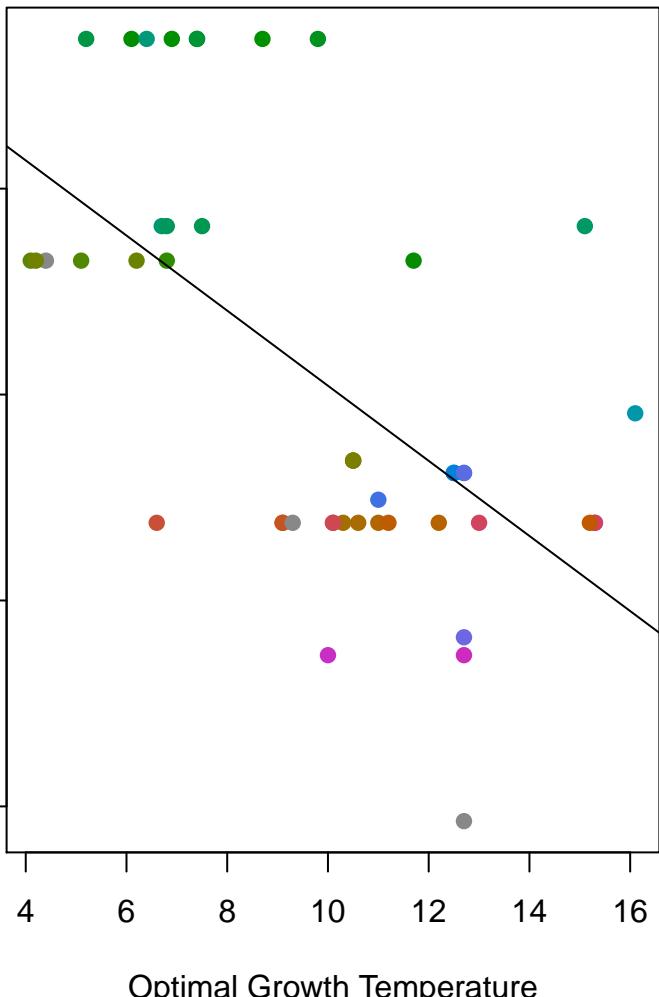
feature.pgfam_id.aromaticity.mean

PGF_01336507

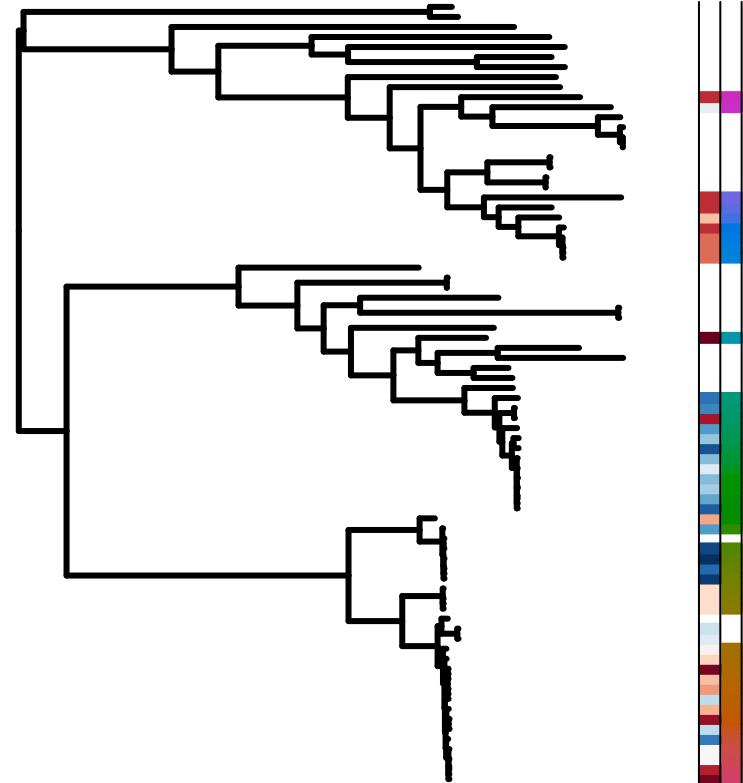
hypothetical protein

$r = -0.599, p = 10^{-5.154}$

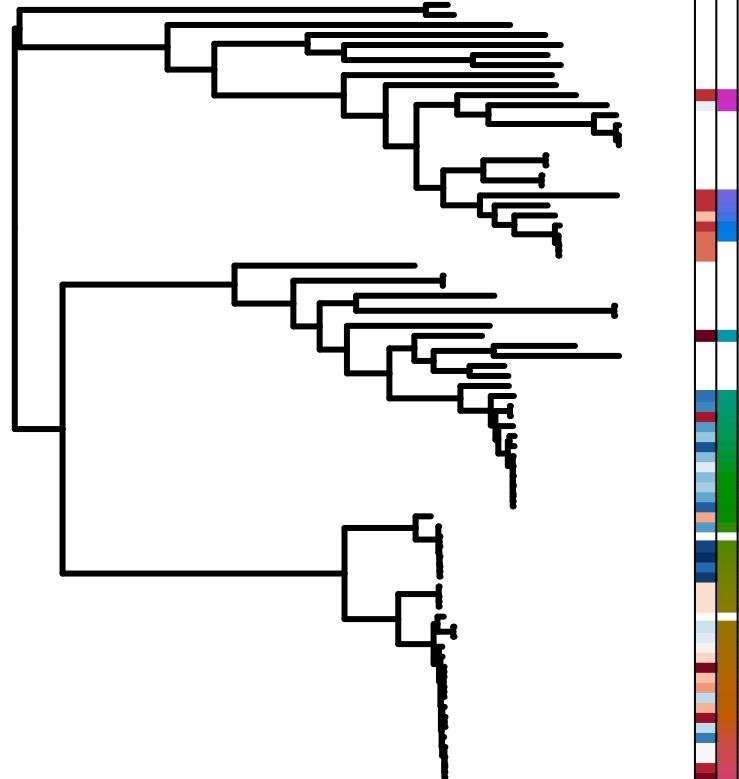
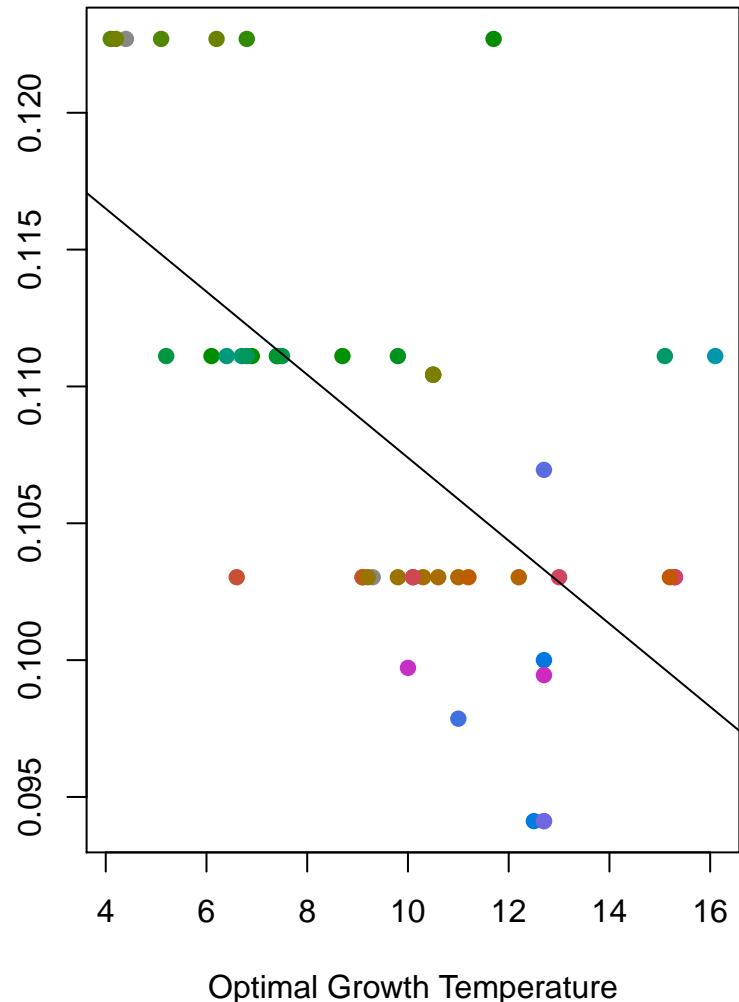
feature.pgfam_id.aromaticity.mean

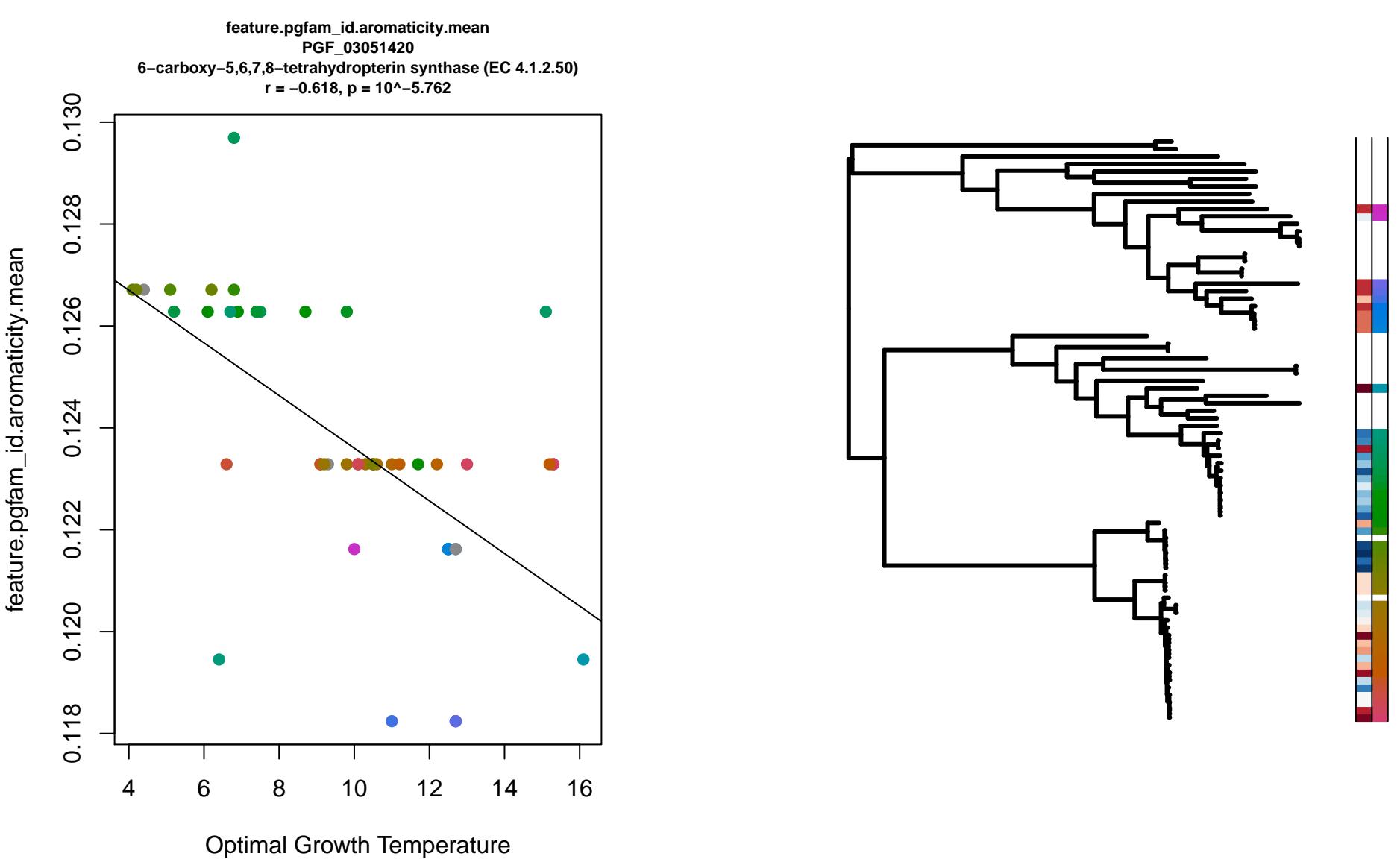


Optimal Growth Temperature



feature.pgfam_id.aromaticity.mean
PGF_09348764
Dihydrofolate reductase (EC 1.5.1.3)
r = -0.607, p = 10^-5.318





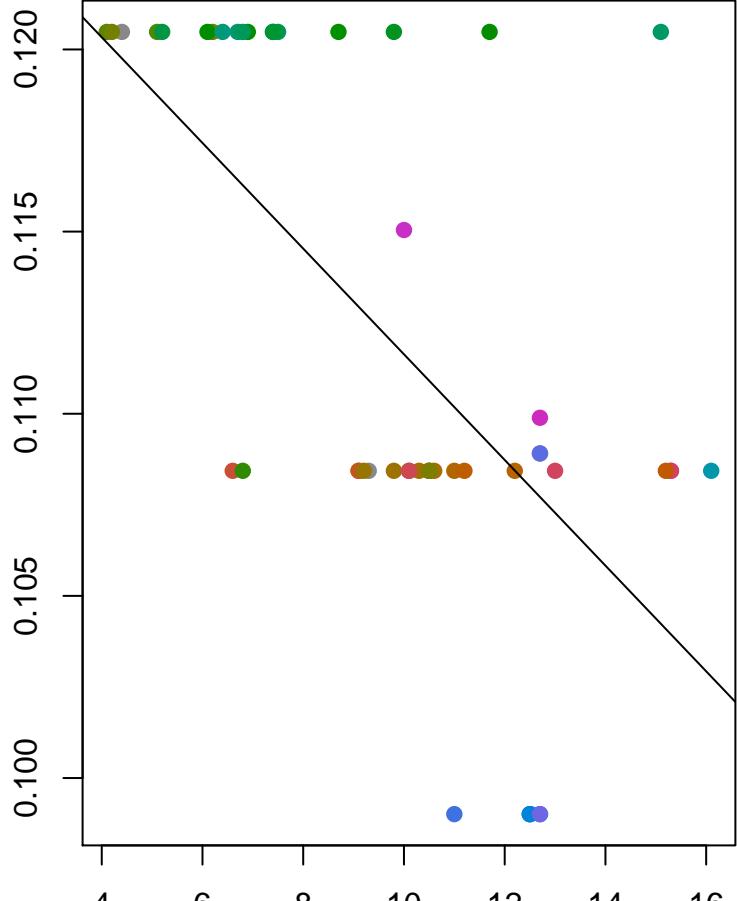
feature.pgfam_id.aromaticity.mean

PGF_02069837

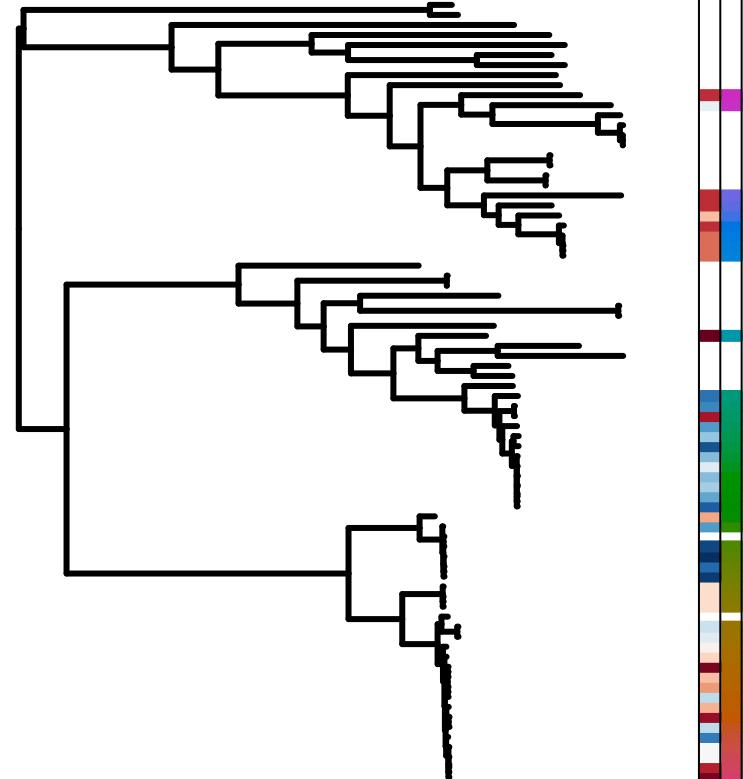
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin

$r = -0.626, p = 10^{-5.944}$

feature.pgfam_id.aromaticity.mean



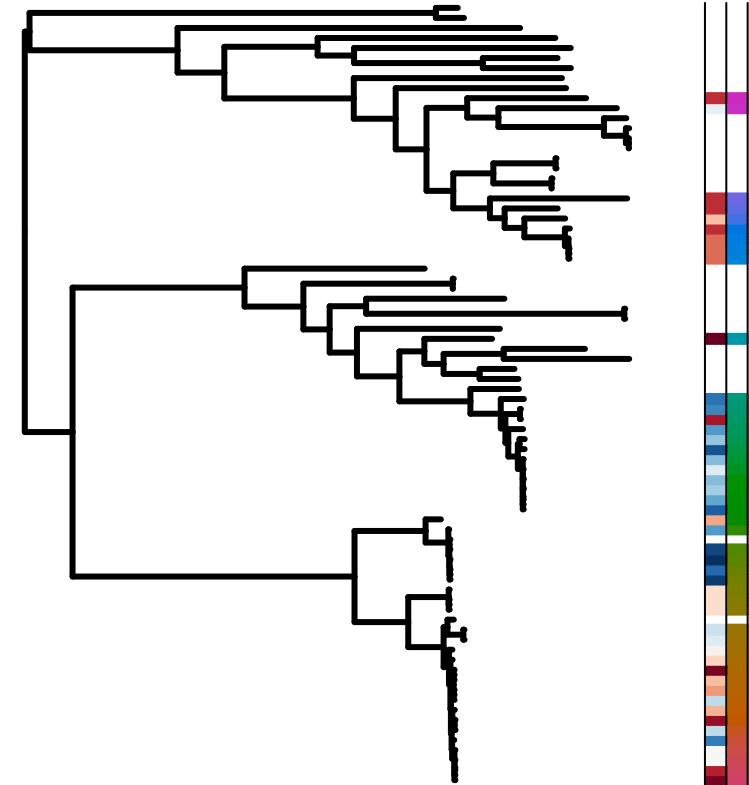
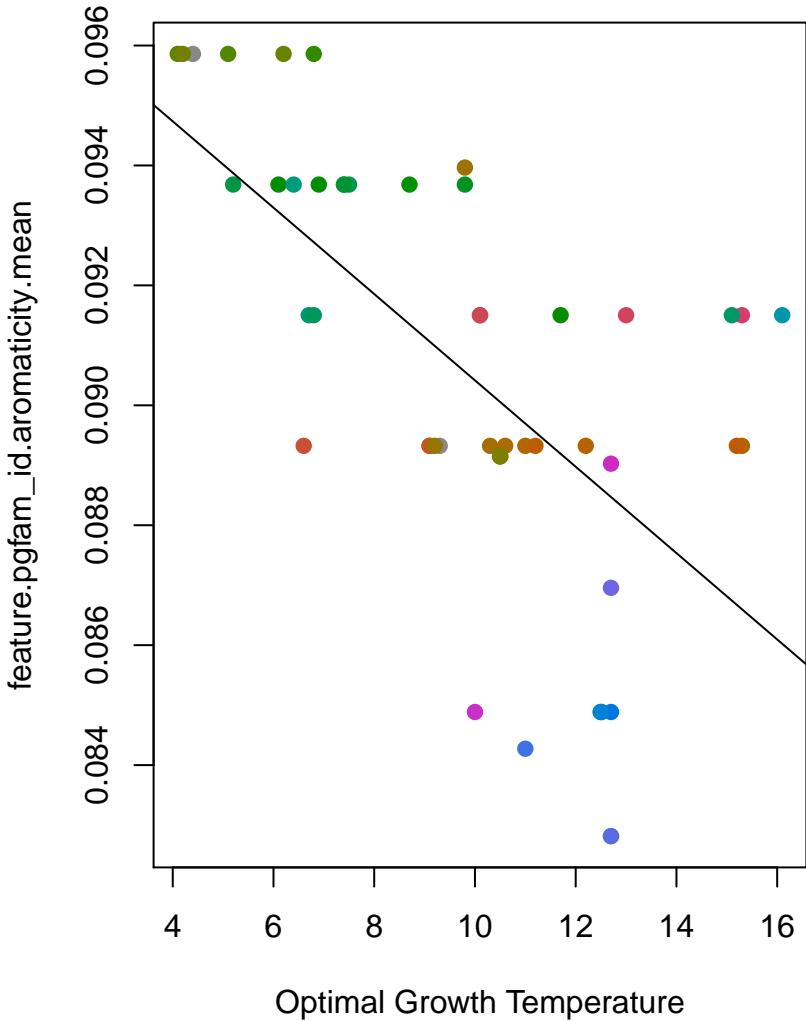
Optimal Growth Temperature



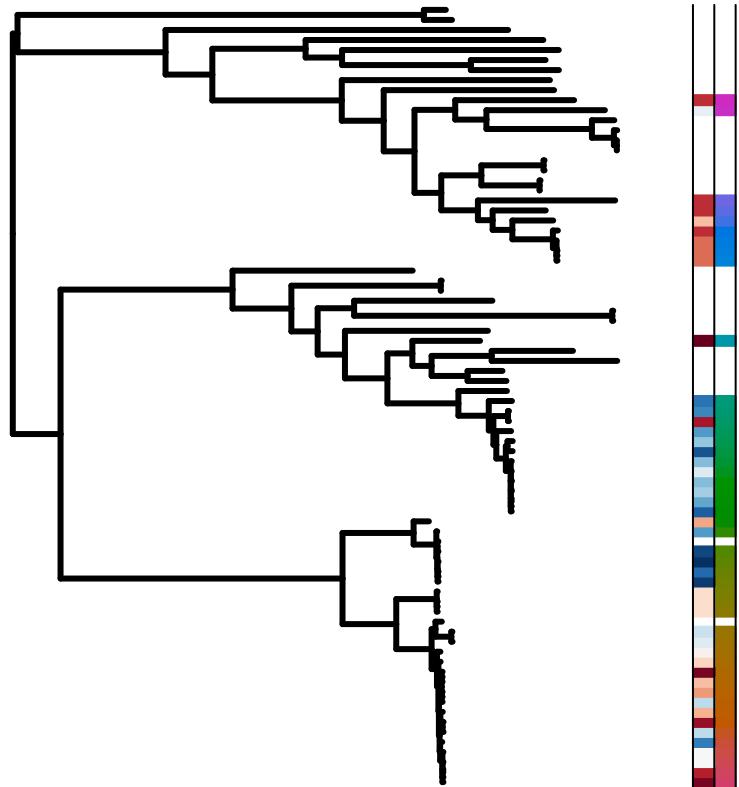
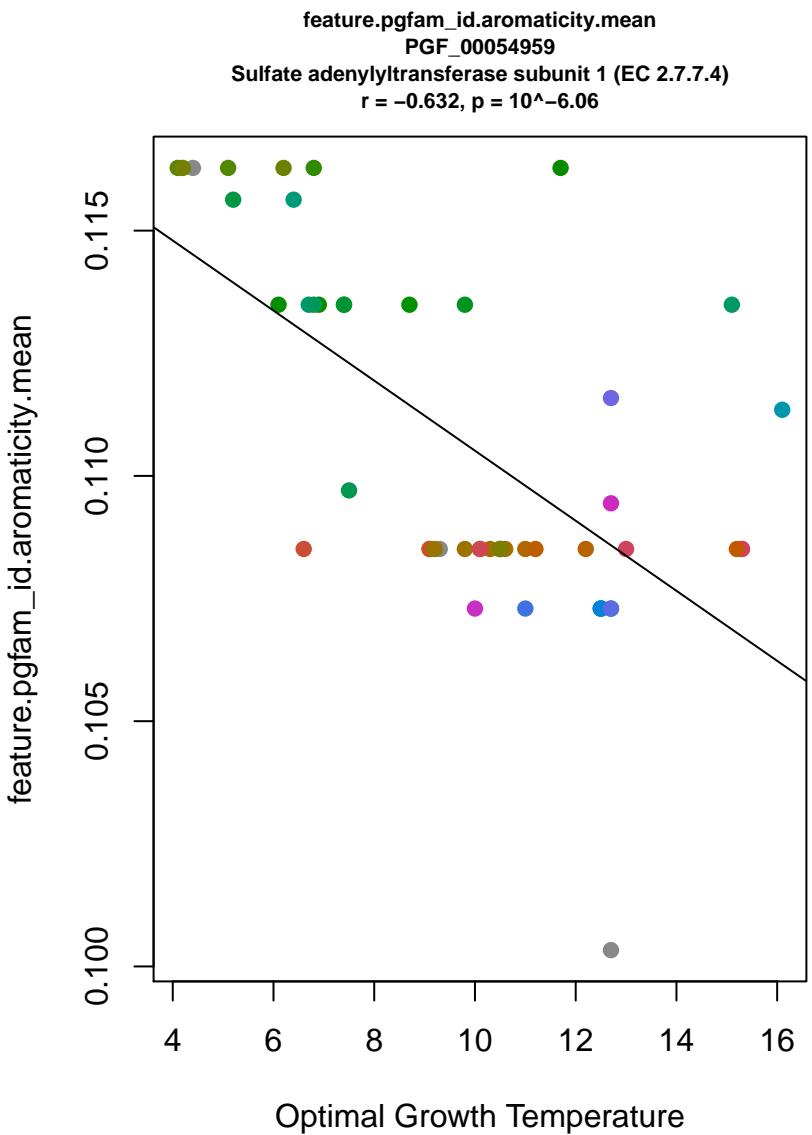
feature.pgfam_id.aromaticity.mean

PGF_06051594

Predicted ATPase related to phosphate starvation-inducible protein PhoH
 $r = -0.631, p = 10^{-6.049}$



Optimal Growth Temperature

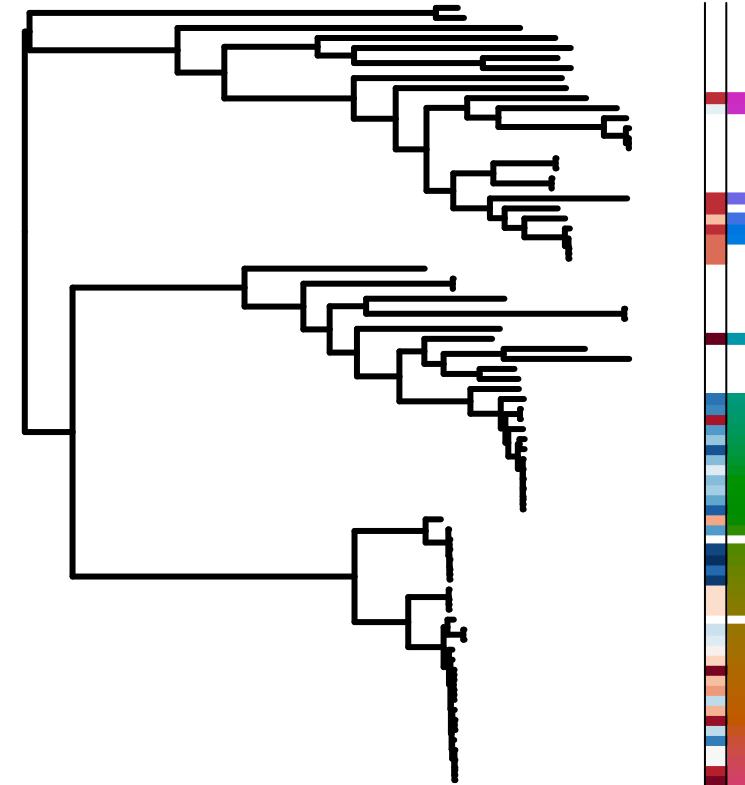
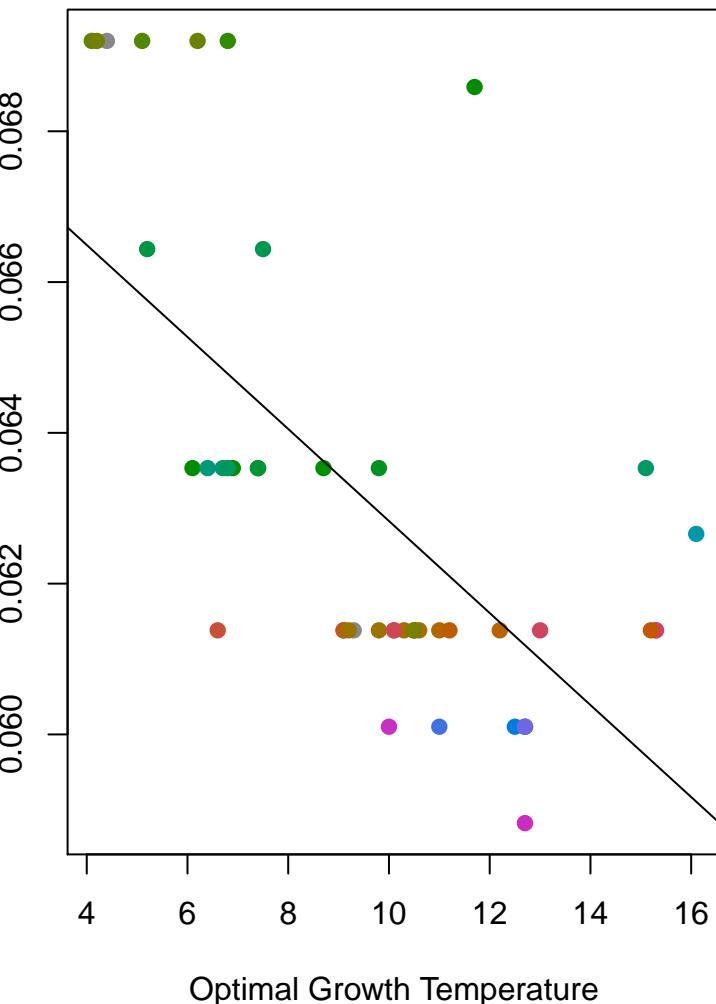
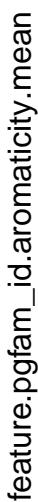


feature.pgfam_id.aromaticity.mean

PGF_04438983

ATP-dependent protease La (EC 3.4.21.53) Type I

$r = -0.651, p = 10^{-6.143}$



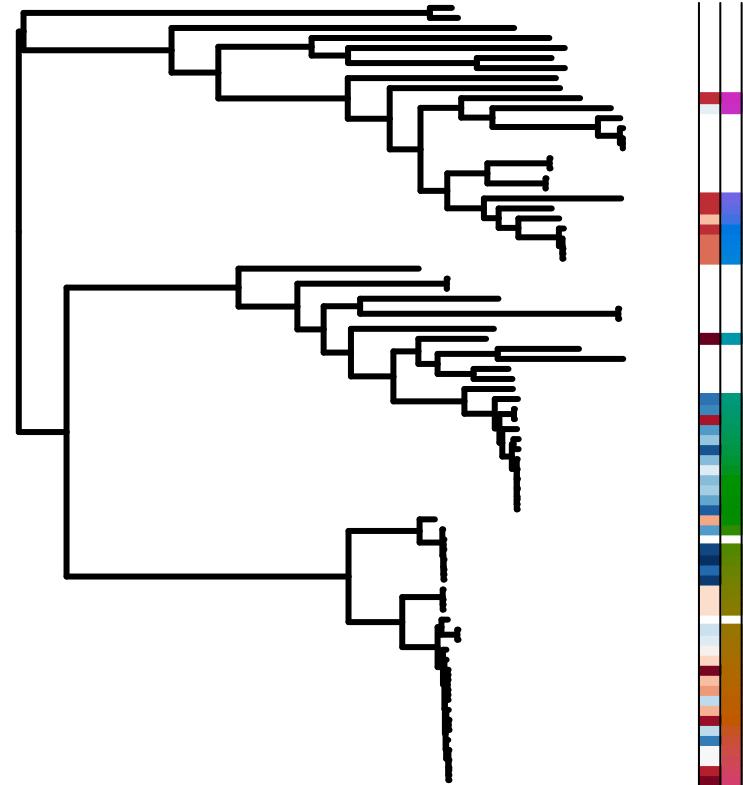
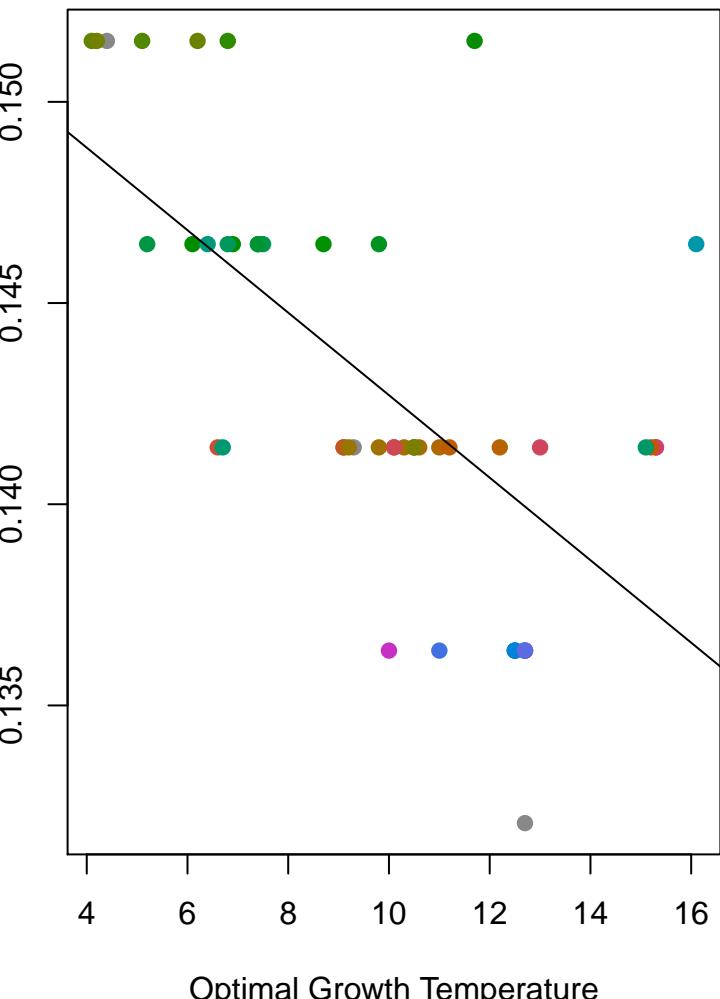
feature.pgfam_id.aromaticity.mean

PGF_06660812

3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)

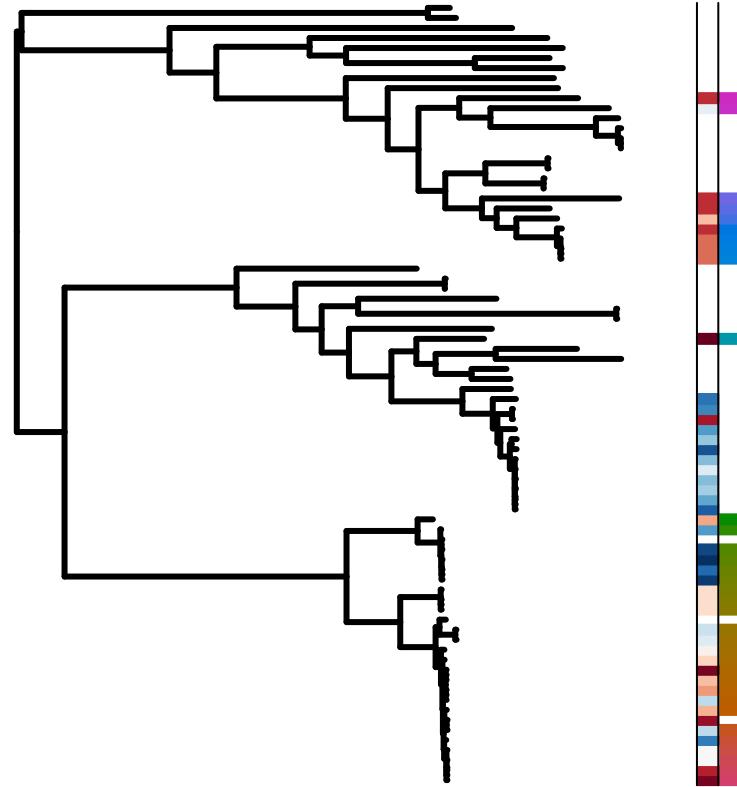
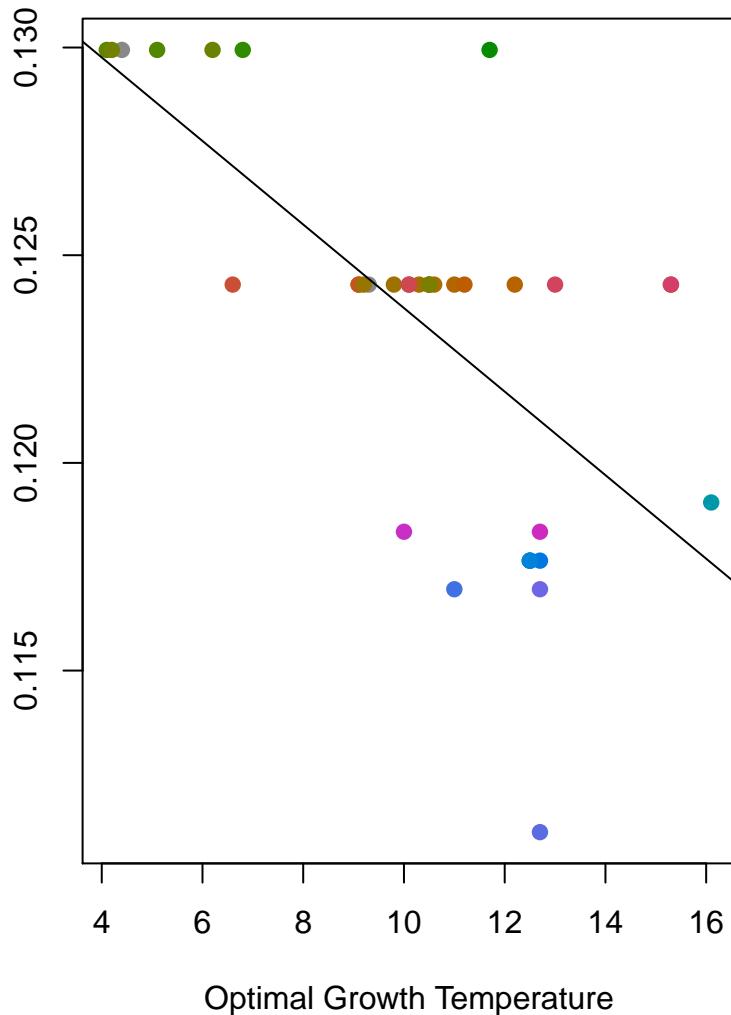
$r = -0.652, p = 10^{-6.524}$

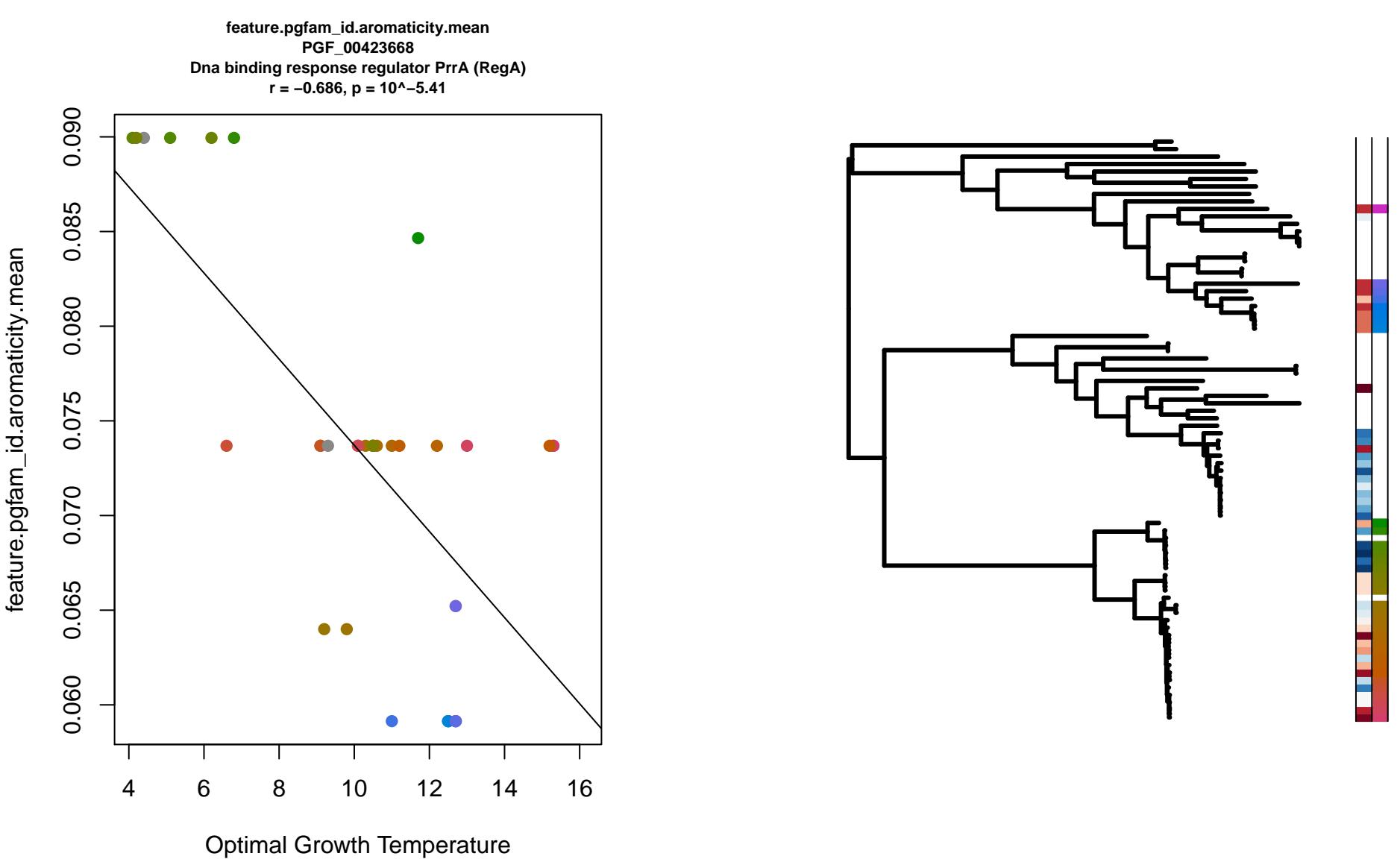
feature.pgfam_id.aromaticity.mean

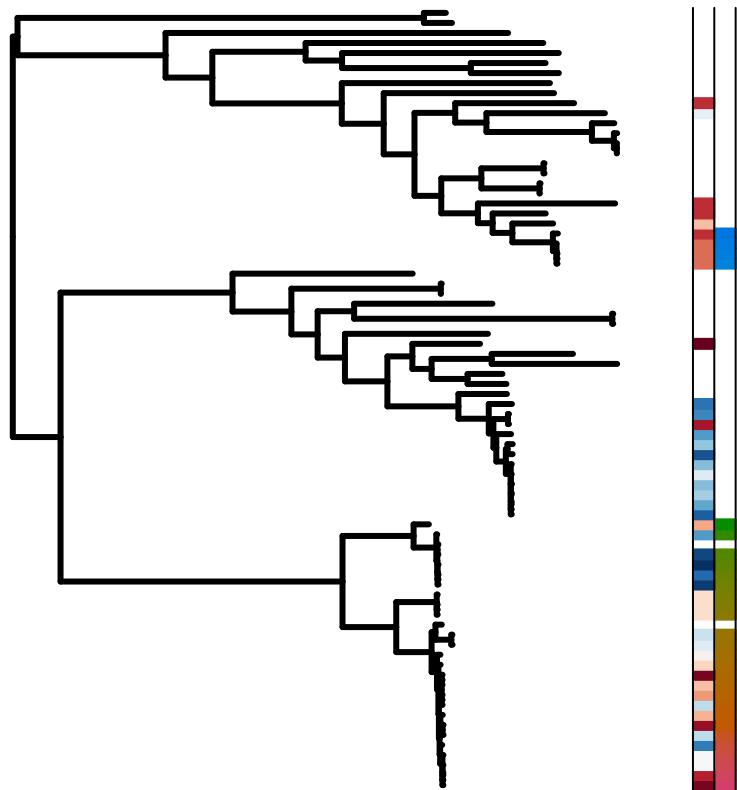
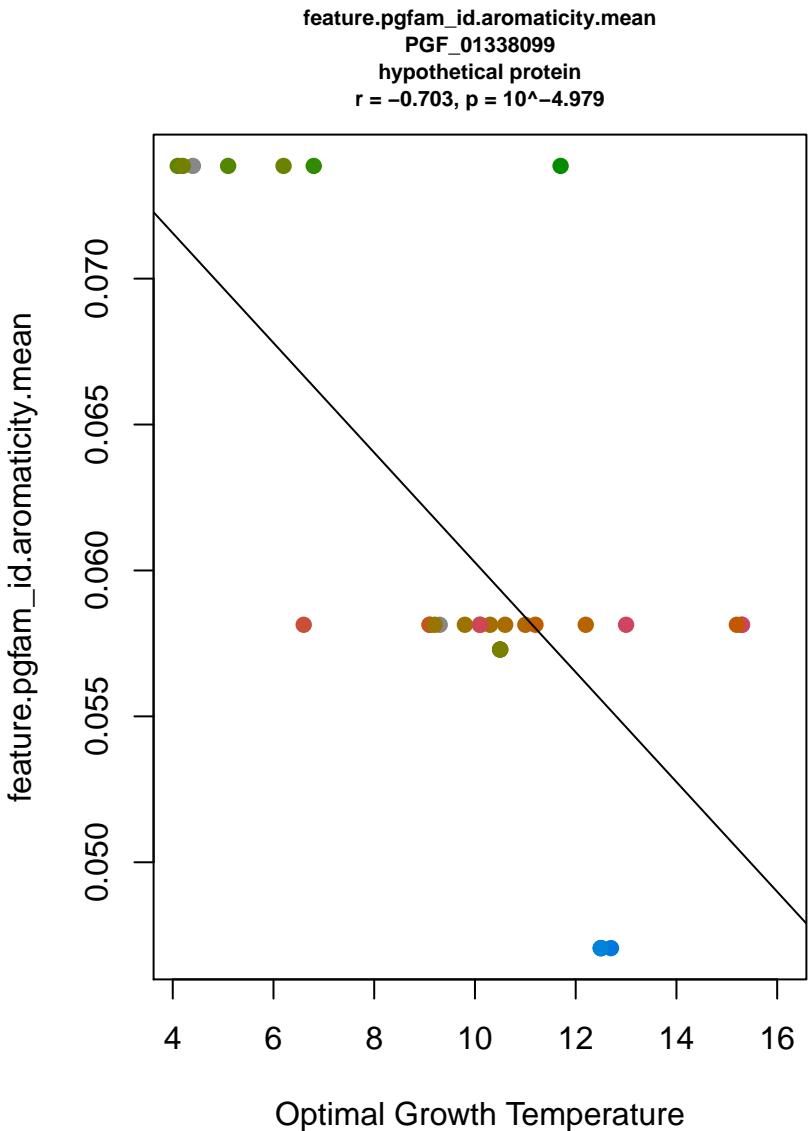


feature.pgfam_id.aromaticity.mean
PGF_03021302
Ureidoglycolate lyase (EC 4.3.2.3)
 $r = -0.658, p = 10^{-4.892}$

feature.pgfam_id.aromaticity.mean





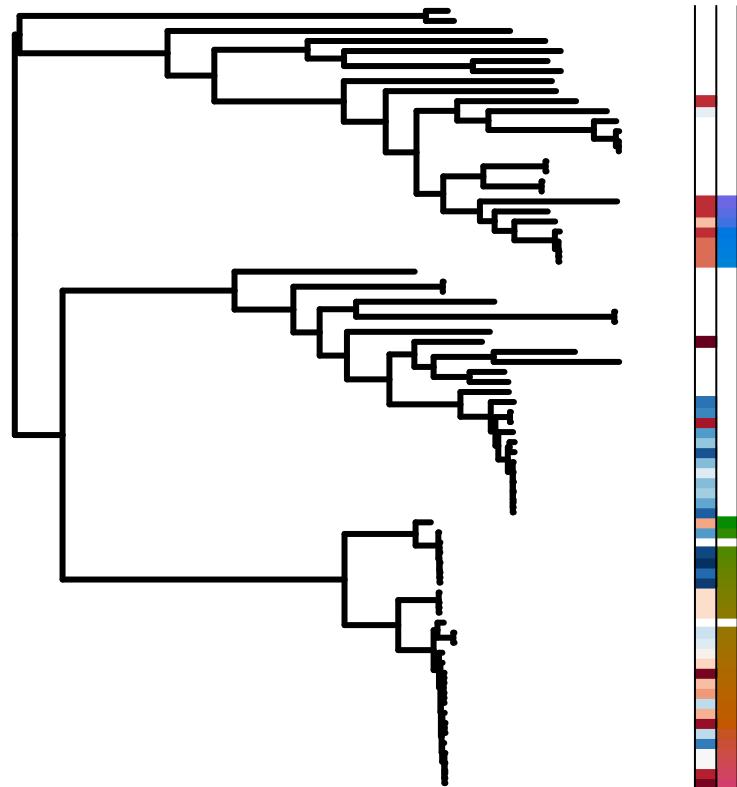
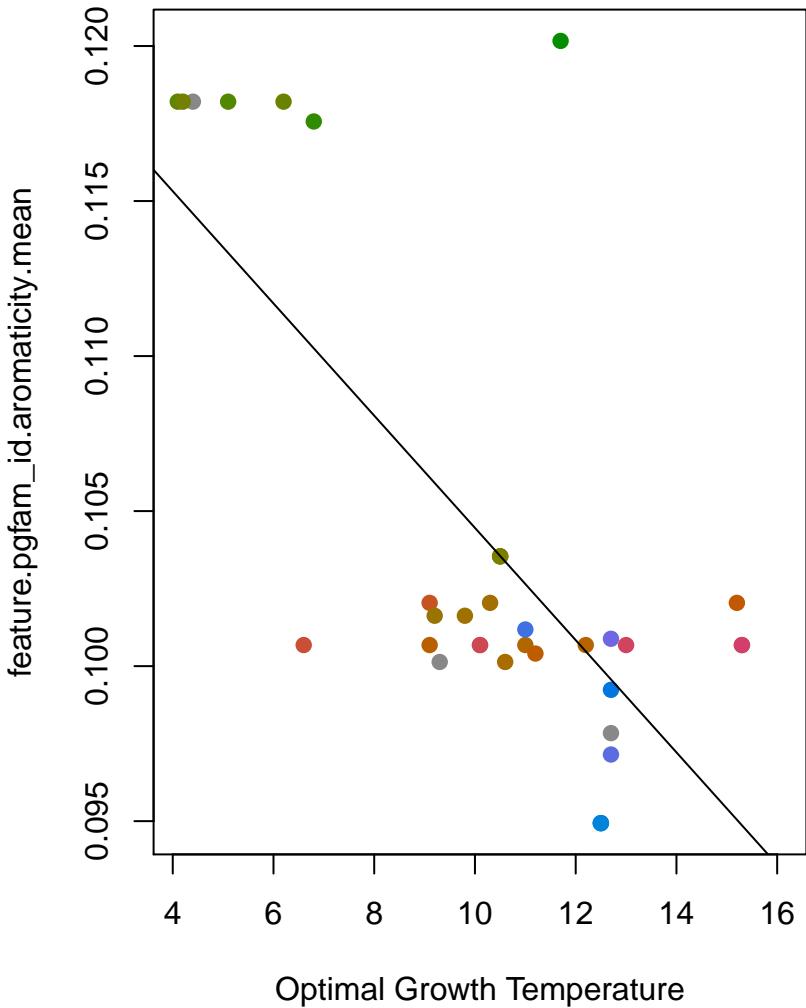


feature.pgfam_id.aromaticity.mean

PGF_00014974

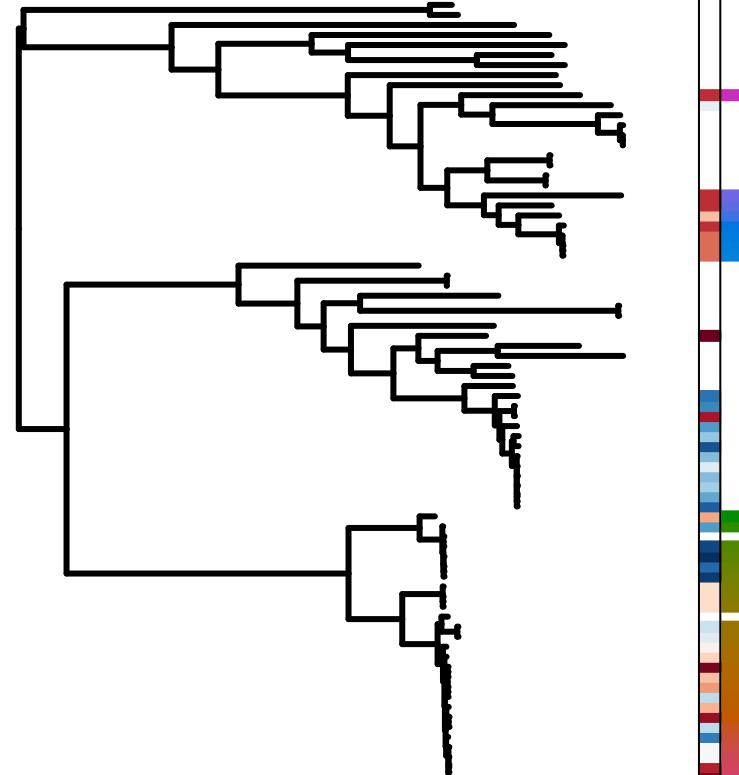
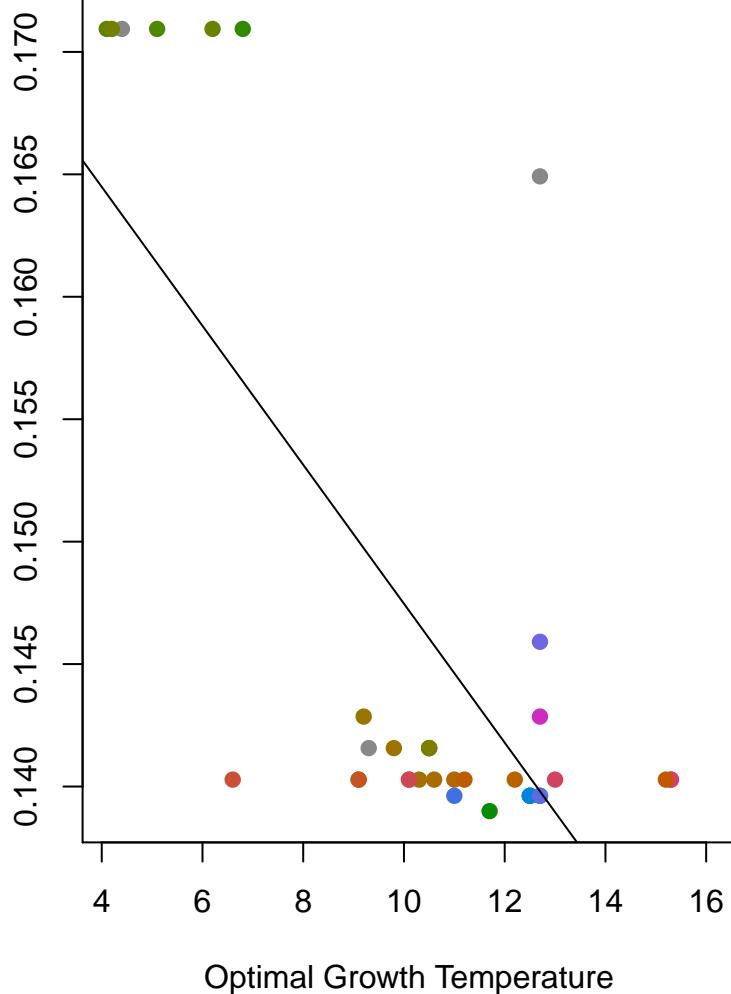
Inter-alpha-trypsin inhibitor domain protein

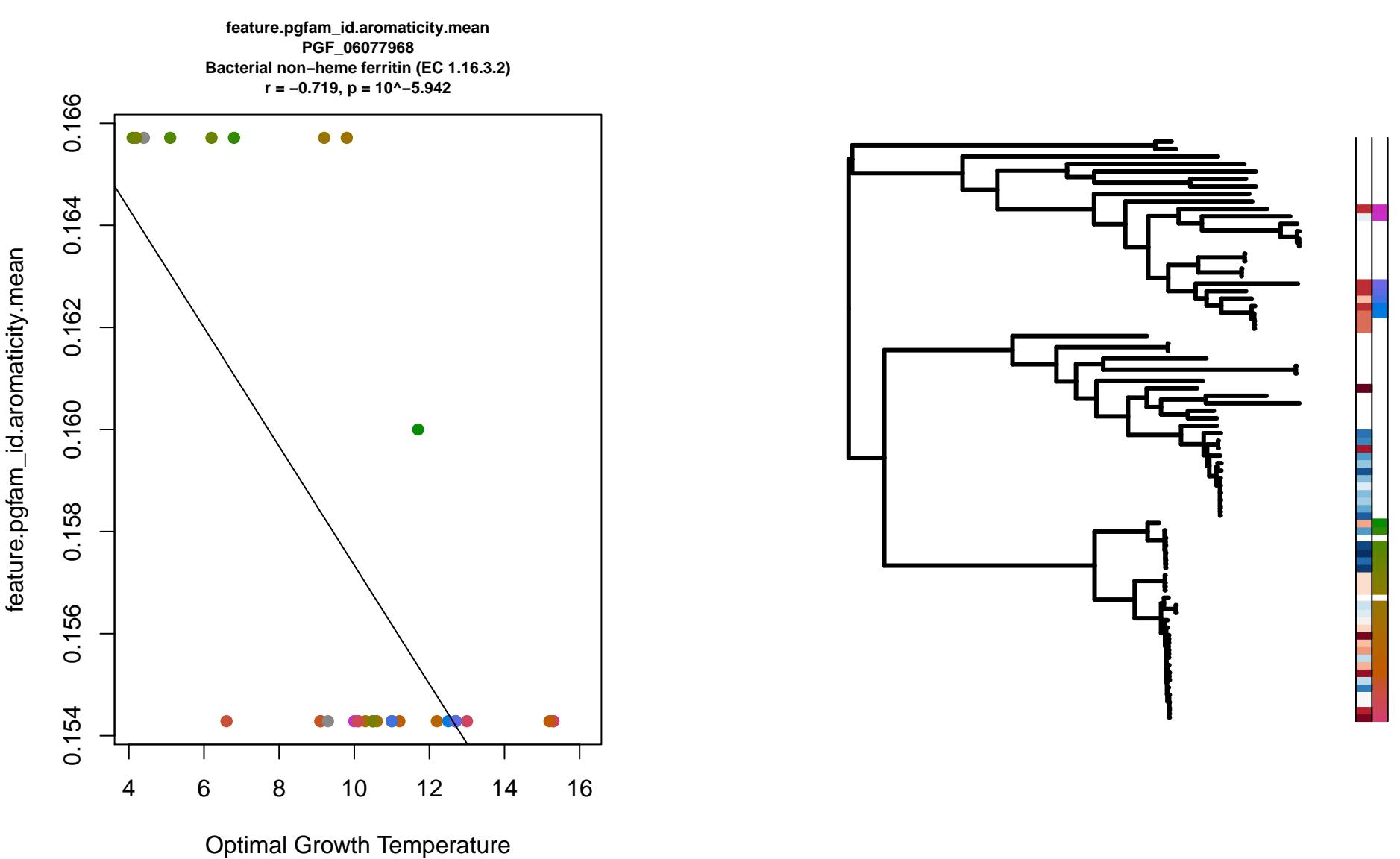
$r = -0.717$, $p = 10^{-5.89}$

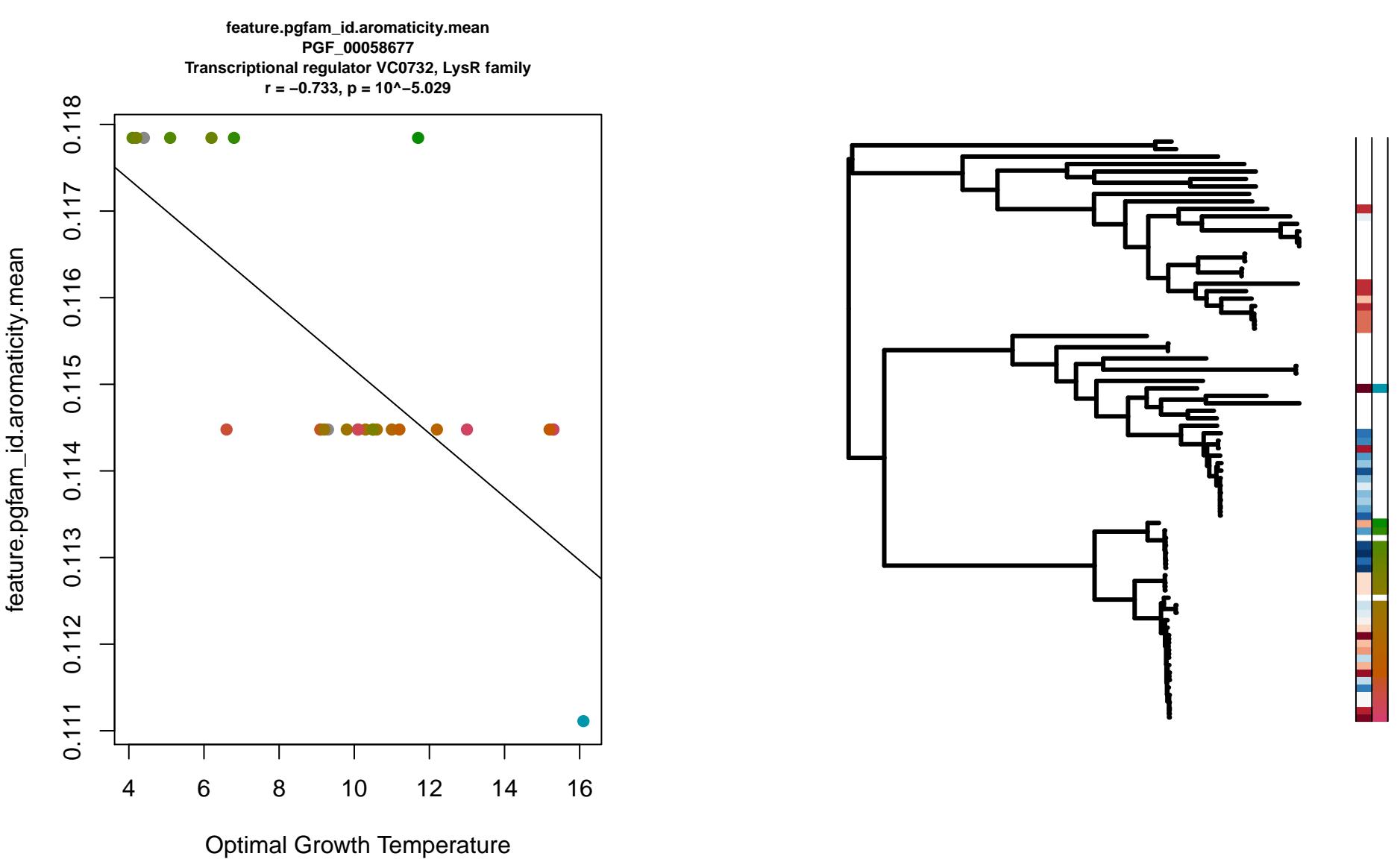


feature.pgfam_id.aromaticity.mean
PGF_00004056
Fatty acid cis/trans isomerase
 $r = -0.719$, $p = 10^{-6.096}$

feature.pgfam_id.aromaticity.mean







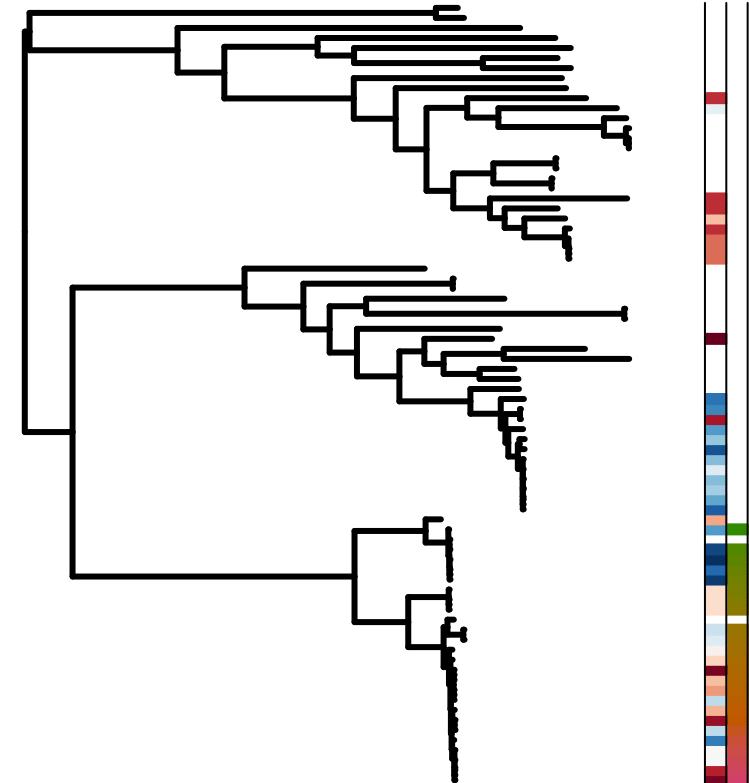
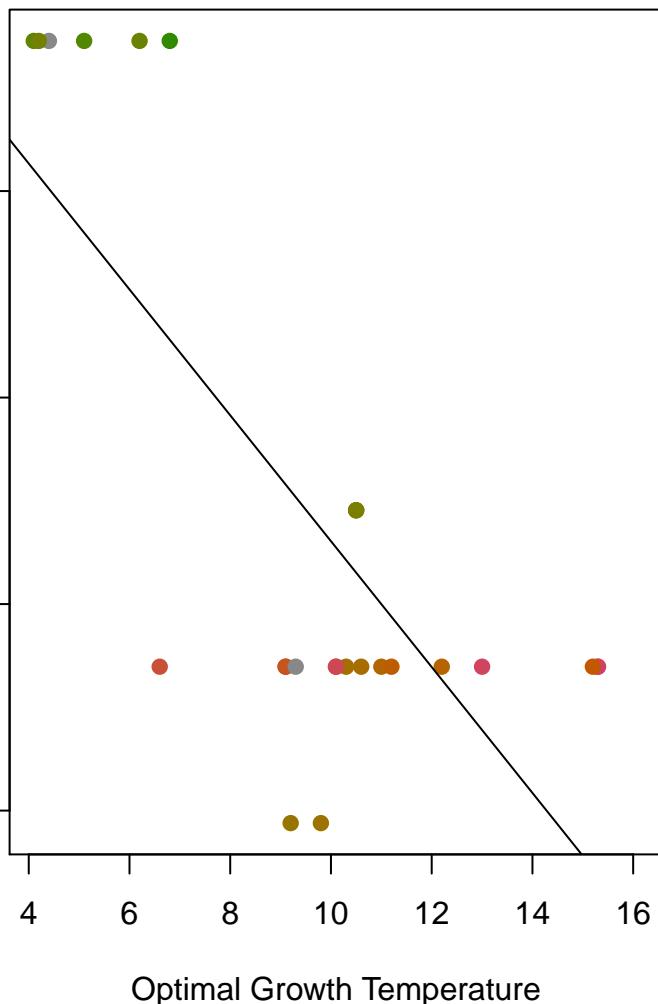
feature.pgfam_id.aromaticity.mean

PGF_11600935

hypothetical protein

$r = -0.739, p = 10^{-4.786}$

feature.pgfam_id.aromaticity.mean



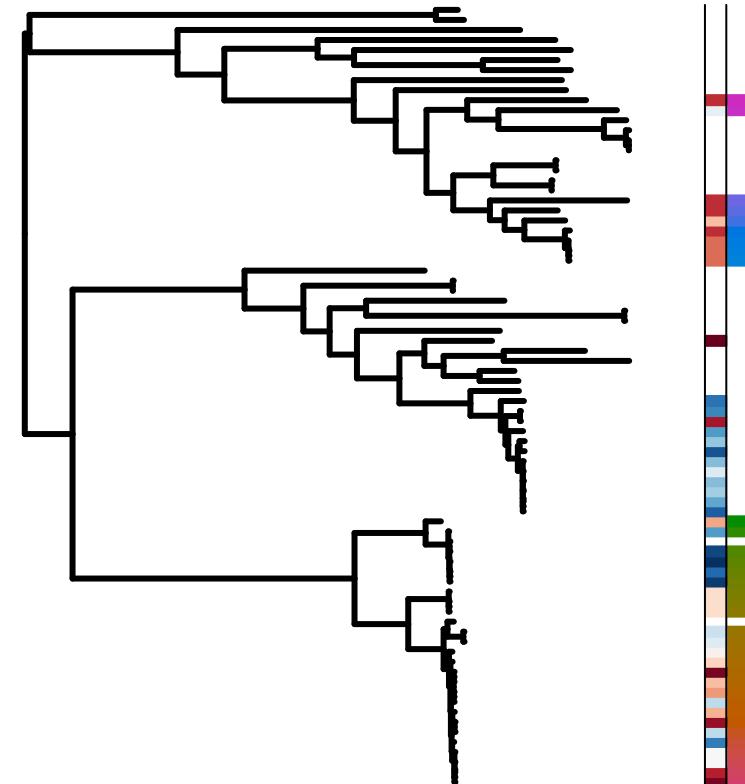
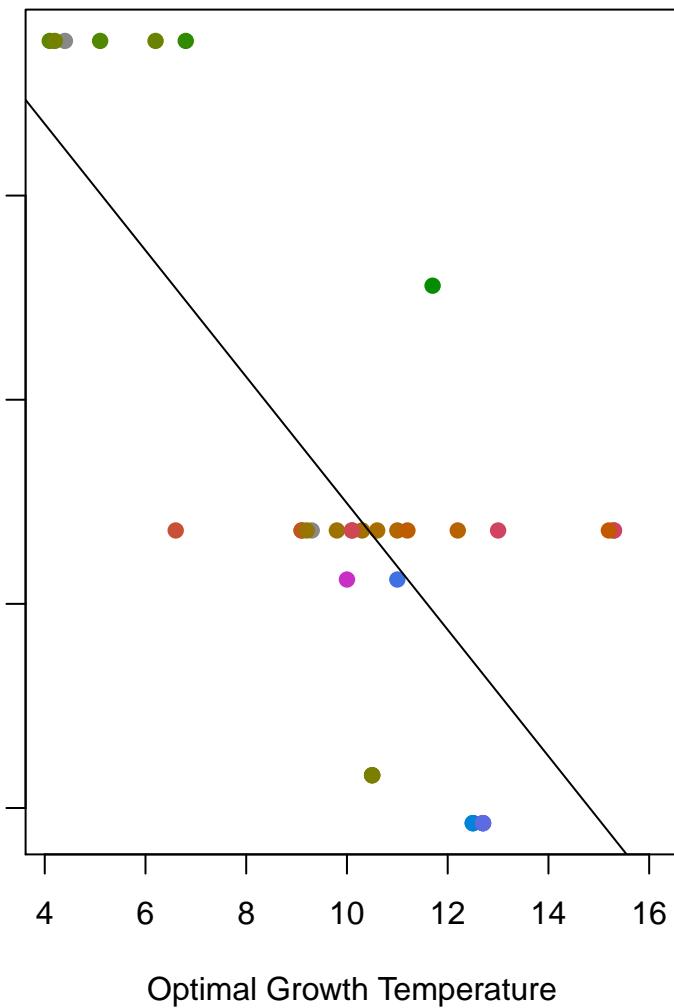
feature.pgfam_id.aromaticity.mean

PGF_01336341

Transcriptional regulator

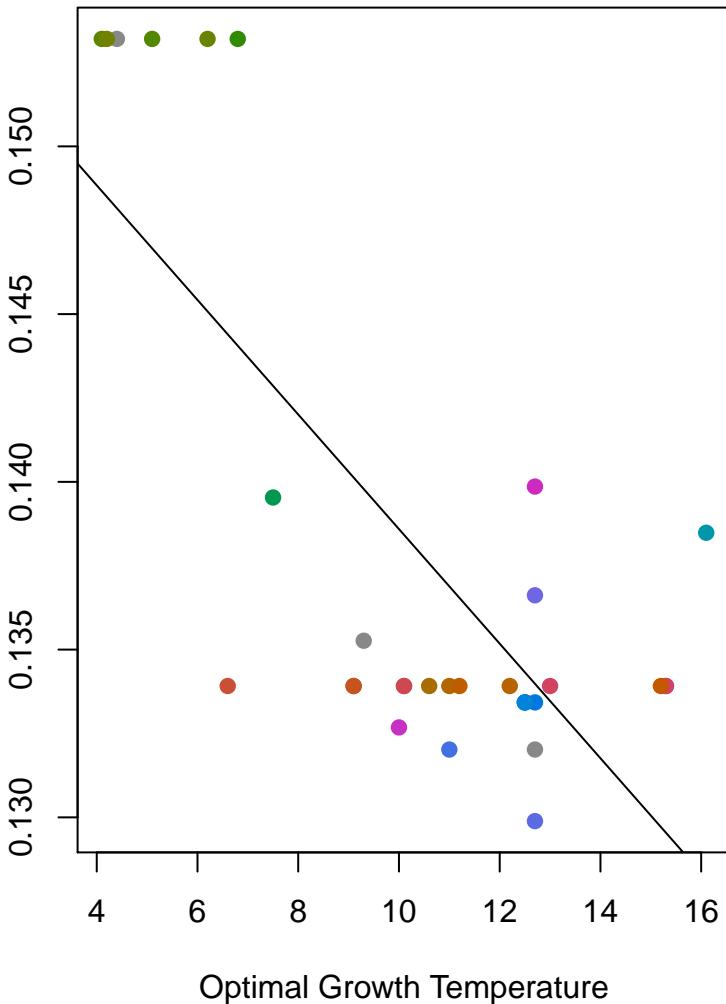
$r = -0.74$, $p = 10^{-6.601}$

feature.pgfam_id.aromaticity.mean

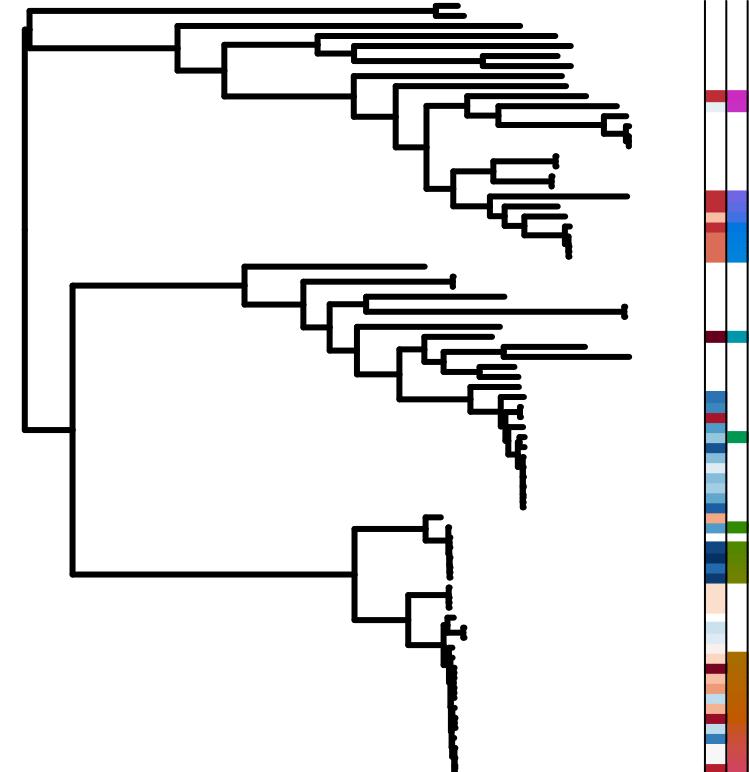


feature.pgfam_id.aromaticity.mean
PGF_06641194
Capsule biosynthesis protein capA
 $r = -0.745$, $p = 10^{-5.991}$

feature.pgfam_id.aromaticity.mean



Optimal Growth Temperature



Legend (Color Key):

- White
- Red
- Blue
- Green
- Orange
- Light Blue
- Dark Blue
- Dark Green
- Dark Orange
- Dark Red
- Dark Purple
- Dark Teal

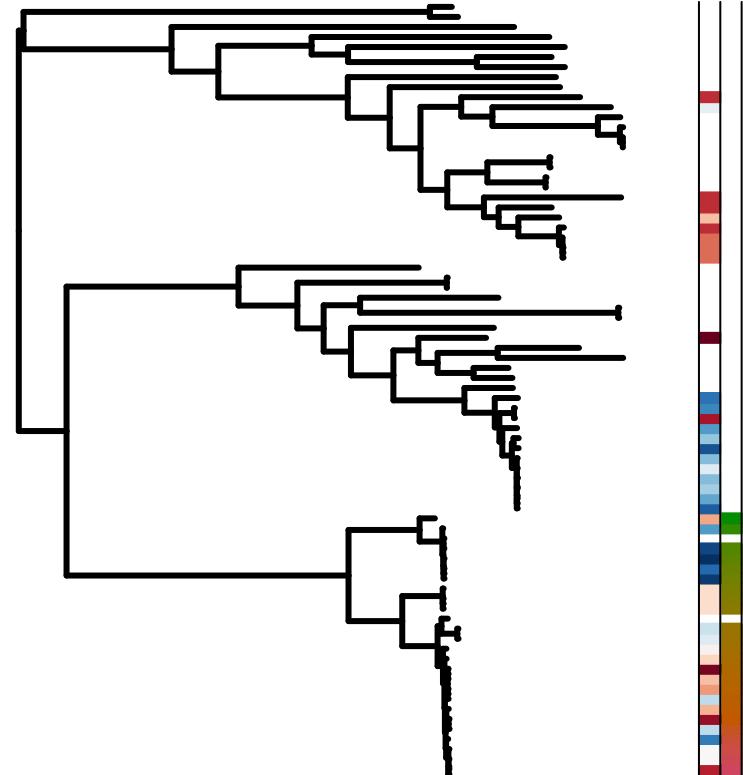
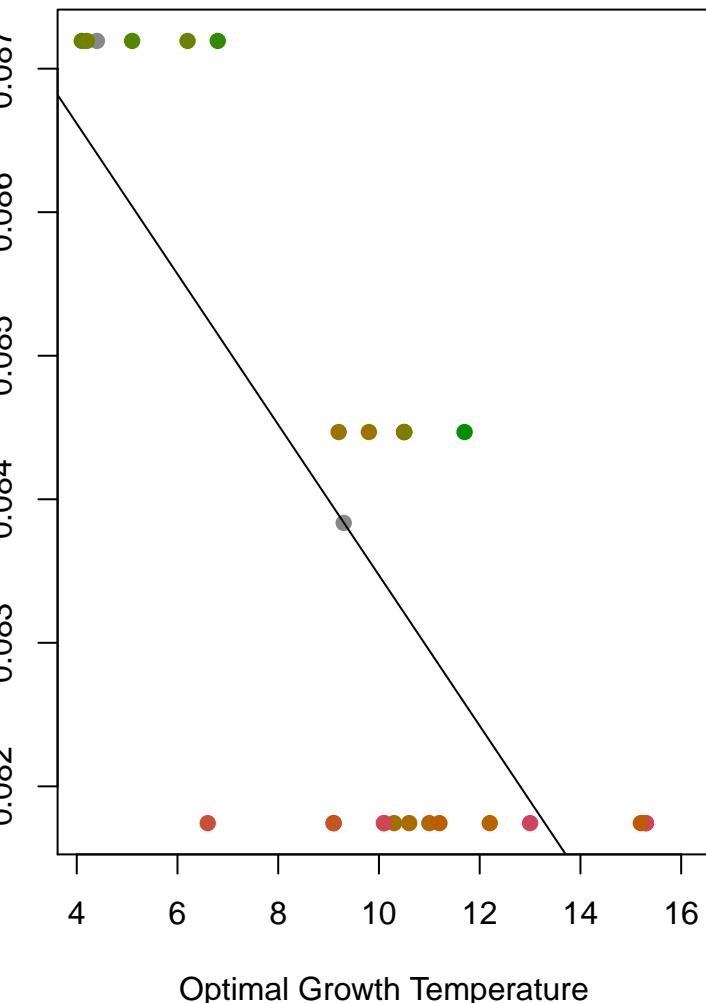
feature.pgfam_id.aromaticity.mean

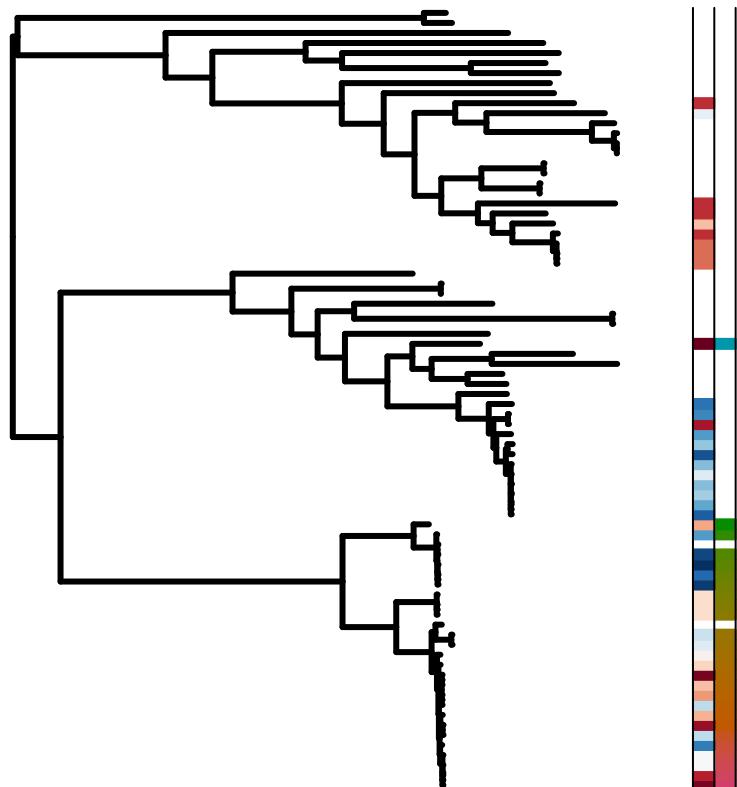
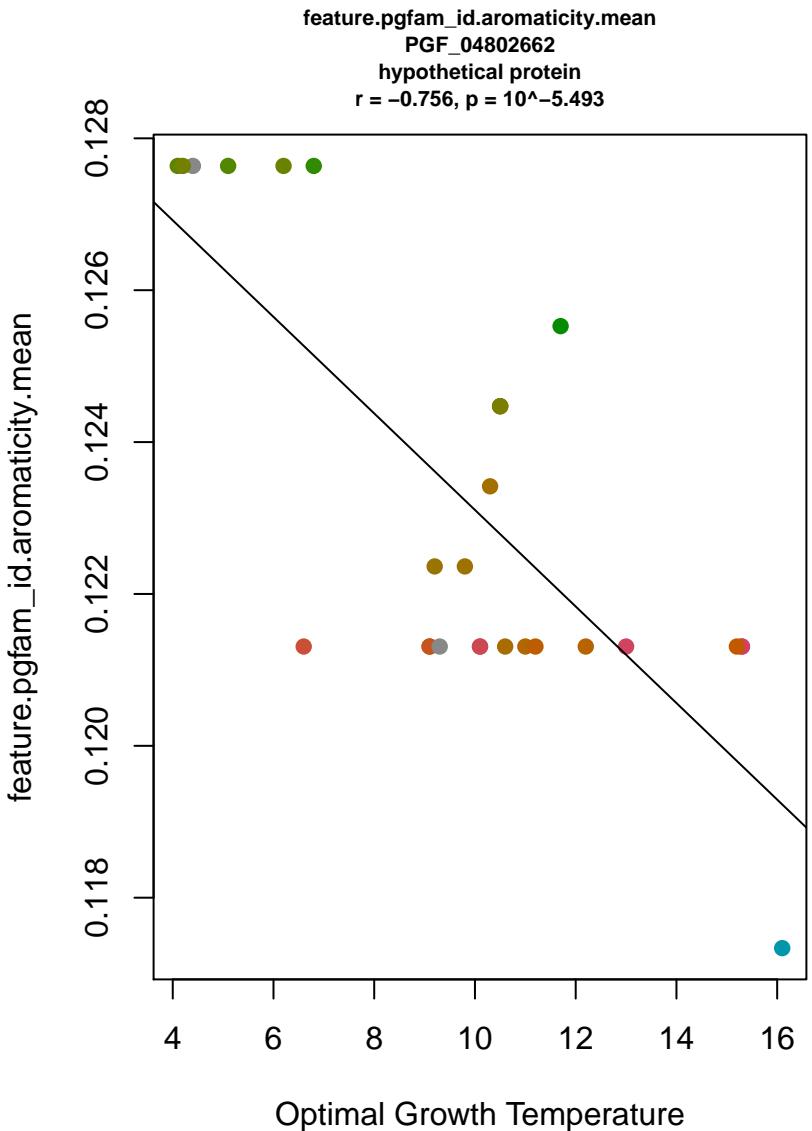
PGF_09674332

hypothetical protein

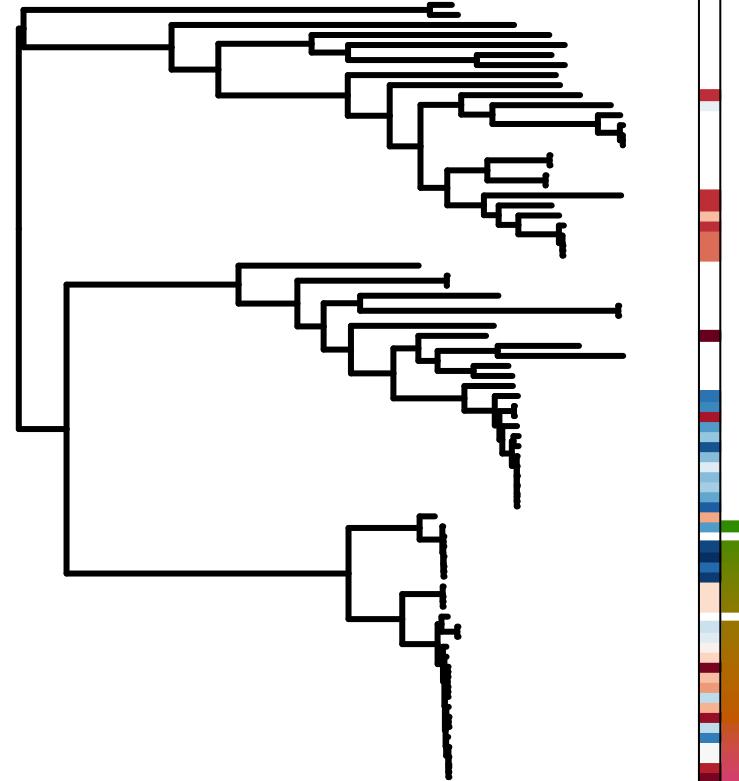
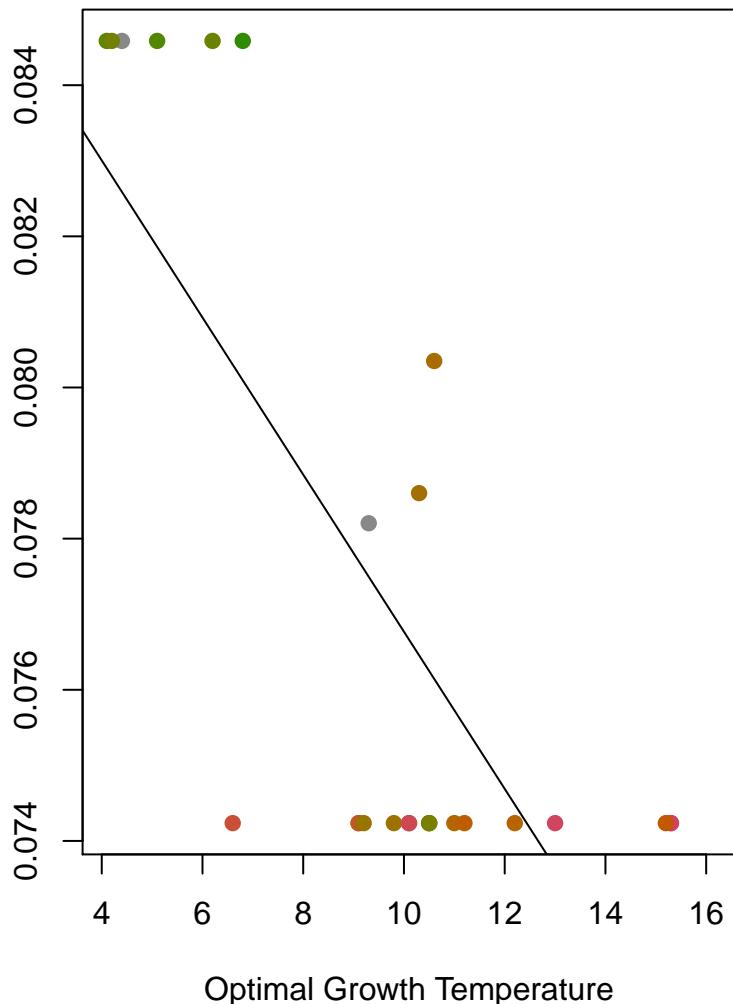
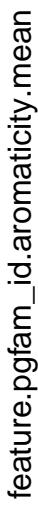
$r = -0.746, p = 10^{-5.105}$

feature.pgfam_id.aromaticity.mean





feature.pgfam_id.aromaticity.mean
PGF_07132870
hypothetical protein
 $r = -0.757, p = 10^{-5.113}$



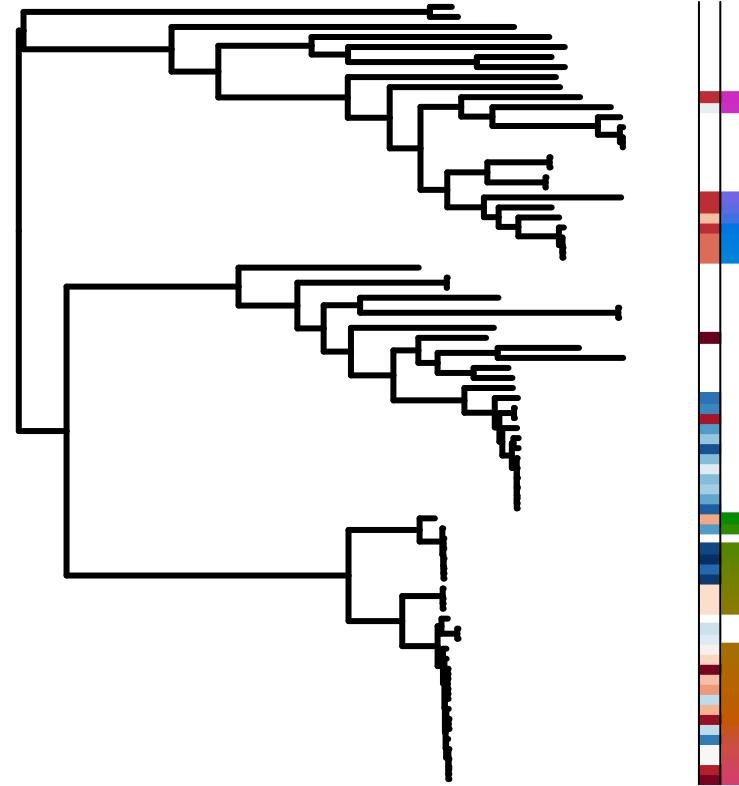
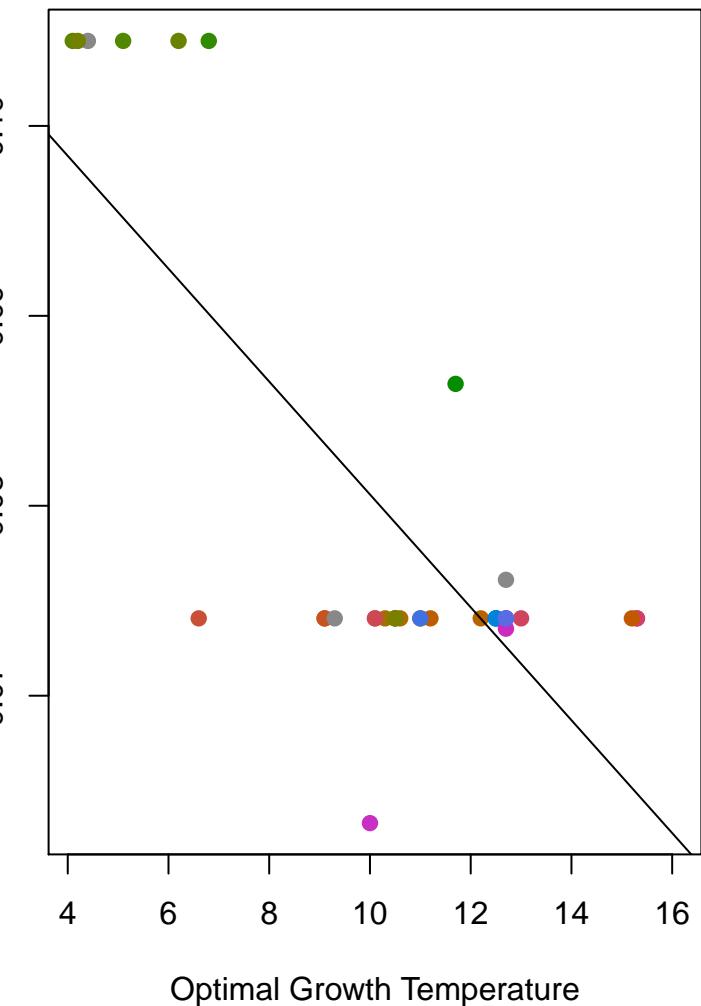
feature.pgfam_id.aromaticity.mean

PGF_00064685

Uncharacterized ferredoxin-like protein YfhL

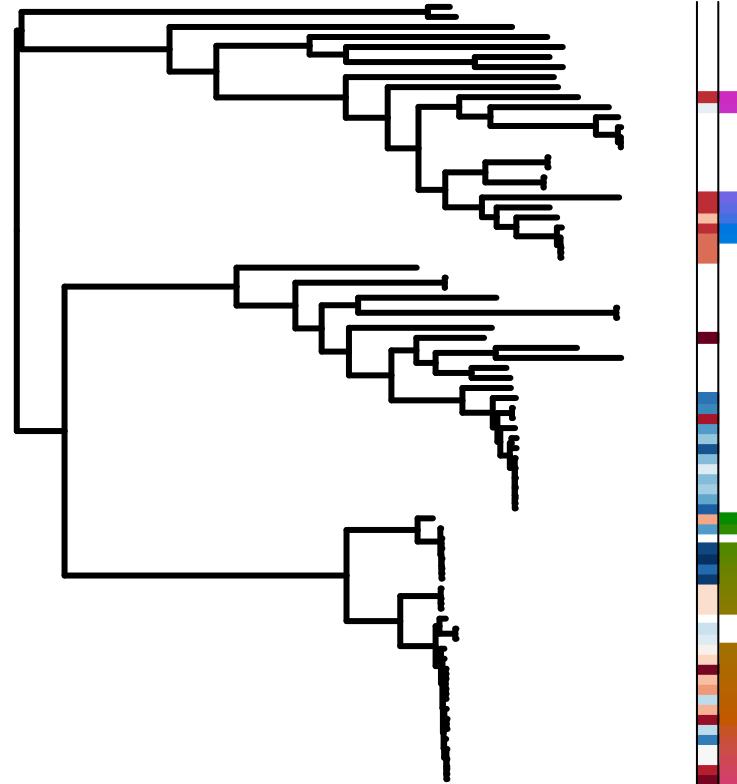
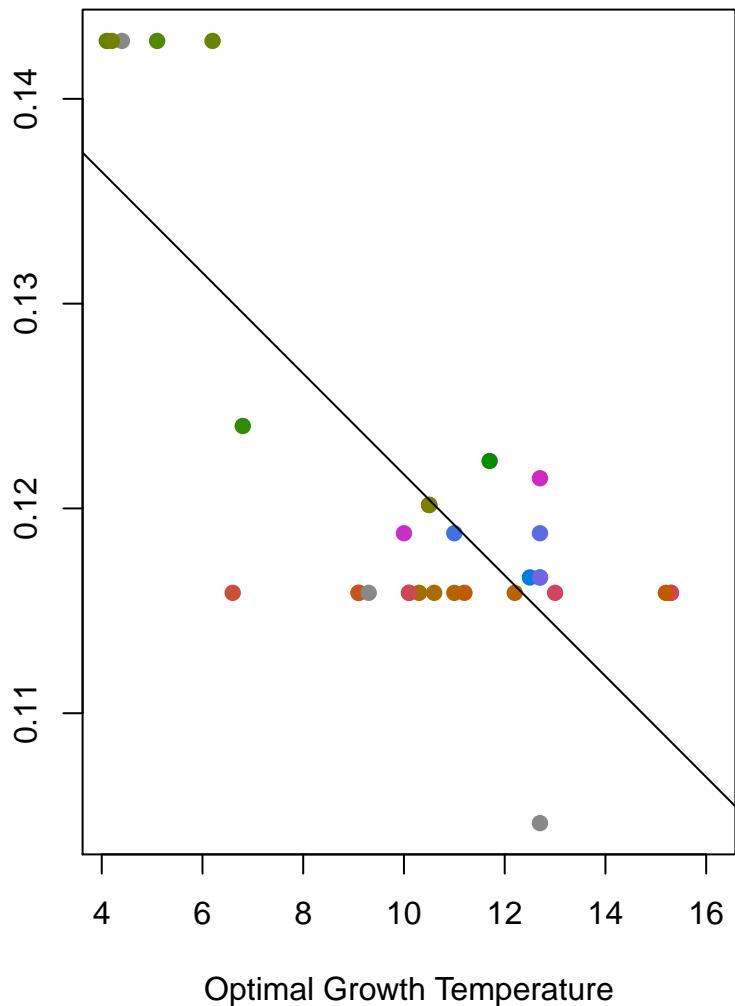
$r = -0.76, p = 10^{-6.914}$

feature.pgfam_id.aromaticity.mean



feature.pgfam_id.aromaticity.mean
PGF_02105064
Uncharacterized protease YegQ
 $r = -0.771$, $p = 10^{-6.825}$

feature.pgfam_id.aromaticity.mean



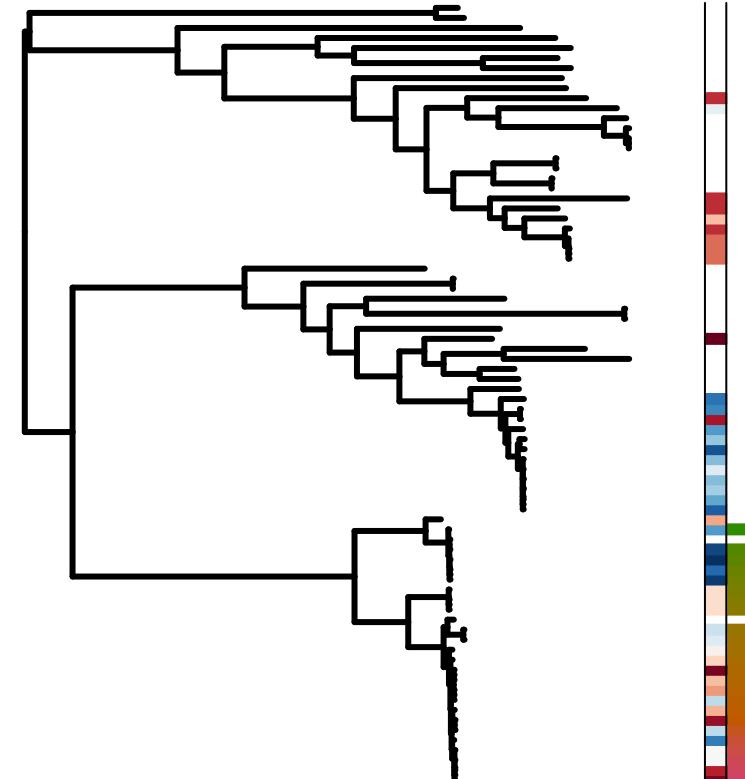
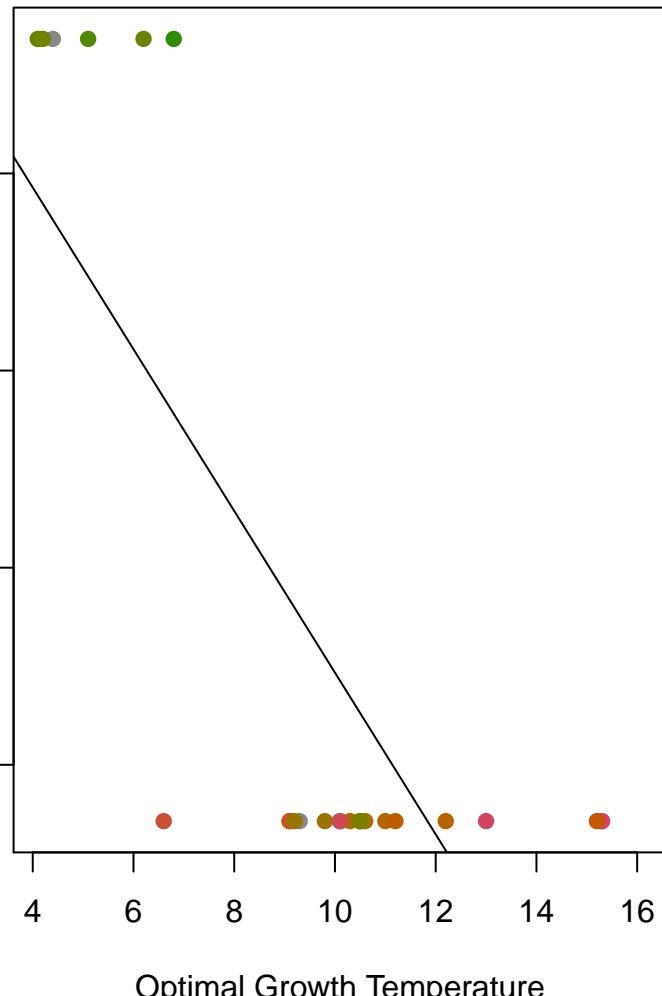
feature.pgfam_id.aromaticity.mean

PGF_12288710

hypothetical protein

$r = -0.775, p = 10^{-5.478}$

feature.pgfam_id.aromaticity.mean



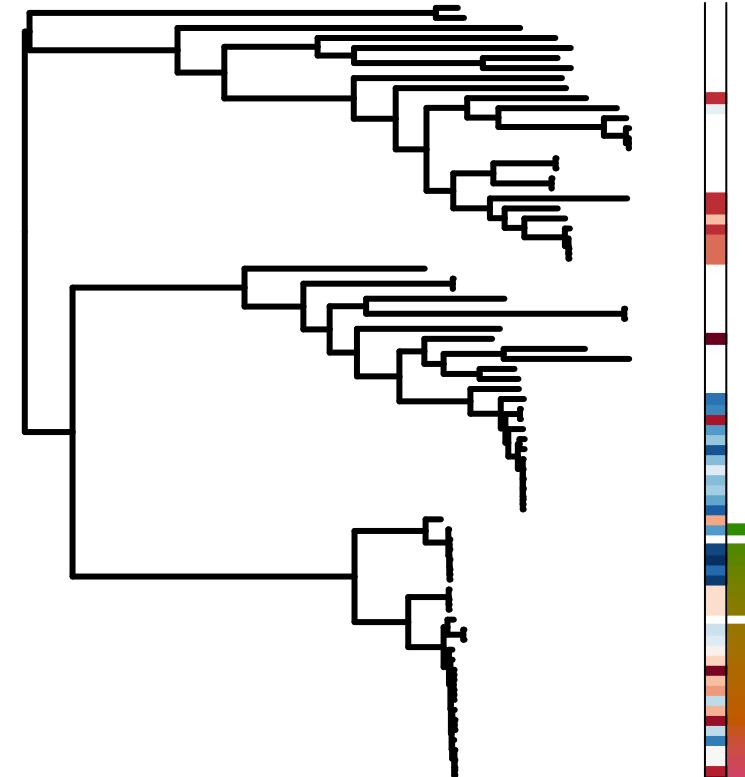
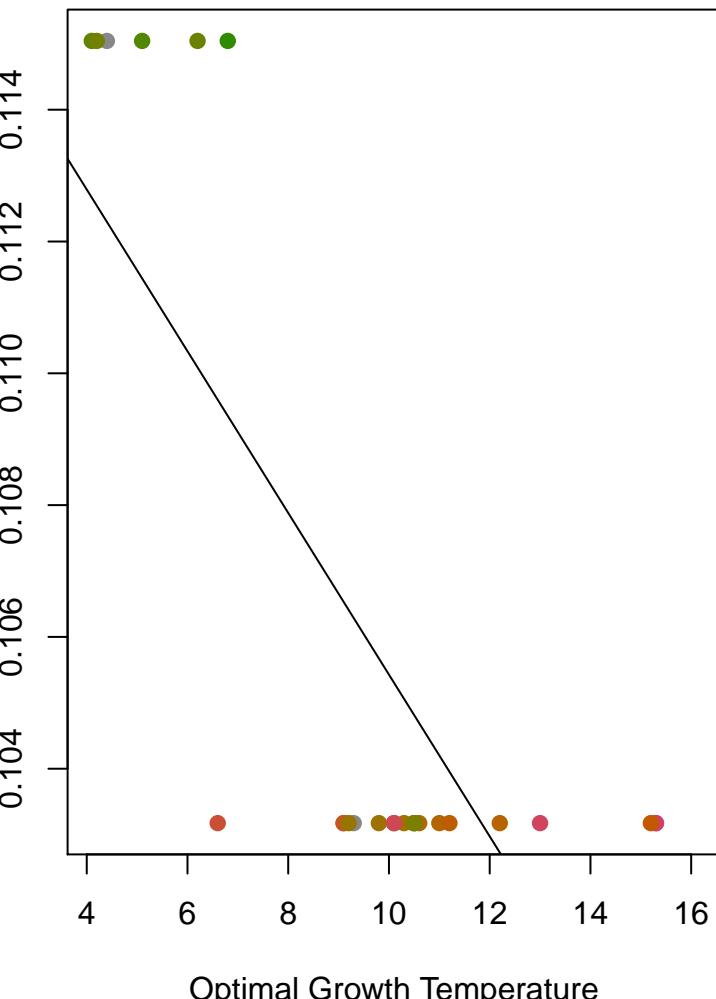
feature.pgfam_id.aromaticity.mean

PGF_12049070

hypothetical protein

$r = -0.775, p = 10^{-5.478}$

feature.pgfam_id.aromaticity.mean



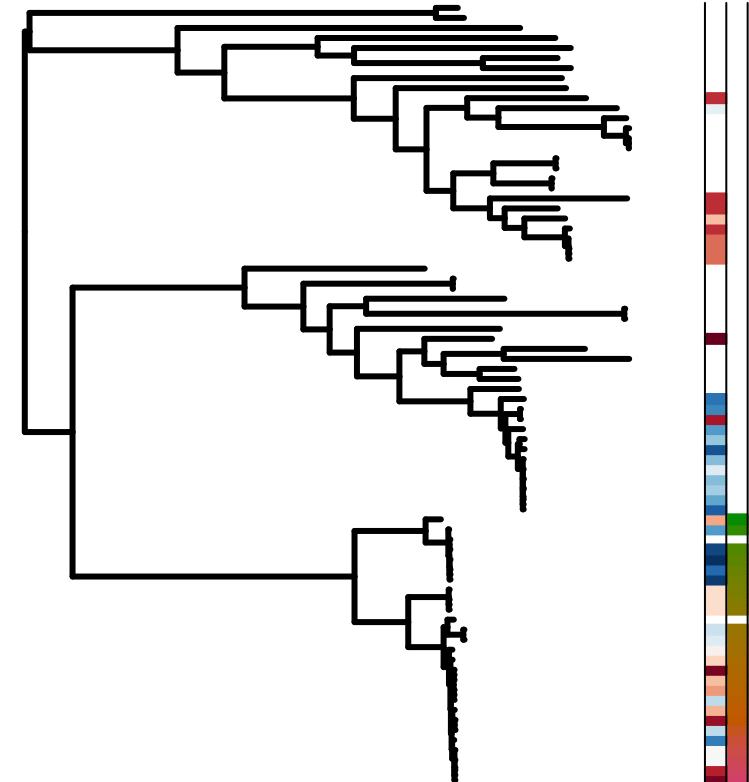
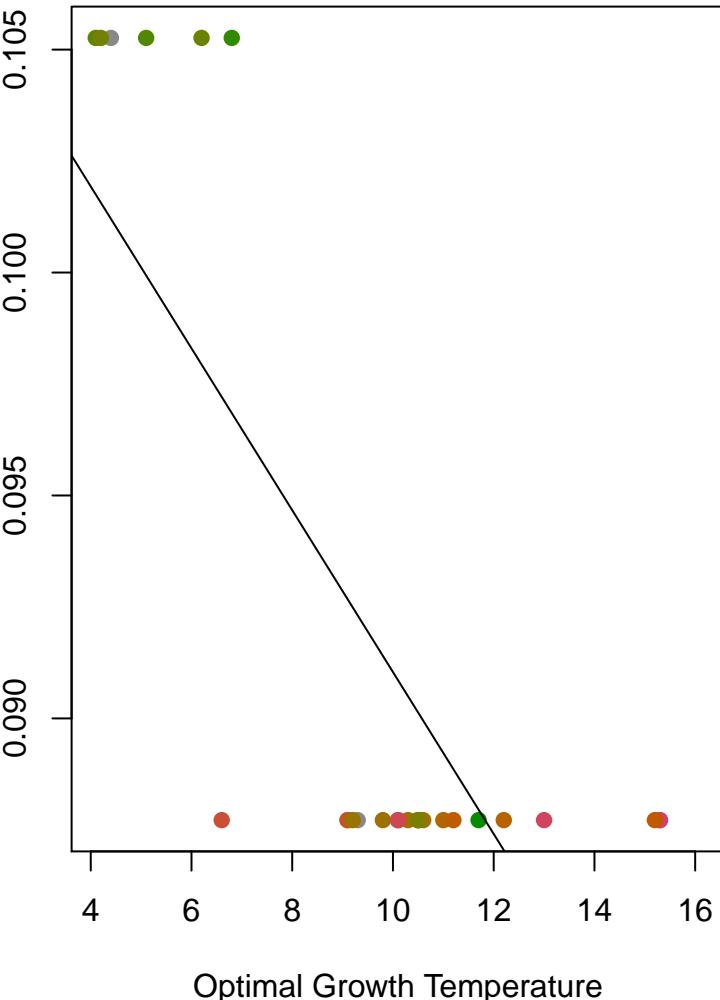
feature.pgfam_id.aromaticity.mean

PGF_08289417

hypothetical protein

$r = -0.778, p = 10^{-5.746}$

feature.pgfam_id.aromaticity.mean



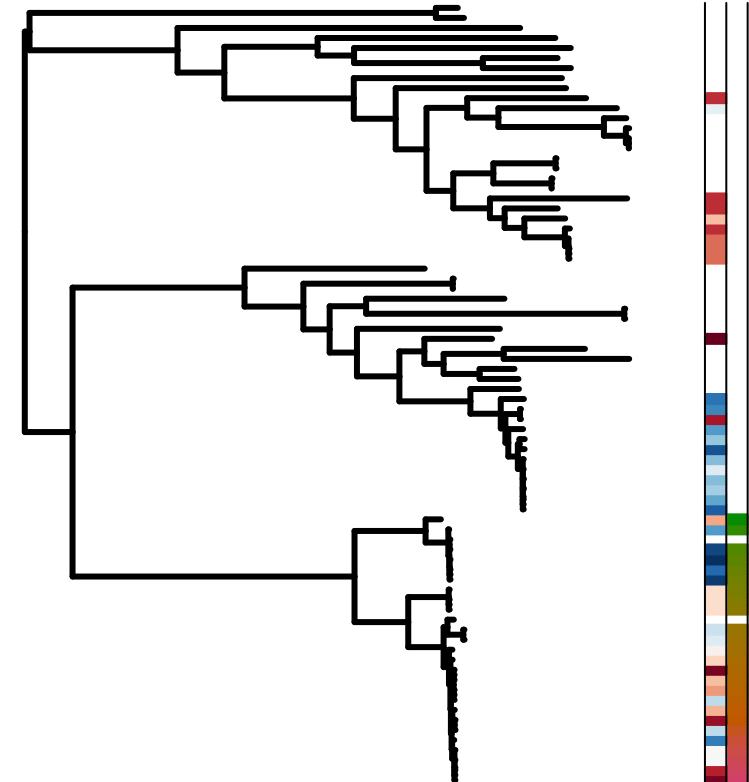
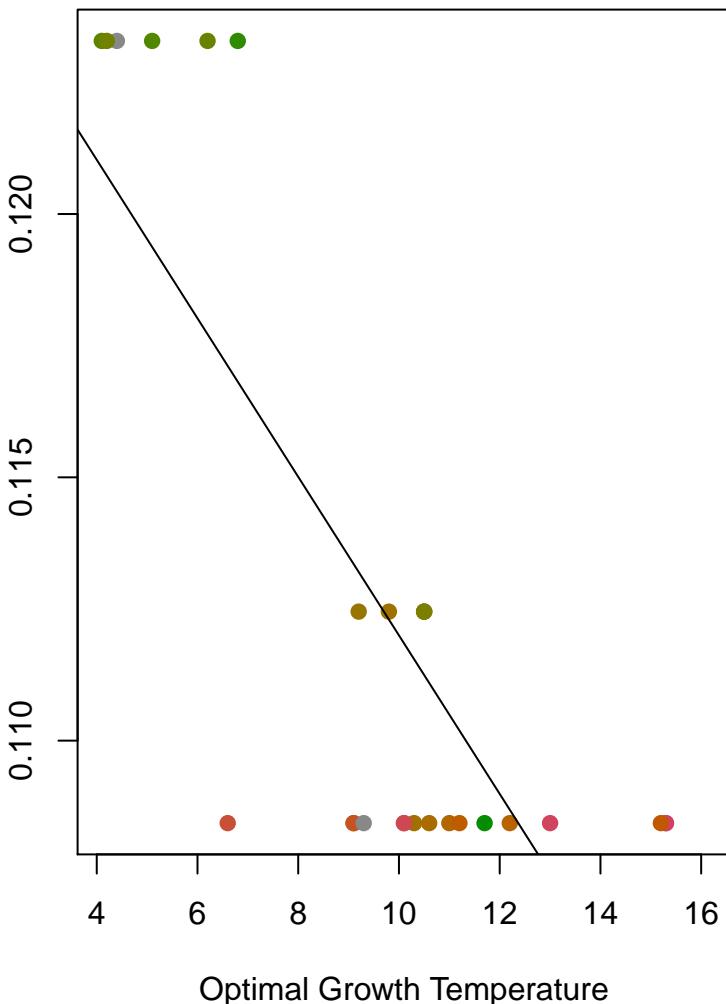
feature.pgfam_id.aromaticity.mean

