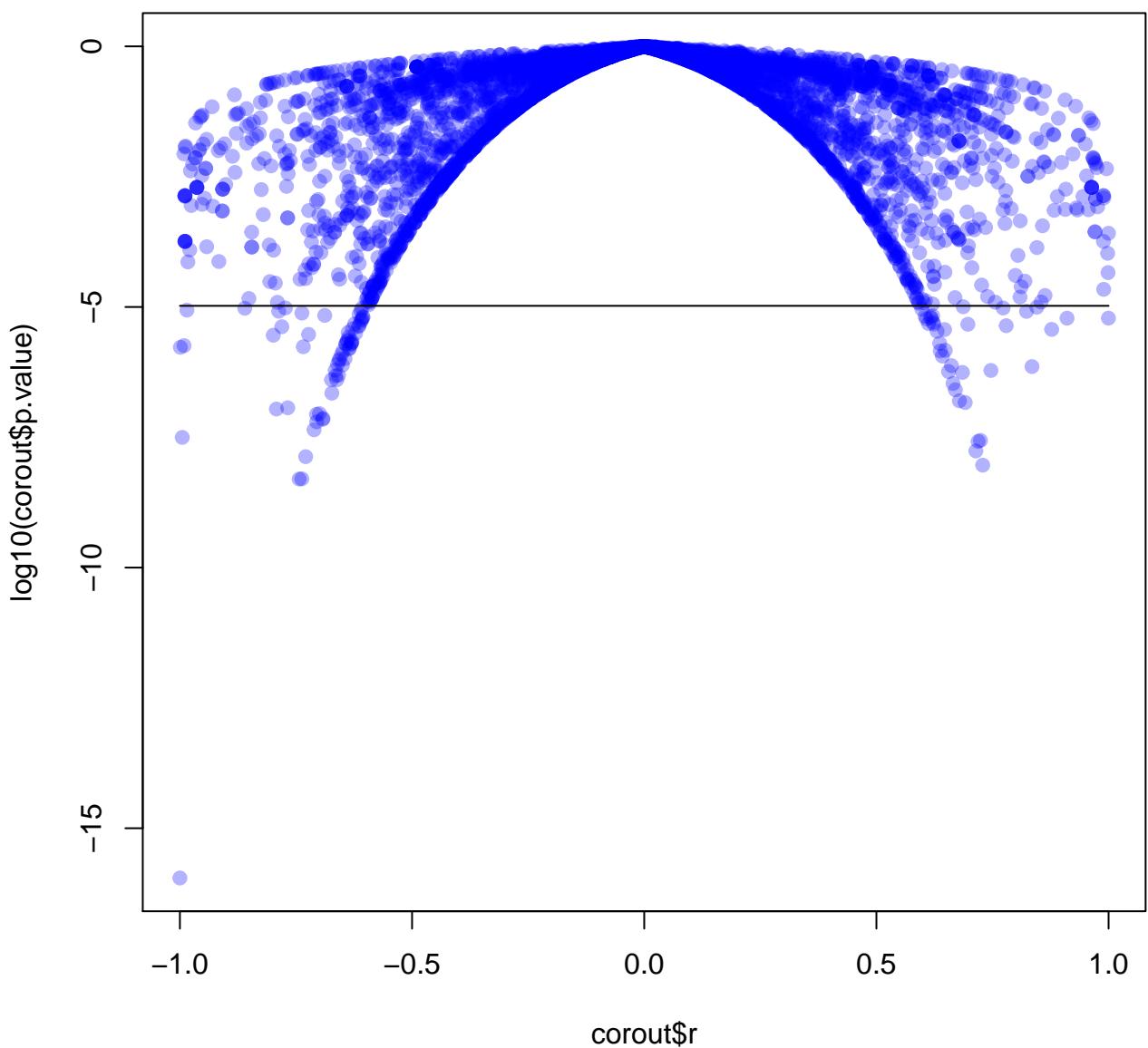
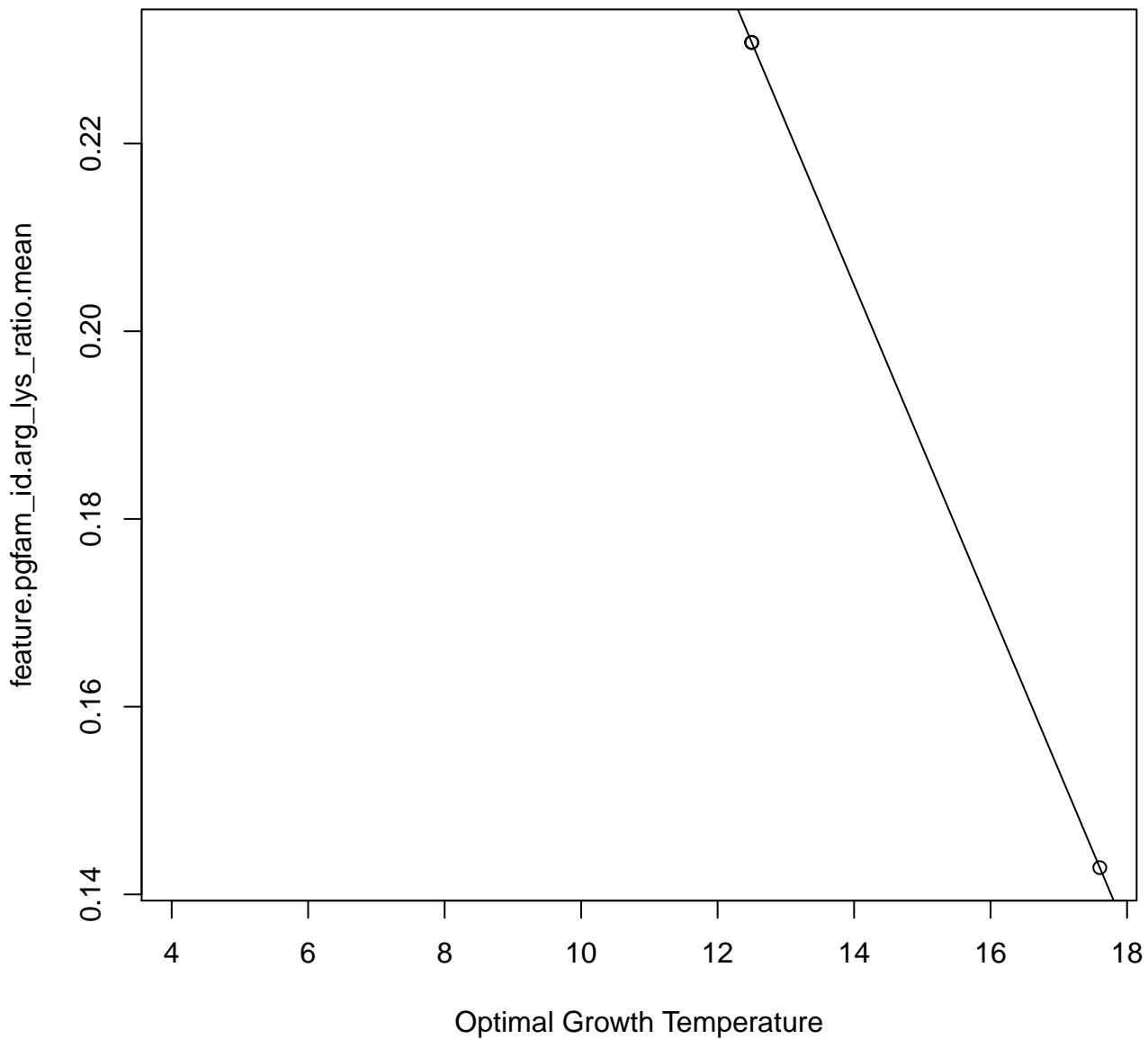


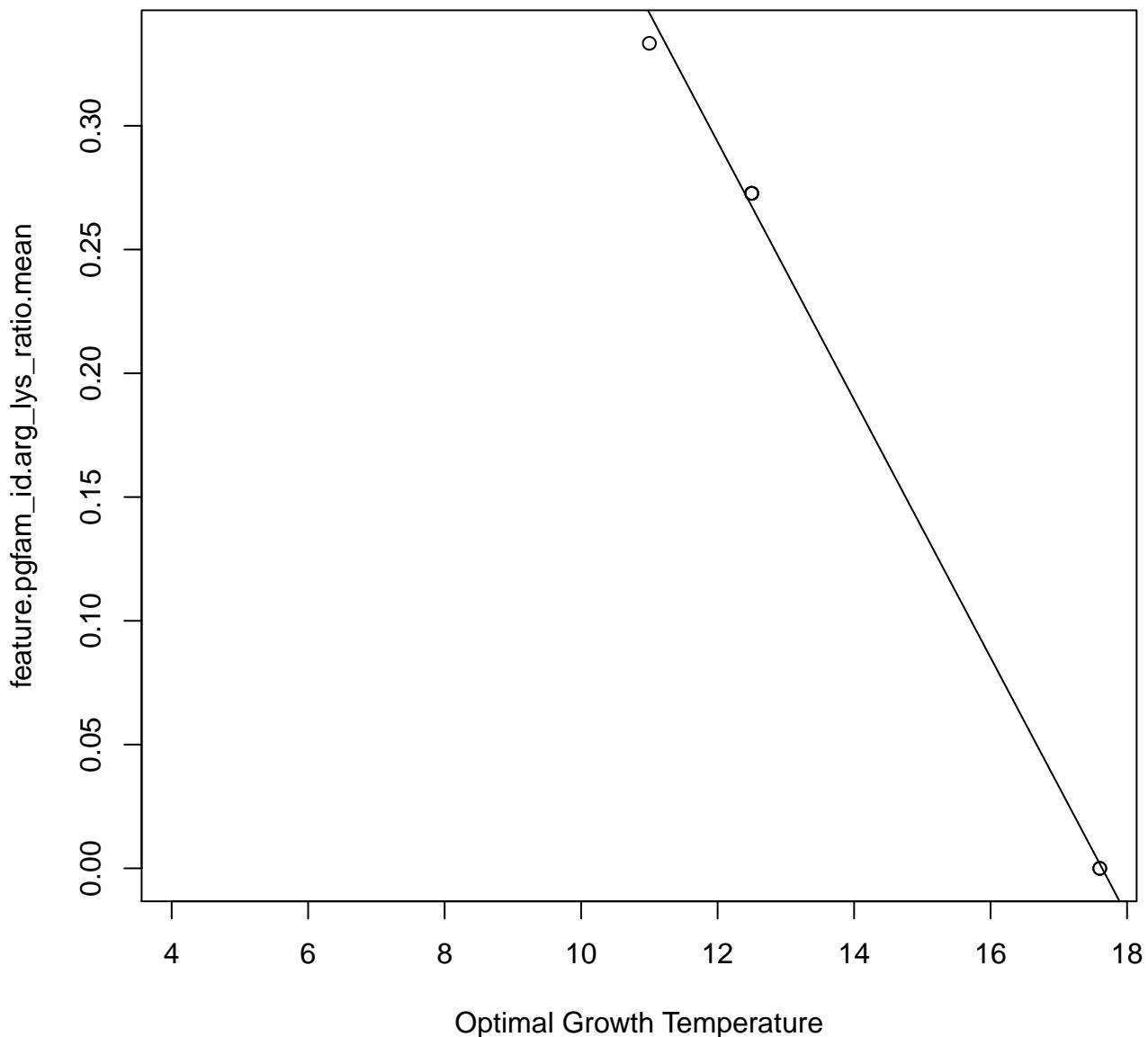
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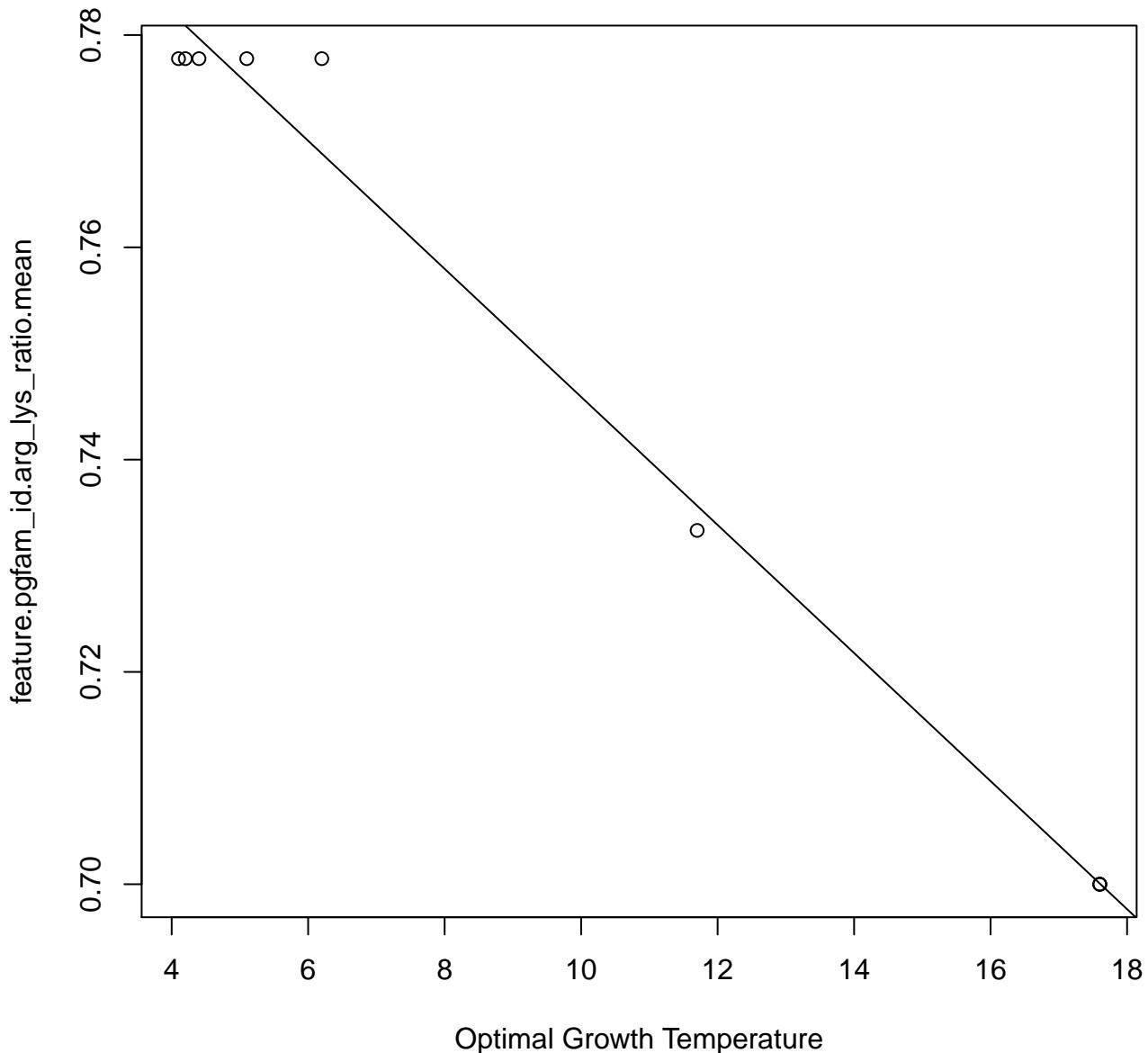
feature.pgfam_id.arg_lys_ratio.mean
PGF_01338089
hypothetical protein



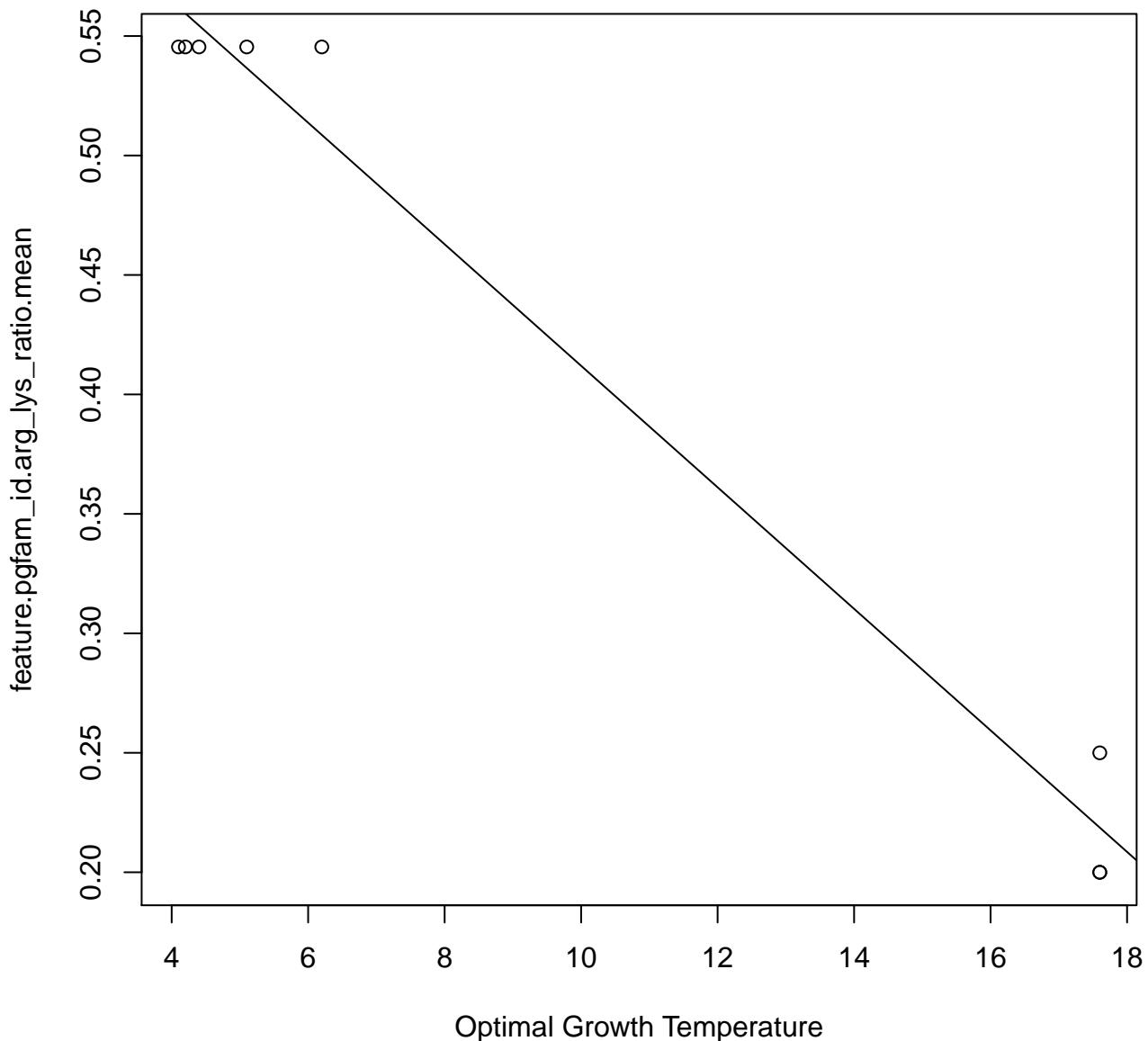
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PGF_01337799
hypothetical protein



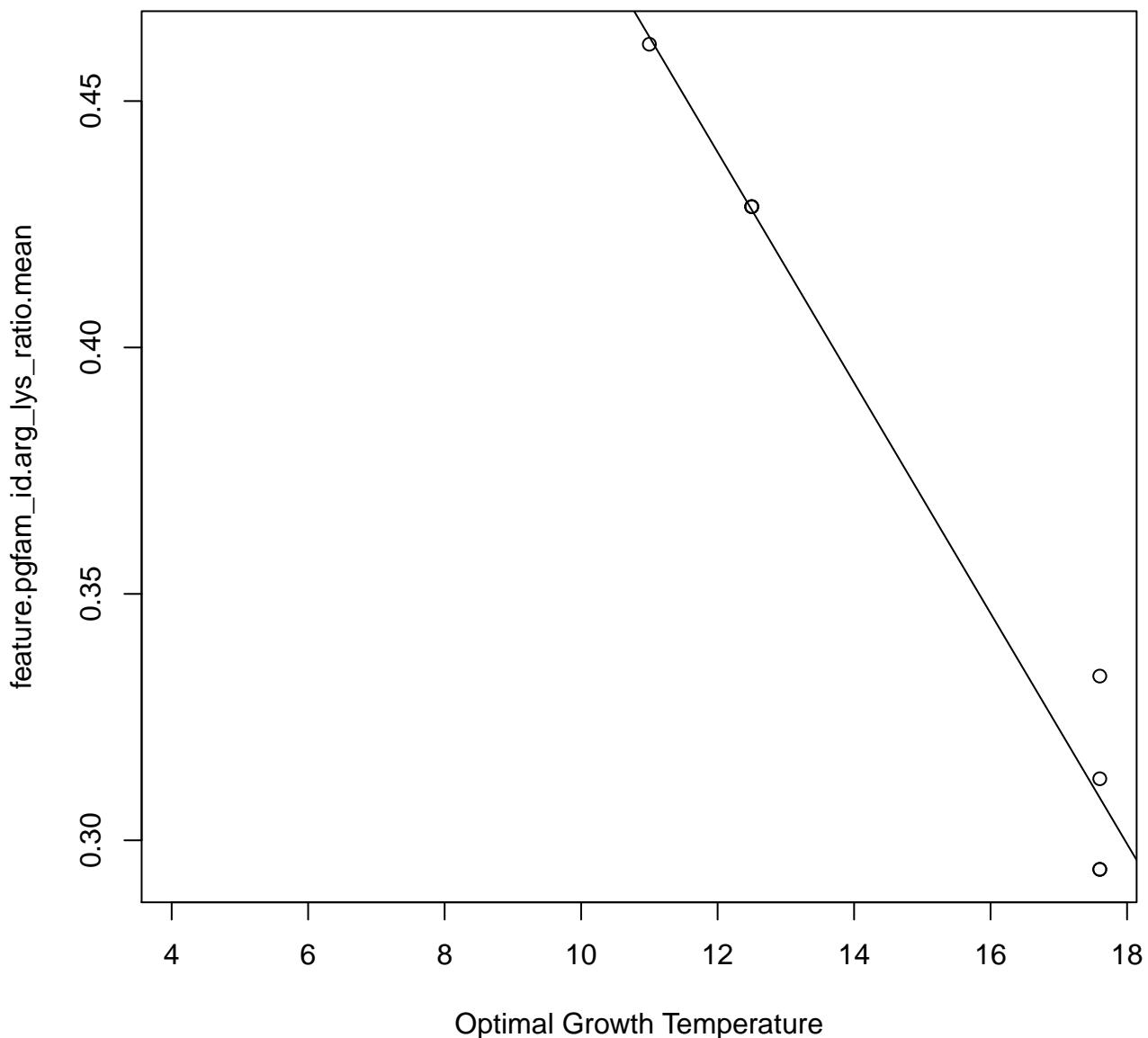
feature.pgfam_id.arg_lys_ratio.mean
PGF_03221663
Phage tail collar domain



feature.pgfam_id.arg_lys_ratio.mean
PGF_01336811
hypothetical protein



feature.pgfam_id.arg_lys_ratio.mean
PGF_01336832
hypothetical protein

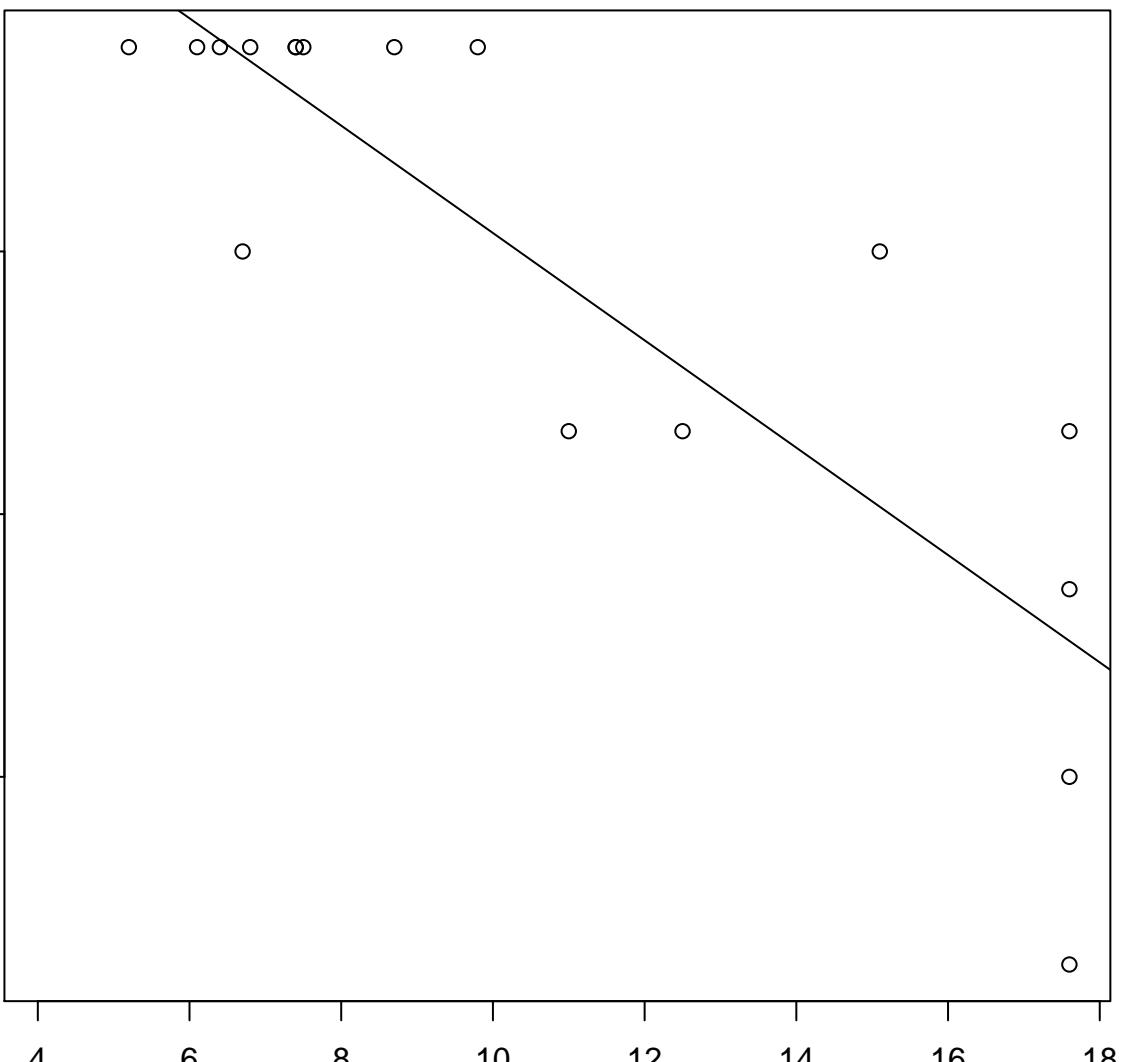


feature.pgfam_id.arg_lys_ratio.mean

PGF_00032999

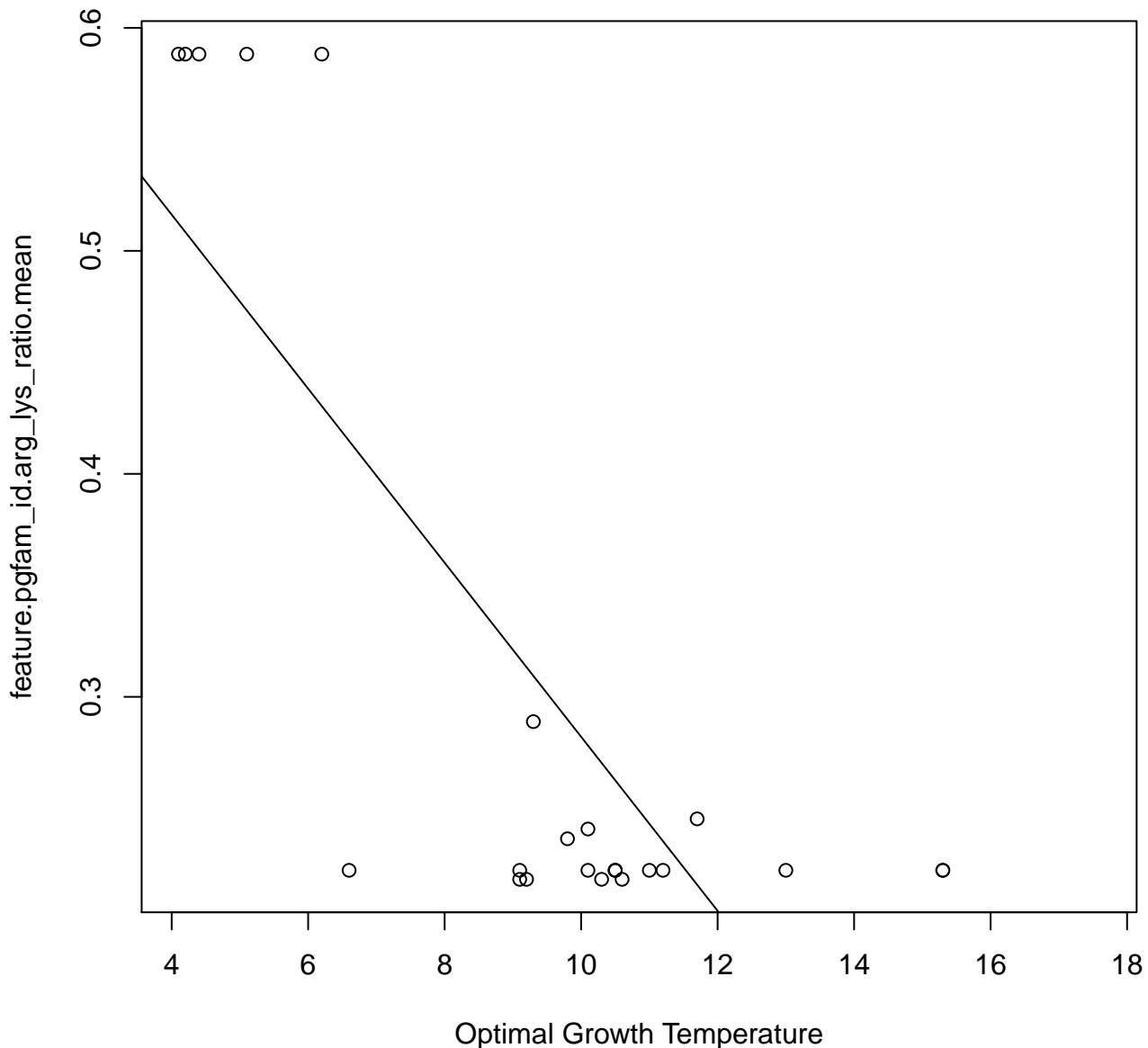
PhbF

feature.pgfam_id.arg_lys_ratio.mean

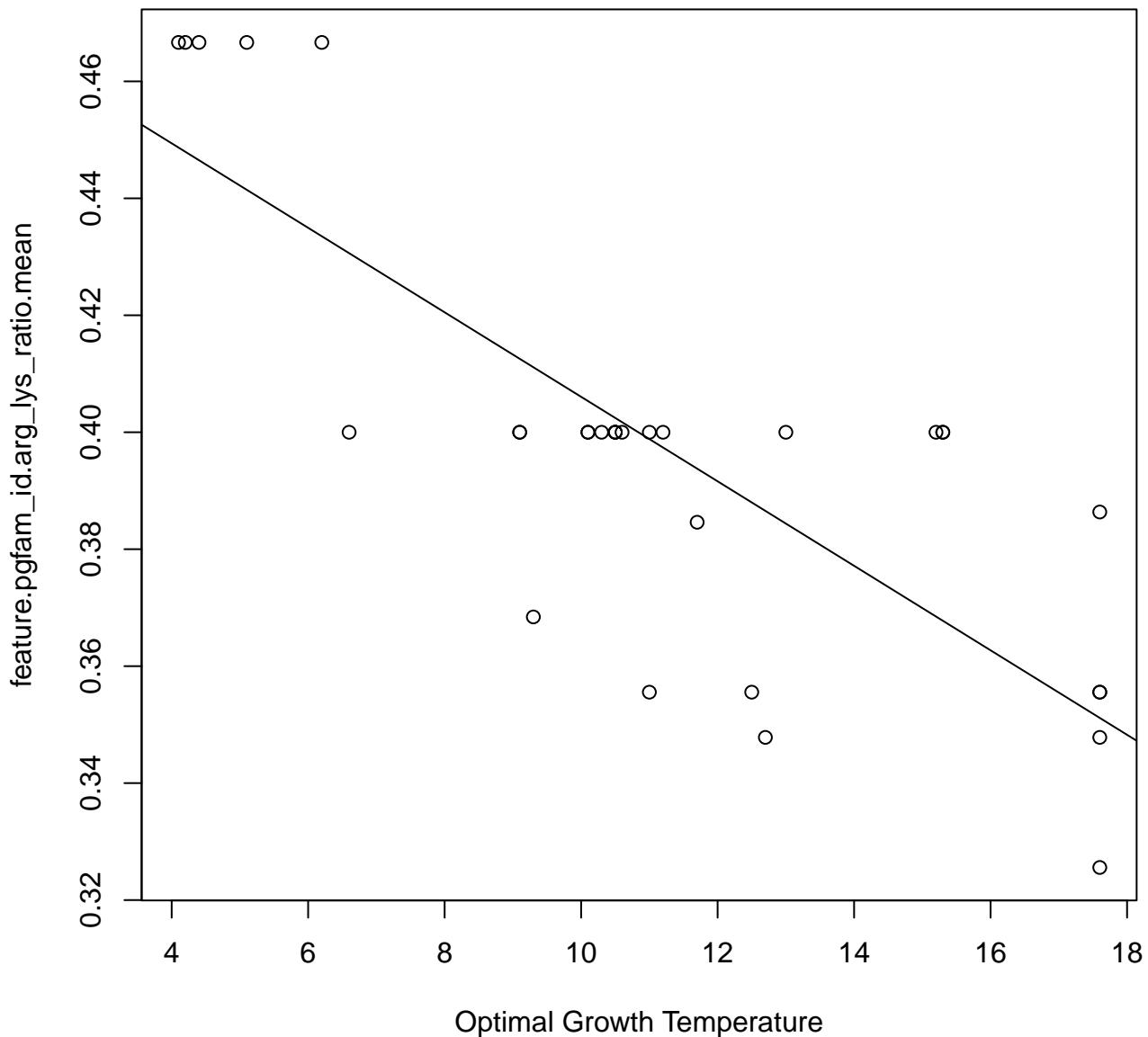


Optimal Growth Temperature

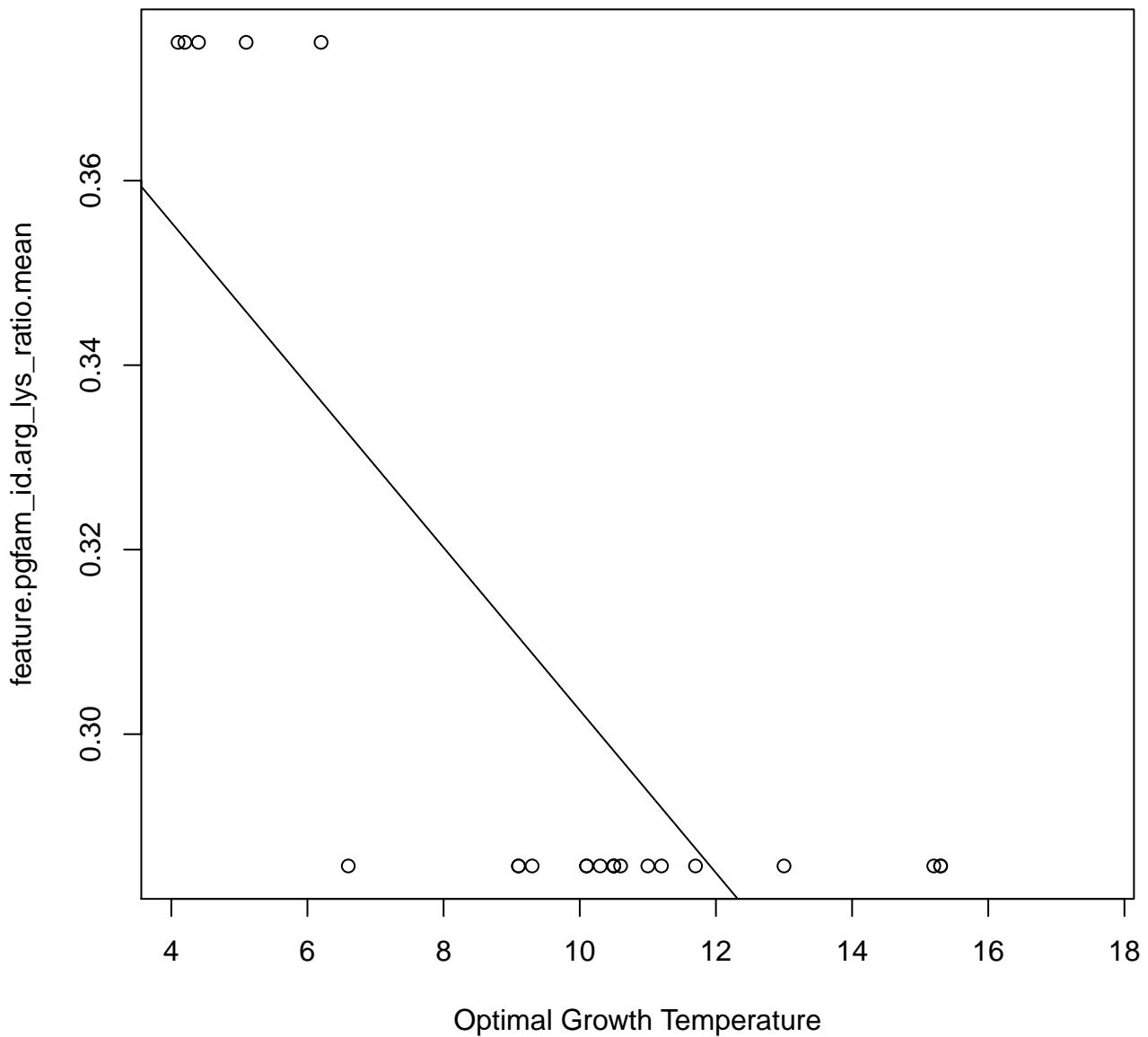
feature.pgfam_id.arg_lys_ratio.mean
PGF_03083319
Maltodextrin glucosidase (EC 3.2.1.20)



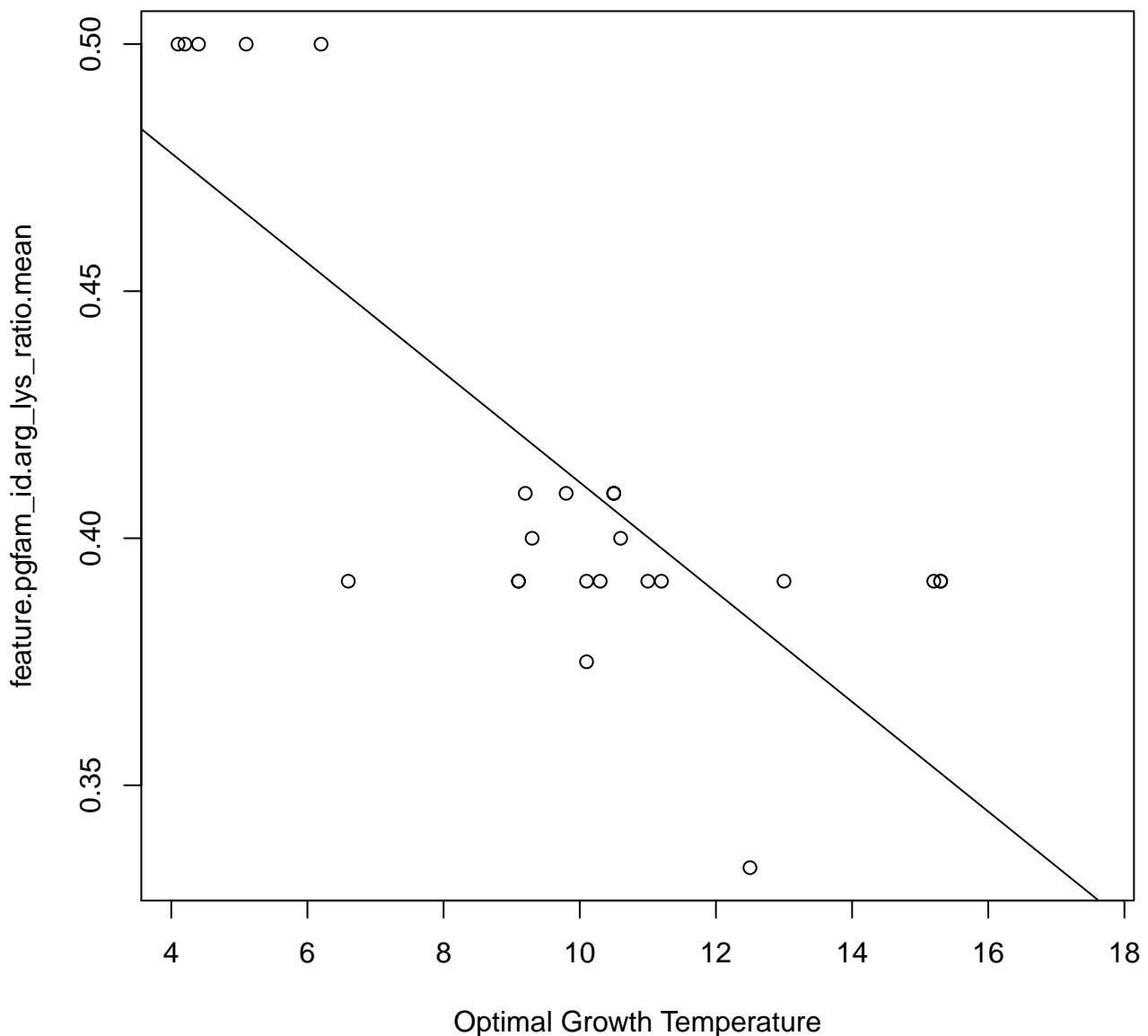
feature.pgfam_id.arg_lys_ratio.mean
PGF_12765299
Two-component system sensor histidine kinase



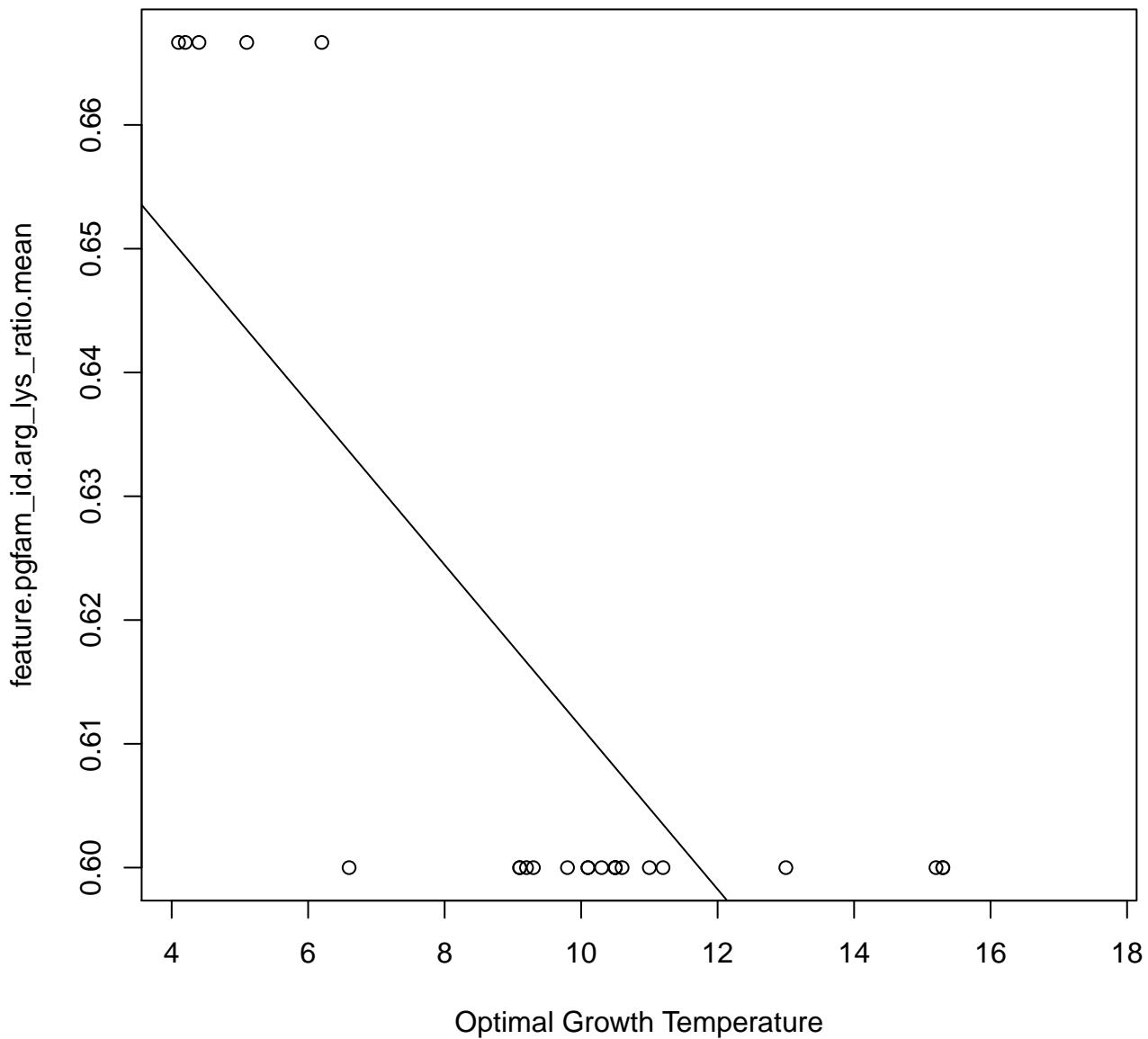
feature.pgfam_id.arg_lys_ratio.mean
PGF_10906072
hypothetical protein



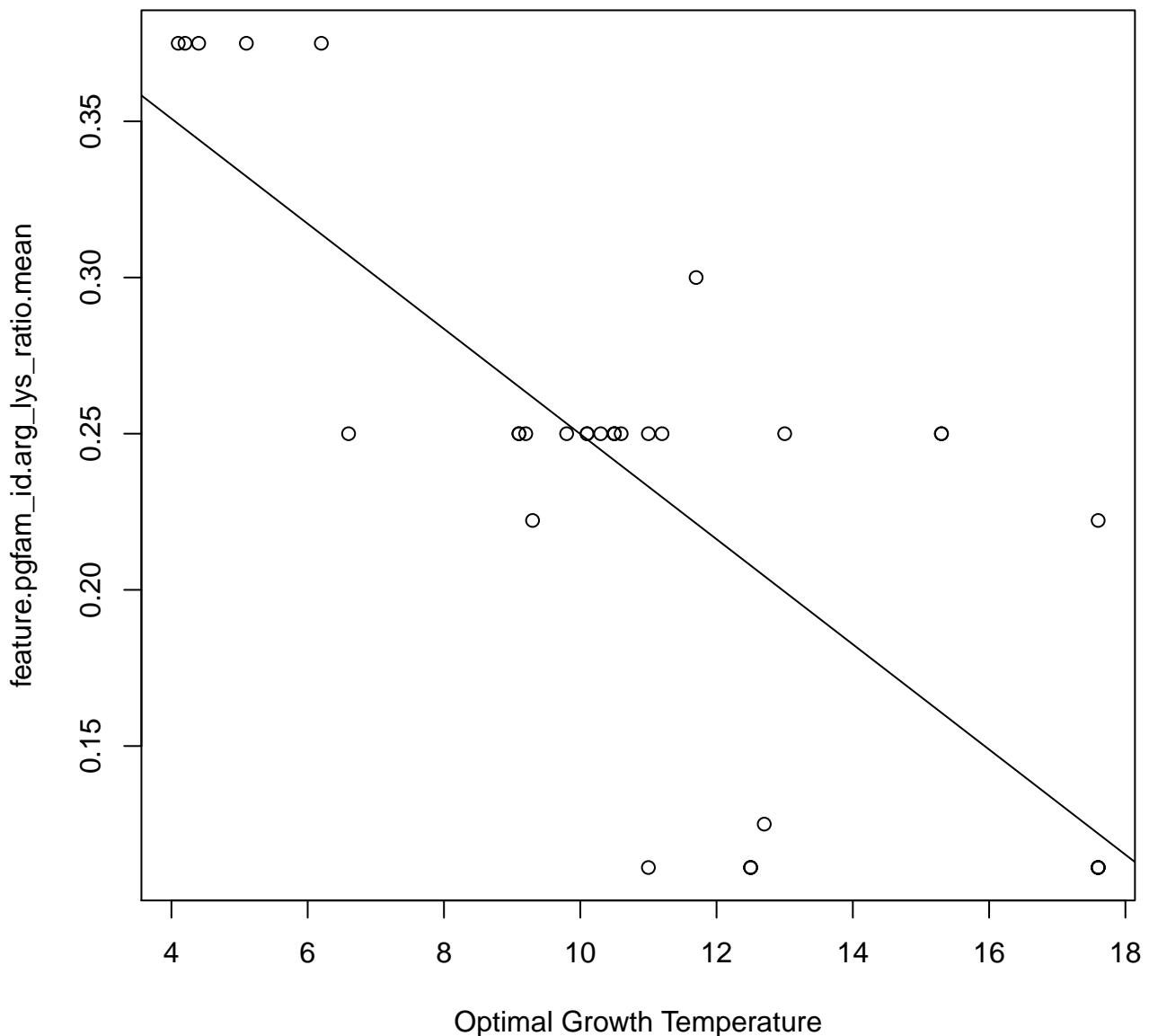
feature.pgfam_id.arg_lys_ratio.mean
PGF_06792096
hypothetical protein



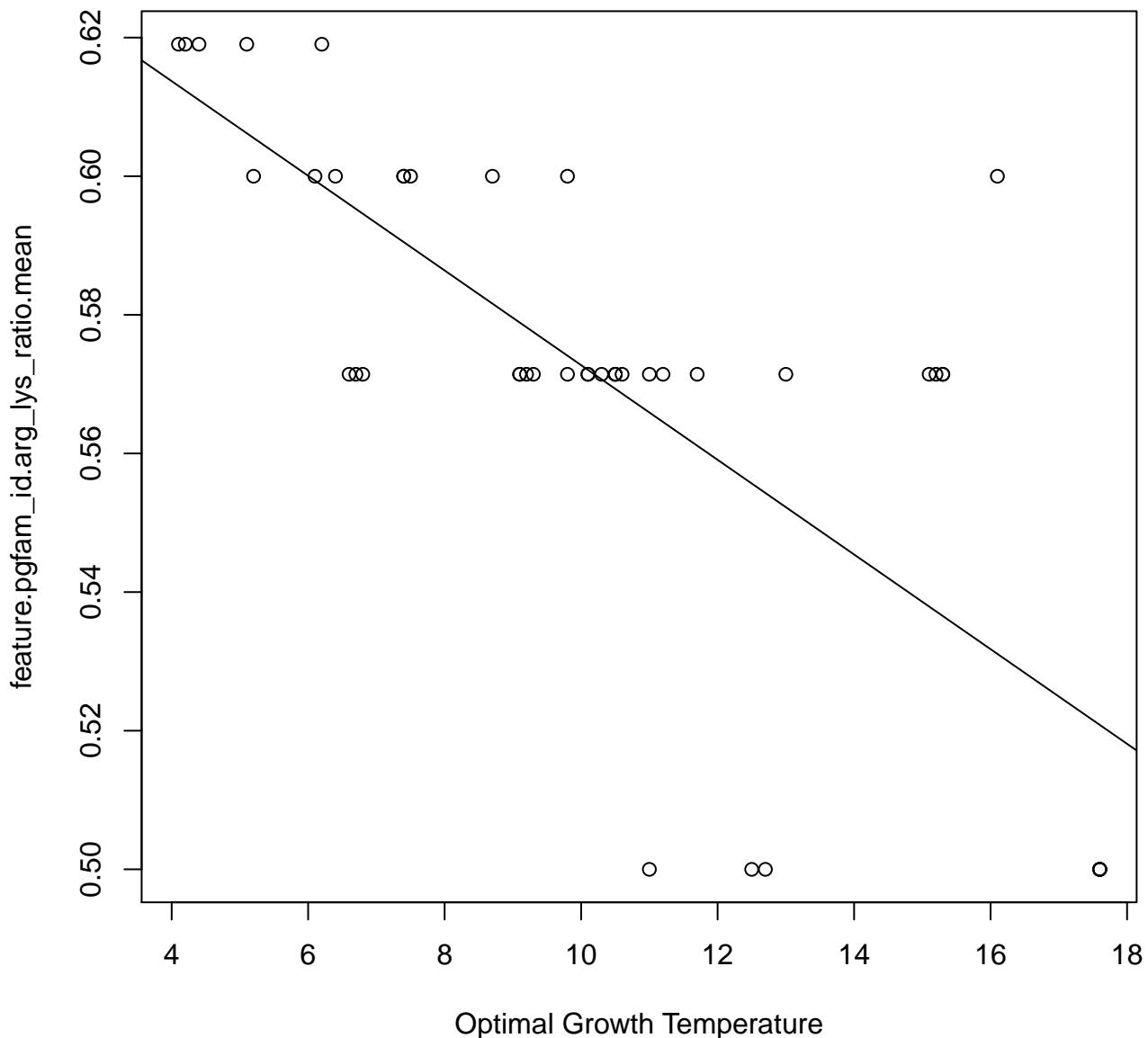
feature.pgfam_id.arg_lys_ratio.mean
PGF_12071964
hypothetical protein



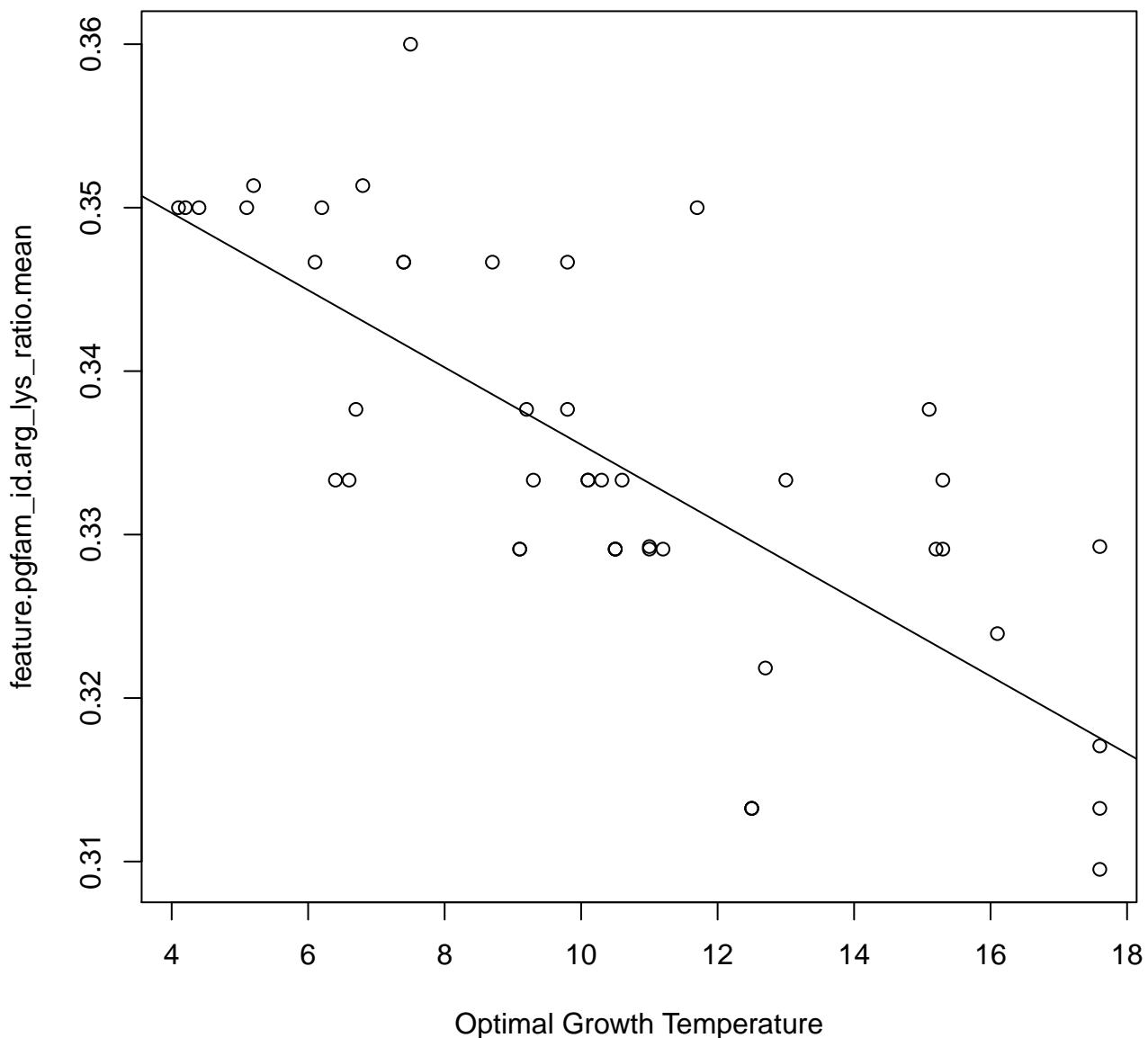
feature.pgfam_id.arg_lys_ratio.mean
PGF_01442793
Putative manganese efflux pump MntP



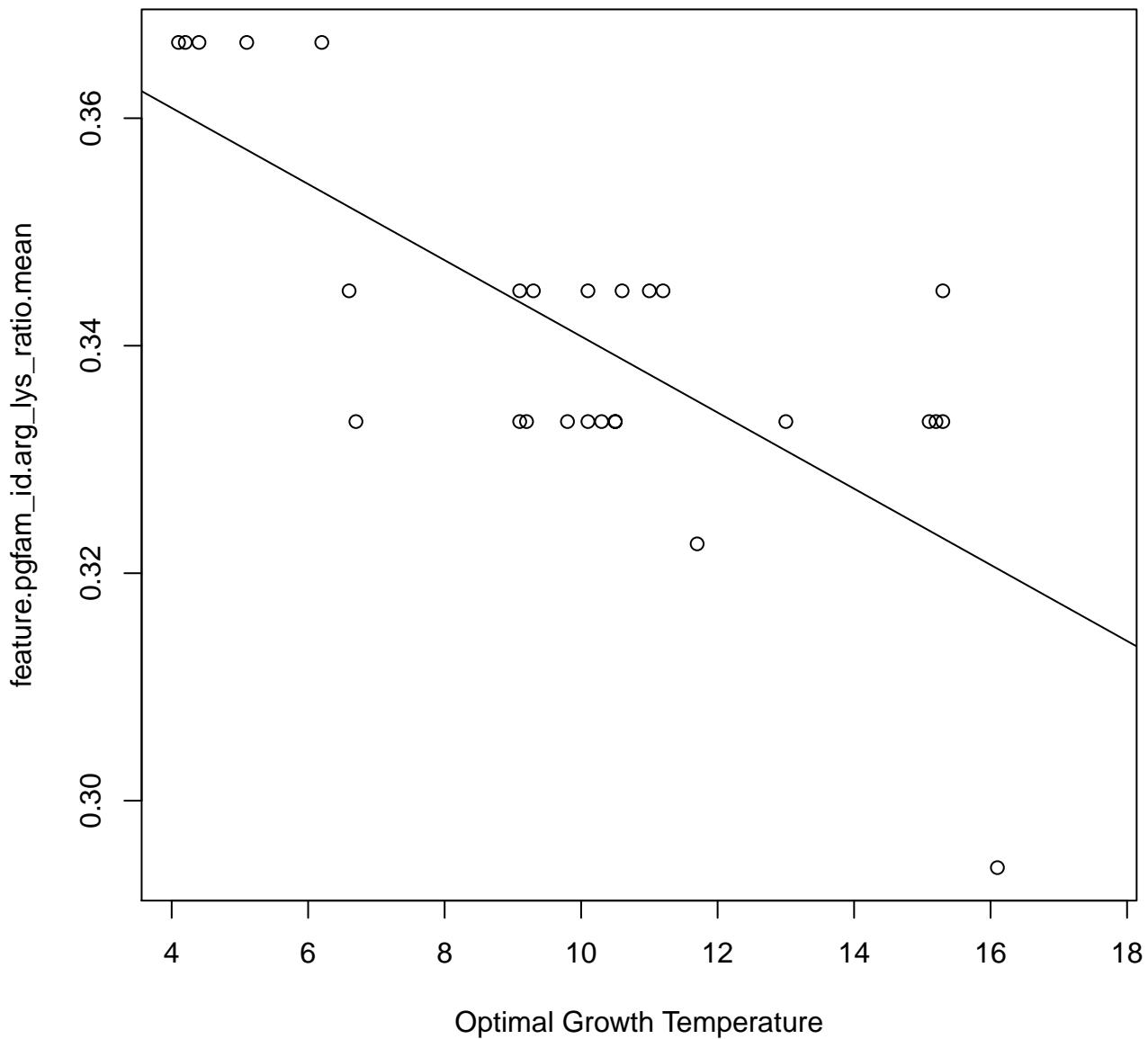
feature.pgfam_id.arg_lys_ratio.mean
PGF_07480521
23S rRNA (pseudouridine(1915)-N(3))-methyltransferase (EC 2.1.1.177)



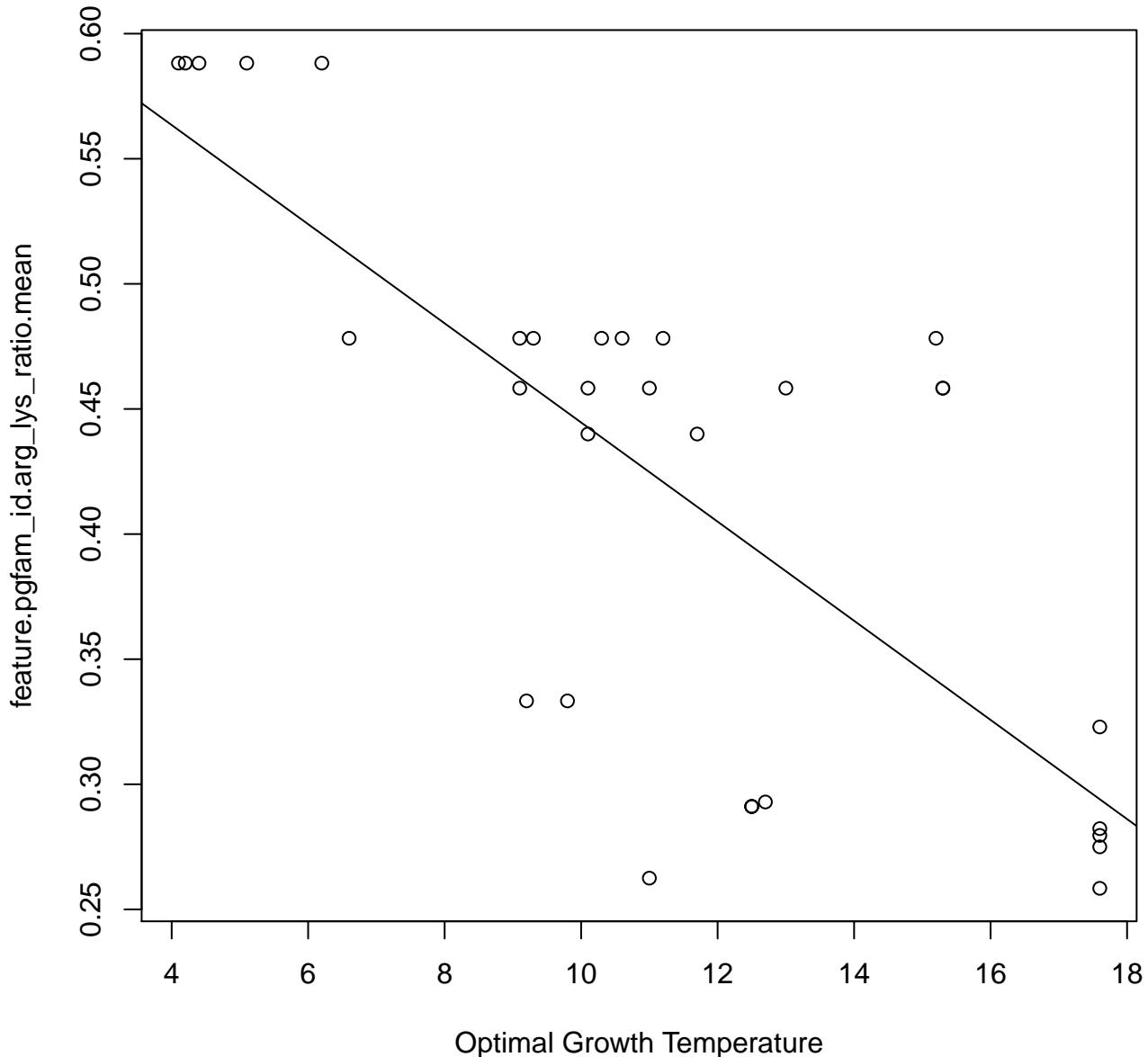
feature.pgfam_id.arg_lys_ratio.mean
PGF_00047484
Related to collagenase



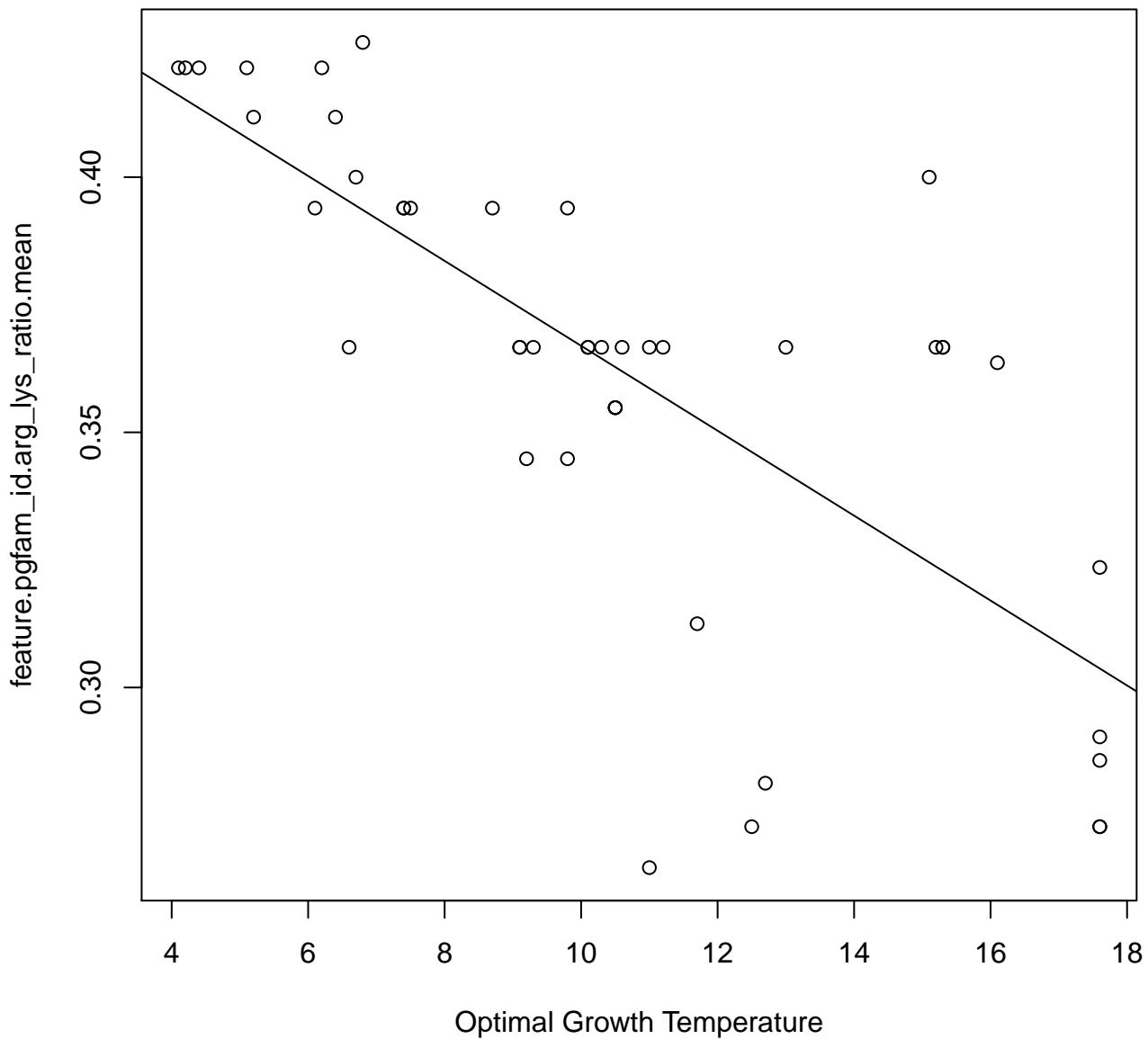
feature.pgfam_id.arg_lys_ratio.mean
PGF_00062002
Tryptophan 2,3-dioxygenase (EC 1.13.11.11)



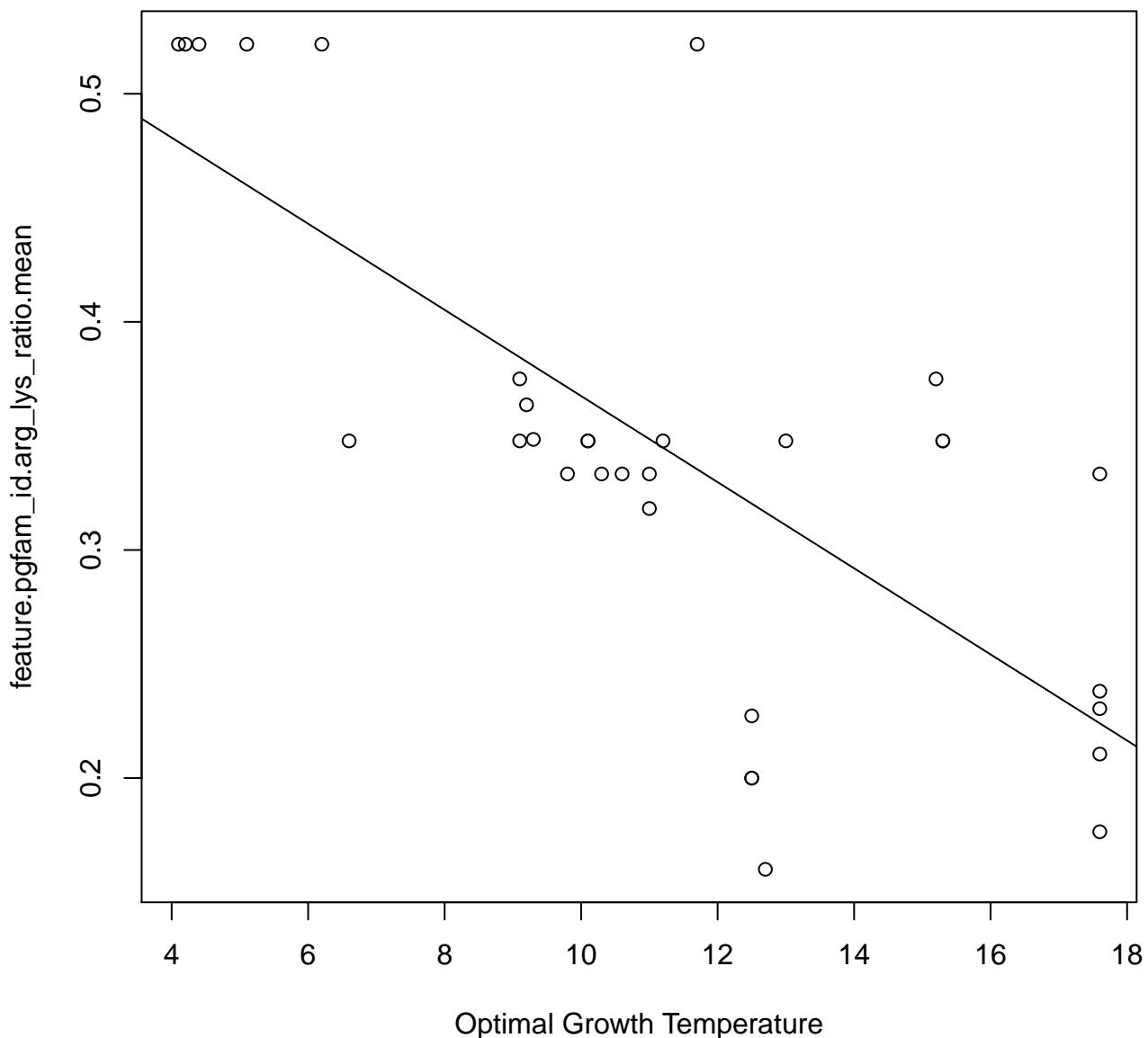
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336501
hypothetical protein



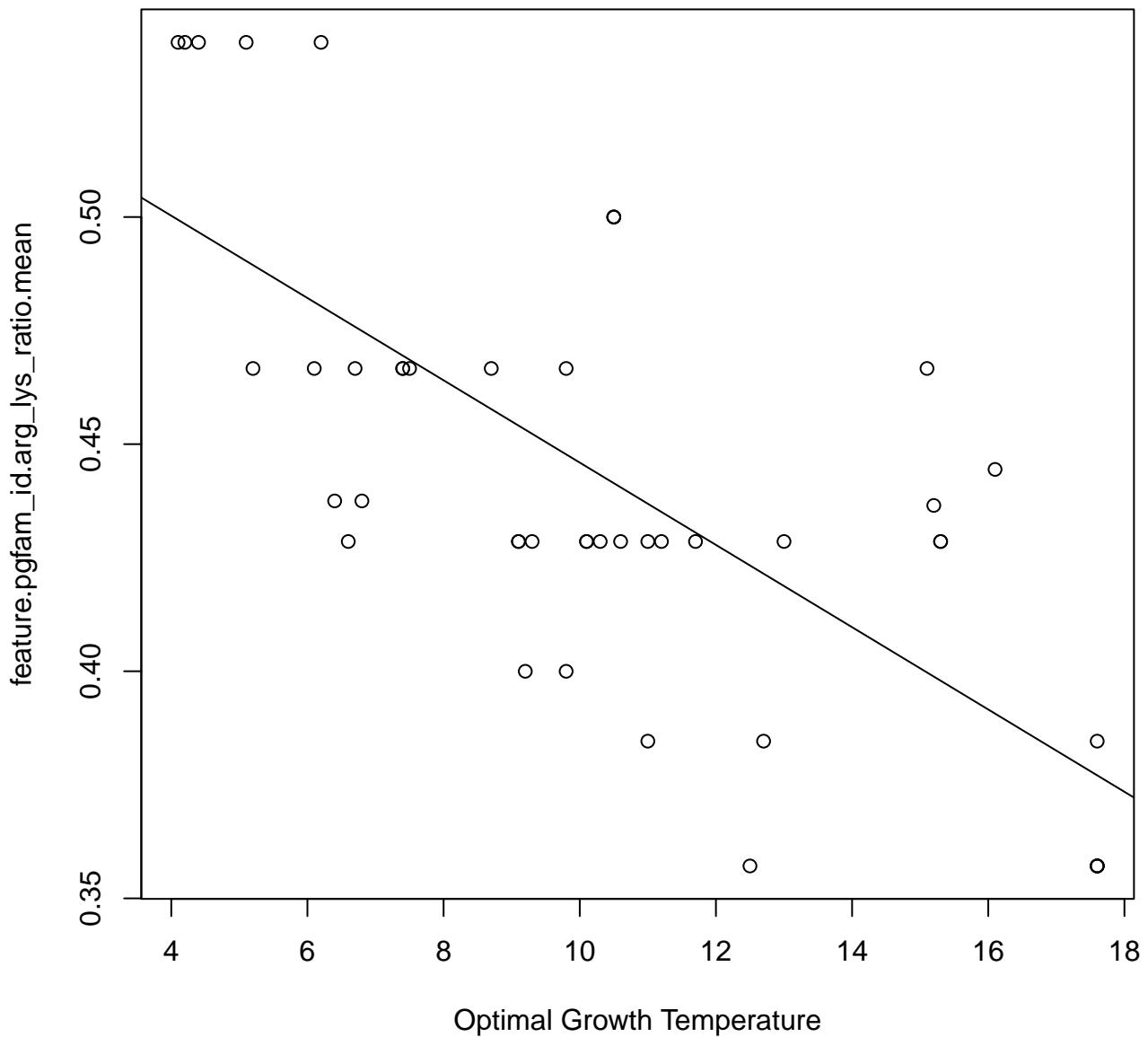
feature.pgfam_id.arg_lys_ratio.mean
PGF_10414515
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)



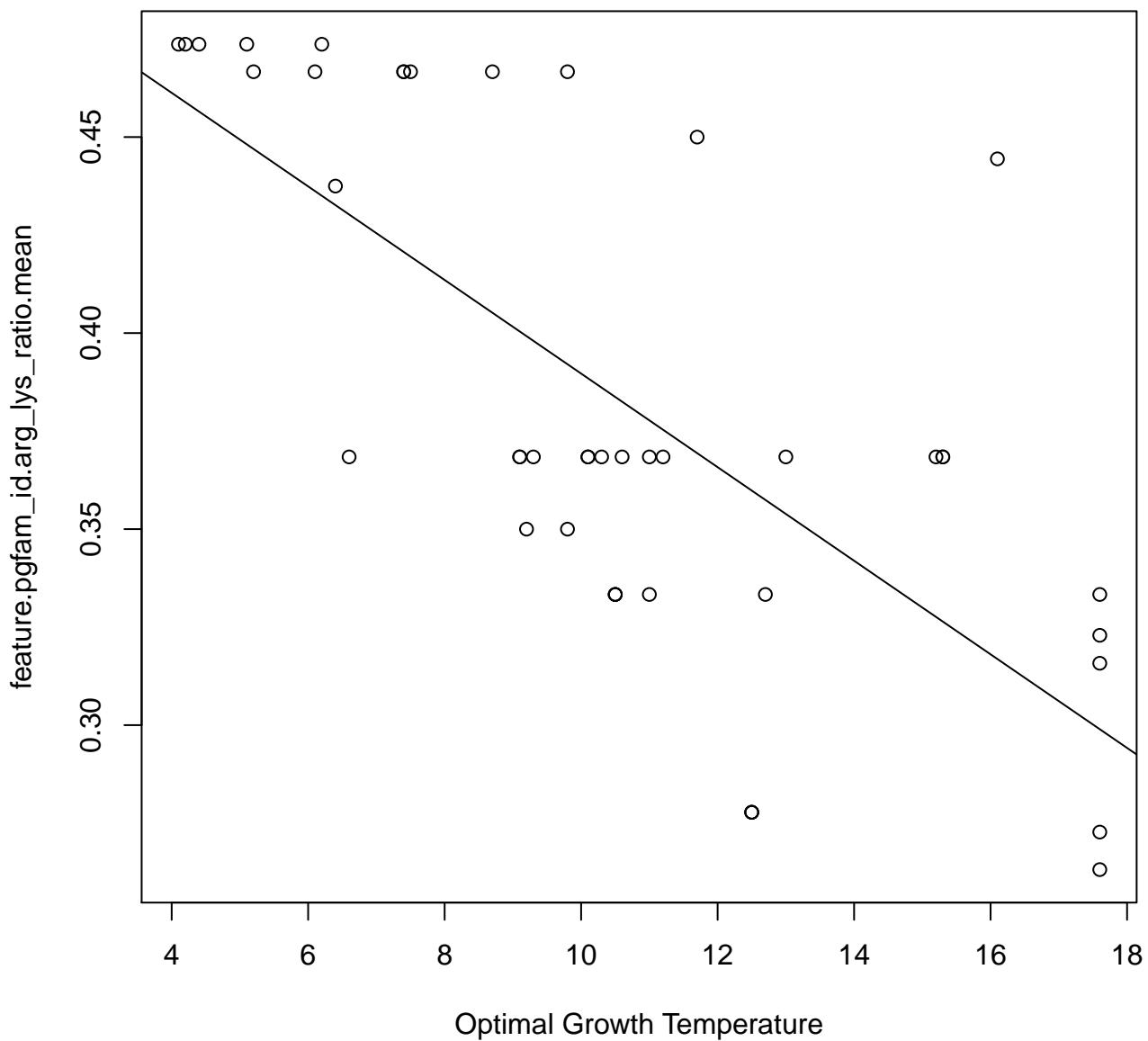
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PGF_01336446
hypothetical protein



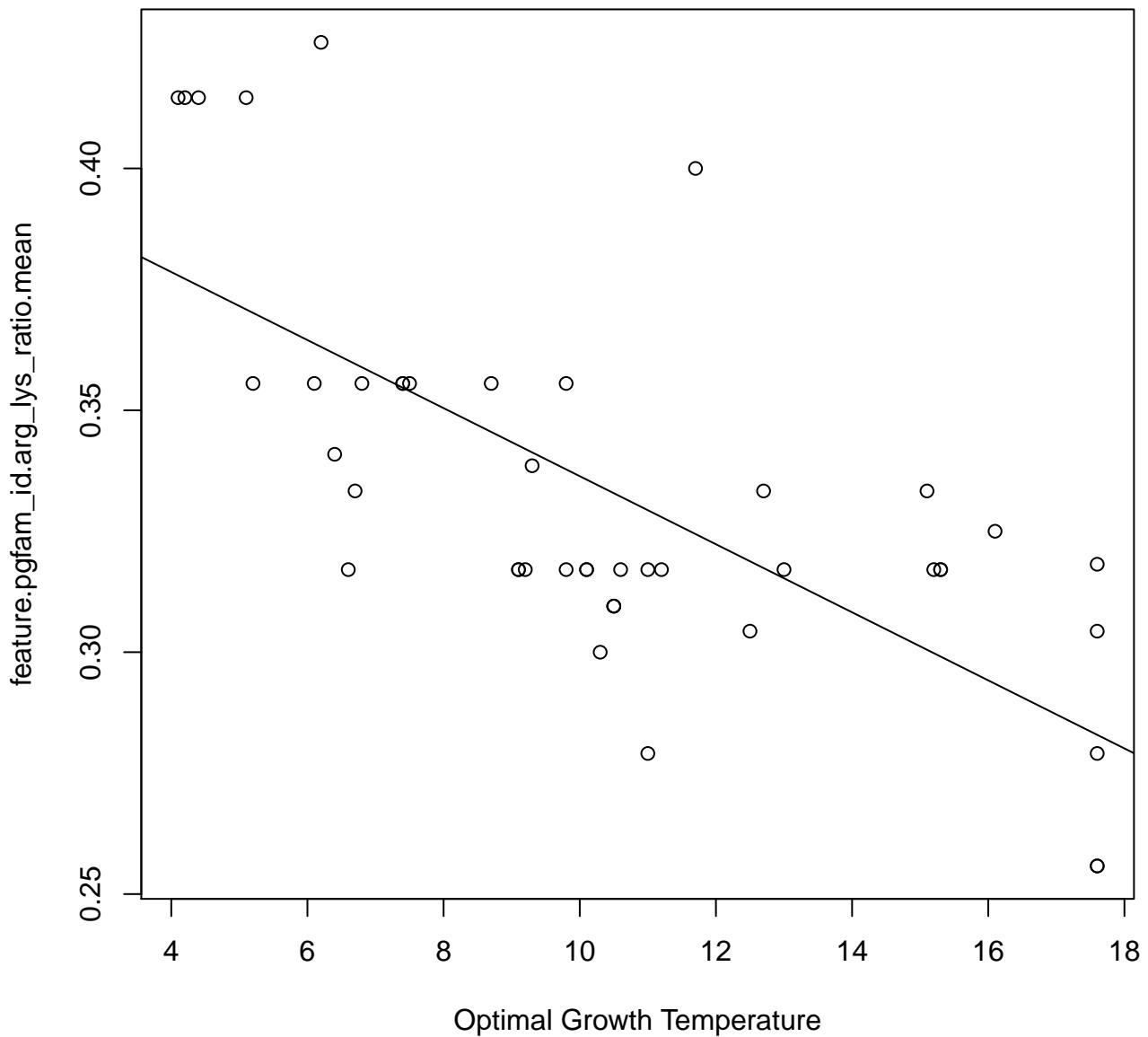
feature.pgfam_id.arg_lys_ratio.mean
PGF_09375481
Uncharacterized protein YfgD, not an arsenate reductase



feature.pgfam_id.arg_lys_ratio.mean
PGF_00035421
Potential queD like 2



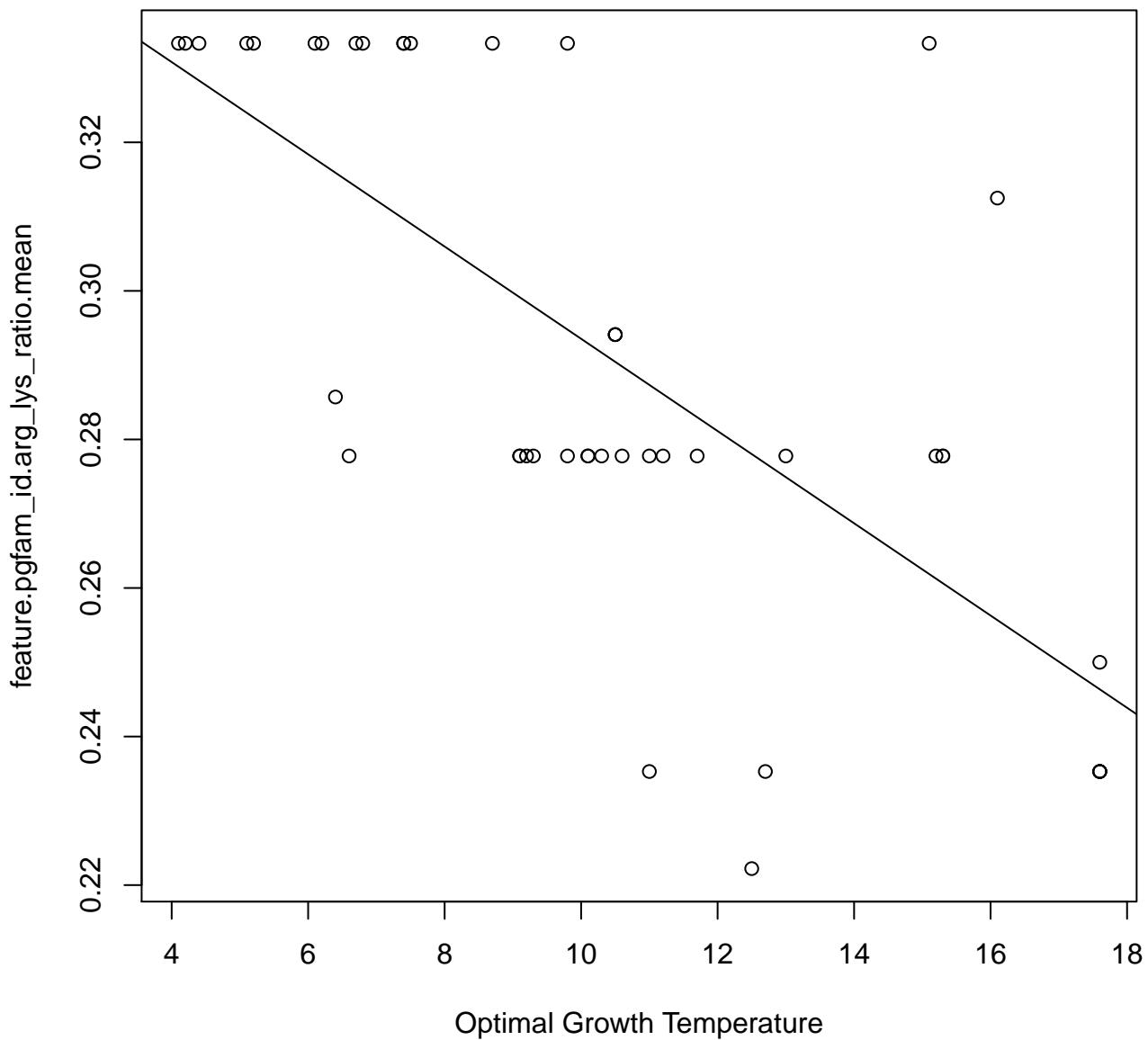
feature.pgfam_id.arg_lys_ratio.mean
PGF_06606669
Alanine transaminase (EC 2.6.1.2)



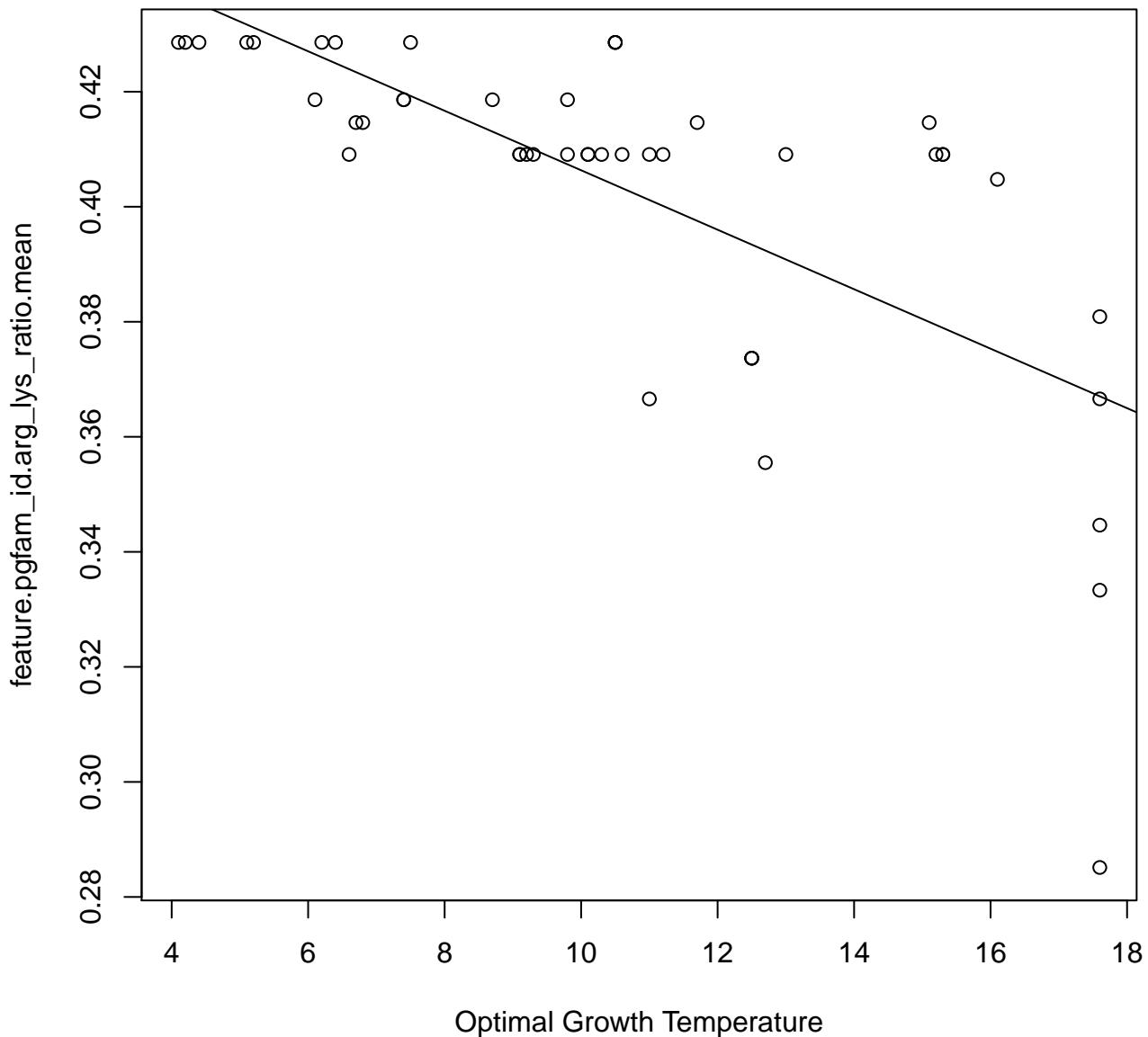
feature.pgfam_id.arg_lys_ratio.mean

PGF_02658061

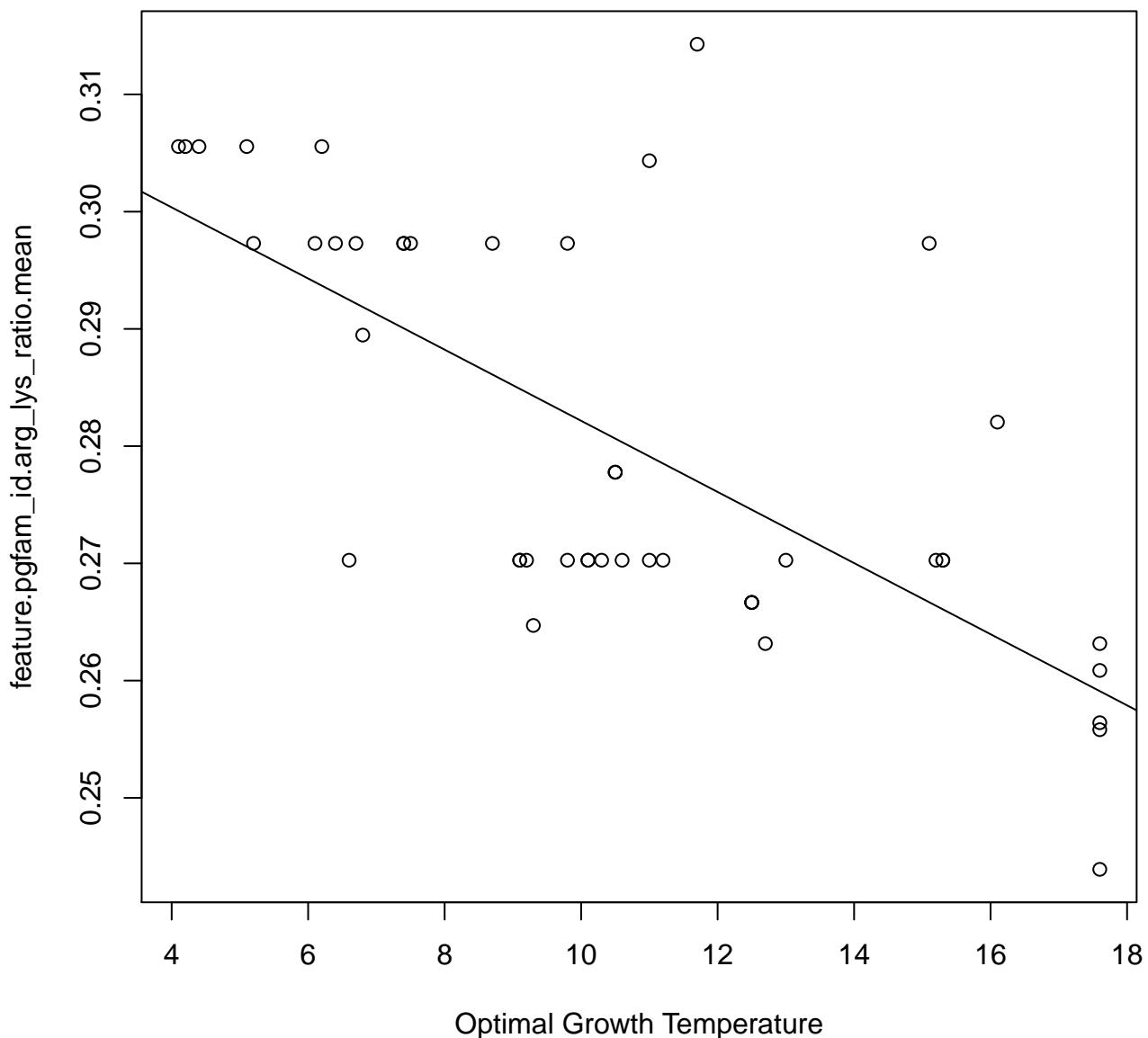
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)



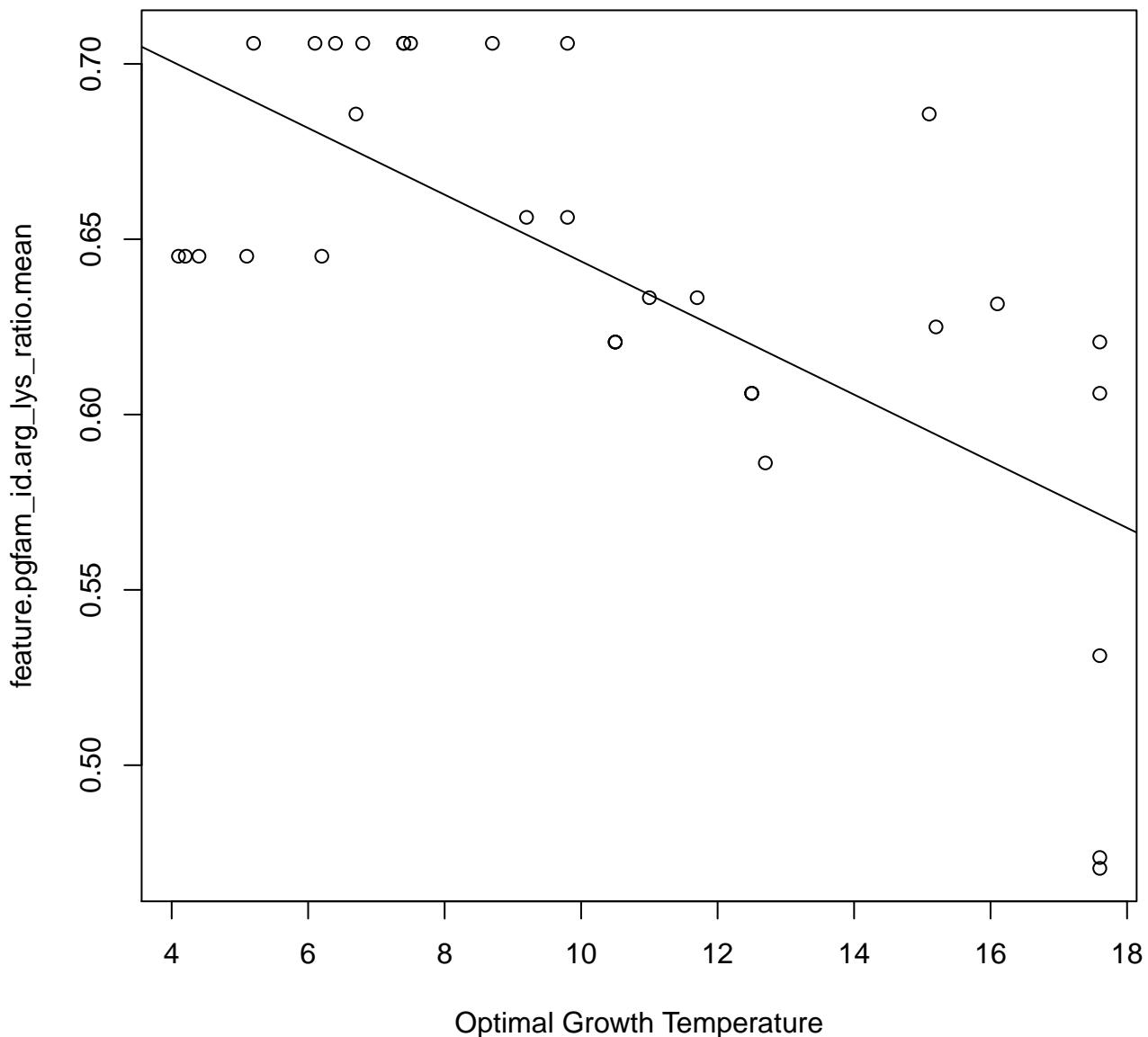
feature.pgfam_id.arg_lys_ratio.mean
PGF_06447349
NADP-dependent malic enzyme (EC 1.1.1.40)



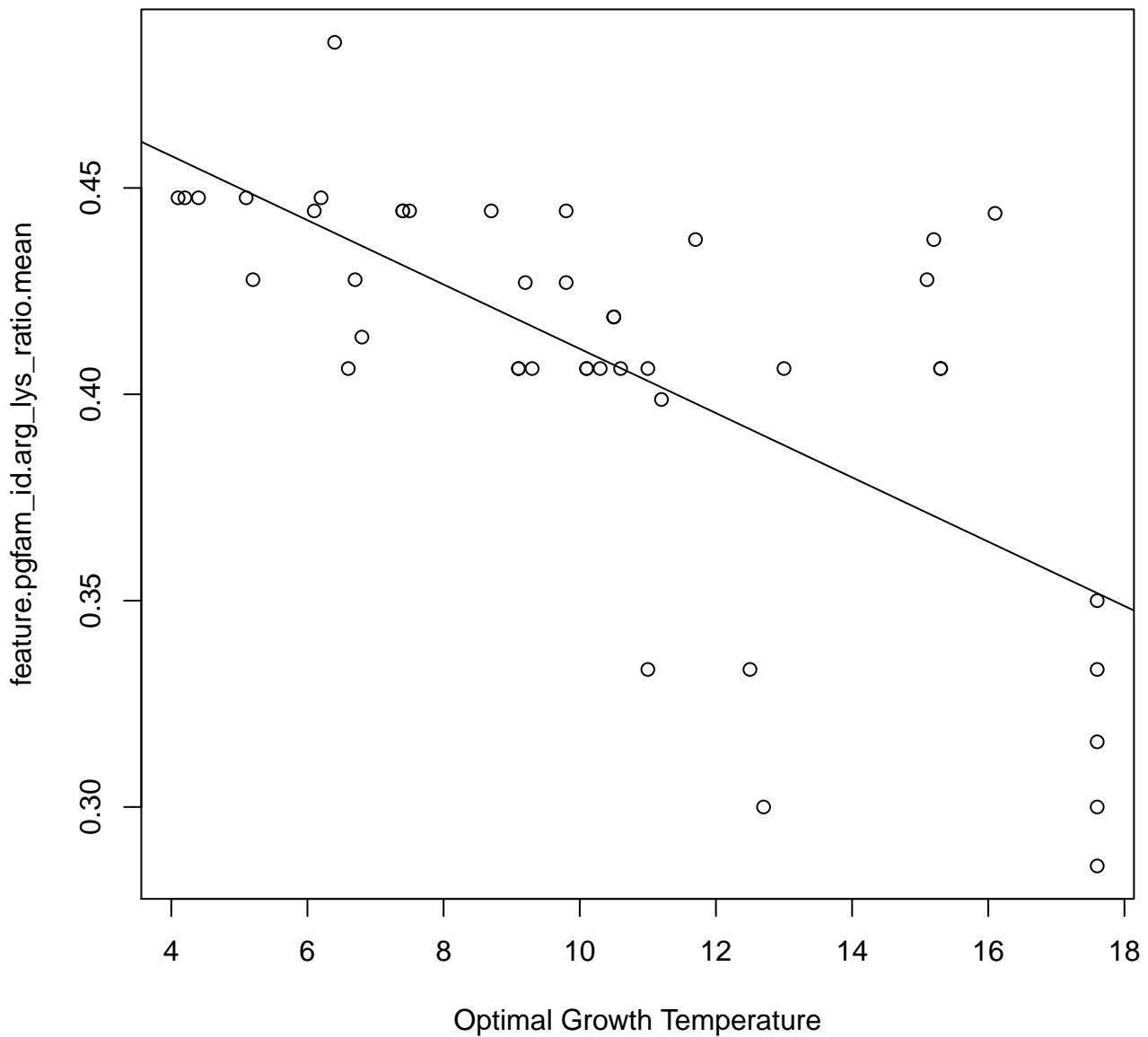
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336369
hypothetical protein



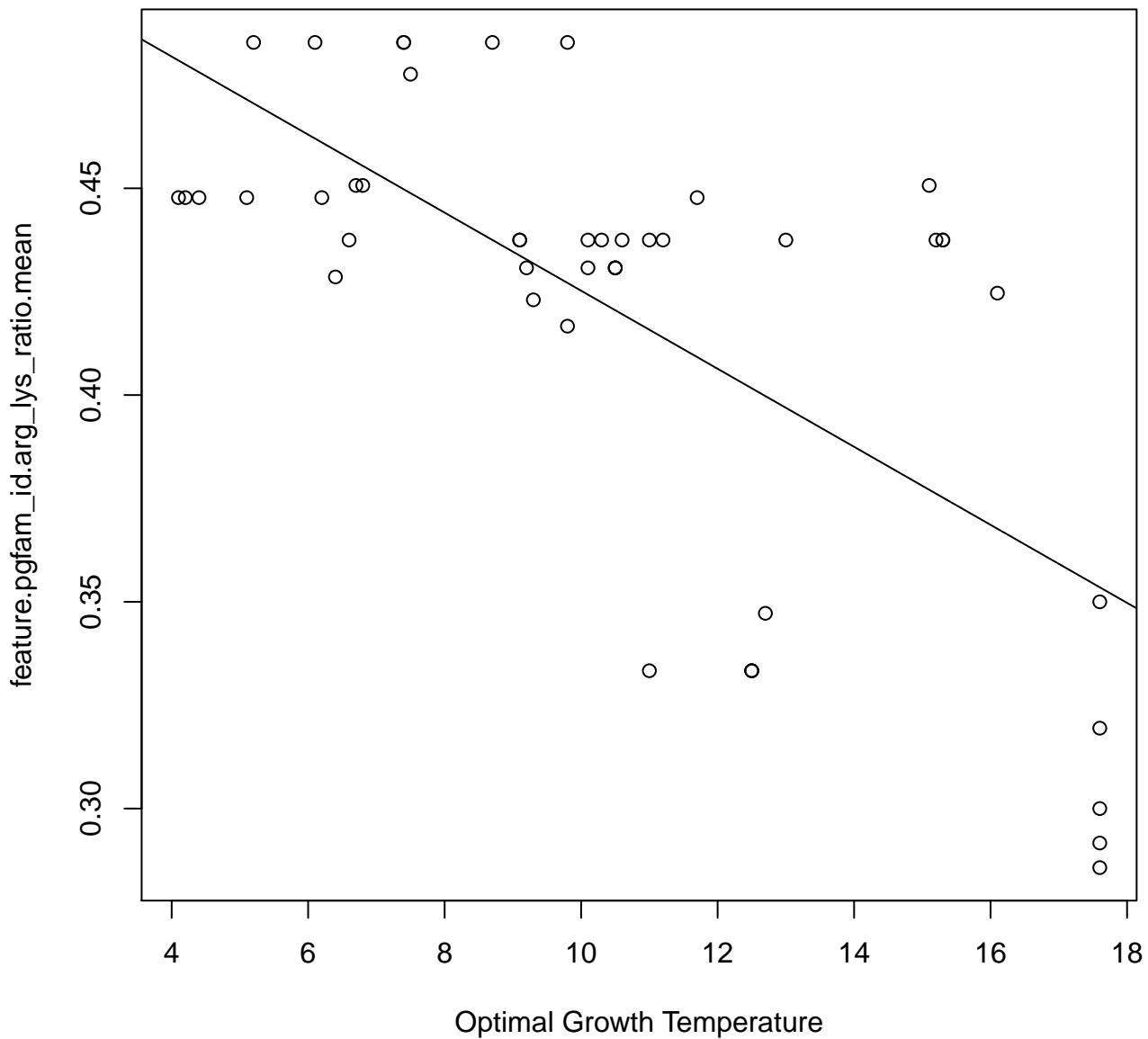
feature.pgfam_id.arg_lys_ratio.mean
PGF_00004481
Ferric iron ABC transporter, permease protein



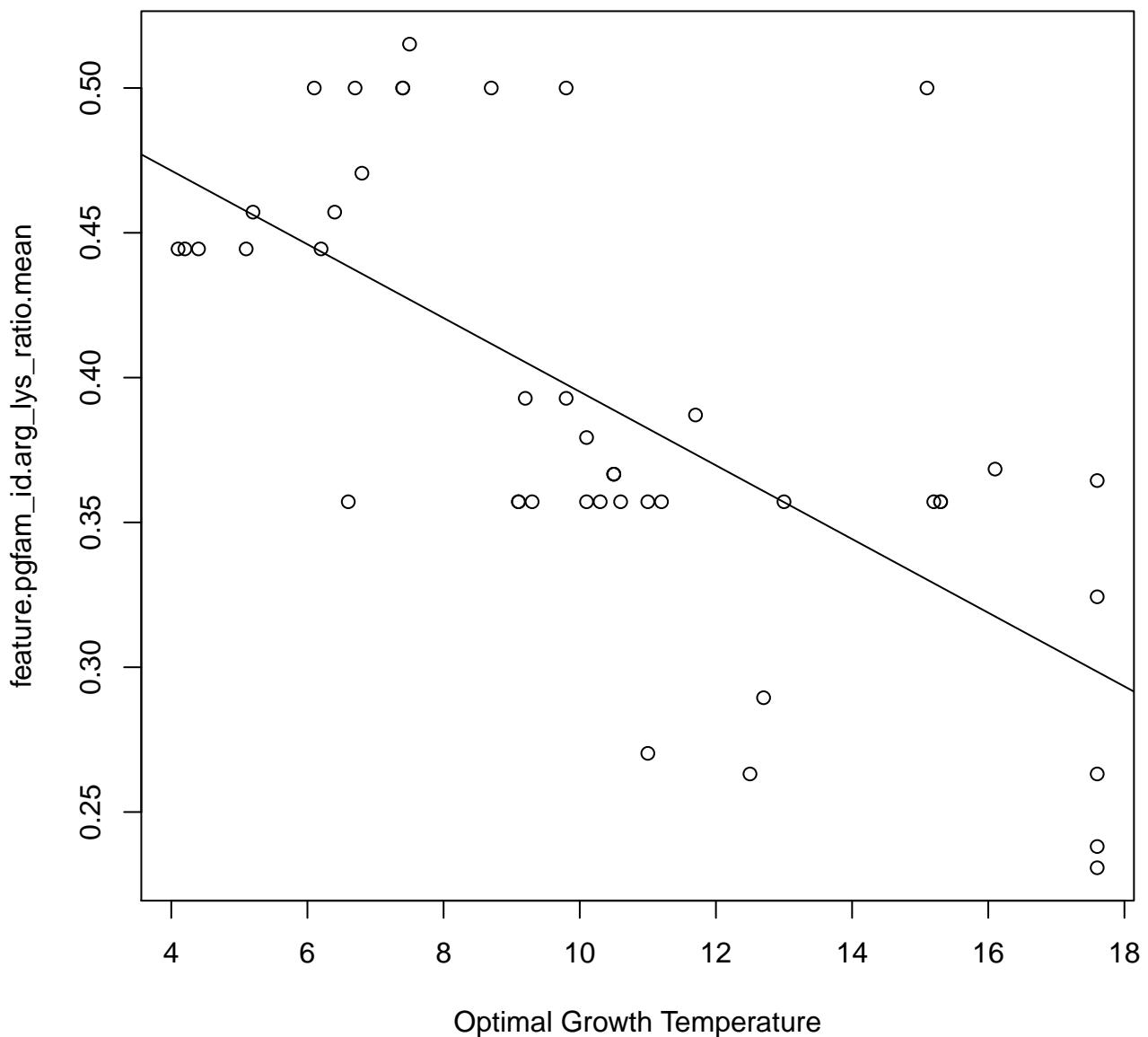
feature.pgfam_id.arg_lys_ratio.mean
PGF_03751076
Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)



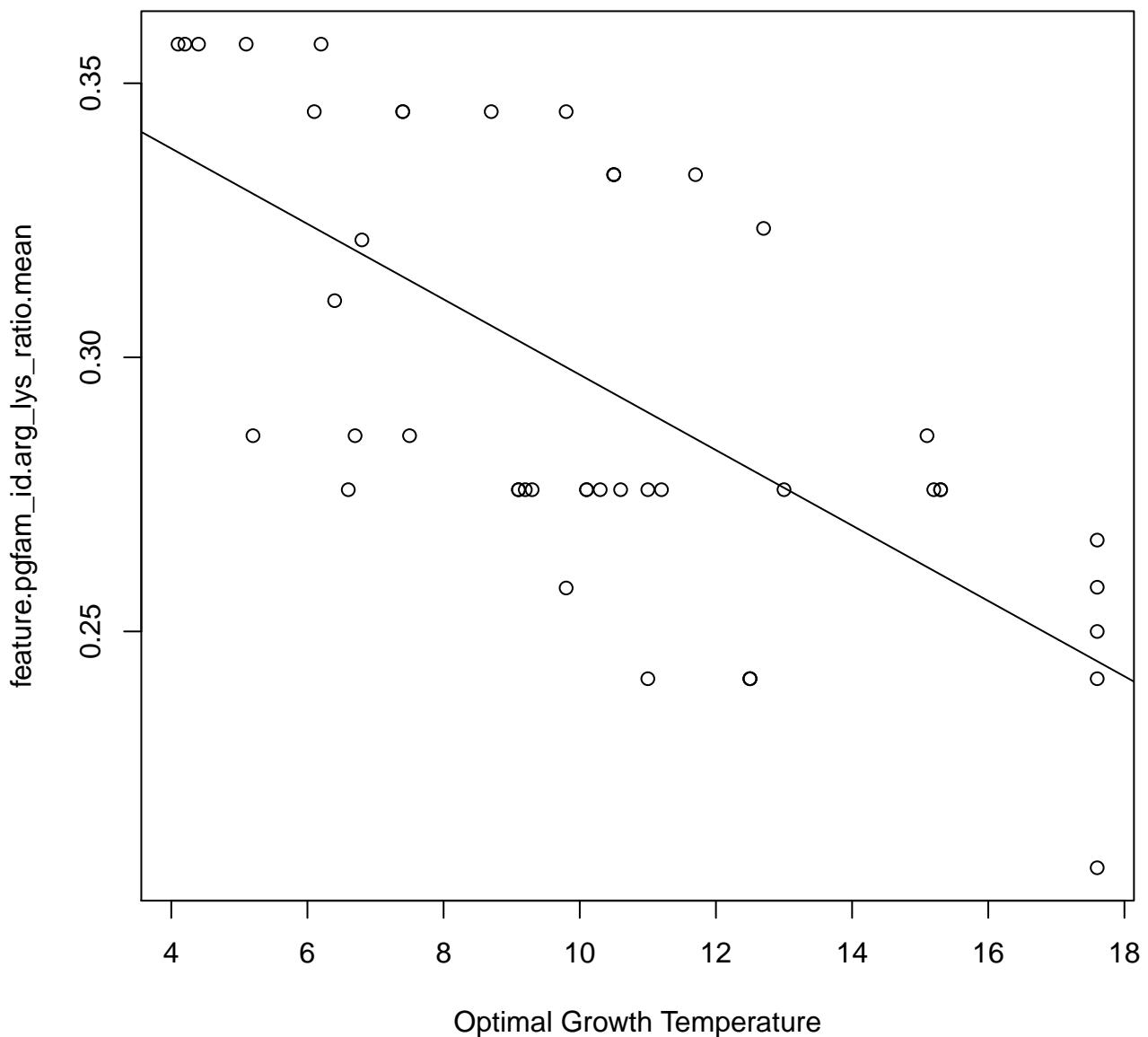
feature.pgfam_id.arg_lys_ratio.mean
PGF_01466819
N-acetyl muramoyl-L-alanine amidase (EC 3.5.1.28)



feature.pgfam_id.arg_lys_ratio.mean
PGF_09566238
Septum-associated rare lipoprotein A



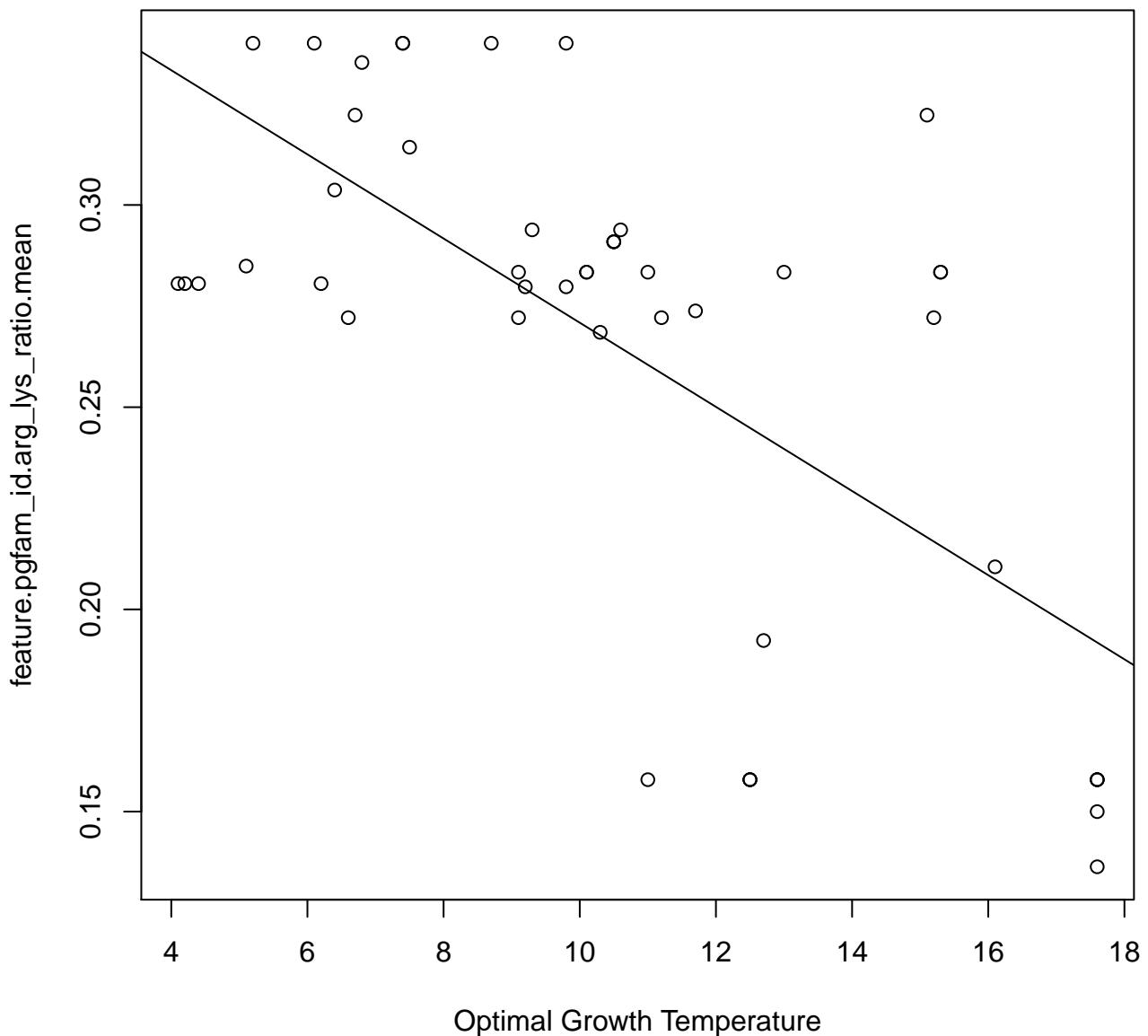
feature.pgfam_id.arg_lys_ratio.mean
PGF_00343871
hypothetical protein



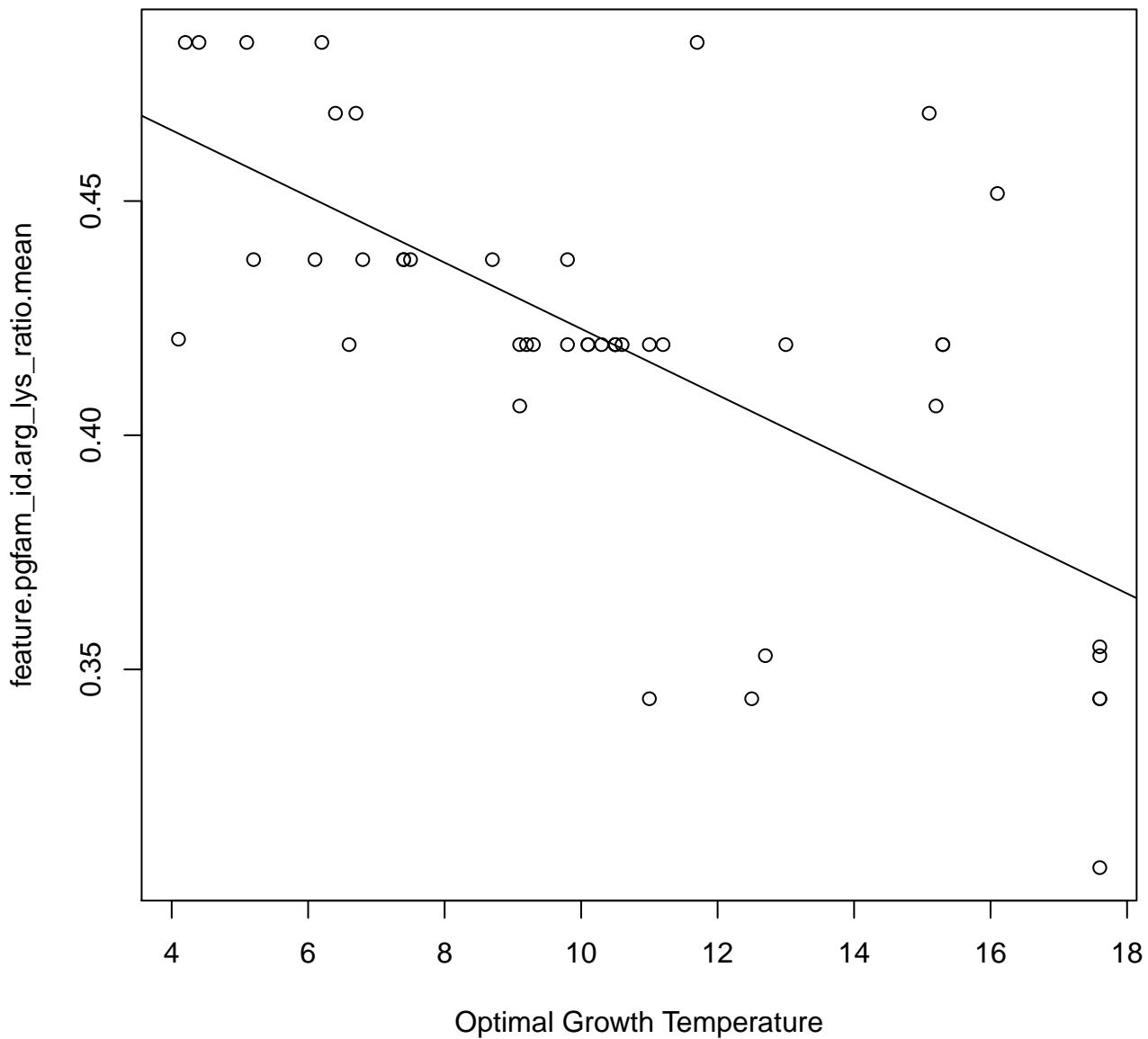
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PGF_00417755

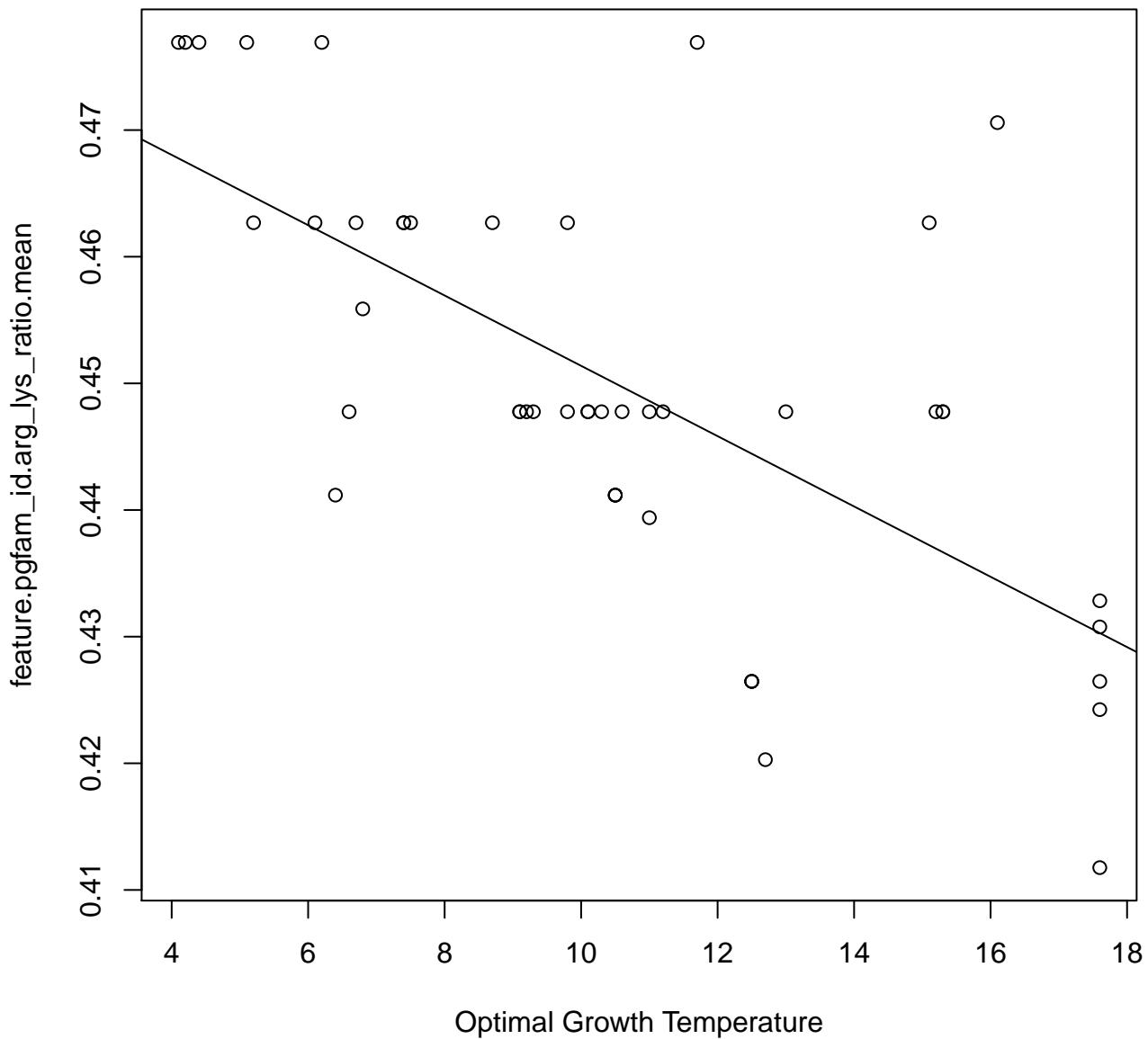
3-demethylubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6-hydroxyphenyl methylase (EC 2.1.1.222)



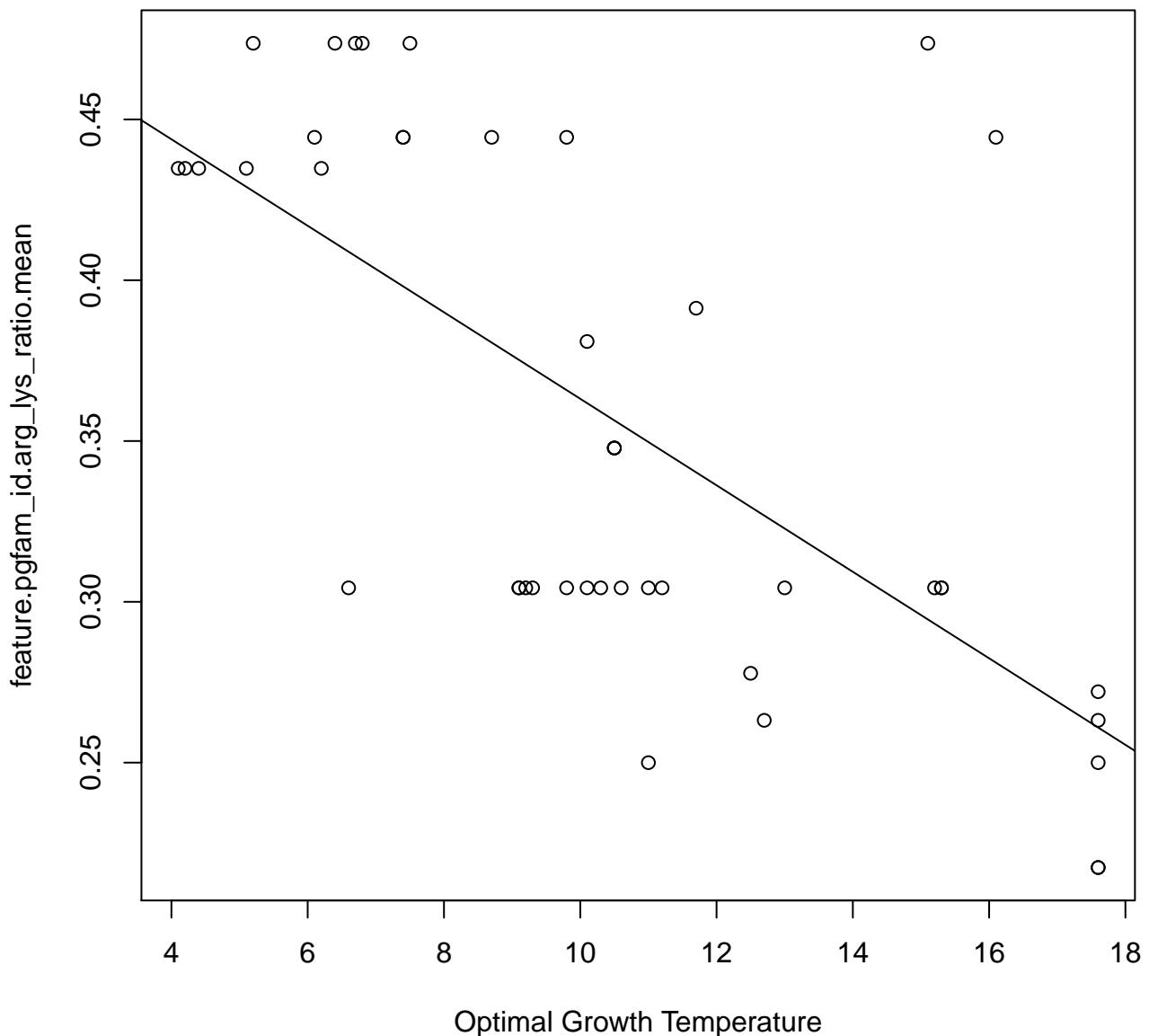
feature.pgfam_id.arg_lys_ratio.mean
PGF_10013303
Isocitrate dehydrogenase [NAD] (EC 1.1.1.41)



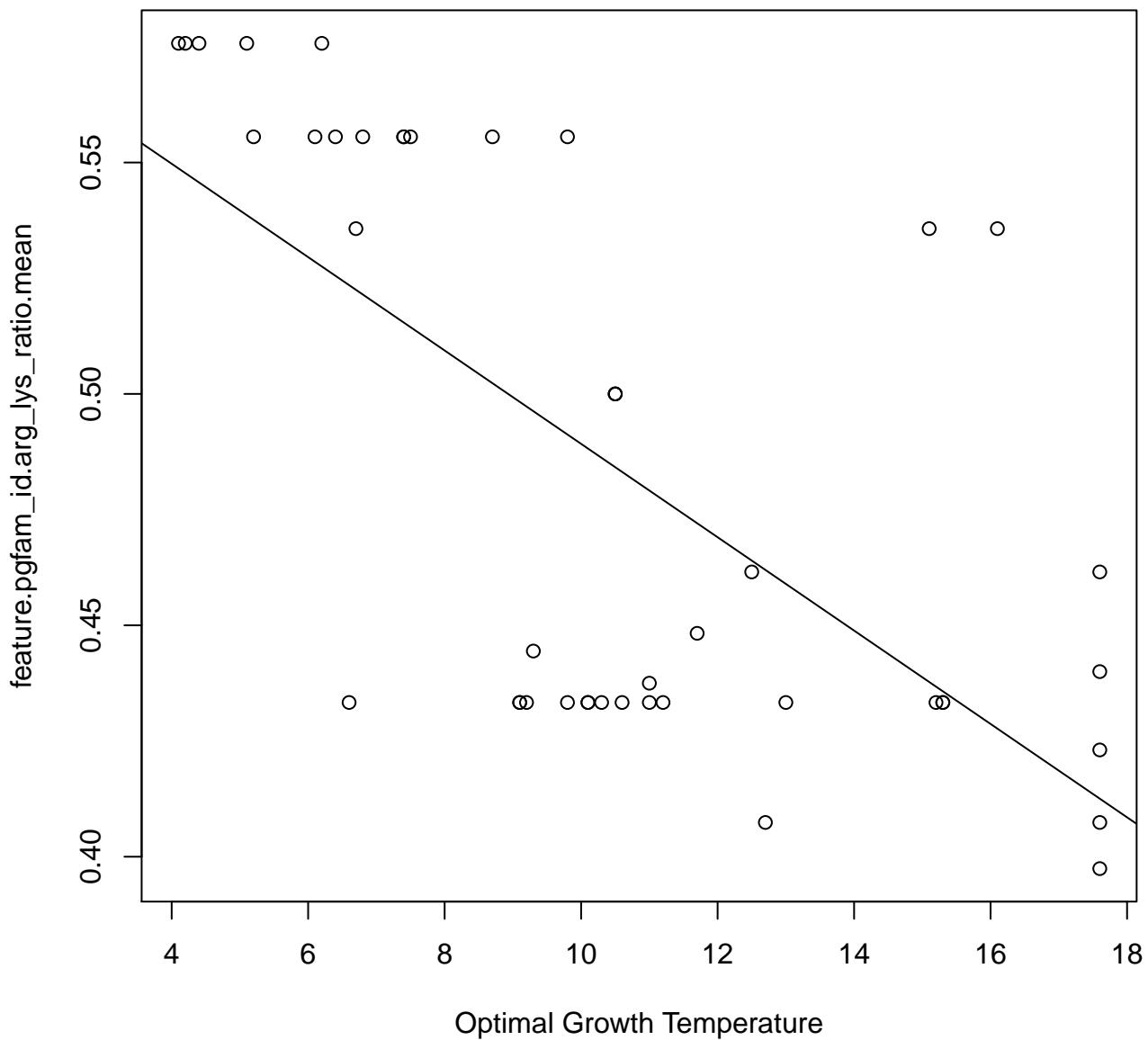
feature.pgfam_id.arg_lys_ratio.mean
PGF_00030643
Peptide chain release factor 3



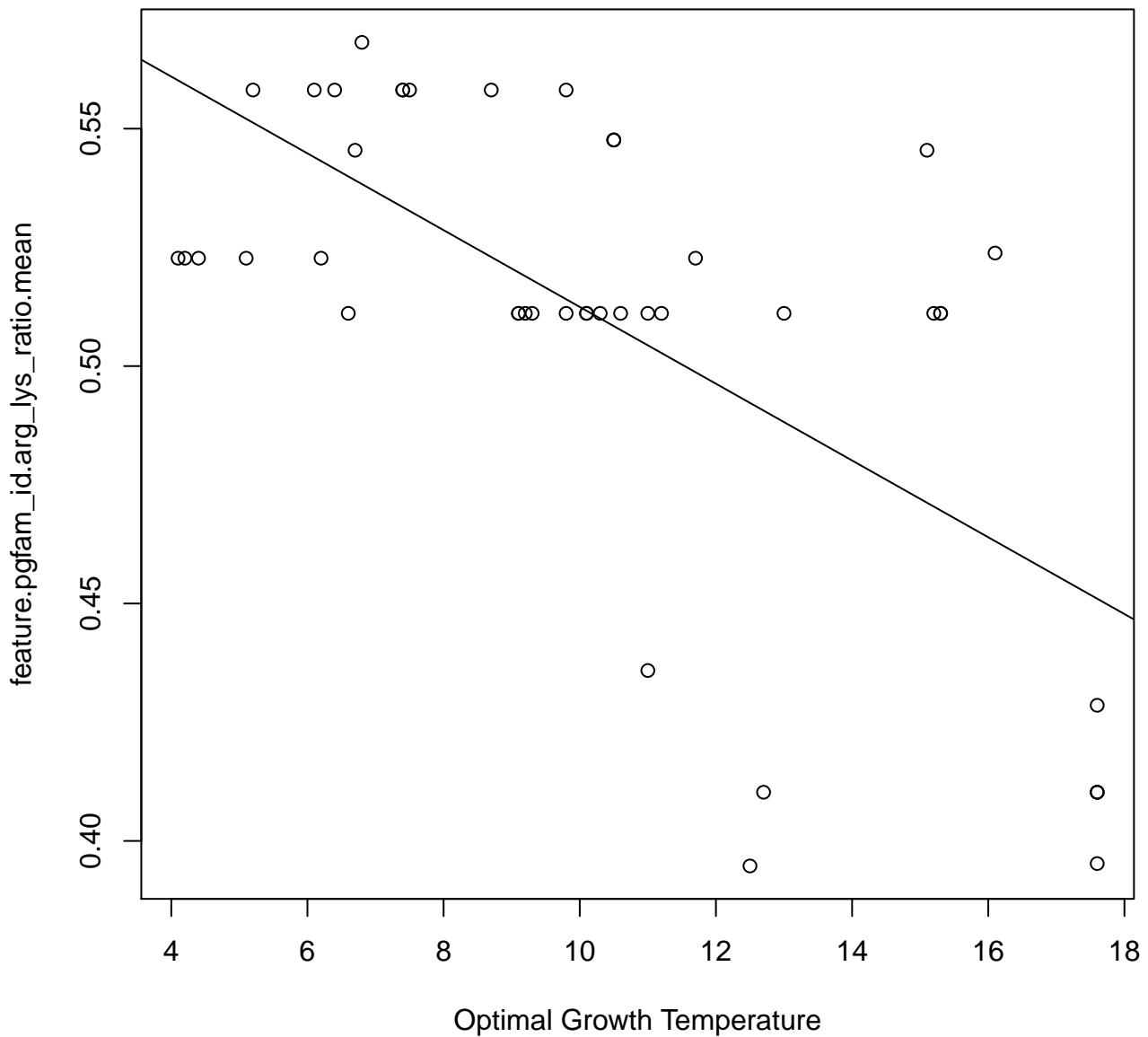
feature.pgfam_id.arg_lys_ratio.mean
PGF_10462808
33 kDa chaperonin HslO



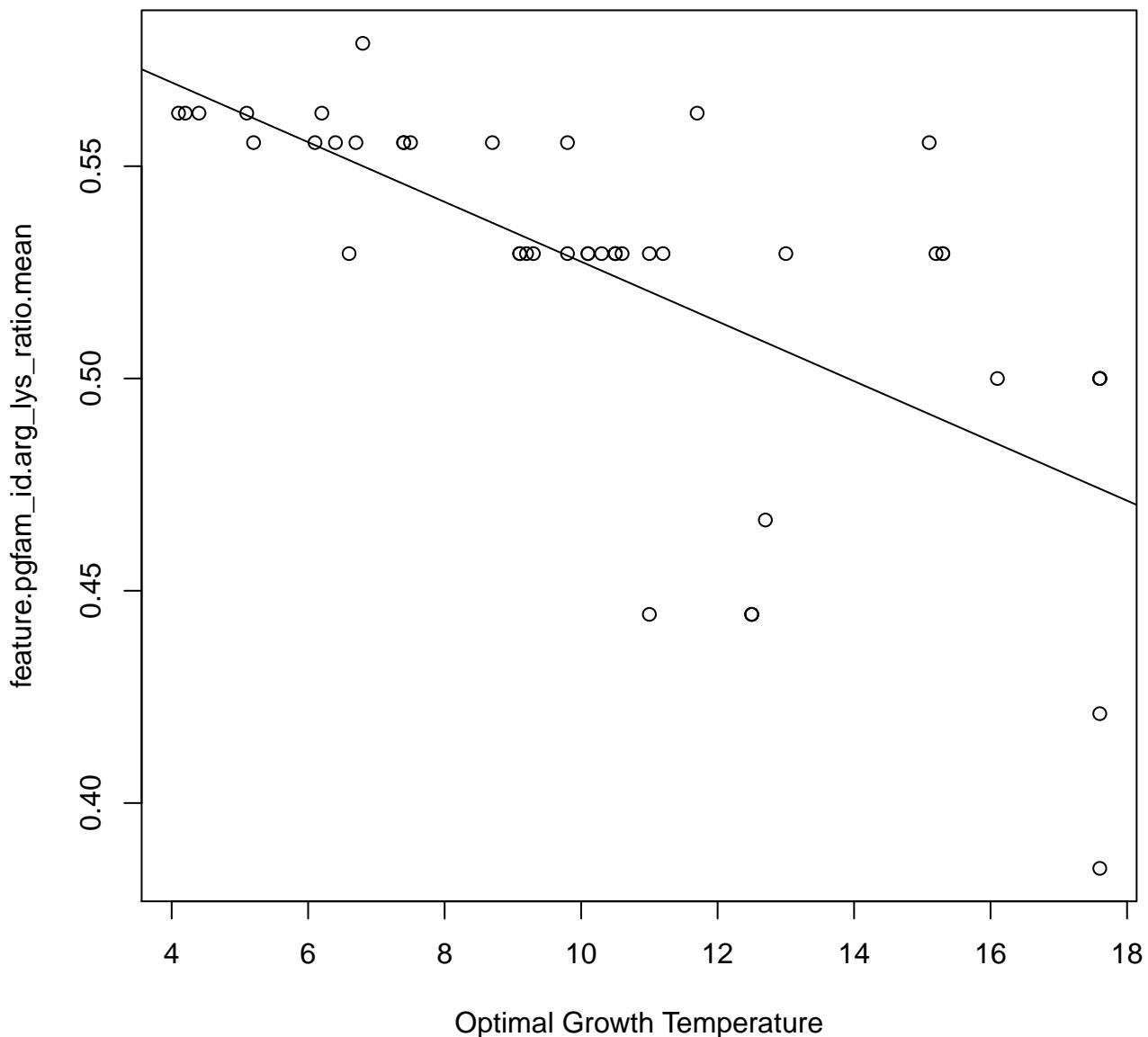
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PGF_06747785
AmpG permease



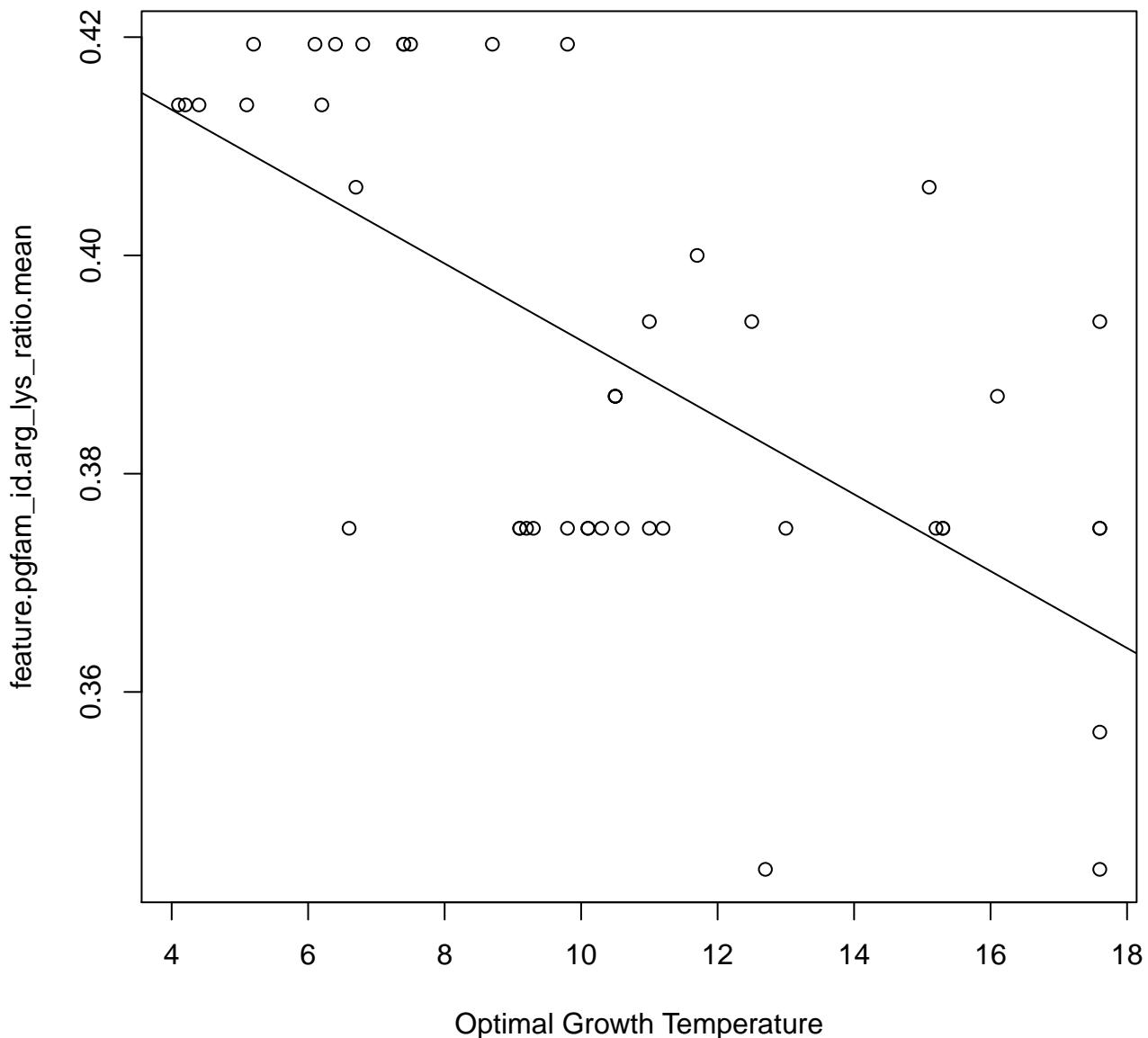
feature.pgfam_id.arg_lys_ratio.mean
PGF_05387084
Gamma-glutamyl phosphate reductase (EC 1.2.1.41)



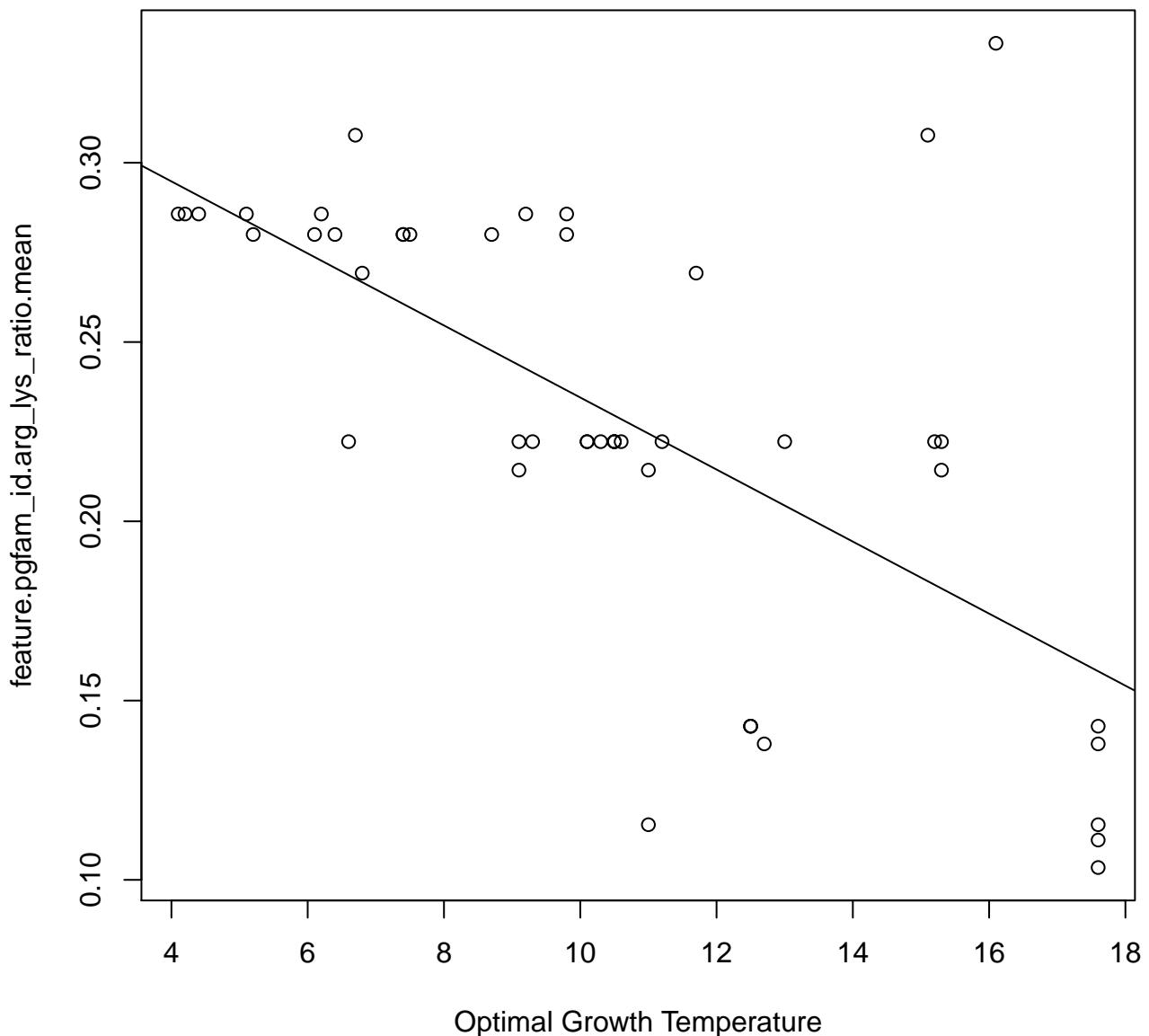
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336380
hypothetical protein



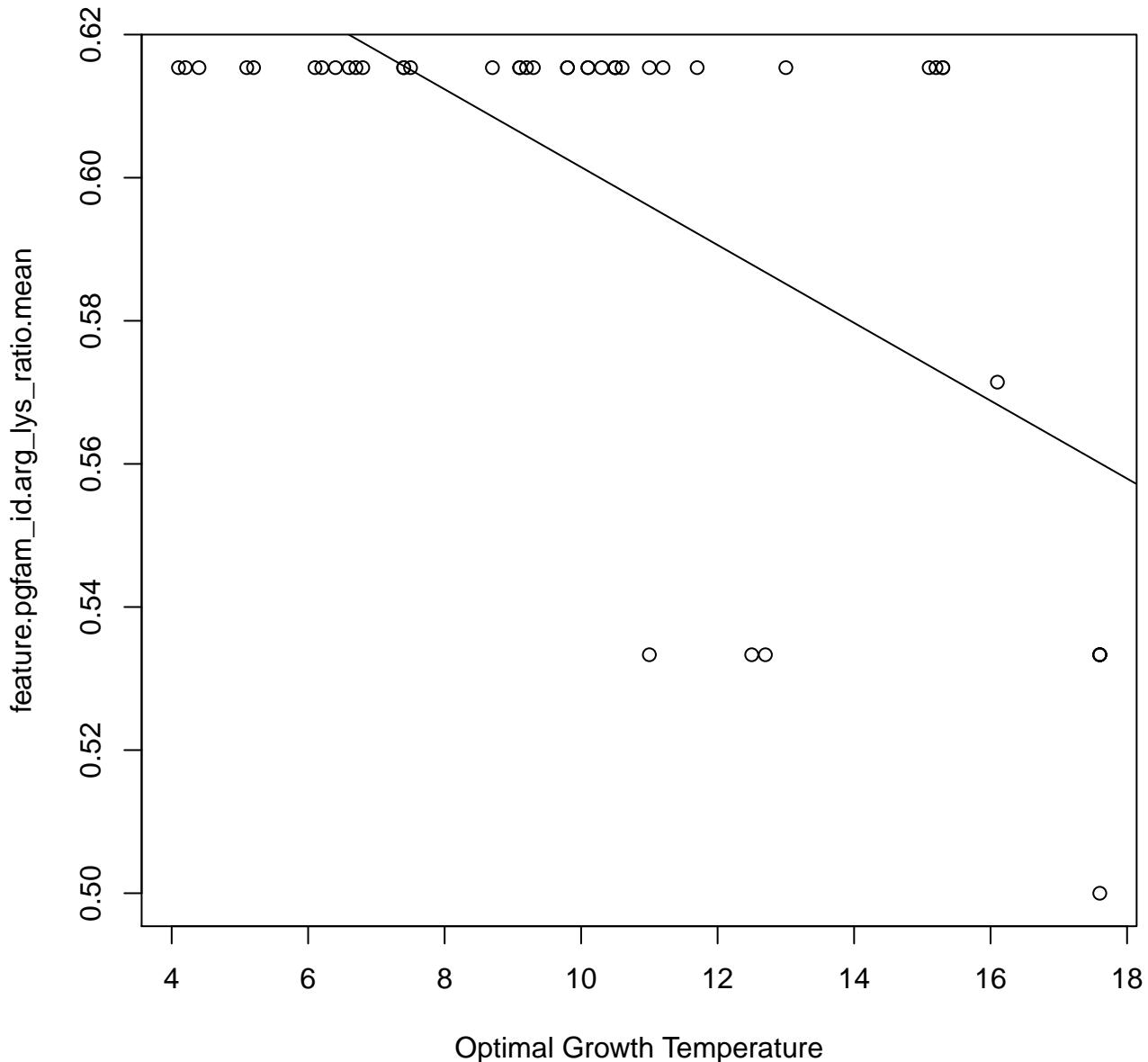
feature.pgfam_id.arg_lys_ratio.mean
PGF_03237586
L-threonine 3-dehydrogenase (EC 1.1.1.103)



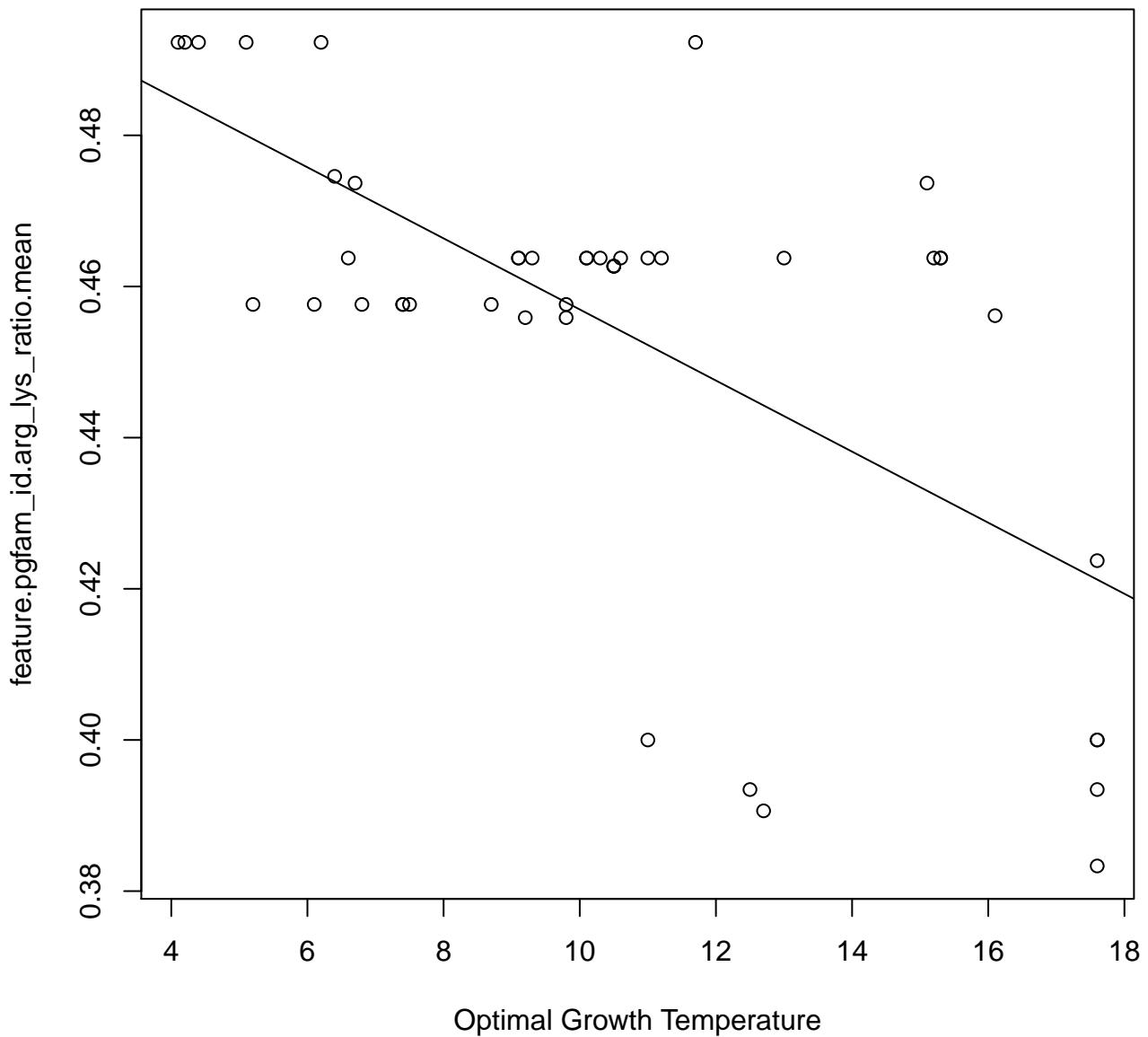
feature.pgfam_id.arg_lys_ratio.mean
PGF_00014140
Inner membrane protein Yedl



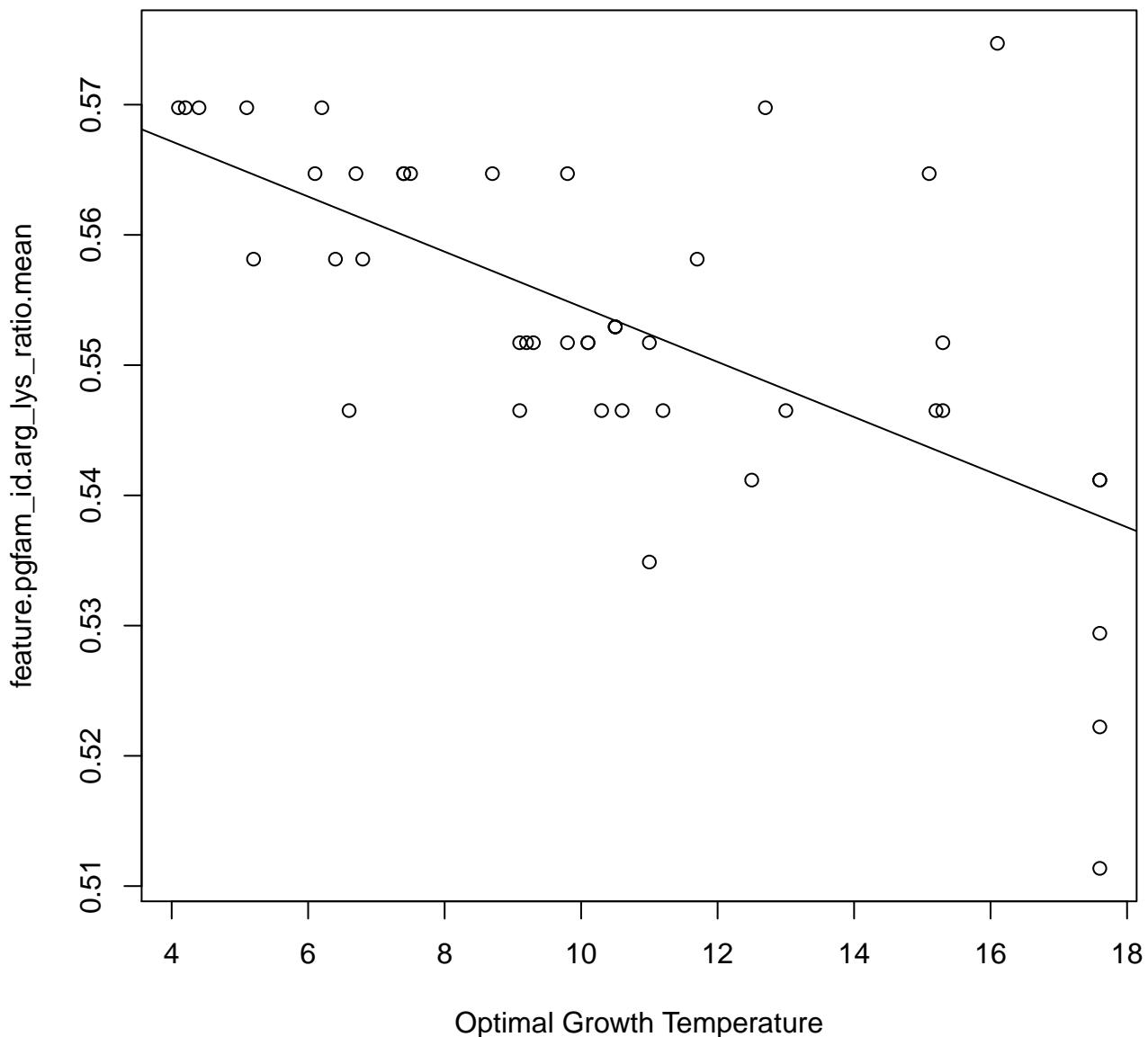
feature.pgfam_id.arg_lys_ratio.mean
PGF_07114837
Phospholipid ABC transporter permease protein MlaE



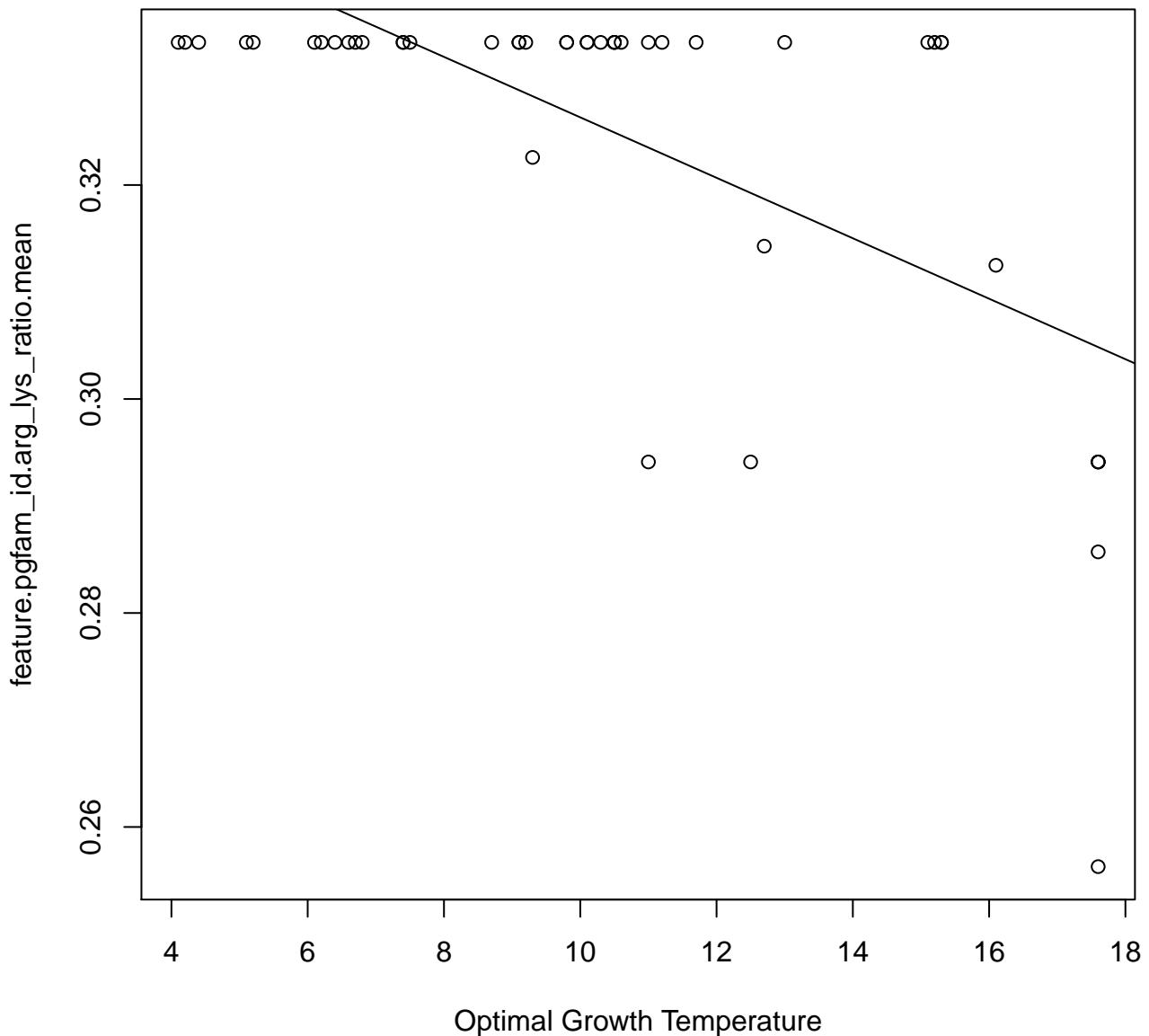
feature.pgfam_id.arg_lys_ratio.mean
PGF_04057876
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)



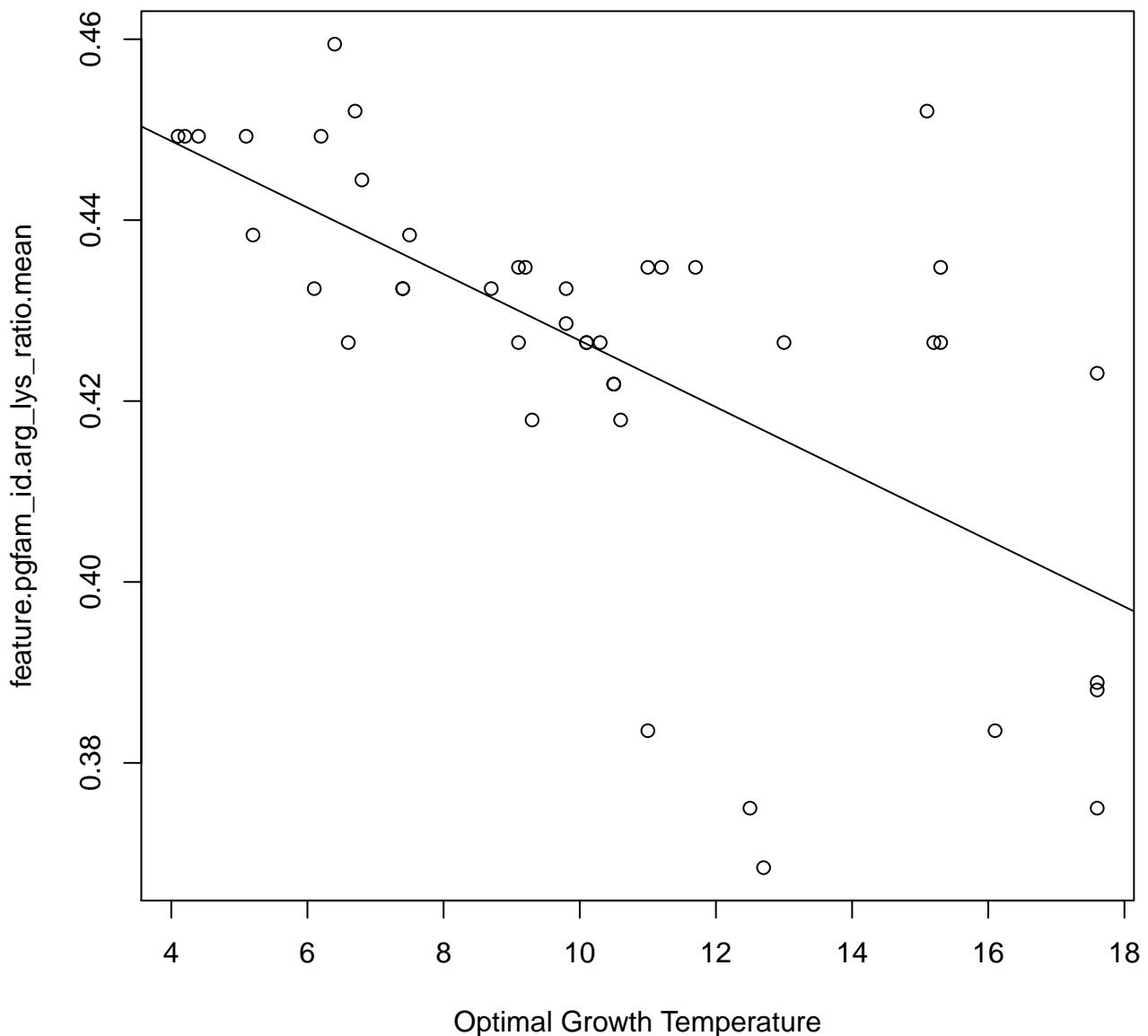
feature.pgfam_id.arg_lys_ratio.mean
PGF_05340948
DNA mismatch repair protein MutS



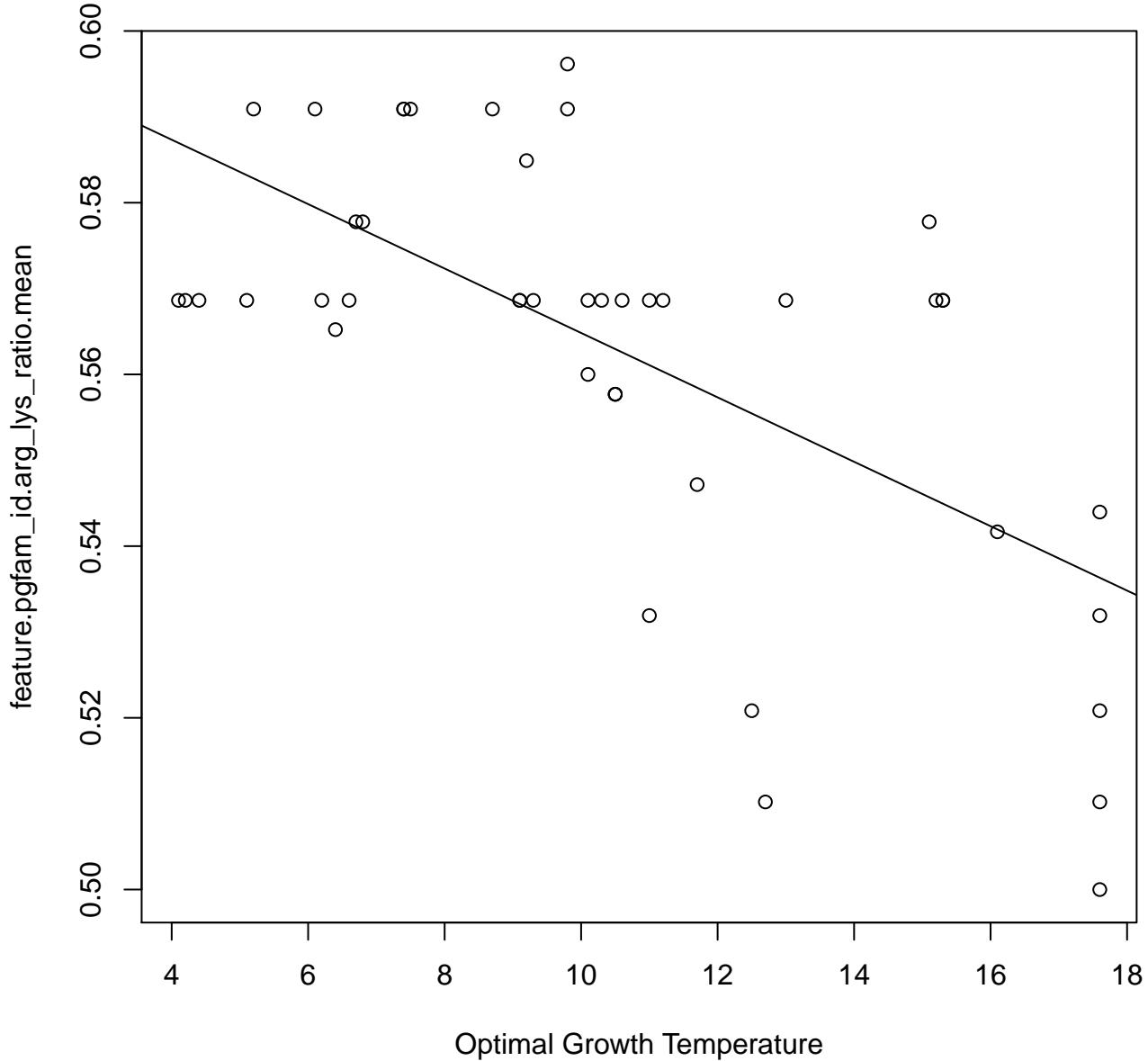
feature.pgfam_id.arg_lys_ratio.mean
PGF_02296690
DNA recombination-dependent growth factor RdgC



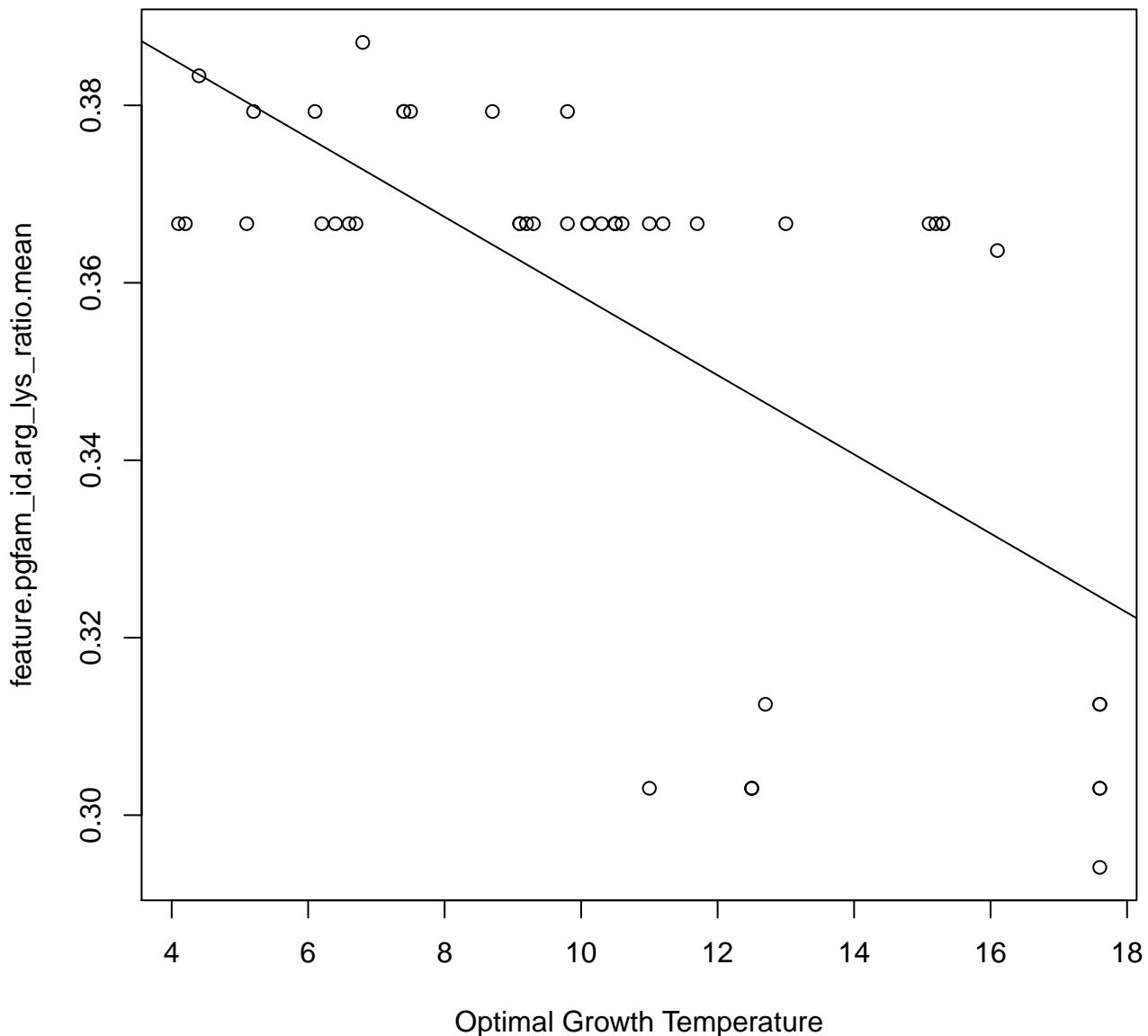
feature.pgfam_id.arg_lys_ratio.mean
PGF_10365126
DNA polymerase III subunits gamma and tau (EC 2.7.7.7)



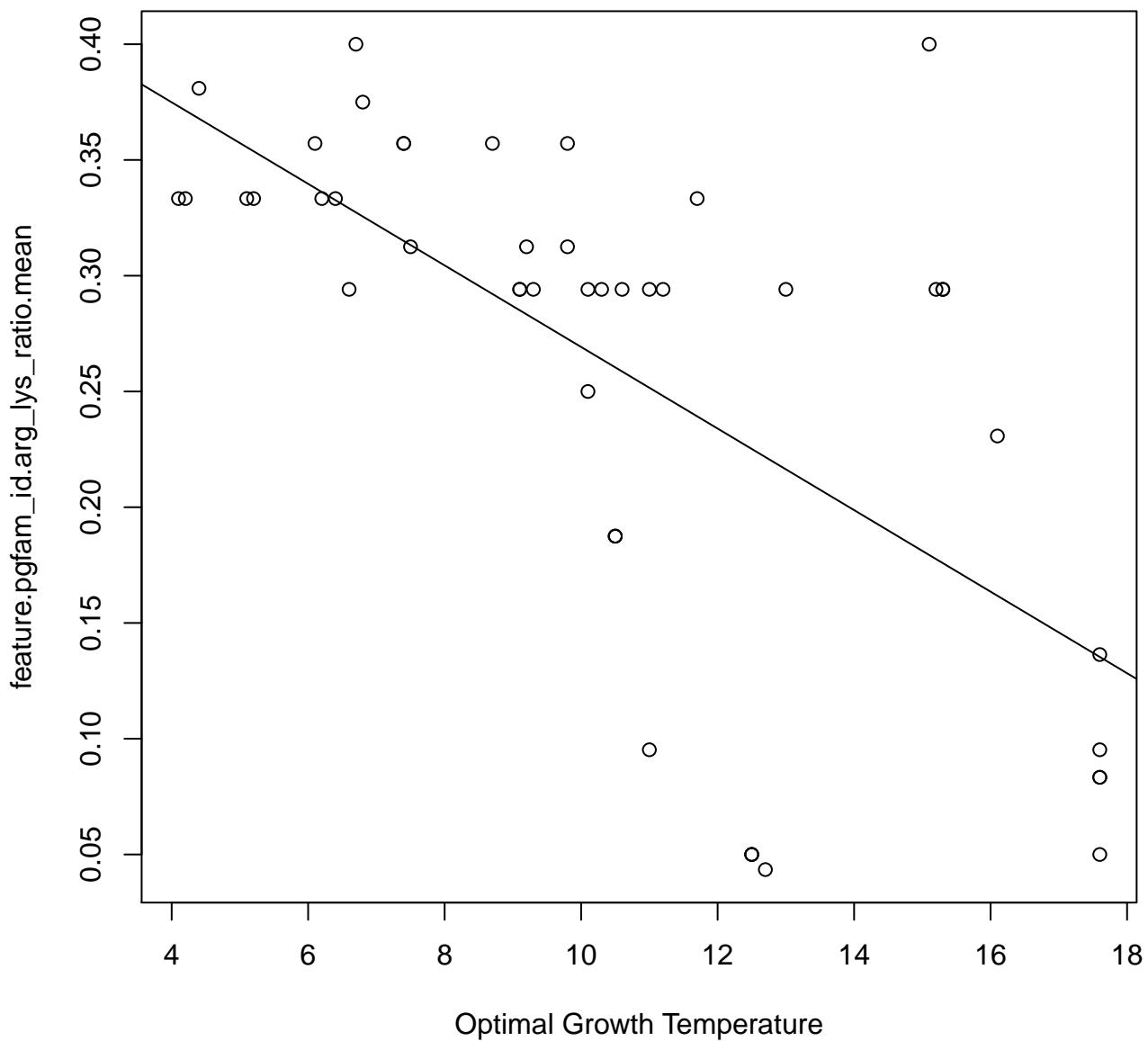
feature.pgfam_id.arg_lys_ratio.mean
PGF_01072302
Phosphate ABC transporter, permease protein PstA (TC 3.A.1.7.1)



feature.pgfam_id.arg_lys_ratio.mean
PGF_00401752
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase (EC 2.1.1.201)



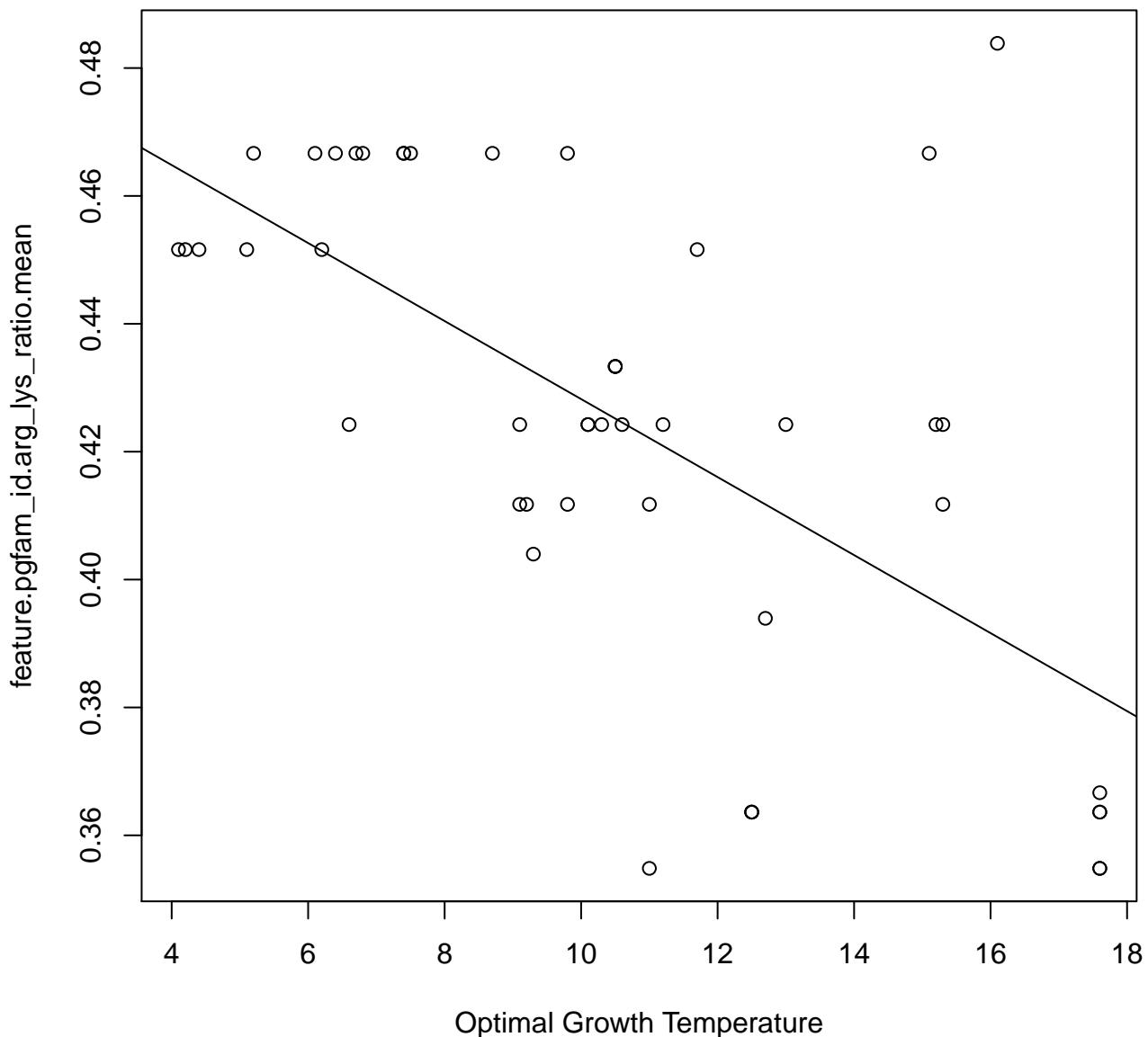
feature.pgfam_id.arg_lys_ratio.mean
PGF_03760224
Dethiobiotin synthase BioD (EC 6.3.3.3)



feature.pgfam_id.arg_lys_ratio.mean

PGF_01737397

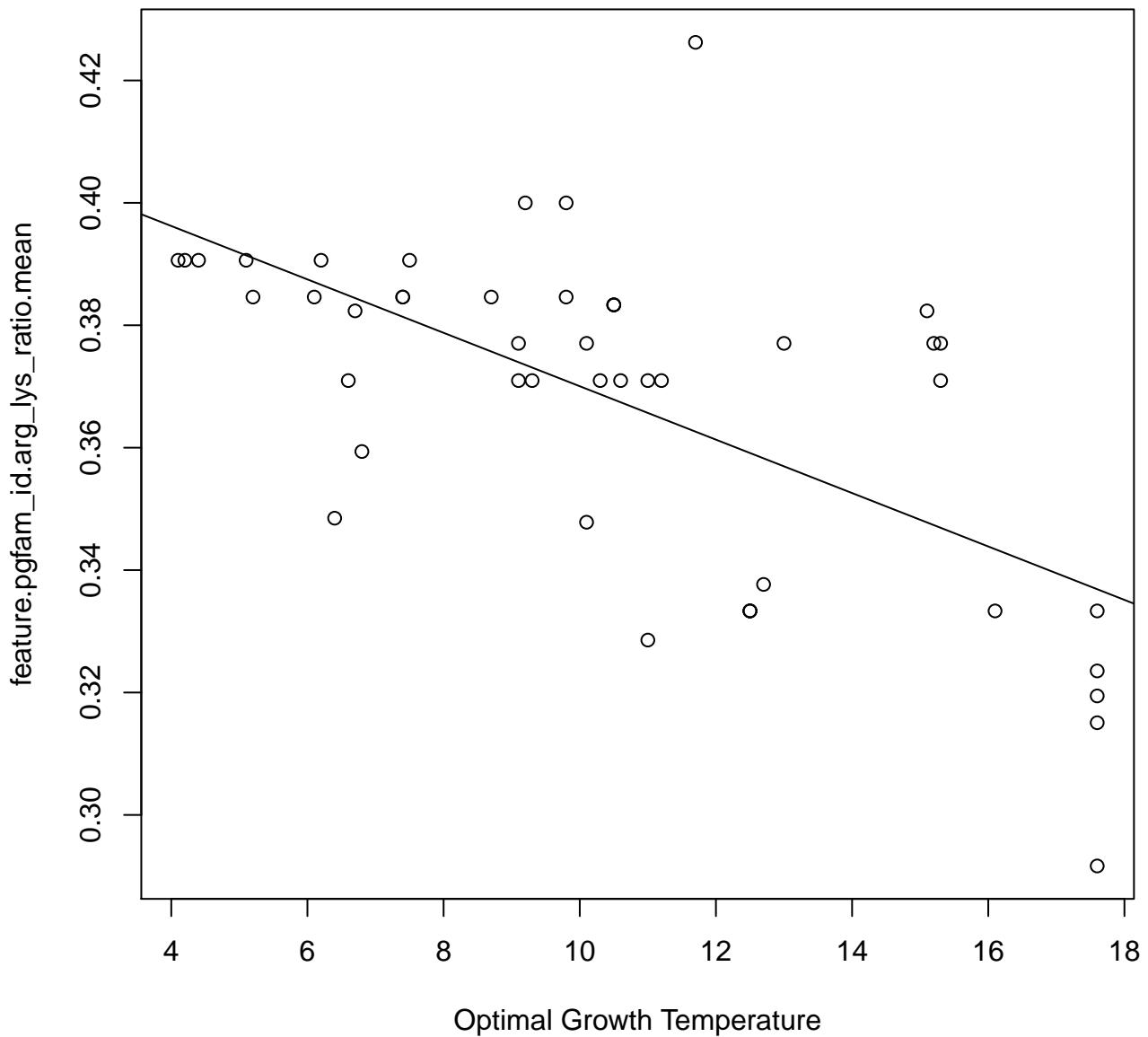
FIG00031715: Predicted metal-dependent phosphoesterases (PHP family)



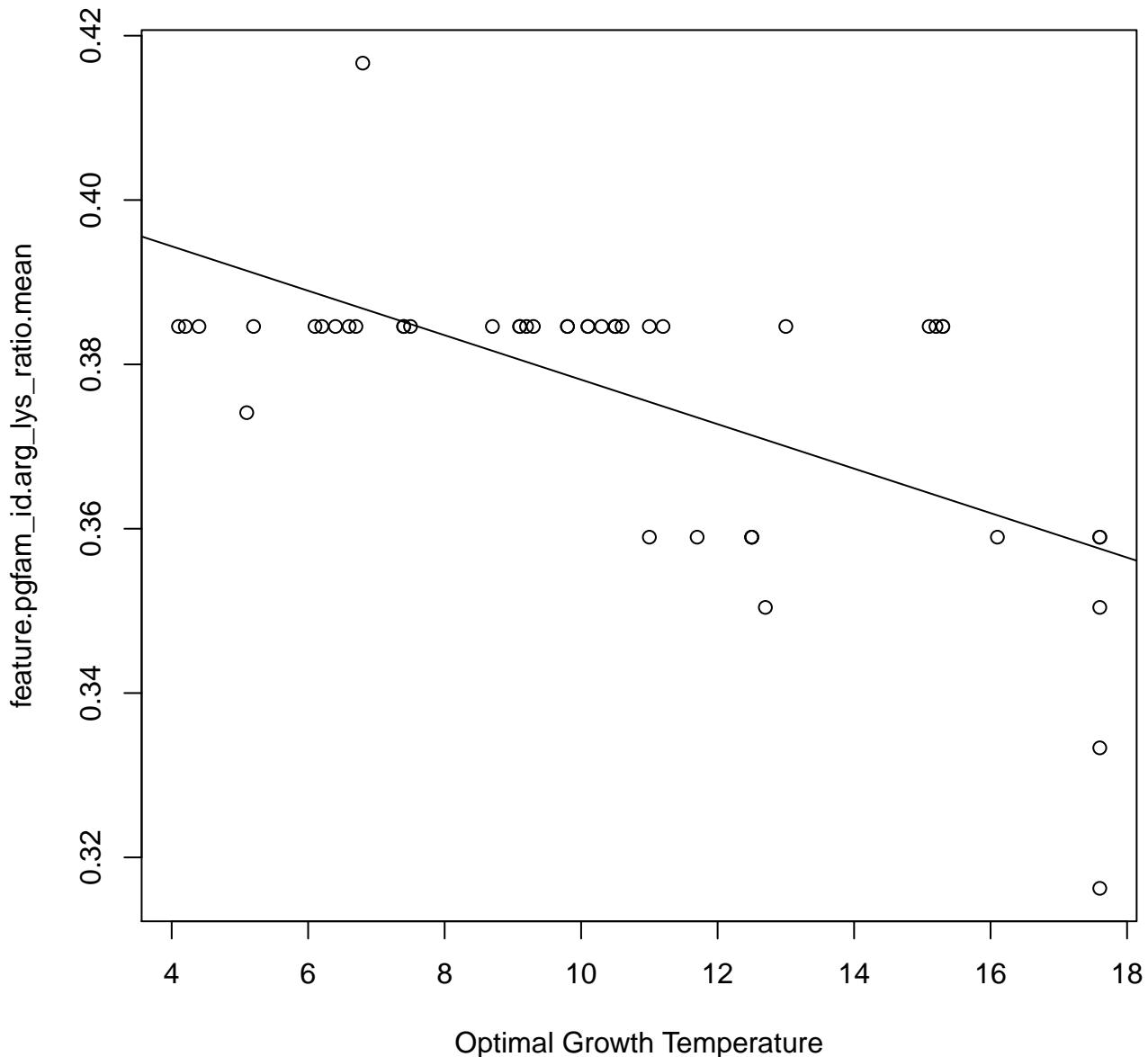
feature.pgfam_id.arg_lys_ratio.mean

PGF_01336321

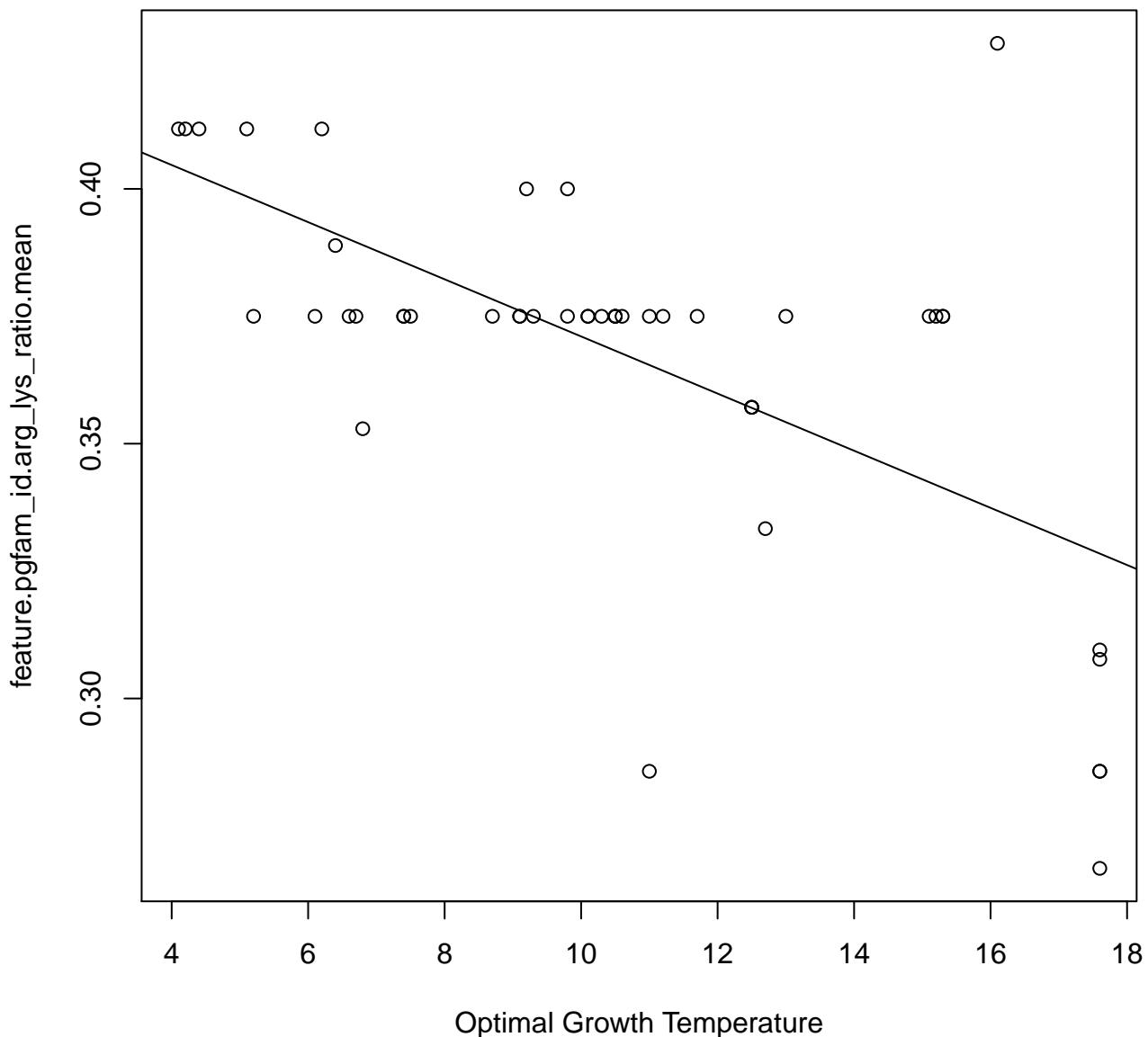
Regulatory sensor-transducer, BlaR1/MecR1 family / TonB family protein



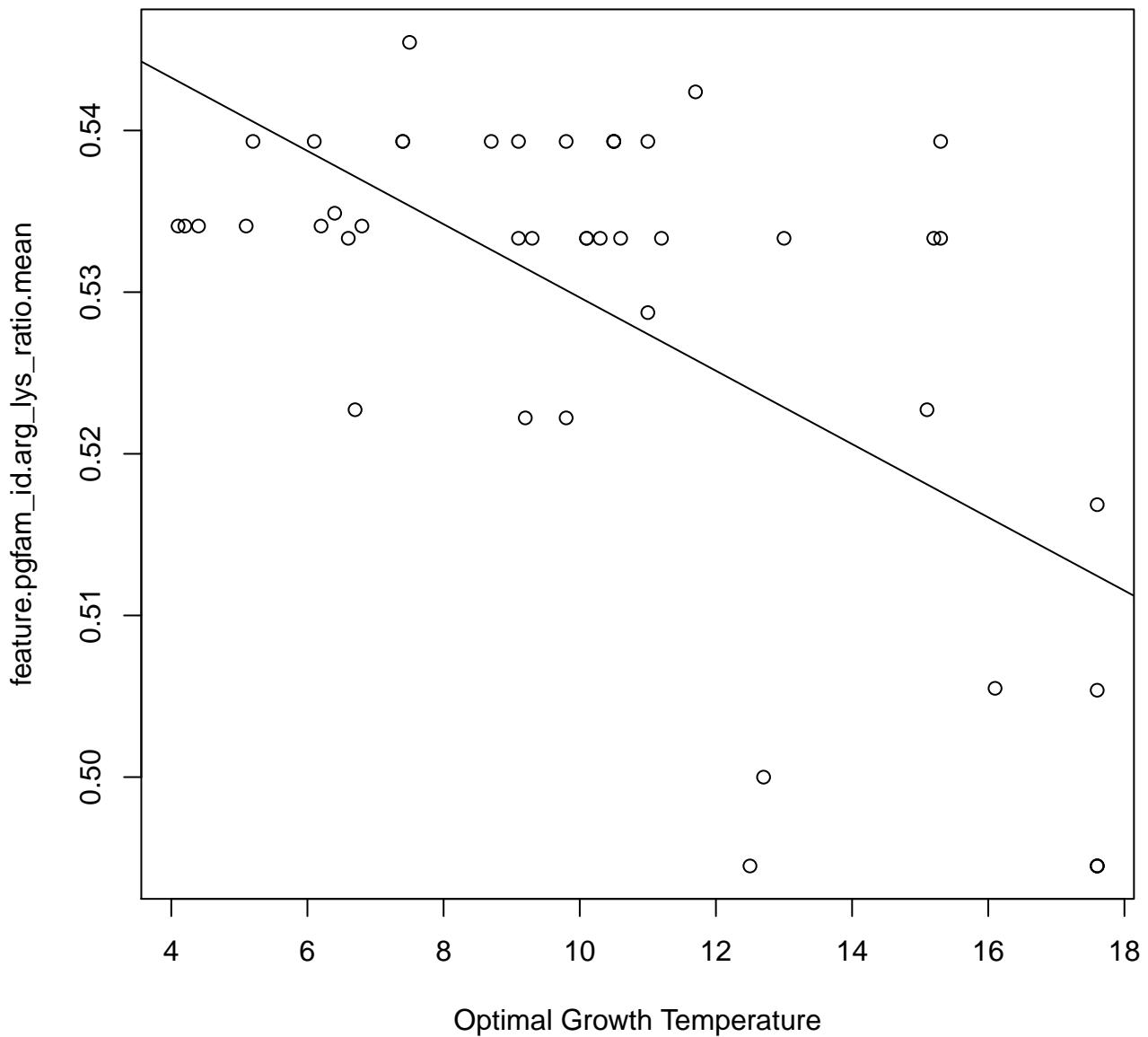
feature.pgfam_id.arg_lys_ratio.mean
PGF_04636538
DNA-binding protein HU-beta



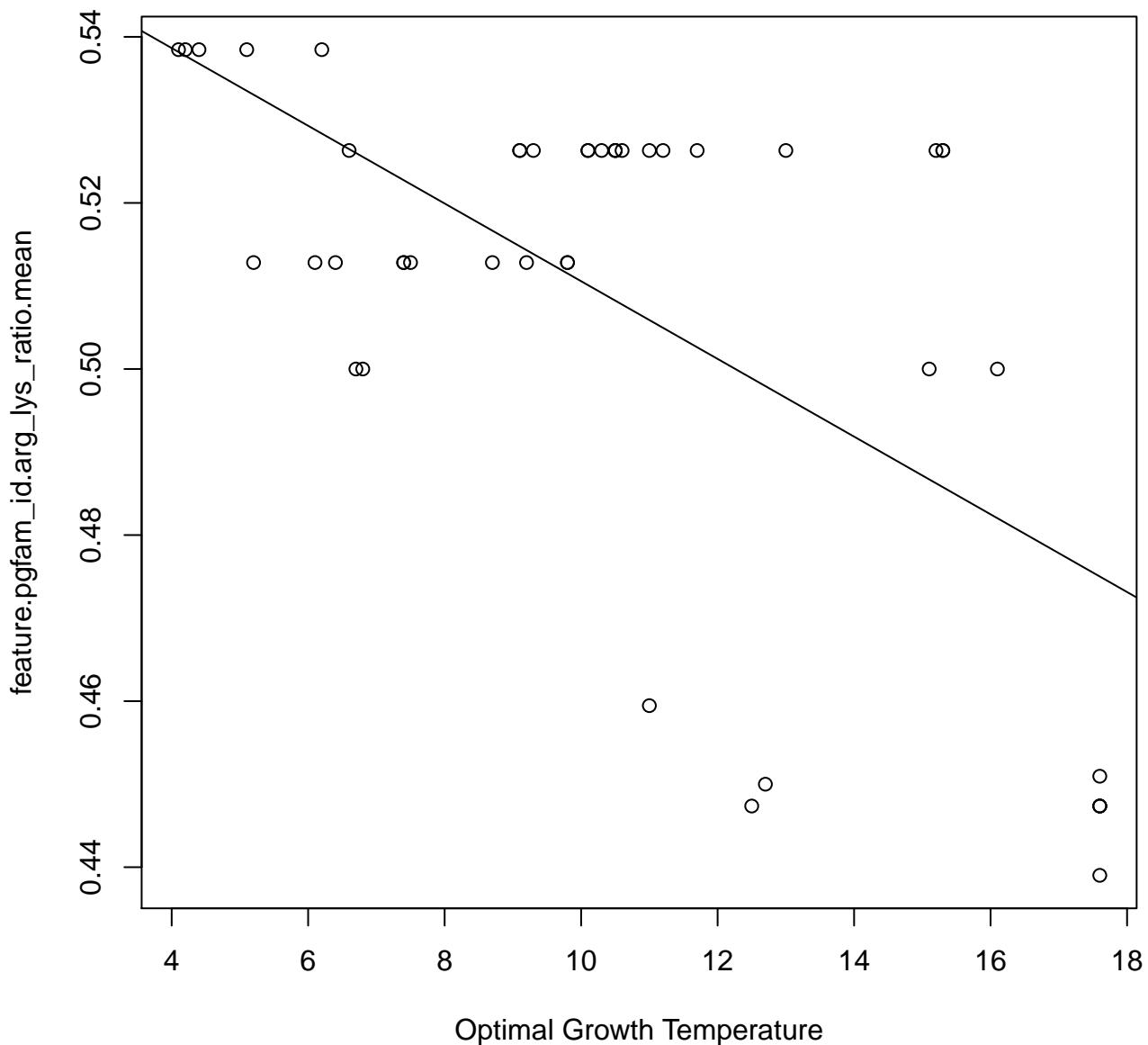
feature.pgfam_id.arg_lys_ratio.mean
PGF_00413232
tRNA 2-thiouridine synthesis protein TusE



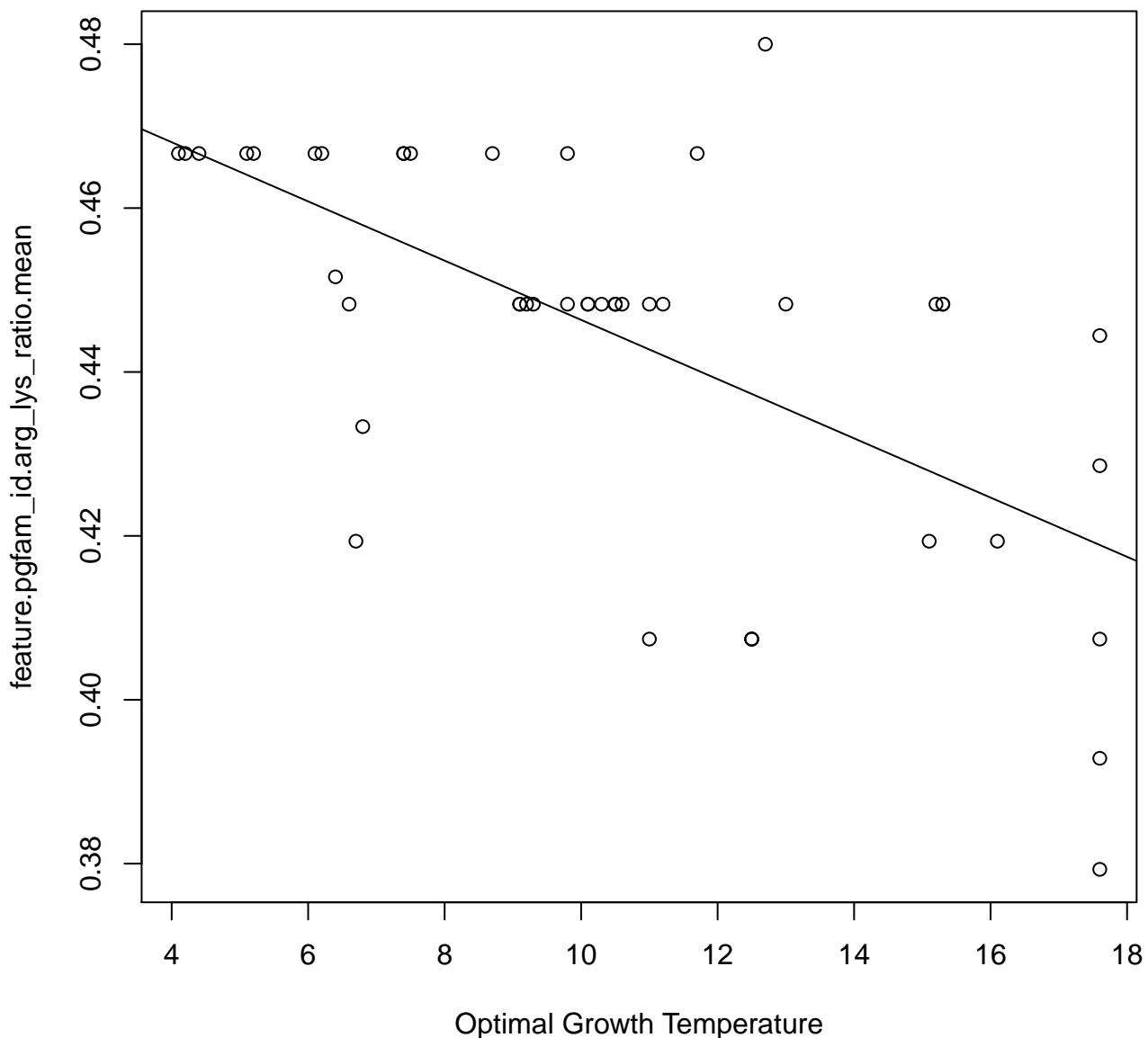
feature.pgfam_id.arg_lys_ratio.mean
PGF_07069408
2-methylcitrate dehydratase (2-methyl-trans-aconitate forming) (EC 4.2.1.117)



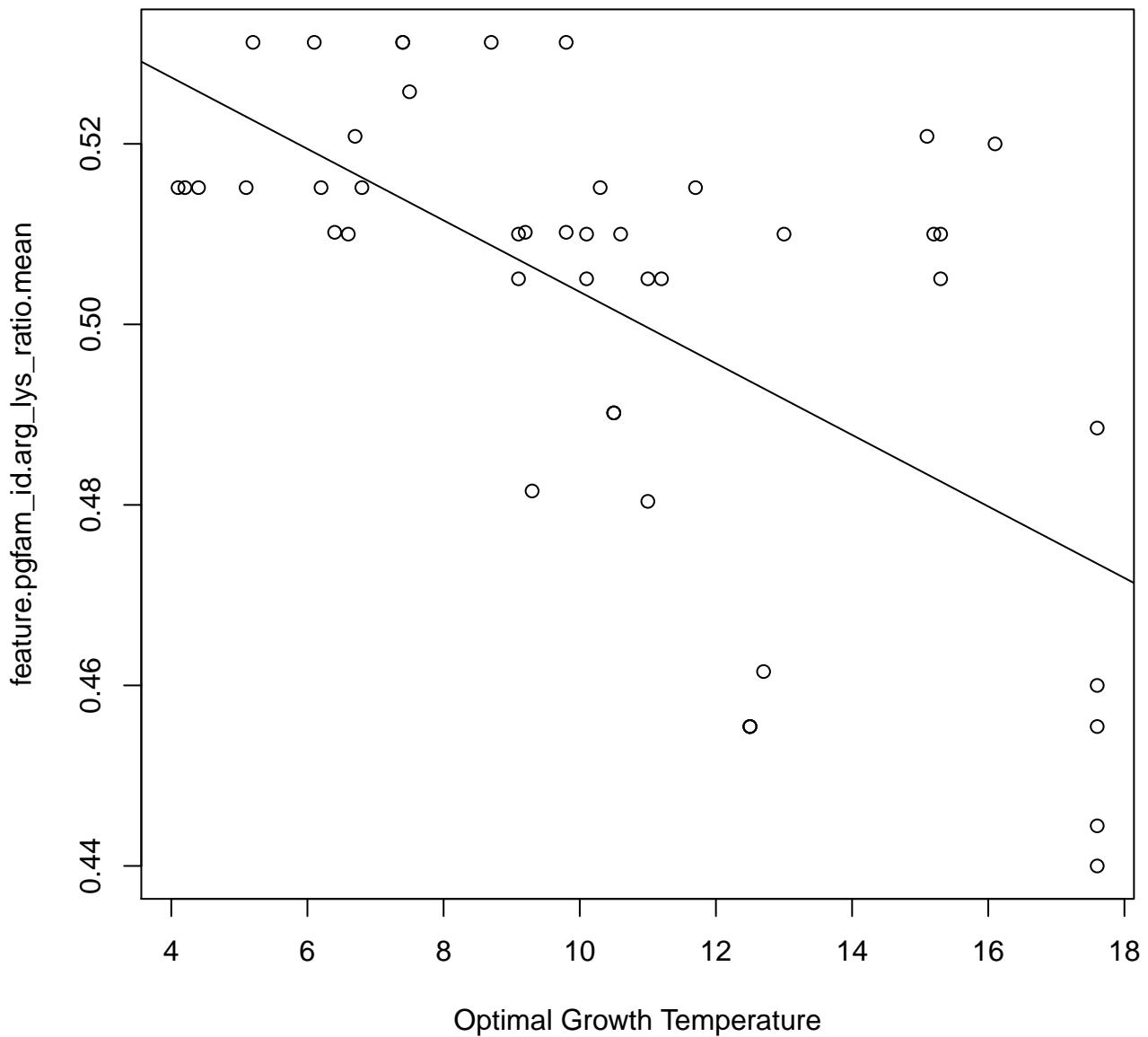
feature.pgfam_id.arg_lys_ratio.mean
PGF_03036276
Citrate synthase (si) (EC 2.3.3.1)



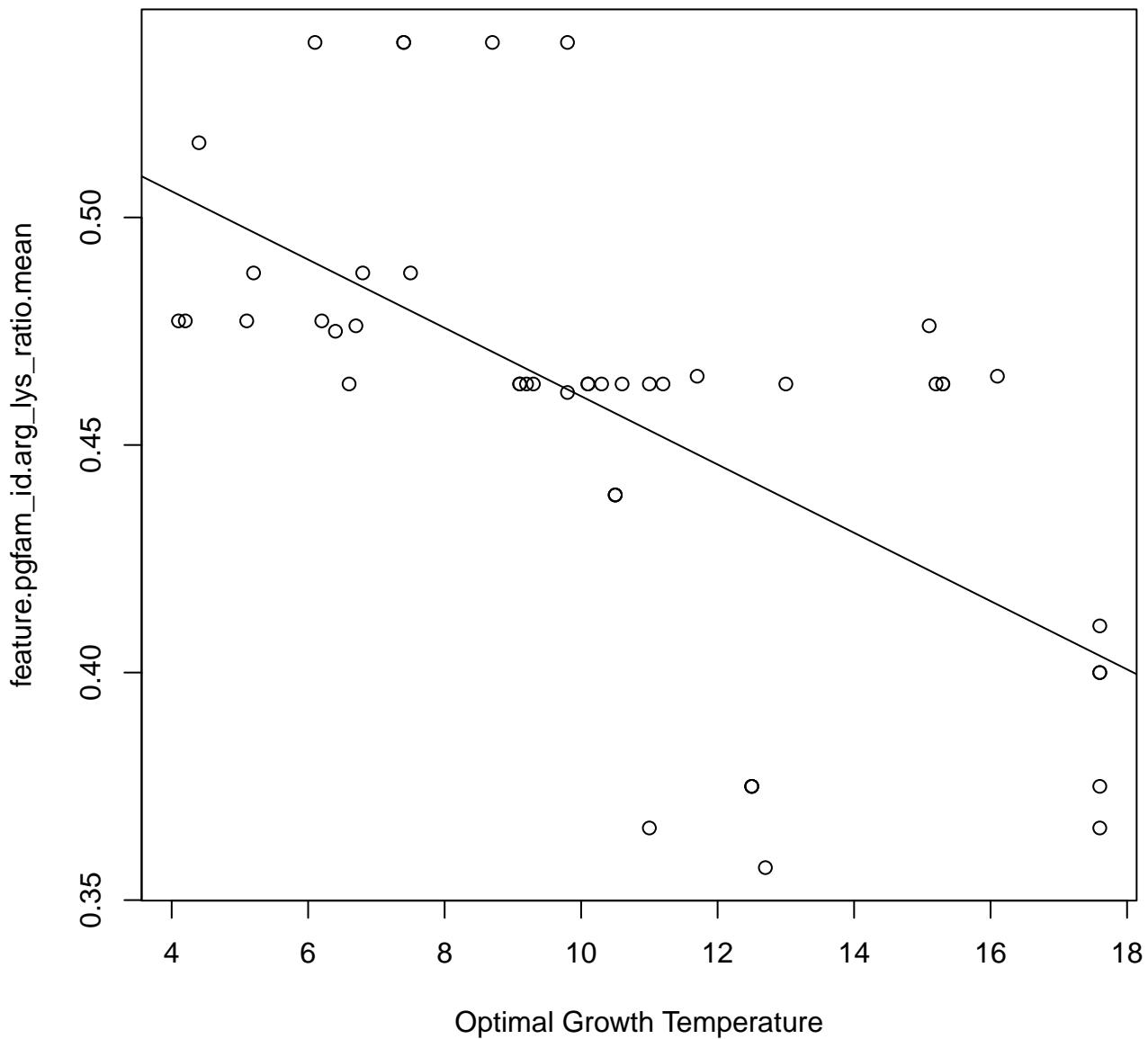
feature.pgfam_id.arg_lys_ratio.mean
PGF_00006983
GTP cyclohydrolase I (EC 3.5.4.16) type 2



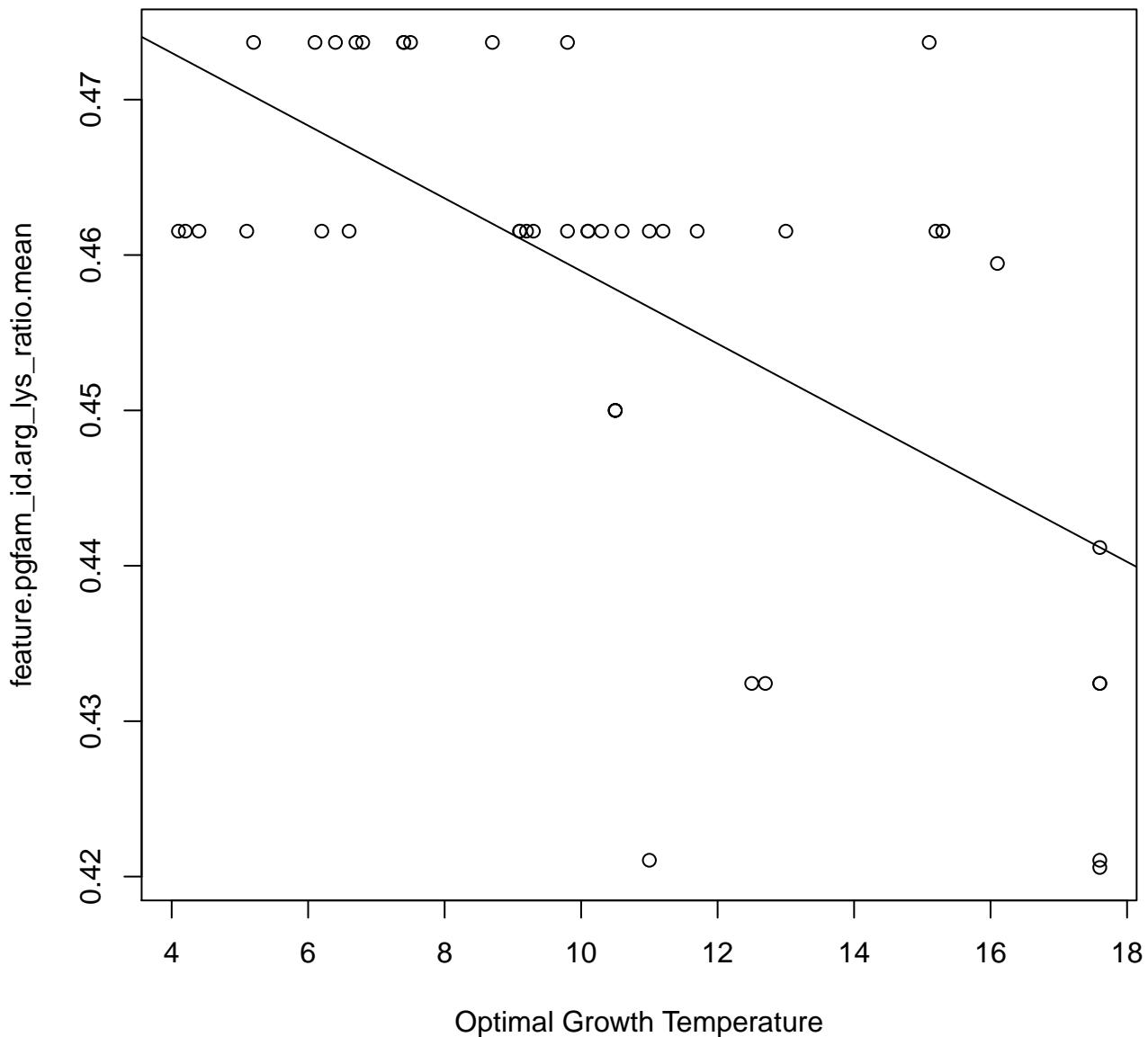
feature.pgfam_id.arg_lys_ratio.mean
PGF_00008595
Glycerol-3-phosphate acyltransferase (EC 2.3.1.15)



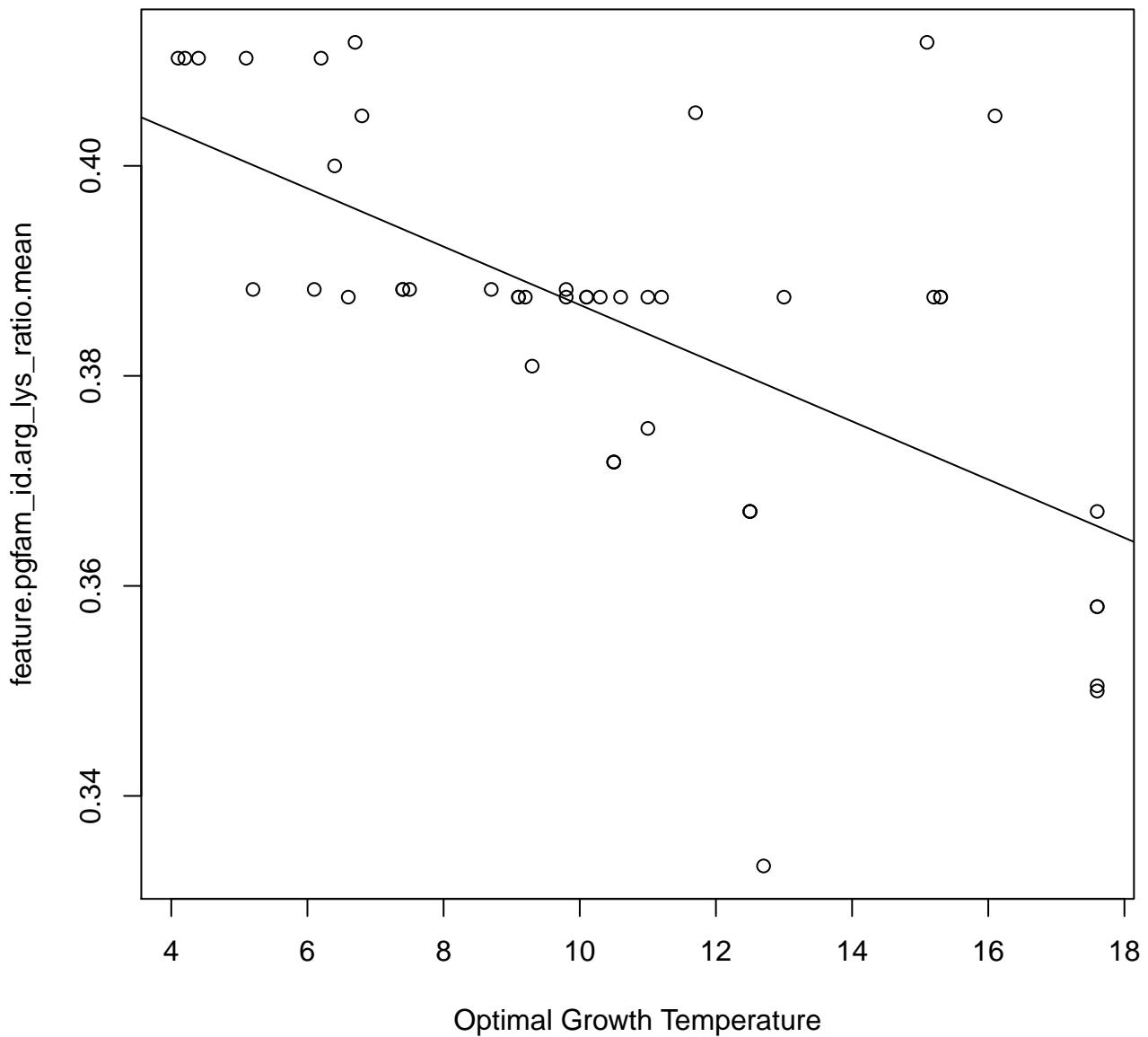
feature.pgfam_id.arg_lys_ratio.mean
PGF_00066867
Xaa-Pro aminopeptidase (EC 3.4.11.9)



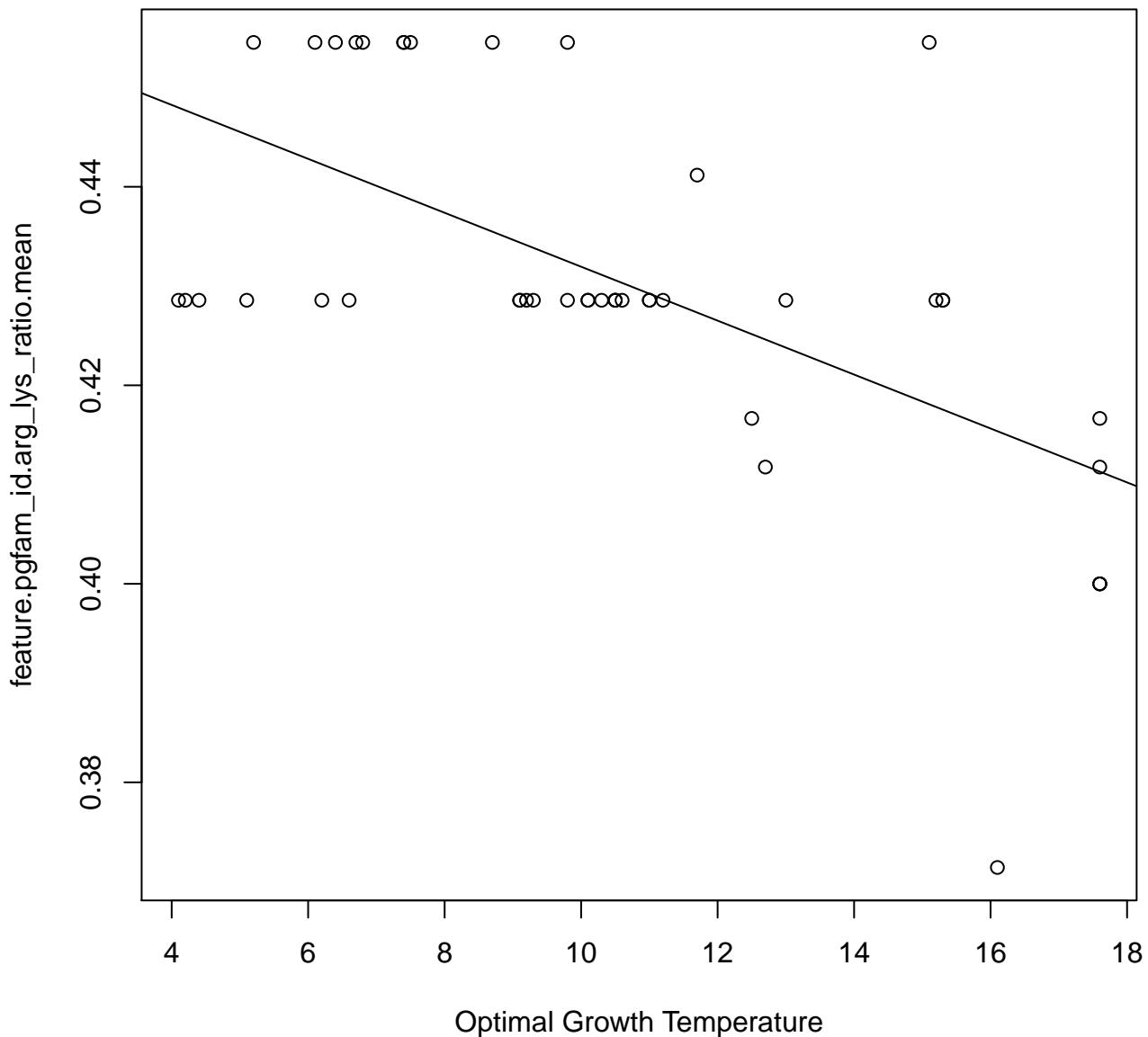
feature.pgfam_id.arg_lys_ratio.mean
PGF_04139053
Uroporphyrinogen III decarboxylase (EC 4.1.1.37)



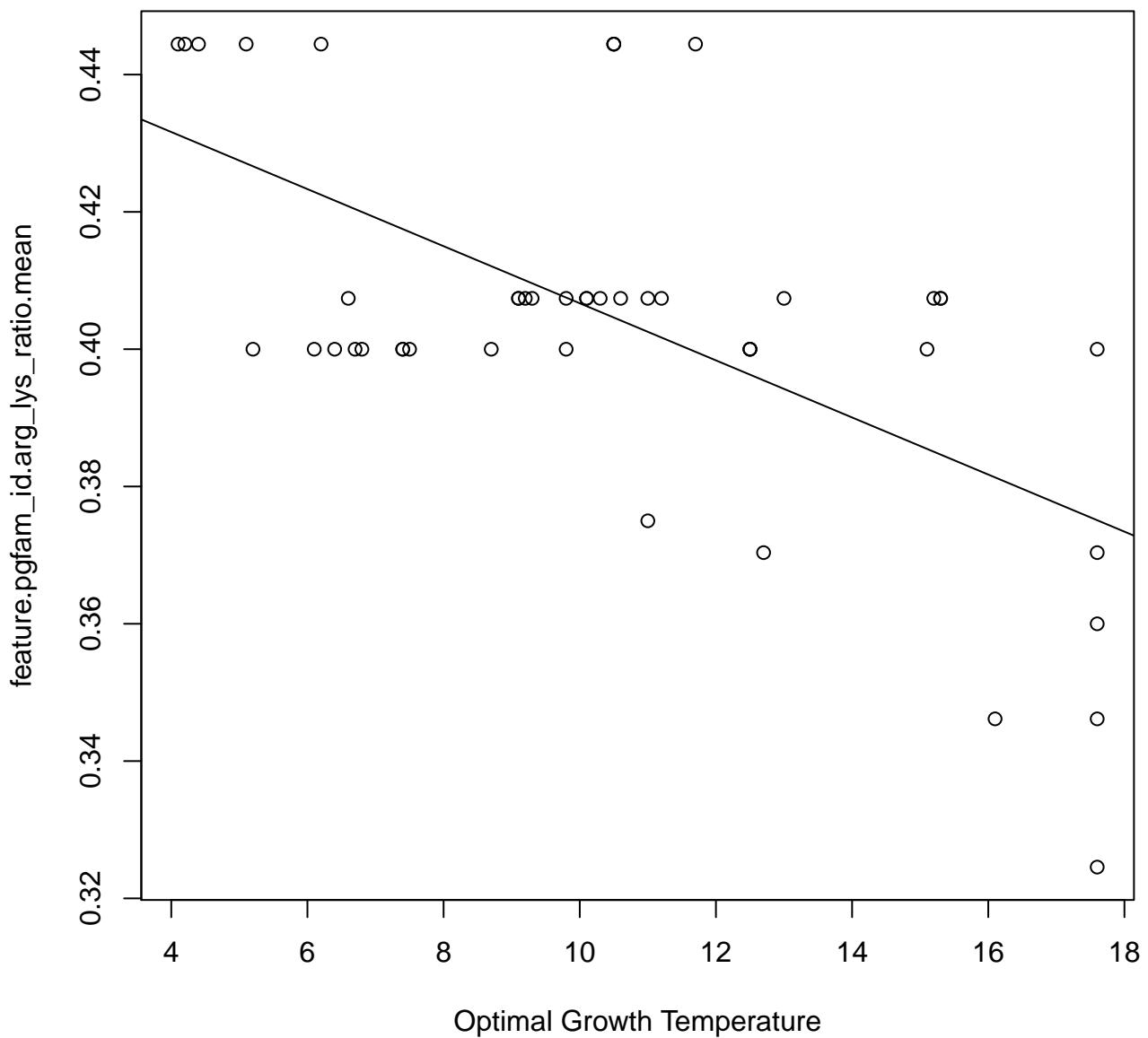
feature.pgfam_id.arg_lys_ratio.mean
PGF_00019567
ATP-dependent protease La (EC 3.4.21.53) Type II



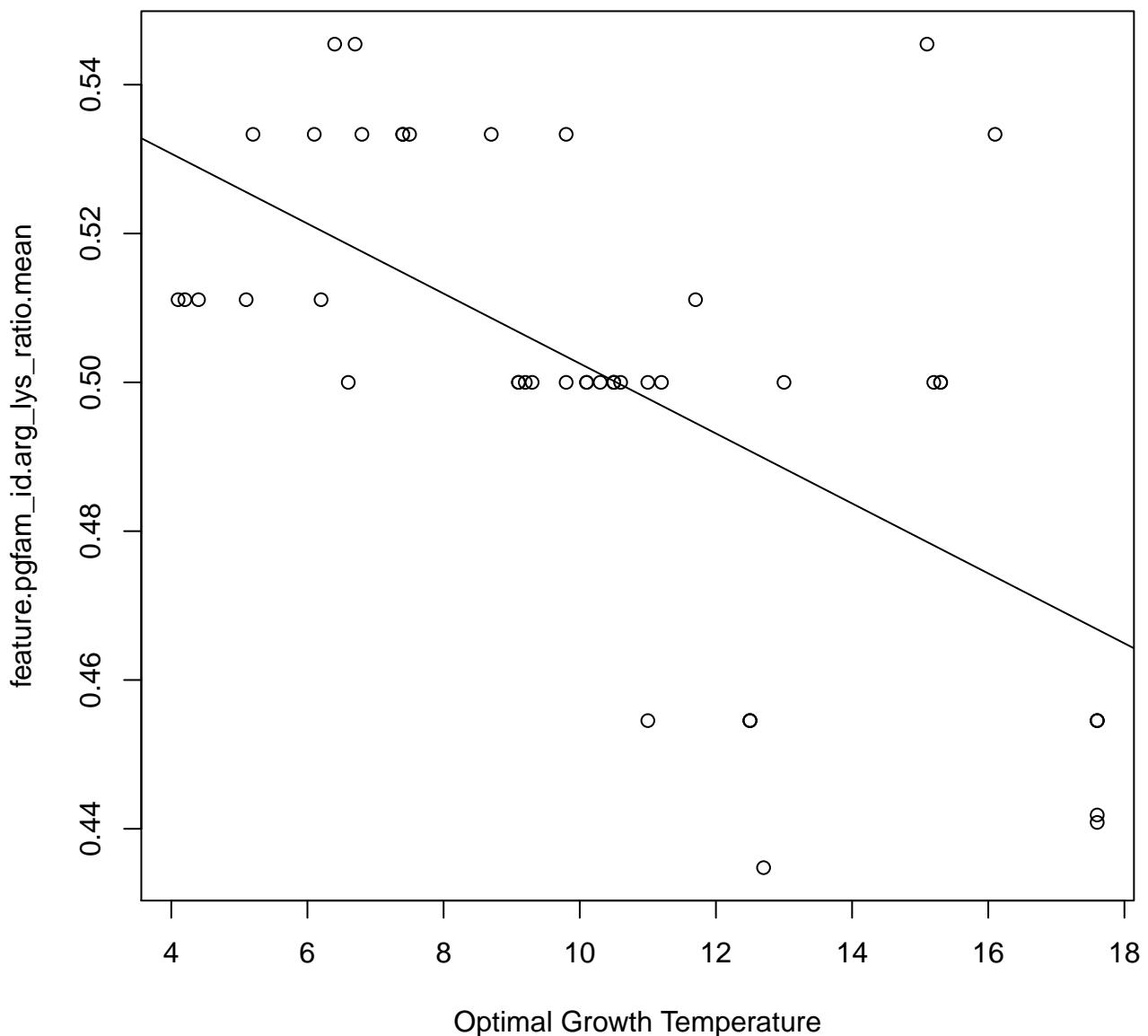
feature.pgfam_id.arg_lys_ratio.mean
PGF_06652053
3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)



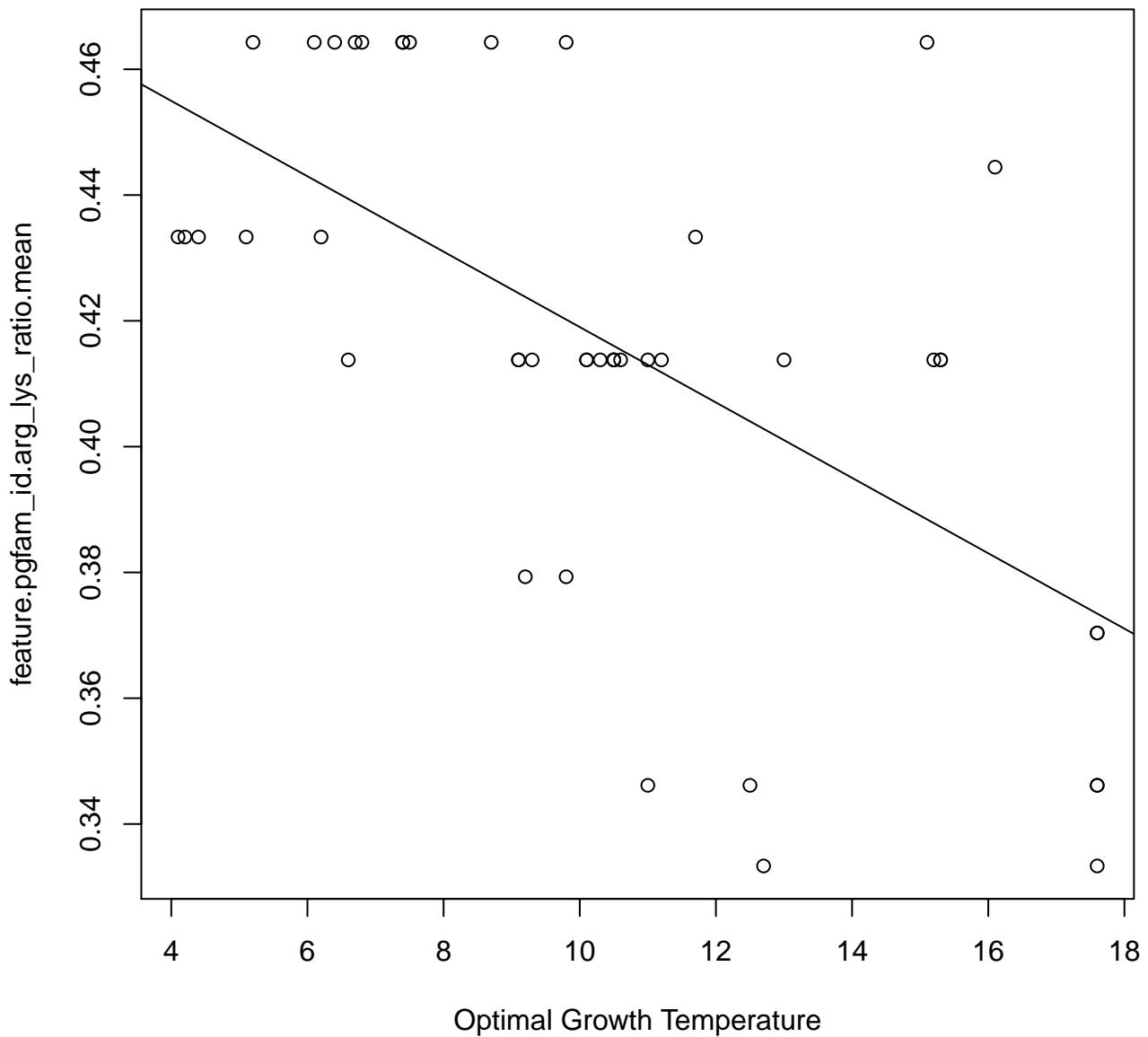
feature.pgfam_id.arg_lys_ratio.mean
PGF_03647550
UPF0234 protein Yitk



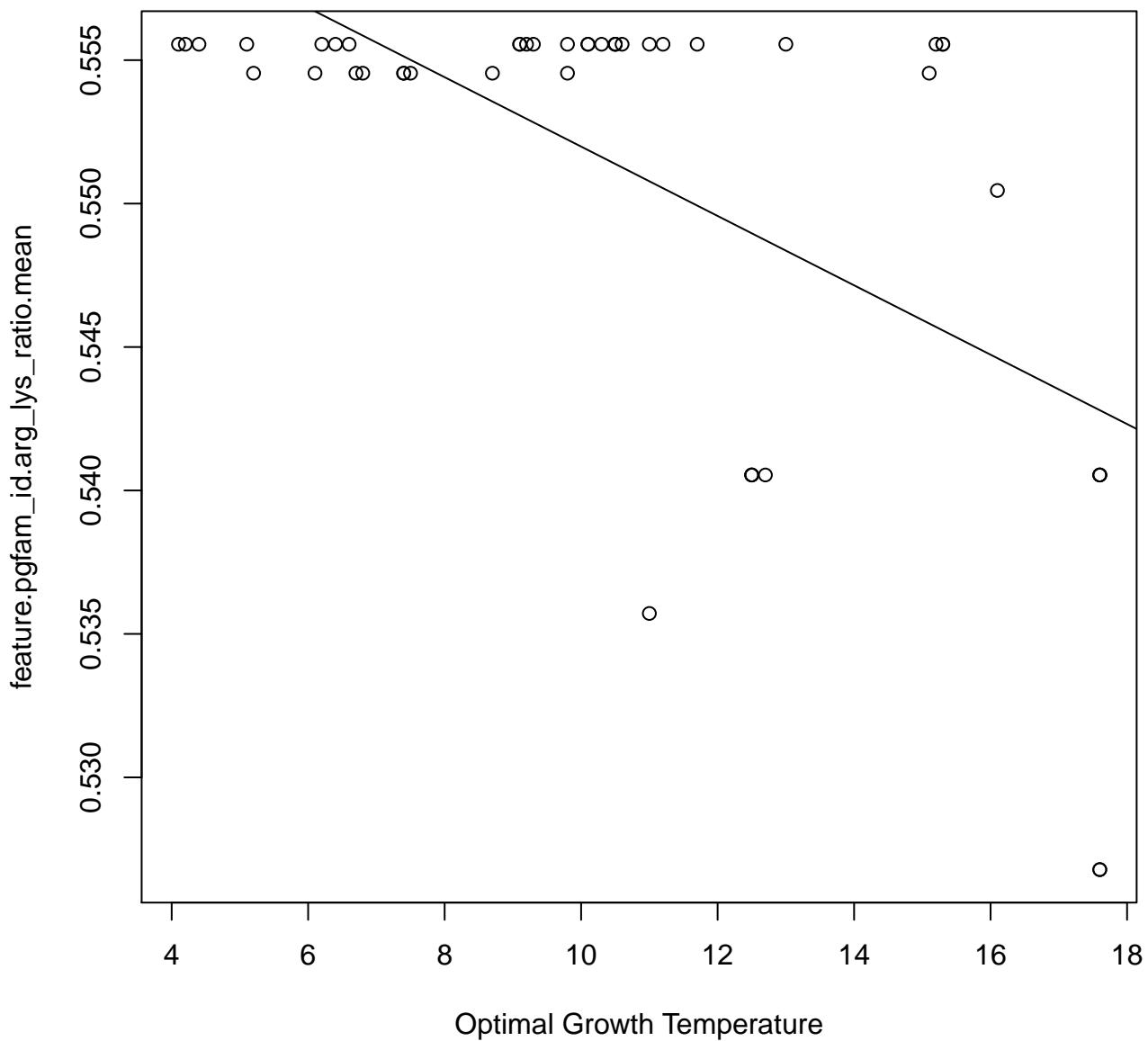
feature.pgfam_id.arg_lys_ratio.mean
PGF_02029783
GTP-binding protein Obg



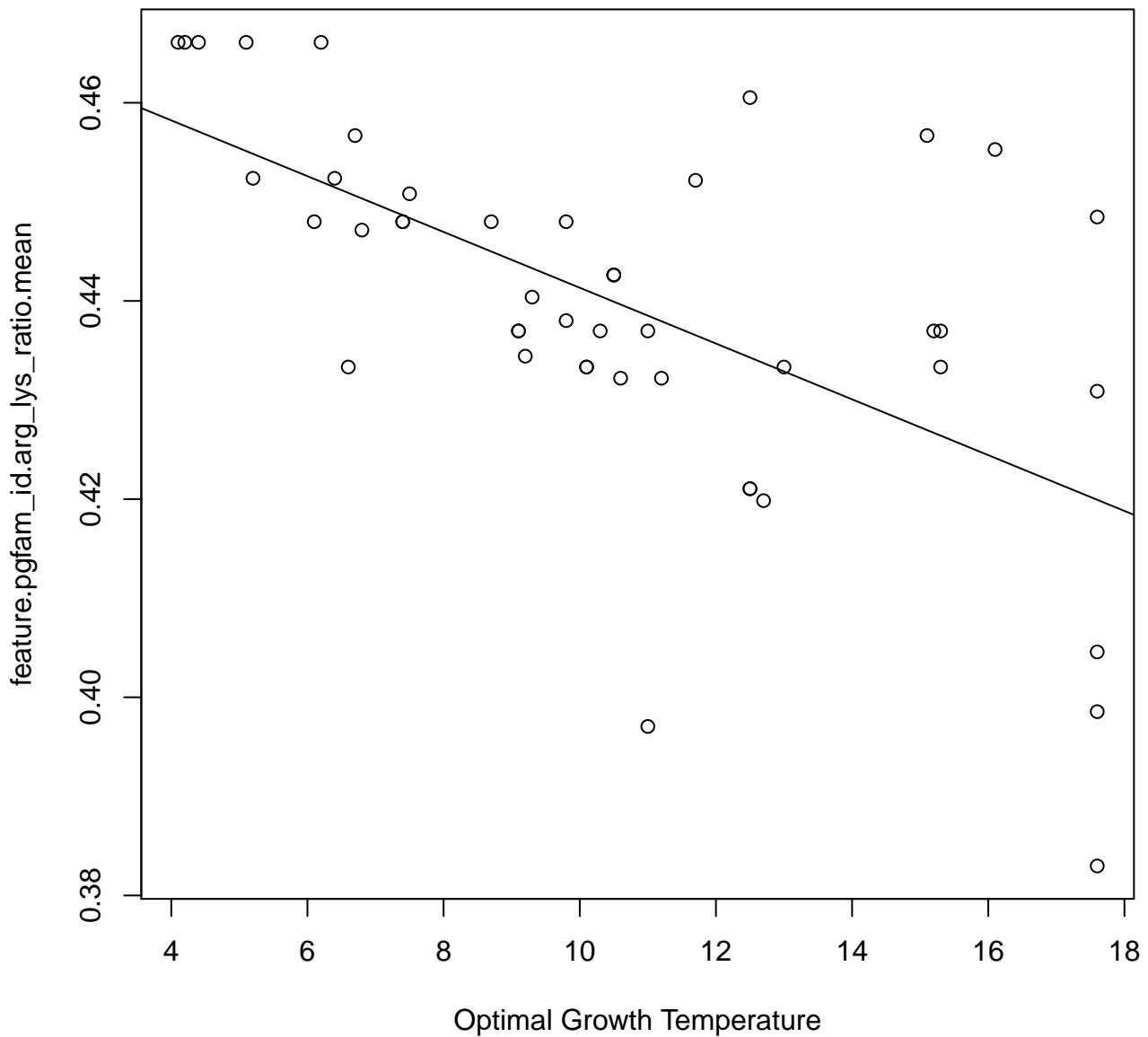
feature.pgfam_id.arg_lys_ratio.mean
PGF_06857975
Cell-division-associated, ABC-transporter-like signaling protein FtsE



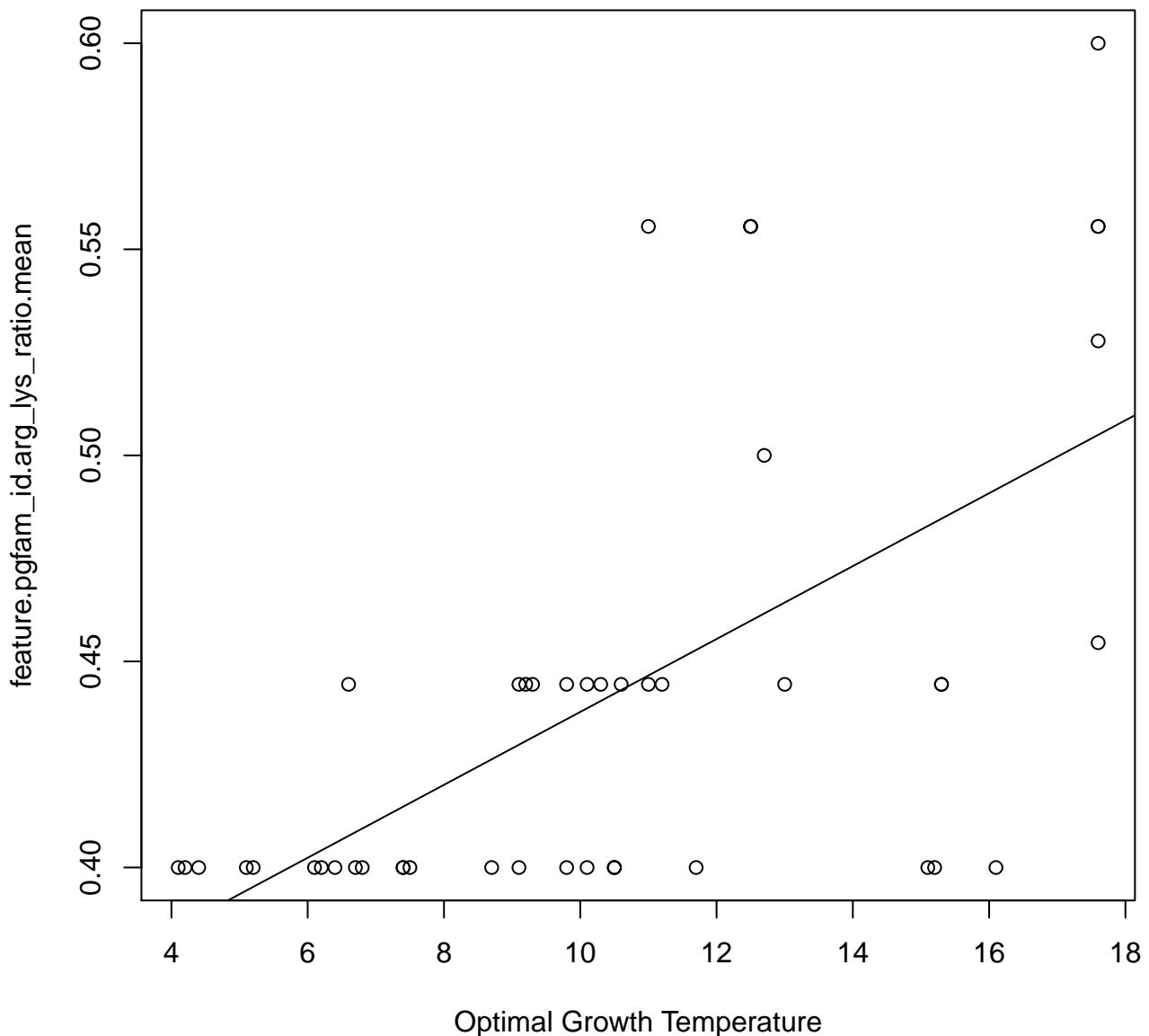
feature.pgfam_id.arg_lys_ratio.mean
PGF_03272313
DNA gyrase subunit A (EC 5.99.1.3)



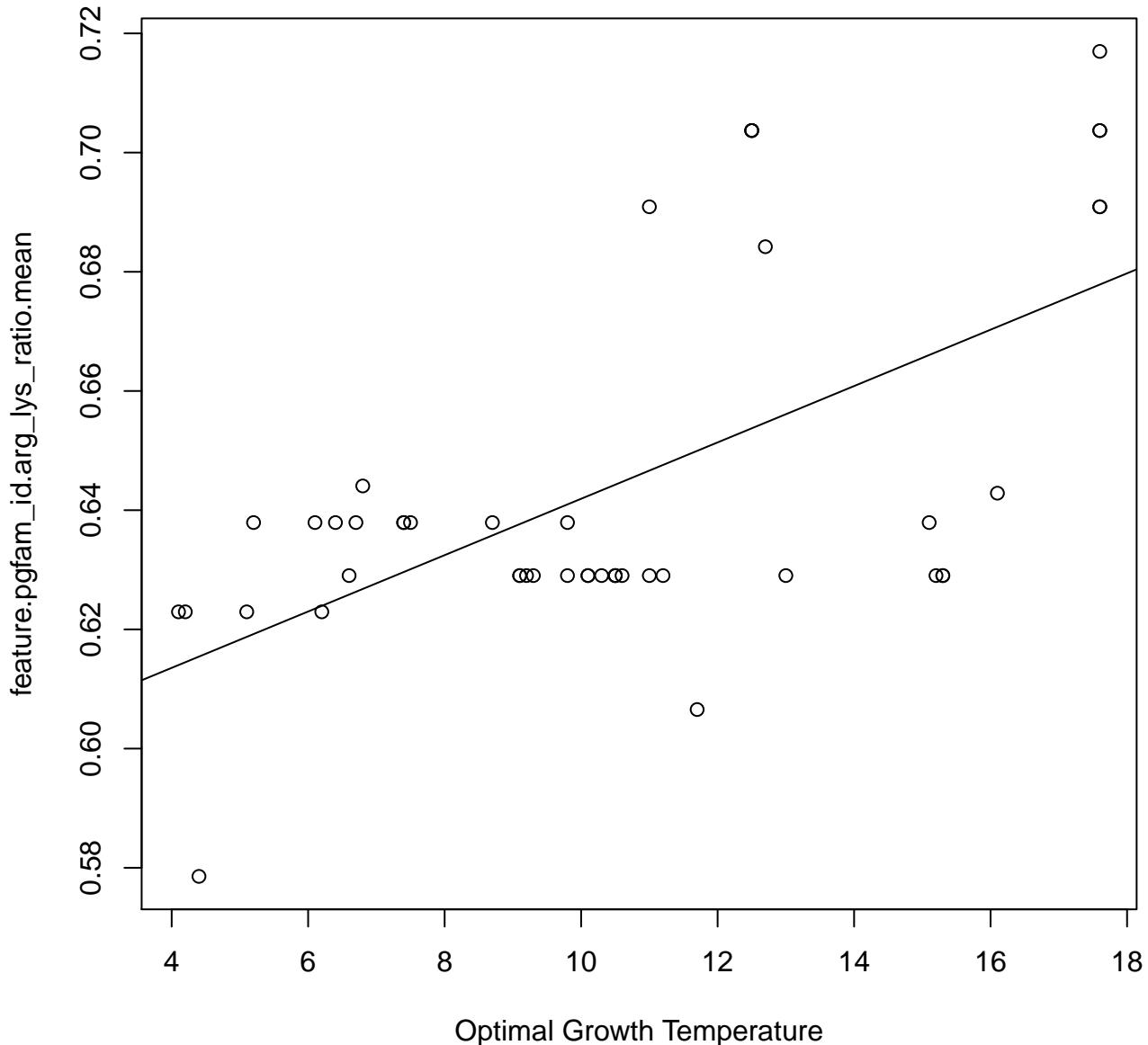
feature.pgfam_id.arg_lys_ratio.mean
PGF_01058419
Exodeoxyribonuclease V beta chain (EC 3.1.11.5)



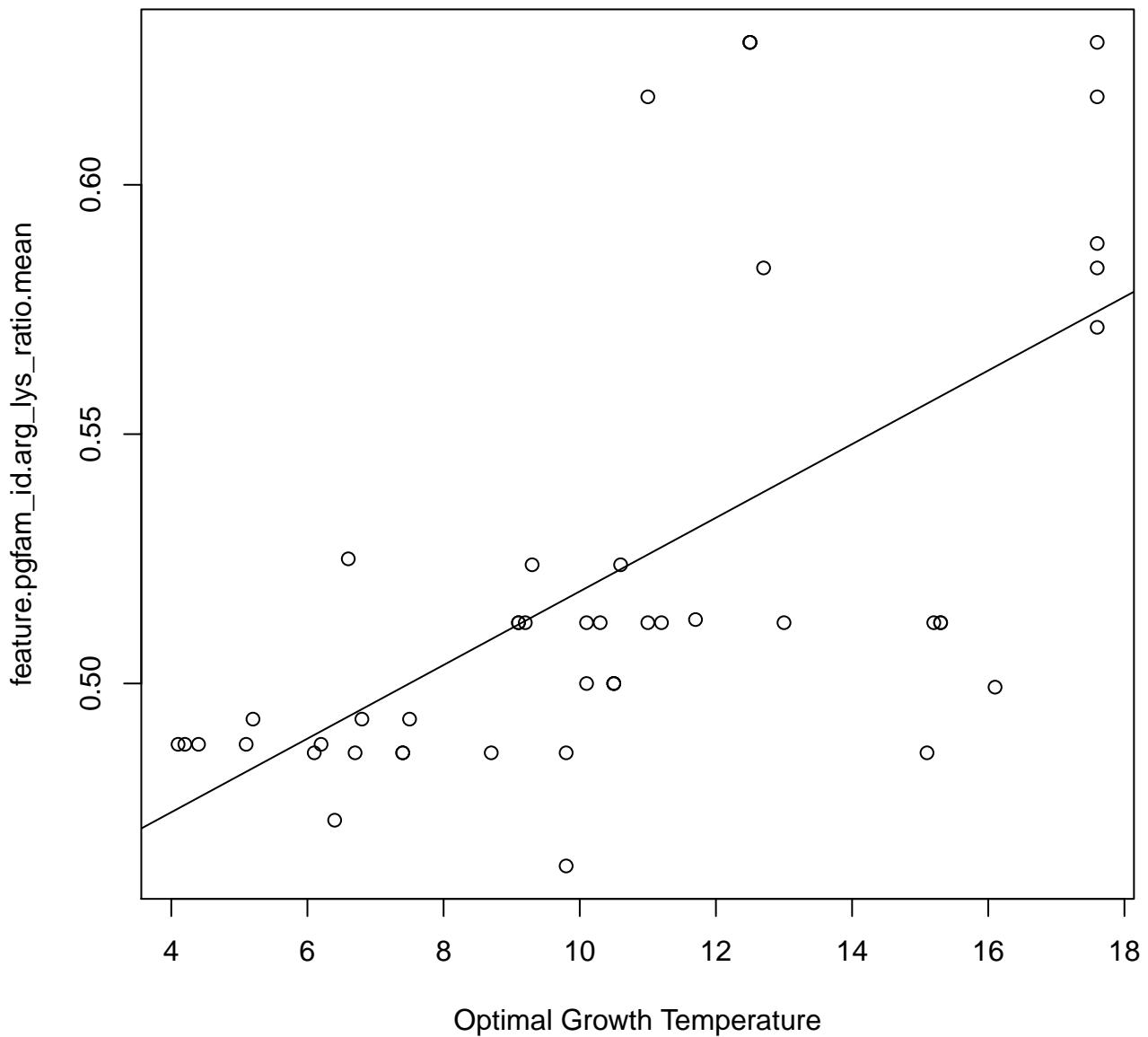
feature.pgfam_id.arg_lys_ratio.mean
PGF_04315180
Protein-export protein SecB (maintains pre-export unfolded state)



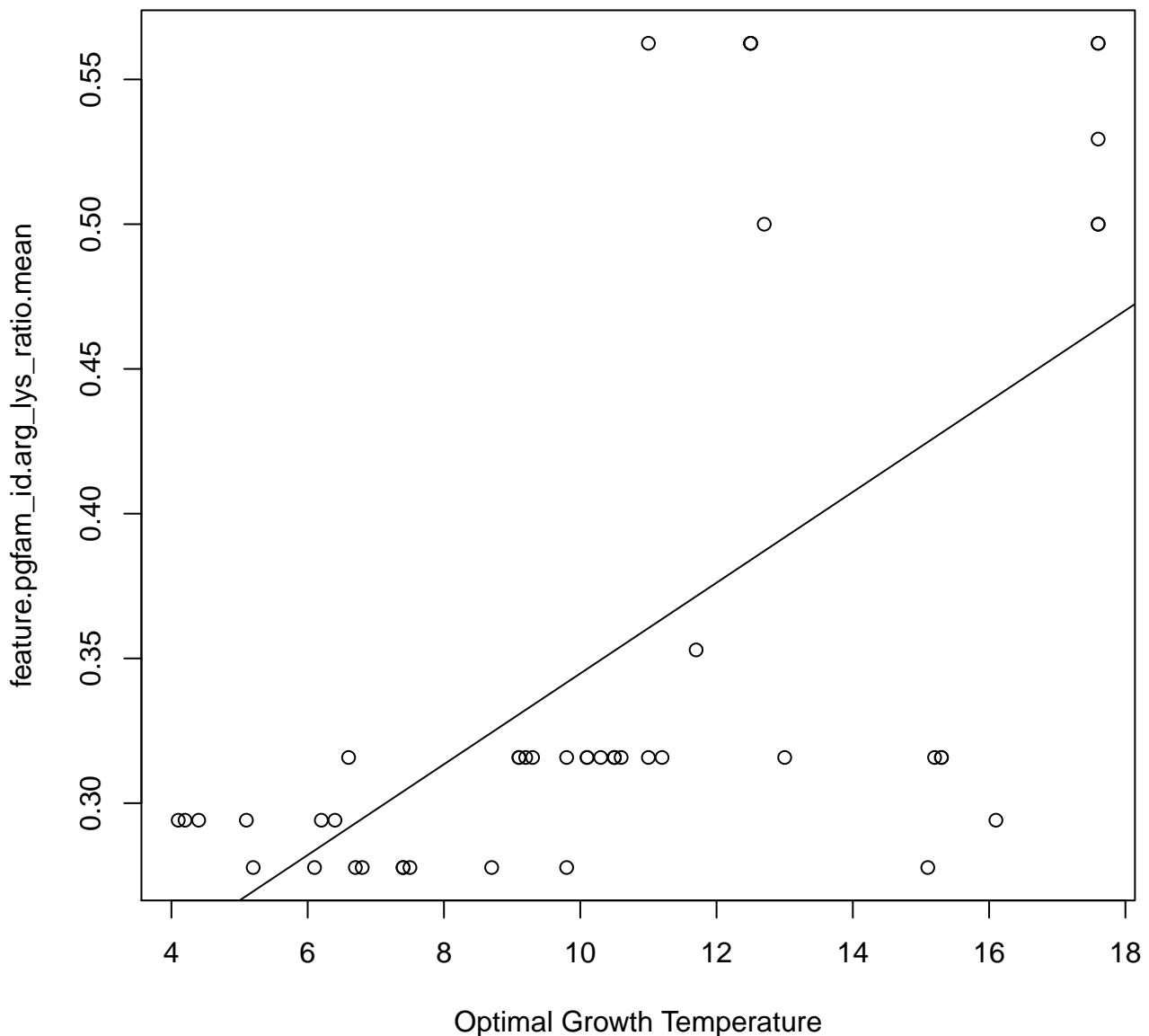
feature.pgfam_id.arg_lys_ratio.mean
PGF_00007028
Ribosome LSU-associated GTP-binding protein HfIX



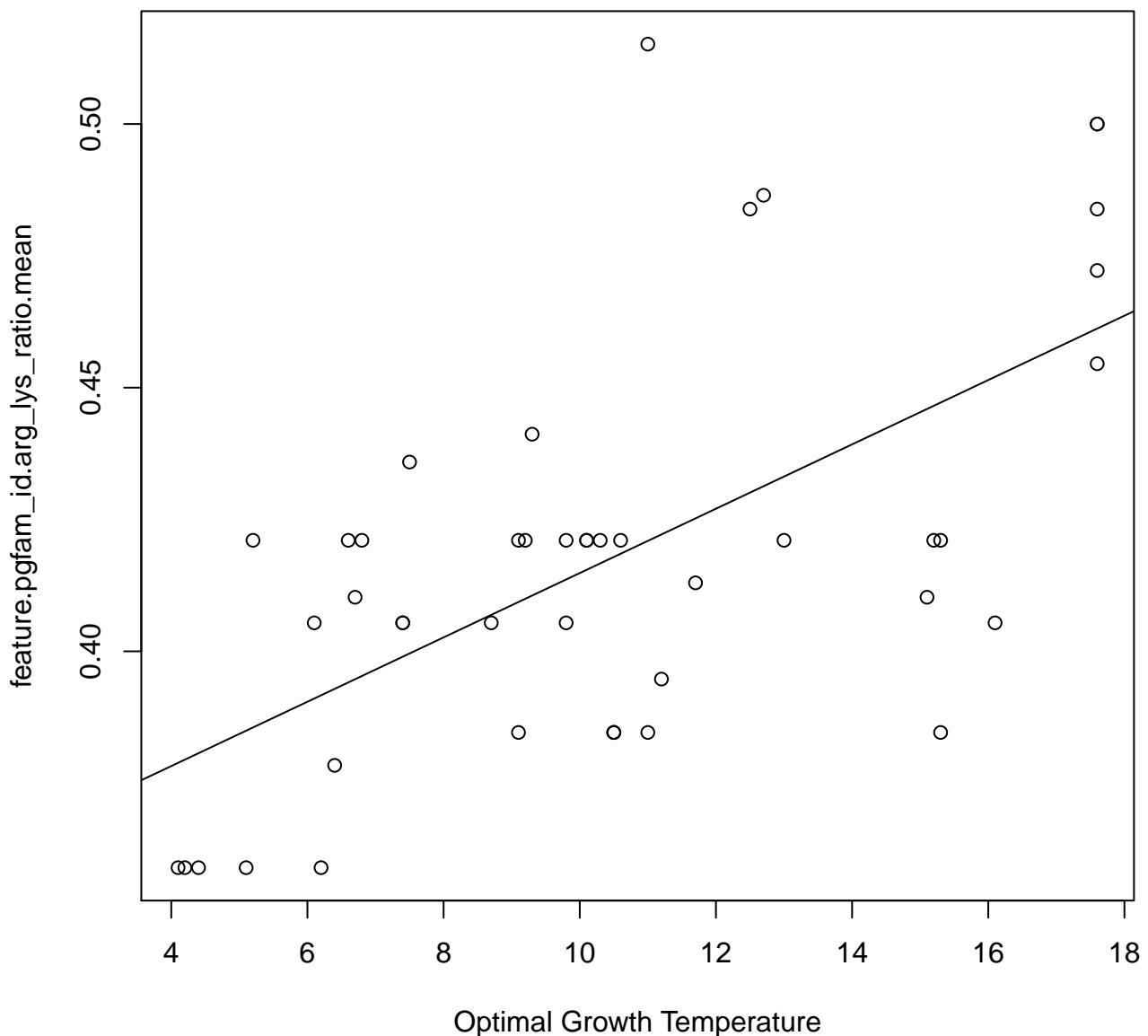
feature.pgfam_id.arg_lys_ratio.mean
PGF_04807486
tRNA dimethylallyltransferase (EC 2.5.1.75)



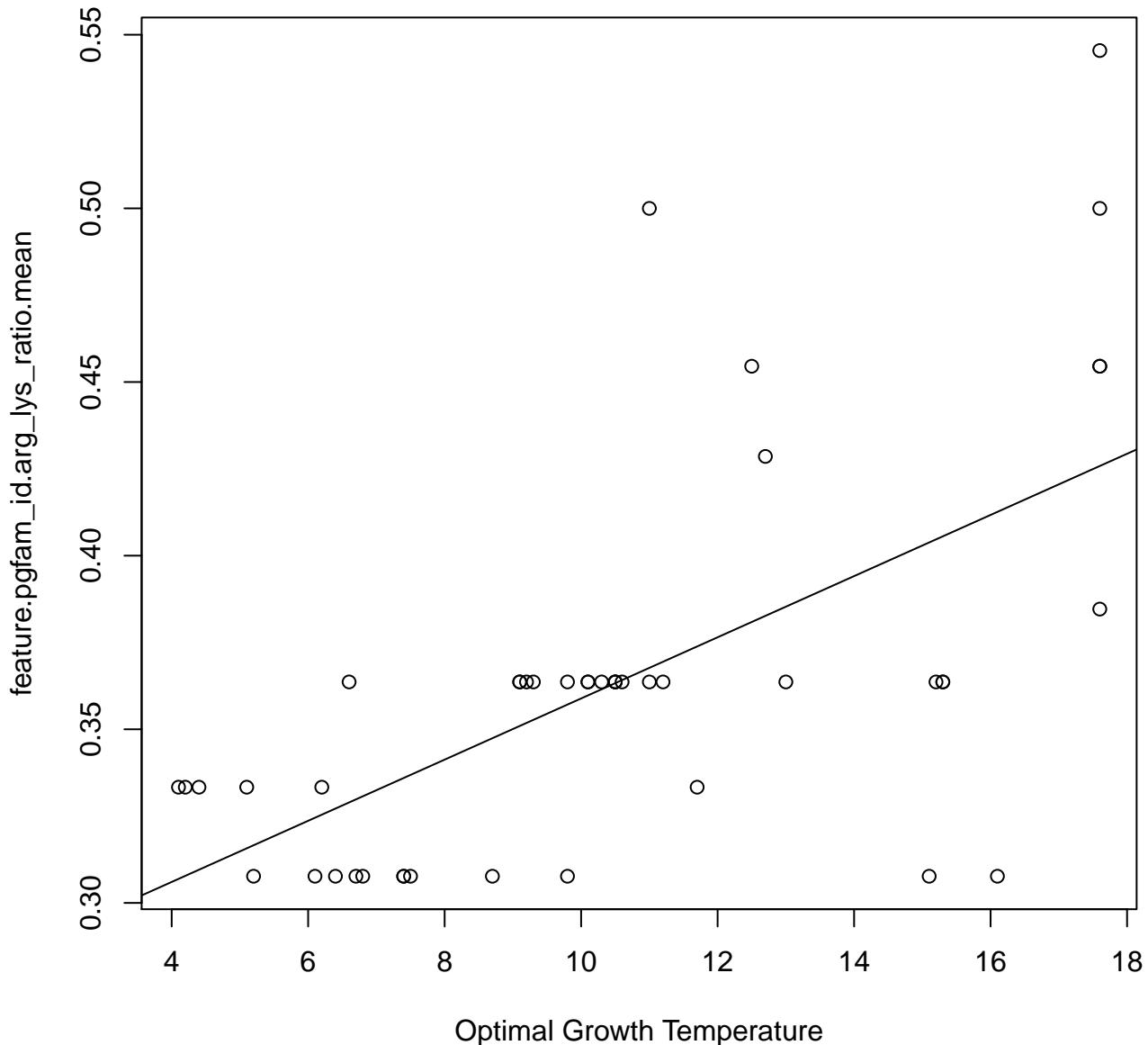
feature.pgfam_id.arg_lys_ratio.mean
PGF_03063012
Chaperone protein HscB



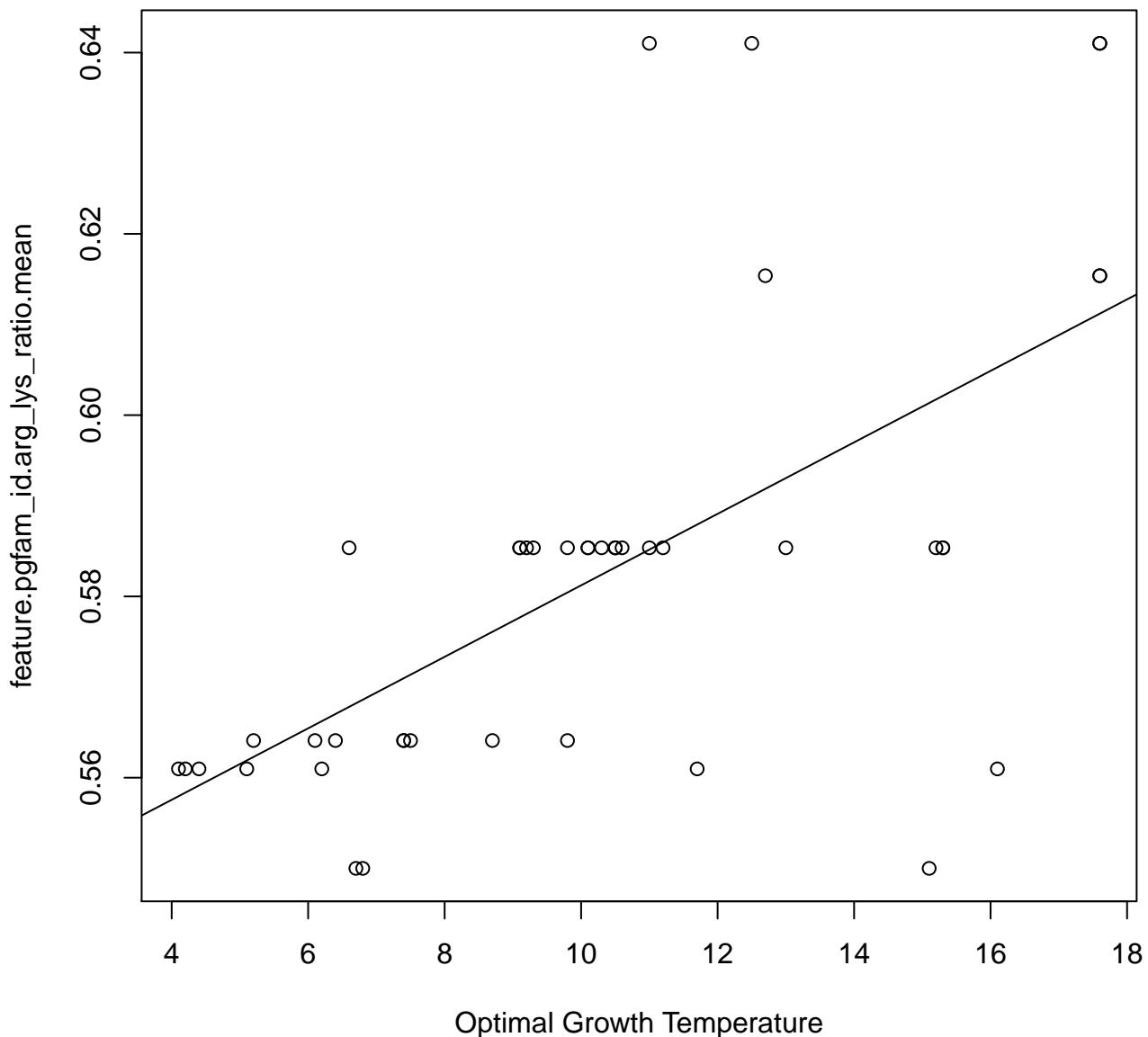
feature.pgfam_id.arg_lys_ratio.mean
PGF_02825604
hypothetical protein



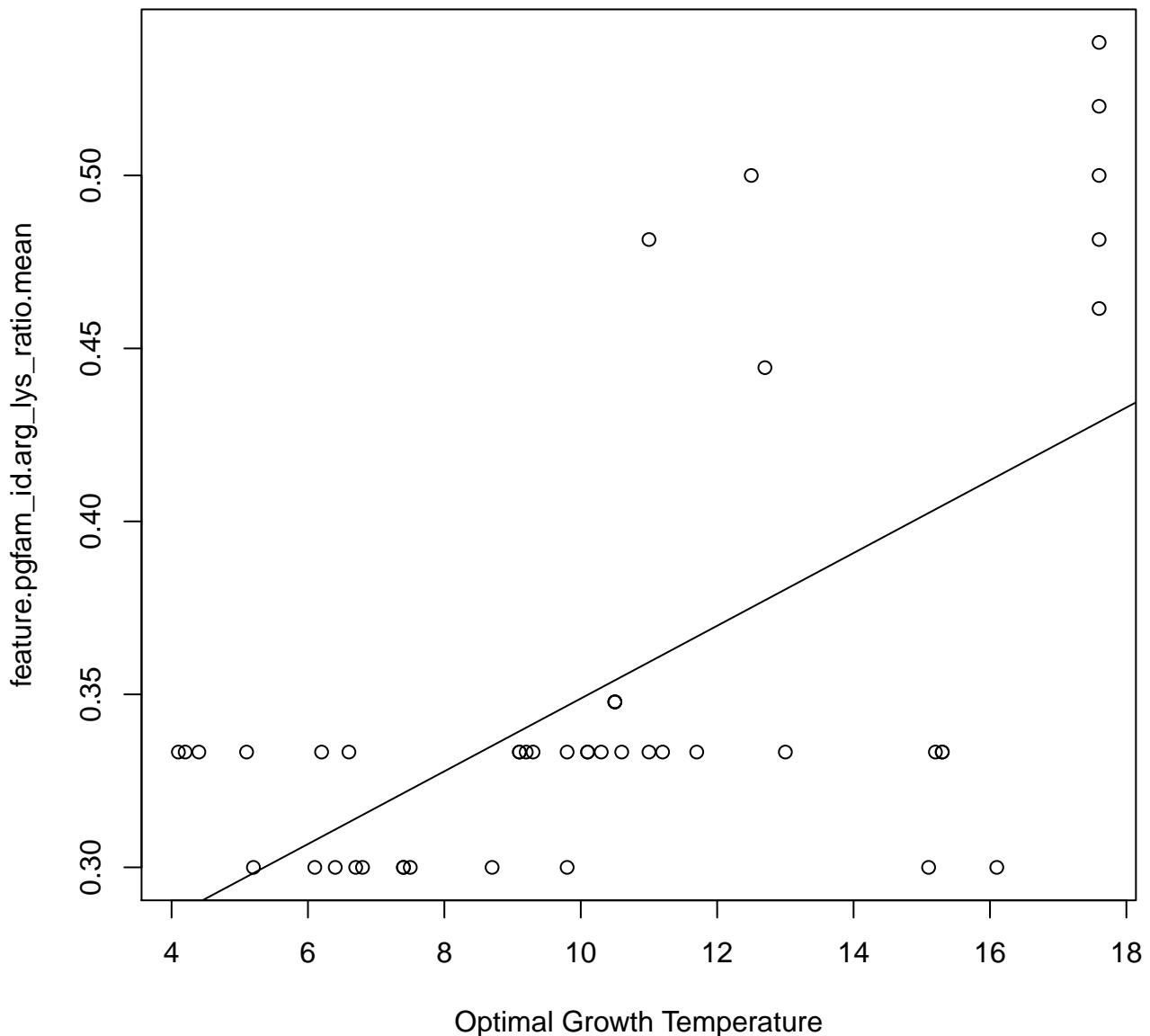
feature.pgfam_id.arg_lys_ratio.mean
PGF_10480638
Cytochrome c oxidase polypeptide III (EC 1.9.3.1)



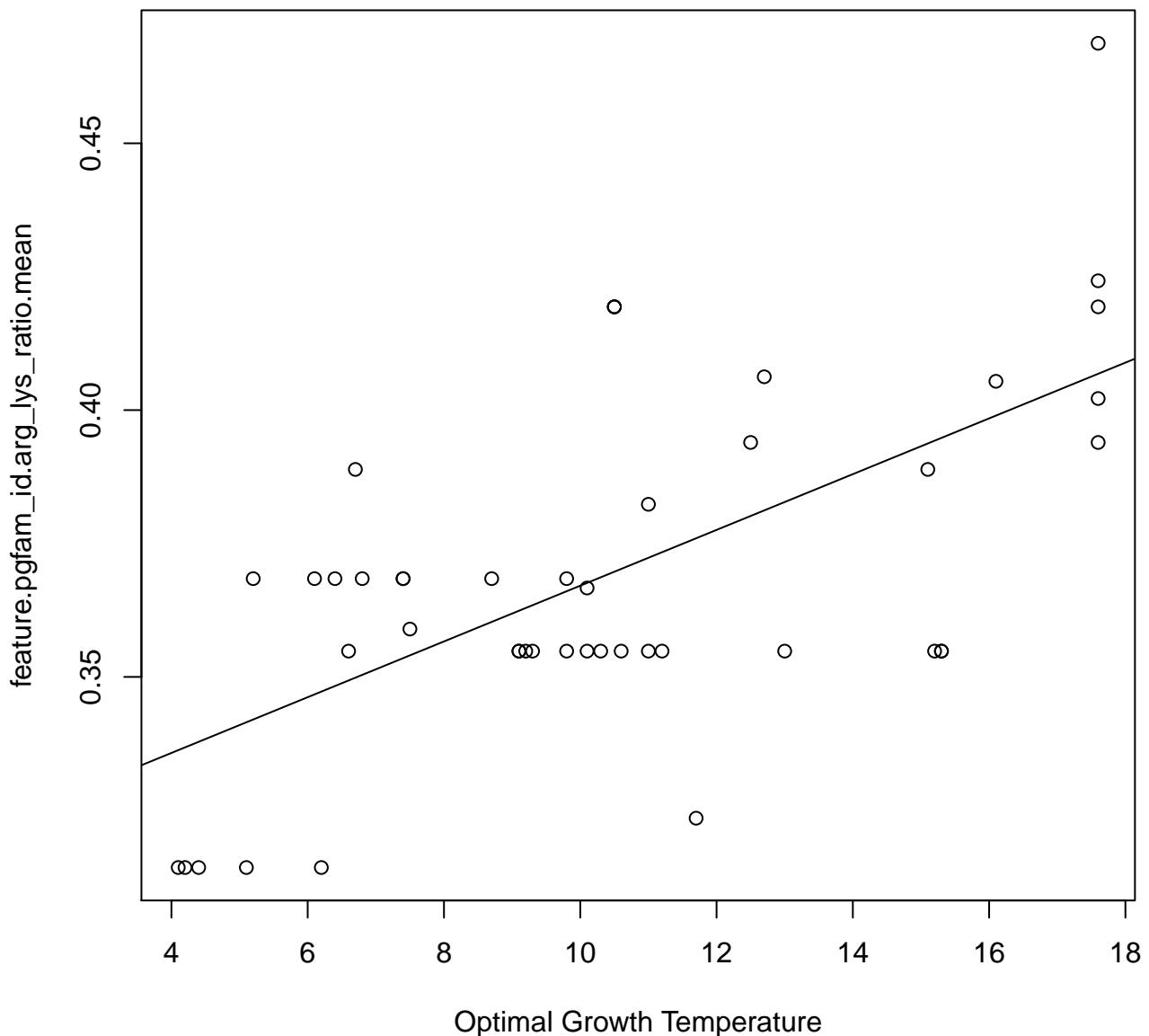
feature.pgfam_id.arg_lys_ratio.mean
PGF_01900675
Flagellar motor switch protein FliM



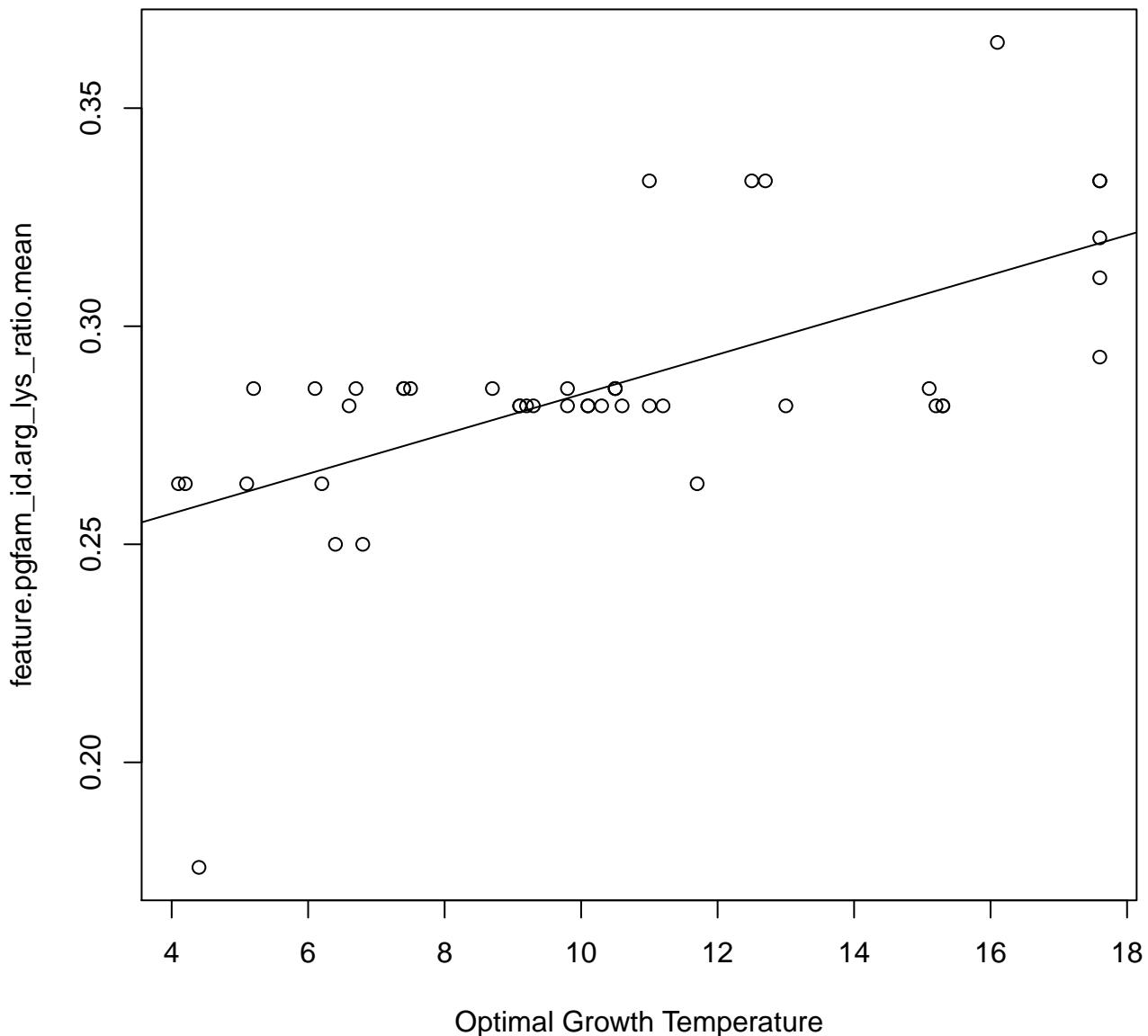
feature.pgfam_id.arg_lys_ratio.mean
PGF_05621995
Prolipoprotein diacylglycerol transferase



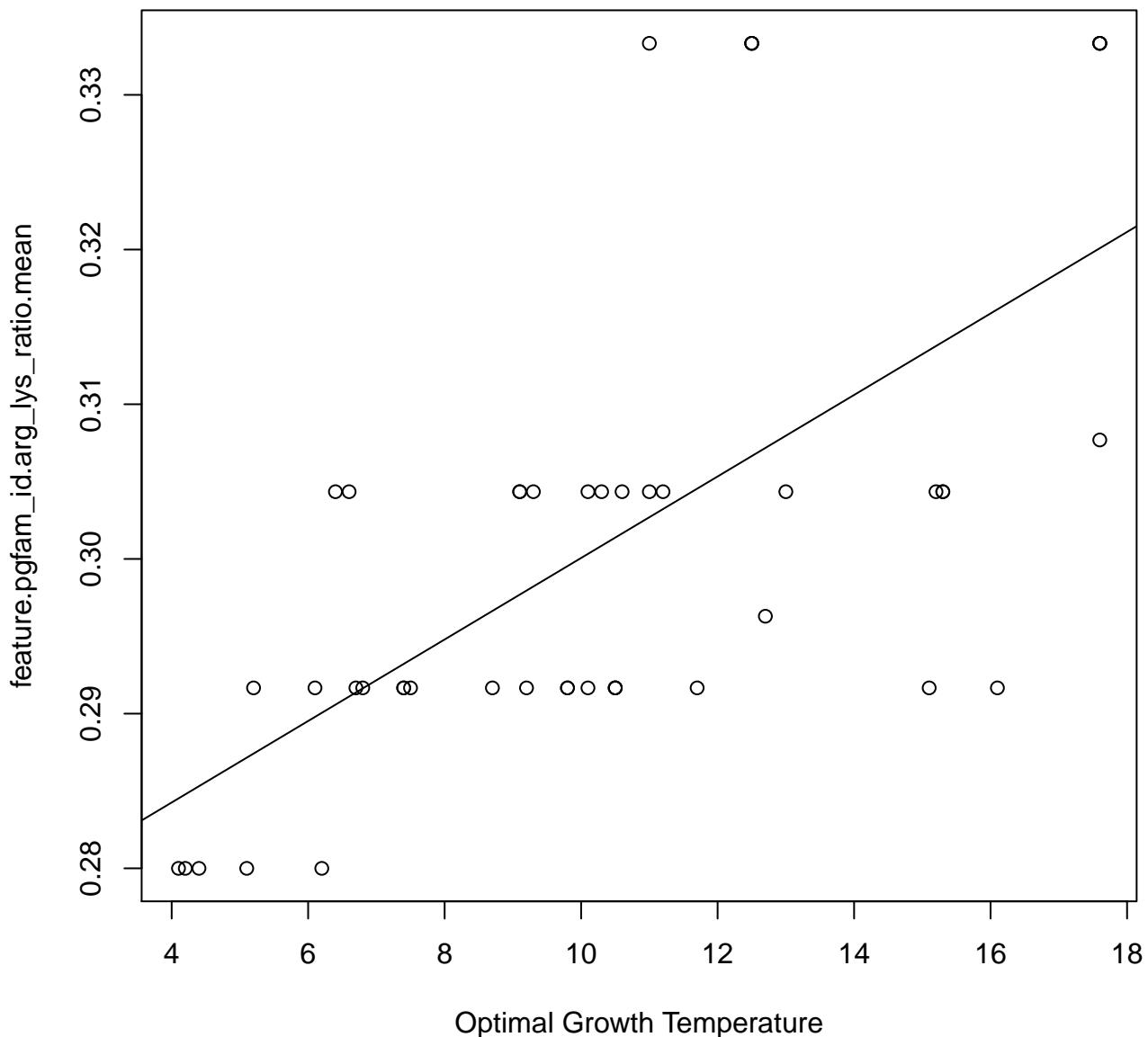
feature.pgfam_id.arg_lys_ratio.mean
PGF_06404031
Proline dipeptidase



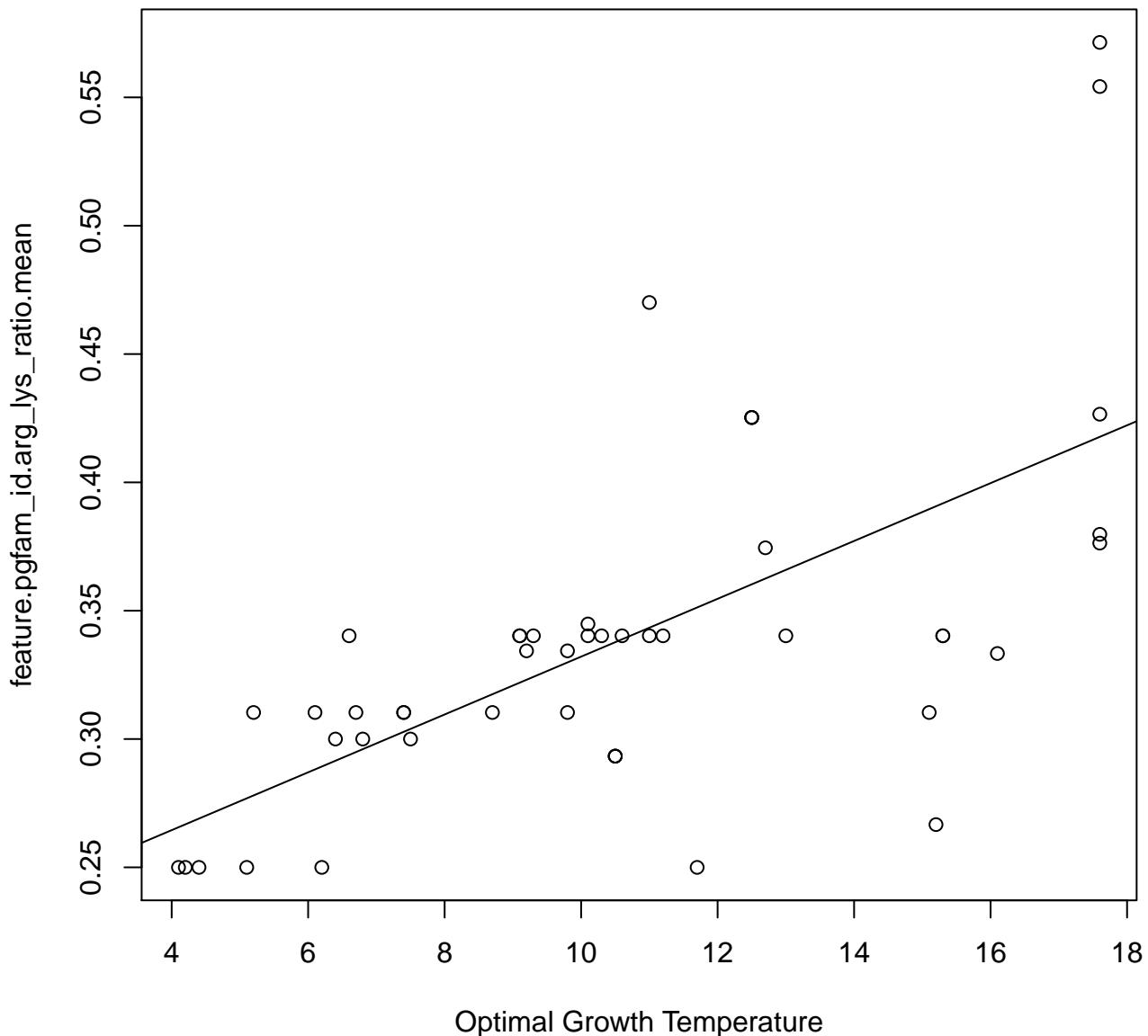
feature.pgfam_id.arg_lys_ratio.mean
PGF_02690675
RidA/YER057c/UK114 superfamily protein



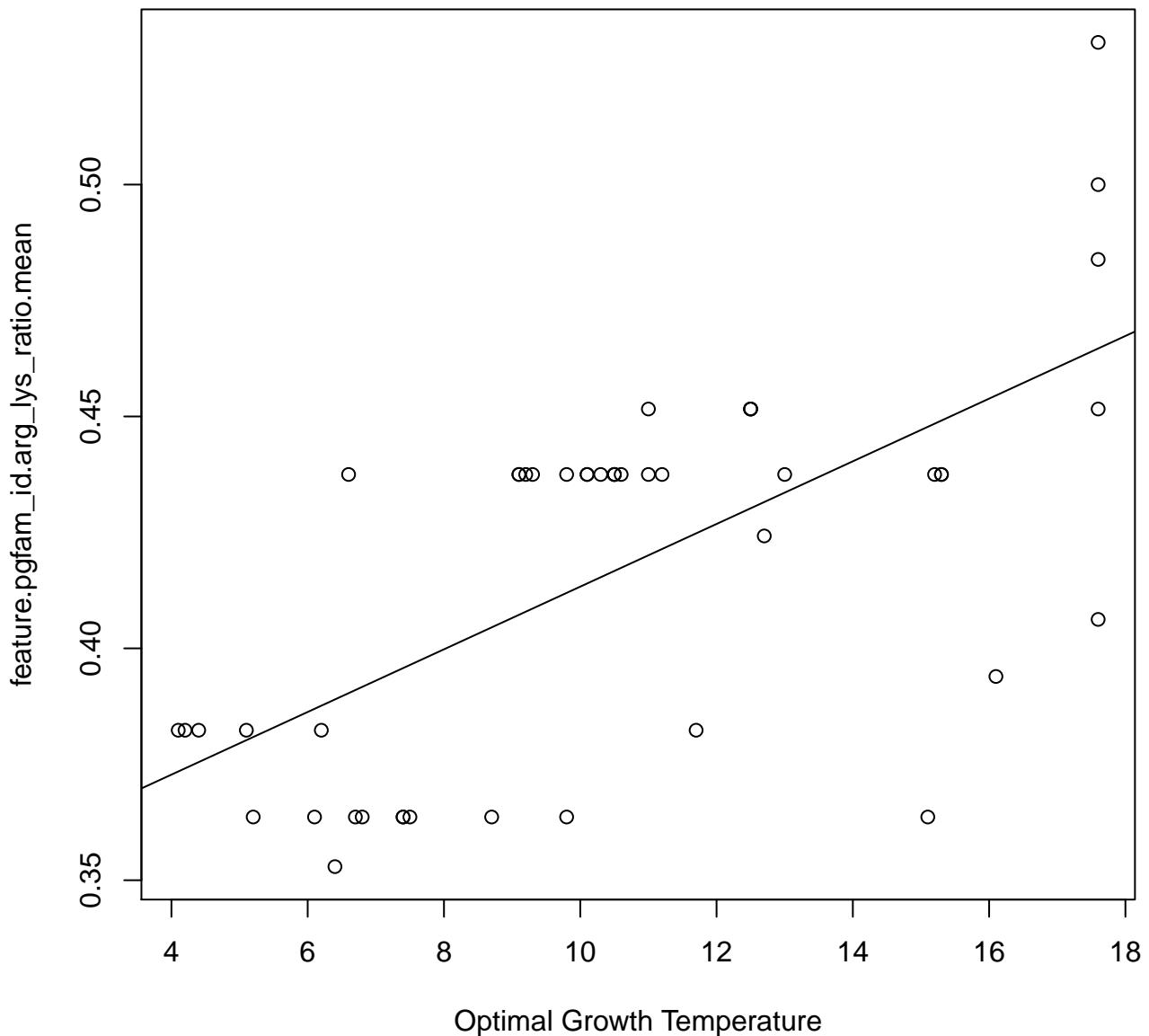
feature.pgfam_id.arg_lys_ratio.mean
PGF_00018952
Malate dehydrogenase (EC 1.1.1.37)



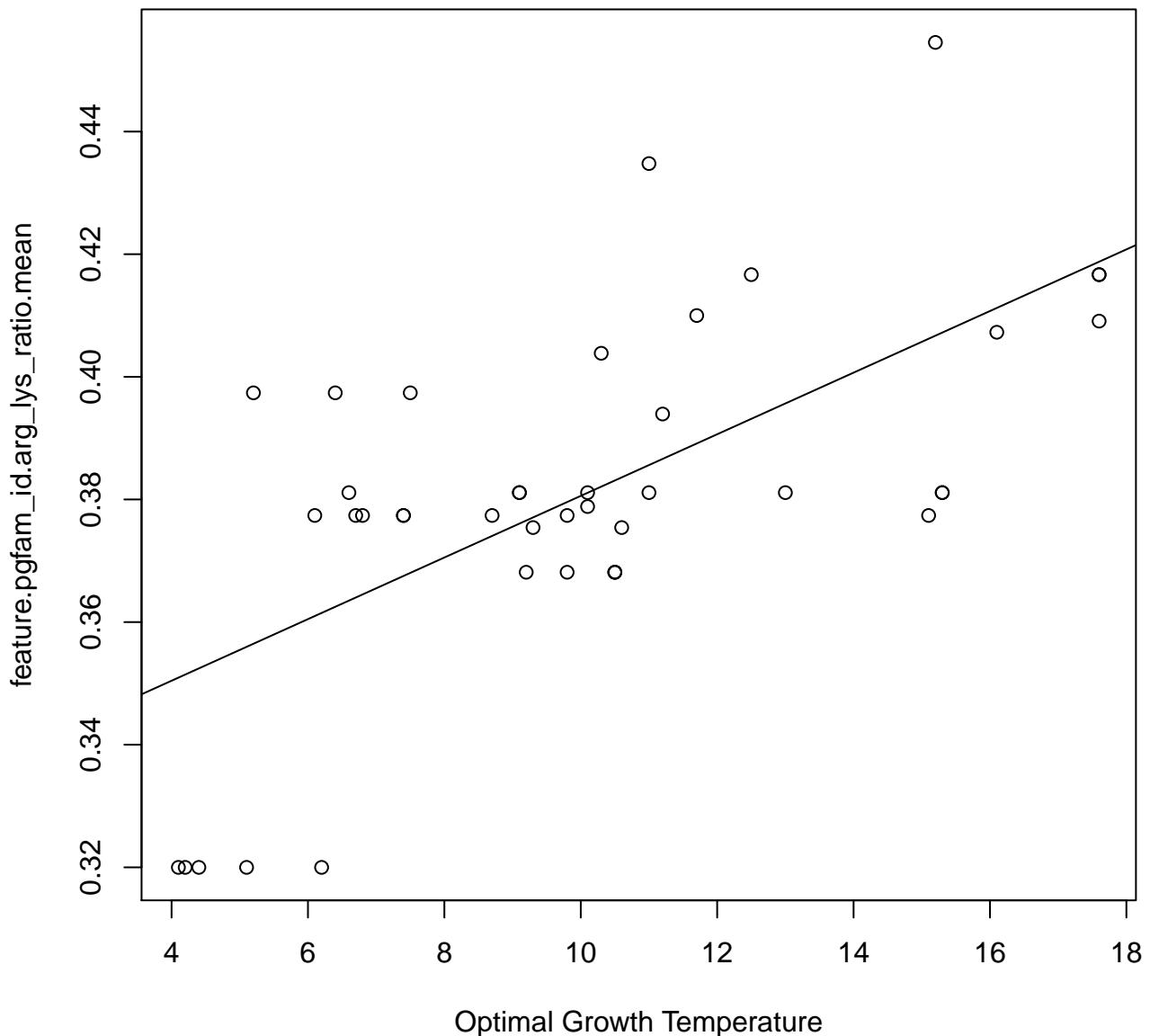
feature.pgfam_id.arg_lys_ratio.mean
PGF_00035194
Adenosine deaminase (EC 3.5.4.4)



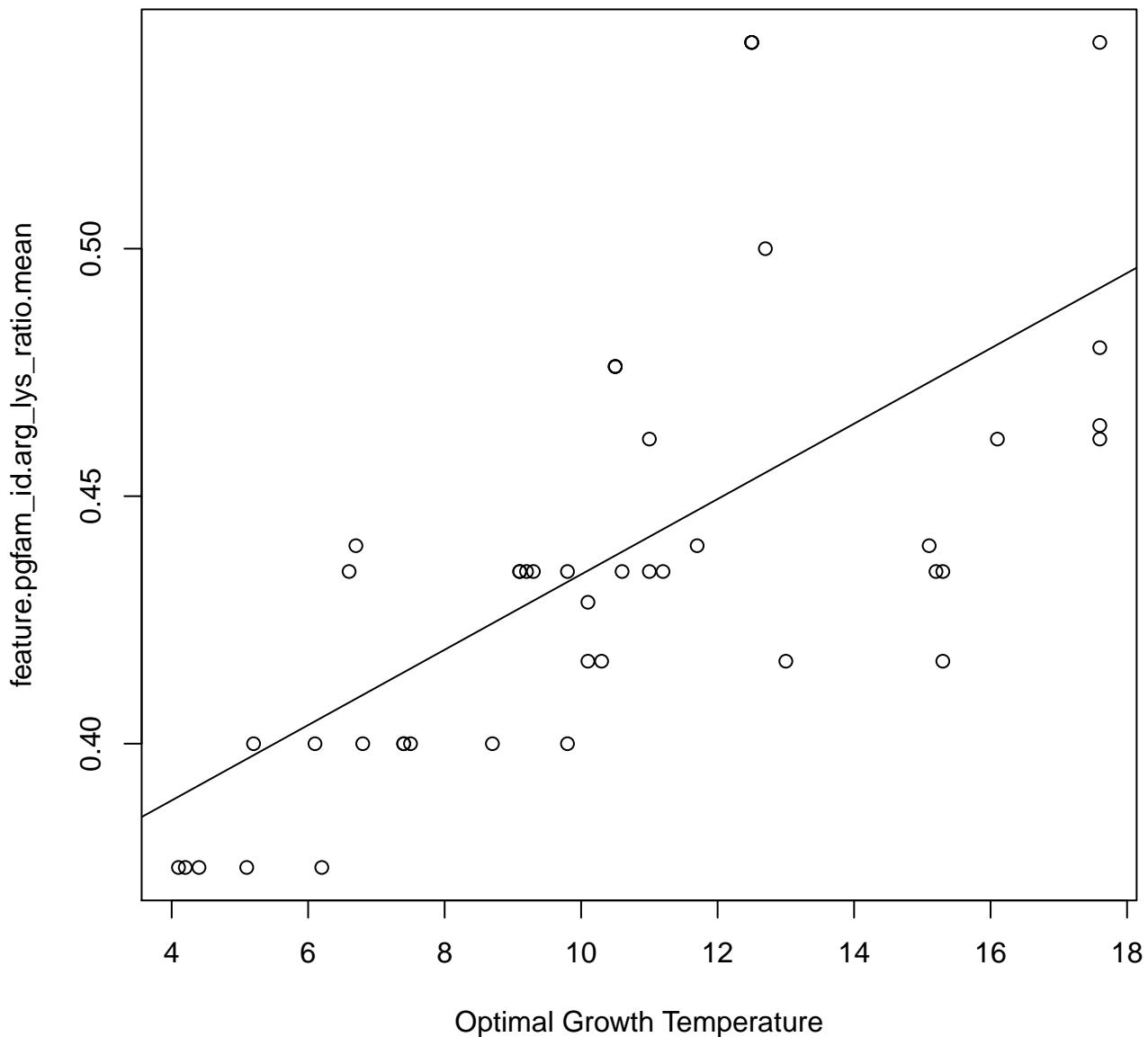
feature.pgfam_id.arg_lys_ratio.mean
PGF_01496598
Chemotaxis protein CheV (EC 2.7.3.-)



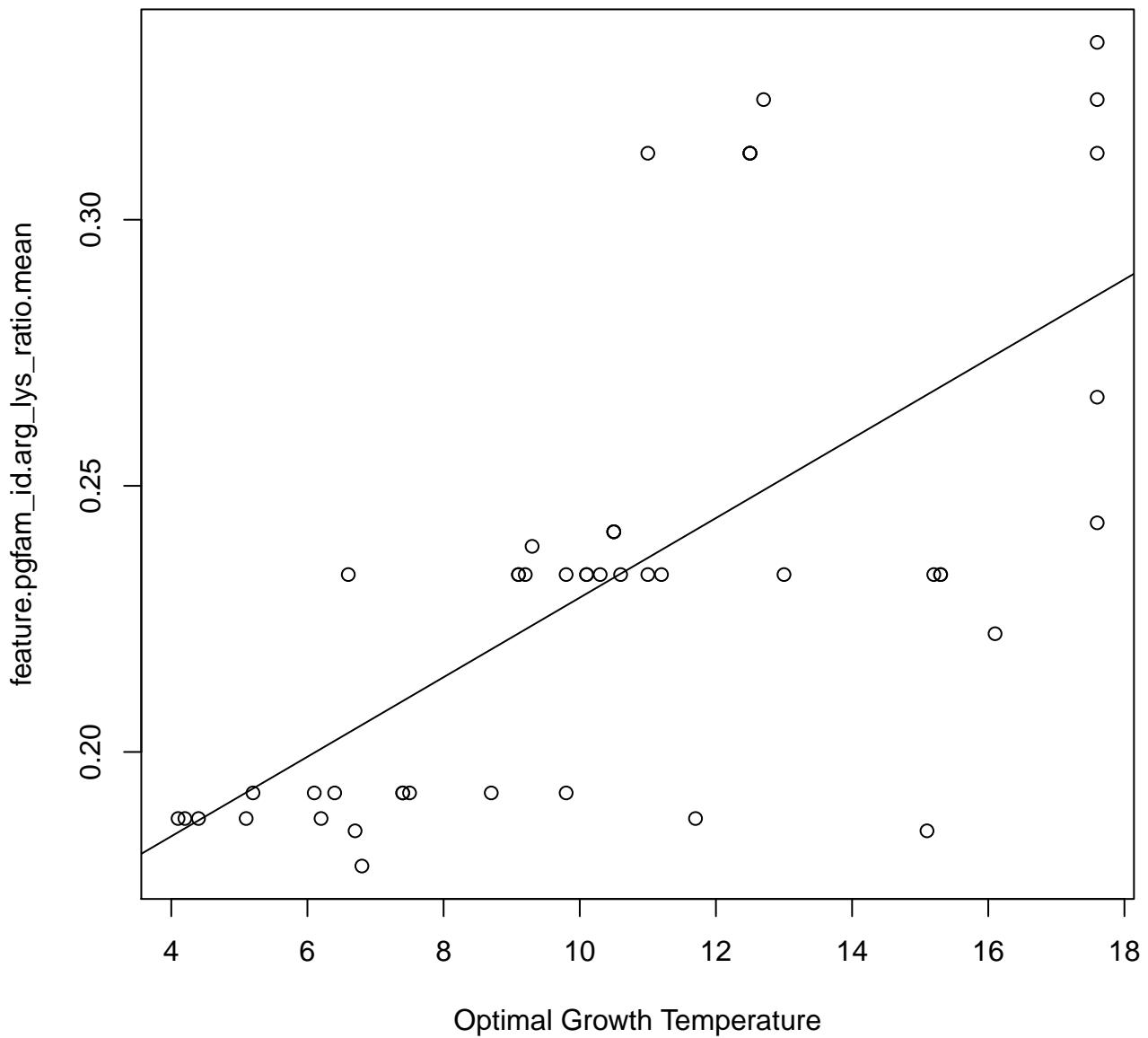
feature.pgfam_id.arg_lys_ratio.mean
PGF_07370053
RNA polymerase sigma-70 factor



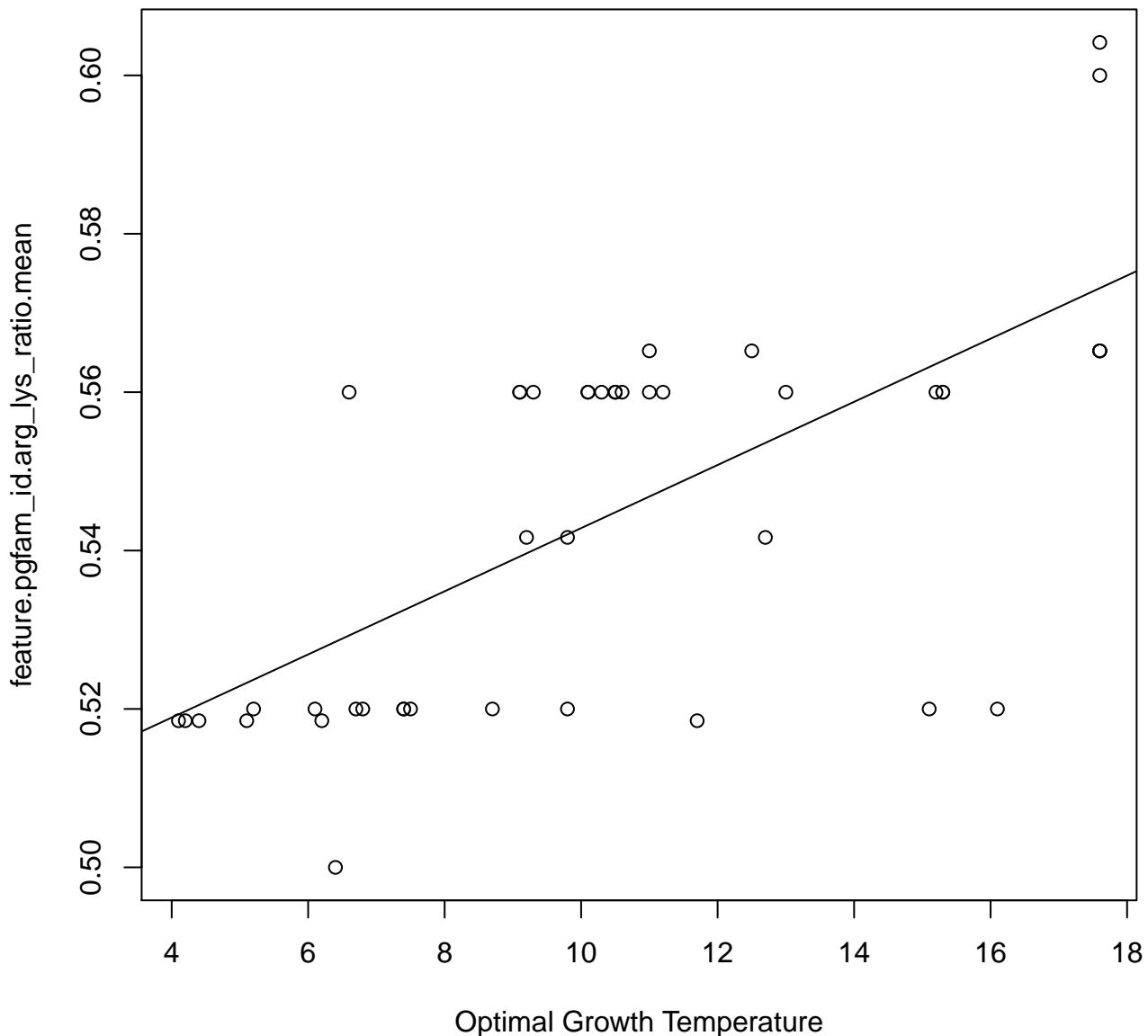
feature.pgfam_id.arg_lys_ratio.mean
PGF_01737958
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)



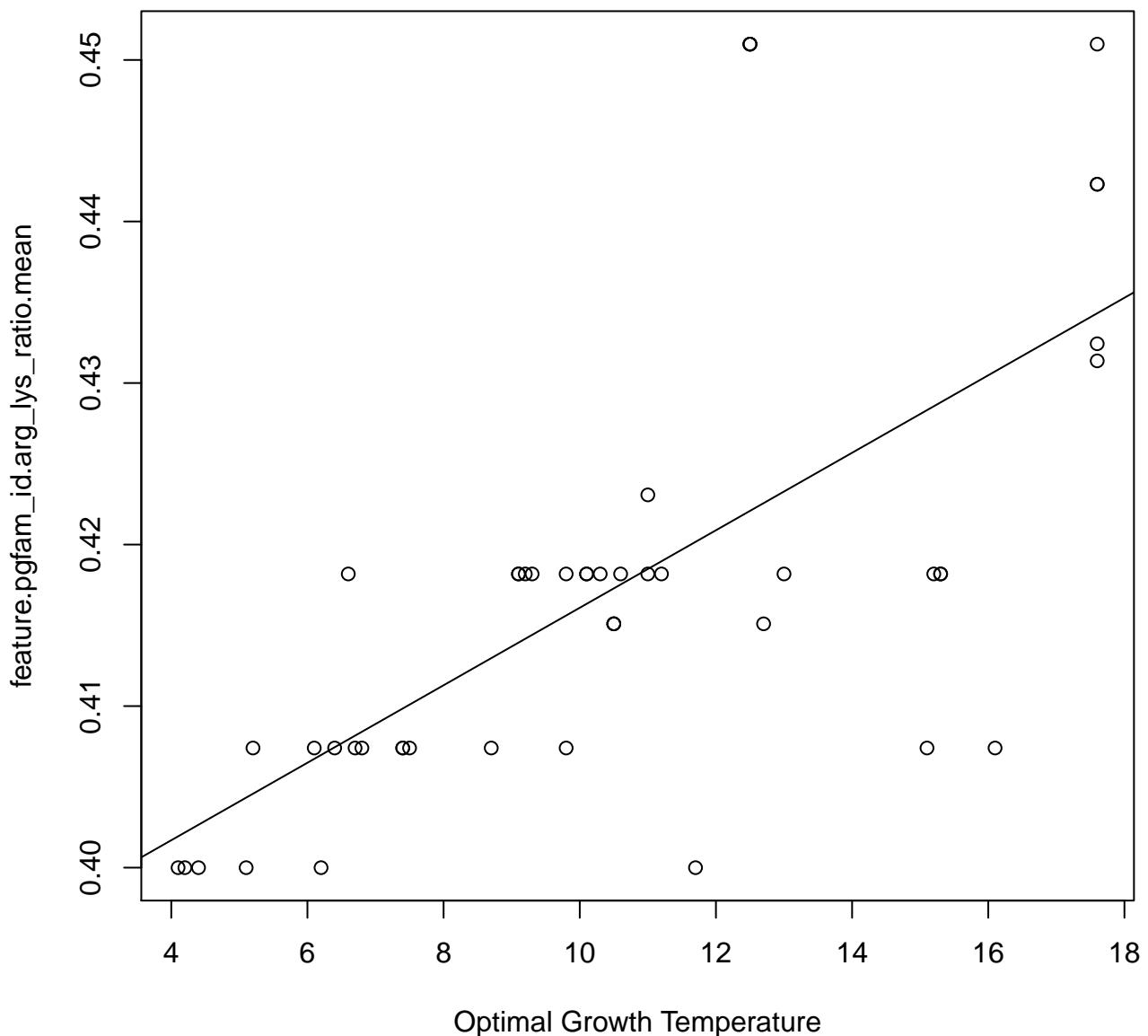
feature.pgfam_id.arg_lys_ratio.mean
PGF_00016850
Branched-chain amino acid dehydrogenase [deaminating] (EC 1.4.1.9)(EC 1.4.1.23)



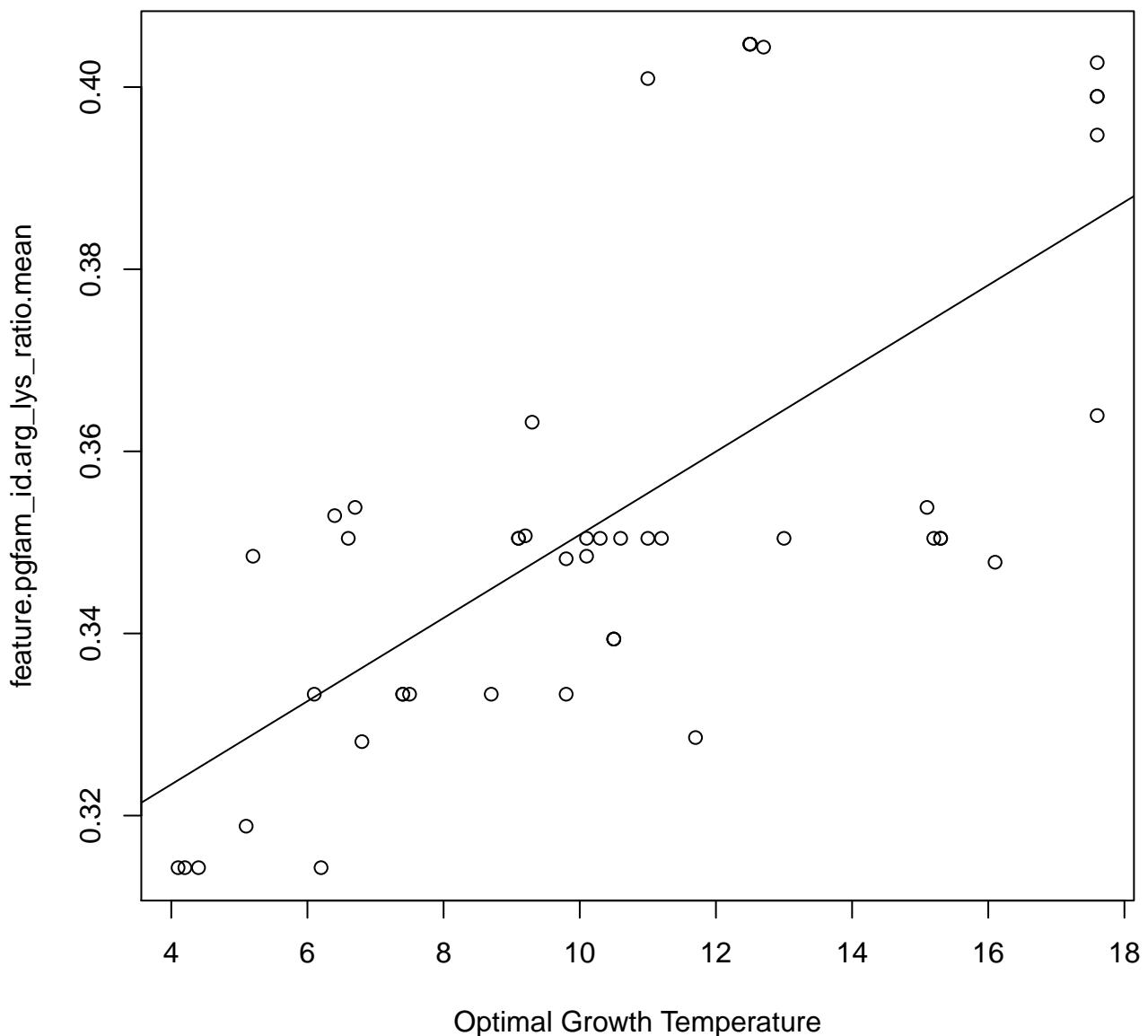
feature.pgfam_id.arg_lys_ratio.mean
PGF_10697445
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)



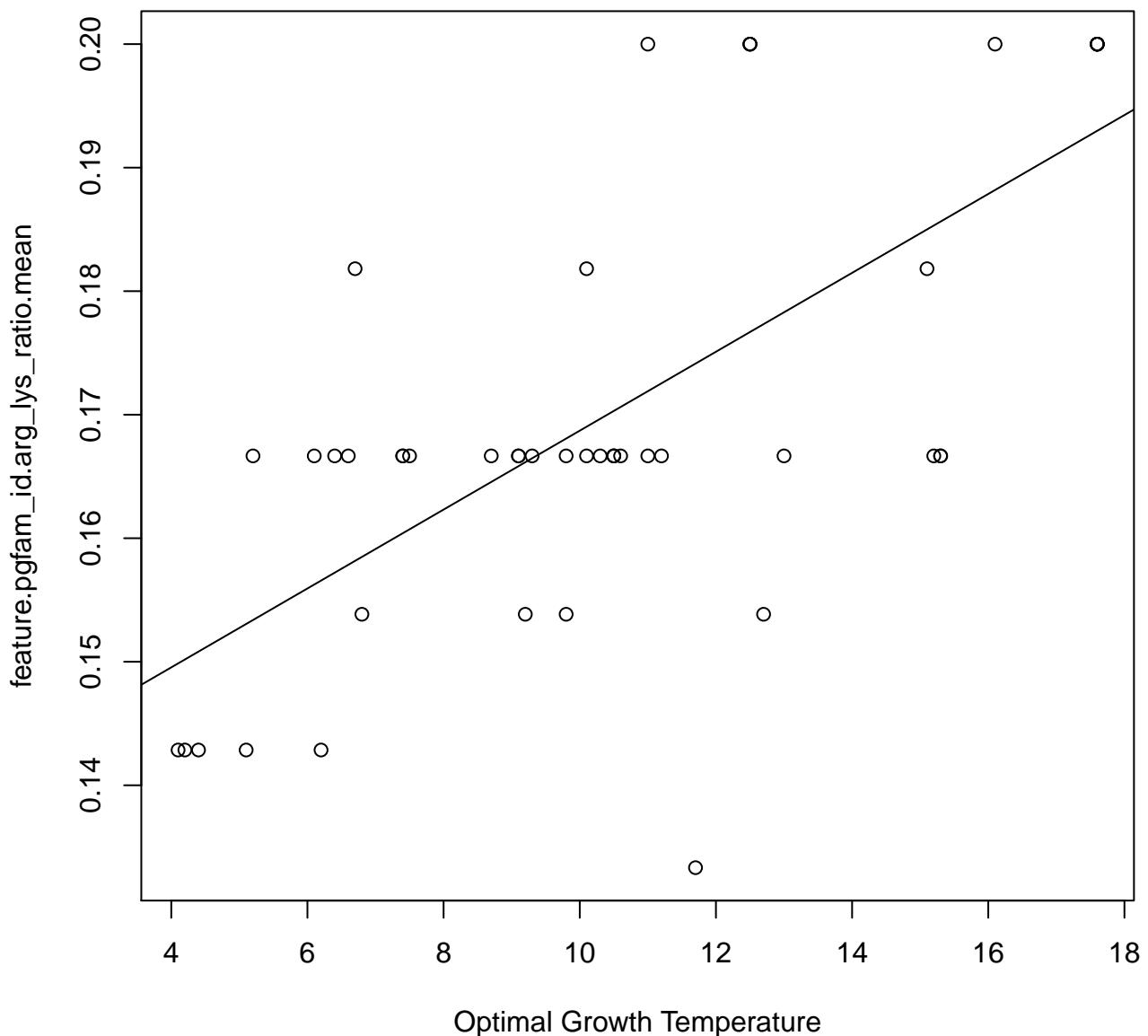
feature.pgfam_id.arg_lys_ratio.mean
PGF_00005384
Flagellar biosynthesis protein FlhA



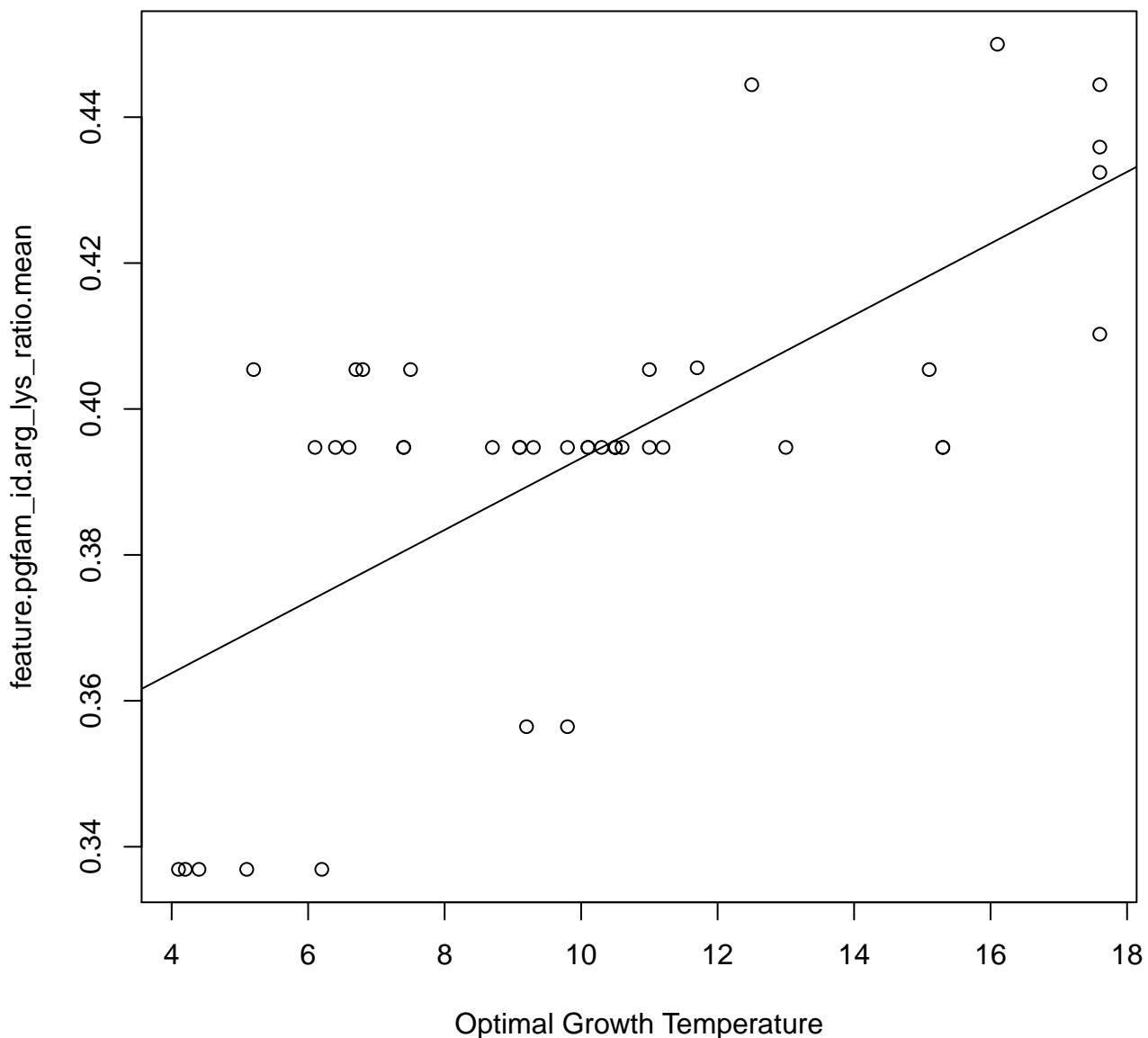
feature.pgfam_id.arg_lys_ratio.mean
PGF_00018965
Malate synthase G (EC 2.3.3.9)



feature.pgfam_id.arg_lys_ratio.mean
PGF_00059675
Antioxidant, AhpC/Tsa family



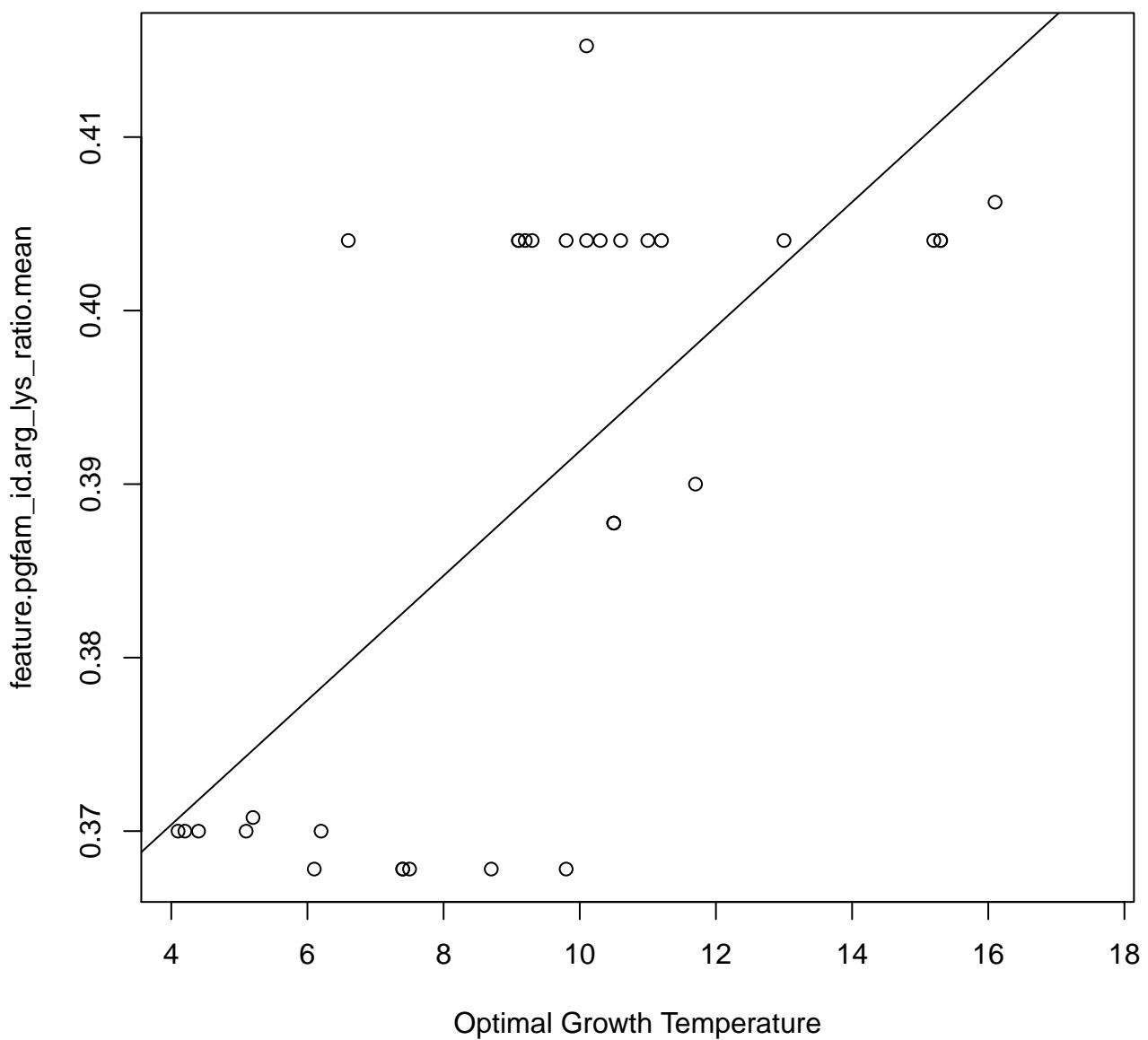
feature.pgfam_id.arg_lys_ratio.mean
PGF_02820072
aminotransferase, Class III pyridoxal-phosphate dependent



feature.pgfam_id.arg_lys_ratio.mean

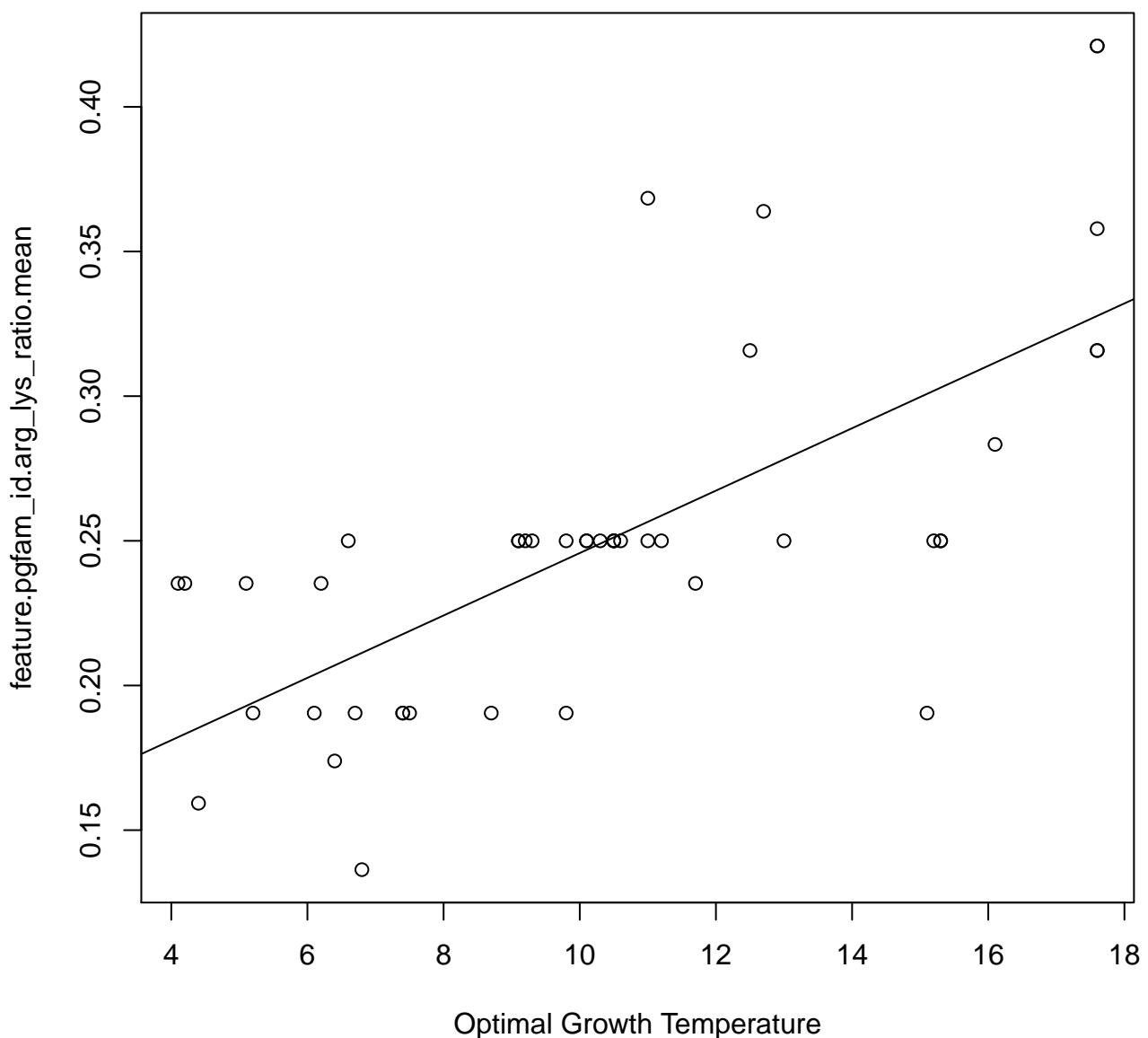
PGF_10437481

hypothetical protein

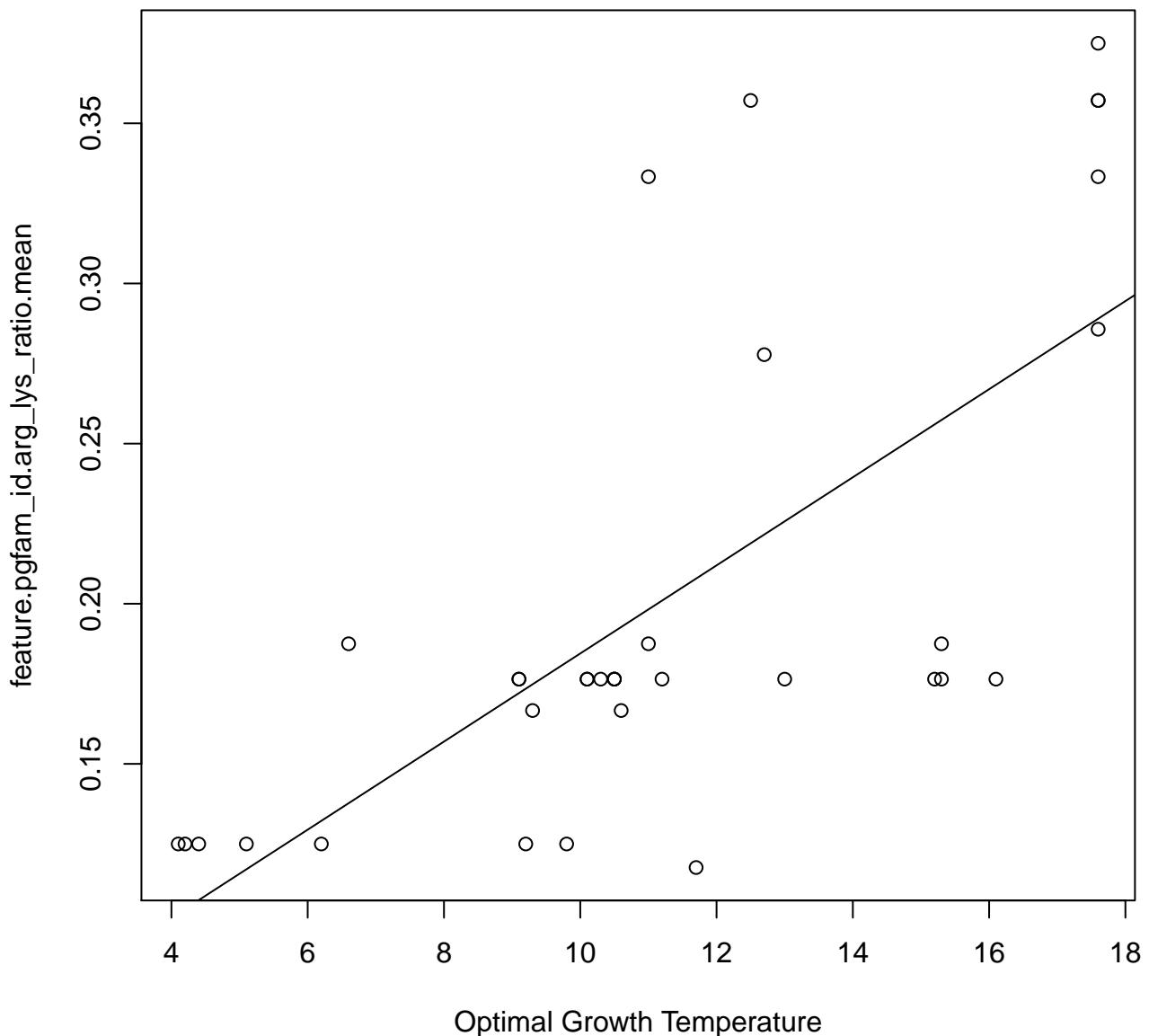


feature.pgfam_id.arg_lys_ratio.mean
PGF_08090639

Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, thiol-disulfide reductase involved in Cu(I) insertion into CoxII Cu(A) ce



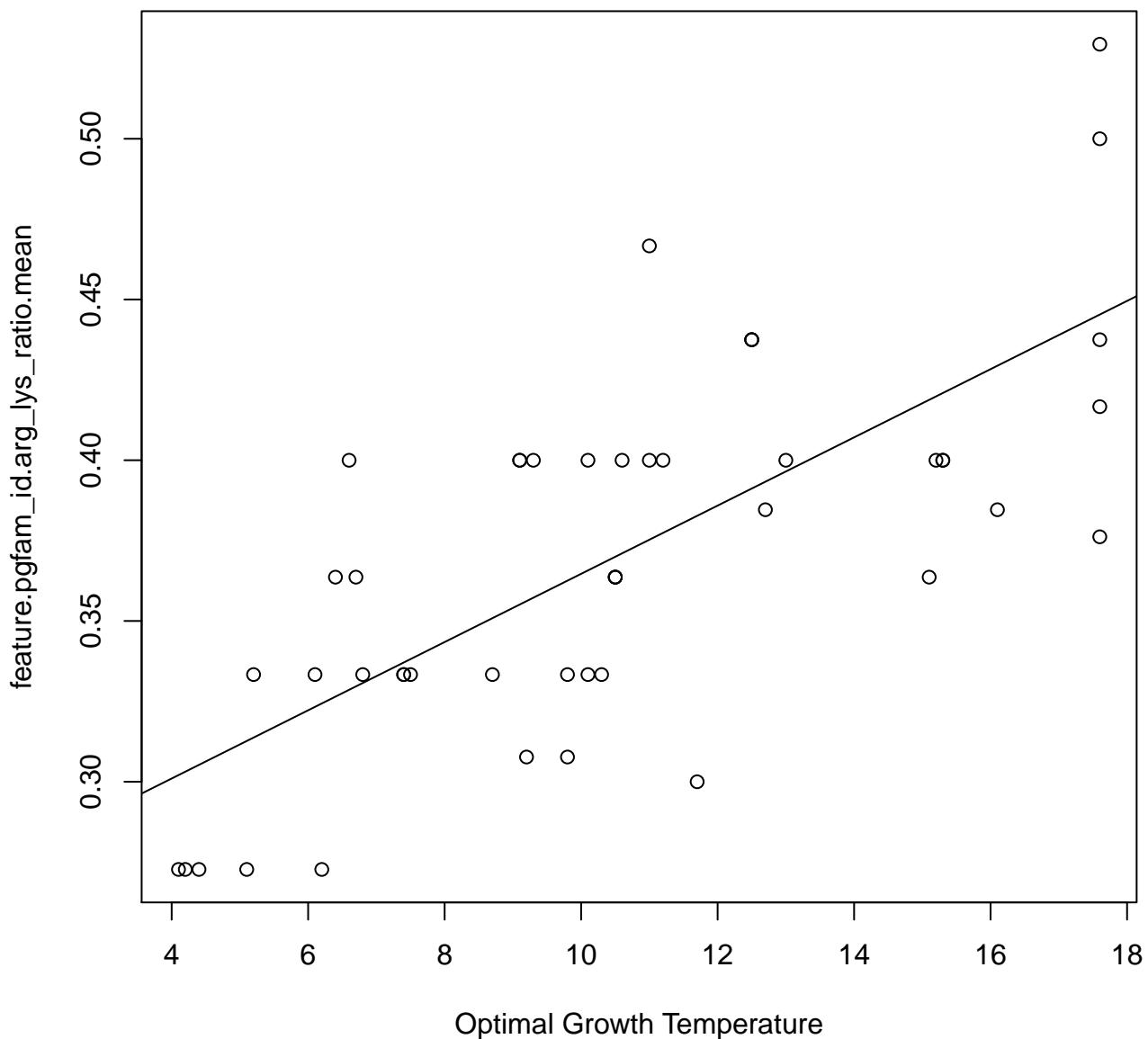
feature.pgfam_id.arg_lys_ratio.mean
PGF_03479908
General secretion pathway protein I



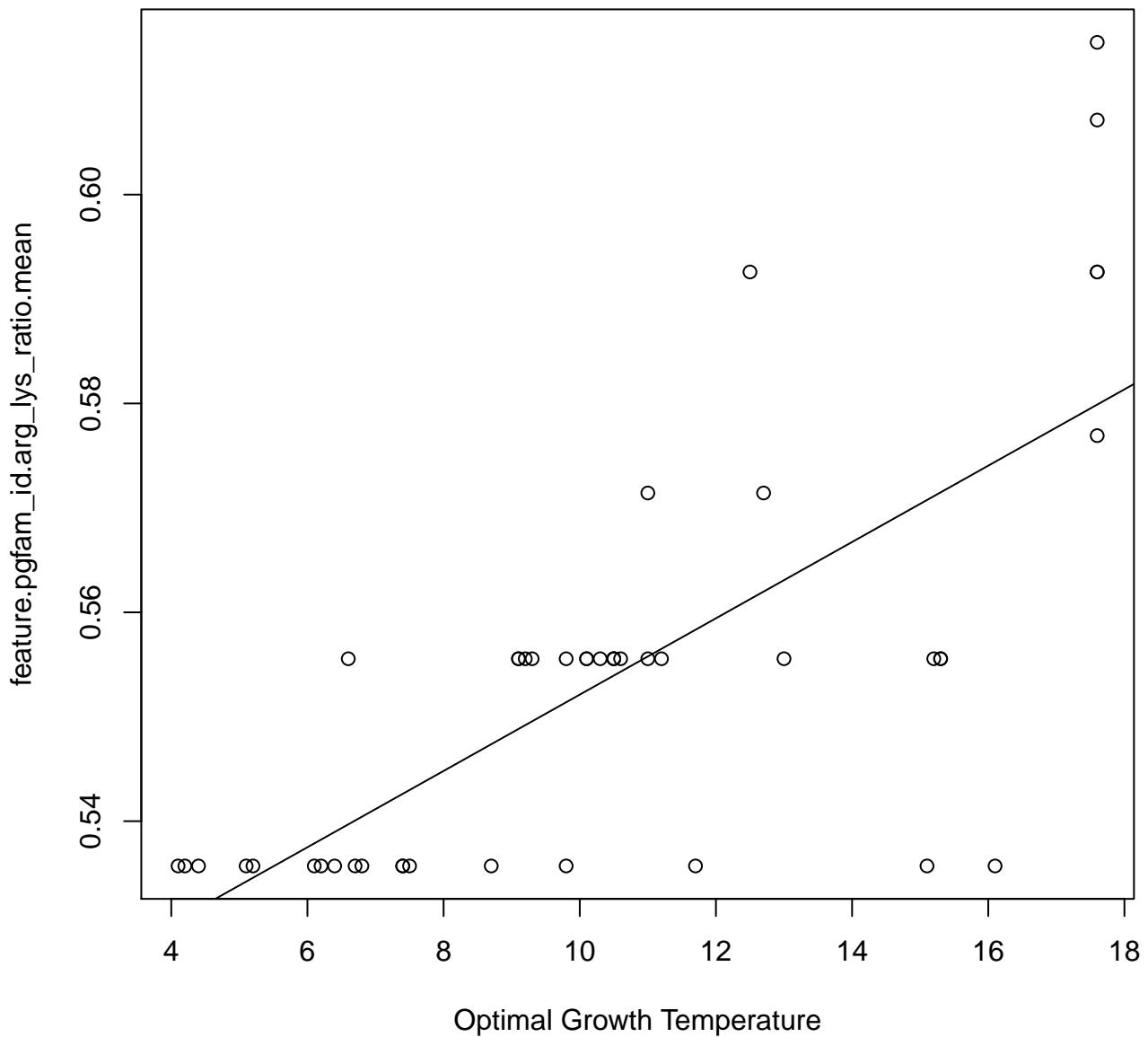
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PGF_00018430

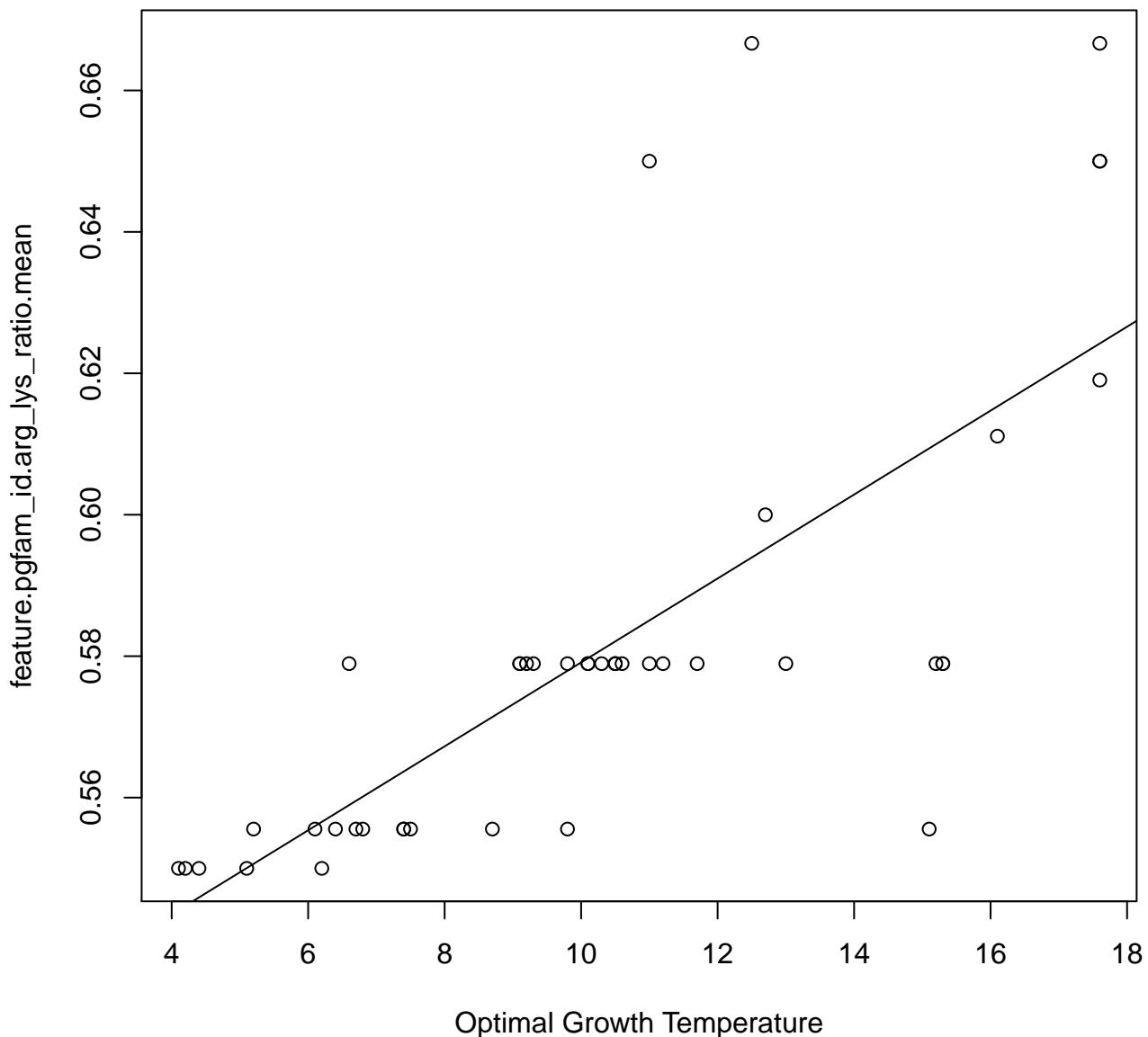
MSHA pilin protein MshB



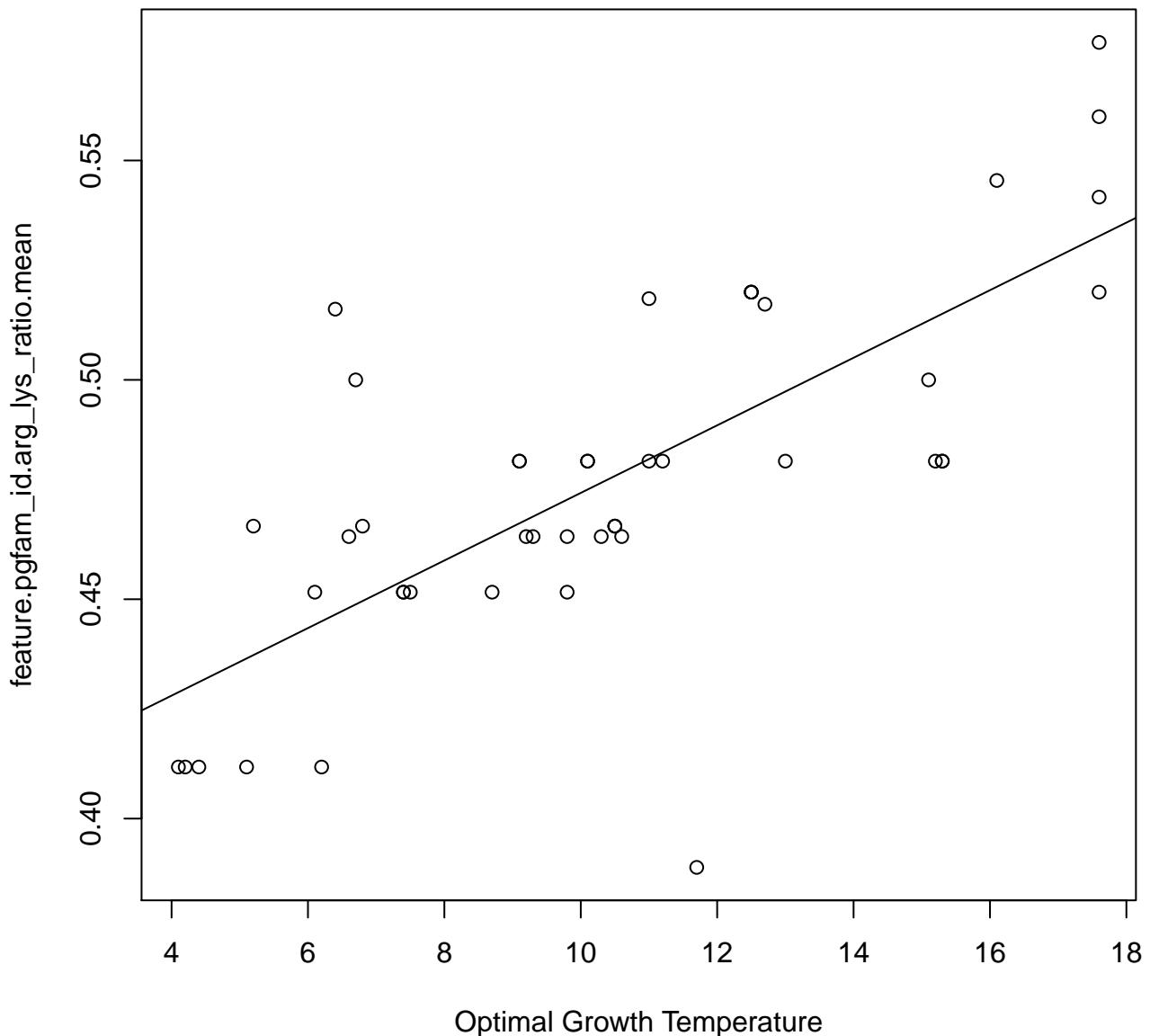
feature.pgfam_id.arg_lys_ratio.mean
PGF_00984073
Phosphate transport system regulatory protein PhoU



feature.pgfam_id.arg_lys_ratio.mean
PGF_03073036
hypothetical protein

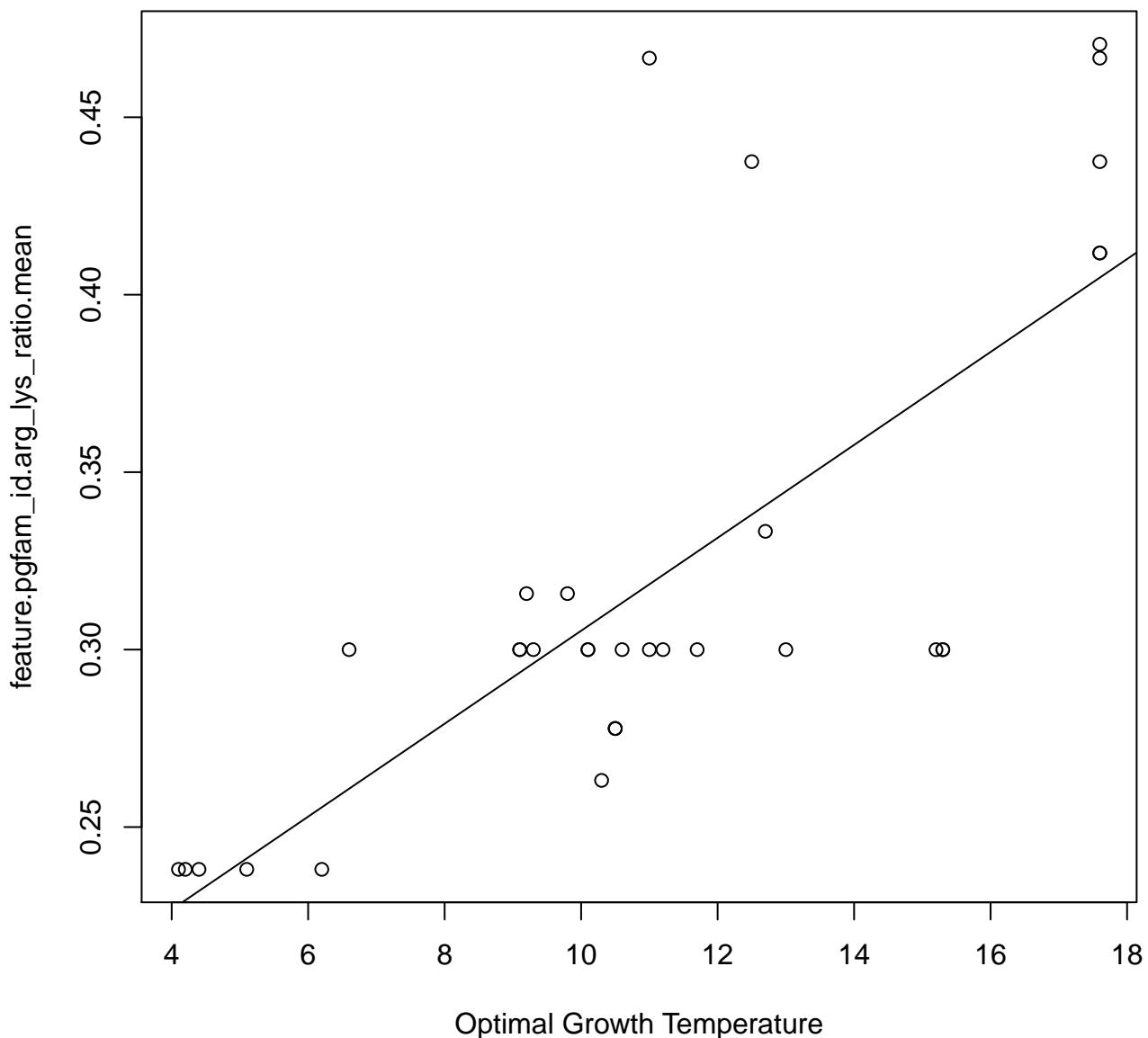


feature.pgfam_id.arg_lys_ratio.mean
PGF_01782190
3-deoxy-D-manno-octulose-4-phosphate kinase (EC 2.7.1.166)



feature.pgfam_id.arg_lys_ratio.mean
PGF_07191133

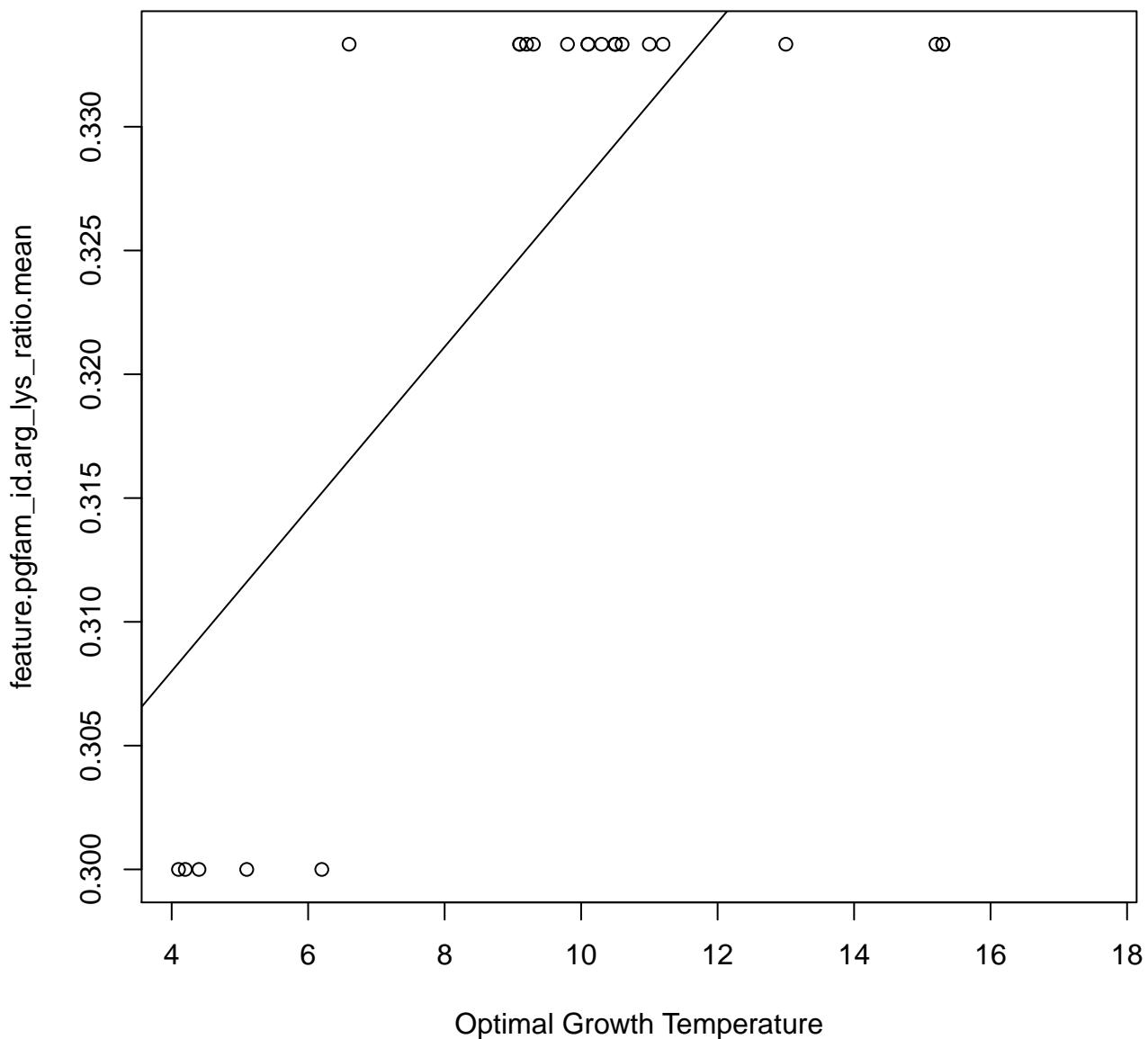
Similar to phosphoglycolate phosphatase, clustered with ribosomal large subunit pseudouridine synthase C



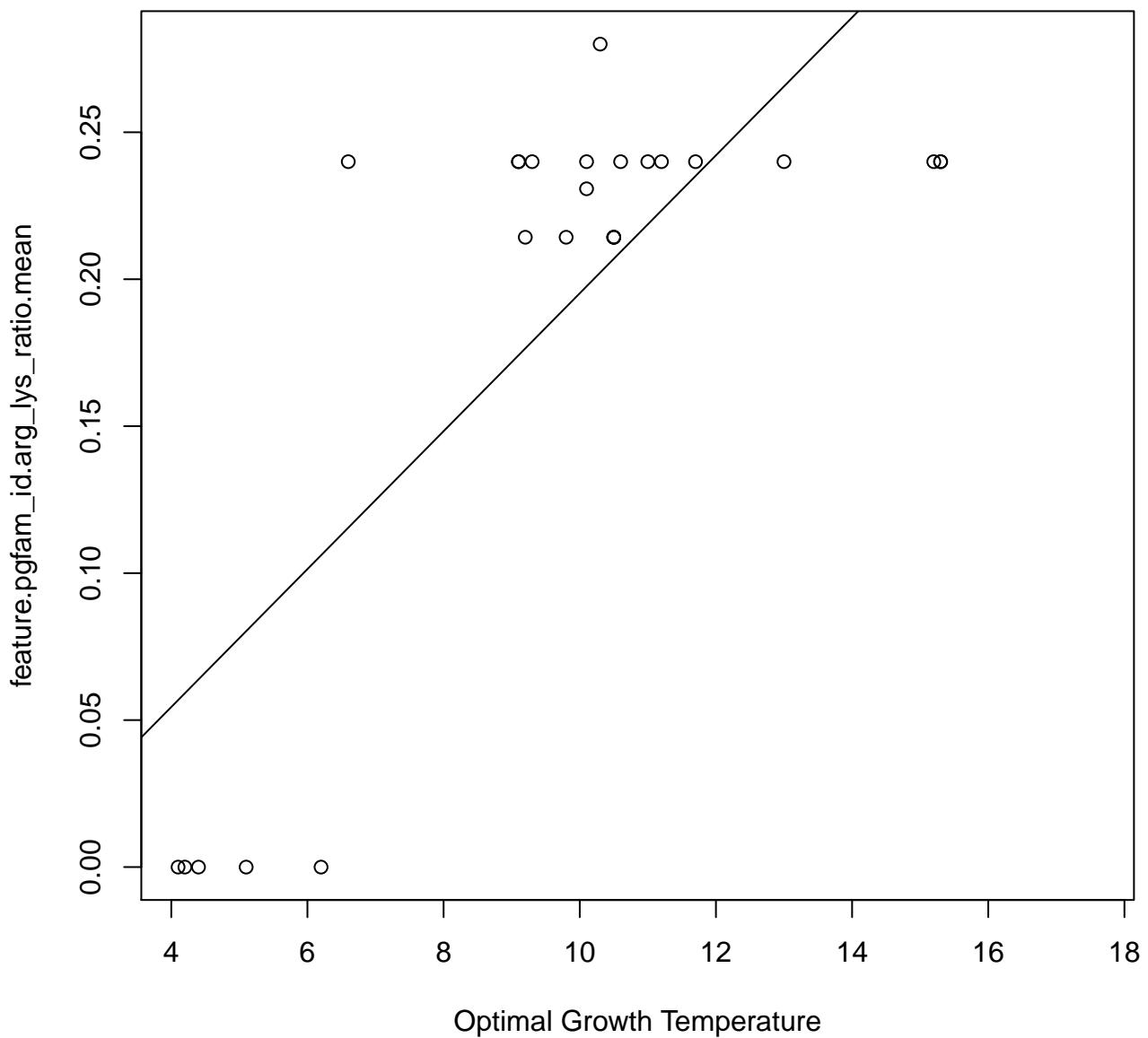
feature.pgfam_id.arg_lys_ratio.mean

PGF_12237460

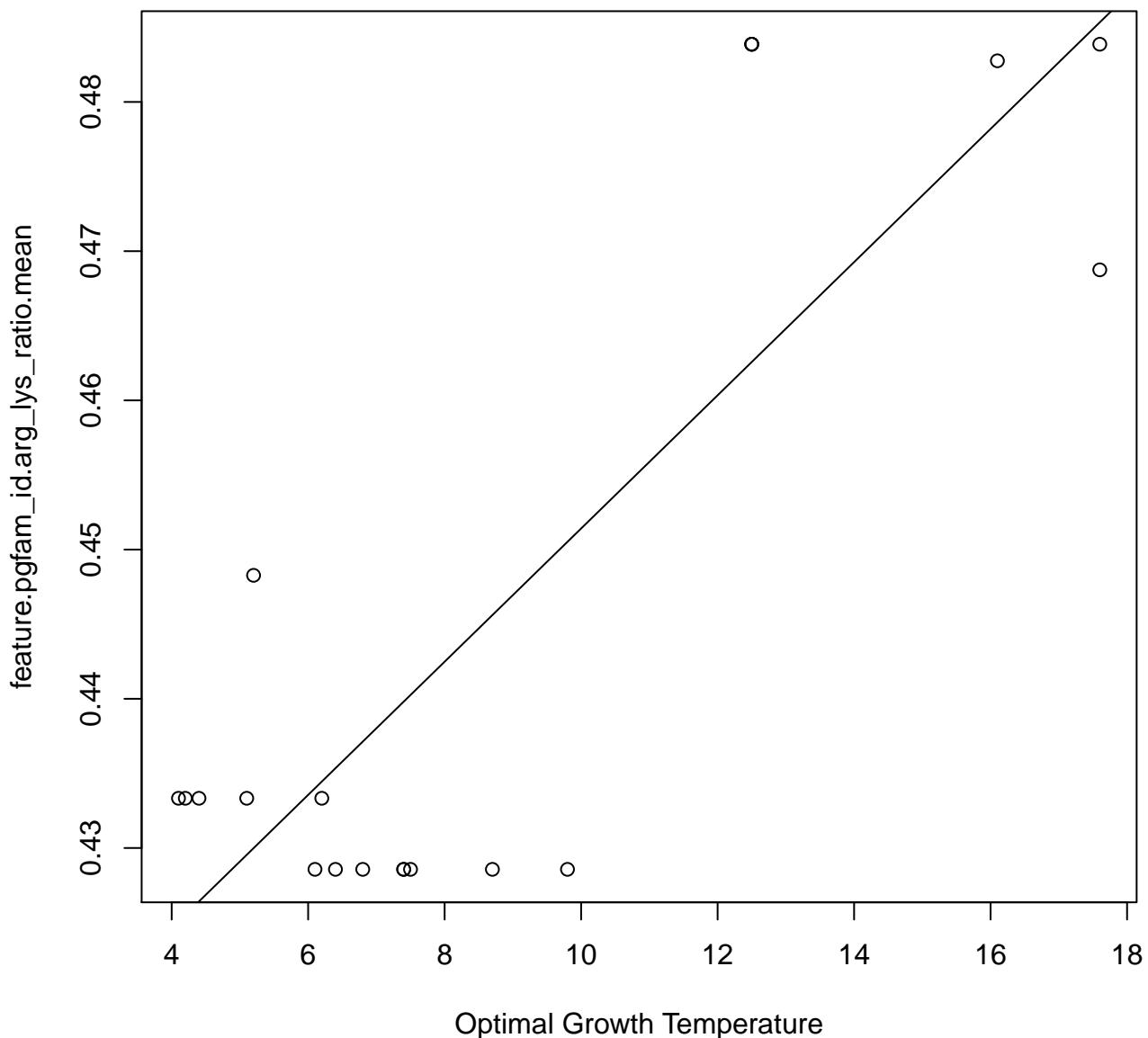
hypothetical protein



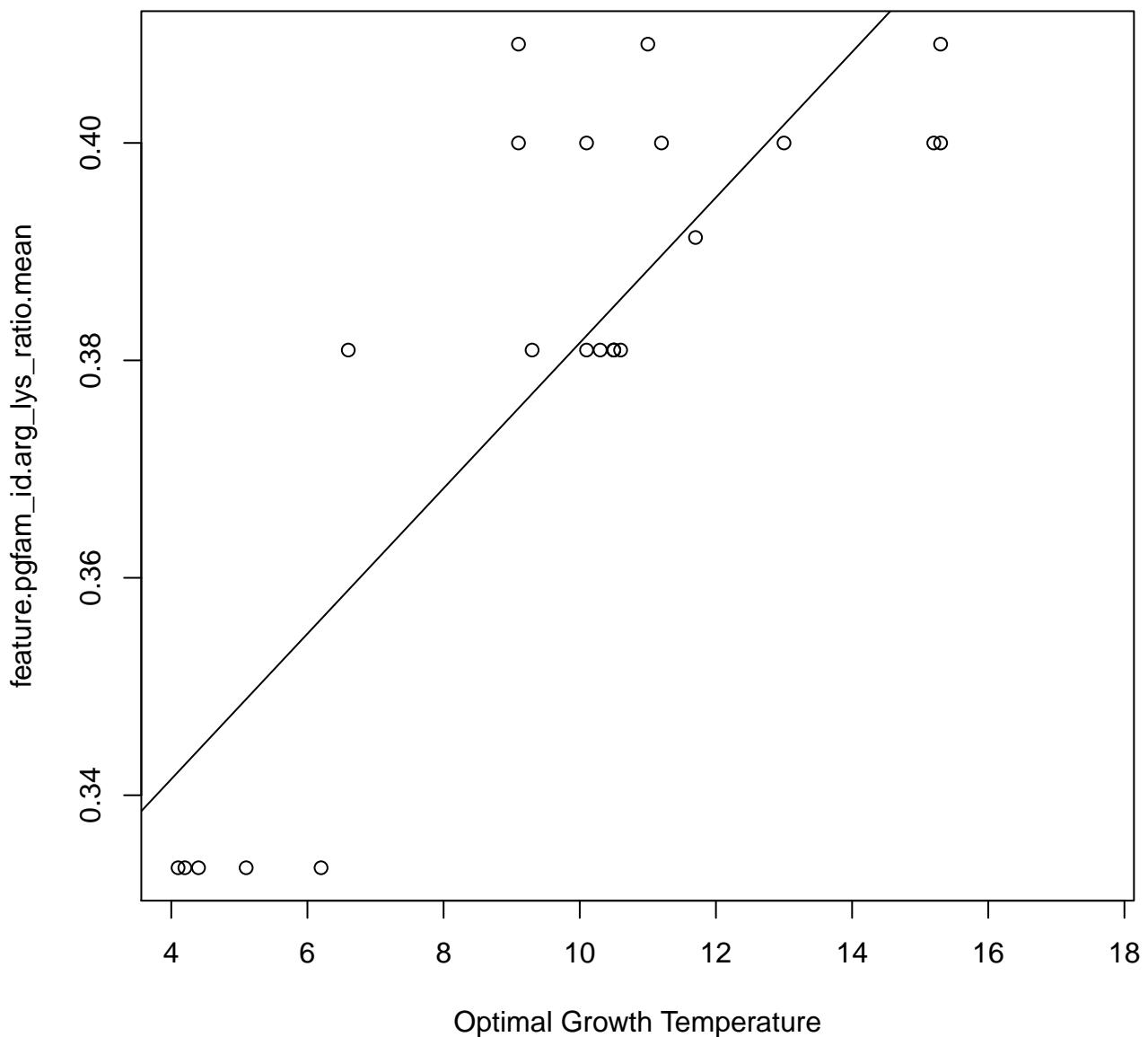
feature.pgfam_id.arg_lys_ratio.mean
PGF_11018774
hypothetical protein



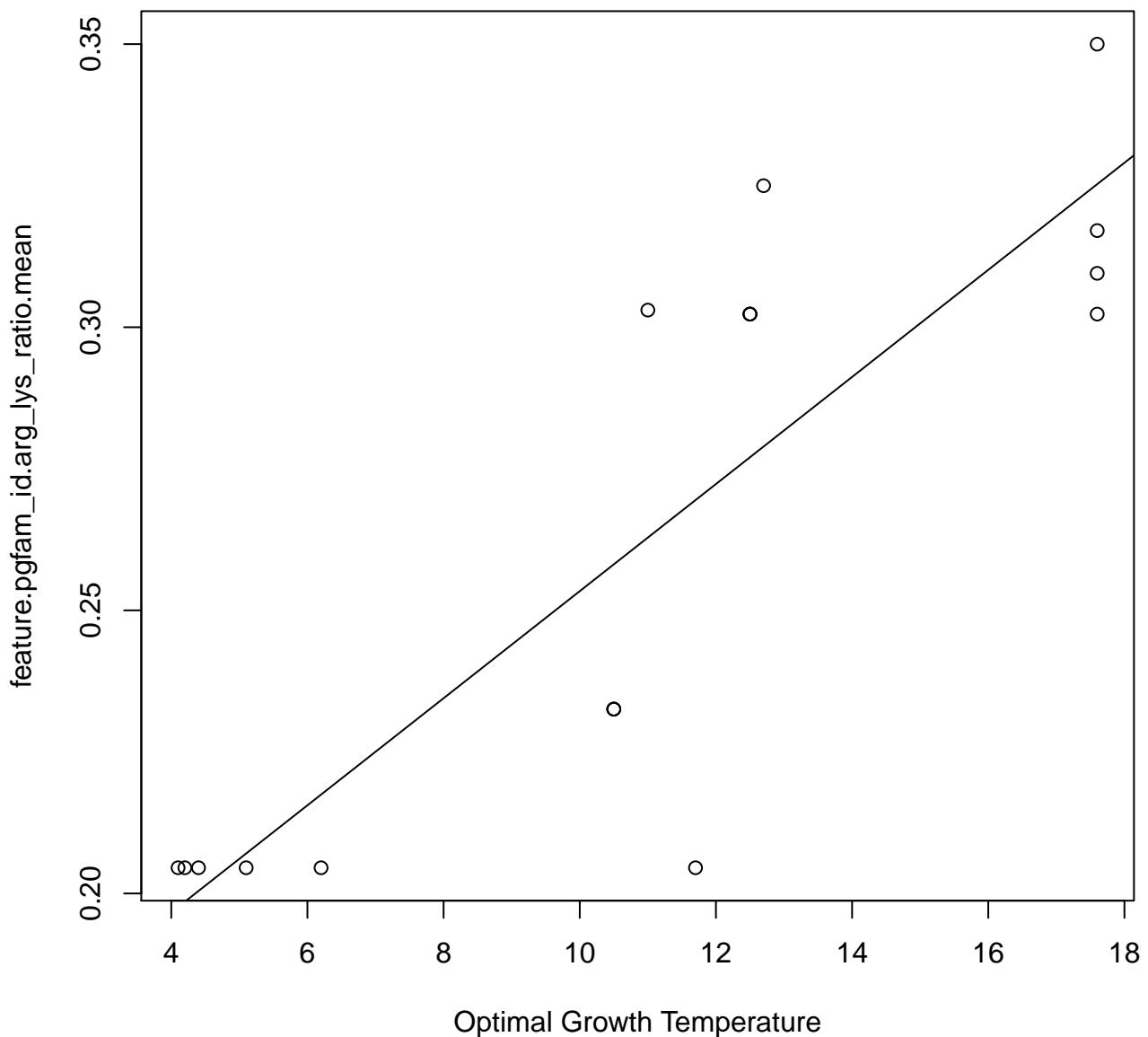
feature.pgfam_id.arg_lys_ratio.mean
PGF_02732386
Glucose/mannose:H⁺ symporter GlcP



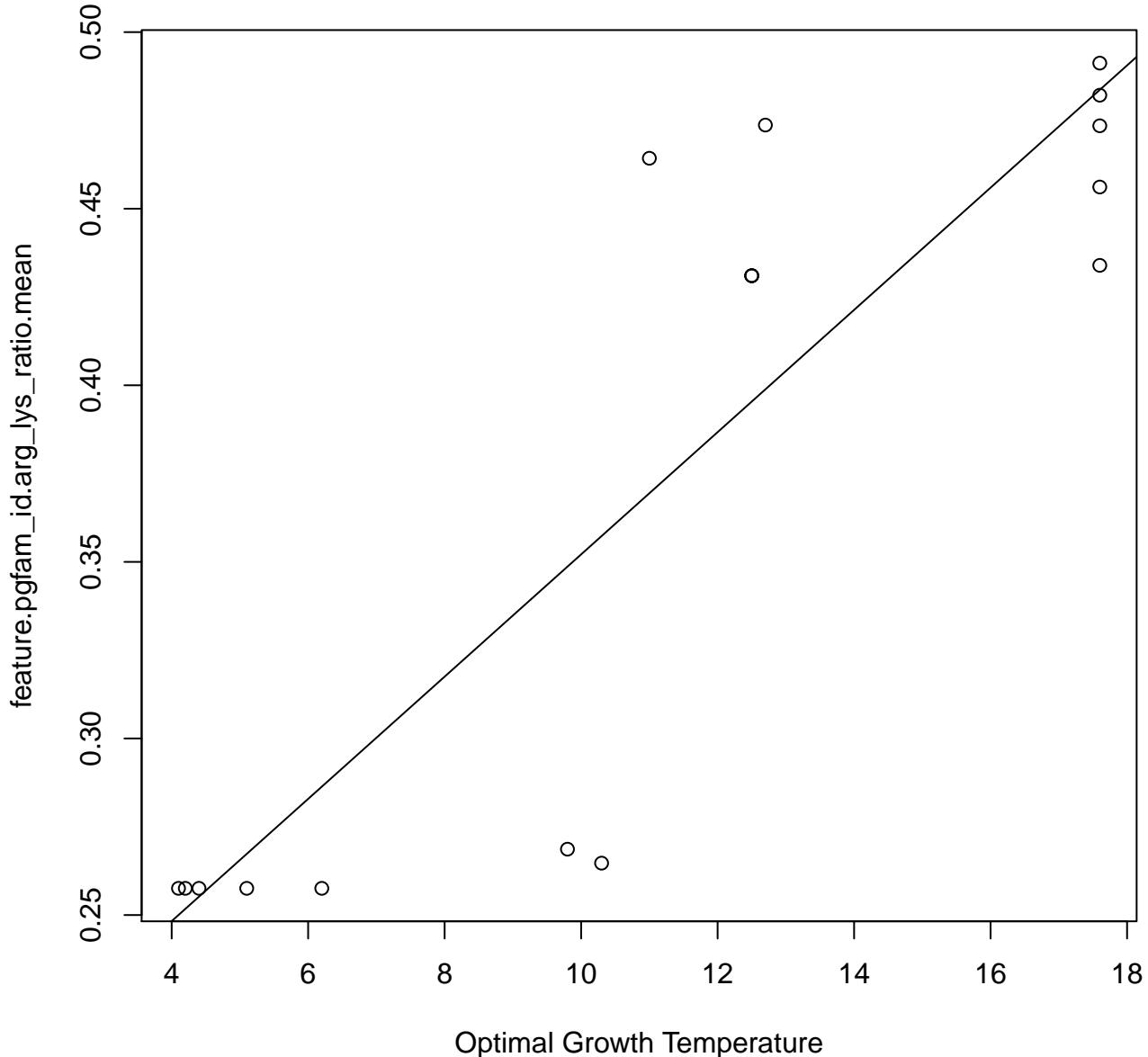
feature.pgfam_id.arg_lys_ratio.mean
PGF_08025863
hypothetical protein



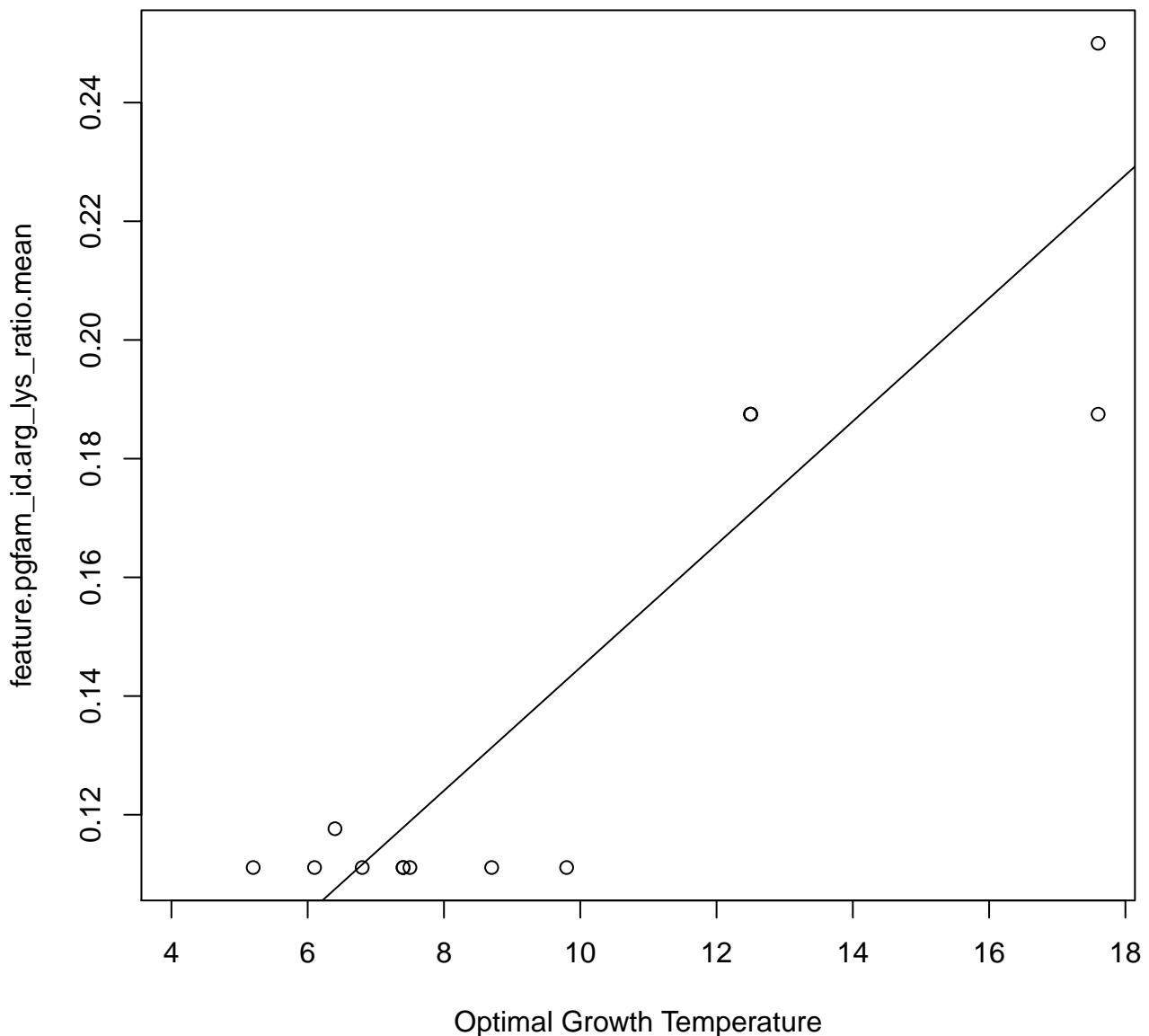
feature.pgfam_id.arg_lys_ratio.mean
PGF_00043931
Allantoinase (EC 3.5.2.5)



feature.pgfam_id.arg_lys_ratio.mean
PGF_00018516
Macrolide-specific ABC-type efflux carrier (TC 3.A.1.122.1)



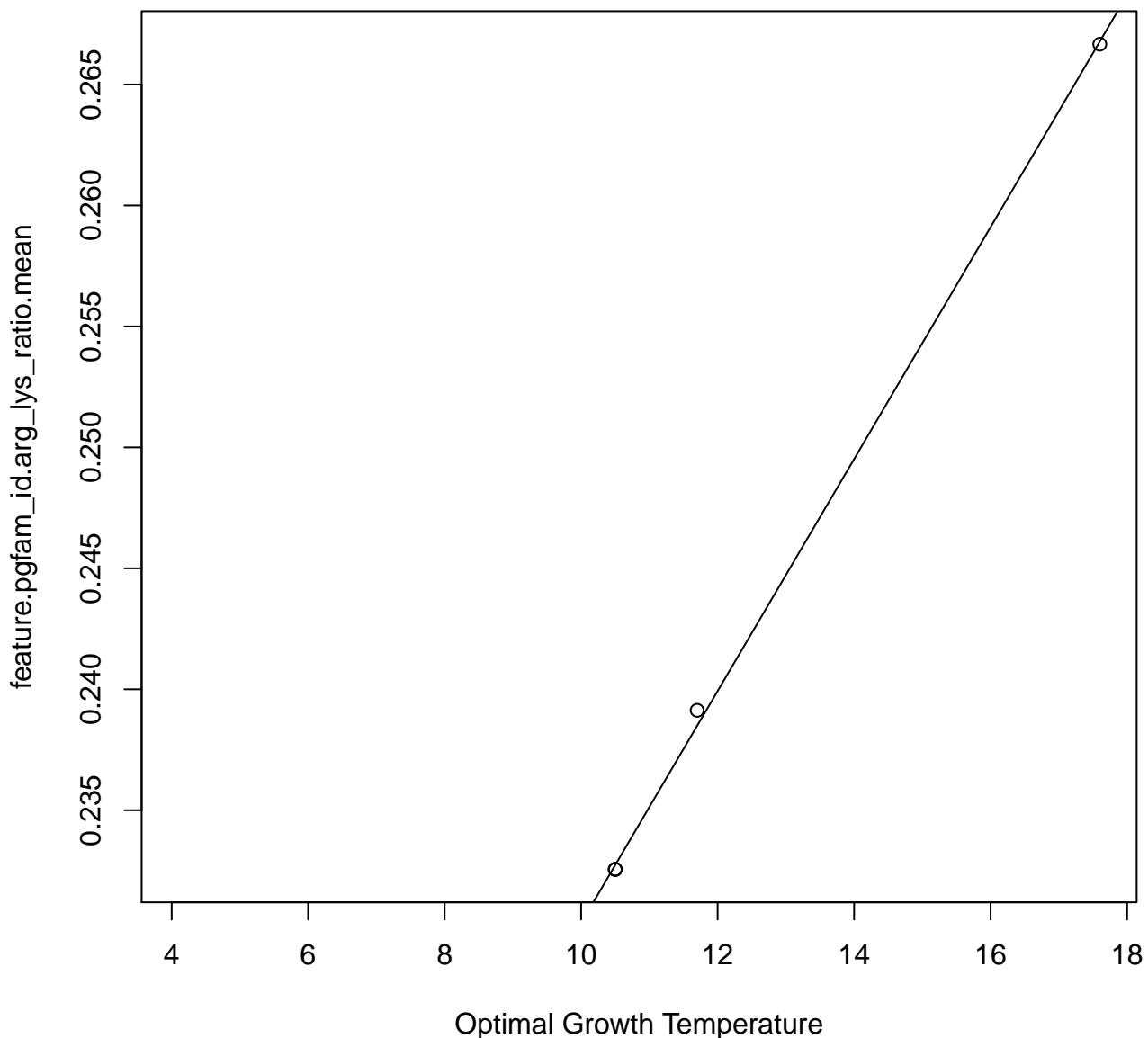
feature.pgfam_id.arg_lys_ratio.mean
PGF_06830555
SapC-like S-layer protein



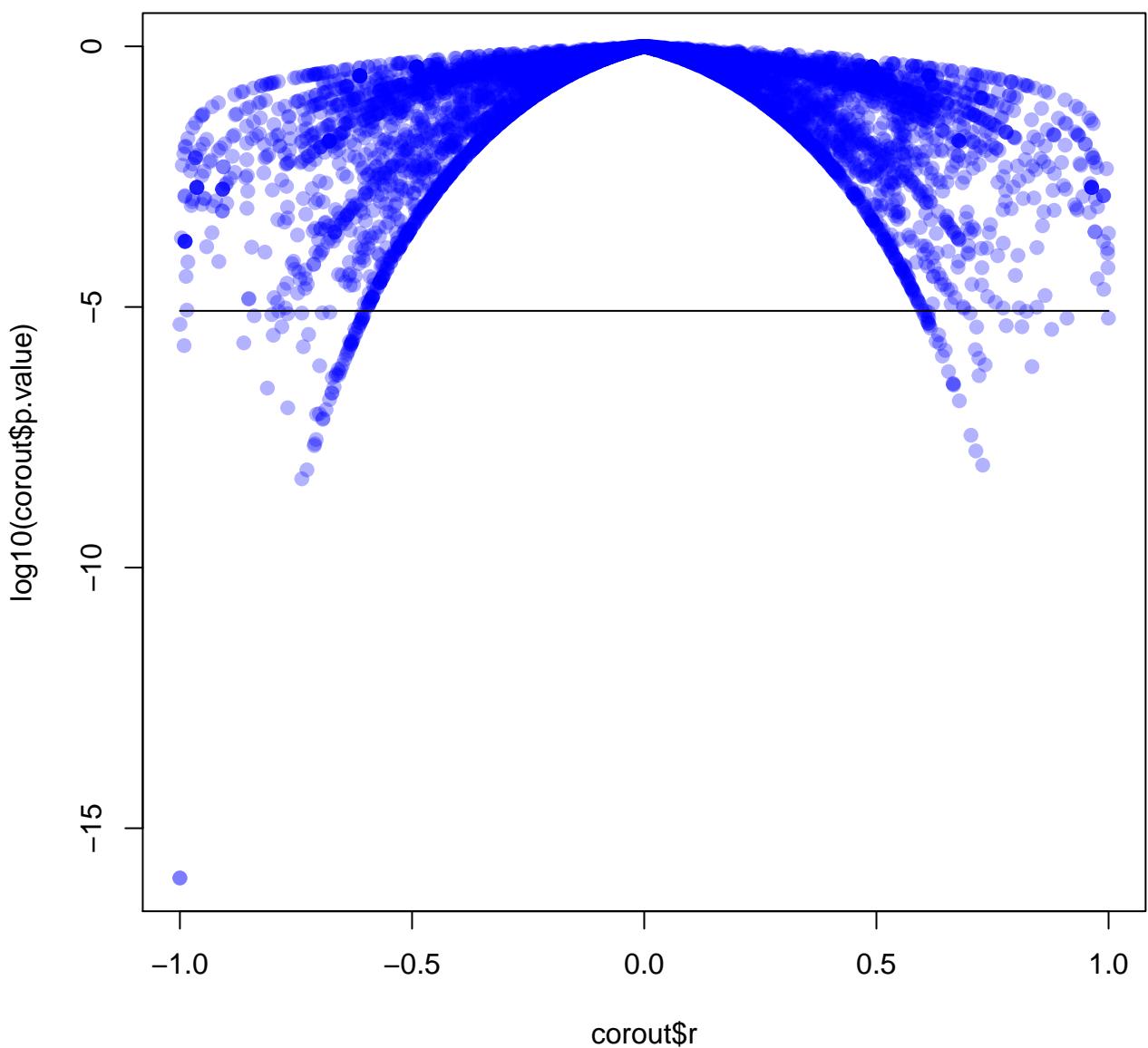
feature.pgfam_id.arg_lys_ratio.mean

PGF_00041322

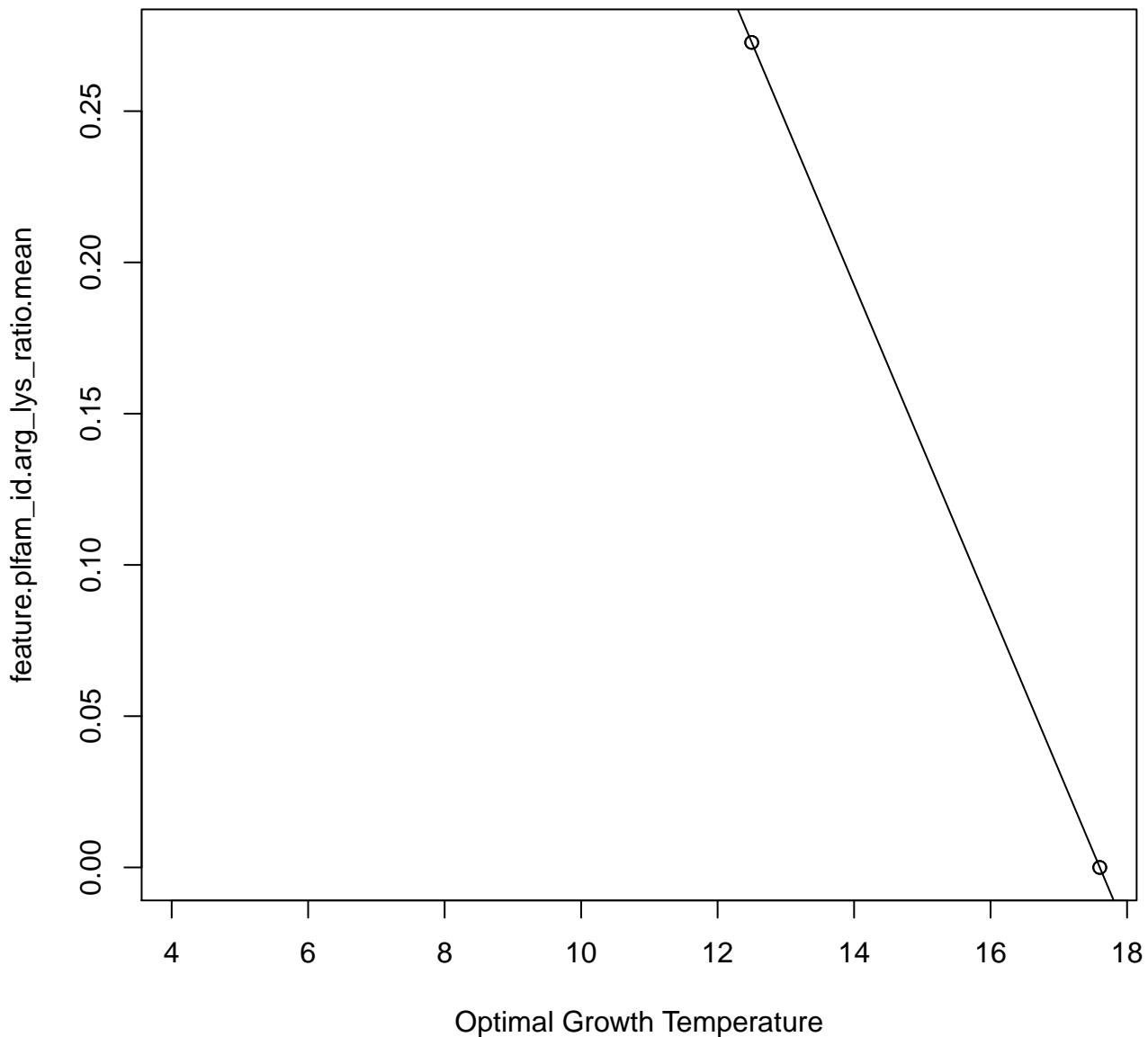
Putative hydrolase



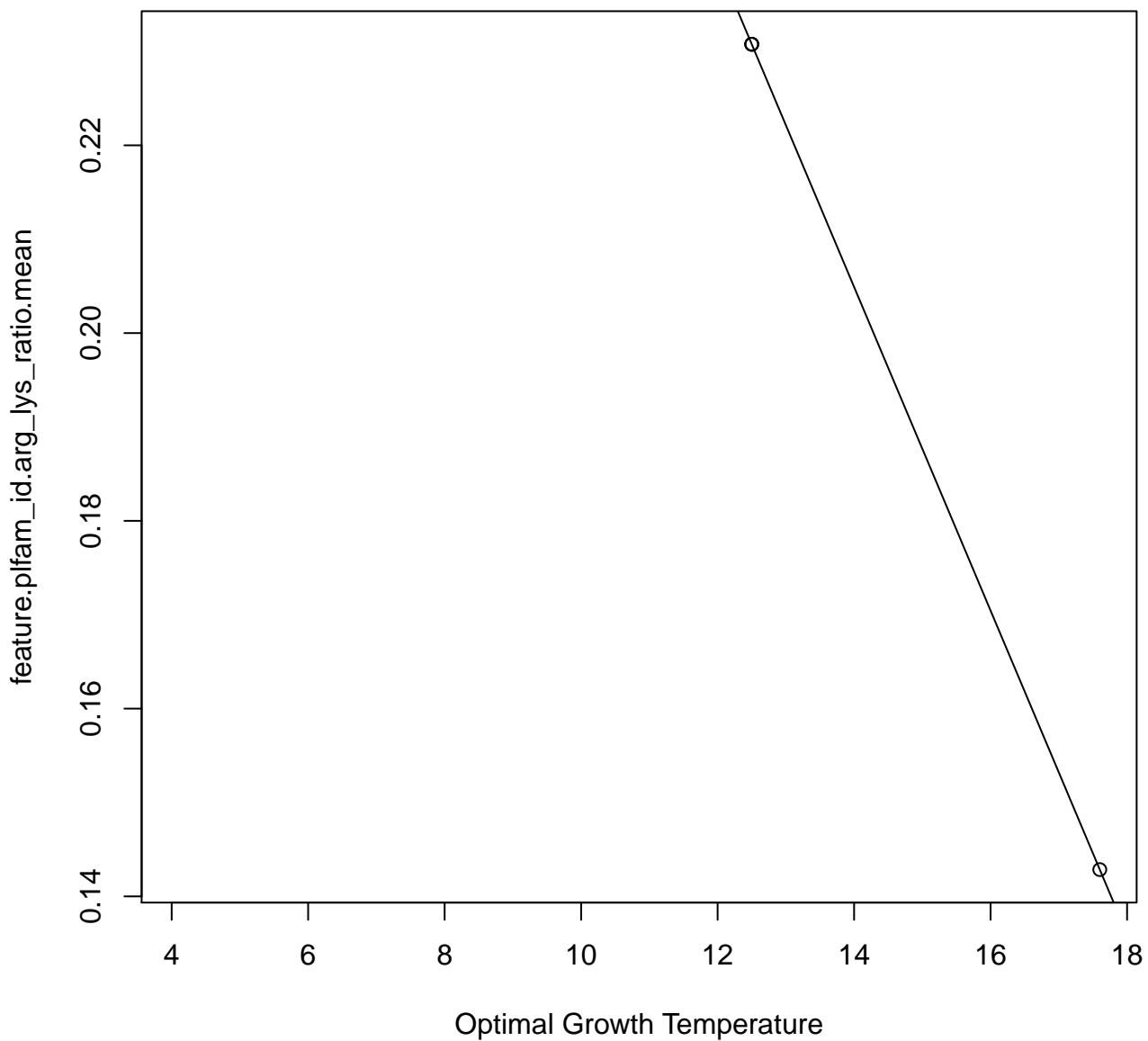
feature.plfam_id.arg_lys_ratio.mean



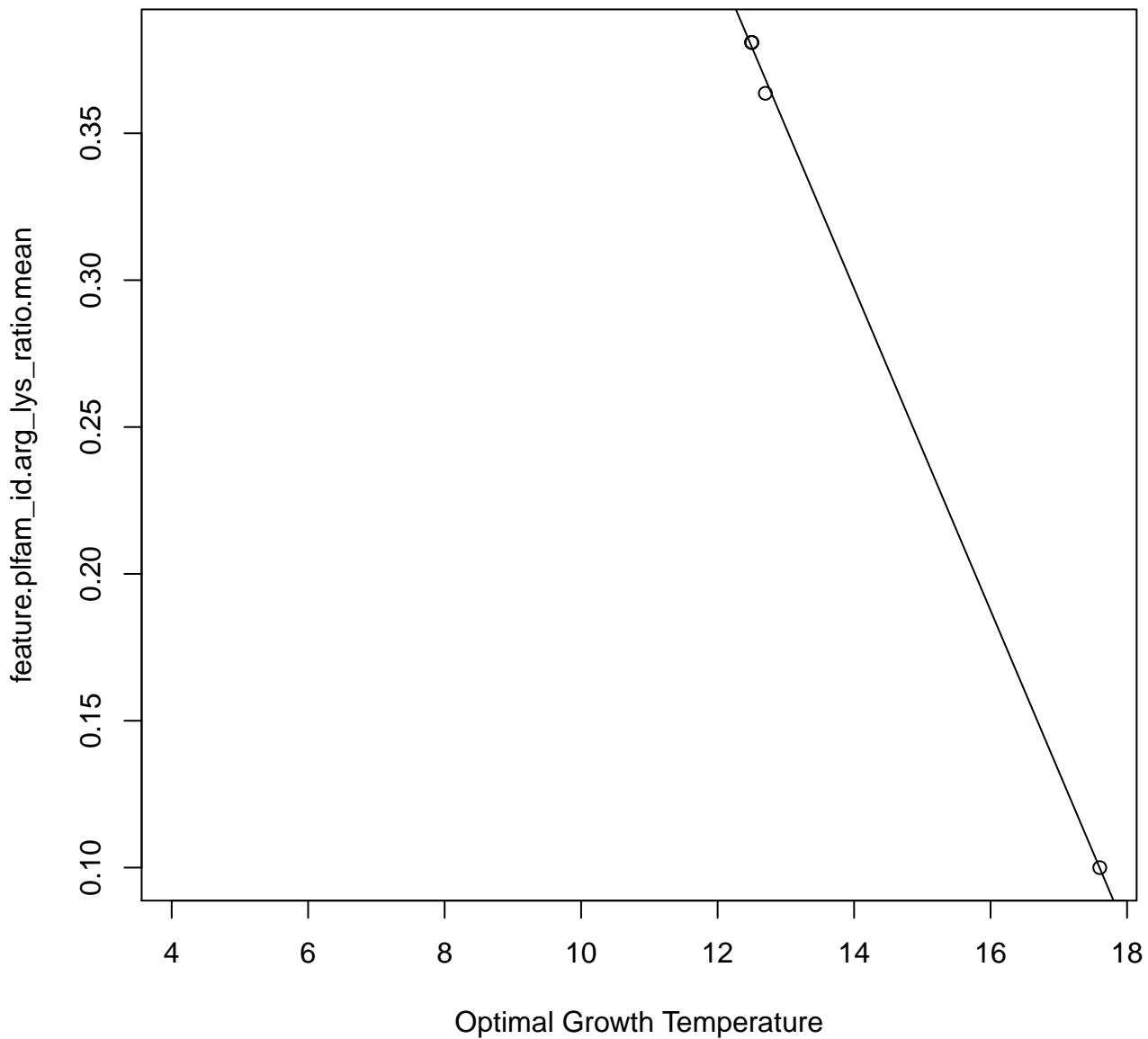
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00005866
hypothetical protein



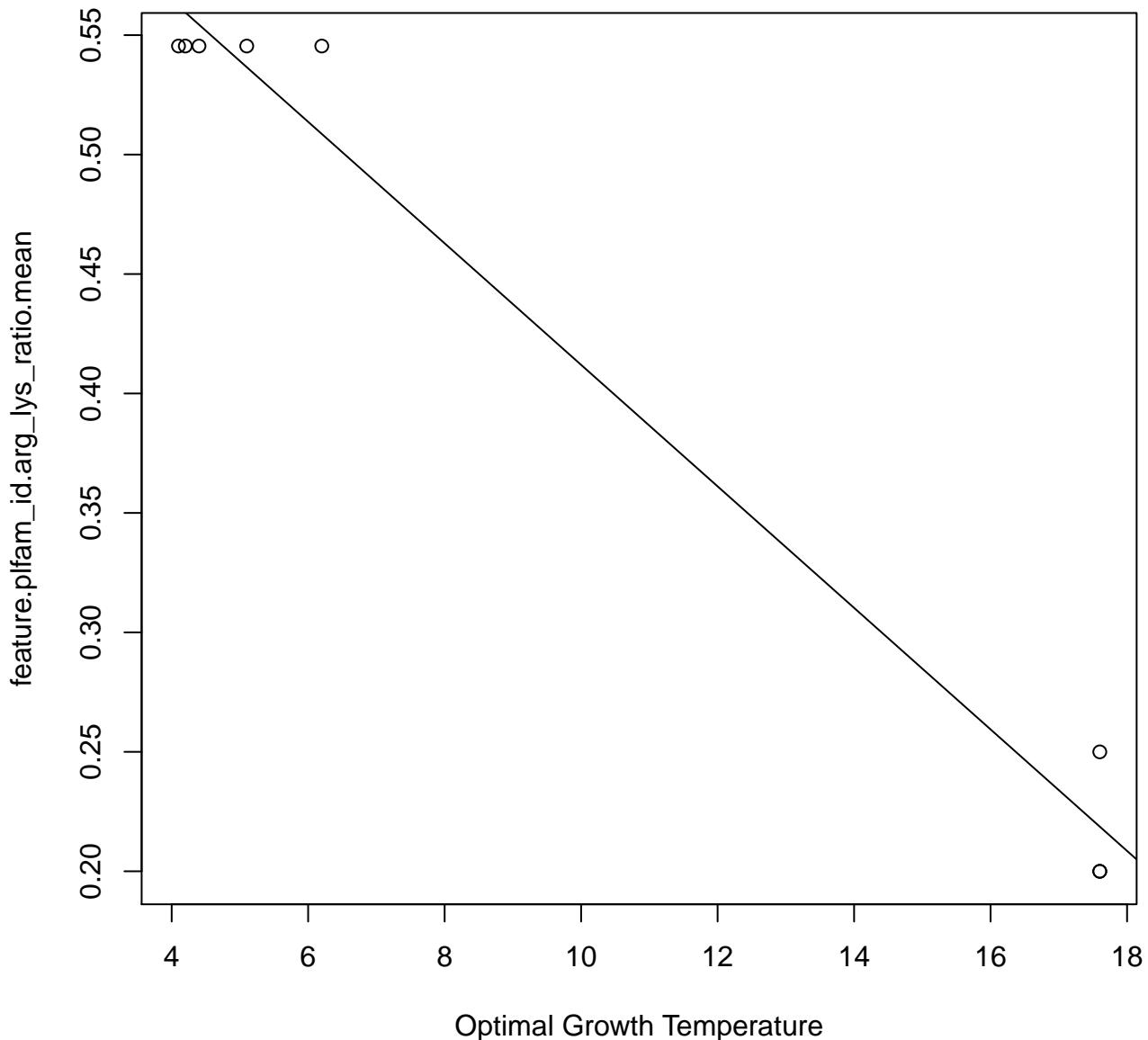
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007934
hypothetical protein



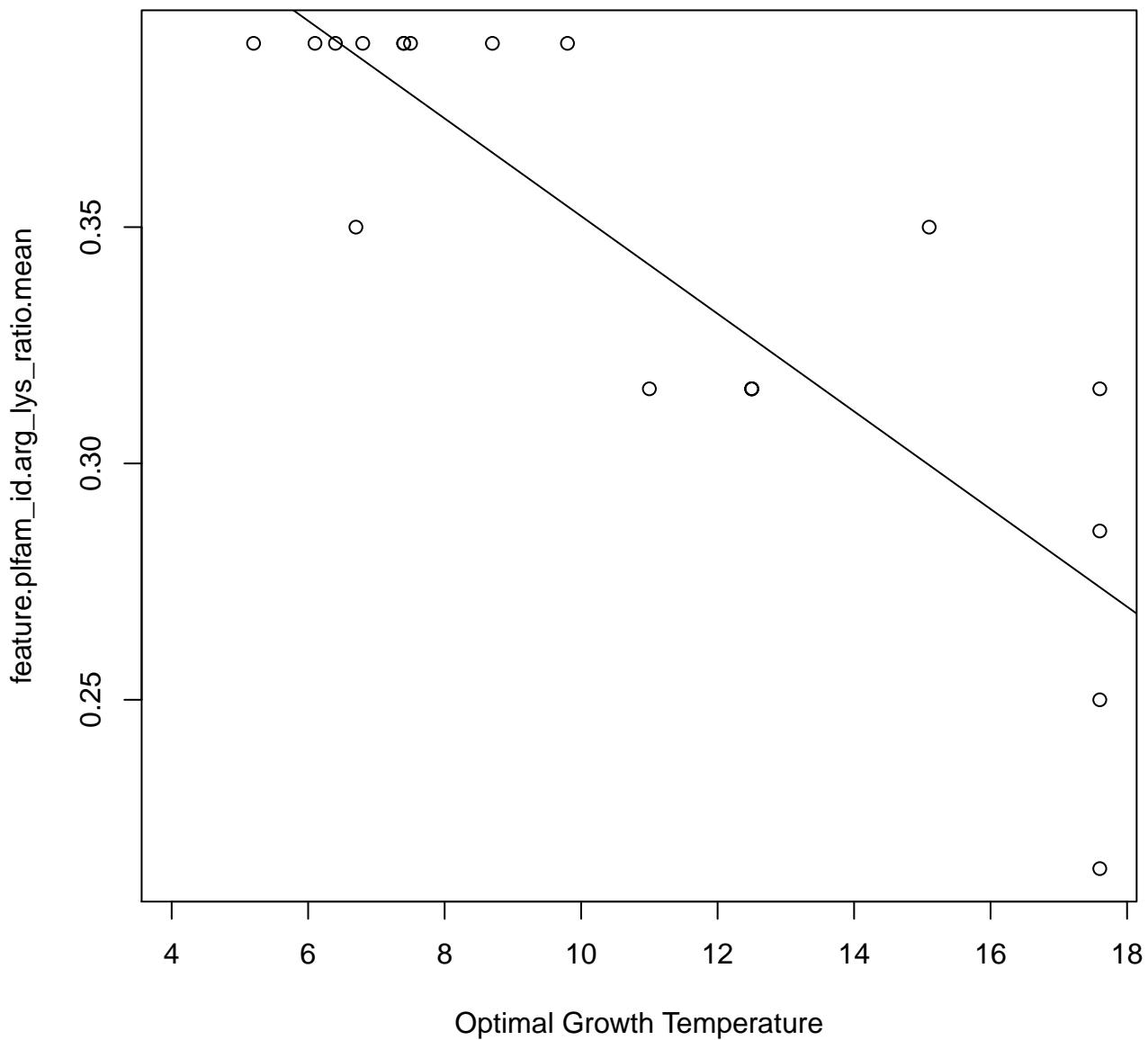
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003832
hypothetical protein



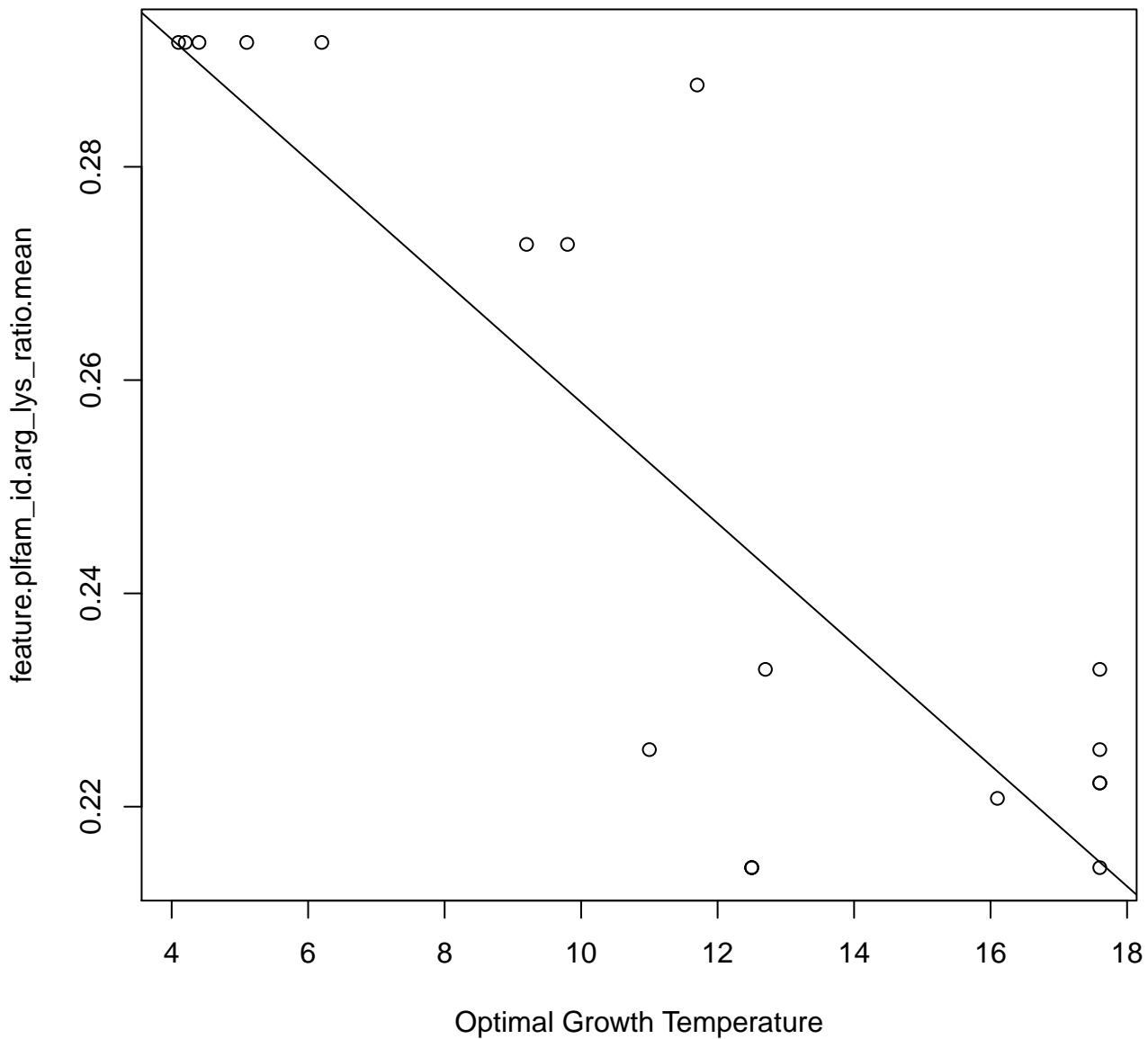
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003941
hypothetical protein



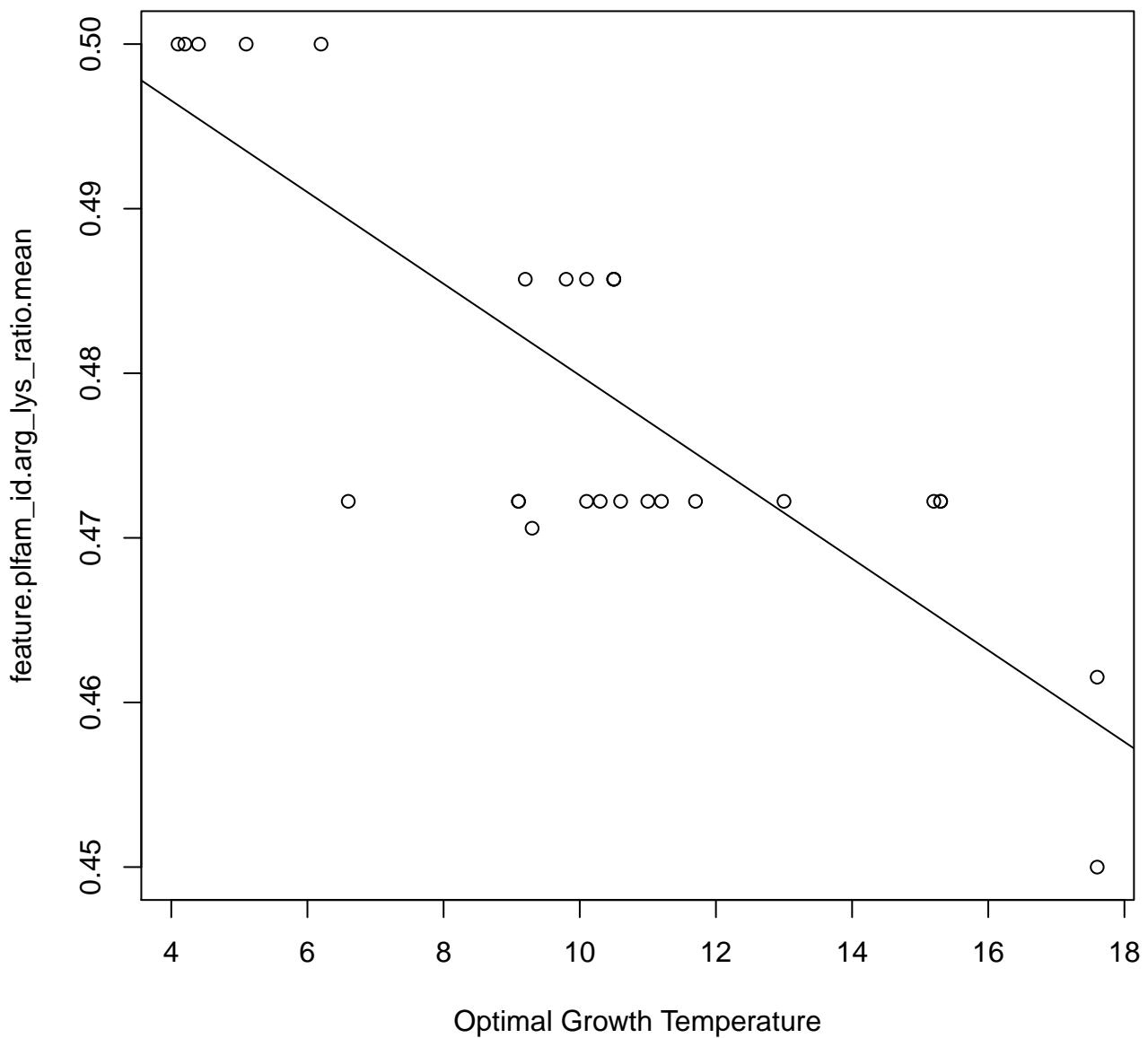
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00014309
PhbF



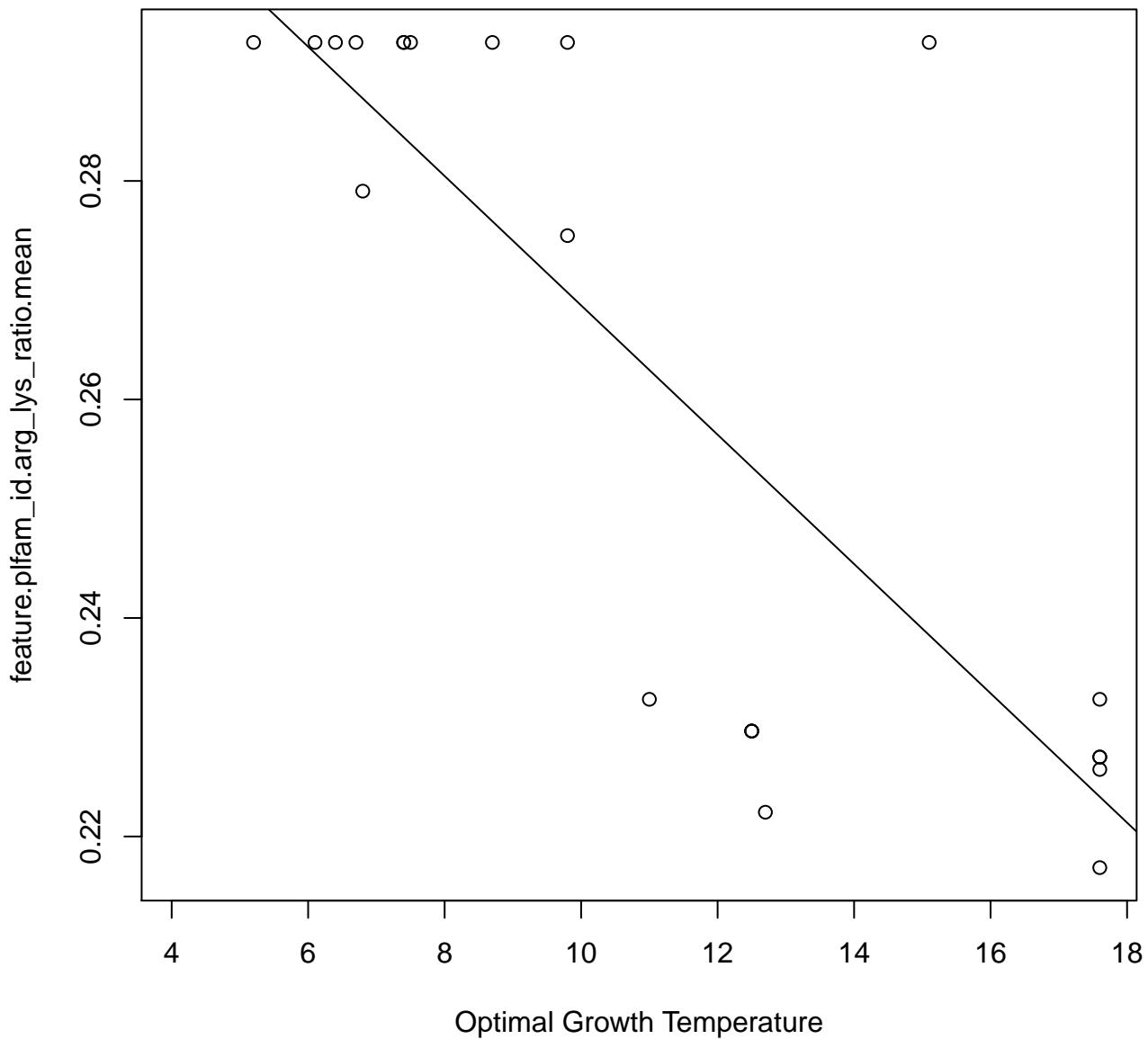
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001859
GGDEF domain protein



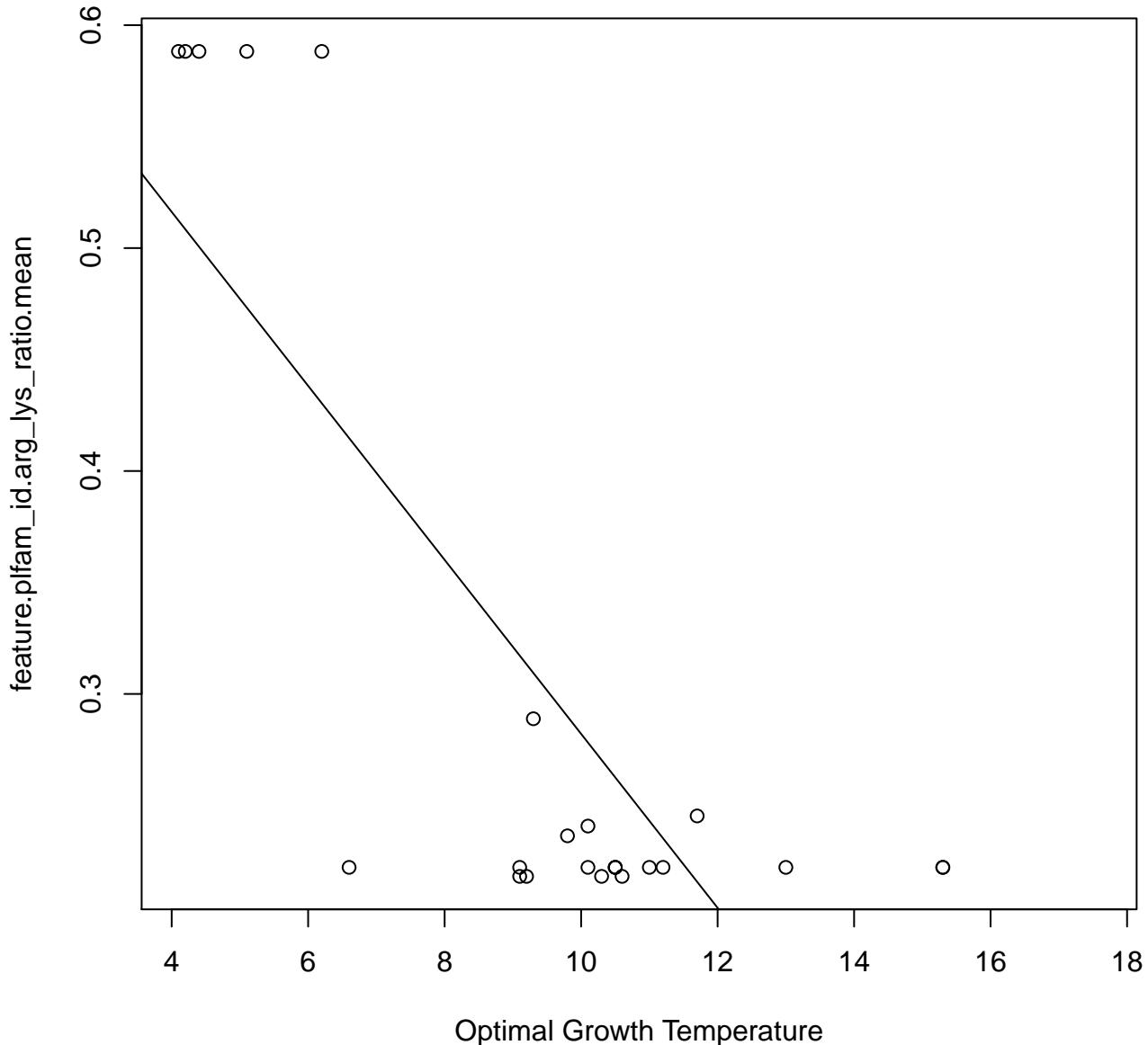
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00005643
hypothetical protein



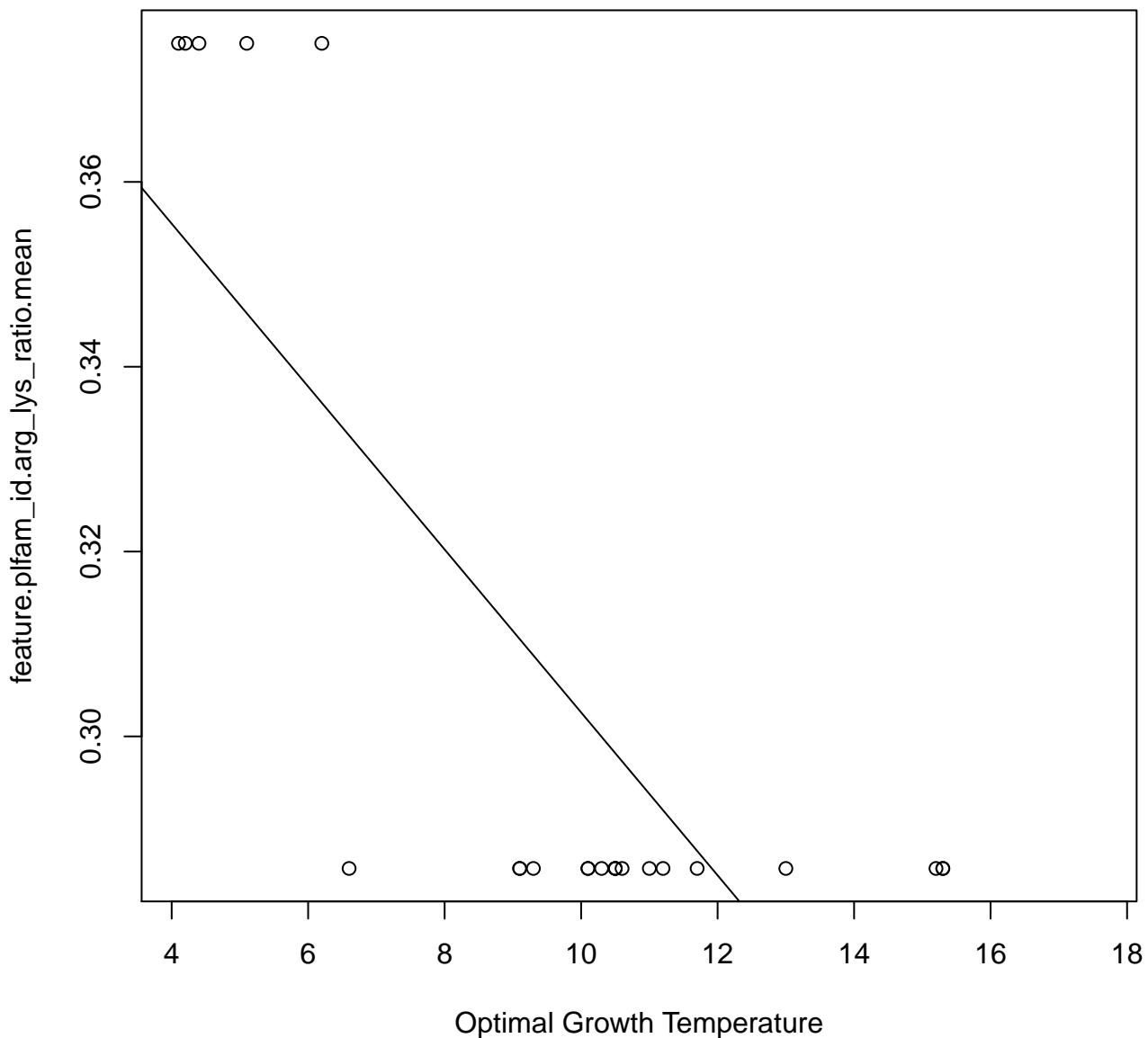
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001182
TRAP transporter solute receptor, unknown substrate 6



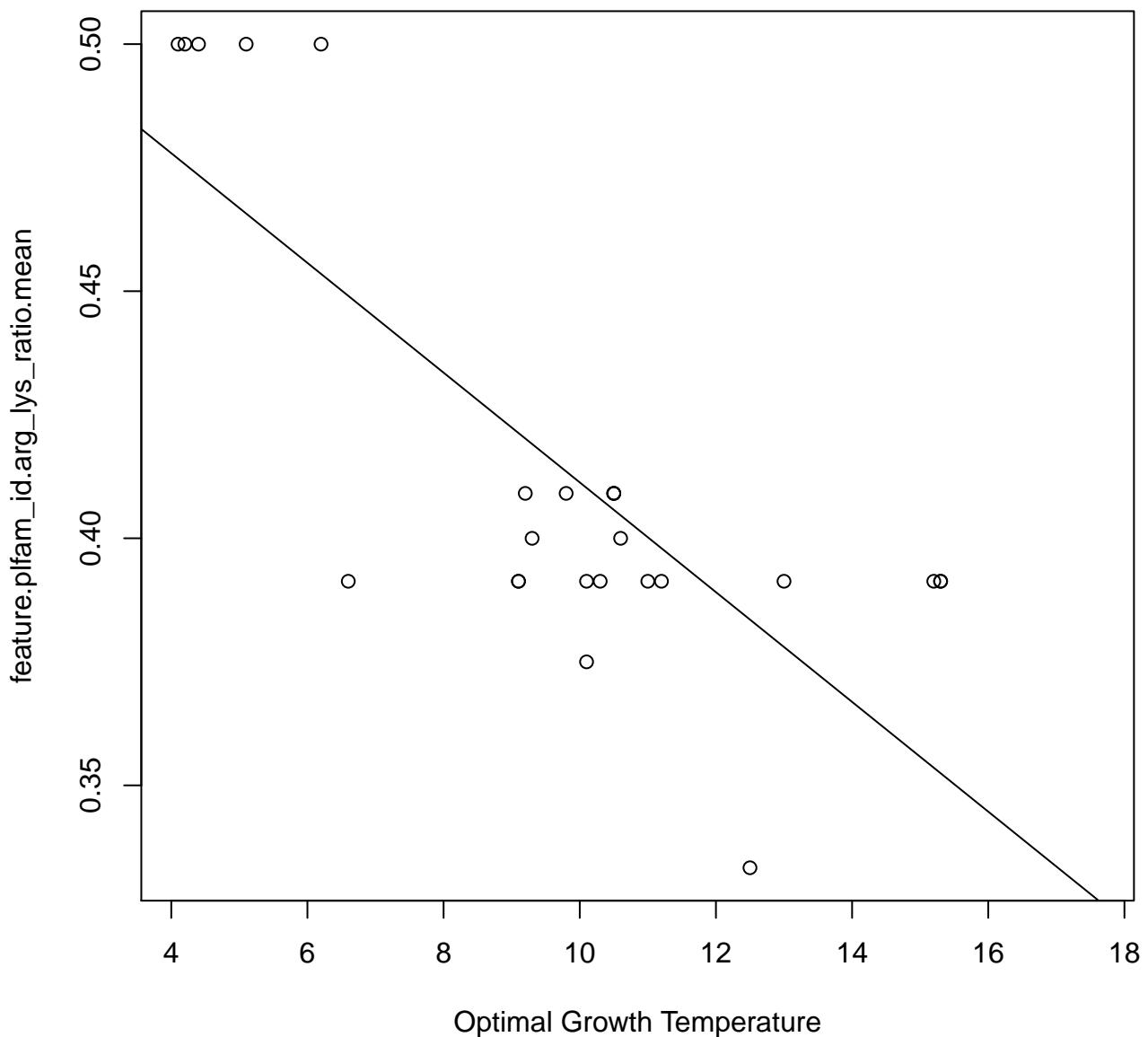
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00017455
Maltodextrin glucosidase (EC 3.2.1.20)



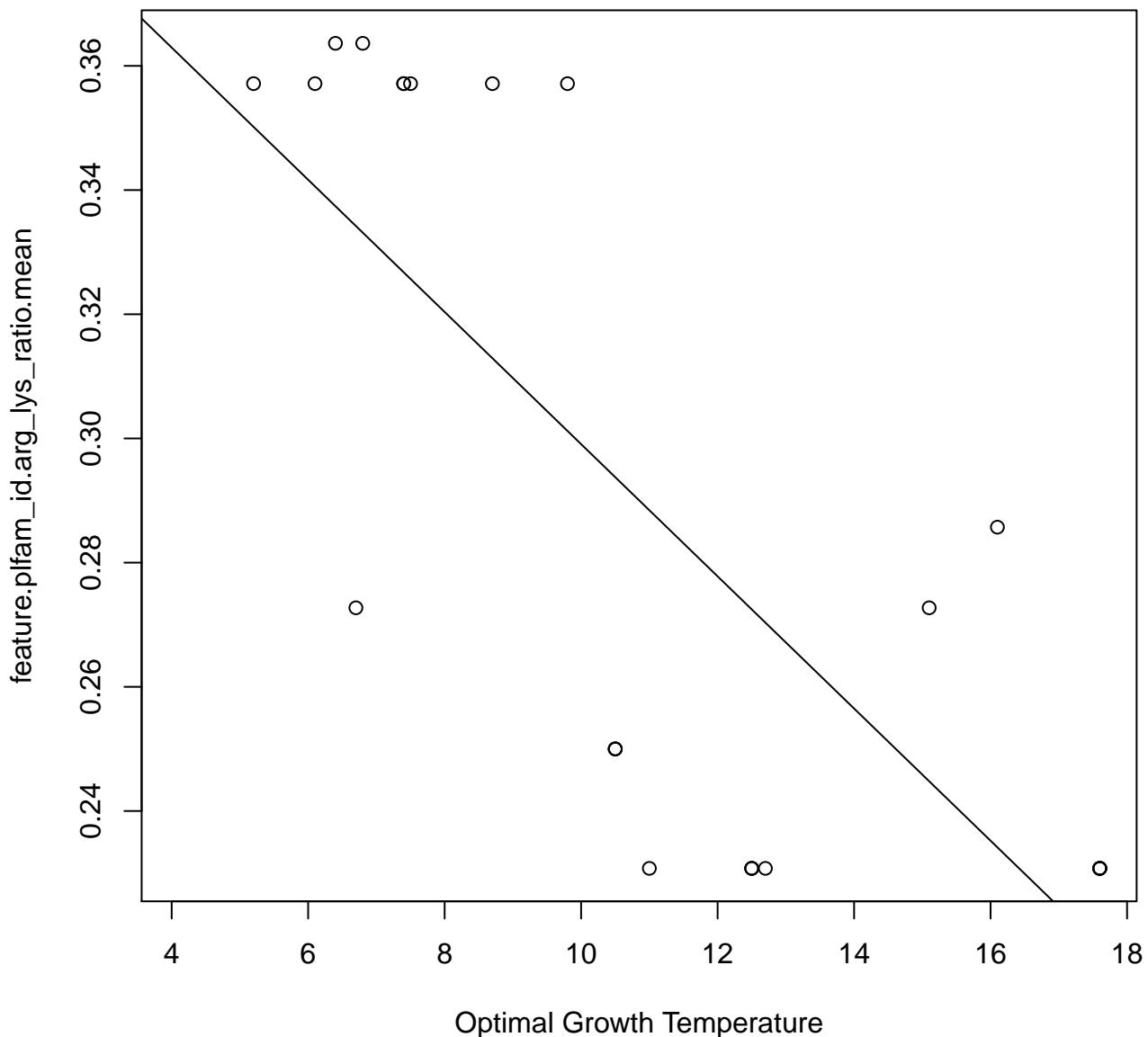
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00029549
hypothetical protein



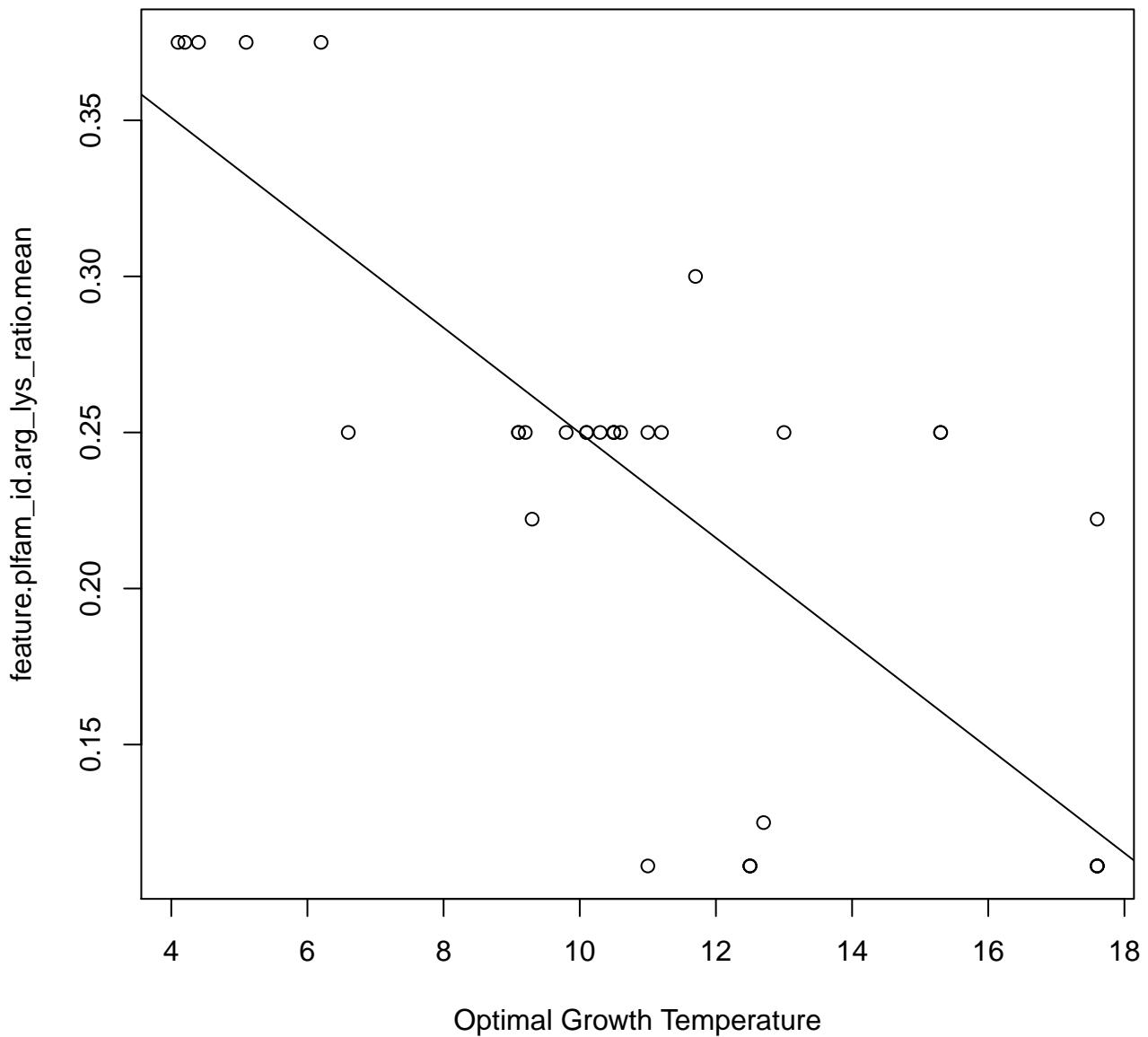
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00014070
hypothetical protein



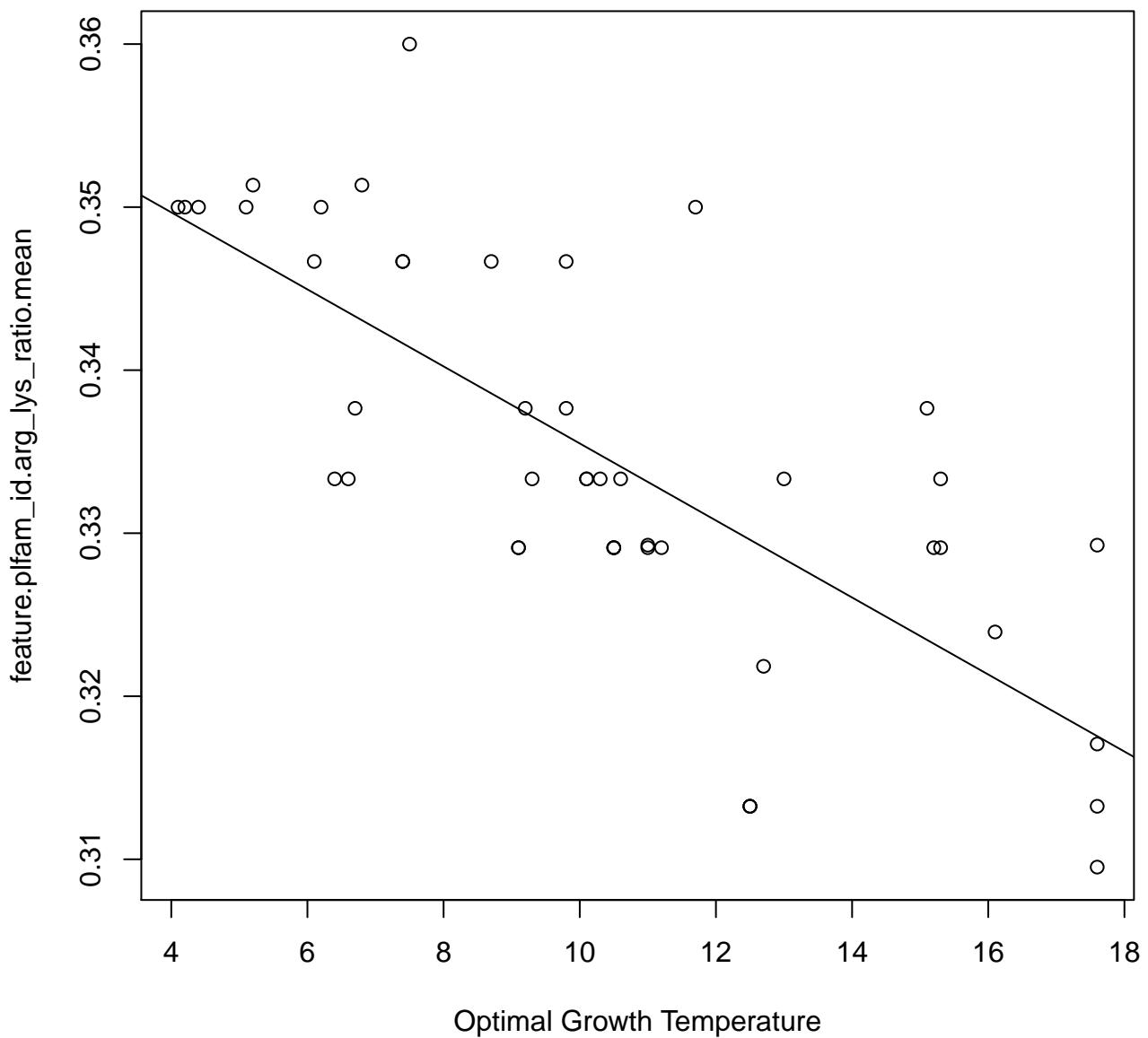
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000318
ATP synthase F0 sector subunit a (EC 3.6.3.14)



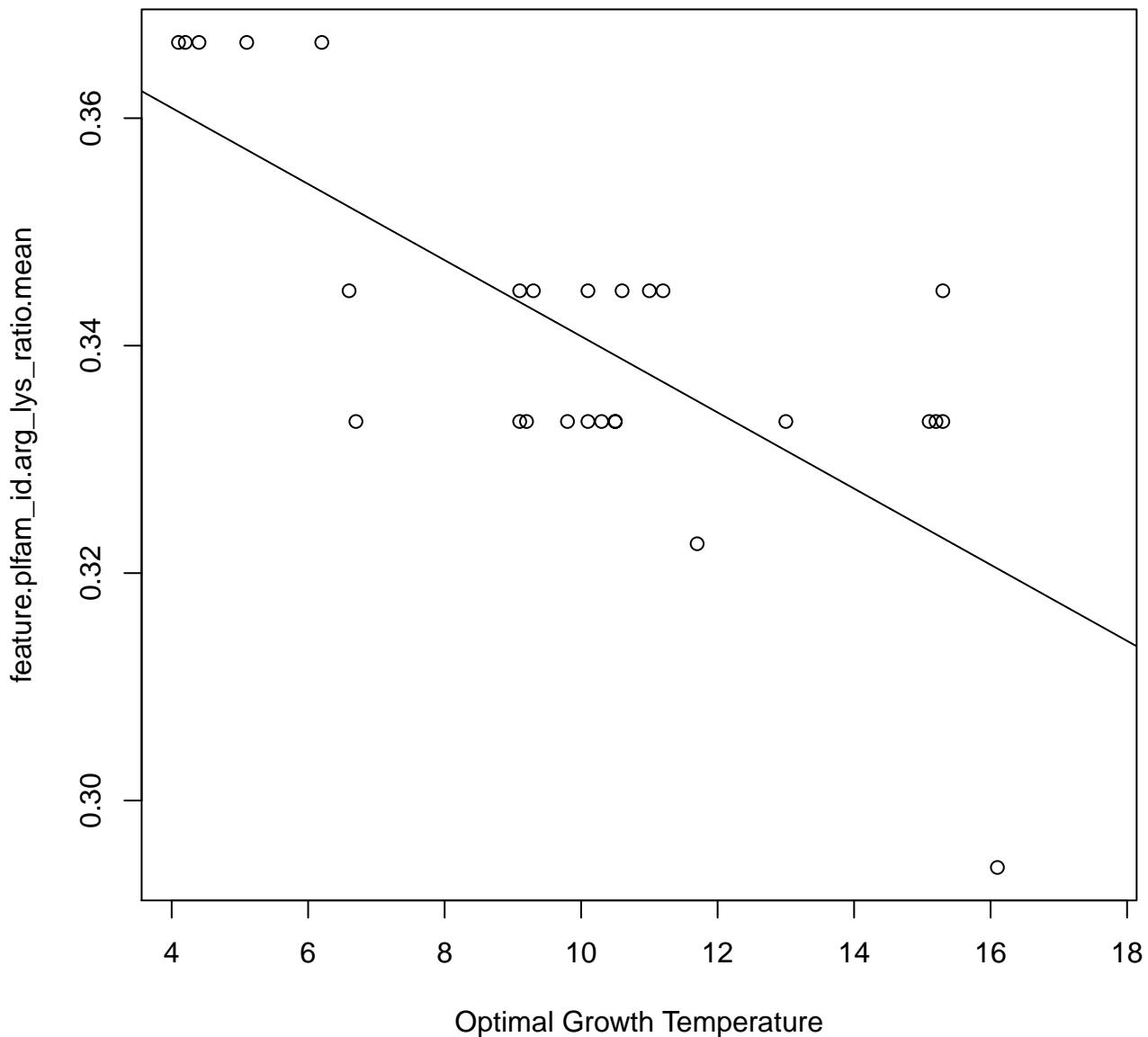
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000991
Putative manganese efflux pump MntP



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002008
Related to collagenase

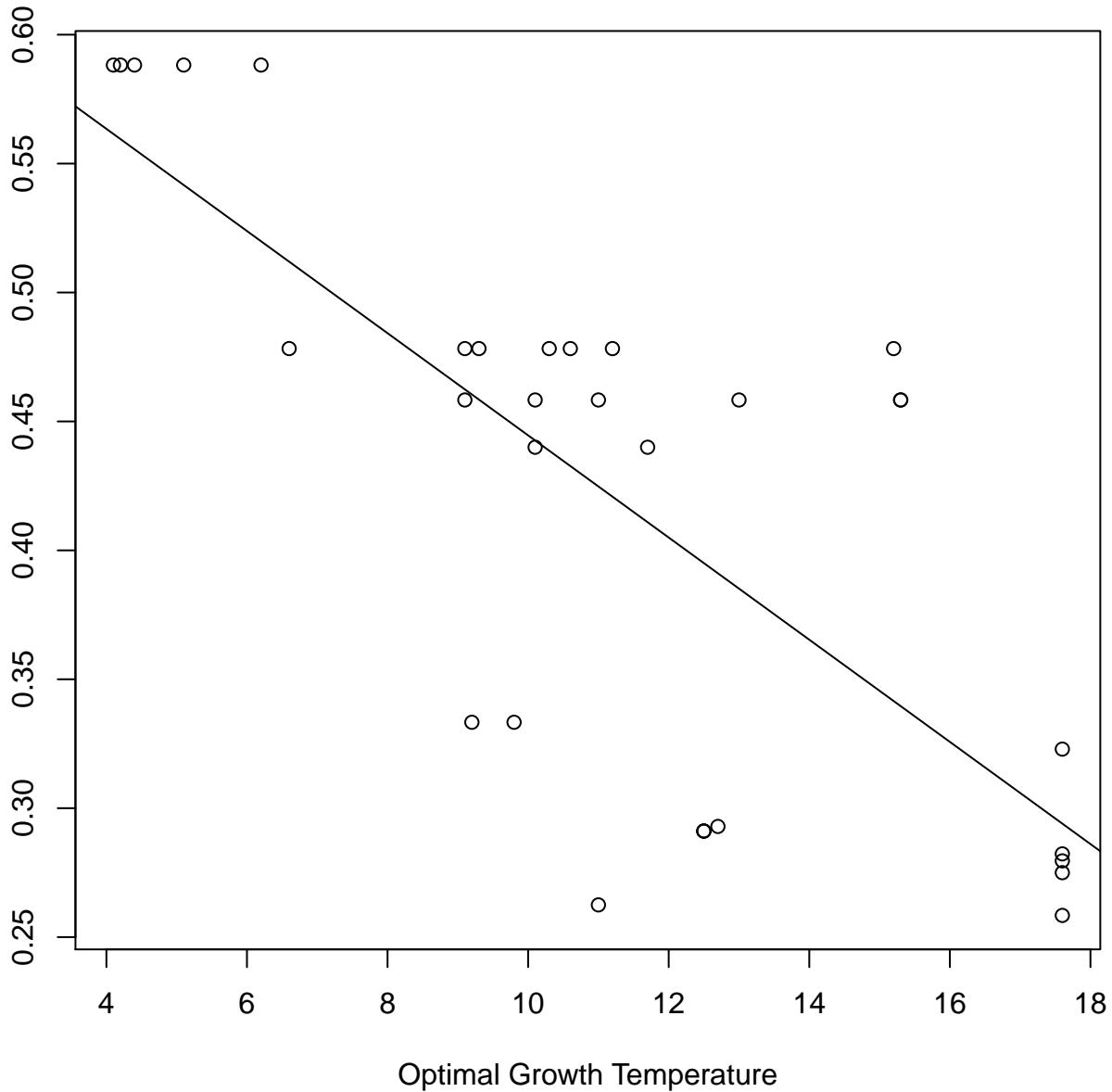


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00016853
Tryptophan 2,3-dioxygenase (EC 1.13.11.11)

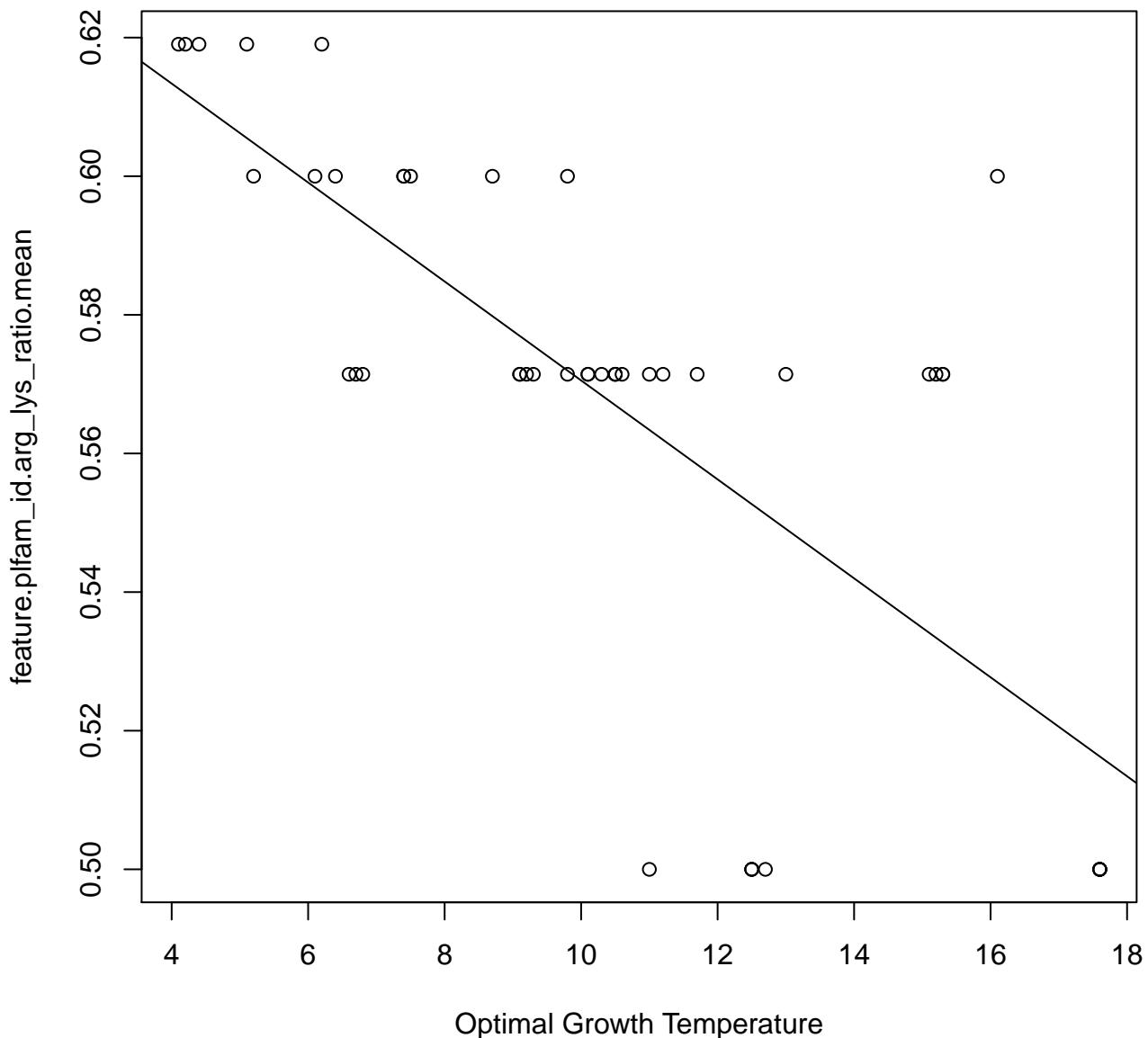


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002434
hypothetical protein

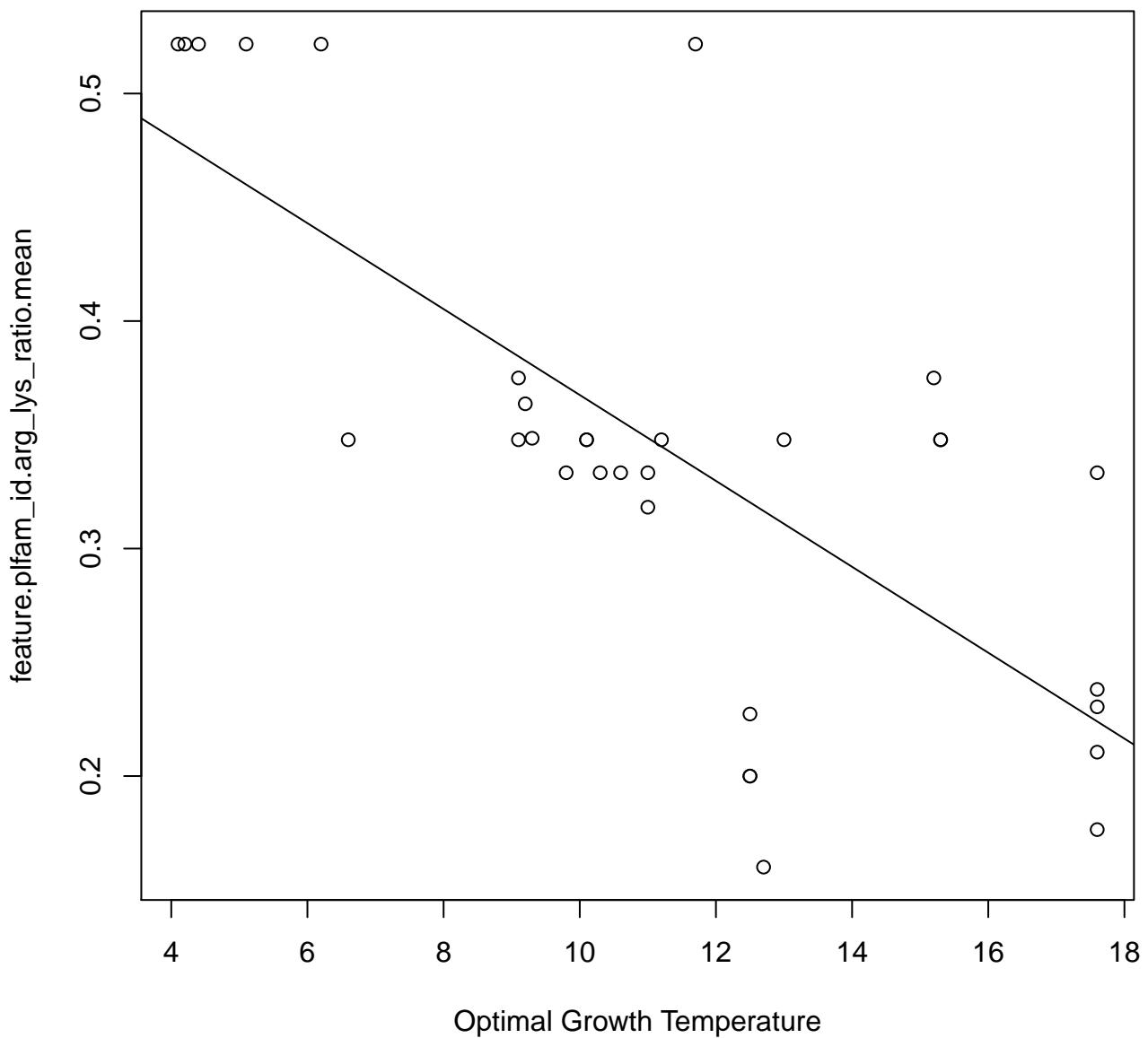
feature.plfam_id.arg_lys_ratio.mean



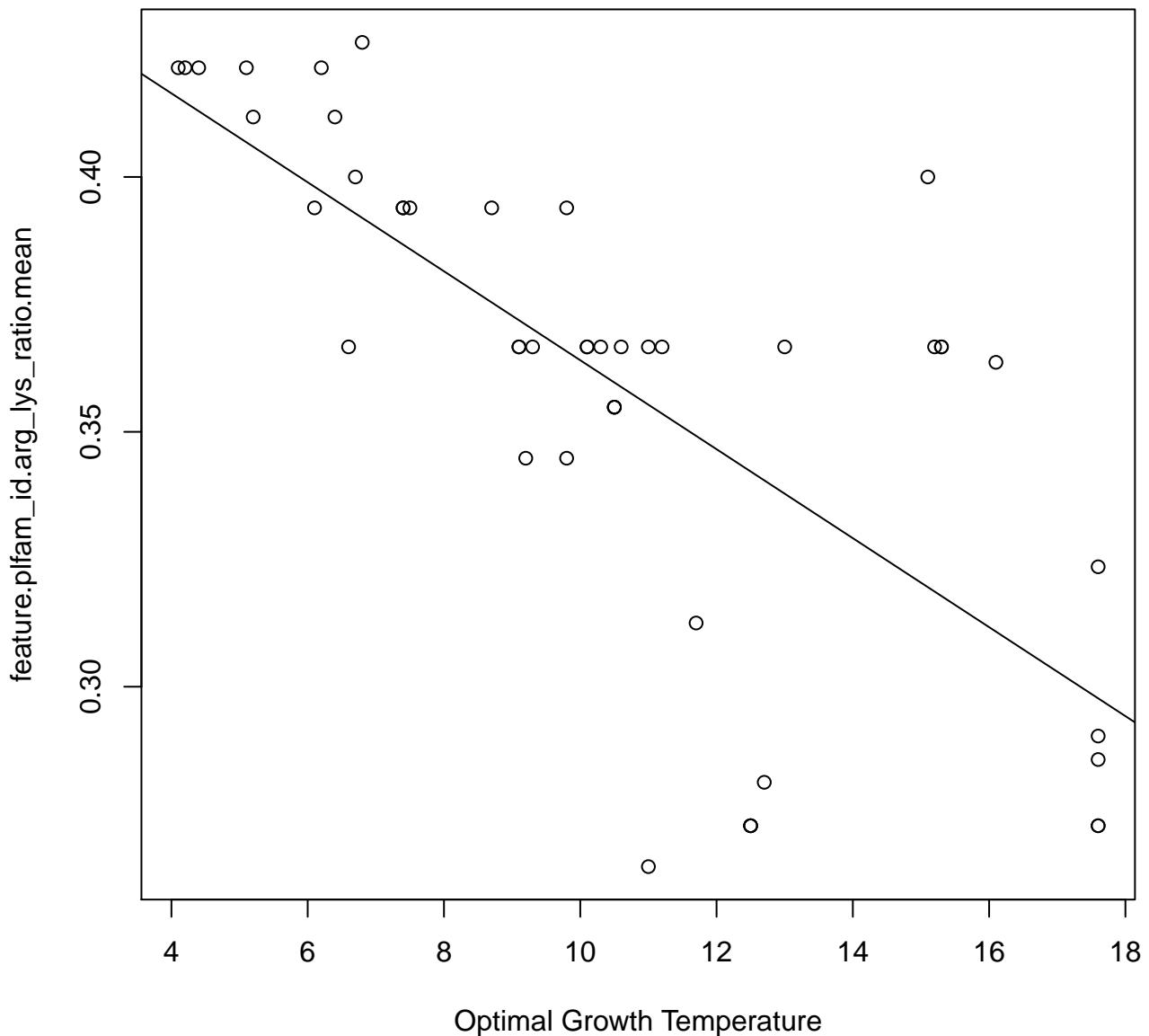
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000260
23S rRNA (pseudouridine(1915)-N(3))-methyltransferase (EC 2.1.1.177)



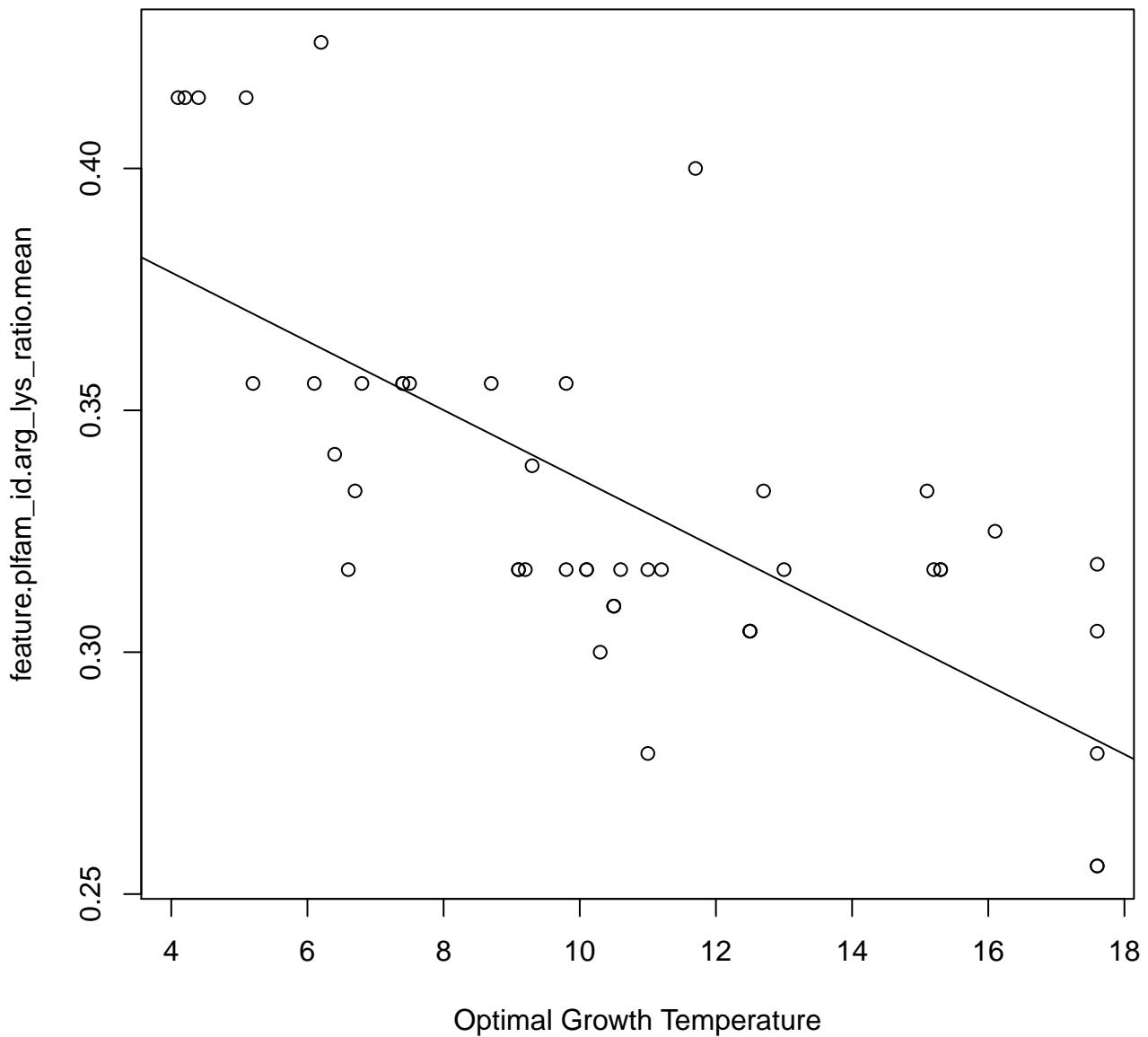
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002358
hypothetical protein



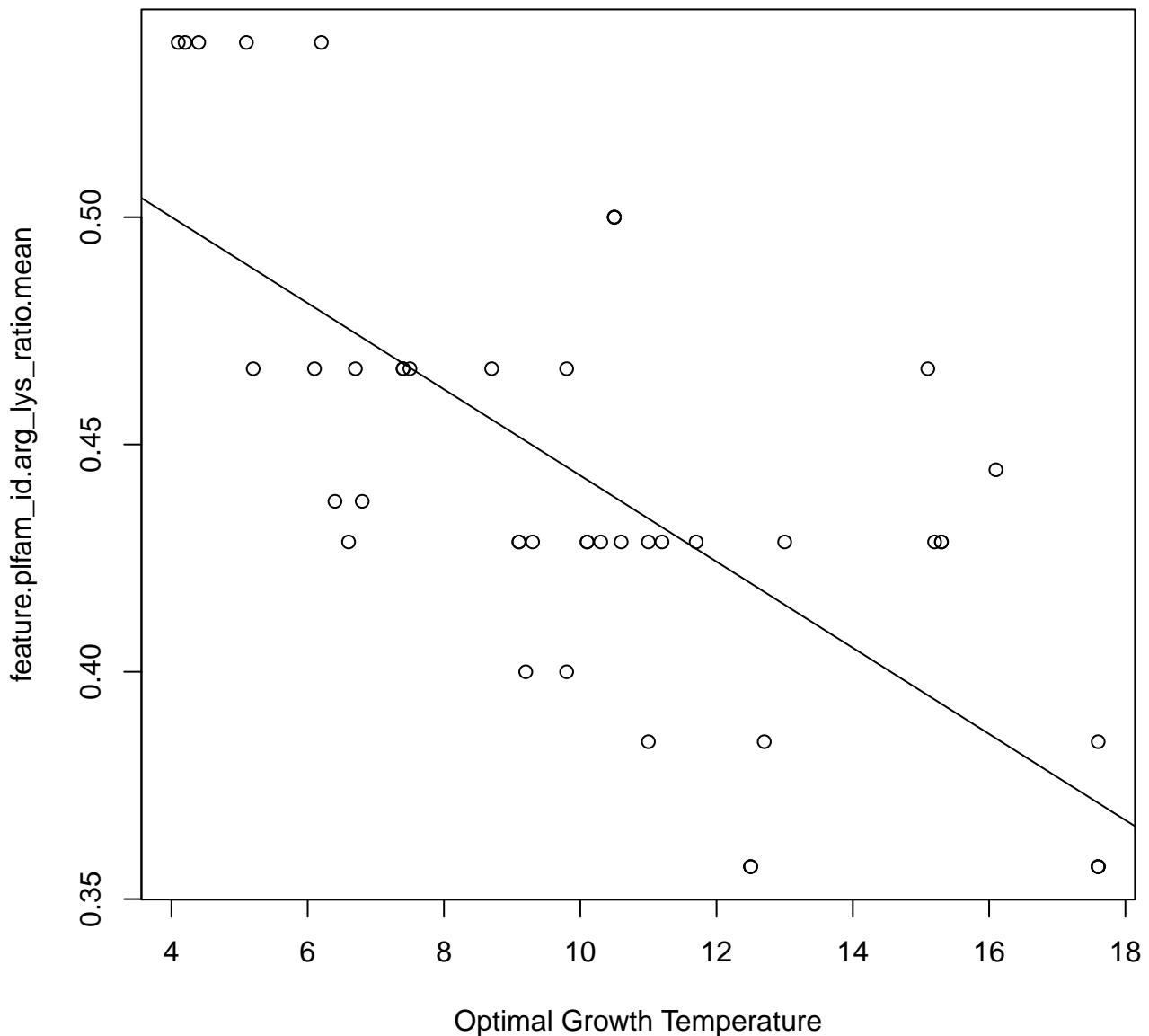
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000670
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)



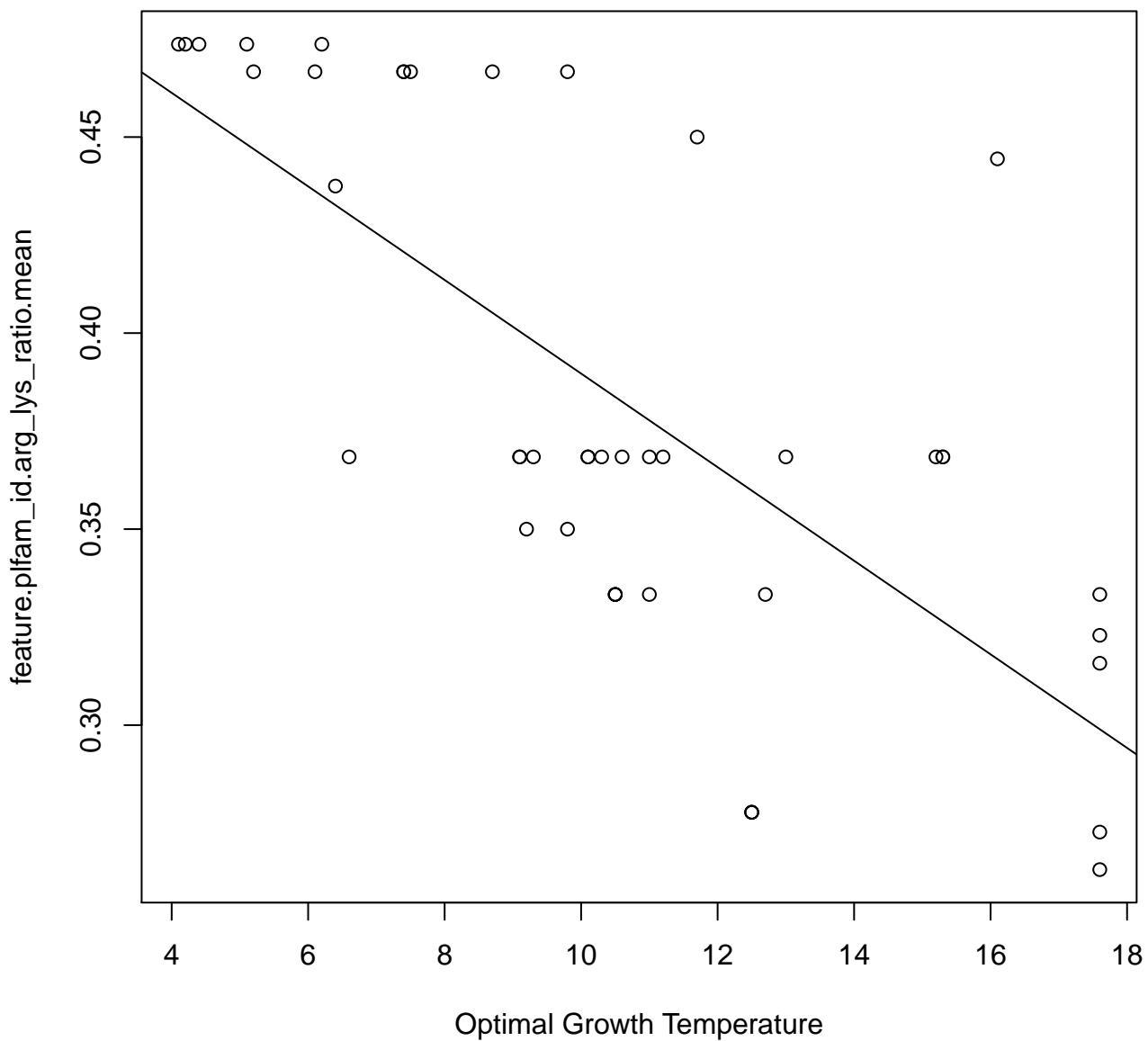
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000740
Alanine transaminase (EC 2.6.1.2)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002875
Uncharacterized protein YfgD, not an arsenate reductase



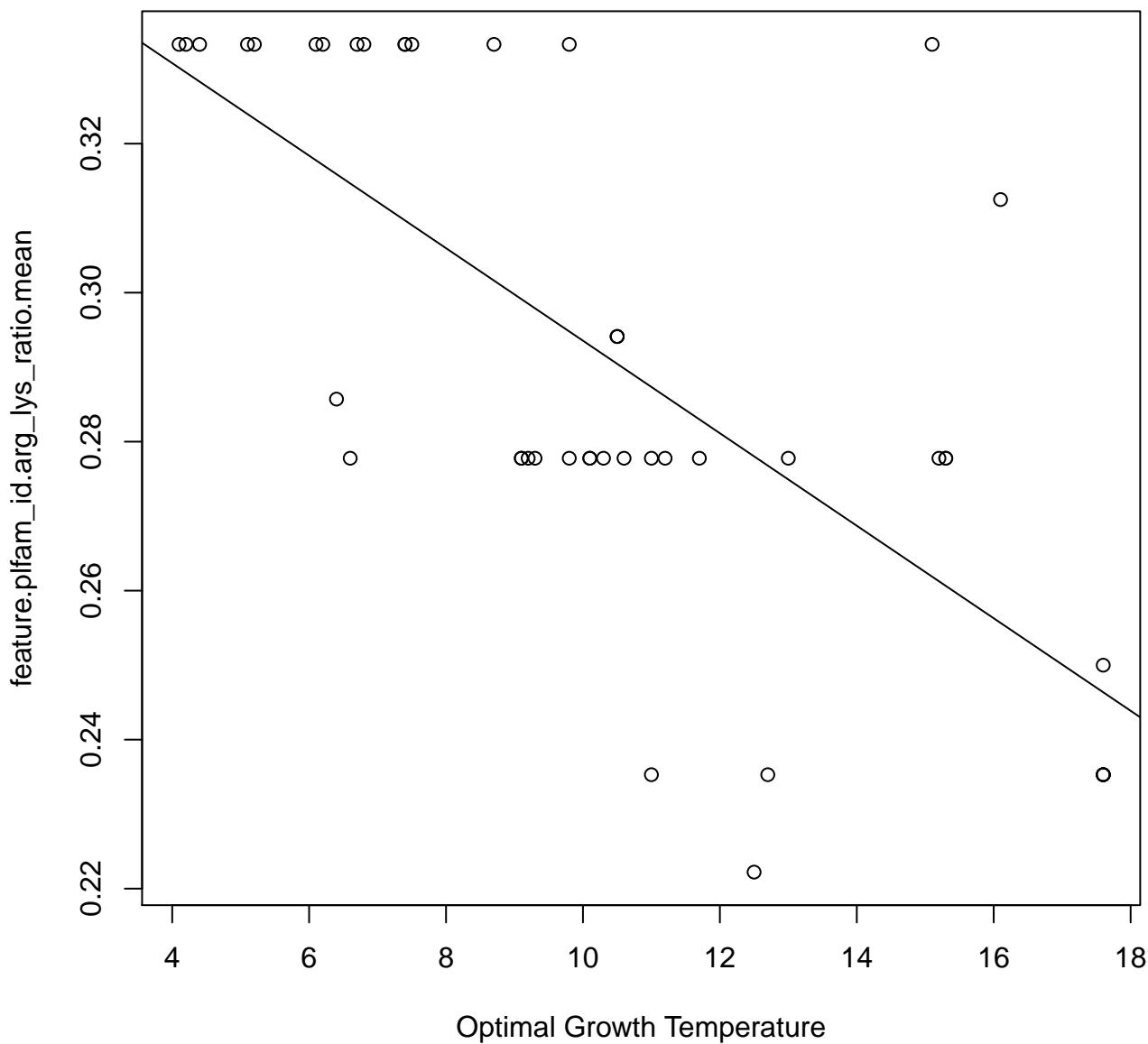
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001927
Potential queD like 2



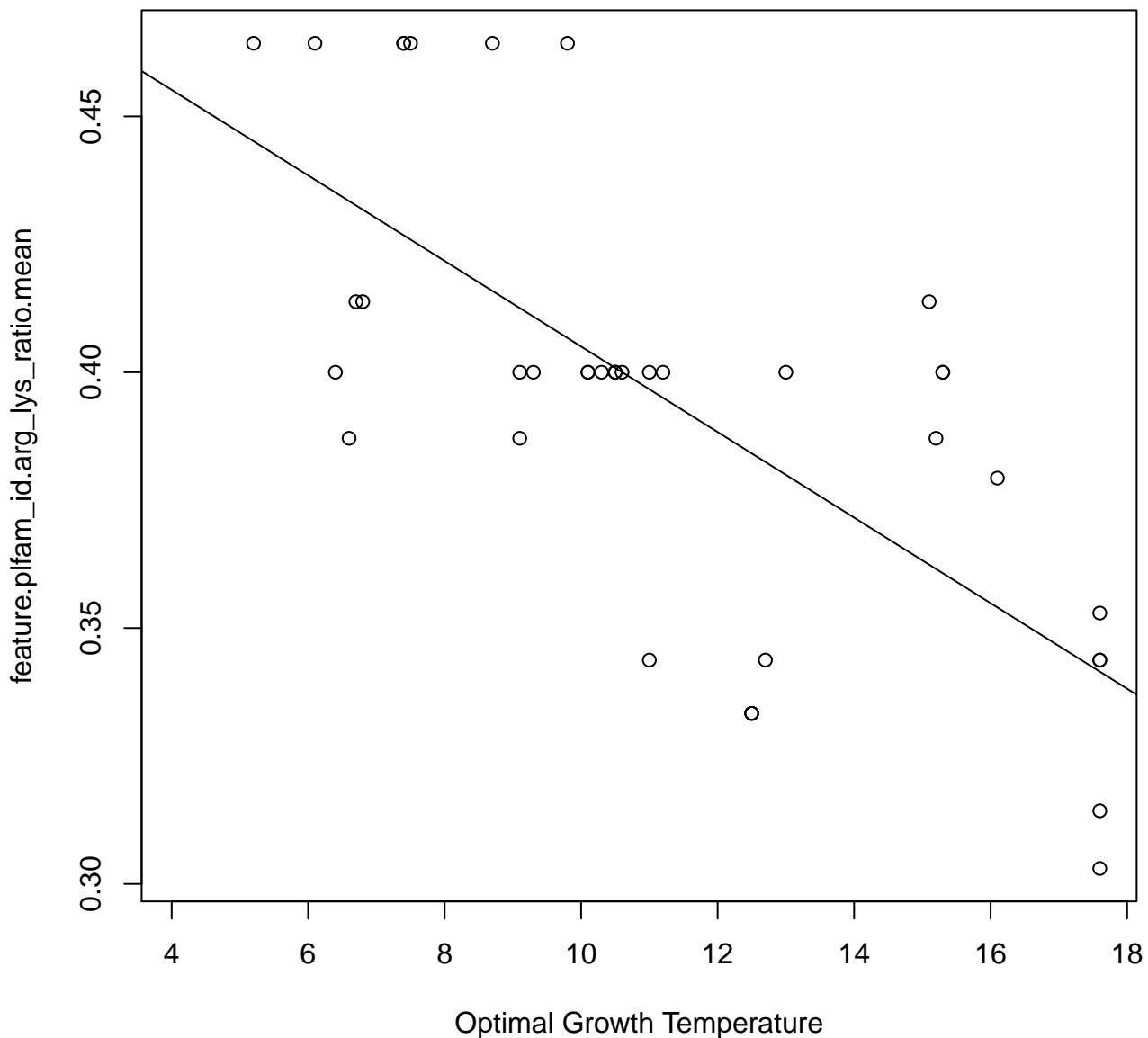
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00028265

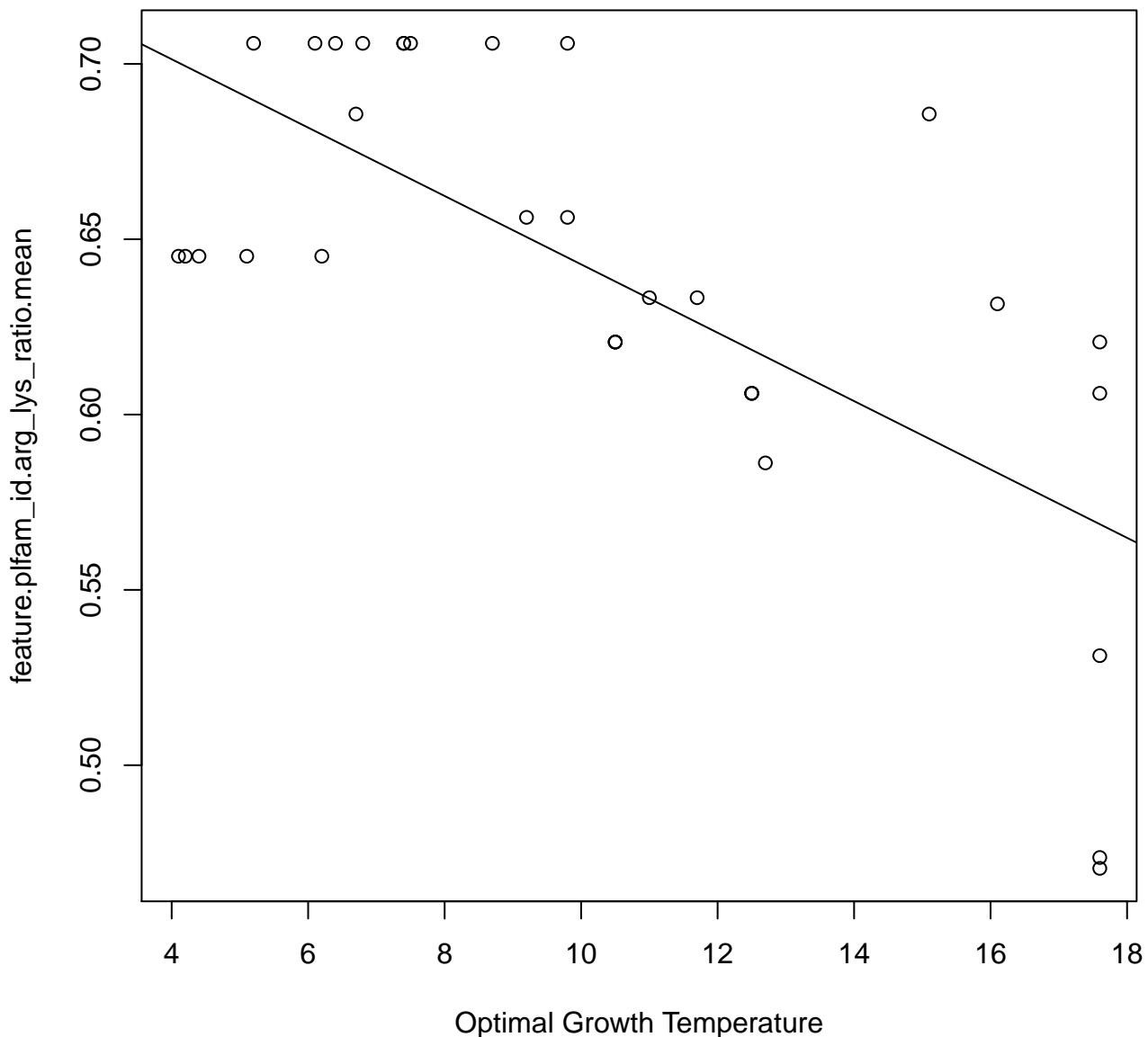
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)



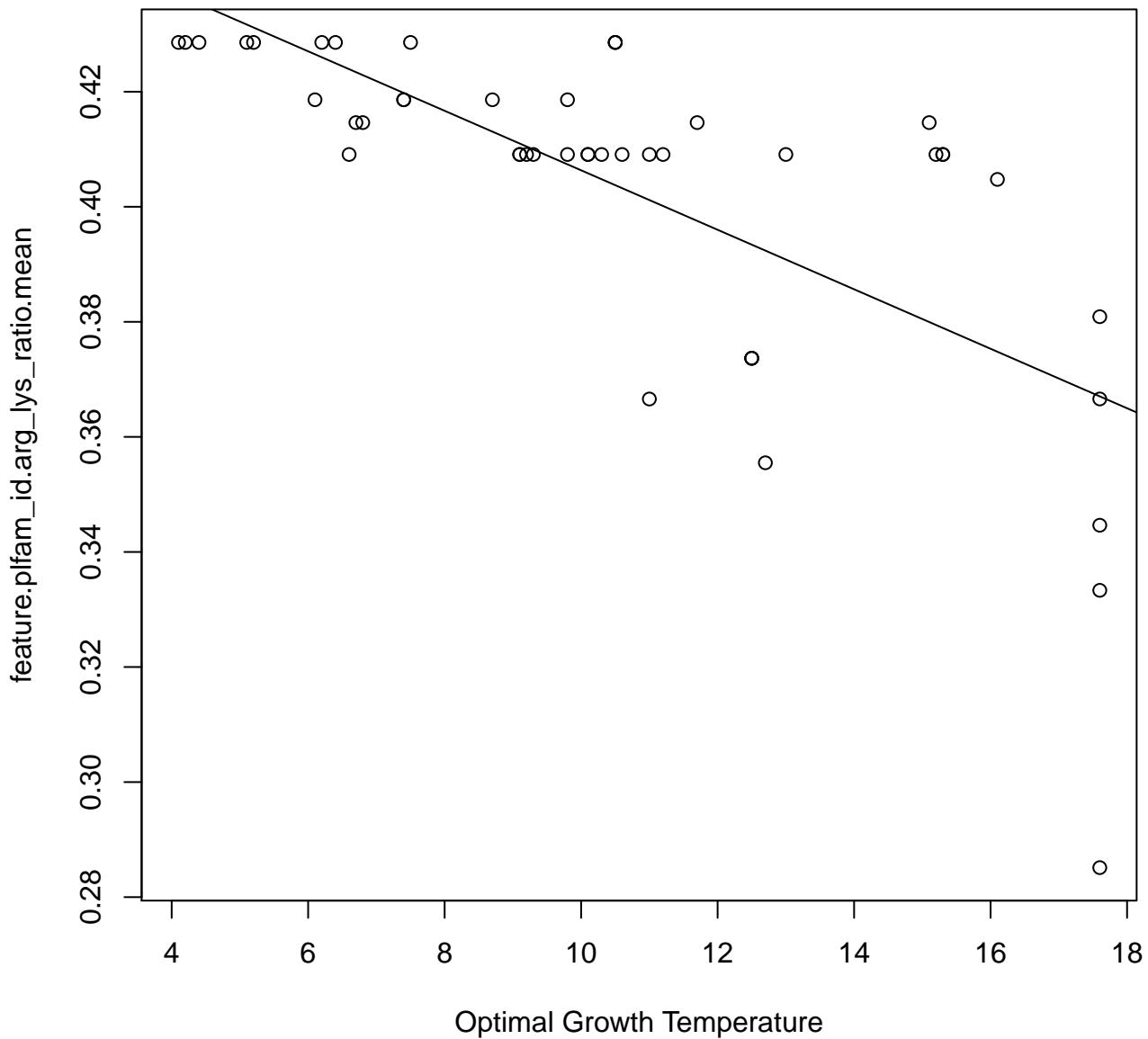
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001343
hypothetical protein



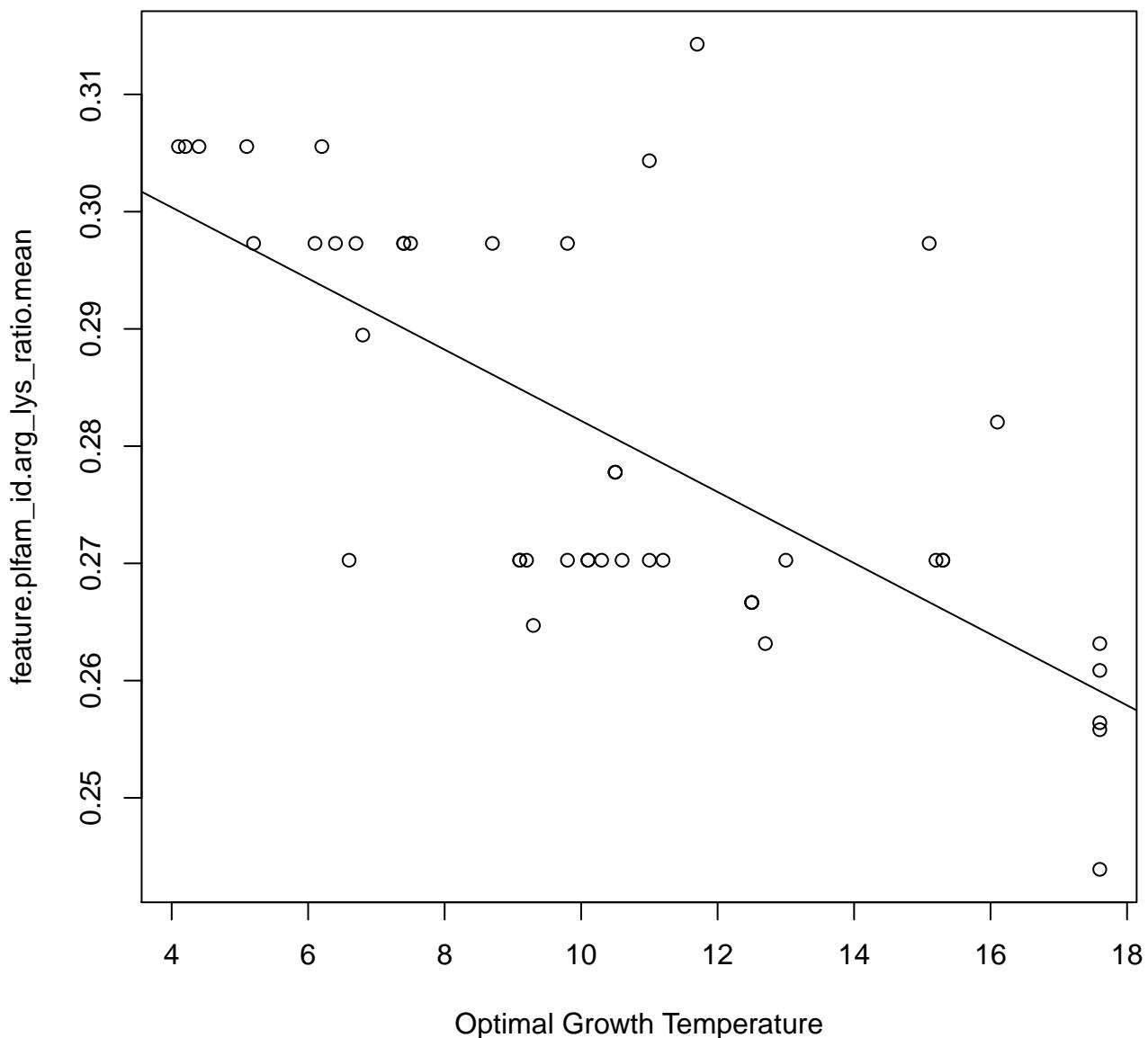
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000801
Ferric iron ABC transporter, permease protein



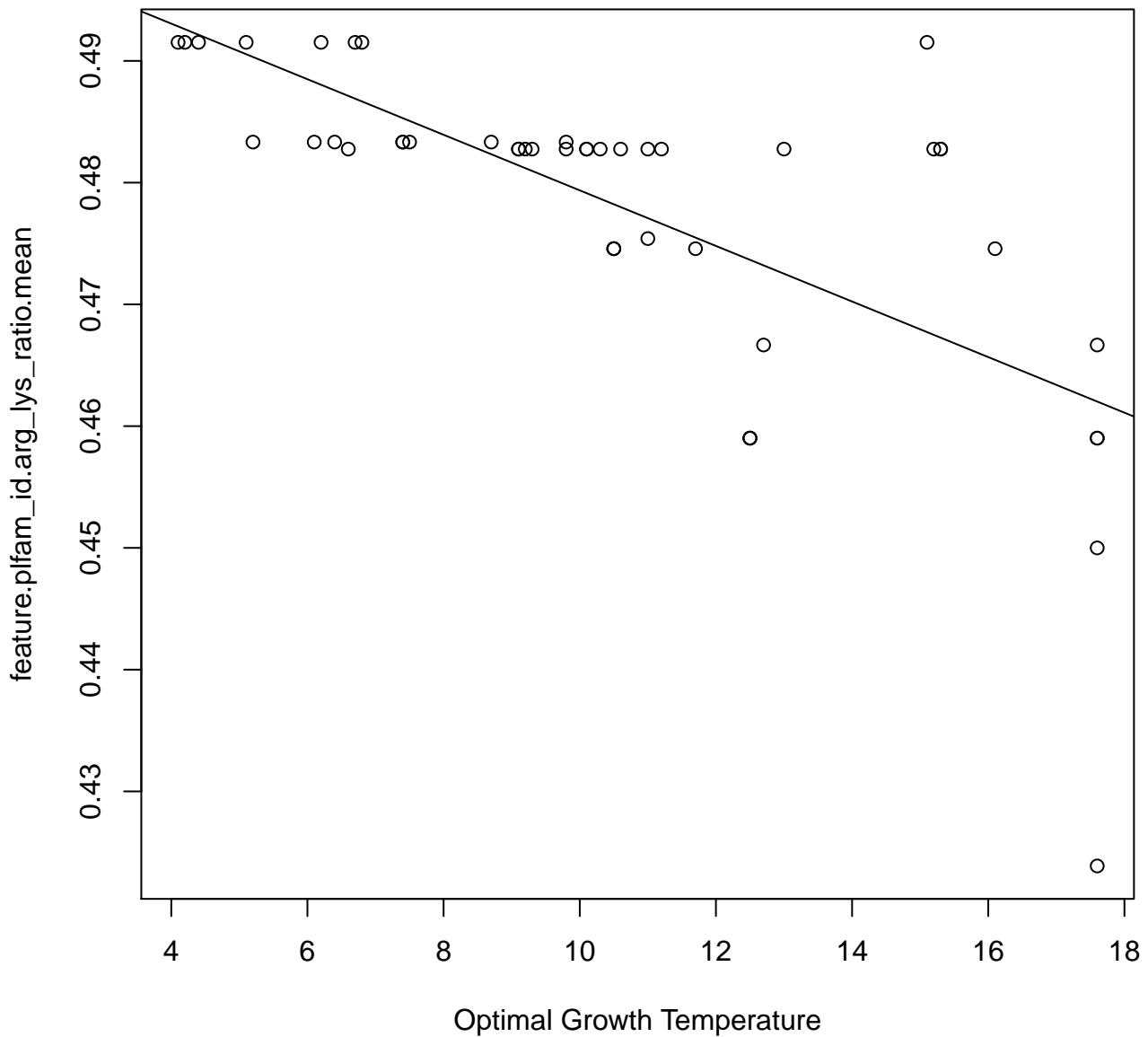
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000010
NADP-dependent malic enzyme (EC 1.1.1.40)



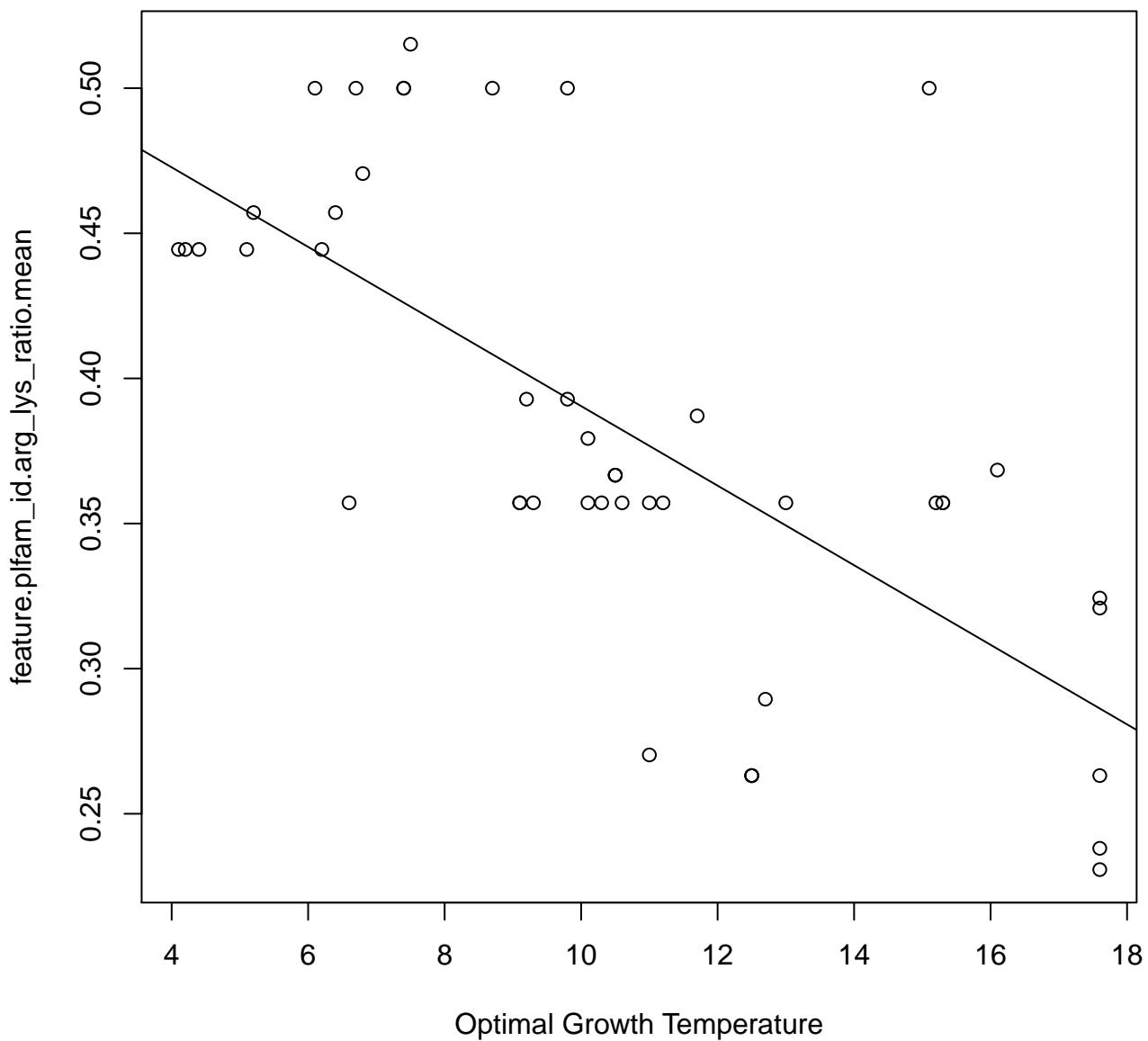
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002251
hypothetical protein



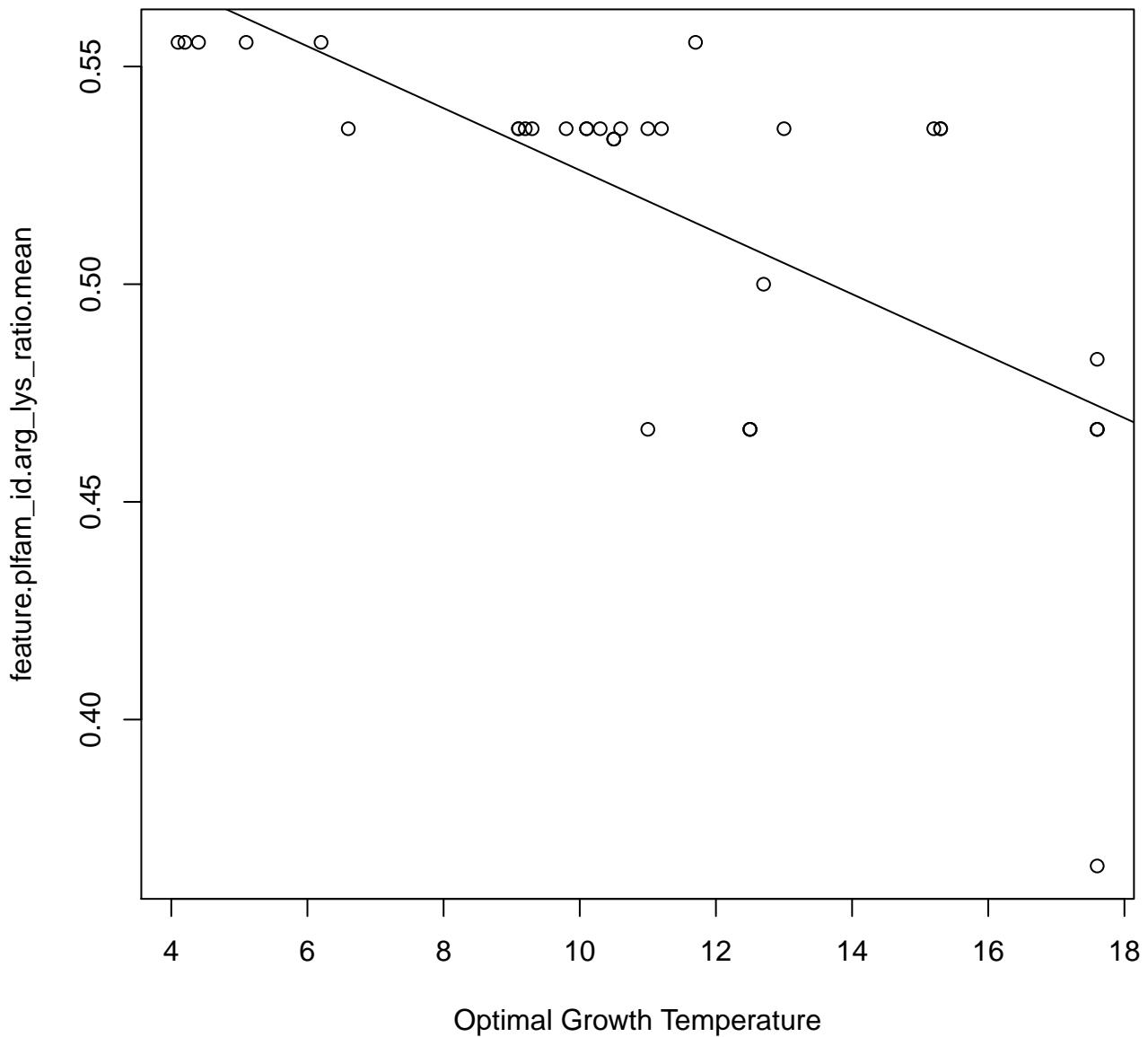
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PLF_28228_00000285
ATP-dependent hsl protease ATP-binding subunit HslU



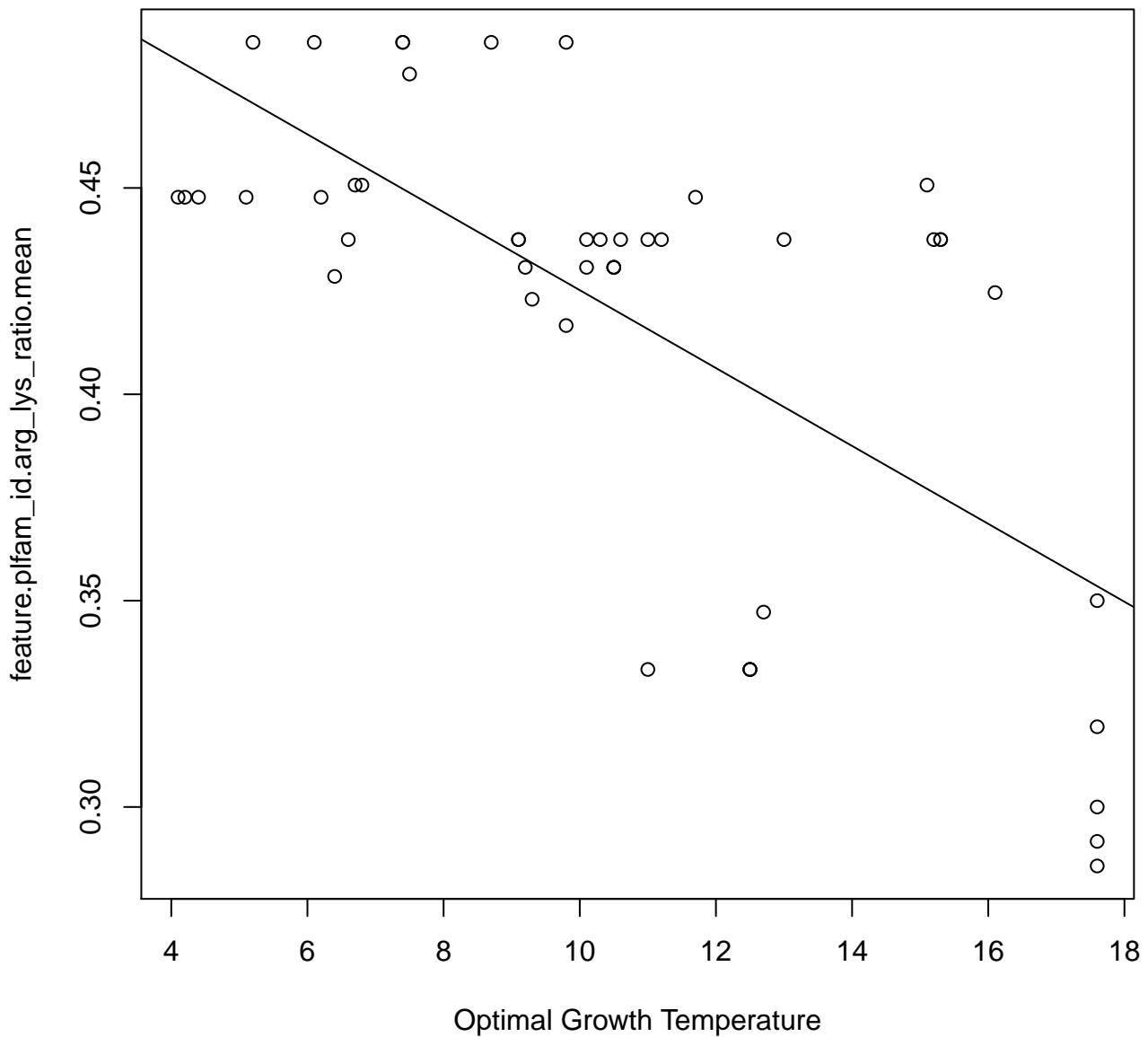
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PLF_28228_00001134
Septum-associated rare lipoprotein A



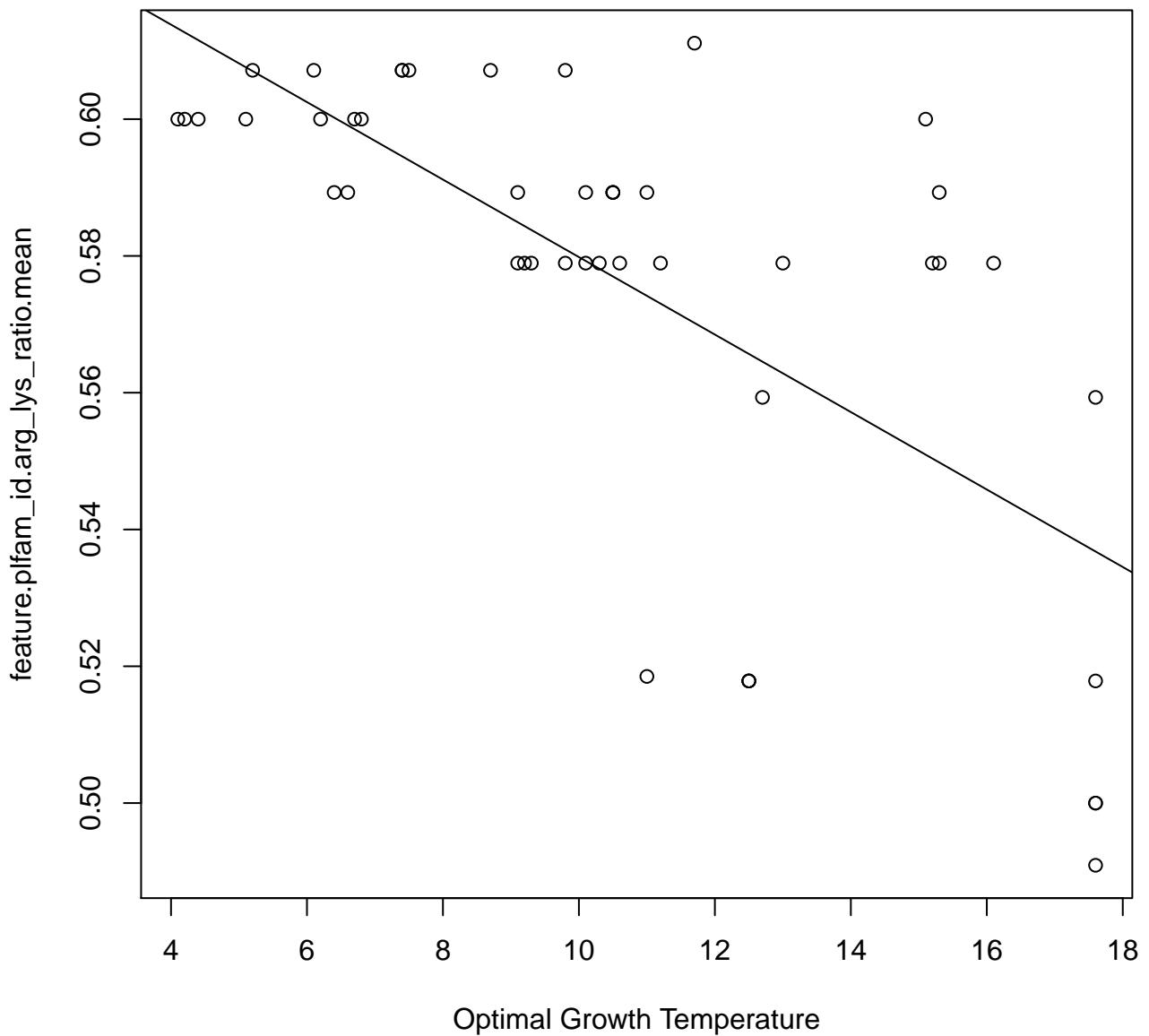
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PLF_28228_00000776
Two-component transcriptional response regulator, OmpR family



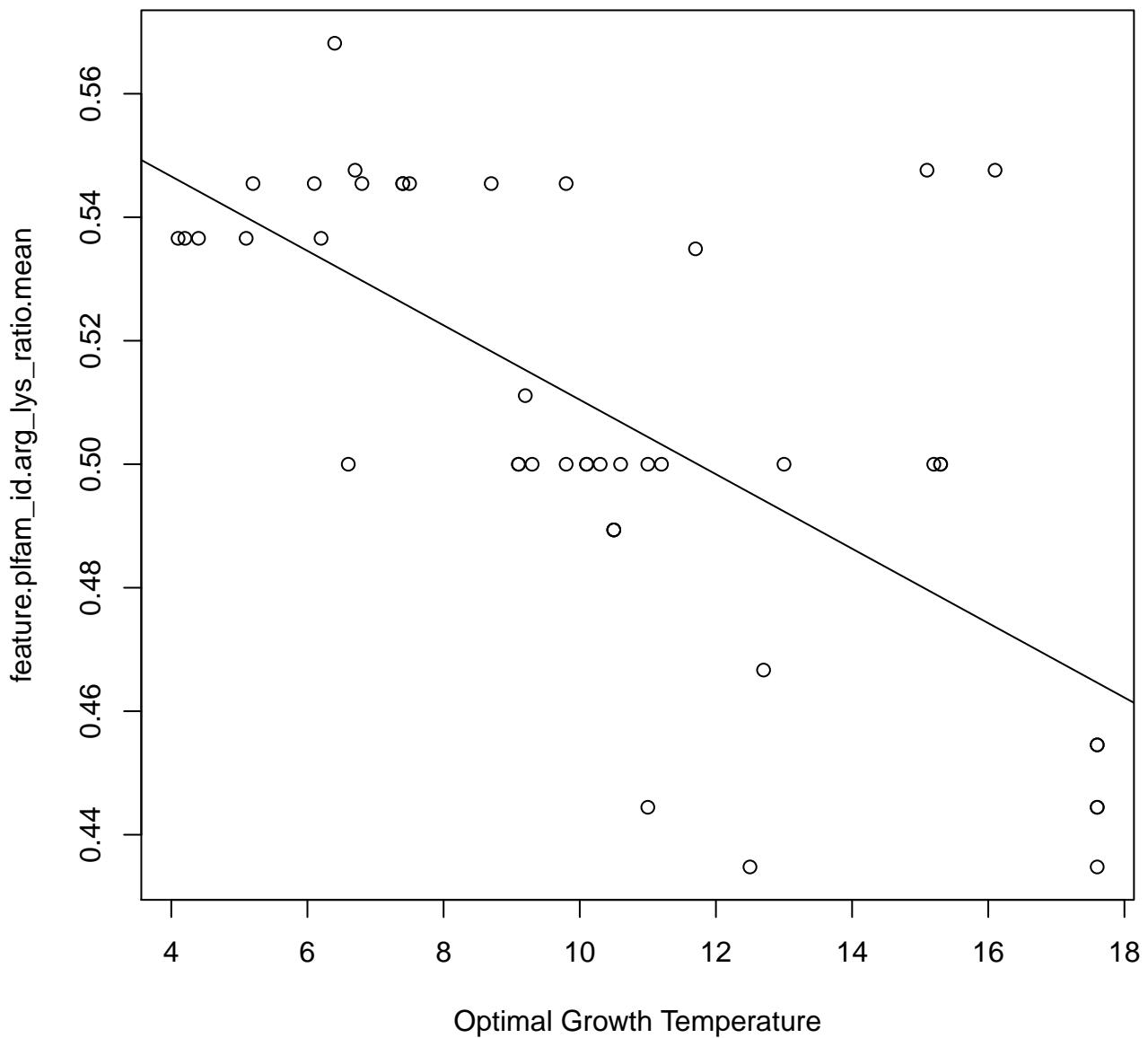
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PLF_28228_00000633
N-acetyl muramoyl-L-alanine amidase (EC 3.5.1.28)



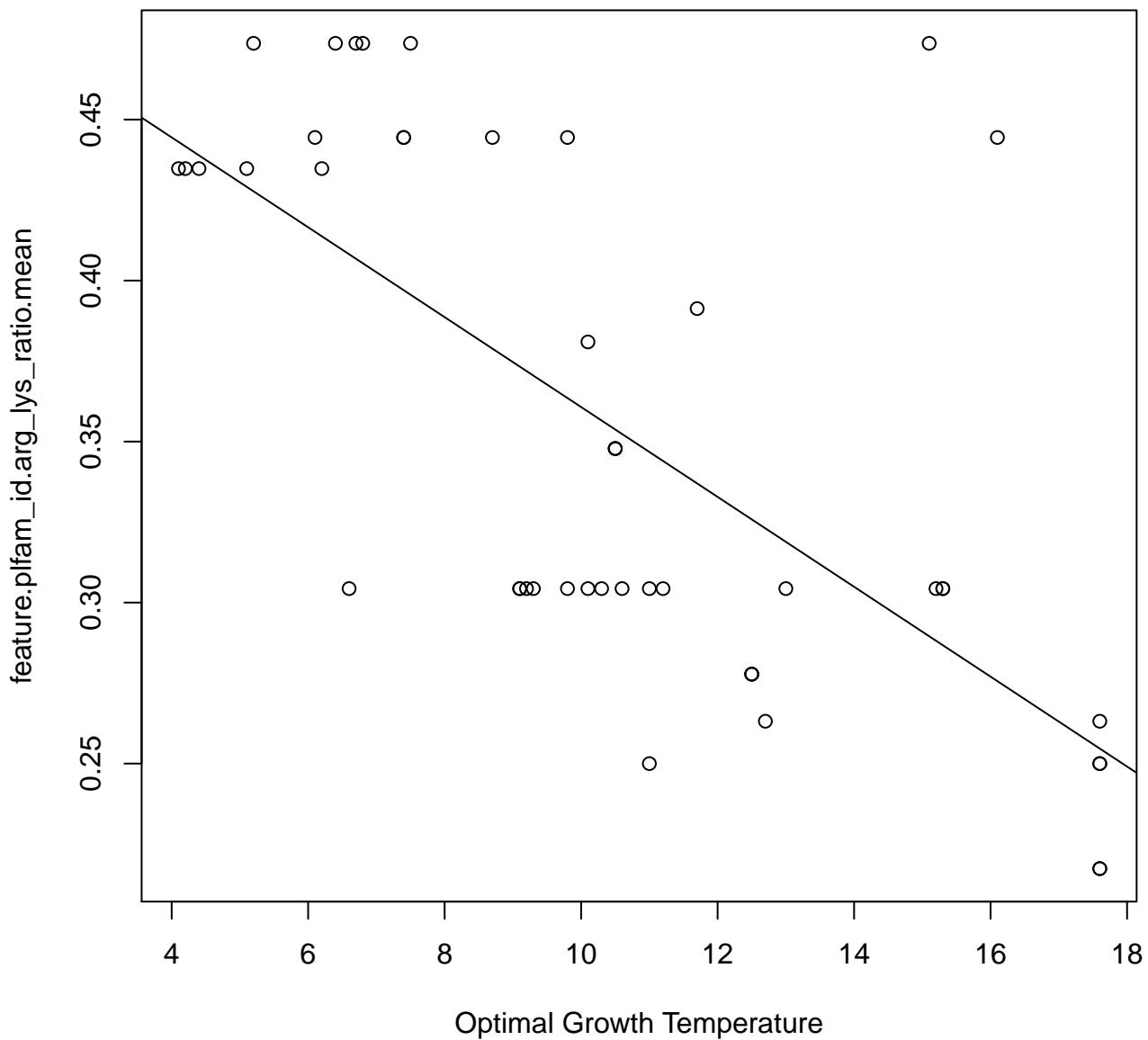
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Inner membrane protein, KefB/KefC family



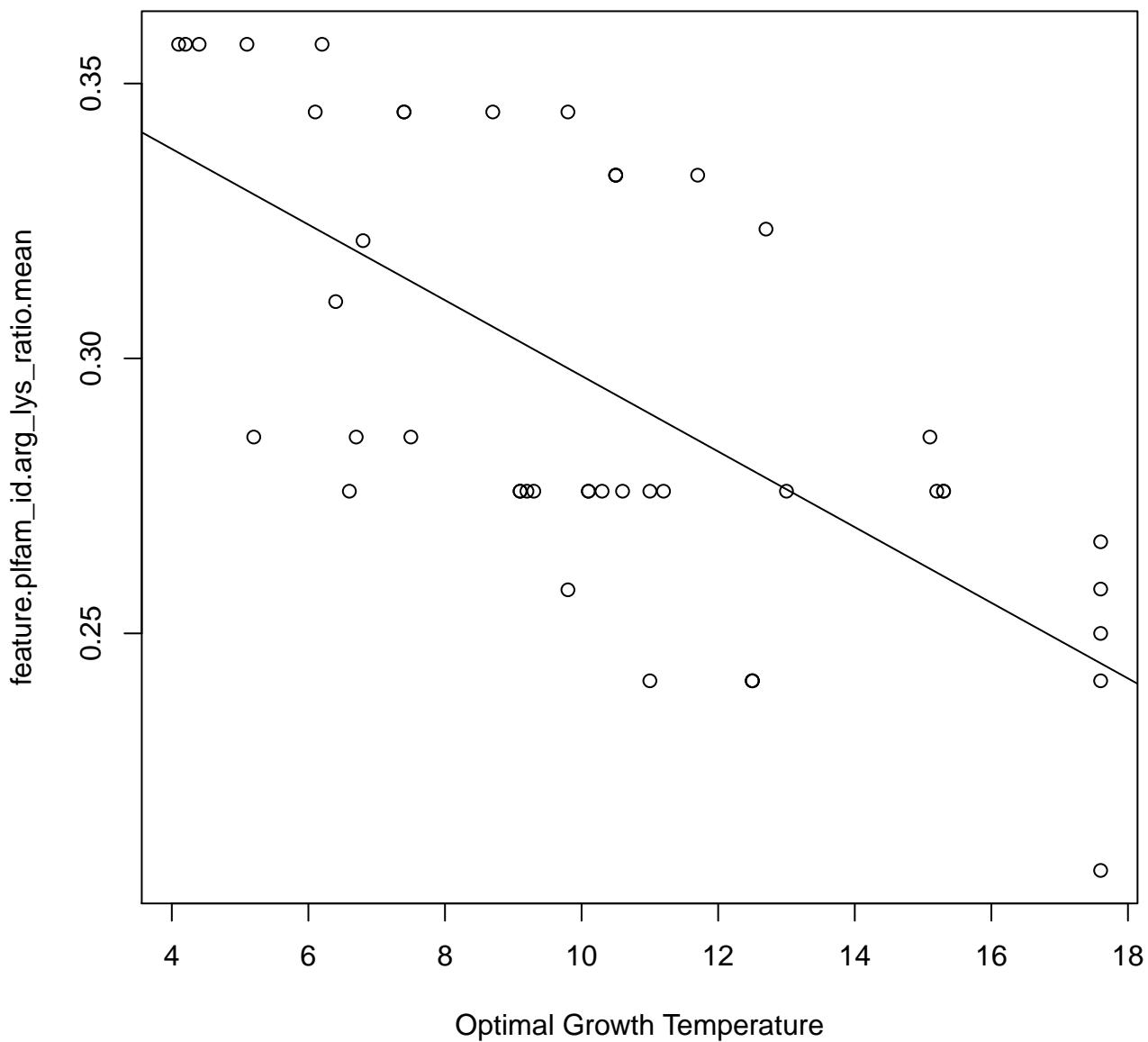
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Cell division protein ZapE



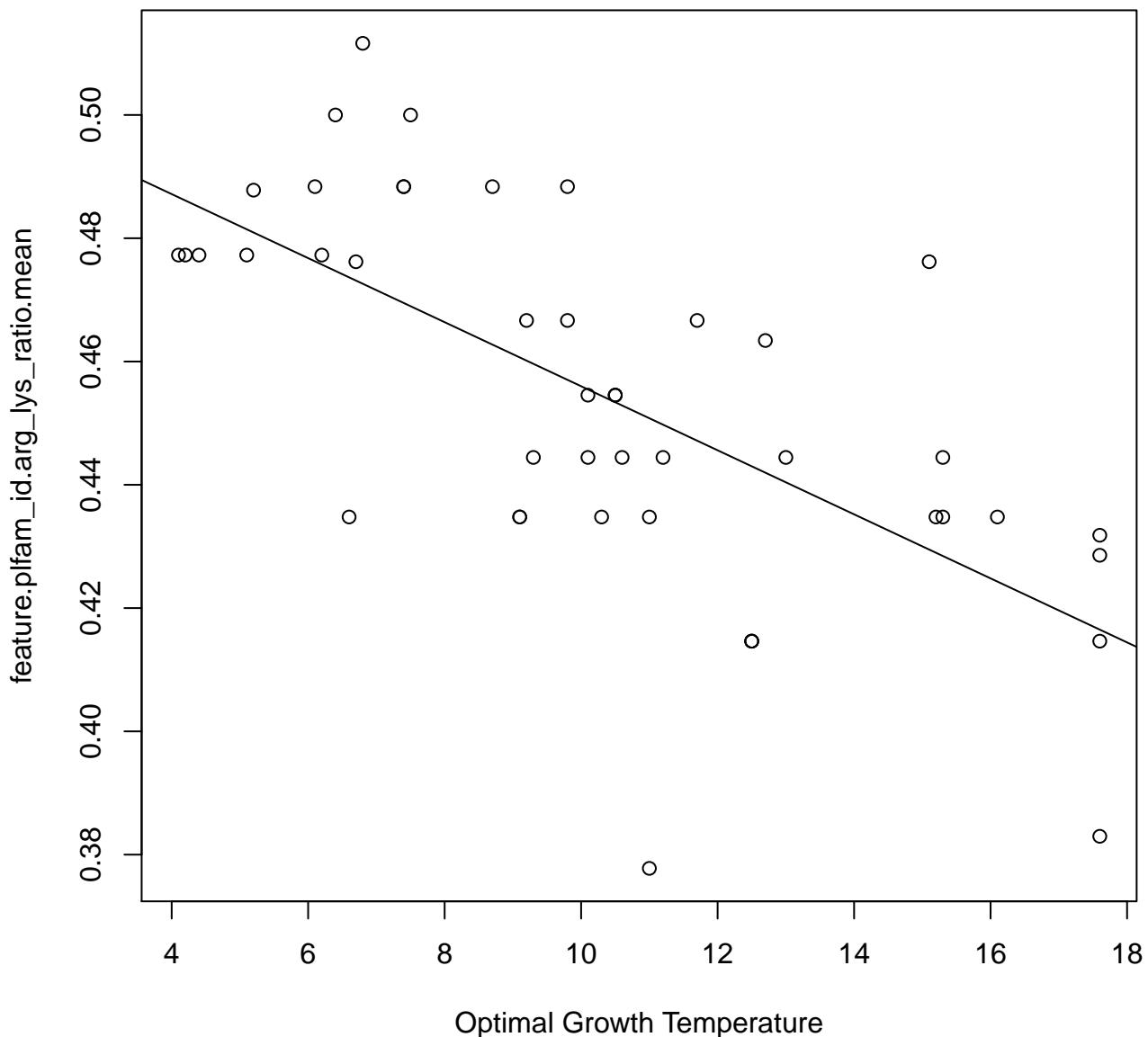
feature.plfam_id.arg_lys_ratio.mean
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33 kDa chaperonin HsIO



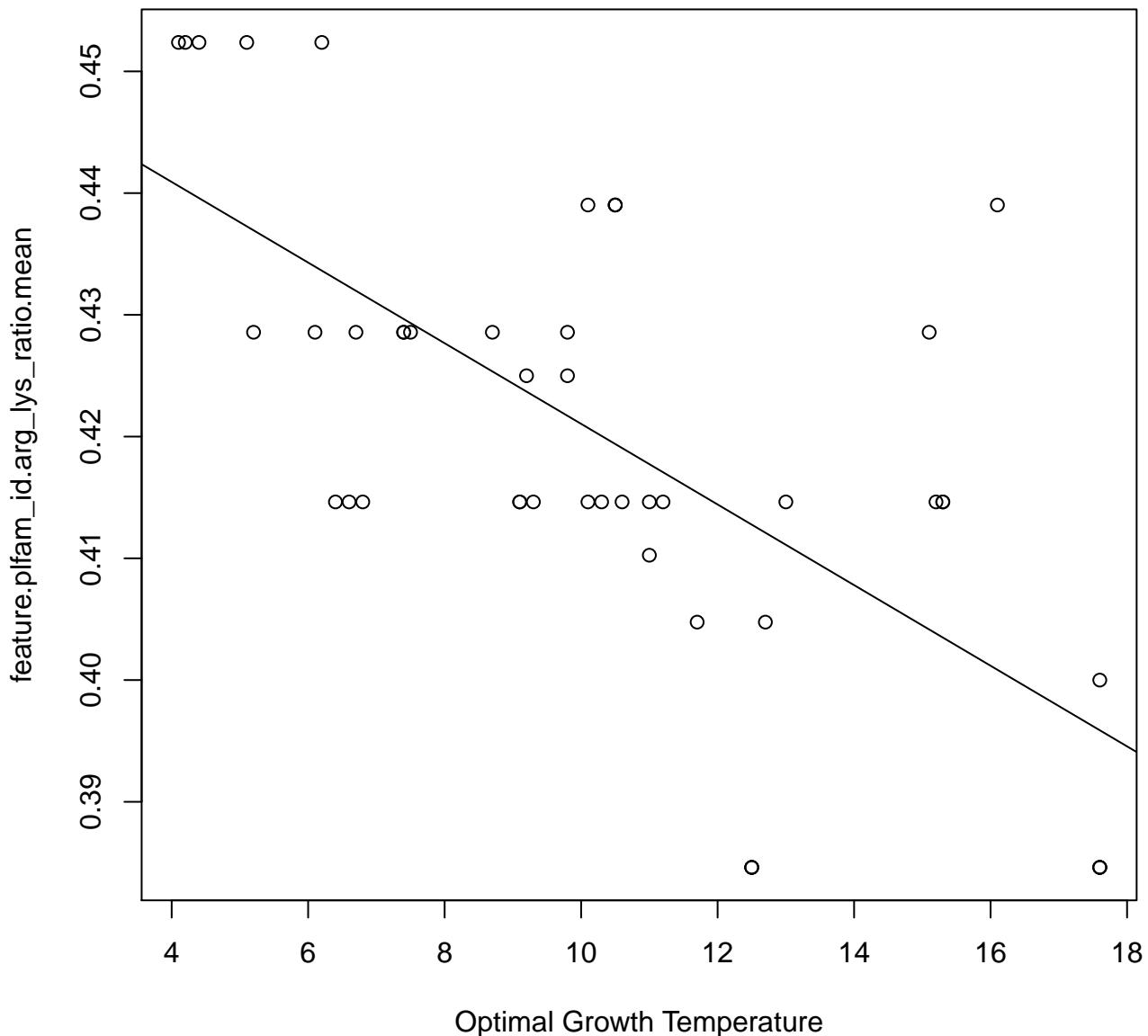
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PLF_28228_00001366
hypothetical protein



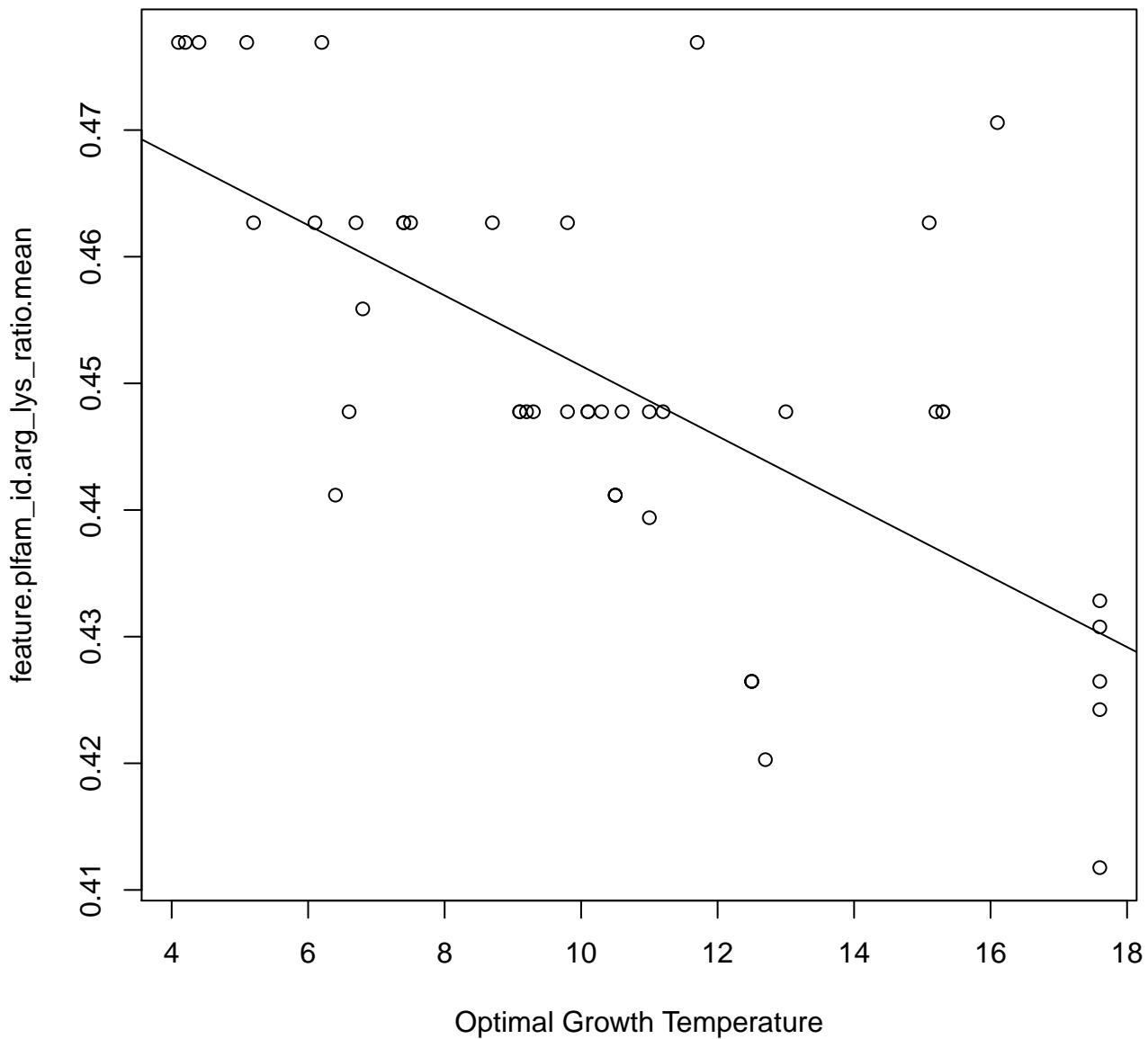
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000141
RND efflux system, membrane fusion protein



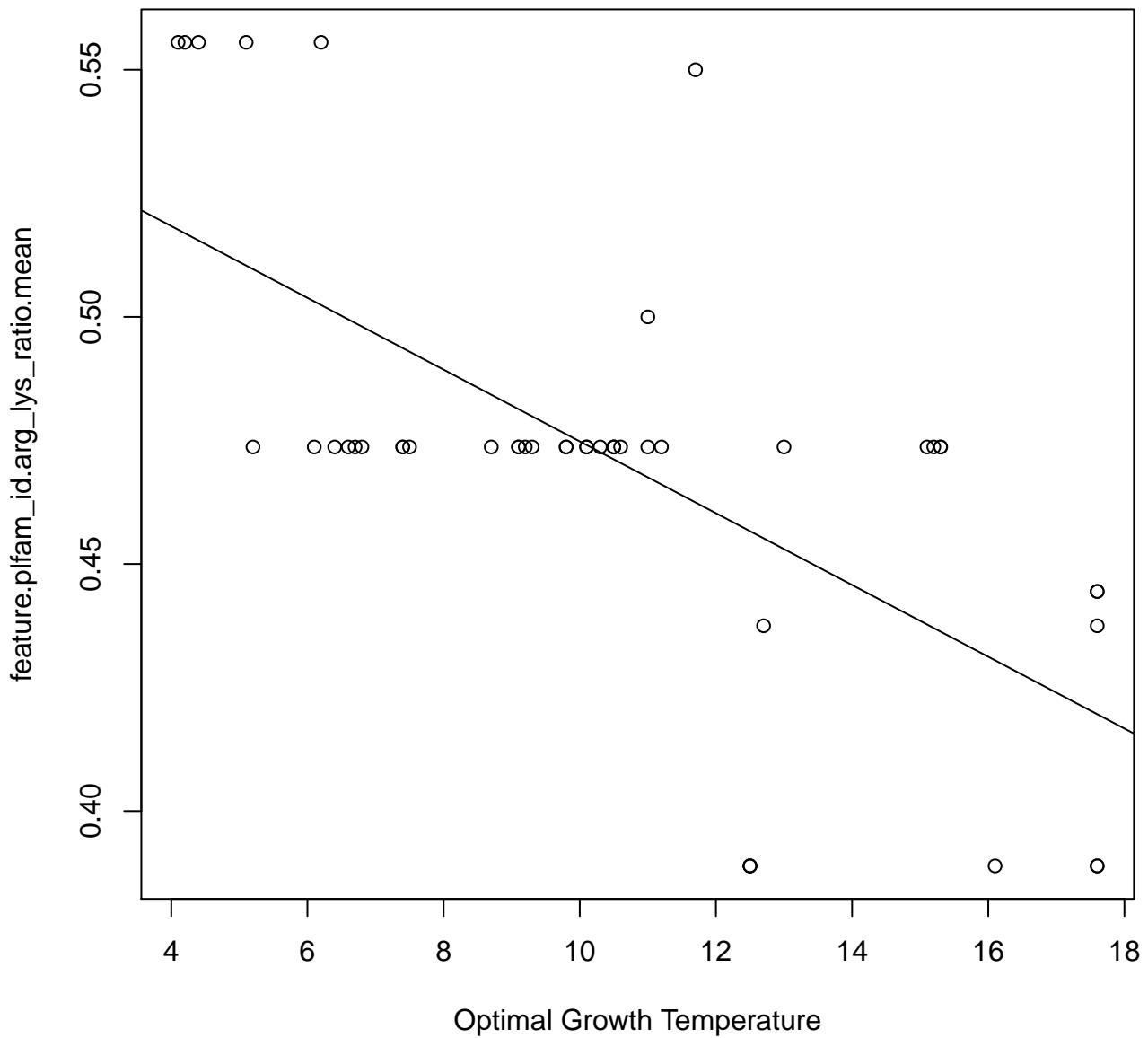
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PLF_28228_00000375
Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)



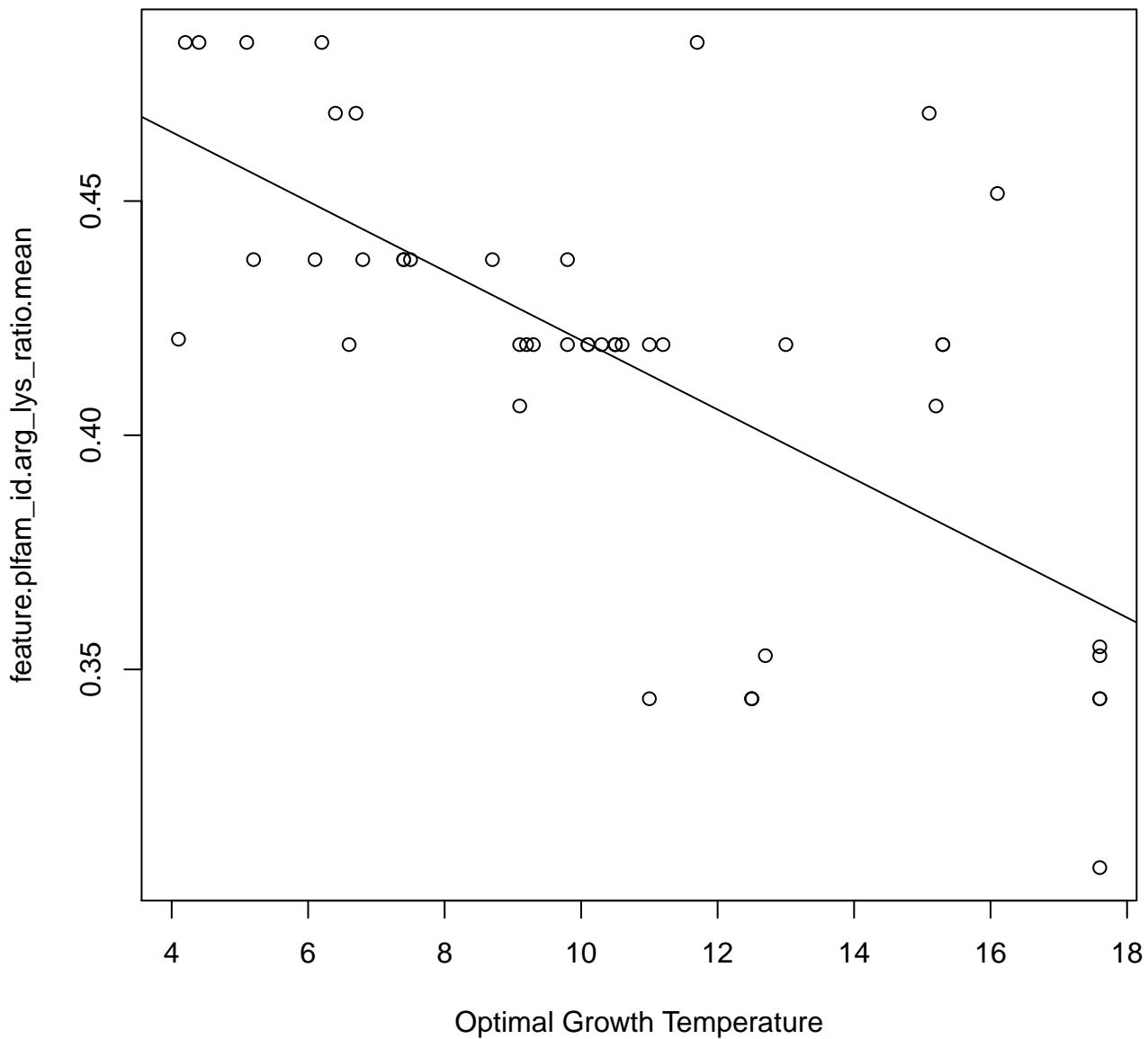
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PLF_28228_00000921
Peptide chain release factor 3



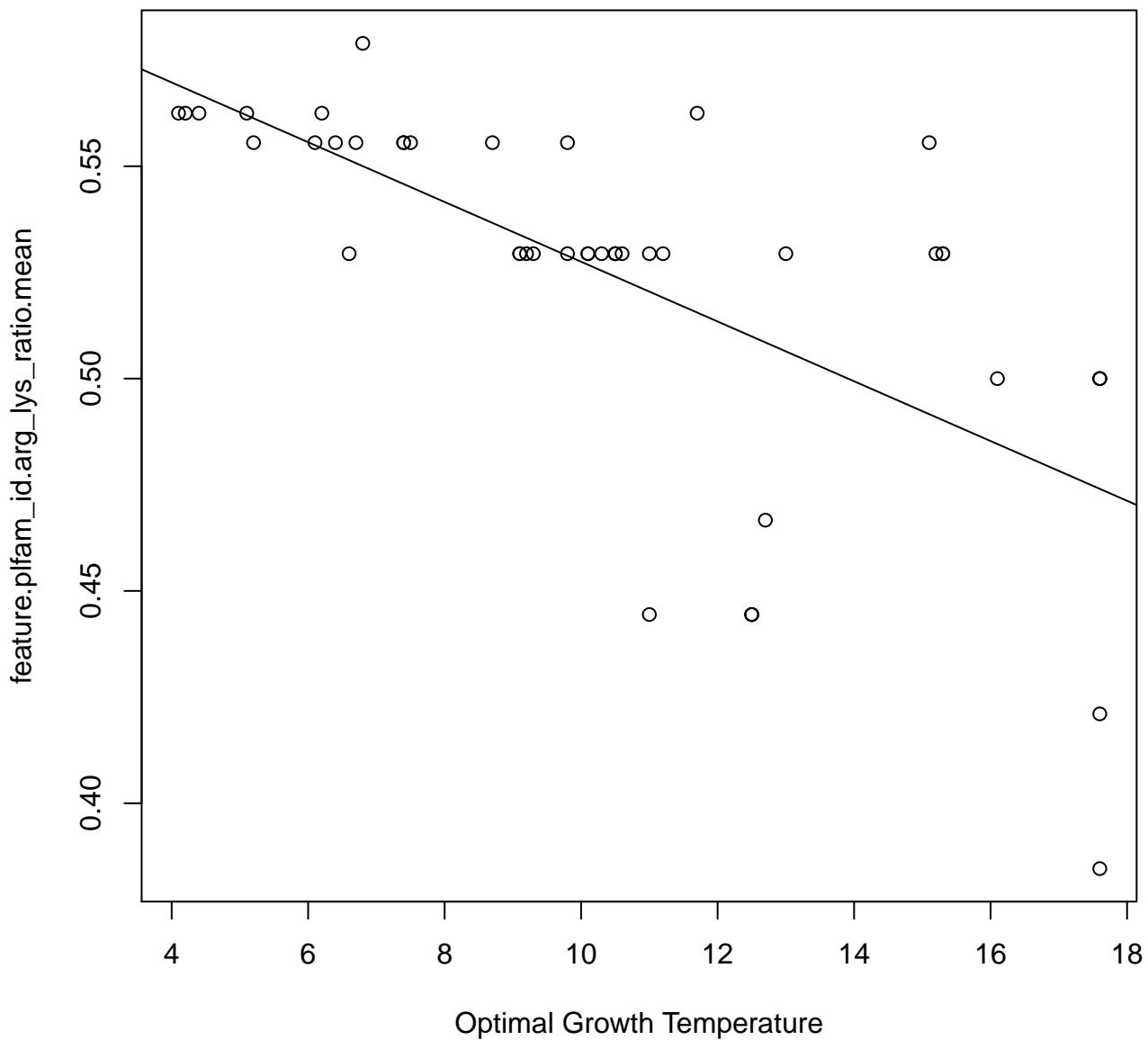
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000522
Inner membrane protein YrbG, predicted calcium/sodium:proton antiporter



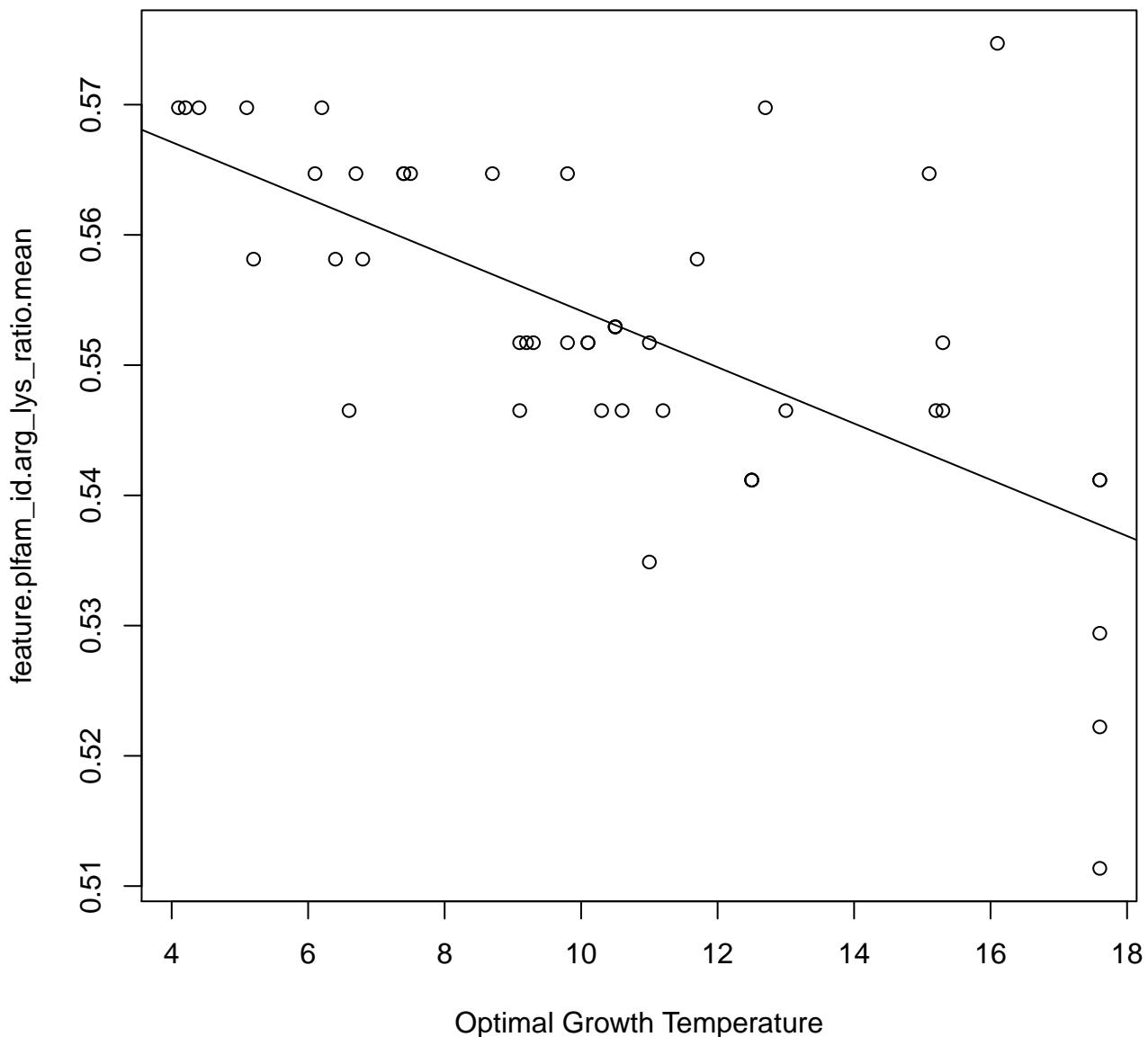
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000536
Isocitrate dehydrogenase [NAD] (EC 1.1.1.41)



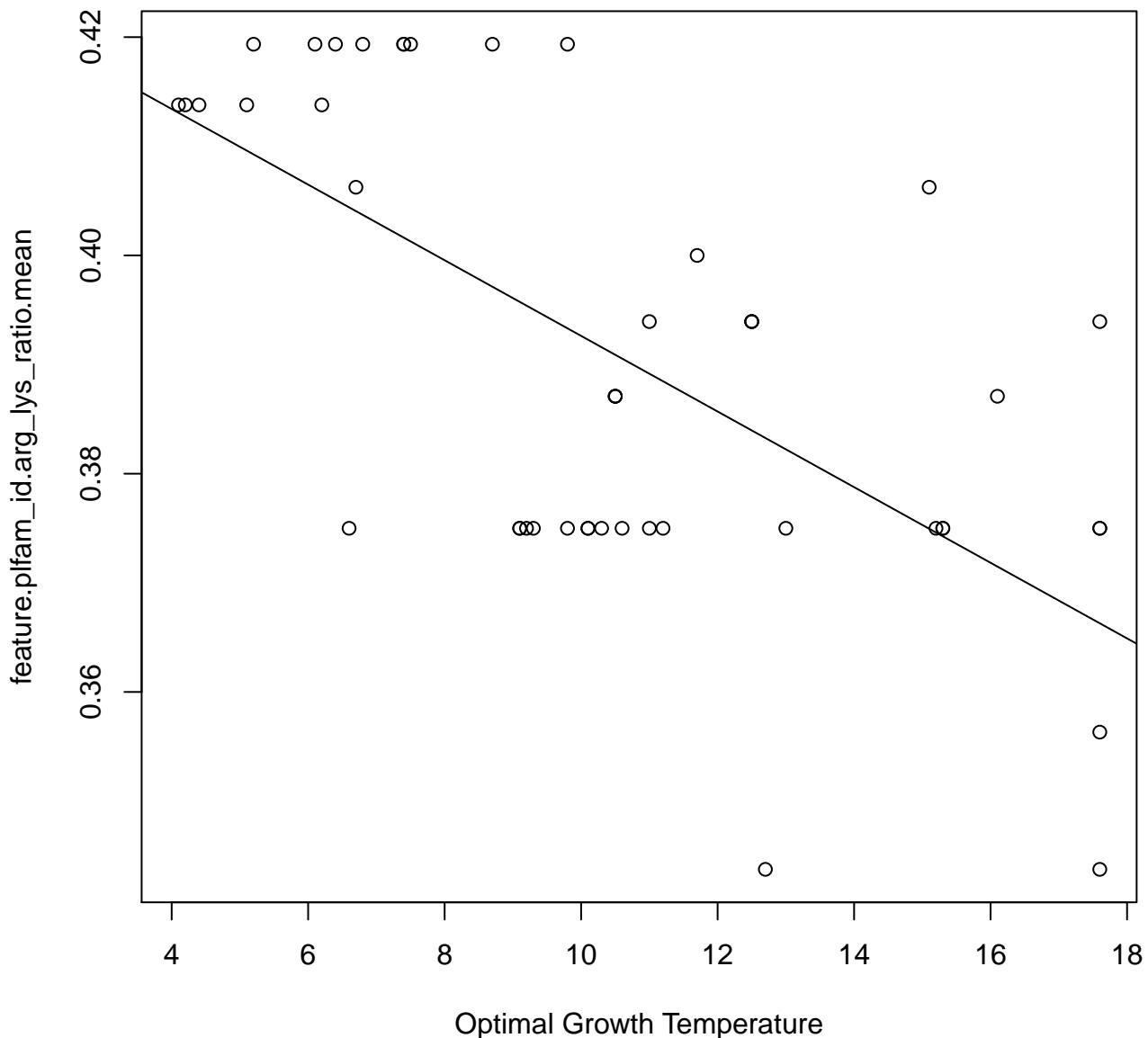
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PLF_28228_00002263
hypothetical protein



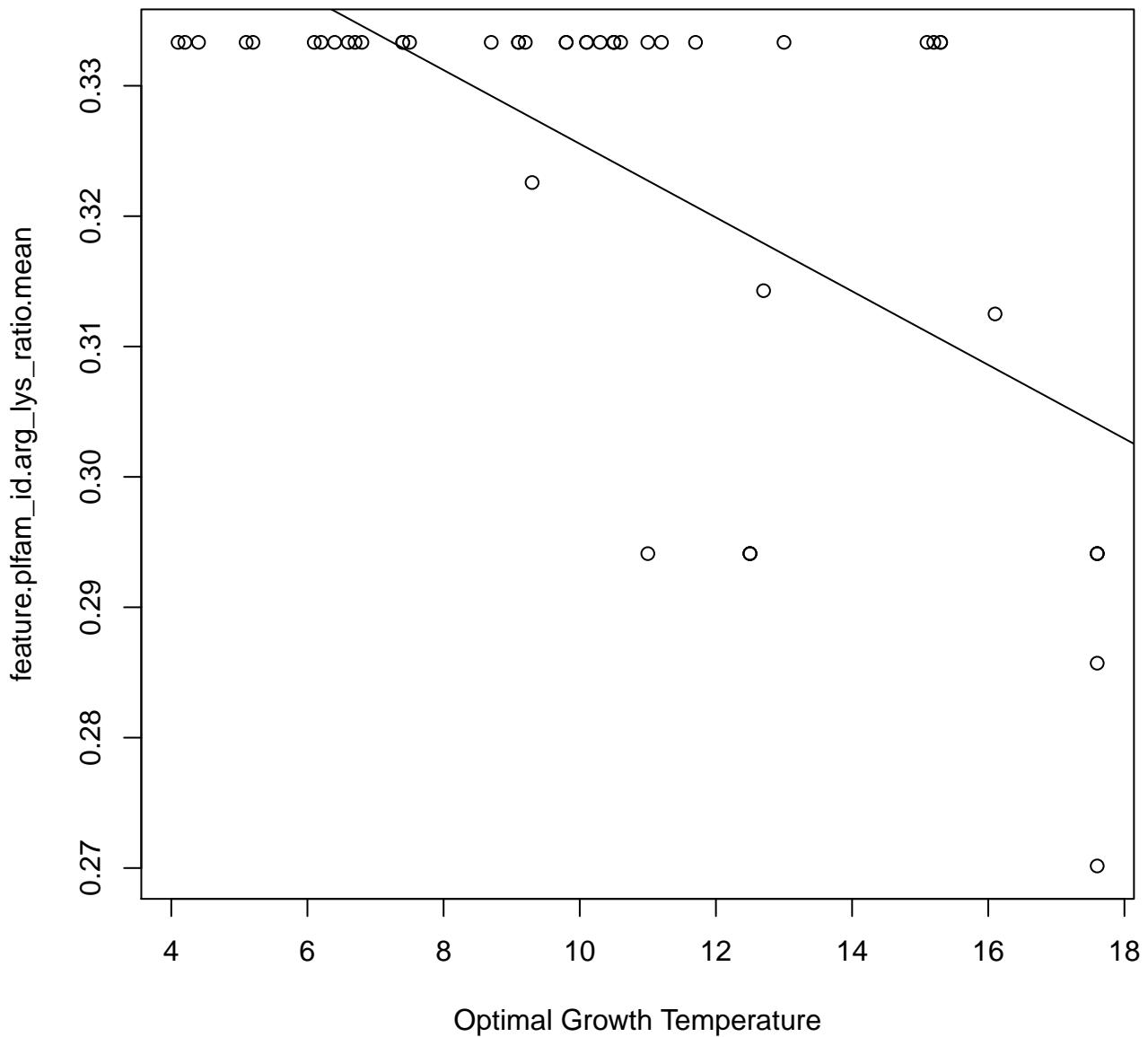
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PLF_28228_00000458
DNA mismatch repair protein MutS



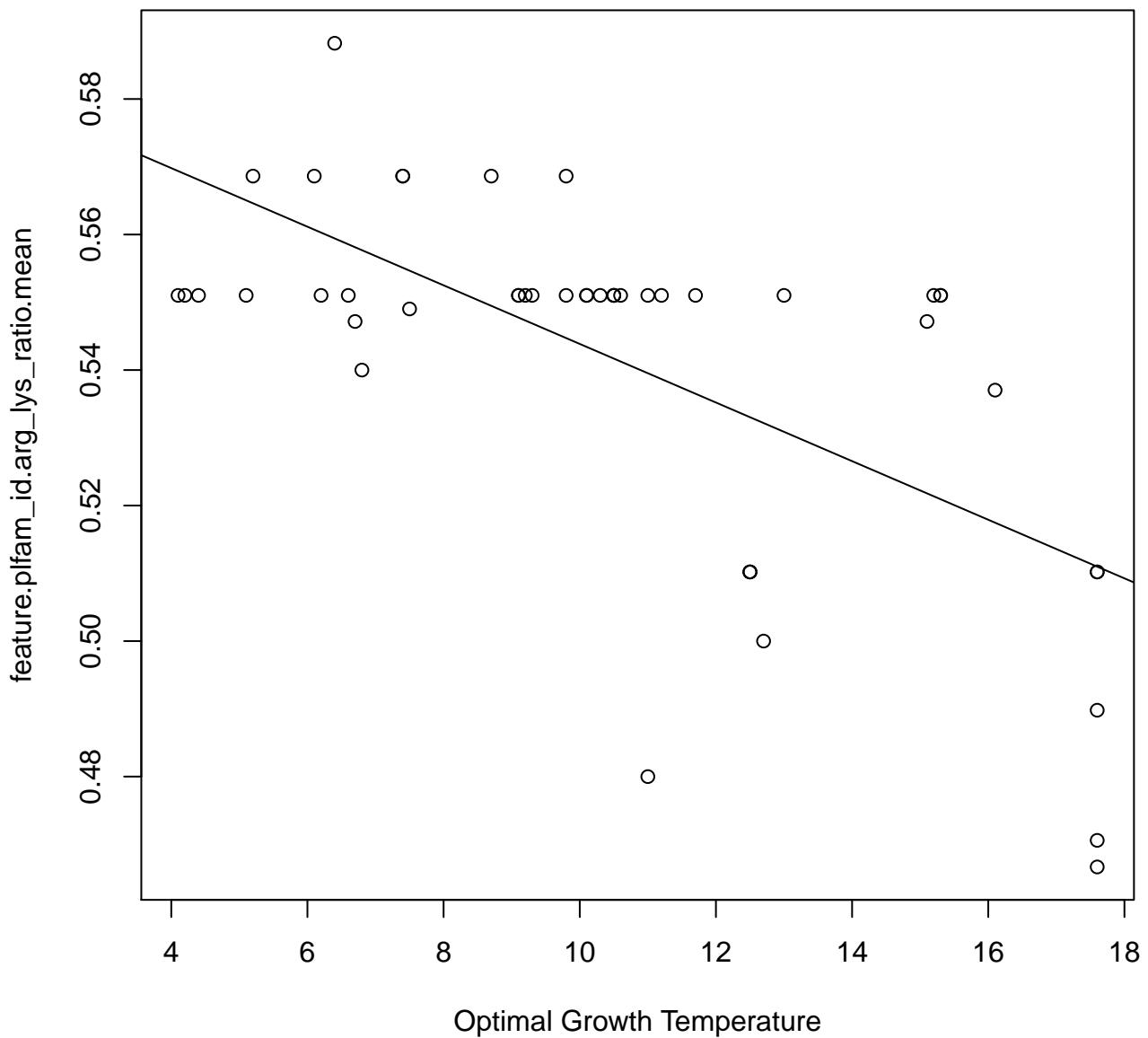
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L-threonine 3-dehydrogenase (EC 1.1.1.103)



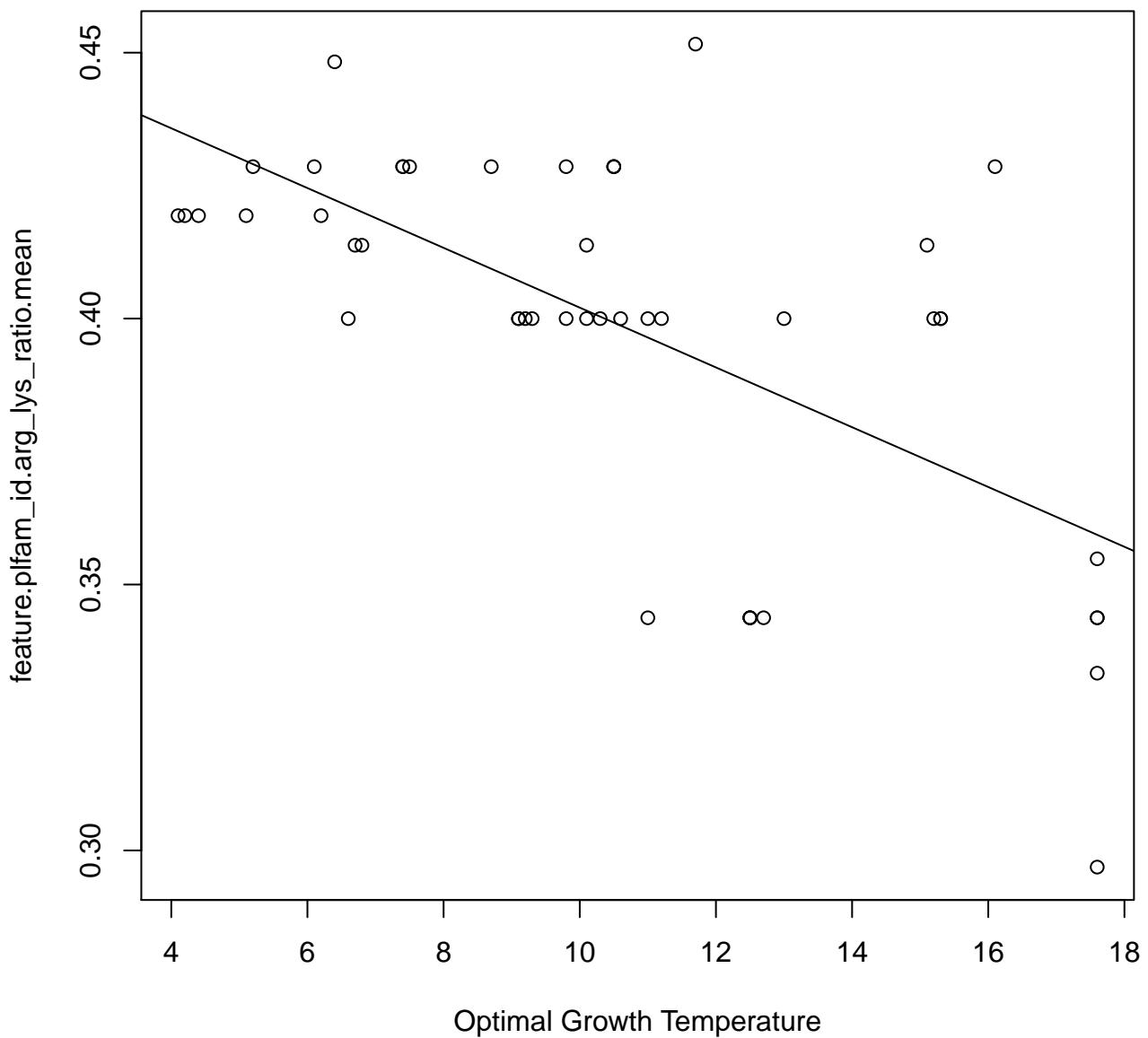
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001624
DNA recombination-dependent growth factor RdgC



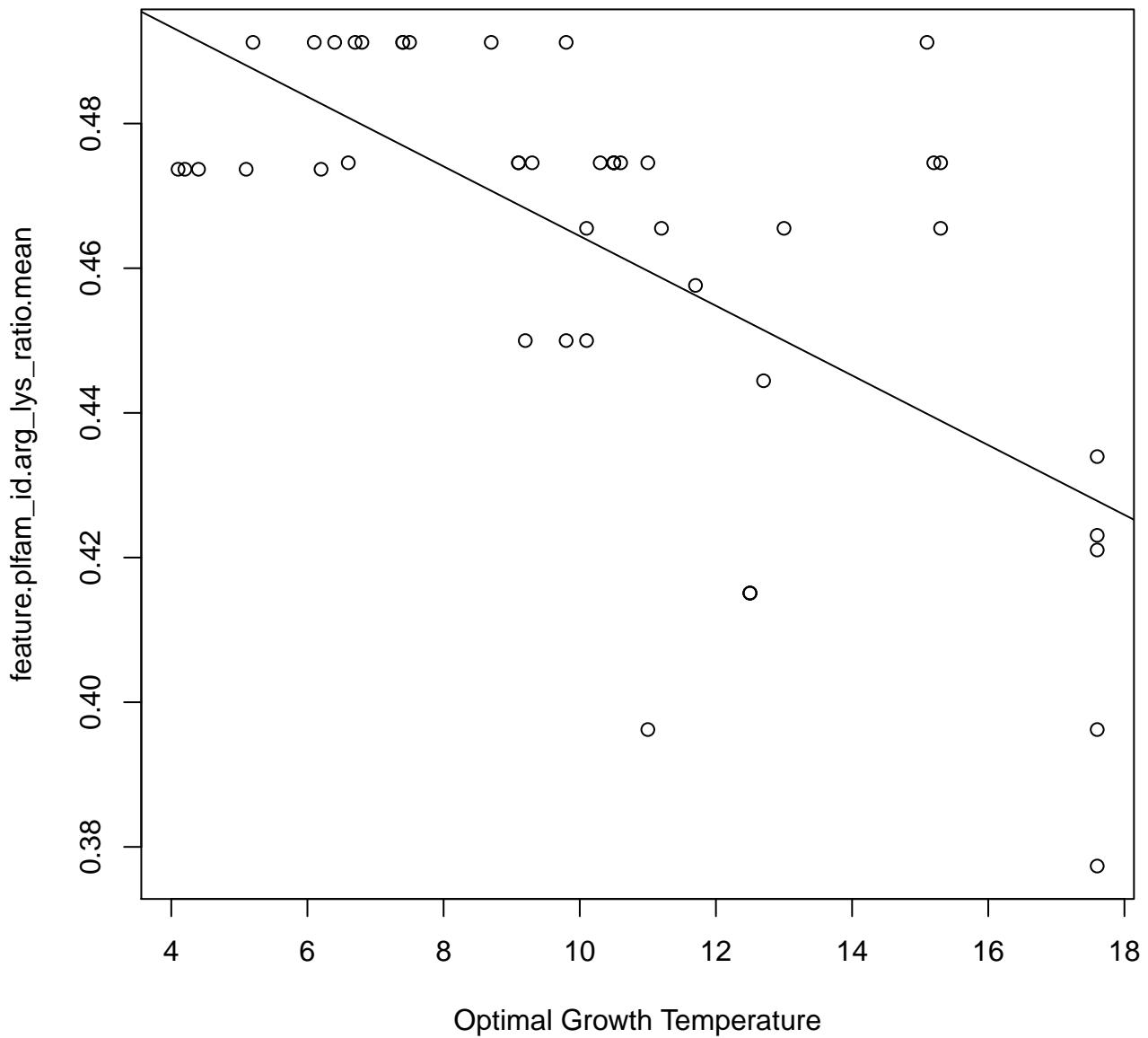
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000848
Flagellar regulatory protein FleQ



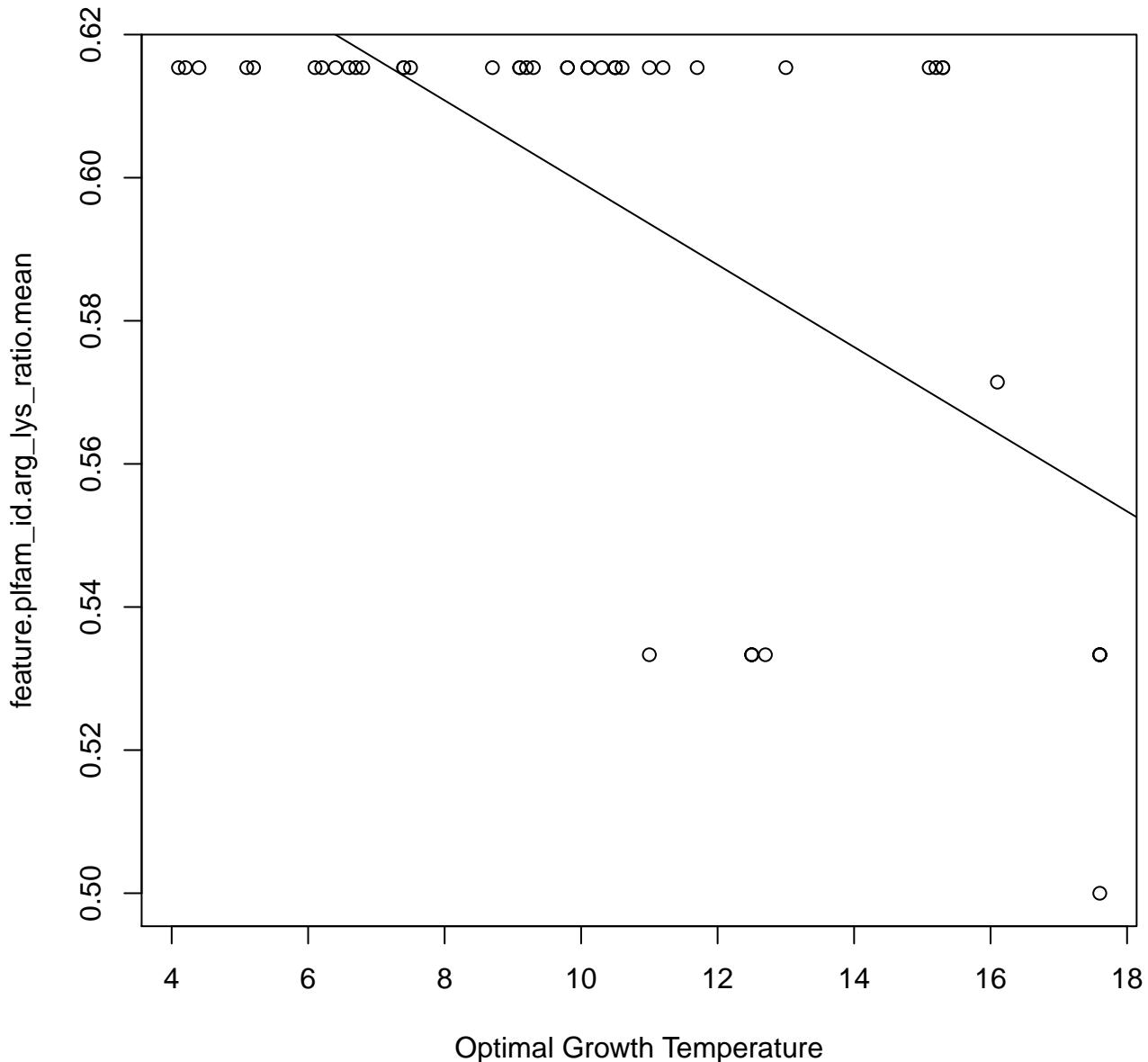
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001174
Sulfate permease



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001635
DNA-binding transcriptional regulator, MocR family / aminotransferase domain



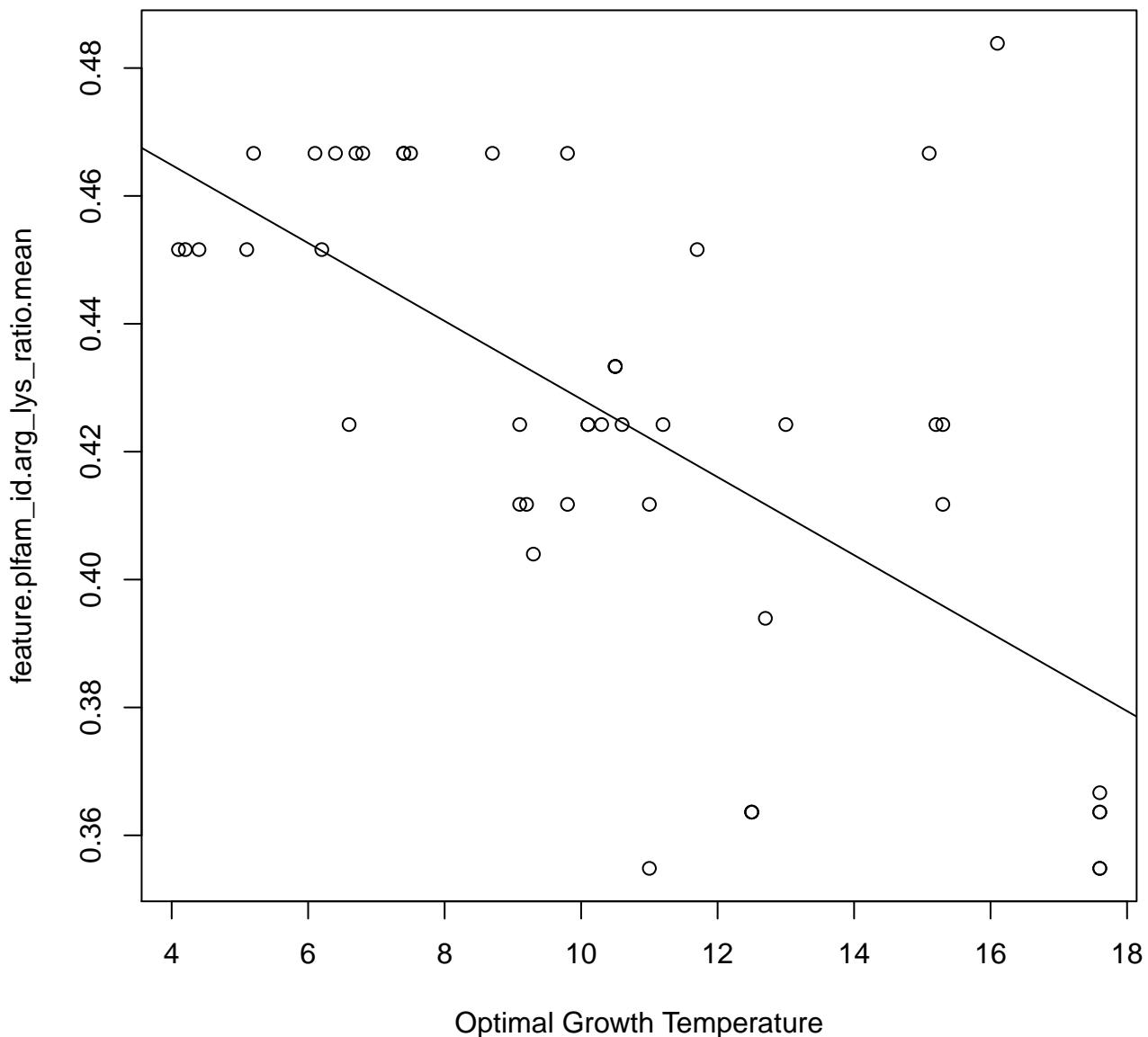
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000963
Phospholipid ABC transporter permease protein MlaE



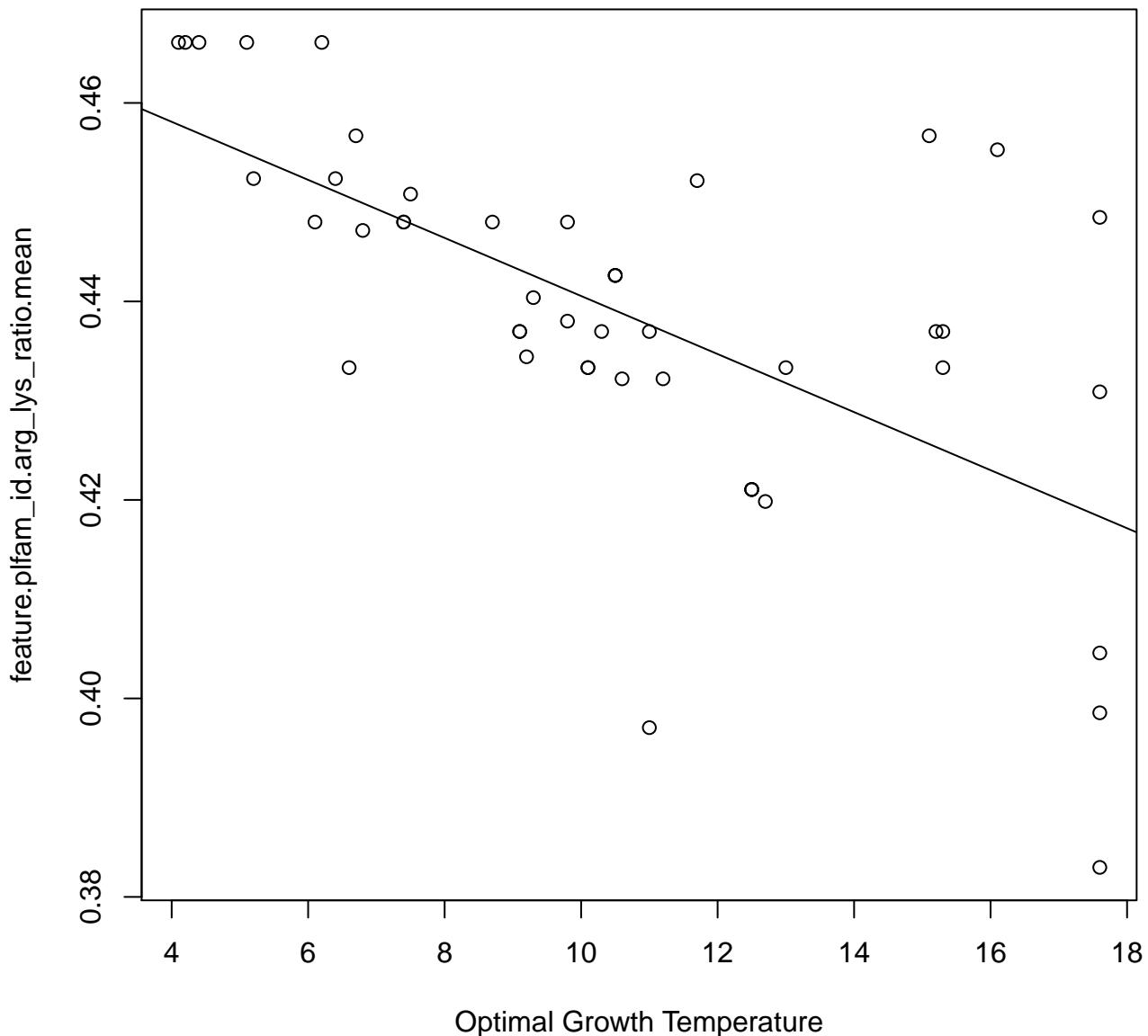
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000340

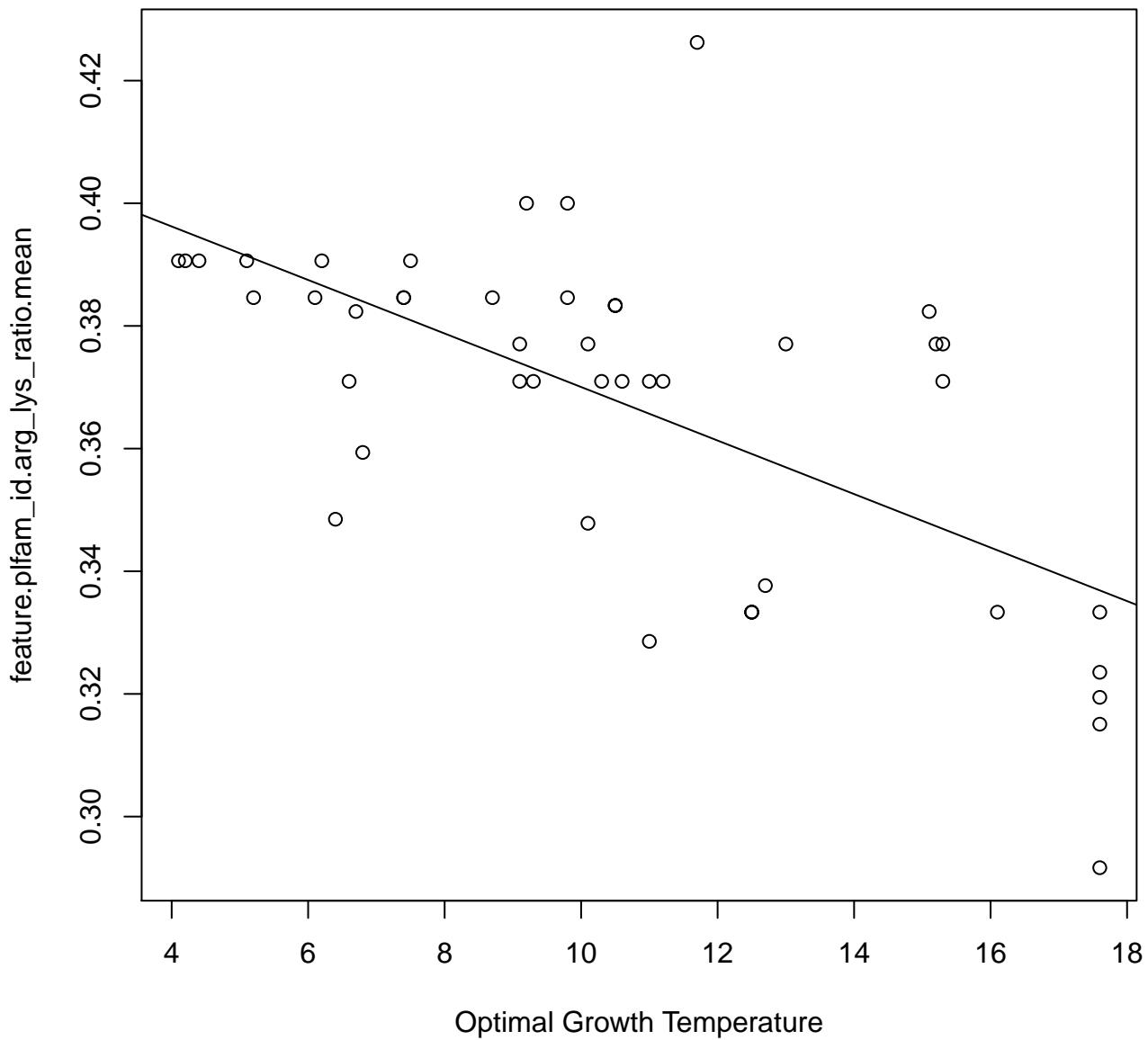
FIG00031715: Predicted metal-dependent phosphoesterases (PHP family)



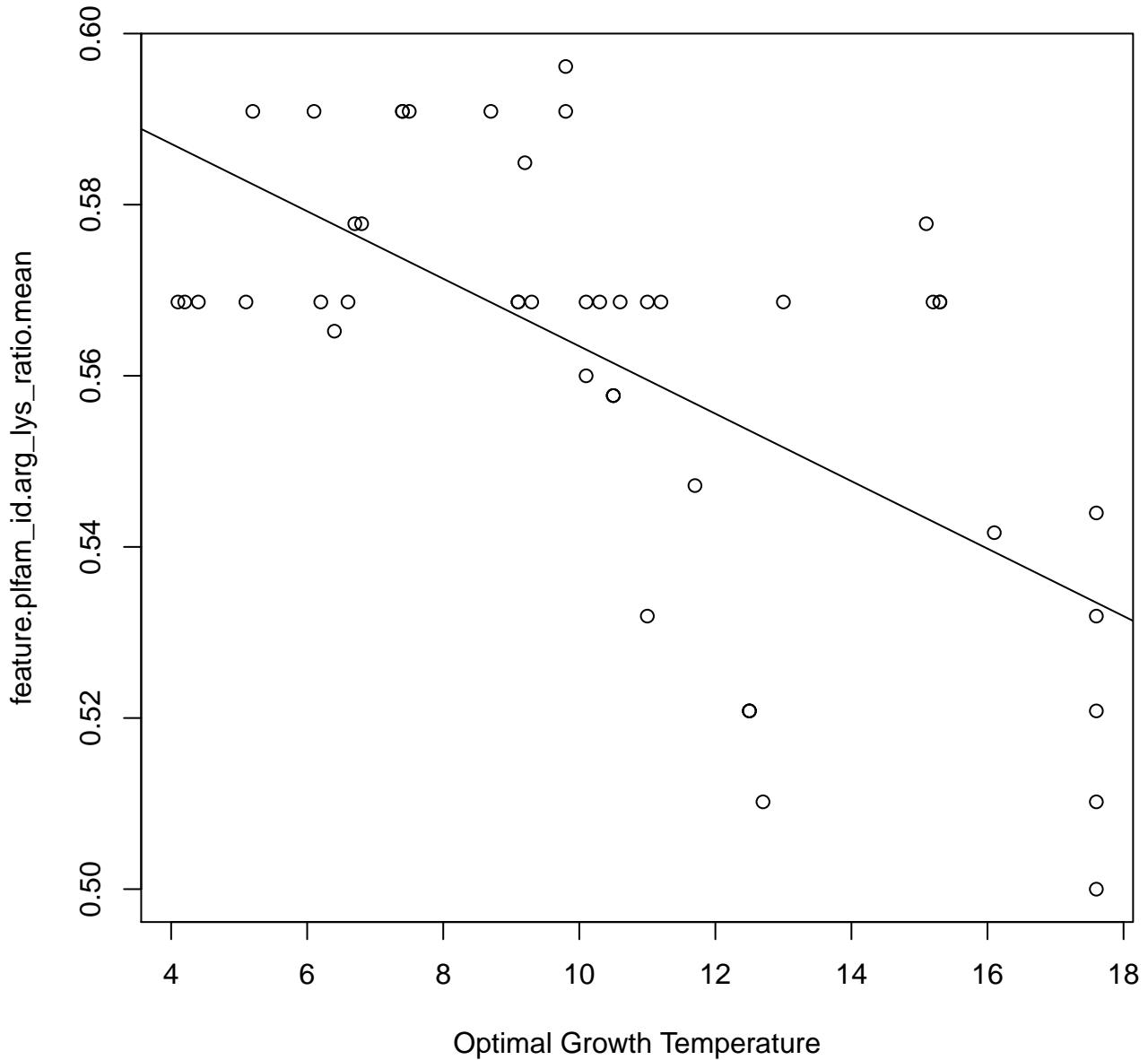
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000333
Exodeoxyribonuclease V beta chain (EC 3.1.11.5)



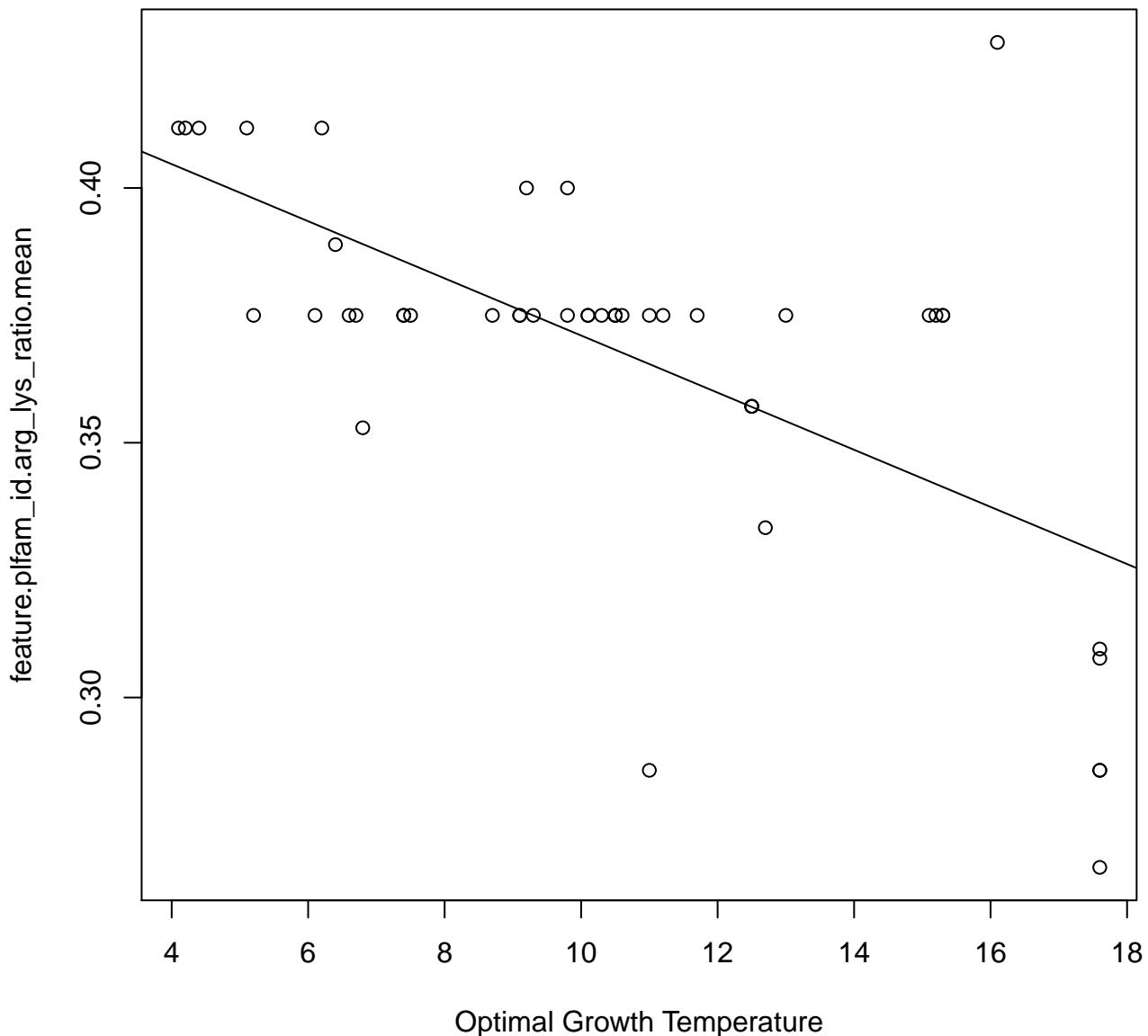
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002007
Regulatory sensor-transducer, BlaR1/MecR1 family / TonB family protein



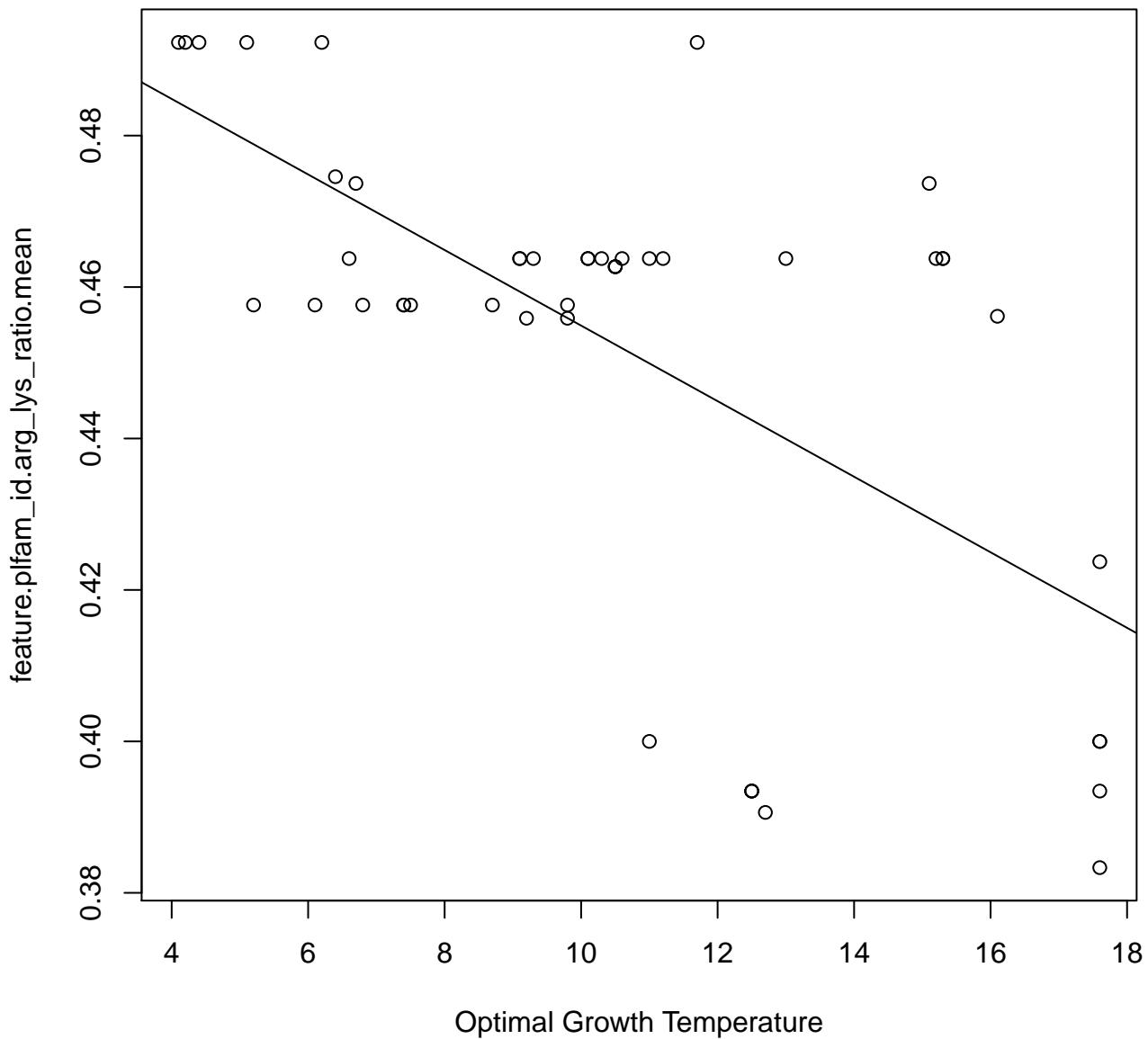
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000948



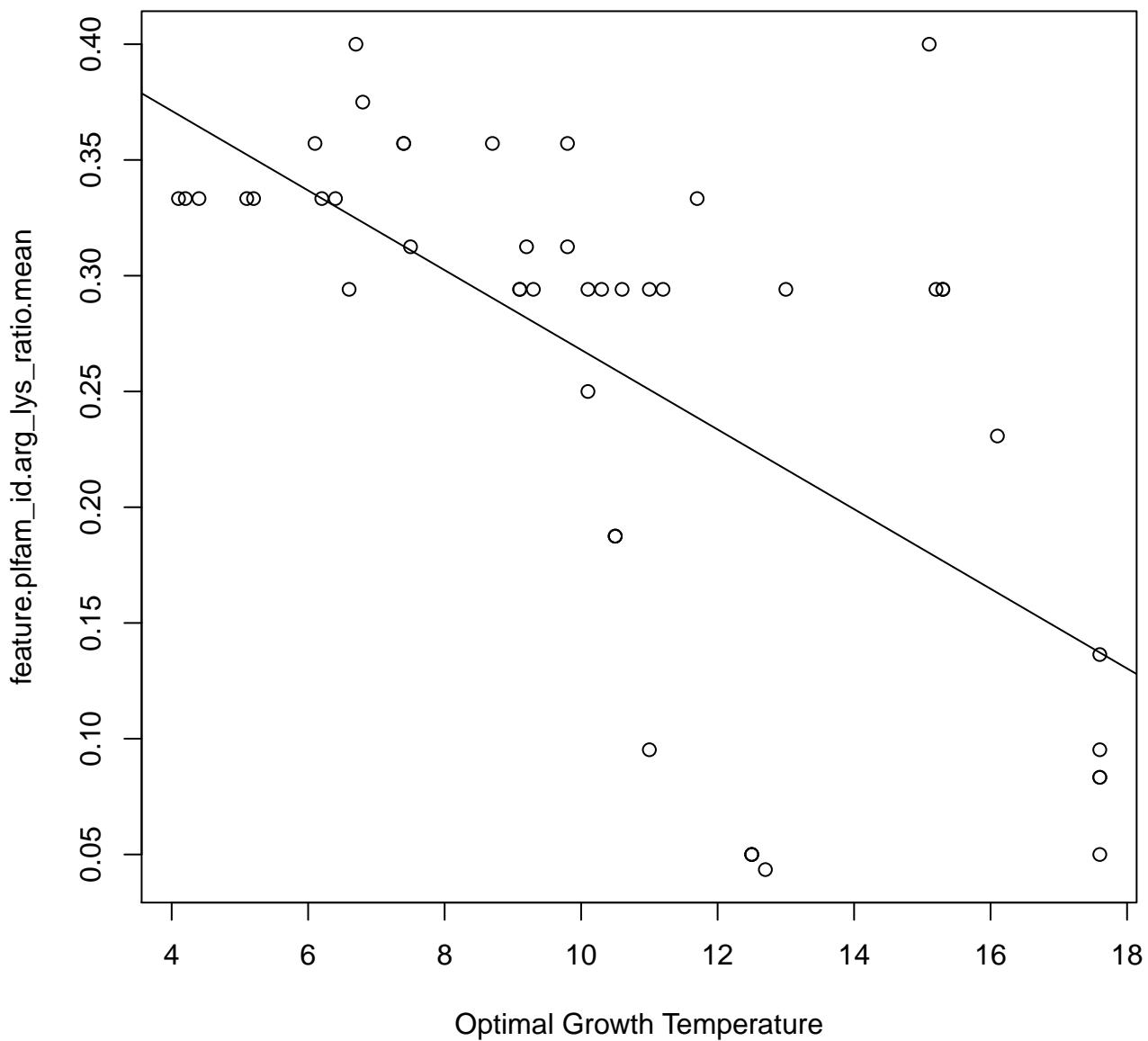
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001402
tRNA 2-thiouridine synthesis protein TusE



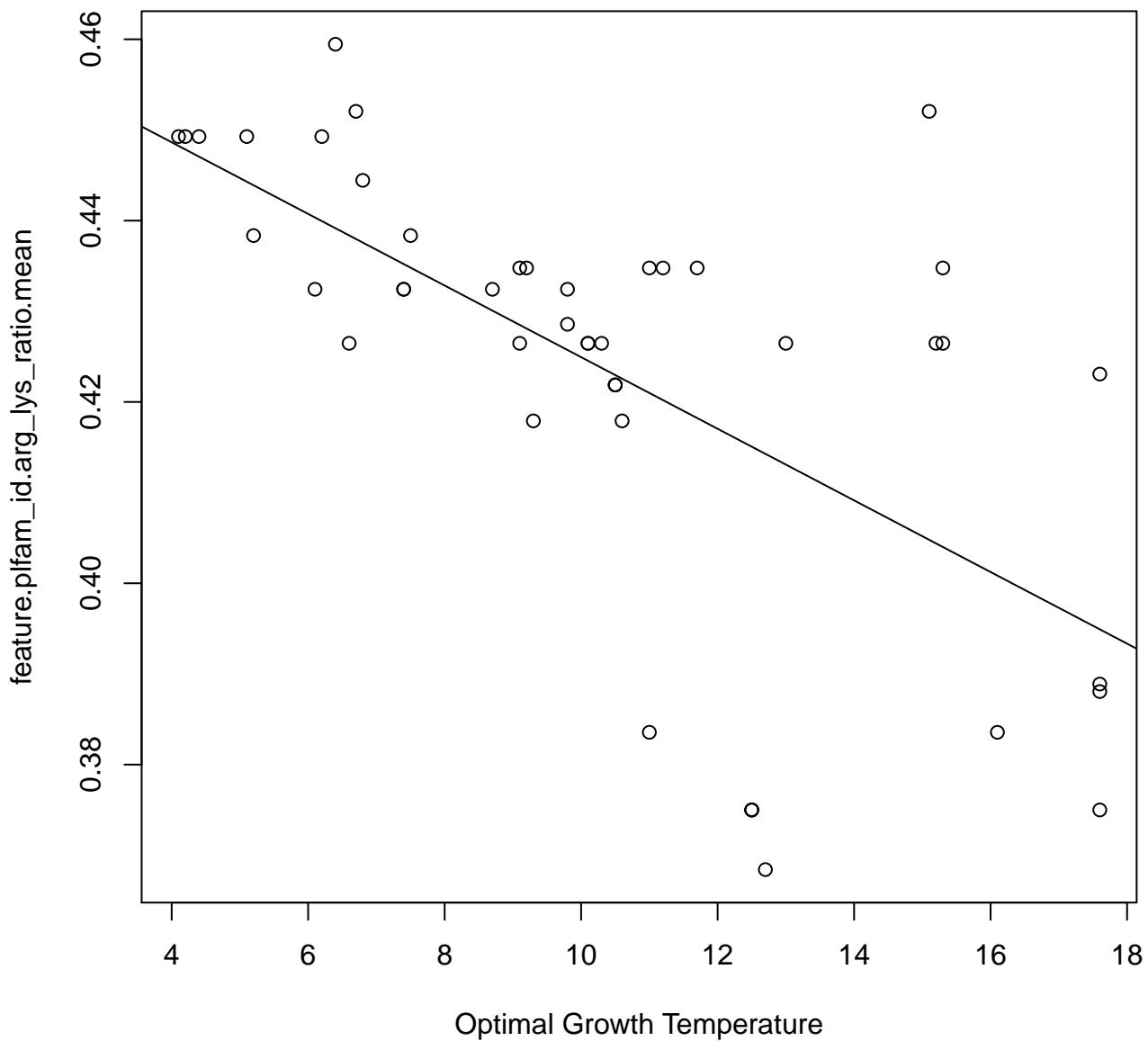
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000614
Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)



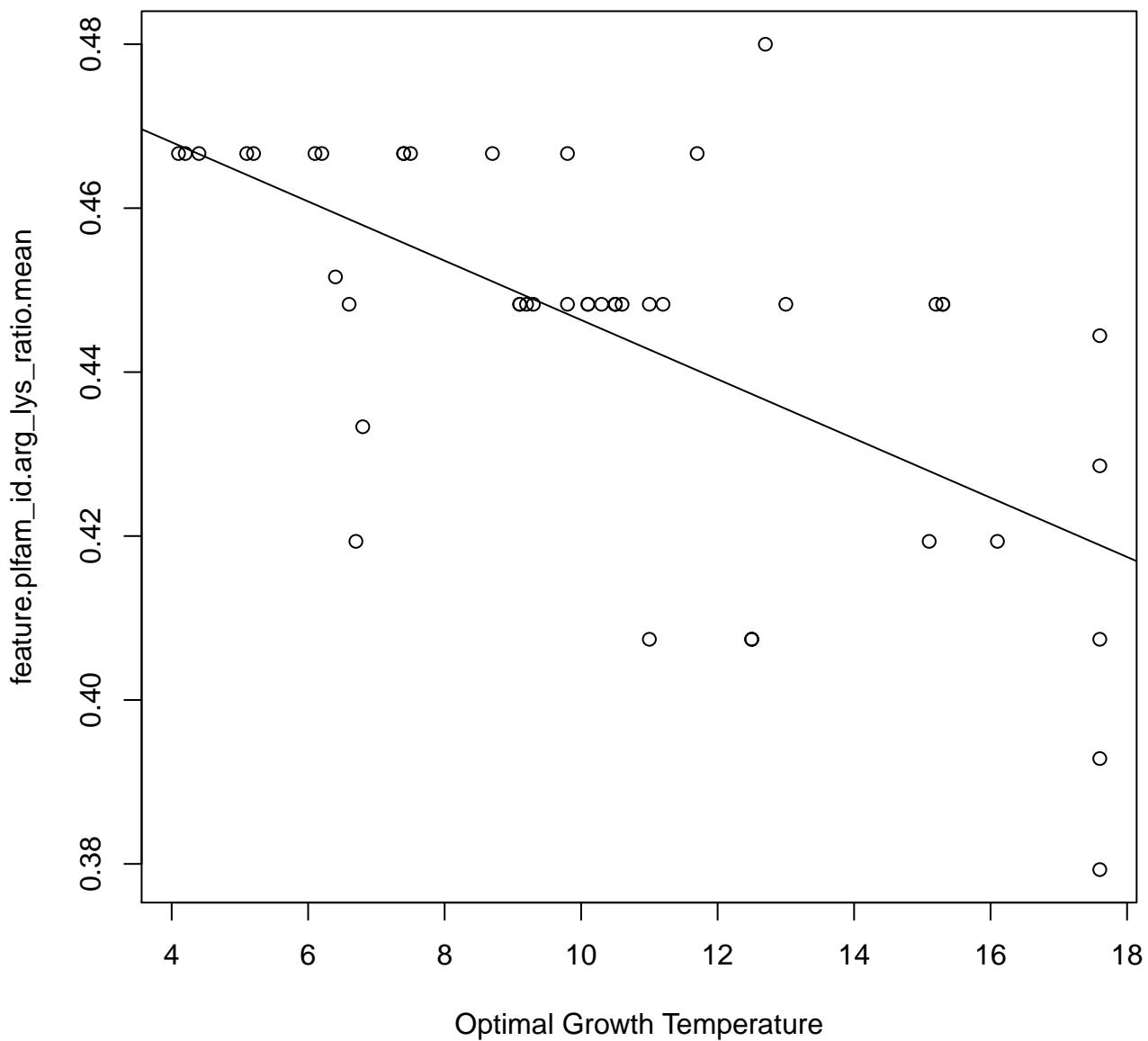
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Dethiobiotin synthase BioD (EC 6.3.3.3)



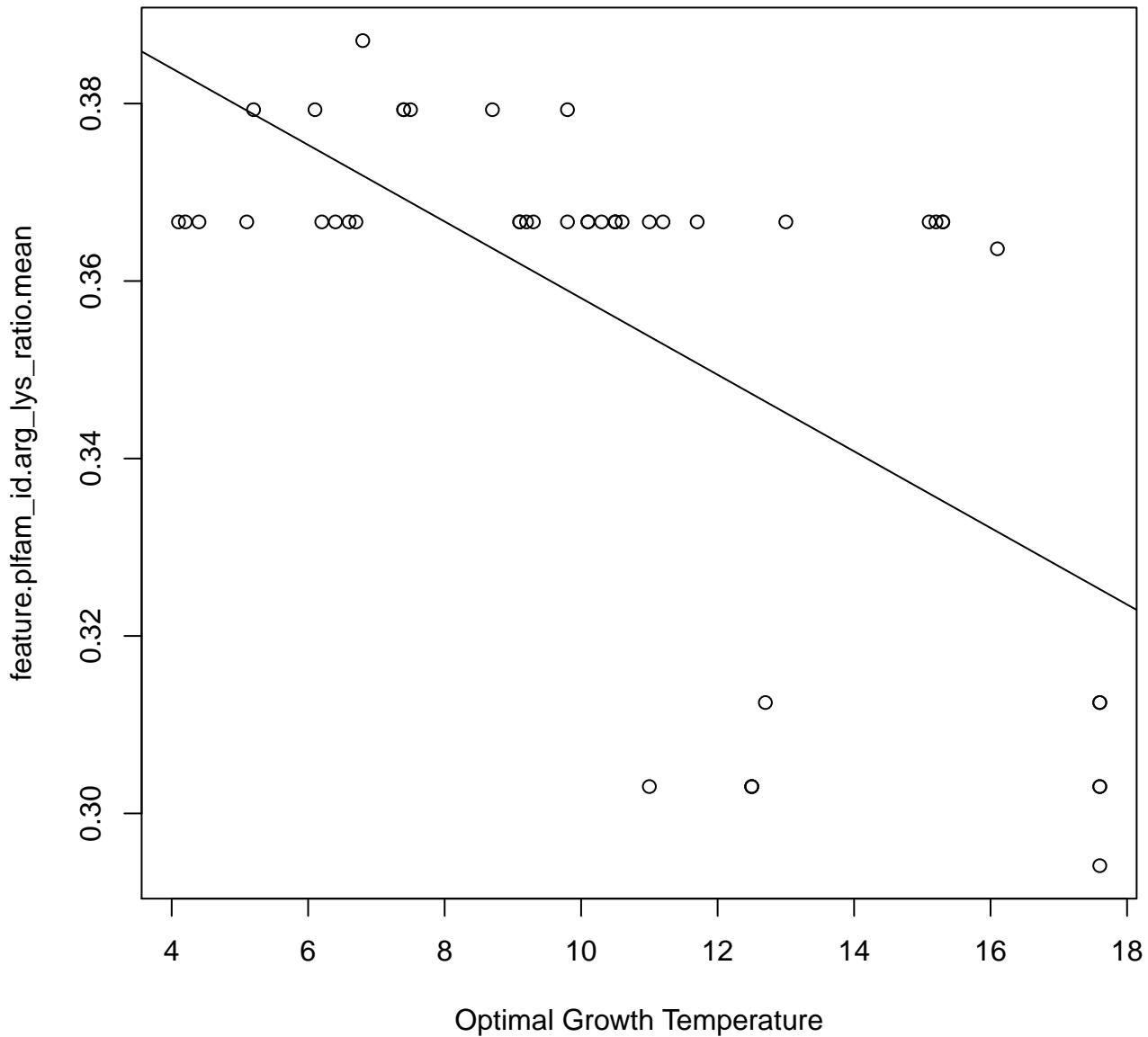
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PLF_28228_00000465
DNA polymerase III subunits gamma and tau (EC 2.7.7.7)



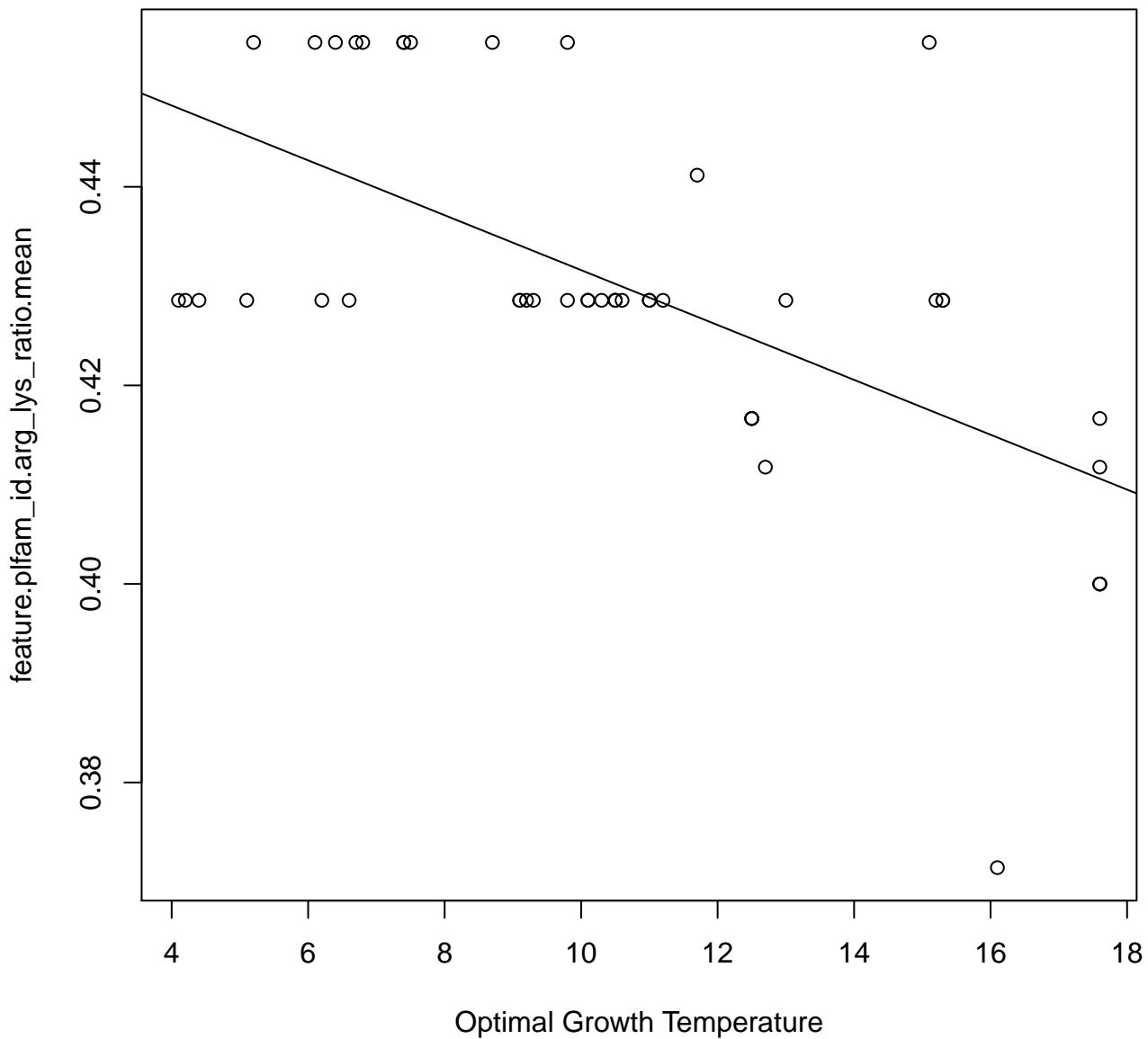
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000865
GTP cyclohydrolase I (EC 3.5.4.16) type 2



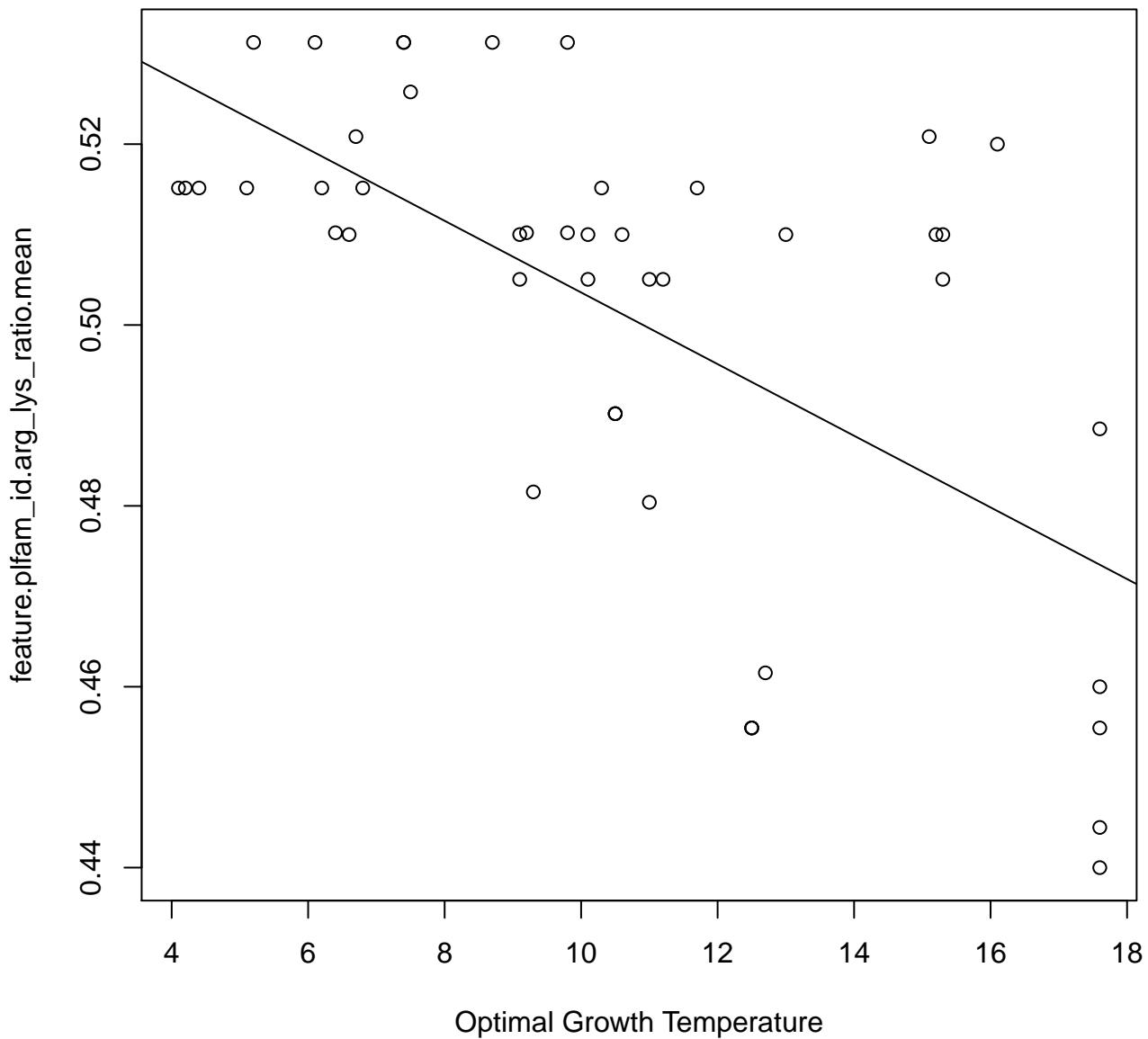
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2-methoxy-6-polyprenyl-1,4-benzoquinol methylase (EC 2.1.1.201)



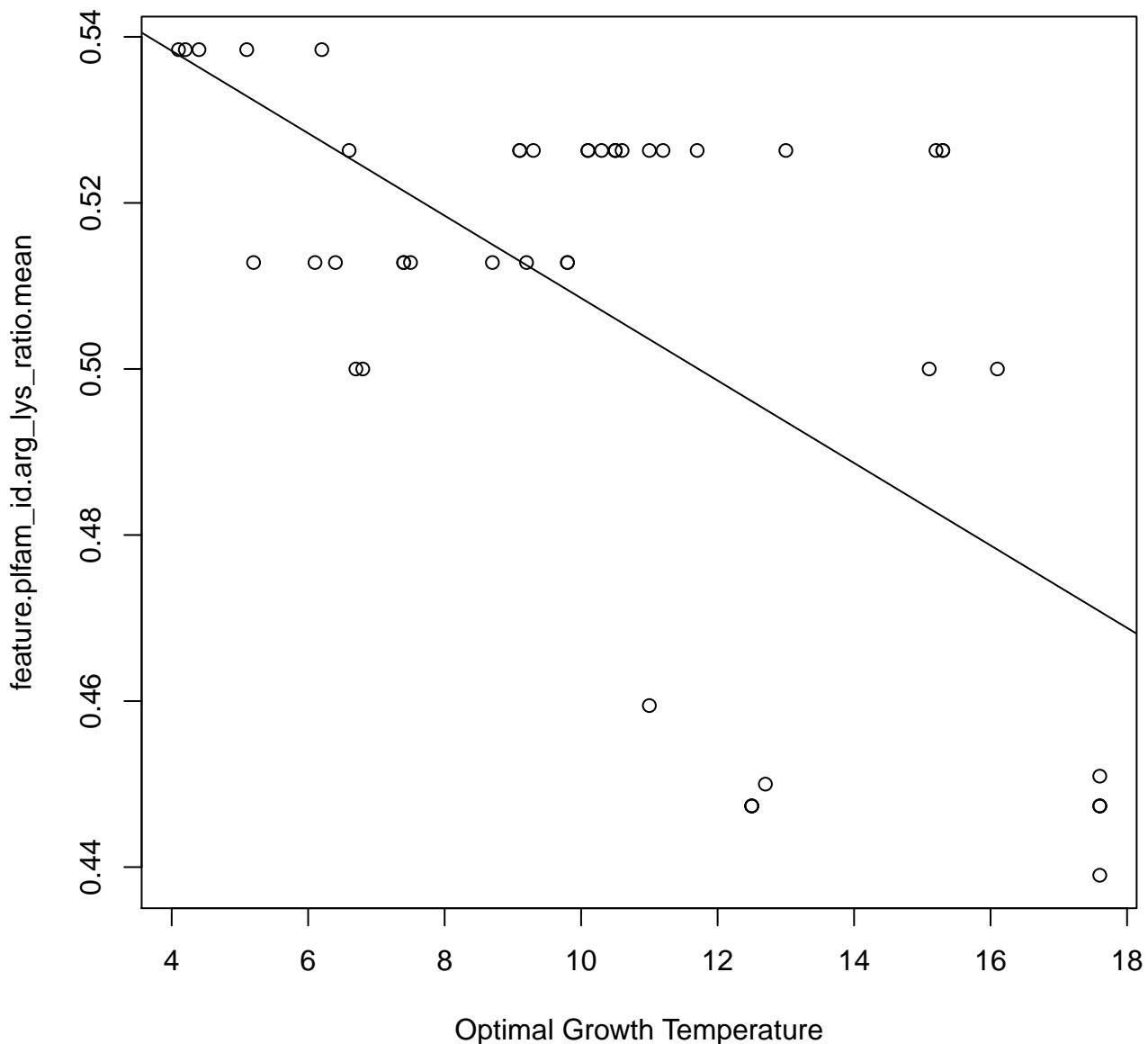
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000221
3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)



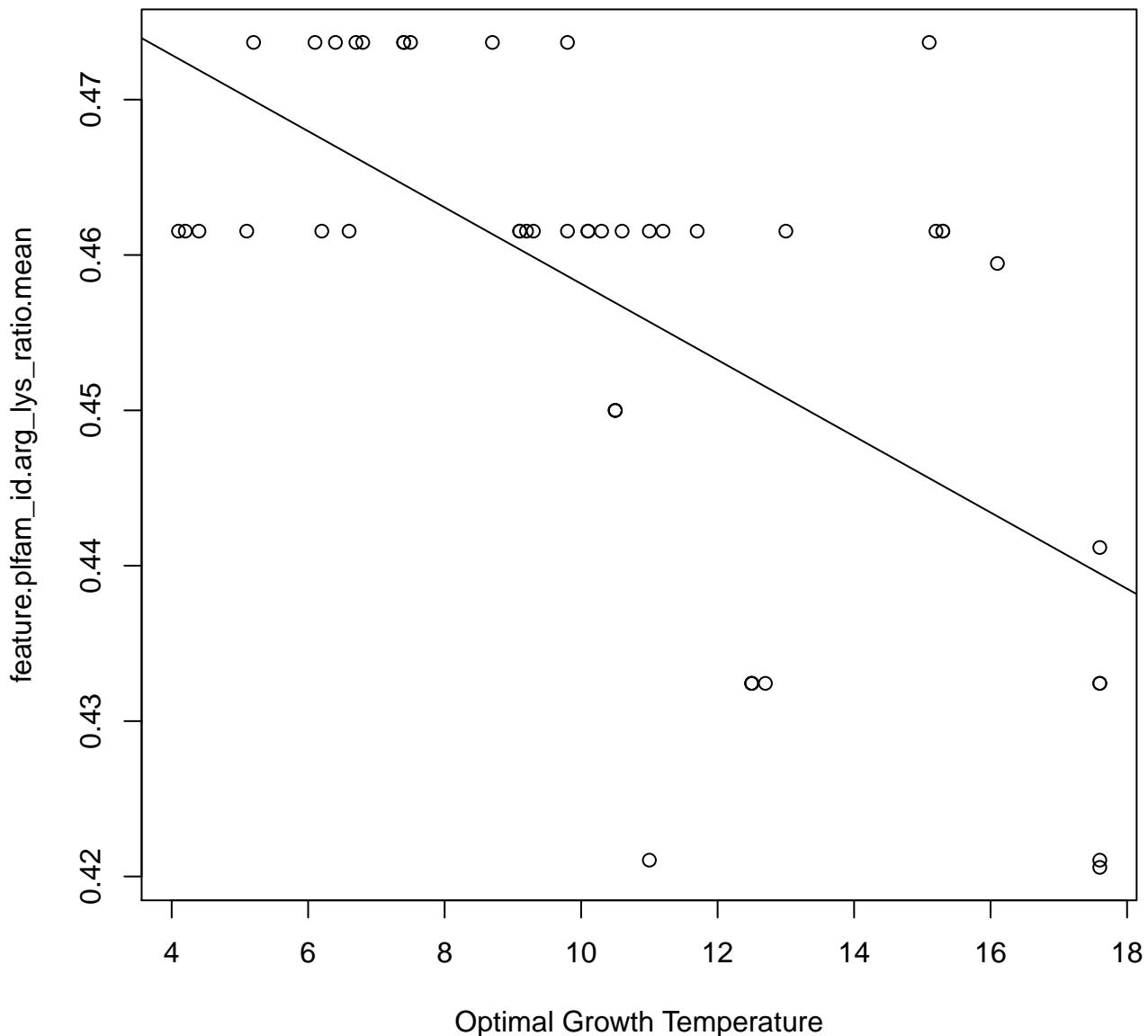
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PLF_28228_00000347
Glycerol-3-phosphate acyltransferase (EC 2.3.1.15)



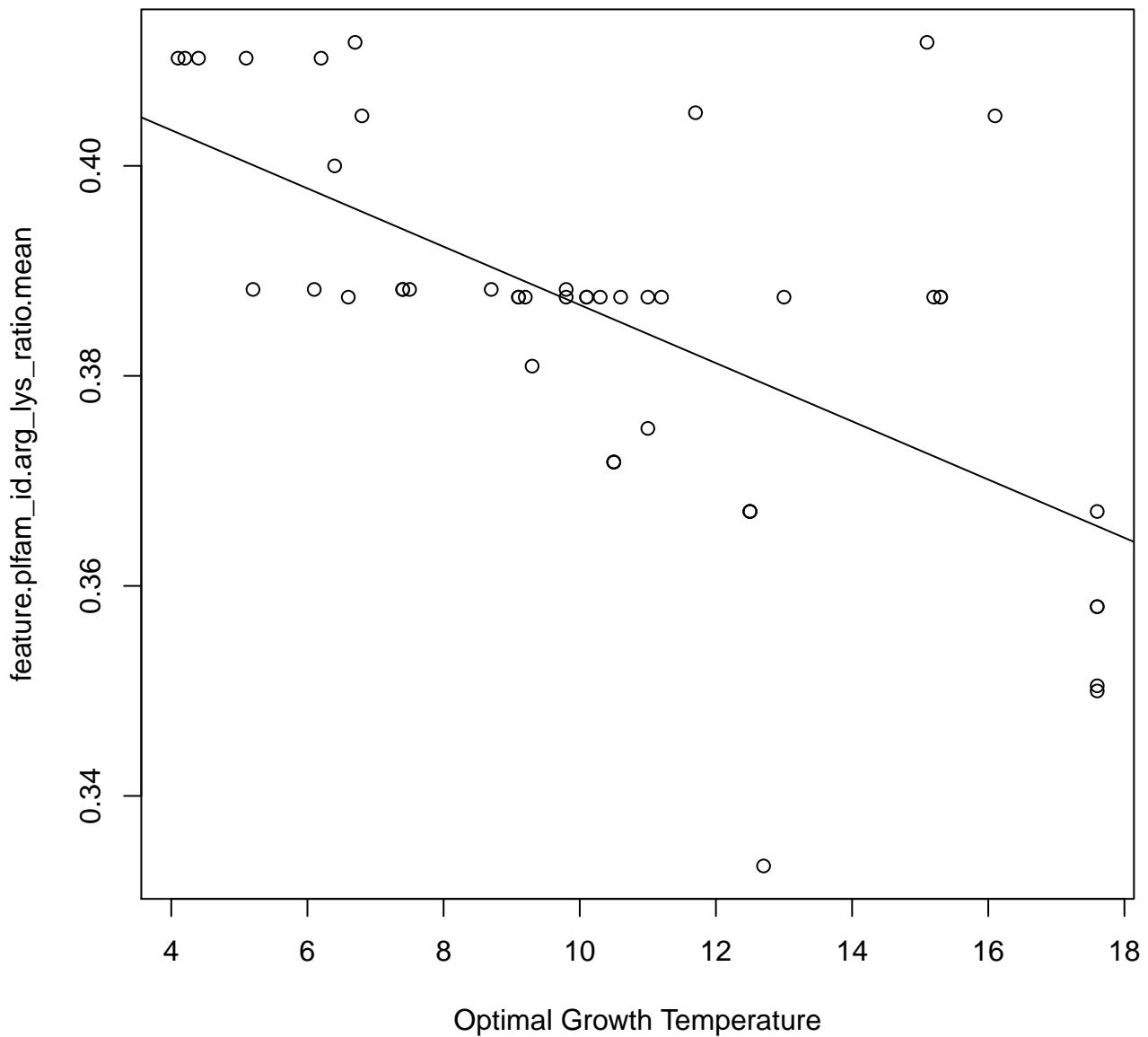
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PLF_28228_00000572
Citrate synthase (si) (EC 2.3.3.1)



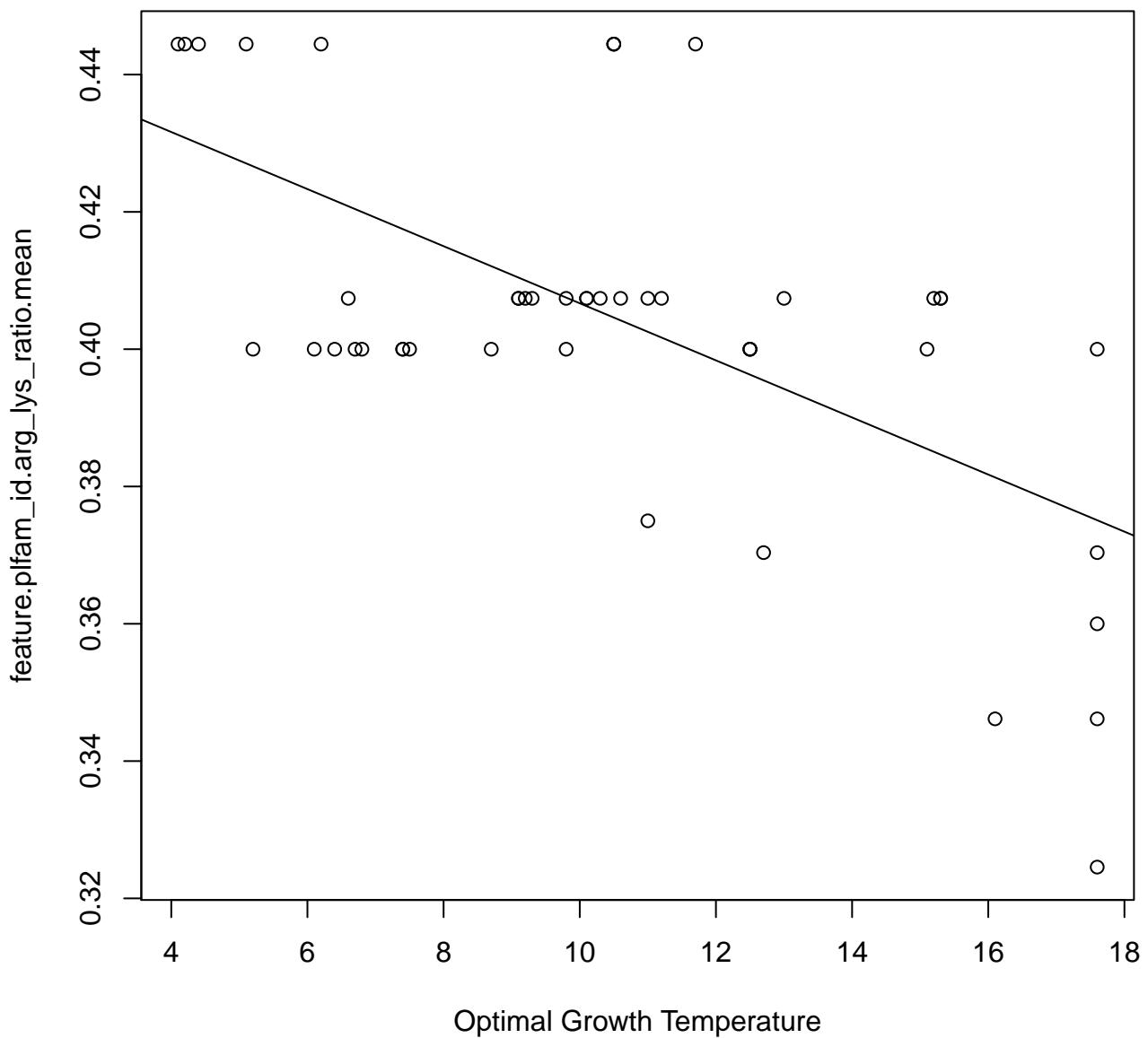
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PLF_28228_00001304
Uroporphyrinogen III decarboxylase (EC 4.1.1.37)



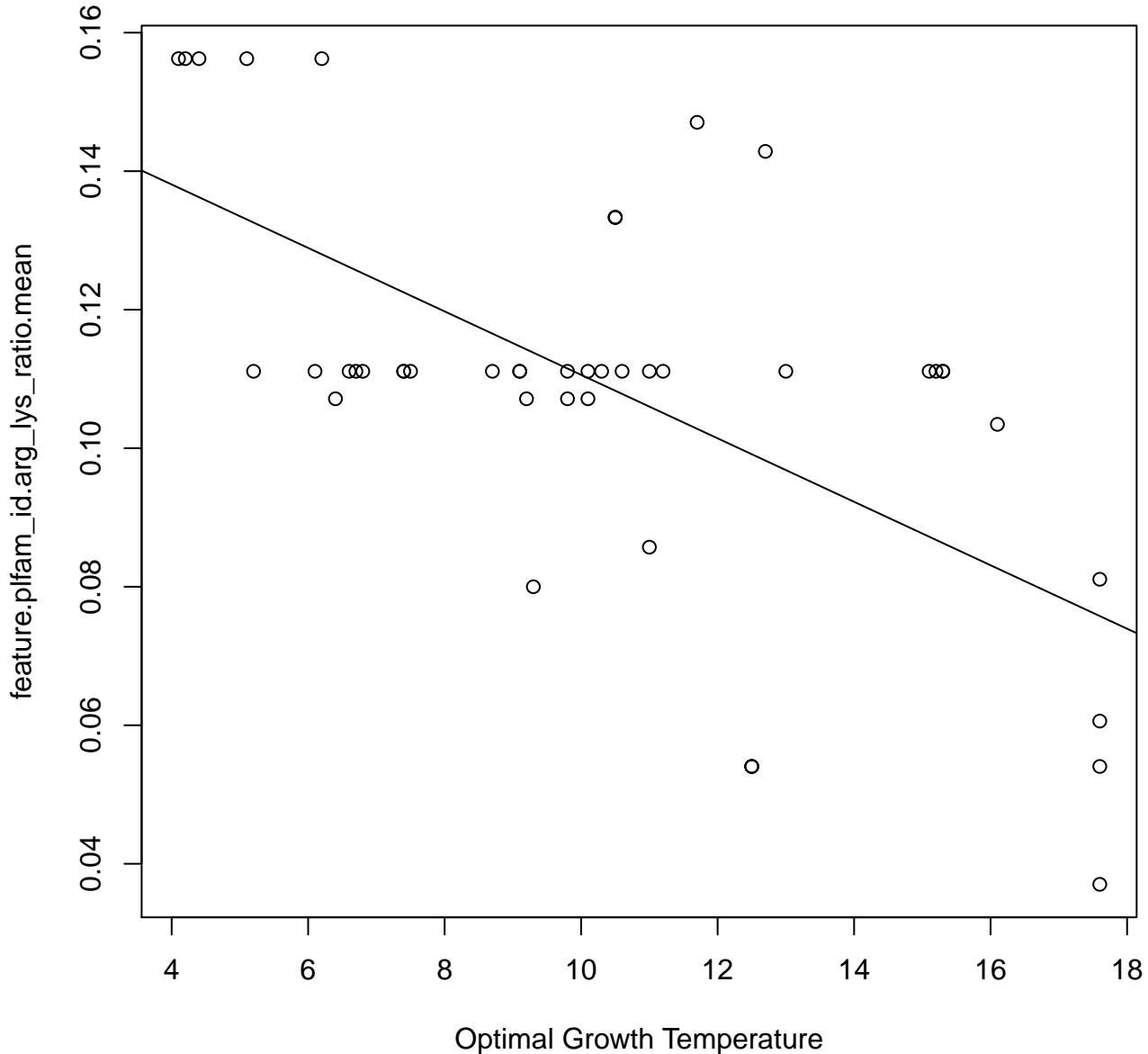
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000729
ATP-dependent protease La (EC 3.4.21.53) Type II



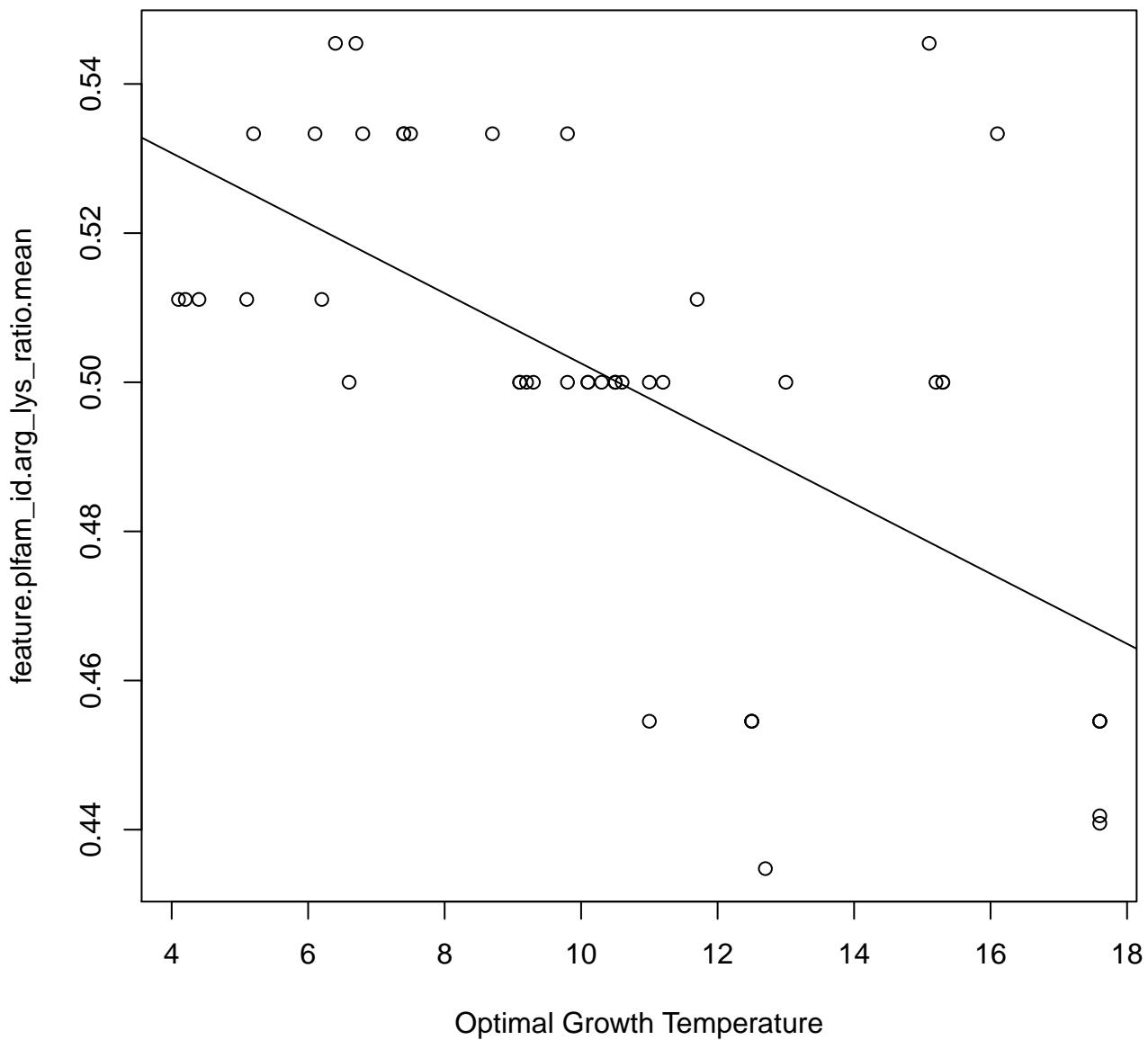
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001533
UPF0234 protein Yitk