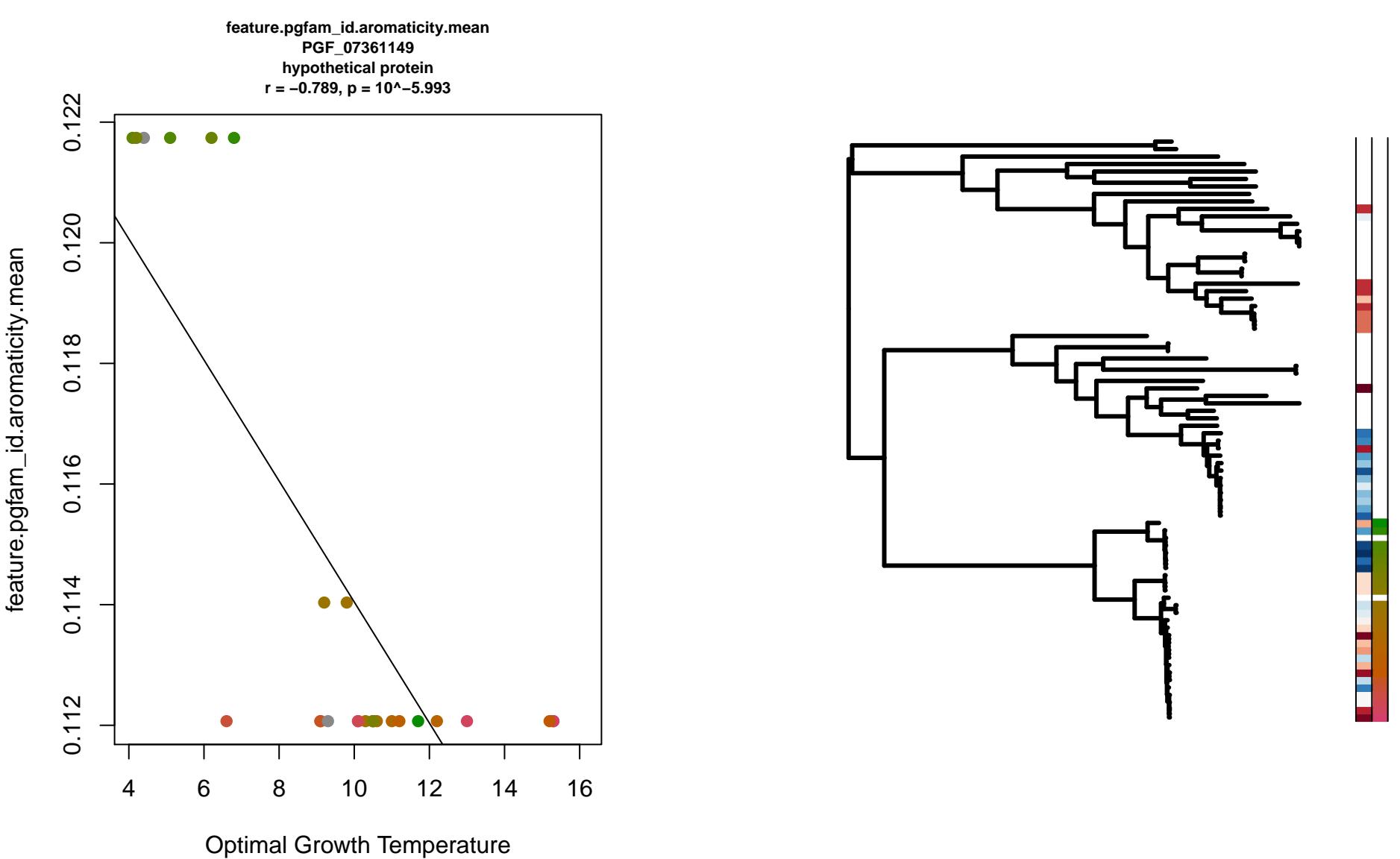
PGF_11018774

hypothetical protein

$r = -0.788, p = 10^{-5.968}$

feature.pgfam_id.aromaticity.mean





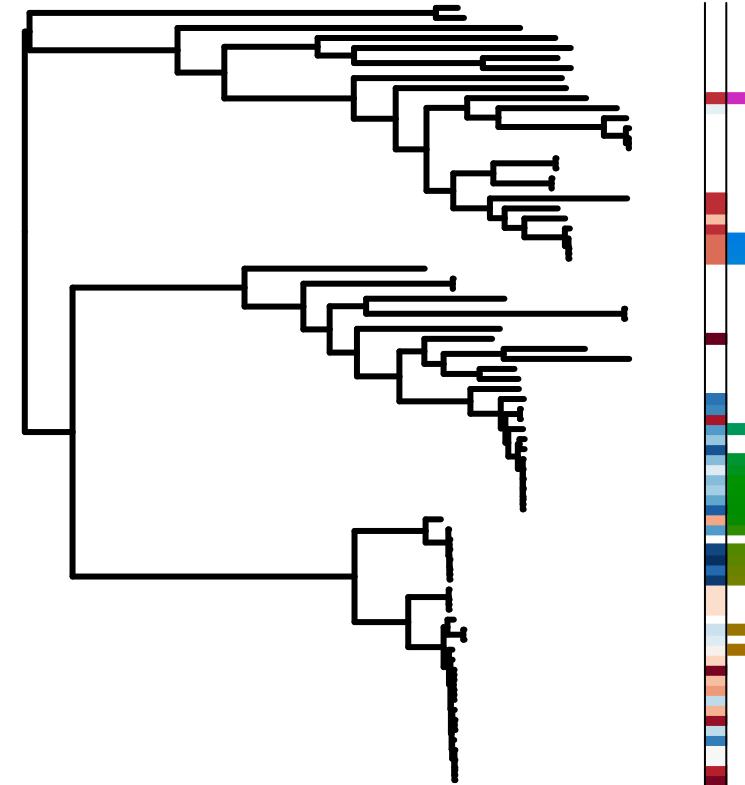
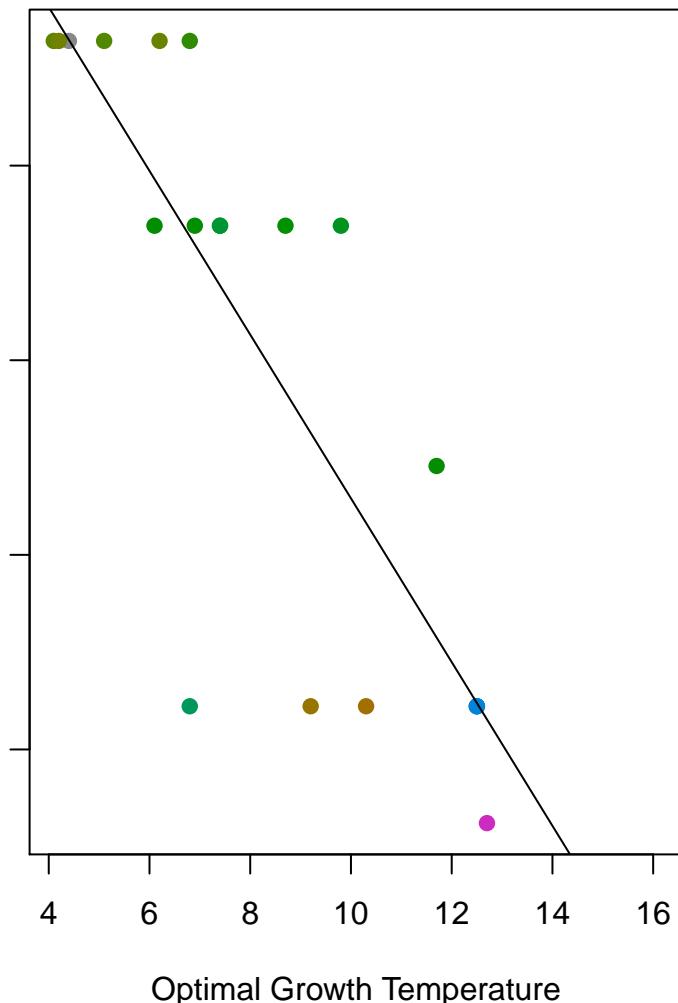
feature.pgfam_id.aromaticity.mean

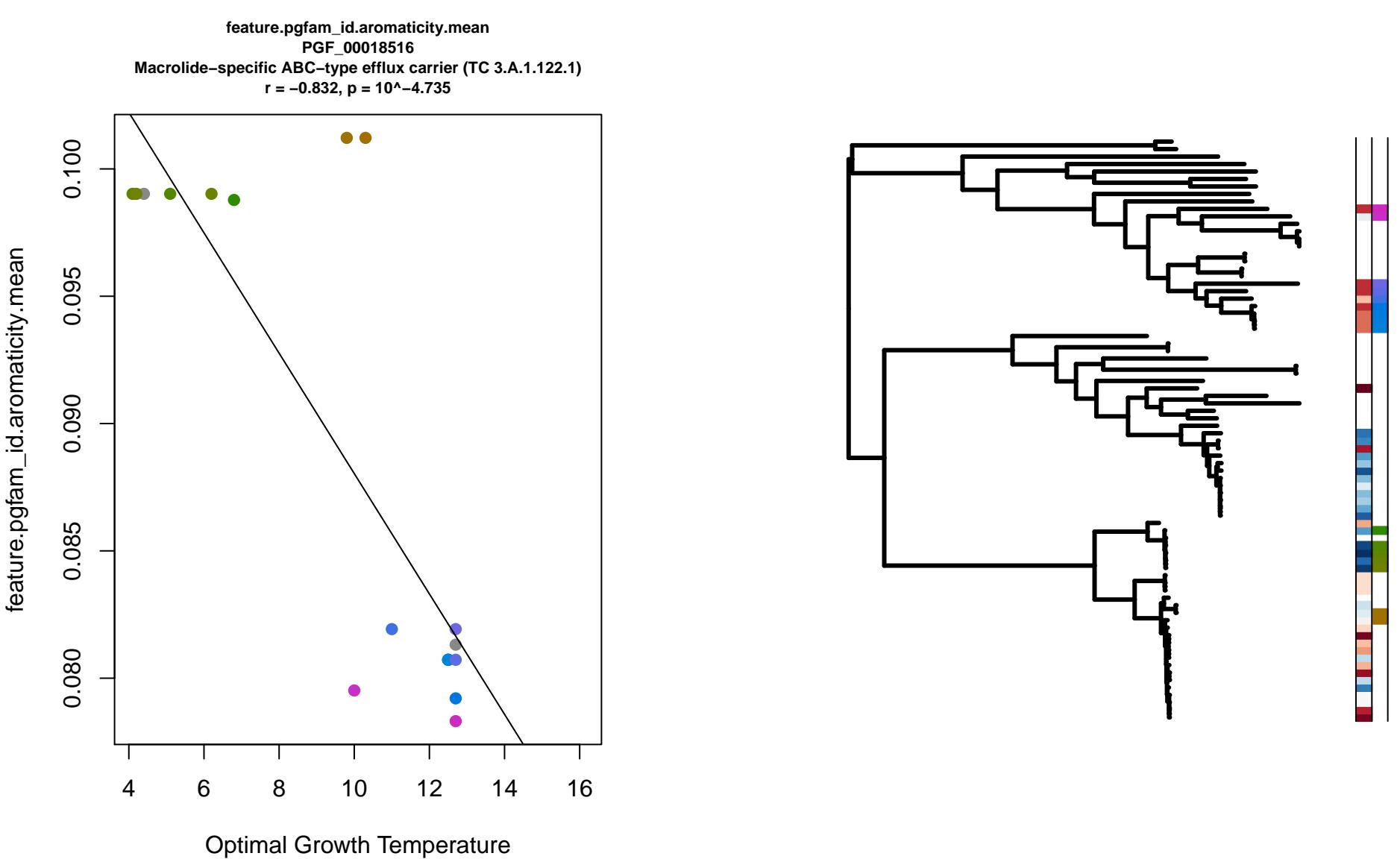
PGF_00257343

hypothetical protein

$r = -0.823, p = 10^{-5.084}$

feature.pgfam_id.aromaticity.mean





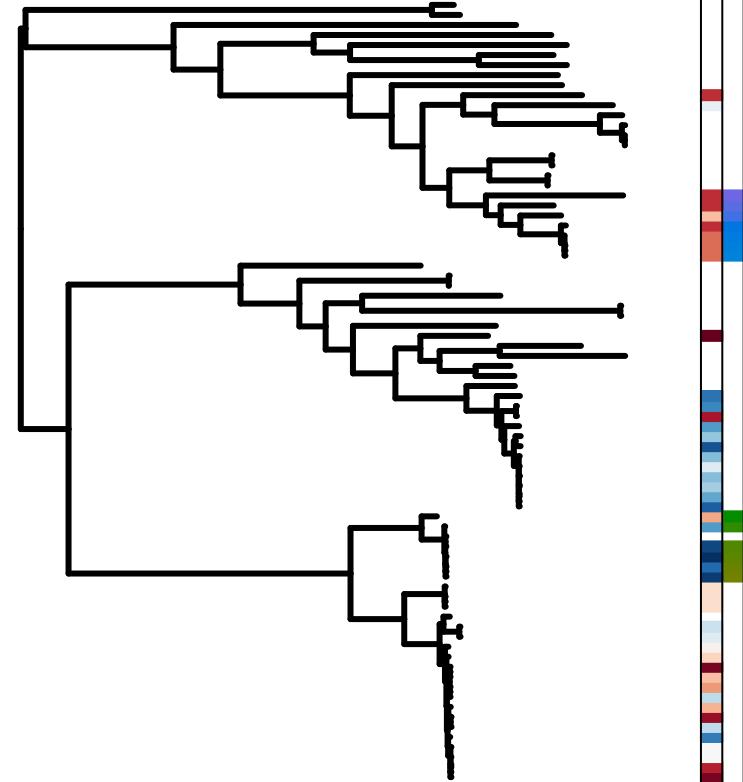
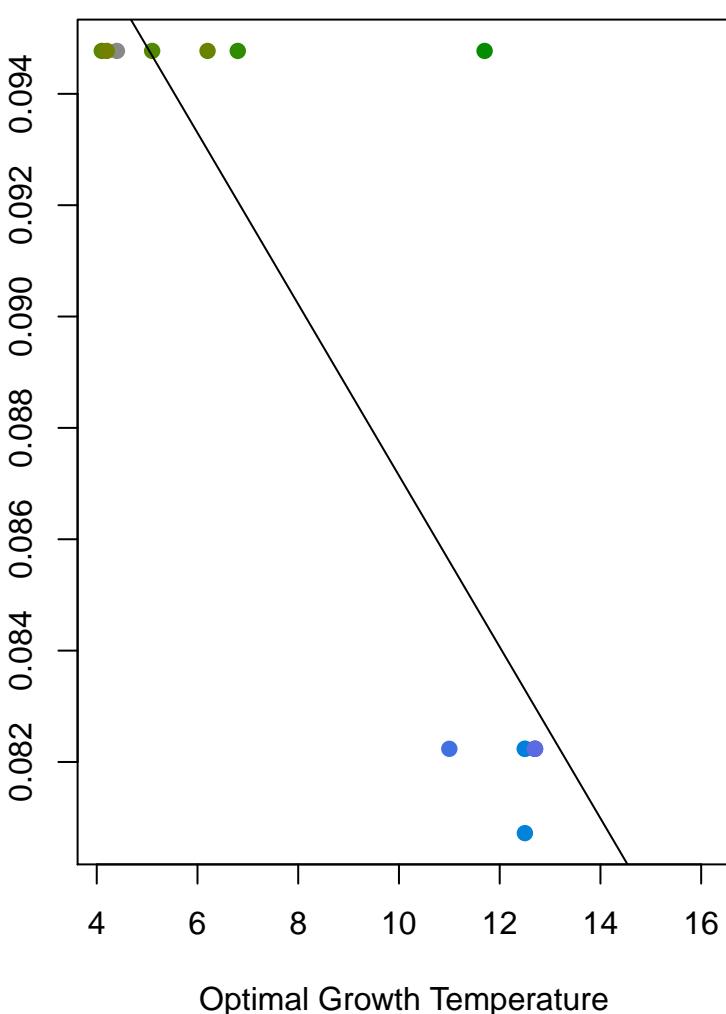
feature.pgfam_id.aromaticity.mean

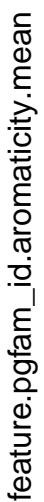
PGF_02964640

1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22)

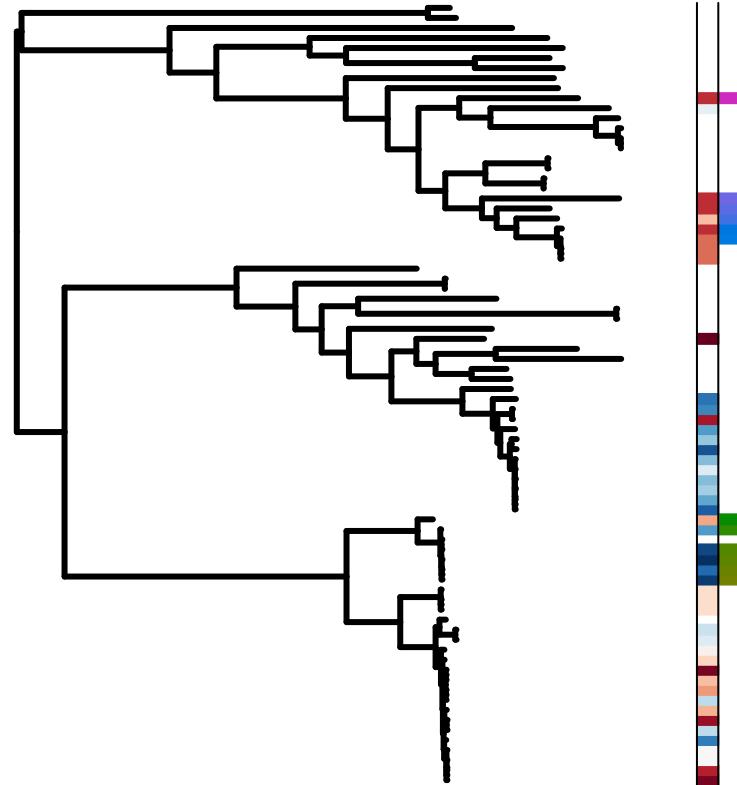
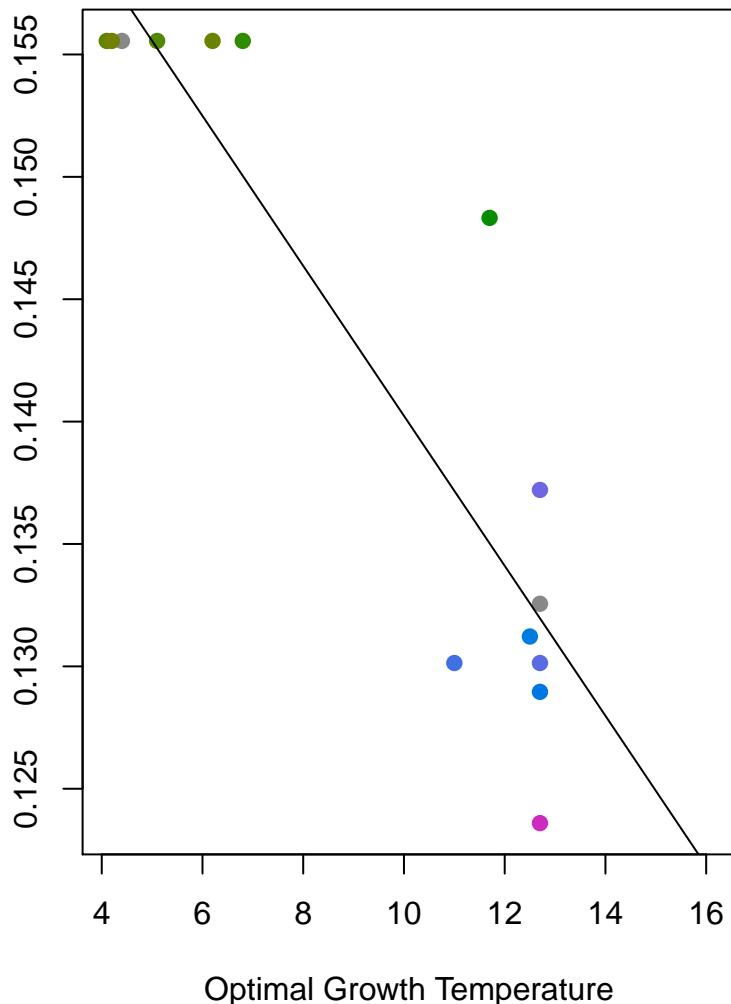
$r = -0.874$, $p = 10^{-4.699}$

feature.pgfam_id.aromaticity.mean





feature.pgfam_id.aromaticity.mean
PGF_12884992
Uncharacterized MFS-type transporter
r = -0.903, p = 10^-5.004



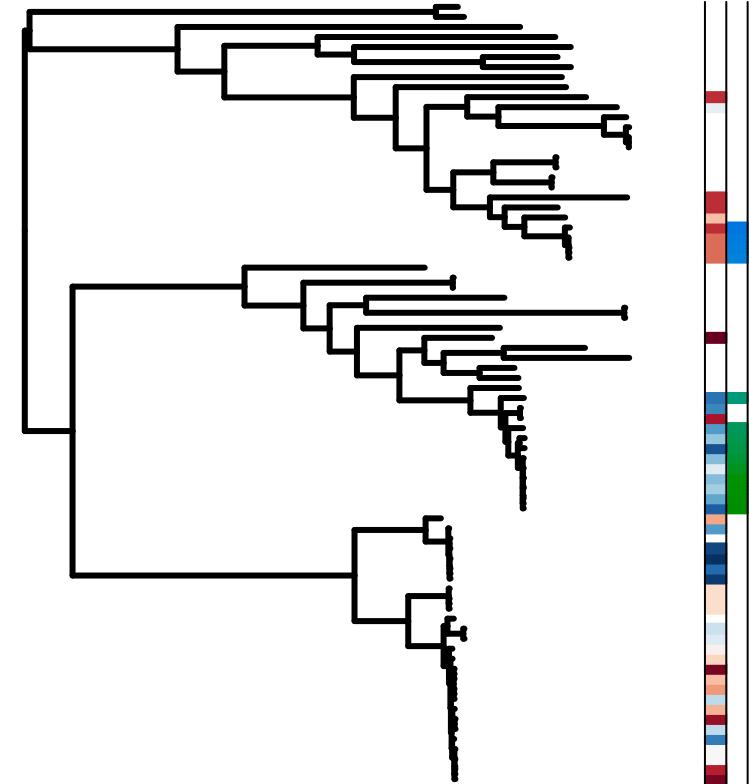
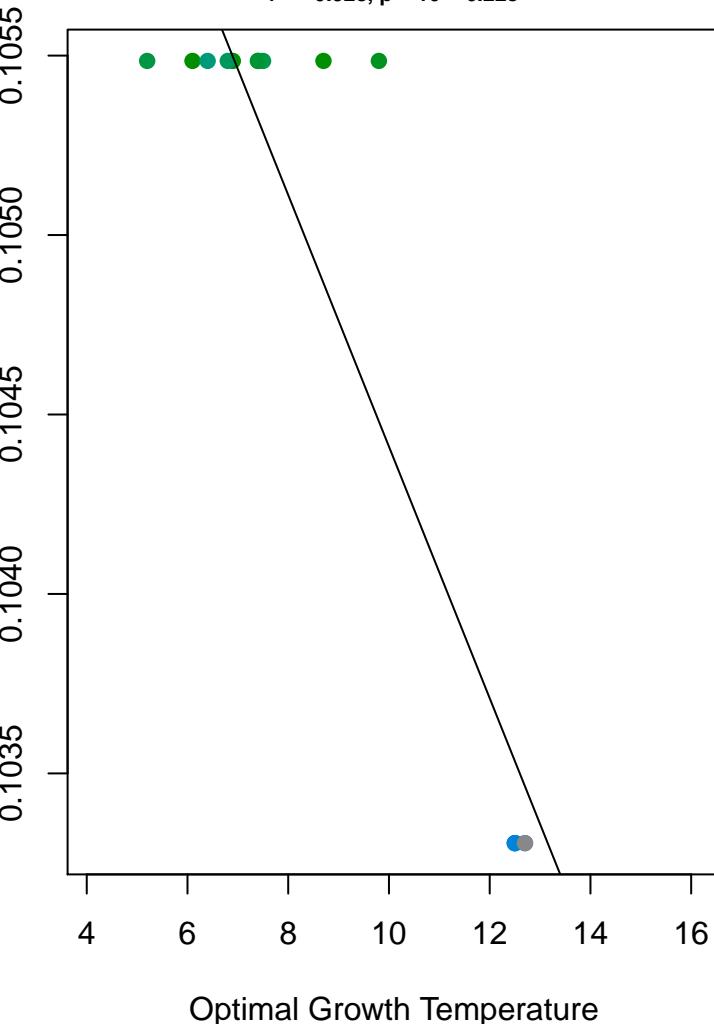
feature.pgfam_id.aromaticity.mean

PGF_06830555

SapC-like S-layer protein

$r = -0.928$, $p = 10^{-6.228}$

feature.pgfam_id.aromaticity.mean

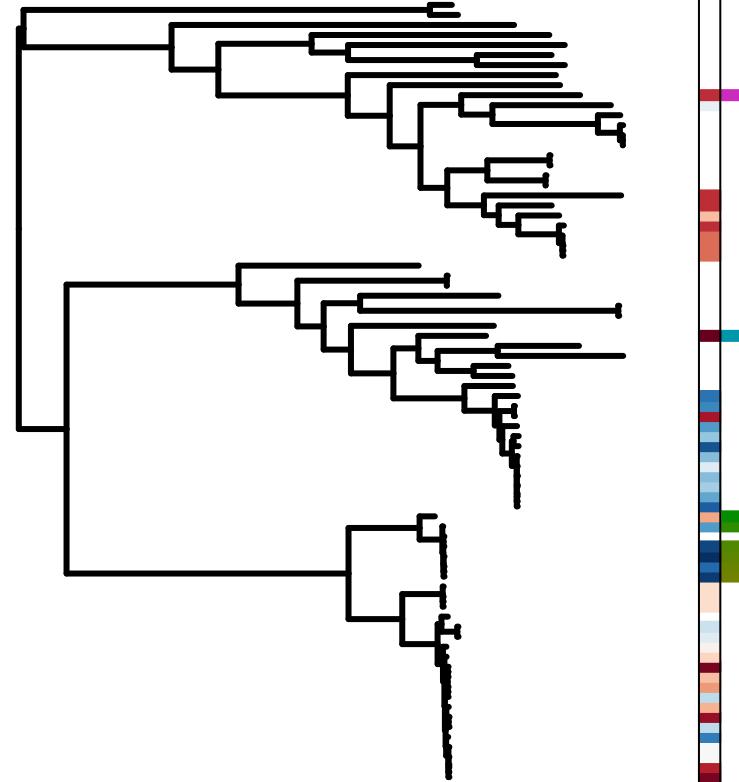
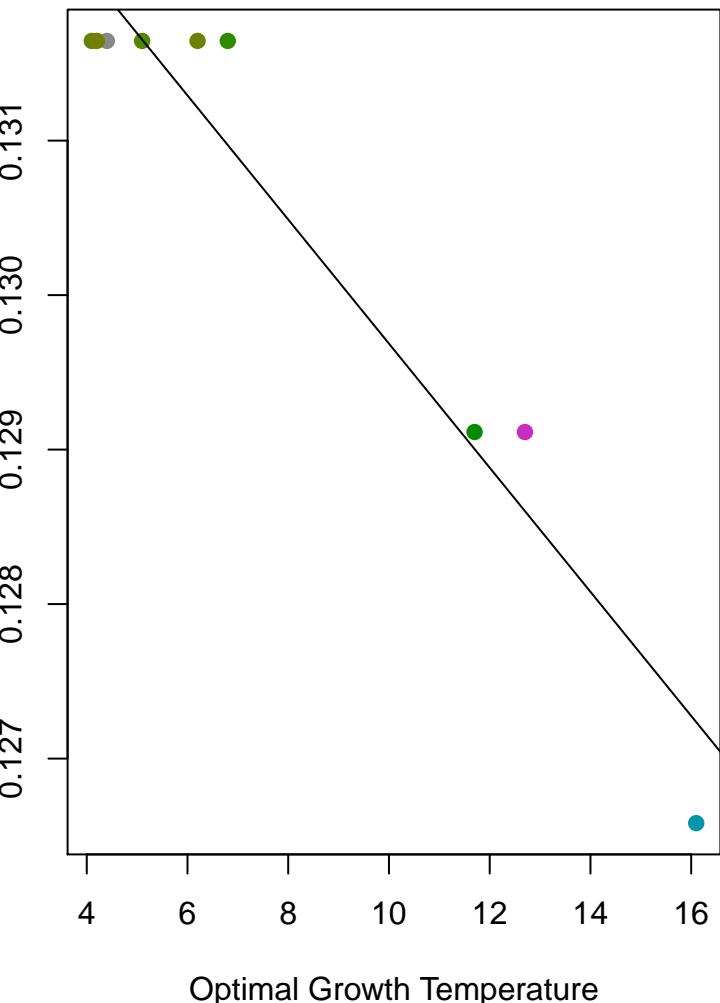


feature.pgfam_id.aromaticity.mean

PGF_00020737

le aminotransferase, PLP-dependent @ Glutamine-dependent 2-keto-4-methylthiobutyrate tra
 $r = -0.967, p = 10^{-4.702}$

feature.pgfam_id.aromaticity.mean



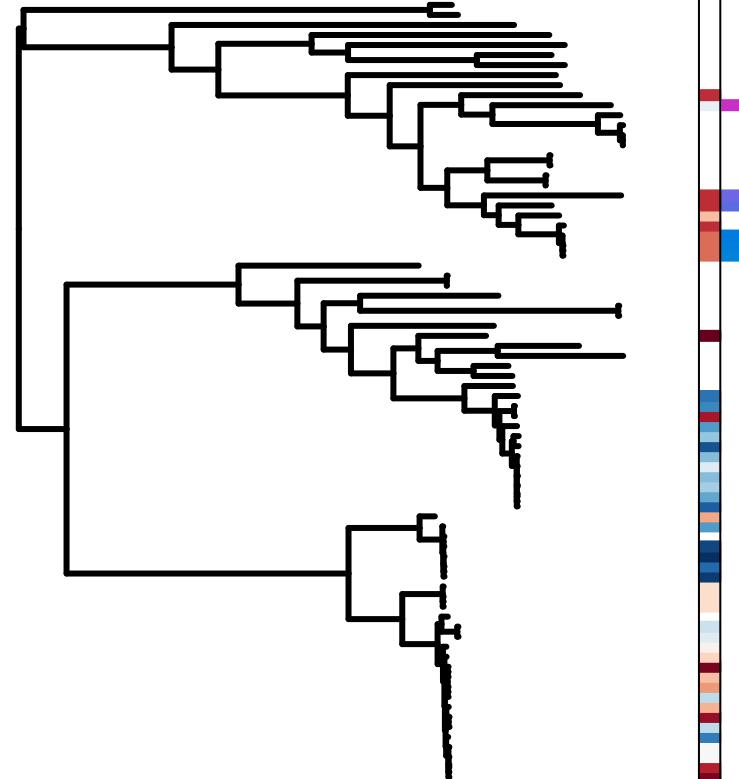
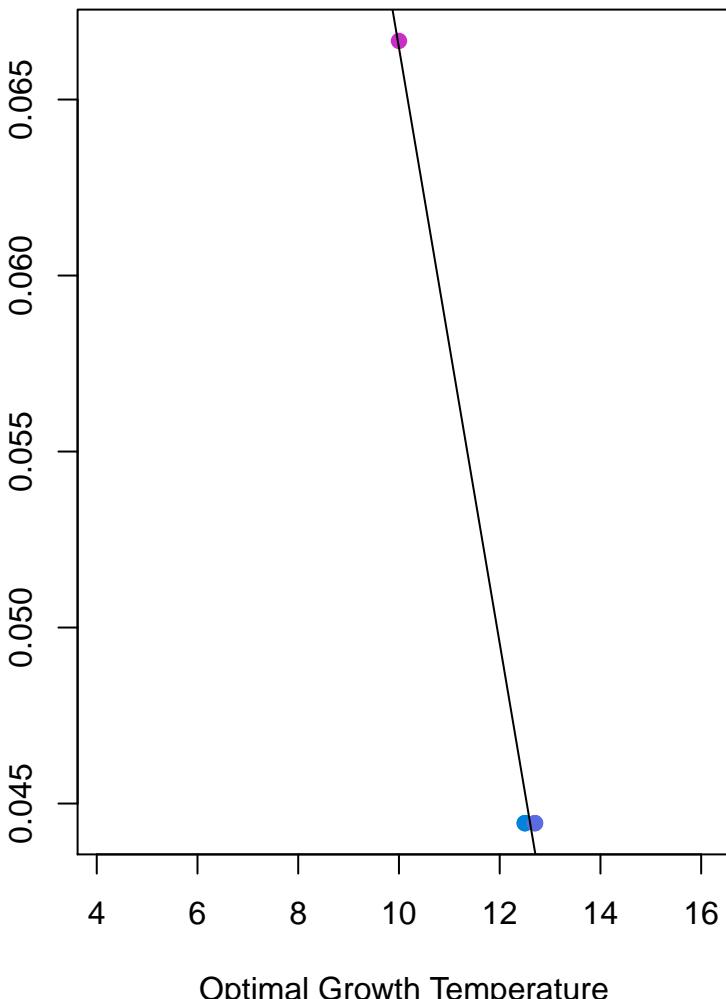
feature.pgfam_id.aromaticity.mean

PGF_01337096

hypothetical protein

$r = -0.995, p = 10^{-5.441}$

feature.pgfam_id.aromaticity.mean



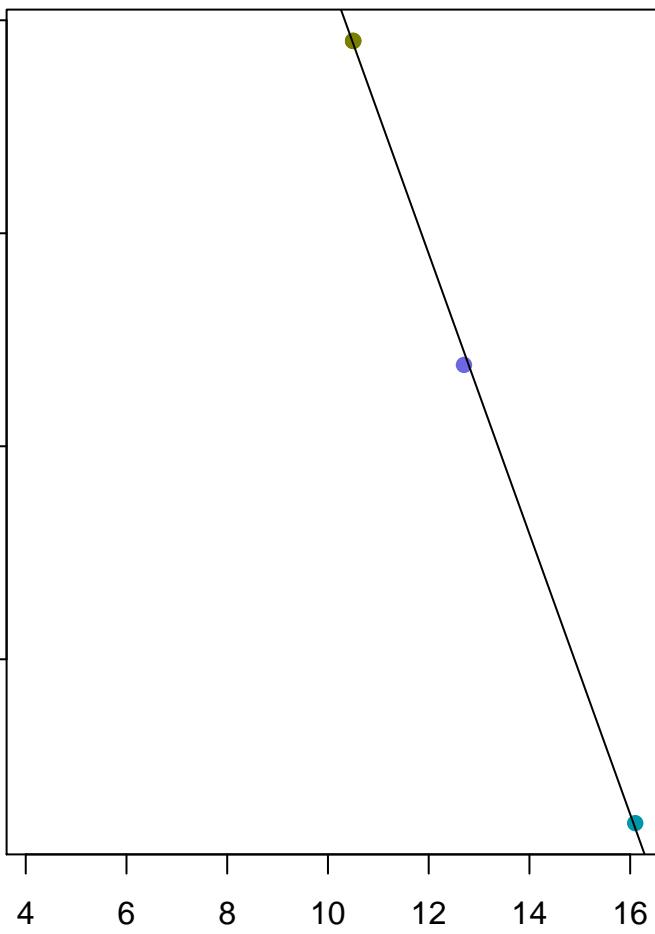
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PGF_04001813

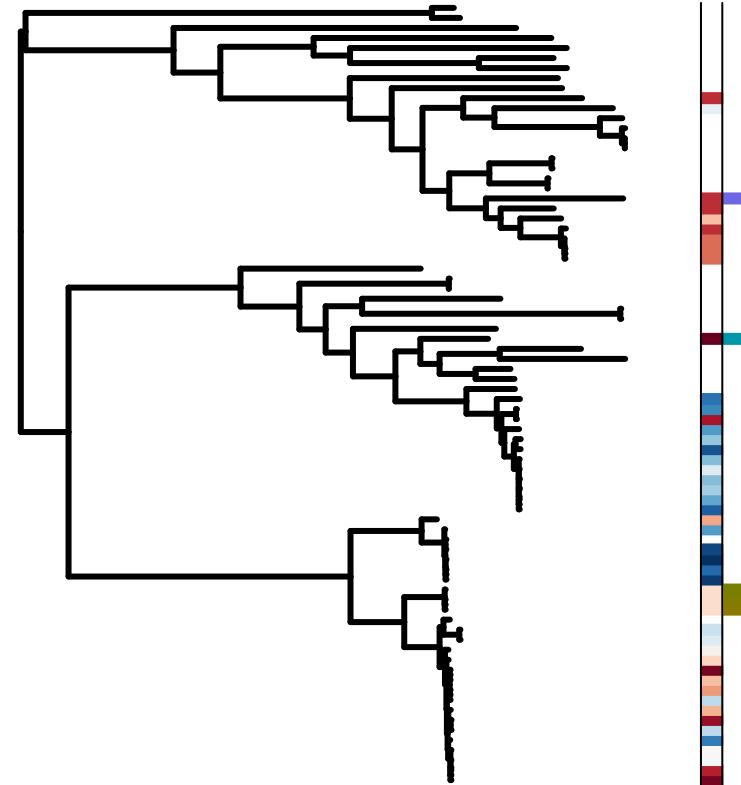
hypothetical protein

$r = -1, p = 10^{-5.375}$

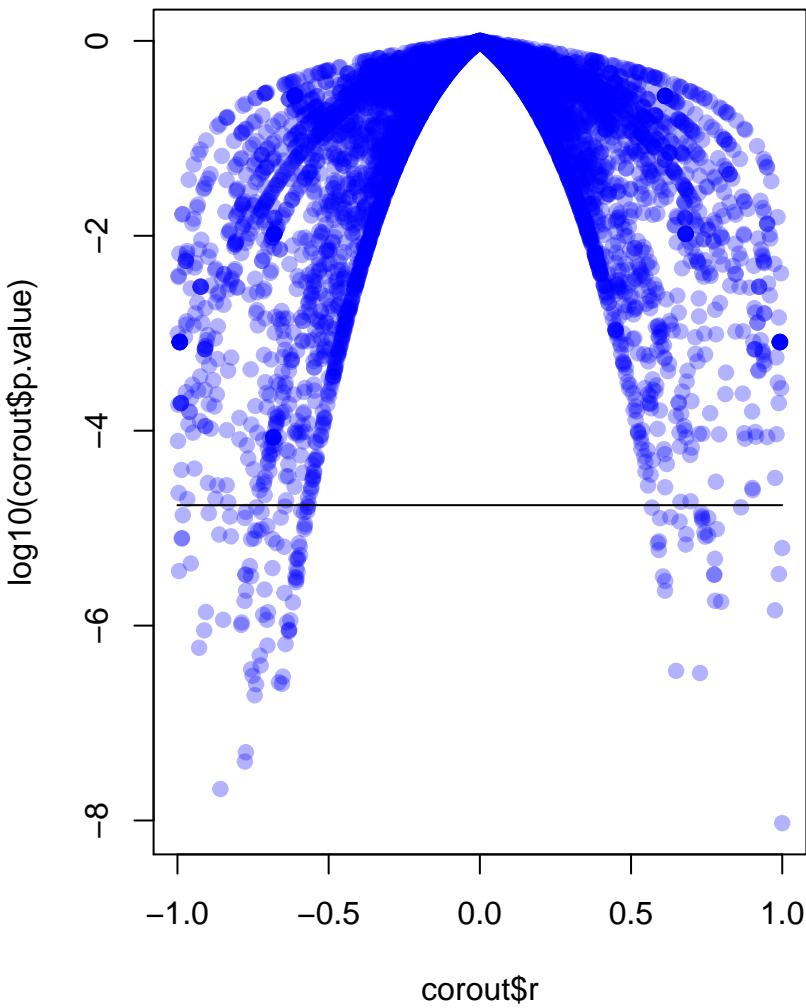
feature.pgfam_id.aromaticity.mean



Optimal Growth Temperature

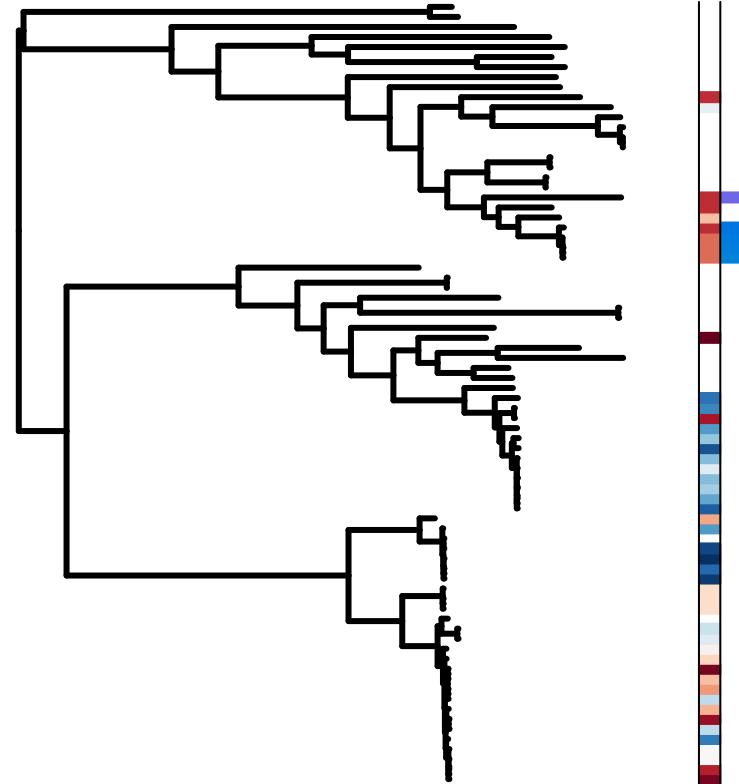
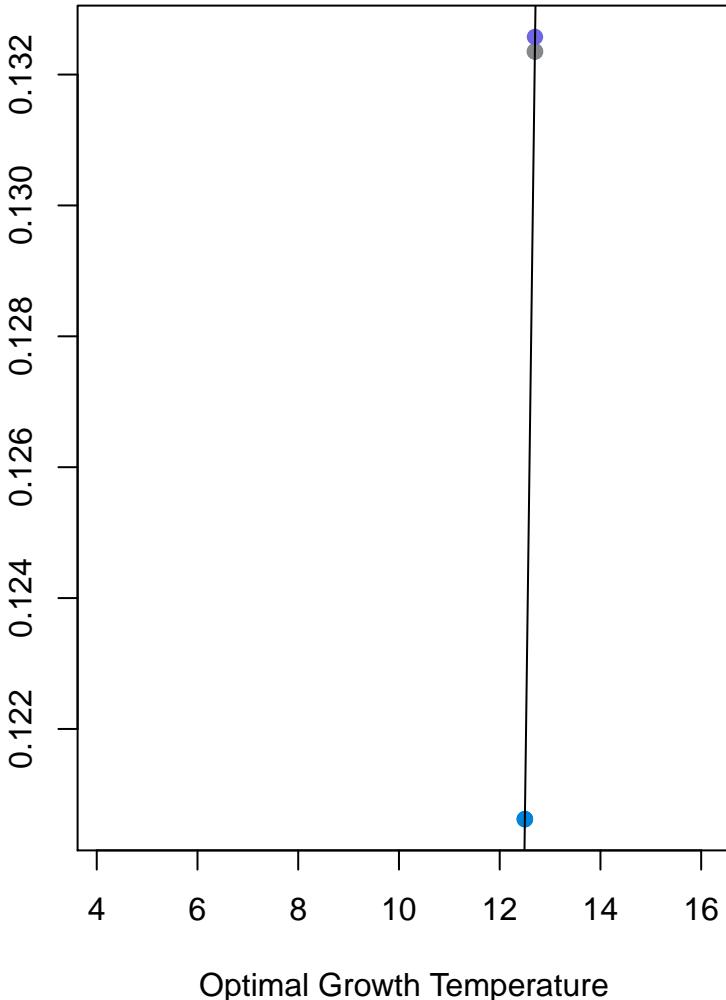


feature.plfam_id.aromaticity.mean



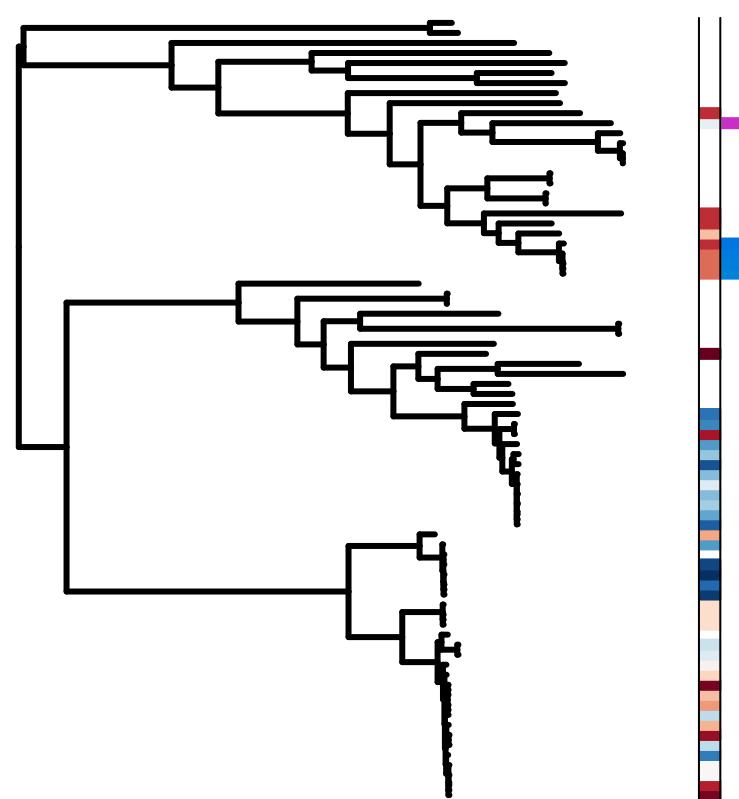
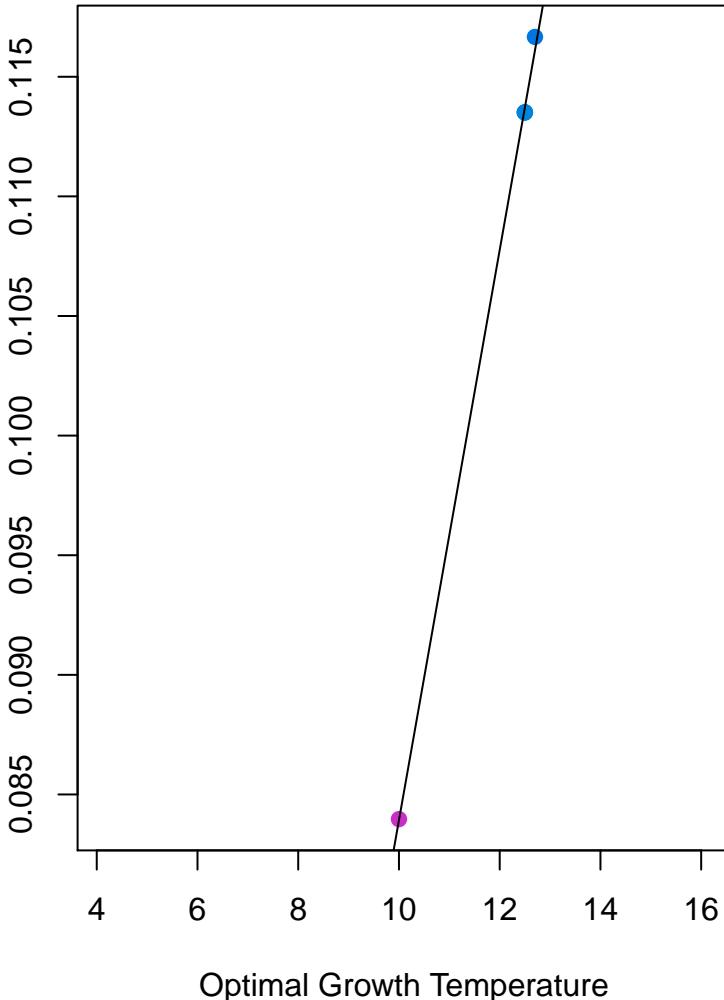
feature.plfam_id.aromaticity.mean
PLF_28228_00018366
hypothetical protein
 $r = 1, p = 10^{-8.027}$

feature.plfam_id.aromaticity.mean



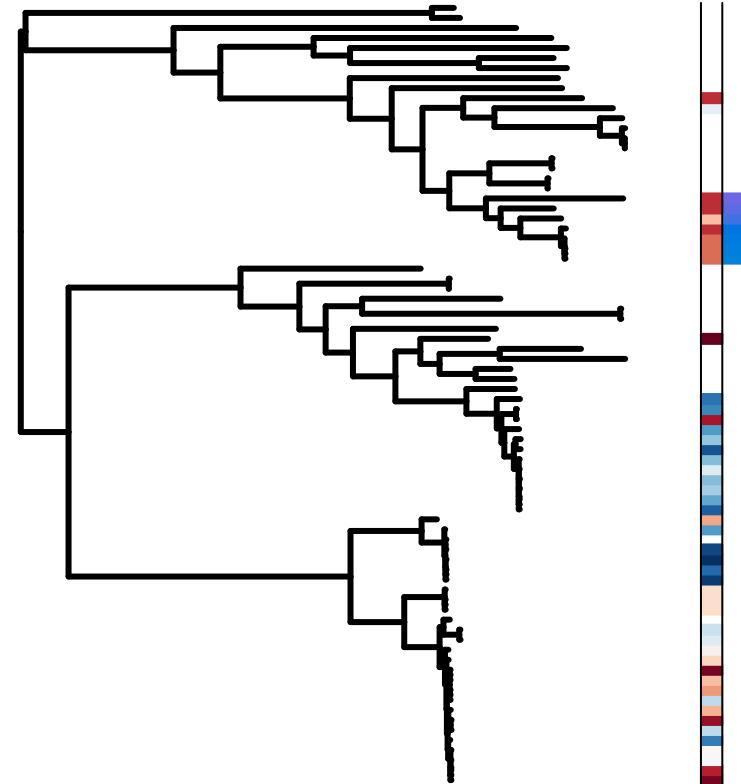
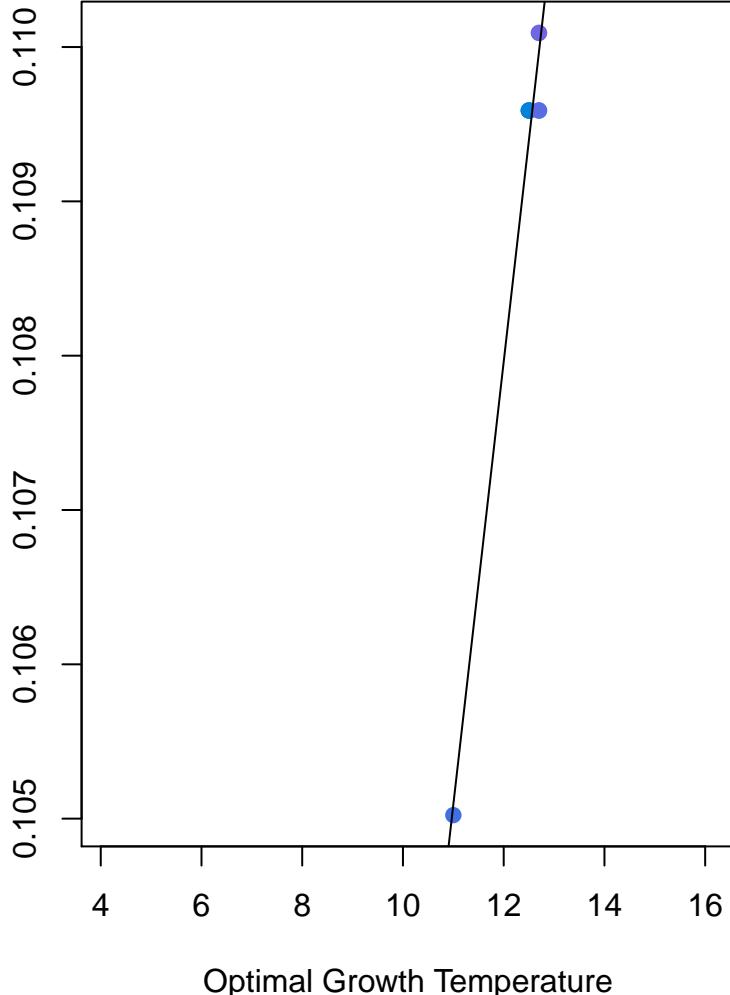
feature.plfam_id.aromaticity.mean
PLF_28228_00004090
hypothetical protein
 $r = 1, p = 10^{-5.204}$

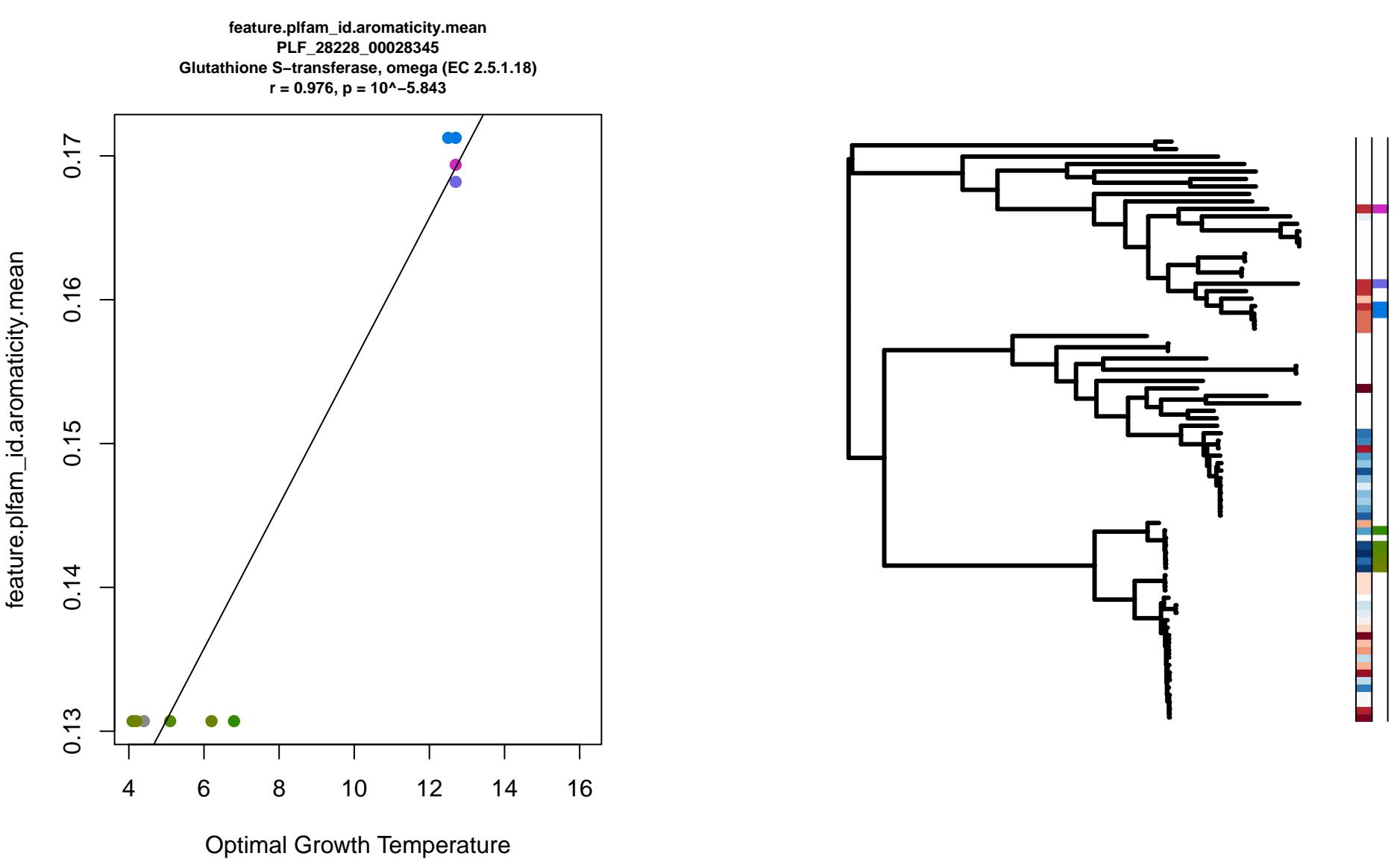
feature.plfam_id.aromaticity.mean



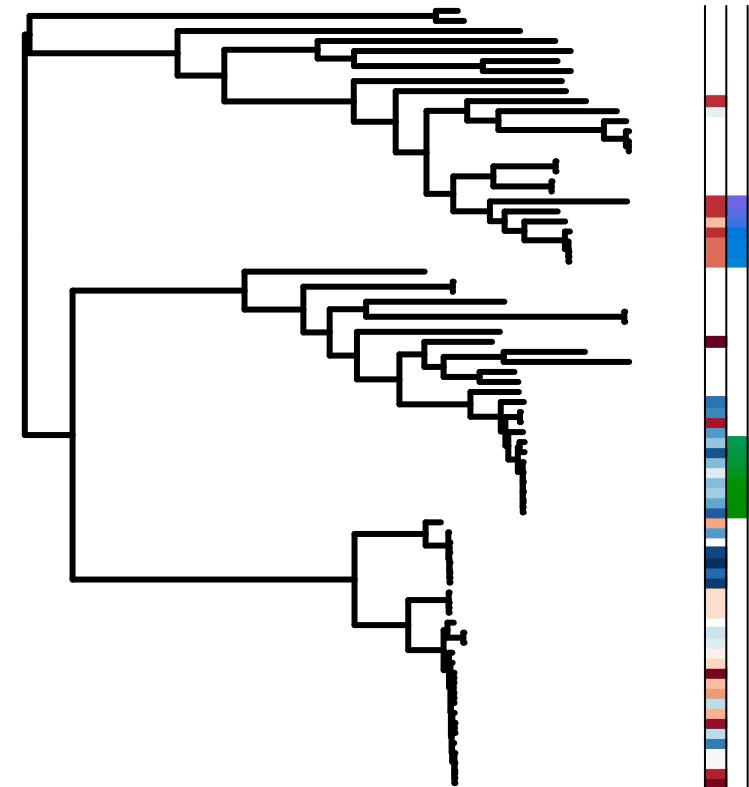
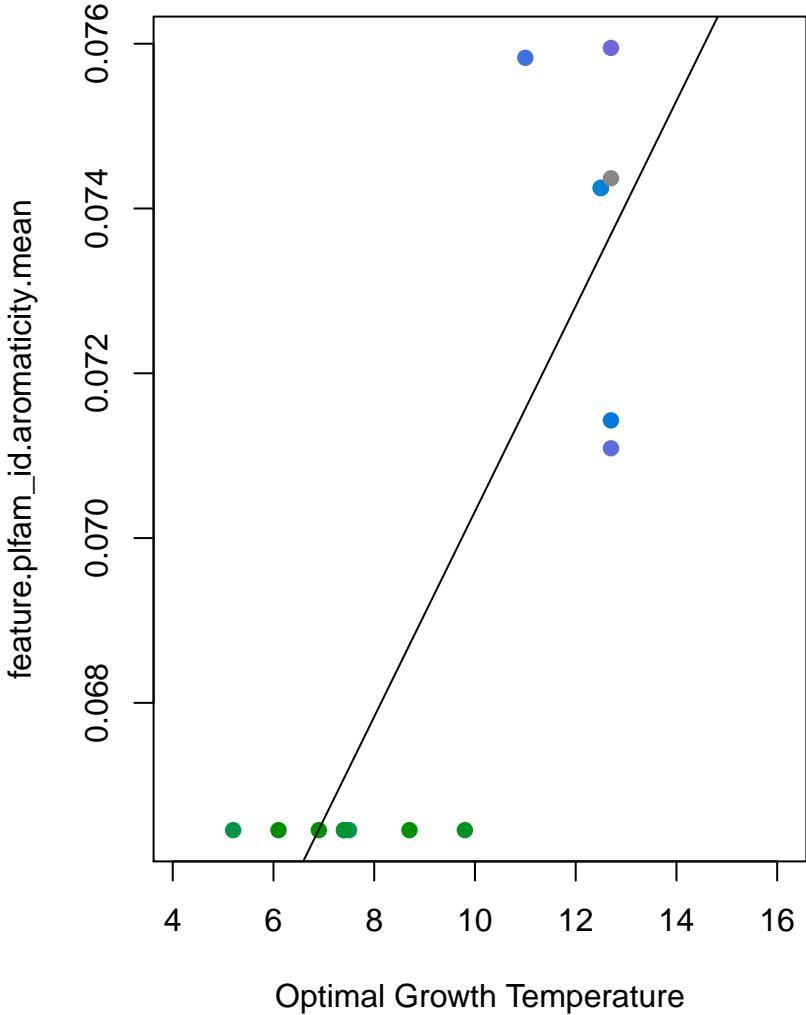
feature.plfam_id.aromaticity.mean
PLF_28228_00003494
Peptidyl-prolyl cis-trans isomerase
 $r = 0.989$, $p = 10^{-5.47}$

feature.plfam_id.aromaticity.mean





feature.plfam_id.aromaticity.mean
PLF_28228_00014411
Methyl-accepting chemotaxis protein
 $r = 0.864, p = 10^{-4.786}$



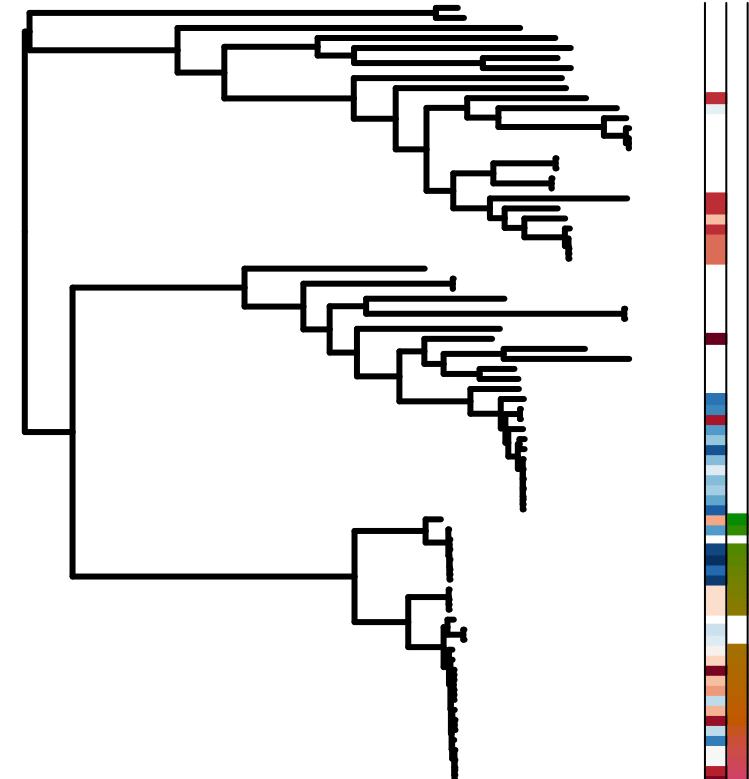
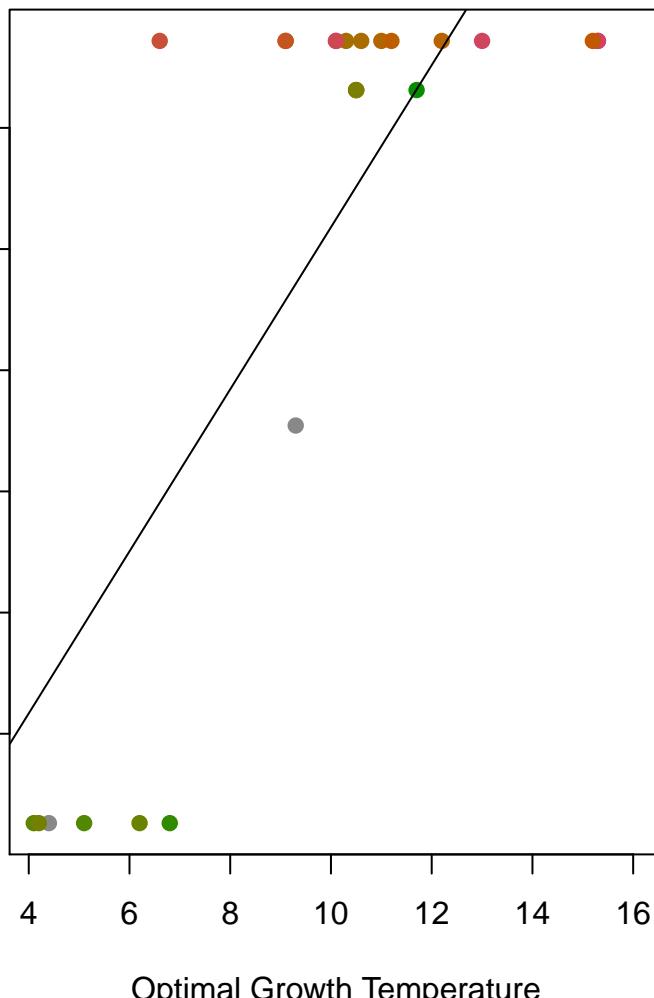
feature.plfam_id.aromaticity.mean

PLF_28228_00022096

Two-component system sensor histidine kinase

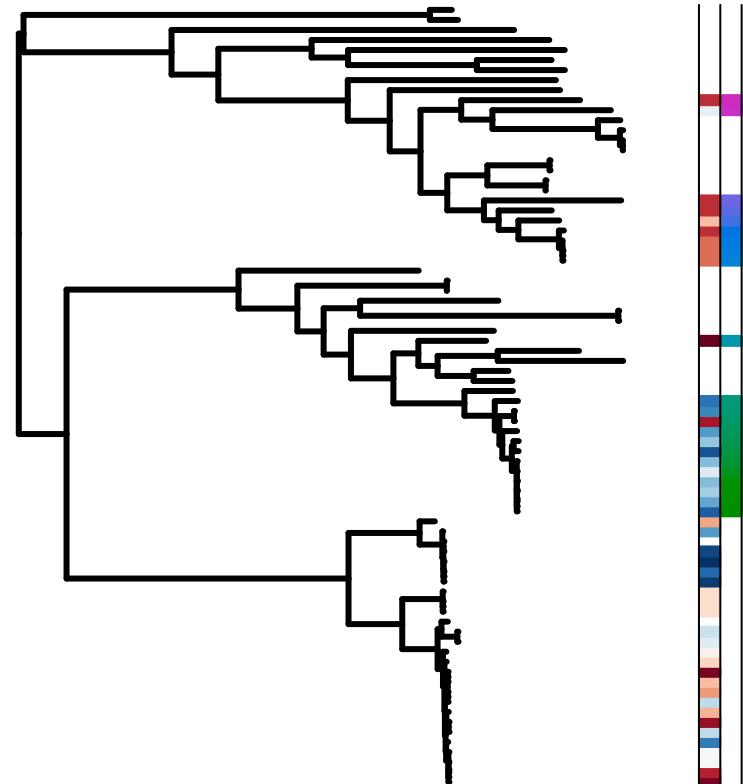
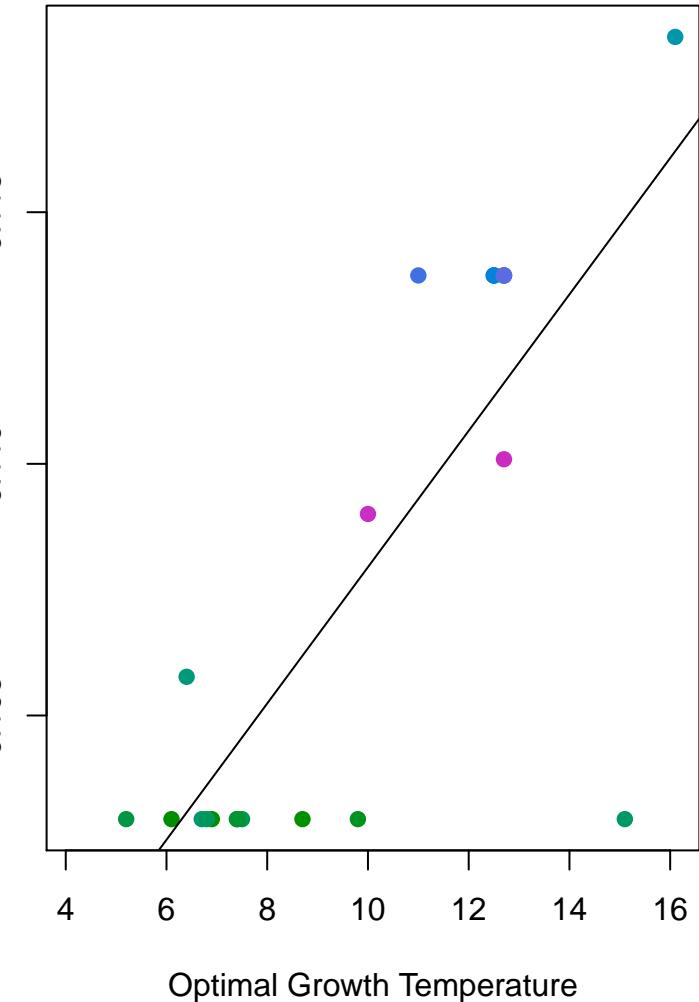
$r = 0.798$, $p = 10^{-5.756}$

feature.plfam_id.aromaticity.mean



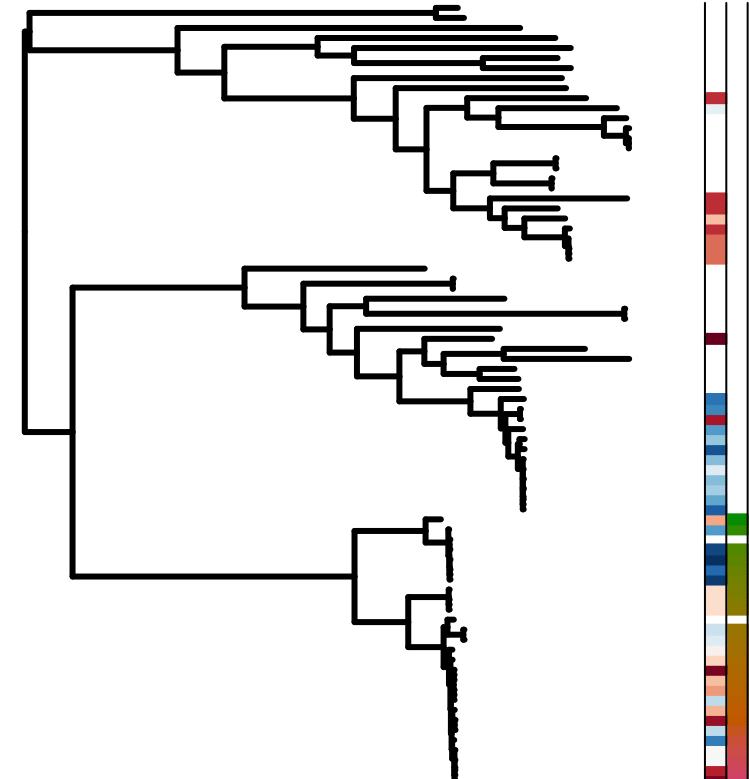
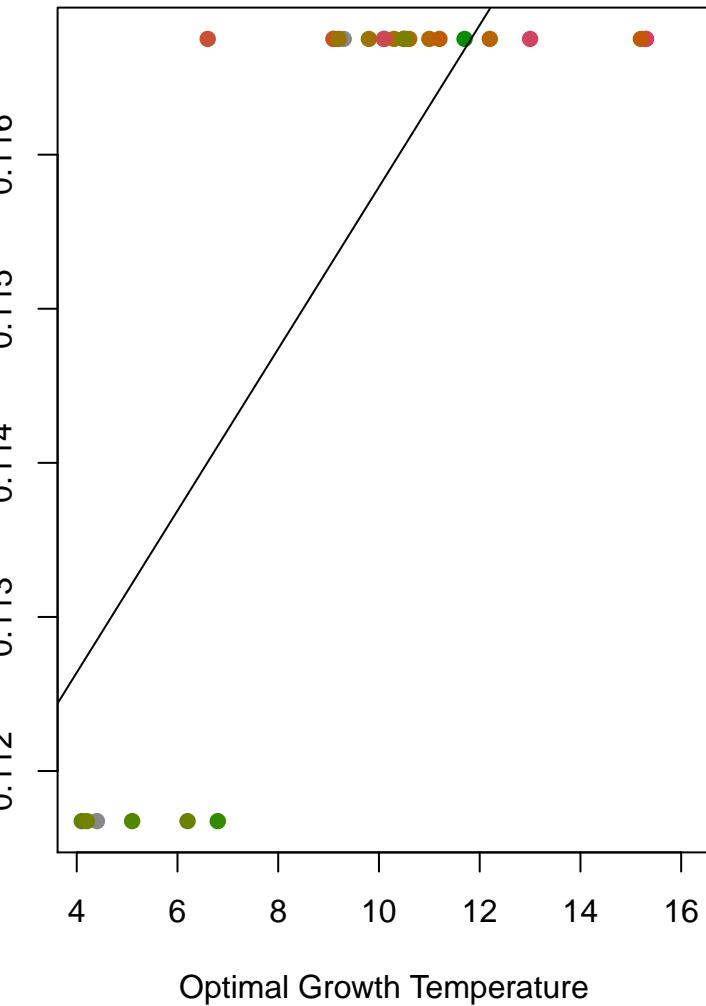
feature.plfam_id.aromaticity.mean
PLF_28228_00002278
hypothetical protein
 $r = 0.784$, $p = 10^{-5.01}$

feature.plfam_id.aromaticity.mean

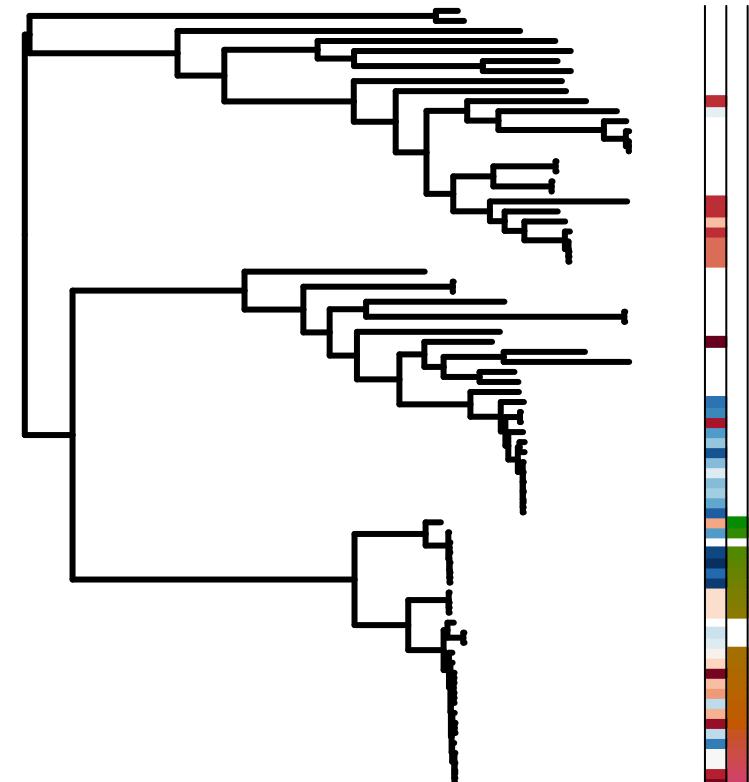
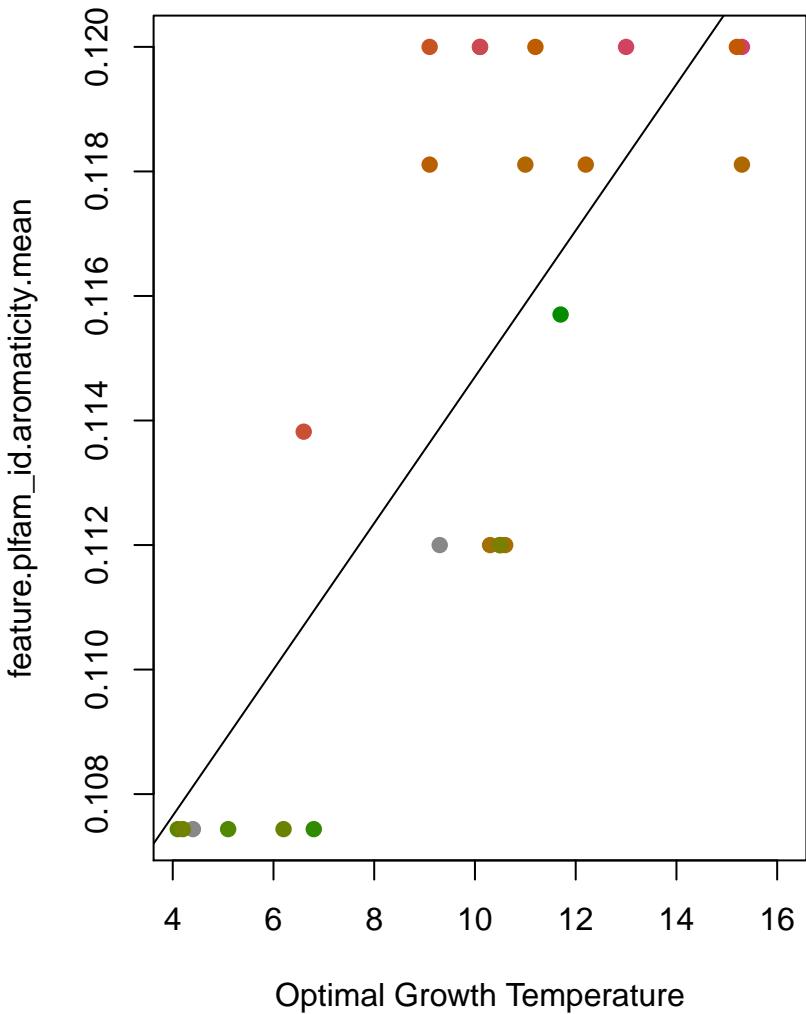


feature.plfam_id.aromaticity.mean
PLF_28228_00032199
Uncharacterized hydrolase DSY2054
 $r = 0.778$, $p = 10^{-5.746}$

feature.plfam_id.aromaticity.mean

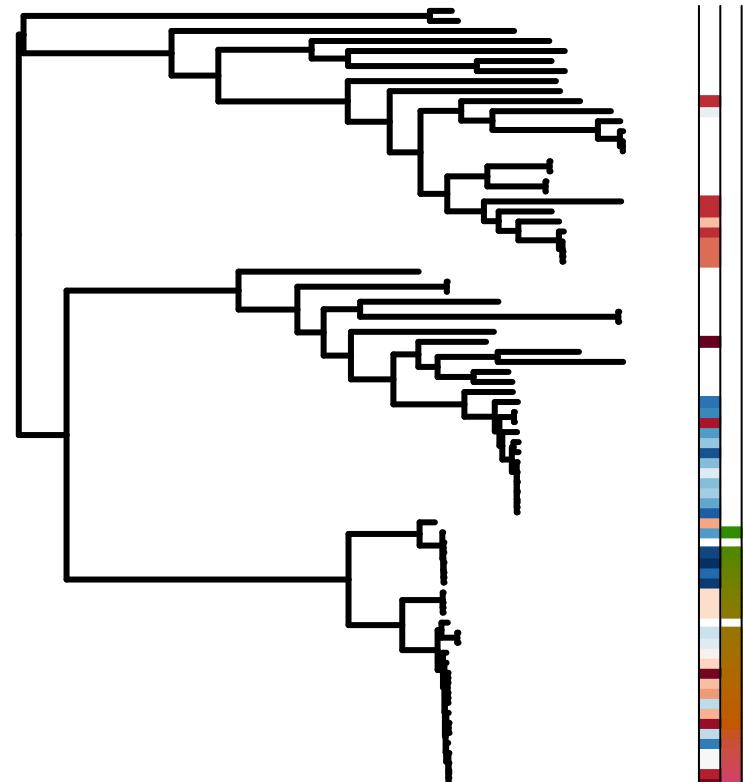
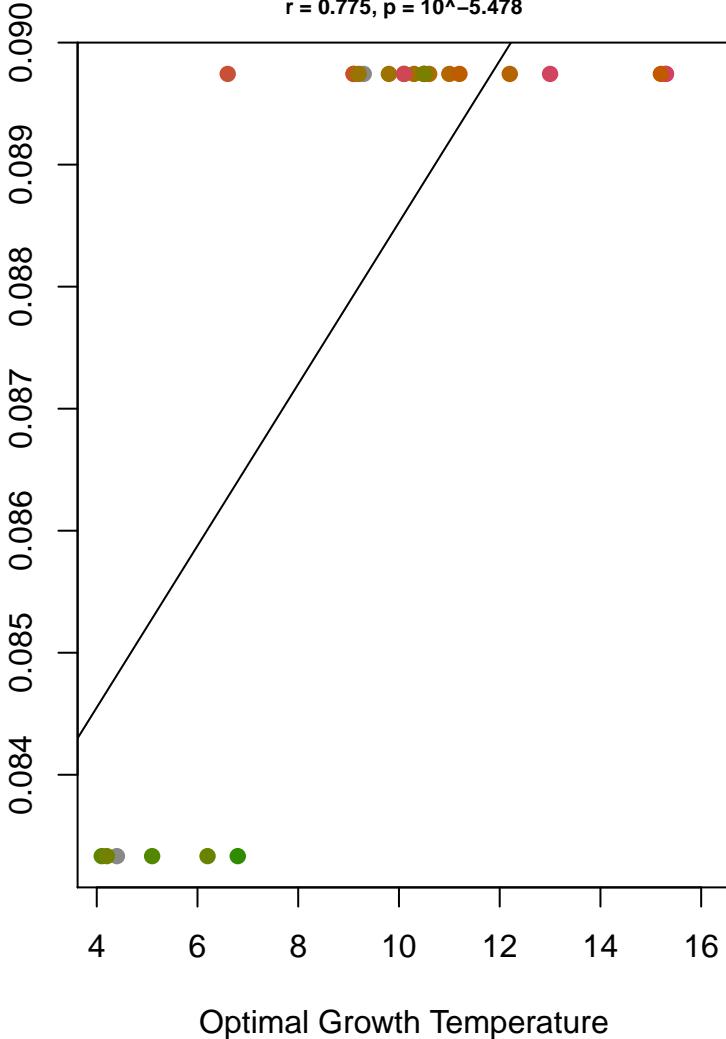


feature.plfam_id.aromaticity.mean
PLF_28228_00020926
hypothetical protein
 $r = 0.777$, $p = 10^{-5.315}$



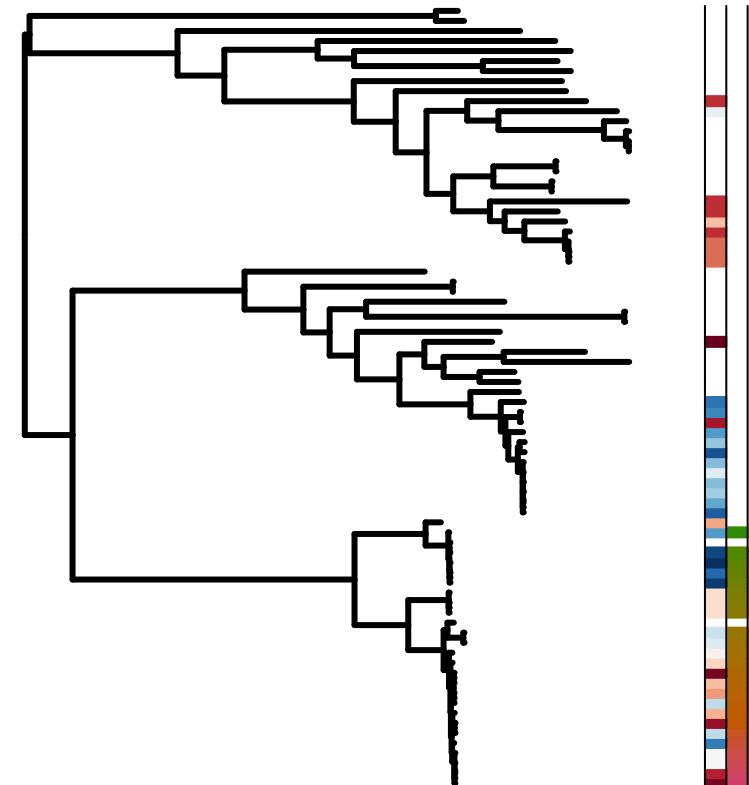
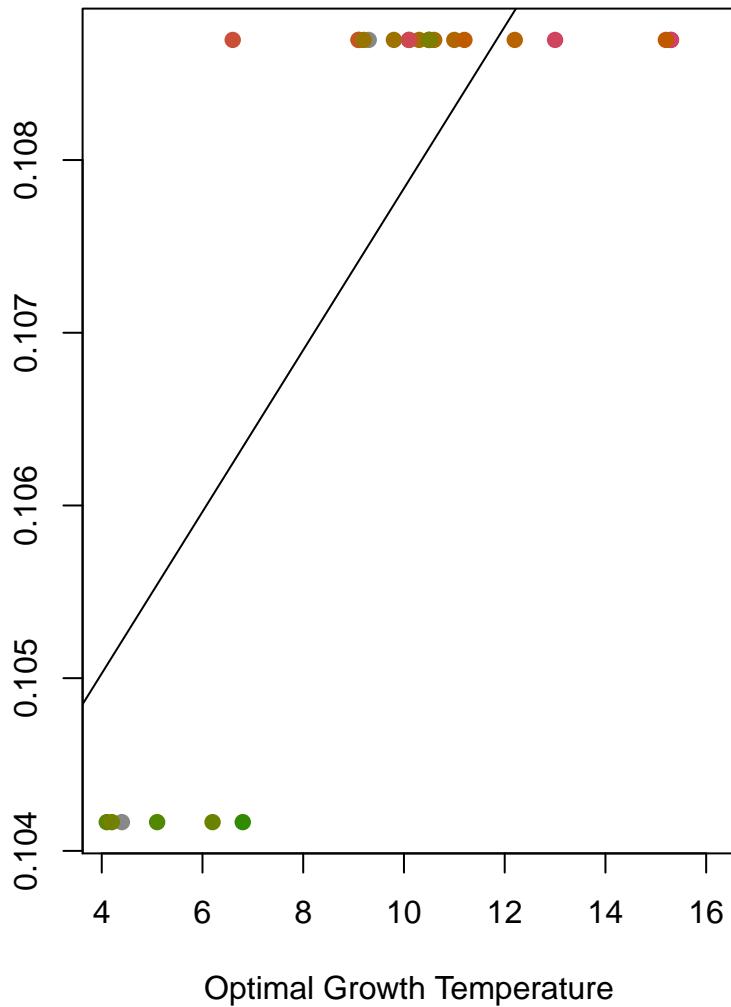
feature.plfam_id.aromaticity.mean
PLF_28228_00015077
hypothetical protein
 $r = 0.775, p = 10^{-5.478}$

feature.plfam_id.aromaticity.mean



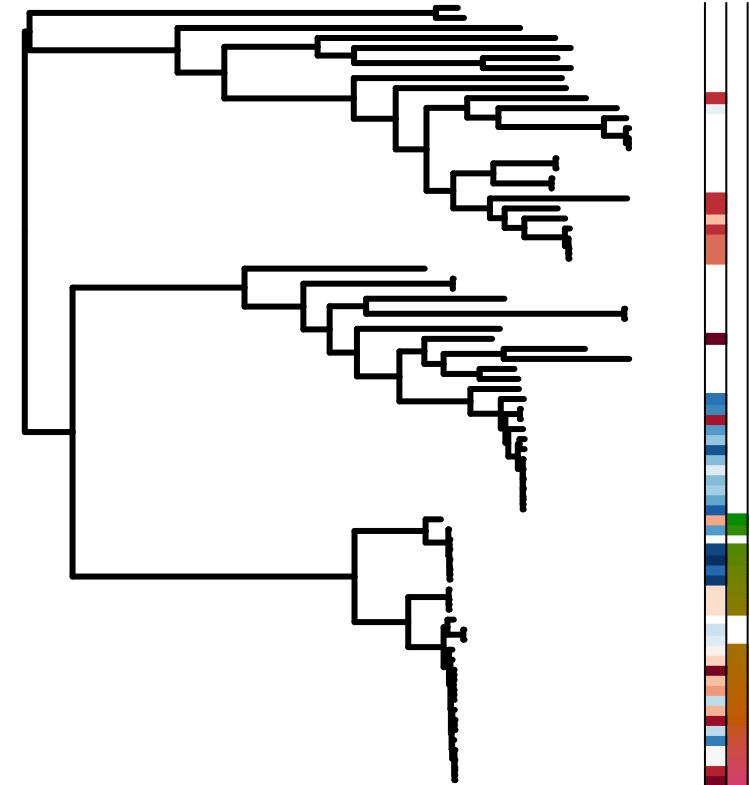
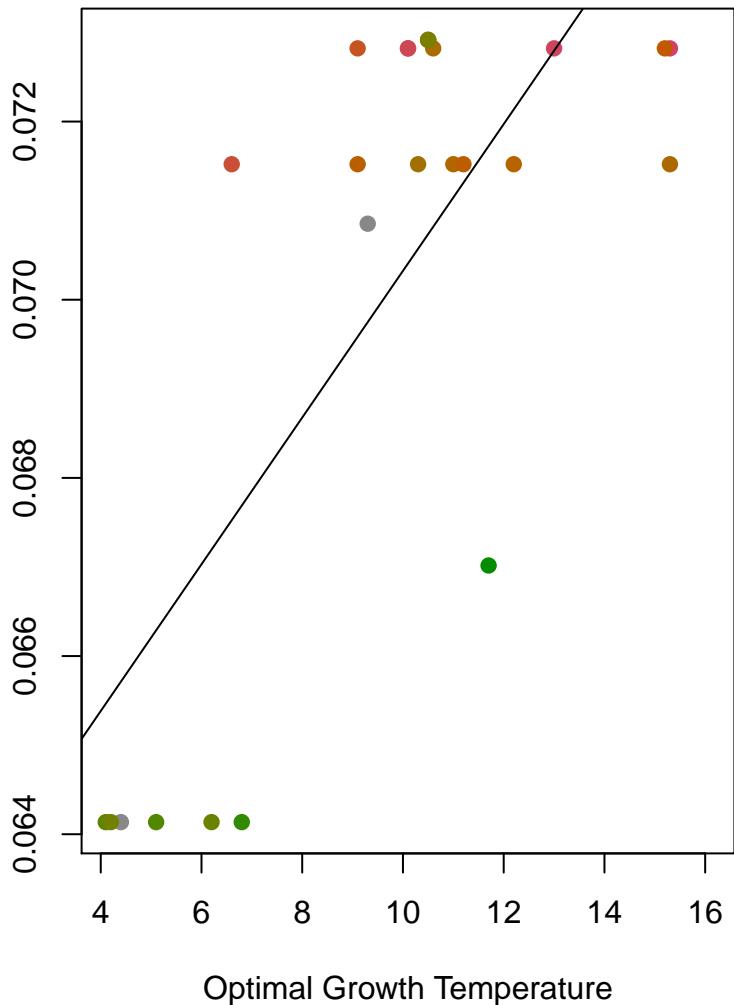
feature.plfam_id.aromaticity.mean
PLF_28228_00029369
hypothetical protein
 $r = 0.775, p = 10^{-5.478}$

feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00015183
FIG00951615: hypothetical protein
 $r = 0.755$, $p = 10^{-4.894}$

feature.plfam_id.aromaticity.mean



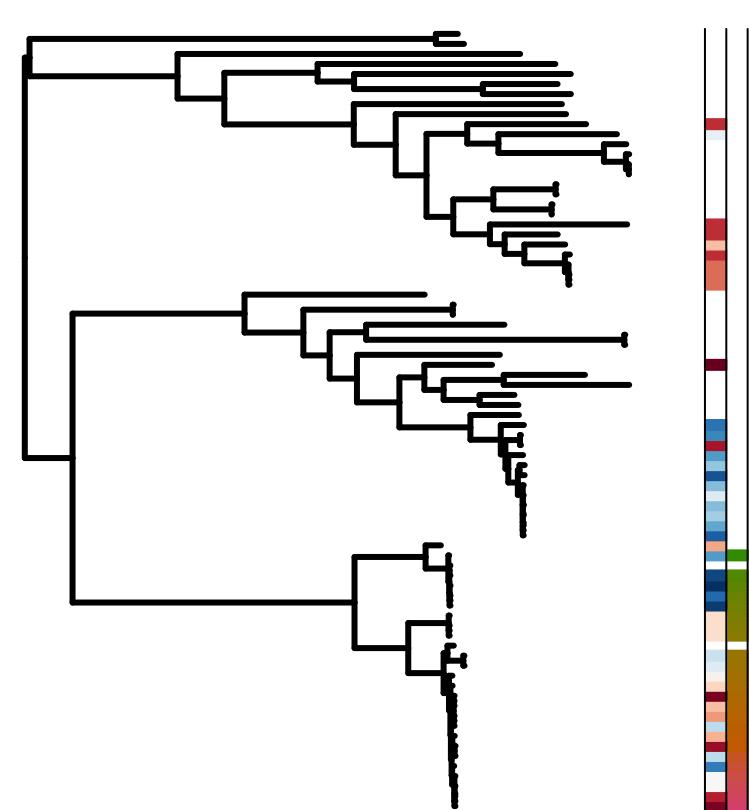
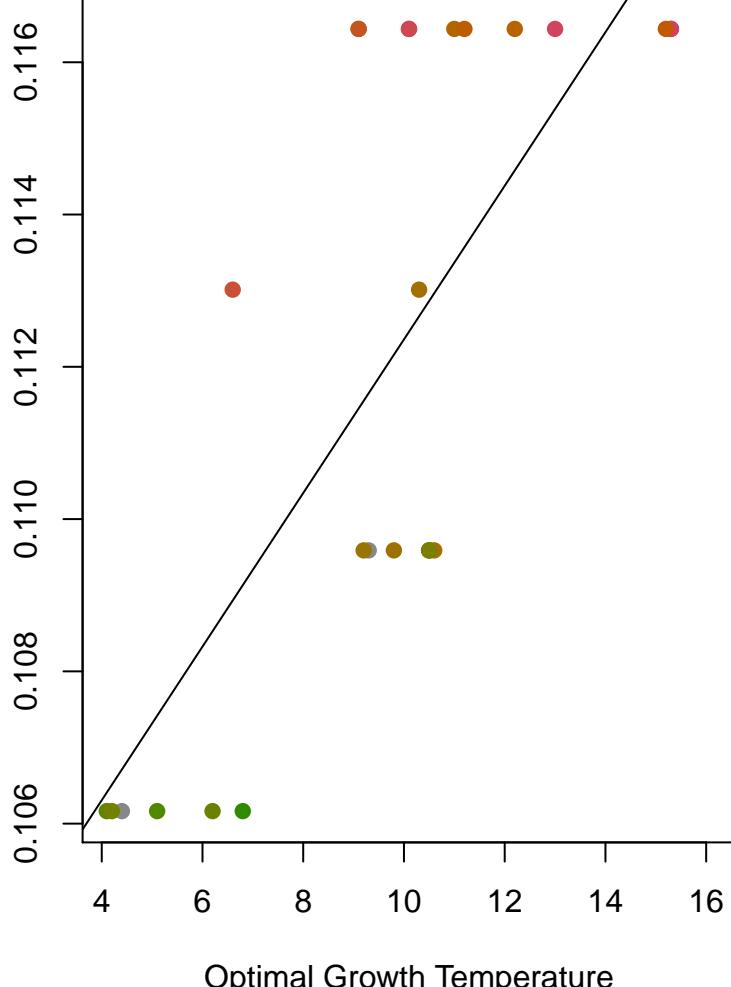
feature.plfam_id.aromaticity.mean

PLF_28228_00023267

Uncharacterized protein conserved in bacteria, NMA0228-like

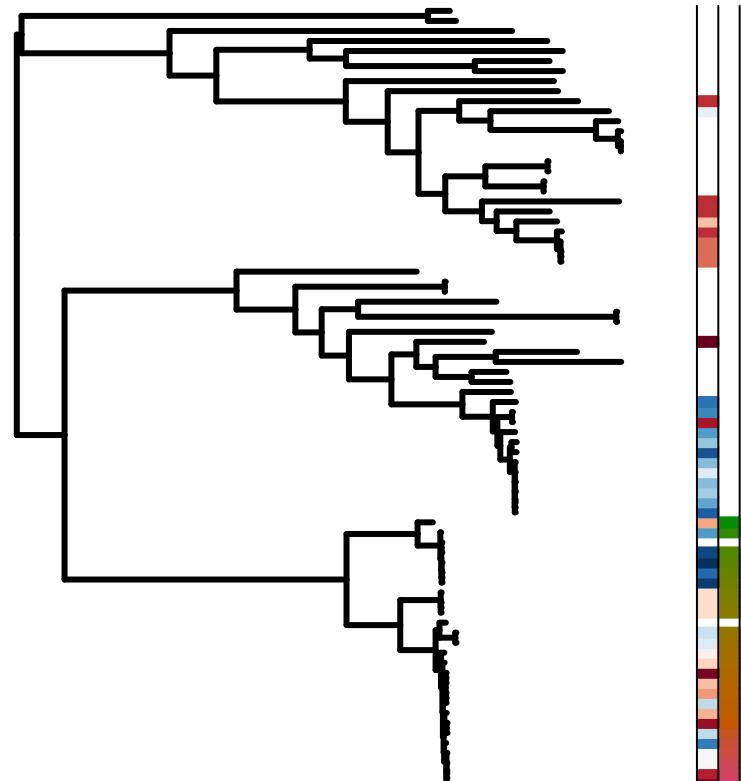
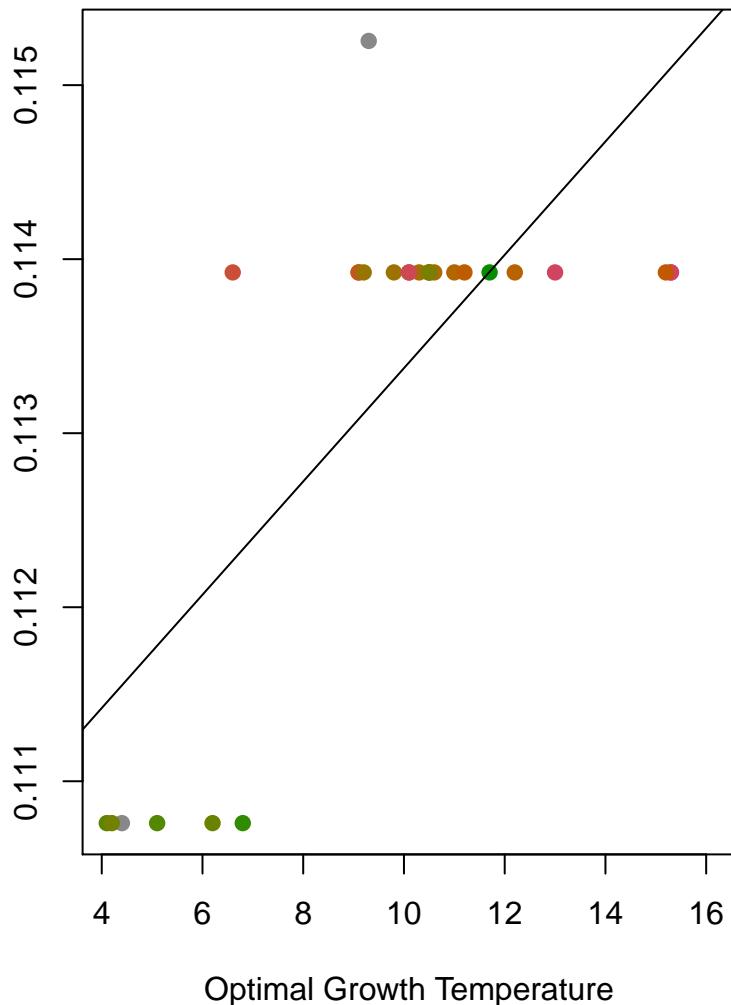
$r = 0.755, p = 10^{-5.073}$

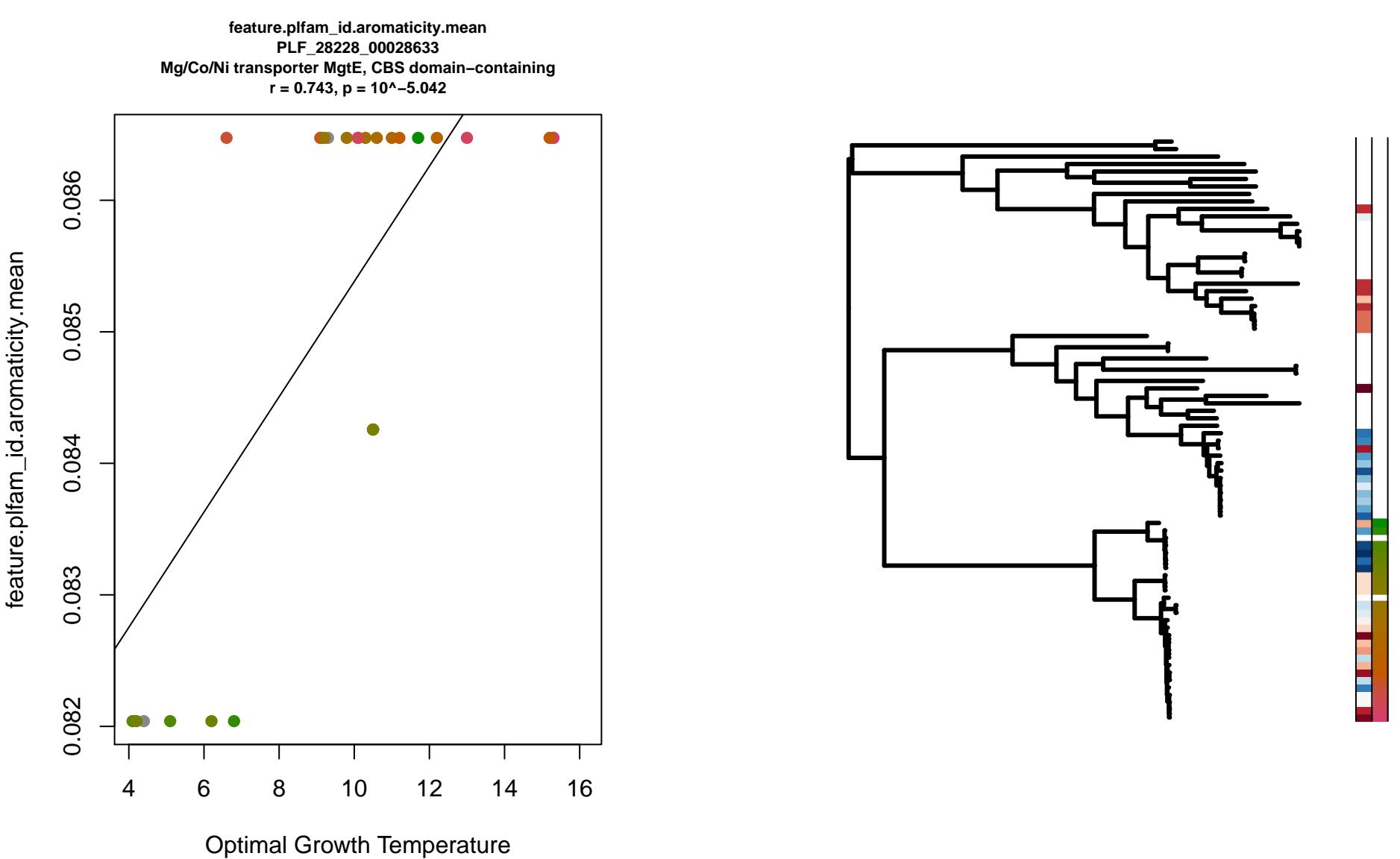
feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00014559
Transcriptional regulator, LysR family
 $r = 0.745$, $p = 10^{-5.088}$

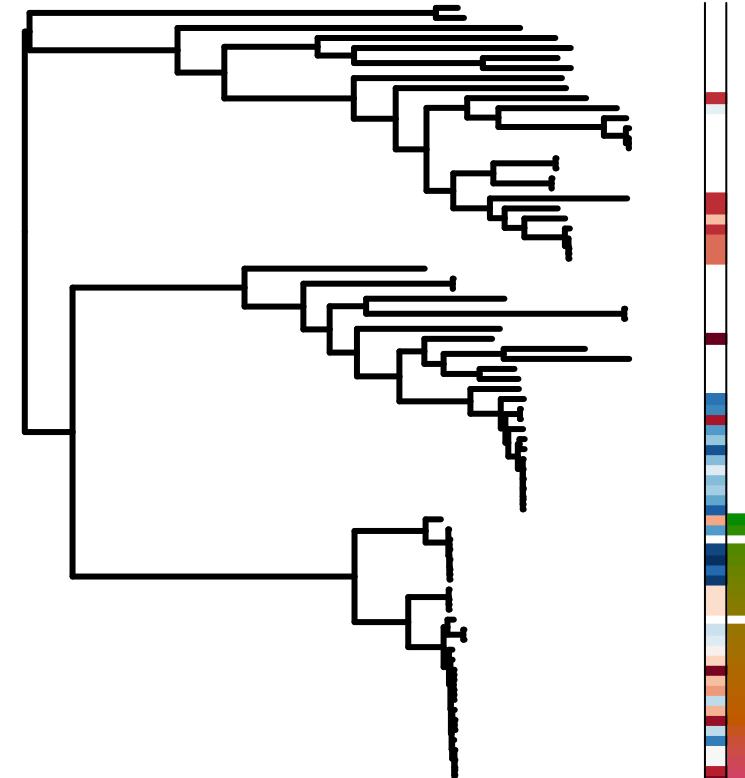
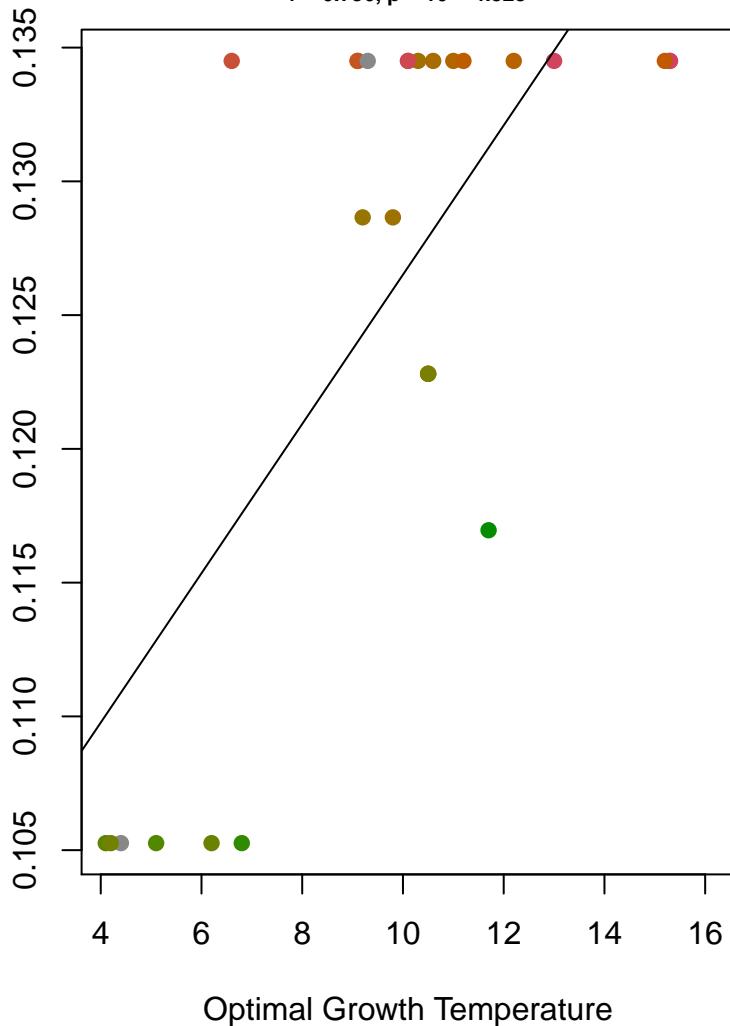
feature.plfam_id.aromaticity.mean





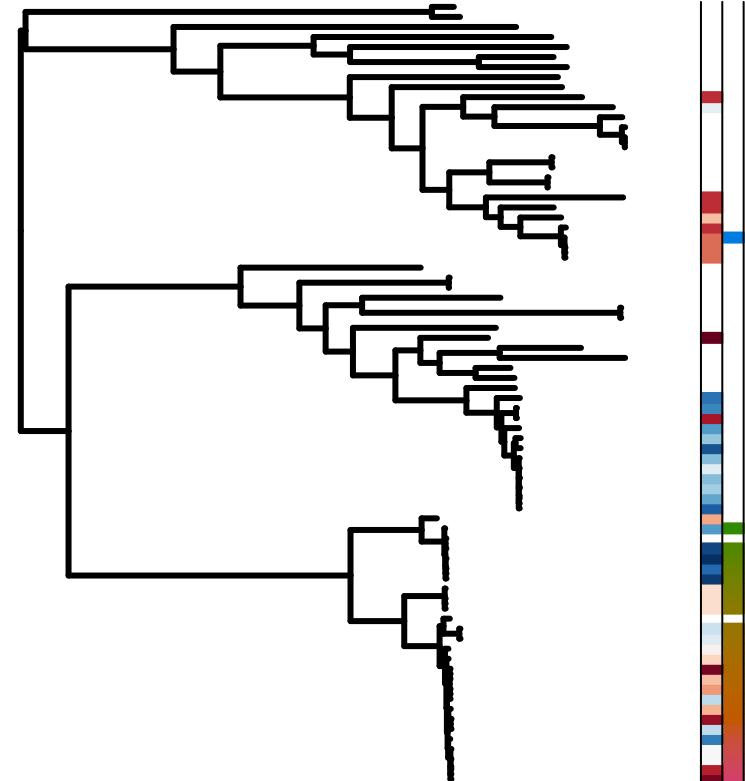
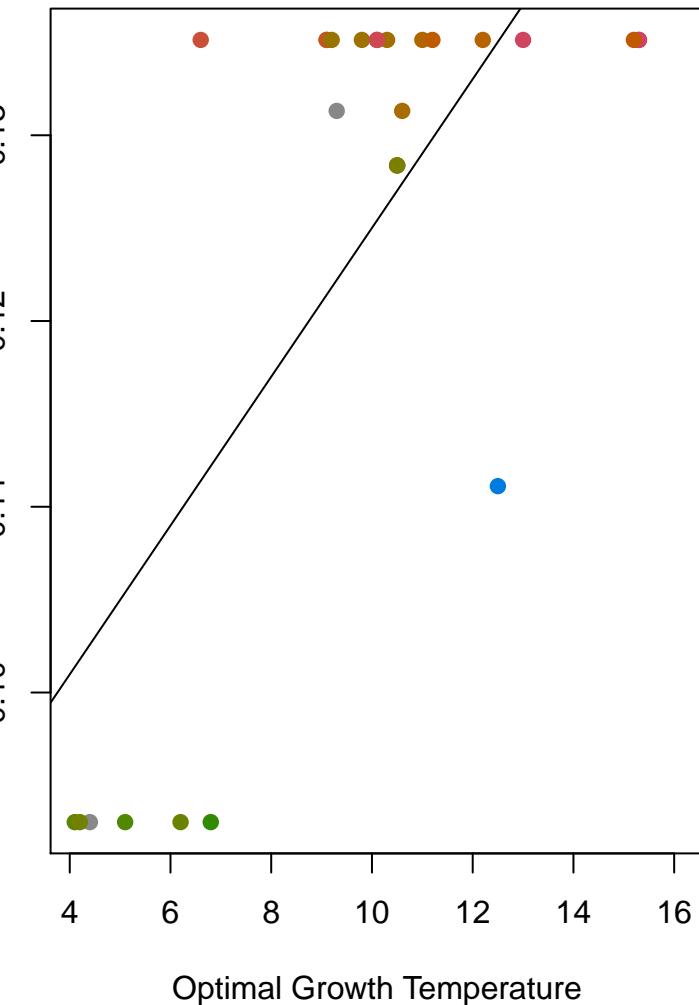
feature.plfam_id.aromaticity.mean
PLF_28228_00031535
hypothetical protein
 $r = 0.736, p = 10^{-4.923}$

feature.plfam_id.aromaticity.mean

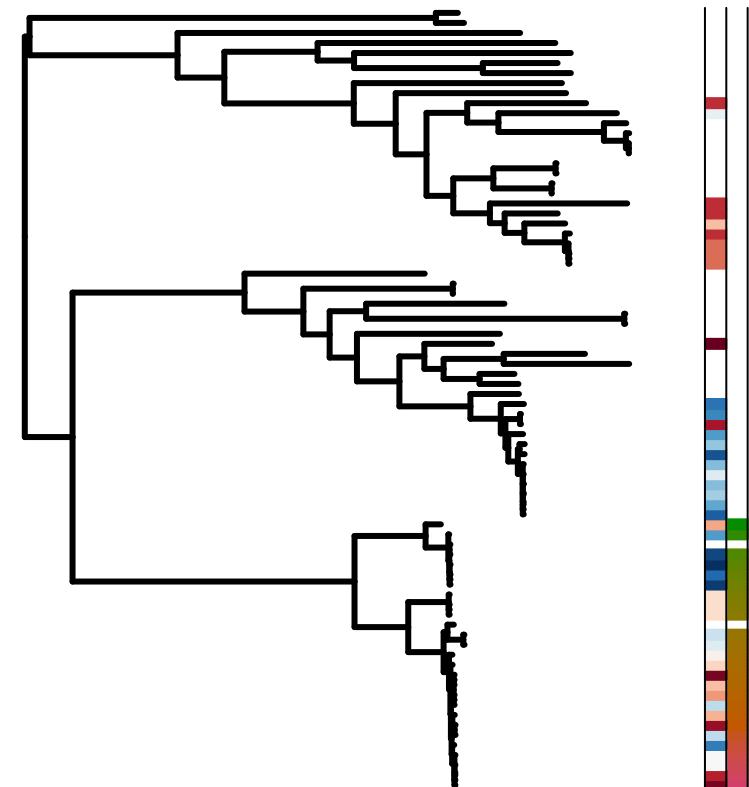
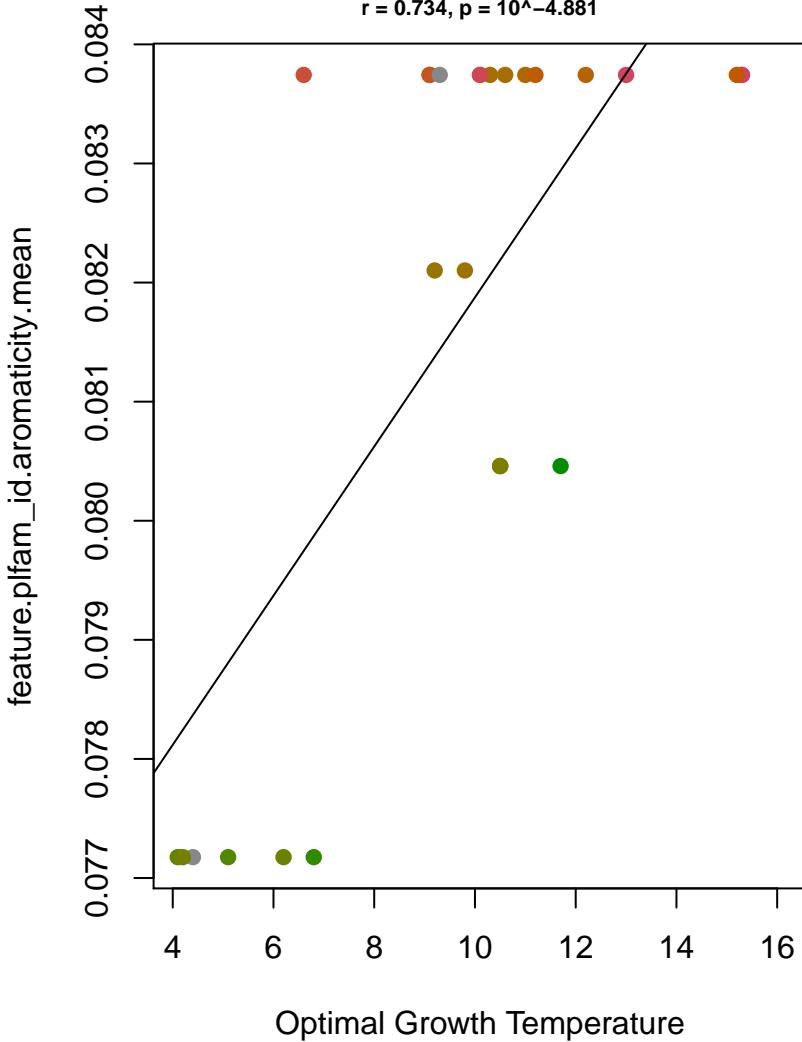


feature.plfam_id.aromaticity.mean
PLF_28228_00014070
hypothetical protein
 $r = 0.735, p = 10^{-4.899}$