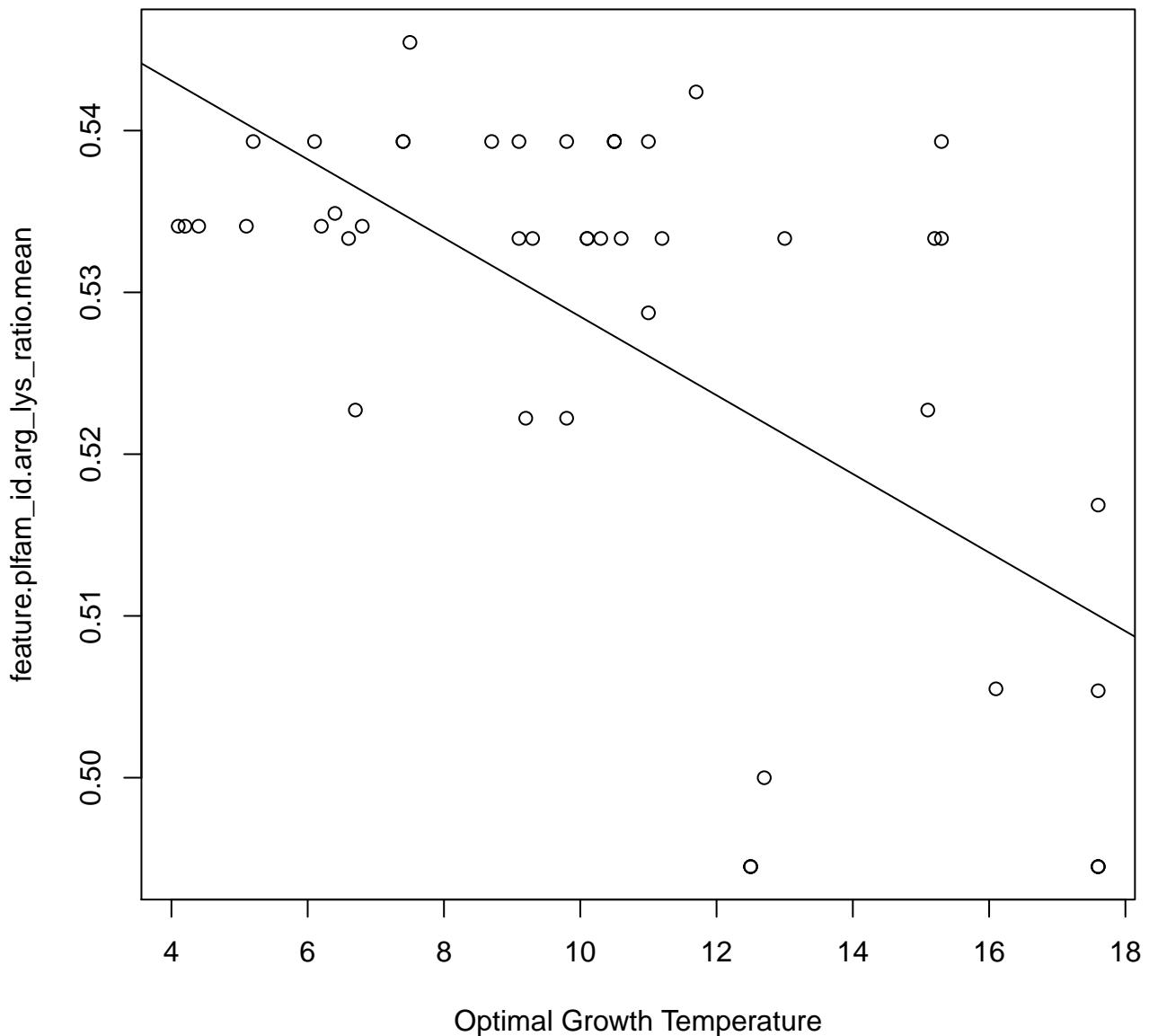
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002049
Septum-associated cell division protein DedD



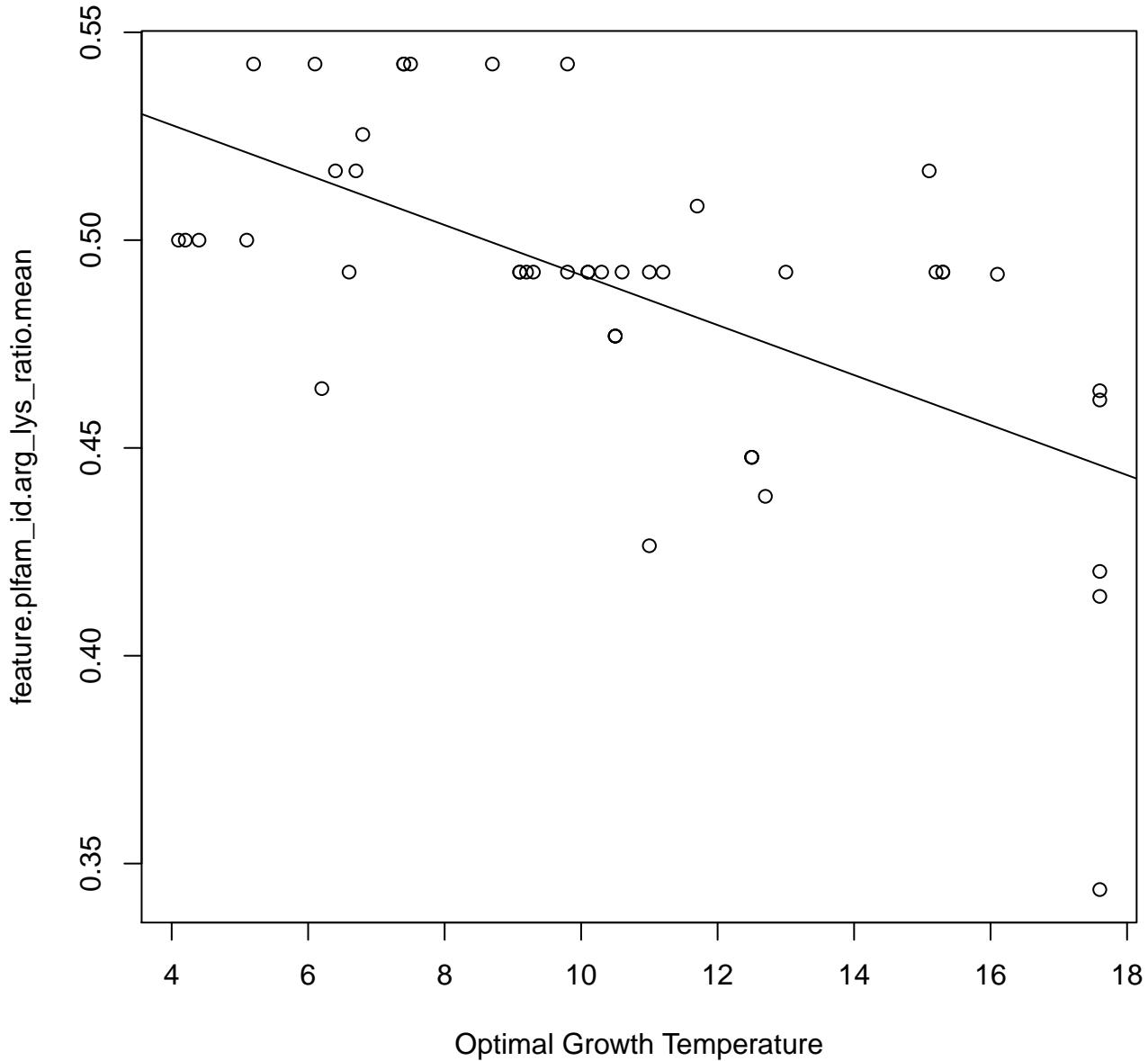
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PLF_28228_00000872
GTP-binding protein Obg



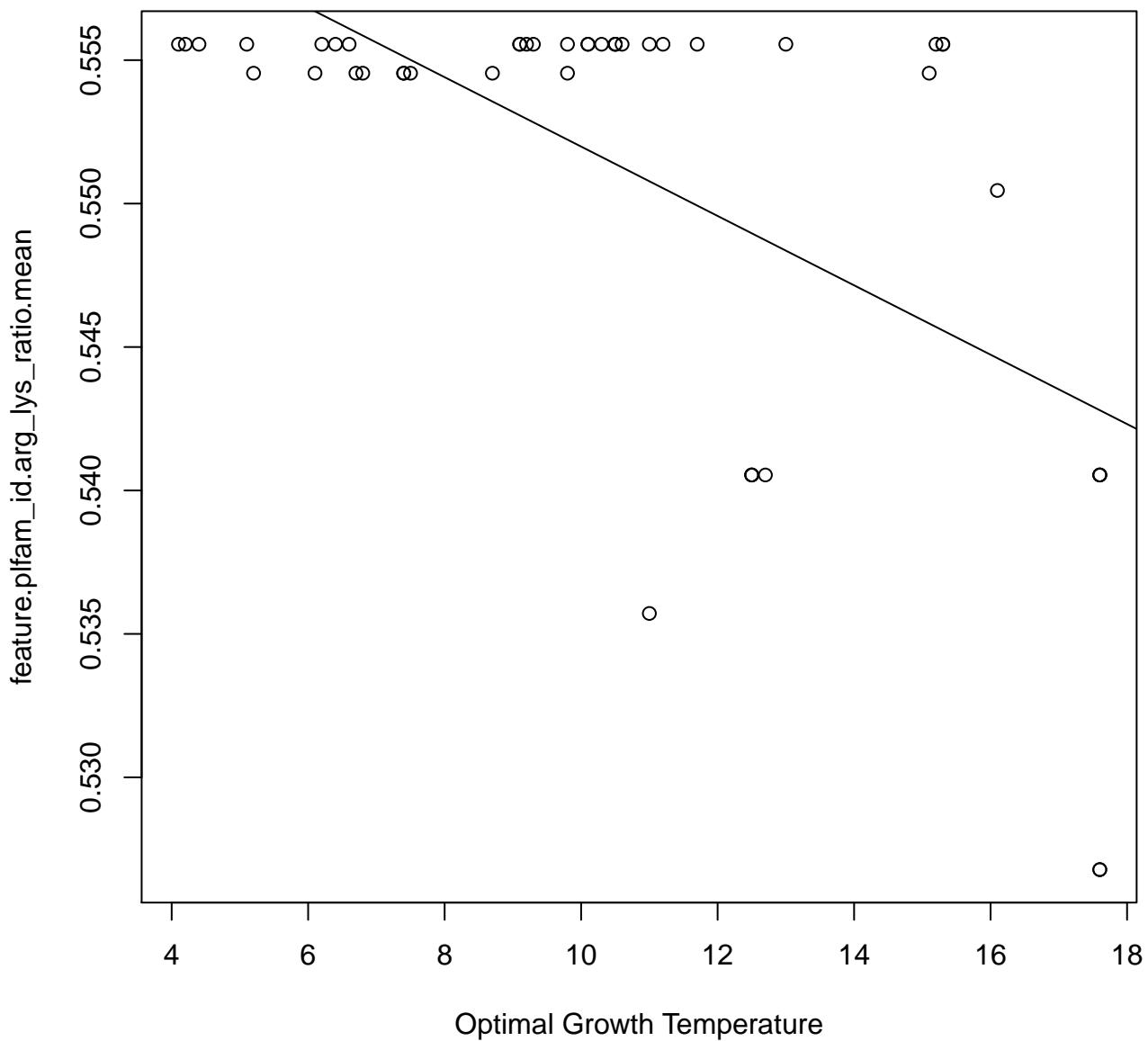
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000248
2-methylcitrate dehydratase (2-methyl-trans-aconitate forming) (EC 4.2.1.117)



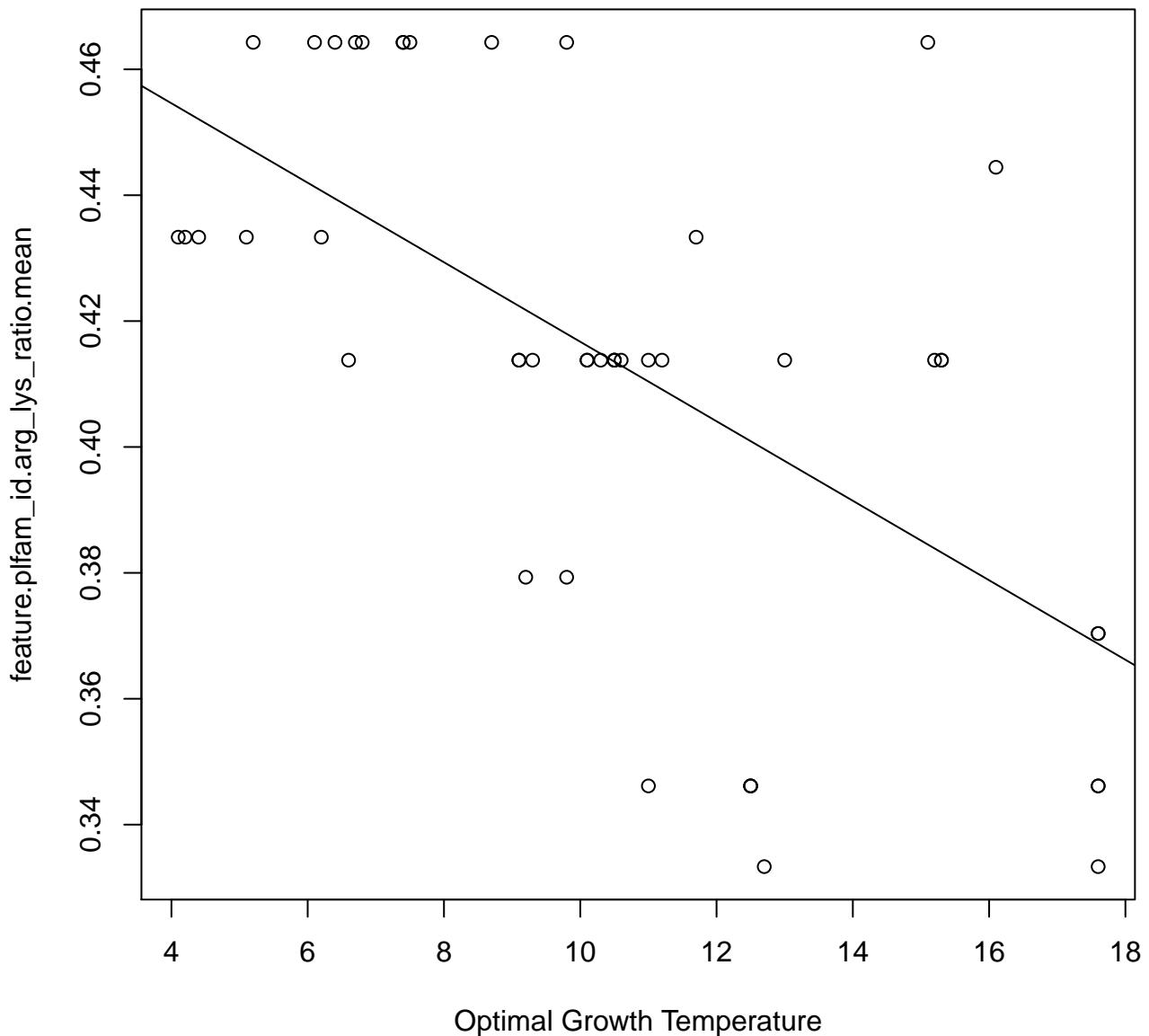
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PLF_28228_00001011
Protein translocase subunit SecD



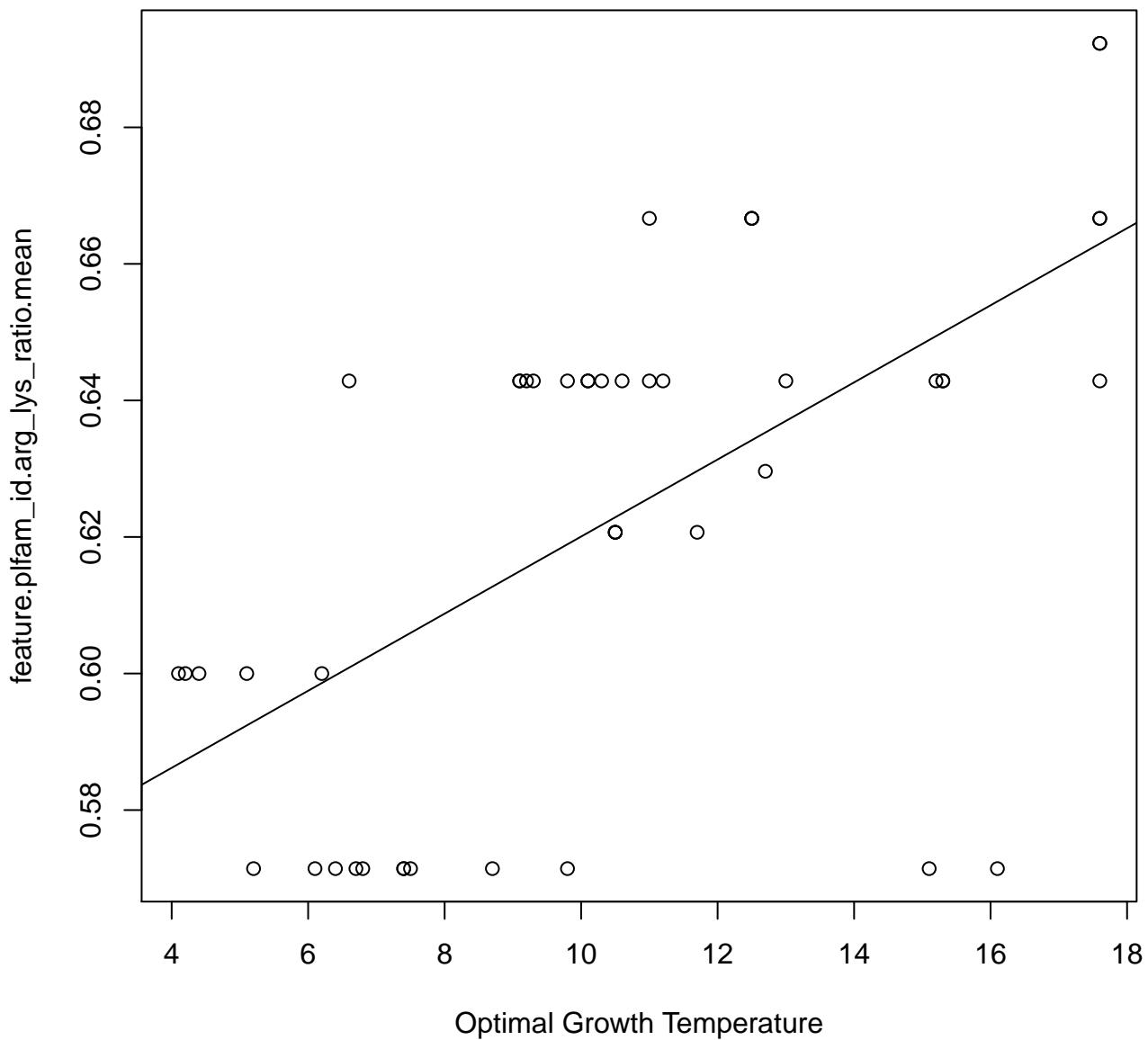
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000454
DNA gyrase subunit A (EC 5.99.1.3)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000557
Cell-division-associated, ABC-transporter-like signaling protein FtsE



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002243
hypothetical protein

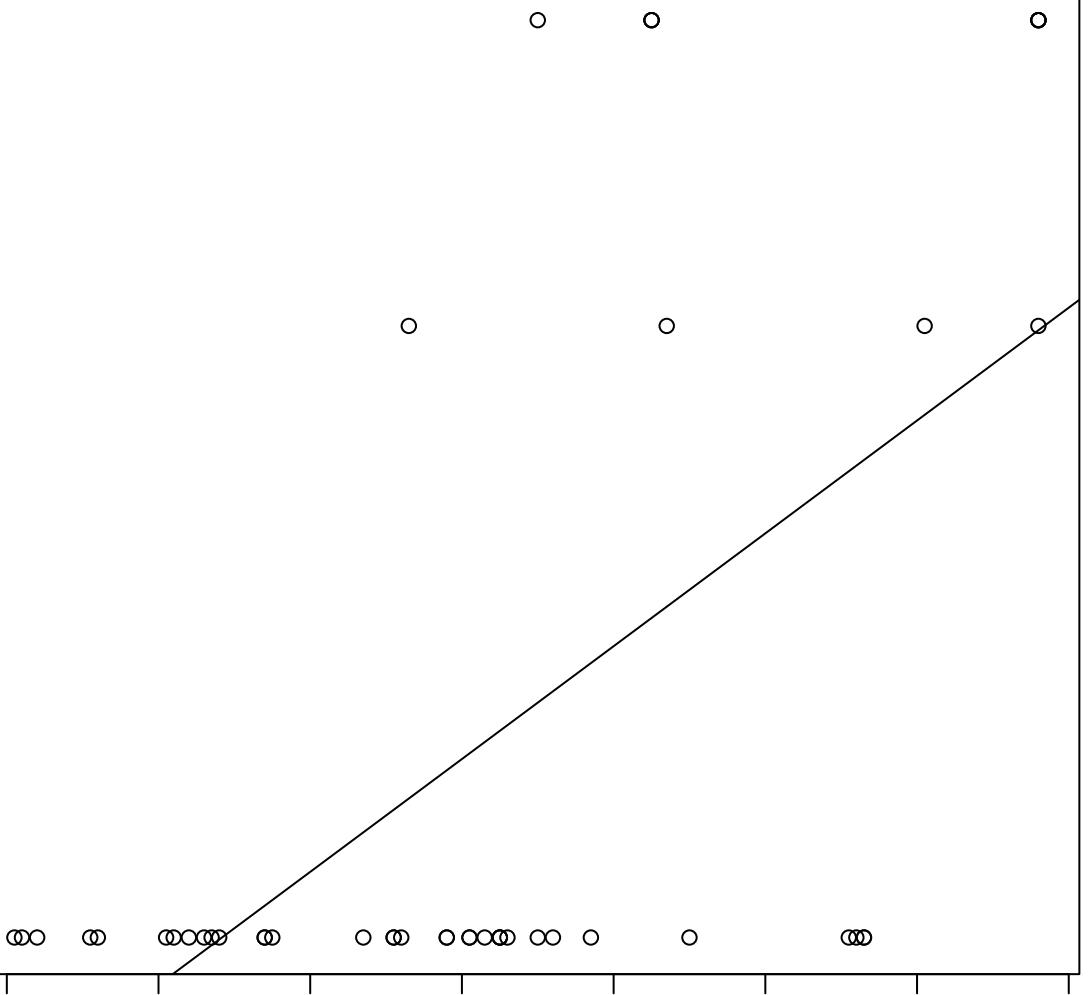


feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000685
LSU ribosomal protein L34p

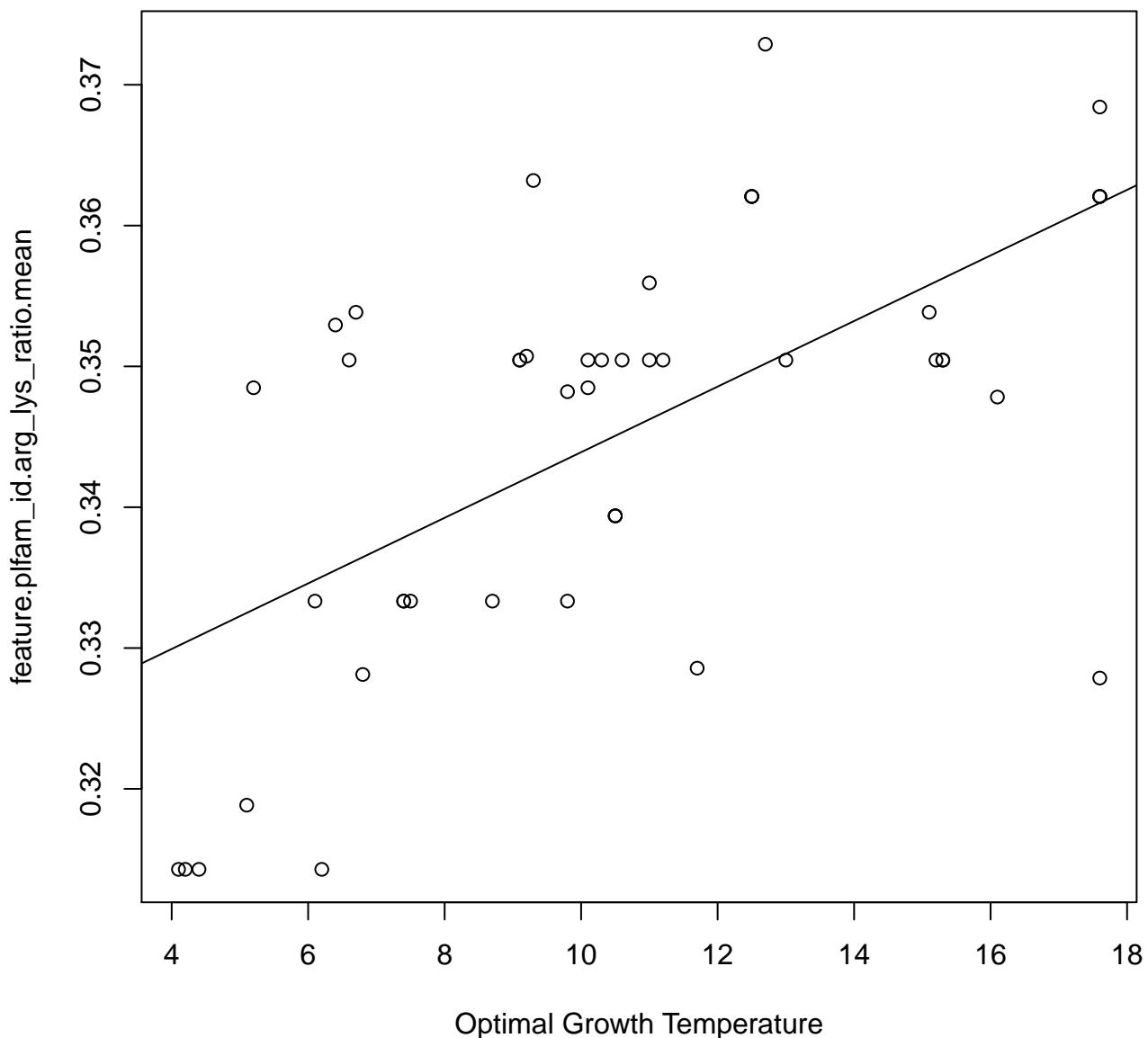
feature.plfam_id.arg_lys_ratio.mean

4 6 8 10 12 14 16 18

Optimal Growth Temperature



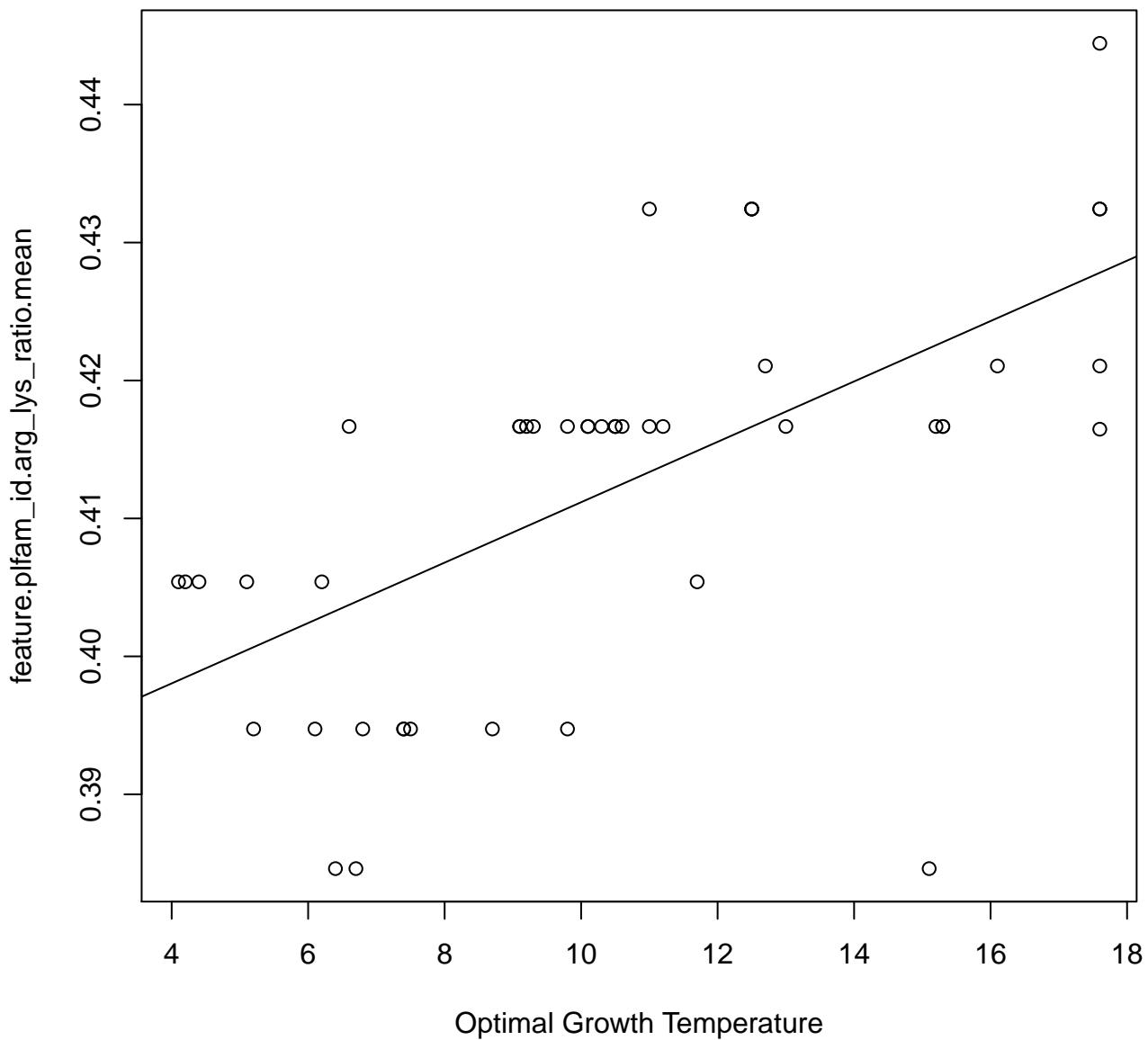
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000597
Malate synthase G (EC 2.3.3.9)



feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000264

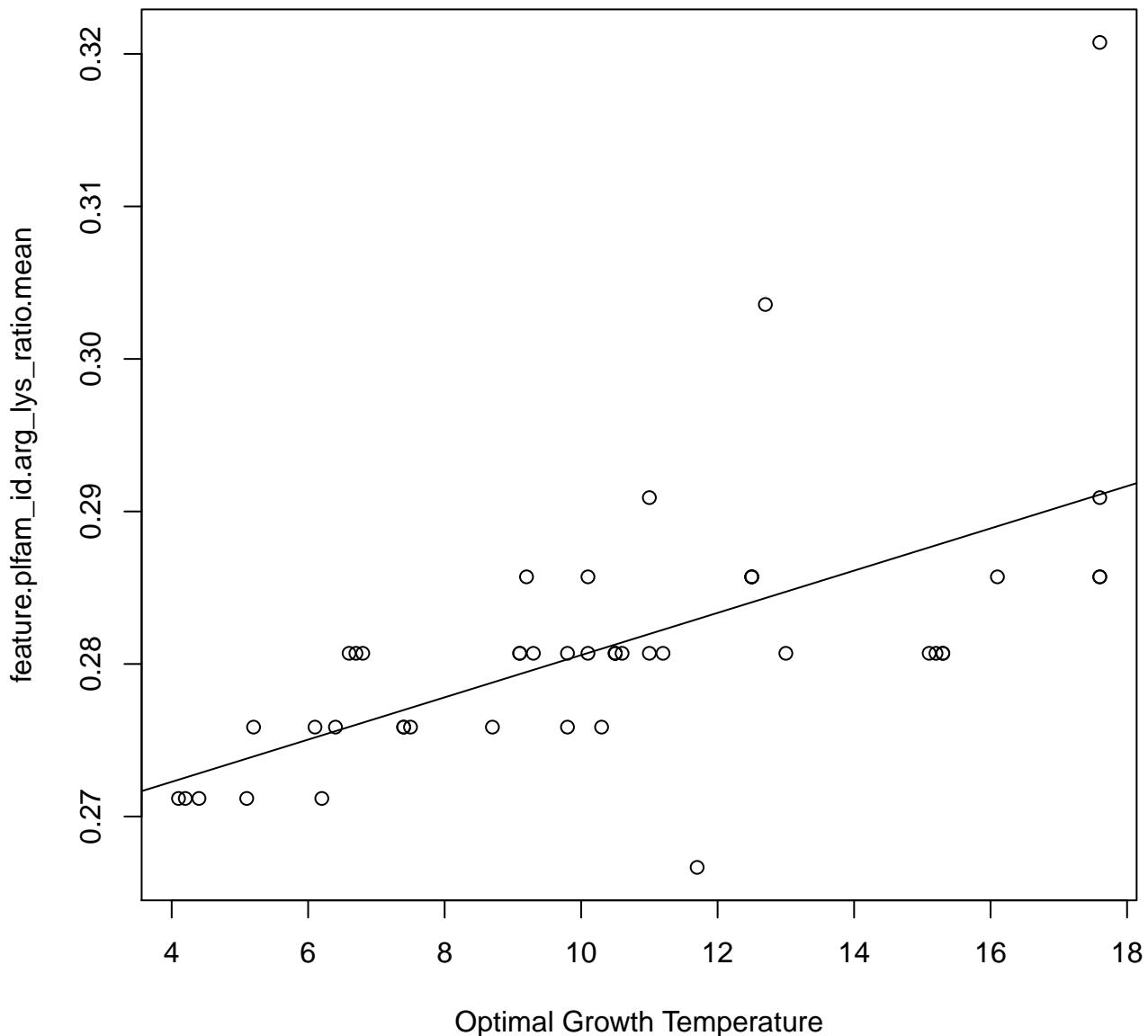
3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25)



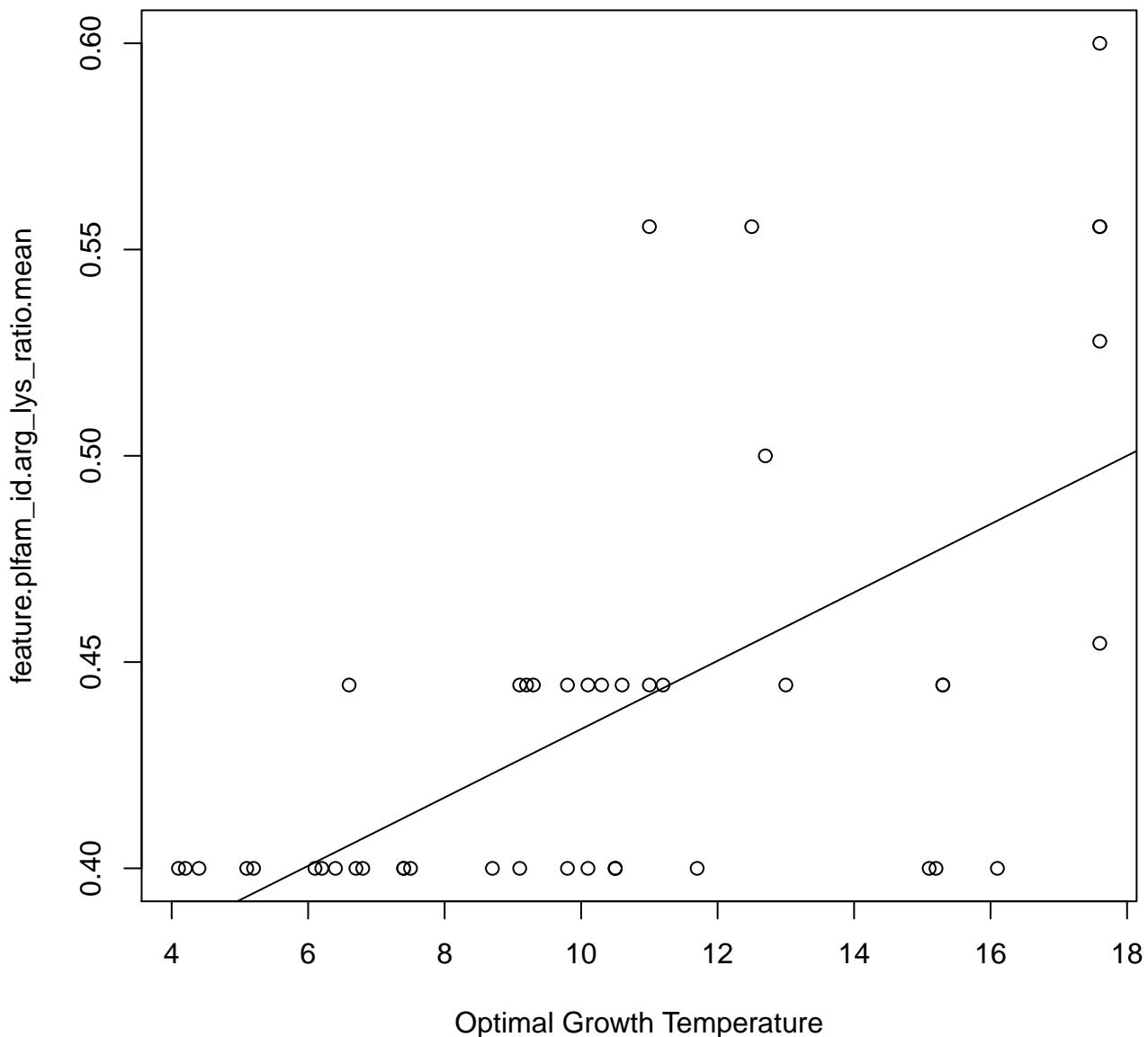
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PLF_28228_00000367

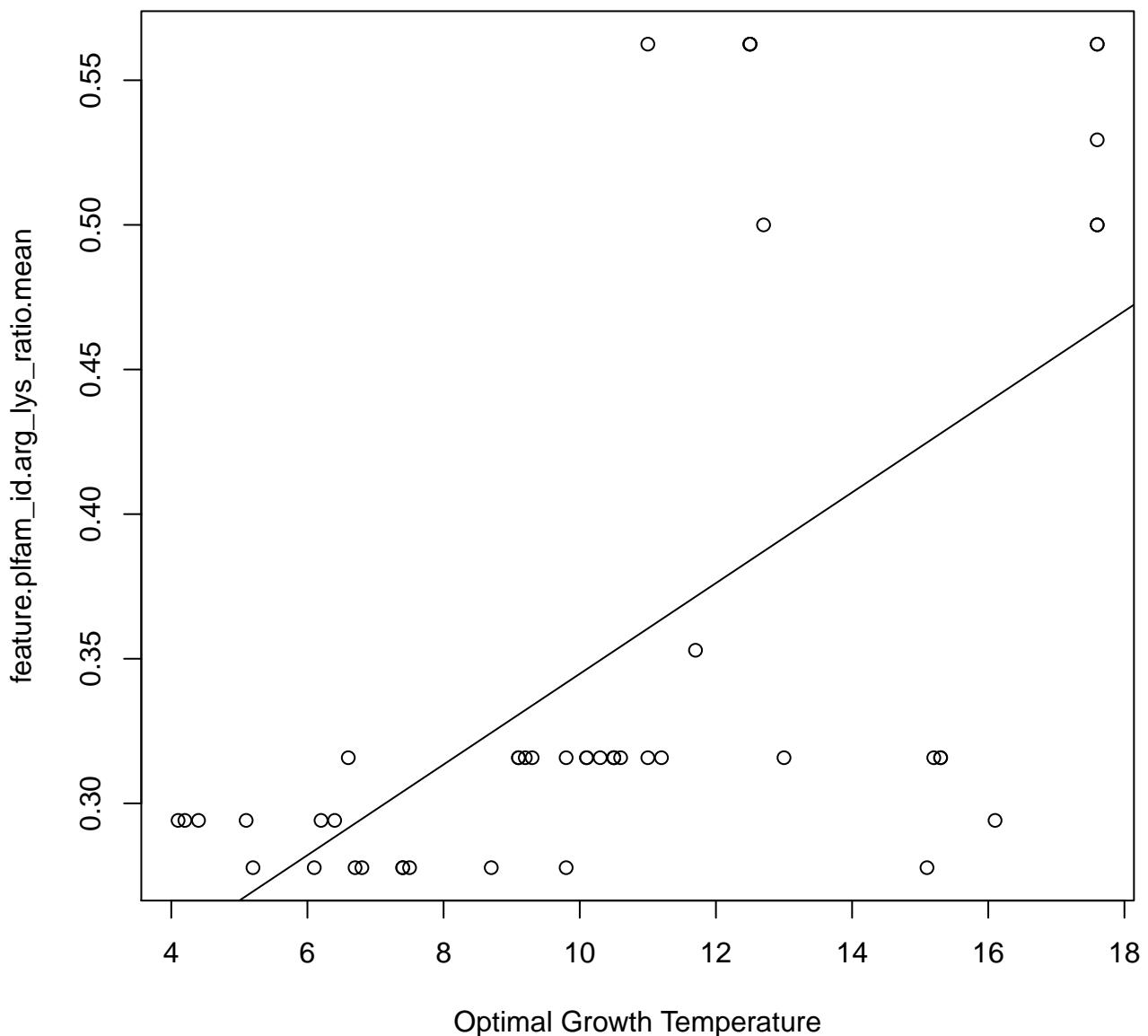
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)



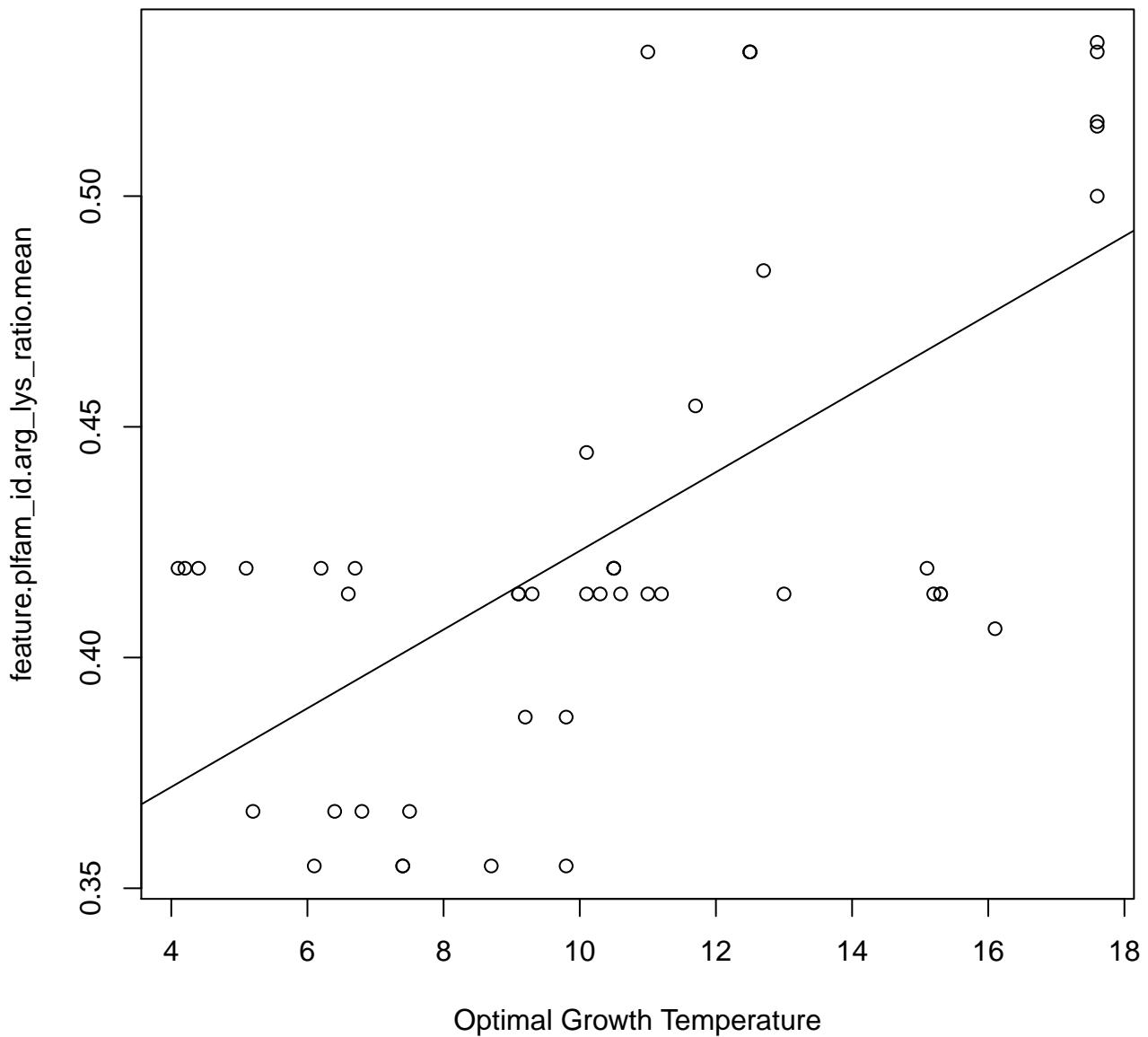
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00027843
Protein-export protein SecB (maintains pre-export unfolded state)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001684
Chaperone protein HscB



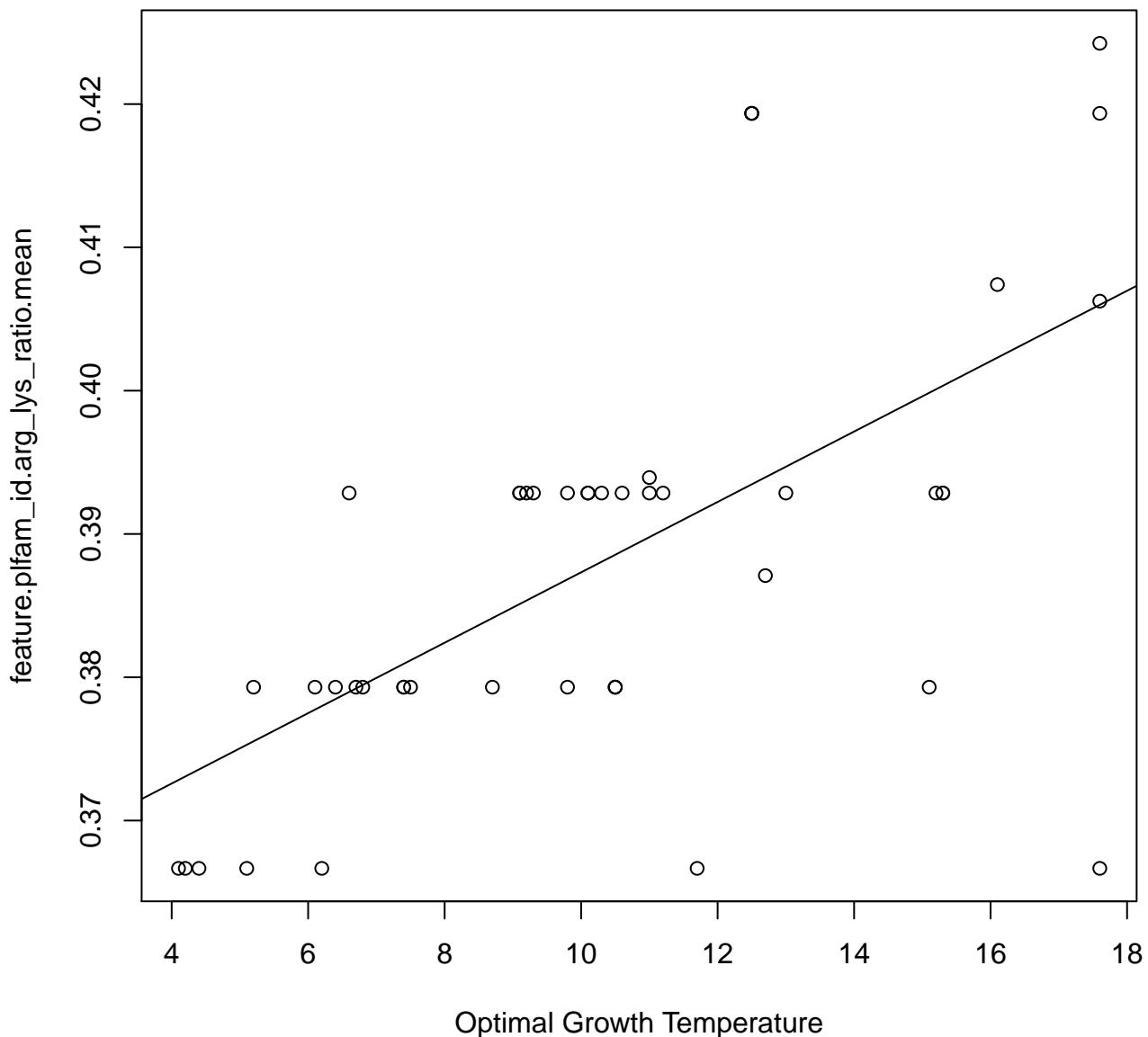
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001084
SSU rRNA pseudouridine(516) synthase (EC 5.4.99.19)



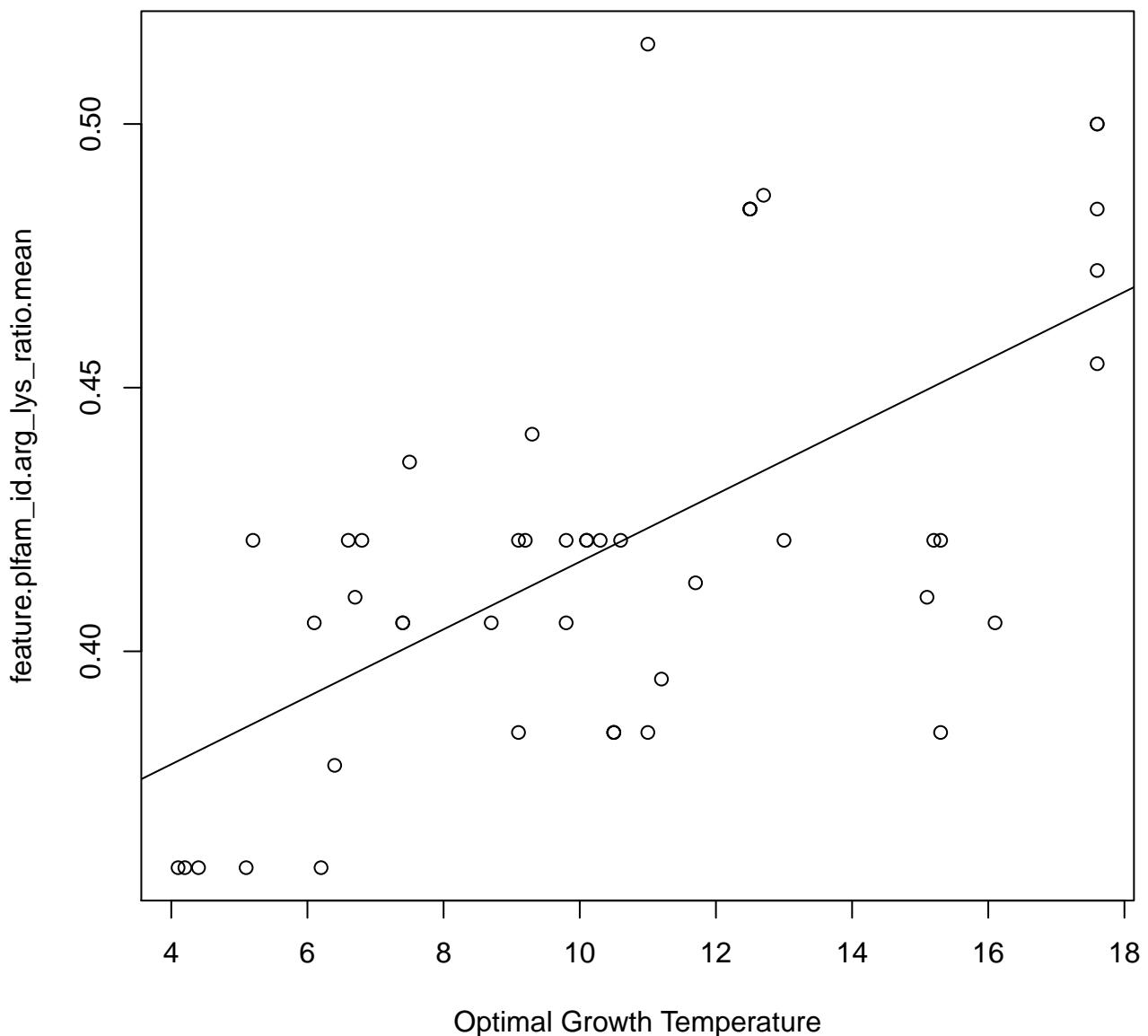
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000103

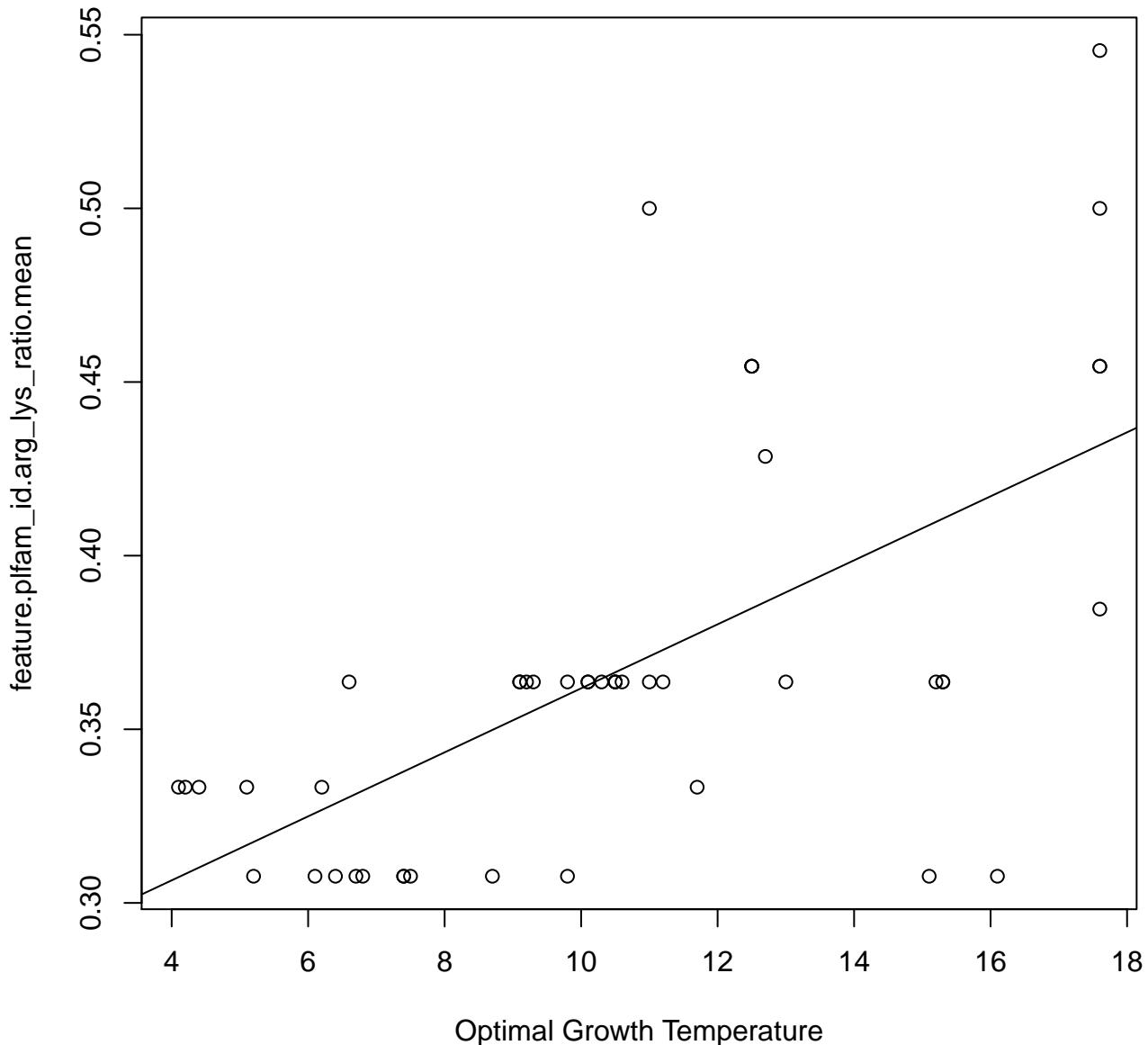
Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)



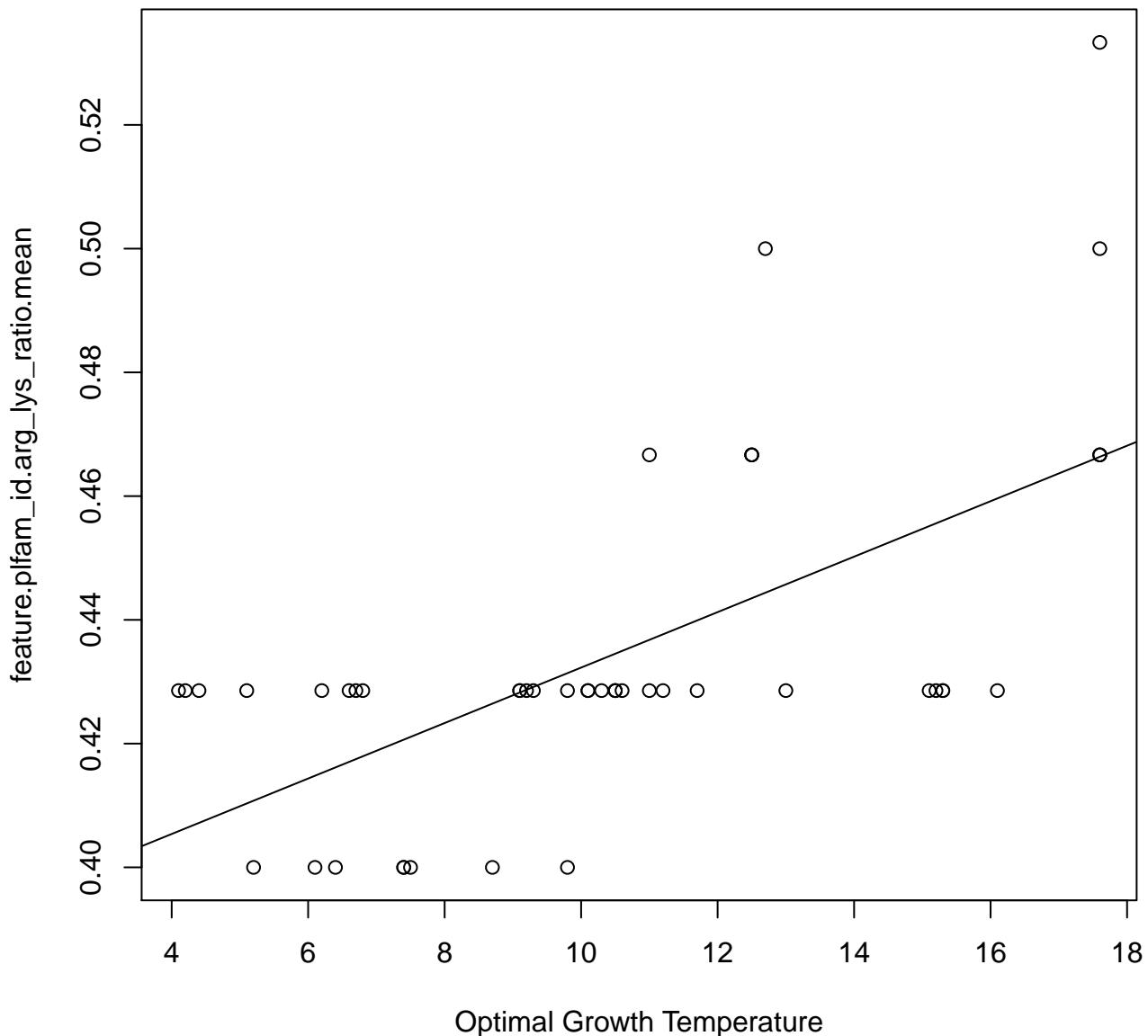
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002359
hypothetical protein



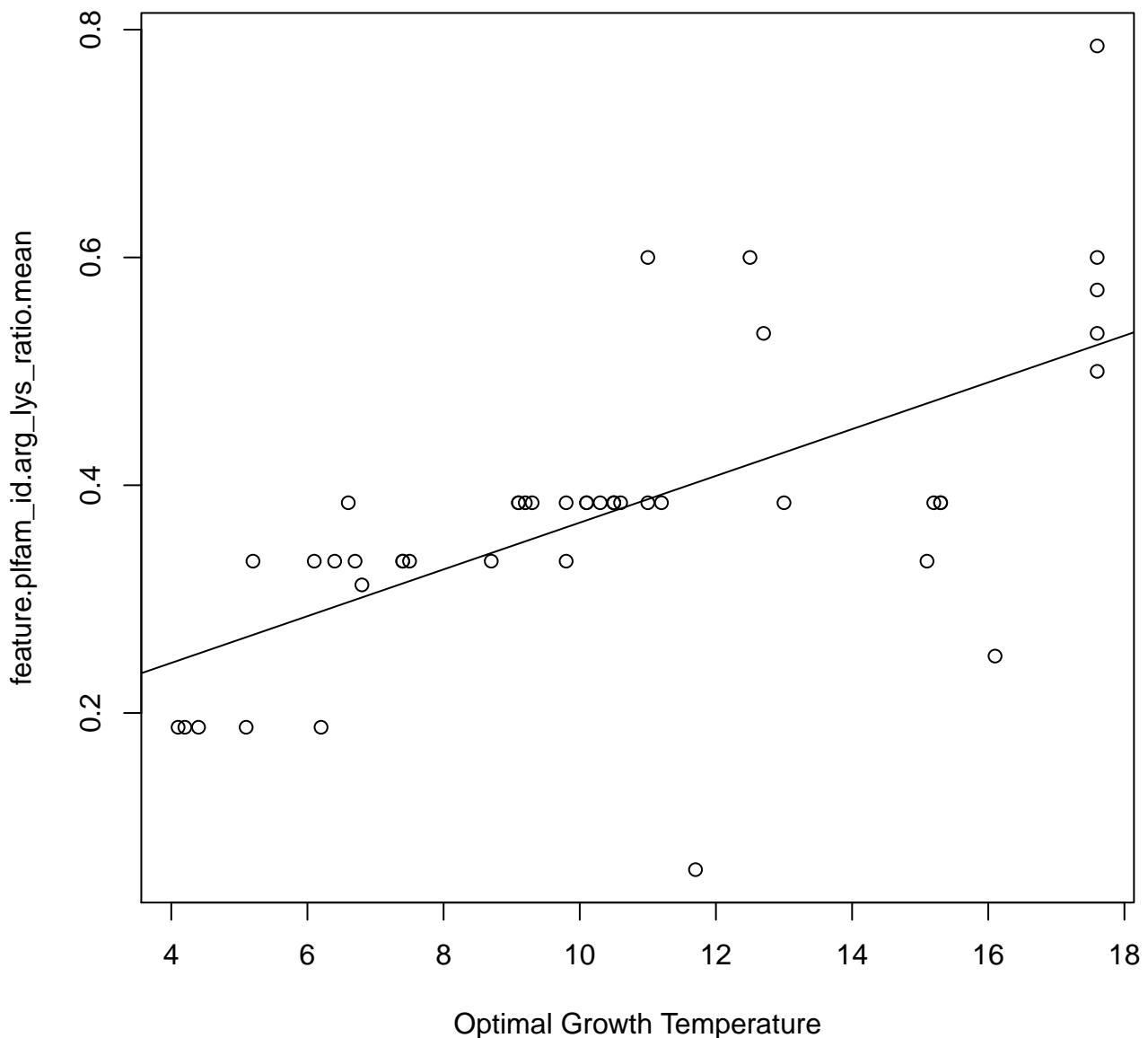
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000439
Cytochrome c oxidase polypeptide III (EC 1.9.3.1)



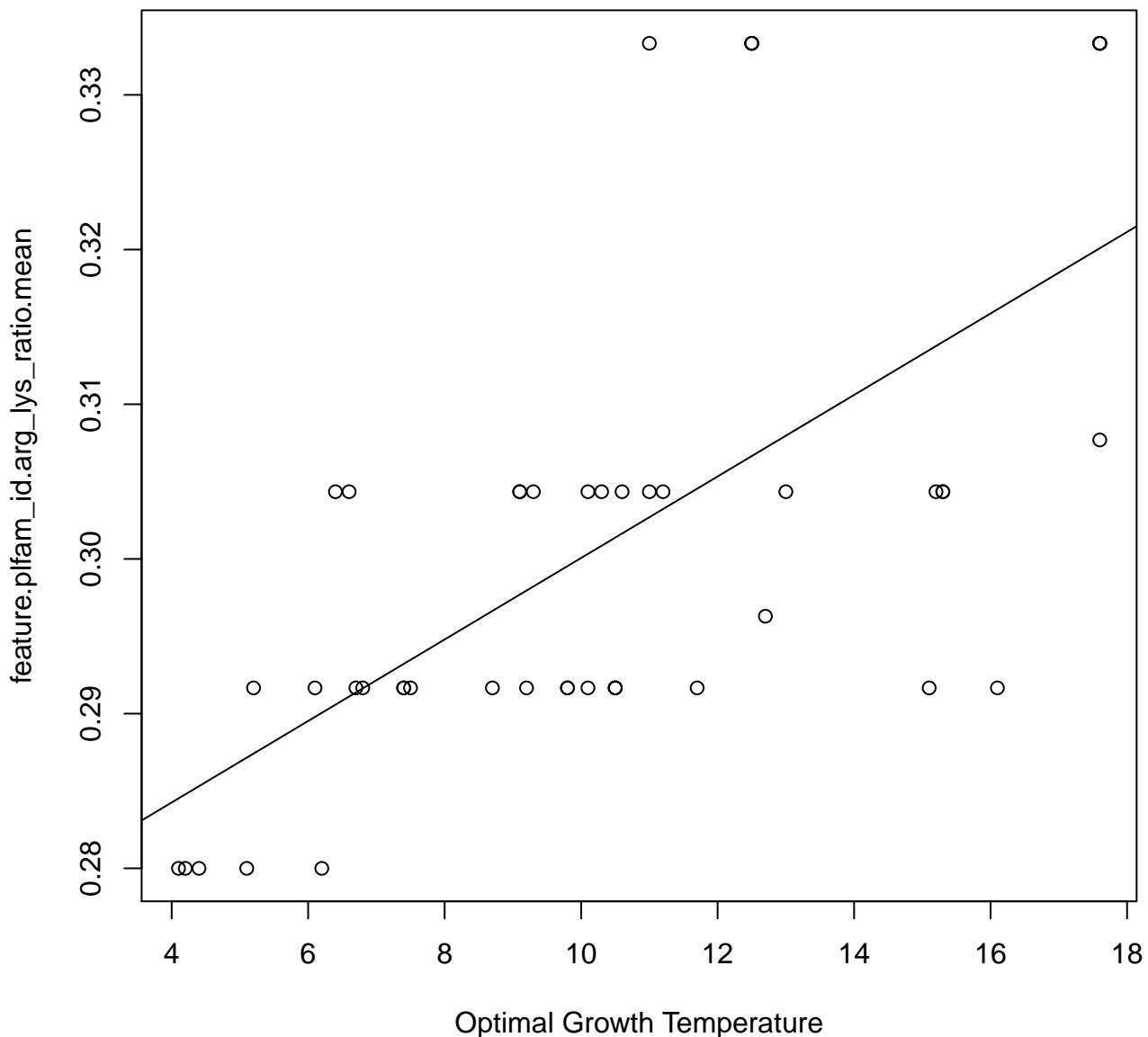
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000838
Flagellar motor rotation protein MotA



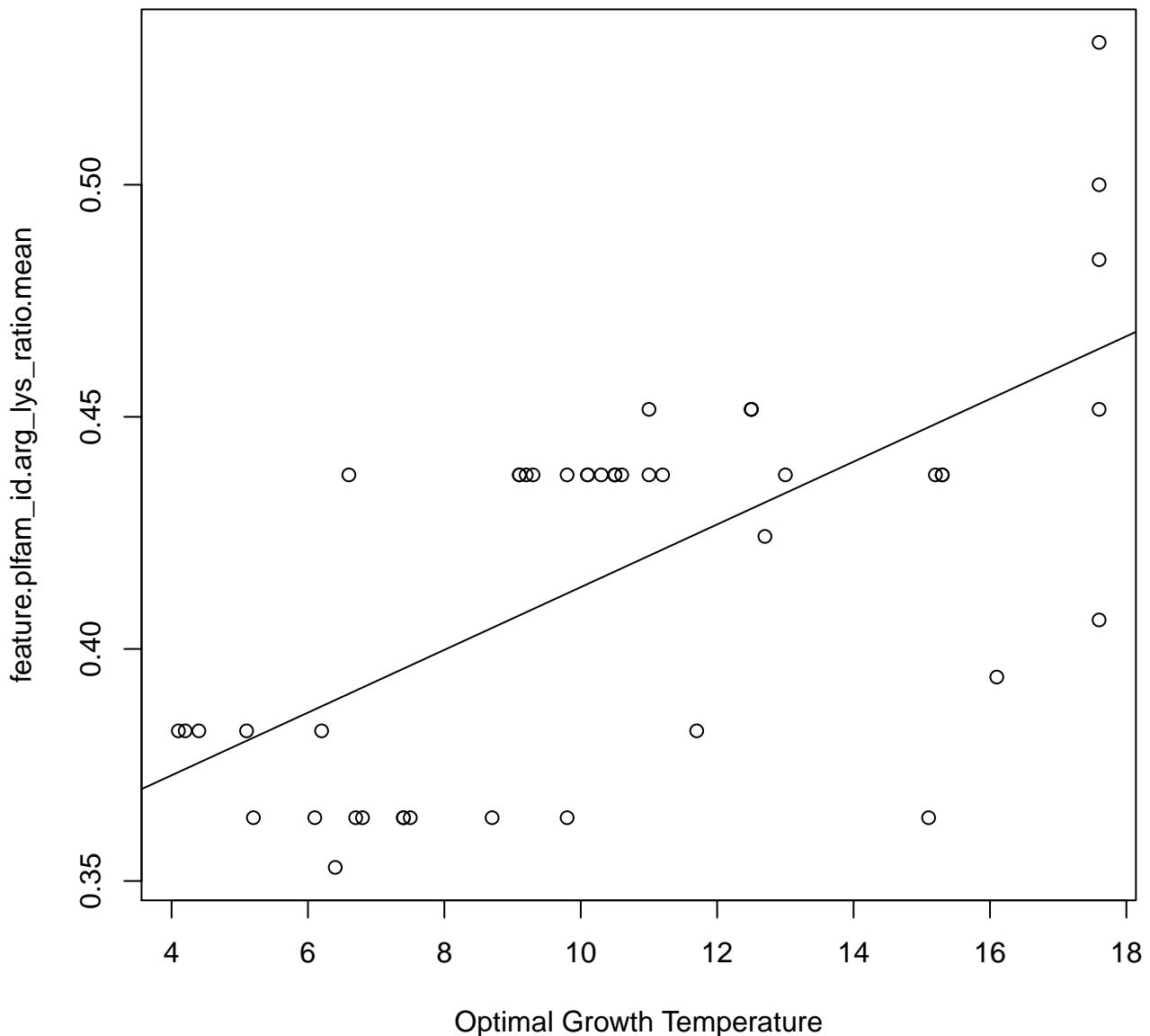
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00015880
Transporter, LysE family



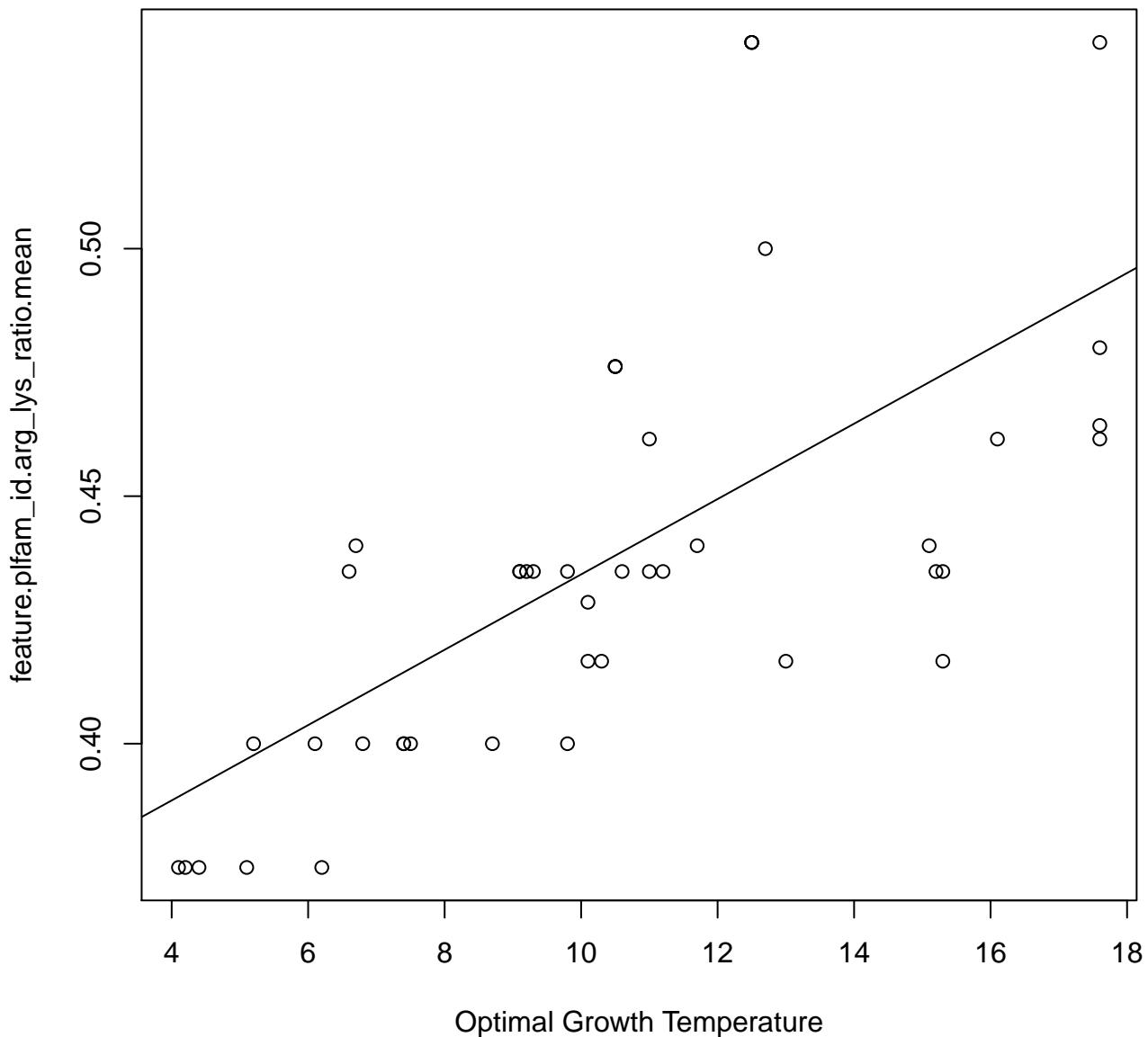
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000596
Malate dehydrogenase (EC 1.1.1.37)



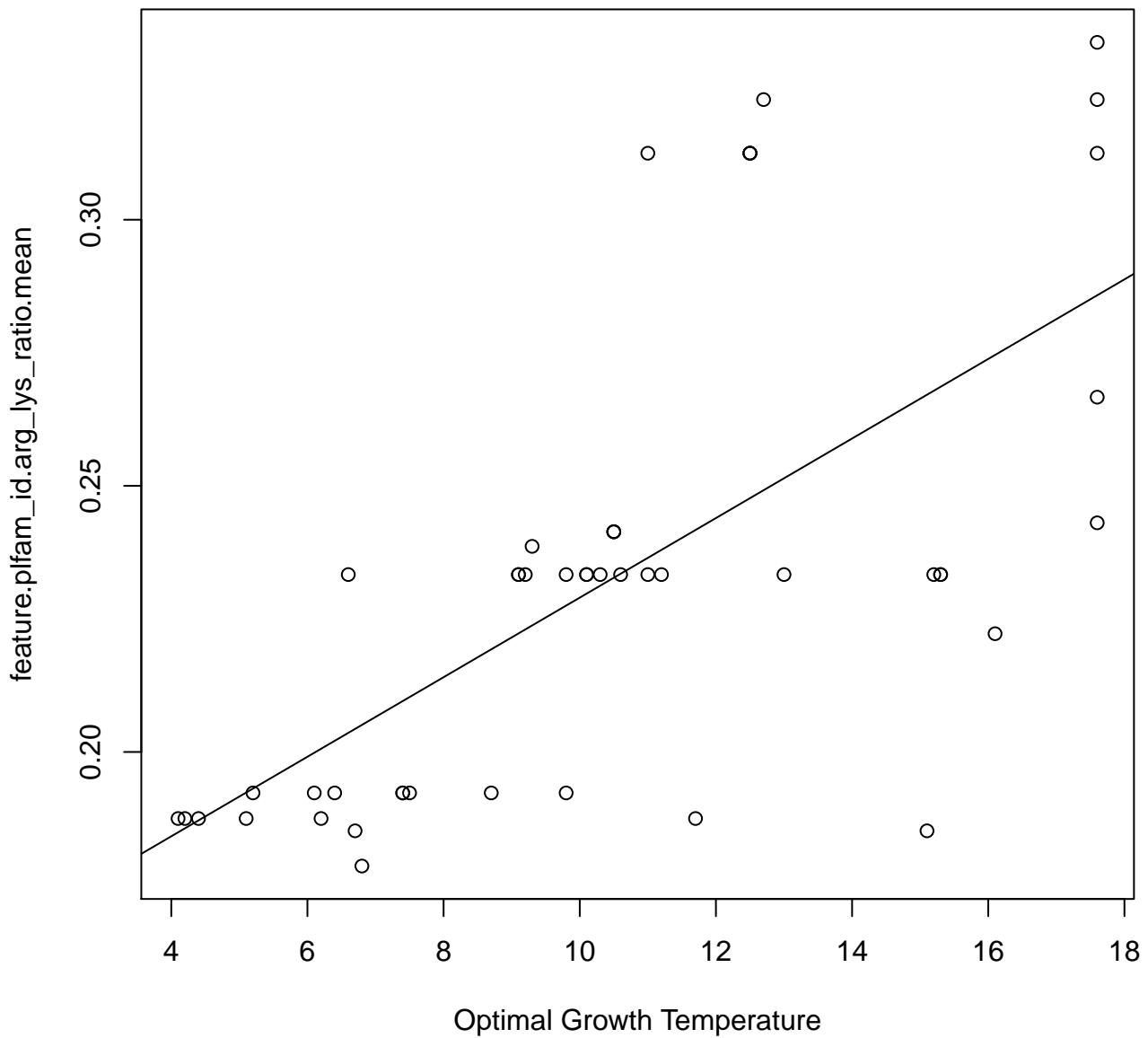
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000099
Chemotaxis protein CheV (EC 2.7.3.-)



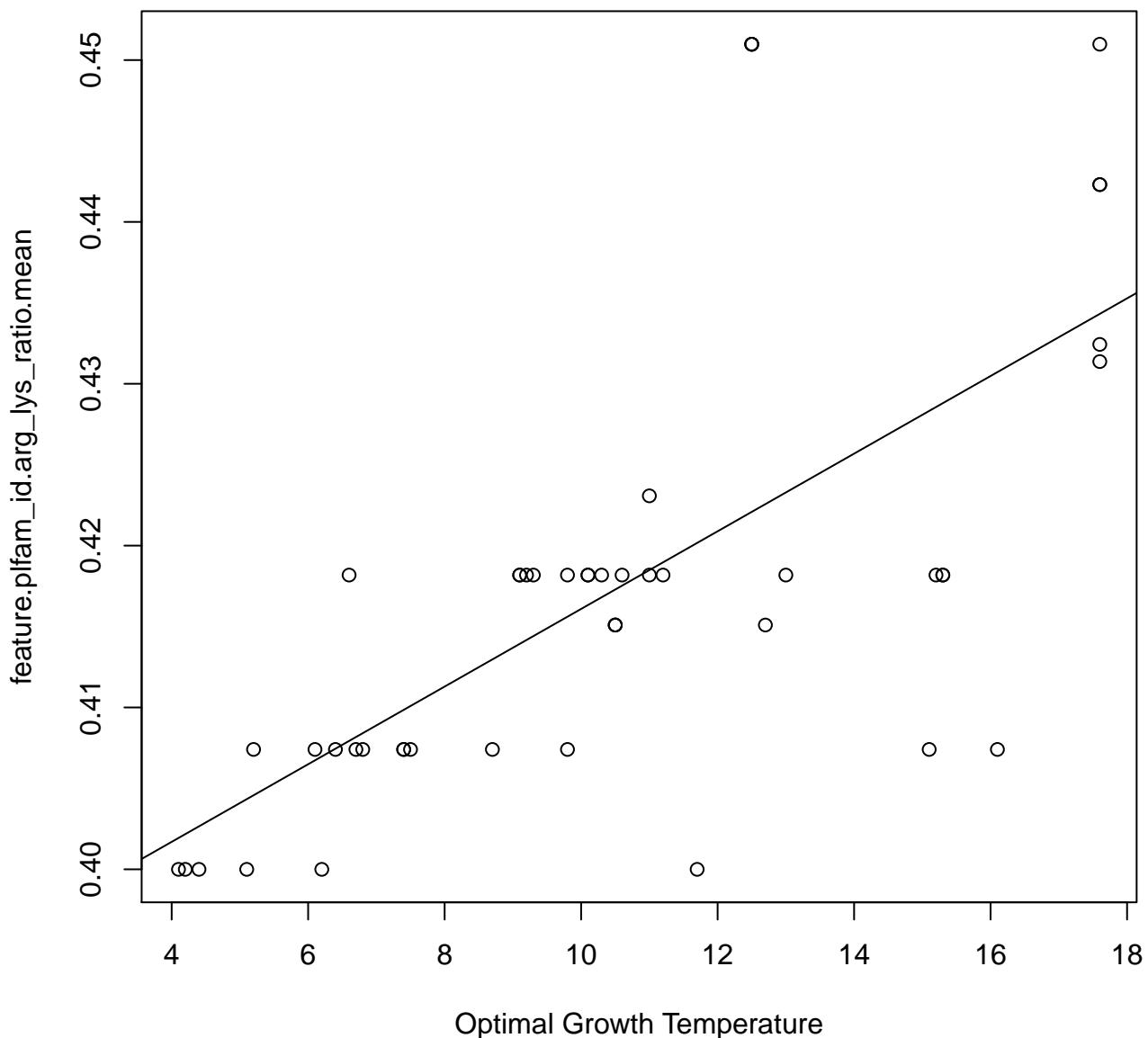
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000242
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000695
Branched-chain amino acid dehydrogenase [deaminating] (EC 1.4.1.9)(EC 1.4.1.23)



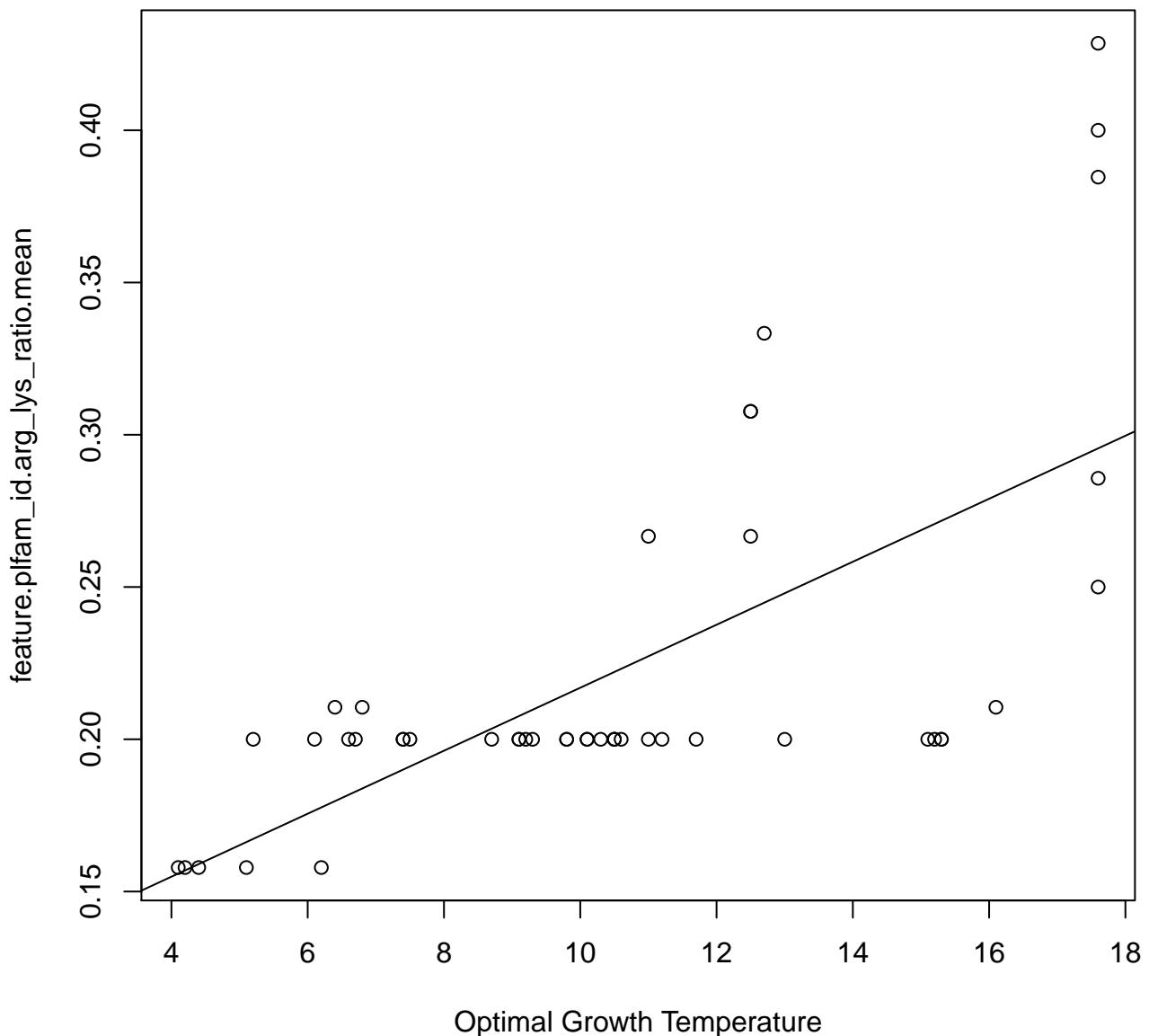
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000484
Flagellar biosynthesis protein FlhA



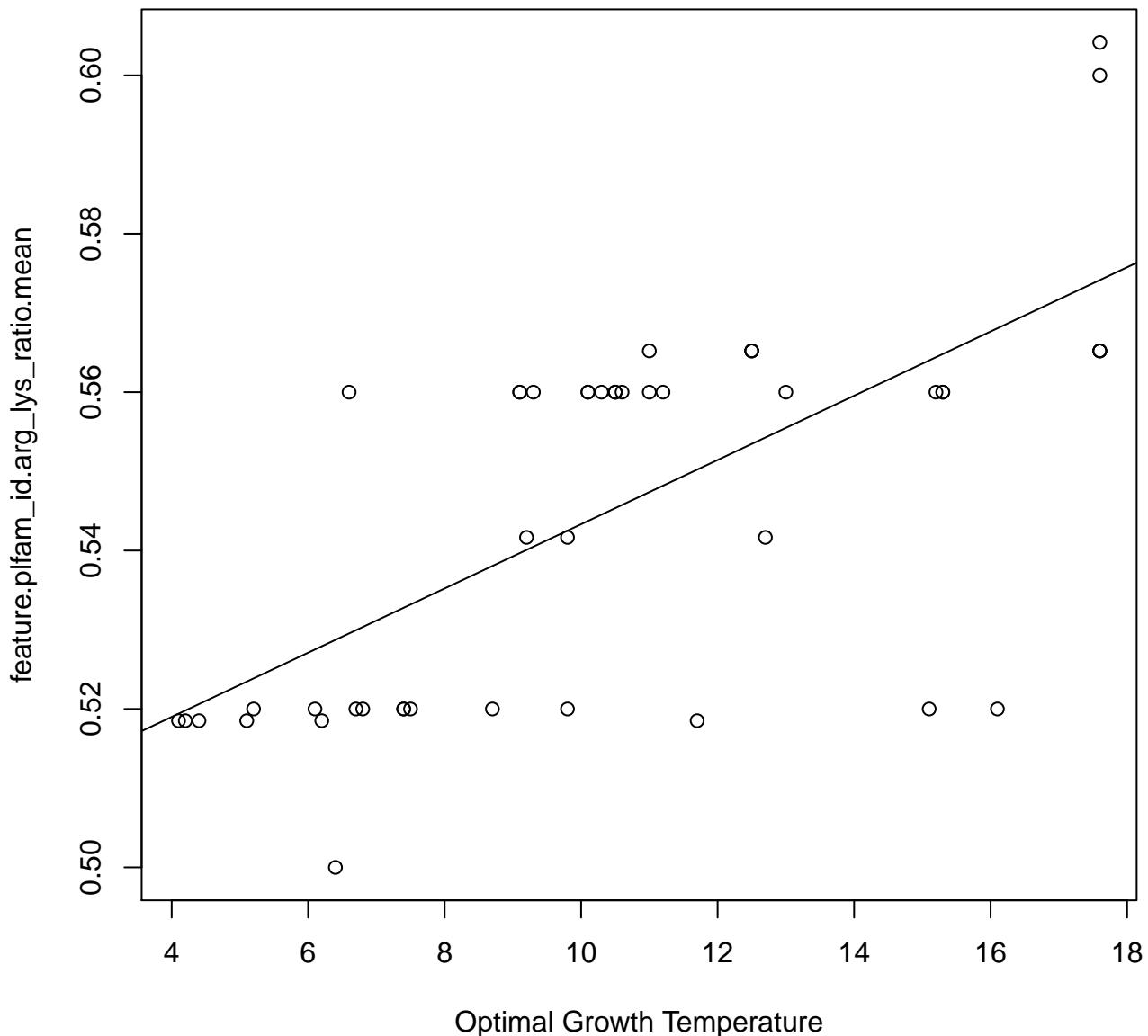
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000226

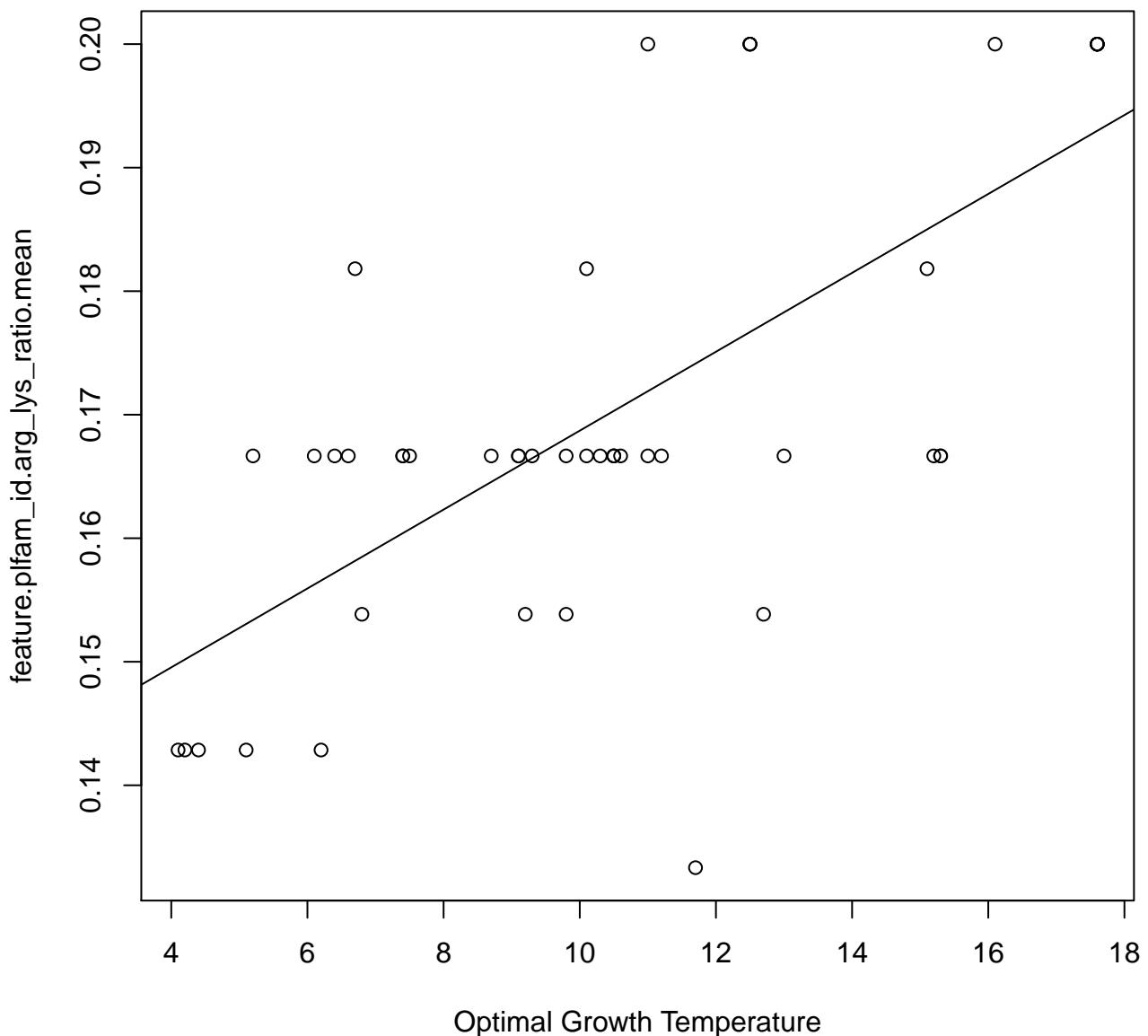
4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)



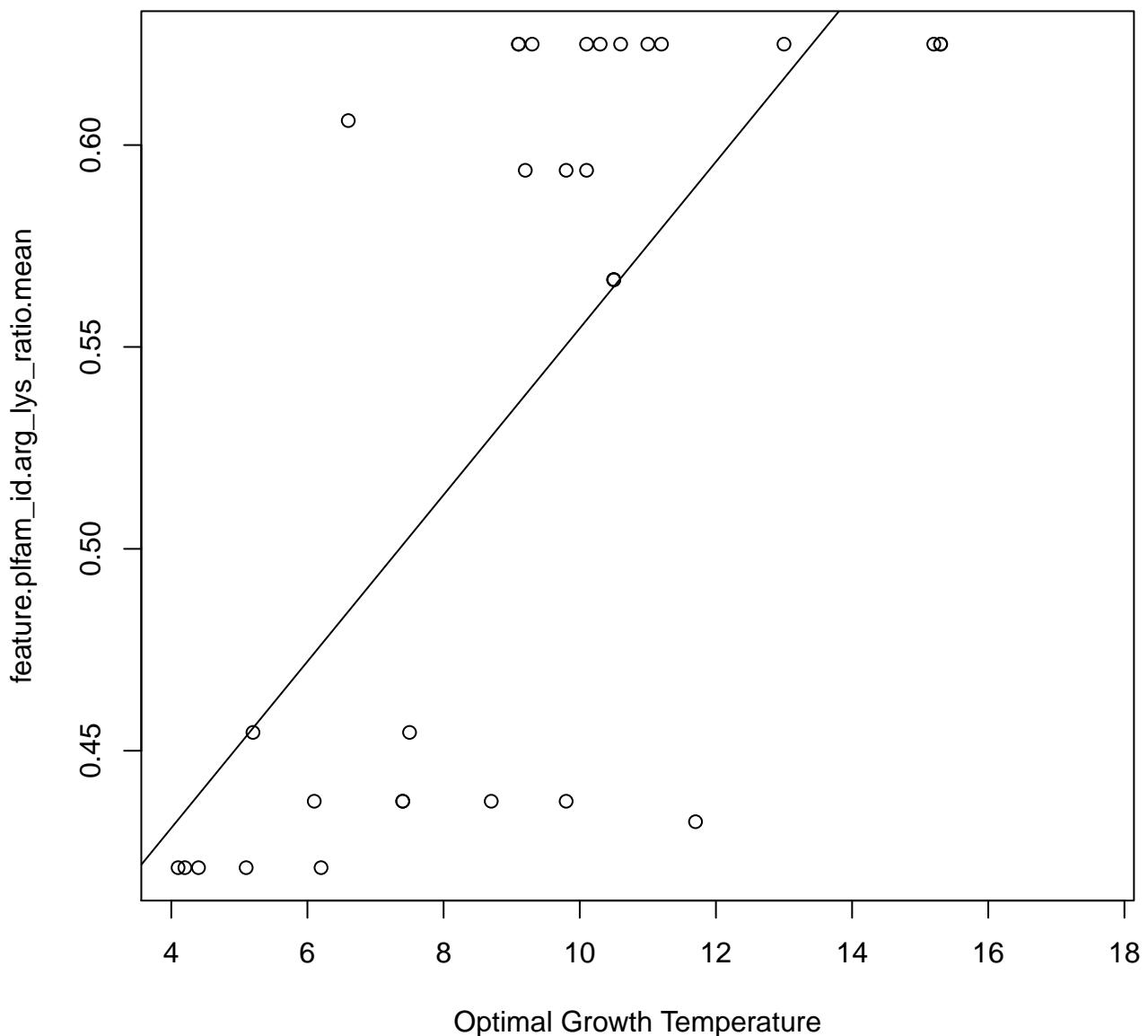
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000955
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)



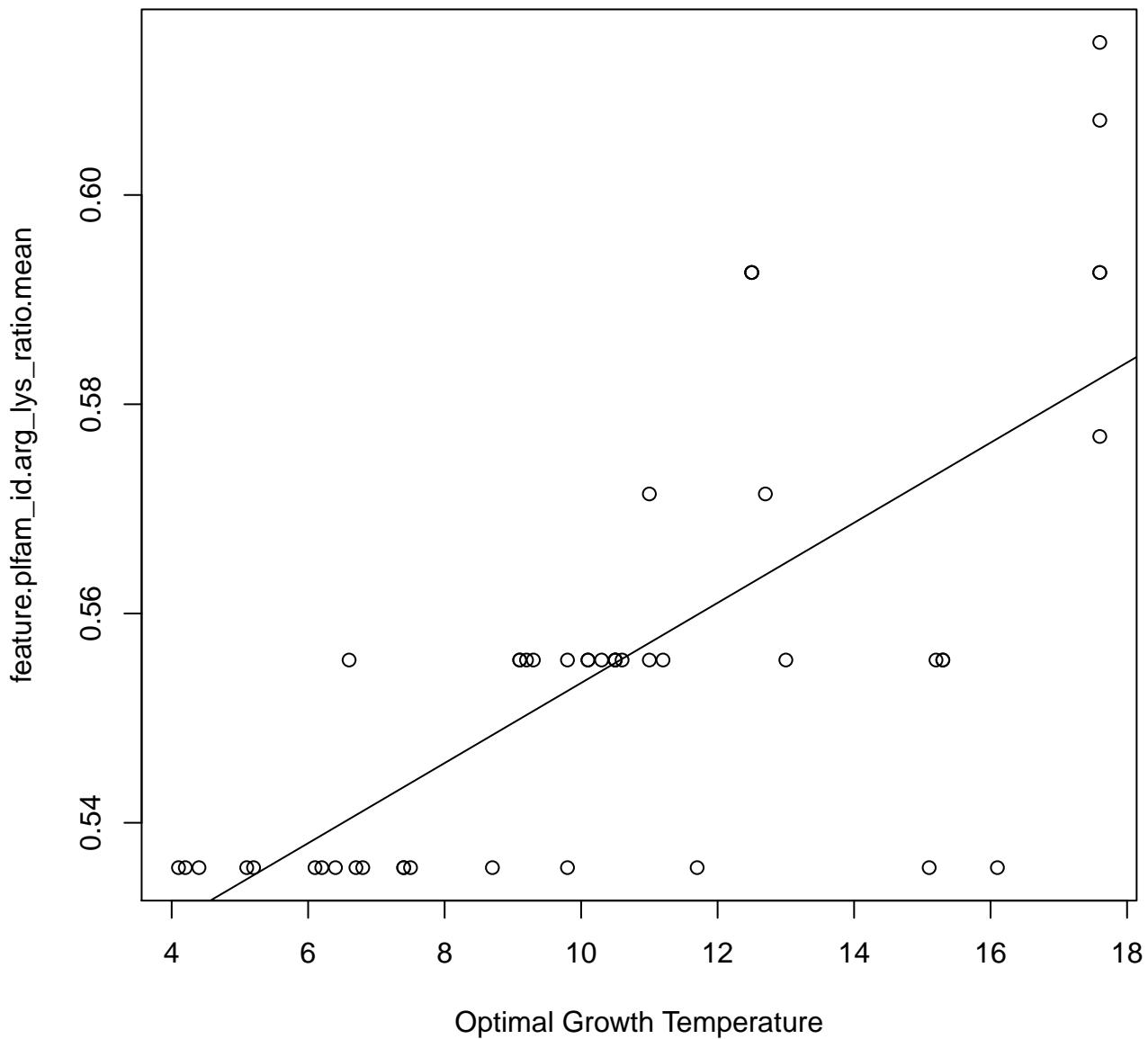
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000115
Antioxidant, AhpC/Tsa family



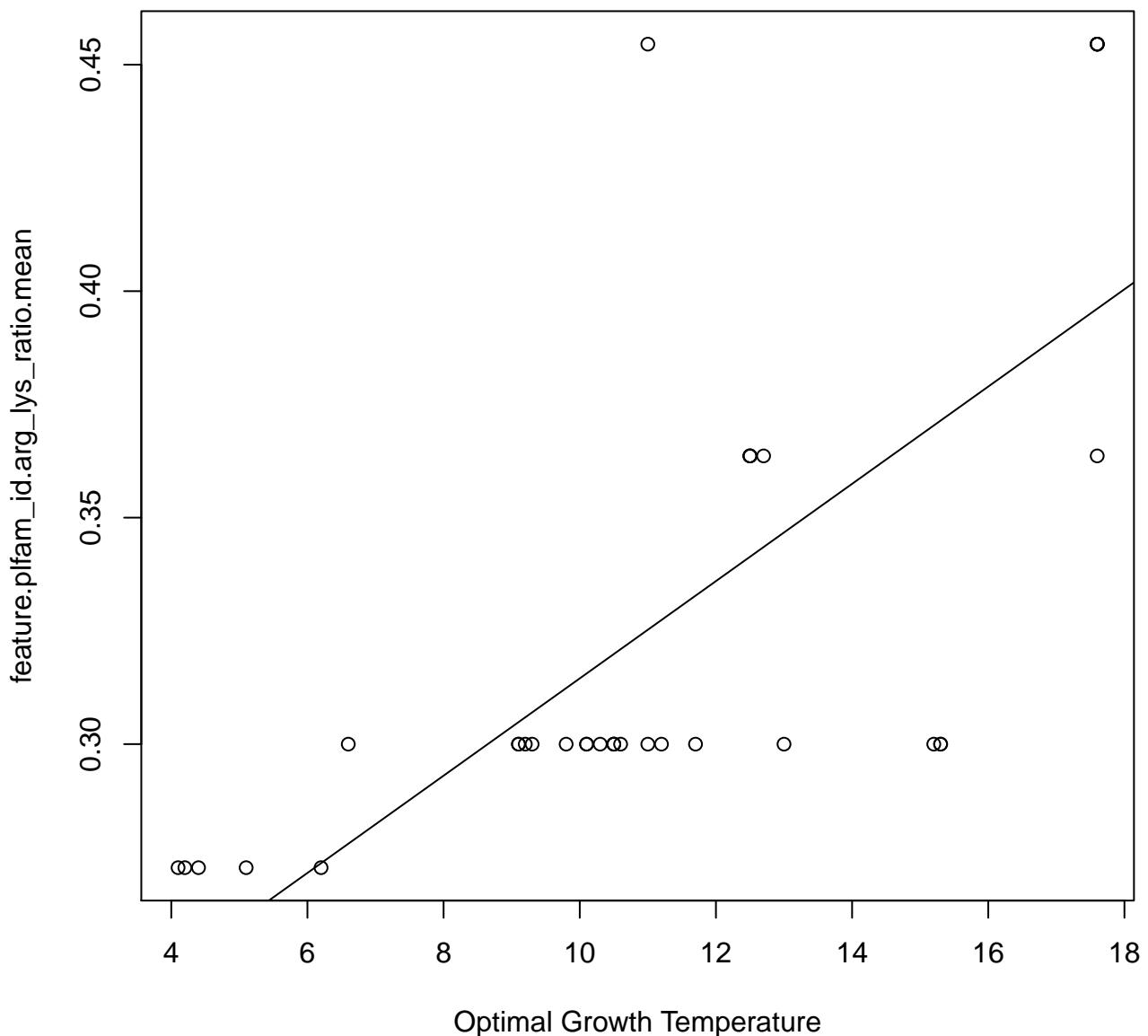
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PLF_28228_00013738
hypothetical protein



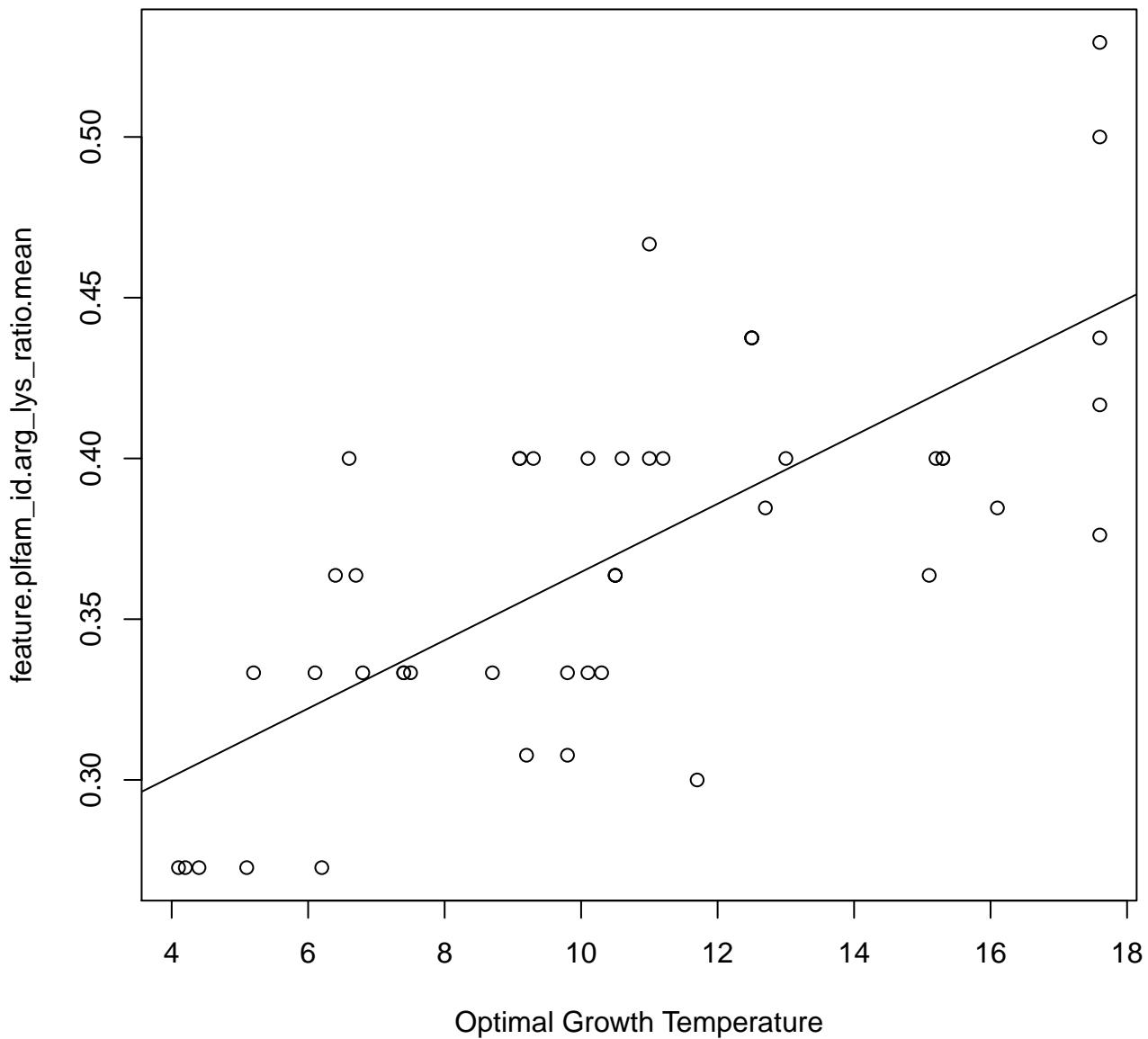
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PLF_28228_00000950
Phosphate transport system regulatory protein PhoU



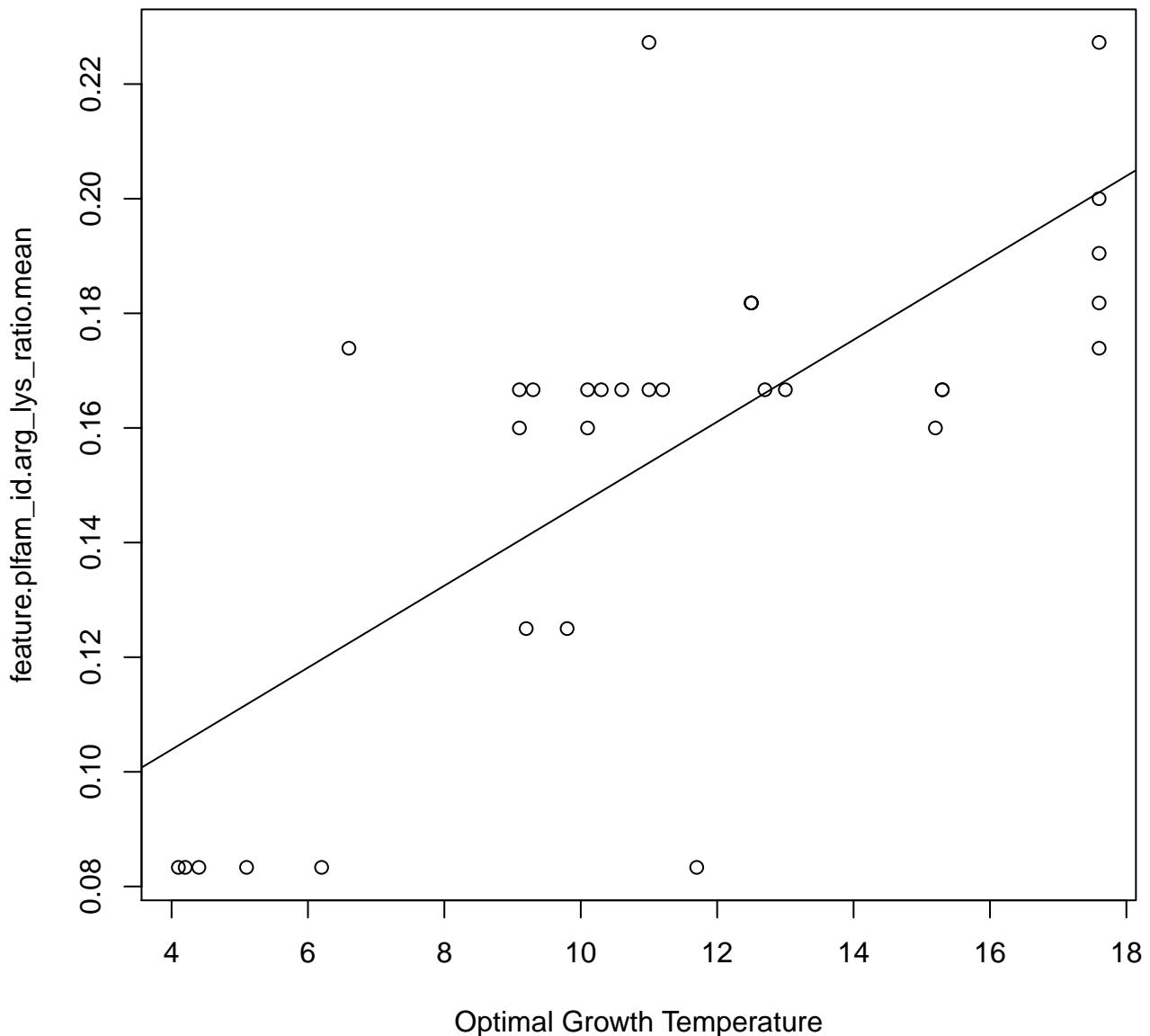
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001915
Phage shock protein C



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001718
MSHA pilin protein MshB



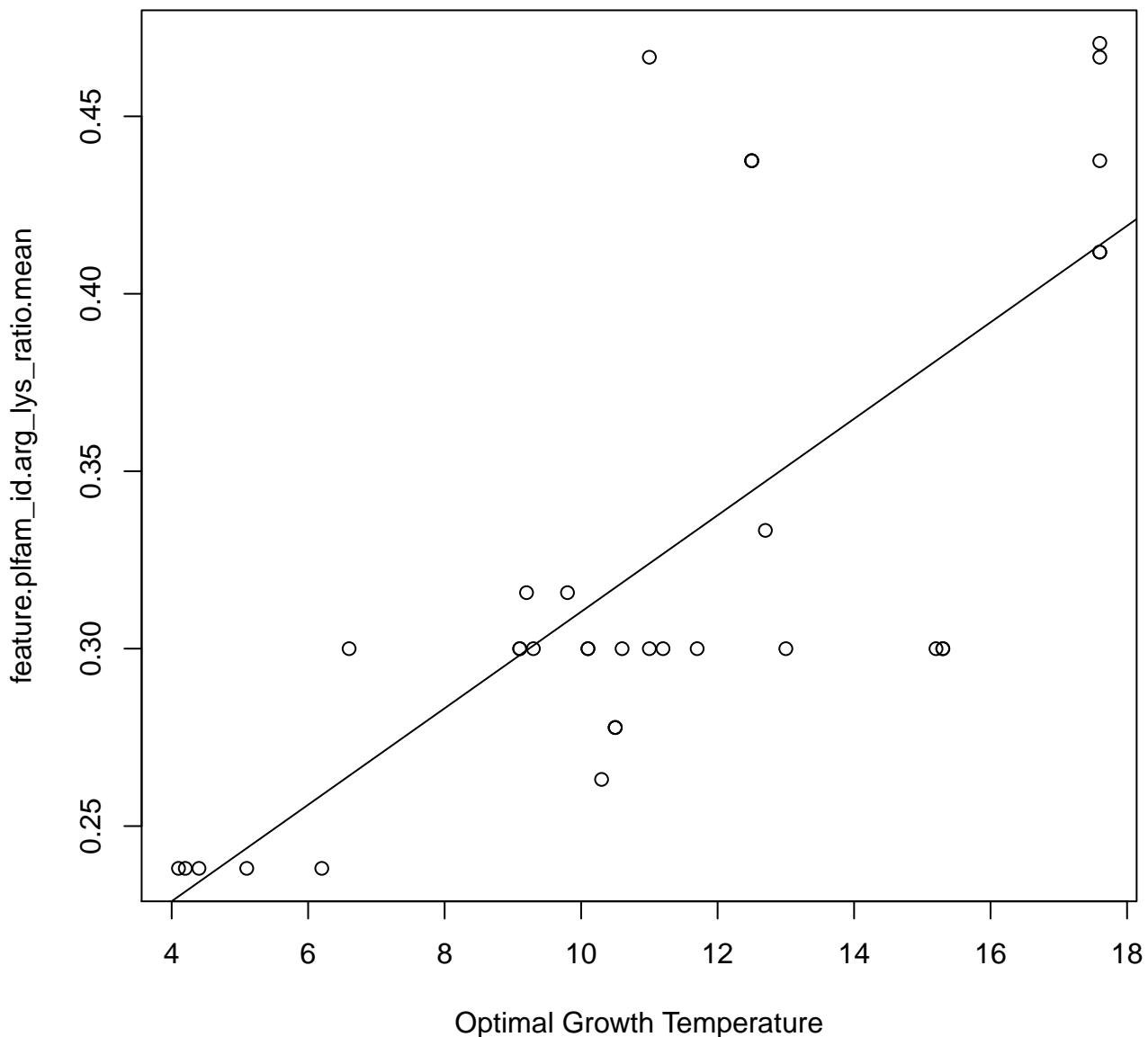
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000629
N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)



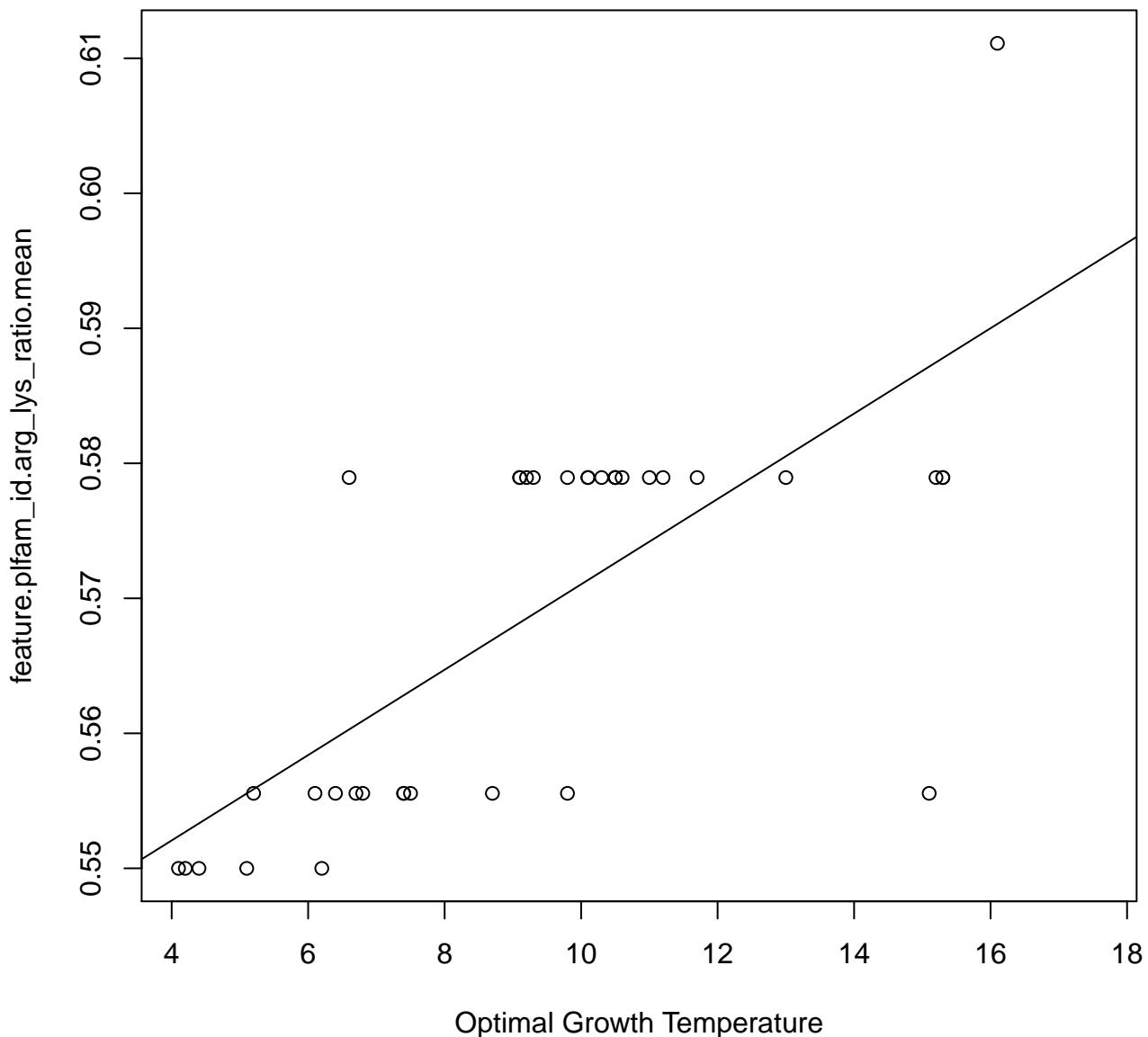
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PLF_28228_00001153

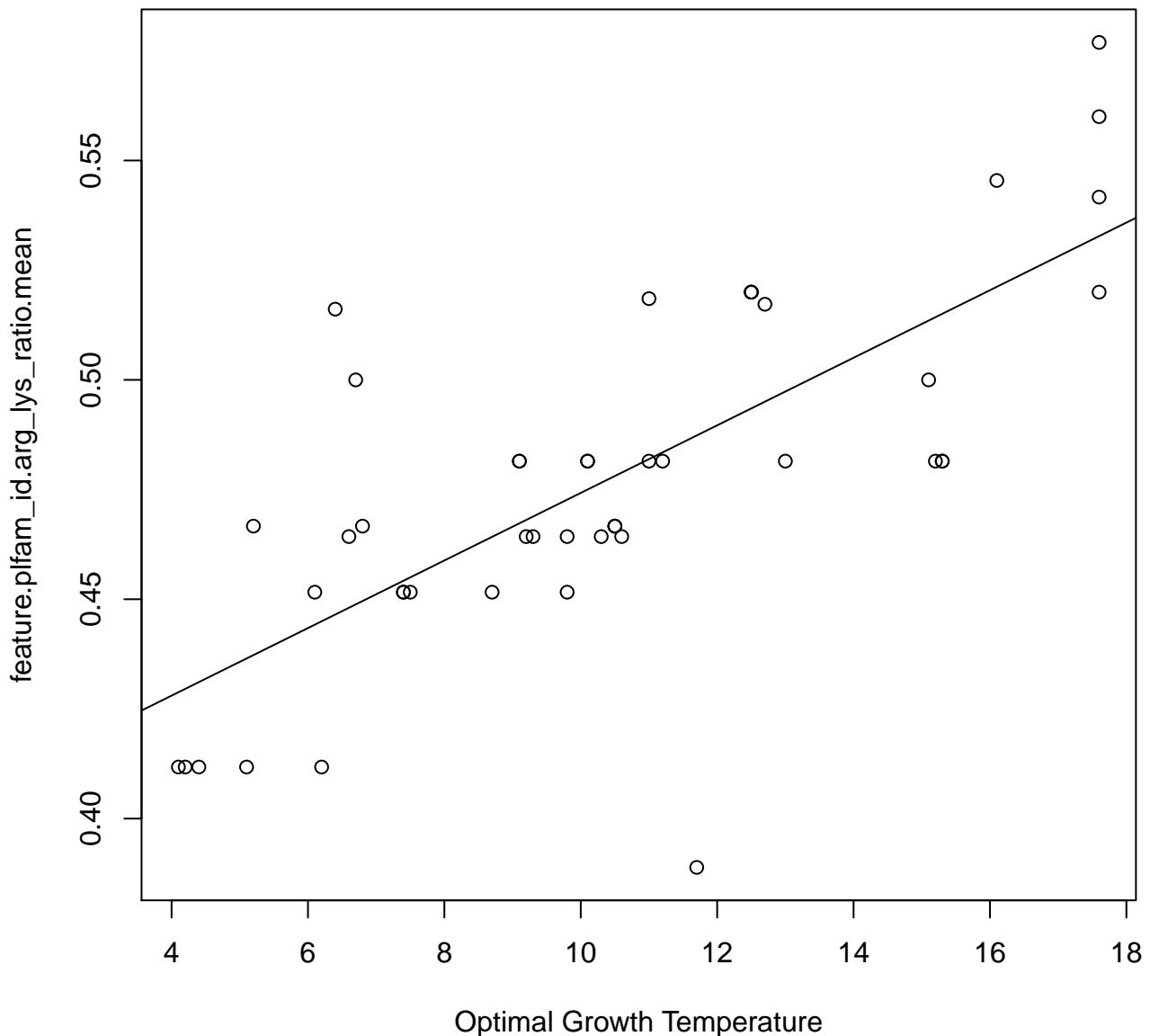
Similar to phosphoglycolate phosphatase, clustered with ribosomal large subunit pseudouridine synthase C



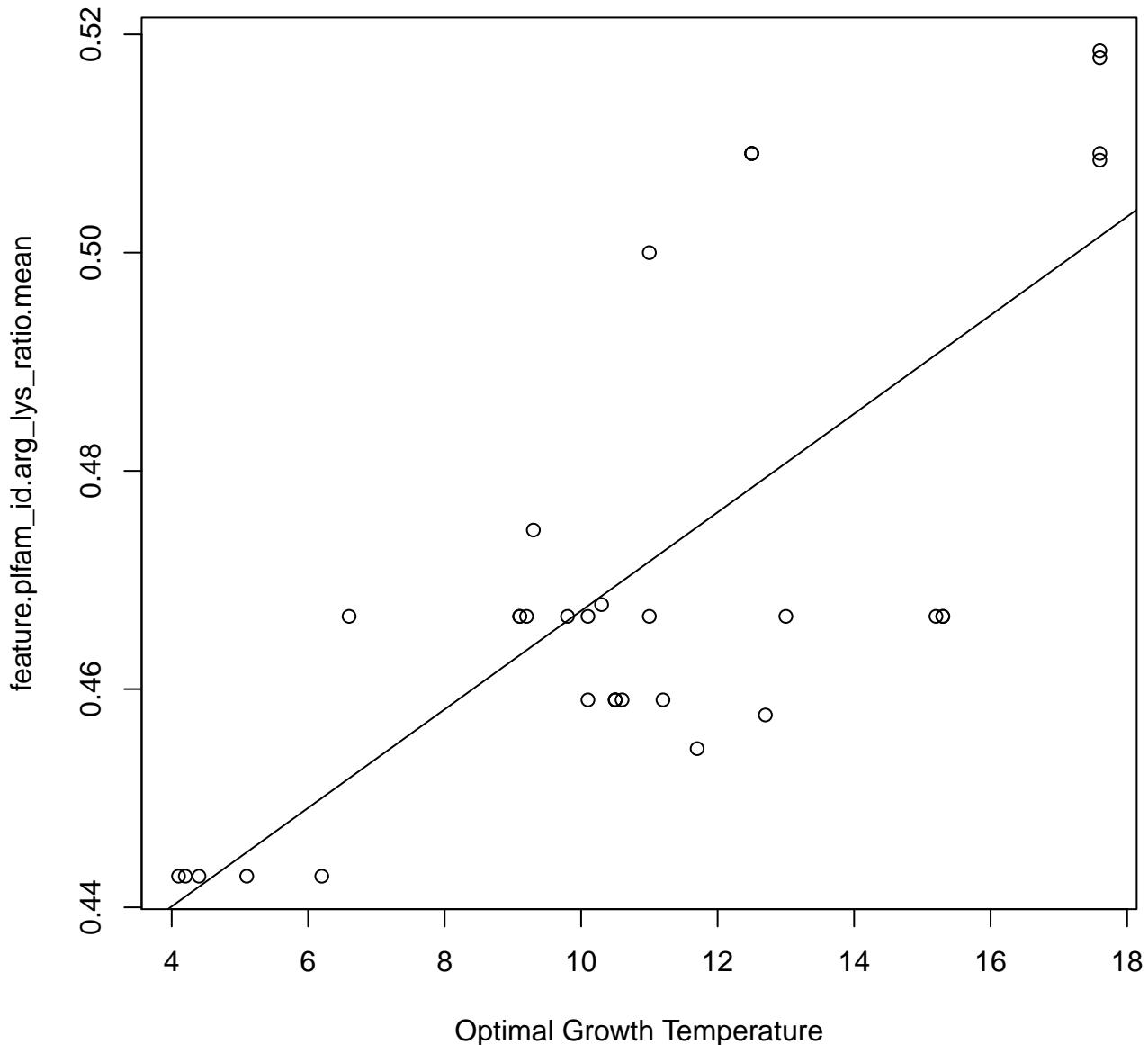
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PLF_28228_00014664
hypothetical protein



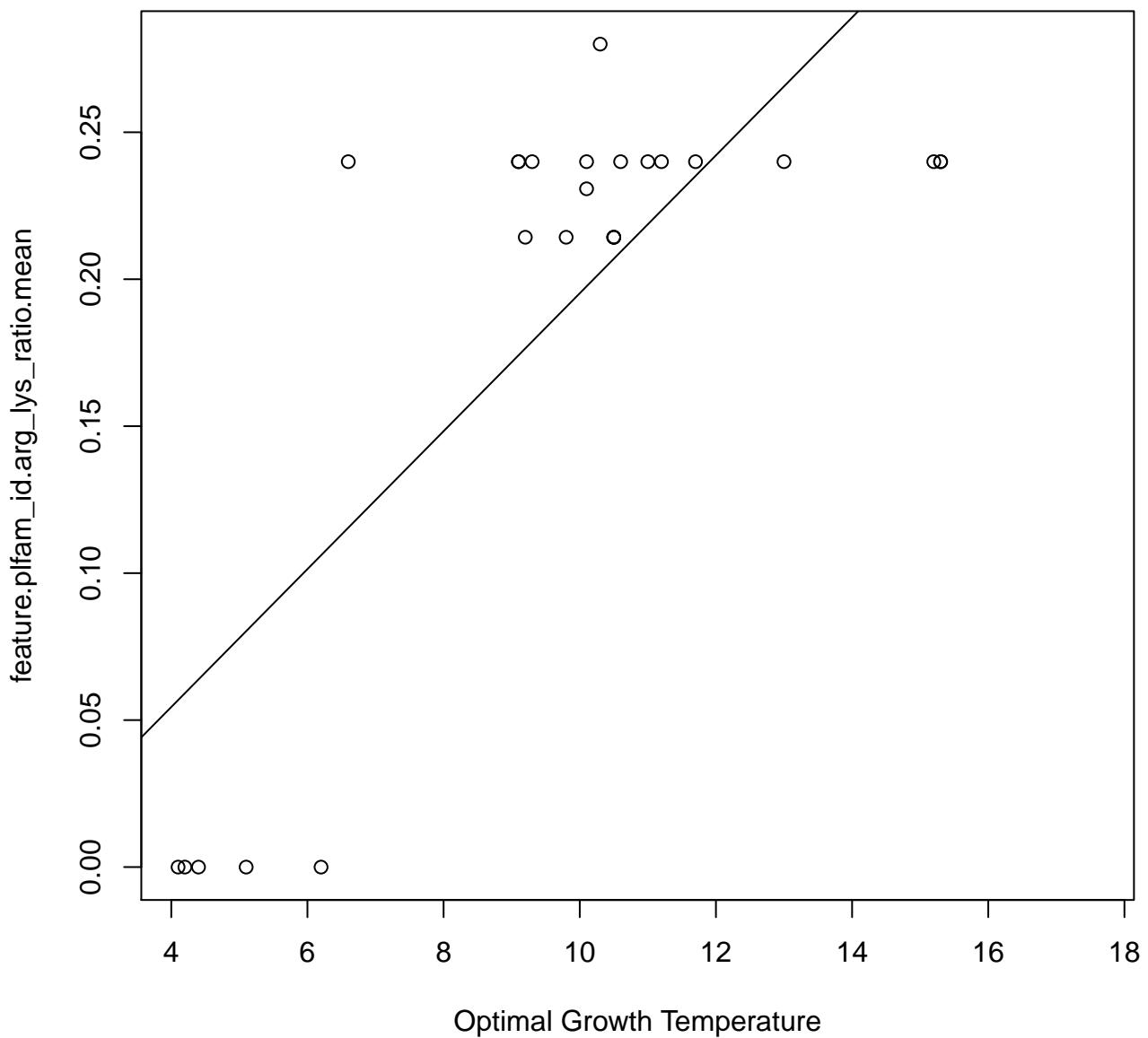
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PLF_28228_00000268
3-deoxy-D-manno-octulose-2'-phosphate kinase (EC 2.7.1.166)



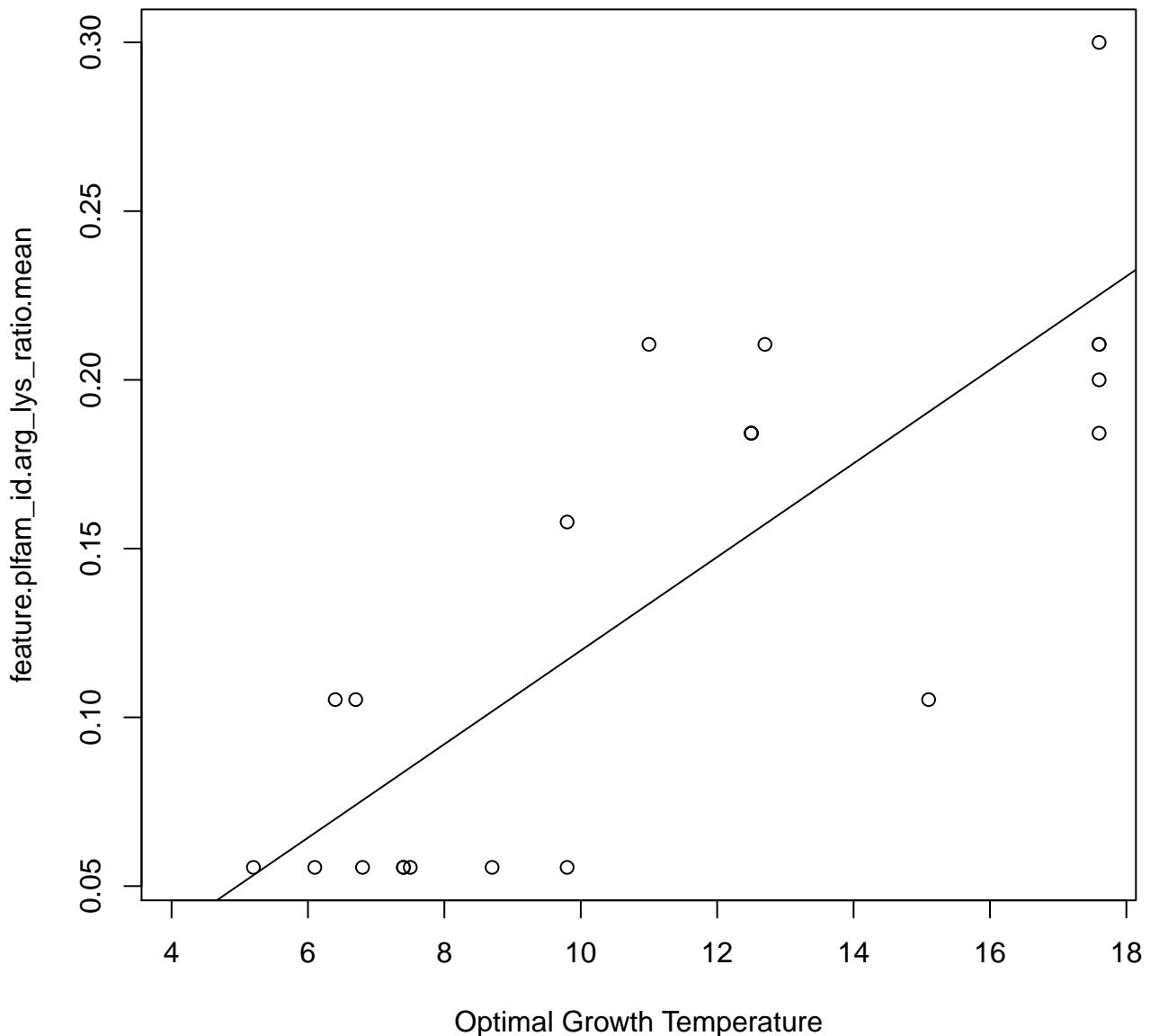
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000474
Ferrichrome–iron receptor



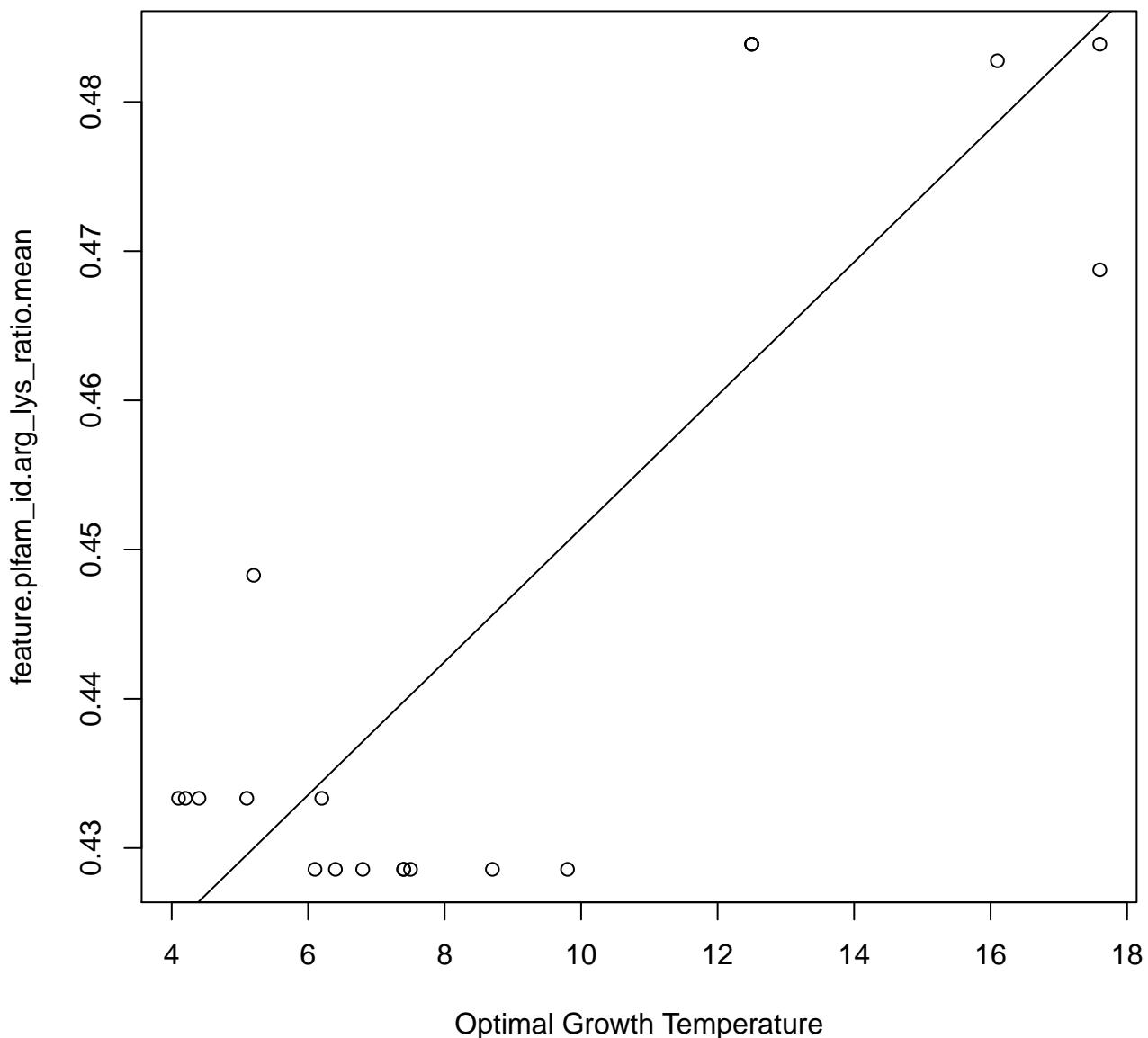
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PLF_28228_00031426
hypothetical protein



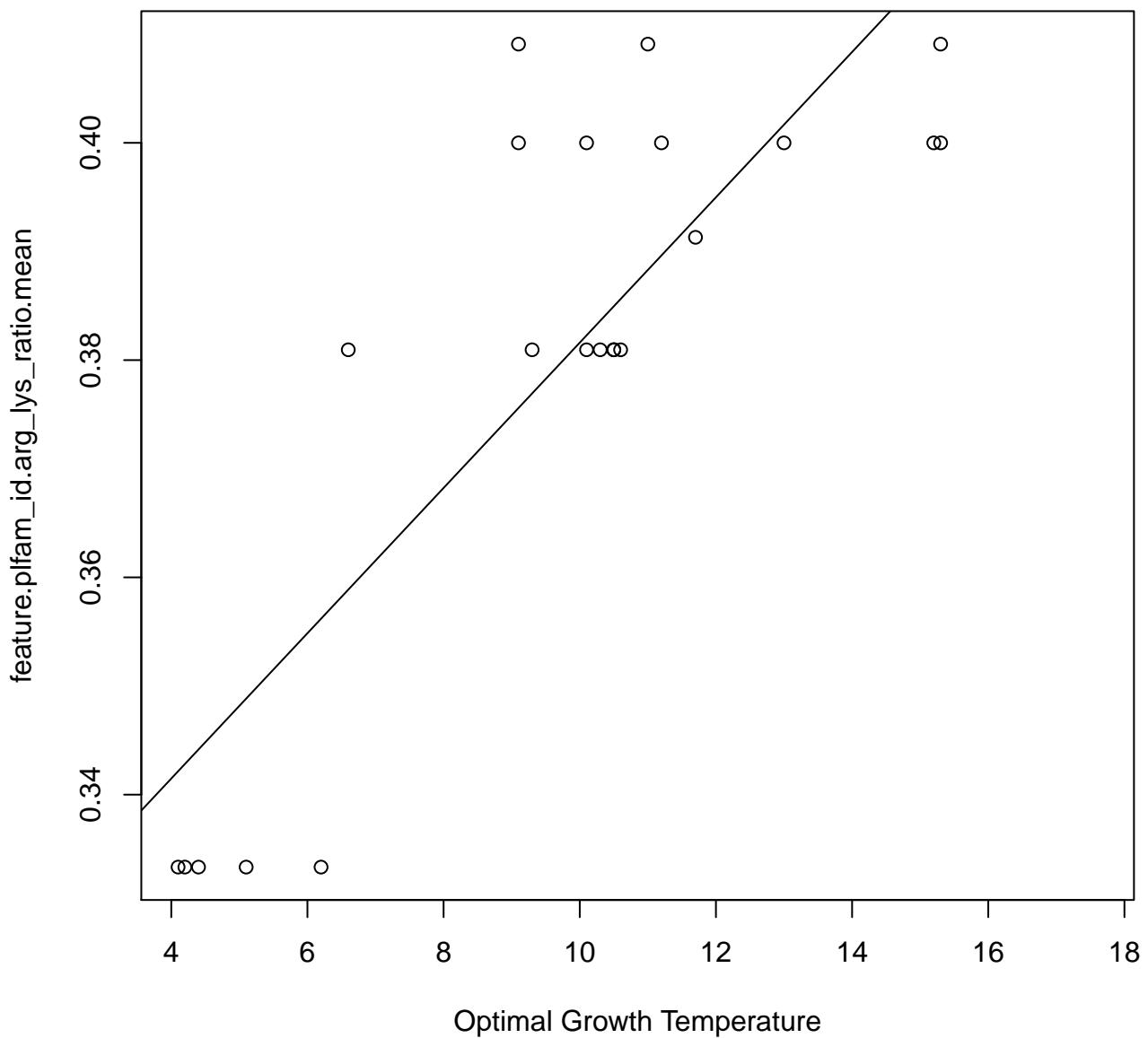
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001180
TRAP dicarboxylate transporter, DctM subunit, unknown substrate 6



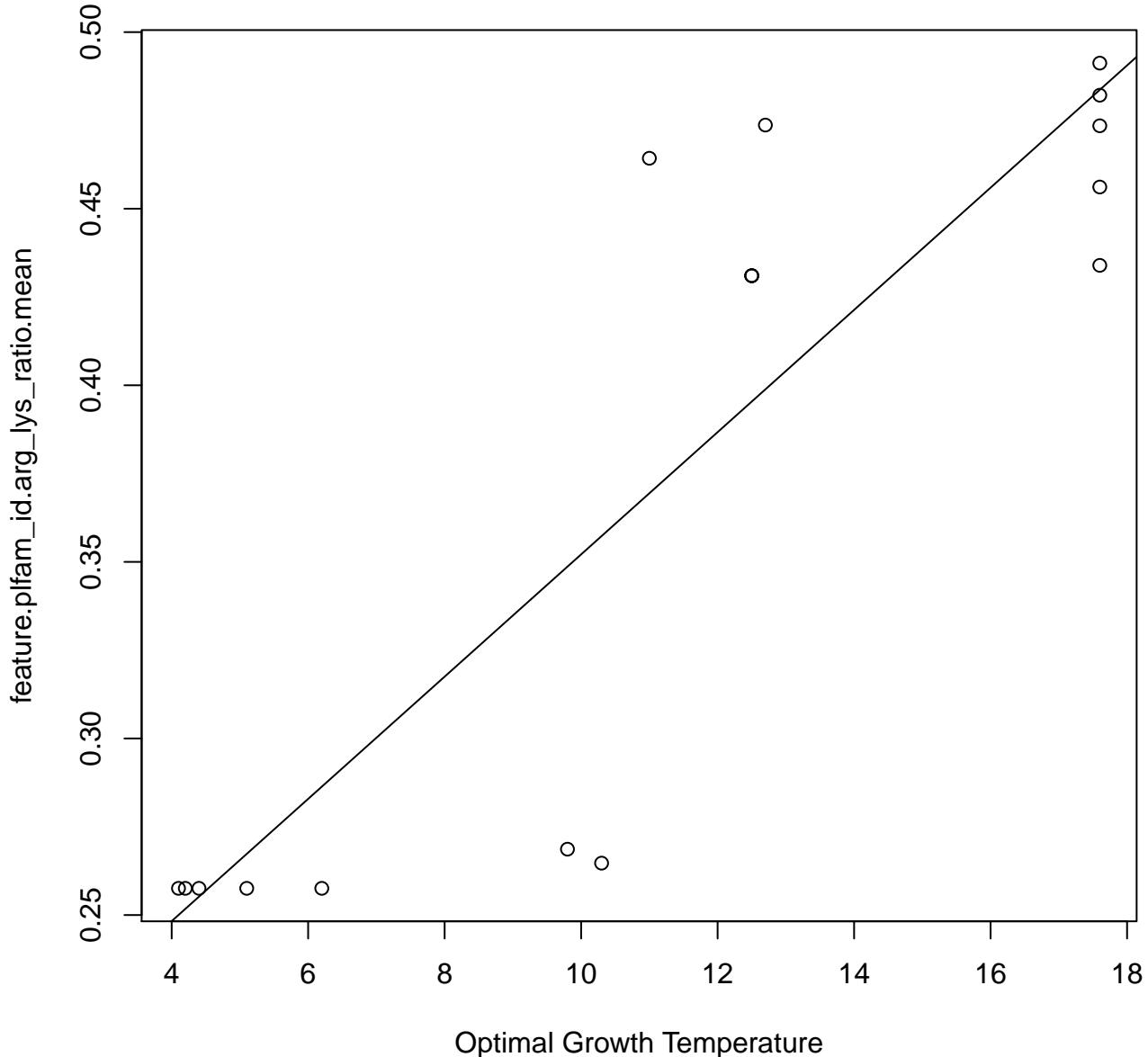
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003471
Glucose/mannose:H⁺ symporter GlcP



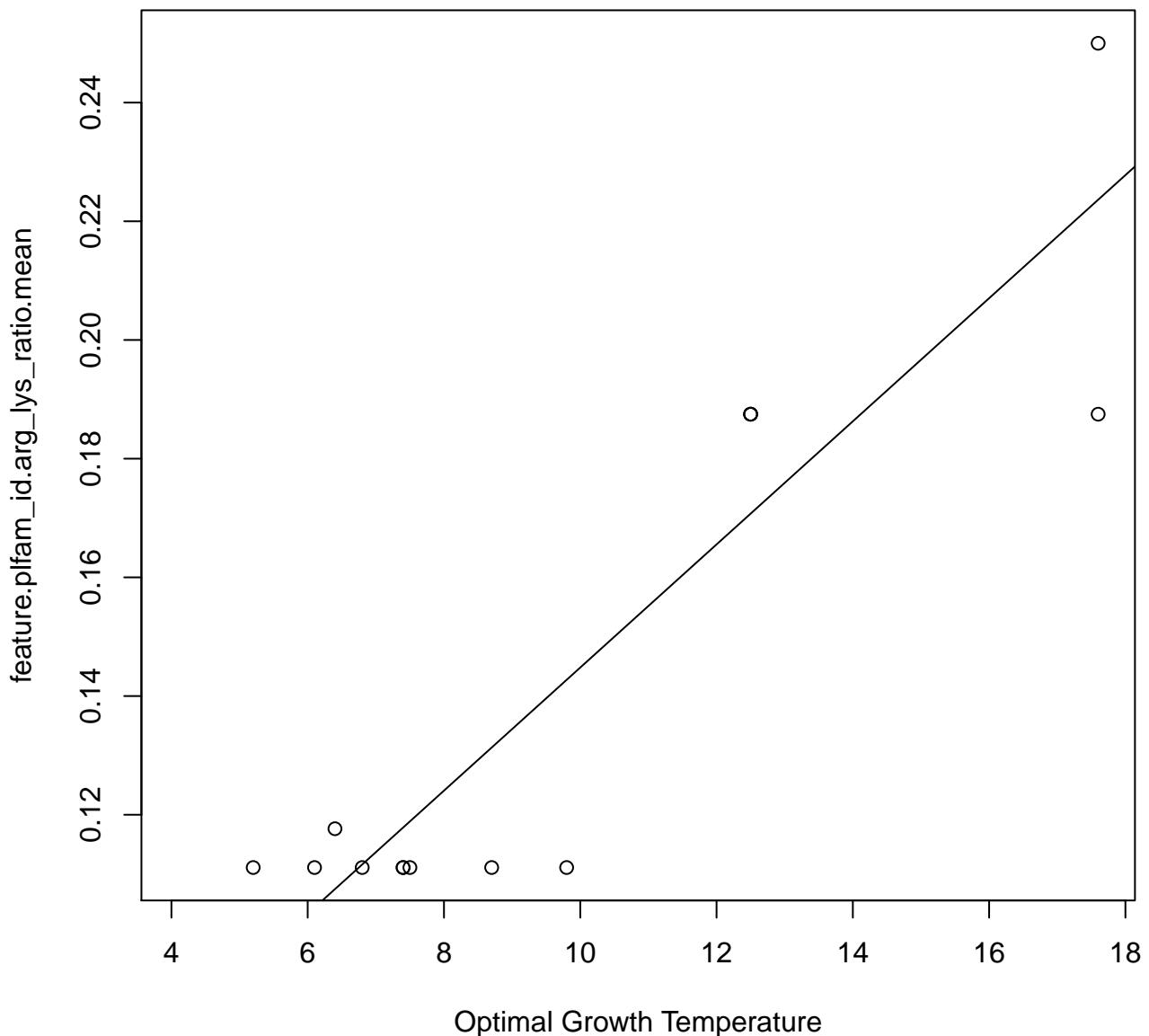
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PLF_28228_00020926
hypothetical protein



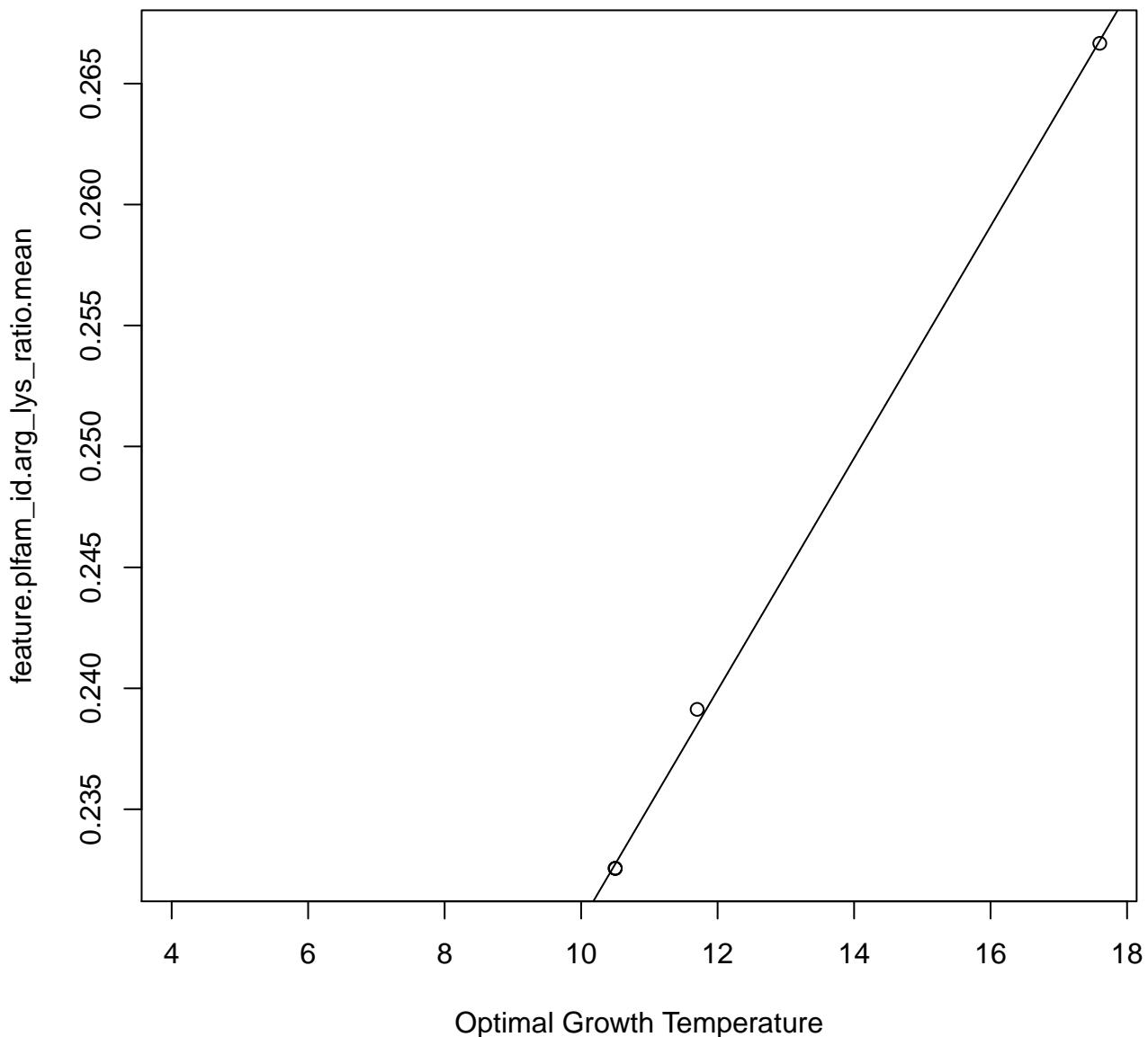
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001719
Macrolide-specific ABC-type efflux carrier (TC 3.A.1.122.1)



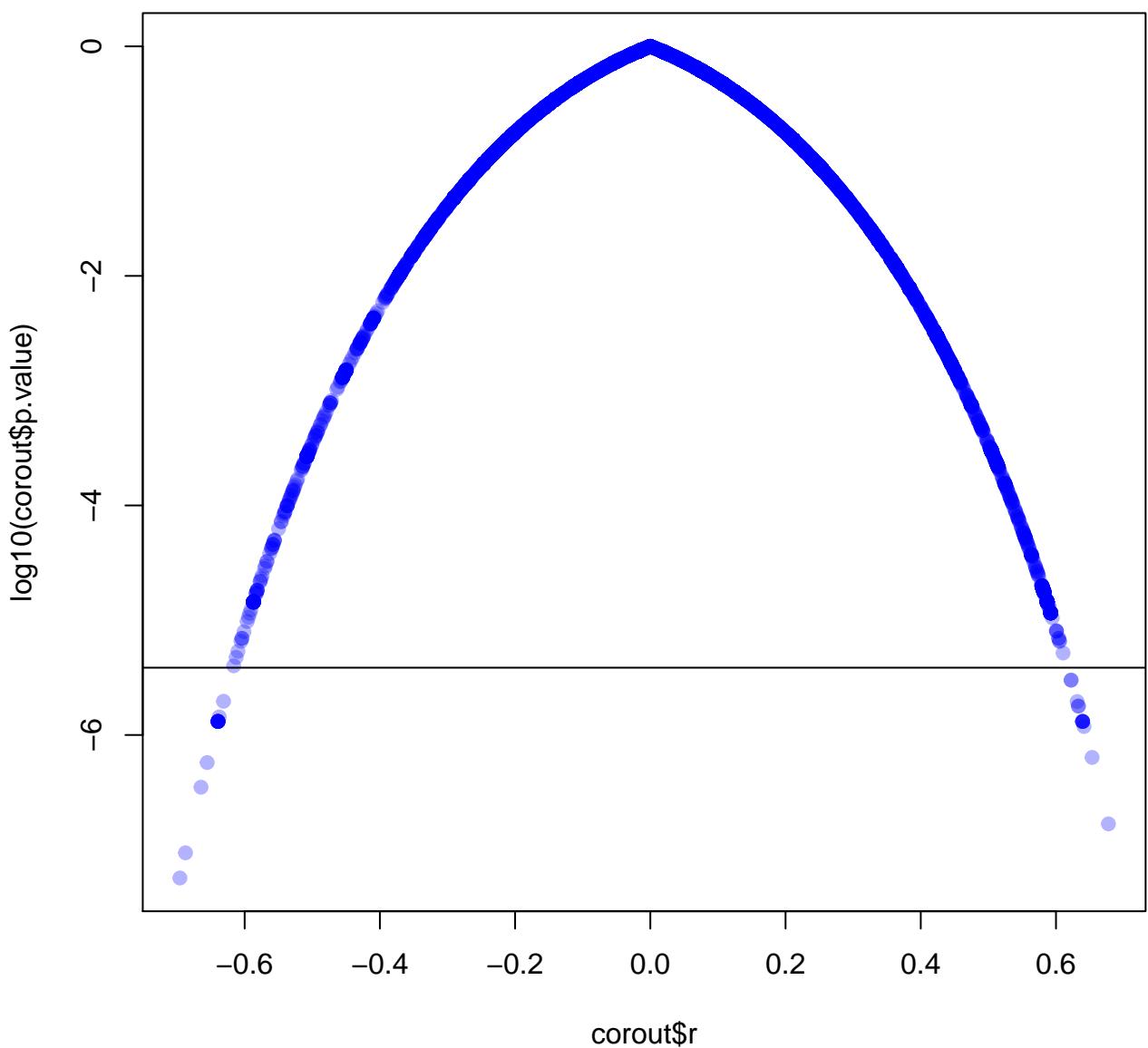
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007378
SapC-like S-layer protein



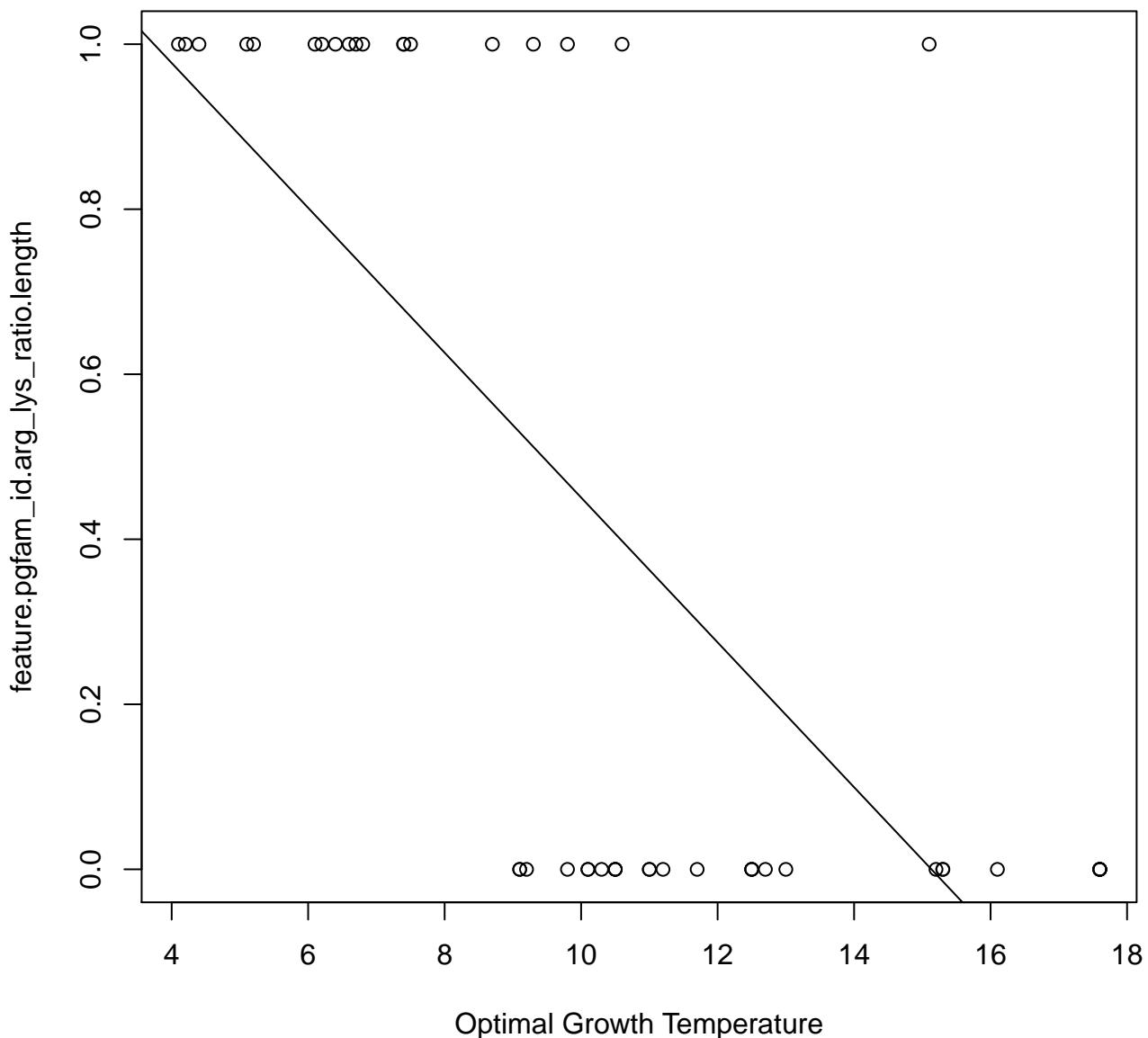
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00005474
Putative hydrolase



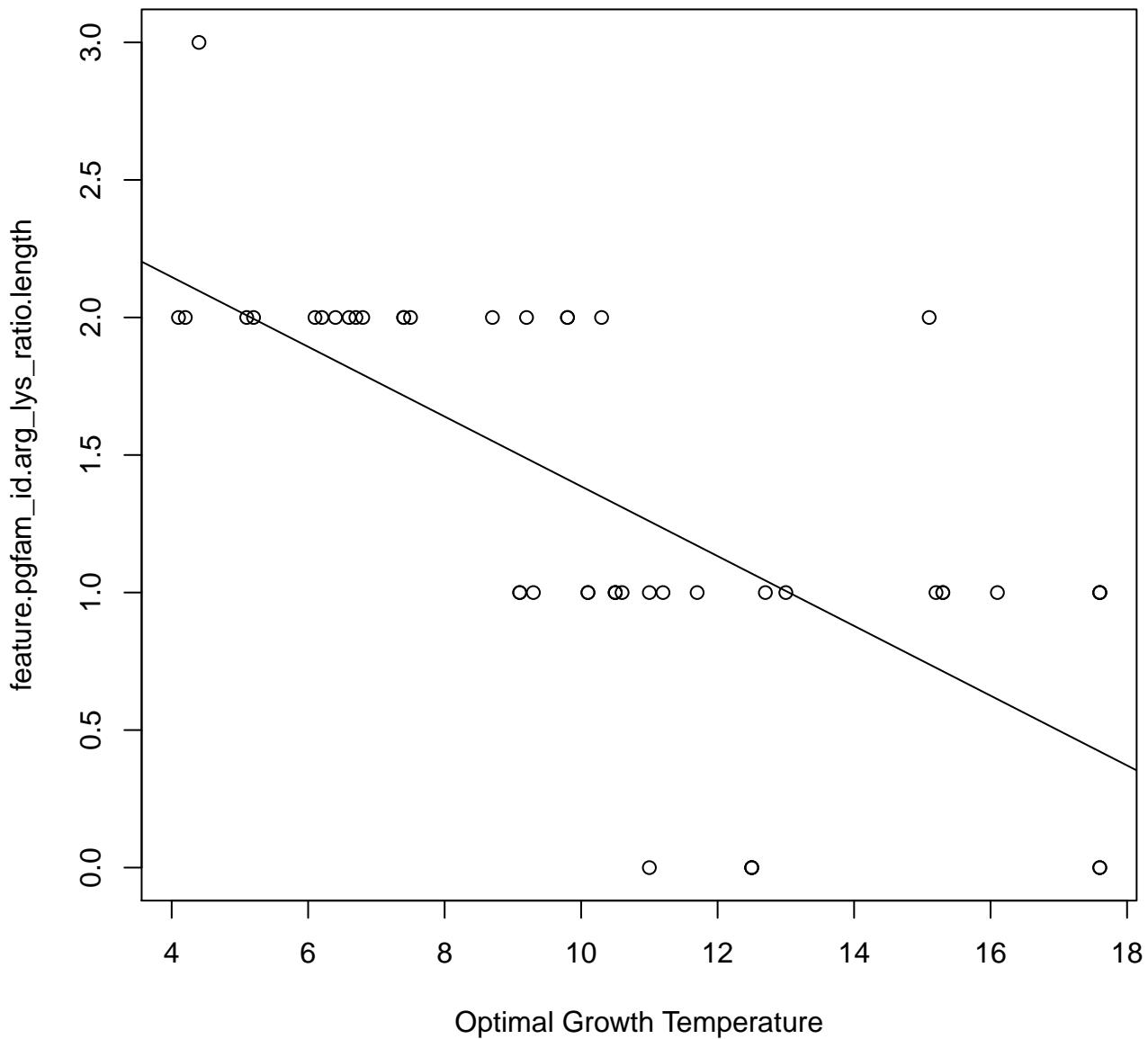
feature.pgfam_id.arg_lys_ratio.length



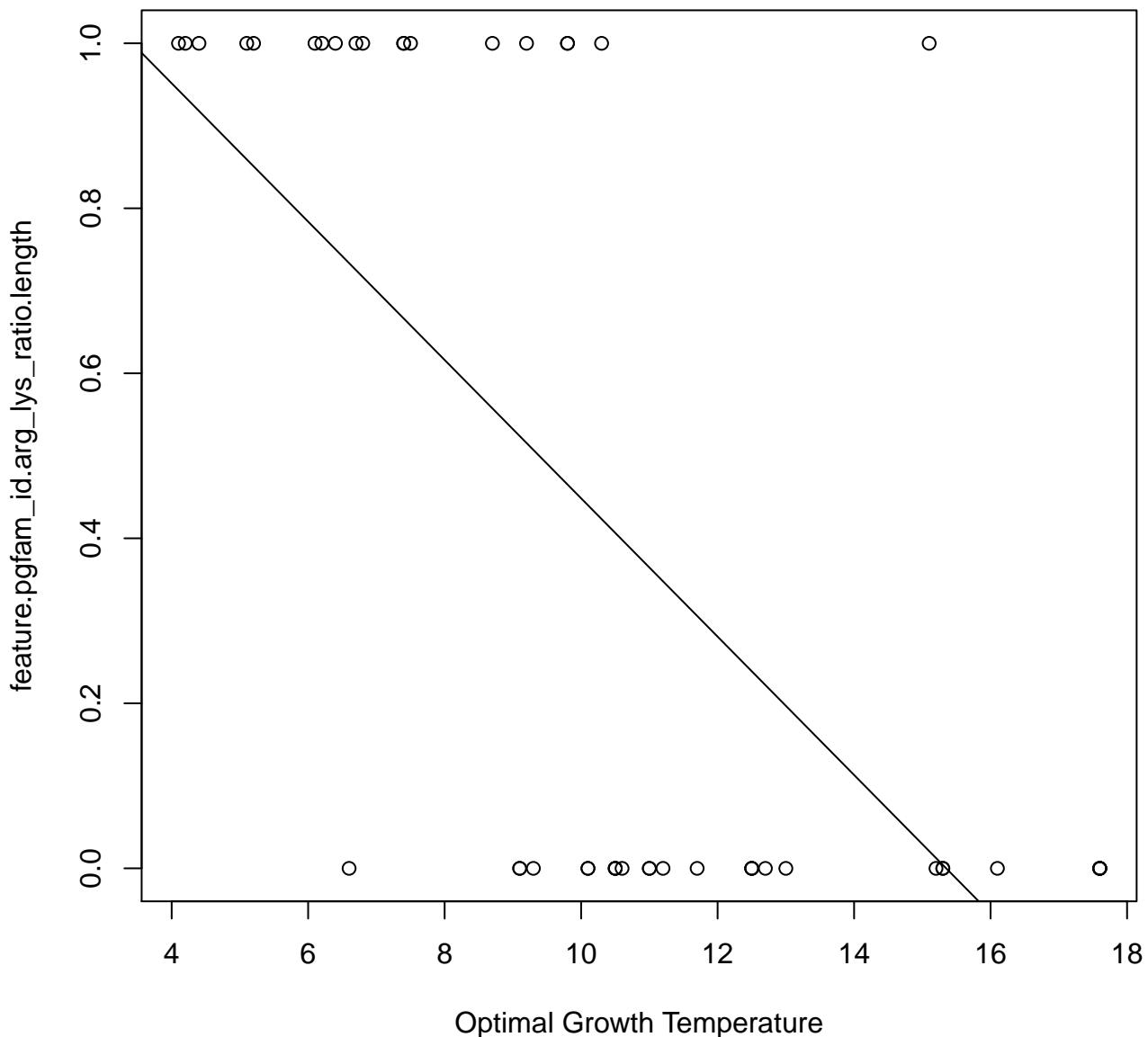
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PGF_07383941
hypothetical protein



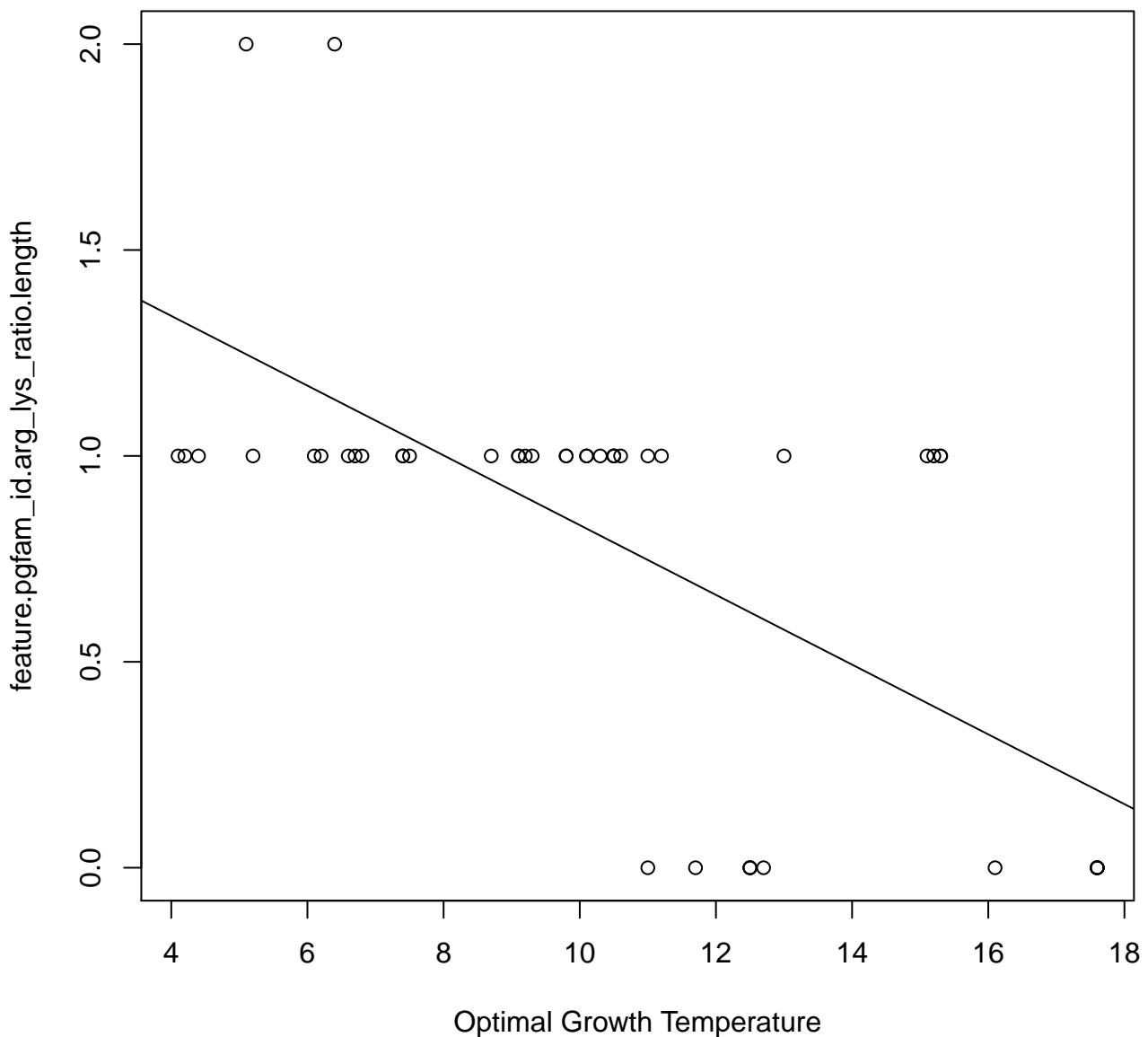
feature.pgfam_id.arg_lys_ratio.length
PGF_07583562
Cysteine desulfurase (EC 2.8.1.7) => SufS



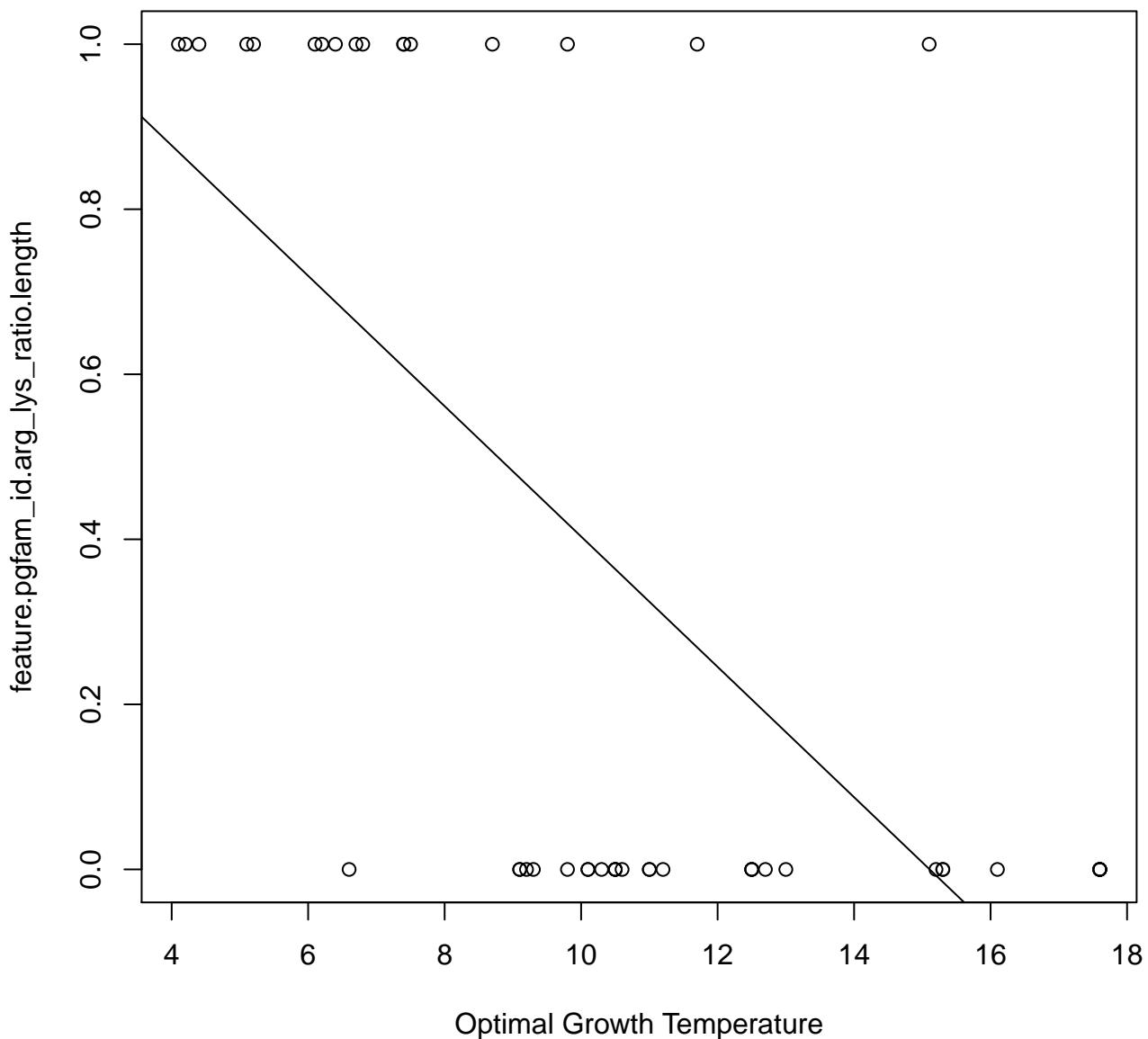
feature.pgfam_id.arg_lys_ratio.length
PGF_00055099
Sulfur acceptor protein => iron-sulfur cluster assembly SuffE



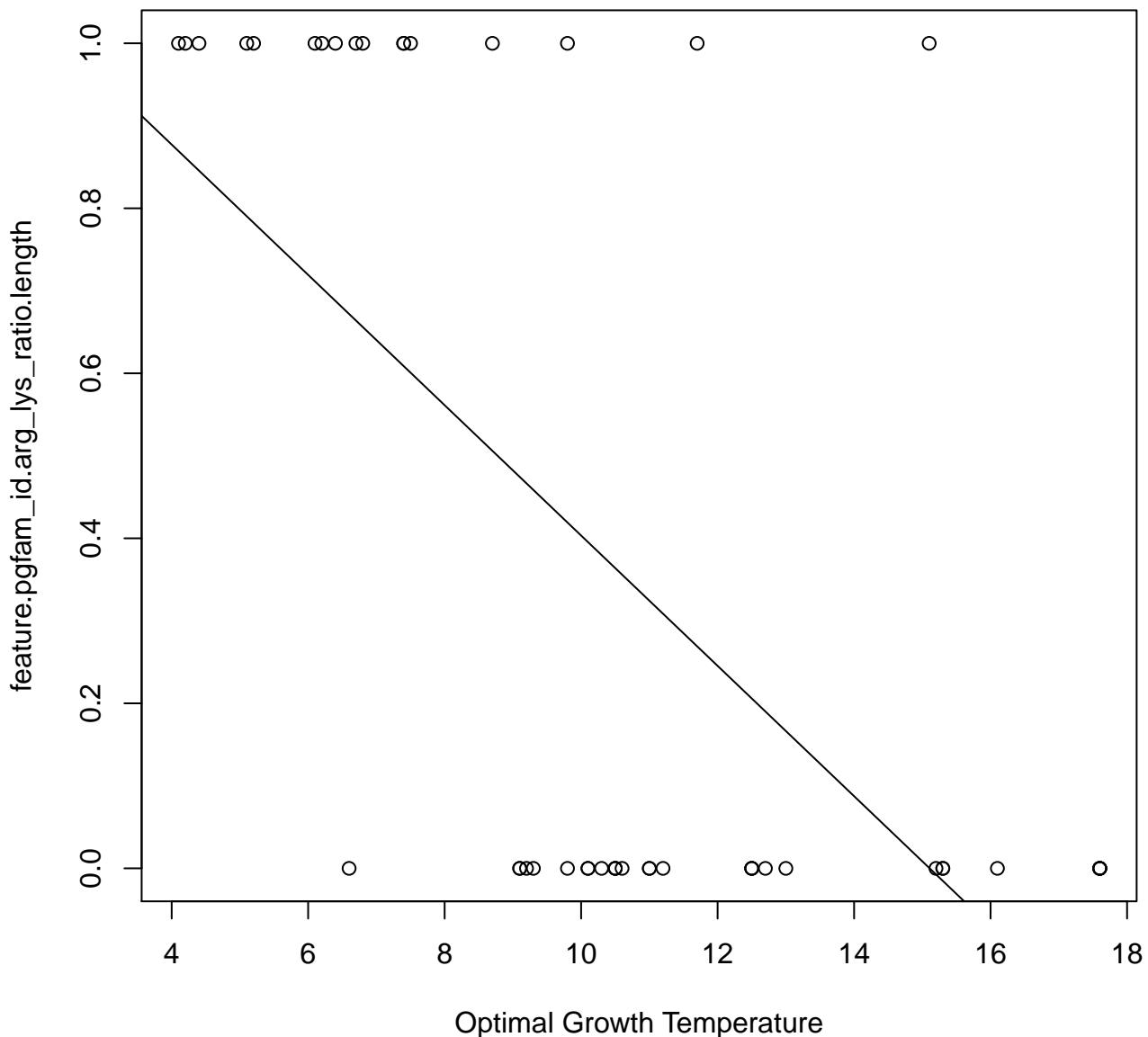
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PGF_00064529
Uncharacterized ABC1 family protein RspH17029_4038



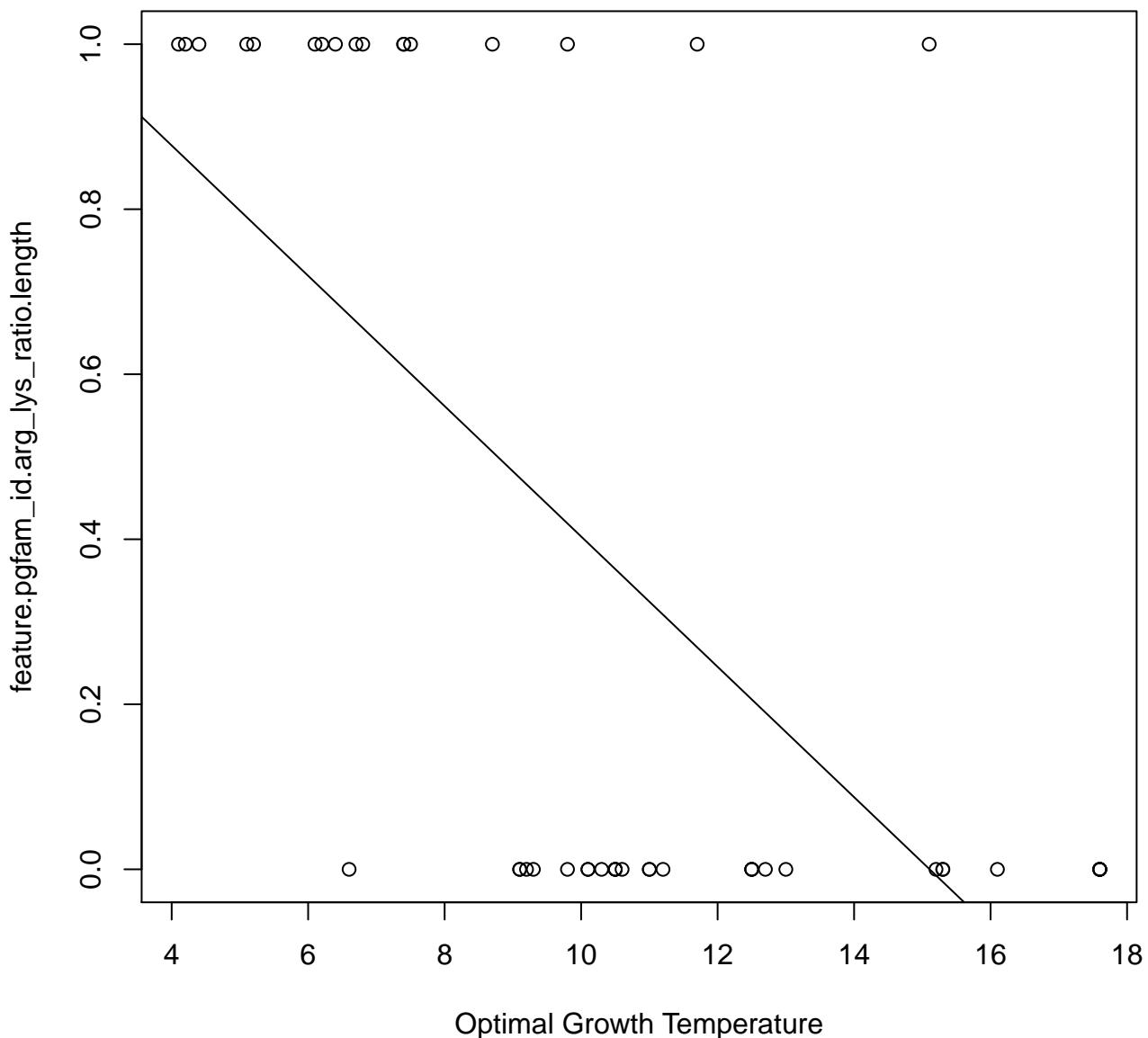
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PGF_00006186
Formate efflux transporter FocA



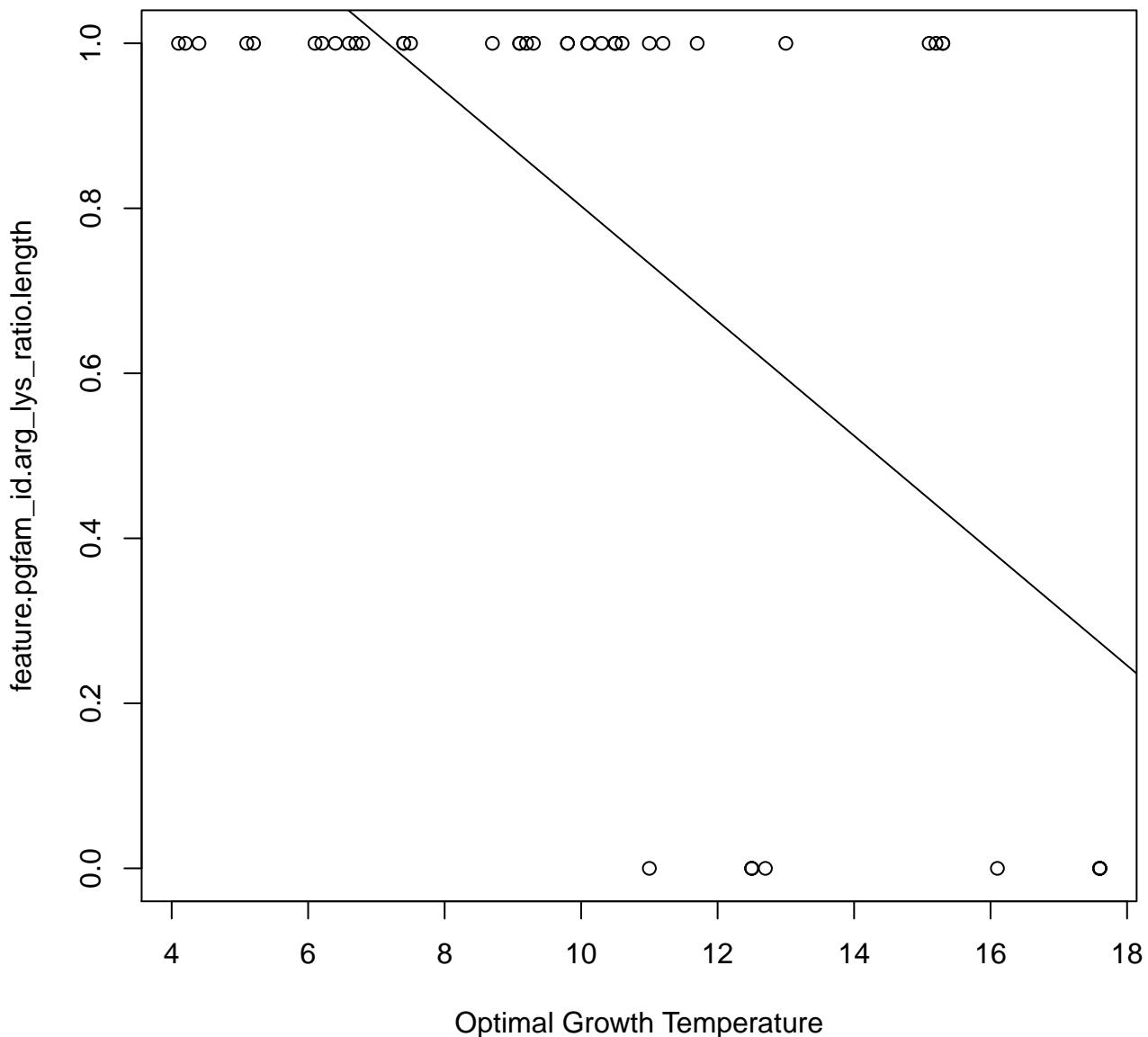
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PGF_00419899
Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)



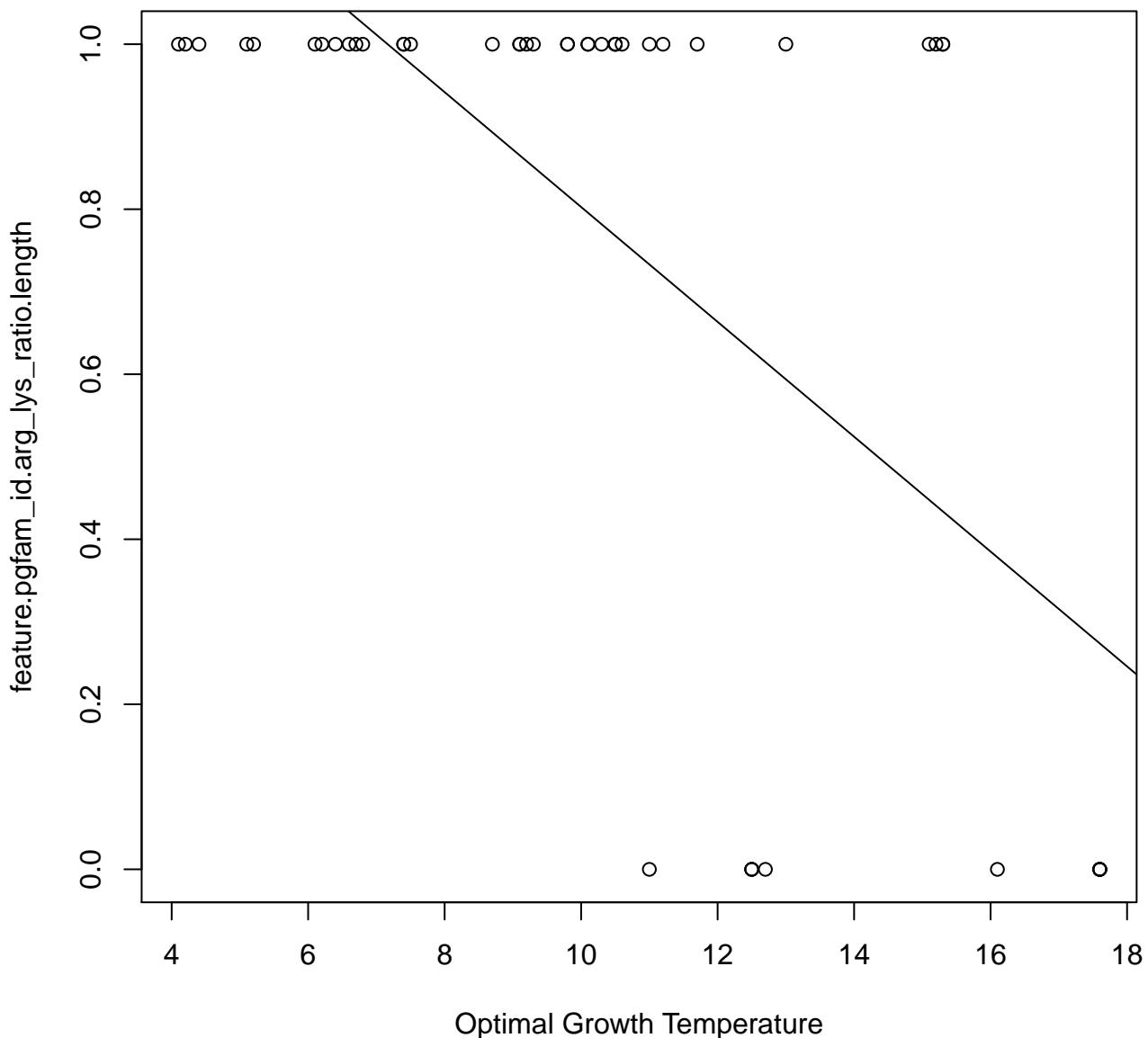
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PGF_01679161
hypothetical protein



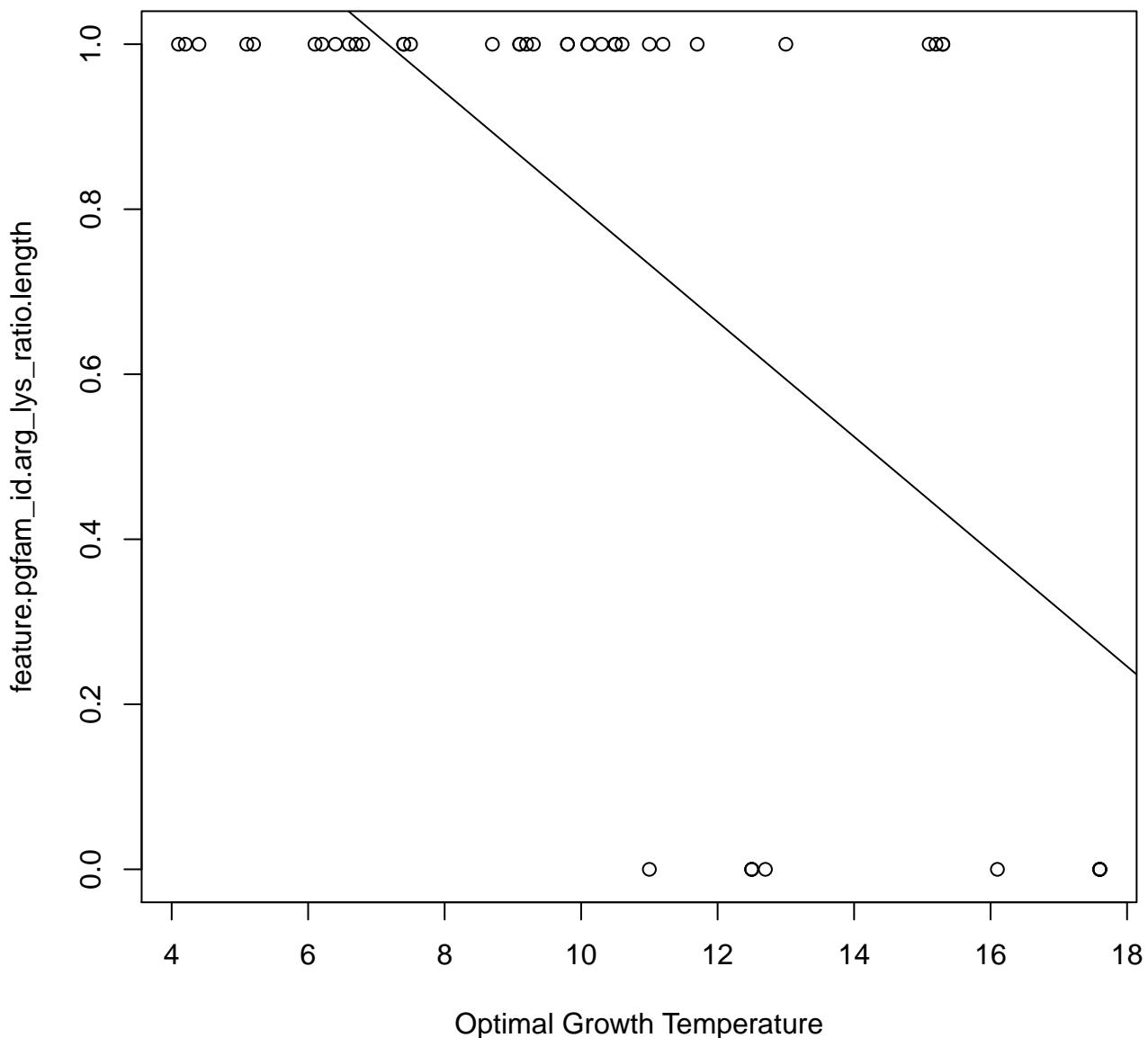
feature.pgfam_id.arg_lys_ratio.length
PGF_00013317
Hypothetical protein in Cyanoglobin locus



feature.pgfam_id.arg_lys_ratio.length
PGF_00305244
hypothetical protein



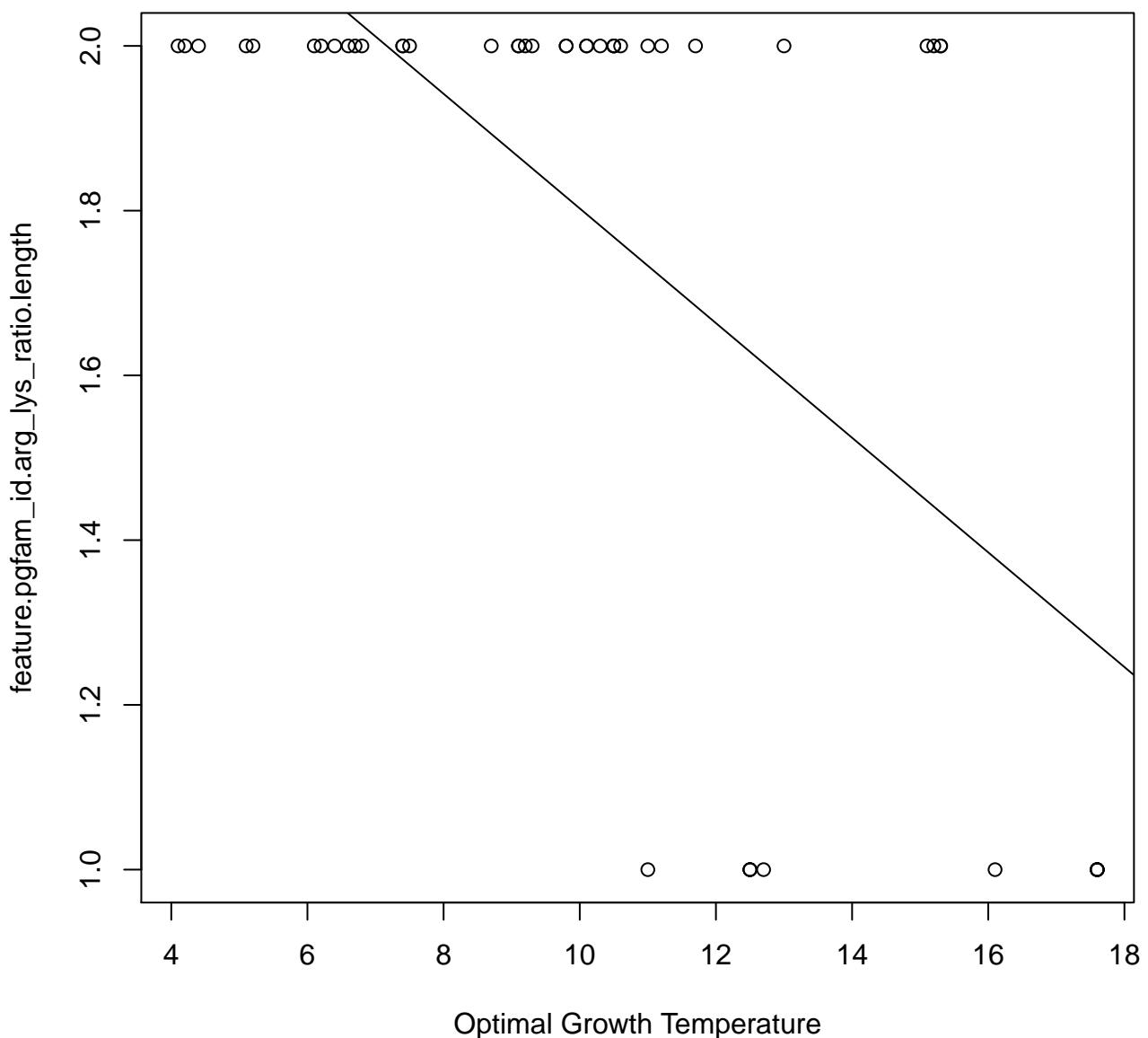
feature.pgfam_id.arg_lys_ratio.length
PGF_00416513
Carbon–nitrogen hydrolase



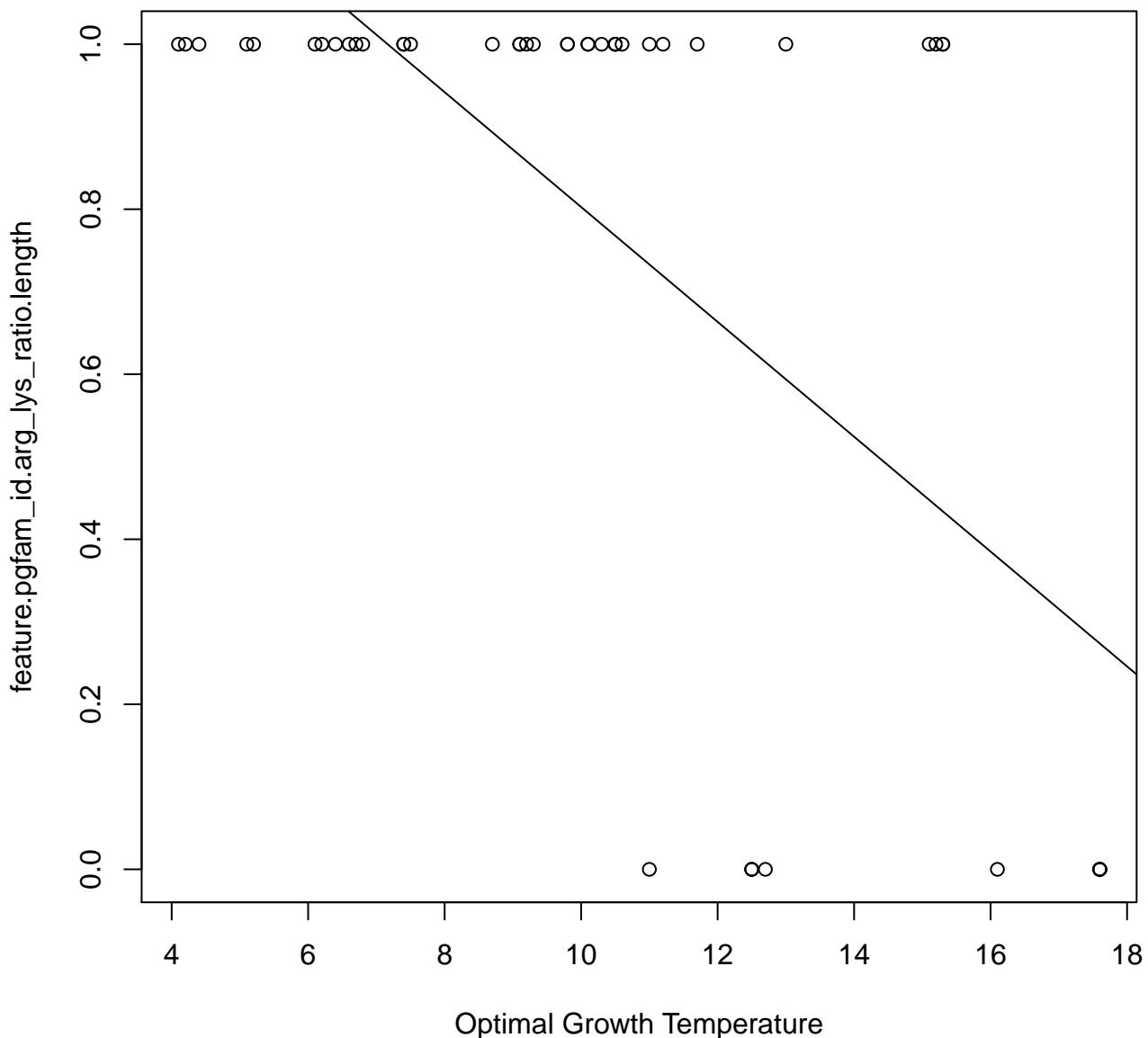
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PGF_00417755

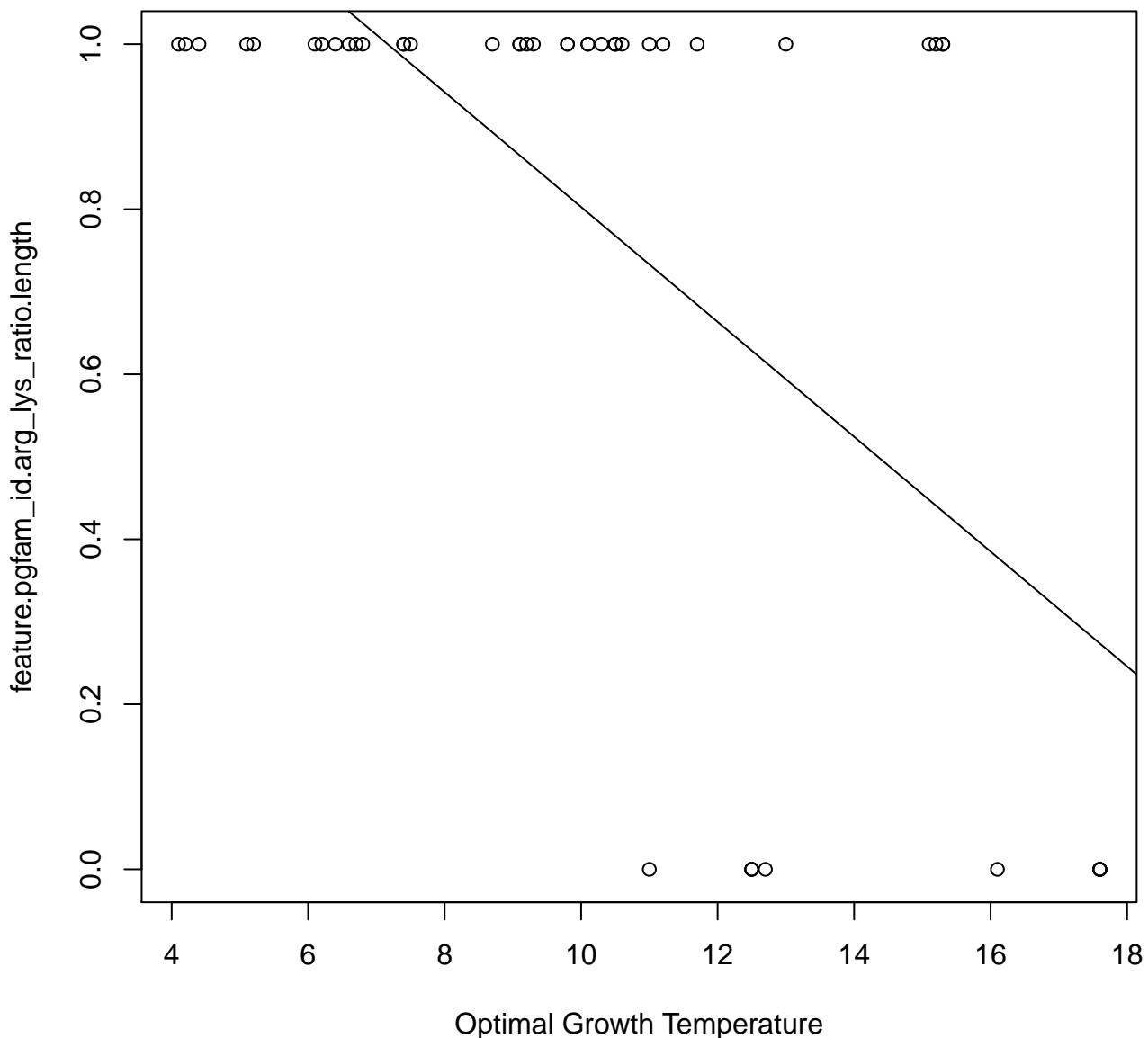
3-demethylubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6-hydroxyphenyl methylase (EC 2.1.1.222)



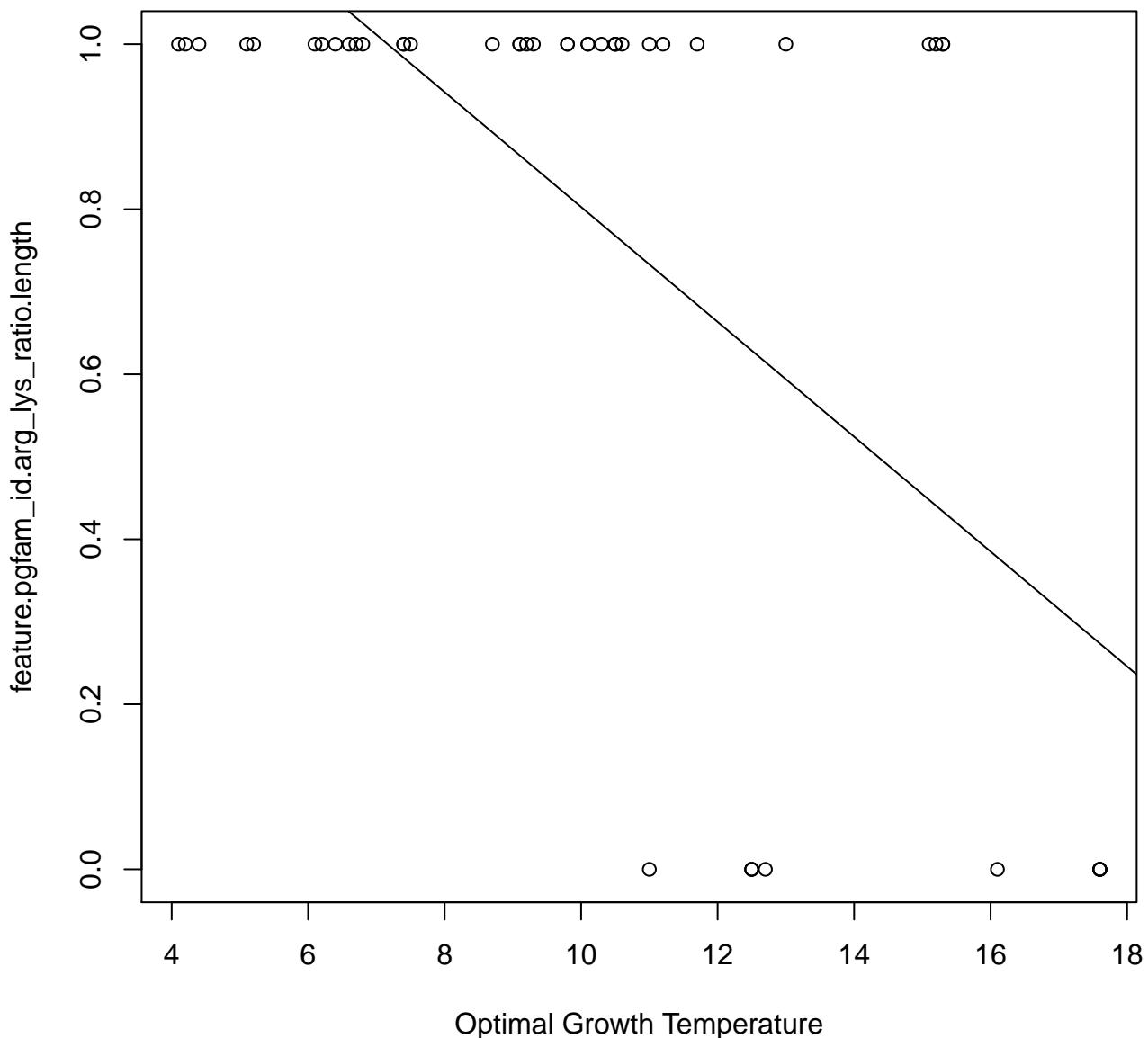
feature.pgfam_id.arg_lys_ratio.length
PGF_03340390
hypothetical protein



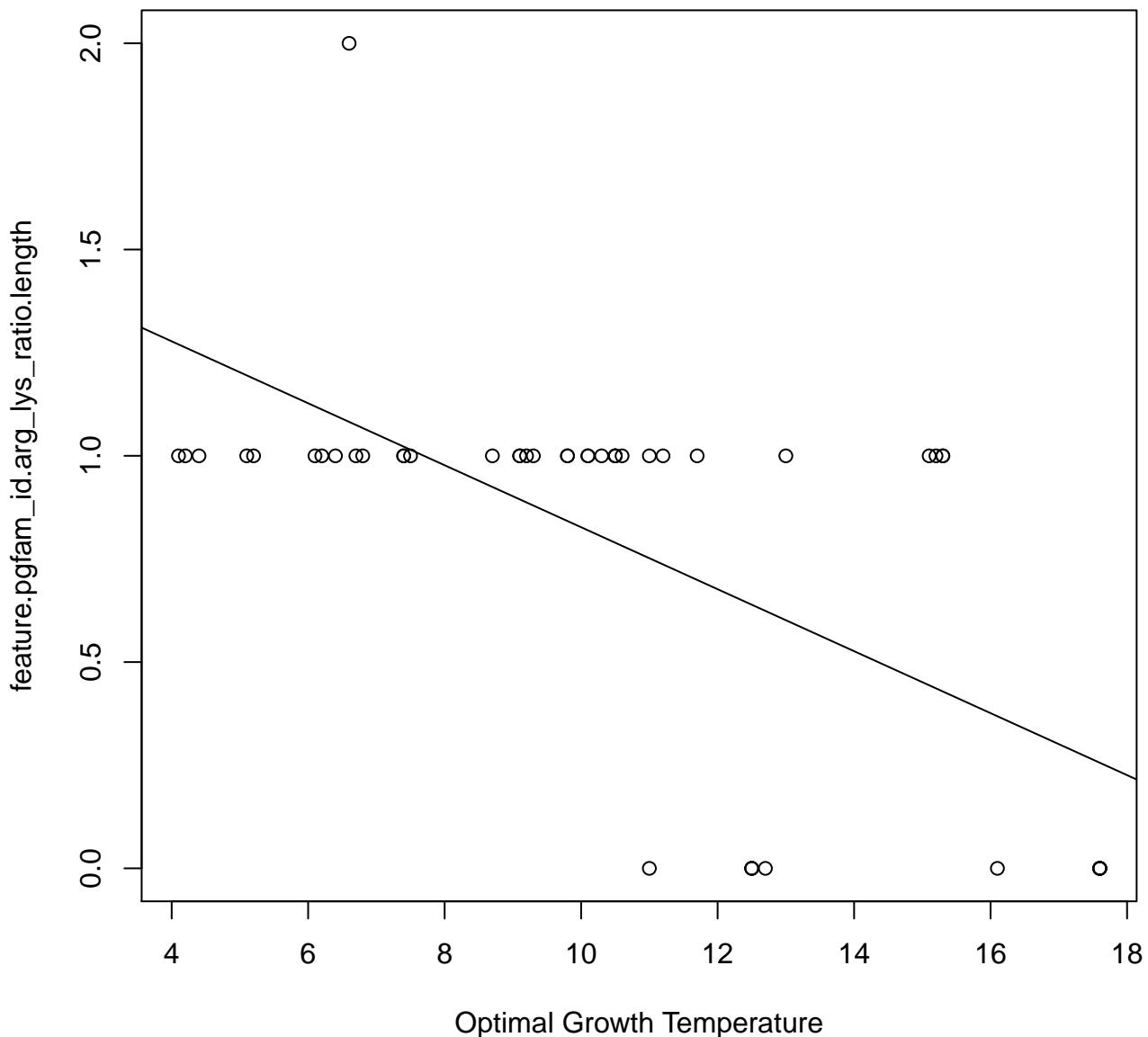
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PGF_04649728
hypothetical protein



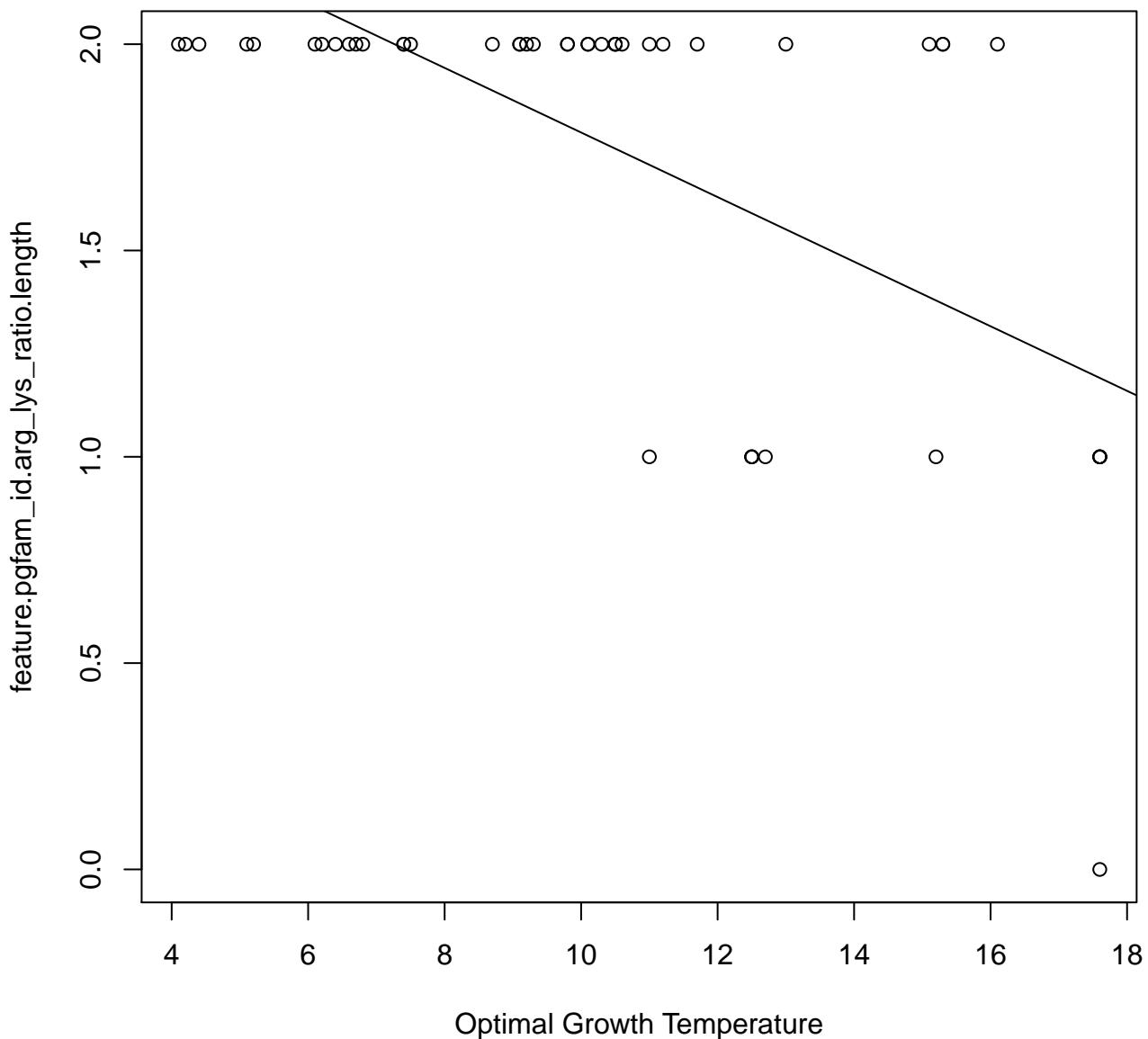
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PGF_06484581
Putative secreted amidase SCO6344



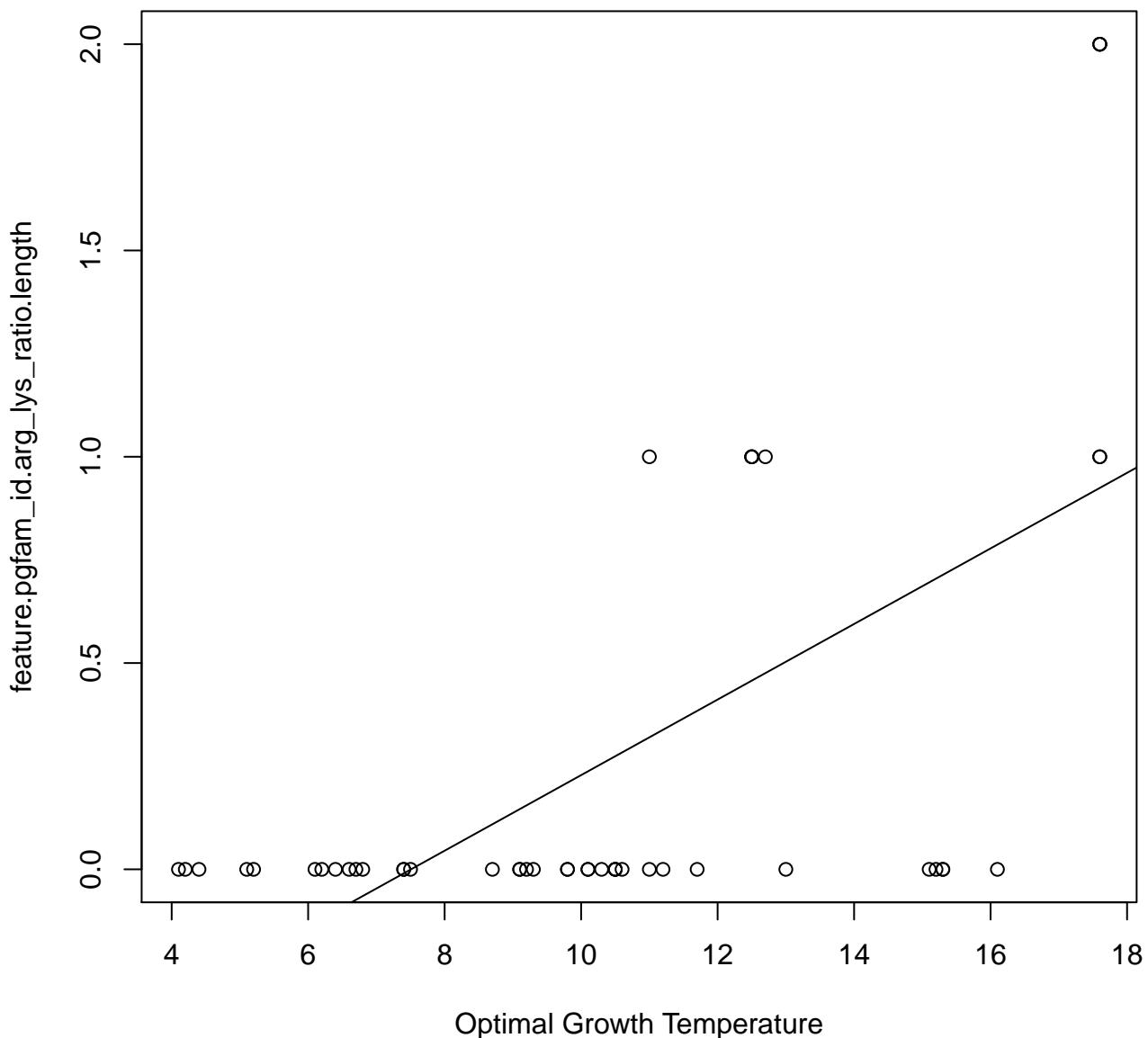
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PGF_10359285
Membrane-bound metal-dependent hydrolase



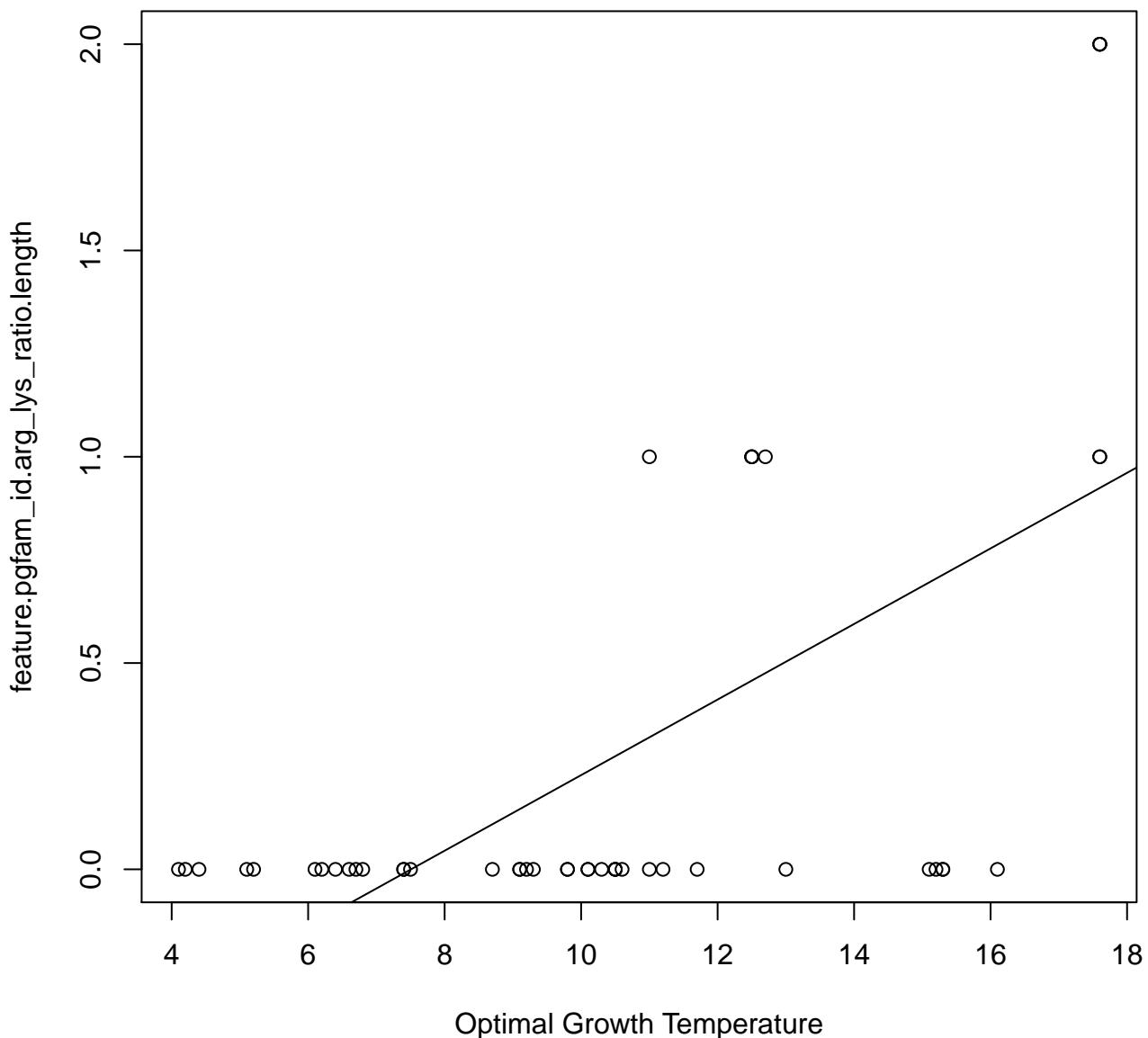
feature.pgfam_id.arg_lys_ratio.length
PGF_00056876
Thymidine phosphorylase (EC 2.4.2.4)



feature.pgfam_id.arg_lys_ratio.length
PGF_00382756
hypothetical protein



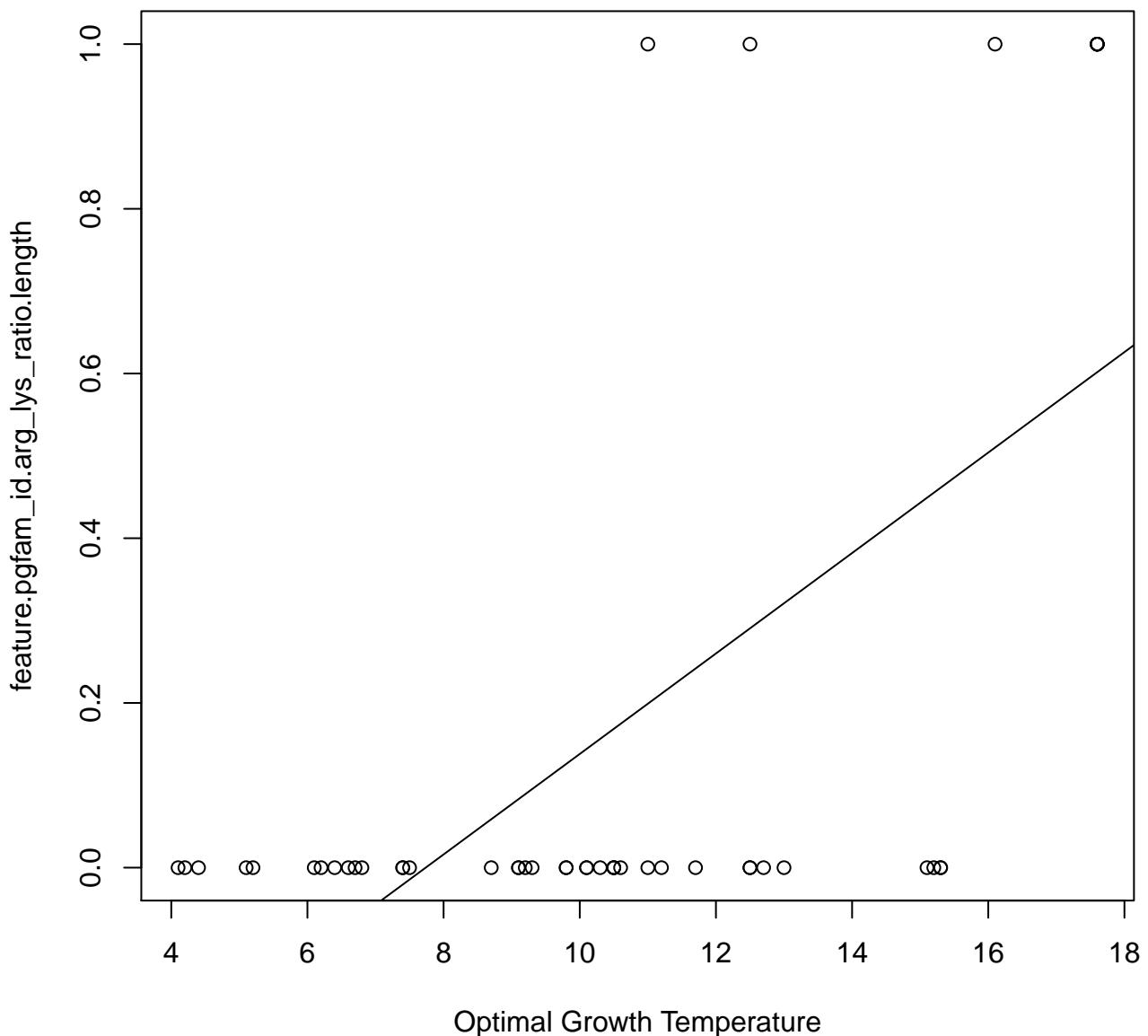
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PGF_00425648
FHA domain protein



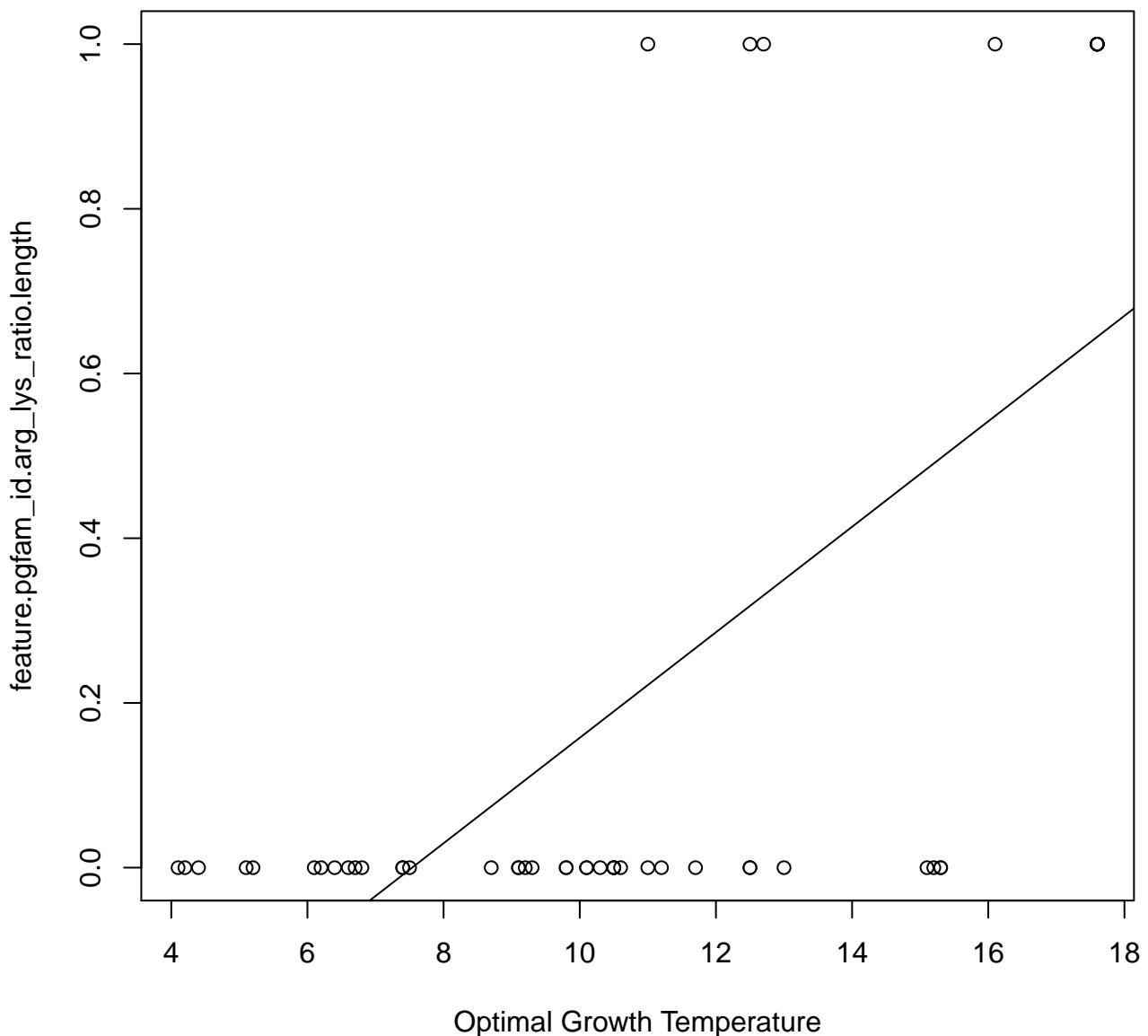
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PGF_06457203

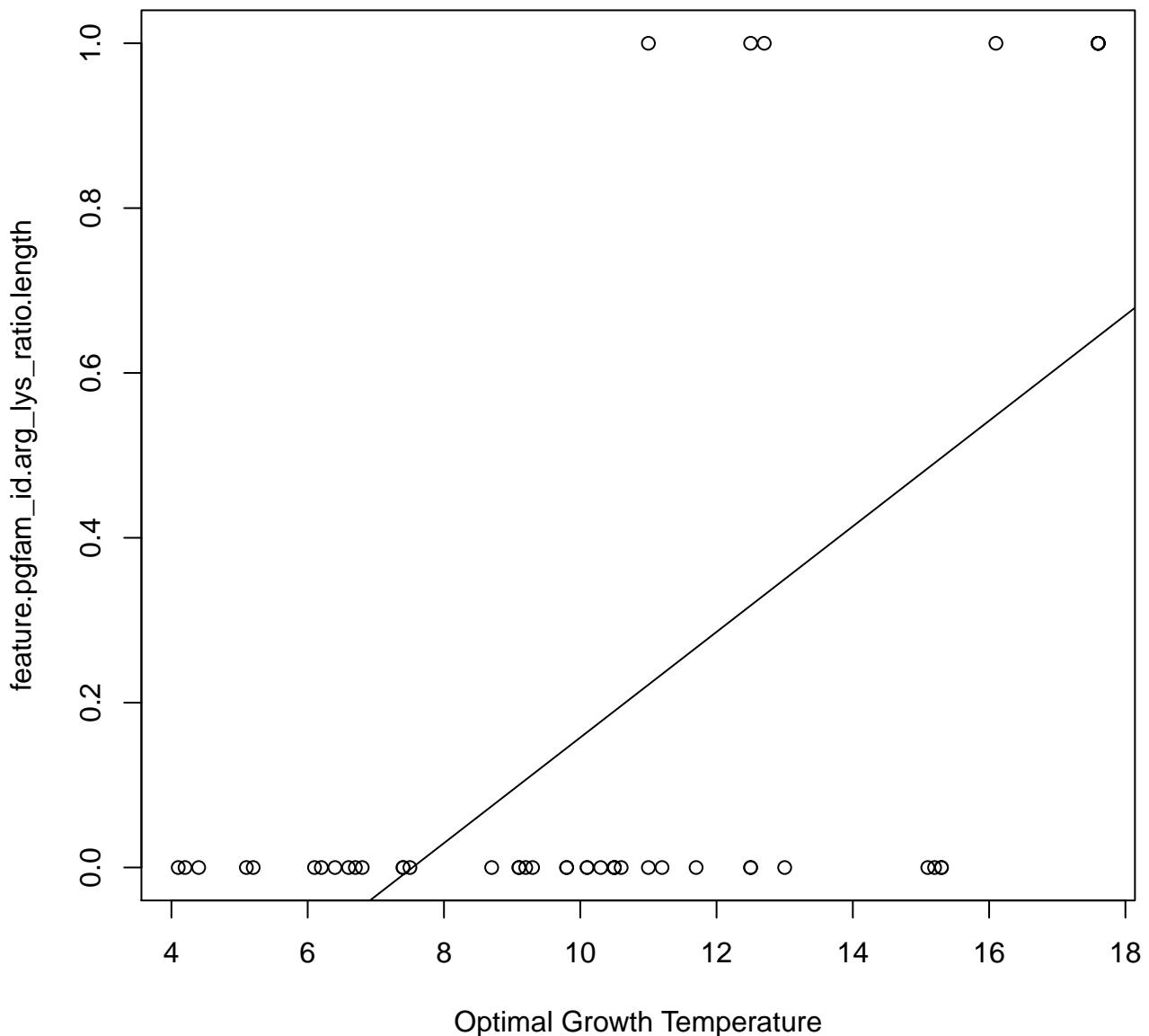
Cytochrome b561



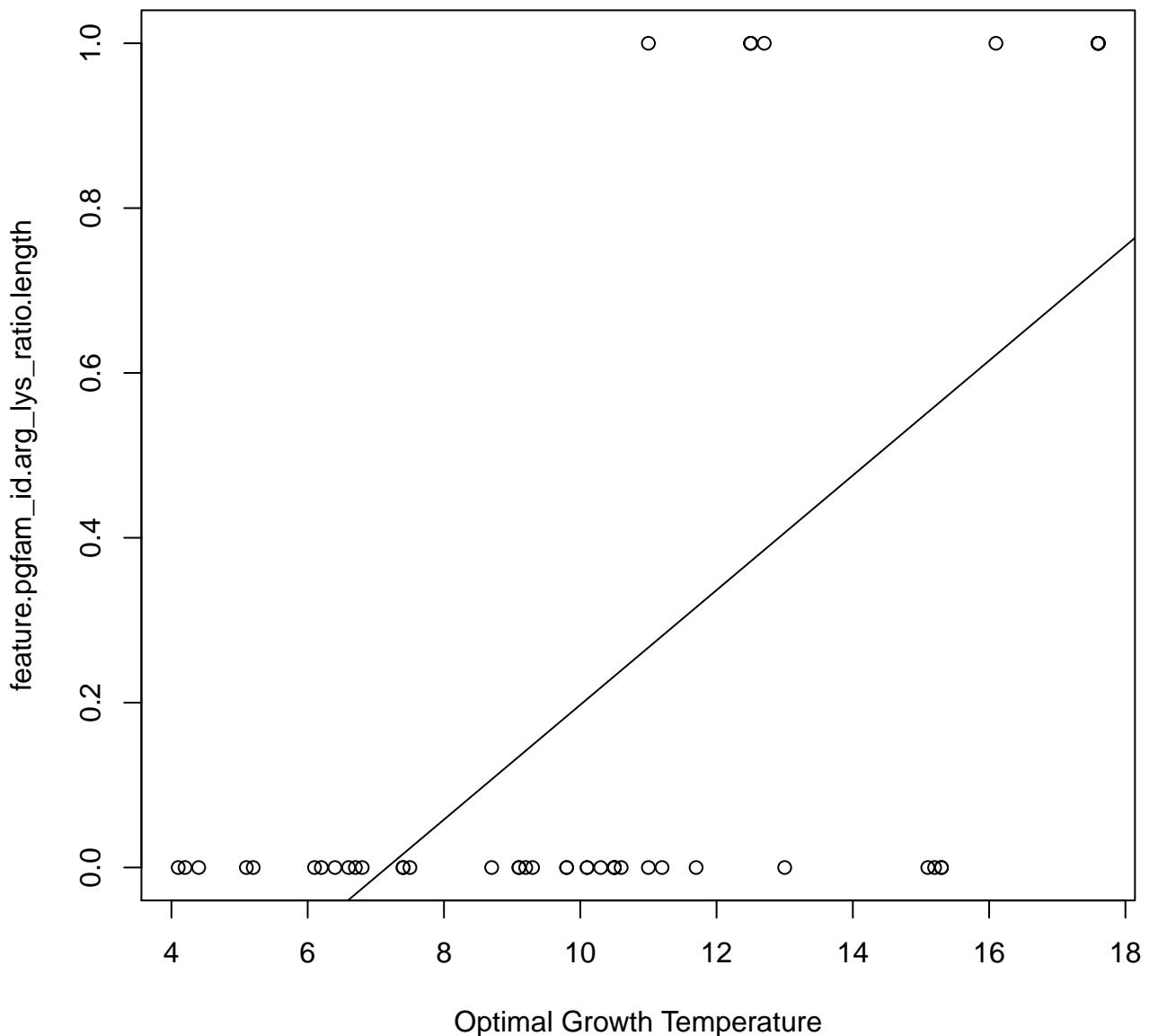
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PGF_02935350
hypothetical protein



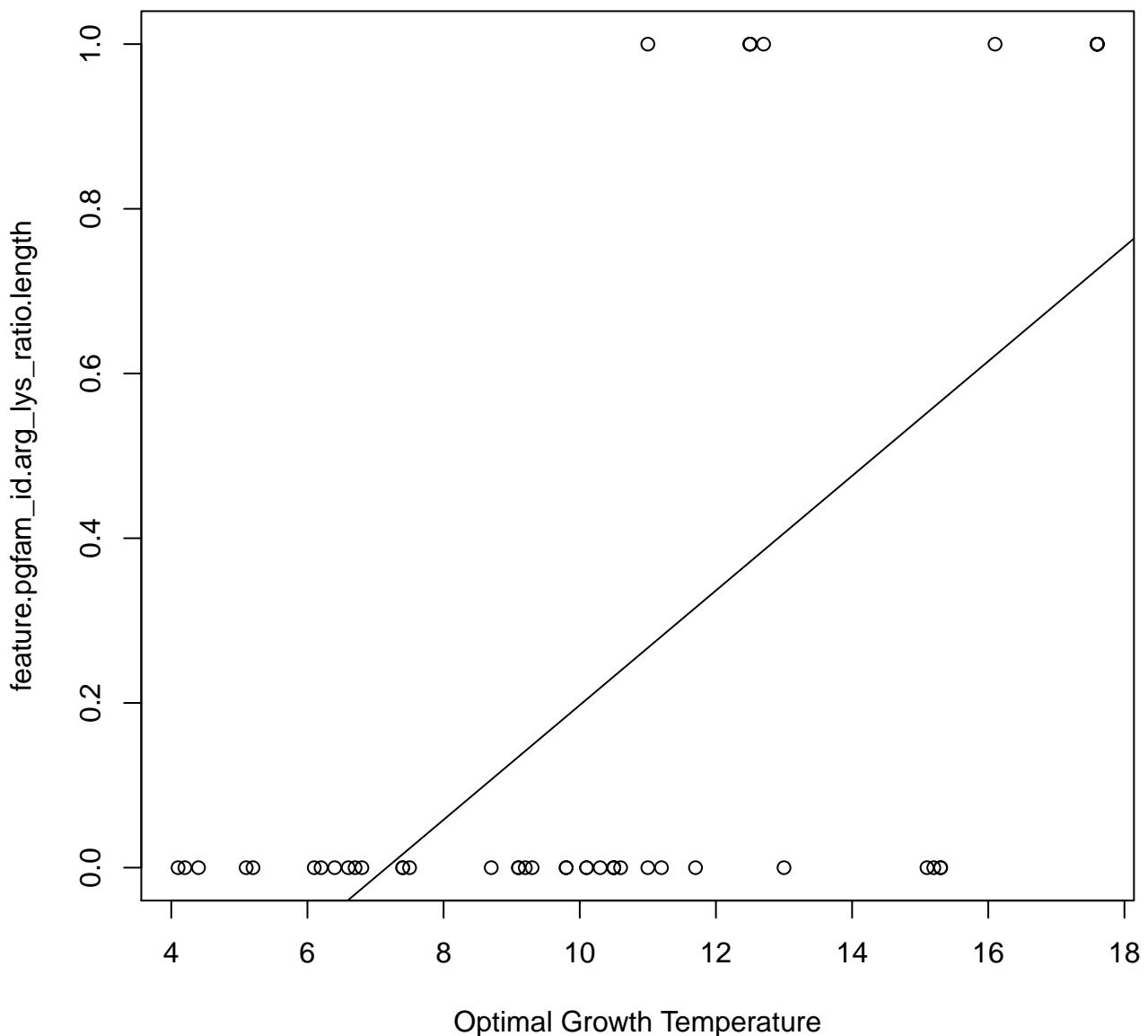
feature.pgfam_id.arg_lys_ratio.length
PGF_12769182
YebG, DNA damage-inducible gene in SOS regulon, expressed in stationary phase



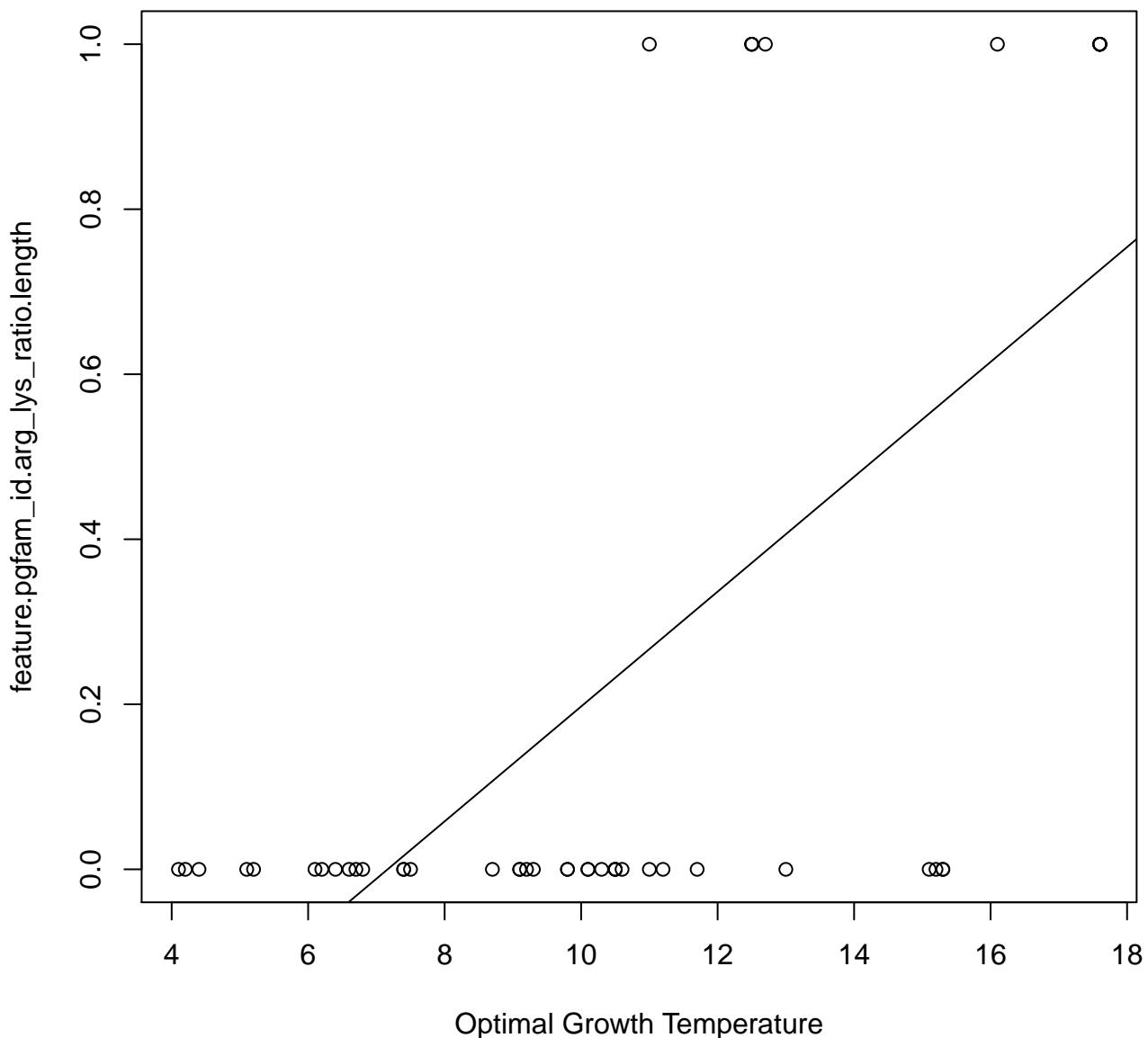
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PGF_00005481
Flagellar hook-length control protein FliK



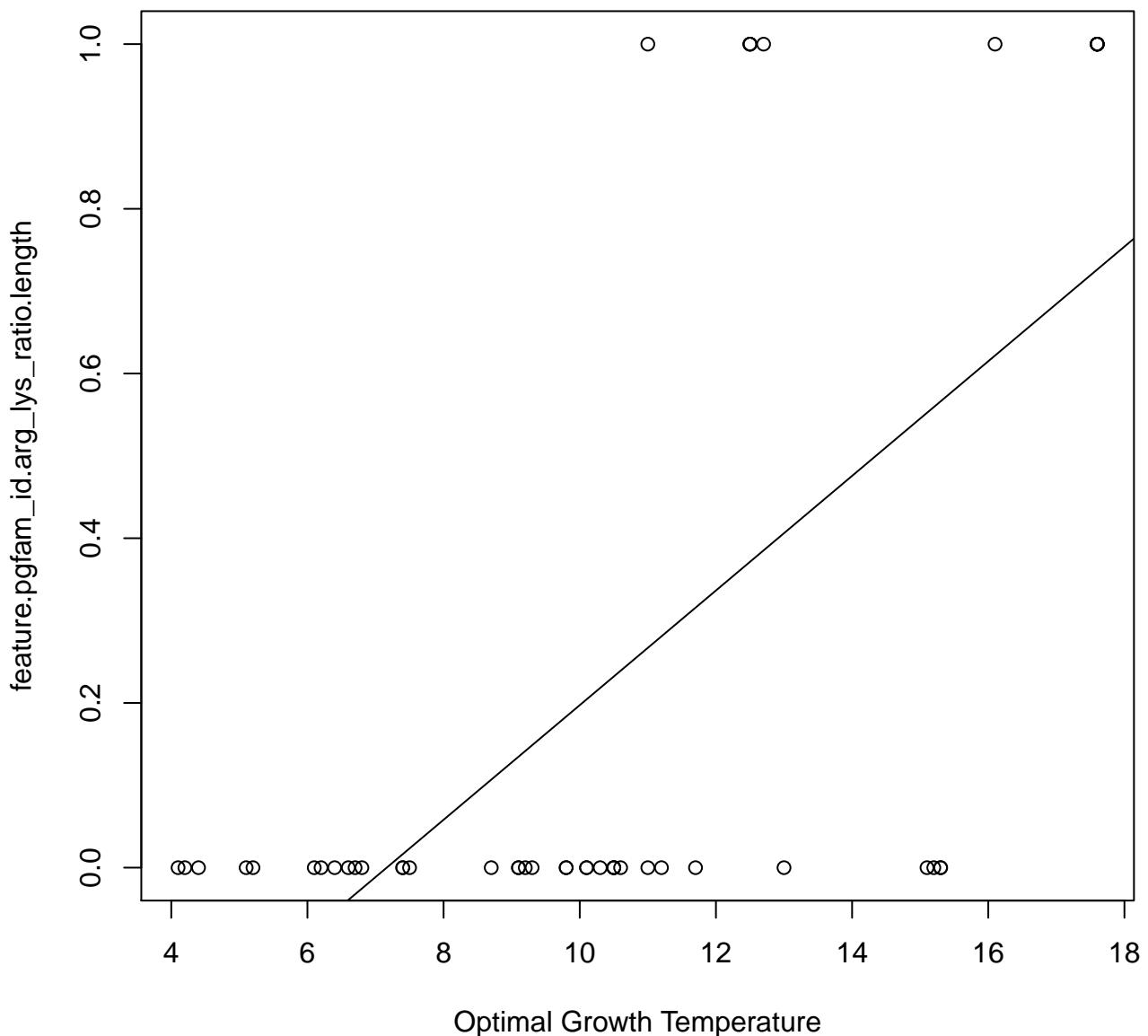
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PGF_00287116
hypothetical protein



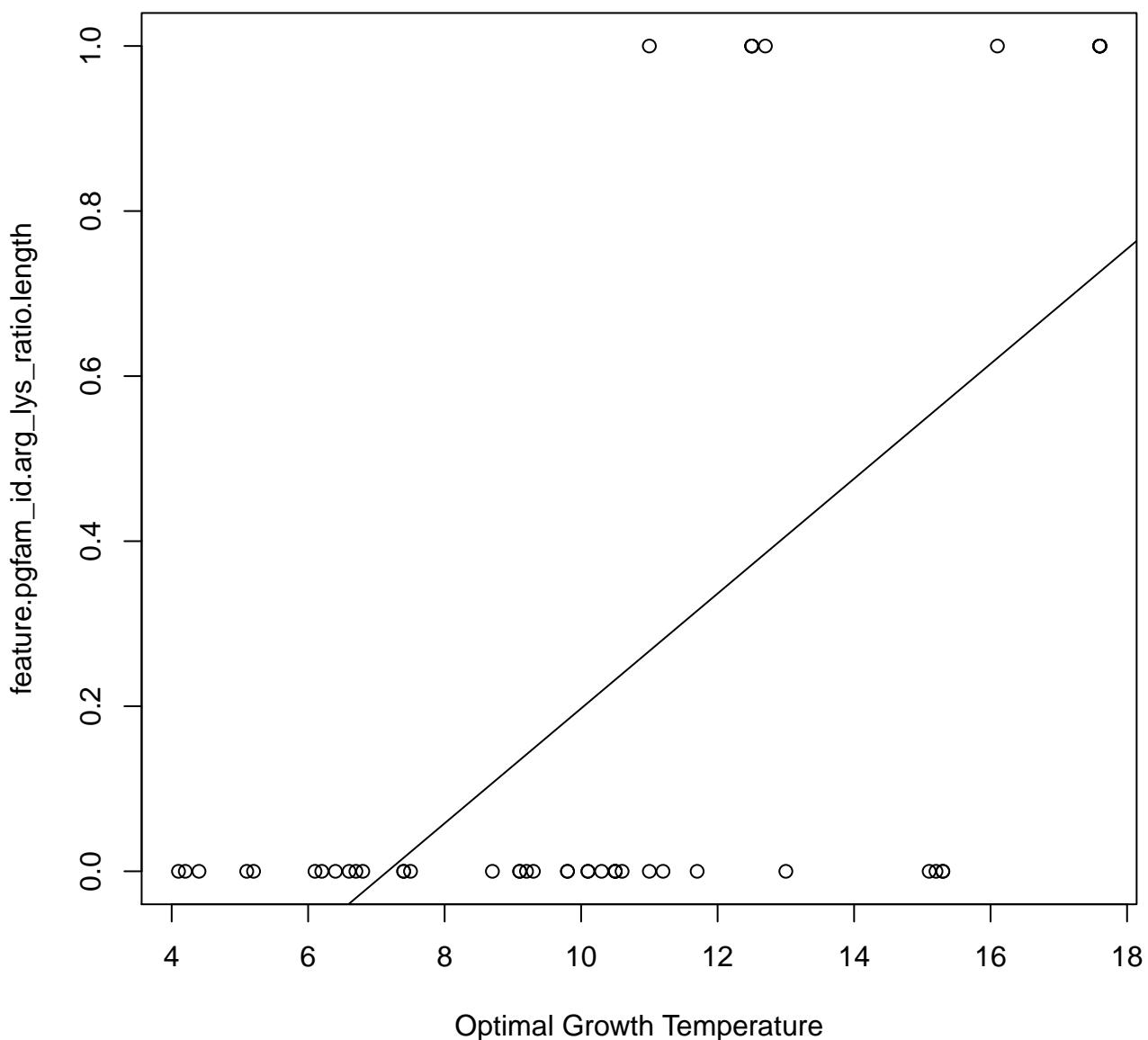
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PGF_00416903
Cell division protein



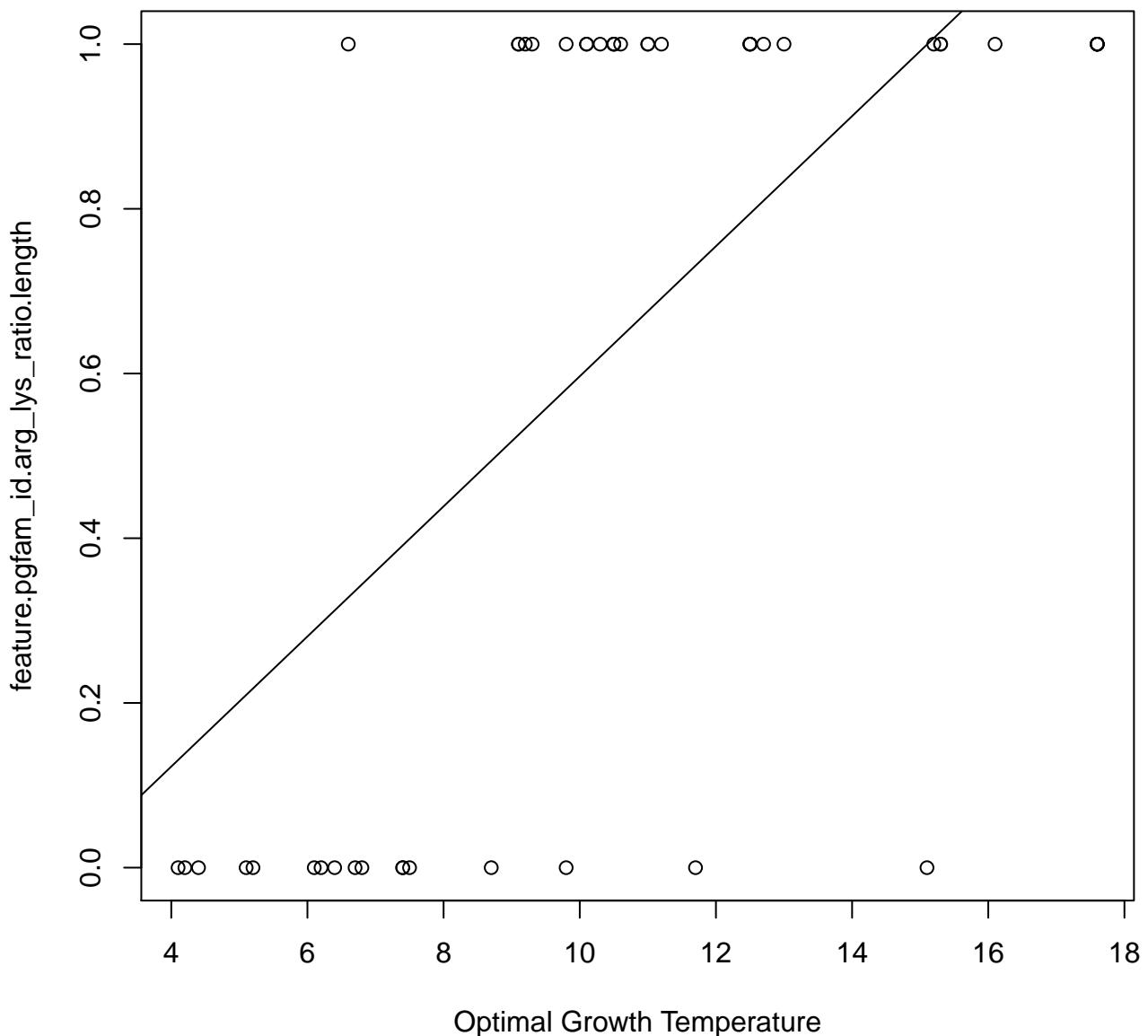
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PGF_01336476
hypothetical protein



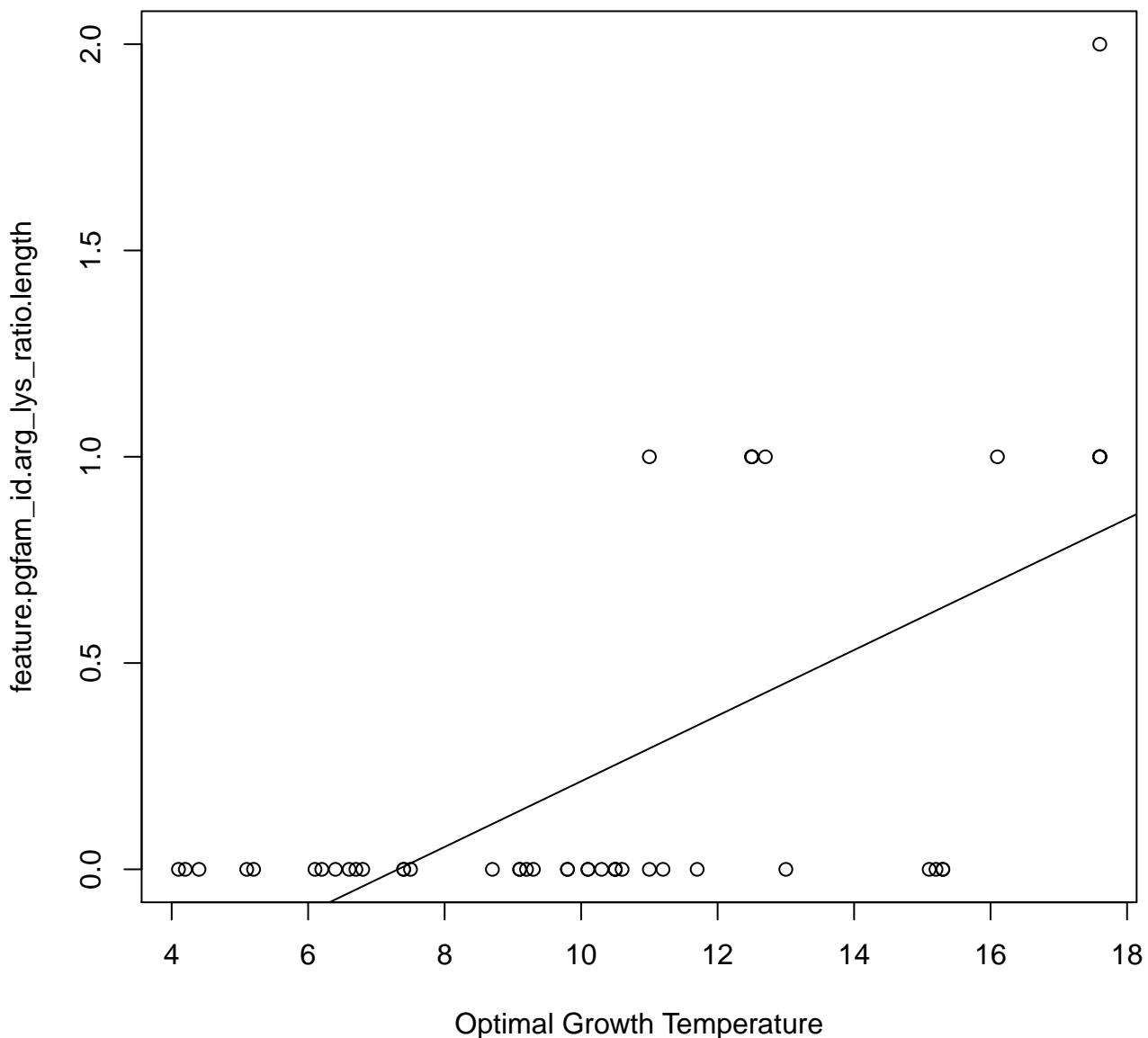
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PGF_01336546
major outer membrane lipoprotein, putative



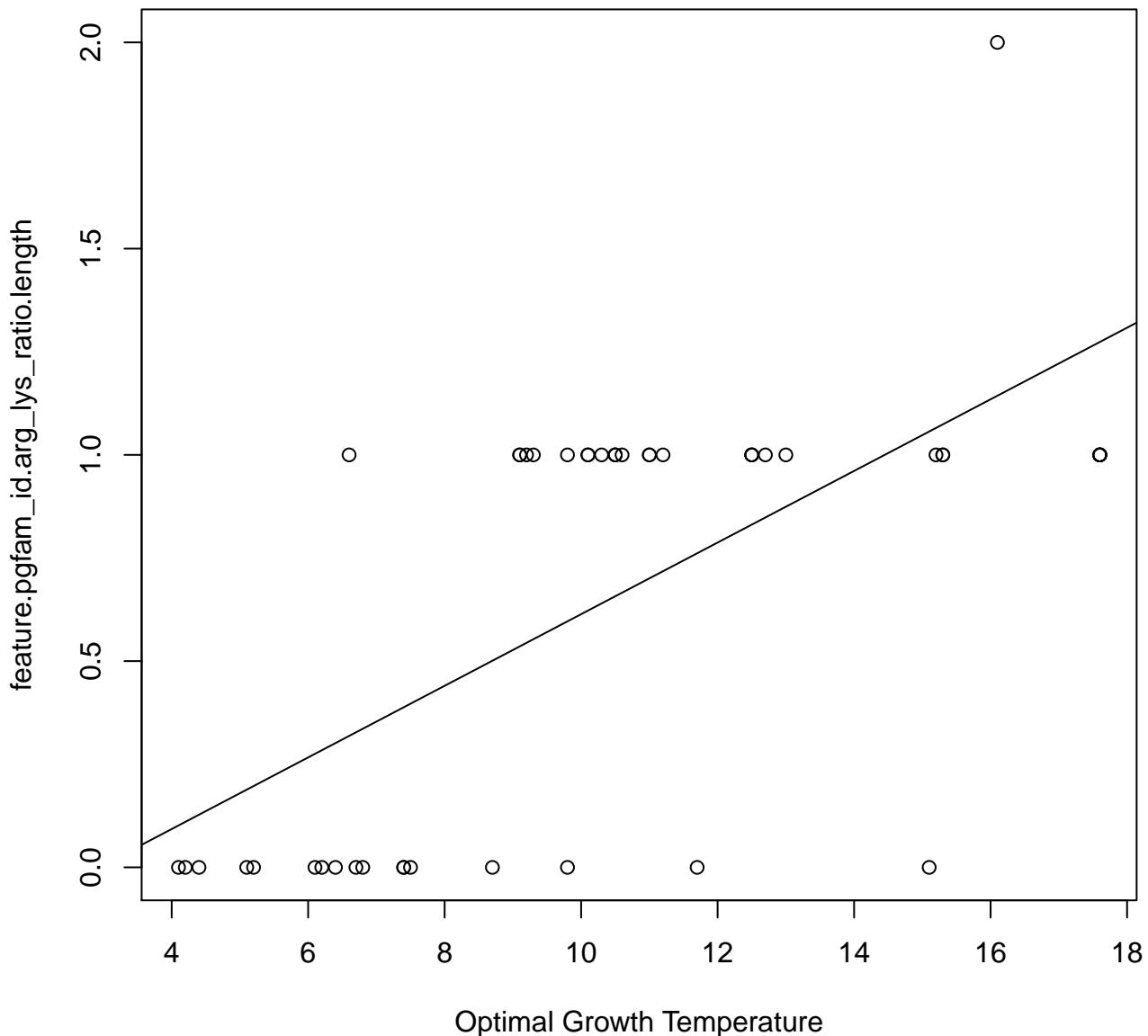
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PGF_00417843
Chorismate--pyruvate lyase (EC 4.1.3.40)



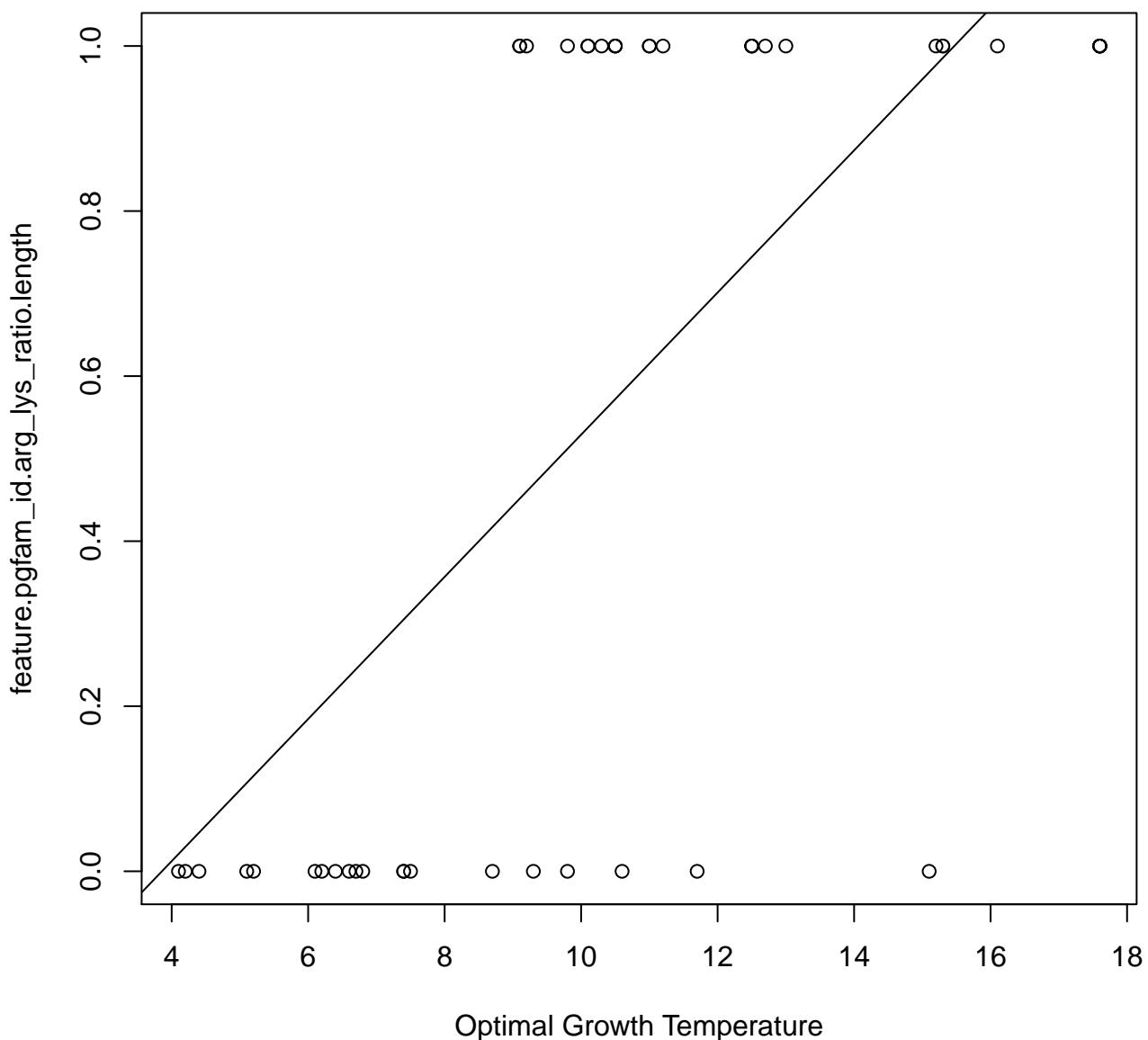
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PGF_01336631
hypothetical protein



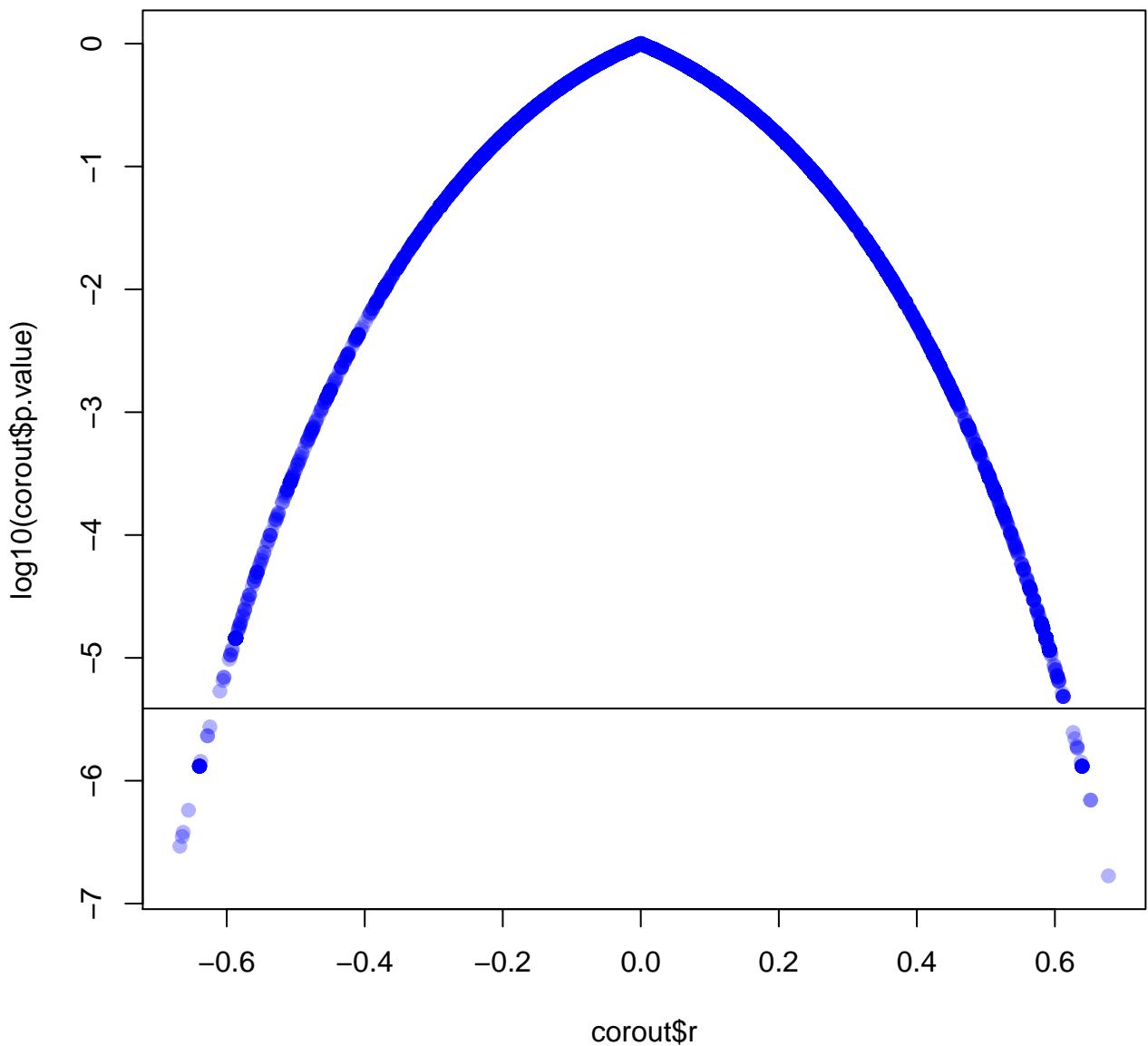
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PGF_03687279
Uncharacterized MFS-type transporter



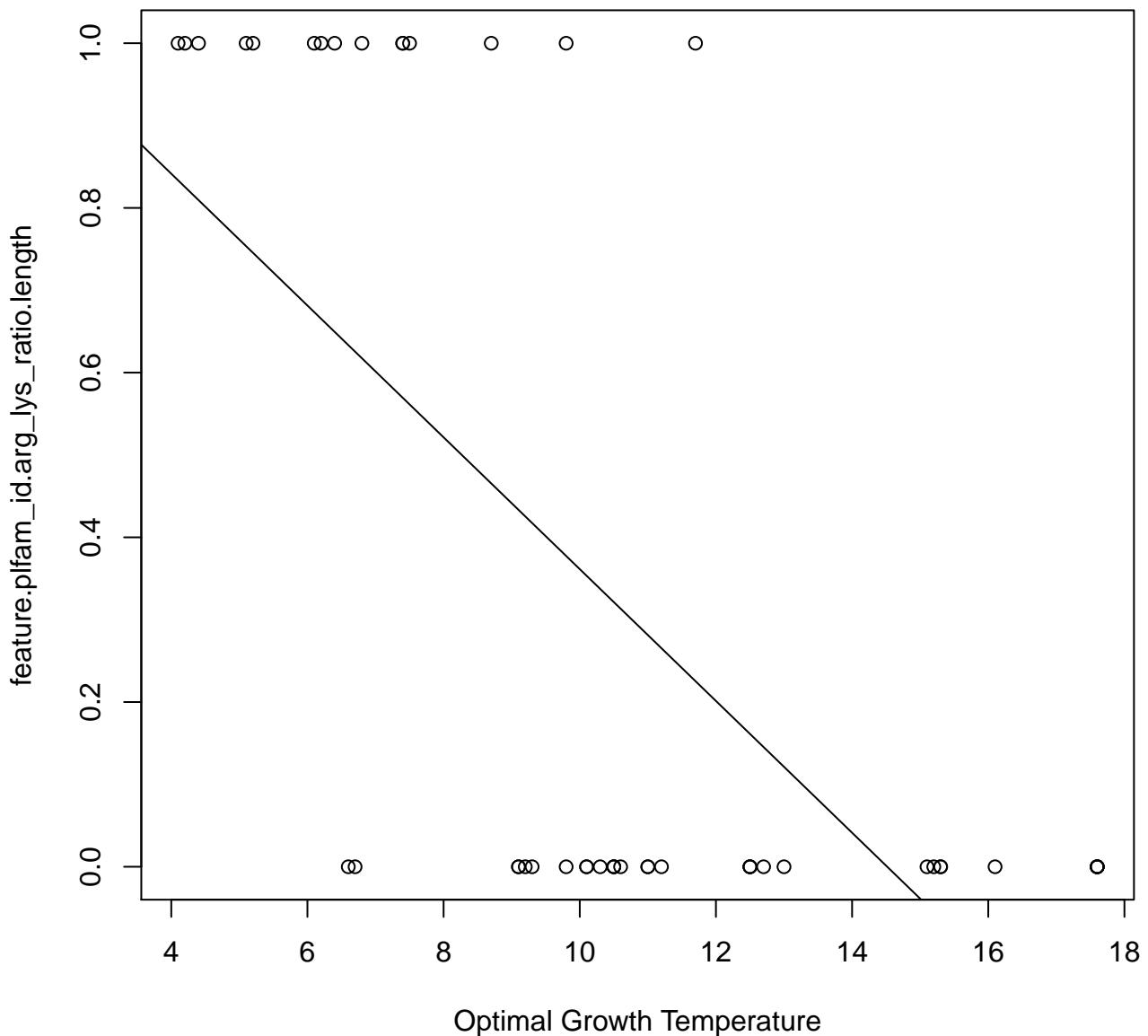
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PGF_01917480
General secretion pathway protein L



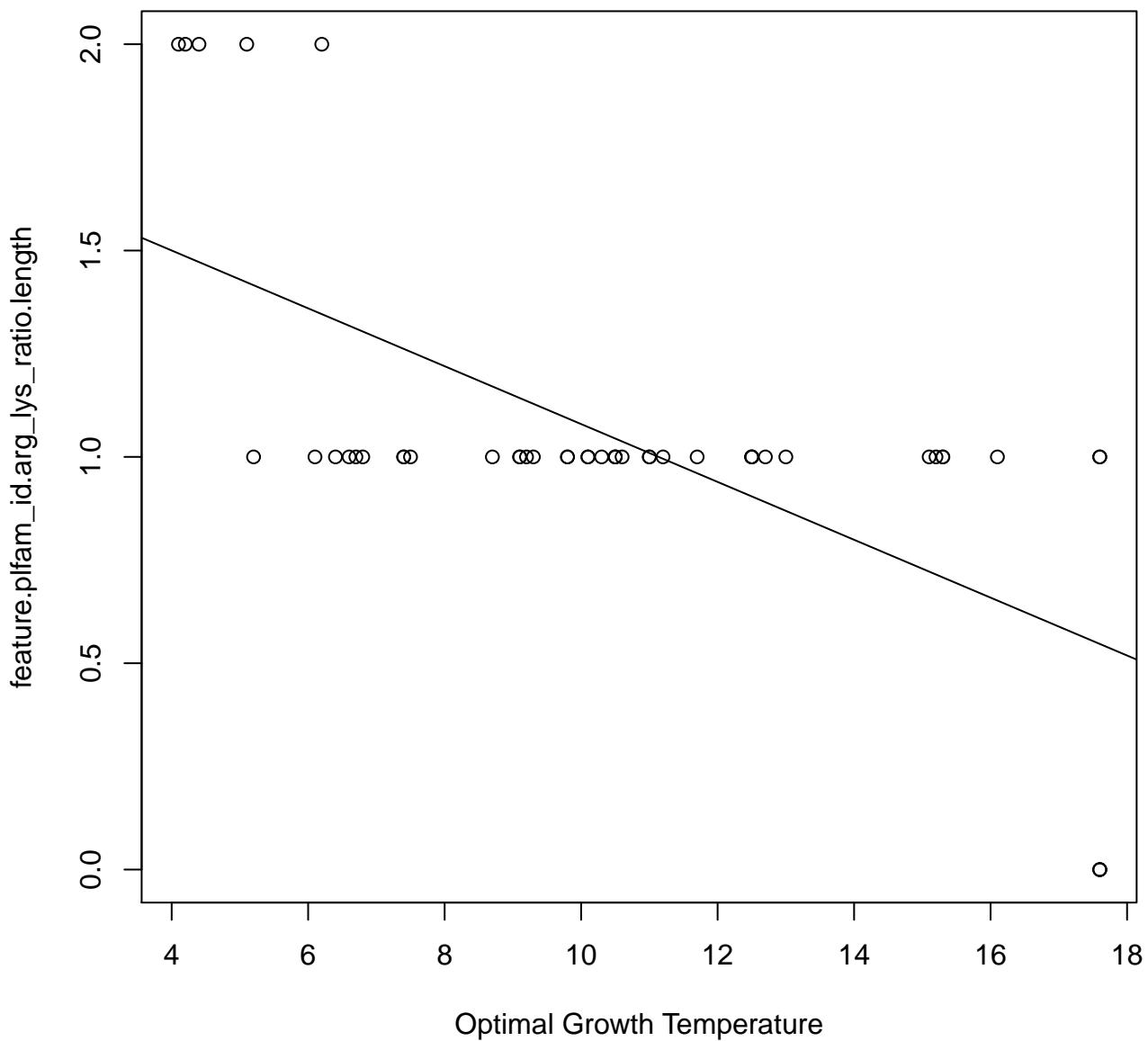
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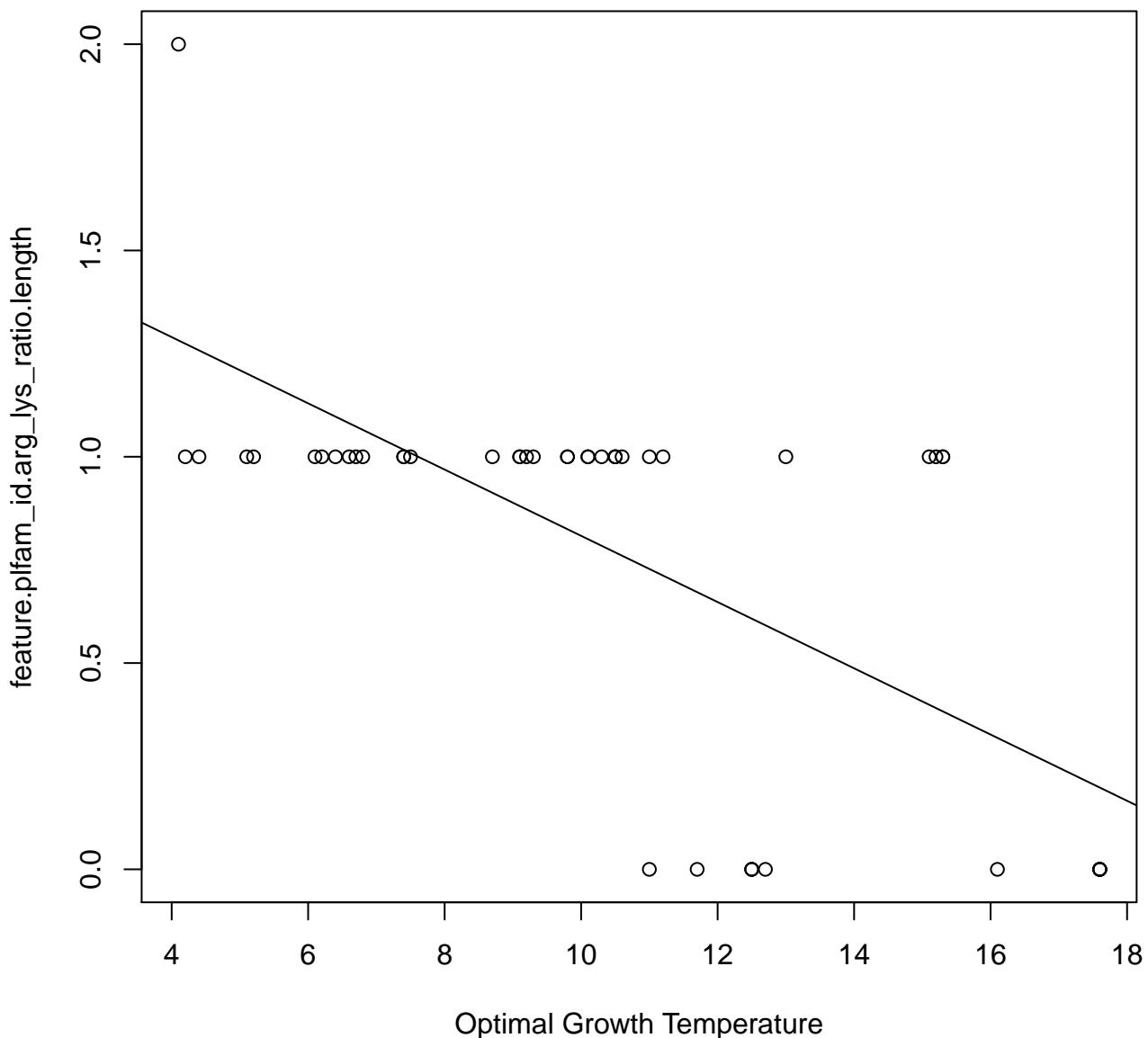
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PLF_28228_00011707
Membrane-bound lytic murein transglycosylase C (EC 3.2.1.n1)



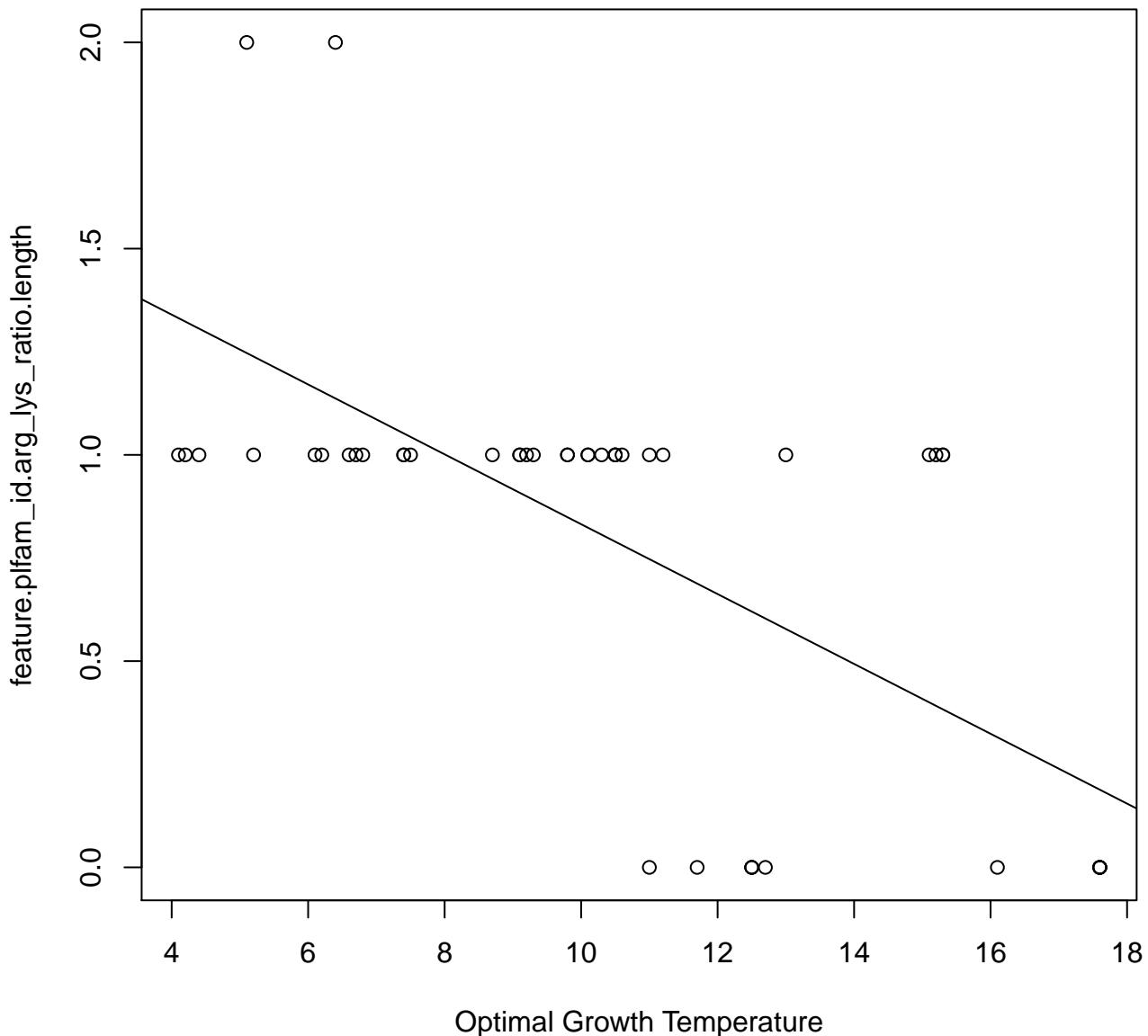
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PLF_28228_00002910
hypothetical protein



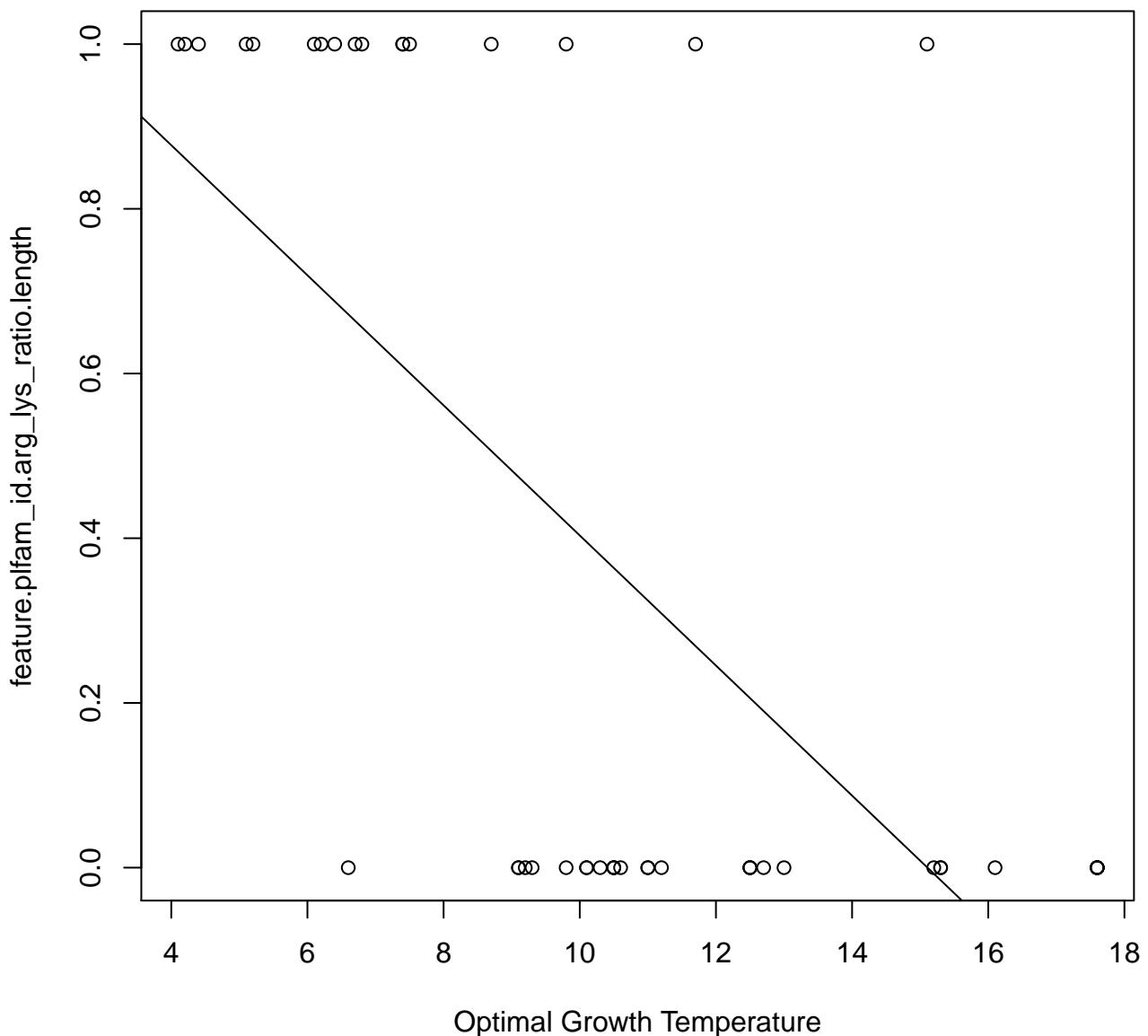
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00018533
ATP-dependent DNA helicase RecQ



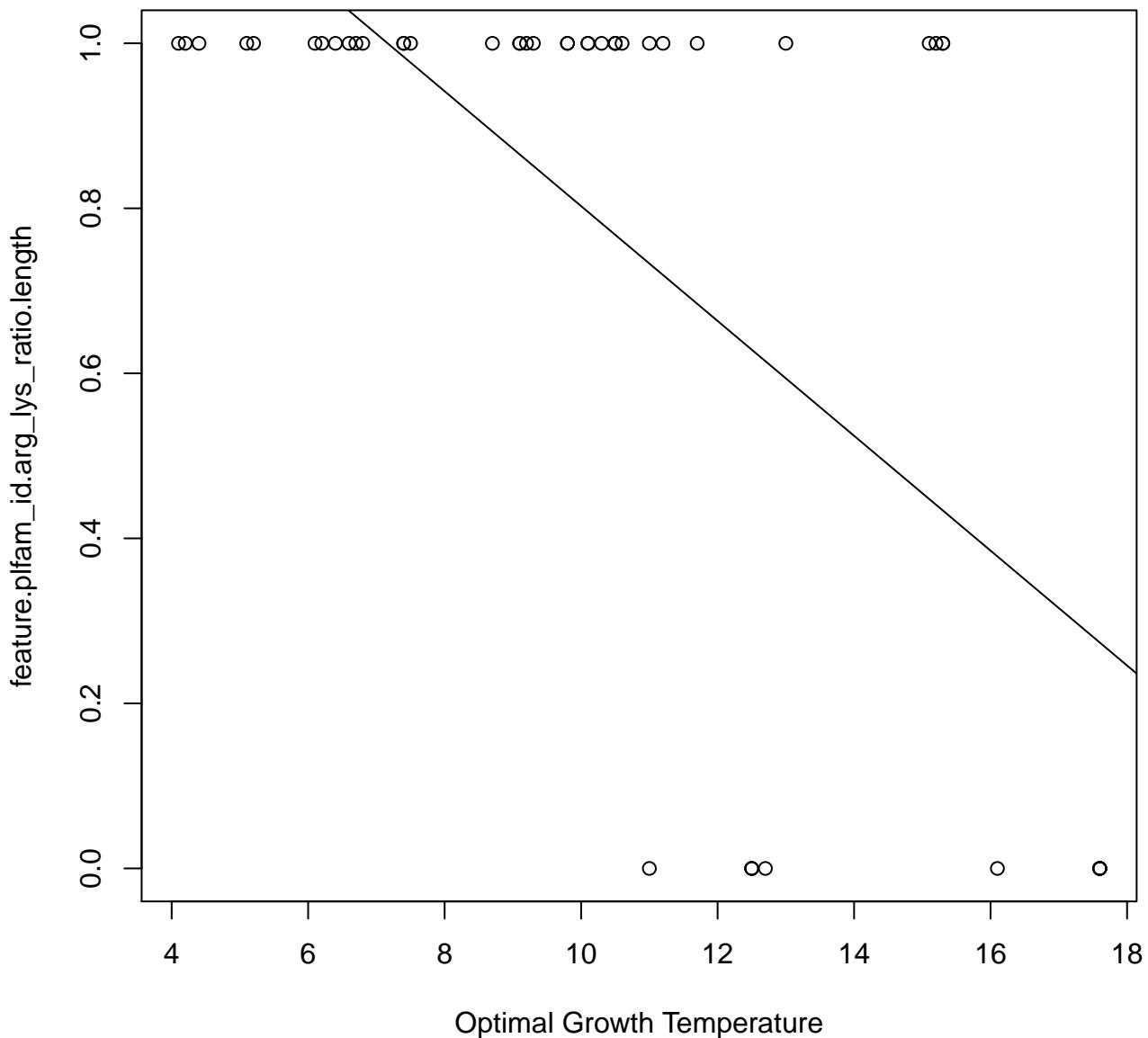
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PLF_28228_00007078
Uncharacterized ABC1 family protein RspH17029_4038



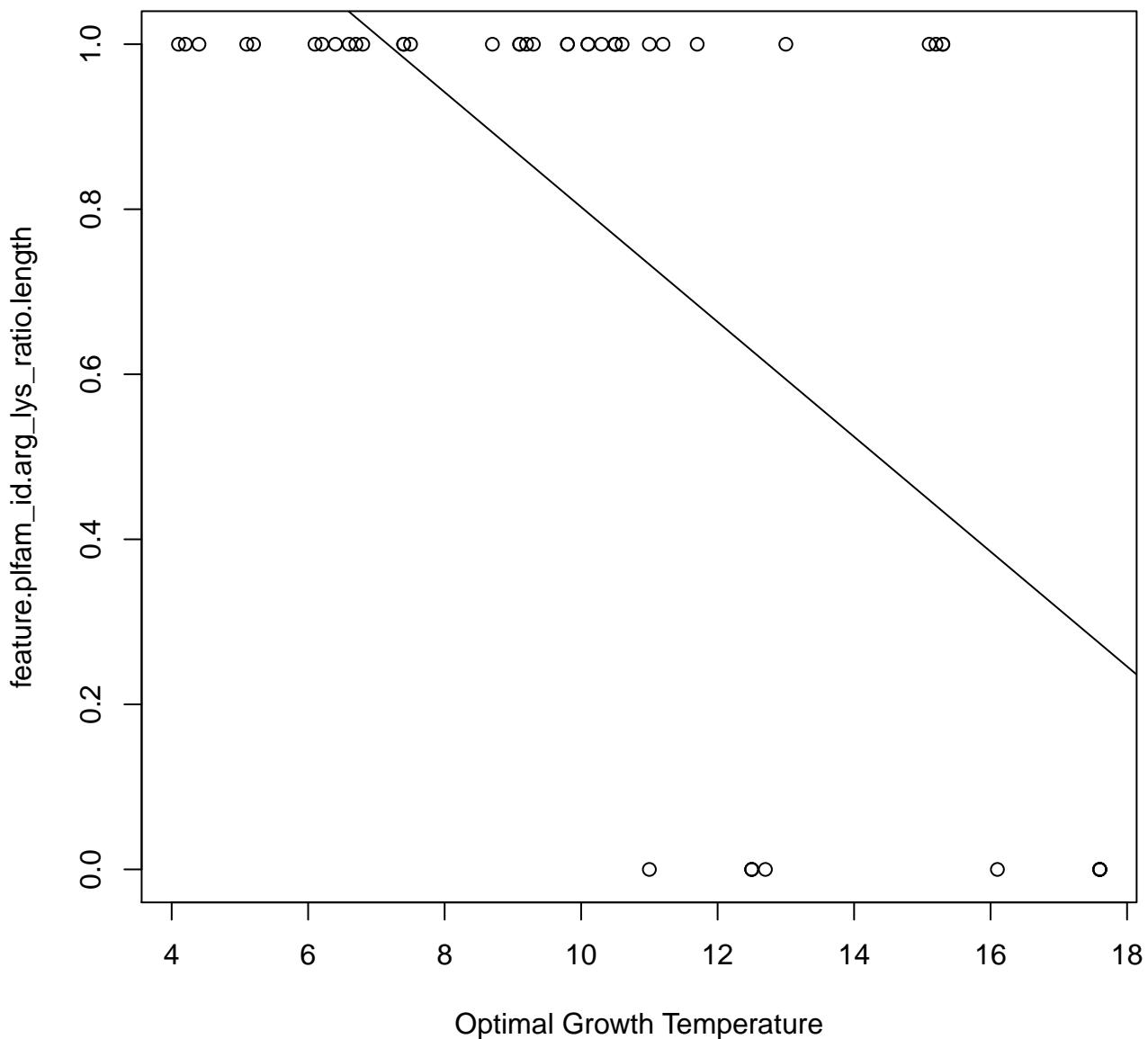
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hypothetical protein



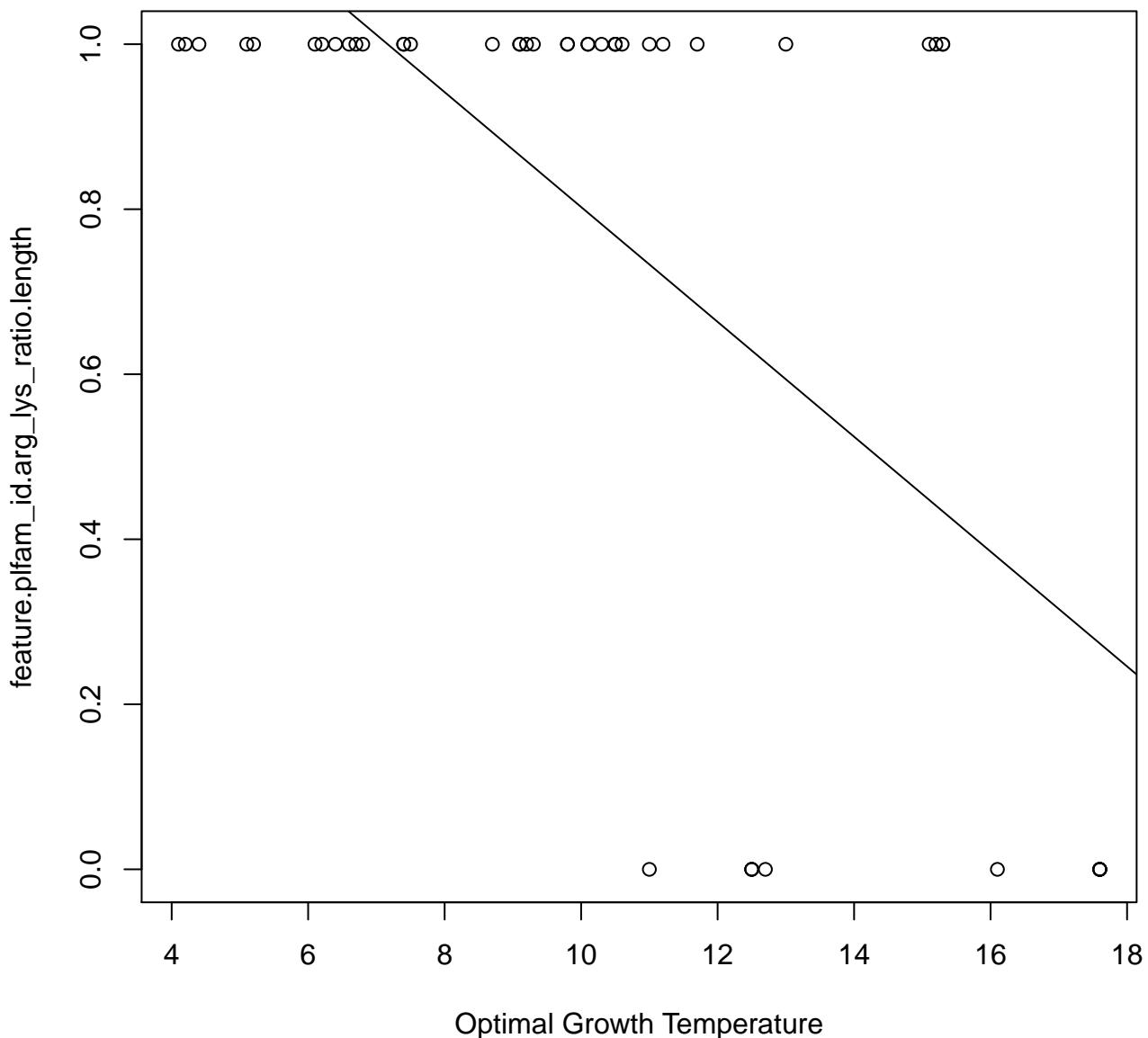
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00006366
Hypothetical protein in Cyanoglobin locus



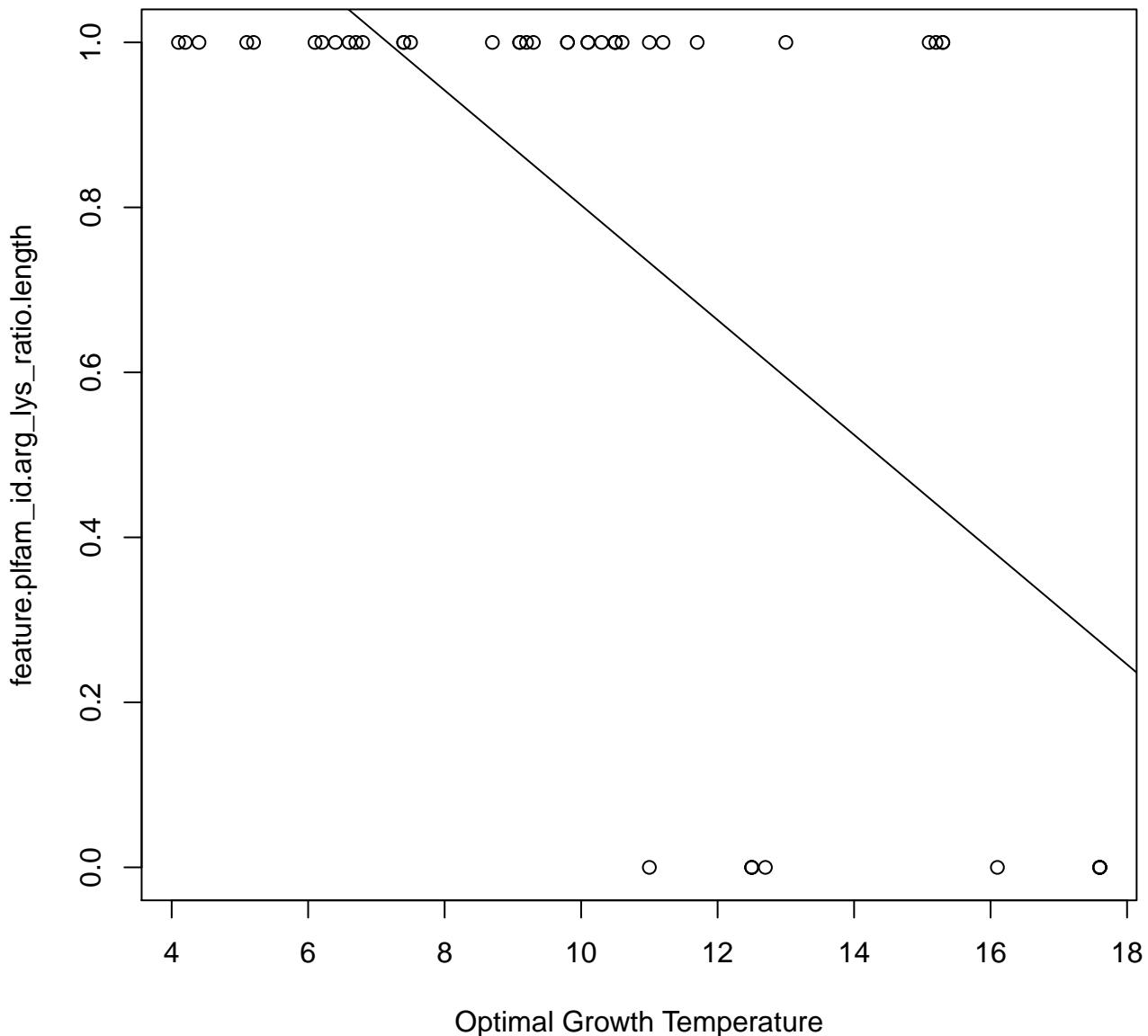
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hypothetical protein



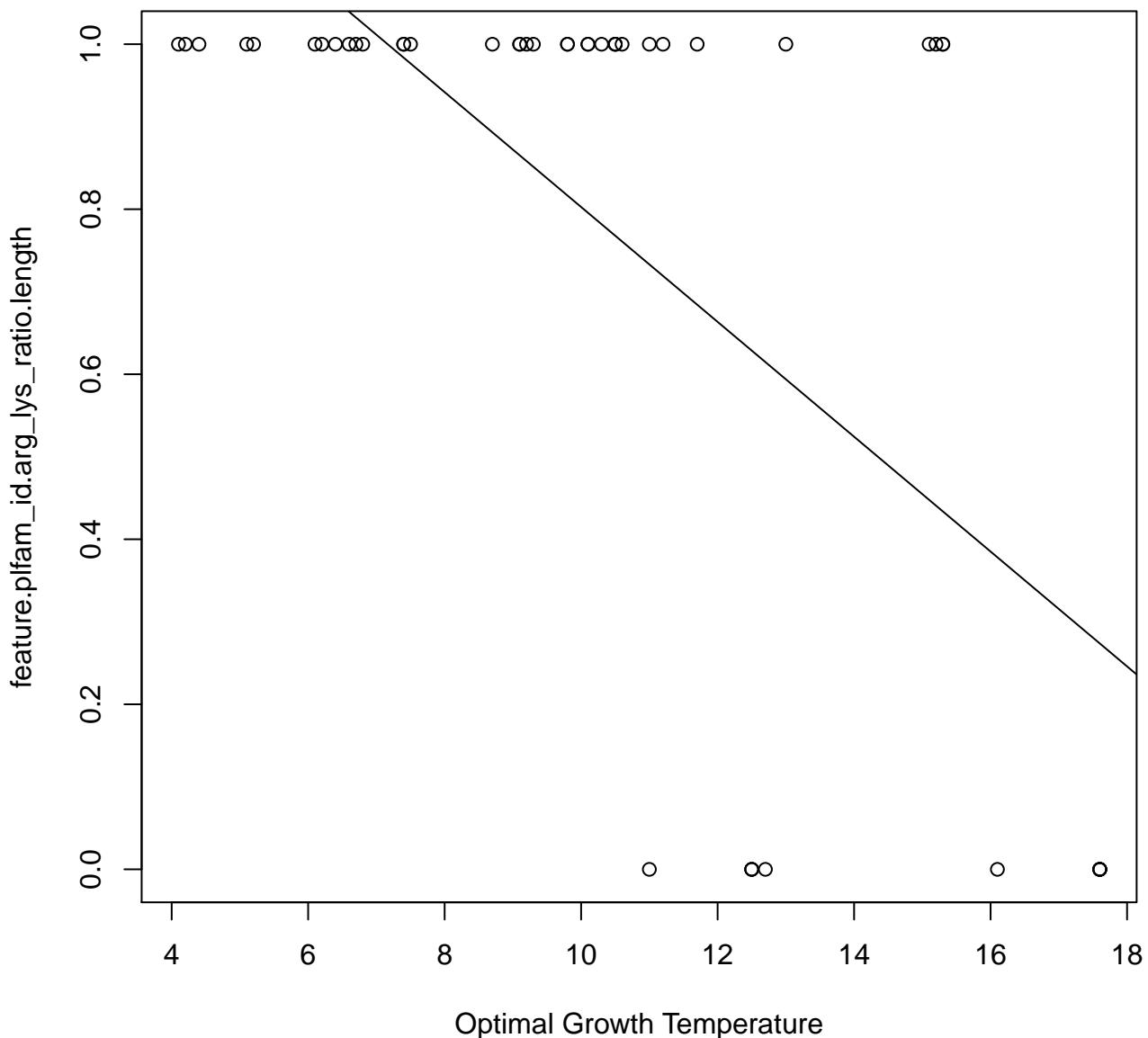
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Glutathione S-transferase (EC 2.5.1.18)



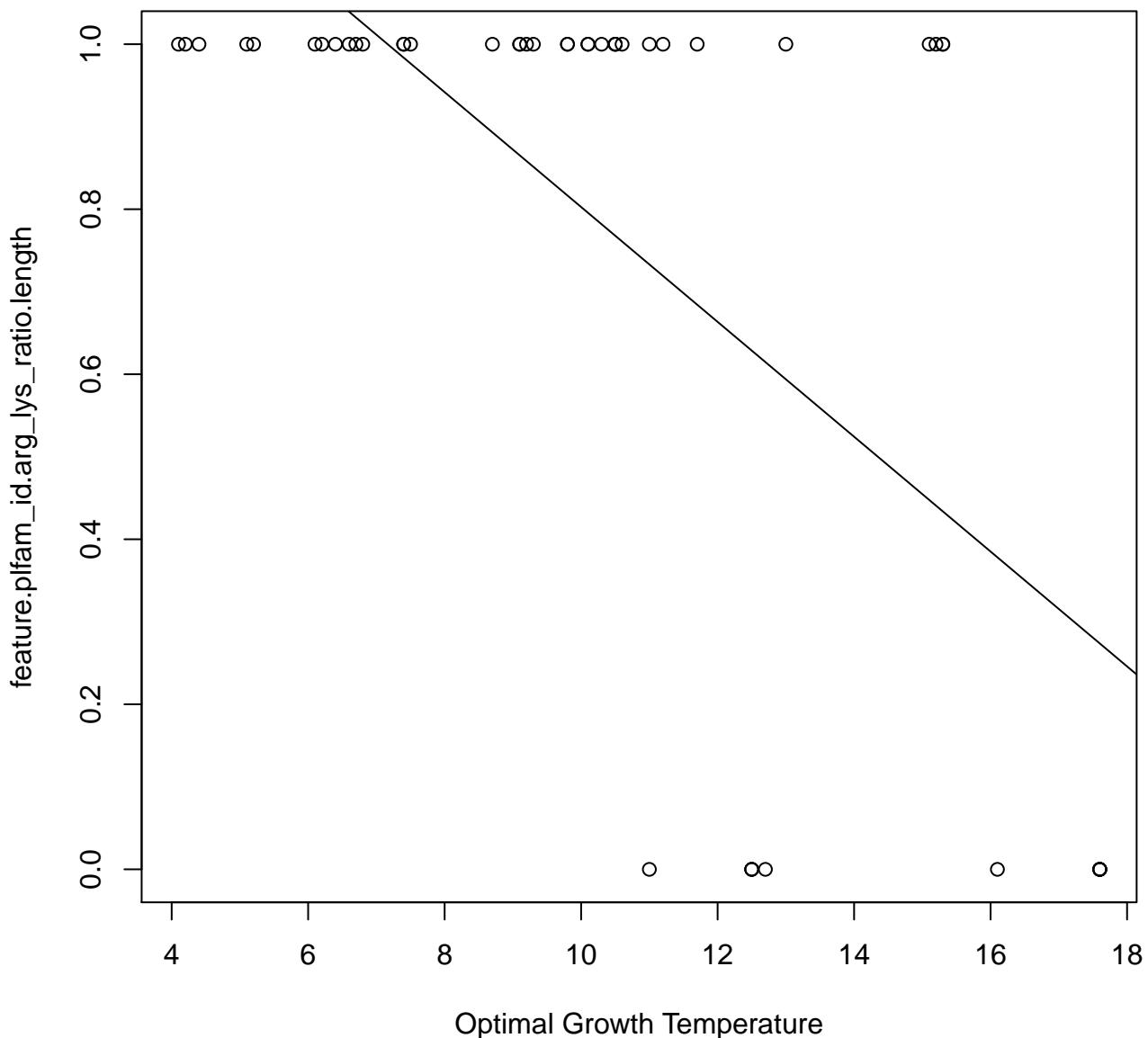
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PLF_28228_00006440
Deoxyribodipyrimidine photolyase, single-strand-specific



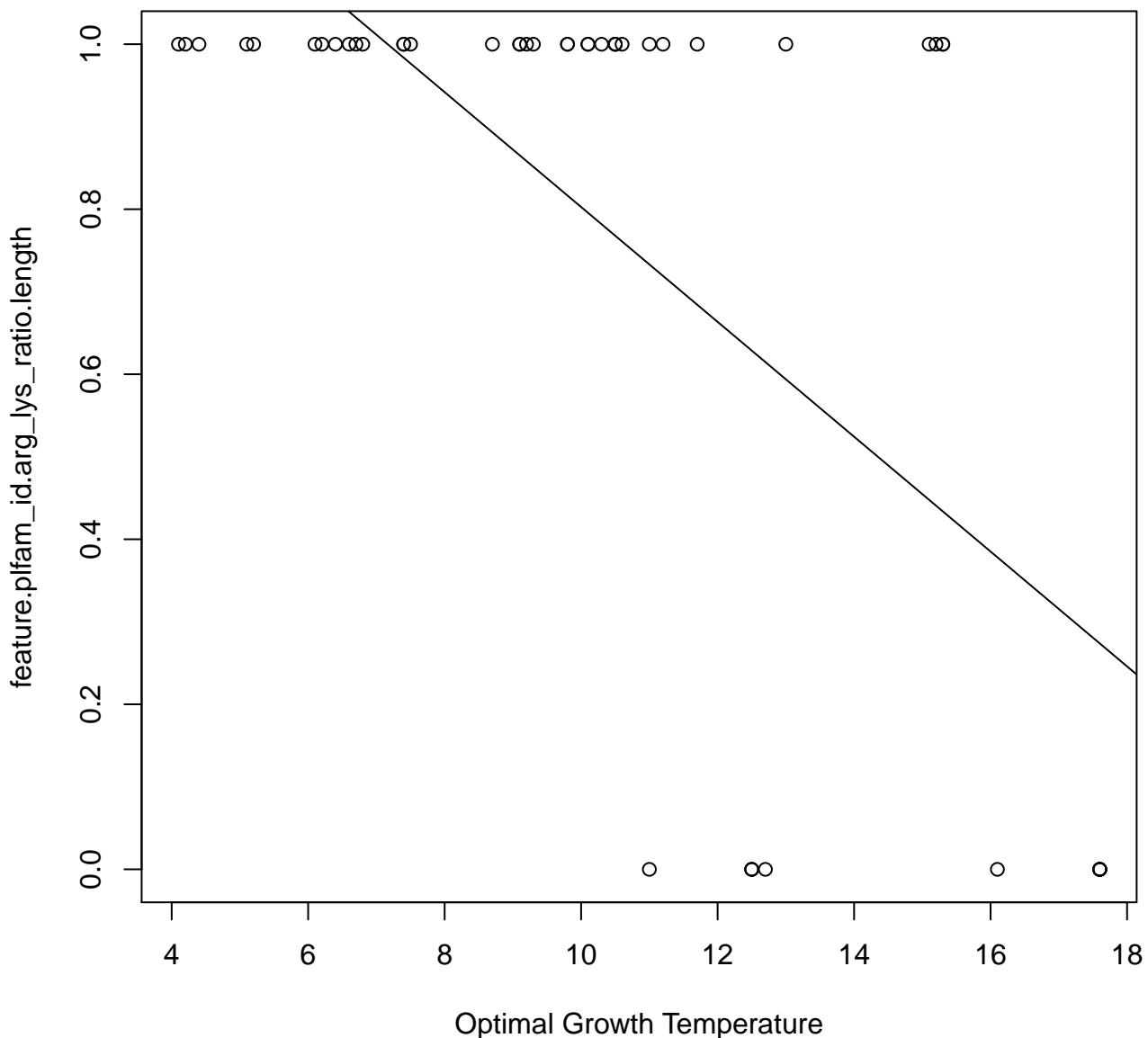
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00006965
Carbon-nitrogen hydrolase



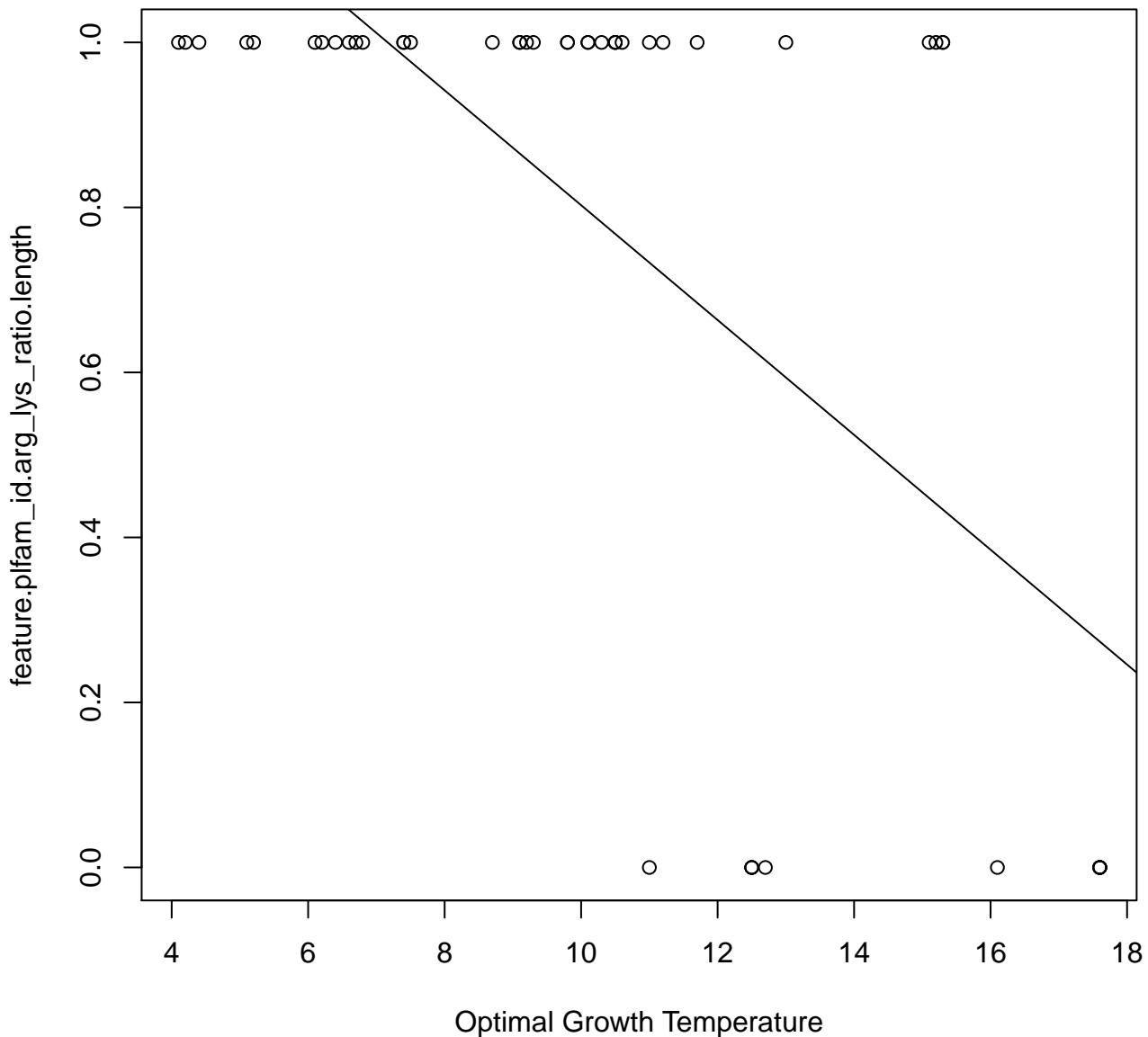
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PLF_28228_00008845
hypothetical protein



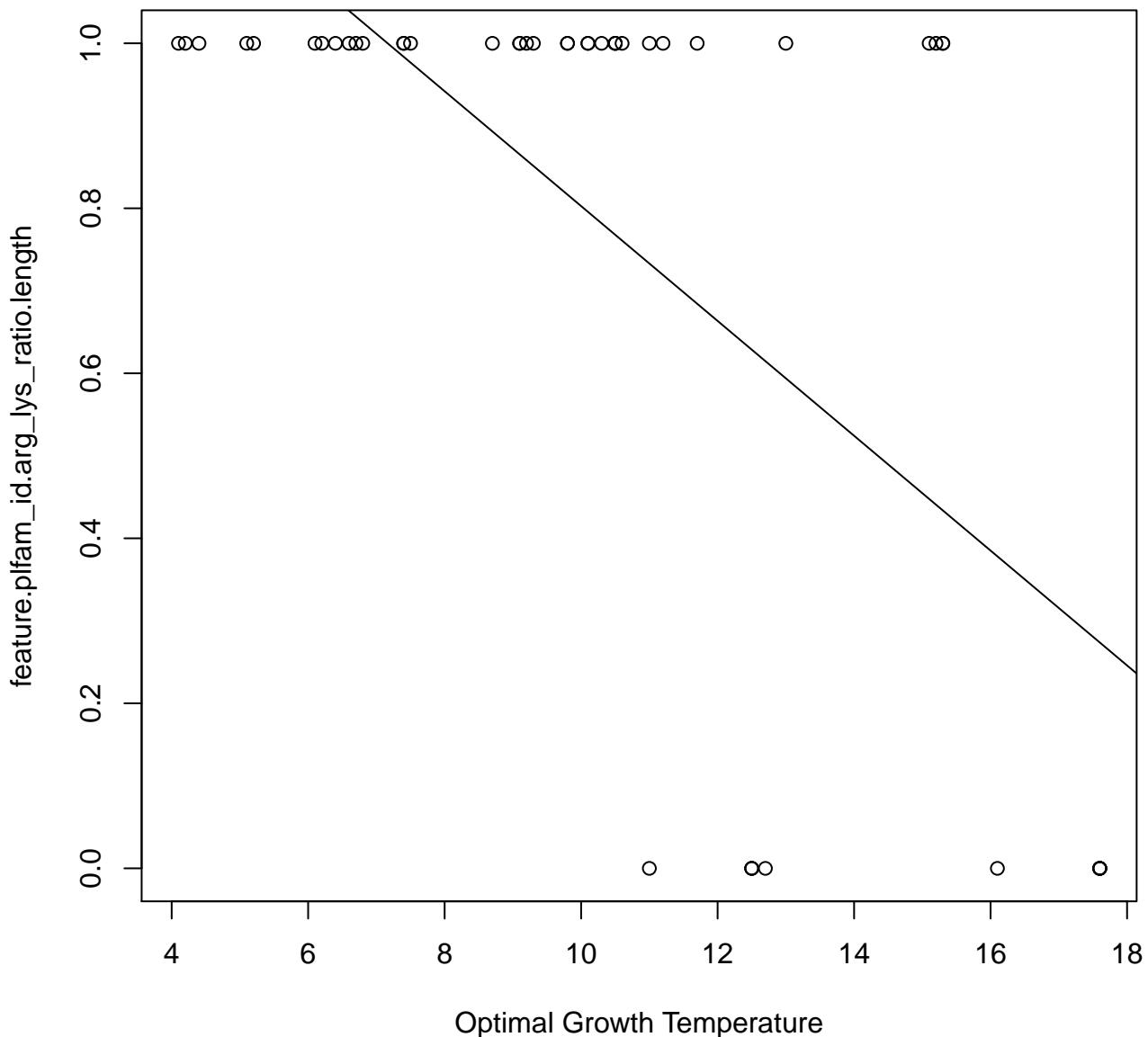
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hypothetical protein



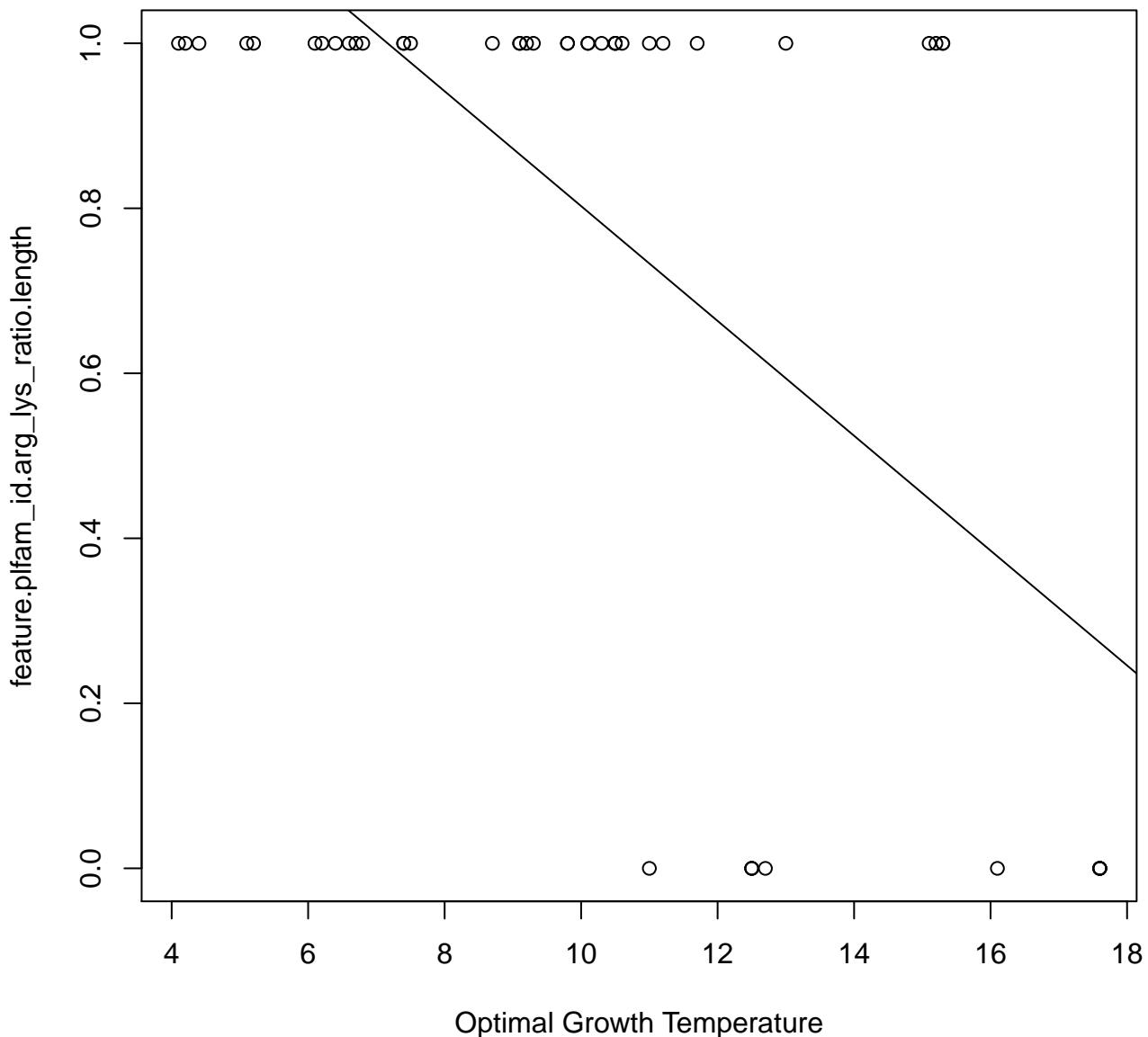
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3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)



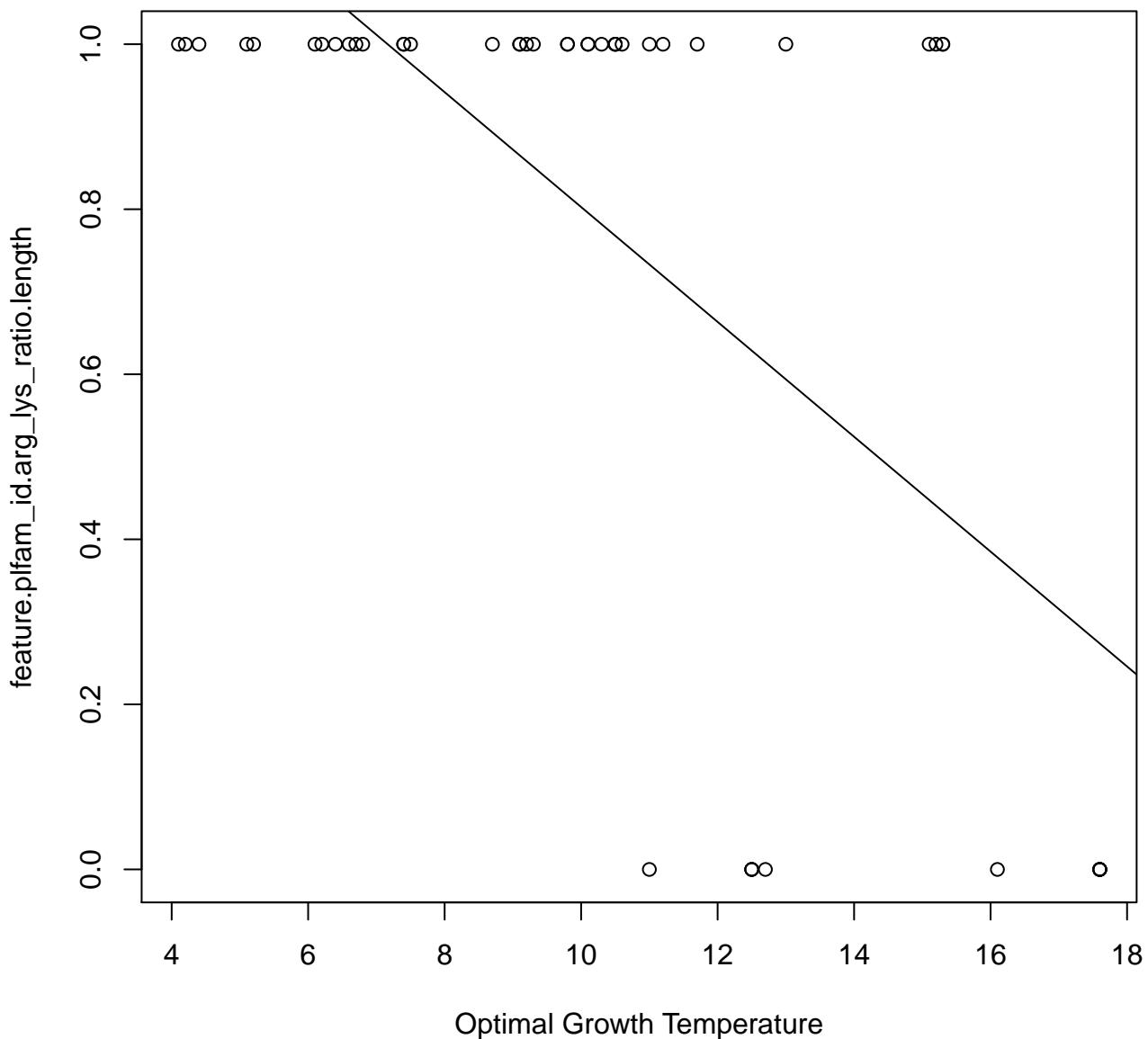
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PLF_28228_00014391
Organic hydroperoxide resistance transcriptional regulator



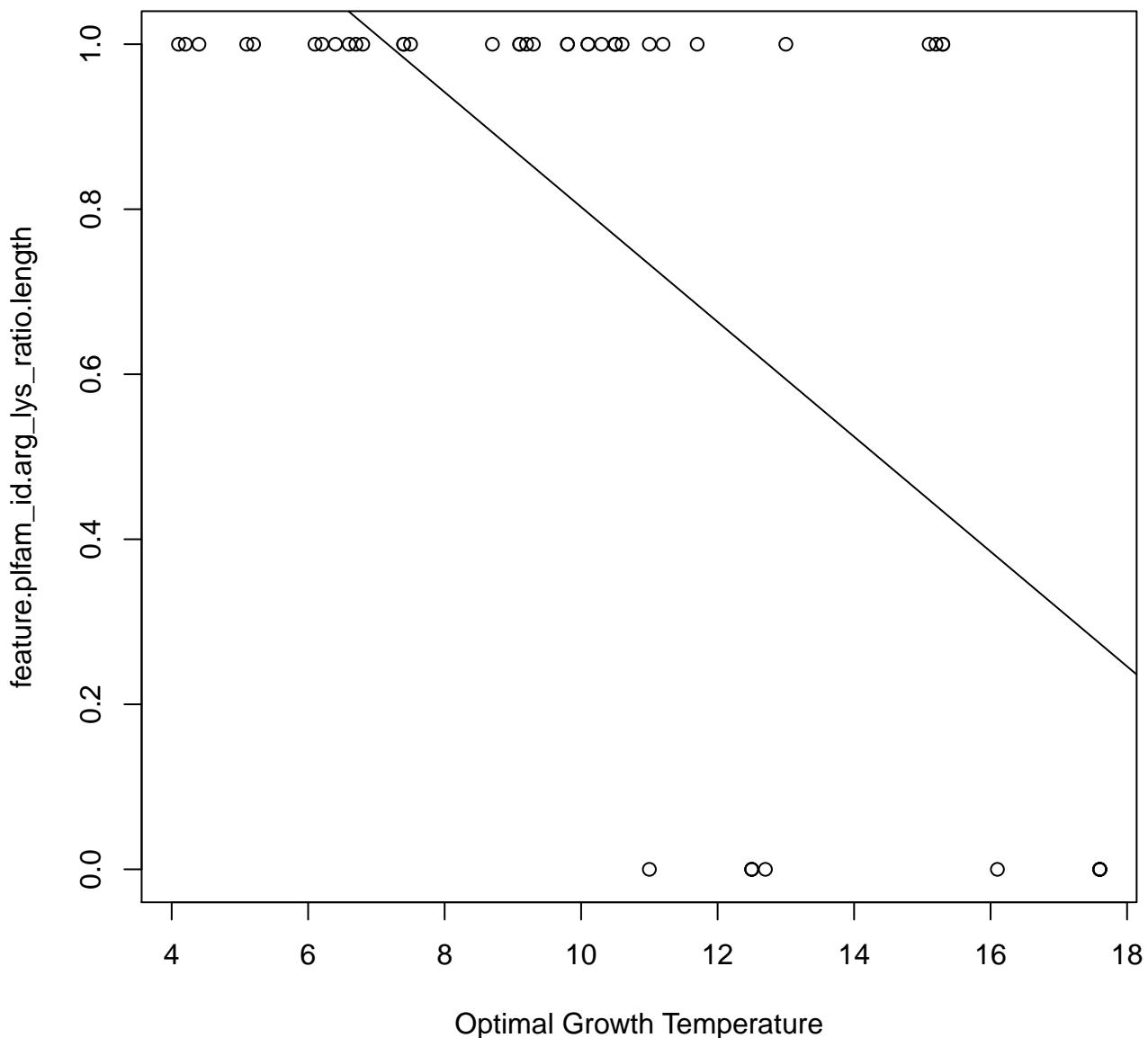
feature.pifam_id.arg_lys_ratio.length
PLF_28228_00014418
Organic hydroperoxide resistance protein



feature.pfam_id.arg_lys_ratio.length
PLF_28228_00015122
hypothetical protein



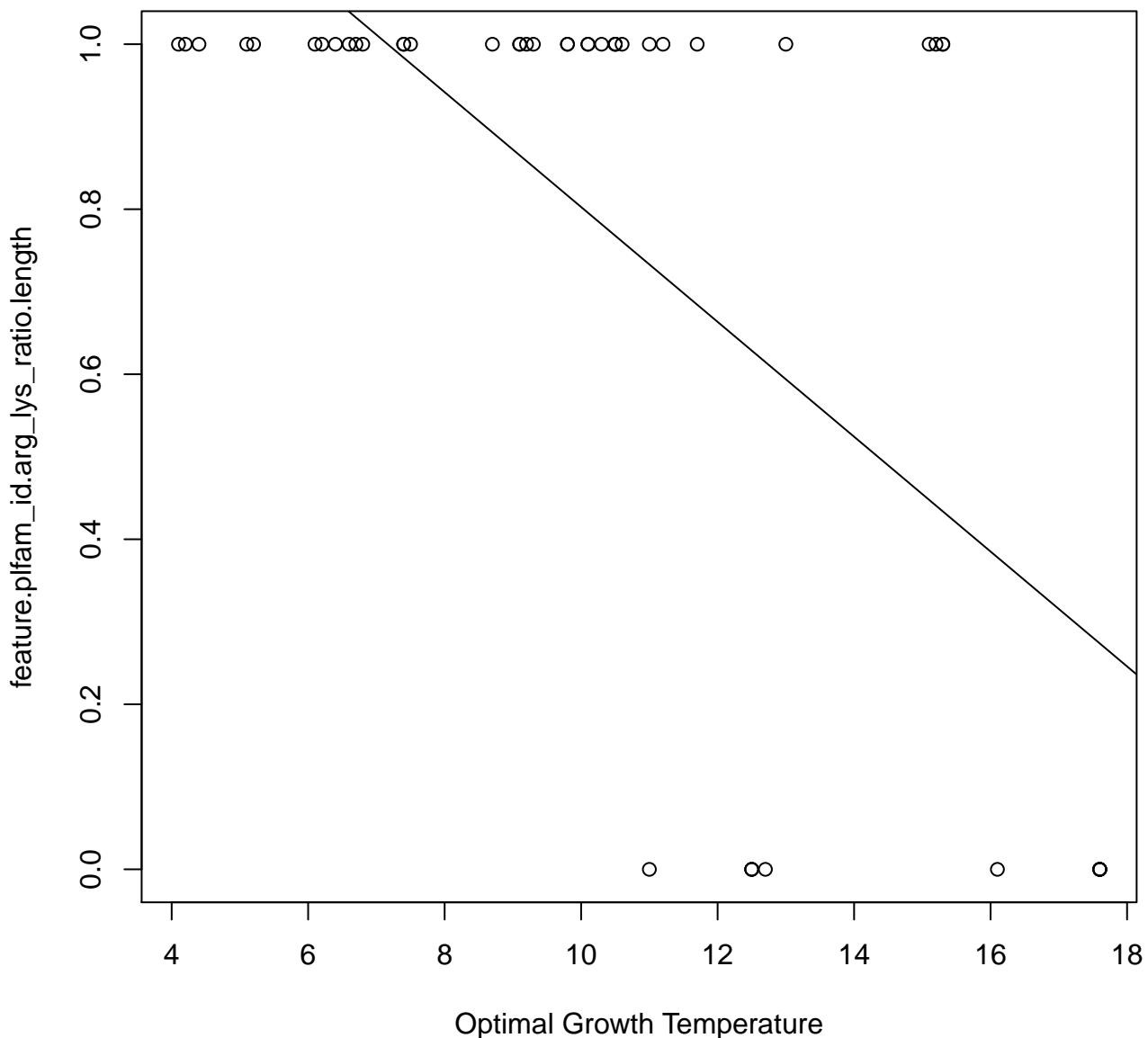
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PLF_28228_00015465
hypothetical protein



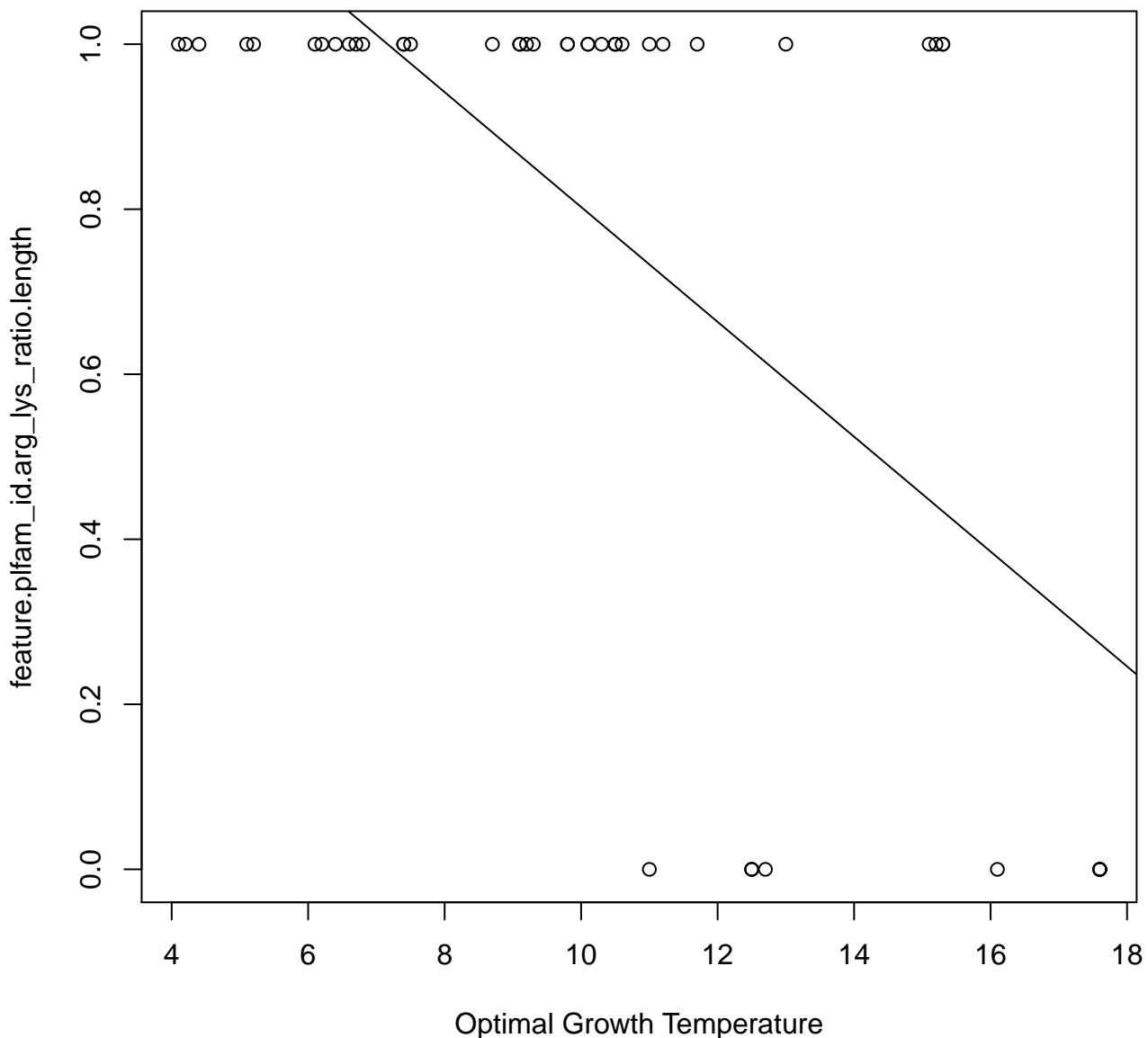
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PLF_28228_00015657

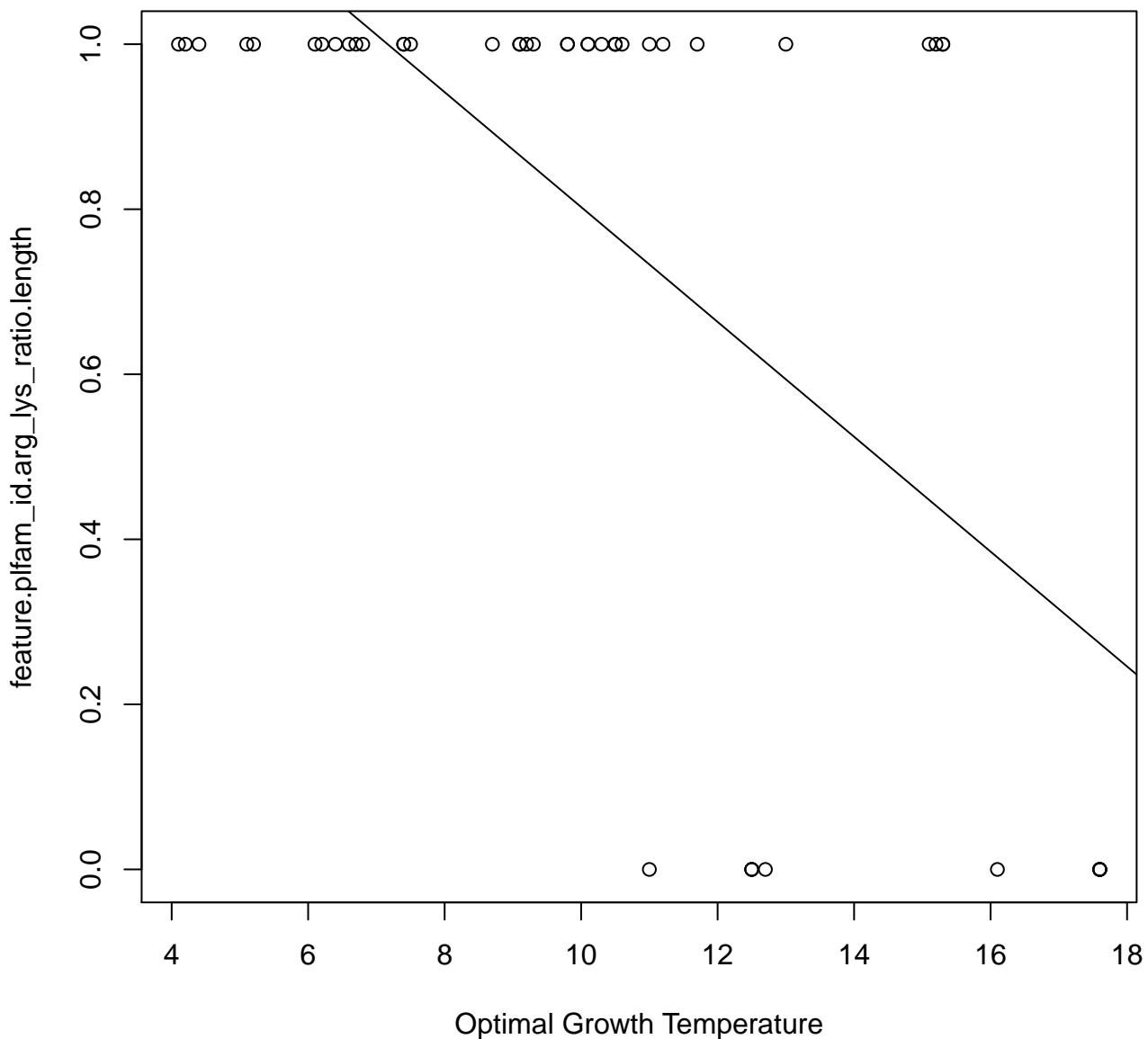
3-demethylubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6-hydroxyphenyl methylase (EC 2.1.1.222)



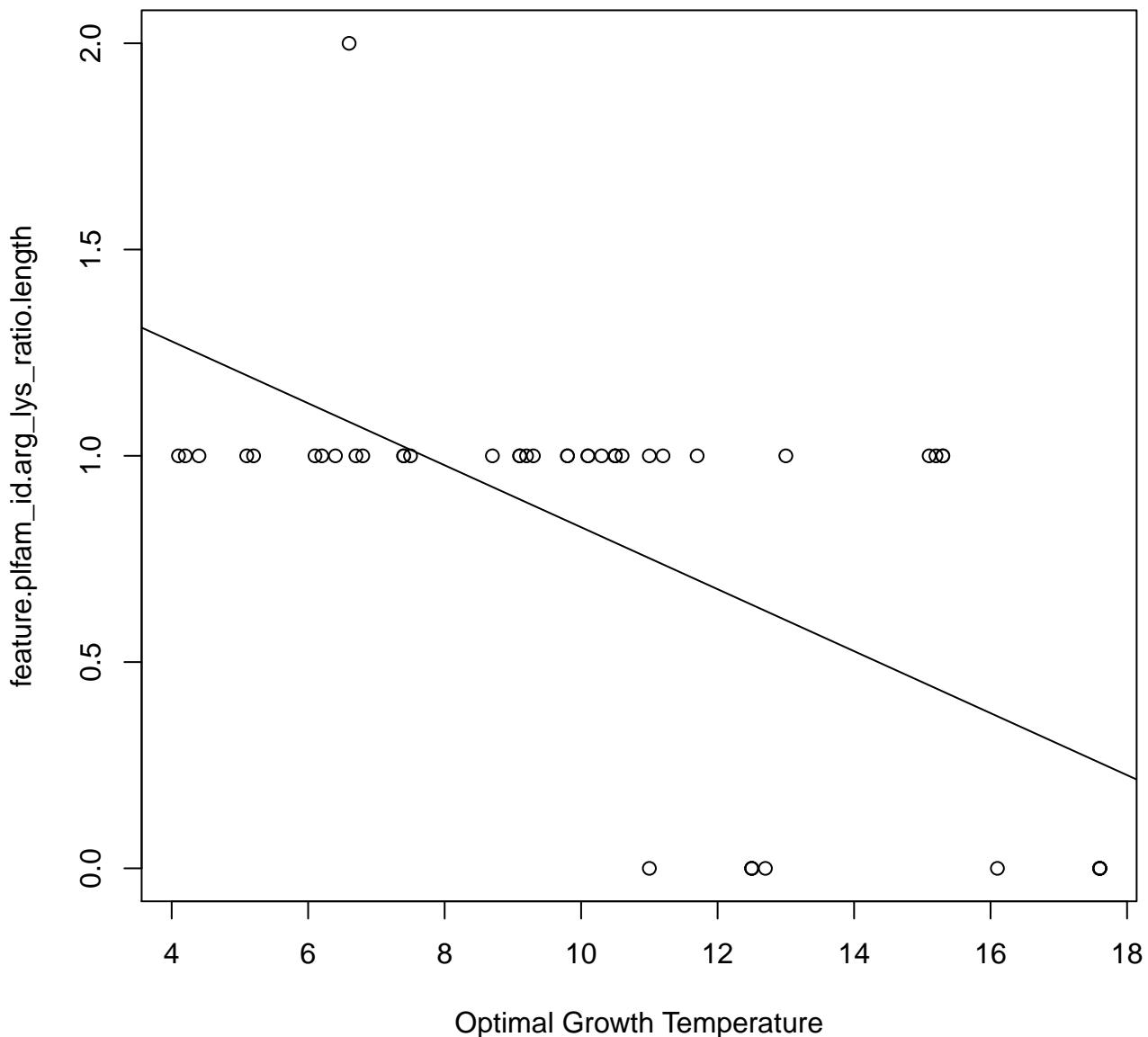
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hypothetical protein



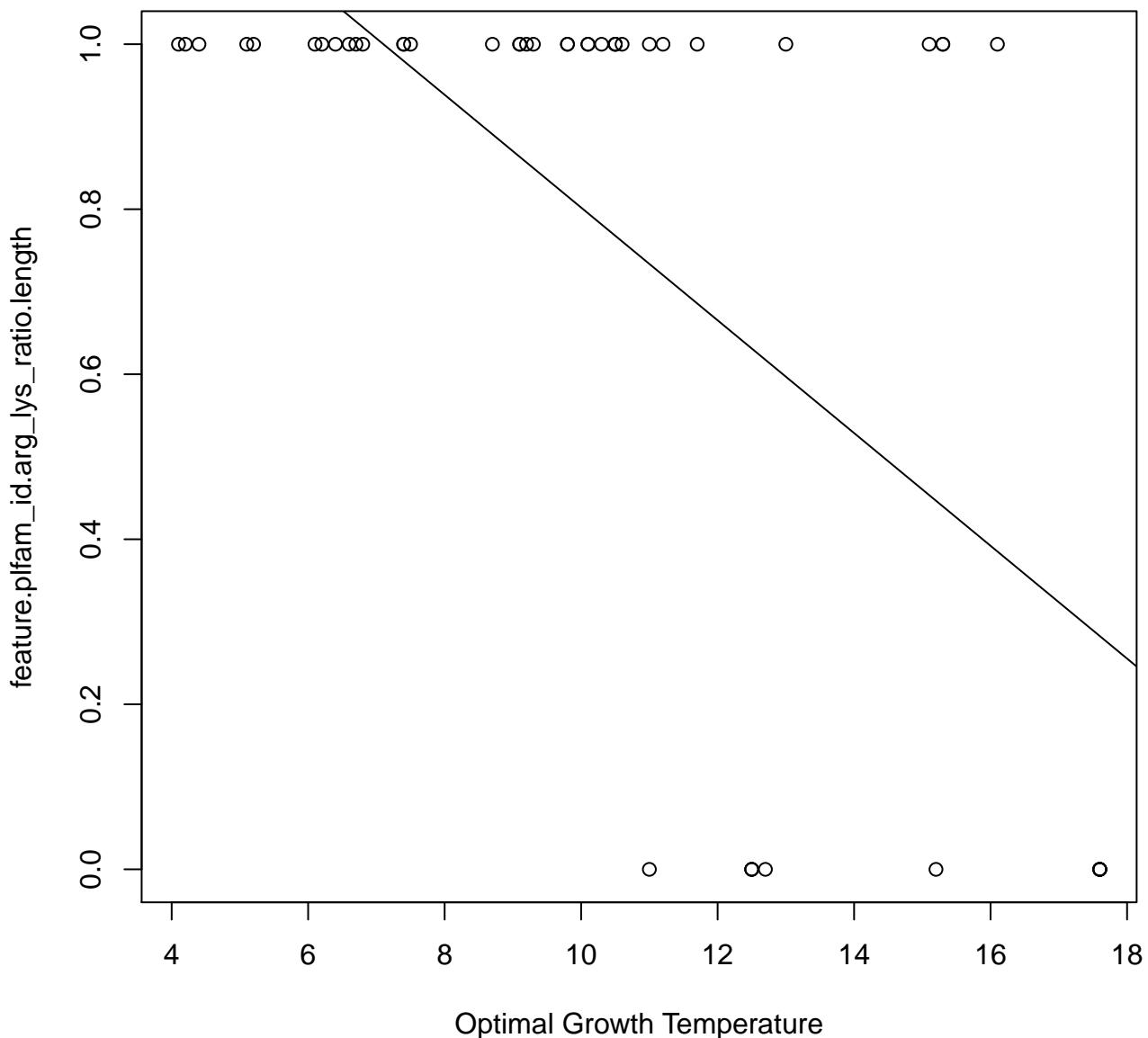
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00017311
Putative secreted amidase SCO6344



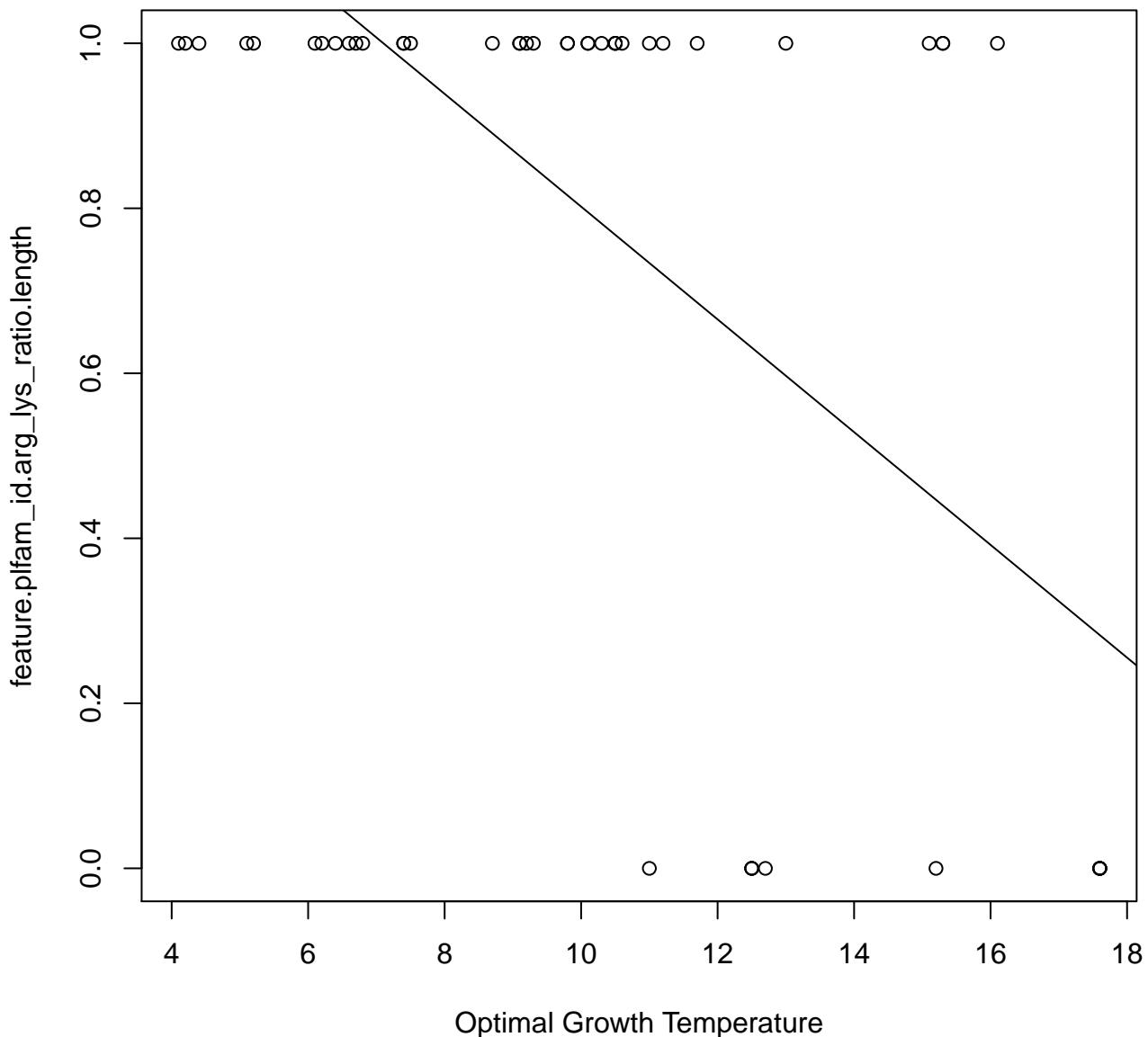
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00006270
Membrane-bound metal-dependent hydrolase



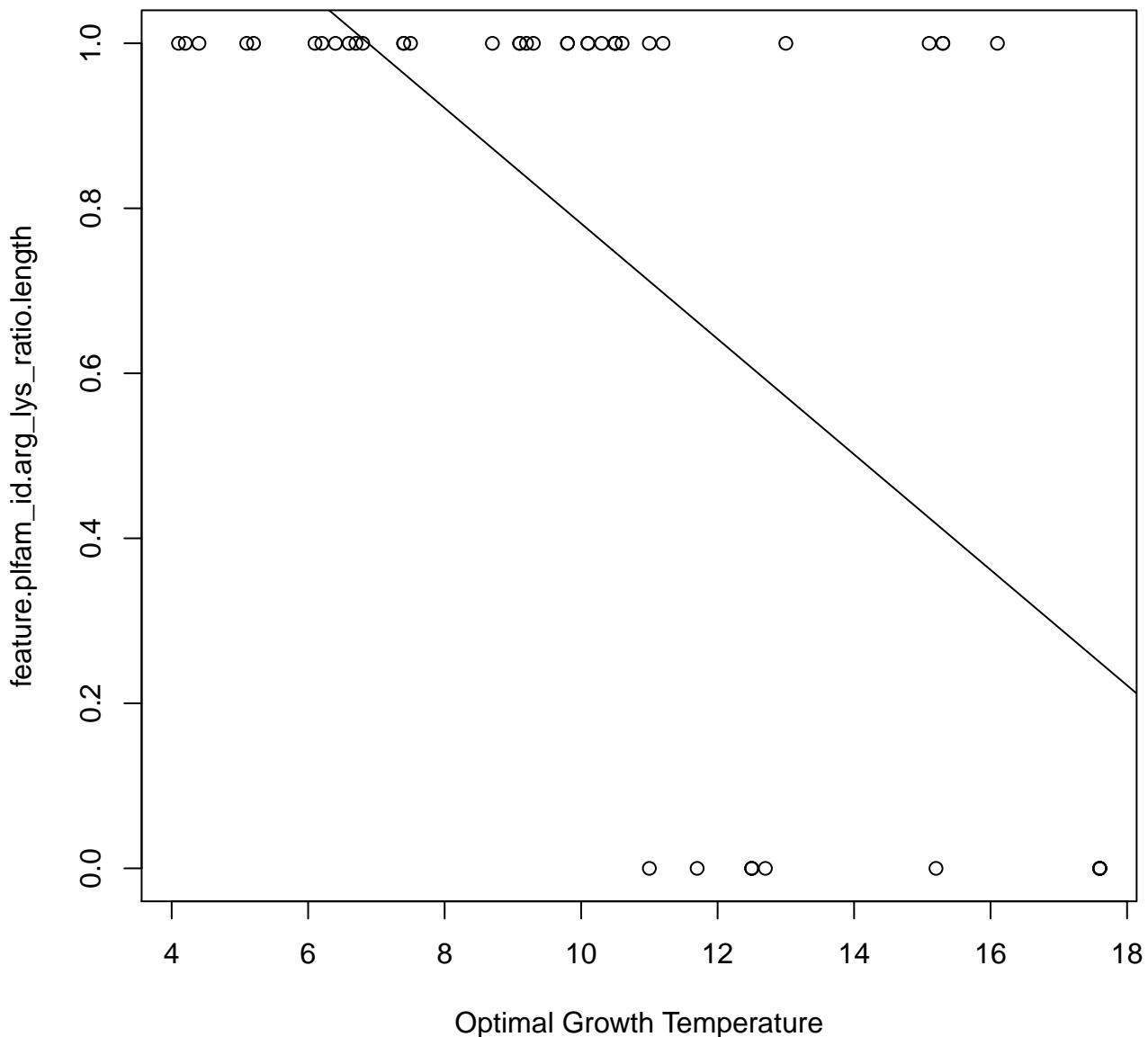
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00018190
Fumarate hydratase class II (EC 4.2.1.2)



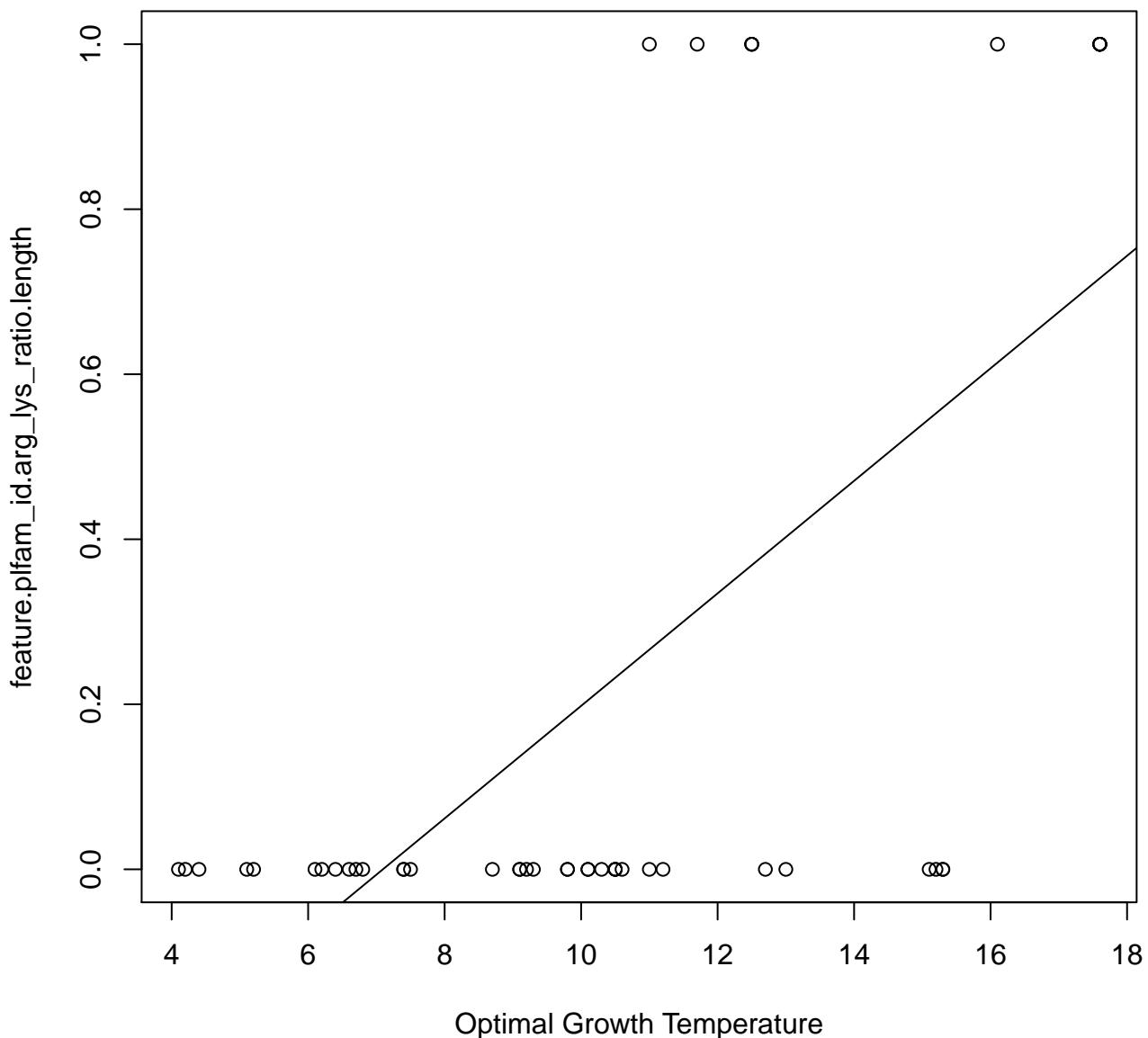
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00022110
Uncharacterized aldehyde oxidase, molybdopterin-binding subunit



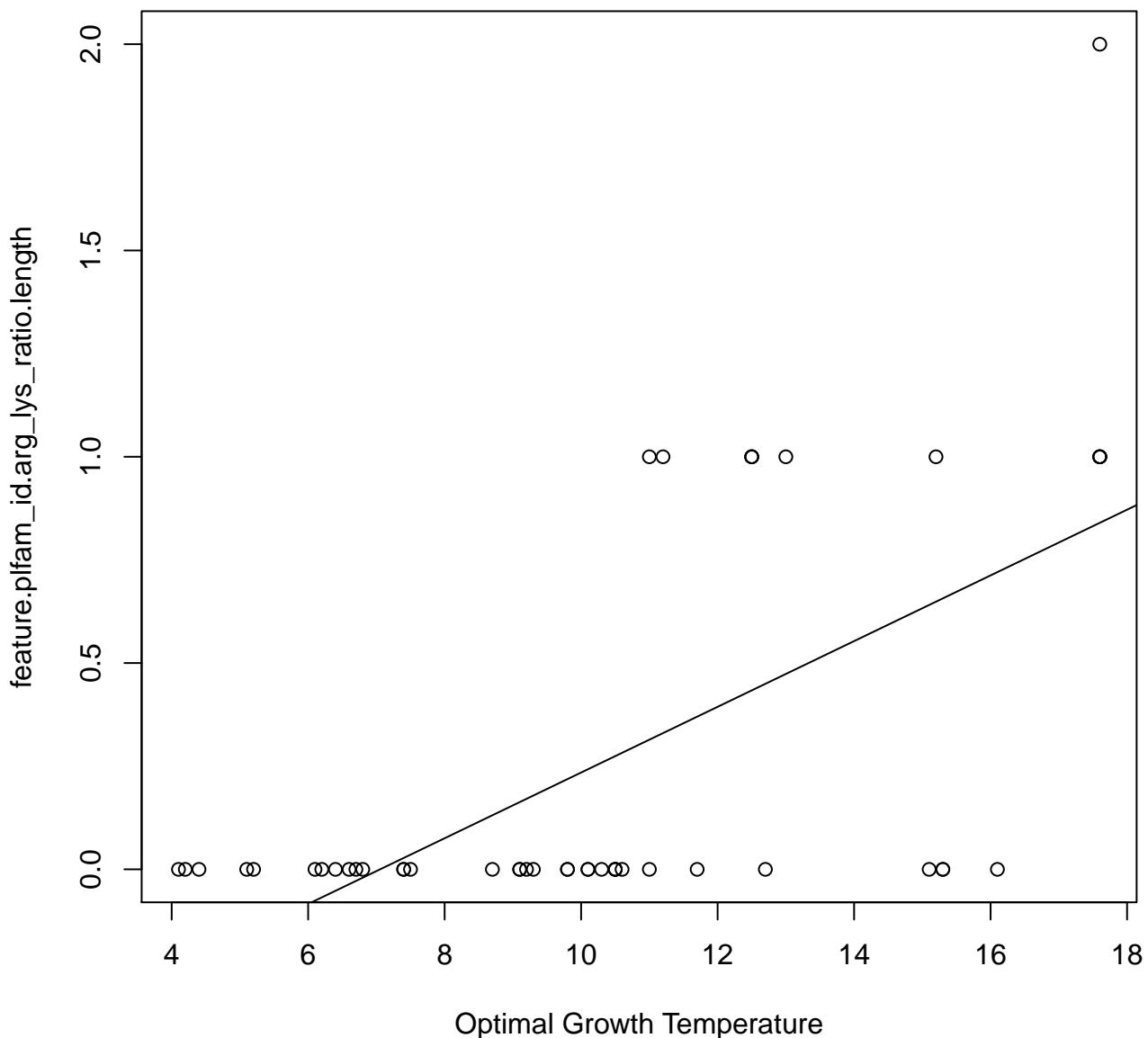
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00011165
Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)



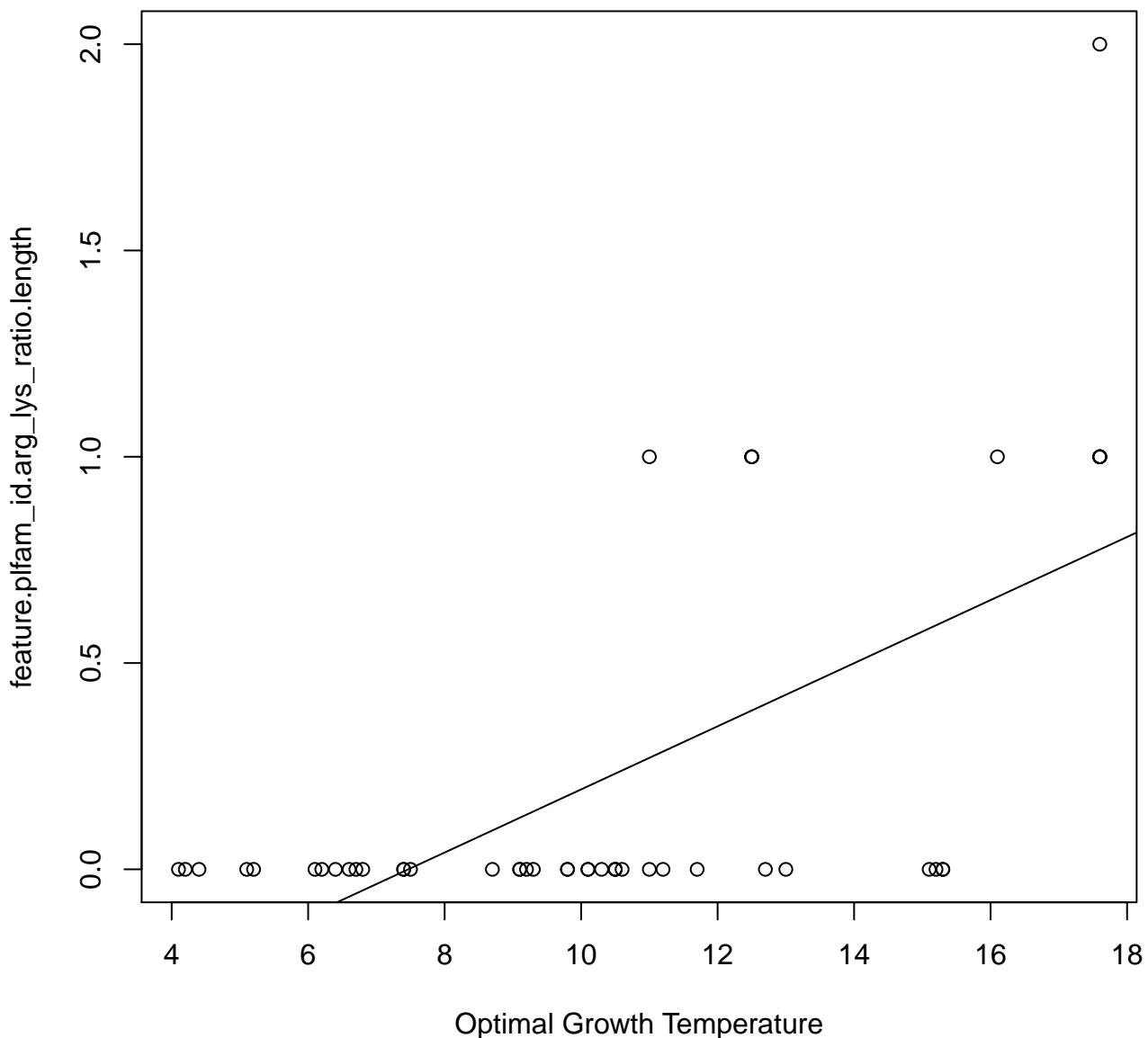
feature.pfam_id.arg_lys_ratio.length
PLF_28228_00001338
hypothetical protein



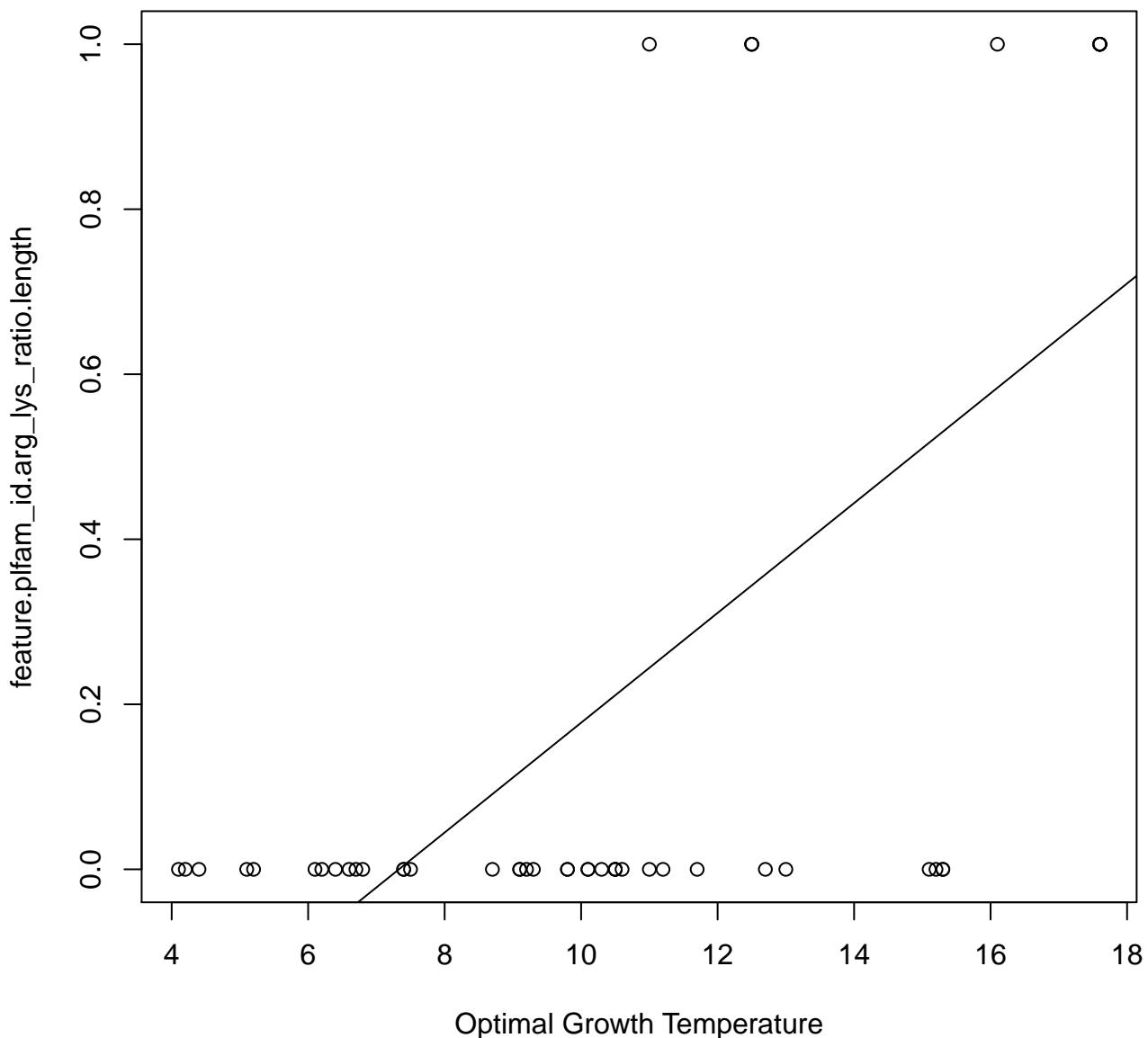
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PLF_28228_00000482
Glyoxalase family protein



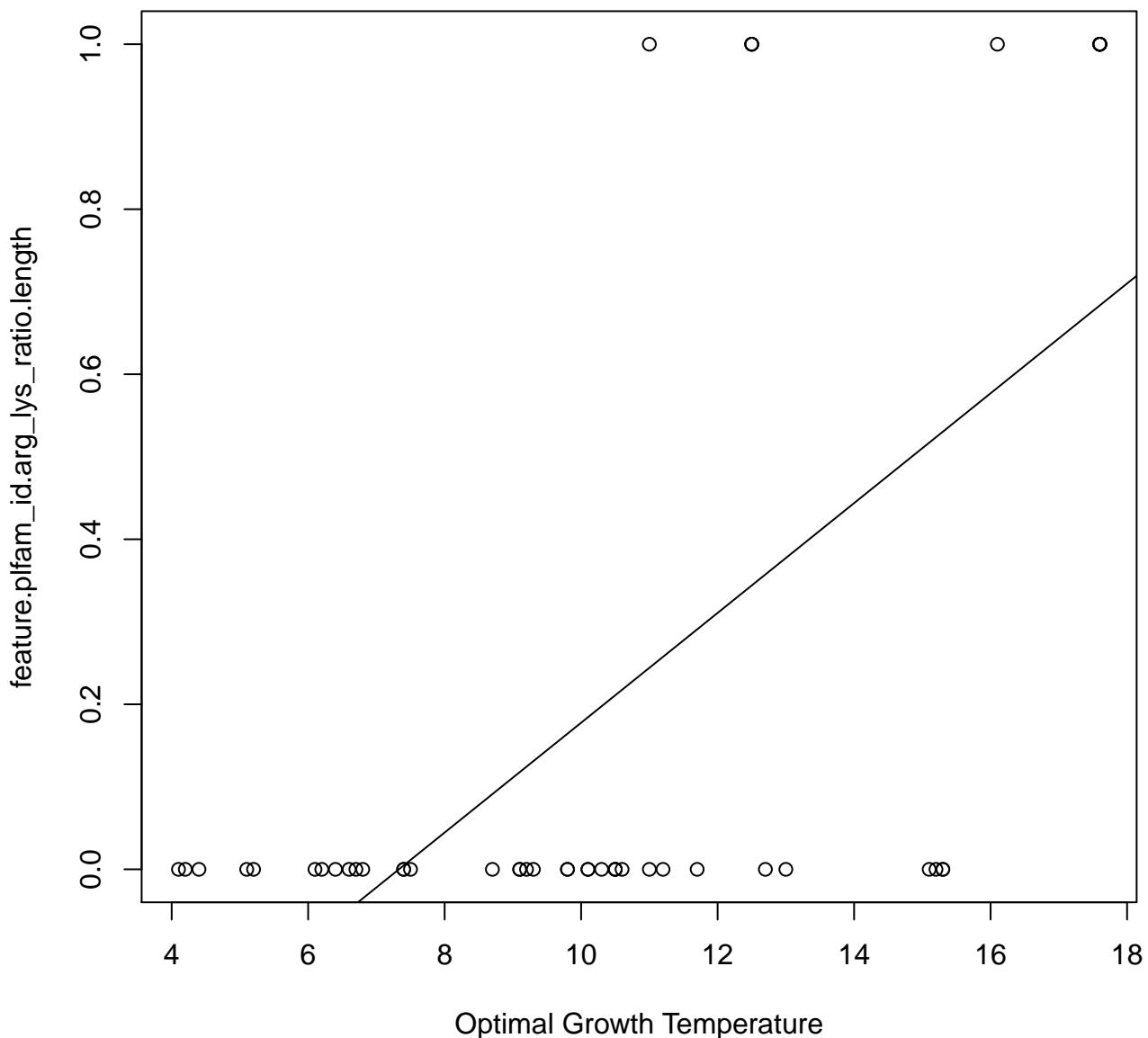
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PLF_28228_00002987
hypothetical protein



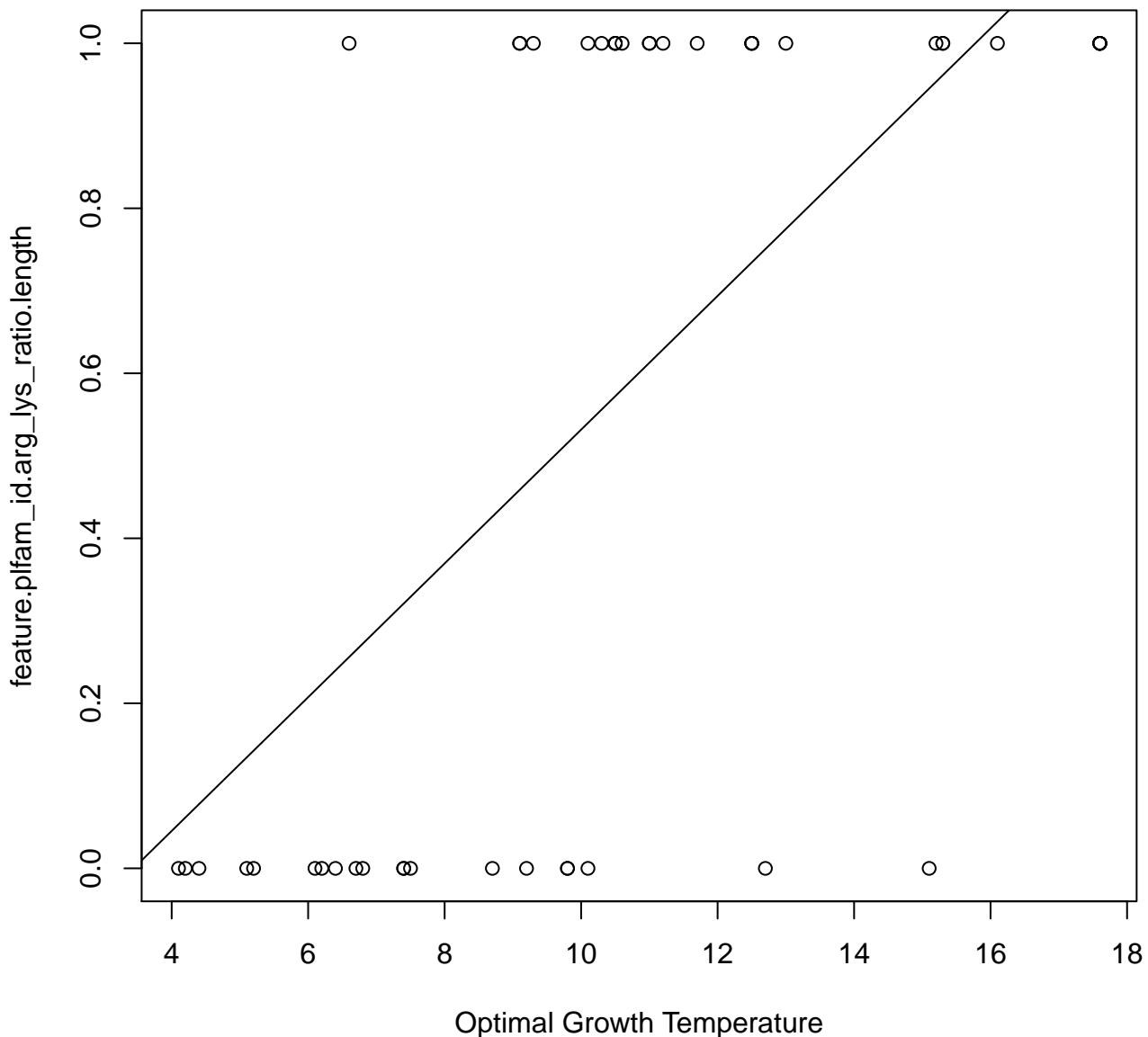
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PLF_28228_00002445
hypothetical protein



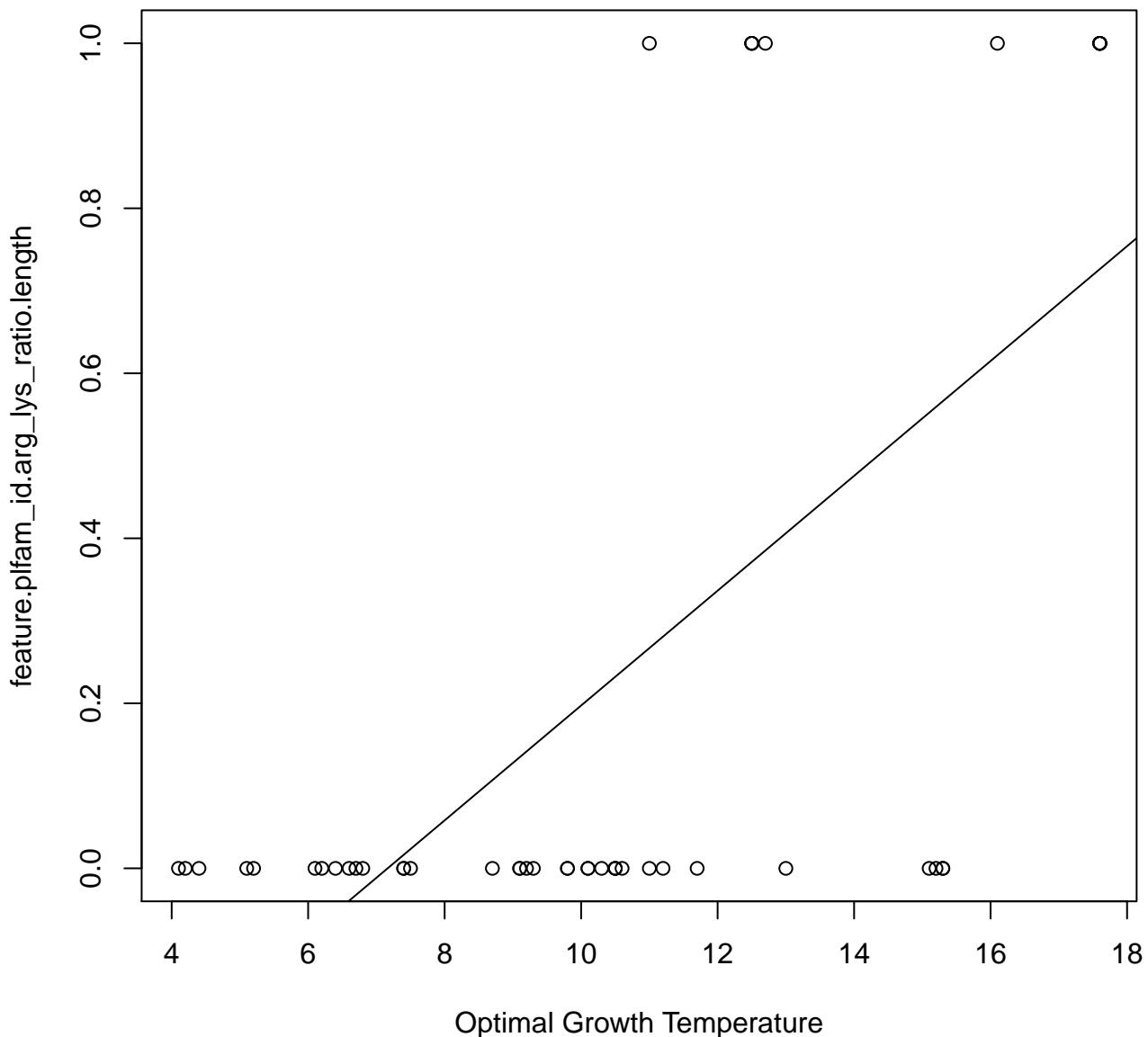
feature_pfam_id.arg_lys_ratio.length
PLF_28228_00002602
Acetyltransferase, GNAT family



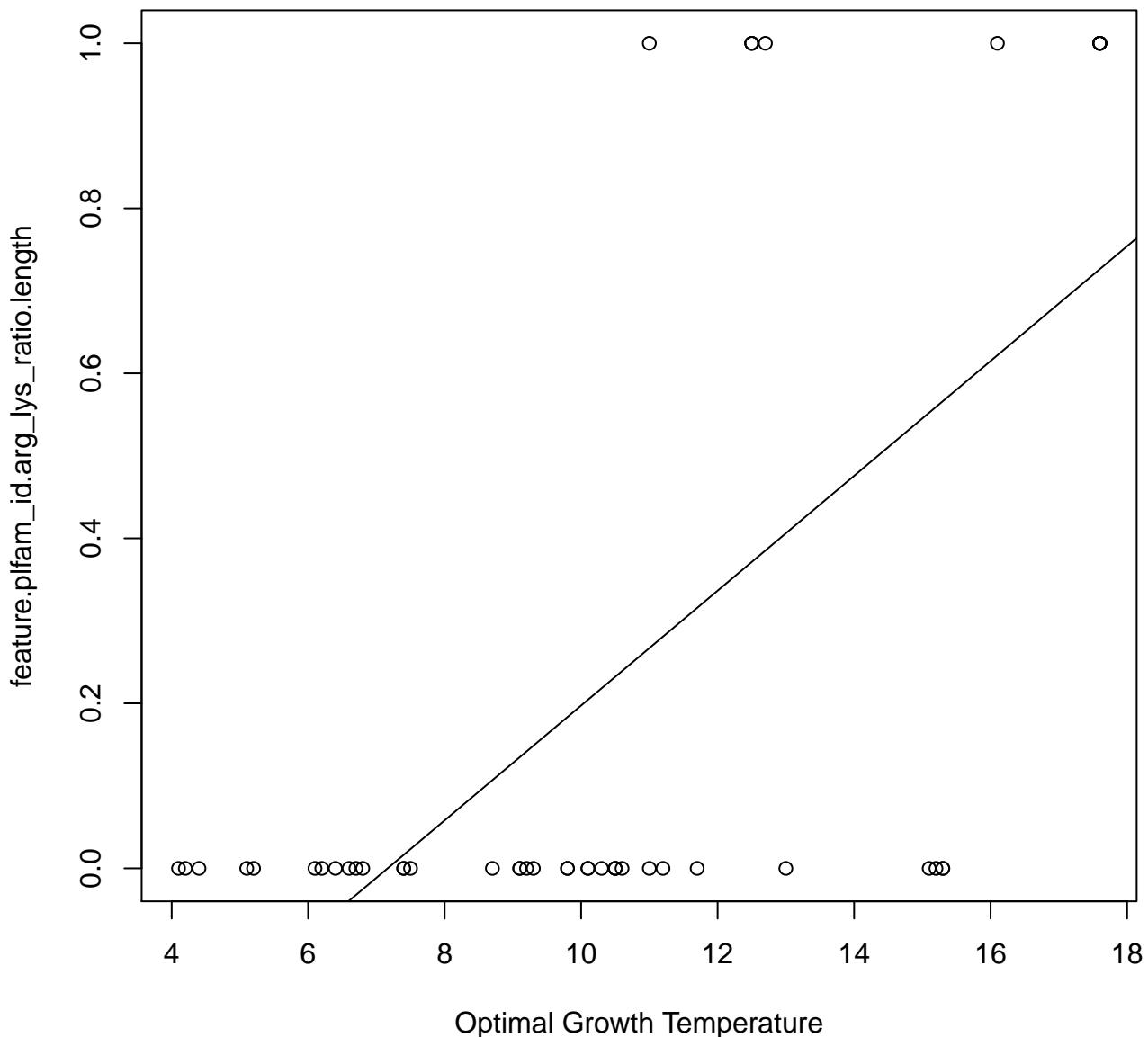
feature.pfam_id.arg_lys_ratio.length
PLF_28228_00002716
3-hydroxybutyrate dehydrogenase (EC 1.1.1.30)



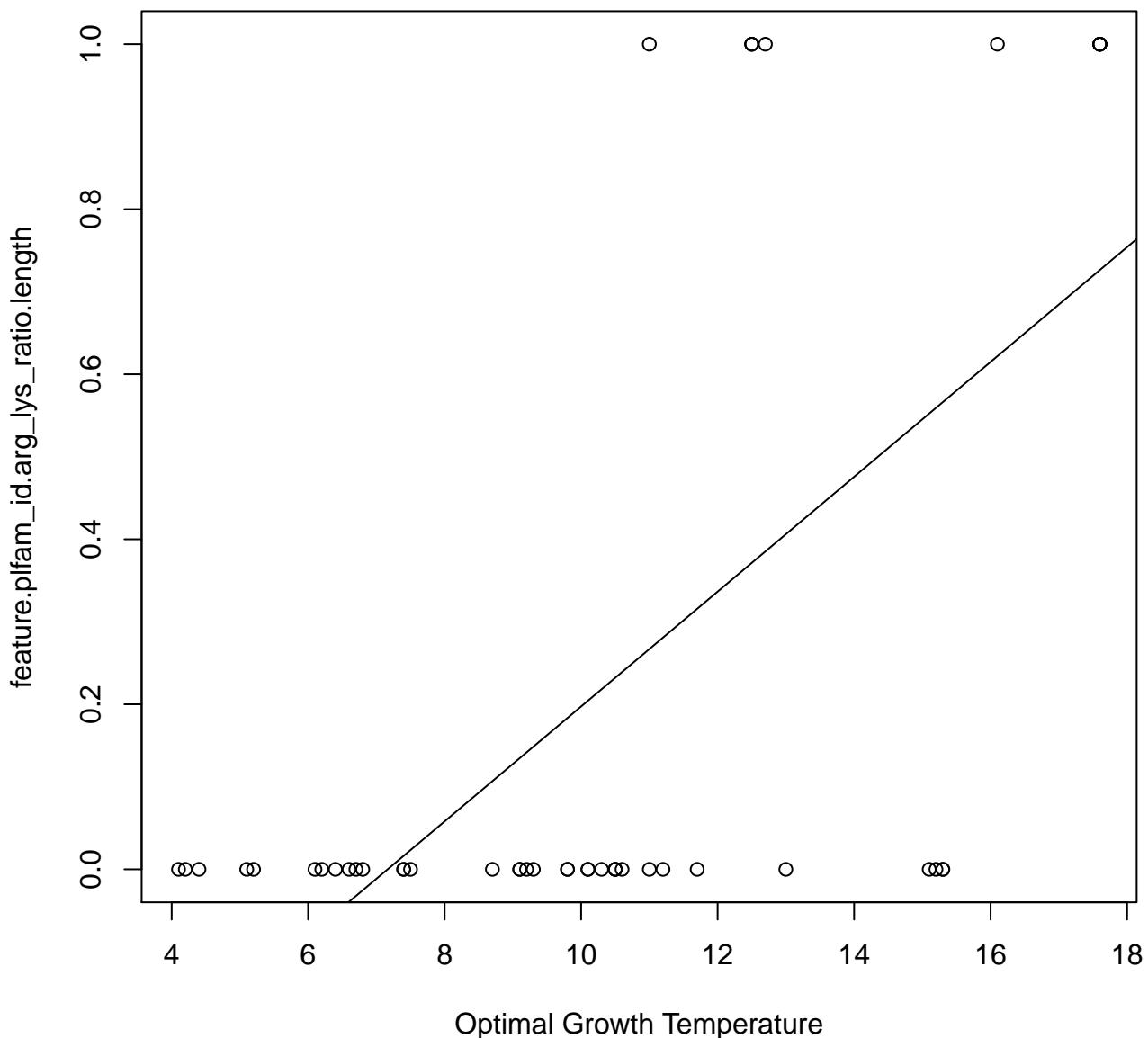
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00000296
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)



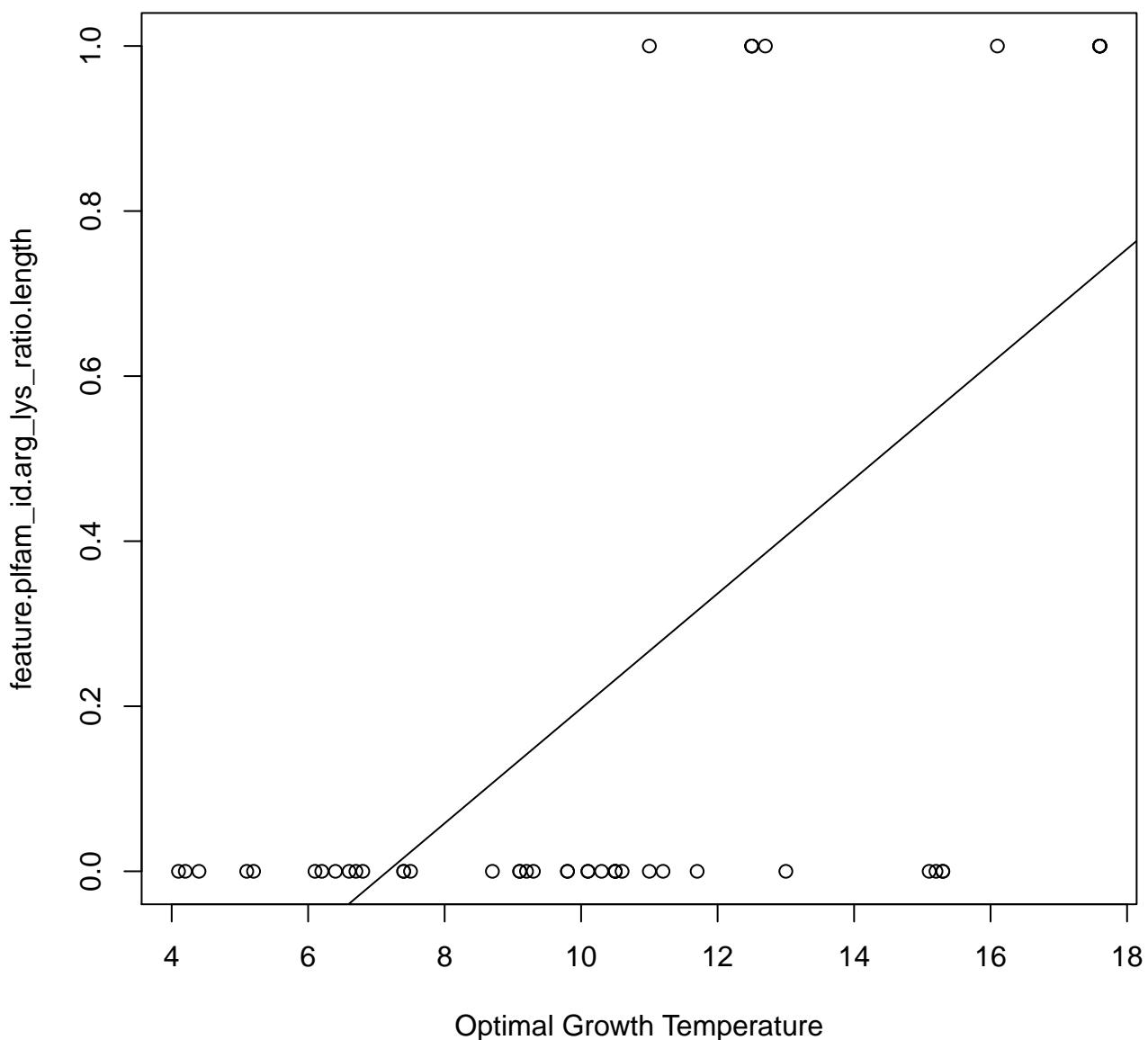
feature_pfam_id.arg_lys_ratio.length
PLF_28228_00000837
Flagellar hook-length control protein FliK



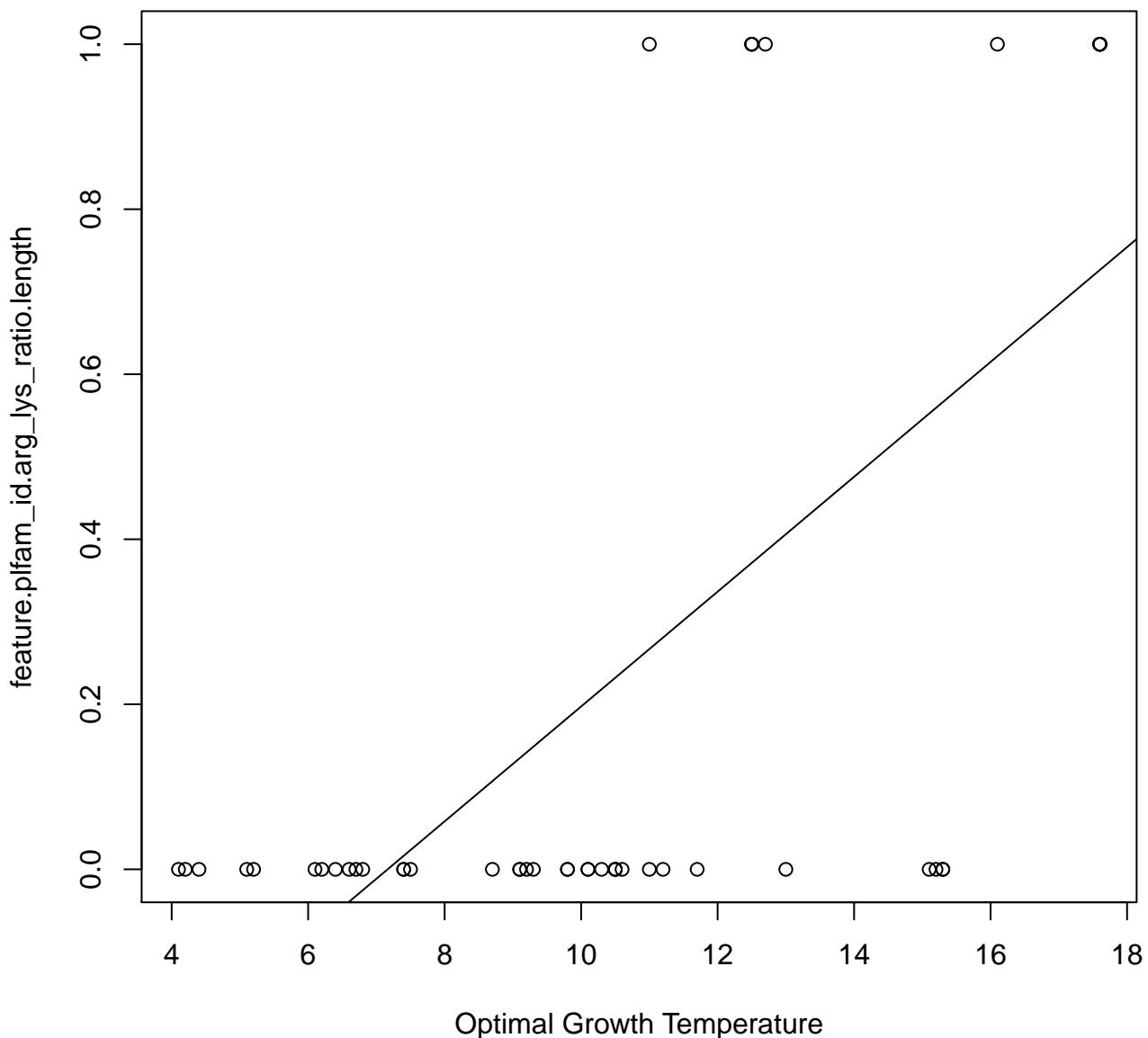
feature_pfam_id.arg_lyc_ratio.length
PLF_28228_00001679
Cell division protein



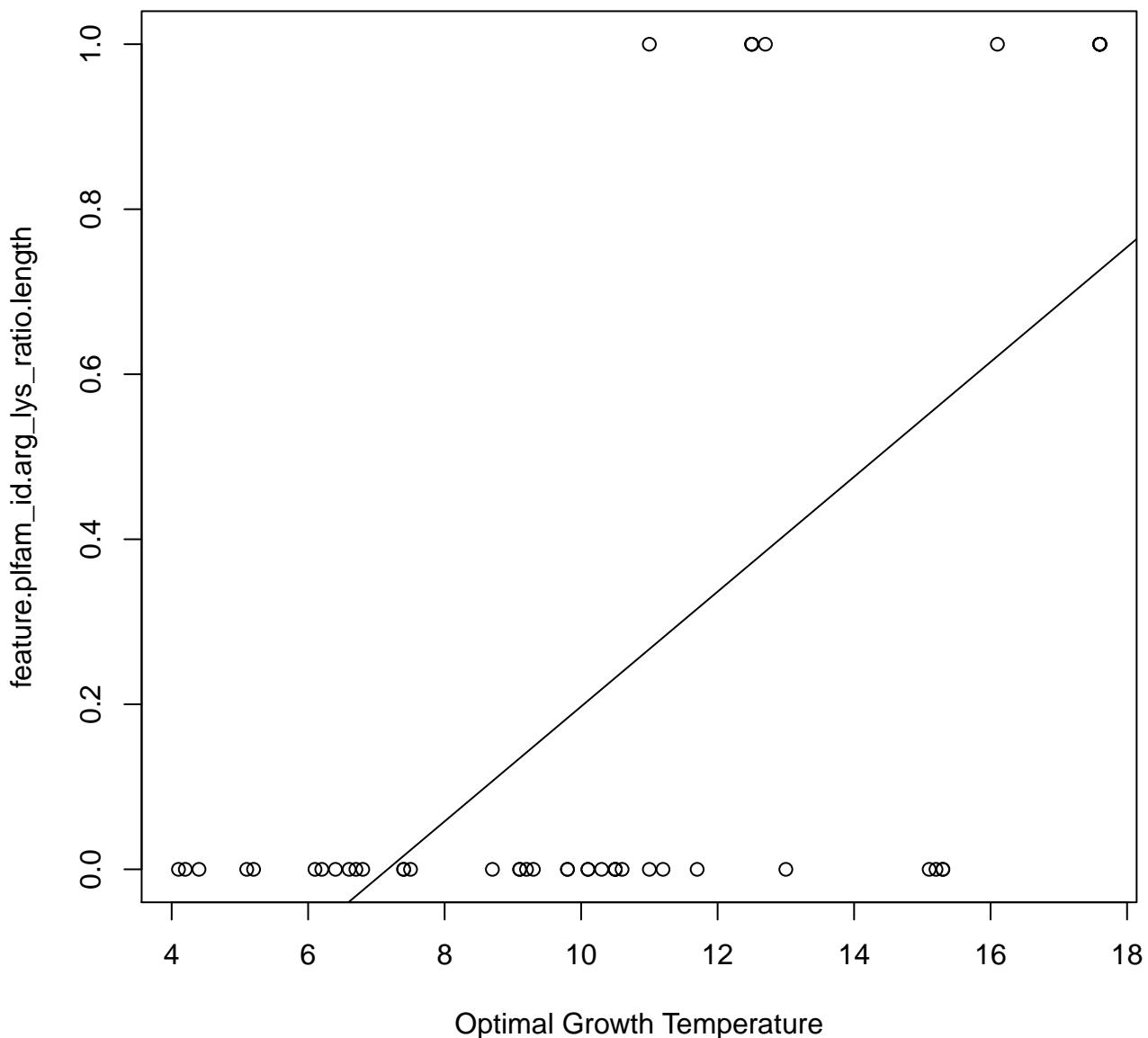
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002208
YebG, DNA damage-inducible gene in SOS regulon, expressed in stationary phase



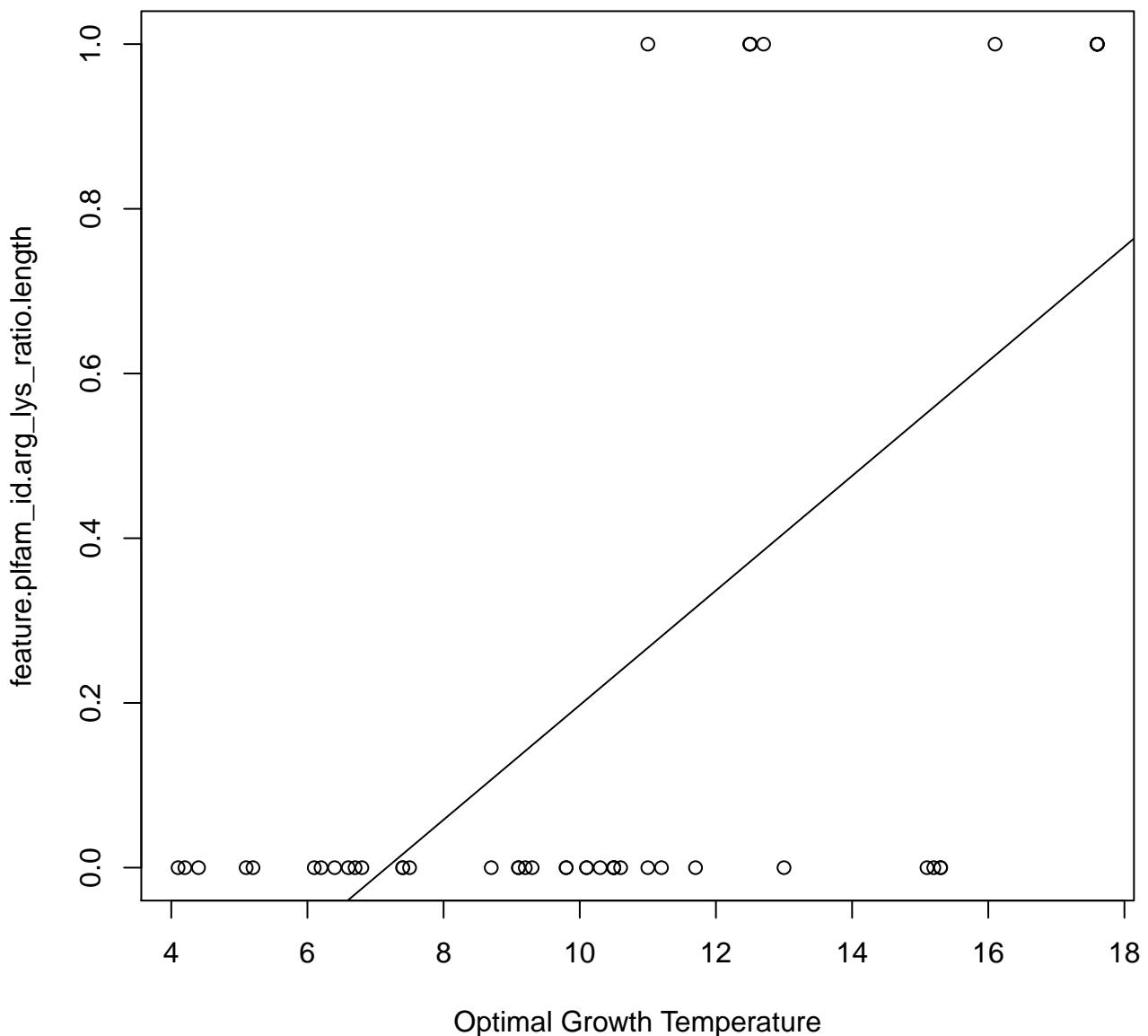
feature_pfam_id_arg_lyc_ratio_length
PLF_28228_00002326
hypothetical protein



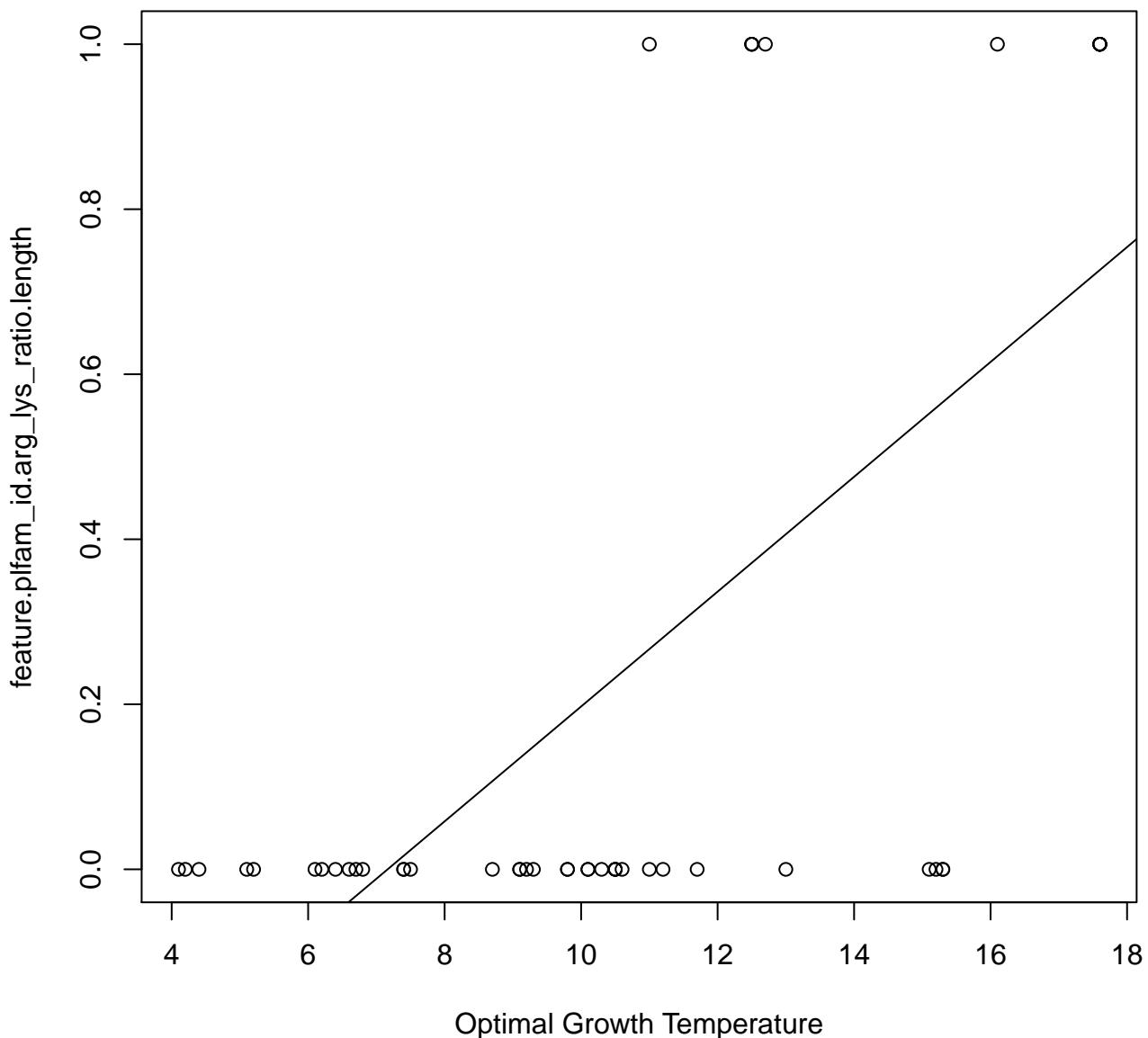
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PLF_28228_00002398
hypothetical protein



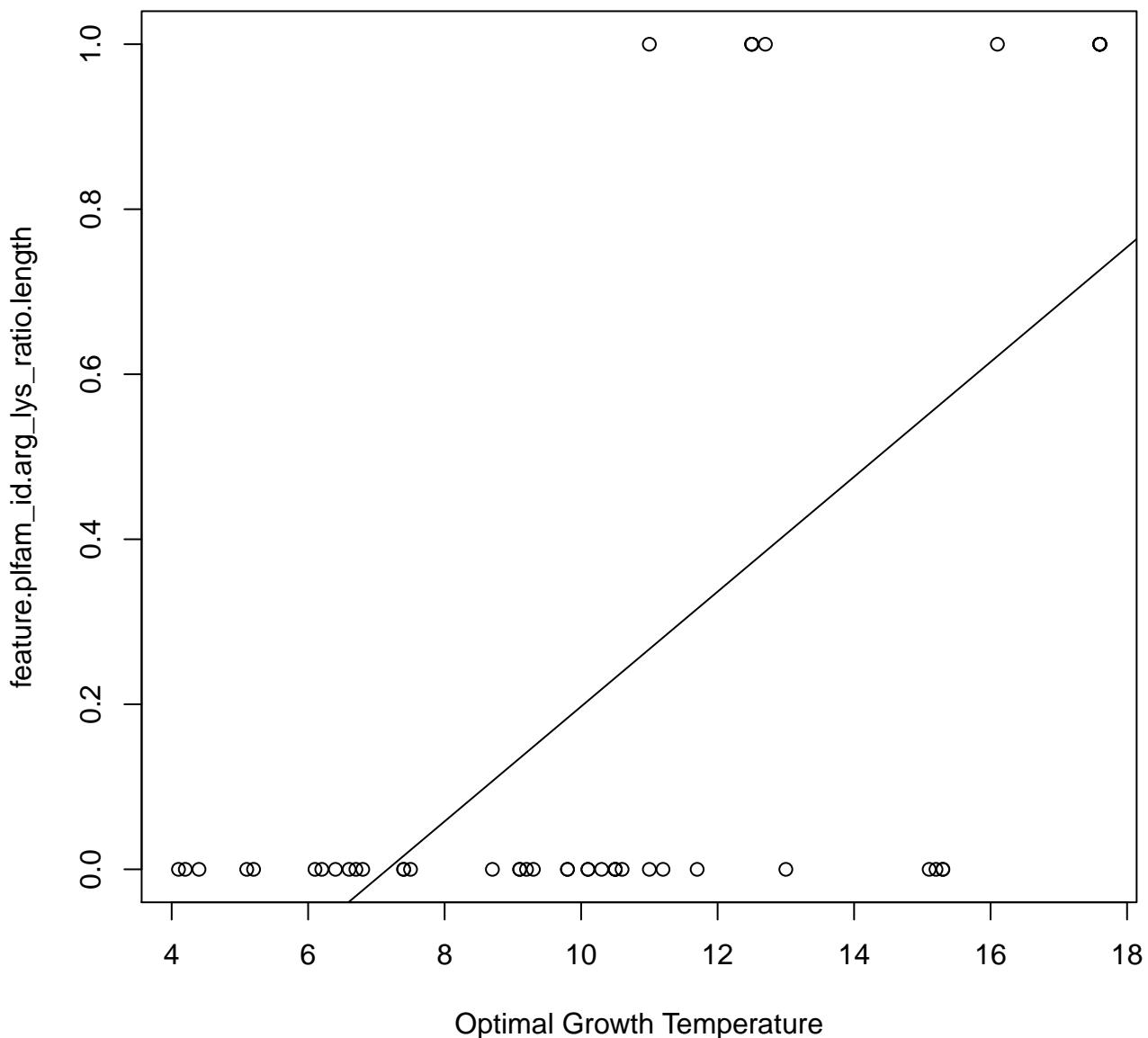
feature_pfam_id_arg_lyc_ratio_length
PLF_28228_00002443
hypothetical protein



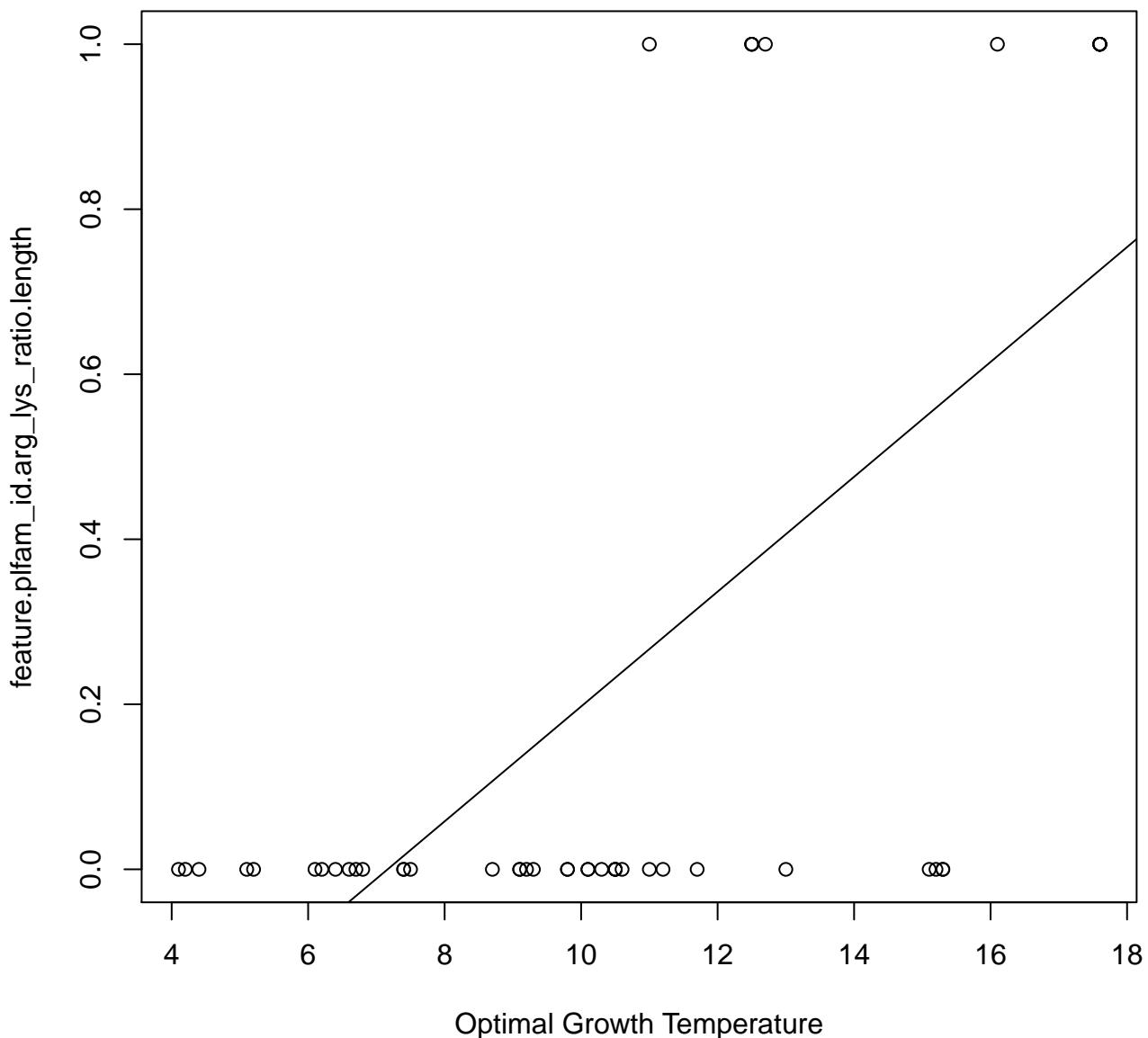
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PLF_28228_00002464
hypothetical protein



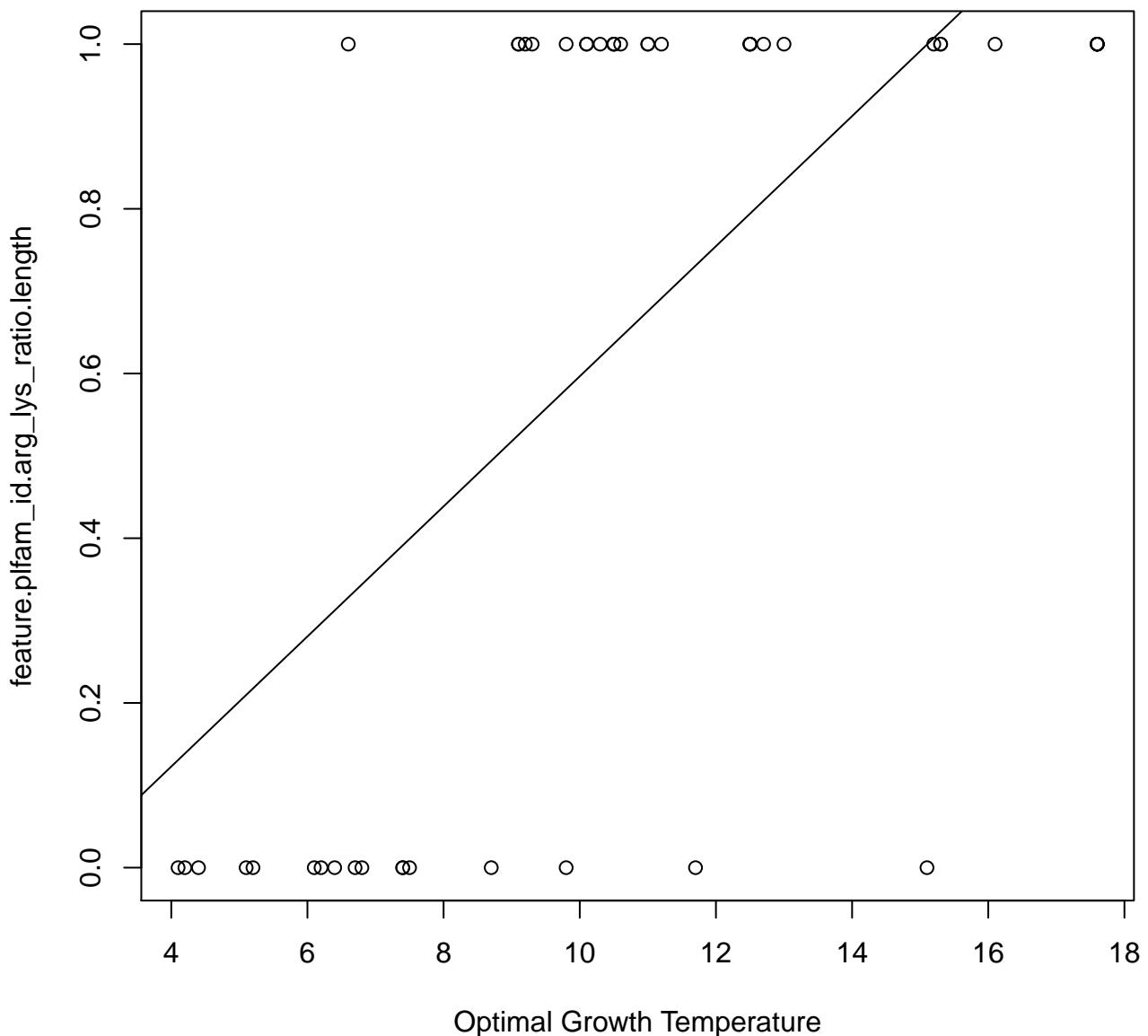
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PLF_28228_00002474
hypothetical protein



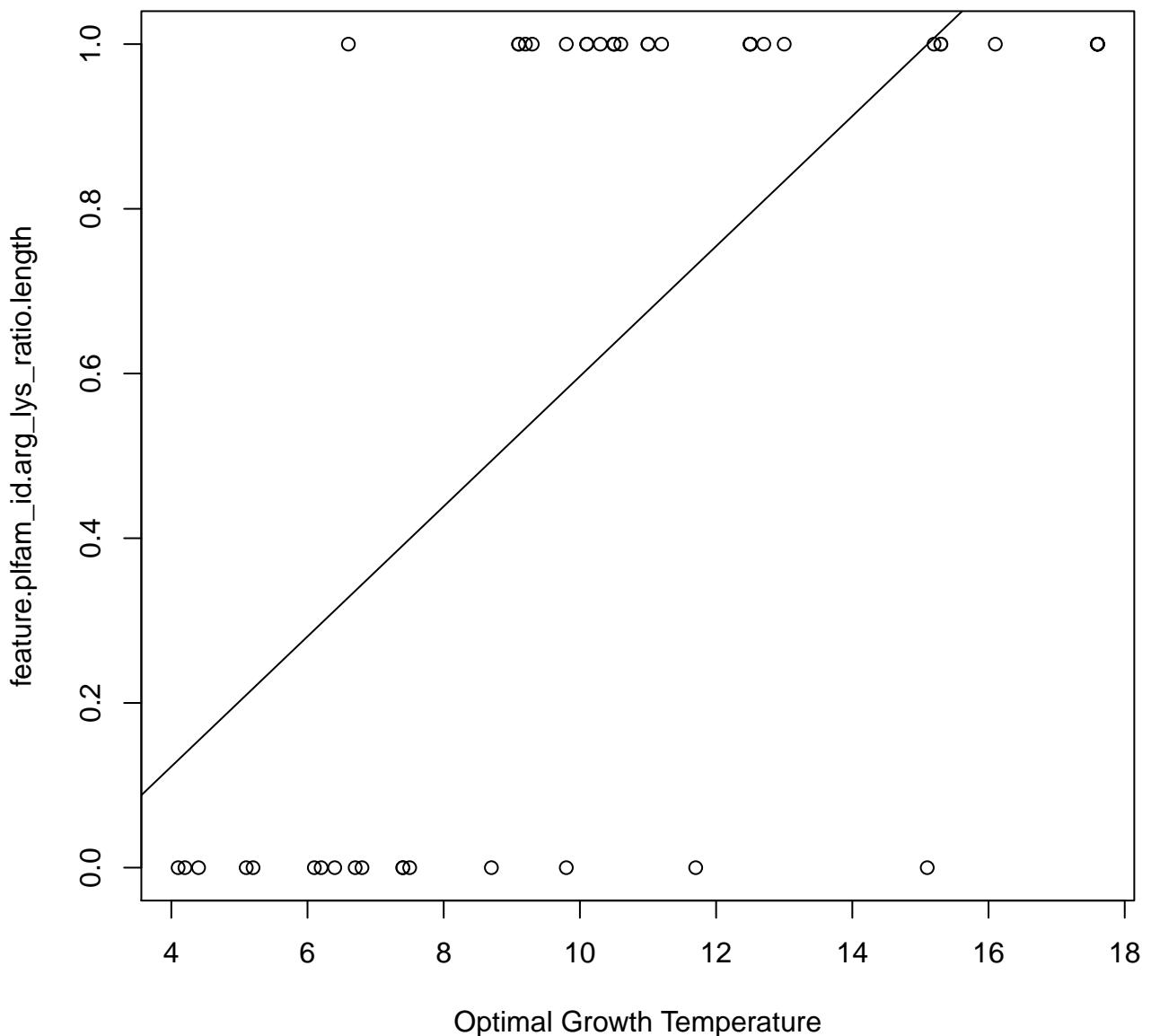
feature_pfam_id.arg_lyc_ratio.length
PLF_28228_00002517
major outer membrane lipoprotein, putative



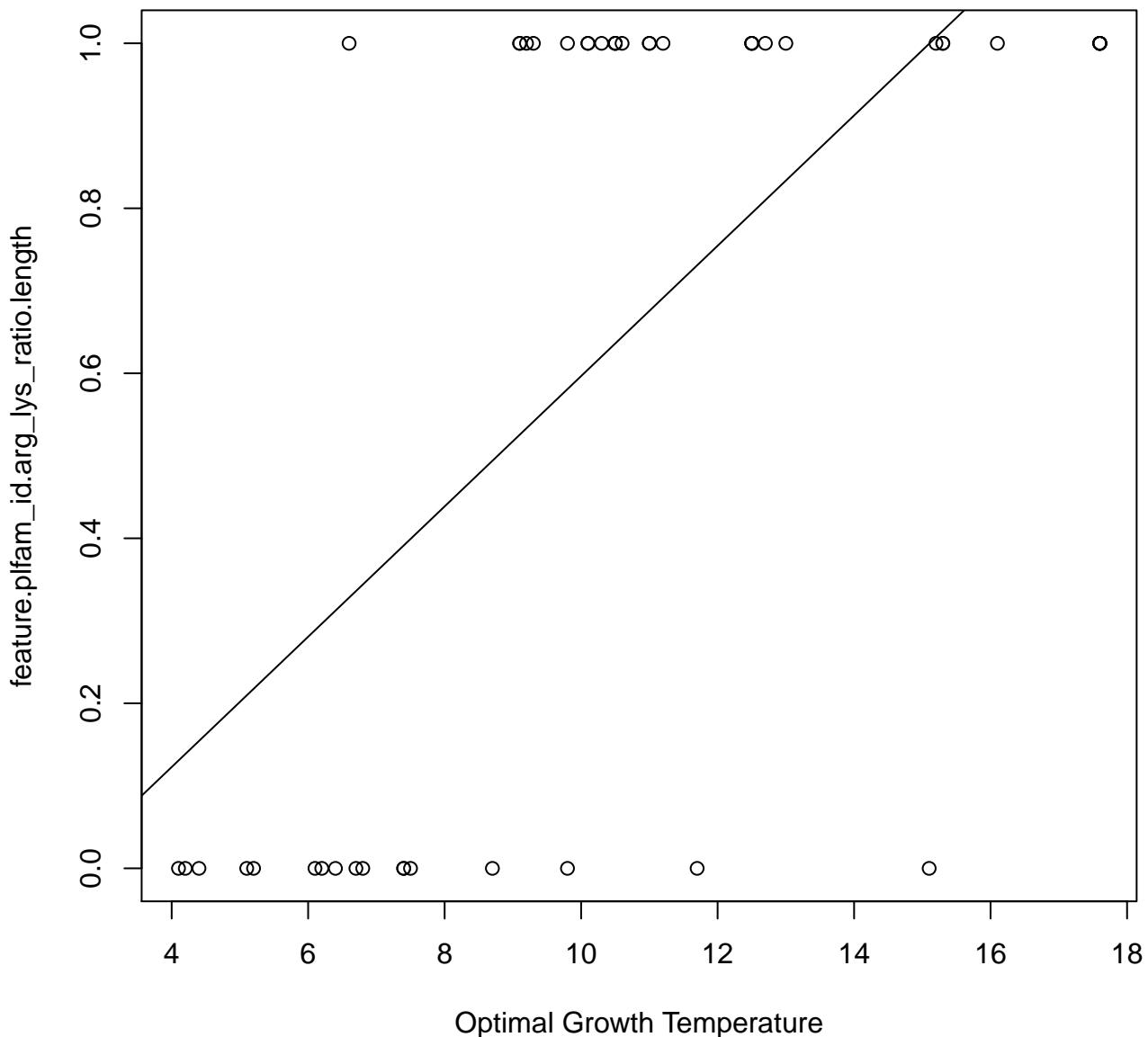
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00001431
Acyltransferase



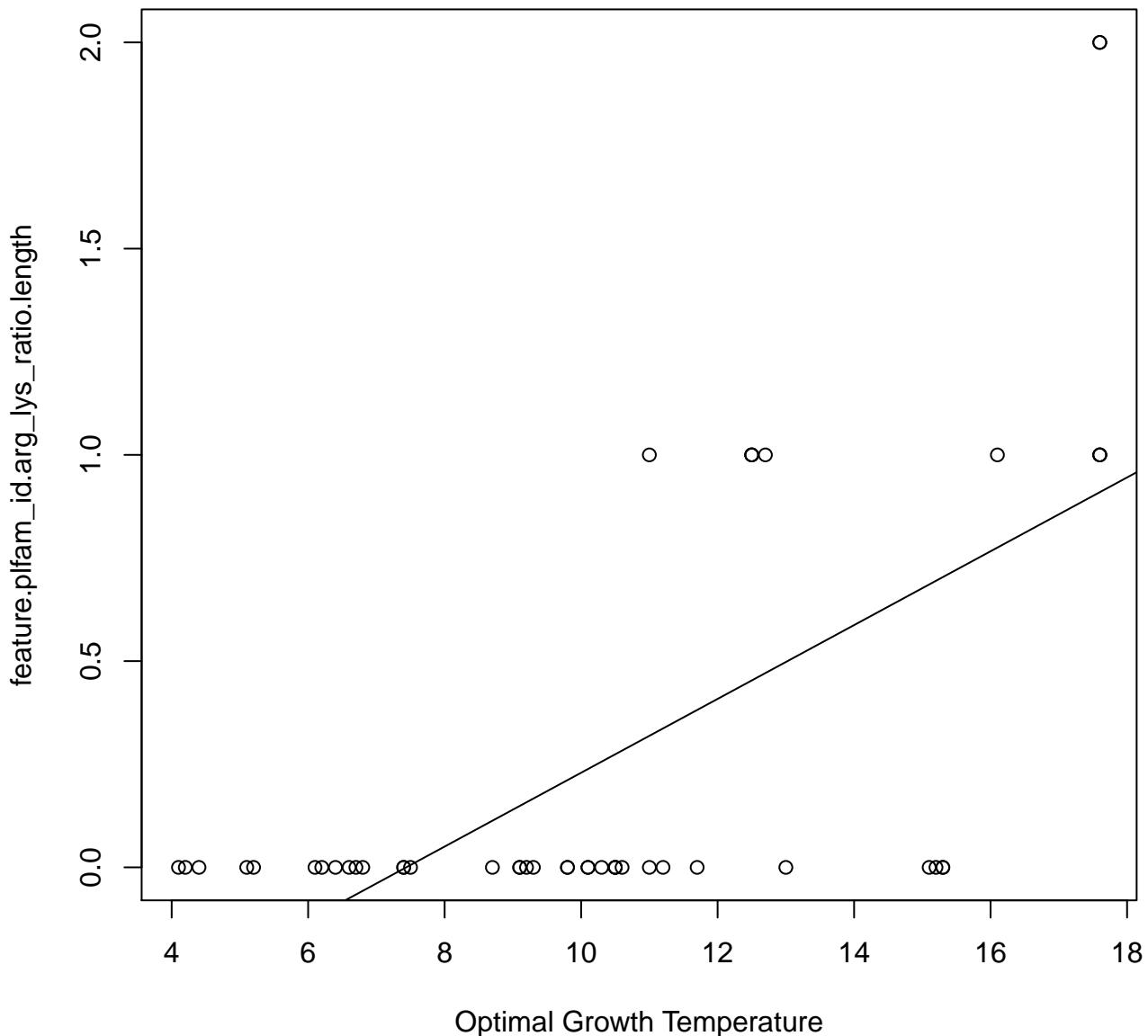
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00001492
Enoyl-CoA hydratase (EC 4.2.1.17)



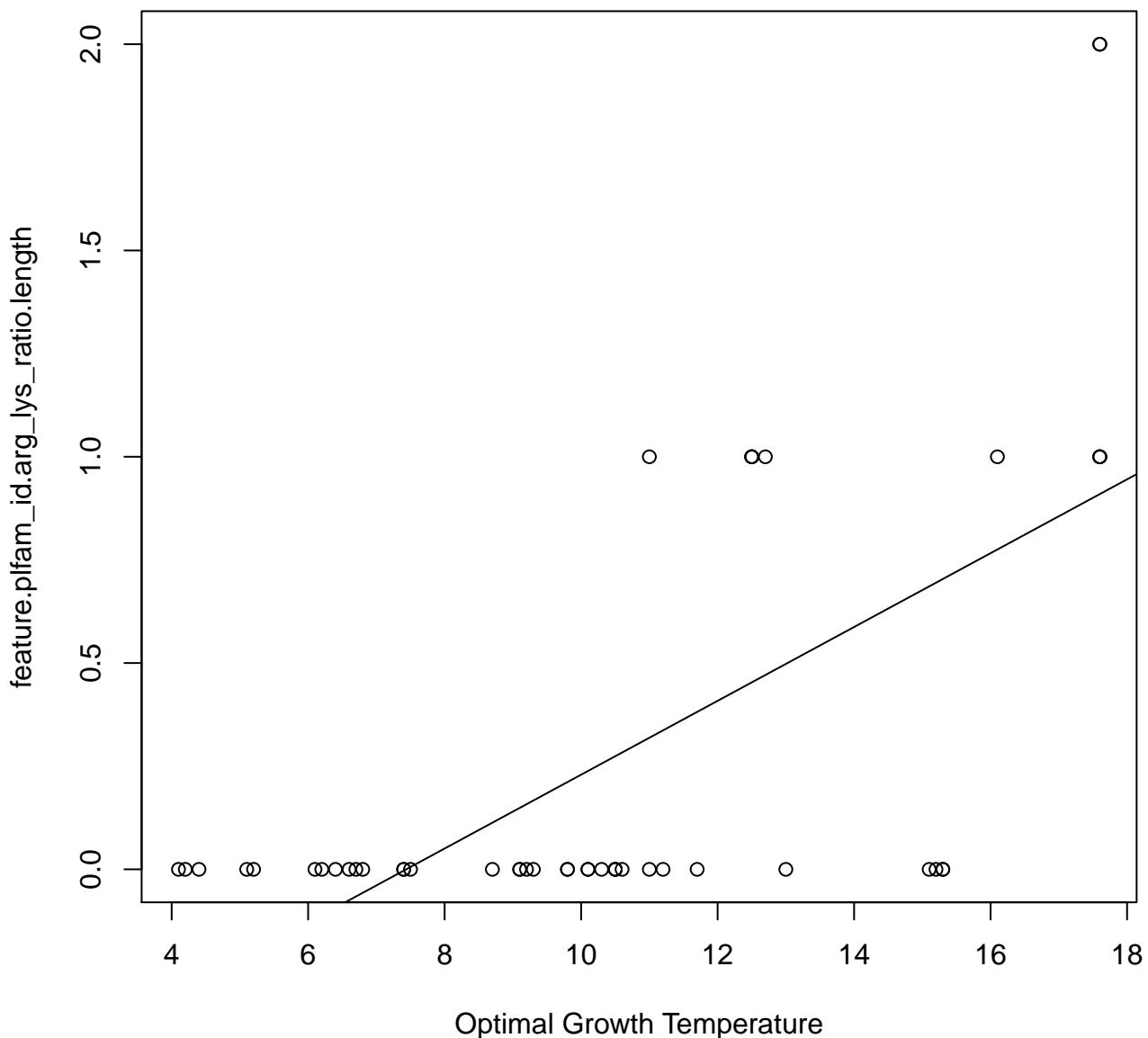
feature.plfam_id.arg_lyc_ratio.length
PLF_28228_00001694
Chorismate--pyruvate lyase (EC 4.1.3.40)



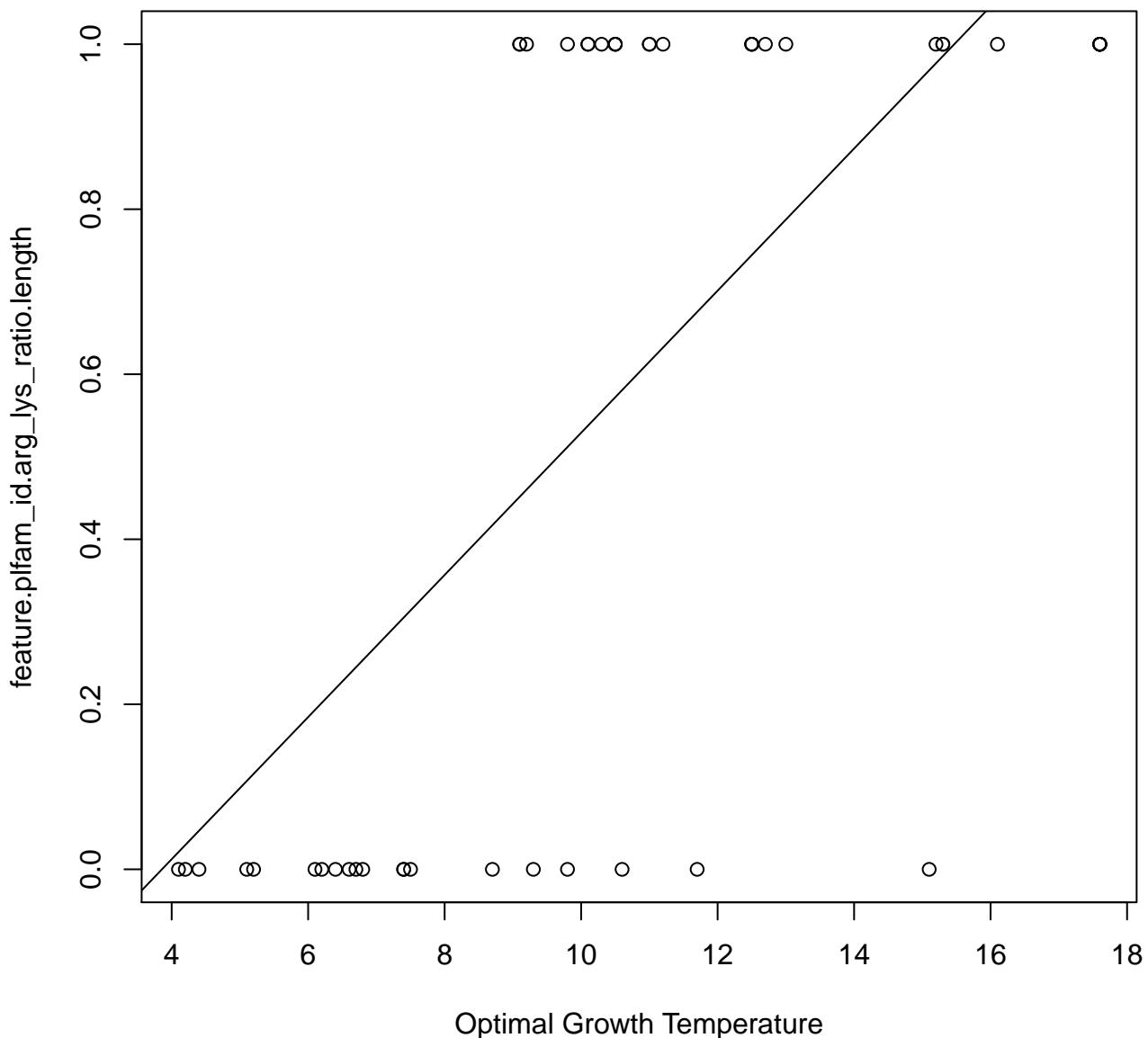
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00001316
dNTP triphosphohydrolase, broad substrate specificity



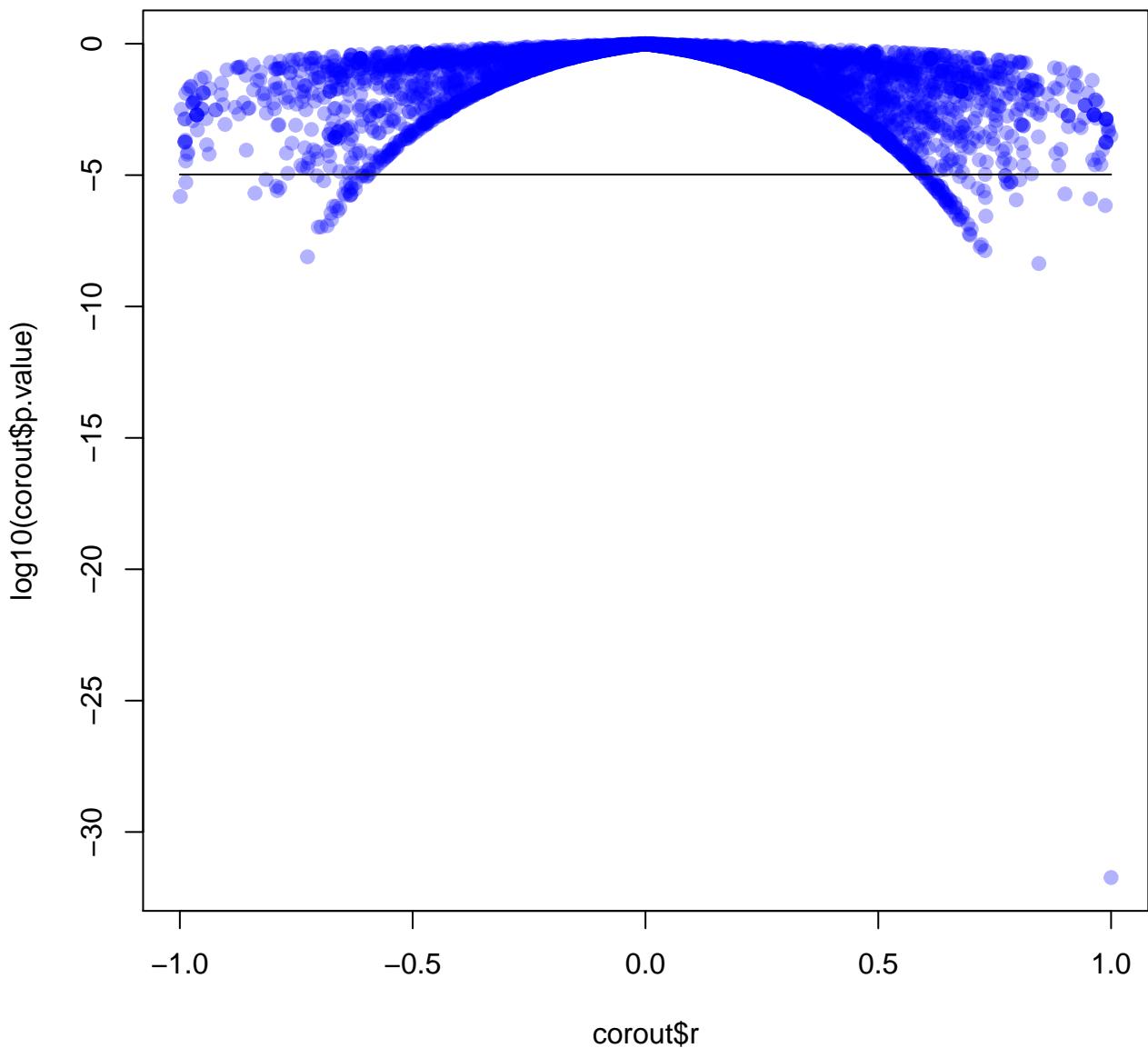
feature.pfam_id.arg_lyc_ratio.length
PLF_28228_00001327
hypothetical protein



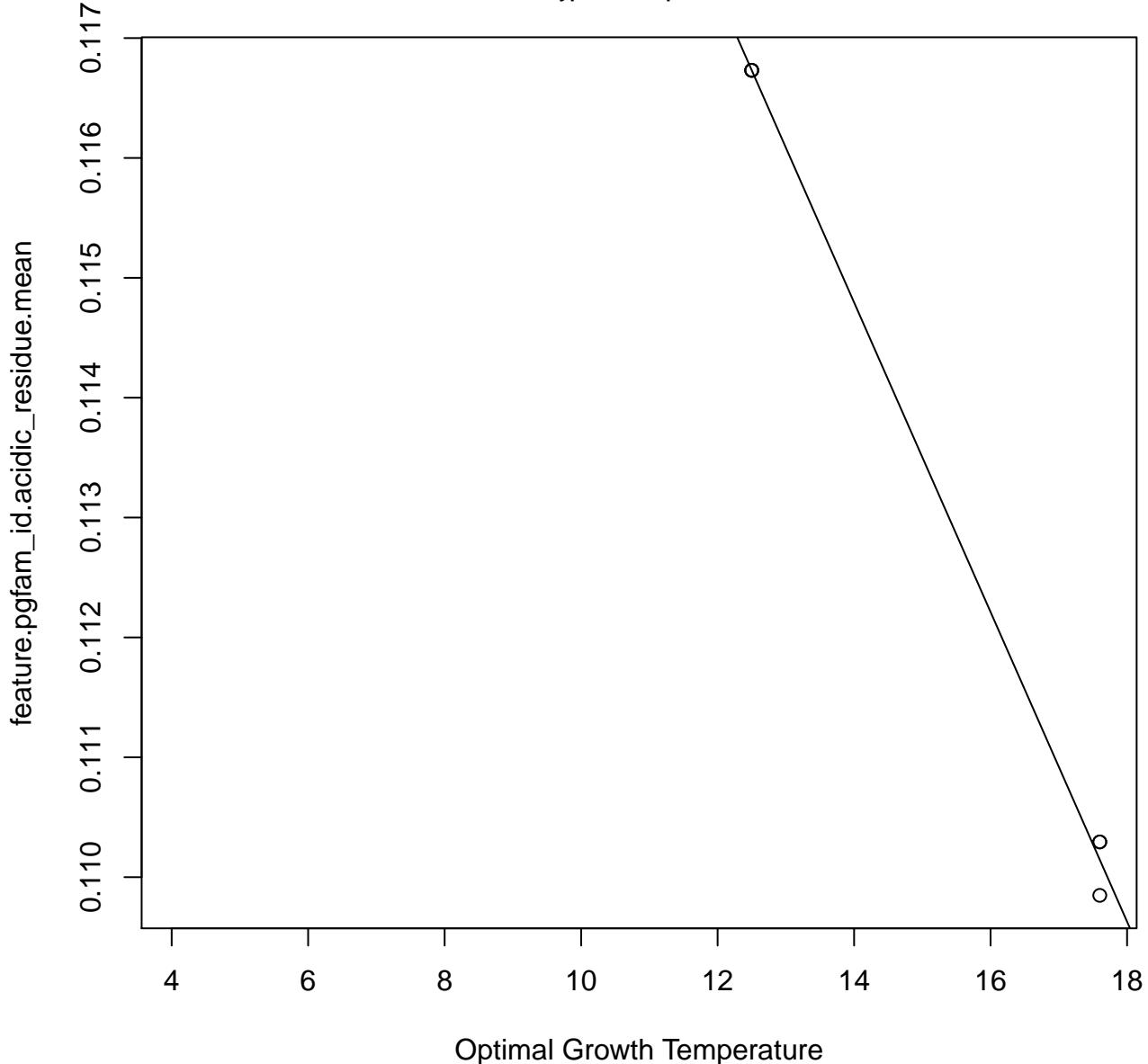
feature_pfam_id.arg_lyc_ratio.length
PLF_28228_00000882
General secretion pathway protein L



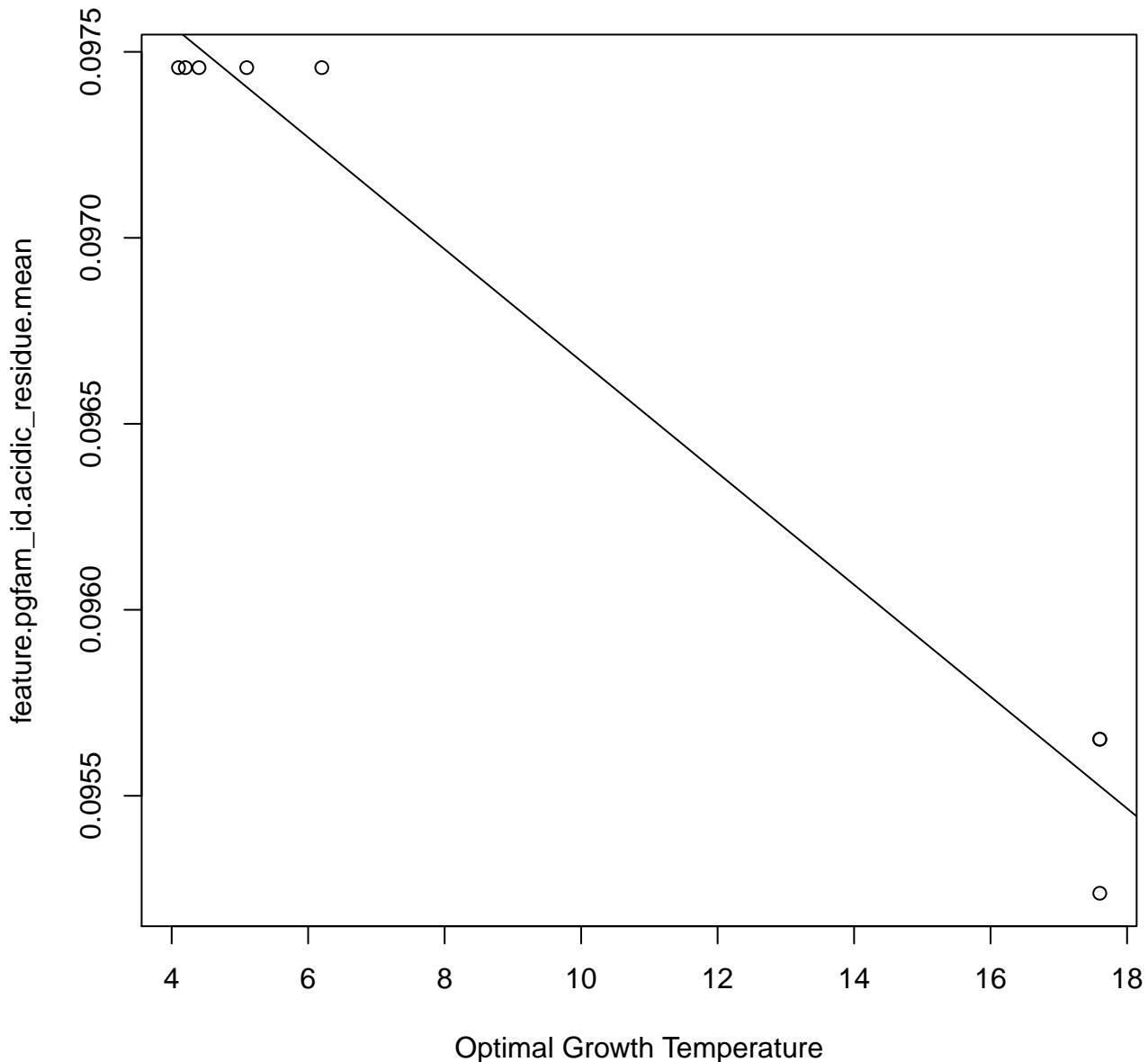
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feature.pgfam_id.acidic_residue.mean
PGF_01336907
hypothetical protein



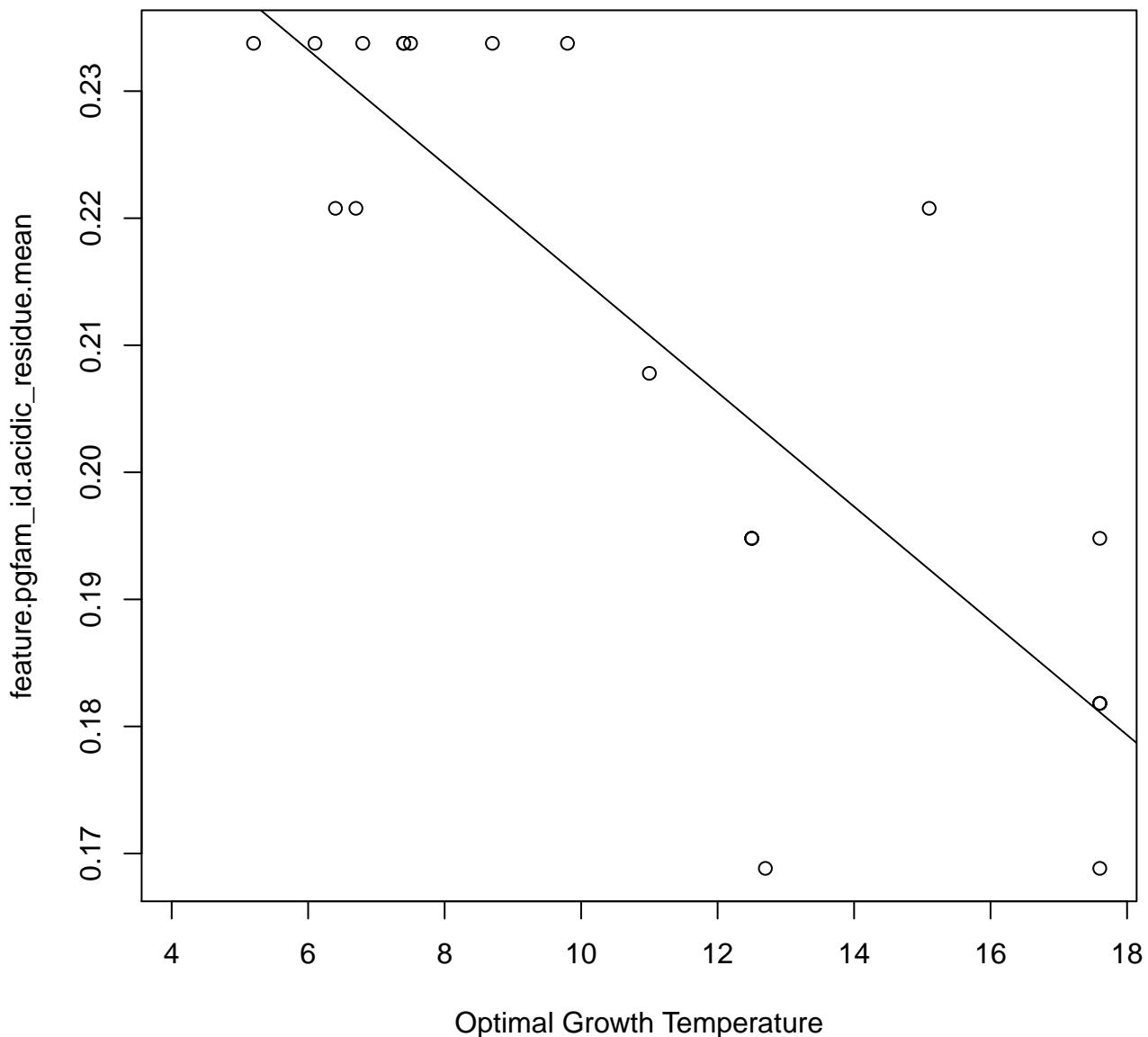
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PGF_01336811
hypothetical protein



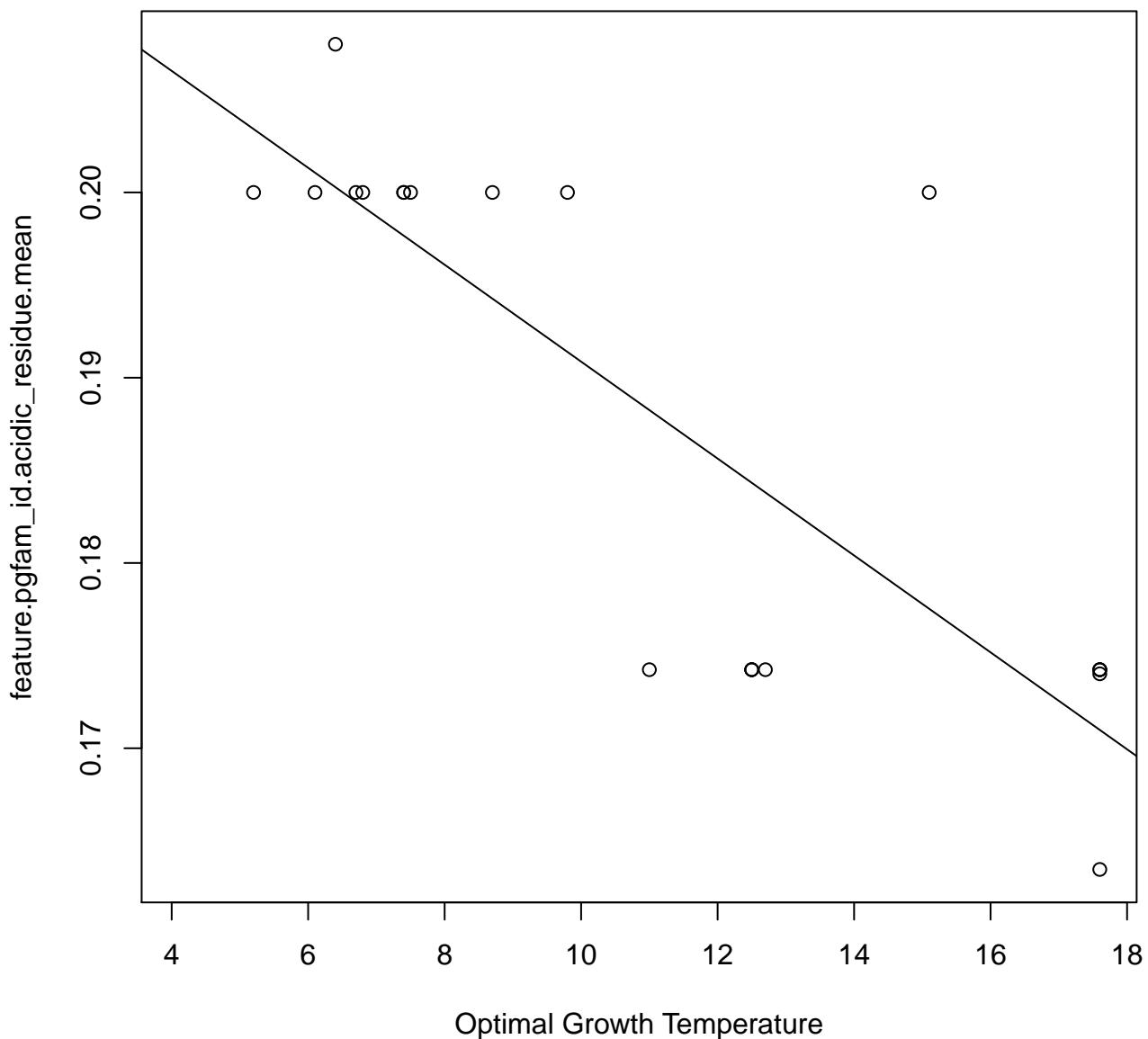
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PGF_01336293

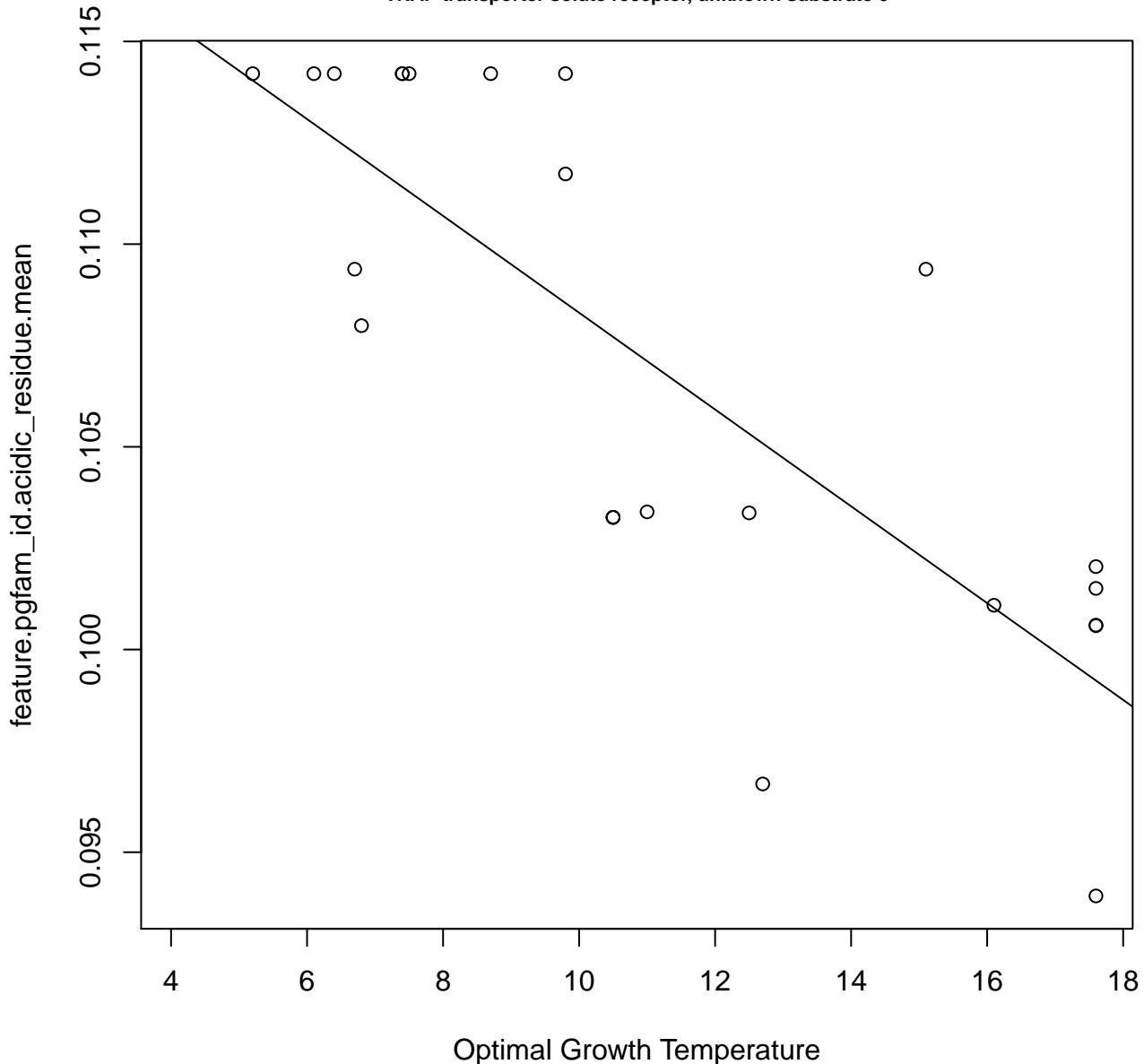
FIG034389 (not subsystem-based): hypothetical protein



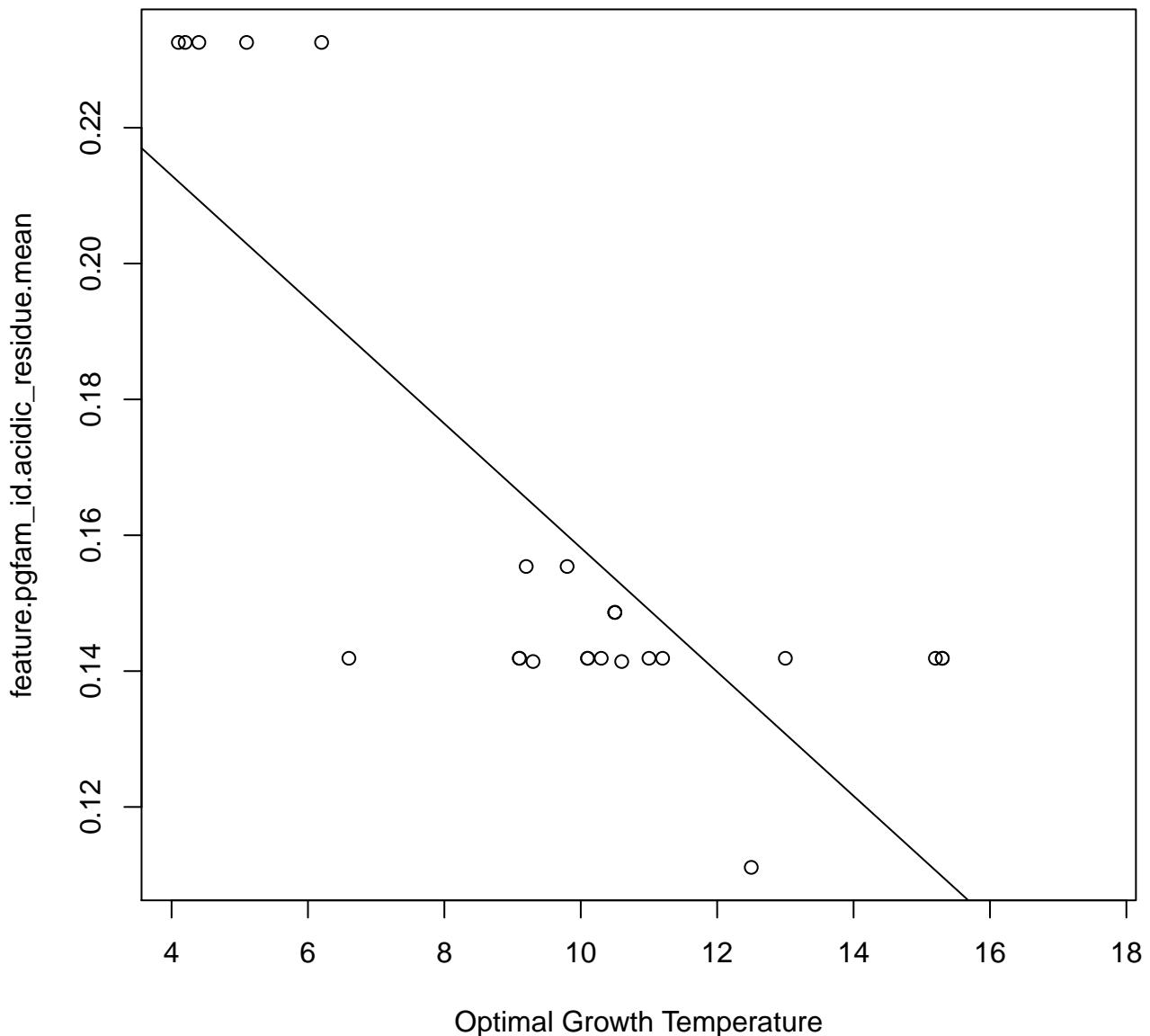
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PGF_01336479
hypothetical protein



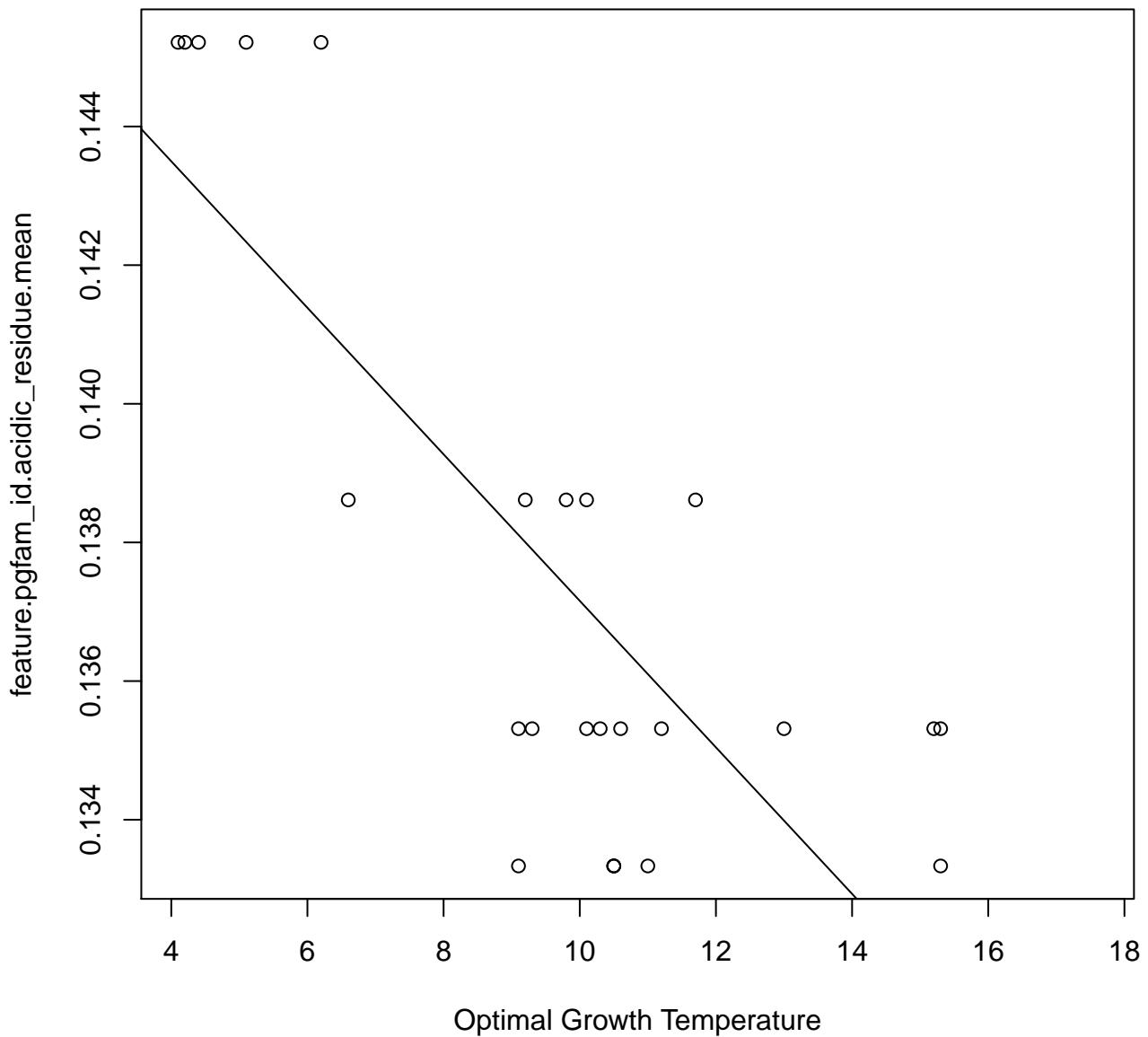
feature.pgfam_id.acidic_residue.mean
PGF_09209650
TRAP transporter solute receptor, unknown substrate 6



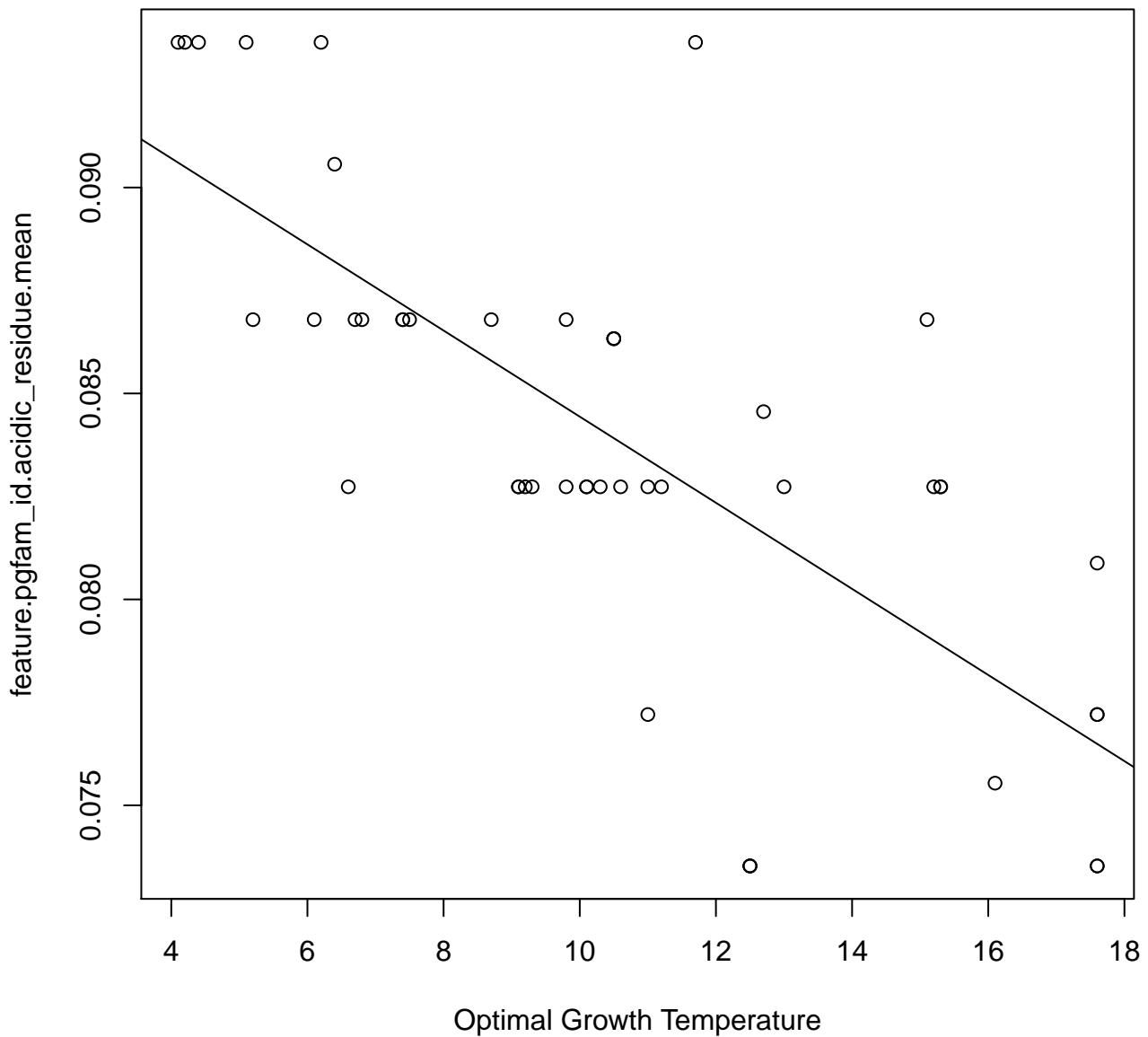
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PGF_06792096
hypothetical protein



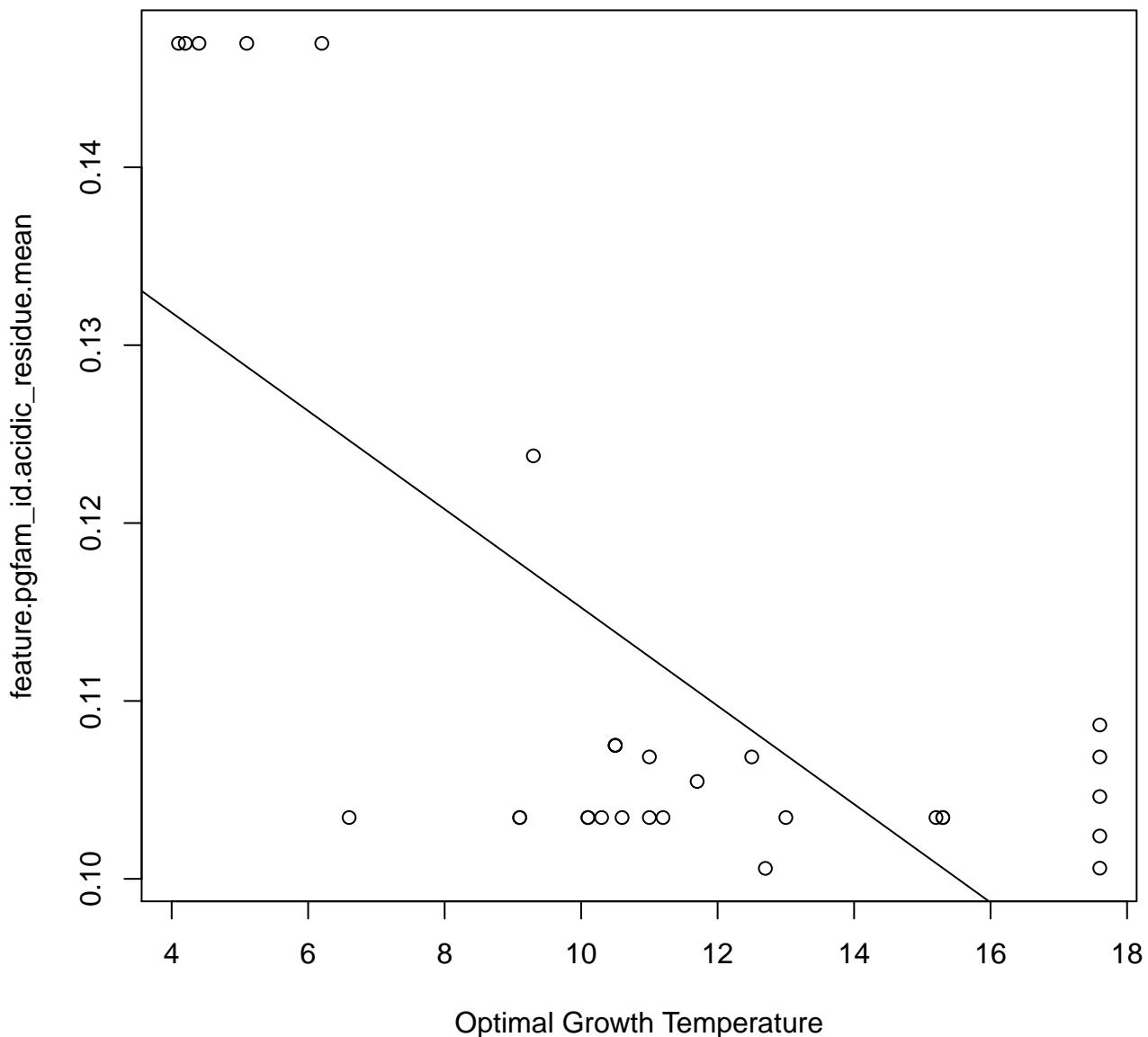
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PGF_12817314
hypothetical protein



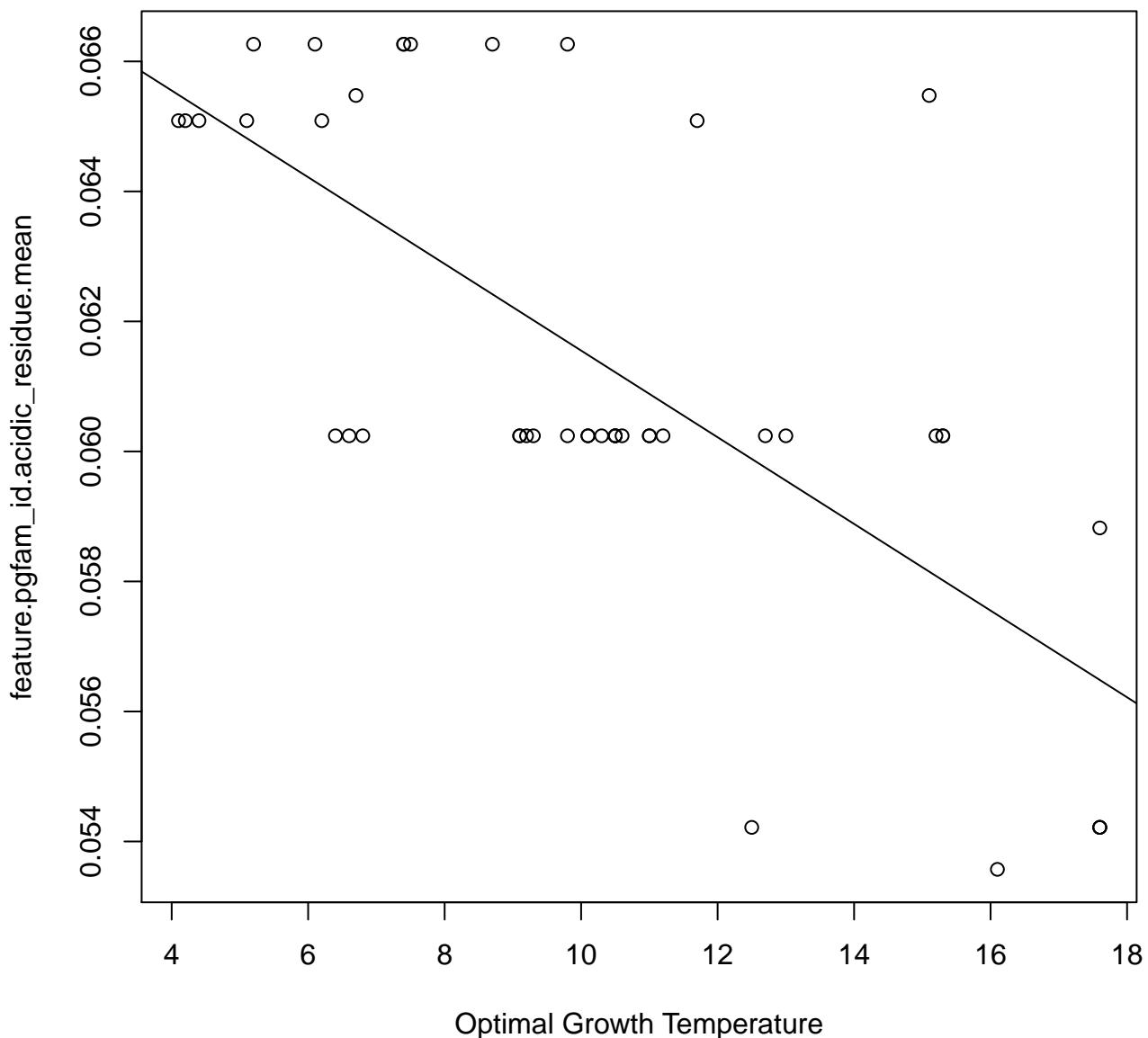
feature.pgfam_id.acidic_residue.mean
PGF_00048554
Caulimovirus viroplasmin / Ribonuclease HI (EC 3.1.26.4)



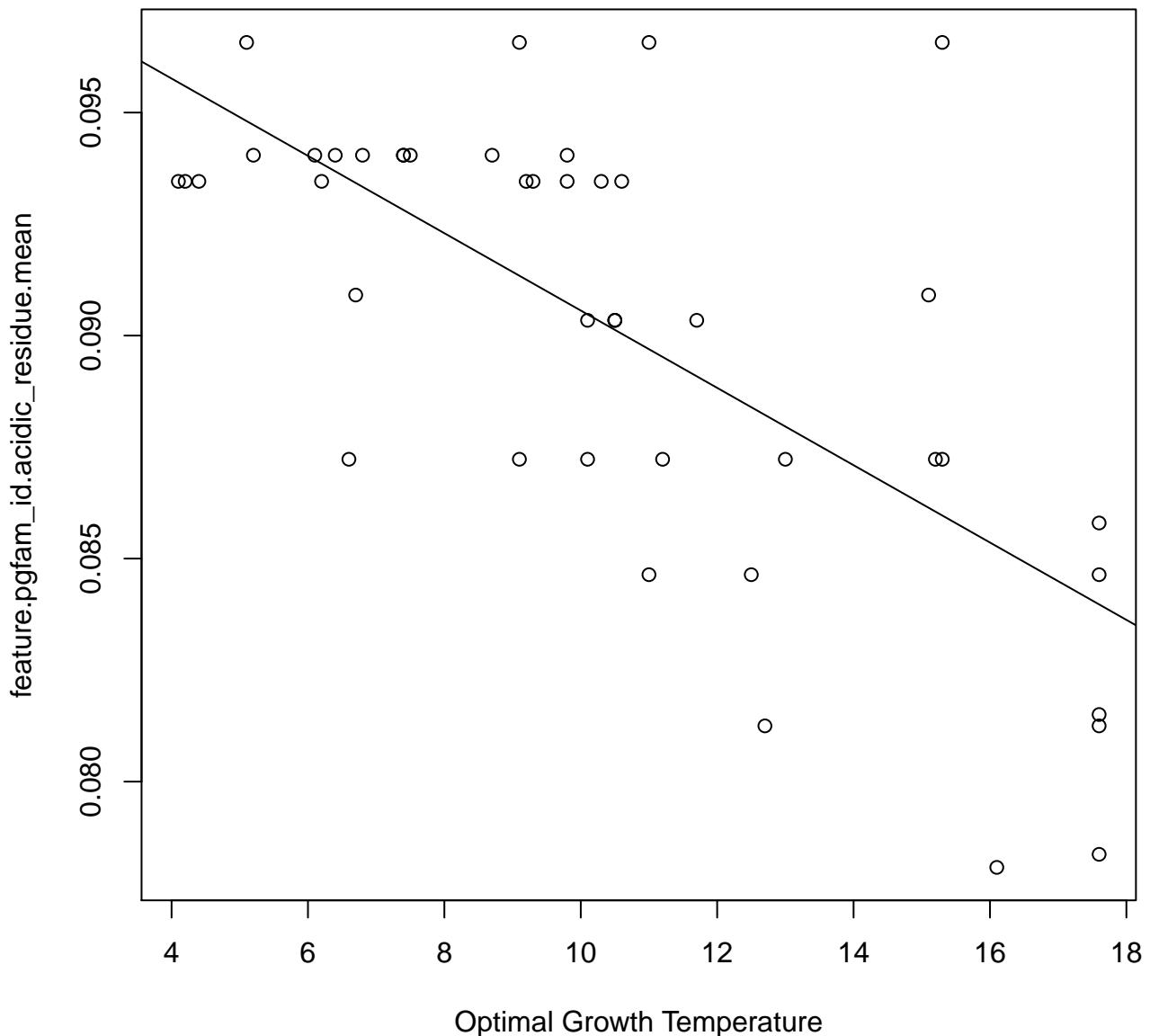
feature.pgfam_id.acidic_residue.mean
PGF_12765299
Two-component system sensor histidine kinase



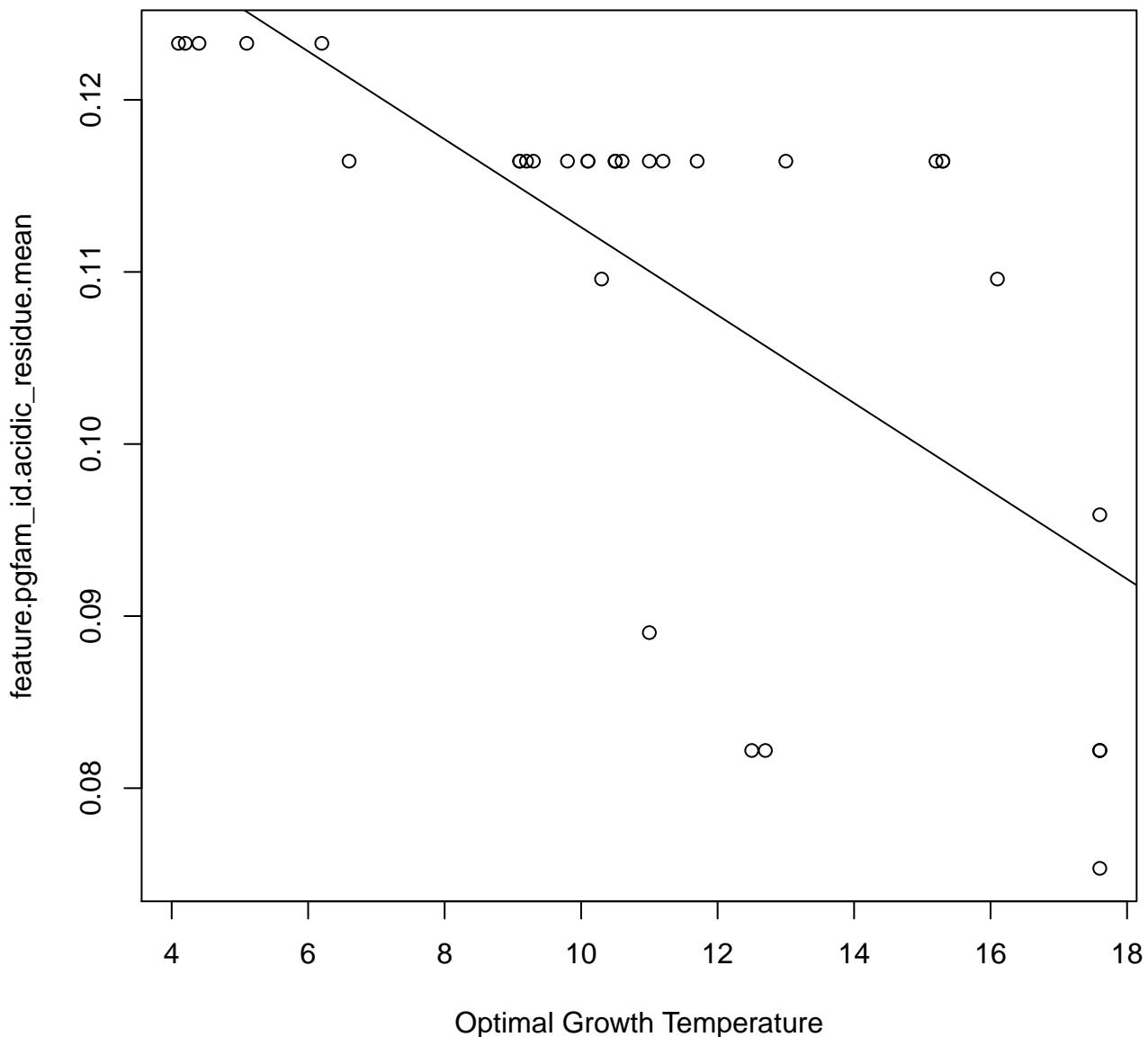
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PGF_03073036
hypothetical protein



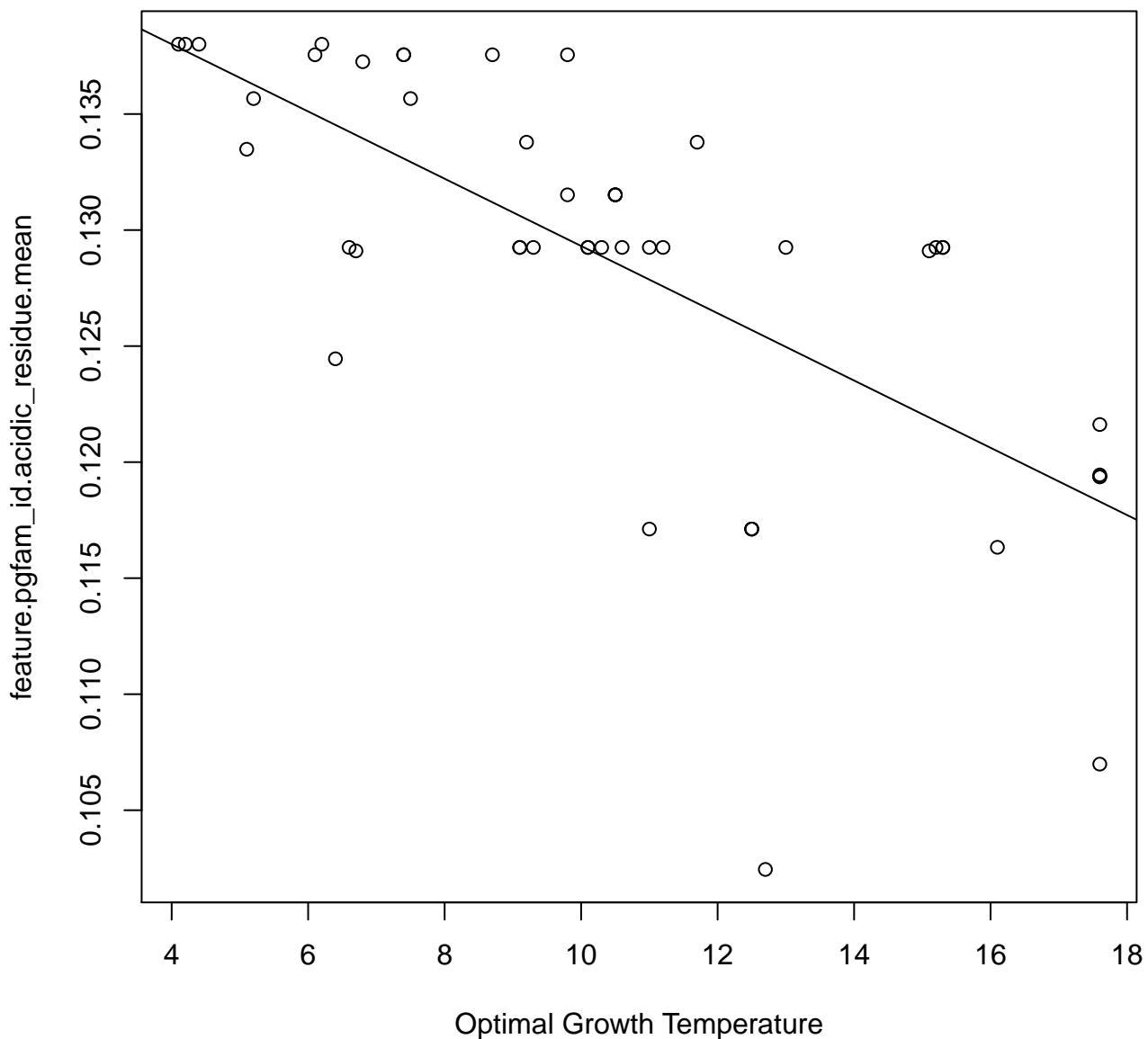
feature.pgfbam_id.acidic_residue.mean
PGF_07668761
Phosphate ABC transporter, substrate-binding protein PstS (TC 3.A.1.7.1)



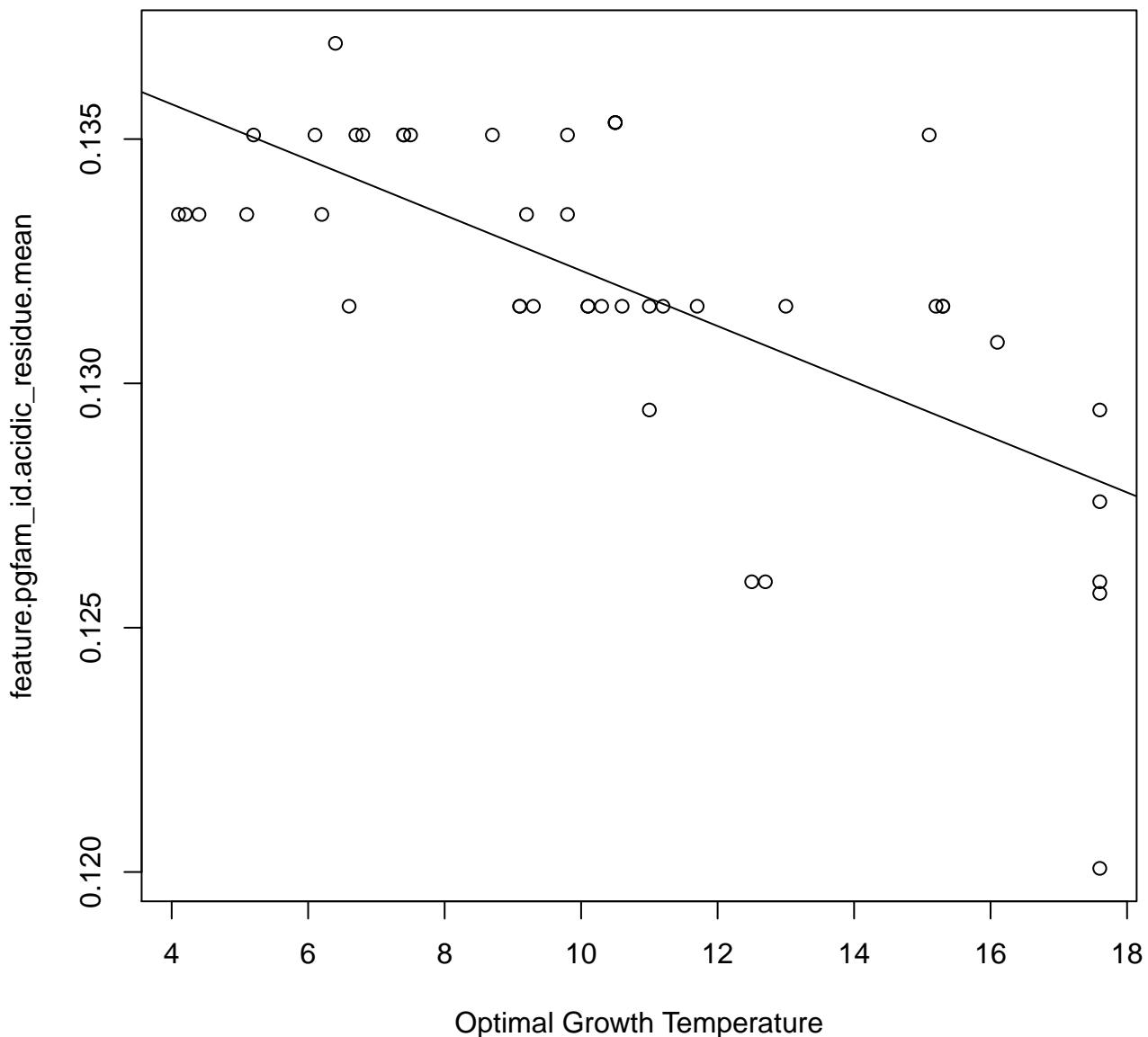
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PGF_03761381
FIG003551: hypothetical protein



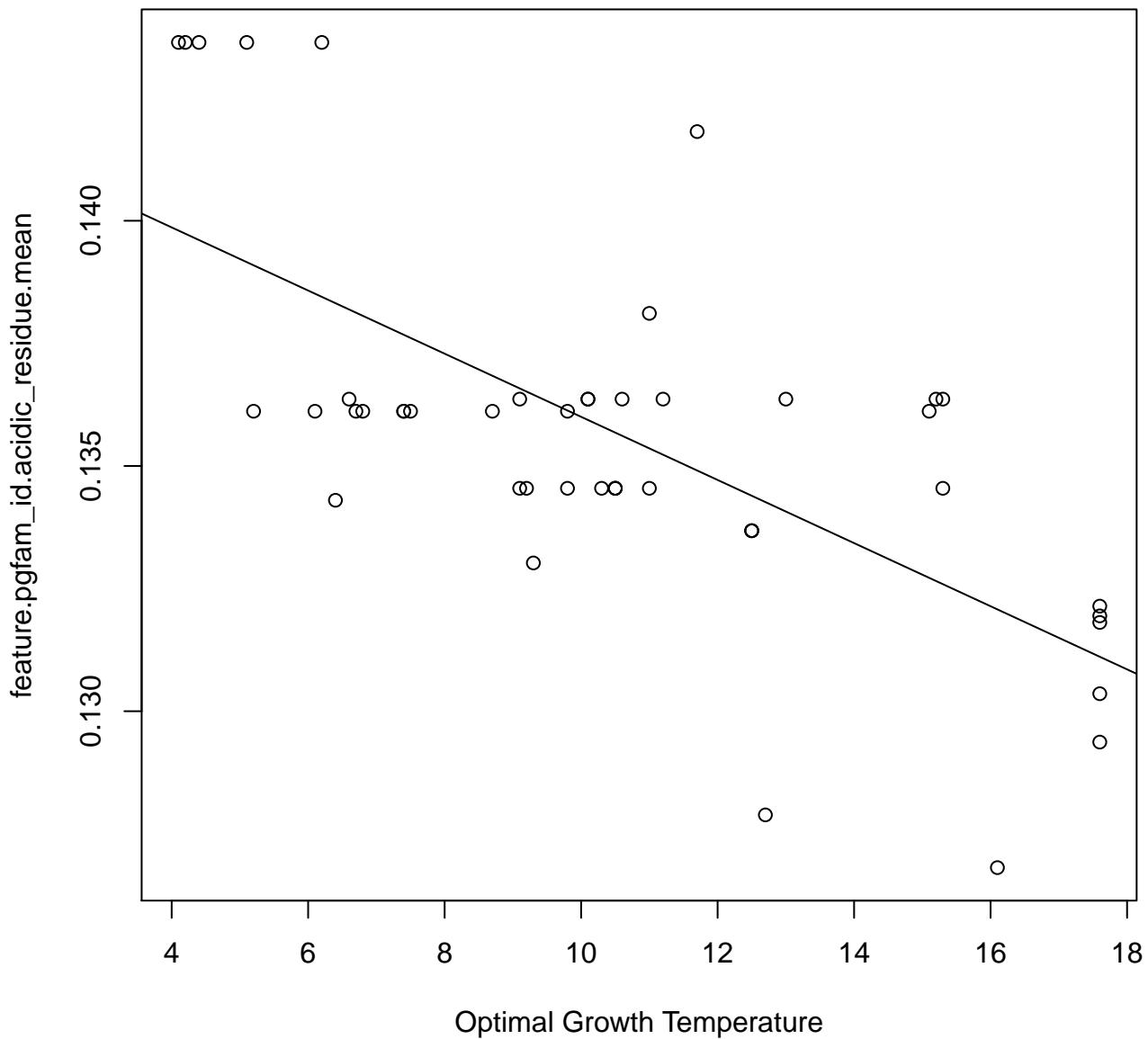
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PGF_03336368
hypothetical protein



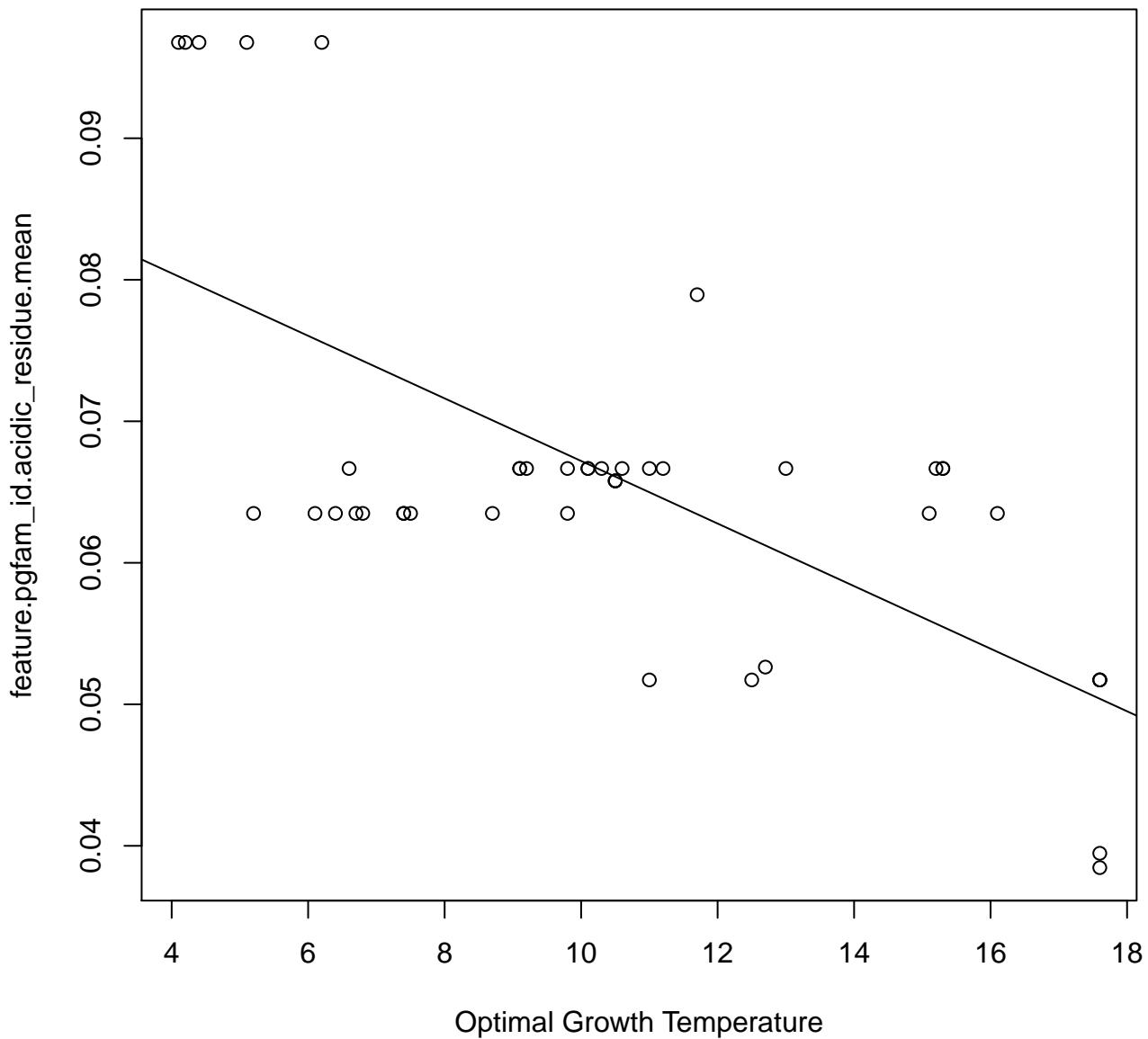
feature.pgfam_id.acidic_residue.mean
PGF_07459509
L-aspartate oxidase (EC 1.4.3.16)



feature.pgfam_id.acidic_residue.mean
PGF_00026525
Nudix hydrolase 3 (EC 3.6.1.-)



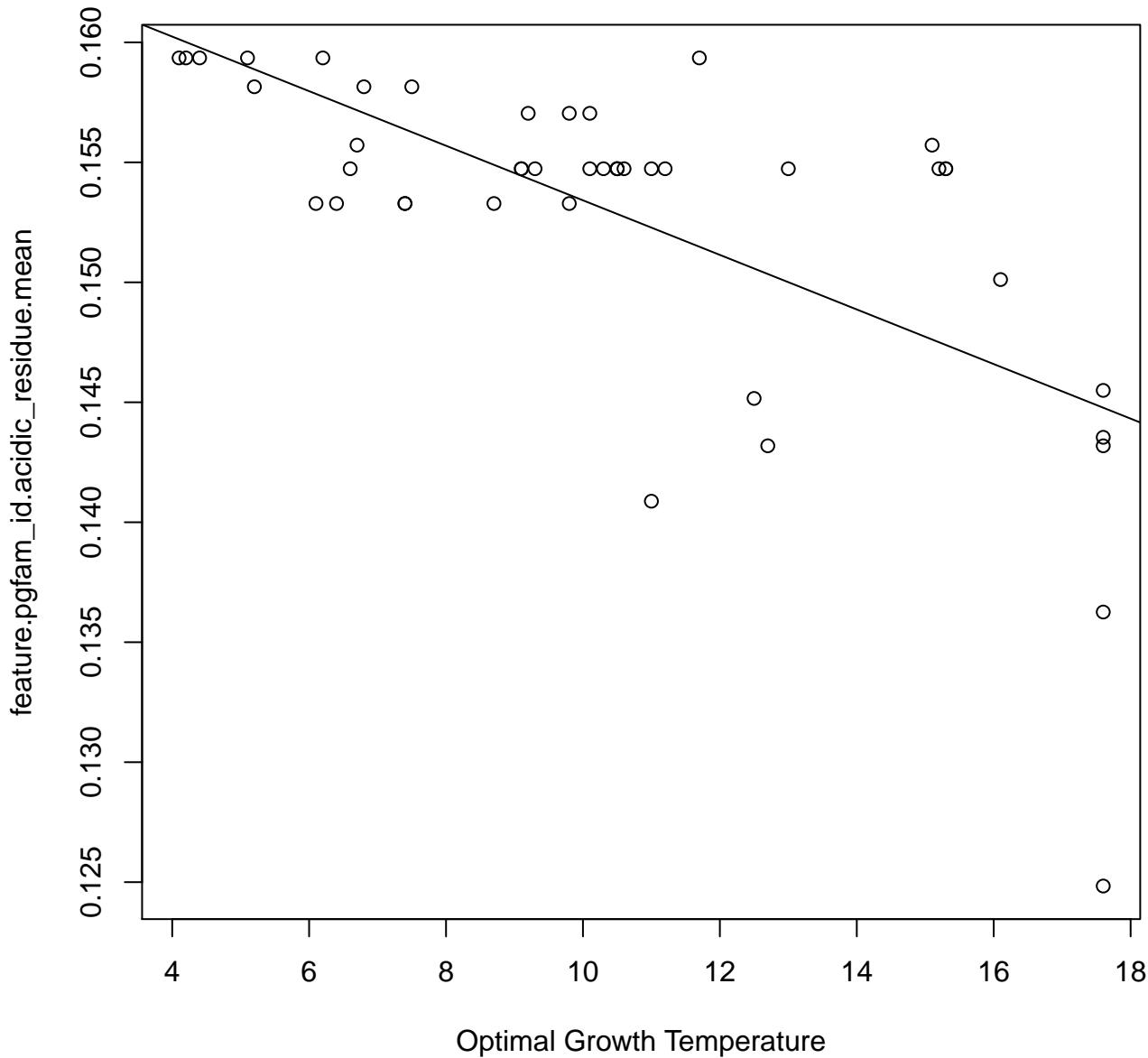
feature.pgfam_id.acidic_residue.mean
PGF_01415873
Uncharacterized membrane protein SO_0290



feature.pgfam_id.acidic_residue.mean

PGF_07075462

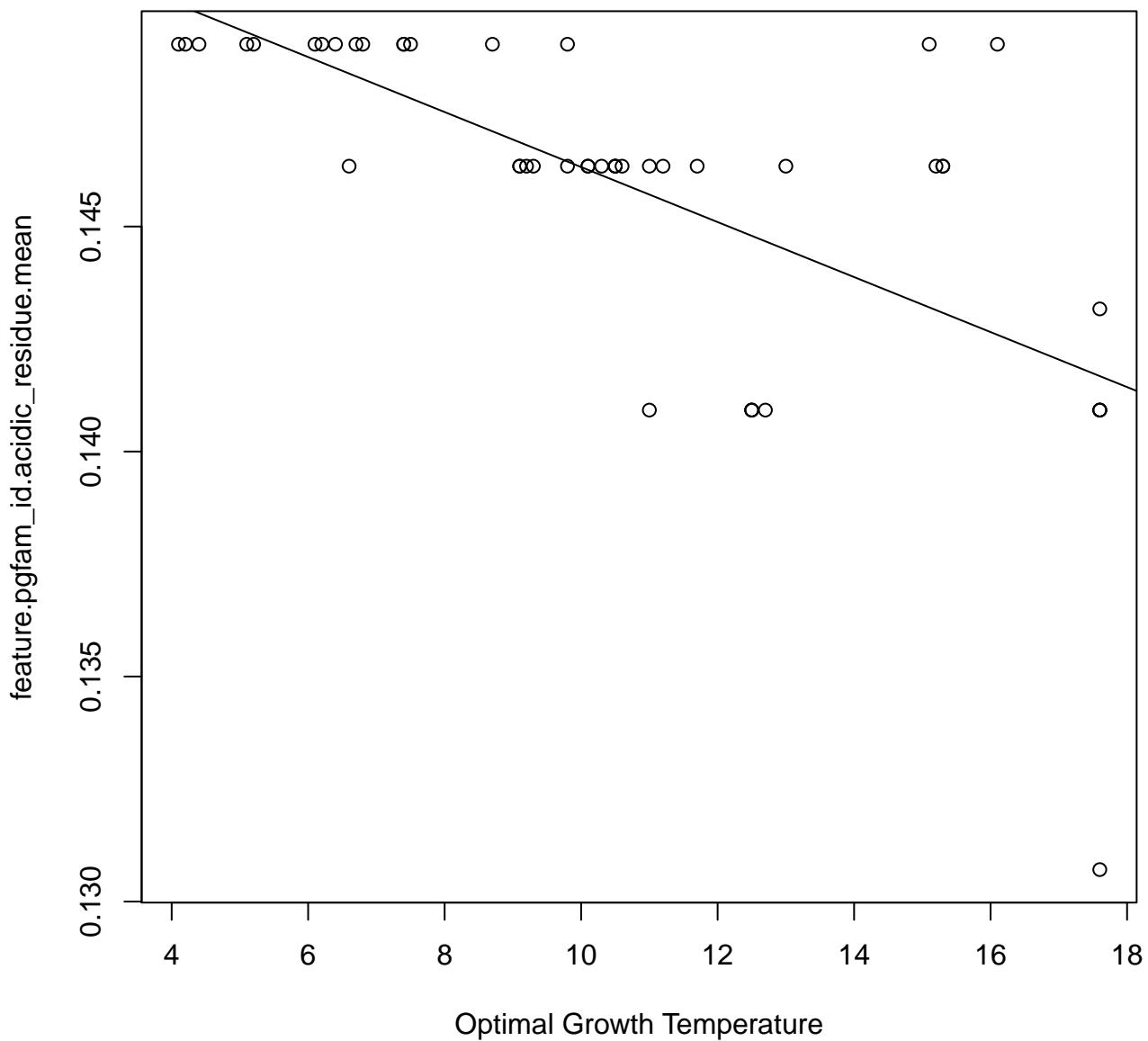
Periplasmic chaperone and peptidyl-prolyl cis-trans isomerase of outer membrane proteins SurA (EC 5.2.1.8)



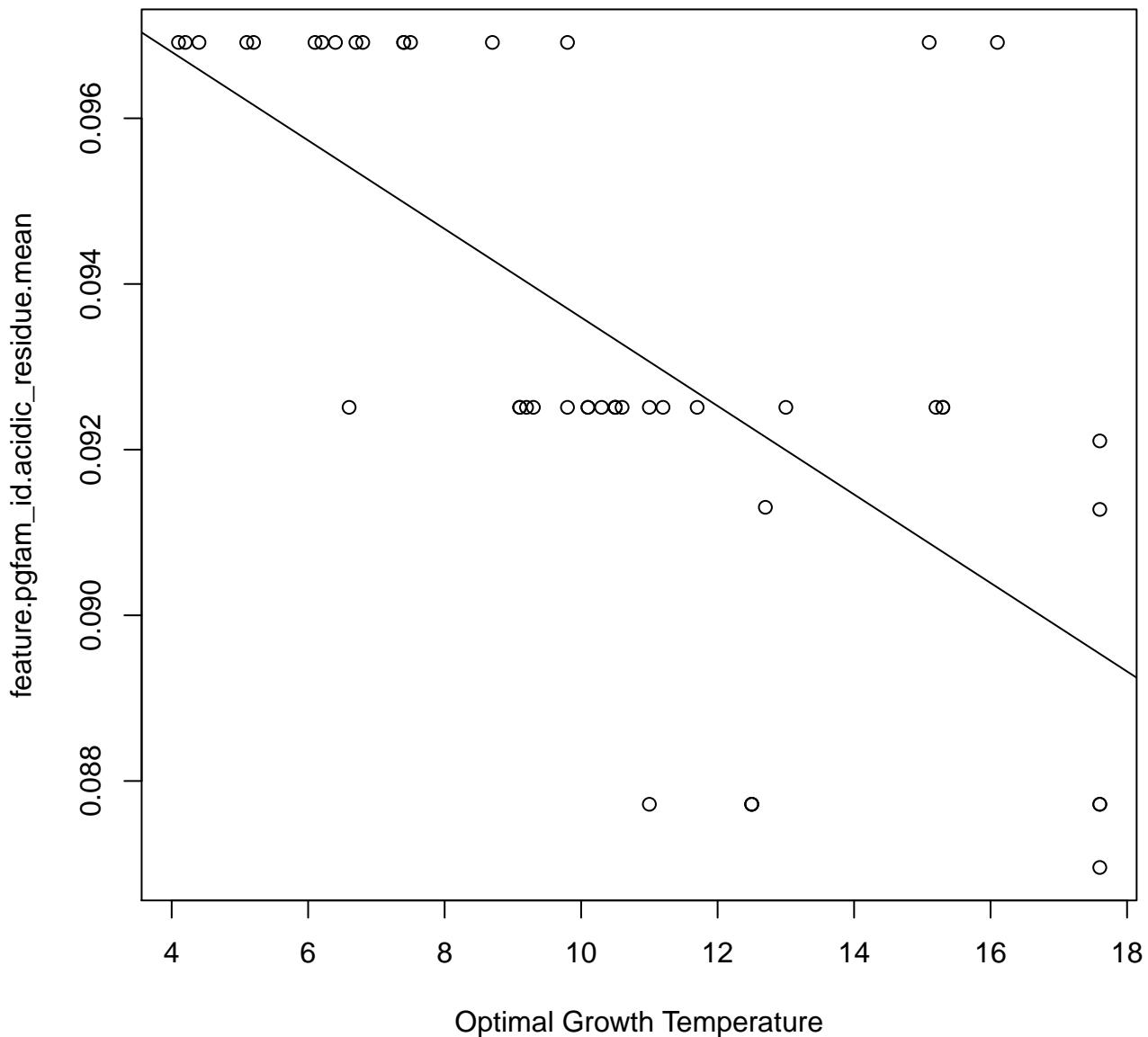
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PGF_00416674

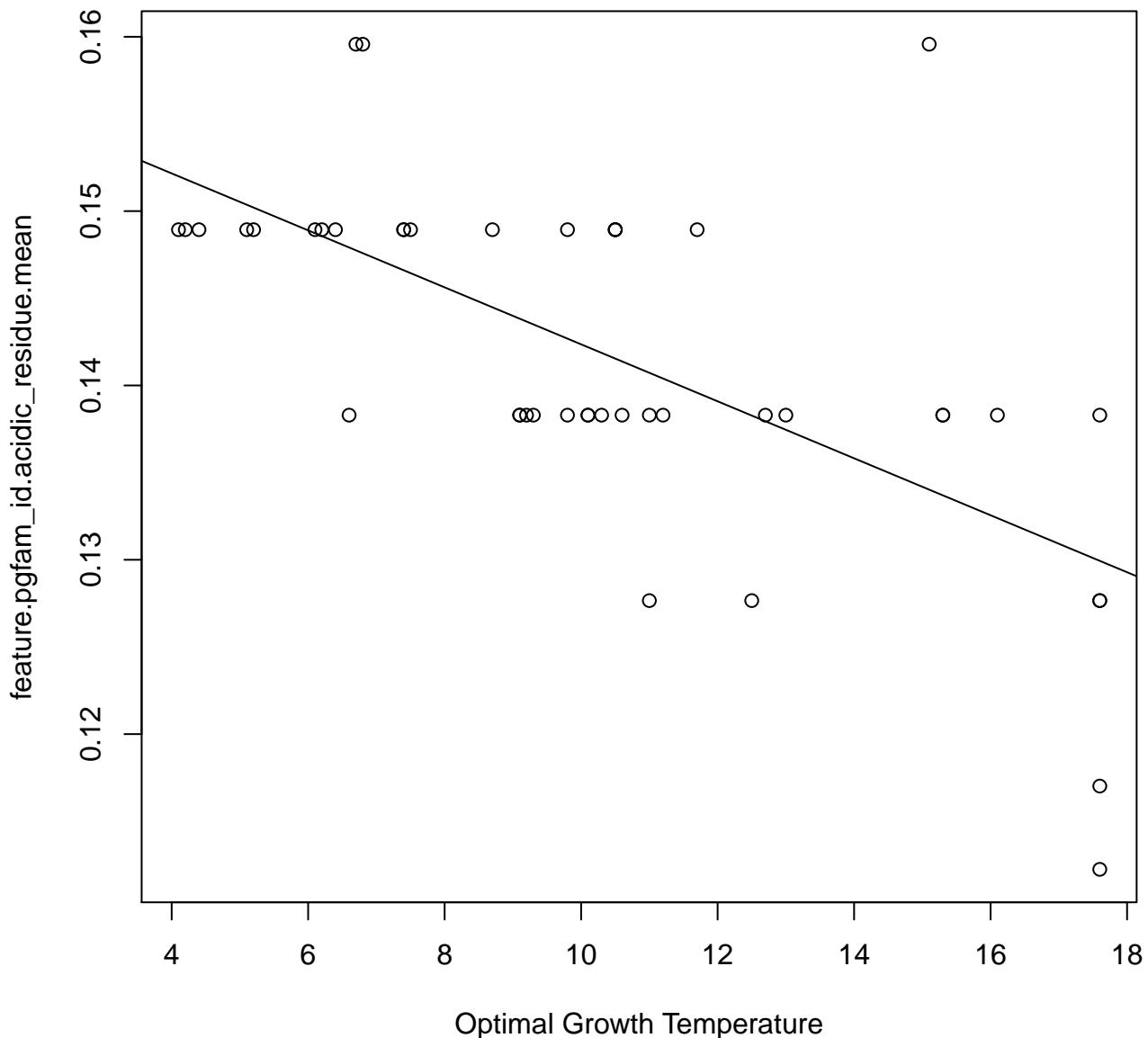
3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25)



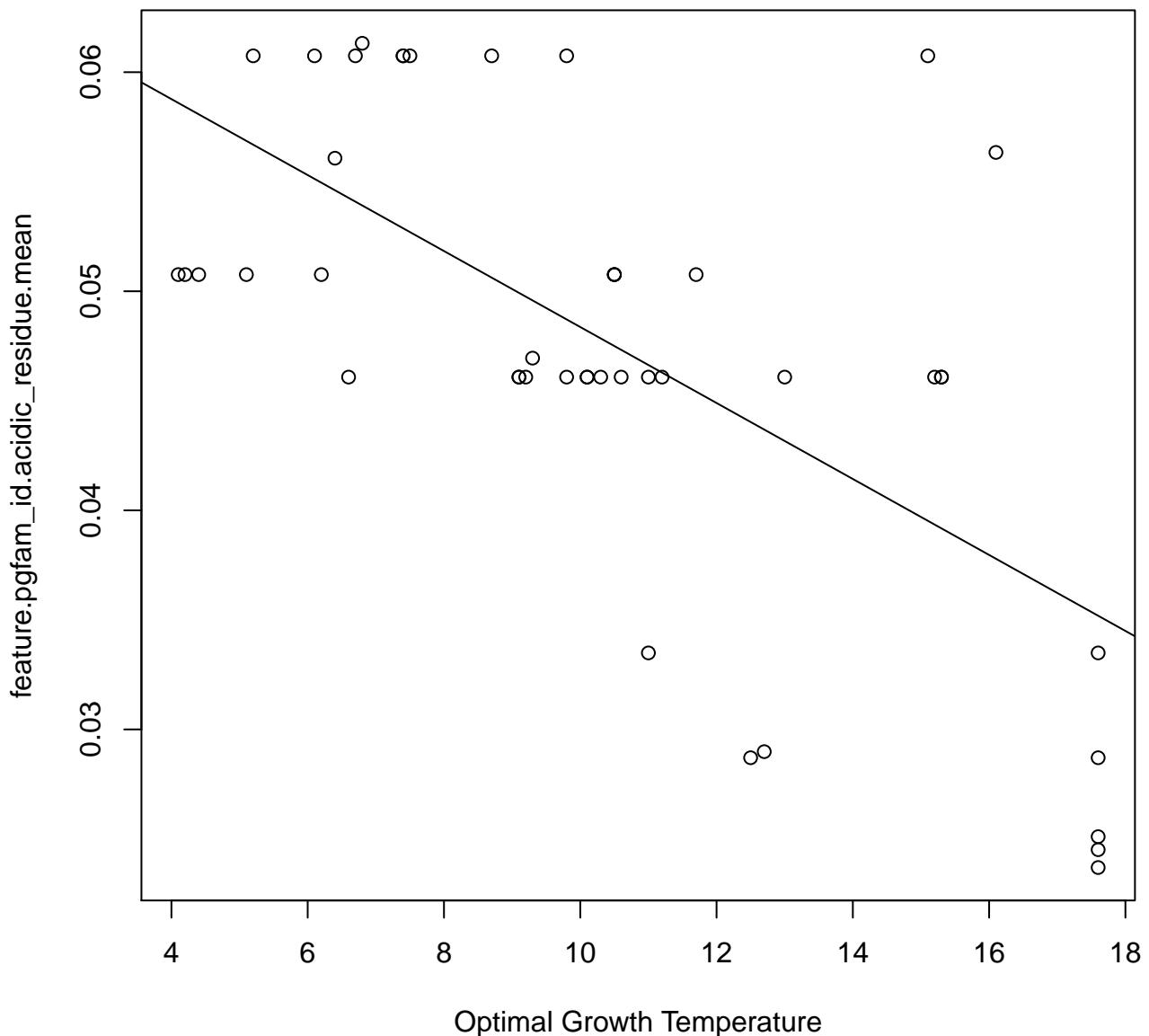
feature.pgfam_id.acidic_residue.mean
PGF_00648054
Tol-Pal system protein TolQ



feature.pgfam_id.acidic_residue.mean
PGF_12809641
hypothetical protein



feature.pgfam_id.acidic_residue.mean
PGF_09587716
Protein-methionine-sulfoxide reductase heme-binding subunit MsrQ



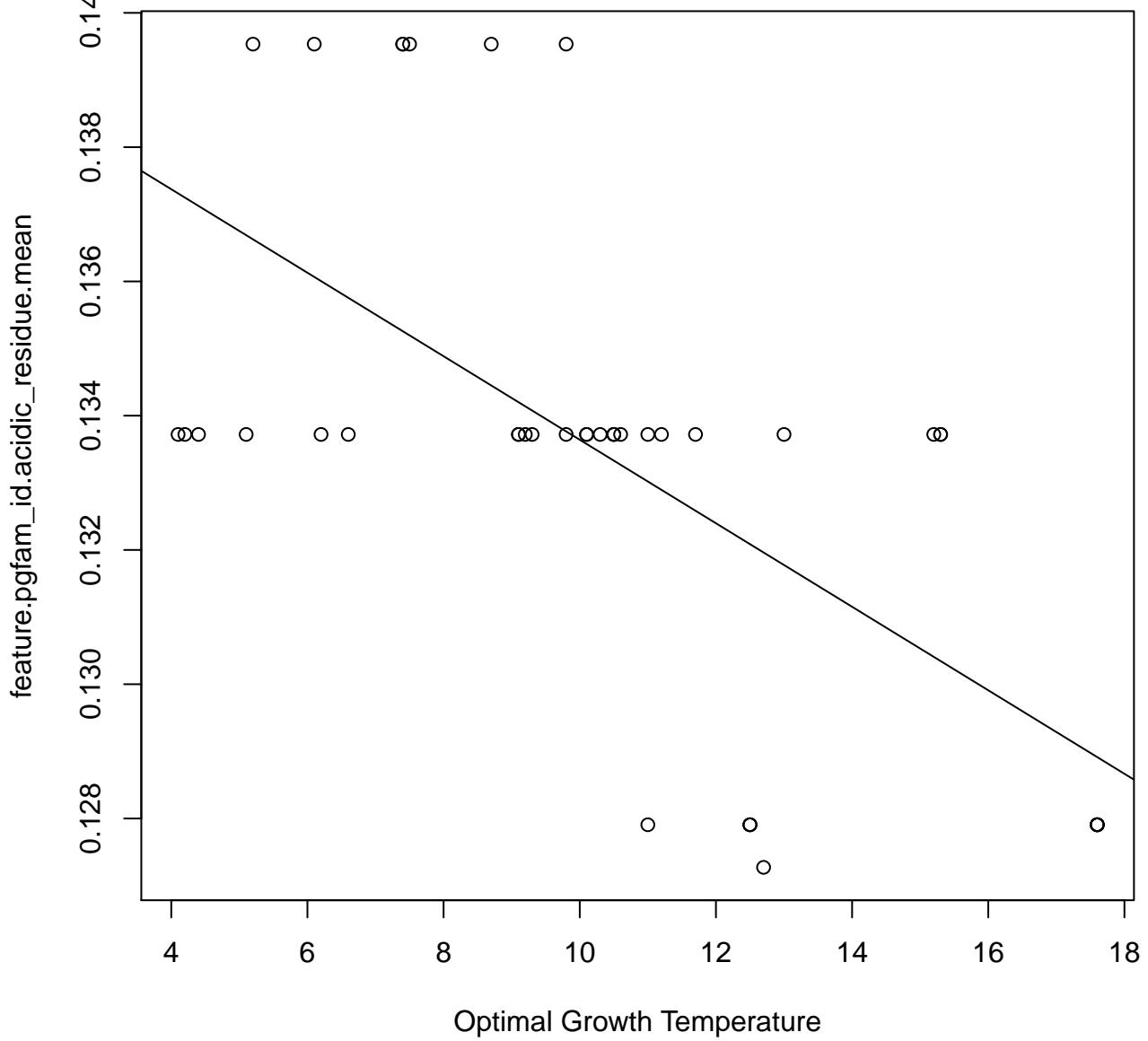
feature.pgfam_id.acidic_residue.mean

PGF_00027740

Periplasmic chaperone of outer membrane proteins Skp @ Outer membrane protein H precursor

feature.pgfam_id.acidic_residue.mean

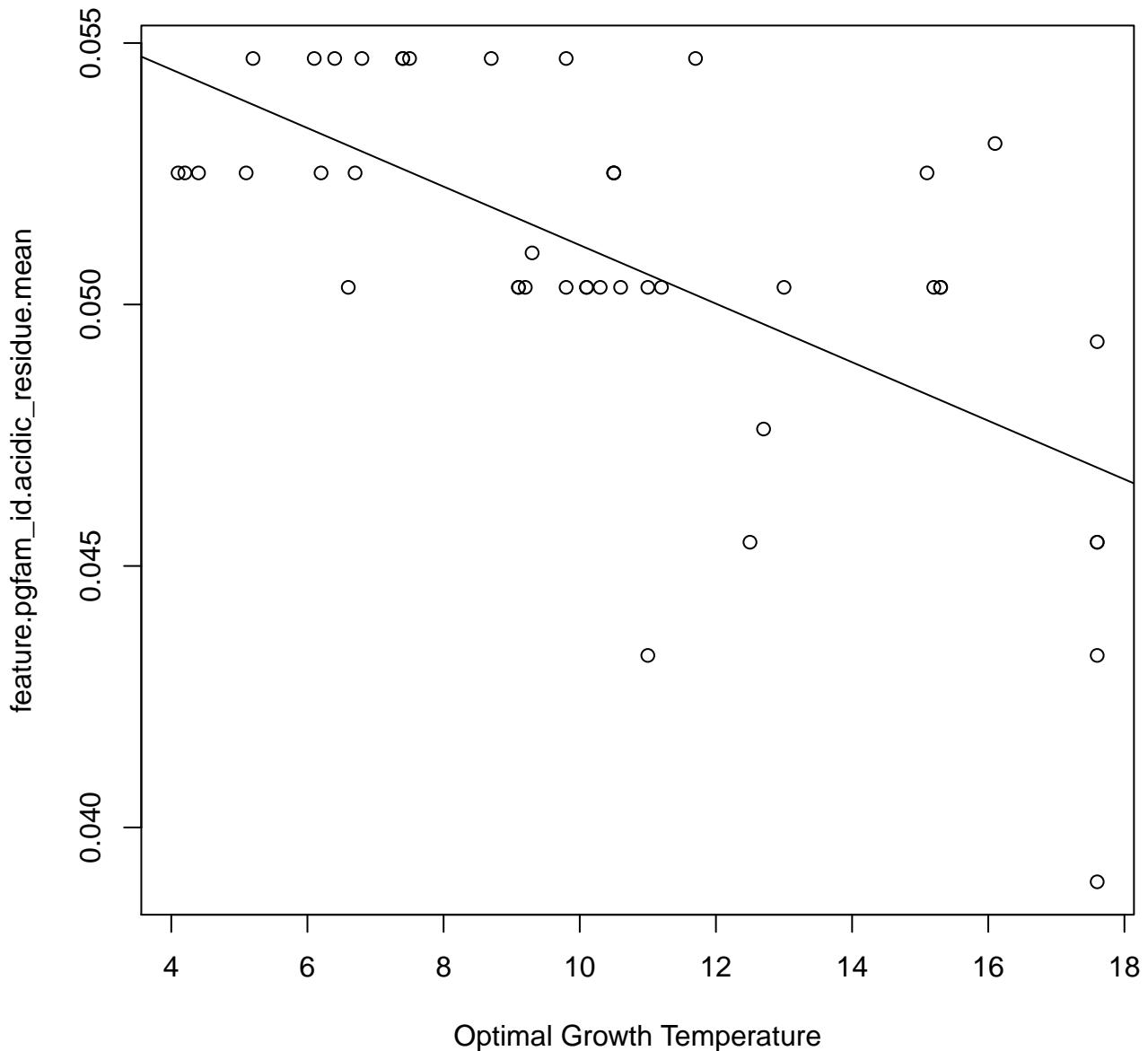
Optimal Growth Temperature



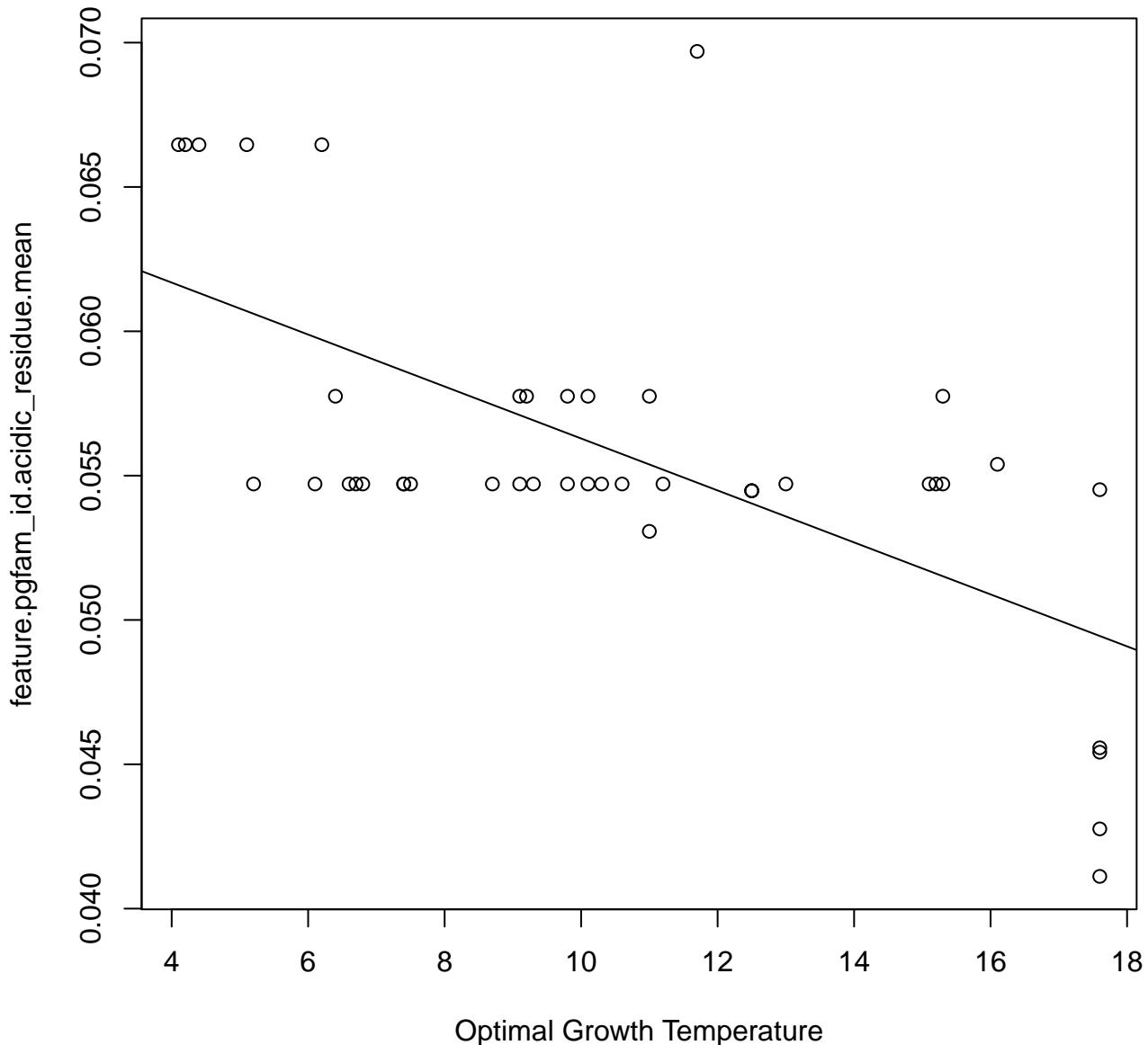
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PGF_08913741

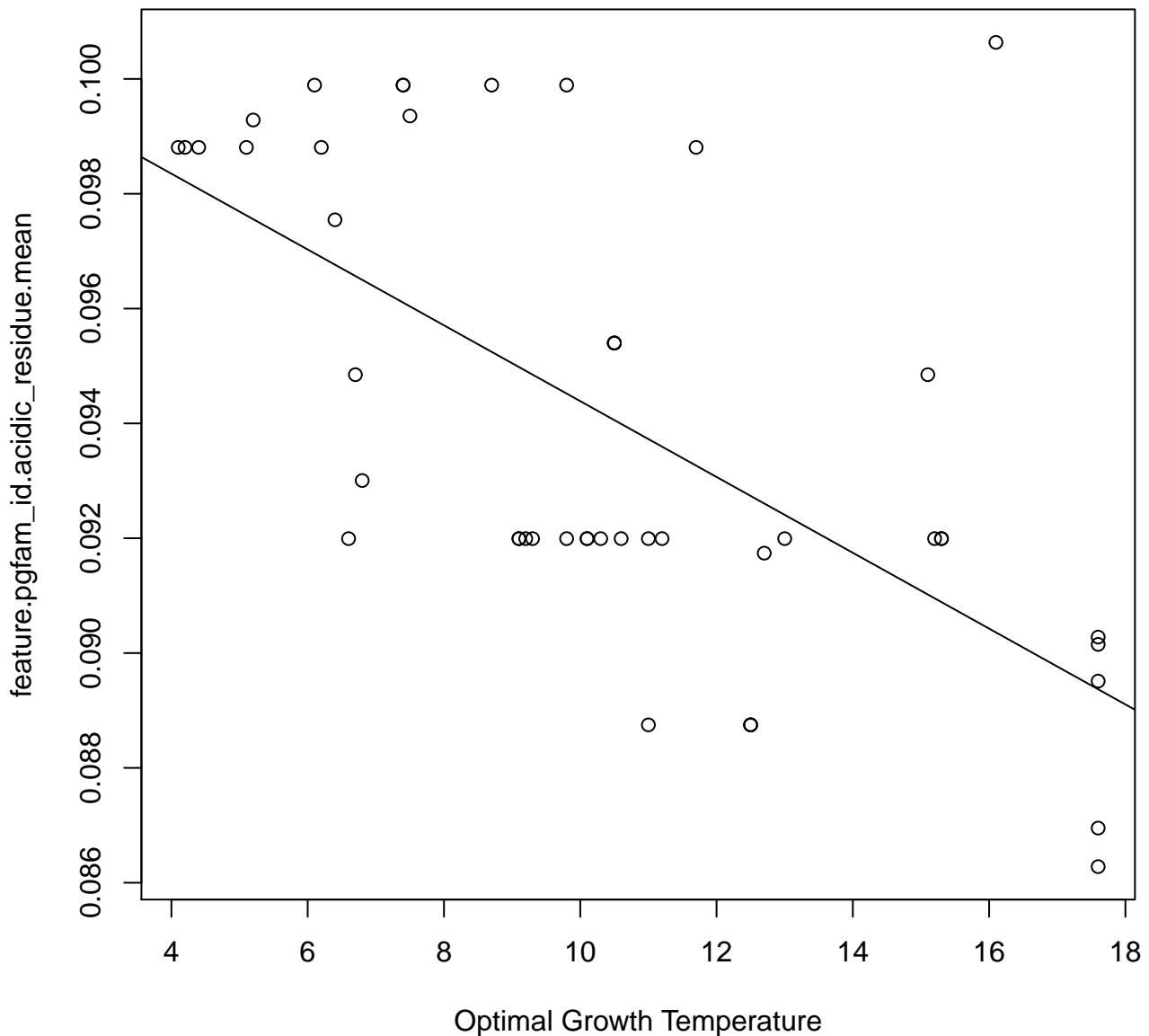
Multi antimicrobial extrusion protein (Na⁽⁺⁾/drug antiporter), MATE family of MDR efflux pumps



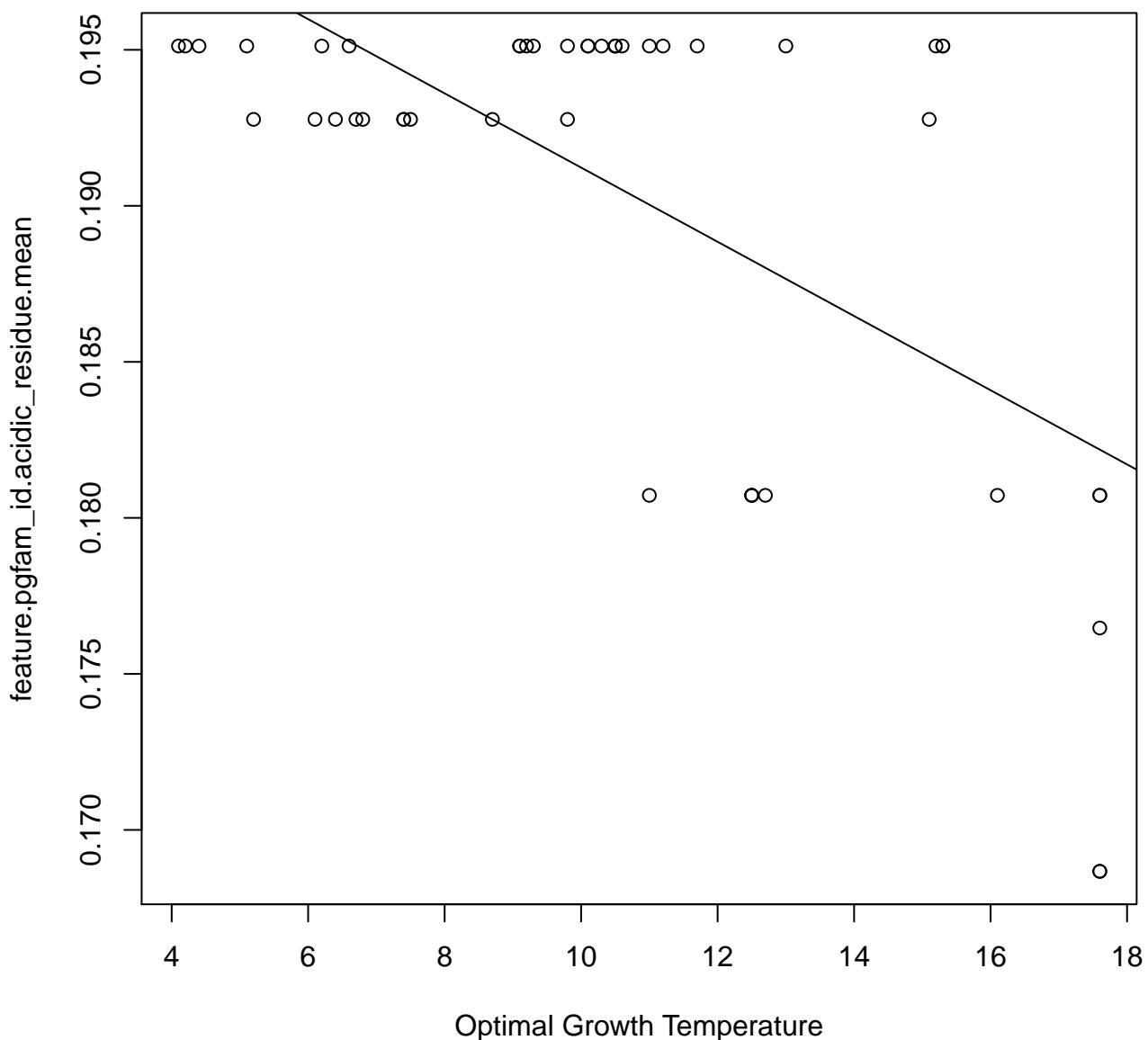
feature.pgfam_id.acidic_residue.mean
PGF_03342342
Uncharacterized membrane protein, YraQ family



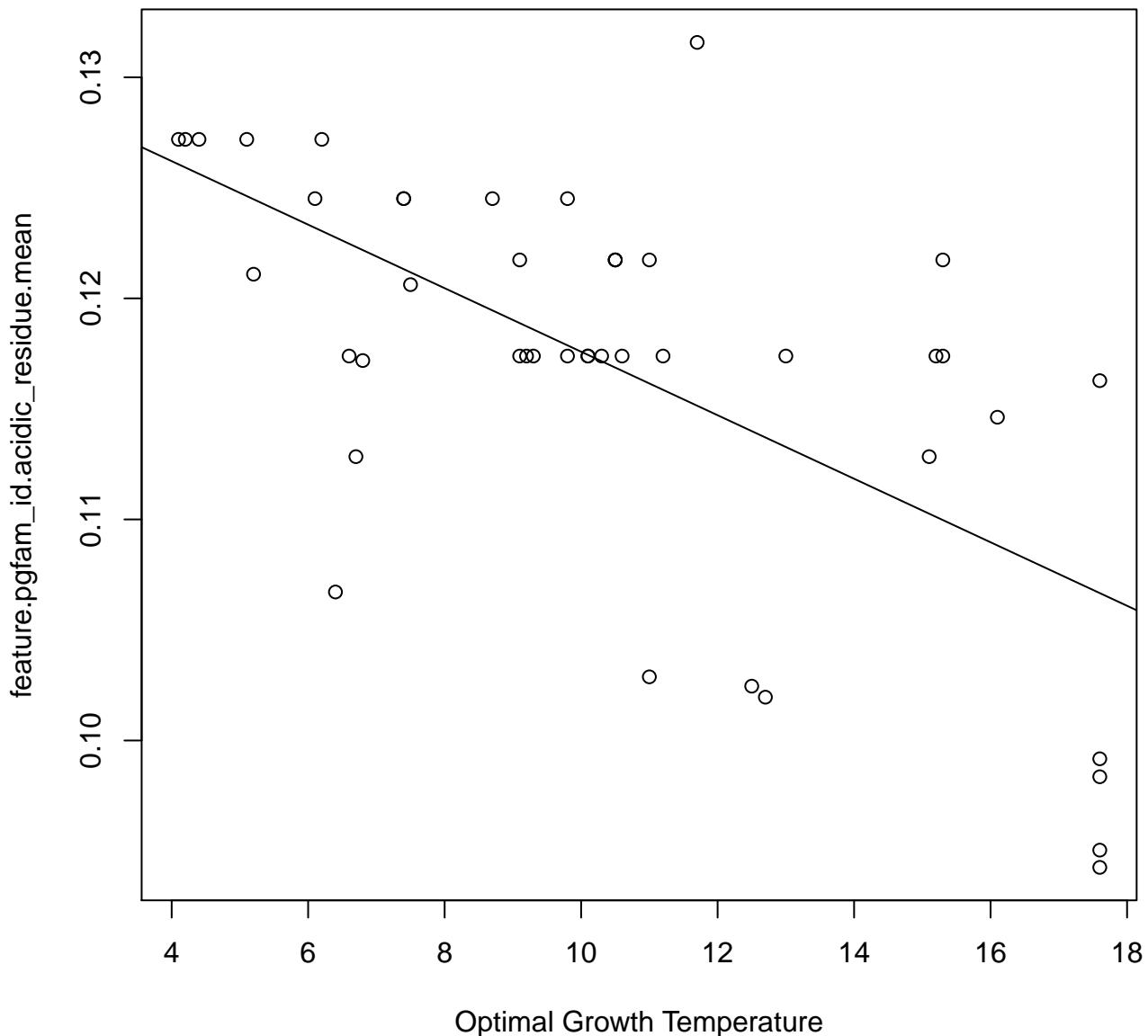
feature.pgfam_id.acidic_residue.mean
PGF_02890229
Gamma-glutamyltranspeptidase (EC 2.3.2.2) @ Glutathione hydrolase (EC 3.4.19.13)



feature.pgfam_id.acidic_residue.mean
PGF_03348849
Uncharacterized protein YqiC



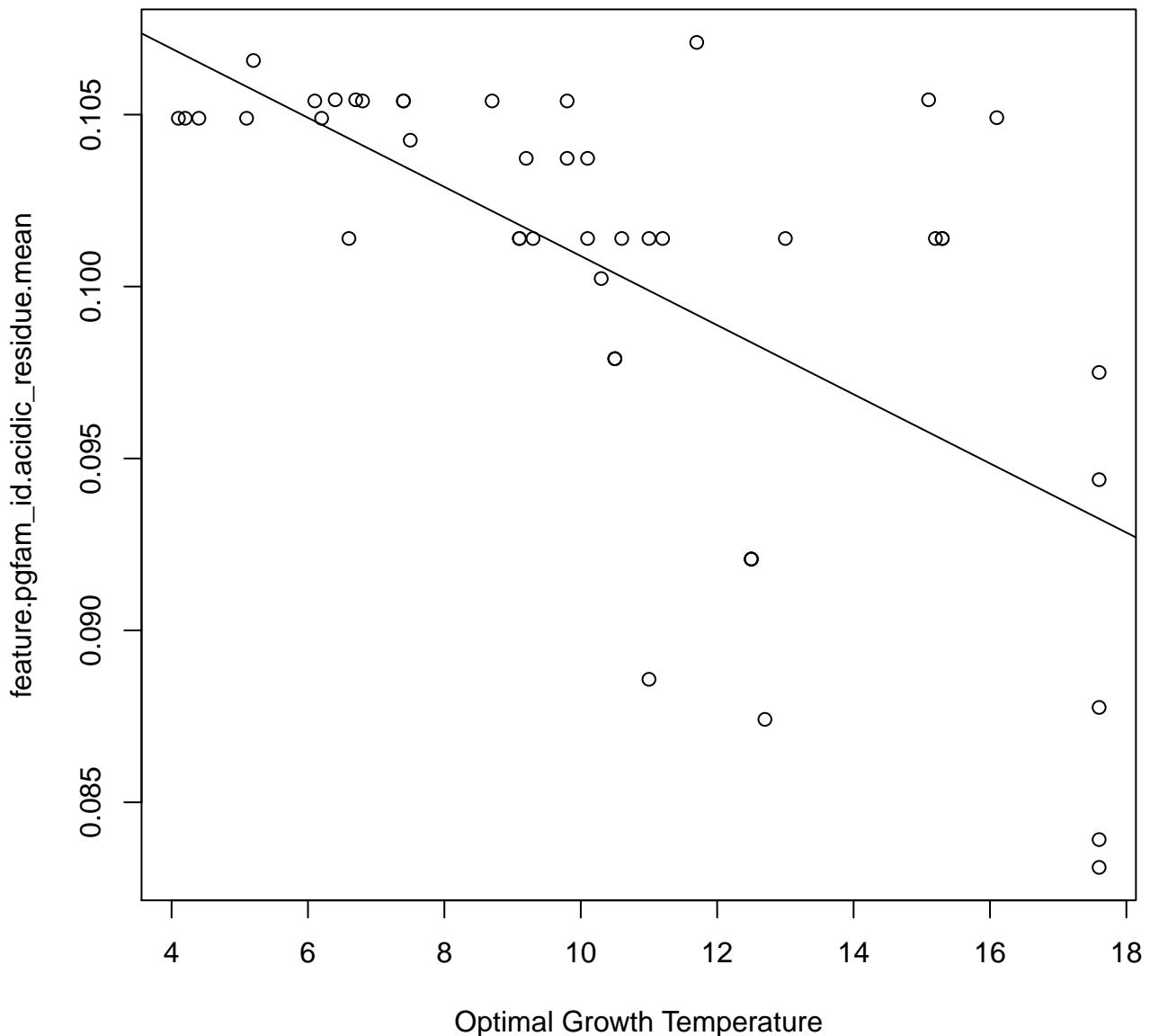
feature.pgfam_id.acidic_residue.mean
PGF_09866709
Outer membrane lipoprotein carrier protein LolA



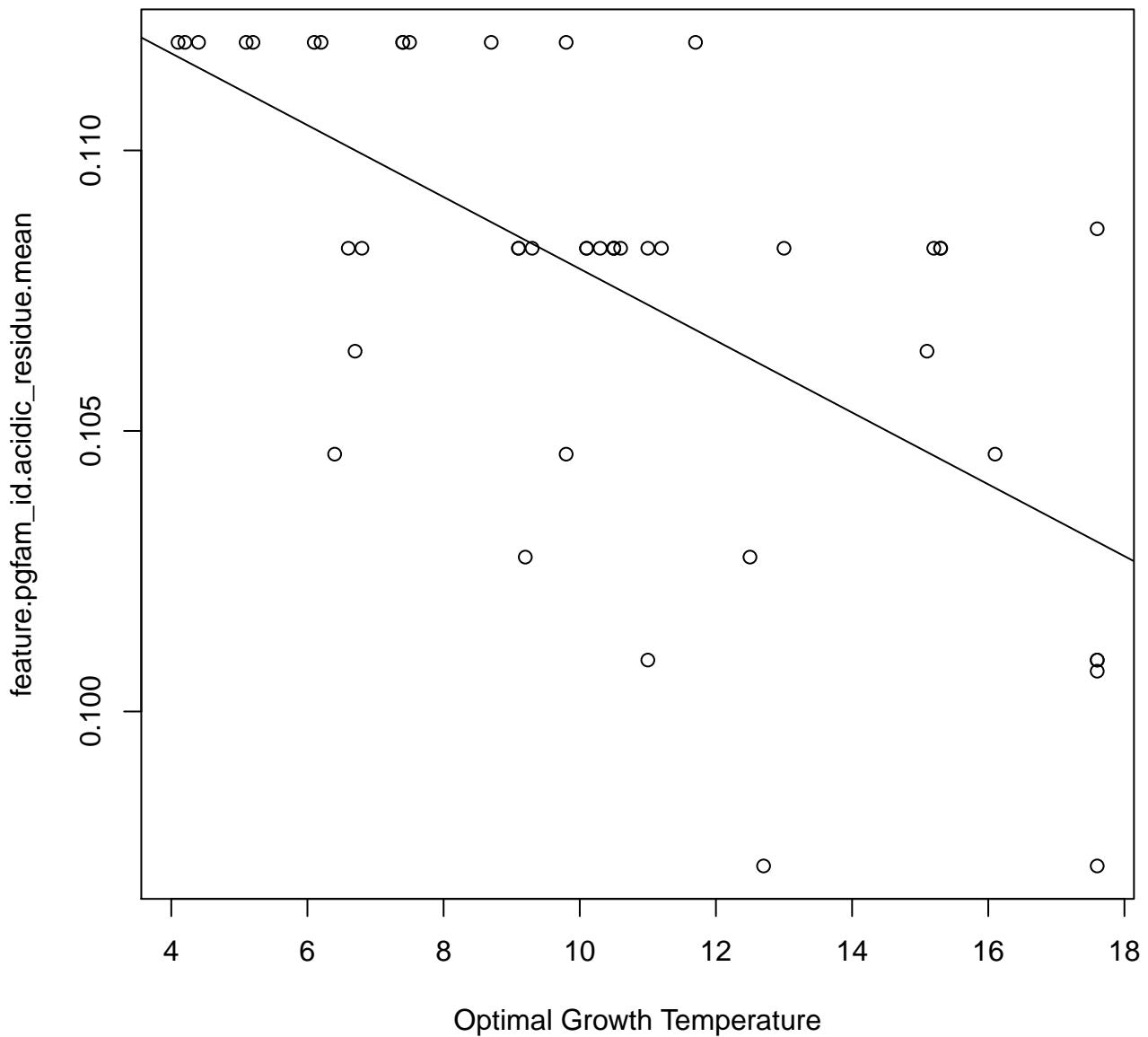
feature.pgfam_id.acidic_residue.mean

PGF_00050214

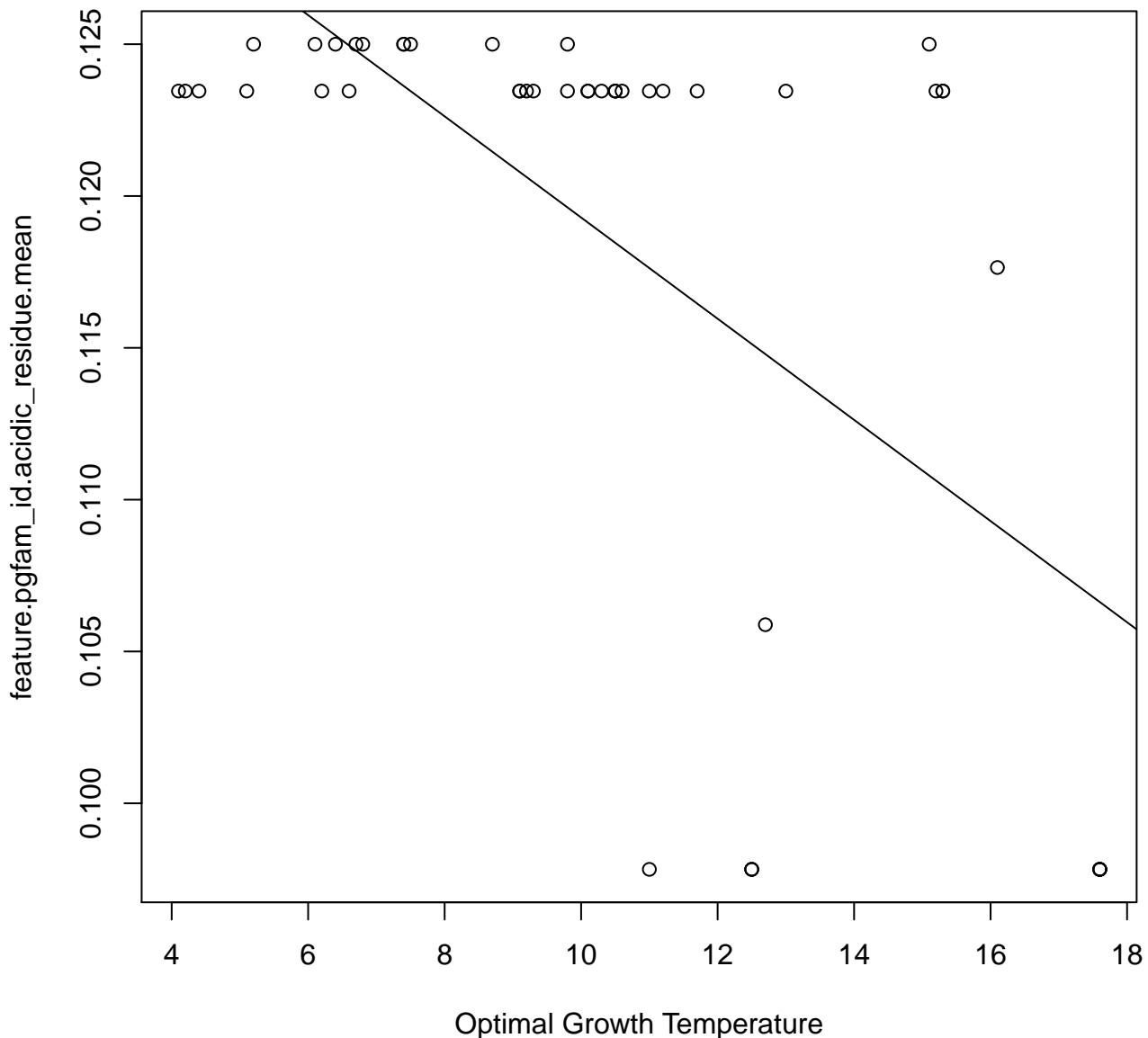
Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain



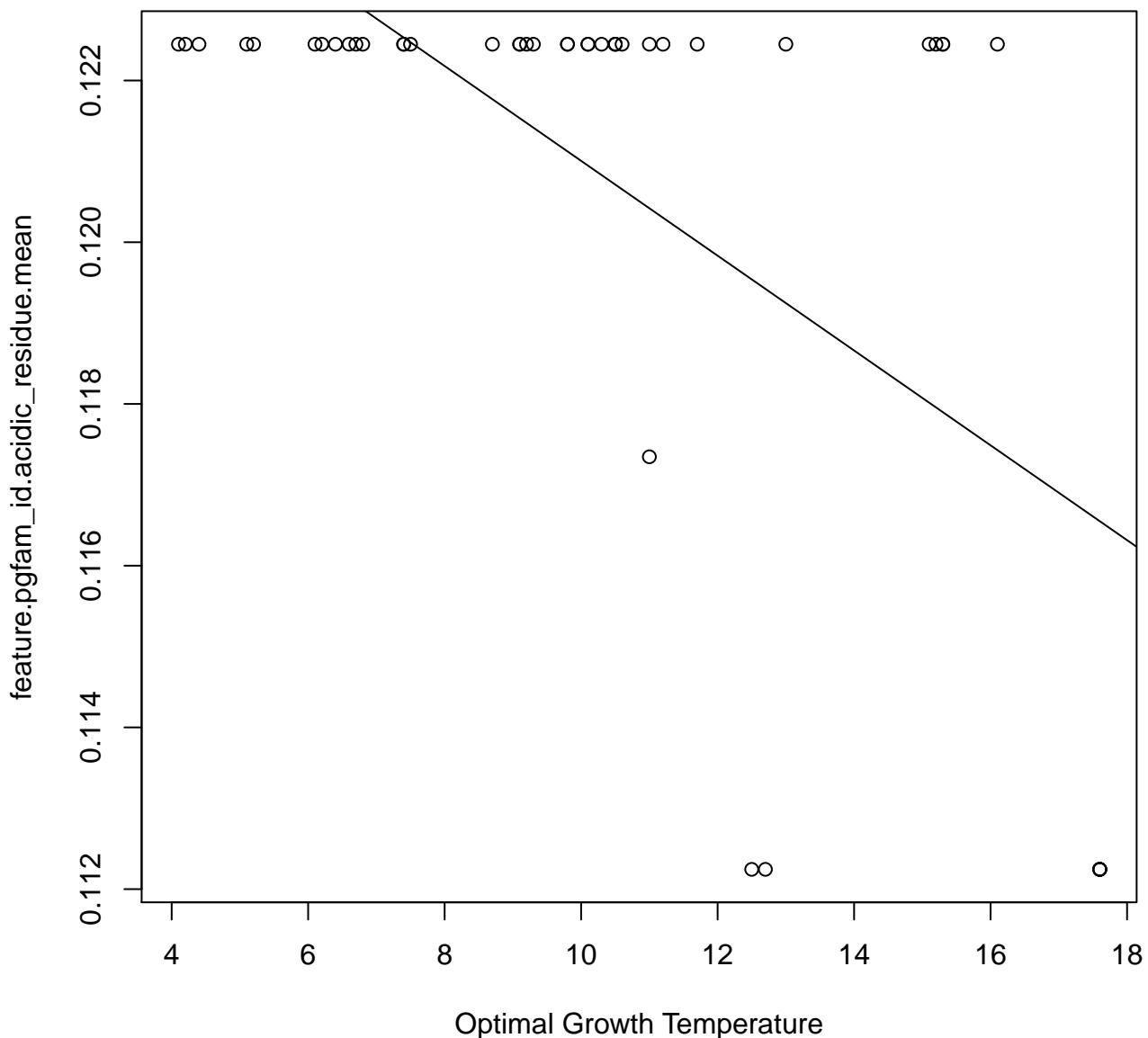
feature.pgfam_id.acidic_residue.mean
PGF_01072302
Phosphate ABC transporter, permease protein PstA (TC 3.A.1.7.1)



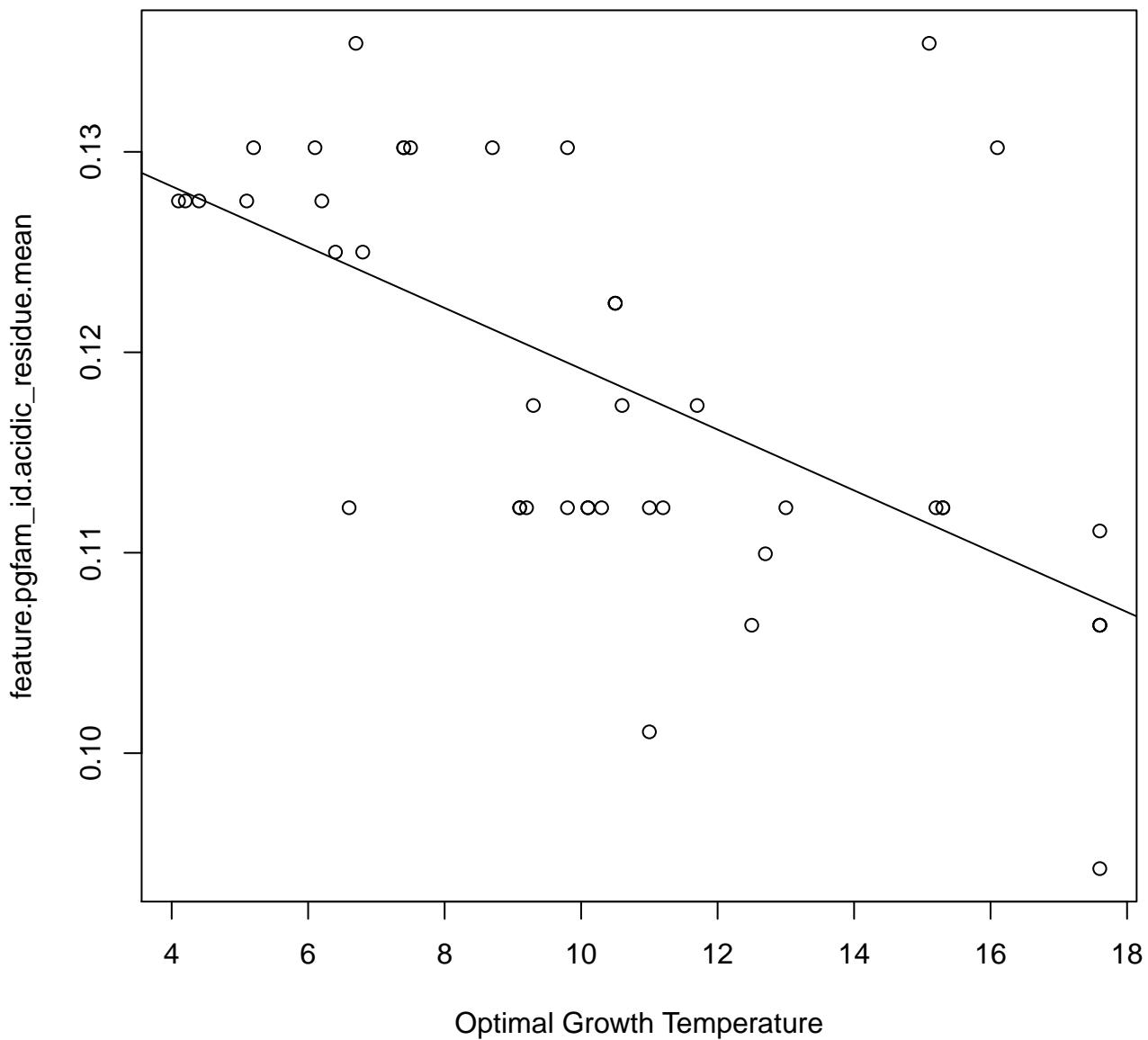
feature.pgfam_id.acidic_residue.mean
PGF_00025216
Acetolactate synthase small subunit (EC 2.2.1.6)



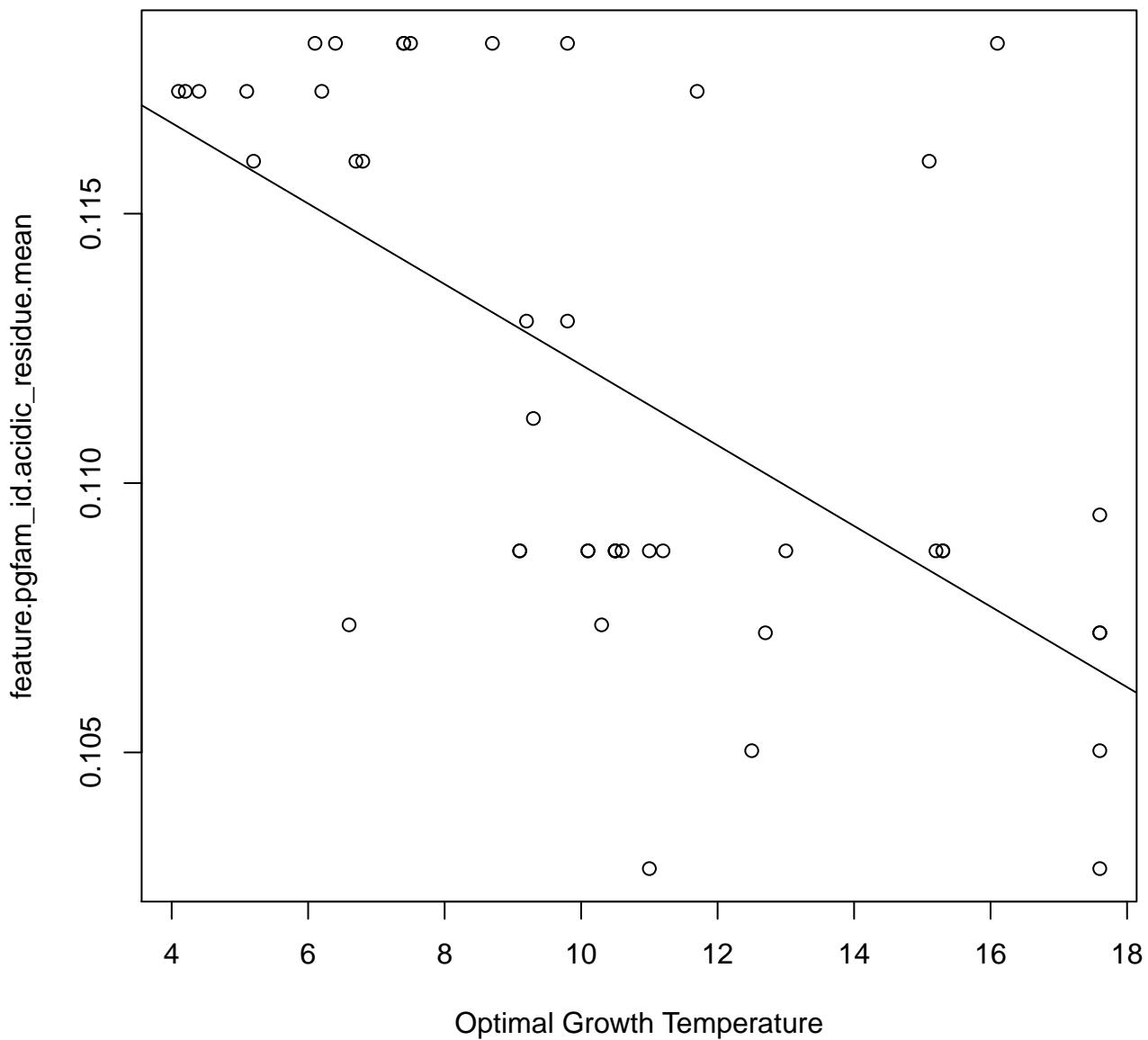
feature.pgfam_id.acidic_residue.mean
PGF_06819459
DnaA initiator-associating protein DiaA



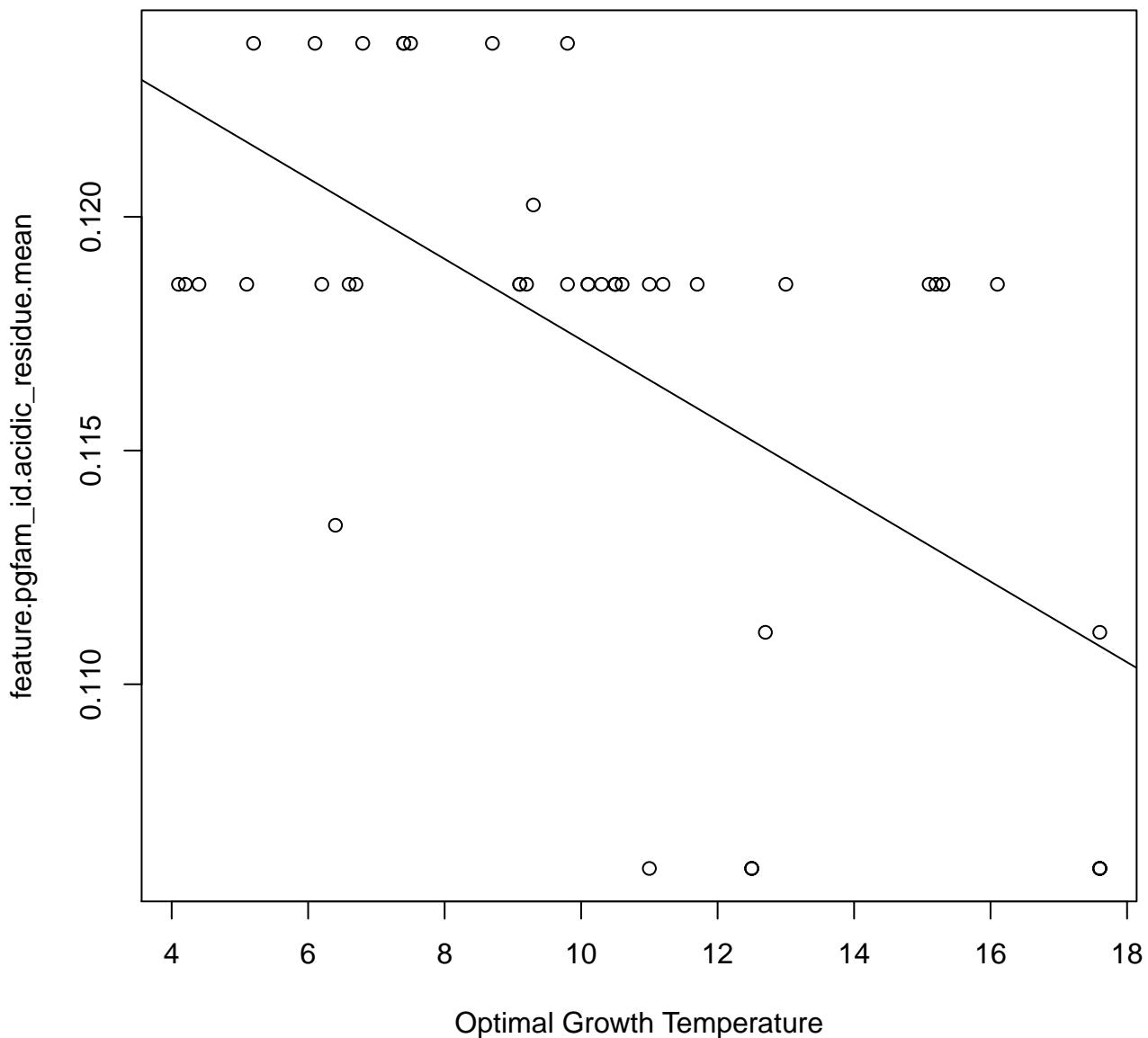
feature.pgfam_id.acidic_residue.mean
PGF_01466629
Type IV pilus biogenesis protein PilN



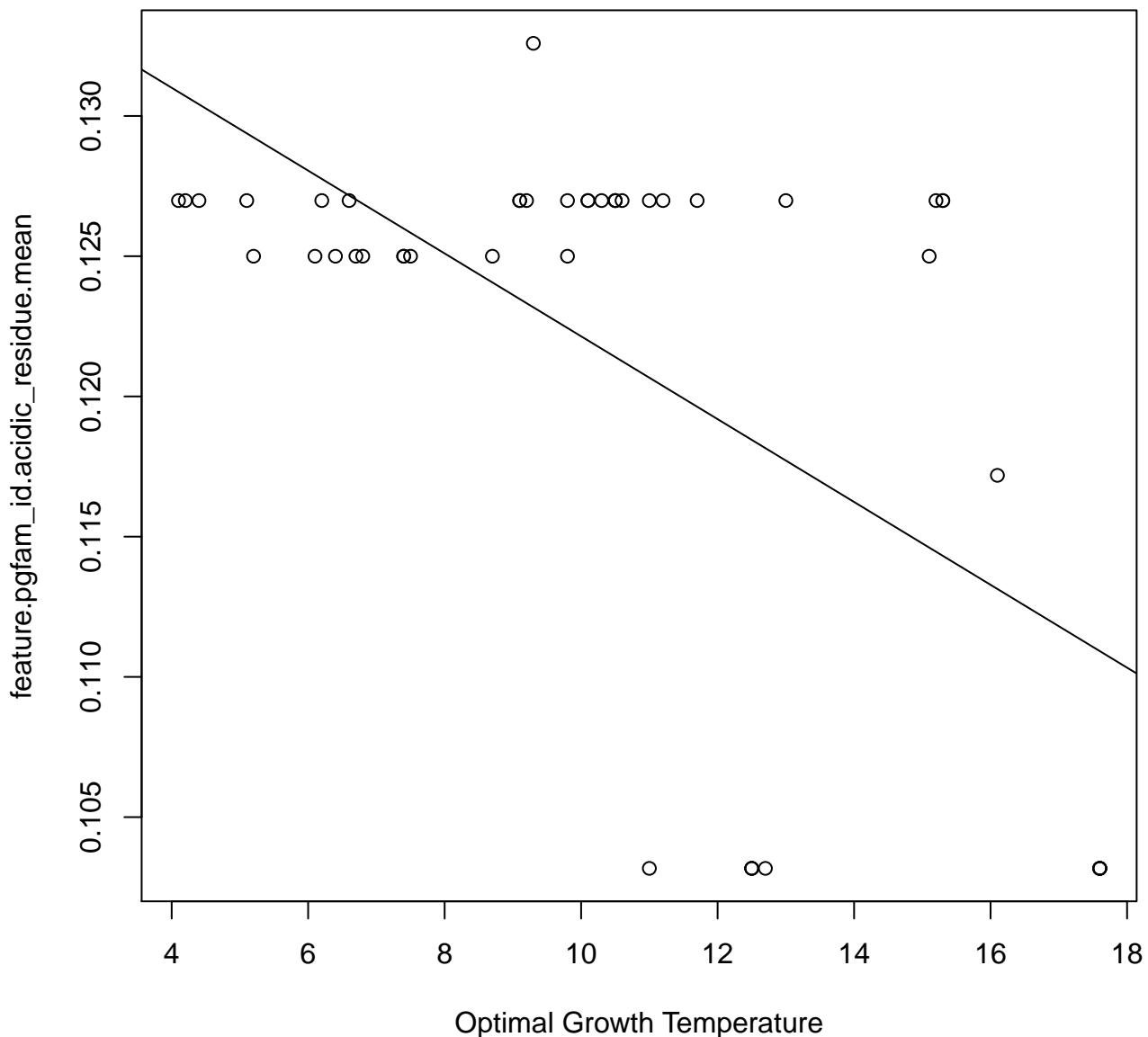
feature.pgfam_id.acidic_residue.mean
PGF_03232027
Transcriptional response regulatory protein GlrR



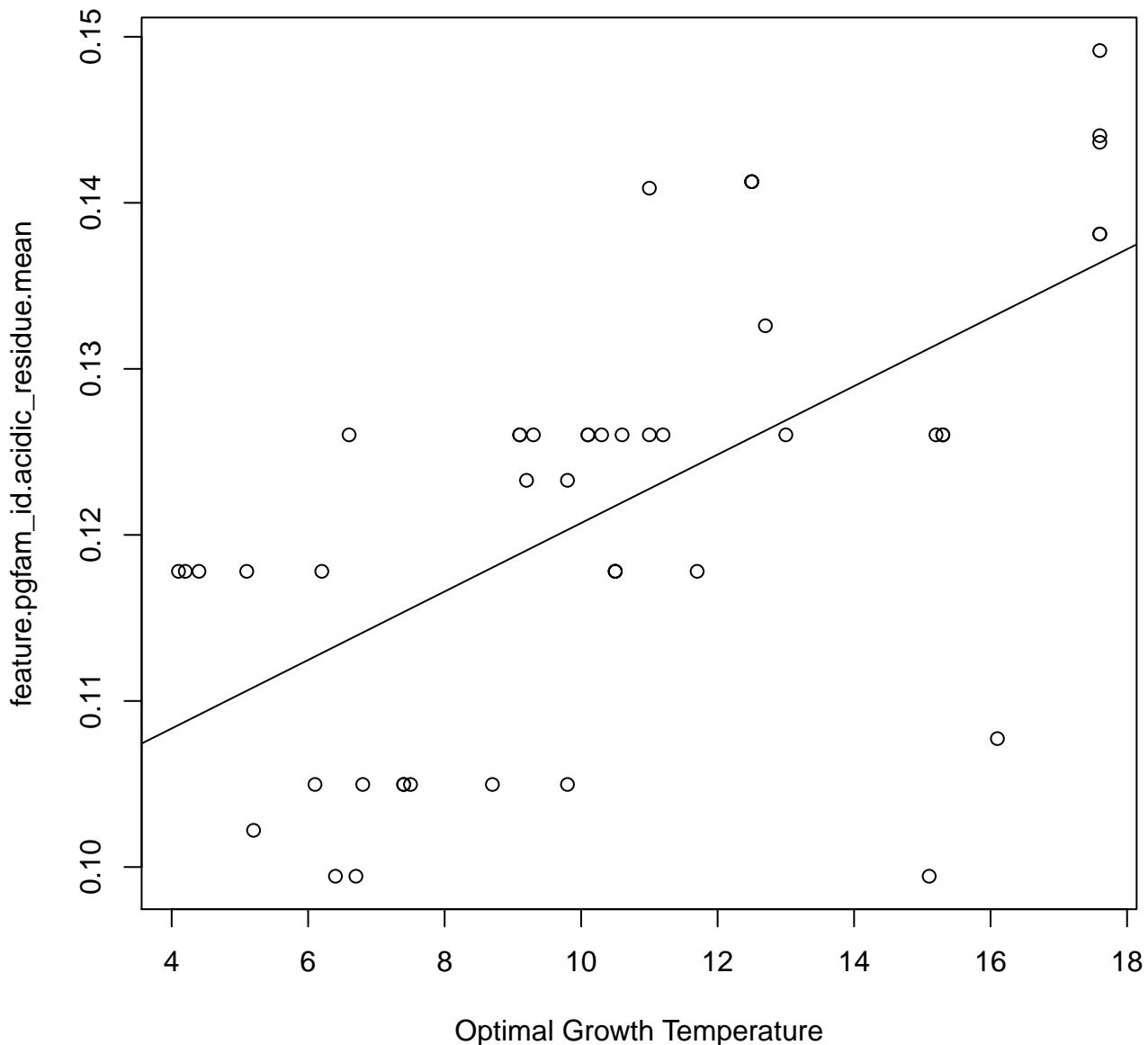
feature.pgfam_id.acidic_residue.mean
PGF_00058666
Transcriptional regulator SlmA, TetR family



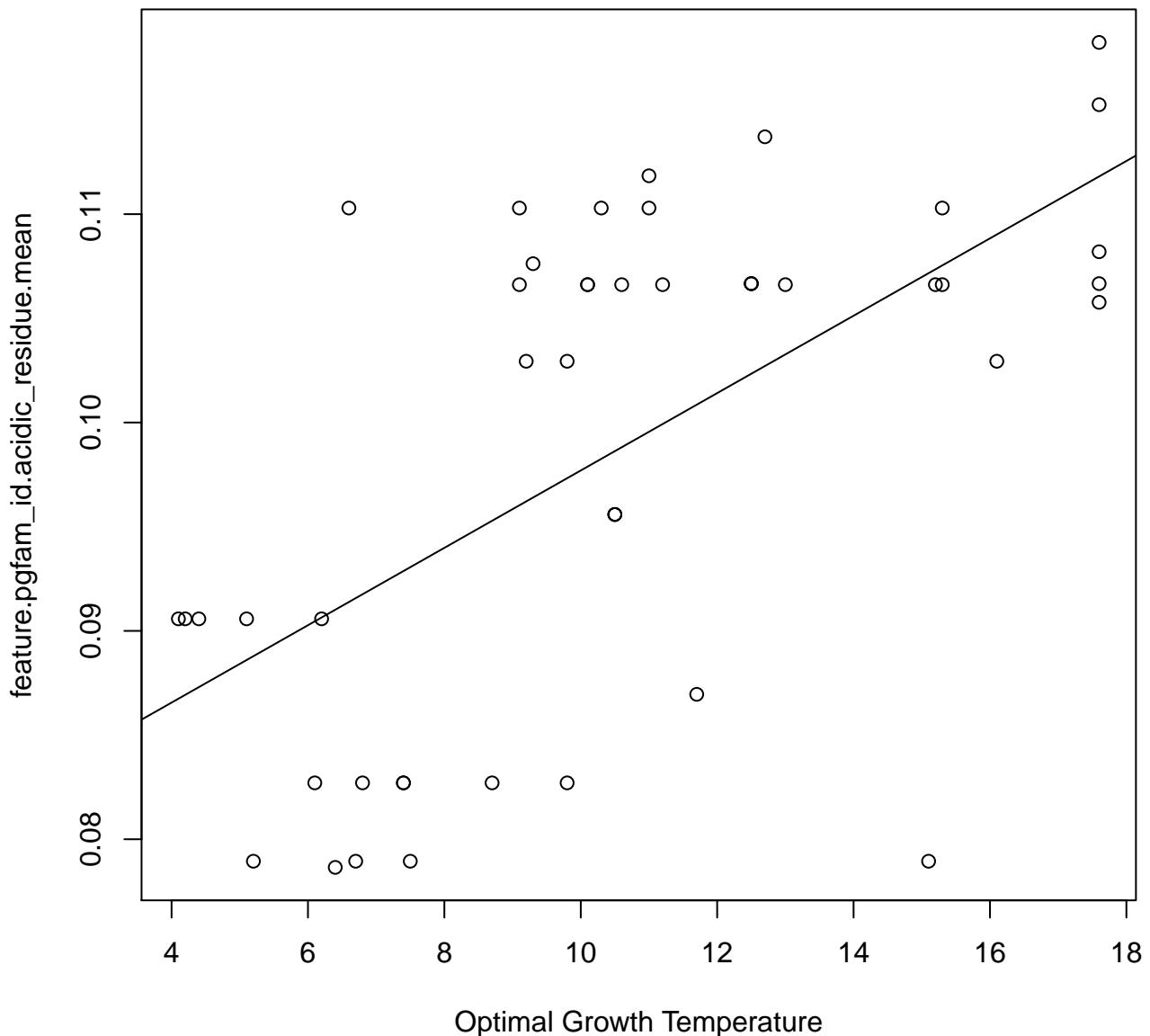
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PGF_00060312
Transcriptional repressor, BlaI/MecI family



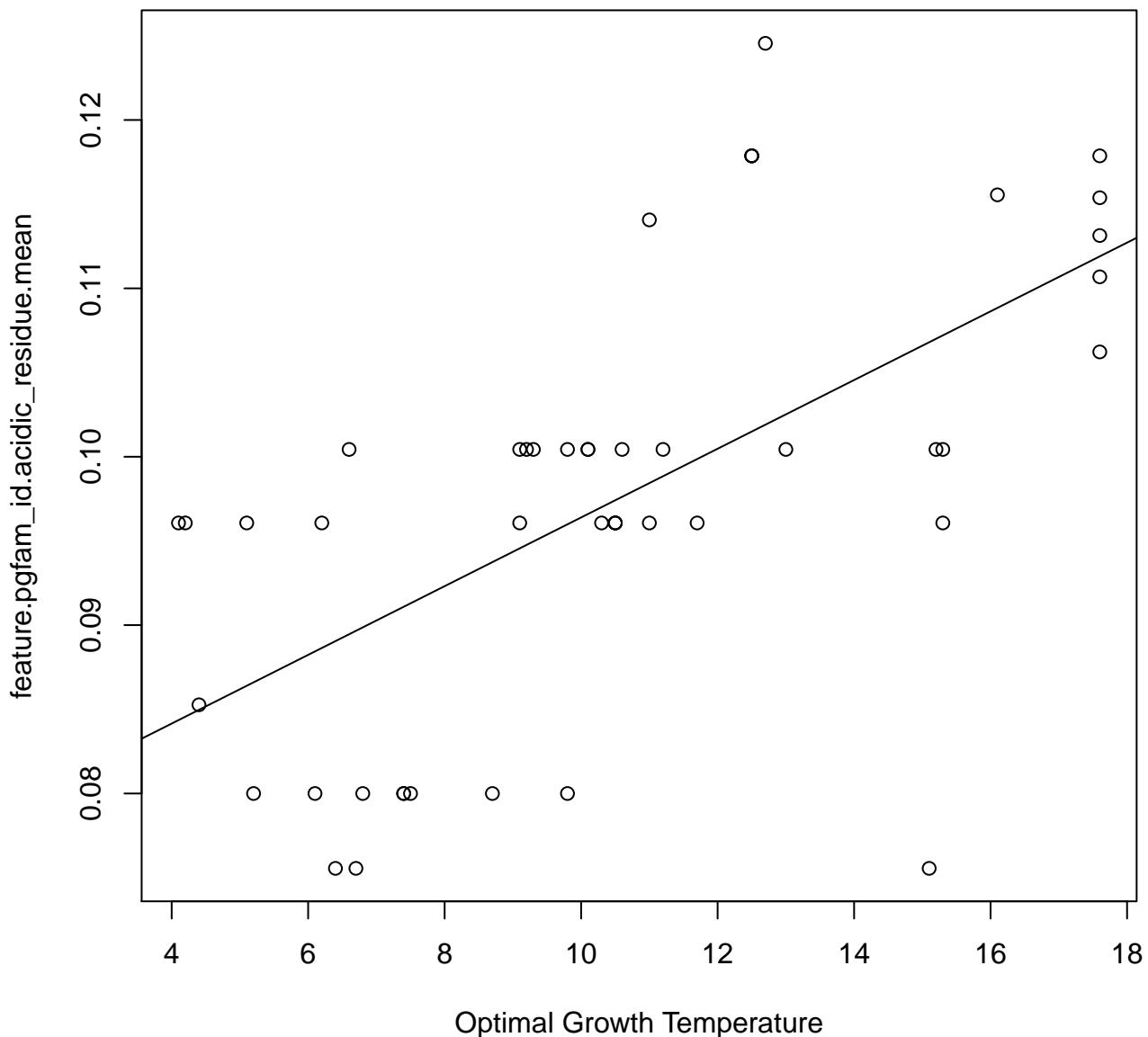
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PGF_00065755
Uncharacterized protein with LysM domain, COG1652



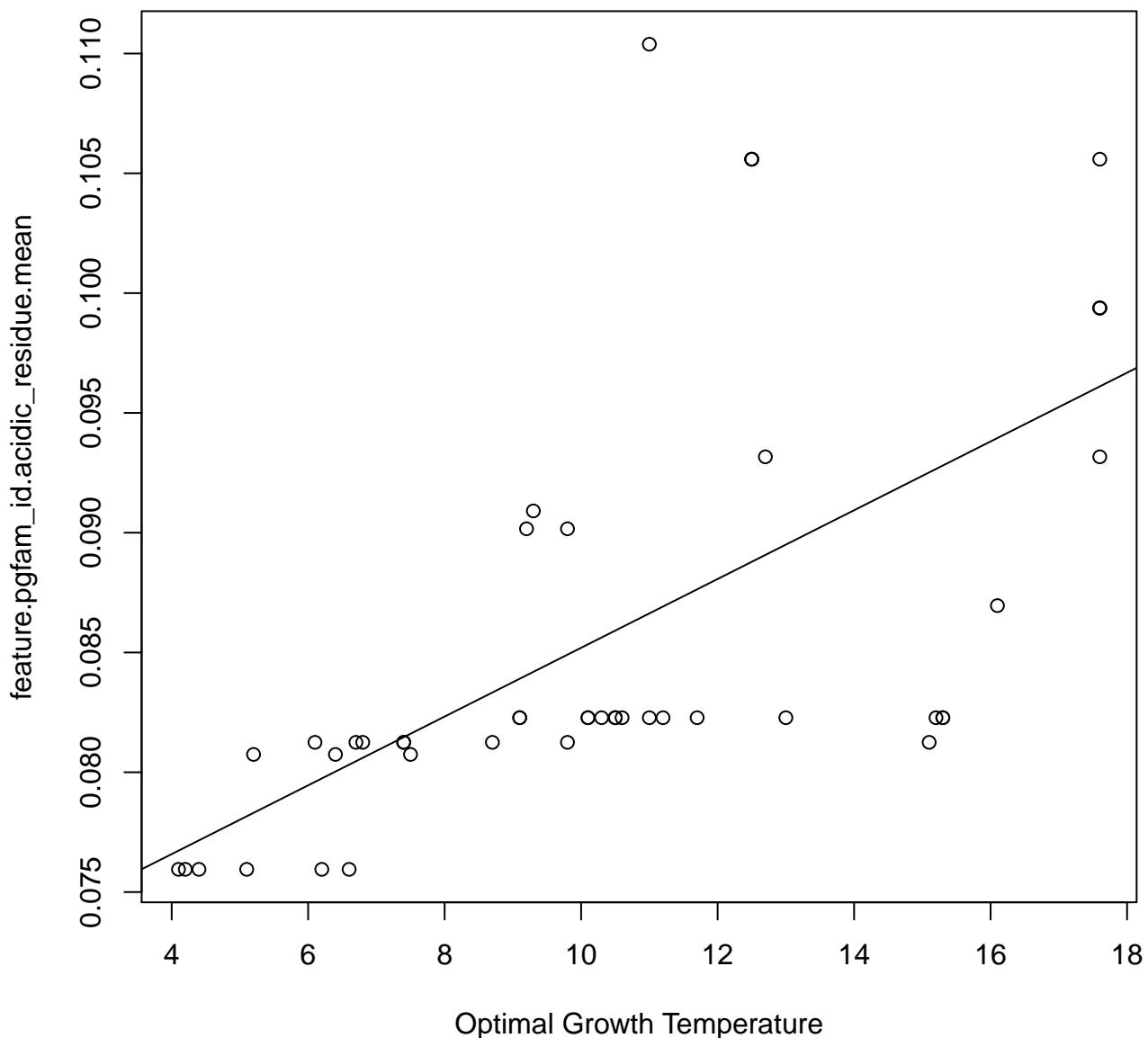
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PGF_00040580
Putative deoxyribonuclease YjjV



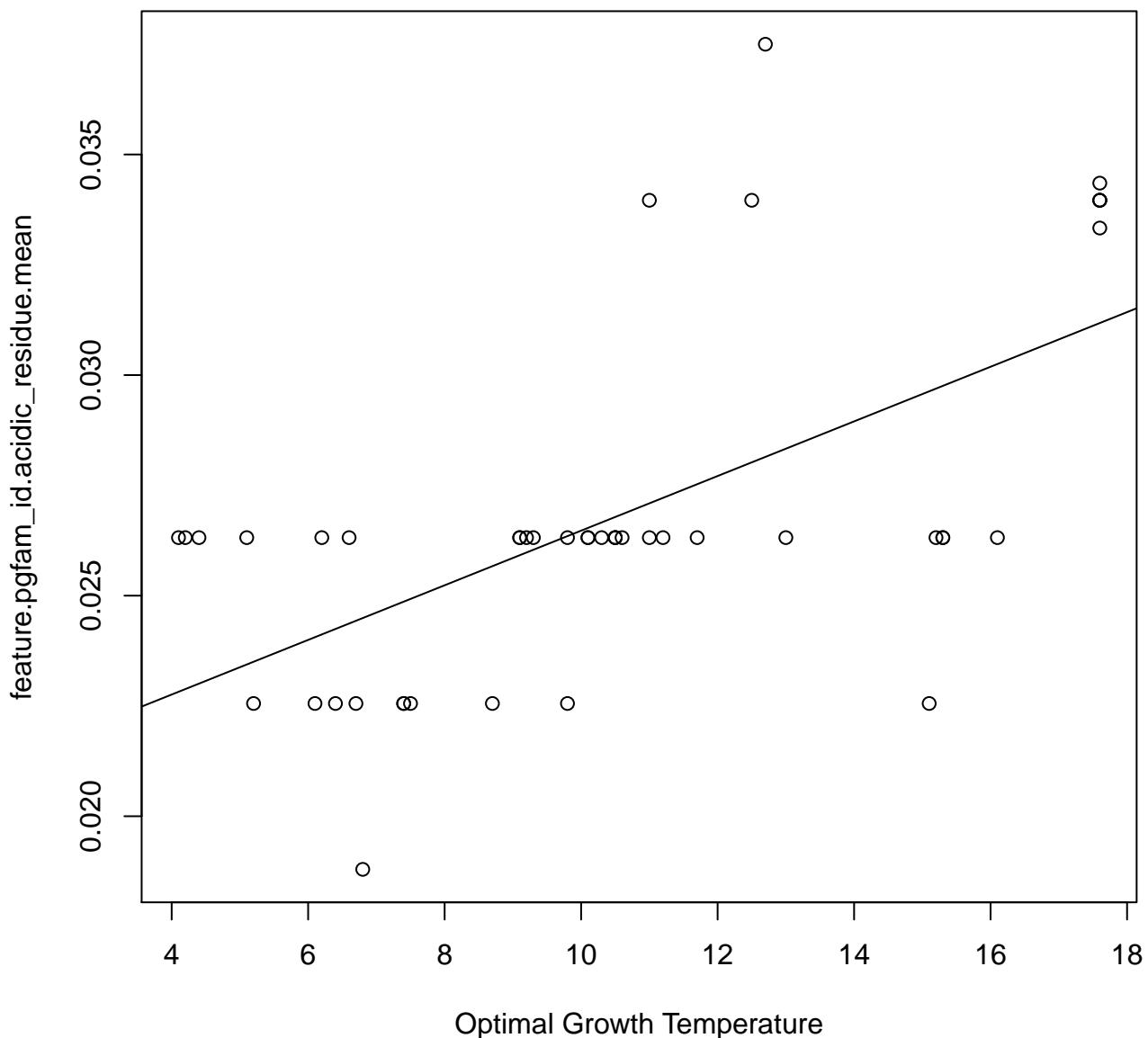
feature.pgfam_id.acidic_residue.mean
PGF_03760224
Dethiobiotin synthase BioD (EC 6.3.3.3)



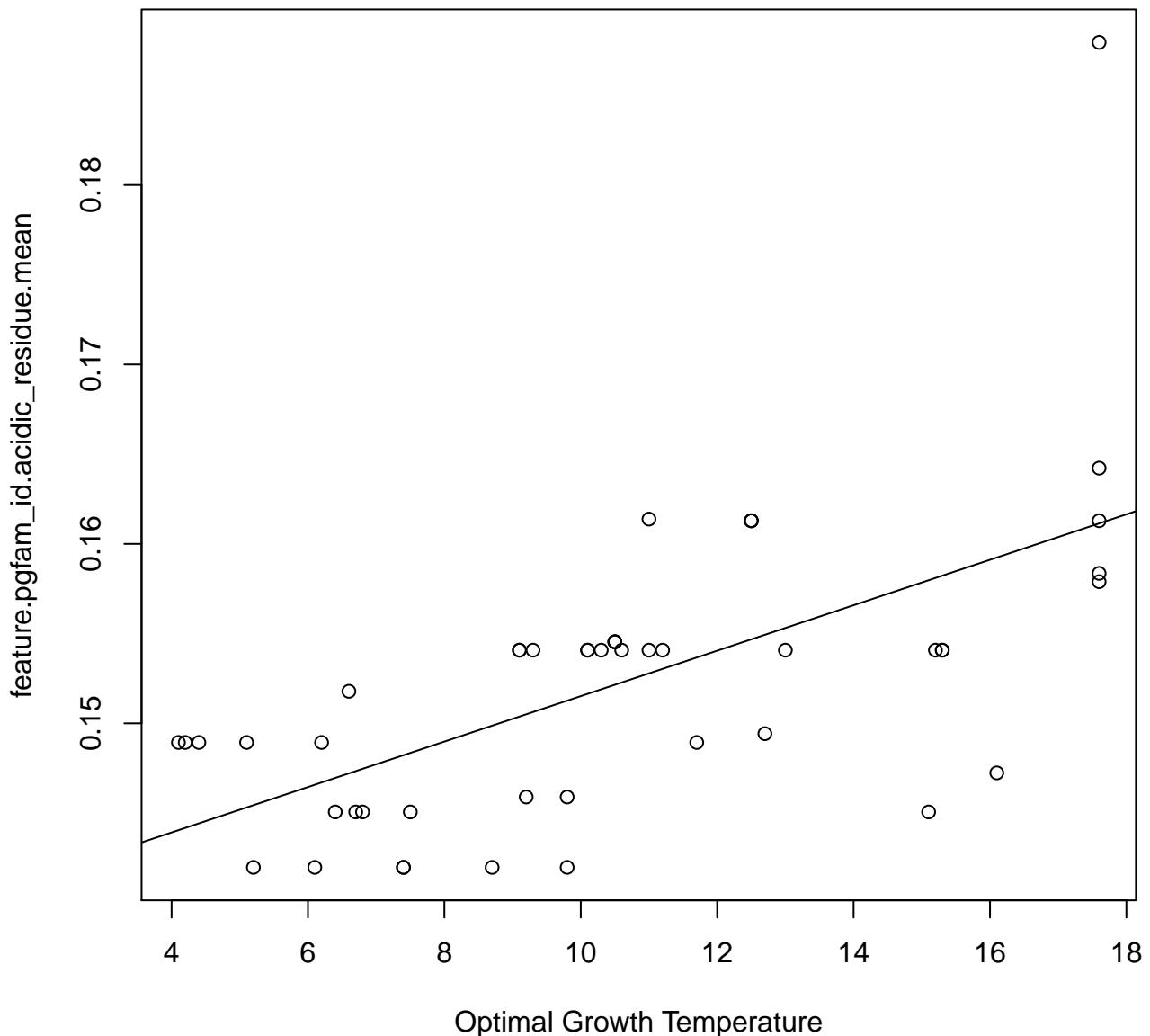
feature.pgfam_id.acidic_residue.mean
PGF_01336366
hypothetical protein



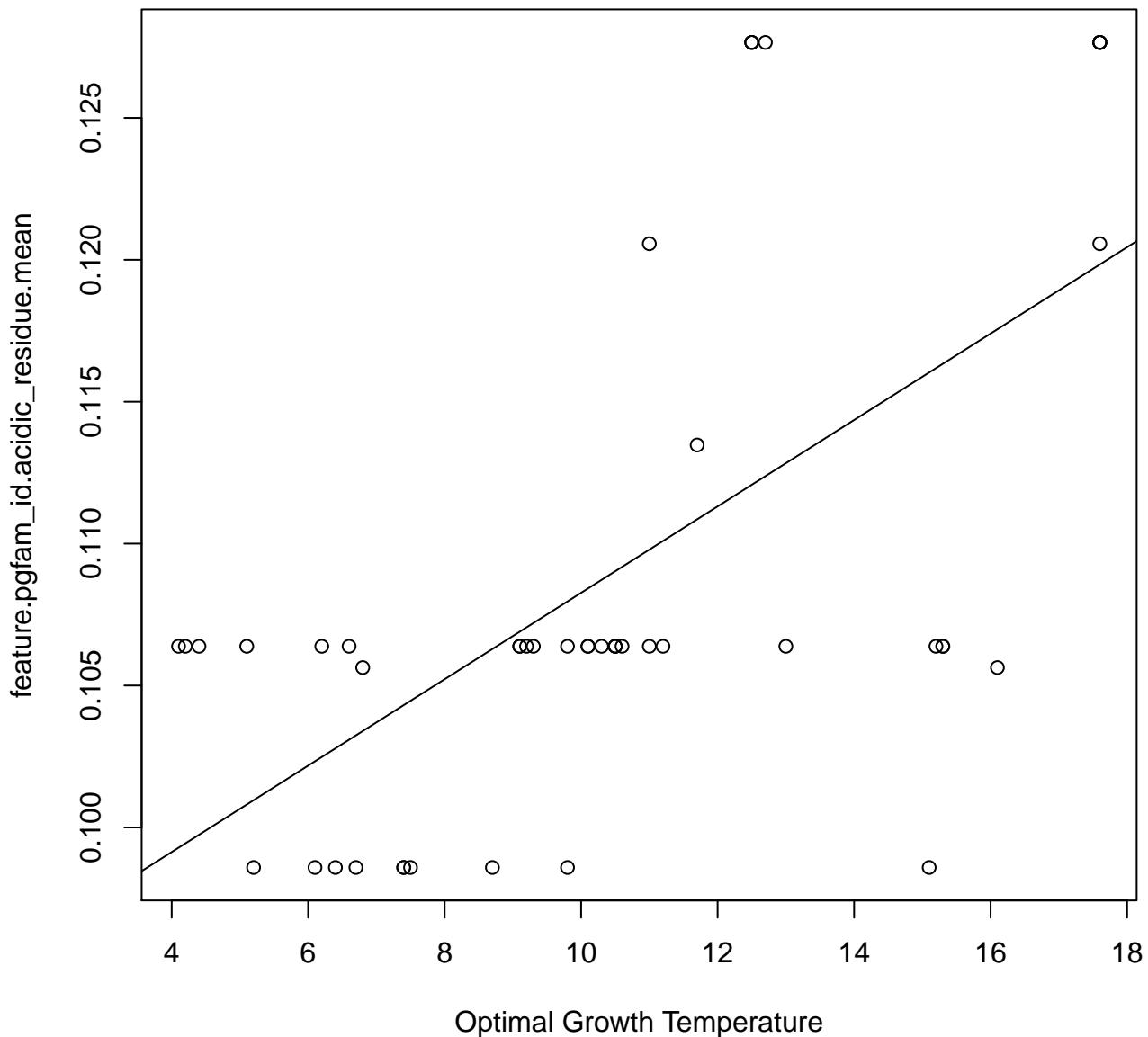
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PGF_03198057
Inner membrane protein YpjD



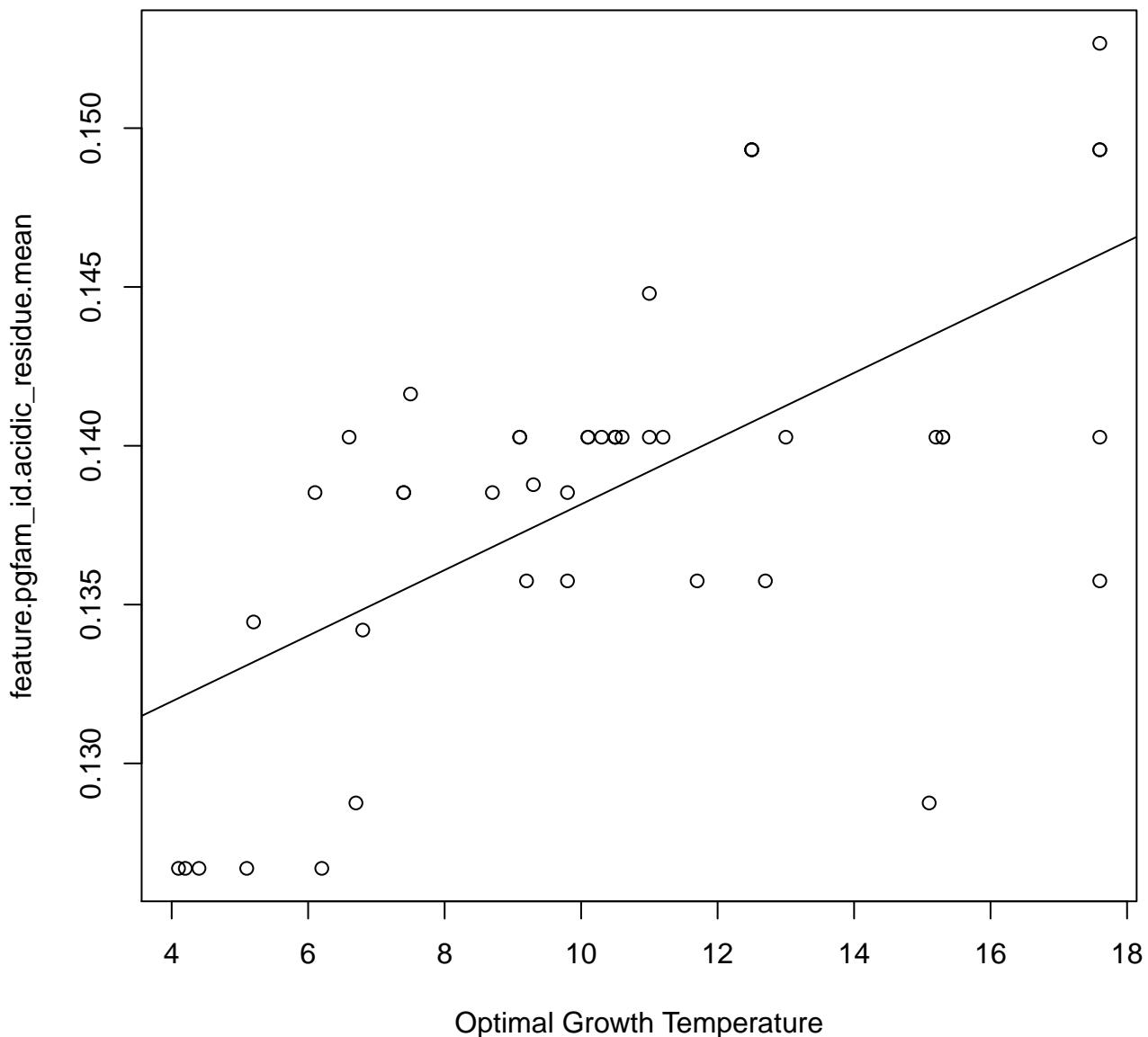
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PGF_00048327
Rhodanese domain protein UPF0176



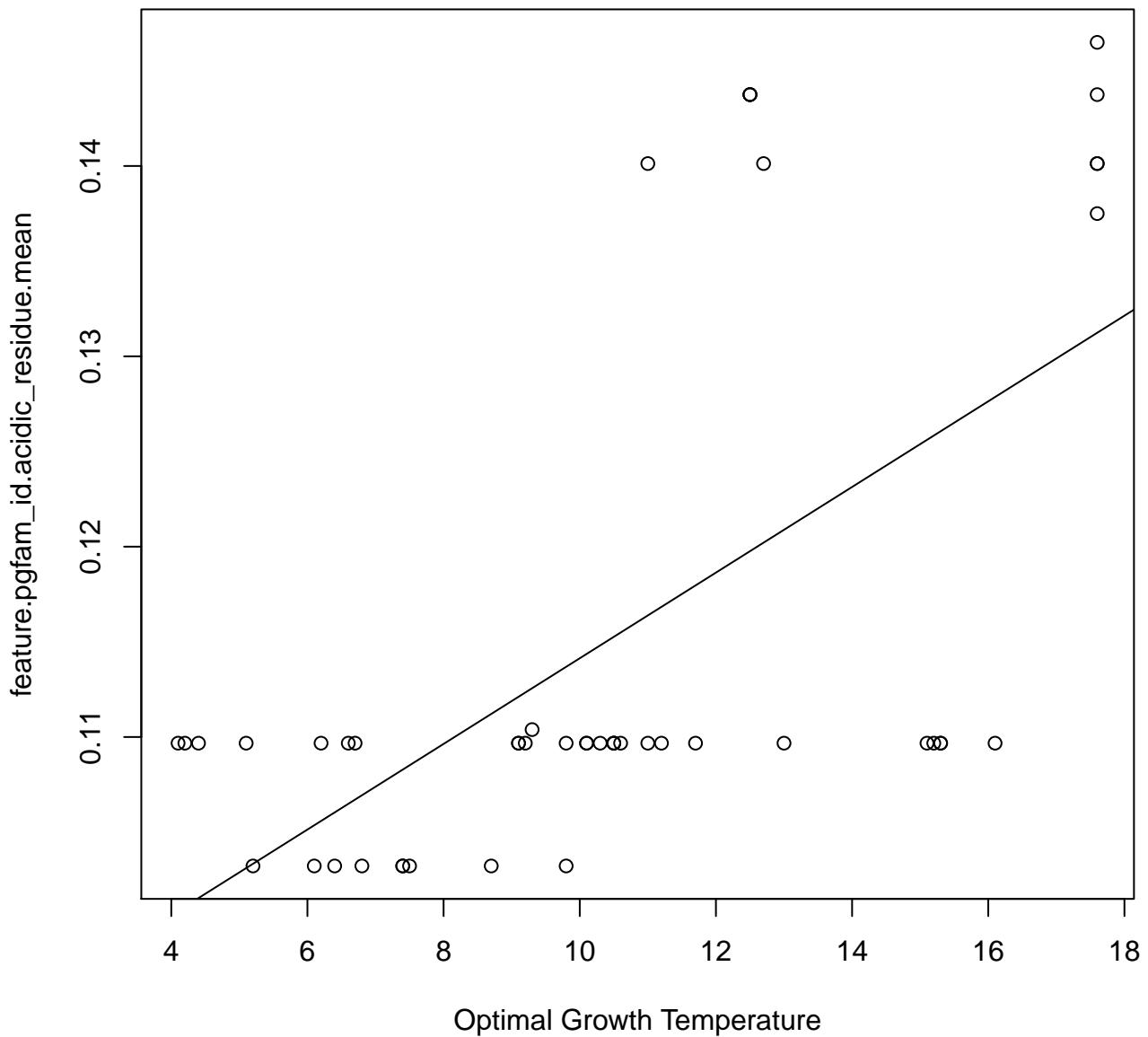
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PGF_00057016
Tol biopolymer transport system, TolR protein



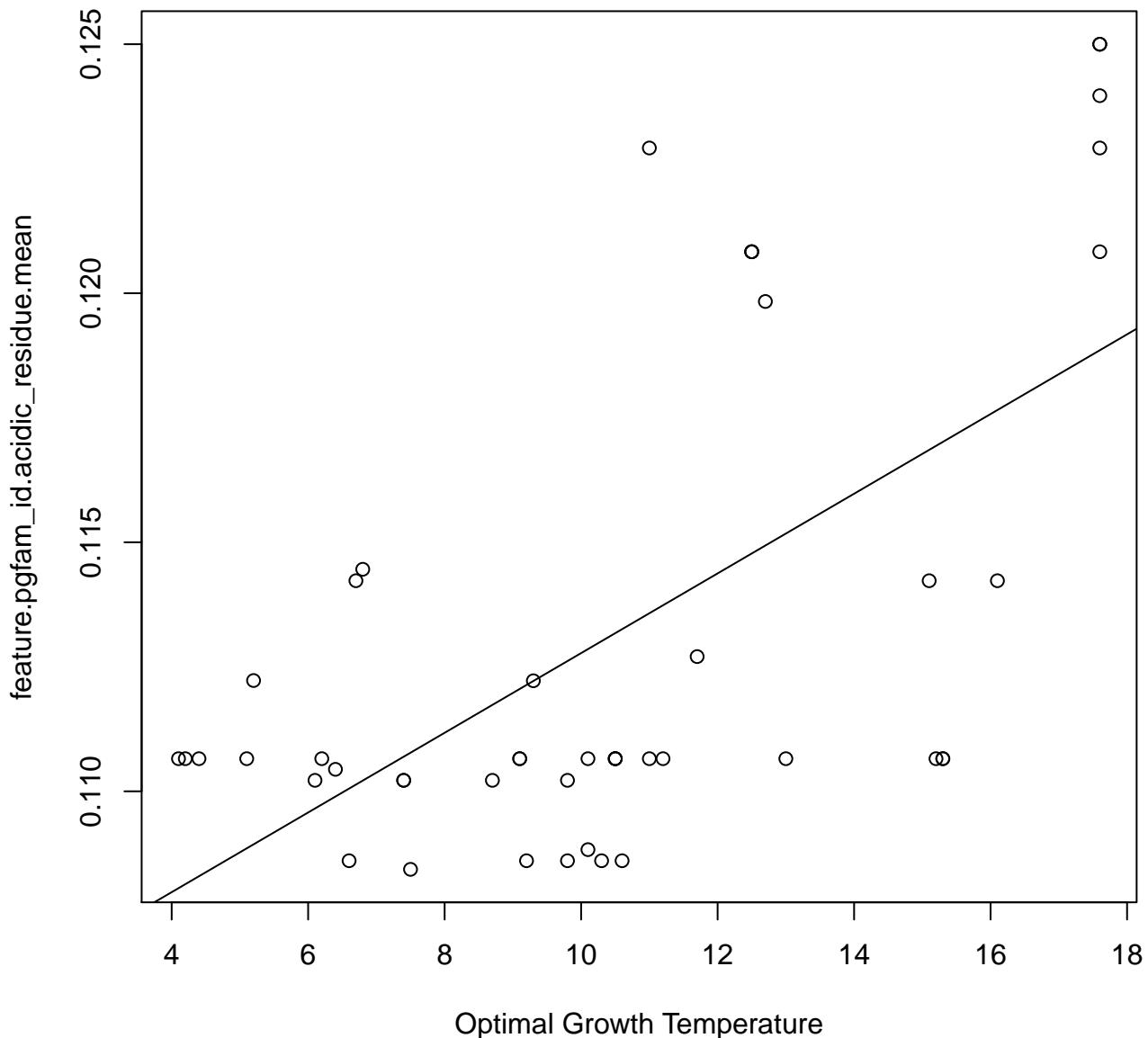
feature.pgfam_id.acidic_residue.mean
PGF_00038573
Protein of unknown function YceH



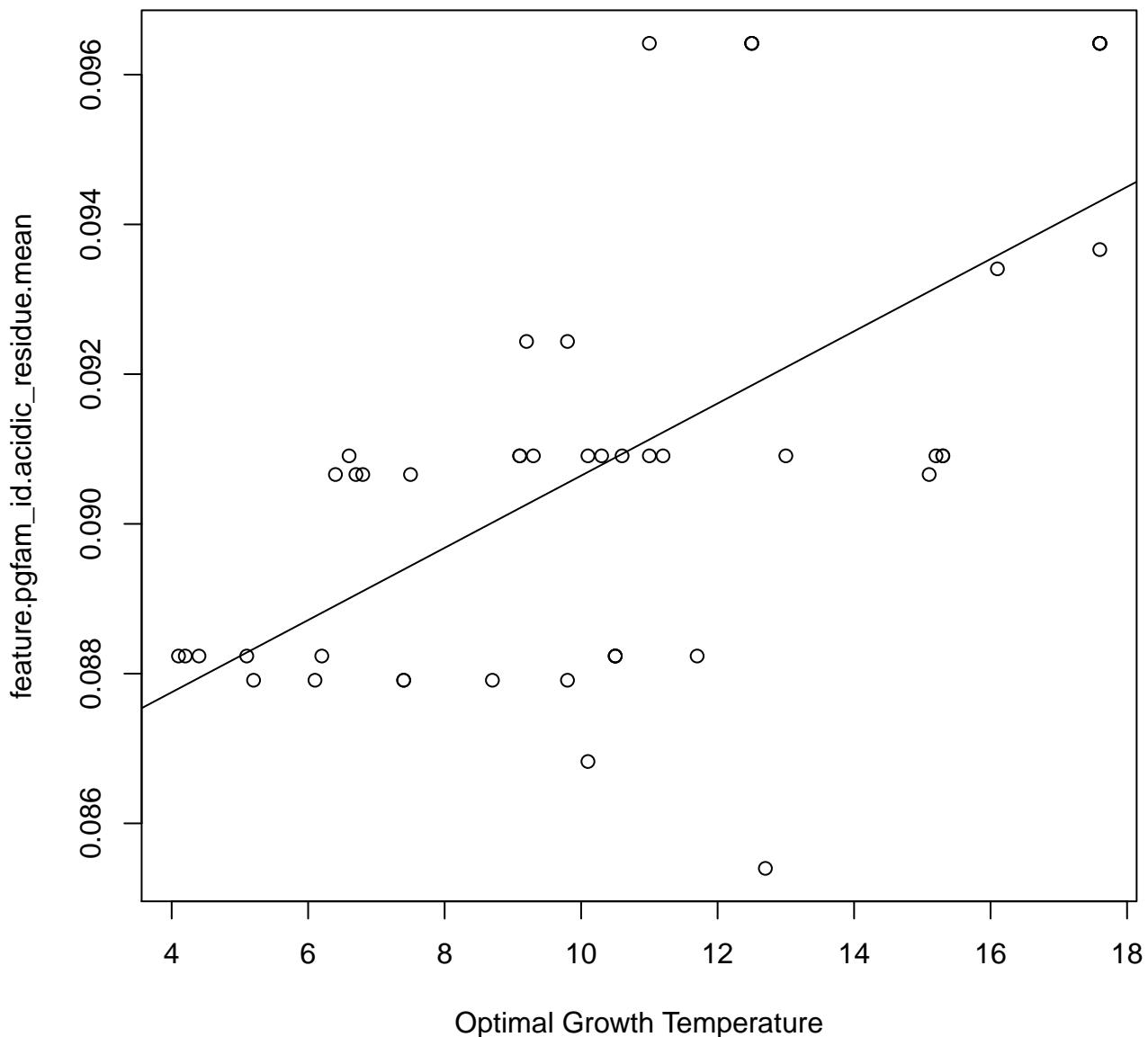
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PGF_00973394
Phospholipid ABC transporter substrate-binding protein MlaD



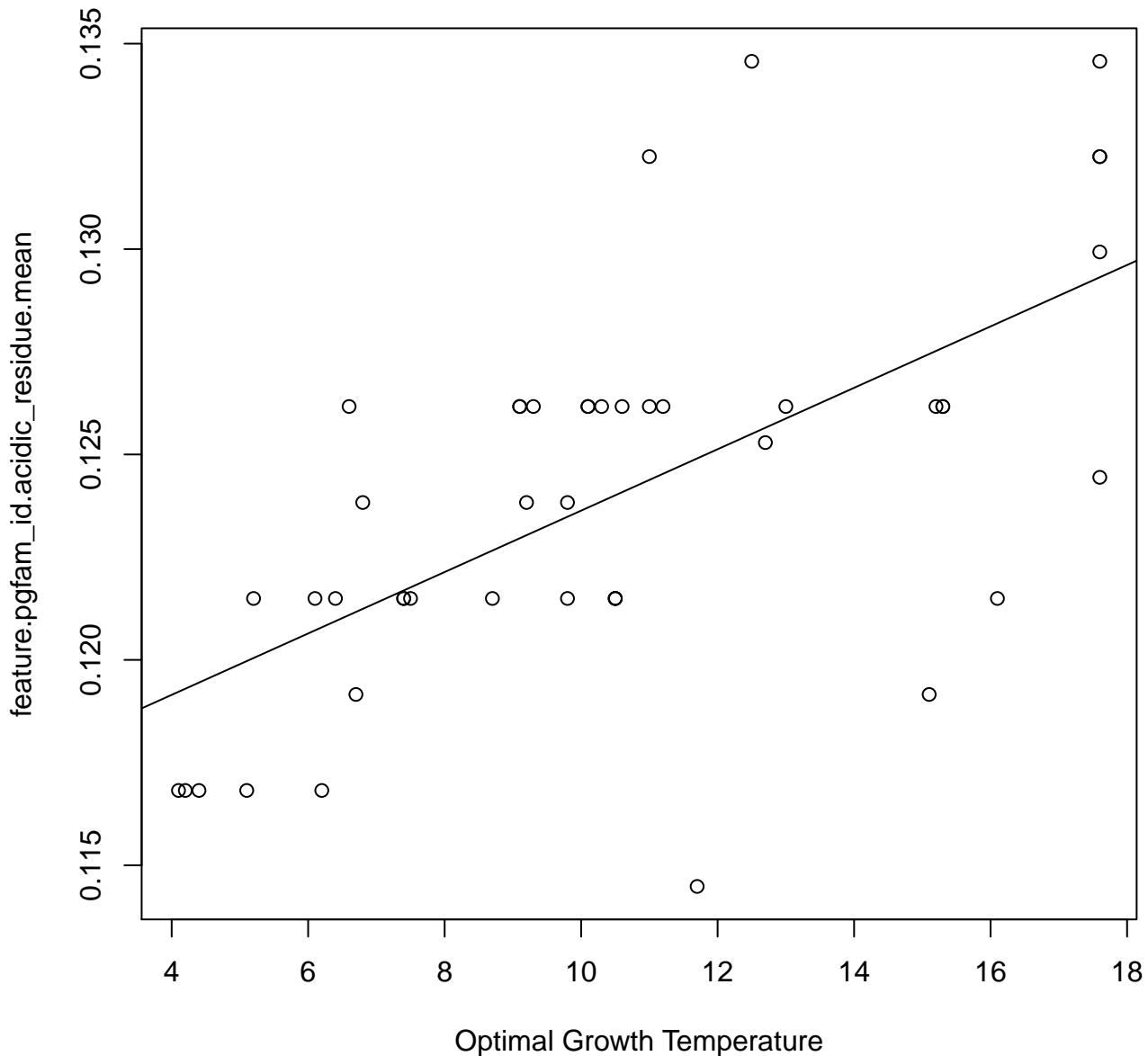
feature.pgfam_id.acidic_residue.mean
PGF_00002980
FIG032621: Hydrolase, alpha/beta hydrolase fold family



feature.pgfam_id.acidic_residue.mean
PGF_00005288
Flagellar P-ring protein Flgl



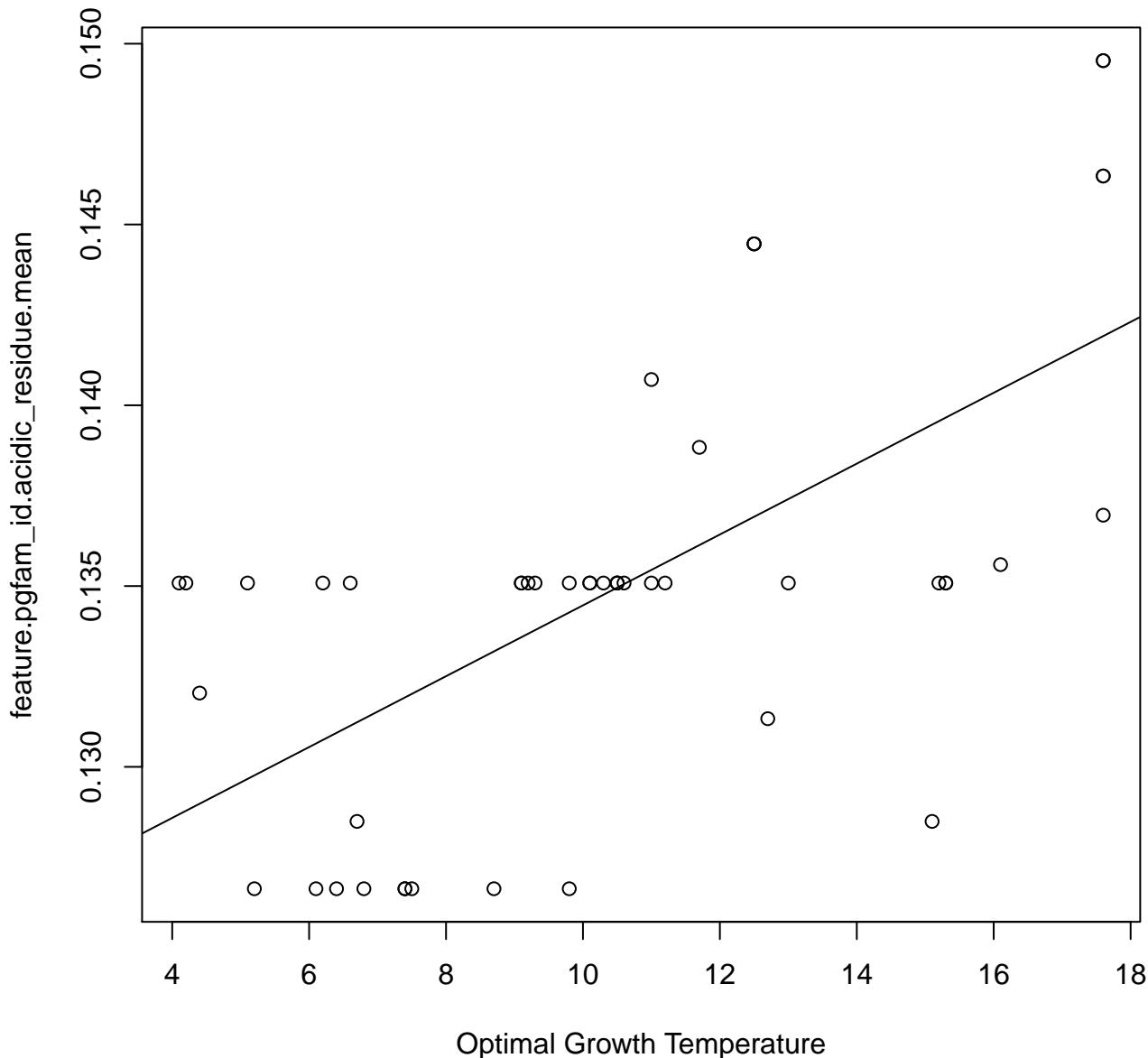
feature.pgfam_id.acidic_residue.mean
PGF_07750515
Phosphoribosylamine--glycine ligase (EC 6.3.4.13)



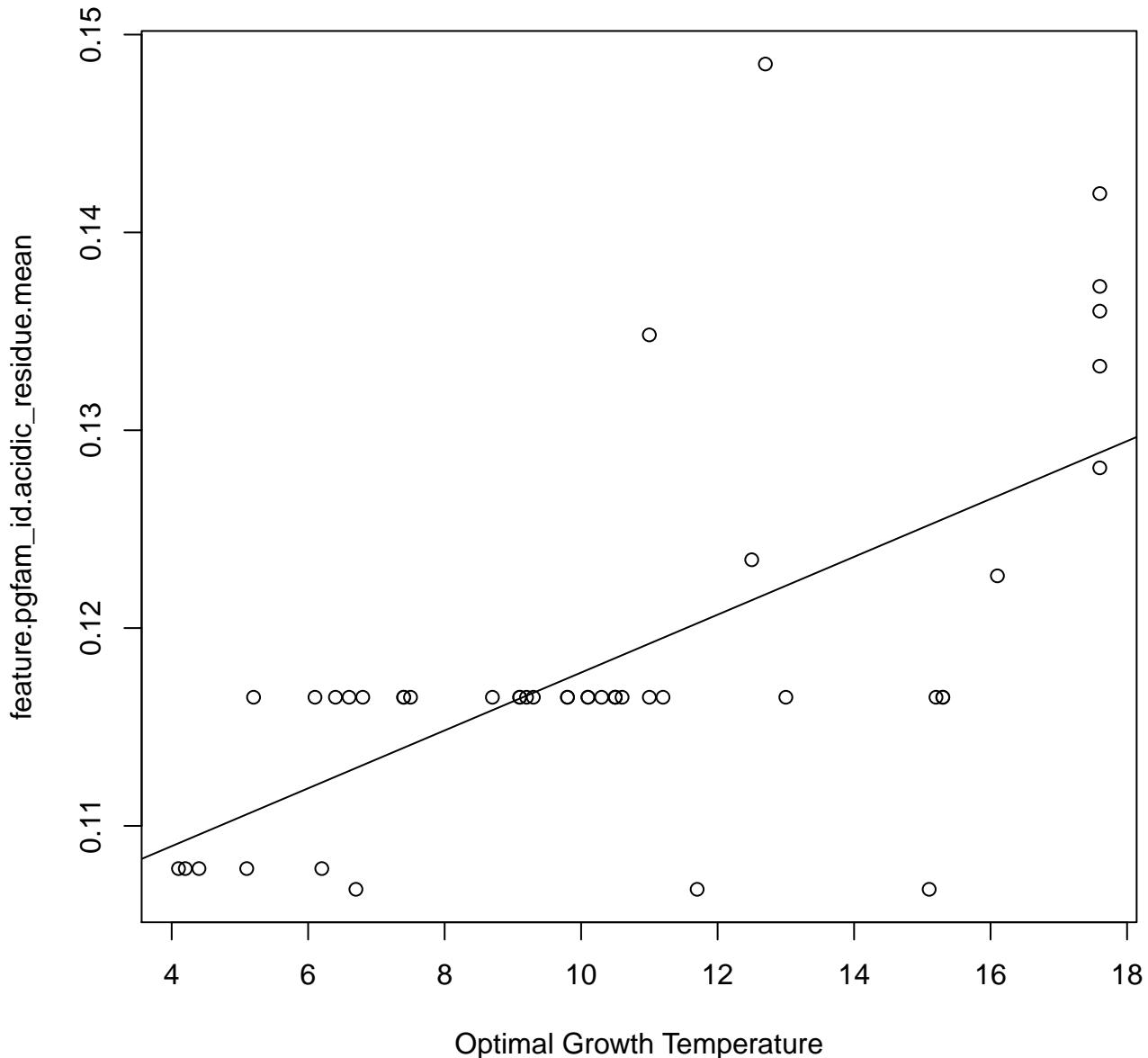
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PGF_00013509