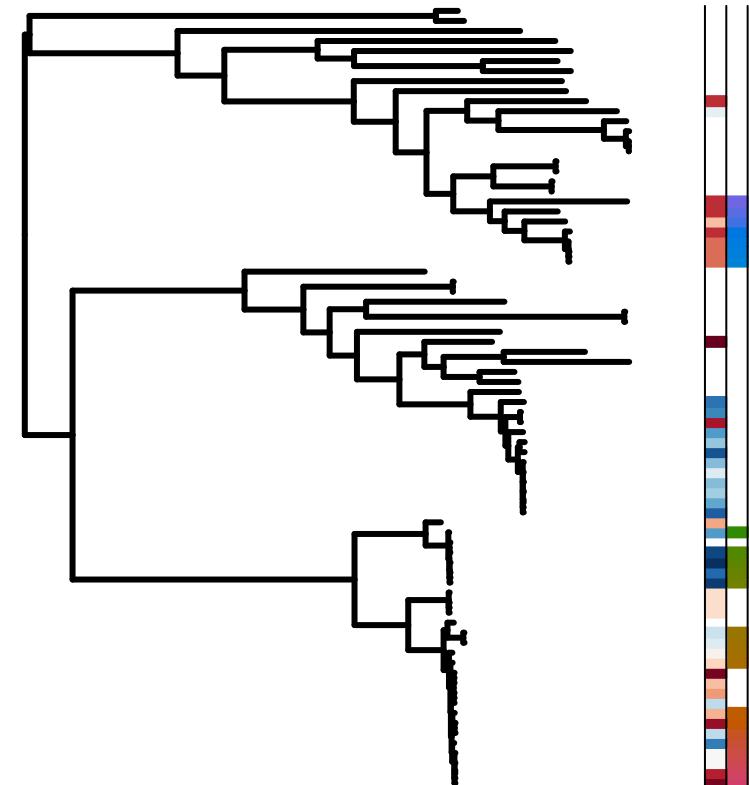
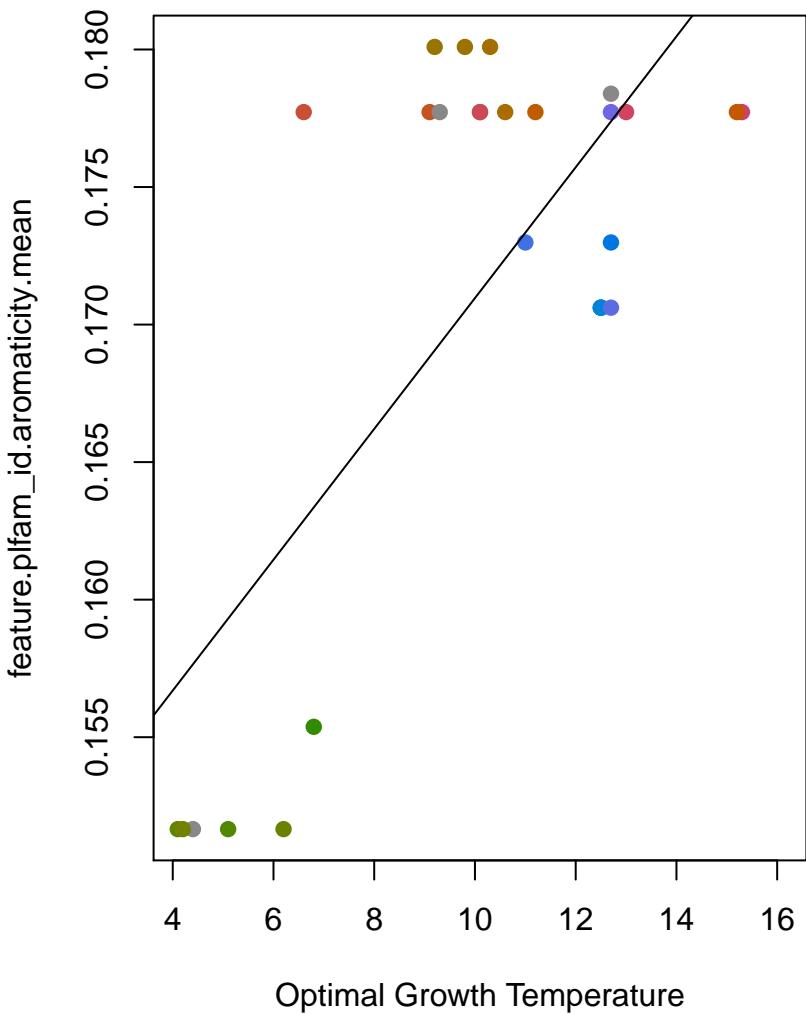
feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00016373
TrkA-C domain protein
 $r = 0.734$, $p = 10^{-4.881}$

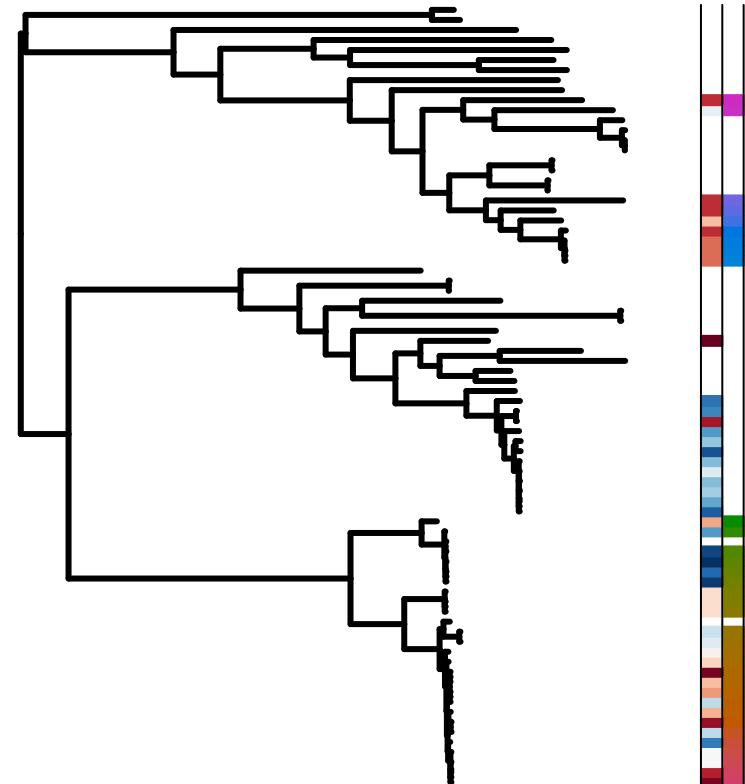
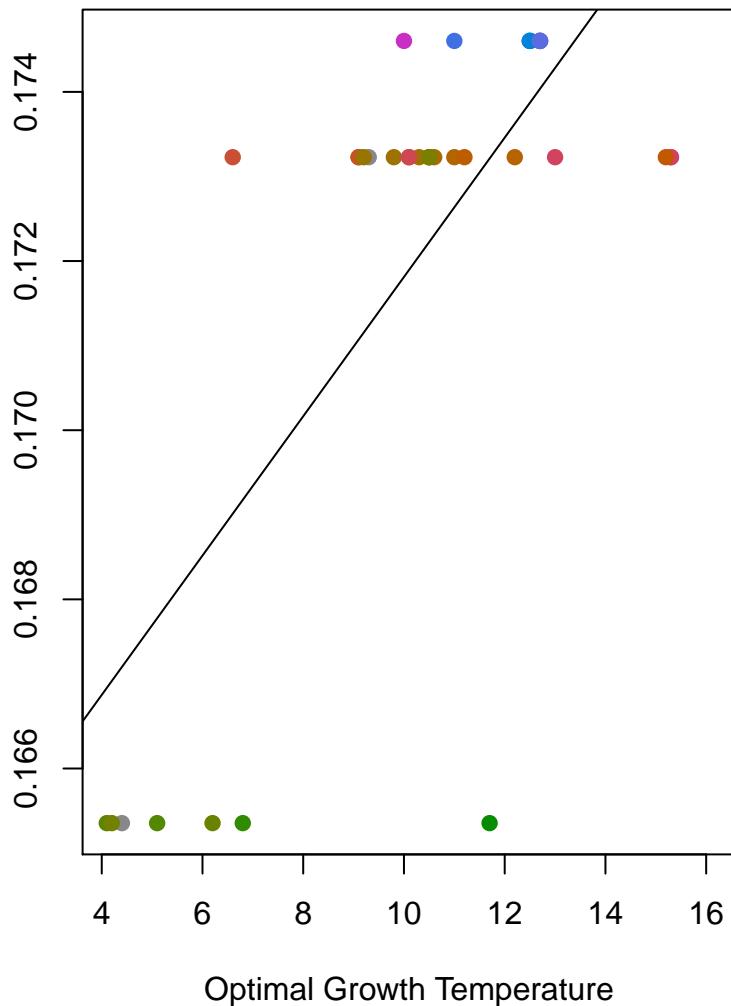


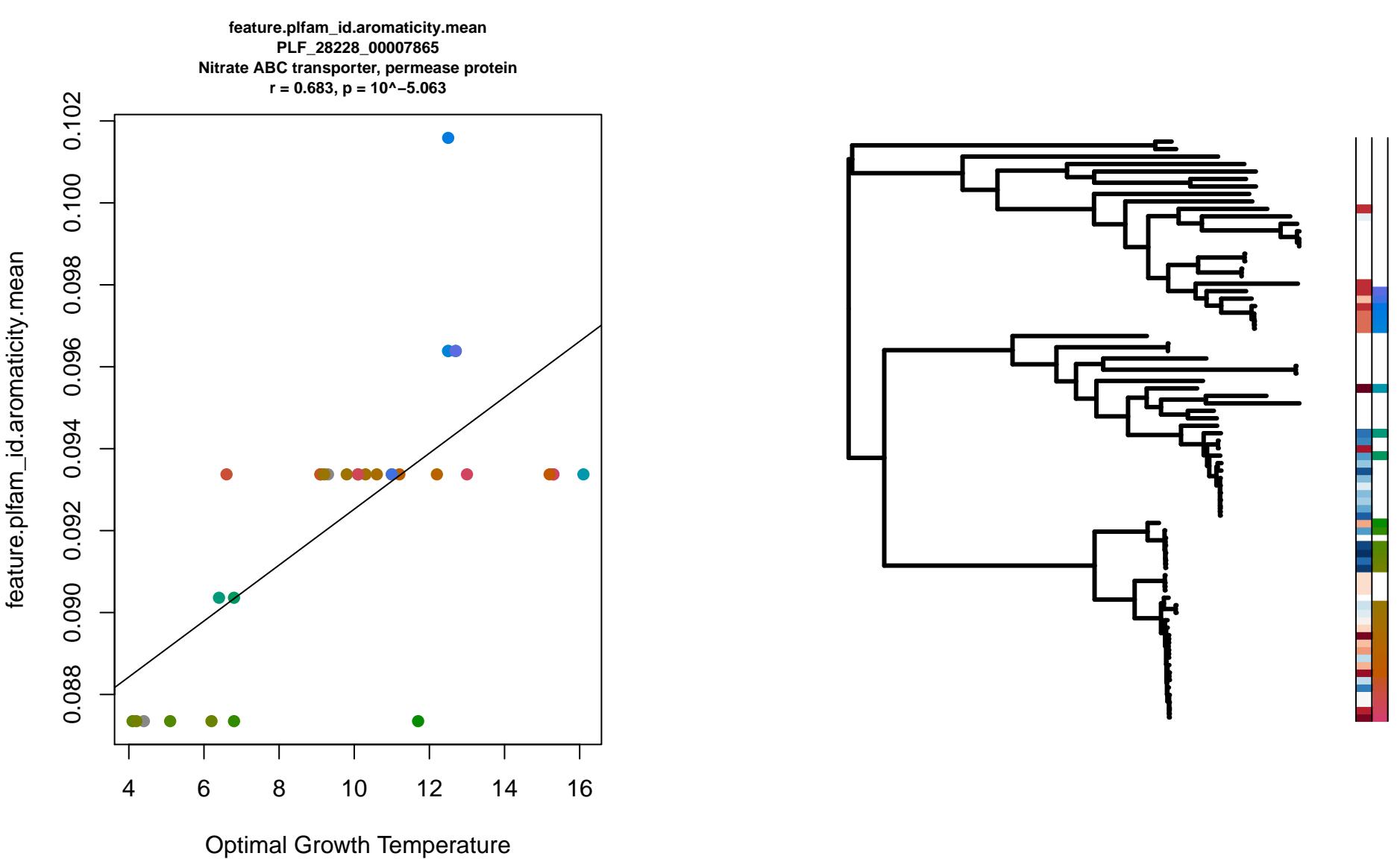
feature.plfam_id.aromaticity.mean
PLF_28228_00018214
hypothetical protein
 $r = 0.732, p = 10^{-4.845}$



feature.plfam_id.aromaticity.mean
PLF_28228_00002252
hypothetical protein
 $r = 0.728, p = 10^{-6.487}$

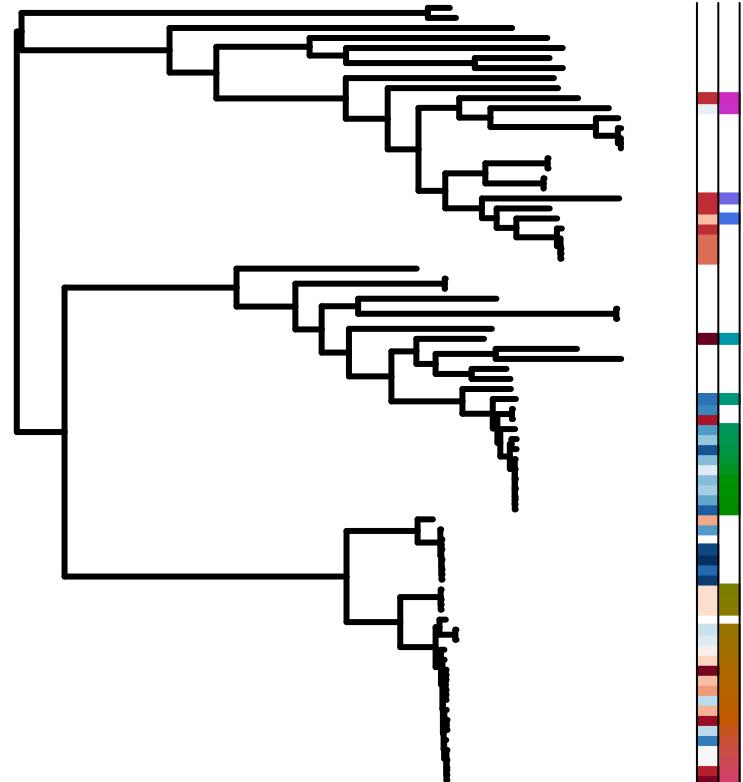
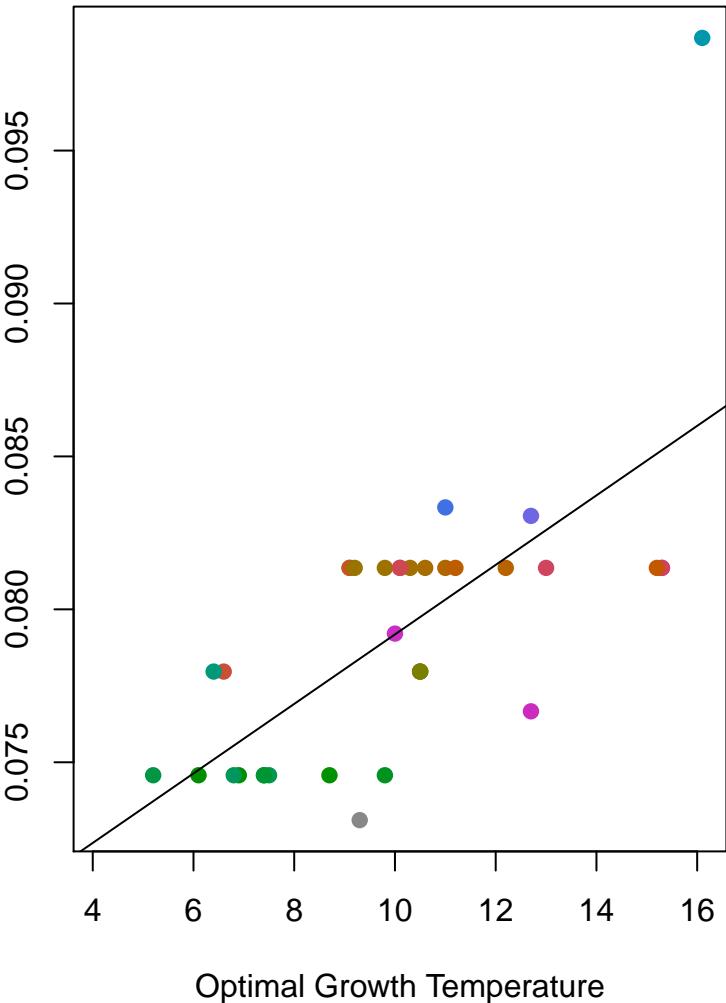
feature.plfam_id.aromaticity.mean





feature.plfam_id.aromaticity.mean
PLF_28228_00002141
Transcriptional regulator, LysR family
 $r = 0.681$, $p = 10^{-5.169}$

feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean

PLF_28228_00001480

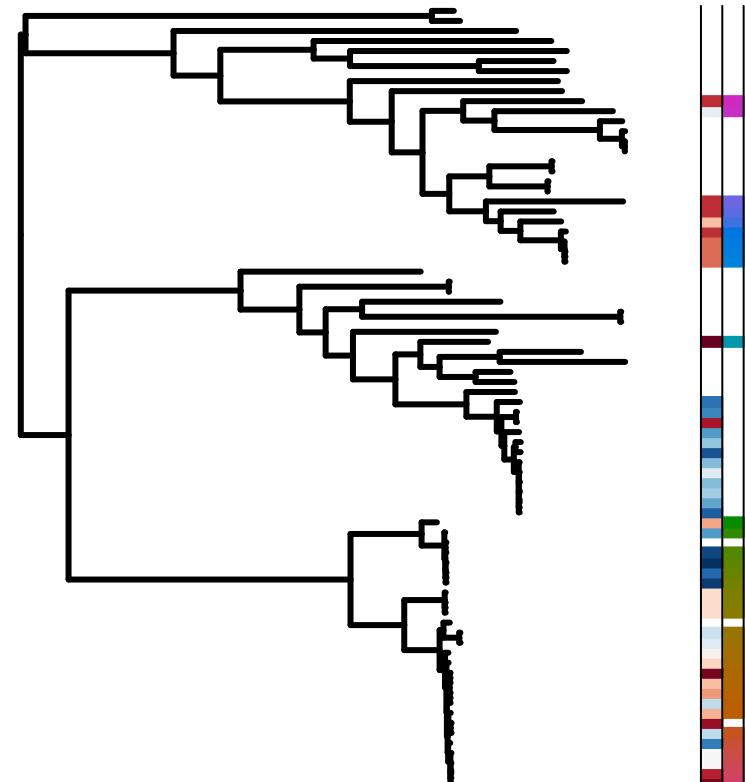
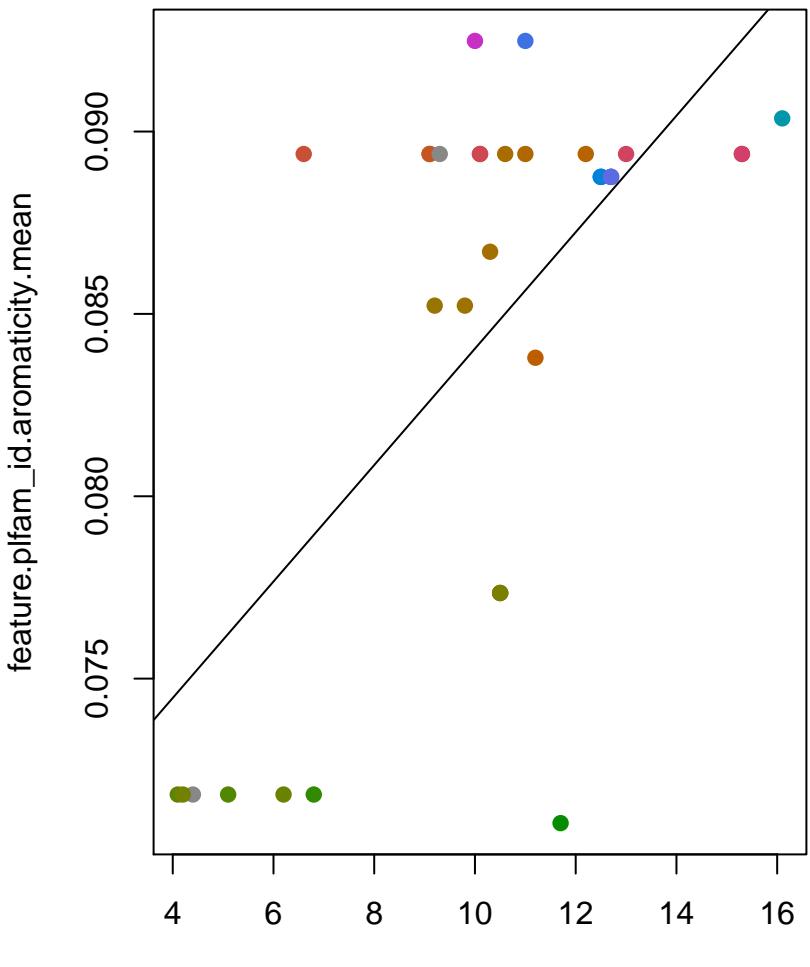
2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline (OHCU) decarboxylase (EC 4.1.1.97)

r = 0.66, p = 10^-4.932

feature.plfam_id.aromaticity.mean

2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline (OHCU) decarboxylase (EC 4.1.1.97)

Optimal Growth Temperature

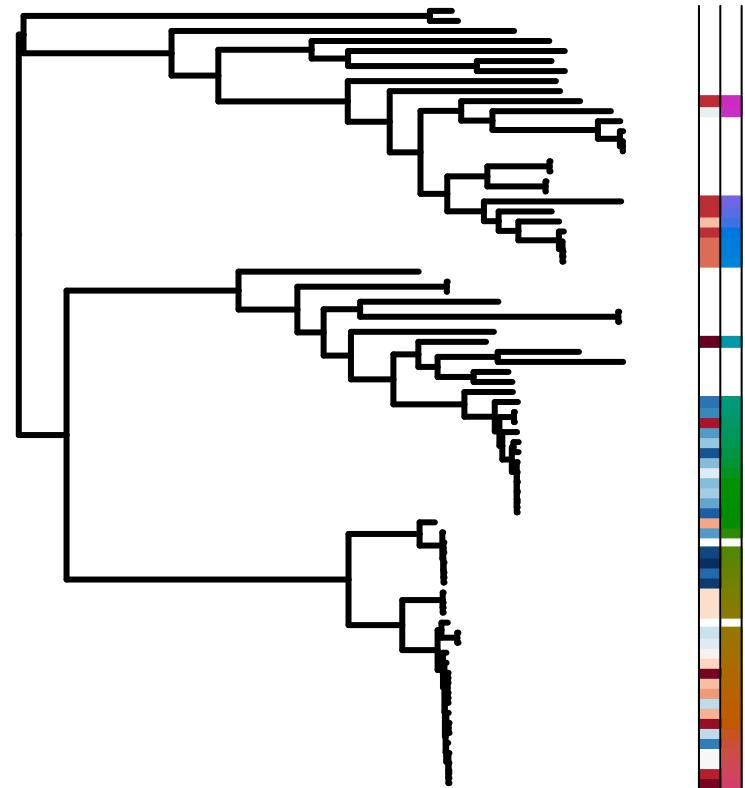
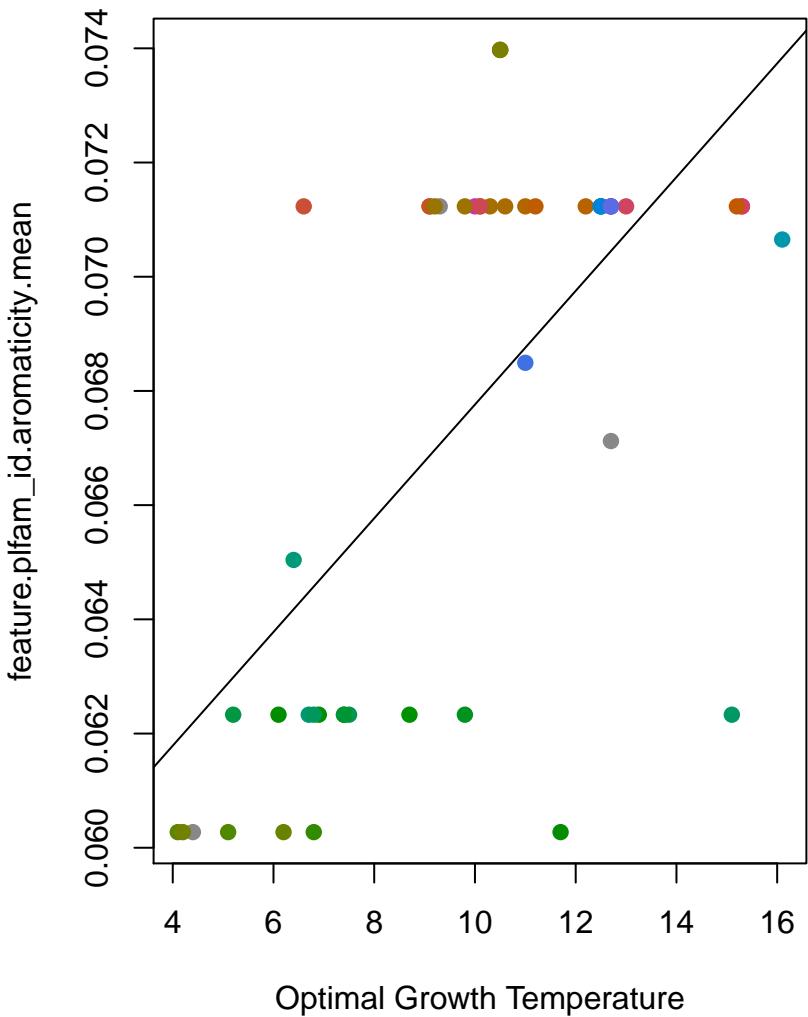


feature.plfam_id.aromaticity.mean

PLF_28228_00001874

Glutamate 5-kinase (EC 2.7.2.11) / RNA-binding C-terminal domain PUA

$r = 0.649$, $p = 10^{-6.465}$

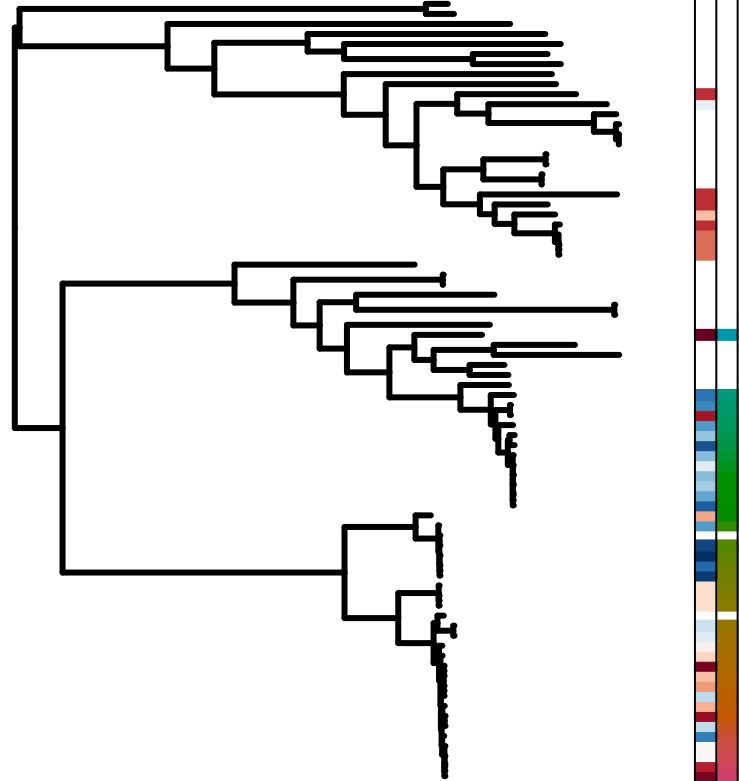
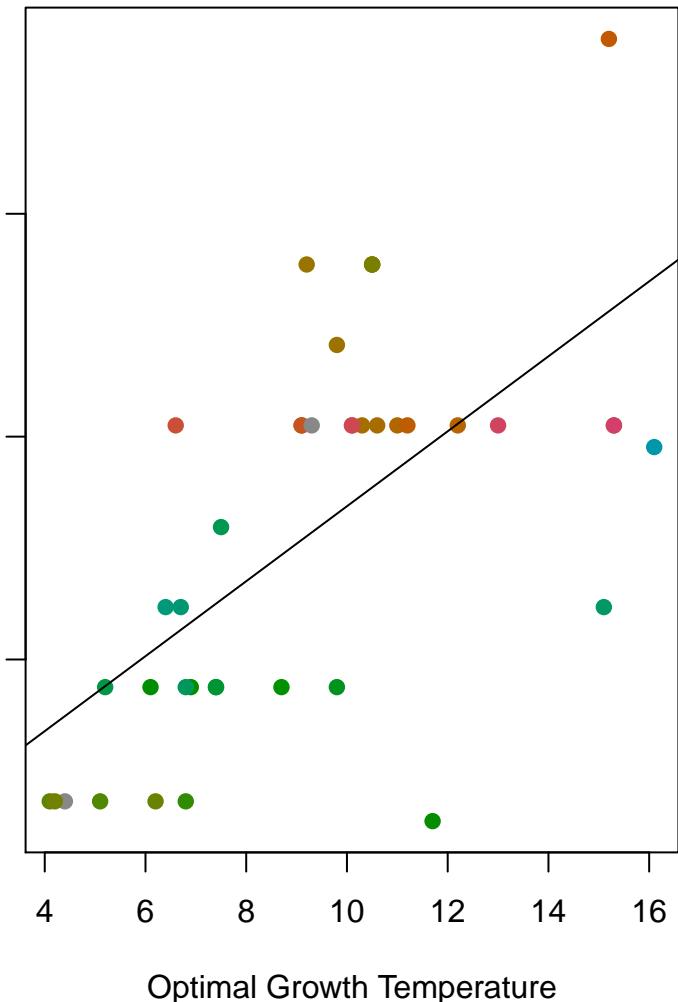
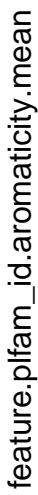


feature.plfam_id.aromaticity.mean

PLF_28228_00015451

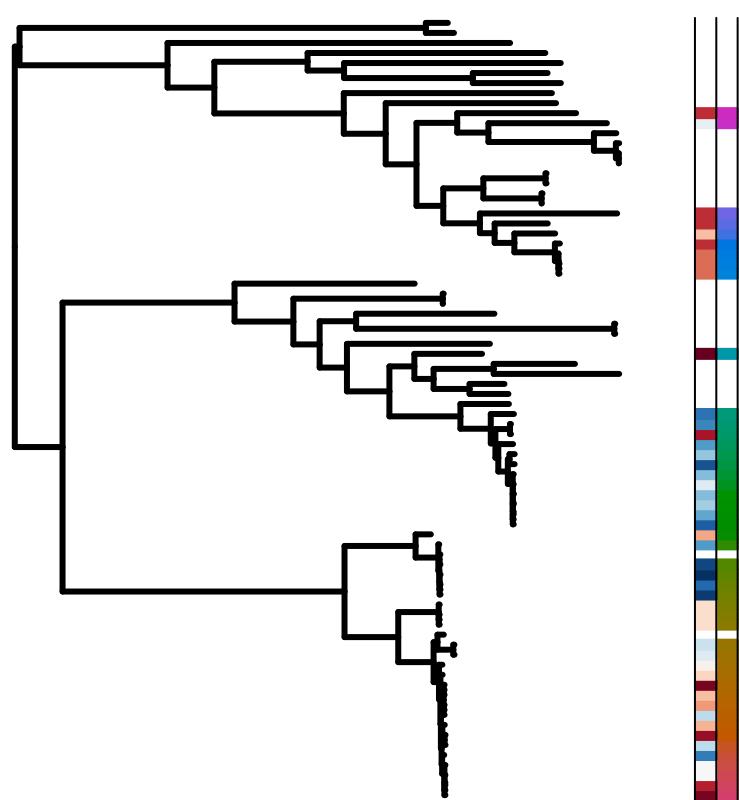
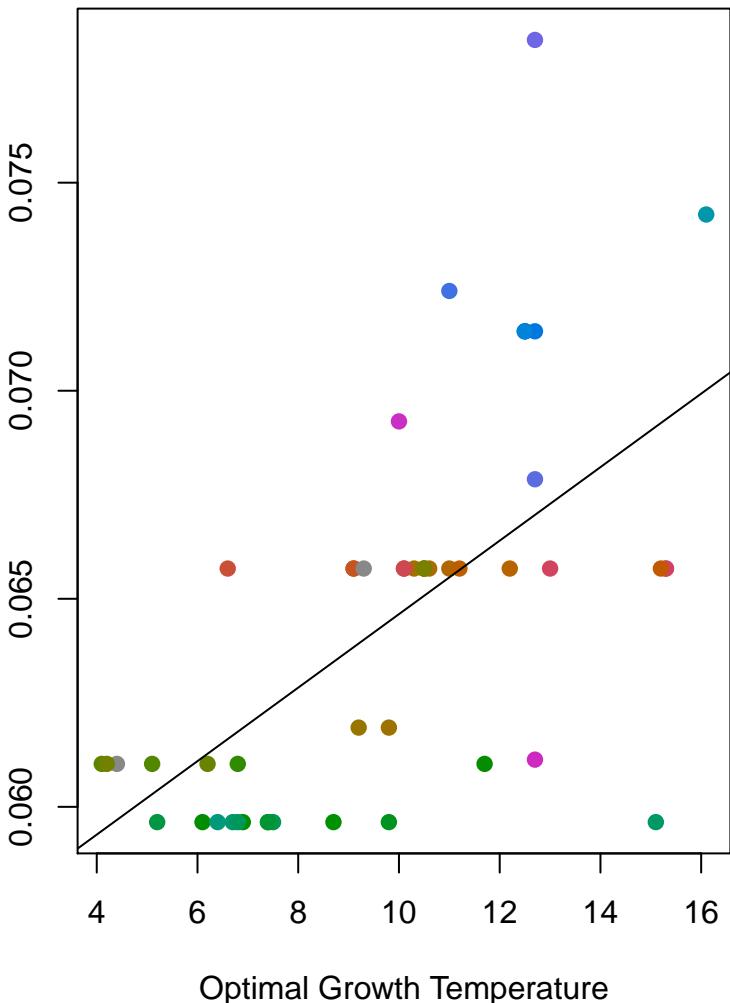
Na(+)–dependent bicarbonate transporter BicA

$r = 0.631$, $p = 10^{-4.887}$



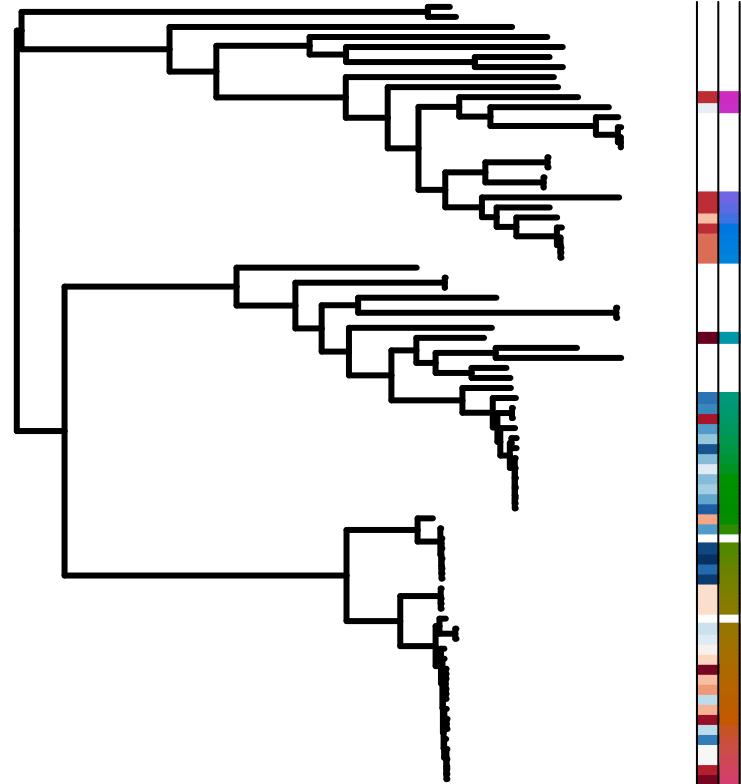
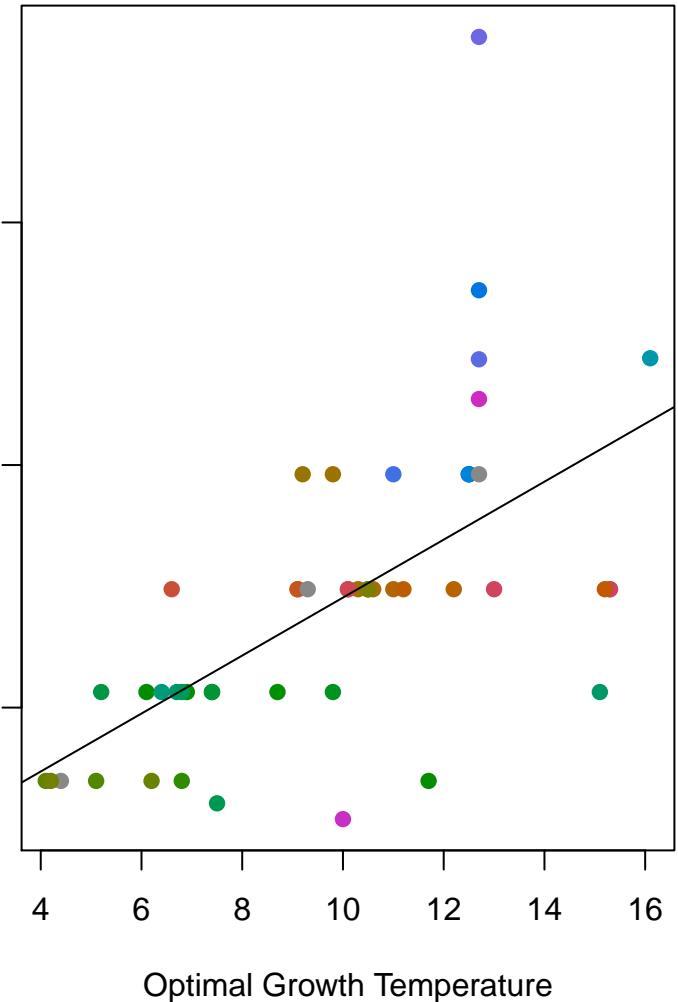
feature.plfam_id.aromaticity.mean
PLF_28228_00000869
GTP-binding protein EngB
 $r = 0.613, p = 10^{-5.543}$

feature.plfam_id.aromaticity.mean



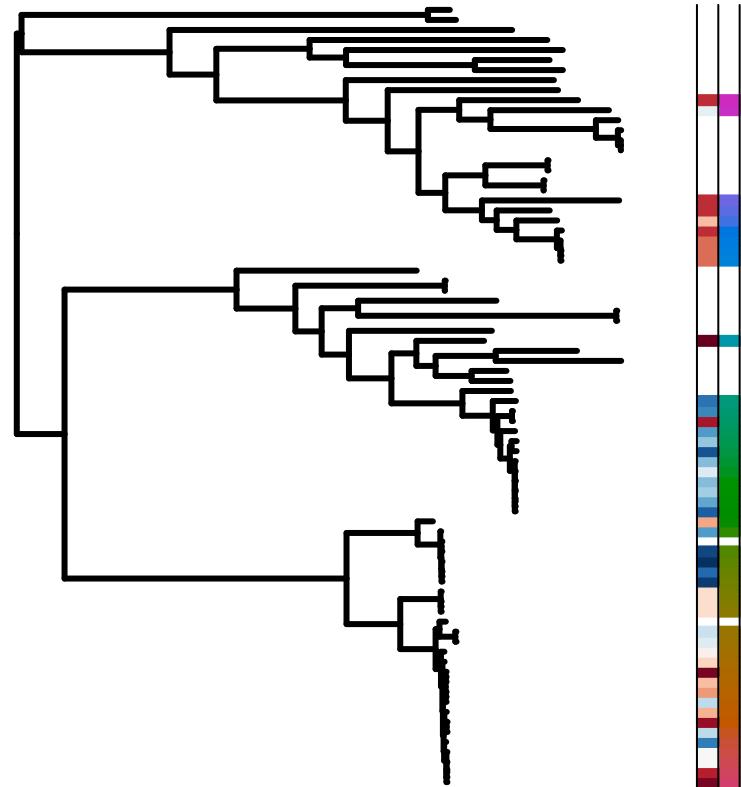
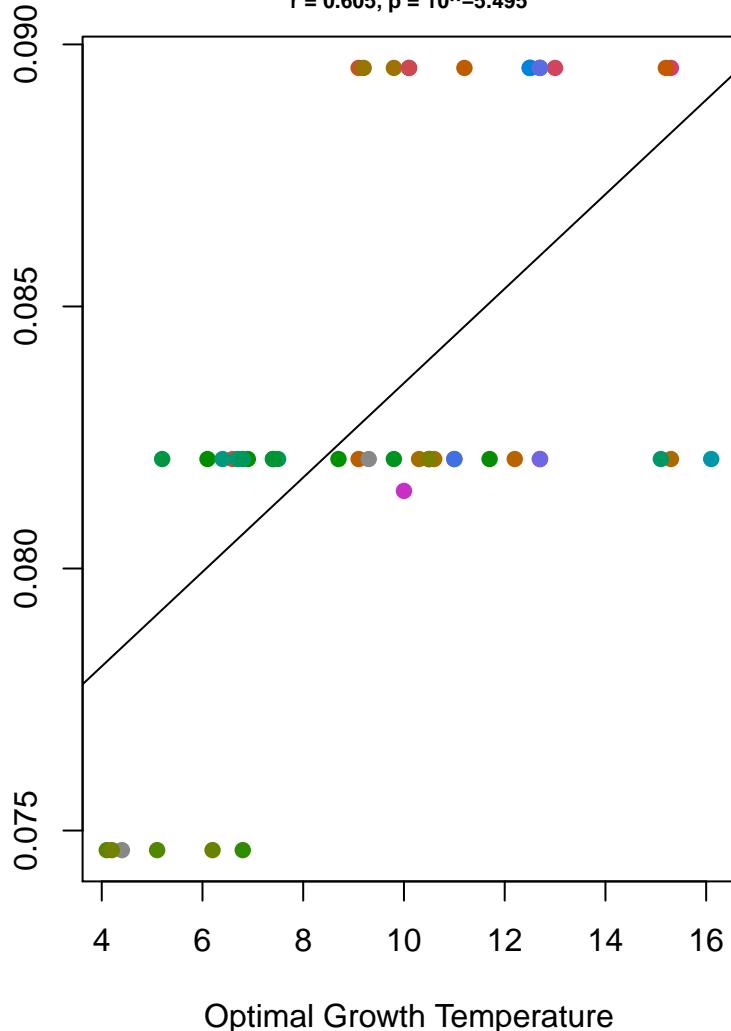
feature.plfam_id.aromaticity.mean
PLF_28228_00002535
Uncharacterized MFS-type transporter
 $r = 0.612$, $p = 10^{-5.641}$

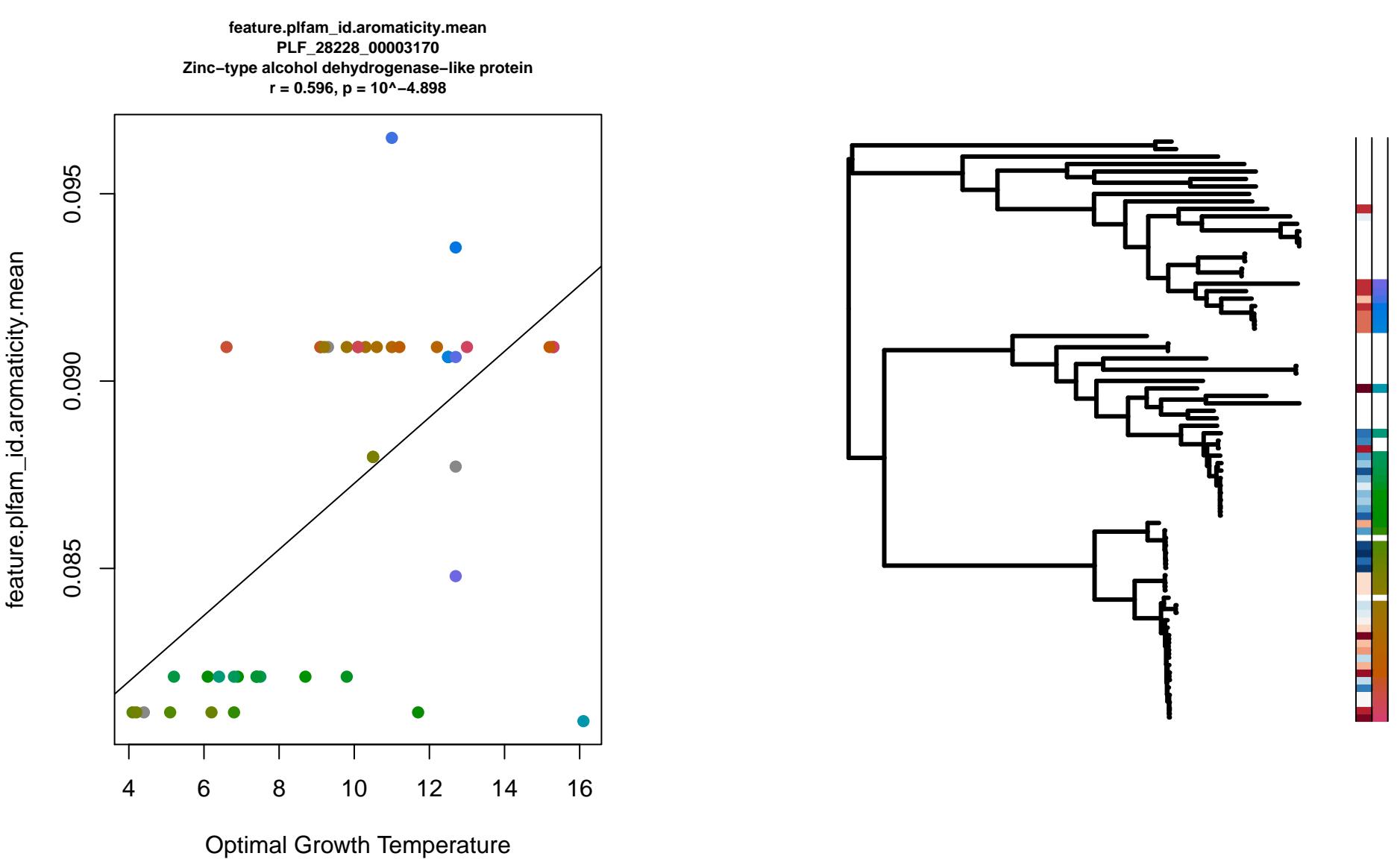
feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00000681
Protein YhfA
 $r = 0.605, p = 10^{-5.495}$

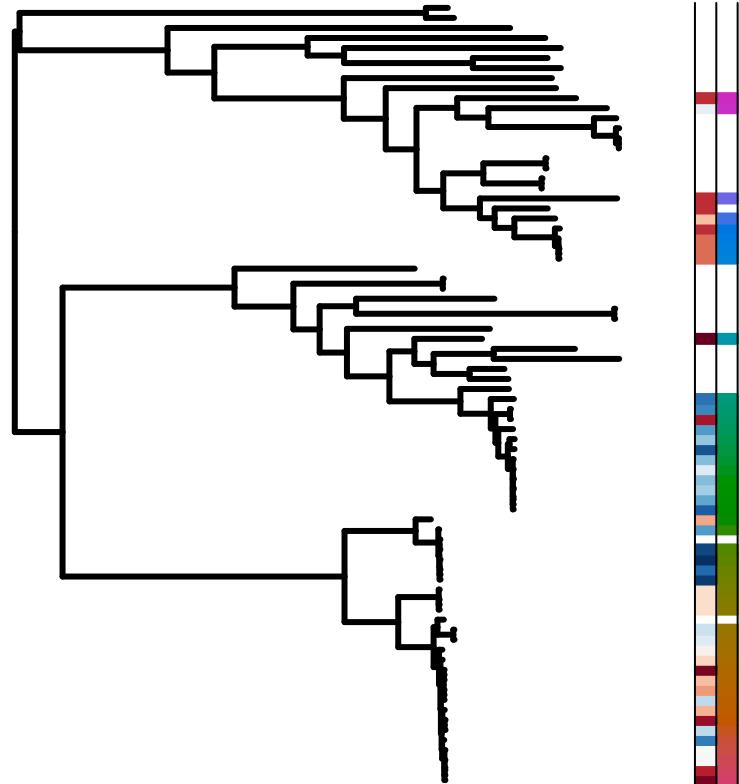
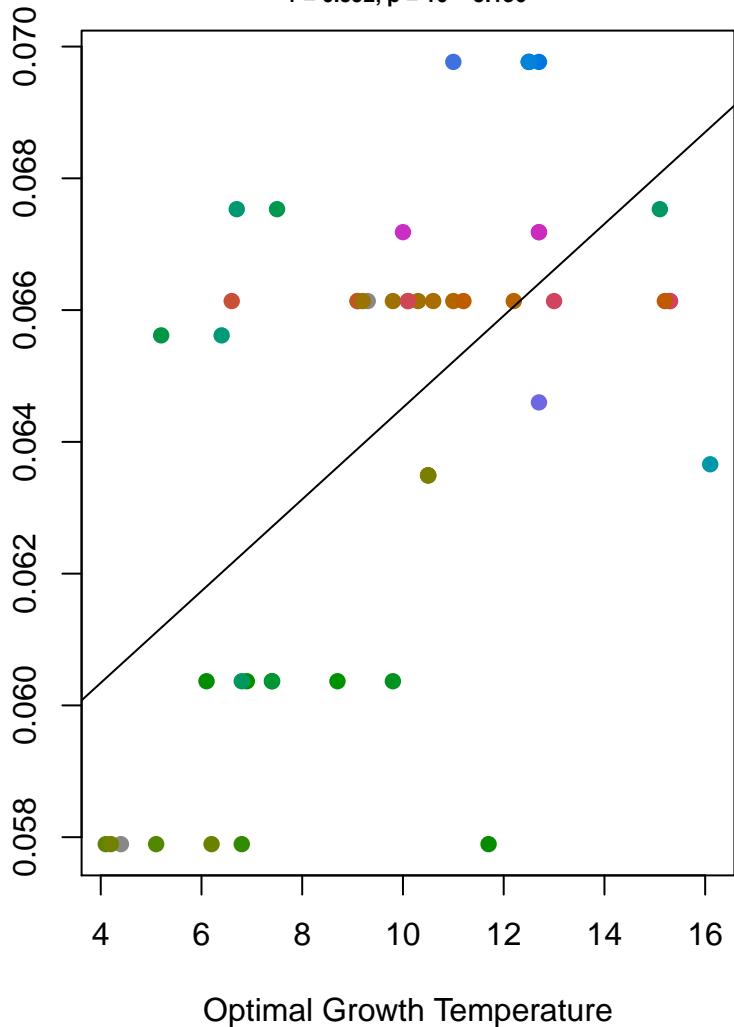
feature.plfam_id.aromaticity.mean



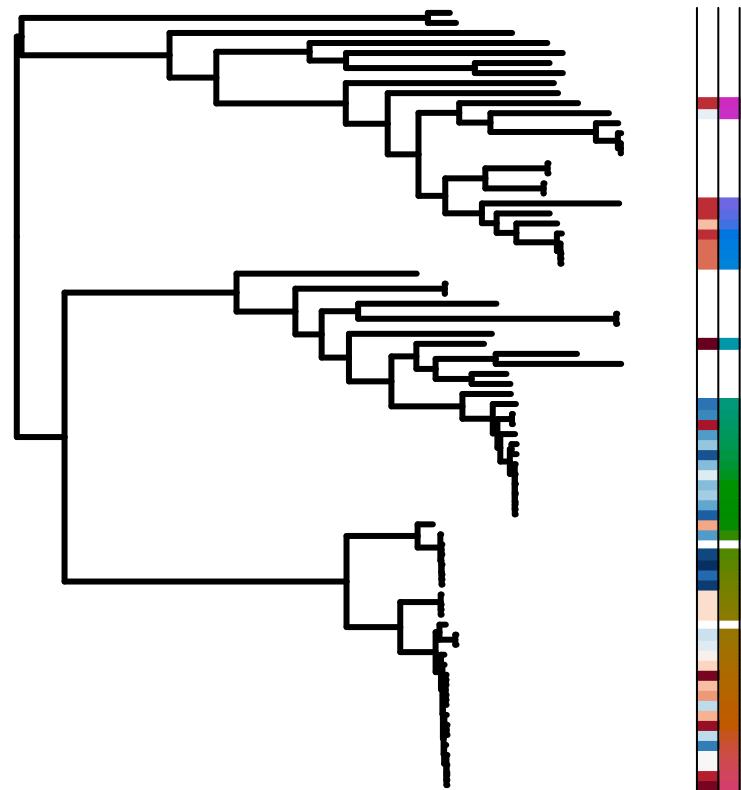
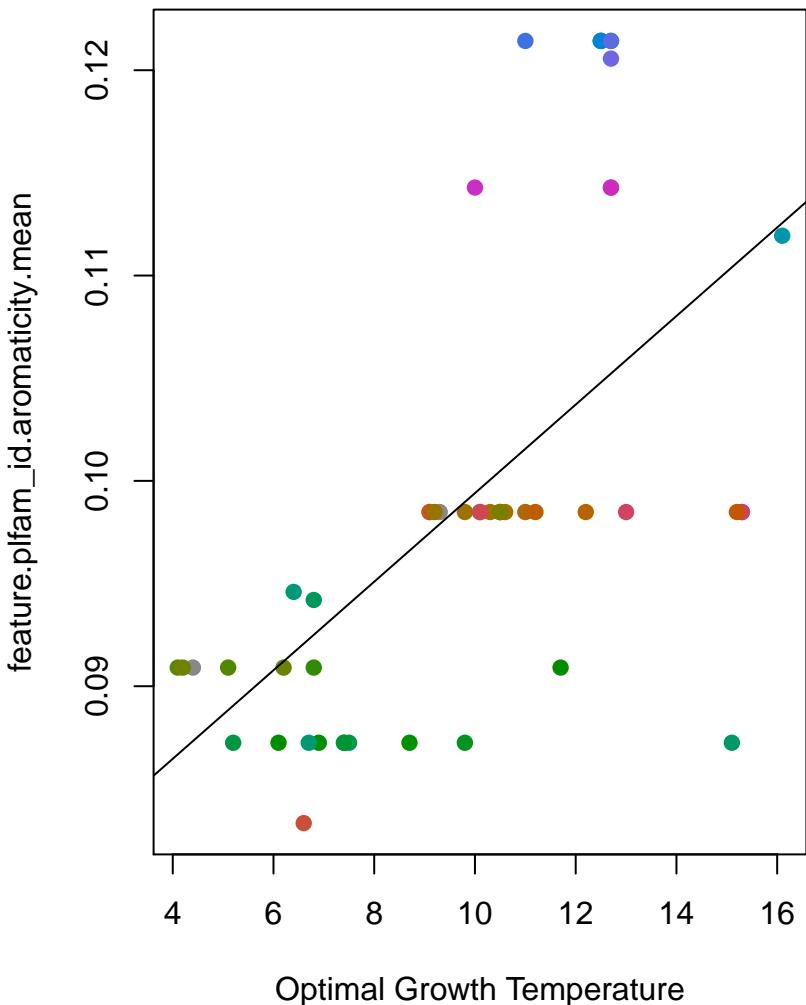


feature.plfam_id.aromaticity.mean
PLF_28228_00001290
Uncharacterized protein SO_3077
 $r = 0.592$, $p = 10^{-5.136}$

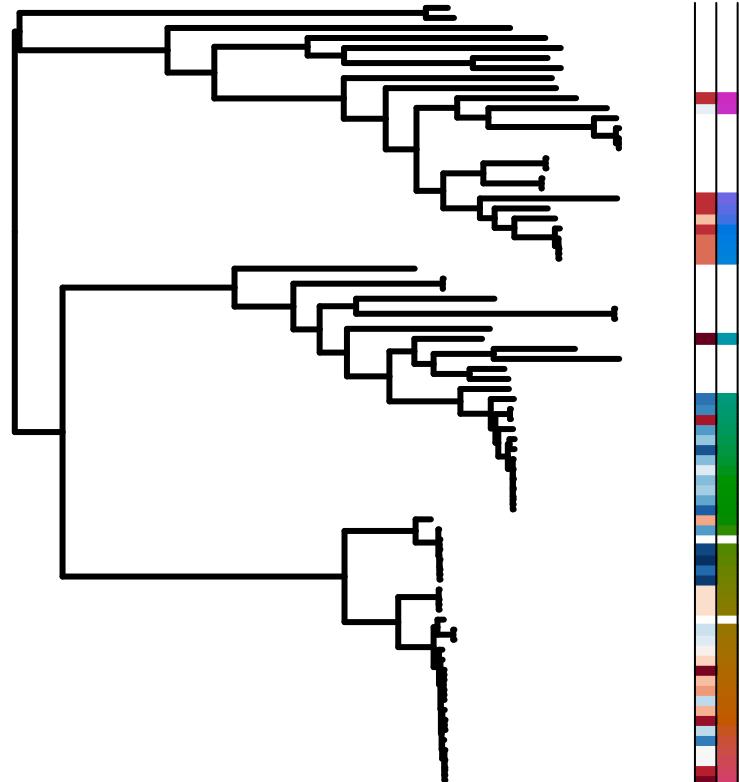
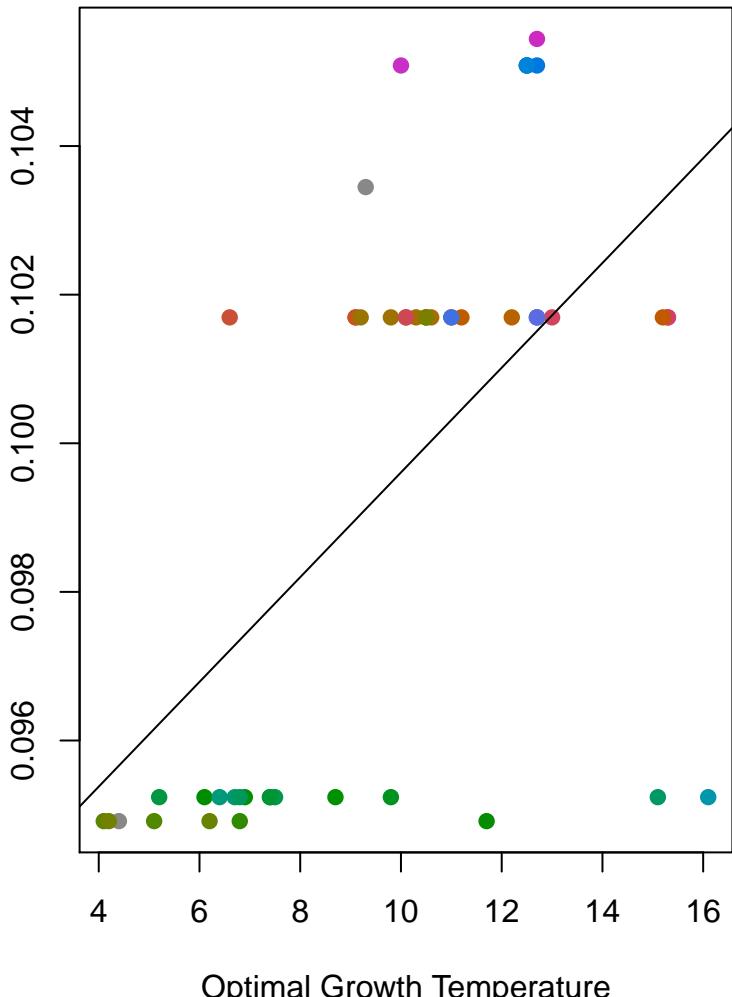
feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00001543
DNA-binding protein, CopG family
 $r = 0.592$, $p = 10^{-5.224}$



feature.plfam_id.aromaticity.mean
PLF_28228_0000094
HfIC protein
 $r = 0.588, p = 10^{-5.153}$

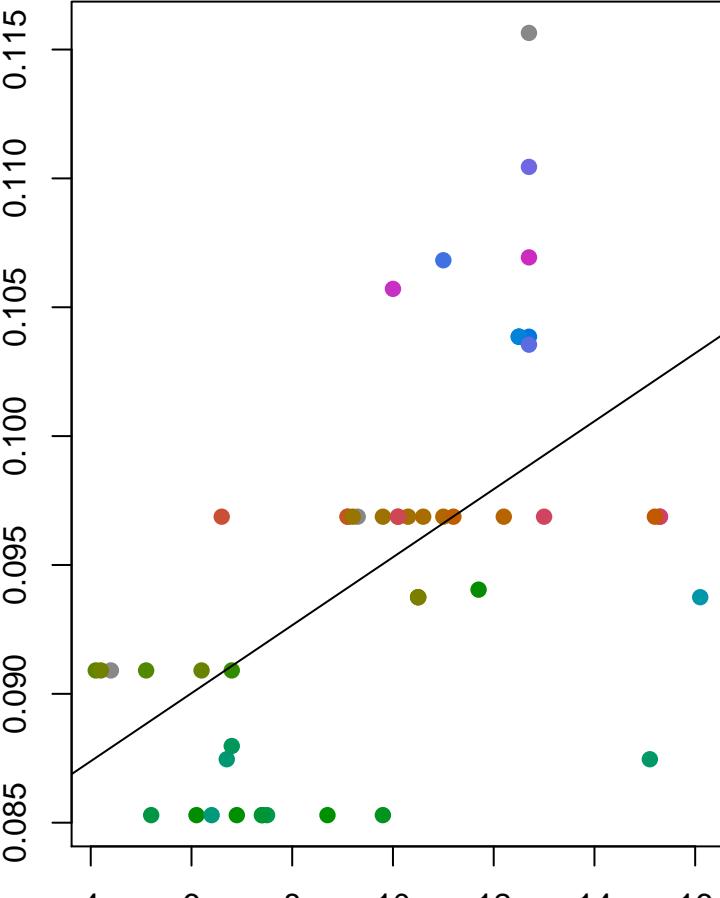


feature.plfam_id.aromaticity.mean

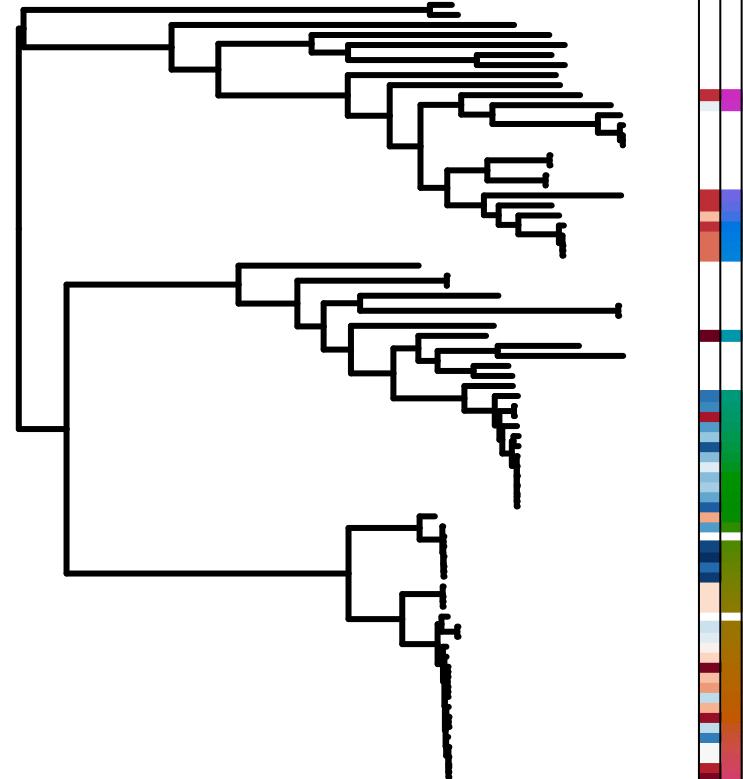
PLF_28228_00002060

Sigma factor RpoE negative regulatory protein RseB precursor
 $r = 0.569, p = 10^{-4.789}$

feature.plfam_id.aromaticity.mean

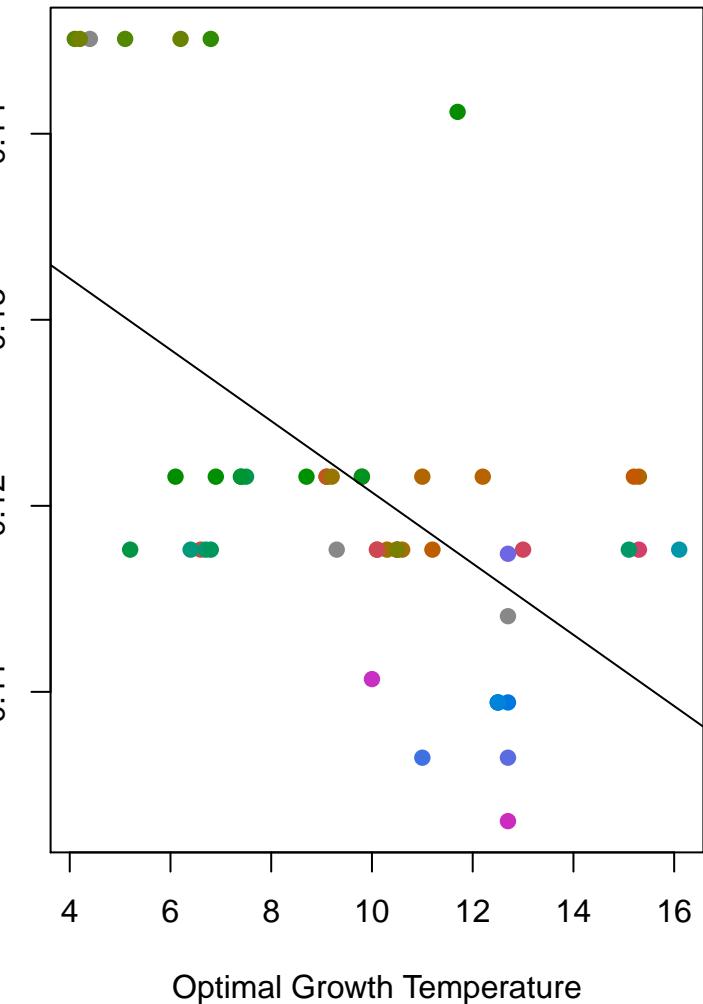


Optimal Growth Temperature

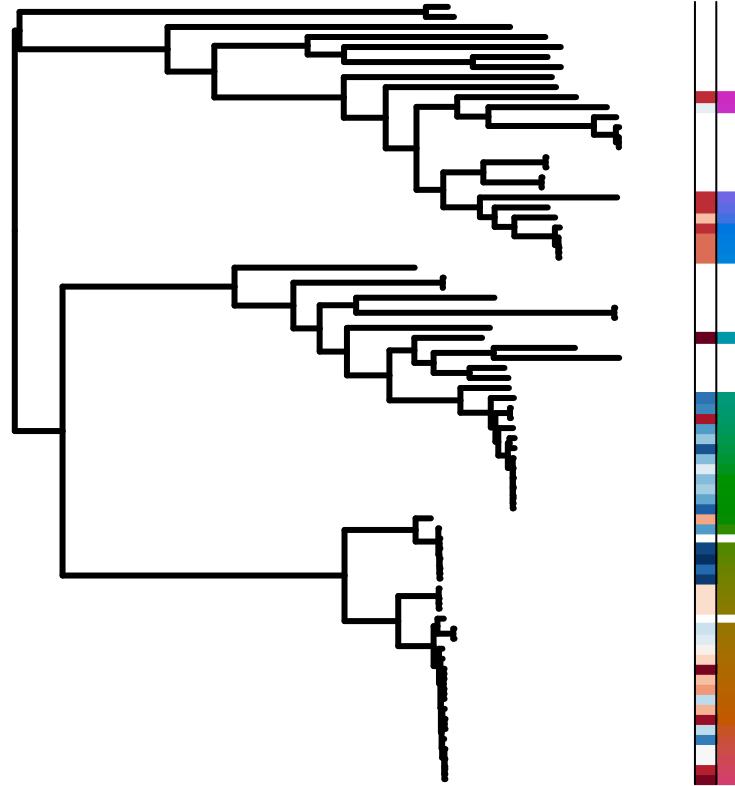


feature.plfam_id.aromaticity.mean
PLF_28228_00000786
Esterase ybfF (EC 3.1.-.-)
 $r = -0.568$, $p = 10^{-4.779}$

feature.plfam_id.aromaticity.mean



Optimal Growth Temperature

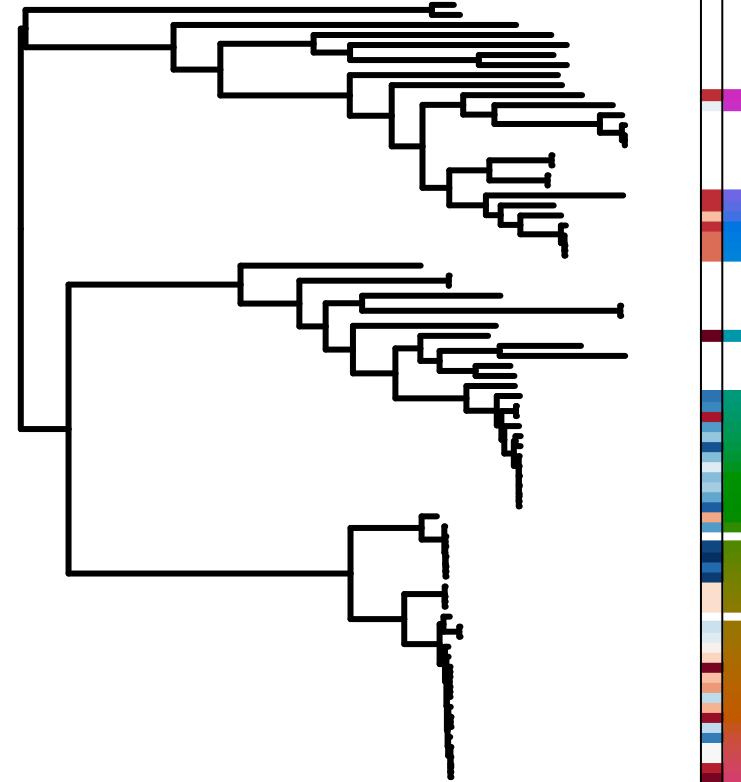
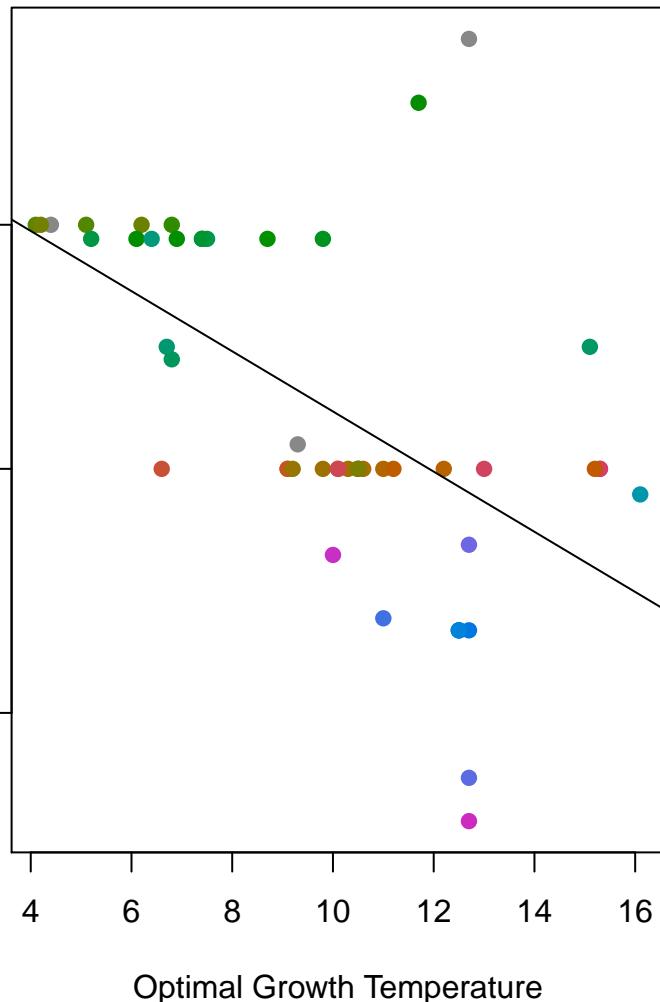
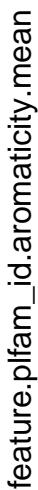


feature.plfam_id.aromaticity.mean

PLF_28228_00000804

Lipid-A-disaccharide synthase (EC 2.4.1.182)

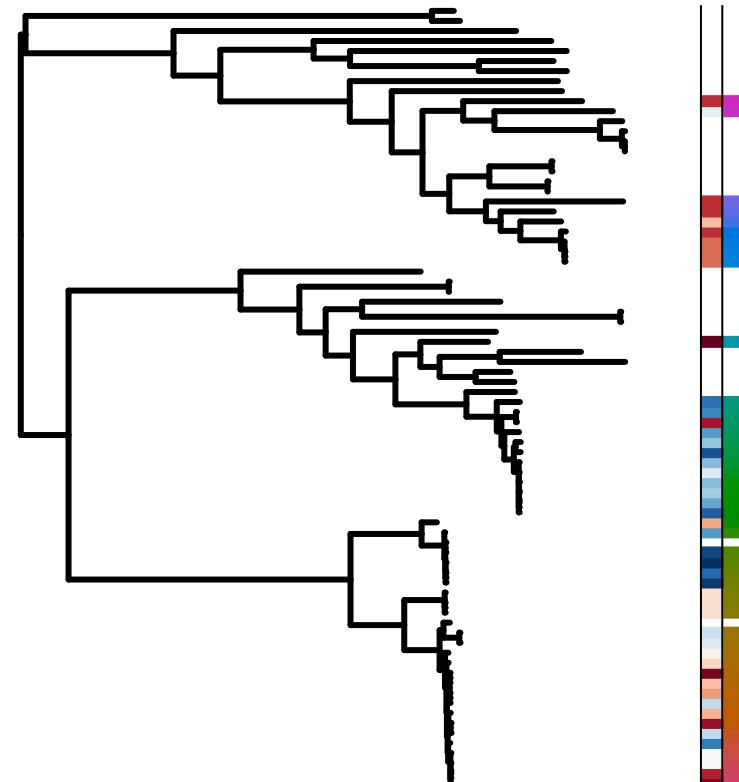
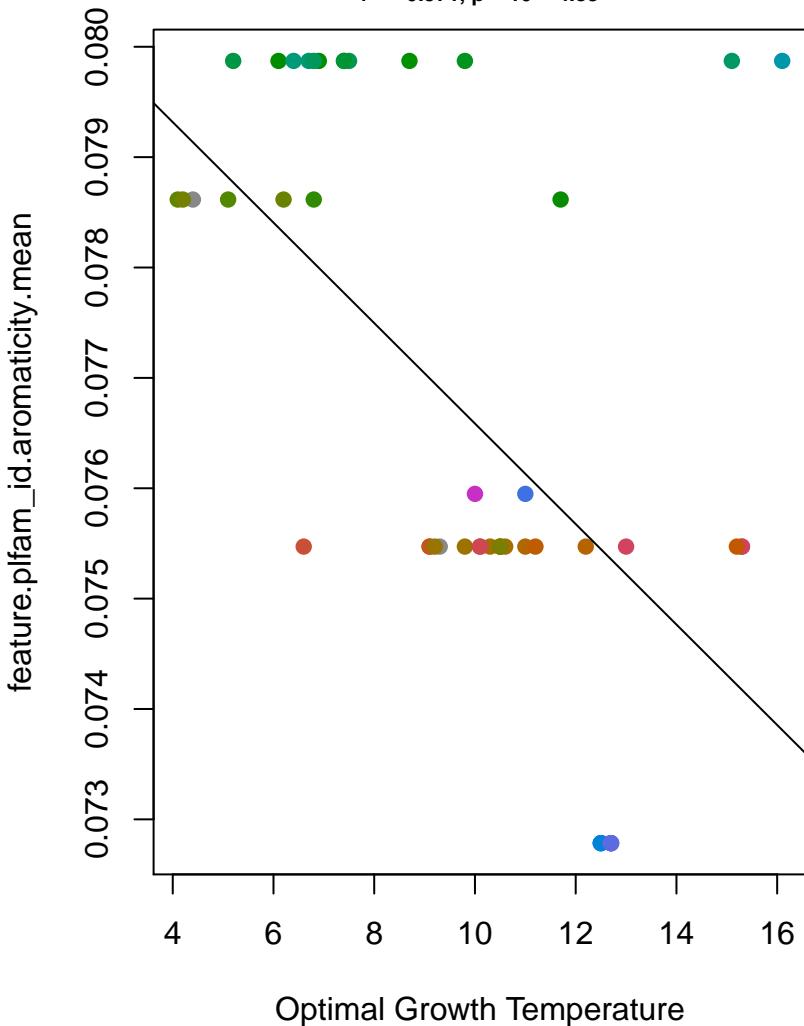
$r = -0.569$, $p = 10^{-4.784}$



feature.plfam_id.aromaticity.mean

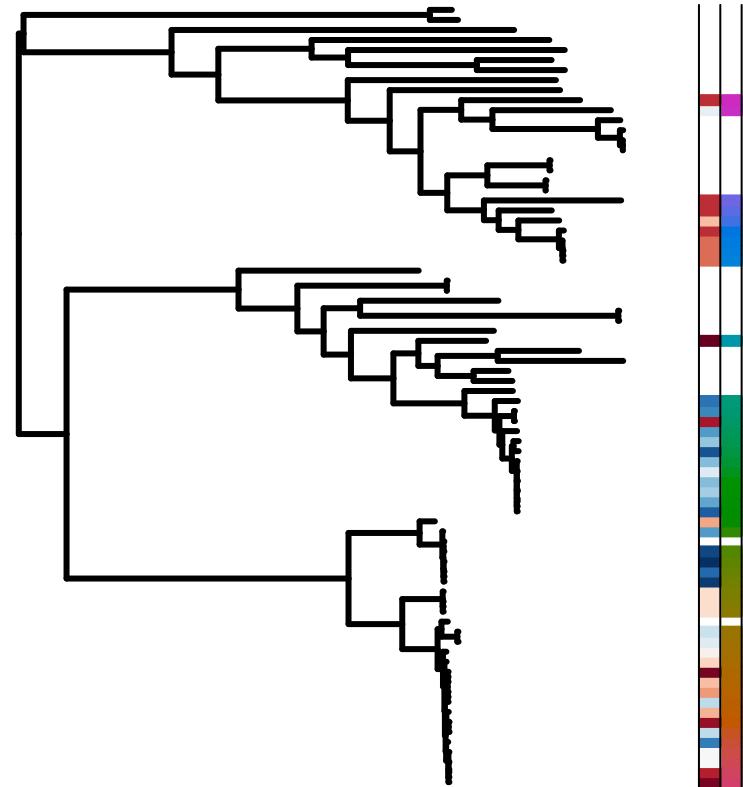
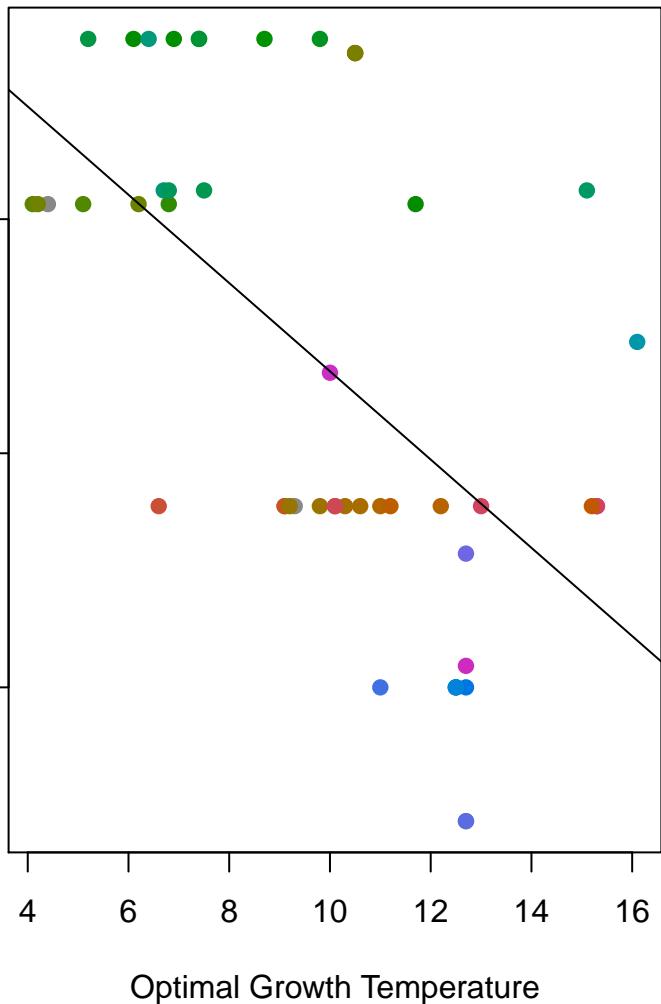
PLF_28228_00000217

16S rRNA (cytosine(1402)-N(4))-methyltransferase (EC 2.1.1.199)
 $r = -0.571$, $p = 10^{-4.83}$

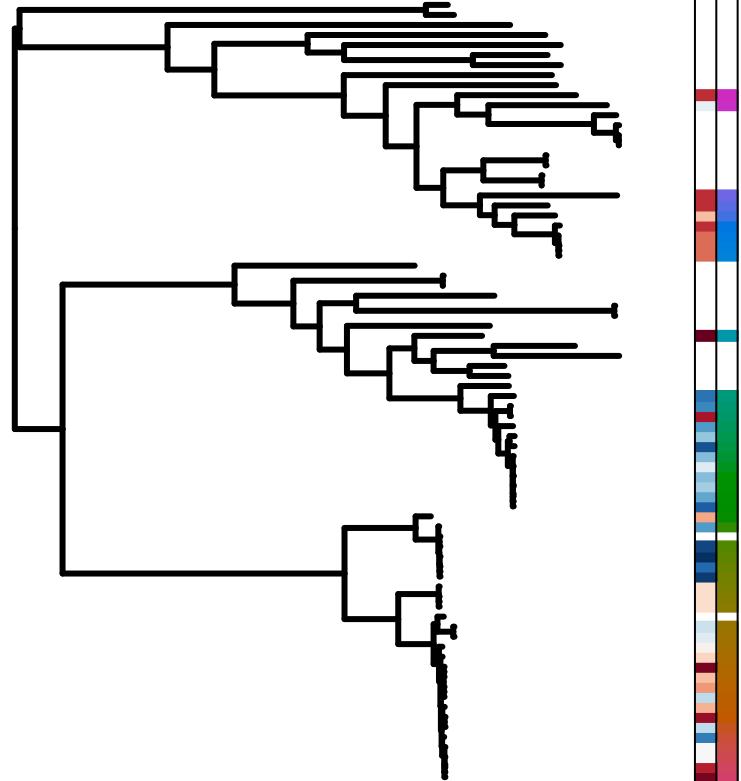
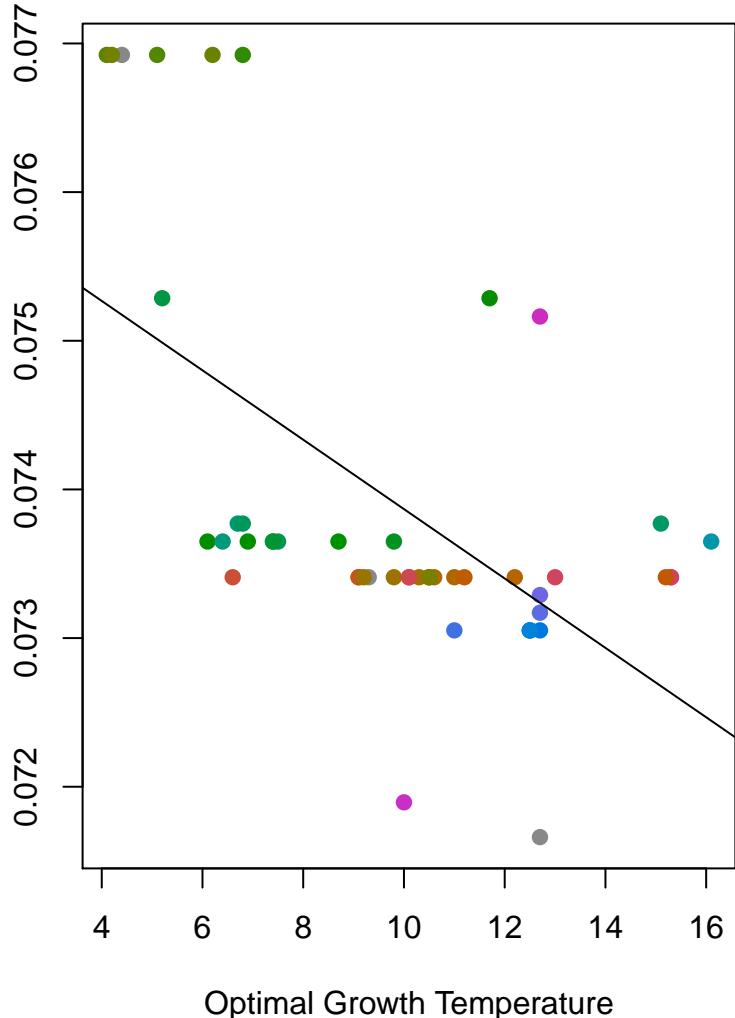
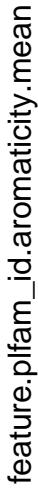


feature.plfam_id.aromaticity.mean
PLF_28228_00000569
FIG022979: MoxR-like ATPases
 $r = -0.578$, $p = 10^{-4.959}$

feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00001039
RNA polymerase sigma factor RpoD
 $r = -0.579$, $p = 10^{-4.984}$

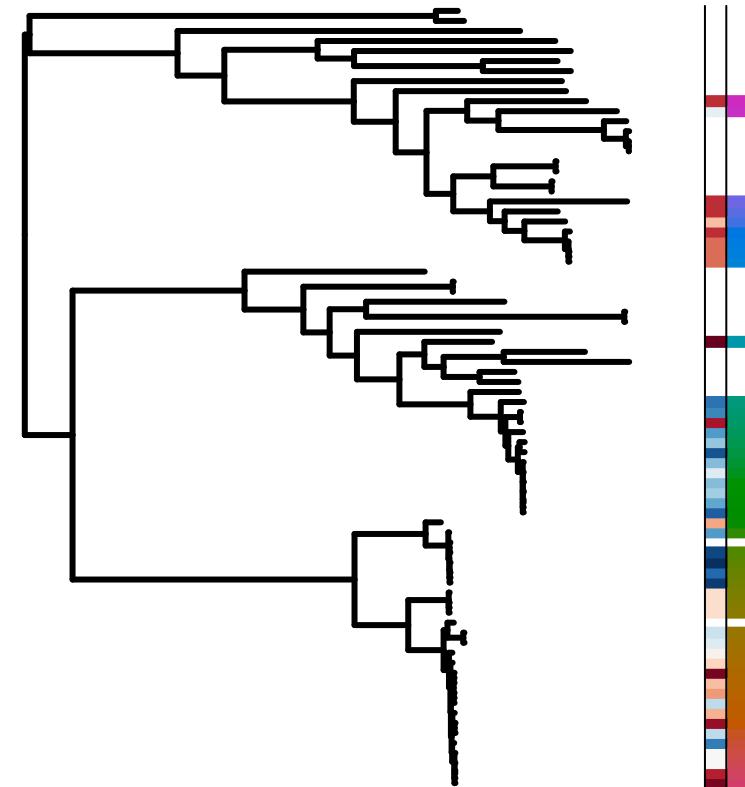
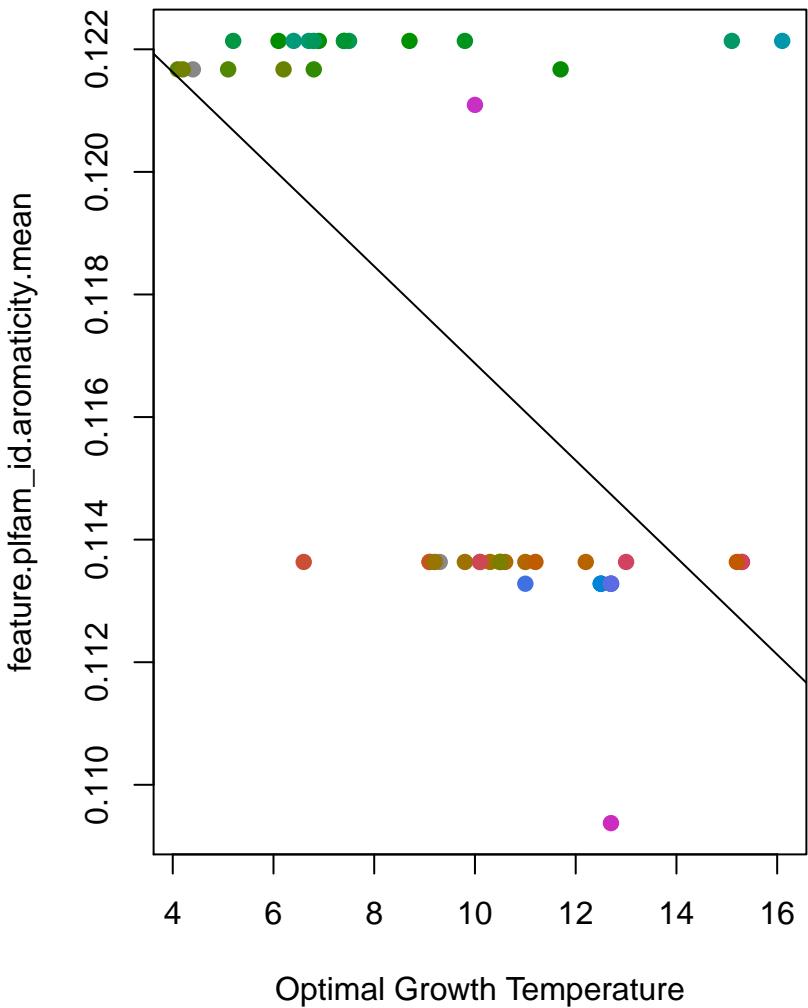


feature.plfam_id.aromaticity.mean

PLF_28228_00000185

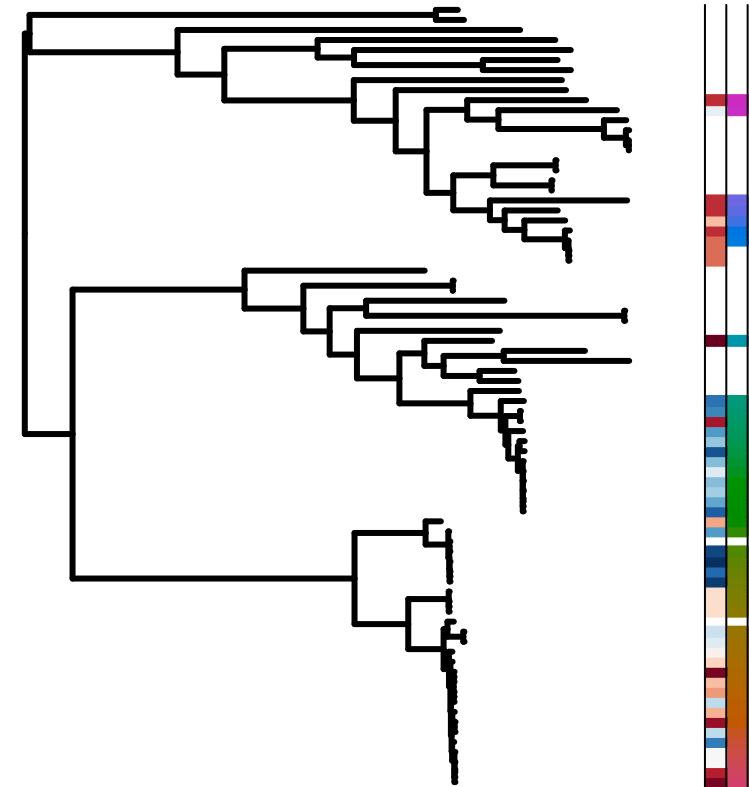
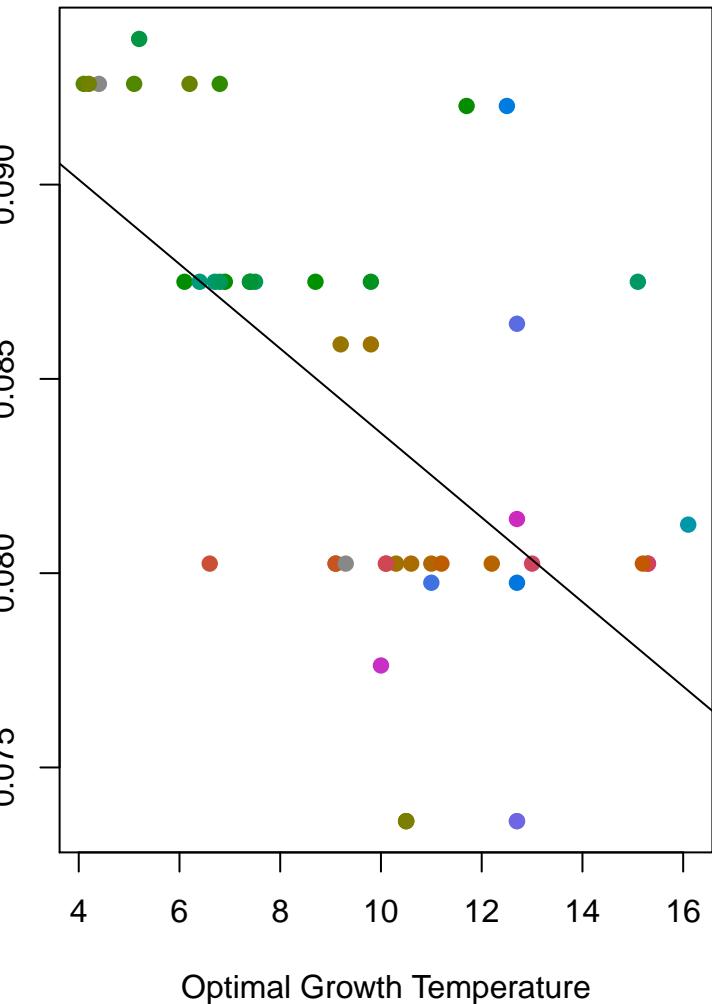
Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129)

$r = -0.581$, $p = 10^{-5.011}$



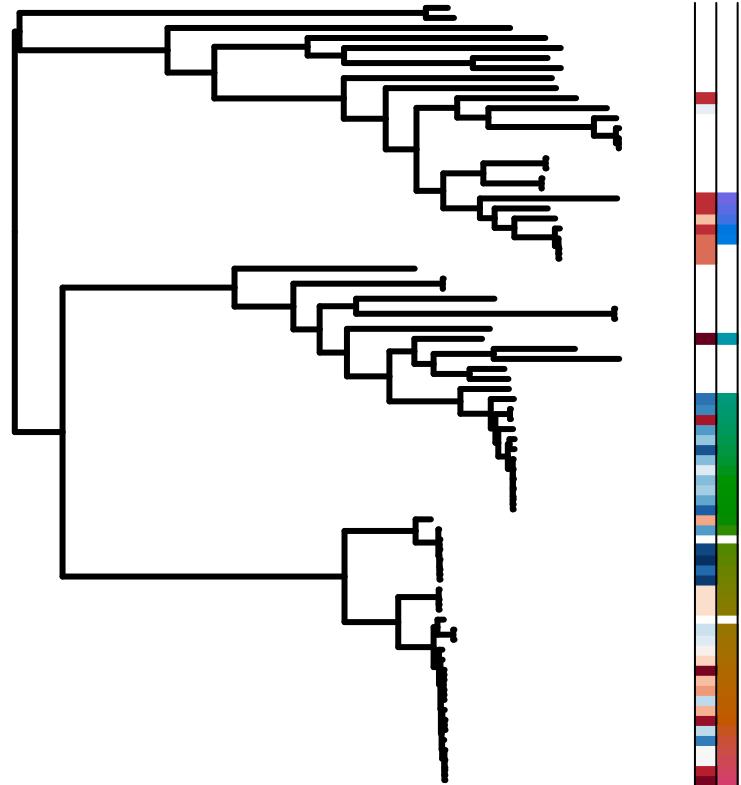
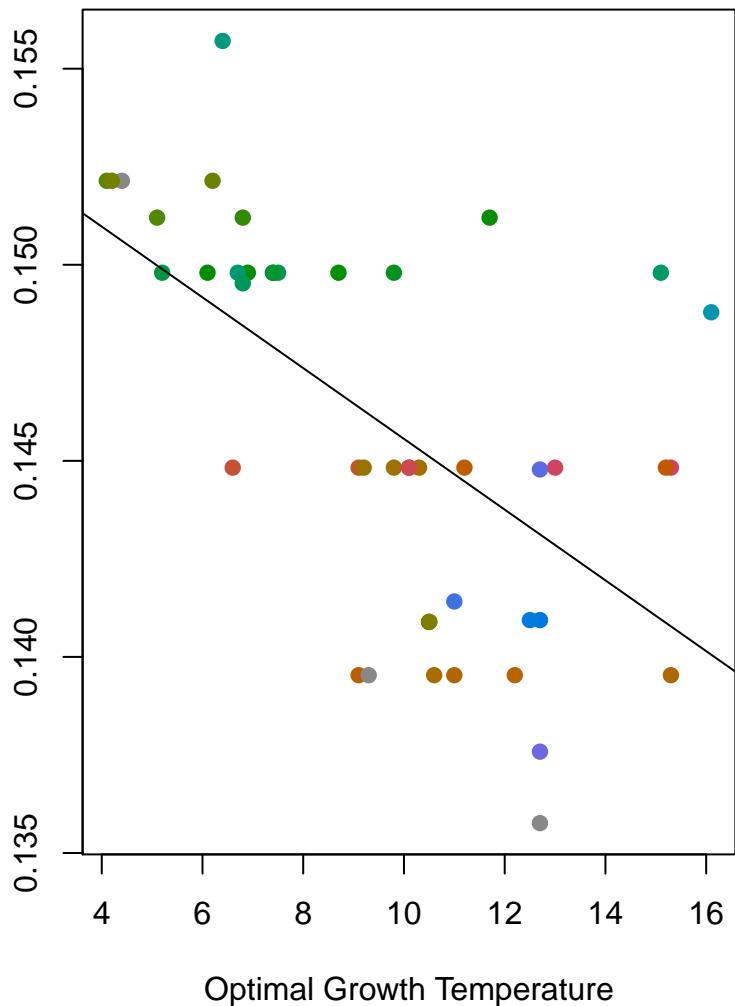
feature.plfam_id.aromaticity.mean
PLF_28228_00028100
Ribonuclease E inhibitor RraA
 $r = -0.582$, $p = 10^{-4.84}$

feature.plfam_id.aromaticity.mean



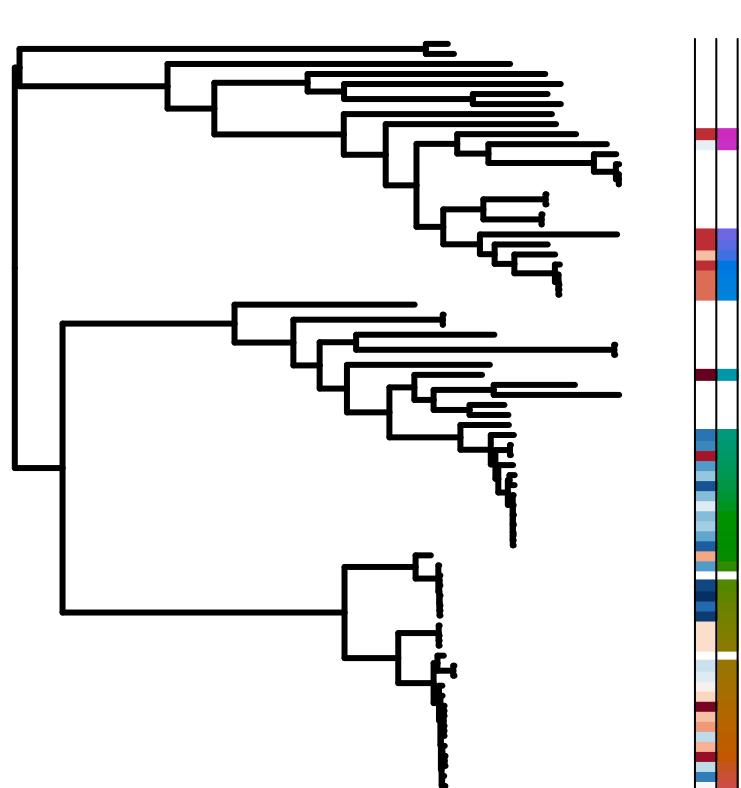
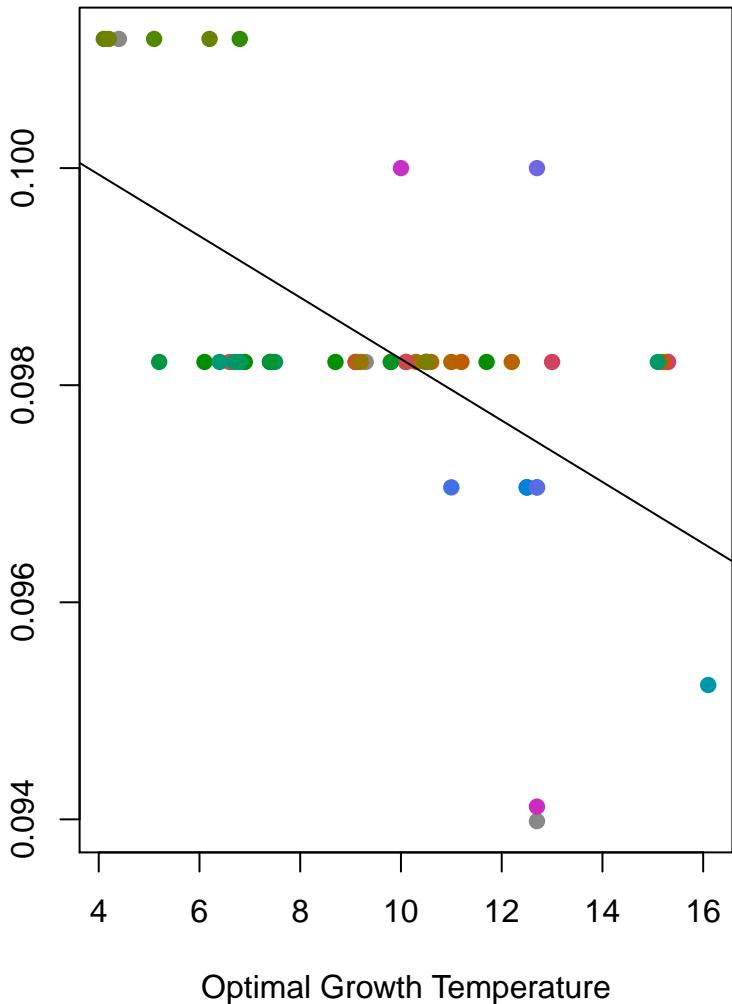
feature.plfam_id.aromaticity.mean
PLF_28228_00028215
Glutathione S-transferase (EC 2.5.1.18)
 $r = -0.591$, $p = 10^{-4.819}$

feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00001275
UDP-glucose 4-epimerase (EC 5.1.3.2)
 $r = -0.595$, $p = 10^{-5.276}$

feature.plfam_id.aromaticity.mean

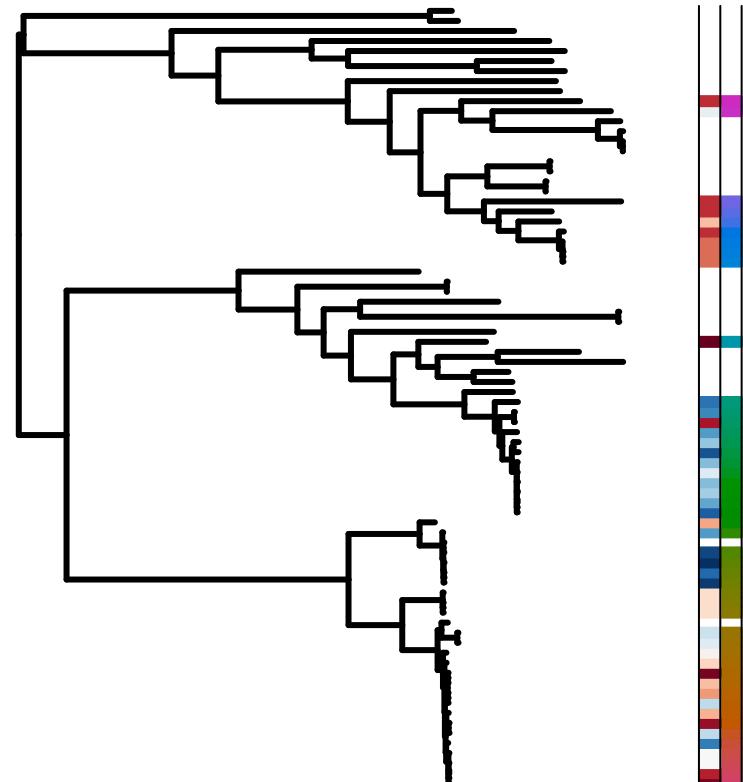
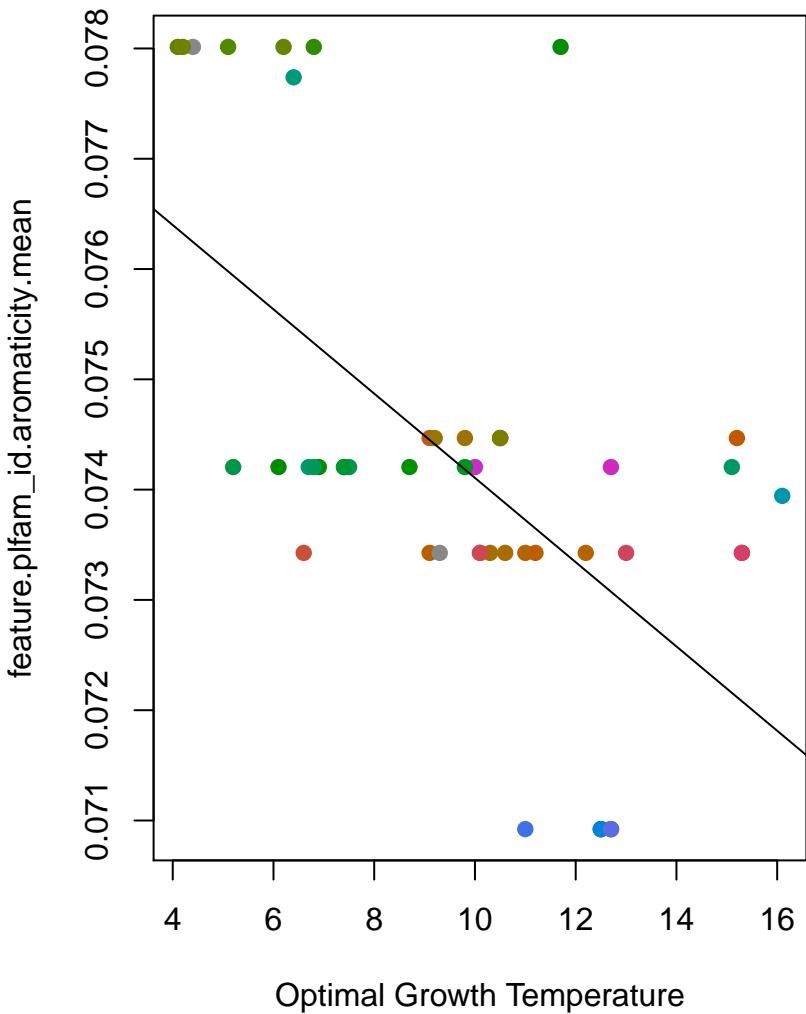


feature.plfam_id.aromaticity.mean

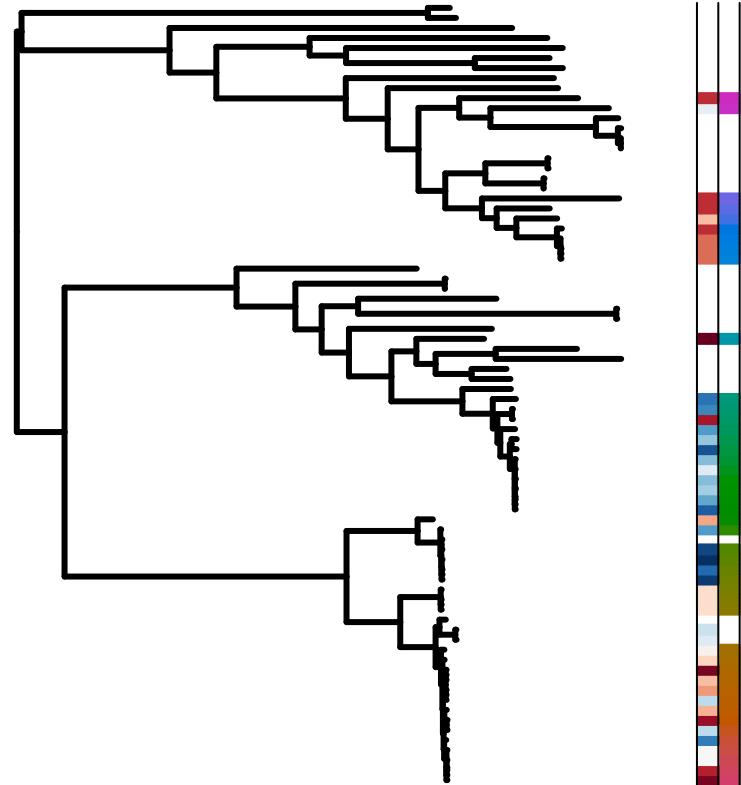
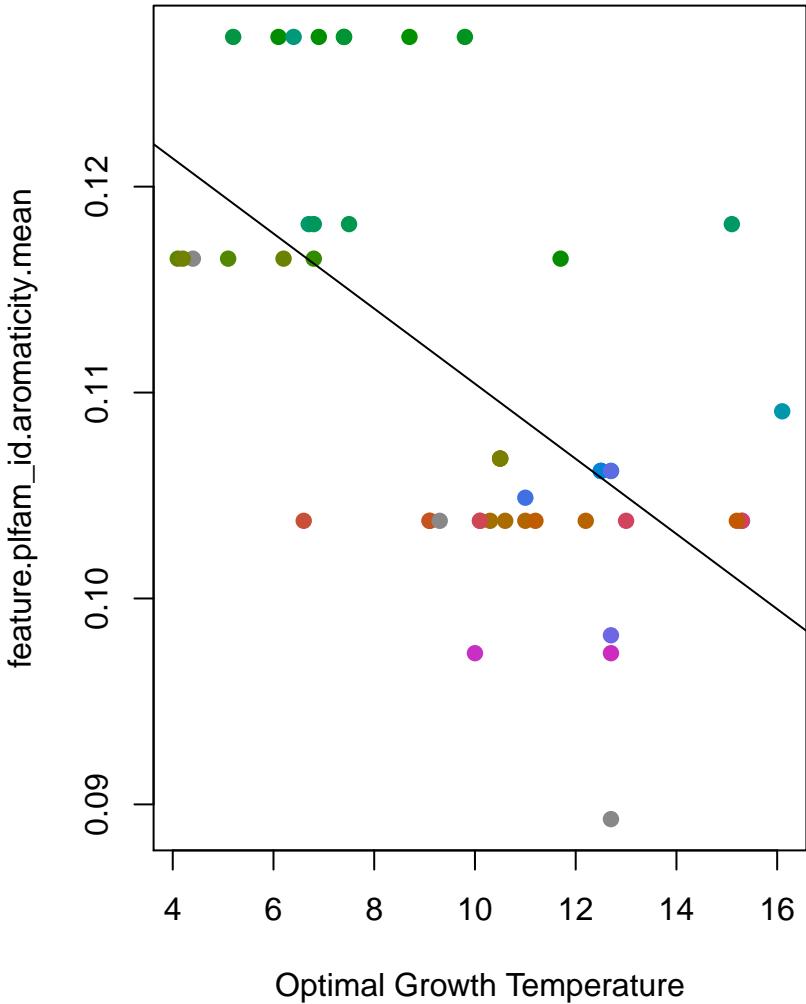
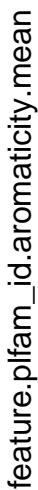
PLF_28228_00000702

16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)

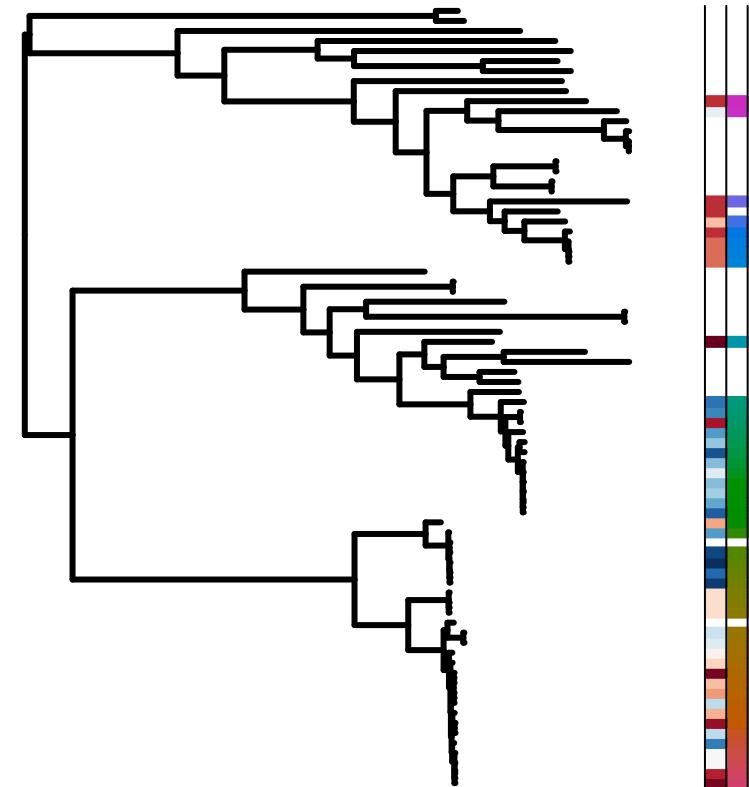
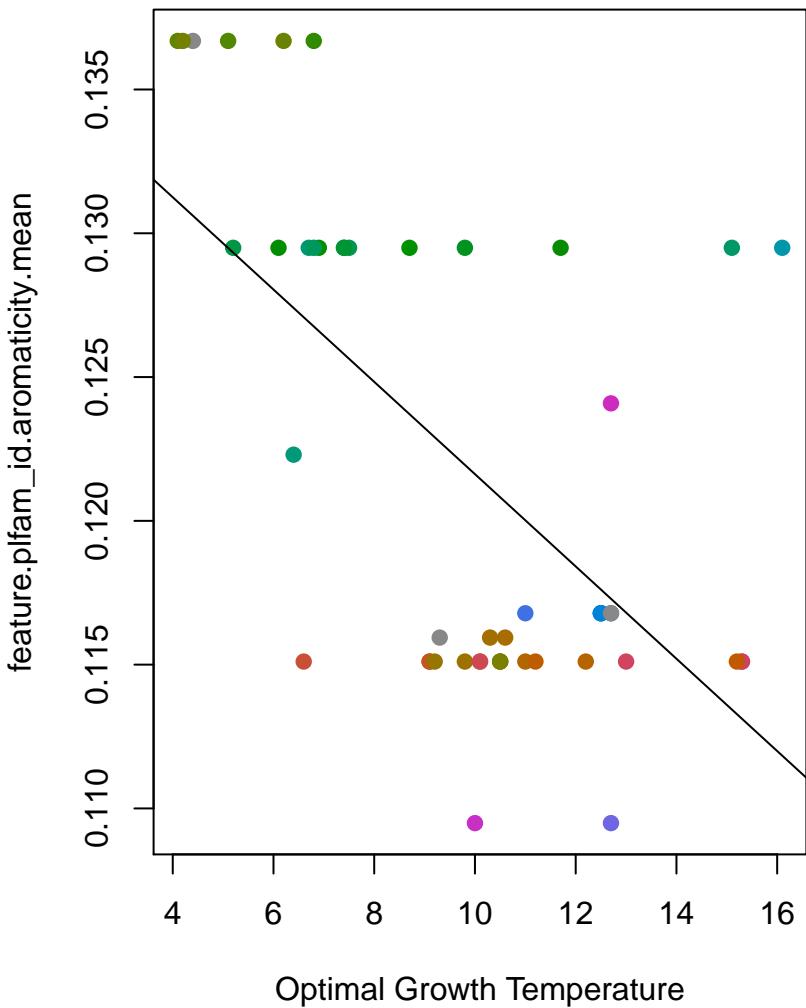
$r = -0.595$, $p = 10^{-5.191}$