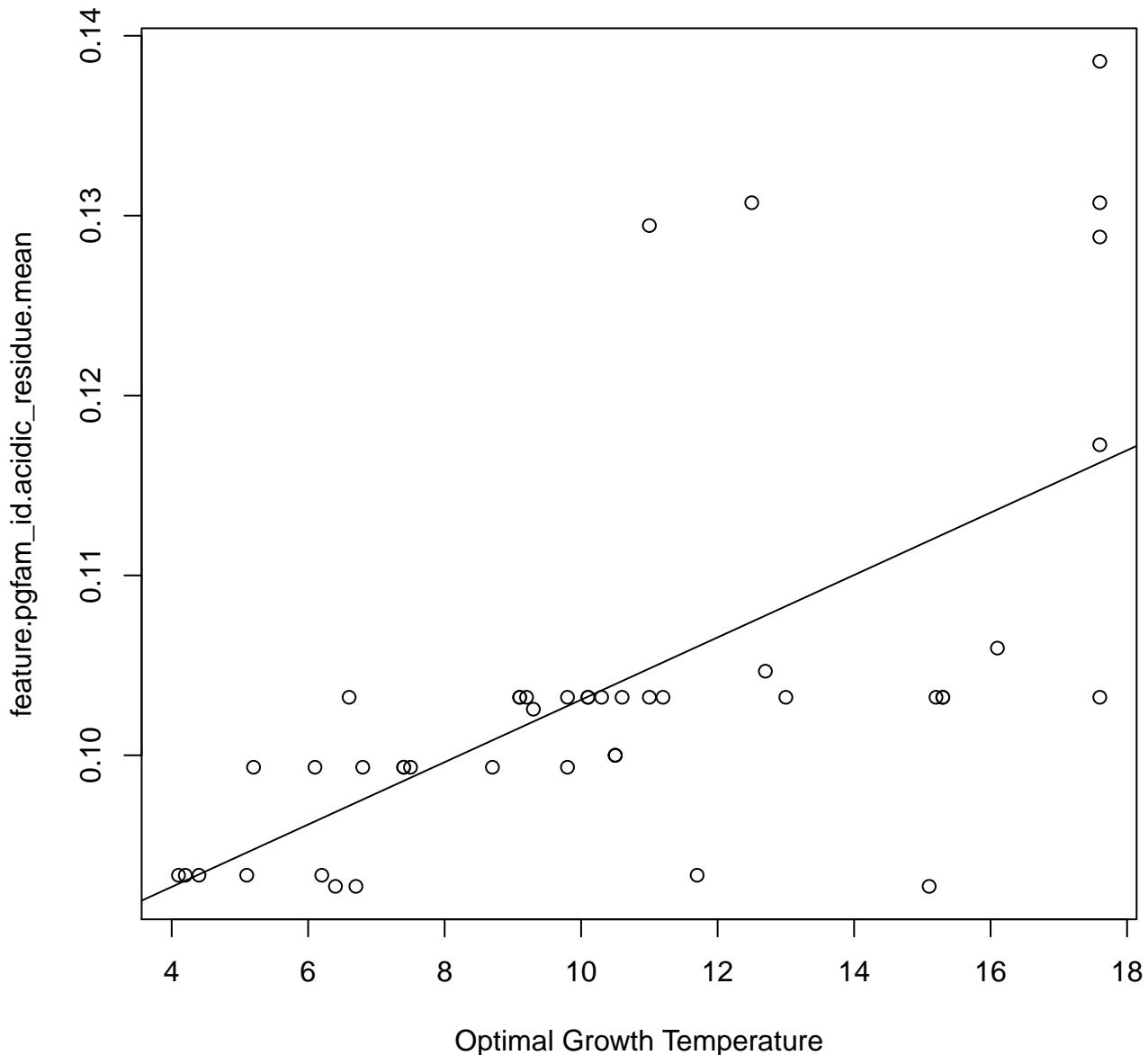
IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)



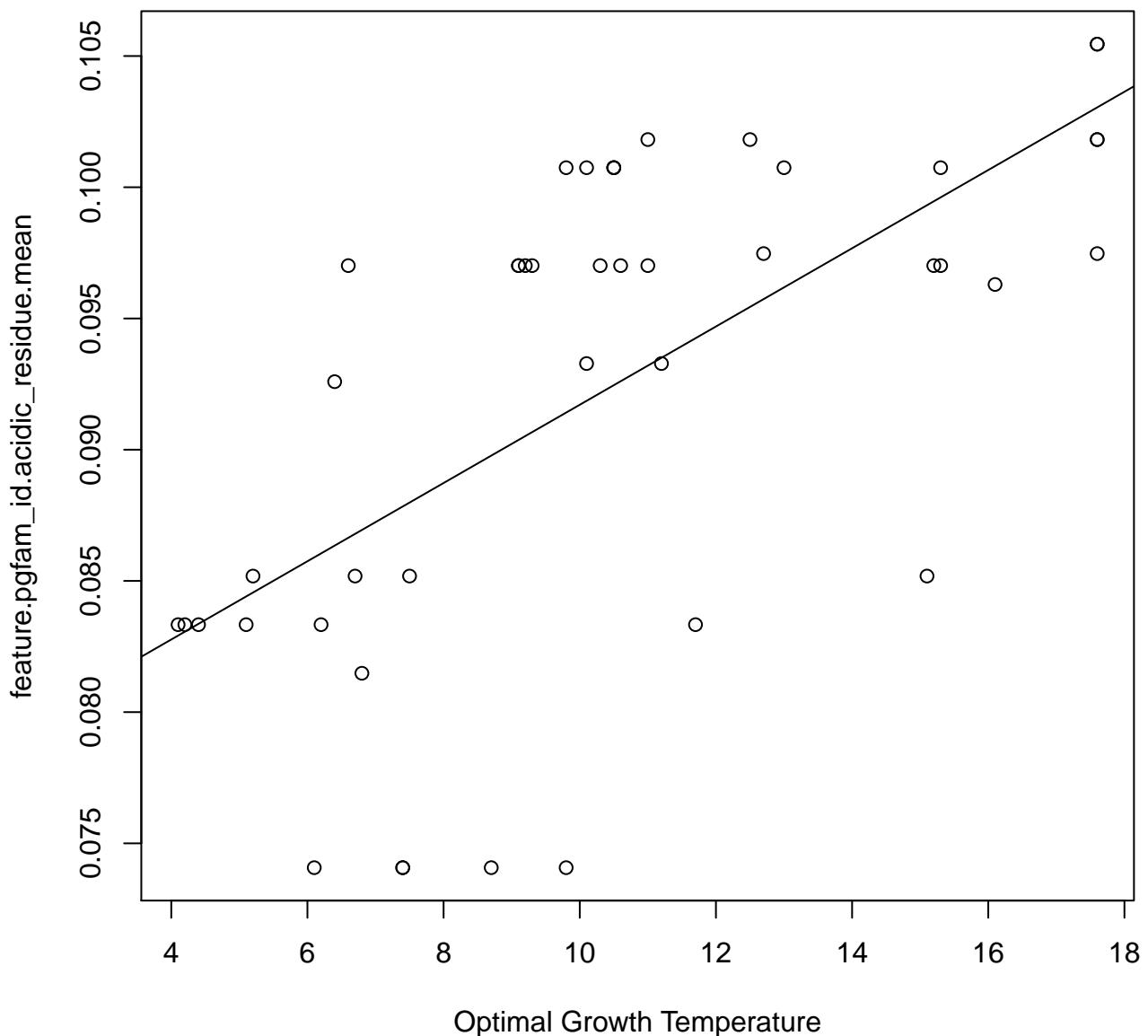
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PGF_08030842
Transcriptional regulator, ArsR family



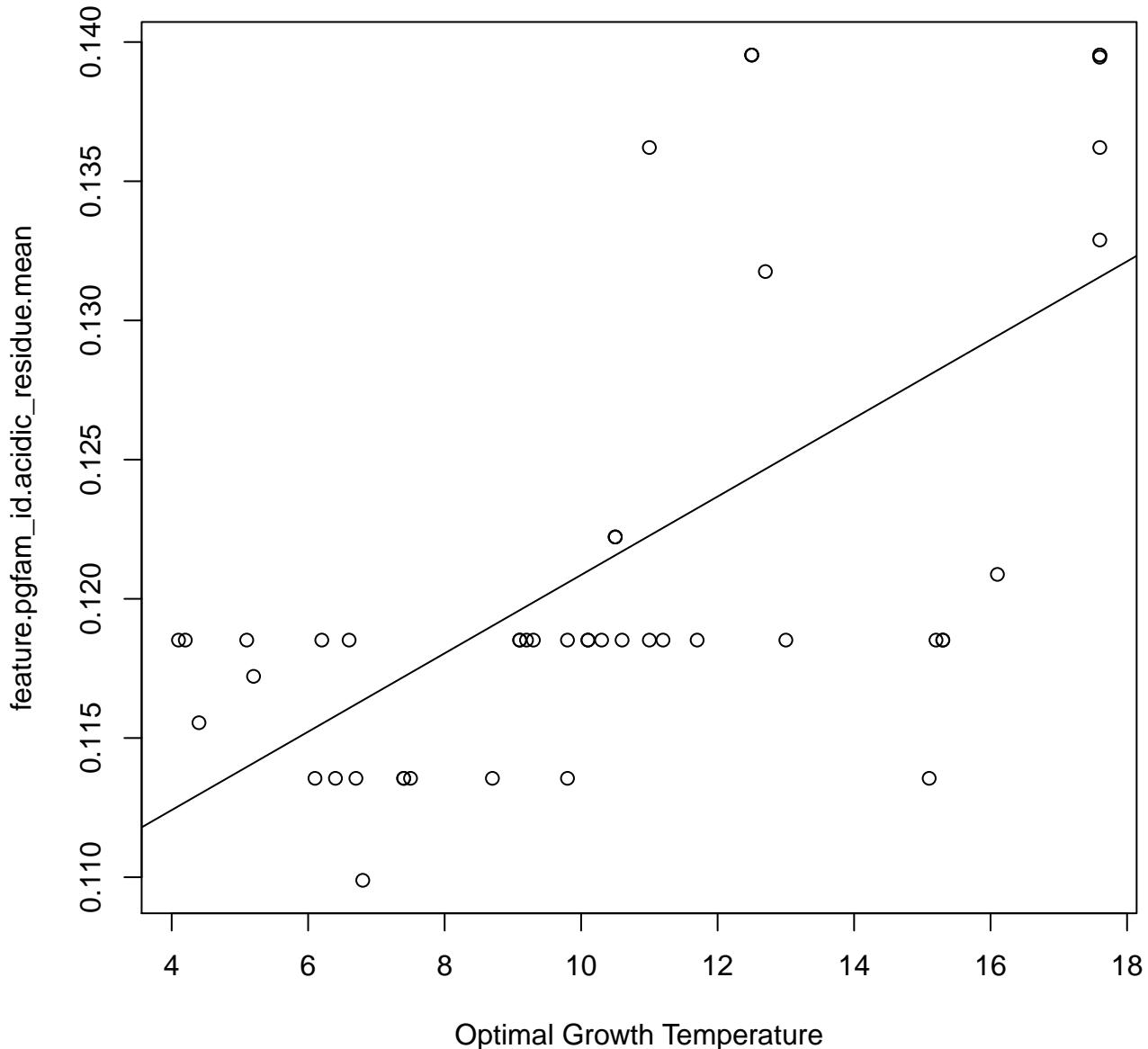
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PGF_07273147
hypothetical protein



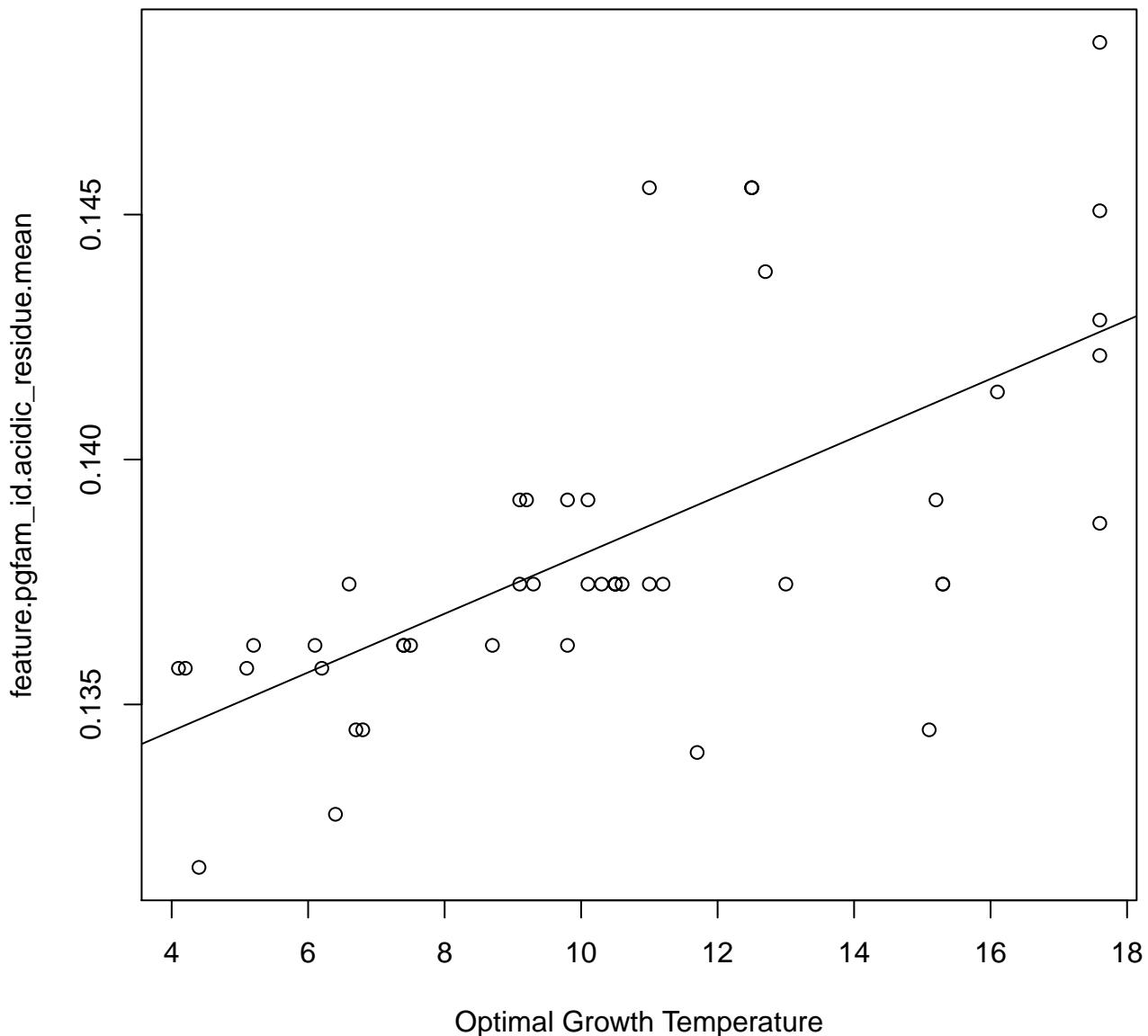
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PGF_08181546
Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)



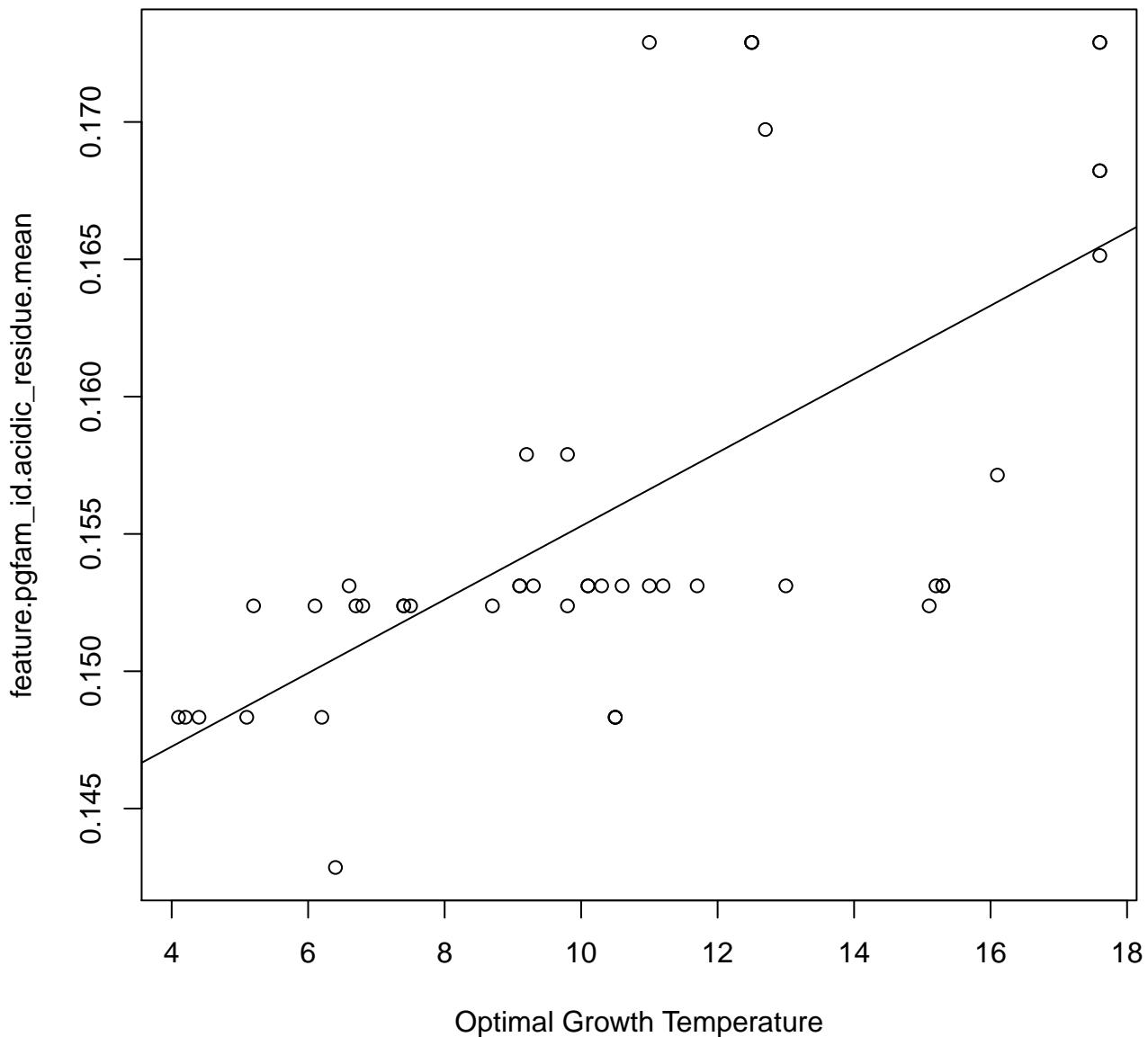
feature.pgfam_id.acidic_residue.mean
PGF_00049827
SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase (EC 2.1.1.182)



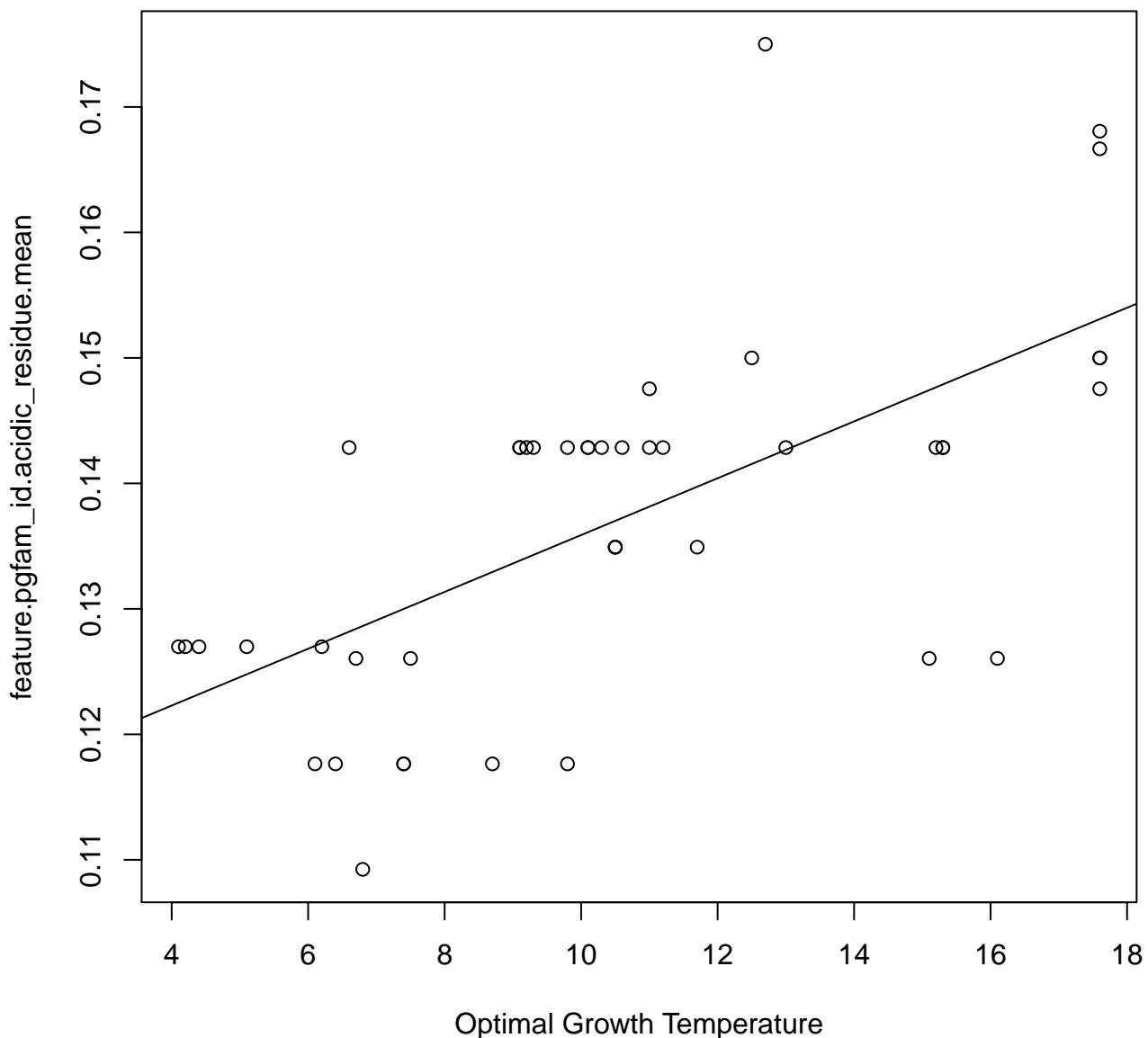
feature.pgfam_id.acidic_residue.mean
PGF_00055052
Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)



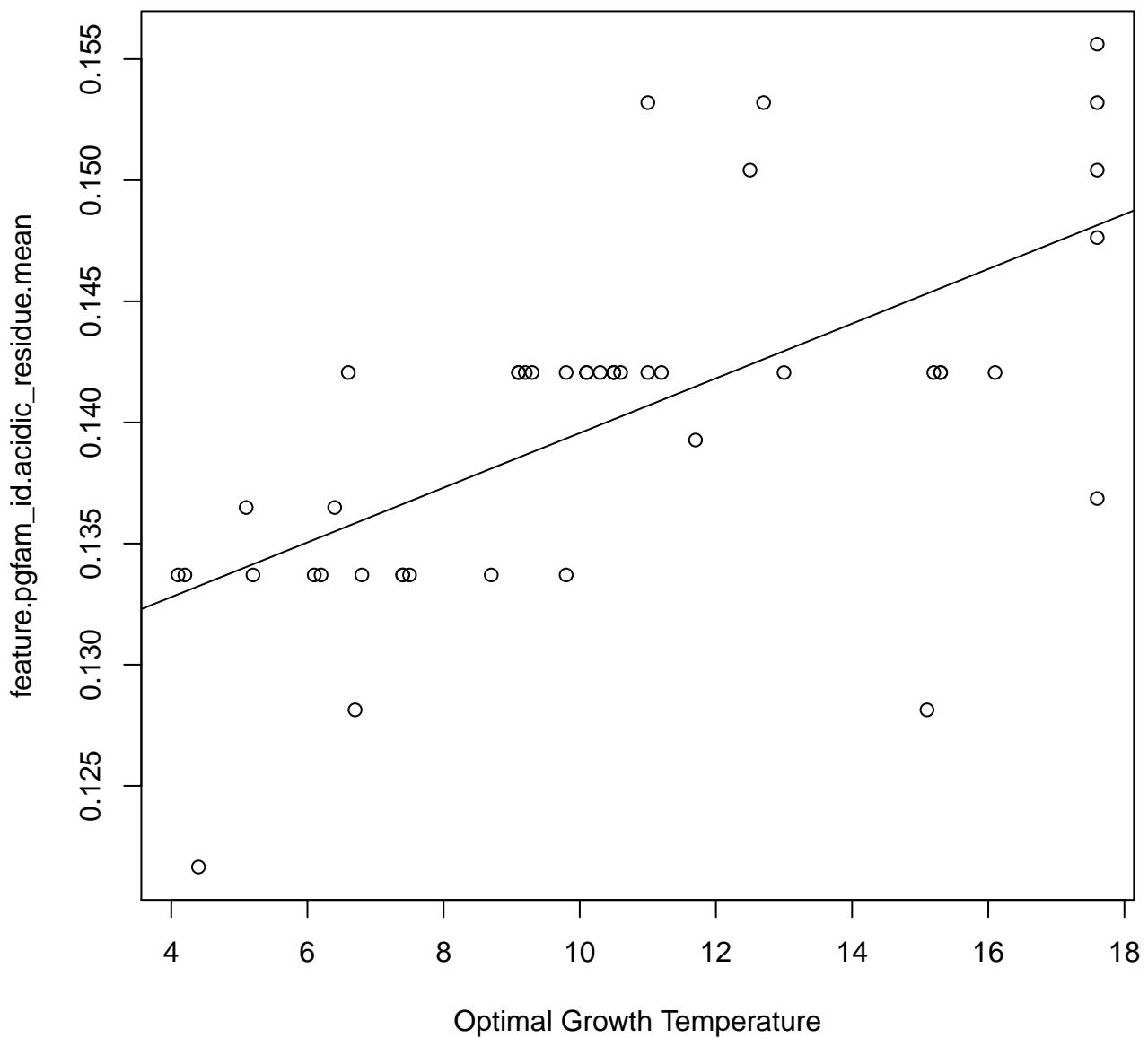
feature.pgfam_id.acidic_residue.mean
PGF_00423436
Dimeric dUTPase (EC 3.6.1.23)



feature.pgfam_id.acidic_residue.mean
PGF_00335891
hypothetical protein



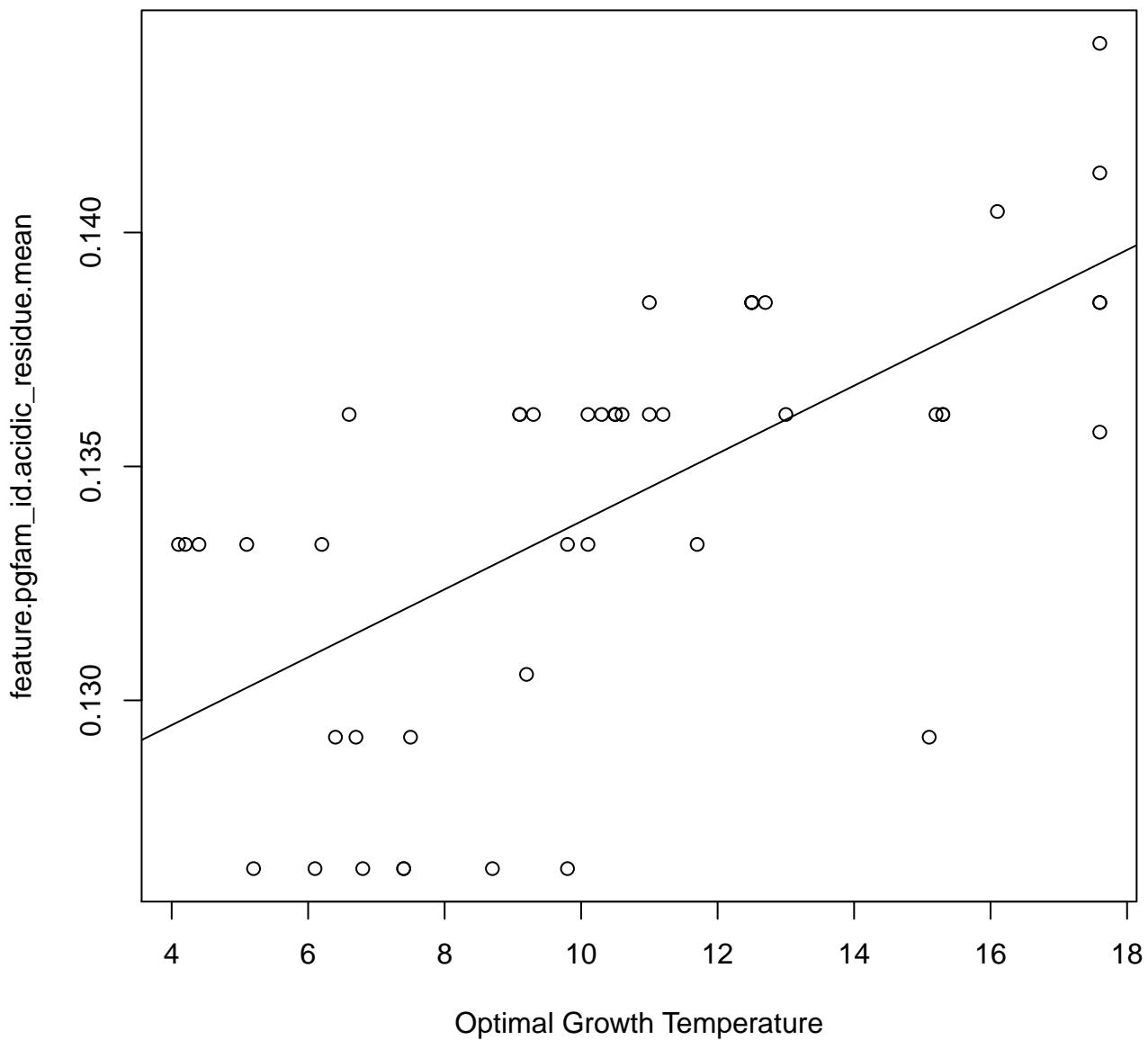
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PGF_10384663
Type IV pilus biogenesis protein PilM



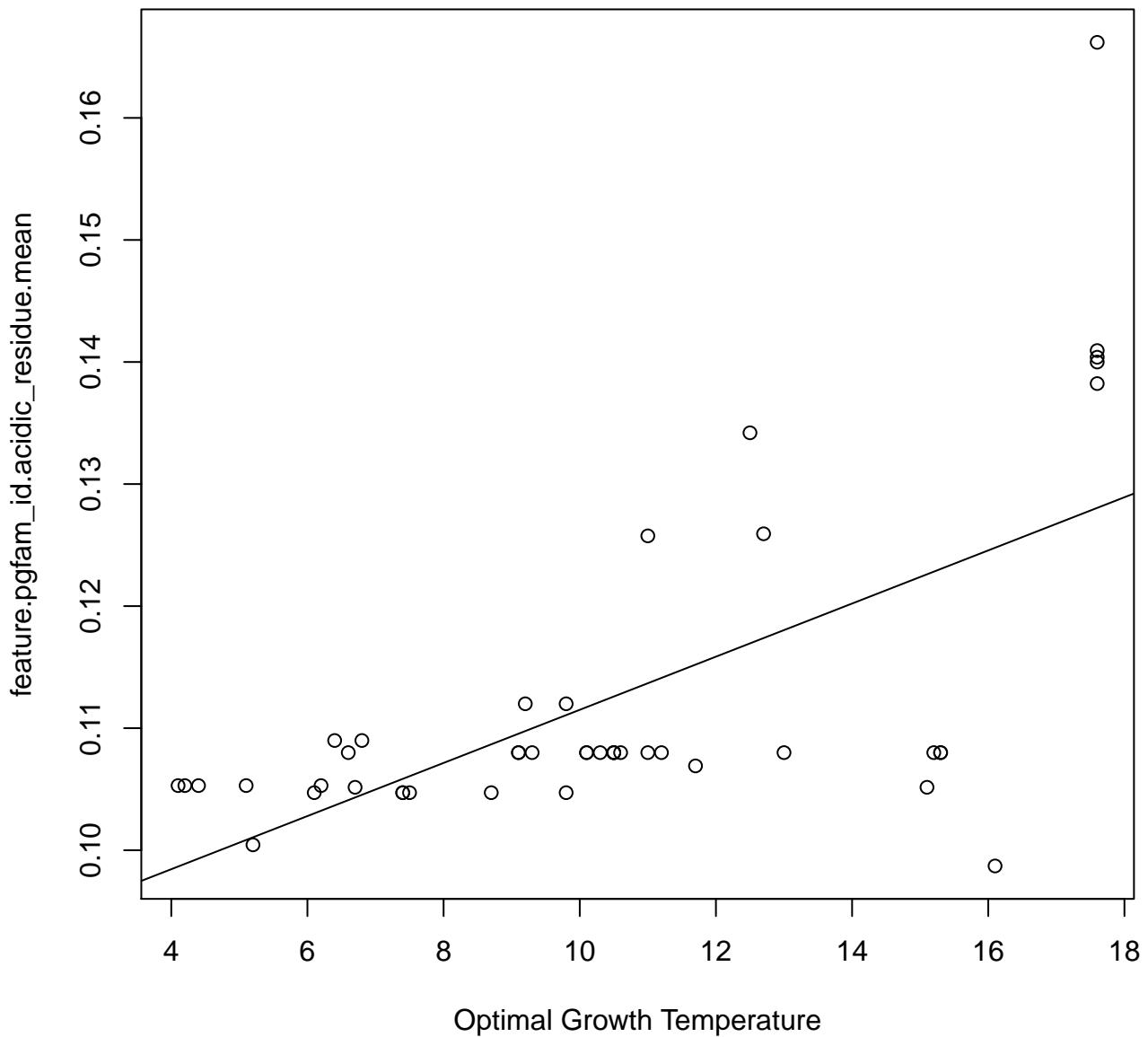
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PGF_00011990

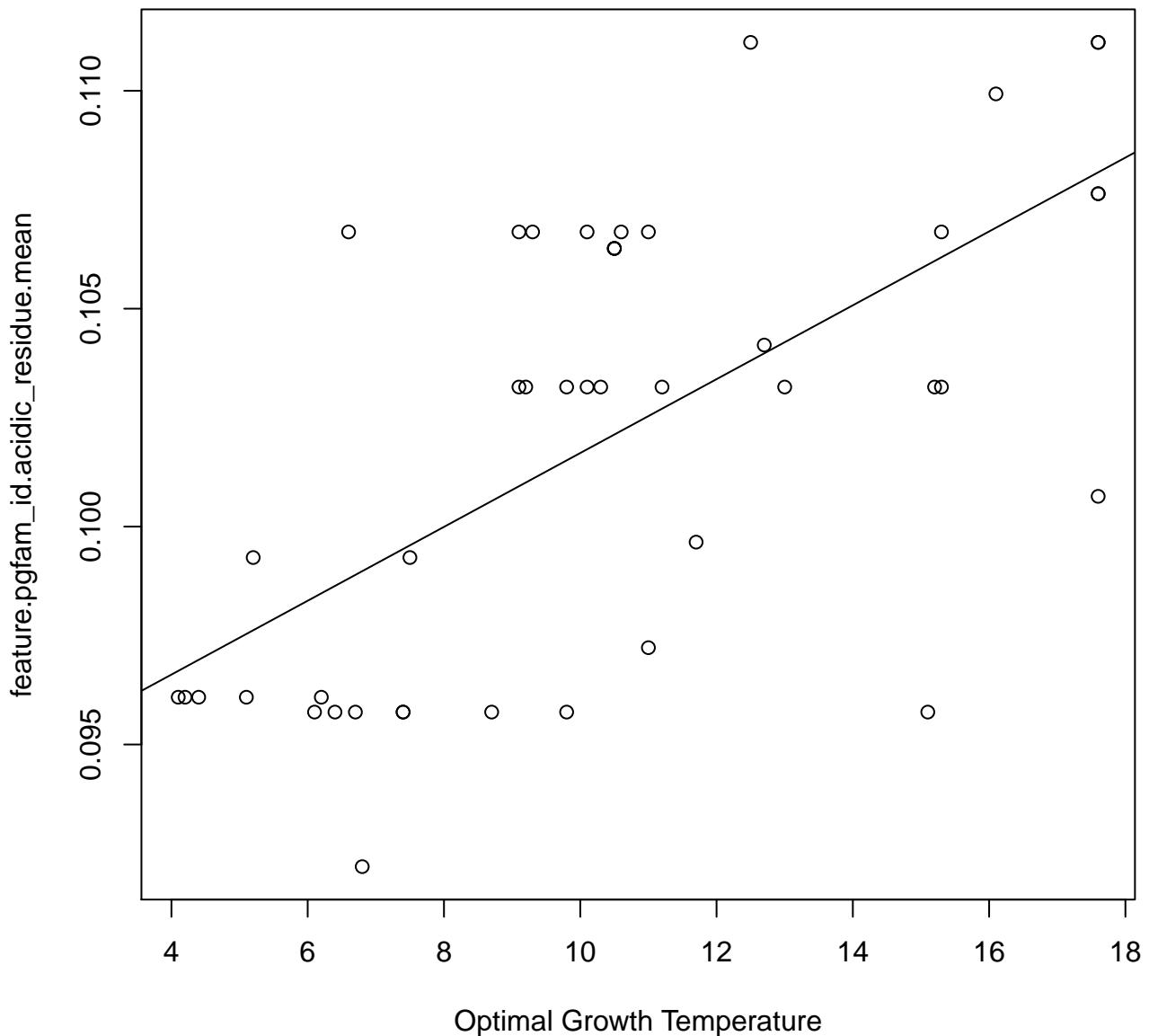
Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)



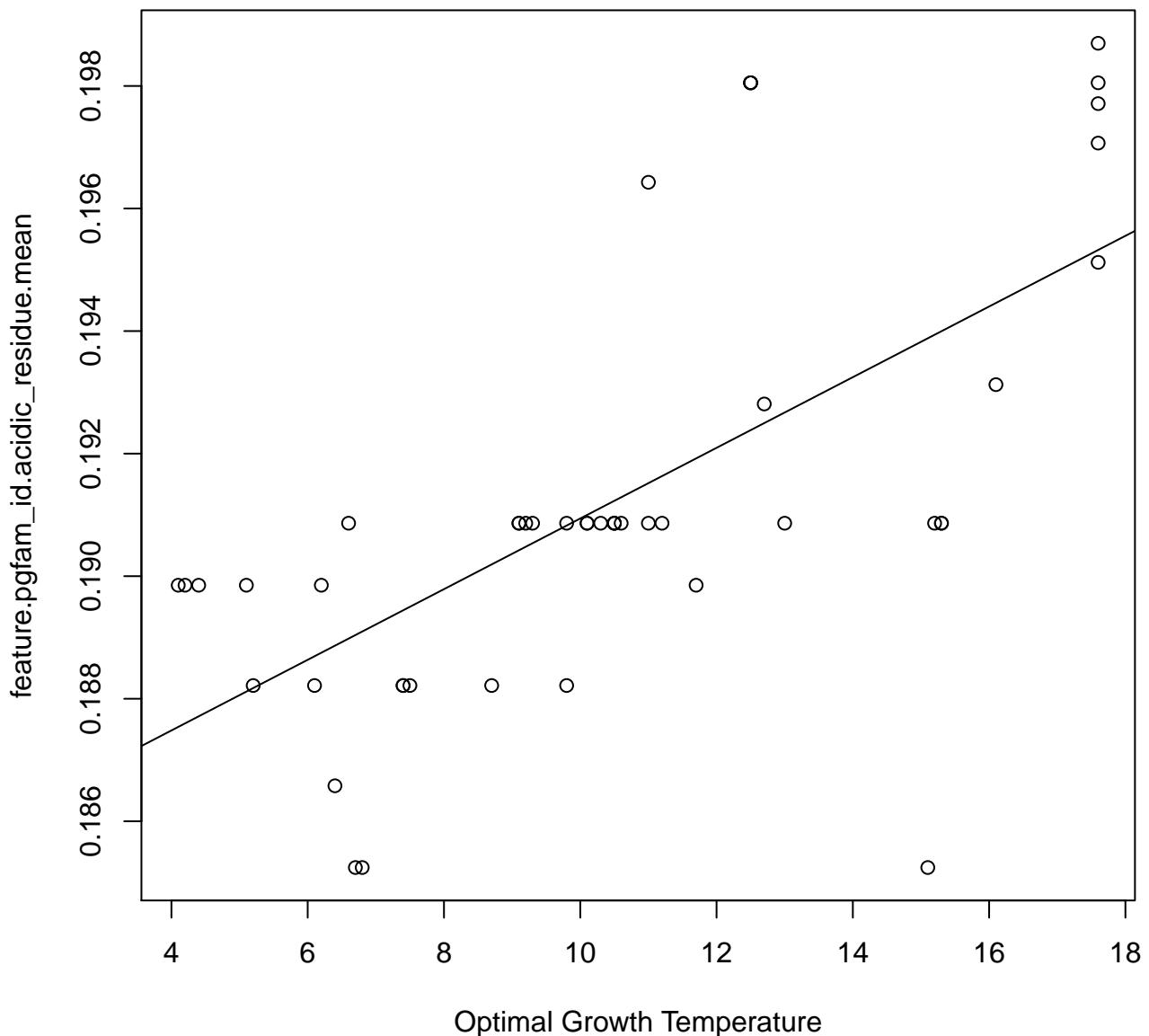
feature.pgfam_id.acidic_residue.mean
PGF_06916058
Uncharacterized S4 RNA-binding-domain protein YbcJ



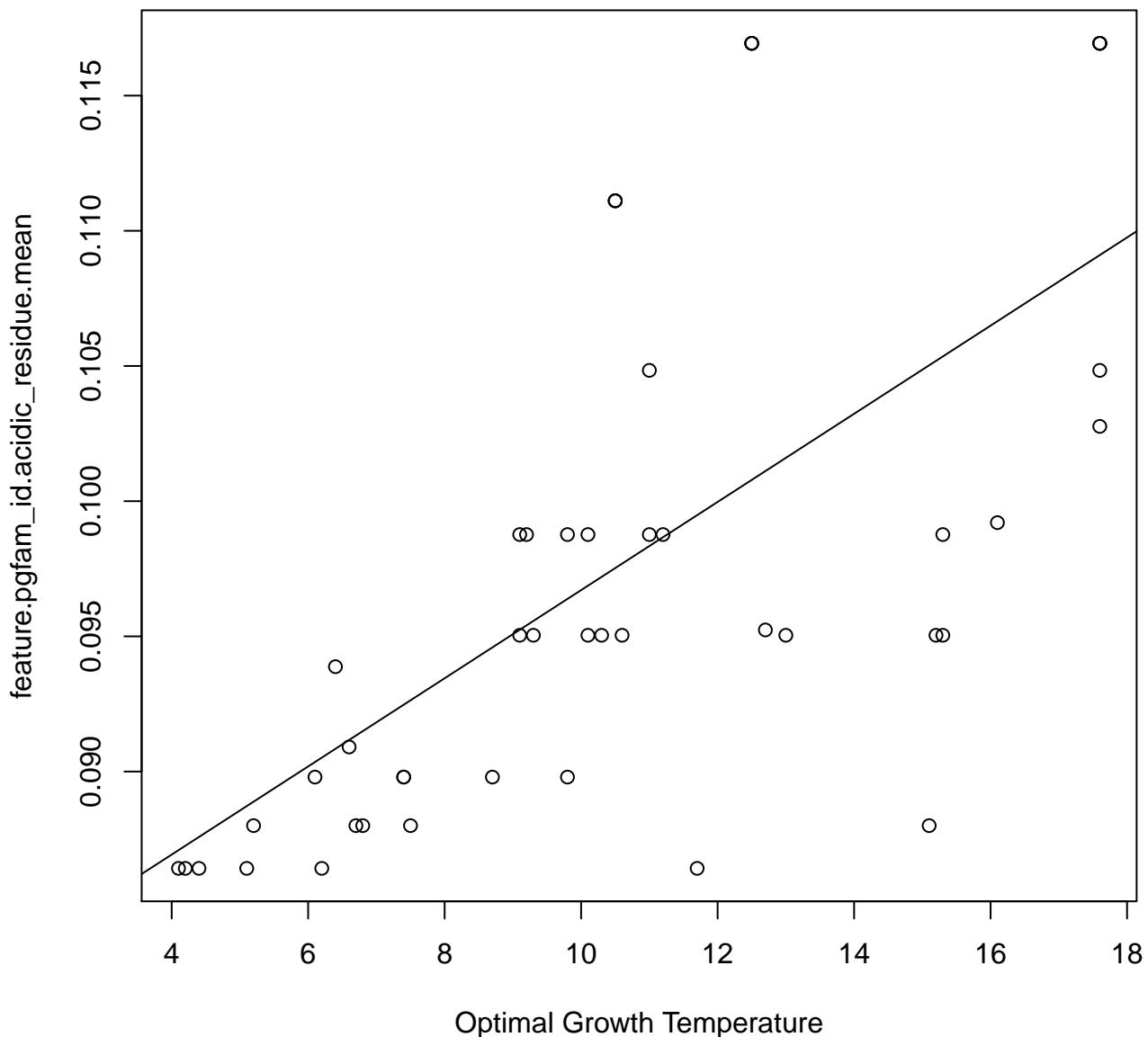
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PGF_00523822
Pantoate--beta-alanine ligase (EC 6.3.2.1)



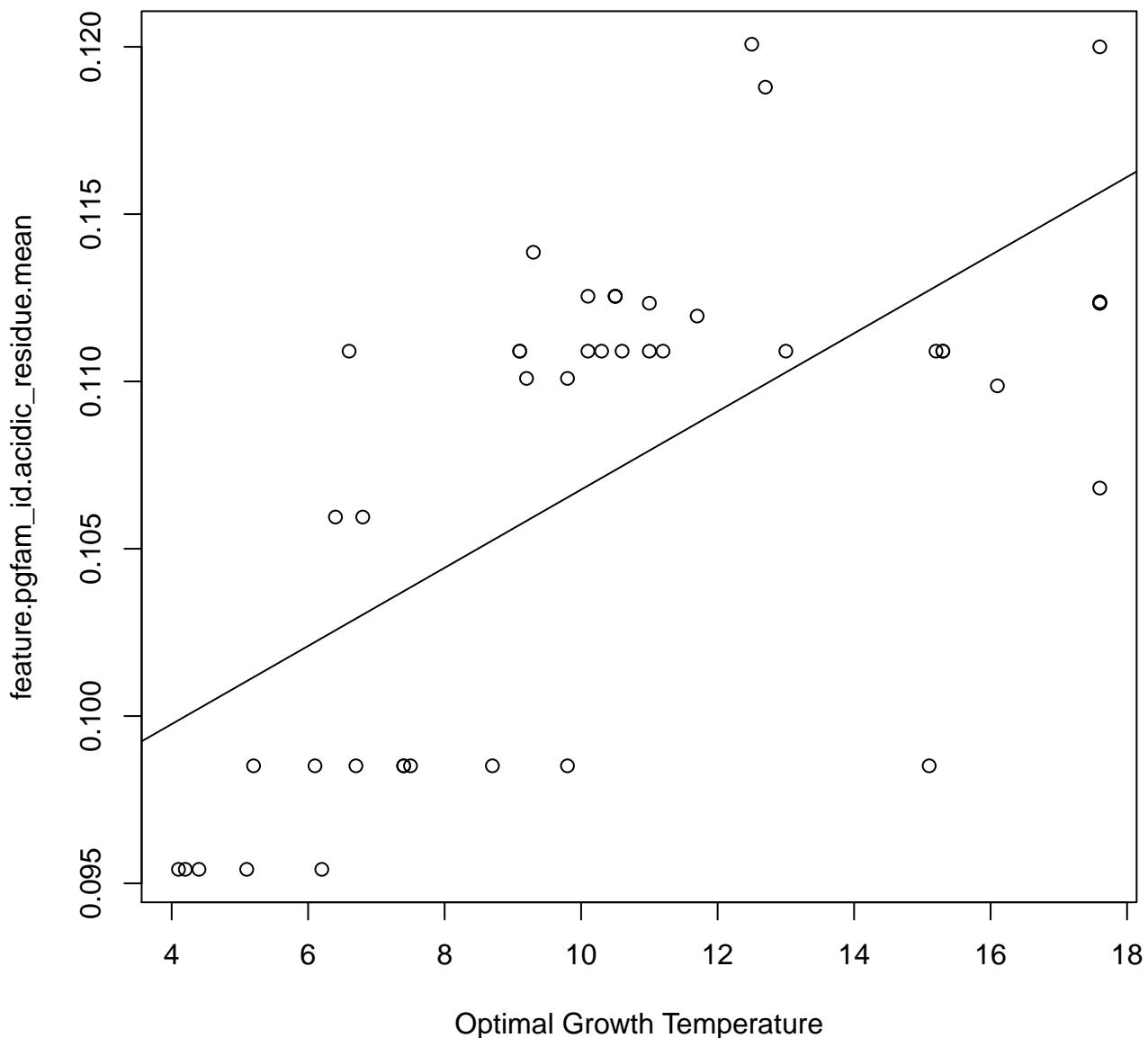
feature.pgfam_id.acidic_residue.mean
PGF_07072582
RNA polymerase sigma factor RpoD



feature.pgfam_id.acidic_residue.mean
PGF_02635429
tRNA (adenine(37)-N6)-methyltransferase



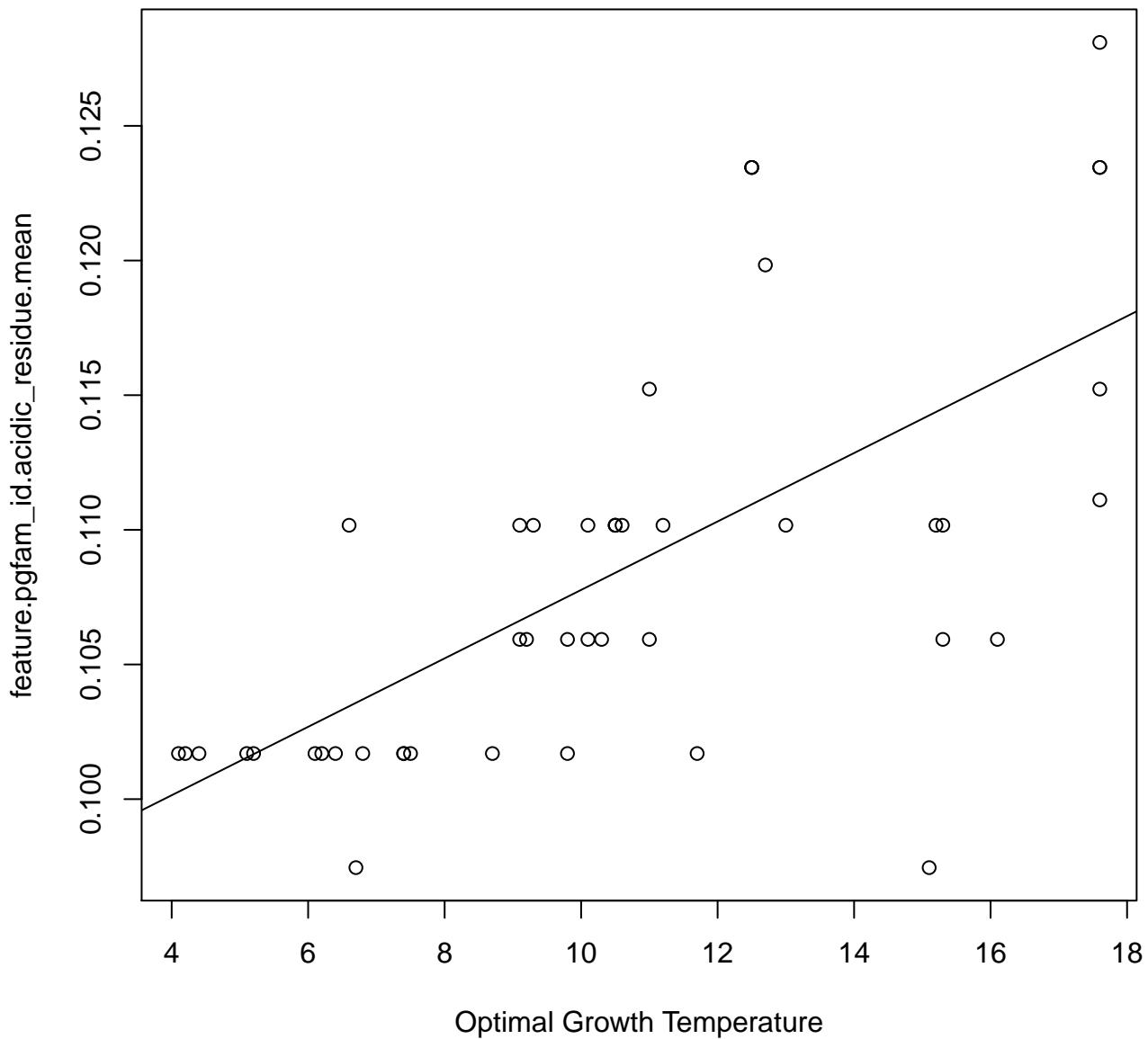
feature.pgfam_id.acidic_residue.mean
PGF_01763633
Sensory box histidine kinase



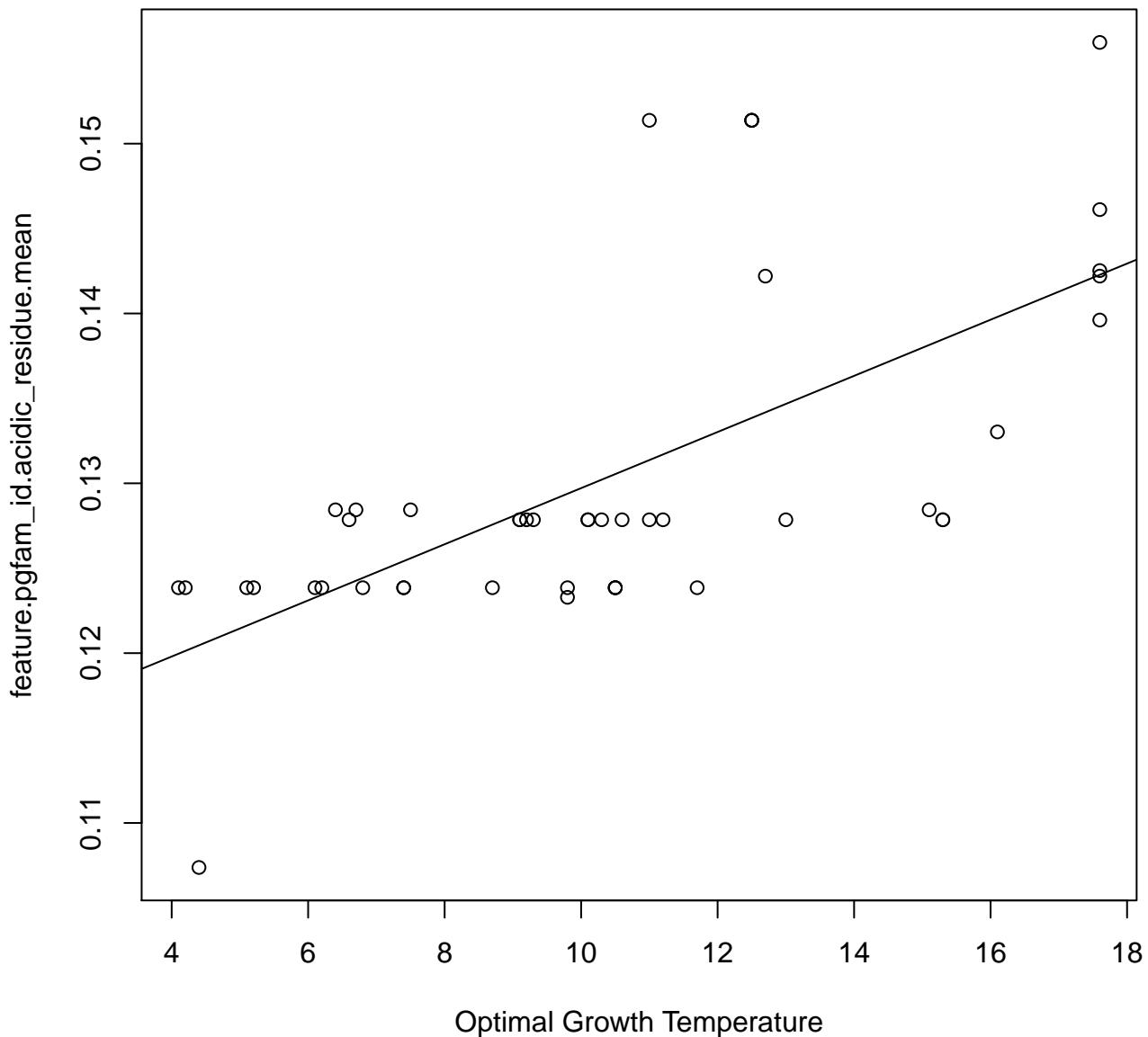
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PGF_00777996

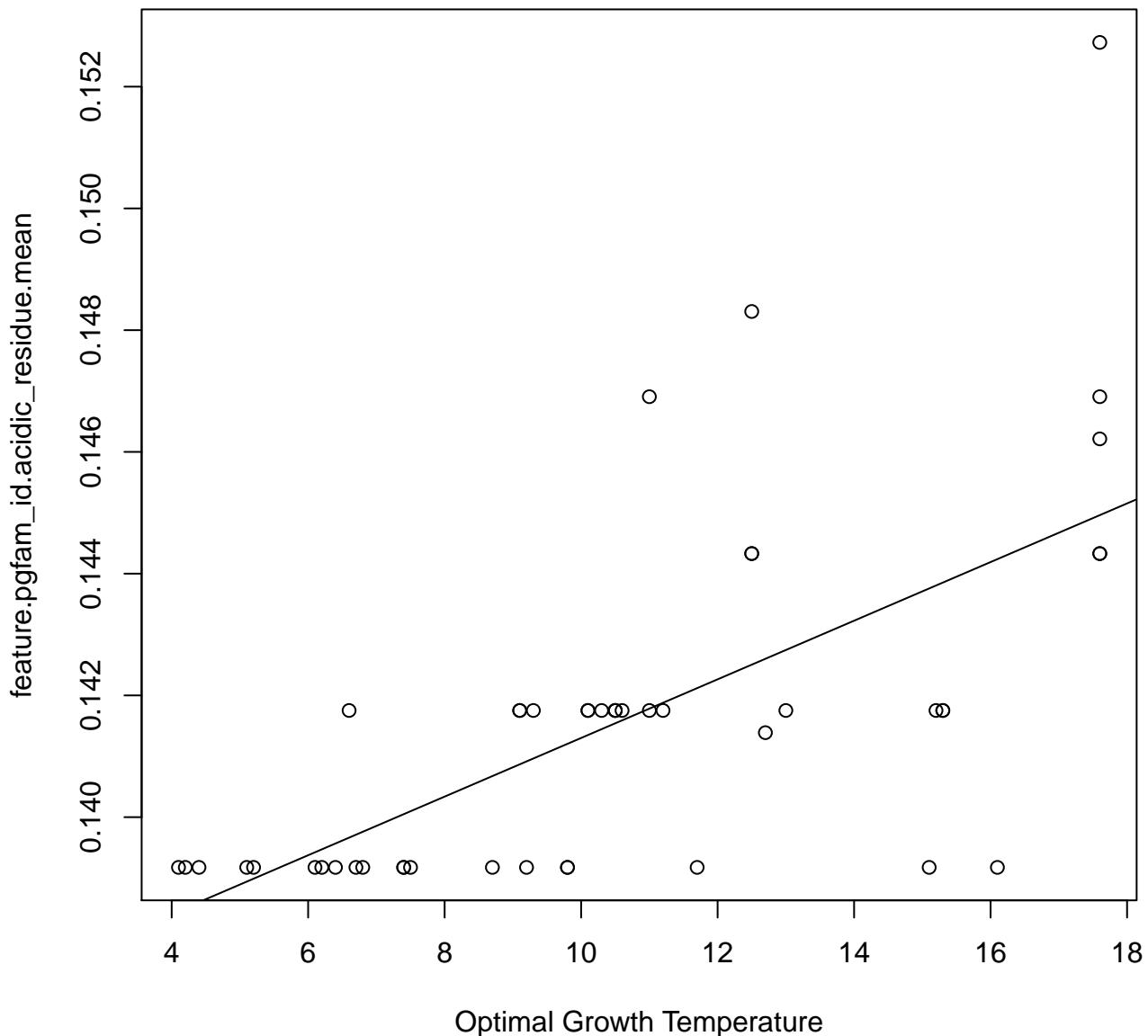
5'-methylthioadenosine nucleosidase (EC 3.2.2.16) @ S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)



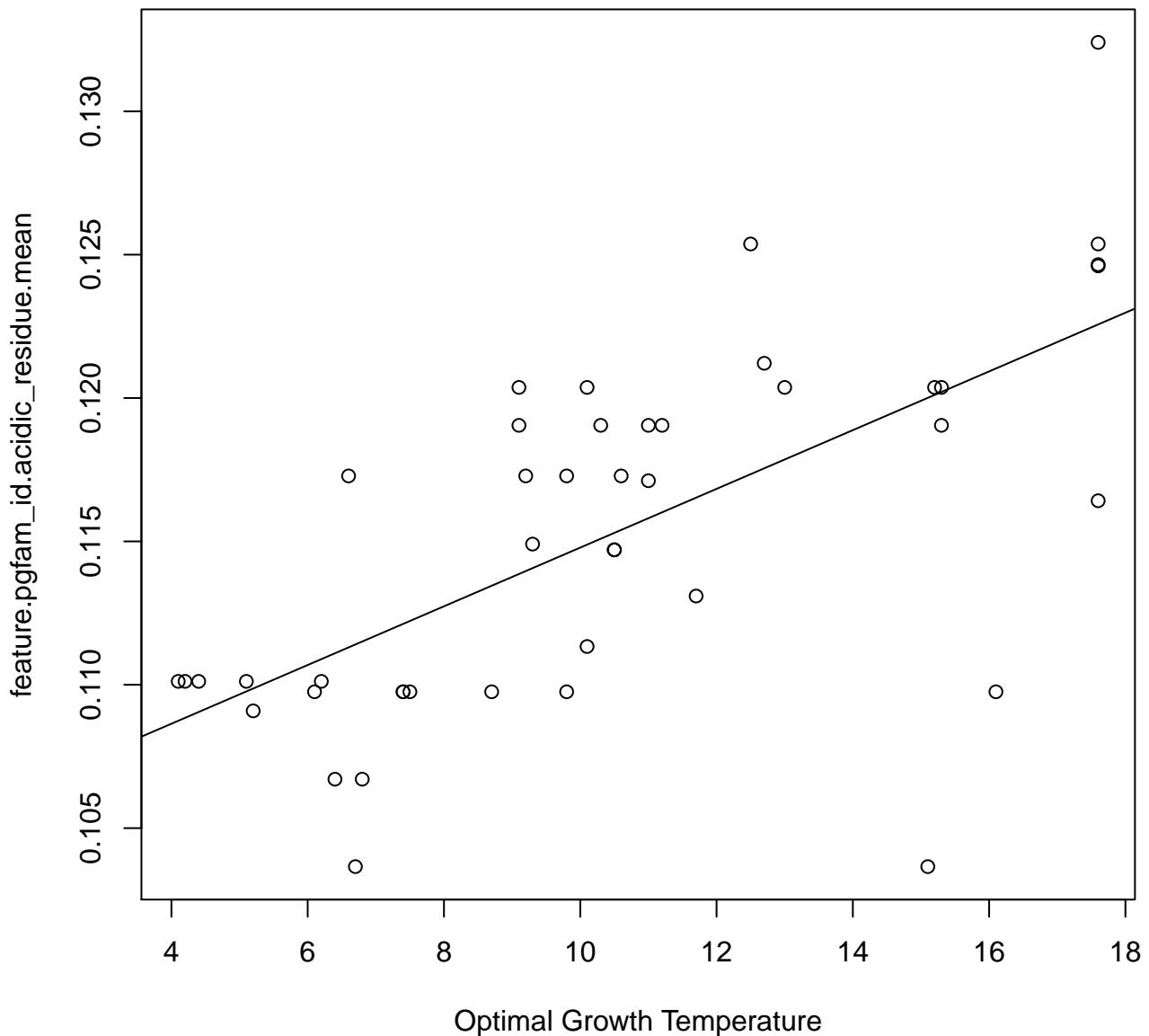
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PGF_00625415
7-cyano-7-deazaguanine synthase (EC 6.3.4.20)



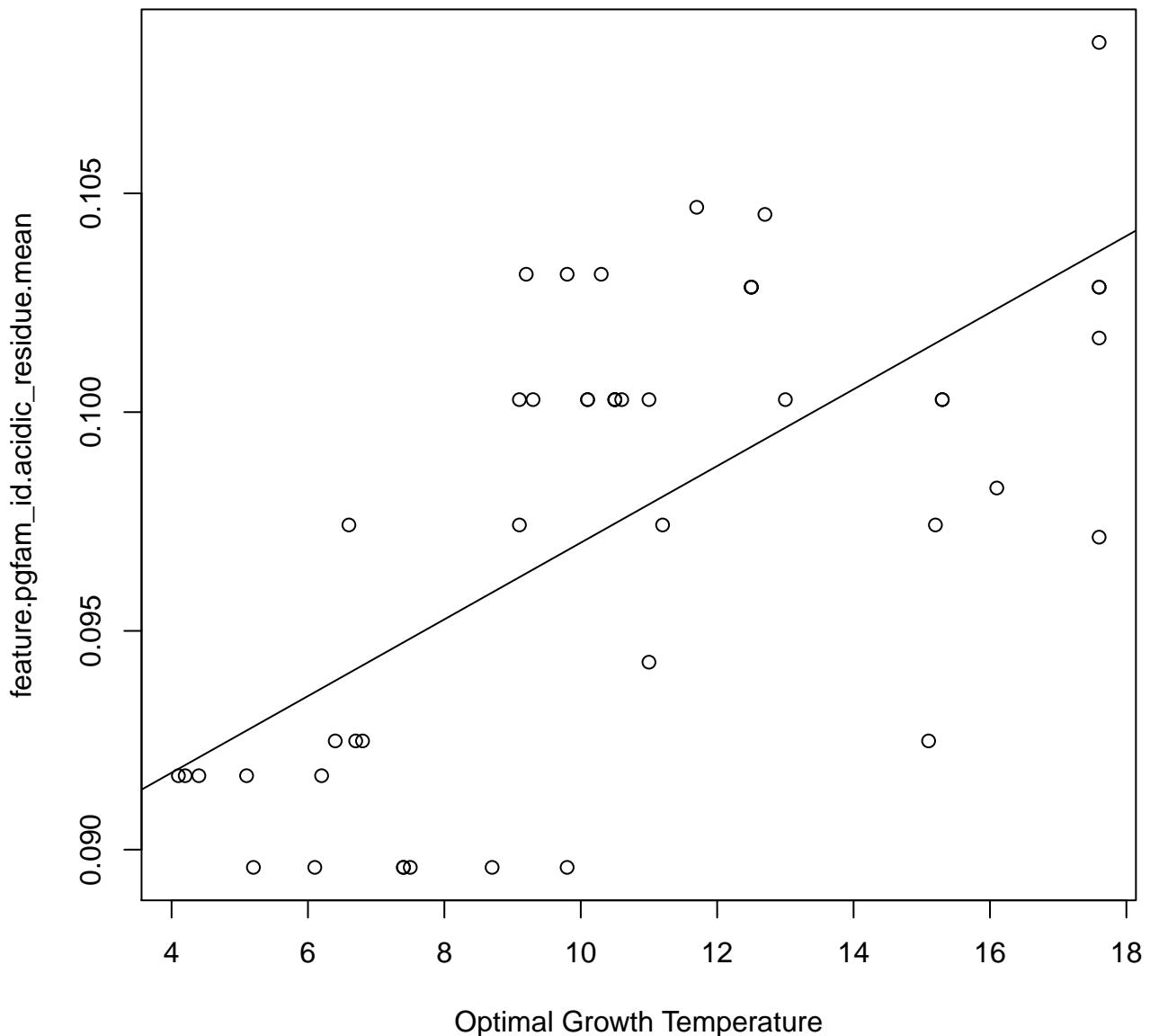
feature.pgfam_id.acidic_residue.mean
PGF_00054528
Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)



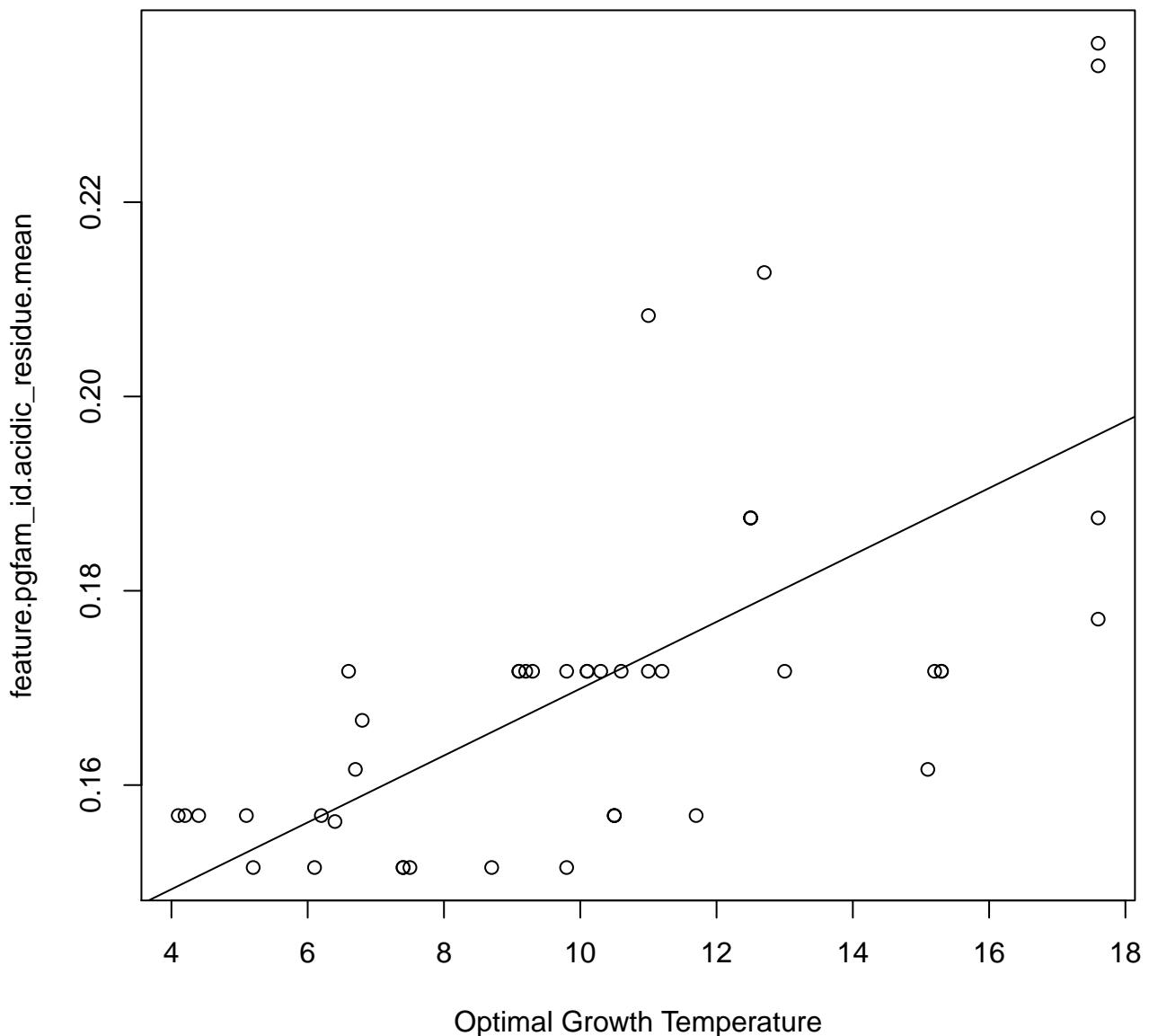
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PGF_06946342
tRNA-dihydrouridine(20/20a) synthase (EC 1.3.1.91)



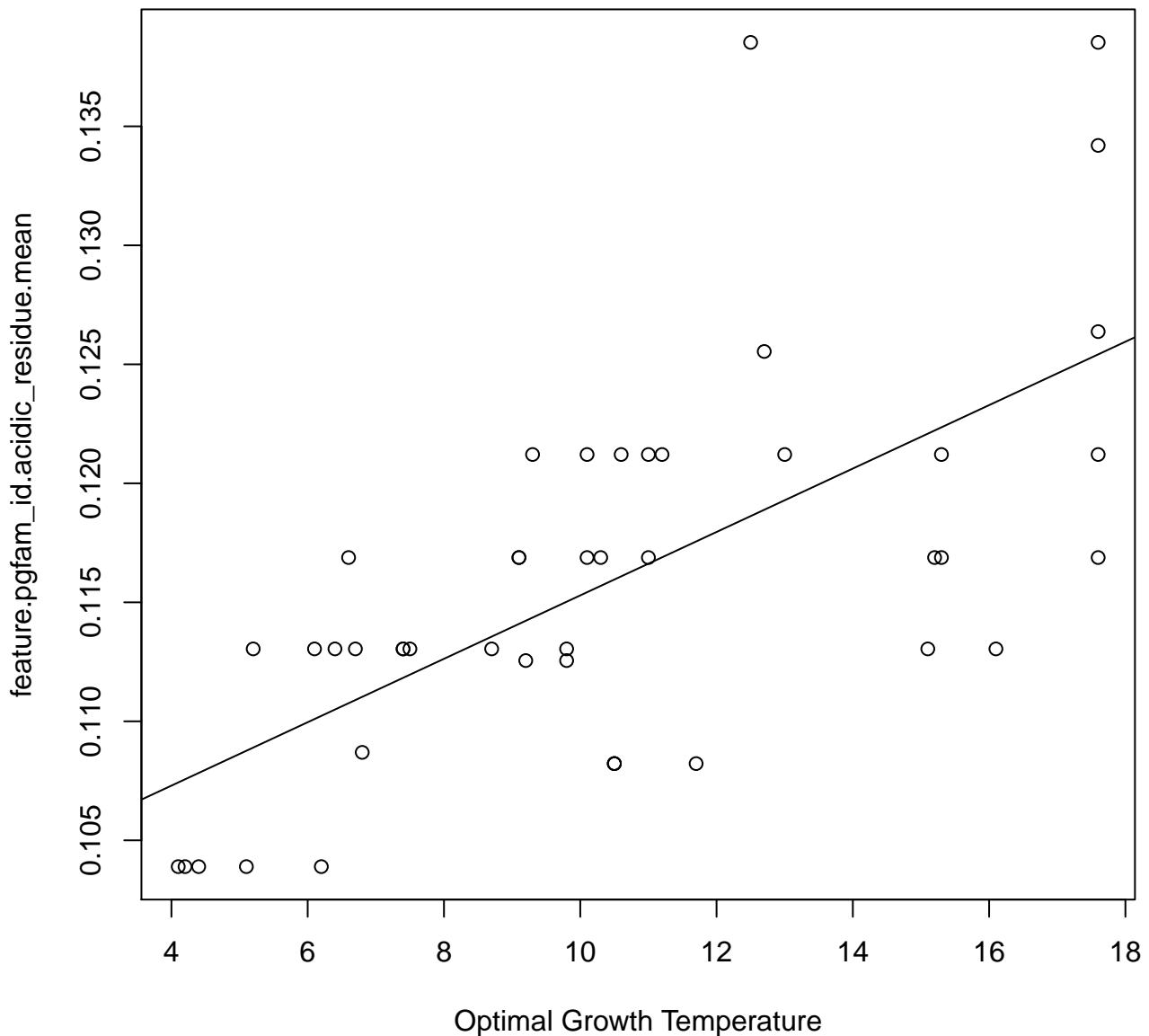
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PGF_03048579
hypothetical protein



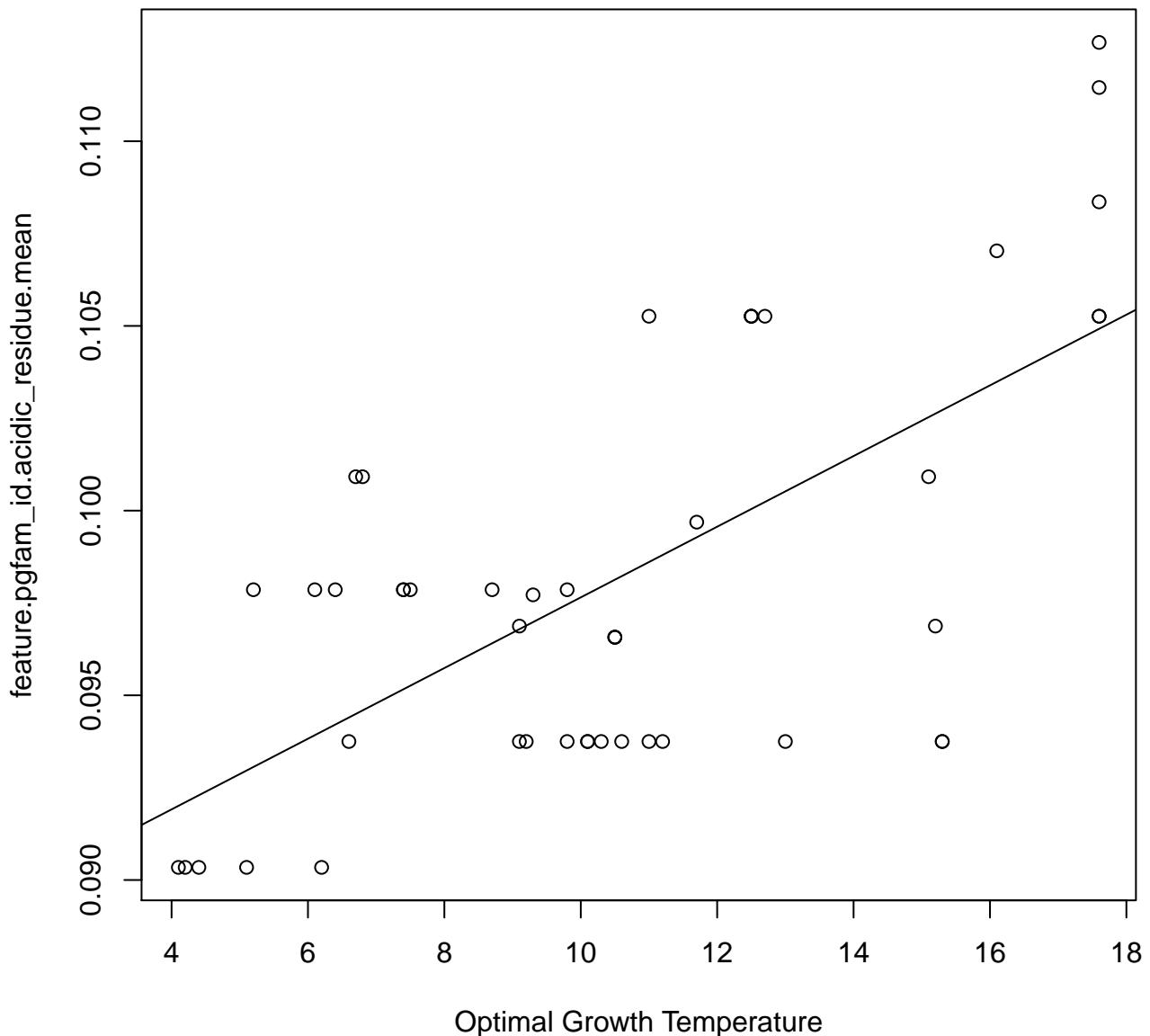
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PGF_00316999
hypothetical protein



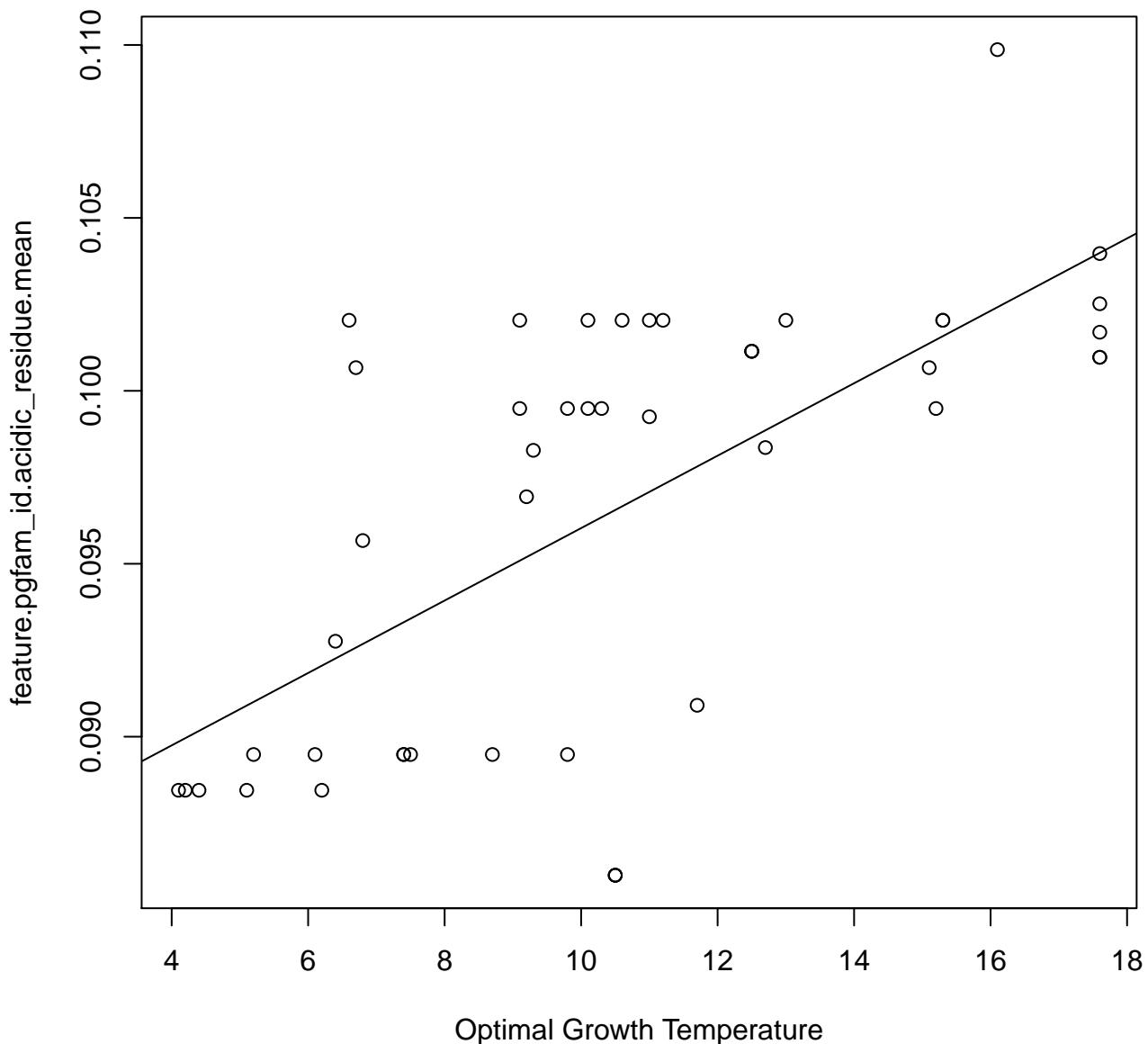
feature.pgfam_id.acidic_residue.mean
PGF_07402119
6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type



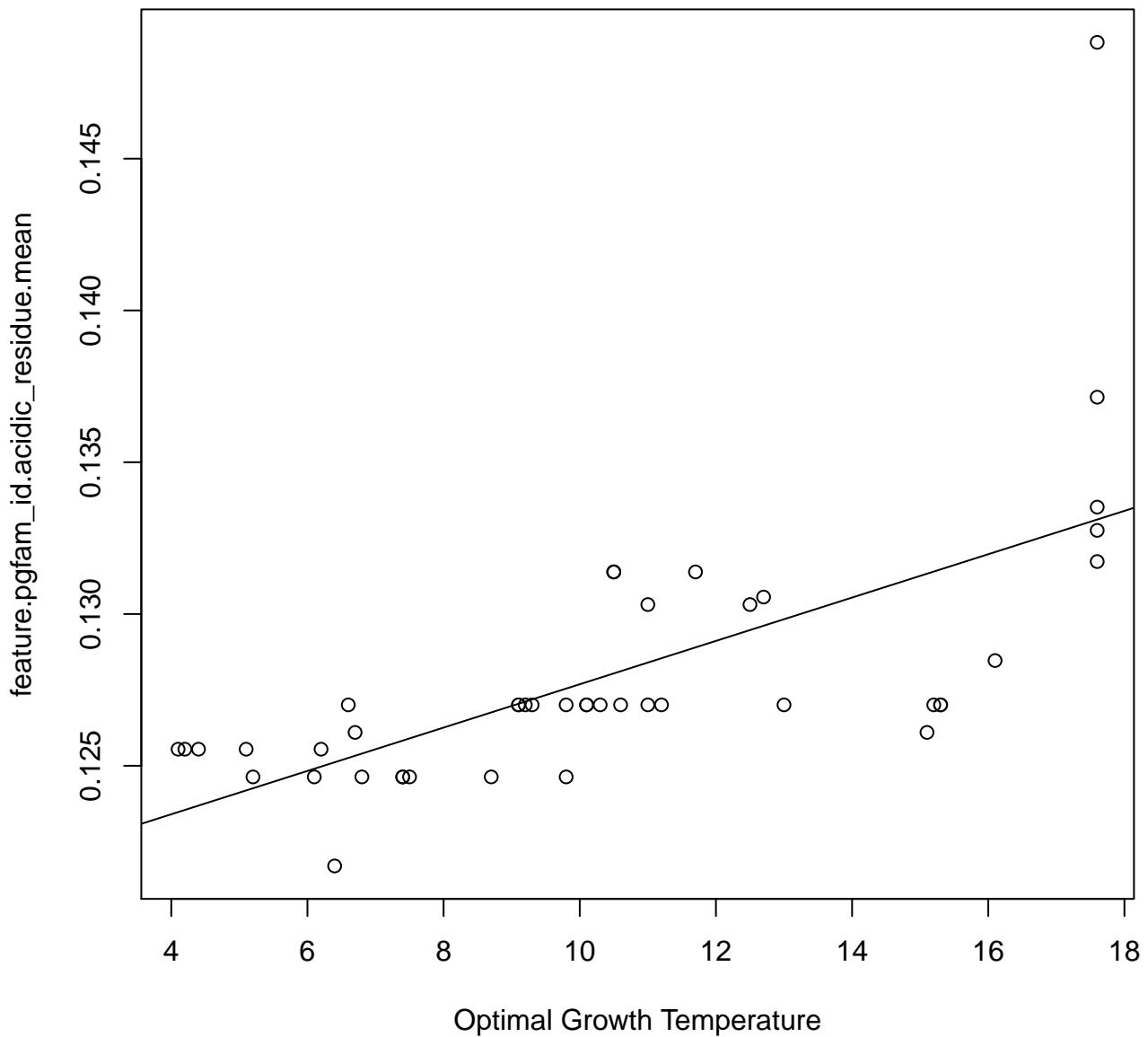
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PGF_03815442
Cytochrome c oxidase (cbb3-type) subunit CcoP (EC 1.9.3.1)



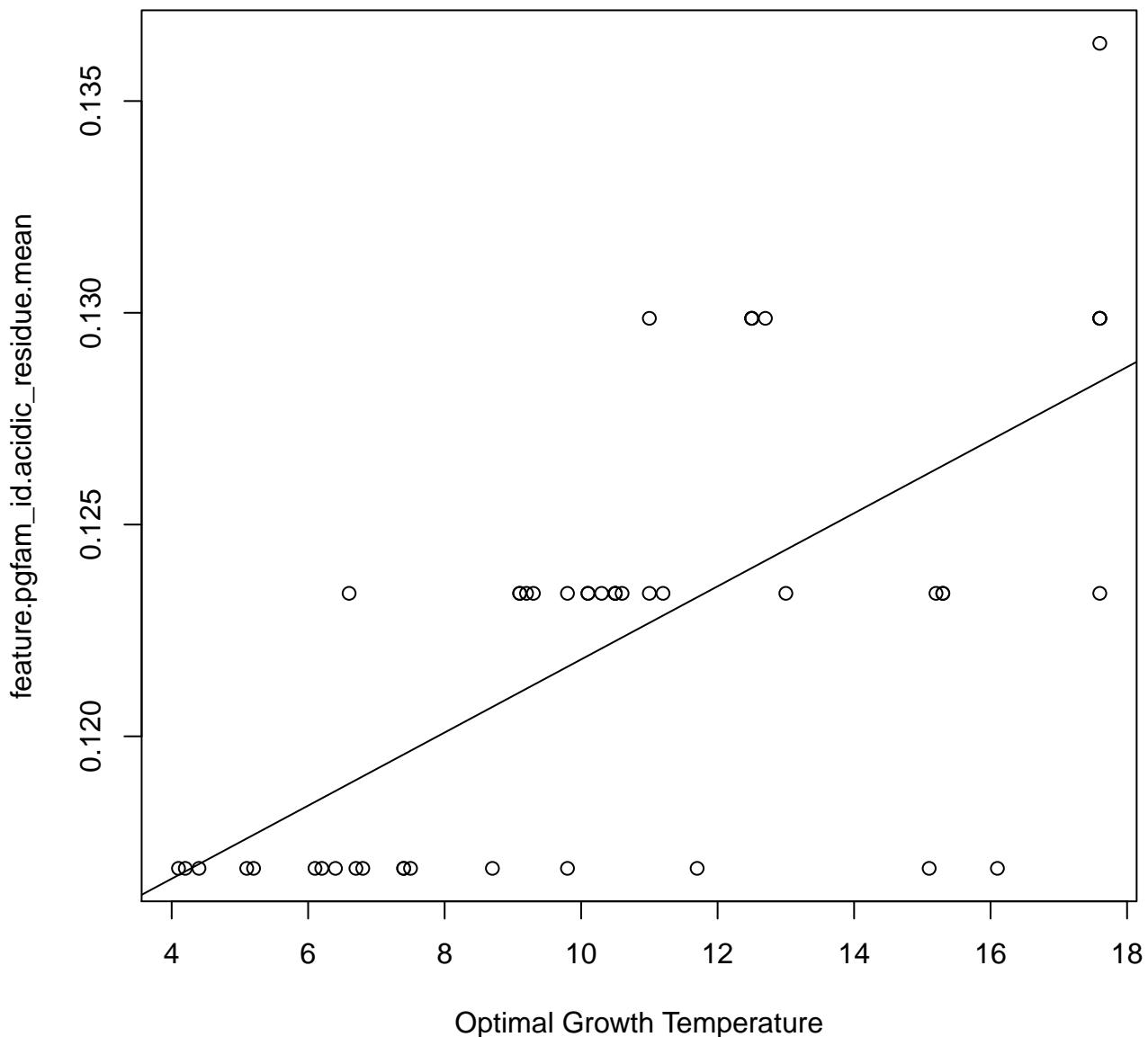
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Type IV pilus biogenesis protein PilF



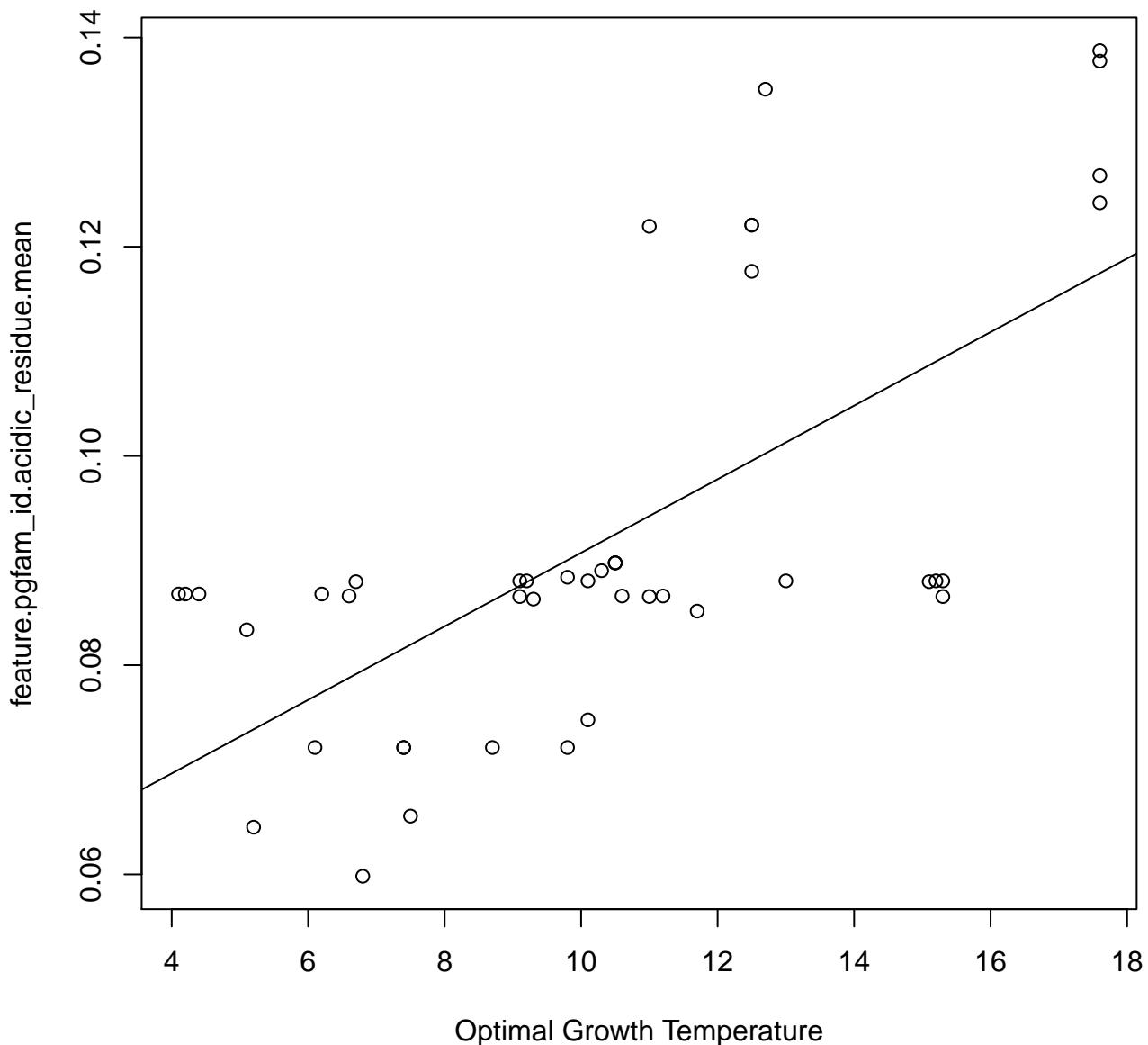
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PGF_00063770
Type IV pilus biogenesis protein PilQ



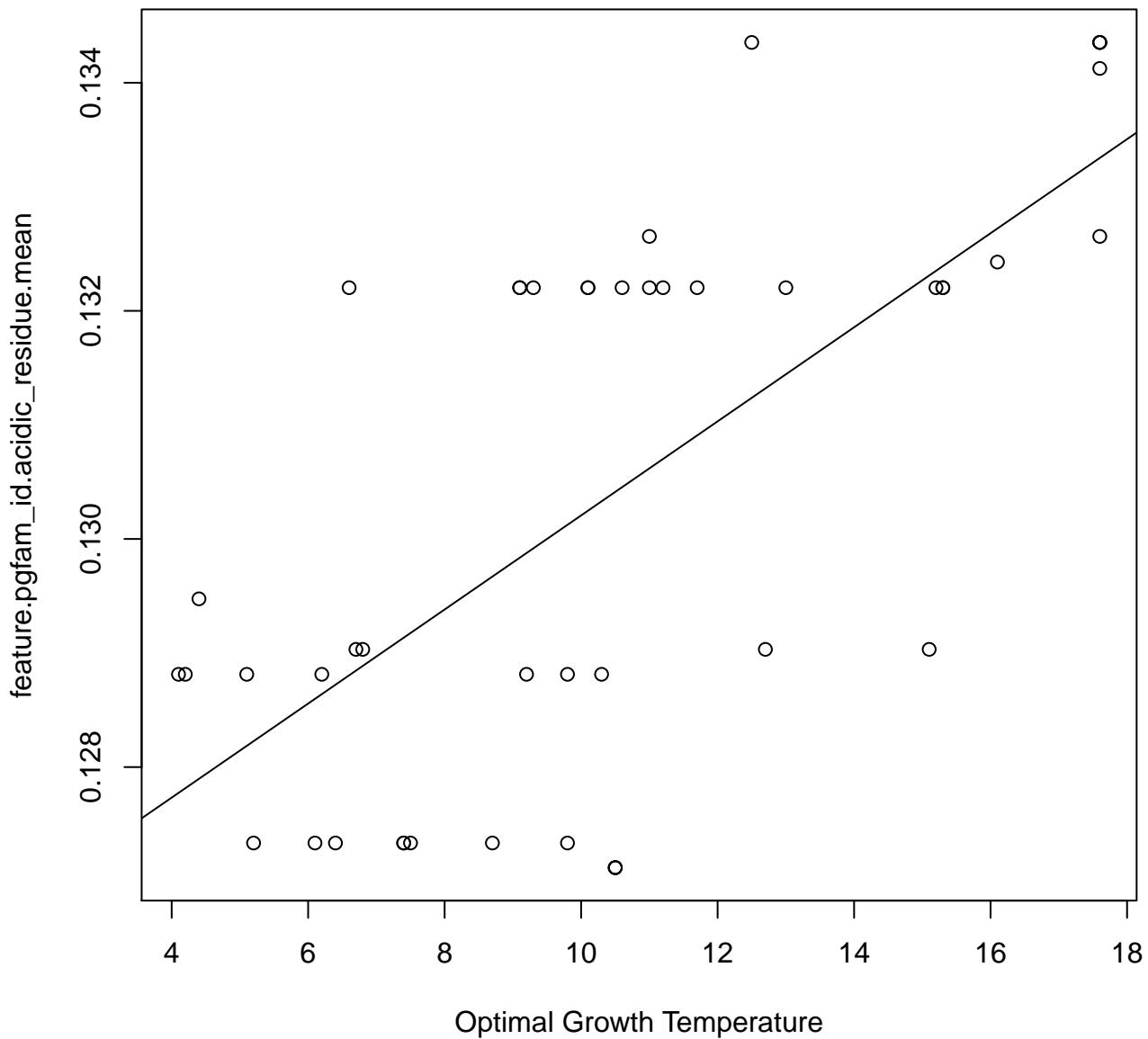
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PGF_00426932
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)



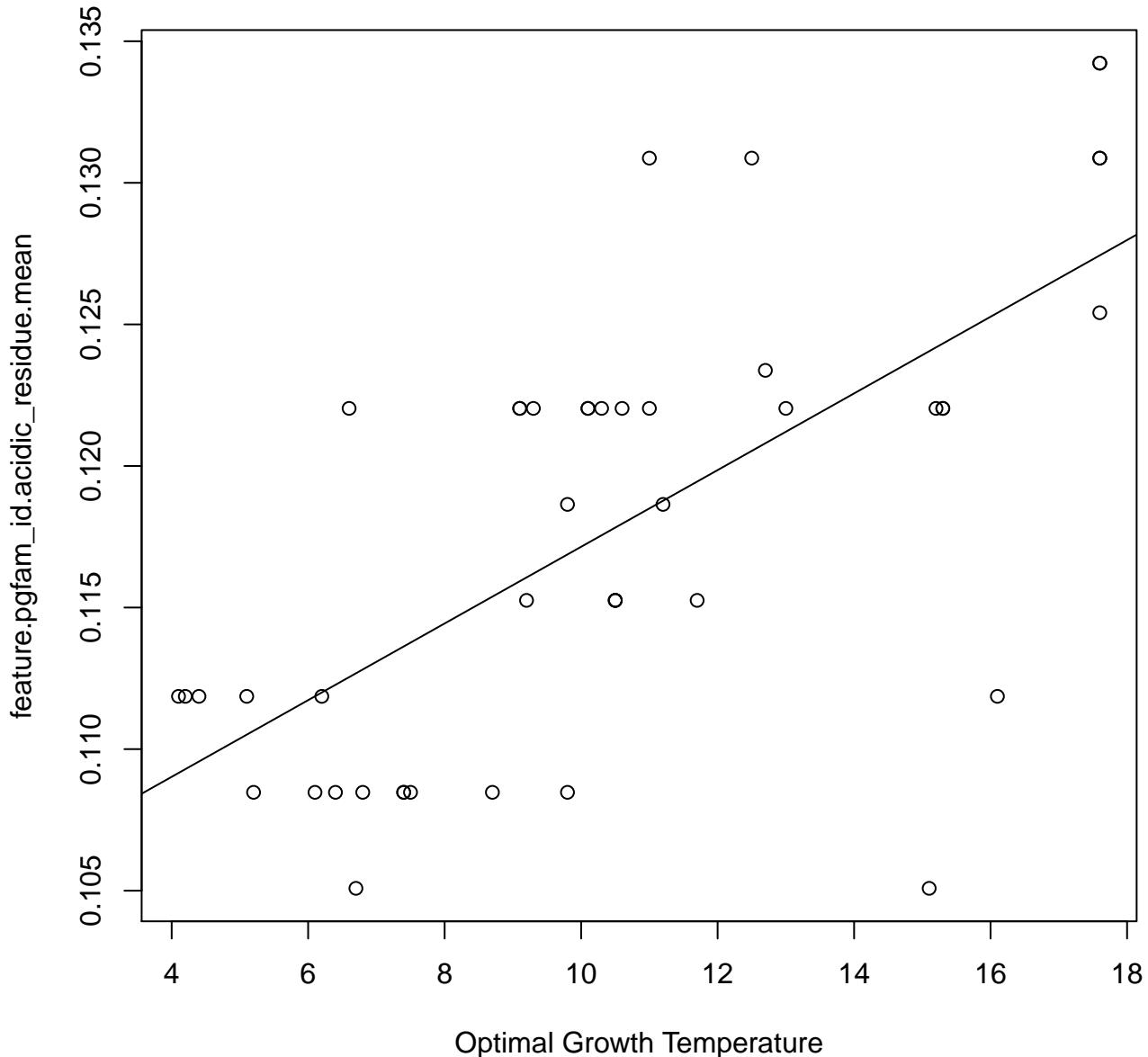
feature.pgfam_id.acidic_residue.mean
PGF_01336427
hypothetical protein



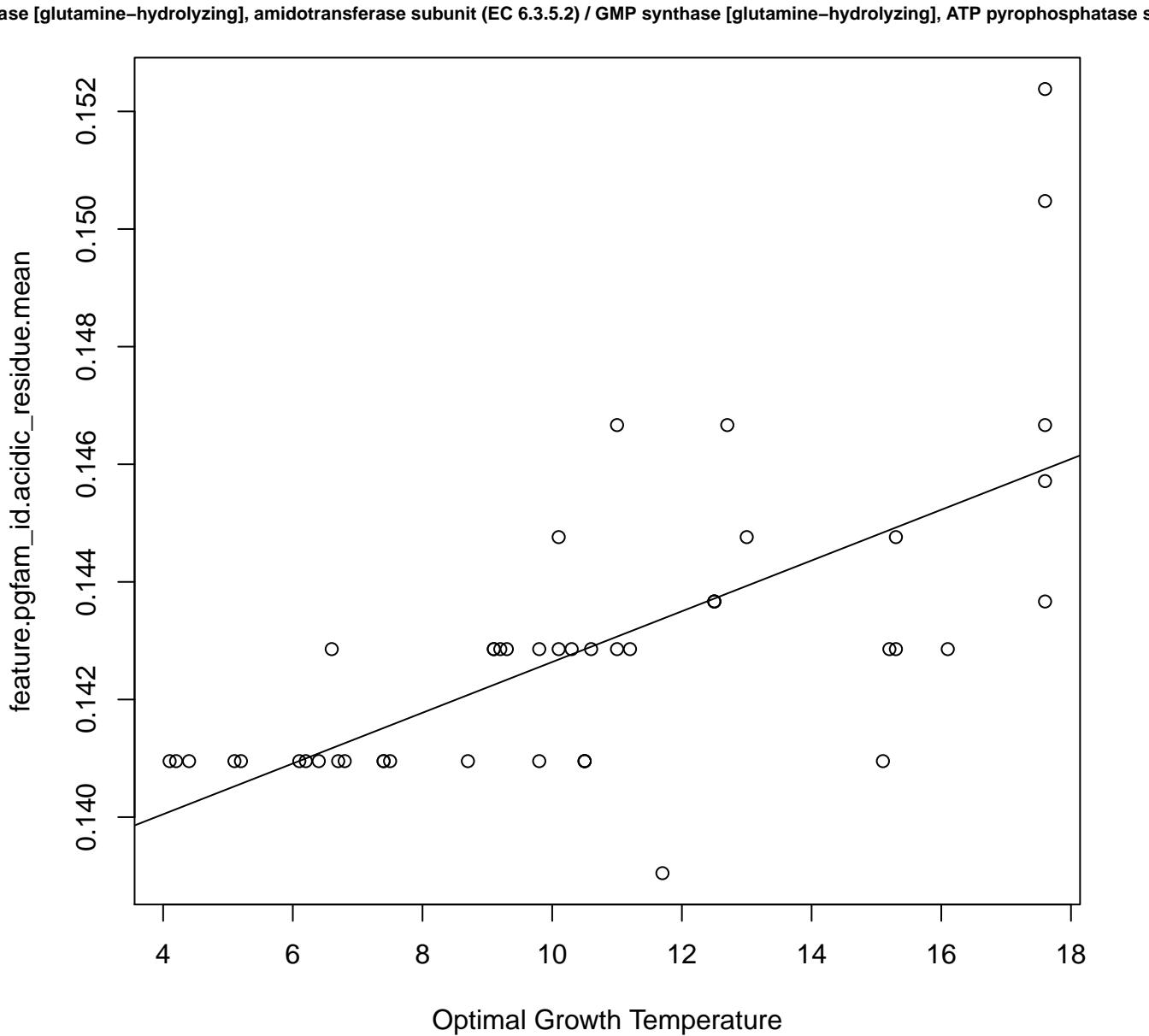
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PGF_08998238
Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)



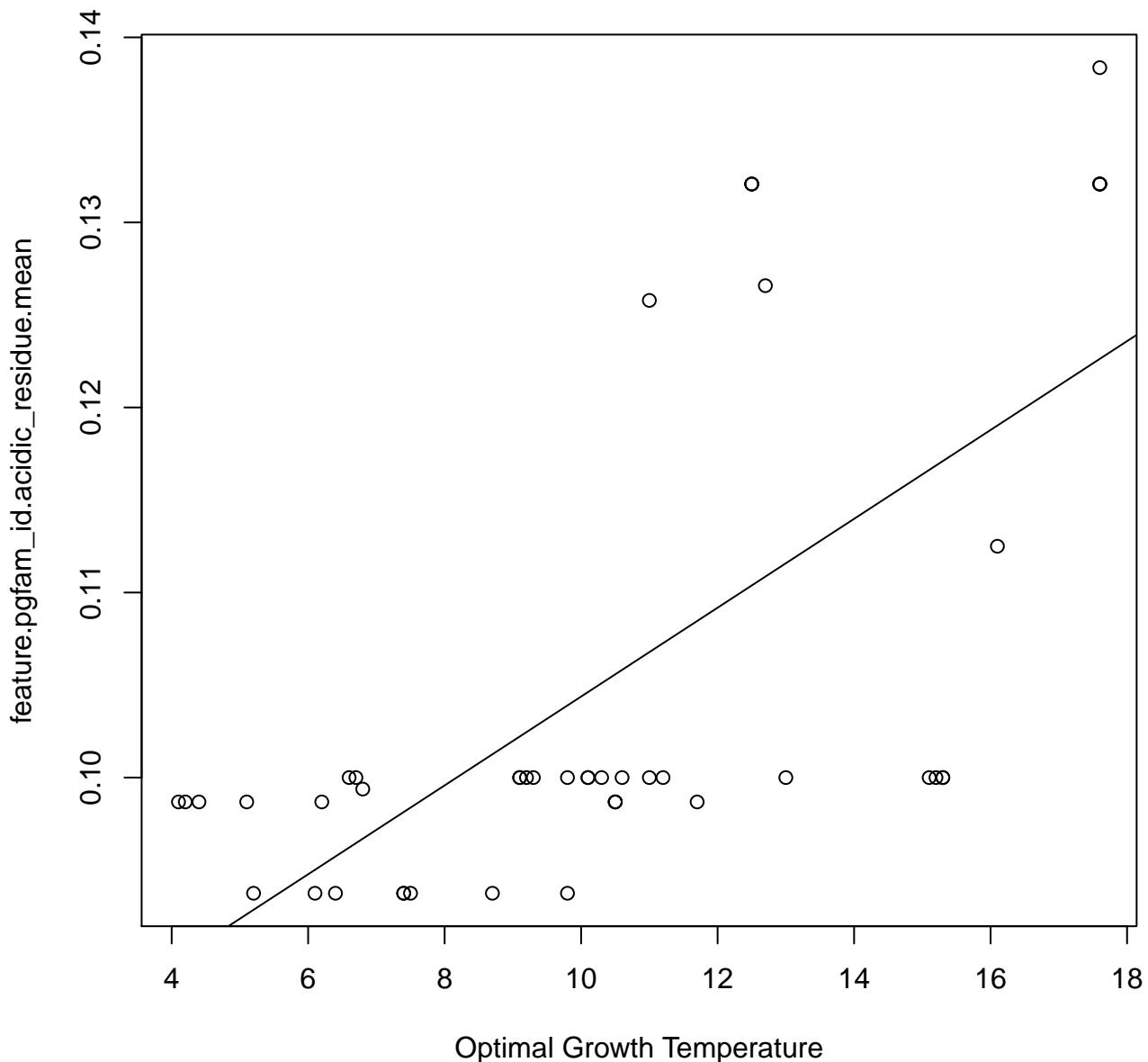
feature.pgfam_id.acidic_residue.mean
PGF_04828114
Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)



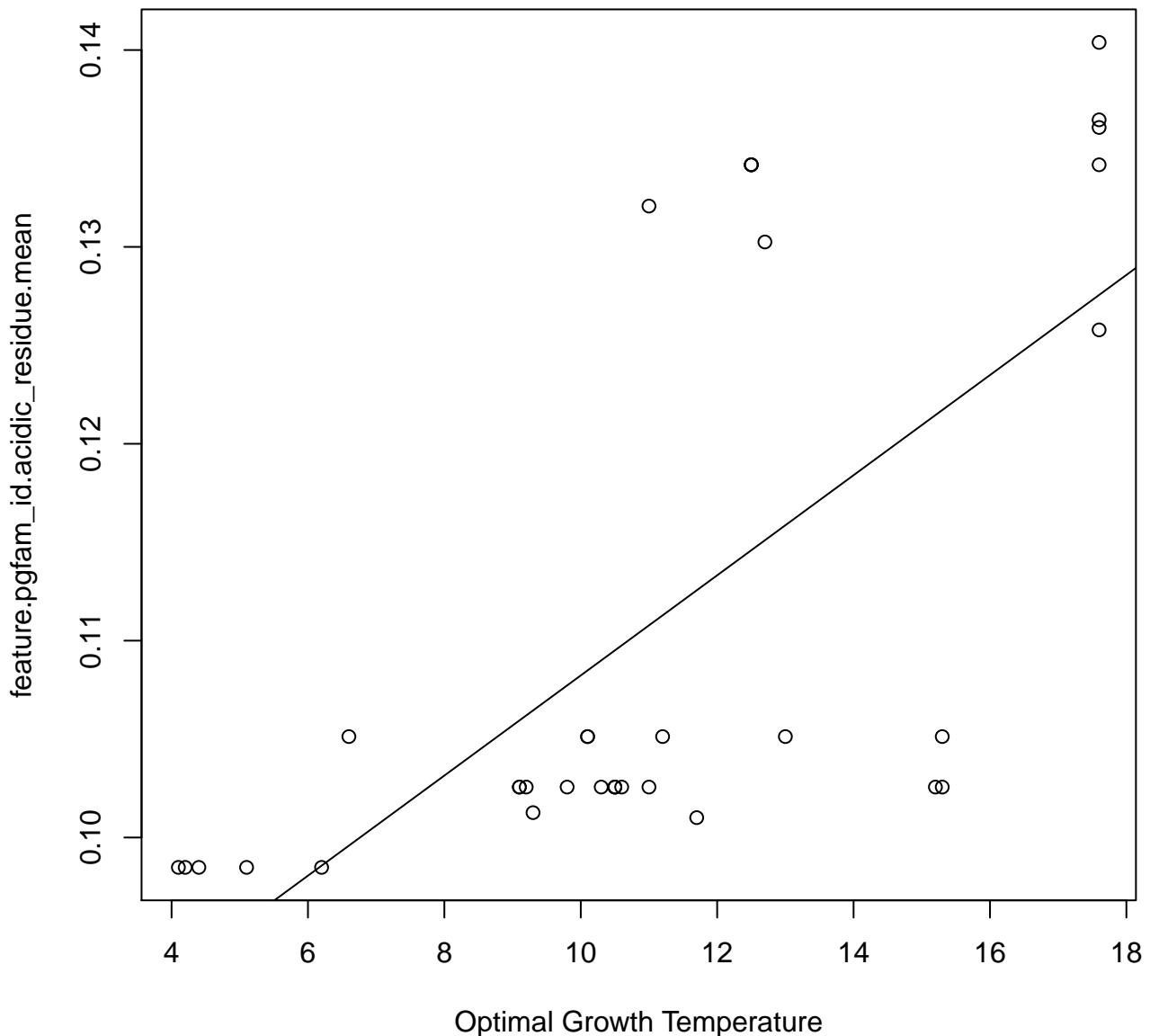
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PGF_00006935



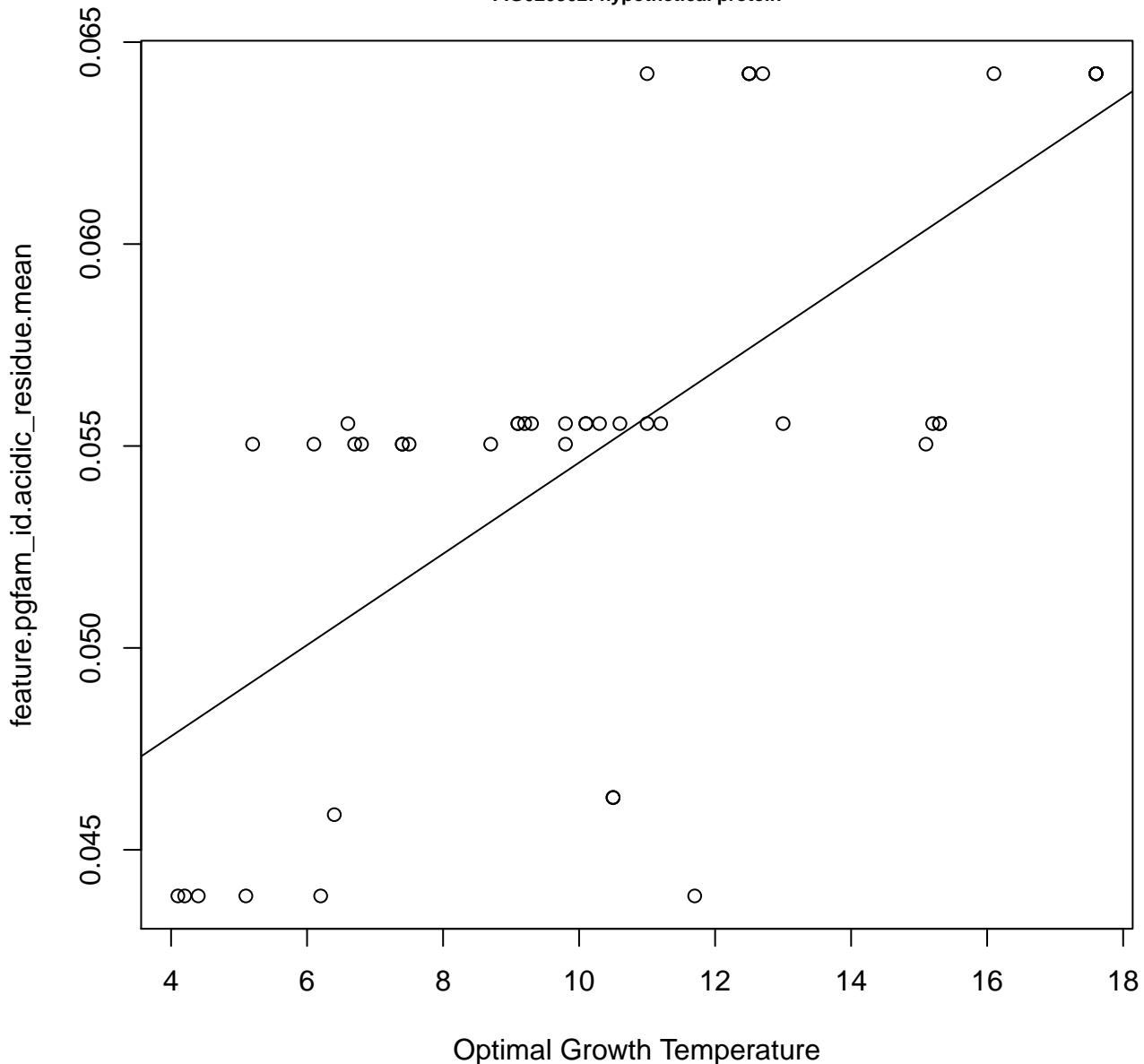
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PGF_00054302
Stringent starvation protein B



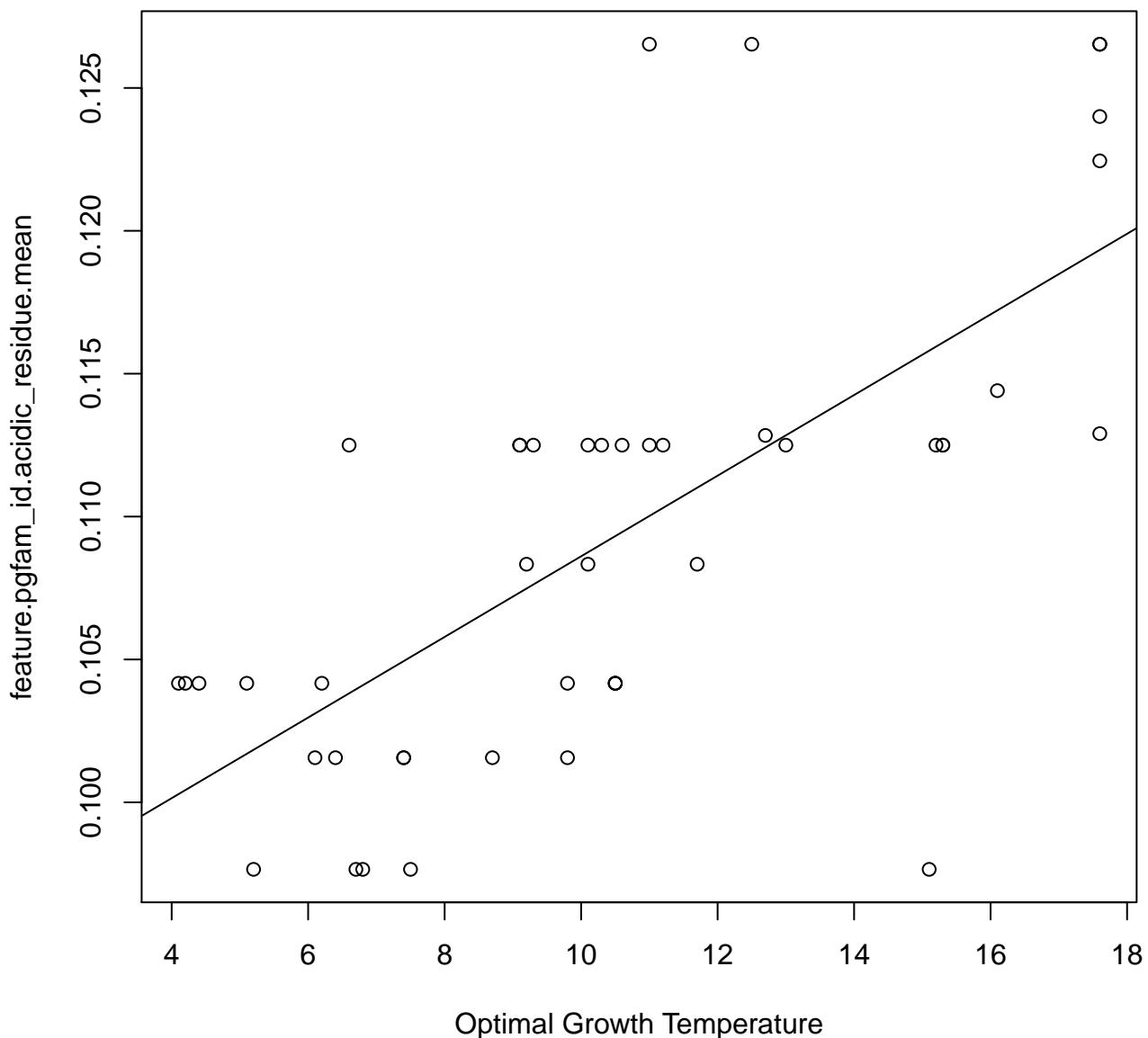
feature.pgfam_id.acidic_residue.mean
PGF_01336373
hypothetical protein



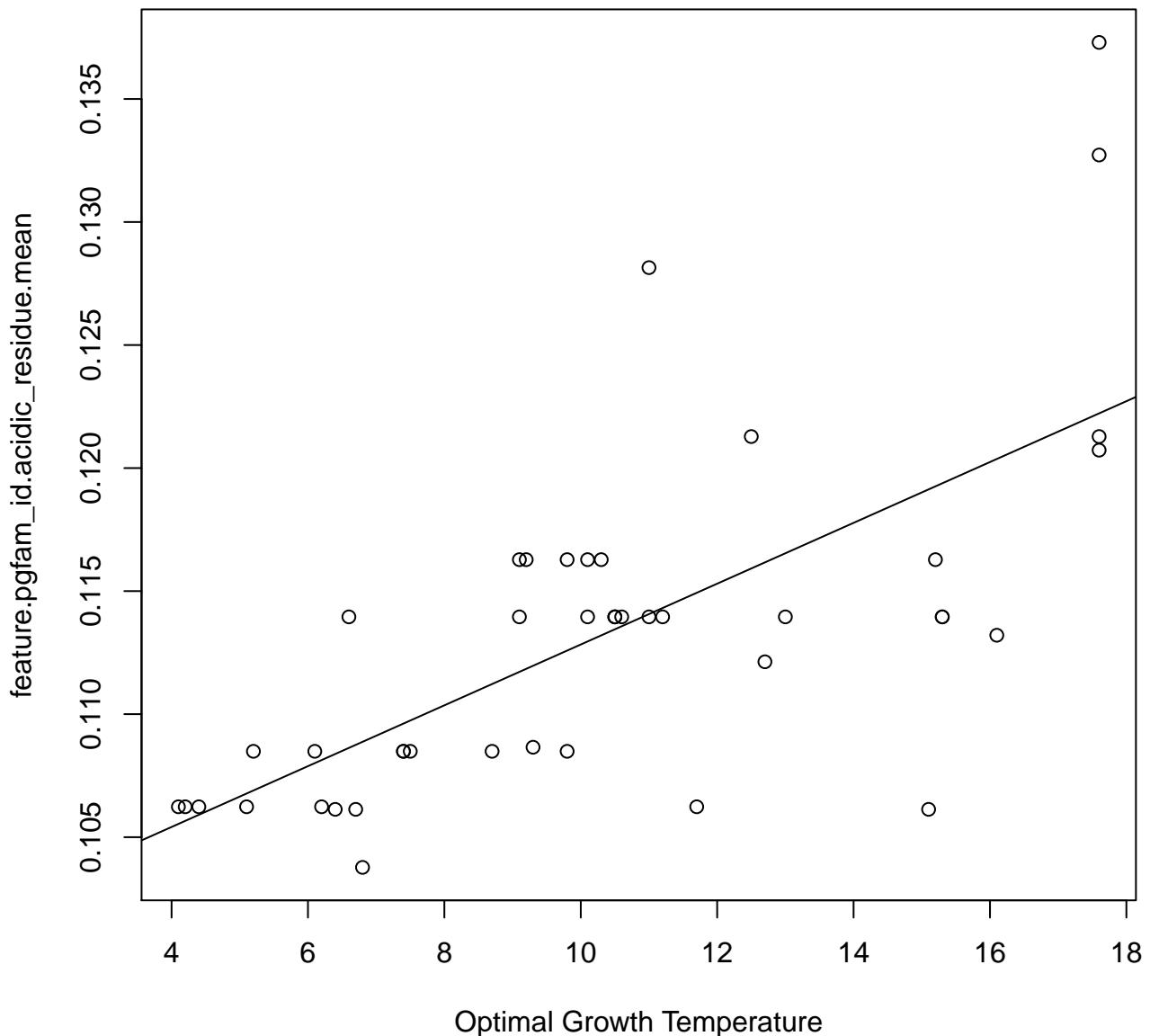
feature.pgfam_id.acidic_residue.mean
PGF_03074033
FIG020302: hypothetical protein



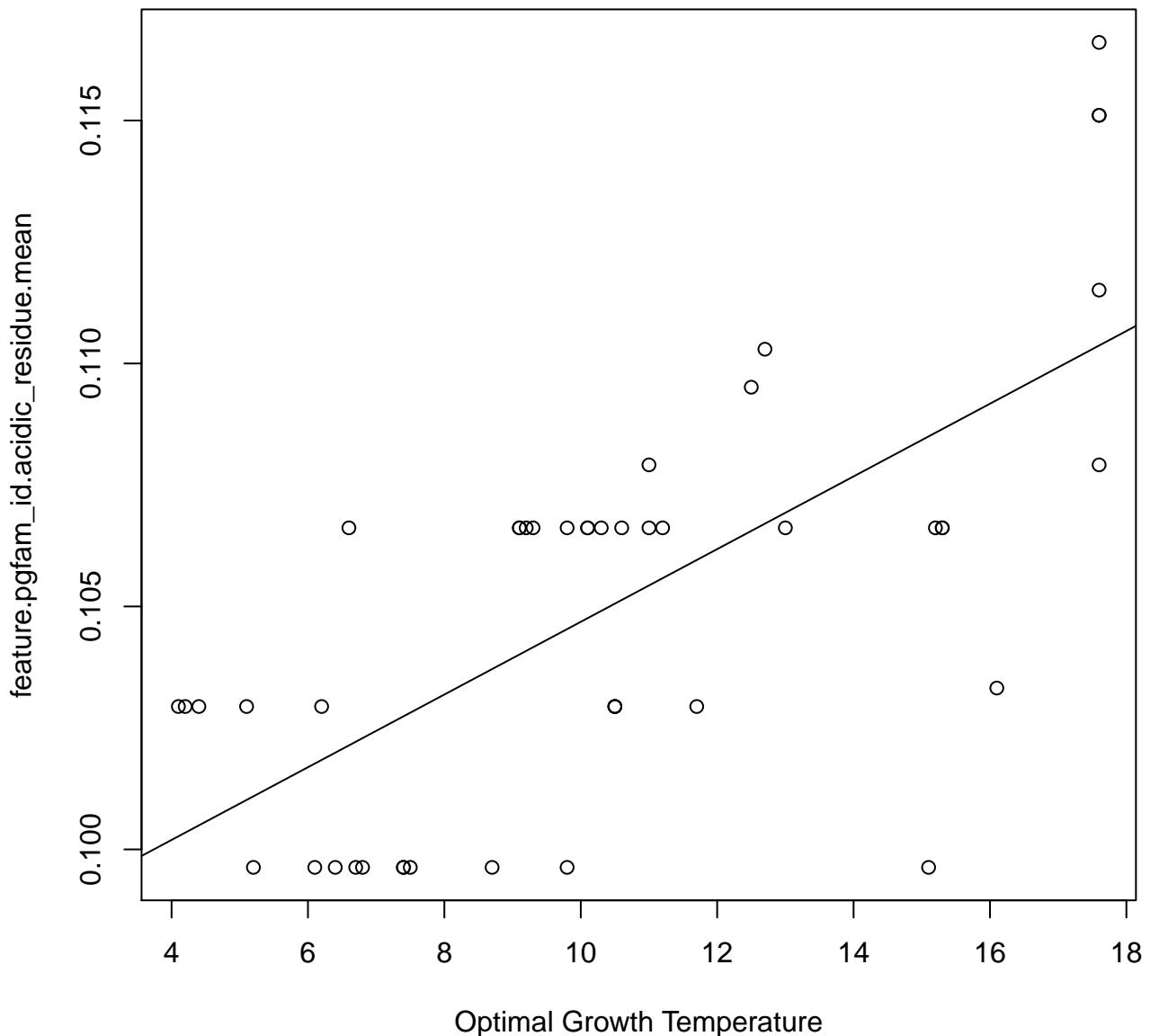
feature.pgfam_id.acidic_residue.mean
PGF_07711219
Histidine utilization repressor



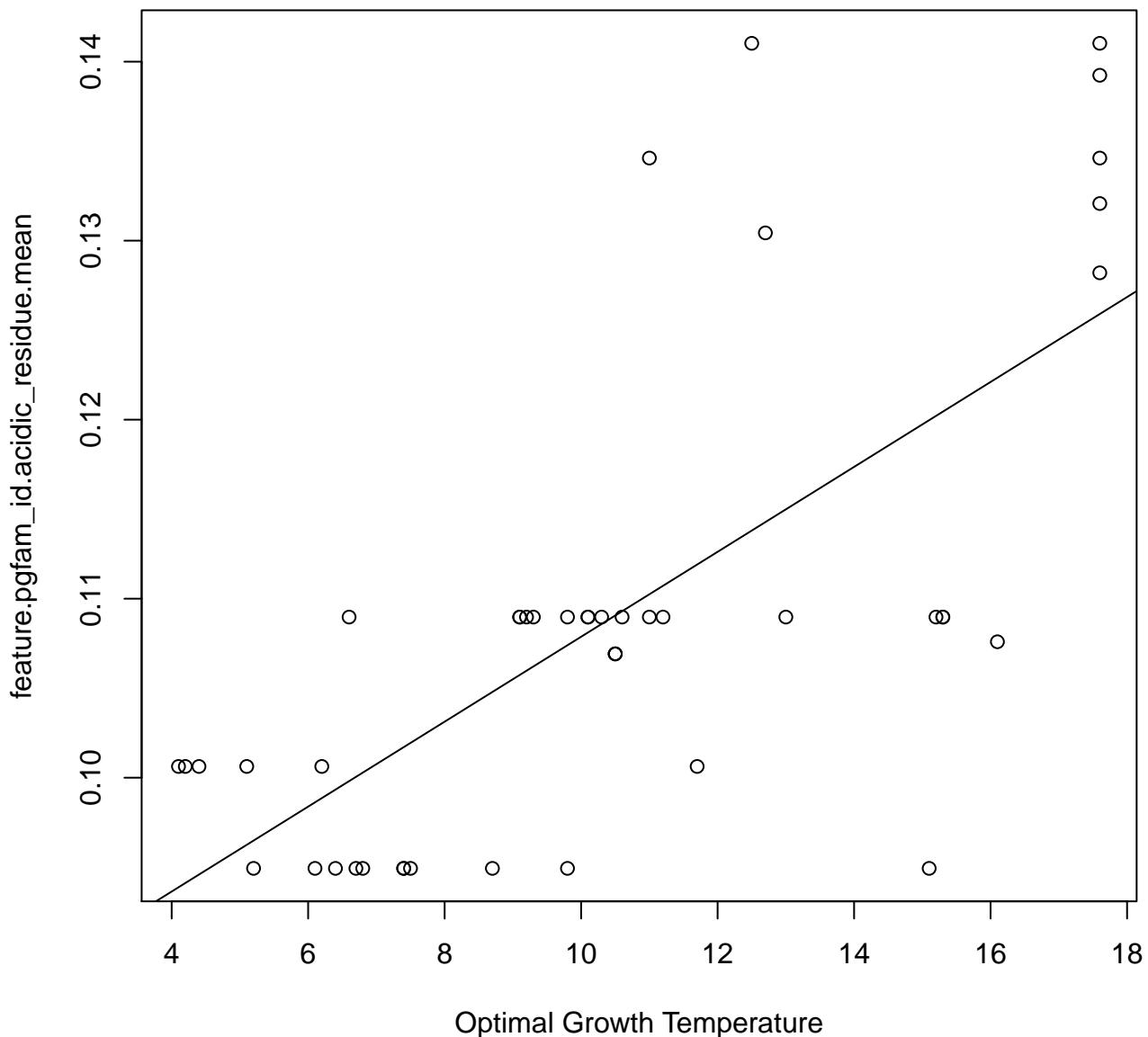
feature.pgfam_id.acidic_residue.mean
PGF_04485073
Dihydrofolate synthase (EC 6.3.2.12) @ Folylpolyglutamate synthase (EC 6.3.2.17)



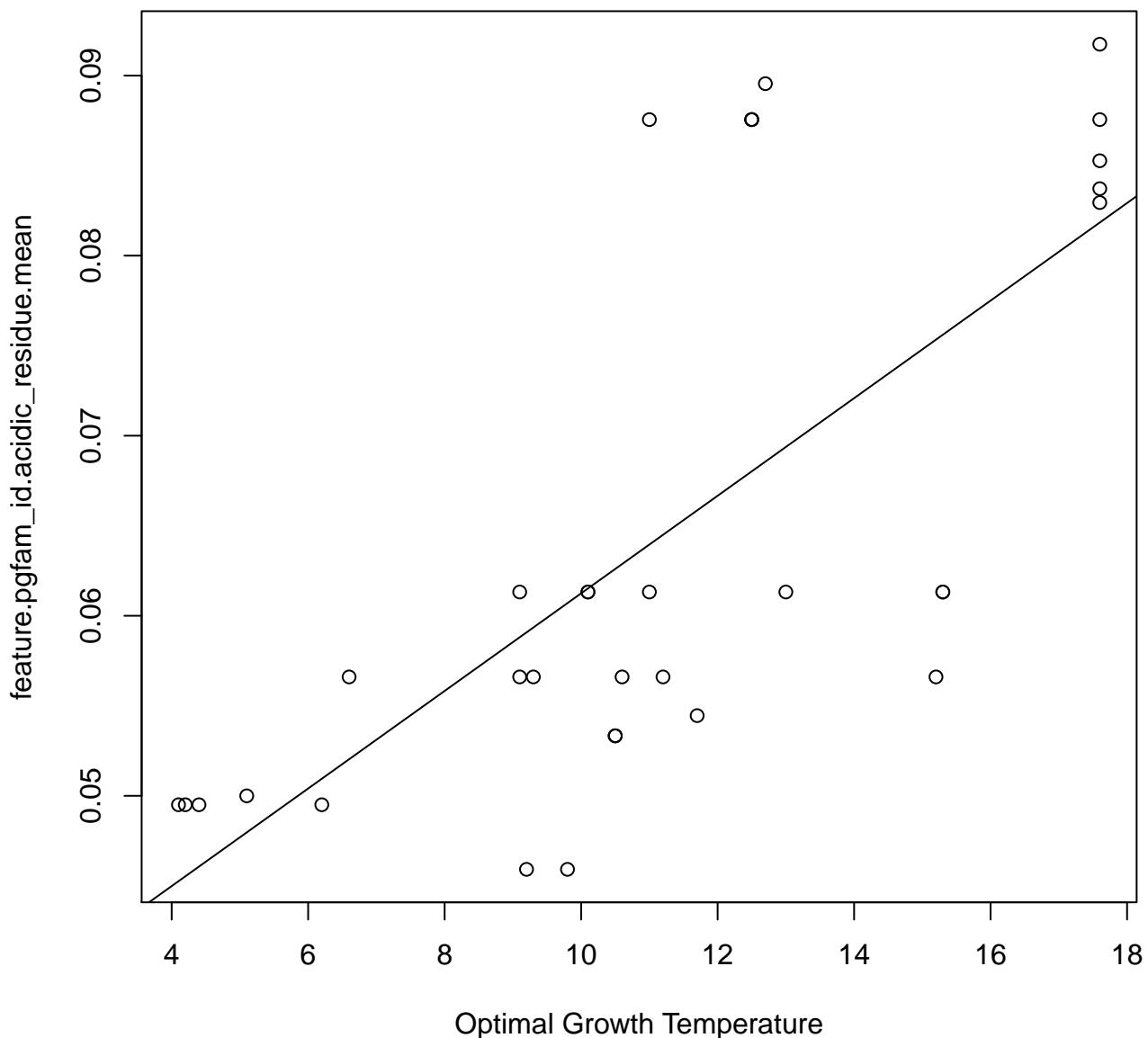
feature.pgfam_id.acidic_residue.mean
PGF_12867503
Methyl-directed repair DNA adenine methylase (EC 2.1.1.72)



feature.pgfam_id.acidic_residue.mean
PGF_00645831
DNA polymerase III chi subunit (EC 2.7.7.7)

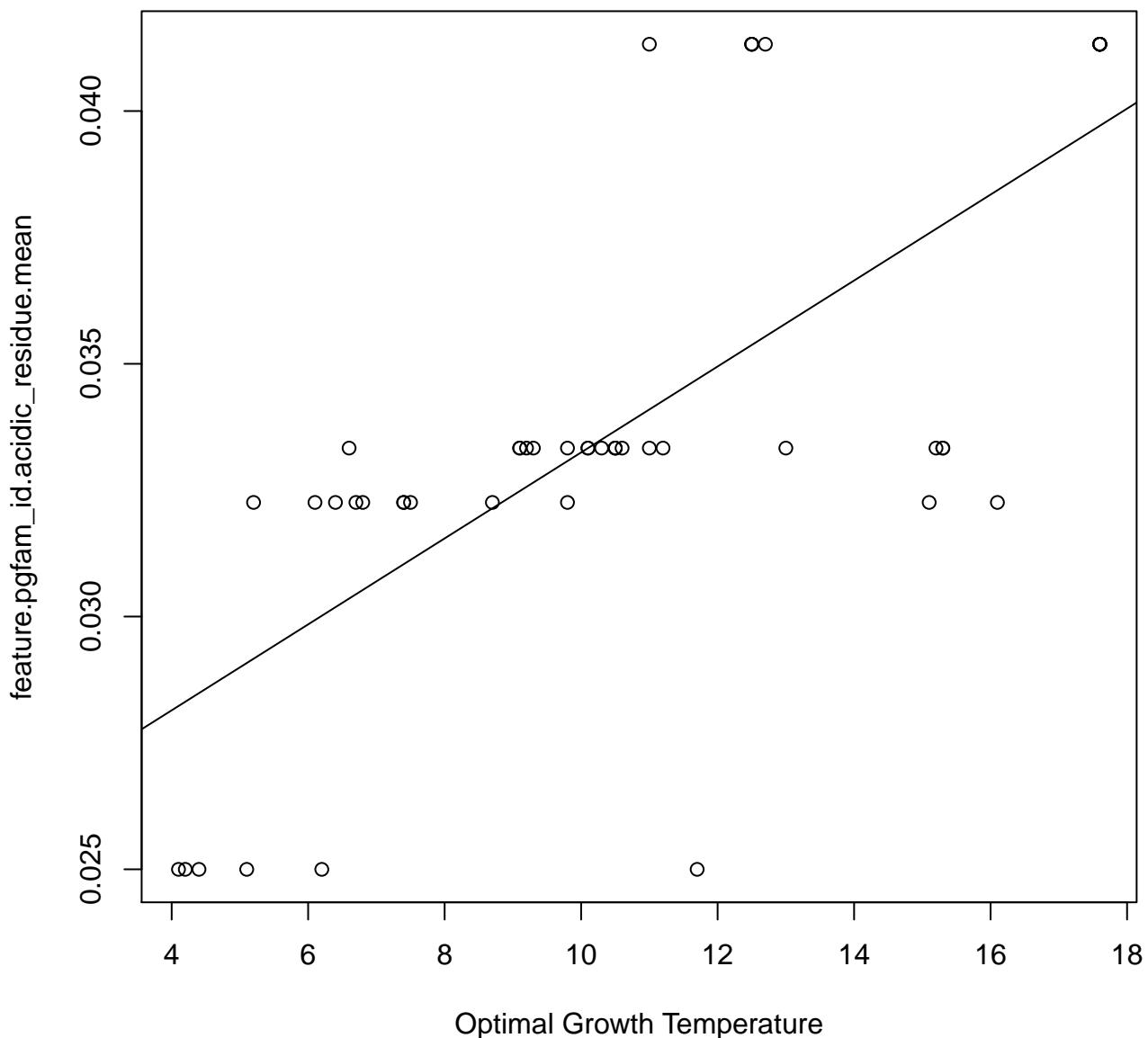


feature.pgfam_id.acidic_residue.mean
PGF_00053527
Soluble lytic murein transglycosylase

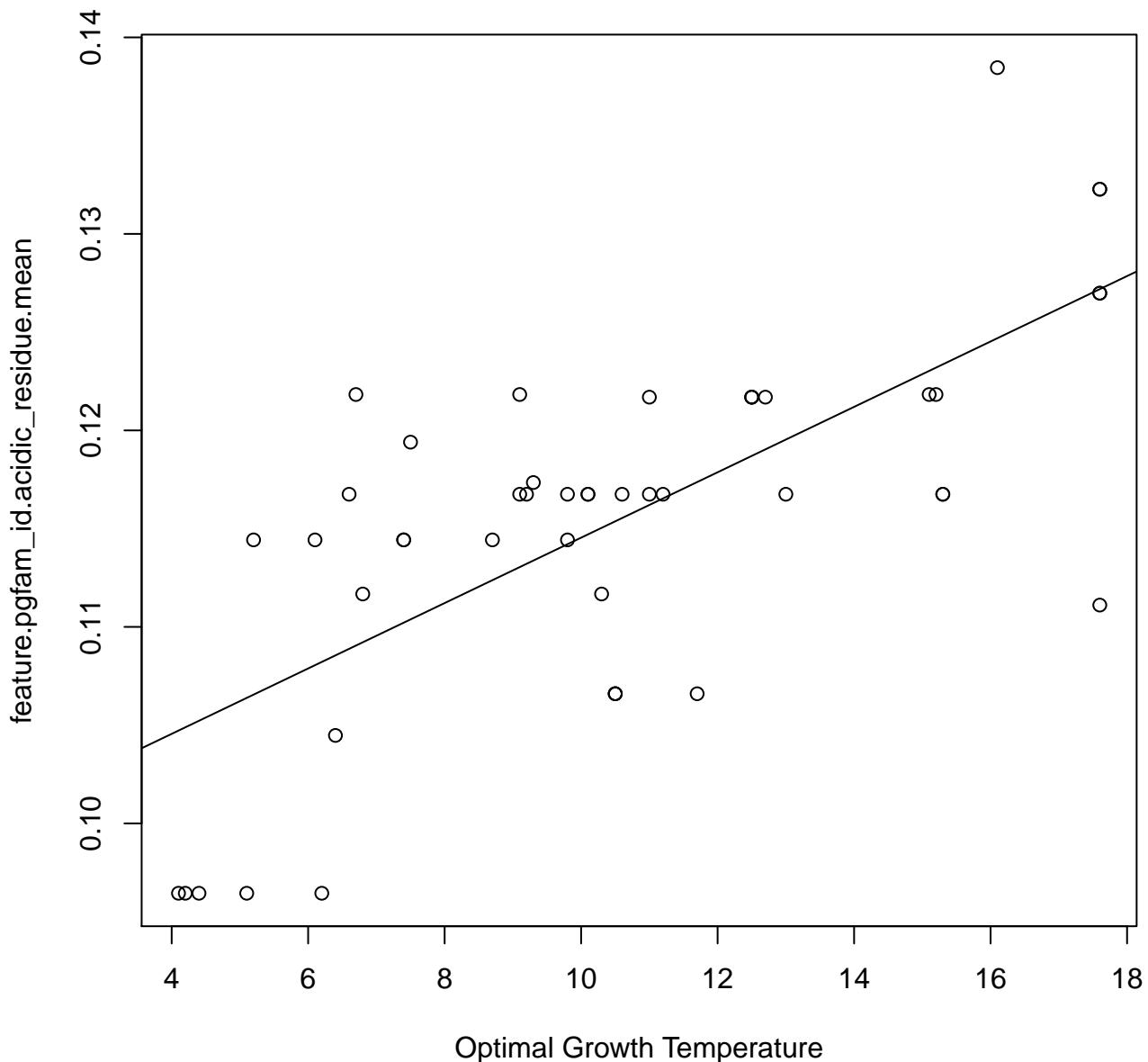


feature.pgfam_id.acidic_residue.mean

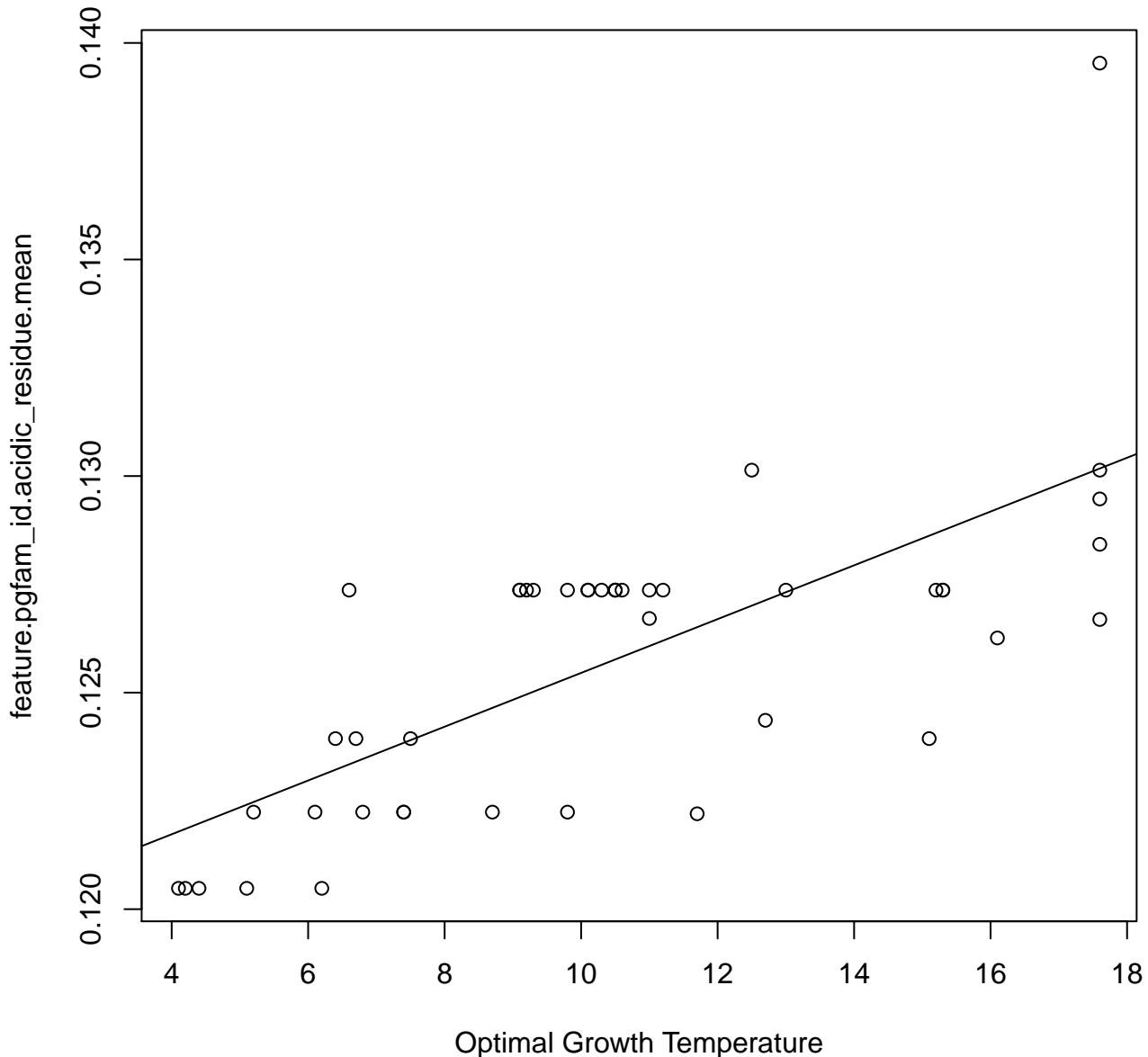
PGF_00425763
FIG002082: Protein SirB2



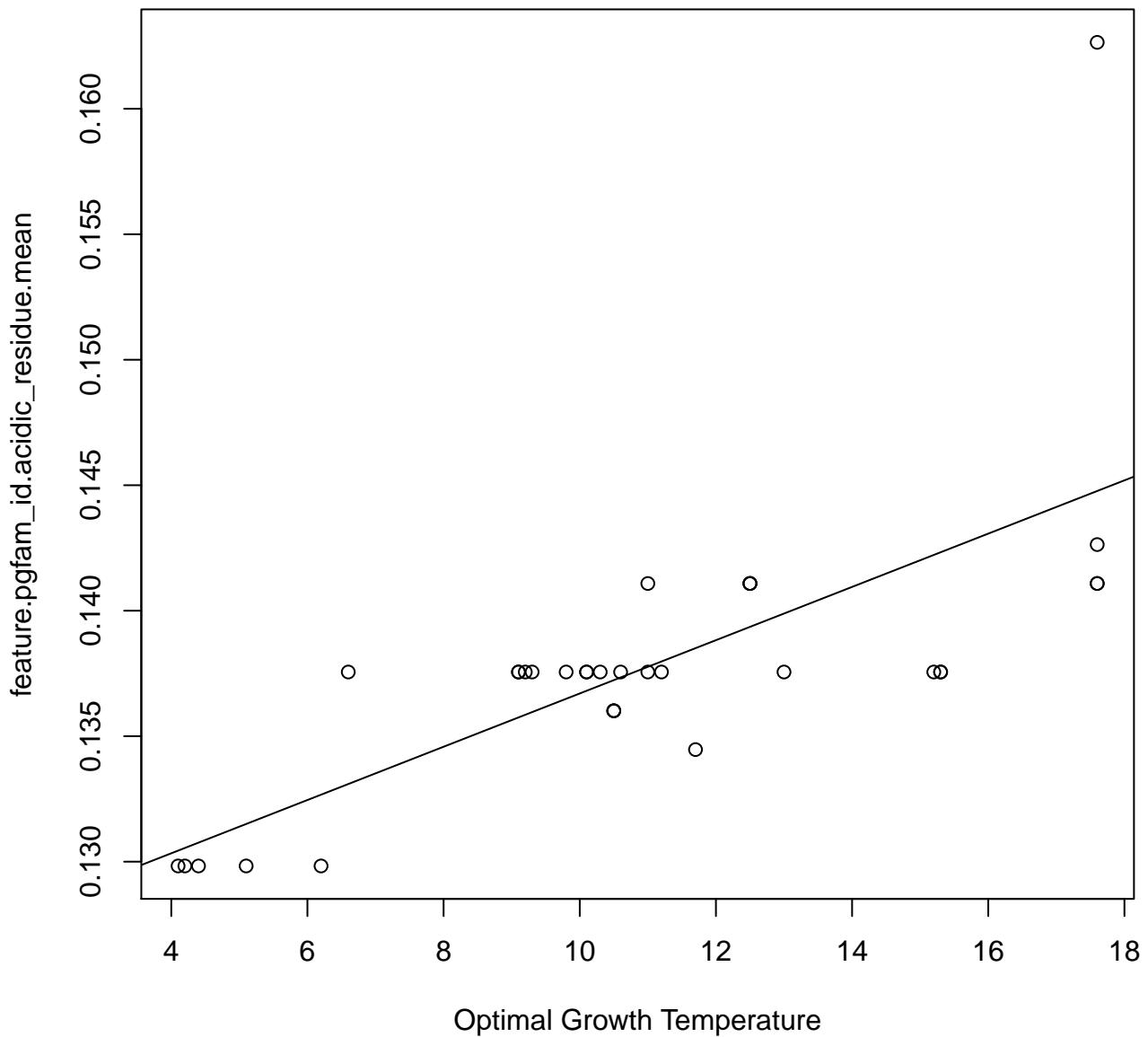
feature.pgfam_id.acidic_residue.mean
PGF_00423914
1,6-anhydro-N-acetylMuramyl-L-alanine amidase



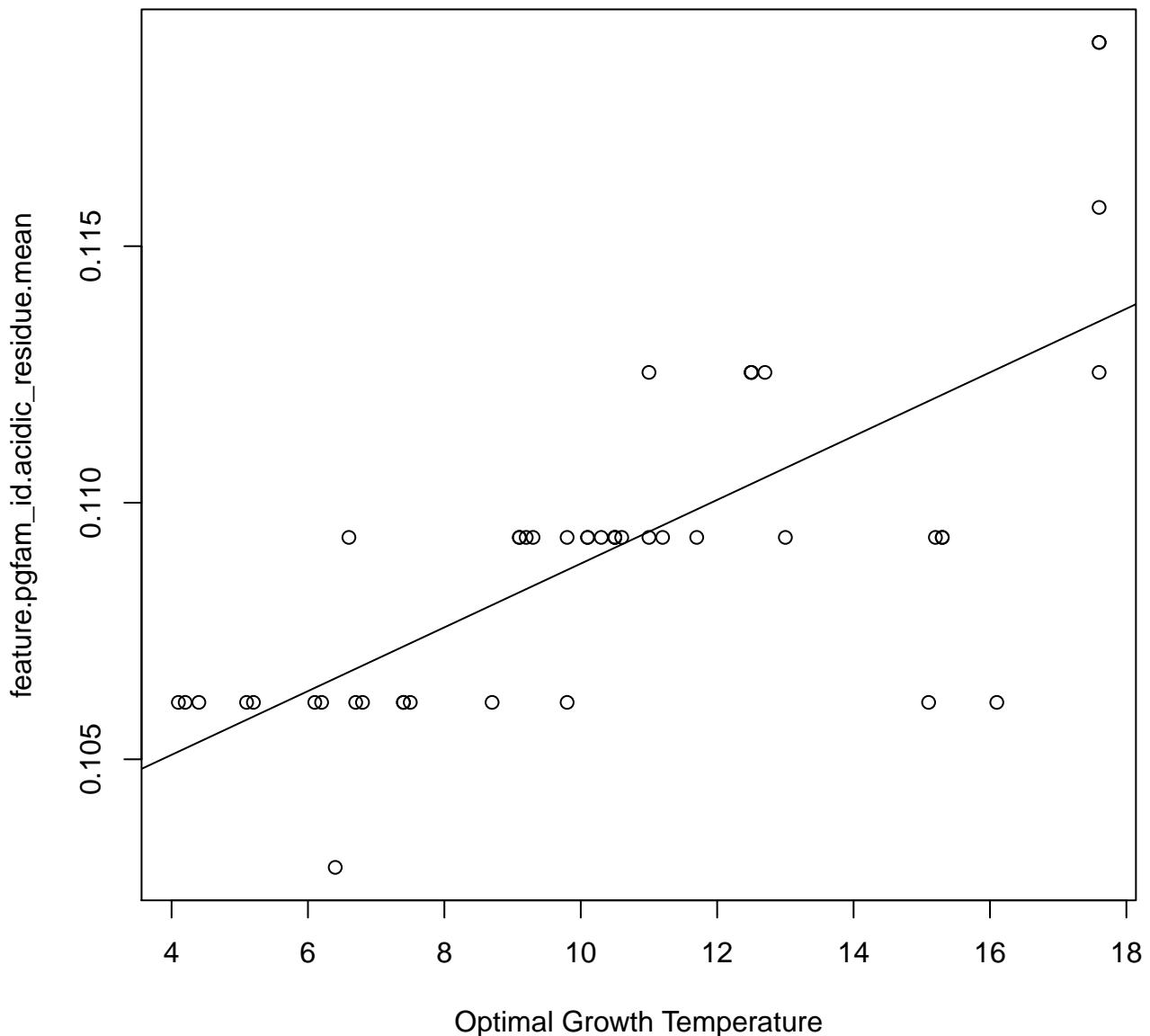
feature.pgfam_id.acidic_residue.mean
PGF_07058357
Single-stranded-DNA-specific exonuclease RecJ



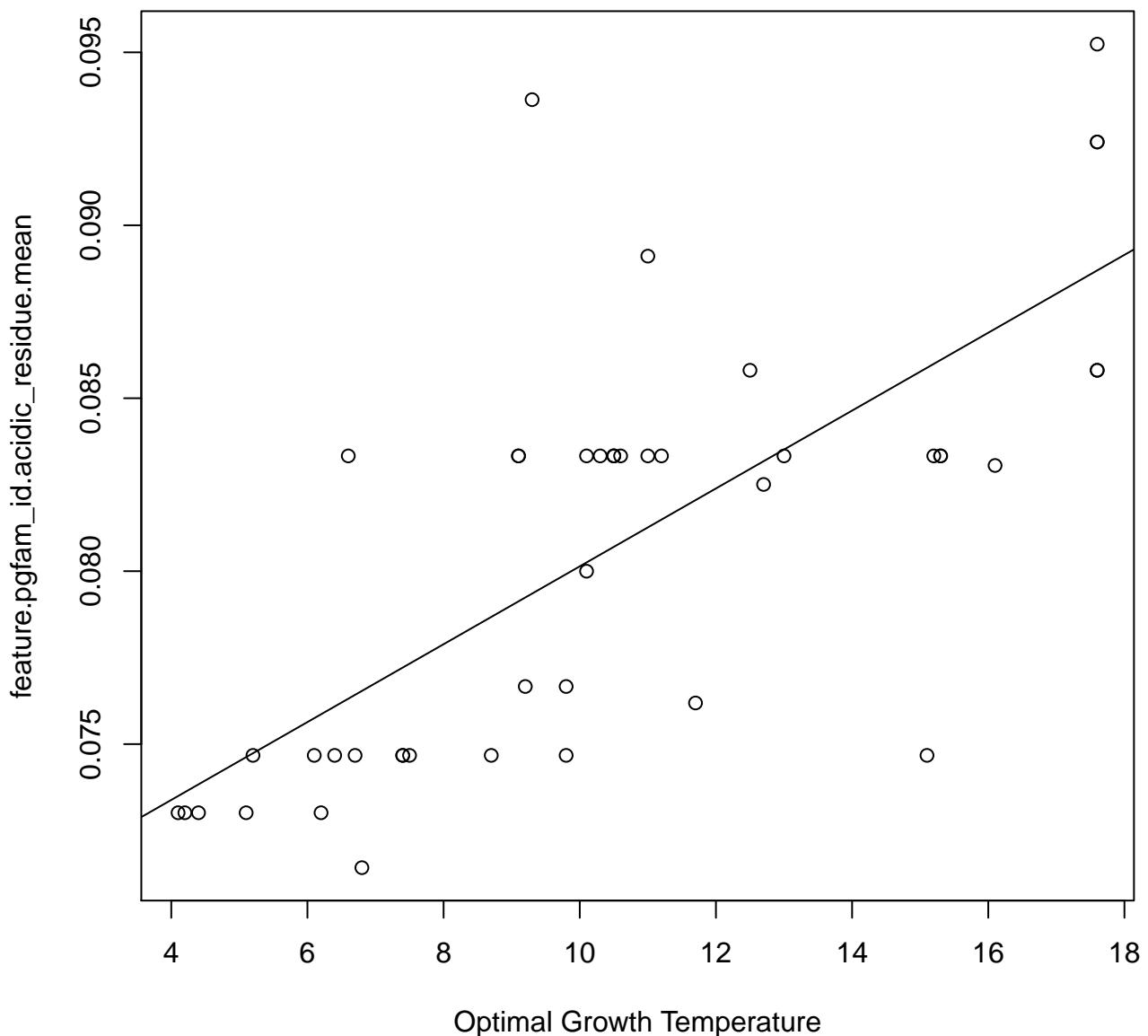
feature.pgfam_id.acidic_residue.mean
PGF_00064667
Argininosuccinate lyase (EC 4.3.2.1) / N-acetylglutamate synthase (EC 2.3.1.1)



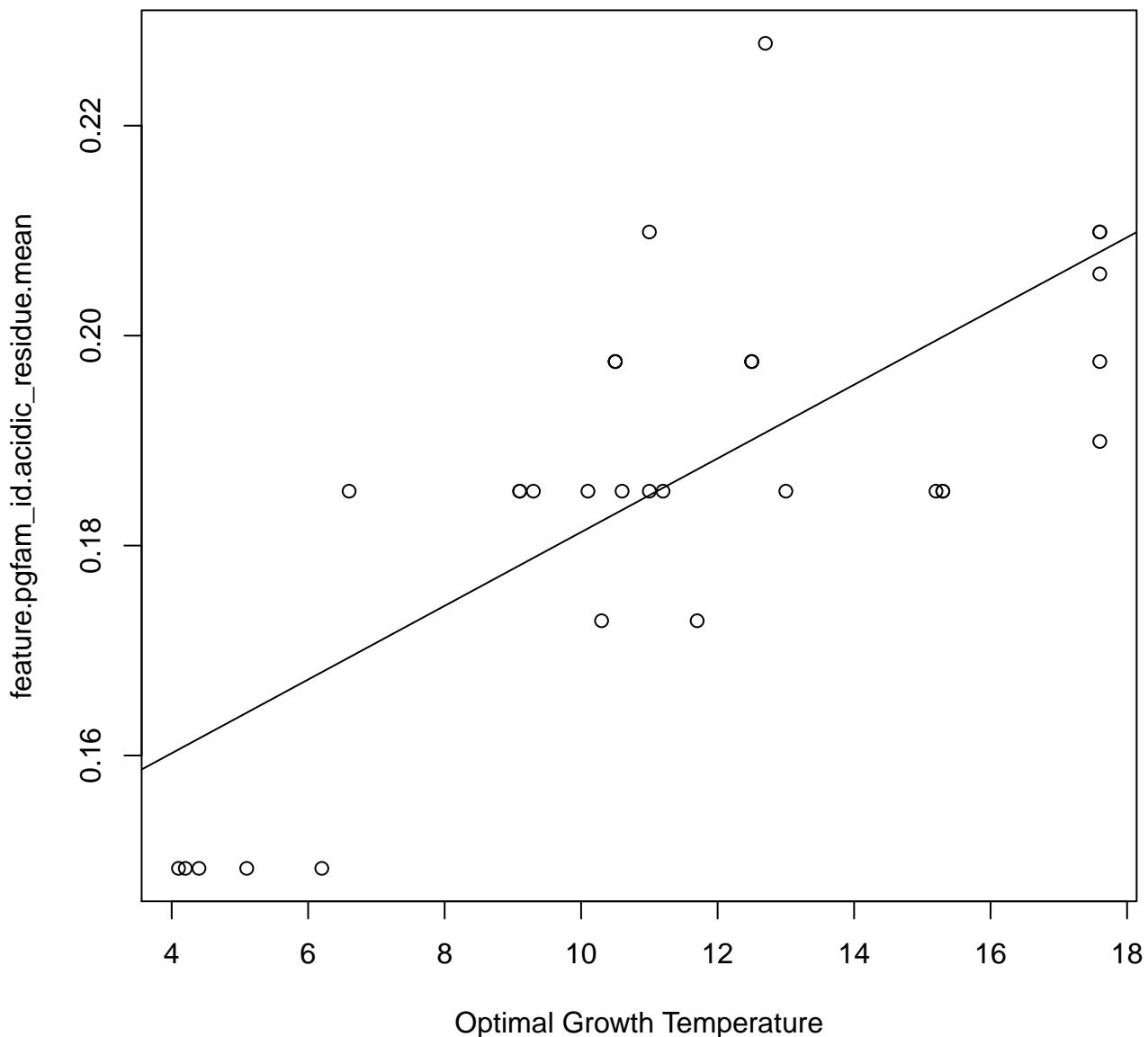
feature.pgfam_id.acidic_residue.mean
PGF_00018952
Malate dehydrogenase (EC 1.1.1.37)



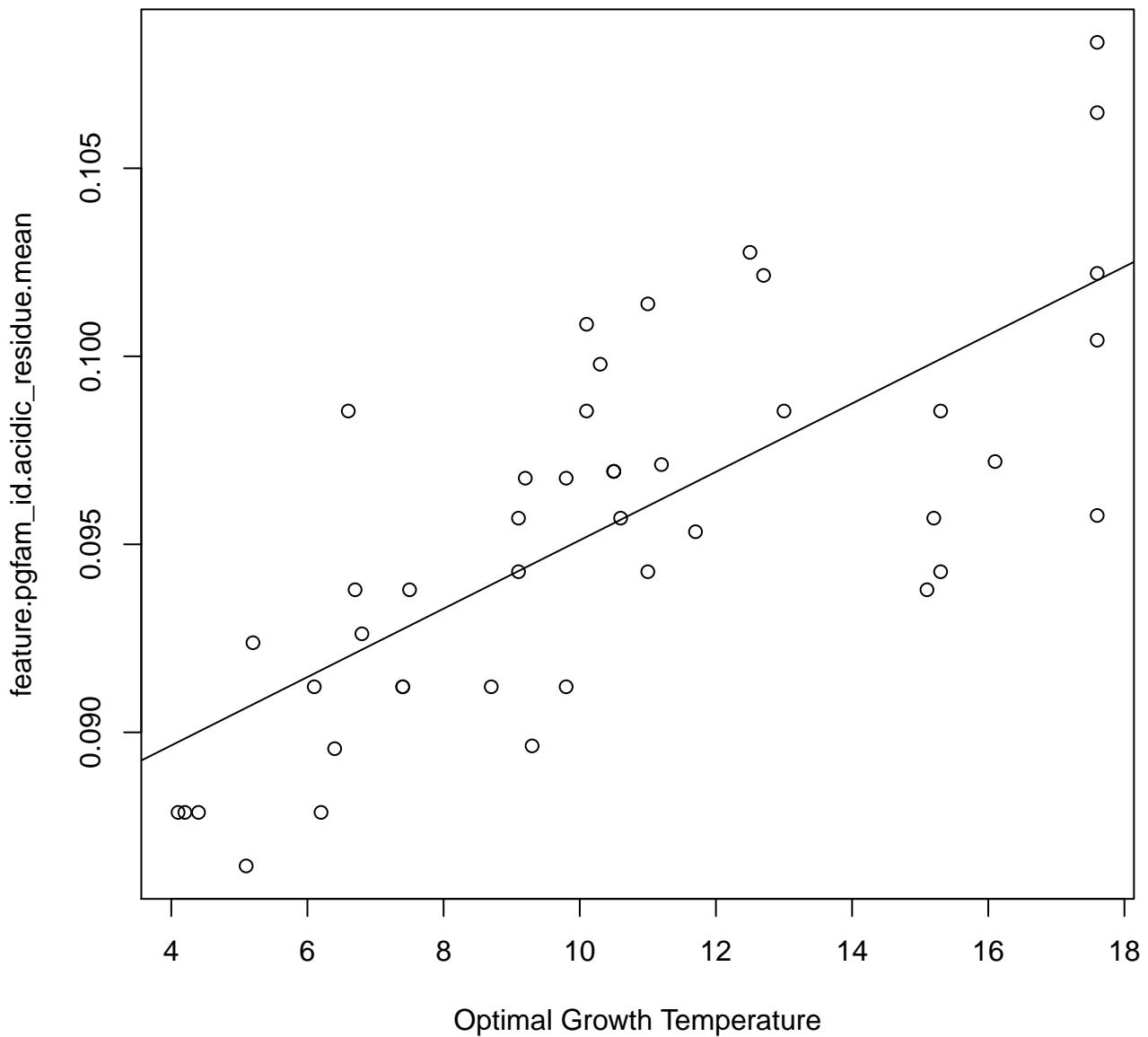
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PGF_05546469
Probable acyltransferase PA0834



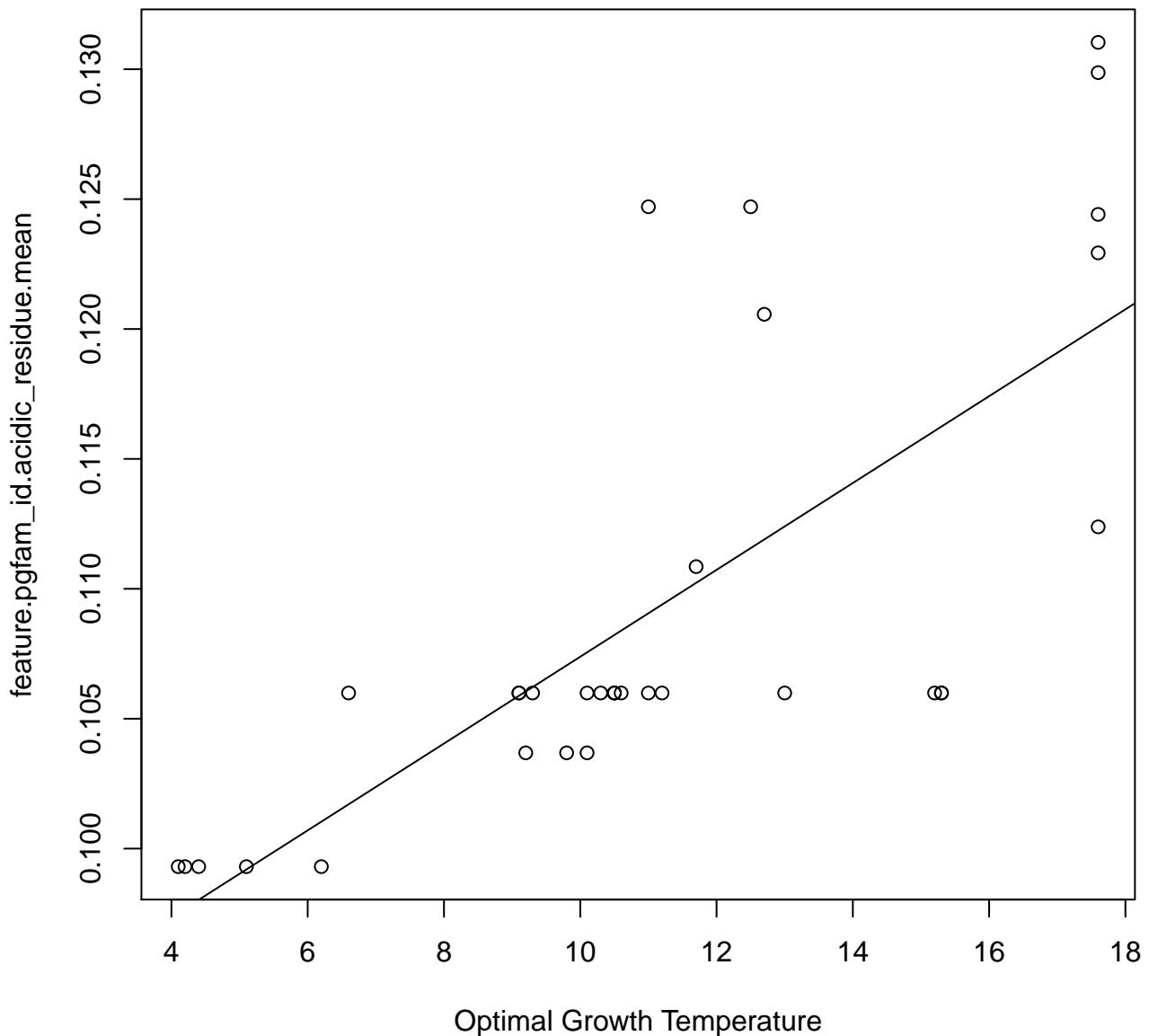
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PGF_00064685
Uncharacterized ferredoxin-like protein YfhL



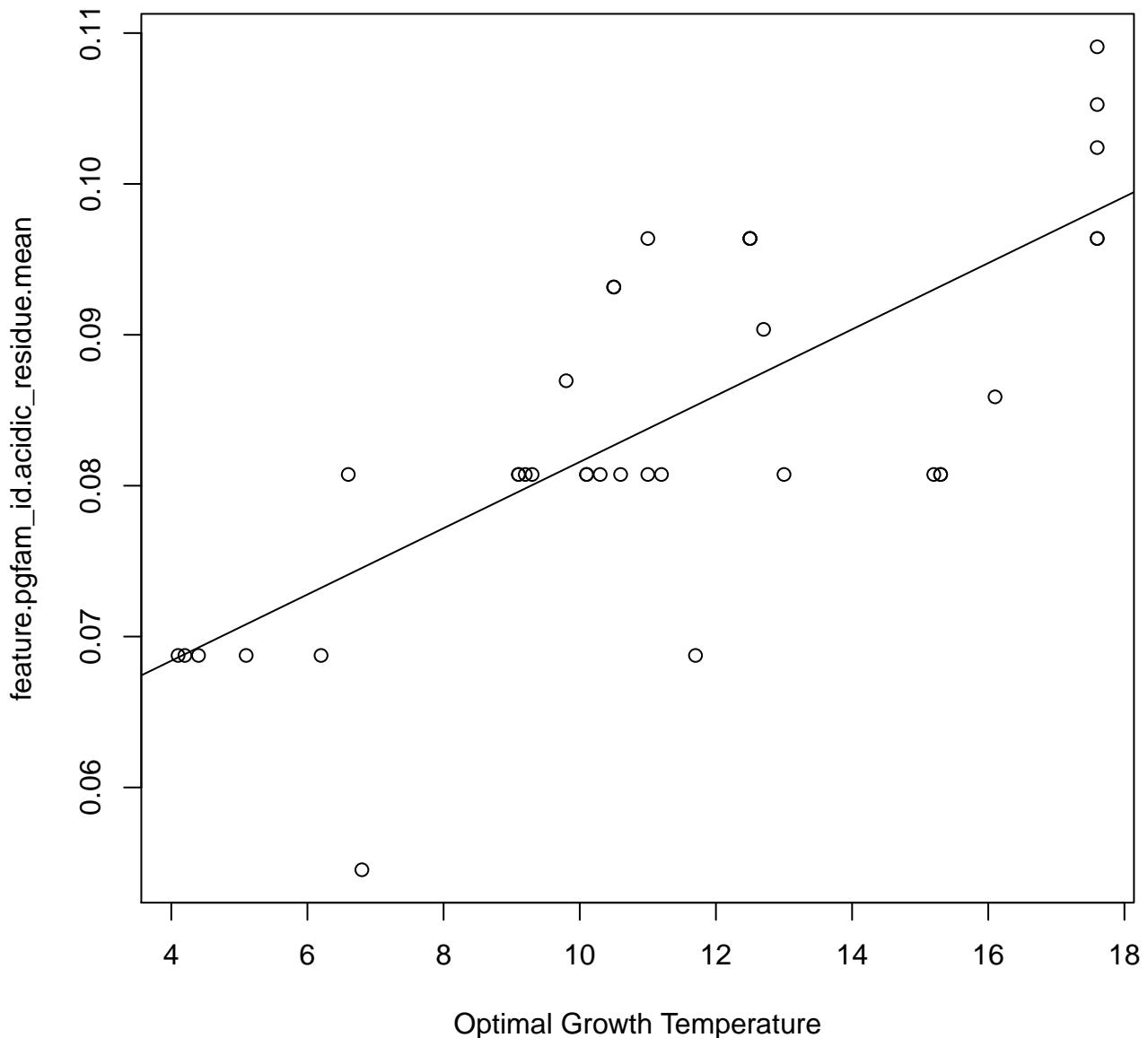
feature.pgfam_id.acidic_residue.mean
PGF_03116630
Membrane-bound lytic murein transglycosylase B



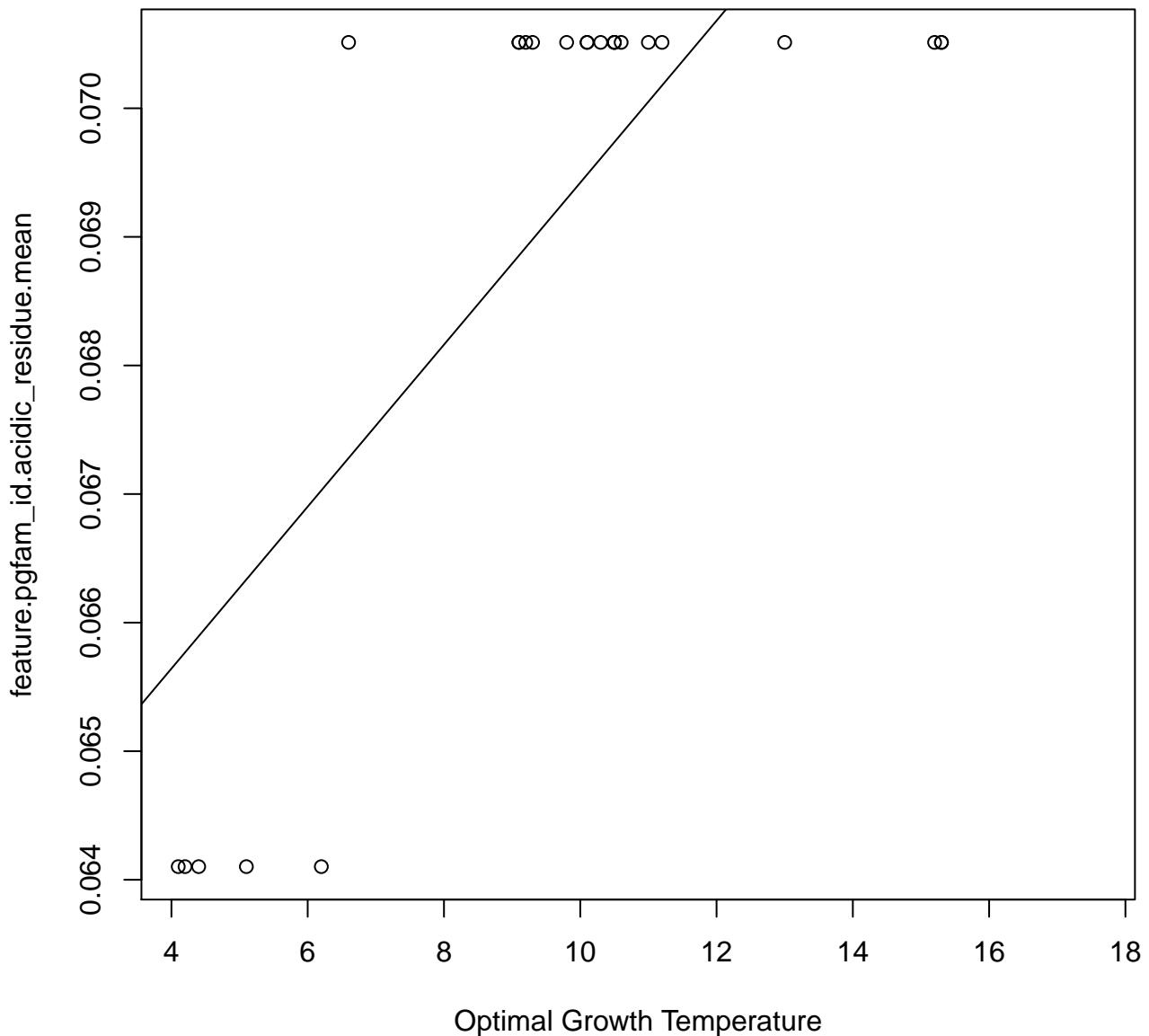
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PGF_00007666
GII1812 protein



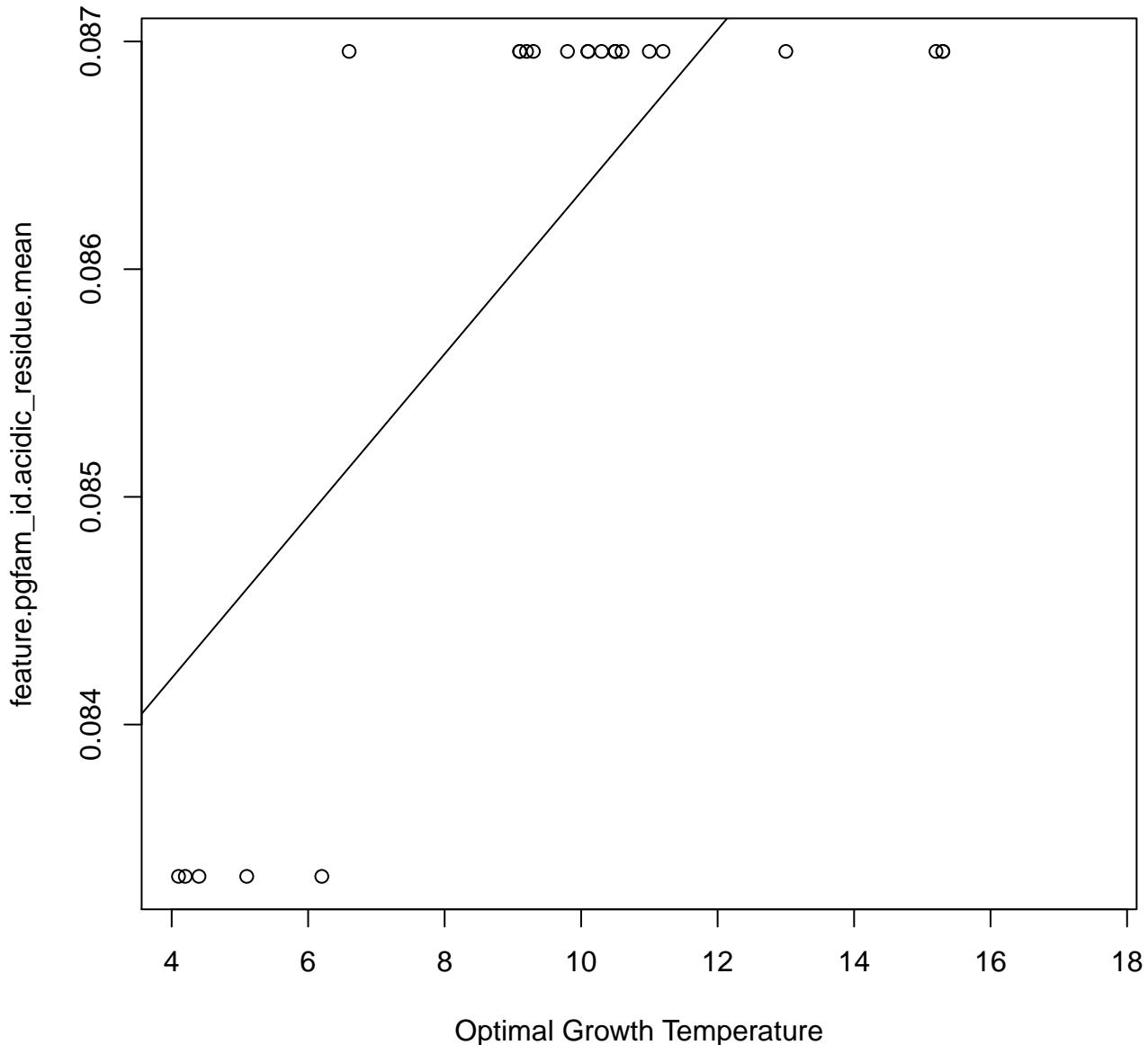
feature.pgfam_id.acidic_residue.mean
PGF_05020380
hypothetical protein



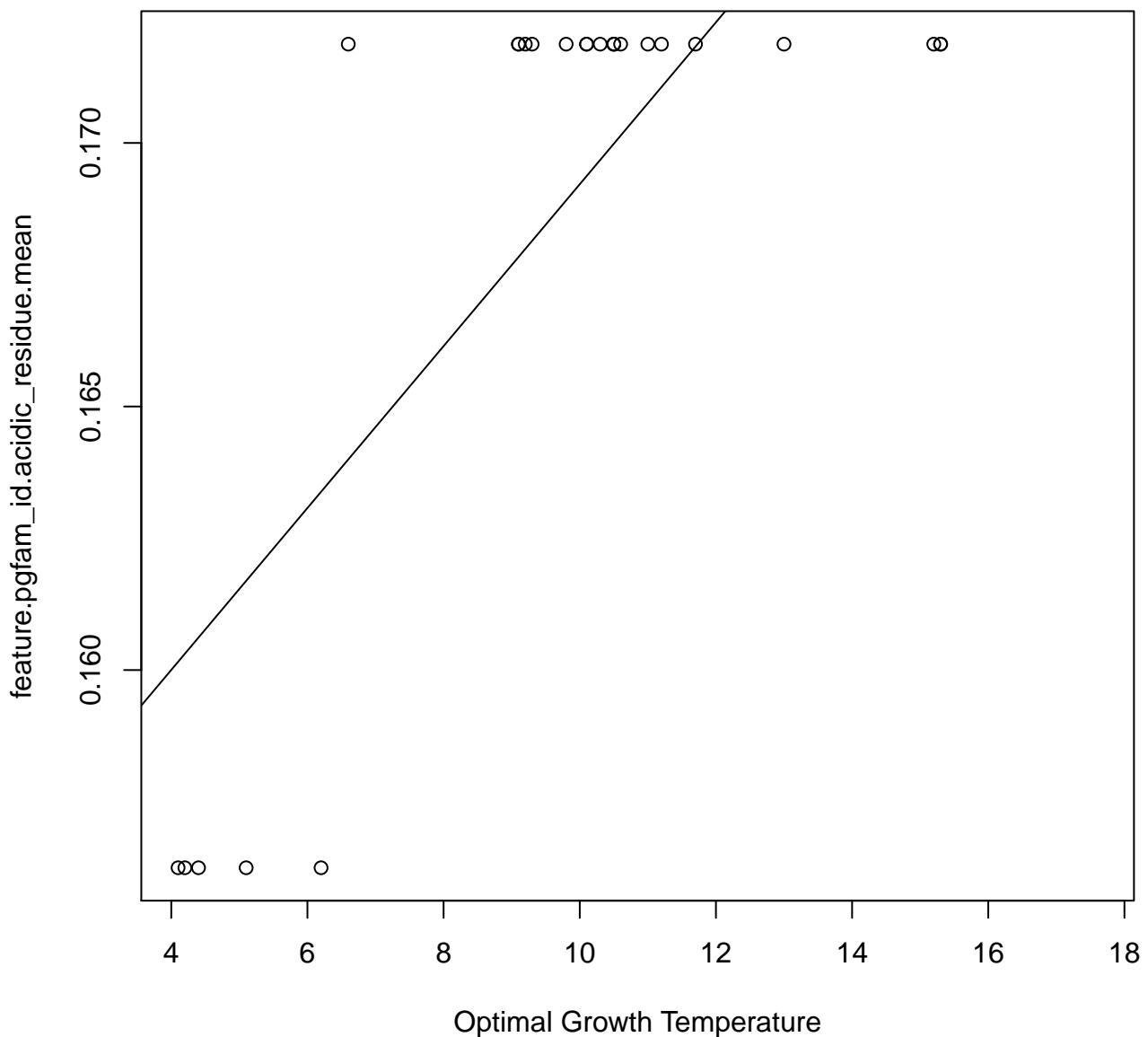
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PGF_04213500
hypothetical protein



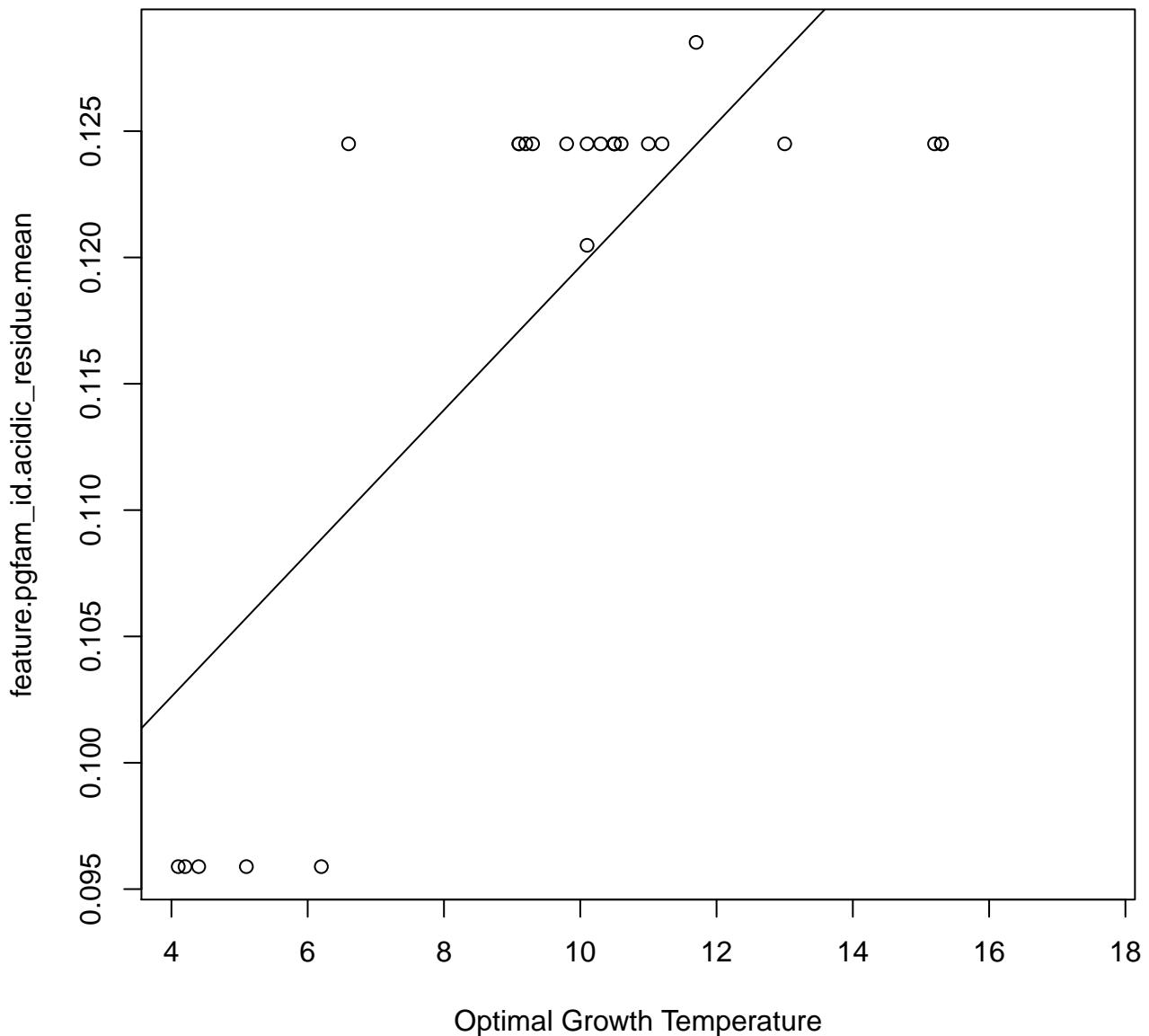
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PGF_12071964
hypothetical protein



feature.pgfam_id.acidic_residue.mean
PGF_07004481
hypothetical protein



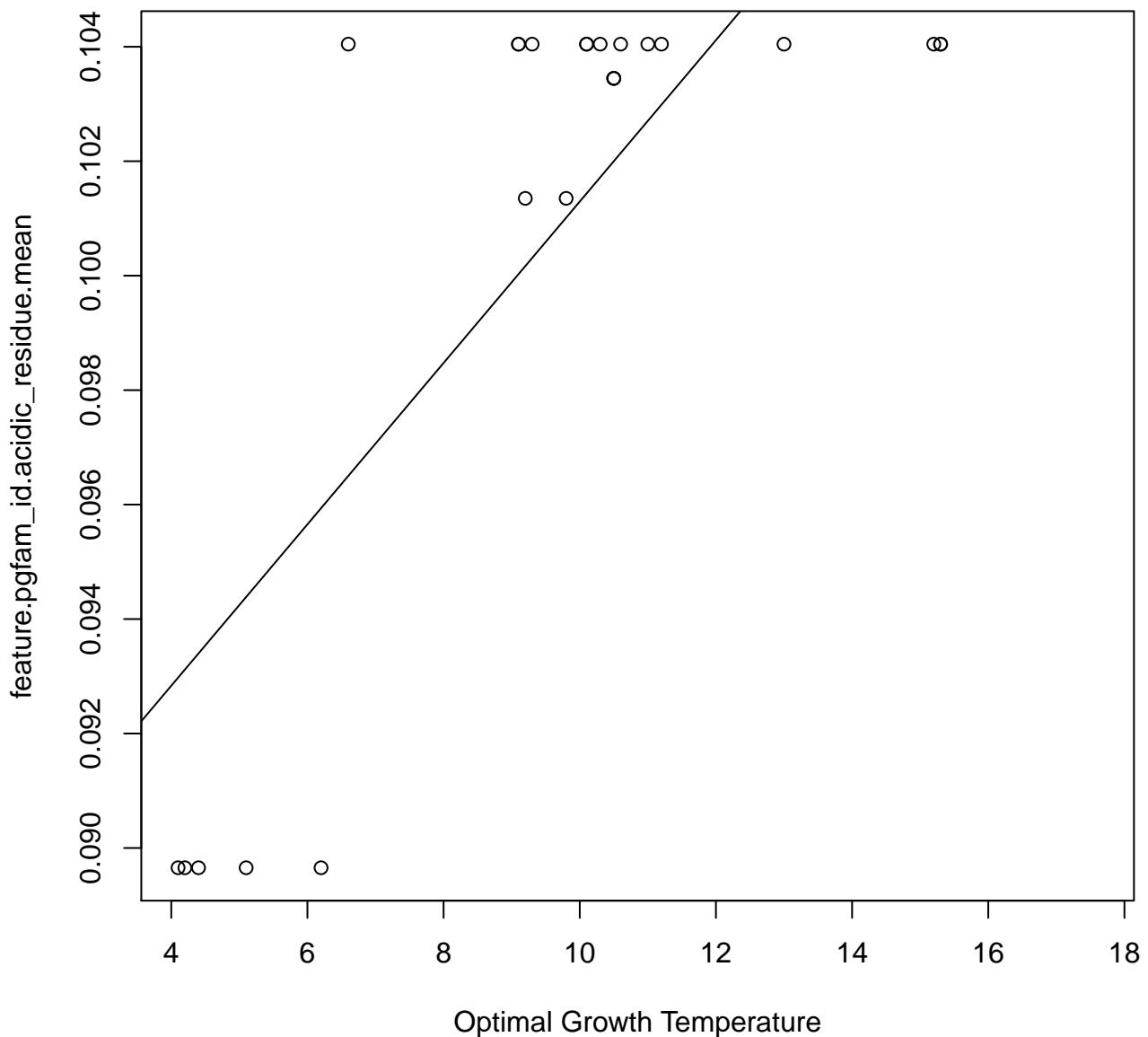
feature.pgfam_id.acidic_residue.mean
PGF_11018774
hypothetical protein



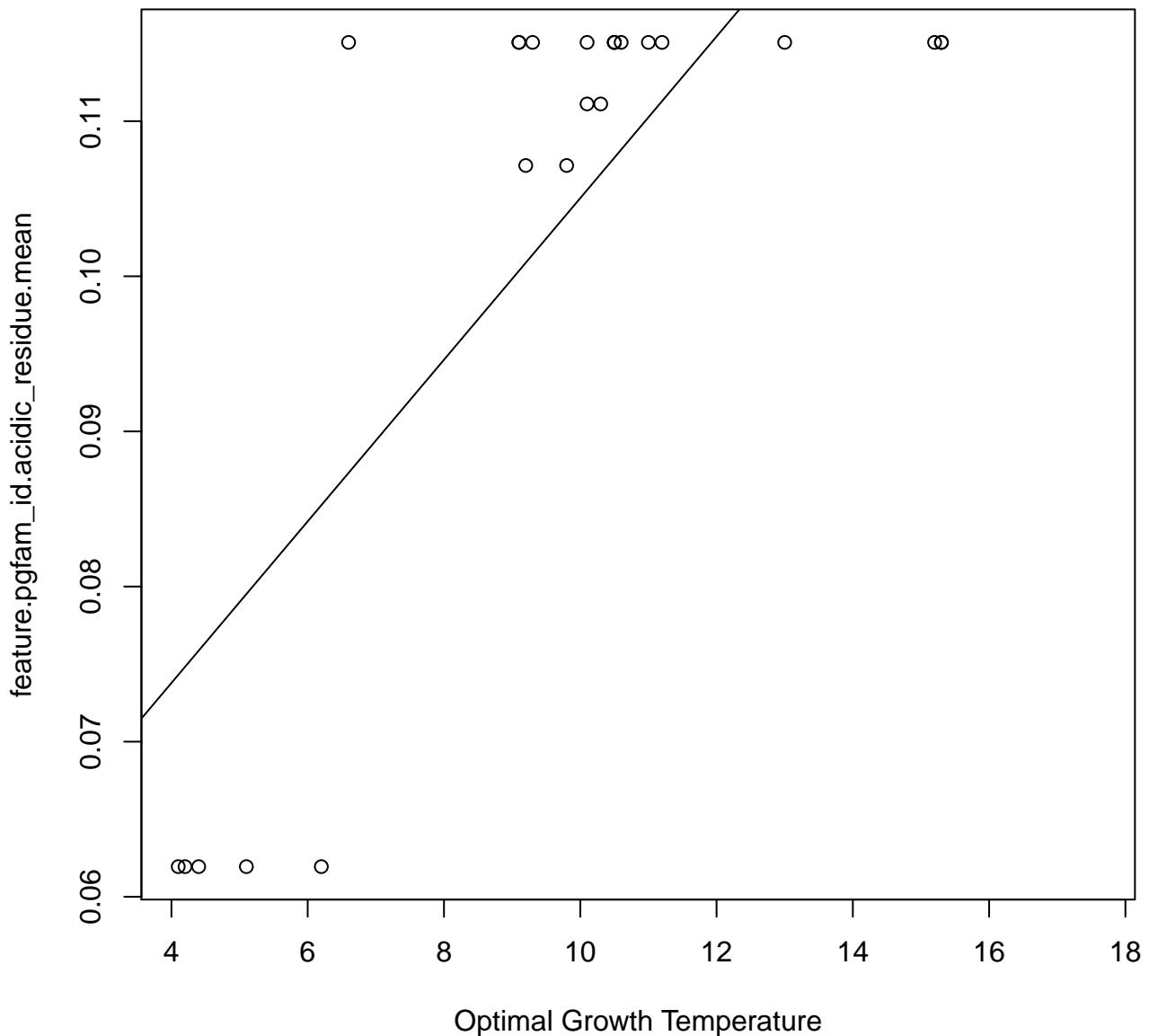
feature.pgfam_id.acidic_residue.mean

PGF_07418929

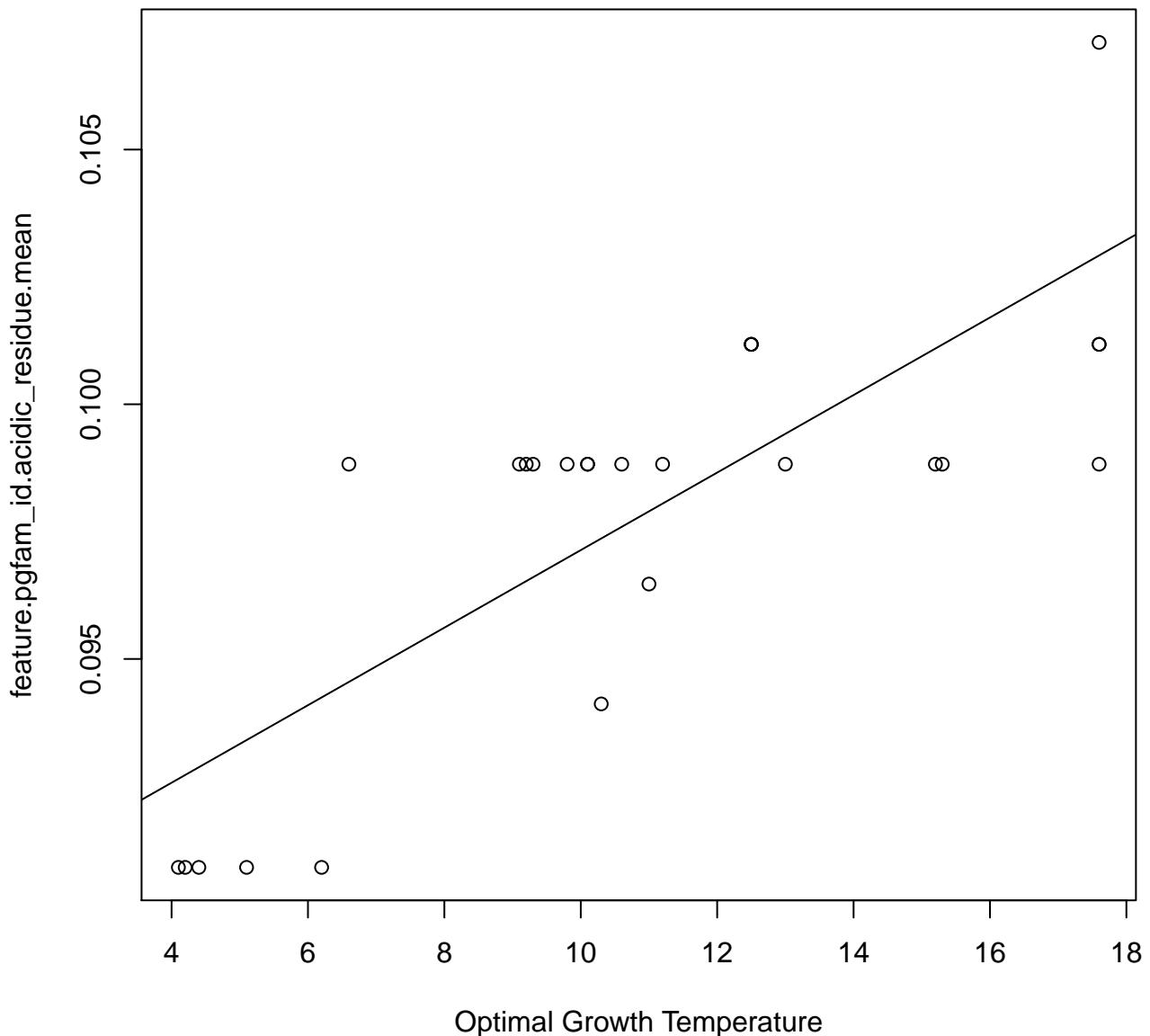
hypothetical protein



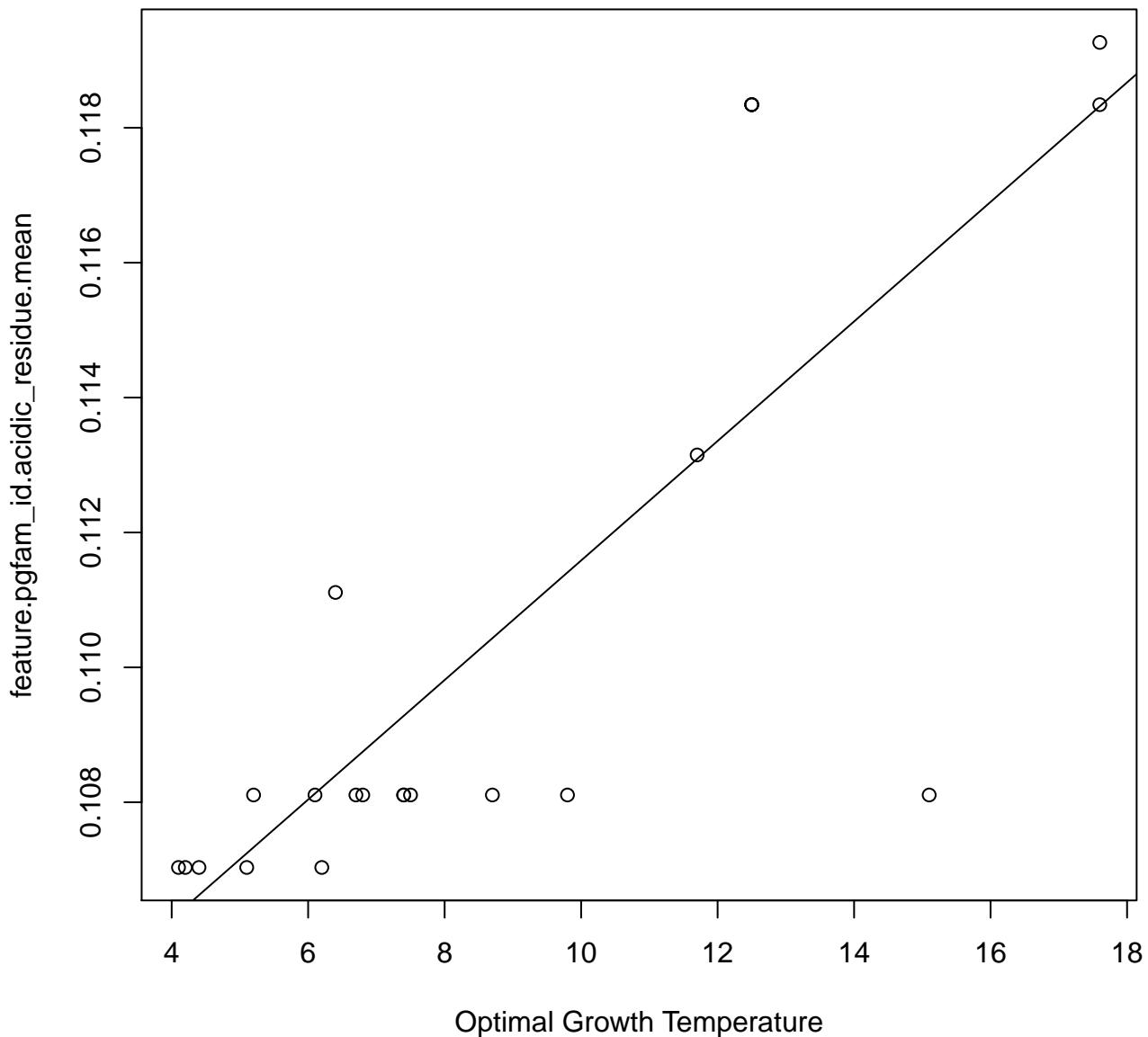
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PGF_12049070
hypothetical protein



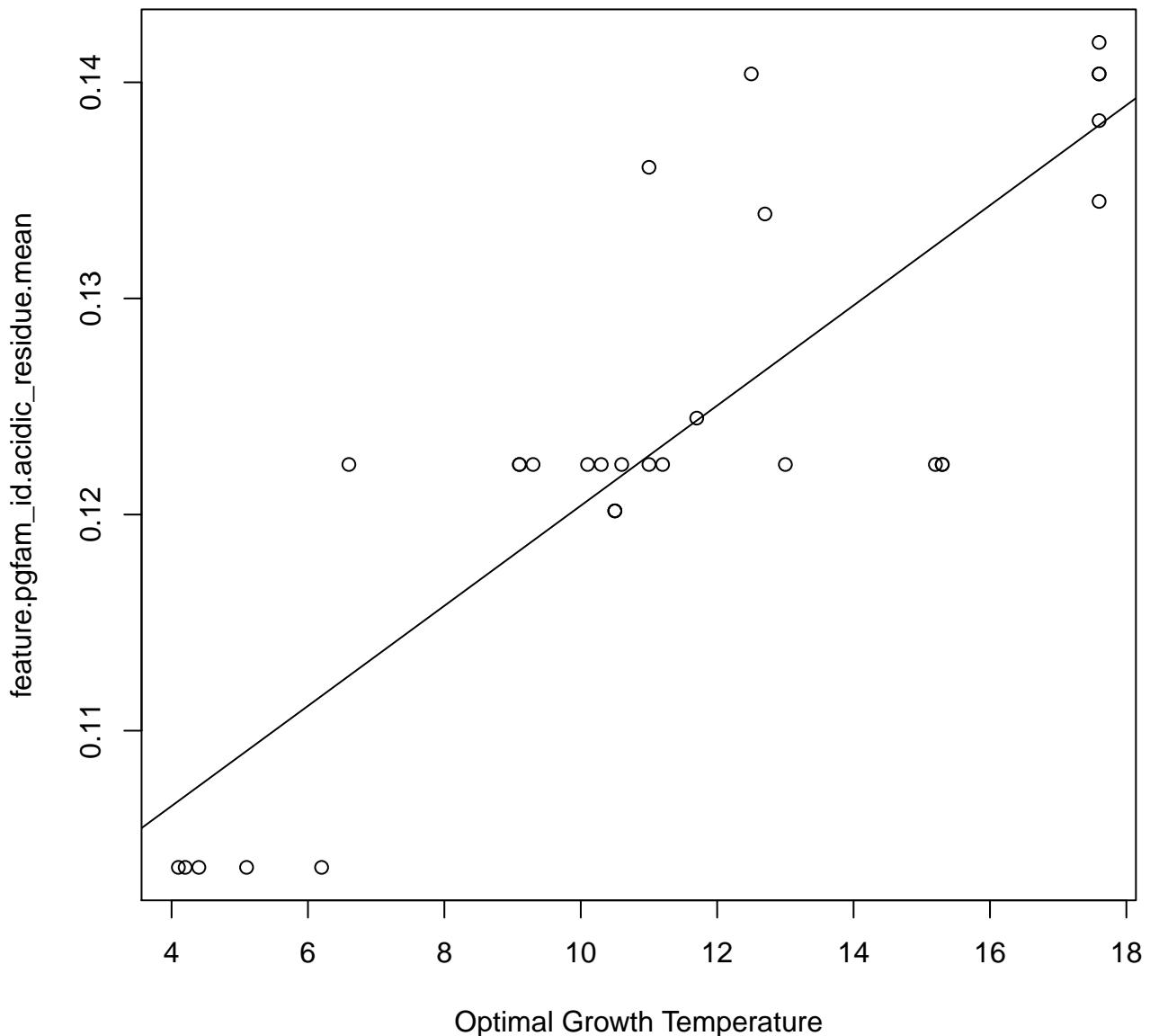
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PGF_00424021
EPS I polysaccharide export outer membrane protein EPSA precursor



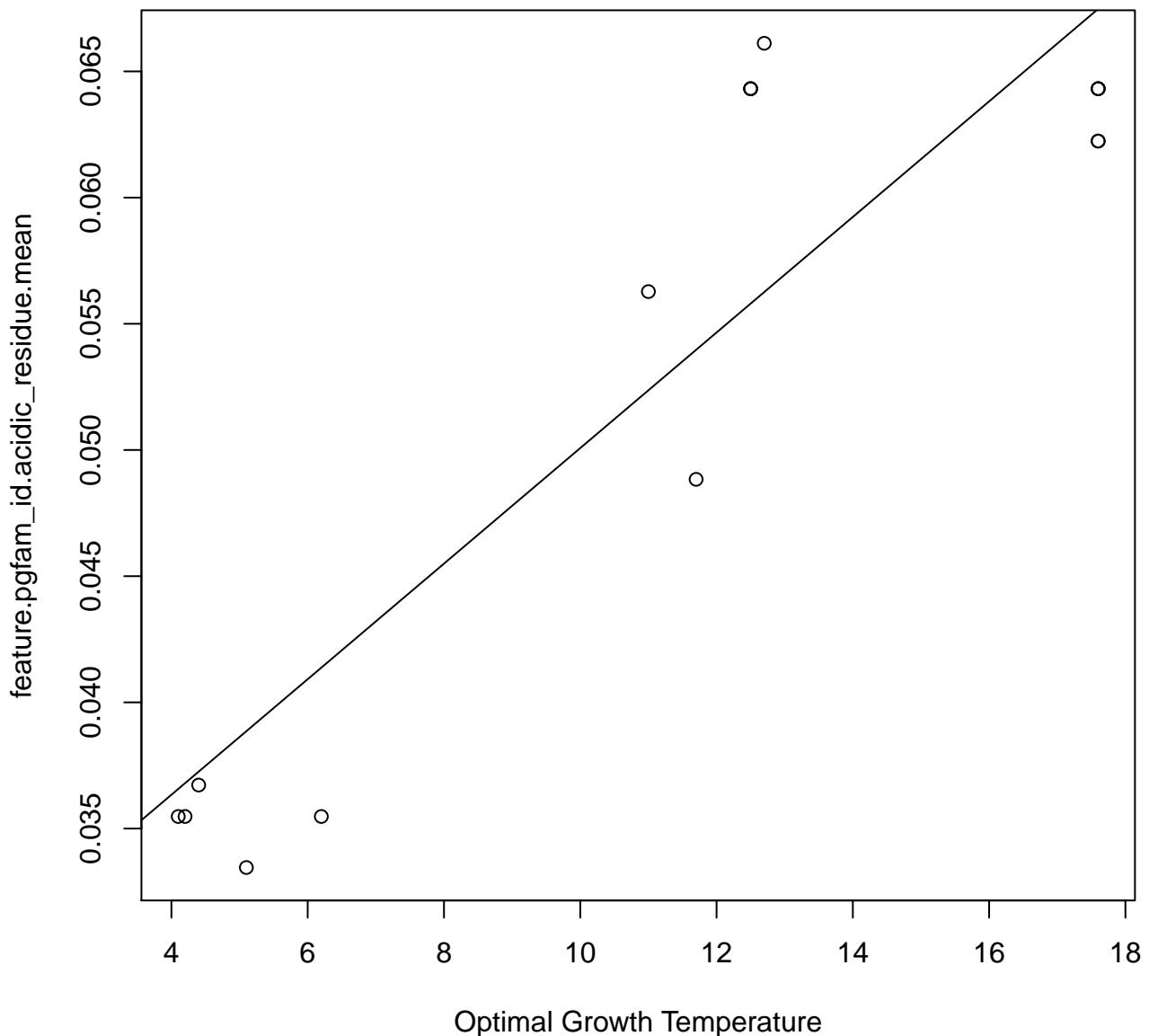
feature.pgfam_id.acidic_residue.mean
PGF_01969379
Acetoin dehydrogenase E1 component beta-subunit (EC 2.3.1.190)



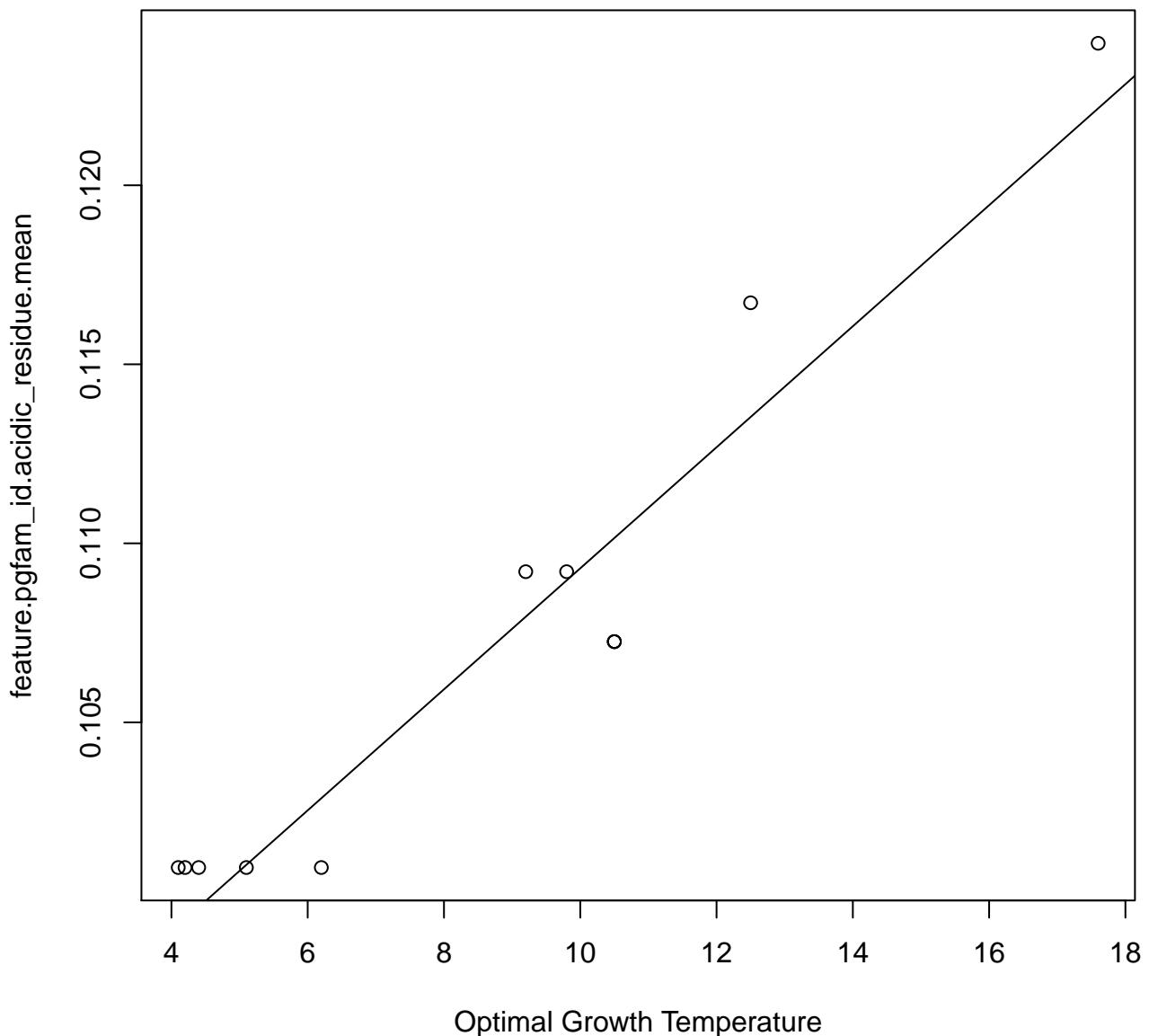
feature.pgfam_id.acidic_residue.mean
PGF_02105064
Uncharacterized protease YegQ



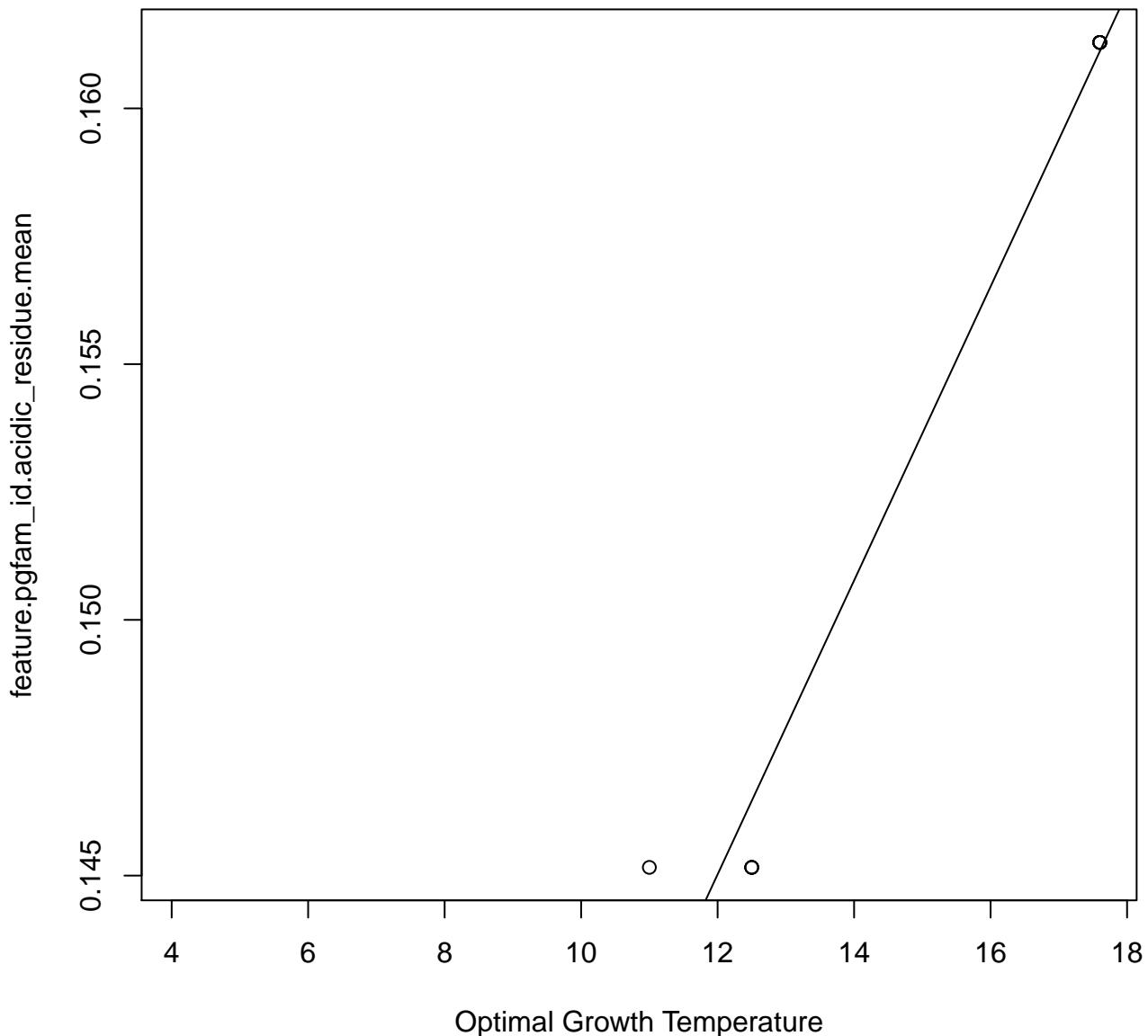
feature.pgfam_id.acidic_residue.mean
PGF_00066964
Xanthine/uracil/thiamine/ascorbate permease family protein



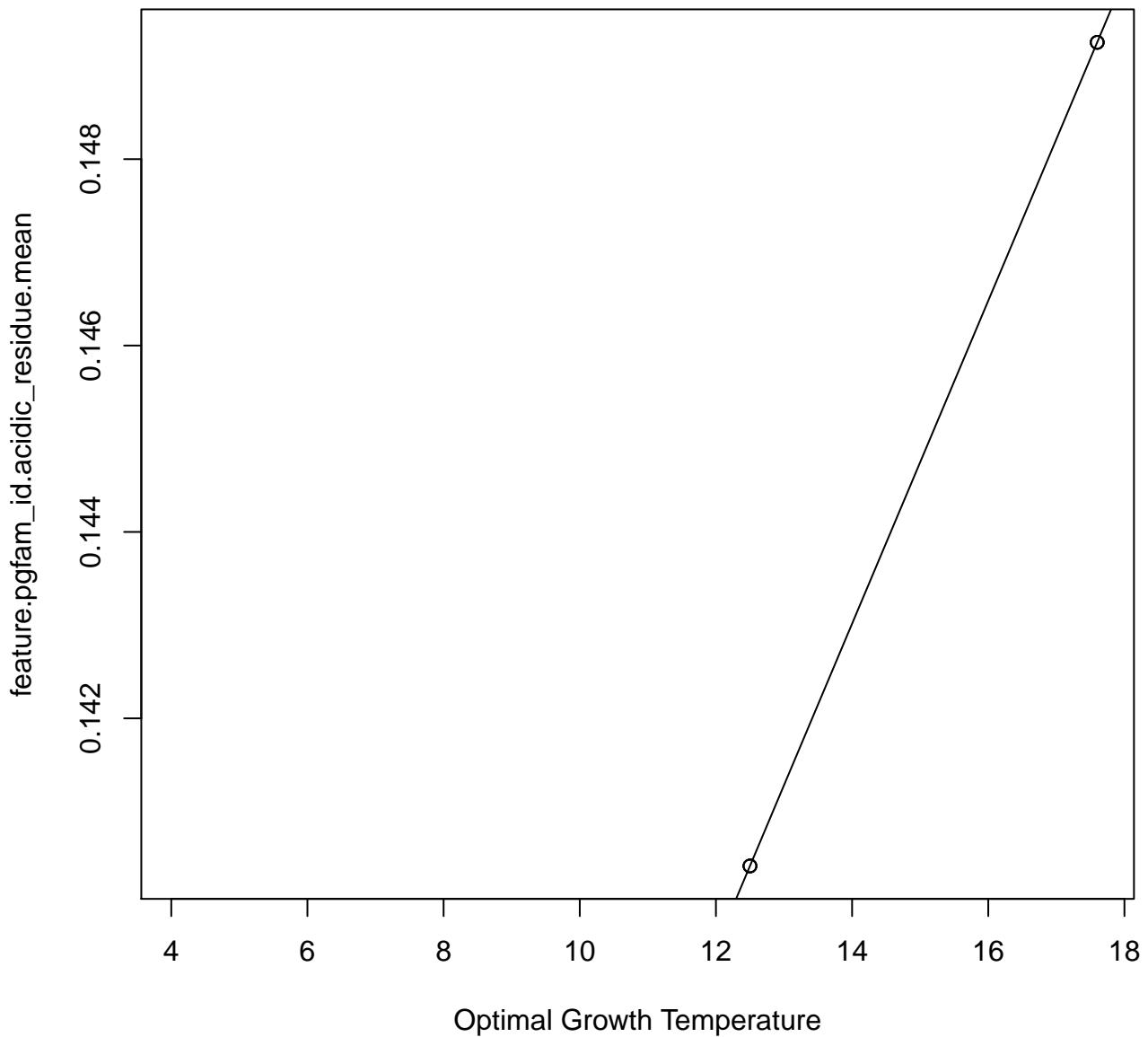
feature.pgfam_id.acidic_residue.mean
PGF_10496736
Transcriptional regulator, AraC family



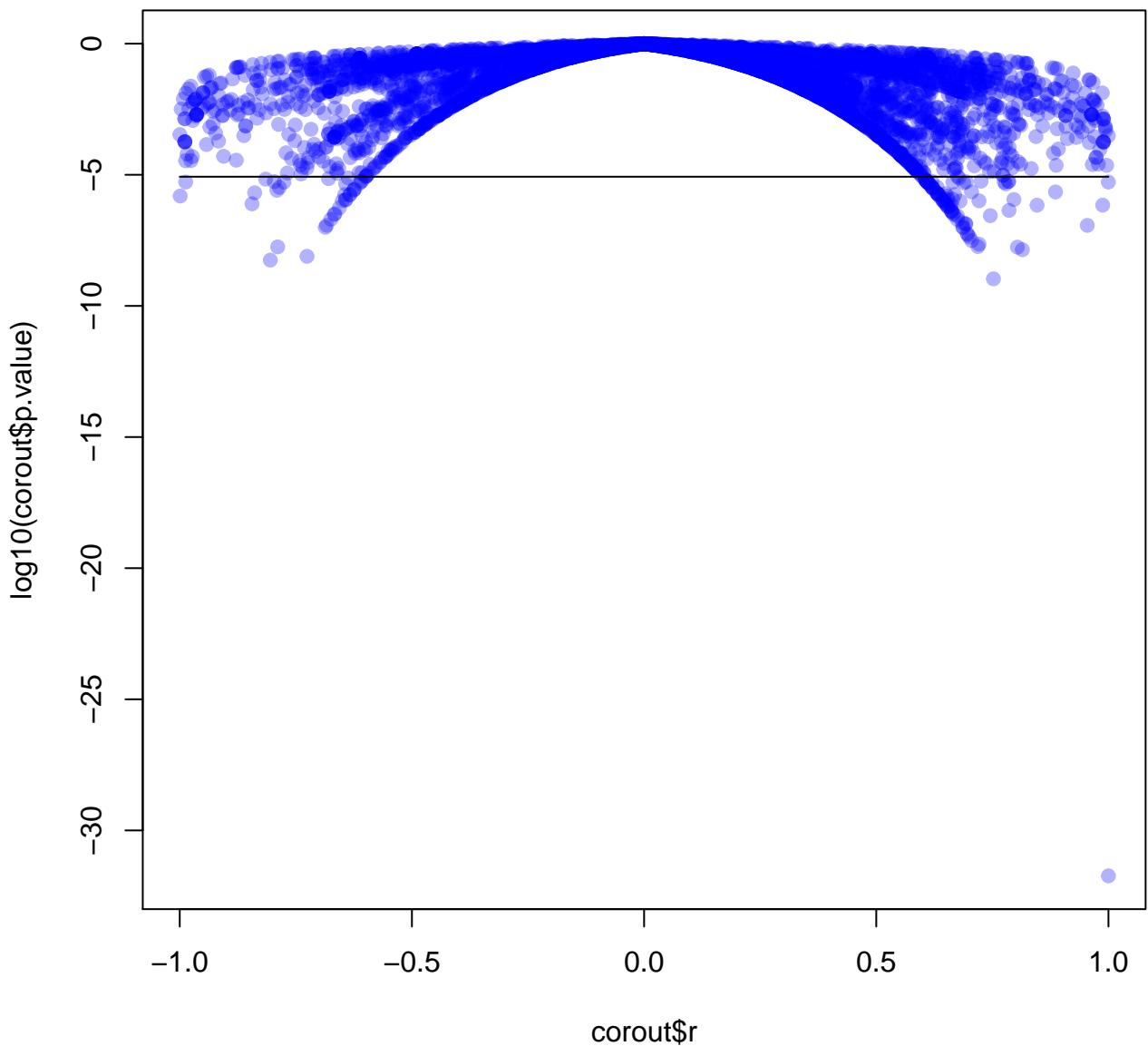
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PGF_00236554
hypothetical protein



feature.pgfam_id.acidic_residue.mean
PGF_01336638
hypothetical protein



feature.plfam_id.acidic_residue.mean

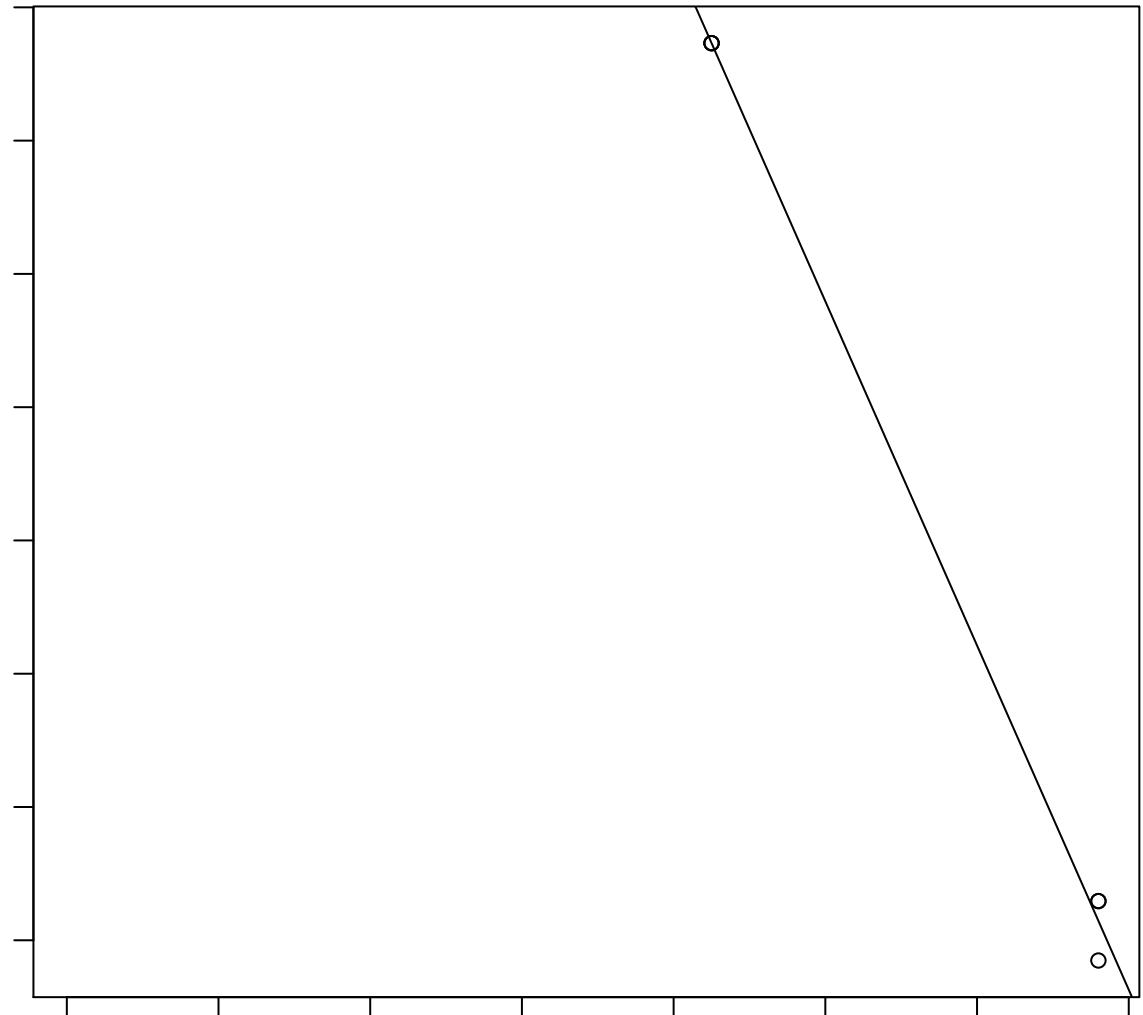


feature.plfam_id.acidic_residue.mean
PLF_28228_00018366
hypothetical protein

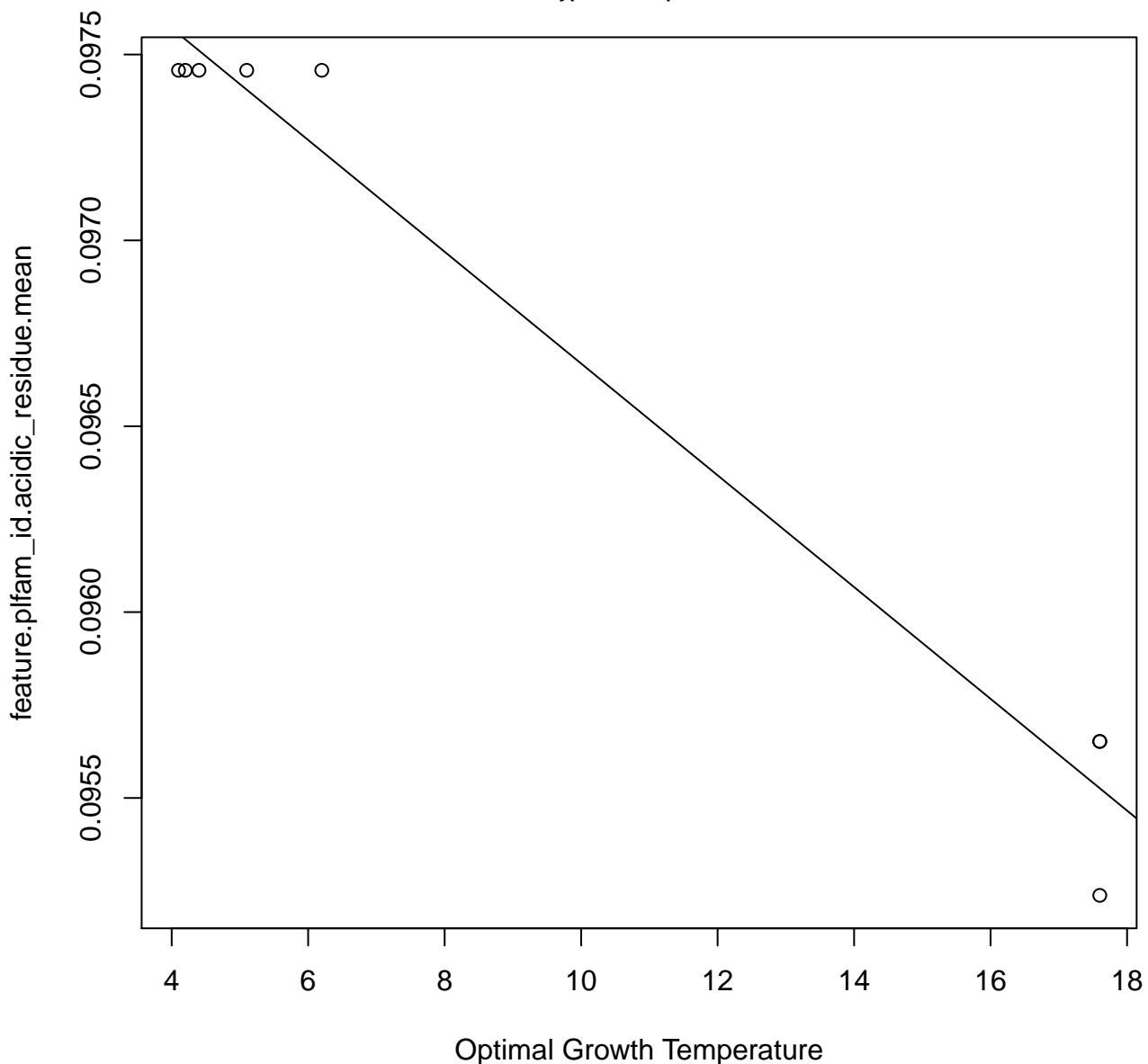
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4 6 8 10 12 14 16 18

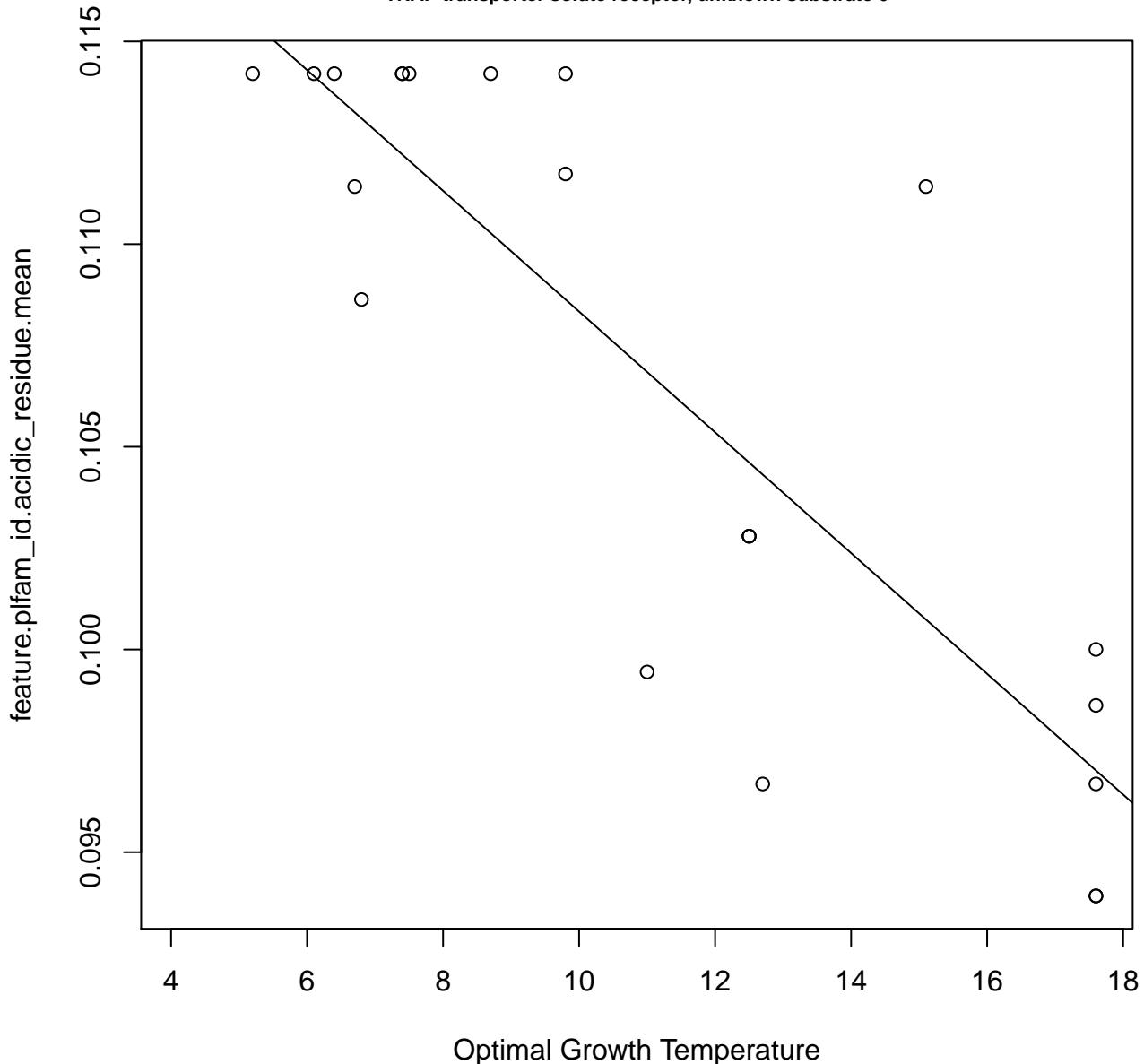
Optimal Growth Temperature



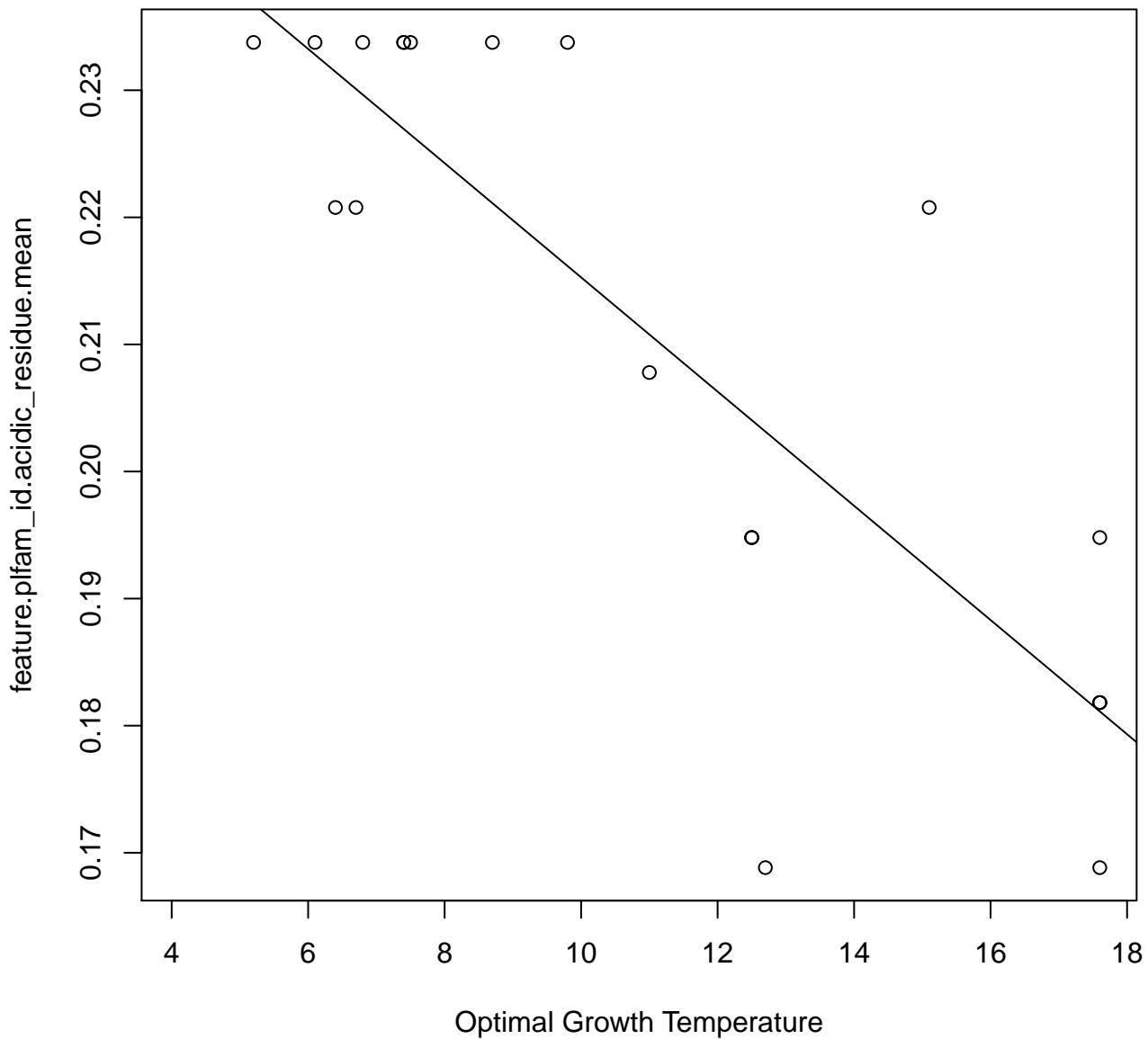
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PLF_28228_00003941
hypothetical protein



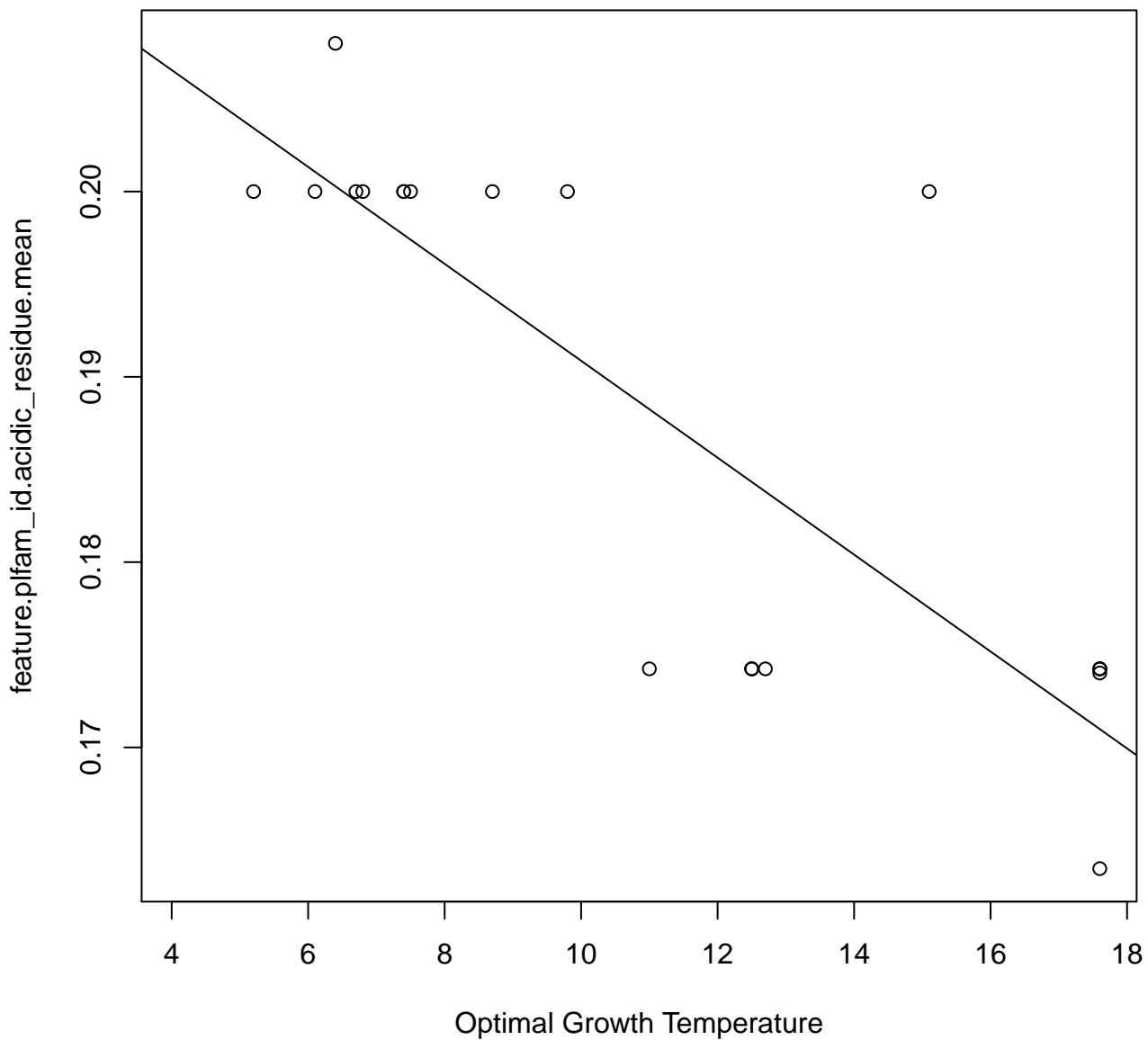
feature.plfam_id.acidic_residue.mean
PLF_28228_00001182
TRAP transporter solute receptor, unknown substrate 6



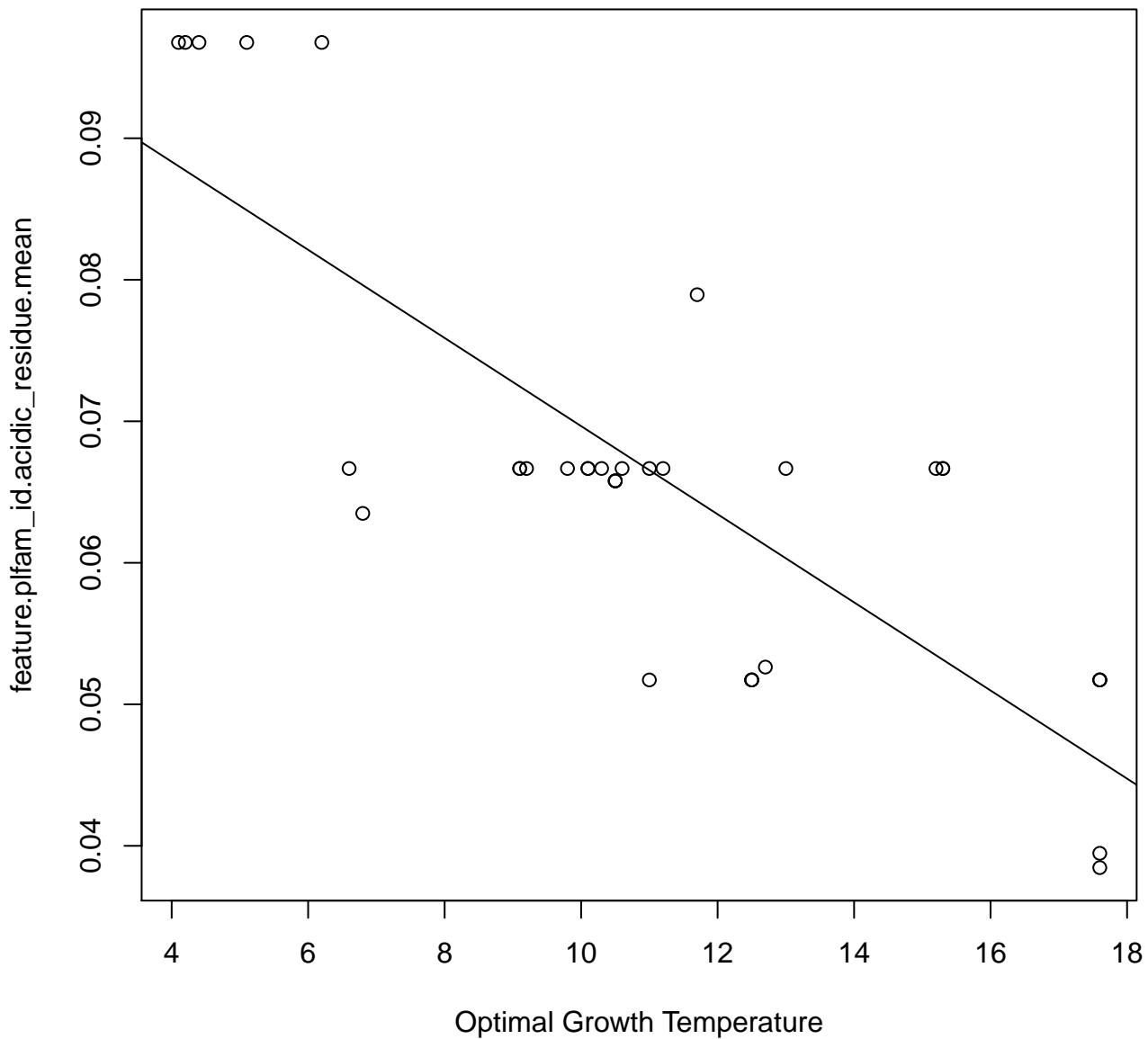
feature.plfam_id.acidic_residue.mean
PLF_28228_00001832
FIG034389 (not subsystem-based): hypothetical protein



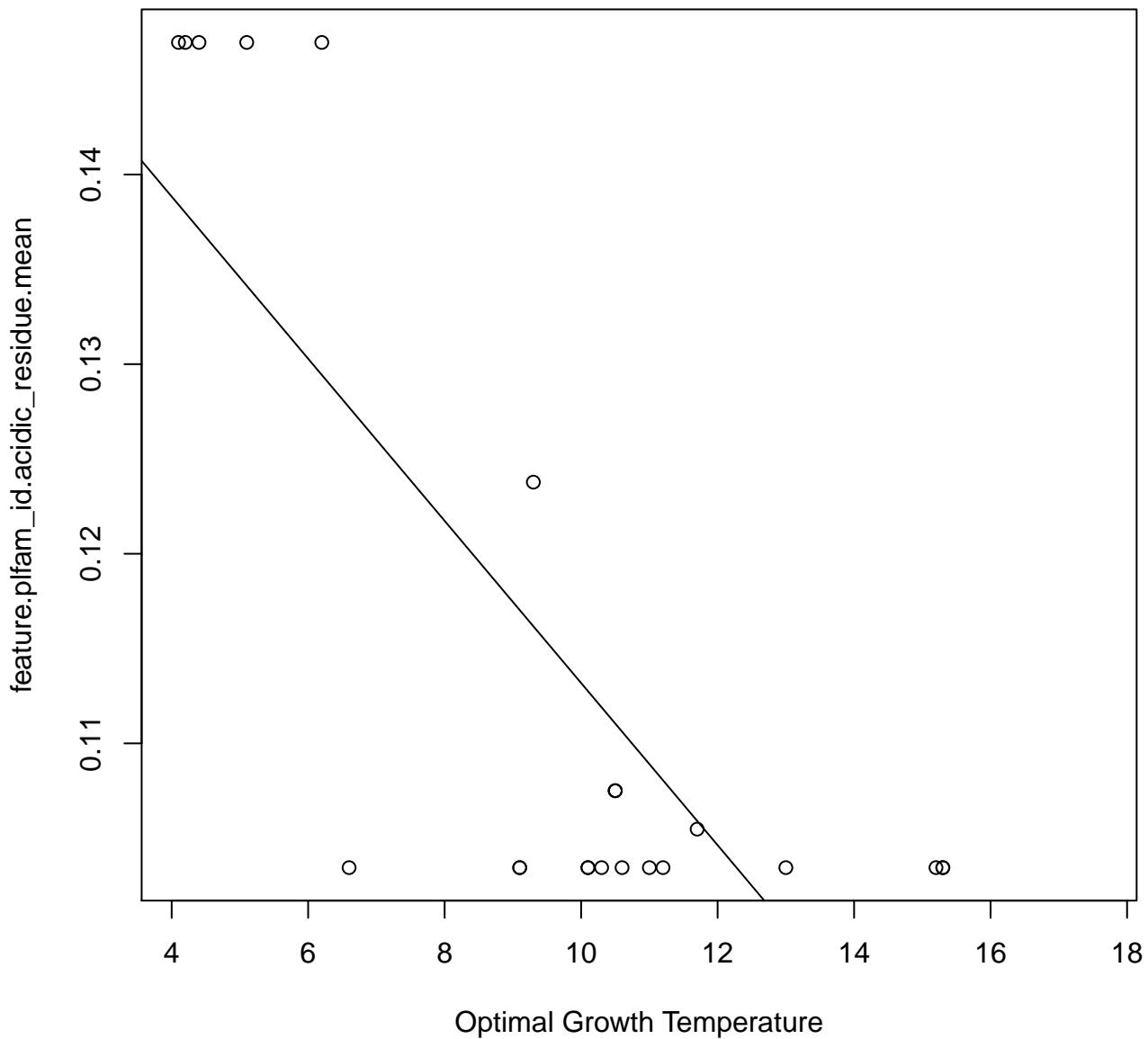
feature.plfam_id.acidic_residue.mean
PLF_28228_00002401
hypothetical protein



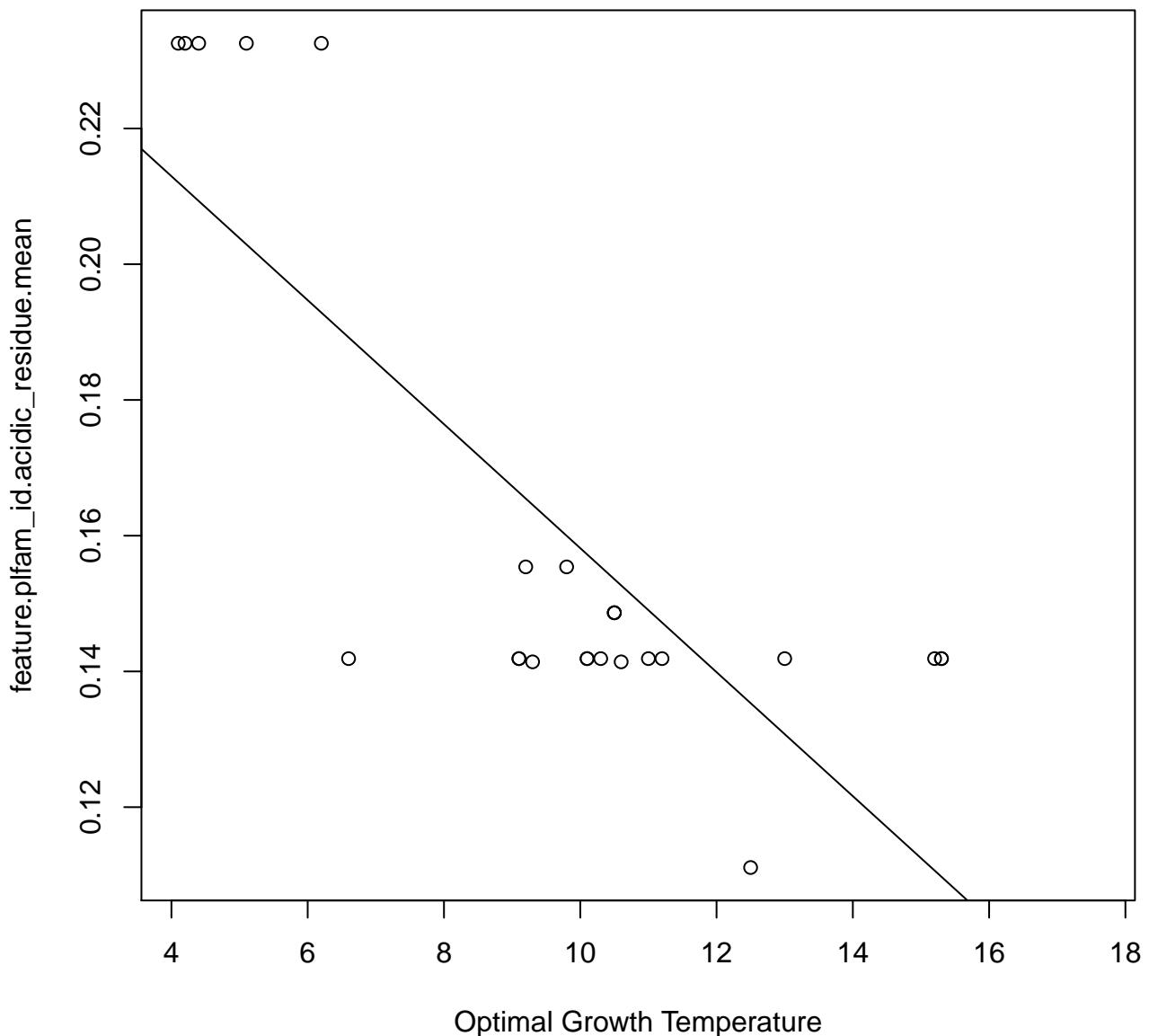
feature.plfam_id.acidic_residue.mean
PLF_28228_00001333
Uncharacterized membrane protein SO_0290



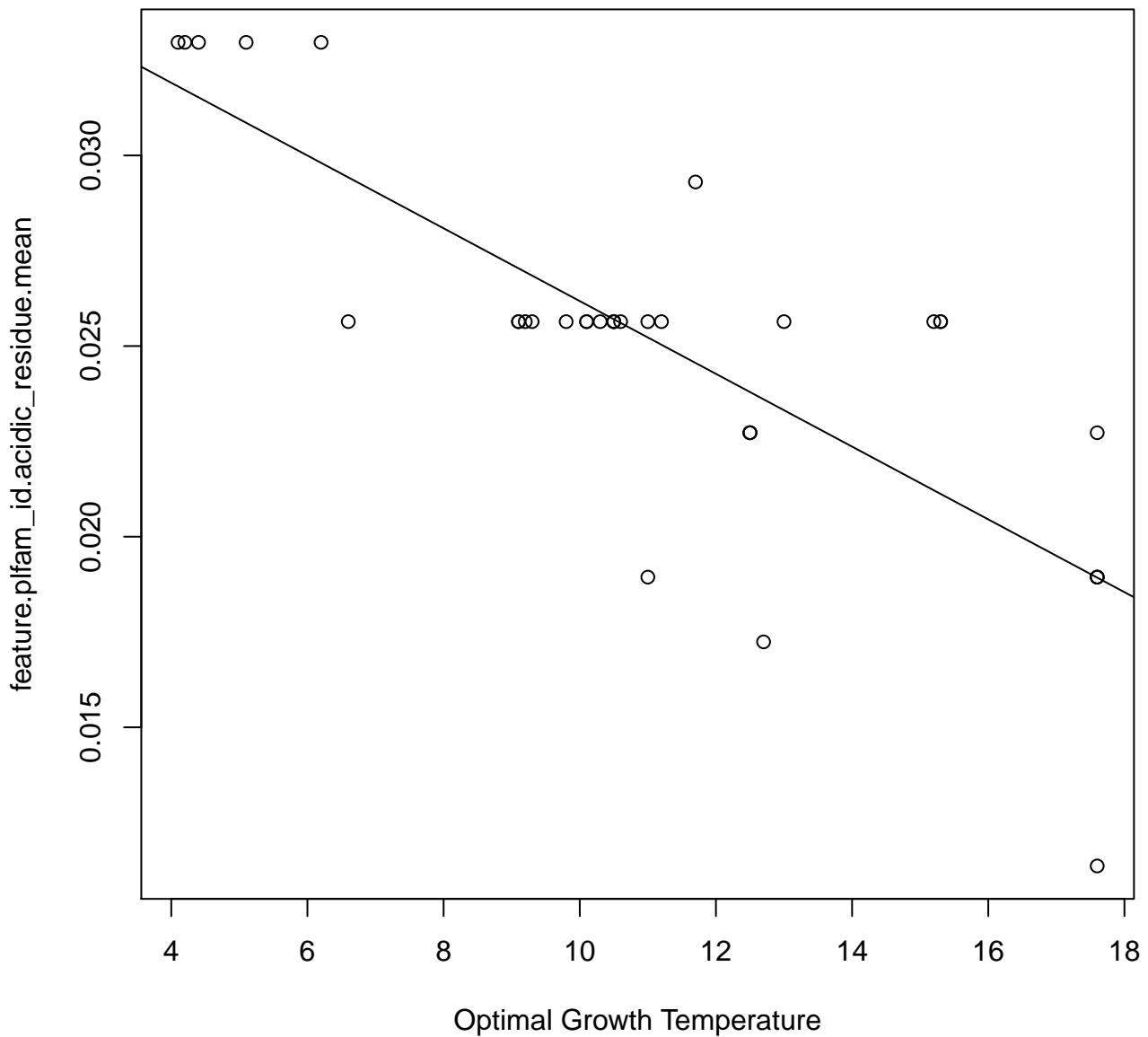
feature.plfam_id.acidic_residue.mean
PLF_28228_00022096
Two-component system sensor histidine kinase



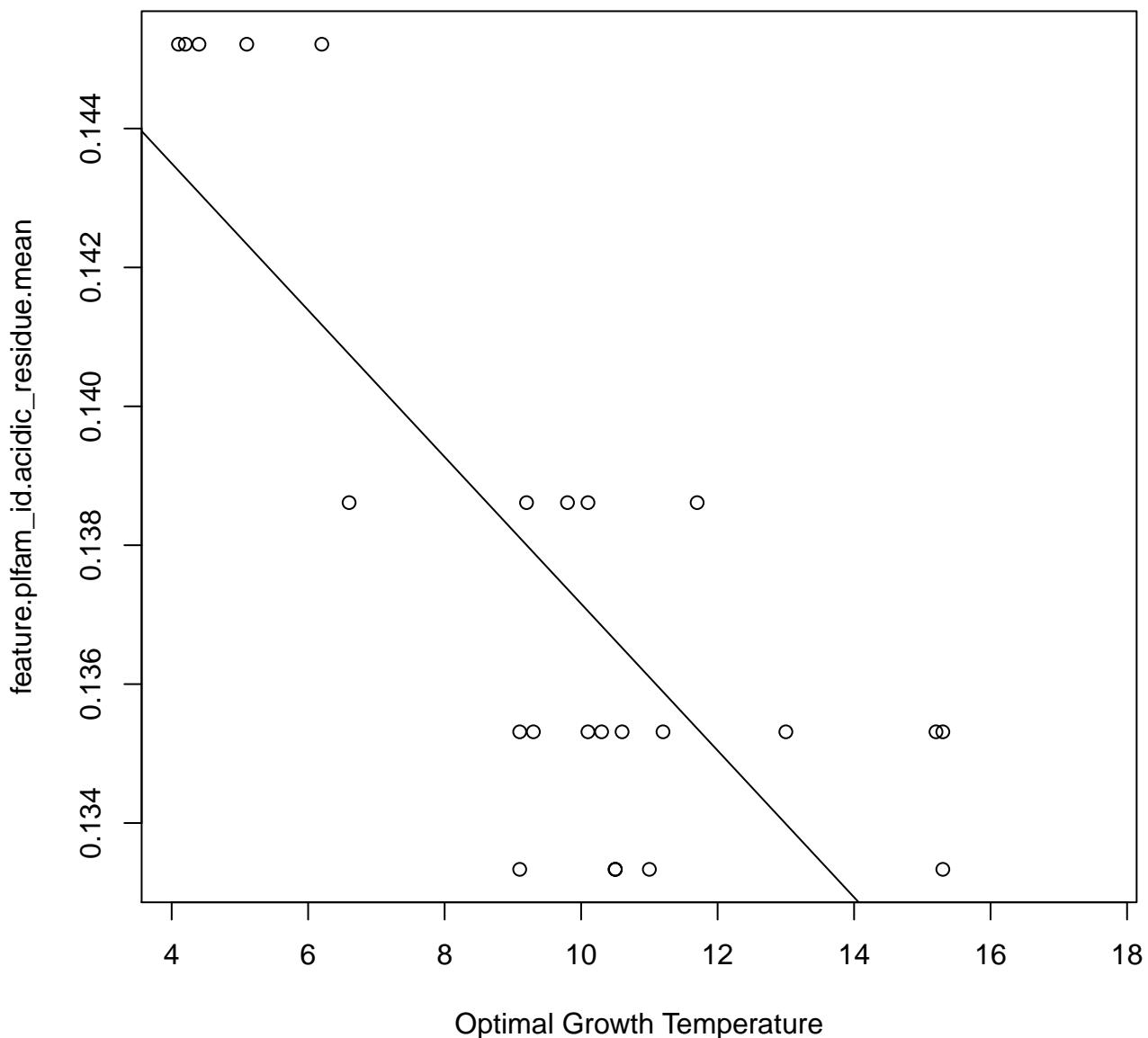
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PLF_28228_00014070
hypothetical protein



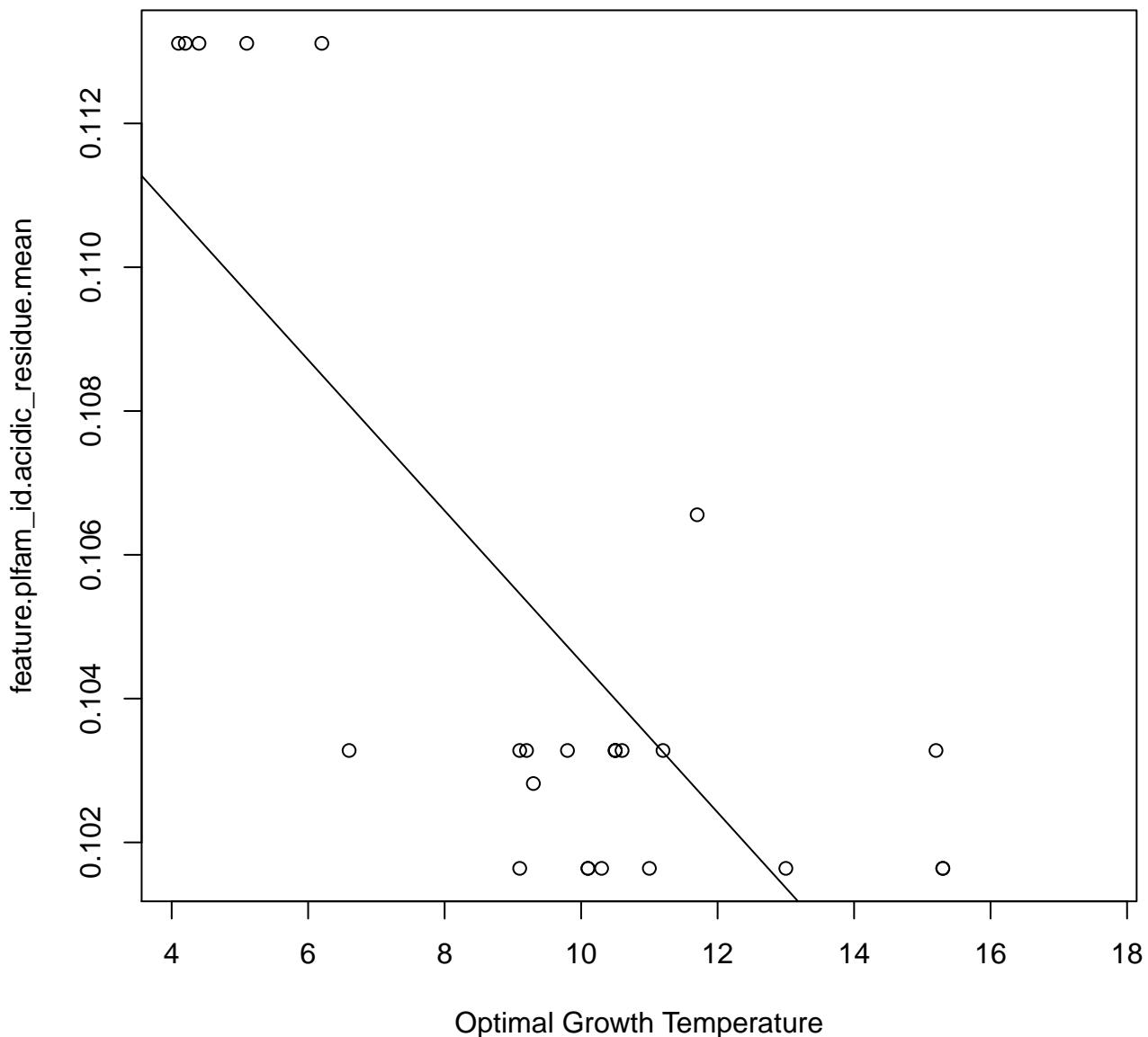
feature.plfam_id.acidic_residue.mean
PLF_28228_00001007
Uncharacterized UPF0721 integral membrane protein



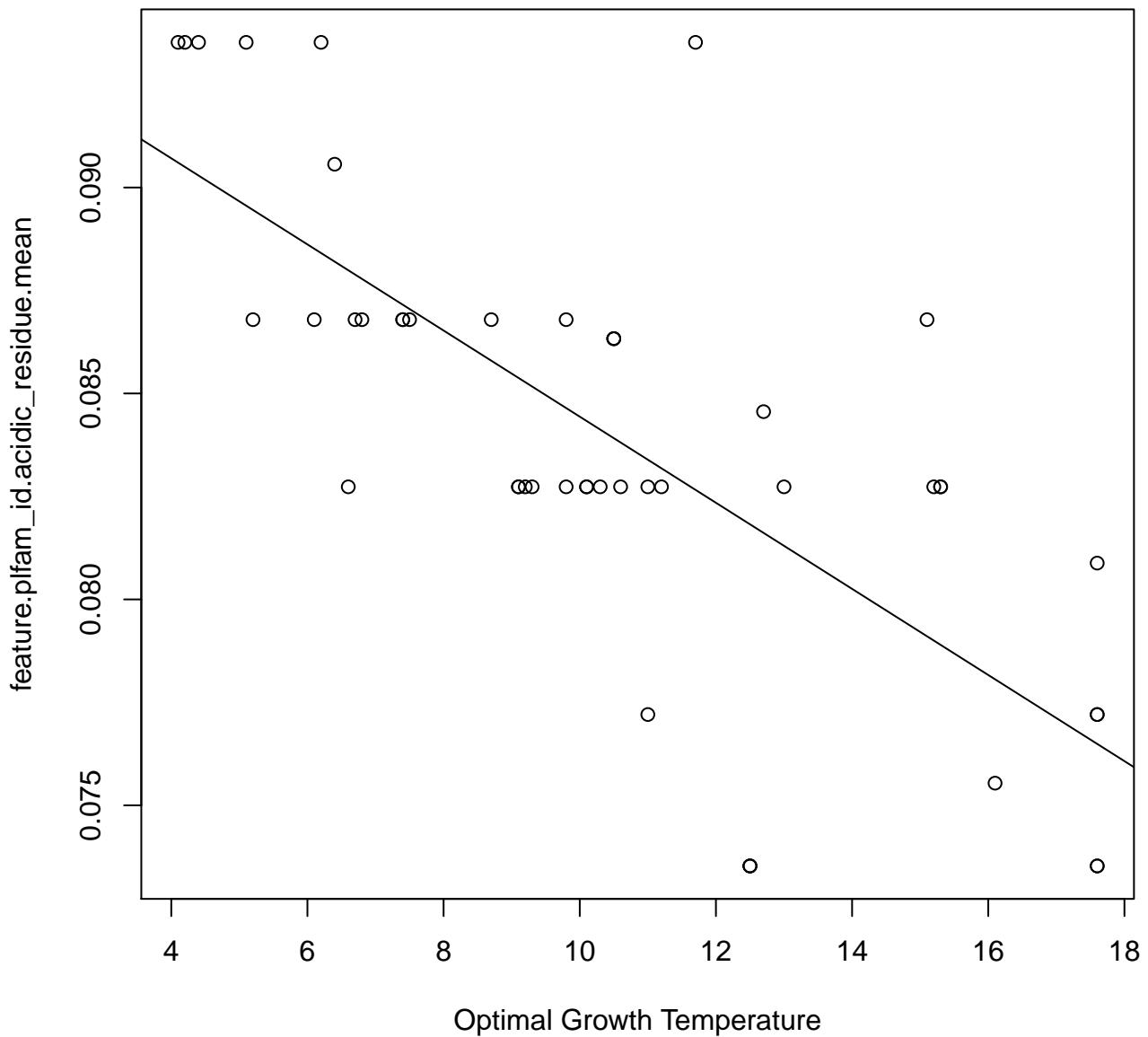
feature.plfam_id.acidic_residue.mean
PLF_28228_00014238
hypothetical protein



feature.plfam_id.acidic_residue.mean
PLF_28228_00028646
hypothetical protein



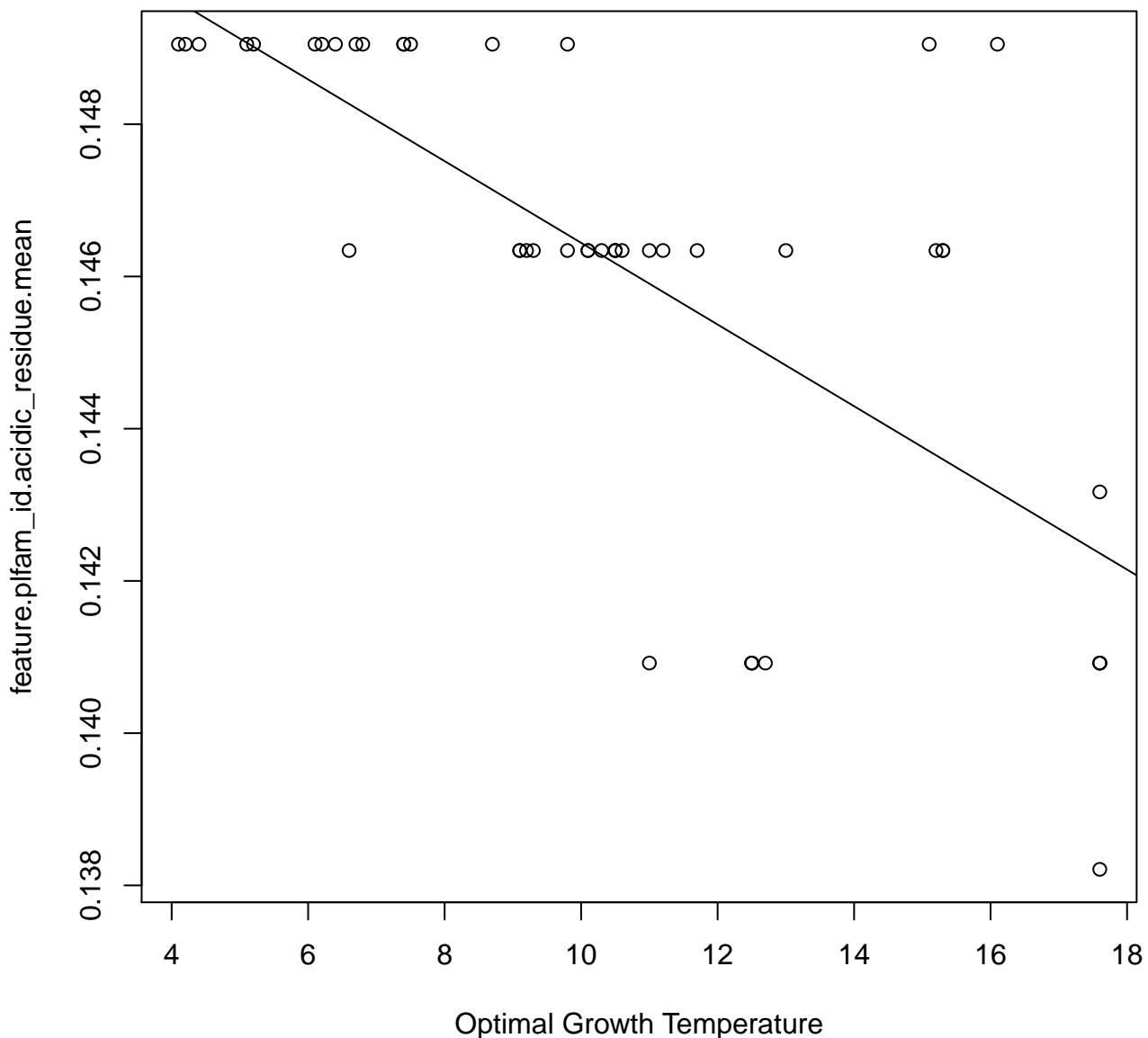
feature.plfam_id.acidic_residue.mean
PLF_28228_00002017
Caulimovirus viroplasmin / Ribonuclease HI (EC 3.1.26.4)



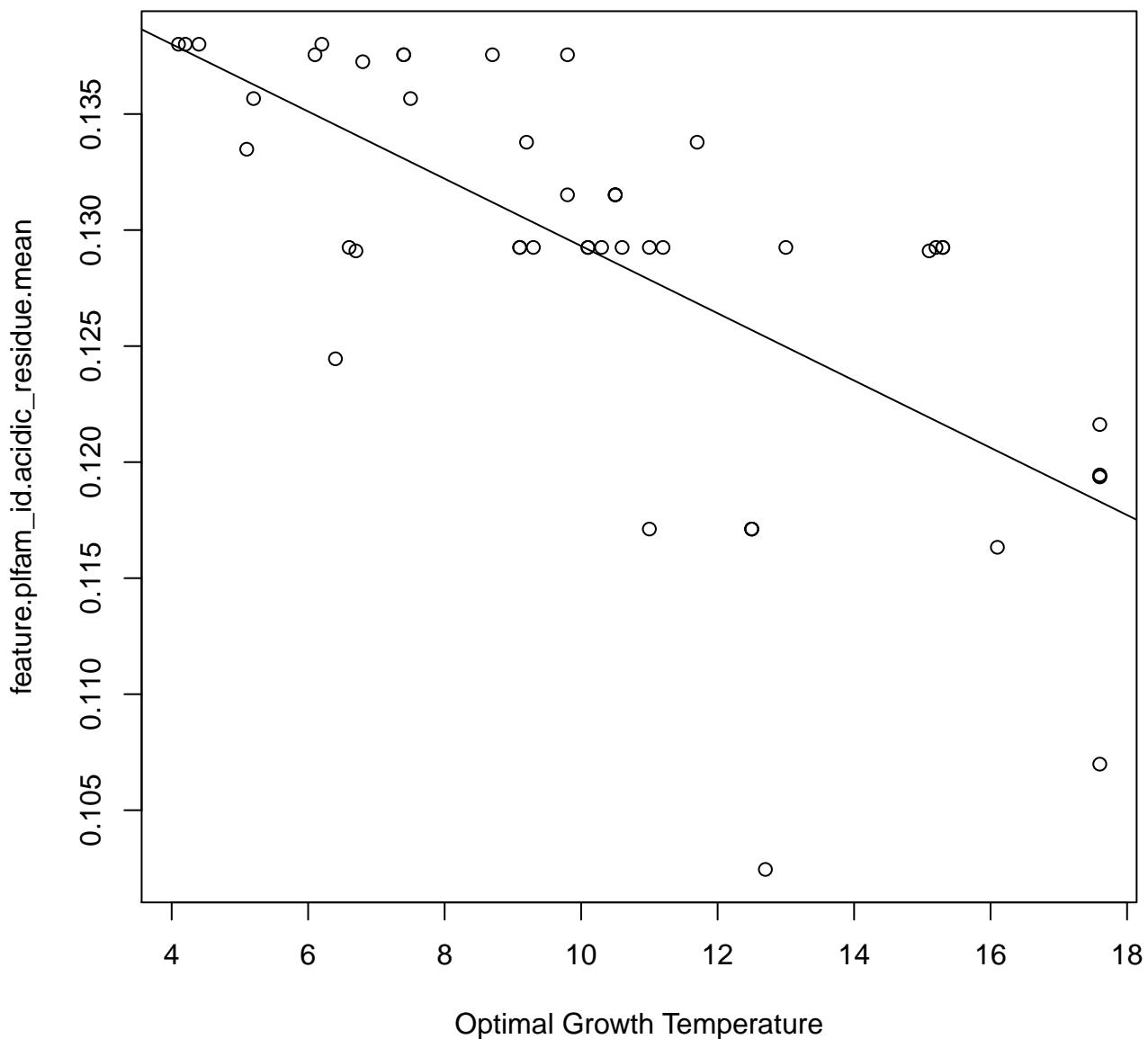
feature.plfam_id.acidic_residue.mean

PLF_28228_00000264

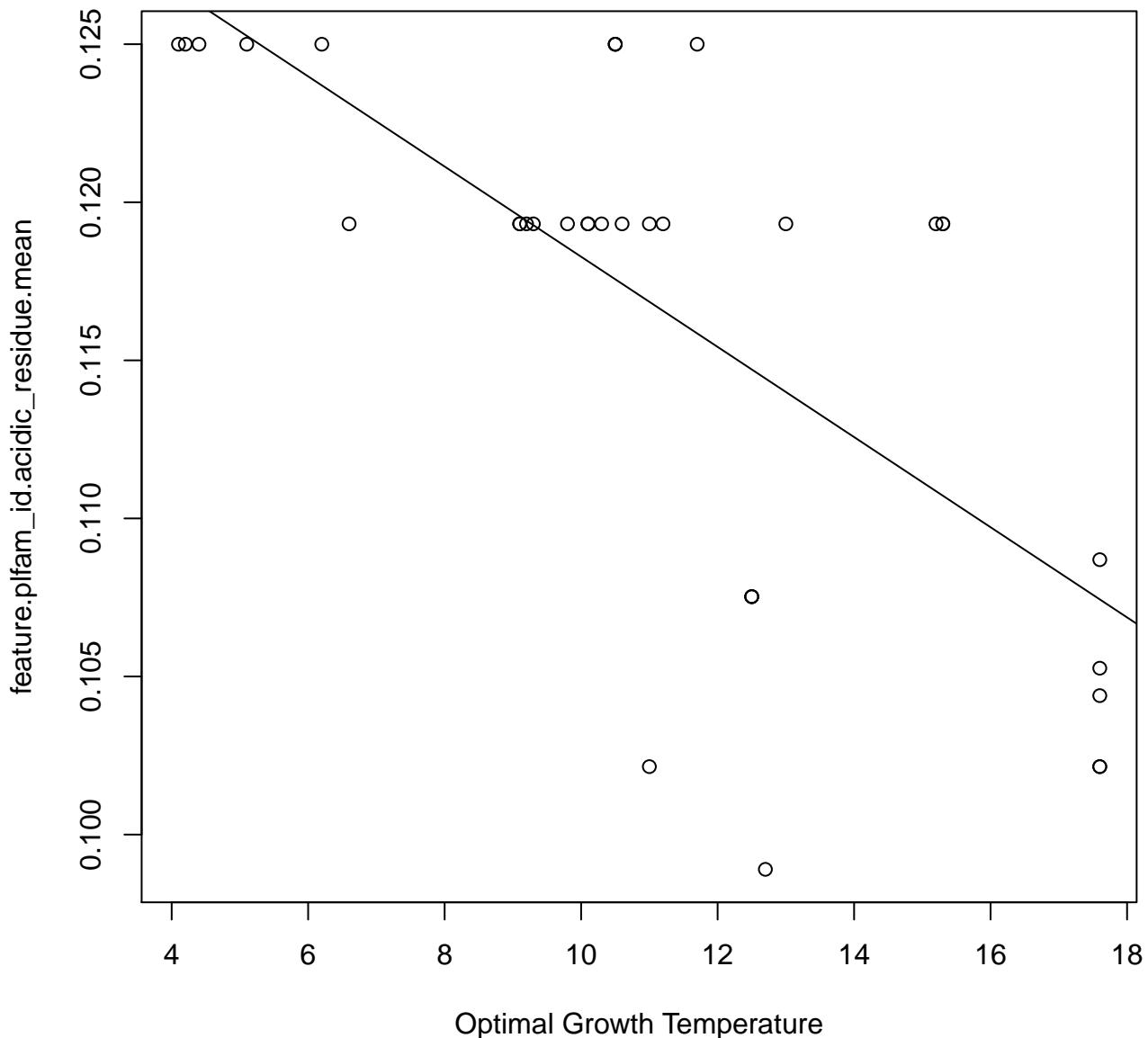
3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25)



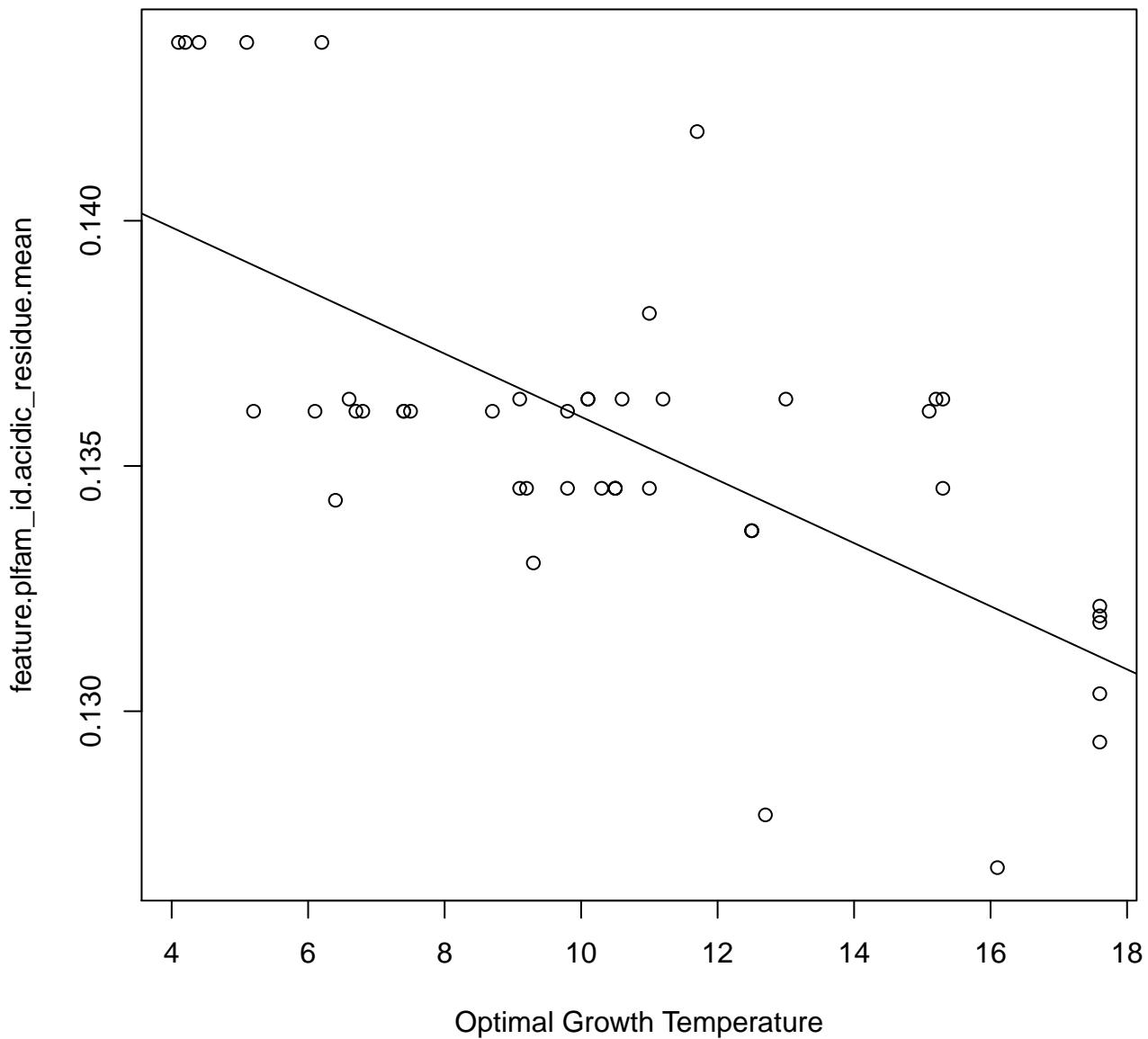
feature.plfam_id.acidic_residue.mean
PLF_28228_00002282
hypothetical protein



feature.plfam_id.acidic_residue.mean
PLF_28228_00001445
Alkyl hydroperoxide reductase subunit C-like protein



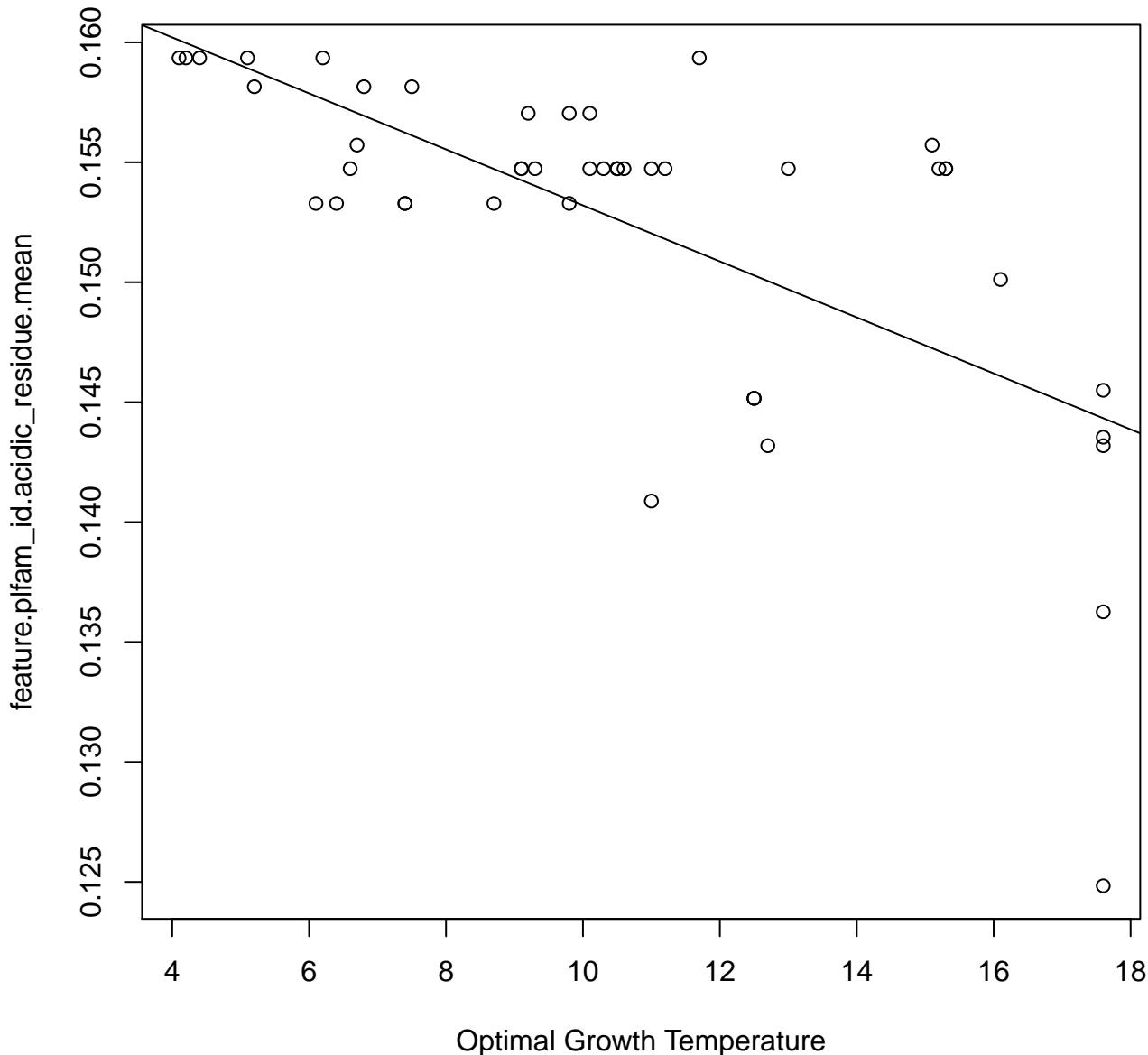
feature.plfam_id.acidic_residue.mean
PLF_28228_00000671
Nudix hydrolase 3 (EC 3.6.1.-)



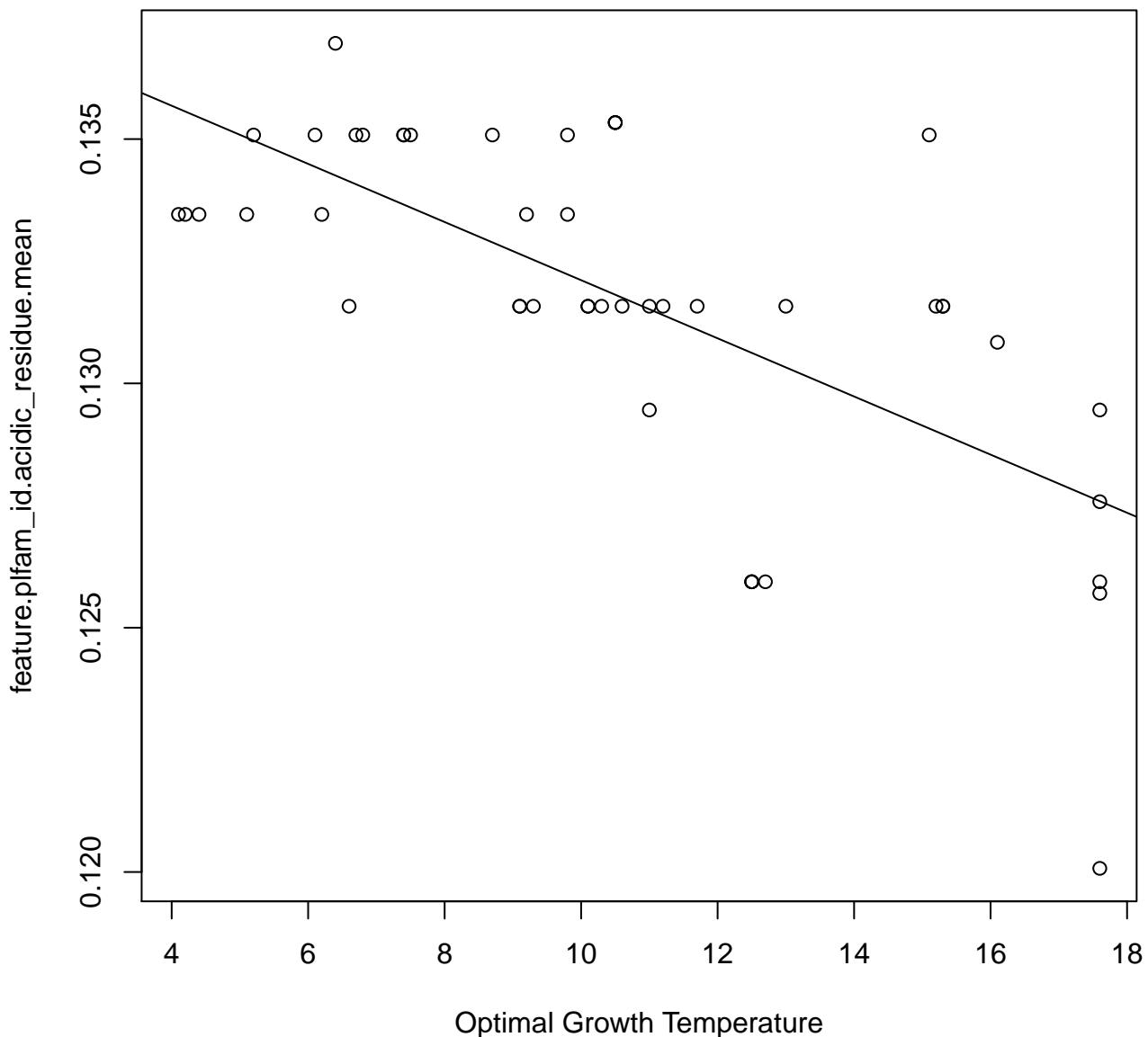
feature.plfam_id.acidic_residue.mean

PLF_28228_00001178

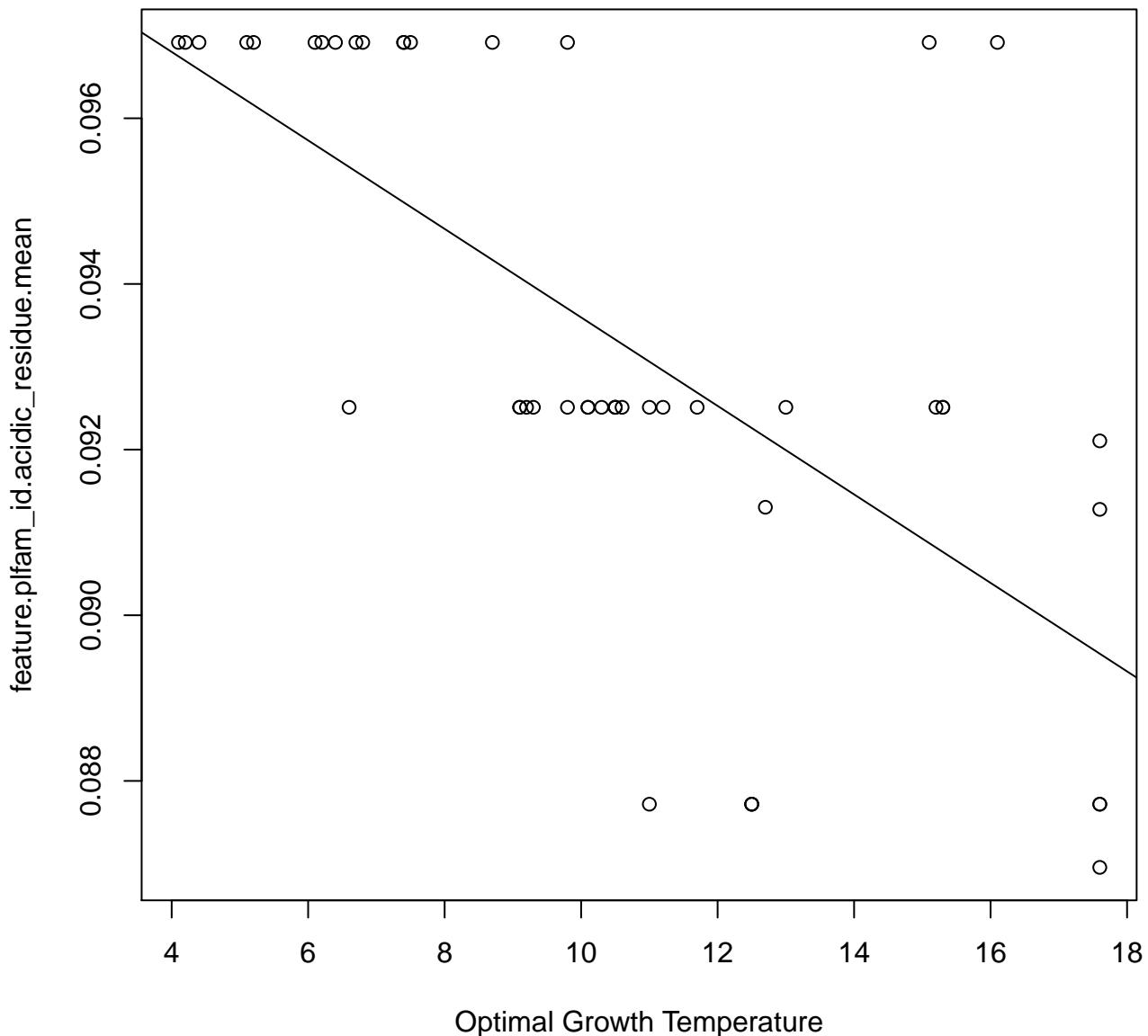
Periplasmic chaperone and peptidyl-prolyl cis-trans isomerase of outer membrane proteins SurA (EC 5.2.1.8)



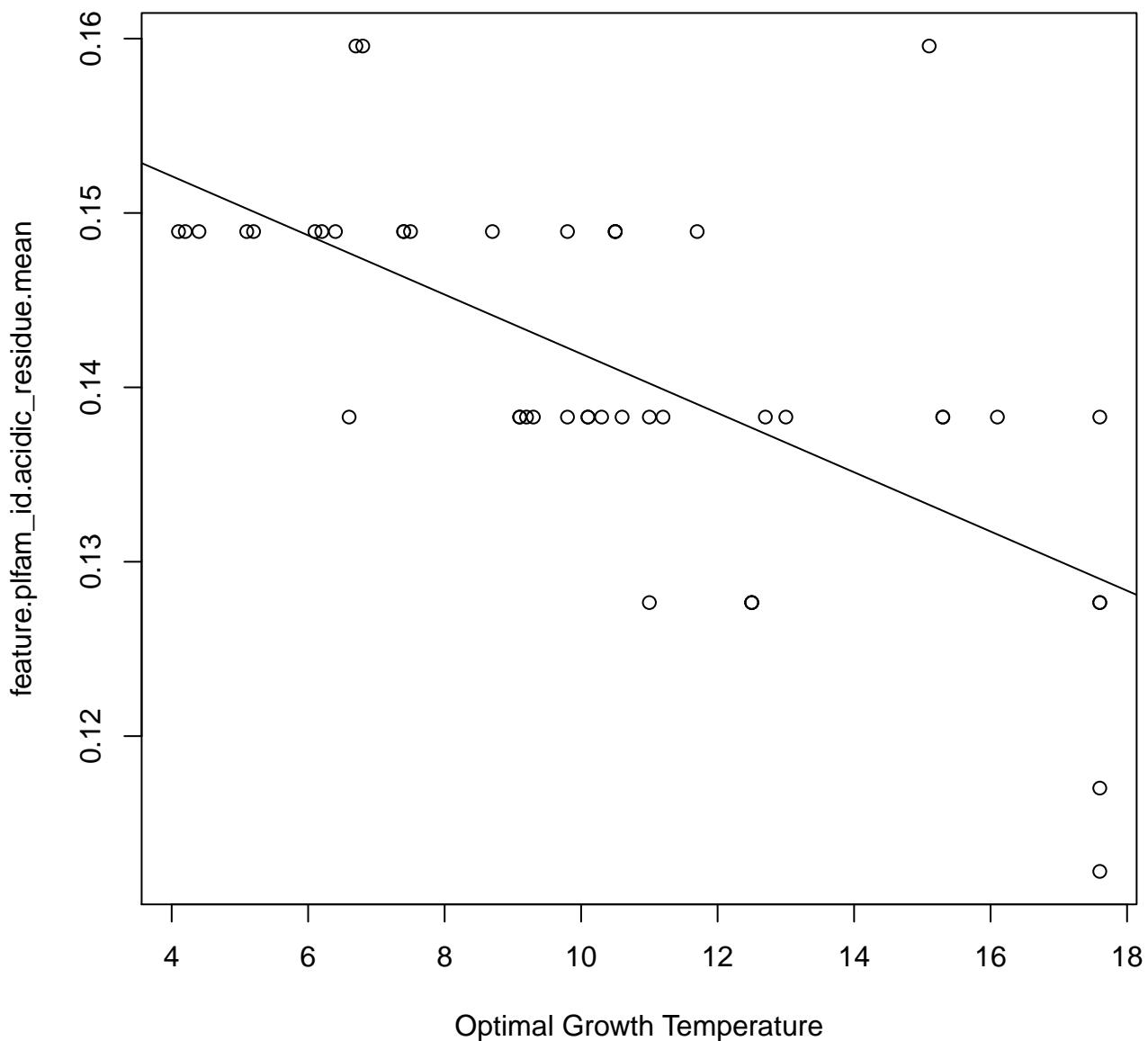
feature.plfam_id.acidic_residue.mean
PLF_28228_00000808
L-aspartate oxidase (EC 1.4.3.16)



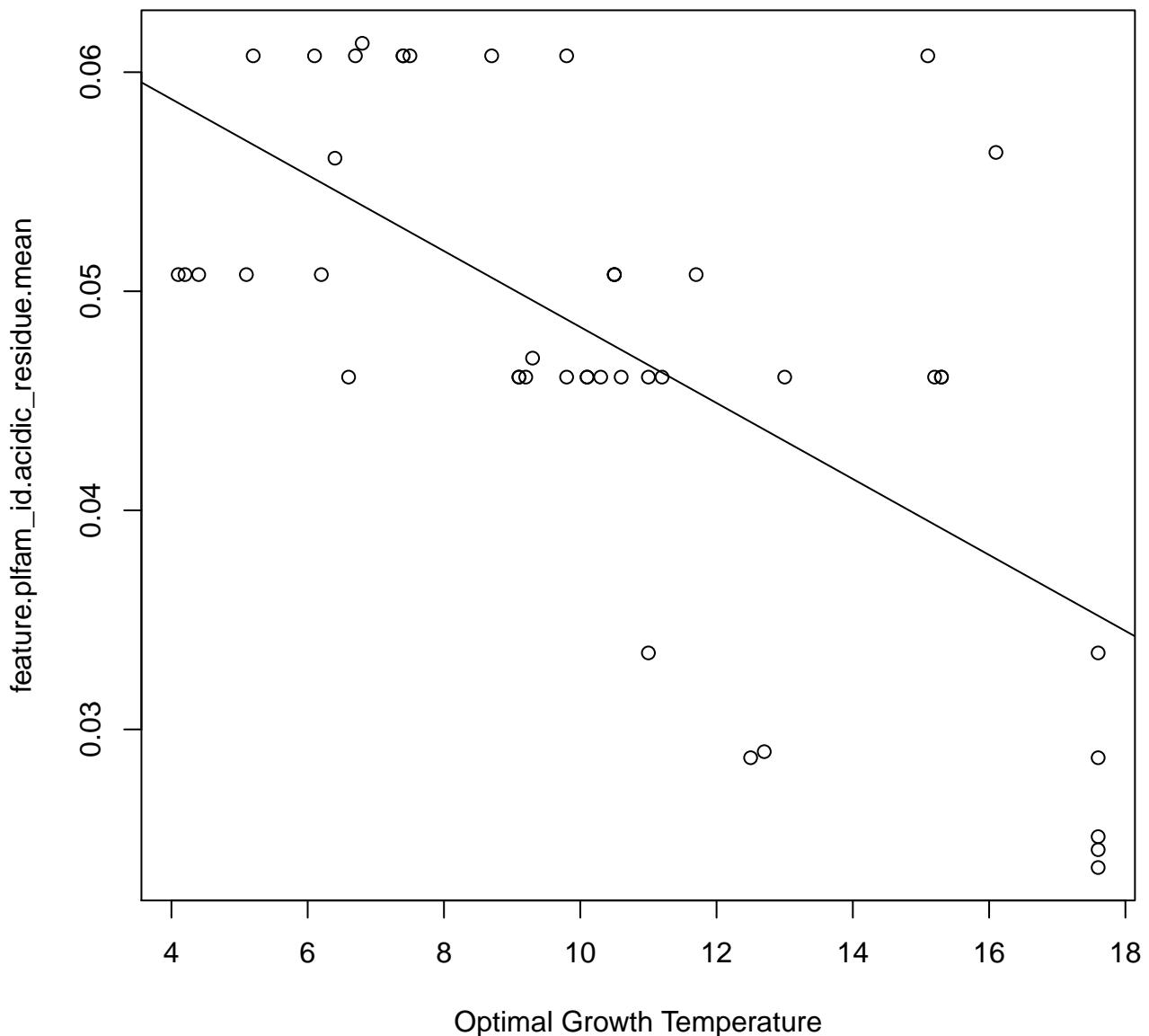
feature.plfam_id.acidic_residue.mean
PLF_28228_00001206
Tol-Pal system protein TolQ



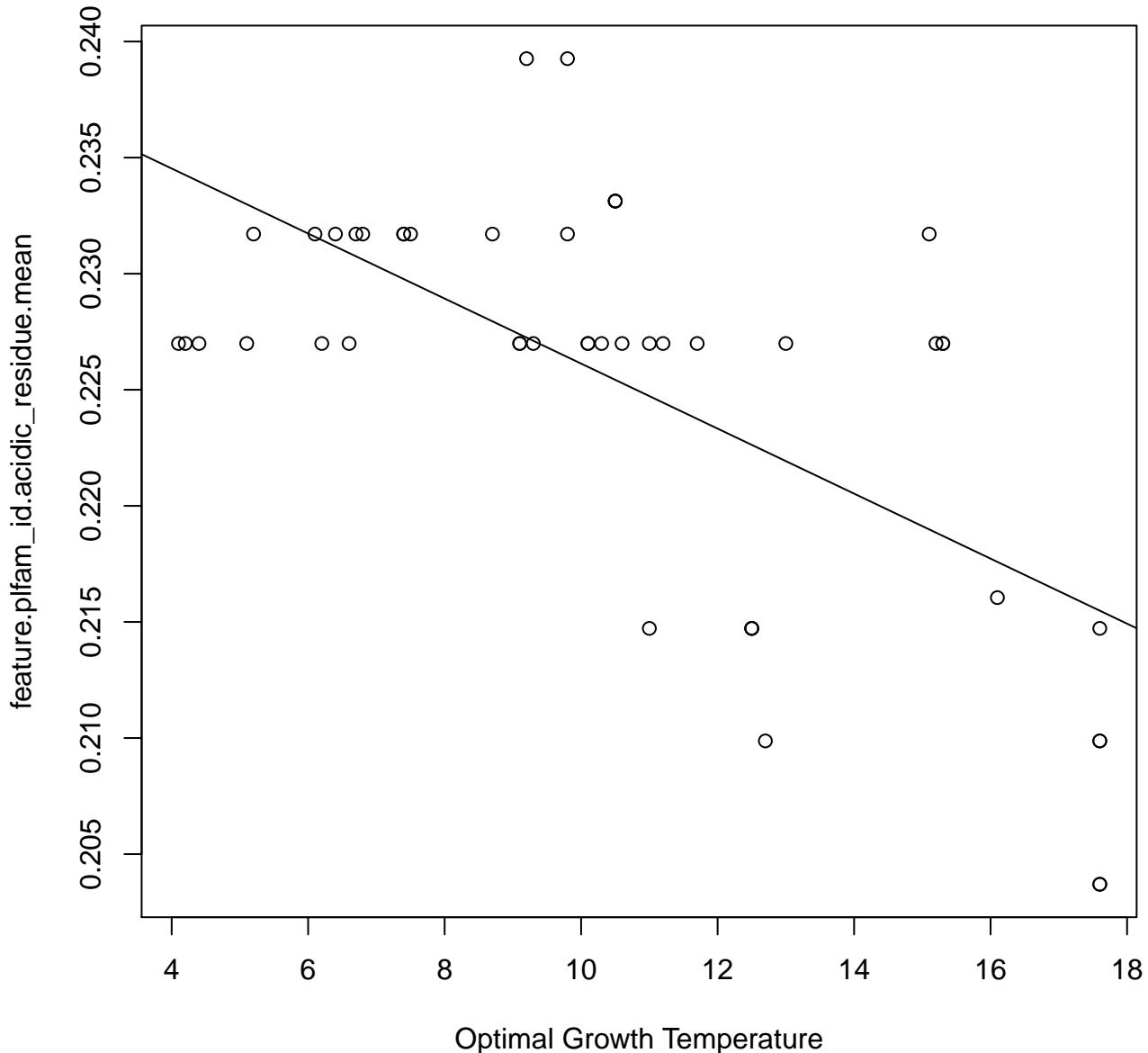
feature.plfam_id.acidic_residue.mean
PLF_28228_00002310
hypothetical protein



feature.plfam_id.acidic_residue.mean
PLF_28228_00002087
Protein-methionine-sulfoxide reductase heme-binding subunit MsrQ



feature.plfam_id.acidic_residue.mean
PLF_28228_00000467
FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)

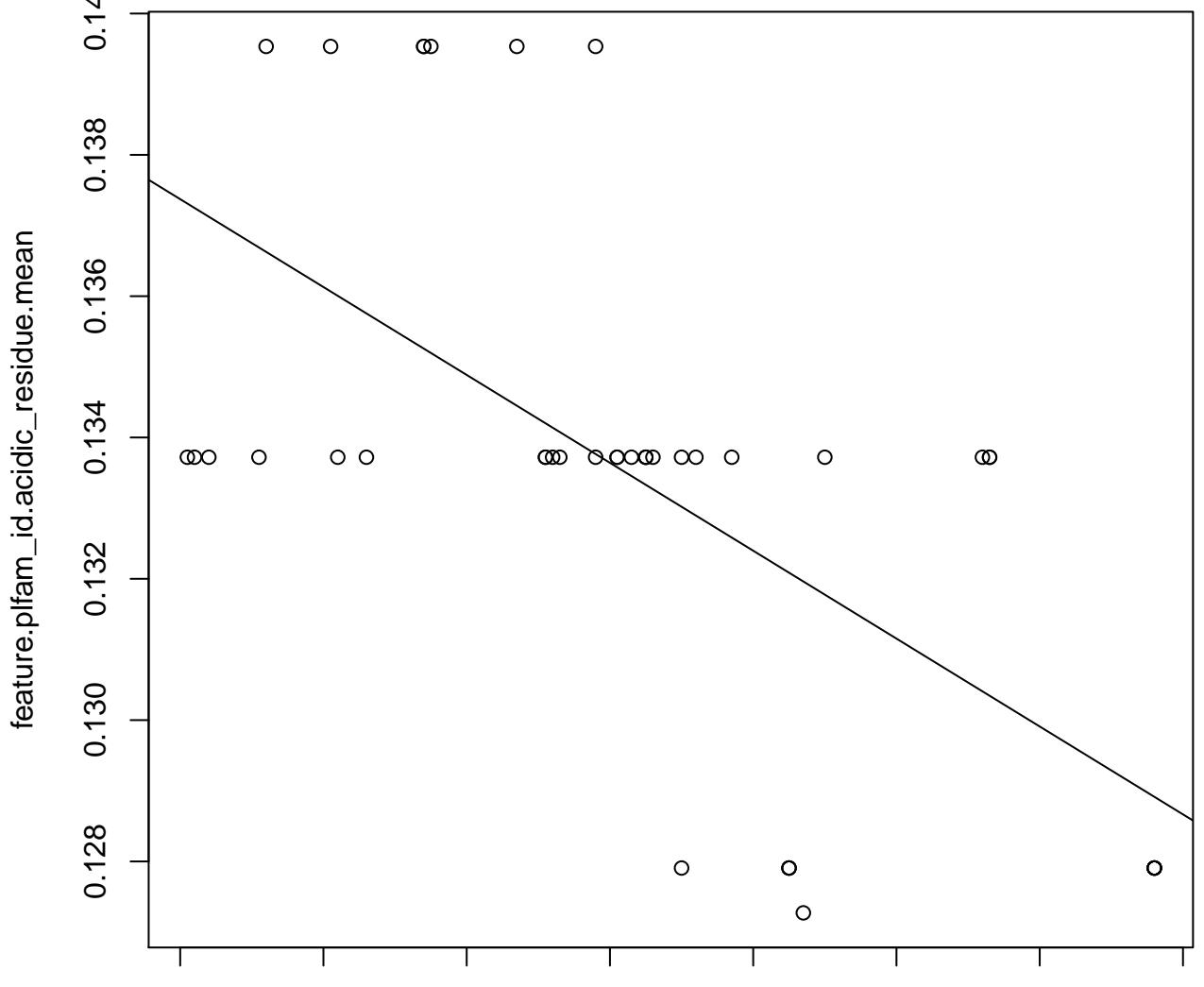


feature.plfam_id.acidic_residue.mean
PLF_28228_00001795

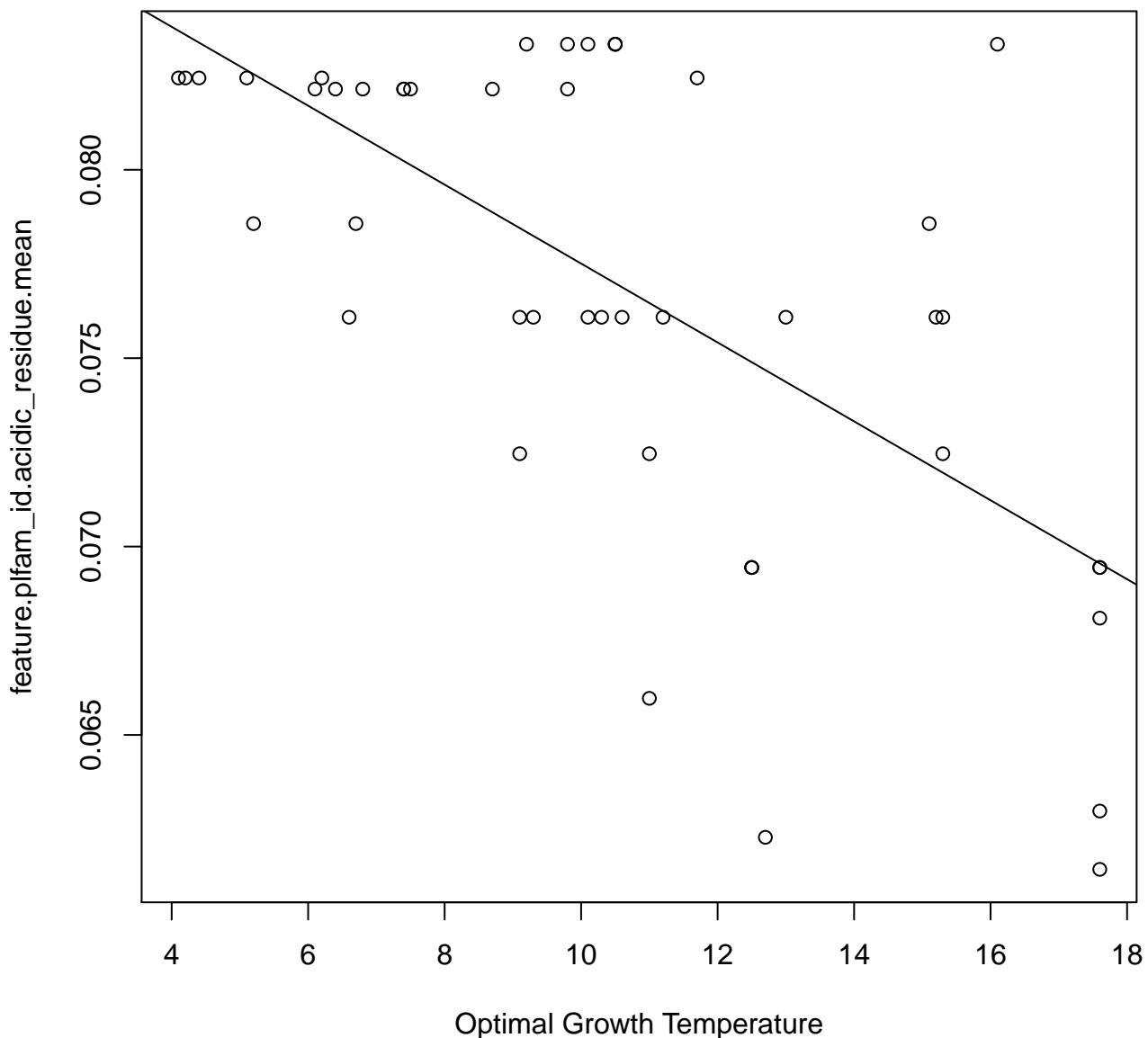
Periplasmic chaperone of outer membrane proteins Skp @ Outer membrane protein H precursor

feature.plfam_id.acidic_residue.mean

Optimal Growth Temperature



feature.plfam_id.acidic_residue.mean
PLF_28228_00000917
Peptidase, M23/M37 family

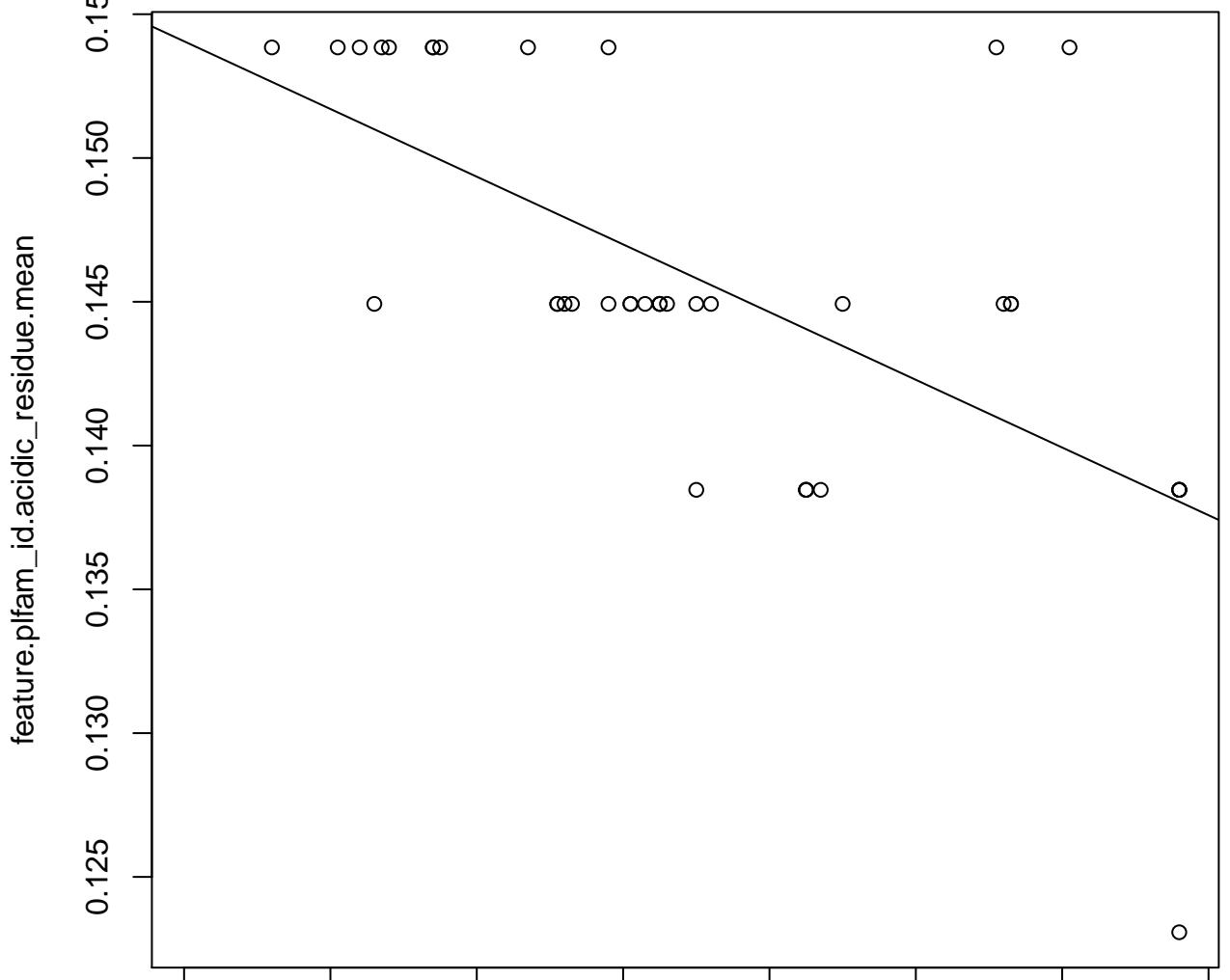


feature.plfam_id.acidic_residue.mean
PLF_28228_00000754
Carbon storage regulator

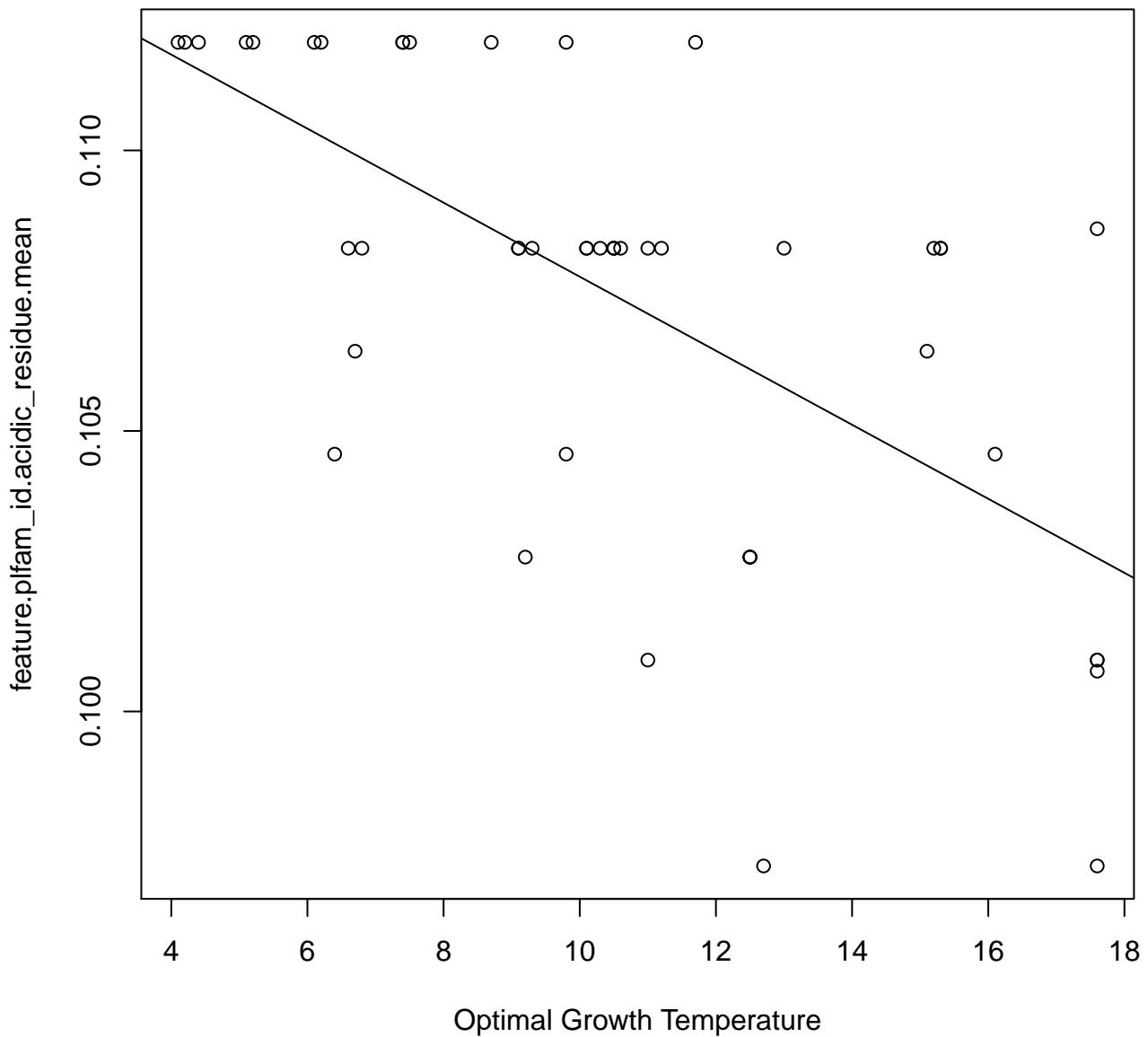
feature.plfam_id.acidic_residue.mean

4 6 8 10 12 14 16 18

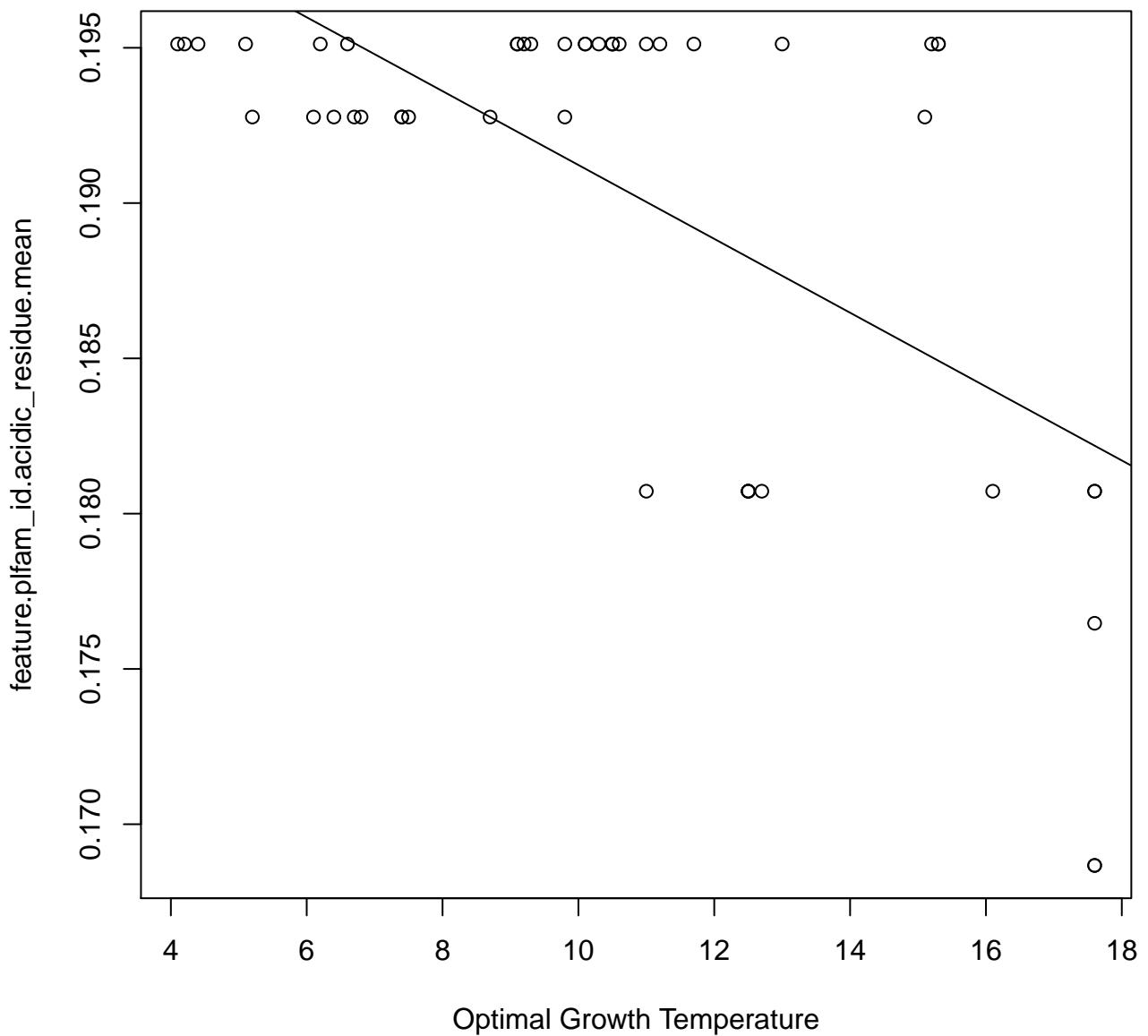
Optimal Growth Temperature



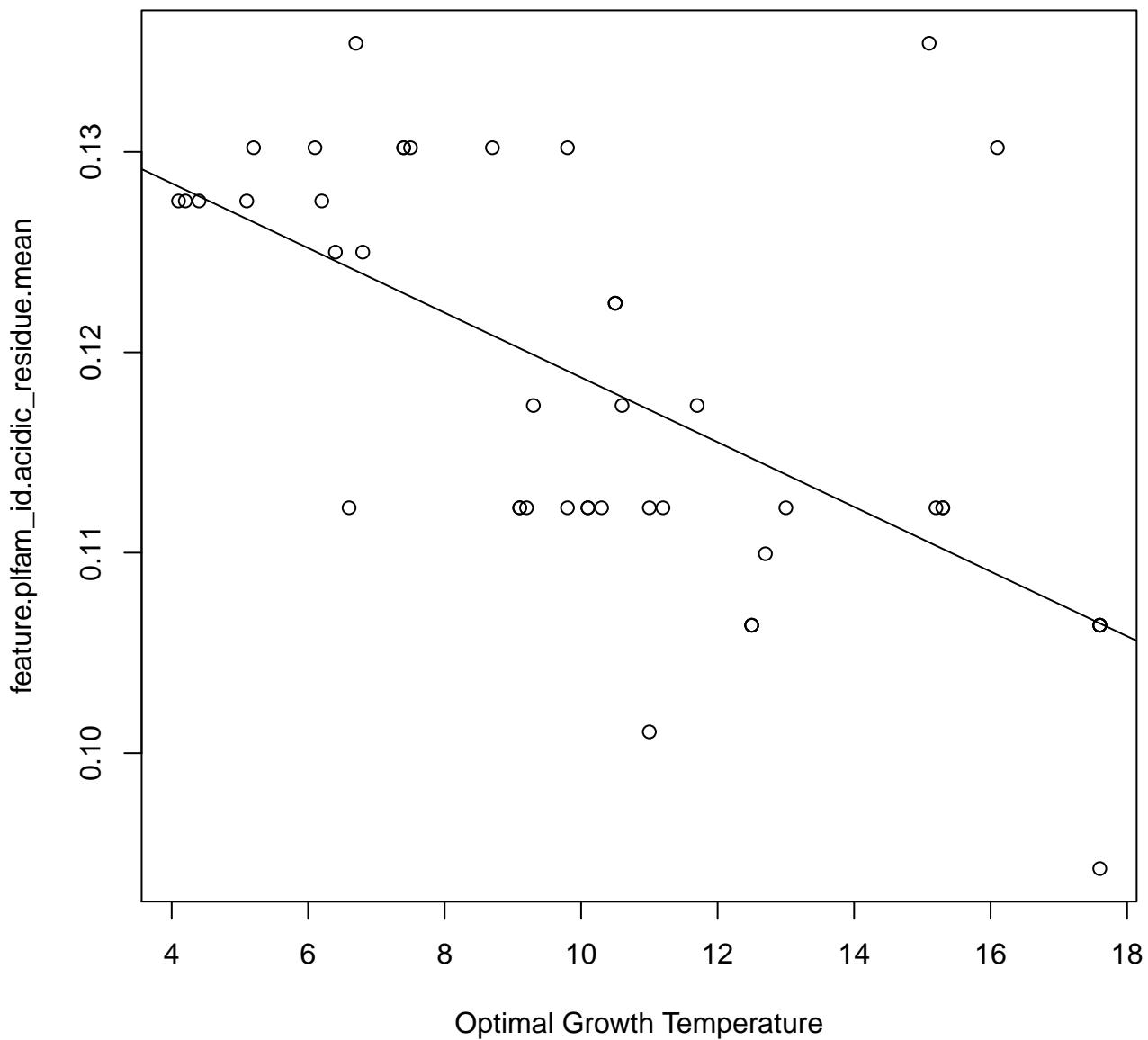
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PLF_28228_00000948
Phosphate ABC transporter, permease protein PstA (TC 3.A.1.7.1)



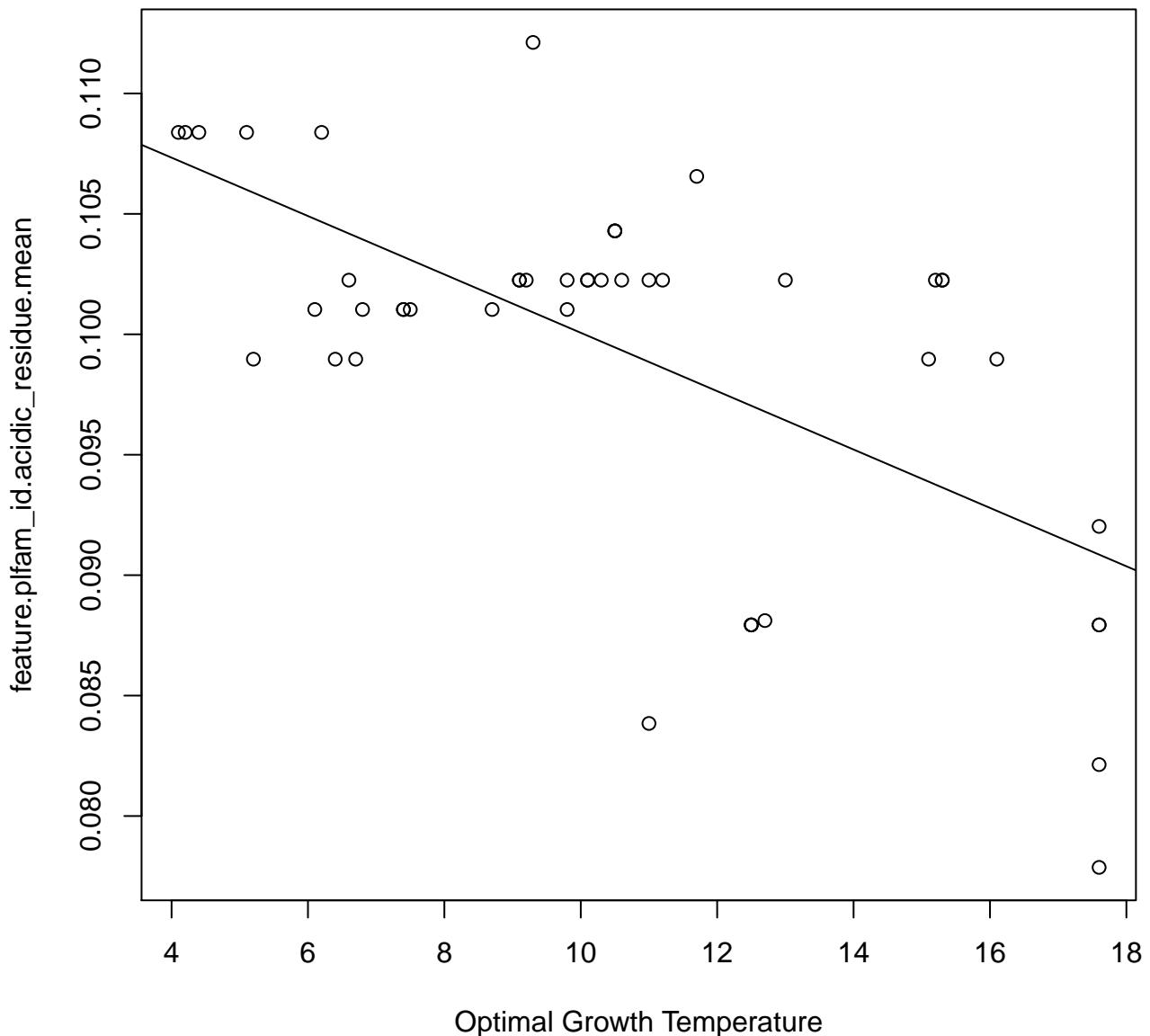
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PLF_28228_00001376
Uncharacterized protein YqIC



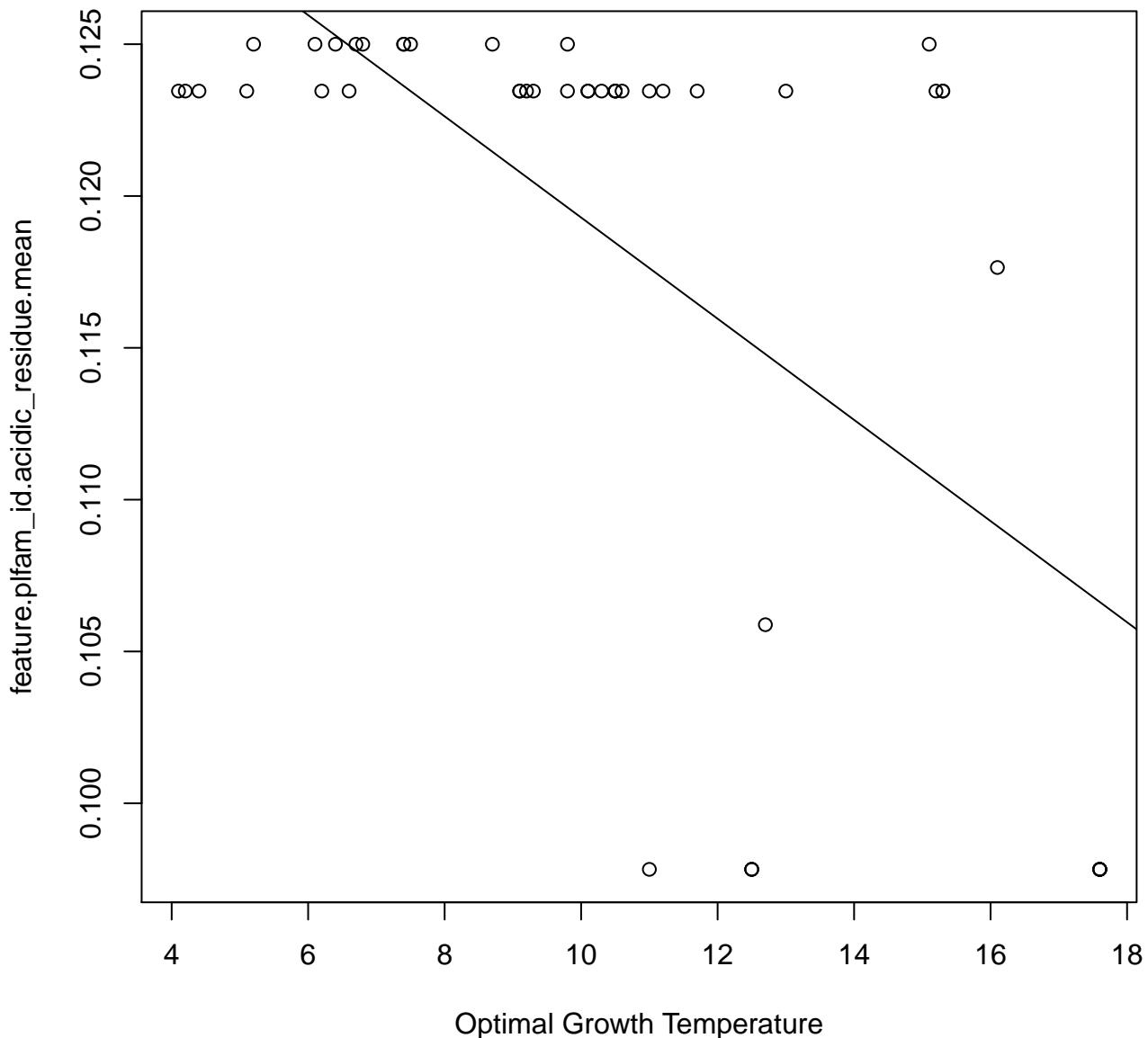
feature.plfam_id.acidic_residue.mean
PLF_28228_00001259
Type IV pilus biogenesis protein PilN



feature.plfam_id.acidic_residue.mean
PLF_28228_00000790
Exported zinc metalloprotease YfgC precursor



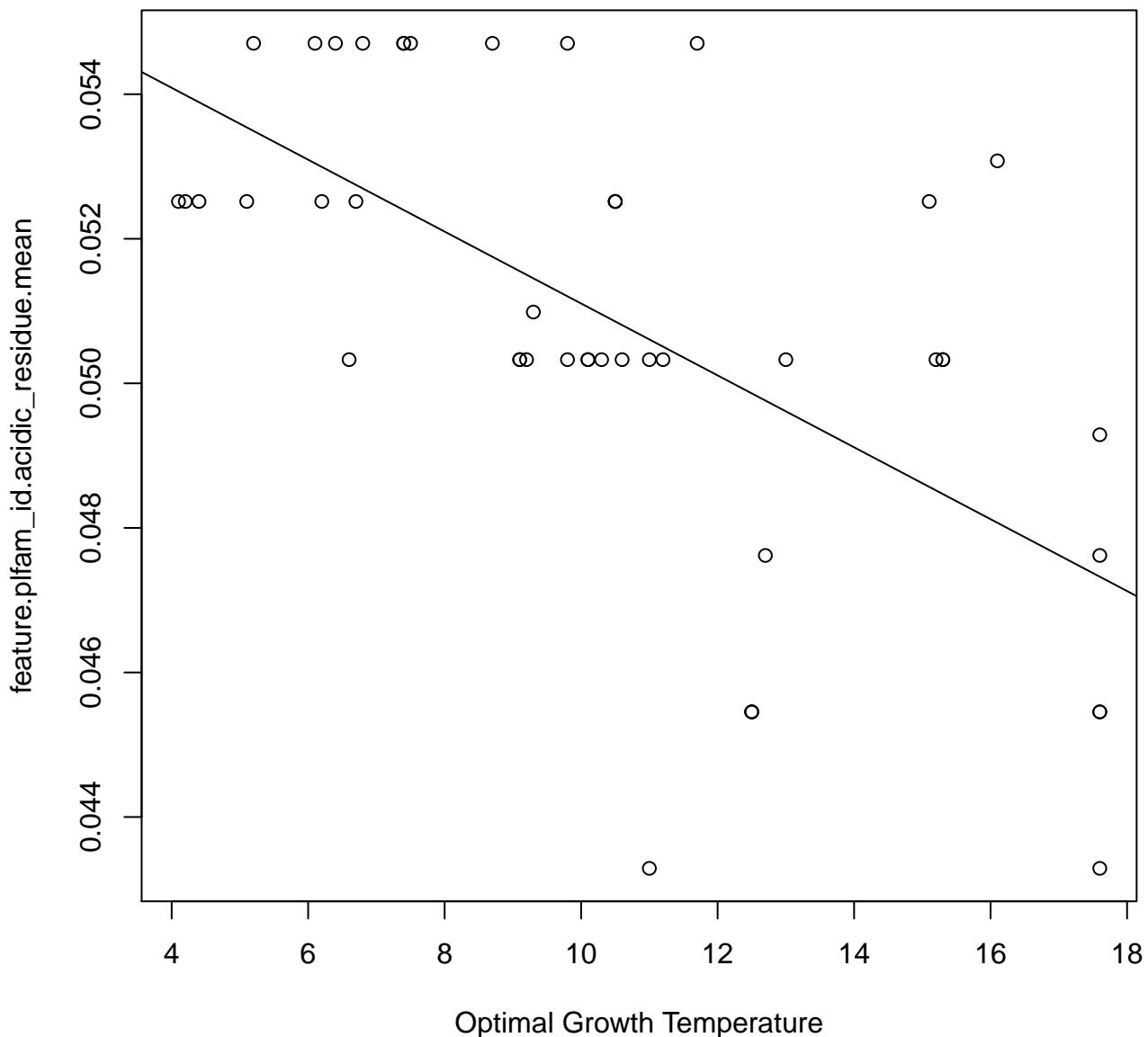
feature.plfam_id.acidic_residue.mean
PLF_28228_00001558
Acetolactate synthase small subunit (EC 2.2.1.6)



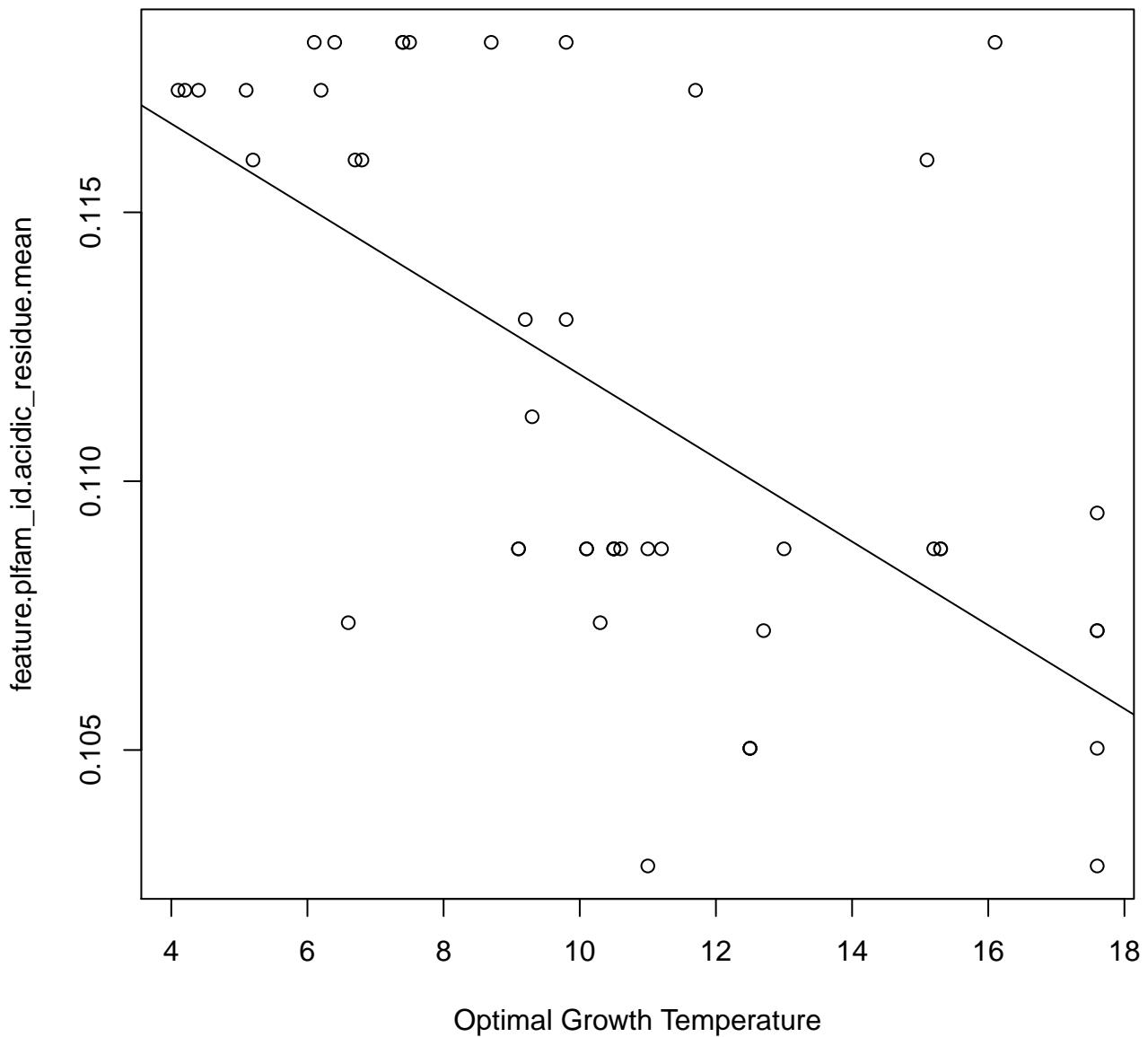
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PLF_28228_00001751

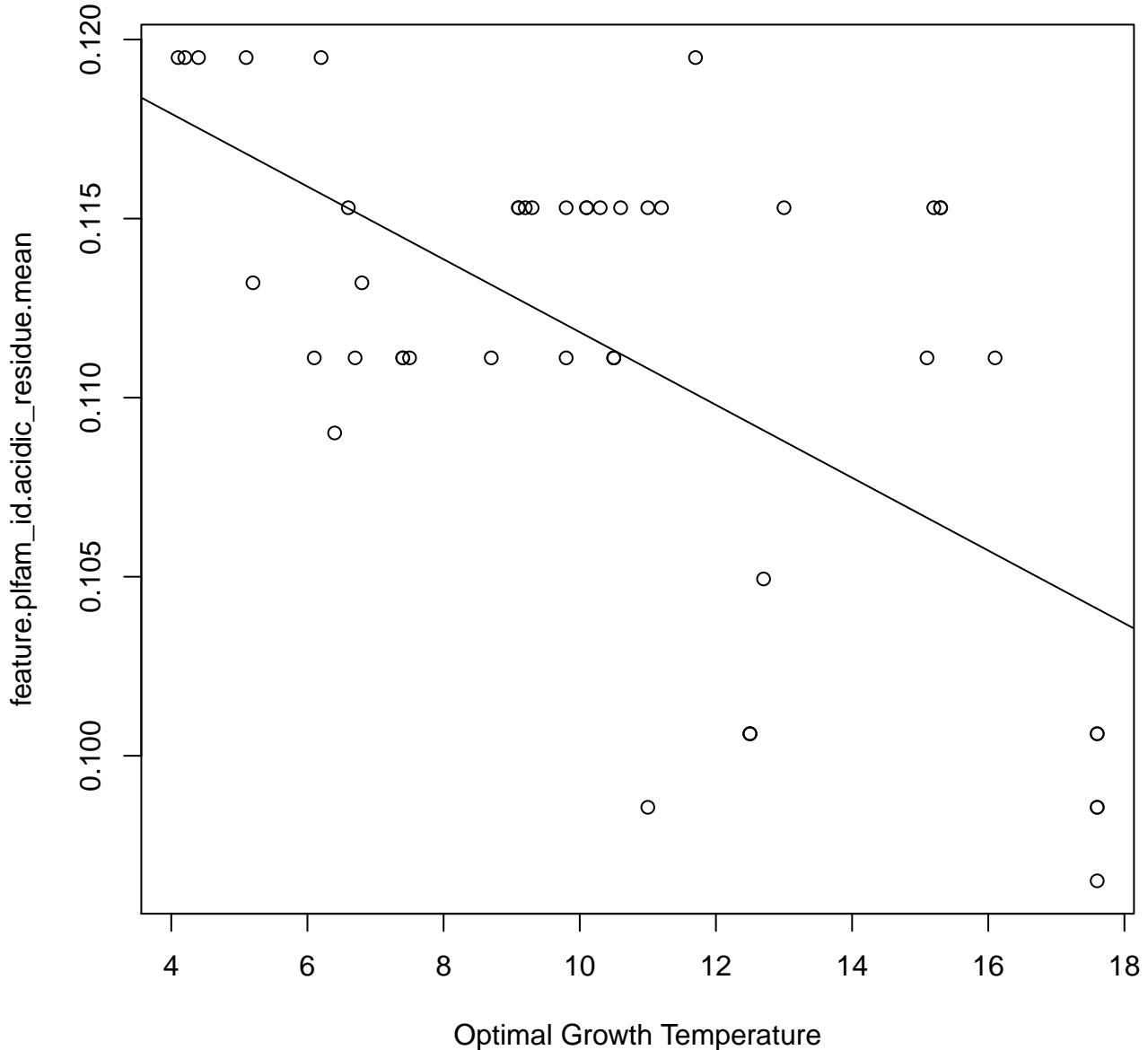
Multi antimicrobial extrusion protein (Na⁽⁺⁾/drug antiporter), MATE family of MDR efflux pumps



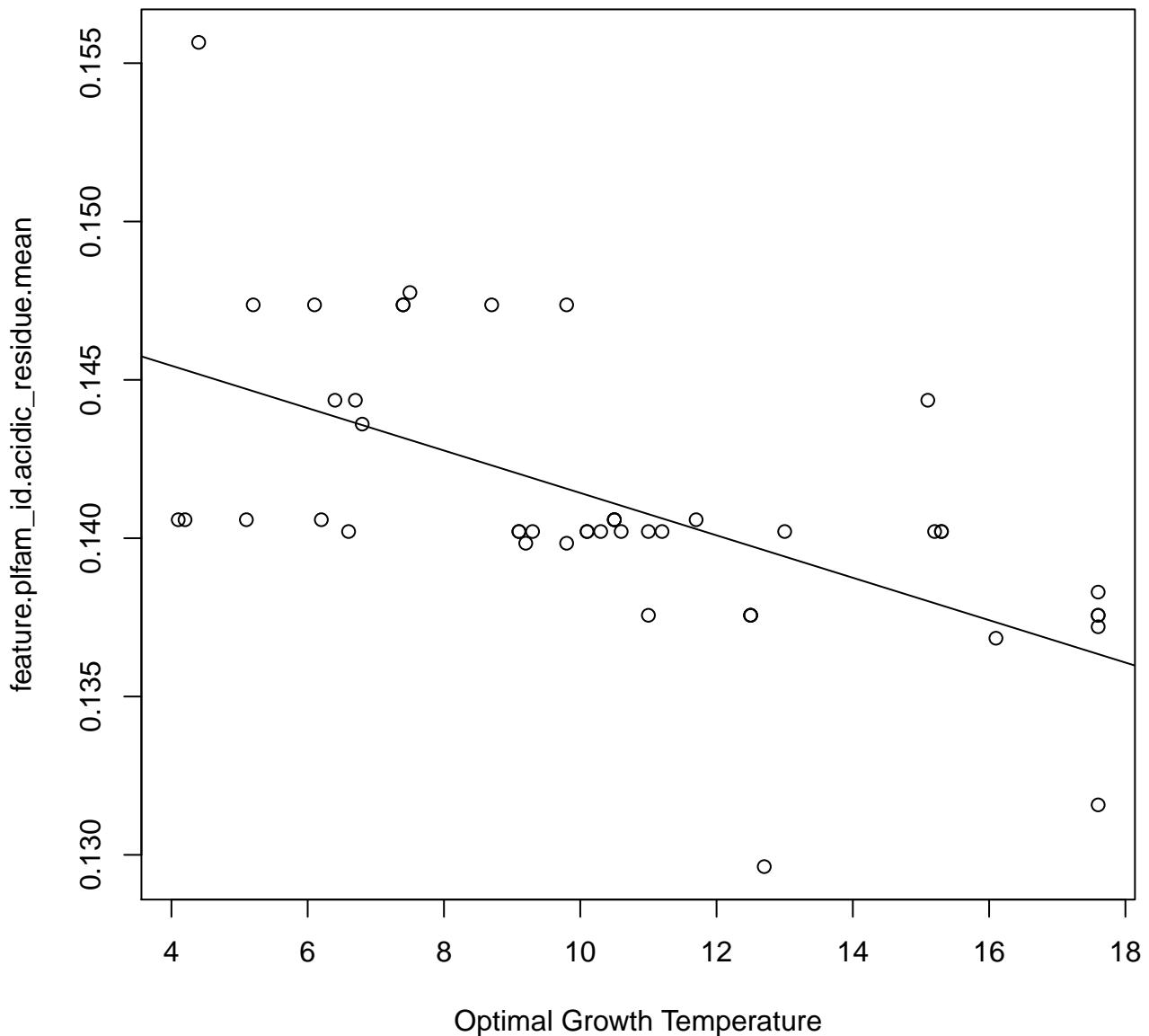
feature.plfam_id.acidic_residue.mean
PLF_28228_00001230
Transcriptional response regulatory protein GlrR



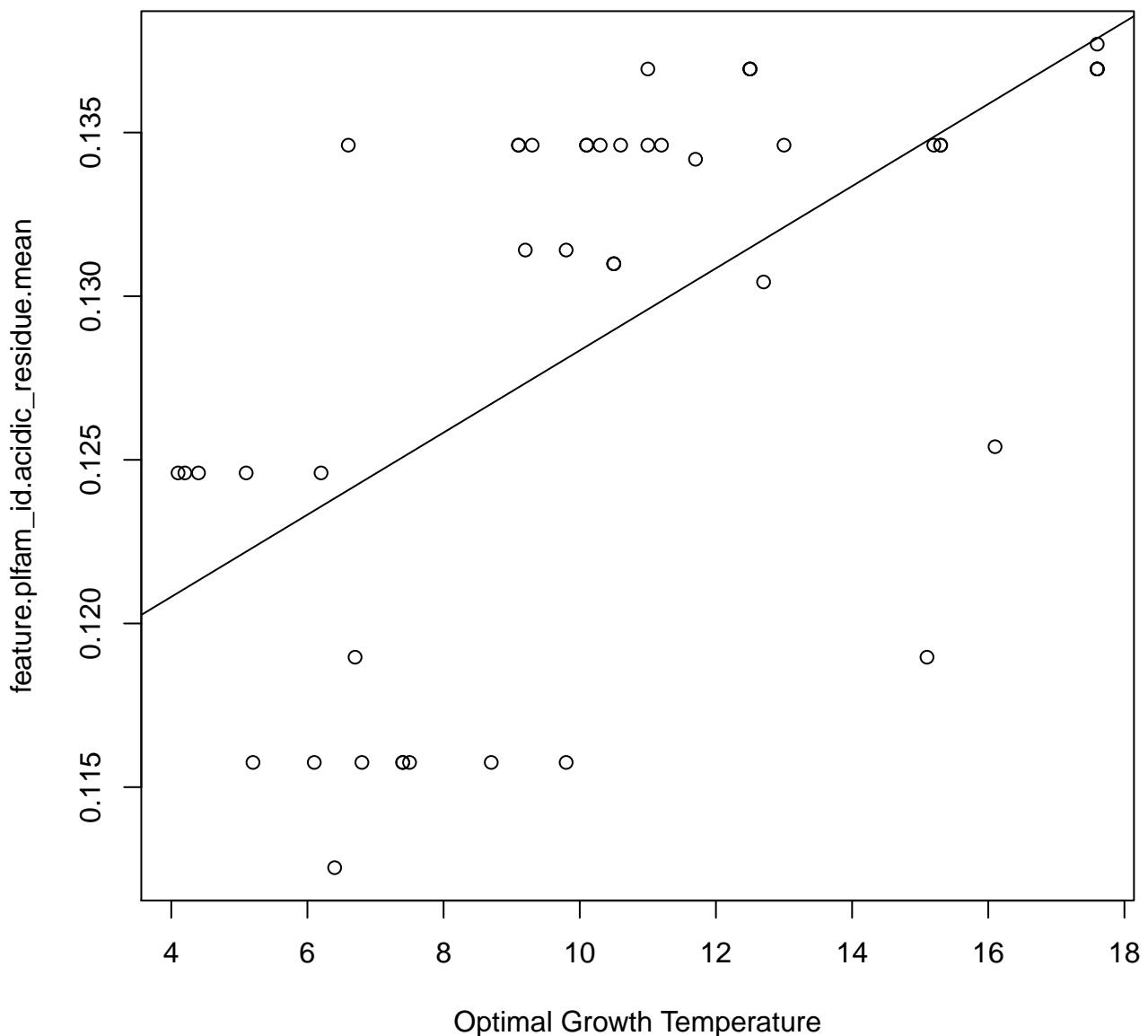
feature.plfam_id.acidic_residue.mean
PLF_28228_00001262
Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation



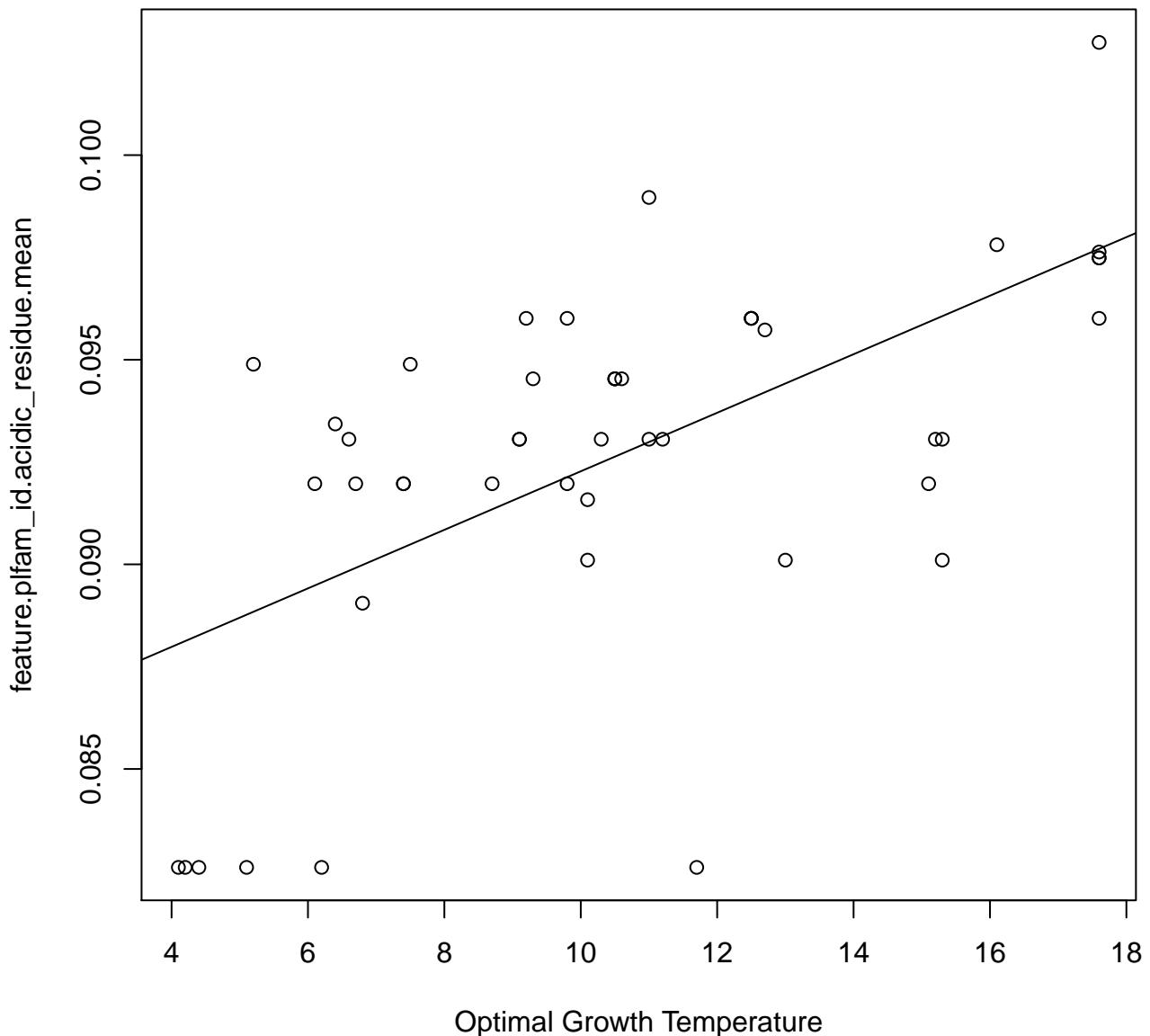
feature.plfam_id.acidic_residue.mean
PLF_28228_00000758
Chaperone protein Dnaj



feature.plfam_id.acidic_residue.mean
PLF_28228_00000841
Flagellar motor rotation protein MotB



feature.plfam_id.acidic_residue.mean
PLF_28228_00002047
Two-component system sensor histidine kinase

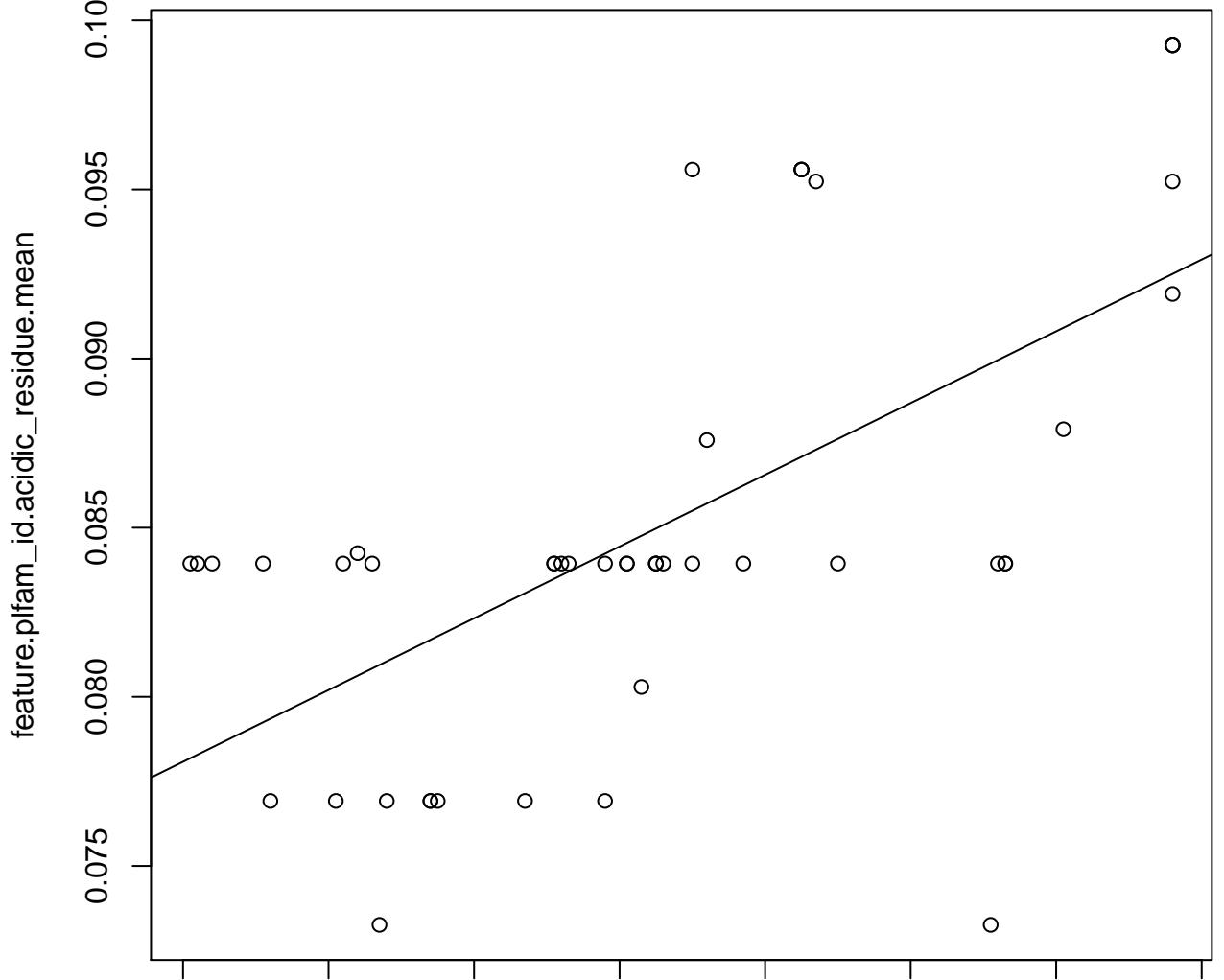


feature.plfam_id.acidic_residue.mean
PLF_28228_00001351
hypothetical protein

feature.plfam_id.acidic_residue.mean

4 6 8 10 12 14 16 18

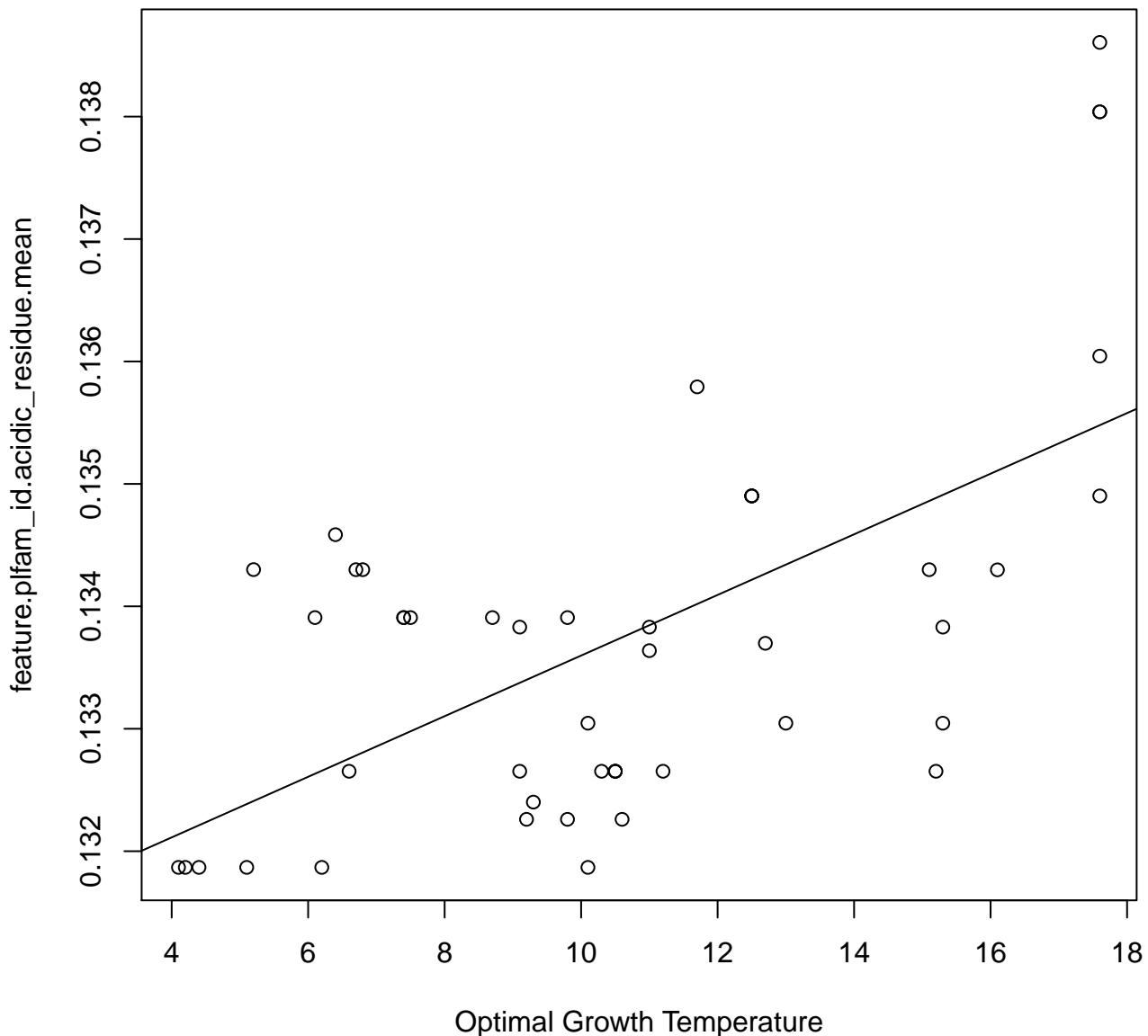
Optimal Growth Temperature



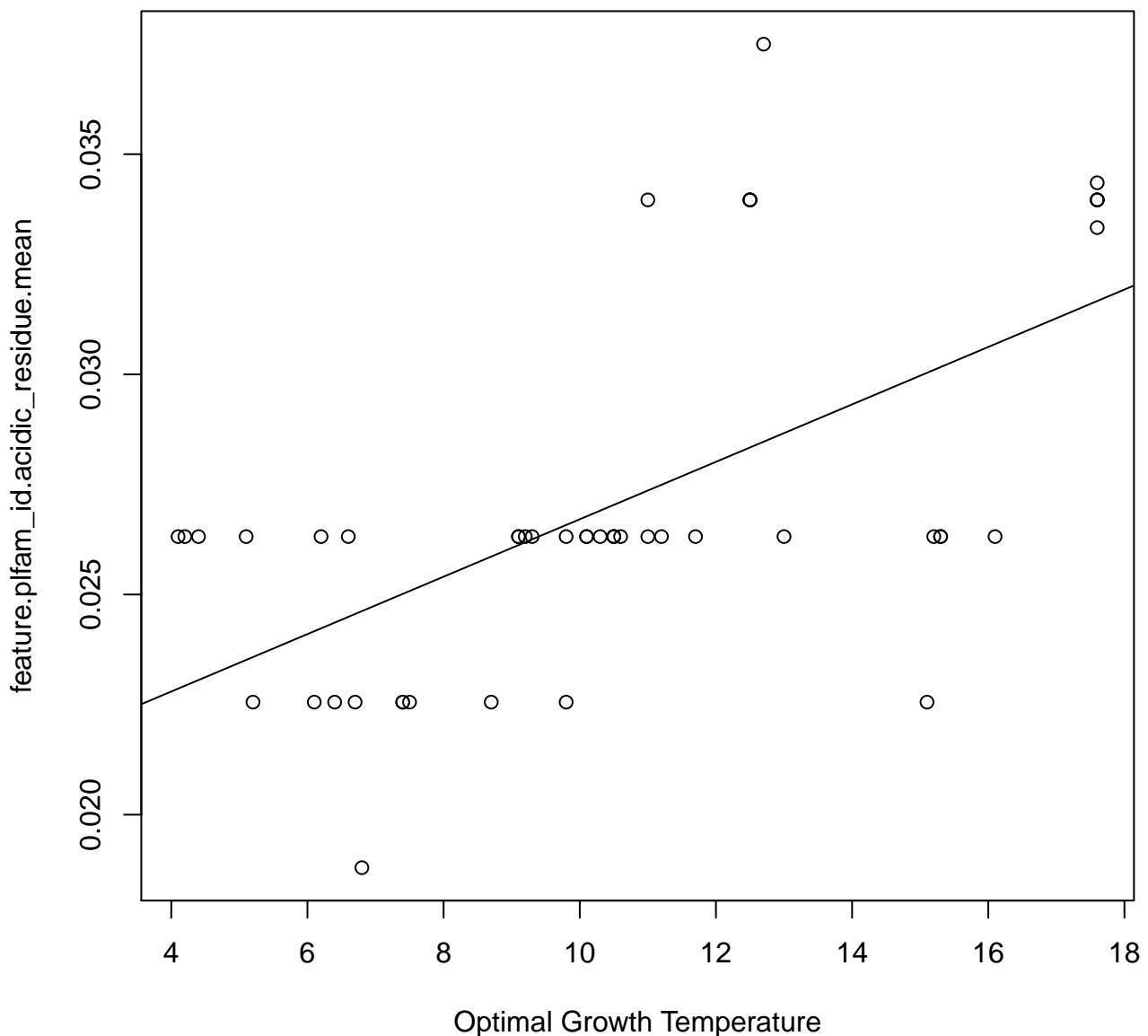
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PLF_28228_00000994

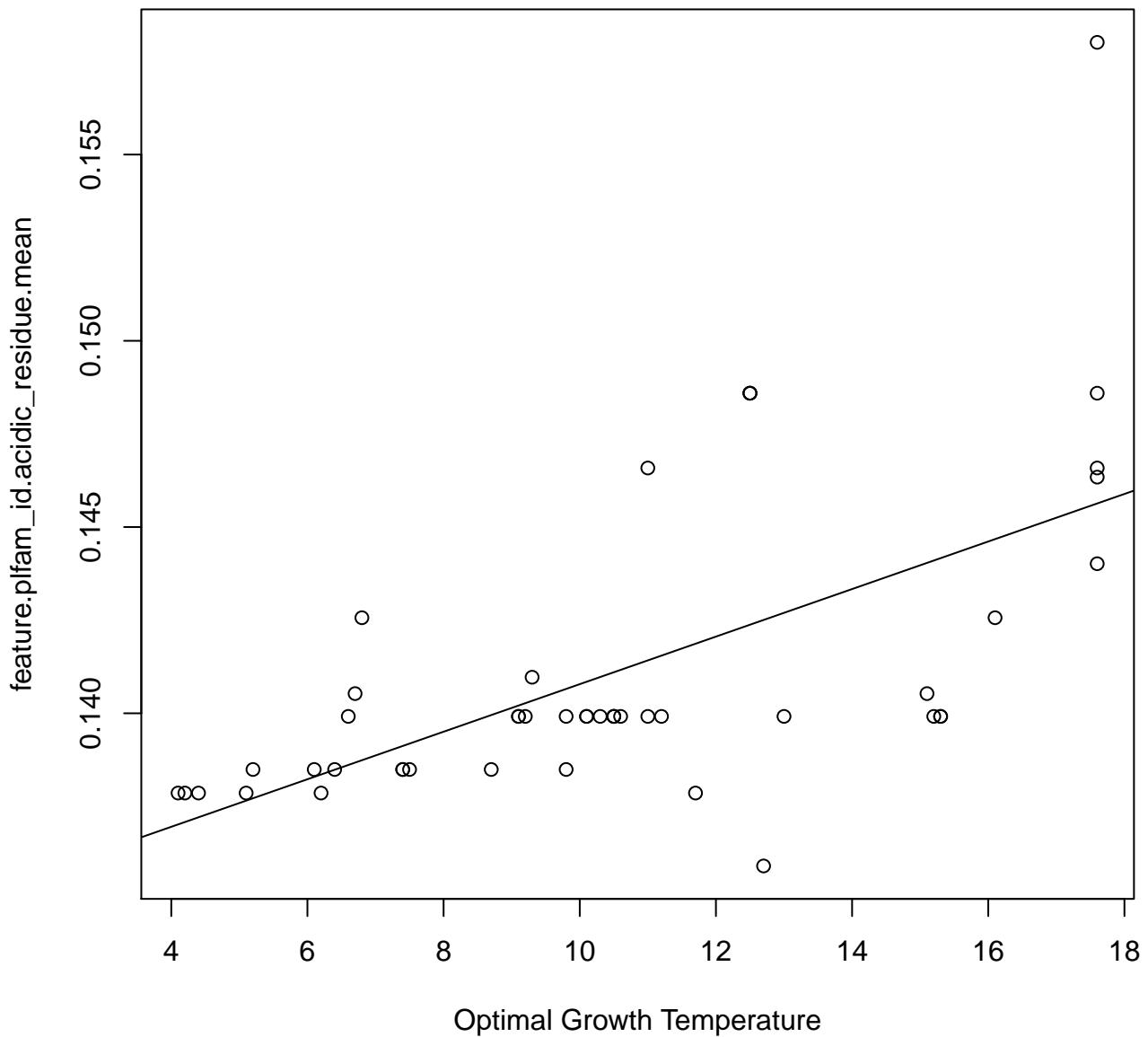
Proline dehydrogenase (EC 1.5.5.2) / Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88)



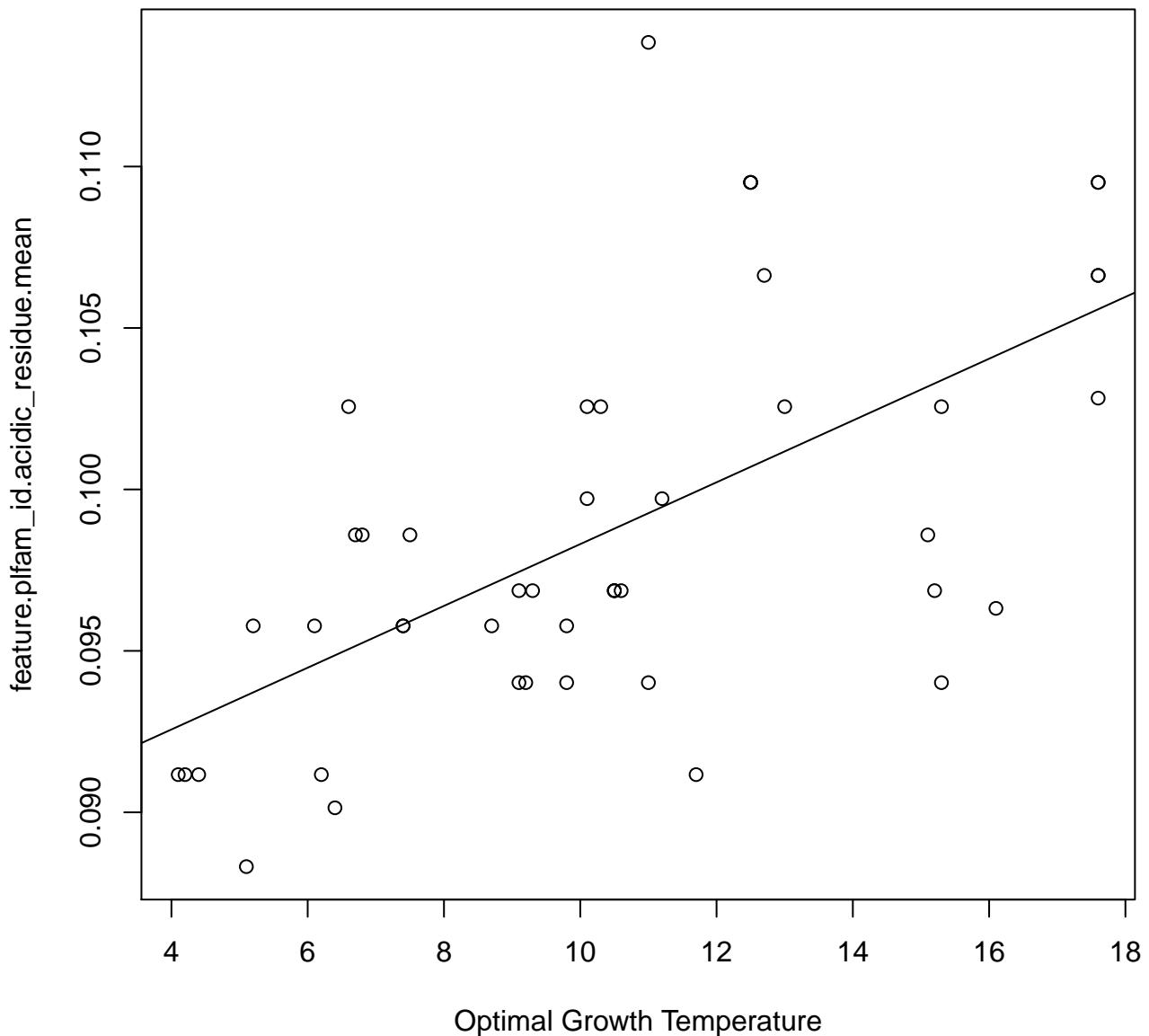
feature.plfam_id.acidic_residue.mean
PLF_28228_00000548
Inner membrane protein YpjD



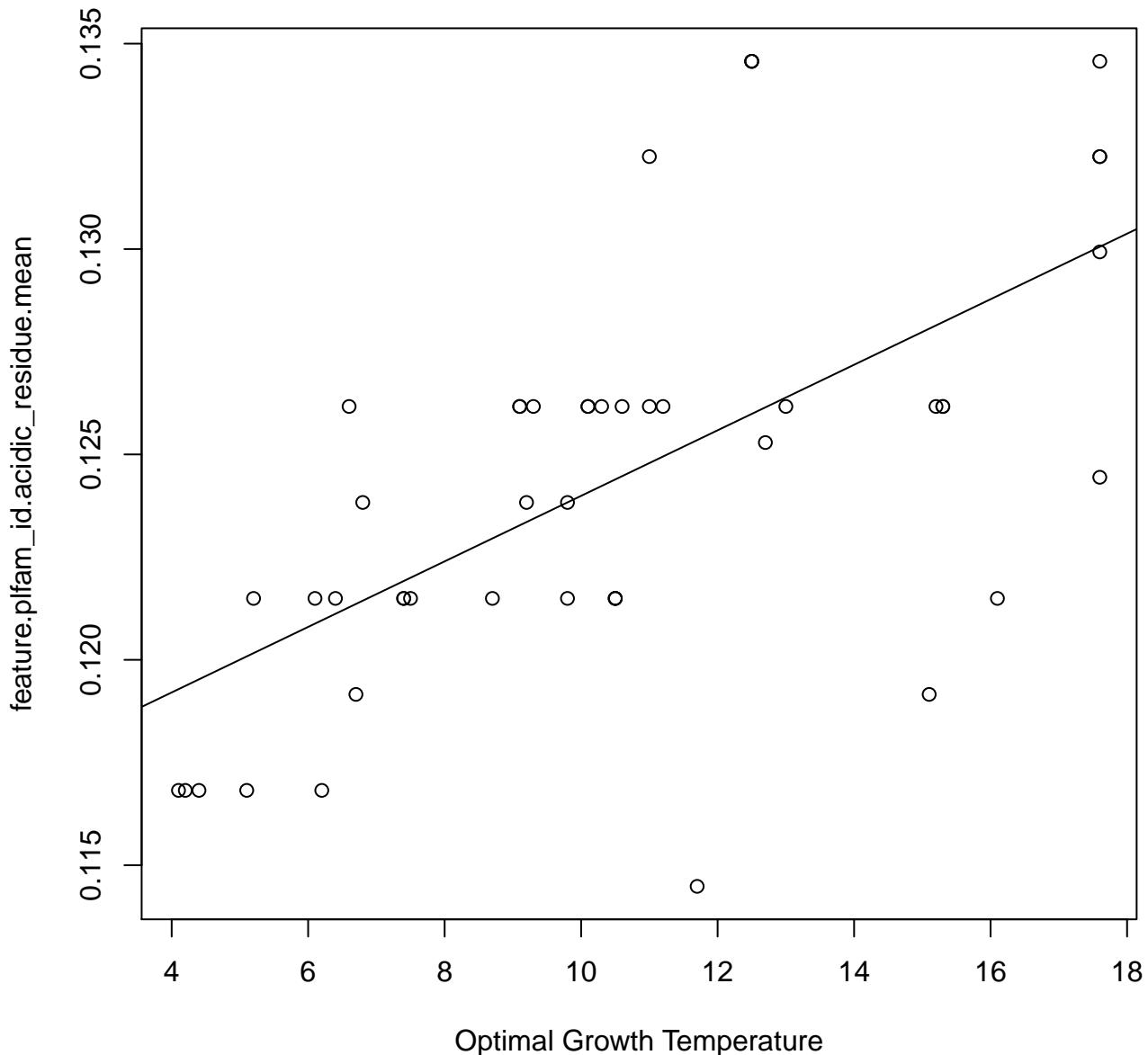
feature.plfam_id.acidic_residue.mean
PLF_28228_00000868
GTP-binding protein EngA



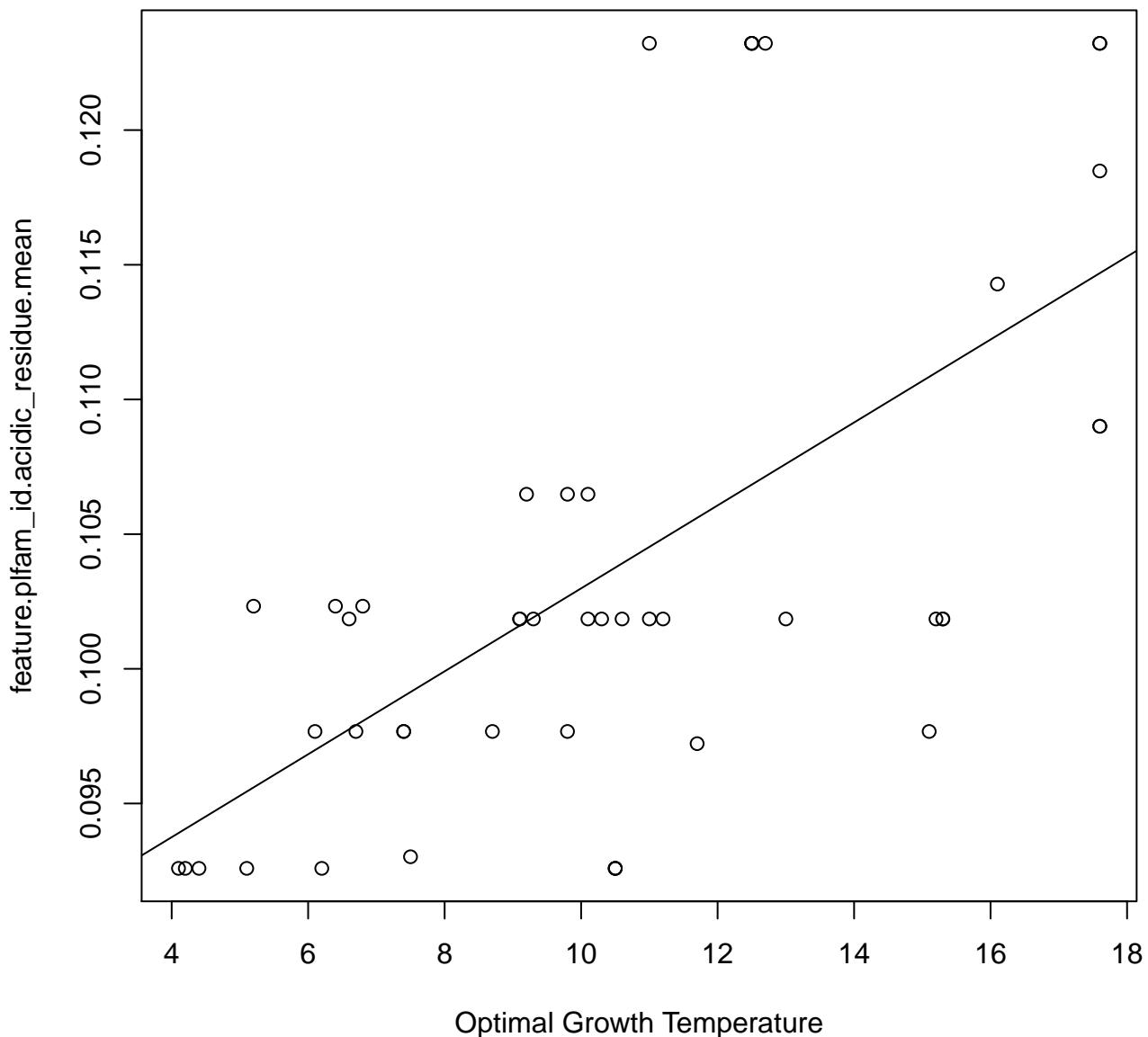
feature.plfam_id.acidic_residue.mean
PLF_28228_00000602
Membrane-bound lytic murein transglycosylase B



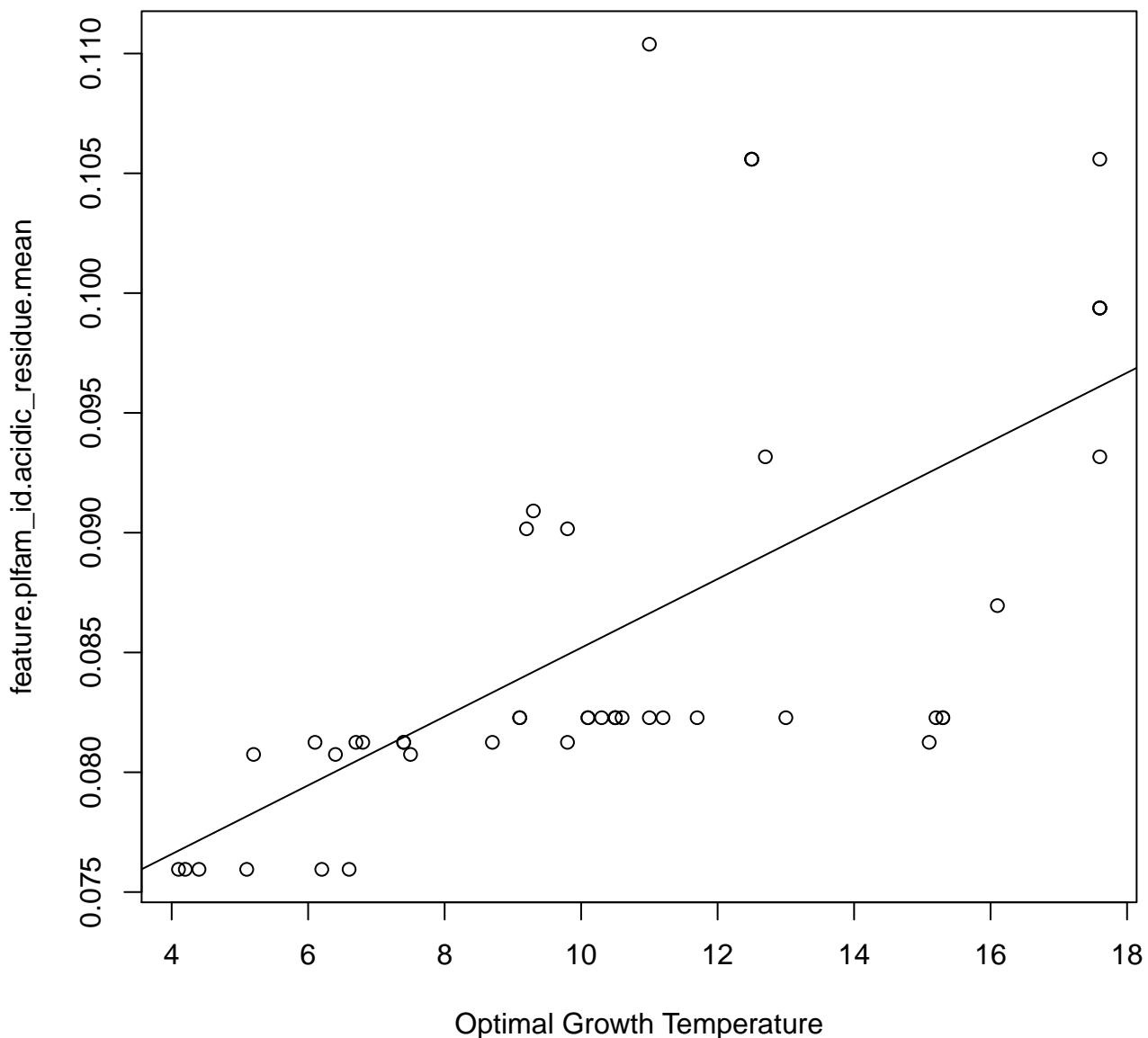
feature.plfam_id.acidic_residue.mean
PLF_28228_00000576
Phosphoribosylamine--glycine ligase (EC 6.3.4.13)



feature.plfam_id.acidic_residue.mean
PLF_28228_00000170
hypothetical protein



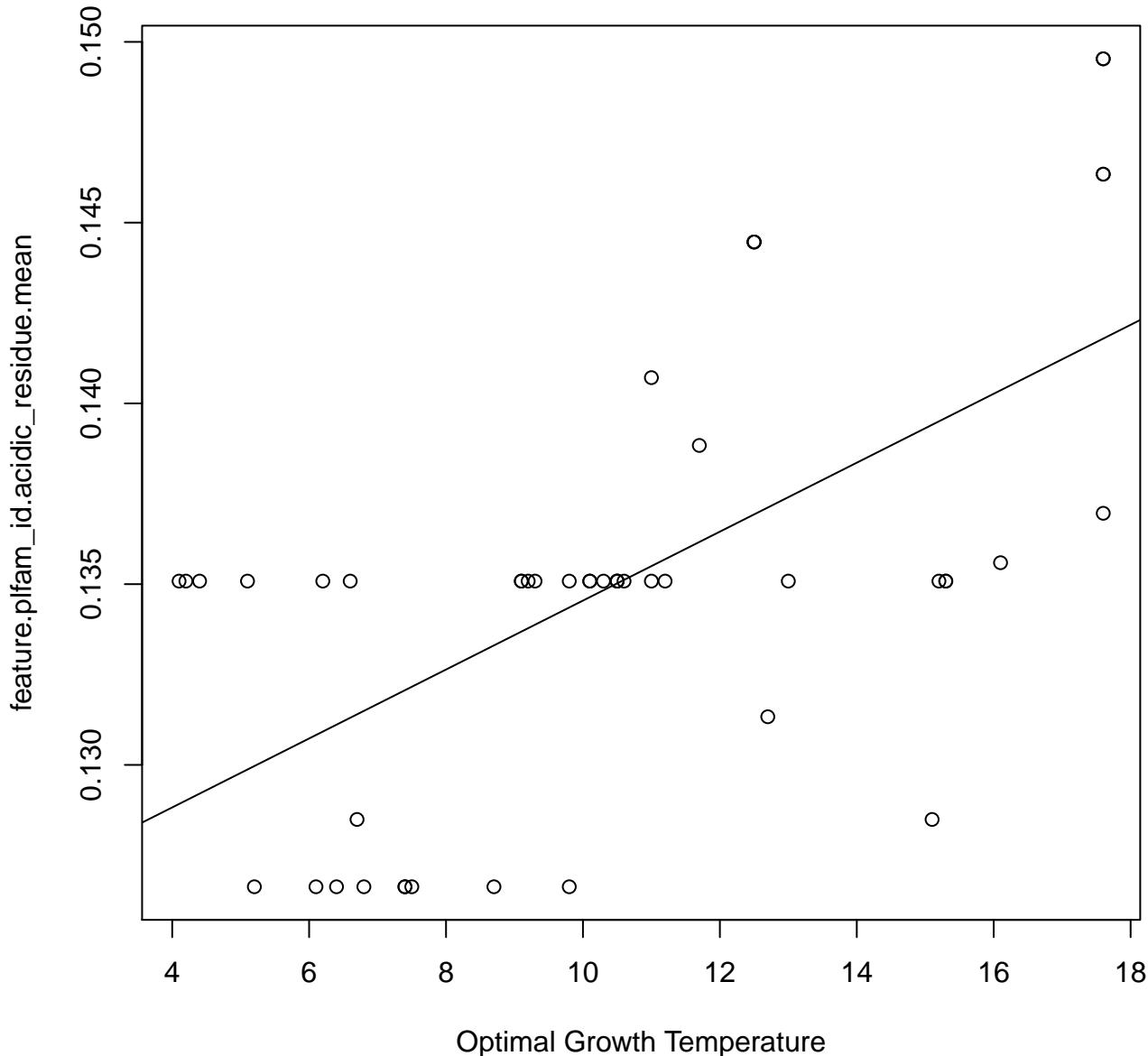
feature.plfam_id.acidic_residue.mean
PLF_28228_00002246
hypothetical protein



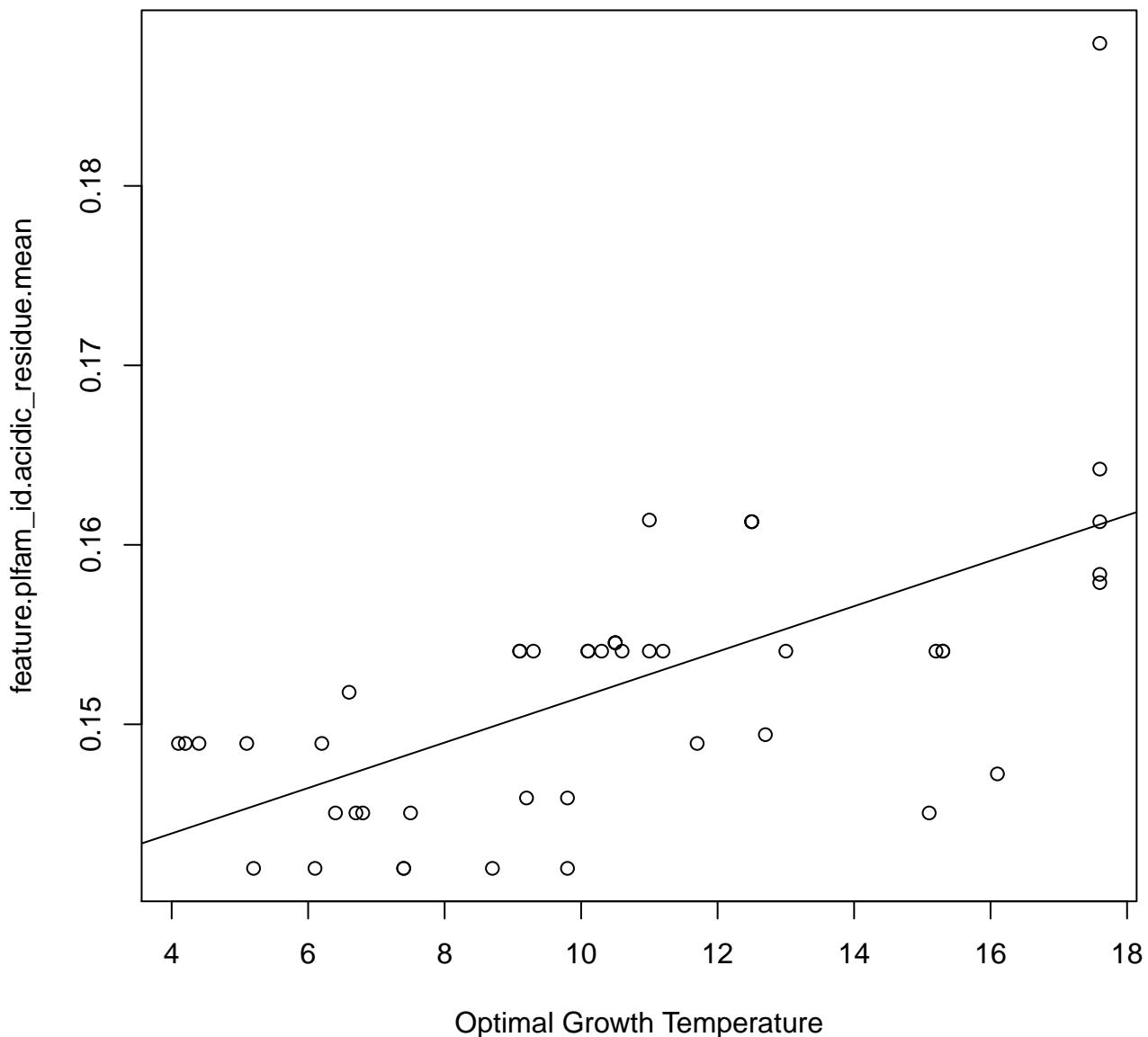
feature.plfam_id.acidic_residue.mean

PLF_28228_00000516

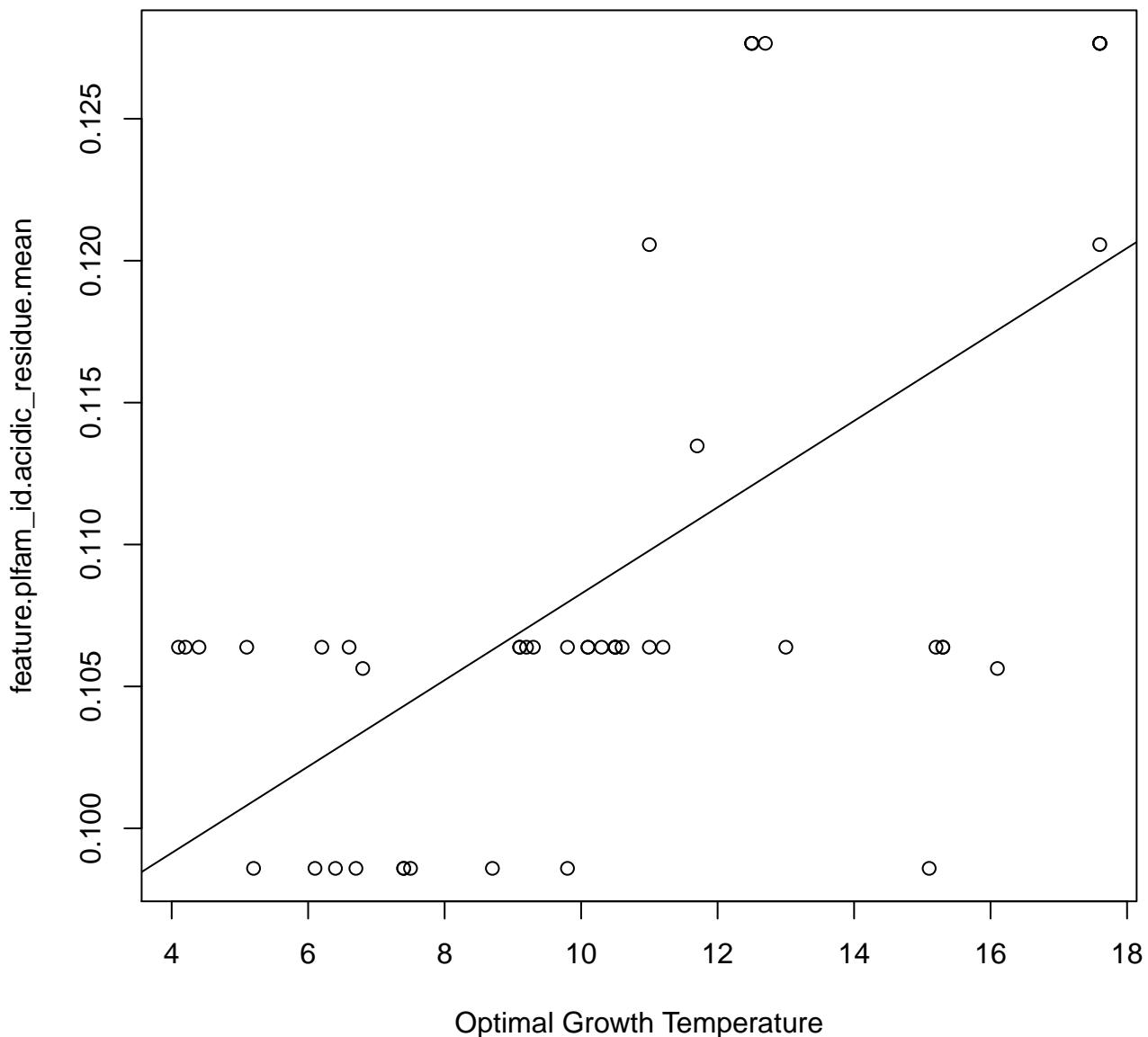
IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)



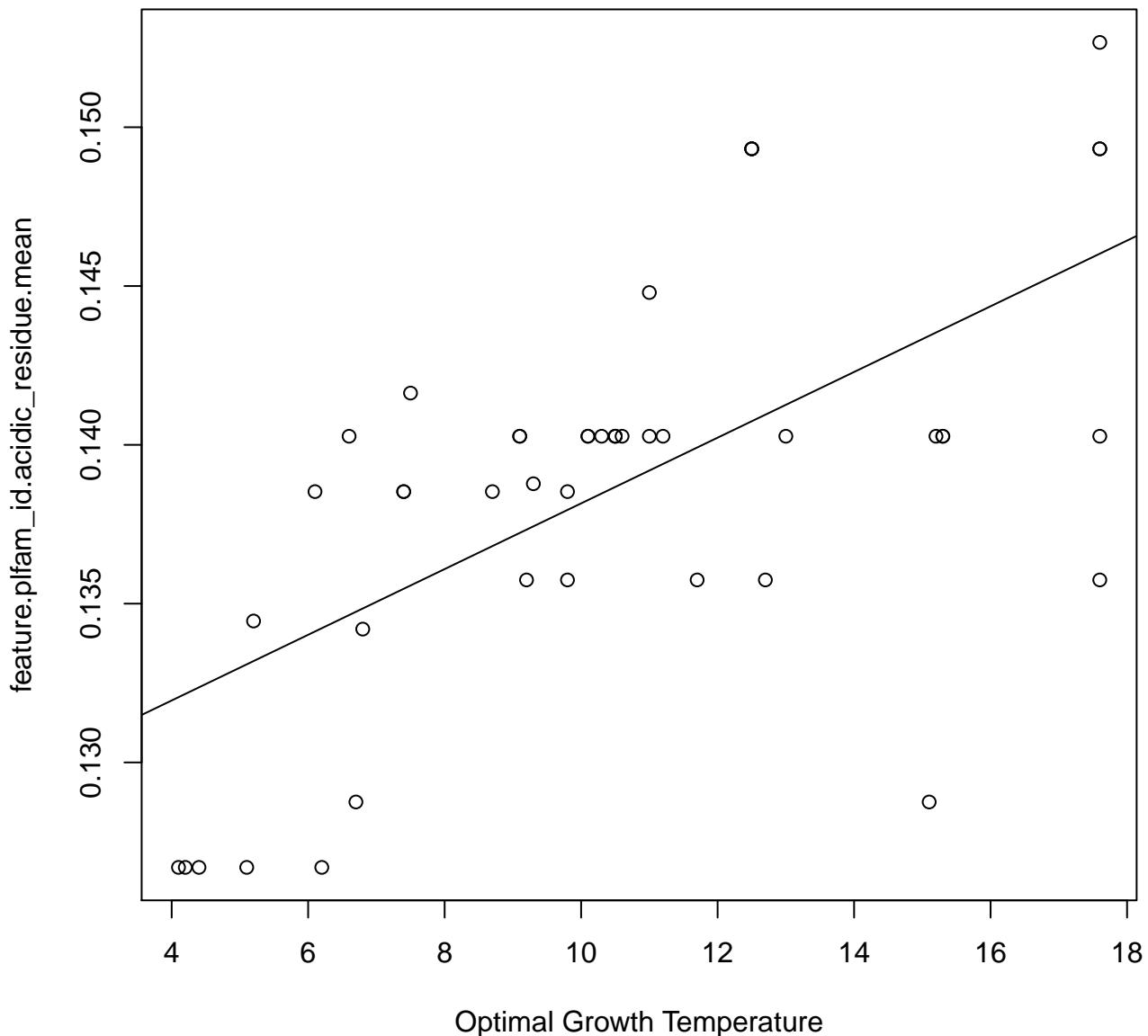
feature.plfam_id.acidic_residue.mean
PLF_28228_00001056
Rhodanese domain protein UPF0176



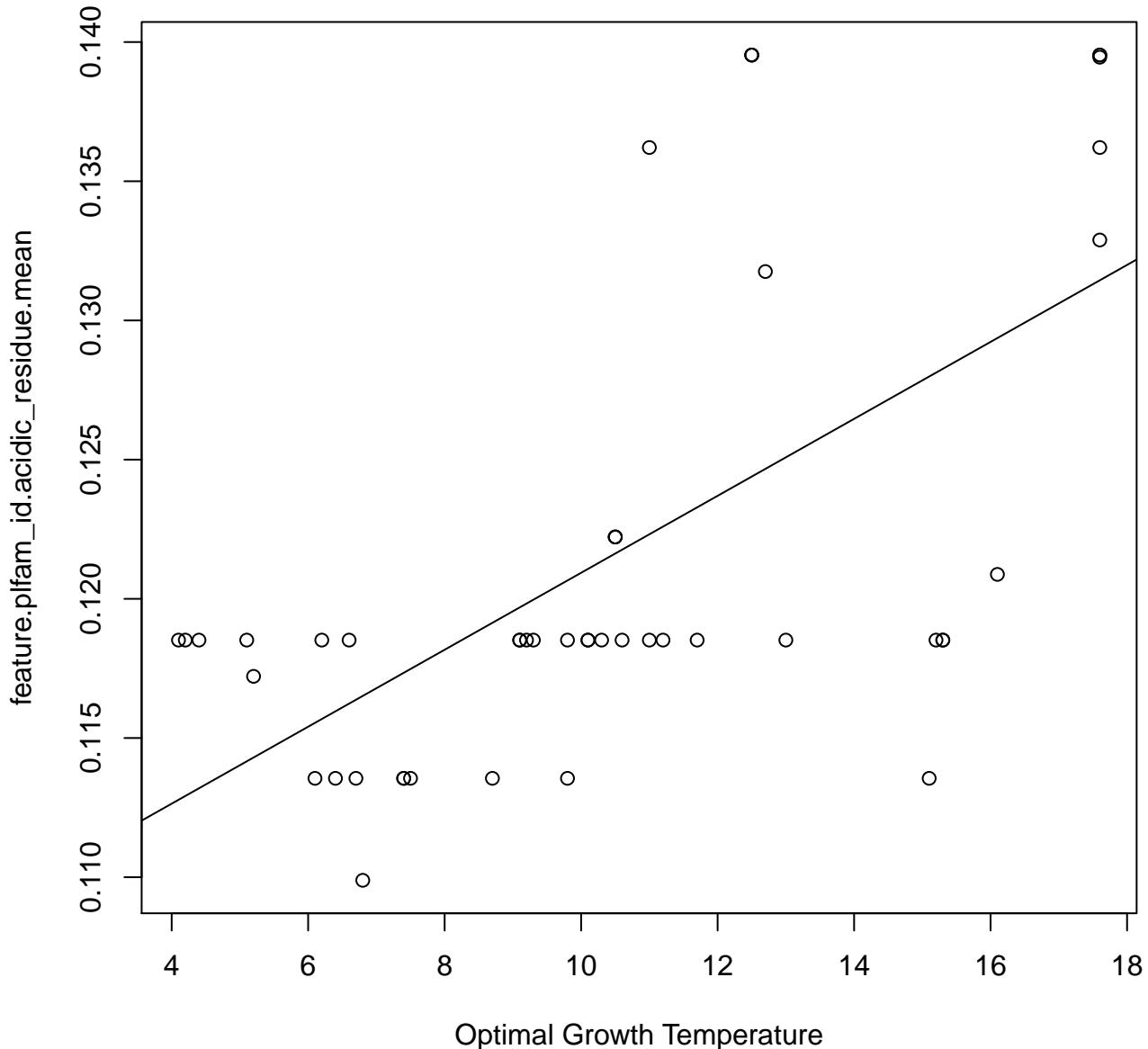
feature.plfam_id.acidic_residue.mean
PLF_28228_00001202
Tol biopolymer transport system, TolR protein



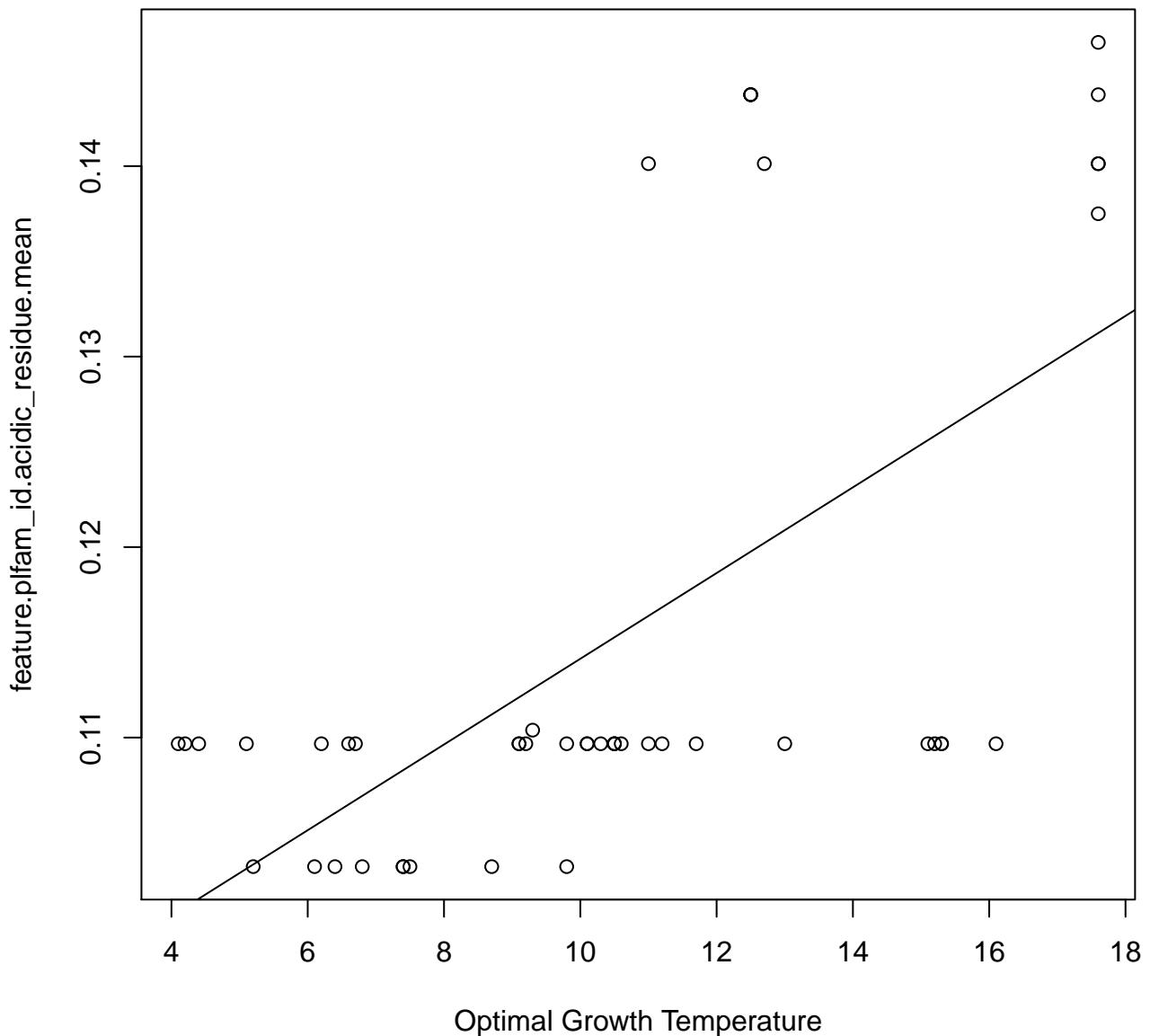
feature.plfam_id.acidic_residue.mean
PLF_28228_00001009
Protein of unknown function YceH



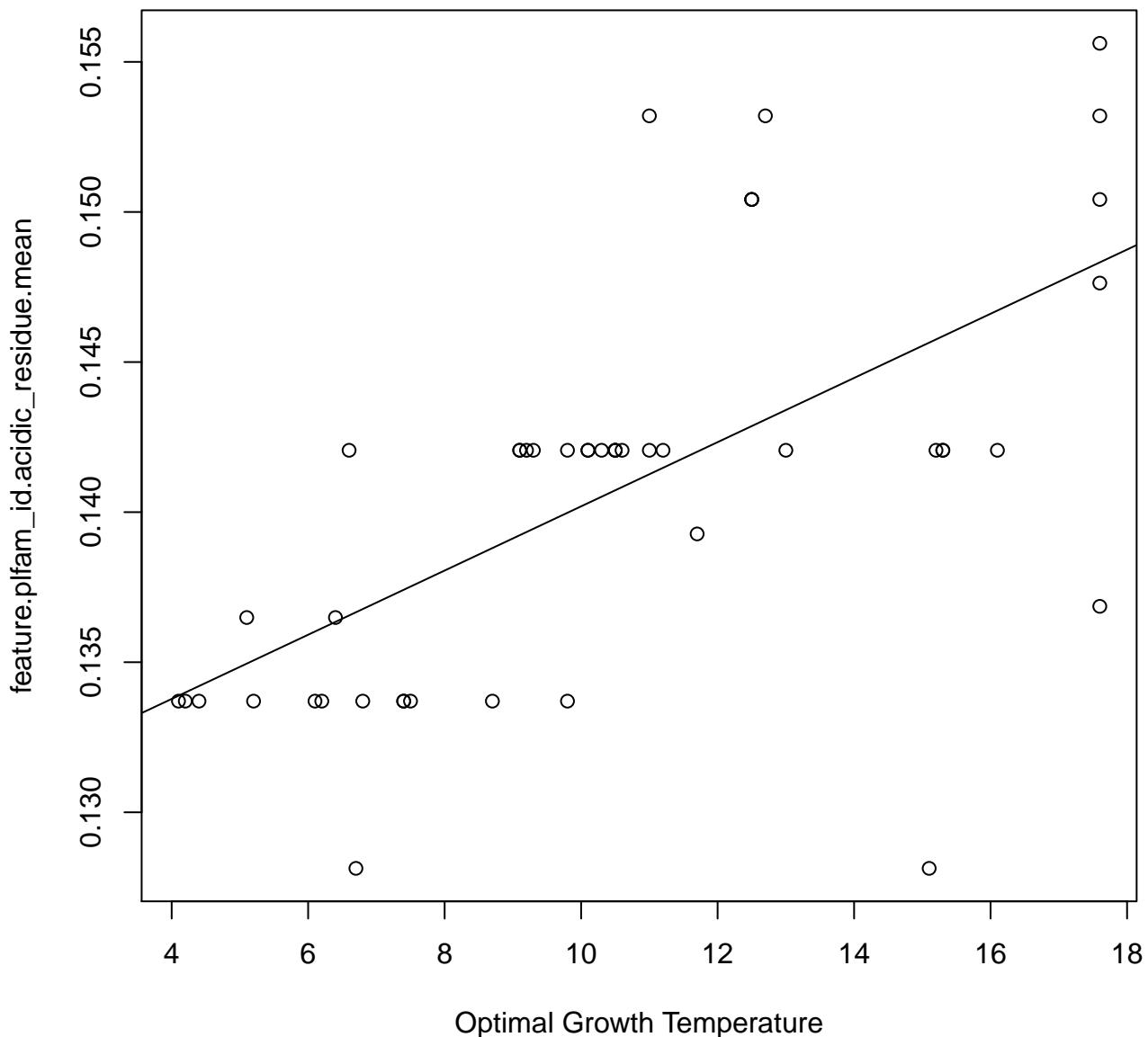
feature.plfam_id.acidic_residue.mean
PLF_28228_00001107
SSU rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase (EC 2.1.1.182)



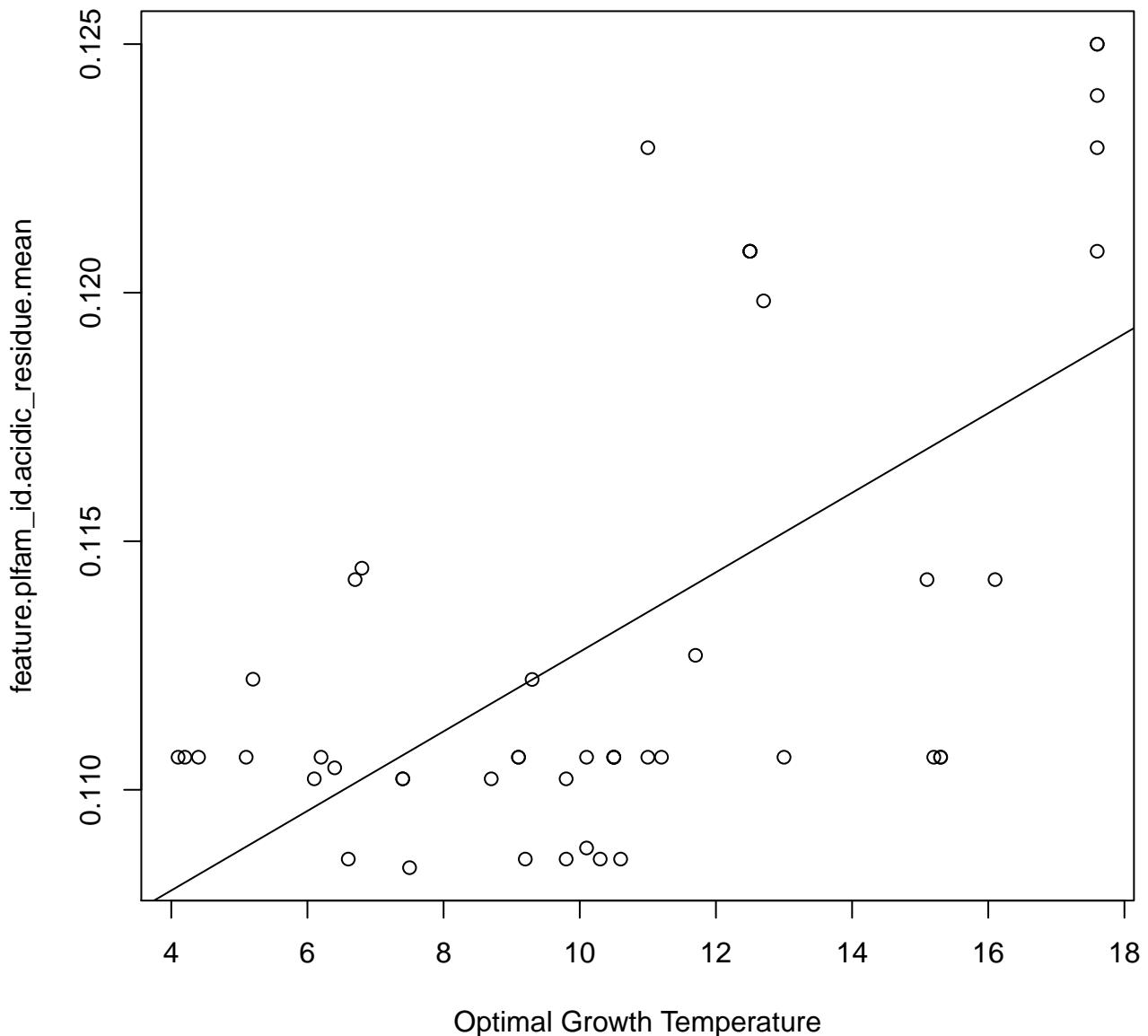
feature.plfam_id.acidic_residue.mean
PLF_28228_00000965
Phospholipid ABC transporter substrate-binding protein MlaD



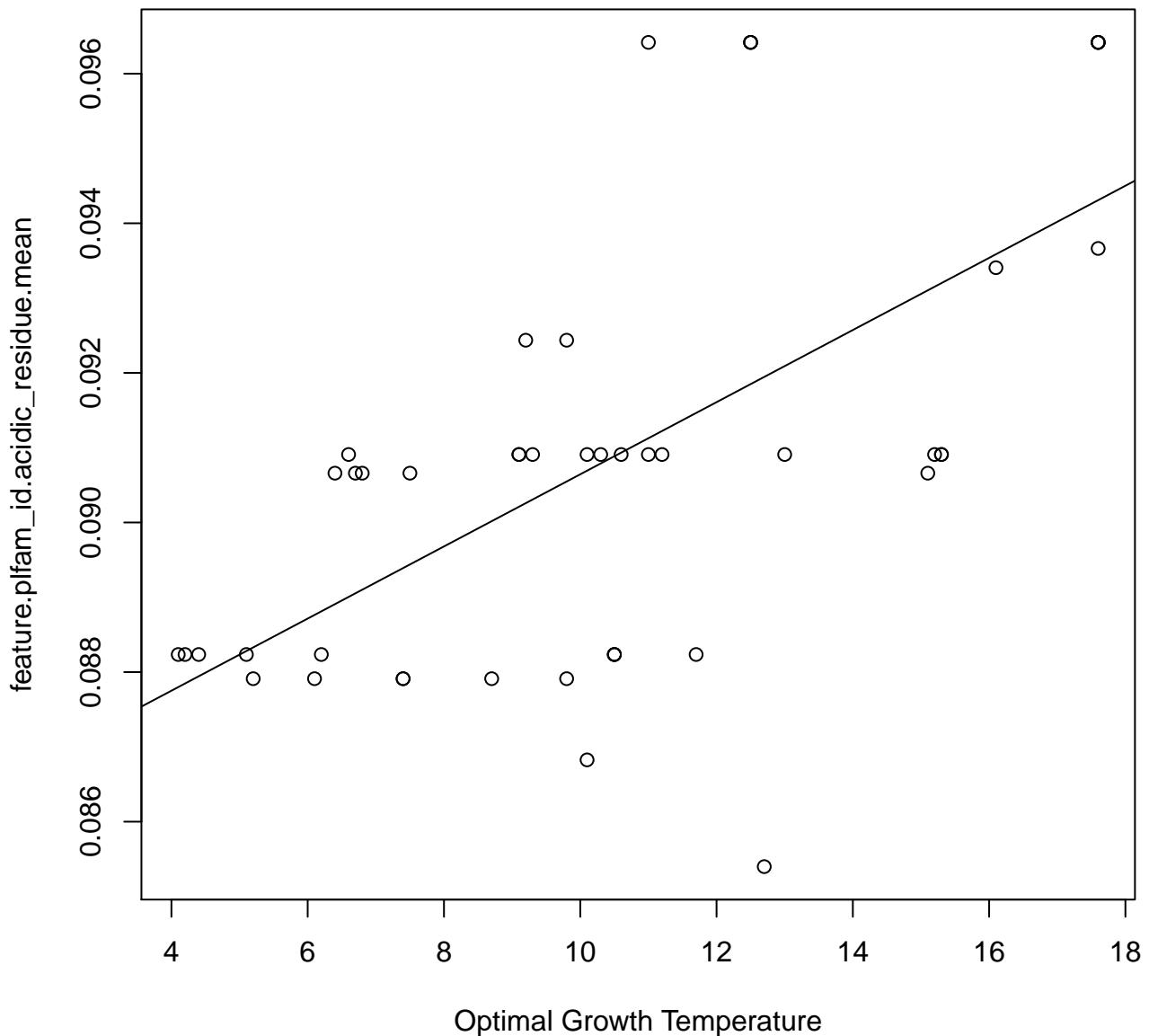
feature.plfam_id.acidic_residue.mean
PLF_28228_00001258
Type IV pilus biogenesis protein PilM



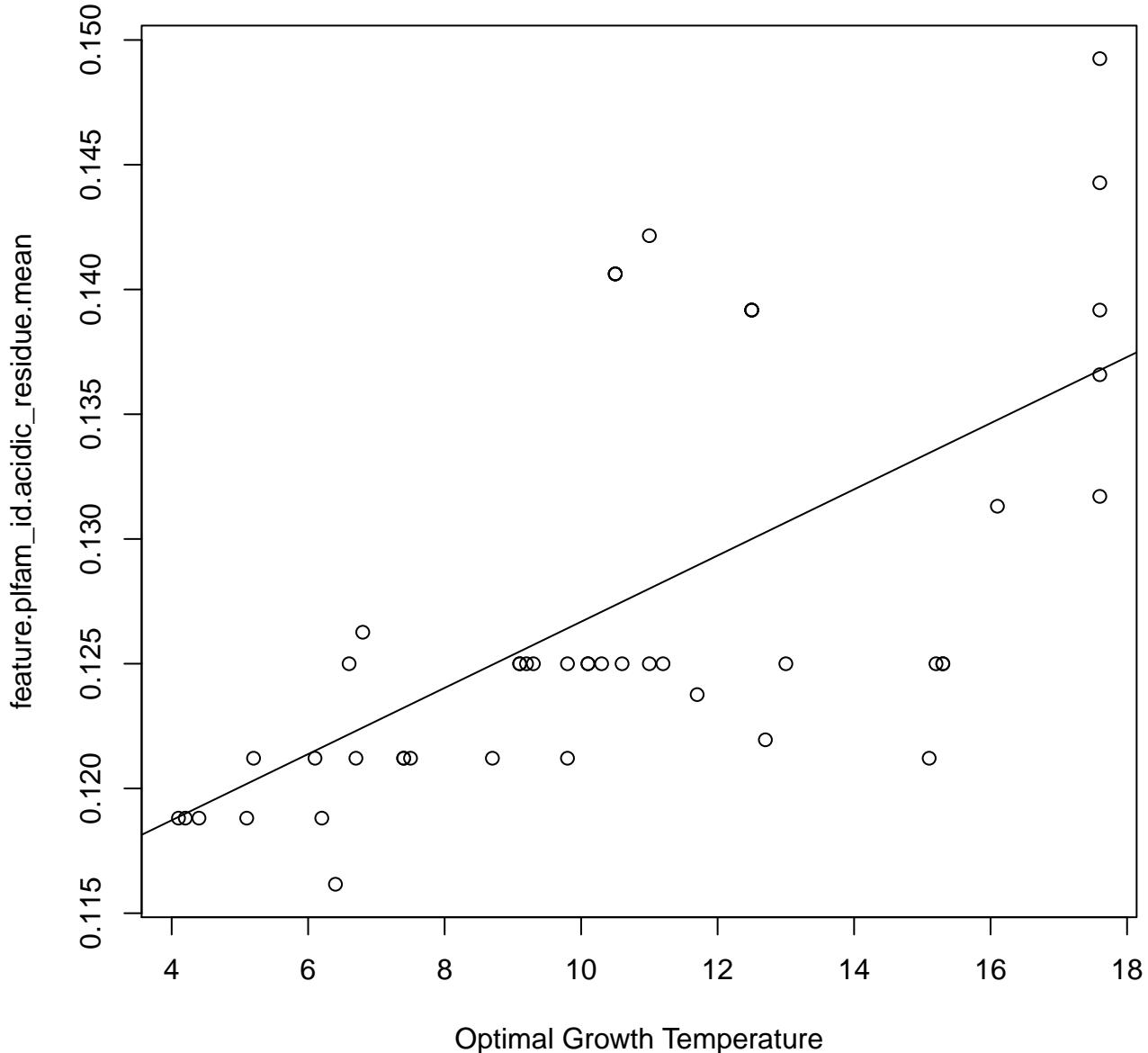
feature.plfam_id.acidic_residue.mean
PLF_28228_00001582
FIG032621: Hydrolase, alpha/beta hydrolase fold family



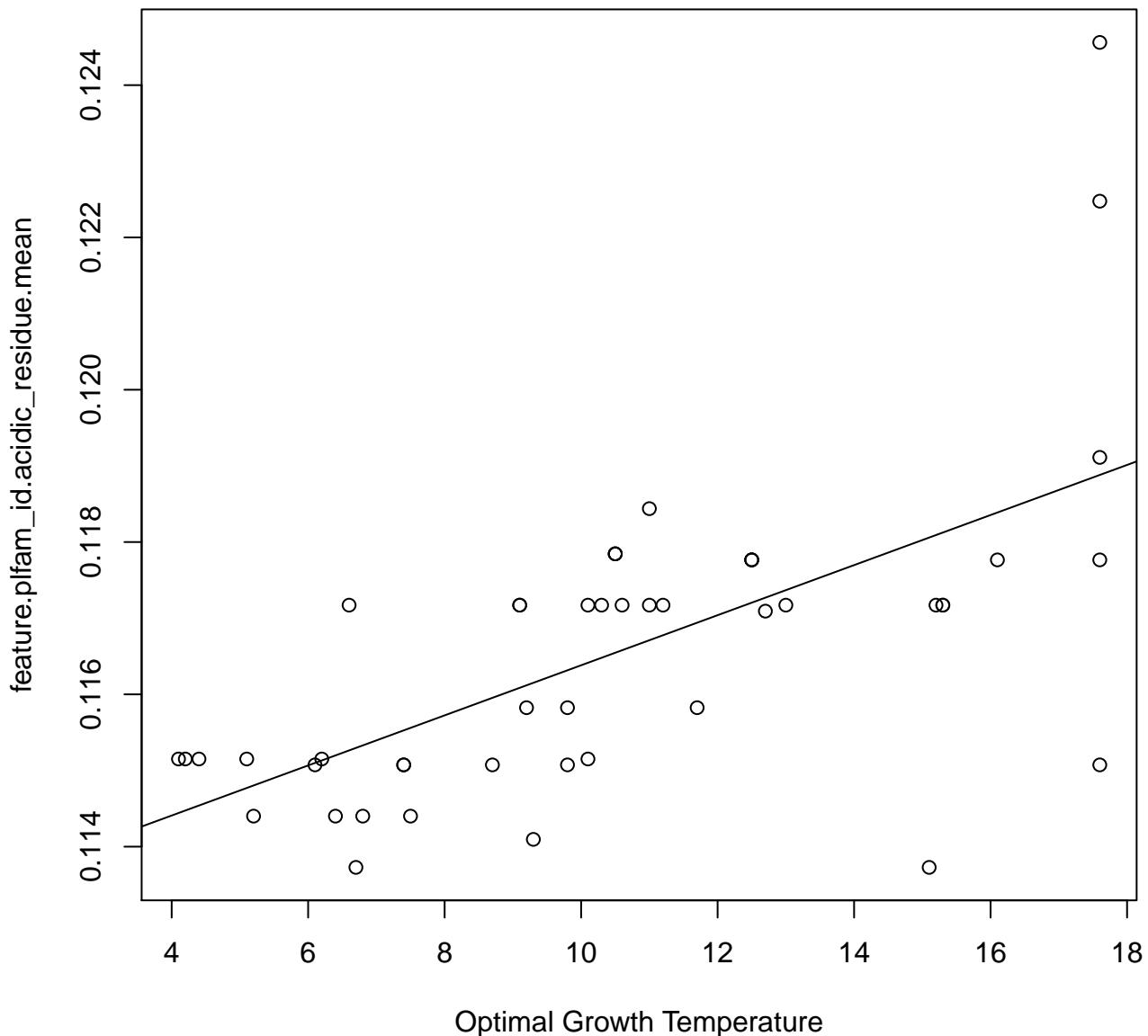
feature.plfam_id.acidic_residue.mean
PLF_28228_00000479
Flagellar P-ring protein FlgI



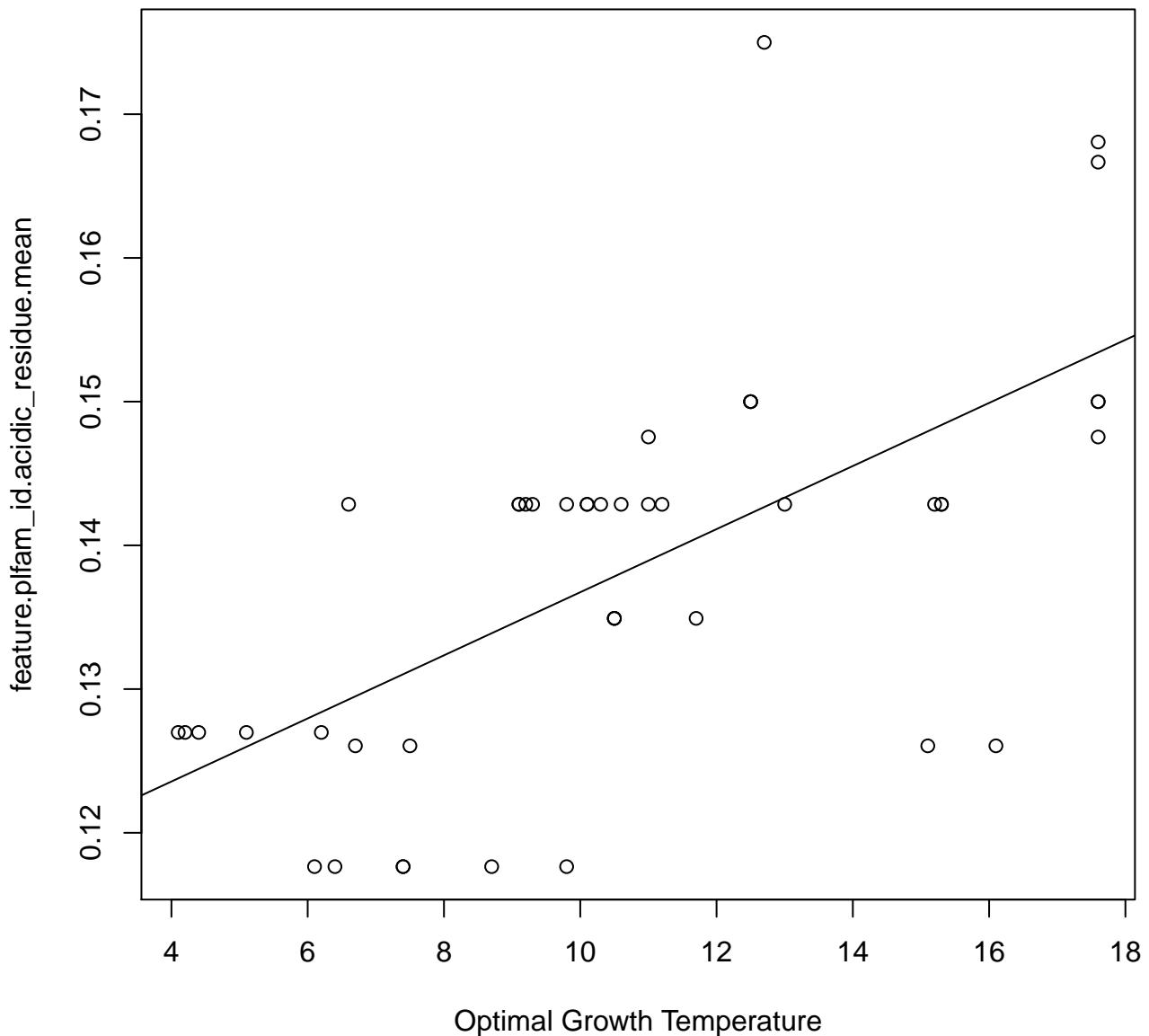
feature.plfam_id.acidic_residue.mean
PLF_28228_00000187
DNA-3-methyladenine glycosylase (EC 3.2.2.20)



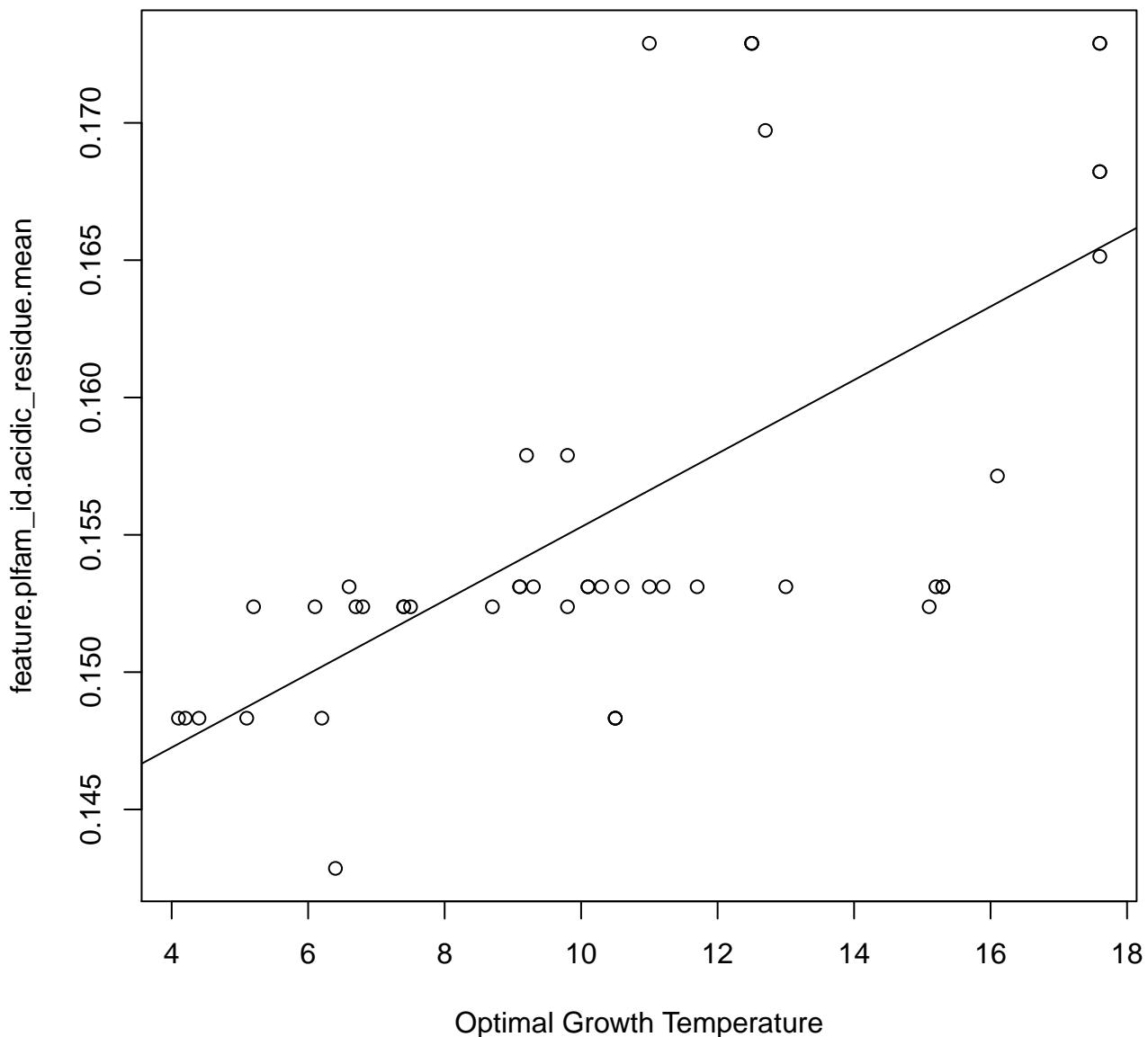
feature.plfam_id.acidic_residue.mean
PLF_28228_00000888
Glutamate synthase [NADPH] large chain (EC 1.4.1.13)



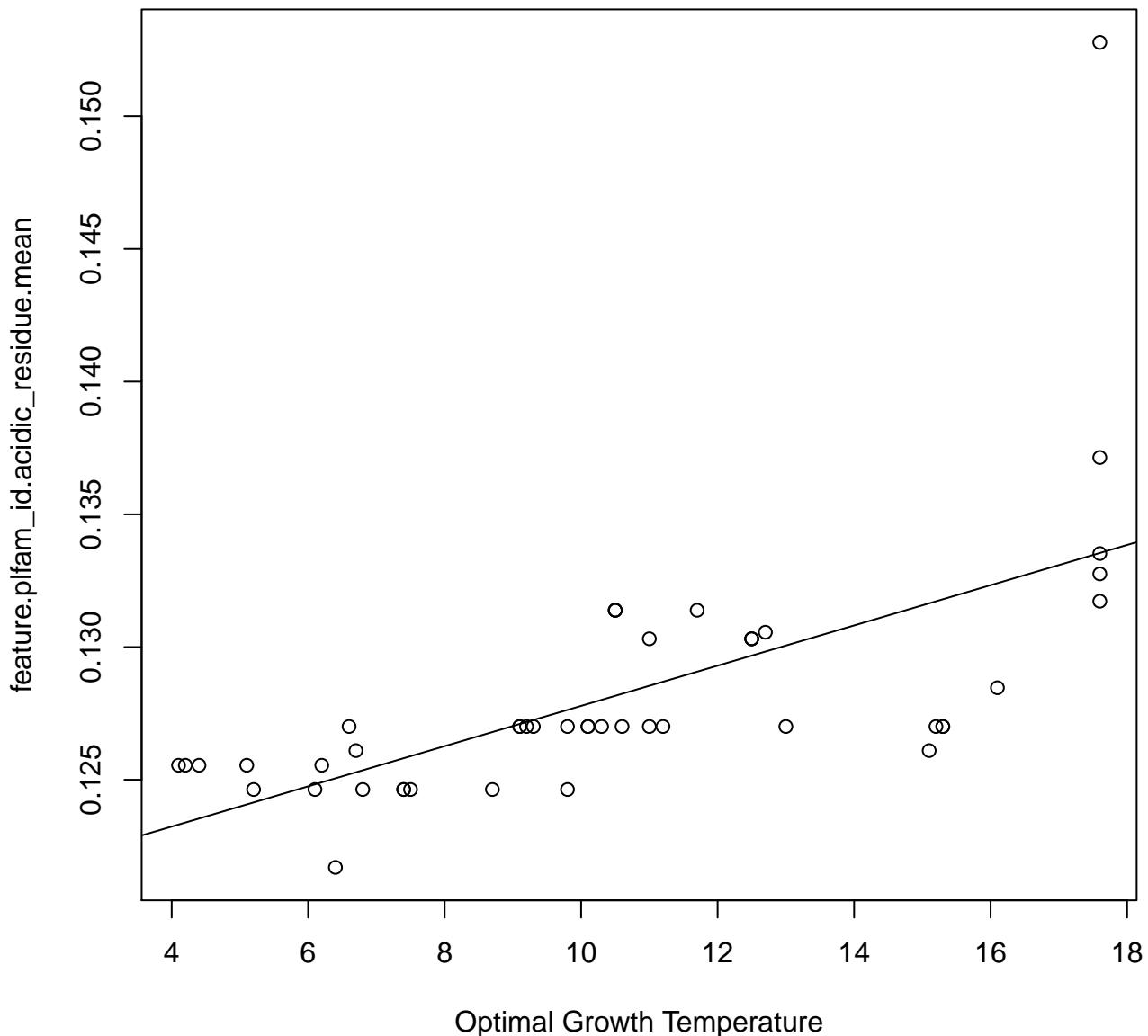
feature.plfam_id.acidic_residue.mean
PLF_28228_00002456
hypothetical protein



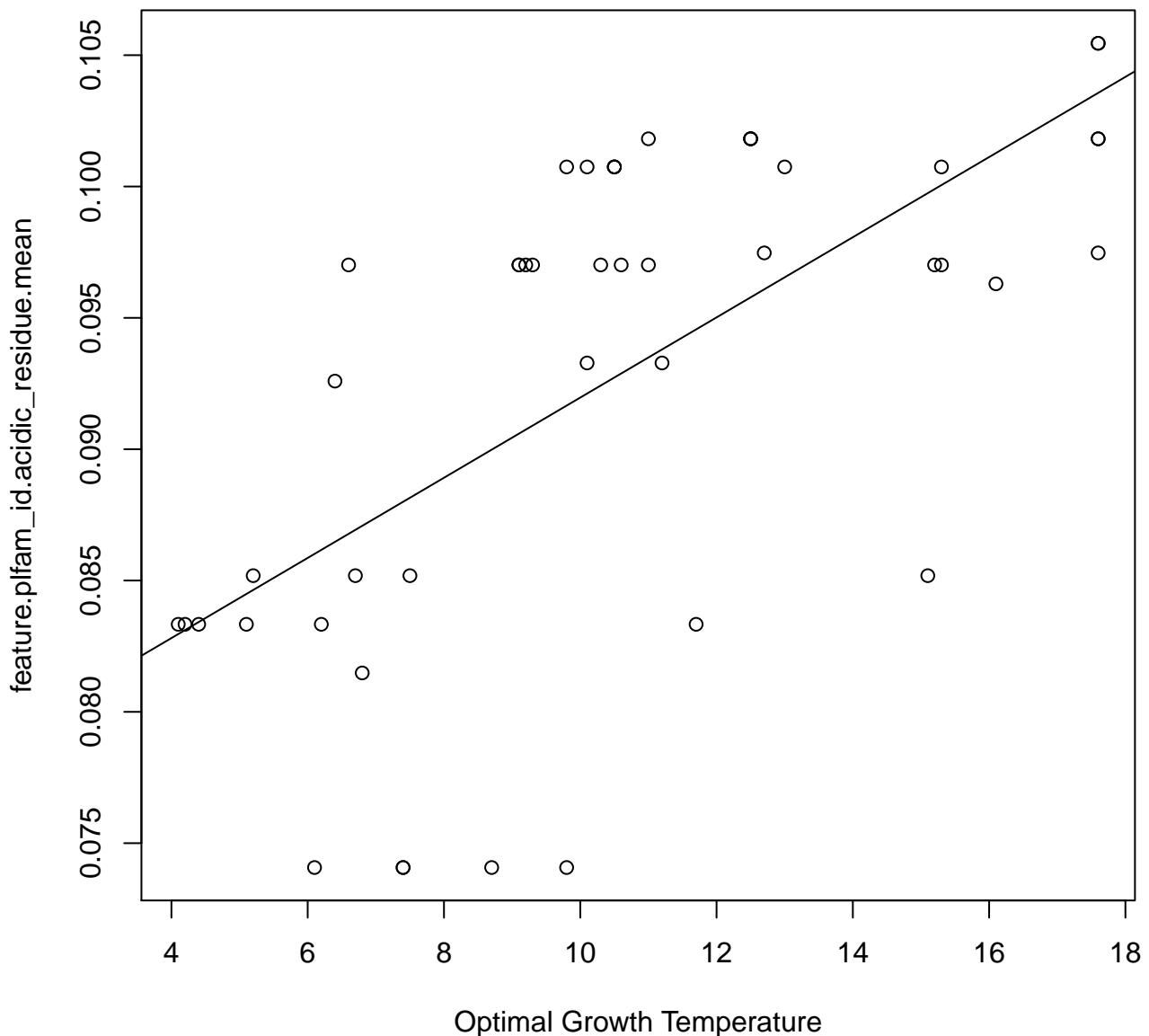
feature.plfam_id.acidic_residue.mean
PLF_28228_00000241
Dimeric dUTPase (EC 3.6.1.23)



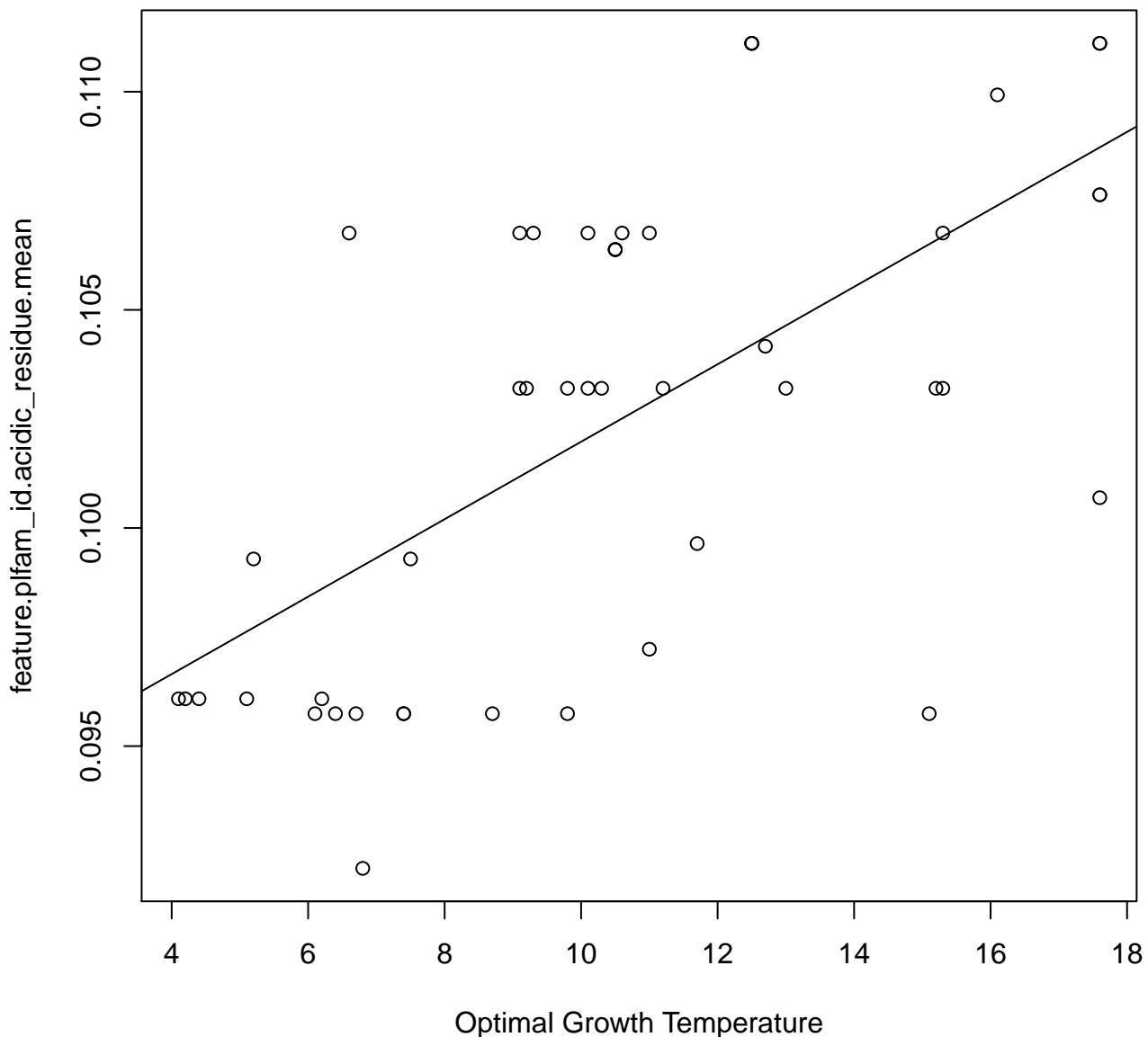
feature.plfam_id.acidic_residue.mean
PLF_28228_00001260
Type IV pilus biogenesis protein PilQ



feature.plfam_id.acidic_residue.mean
PLF_28228_00001140
Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)



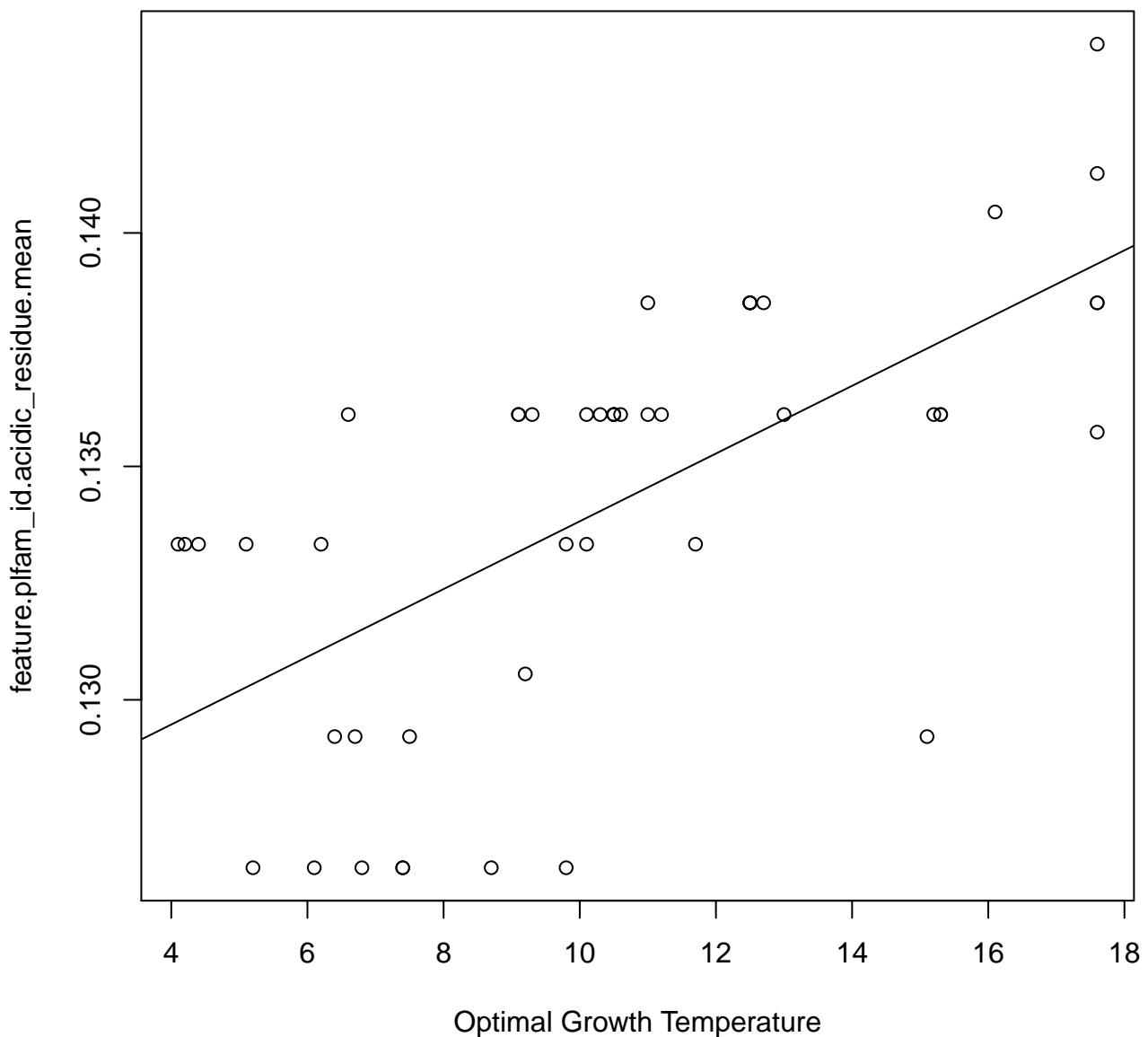
feature.plfam_id.acidic_residue.mean
PLF_28228_00000908
Pantoate--beta-alanine ligase (EC 6.3.2.1)



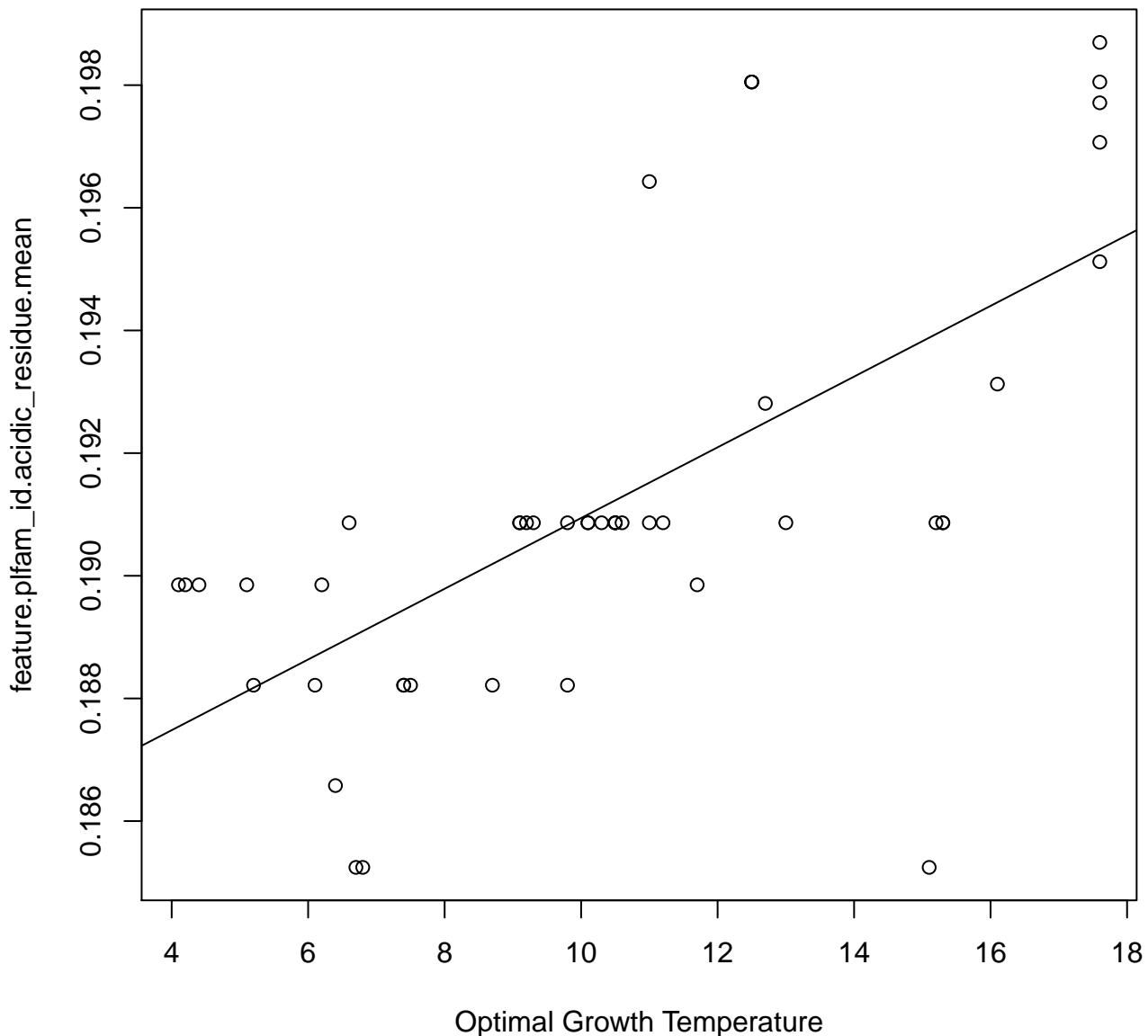
feature.plfam_id.acidic_residue.mean

PLF_28228_00000500

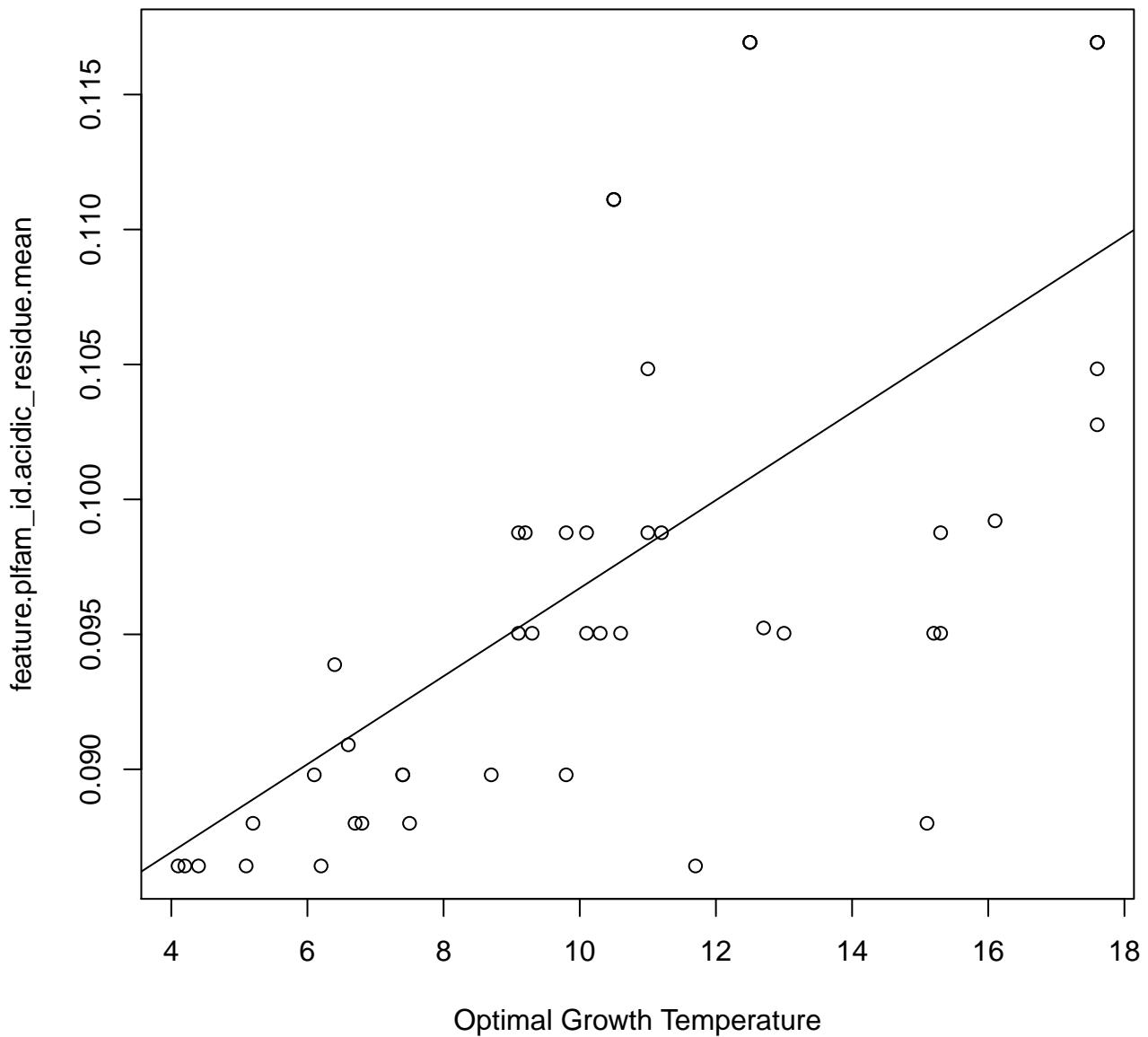
Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)



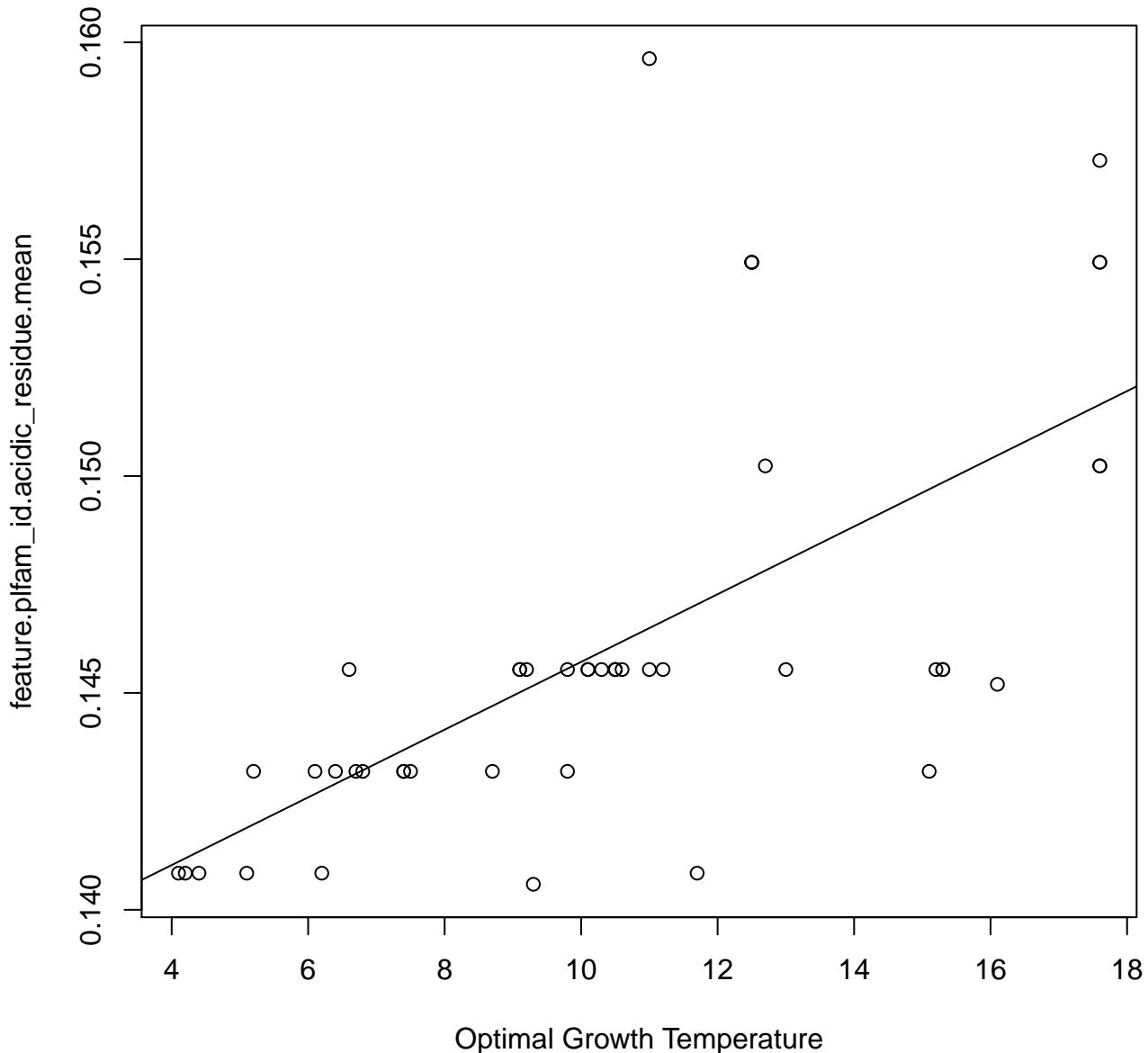
feature.plfam_id.acidic_residue.mean
PLF_28228_00001039
RNA polymerase sigma factor RpoD



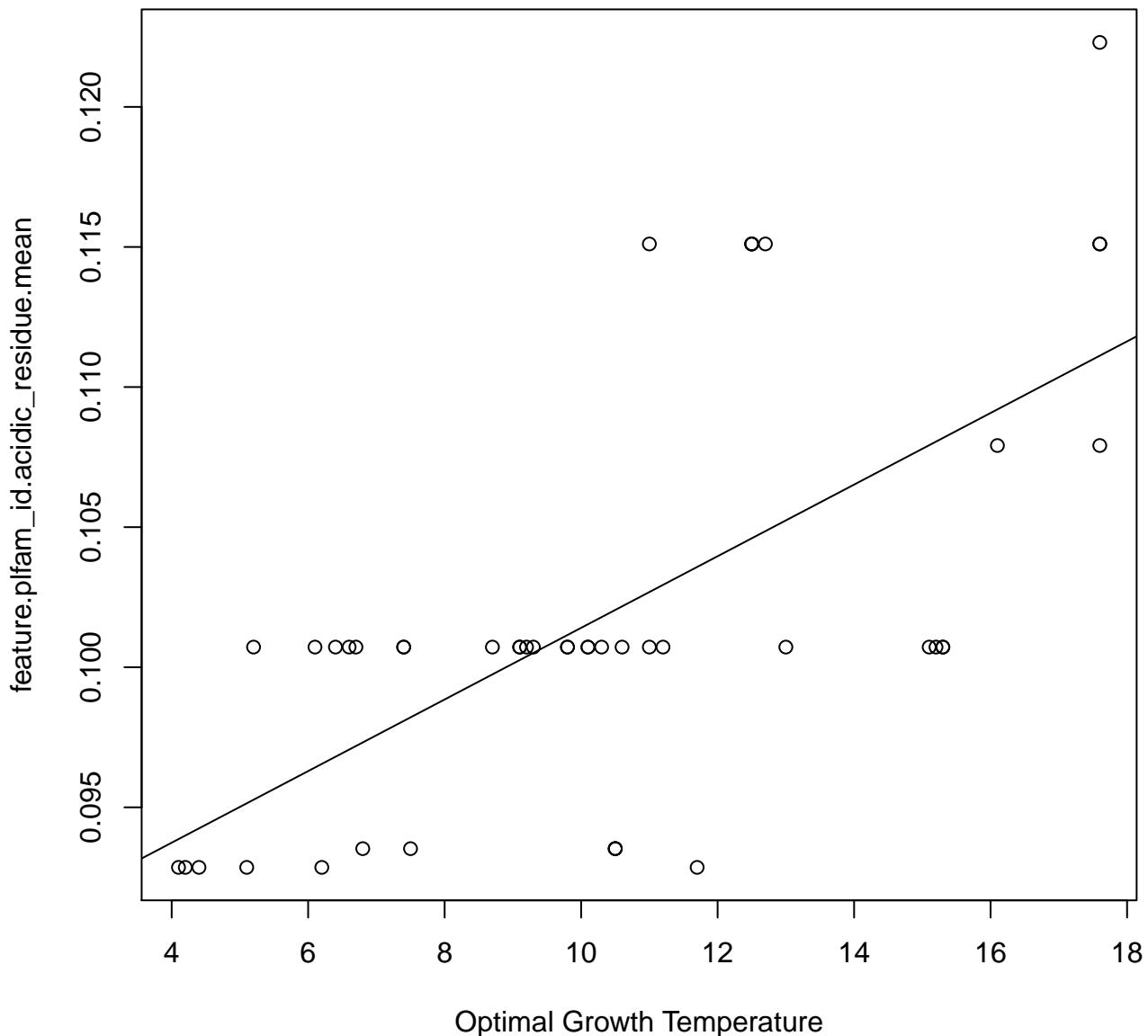
feature.plfam_id.acidic_residue.mean
PLF_28228_00001104
tRNA (adenine(37)-N6)-methyltransferase



feature.plfam_id.acidic_residue.mean
PLF_28228_00001139
Seryl-tRNA synthetase (EC 6.1.1.11)



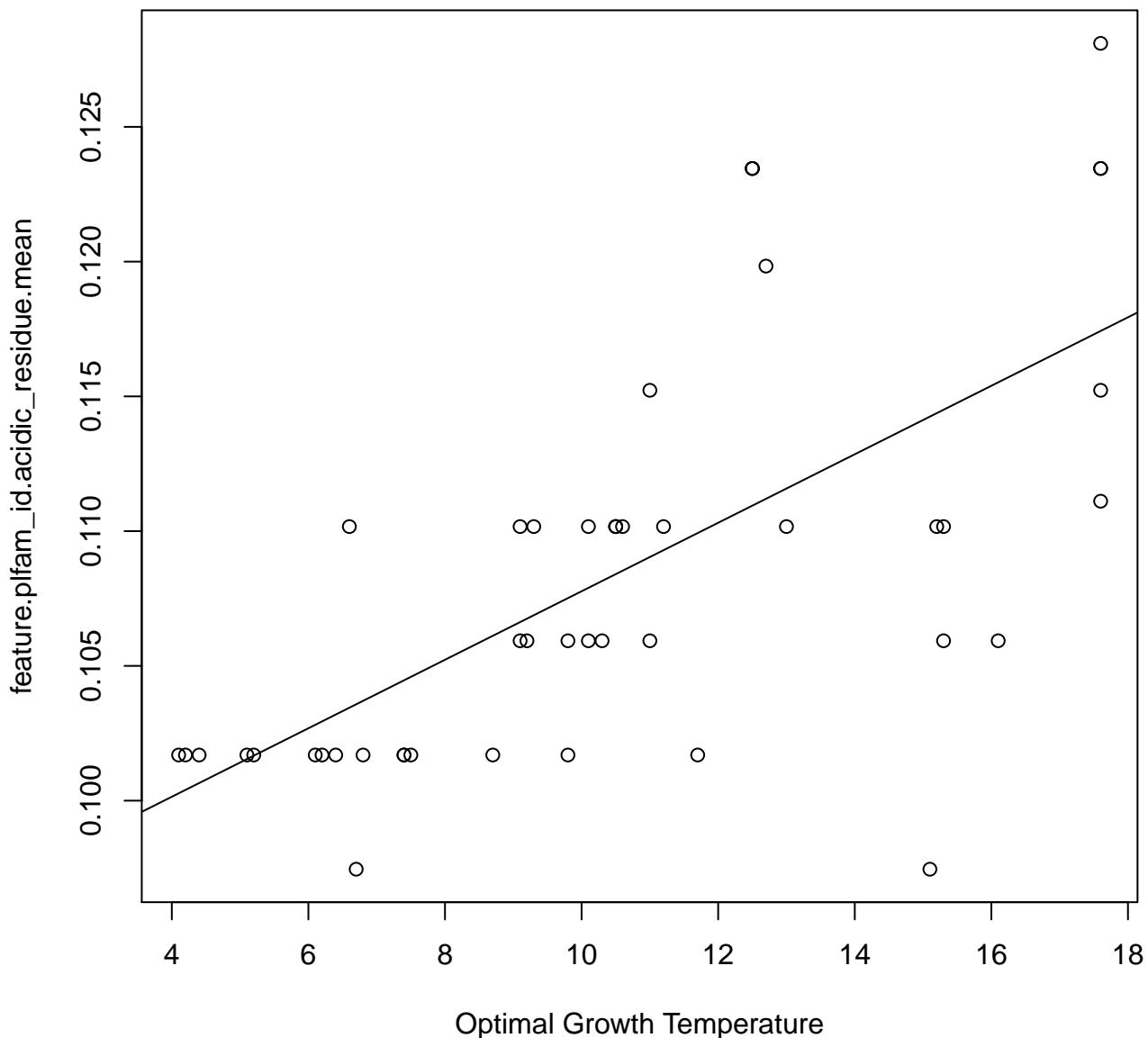
feature.plfam_id.acidic_residue.mean
PLF_28228_00001597
Cytidine deaminase (EC 3.5.4.5)



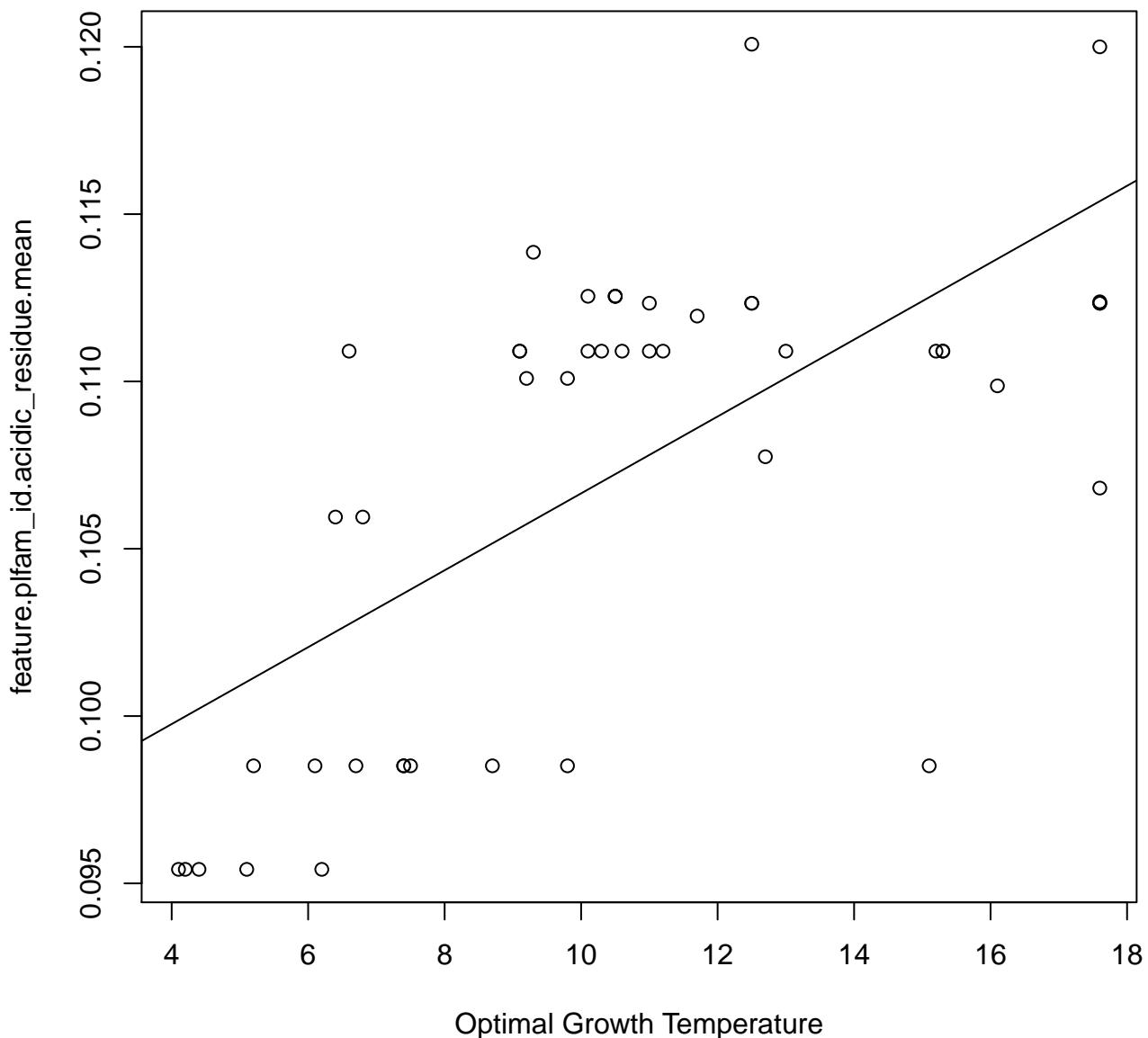
feature.plfam_id.acidic_residue.mean

PLF_28228_00000295

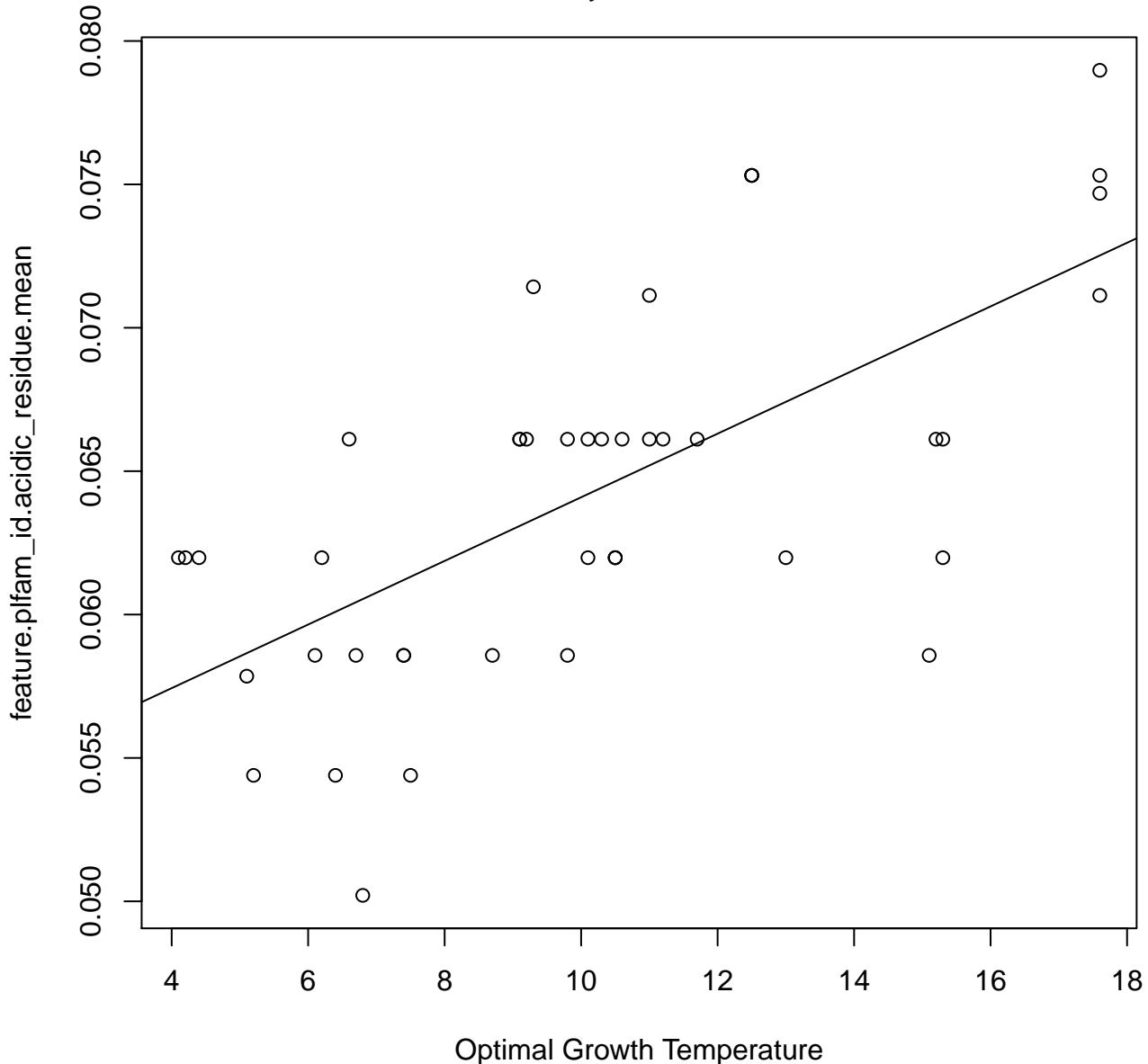
5'-methylthioadenosine nucleosidase (EC 3.2.2.16) @ S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)



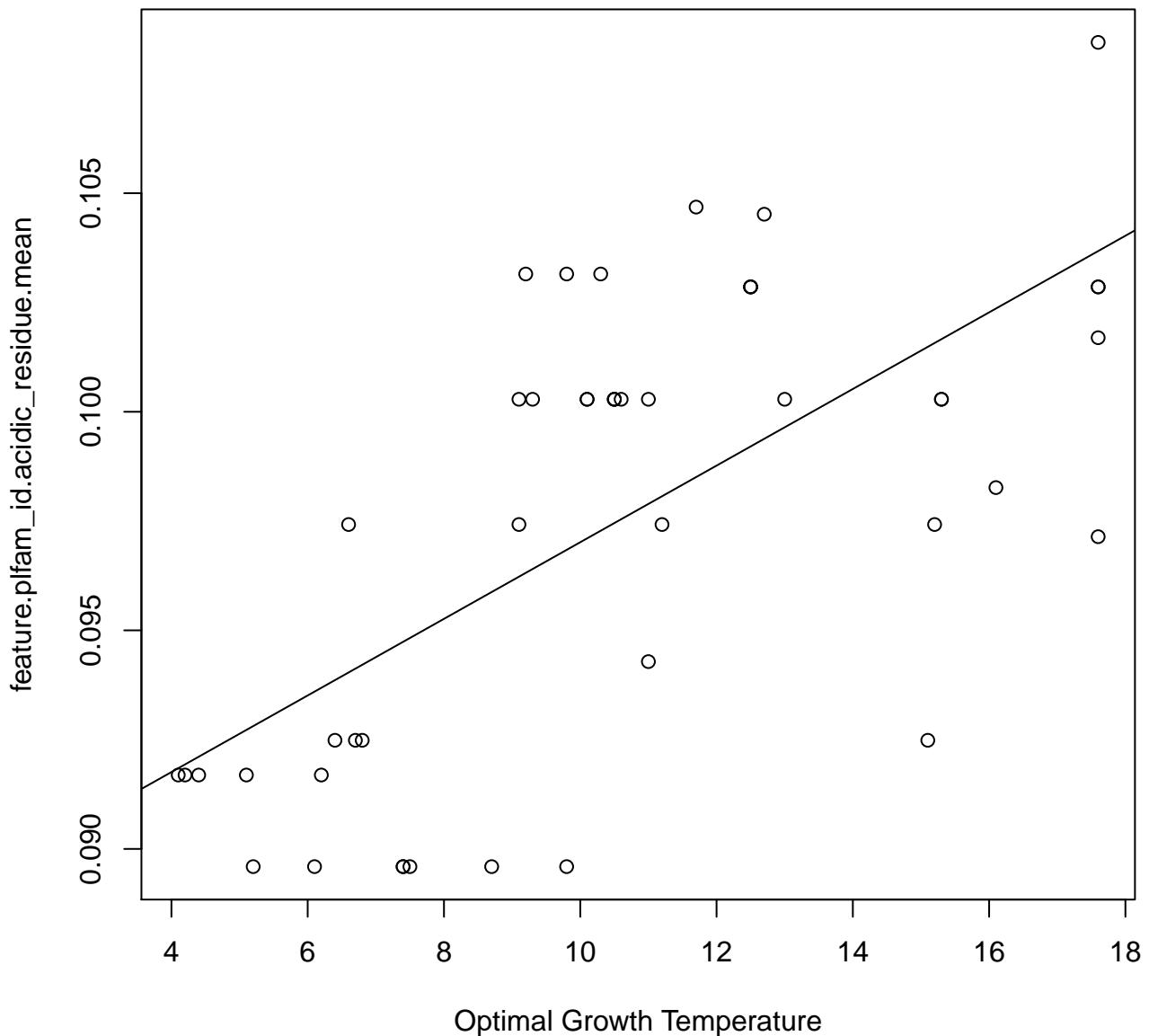
feature.plfam_id.acidic_residue.mean
PLF_28228_00000147
Sensory box histidine kinase



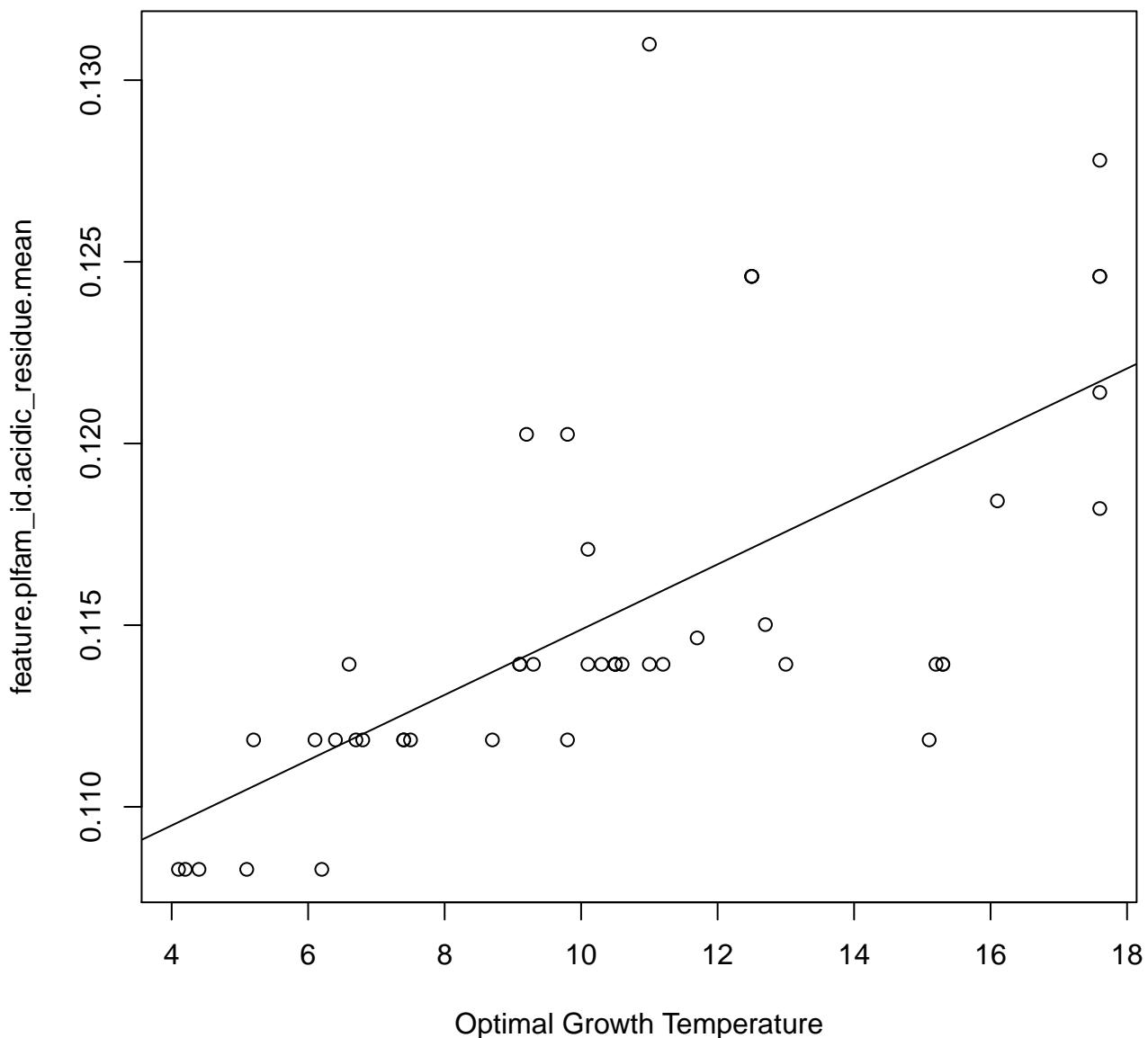
feature.plfam_id.acidic_residue.mean
PLF_28228_00003357
Cytochrome b



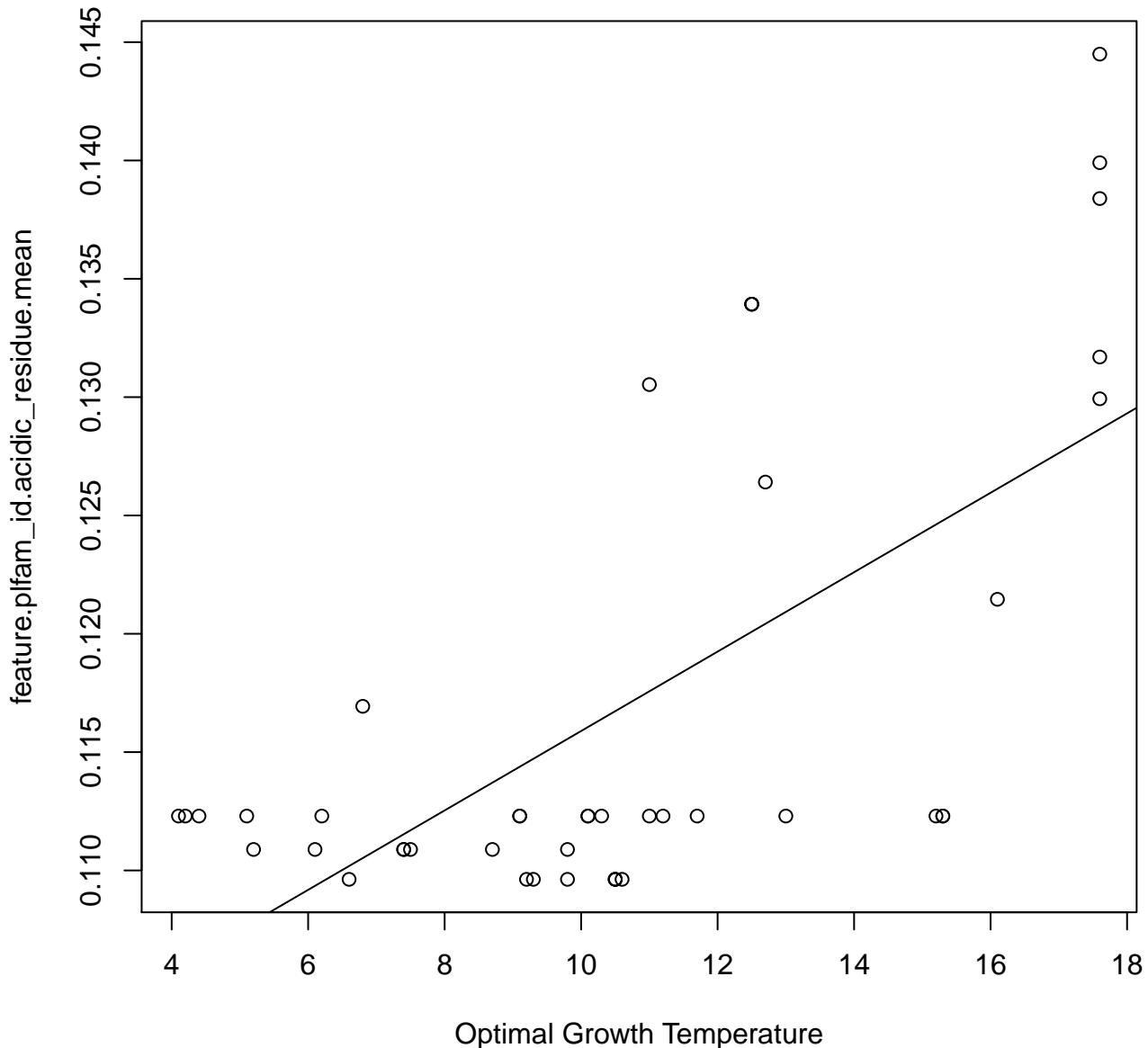
feature.plfam_id.acidic_residue.mean
PLF_28228_00002415
hypothetical protein



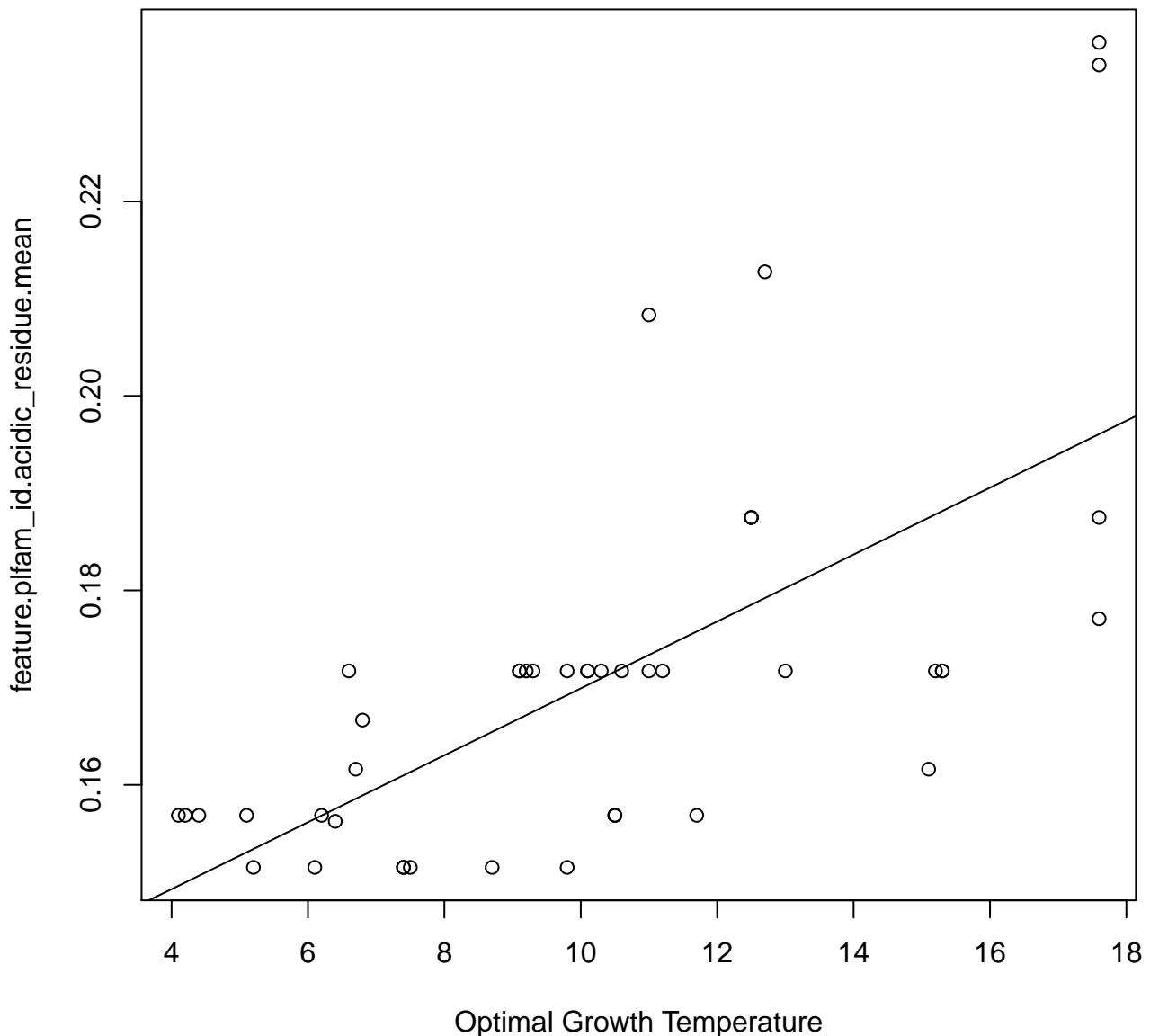
feature.plfam_id.acidic_residue.mean
PLF_28228_00000677
Ornithine carbamoyltransferase (EC 2.1.3.3)



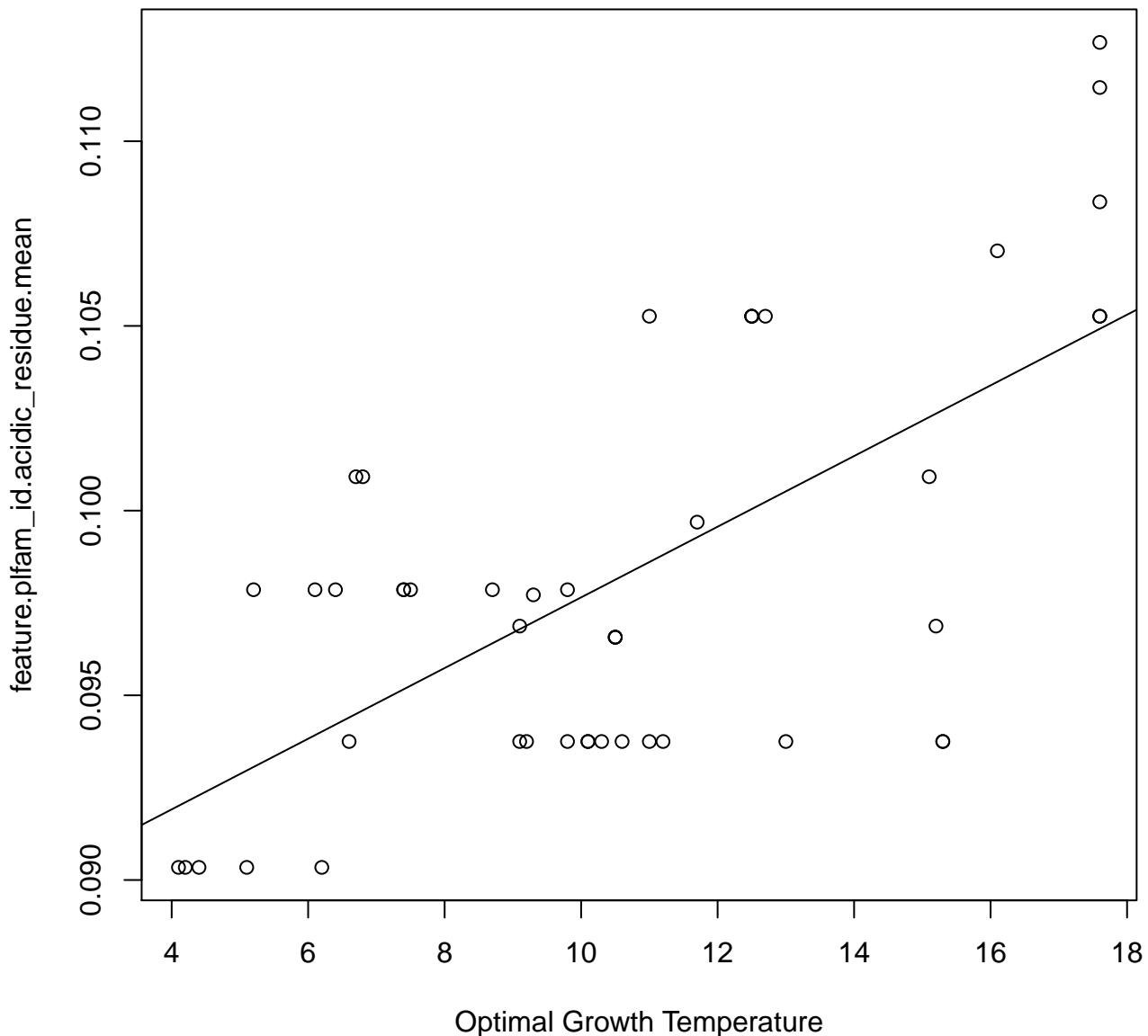
feature.plfam_id.acidic_residue.mean
PLF_28228_00000988
CzcABC family efflux RND transporter, membrane fusion protein



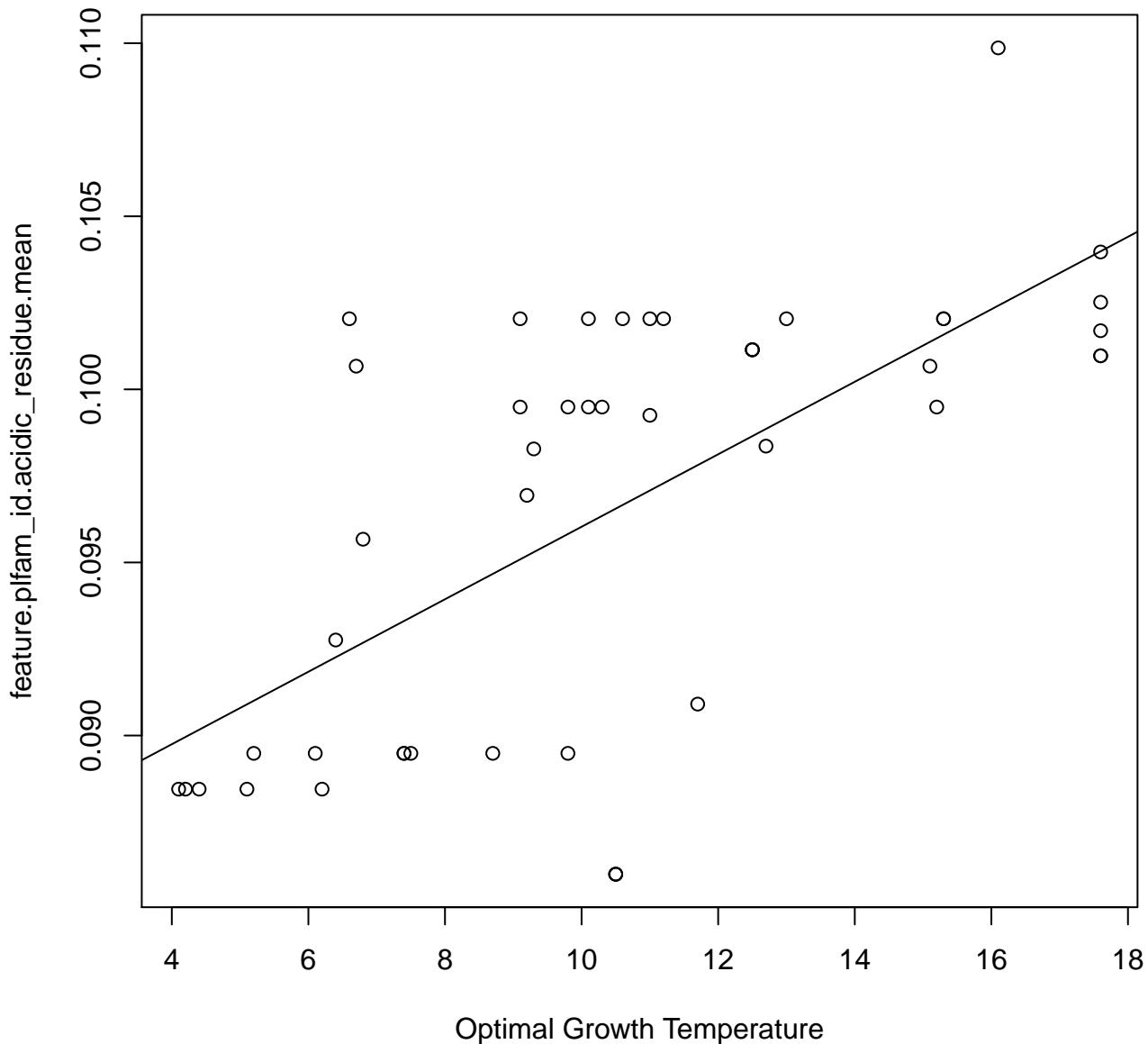
feature.plfam_id.acidic_residue.mean
PLF_28228_00002979
hypothetical protein



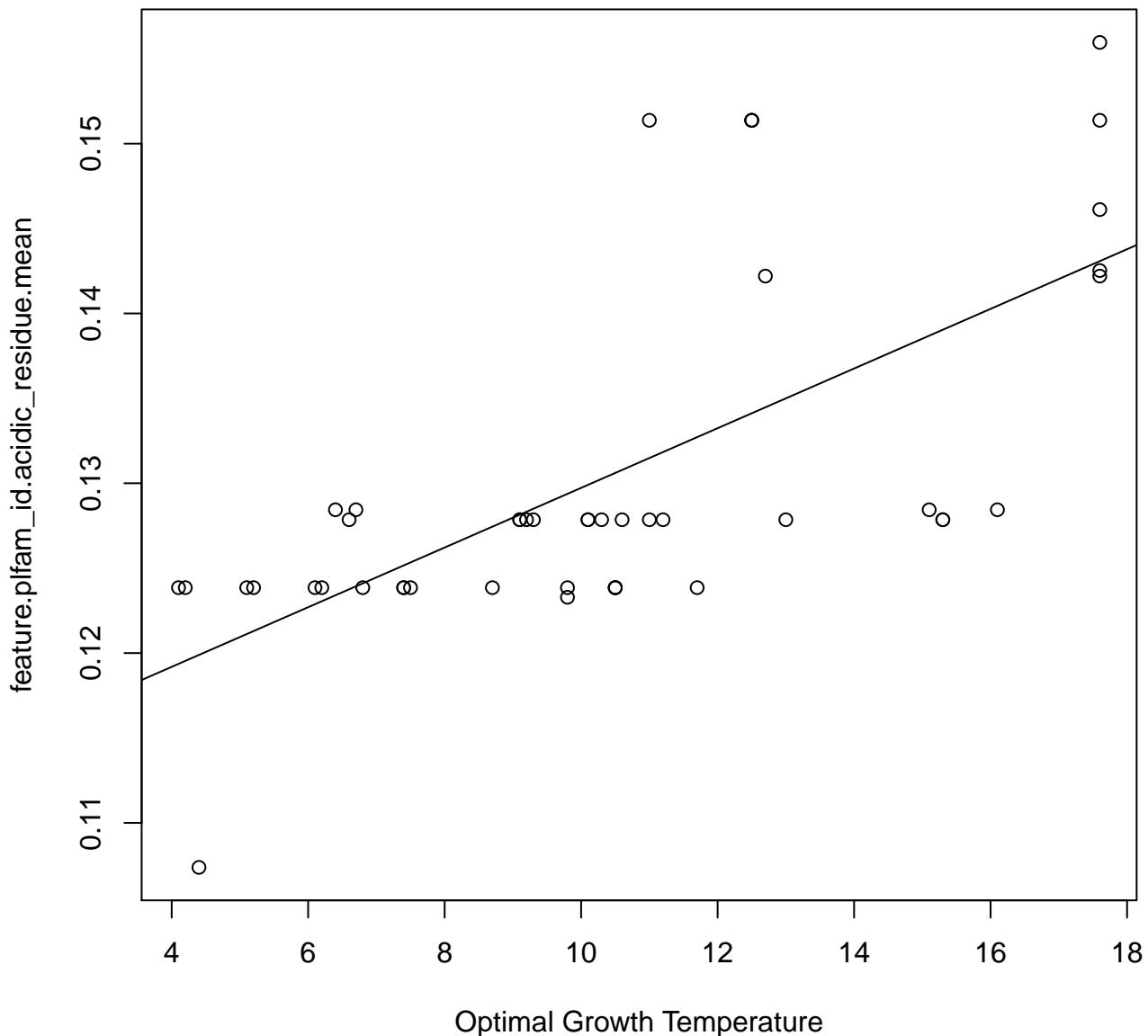
feature.plfam_id.acidic_residue.mean
PLF_28228_00000436
Cytochrome c oxidase (cbb3-type) subunit CcoP (EC 1.9.3.1)



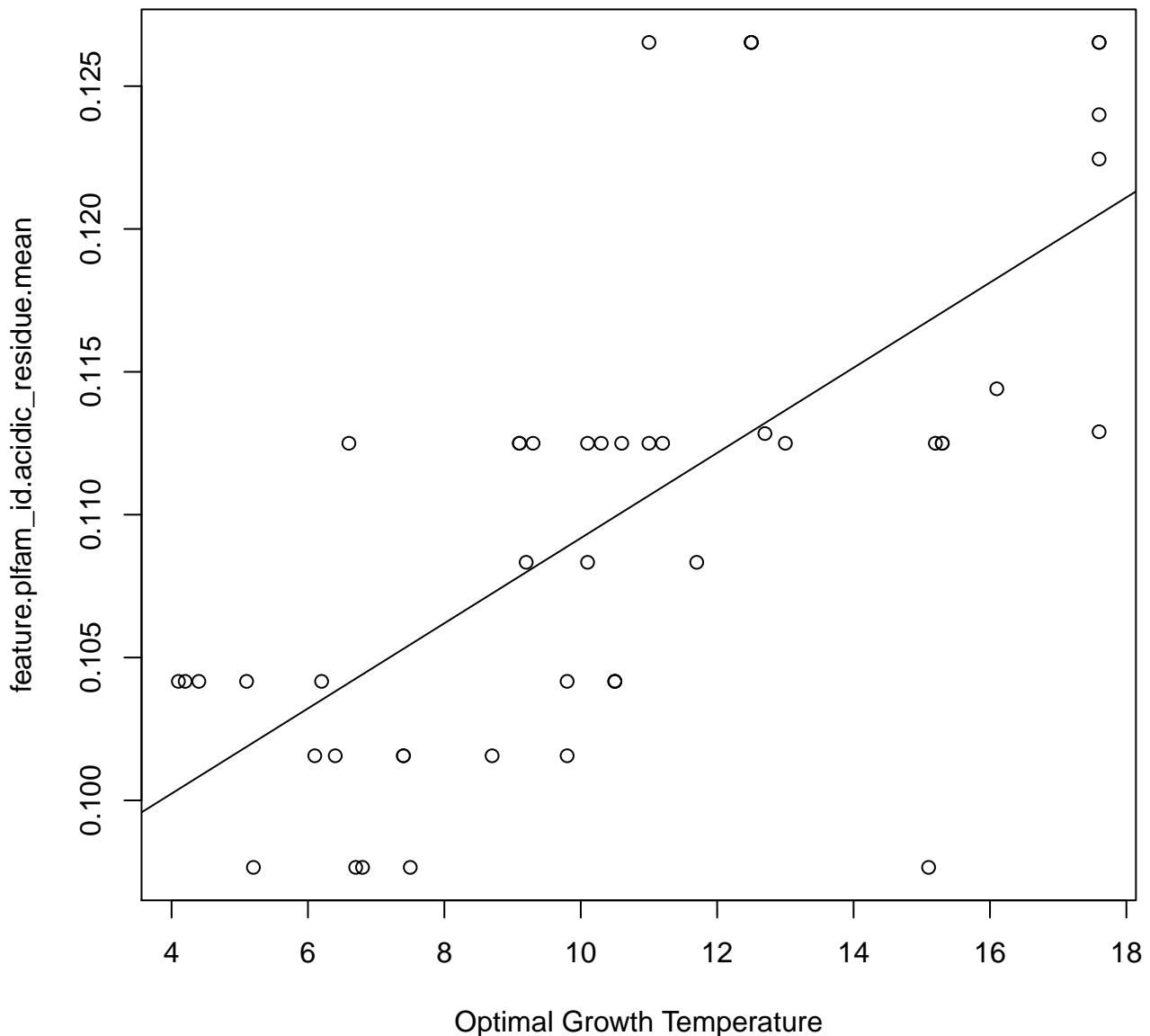
feature.plfam_id.acidic_residue.mean
PLF_28228_00002173
Type IV pilus biogenesis protein PilF



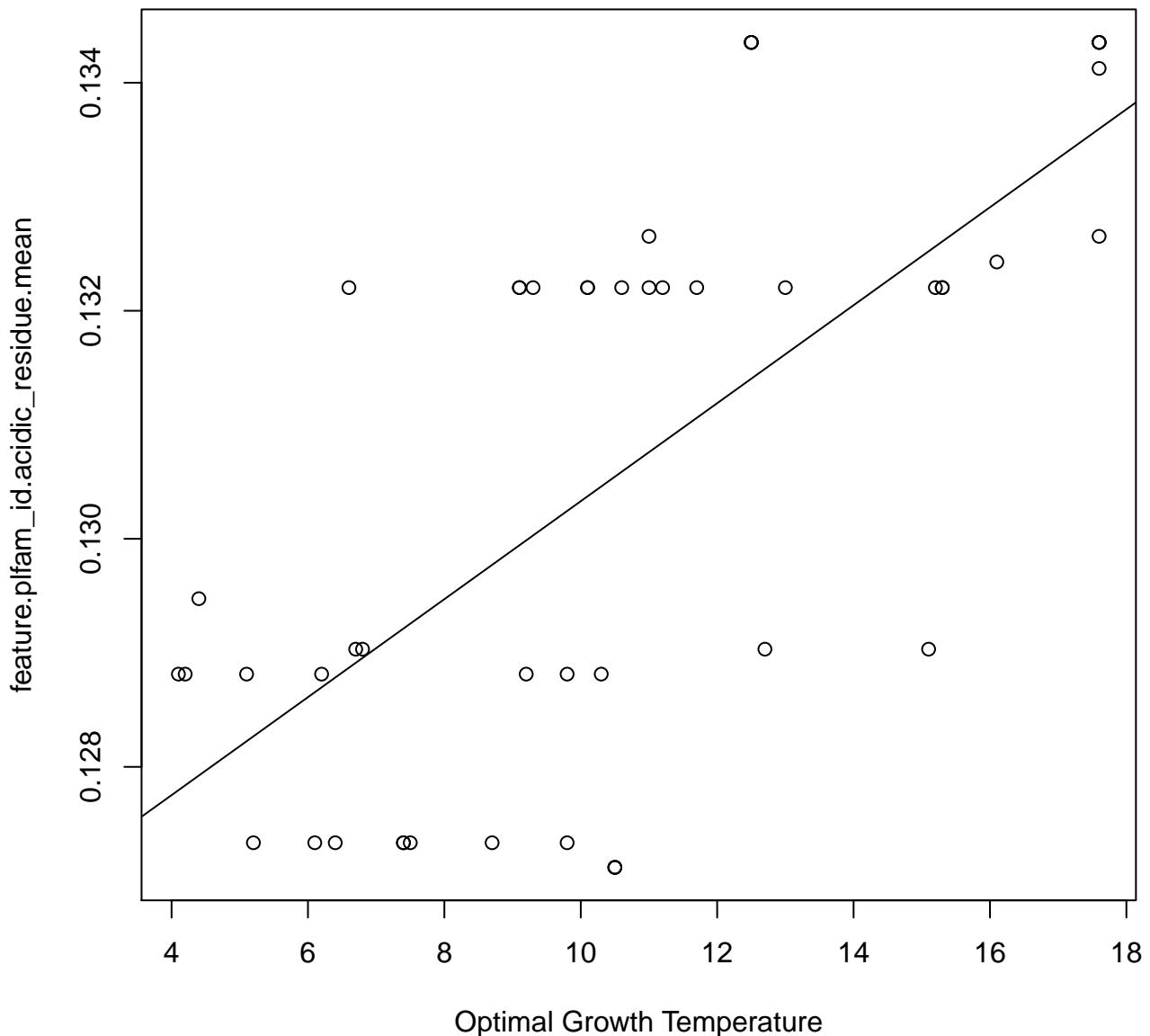
feature.plfam_id.acidic_residue.mean
PLF_28228_00000076
7-cyano-7-deazaguanine synthase (EC 6.3.4.20)



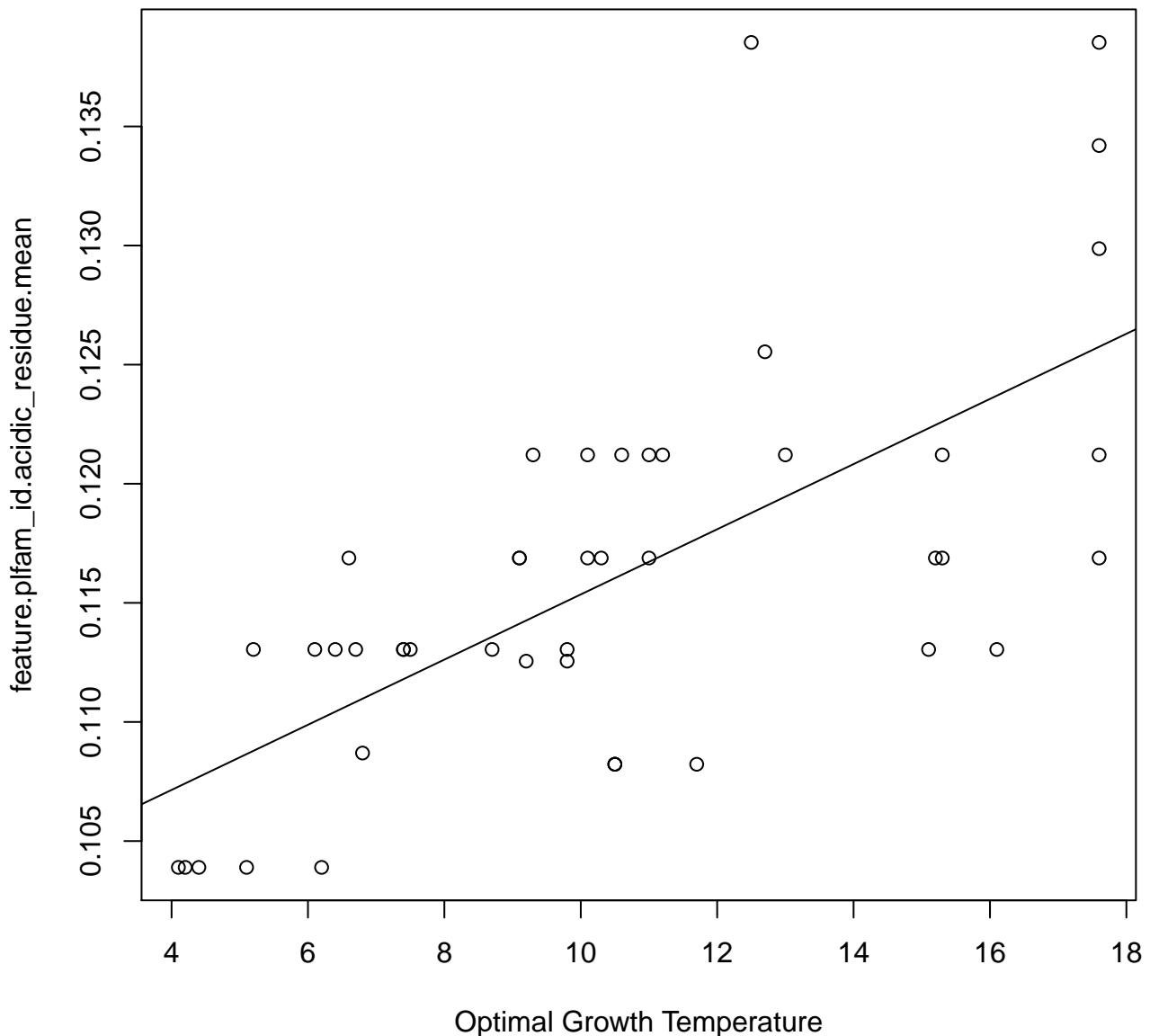
feature.plfam_id.acidic_residue.mean
PLF_28228_00000498
Histidine utilization repressor



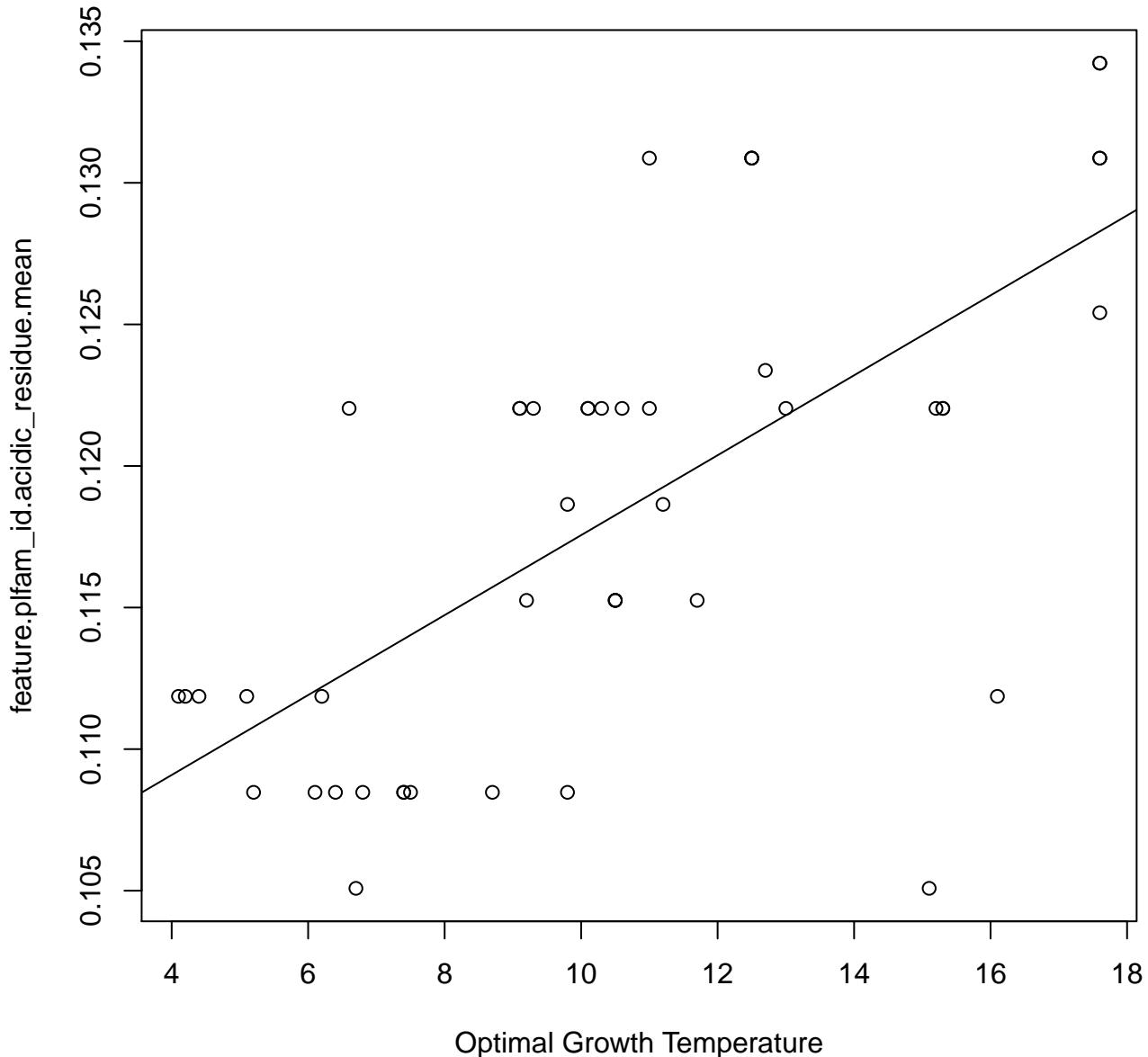
feature.plfam_id.acidic_residue.mean
PLF_28228_00001165
Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)



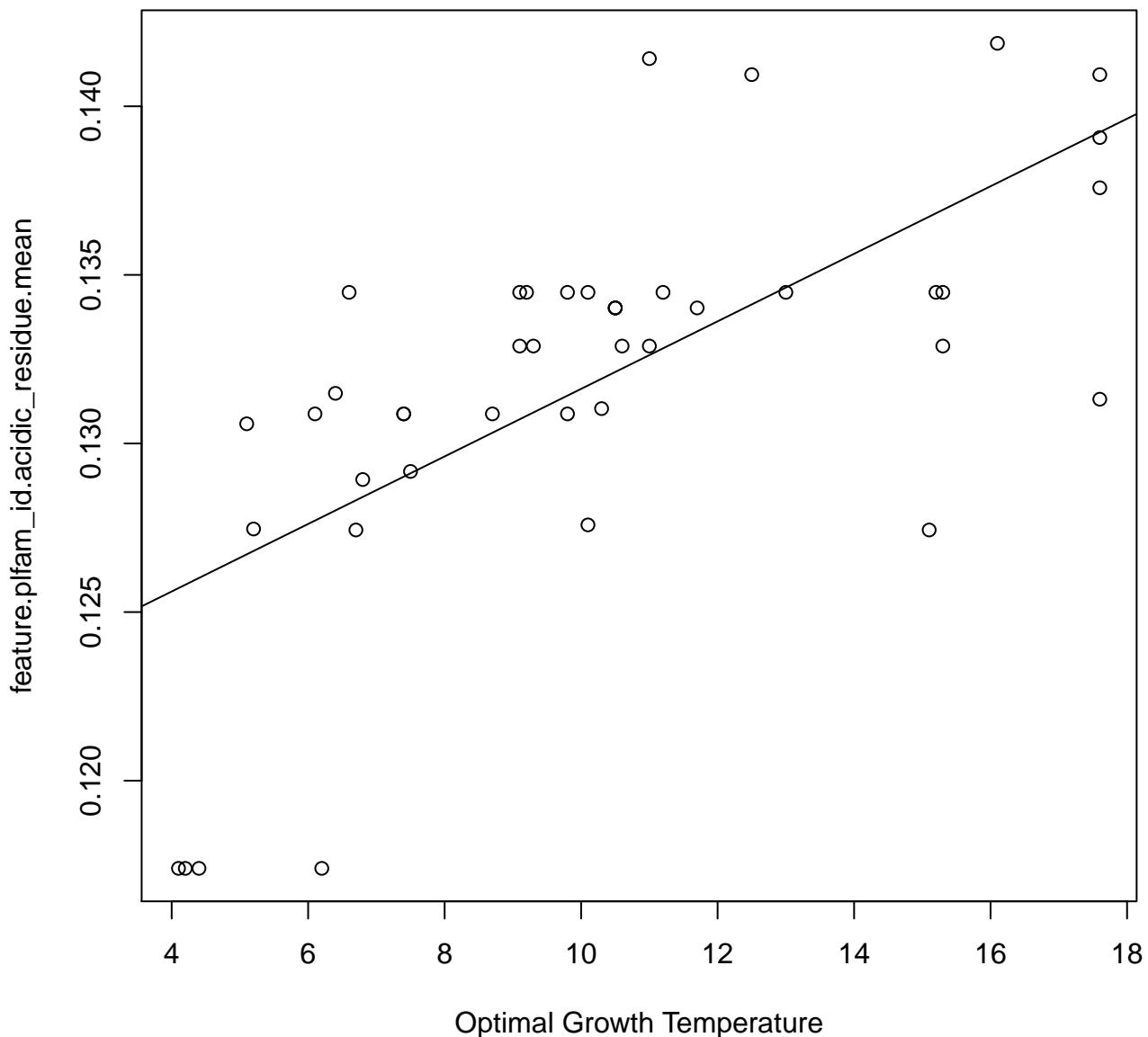
feature.plfam_id.acidic_residue.mean
PLF_28228_00028099
6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type



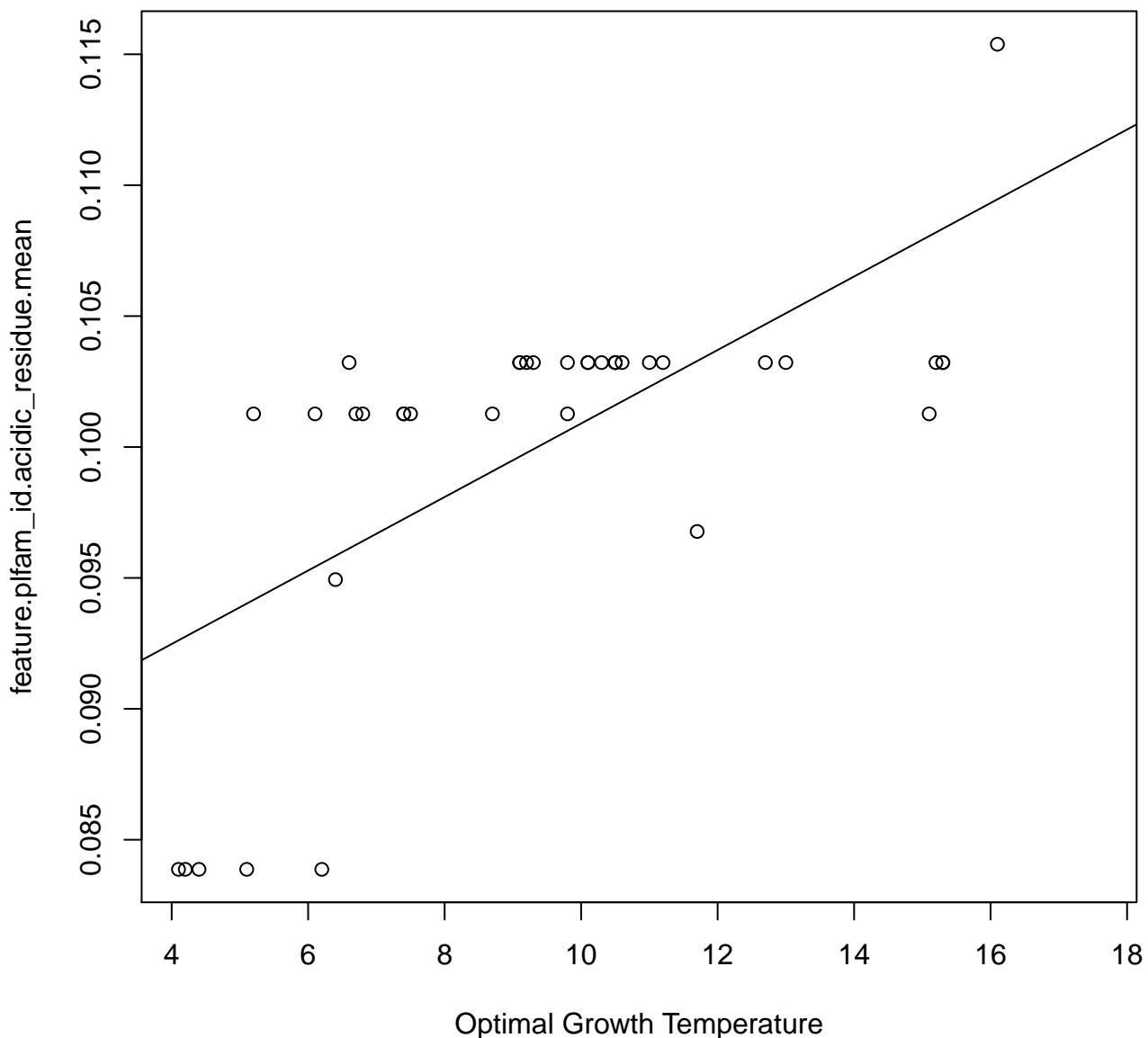
feature.plfam_id.acidic_residue.mean
PLF_28228_00001035
Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)



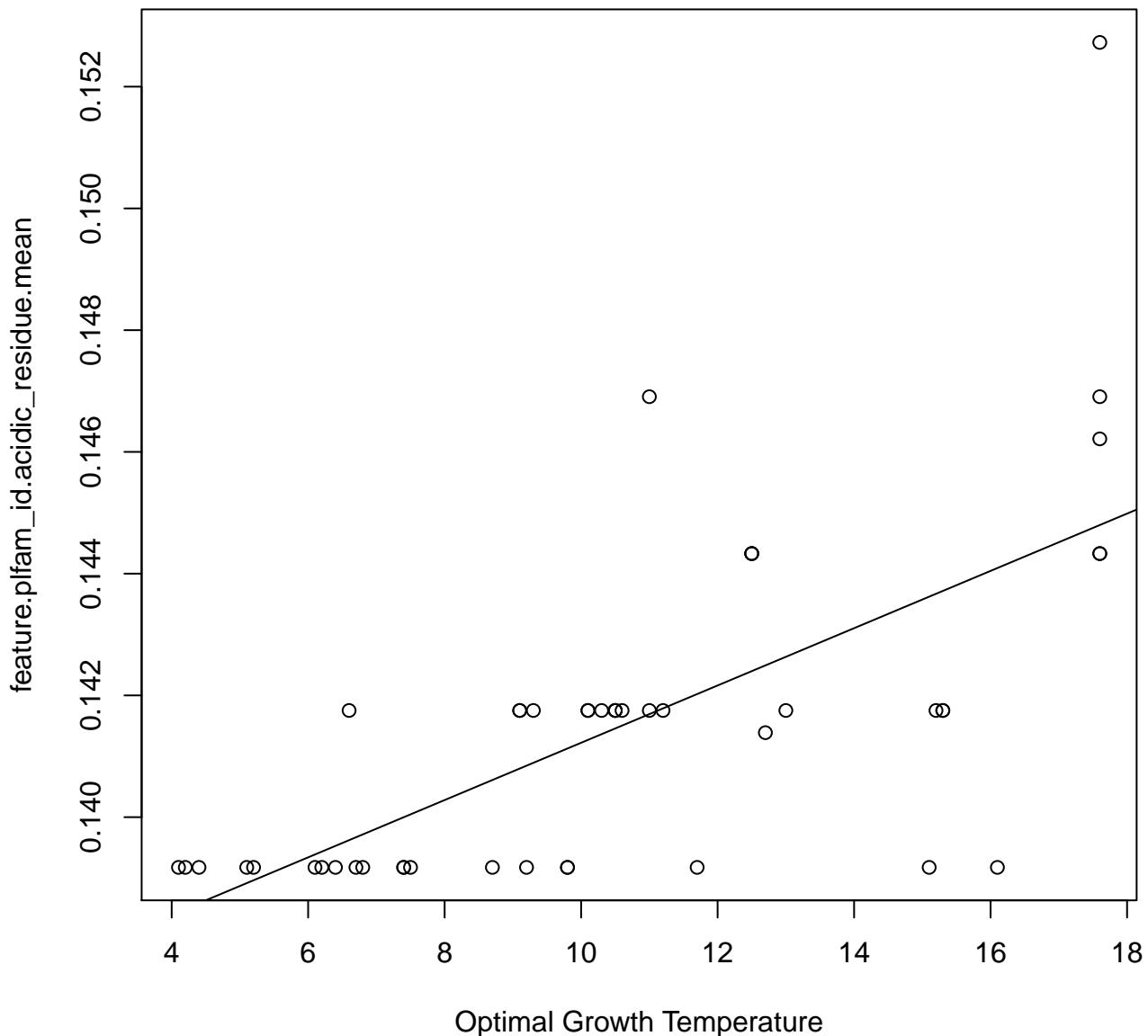
feature.plfam_id.acidic_residue.mean
PLF_28228_00028215
Glutathione S-transferase (EC 2.5.1.18)



feature.plfam_id.acidic_residue.mean
PLF_28228_00015721
Uncharacterized aldehyde oxidase, 2Fe–2S subunit



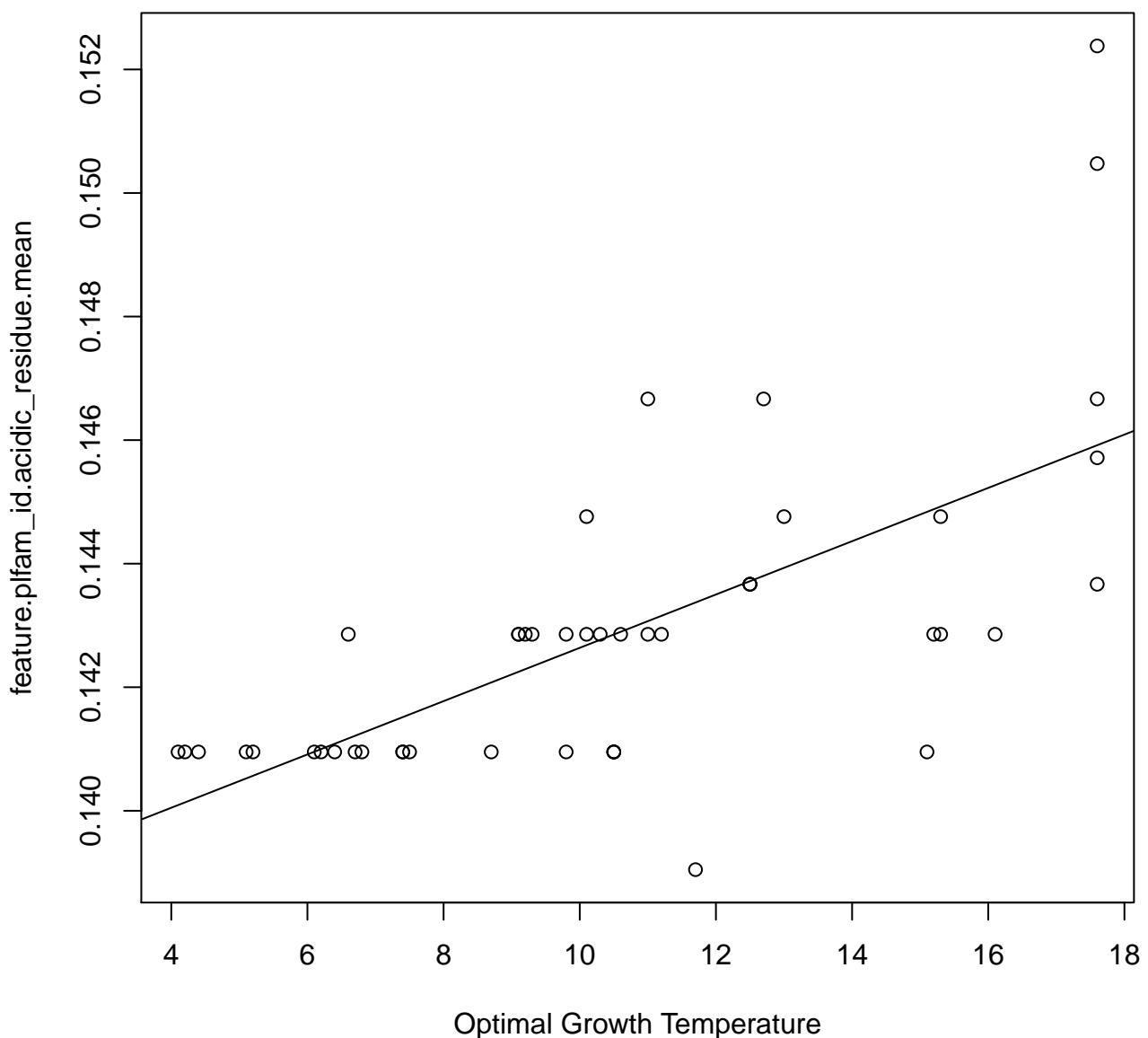
feature.plfam_id.acidic_residue.mean
PLF_28228_00001168
Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)



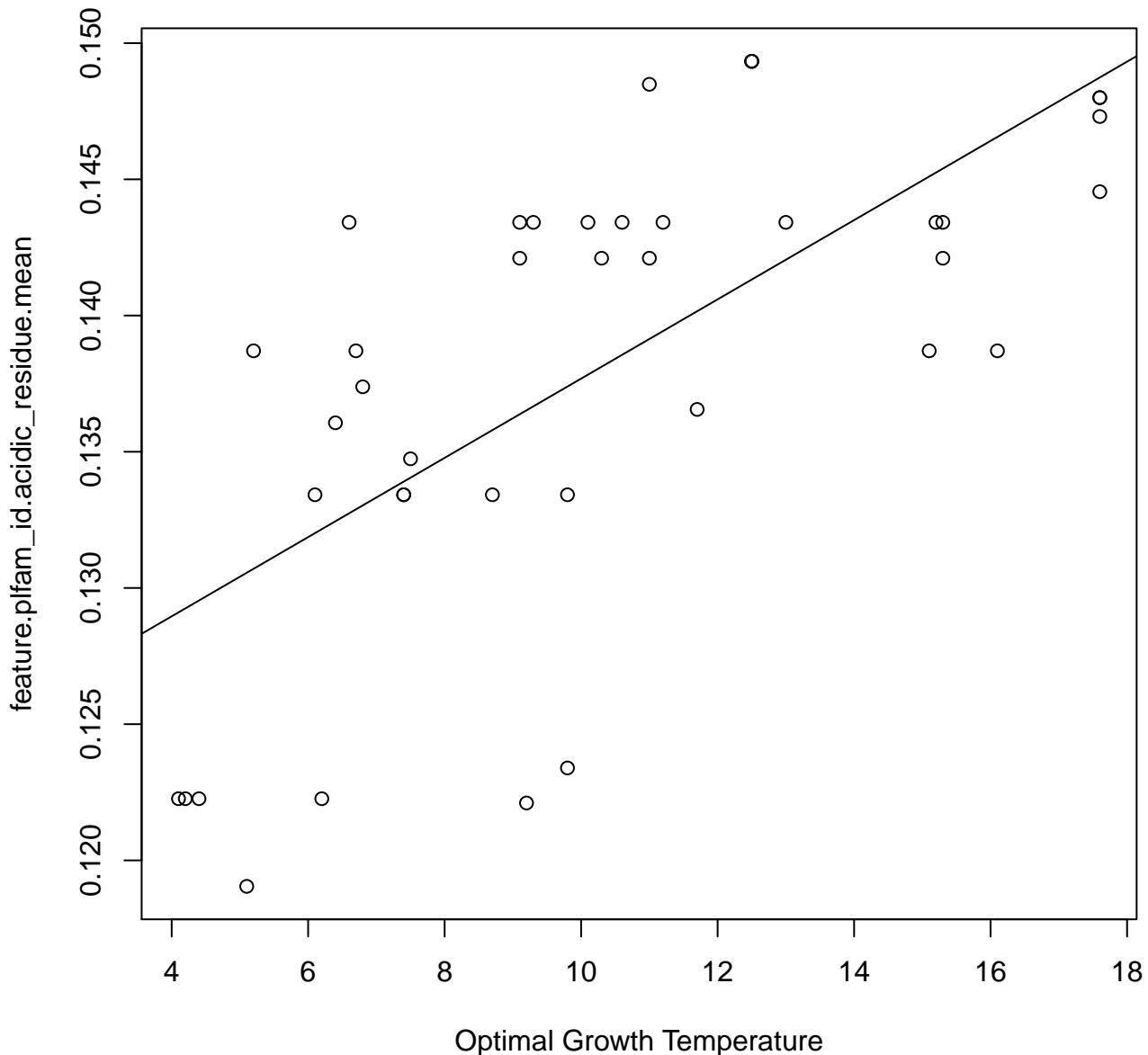
feature.plfam_id.acidic_residue.mean

PLF_28228_00000863

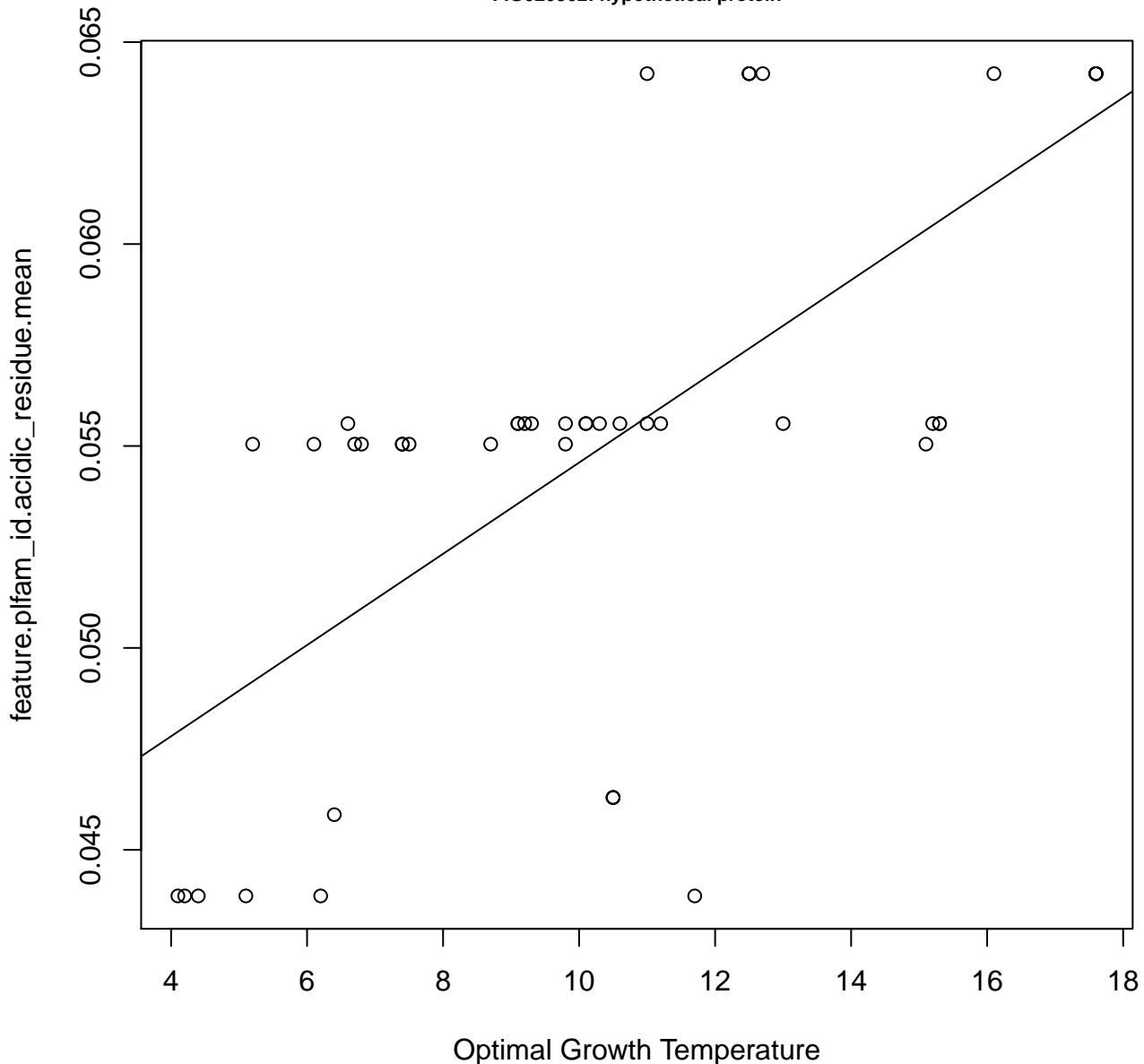
ase [glutamine–hydrolyzing], amidotransferase subunit (EC 6.3.5.2) / GMP synthase [glutamine–hydrolyzing], ATP pyrophosphatase s



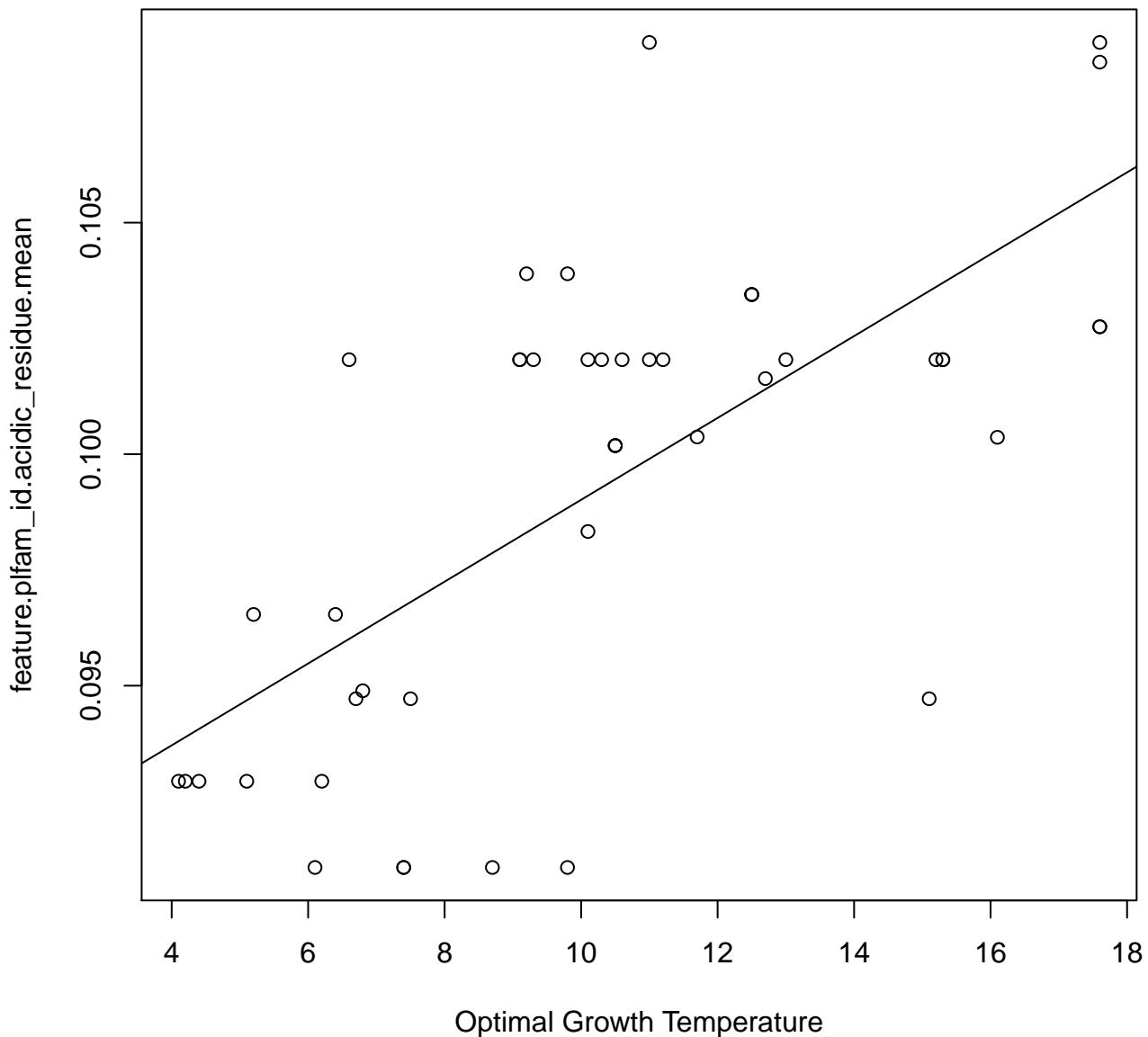
feature.plfam_id.acidic_residue.mean
PLF_28228_00001207
TonB-dependent receptor



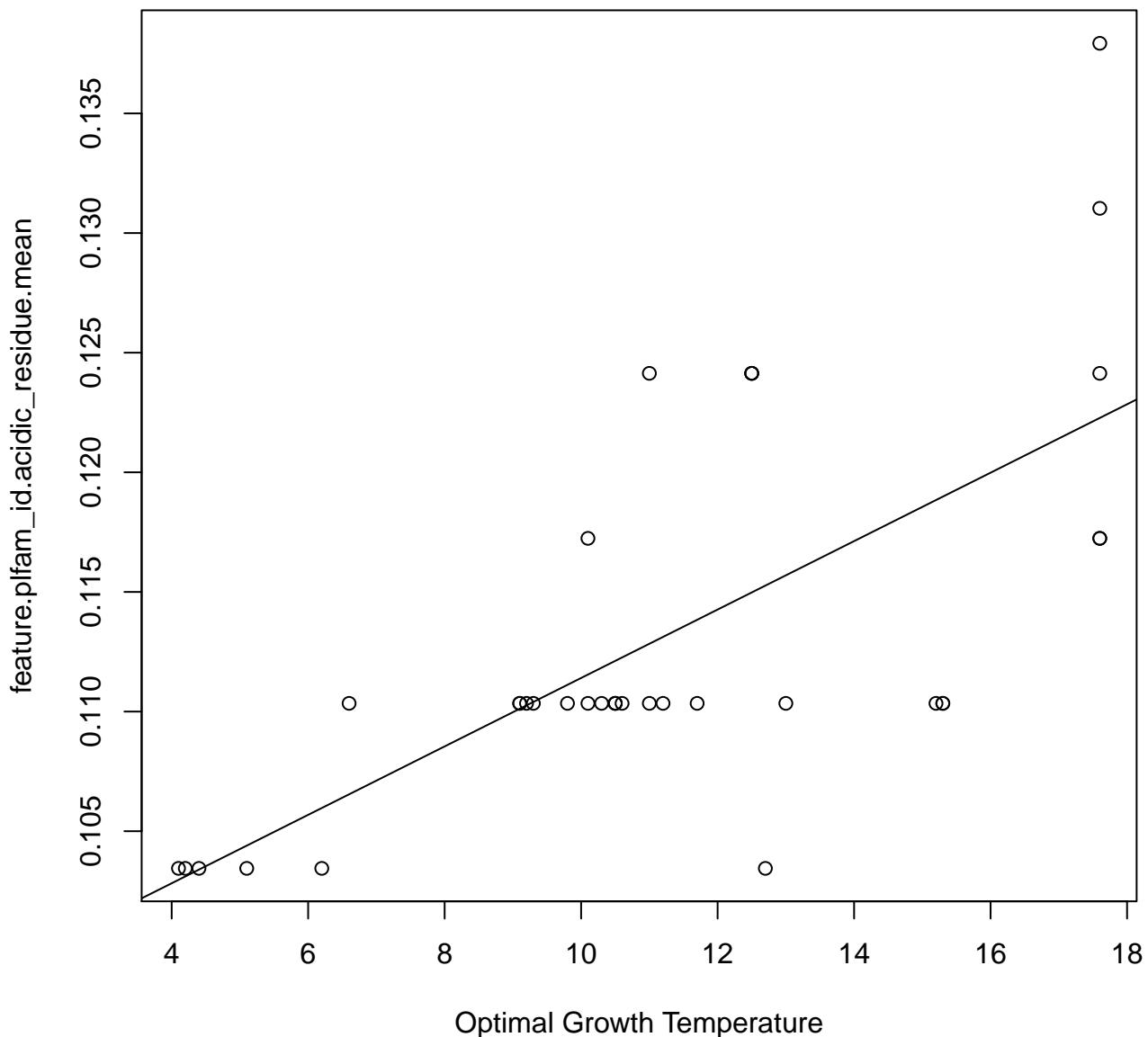
feature.plfam_id.acidic_residue.mean
PLF_28228_00001687
FIG020302: hypothetical protein



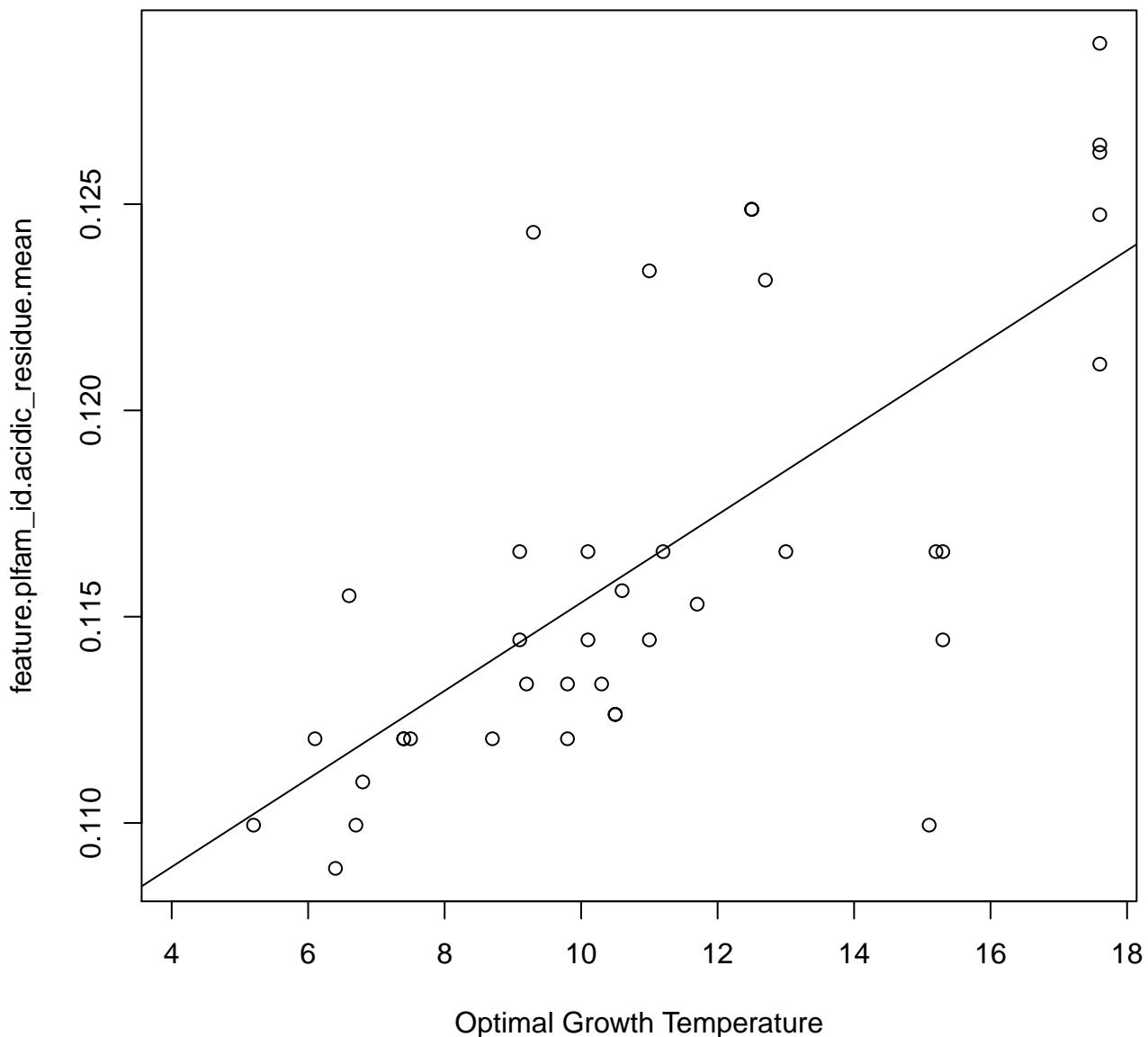
feature.plfam_id.acidic_residue.mean
PLF_28228_00002742
Glucose-6-phosphate isomerase (EC 5.3.1.9)



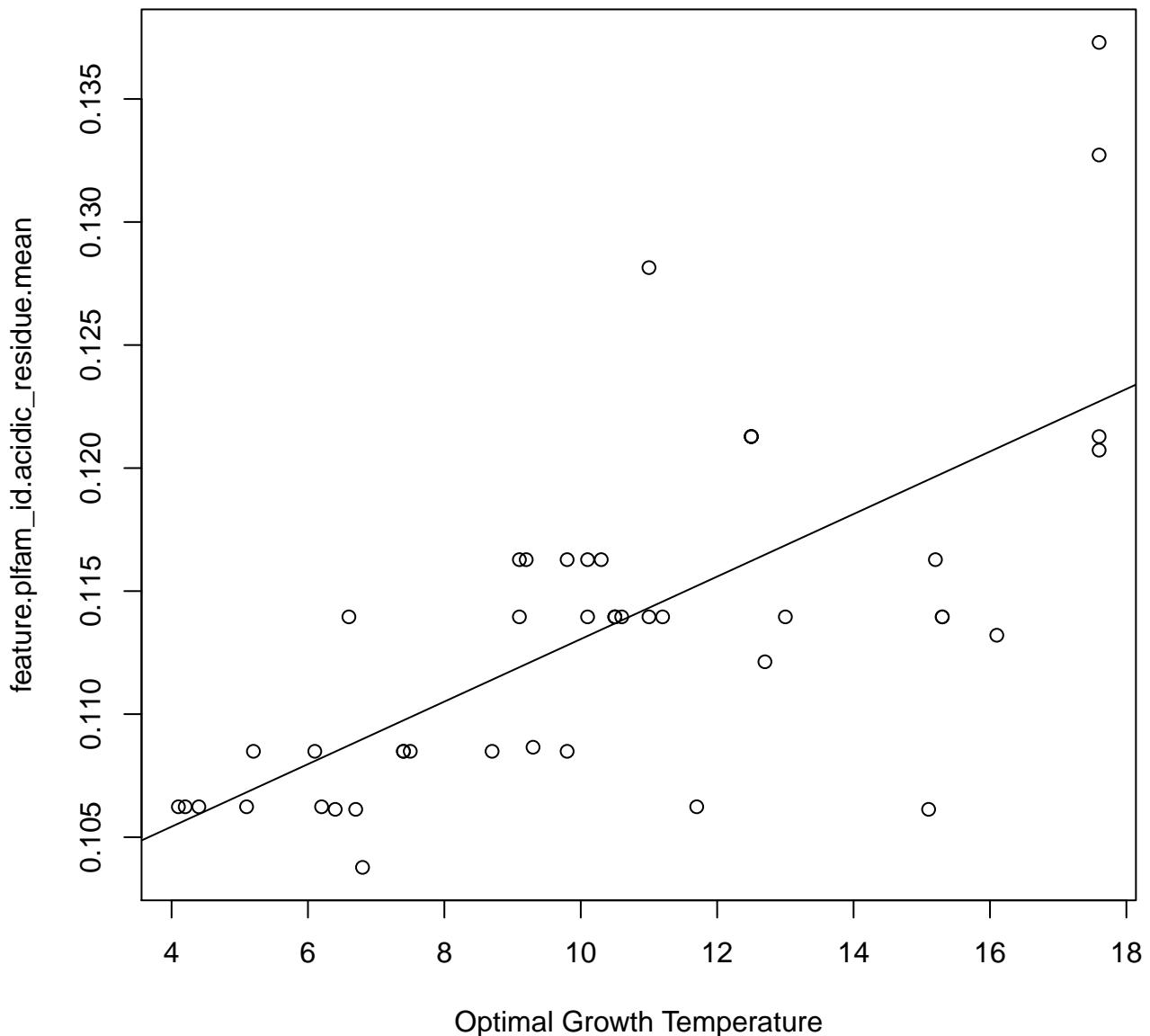
feature.plfam_id.acidic_residue.mean
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D-aminoacyl-tRNA deacylase (EC 3.1.1.96)



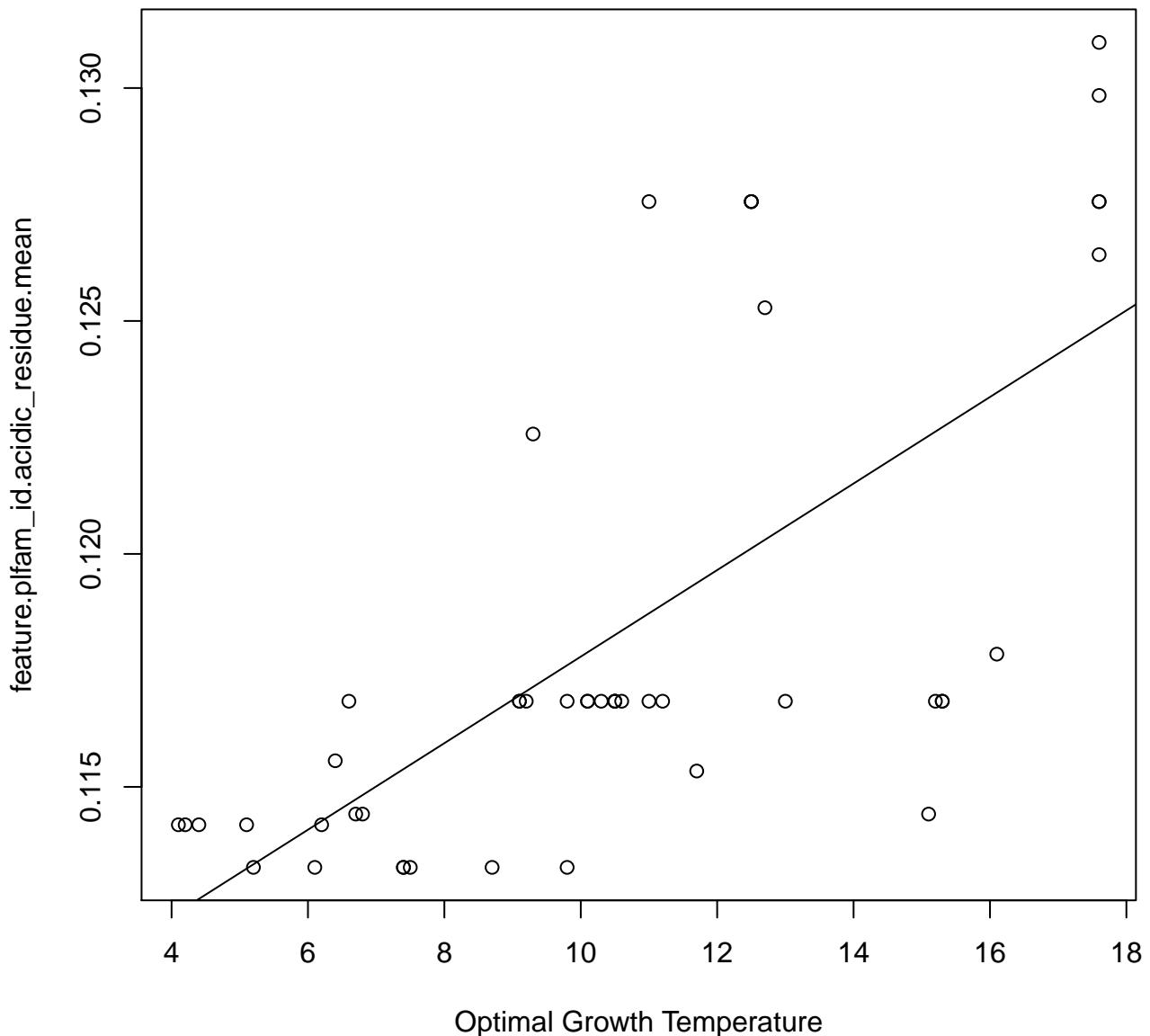
feature.plfam_id.acidic_residue.mean
PLF_28228_00002166
Pullulanase (EC 3.2.1.41)



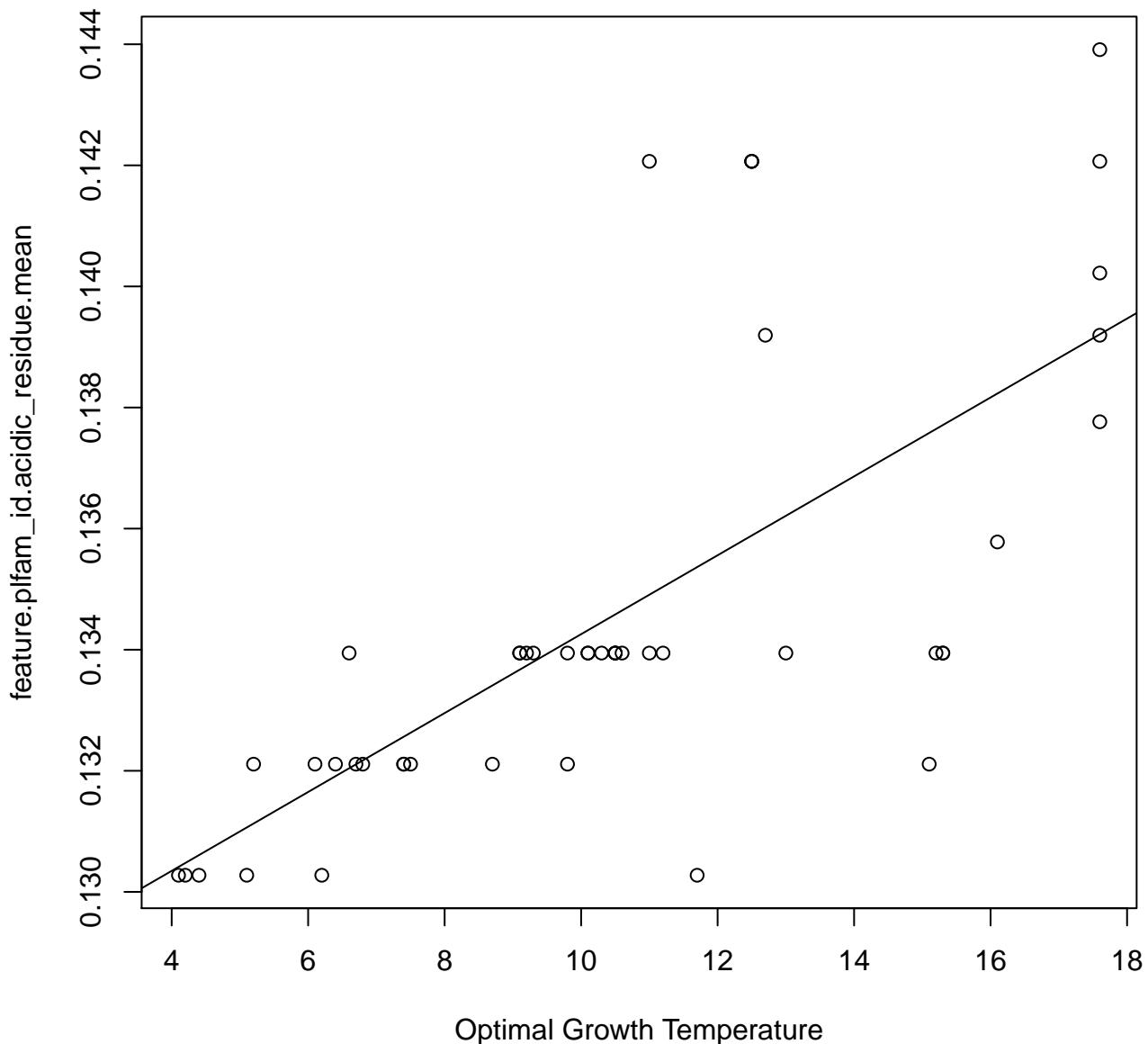
feature.plfam_id.acidic_residue.mean
PLF_28228_00000365
Dihydrofolate synthase (EC 6.3.2.12) @ Folylpolyglutamate synthase (EC 6.3.2.17)



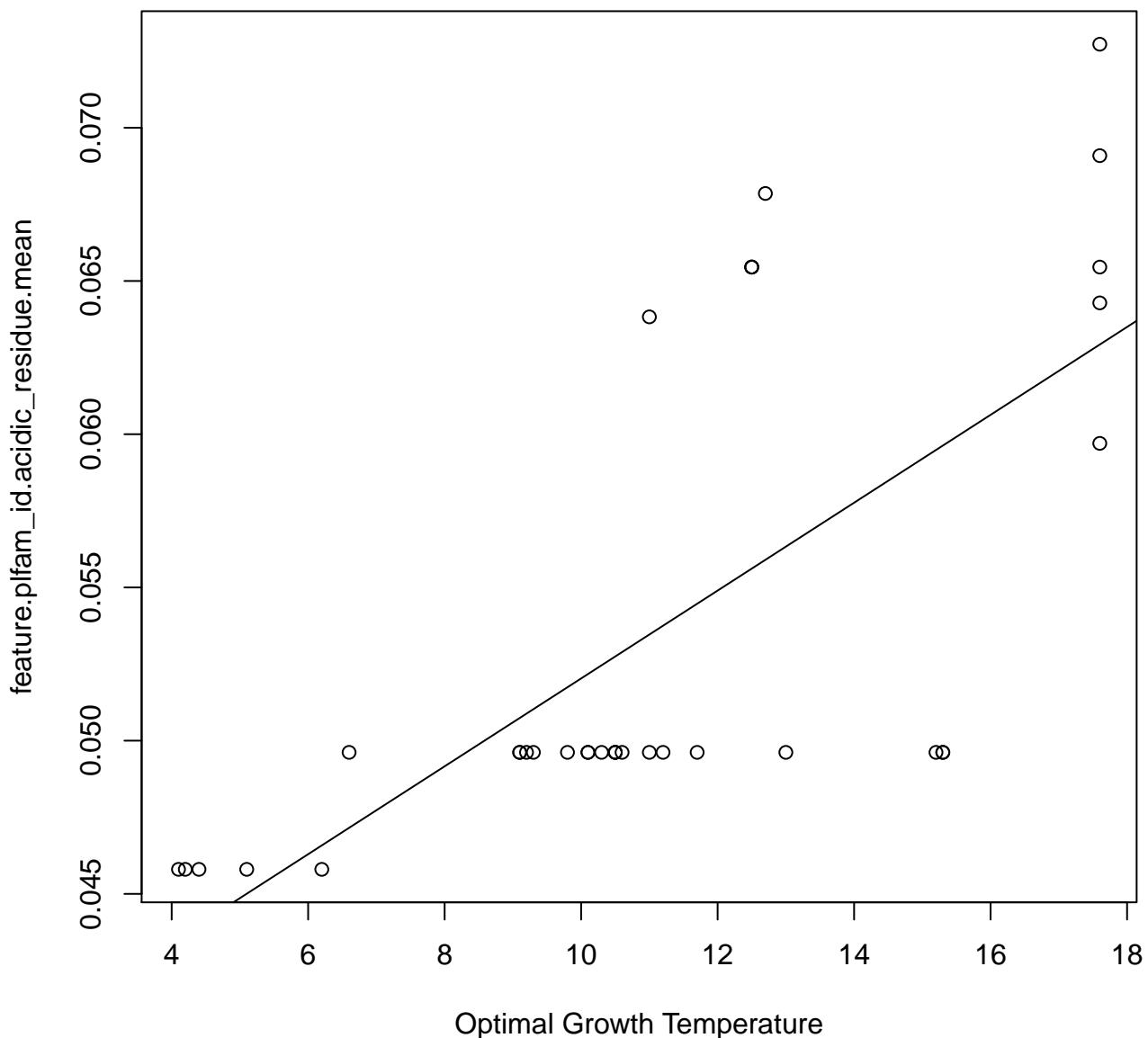
feature.plfam_id.acidic_residue.mean
PLF_28228_00001314
[Protein-PII] uridylyltransferase (EC 2.7.7.59) / [Protein-PII]-UMP uridylyl-removing enzyme



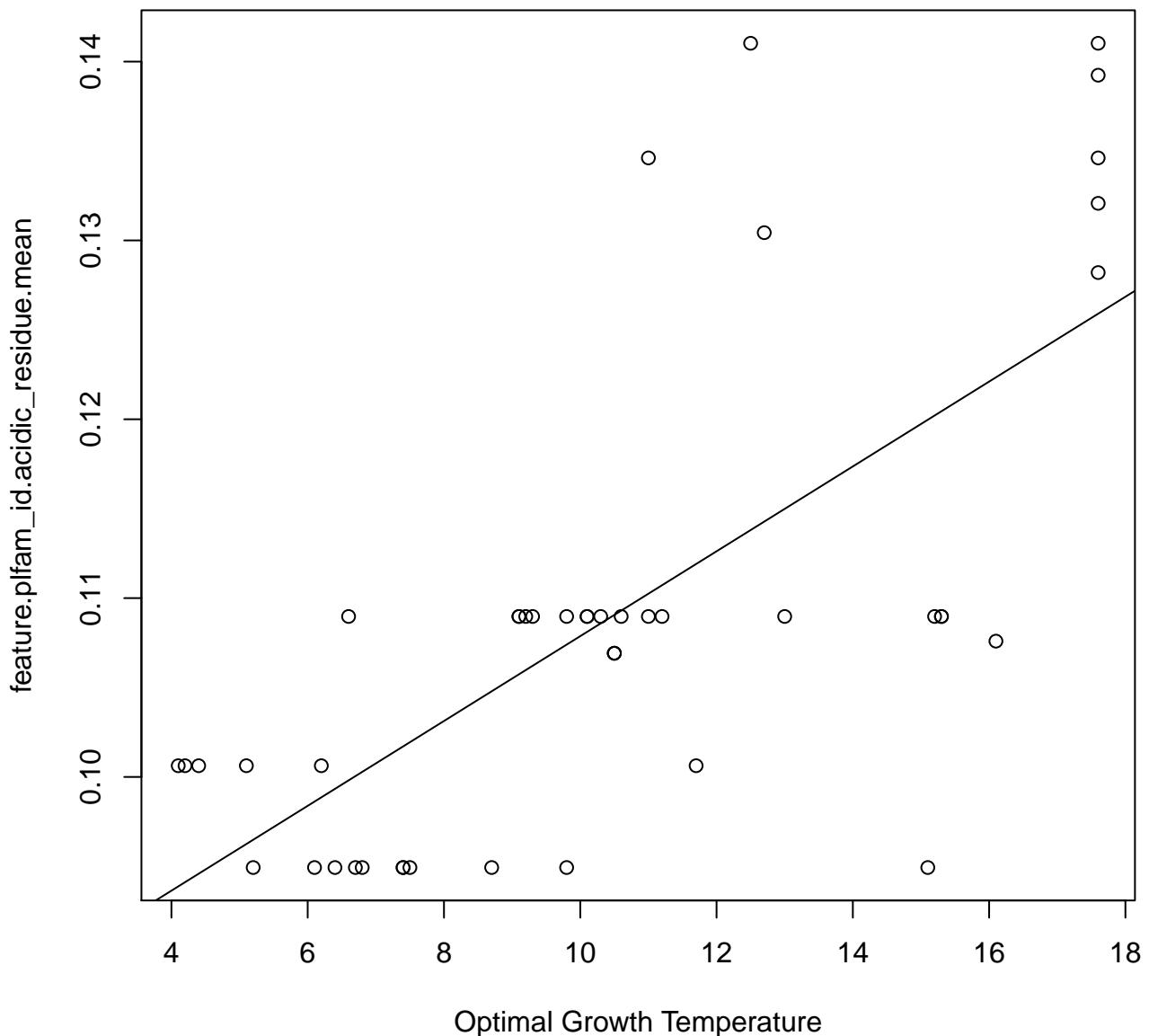
feature.plfam_id.acidic_residue.mean
PLF_28228_00000542
CTP synthase (EC 6.3.4.2)



feature.plfam_id.acidic_residue.mean
PLF_28228_00001359
hypothetical protein



feature.plfam_id.acidic_residue.mean
PLF_28228_00016412
DNA polymerase III chi subunit (EC 2.7.7.7)

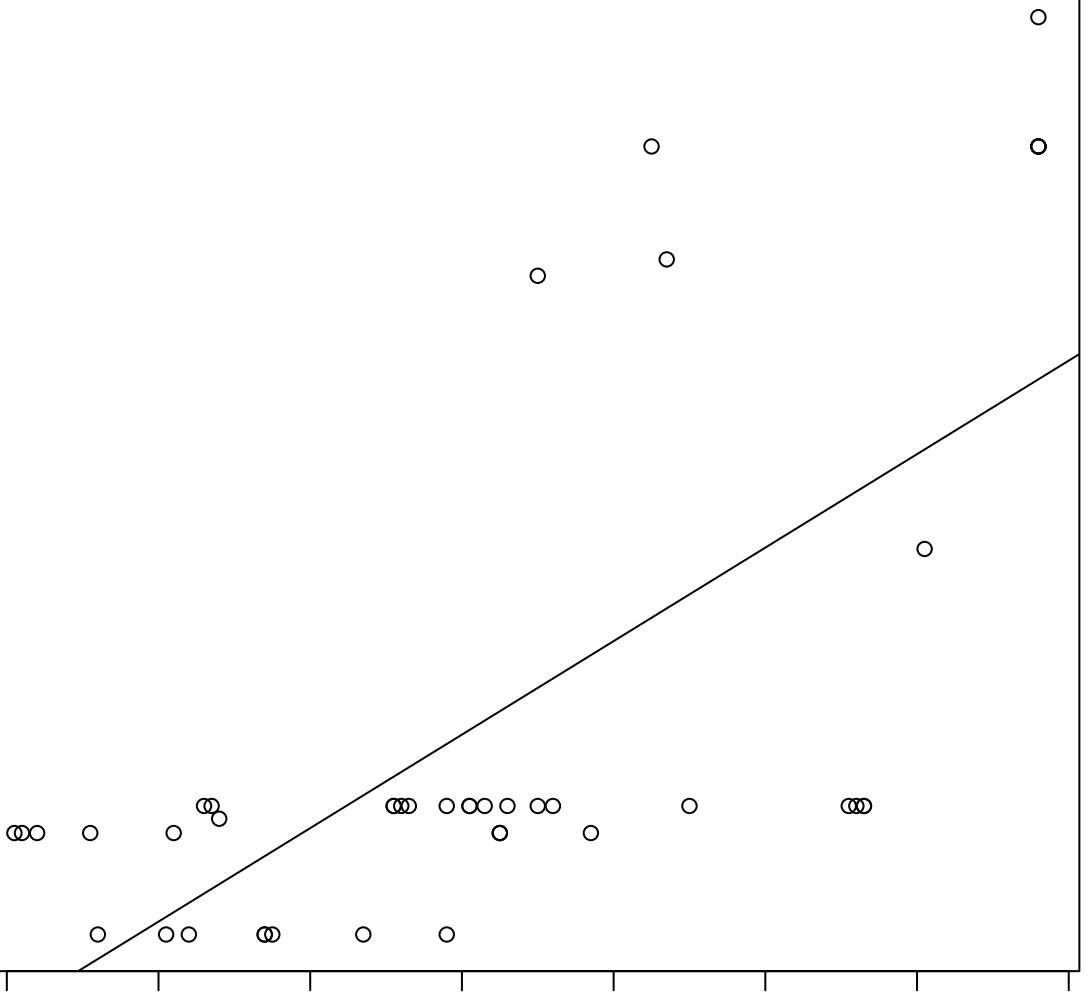


feature.plfam_id.acidic_residue.mean
PLF_28228_00027966
Stringent starvation protein B

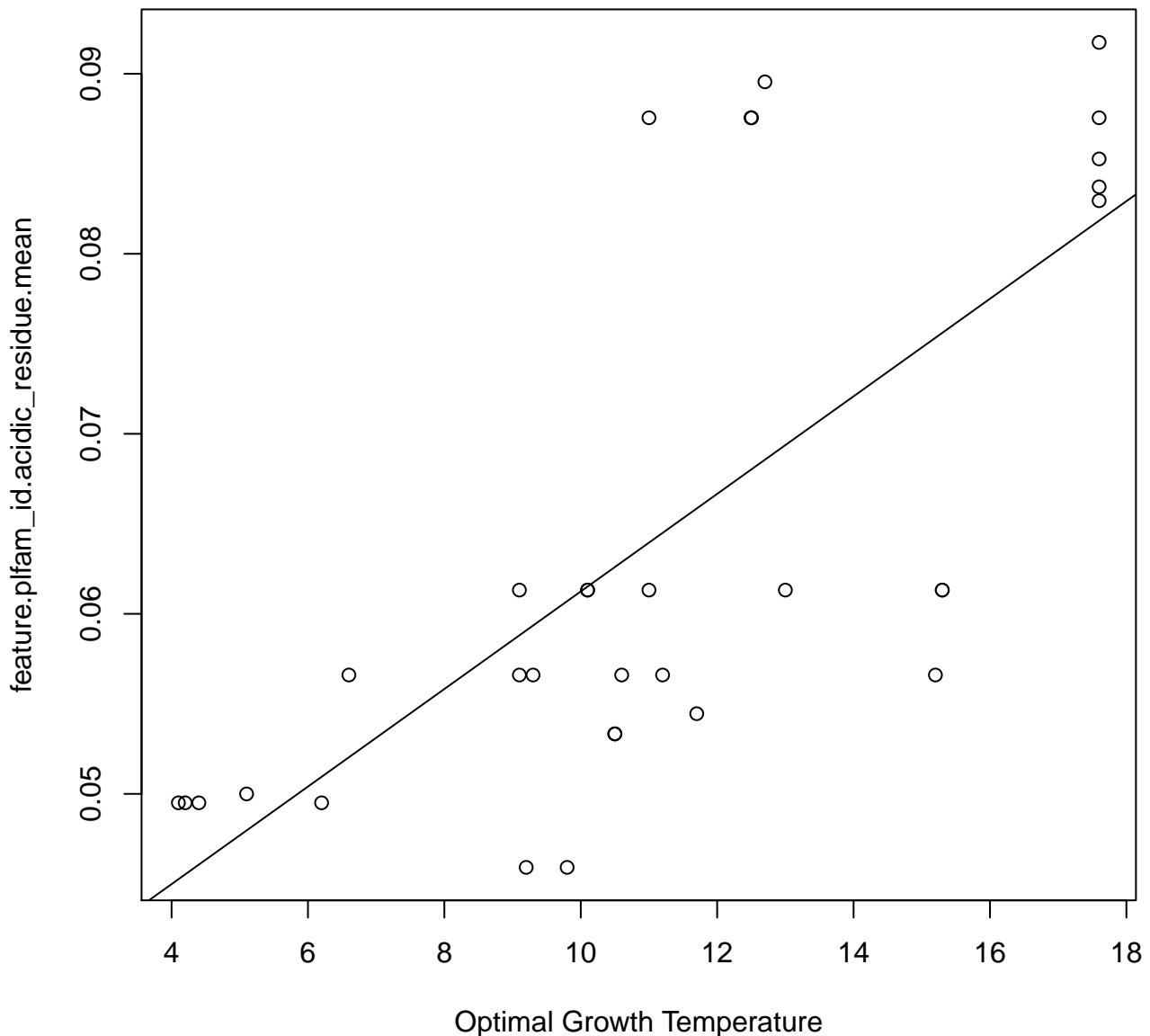
feature.plfam_id.acidic_residue.mean

4 6 8 10 12 14 16 18

Optimal Growth Temperature



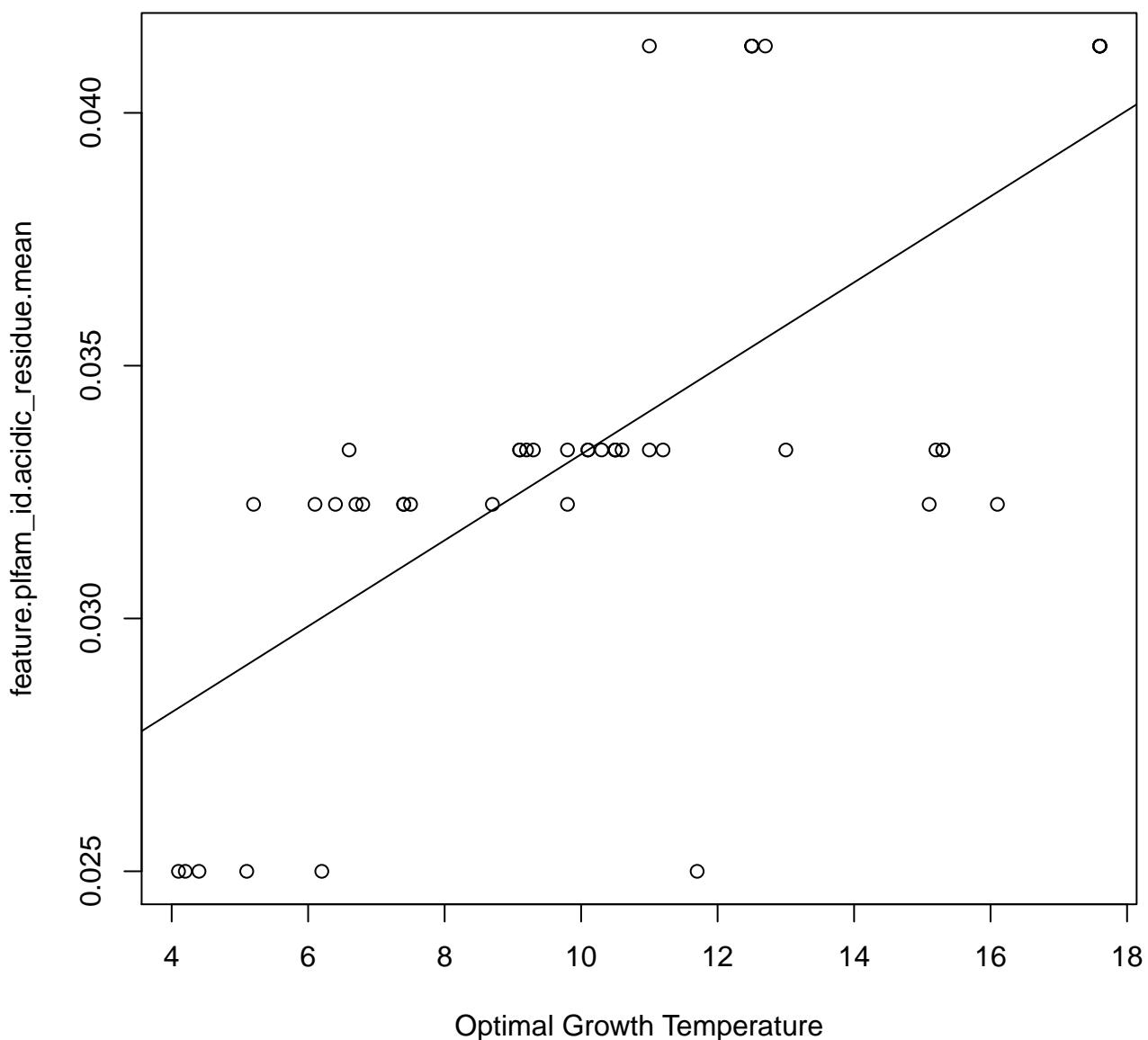
feature.plfam_id.acidic_residue.mean
PLF_28228_00002079
Soluble lytic murein transglycosylase



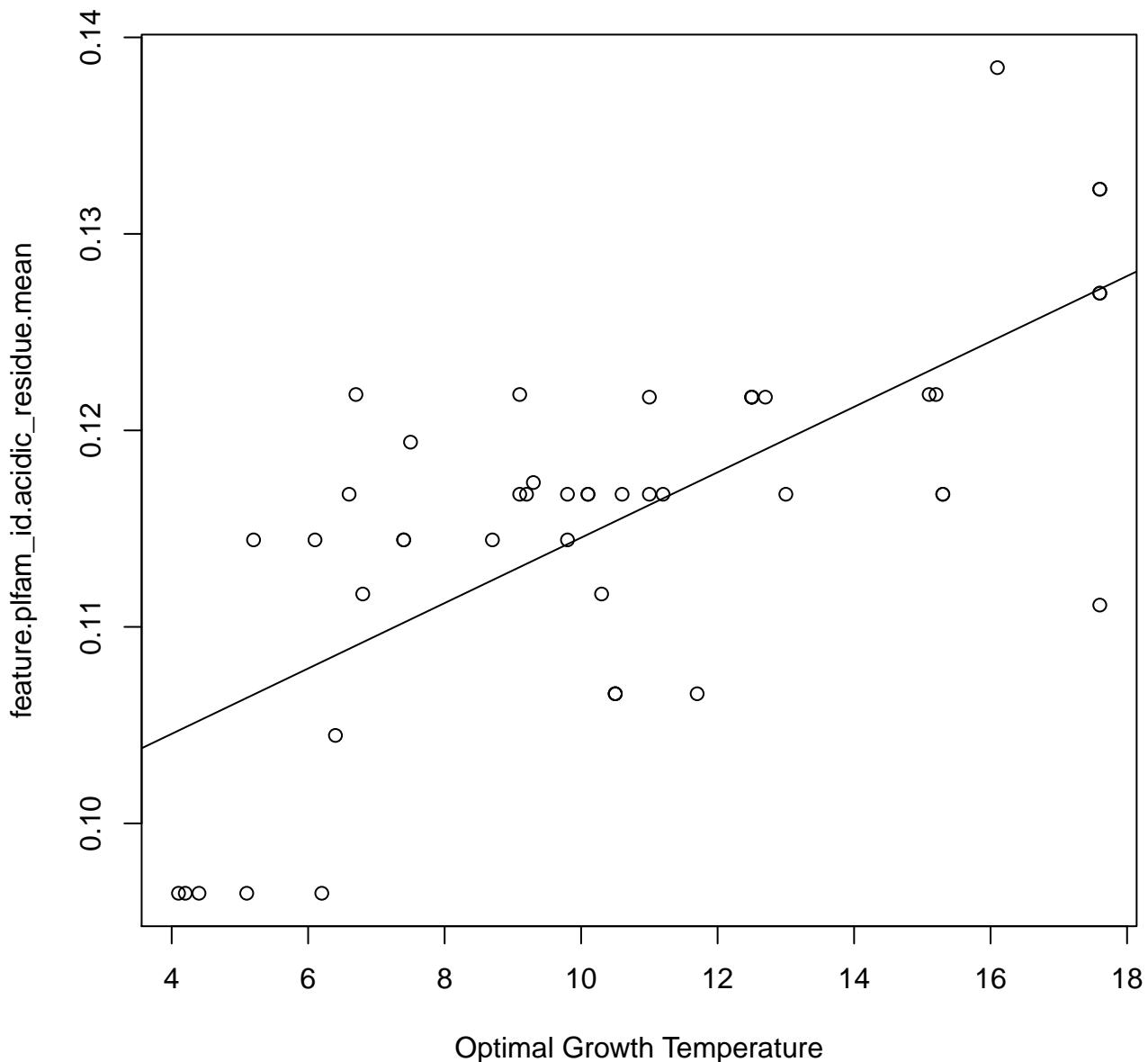
feature.plfam_id.acidic_residue.mean

PLF_28228_00001535

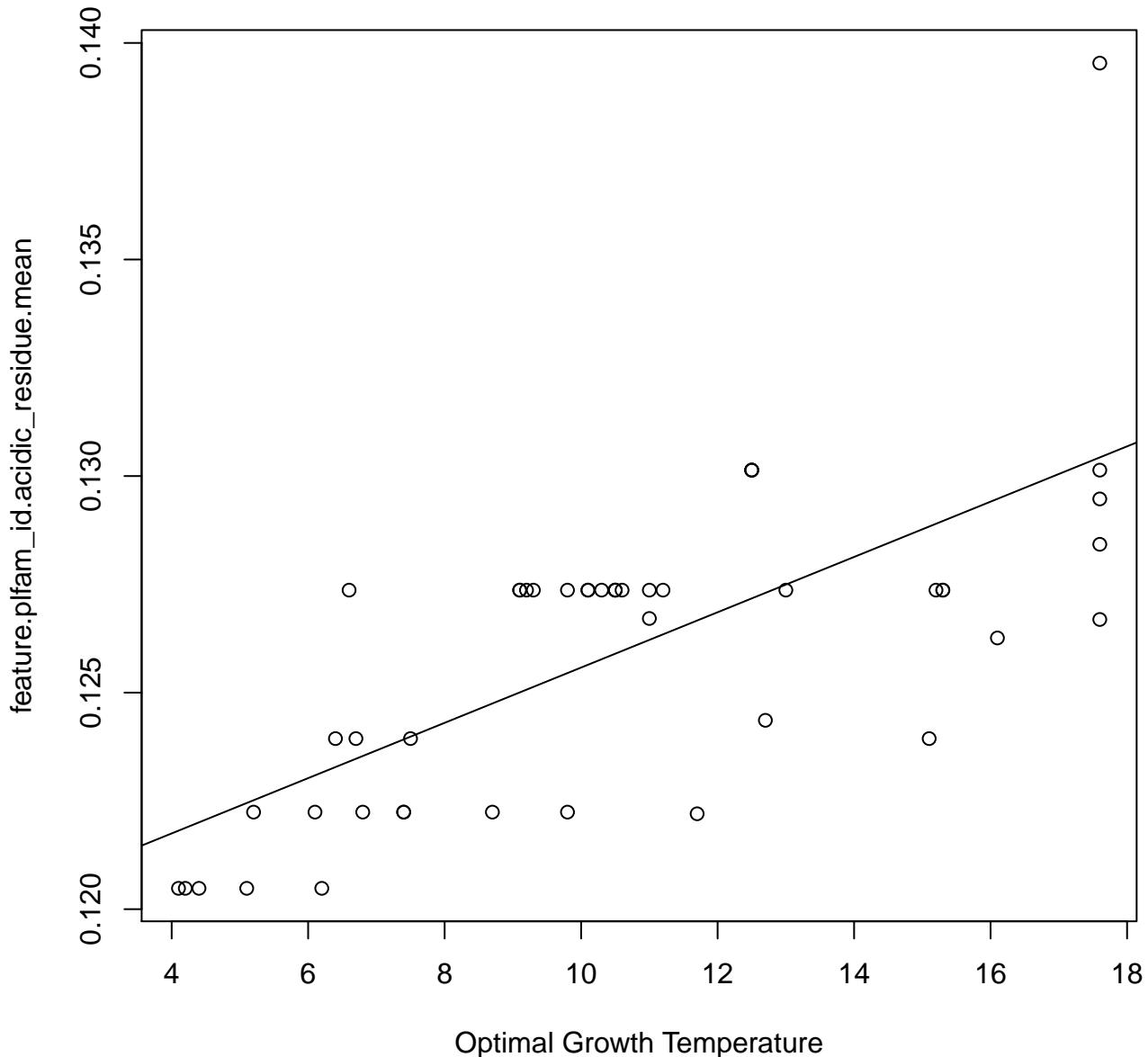
FIG002082: Protein SirB2



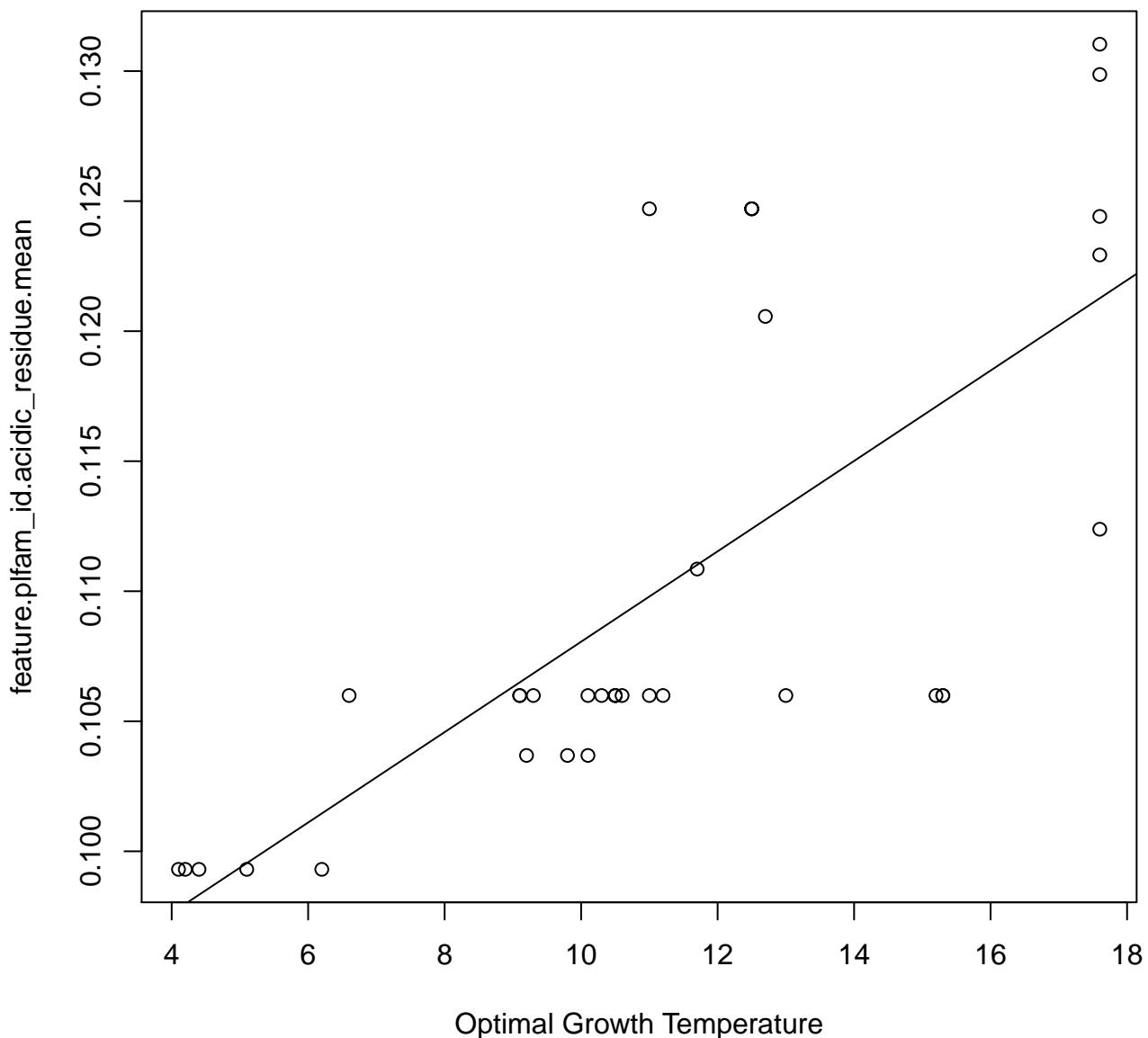
feature.plfam_id.acidic_residue.mean
PLF_28228_00000212
1,6-anhydro-N-acetylMuramyl-L-alanine amidase



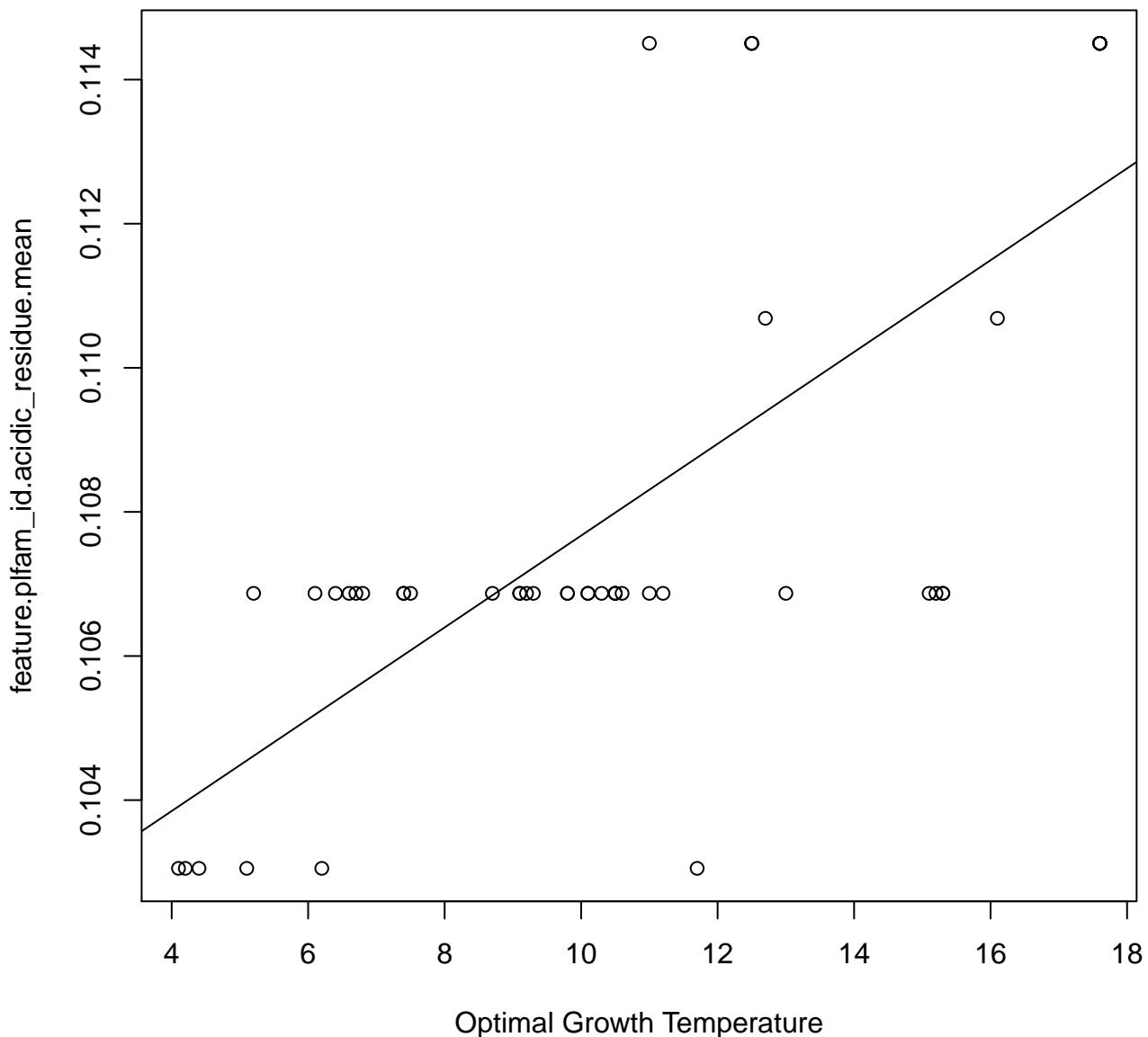
feature.plfam_id.acidic_residue.mean
PLF_28228_00001155
Single-stranded-DNA-specific exonuclease RecJ



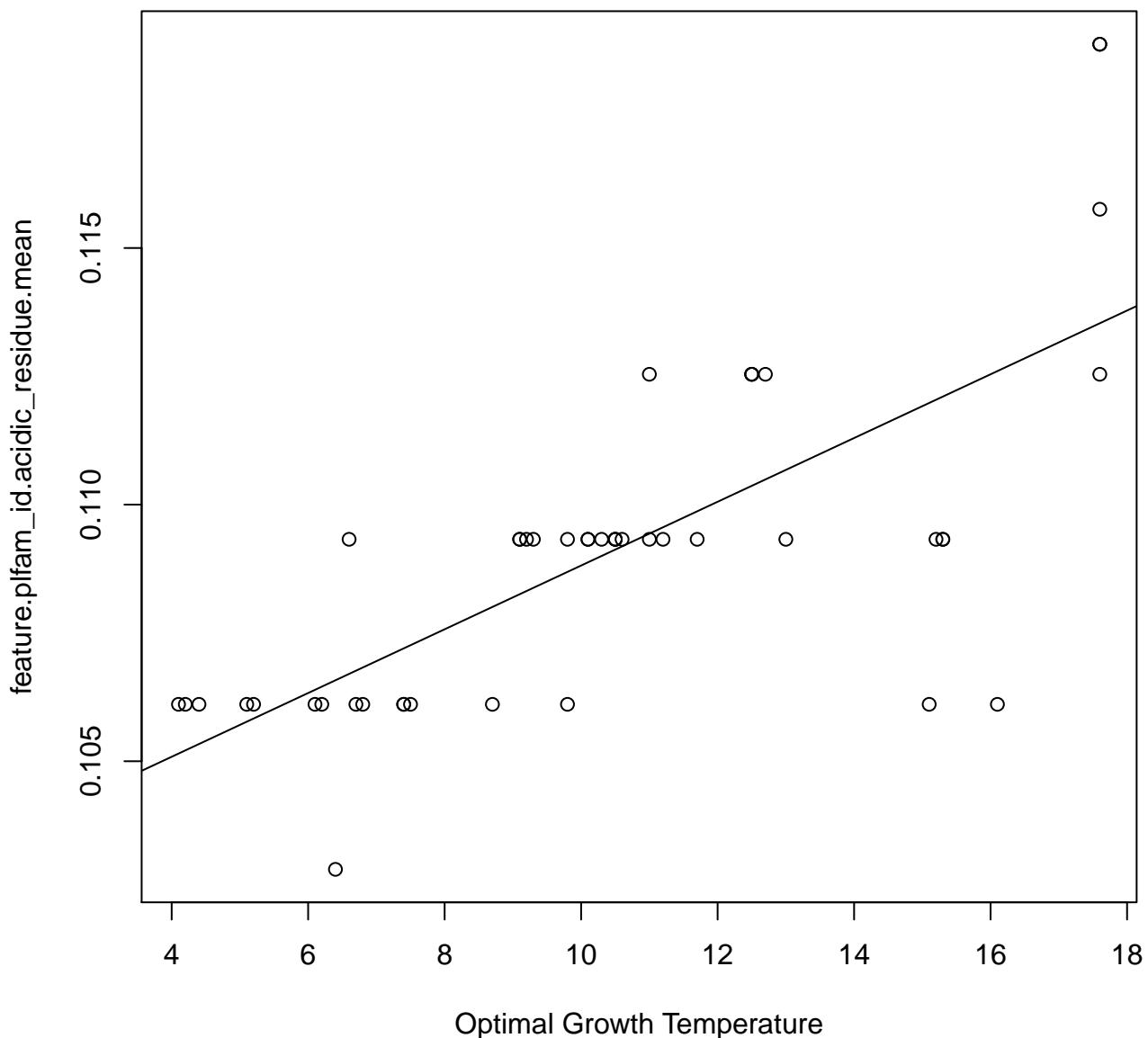
feature.plfam_id.acidic_residue.mean
PLF_28228_00001872
GII1812 protein



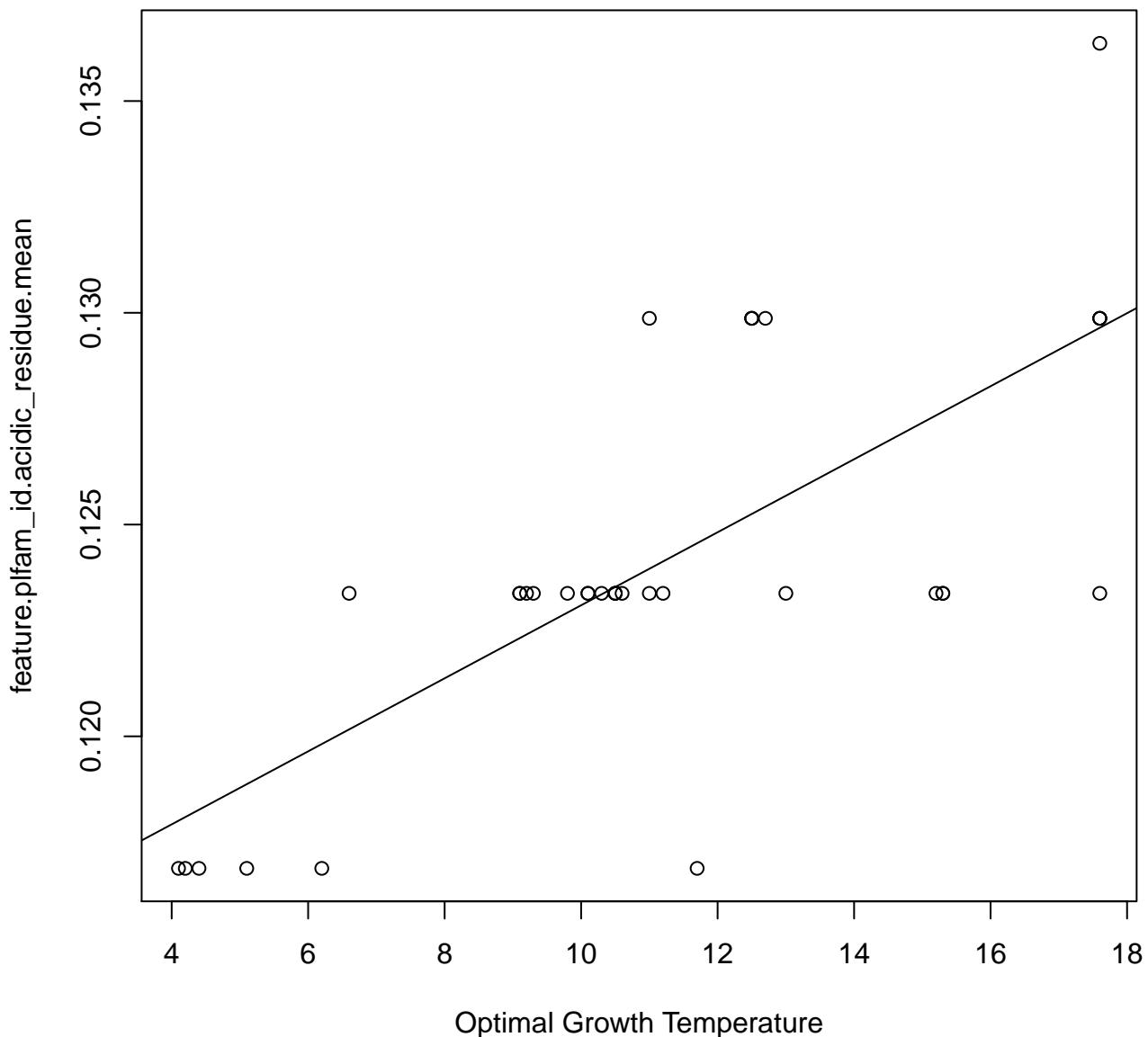
feature.plfam_id.acidic_residue.mean
PLF_28228_00000803
Flagellar basal-body rod protein FlgG



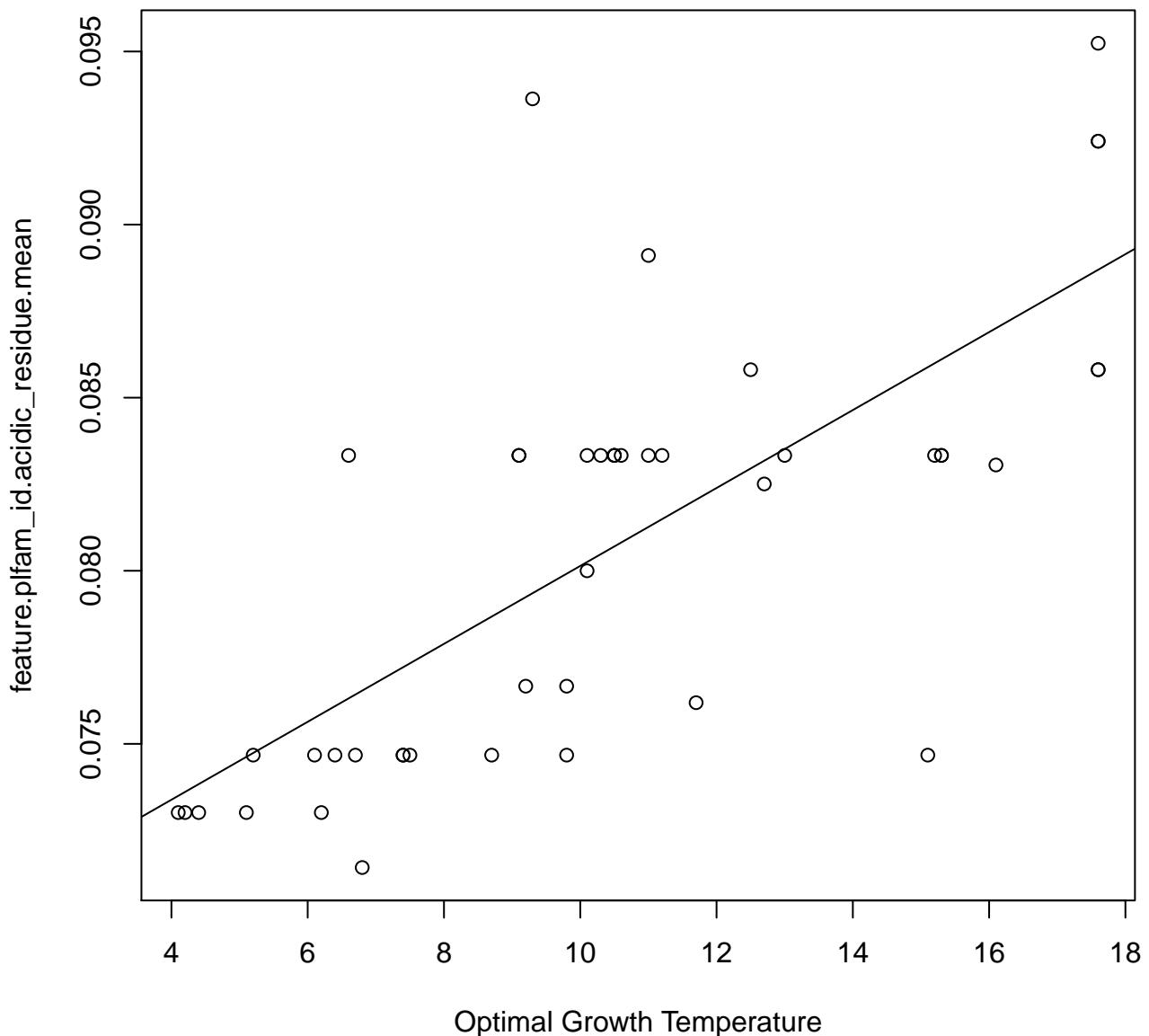
feature.plfam_id.acidic_residue.mean
PLF_28228_00000596
Malate dehydrogenase (EC 1.1.1.37)



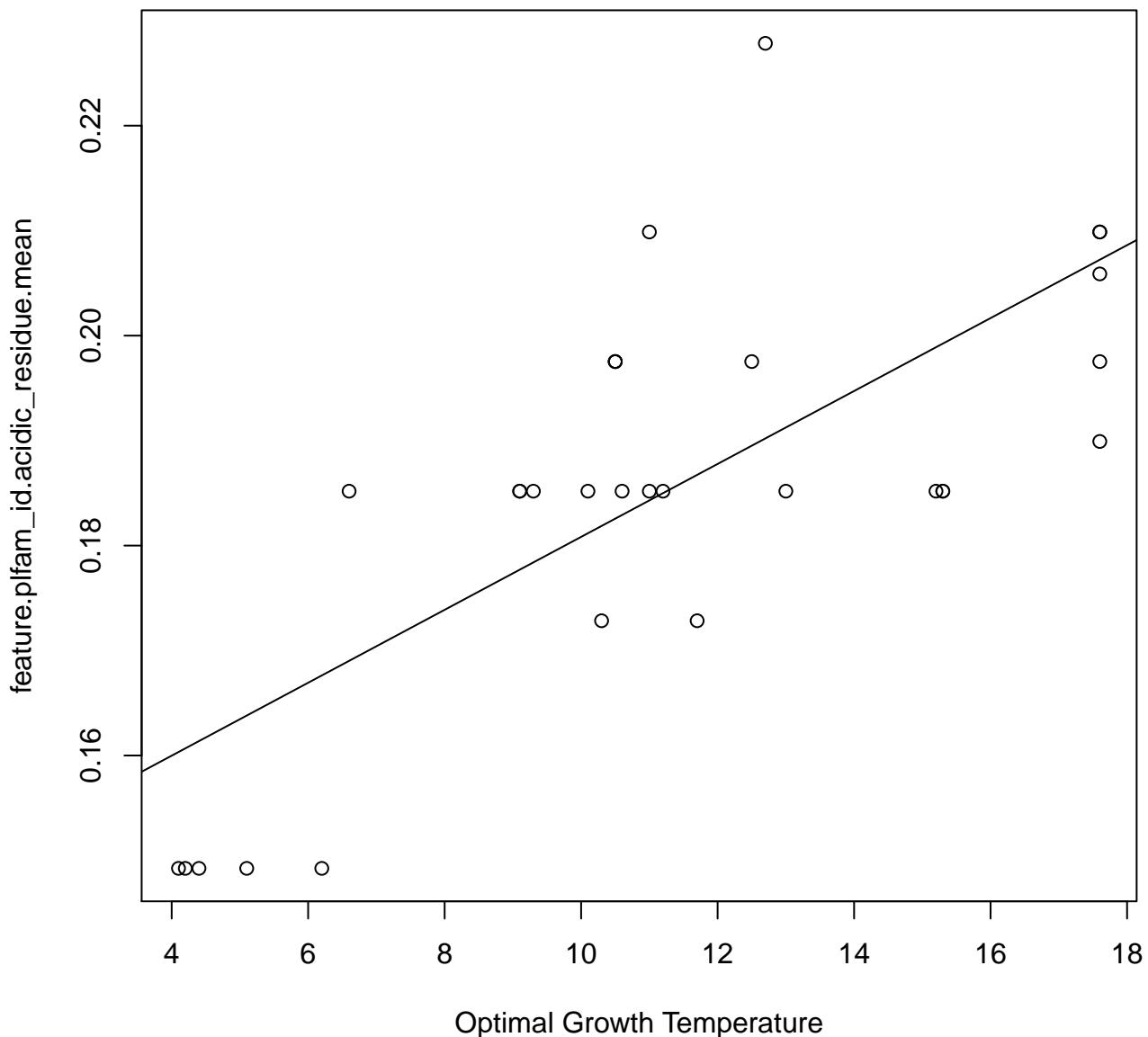
feature.plfam_id.acidic_residue.mean
PLF_28228_00000300
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)



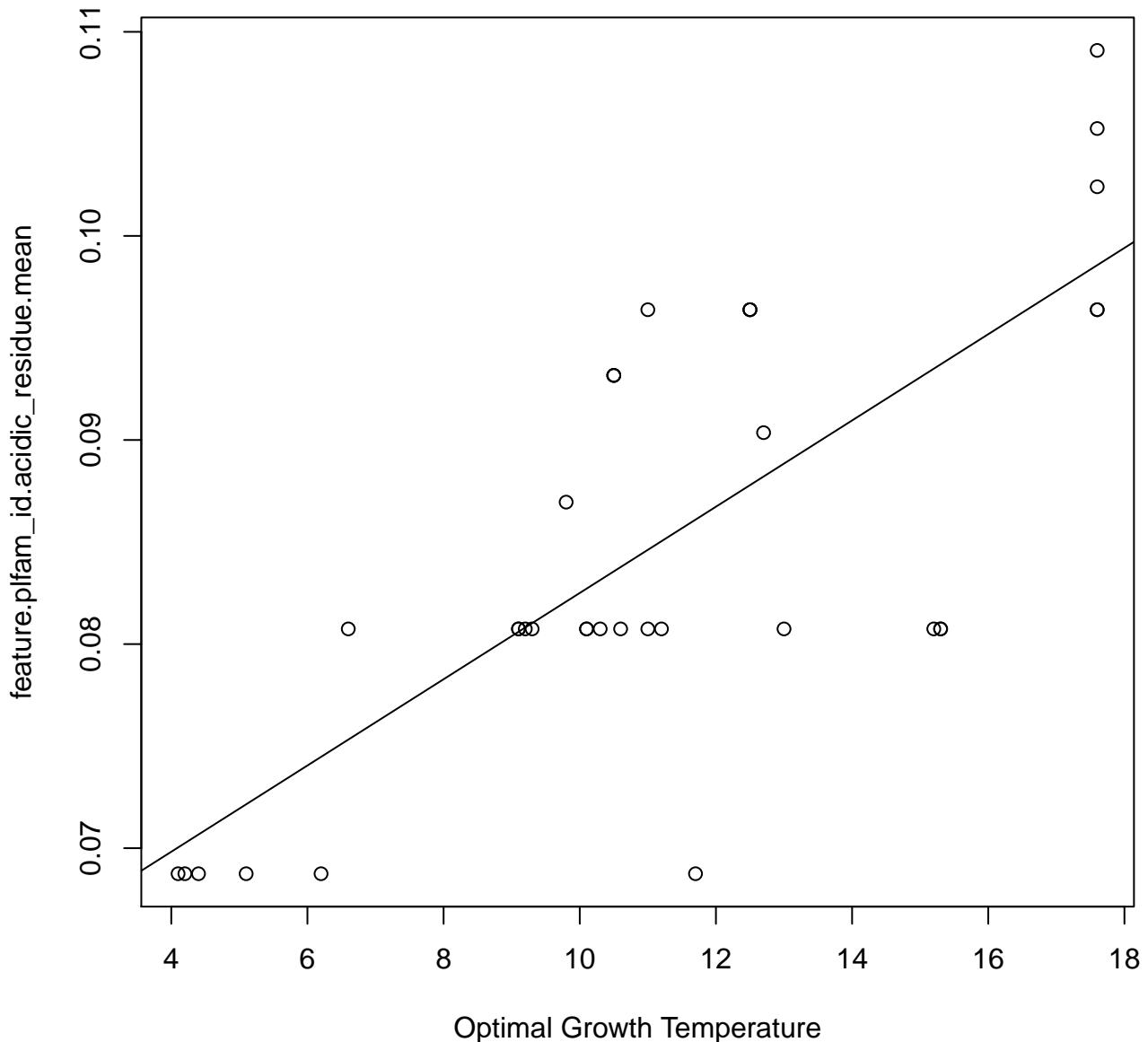
feature.plfam_id.acidic_residue.mean
PLF_28228_00016541
Probable acyltransferase PA0834



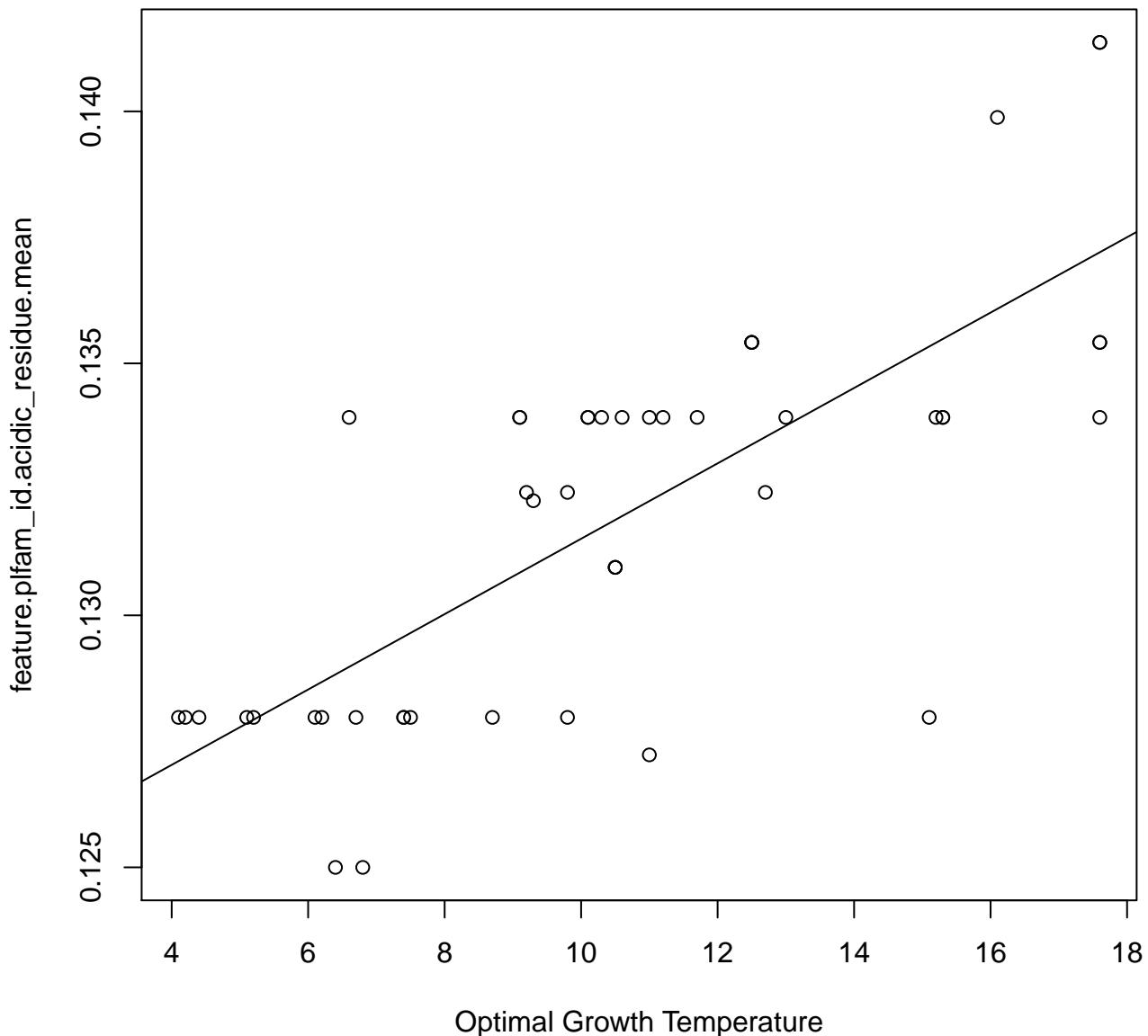
feature.plfam_id.acidic_residue.mean
PLF_28228_00014184
Uncharacterized ferredoxin-like protein YfhL



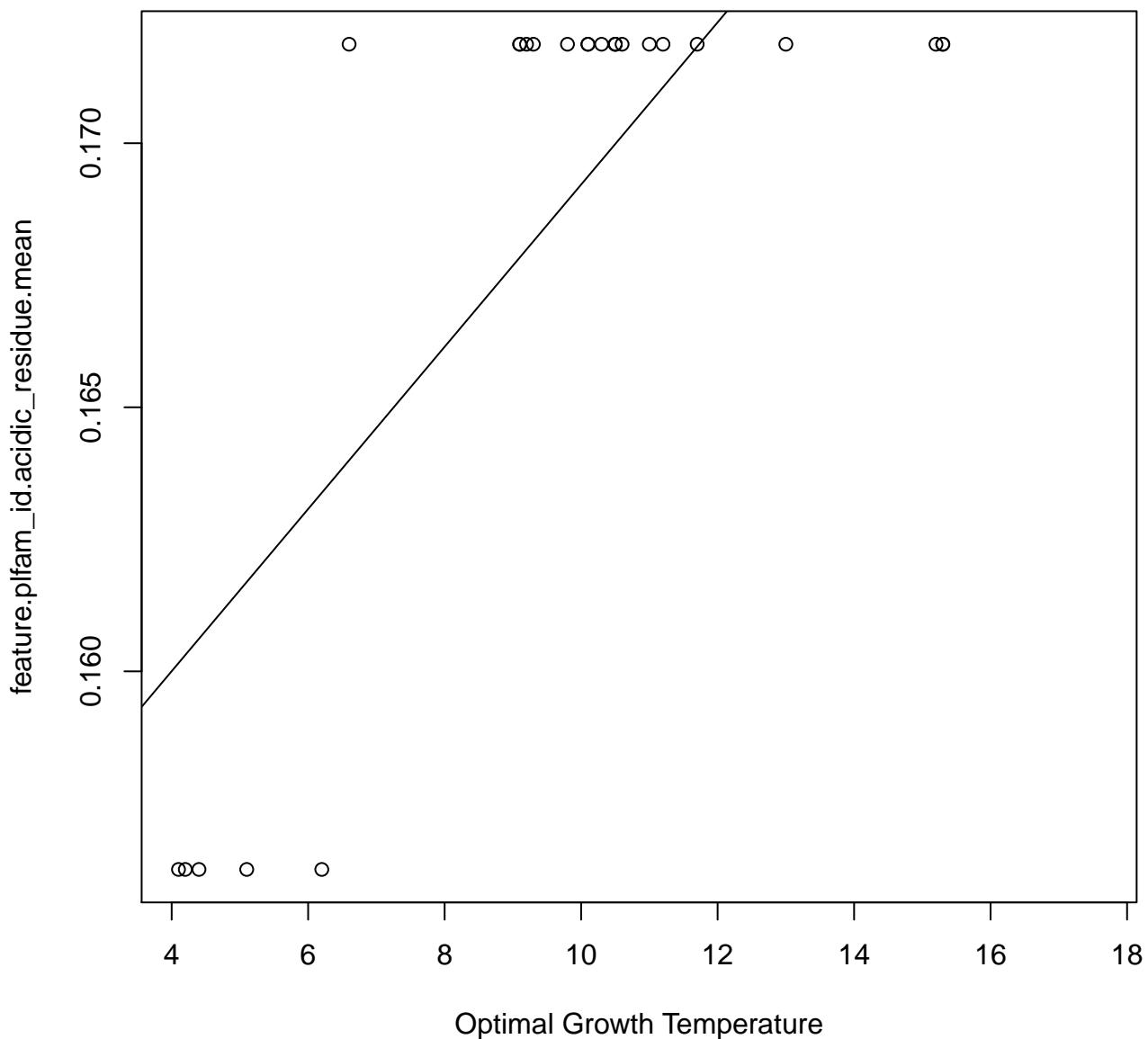
feature.plfam_id.acidic_residue.mean
PLF_28228_00001337
hypothetical protein