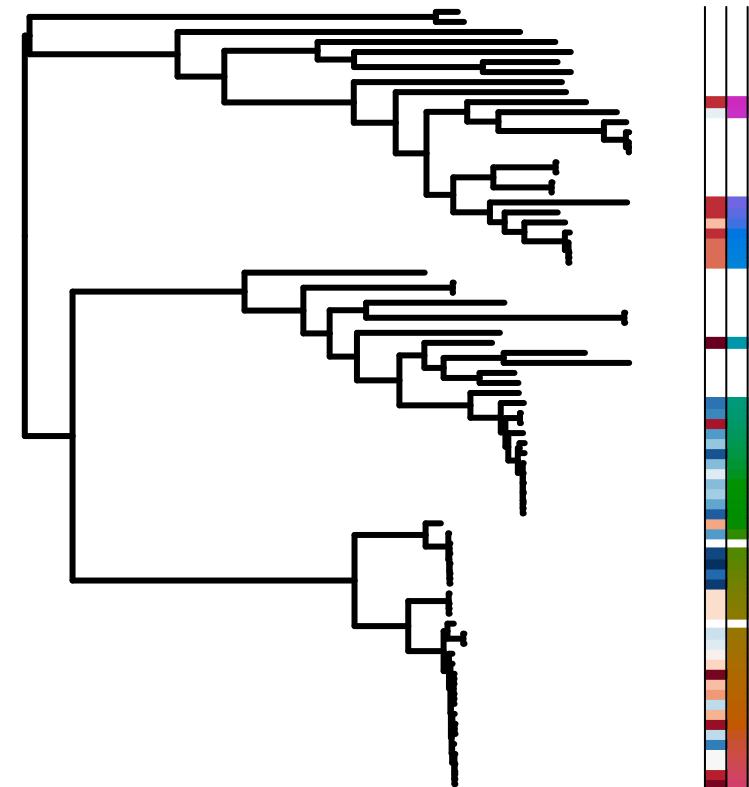
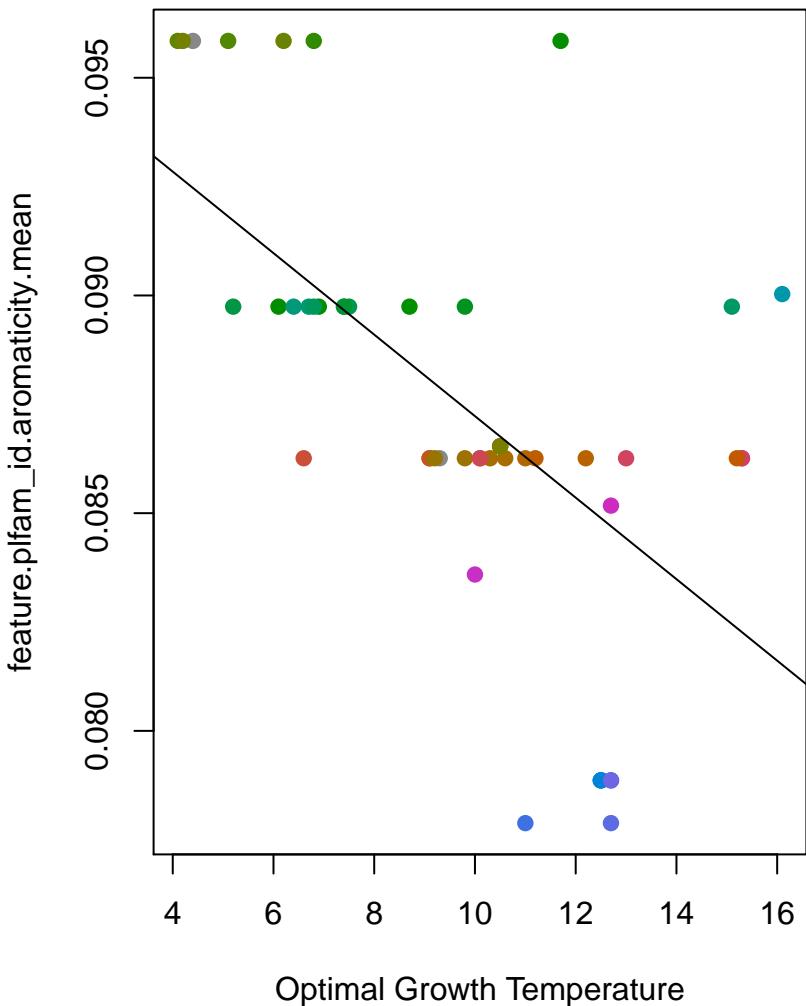
feature.plfam_id.aromaticity.mean
PLF_28228_00002444
hypothetical protein
 $r = -0.599, p = 10^{-5.154}$



feature.plfam_id.aromaticity.mean
PLF_28228_00001562
Acetyltransferase, GNAT family
 $r = -0.601$, $p = 10^{-5.307}$



feature.plfam_id.aromaticity.mean
PLF_28228_00000770
D-alanine--D-alanine ligase (EC 6.3.2.4)
 $r = -0.602$, $p = 10^{-5.322}$



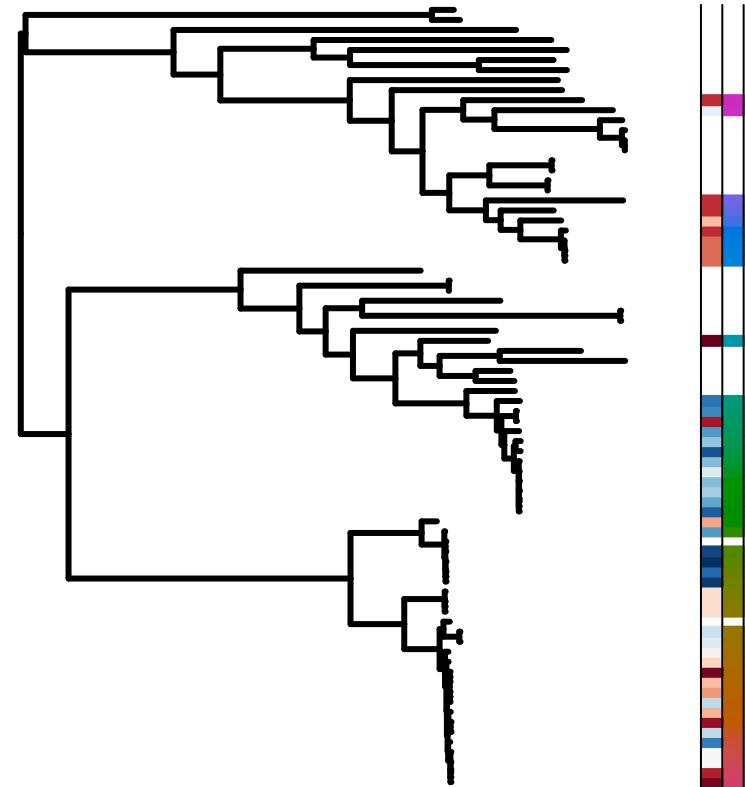
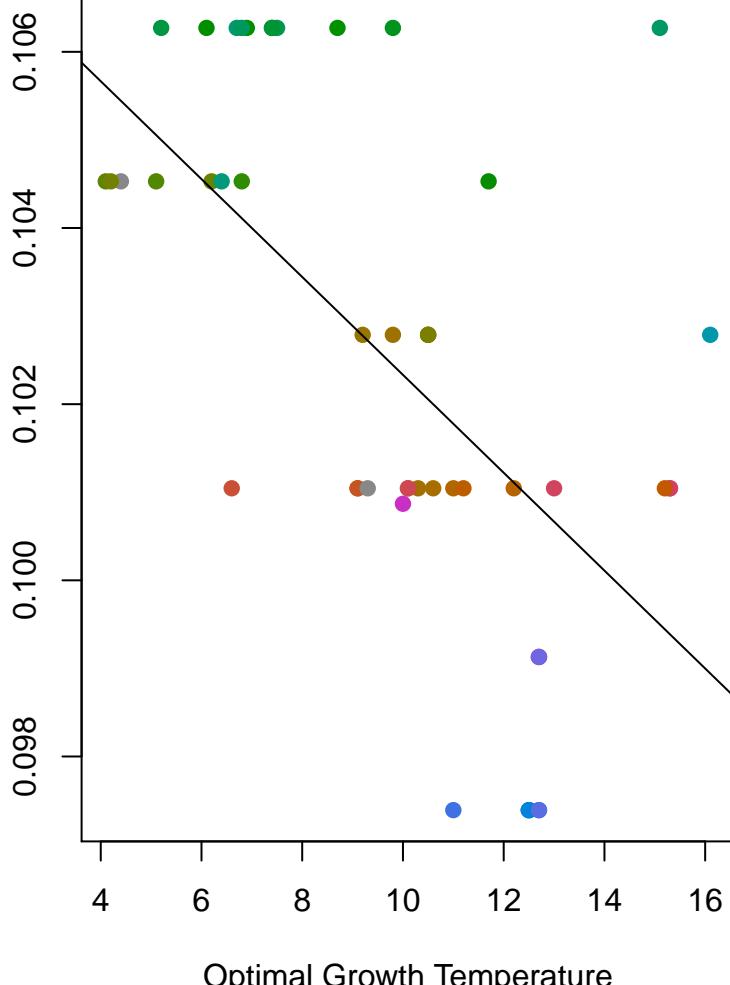
feature.plfam_id.aromaticity.mean

PLF_28228_00000731

Acetolactate synthase large subunit (EC 2.2.1.6)

$r = -0.603, p = 10^{-5.448}$

feature.plfam_id.aromaticity.mean

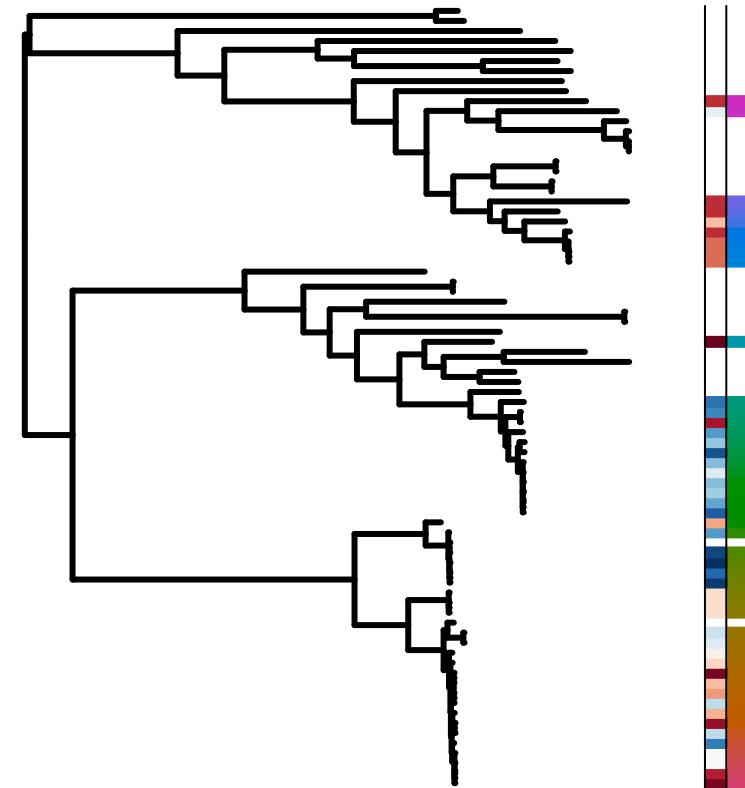
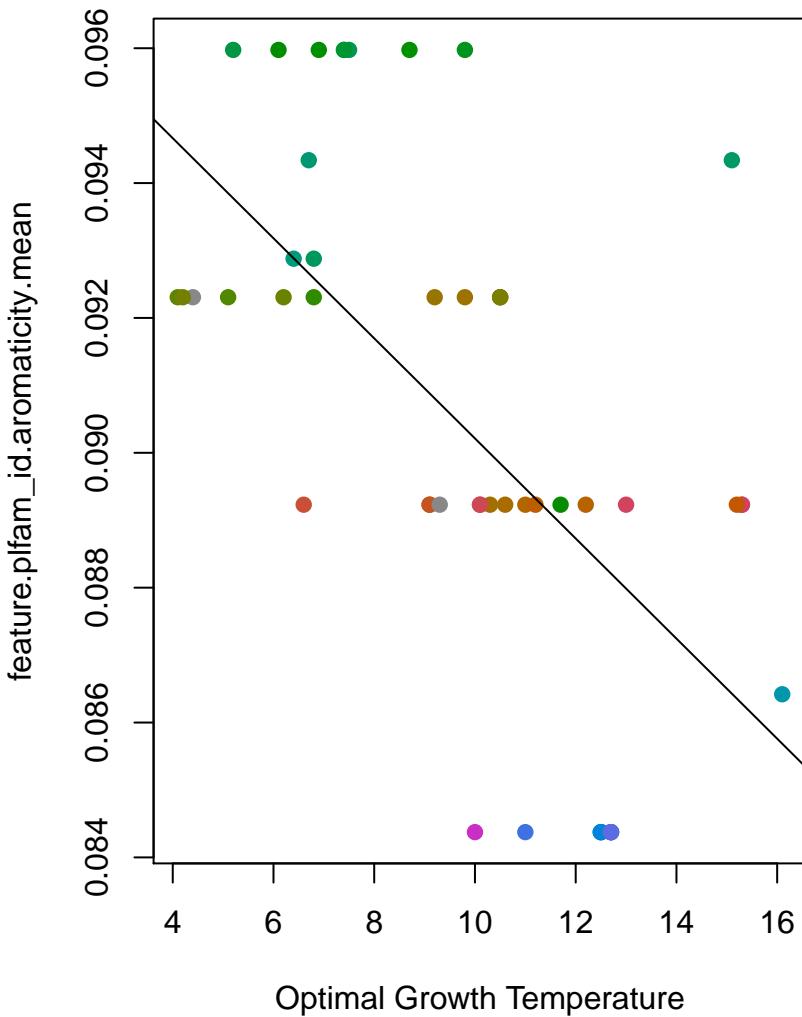


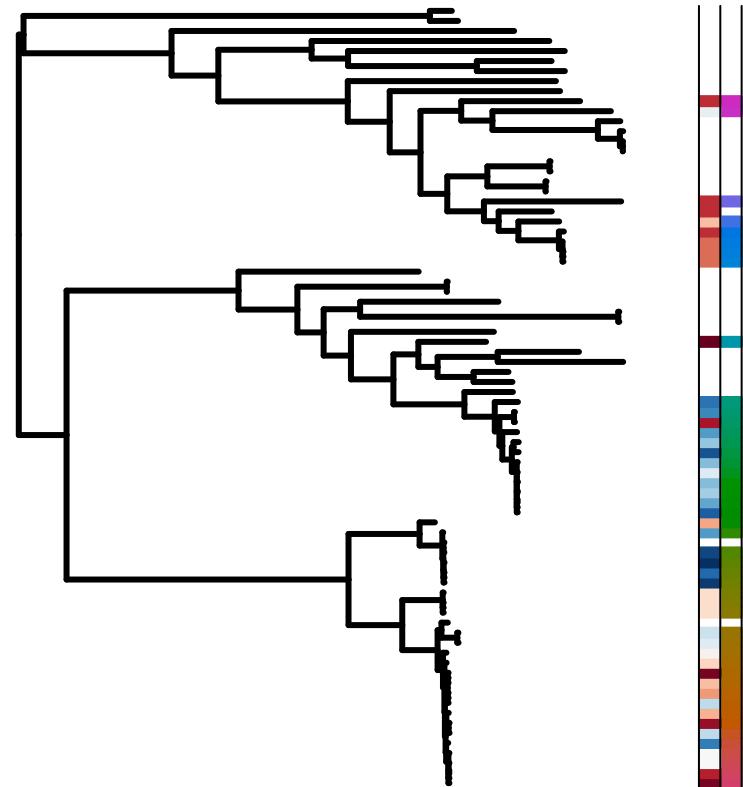
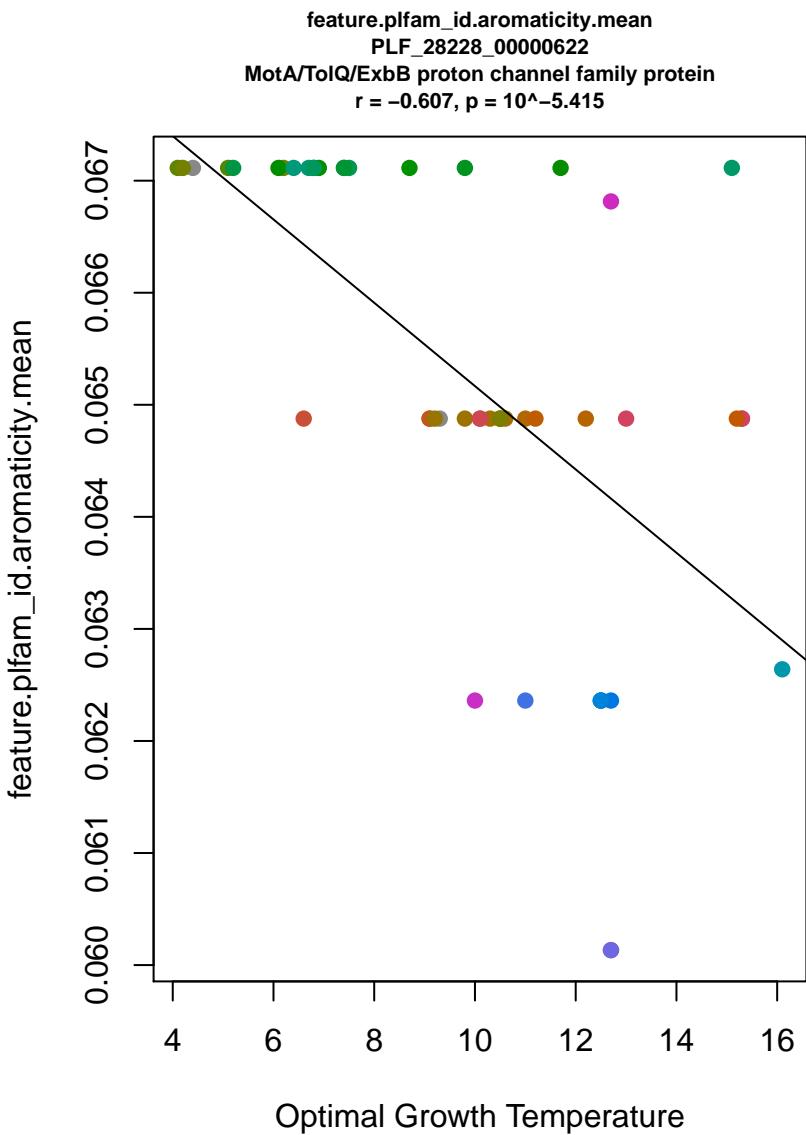
feature.plfam_id.aromaticity.mean

PLF_28228_00001186

Thiamine-monophosphate kinase (EC 2.7.4.16)

$r = -0.606$, $p = 10^{-5.51}$





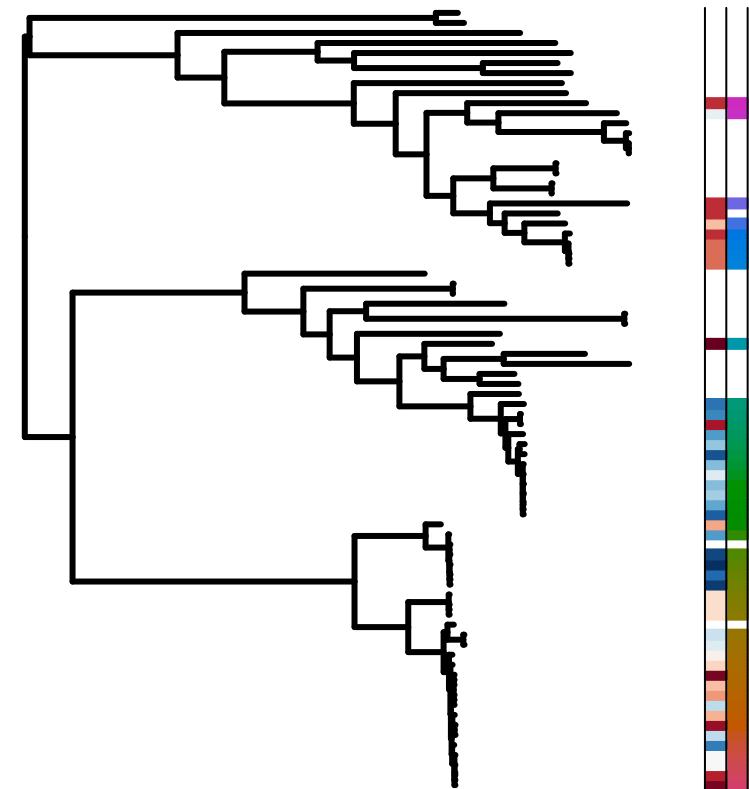
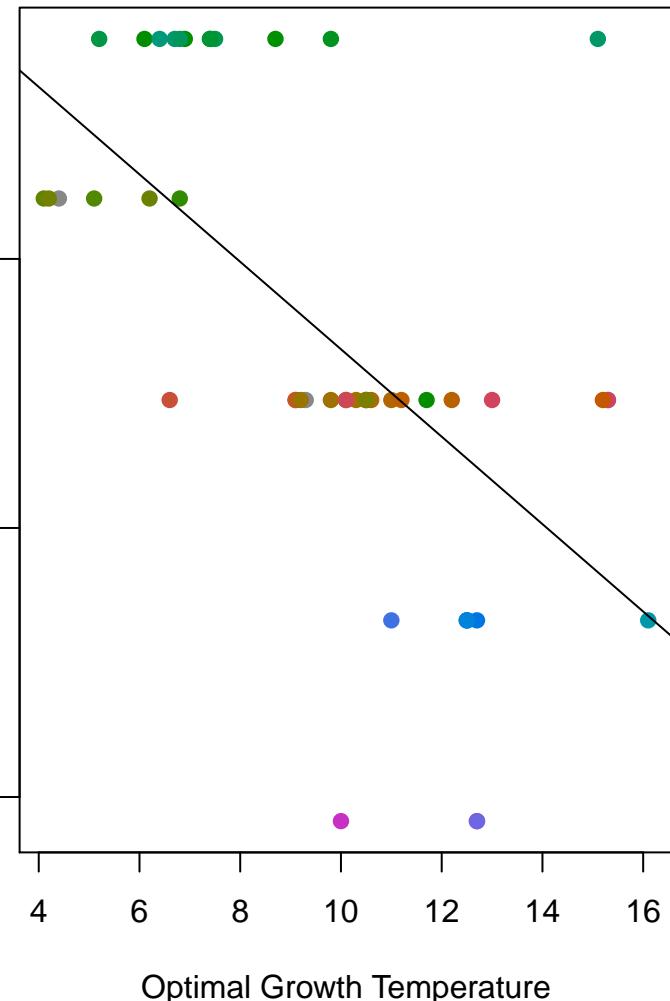
feature.plfam_id.aromaticity.mean

PLF_28228_00000719

4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)

$r = -0.607$, $p = 10^{-5.315}$

feature.plfam_id.aromaticity.mean



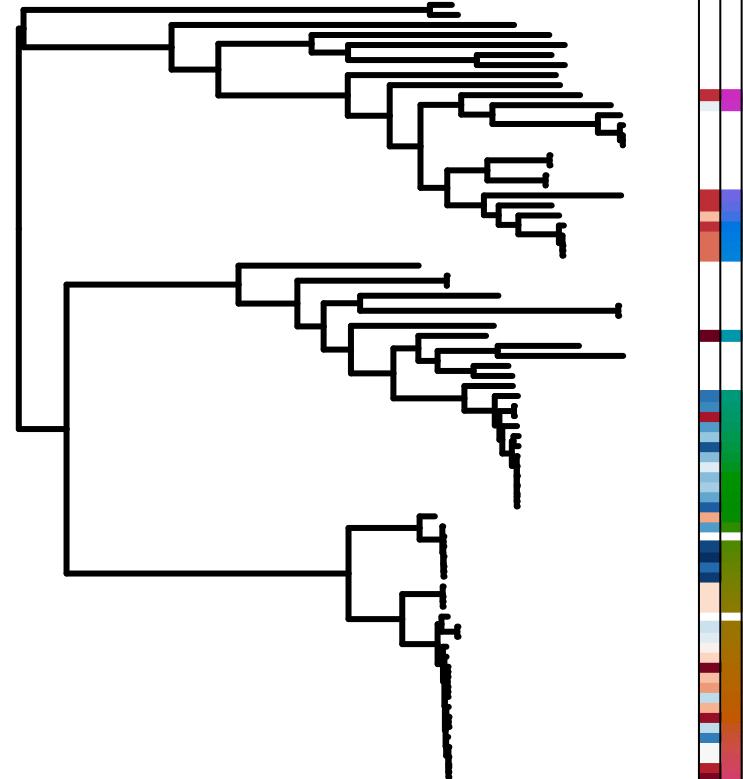
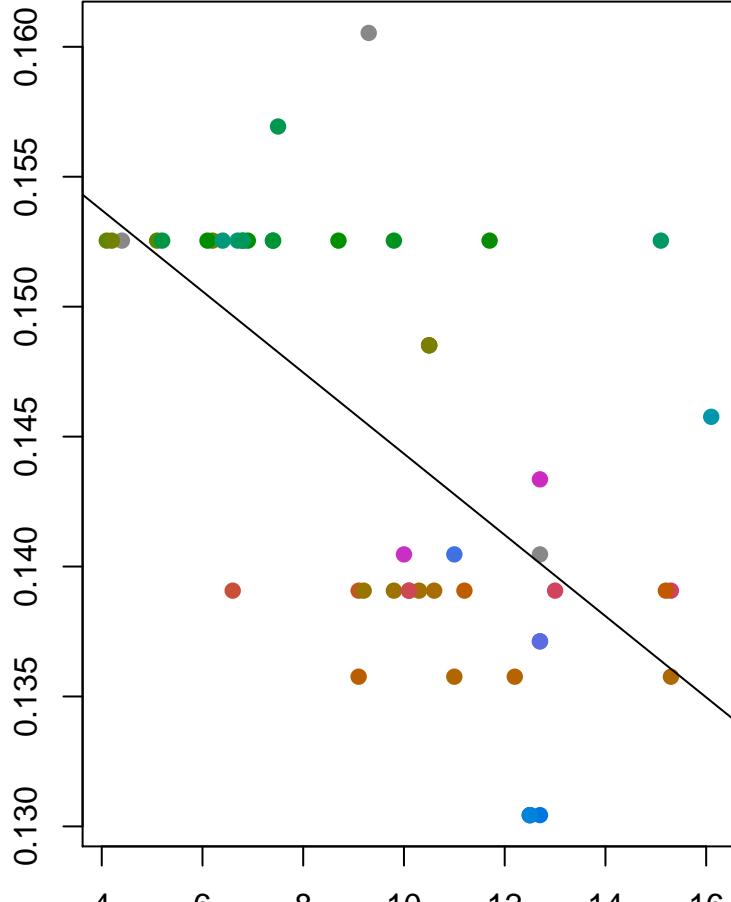
feature.plfam_id.aromaticity.mean

PLF_28228_00001911

Permease of the drug/metabolite transporter (DMT) superfamily

$r = -0.607, p = 10^{-5.53}$

feature.plfam_id.aromaticity.mean



Optimal Growth Temperature

feature.plfam_id.aromaticity.mean

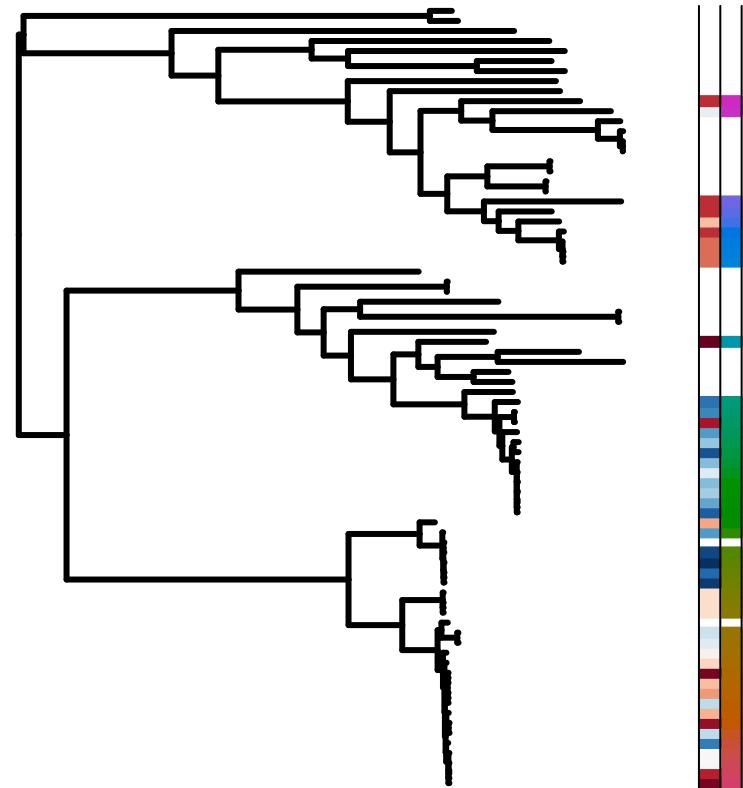
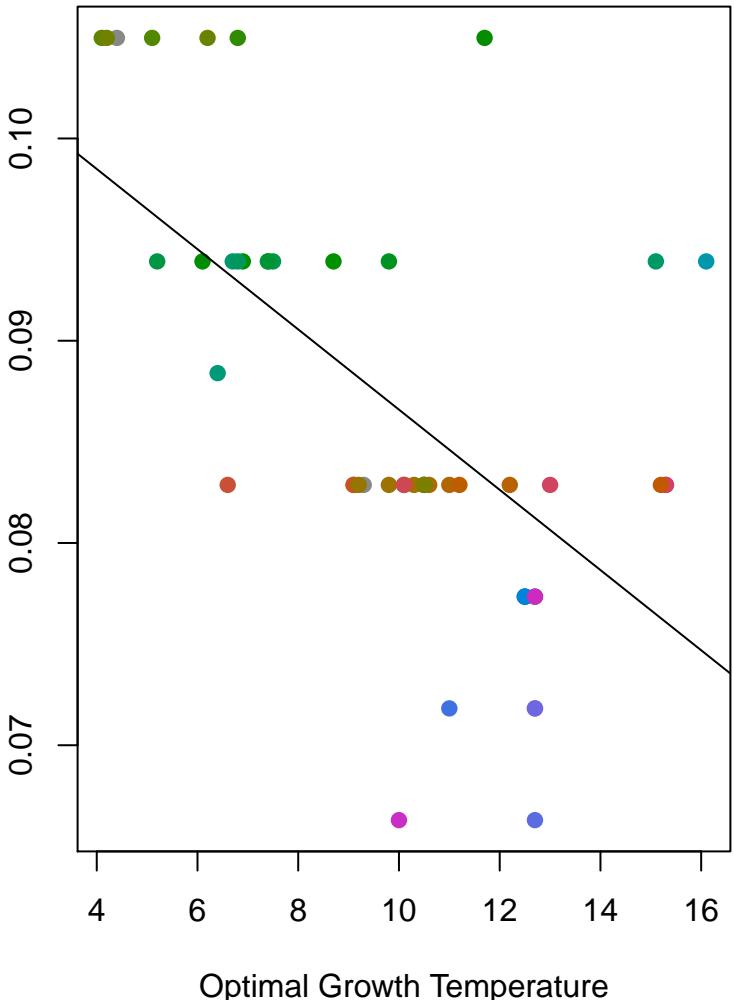
PLF_28228_00000267

3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)

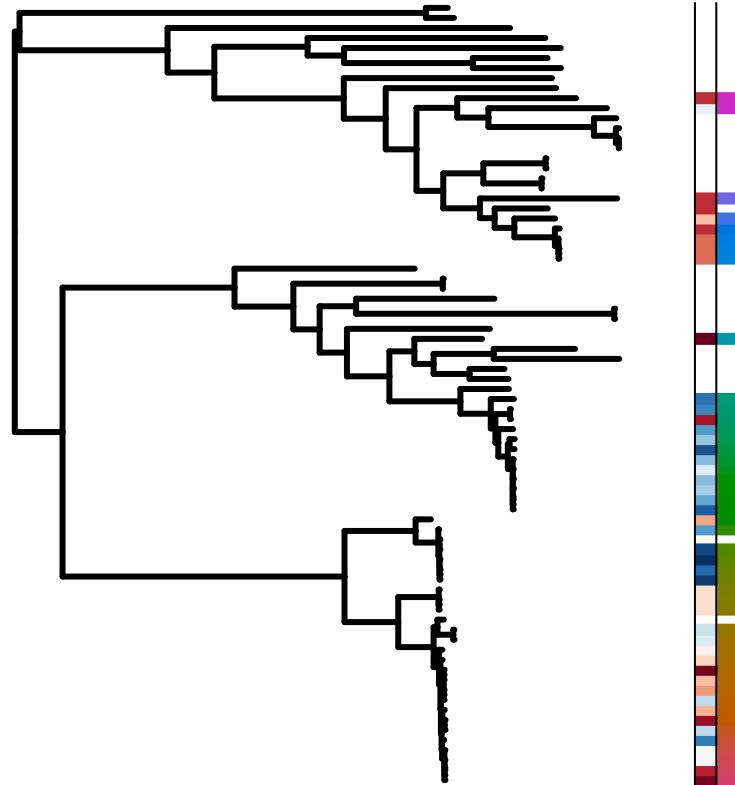
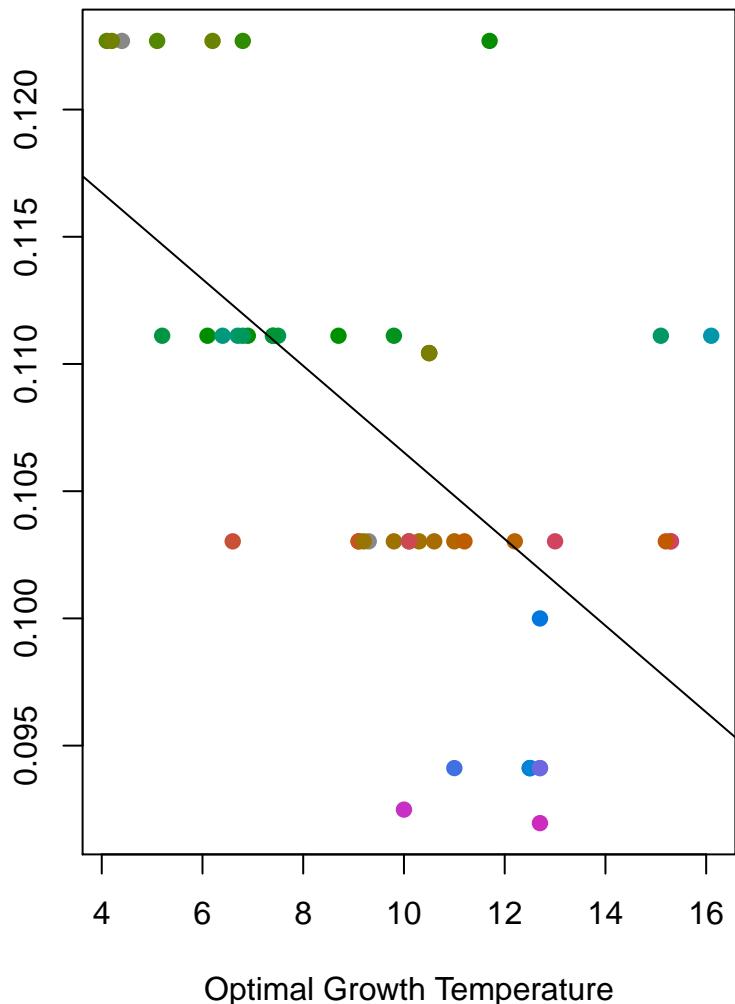
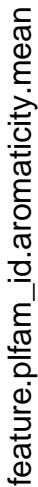
$r = -0.608, p = 10^{-5.554}$

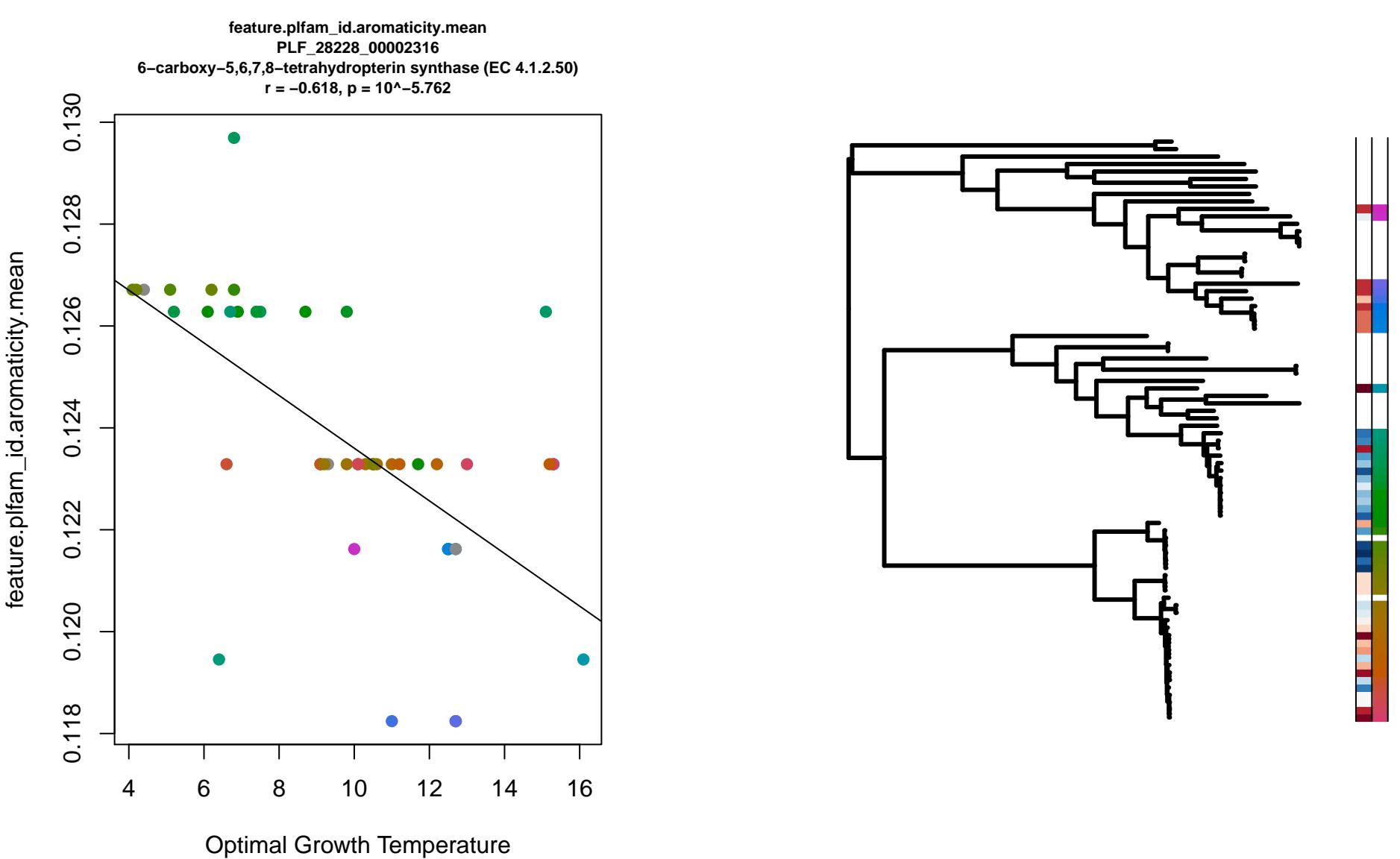
feature.plfam_id.aromaticity.mean

3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)
 $r = -0.608, p = 10^{-5.554}$



feature.plfam_id.aromaticity.mean
PLF_28228_00000781
Dihydrofolate reductase (EC 1.5.1.3)
 $r = -0.611, p = 10^{-5.503}$





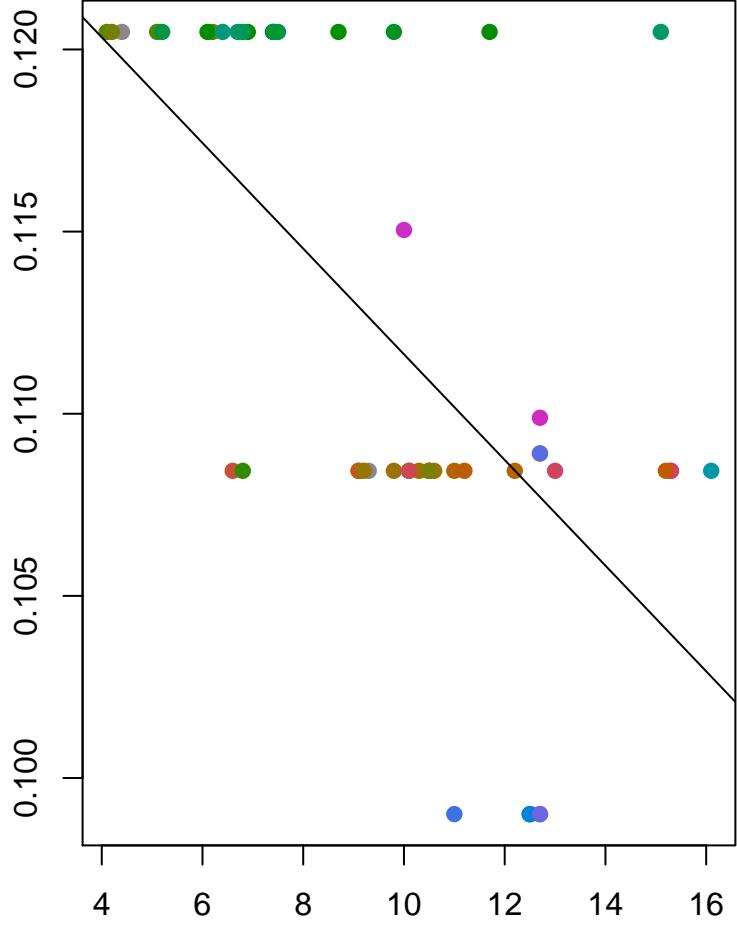
feature.plfam_id.aromaticity.mean

PLF_28228_00001310

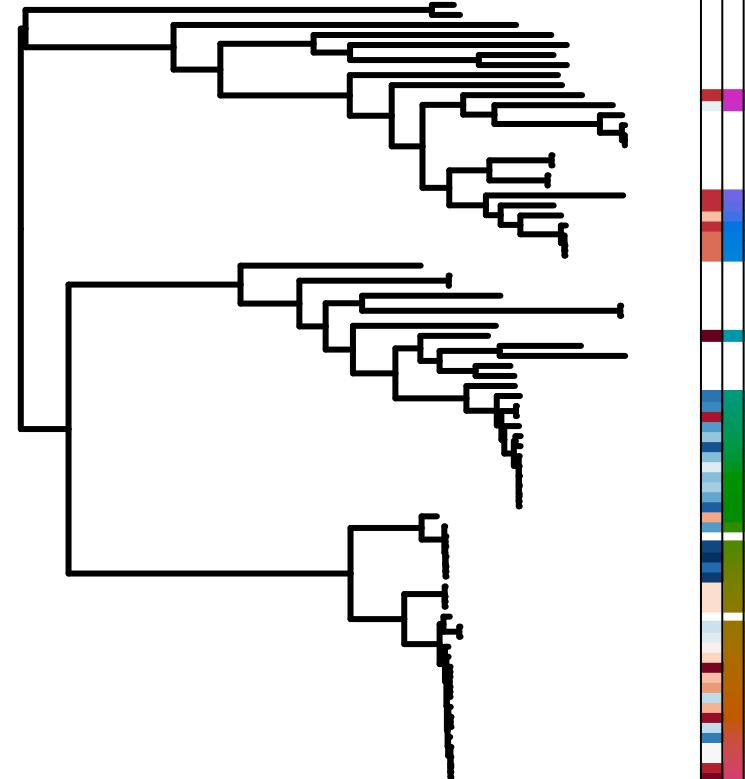
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin

$r = -0.626, p = 10^{-5.944}$

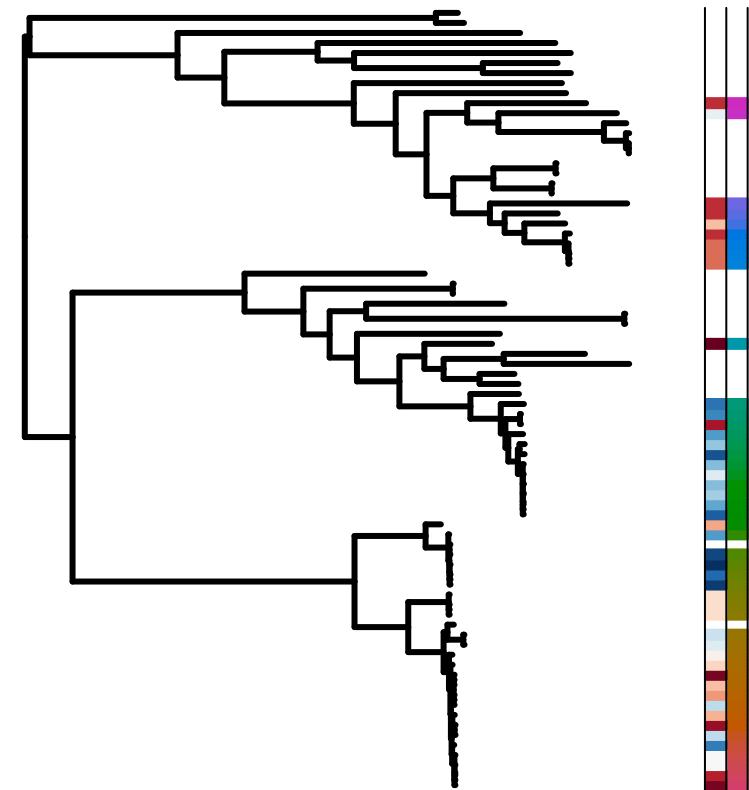
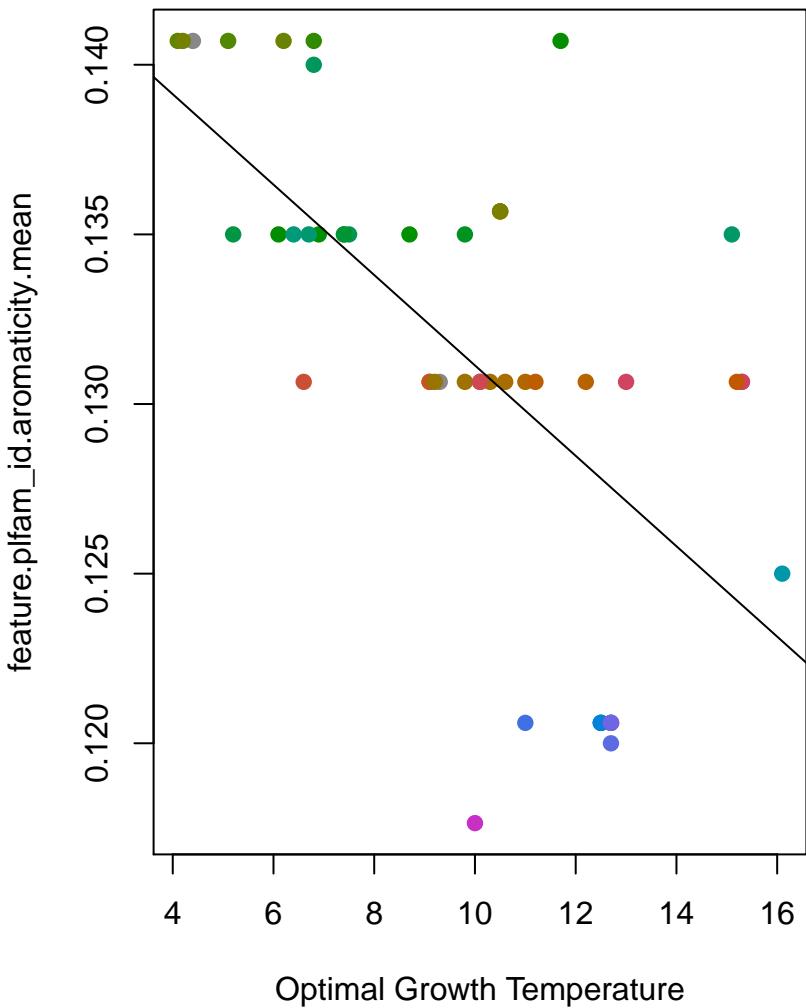
feature.plfam_id.aromaticity.mean



Optimal Growth Temperature



feature.plfam_id.aromaticity.mean
PLF_28228_00000546
Carbonic anhydrase, beta class (EC 4.2.1.1)
 $r = -0.631$, $p = 10^{-6.041}$

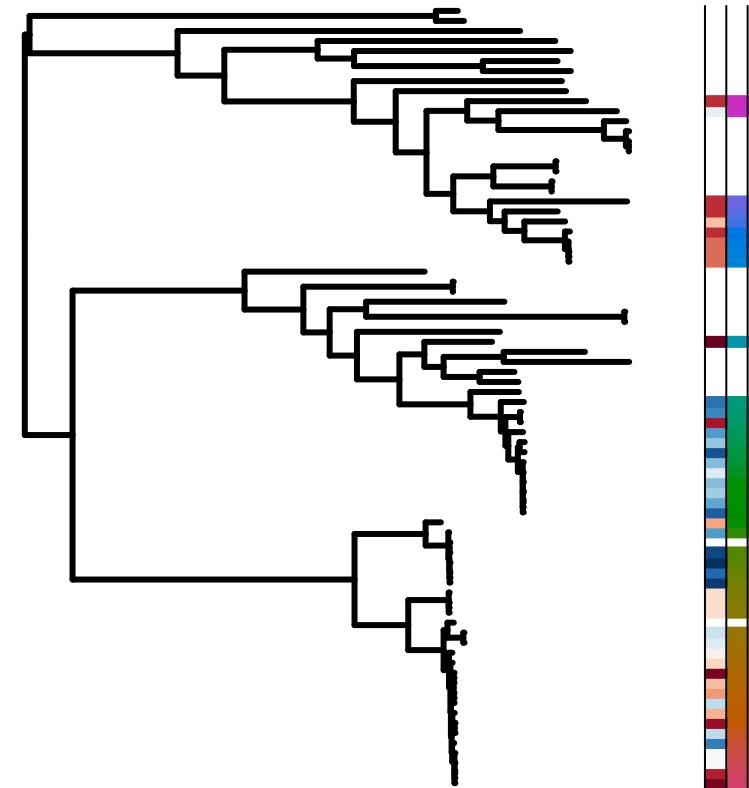
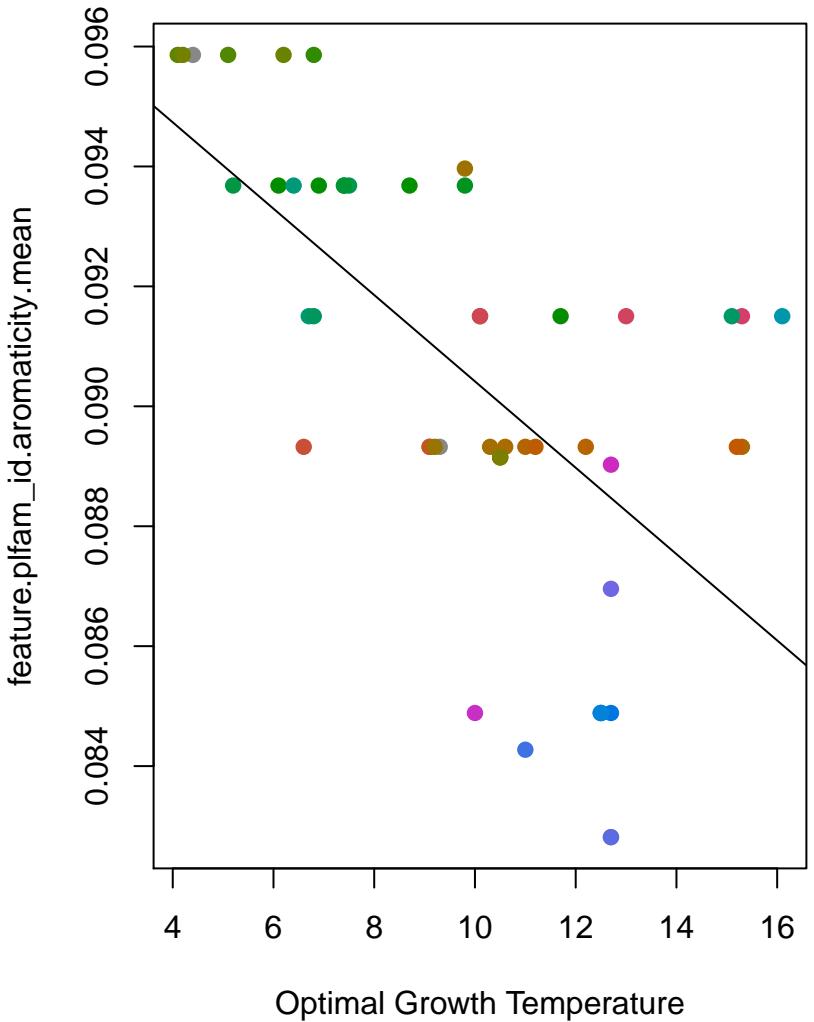


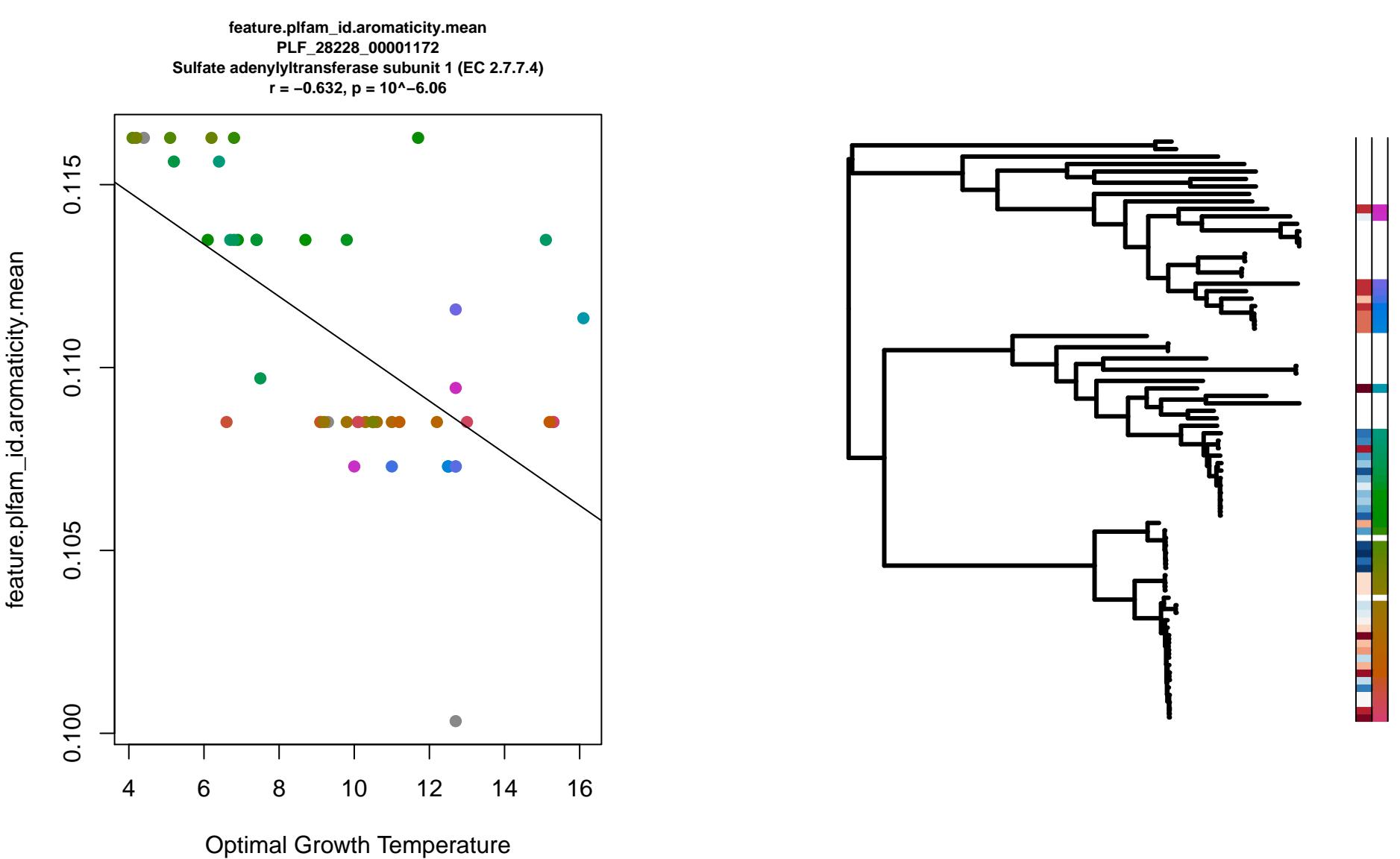
feature.plfam_id.aromaticity.mean

PLF_28228_00000981

Predicted ATPase related to phosphate starvation-inducible protein PhoH

$r = -0.631, p = 10^{-6.049}$





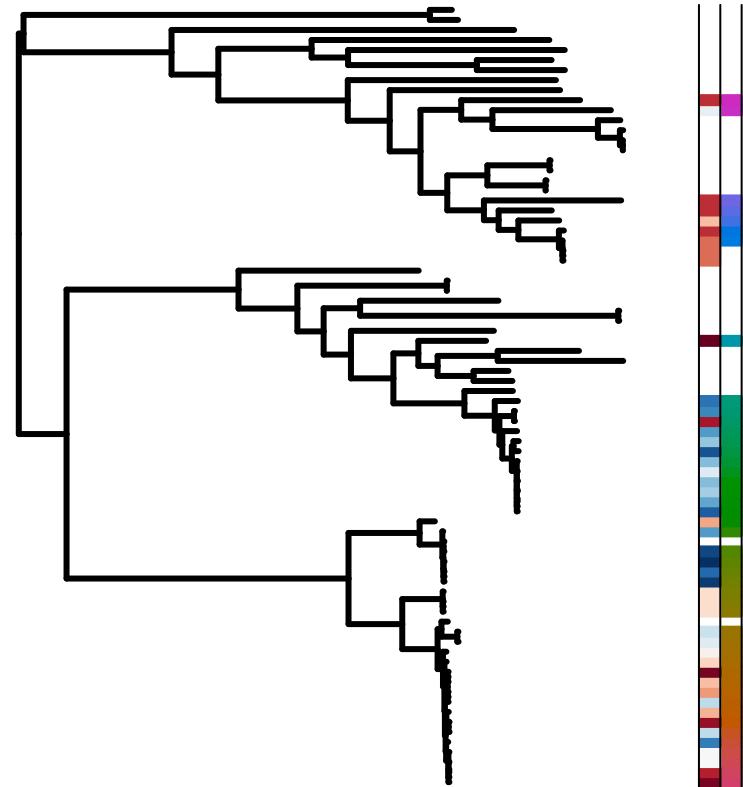
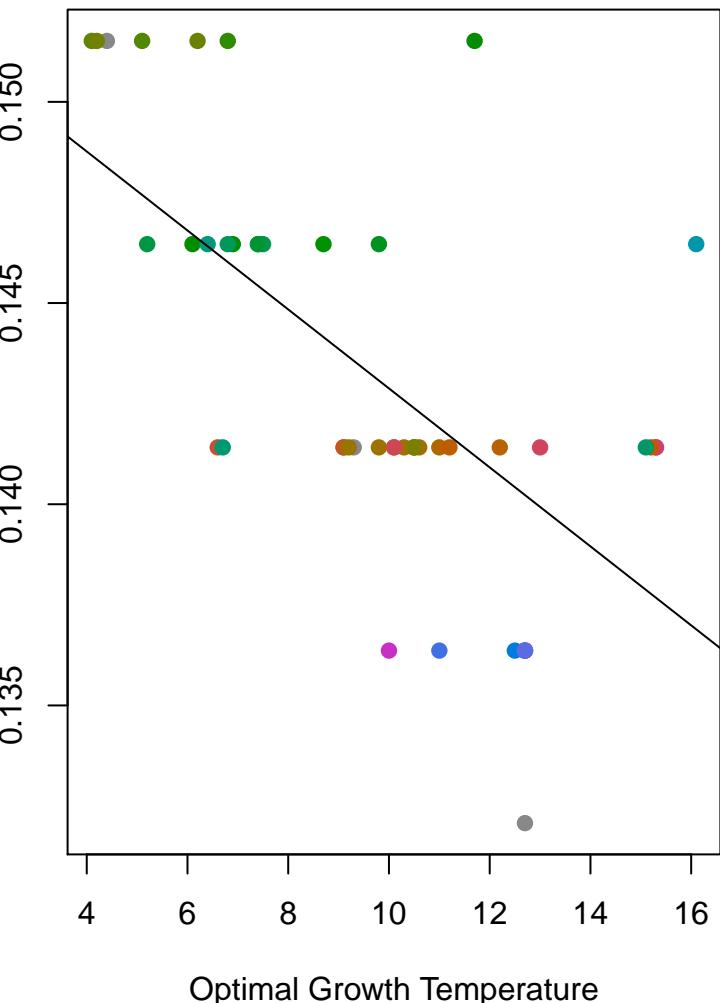
feature.plfam_id.aromaticity.mean

PLF_28228_00028151

3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)

$r = -0.638, p = 10^{-5.969}$

feature.plfam_id.aromaticity.mean



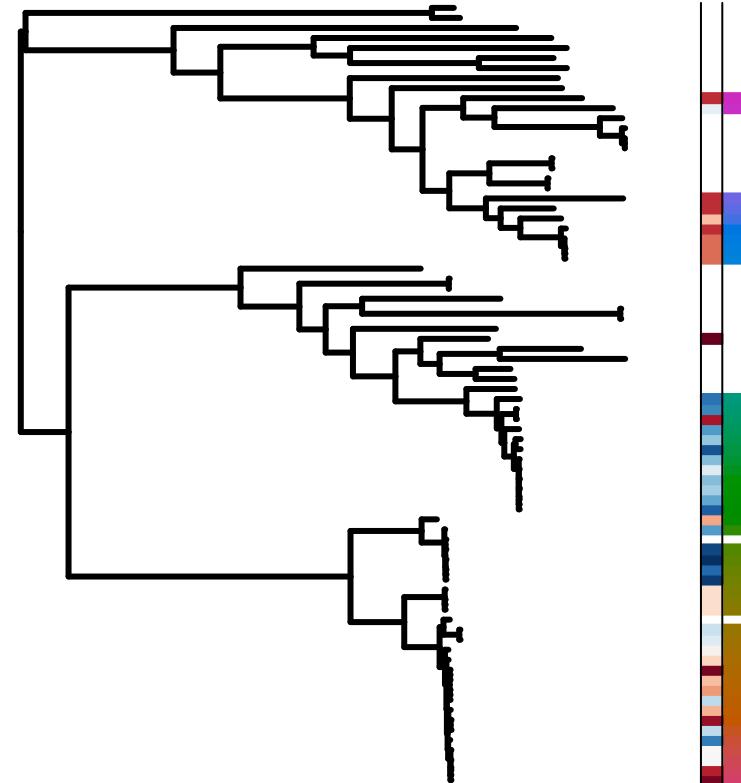
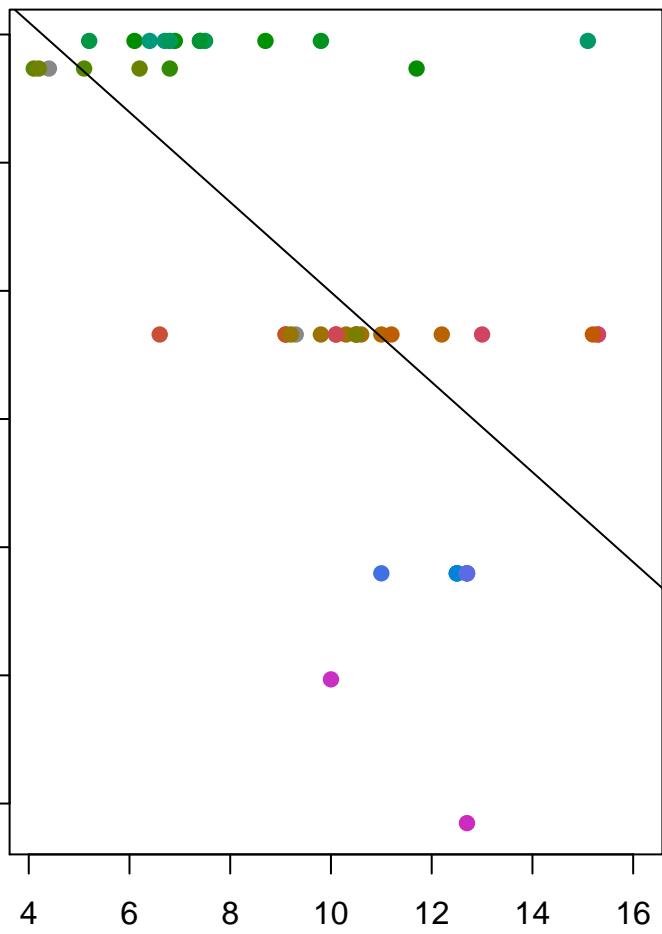
feature.plfam_id.aromaticity.mean

PLF_28228_00001635

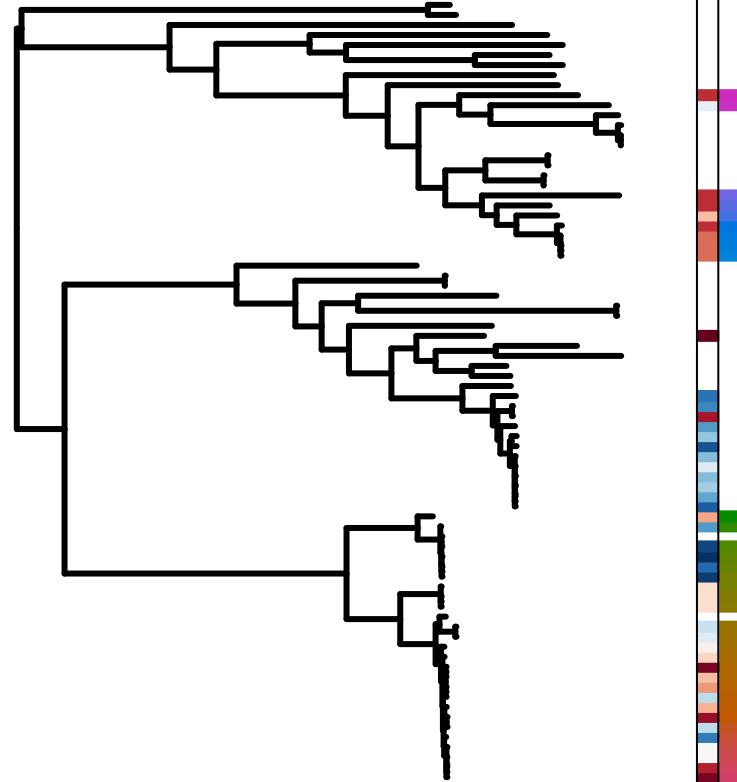
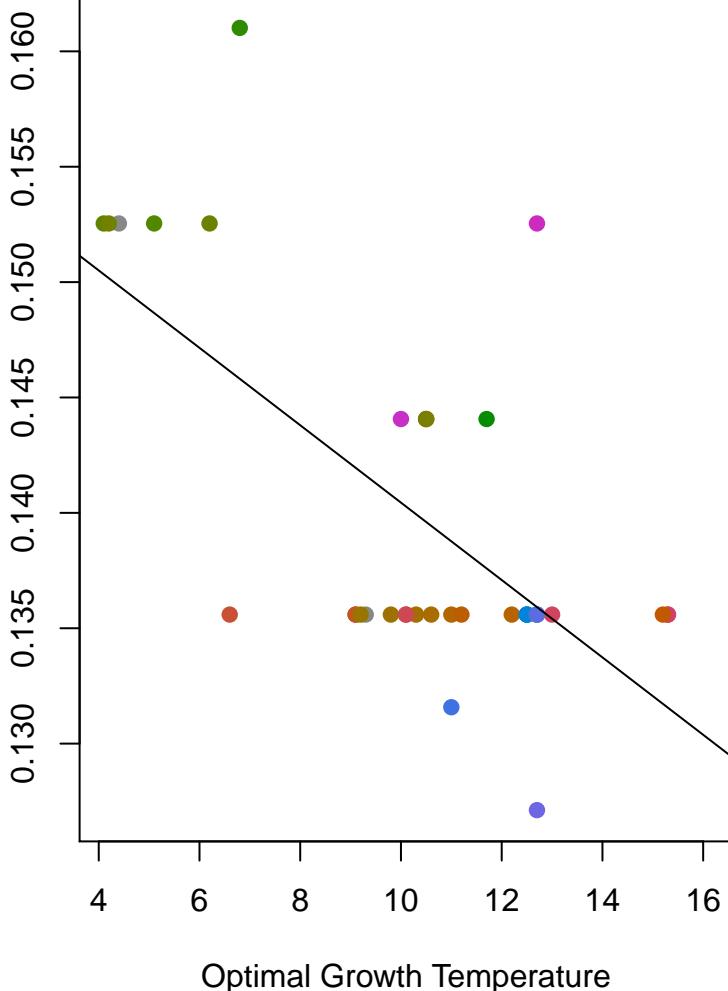
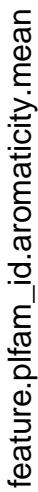
DNA-binding transcriptional regulator, MocR family / aminotransferase domain

$r = -0.643, p = 10^{-6.19}$

feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00002486
hypothetical protein
 $r = -0.645$, $p = 10^{-4.4779}$



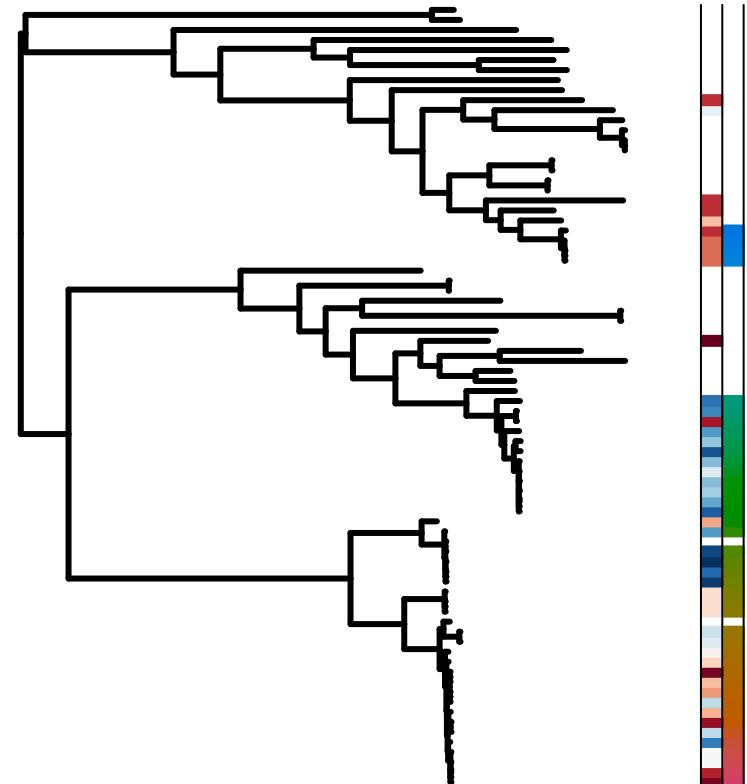
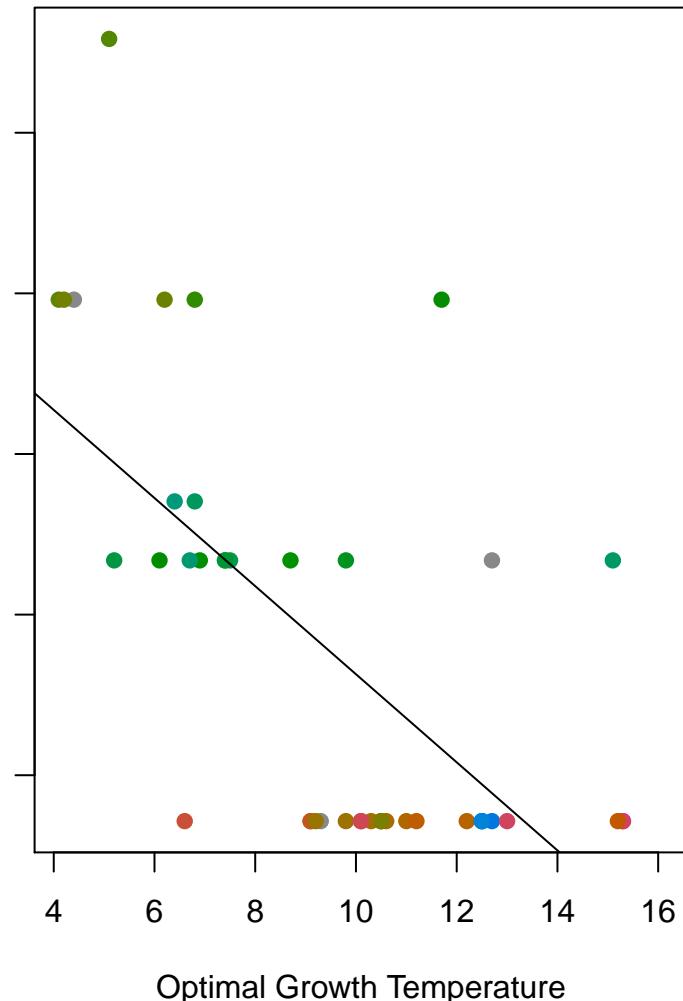
feature.plfam_id.aromaticity.mean

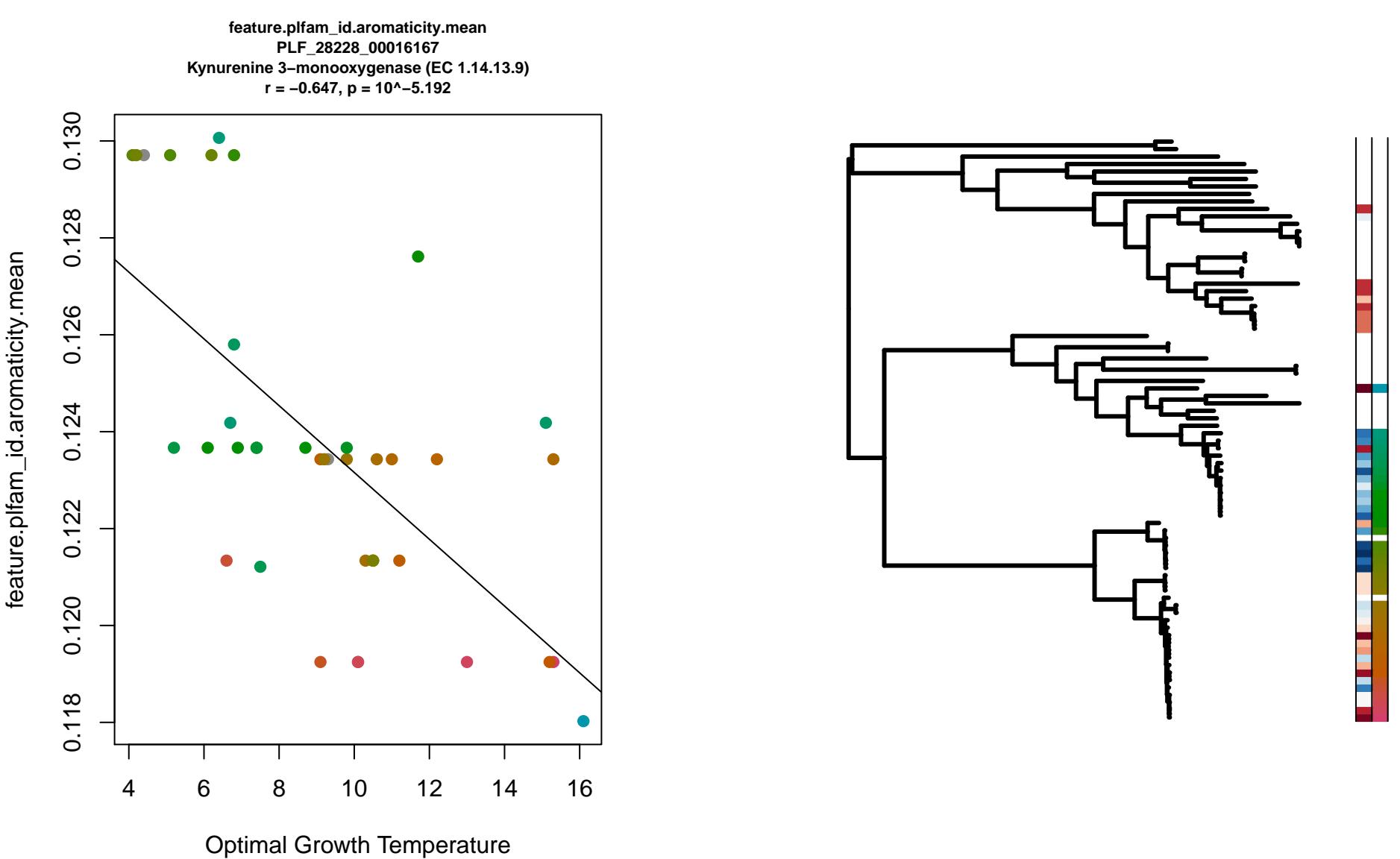
PLF_28228_00007842

Efflux ABC transporter, ATP-binding protein

$r = -0.646$, $p = 10^{-5.664}$

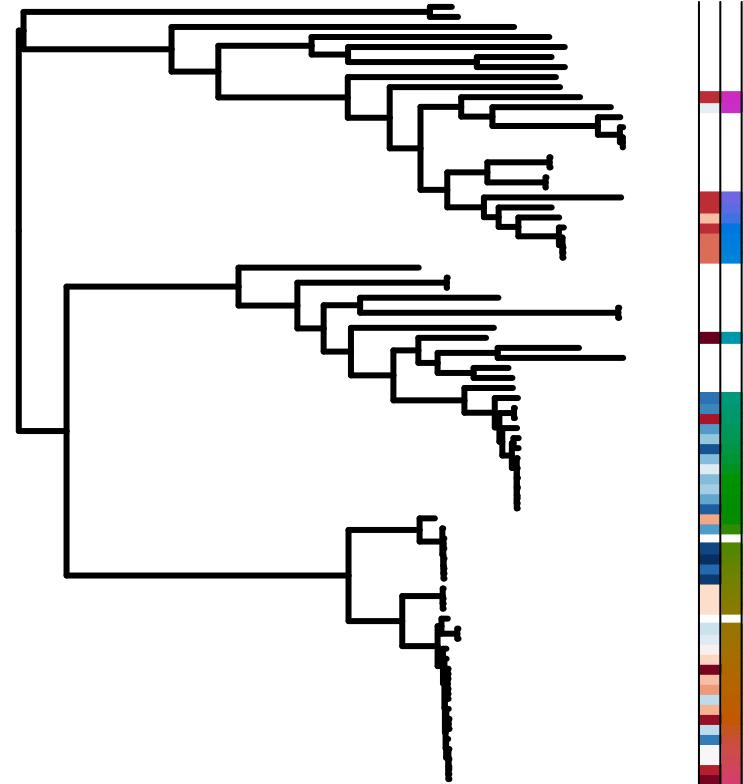
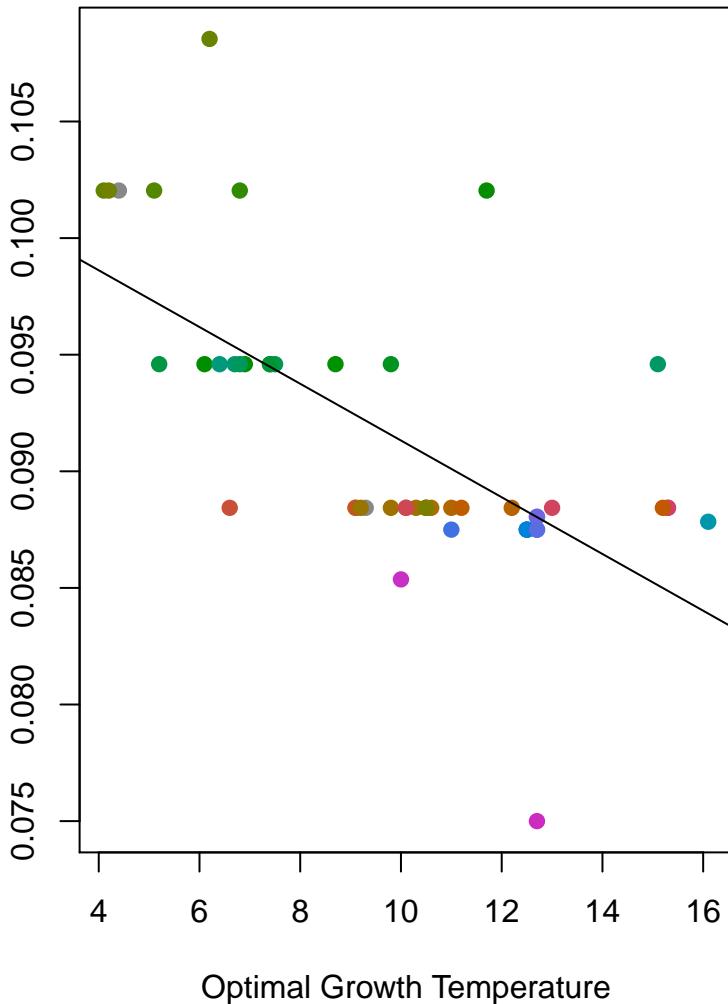
feature.plfam_id.aromaticity.mean





feature.plfam_id.aromaticity.mean
PLF_28228_00001047
RNA-binding protein
 $r = -0.652$, $p = 10^{-6.524}$

feature.plfam_id.aromaticity.mean



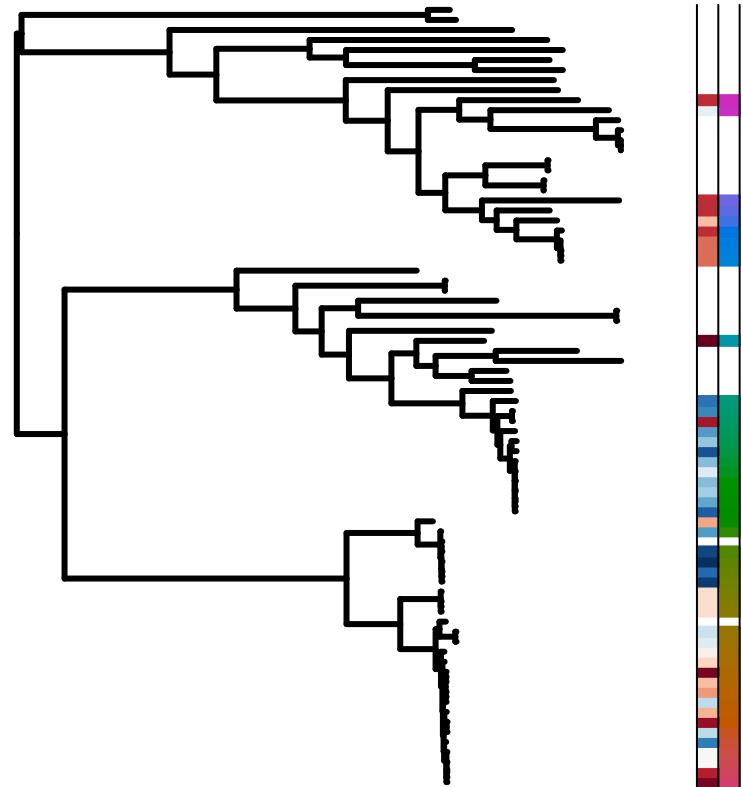
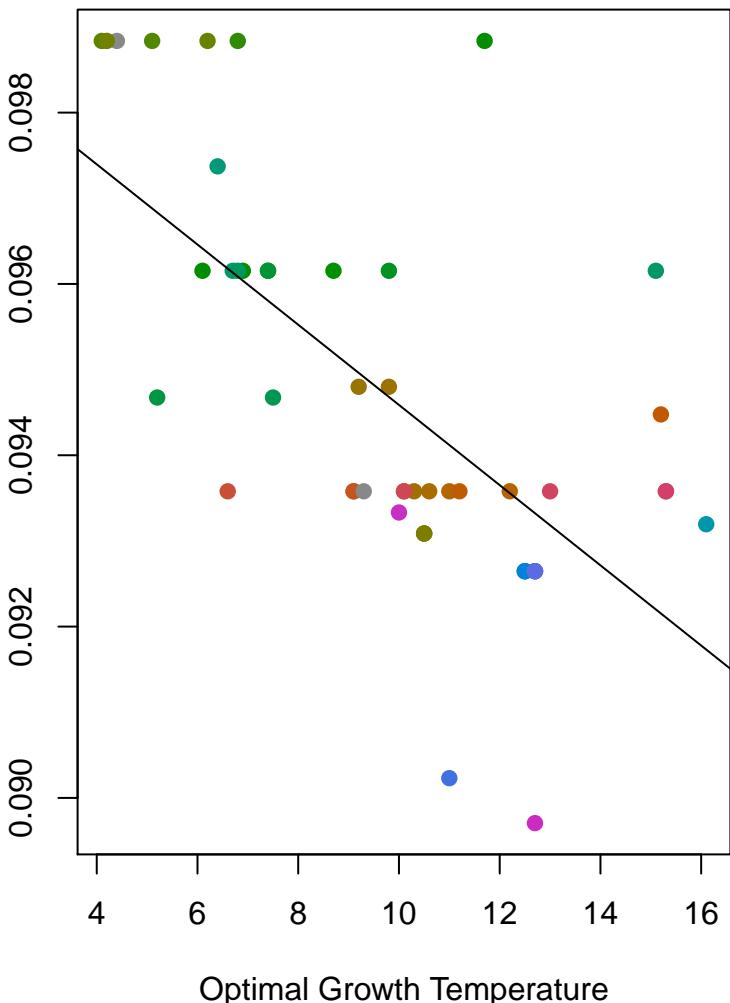
feature.plfam_id.aromaticity.mean

PLF_28228_00000071

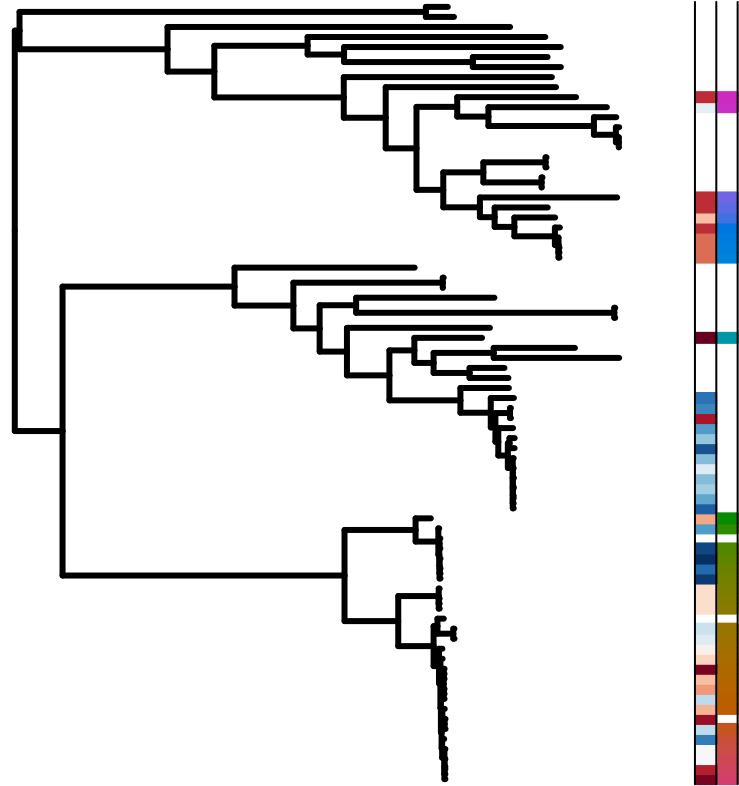
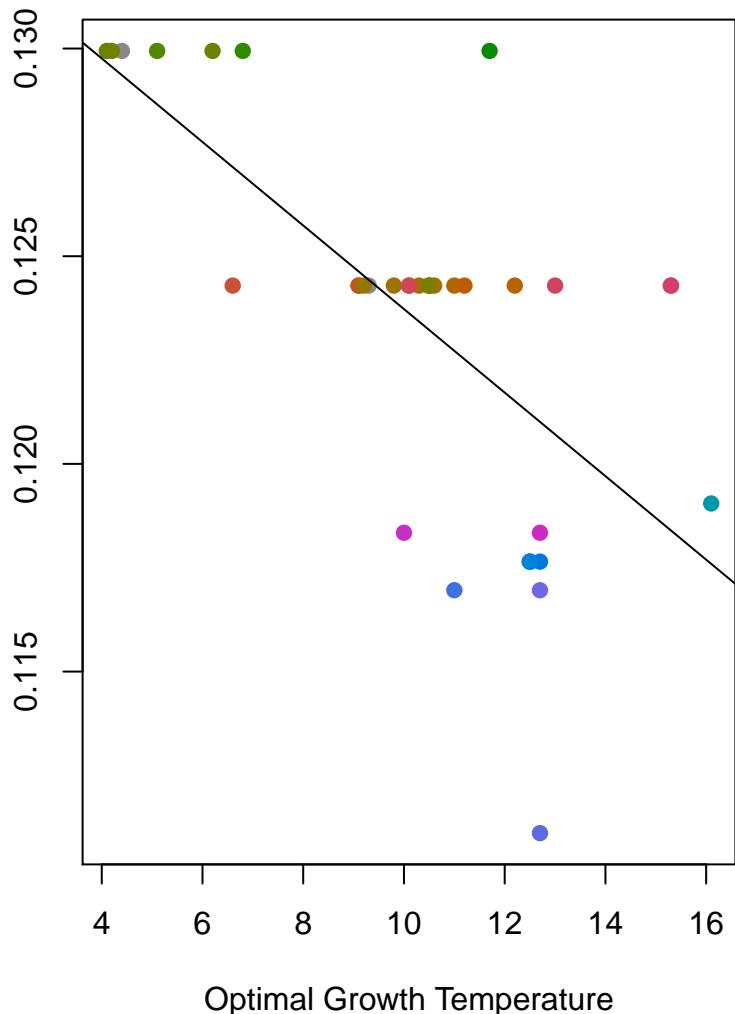
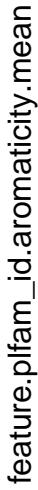
2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)

$r = -0.655, p = 10^{-6.598}$

feature.plfam_id.aromaticity.mean

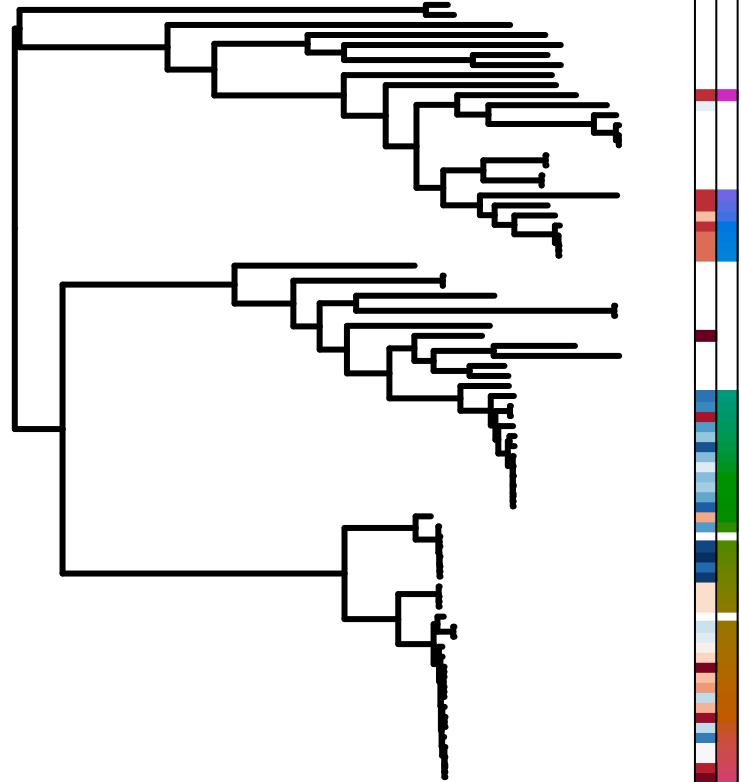
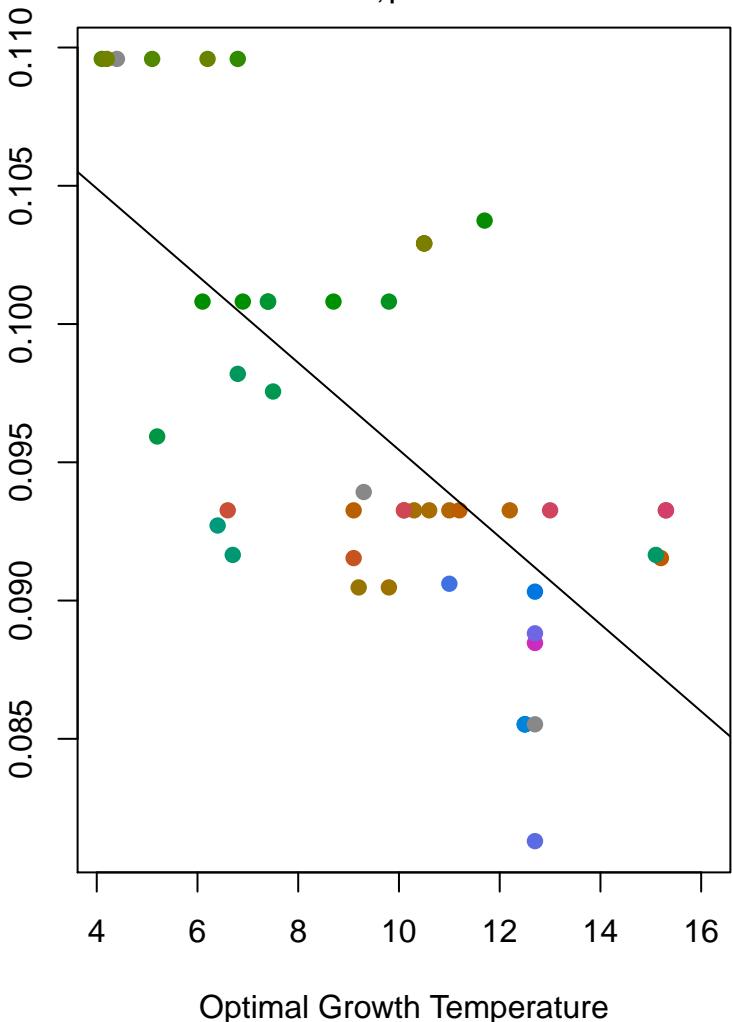


feature.plfam_id.aromaticity.mean
PLF_28228_00002195
Ureidoglycolate lyase (EC 4.3.2.3)
 $r = -0.658$, $p = 10^{-4.892}$



feature.plfam_id.aromaticity.mean
PLF_28228_00002320
hypothetical protein
 $r = -0.664$, $p = 10^{-6.582}$

feature.plfam_id.aromaticity.mean



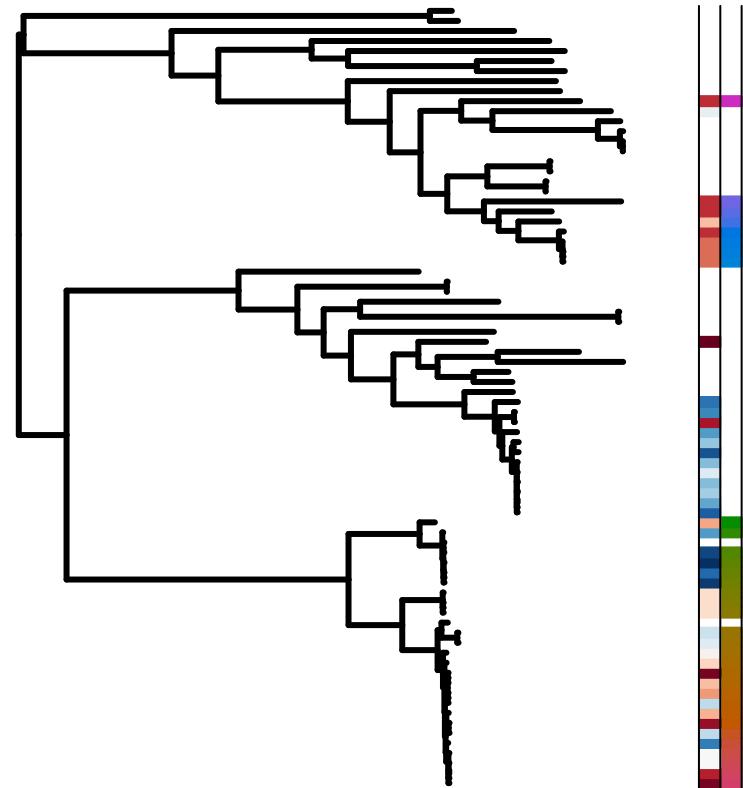
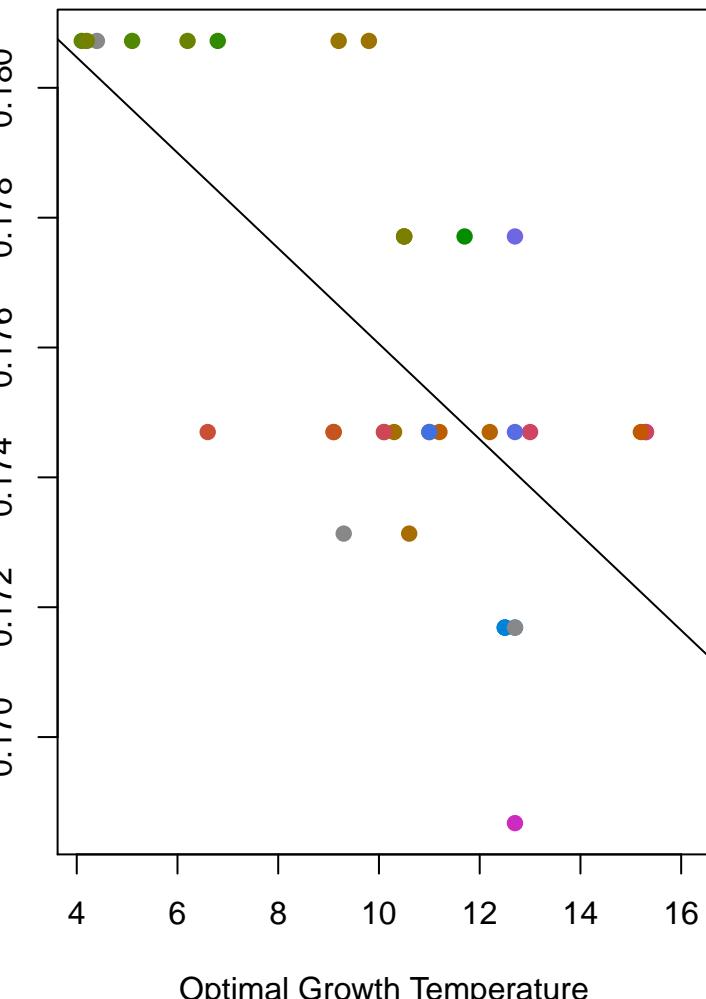
feature.plfam_id.aromaticity.mean

PLF_28228_00002715

Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)

$r = -0.673$, $p = 10^{-5.154}$

feature.plfam_id.aromaticity.mean

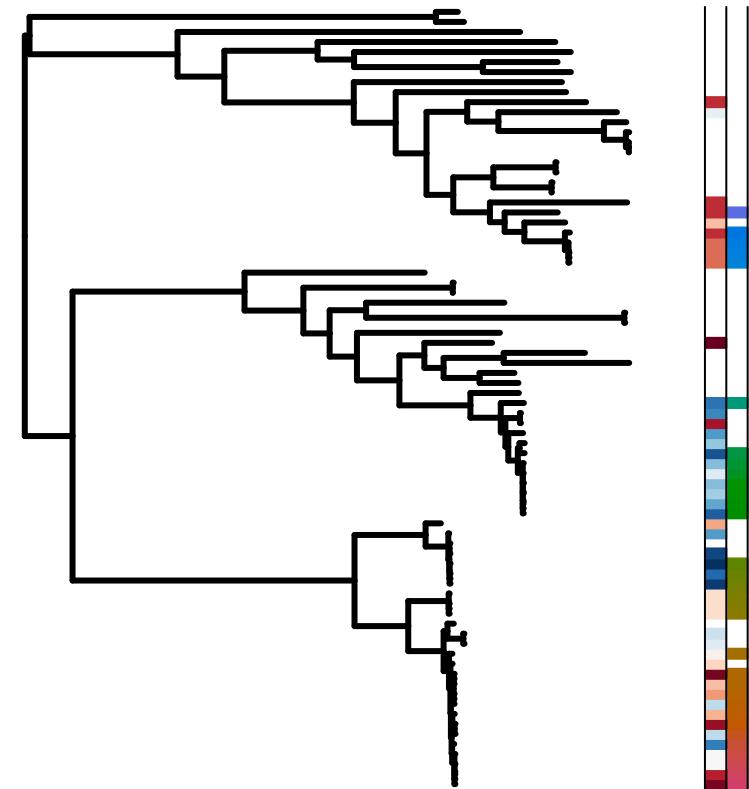
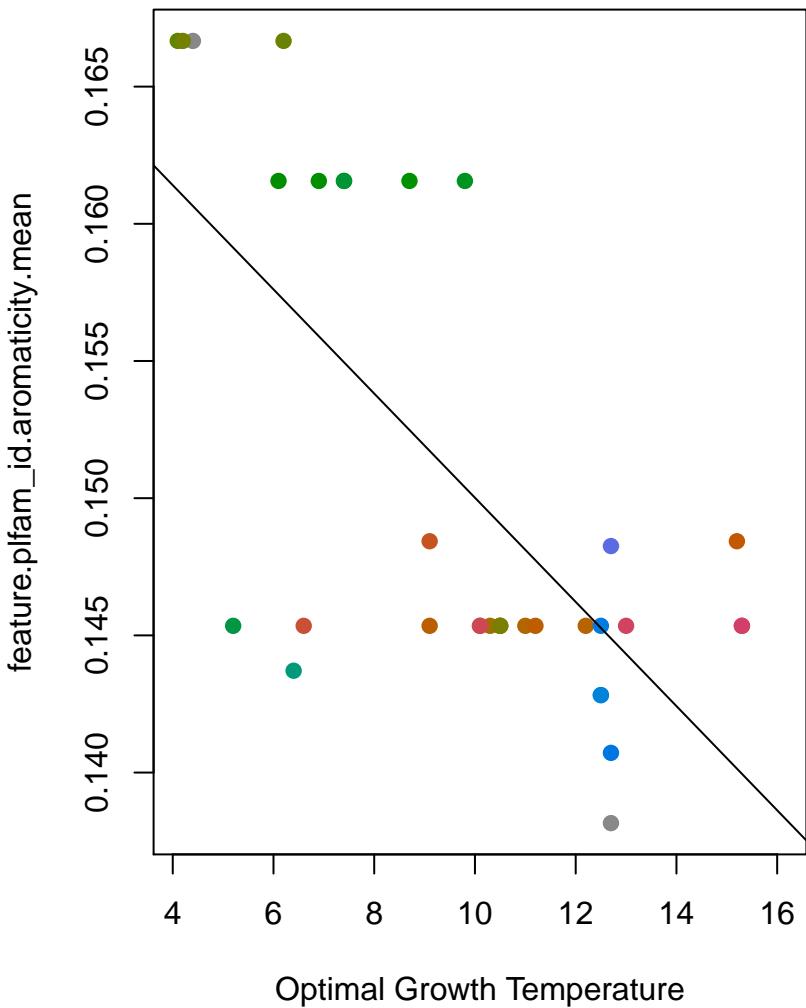


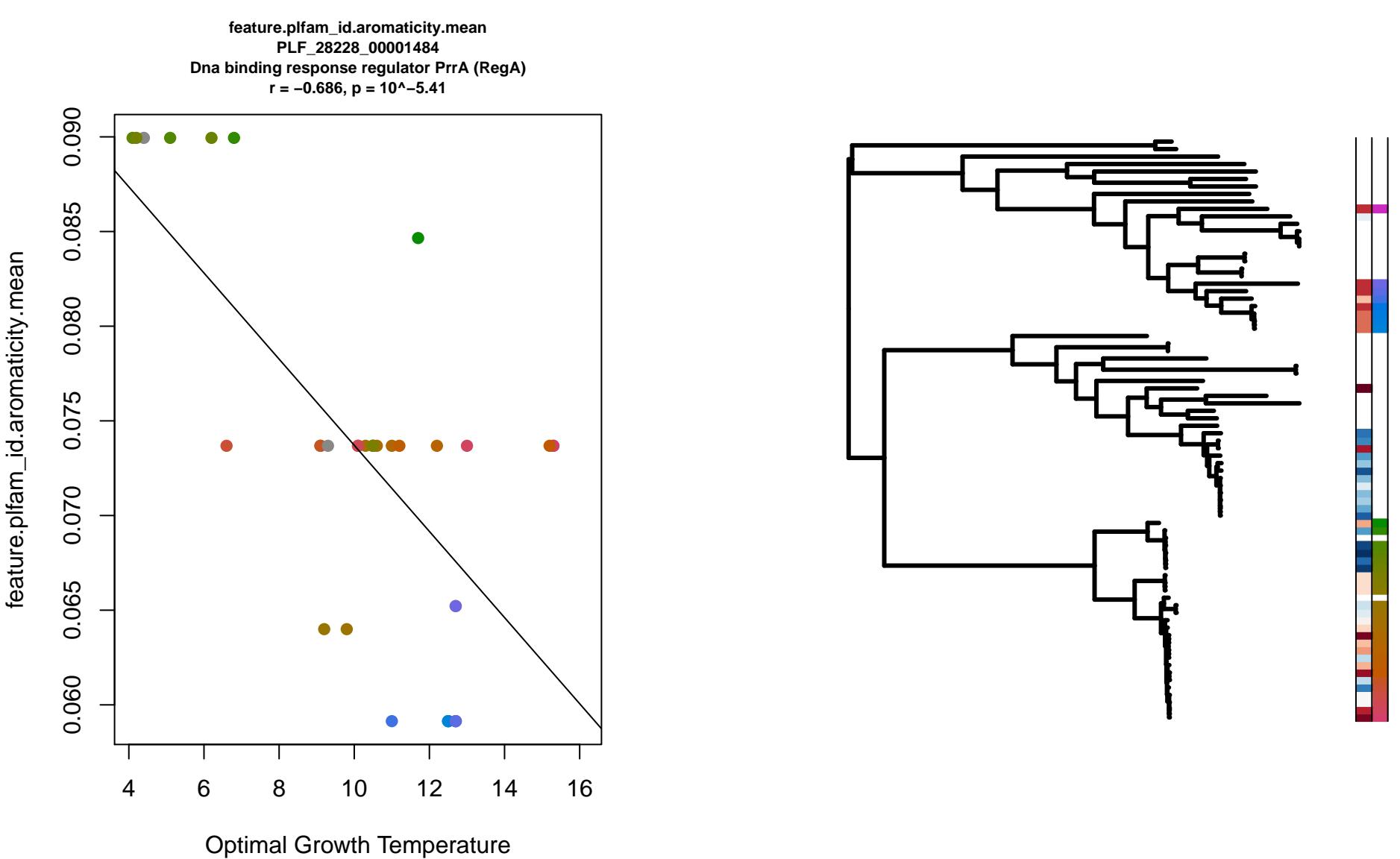
feature.plfam_id.aromaticity.mean

PLF_28228_00003783

UDP-glucuronate 5'-epimerase (EC 5.1.3.12)

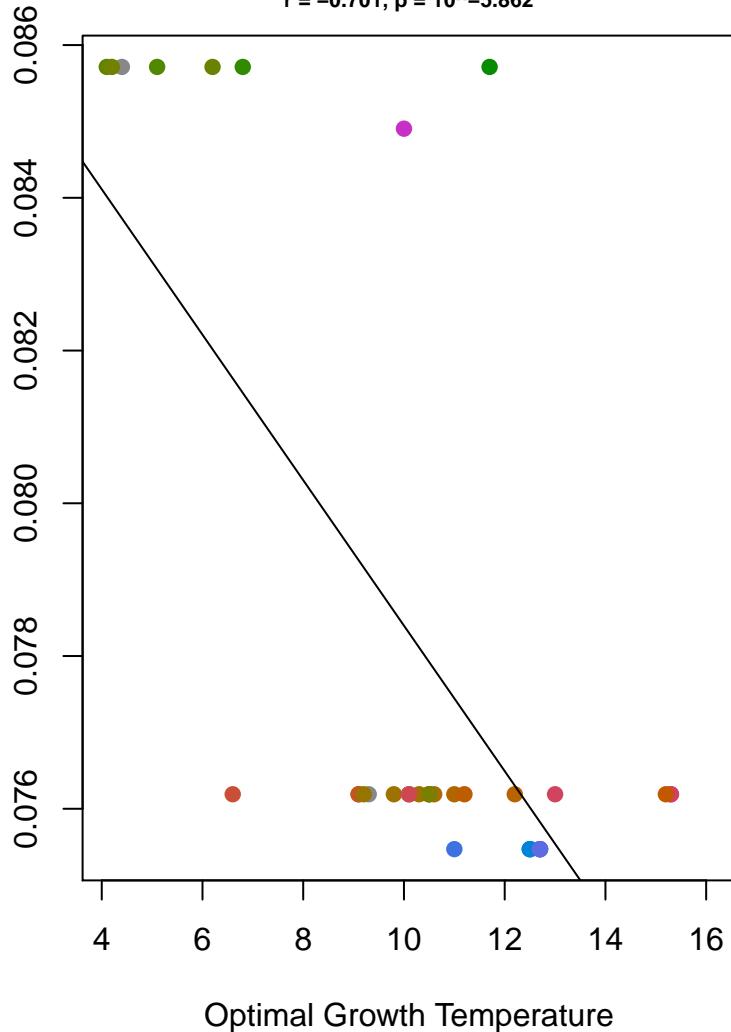
$r = -0.685, p = 10^{-5.113}$



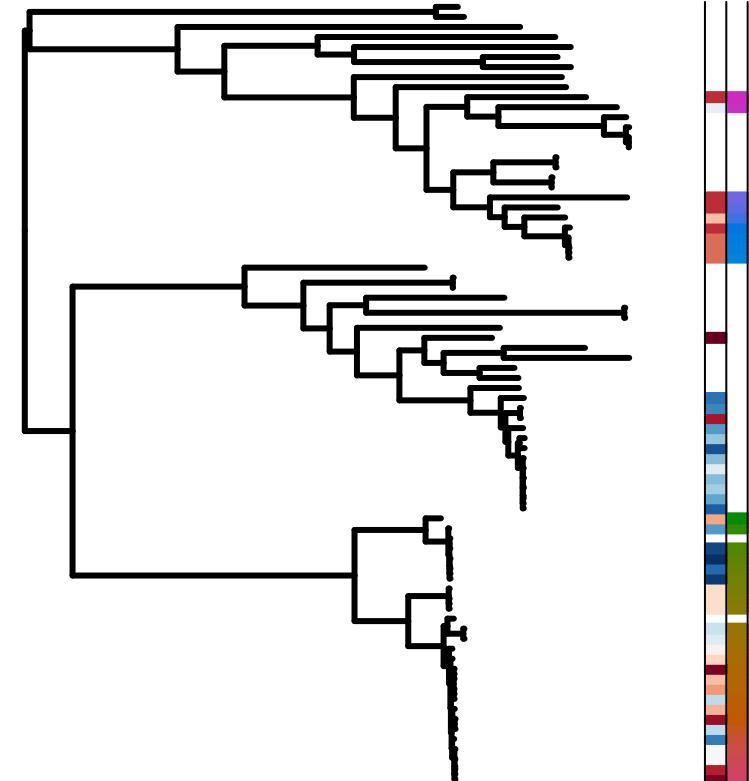


feature.plfam_id.aromaticity.mean
PLF_28228_00001083
Ribosomal silencing factor RsfA
 $r = -0.701$, $p = 10^{-5.862}$

feature.plfam_id.aromaticity.mean

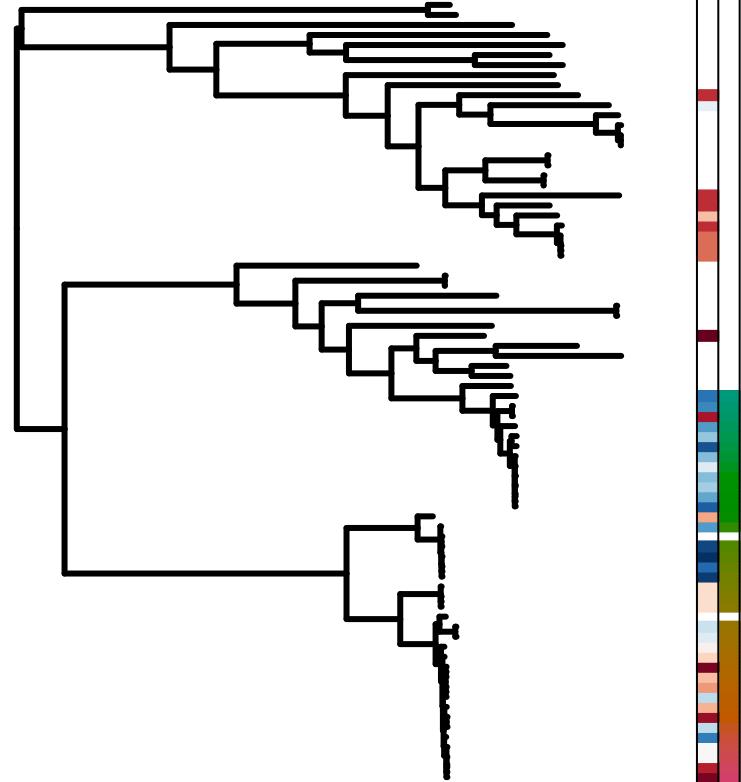
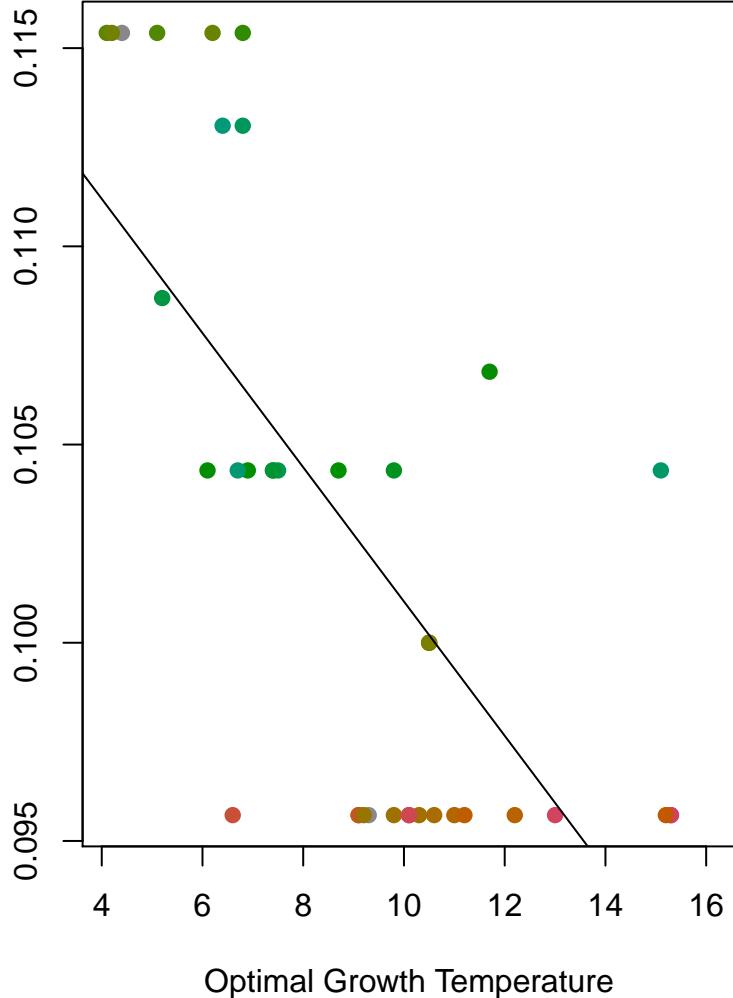