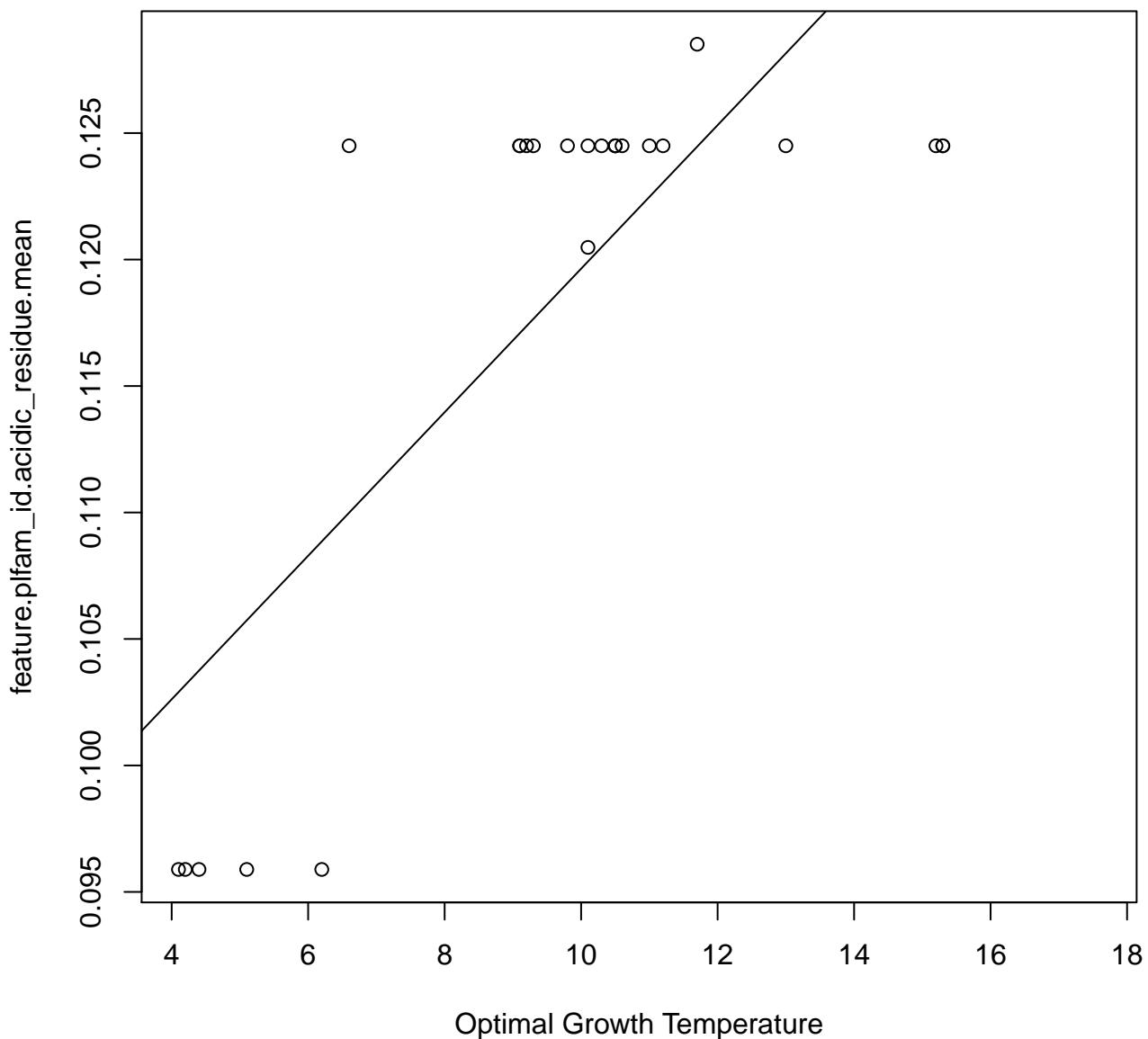
feature.plfam_id.acidic_residue.mean
PLF_28228_00001734
Methyl-accepting chemotaxis sensor/transducer protein



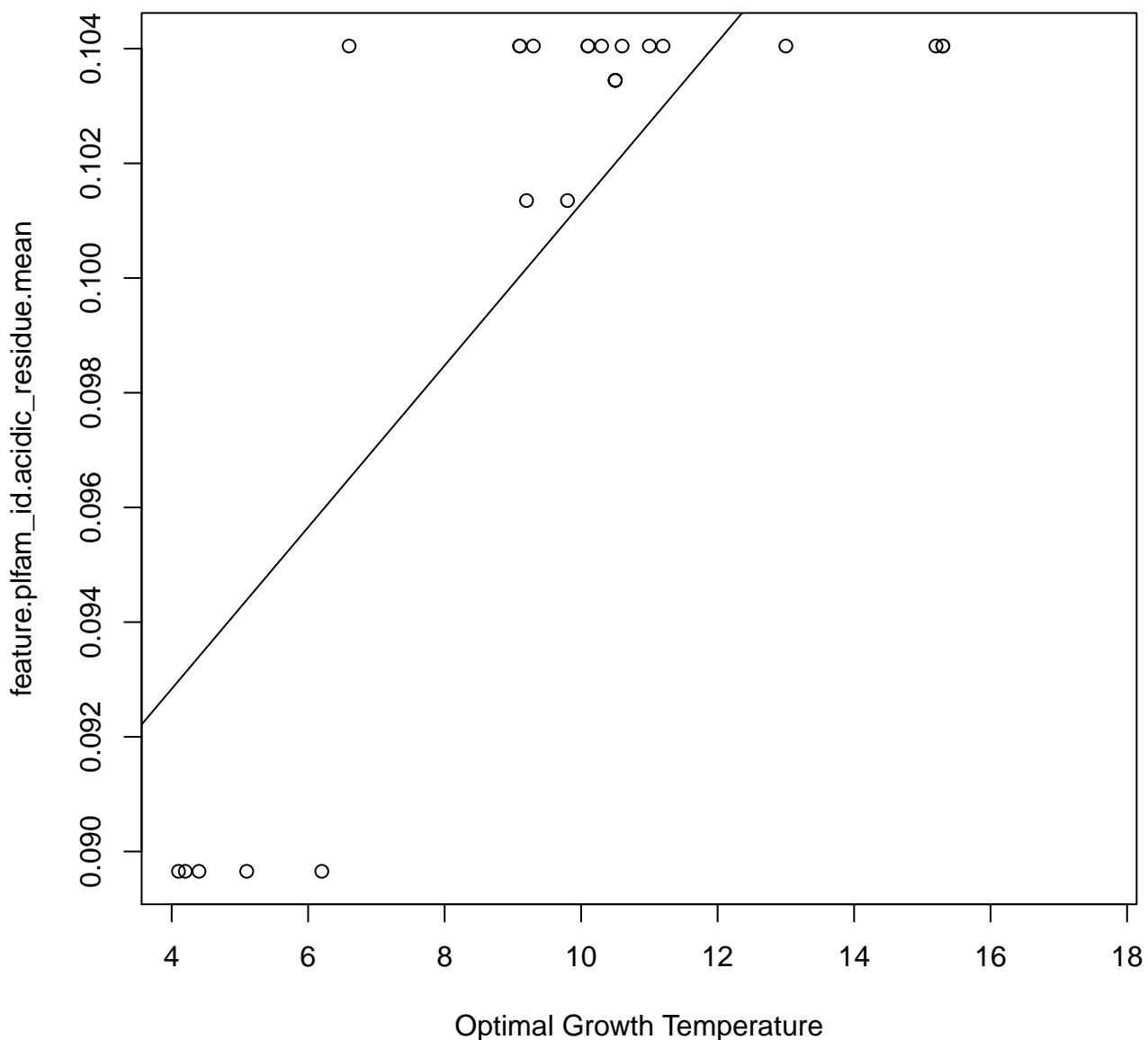
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PLF_28228_00016786
hypothetical protein



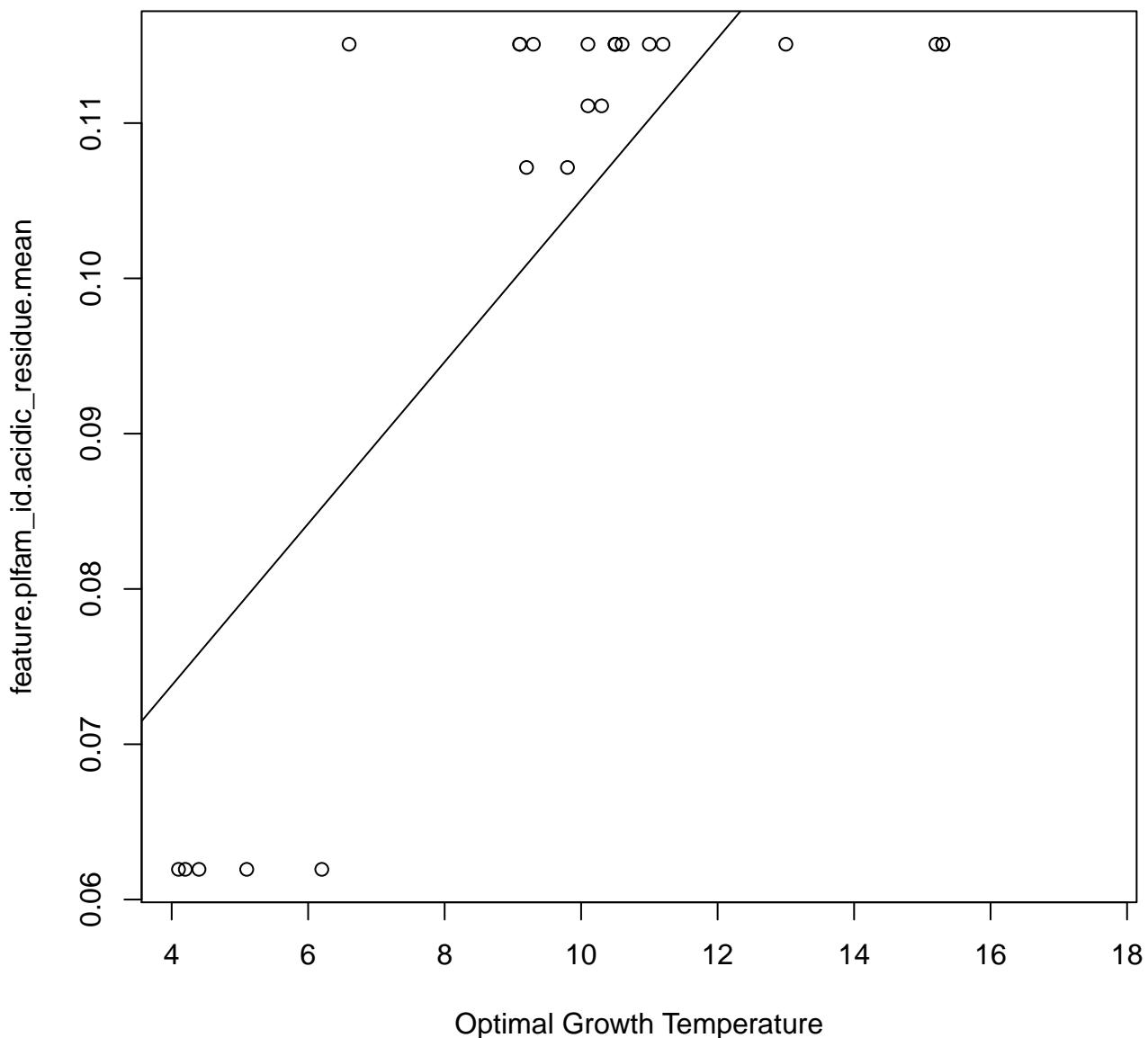
feature.plfam_id.acidic_residue.mean
PLF_28228_00031426
hypothetical protein



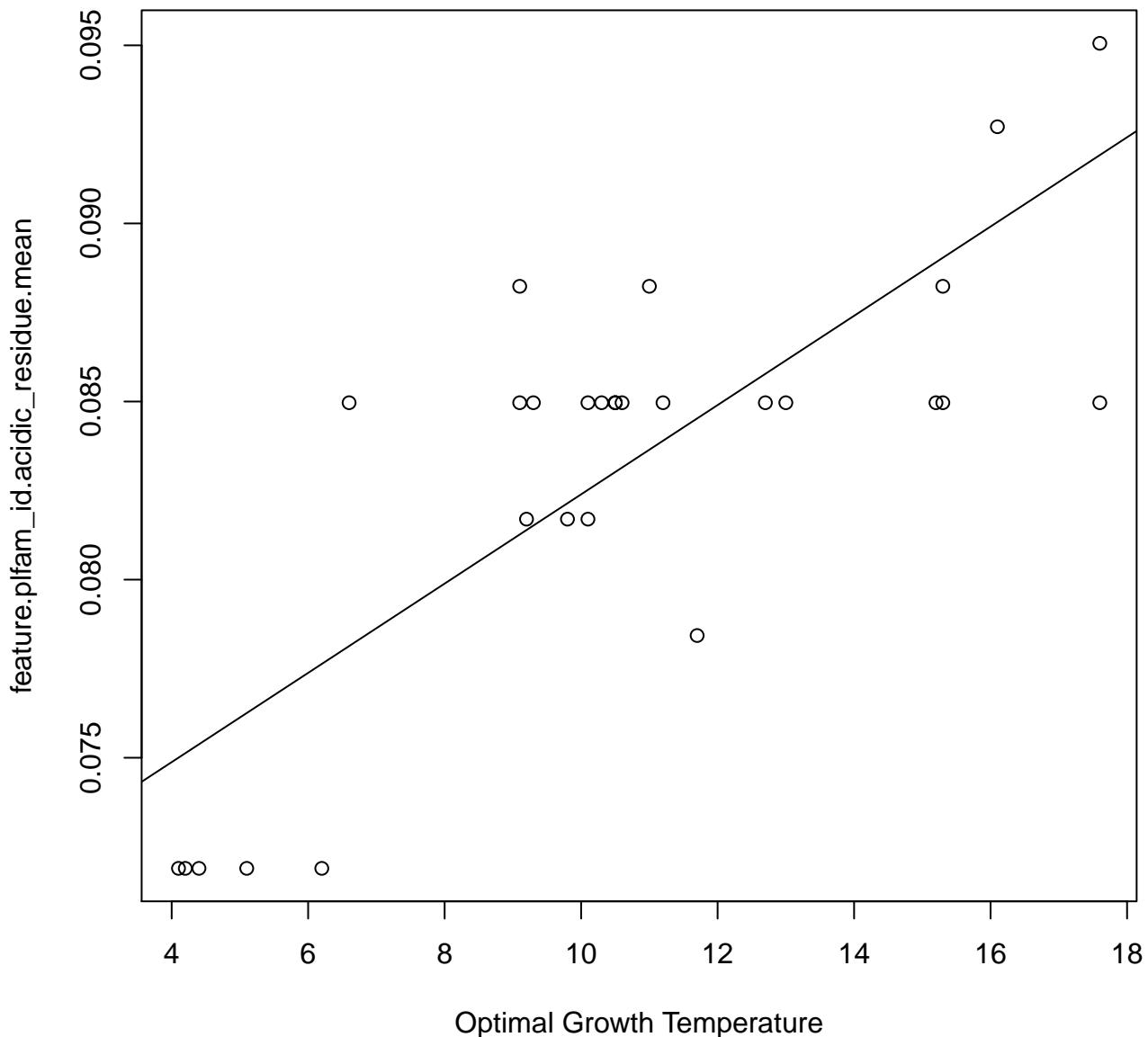
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PLF_28228_00015220
hypothetical protein



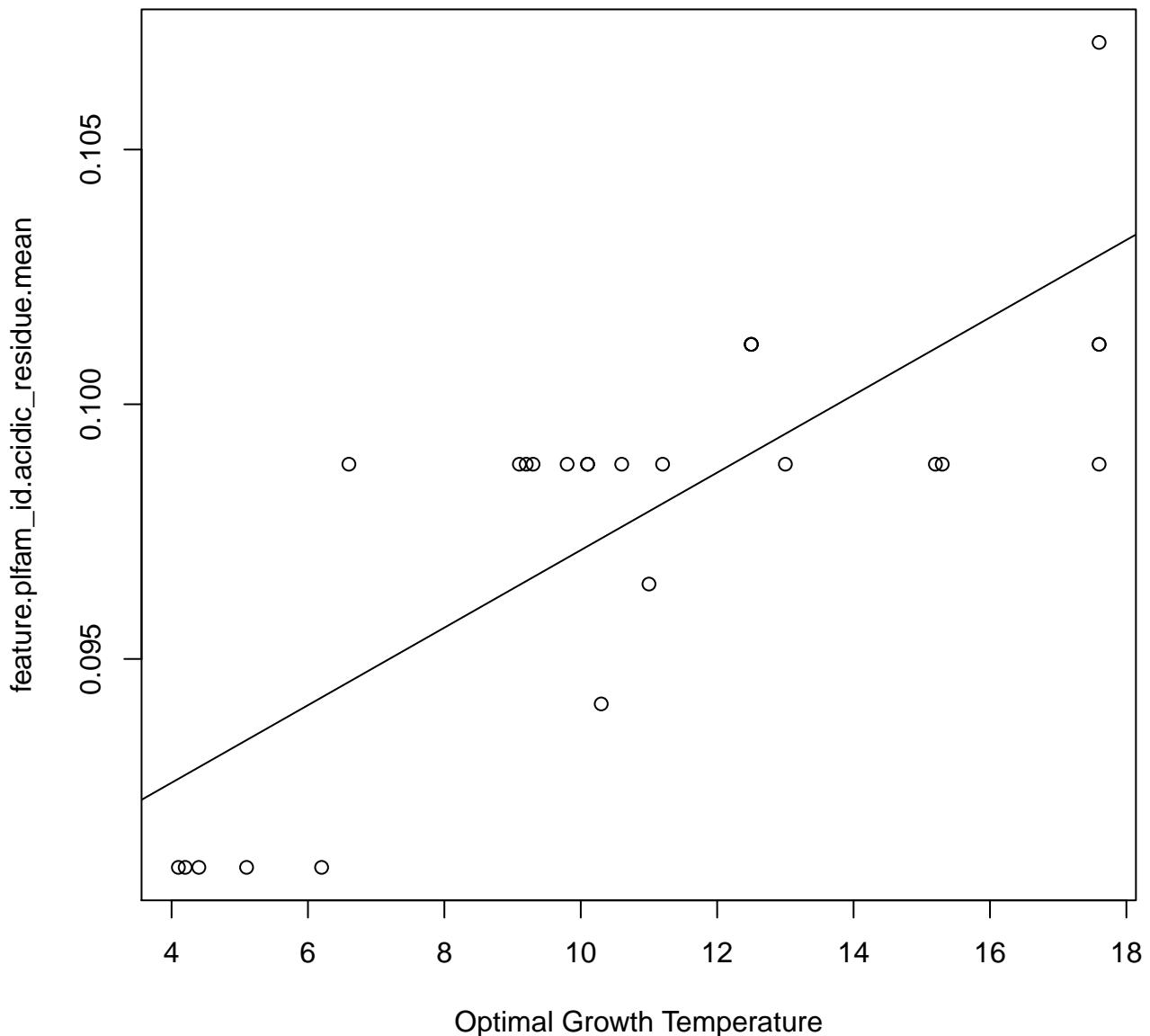
feature.plfam_id.acidic_residue.mean
PLF_28228_00030076
hypothetical protein



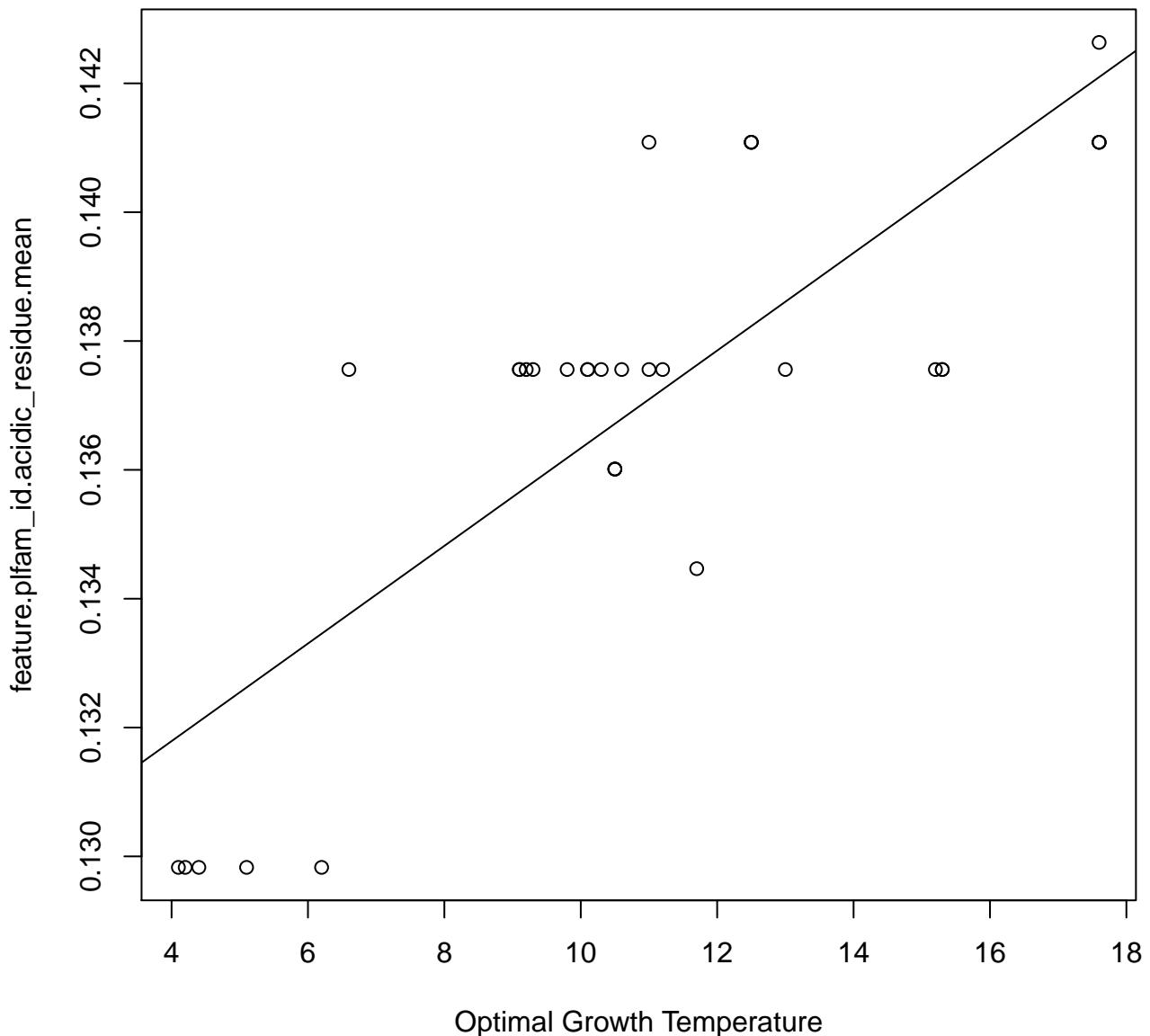
feature.plfam_id.acidic_residue.mean
PLF_28228_00002780
Protein translocase subunit SecF



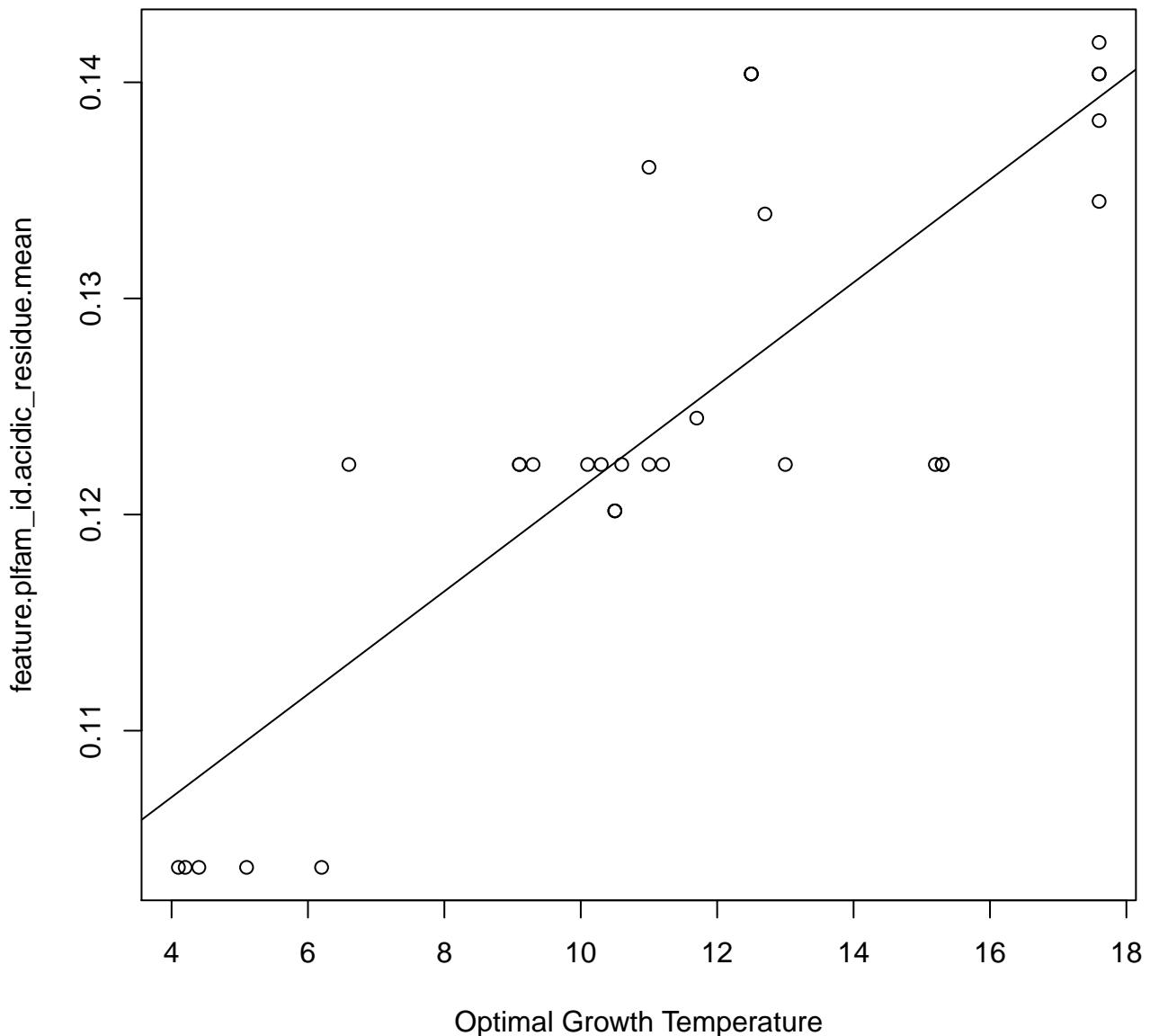
feature.plfam_id.acidic_residue.mean
PLF_28228_00003089
EPS I polysaccharide export outer membrane protein EPSA precursor



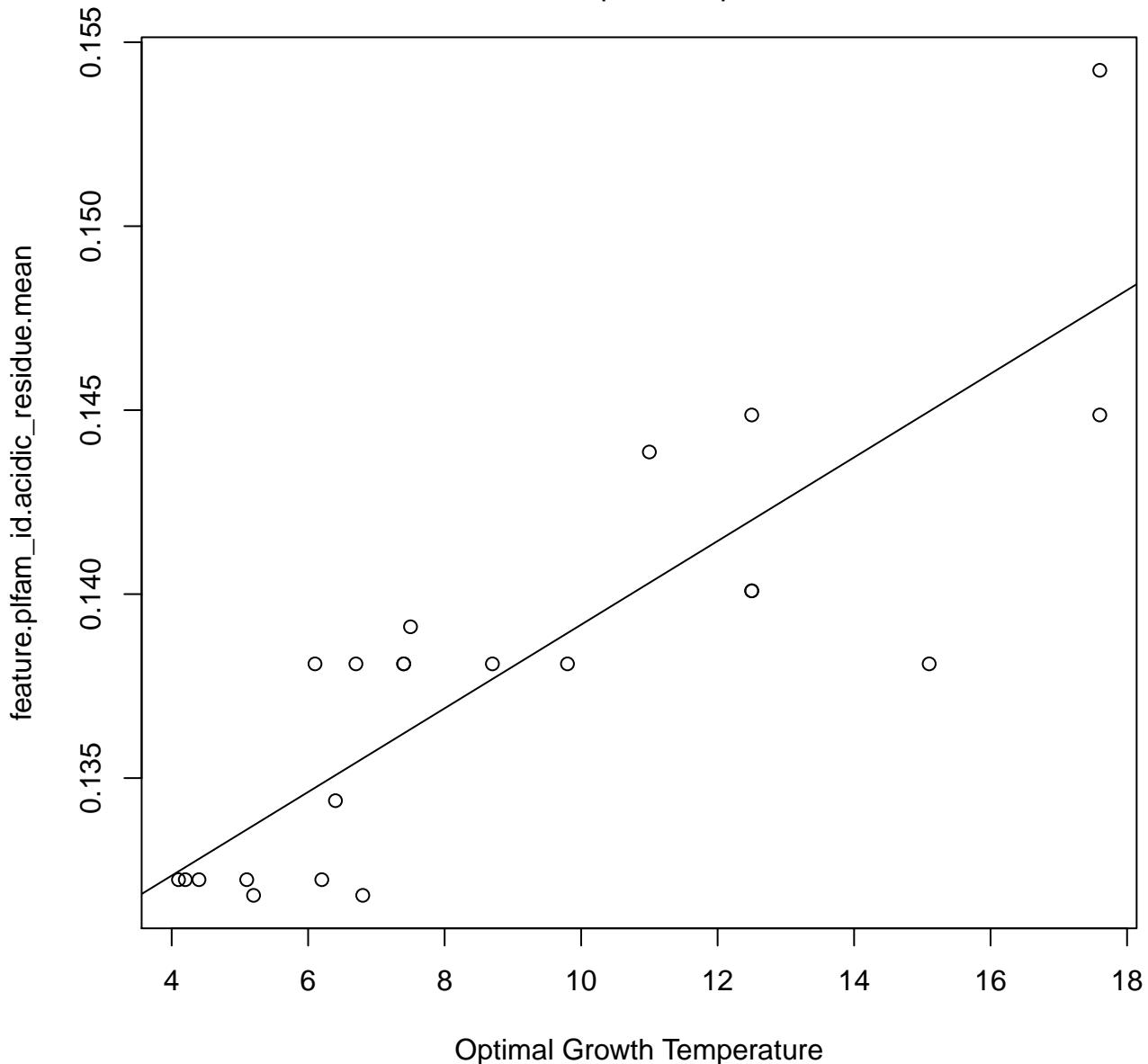
feature.plfam_id.acidic_residue.mean
PLF_28228_00007395
Argininosuccinate lyase (EC 4.3.2.1) / N-acetylglutamate synthase (EC 2.3.1.1)



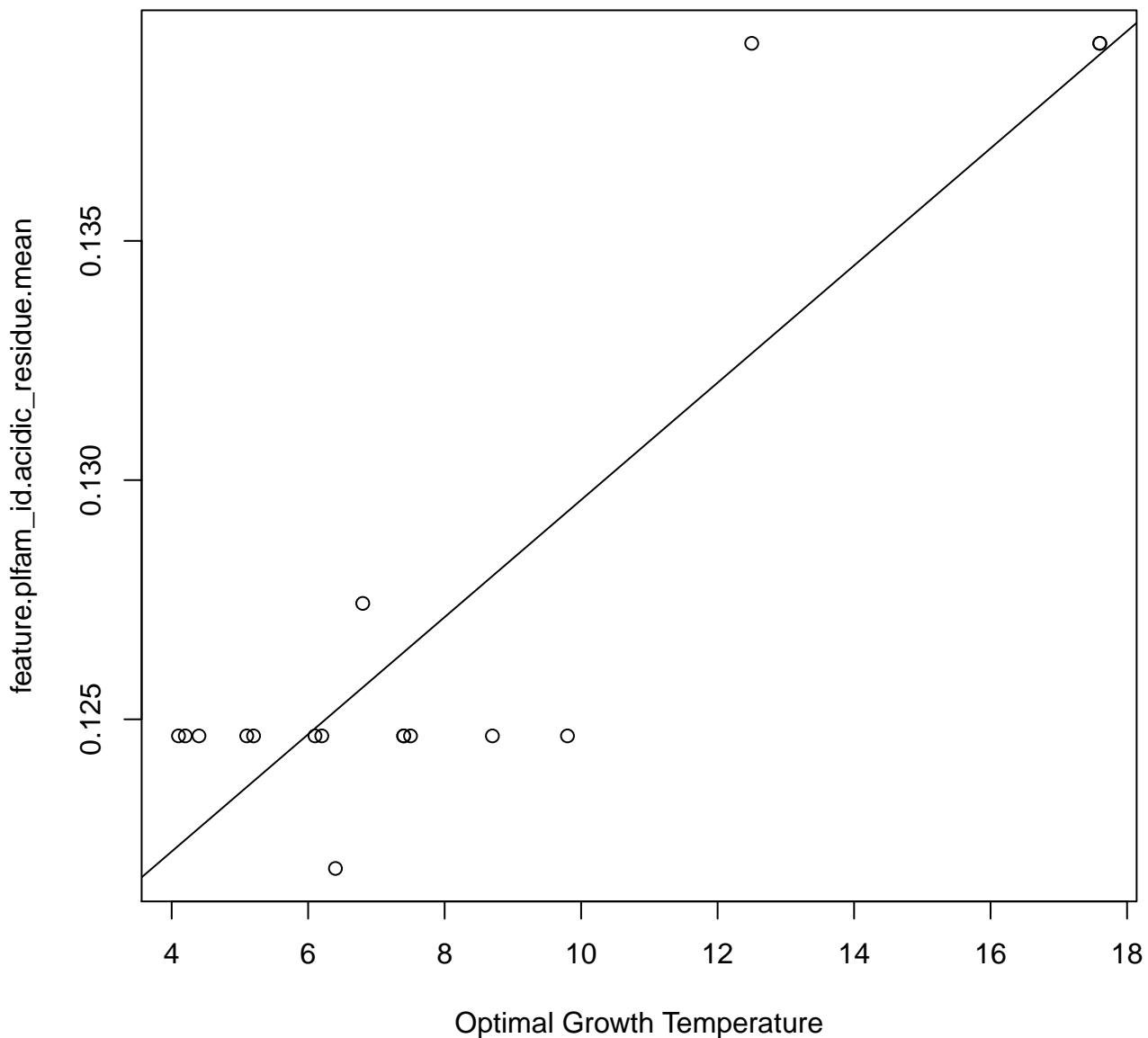
feature.plfam_id.acidic_residue.mean
PLF_28228_00001289
Uncharacterized protease YegQ



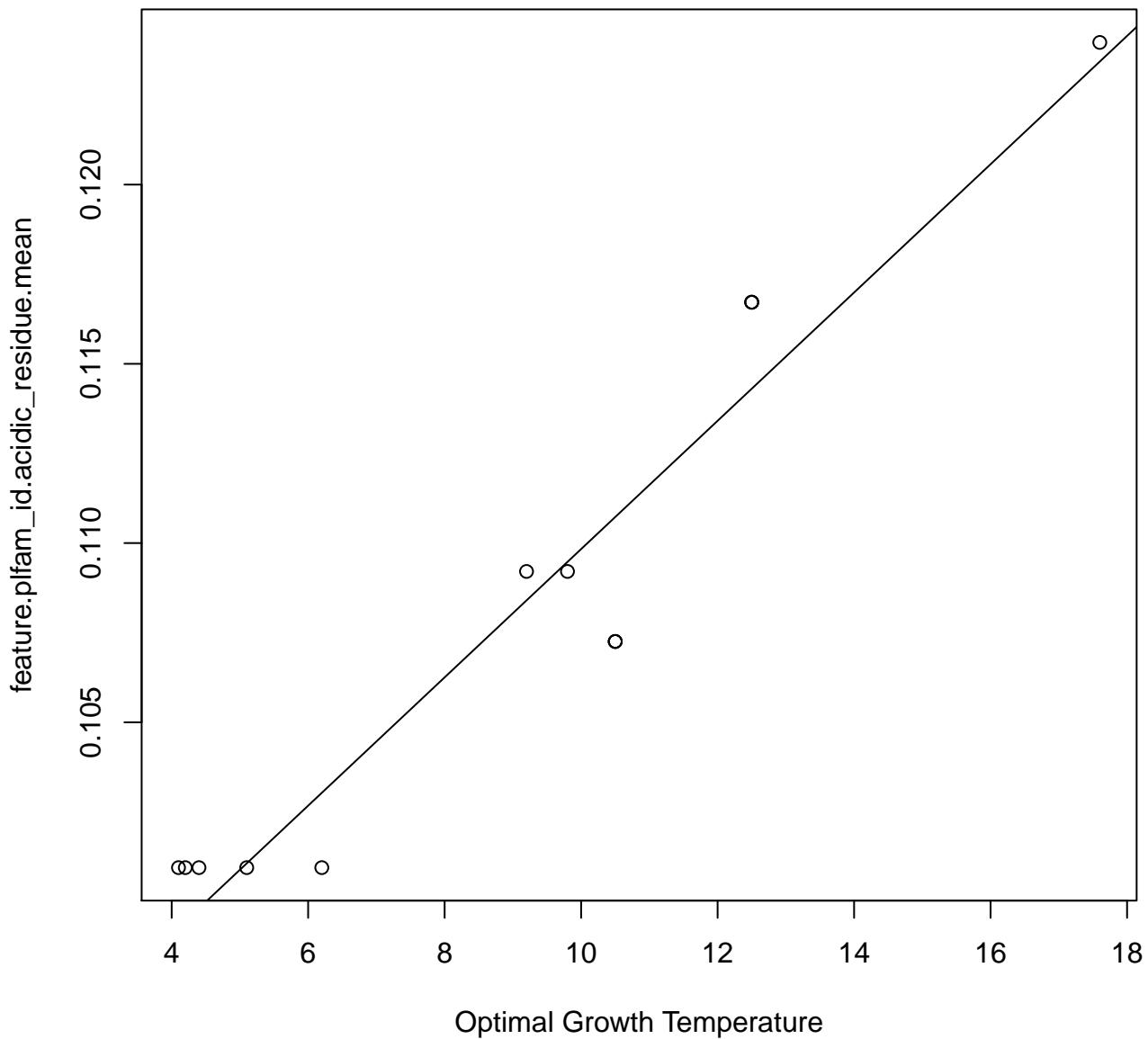
feature.plfam_id.acidic_residue.mean
PLF_28228_00004171
TonB-dependent receptor



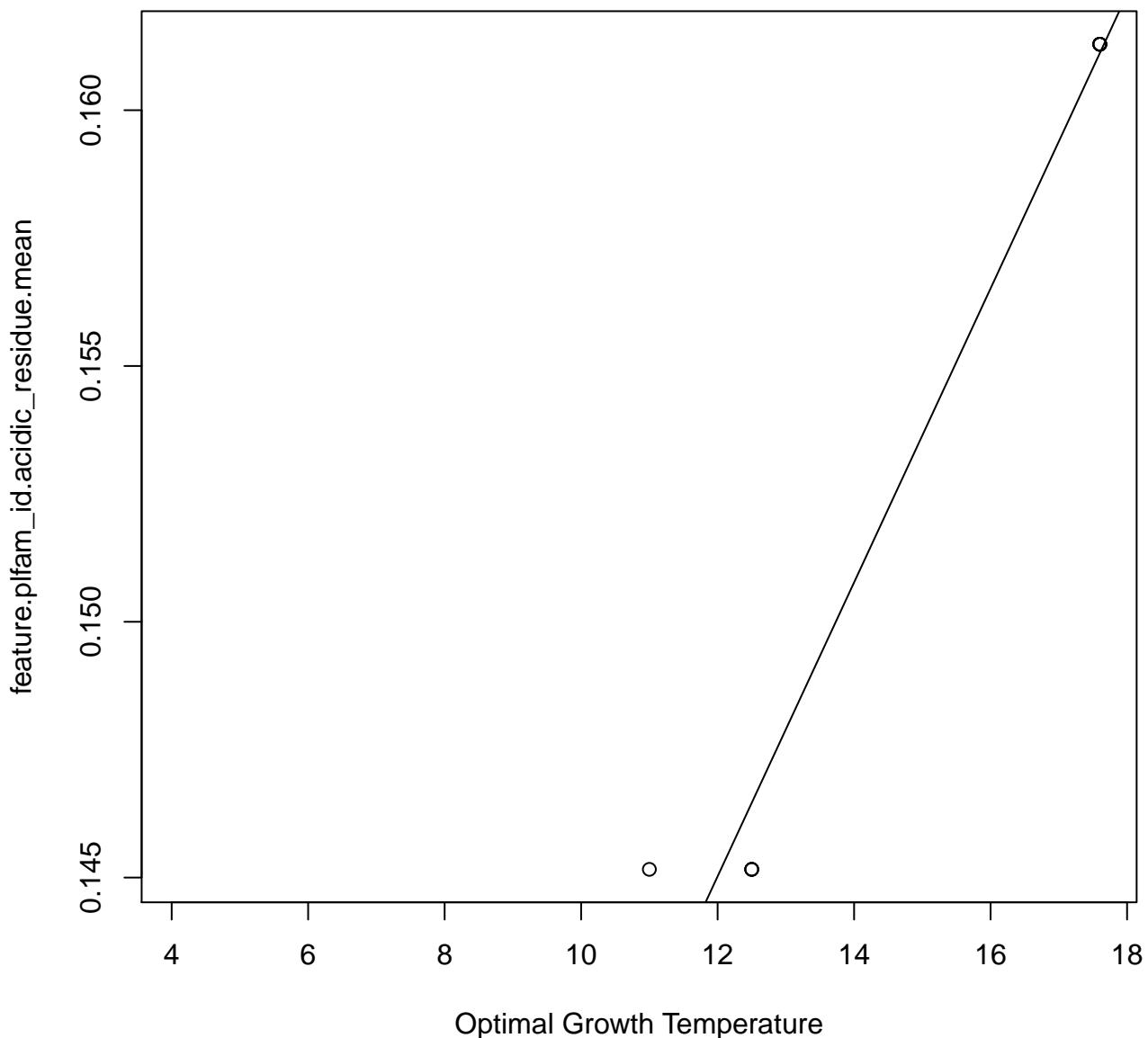
feature.plfam_id.acidic_residue.mean
PLF_28228_00028262
Iron siderophore sensor protein



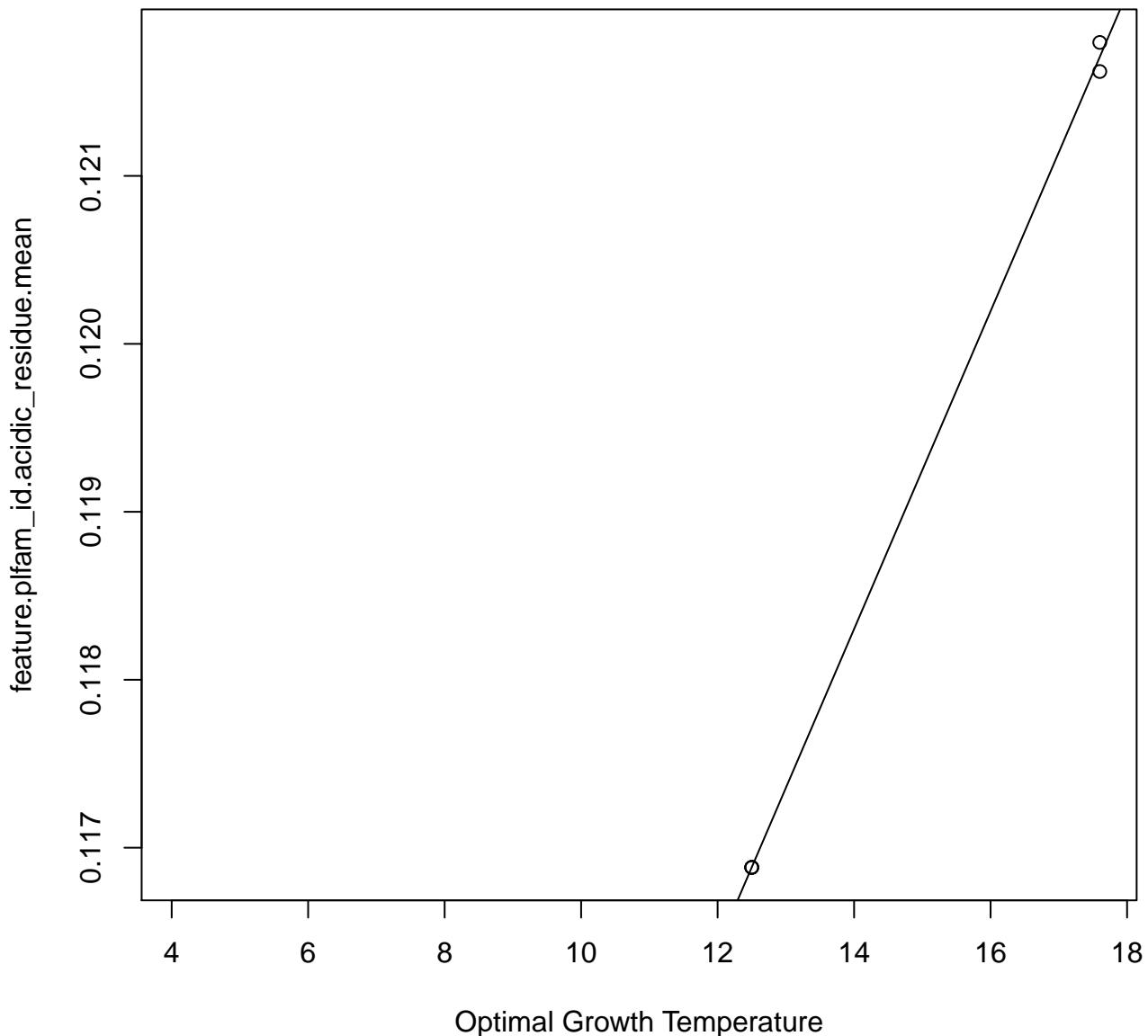
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PLF_28228_00007837
Transcriptional regulator, AraC family



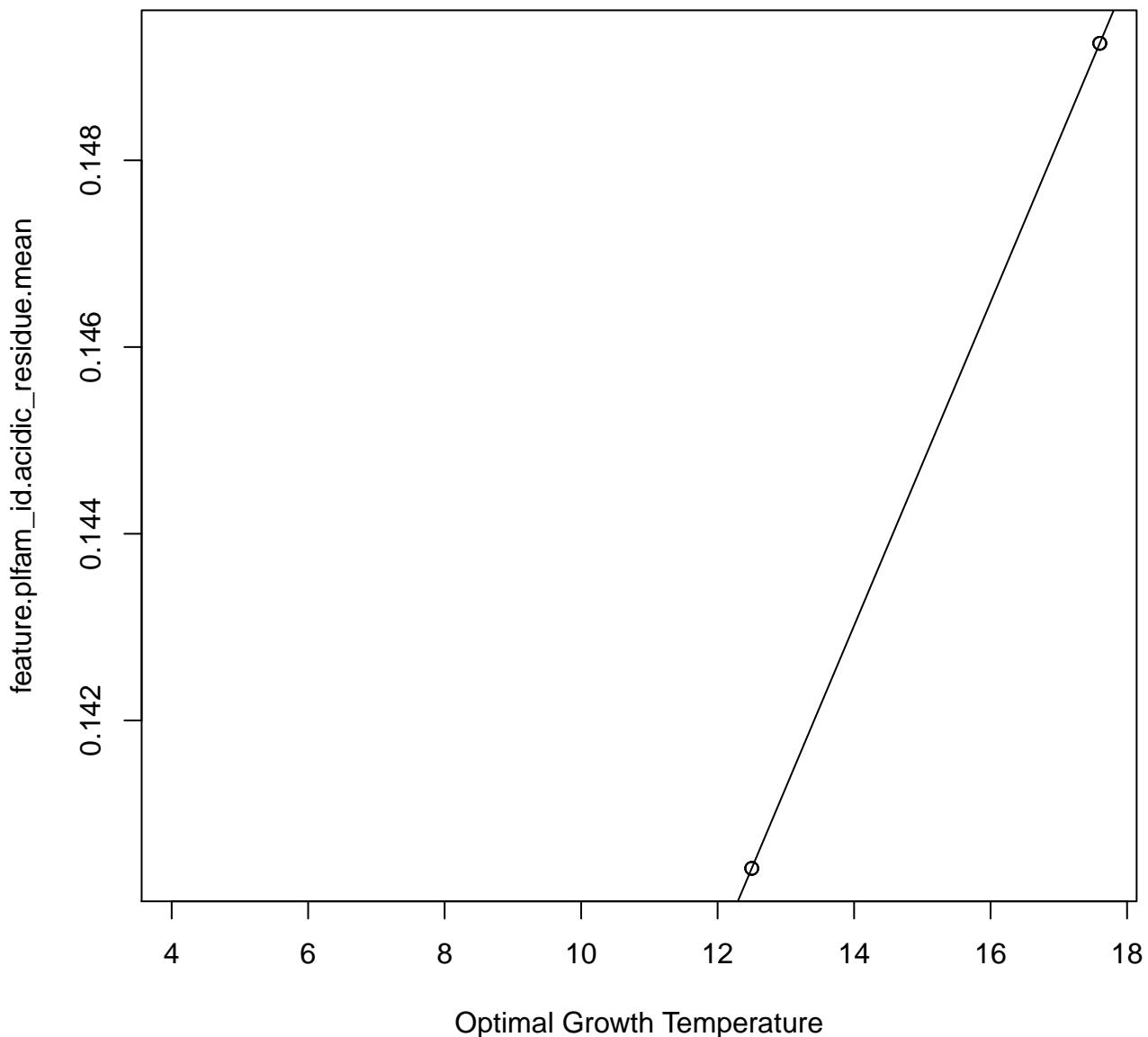
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hypothetical protein



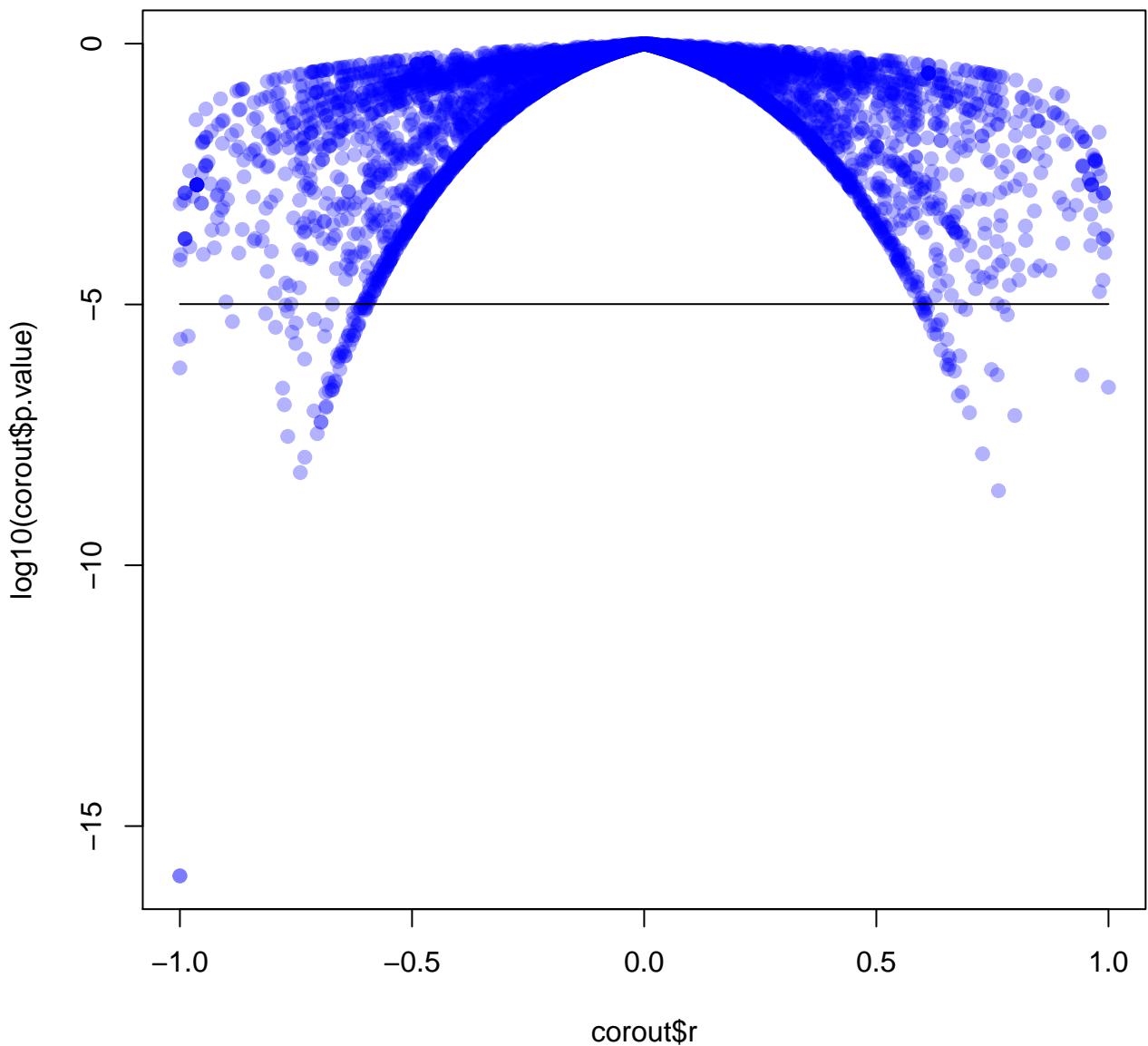
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Regulatory protein LuxR



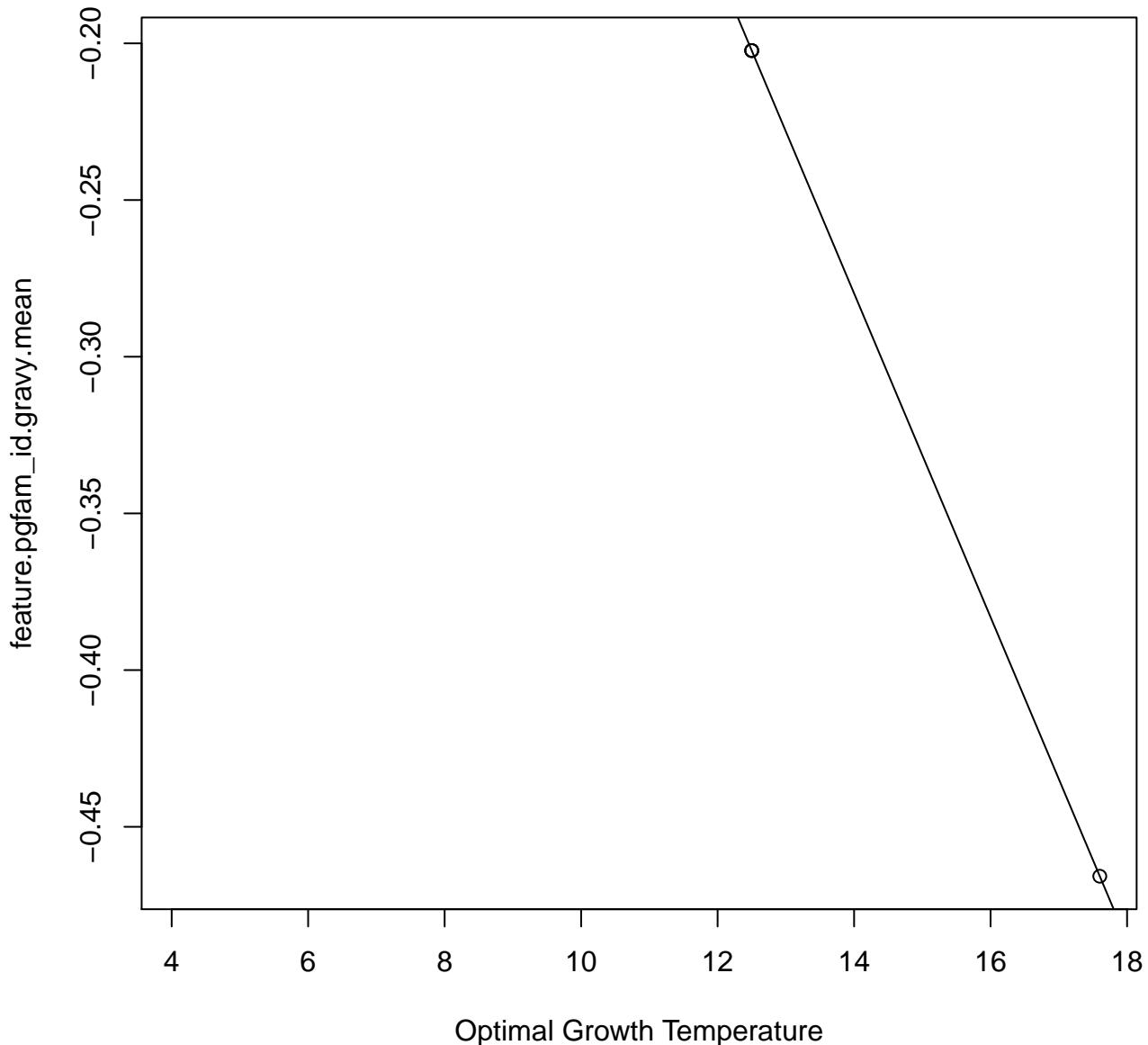
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hypothetical protein



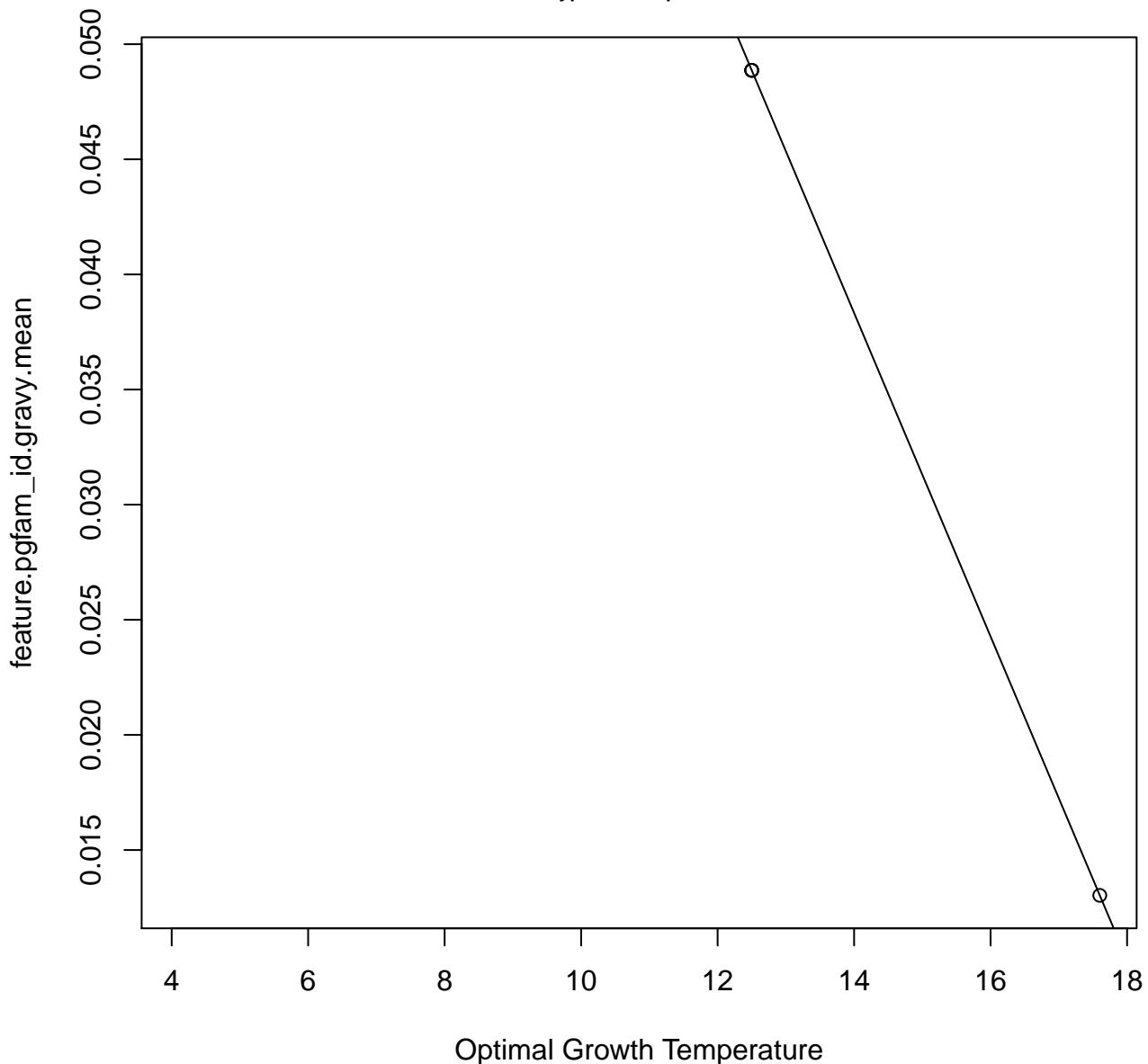
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feature.pgfam_id.gravy.mean
PGF_00211286
hypothetical protein

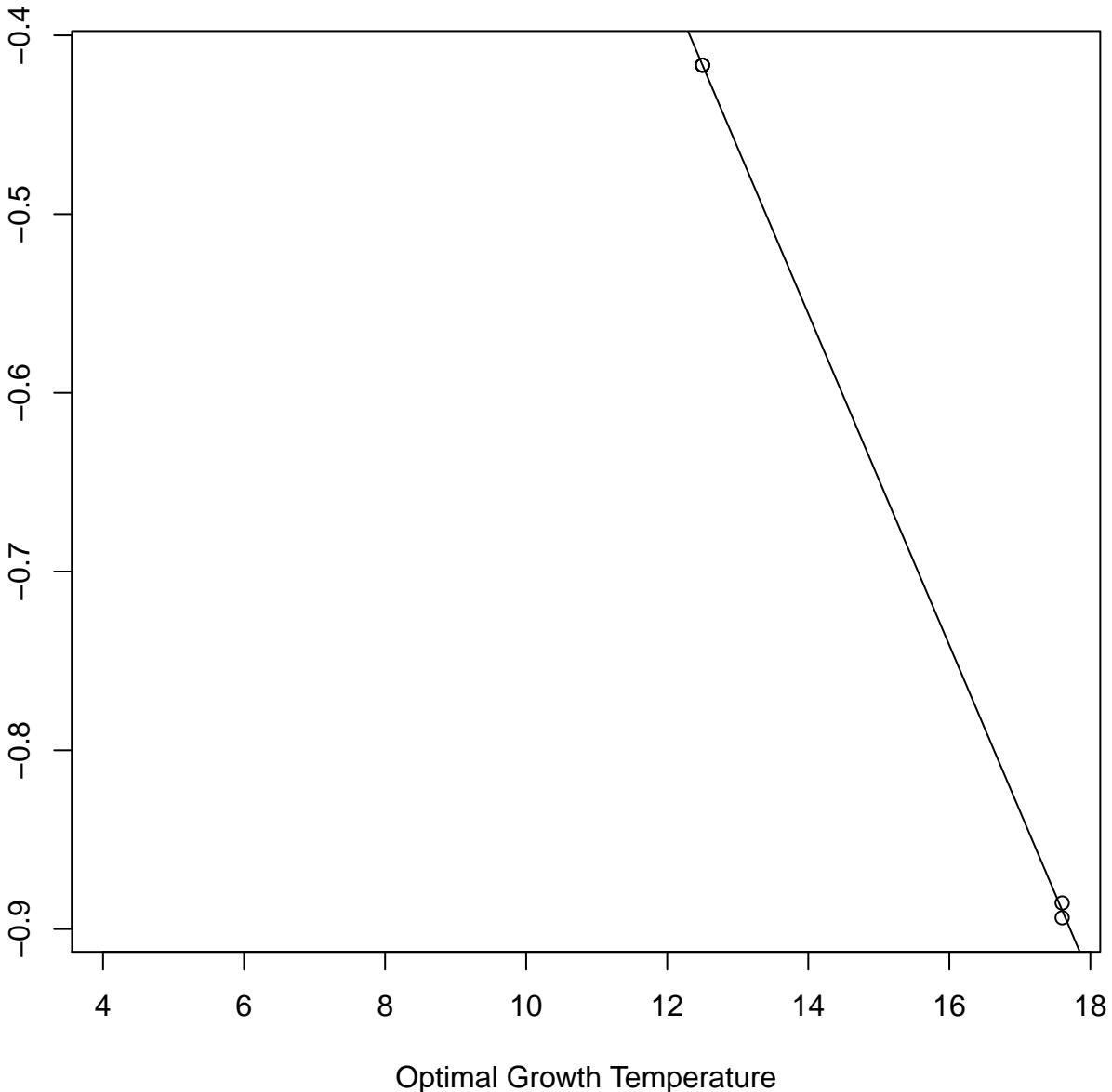


feature.pgfam_id.gravy.mean
PGF_00336673
hypothetical protein

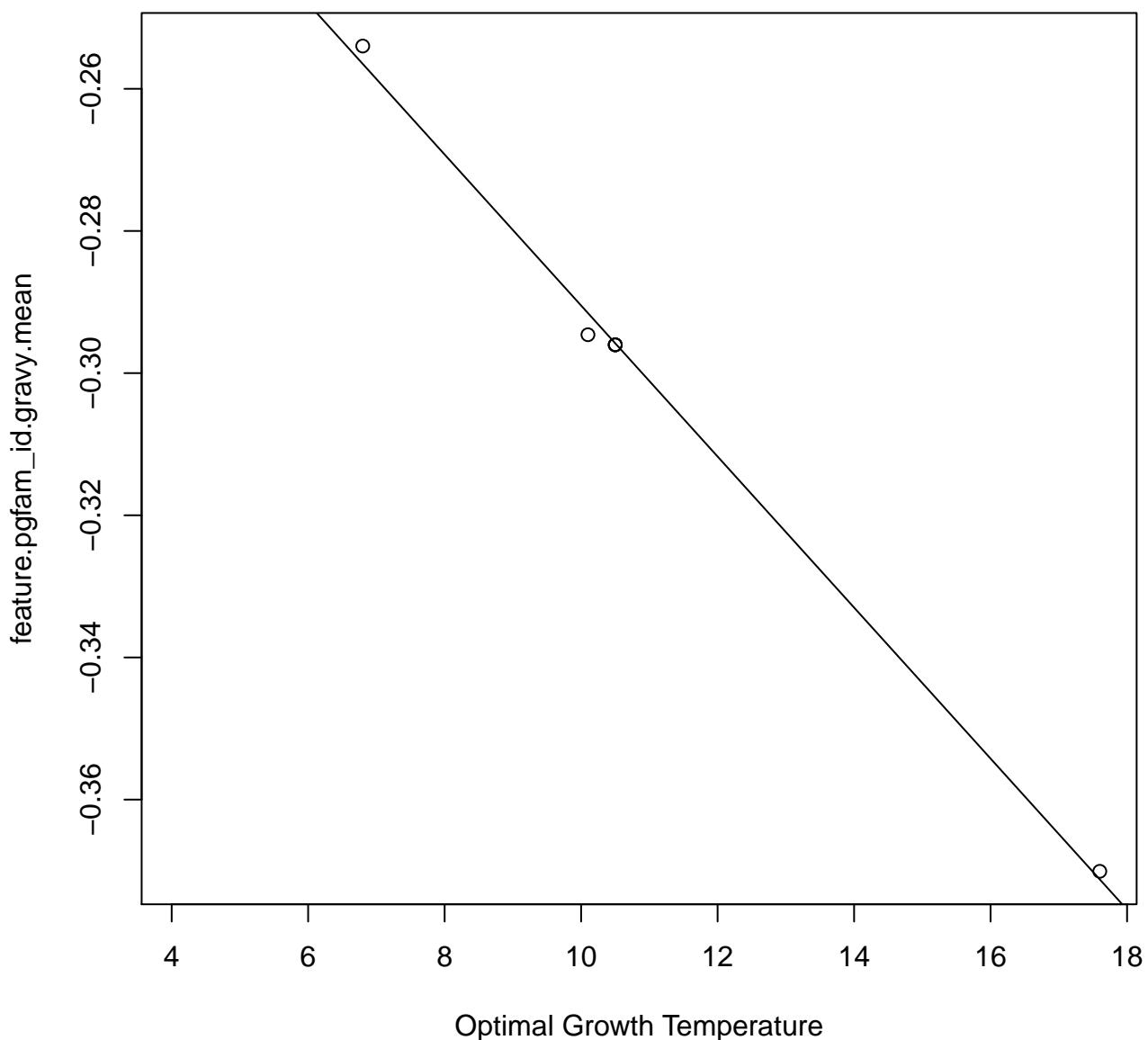


feature.pgfam_id.gravy.mean
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hypothetical protein

feature.pgfam_id.gravy.mean

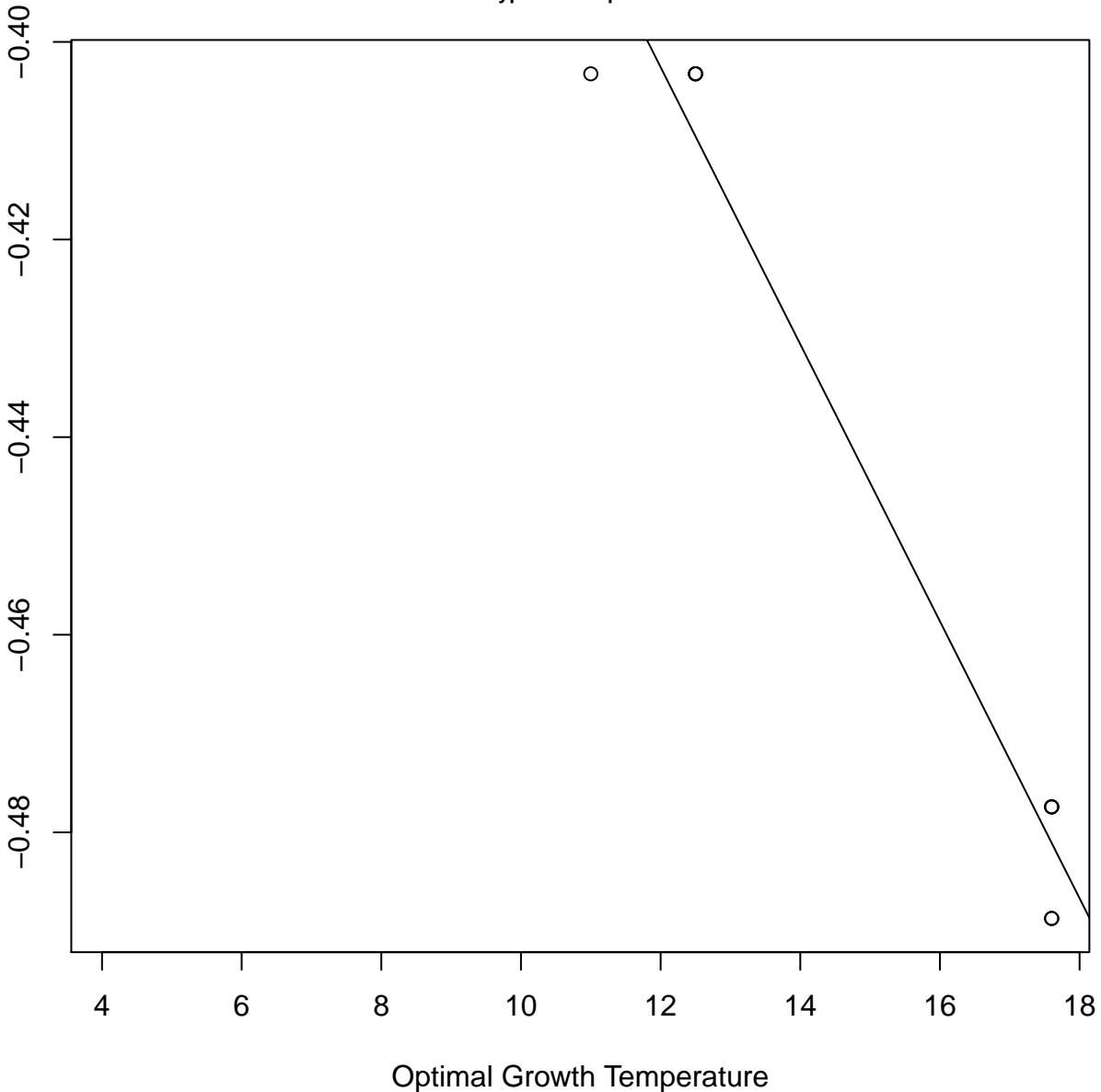


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PGF_00415824
FIG00640418: hypothetical protein

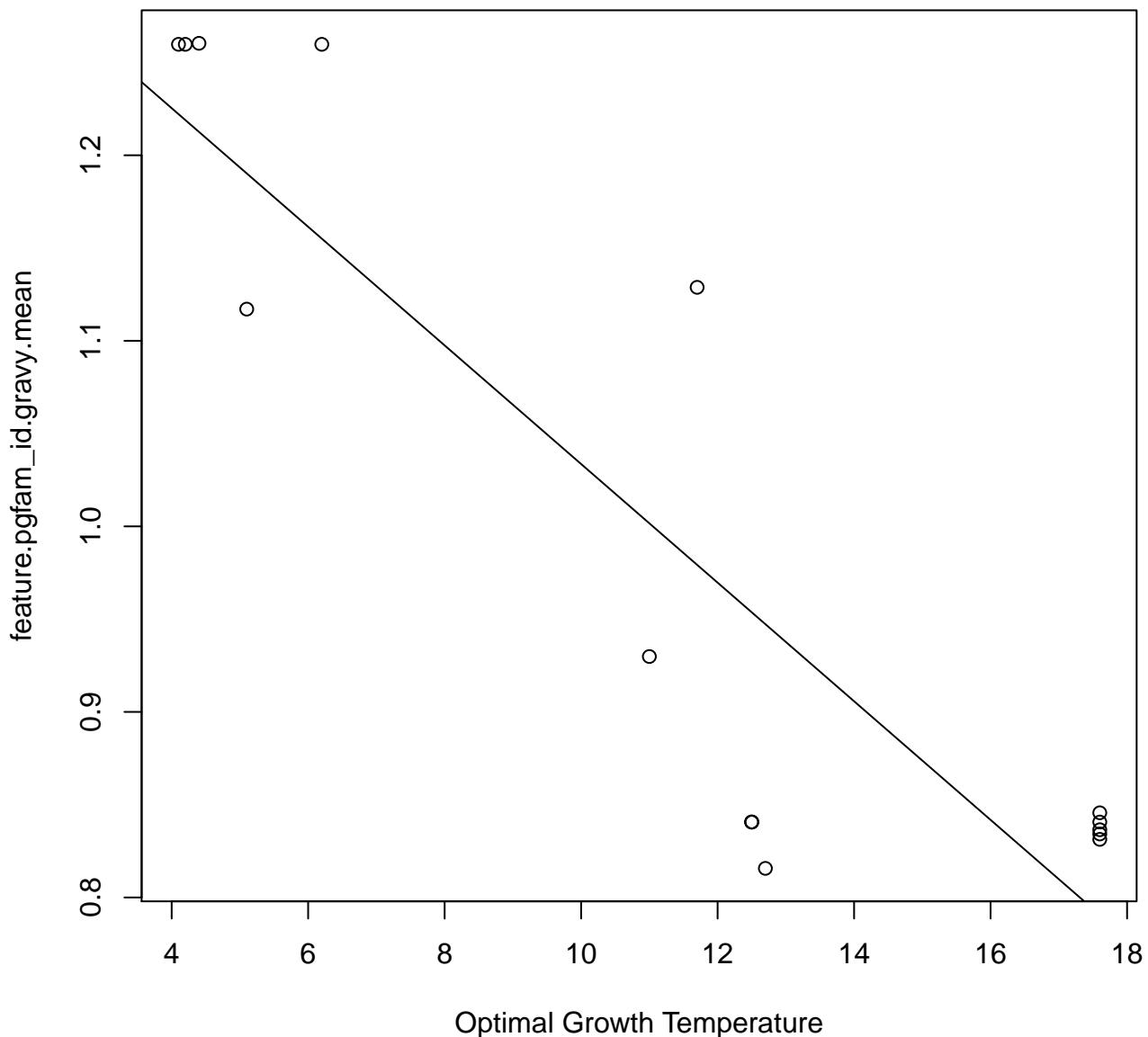


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hypothetical protein

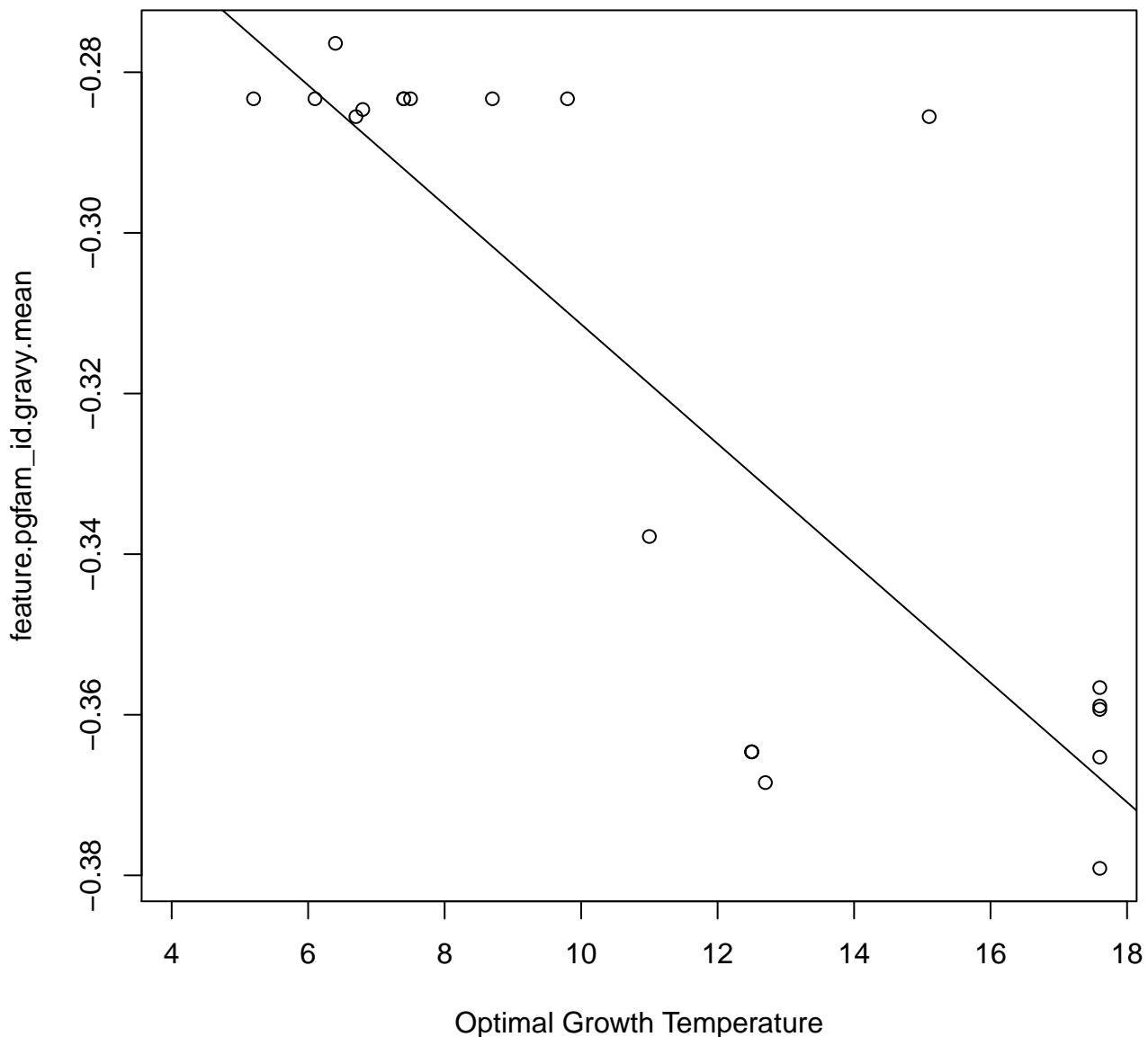
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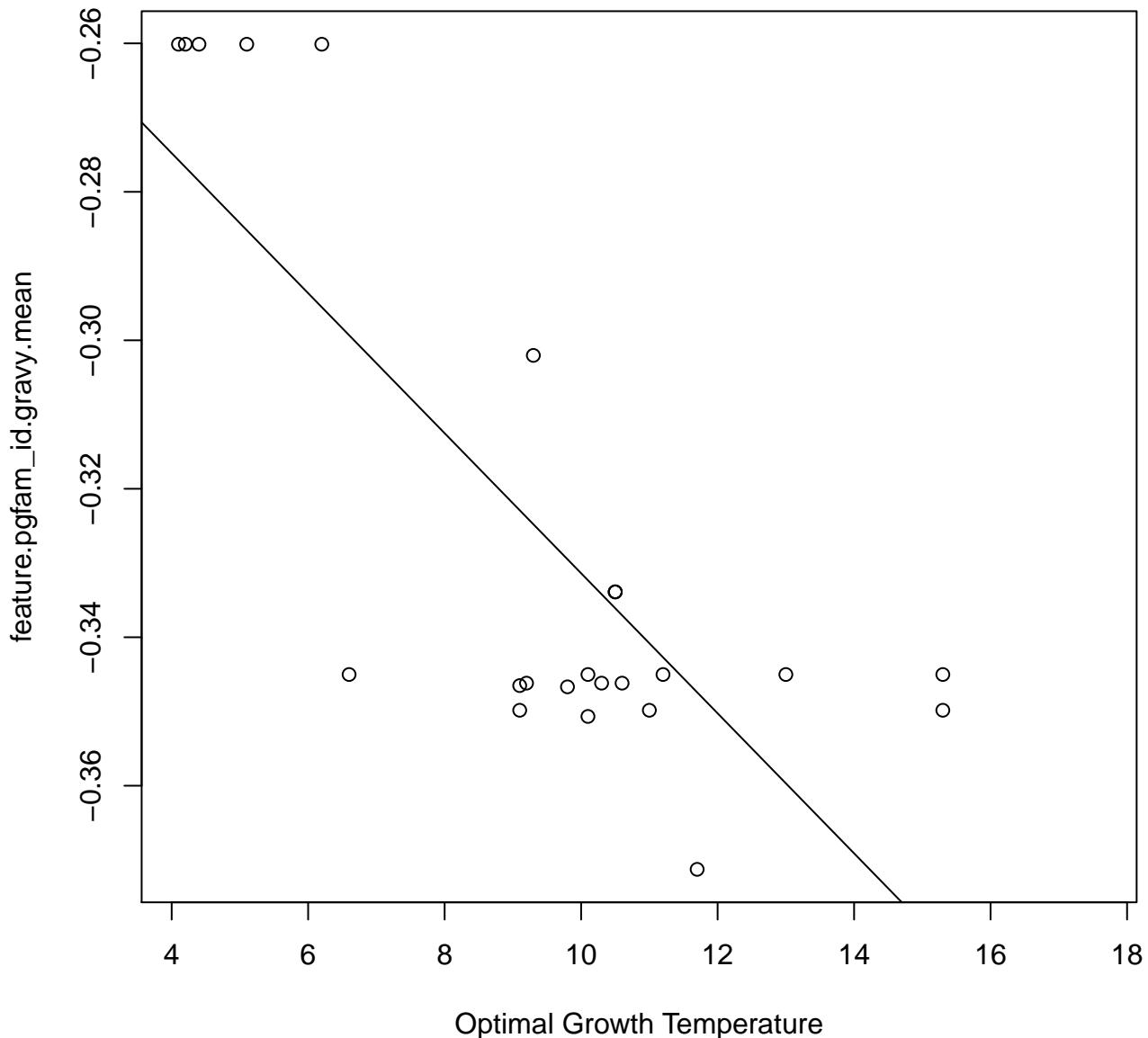
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PGF_00066964
Xanthine/uracil/thiamine/ascorbate permease family protein



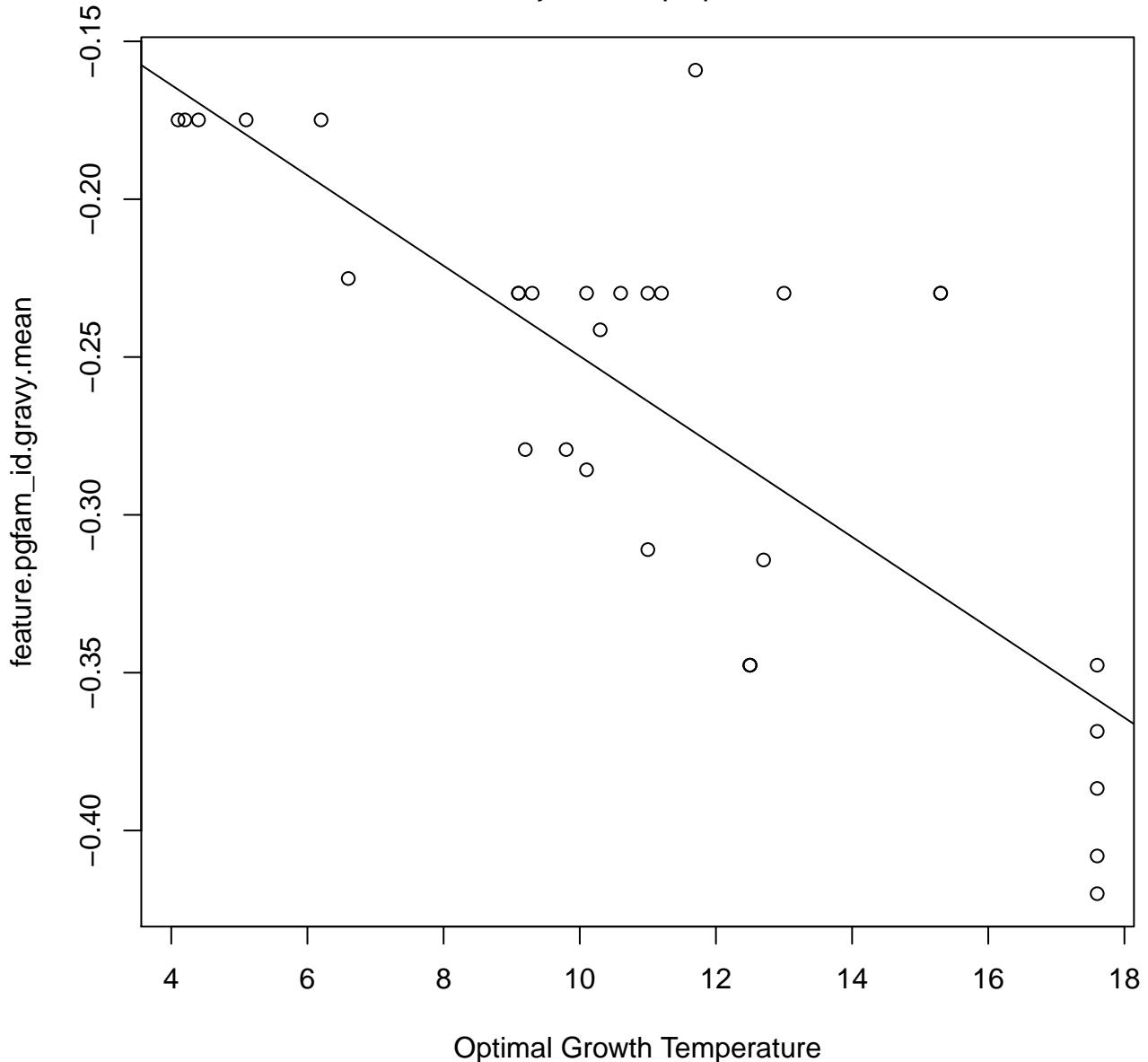
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ATP-dependent RNA helicase SO1501



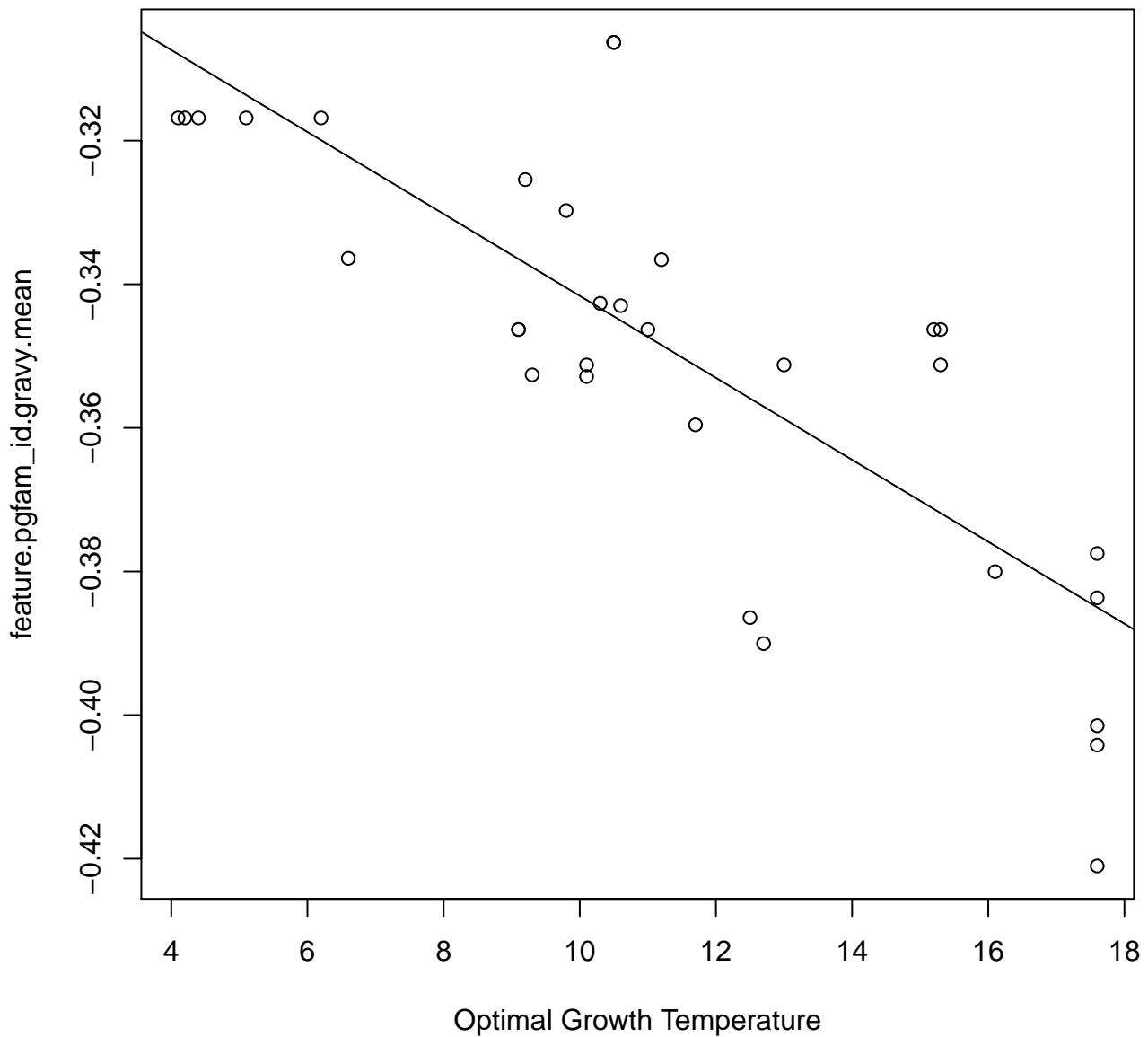
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PGF_03083319
Maltodextrin glucosidase (EC 3.2.1.20)



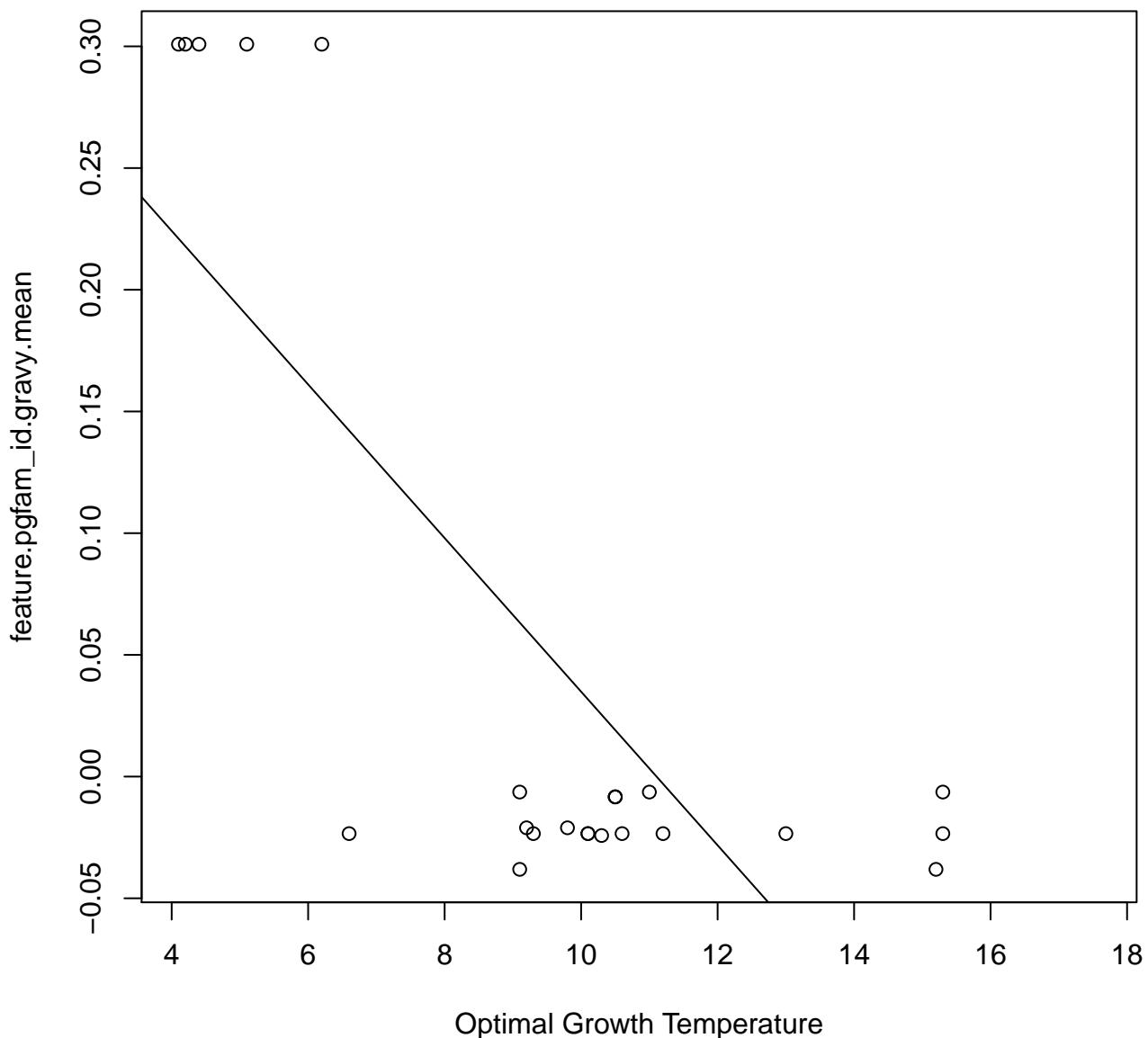
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Alkylated DNA repair protein



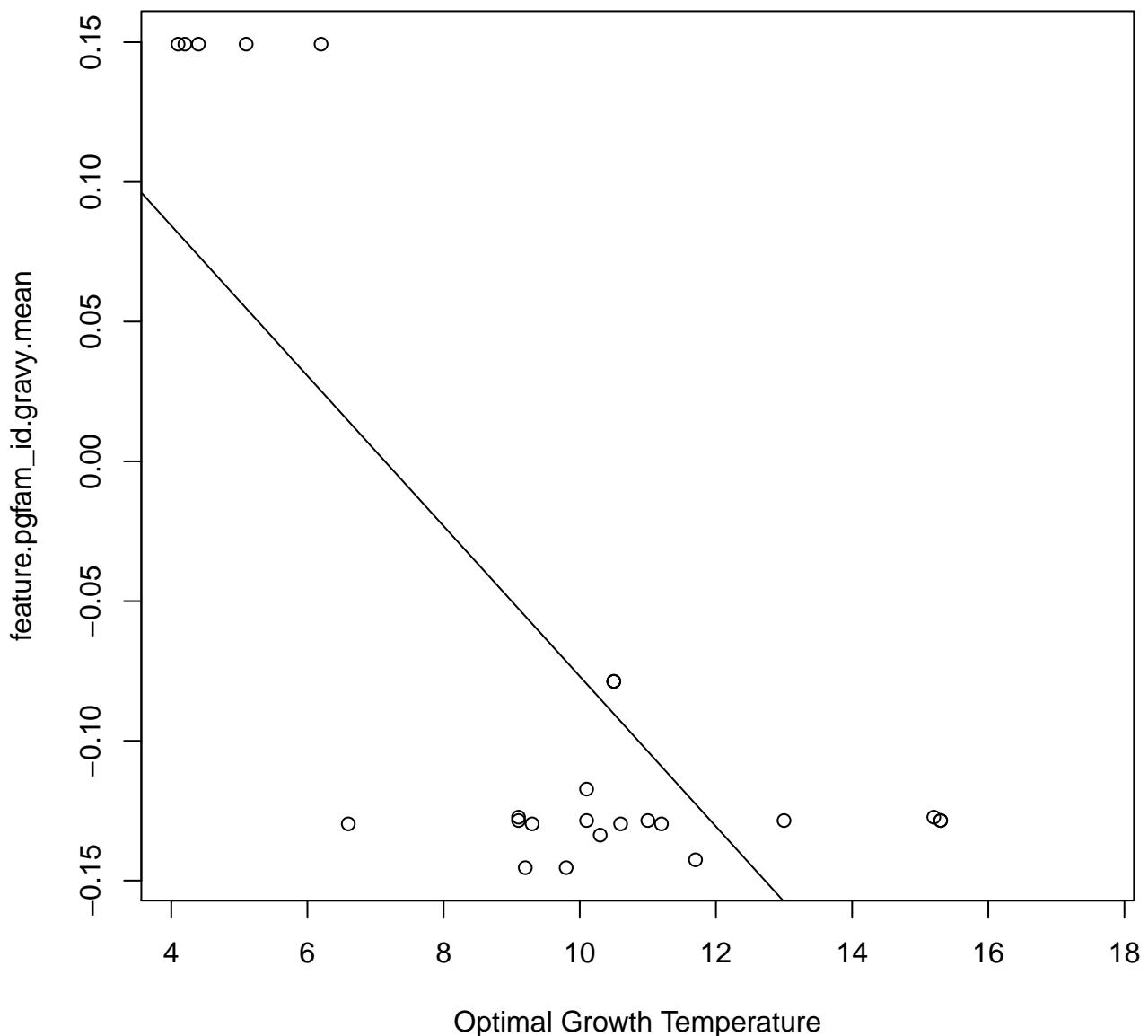
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PGF_12728693
Two-component system sensor histidine kinase/response regulator hybrid



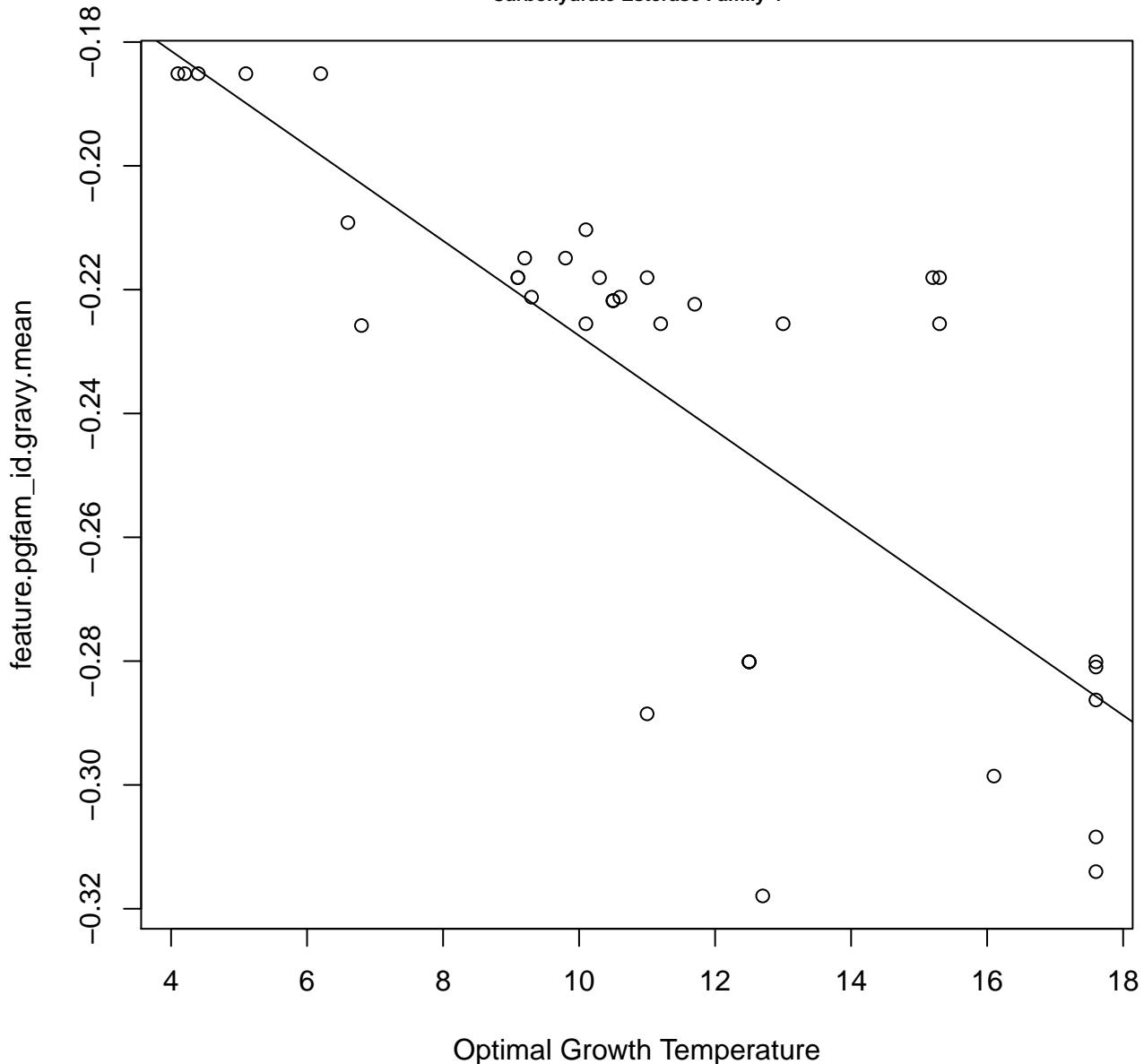
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PGF_12049070
hypothetical protein



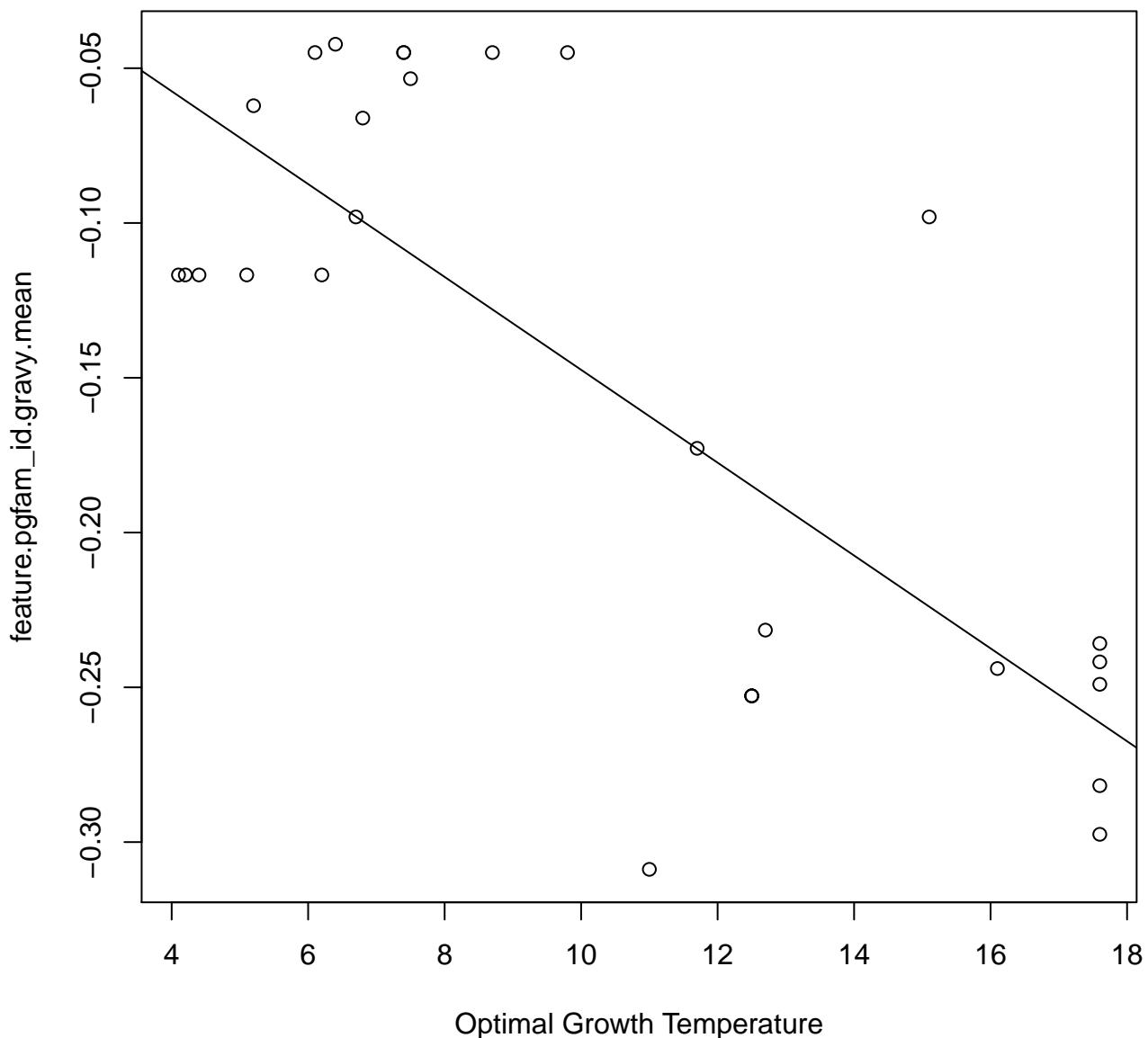
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PGF_11018774
hypothetical protein



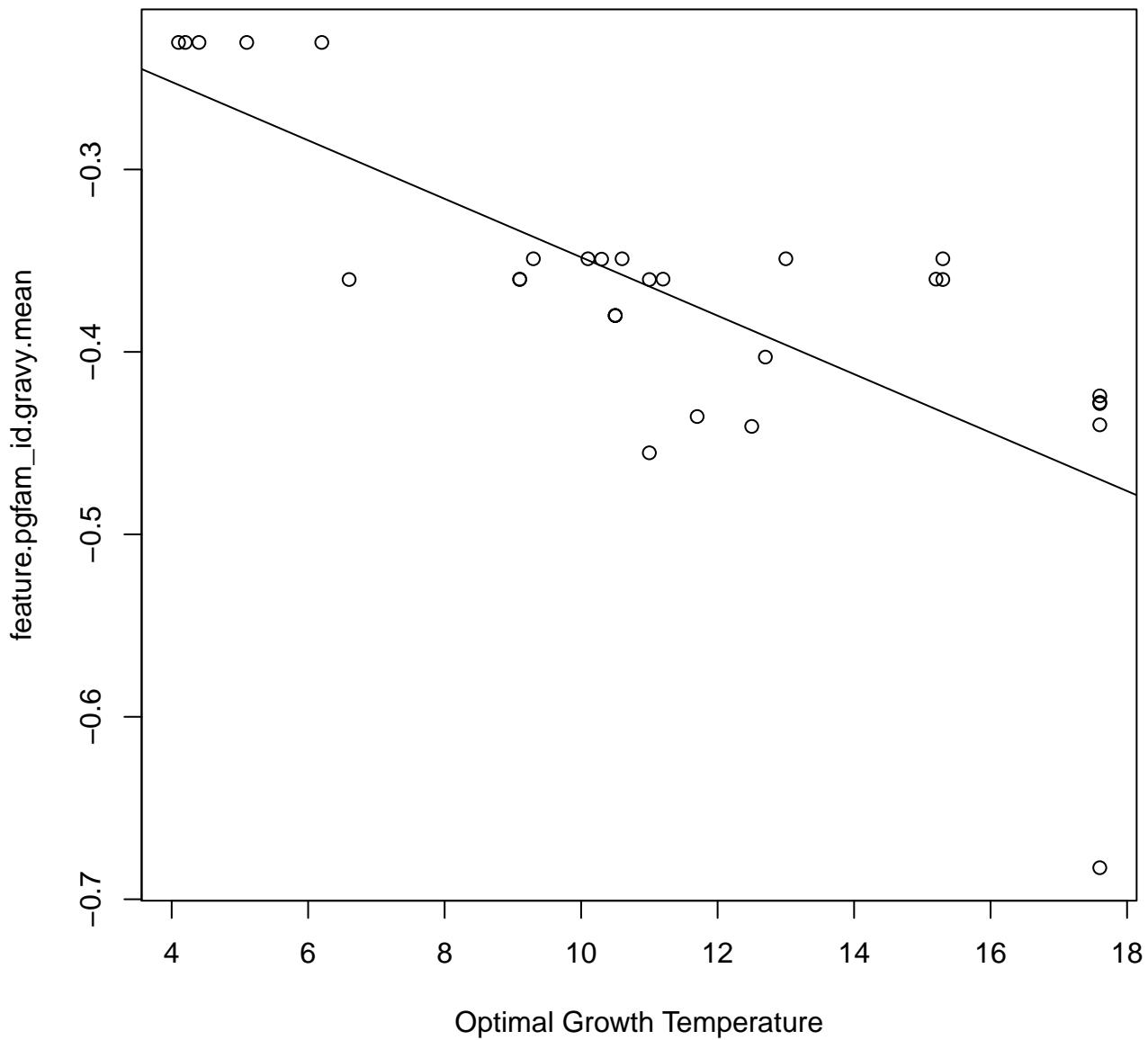
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Carbohydrate Esterase Family 4



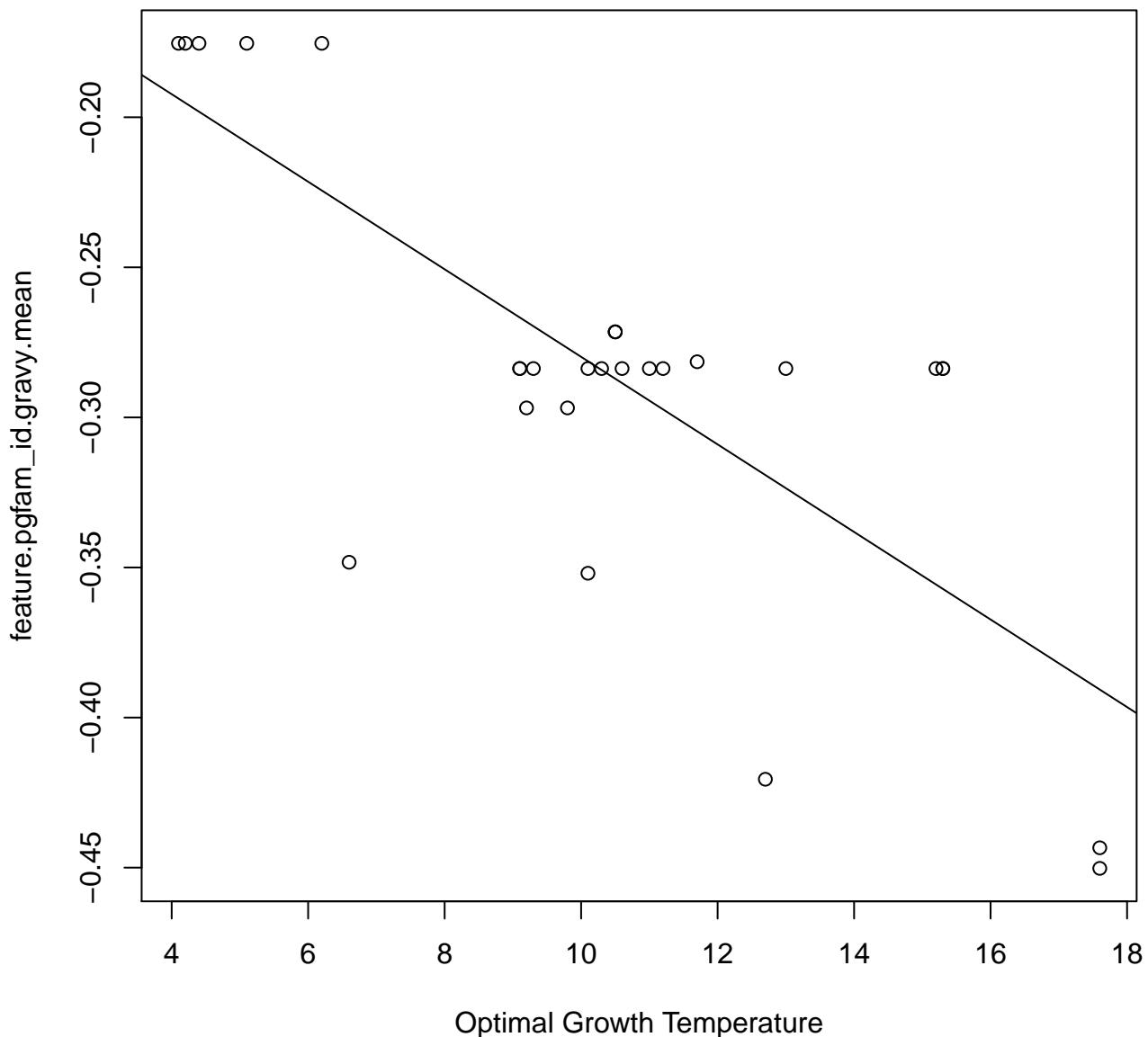
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FIG004599: Hypothetical protein



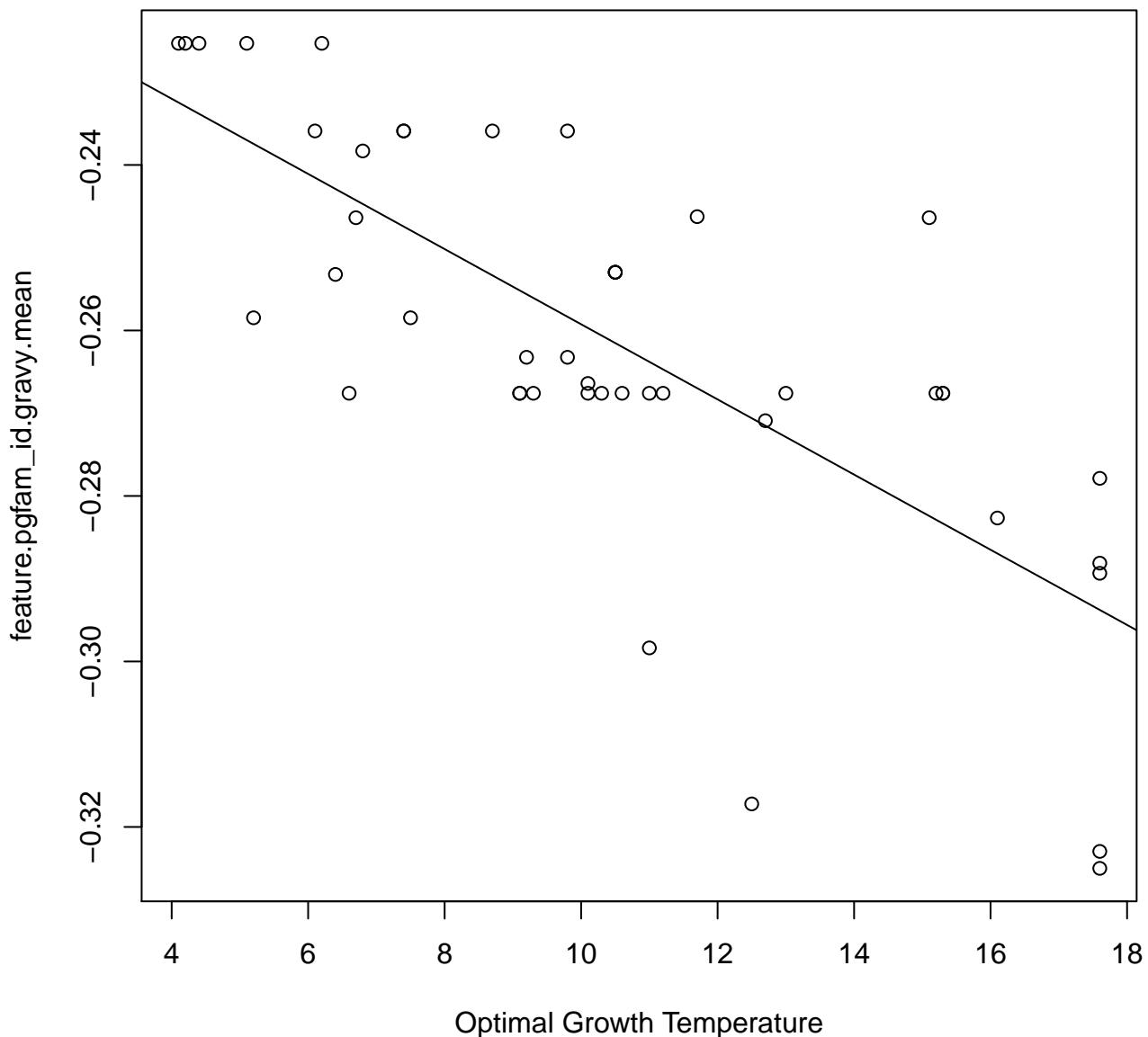
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PGF_02105064
Uncharacterized protease YegQ



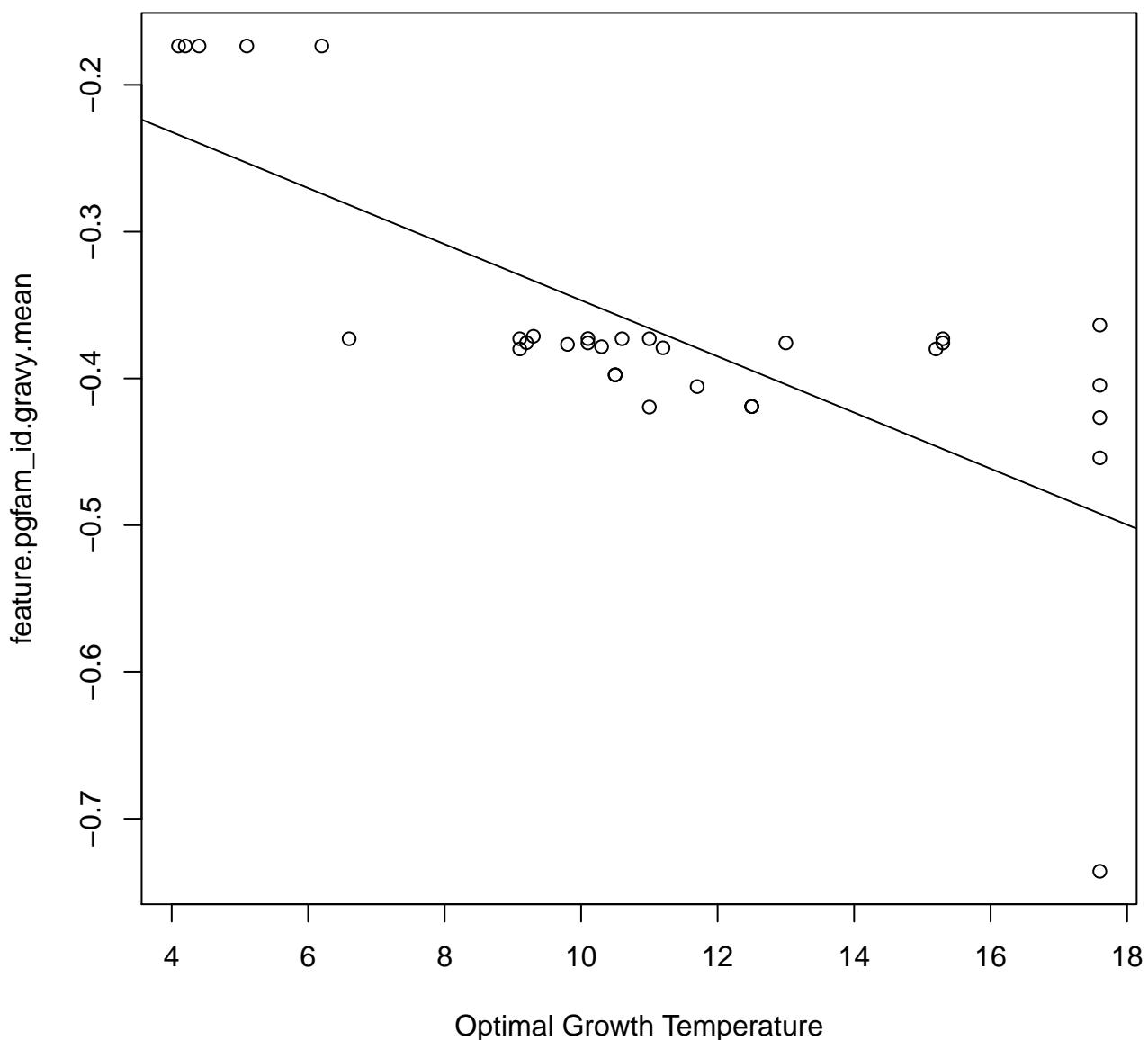
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Chemotaxis protein CheD



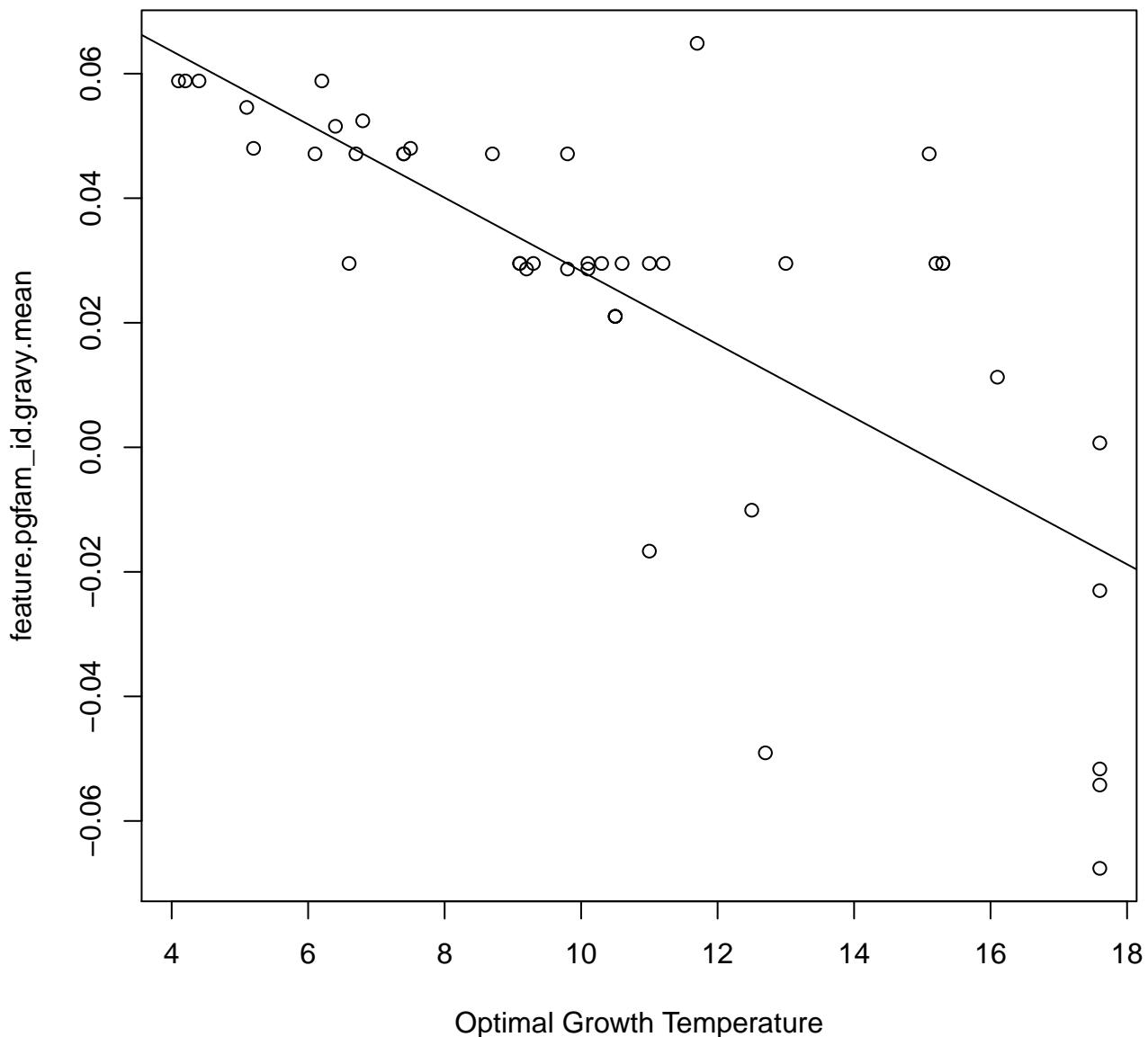
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16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)



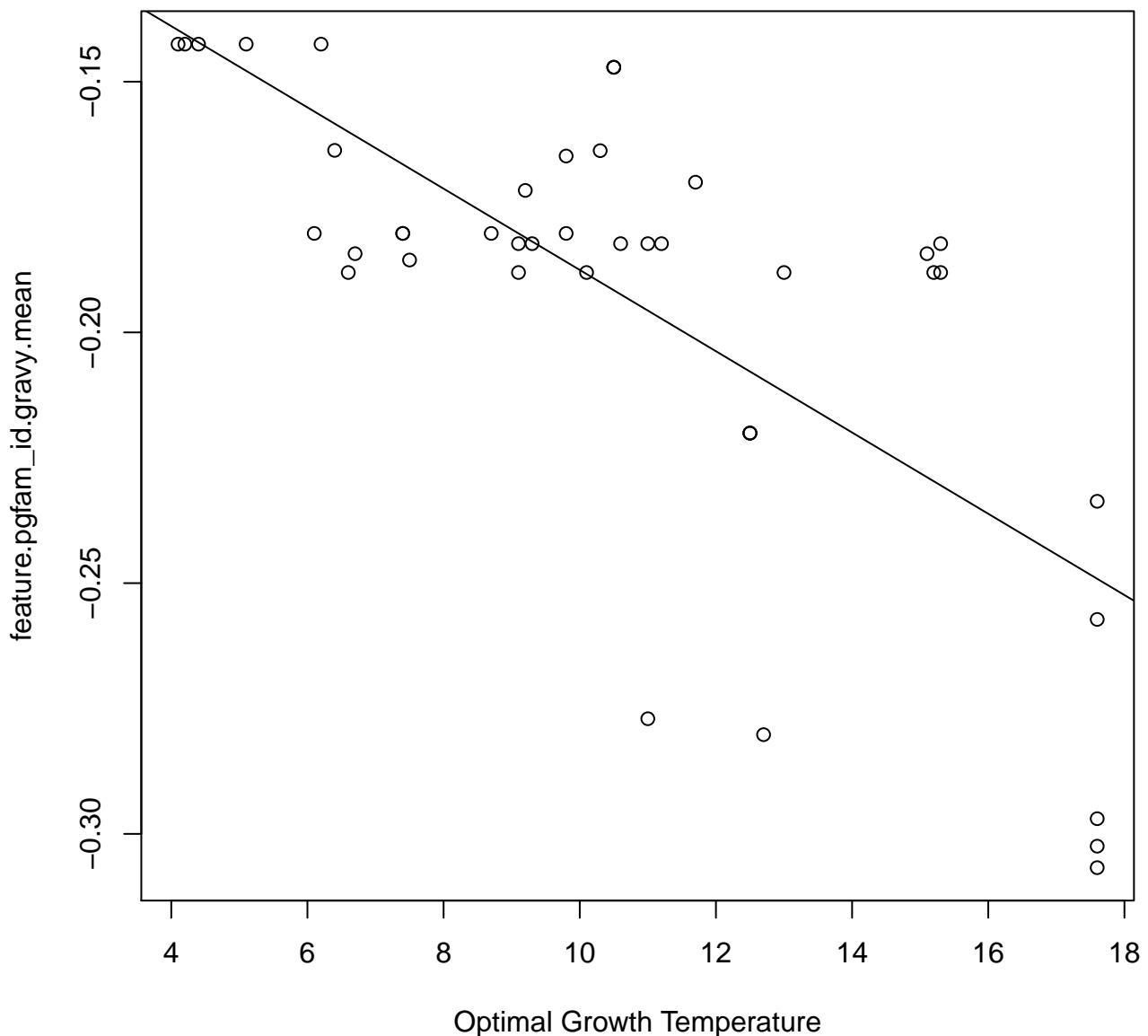
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Fatty acid cis/trans isomerase



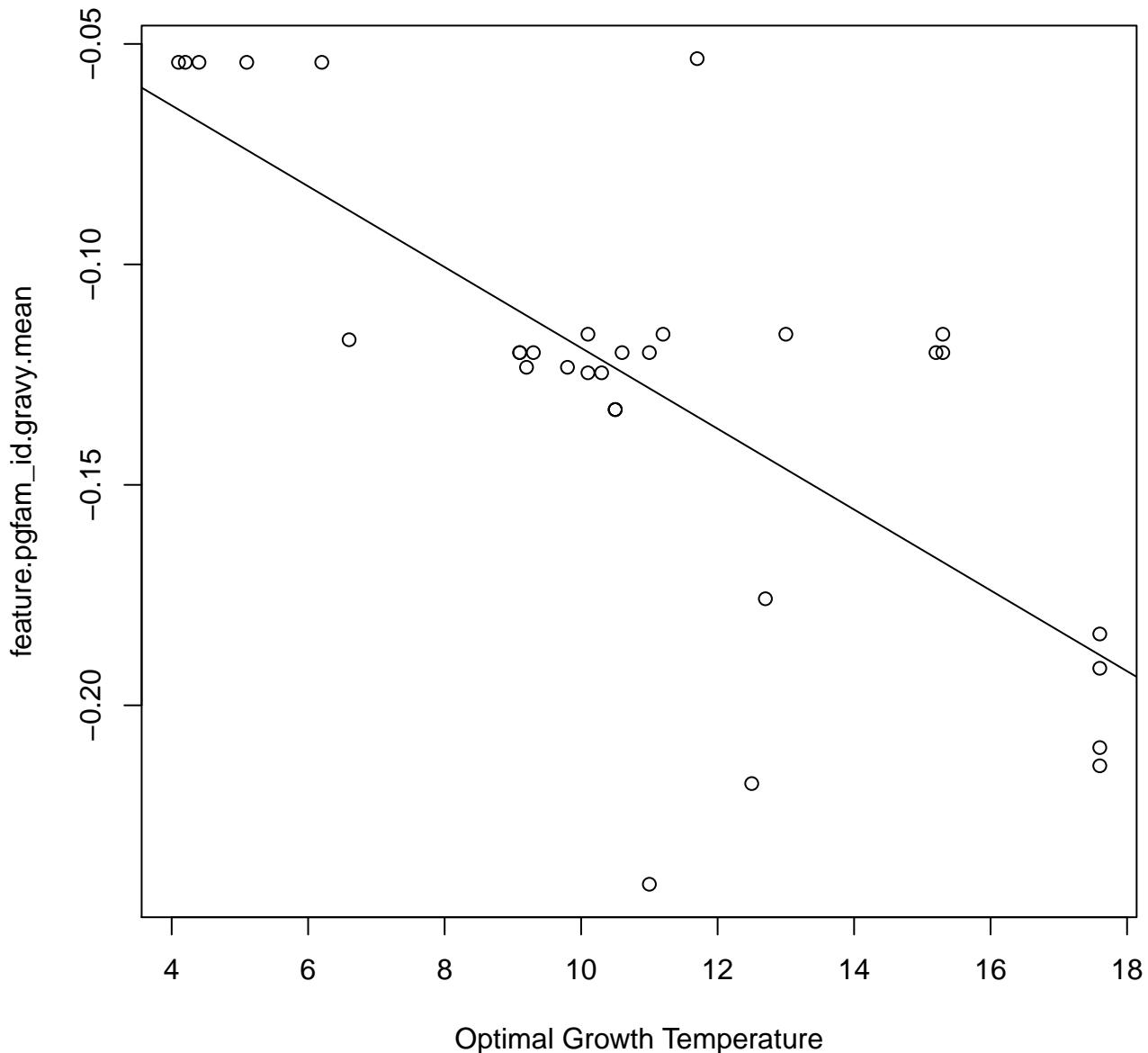
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3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)



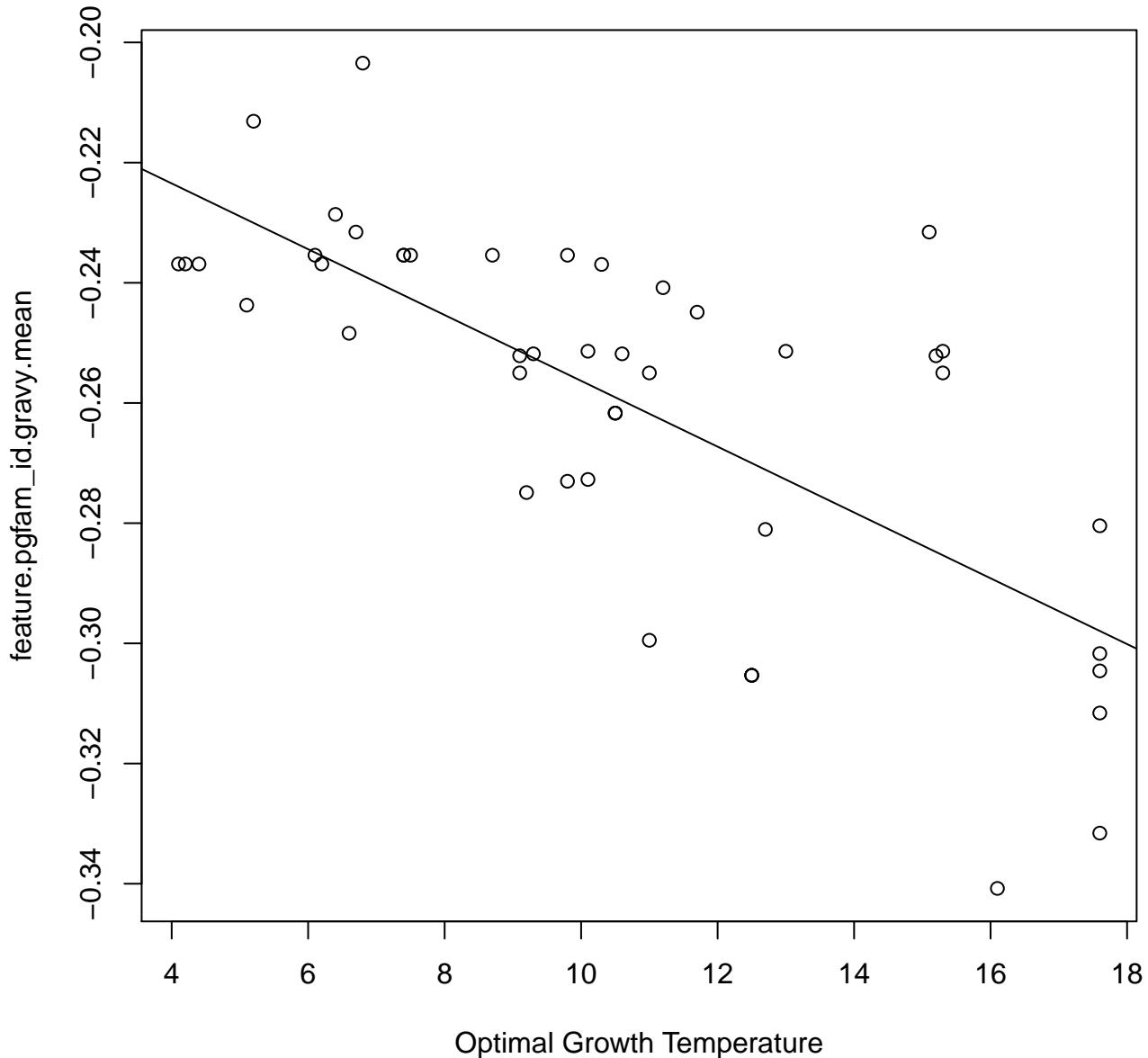
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Peptidase M20:Peptidase M28 precursor



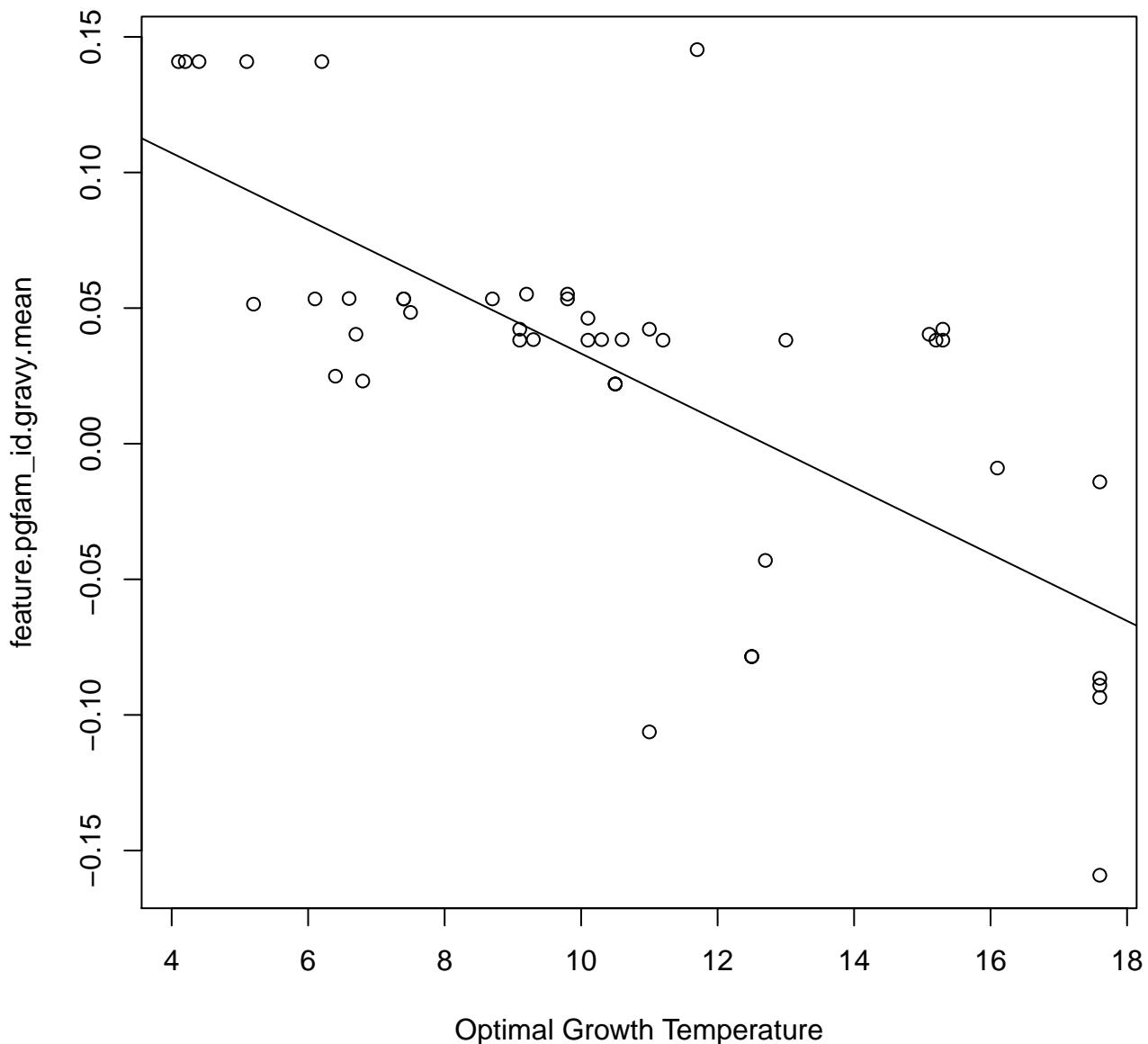
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PGF_10506184
Transcriptional regulator, AcrR family



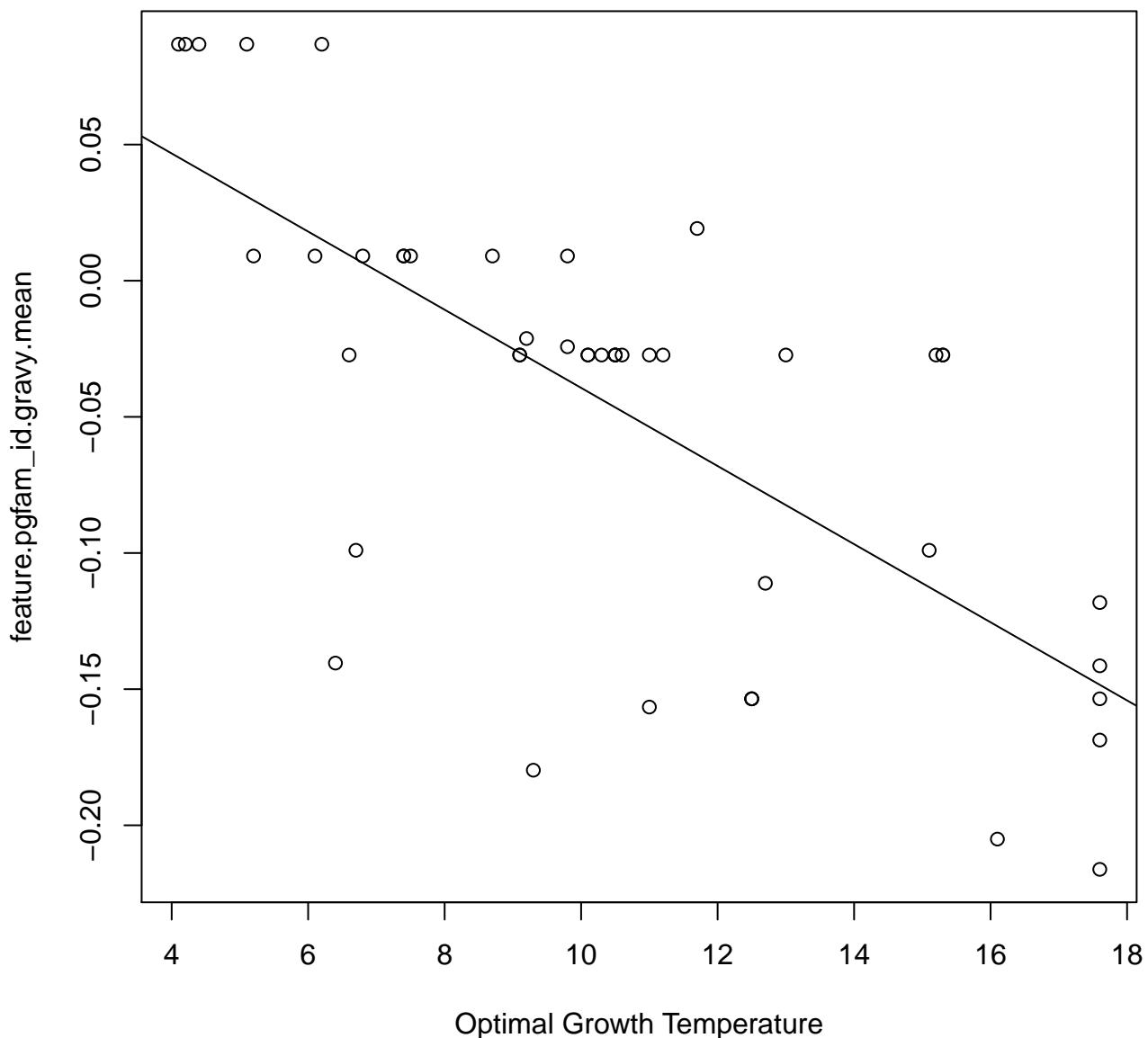
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Peptidase, M23/M37 family



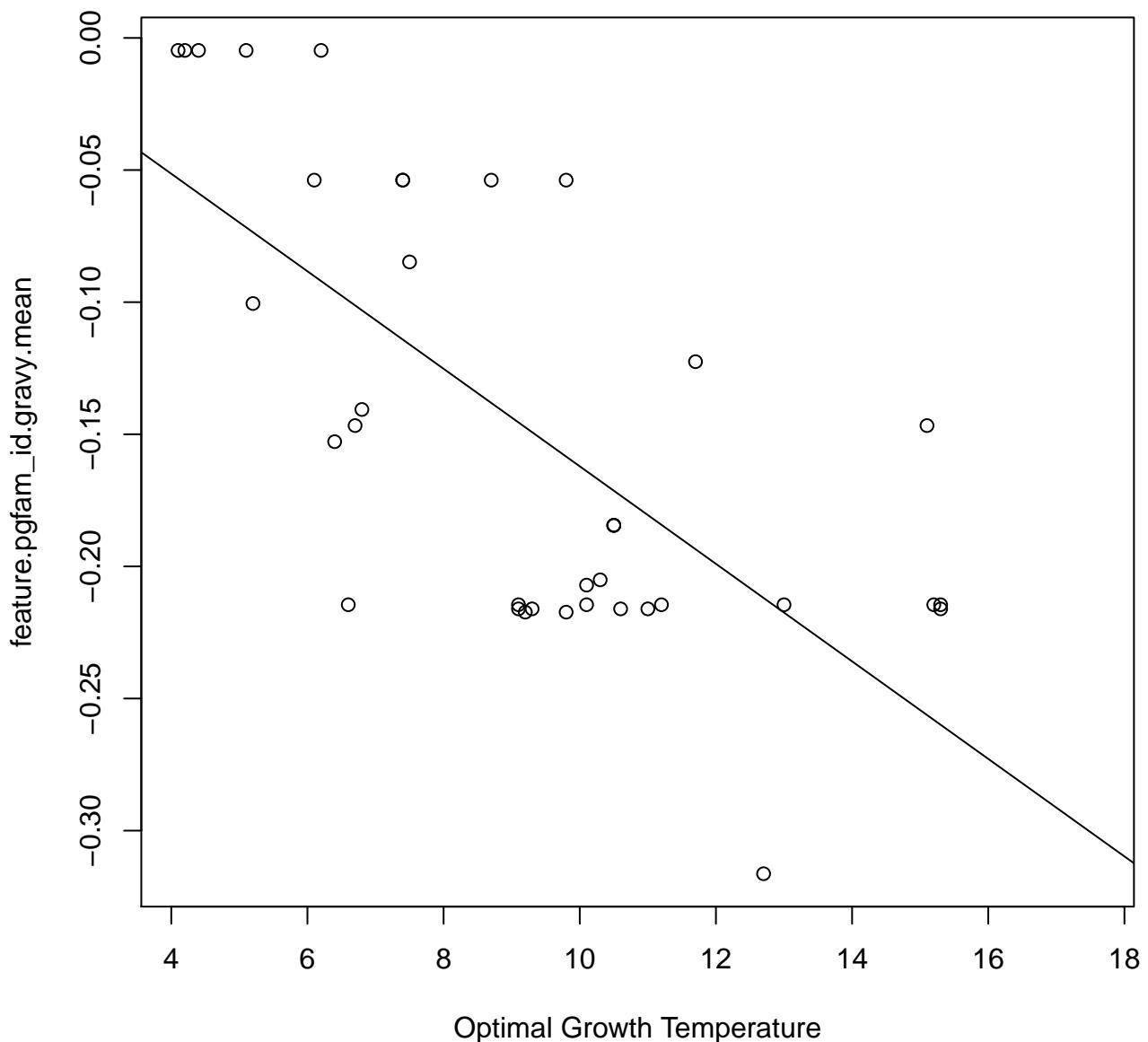
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PGF_03772086
Sensor histidine kinase GirK



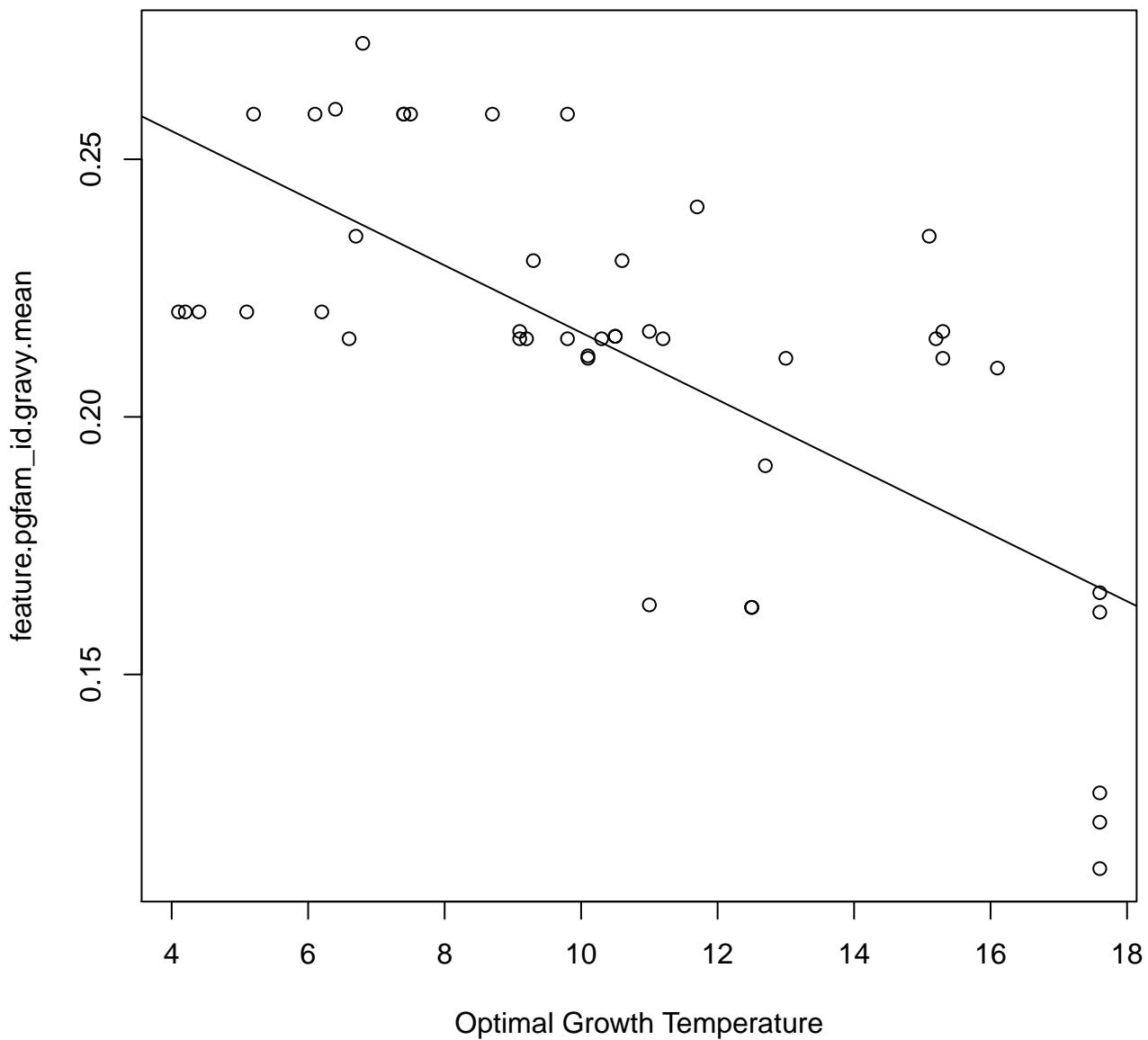
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PGF_01336539
hypothetical protein



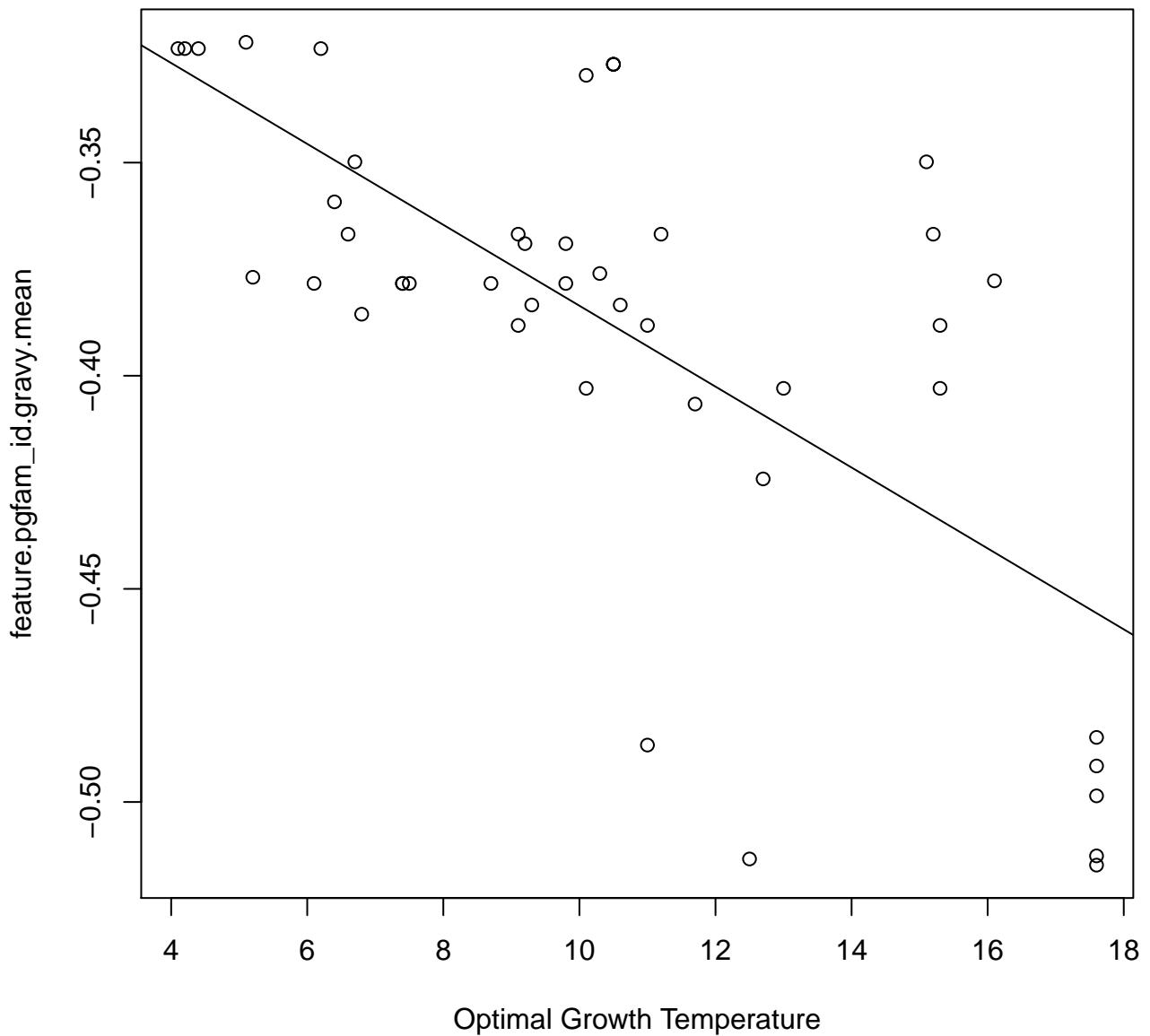
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PGF_01338555
hypothetical protein



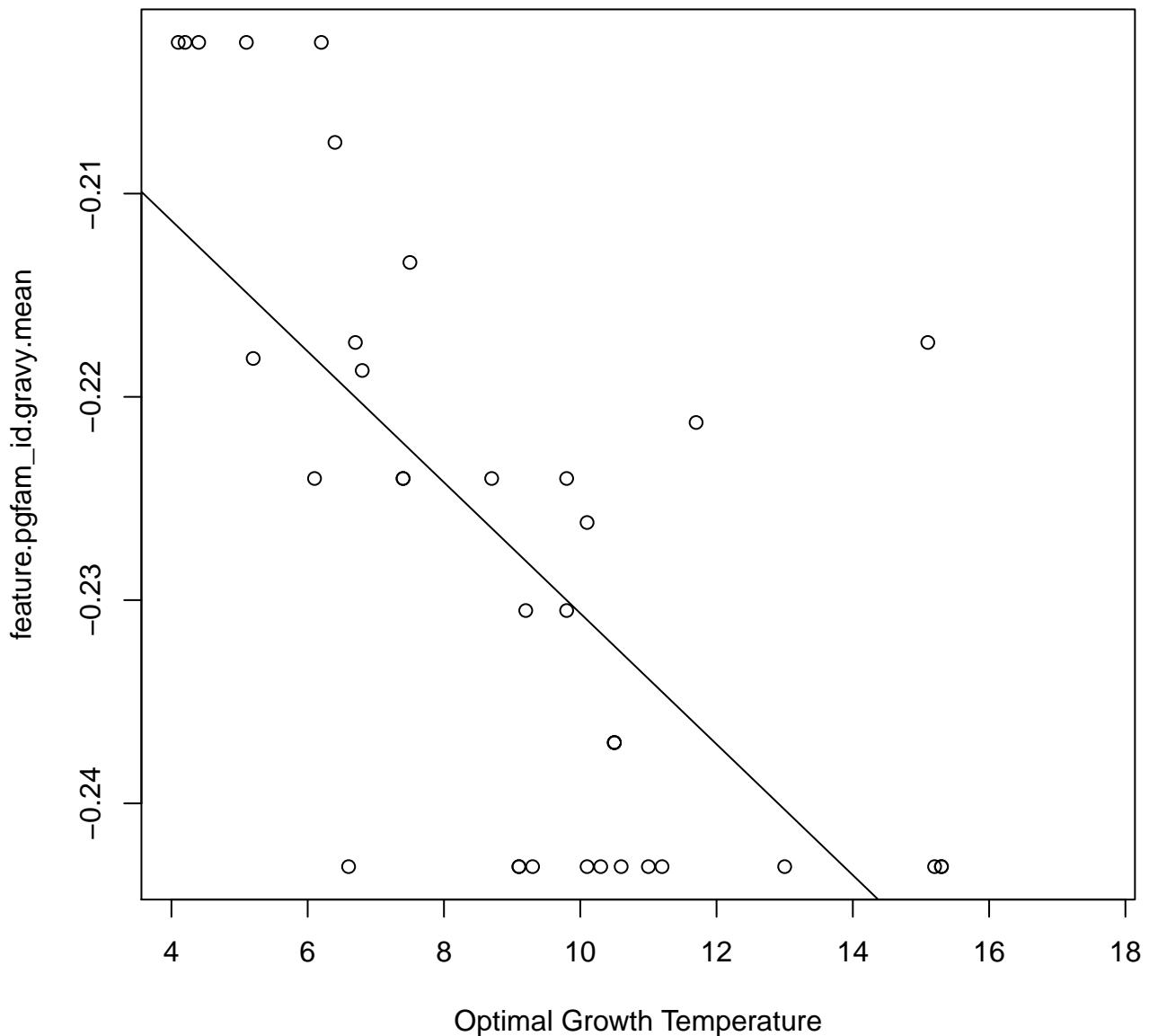
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PGF_00003478
FIG123464: Polysaccharide export protein



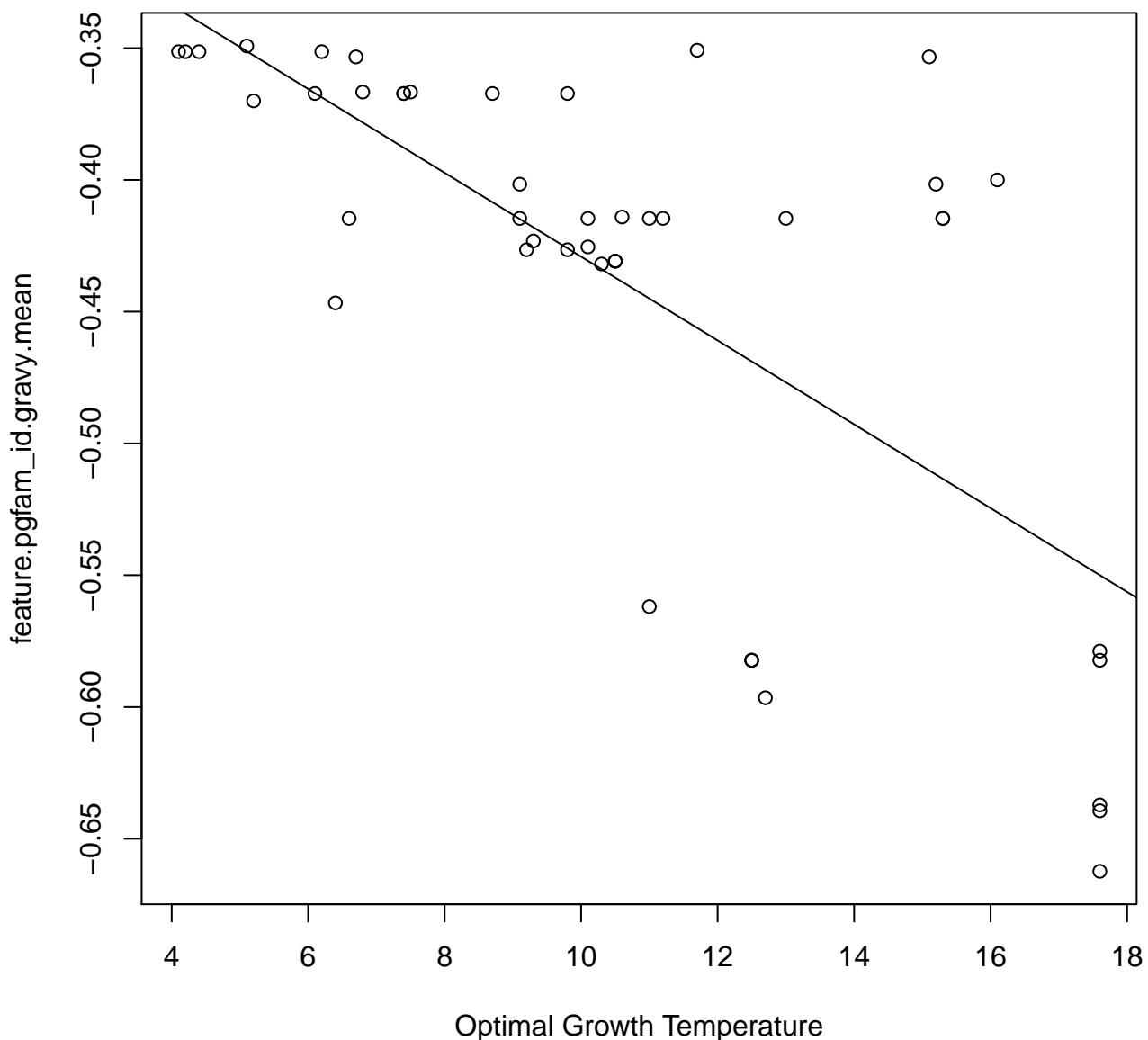
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23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)



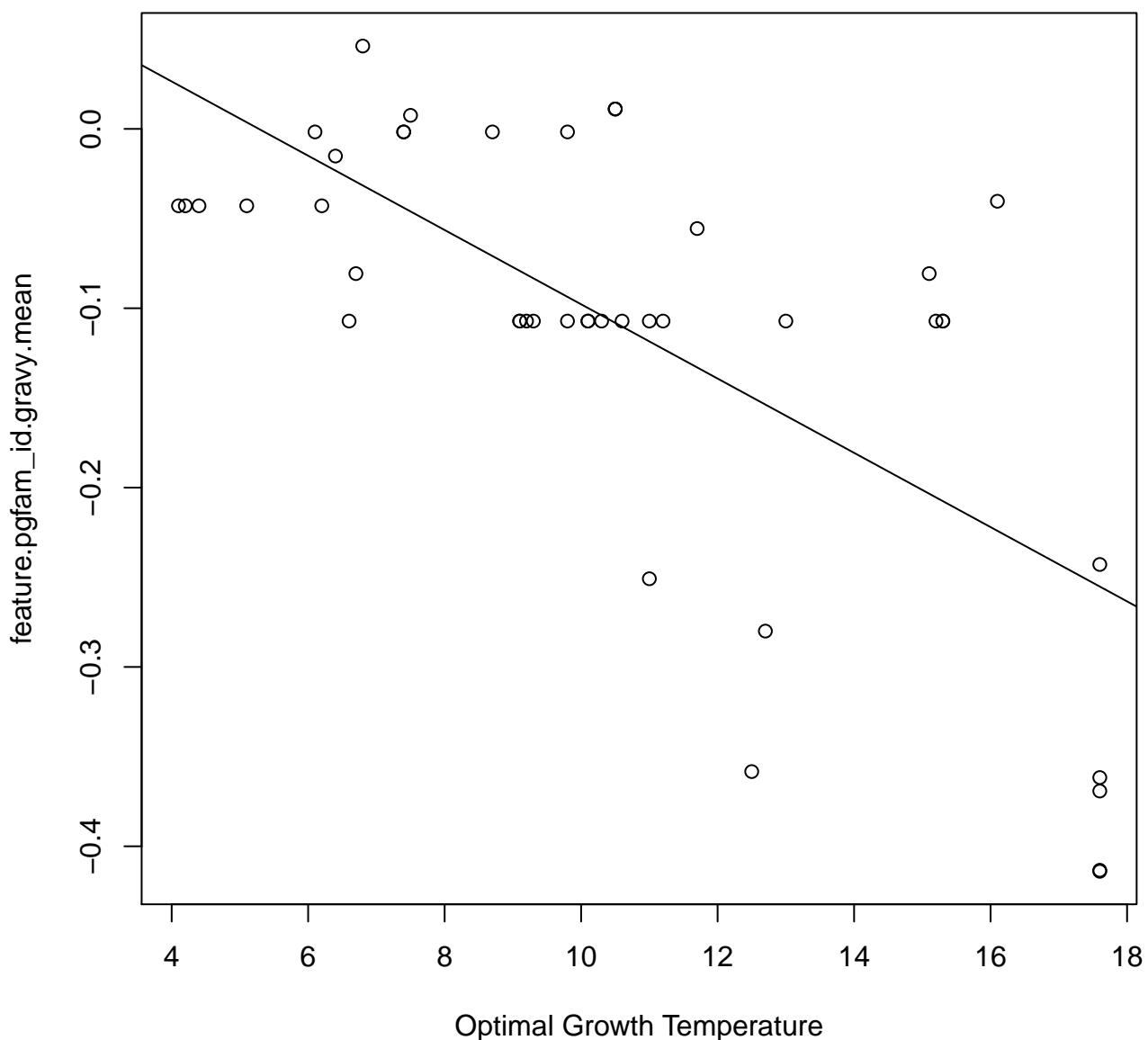
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PGF_00416513
Carbon–nitrogen hydrolase



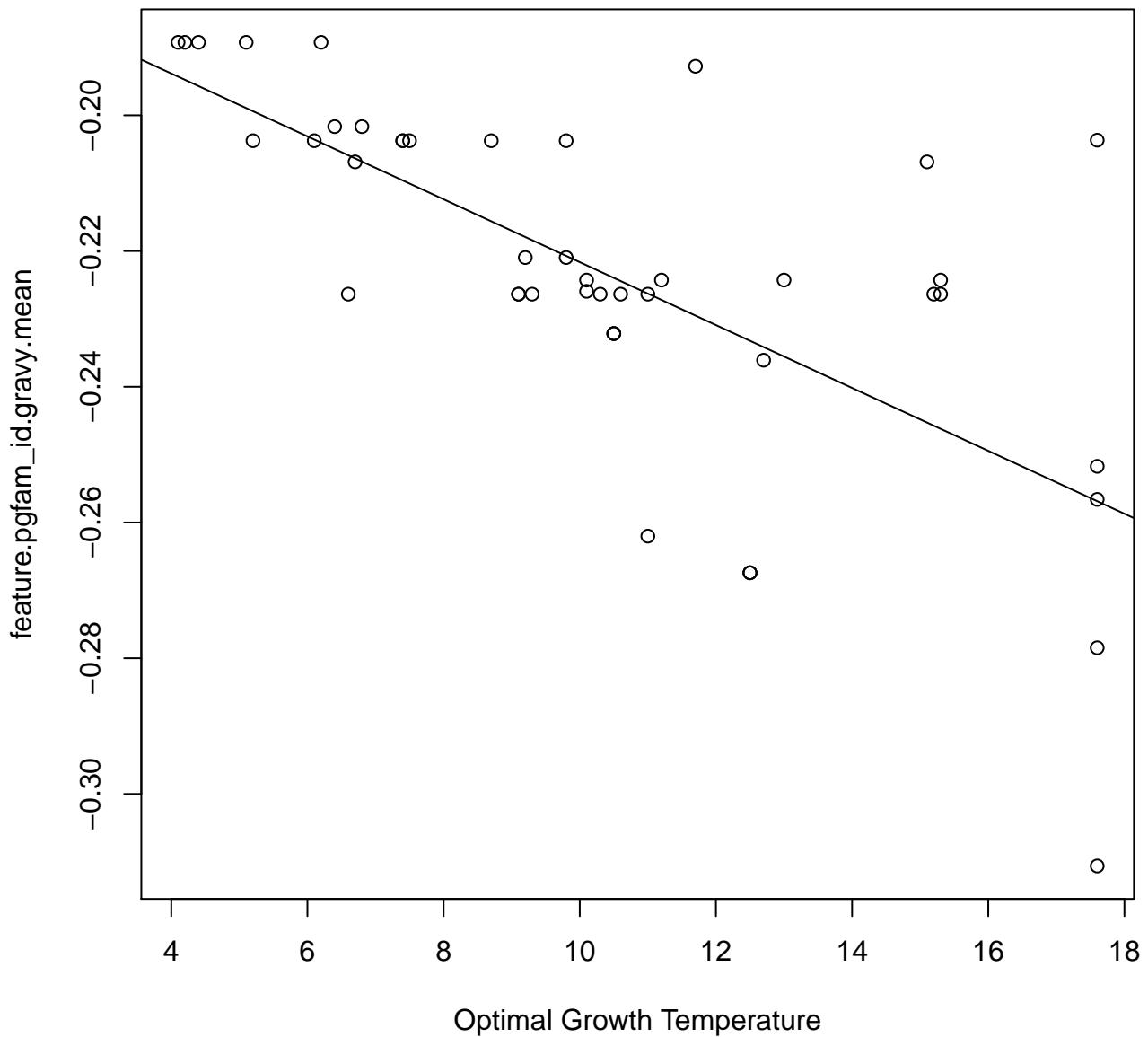
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PGF_00064199
UPF0115 protein YfcN



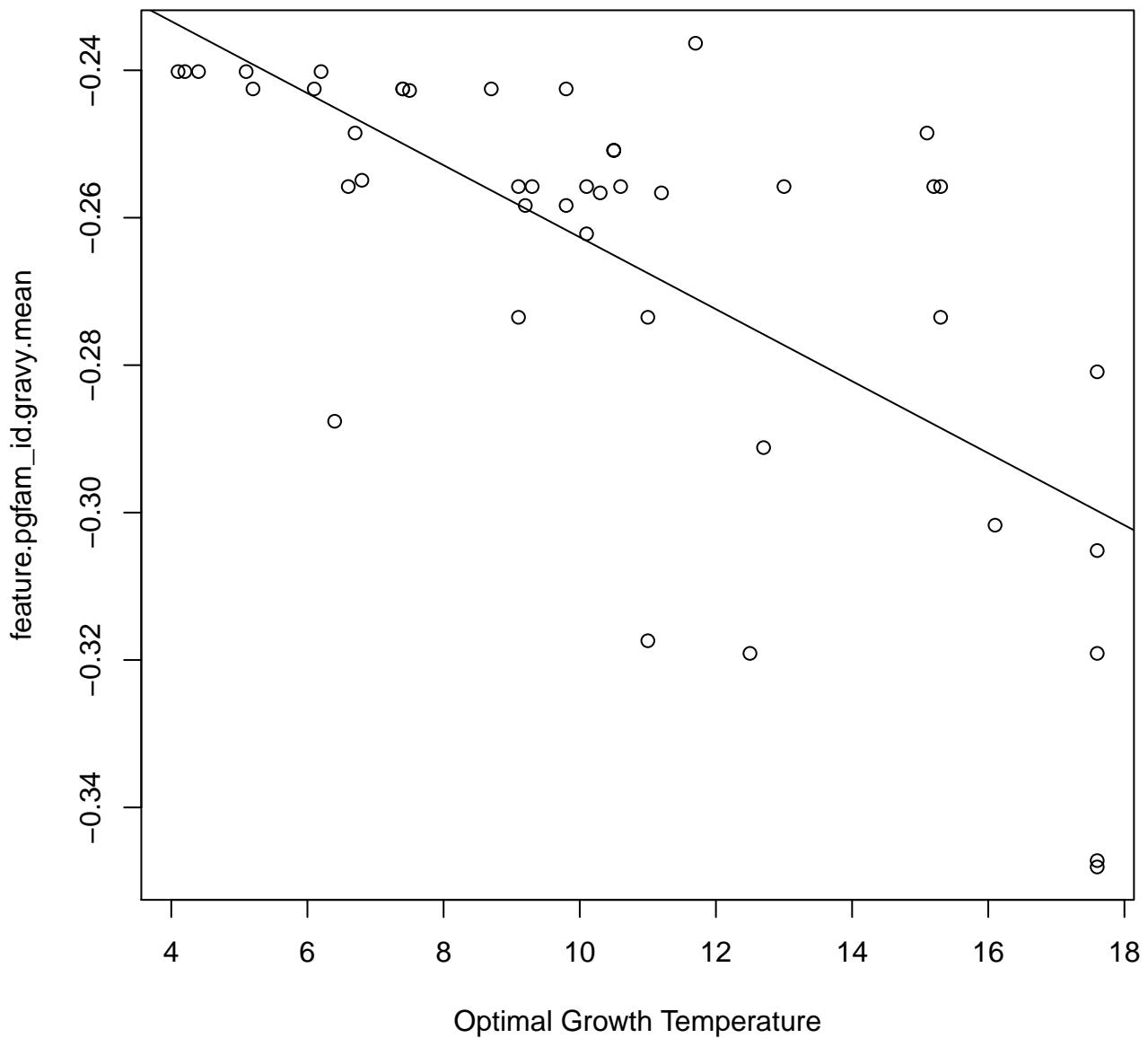
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PGF_00335891
hypothetical protein



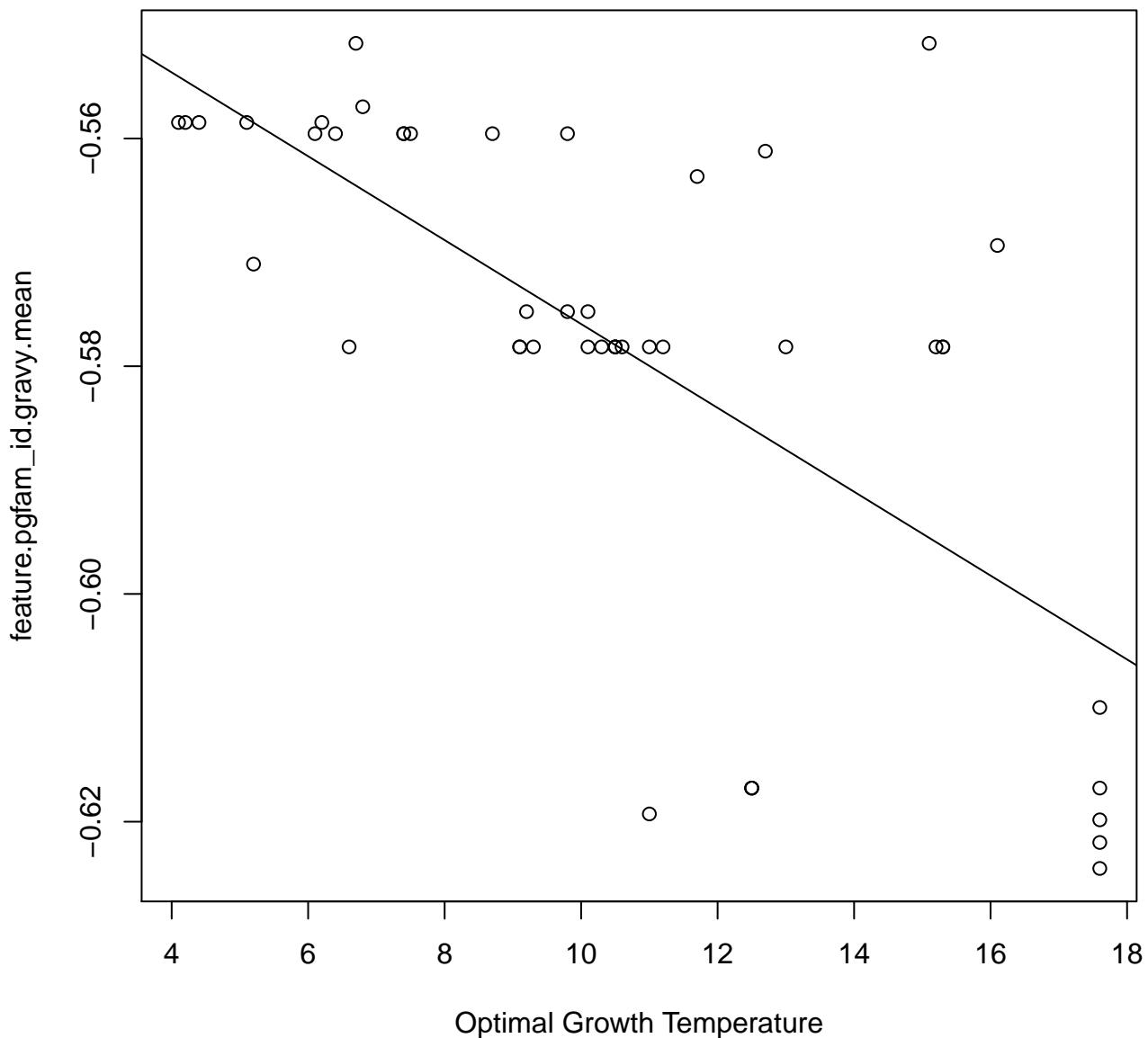
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PGF_06775354
DNA-binding transcriptional regulator, MocR family / aminotransferase domain



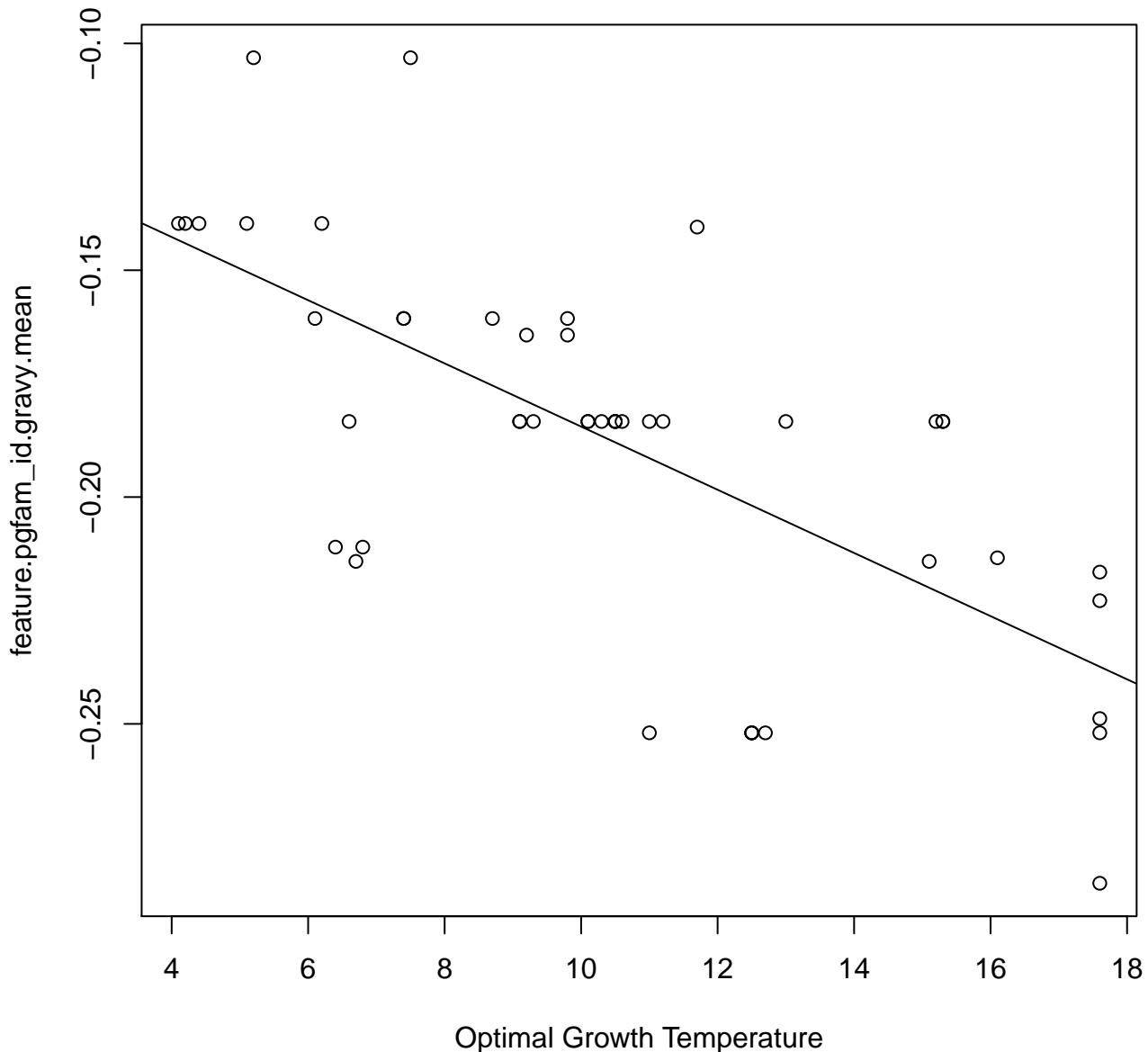
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PGF_09676755
Nitrogen regulation protein NR(I), GlnG (=NtrC)



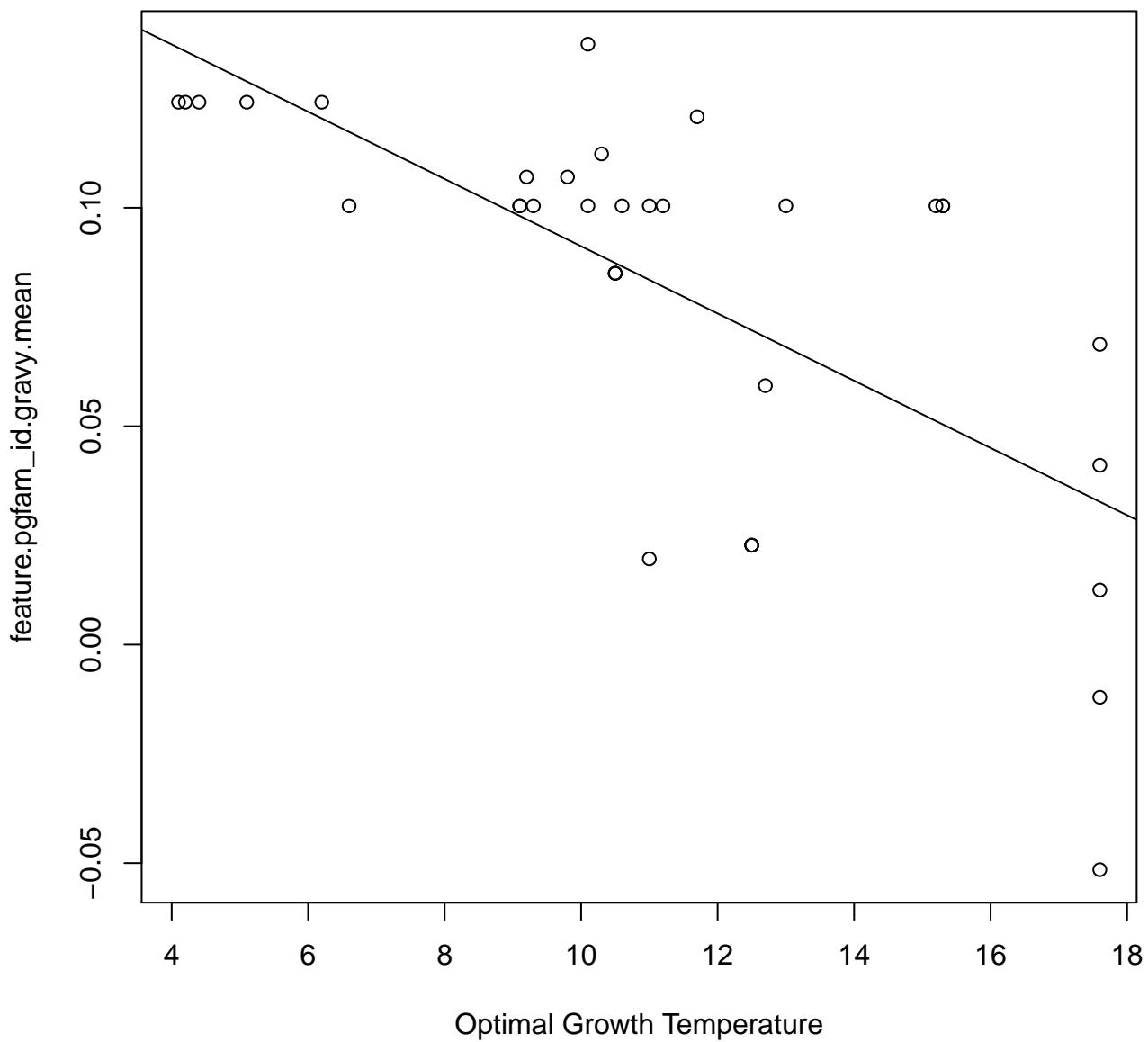
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RNA polymerase sigma factor RpoD



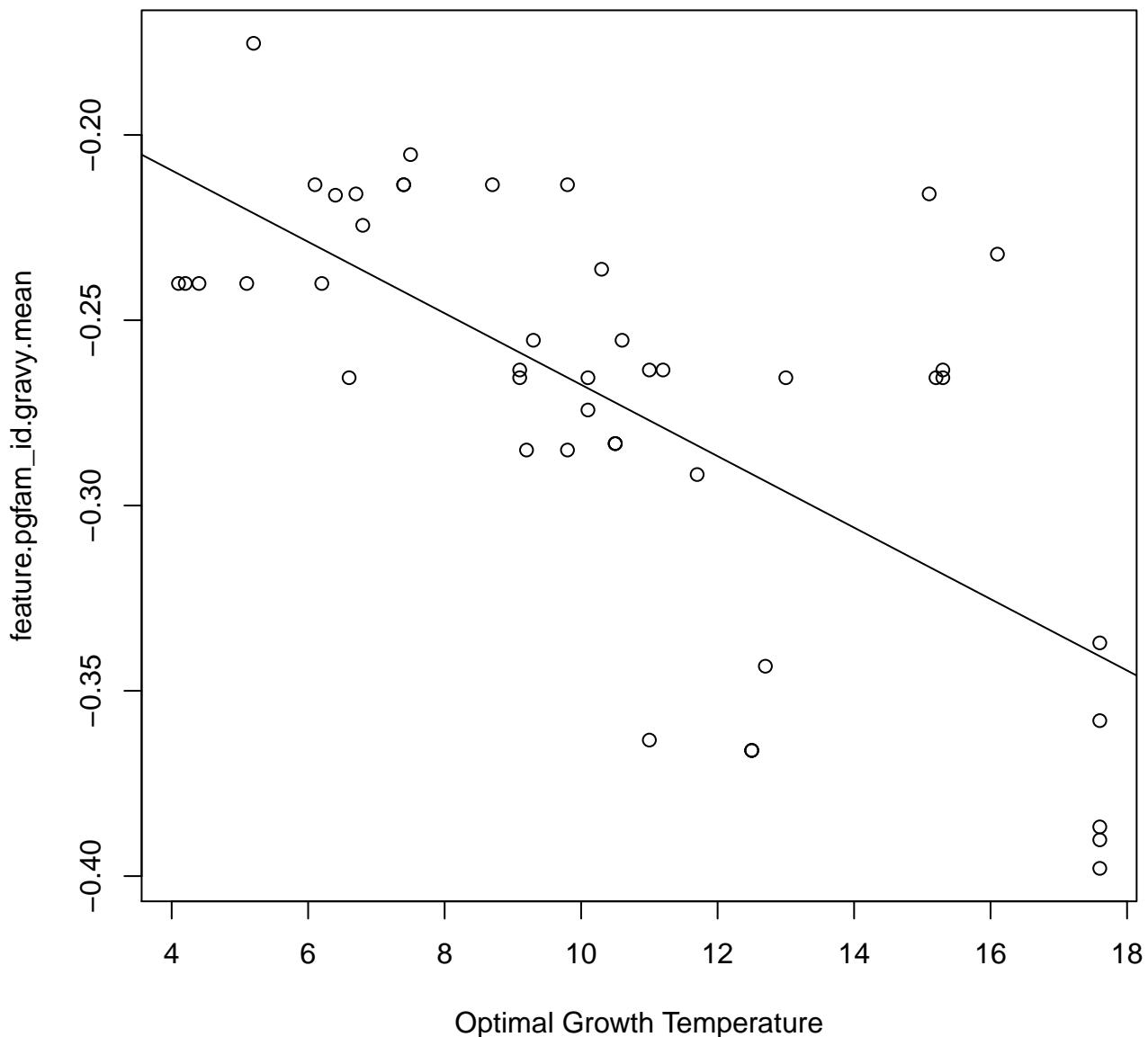
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Iron-sulfur cluster assembly scaffold protein IscU



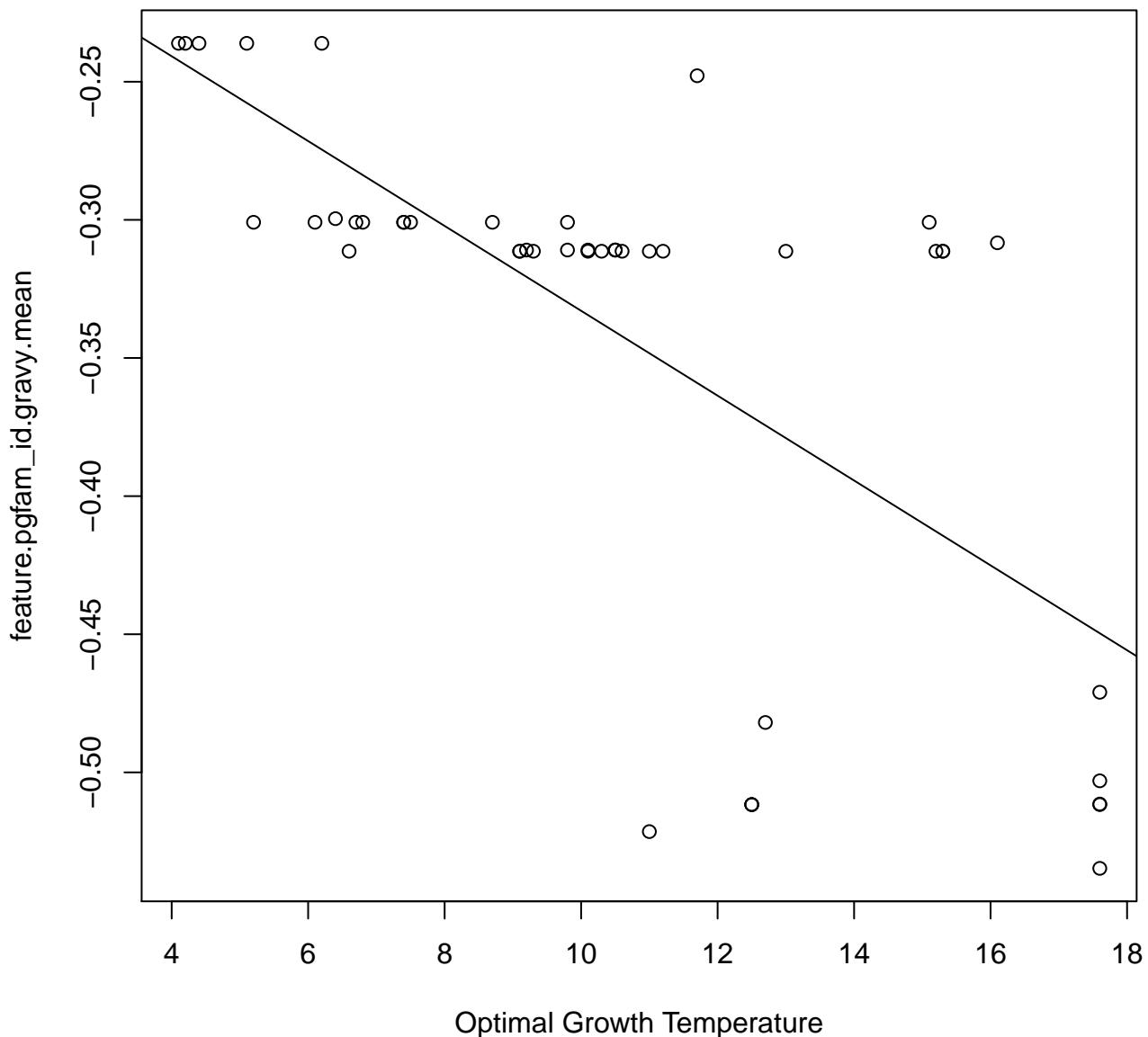
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PGF_01336399
hypothetical protein



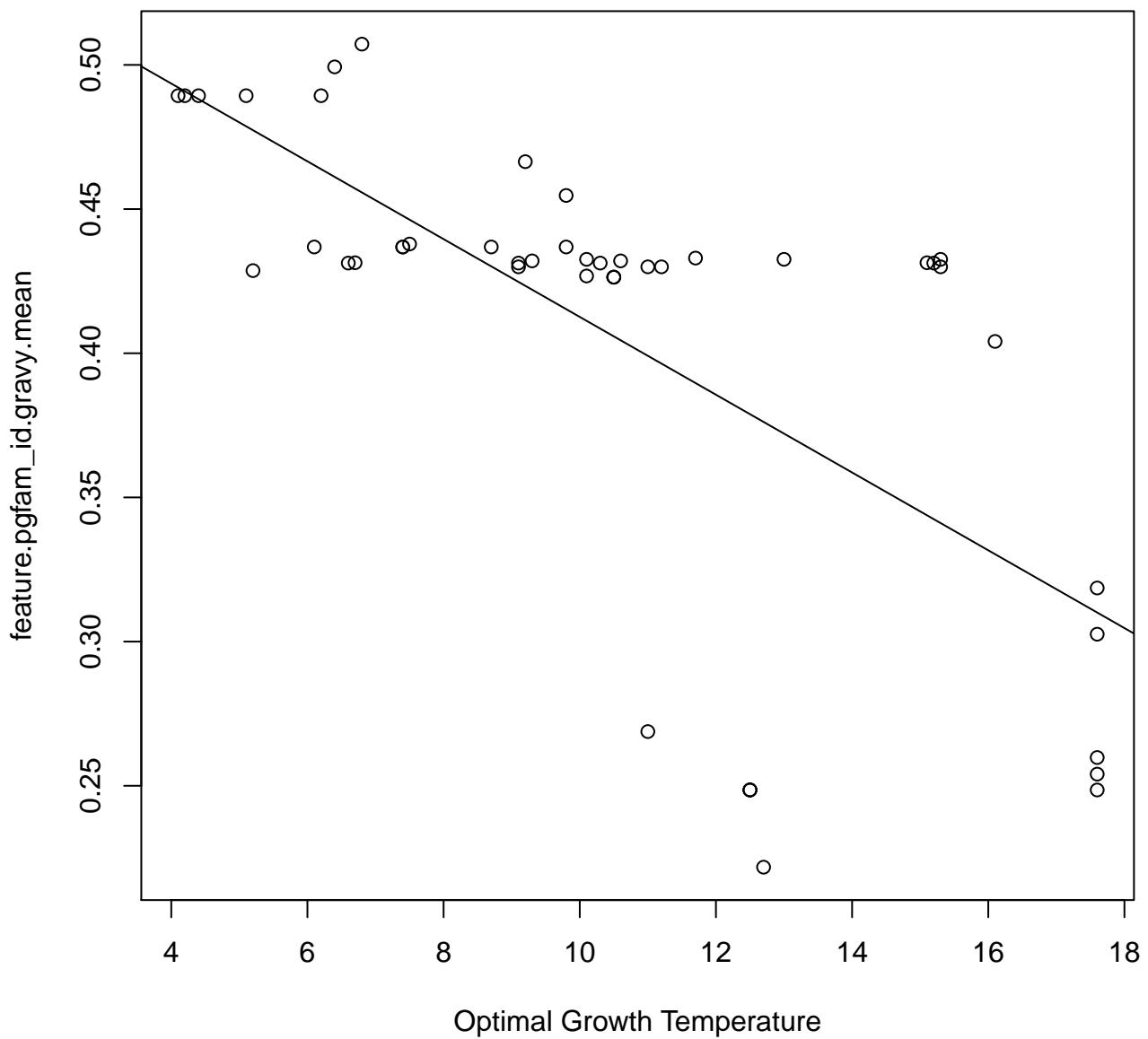
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NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.13)



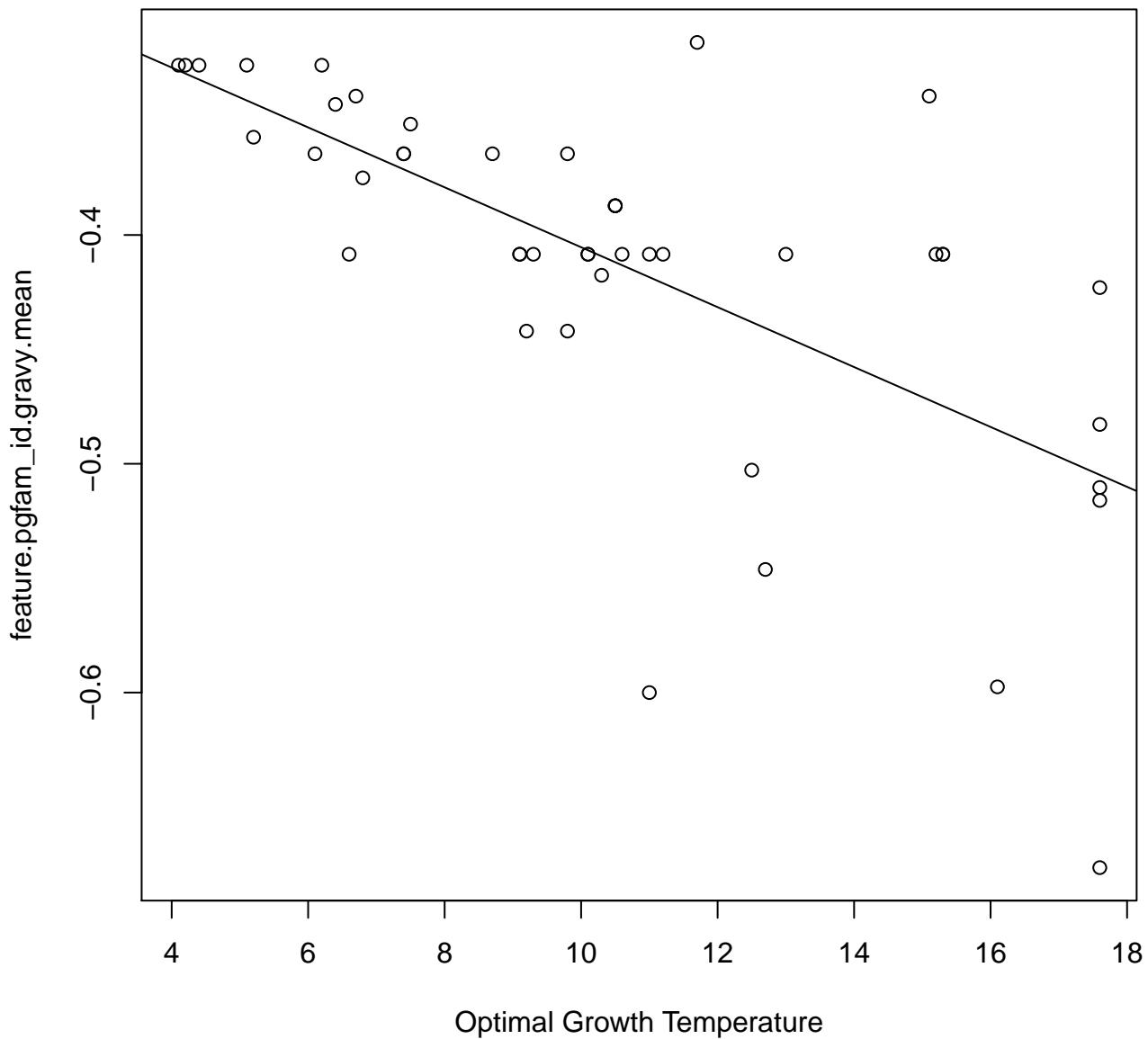
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Ribonuclease III (EC 3.1.26.3)



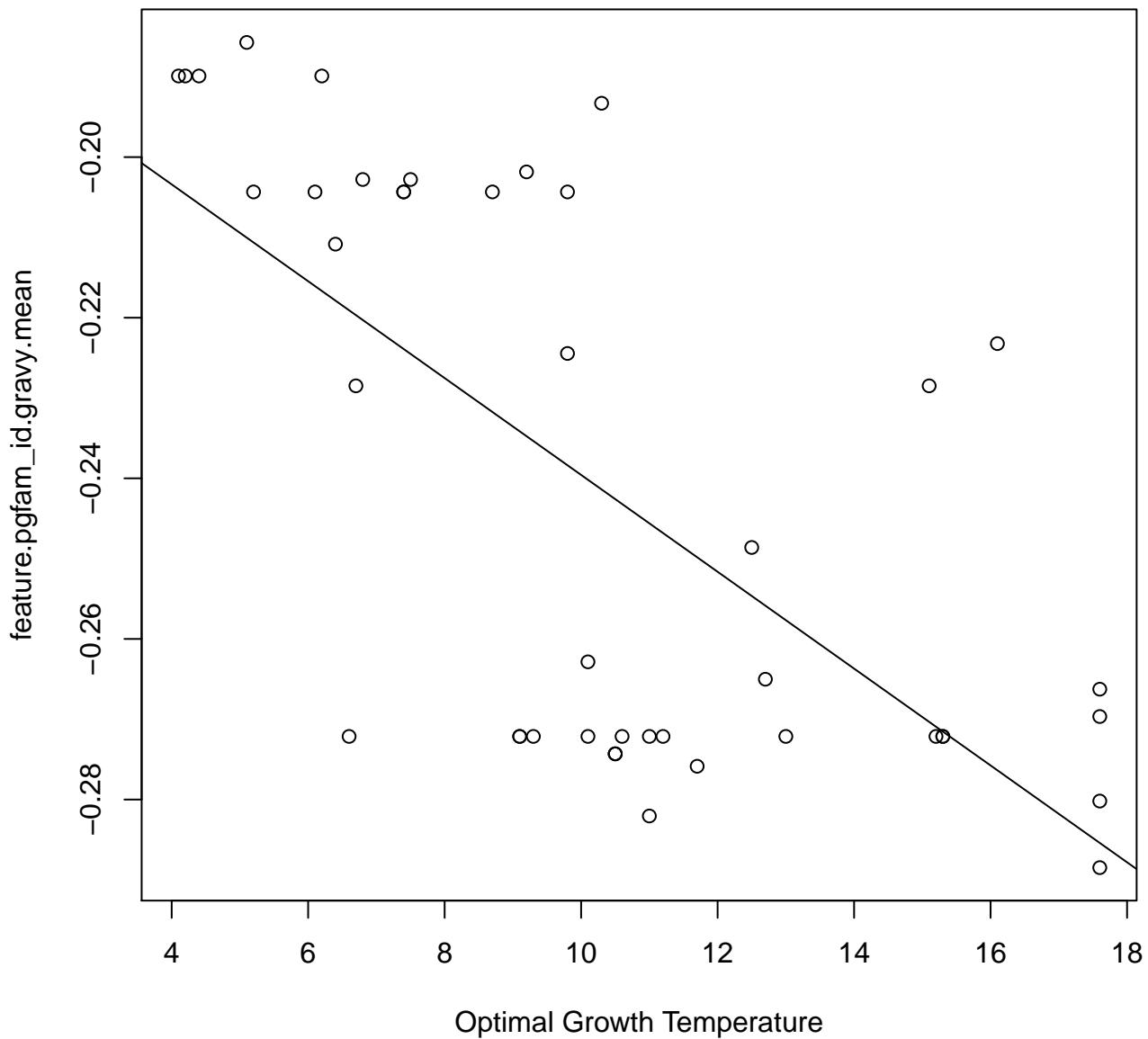
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PGF_03961195
AmpE protein



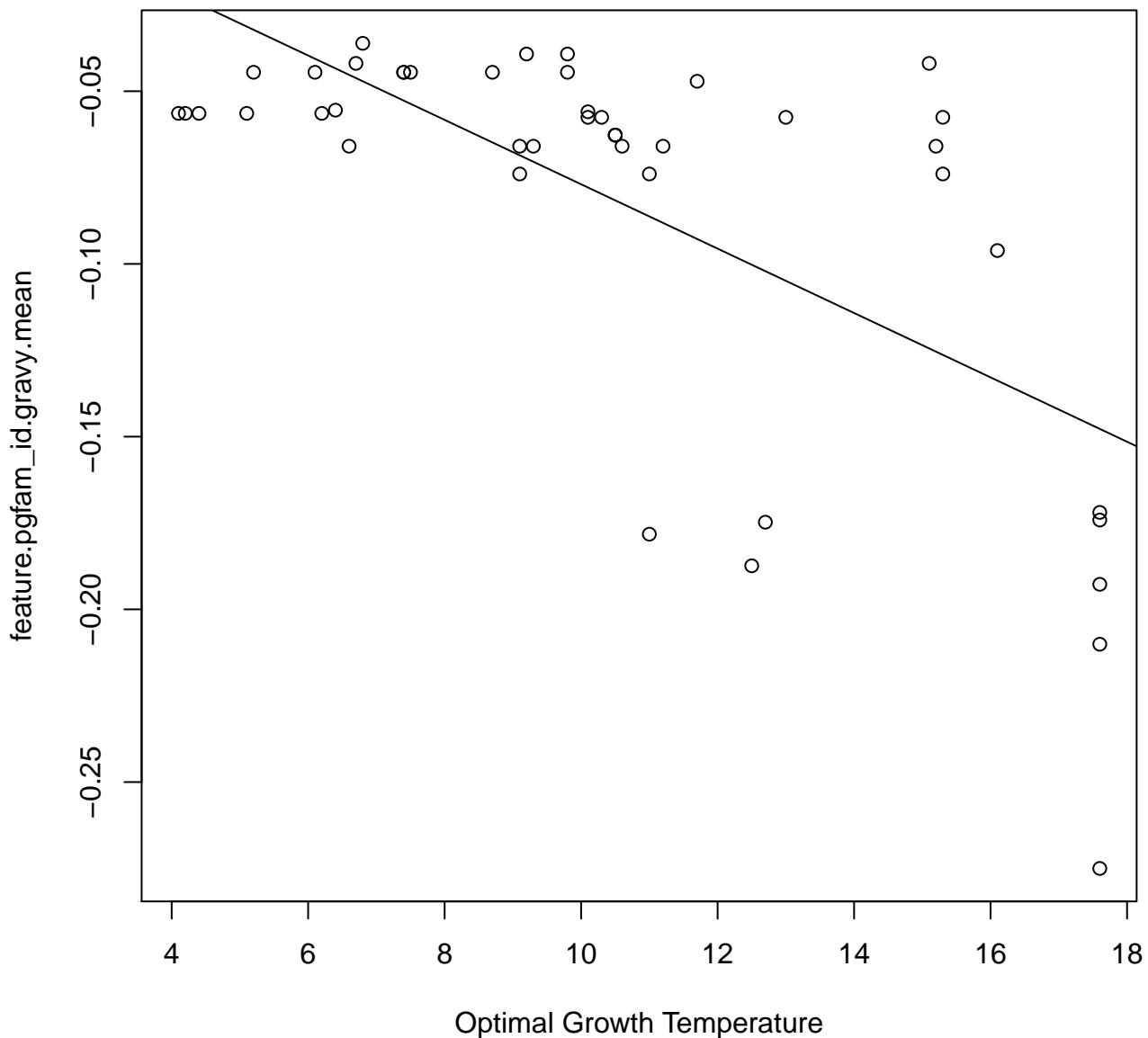
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PGF_06916058
Uncharacterized S4 RNA-binding-domain protein YbcJ



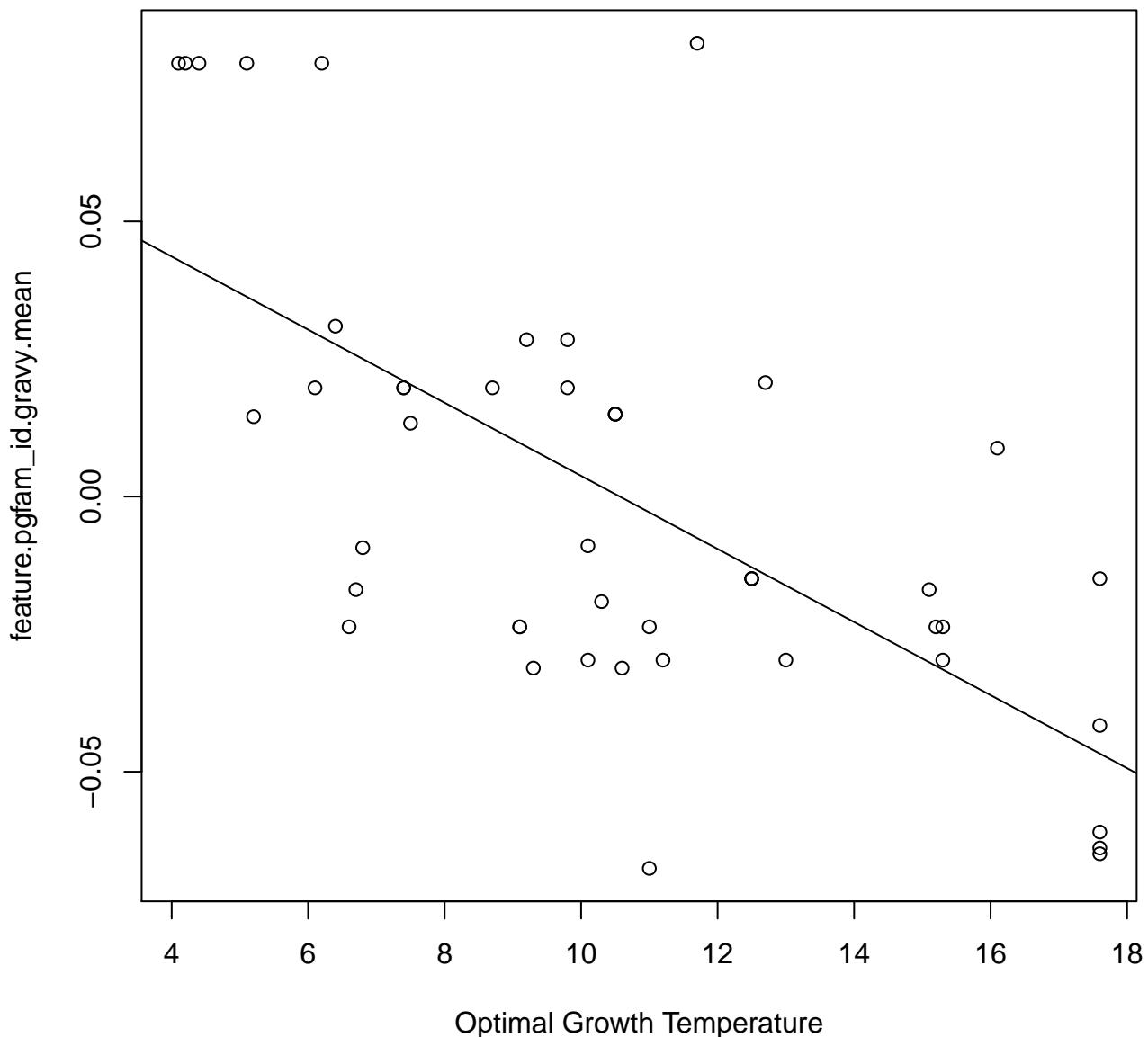
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GTP 3',8'-cyclase (EC 4.1.99.22)



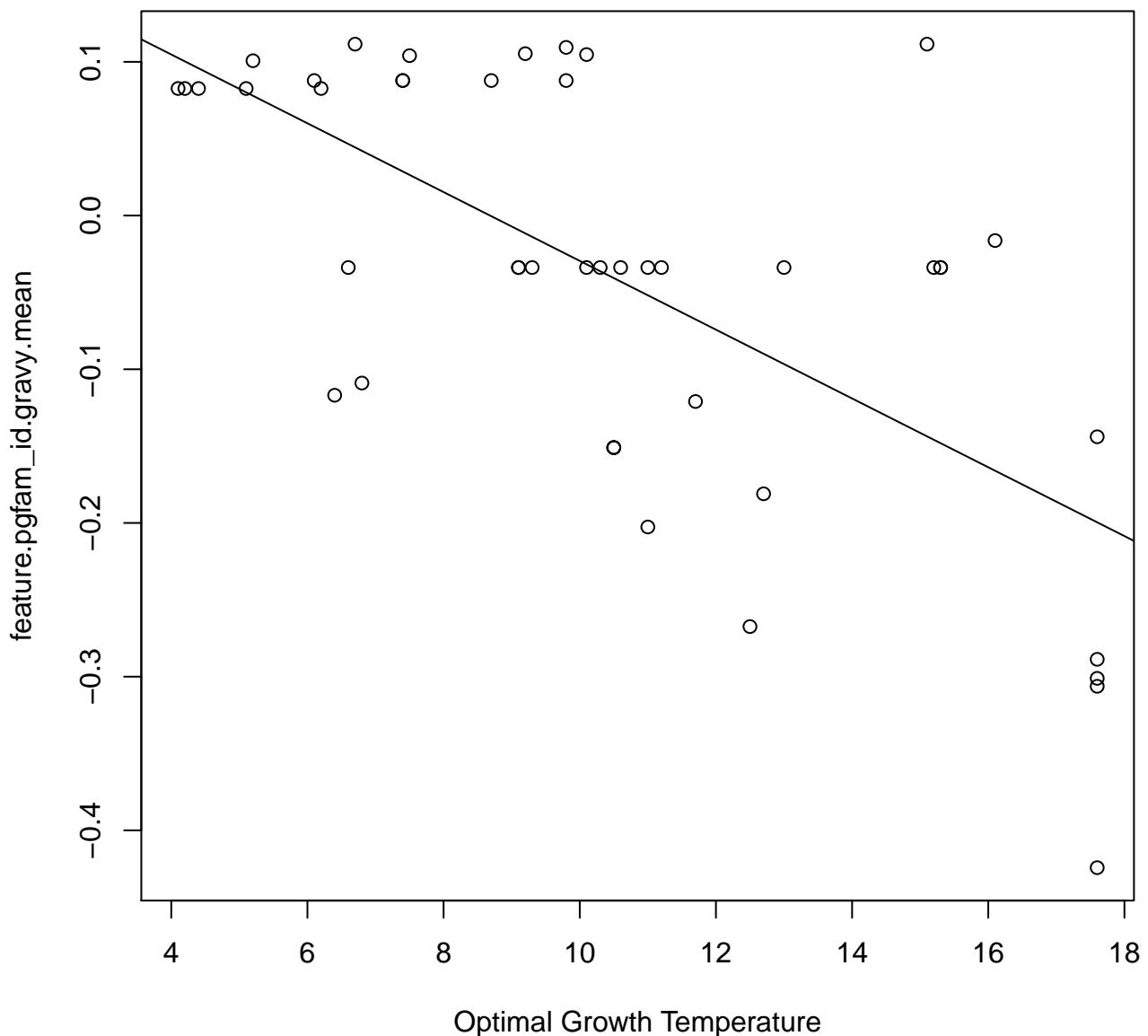
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PGF_10097367
Porphobilinogen deaminase (EC 2.5.1.61)



feature.pgfam_id.gravy.mean
PGF_00846740
Orn/DAP/Arg family decarboxylase



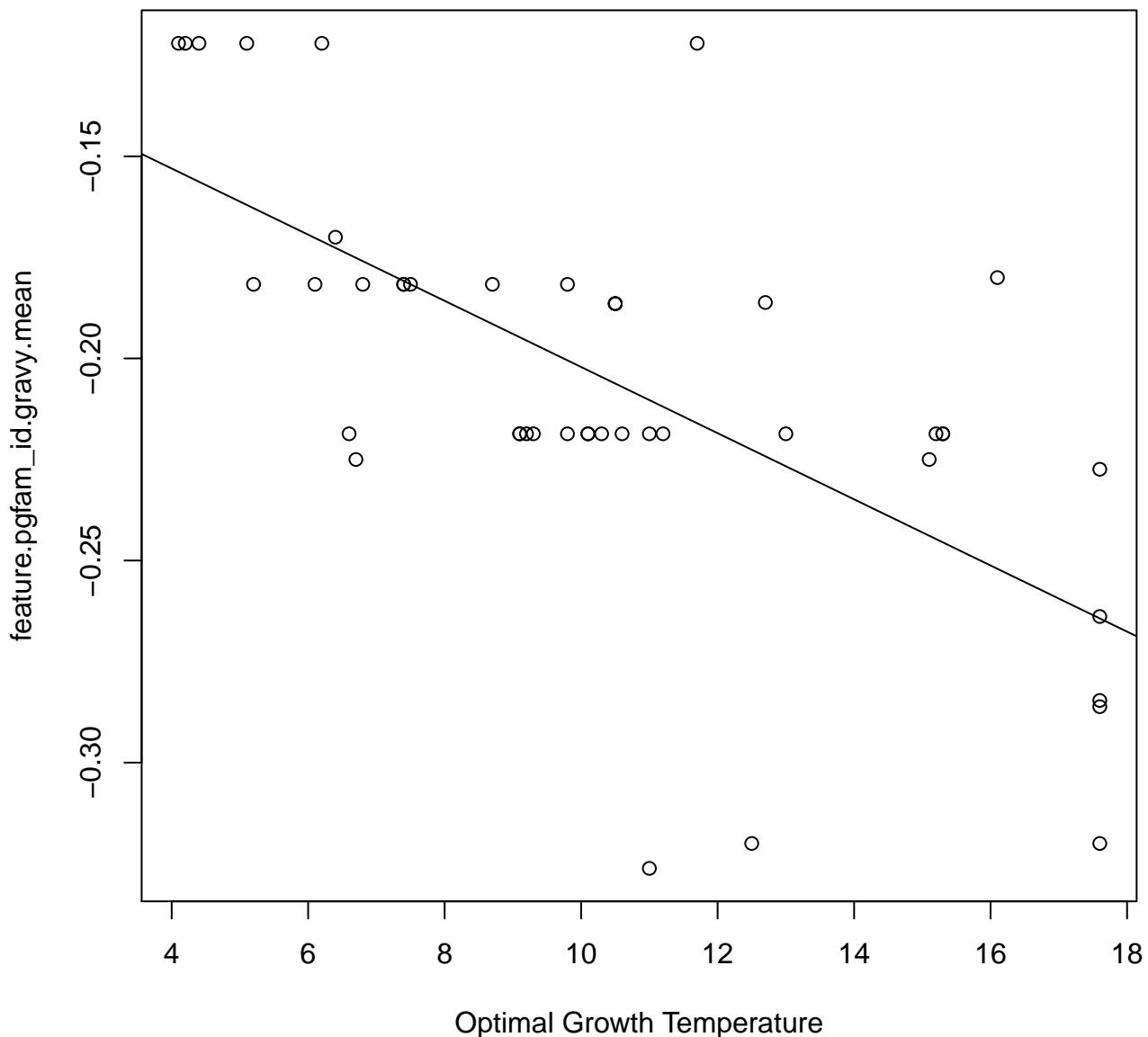
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PGF_00751789
hypothetical protein



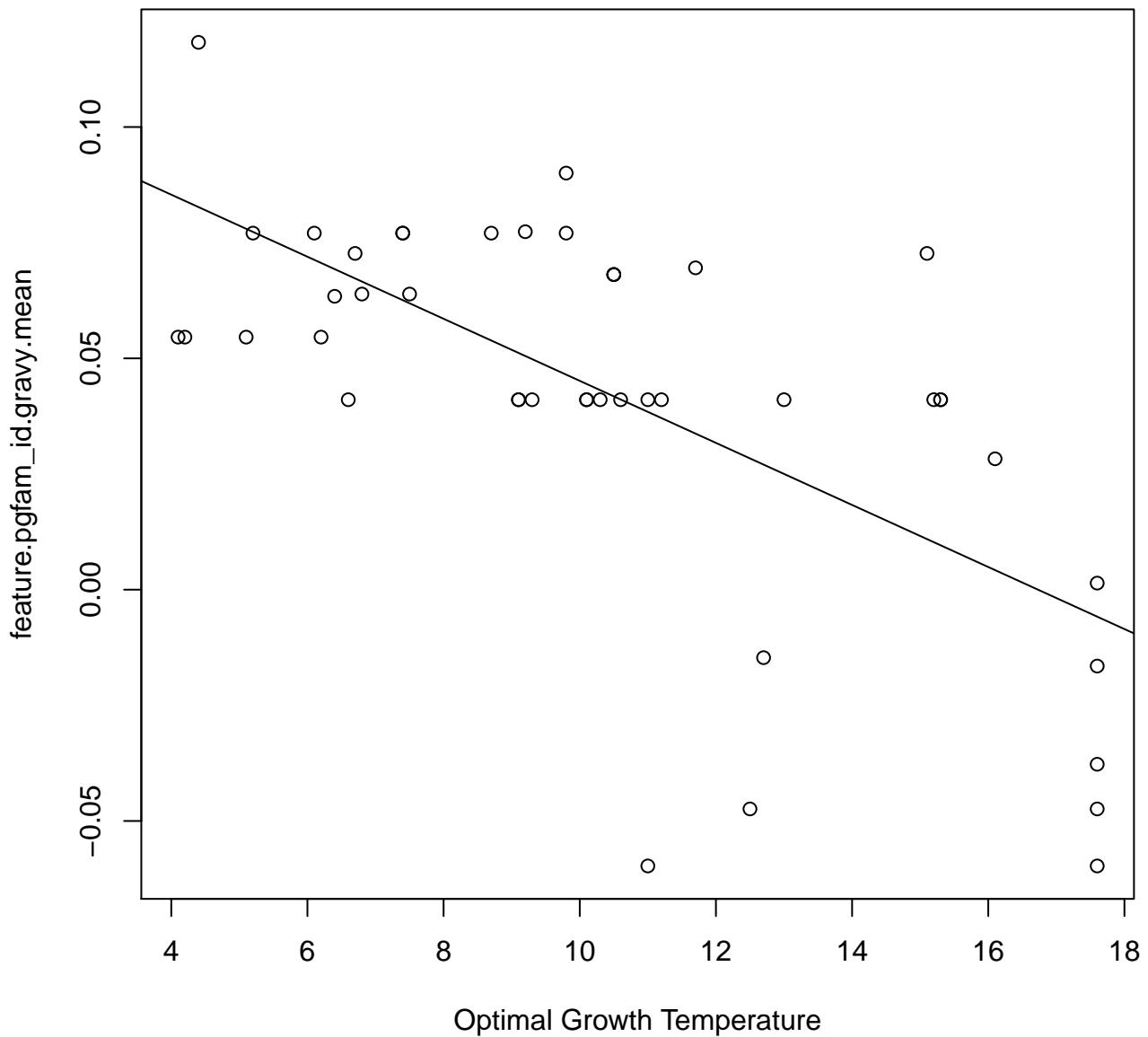
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PGF_07550057

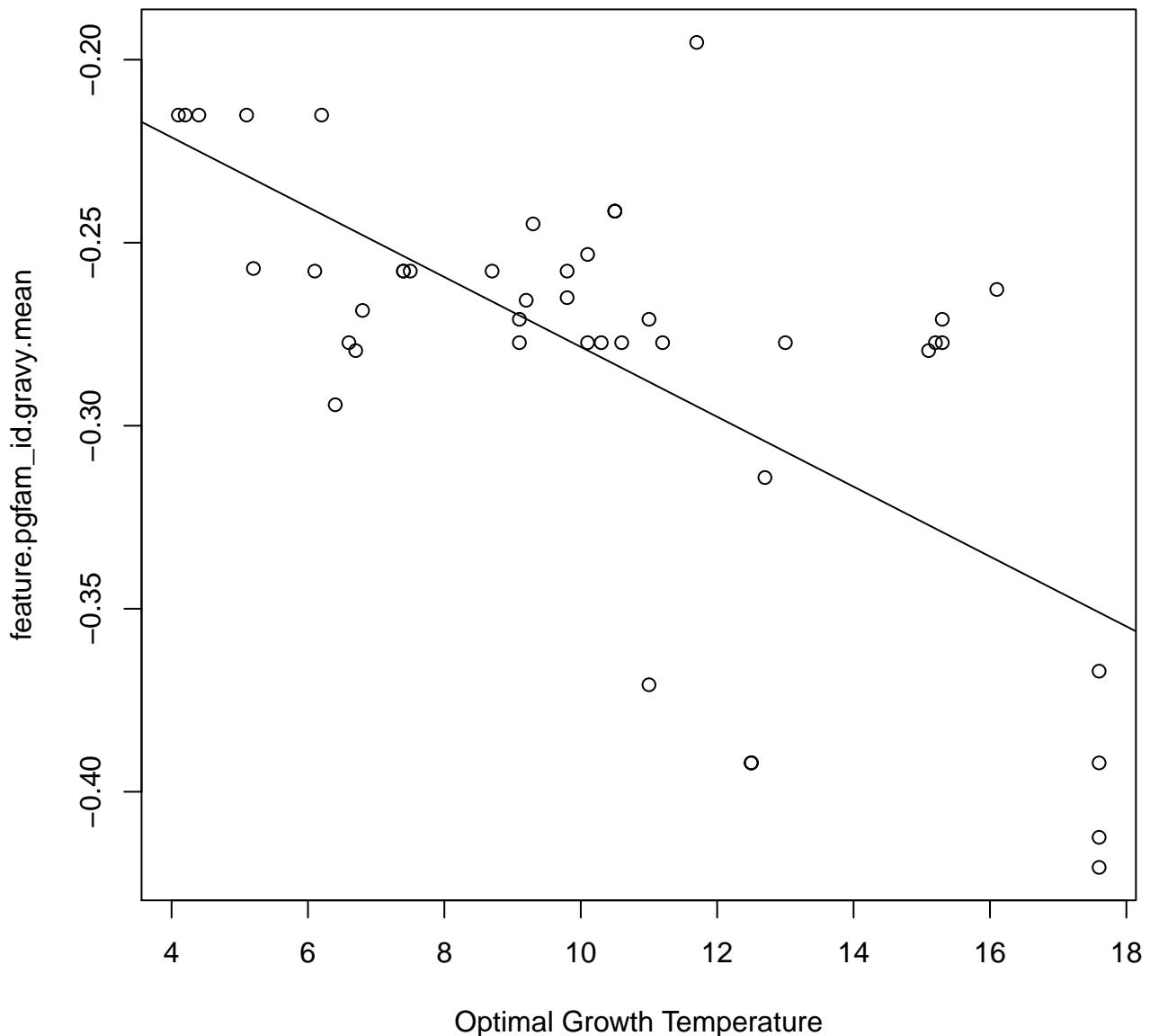
FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster



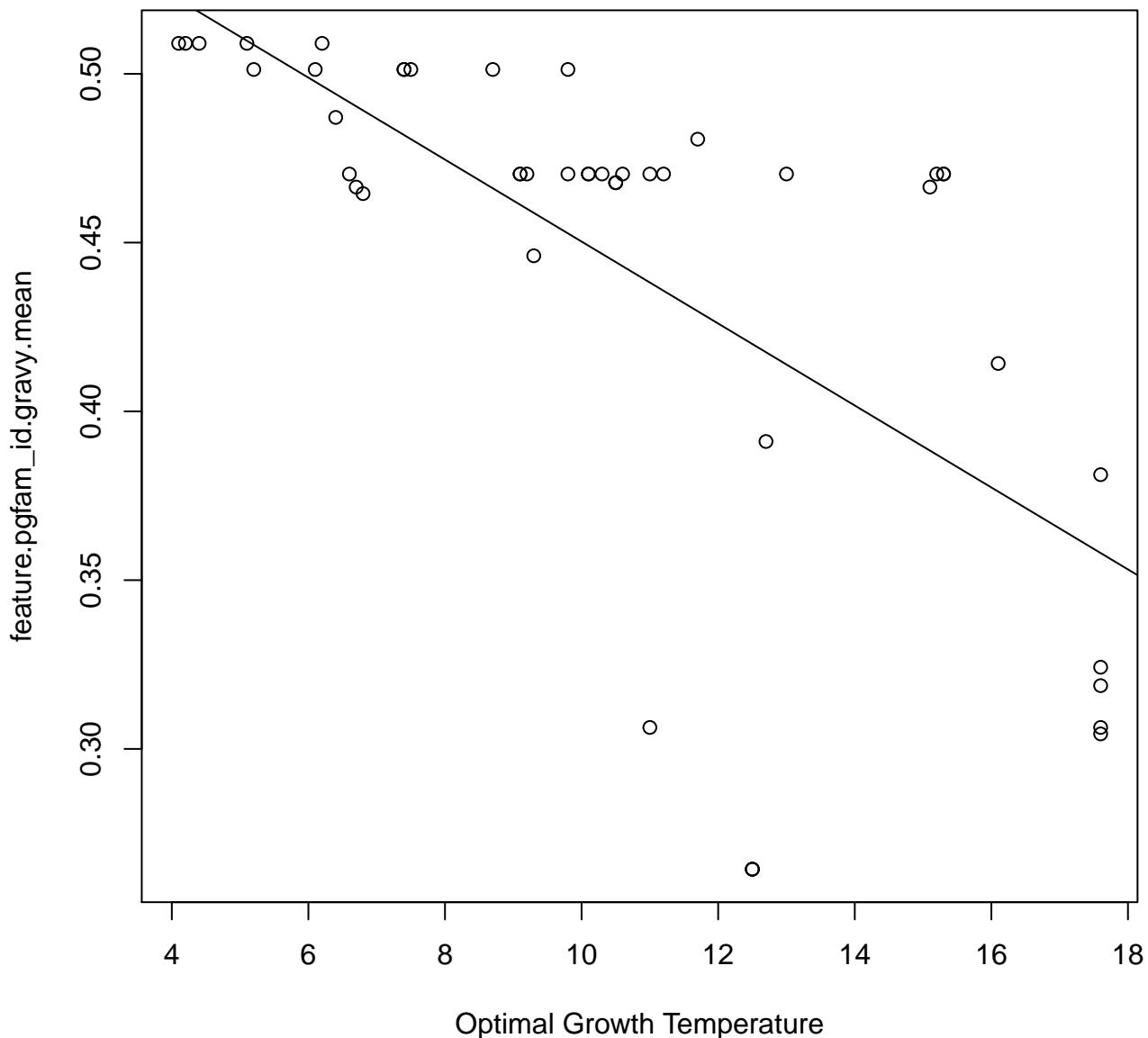
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PGF_03189552
Holliday junction ATP-dependent DNA helicase RuvA (EC 3.6.4.12)



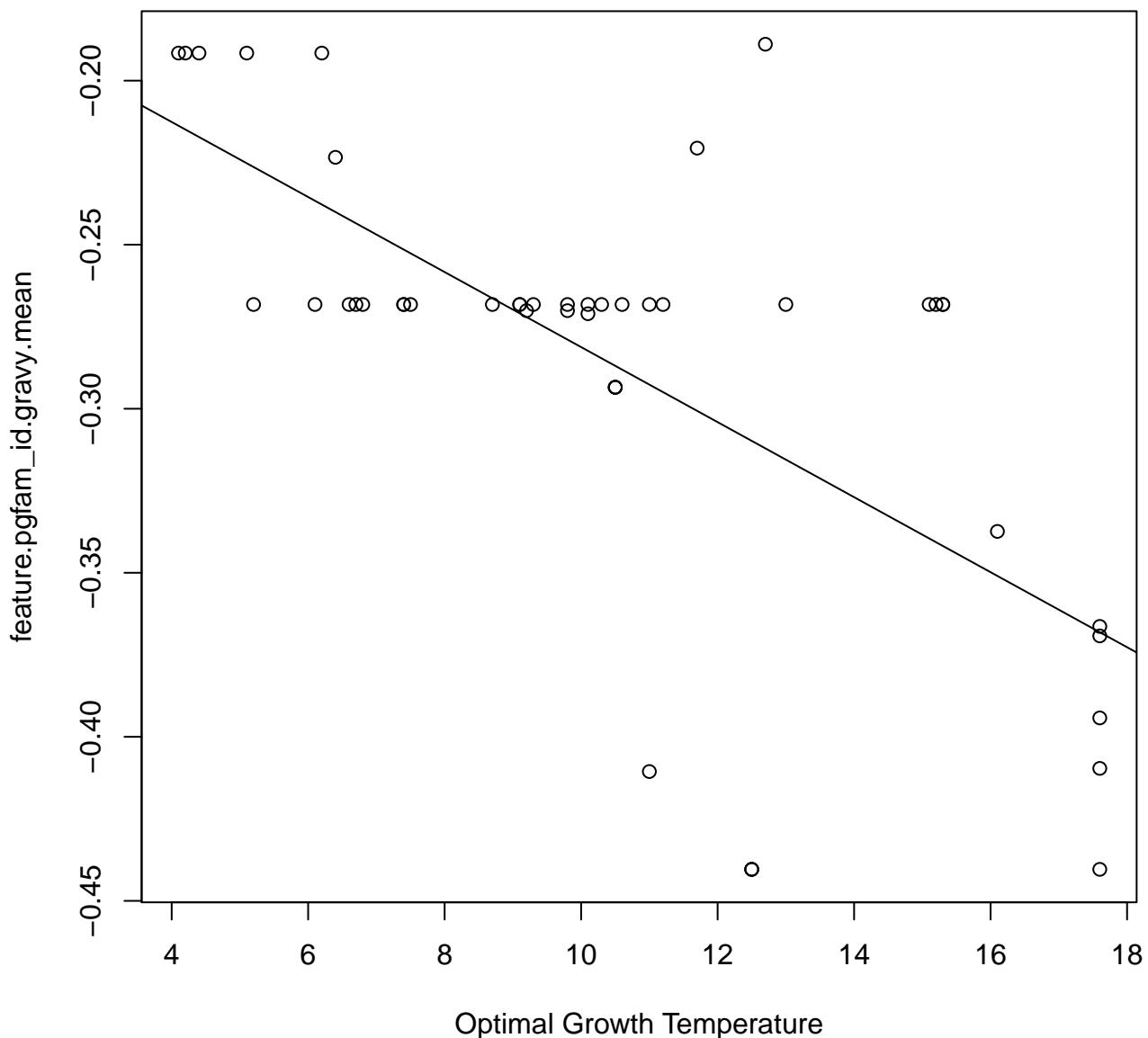
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PGF_00055549
TPR domain protein, putative component of TonB system



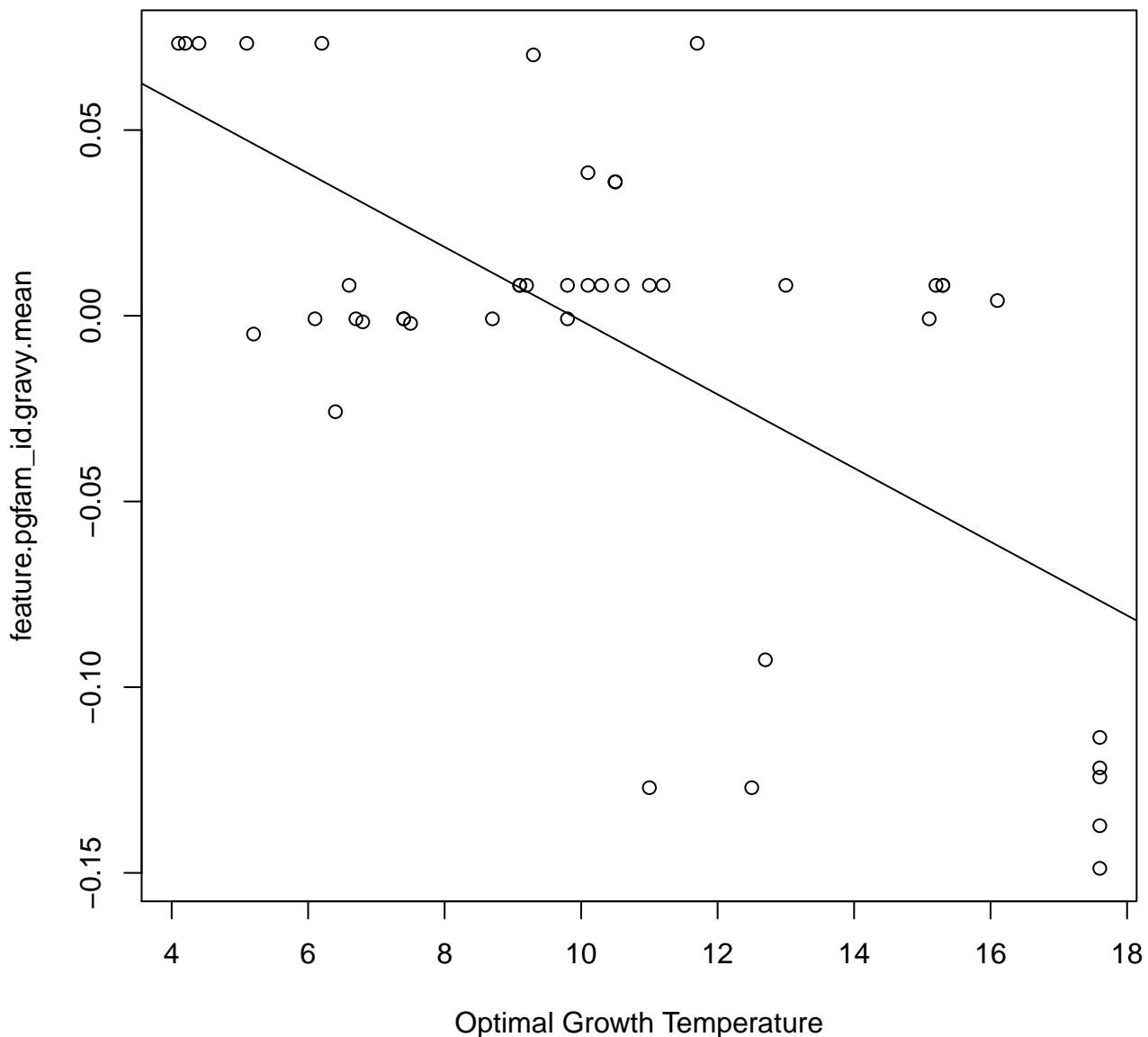
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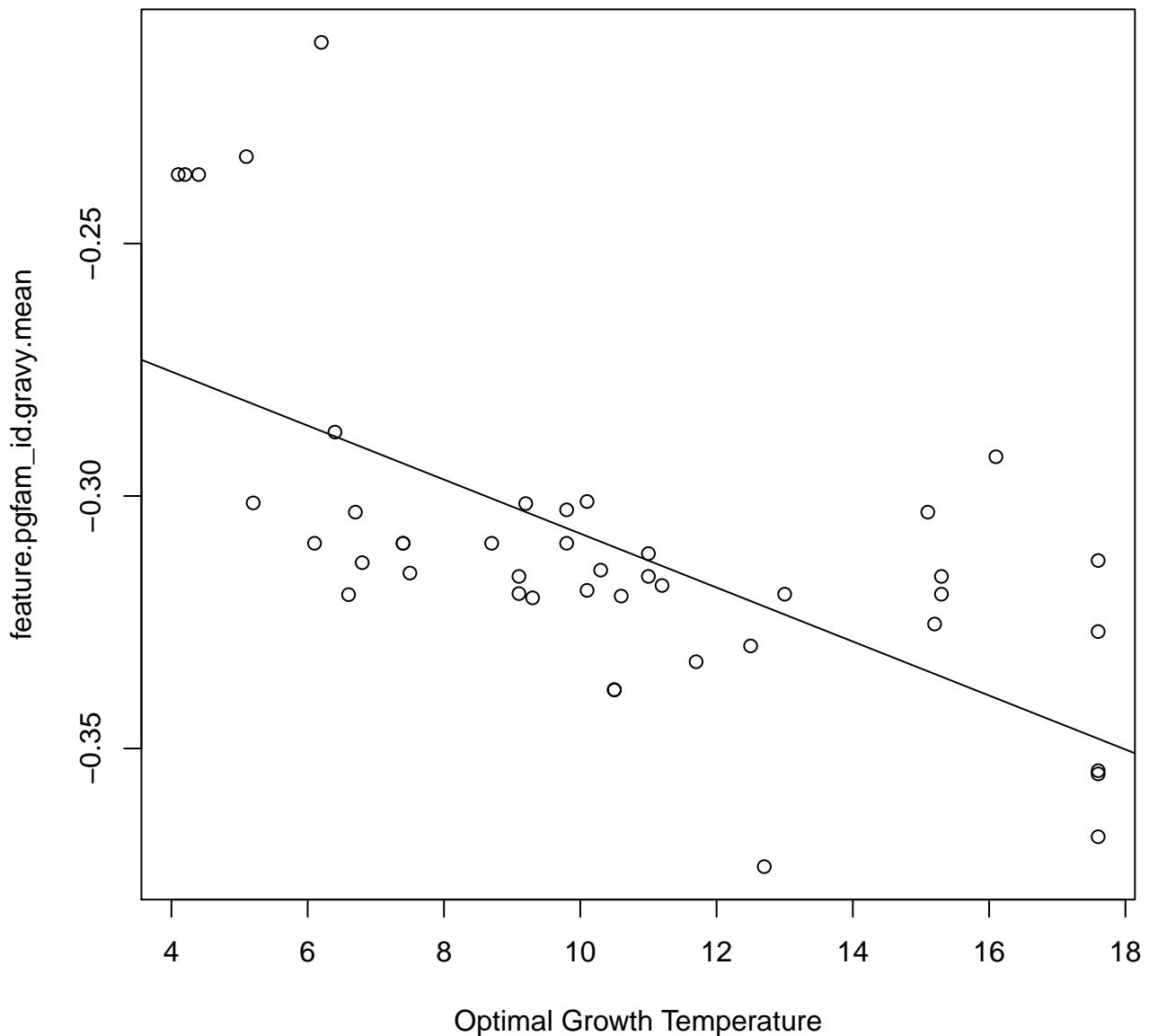
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PGF_00649271
Cell division protein BolA



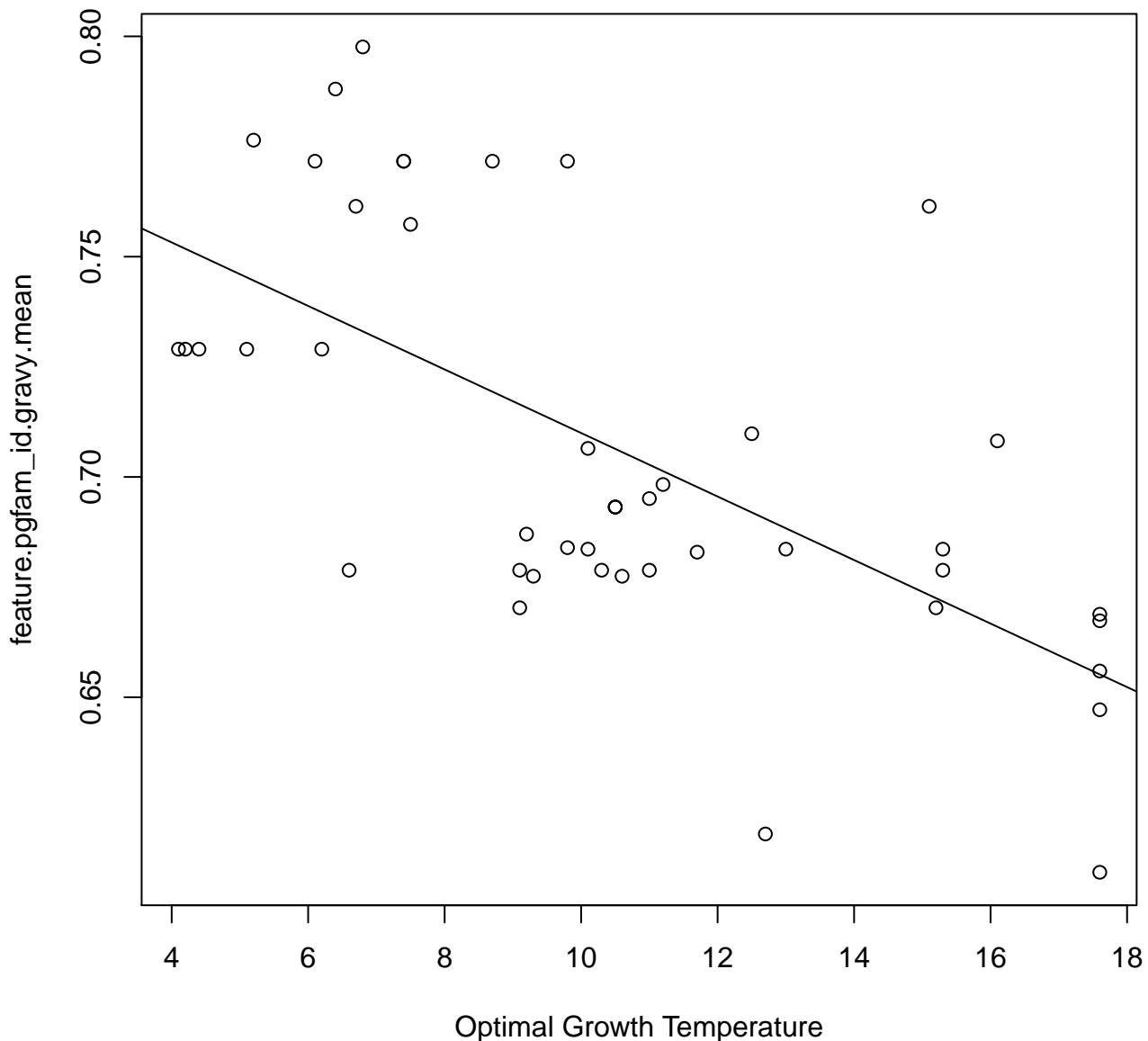
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PGF_06023067
Carboxy-S-adenosyl-L-methionine synthase



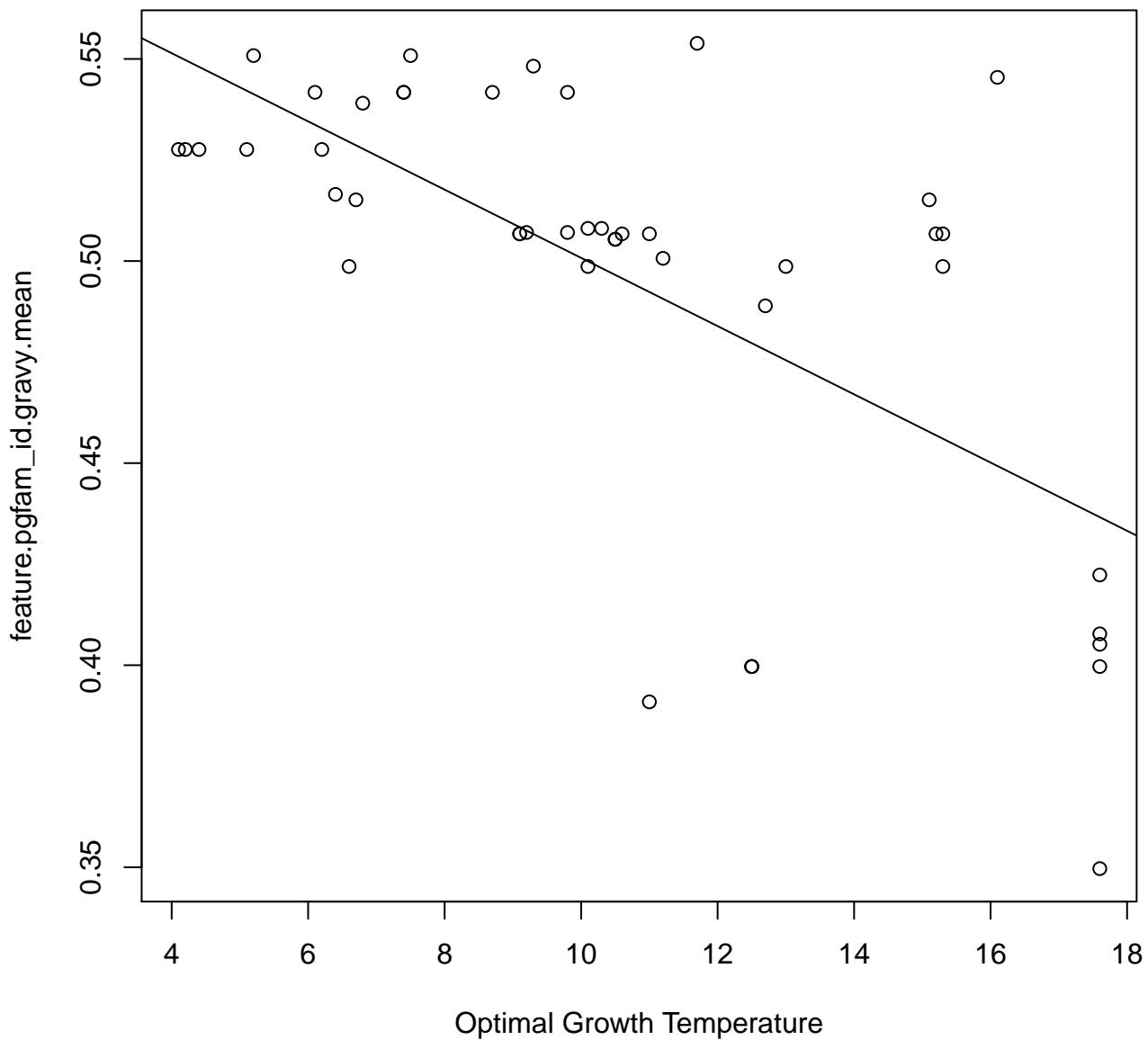
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PGF_10537966
TonB-dependent receptor



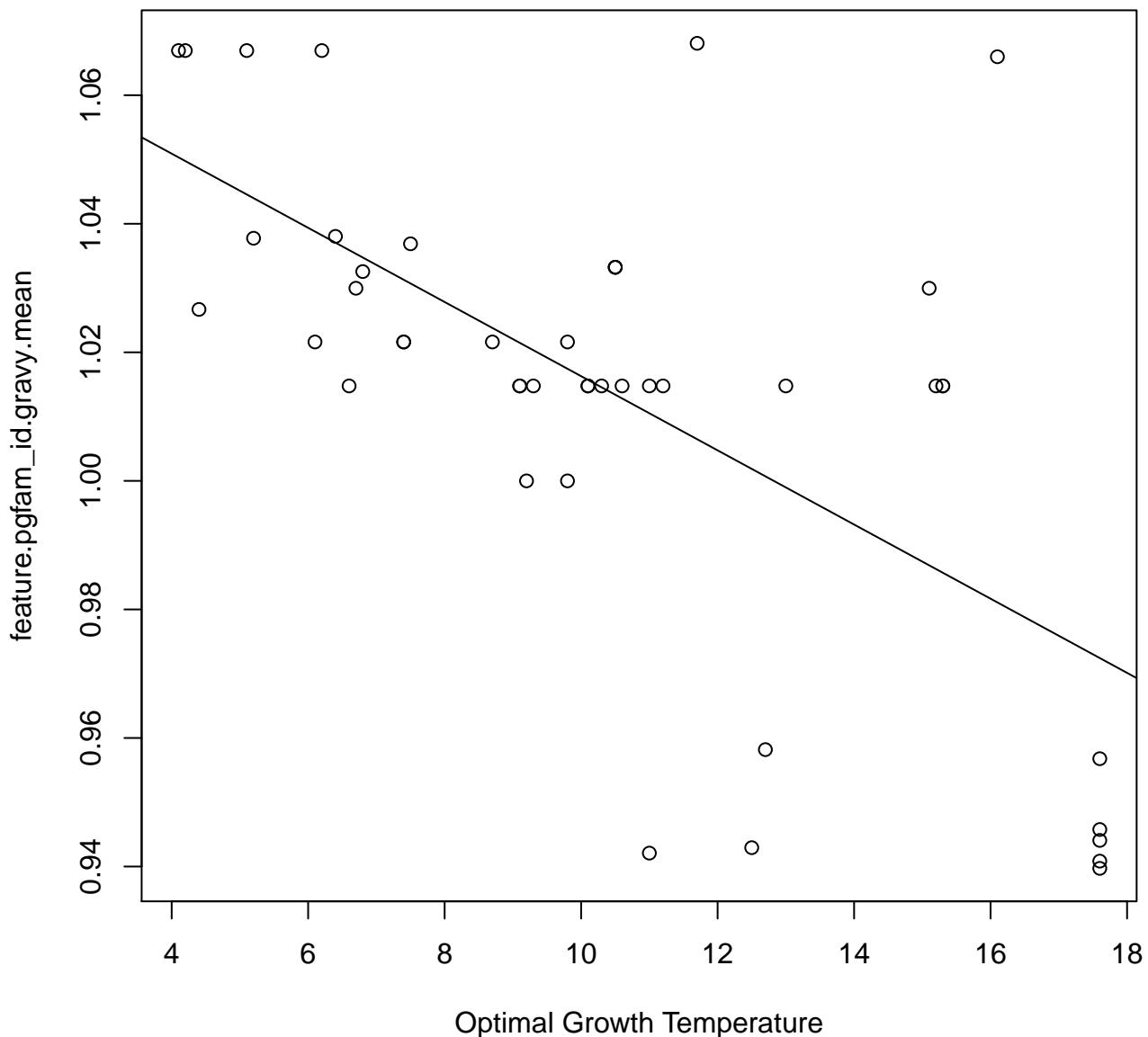
feature.pgfam_id.gravy.mean
PGF_09449034
Leader peptidase (Prephilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-)



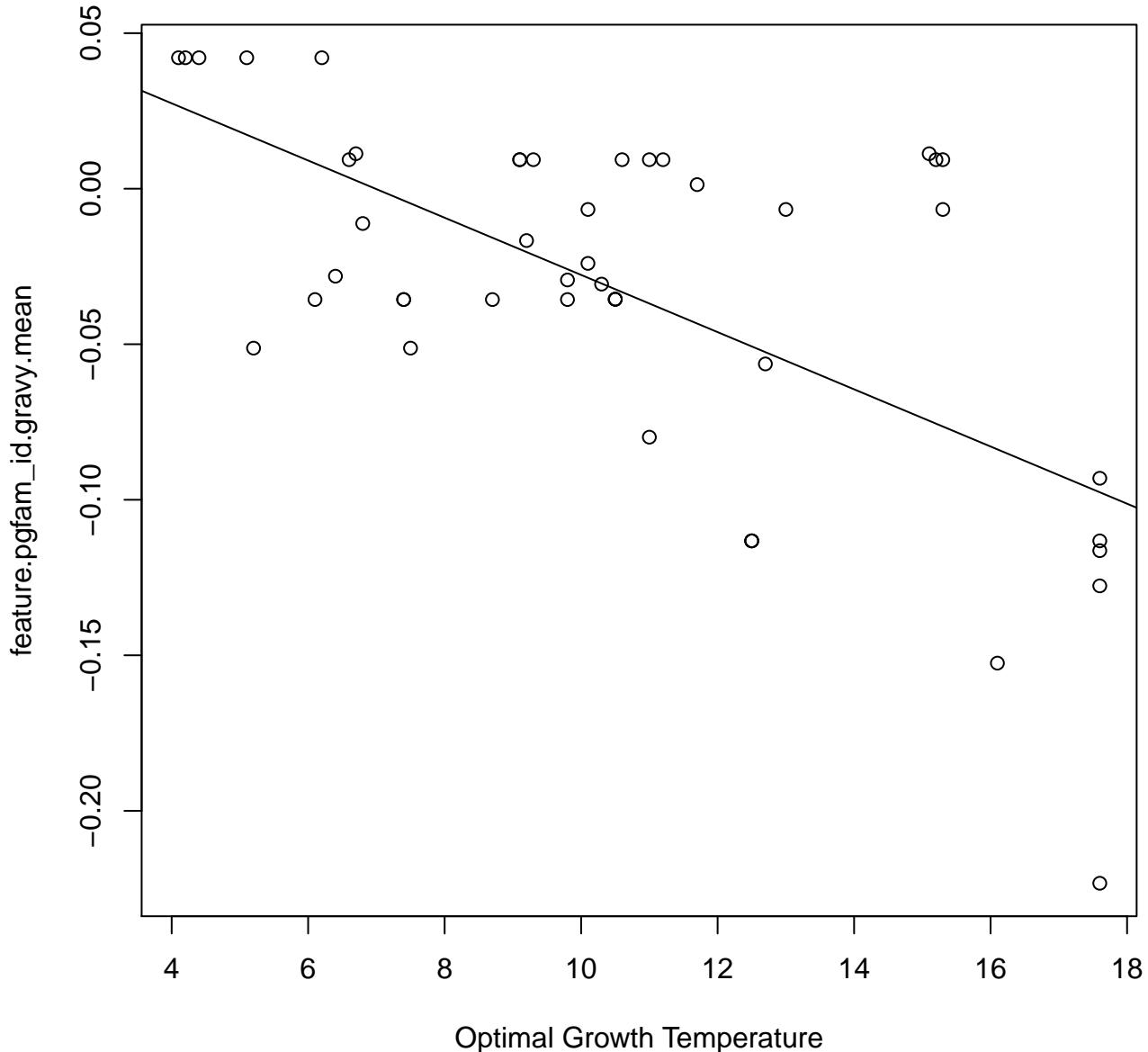
feature.pfam_id.gravy.mean
PGF_01336260
Mechanosensitive ion channel family protein



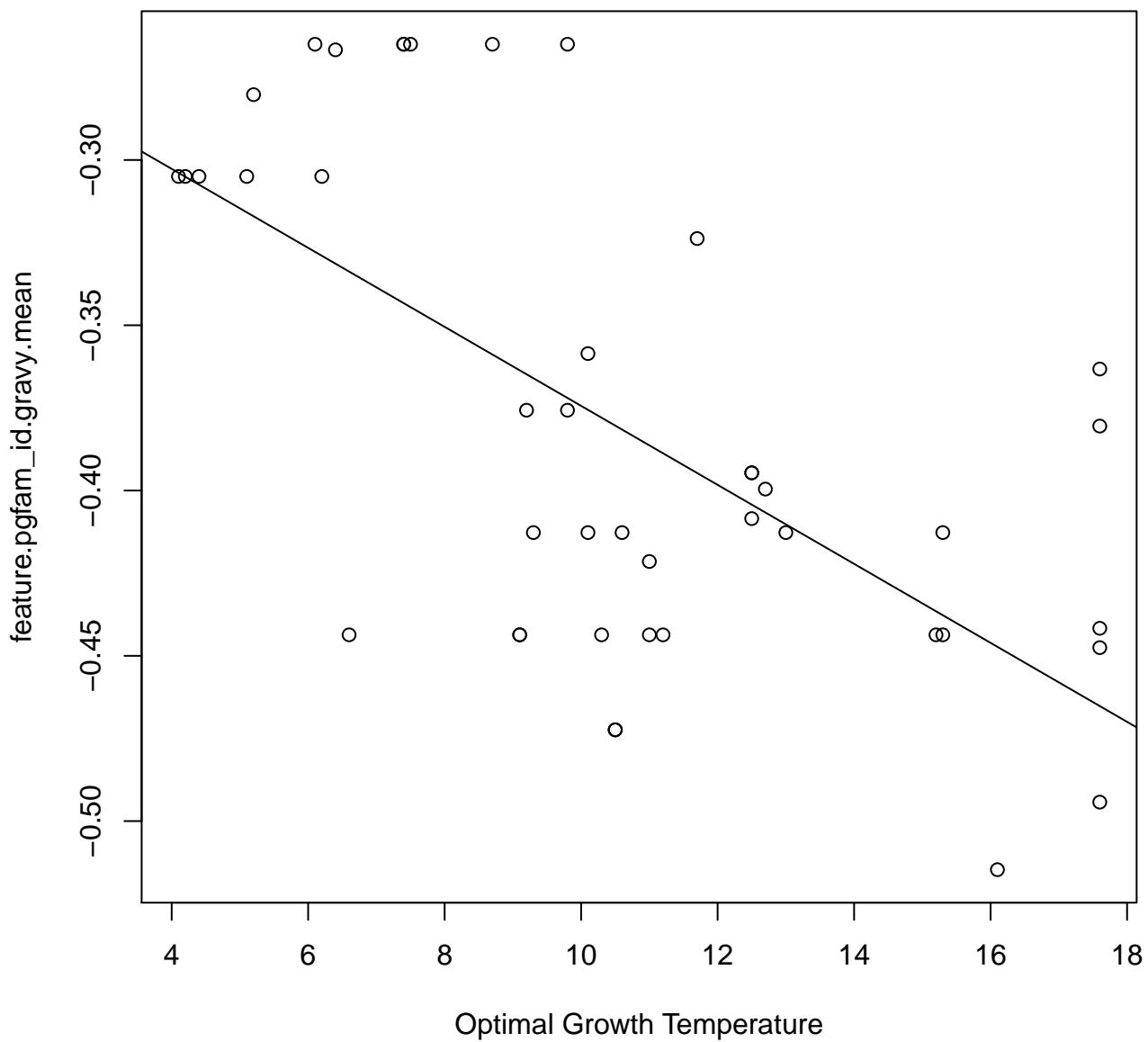
feature.pgfam_id.gravy.mean
PGF_06866315
Uncharacterized UPF0118 membrane protein



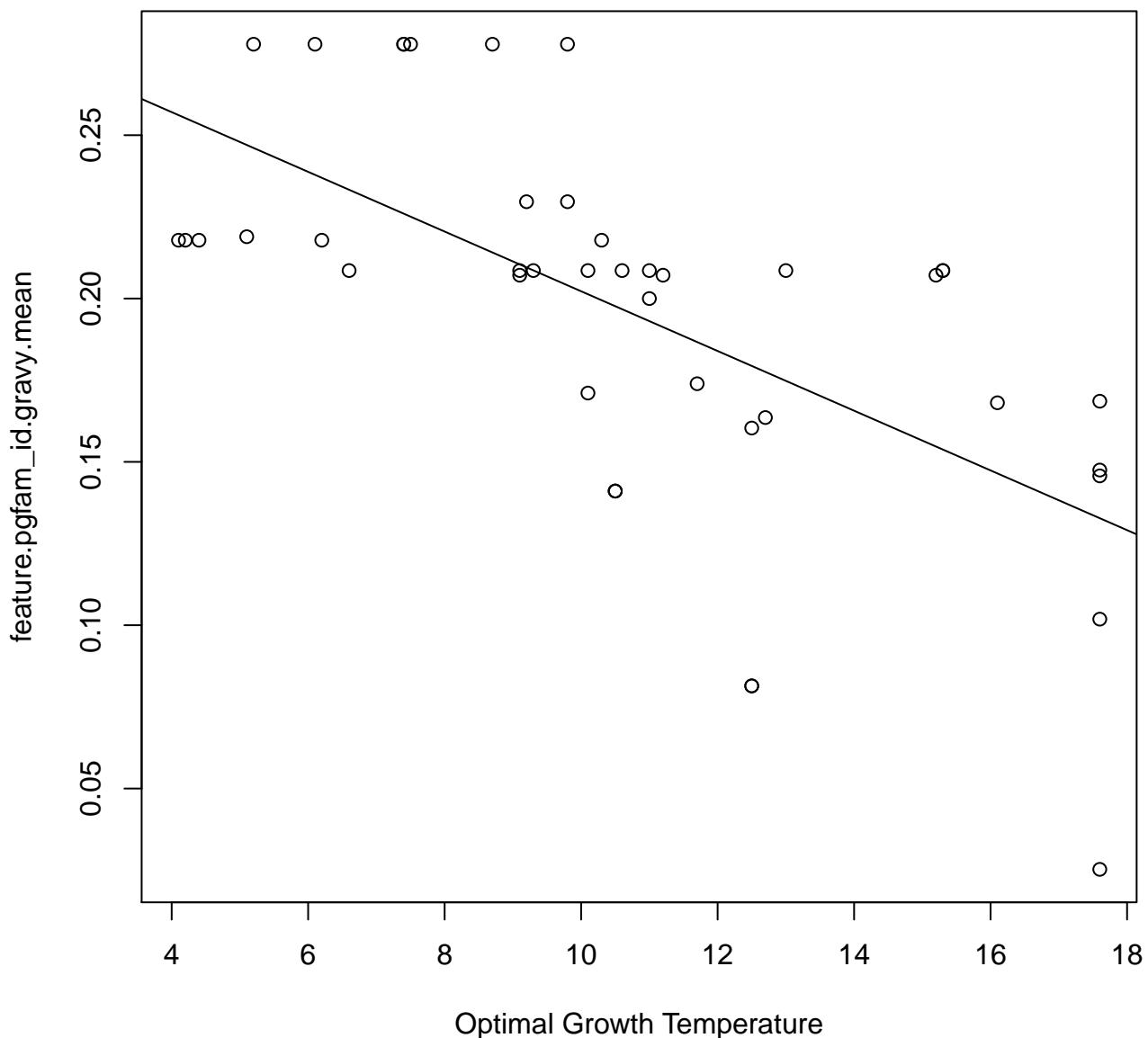
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PGF_00054302
Stringent starvation protein B



feature.pgfam_id.gravy.mean
PGF_00035421
Potential queD like 2



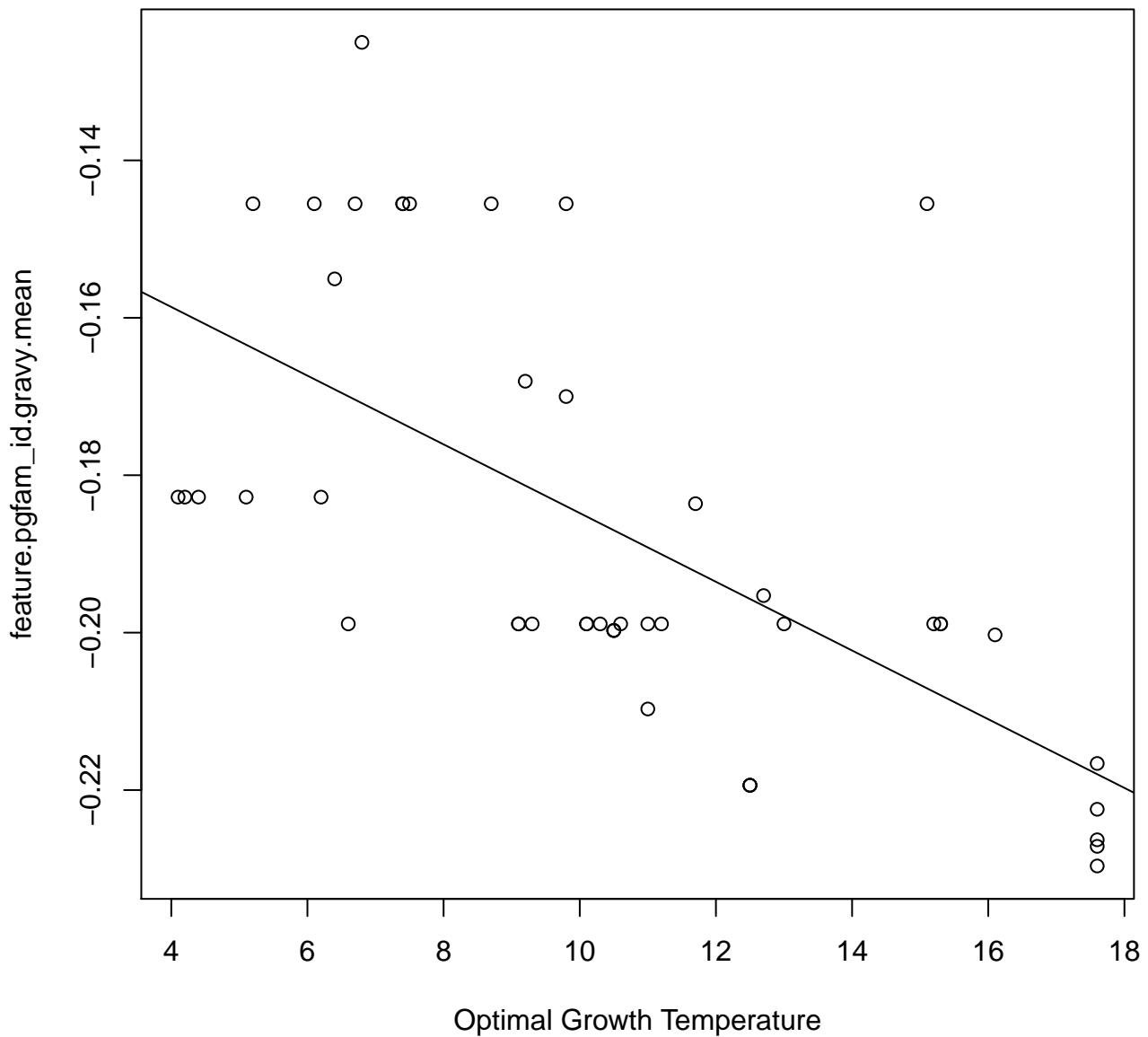
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PGF_01336378
hypothetical protein



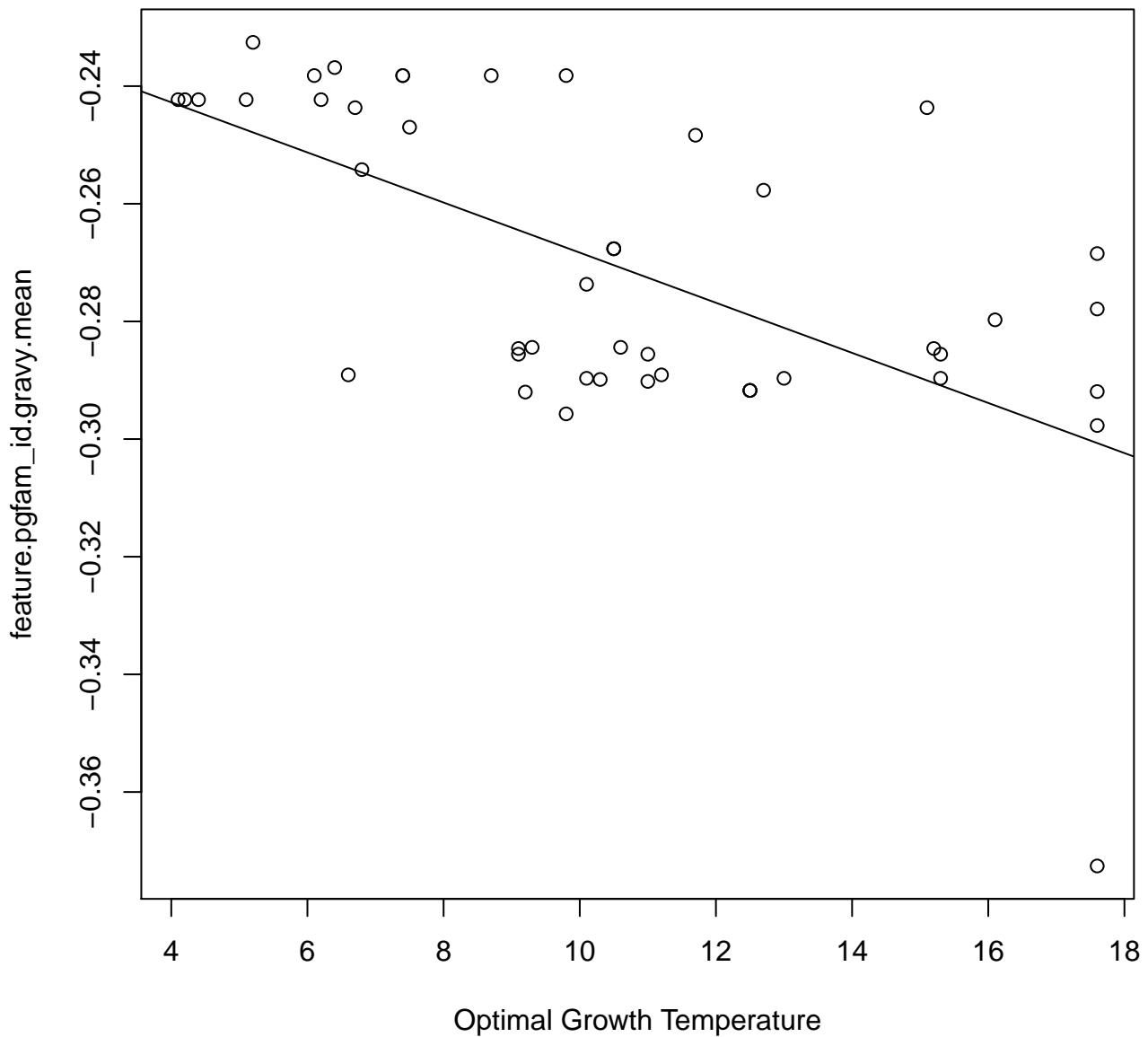
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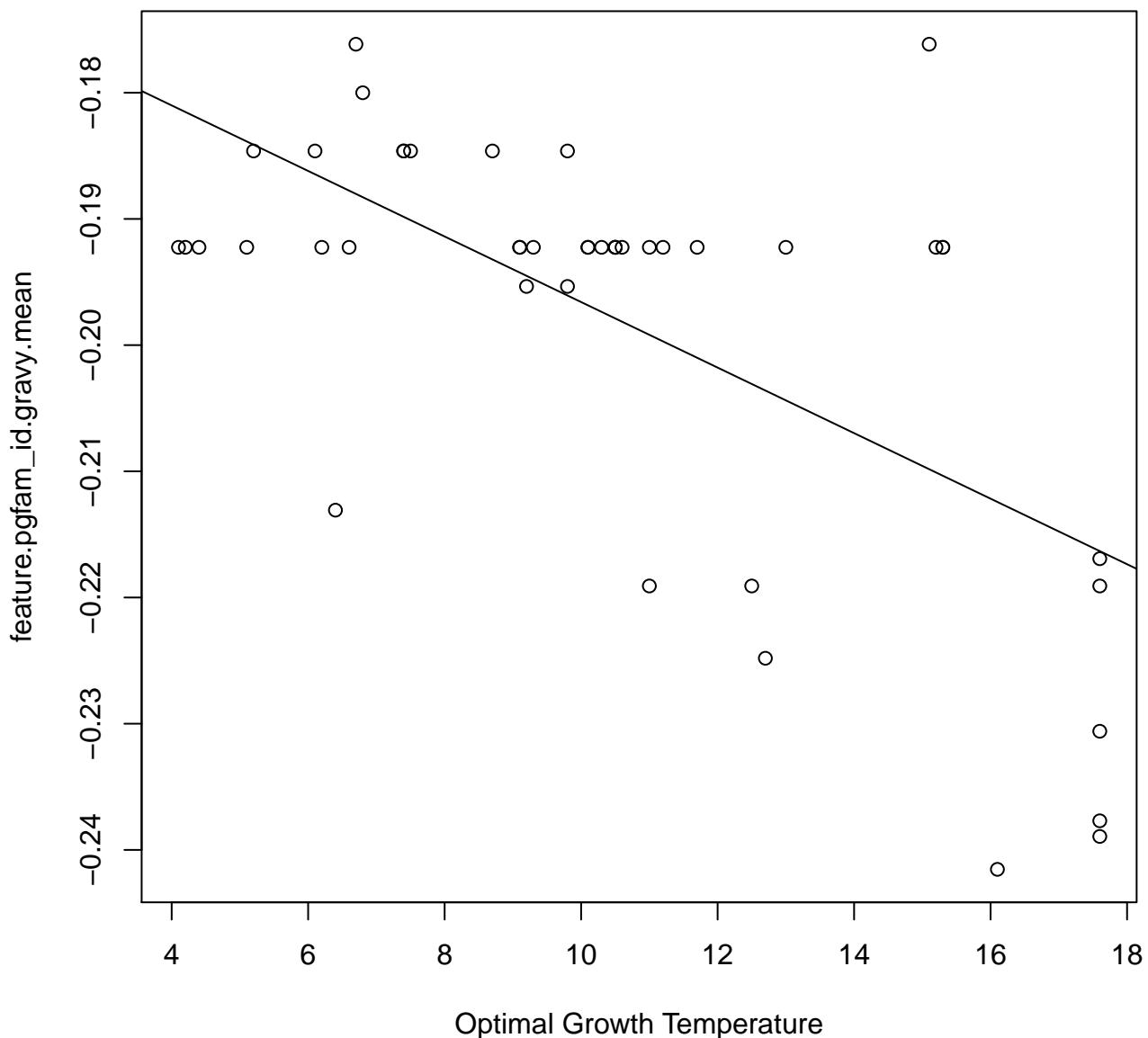
Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)



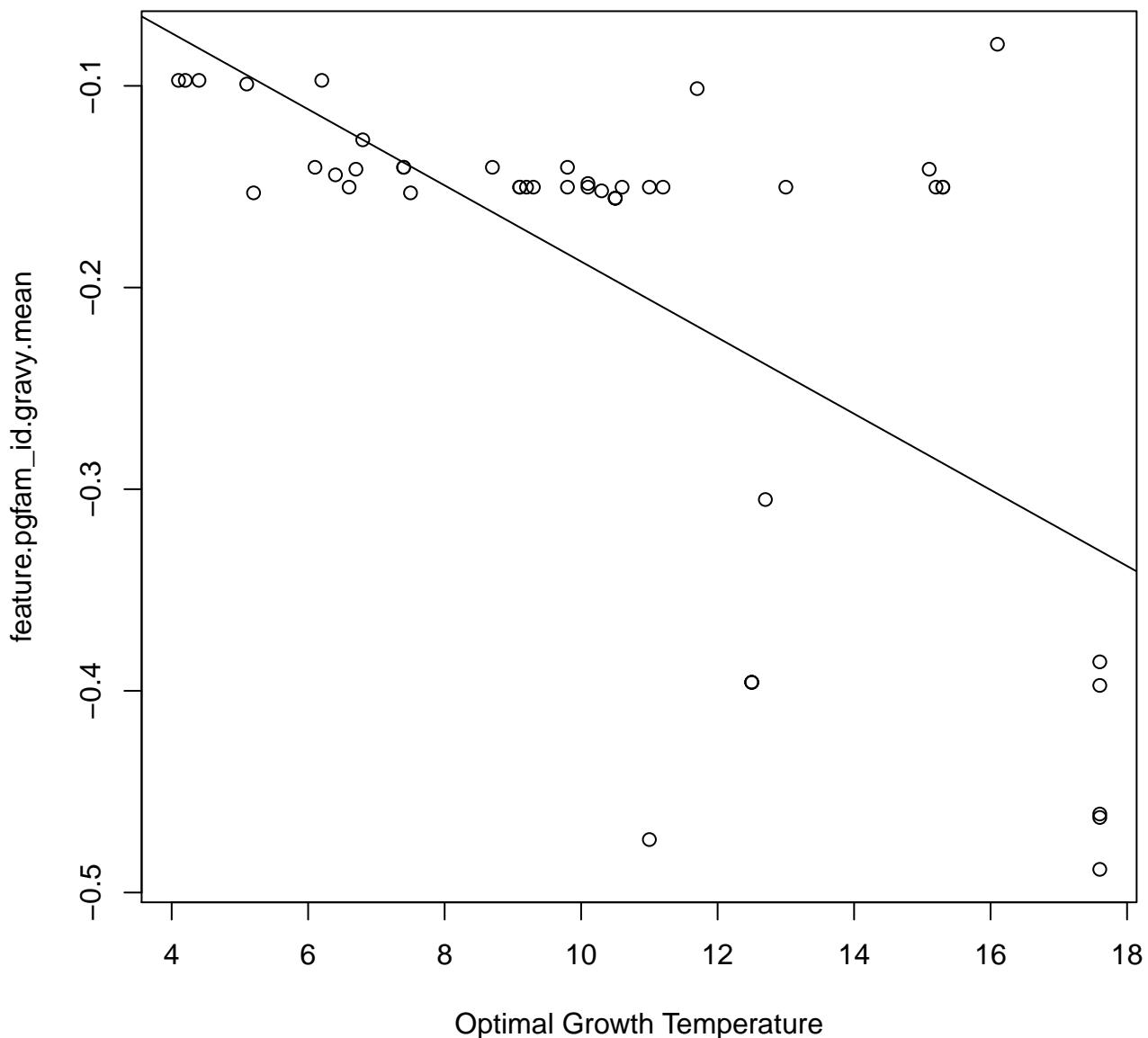
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2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)



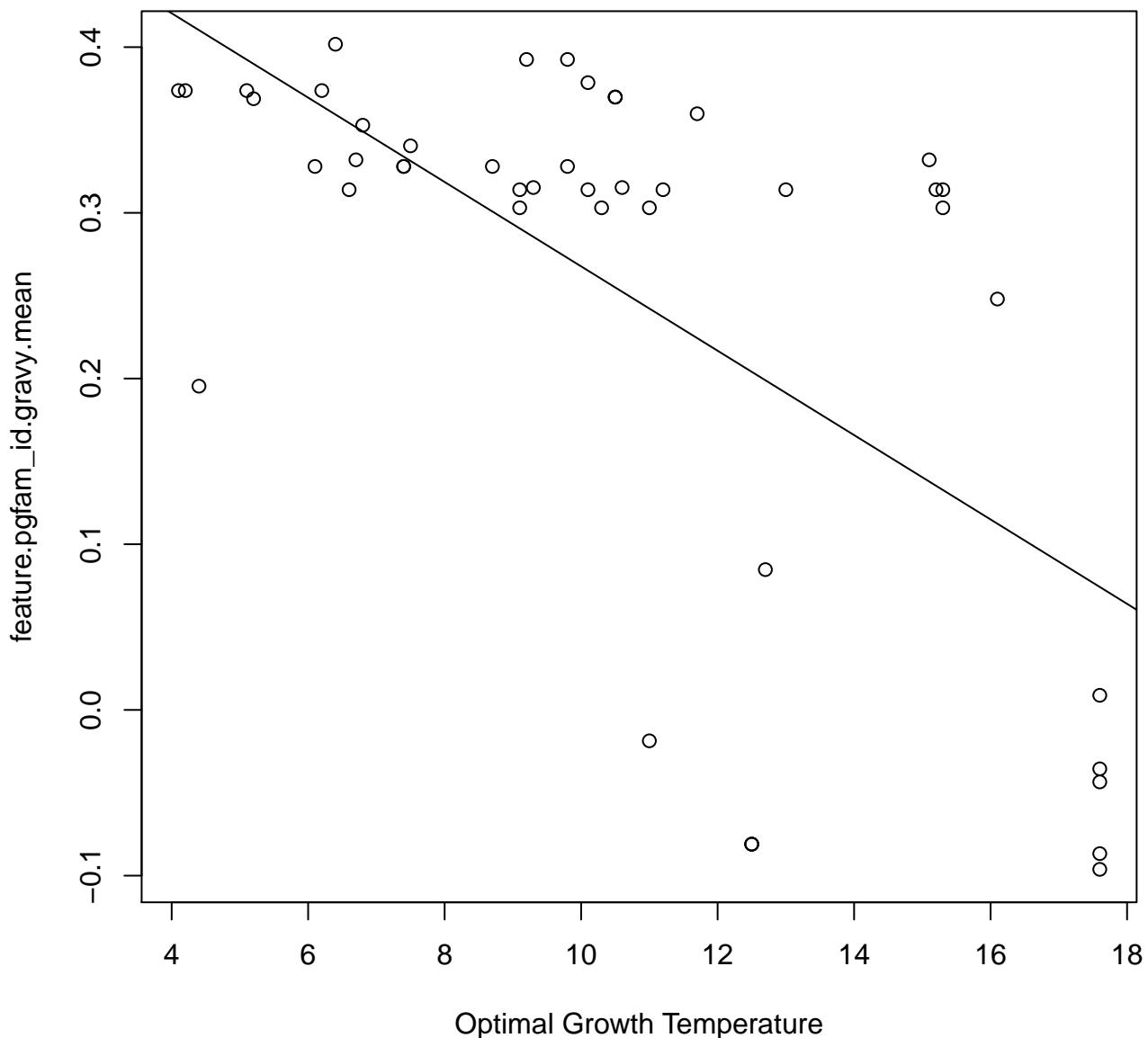
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PGF_09438139
Flagellar motor switch protein FliN



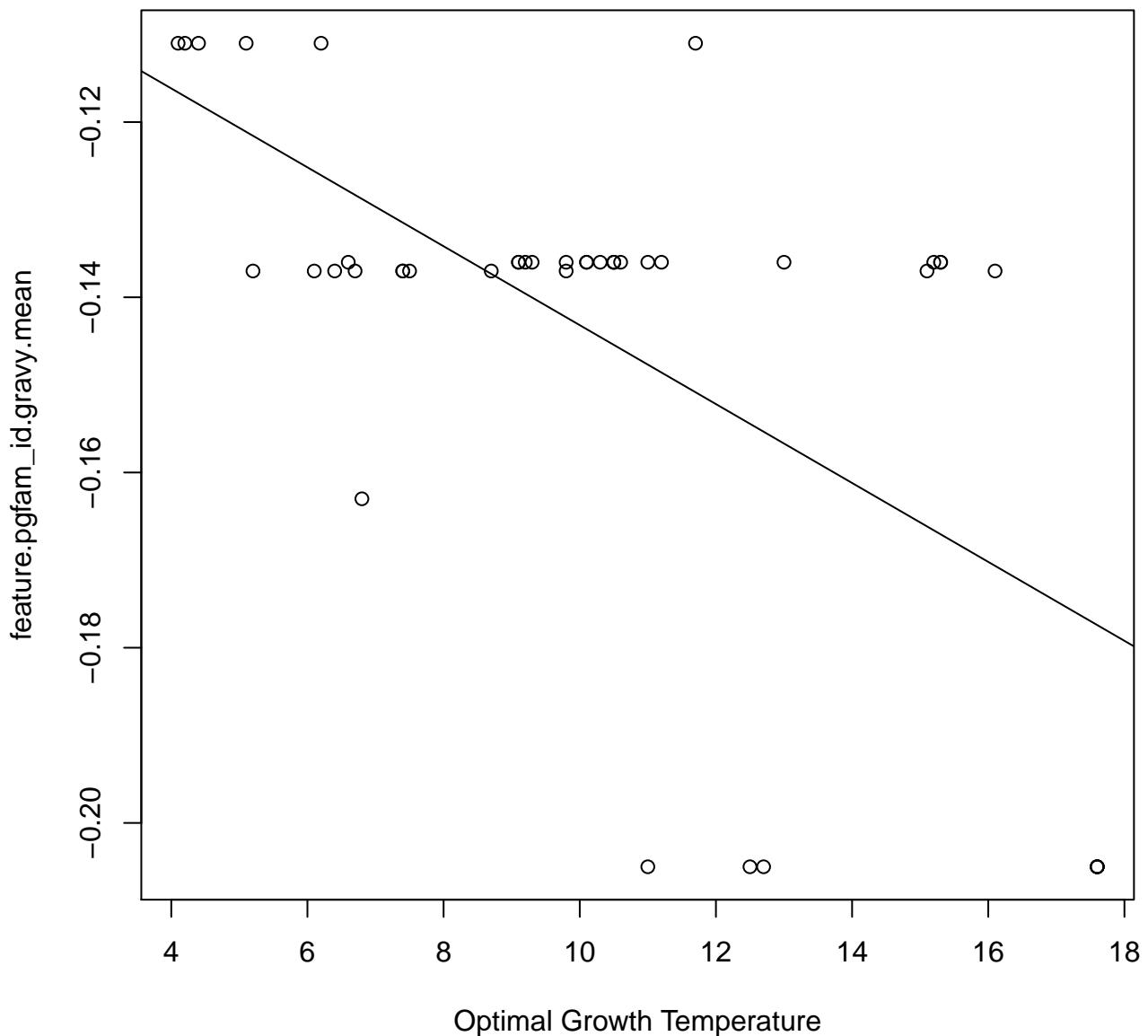
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PGF_01484108
Electron transport complex protein RnfG



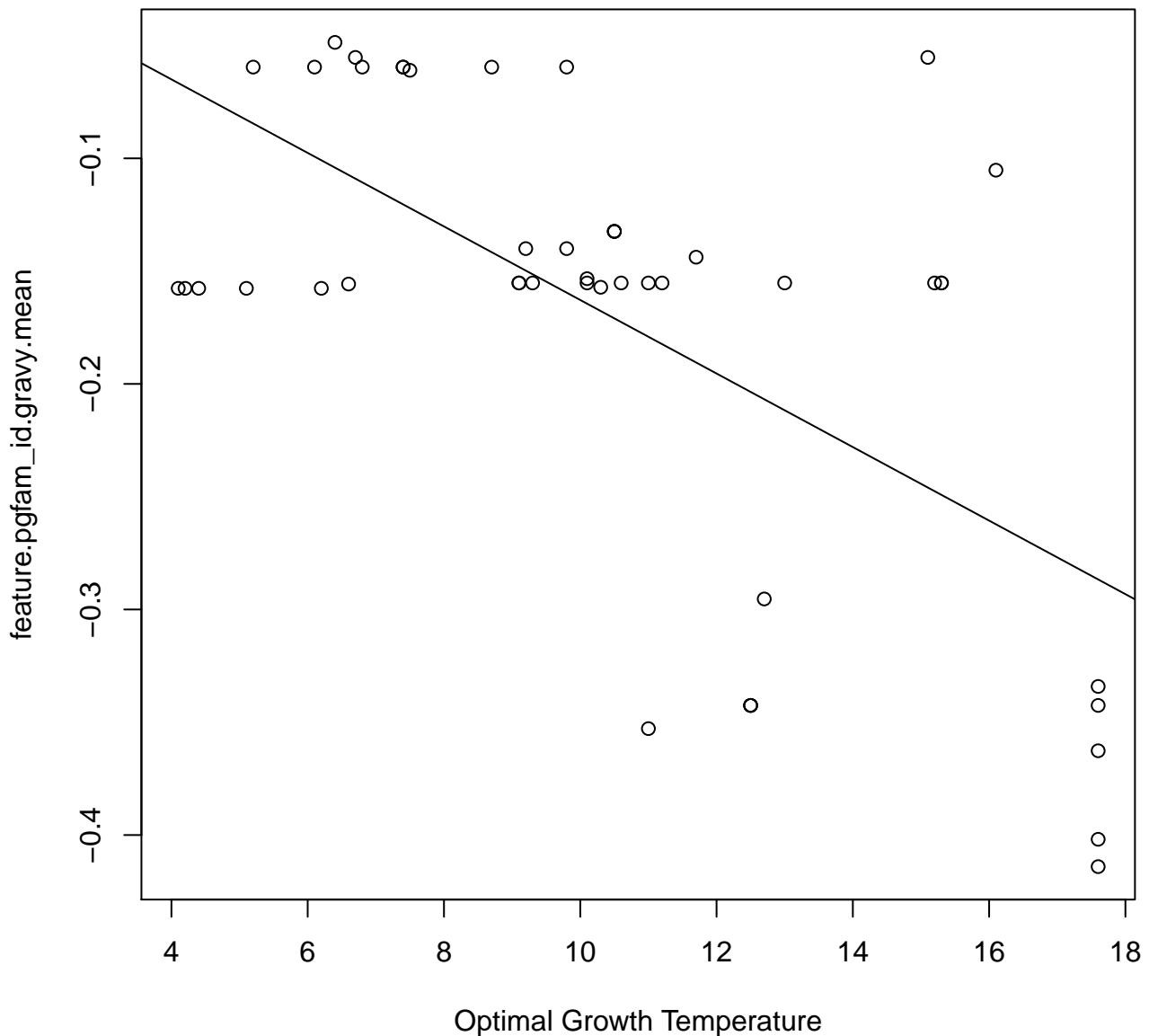
feature.pgfam_id.gravy.mean
PGF_03760224
Dethiobiotin synthase BioD (EC 6.3.3.3)



feature.pgfam_id.gravy.mean
PGF_03990071
LSU ribosomal protein L23p (L23Ae)



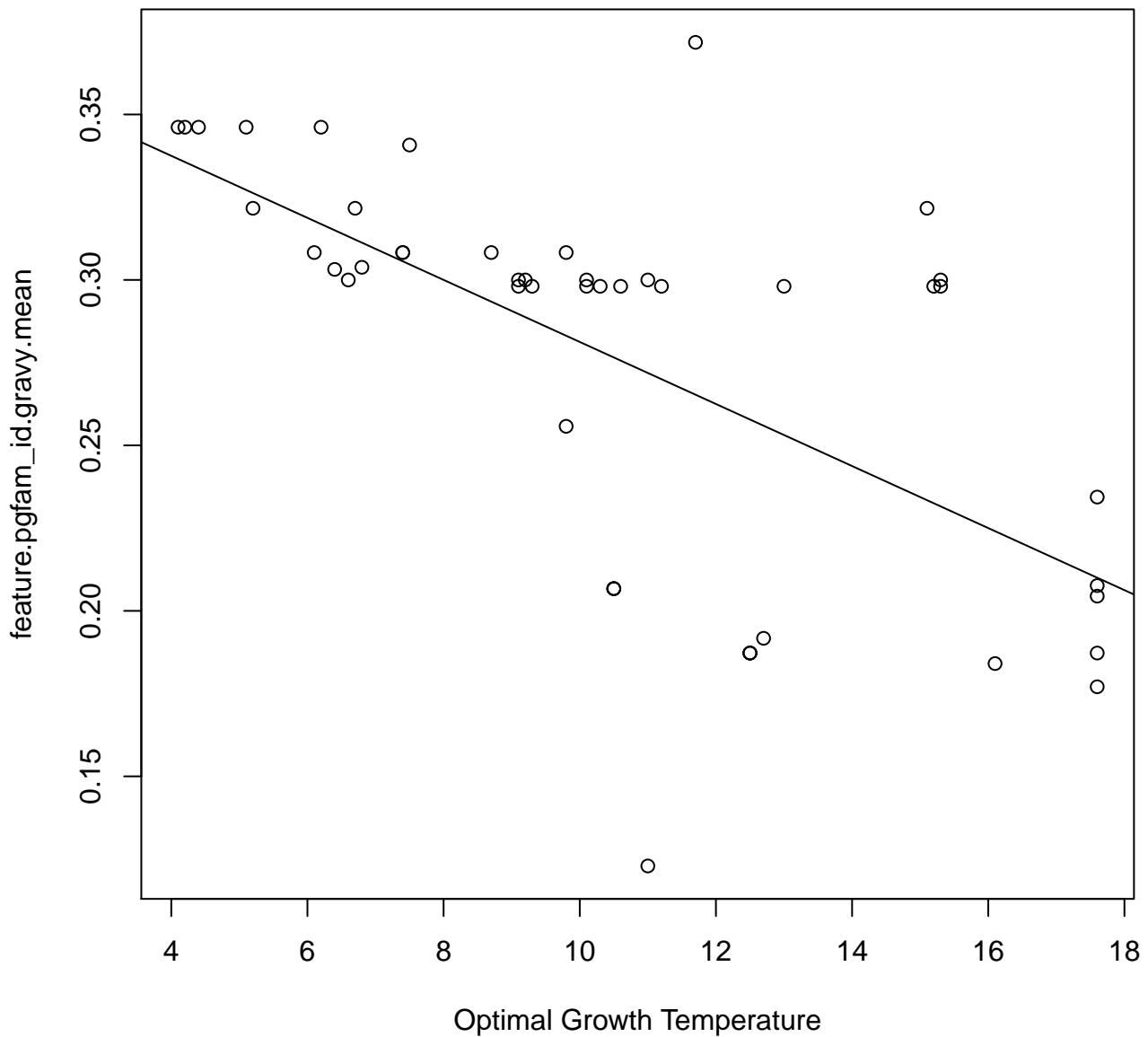
feature.pgfam_id.gravy.mean
PGF_00031127
Periplasmic thiol:disulfide interchange protein DsbA



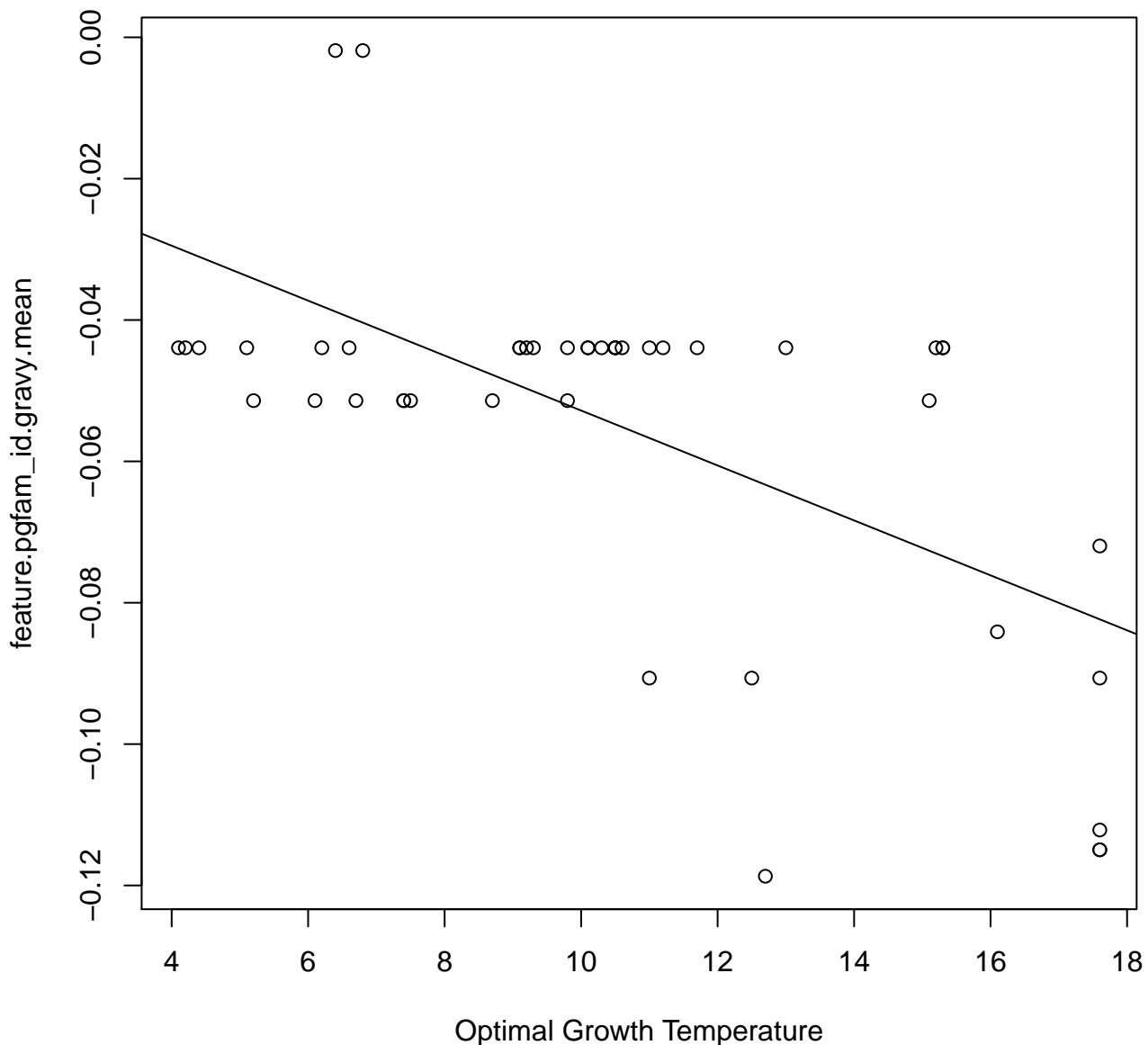
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PGF_00846351

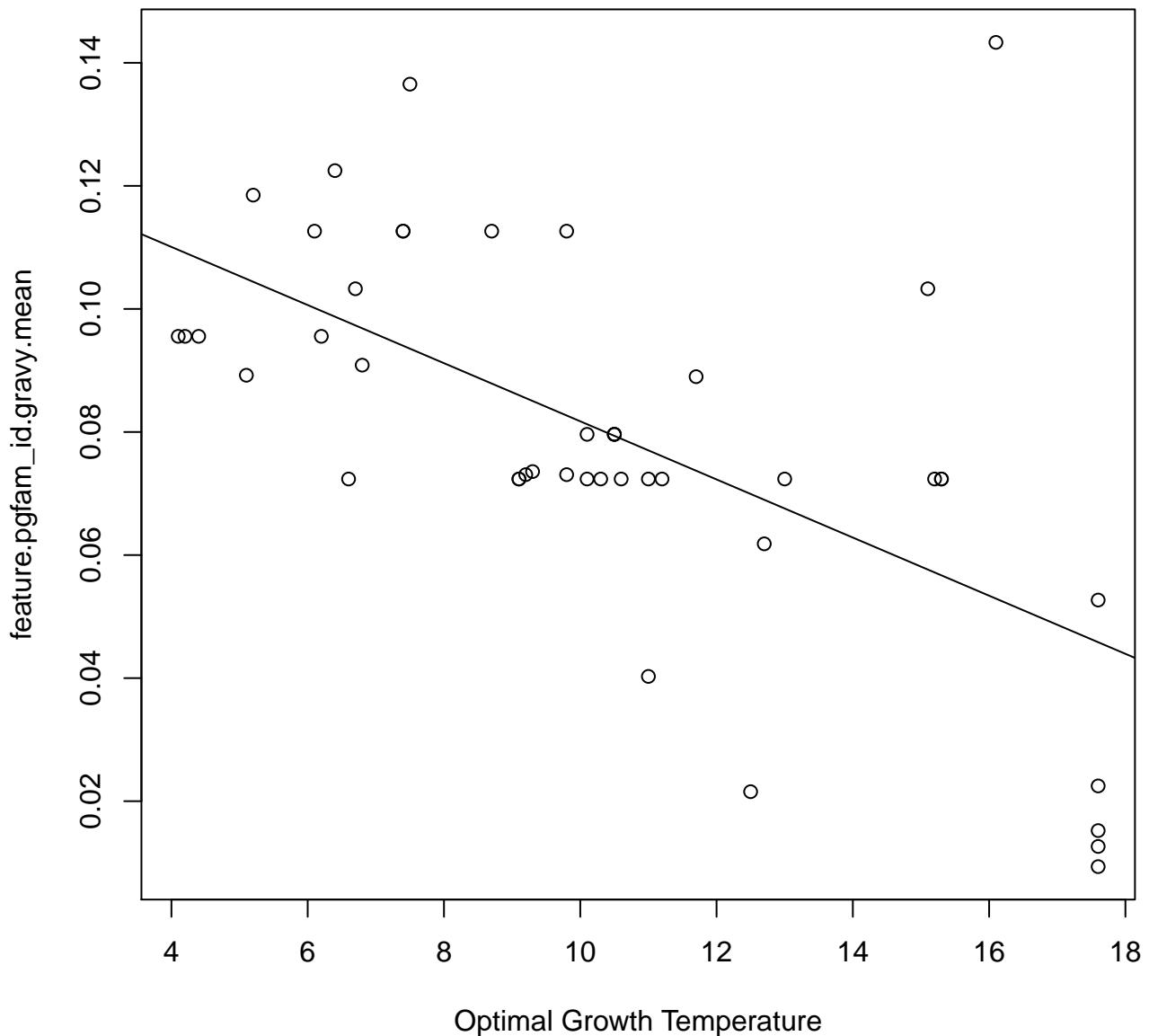
Peptidylprolyl isomerase, FKBP-type (EC 5.2.1.8) / Macrophage infectivity potentiator



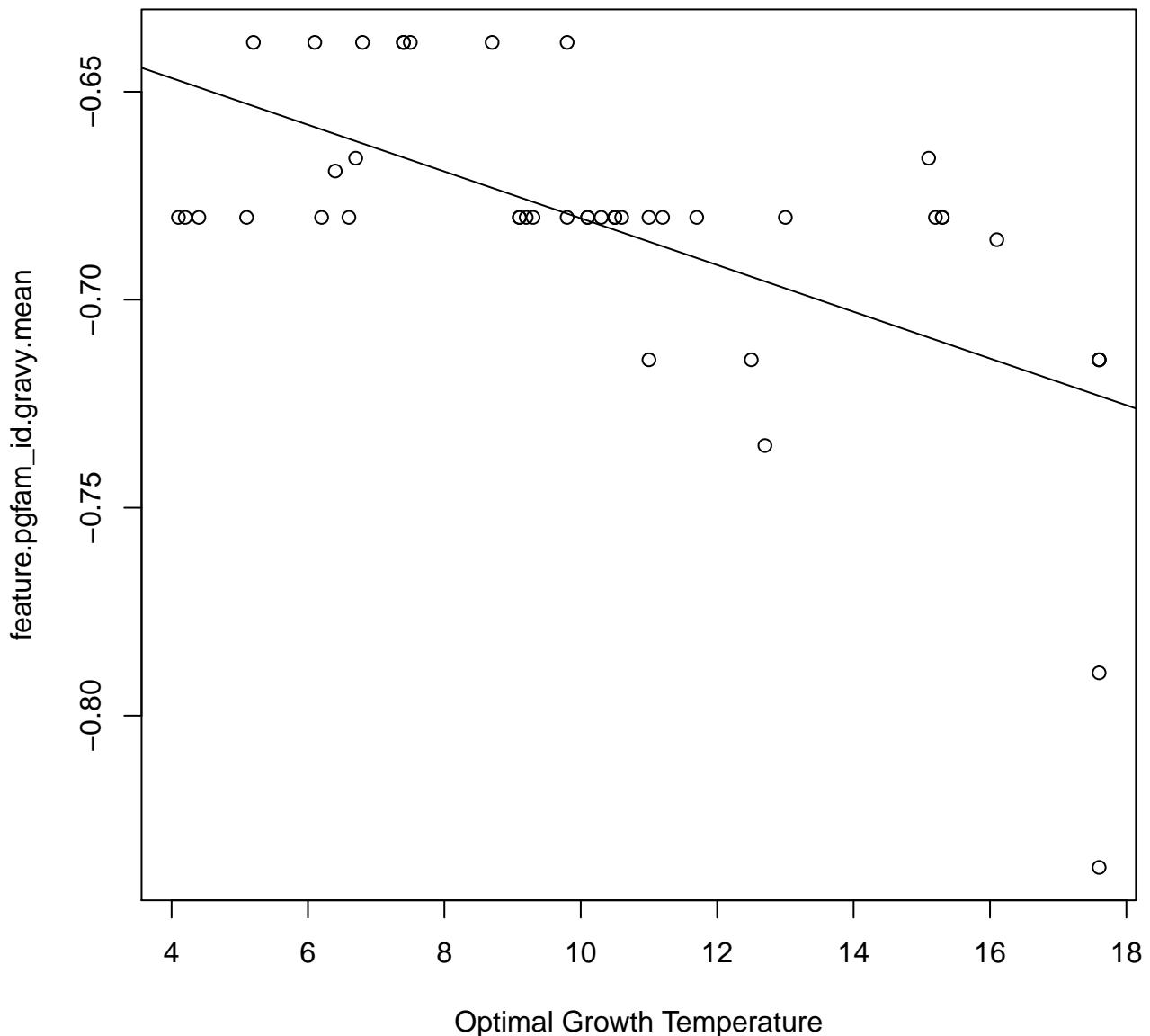
feature.pgfam_id.gravy.mean
PGF_05931407
Iron-sulfur cluster assembly iron binding protein IscA



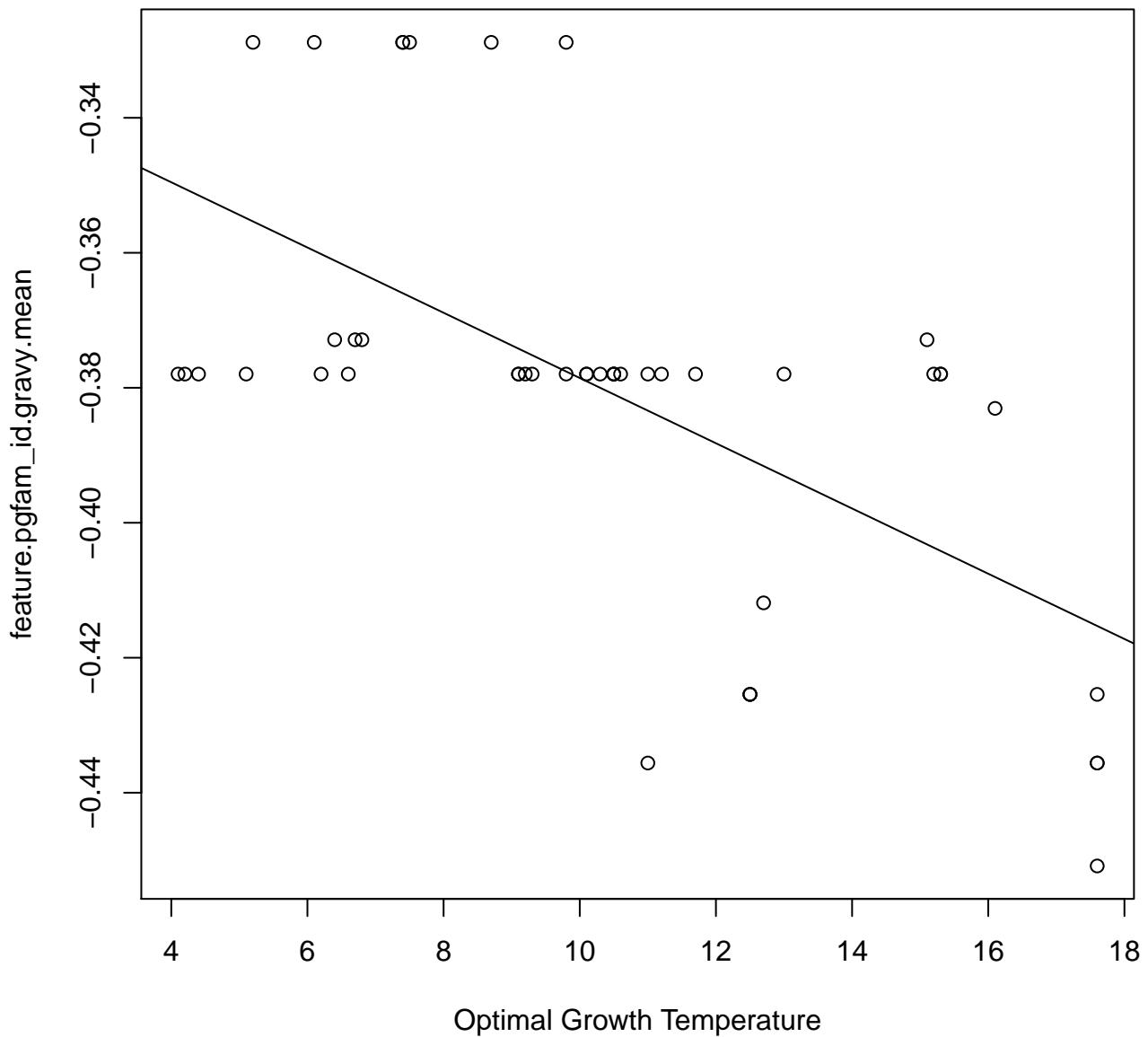
feature.pgfam_id.gravy.mean
PGF_09019918
Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)



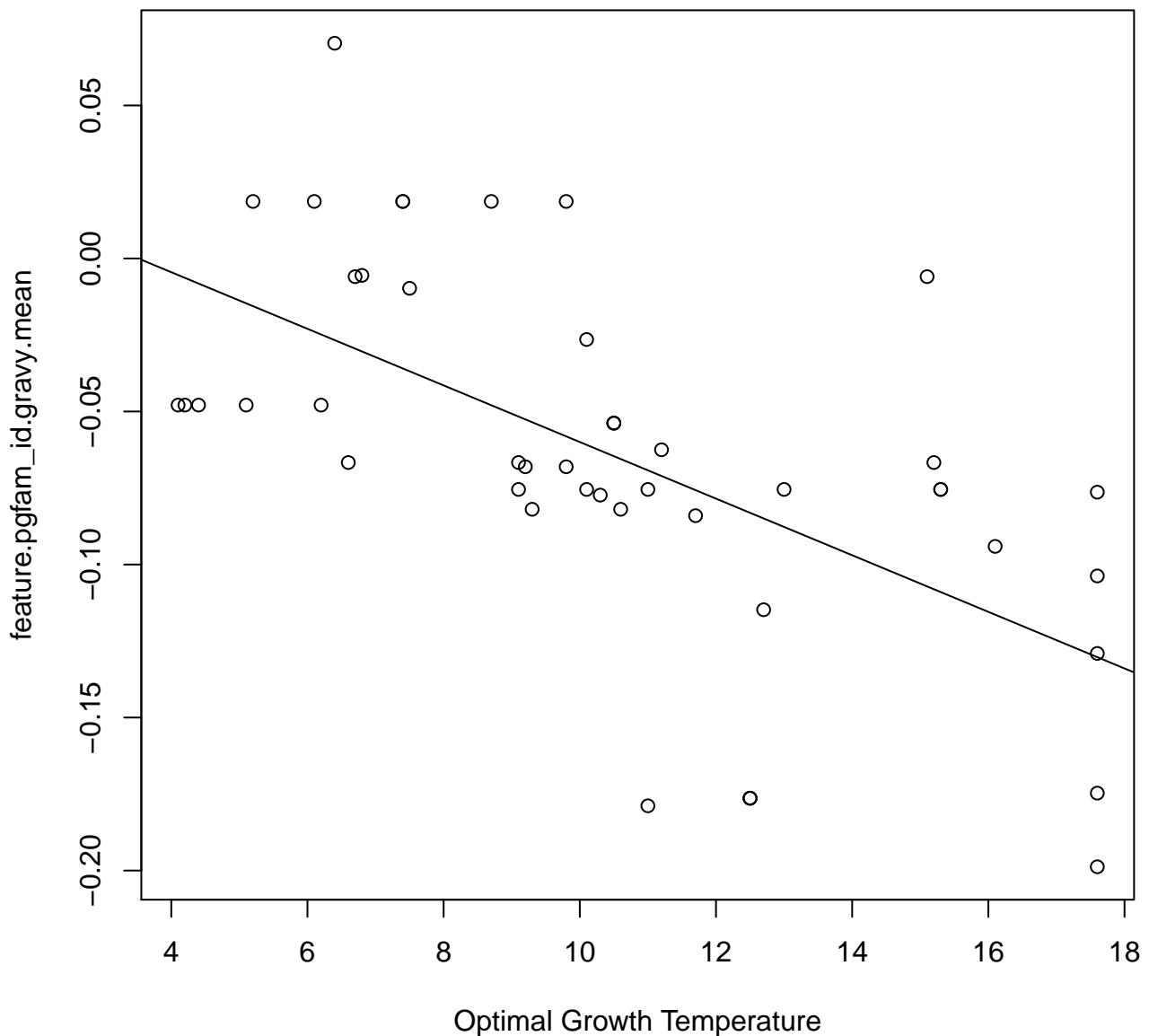
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PGF_03793164
Integration host factor alpha subunit



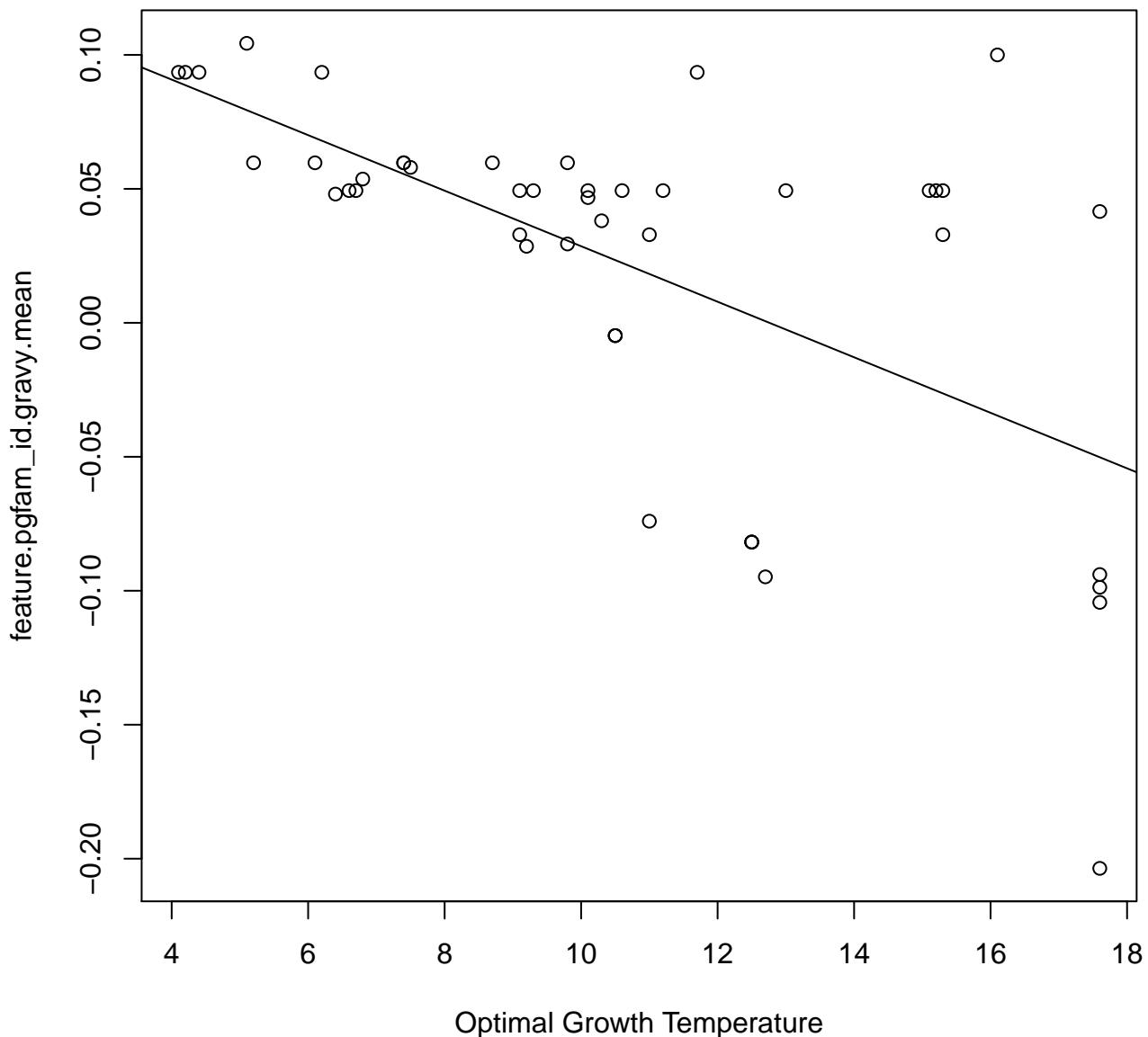
feature.pgfam_id.gravy.mean
PGF_00016395
LSU ribosomal protein L30p (L7e)