Optimal Growth Temperature



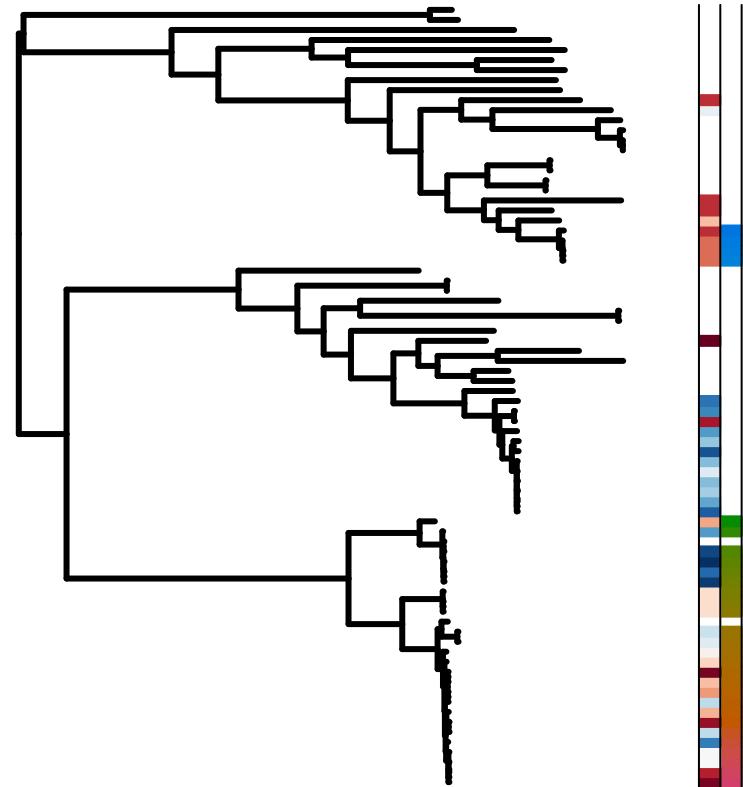
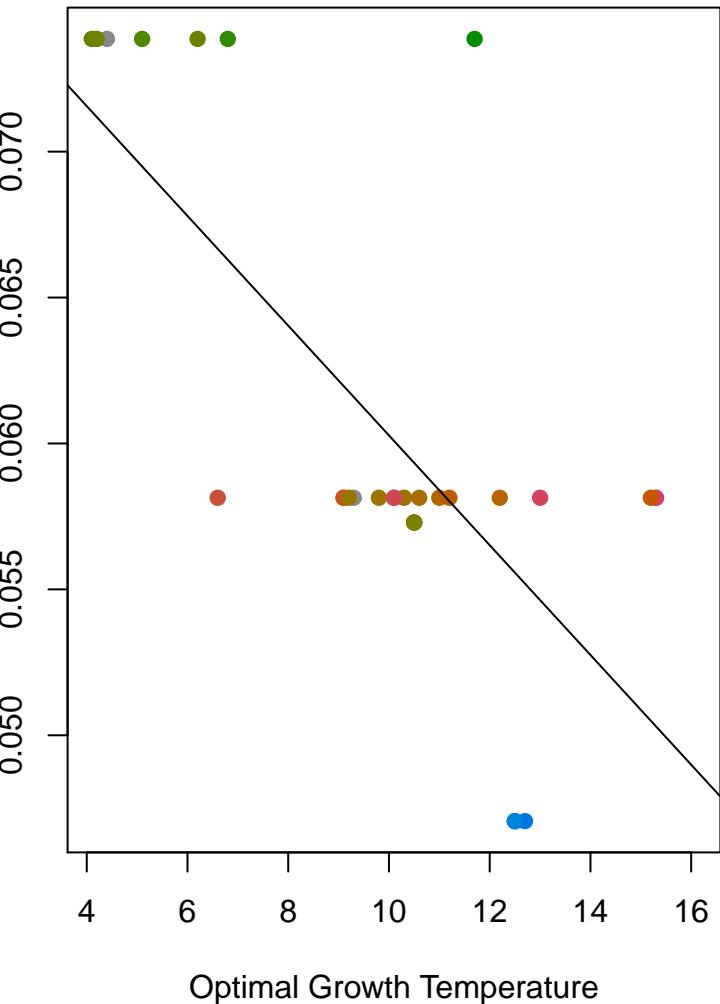
feature.plfam_id.aromaticity.mean
PLF_28228_00006398
hypothetical protein
 $r = -0.702$, $p = 10^{-6.205}$

feature.plfam_id.aromaticity.mean



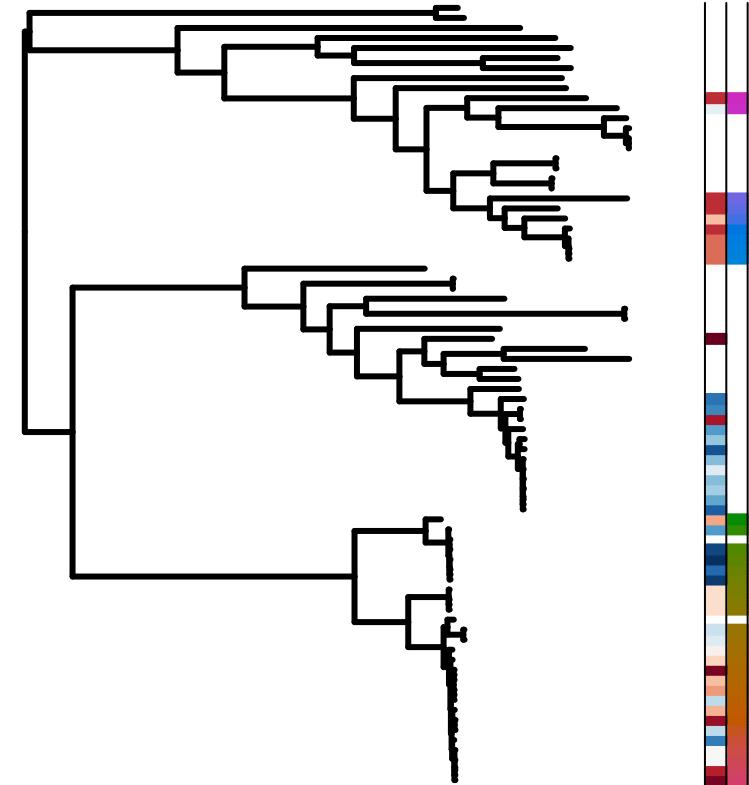
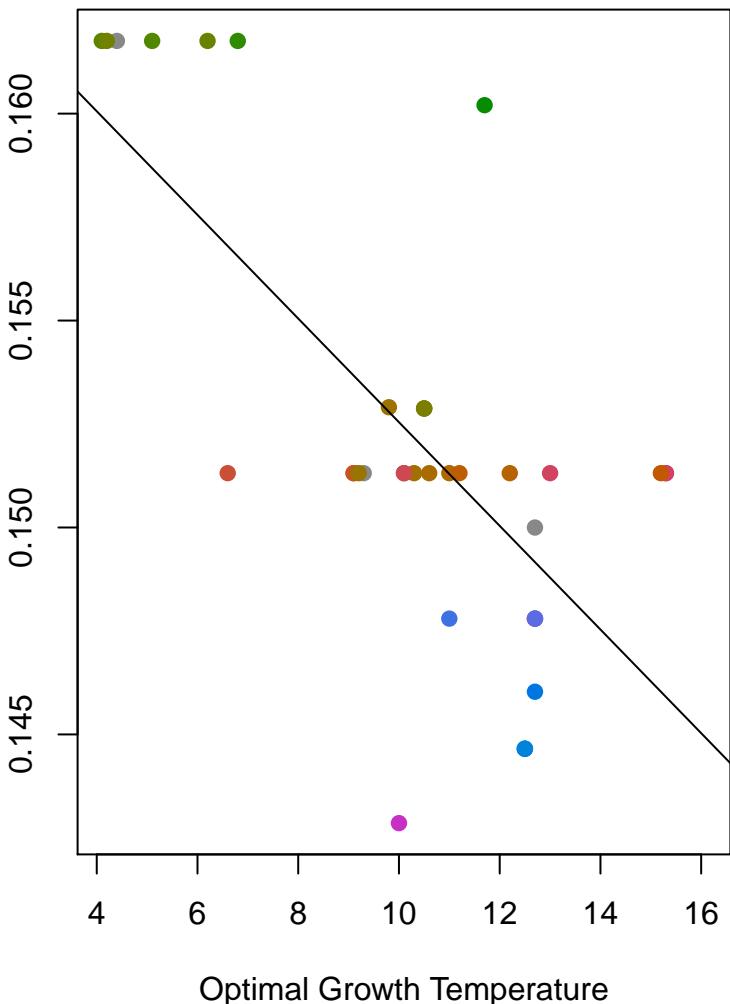
feature.plfam_id.aromaticity.mean
PLF_28228_00007976
hypothetical protein
 $r = -0.703$, $p = 10^{-4.979}$

feature.plfam_id.aromaticity.mean



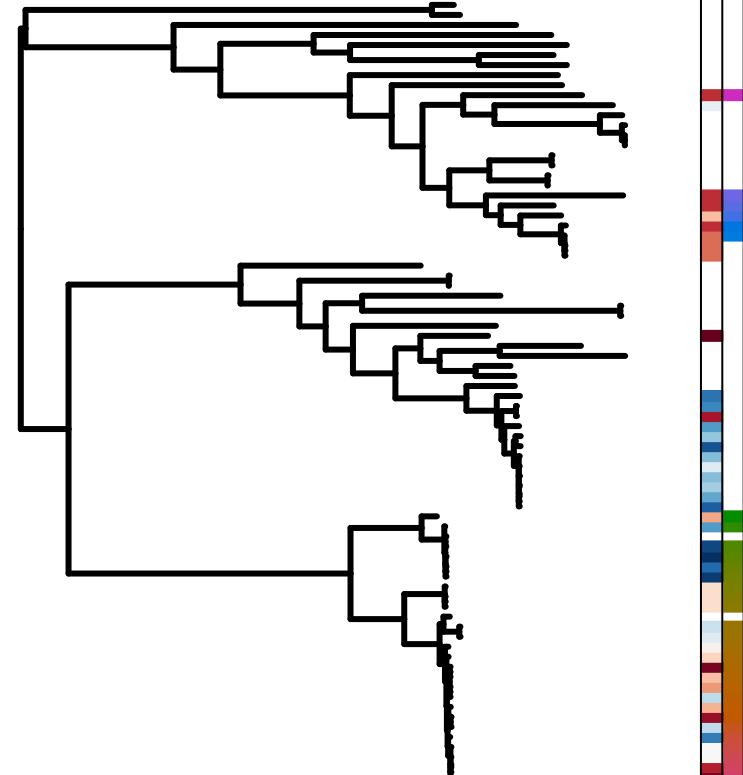
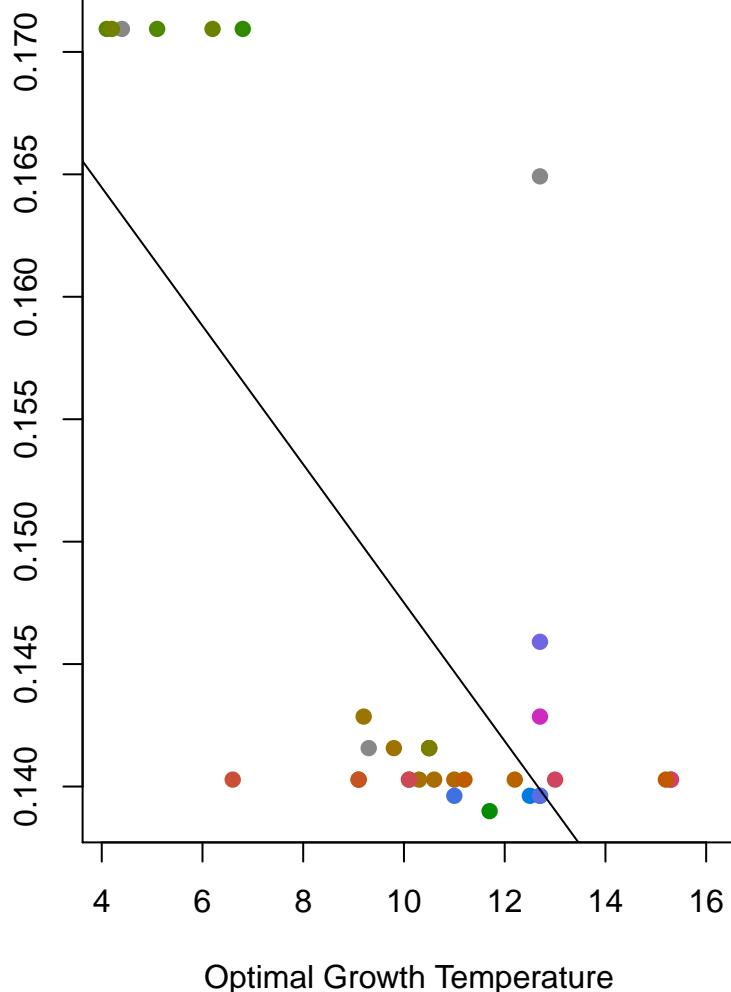
feature.plfam_id.aromaticity.mean
PLF_28228_00001949
Proline iminopeptidase (EC 3.4.11.5)
 $r = -0.704$, $p = 10^{-5.941}$

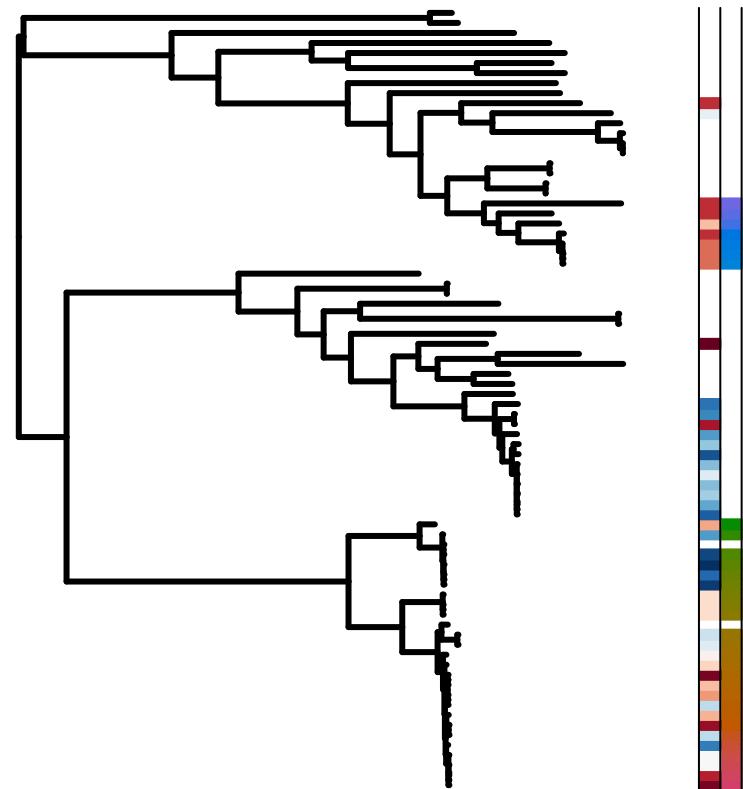
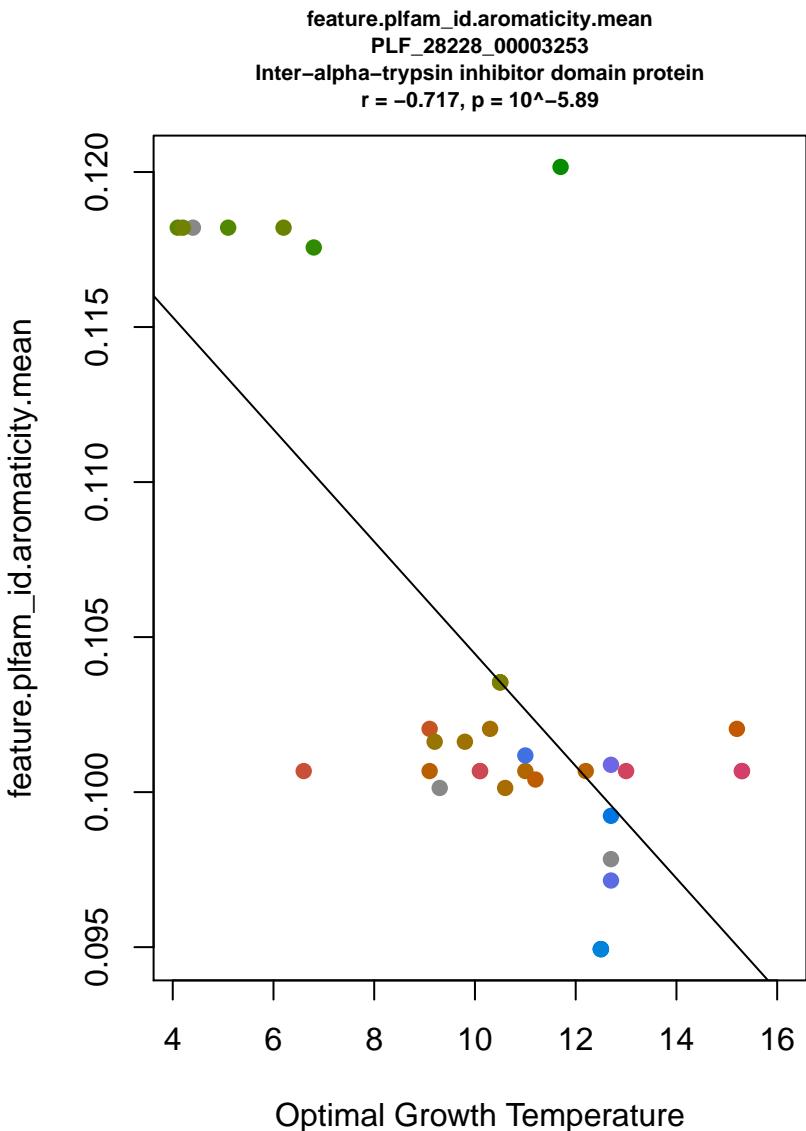
feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00028047
Fatty acid cis/trans isomerase
 $r = -0.712$, $p = 10^{-5.63}$

feature.plfam_id.aromaticity.mean





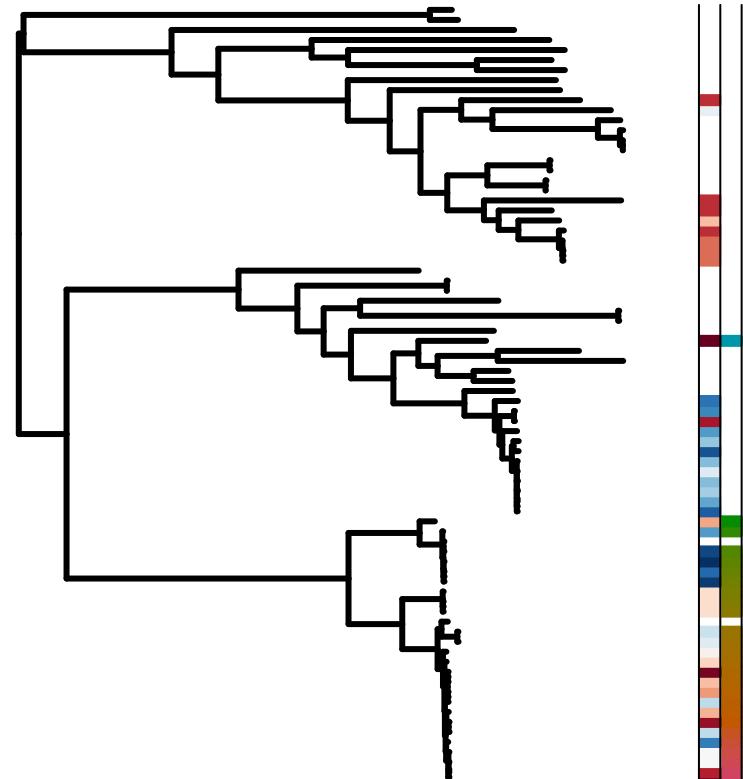
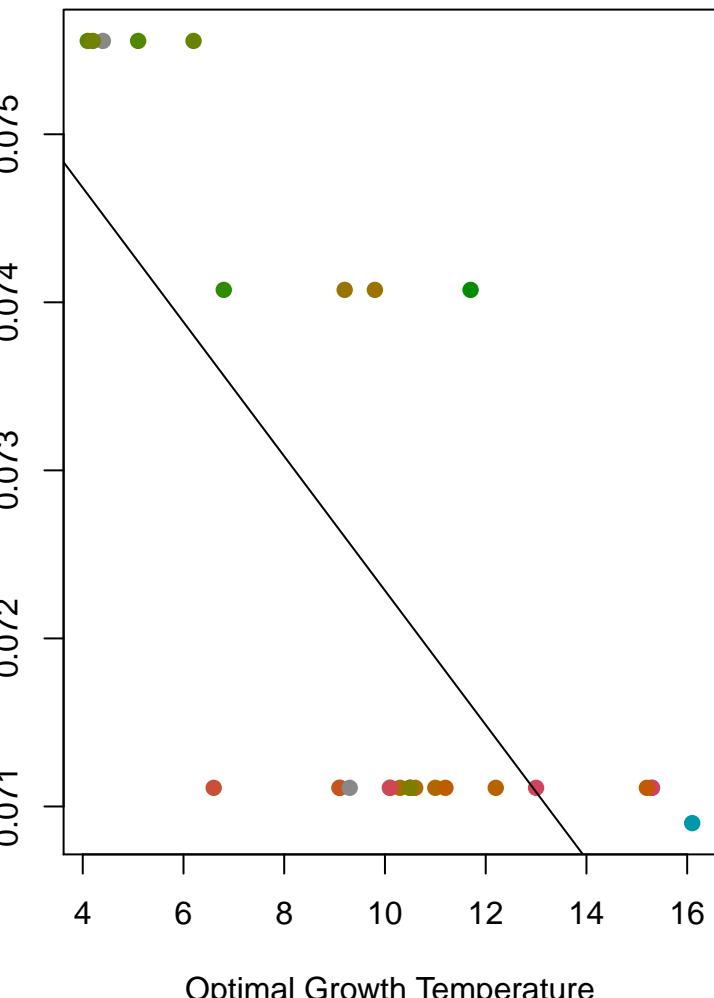
feature.plfam_id.aromaticity.mean

PLF_28228_00022158

Methyl-accepting chemotaxis sensor/transducer protein

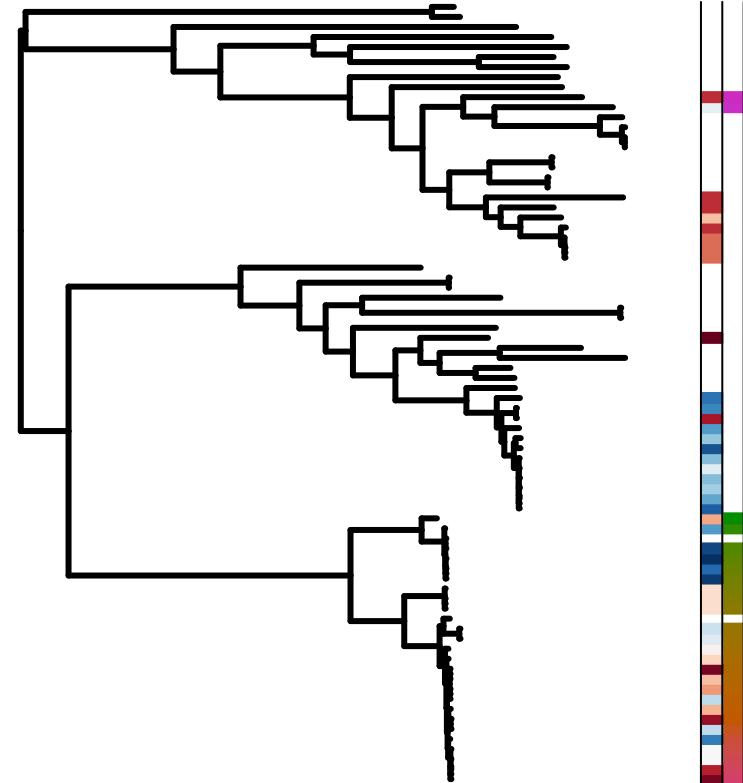
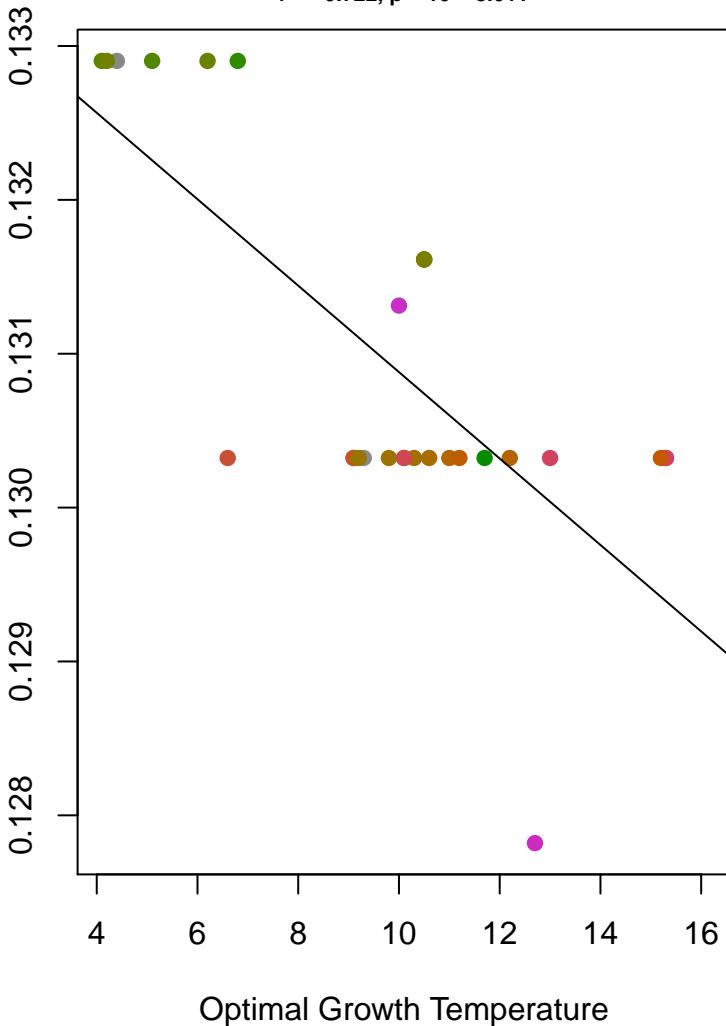
$r = -0.722, p = 10^{-4.836}$

feature.plfam_id.aromaticity.mean



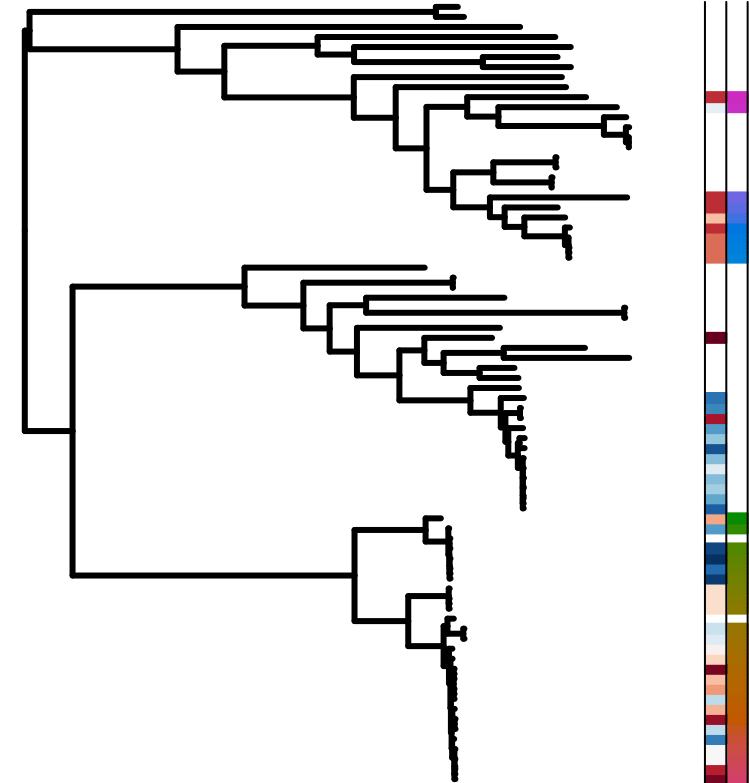
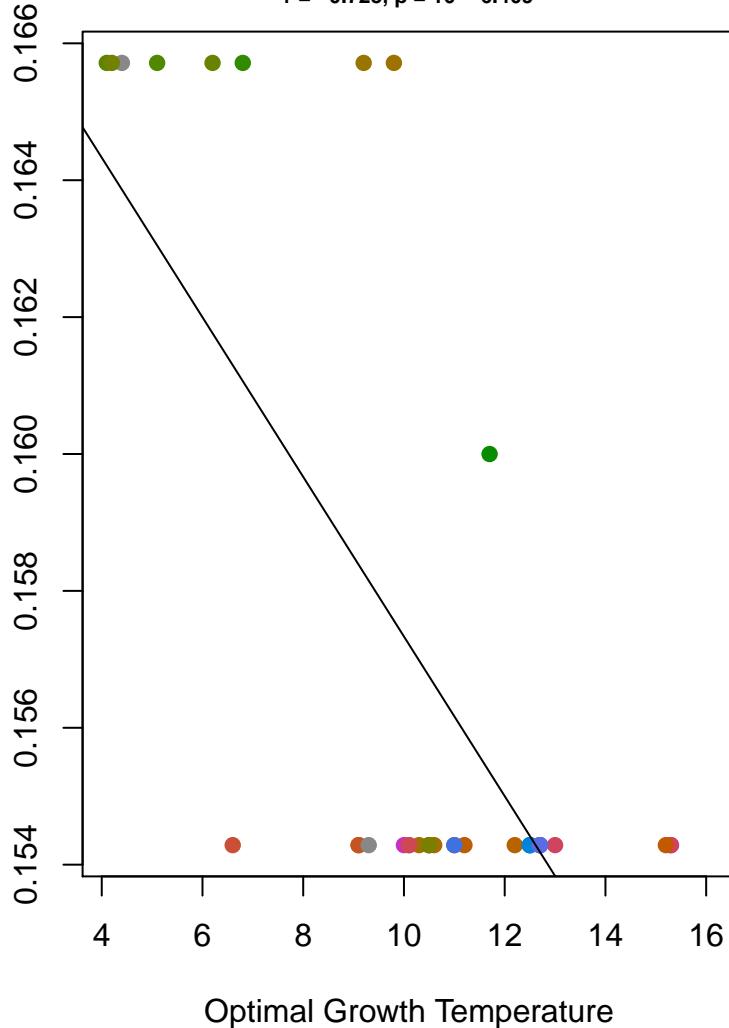
feature.plfam_id.aromaticity.mean
PLF_28228_00002575
Dipeptidyl peptidase IV
 $r = -0.722$, $p = 10^{-5.011}$

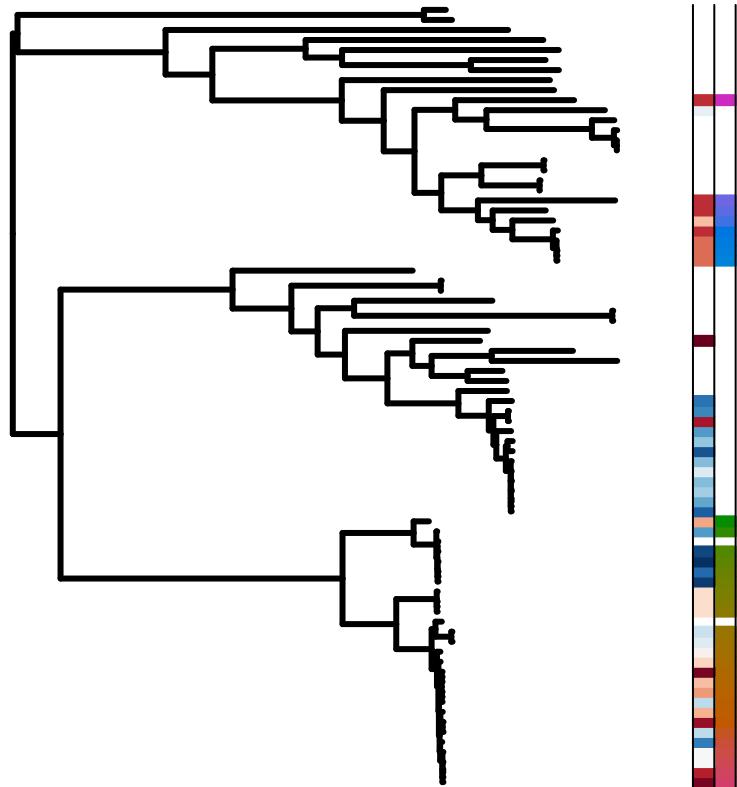
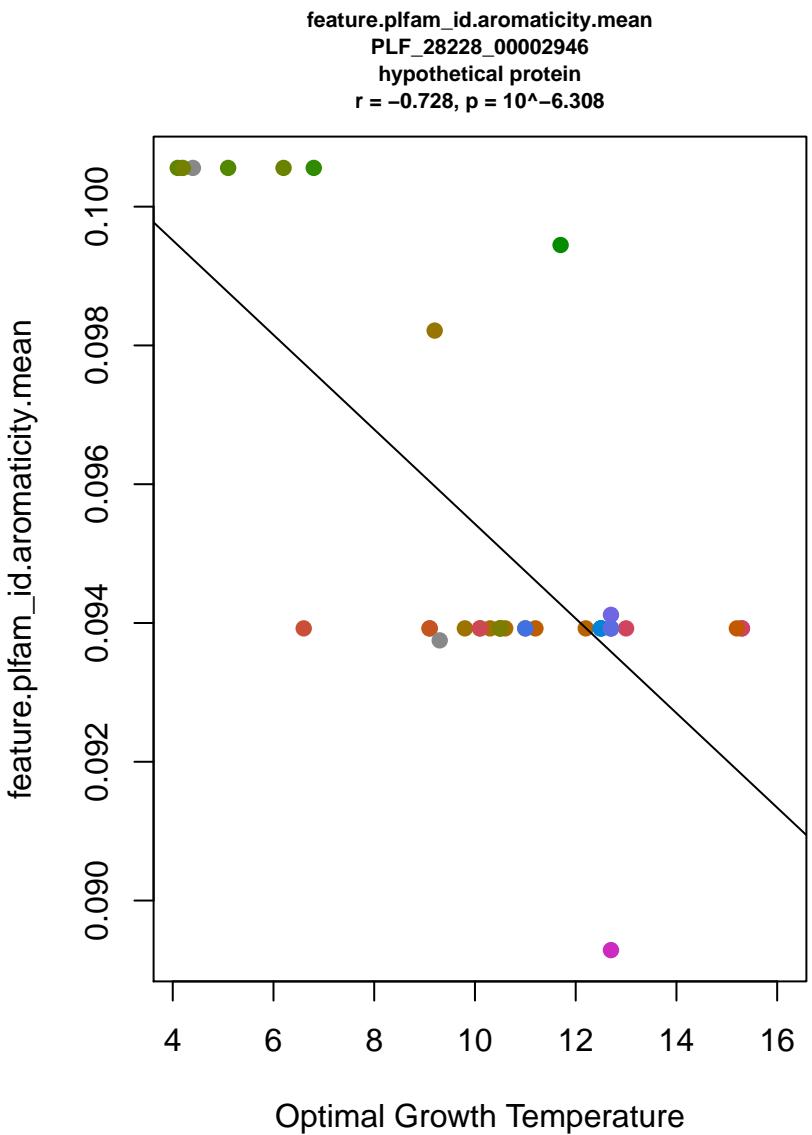
feature.plfam_id.aromaticity.mean

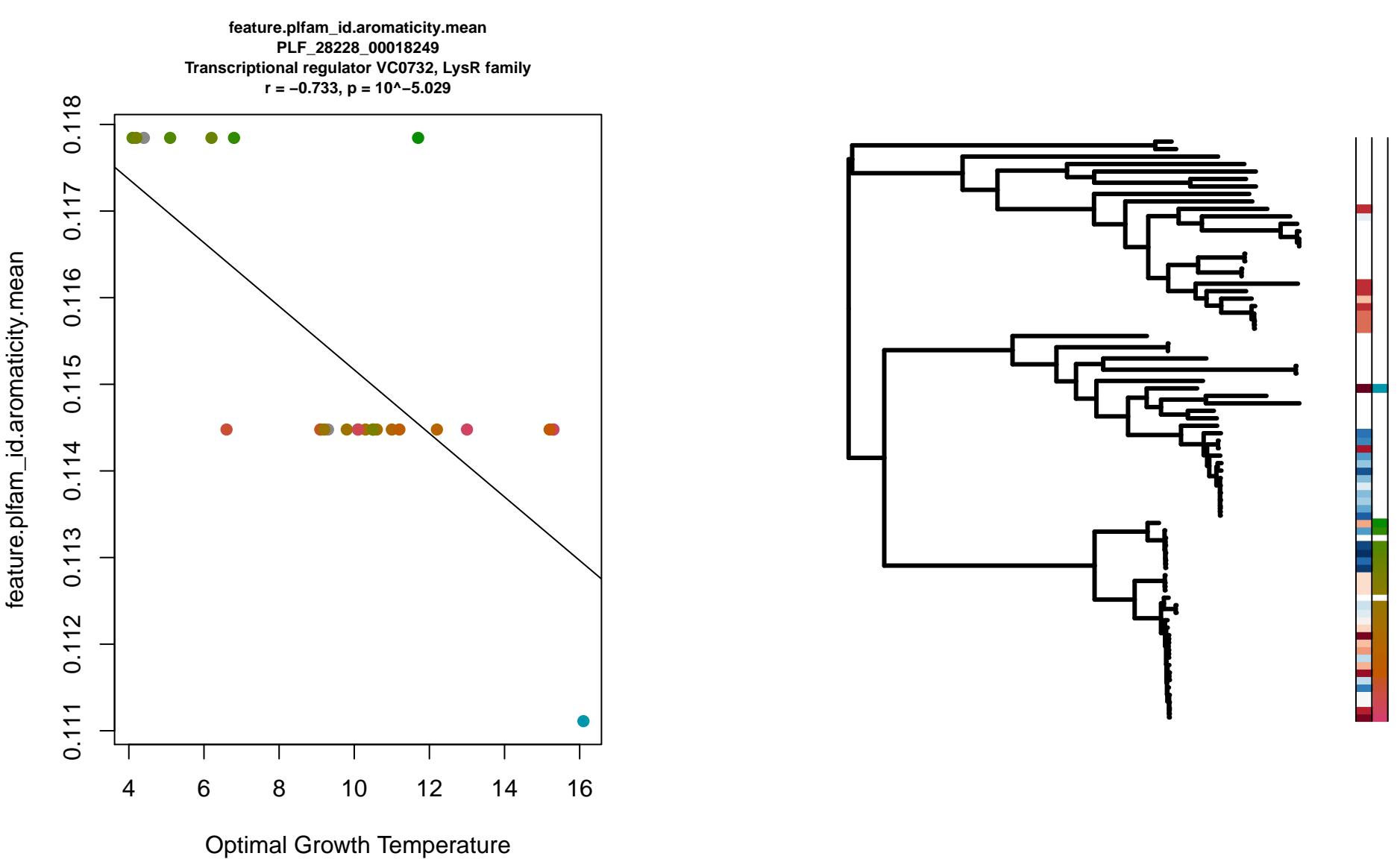


feature.plfam_id.aromaticity.mean
PLF_28228_00001835
Bacterial non-heme ferritin (EC 1.16.3.2)
 $r = -0.725$, $p = 10^{-6.409}$

feature.plfam_id.aromaticity.mean

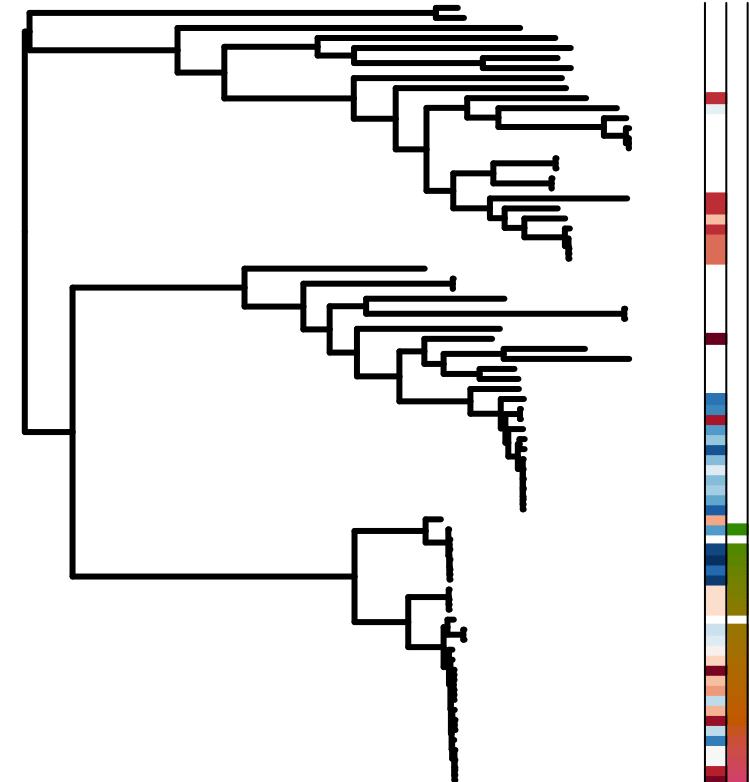
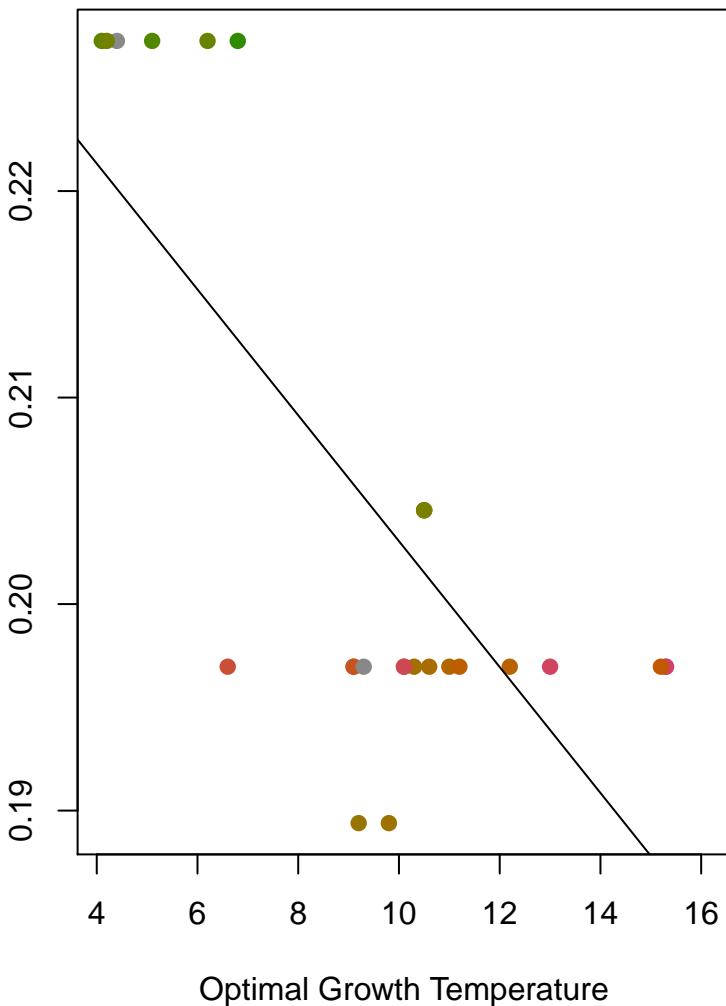






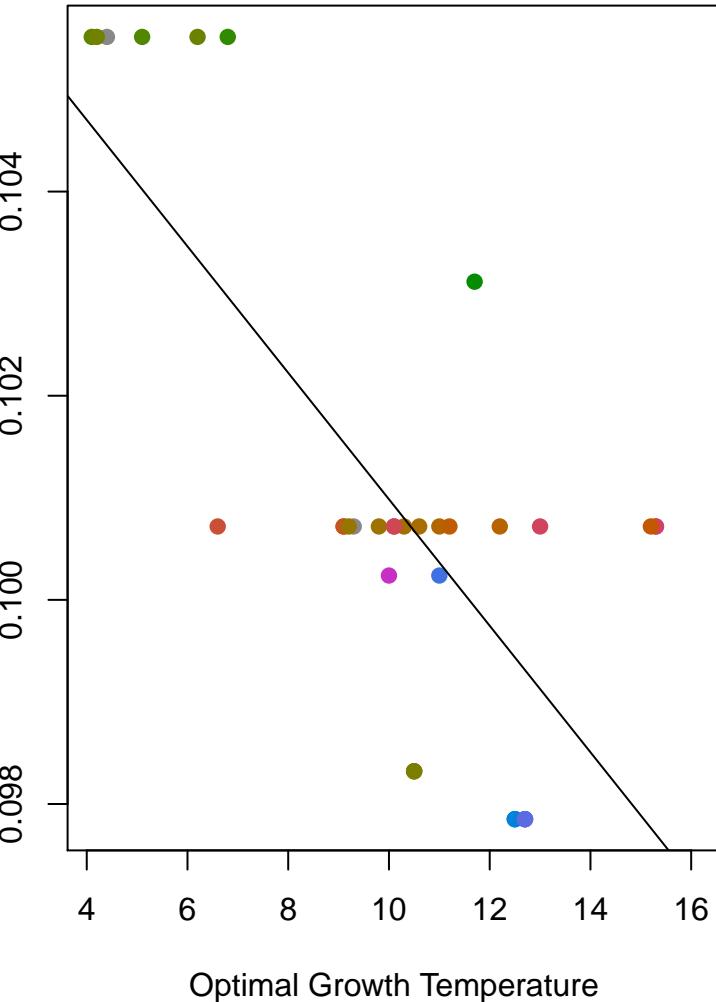
feature.plfam_id.aromaticity.mean
PLF_28228_00030864
hypothetical protein
 $r = -0.739$, $p = 10^{-4.786}$

feature.plfam_id.aromaticity.mean

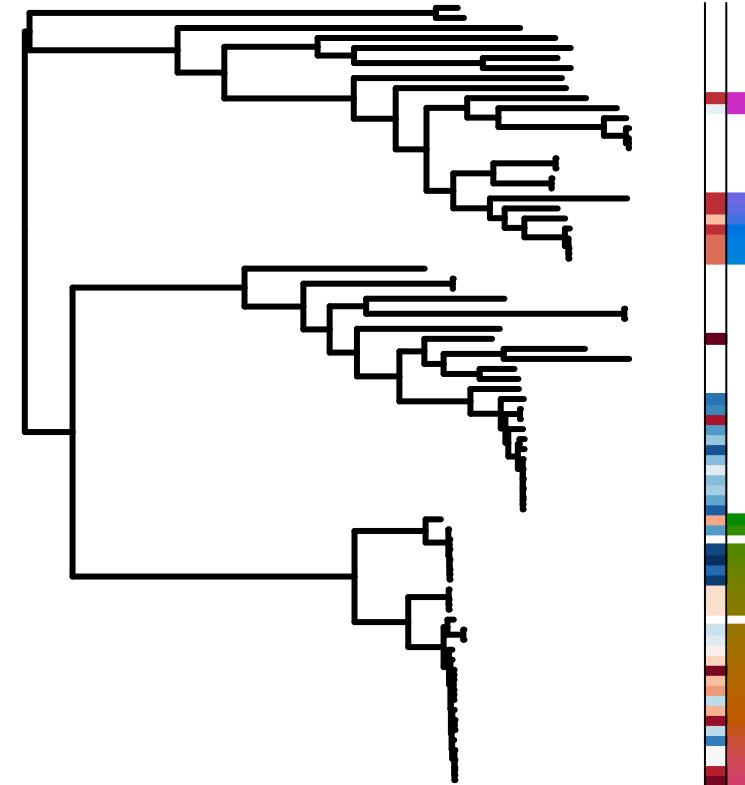


feature.plfam_id.aromaticity.mean
PLF_28228_00002118
Transcriptional regulator
 $r = -0.74$, $p = 10^{-6.601}$

feature.plfam_id.aromaticity.mean

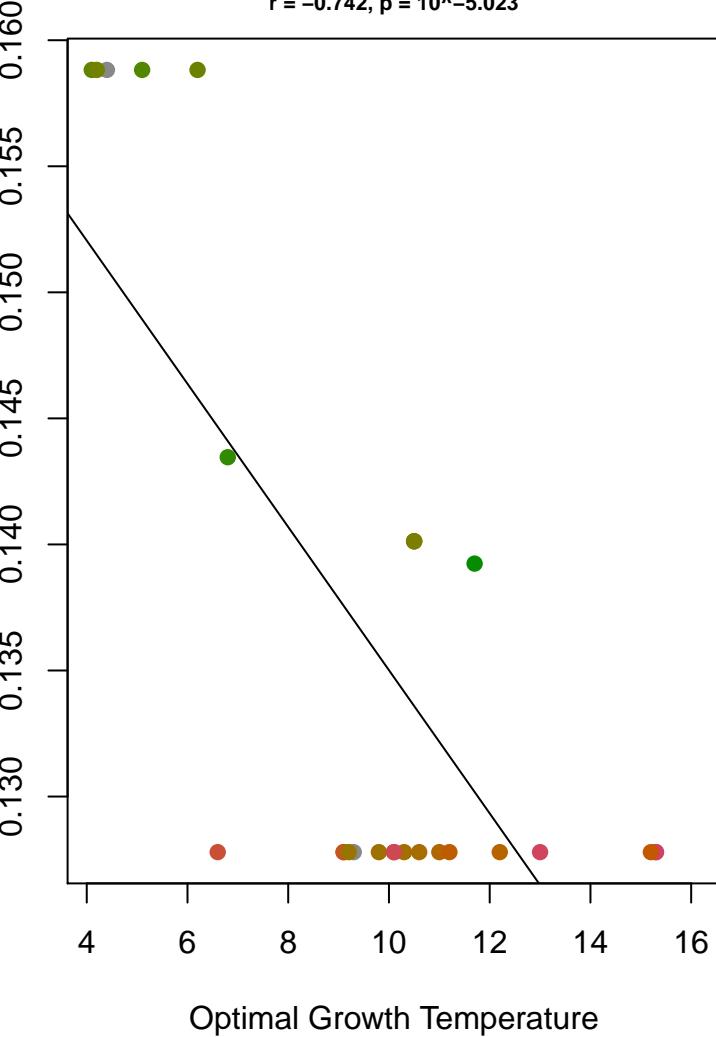


Optimal Growth Temperature

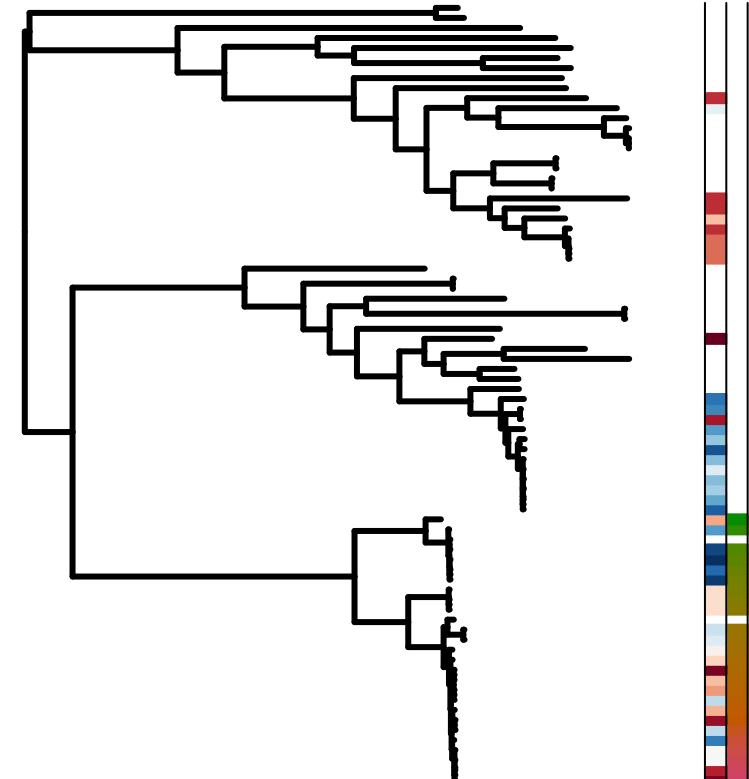


feature.plfam_id.aromaticity.mean
PLF_28228_00011660
Agmatinase (EC 3.5.3.11)
 $r = -0.742$, $p = 10^{-5.023}$

feature.plfam_id.aromaticity.mean



Optimal Growth Temperature



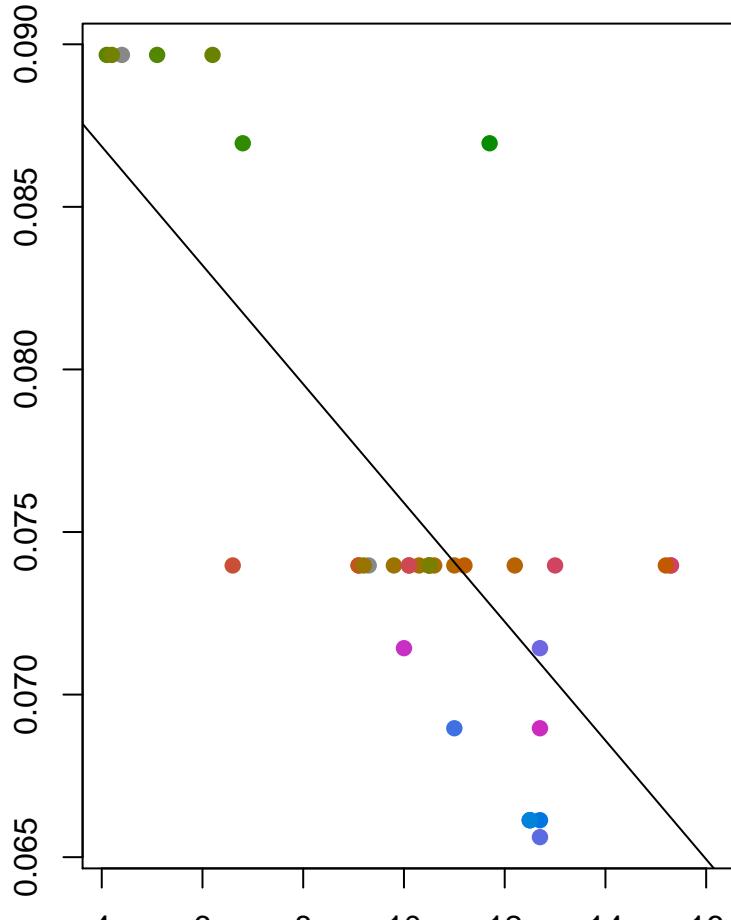
feature.plfam_id.aromaticity.mean

PLF_28228_00001942

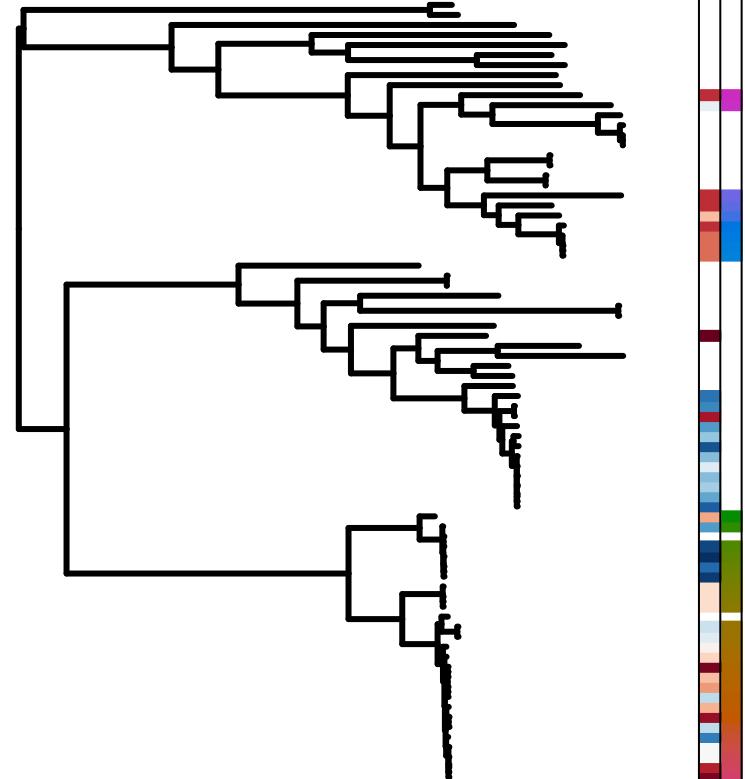
CzcABC family efflux RND transporter, membrane fusion protein

$r = -0.745, p = 10^{-6.715}$

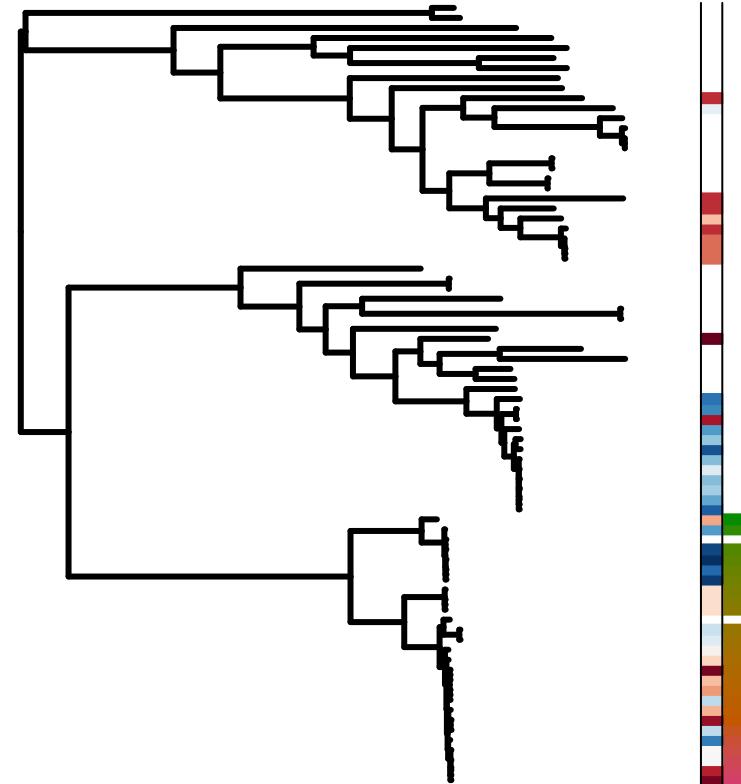
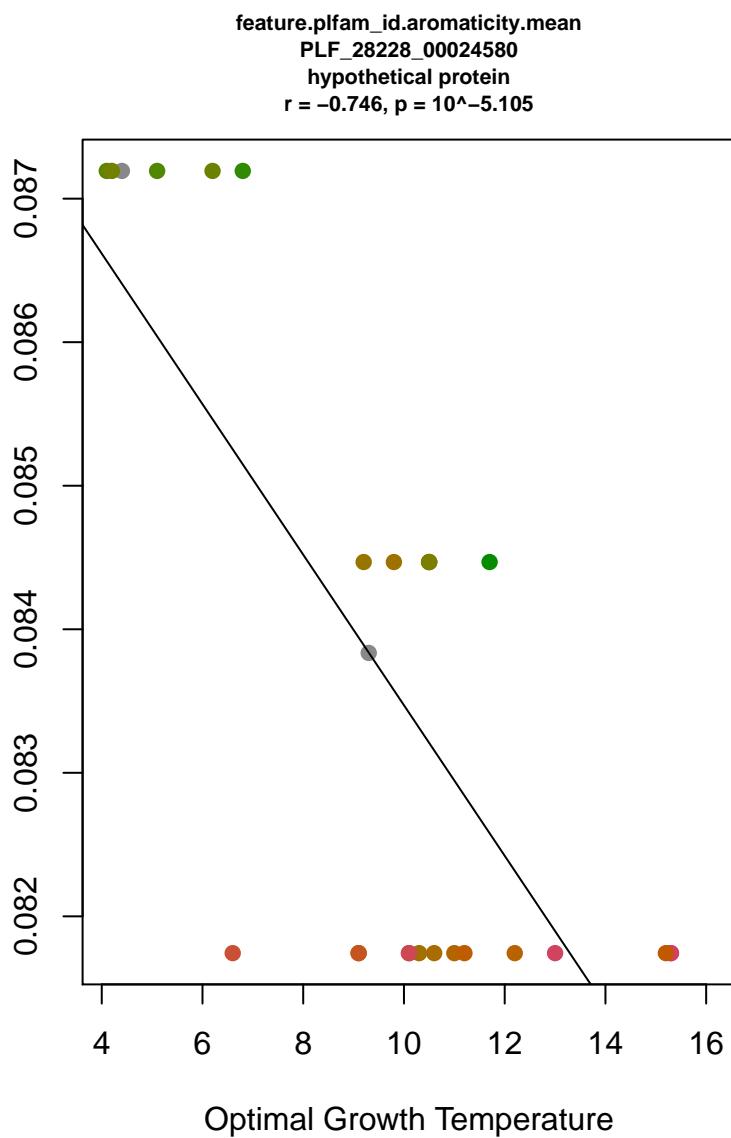
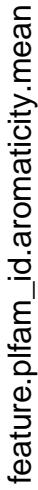
feature.plfam_id.aromaticity.mean



Optimal Growth Temperature

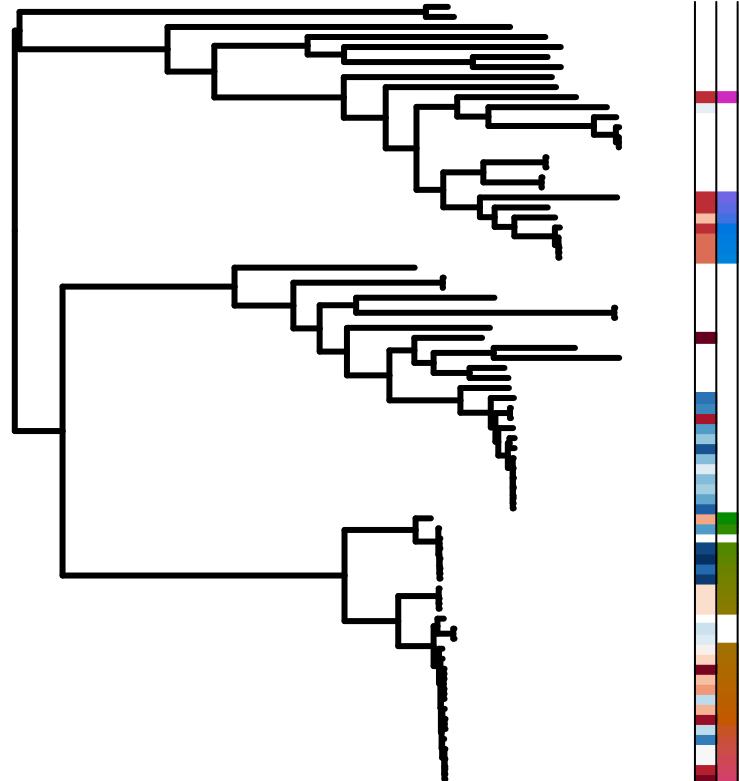
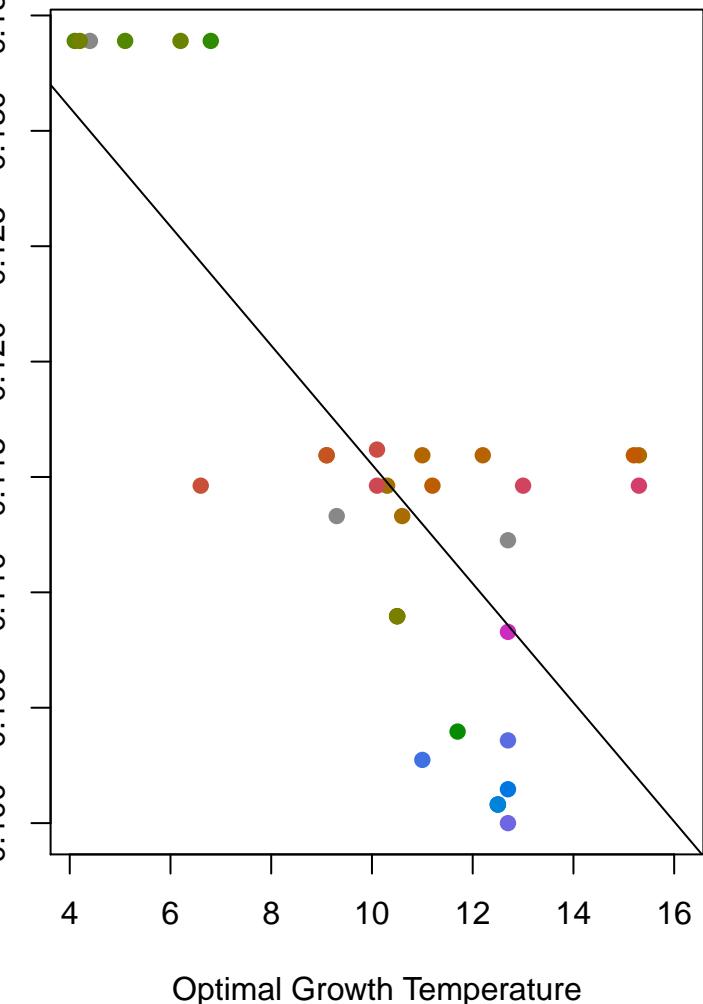


feature.plfam_id.aromaticity.mean
PLF_28228_00024580
hypothetical protein
 $r = -0.746$, $p = 10^{-5.105}$



feature.plfam_id.aromaticity.mean
PLF_28228_00002829
TonB-dependent receptor
 $r = -0.751$, $p = 10^{-6.515}$

feature.plfam_id.aromaticity.mean



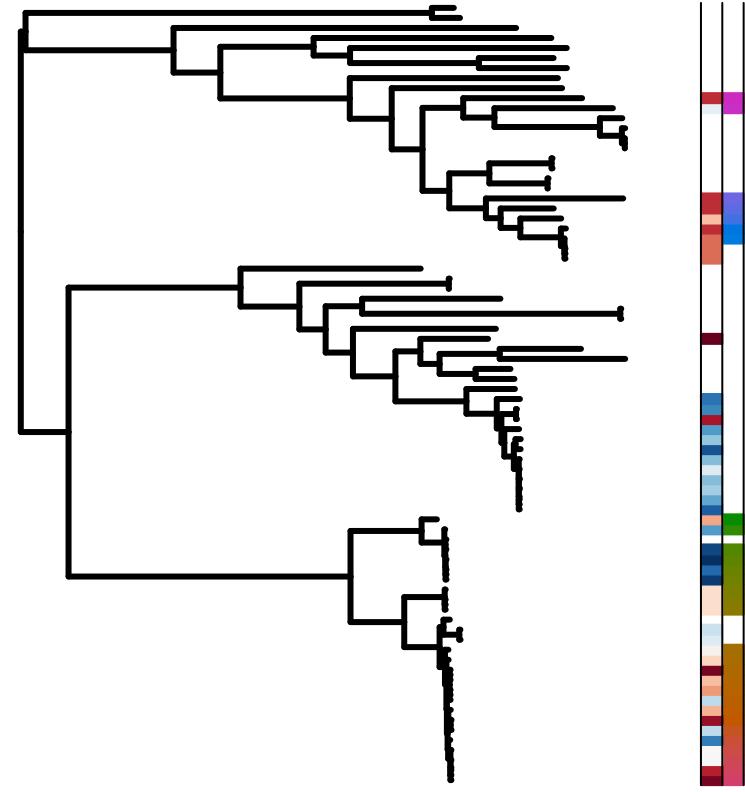
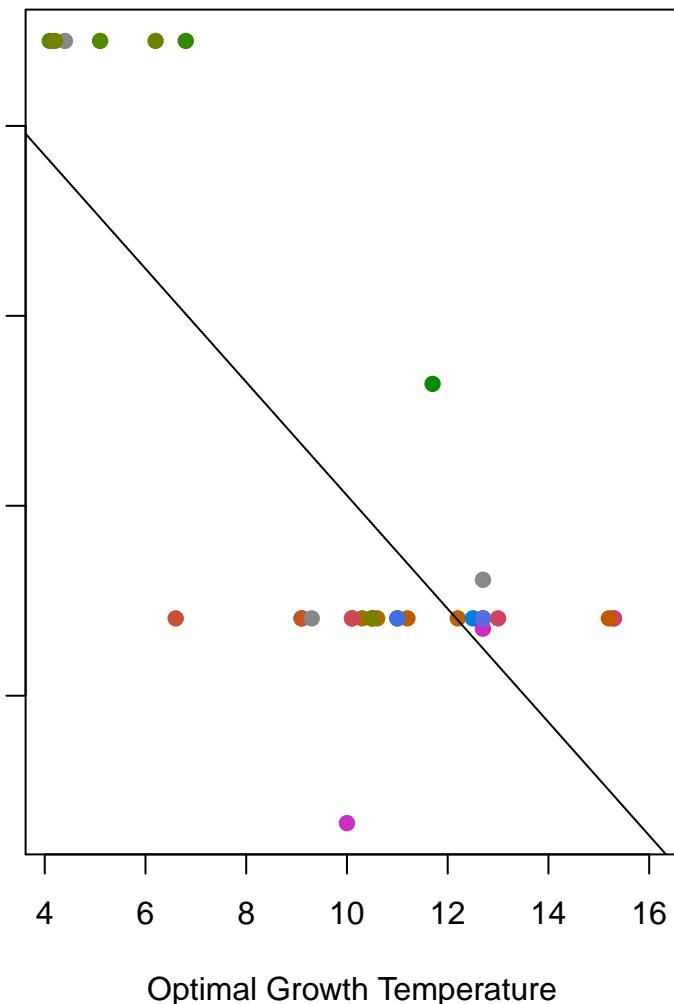
feature.plfam_id.aromaticity.mean

PLF_28228_00014184

Uncharacterized ferredoxin-like protein YfhL

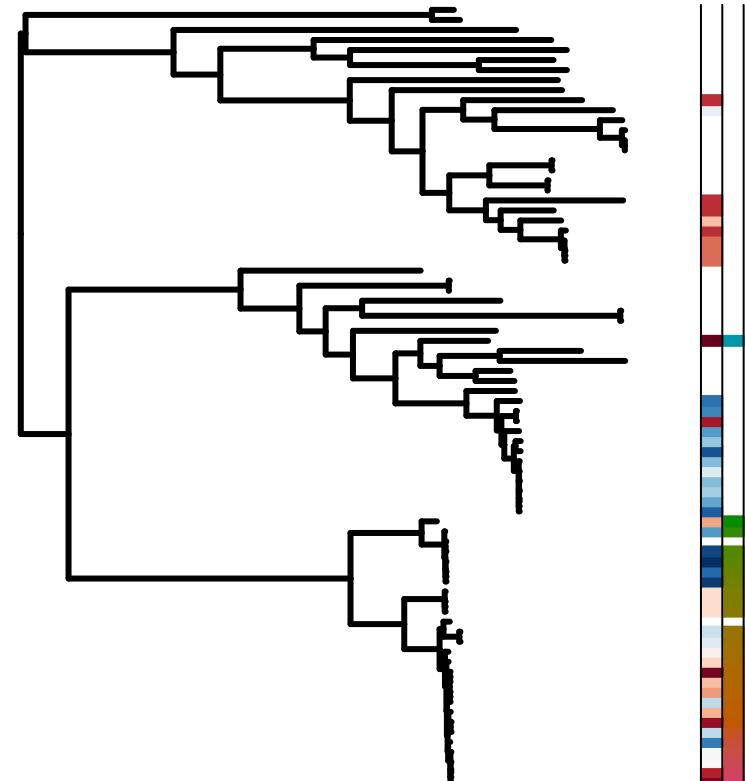
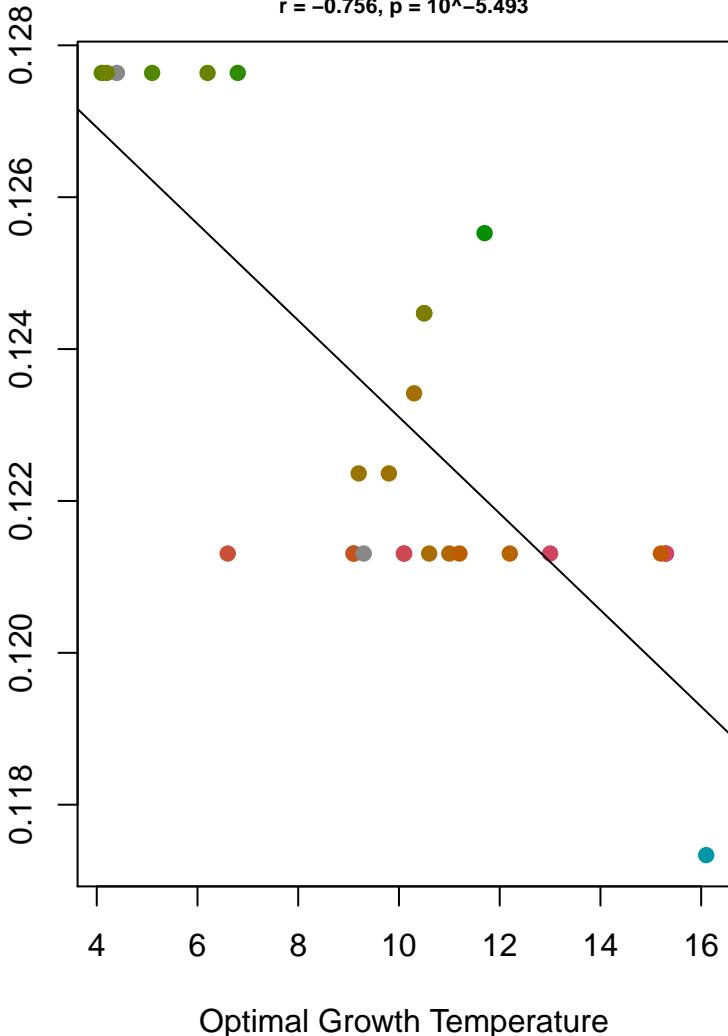
$r = -0.756, p = 10^{-6.448}$

feature.plfam_id.aromaticity.mean



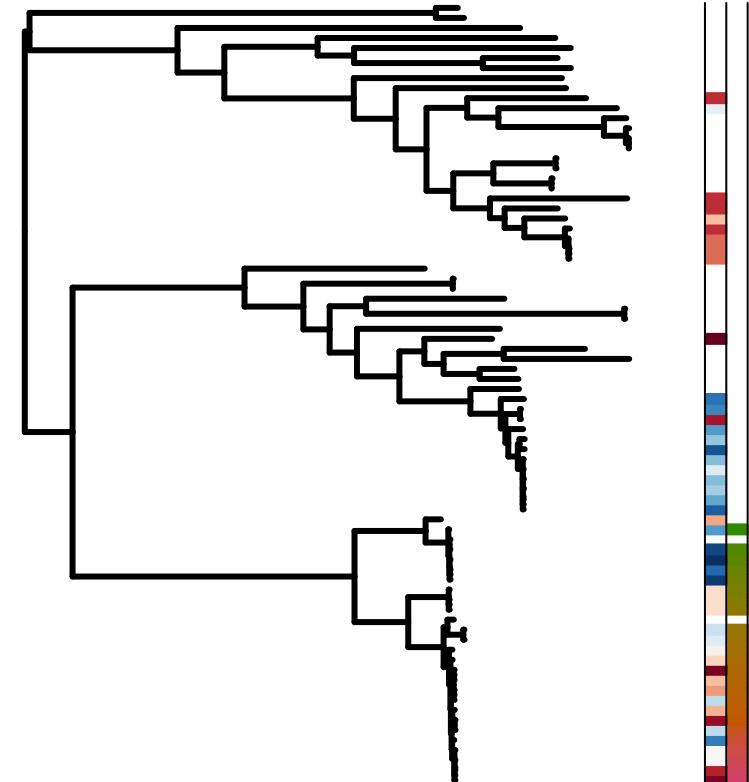
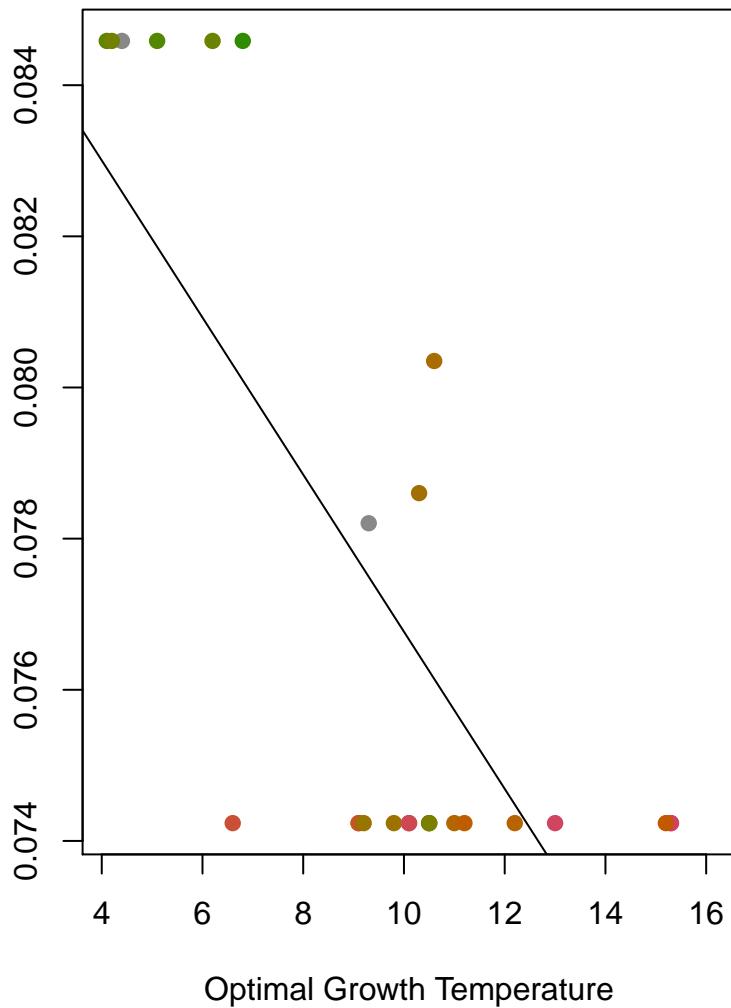
feature.plfam_id.aromaticity.mean
PLF_28228_00013222
hypothetical protein
 $r = -0.756$, $p = 10^{-5.493}$

feature.plfam_id.aromaticity.mean



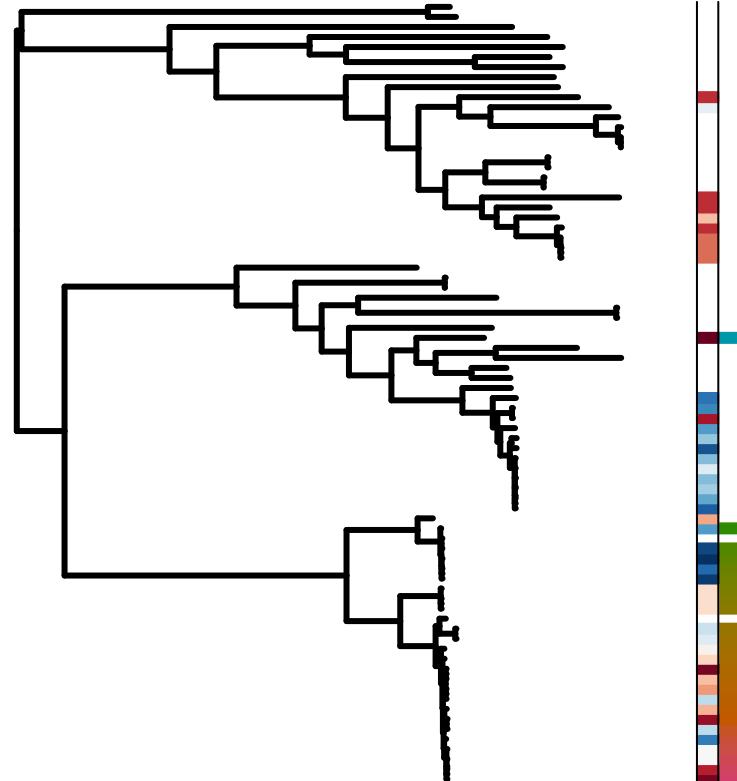
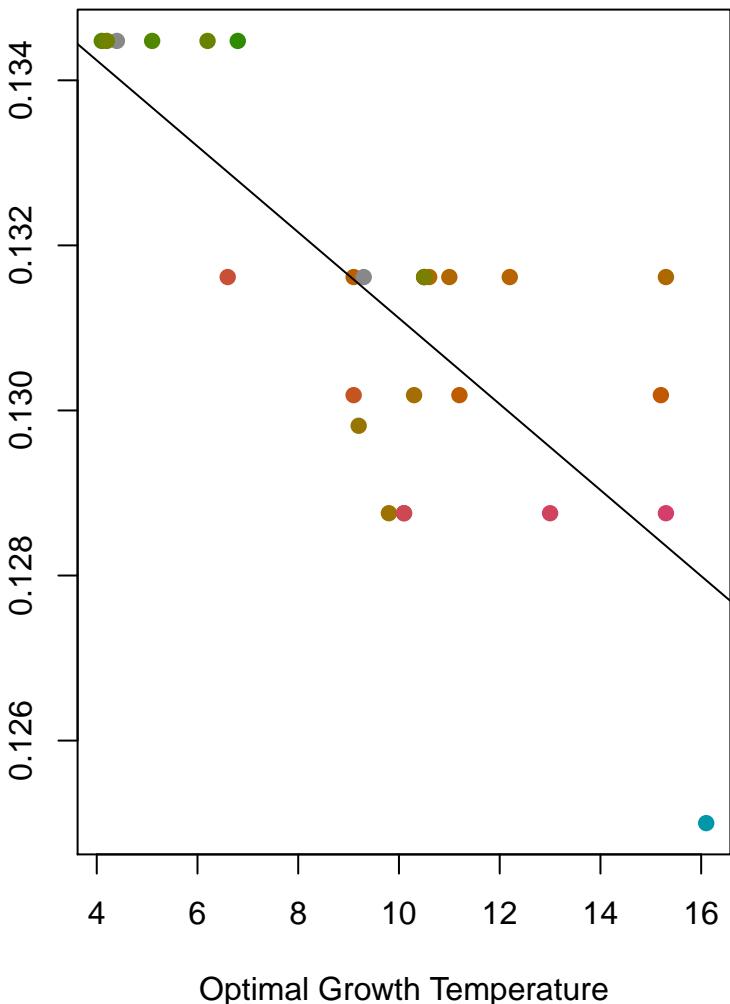
feature.plfam_id.aromaticity.mean
PLF_28228_00015307
hypothetical protein
 $r = -0.757$, $p = 10^{-5.113}$

feature.plfam_id.aromaticity.mean



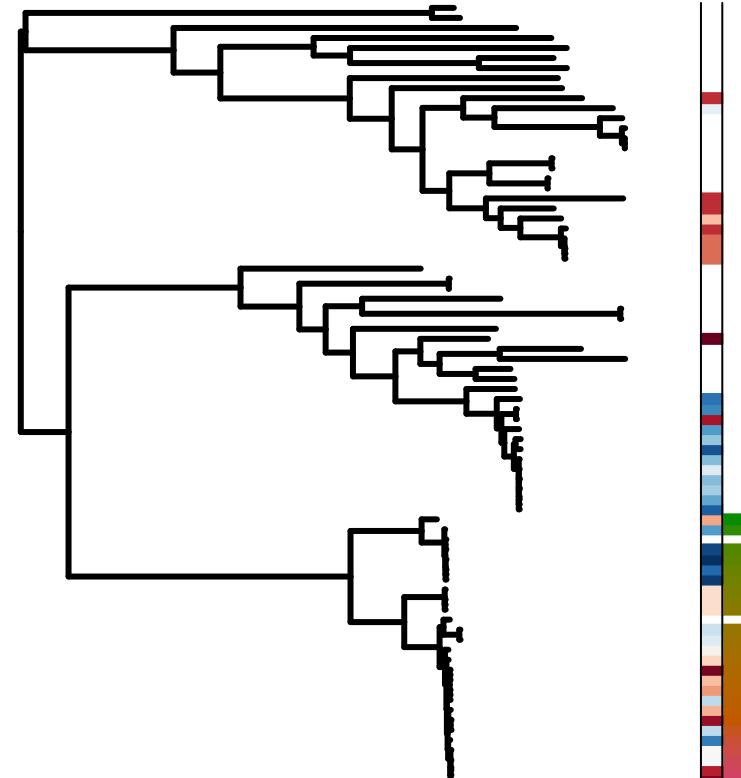
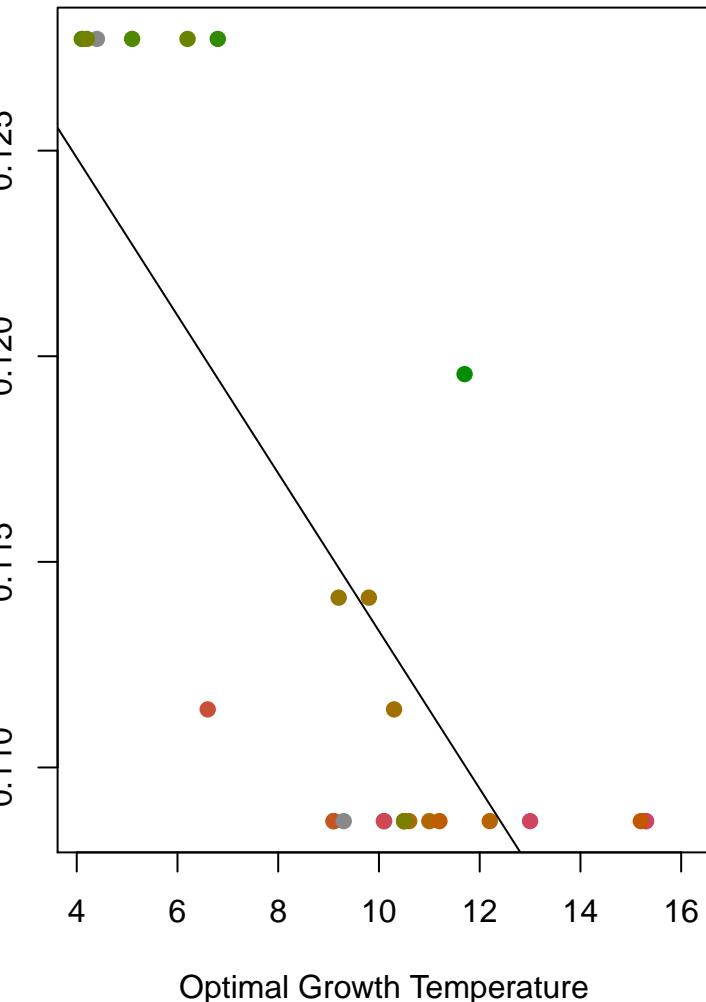
feature.plfam_id.aromaticity.mean
PLF_28228_00016855
hypothetical protein
 $r = -0.761$, $p = 10^{-5.389}$

feature.plfam_id.aromaticity.mean



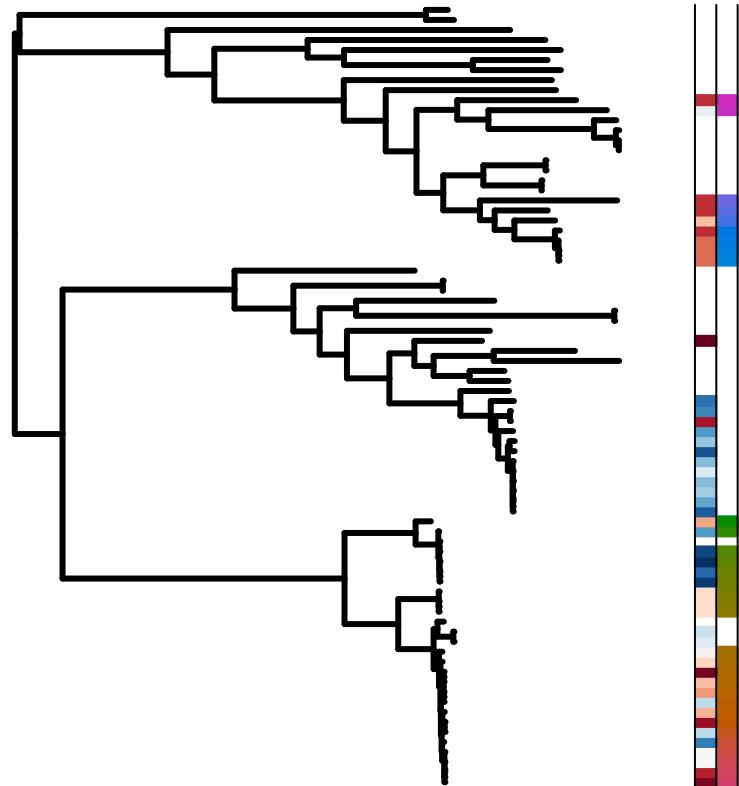
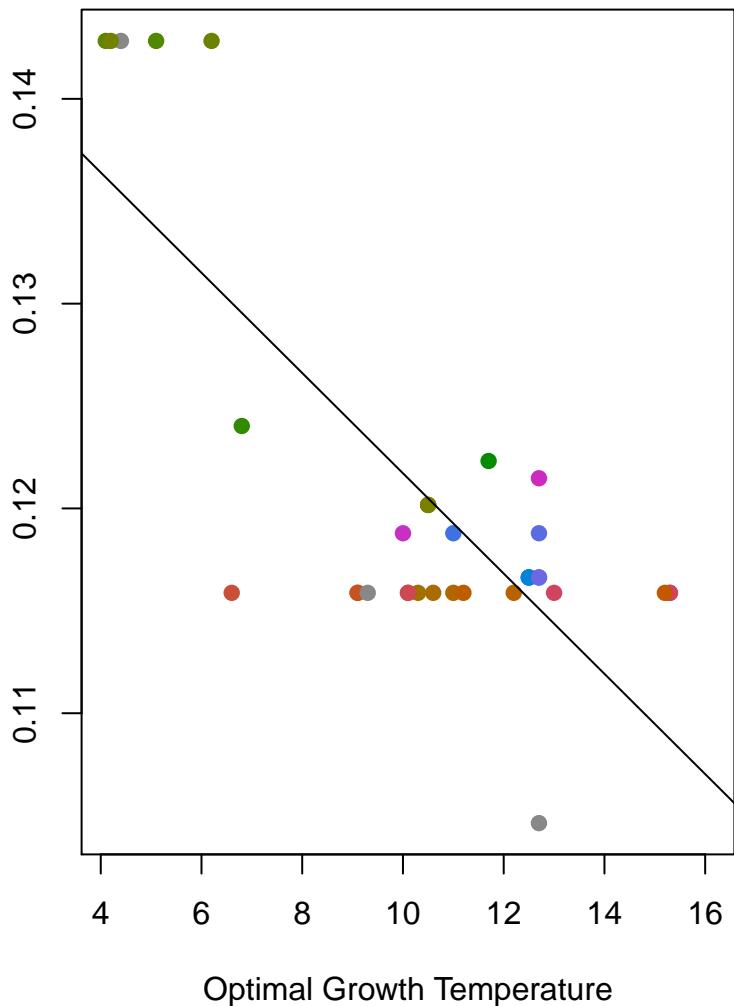
feature.plfam_id.aromaticity.mean
PLF_28228_00032200
hypothetical protein
 $r = -0.773$, $p = 10^{-5.641}$

feature.plfam_id.aromaticity.mean



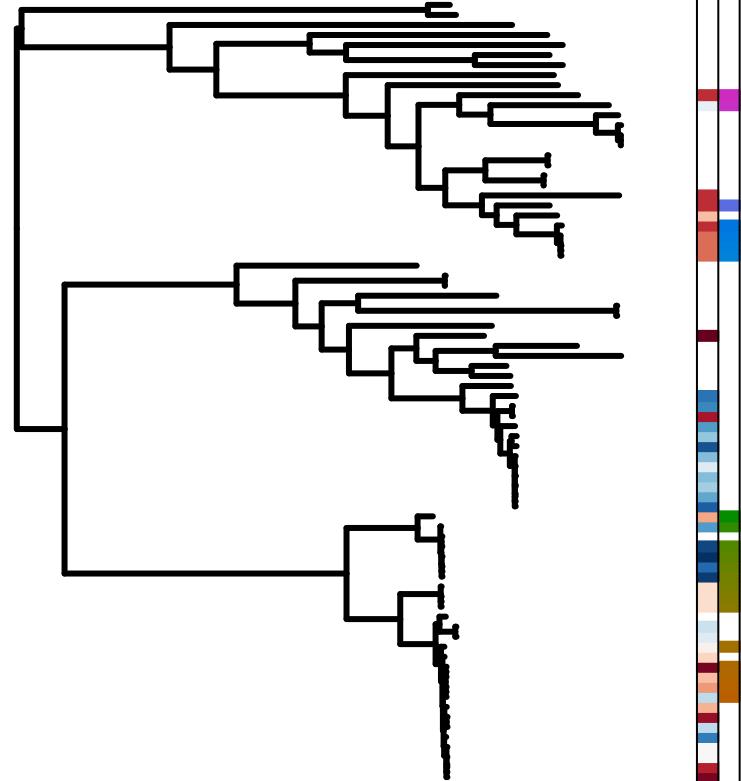
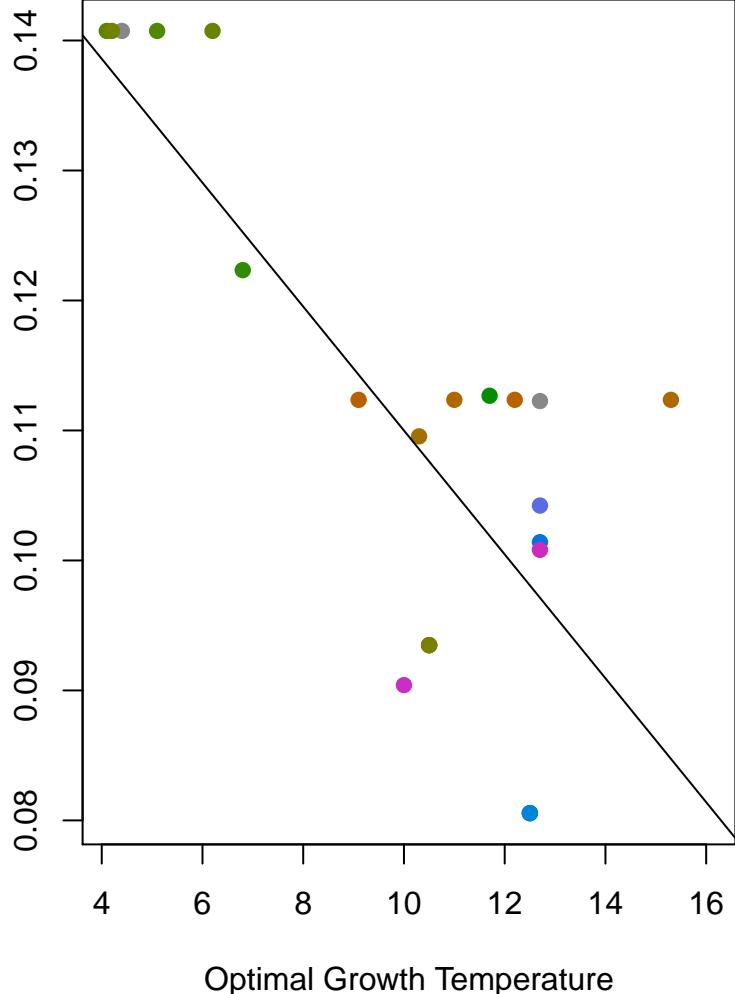
feature.plfam_id.aromaticity.mean
PLF_28228_00001289
Uncharacterized protease YegQ
 $r = -0.774$, $p = 10^{-7.299}$

feature.plfam_id.aromaticity.mean



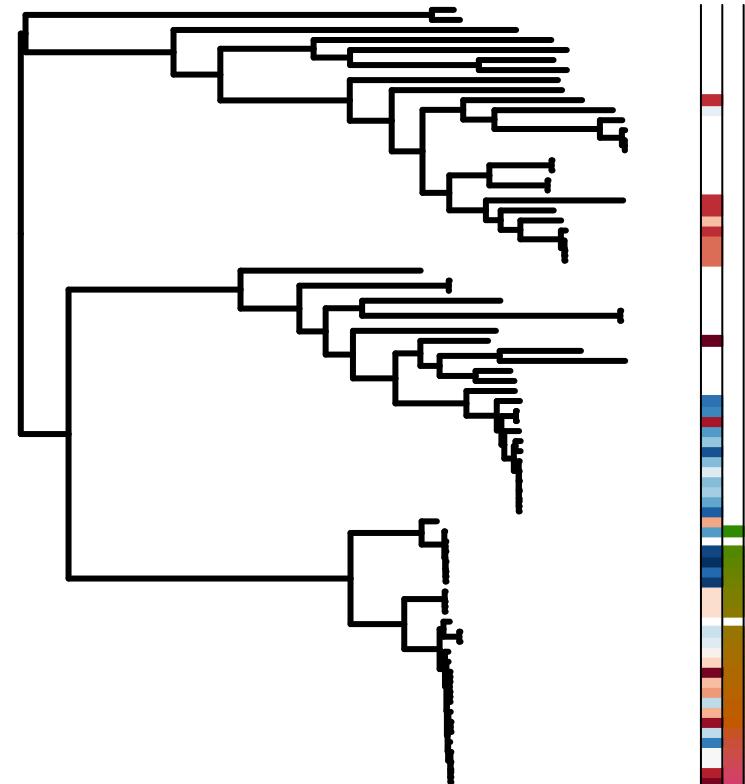
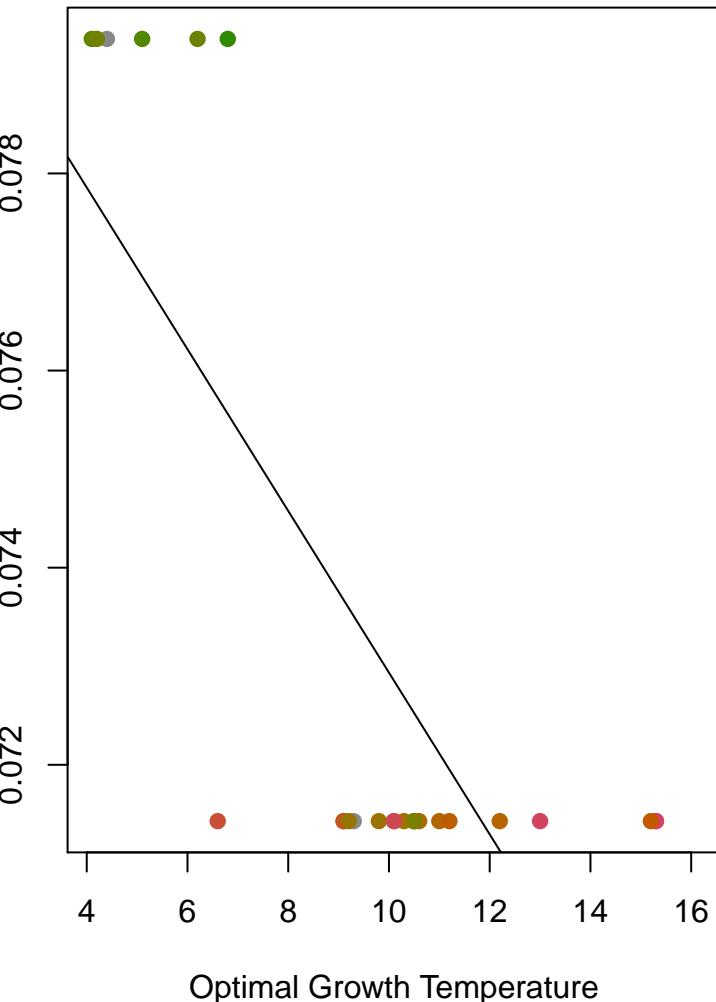
feature.plfam_id.aromaticity.mean
PLF_28228_00001912
Phage integrase
 $r = -0.774$, $p = 10^{-4.833}$

feature.plfam_id.aromaticity.mean



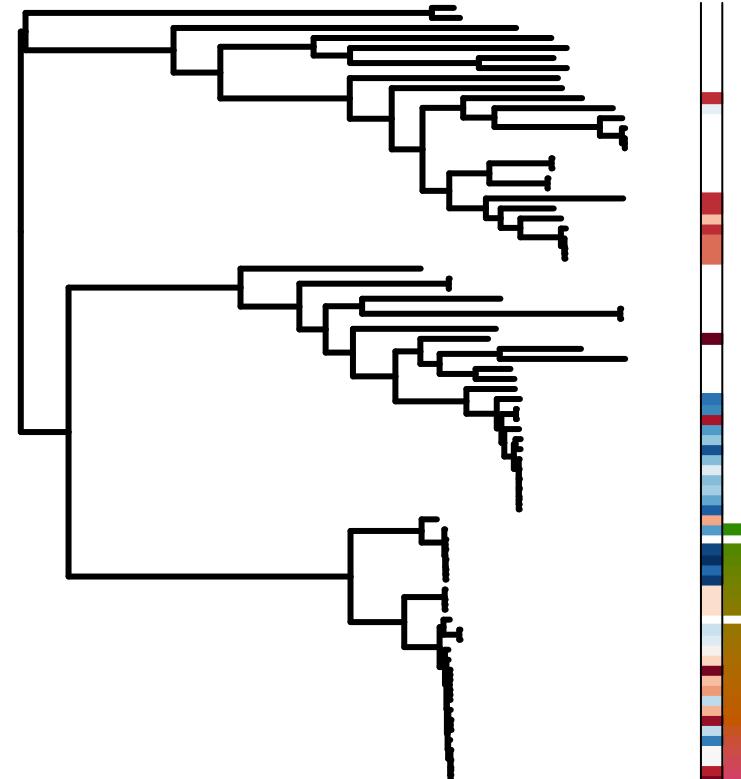
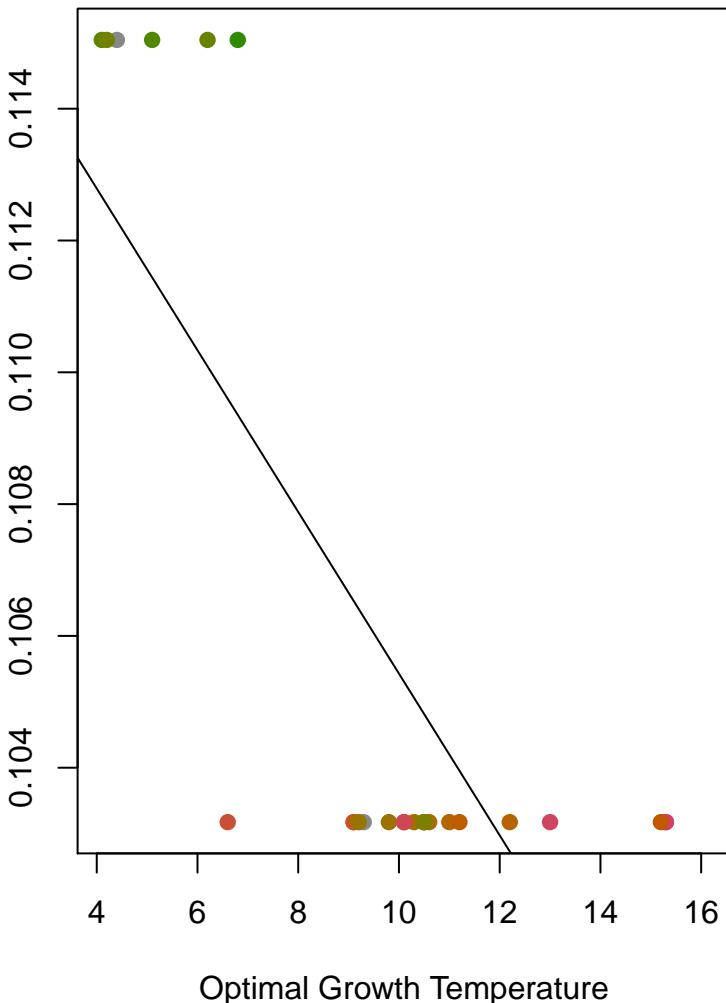
feature.plfam_id.aromaticity.mean
PLF_28228_00030463
hypothetical protein
 $r = -0.775$, $p = 10^{-5.478}$

feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00030076
hypothetical protein
 $r = -0.775$, $p = 10^{-5.478}$

feature.plfam_id.aromaticity.mean



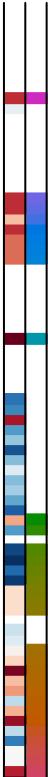
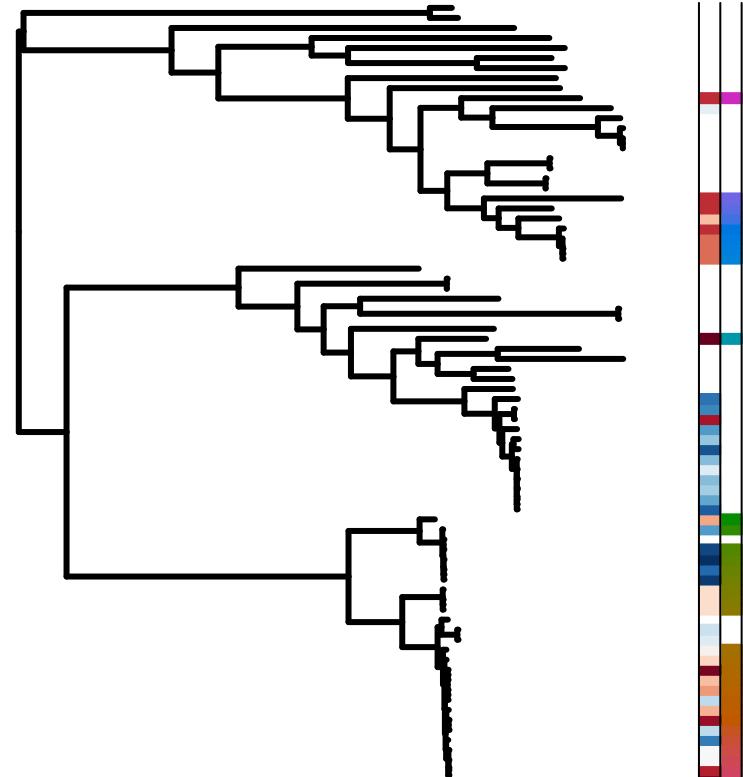
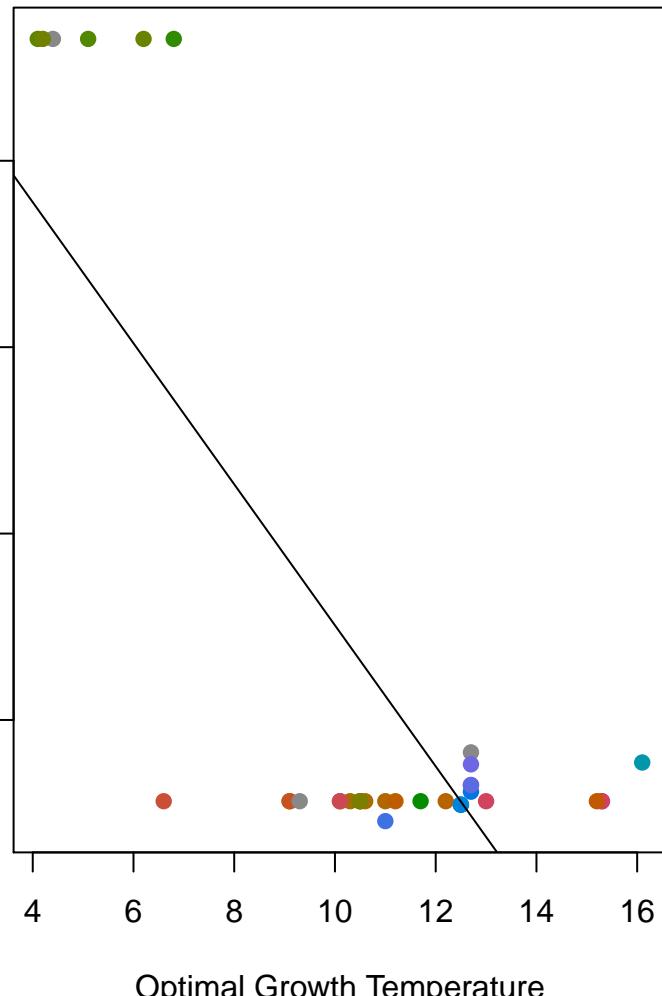
feature.plfam_id.aromaticity.mean

PLF_28228_00002798

Two-component transcriptional response regulator, OmpR family

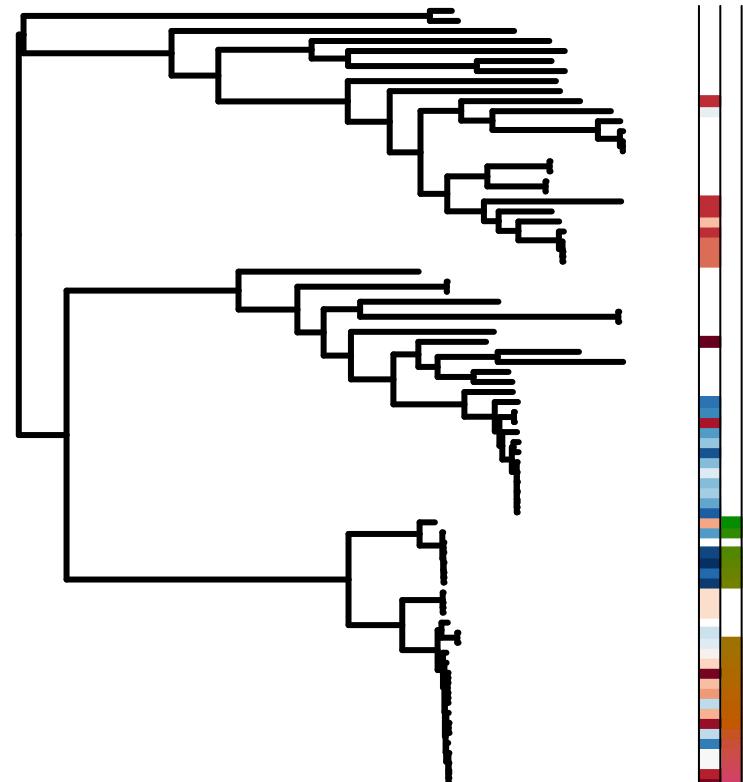
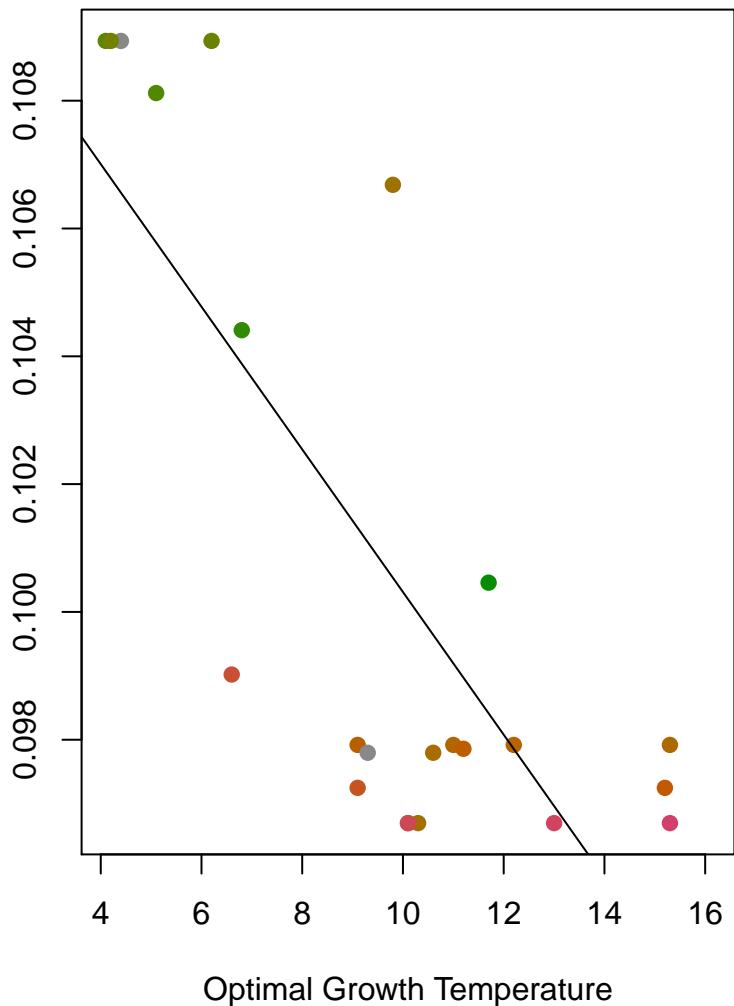
$r = -0.777$, $p = 10^{-7.395}$

feature.plfam_id.aromaticity.mean



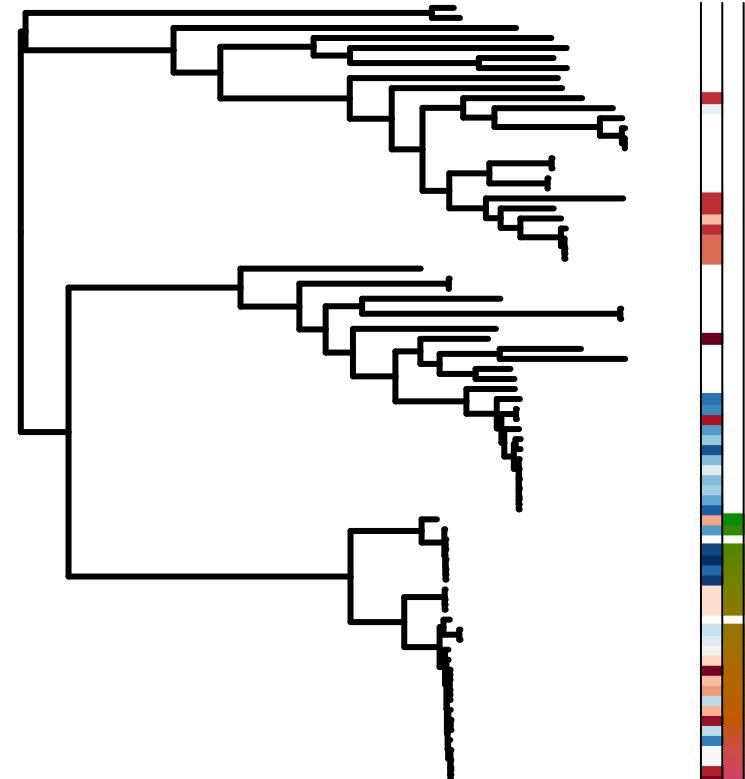
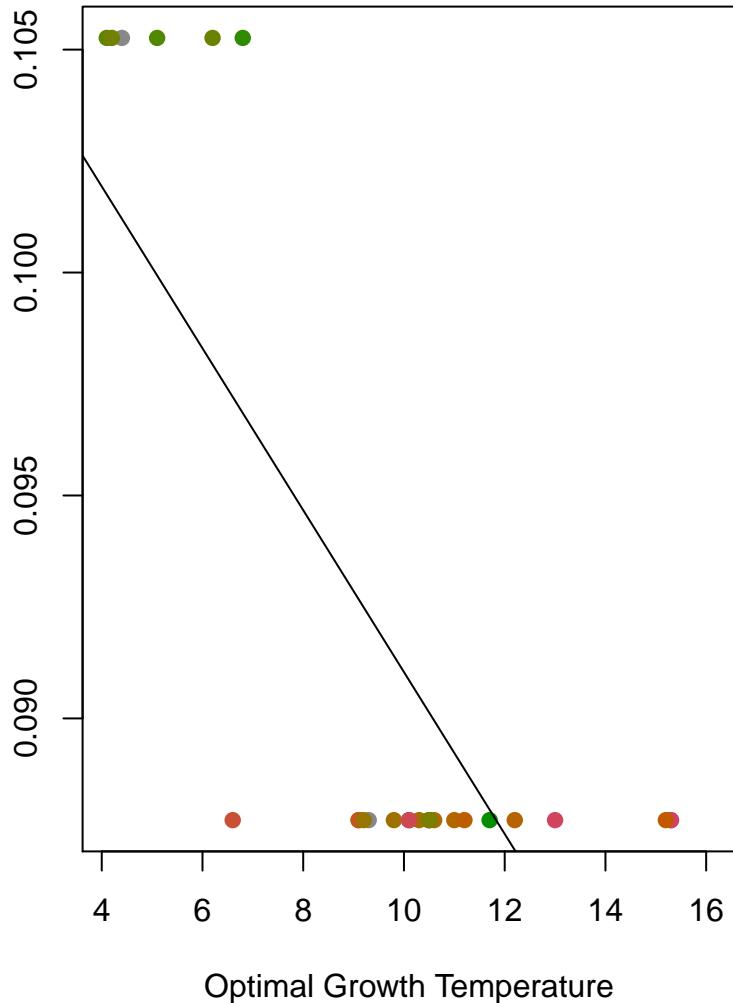
feature.plfam_id.aromaticity.mean
PLF_28228_00005302
hypothetical protein
 $r = -0.777$, $p = 10^{-4.895}$

feature.plfam_id.aromaticity.mean

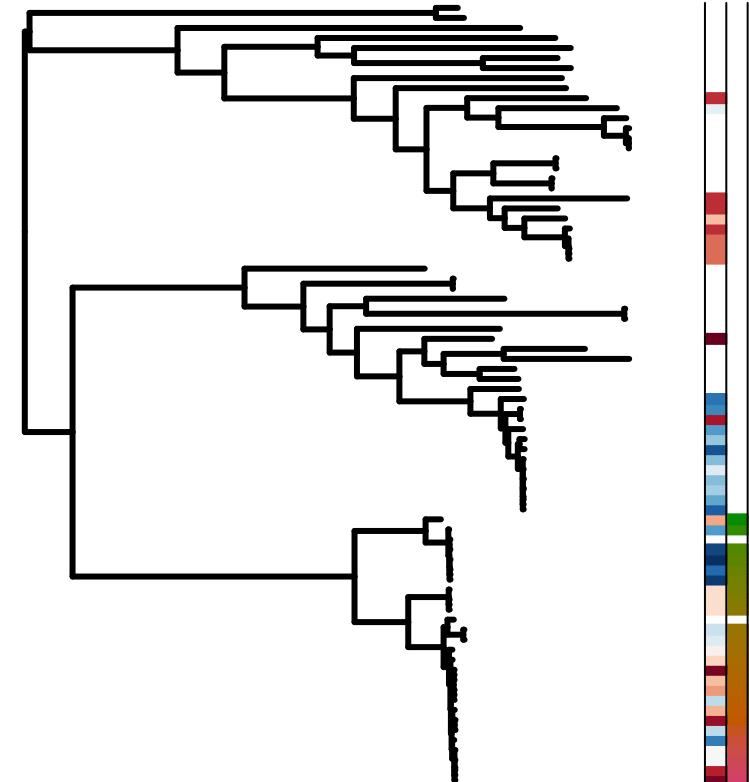
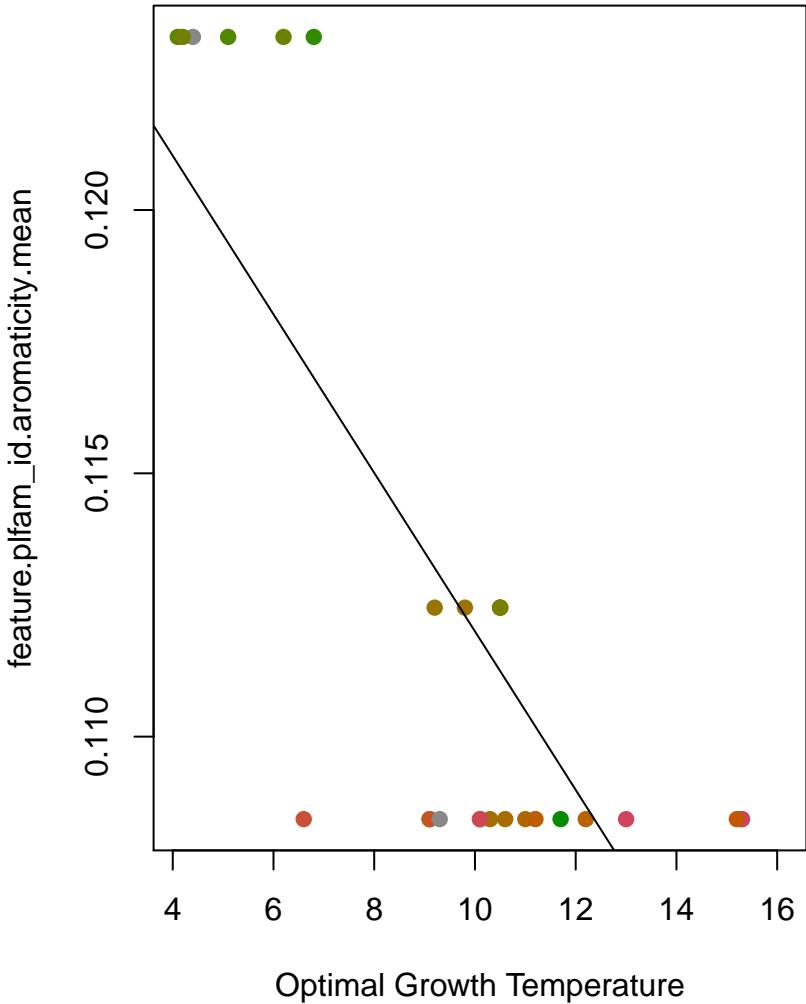
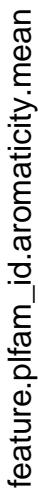


feature.plfam_id.aromaticity.mean
PLF_28228_00022617
hypothetical protein
 $r = -0.778$, $p = 10^{-5.746}$

feature.plfam_id.aromaticity.mean

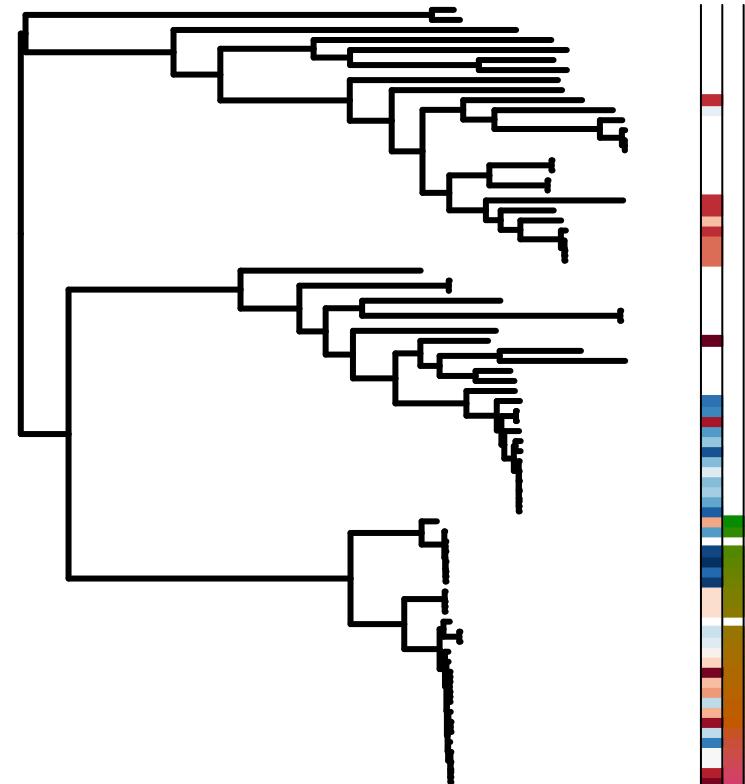
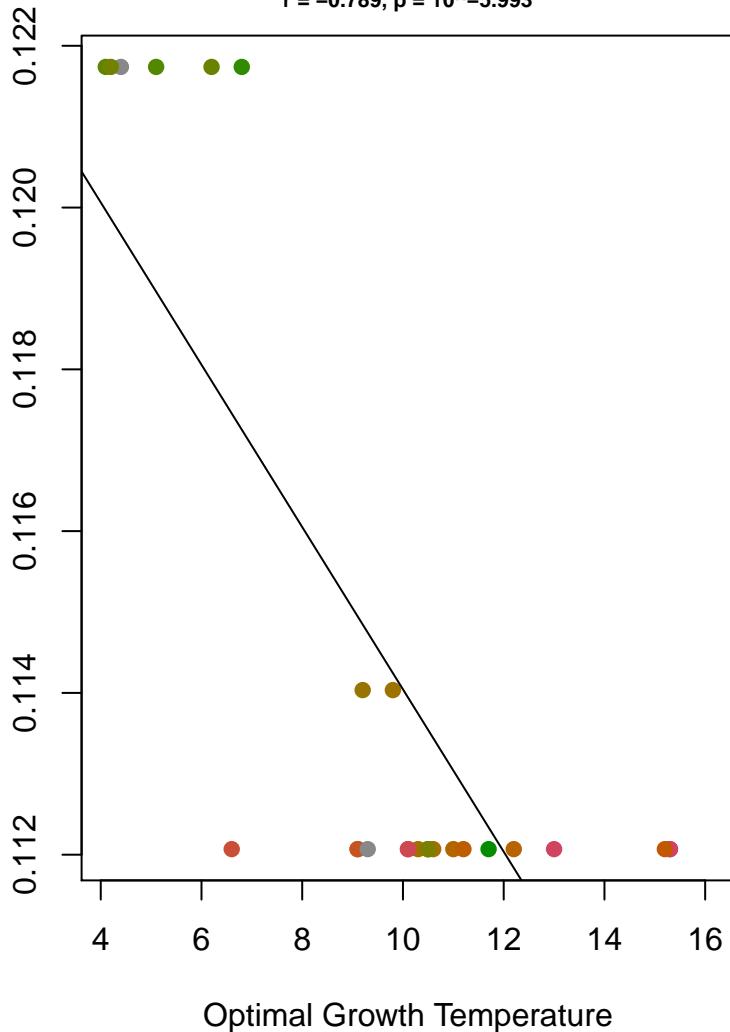


feature.plfam_id.aromaticity.mean
PLF_28228_00031426
hypothetical protein
 $r = -0.788, p = 10^{-5.968}$



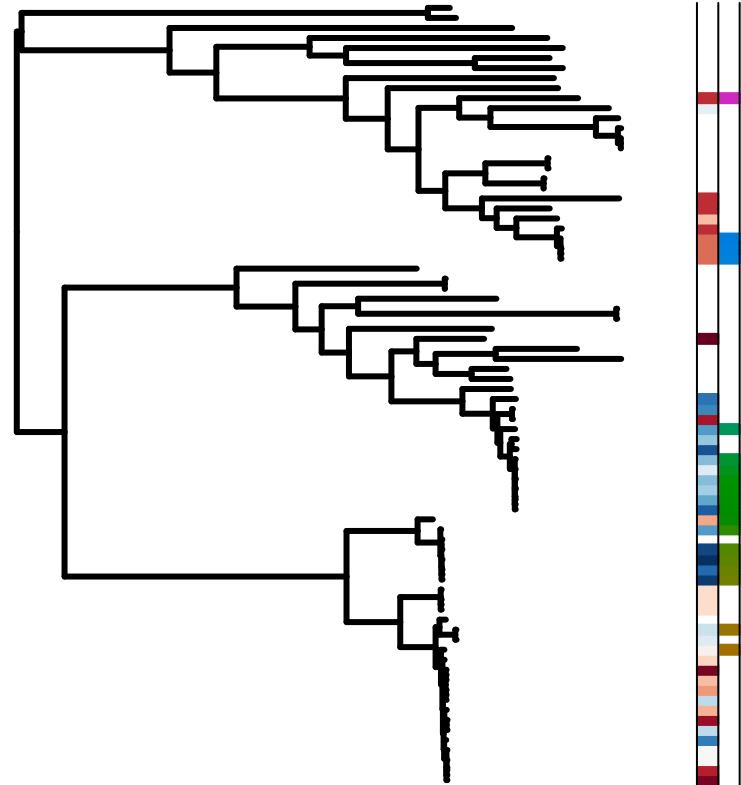
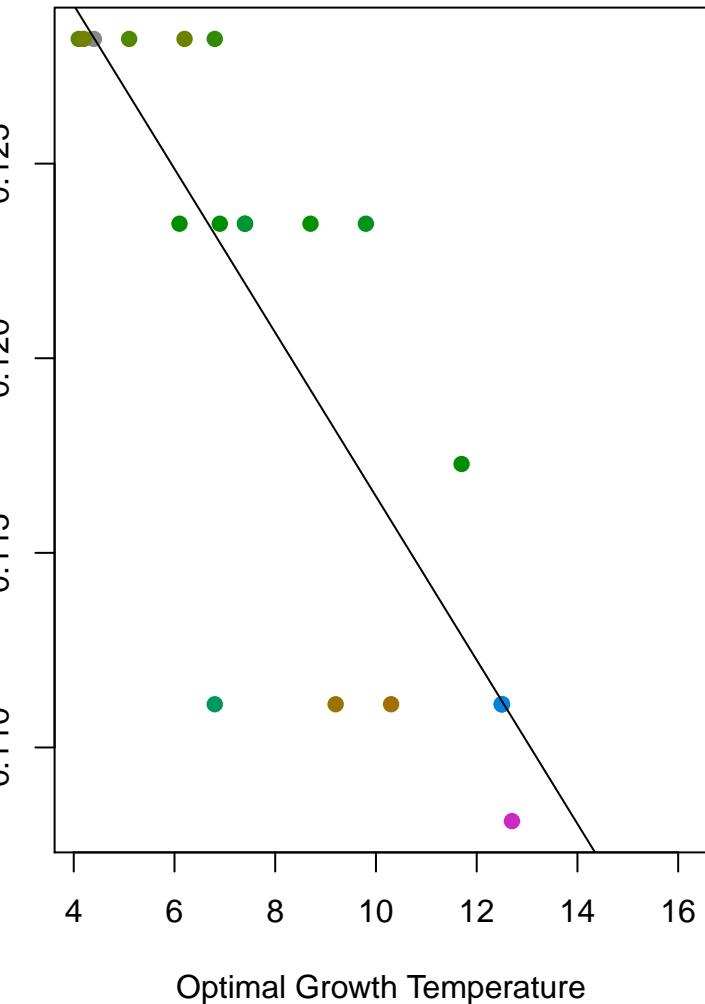
feature.plfam_id.aromaticity.mean
PLF_28228_00016319
hypothetical protein
 $r = -0.789$, $p = 10^{-5.993}$

feature.plfam_id.aromaticity.mean



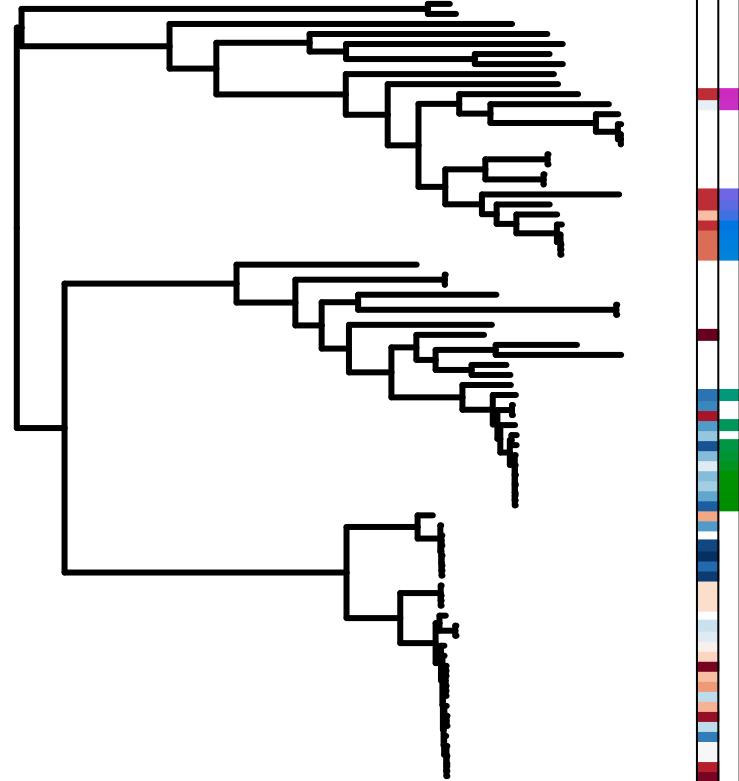
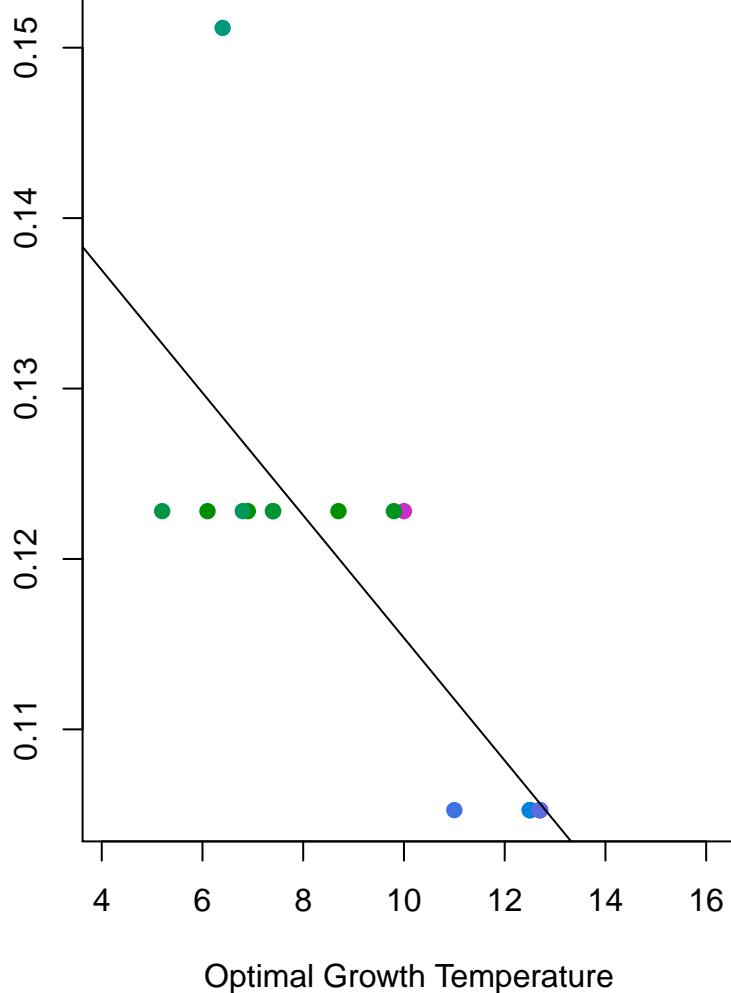
feature.plfam_id.aromaticity.mean
PLF_28228_00005149
hypothetical protein
 $r = -0.823$, $p = 10^{-5.084}$

feature.plfam_id.aromaticity.mean



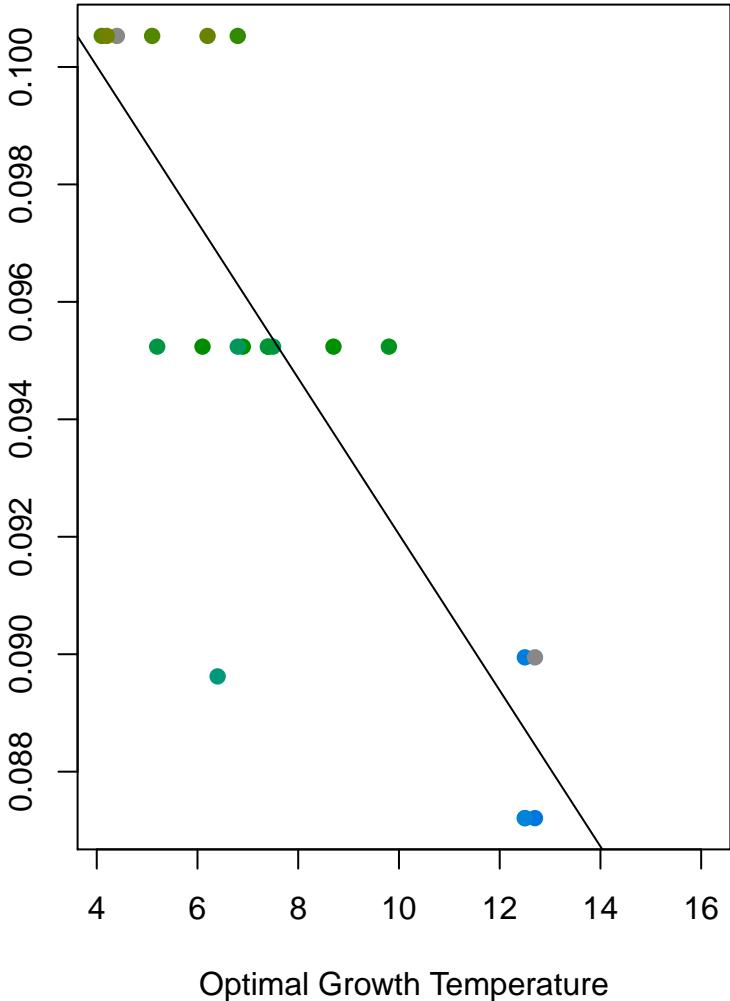
feature.plfam_id.aromaticity.mean
PLF_28228_00002024
Ribosome modulation factor
 $r = -0.826$, $p = 10^{-4.881}$

feature.plfam_id.aromaticity.mean

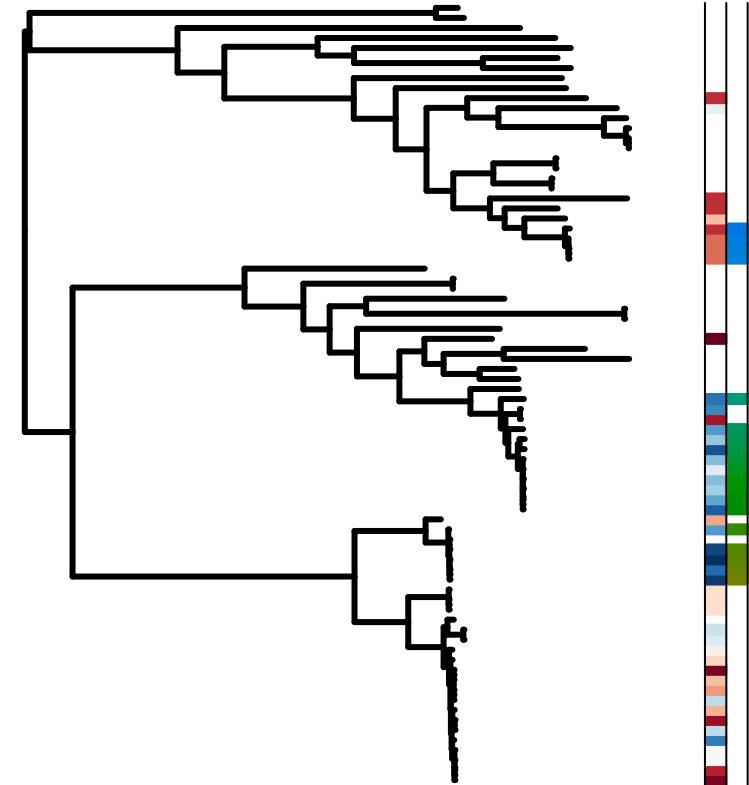


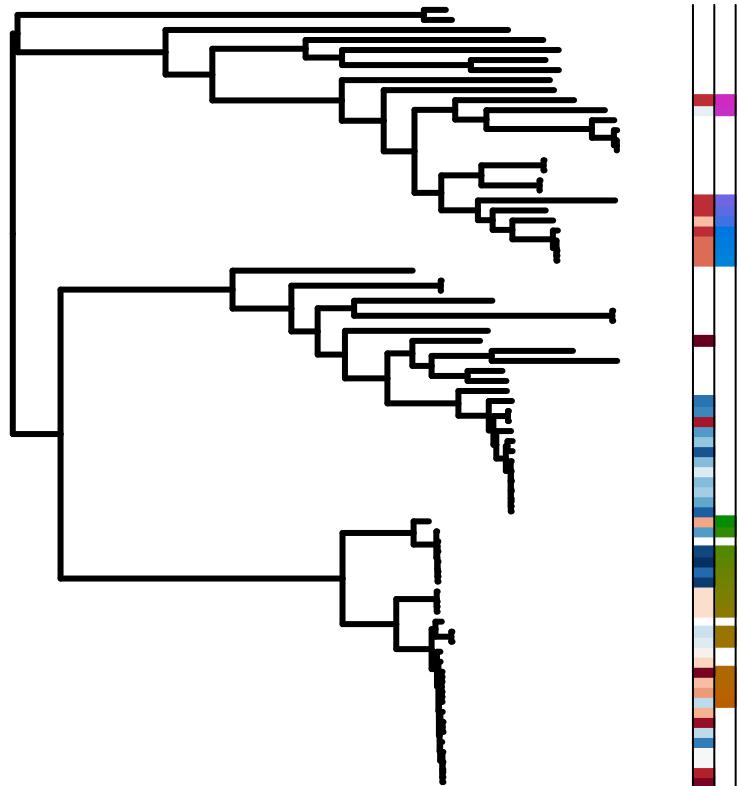
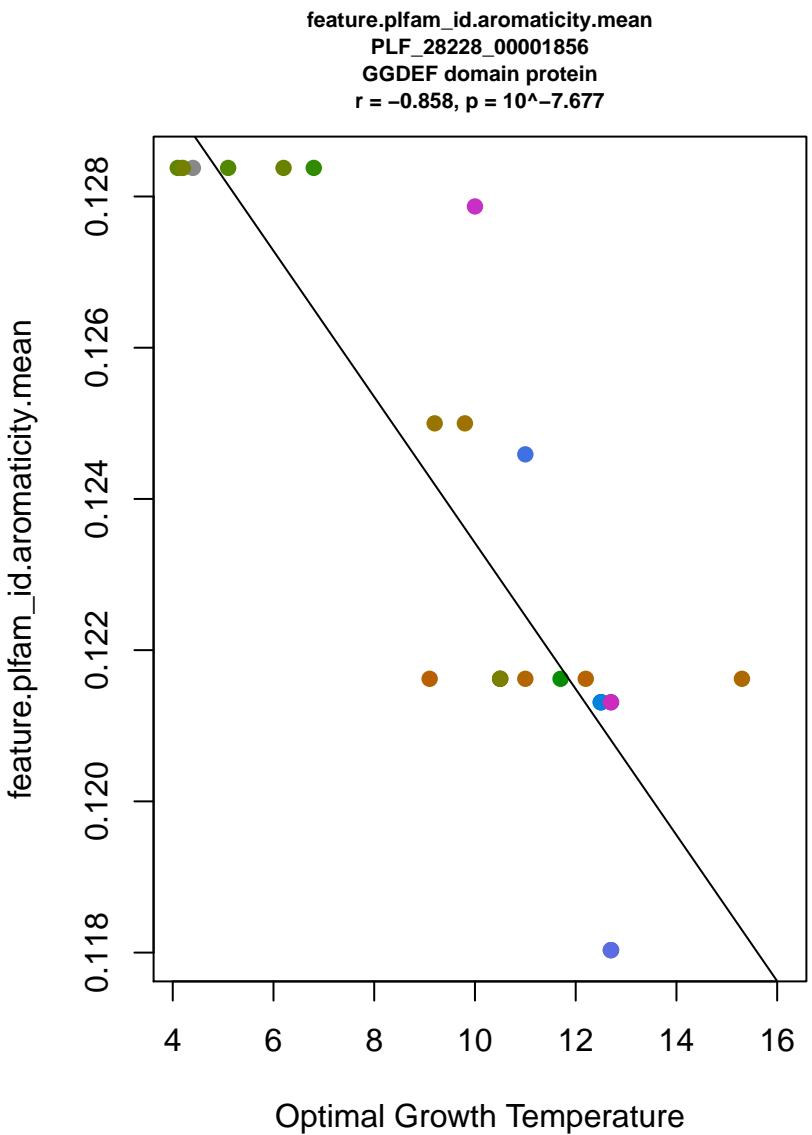
feature.plfam_id.aromaticity.mean
PLF_28228_00014224
FIG006045: Sigma factor, ECF subfamily
 $r = -0.849$, $p = 10^{-5.941}$

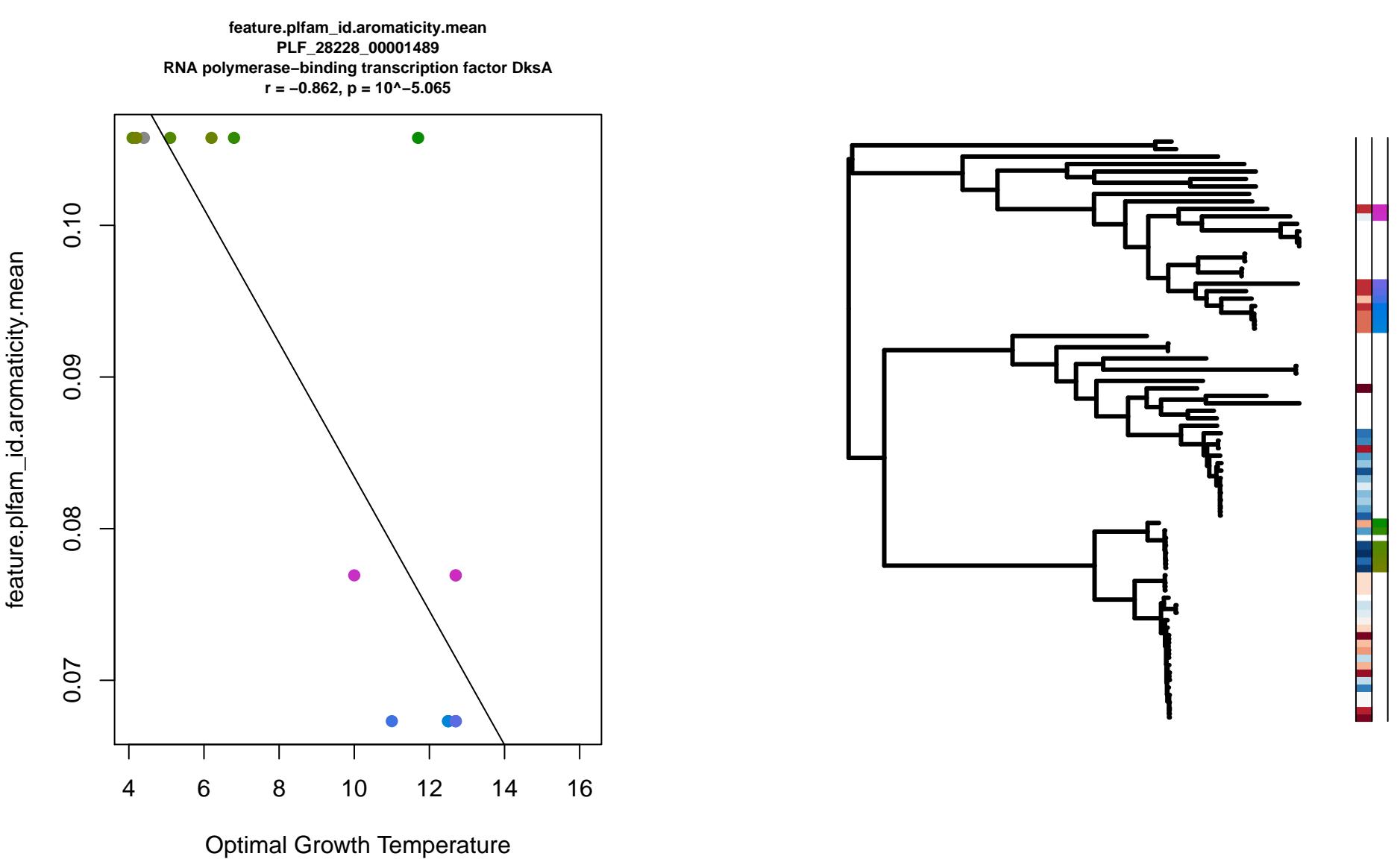
feature.plfam_id.aromaticity.mean



Optimal Growth Temperature







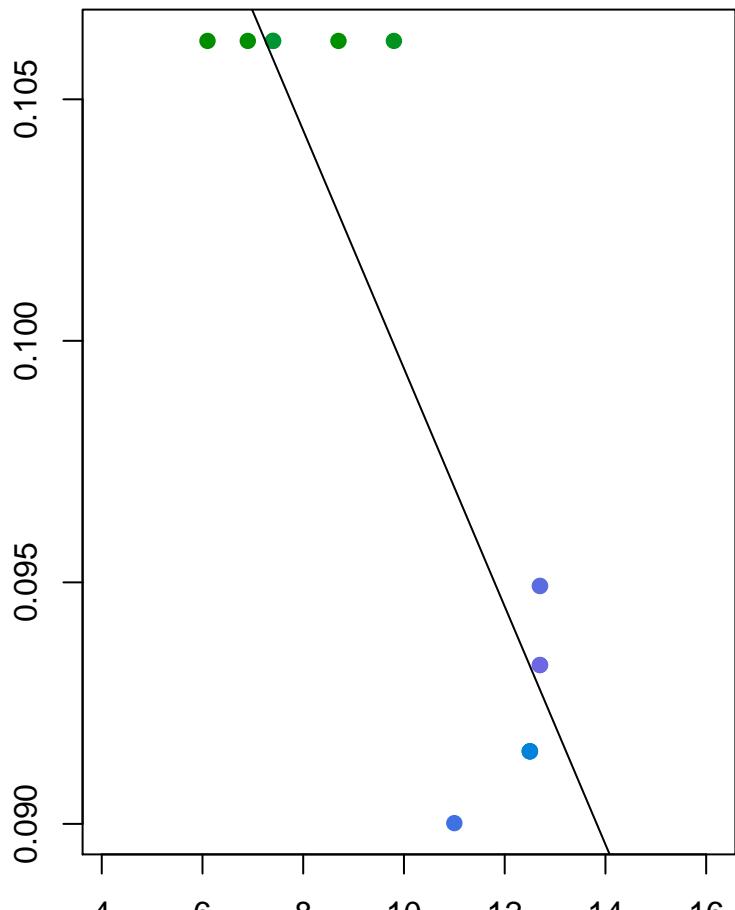
feature.plfam_id.aromaticity.mean

PLF_28228_00003666

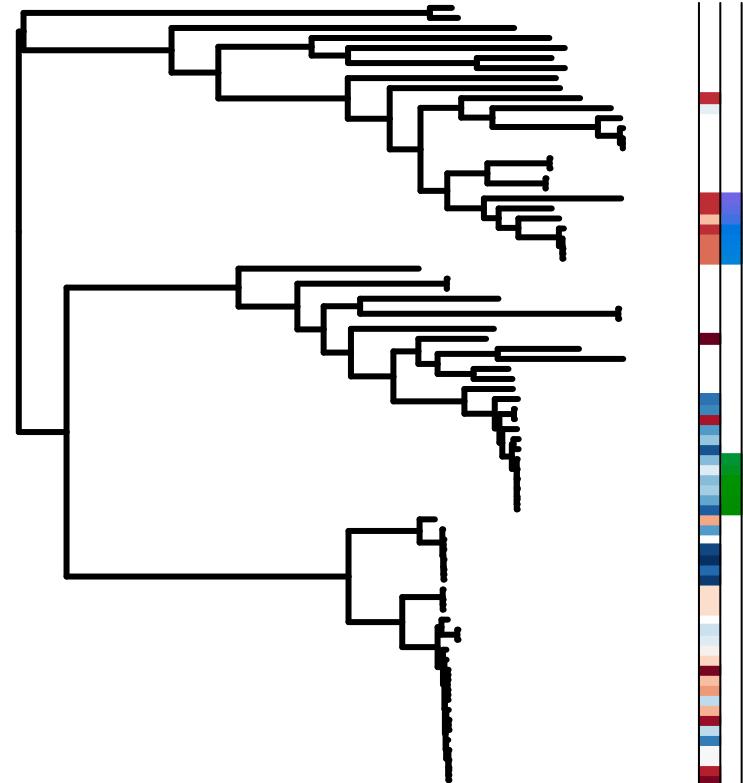
Signal transduction histidine kinase regulating C4-dicarboxylate transport system

$r = -0.896, p = 10^{-4.846}$

feature.plfam_id.aromaticity.mean



Optimal Growth Temperature



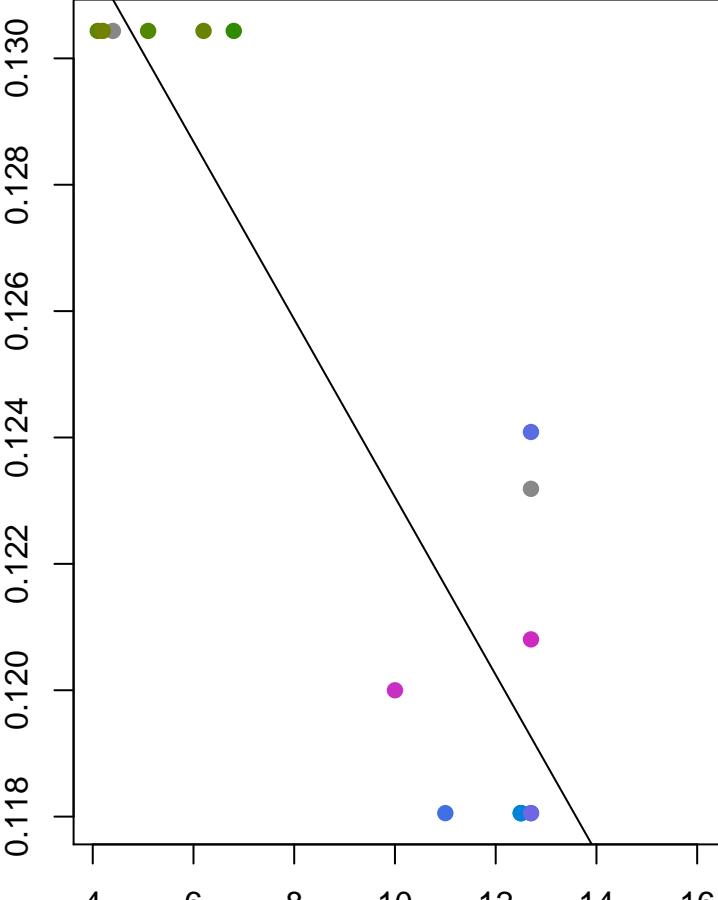
feature.plfam_id.aromaticity.mean

PLF_28228_00001794

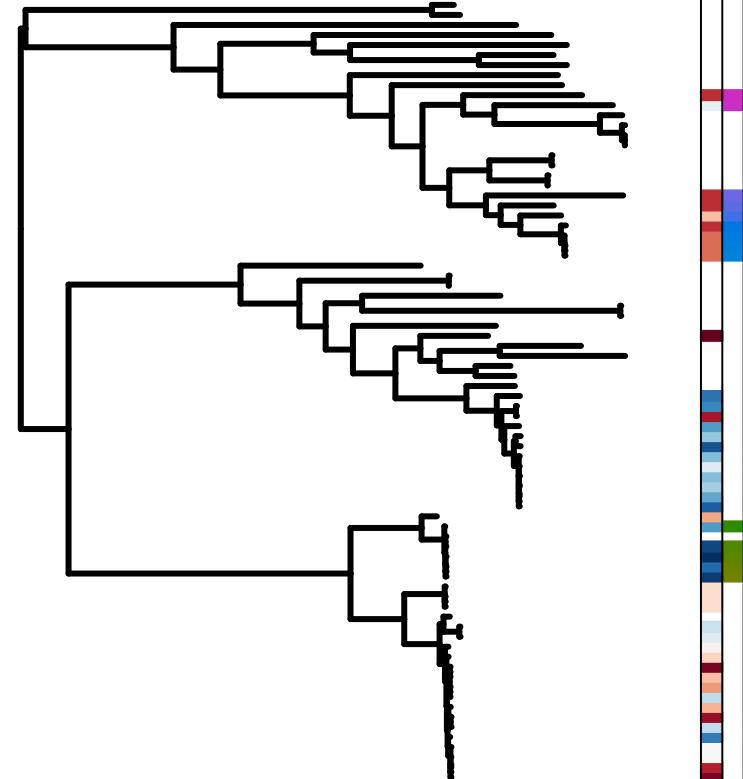
Outer membrane beta-barrel assembly protein BamE

$r = -0.906$, $p = 10^{-5.861}$

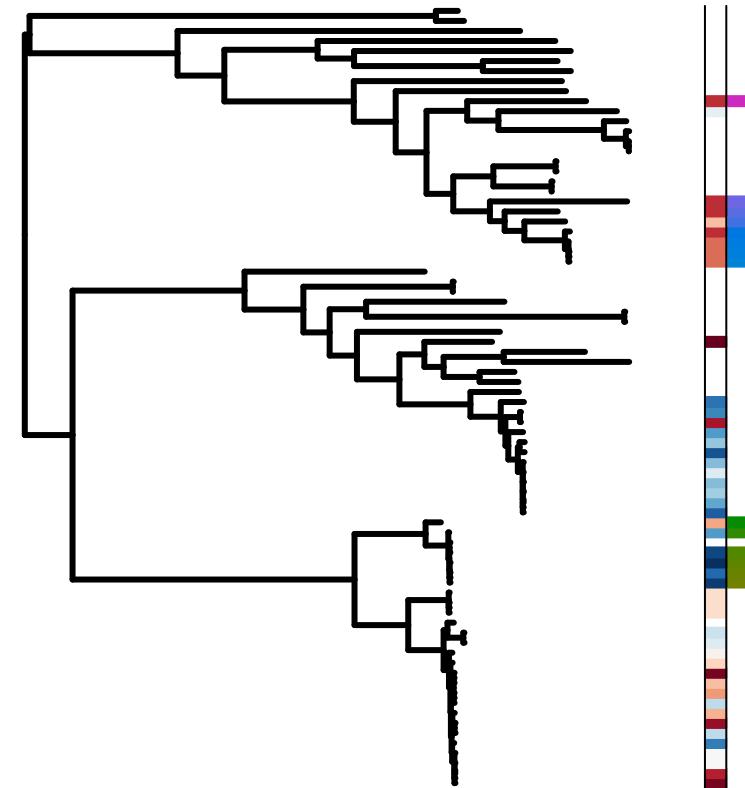
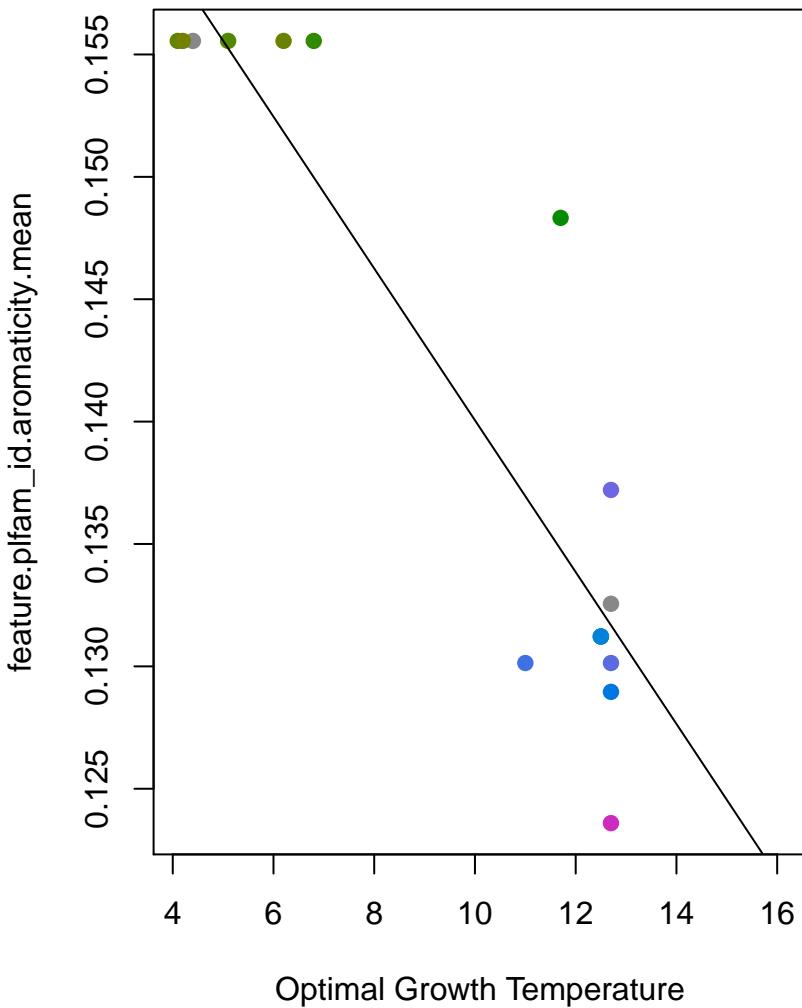
feature.plfam_id.aromaticity.mean



Optimal Growth Temperature

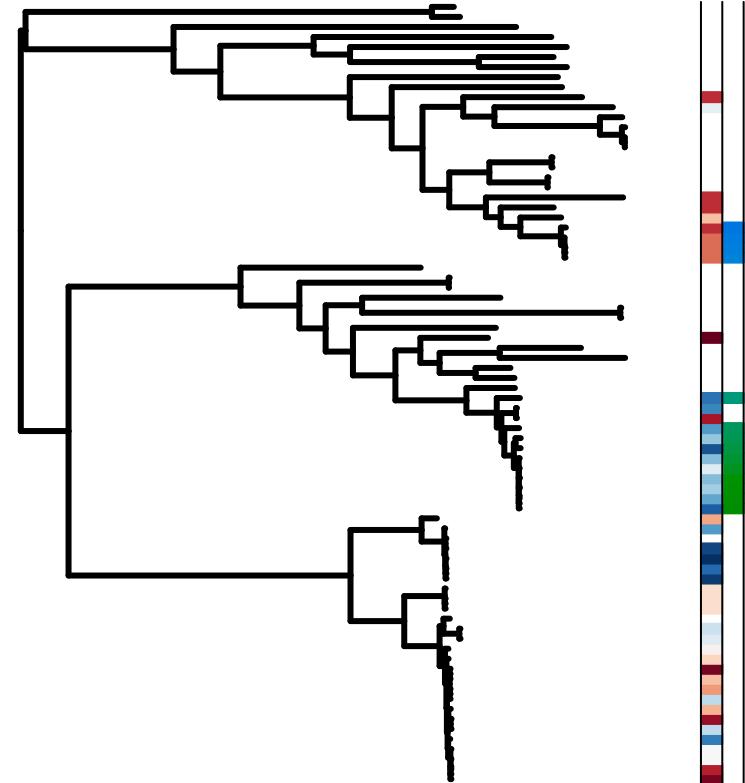
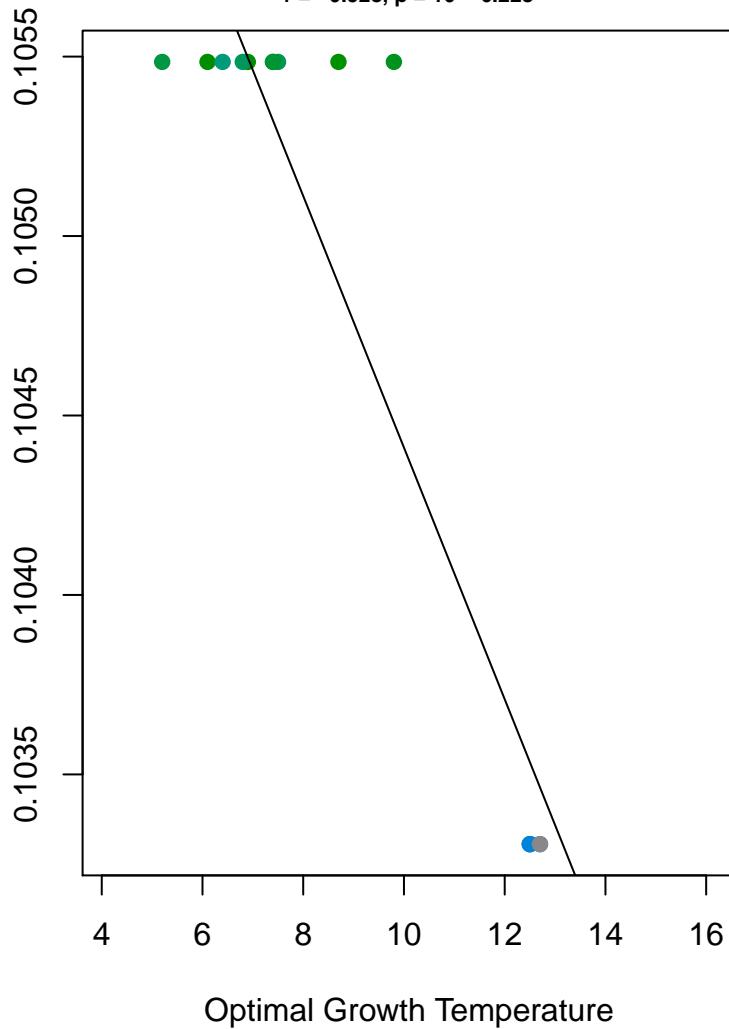


feature.plfam_id.aromaticity.mean
PLF_28228_00002761
Uncharacterized MFS-type transporter
 $r = -0.912$, $p = 10^{-6.049}$



feature.plfam_id.aromaticity.mean
PLF_28228_00007378
SapC-like S-layer protein
 $r = -0.928$, $p = 10^{-6.228}$

feature.plfam_id.aromaticity.mean



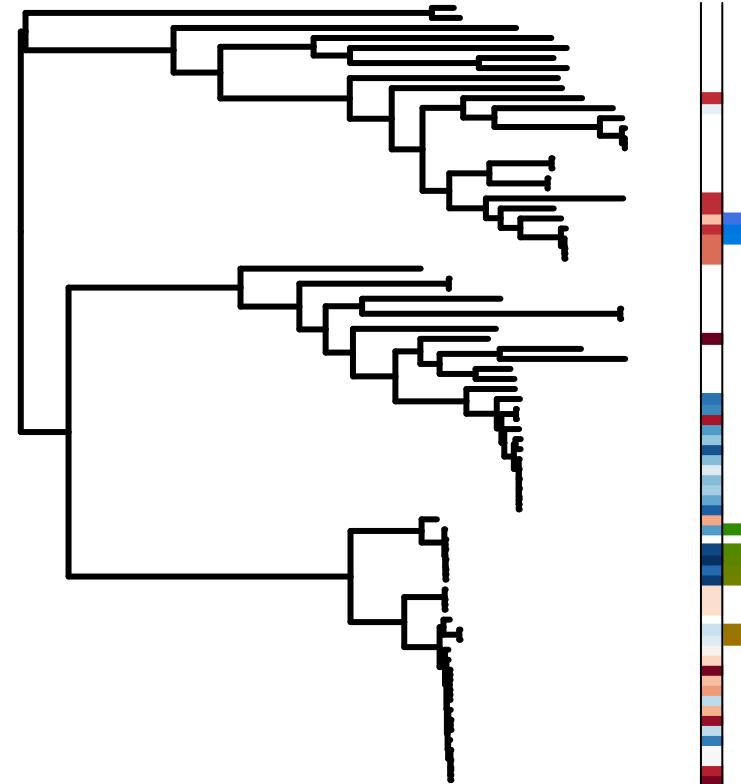
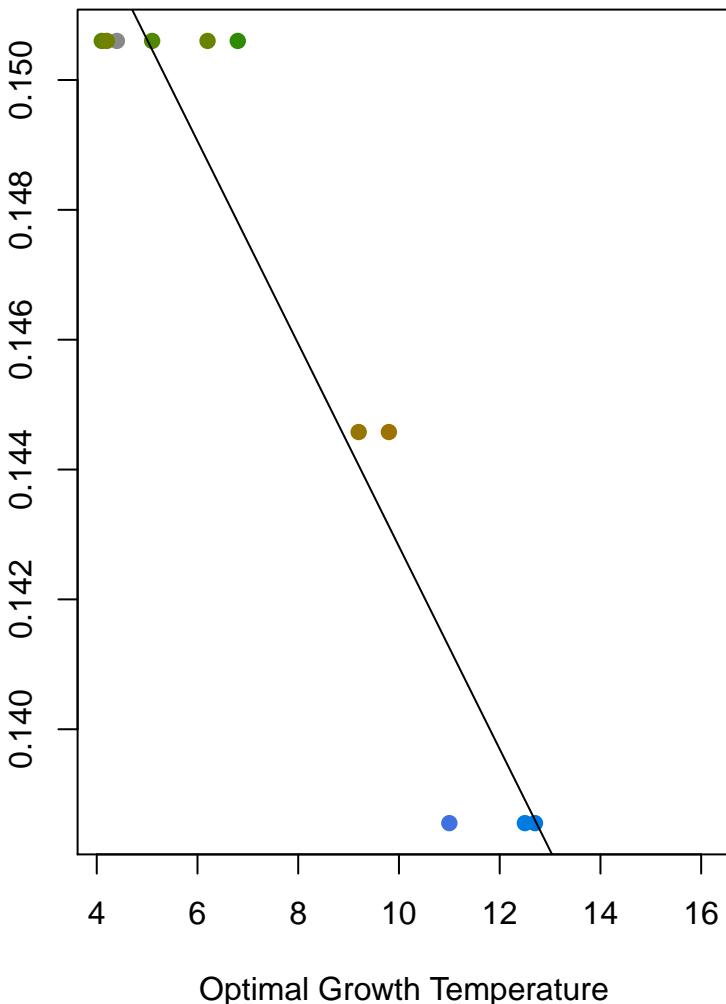
feature.plfam_id.aromaticity.mean

PLF_28228_00028582

Peptide-methionine (S)-S-oxide reductase MsrA (EC 1.8.4.11)

$r = -0.956$, $p = 10^{-5.362}$

feature.plfam_id.aromaticity.mean



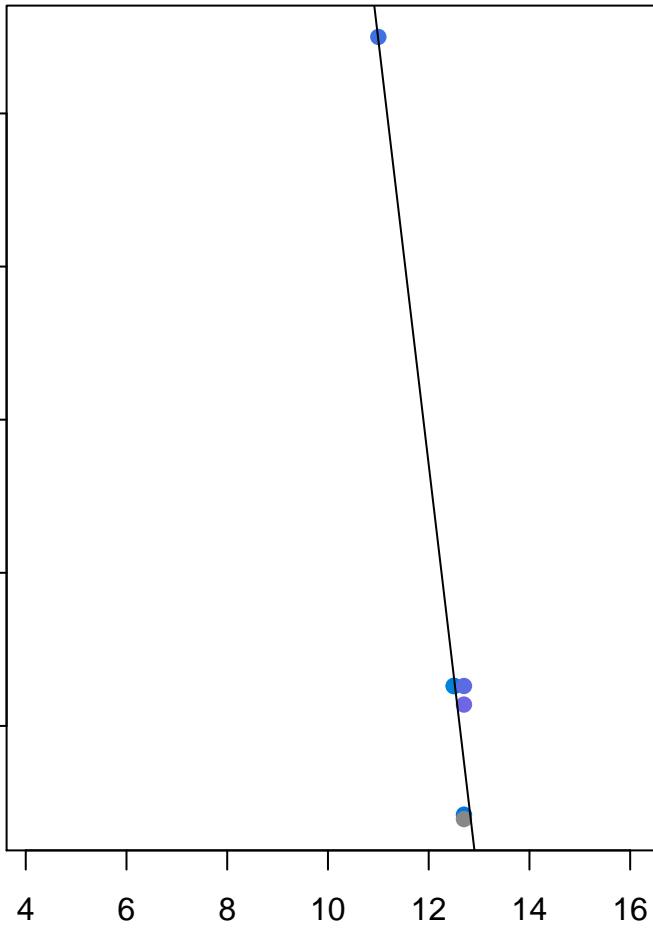
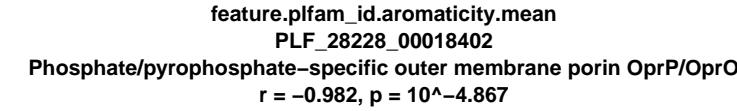
feature.plfam_id.aromaticity.mean

PLF_28228_00018402

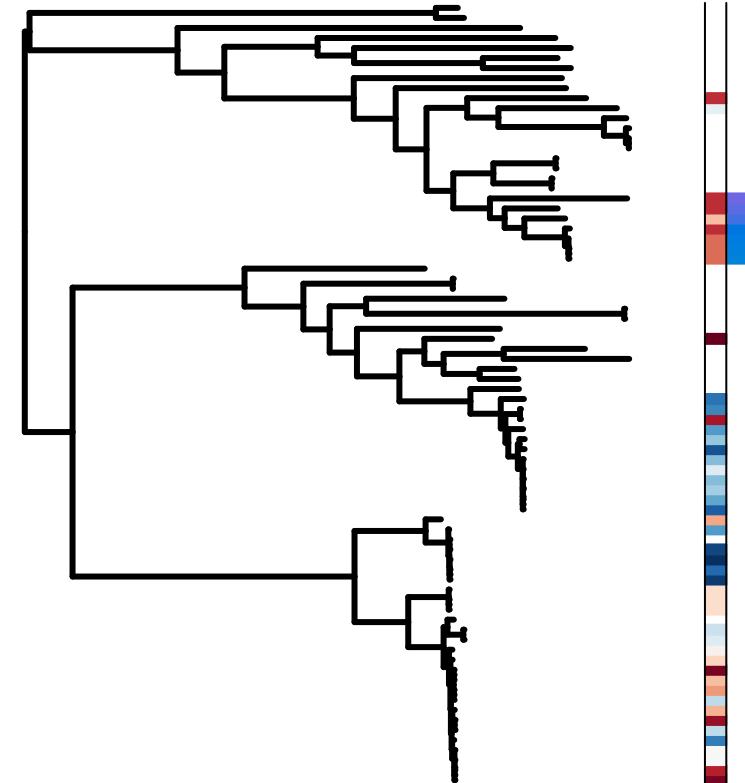
Phosphate/pyrophosphate-specific outer membrane porin OprP/OprO

$r = -0.982, p = 10^{-4.867}$

feature.plfam_id.aromaticity.mean

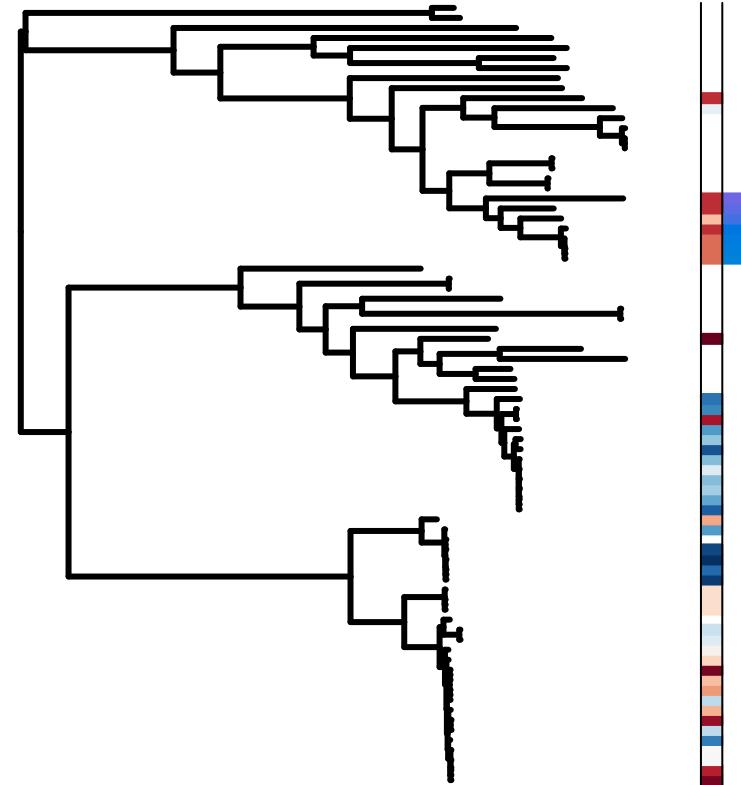
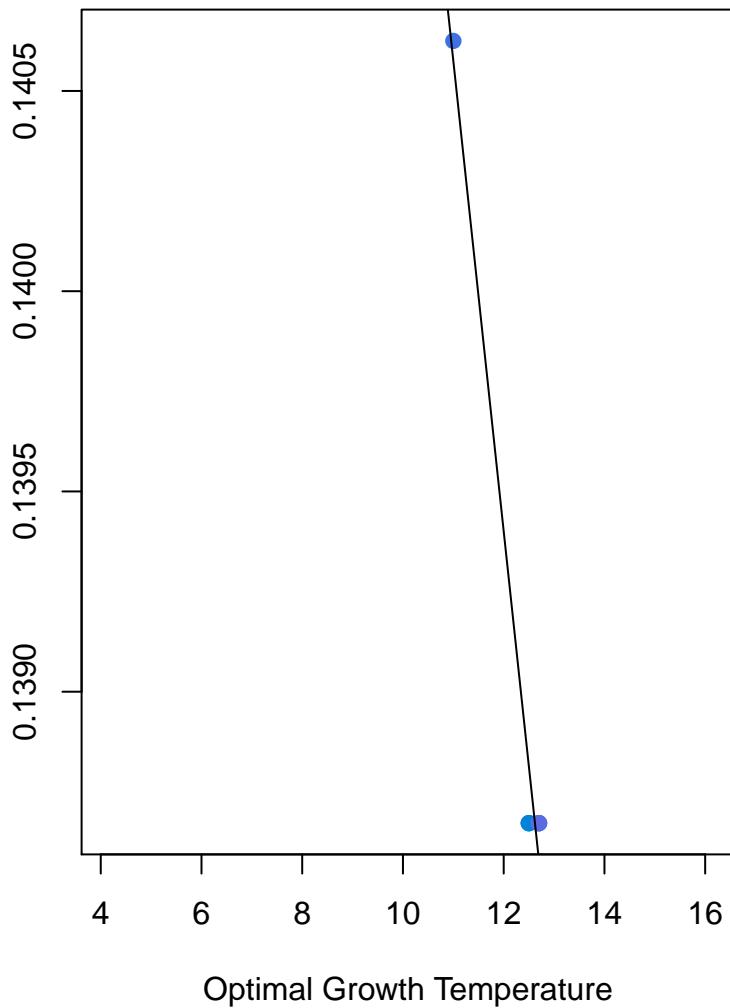


Optimal Growth Temperature



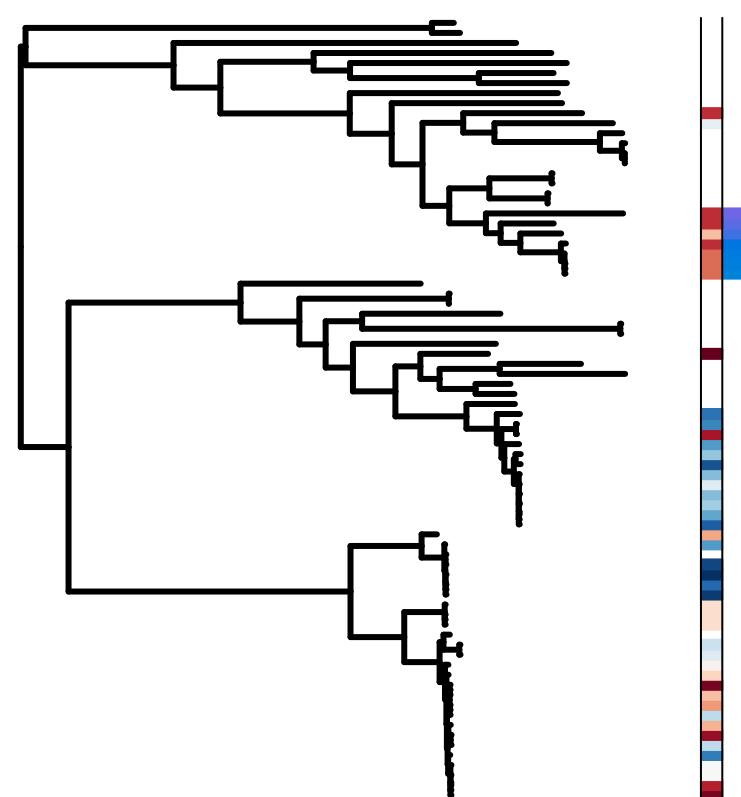
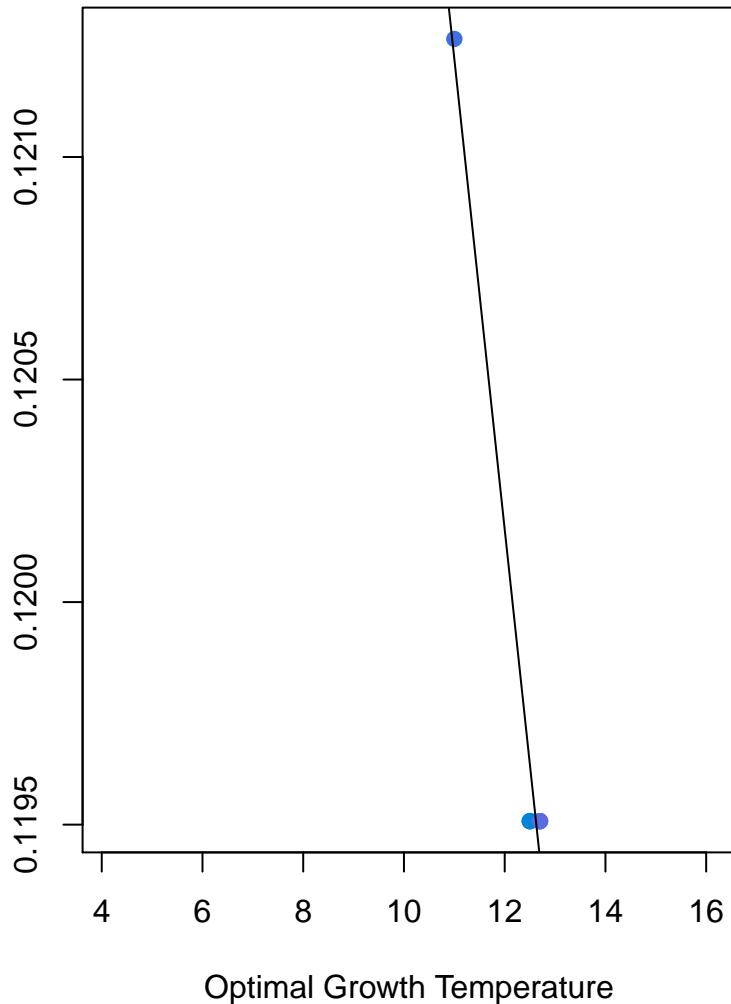
feature.plfam_id.aromaticity.mean
PLF_28228_00003079
Arylsulfatase (EC 3.1.6.1)
 $r = -0.985$, $p = 10^{-5.104}$

feature.plfam_id.aromaticity.mean



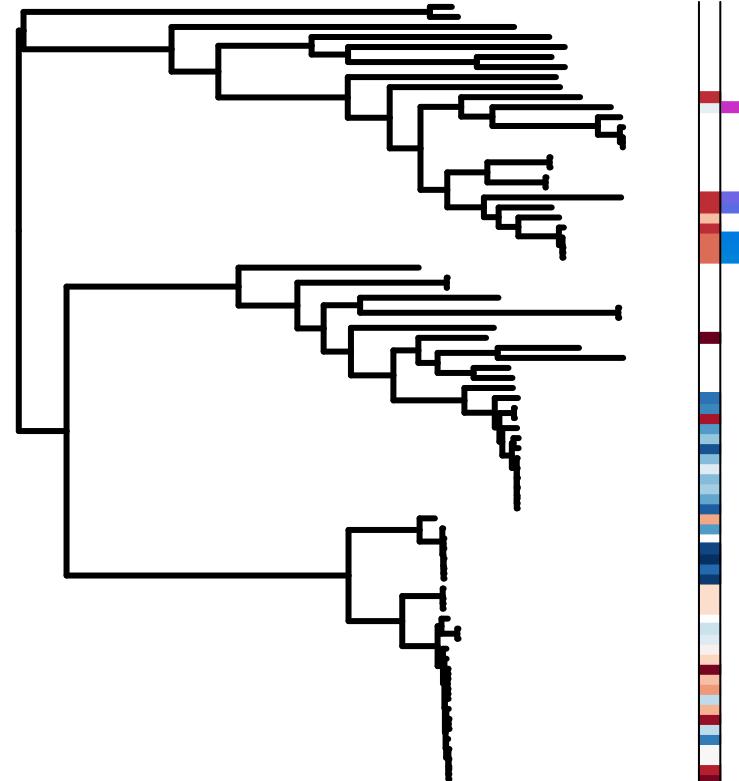
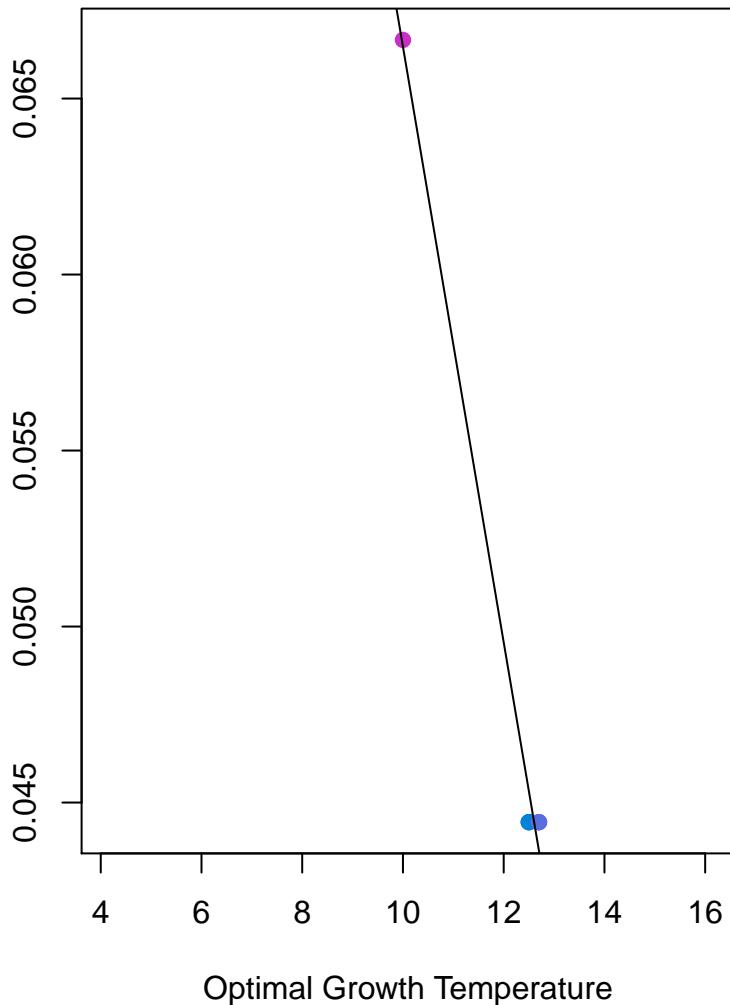
feature.plfam_id.aromaticity.mean
PLF_28228_00018479
hypothetical protein
 $r = -0.985$, $p = 10^{-5.104}$

feature.plfam_id.aromaticity.mean

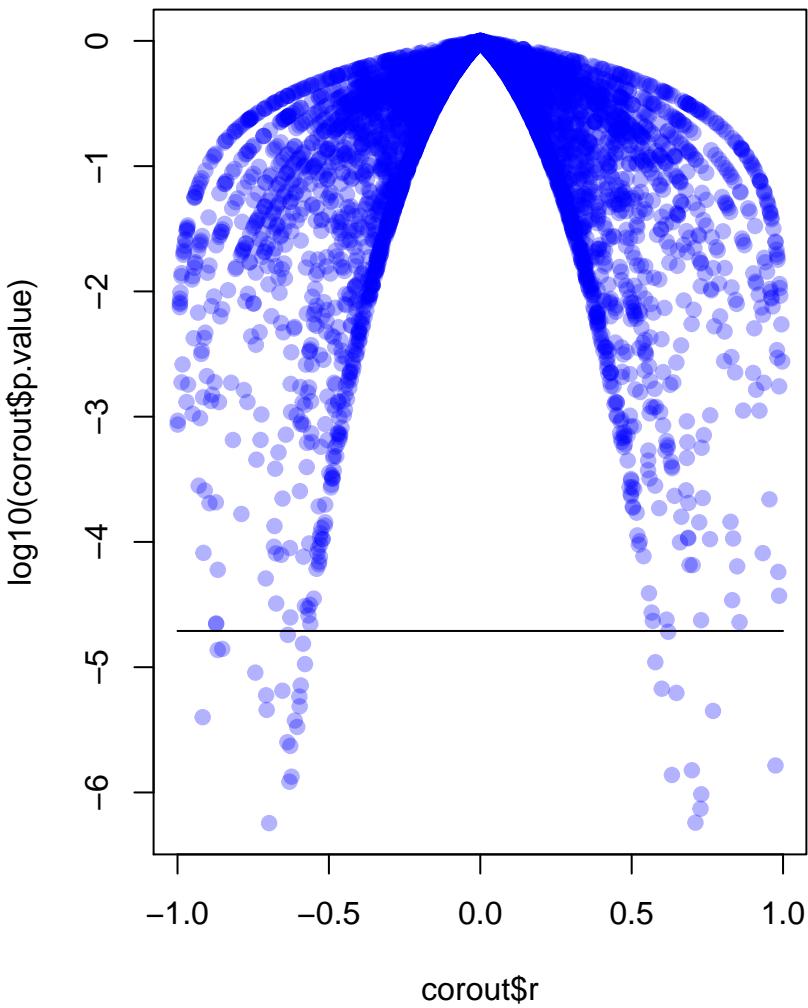


feature.plfam_id.aromaticity.mean
PLF_28228_00004382
hypothetical protein
 $r = -0.995$, $p = 10^{-5.441}$

feature.plfam_id.aromaticity.mean



`feature.pgfam_id.aliphatic_index.mean`



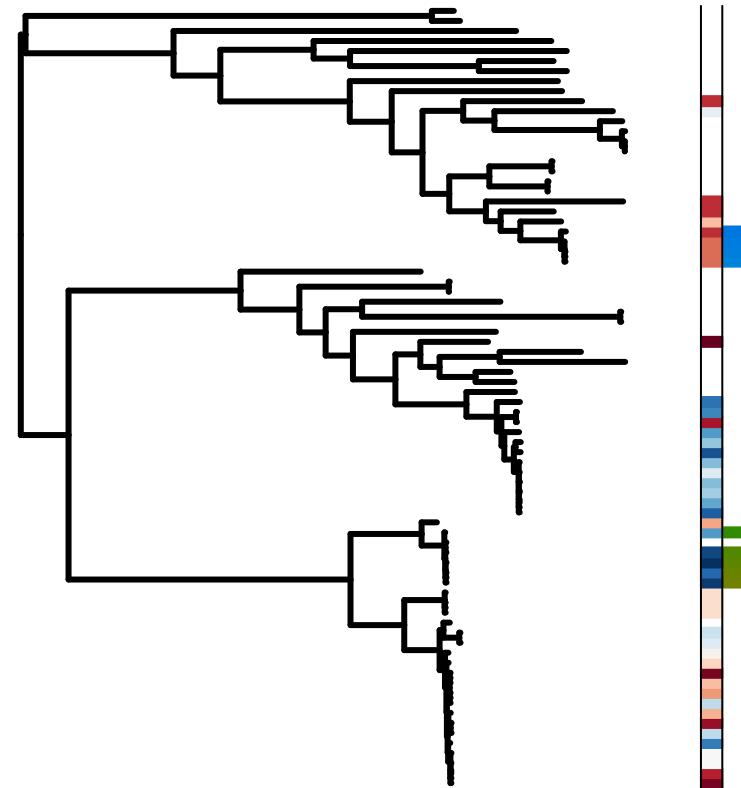
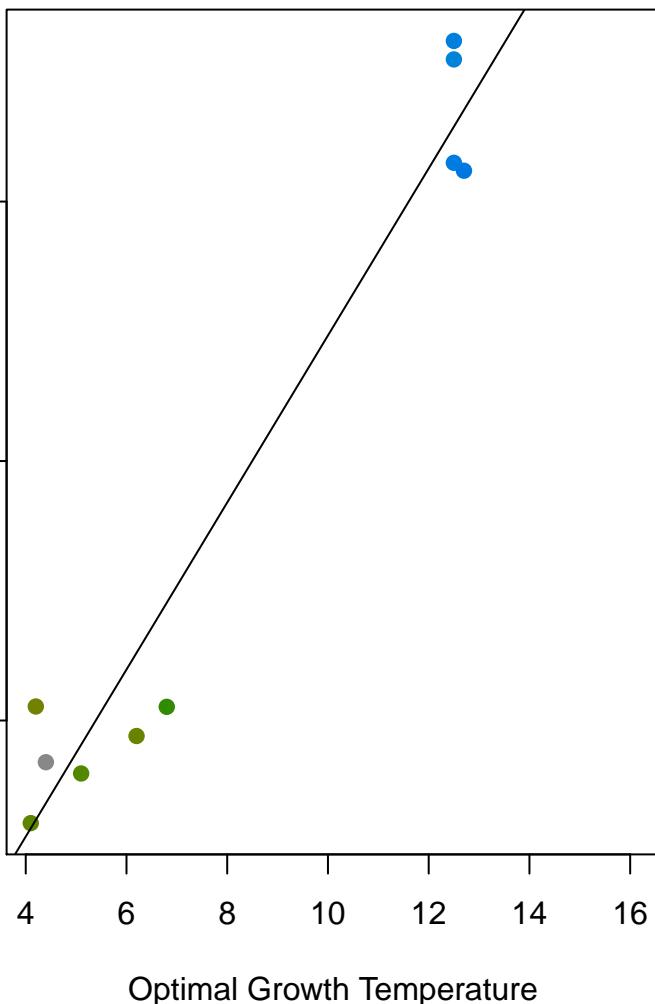
feature.pgfam_id.aliphatic_index.mean

PGF_01338043

hypothetical protein

$r = 0.975, p = 10^{-5.785}$

feature.pgfam_id.aliphatic_index.mean



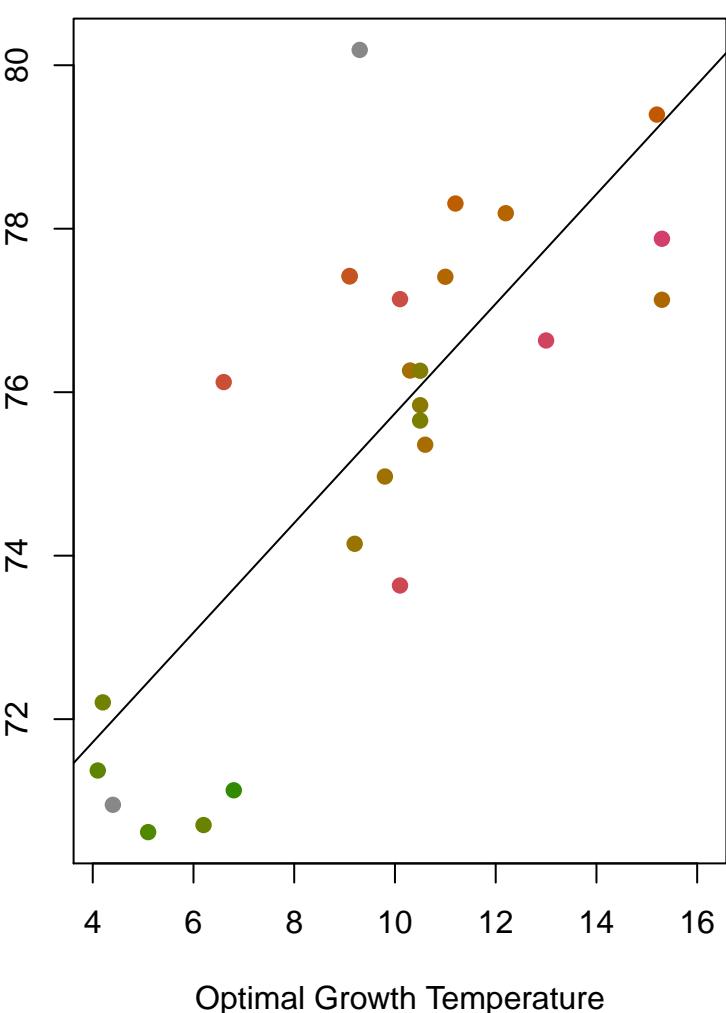
feature.pgfam_id.aliphatic_index.mean

PGF_12159935

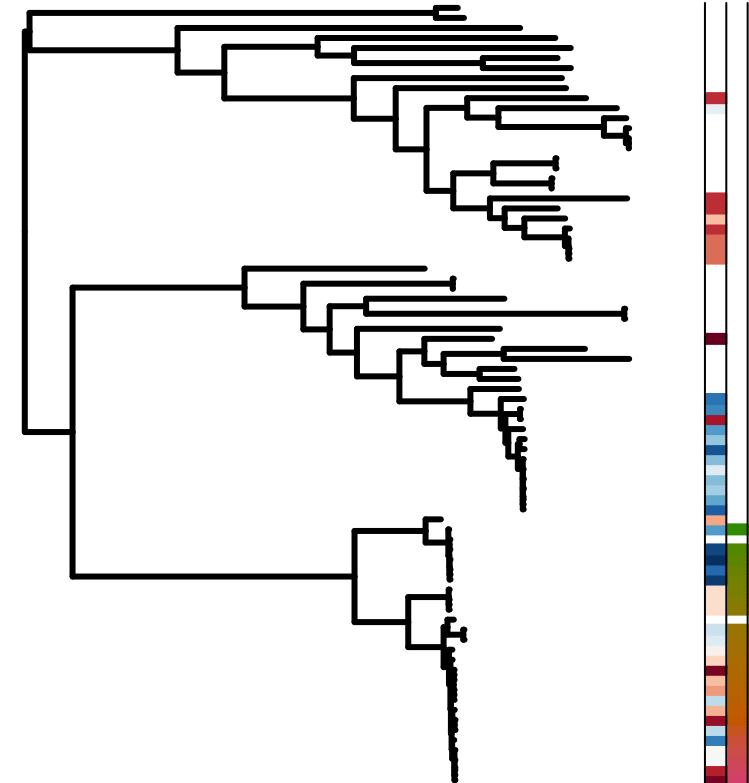
hypothetical protein

$r = 0.769, p = 10^{-5.349}$

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature



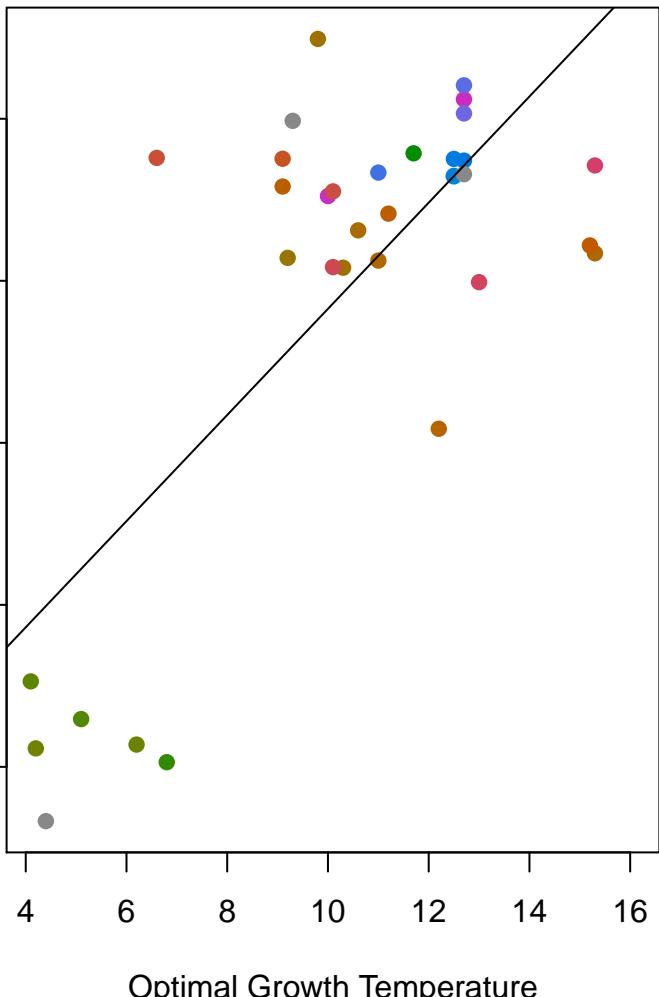
feature.pgfam_id.aliphatic_index.mean

PGF_01336501

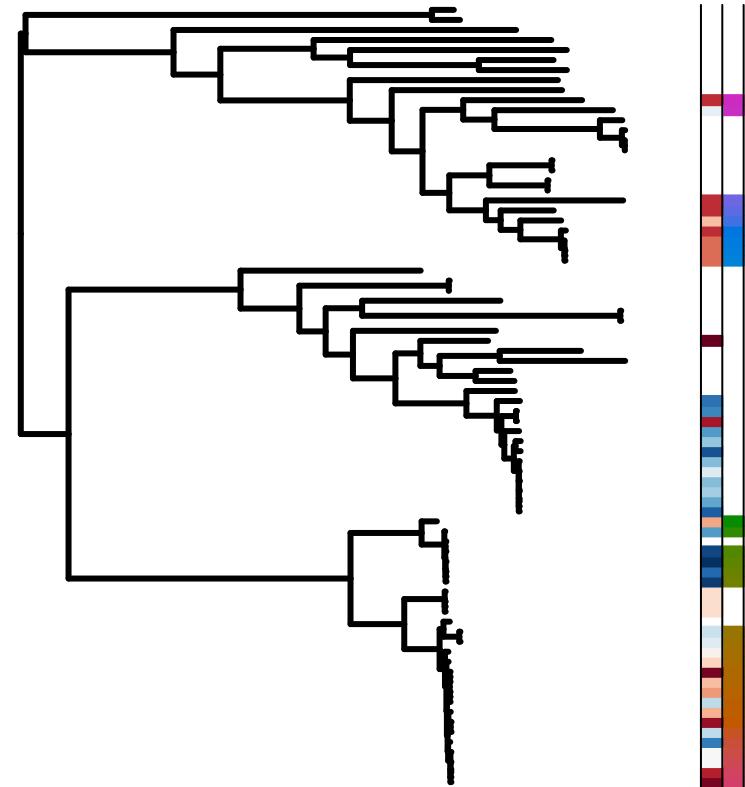
hypothetical protein

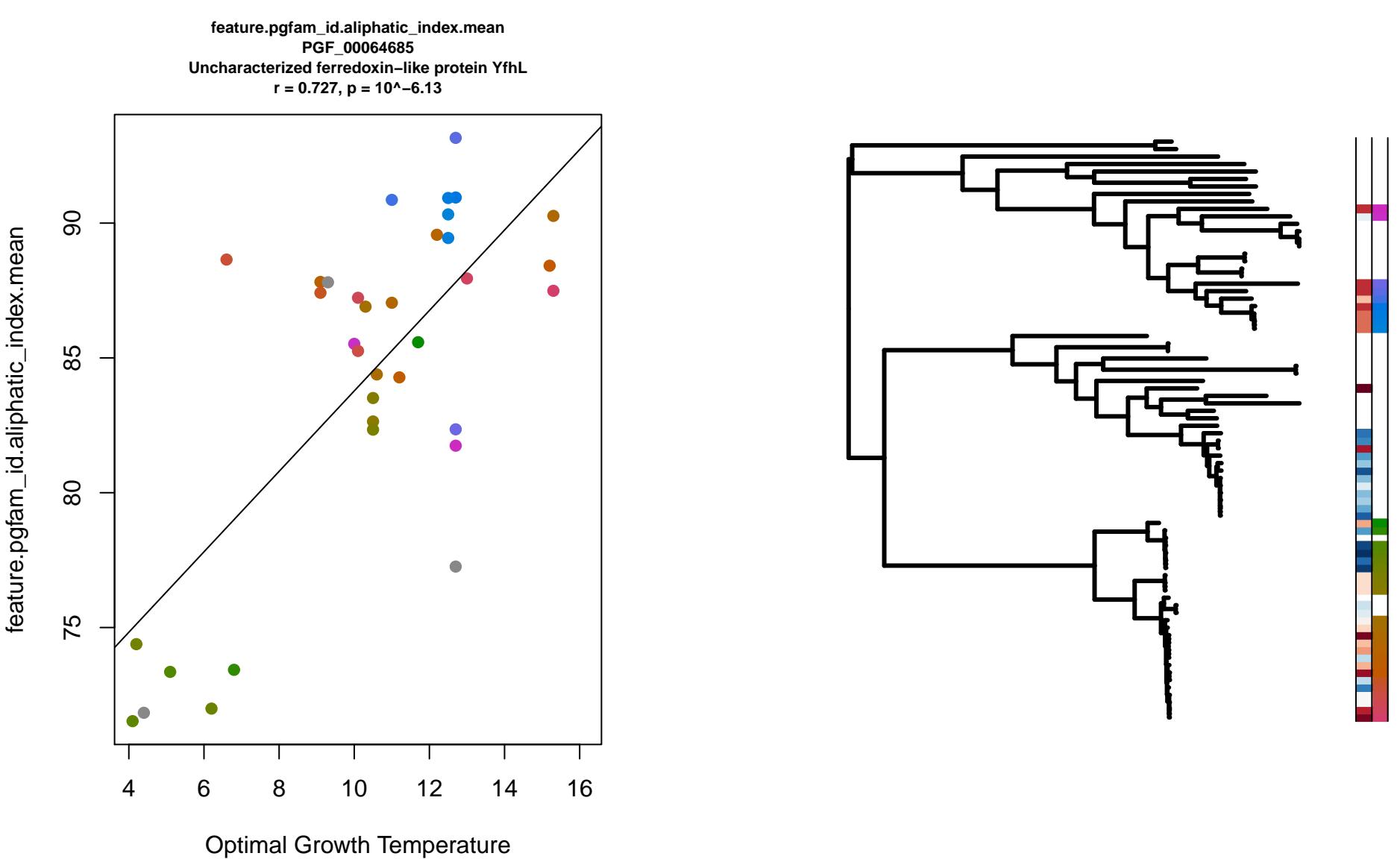
r = 0.73, p = 10^-6.015

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature





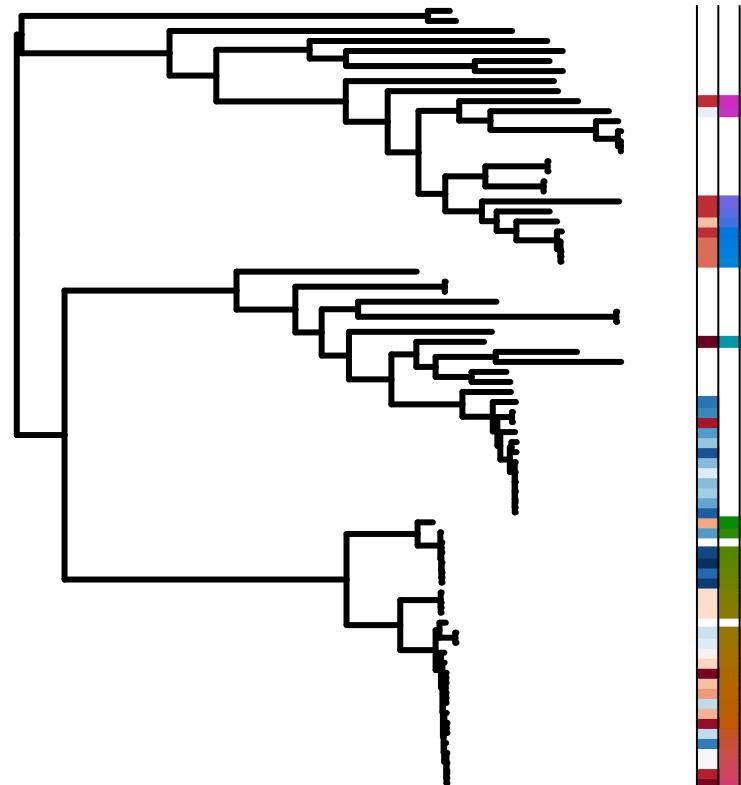
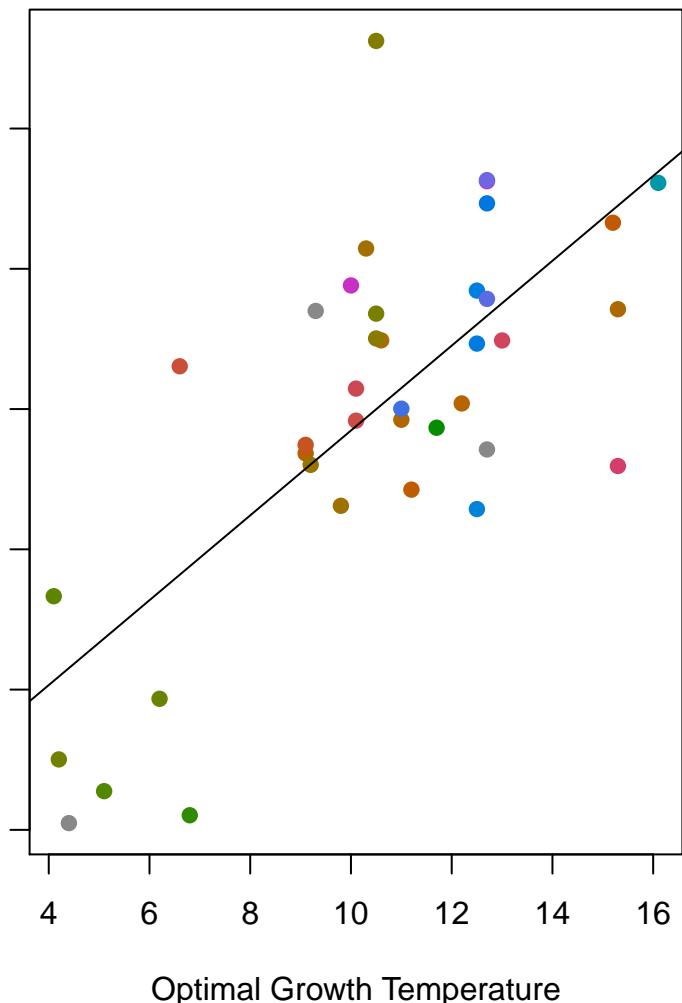
feature.pgfam_id.aliphatic_index.mean

PGF_07675395

Flagellar protein FliJ

$r = 0.711, p = 10^{-6.241}$

feature.pgfam_id.aliphatic_index.mean

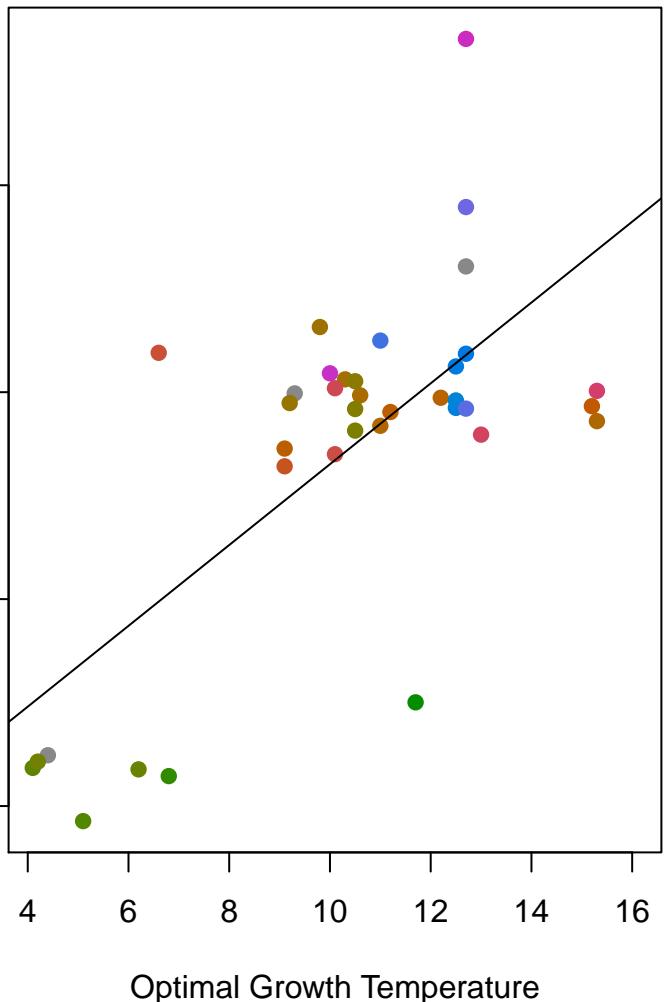


feature.pgfam_id.aliphatic_index.mean

PGF_02790700

ylcobinamide kinase (EC 2.7.1.156) / Adenosylcobinamide-phosphate guanylyltransferase (EC :
 $r = 0.699, p = 10^{-5.823}$

feature.pgfam_id.aliphatic_index.mean



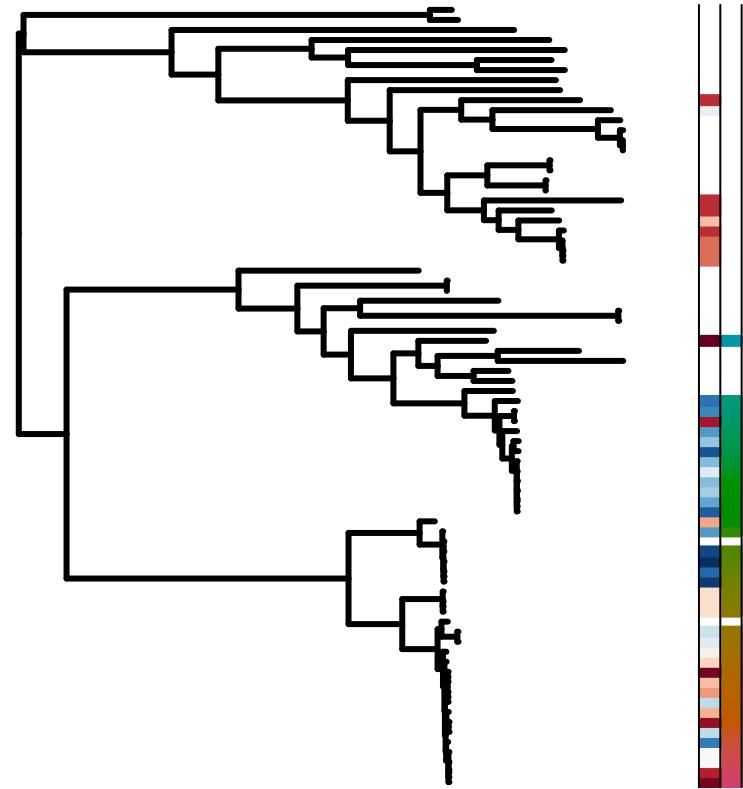
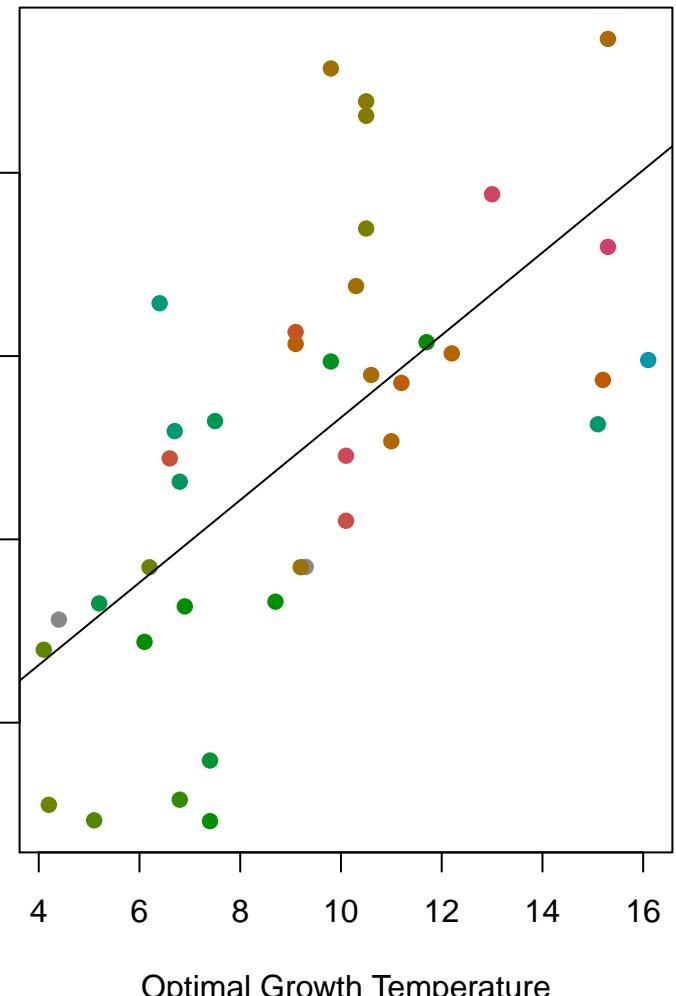
feature.pgfam_id.aliphatic_index.mean

PGF_10373609

CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)

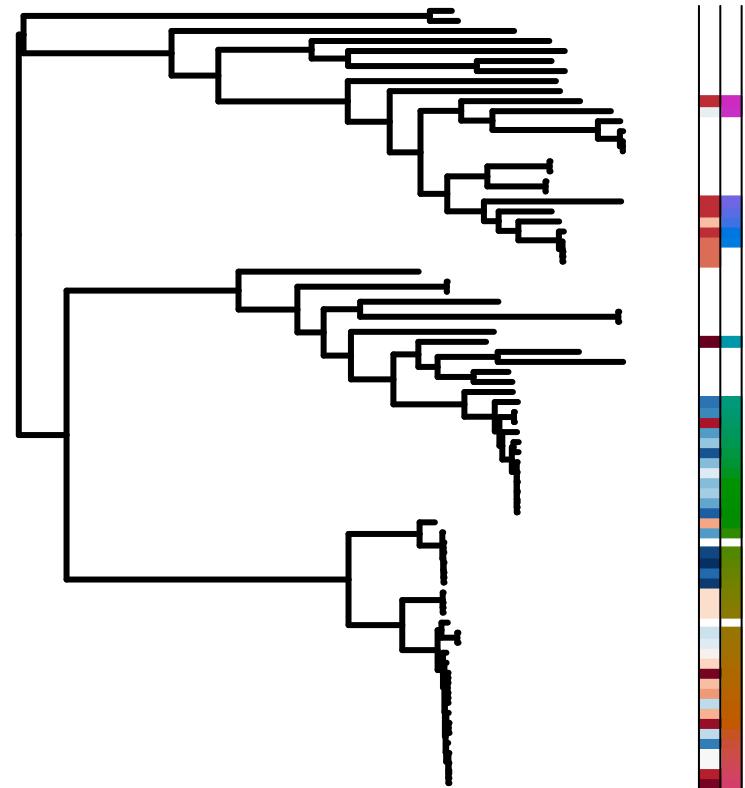
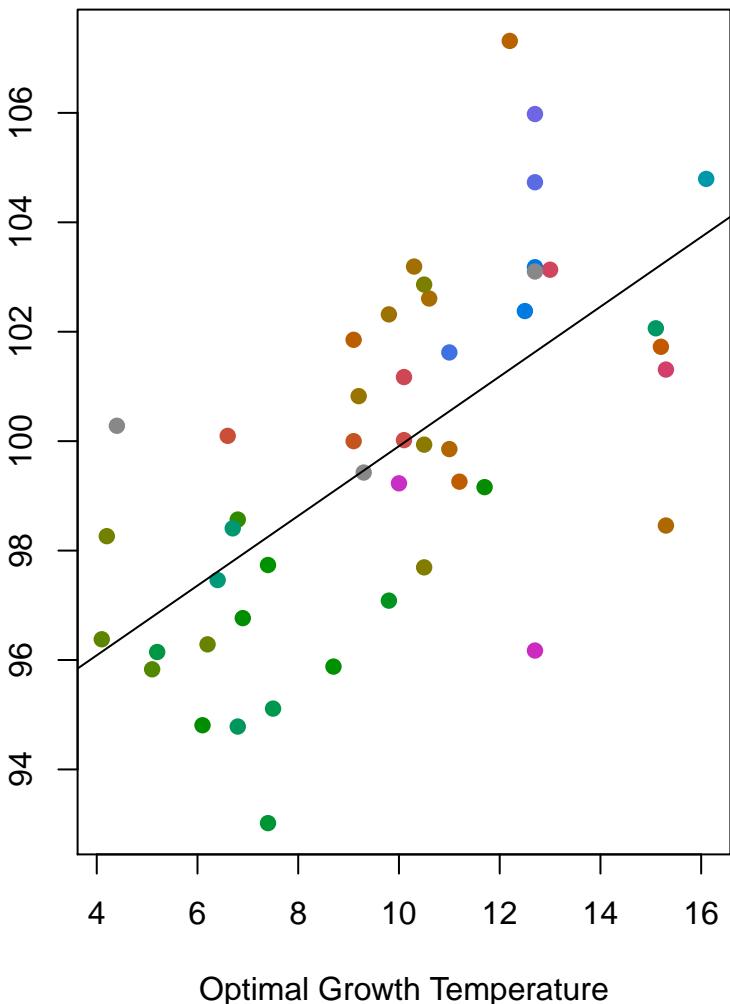
$r = 0.648$, $p = 10^{-5.206}$

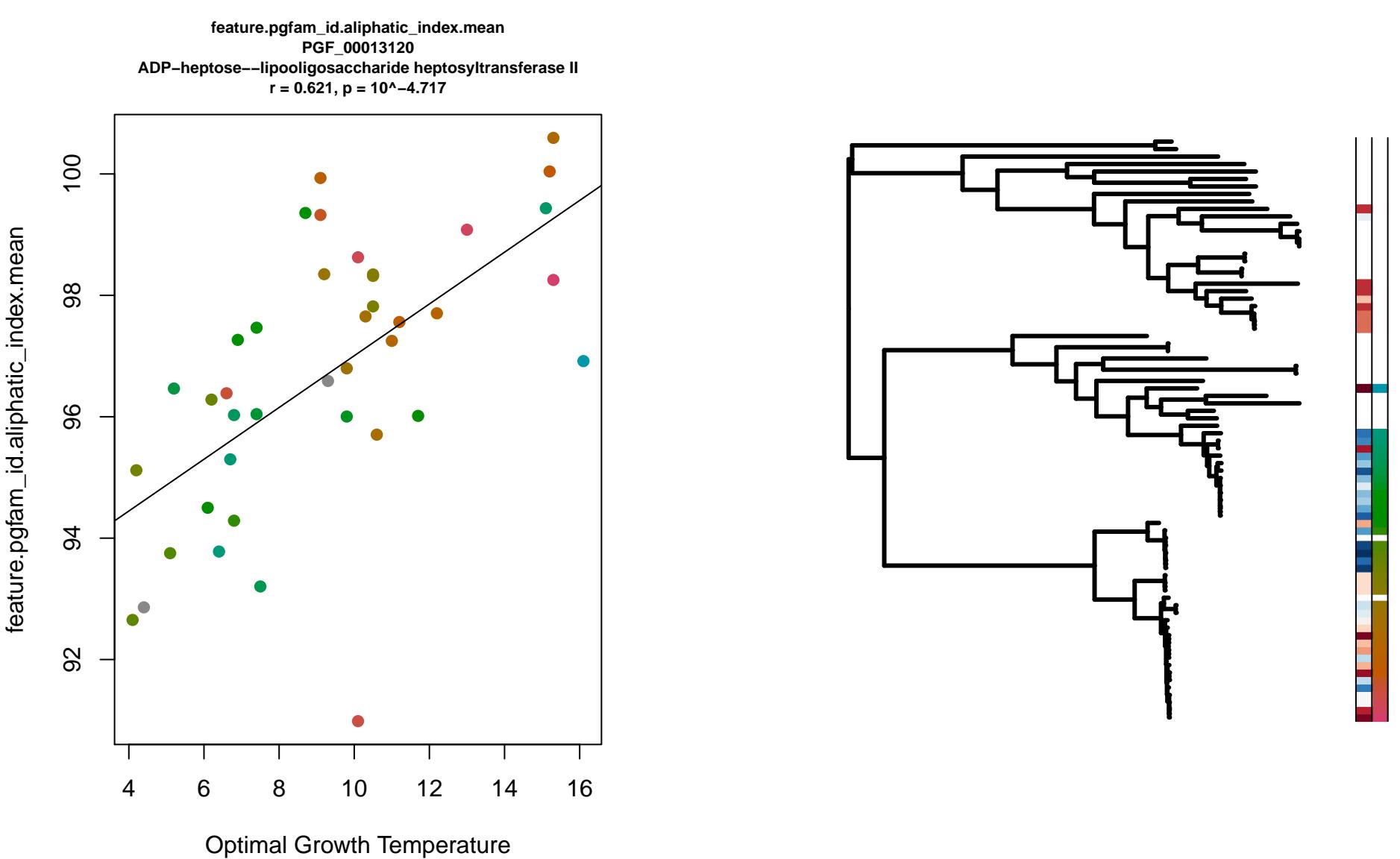
feature.pgfam_id.aliphatic_index.mean



feature.pgfam_id.aliphatic_index.mean
PGF_10454652
UPF0758 family protein
 $r = 0.633, p = 10^{-5.86}$

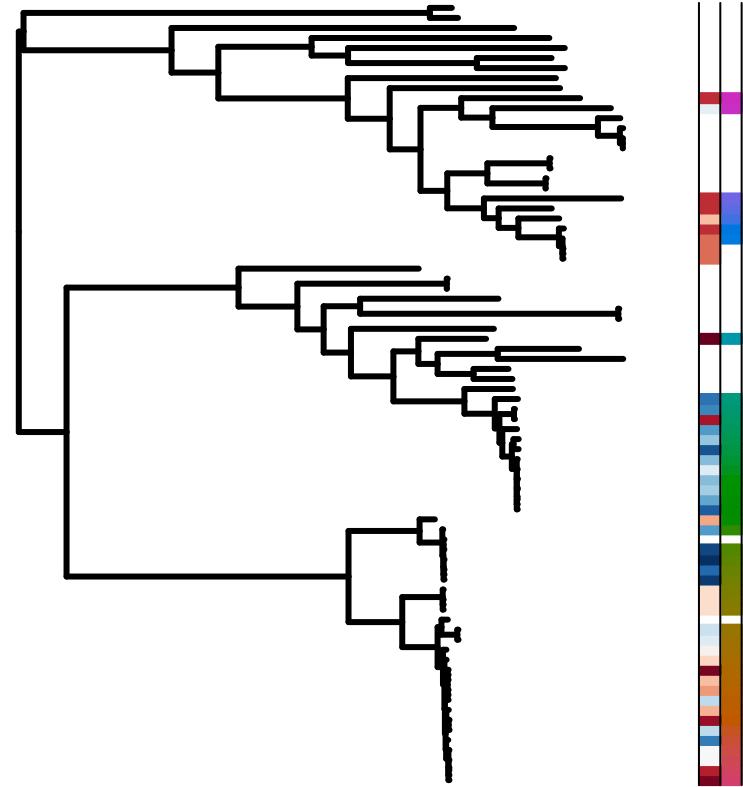
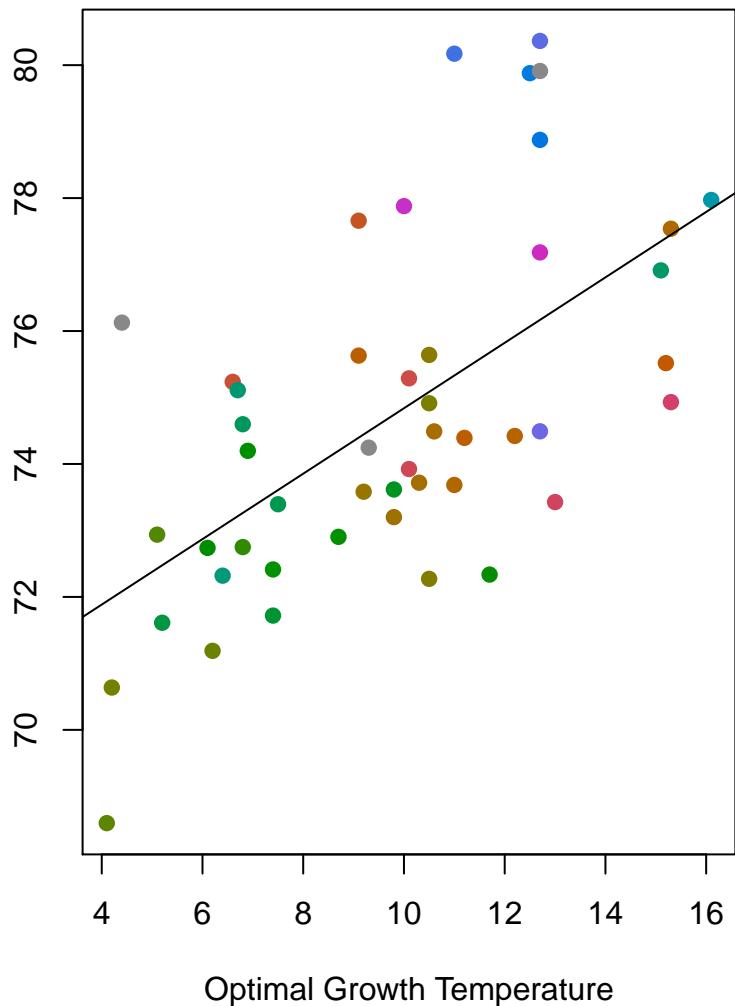
feature.pgfam_id.aliphatic_index.mean





feature.pgfam_id.aliphatic_index.mean
PGF_07179577
Flagellar basal-body rod protein FlgF
 $r = 0.599$, $p = 10^{-5.172}$

feature.pgfam_id.aliphatic_index.mean

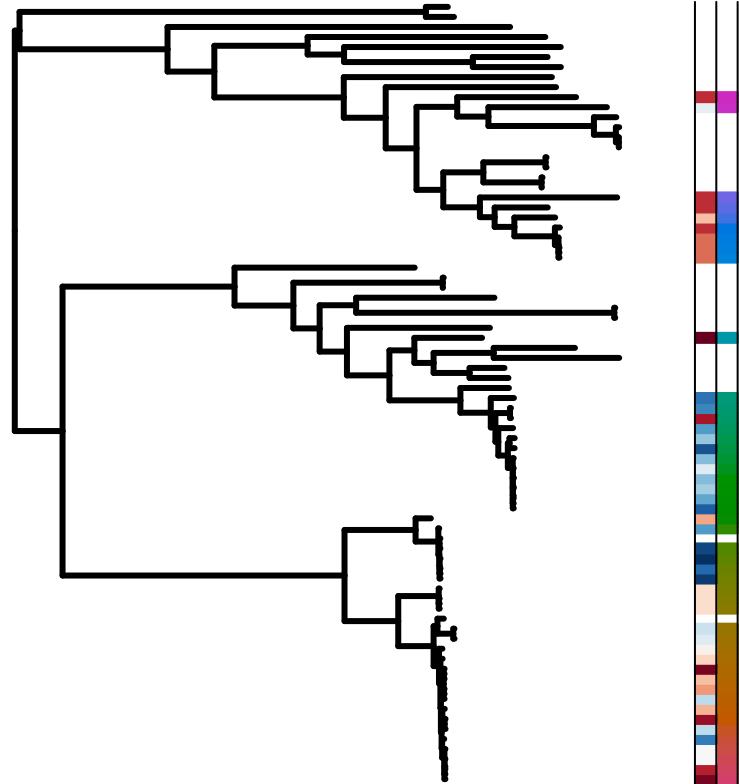
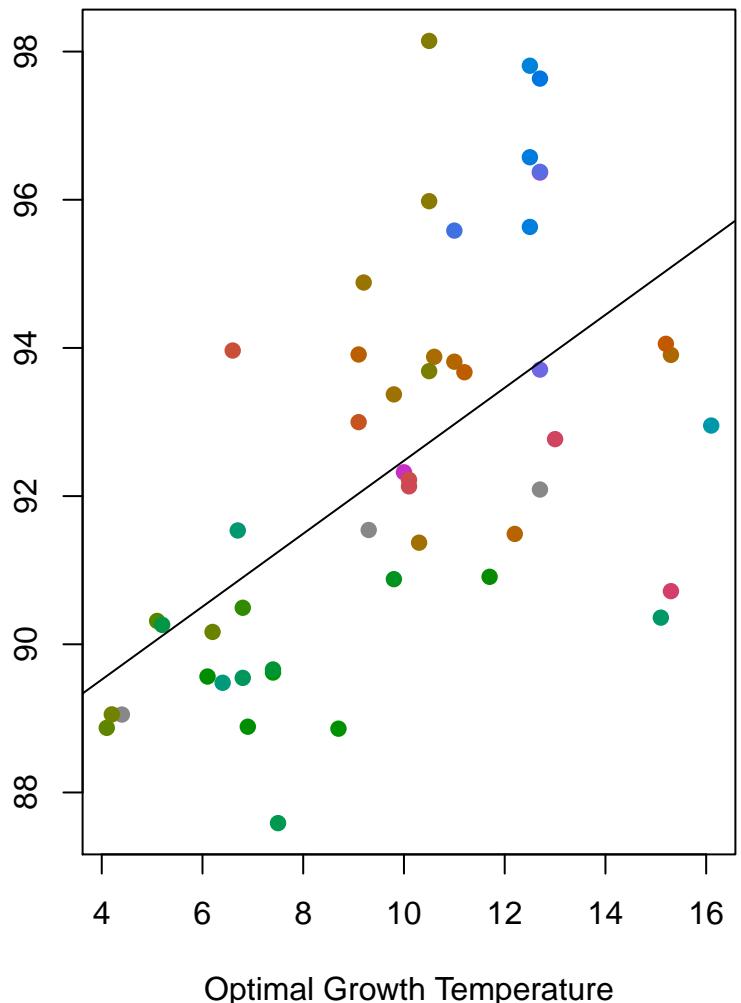


feature.pgfam_id.aliphatic_index.mean

PGF_00417755

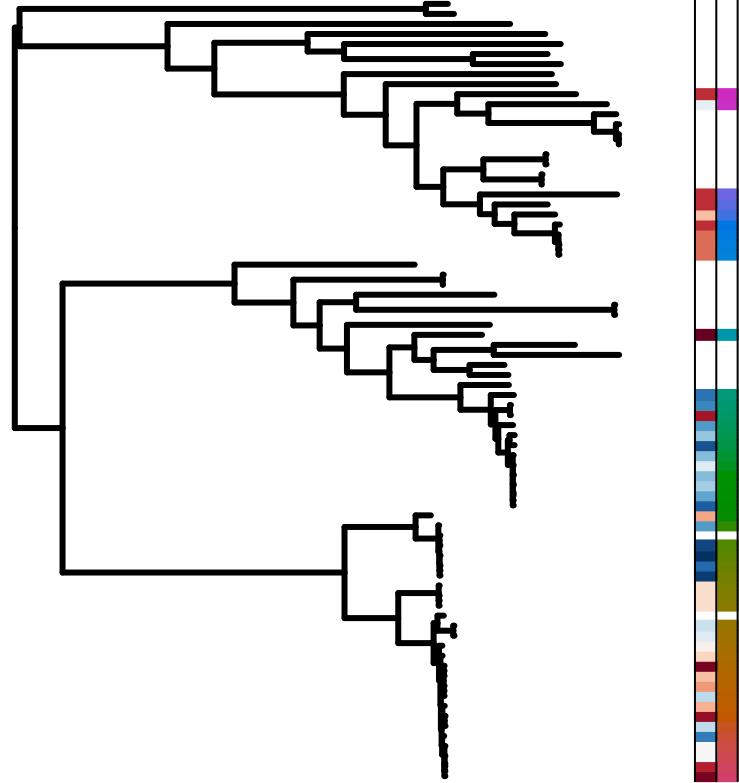
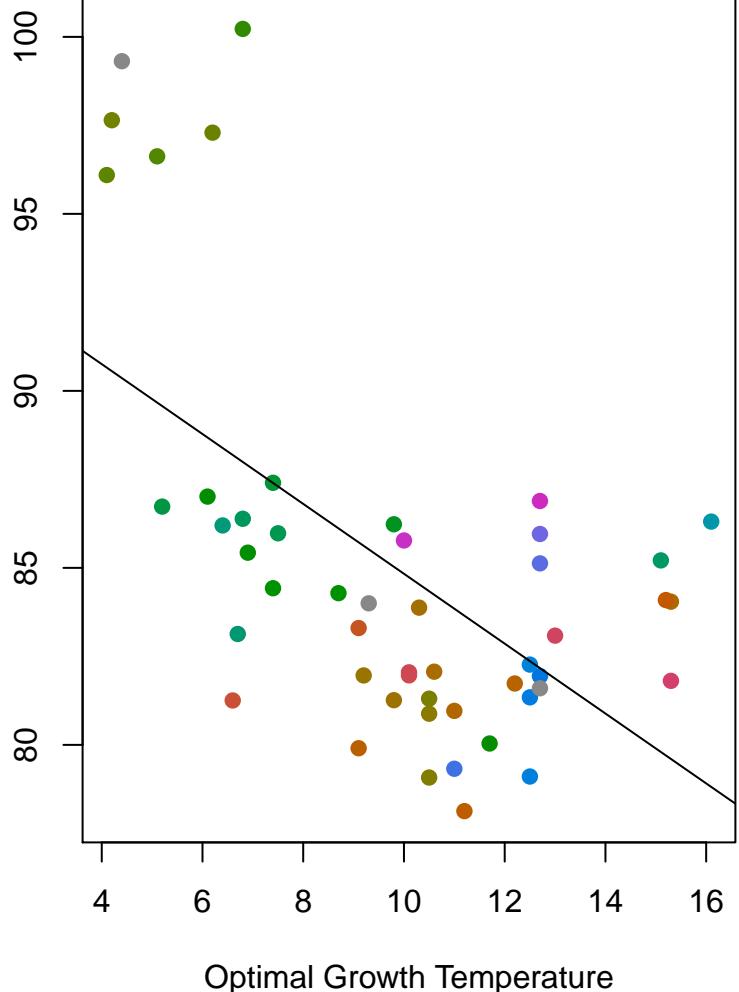
ubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6-hydroxyphenyl methylase (E)
 $r = 0.578, p = 10^{-4.96}$

feature.pgfam_id.aliphatic_index.mean



feature.pgfam_id.aliphatic_index.mean
PGF_00039503
Putative NAD(P)H nitroreductase YdjA
 $r = -0.579$, $p = 10^{-4.975}$

feature.pgfam_id.aliphatic_index.mean



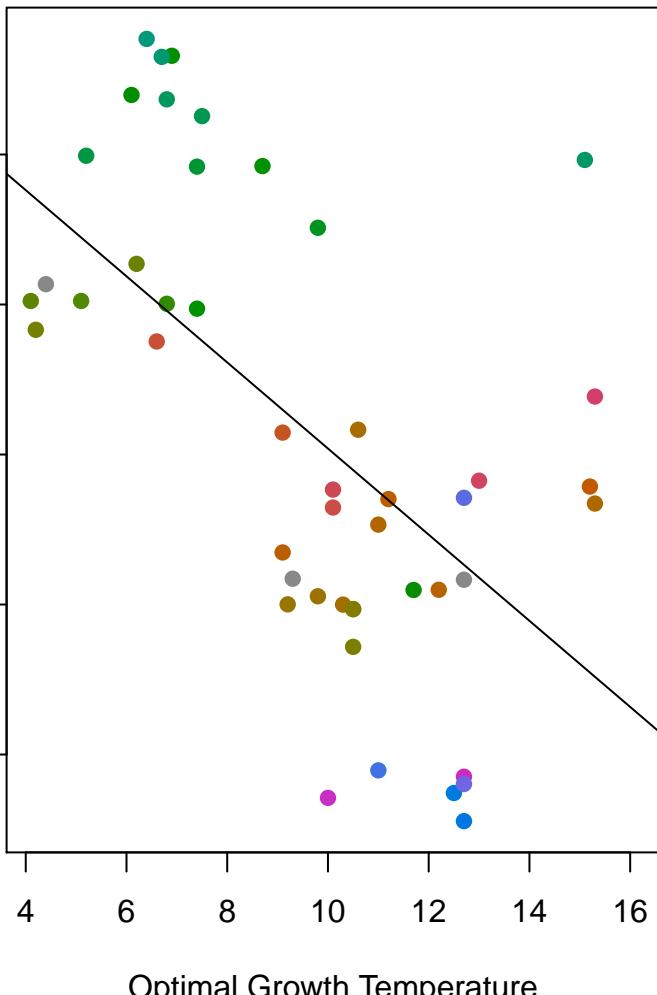
feature.pgfam_id.aliphatic_index.mean

PGF_00707140

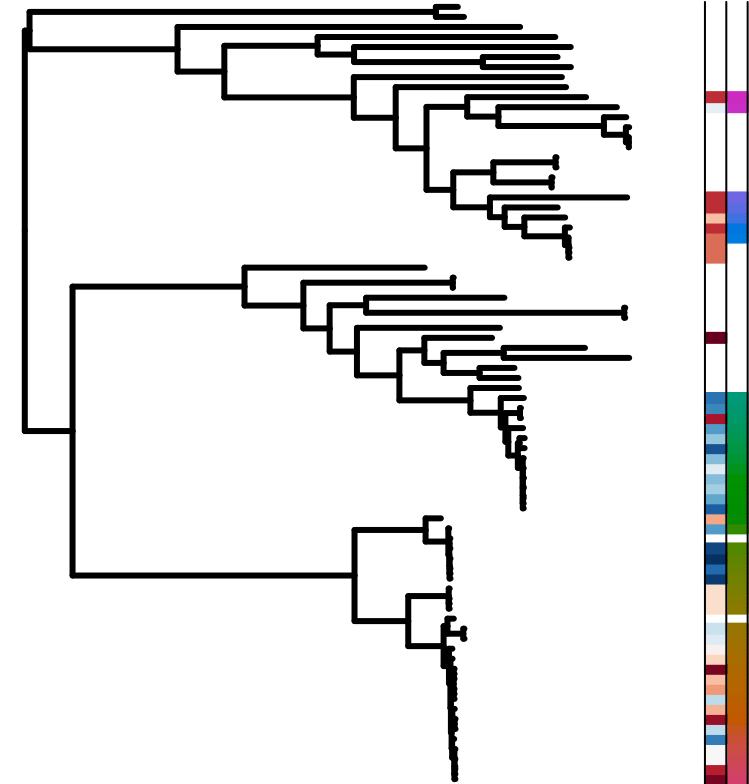
Cys-tRNA(Pro) deacylase YbaK

$r = -0.585, p = 10^{-4.813}$

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature



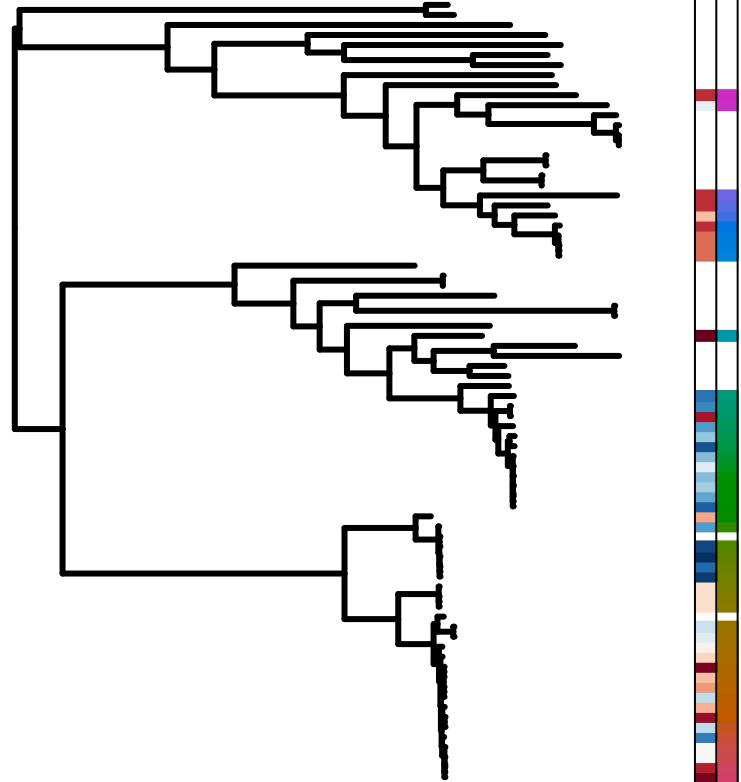
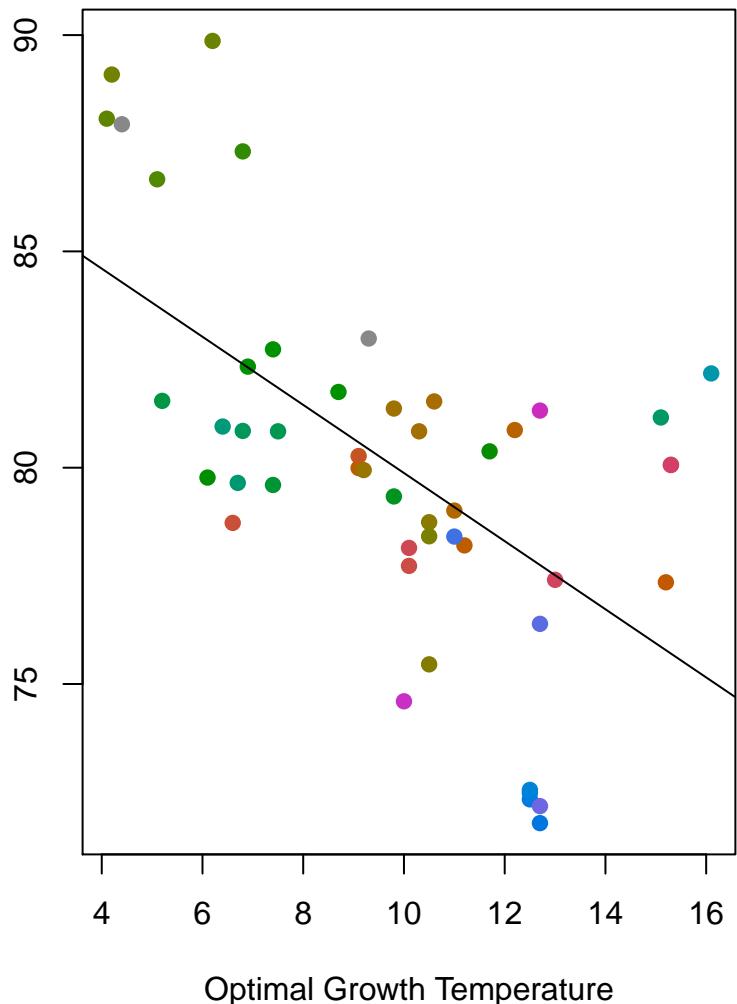


feature.pgfam_id.aliphatic_index.mean

PGF_01782190

3-deoxy-D-manno-octulosonic acid kinase (EC 2.7.1.166)

$r = -0.593, p = 10^{-5.145}$

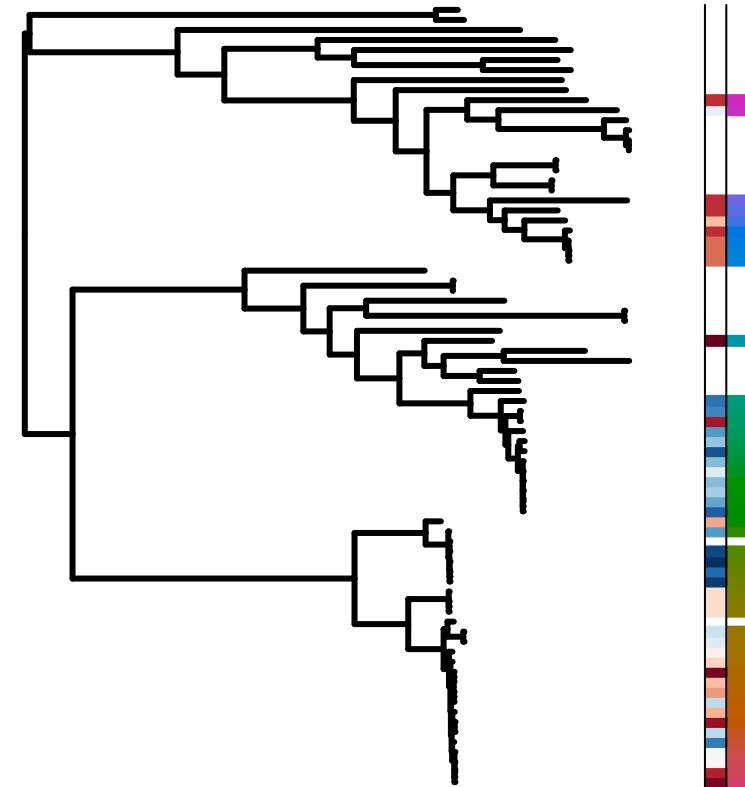
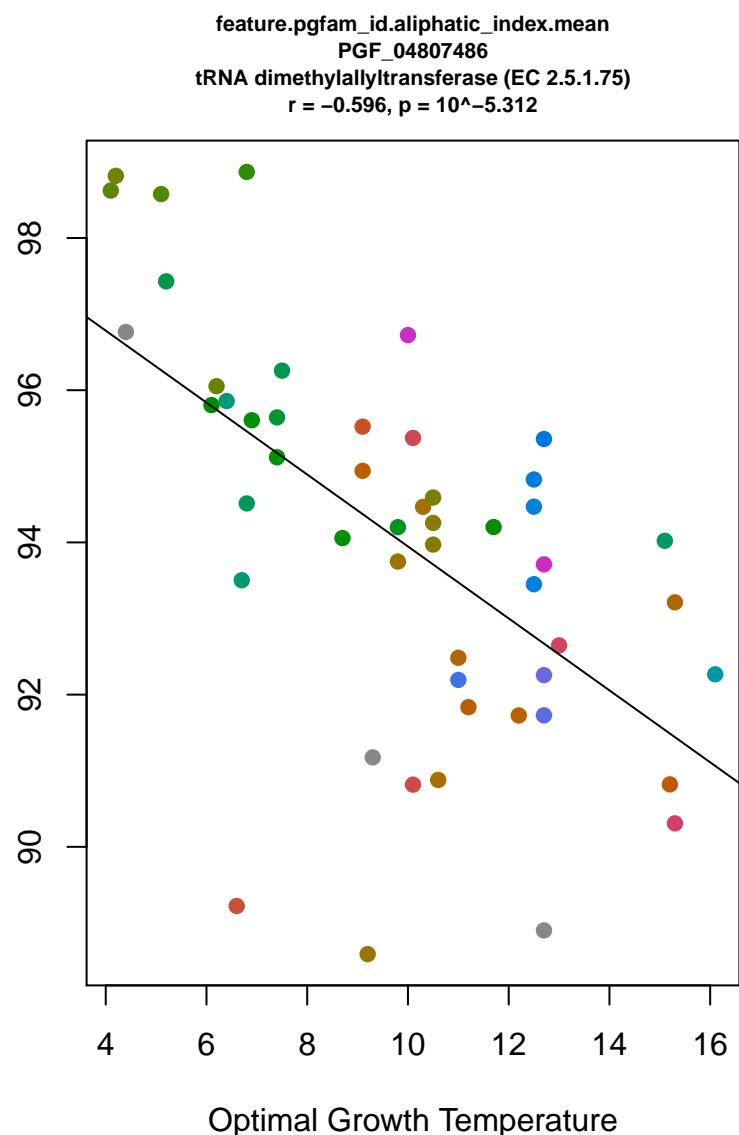


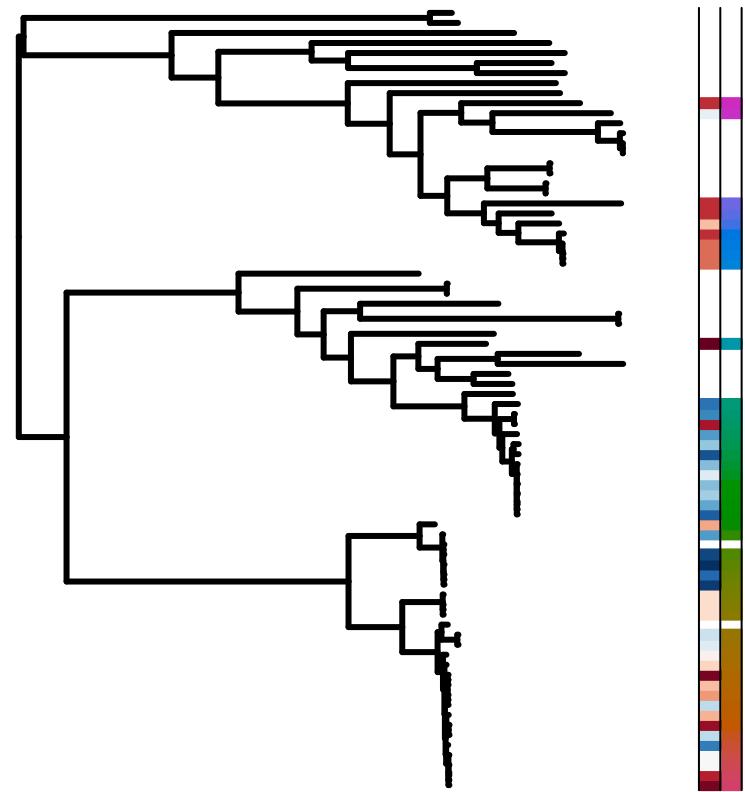
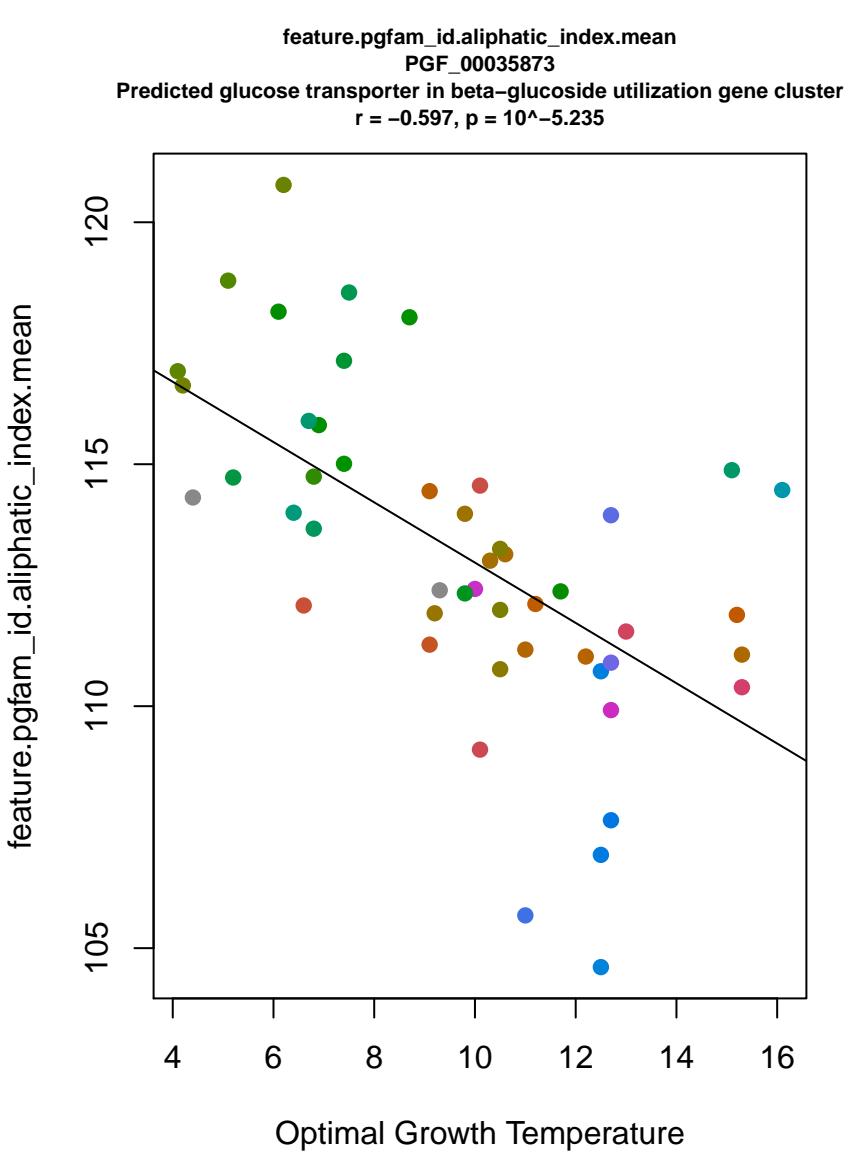
feature.pgfam_id.aliphatic_index.mean

PGF_04807486

tRNA dimethylallyltransferase (EC 2.5.1.75)

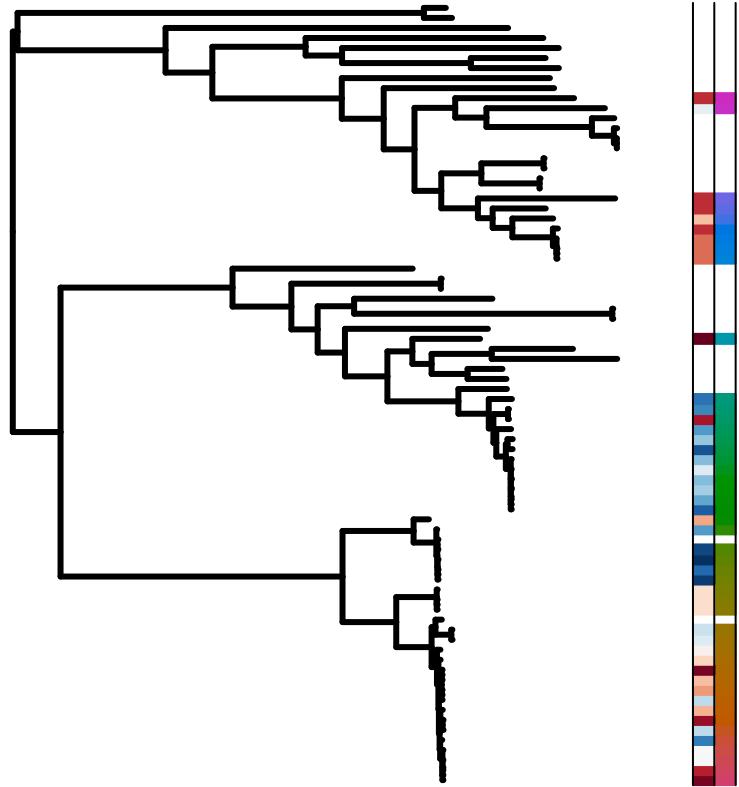
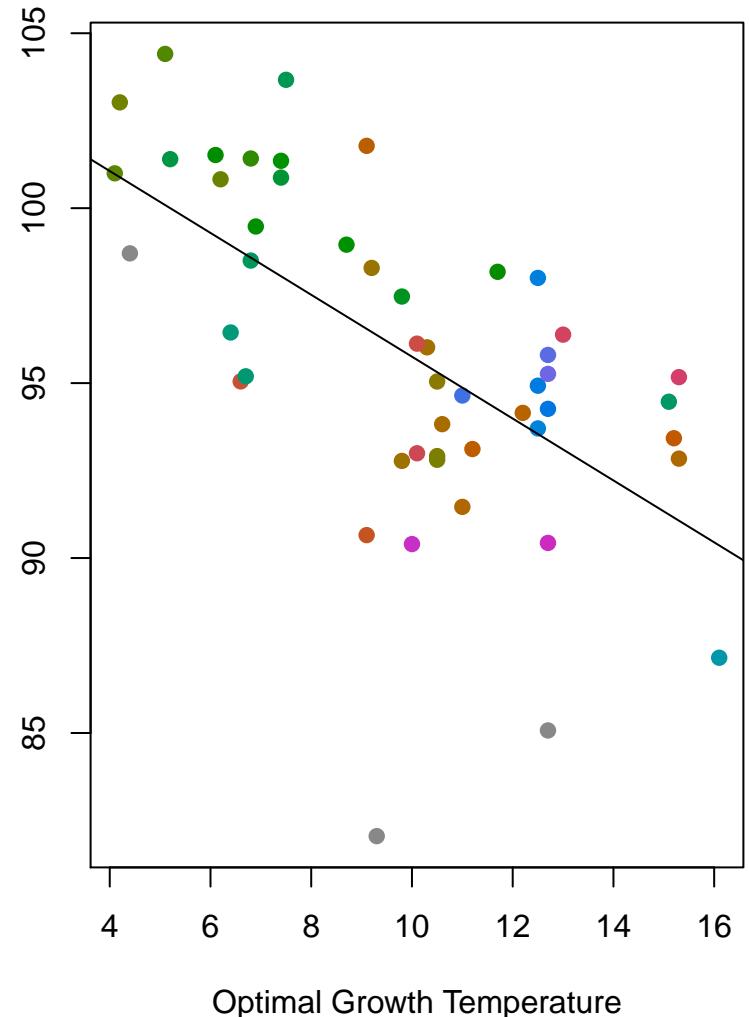
$r = -0.596$, $p = 10^{-5.312}$





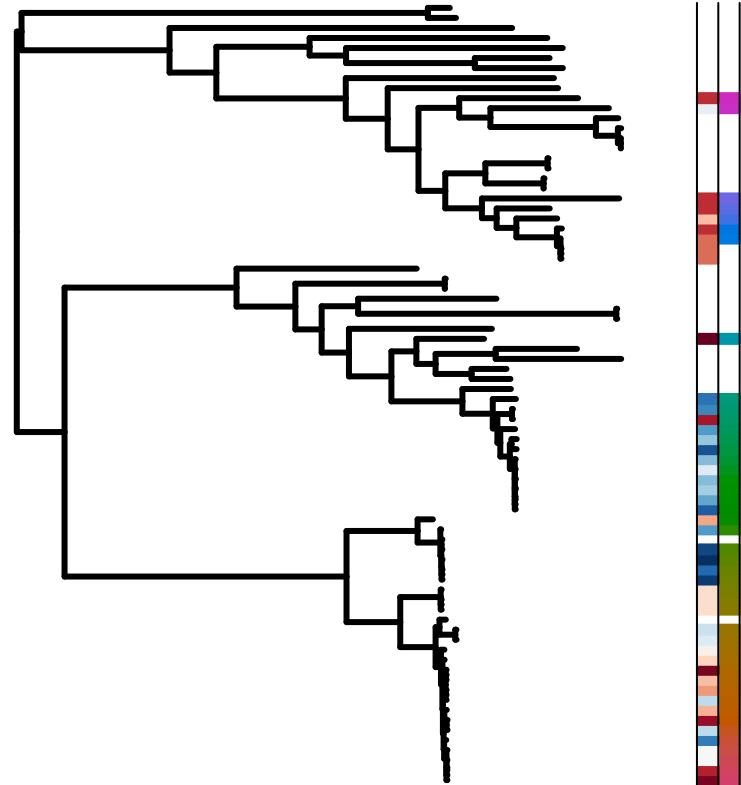
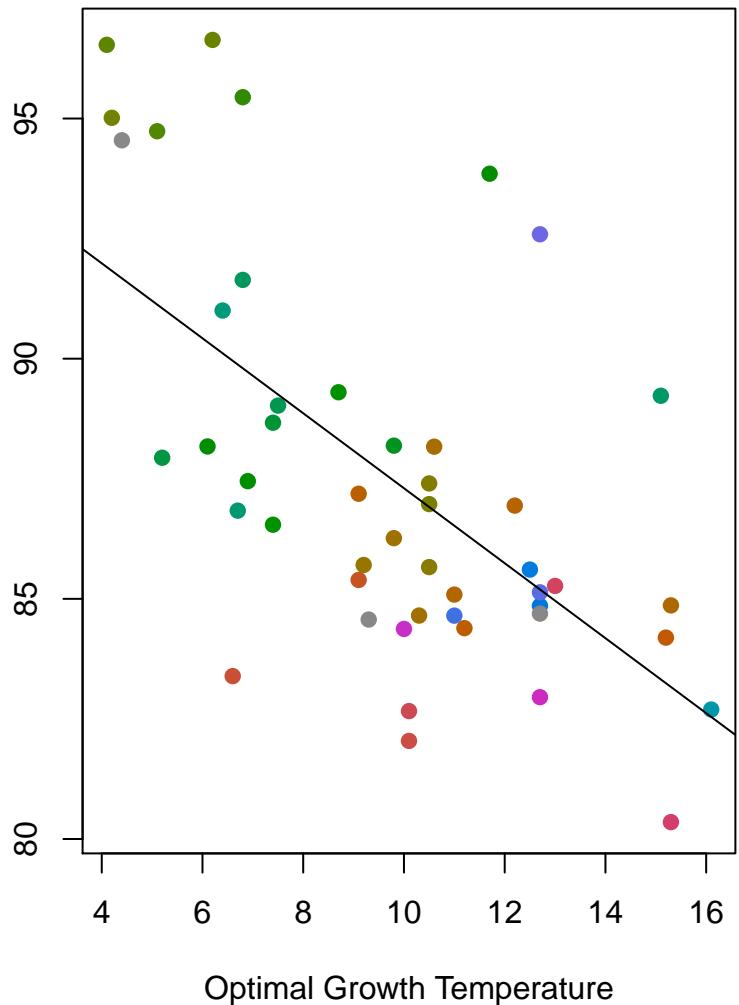


feature.pgfam_id.aliphatic_index.mean
PGF_01336539
hypothetical protein
 $r = -0.605, p = 10^{-5.477}$



feature.pgfam_id.aliphatic_index.mean
PGF_07058319
General secretion pathway protein K
 $r = -0.612$, $p = 10^{-5.426}$

feature.pgfam_id.aliphatic_index.mean



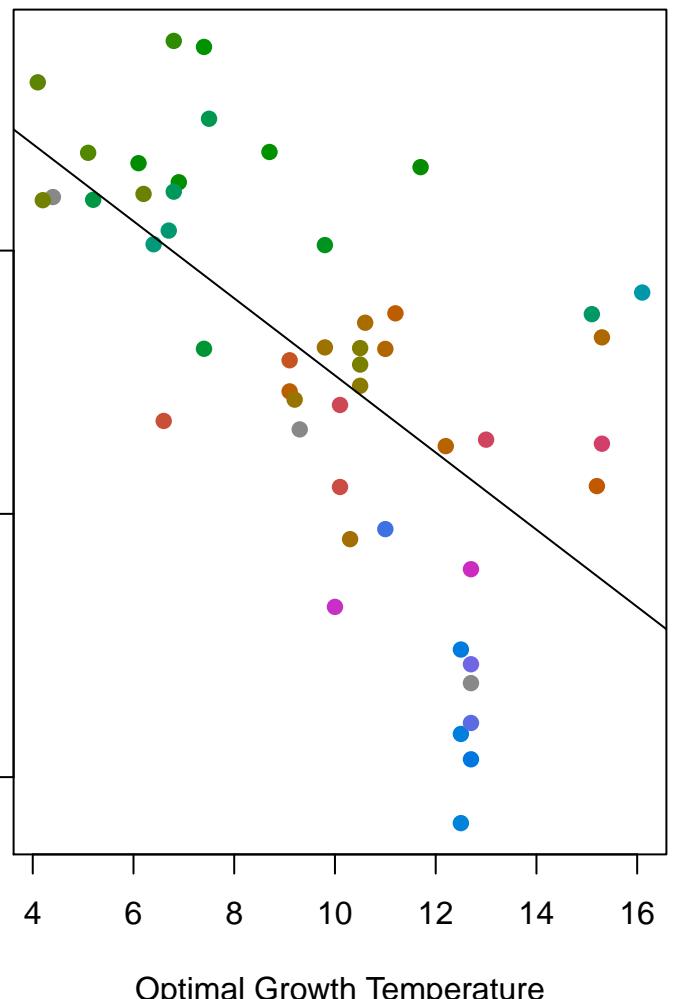
feature.pgfam_id.aliphatic_index.mean

PGF_02473279

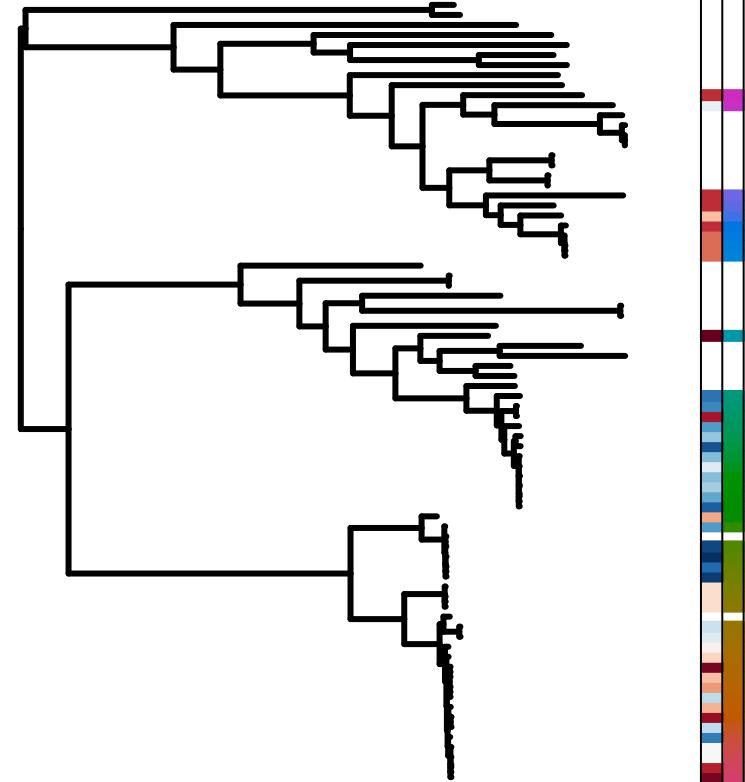
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)

$r = -0.623, p = 10^{-5.874}$

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature



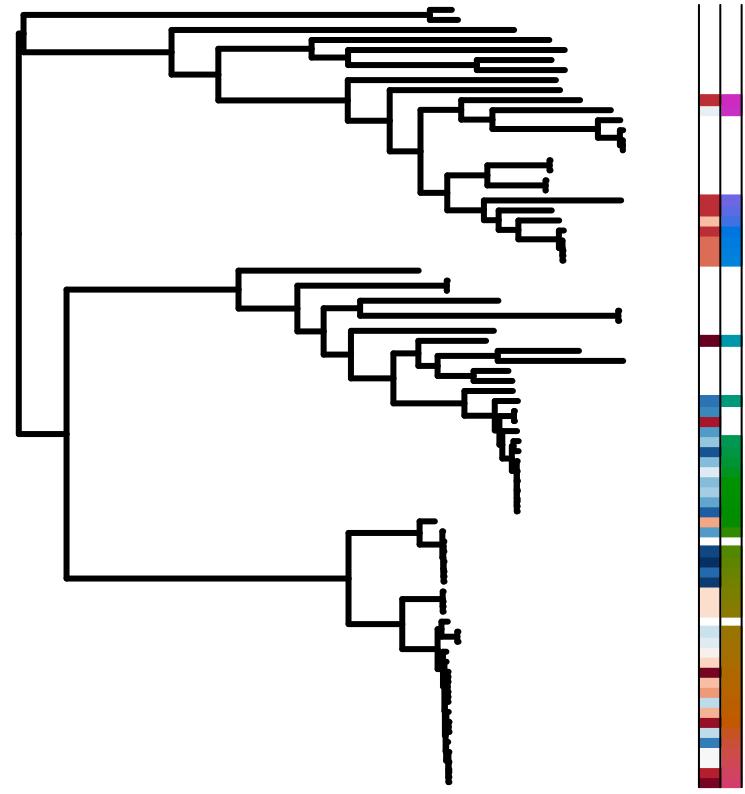
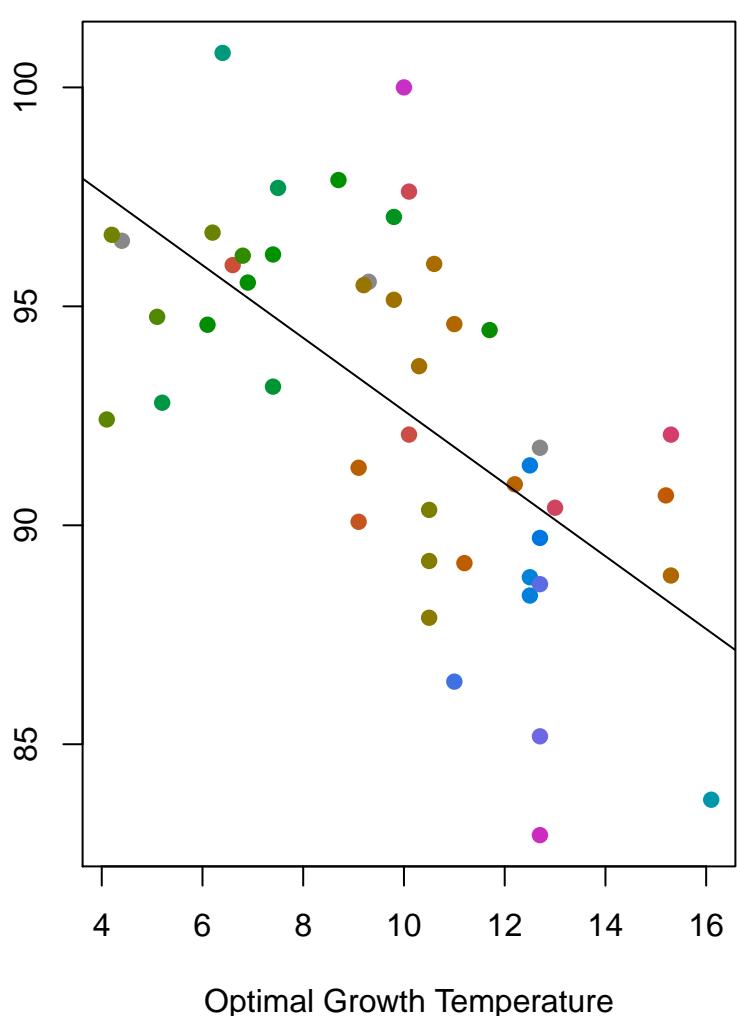
feature.pgfam_id.aliphatic_index.mean

PGF_00035421

Potential queD like 2

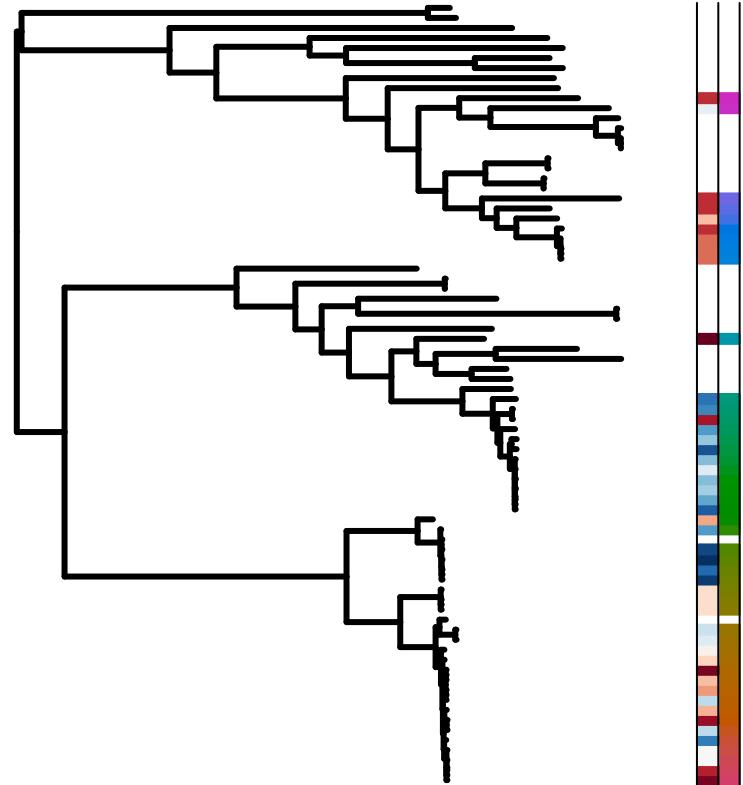
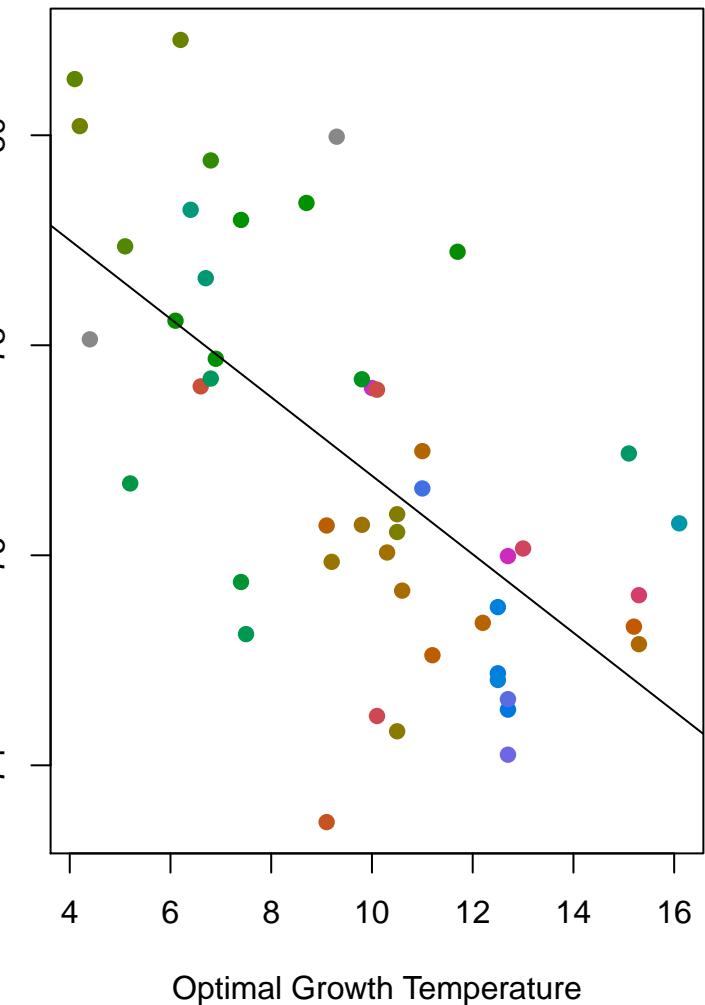
$r = -0.628$, $p = 10^{-5.629}$

feature.pgfam_id.aliphatic_index.mean



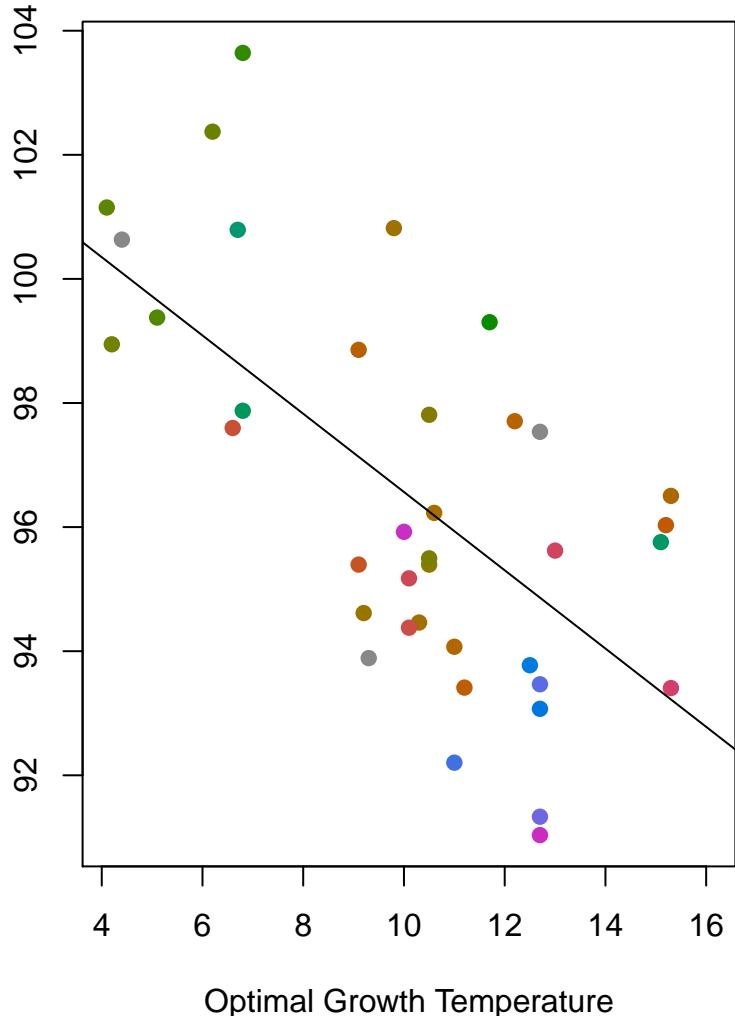
feature.pgfam_id.aliphatic_index.mean
PGF_00016431
LSU ribosomal protein L3p (L3e)
 $r = -0.63$, $p = 10^{-5.914}$

feature.pgfam_id.aliphatic_index.mean

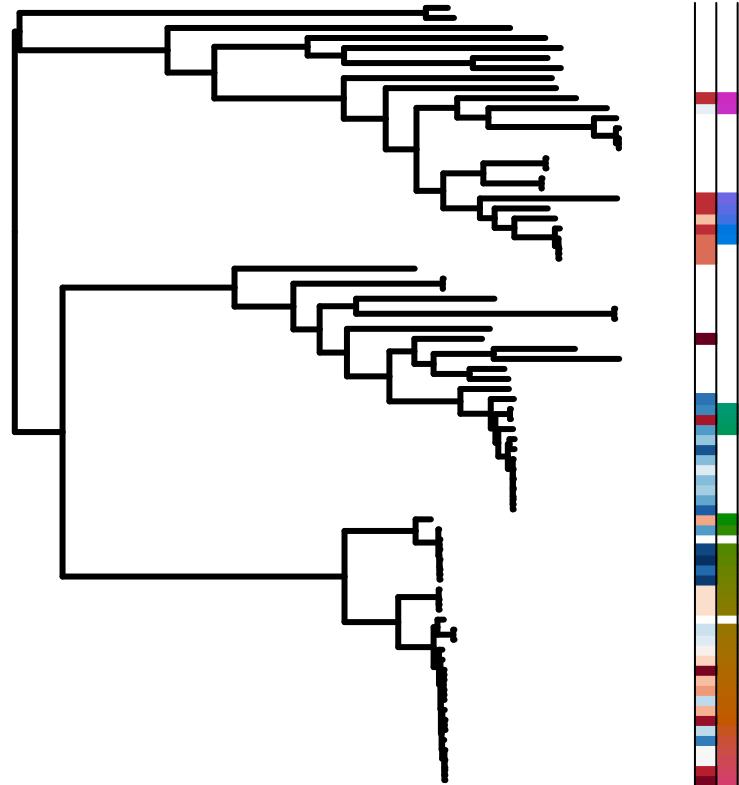


feature.pgfam_id.aliphatic_index.mean
PGF_05554840
Cobyric acid synthase (EC 6.3.5.10)
 $r = -0.636$, $p = 10^{-4.742}$

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature



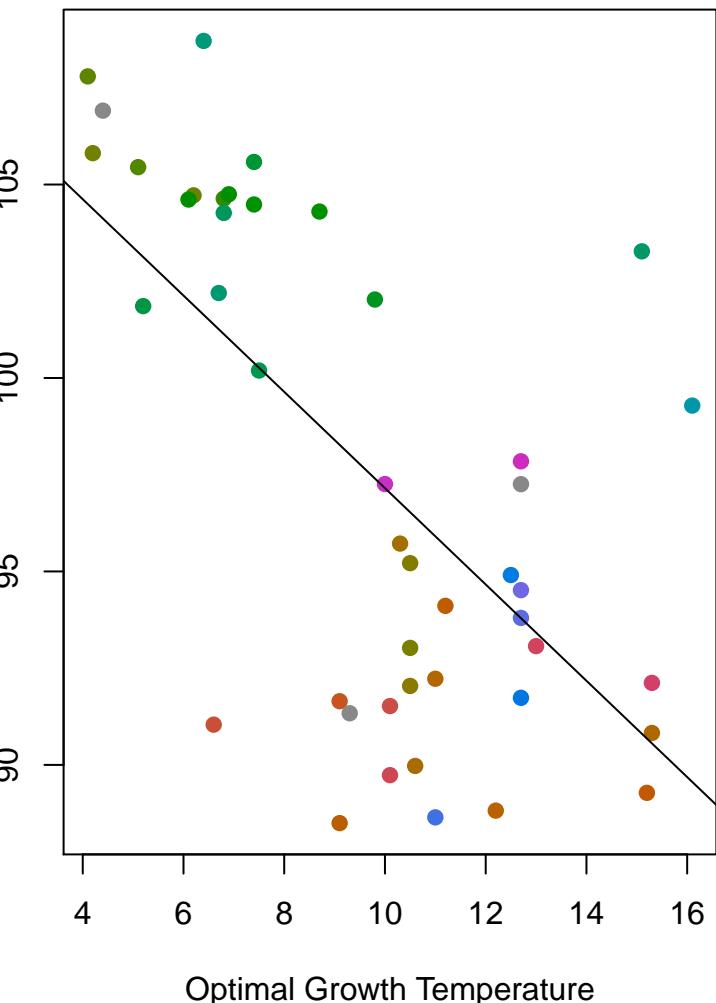
feature.pgfam_id.aliphatic_index.mean

PGF_03774796

Flagellar biosynthesis protein FliS

$r = -0.637, p = 10^{-5.599}$

feature.pgfam_id.aliphatic_index.mean



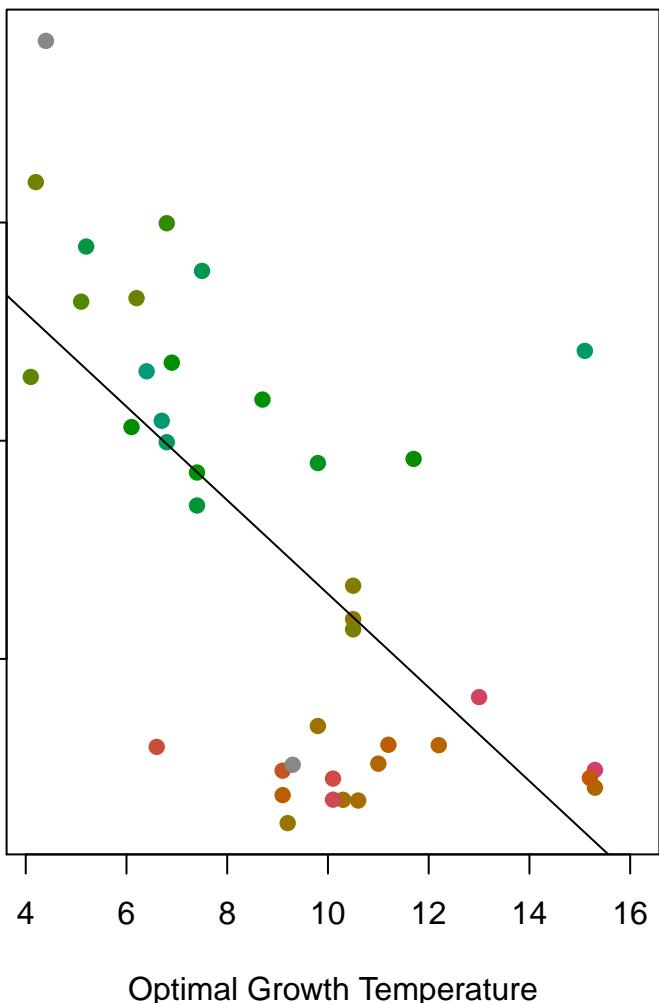
feature.pgfam_id.aliphatic_index.mean

PGF_00305244

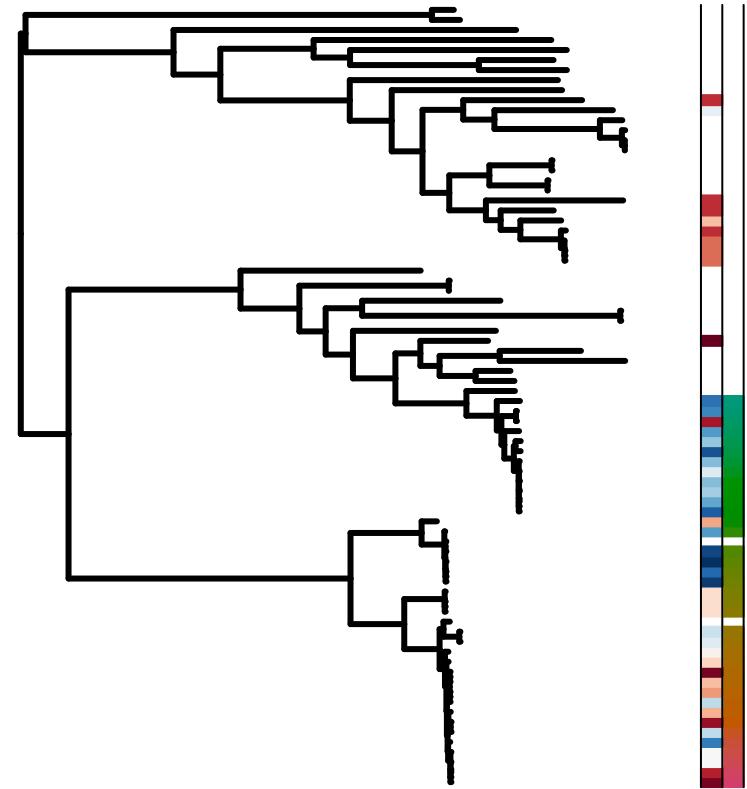
hypothetical protein

$r = -0.653, p = 10^{-5.188}$

feature.pgfam_id.aliphatic_index.mean

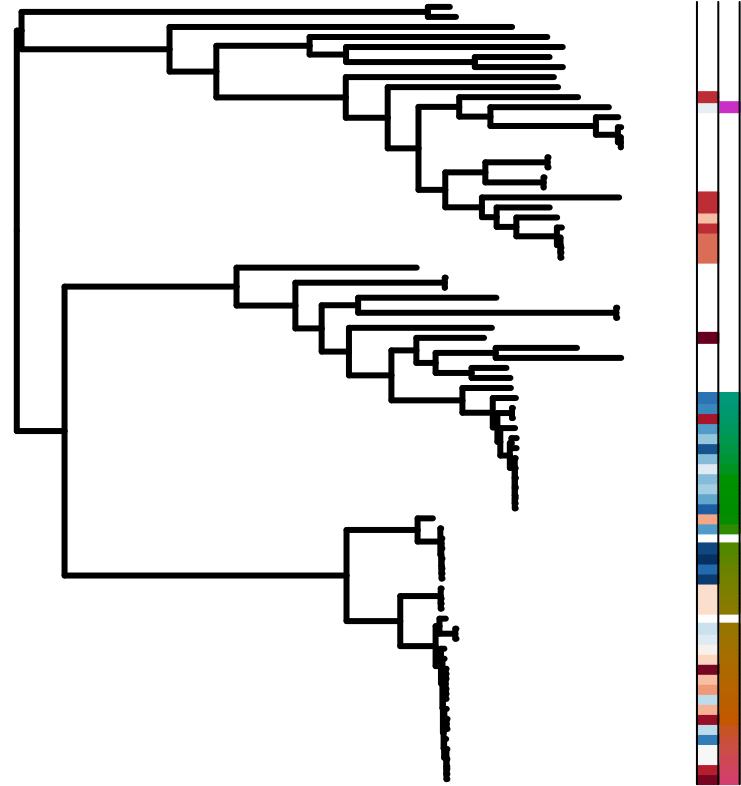
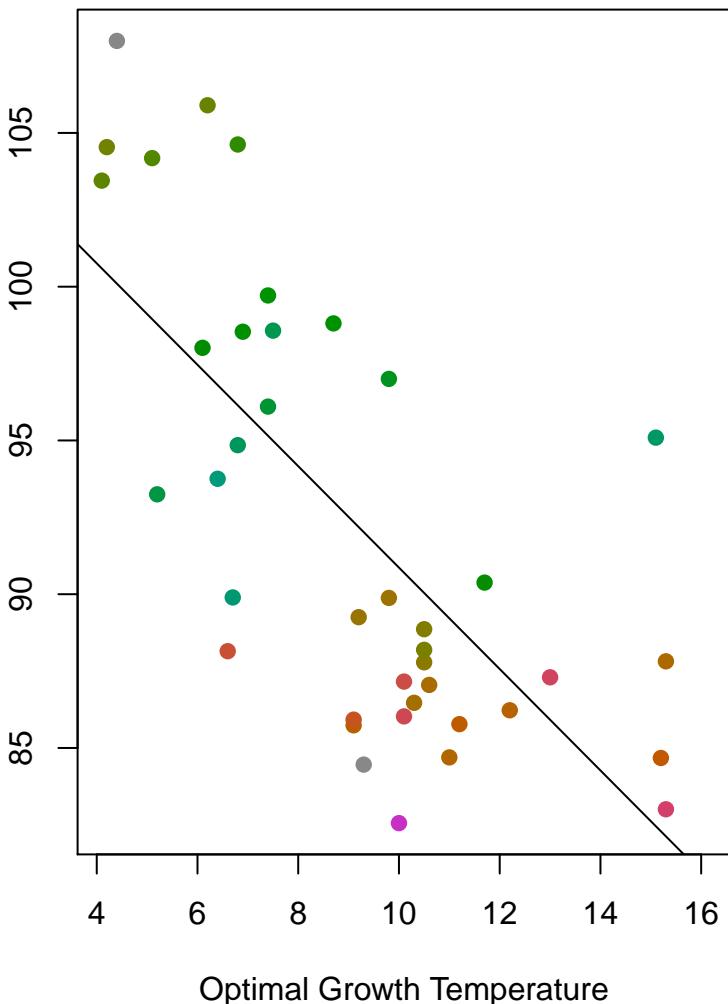


Optimal Growth Temperature



feature.pgfam_id.aliphatic_index.mean
PGF_01338555
hypothetical protein
 $r = -0.697$, $p = 10^{-6.245}$

feature.pgfam_id.aliphatic_index.mean



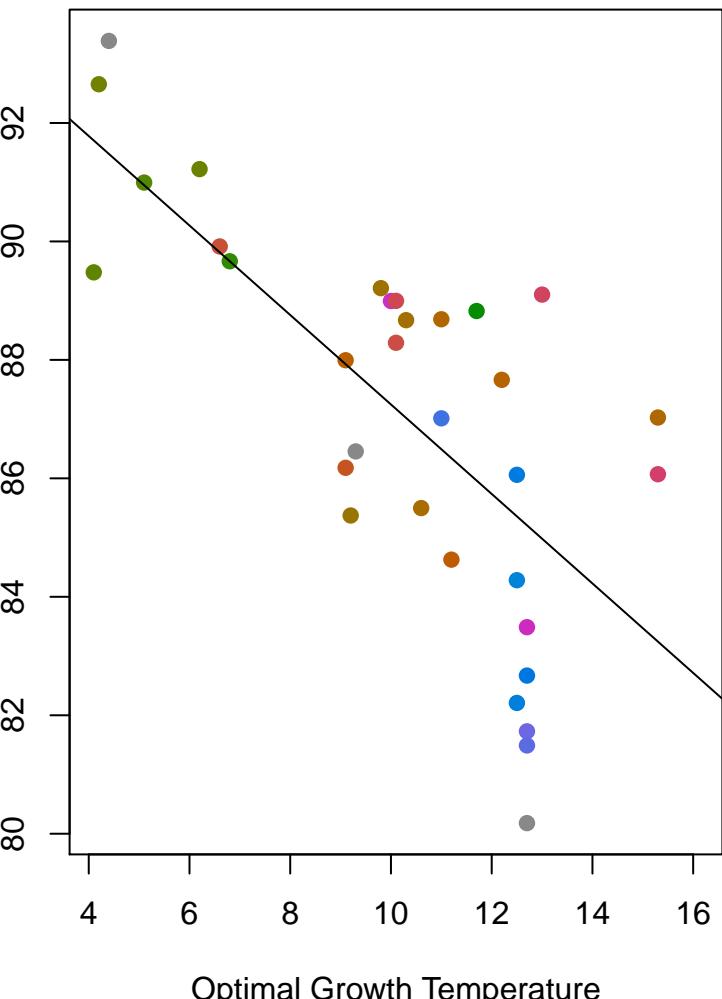
feature.pgfam_id.aliphatic_index.mean

PGF_03940803

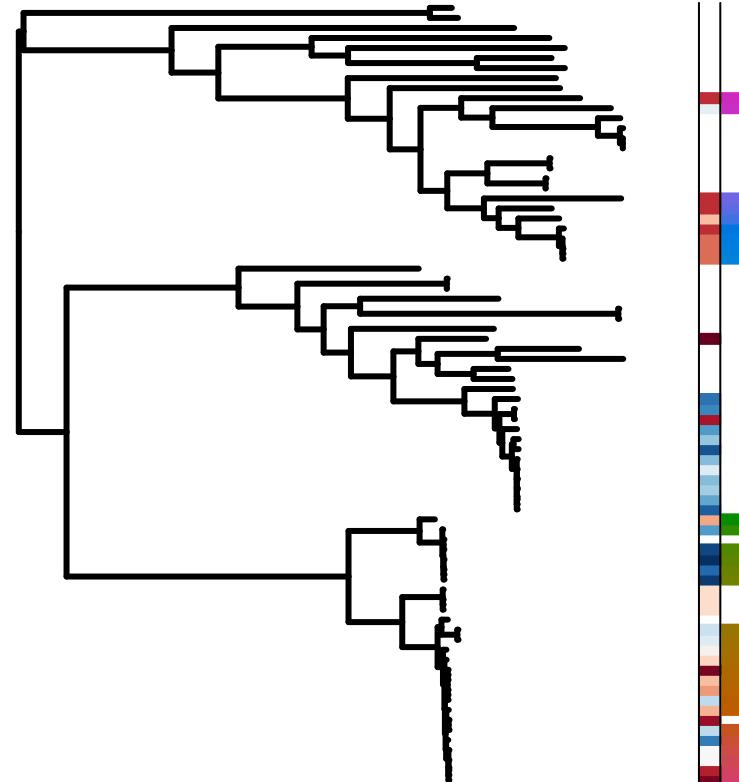
Alkylated DNA repair protein

$r = -0.705, p = 10^{-5.341}$

feature.pgfam_id.aliphatic_index.mean

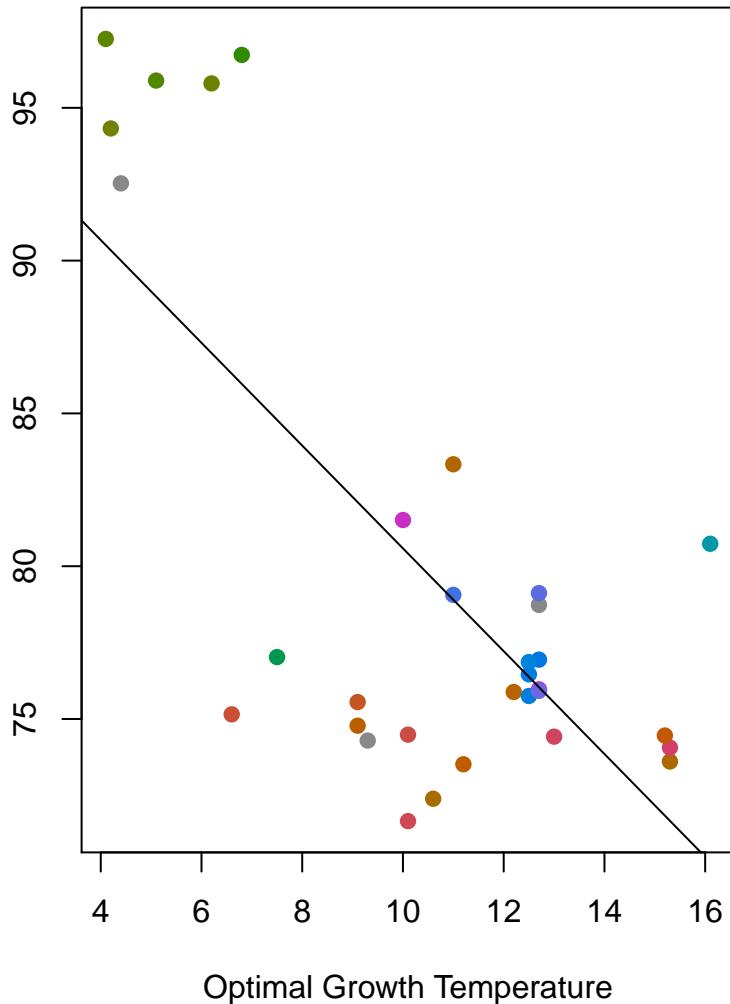


Optimal Growth Temperature

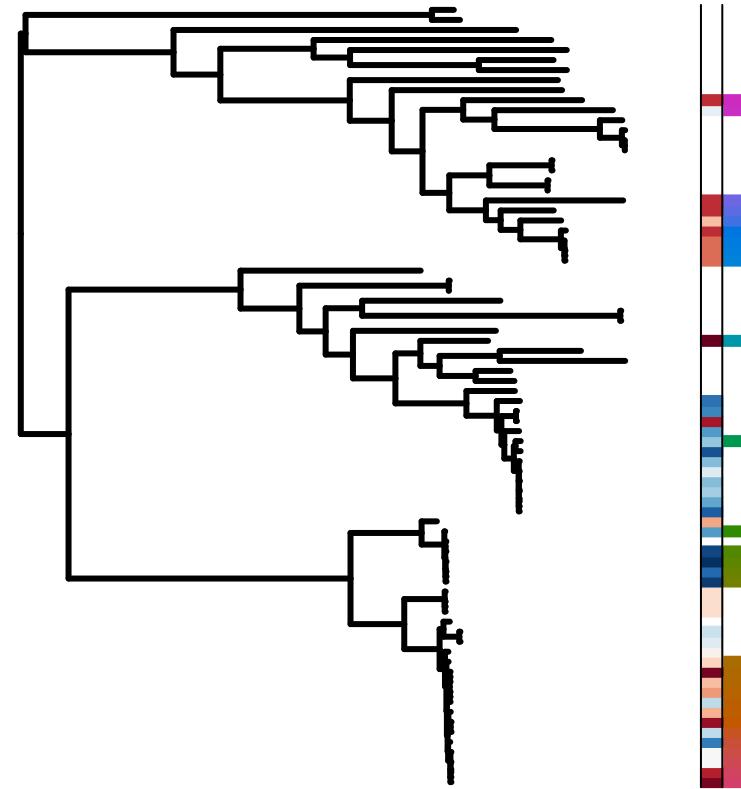


feature.pgfam_id.aliphatic_index.mean
PGF_06641194
Capsule biosynthesis protein capA
 $r = -0.707$, $p = 10^{-5.224}$

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature



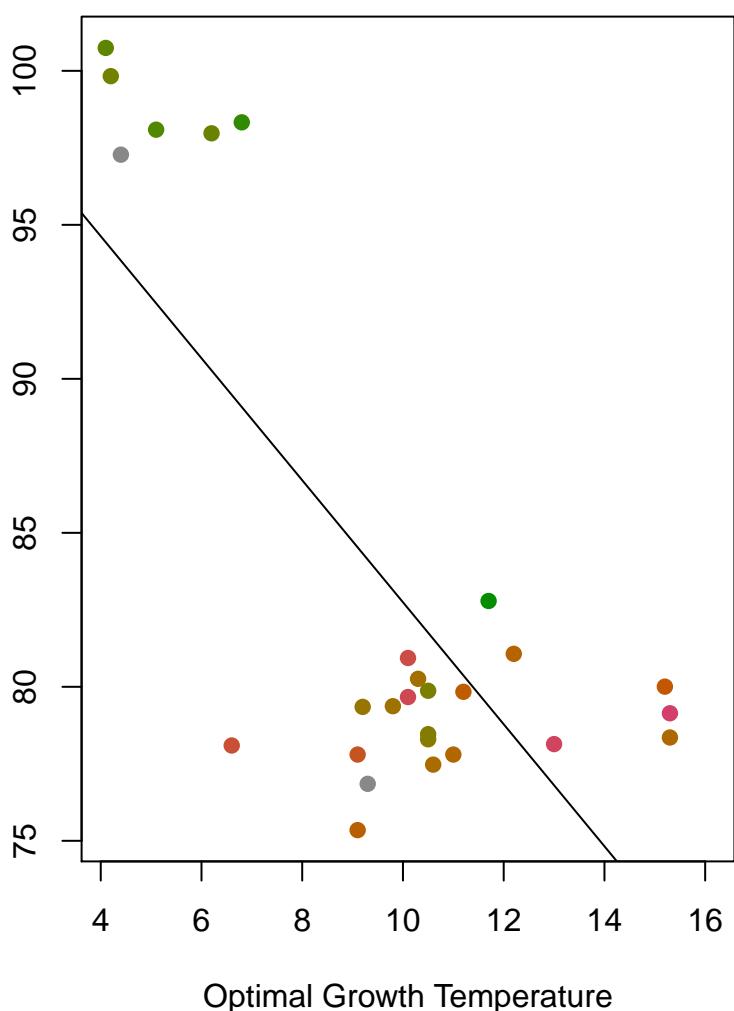
feature.pgfam_id.aliphatic_index.mean

PGF_11018774

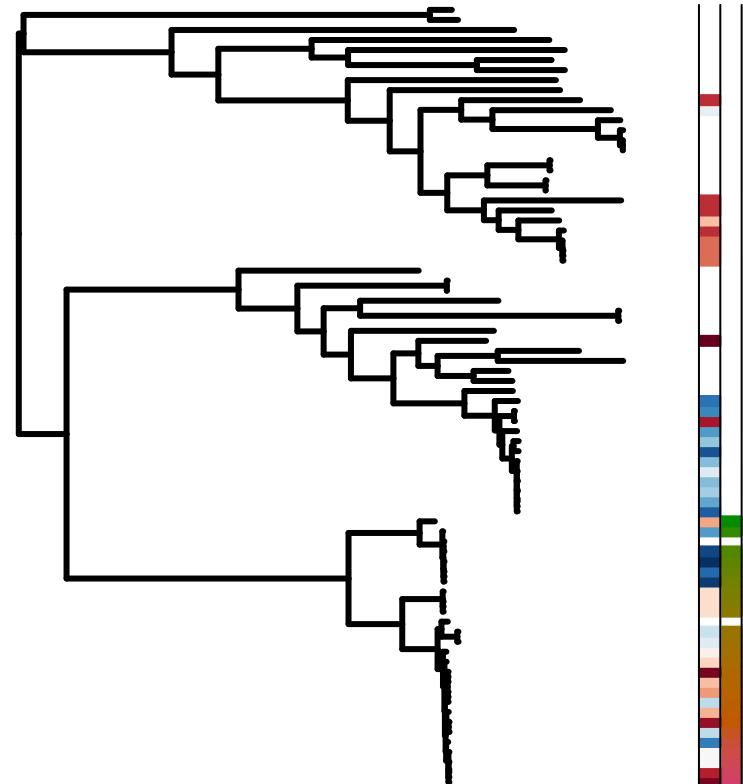
hypothetical protein

$r = -0.743, p = 10^{-5.043}$

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature

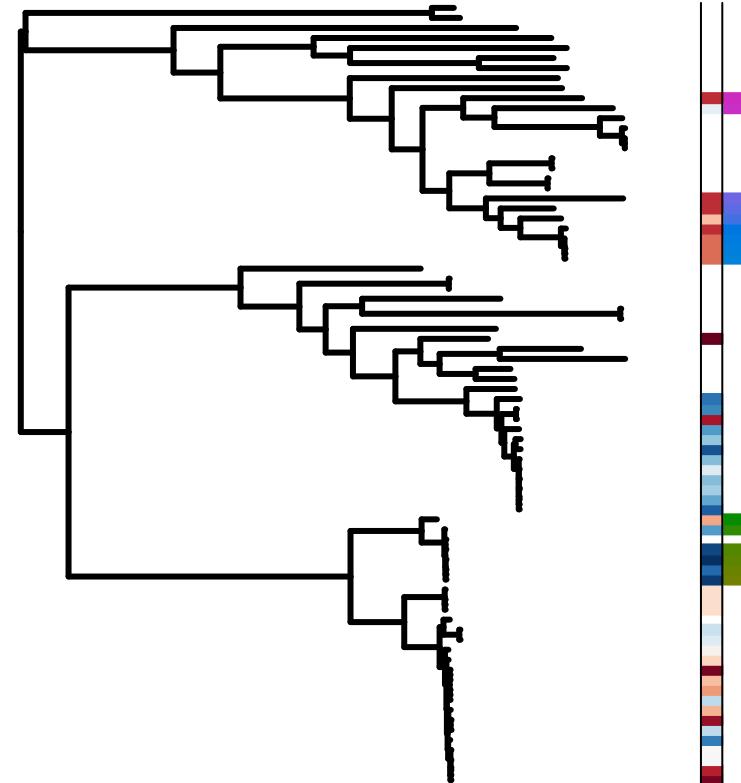
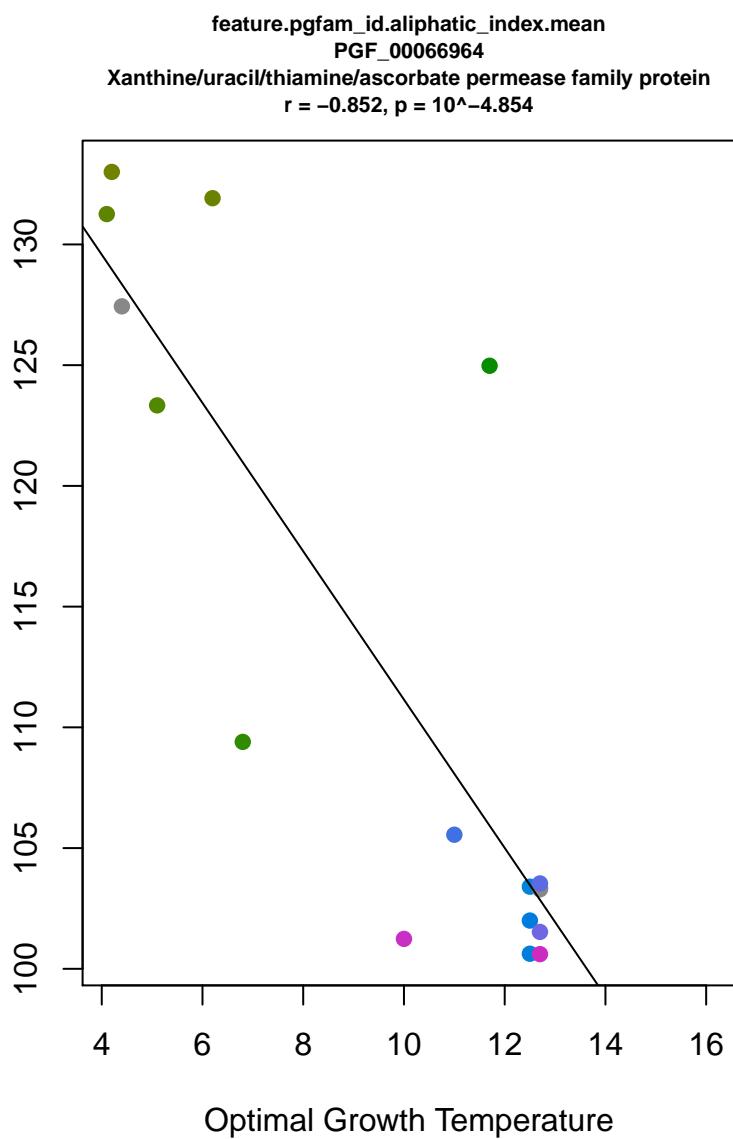
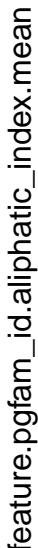


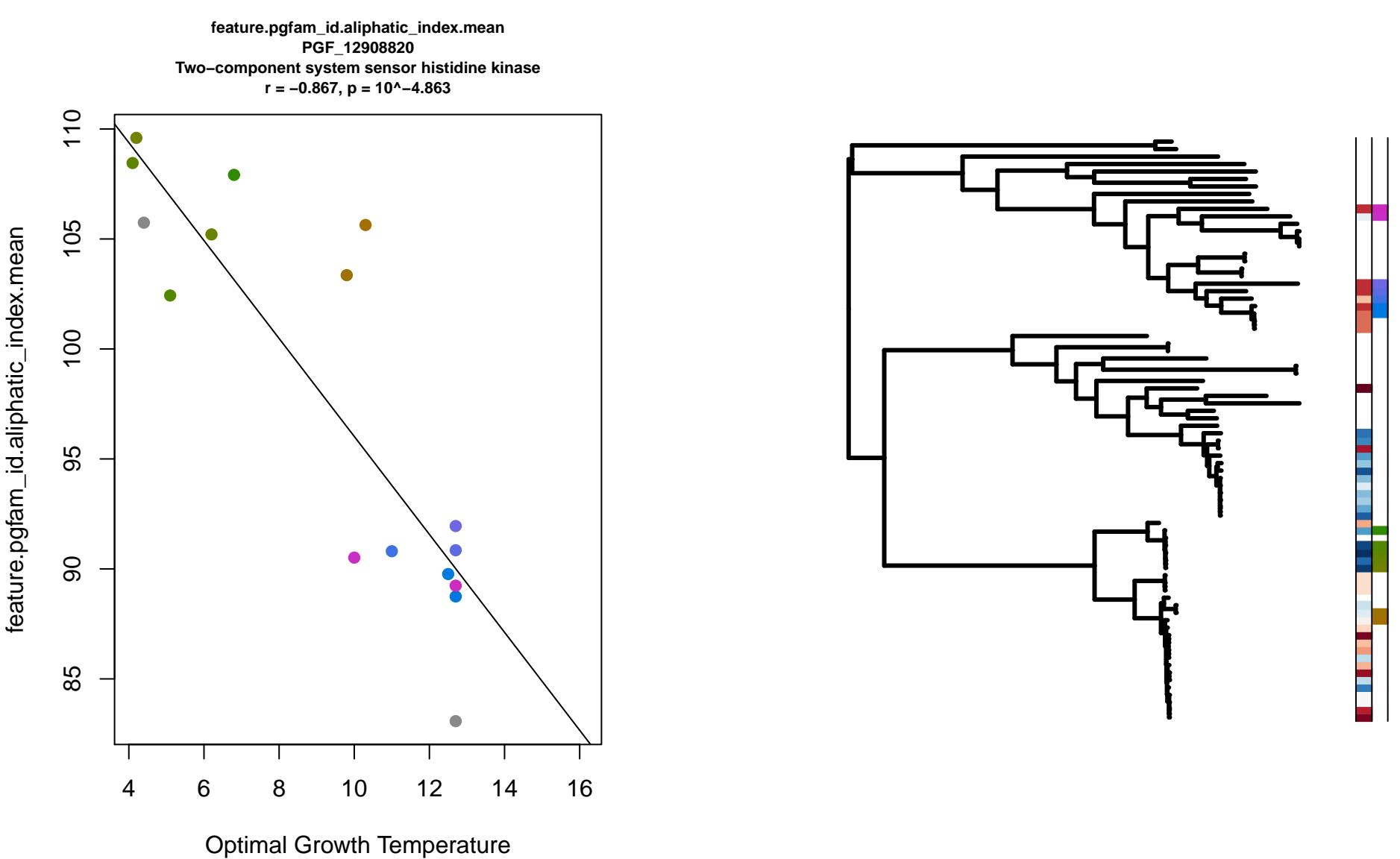
feature.pgfam_id.aliphatic_index.mean

PGF_00066964

Xanthine/uracil/thiamine/ascorbate permease family protein

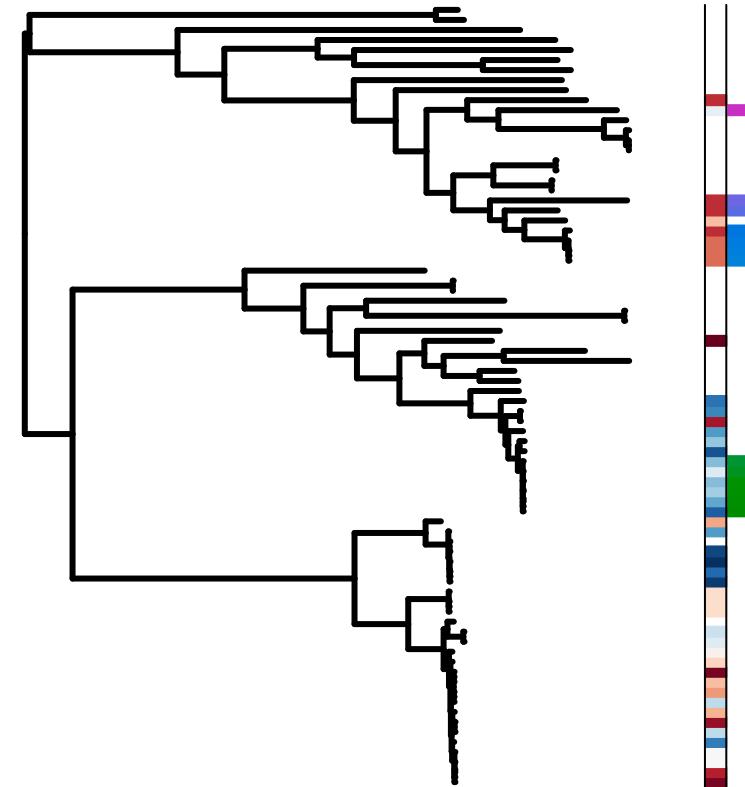
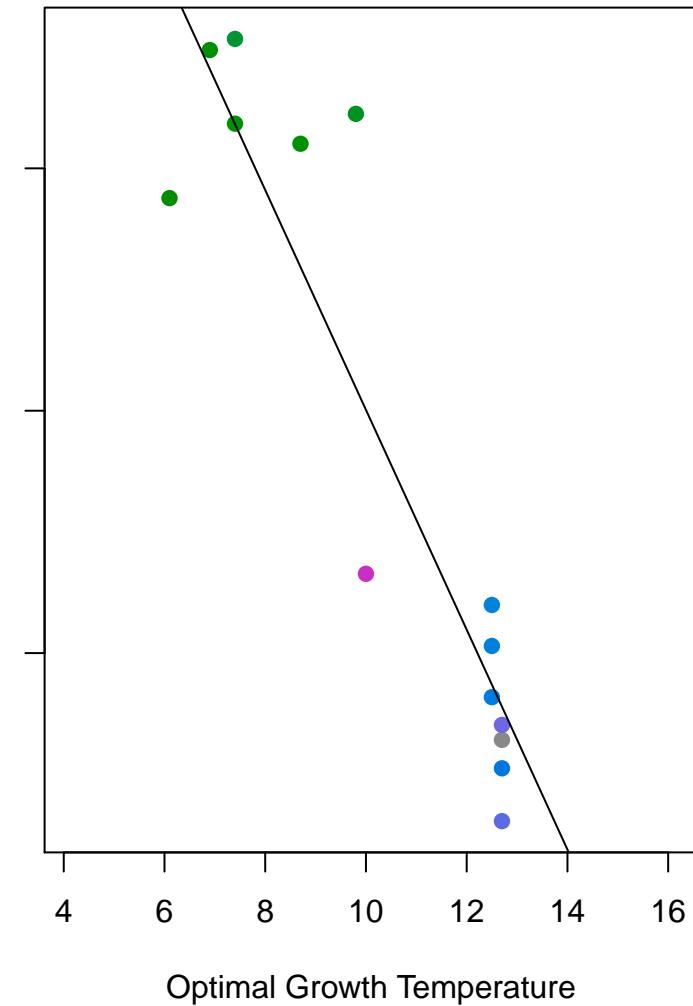
$$r = -0.852, p = 10^{-4.854}$$



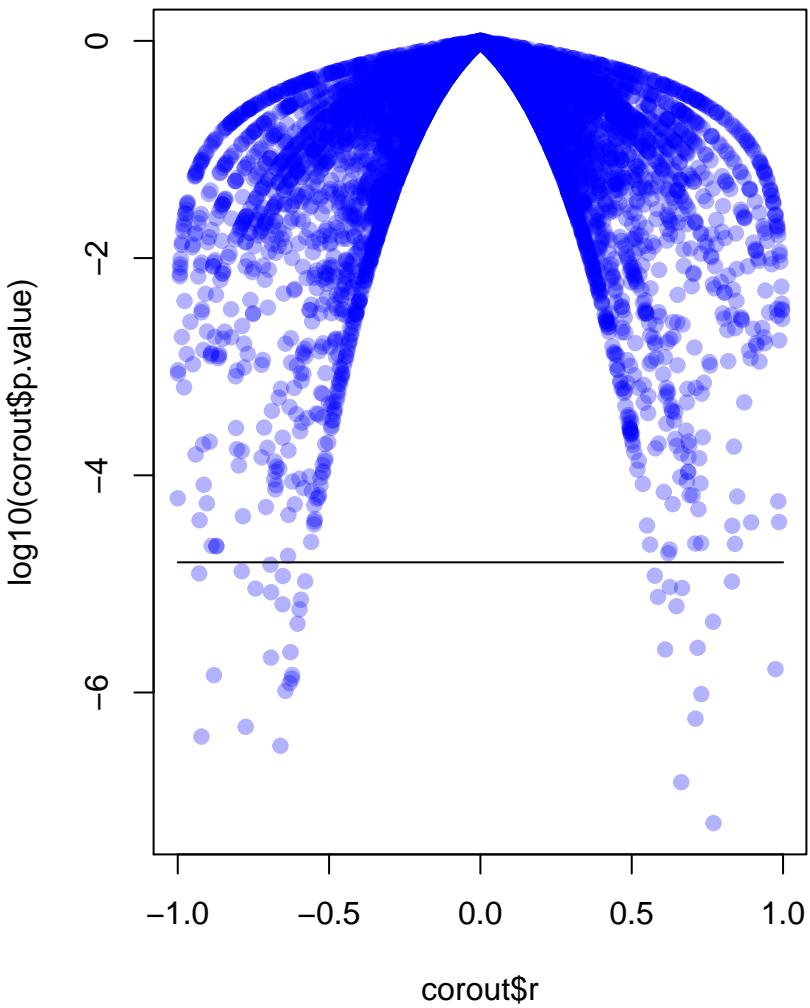


feature.pgfam_id.aliphatic_index.mean
PGF_00045708
Alpha-1,2-fucosyltransferase
 $r = -0.917$, $p = 10^{-5.399}$

feature.pgfam_id.aliphatic_index.mean

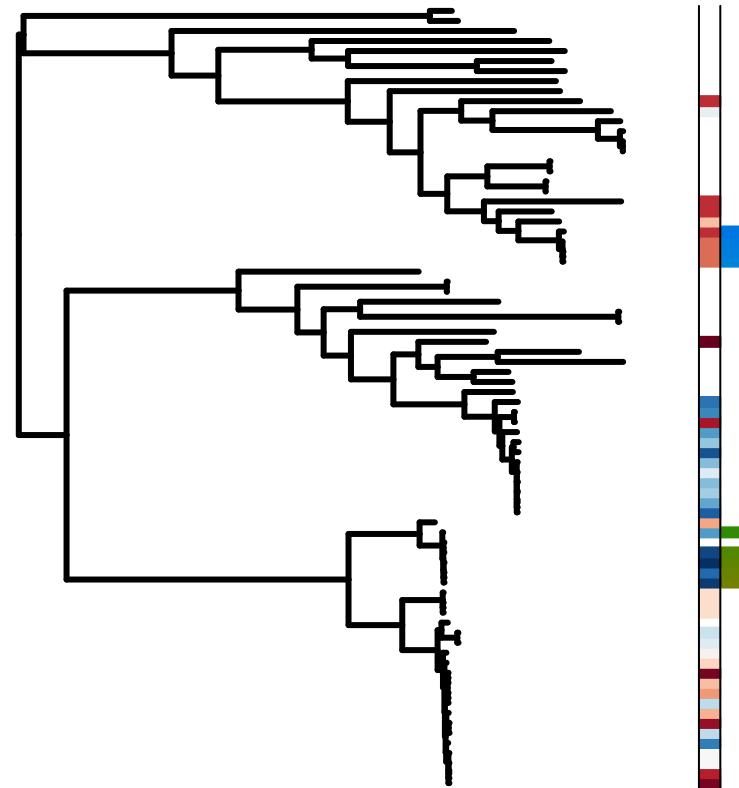
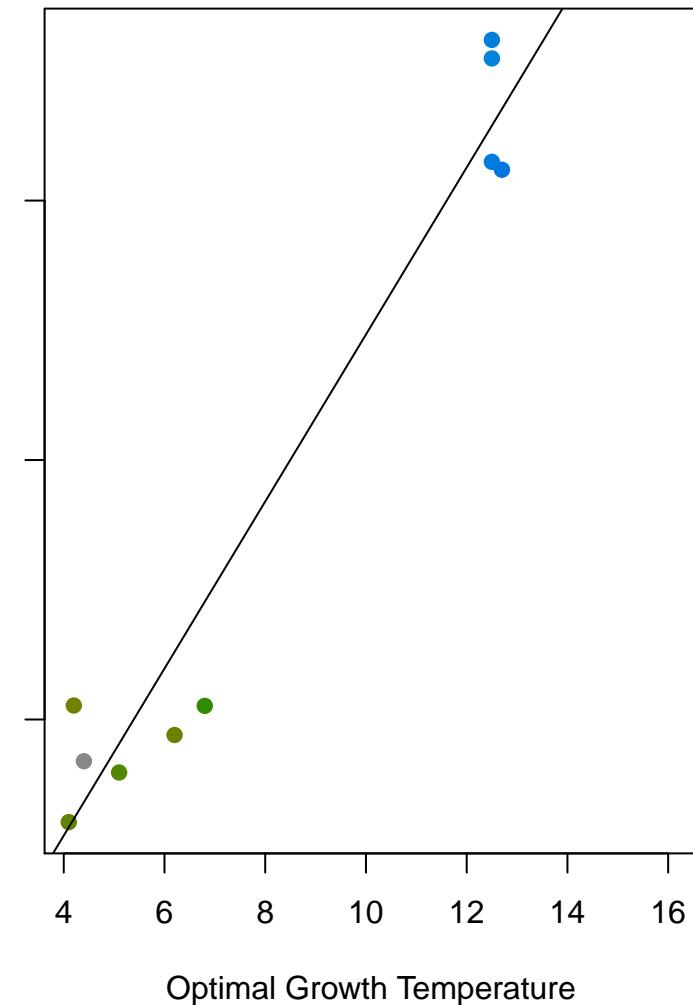


feature.plfam_id.aliphatic_index.mean



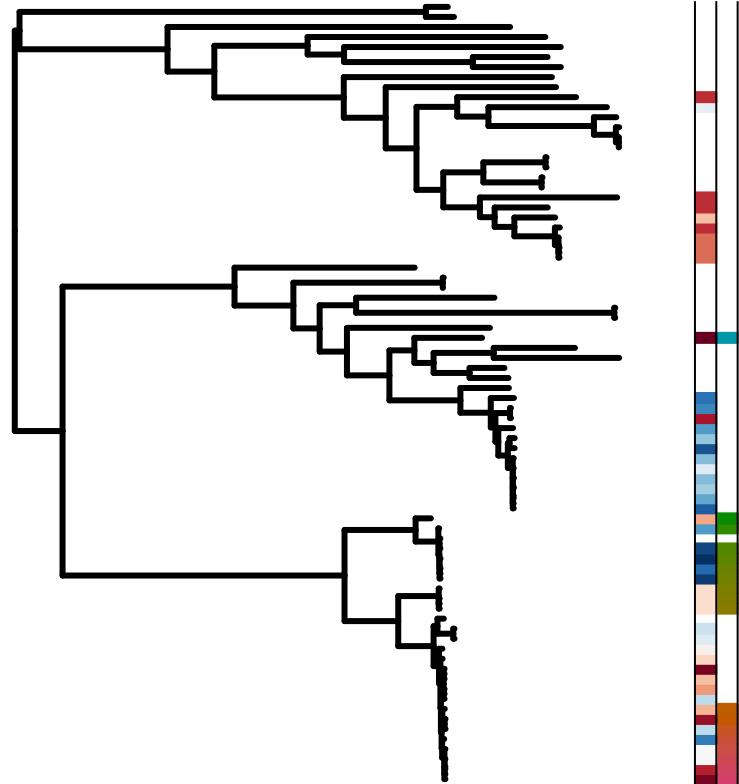
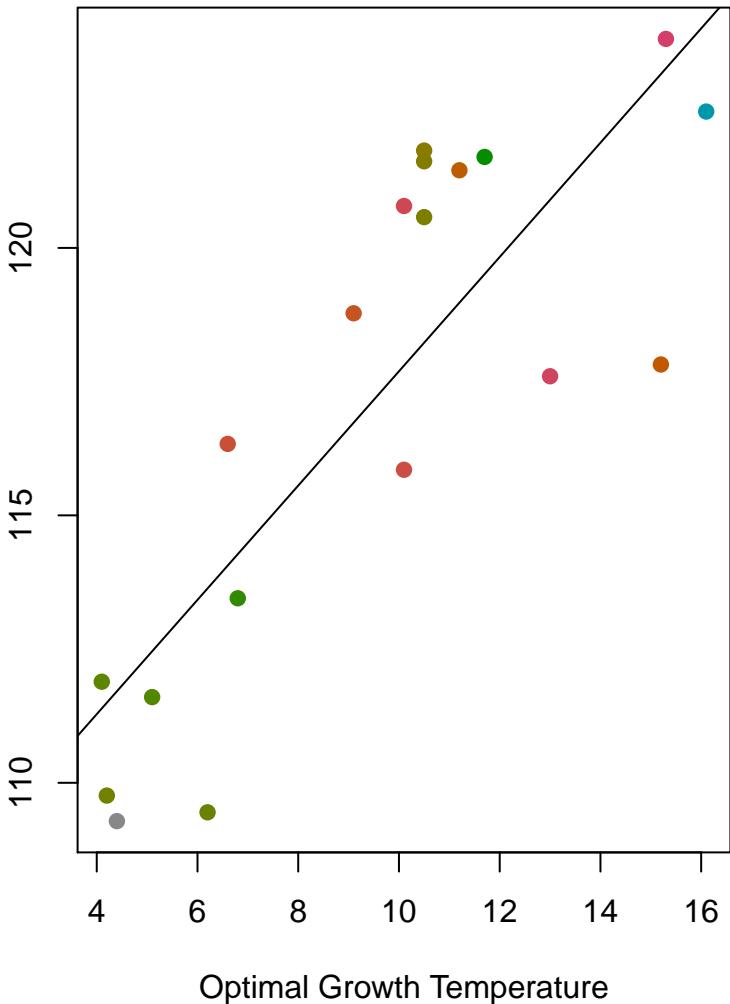
feature.plfam_id.aliphatic_index.mean
PLF_28228_00007839
hypothetical protein
 $r = 0.975, p = 10^{-5.785}$

feature.plfam_id.aliphatic_index.mean



feature.plfam_id.aliphatic_index.mean
PLF_28228_00015556
hypothetical protein
 $r = 0.831, p = 10^{-4.979}$

feature.plfam_id.aliphatic_index.mean



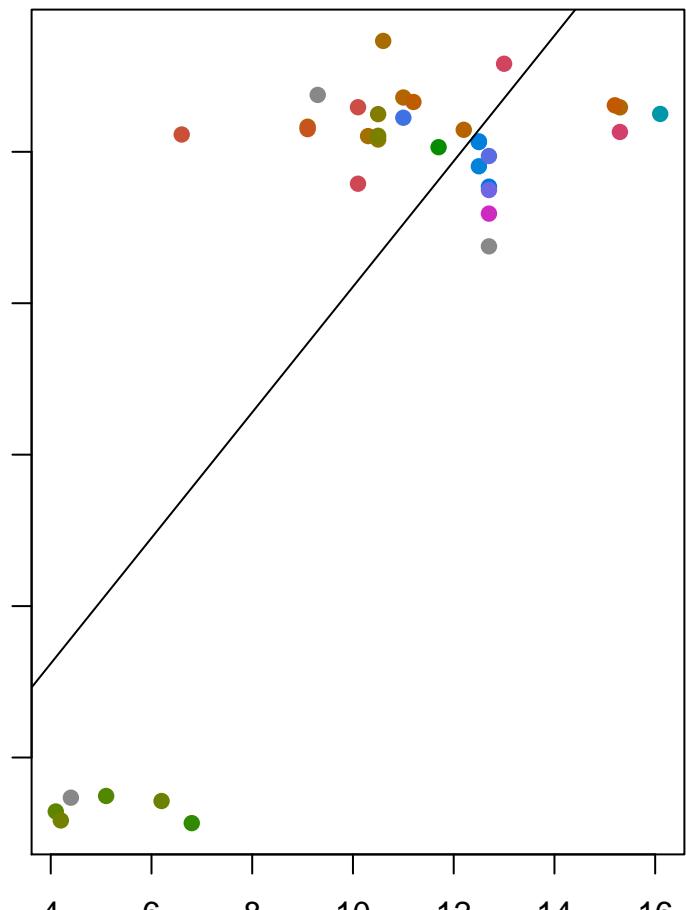
feature.plfam_id.aliphatic_index.mean

PLF_28228_00002798

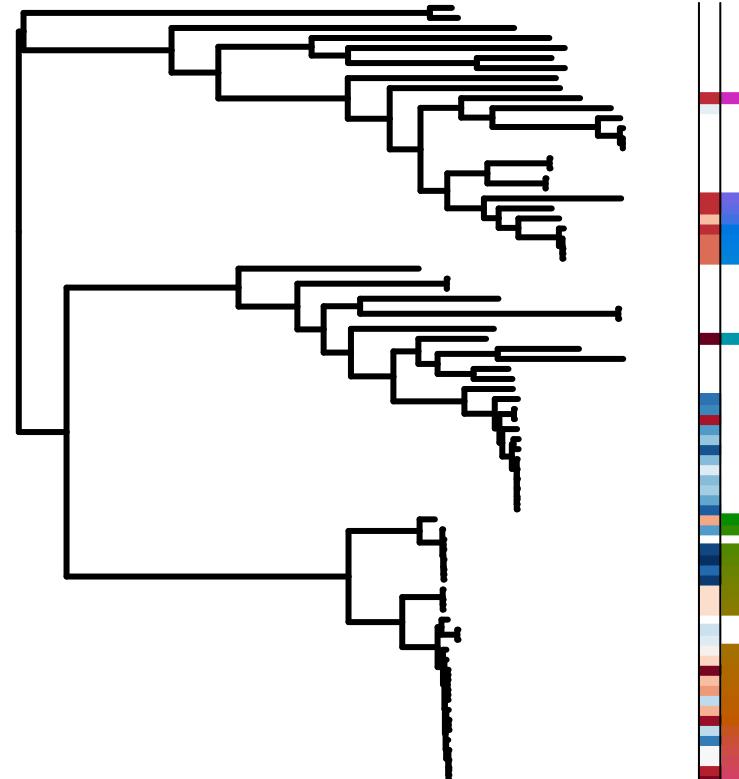
Two-component transcriptional response regulator, OmpR family

r = 0.77, p = 10^-7.203

feature.plfam_id.aliphatic_index.mean

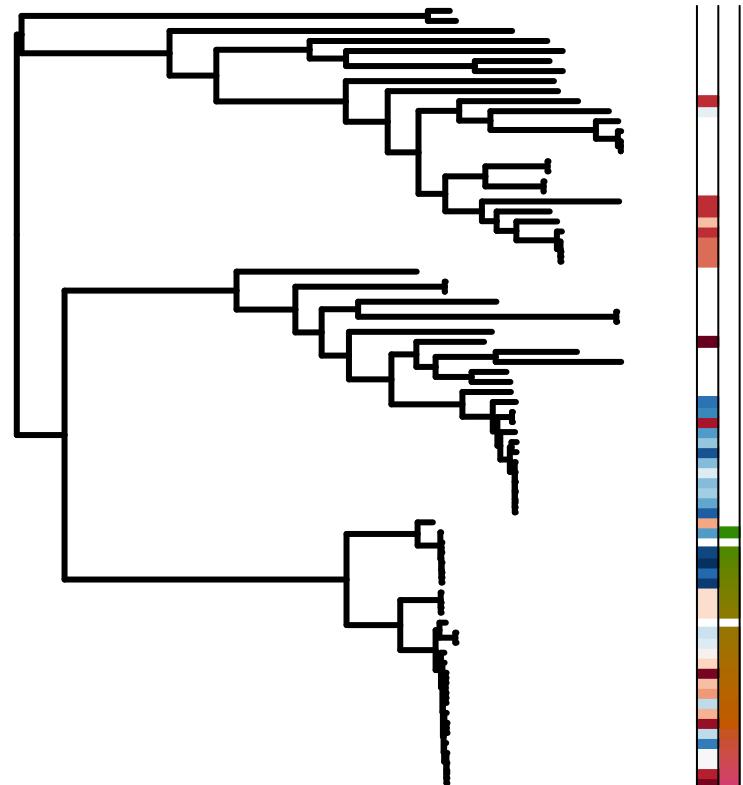
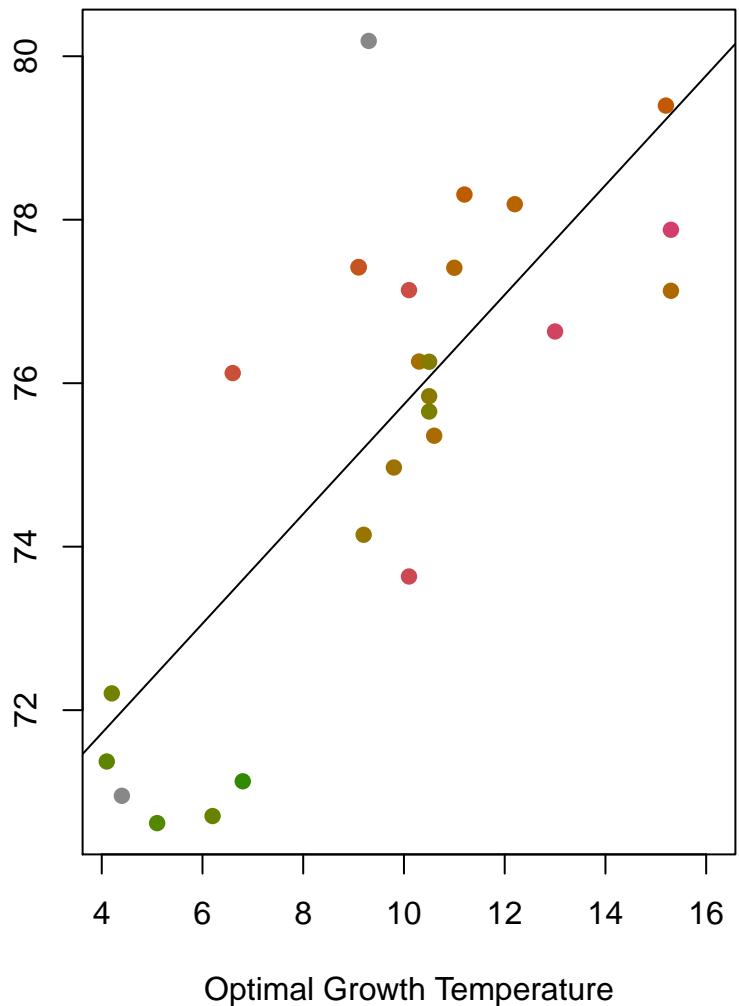


Optimal Growth Temperature



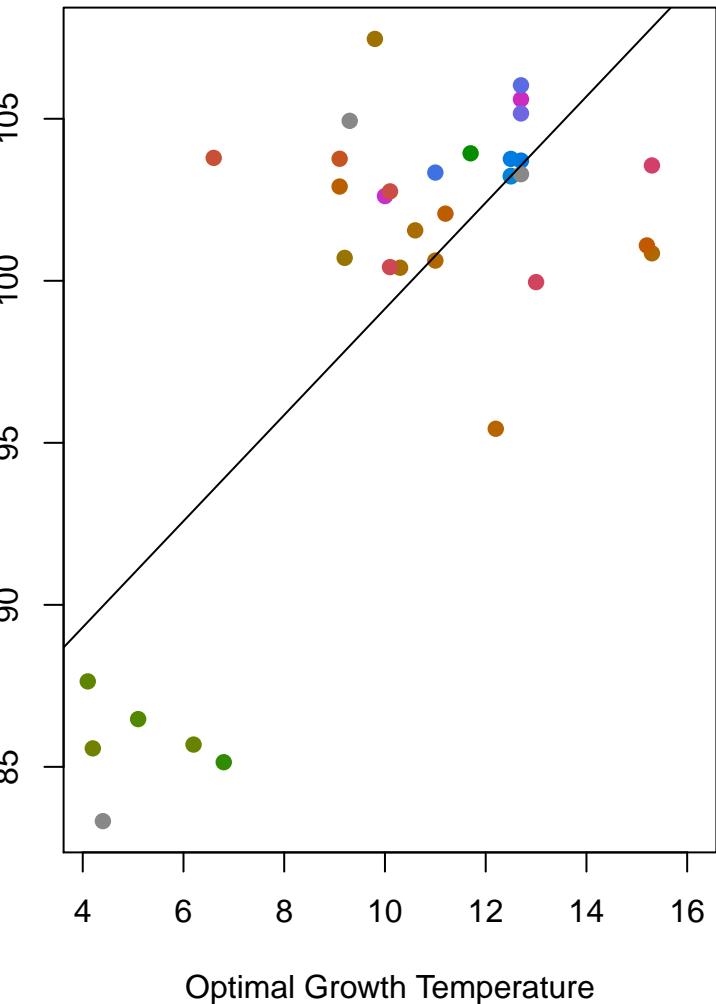
feature.plfam_id.aliphatic_index.mean
PLF_28228_00031666
hypothetical protein
 $r = 0.769, p = 10^{-5.349}$

feature.plfam_id.aliphatic_index.mean

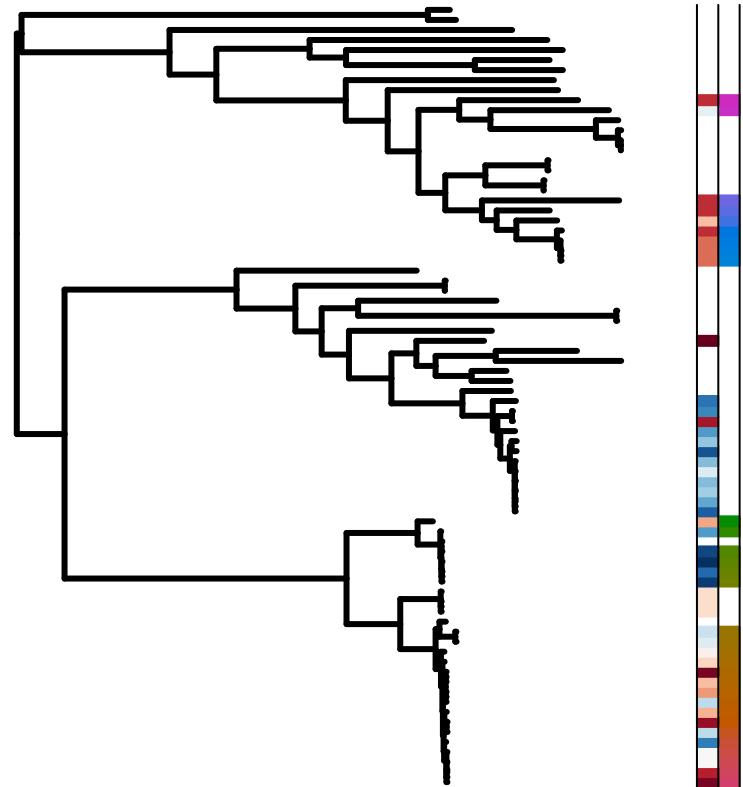


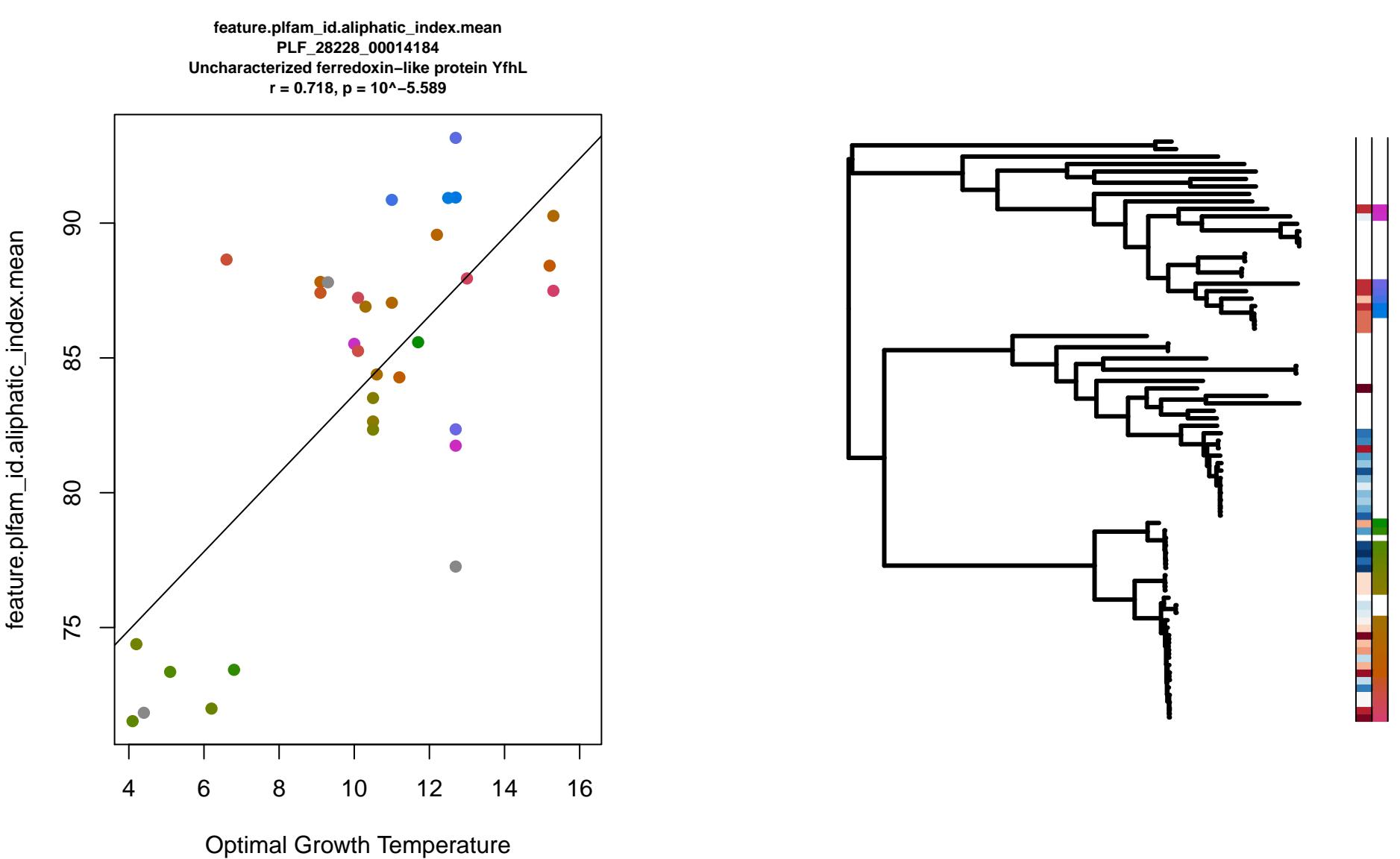
feature.plfam_id.aliphatic_index.mean
PLF_28228_00002434
hypothetical protein
 $r = 0.73, p = 10^{-6.015}$

feature.plfam_id.aliphatic_index.mean



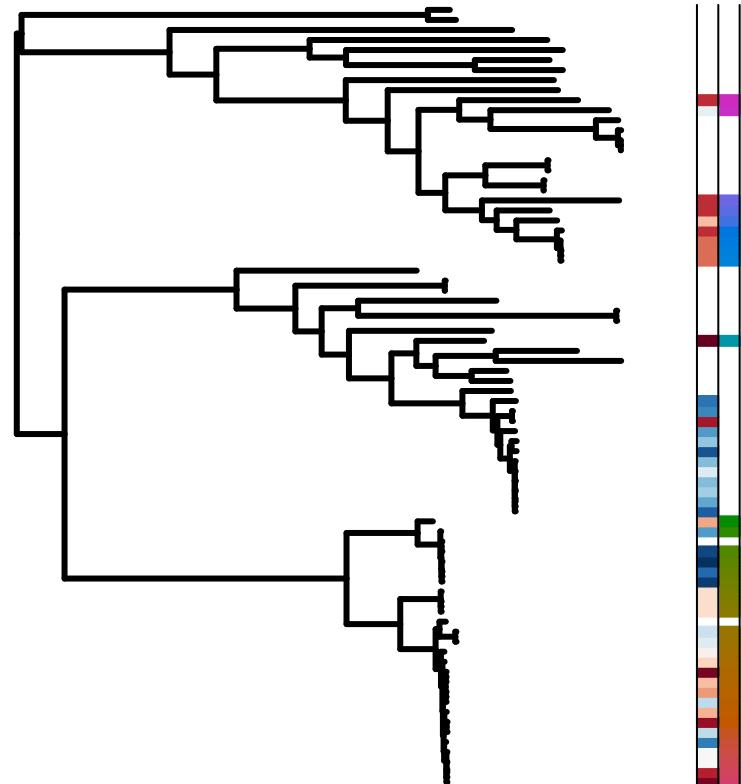
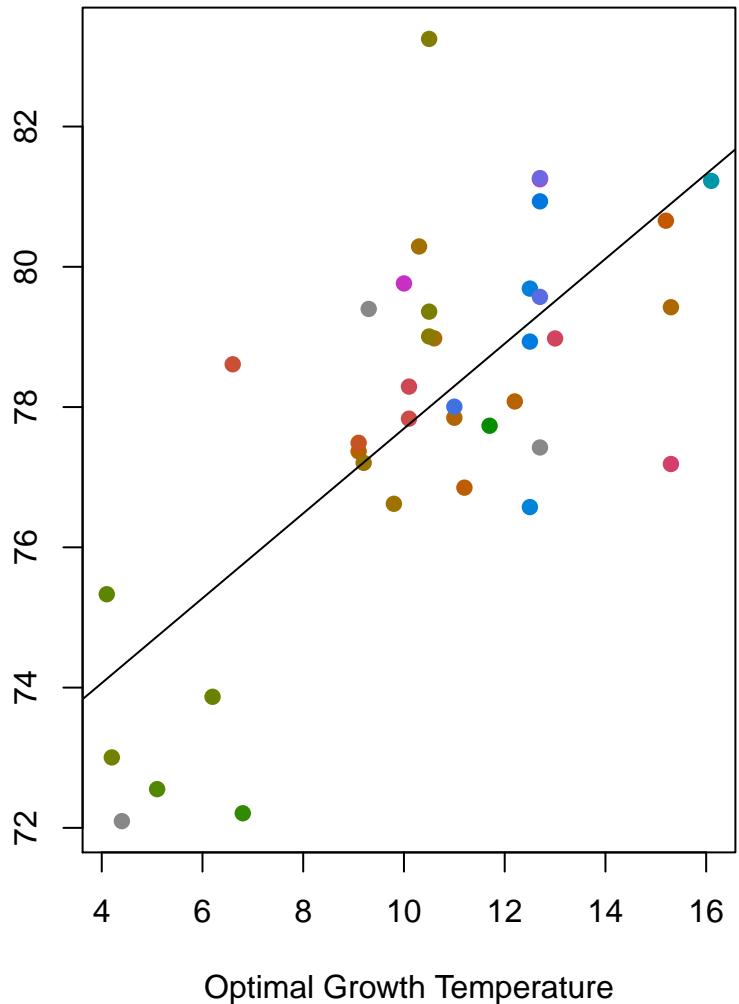
Optimal Growth Temperature





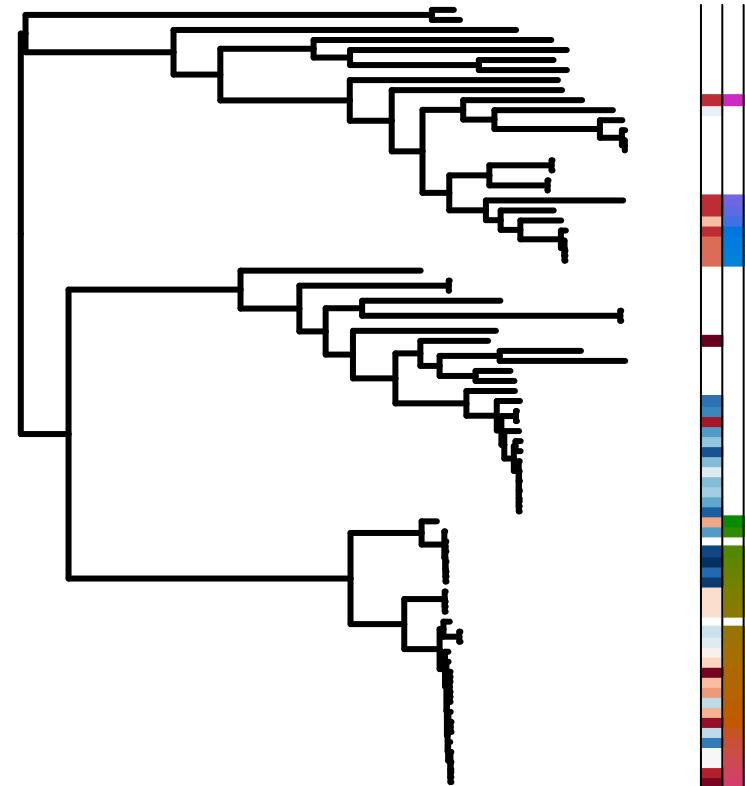
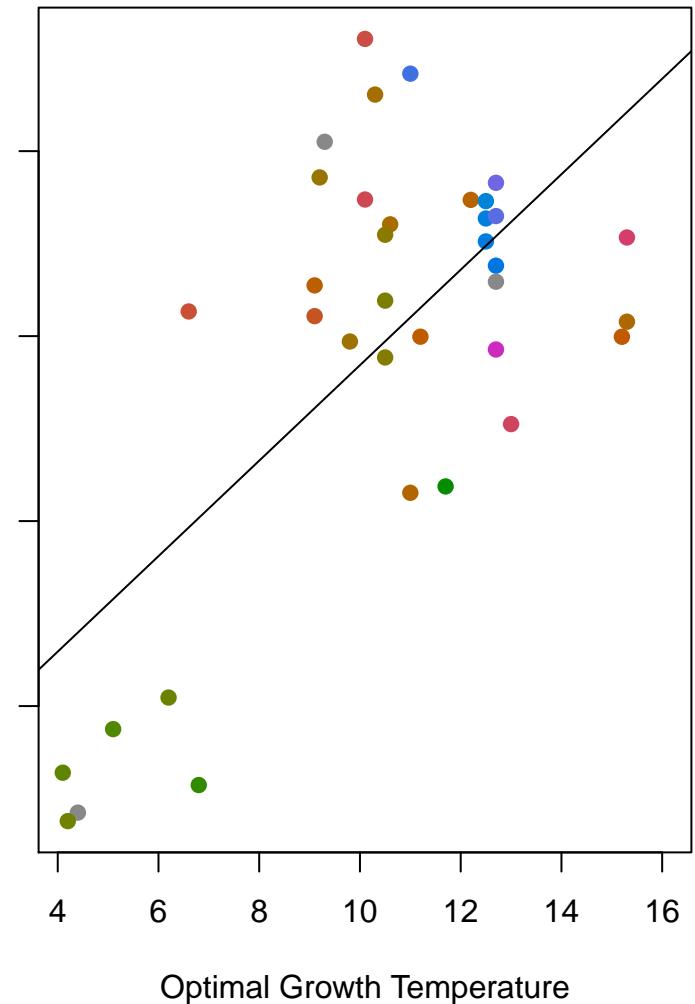
feature.plfam_id.aliphatic_index.mean
PLF_28228_00001844
Flagellar protein FliJ
 $r = 0.711, p = 10^{-6.241}$

feature.plfam_id.aliphatic_index.mean



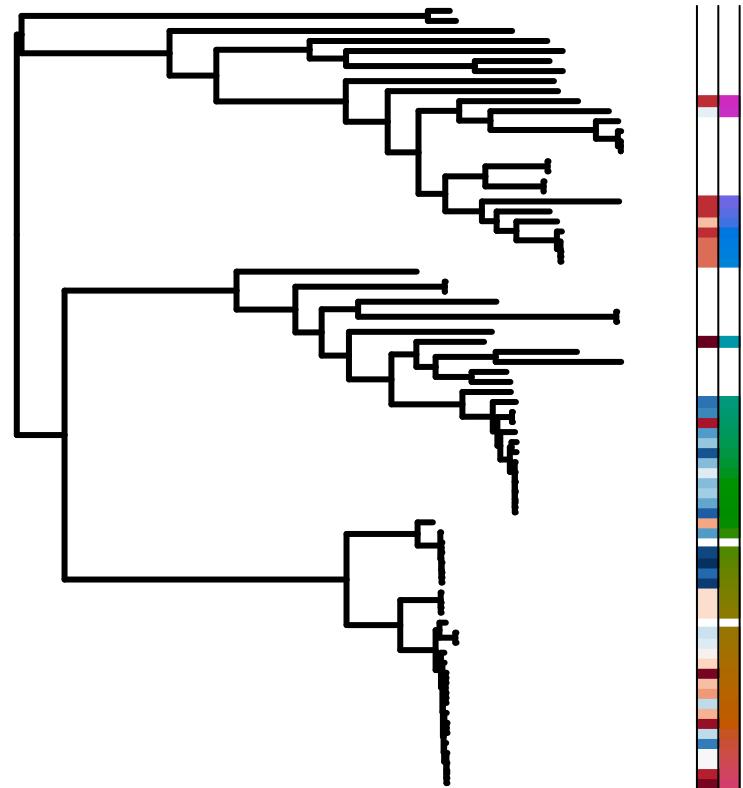
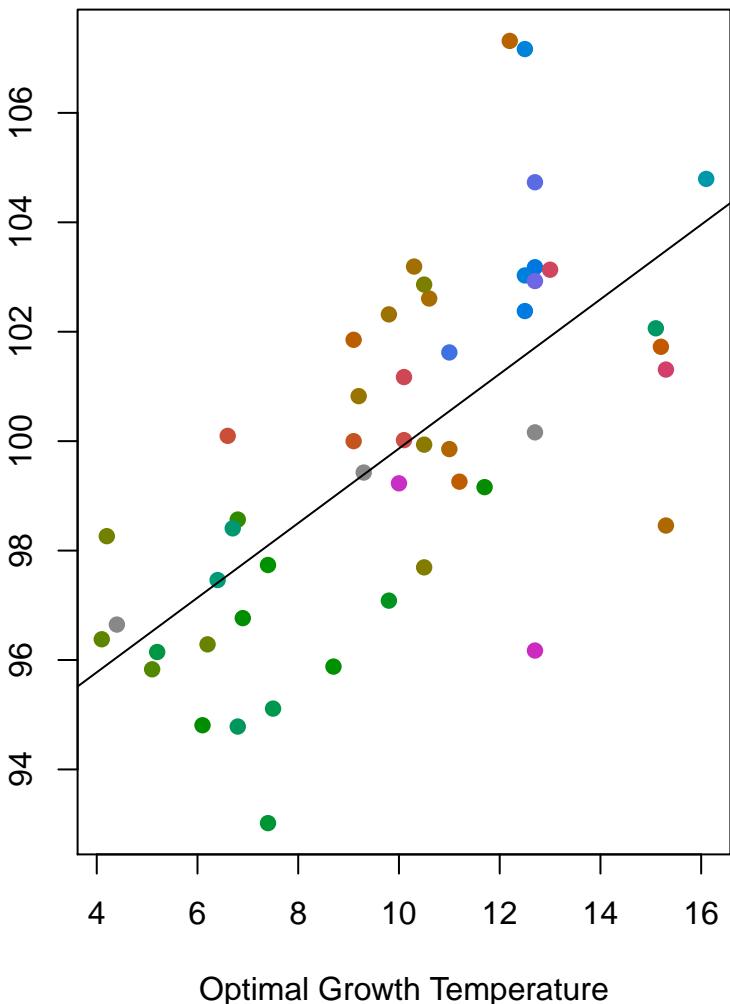
feature.plfam_id.aliphatic_index.mean
PLF_28228_00002946
hypothetical protein
 $r = 0.666$, $p = 10^{-5.038}$

feature.plfam_id.aliphatic_index.mean



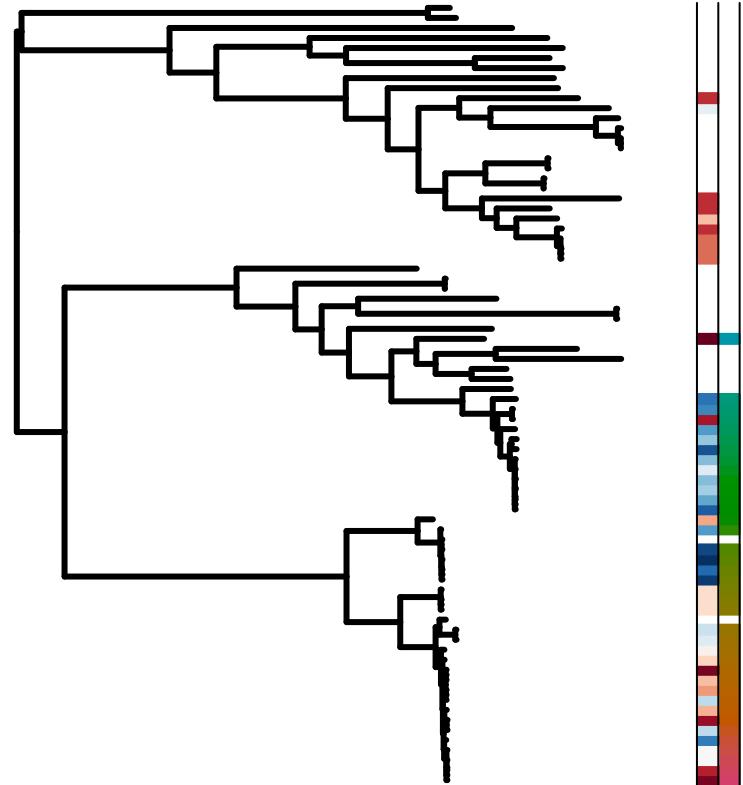
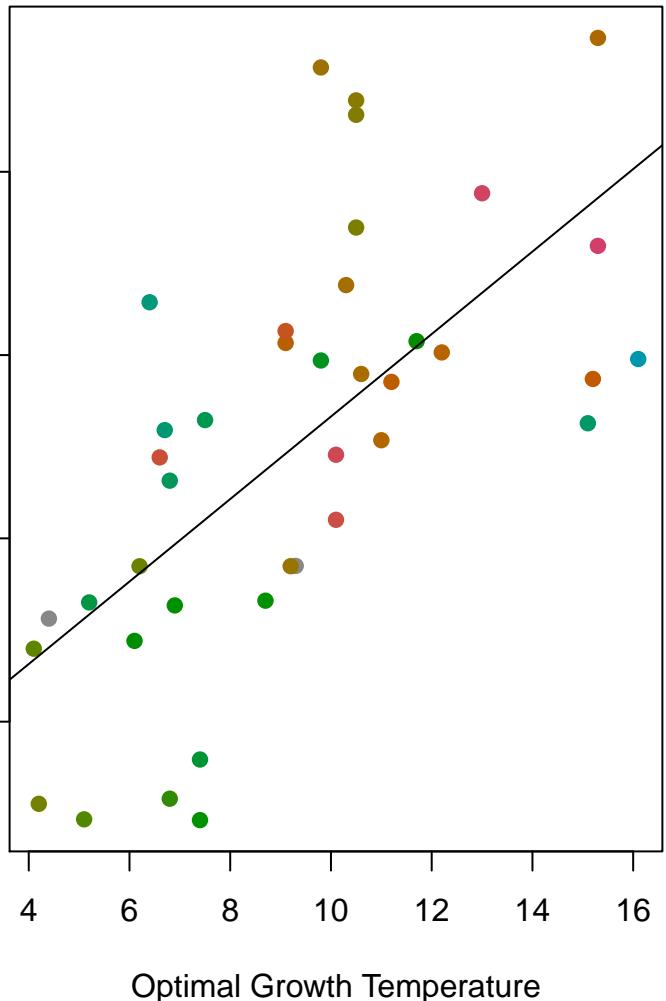
feature.plfam_id.aliphatic_index.mean
PLF_28228_00000039
UPF0758 family protein
 $r = 0.664, p = 10^{-6.826}$

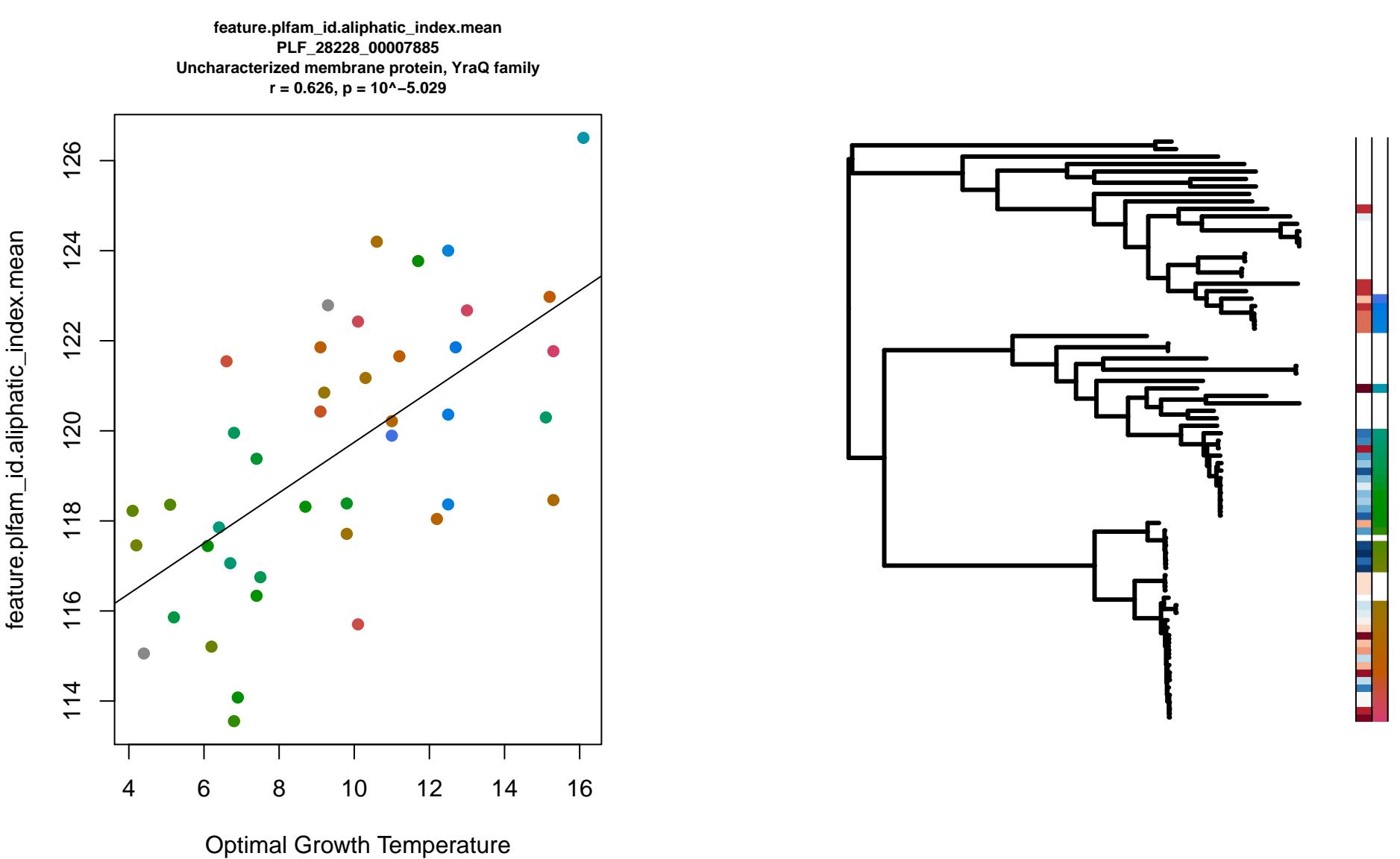
feature.plfam_id.aliphatic_index.mean



feature.plfam_id.aliphatic_index.mean
PLF_28228_00014025
CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)
 $r = 0.648$, $p = 10^{-5.206}$

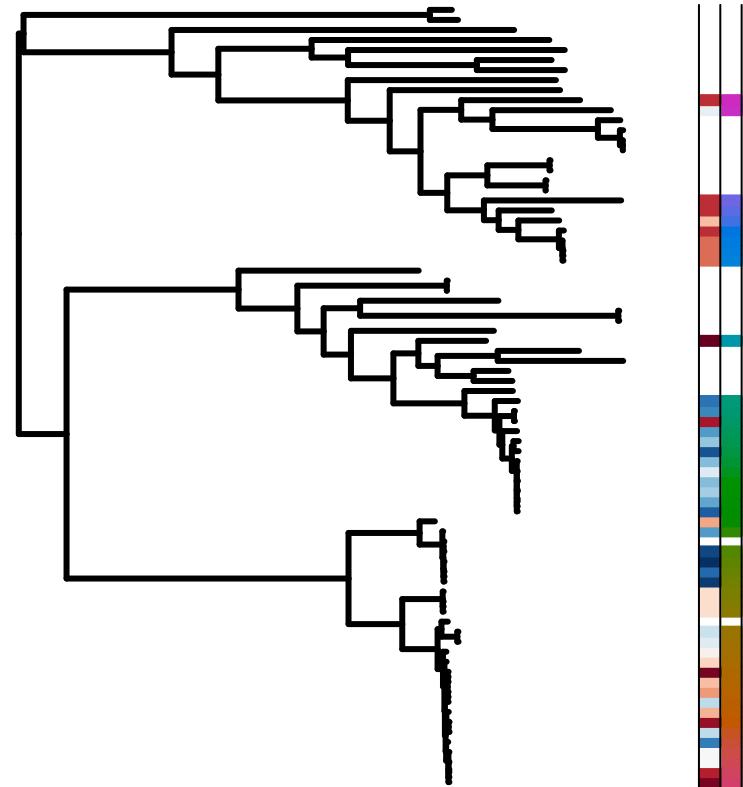
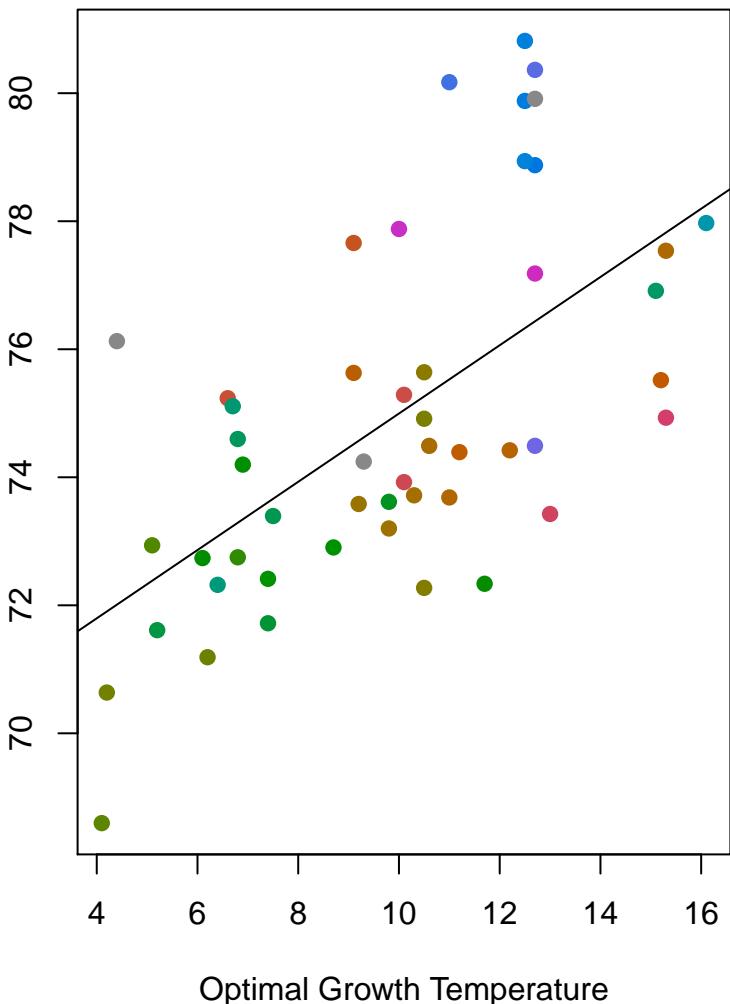
feature.plfam_id.aliphatic_index.mean





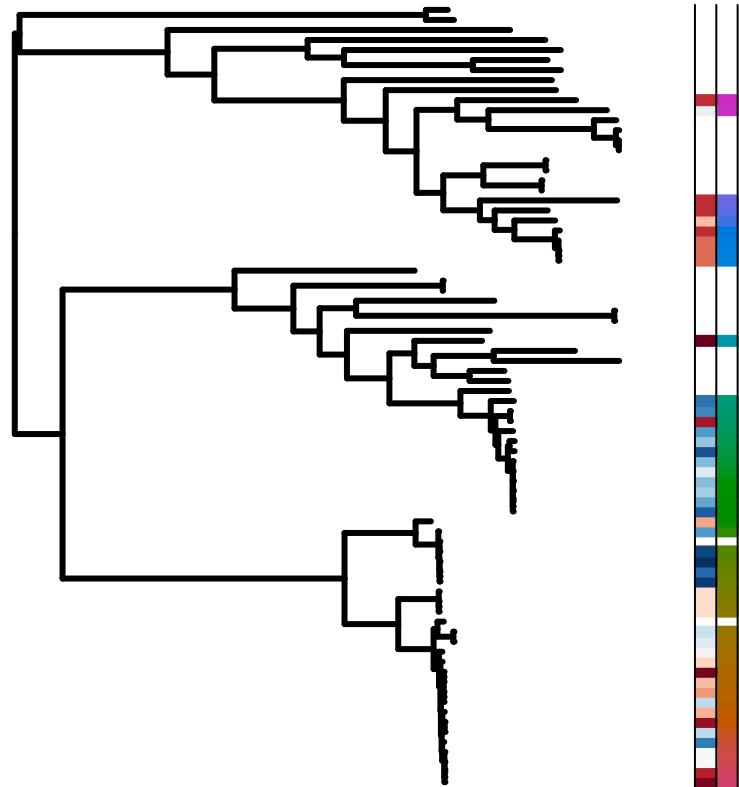
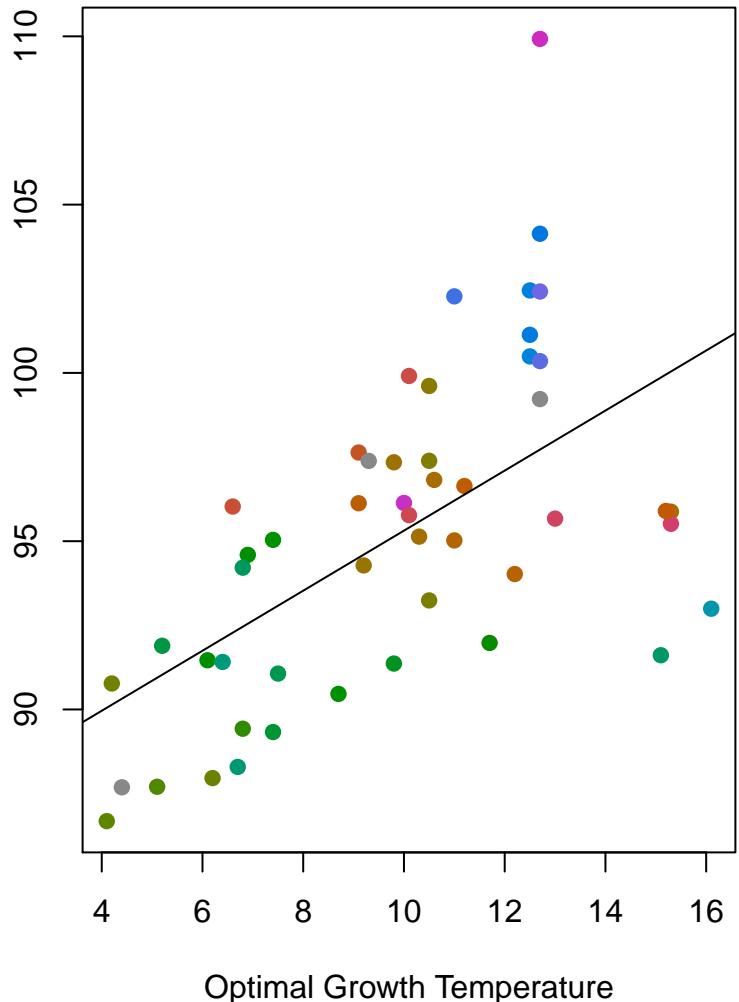
feature.plfam_id.aliphatic_index.mean
PLF_28228_00000483
Flagellar basal-body rod protein FlgF
 $r = 0.611$, $p = 10^{-5.604}$

feature.plfam_id.aliphatic_index.mean



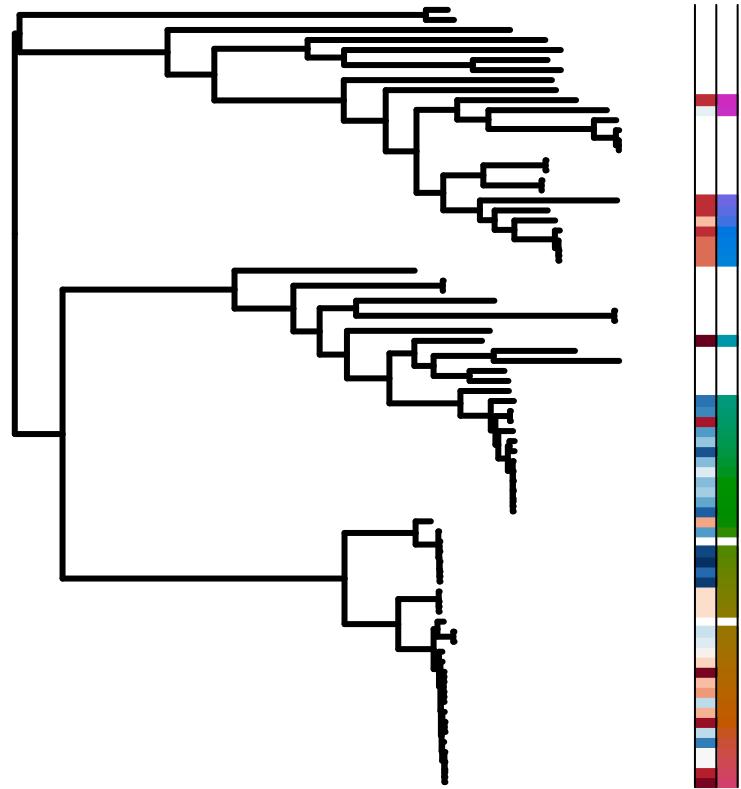
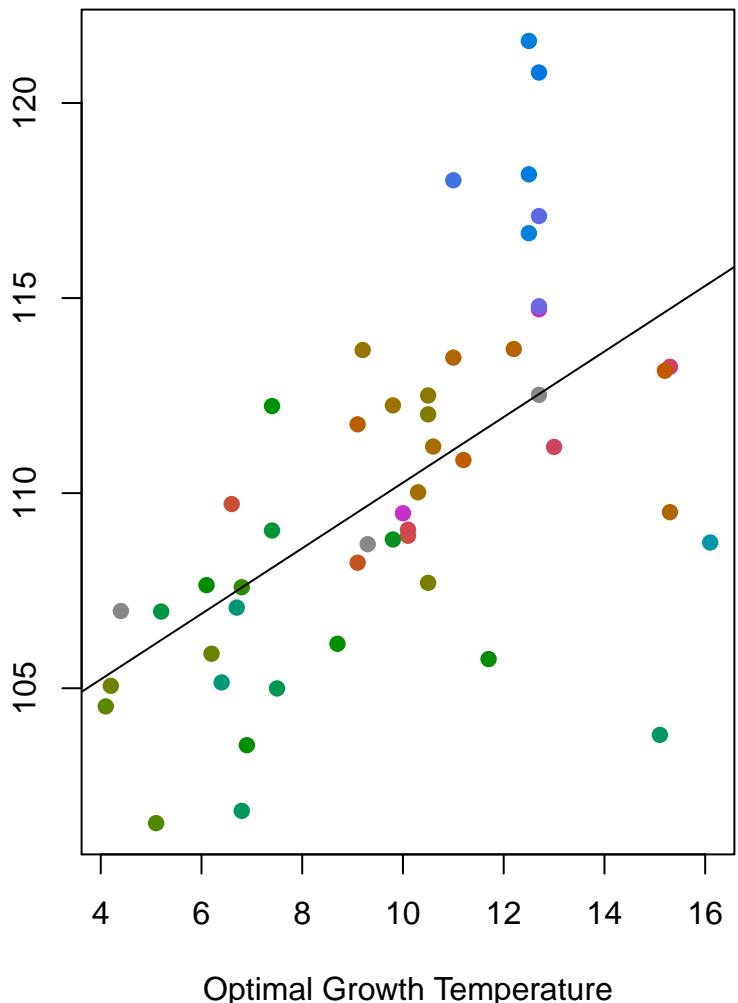
feature.plfam_id.aliphatic_index.mean
PLF_28228_00000786
Esterase ybfF (EC 3.1.-.-)
 $r = 0.587$, $p = 10^{-5.12}$

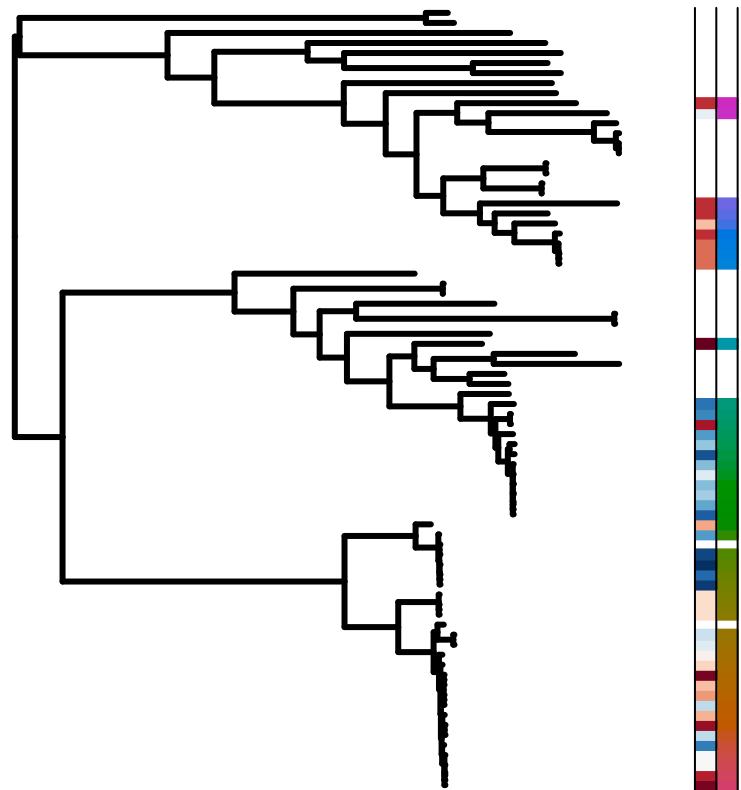
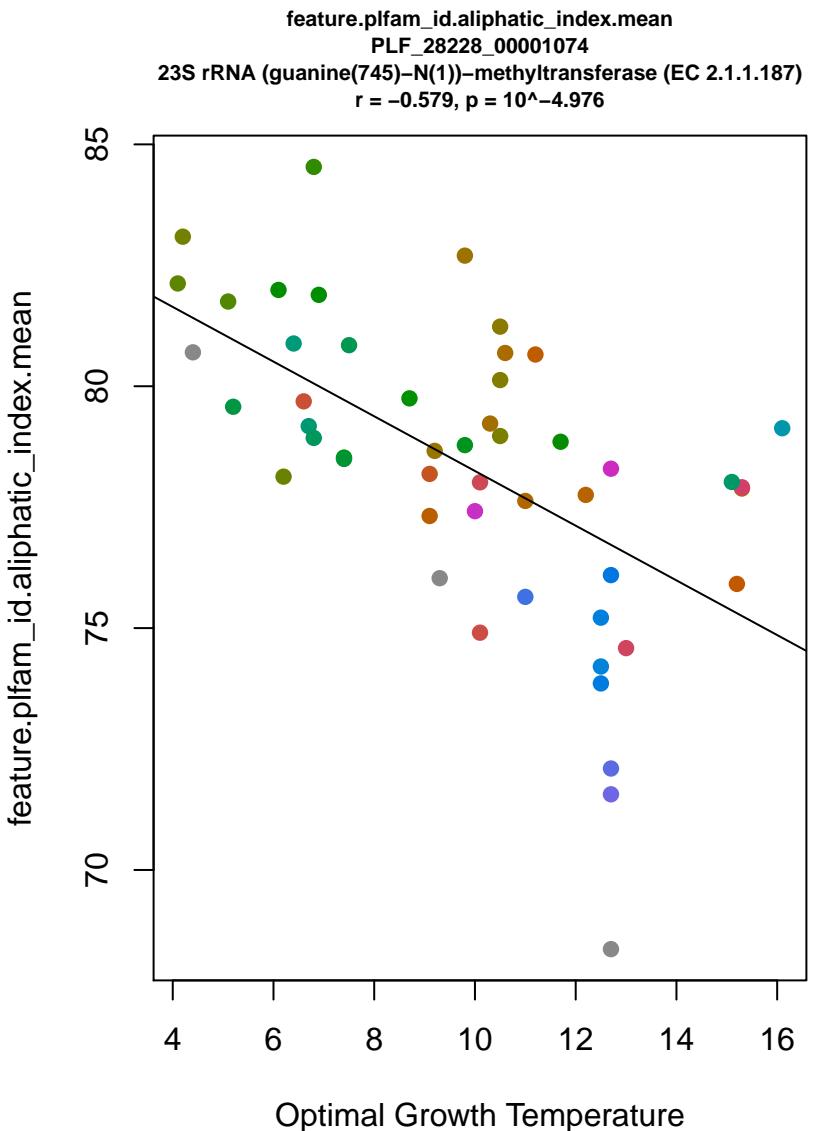
feature.plfam_id.aliphatic_index.mean

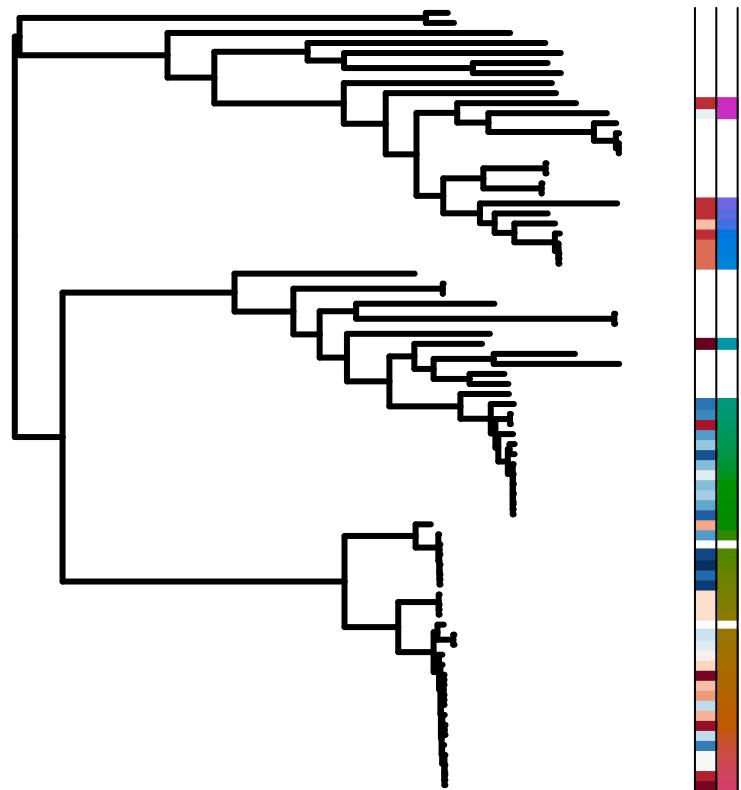
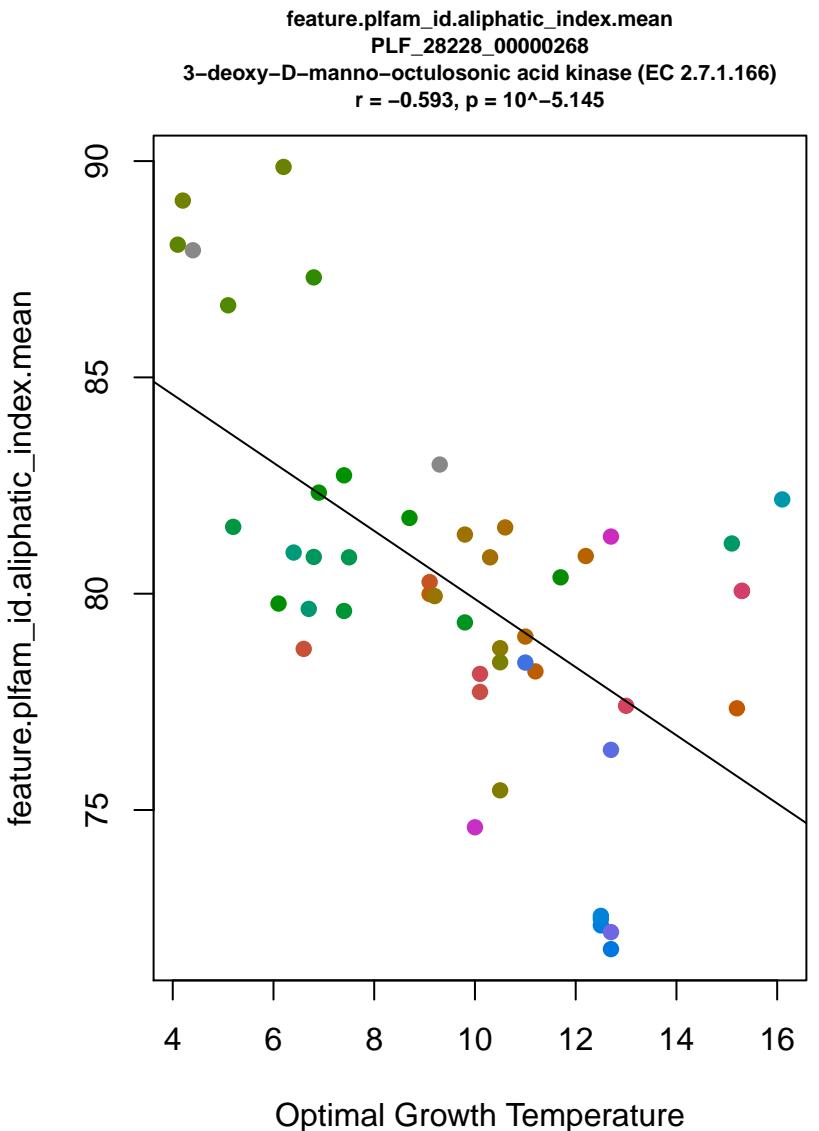


feature.plfam_id.aliphatic_index.mean
PLF_28228_00002183
UPF0352 protein YejL
 $r = 0.576$, $p = 10^{-4.925}$

feature.plfam_id.aliphatic_index.mean







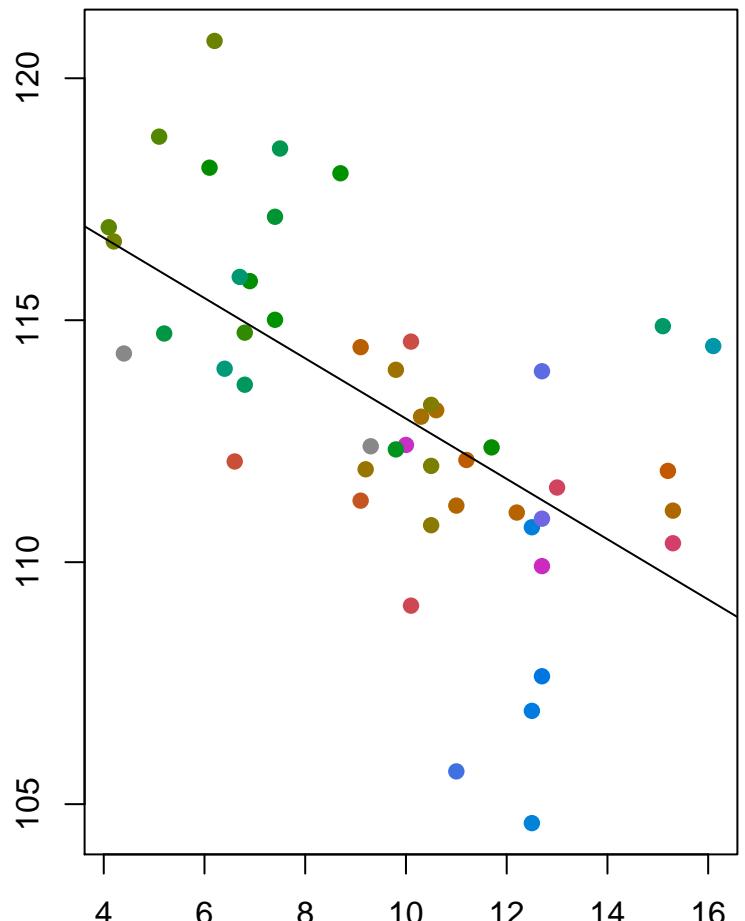
feature.plfam_id.aliphatic_index.mean

PLF_28228_00000983

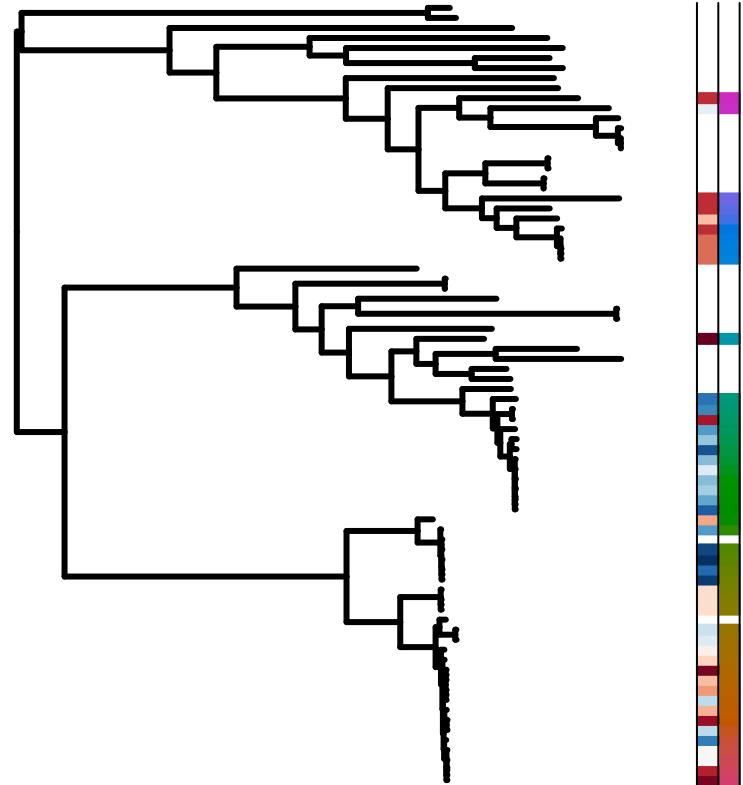
Predicted glucose transporter in beta-glucoside utilization gene cluster

$r = -0.597, p = 10^{-5.235}$

feature.plfam_id.aliphatic_index.mean

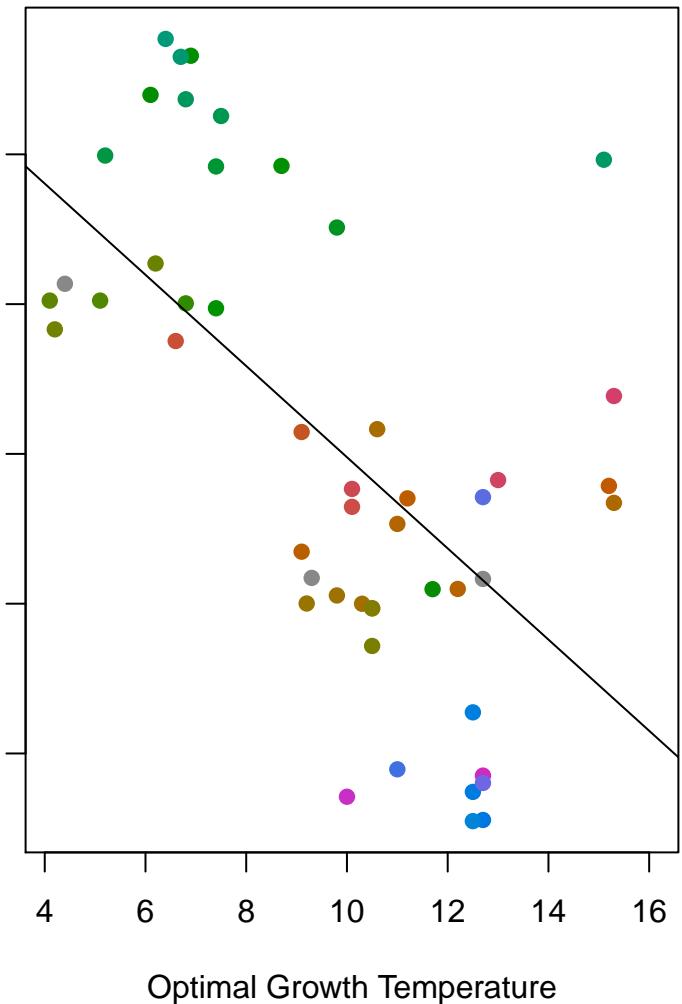


Optimal Growth Temperature



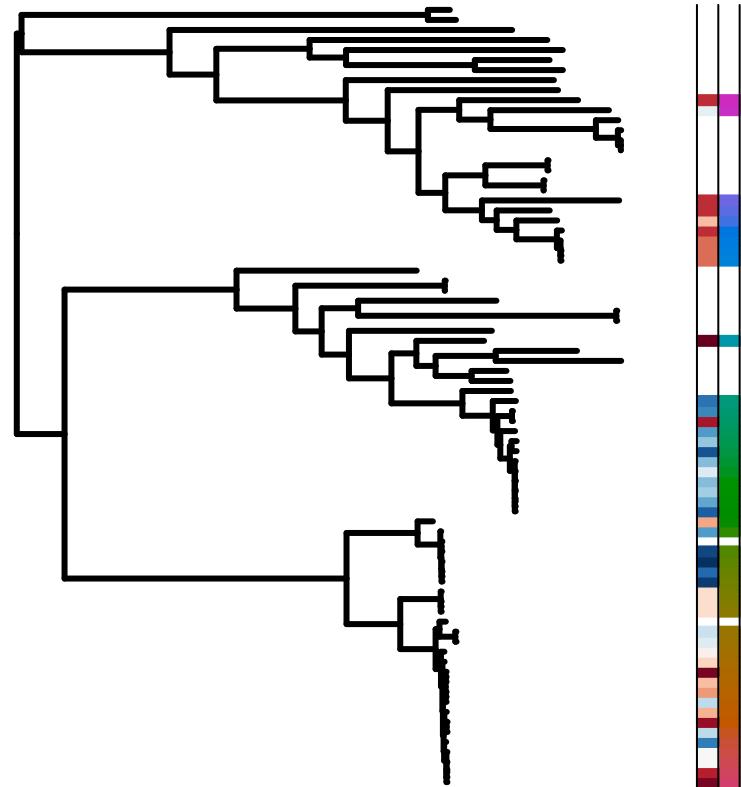
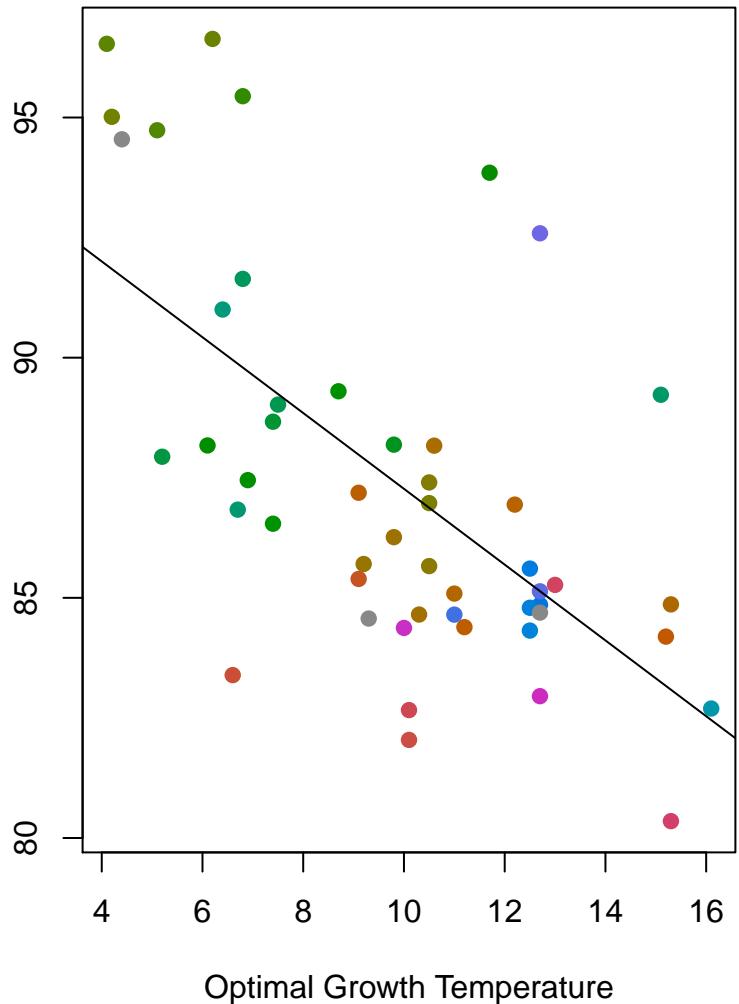
feature.plfam_id.aliphatic_index.mean
PLF_28228_00000425
Cys-tRNA(Pro) deacylase YbaK
 $r = -0.604$, $p = 10^{-5.367}$

feature.plfam_id.aliphatic_index.mean



feature.plfam_id.aliphatic_index.mean
PLF_28228_00001868
General secretion pathway protein K
 $r = -0.622$, $p = 10^{-5.839}$

feature.plfam_id.aliphatic_index.mean



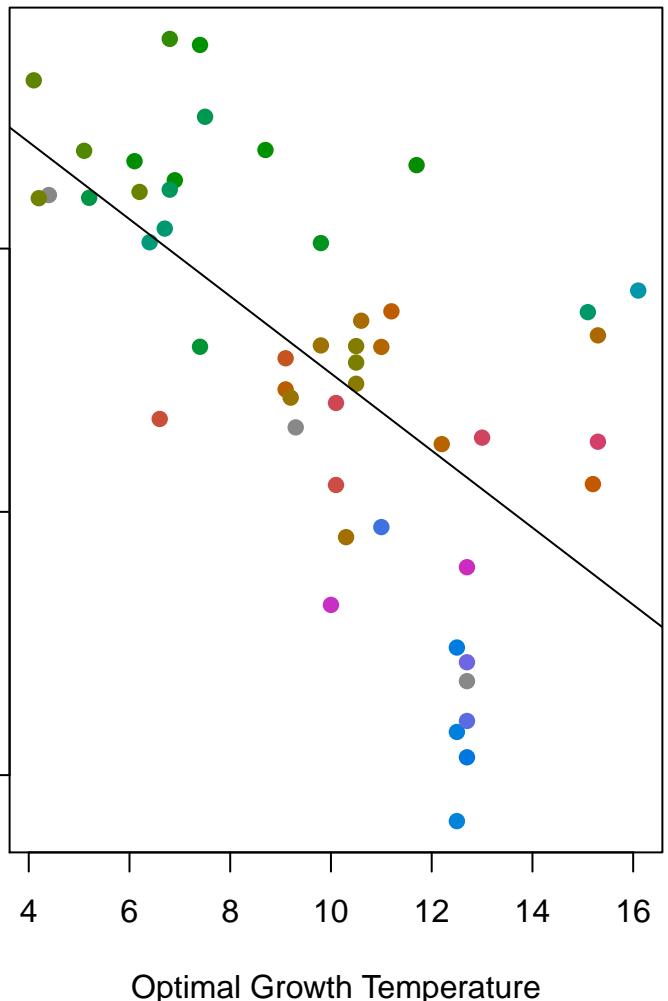
feature.plfam_id.aliphatic_index.mean

PLF_28228_00001395

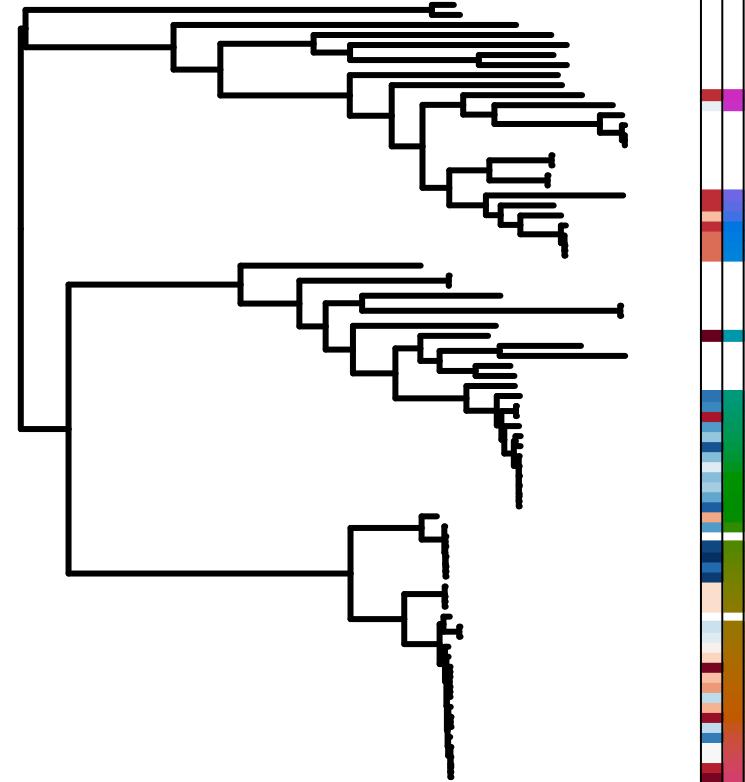
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)

$r = -0.623$, $p = 10^{-5.874}$

feature.plfam_id.aliphatic_index.mean

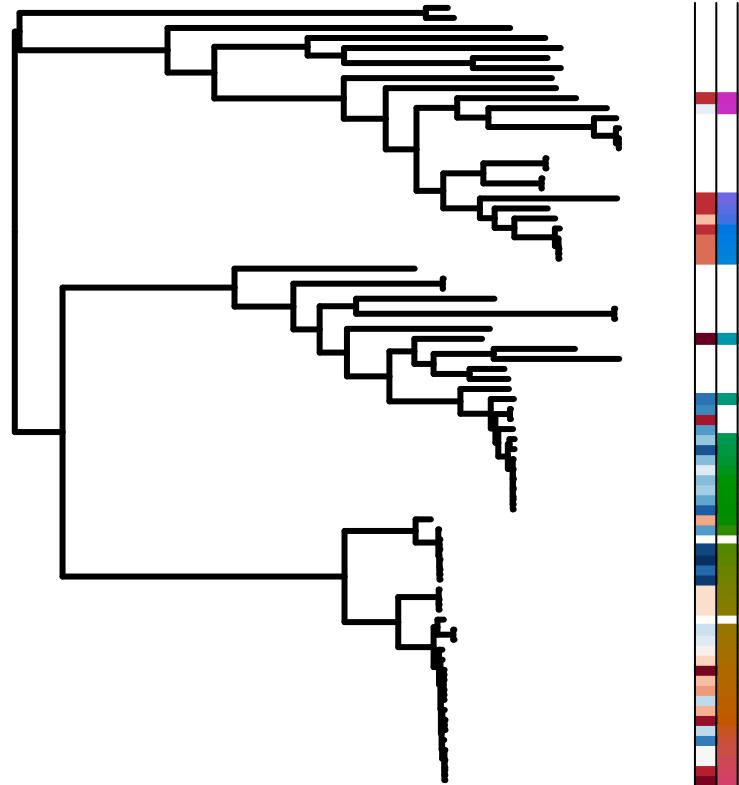
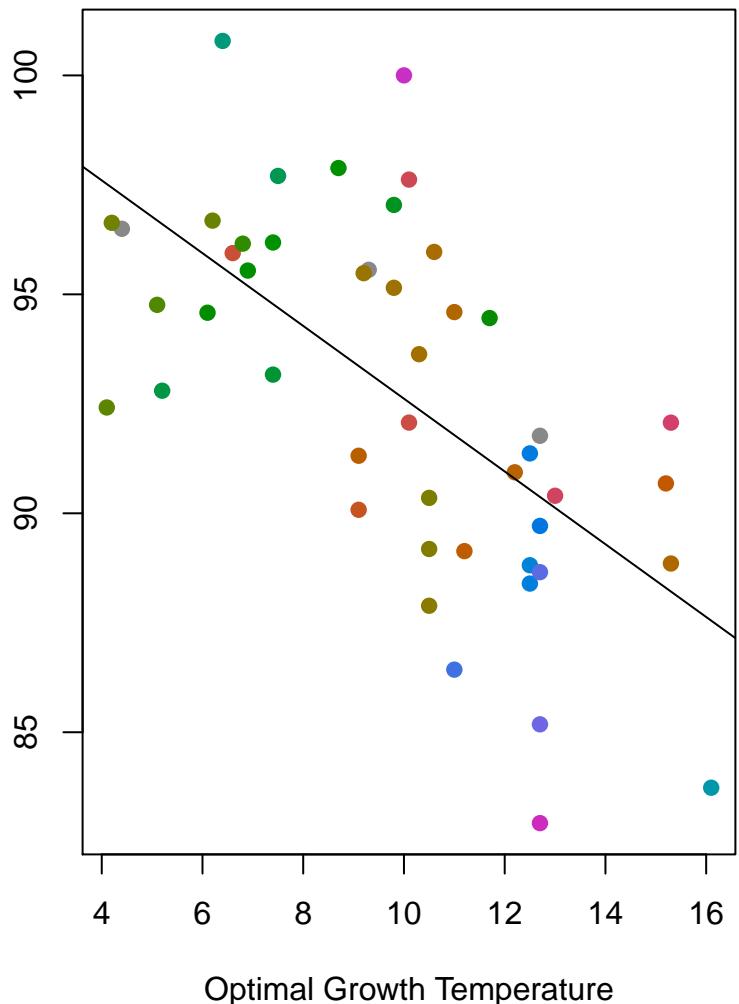


Optimal Growth Temperature



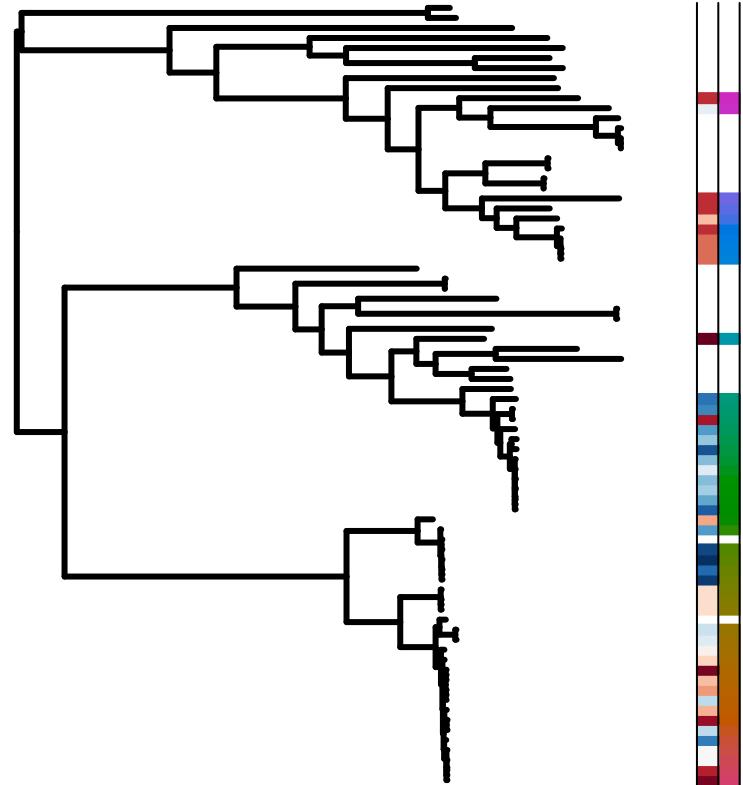
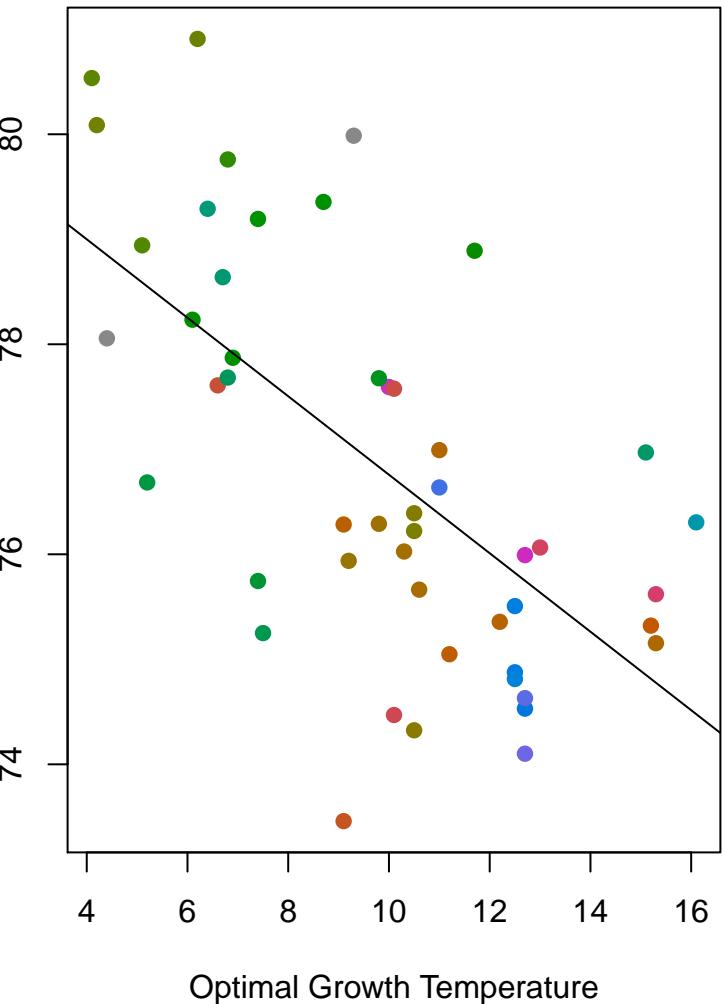
feature.plfam_id.aliphatic_index.mean
PLF_28228_00001927
Potential queD like 2
 $r = -0.628$, $p = 10^{-5.629}$

feature.plfam_id.aliphatic_index.mean



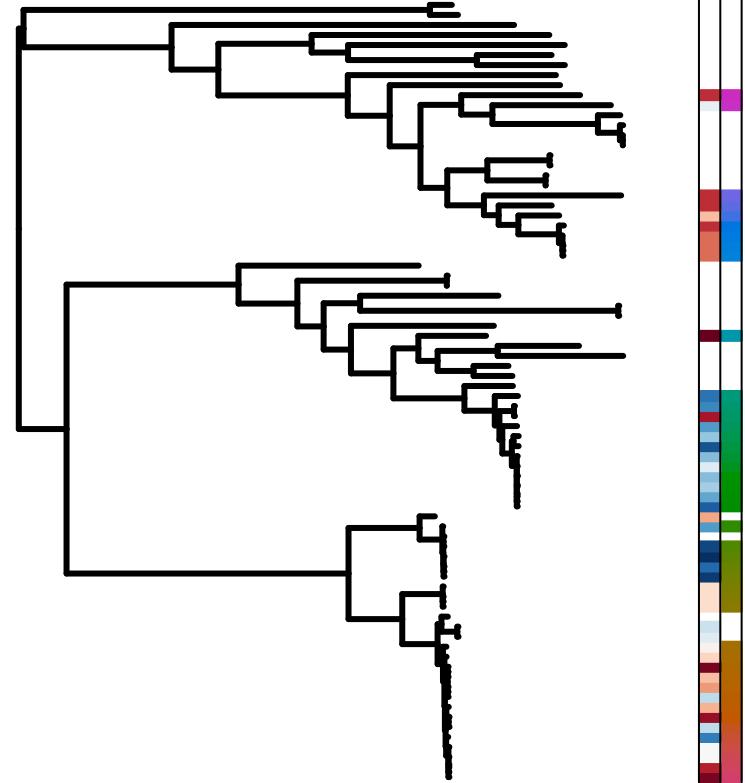
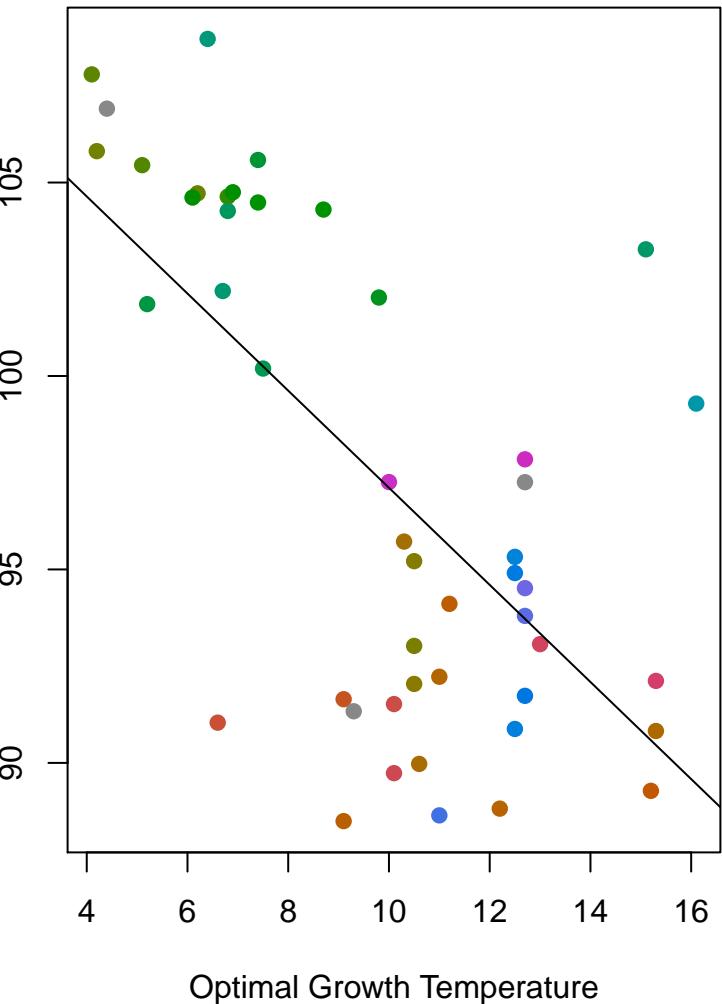
feature.plfam_id.aliphatic_index.mean
PLF_28228_00000687
LSU ribosomal protein L3p (L3e)
 $r = -0.63$, $p = 10^{-5.914}$

feature.plfam_id.aliphatic_index.mean



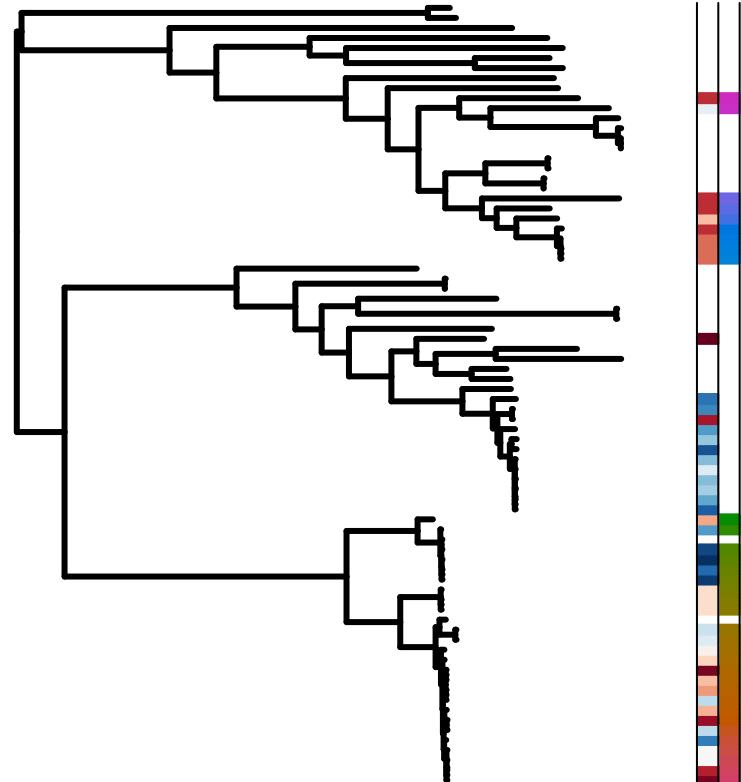
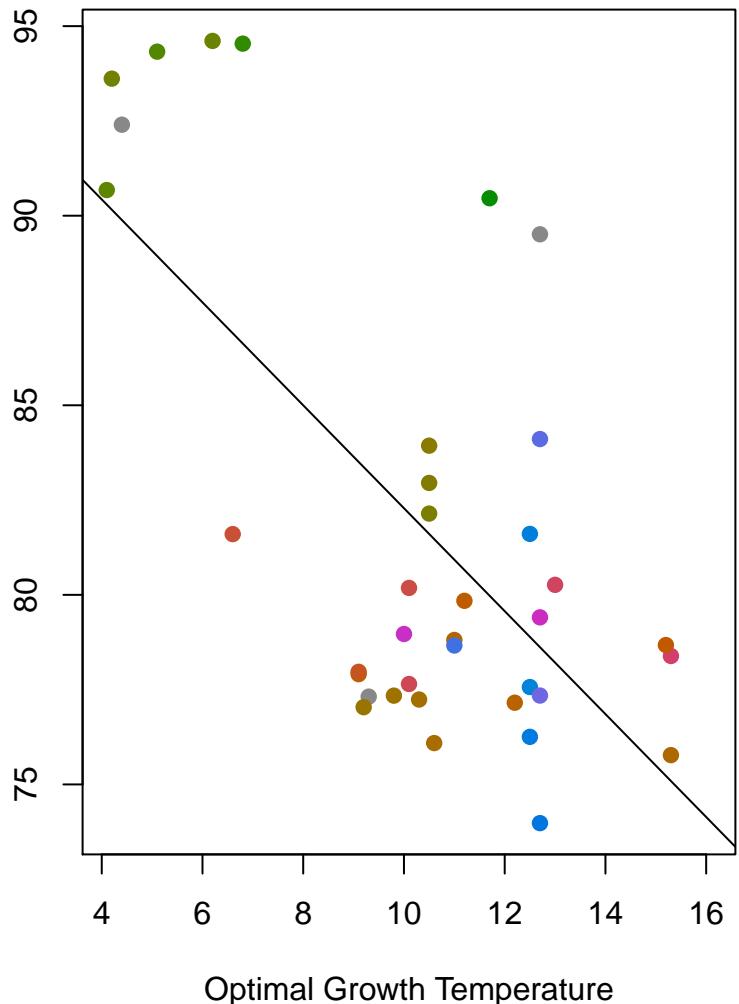
feature.plfam_id.aliphatic_index.mean
PLF_28228_00001839
Flagellar biosynthesis protein FliS
 $r = -0.644$, $p = 10^{-5.985}$

feature.plfam_id.aliphatic_index.mean



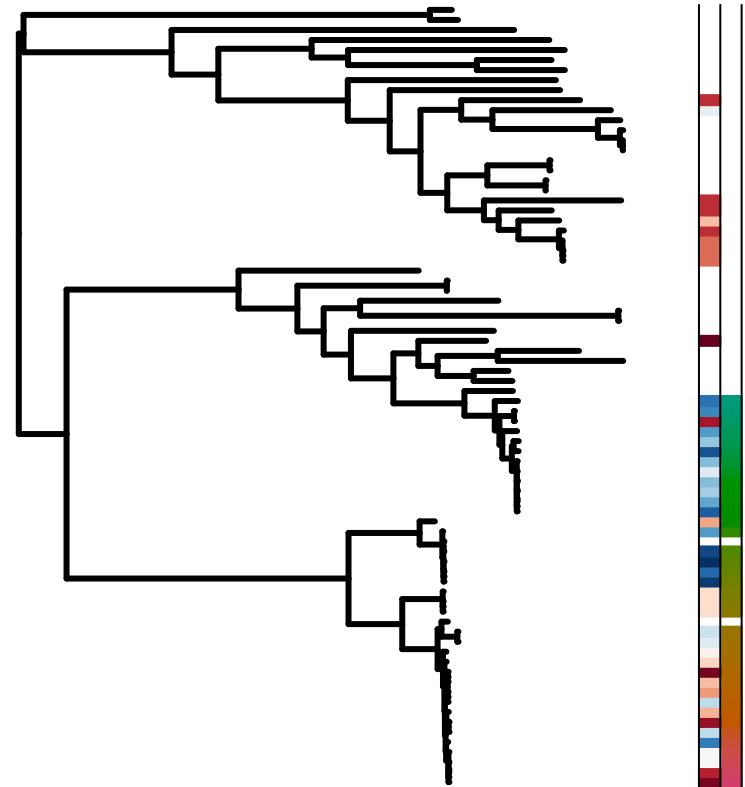
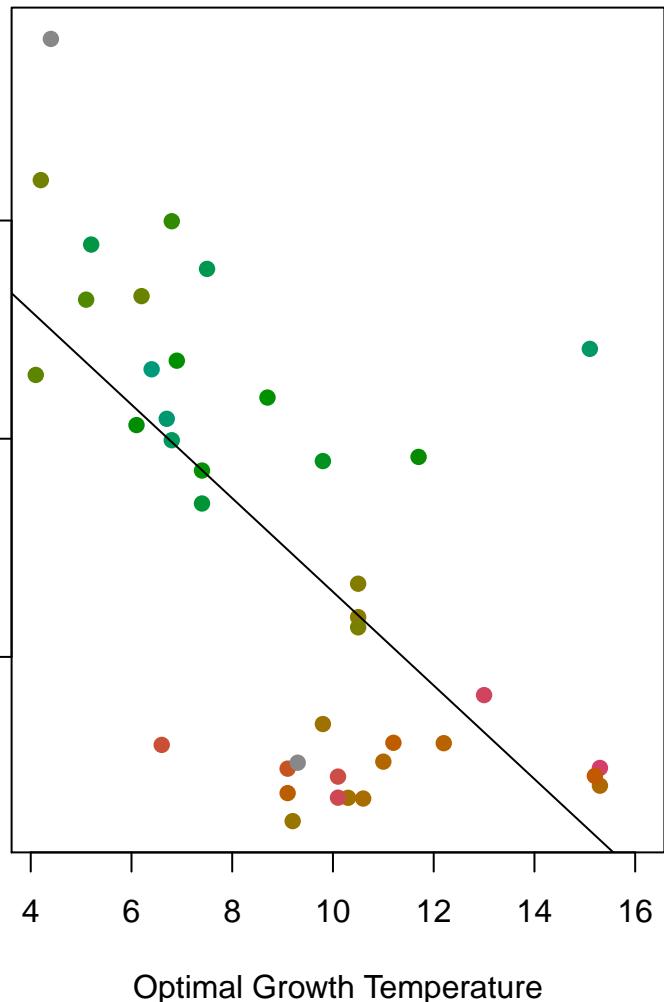
feature.plfam_id.aliphatic_index.mean
PLF_28228_00002276
hypothetical protein
 $r = -0.653, p = 10^{-4.927}$

feature.plfam_id.aliphatic_index.mean



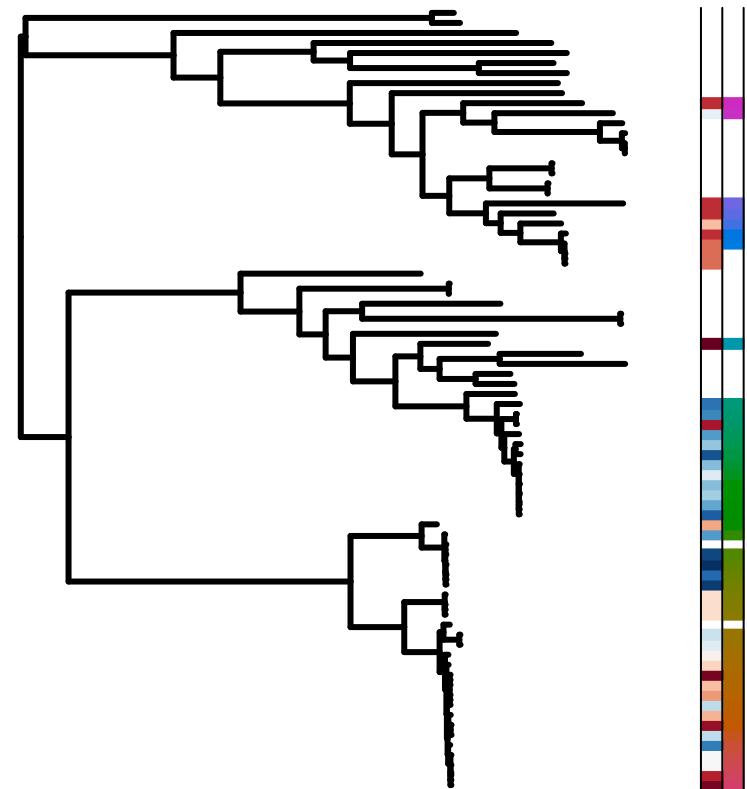
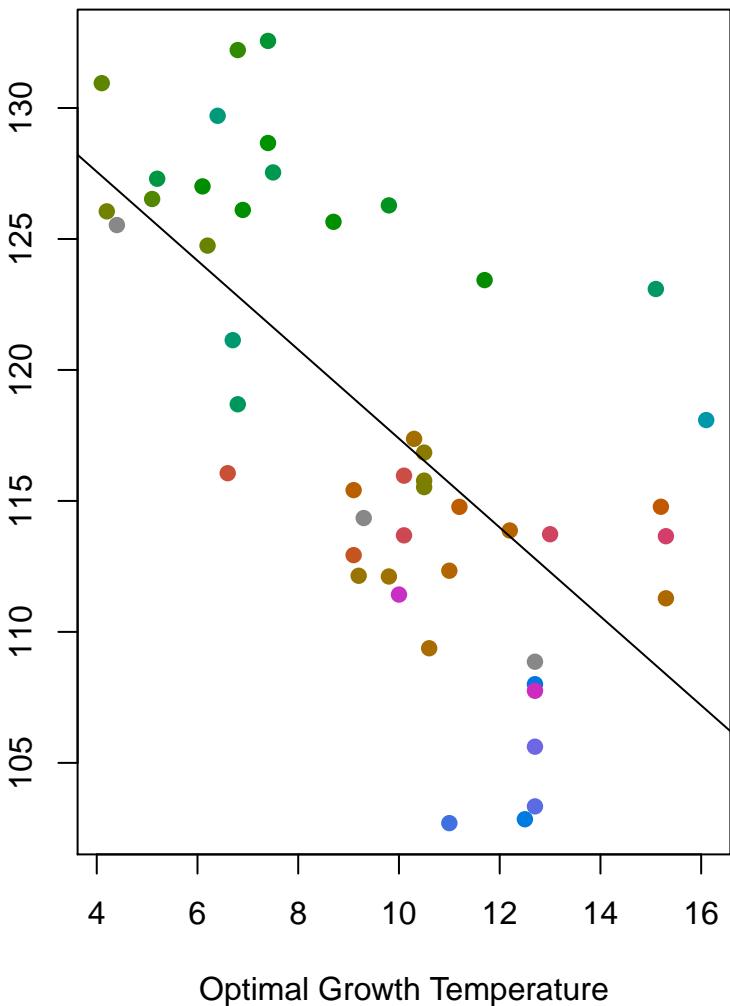
feature.plfam_id.aliphatic_index.mean
PLF_28228_00015122
hypothetical protein
 $r = -0.653$, $p = 10^{-5.188}$

feature.plfam_id.aliphatic_index.mean



feature.plfam_id.aliphatic_index.mean
PLF_28228_00015880
Transporter, LysE family
 $r = -0.661$, $p = 10^{-6.491}$

feature.plfam_id.aliphatic_index.mean



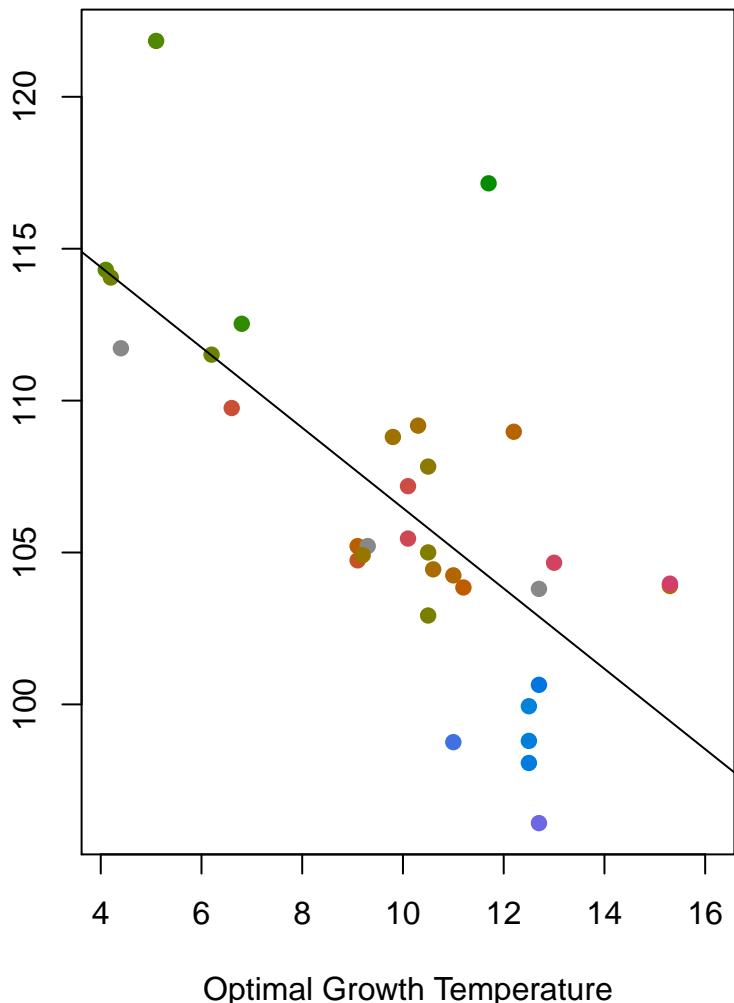
feature.plfam_id.aliphatic_index.mean

PLF_28228_00002612

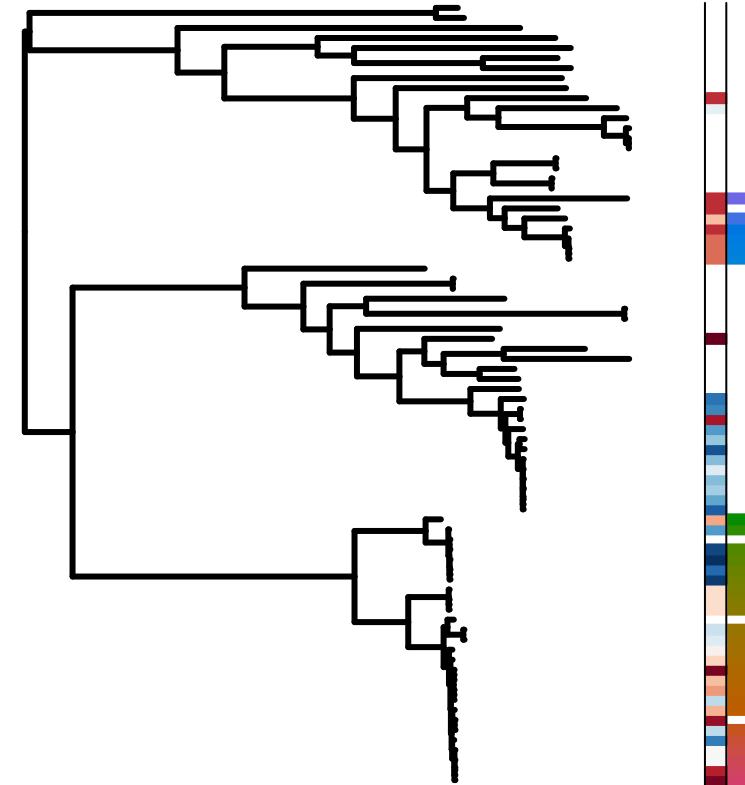
FIG026291: Hypothetical periplasmic protein

$r = -0.691, p = 10^{-5.077}$

feature.plfam_id.aliphatic_index.mean

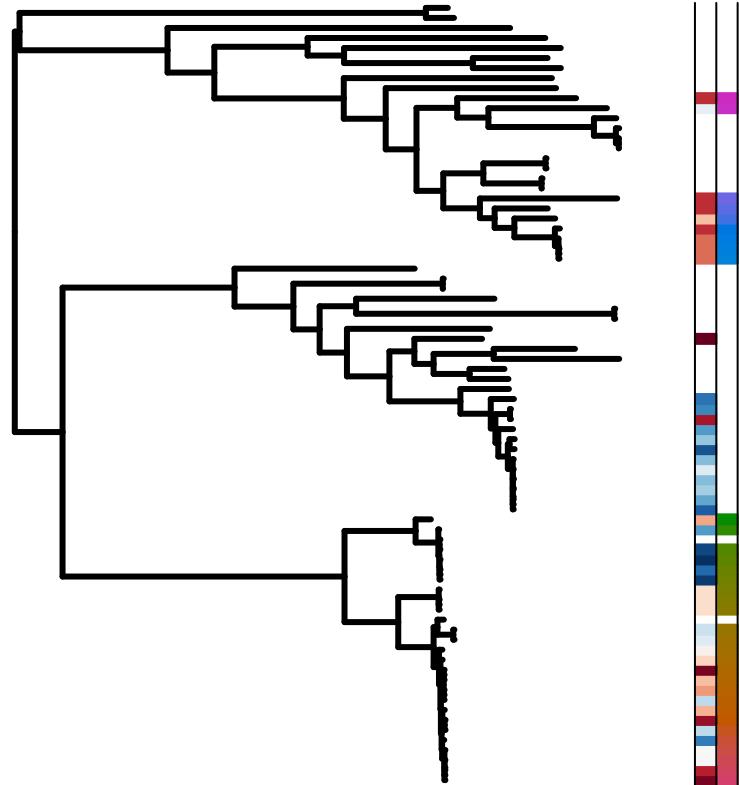
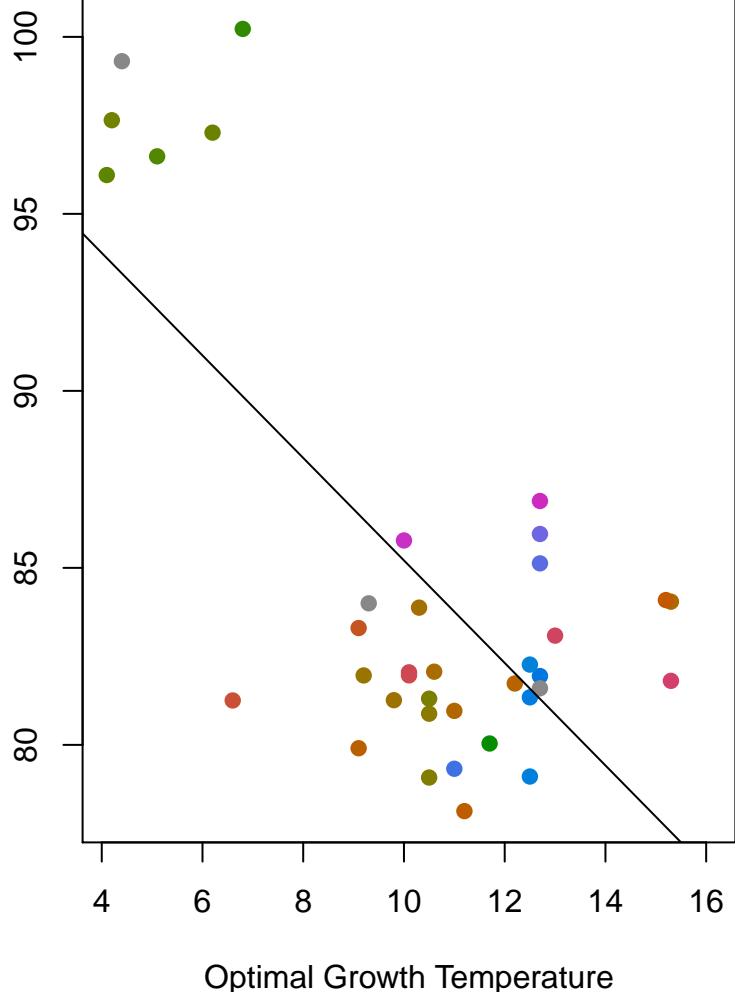


Optimal Growth Temperature



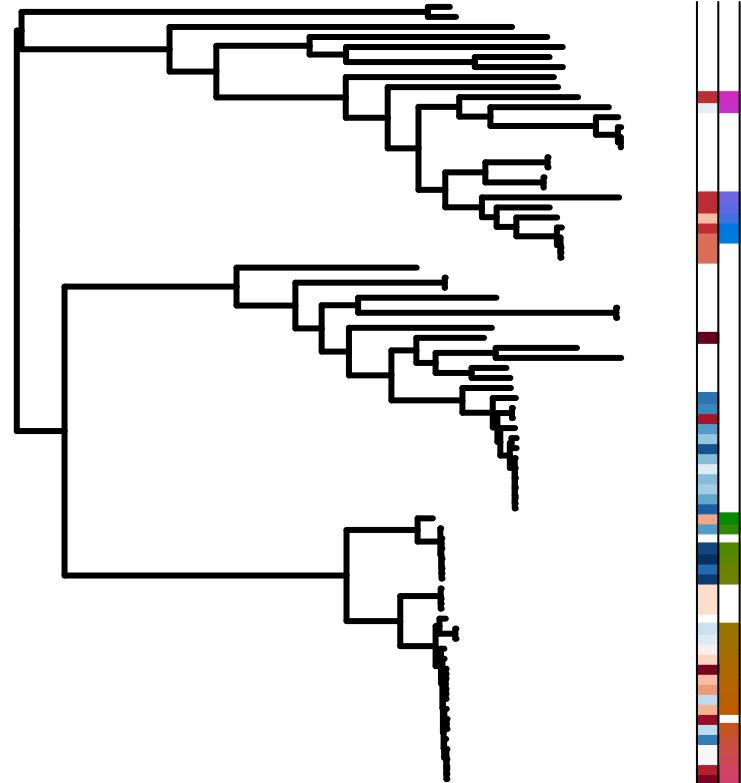
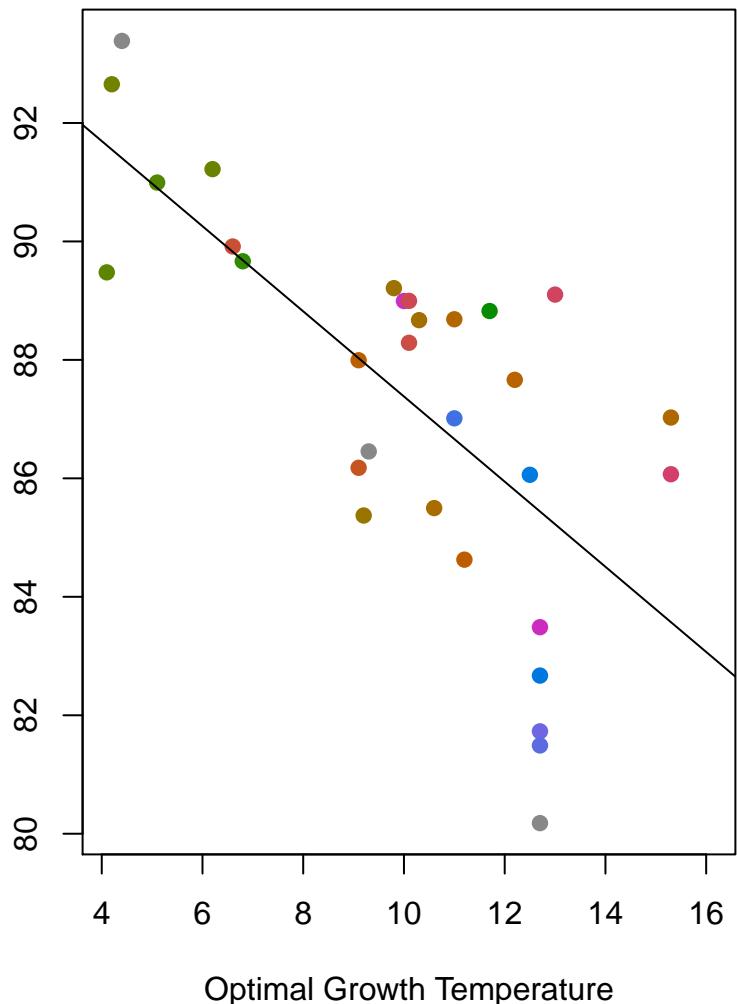
feature.plfam_id.aliphatic_index.mean
PLF_28228_00001024
Putative NAD(P)H nitroreductase YdjA
 $r = -0.692$, $p = 10^{-5.679}$

feature.plfam_id.aliphatic_index.mean



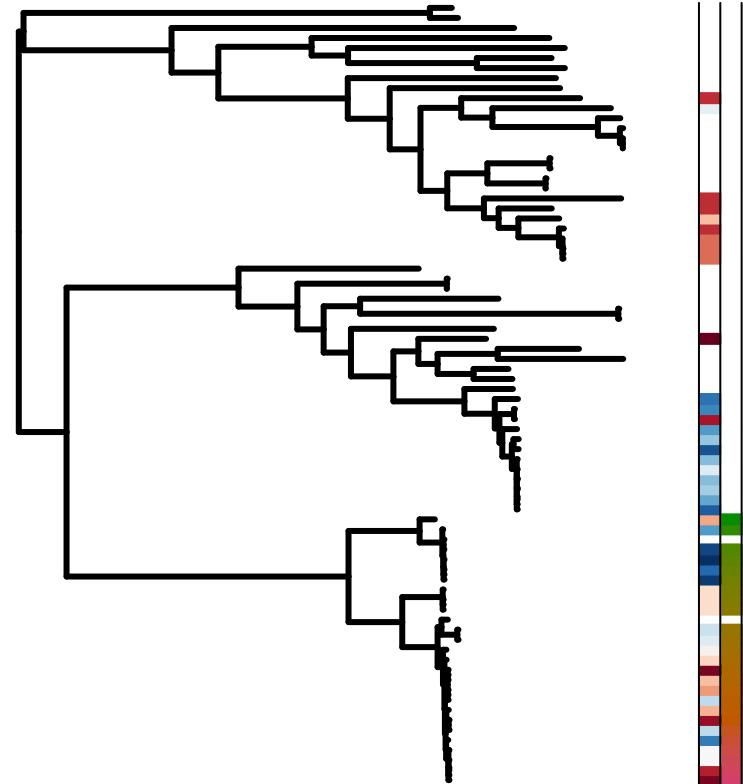
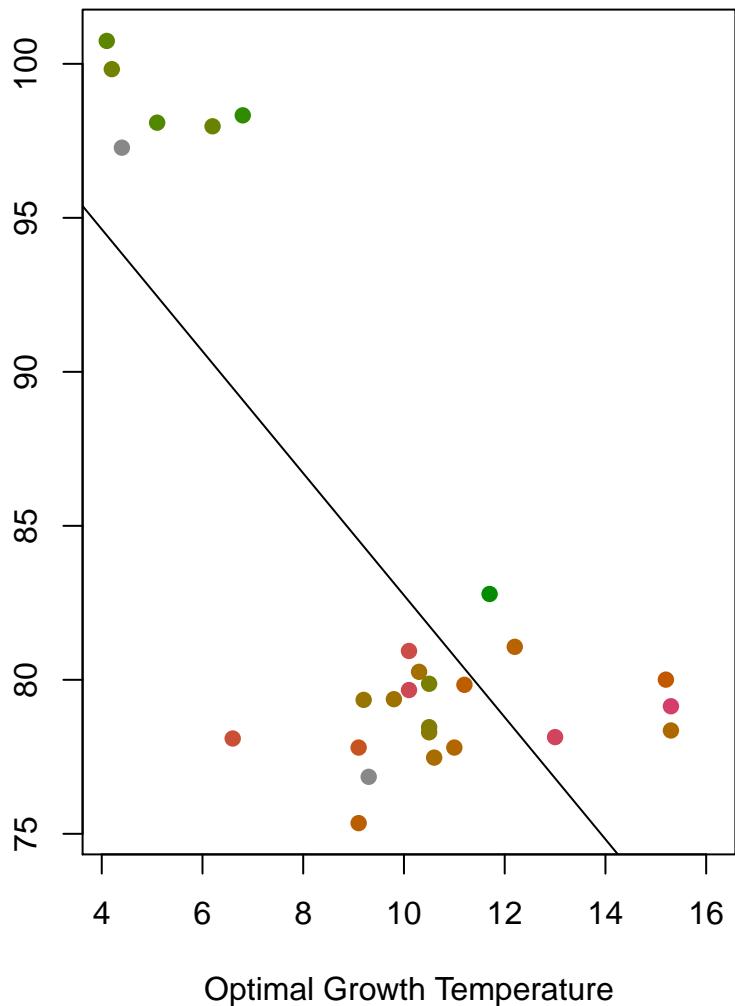
feature.plfam_id.aliphatic_index.mean
PLF_28228_00017084
Alkylated DNA repair protein
 $r = -0.694$, $p = 10^{-4.823}$

feature.plfam_id.aliphatic_index.mean



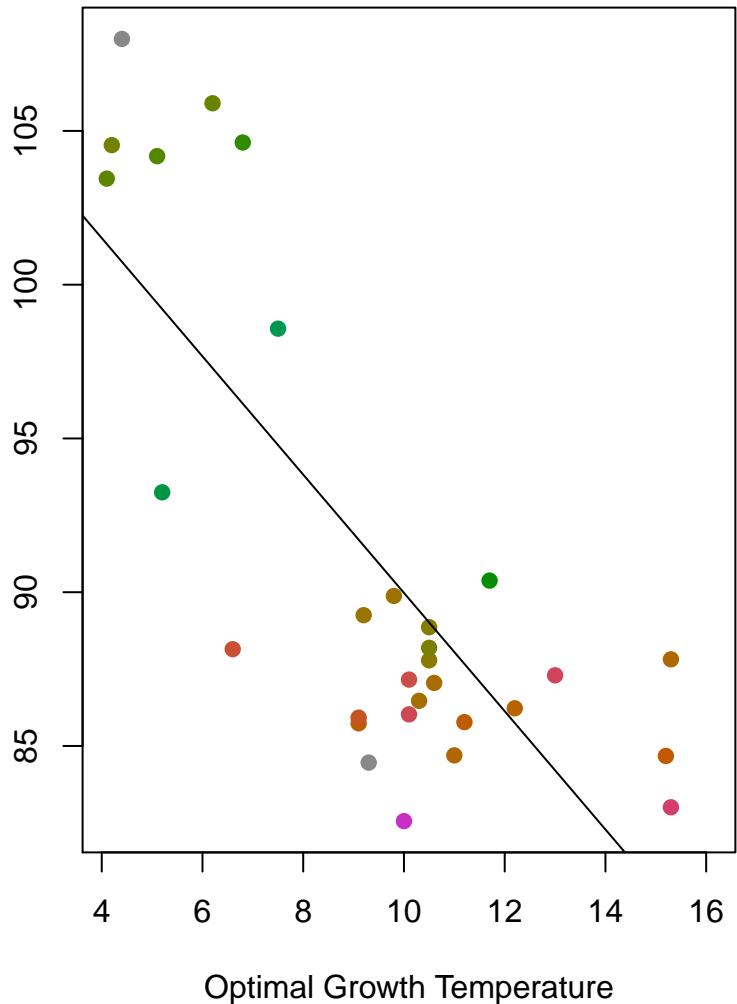
feature.plfam_id.aliphatic_index.mean
PLF_28228_00031426
hypothetical protein
 $r = -0.743$, $p = 10^{-5.043}$

feature.plfam_id.aliphatic_index.mean

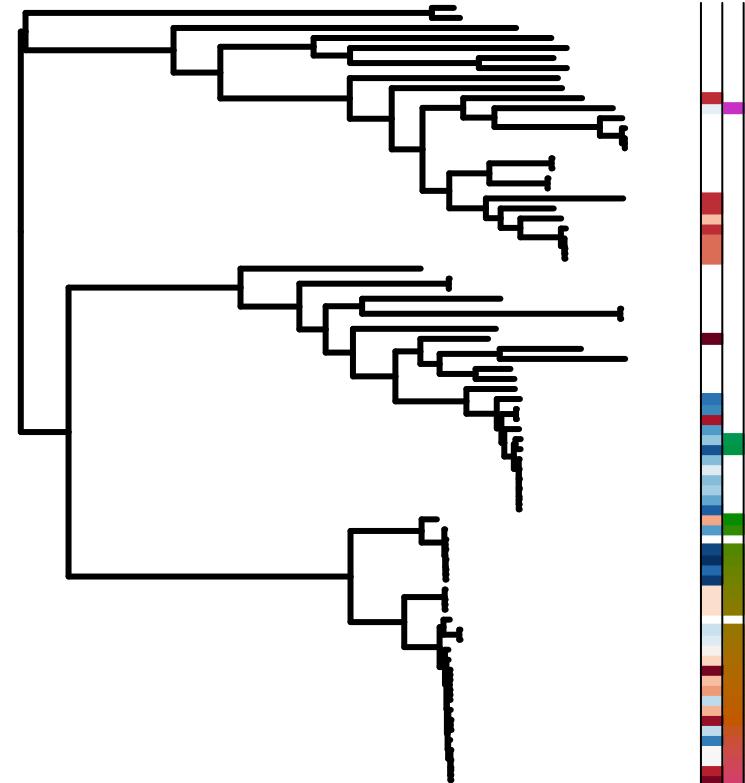


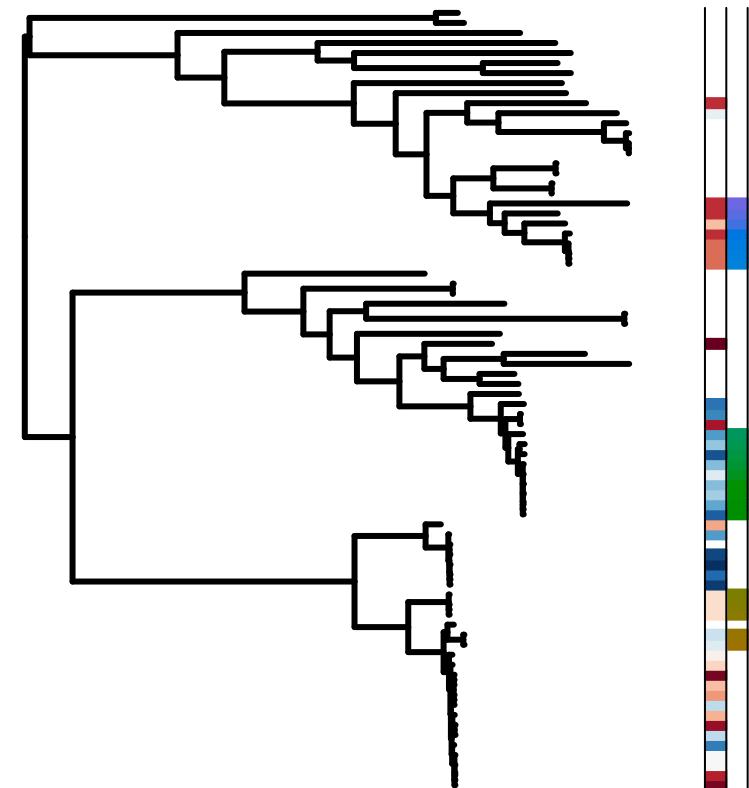
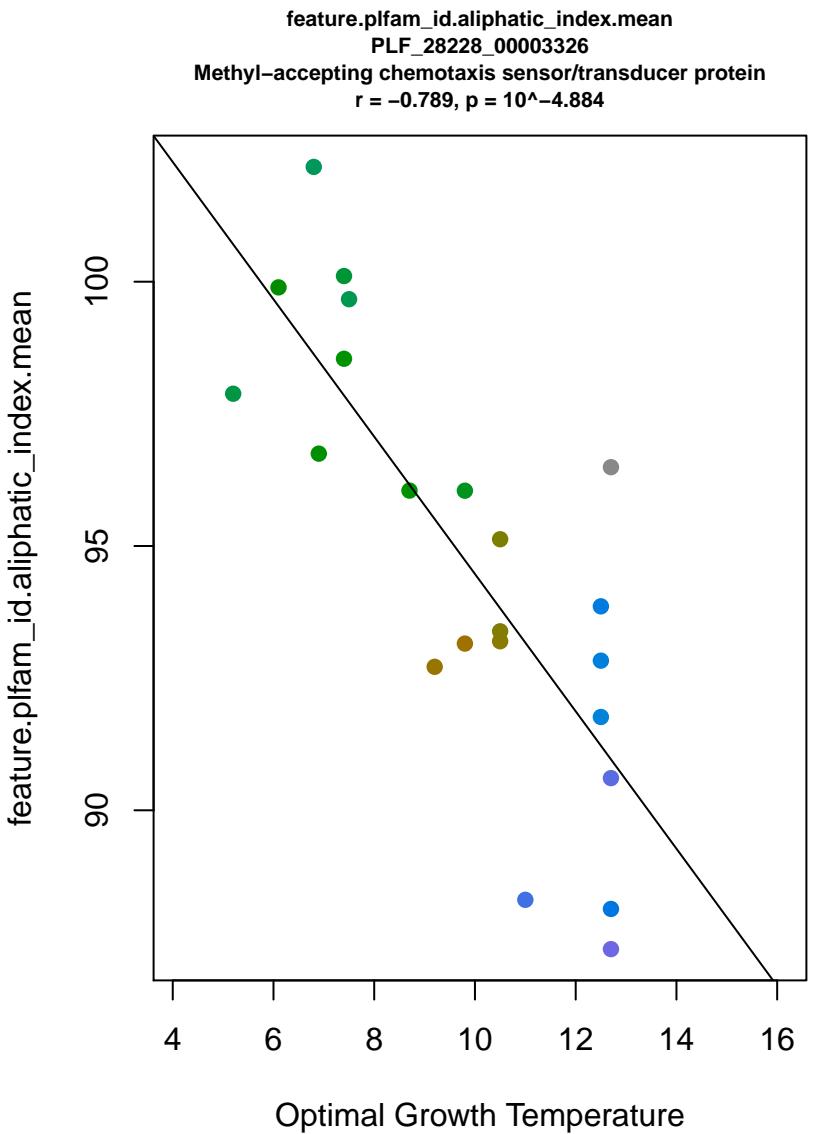
feature.plfam_id.aliphatic_index.mean
PLF_28228_00008631
hypothetical protein
 $r = -0.775$, $p = 10^{-6.316}$

feature.plfam_id.aliphatic_index.mean



Optimal Growth Temperature



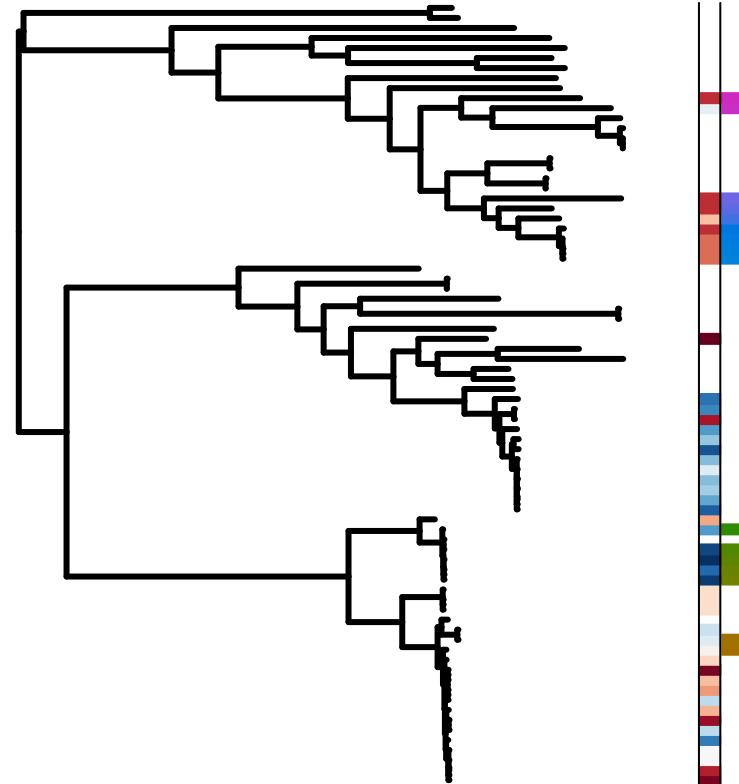
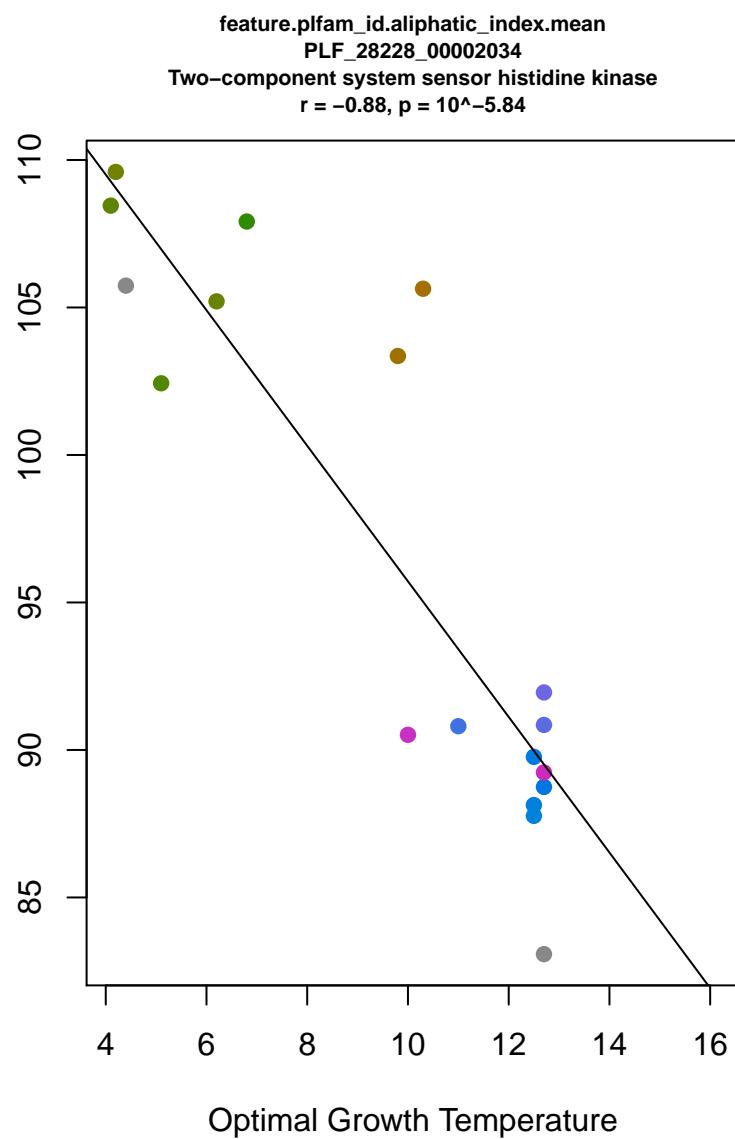
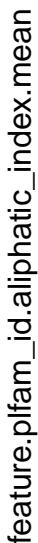


feature_pfam_id.aliphatic_index.mean

PLF_28228_00002034

Two-component system sensor histidine kinase

$r = -0.88, p = 10^{-5.84}$

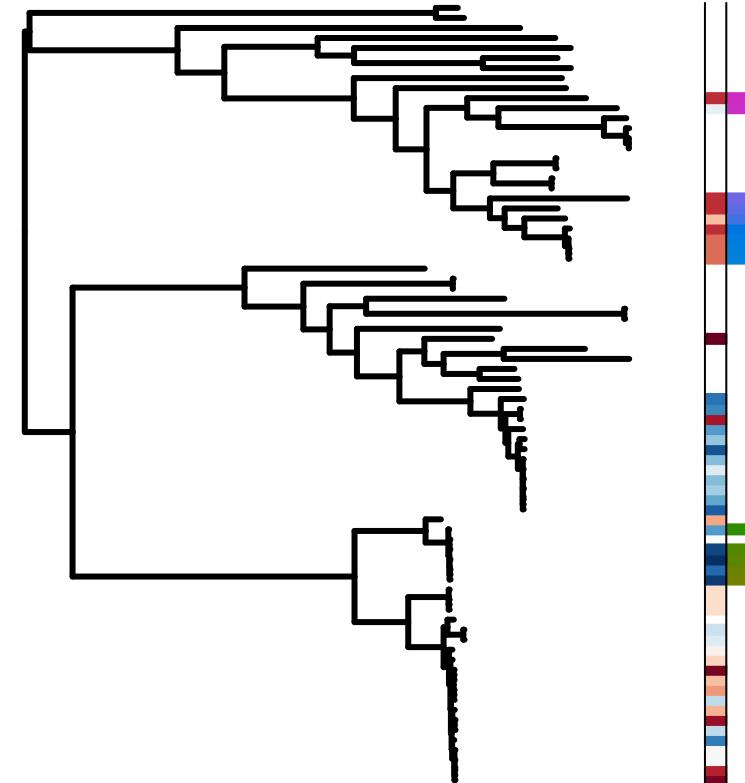
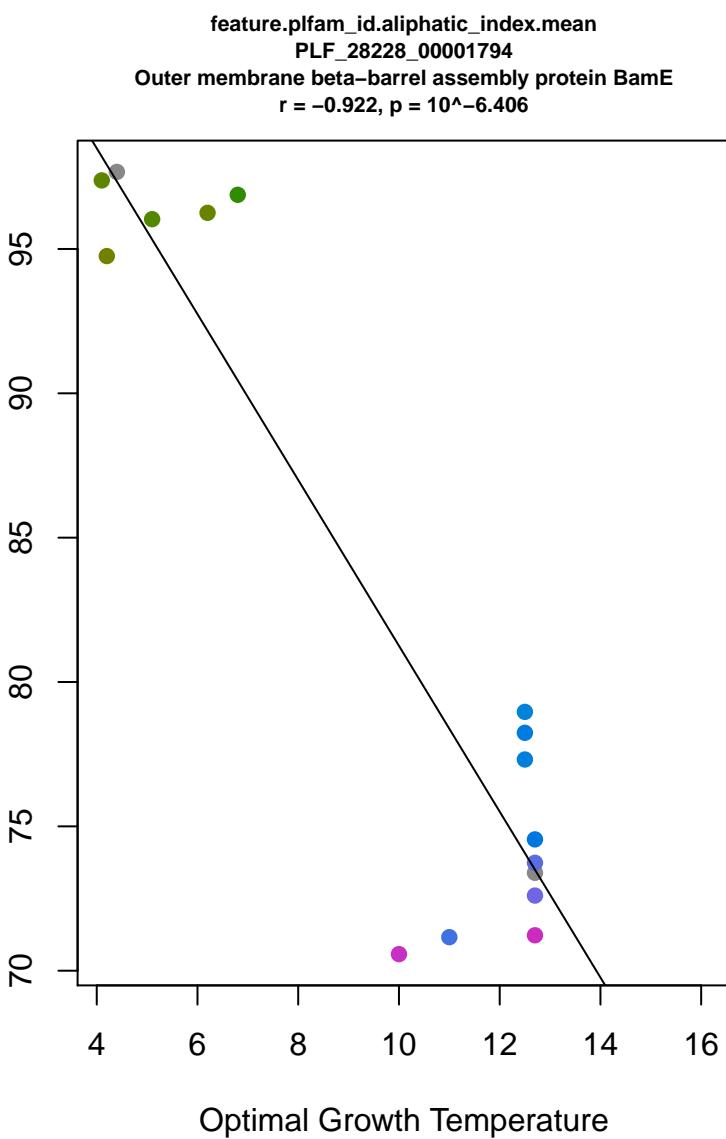


feature_pfam_id.aliphatic_index.mean

PLF_28228_00001794

Outer membrane beta-barrel assembly protein BamE

$r = -0.922$, $p = 10^{-6.406}$



feature.plfam_id.aliphatic_index.mean
PLF_28228_00007748
EAL domain protein
 $r = -0.929$, $p = 10^{-4.904}$

feature.plfam_id.aliphatic_index.mean