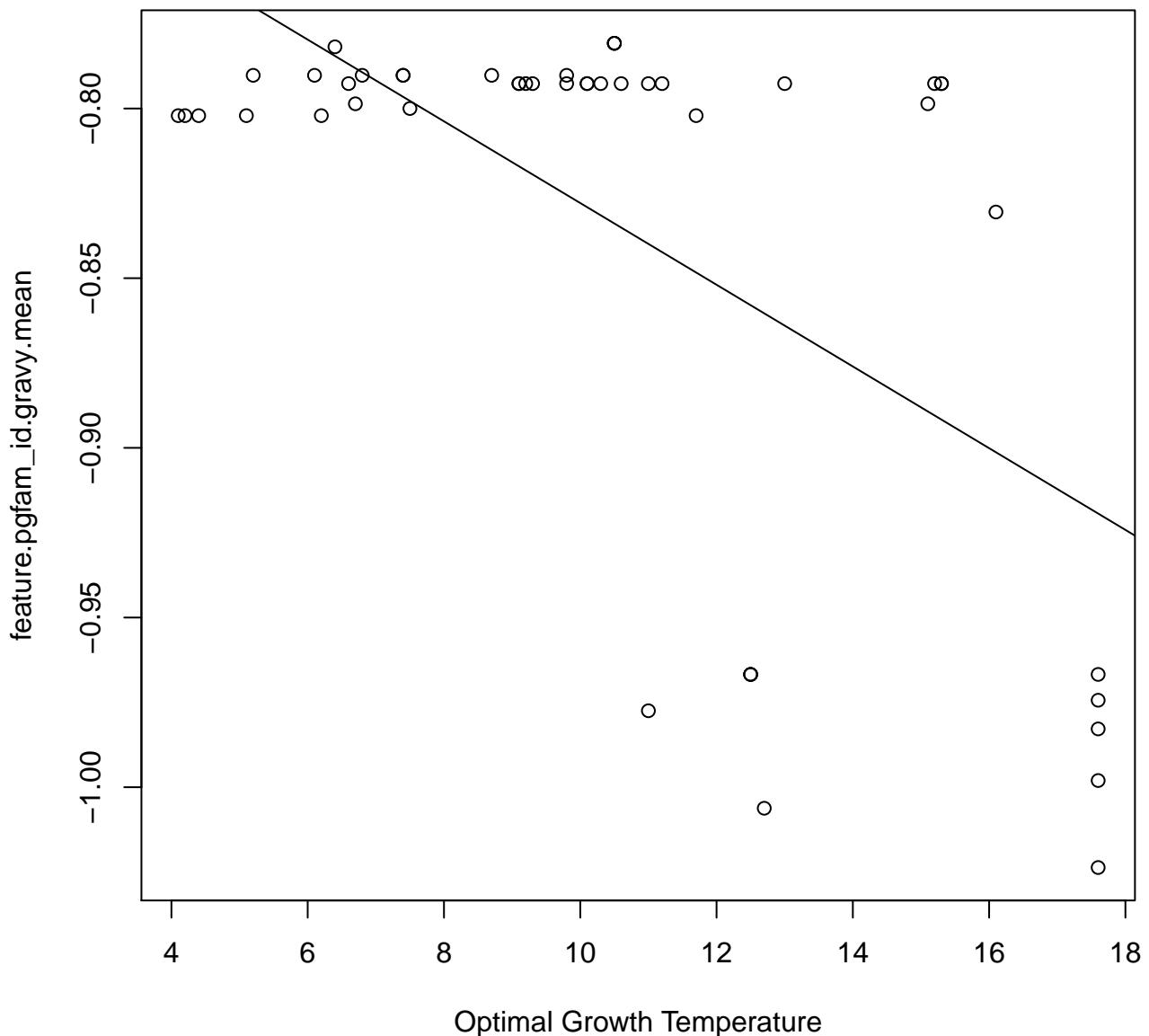
feature.pgfam_id.gravy.mean
PGF_00016919
Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)



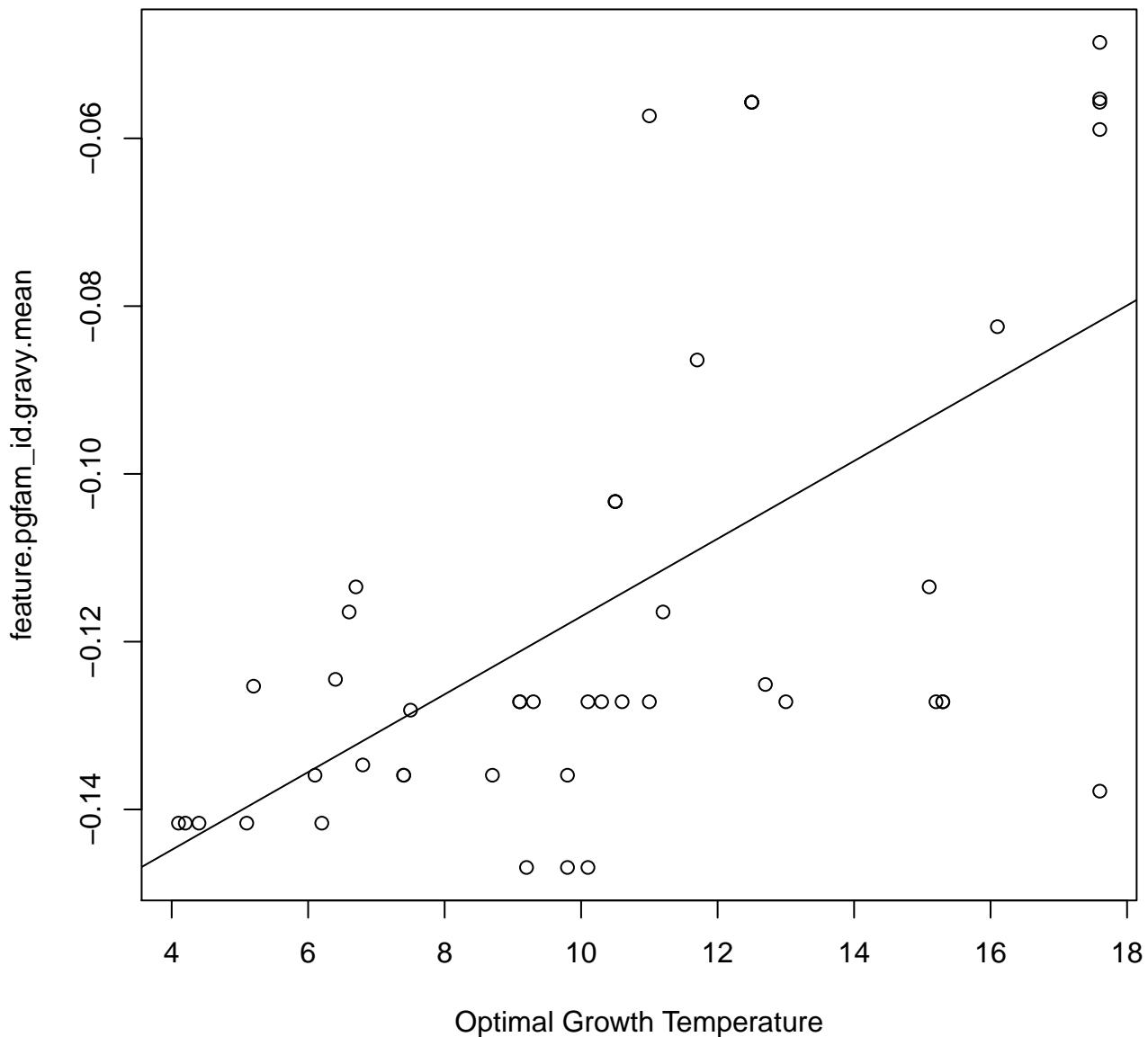
feature.pgfam_id.gravy.mean
PGF_00777371
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)



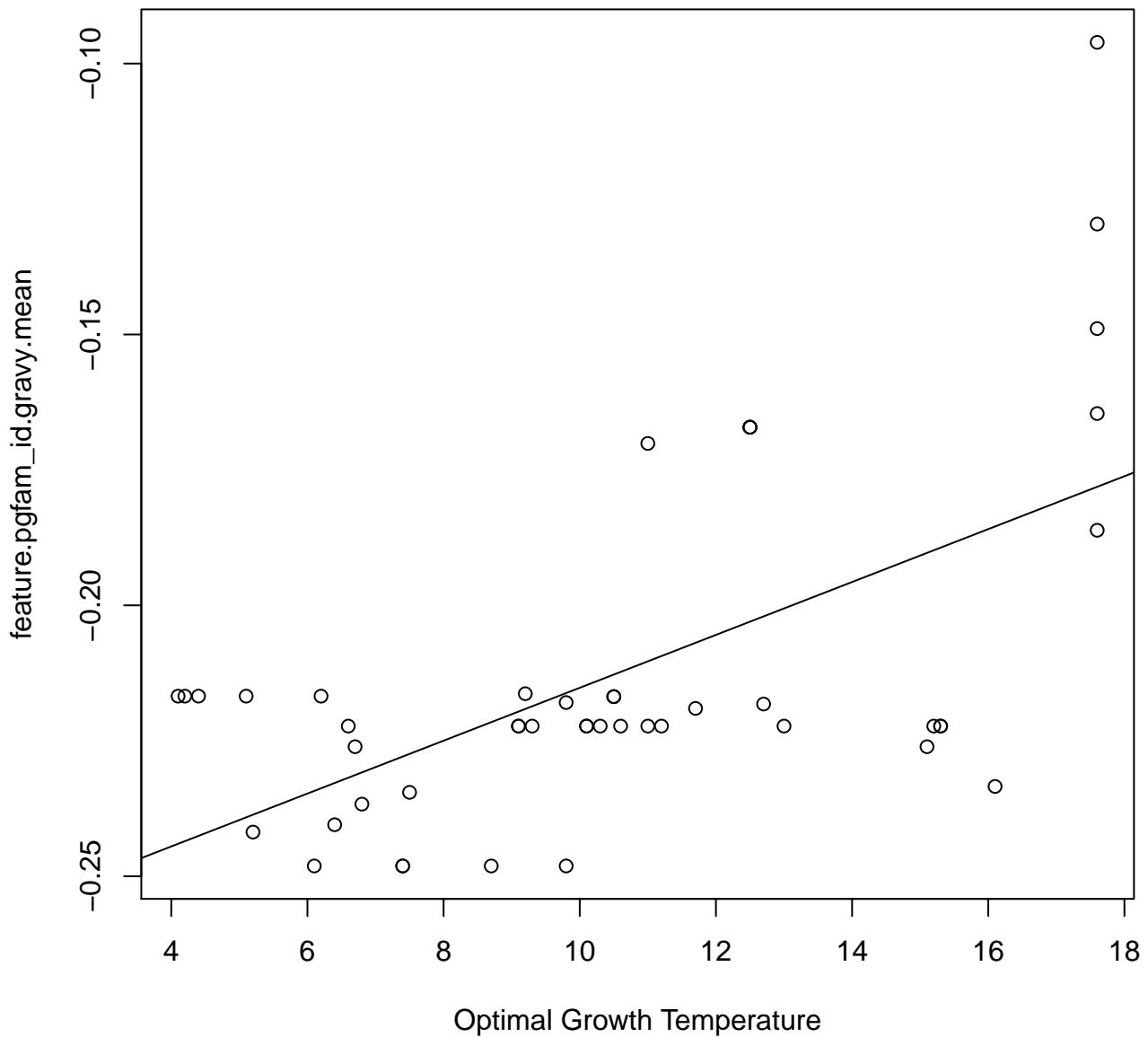
feature.pgfam_id.gravy.mean
PGF_00048829
LSU rRNA pseudouridine(2605) synthase (EC 5.4.99.22)



feature.pgfam_id.gravy.mean
PGF_00045900
Pyridoxine 5'-phosphate synthase (EC 2.6.99.2)

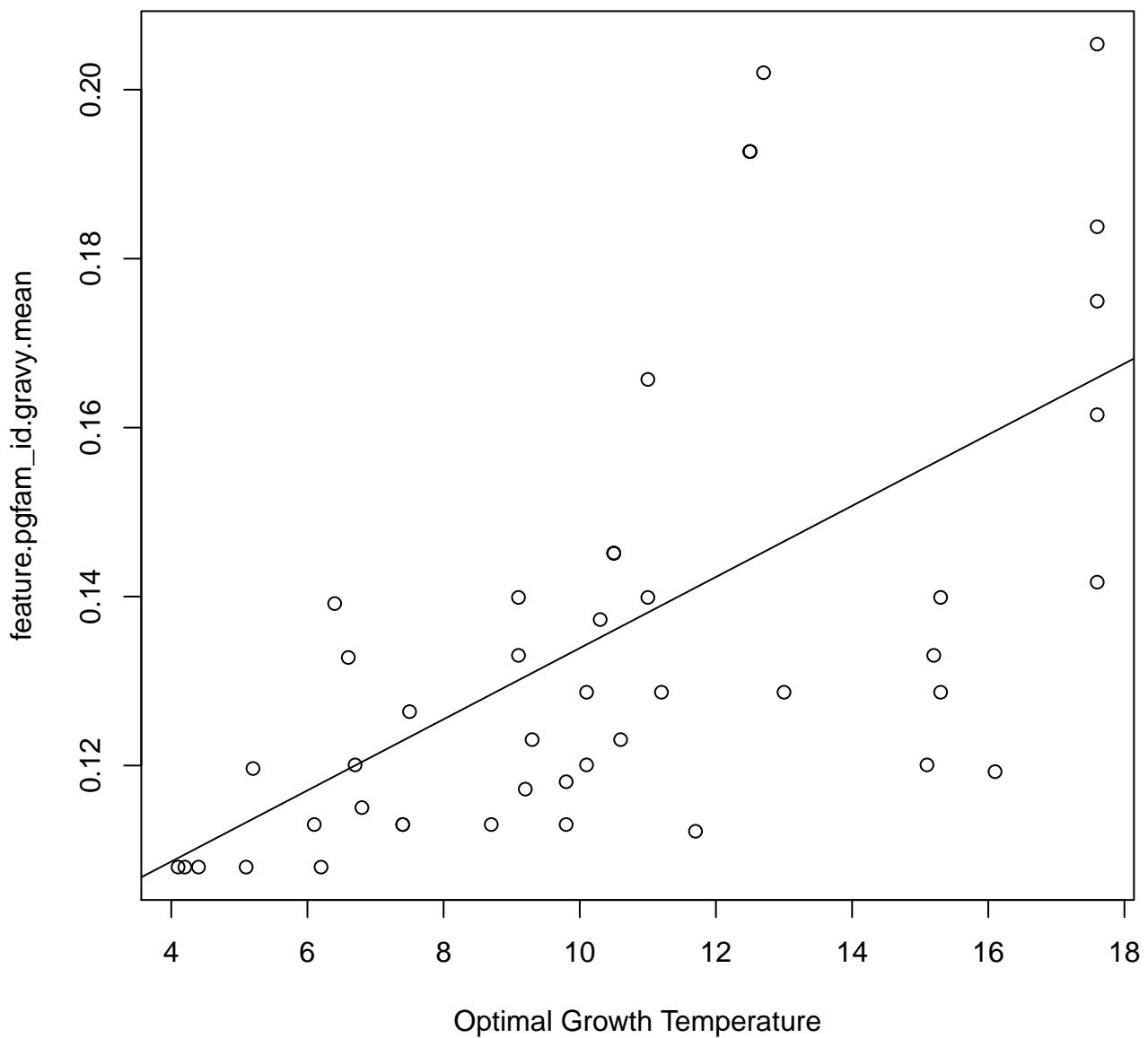


feature.pgfam_id.gravy.mean
PGF_00068042
Arginase/agmatinase/formiminoglutamate hydrolase, arginase family

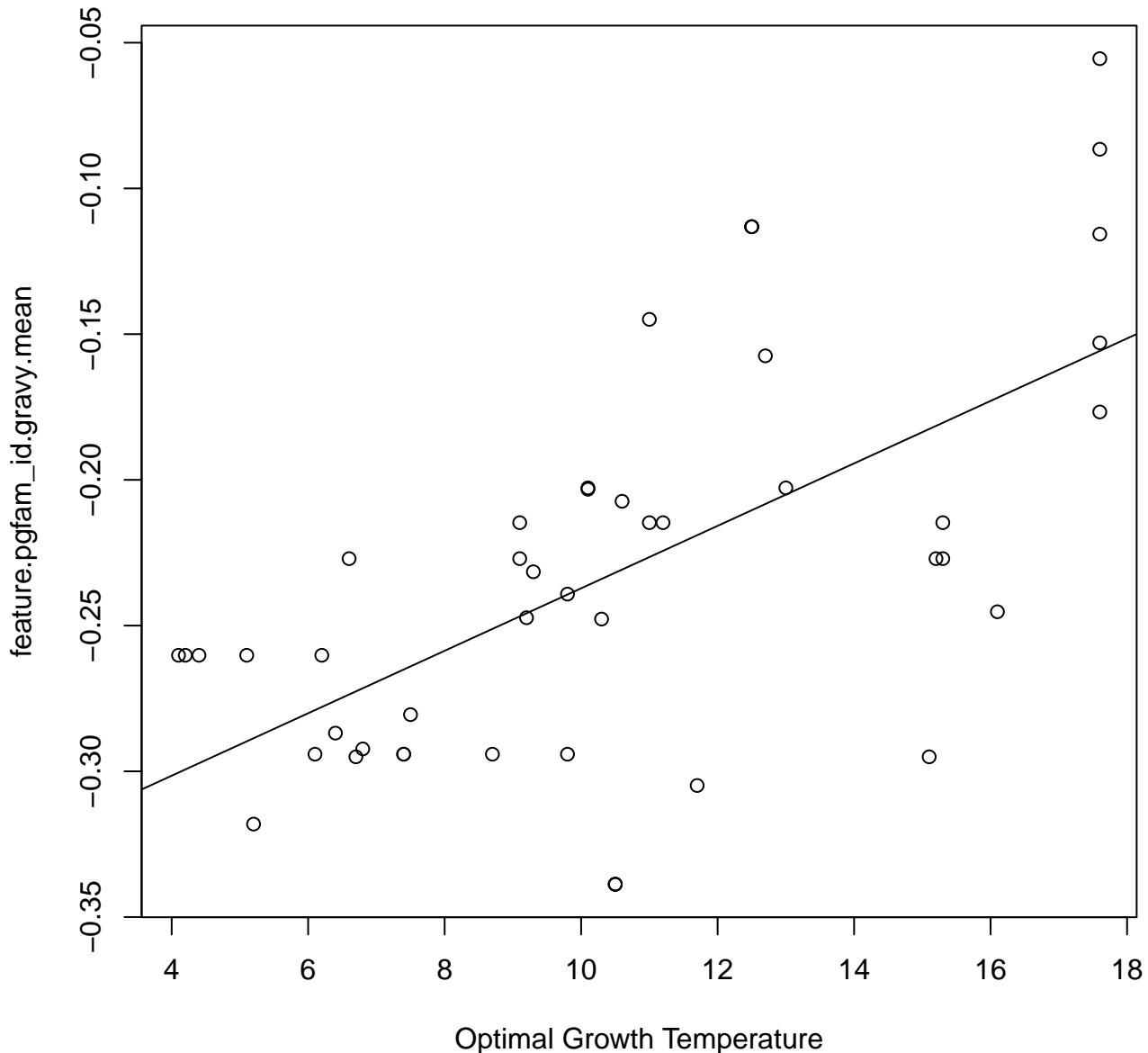


feature.pgfam_id.gravy.mean
PGF_03364965

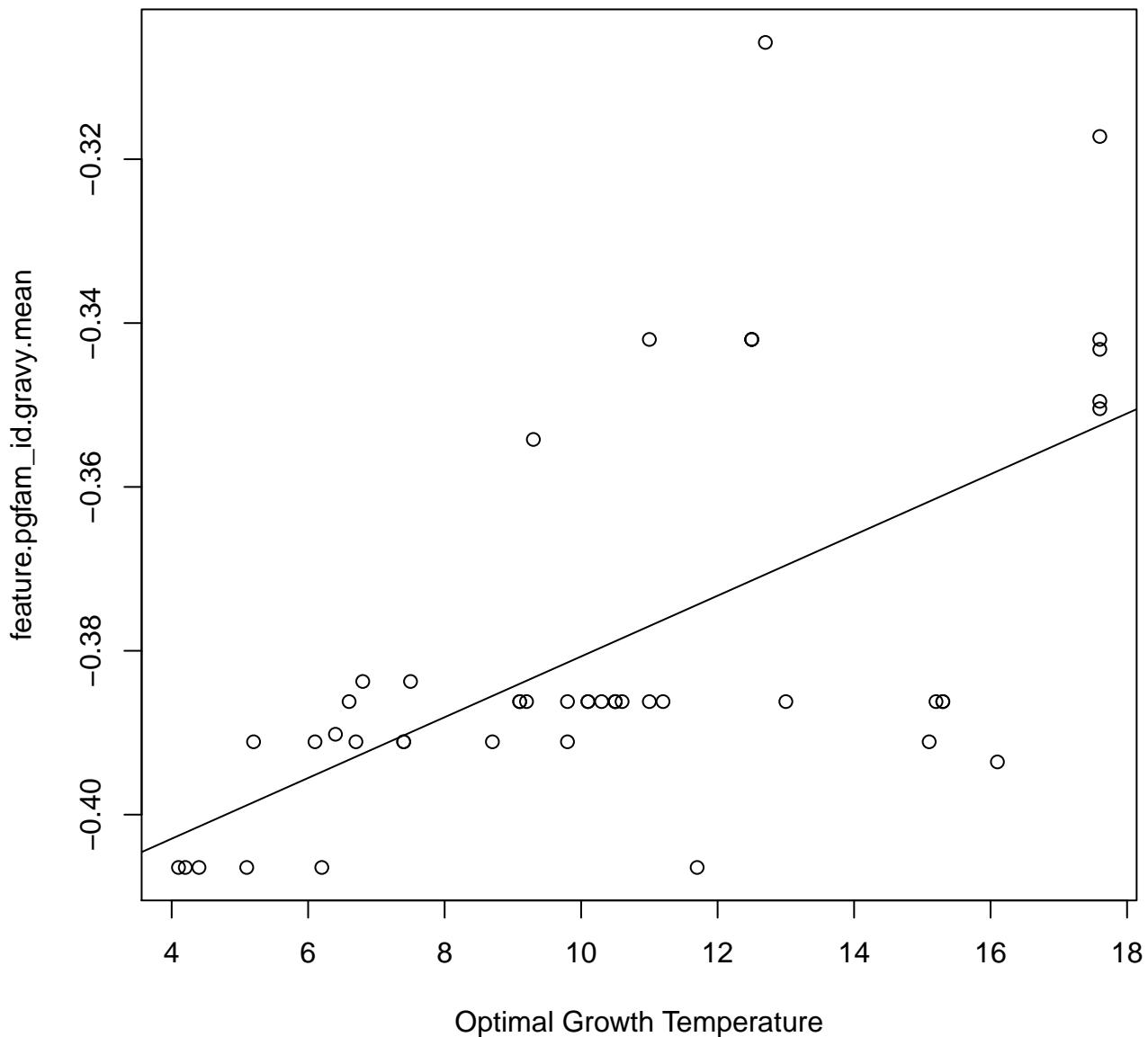
Type cbb3 cytochrome oxidase biogenesis protein Ccol; Copper-translocating P-type ATPase (EC 3.6.3.4)



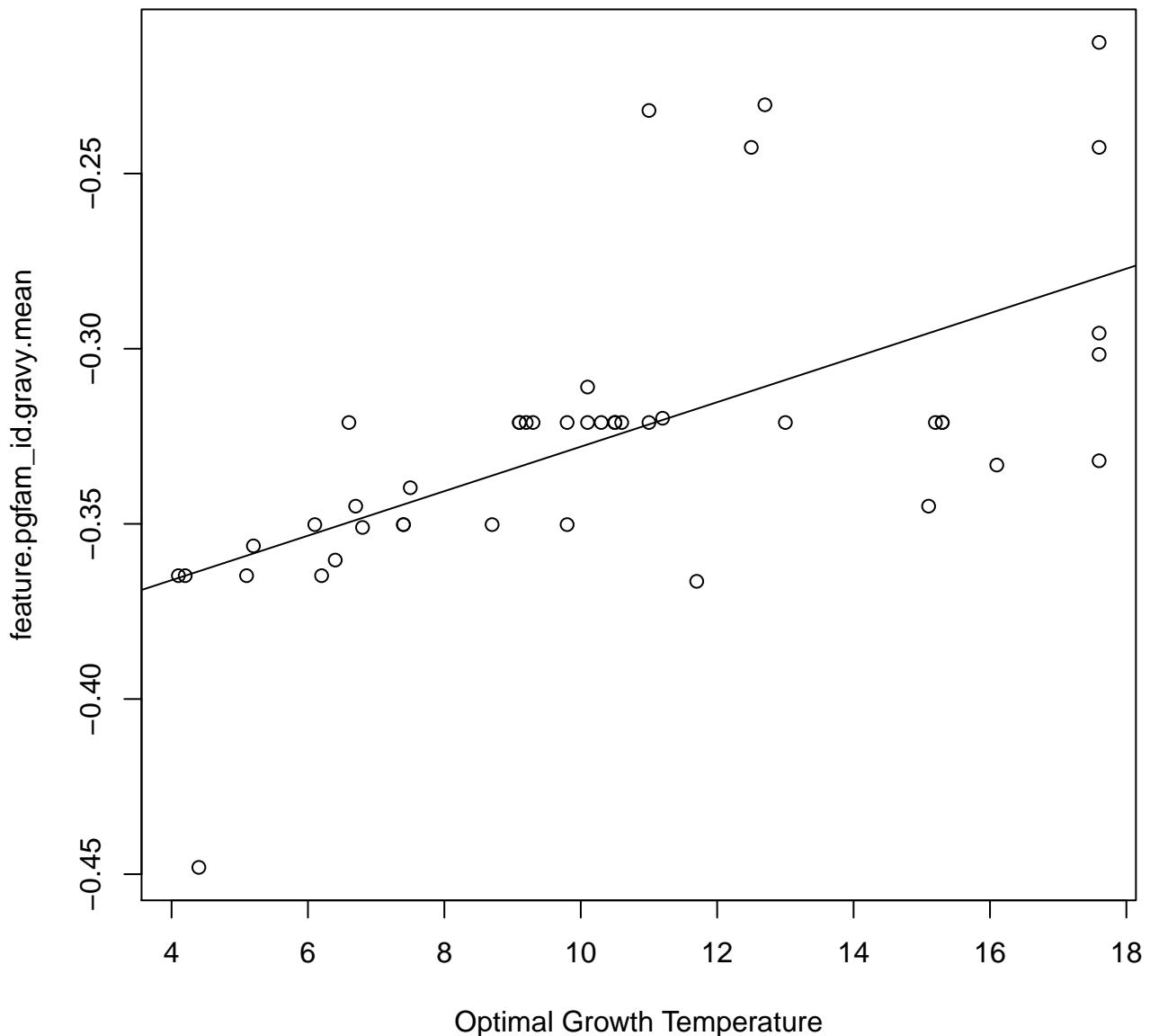
feature.pgfam_id.gravy.mean
PGF_00116812
Hydrolase SM_b20688, alpha/beta fold family



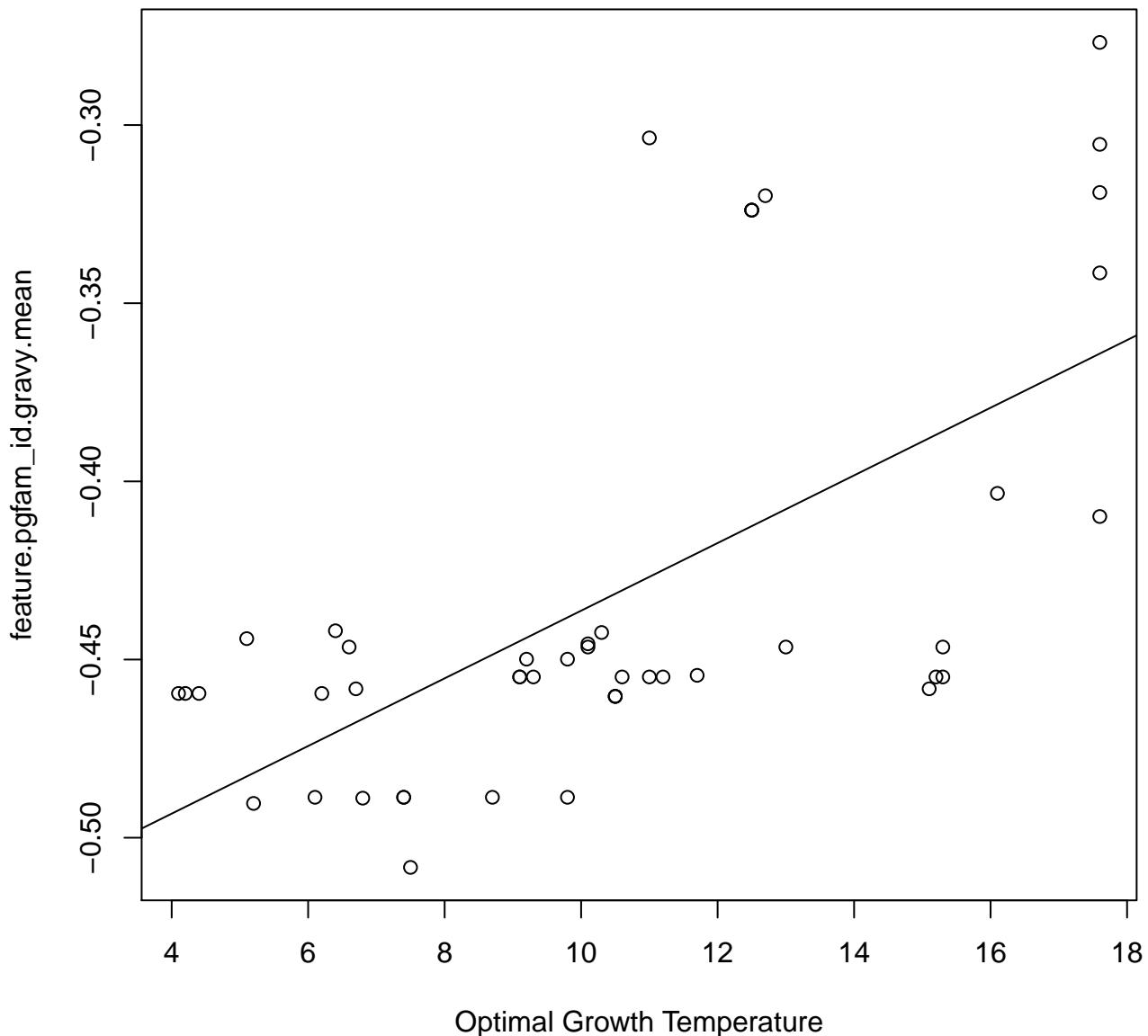
feature.pgfam_id.gravy.mean
PGF_02019462
Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)



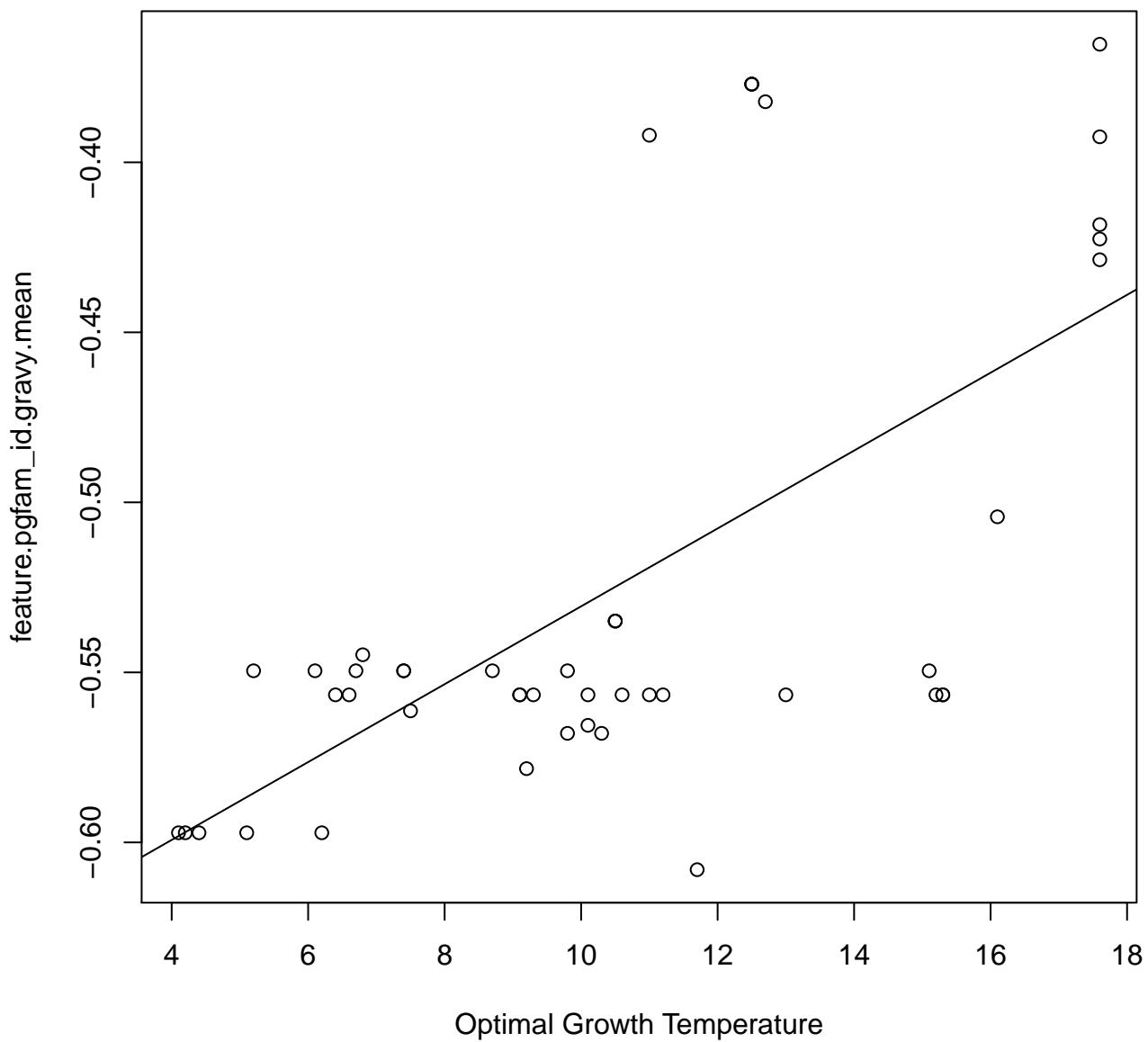
feature.pgfam_id.gravy.mean
PGF_07179577
Flagellar basal-body rod protein FlgF



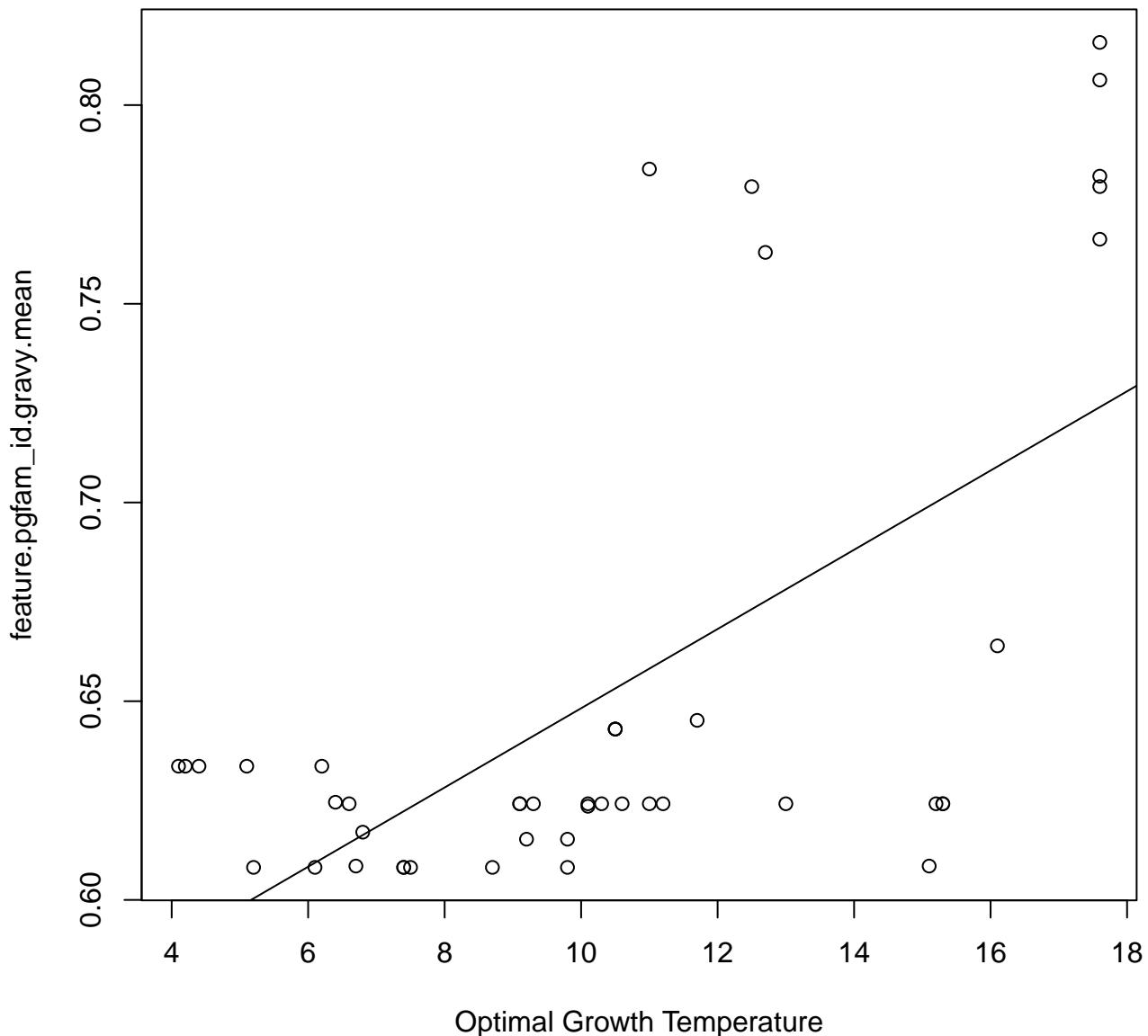
feature.pgfam_id.gravy.mean
PGF_03336368
hypothetical protein



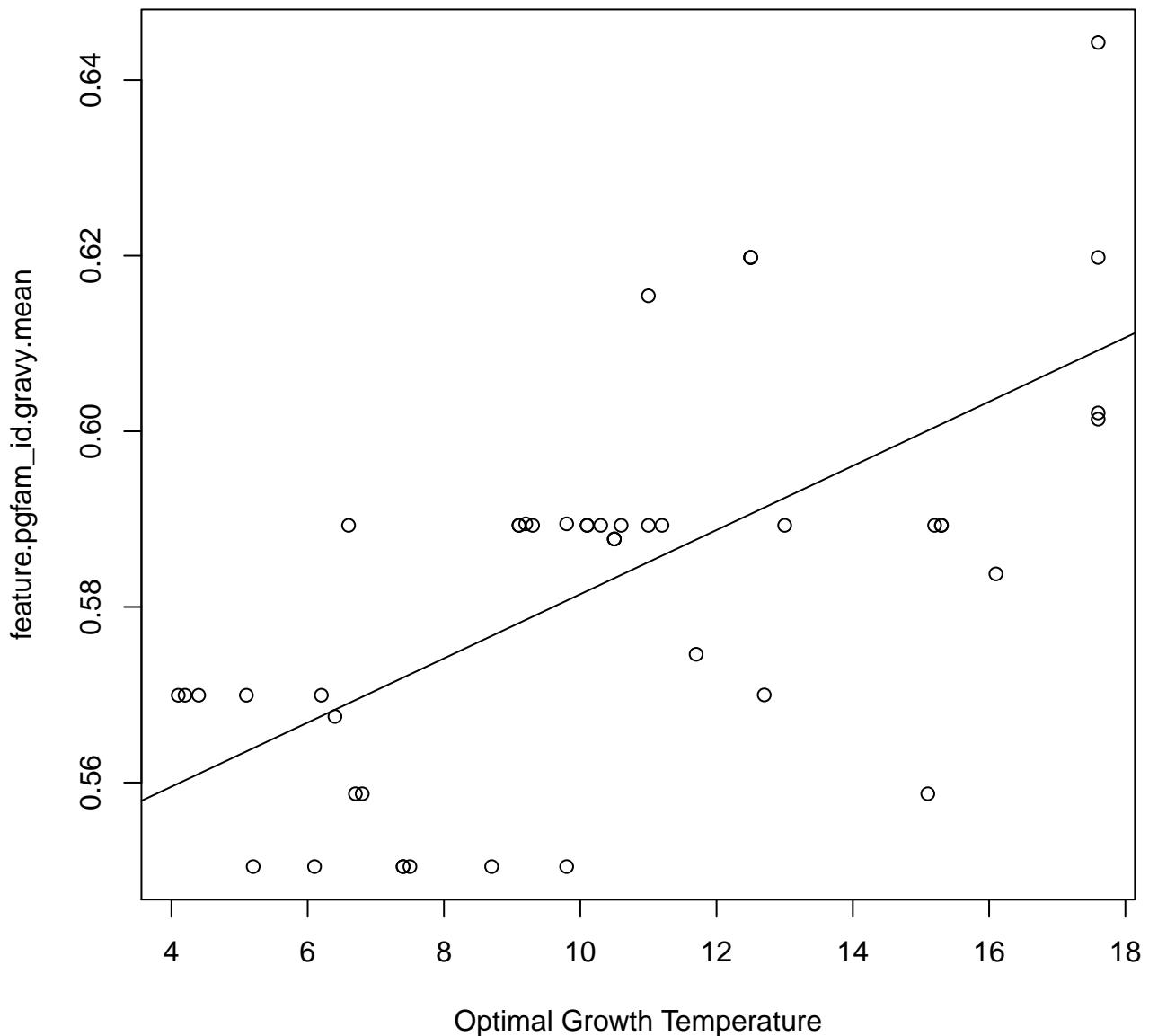
feature.pgfam_id.gravy.mean
PGF_00002640
FIG021625: hypothetical protein



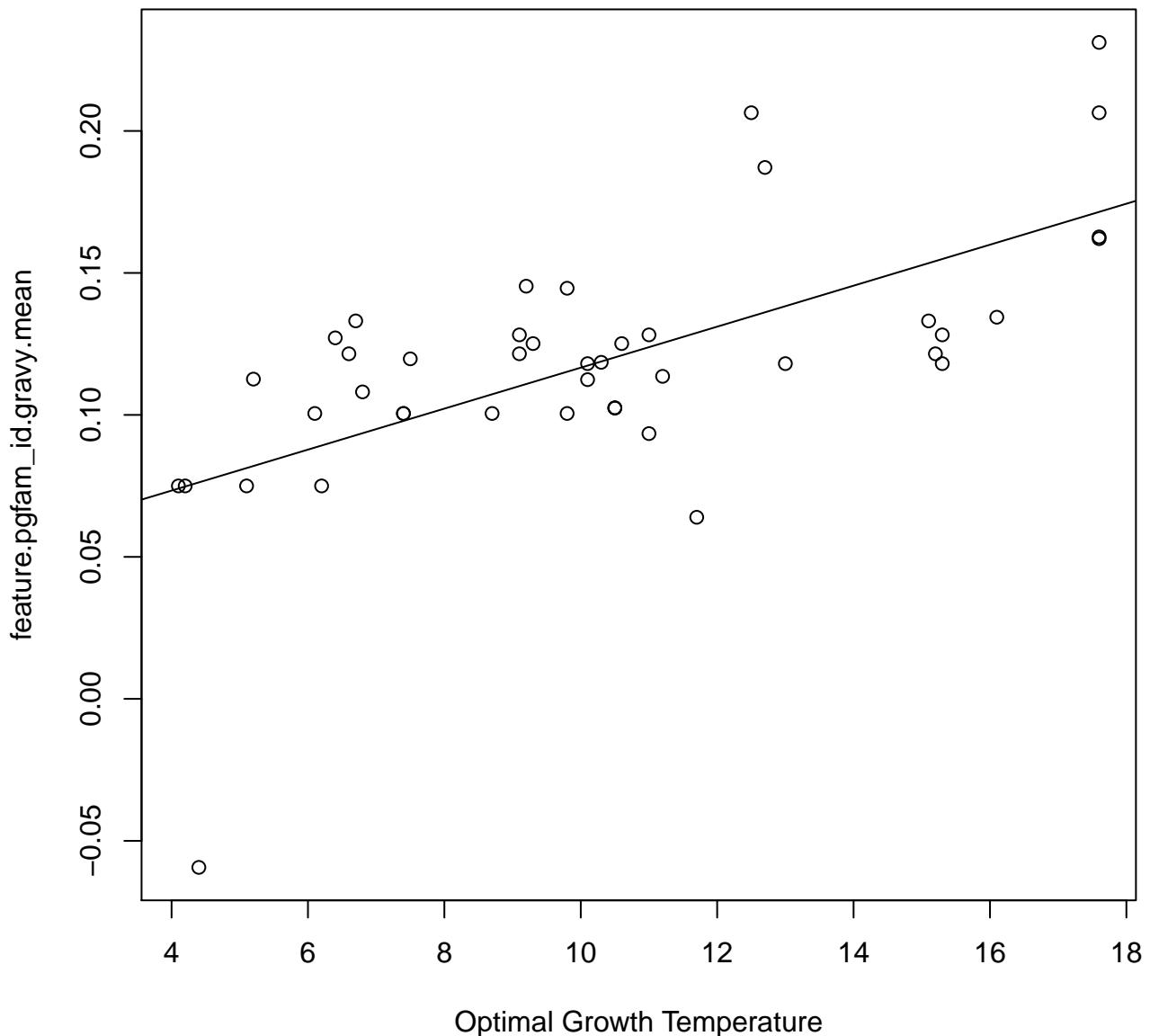
feature.pgfam_id.gravy.mean
PGF_07157721
Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB



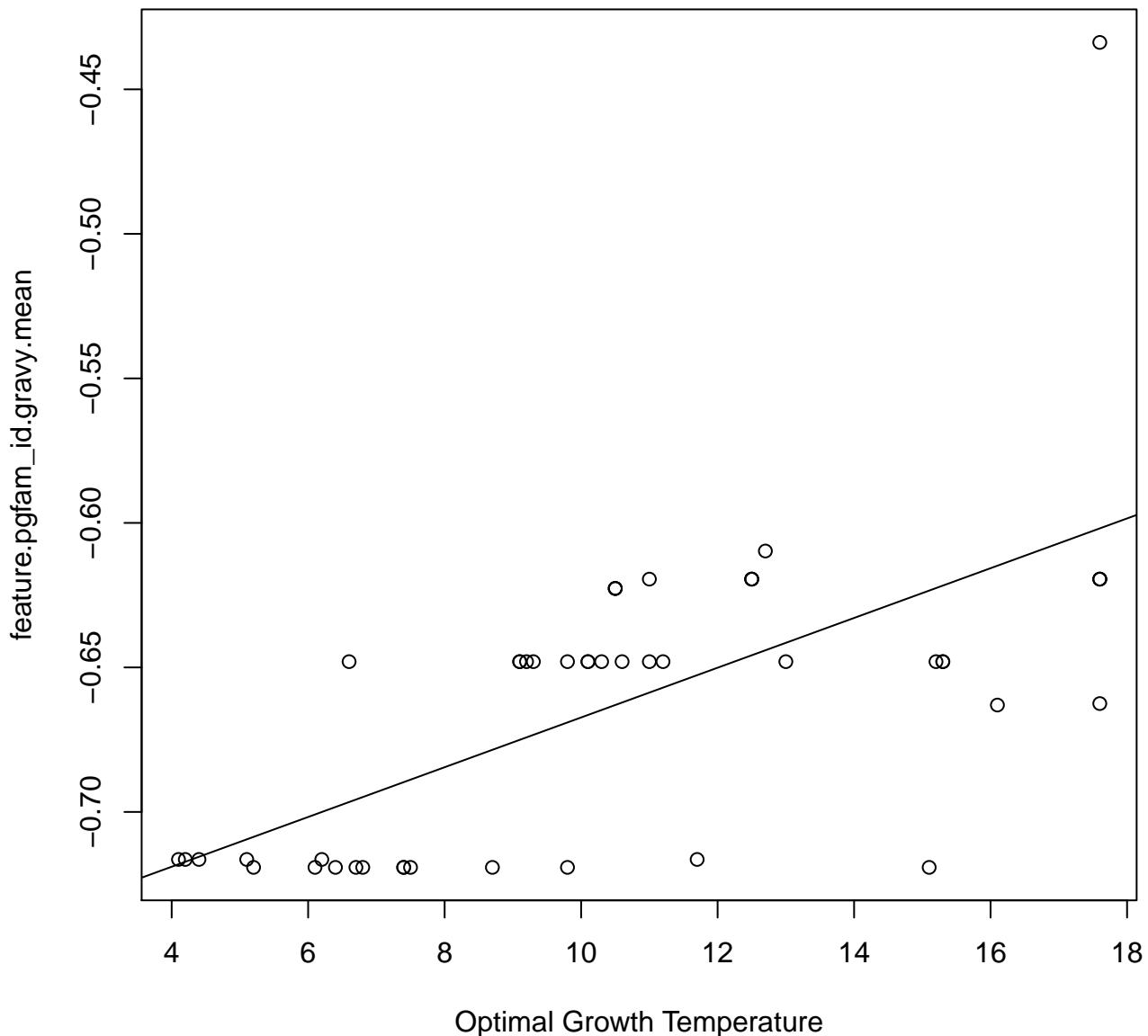
feature.pgfam_id.gravy.mean
PGF_00024619
Acetate permease ActP (cation/acetate symporter)



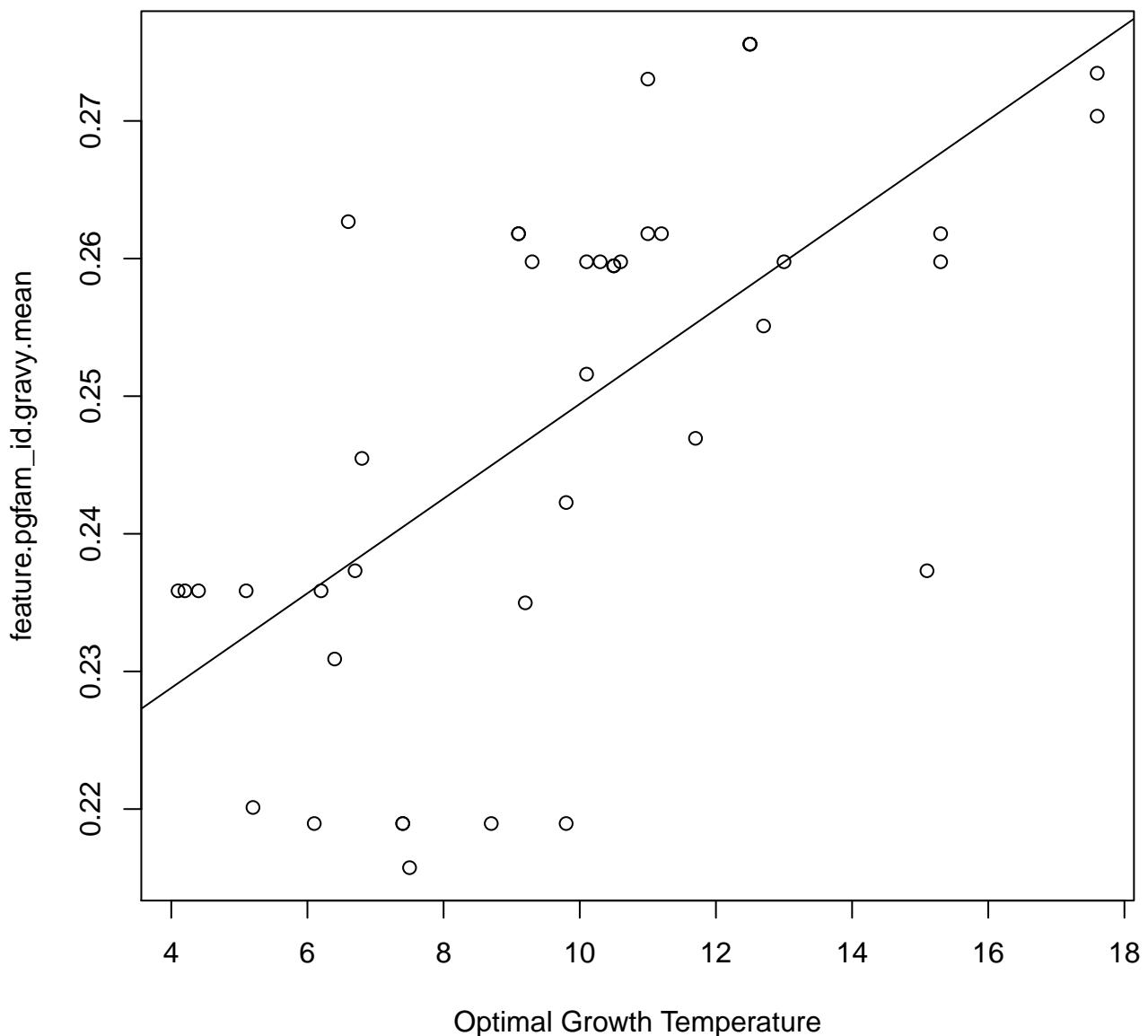
feature.pgfam_id.gravy.mean
PGF_00911329
Acryloyl-CoA reductase Acul/YhdH (EC 1.3.1.84)



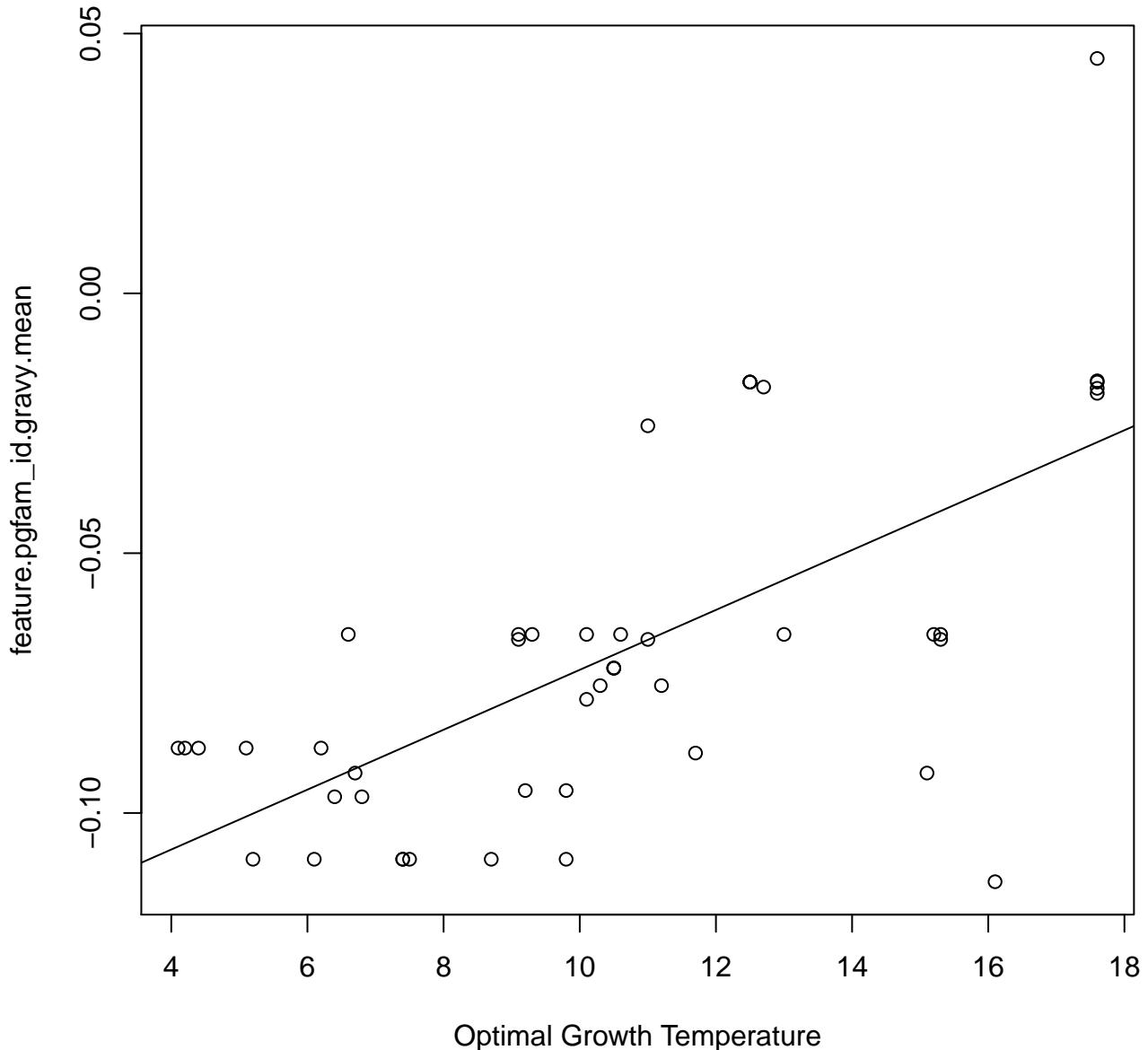
feature.pgfam_id.gravy.mean
PGF_00502502
Cold shock protein of CSP family => CspD (naming convention as in E.coli)



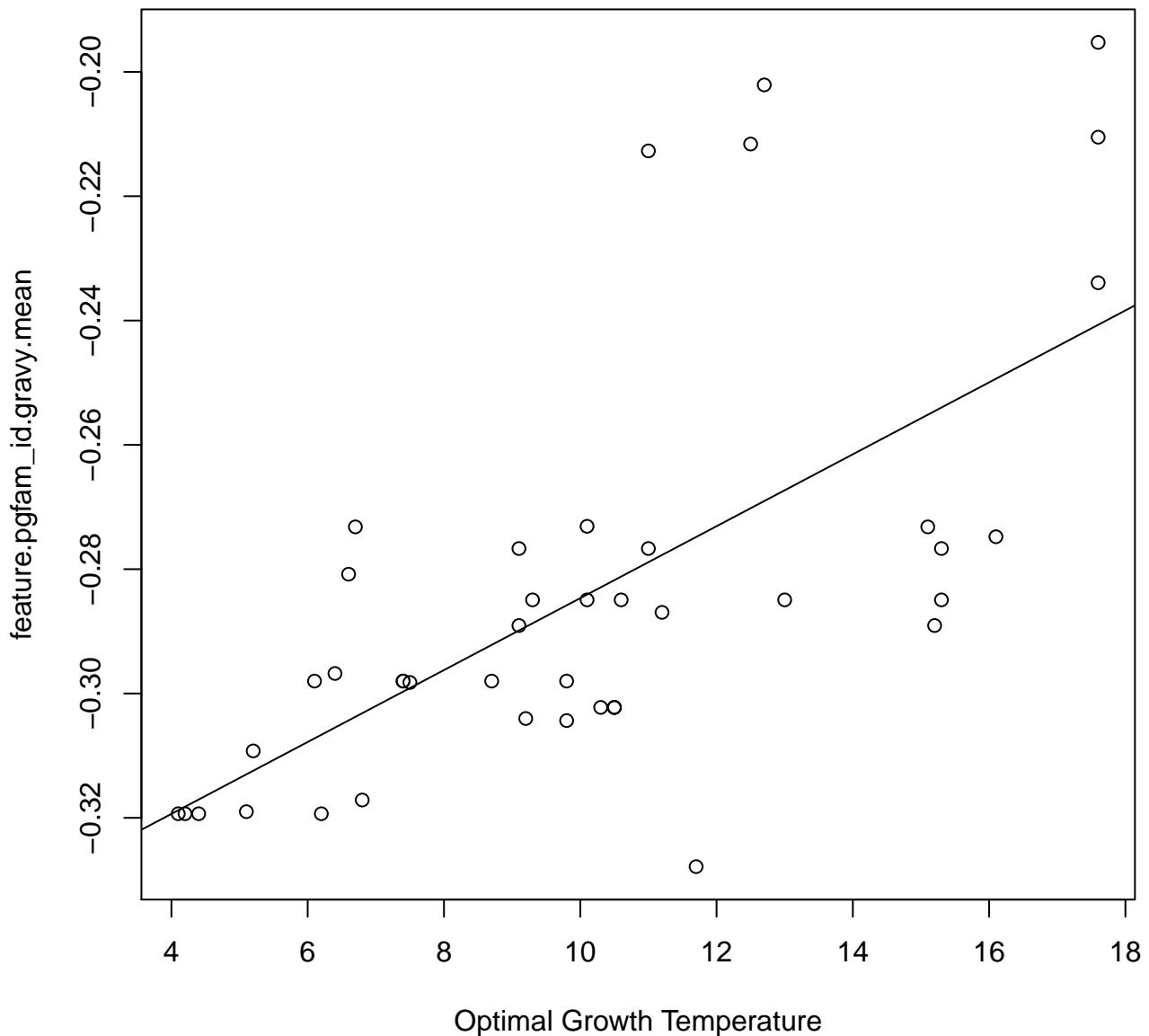
feature.pgfam_id.gravy.mean
PGF_05770898
Selenide,water dikinase (EC 2.7.9.3)



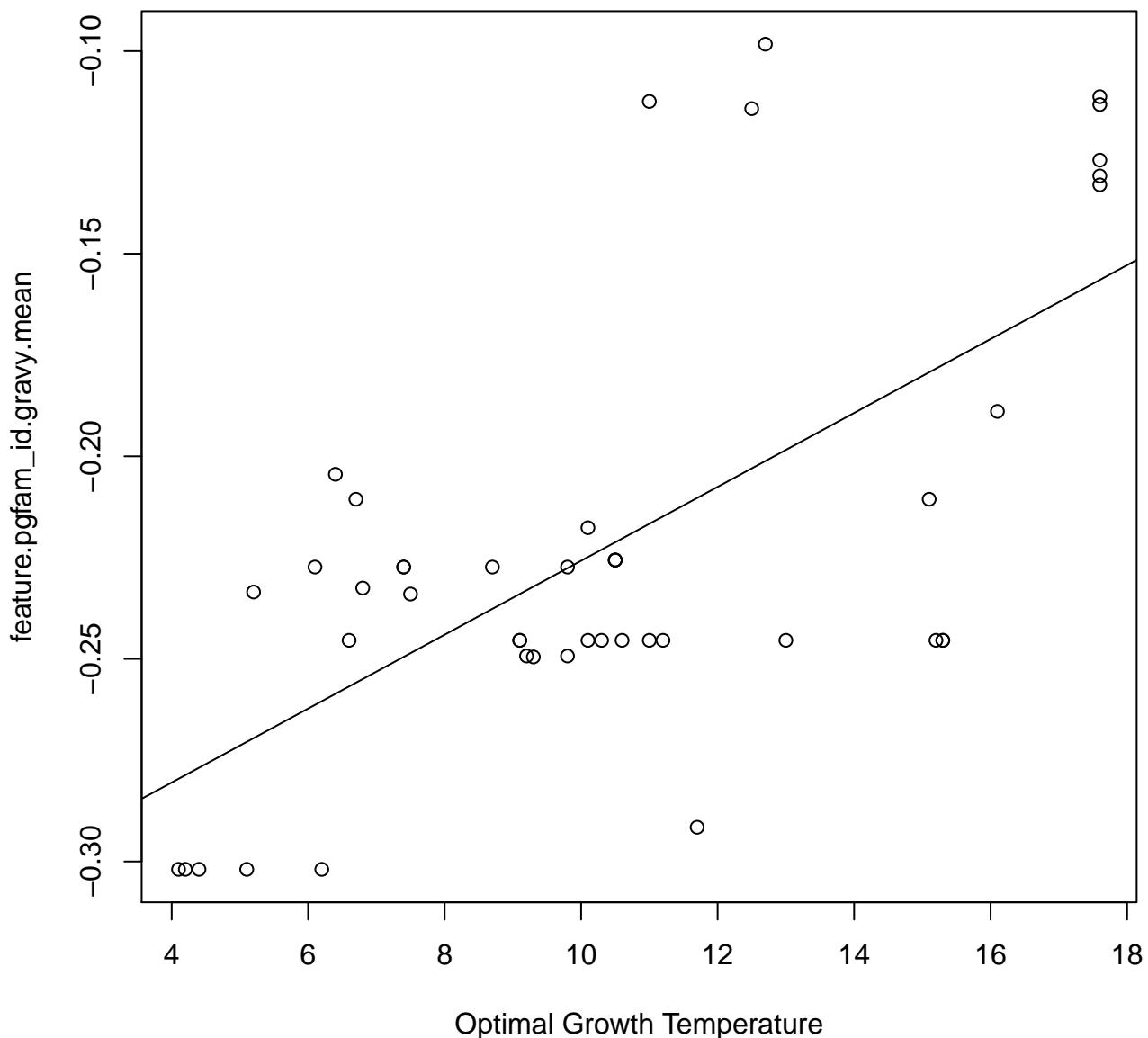
feature.pgfam_id.gravy.mean
PGF_00015701
Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)



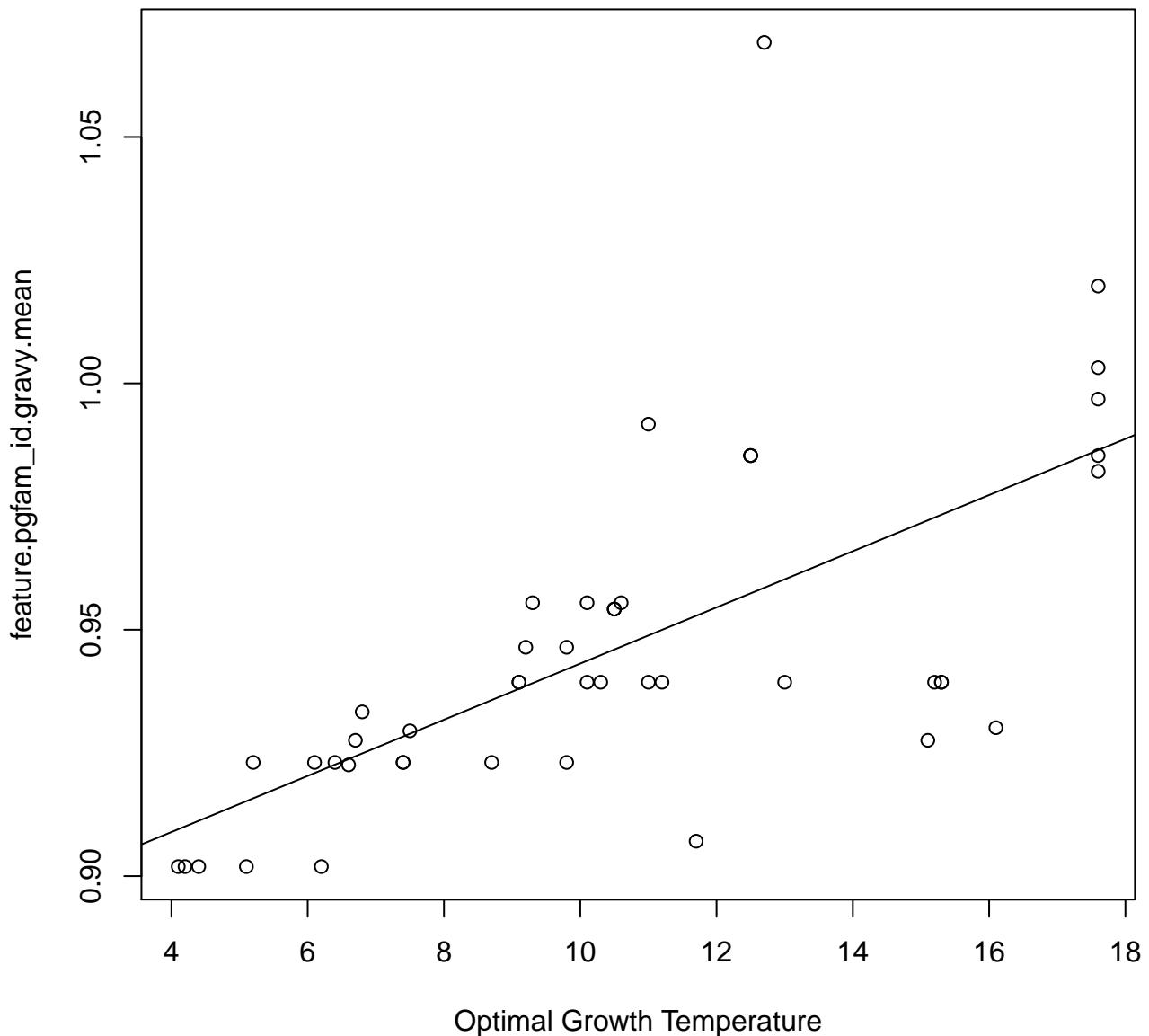
feature.pgfam_id.gravy.mean
PGF_04883561
Assimilatory nitrate reductase large subunit (EC 1.7.99.4)



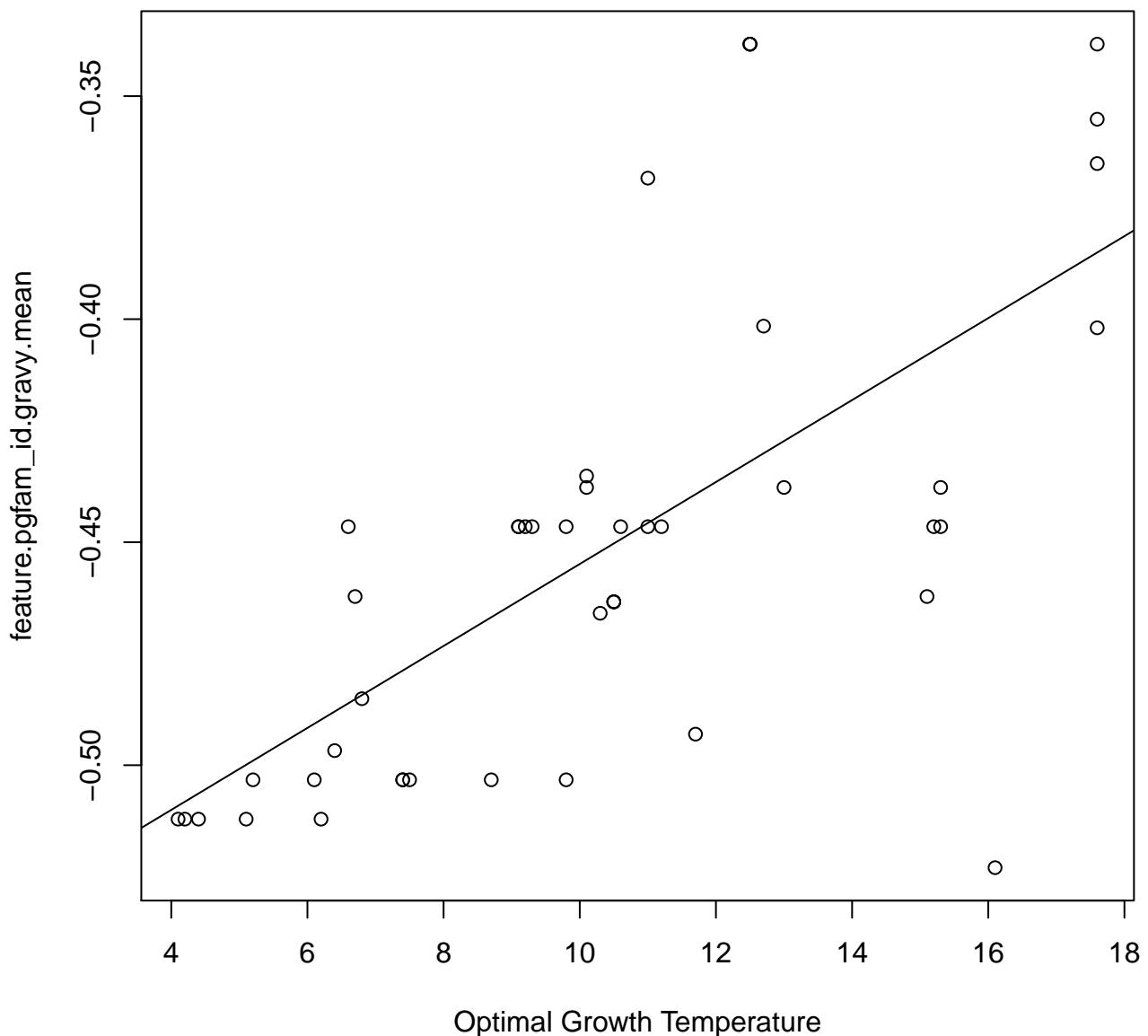
feature.pgfam_id.gravy.mean
PGF_06404031
Proline dipeptidase



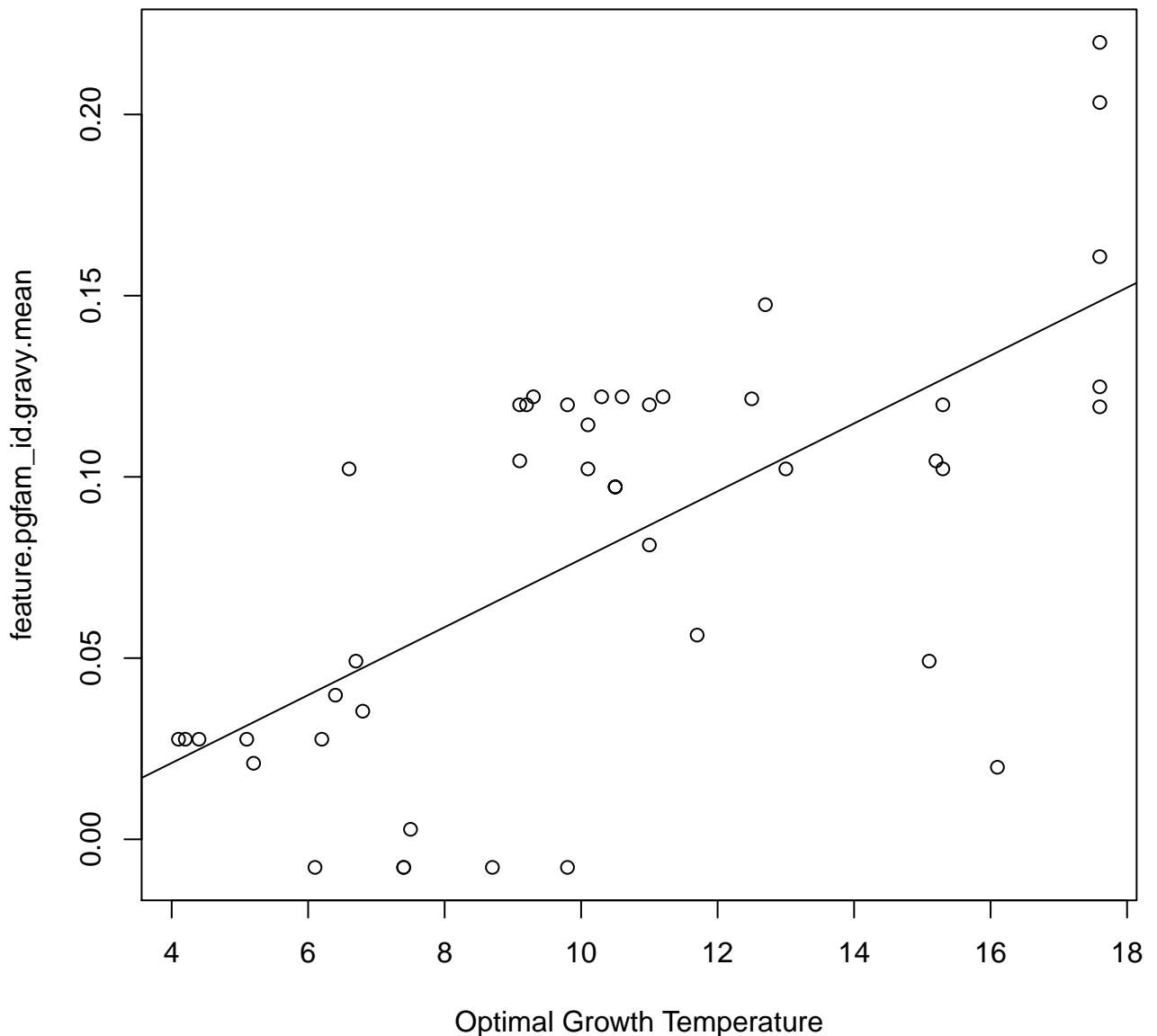
feature.pgfam_id.gravy.mean
PGF_06458877
Phosphatidylglycerophosphatase A (EC 3.1.3.27)



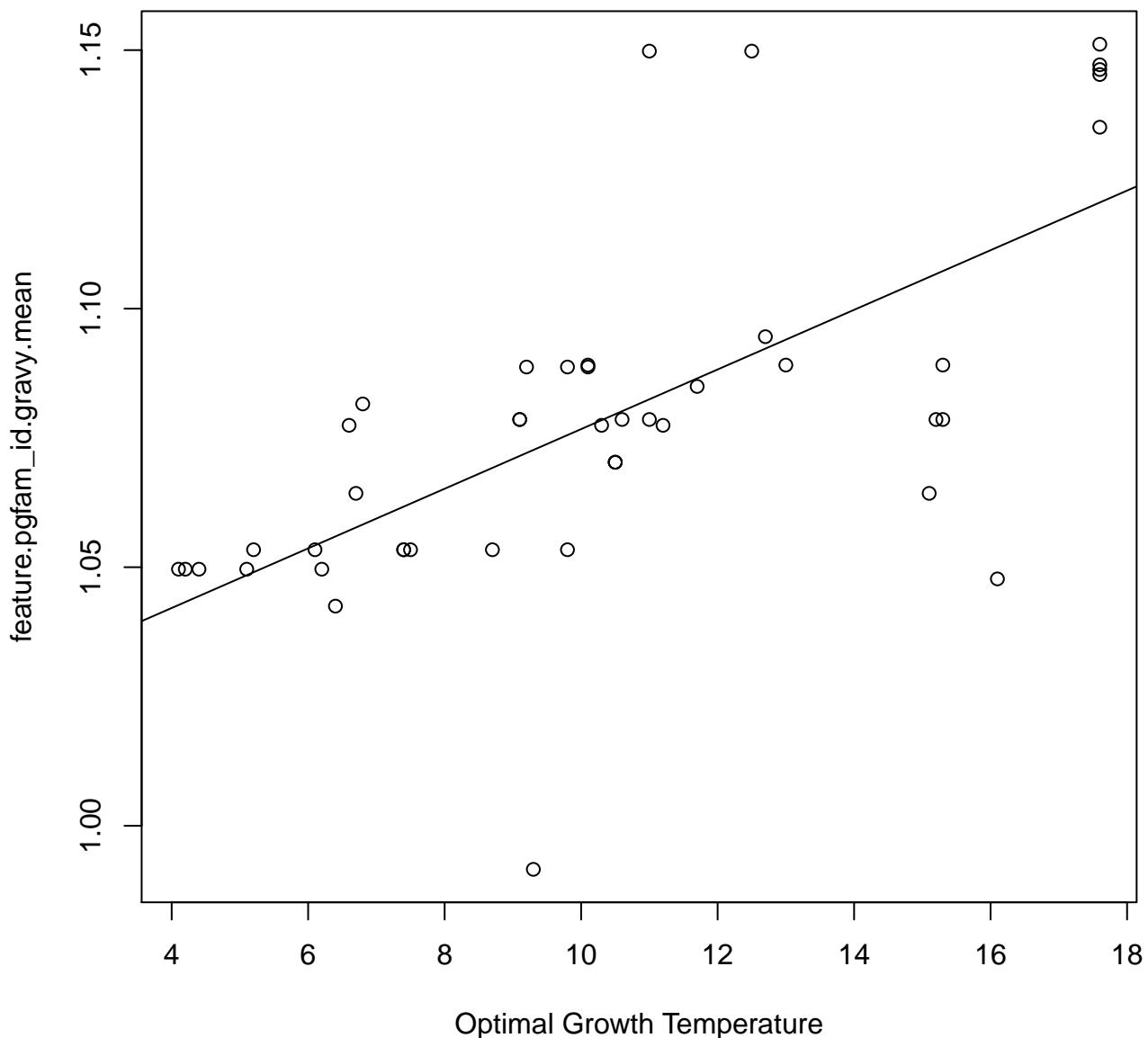
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tRNA (guanine(37)-N(1))-methyltransferase (EC 2.1.1.228)



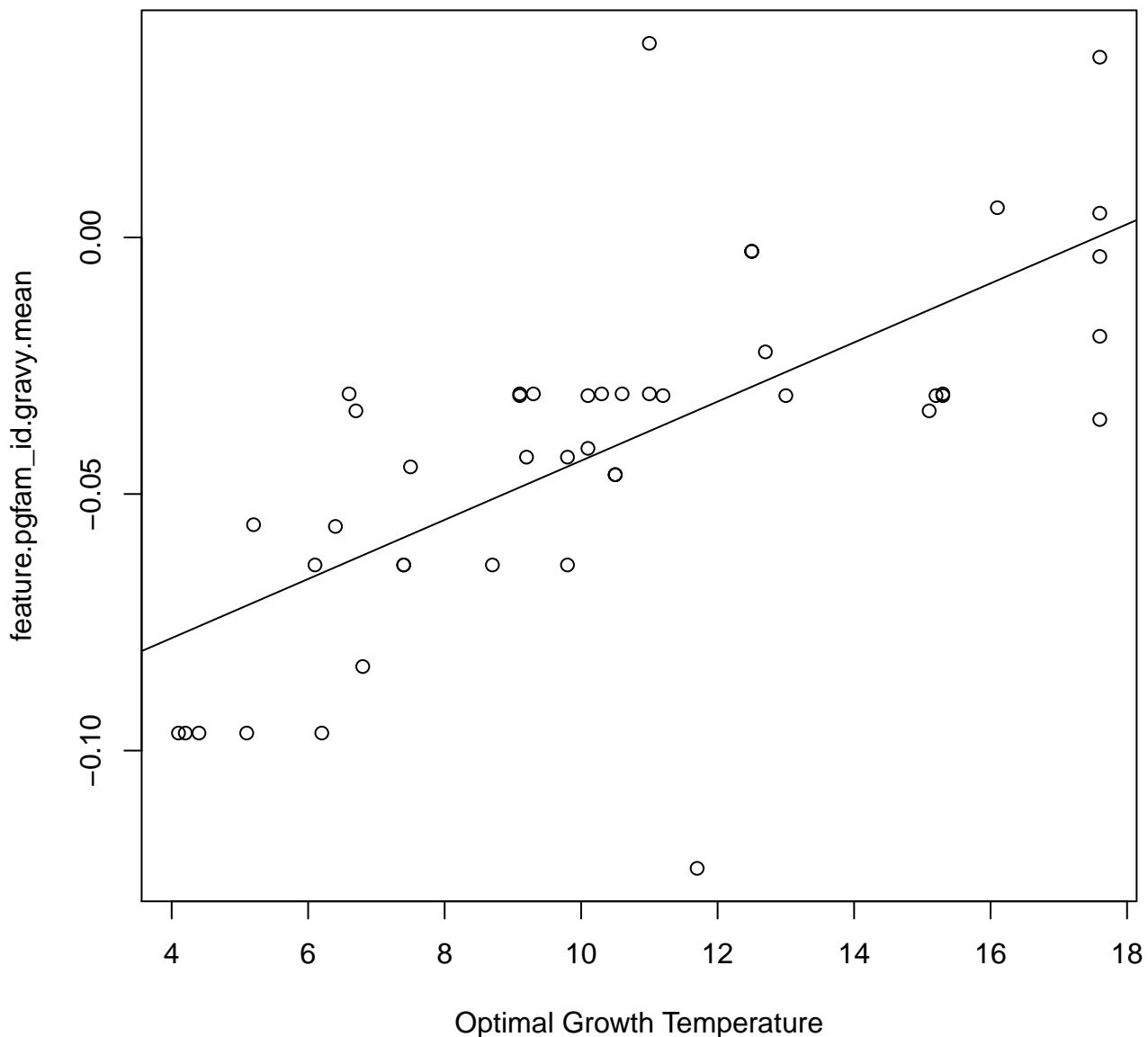
feature.pgfam_id.gravy.mean
PGF_06894101
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)



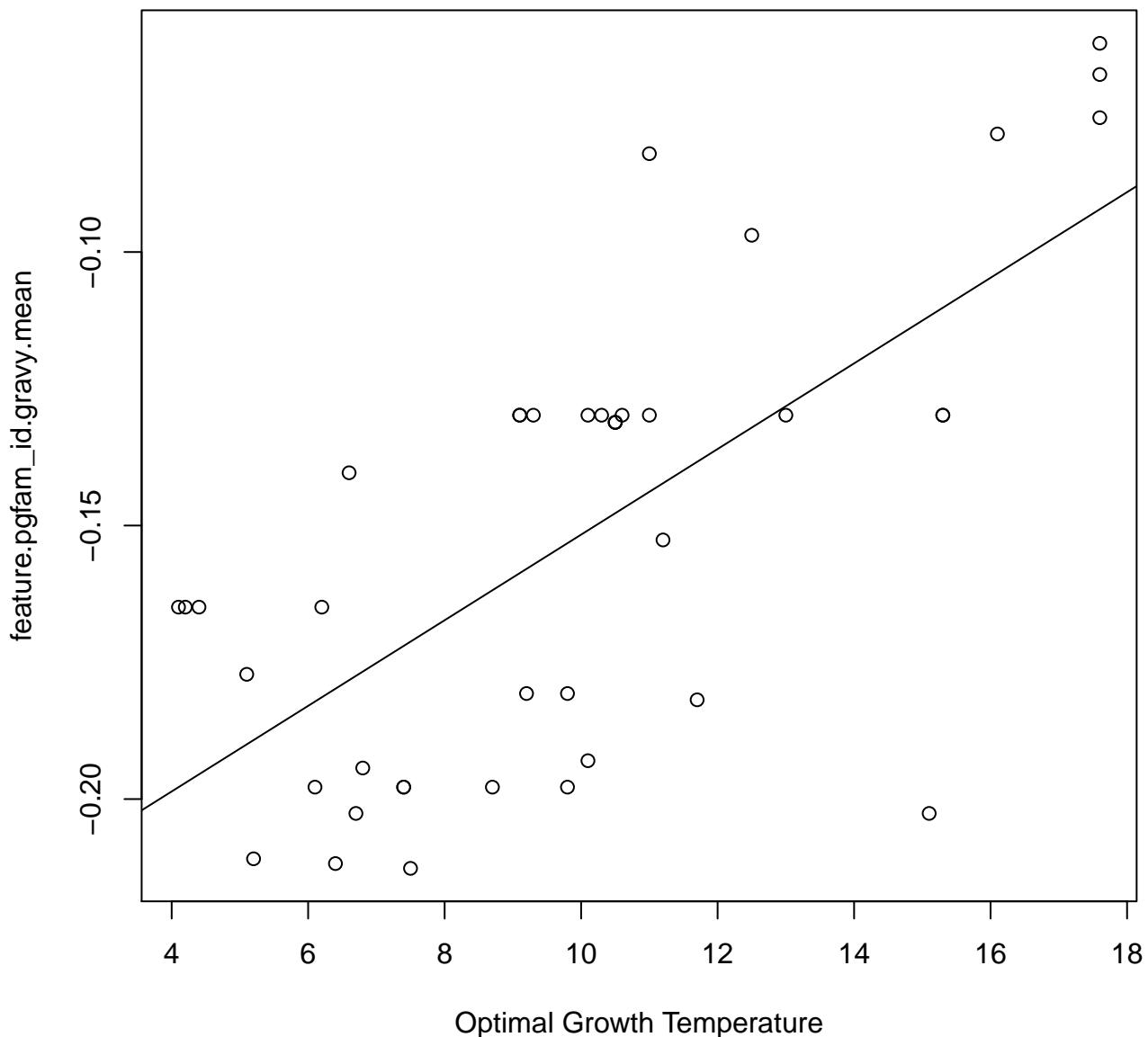
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PGF_03198057
Inner membrane protein YpjD



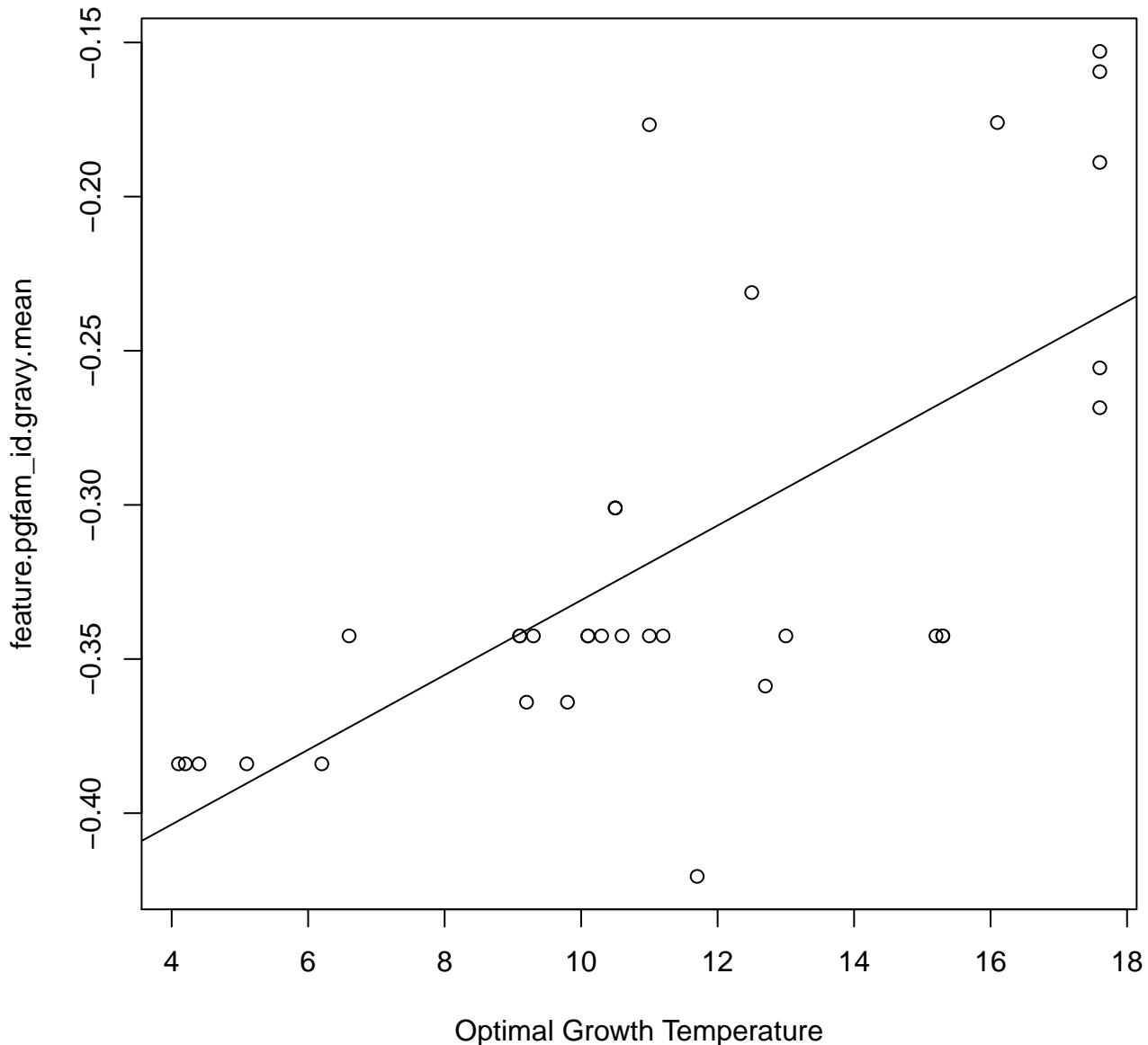
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PGF_03051420
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



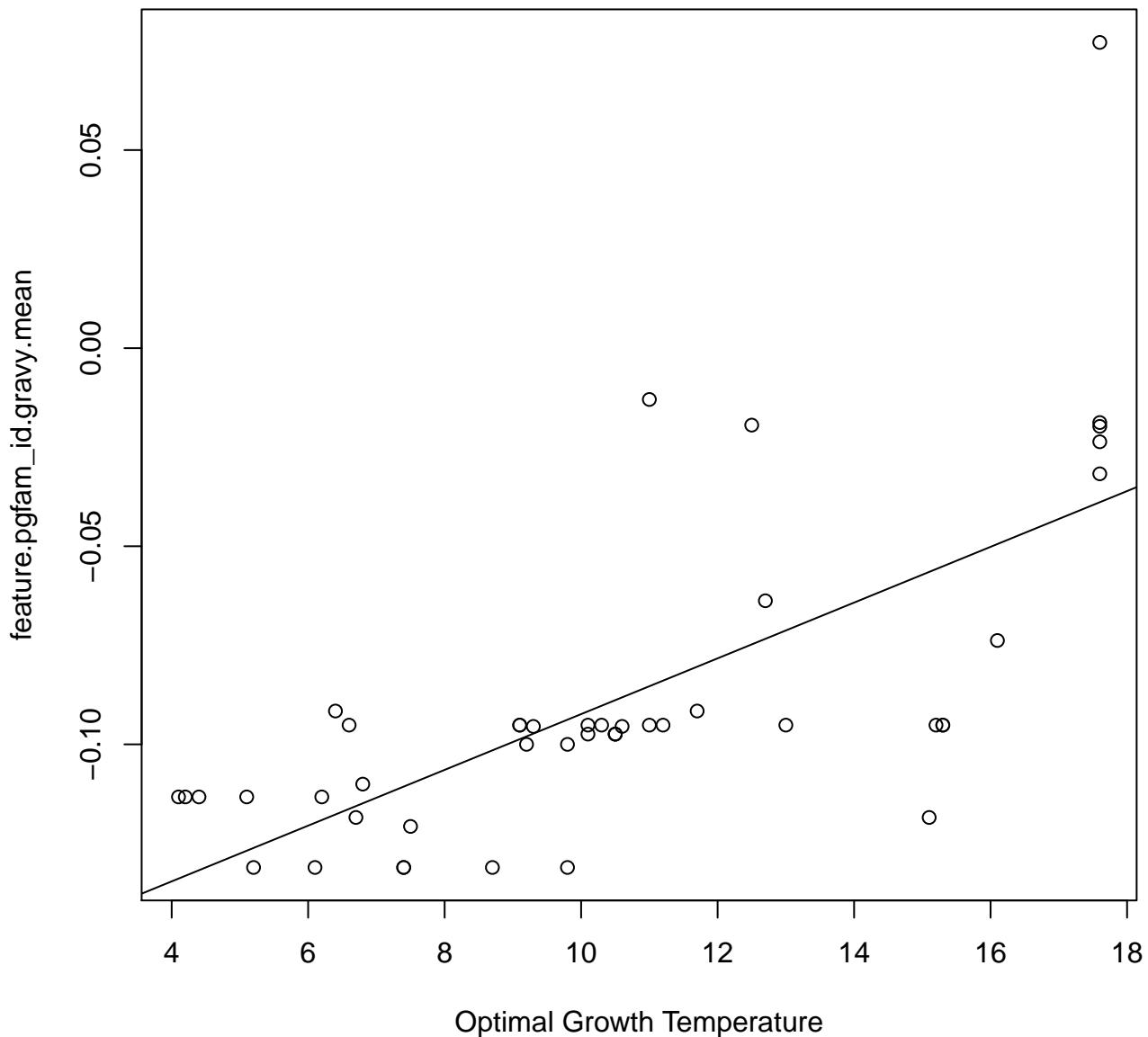
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PGF_03832998
FIG111991: hypothetical protein



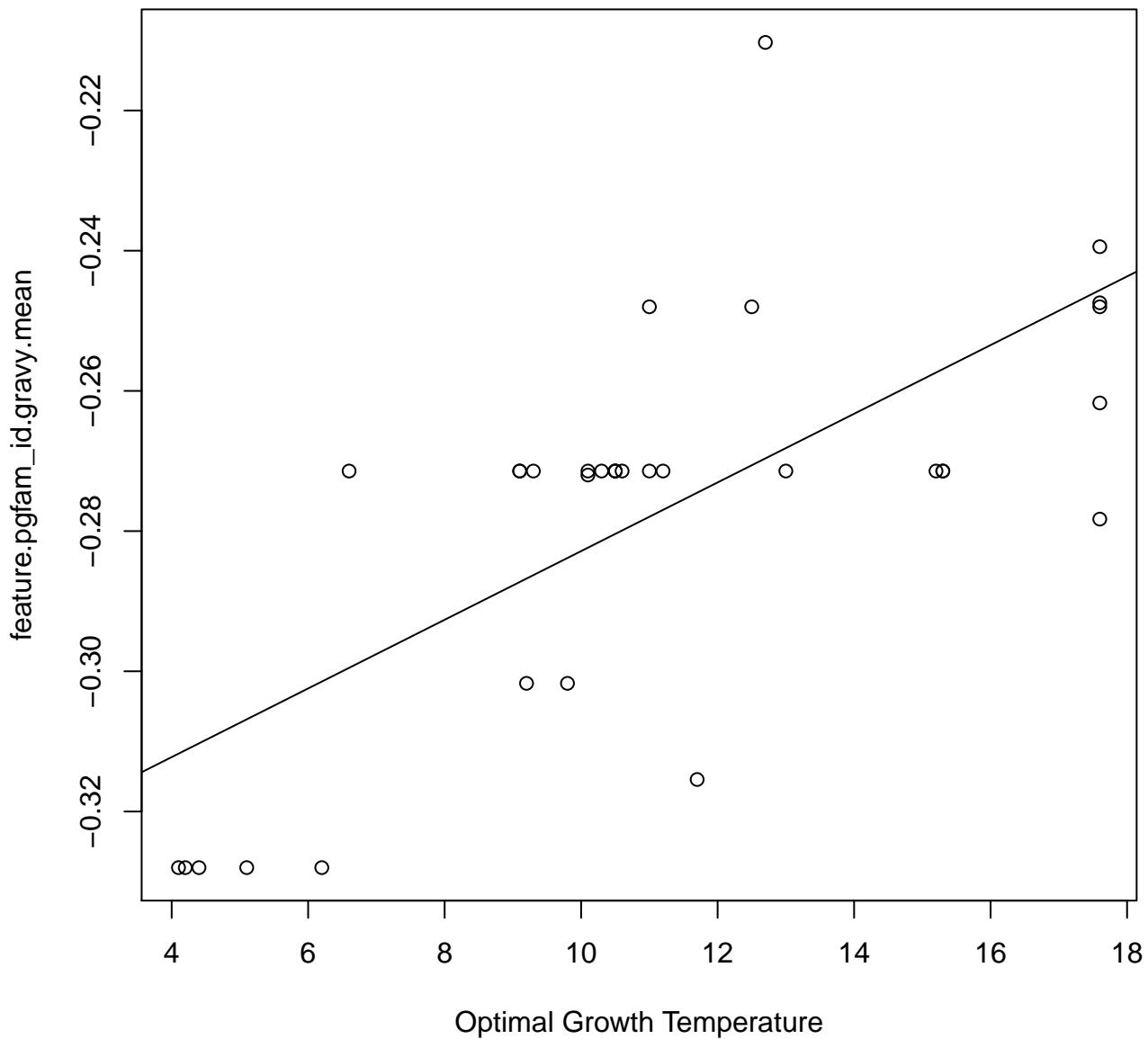
feature.pgfam_id.gravy.mean
PGF_12908301
RNA polymerase ECF-type sigma factor



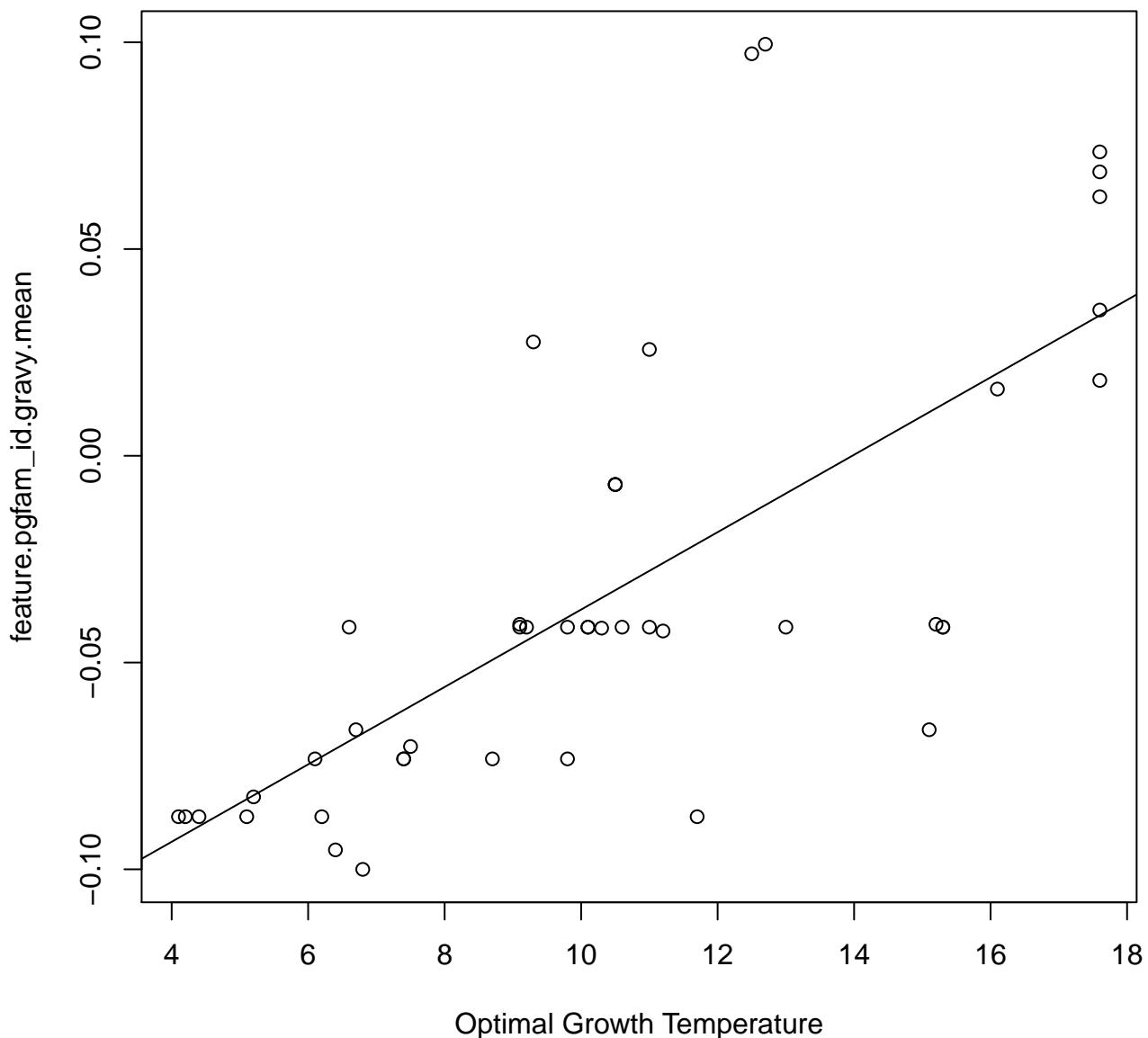
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PGF_00423732
4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.7.4)



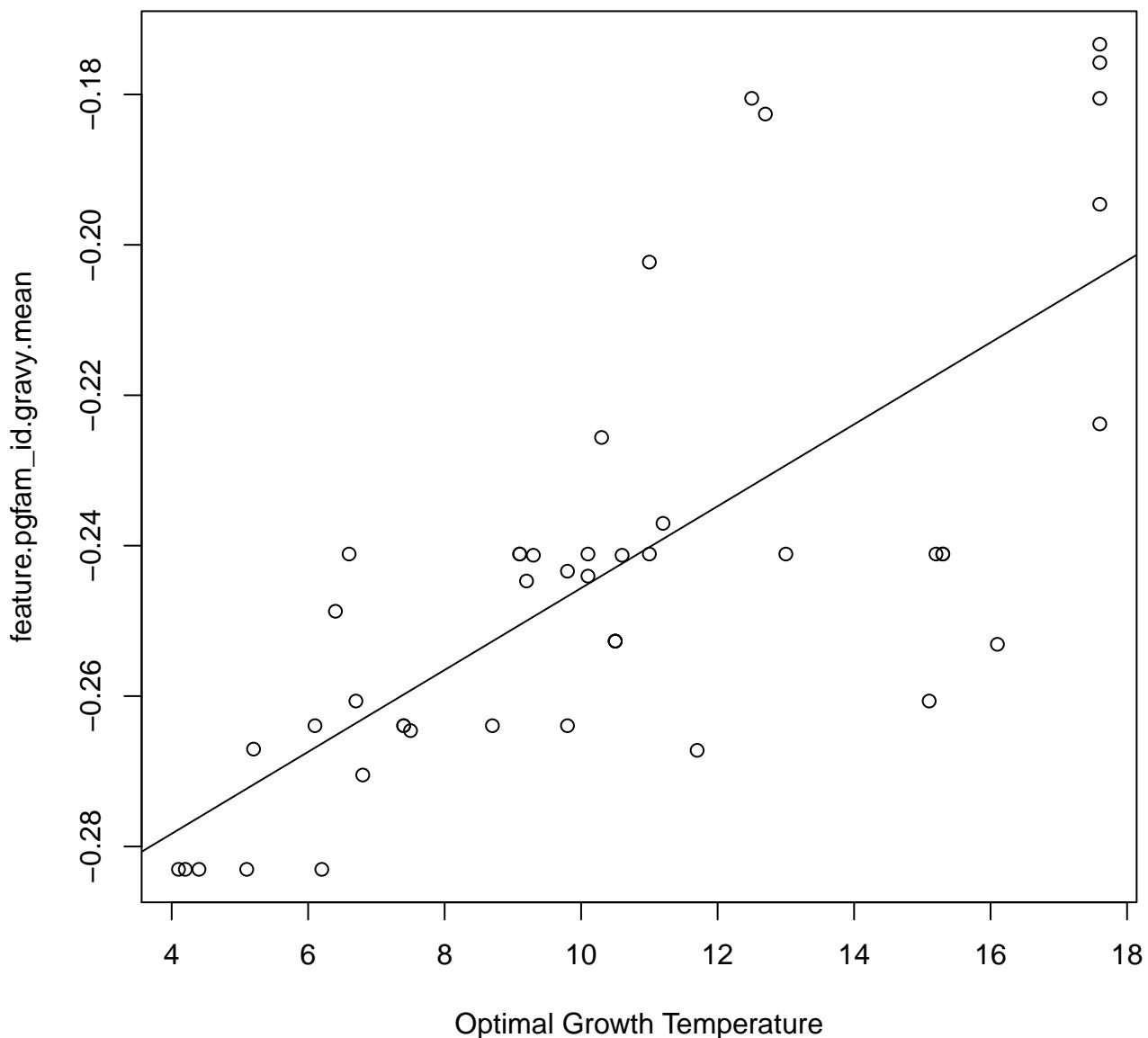
feature.pgfam_id.gravy.mean
PGF_06077968
Bacterial non-heme ferritin (EC 1.16.3.2)



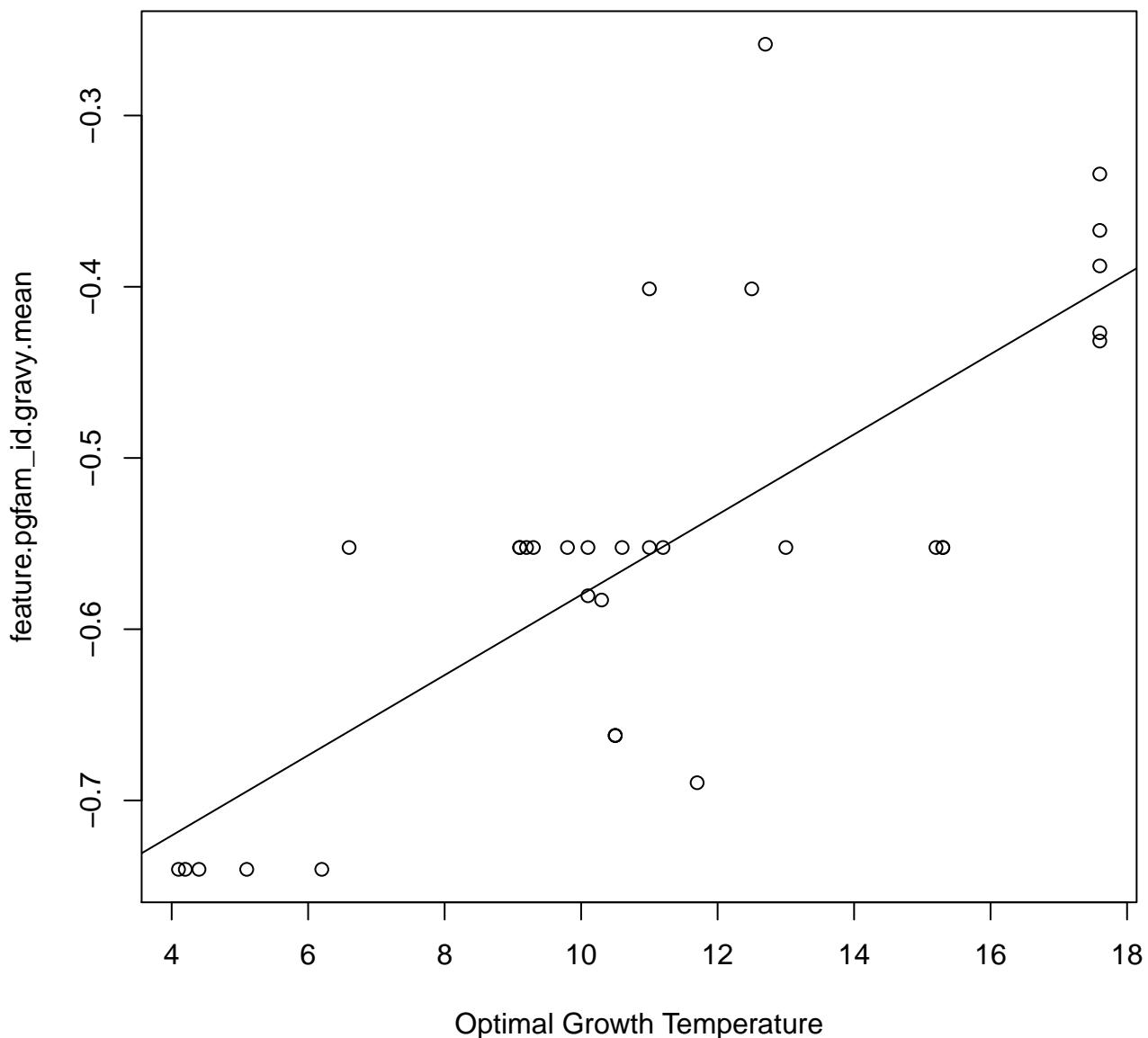
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Histidinol dehydrogenase (EC 1.1.1.23)



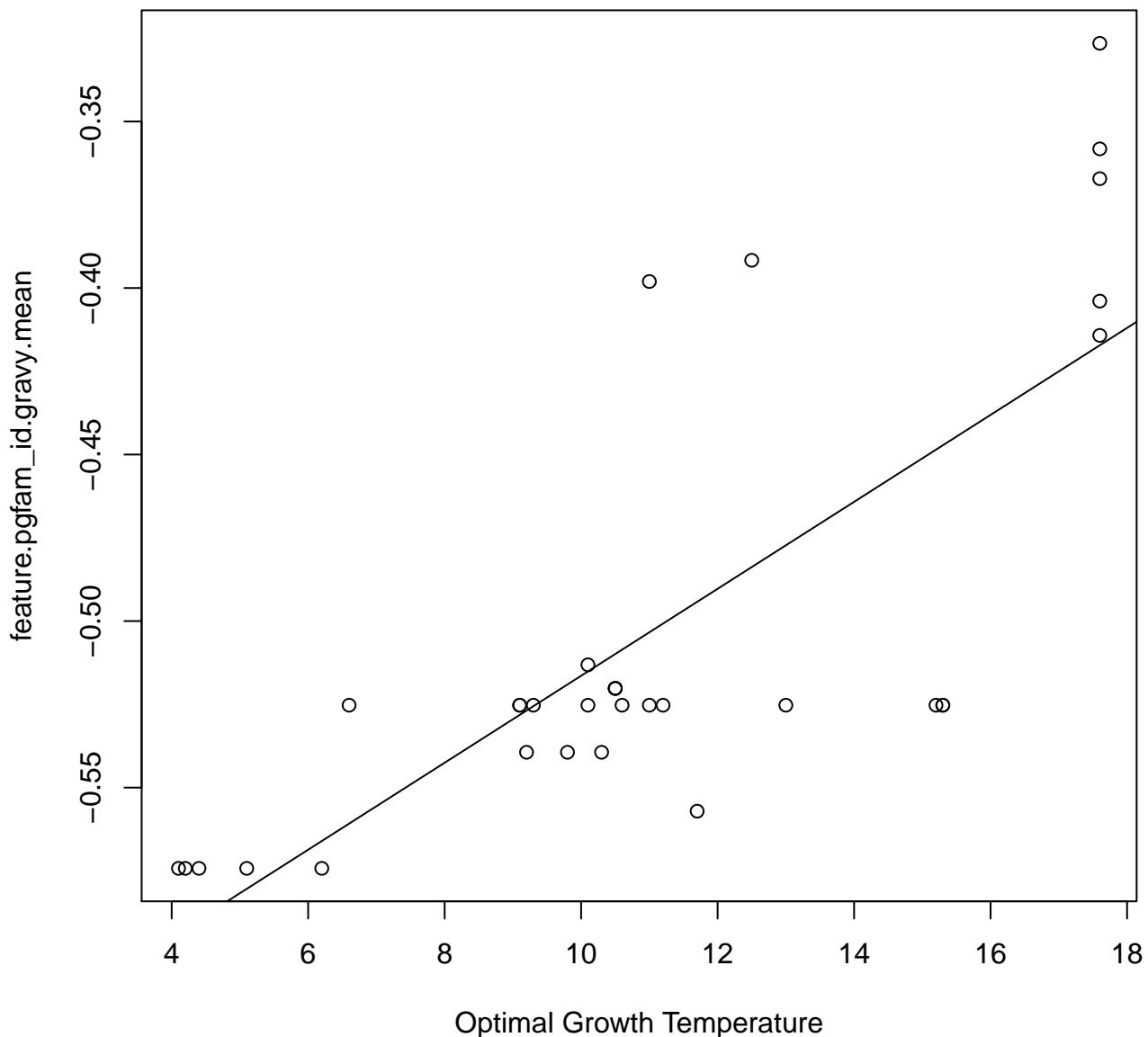
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PGF_12698553
Protein kinase



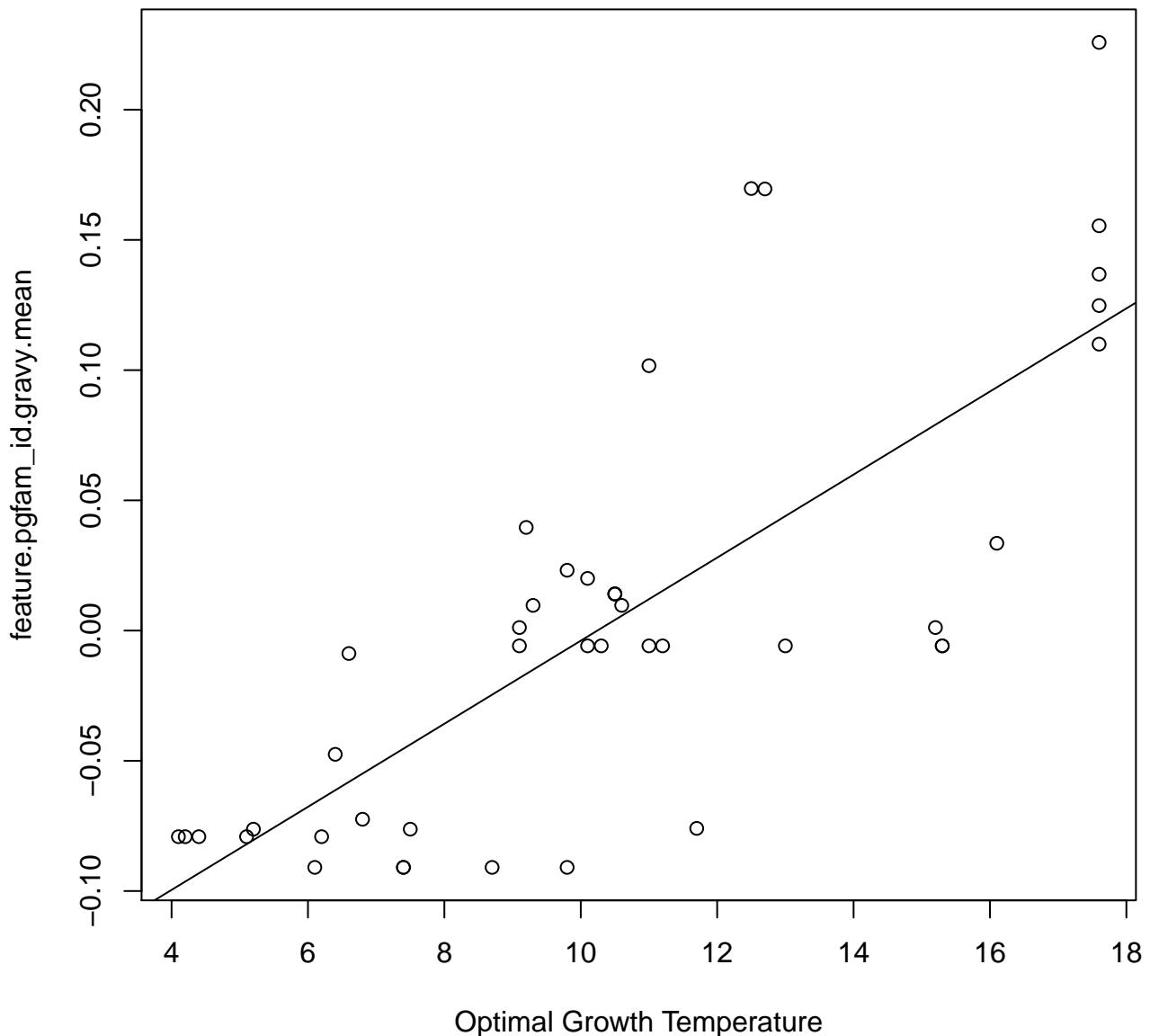
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Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)



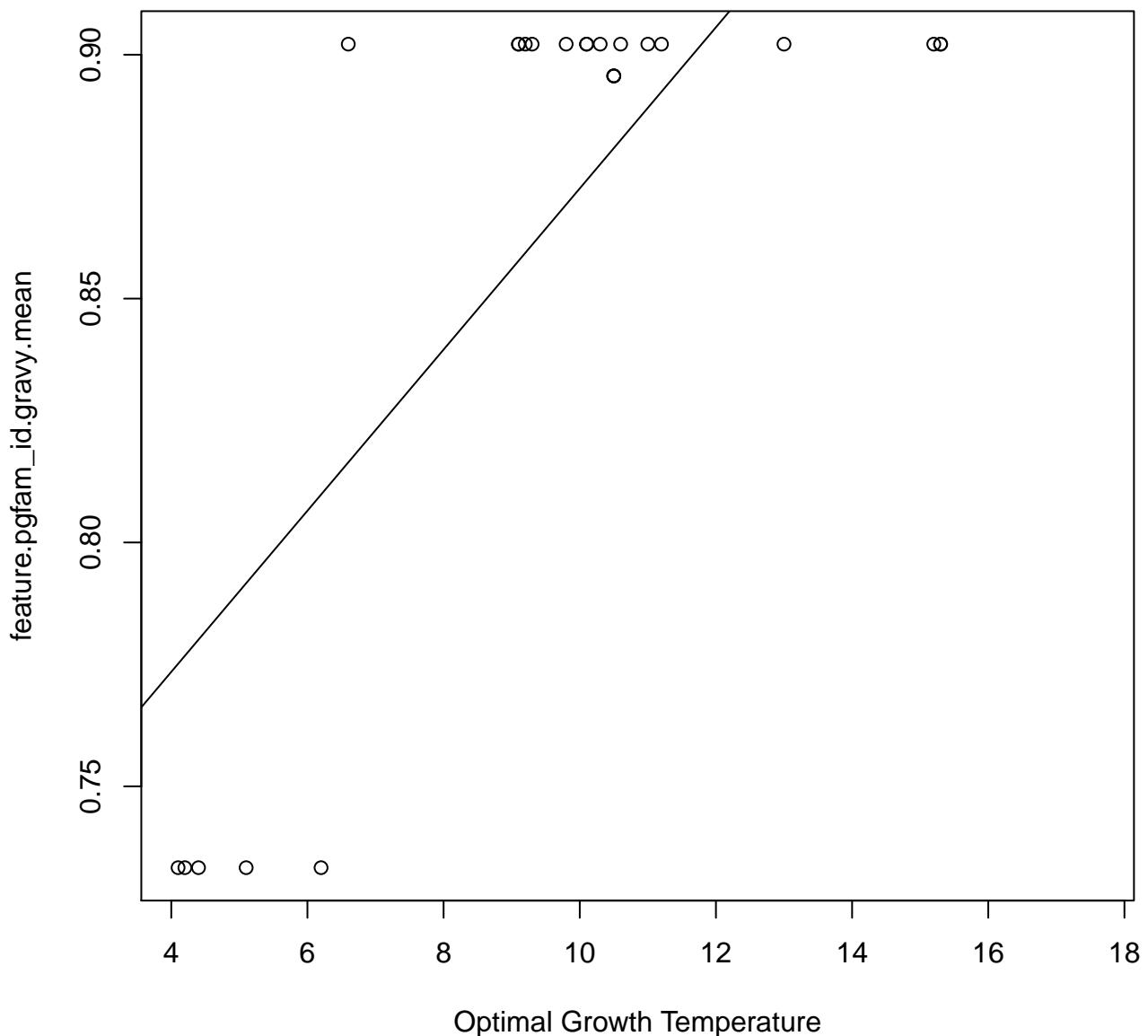
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GTP cyclohydrolase II (EC 3.5.4.25)



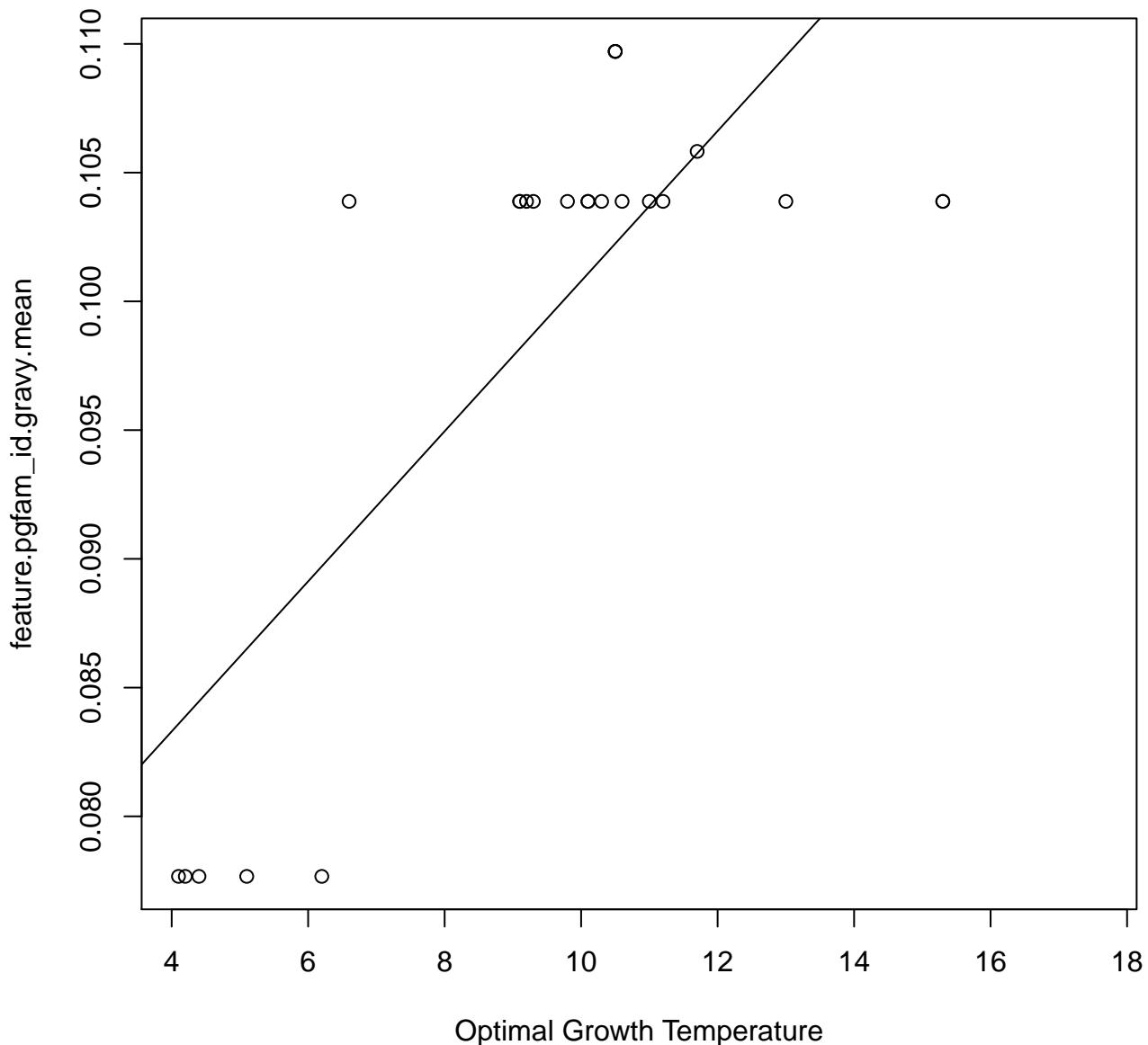
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PGF_02007855
Zinc-type alcohol dehydrogenase-like protein



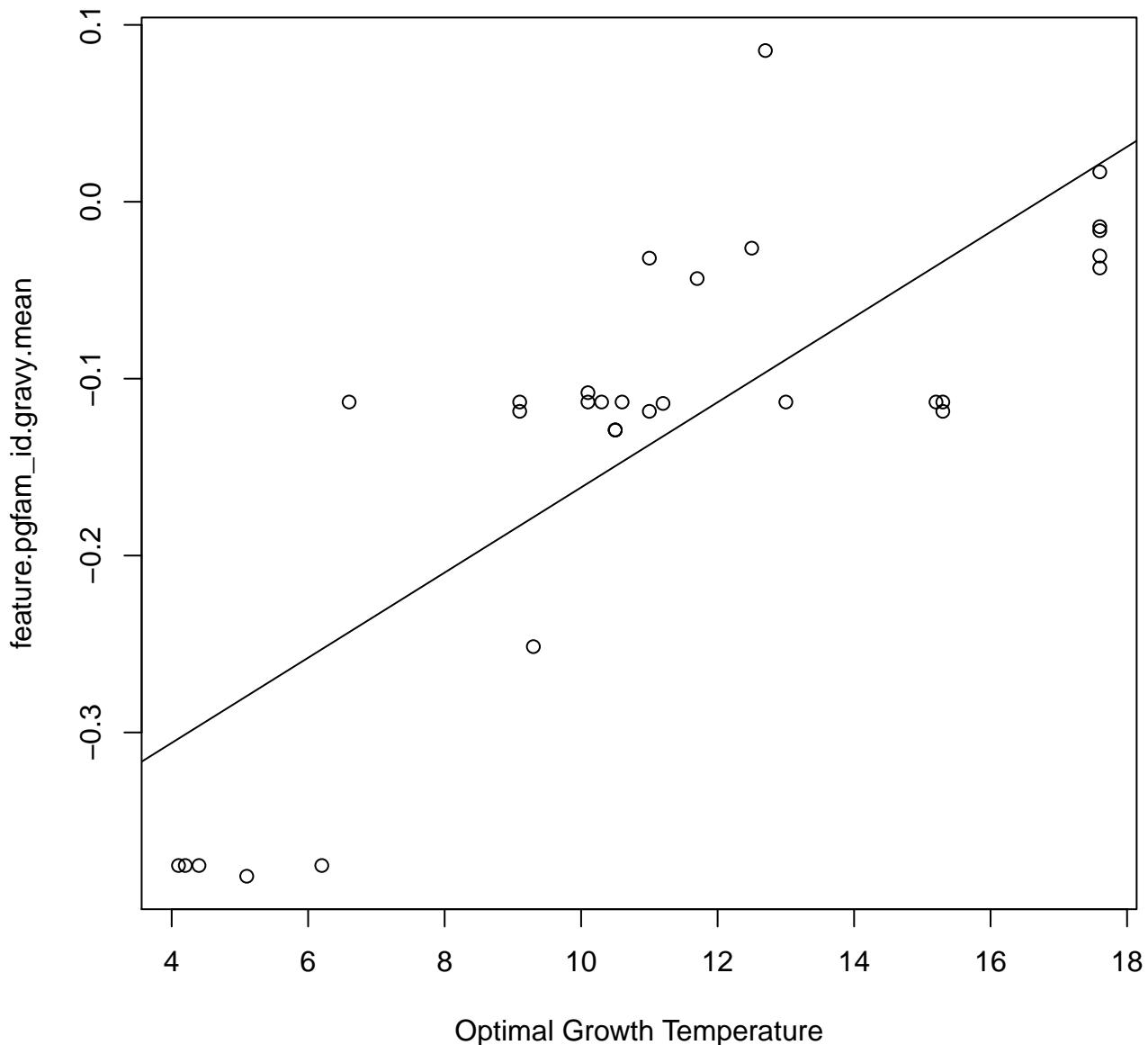
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PGF_12071964
hypothetical protein



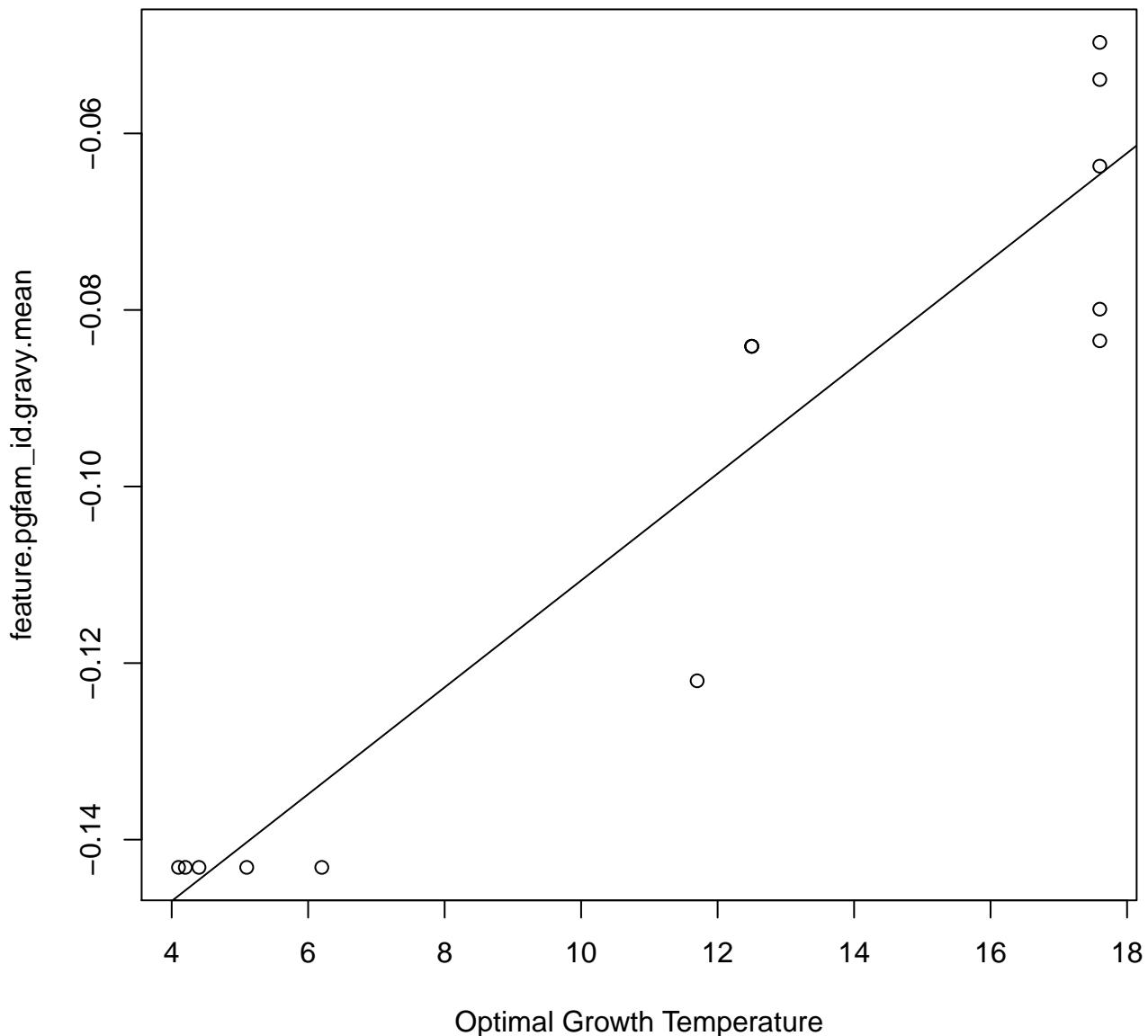
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PGF_07210740
hypothetical protein



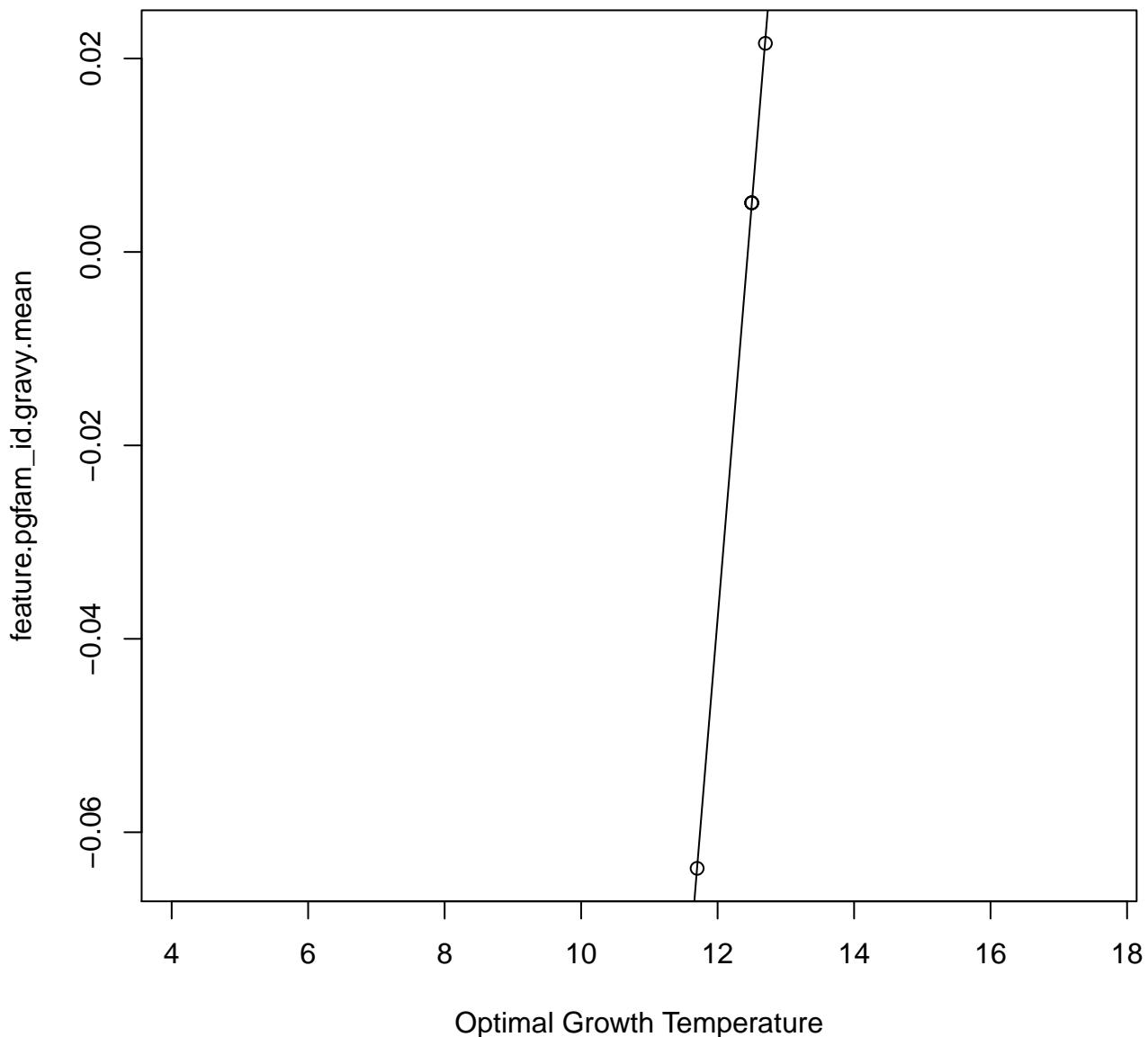
feature.pgfam_id.gravy.mean
PGF_12765299
Two-component system sensor histidine kinase



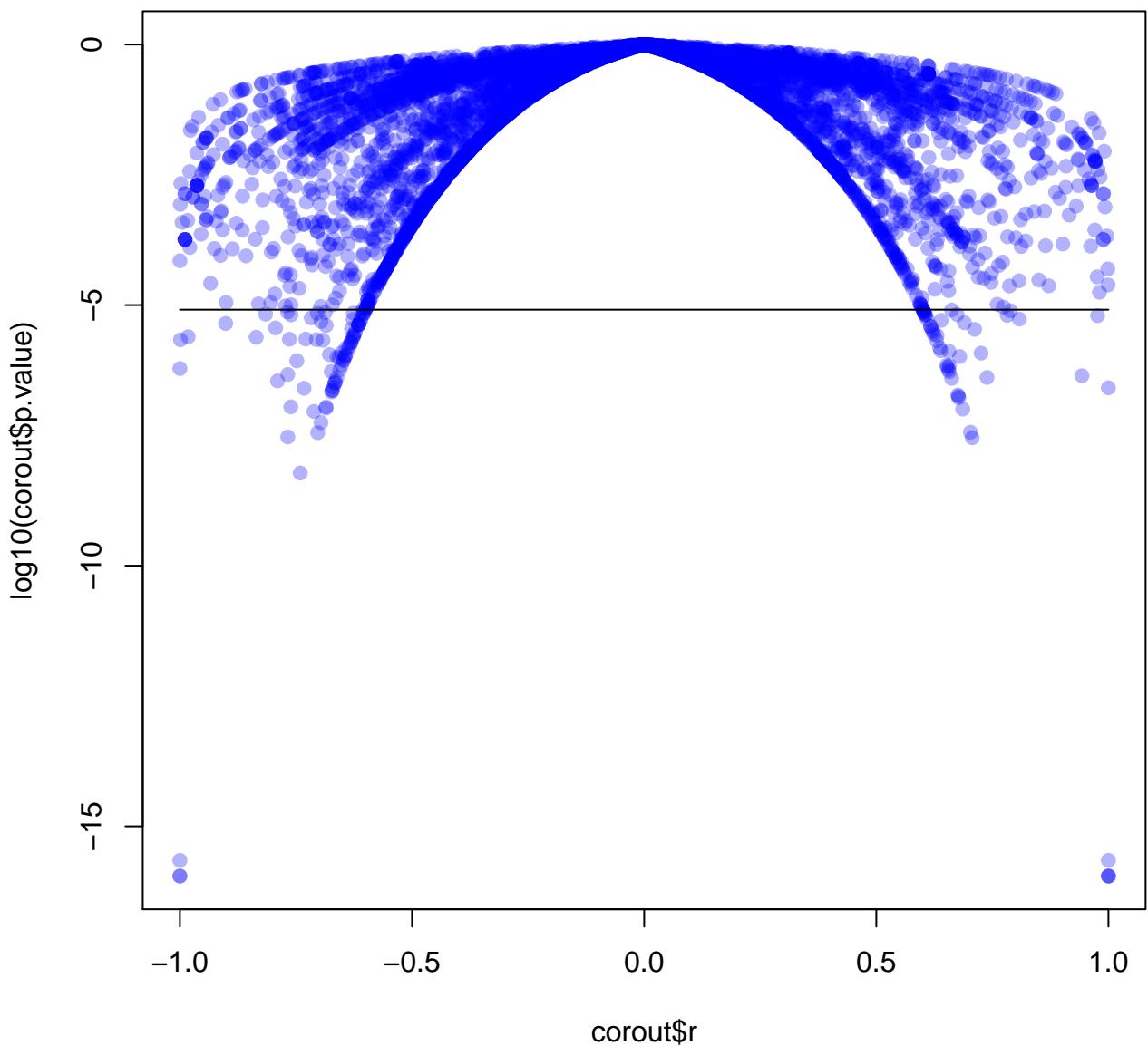
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PGF_00036950
Agglutinin-like sequence 9



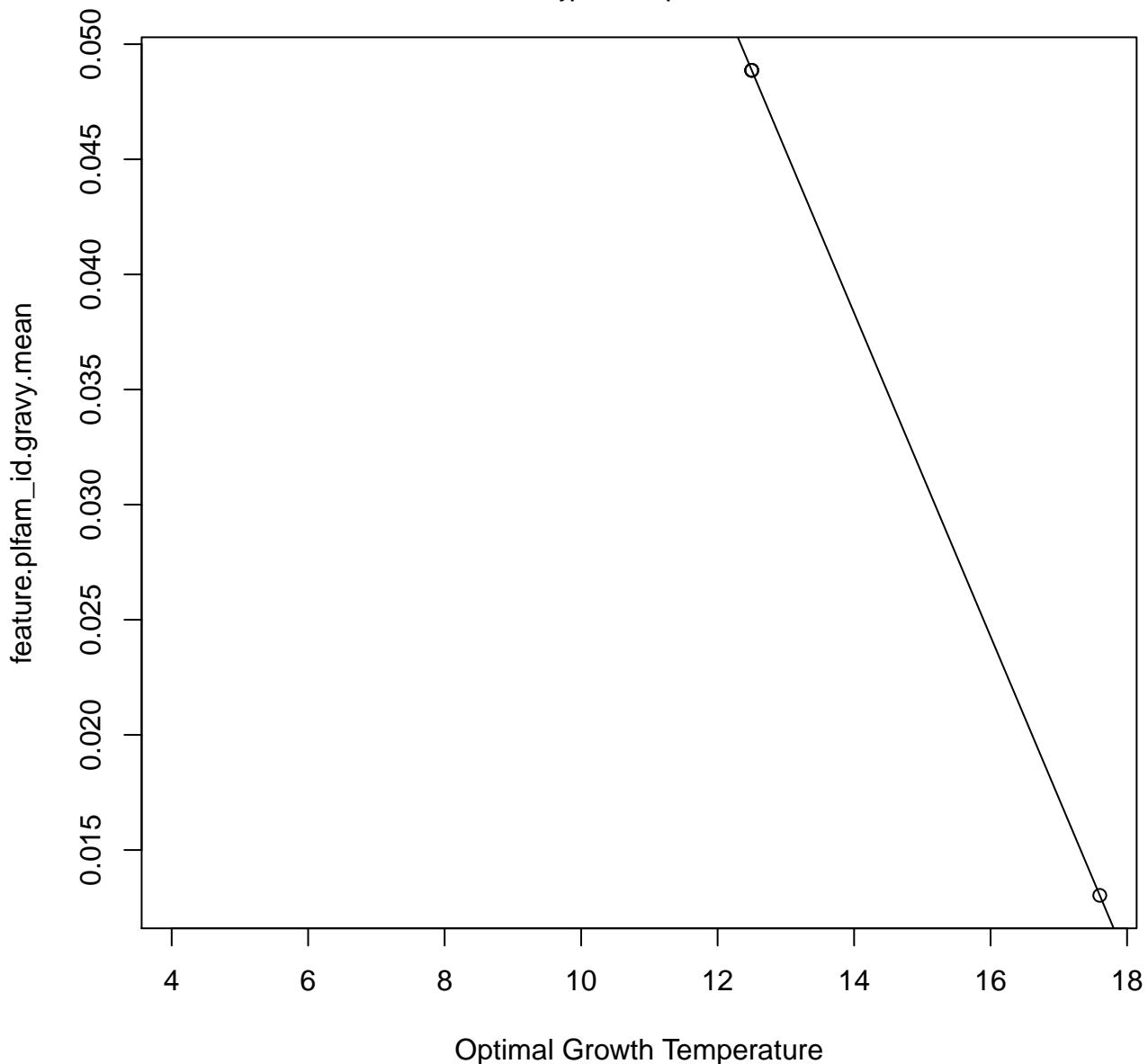
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Probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)



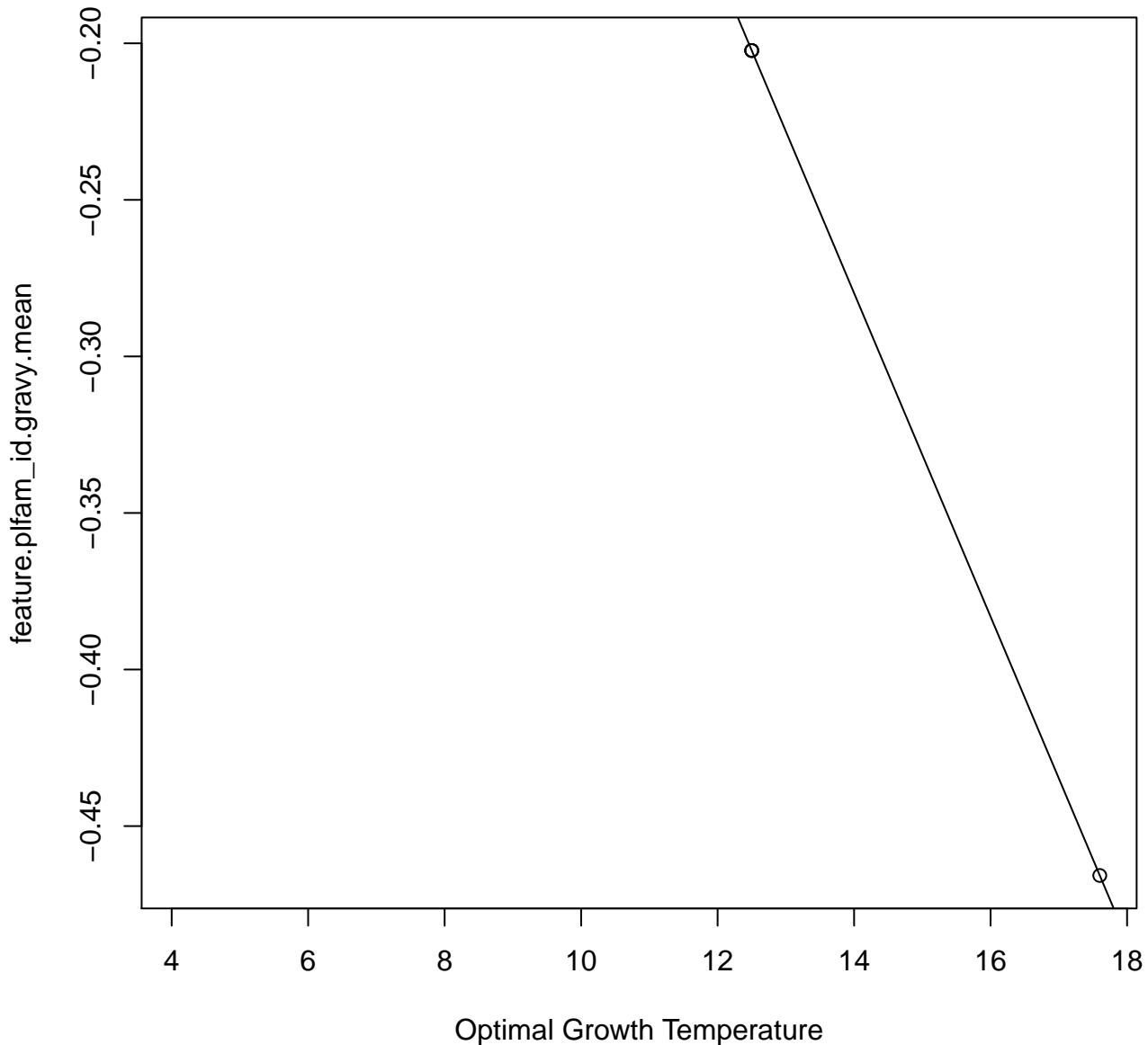
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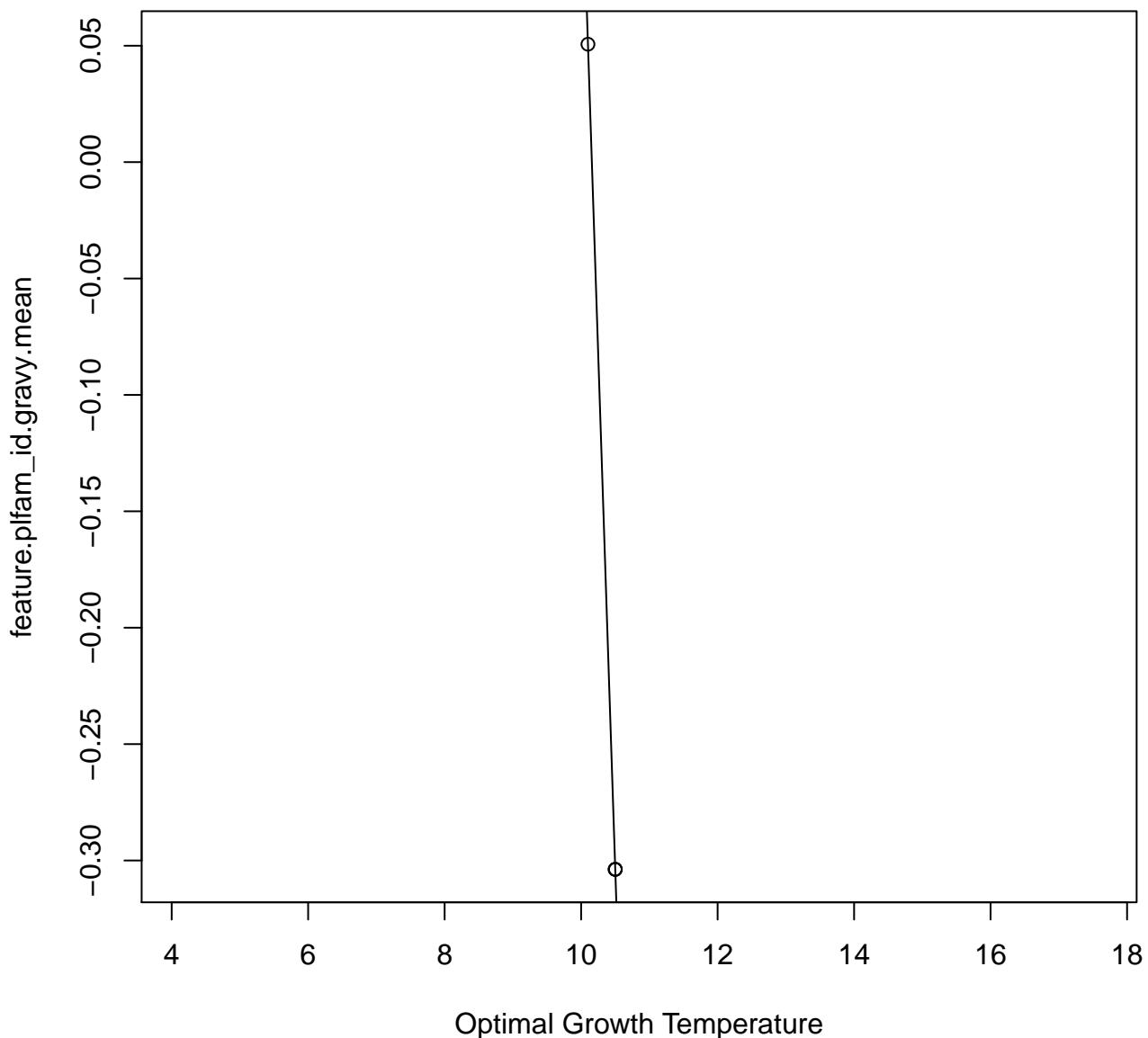
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hypothetical protein



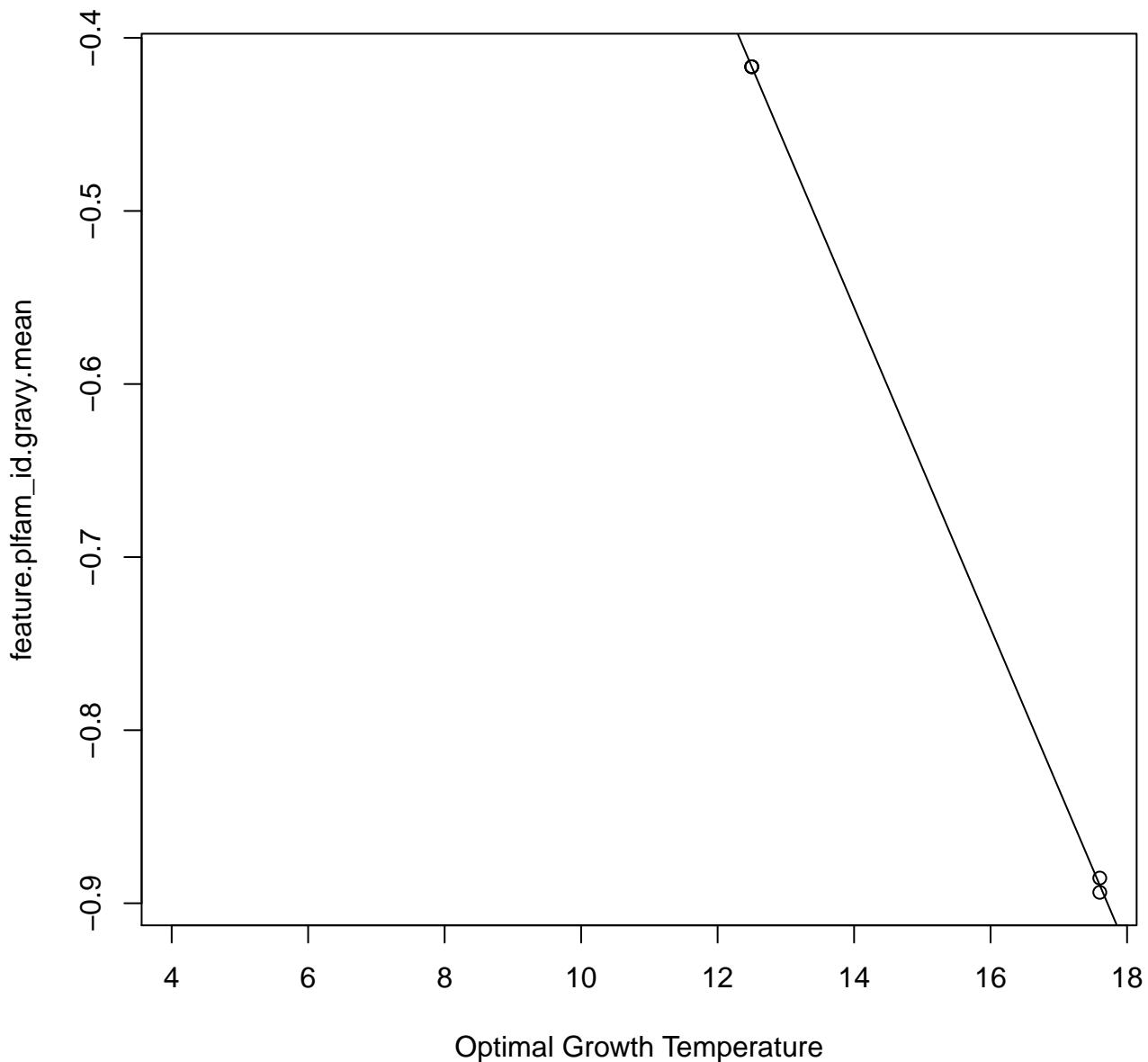
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hypothetical protein



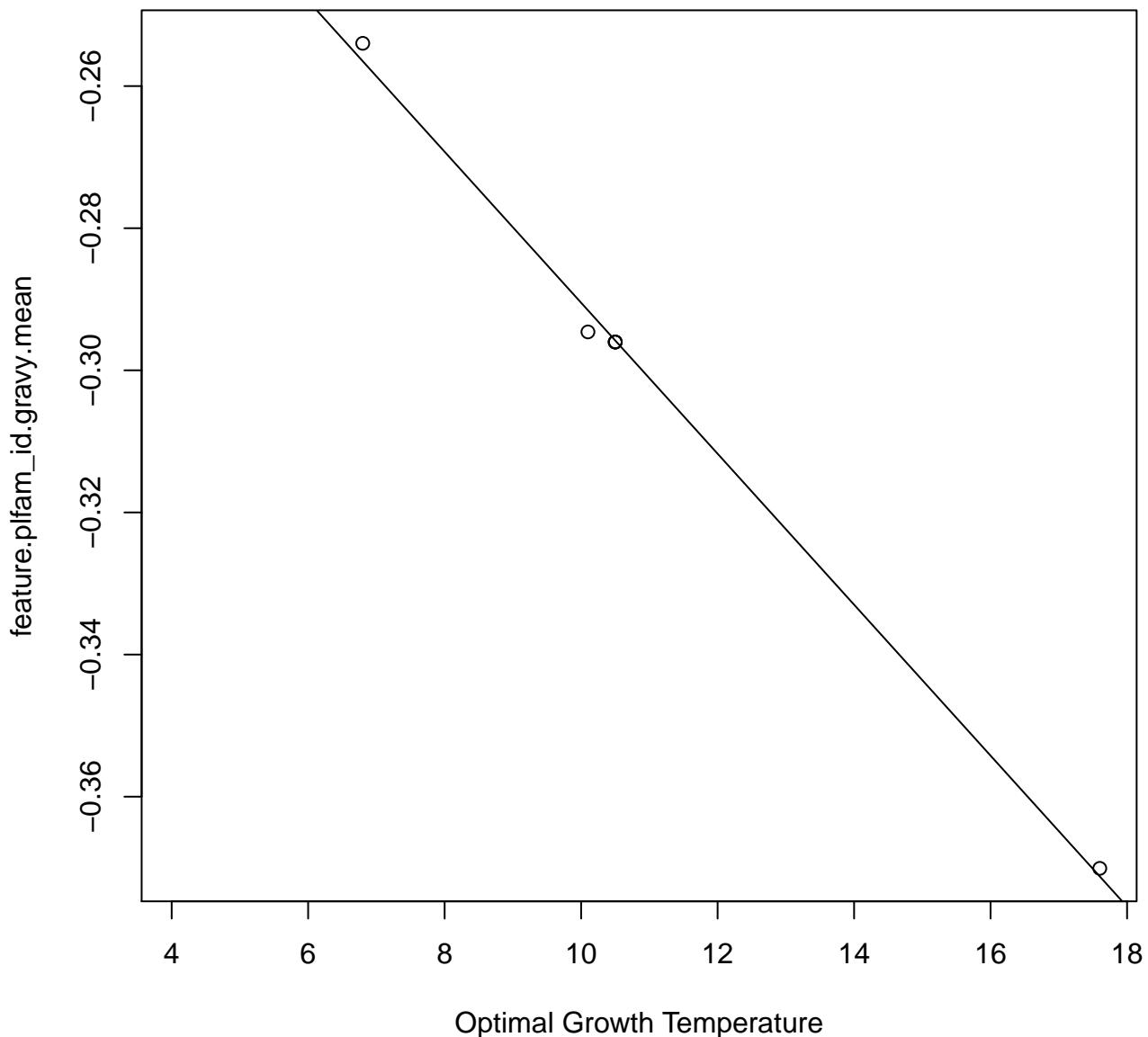
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PLF_28228_00015840
hypothetical protein



feature.pifam_id.gravy.mean
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hypothetical protein

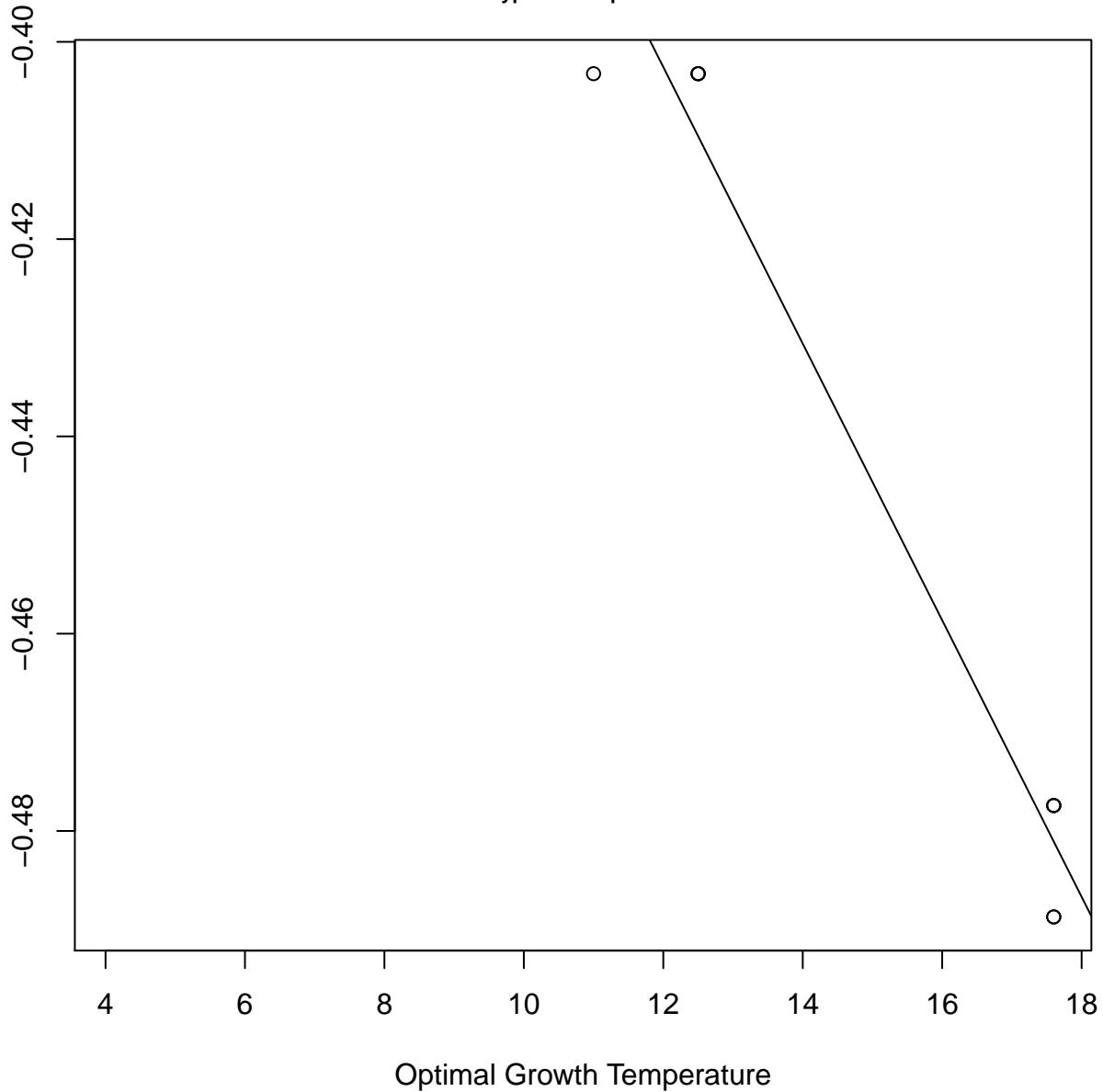


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FIG00640418: hypothetical protein

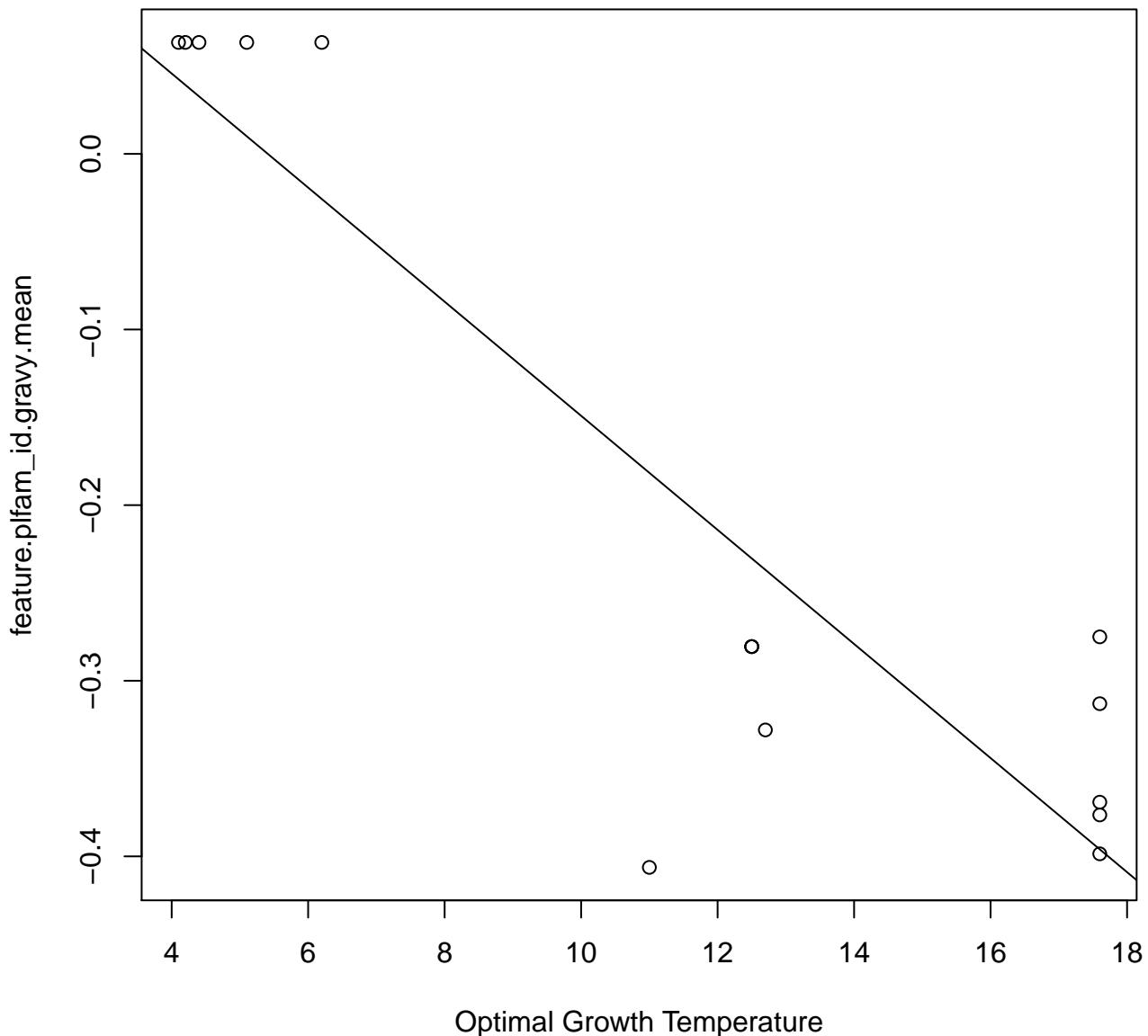


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hypothetical protein

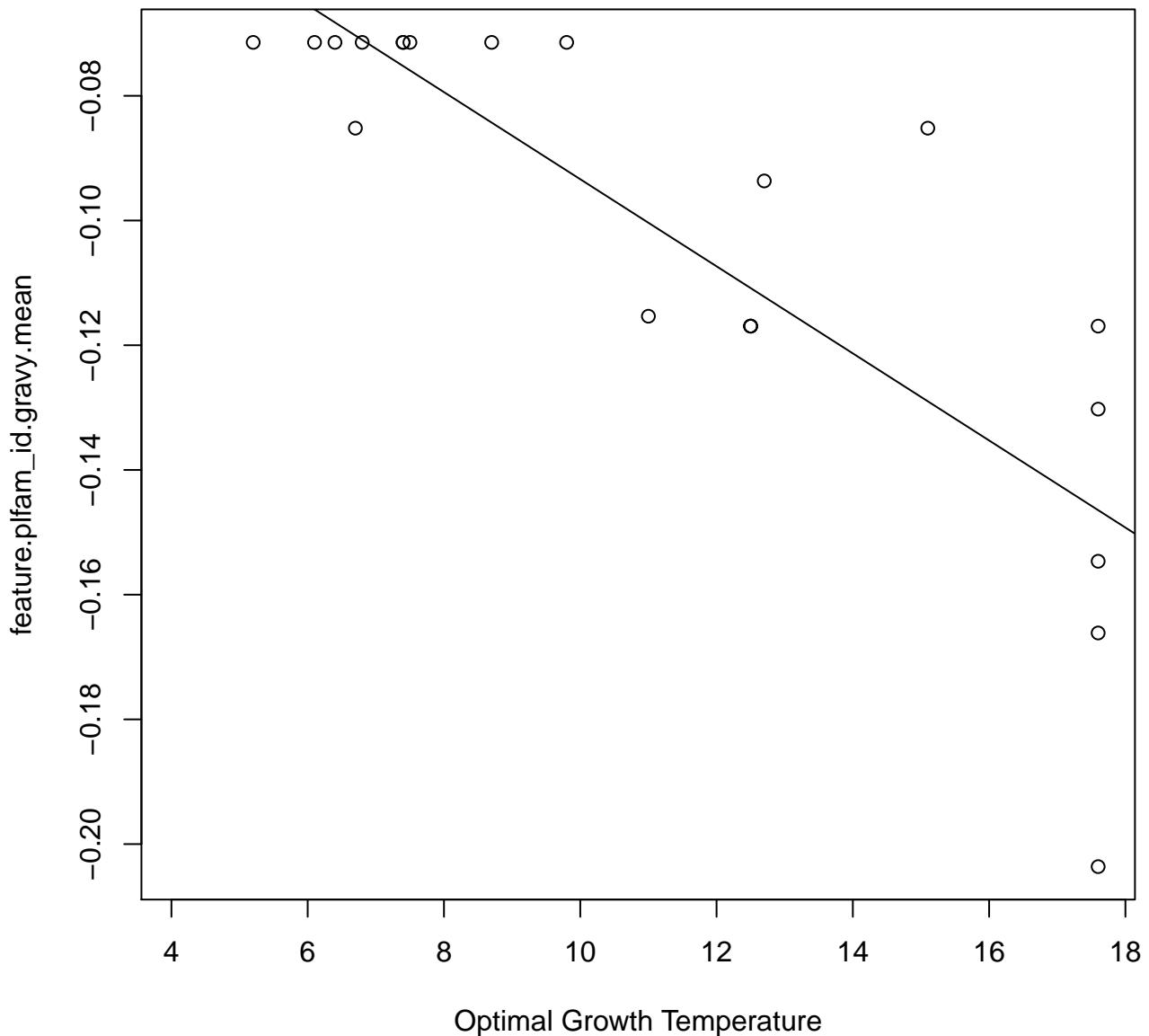
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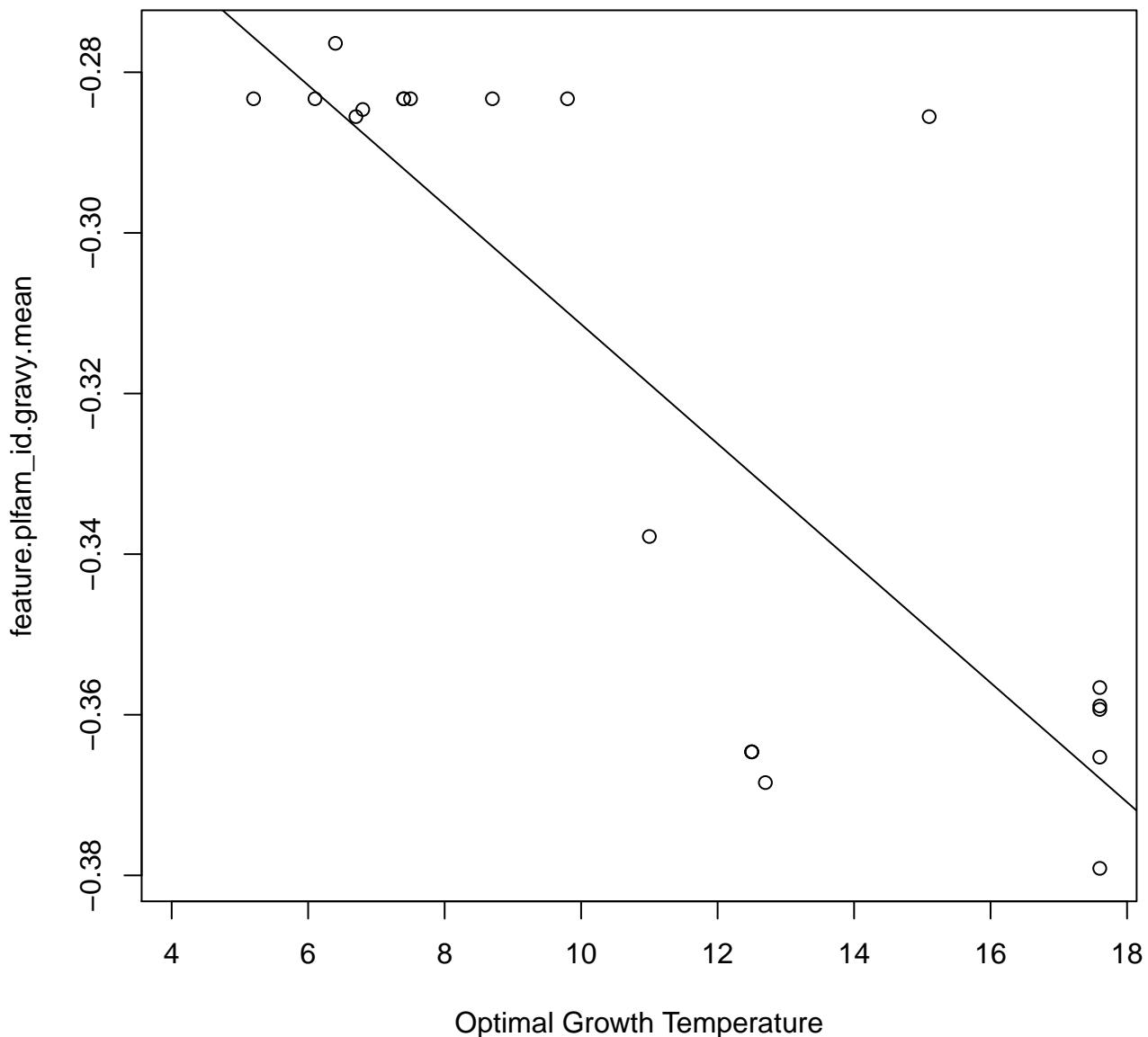
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PLF_28228_00001794
Outer membrane beta-barrel assembly protein BamE



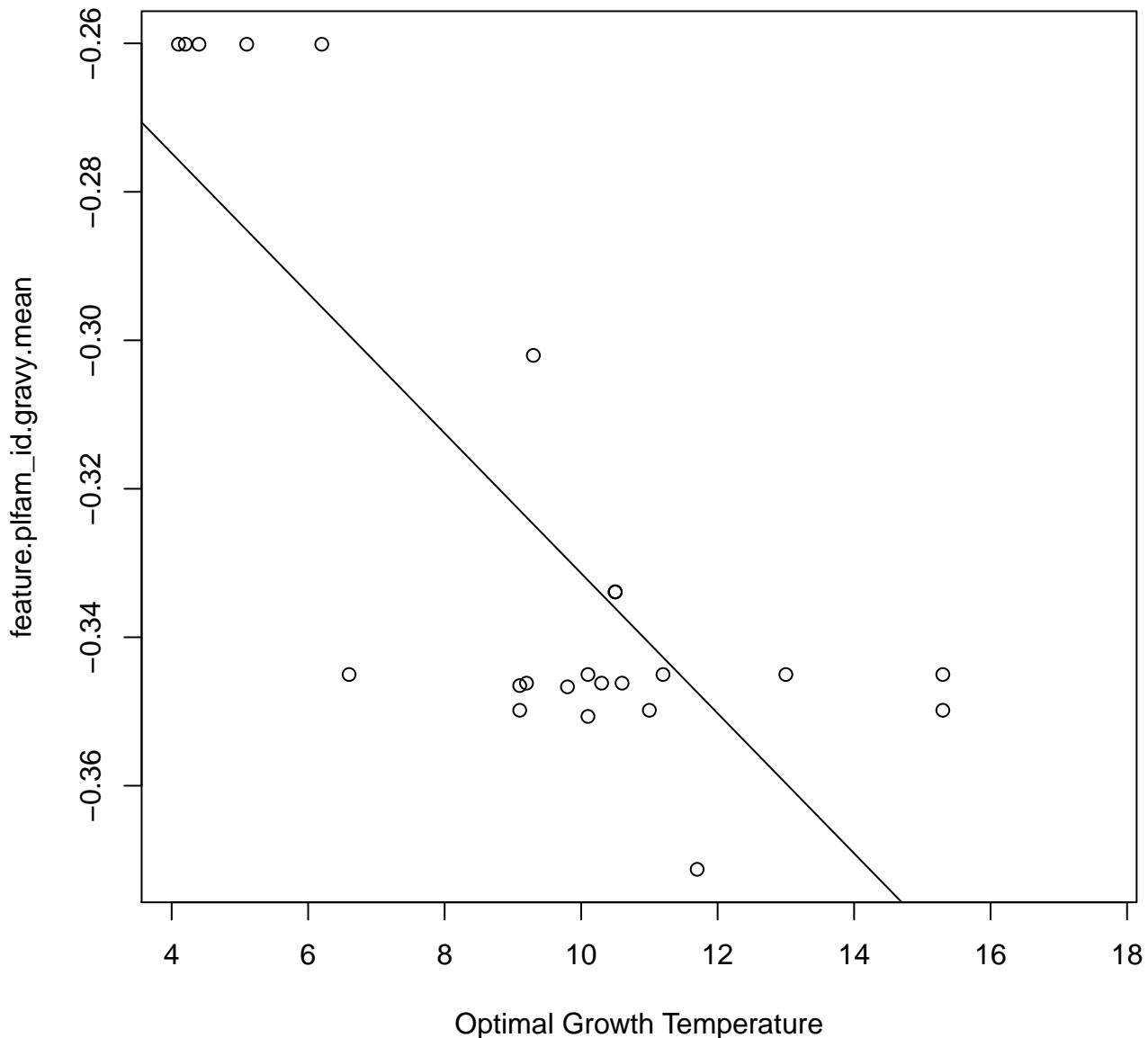
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Alkyl hydroperoxide reductase protein C (EC 1.11.1.15)



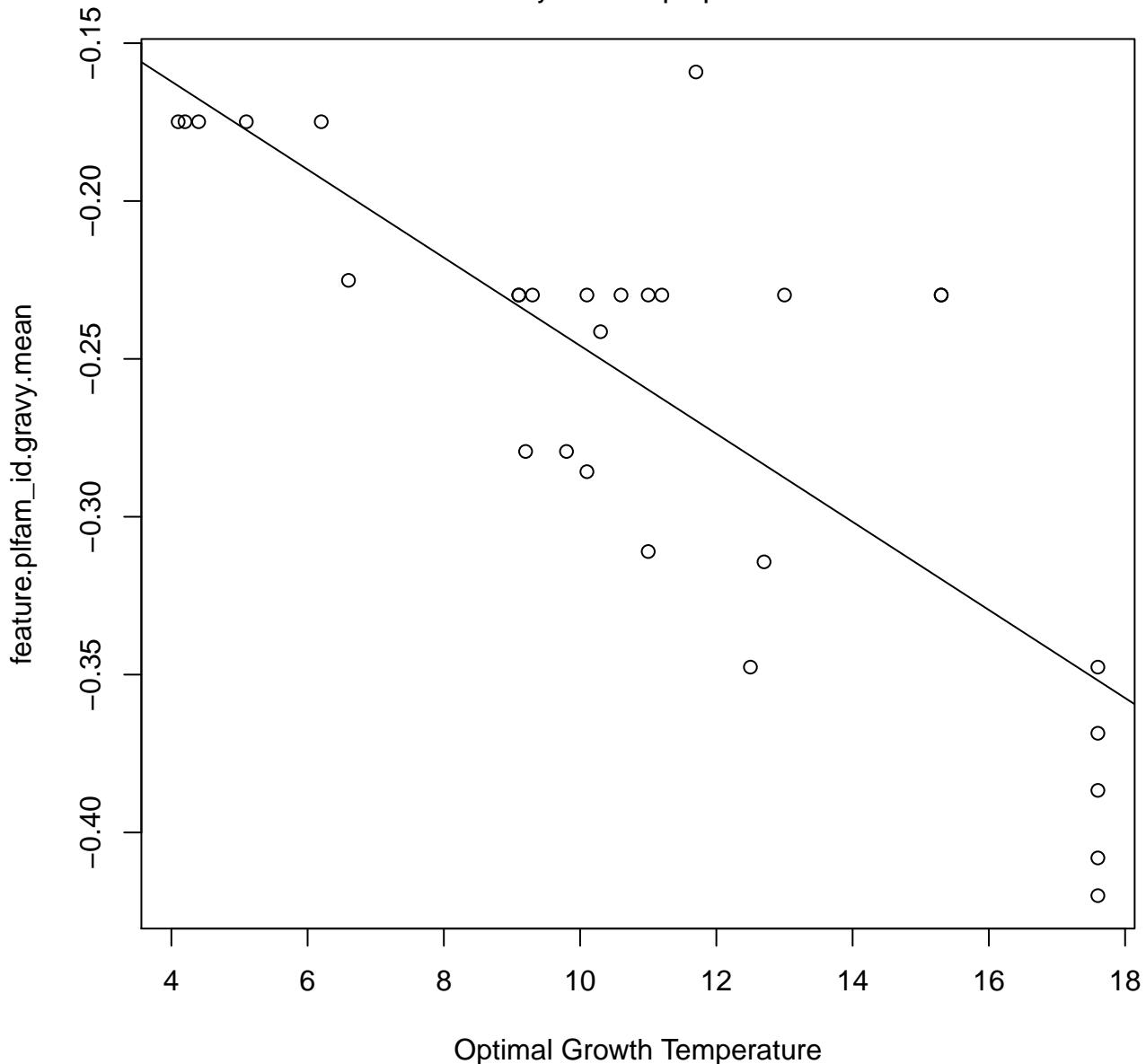
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ATP-dependent RNA helicase SO1501



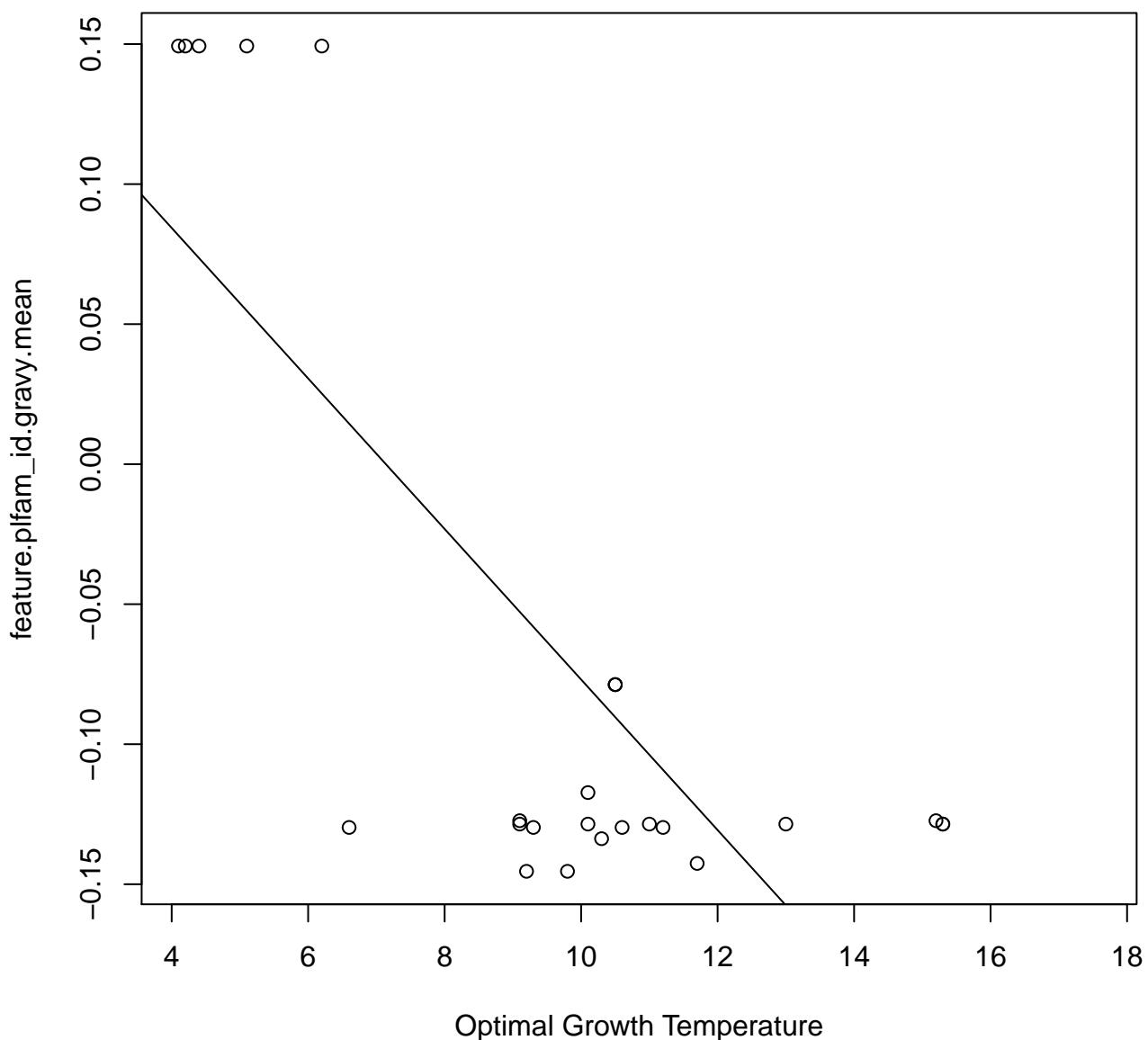
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Maltodextrin glucosidase (EC 3.2.1.20)



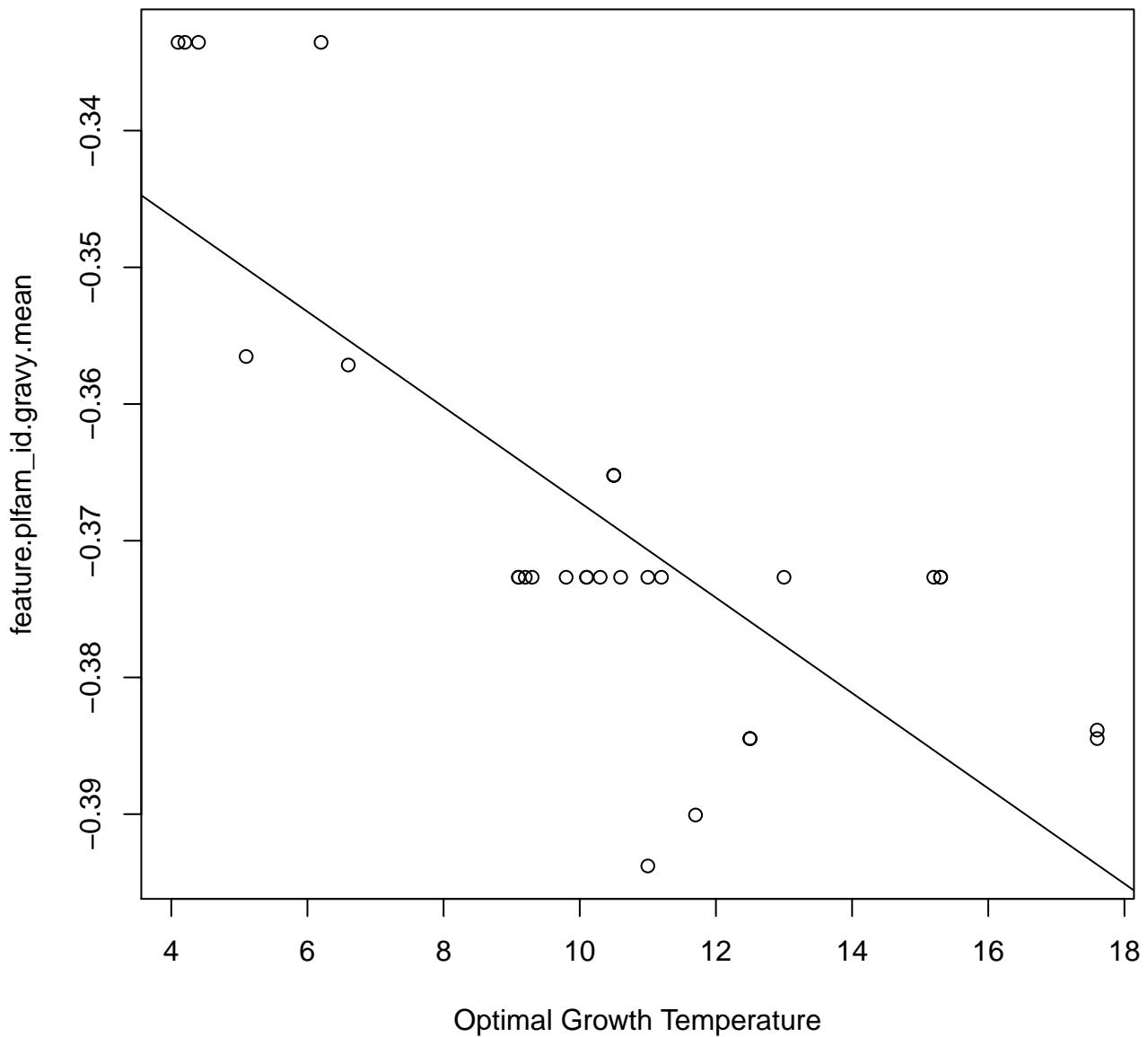
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Alkylated DNA repair protein



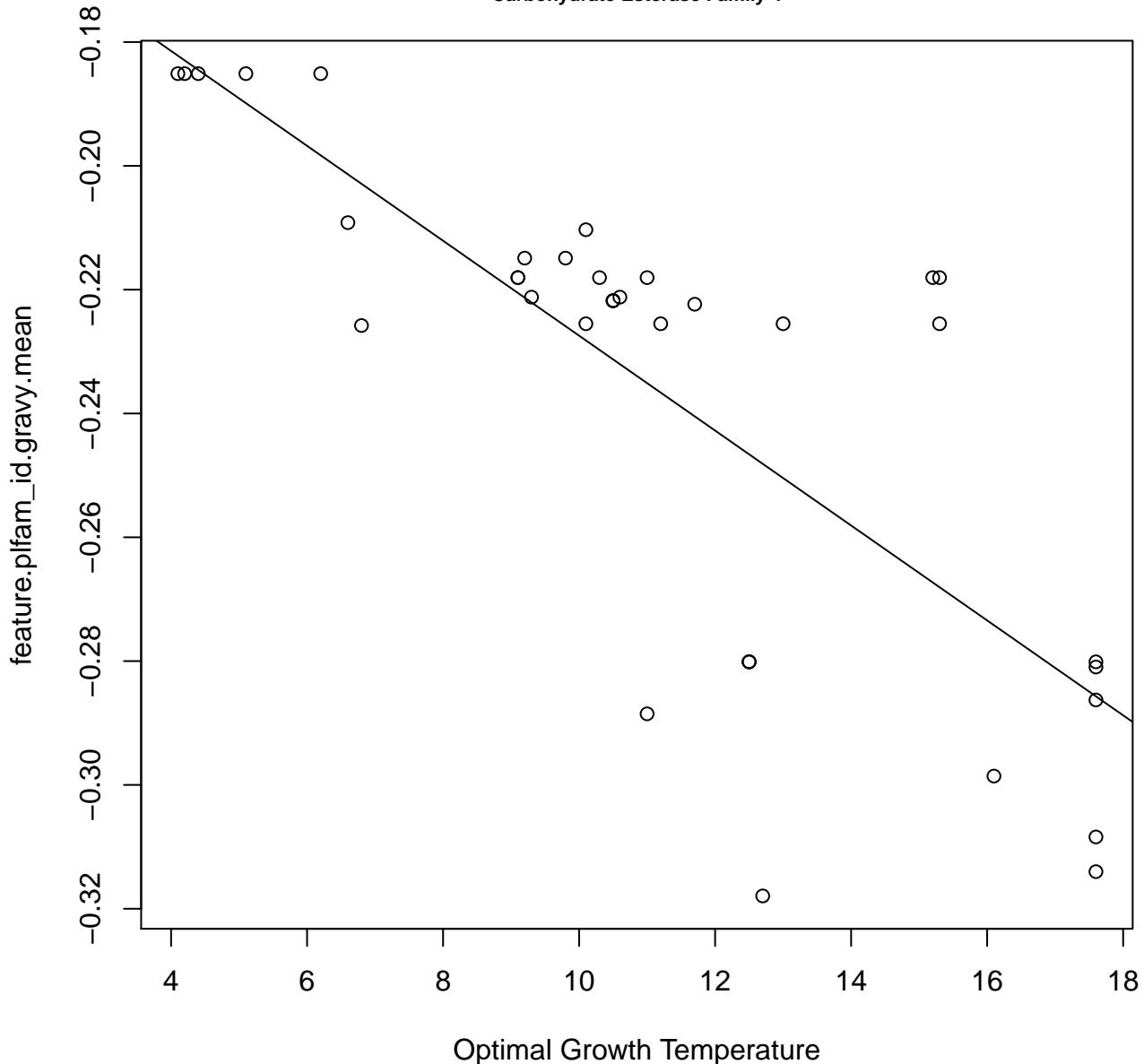
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PLF_28228_00031426
hypothetical protein



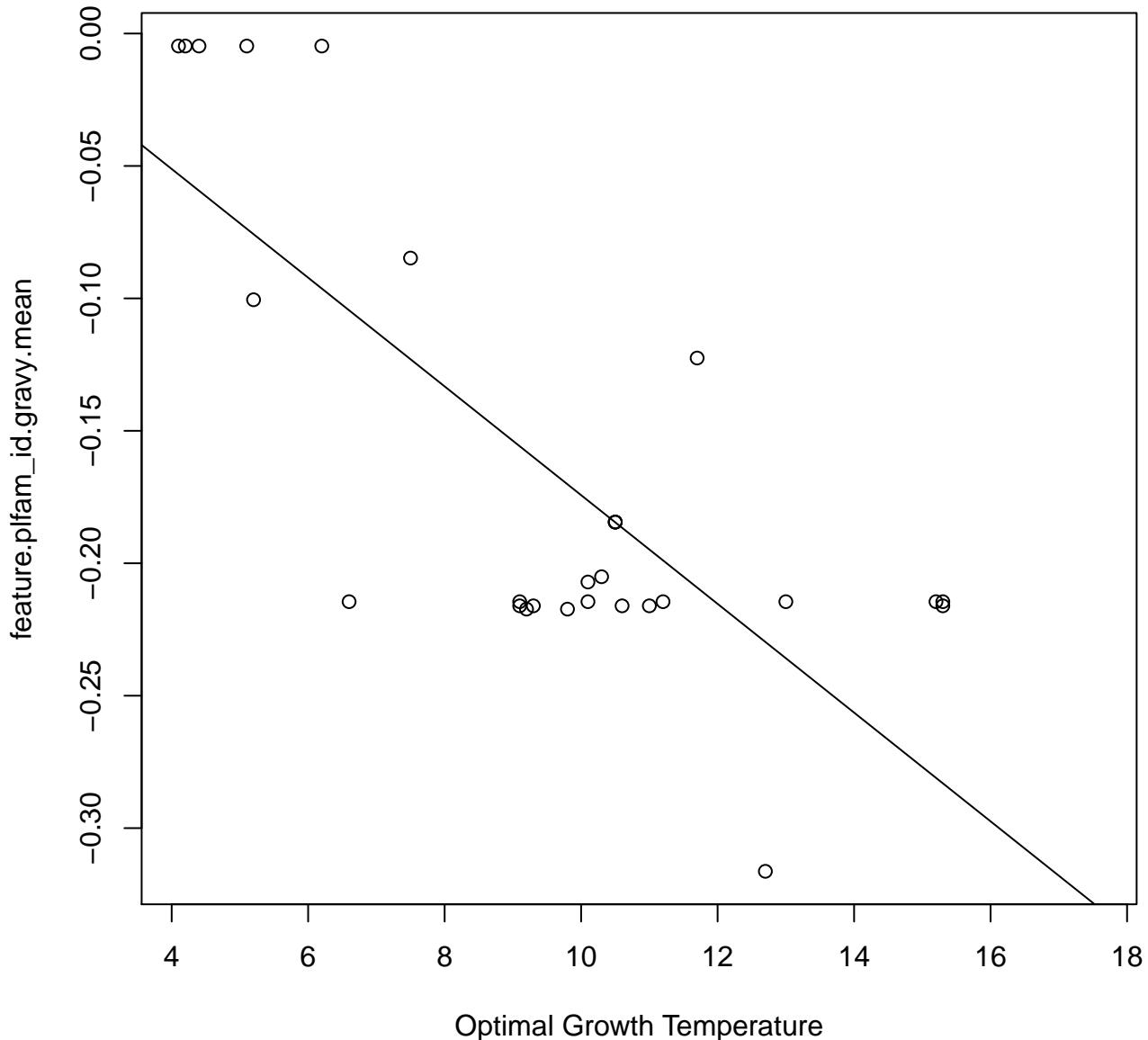
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hypothetical protein



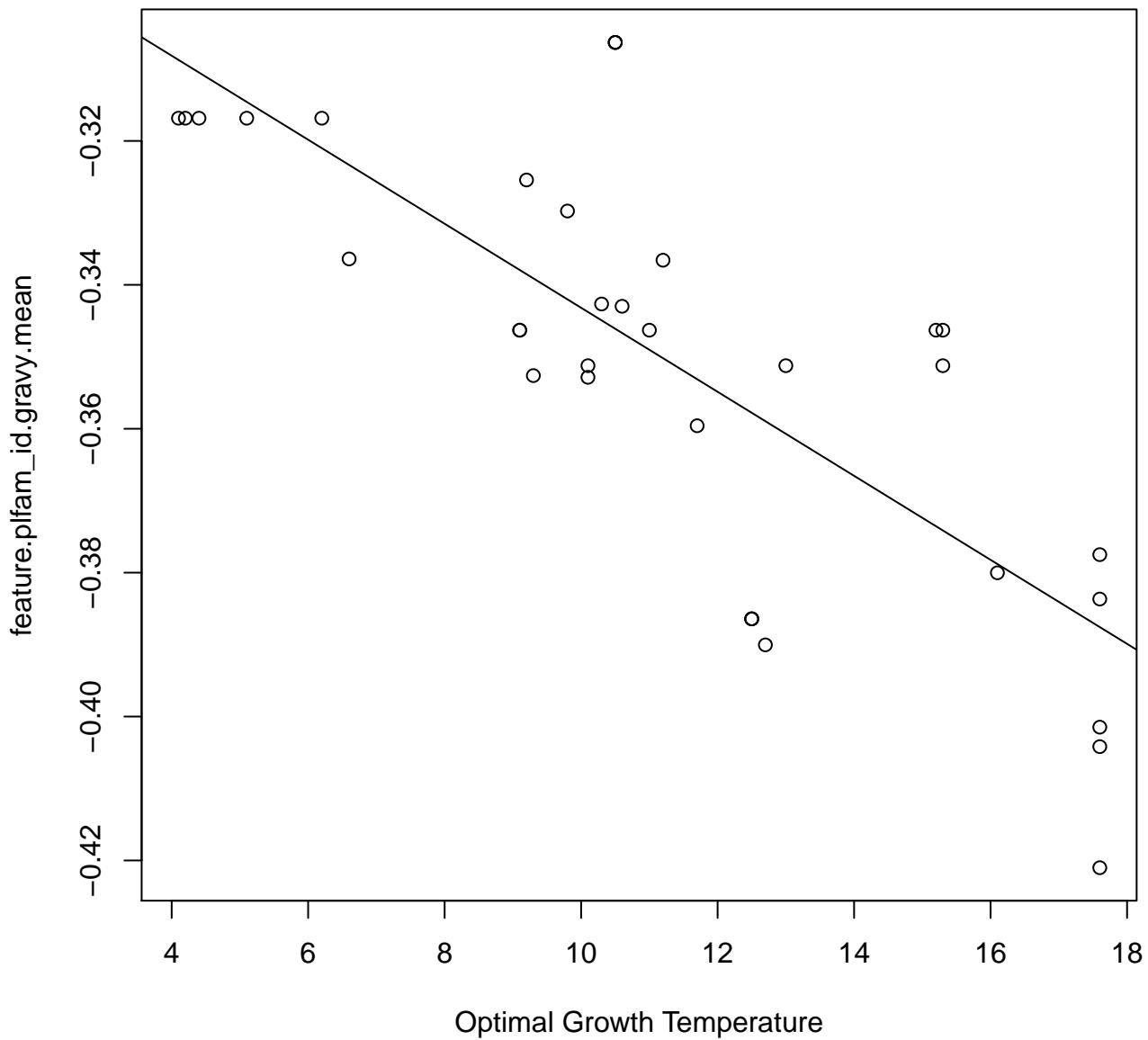
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Carbohydrate Esterase Family 4



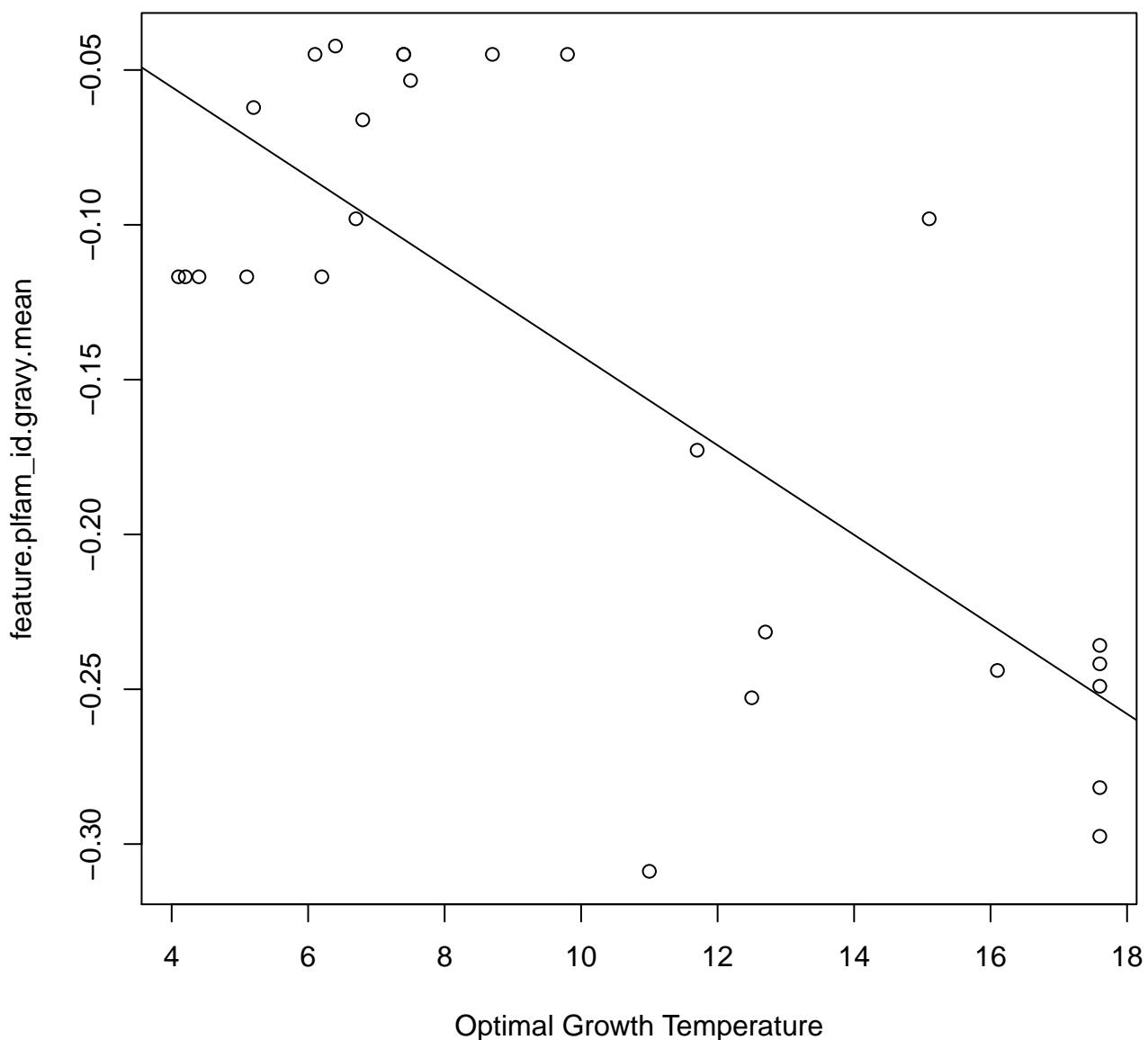
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hypothetical protein



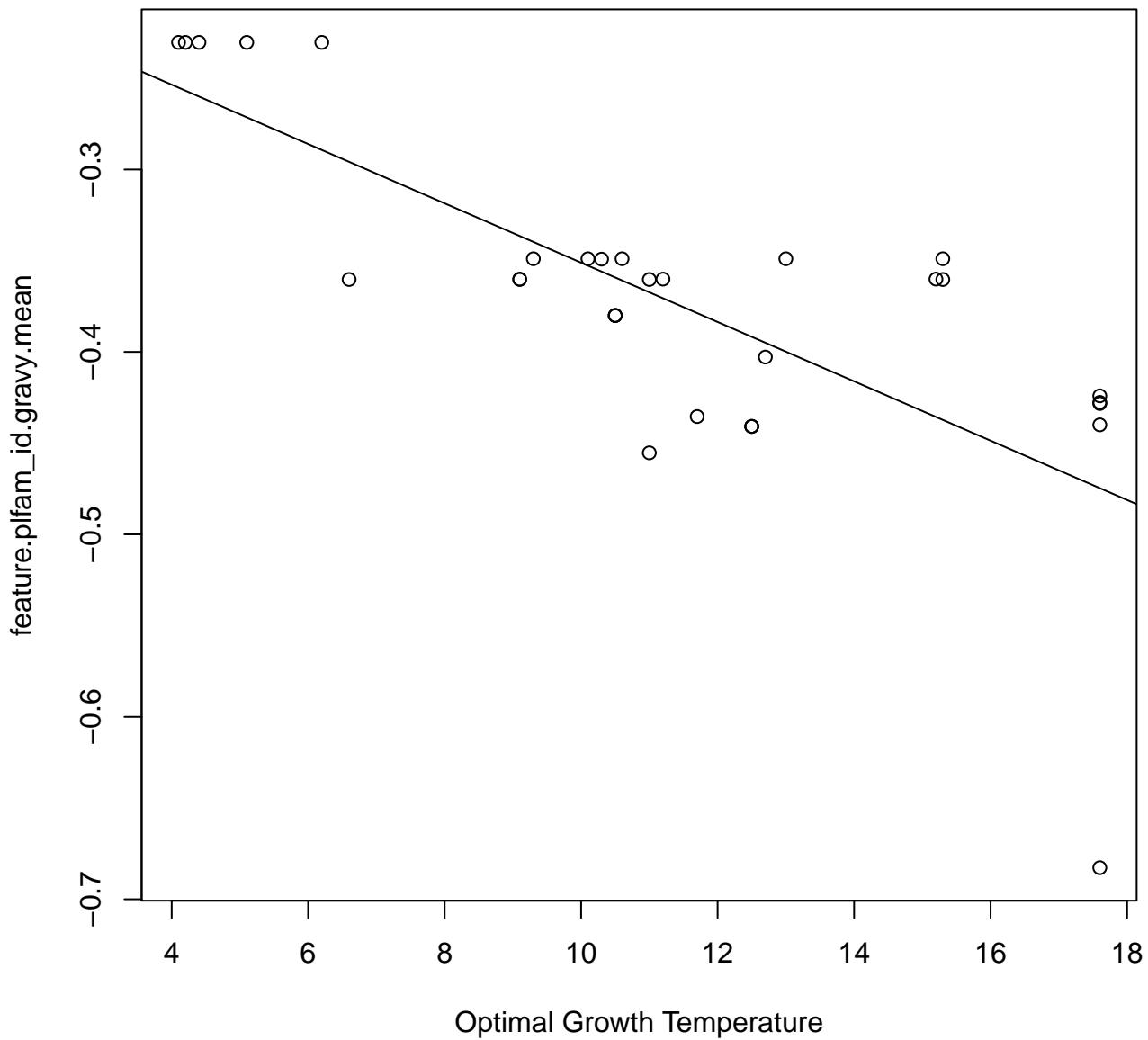
feature.plfam_id.gravy.mean
PLF_28228_00002160
Two-component system sensor histidine kinase/response regulator hybrid



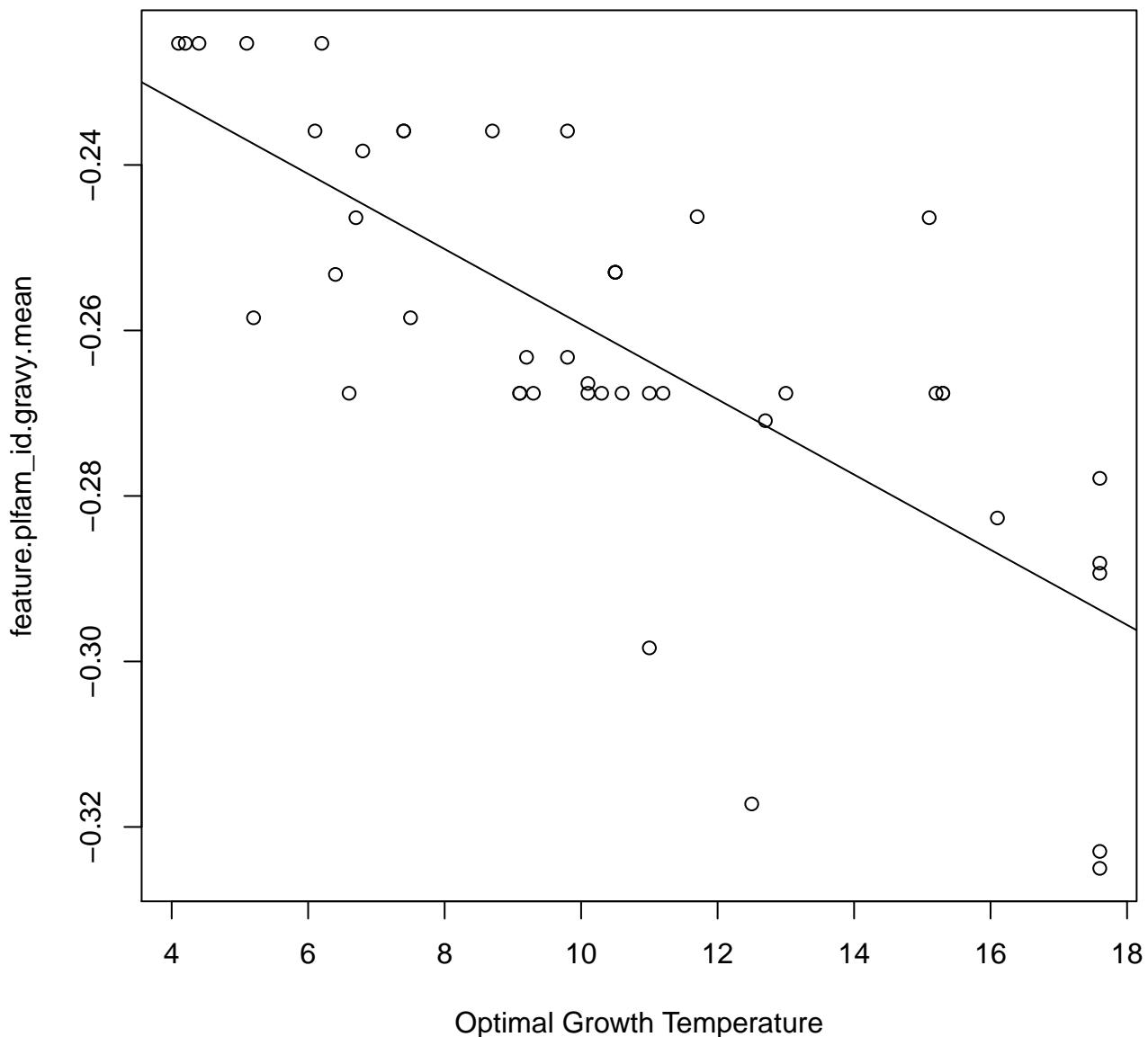
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PLF_28228_00022139
FIG004599: Hypothetical protein



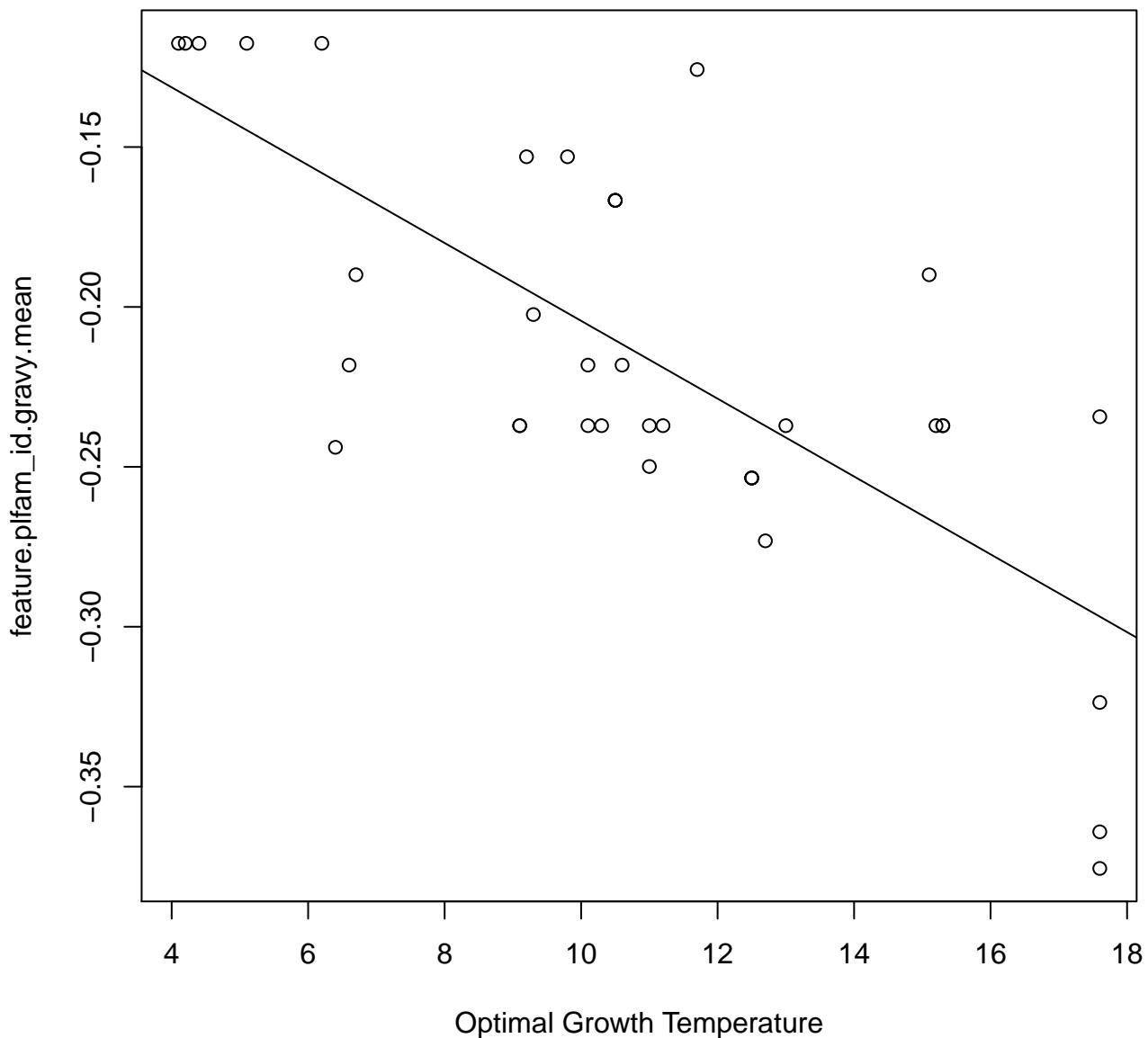
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PLF_28228_00001289
Uncharacterized protease YegQ



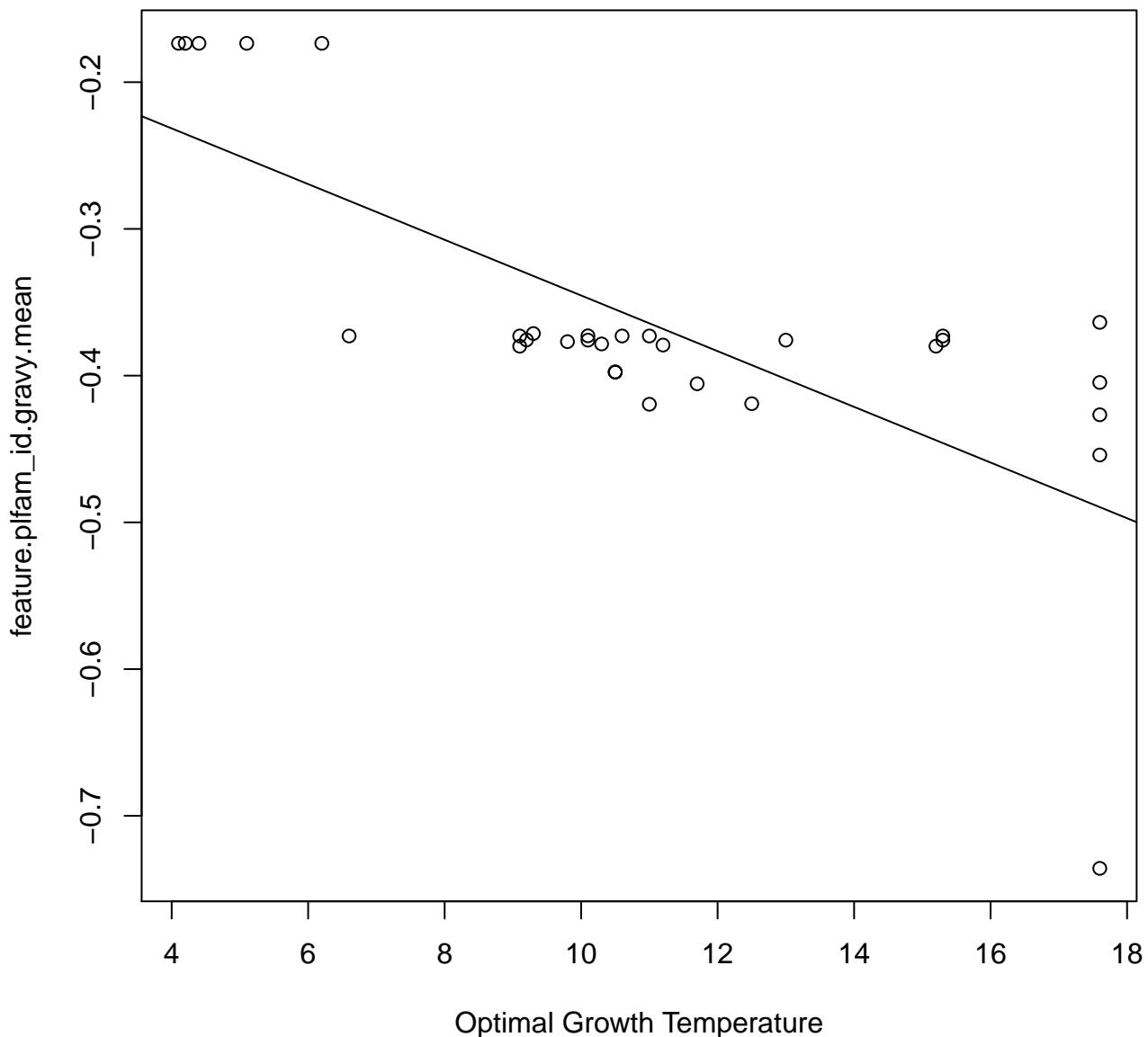
feature.plfam_id.gravy.mean
PLF_28228_00027836
16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)



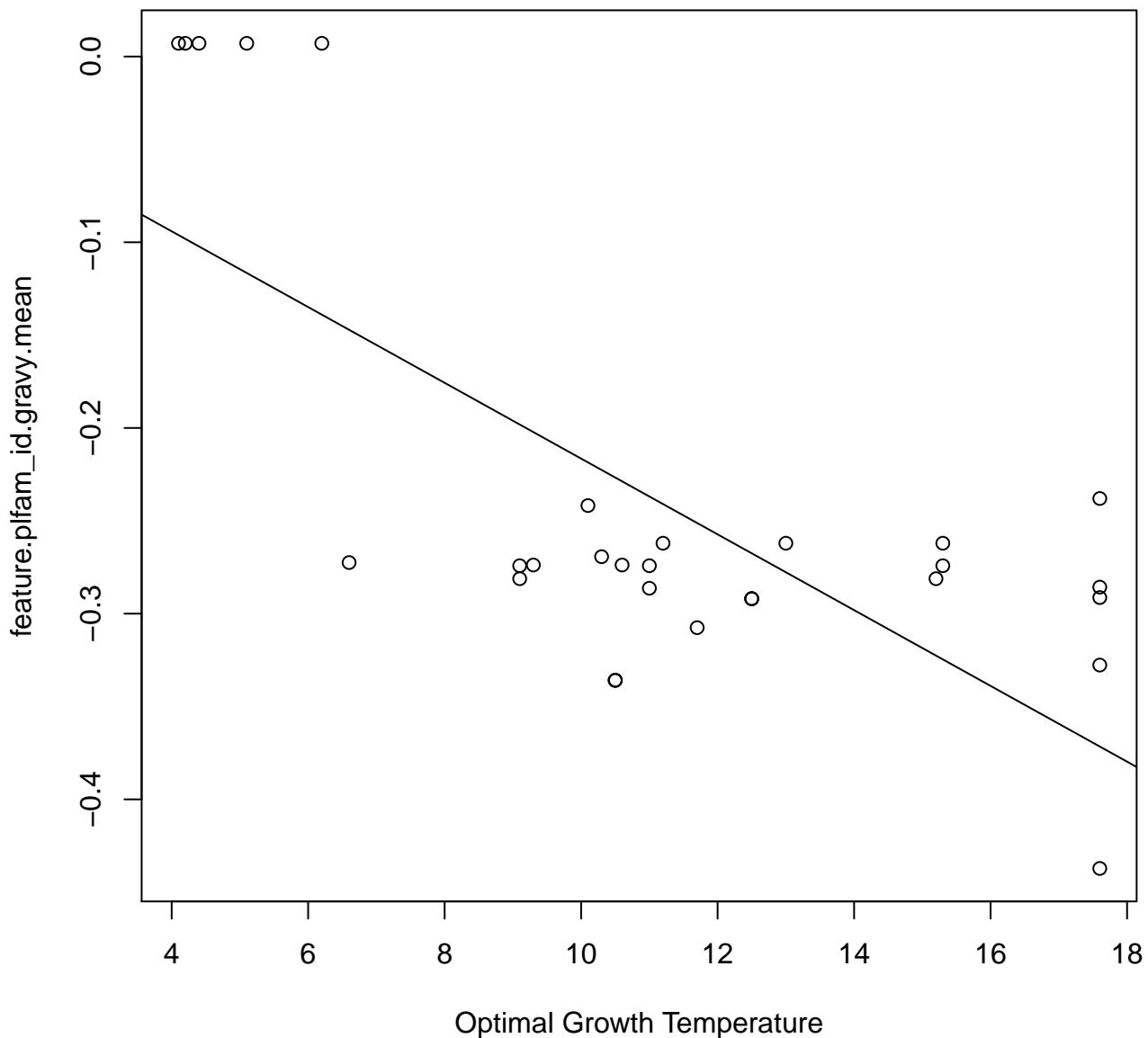
feature.plfam_id.gravy.mean
PLF_28228_00001370
hypothetical protein



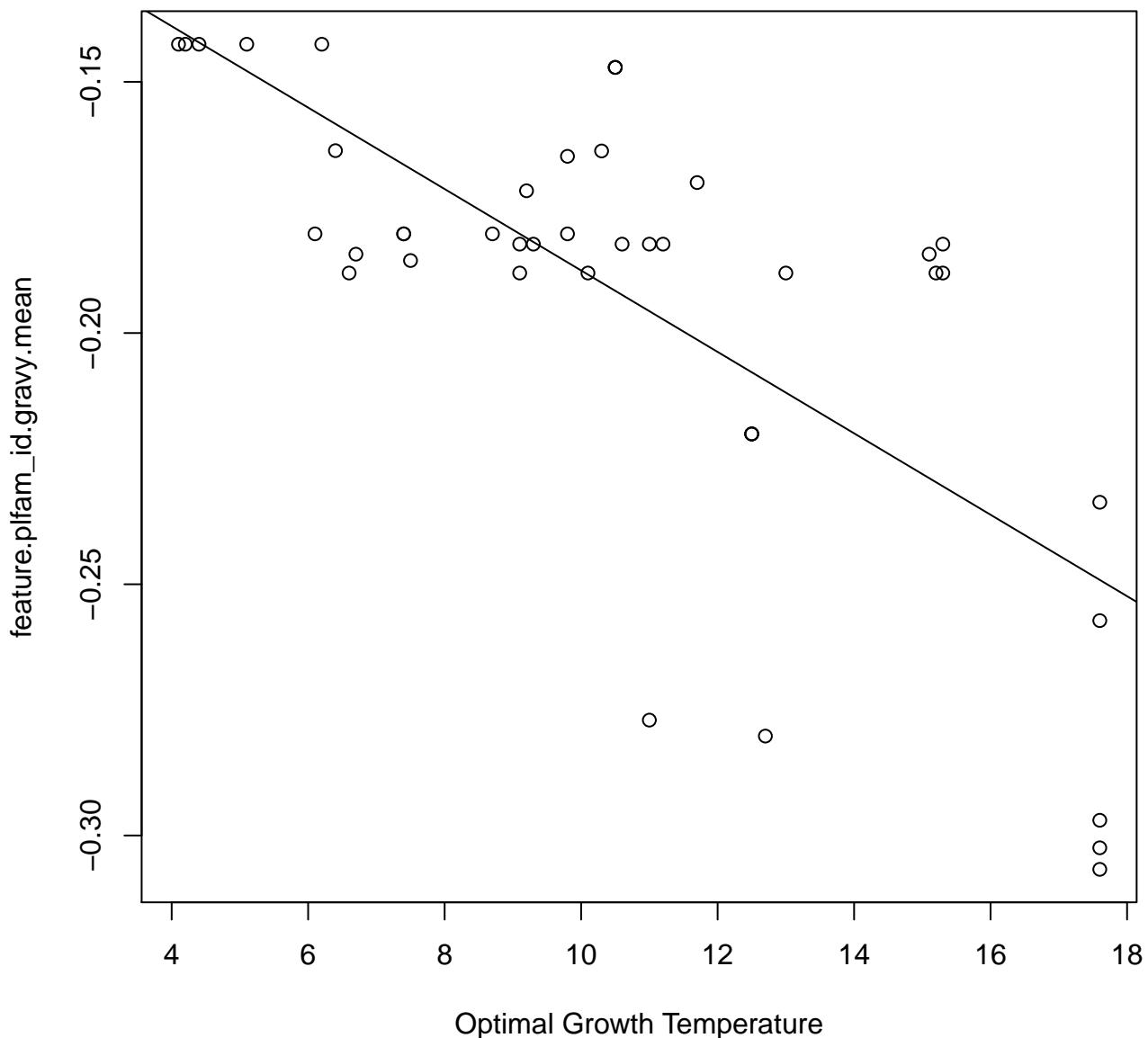
feature.plfam_id.gravy.mean
PLF_28228_00028047
Fatty acid cis/trans isomerase



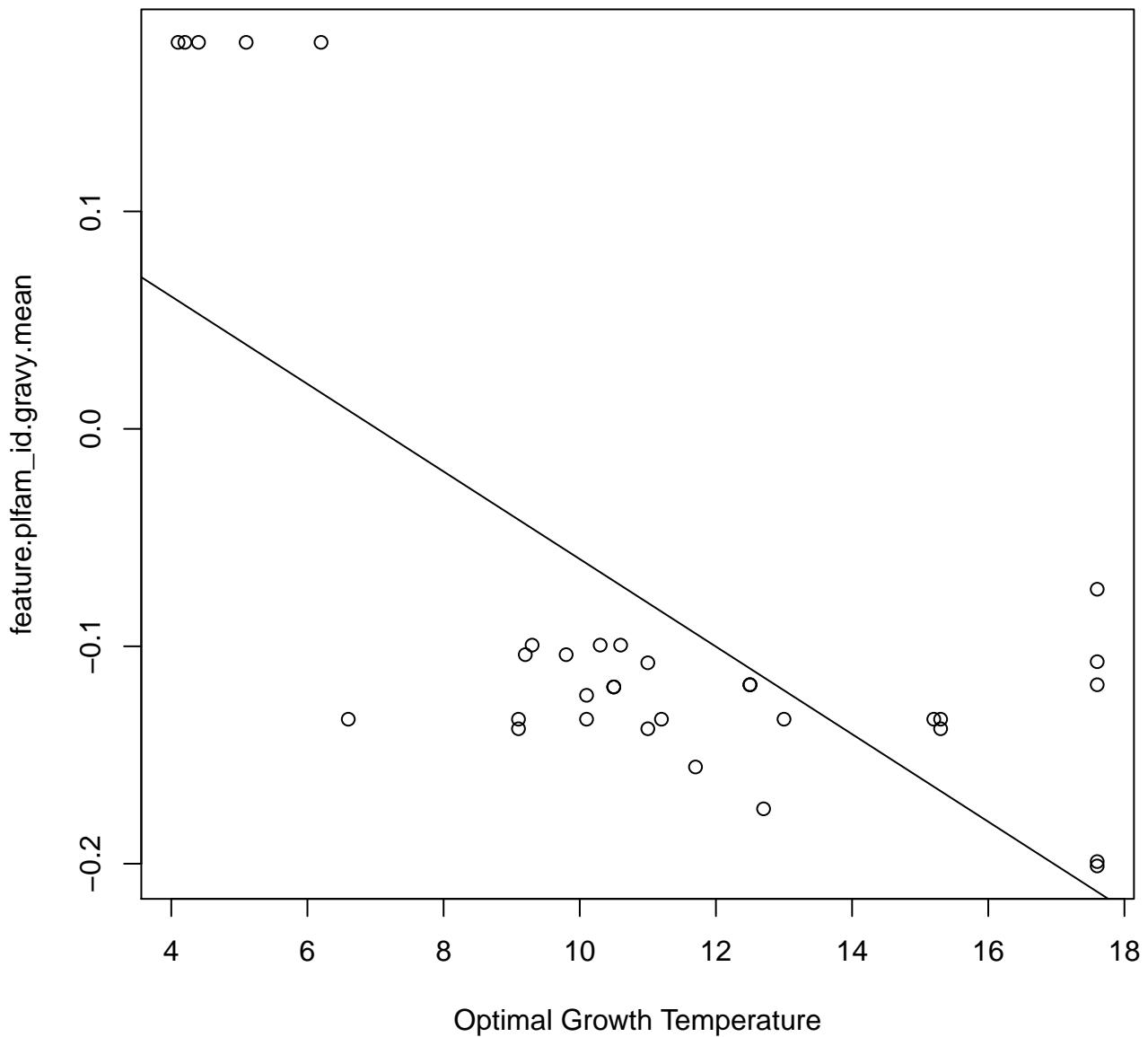
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TonB-dependent receptor



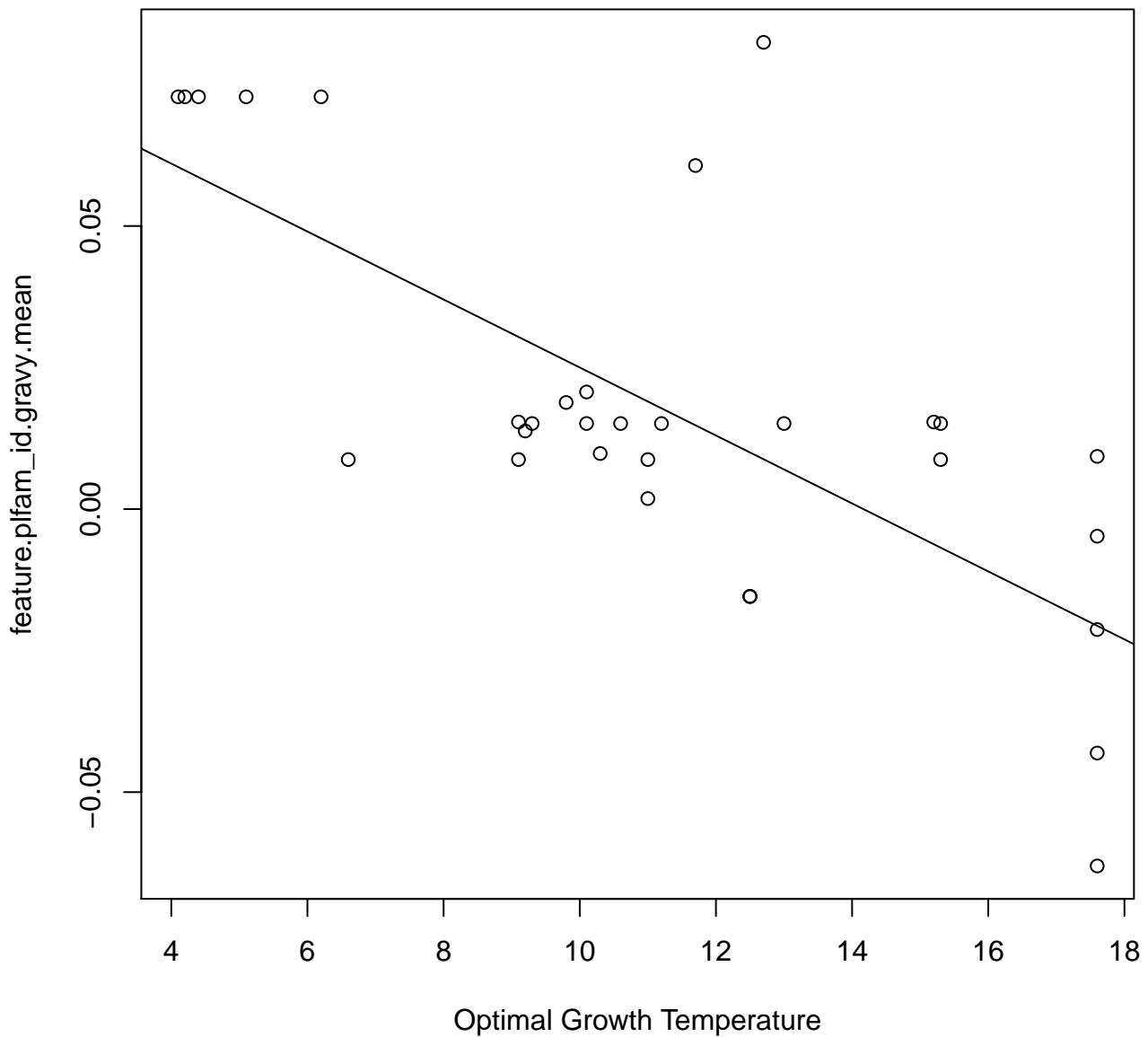
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Peptidase M20:Peptidase M28 precursor



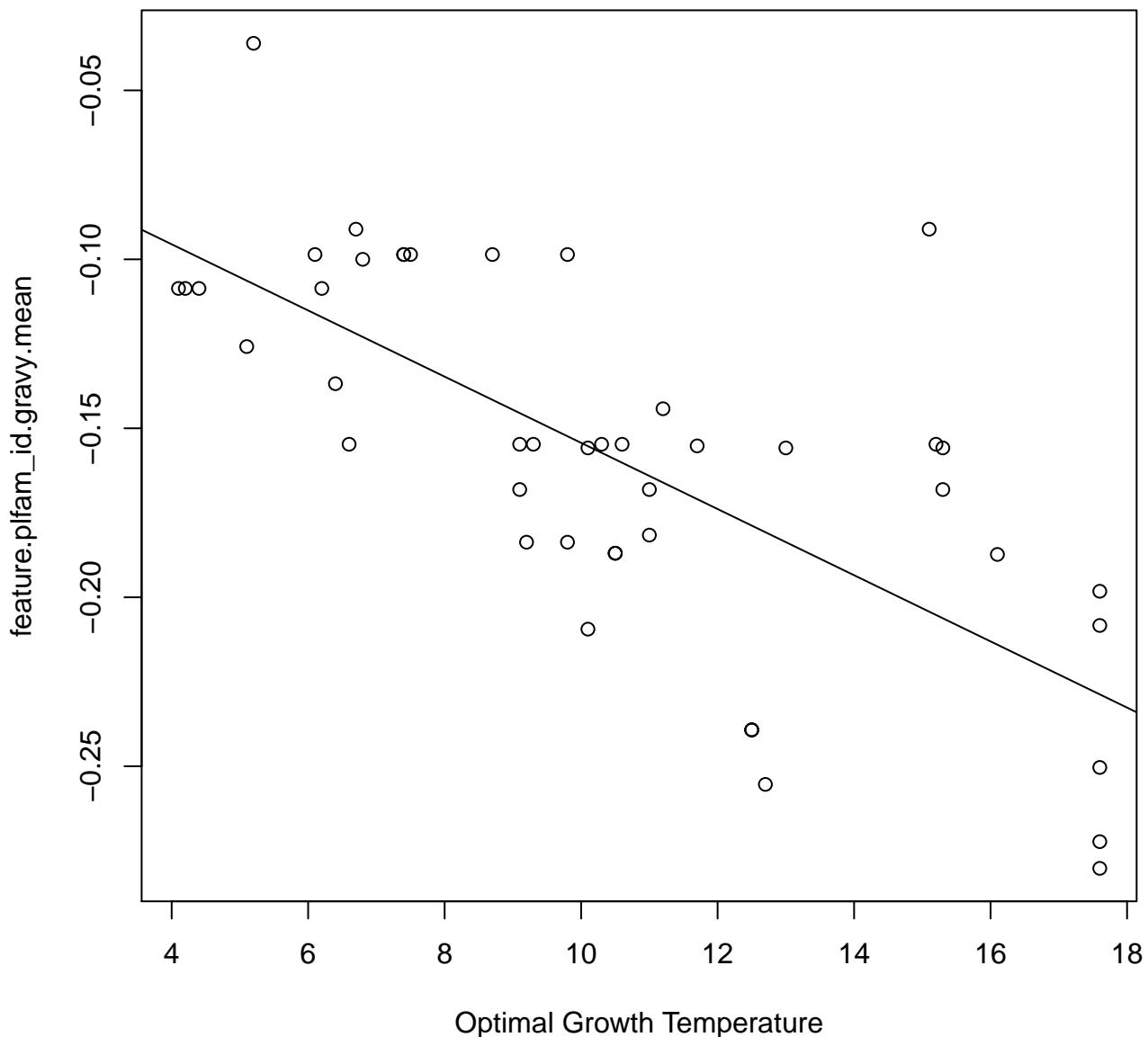
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Putative NAD(P)H nitroreductase YdjA



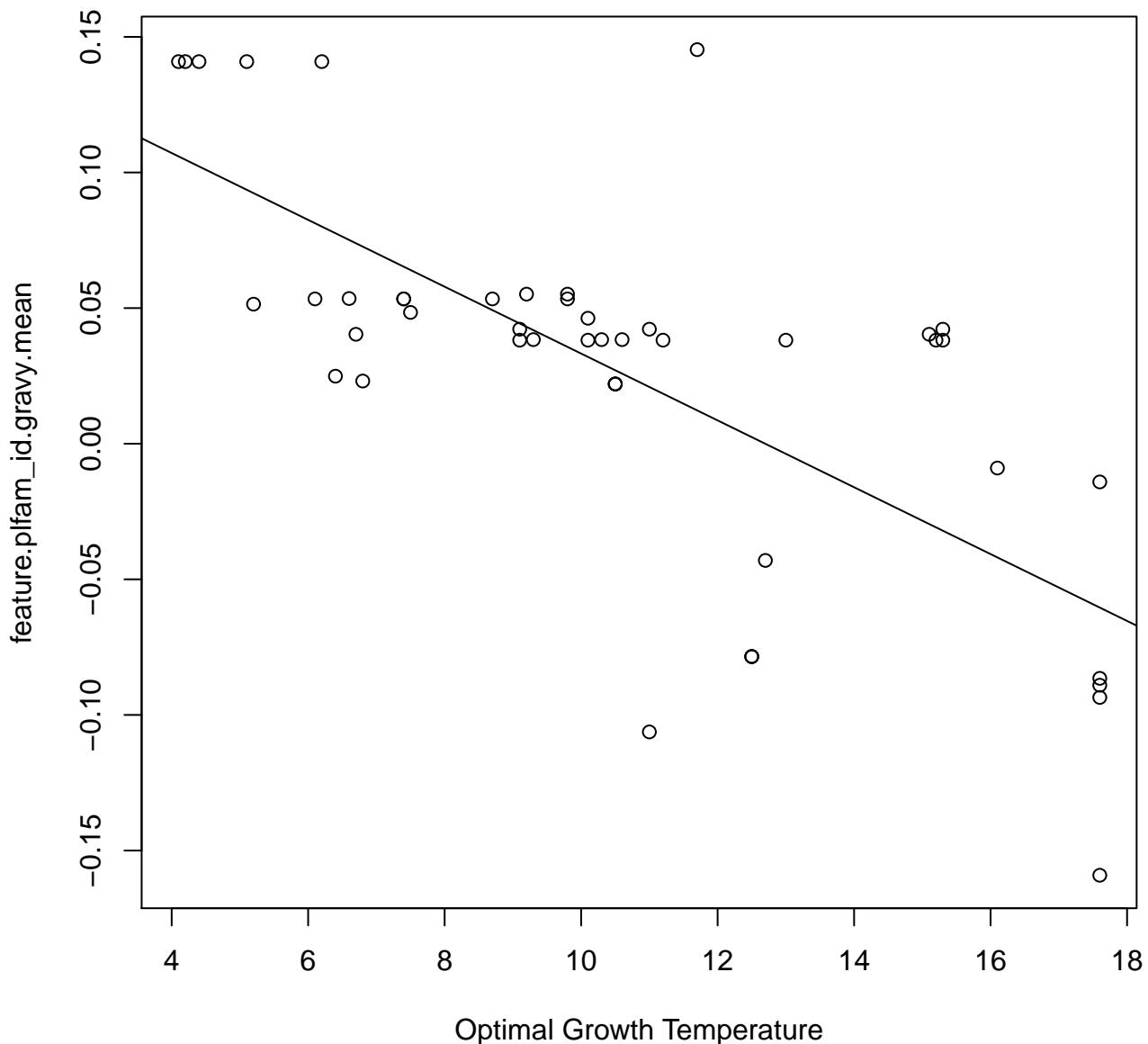
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N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)



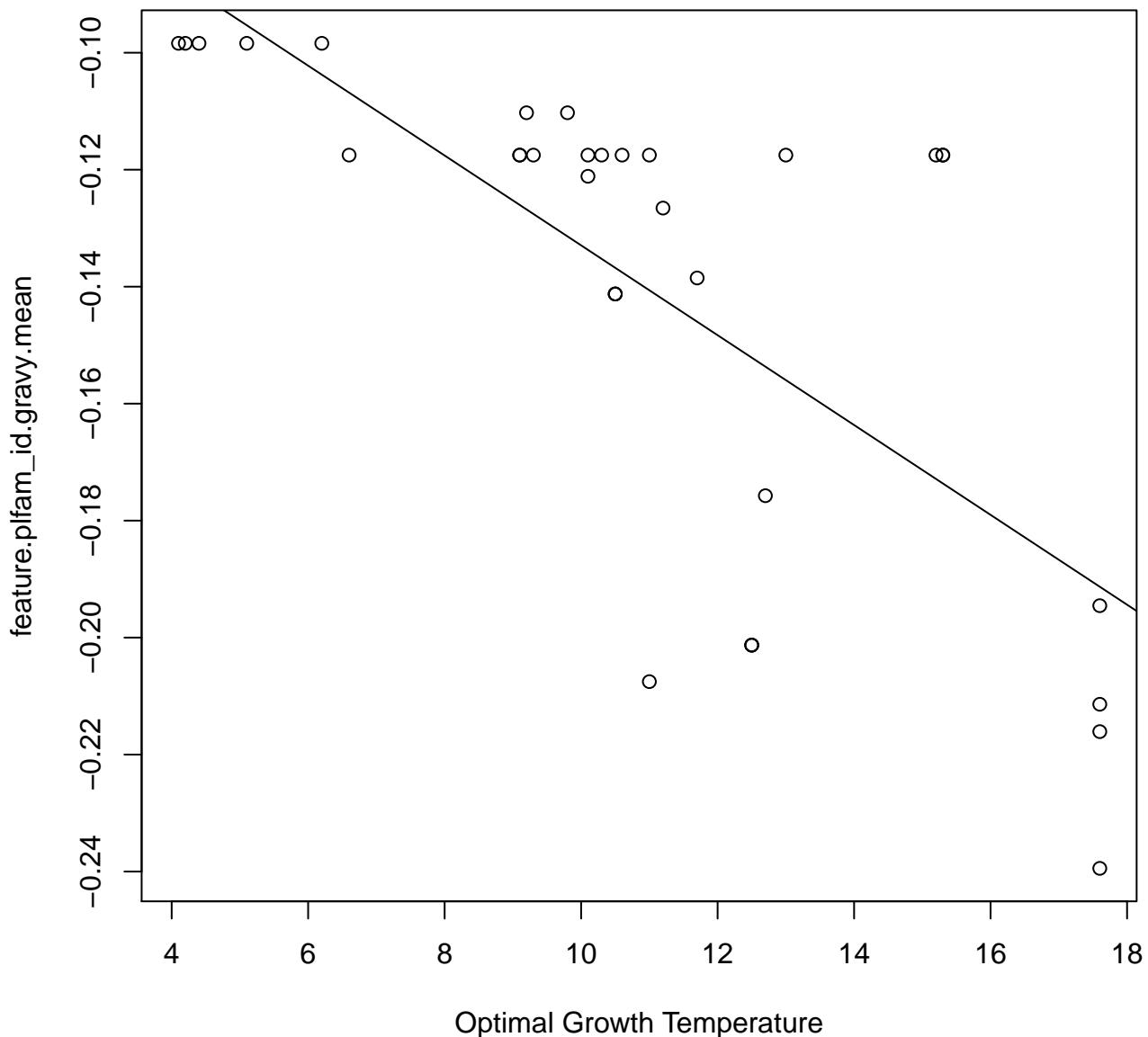
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Peptidase, M23/M37 family



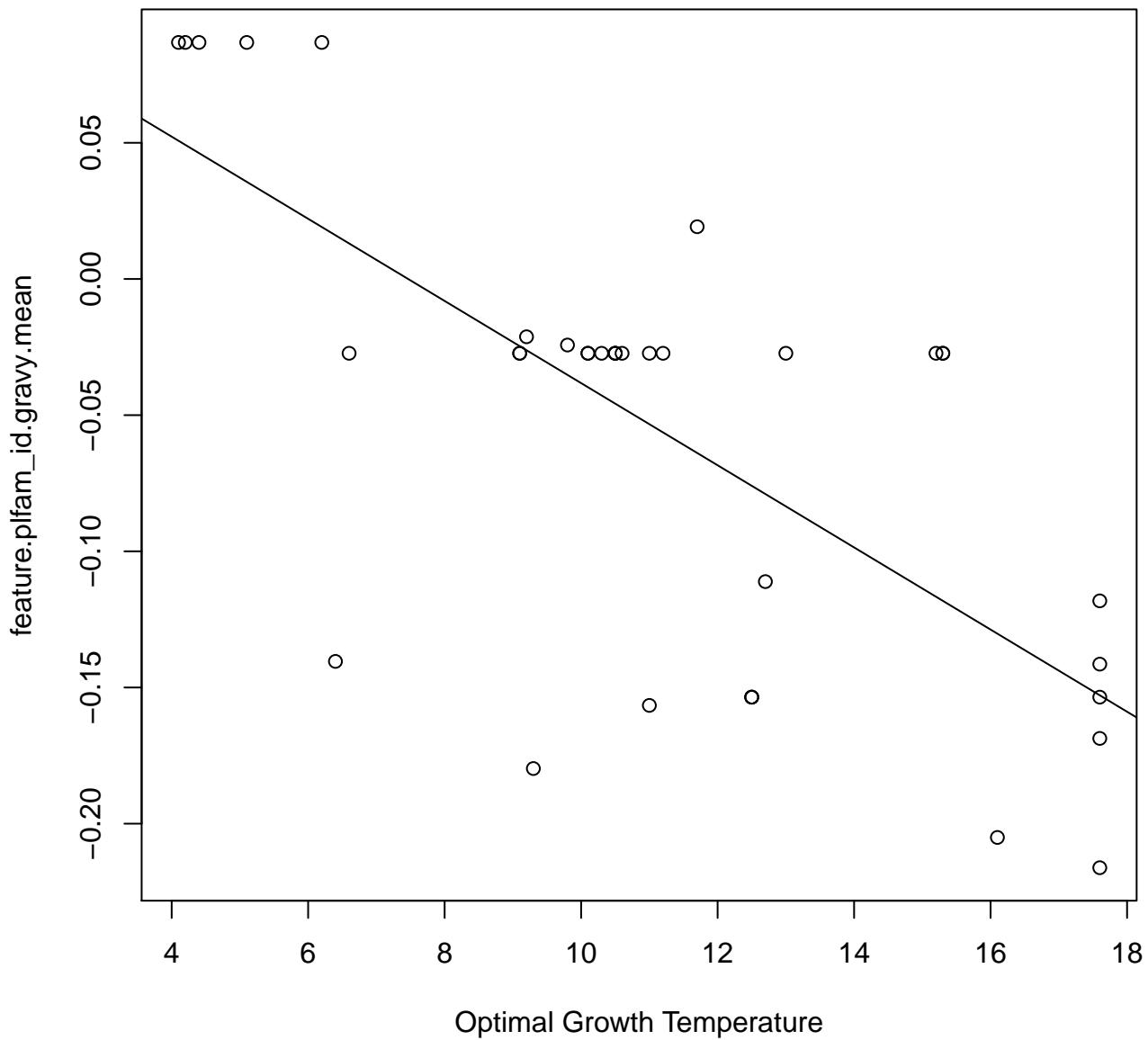
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Sensor histidine kinase GlrK



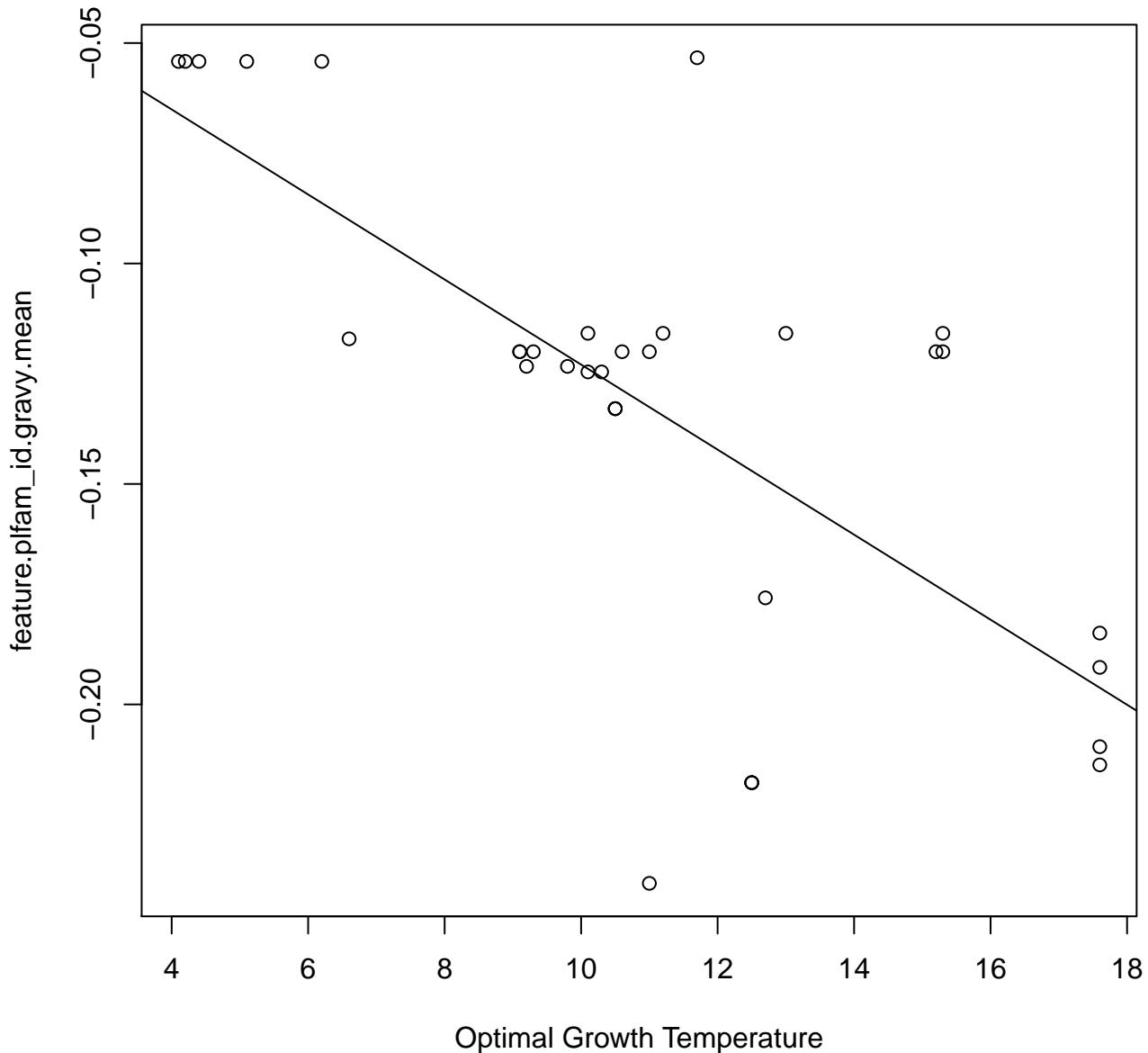
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Methyl-accepting chemotaxis sensor/transducer protein



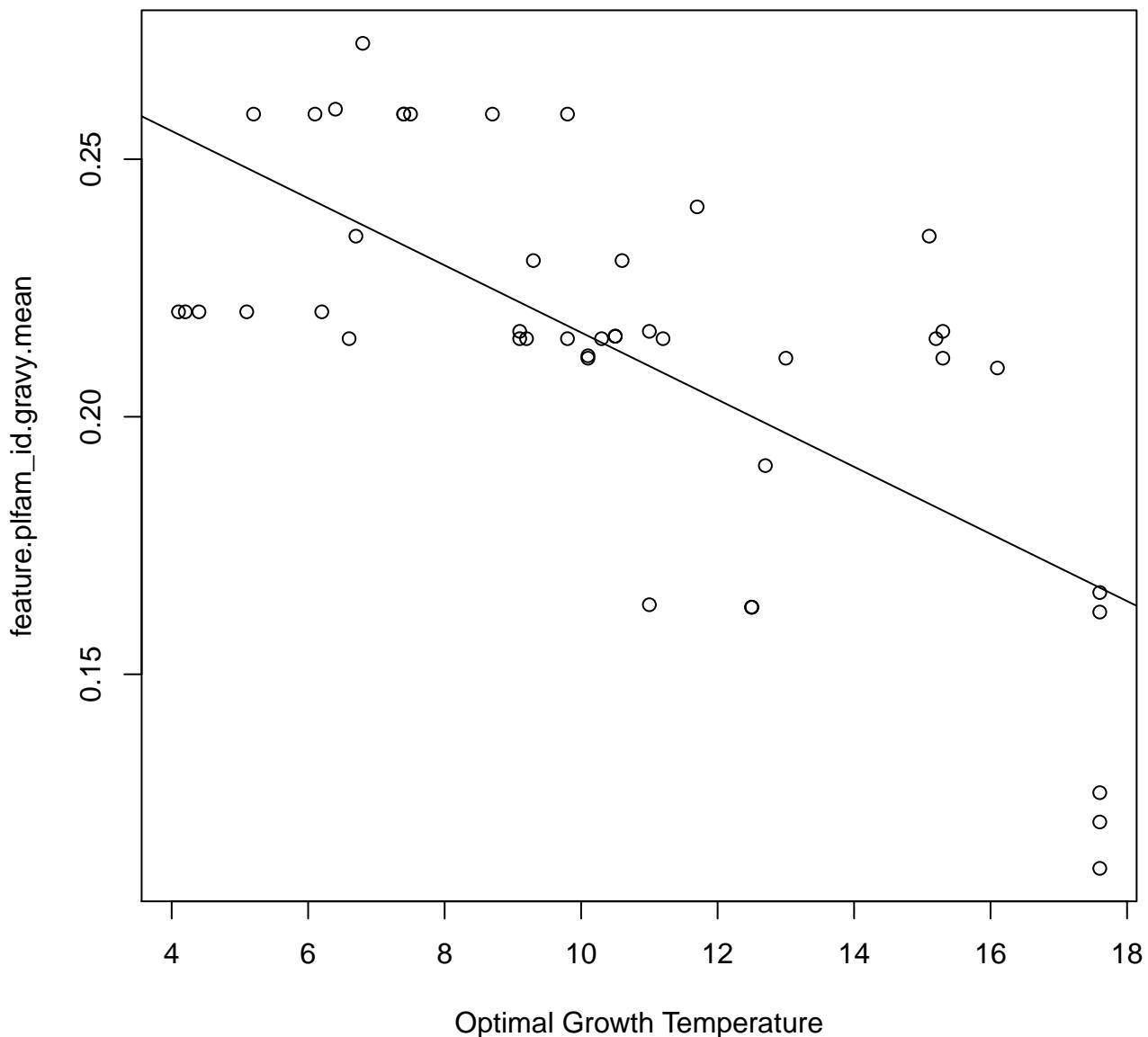
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hypothetical protein



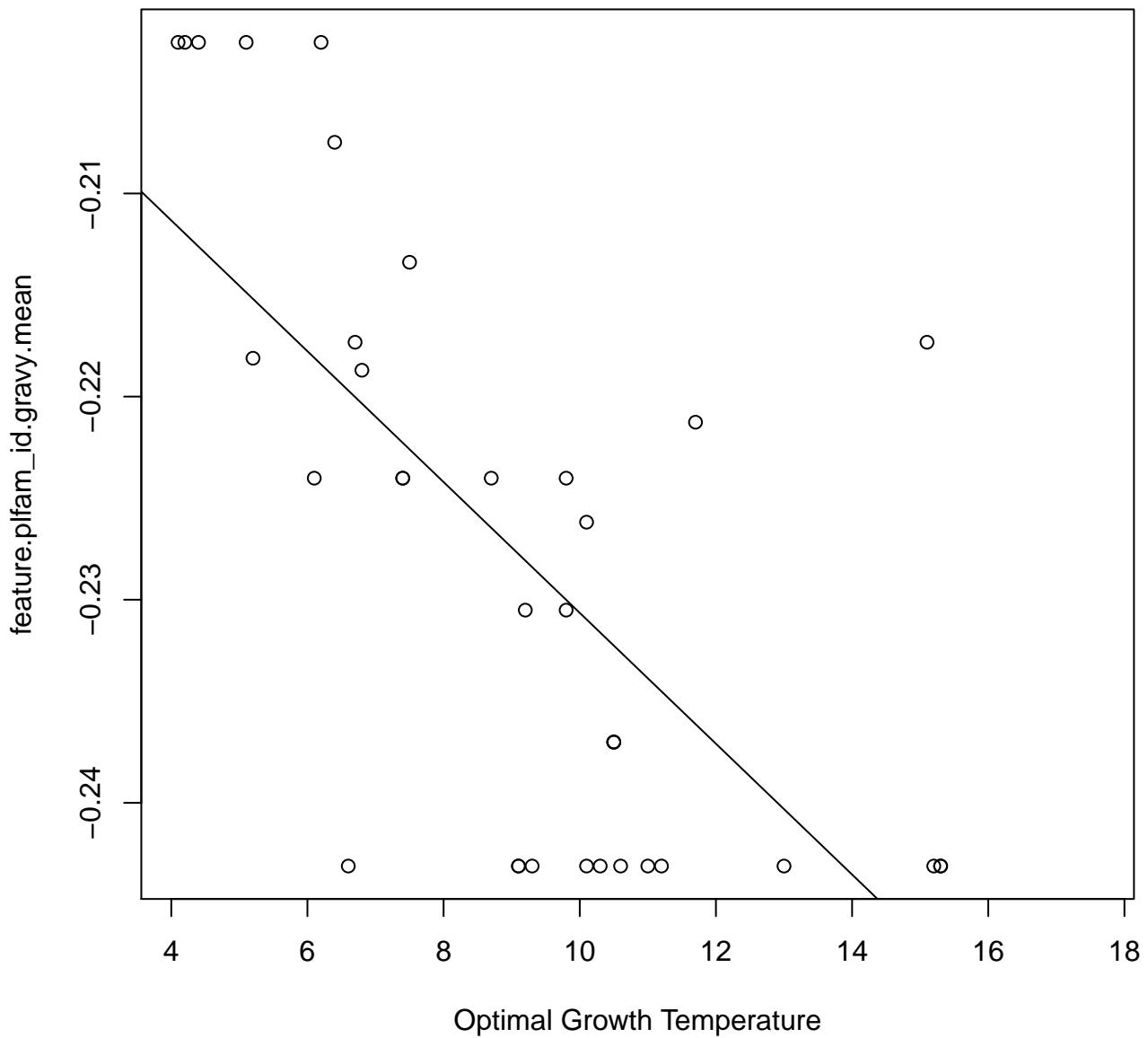
feature.plfam_id.gravy.mean
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Transcriptional regulator, AcrR family



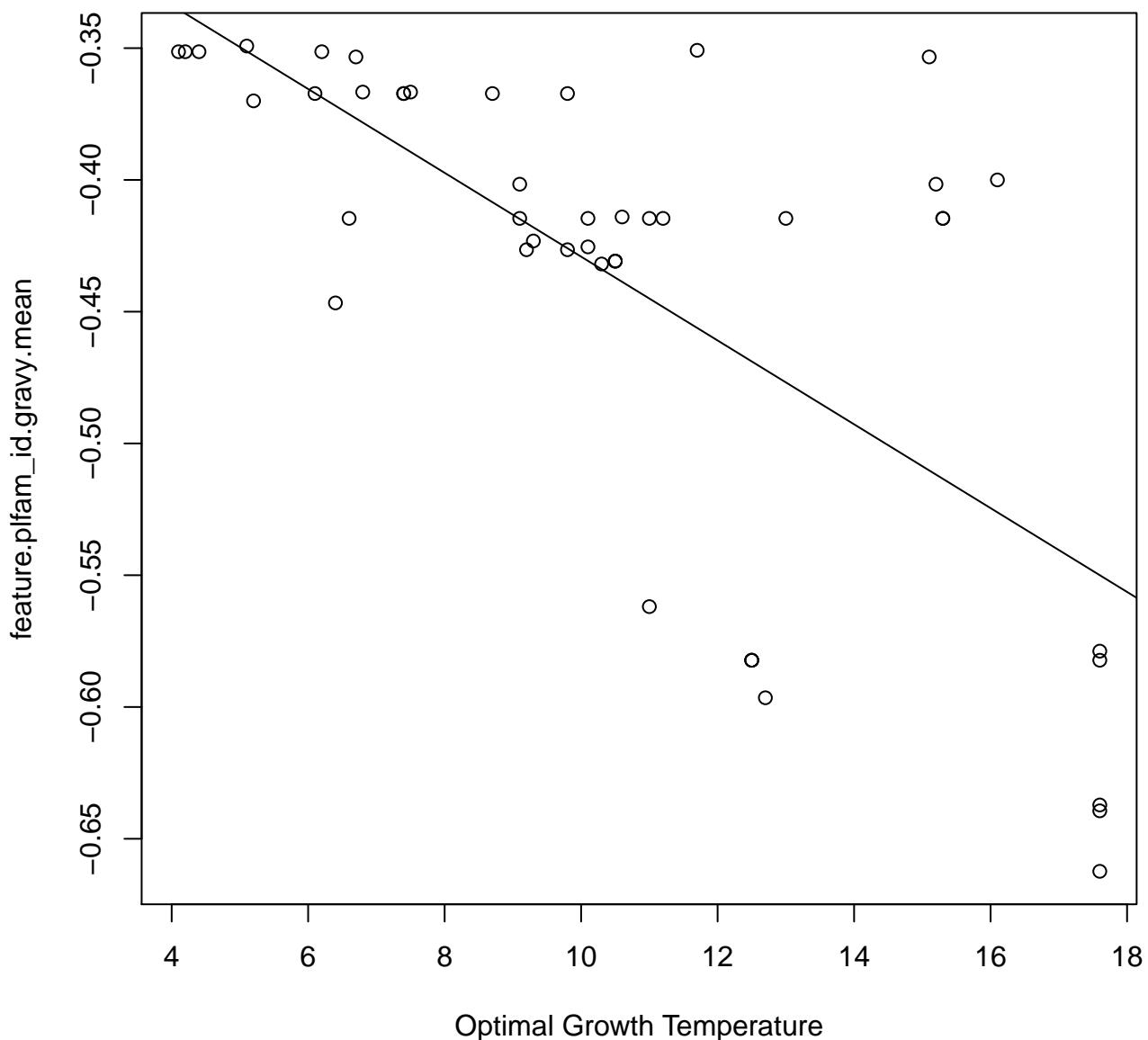
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FIG123464: Polysaccharide export protein



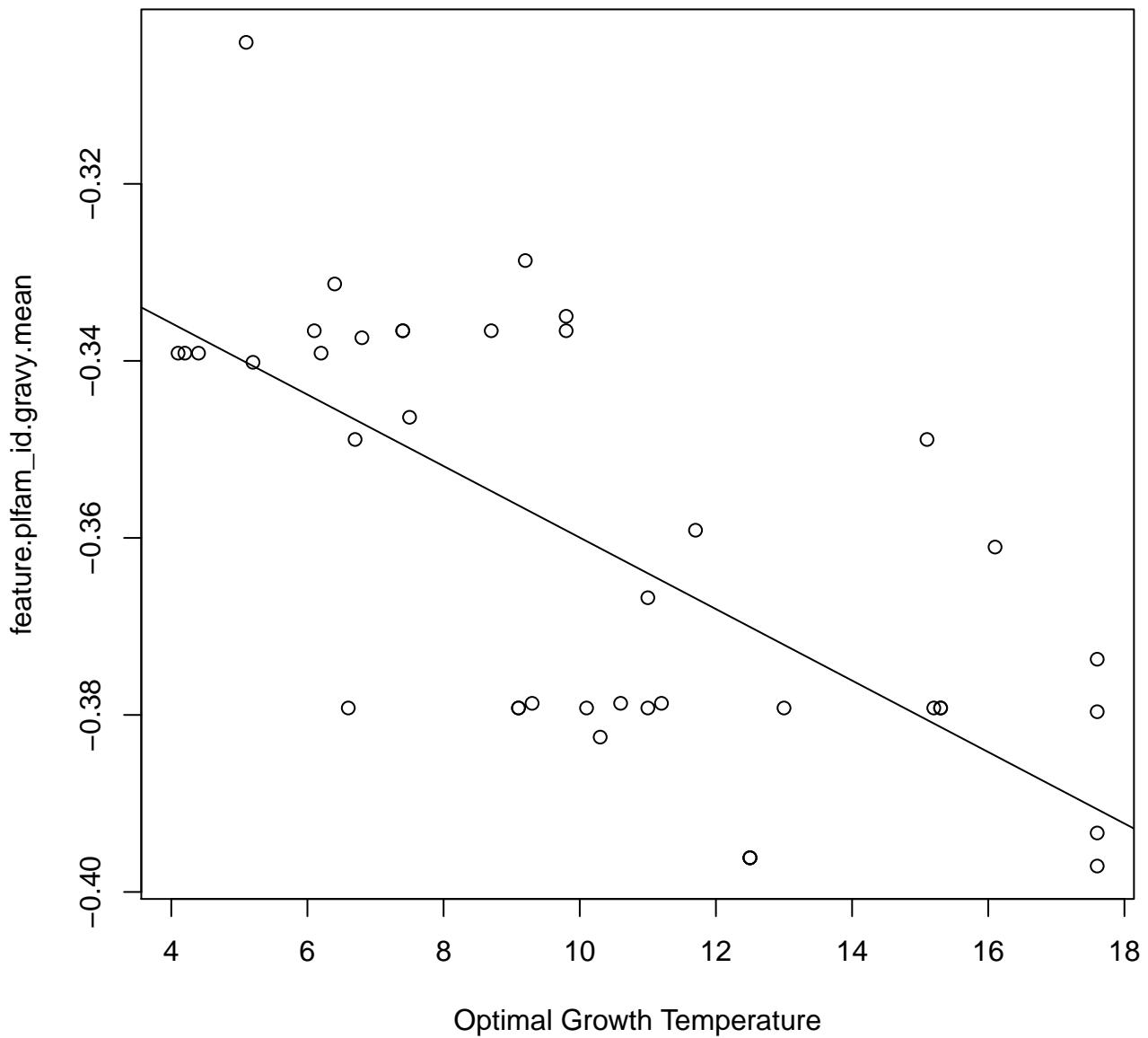
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Carbon–nitrogen hydrolase



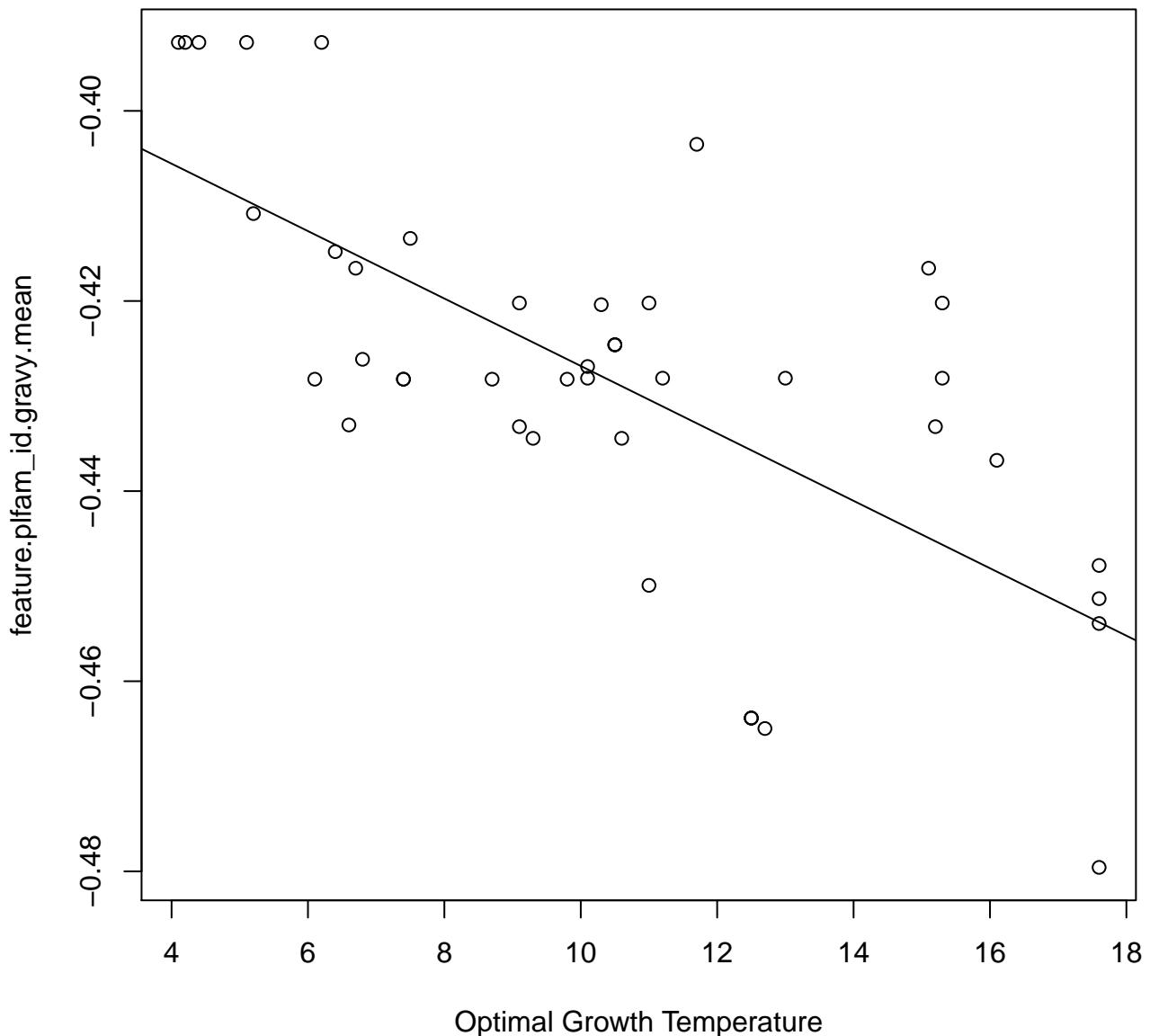
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UPF0115 protein YfcN



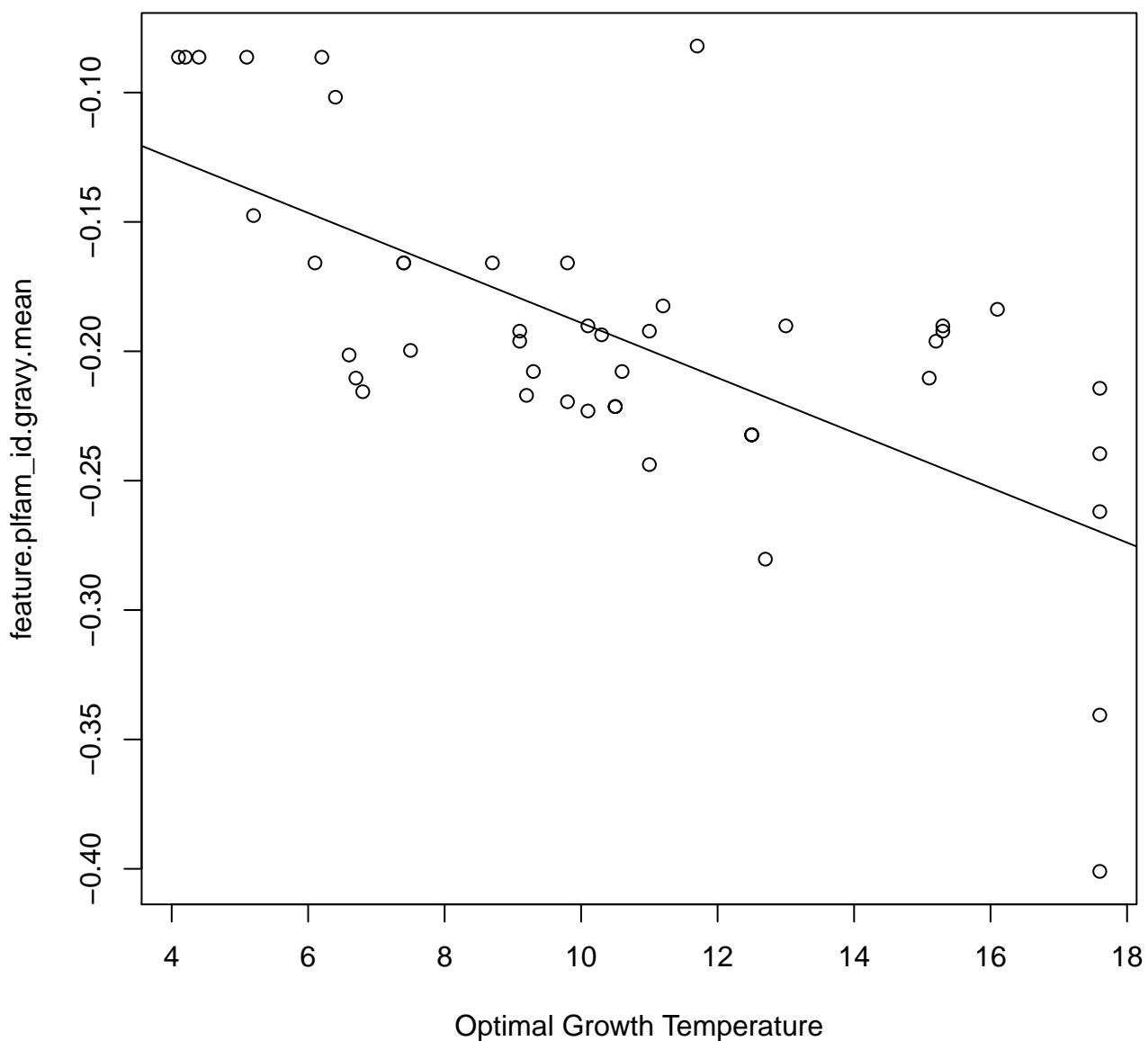
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TonB-dependent receptor



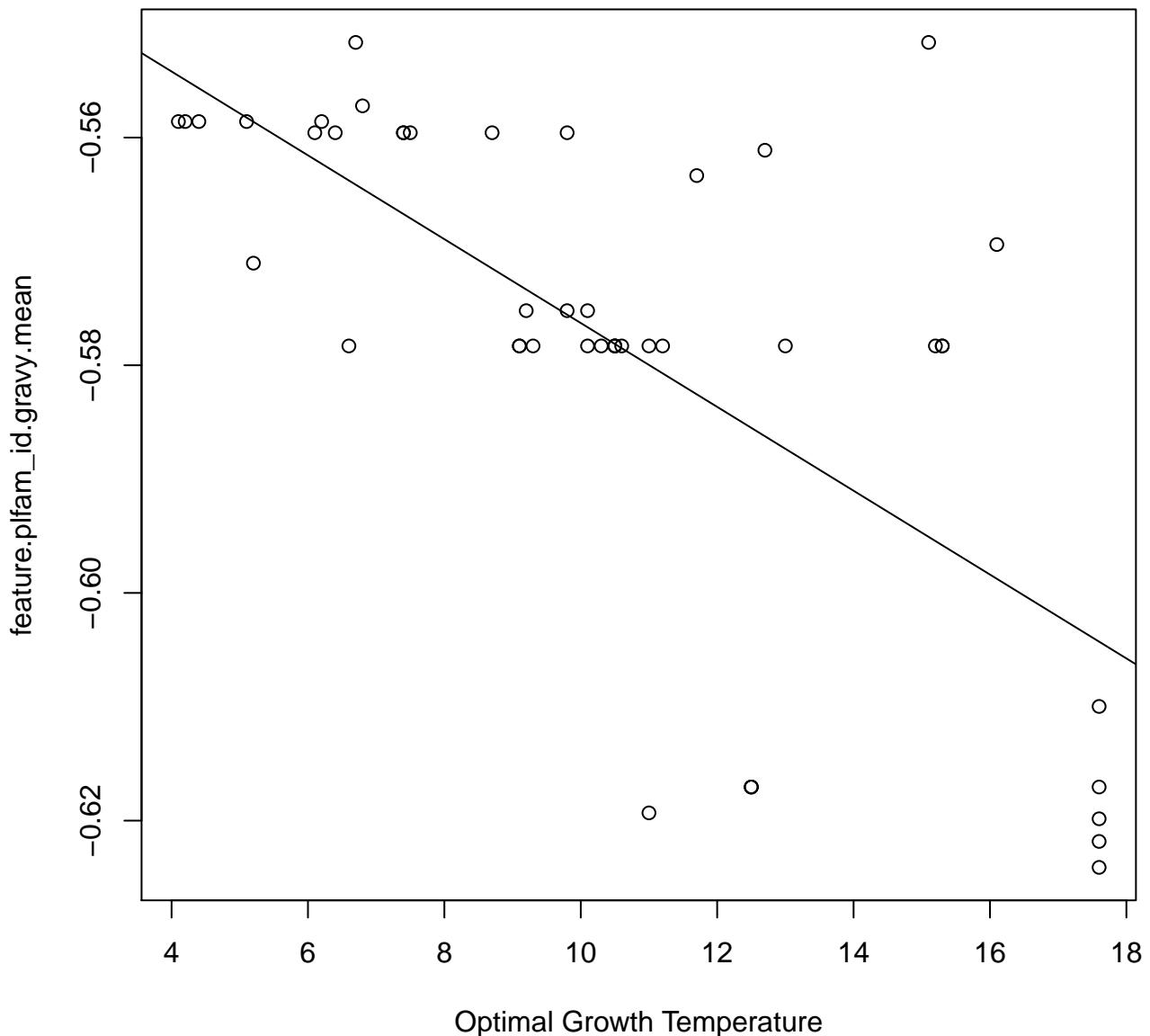
feature.plfam_id.gravy.mean
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Glucose-methanol-choline (GMC) oxidoreductase:NAD binding site



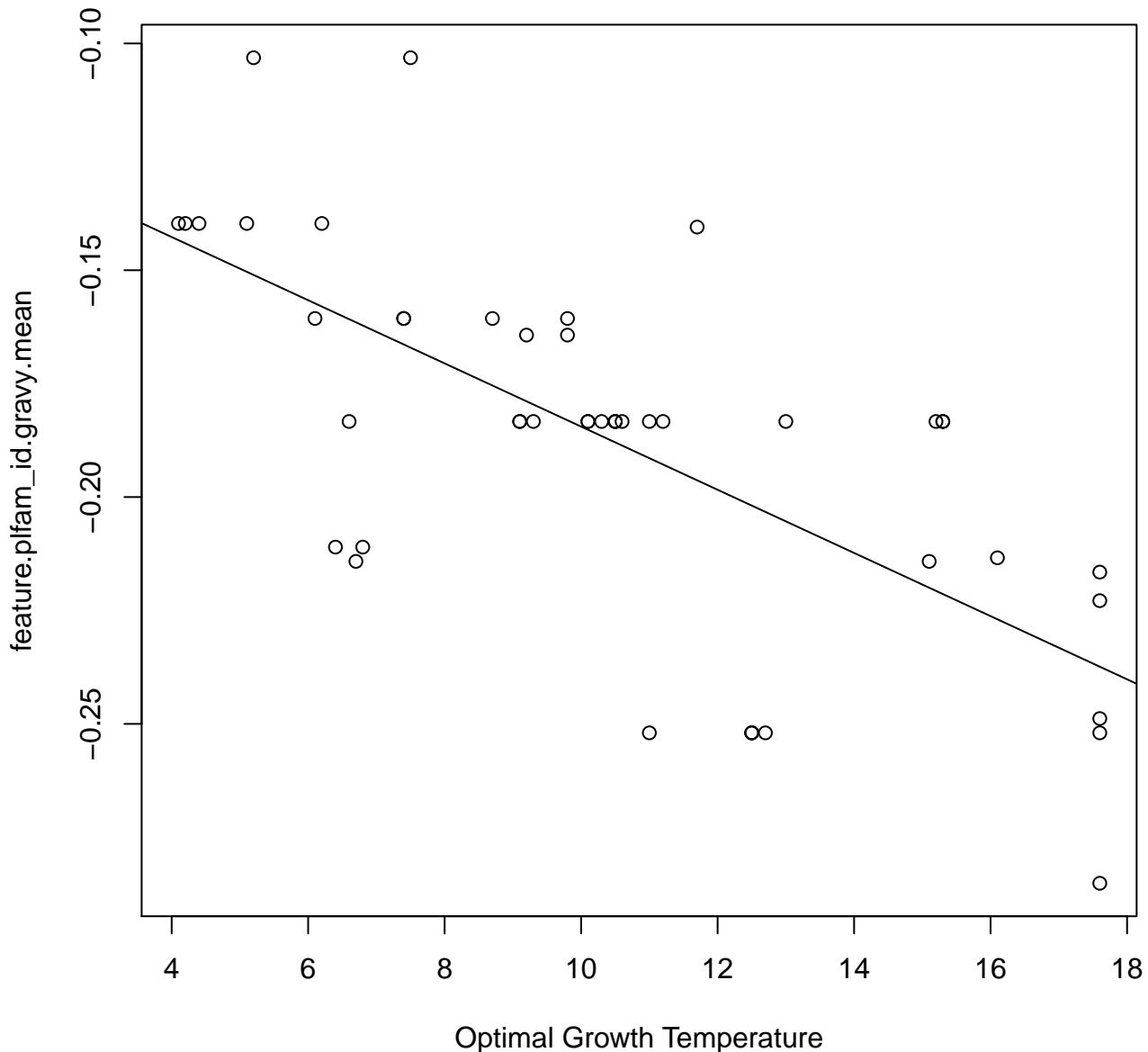
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hypothetical protein



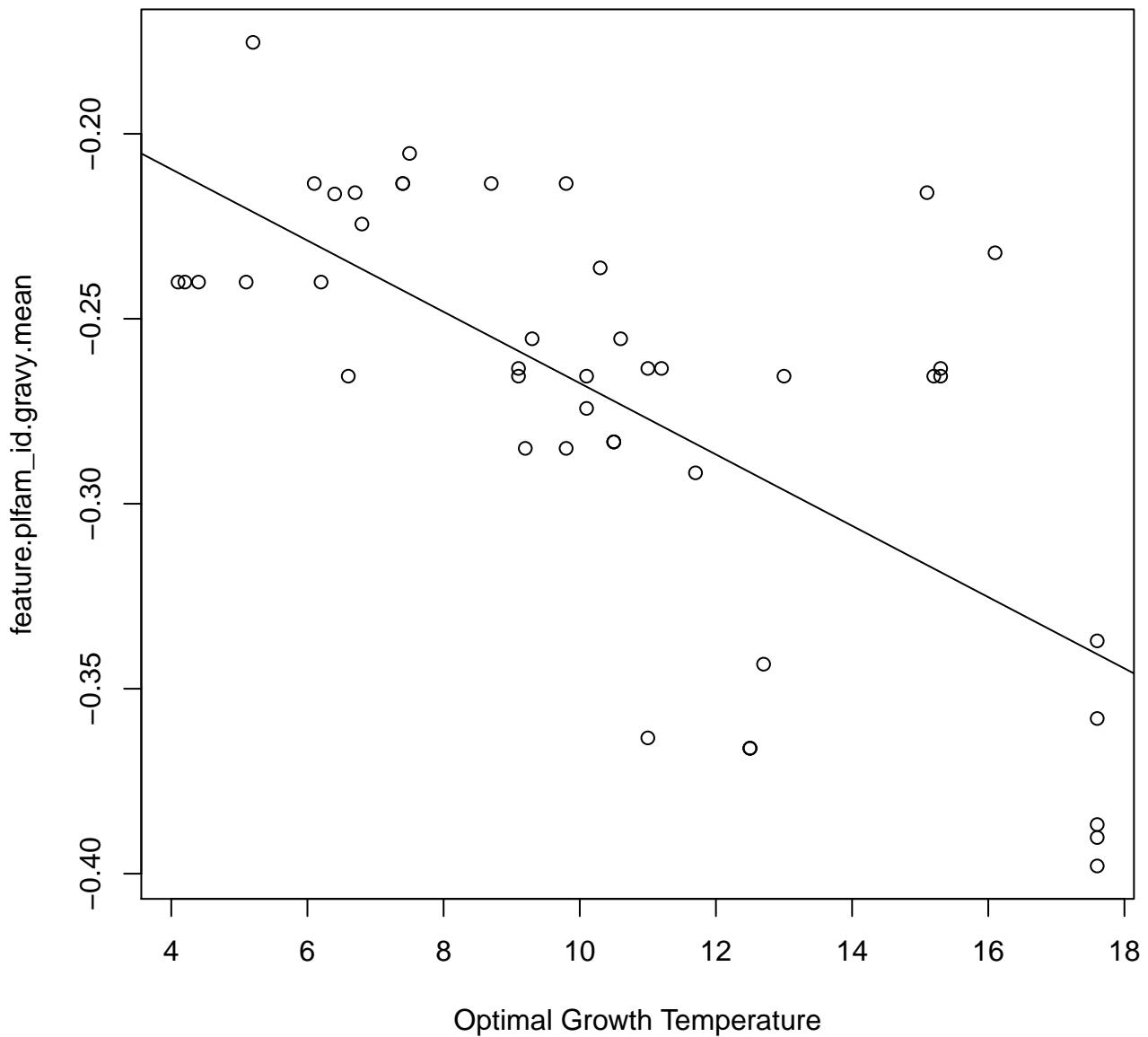
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RNA polymerase sigma factor RpoD



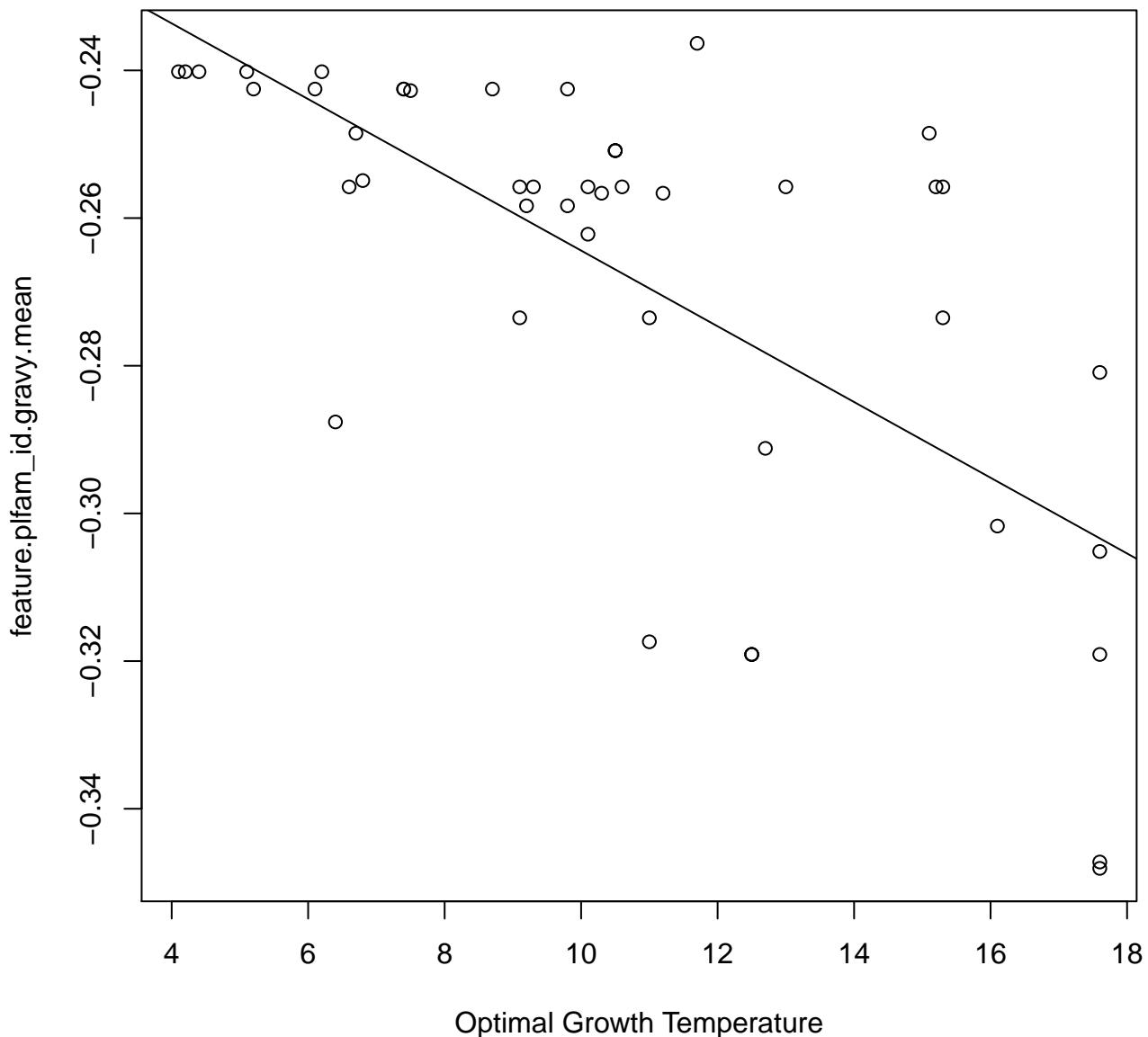
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Iron-sulfur cluster assembly scaffold protein IscU



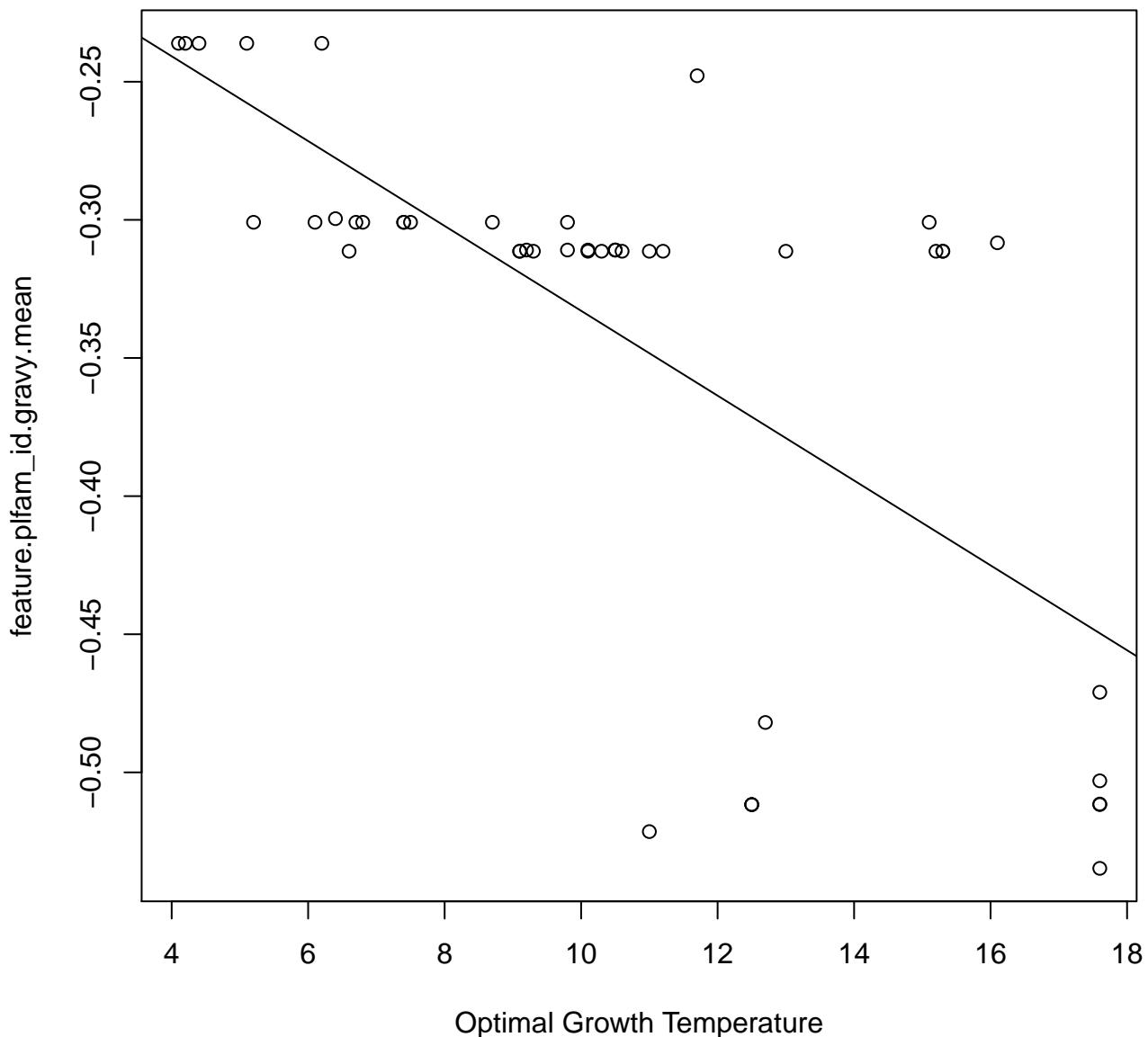
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NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.13)



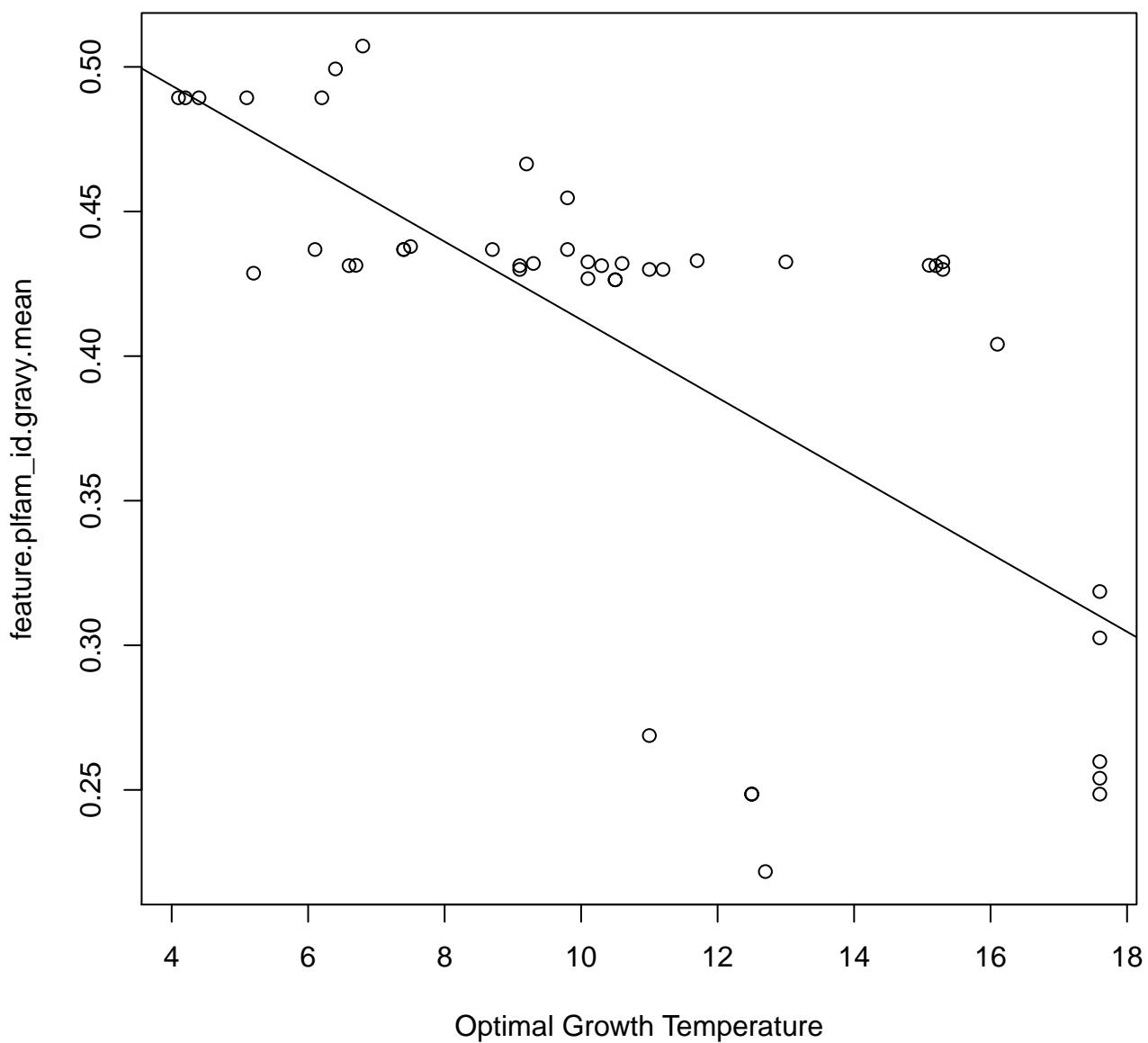
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Nitrogen regulation protein NR(I), GlnG (=NtrC)



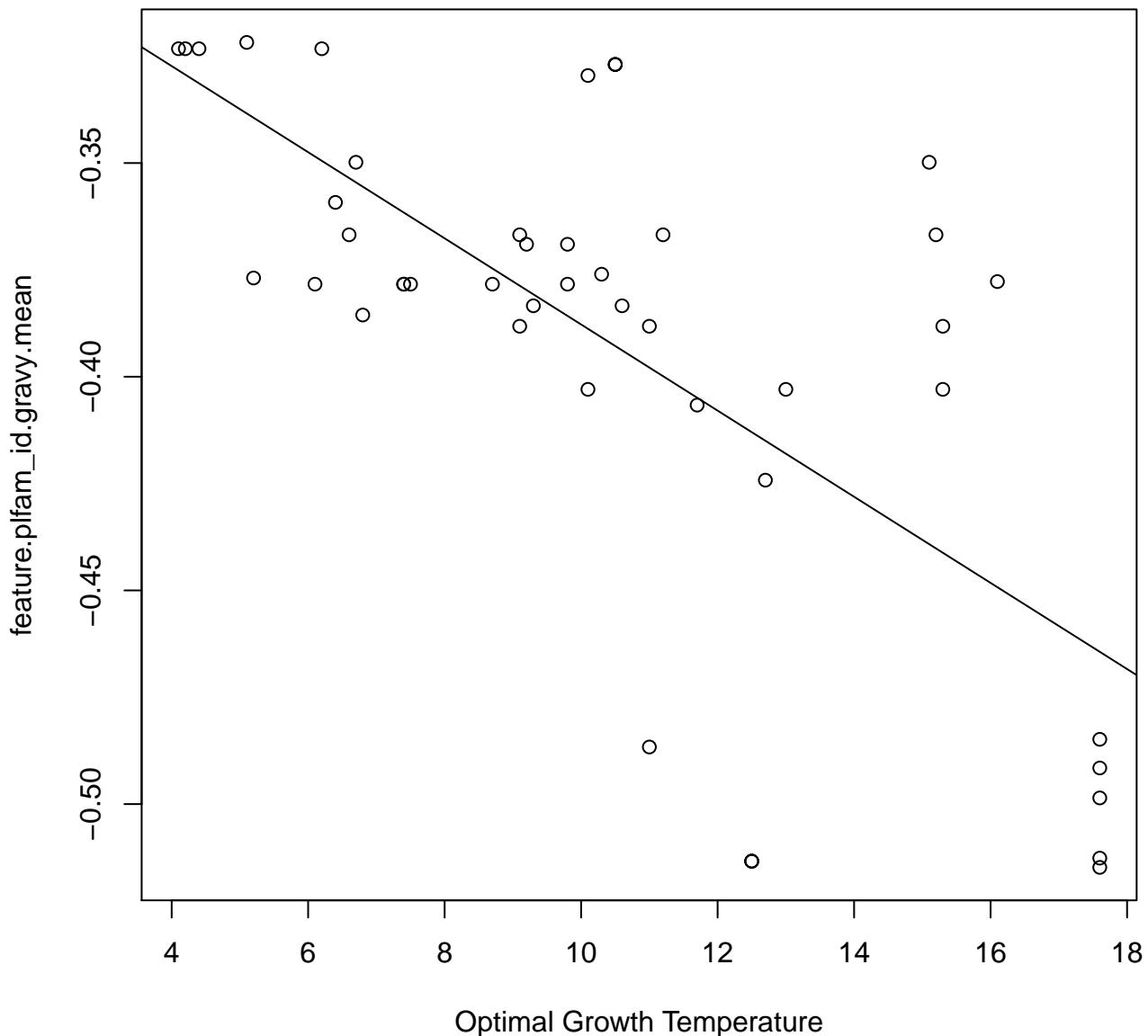
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Ribonuclease III (EC 3.1.26.3)



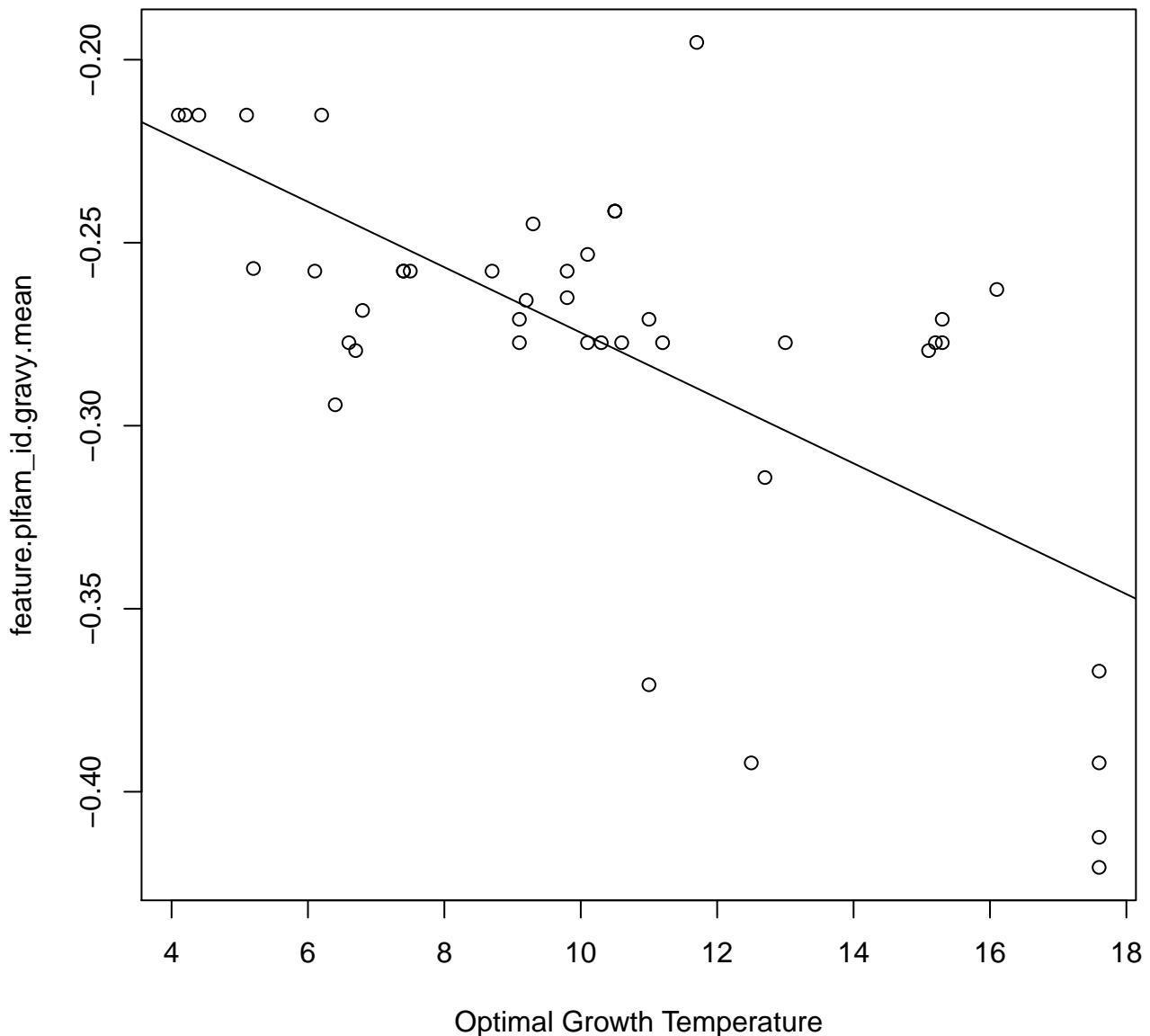
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AmpE protein



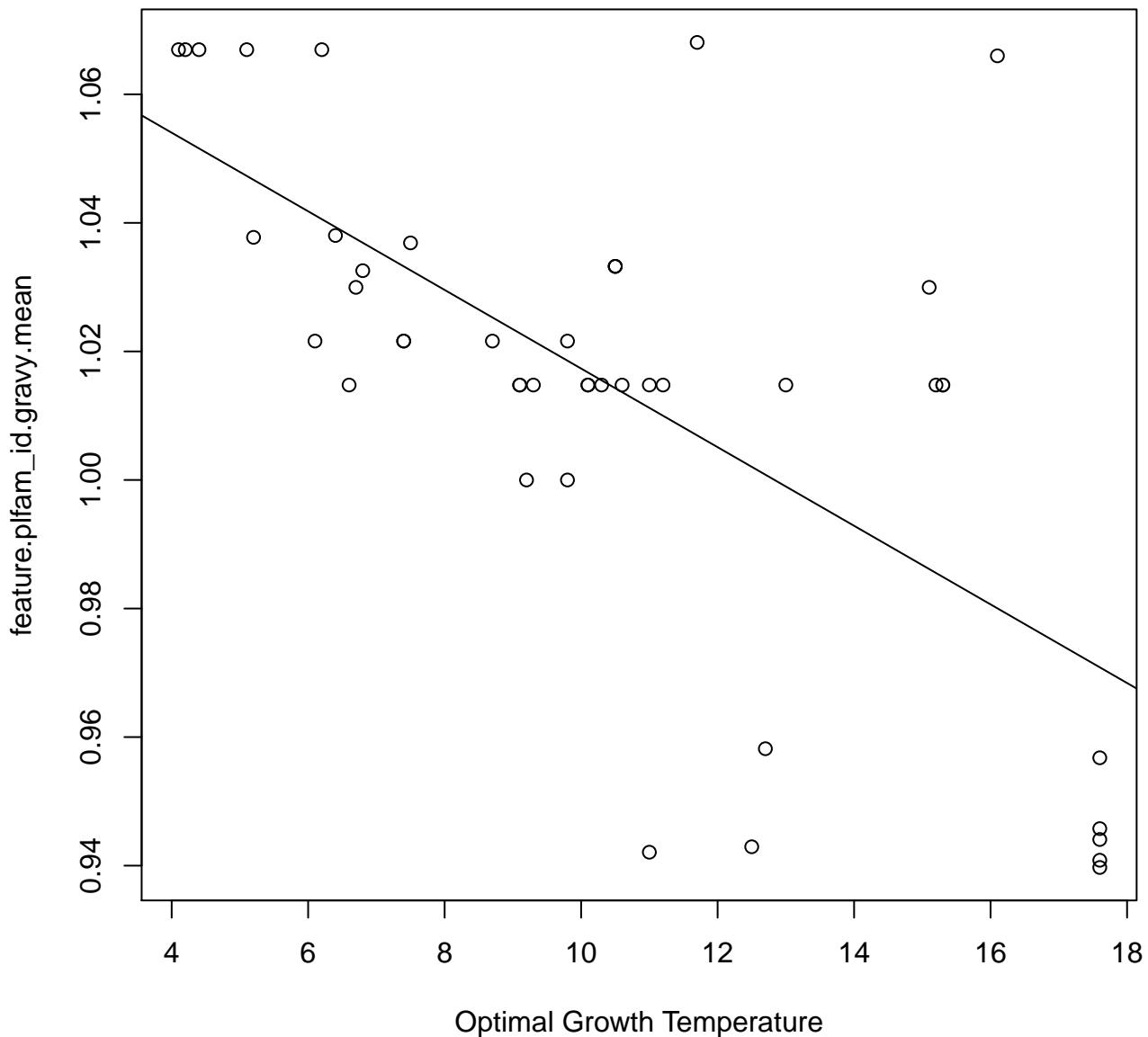
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23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)



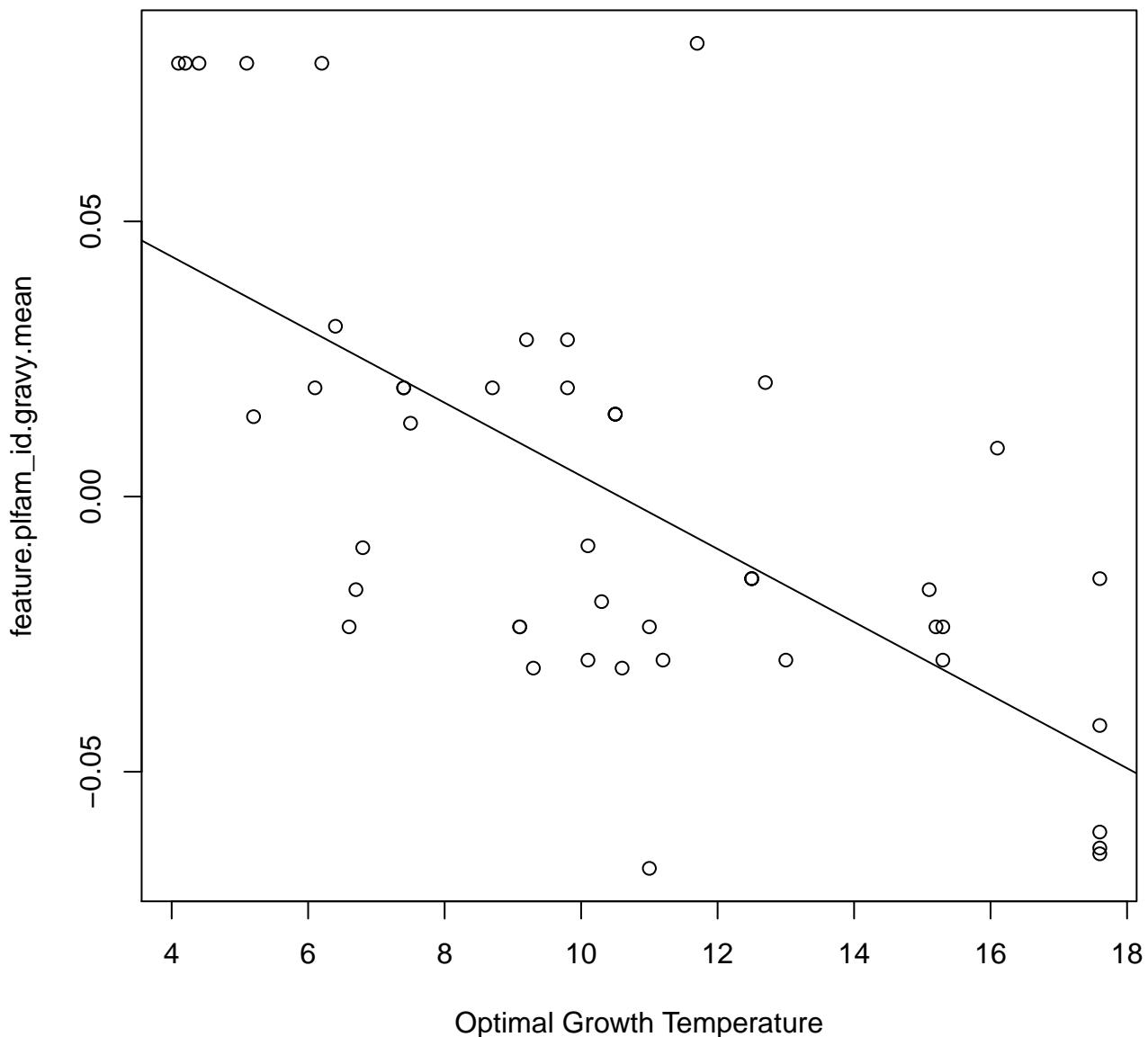
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TPR domain protein, putative component of TonB system



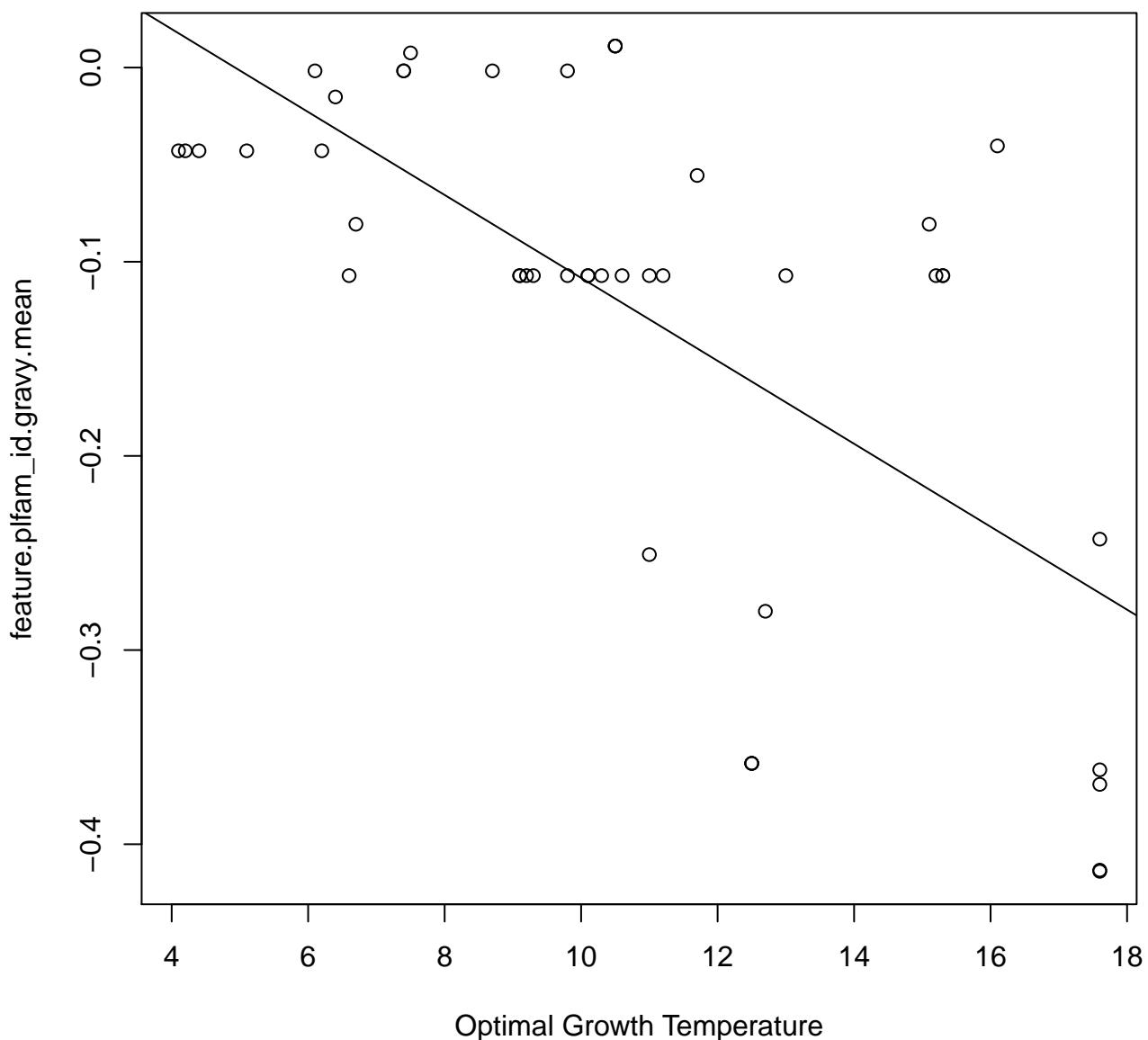
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Uncharacterized UPF0118 membrane protein



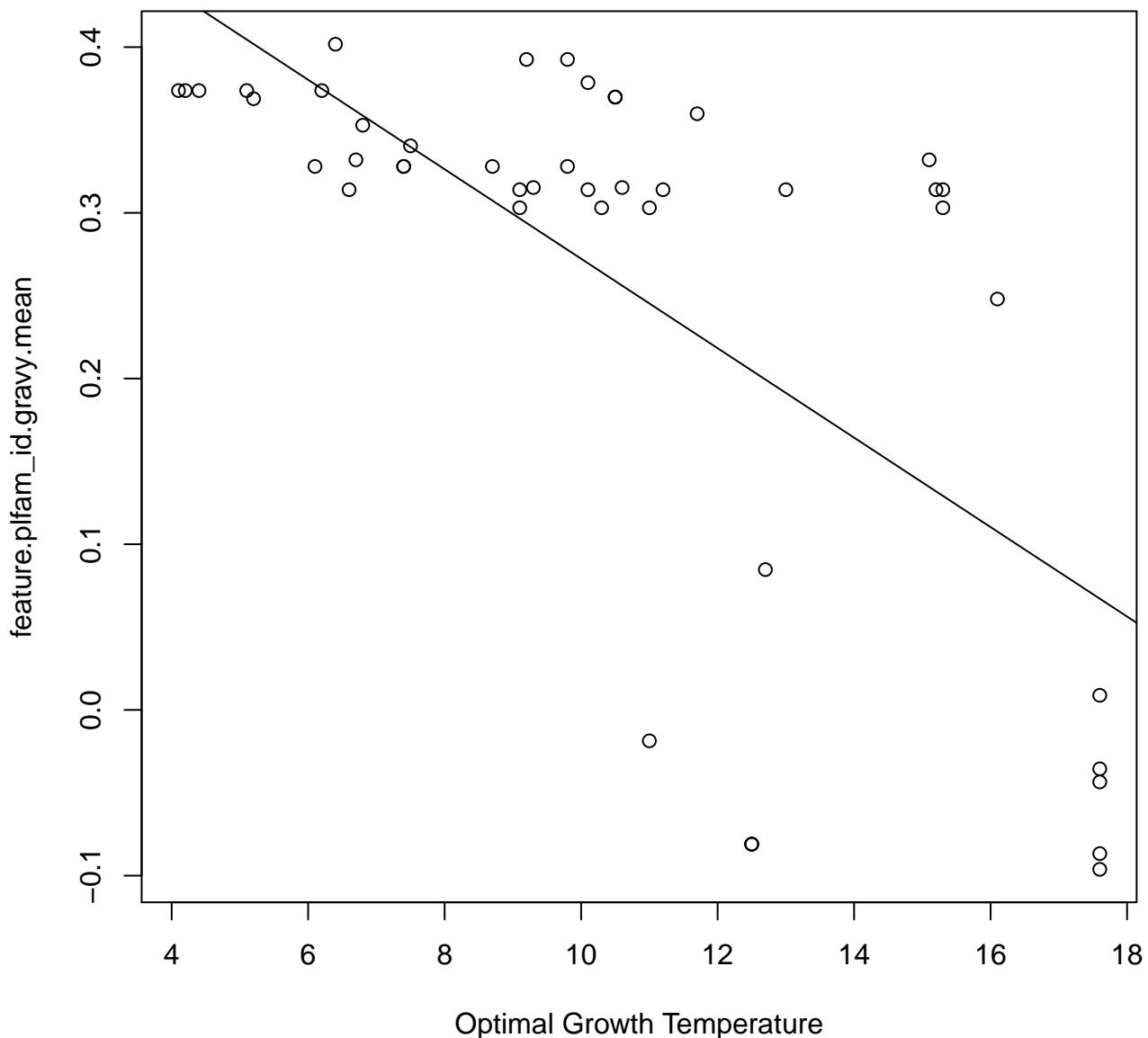
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Orn/DAP/Arg family decarboxylase



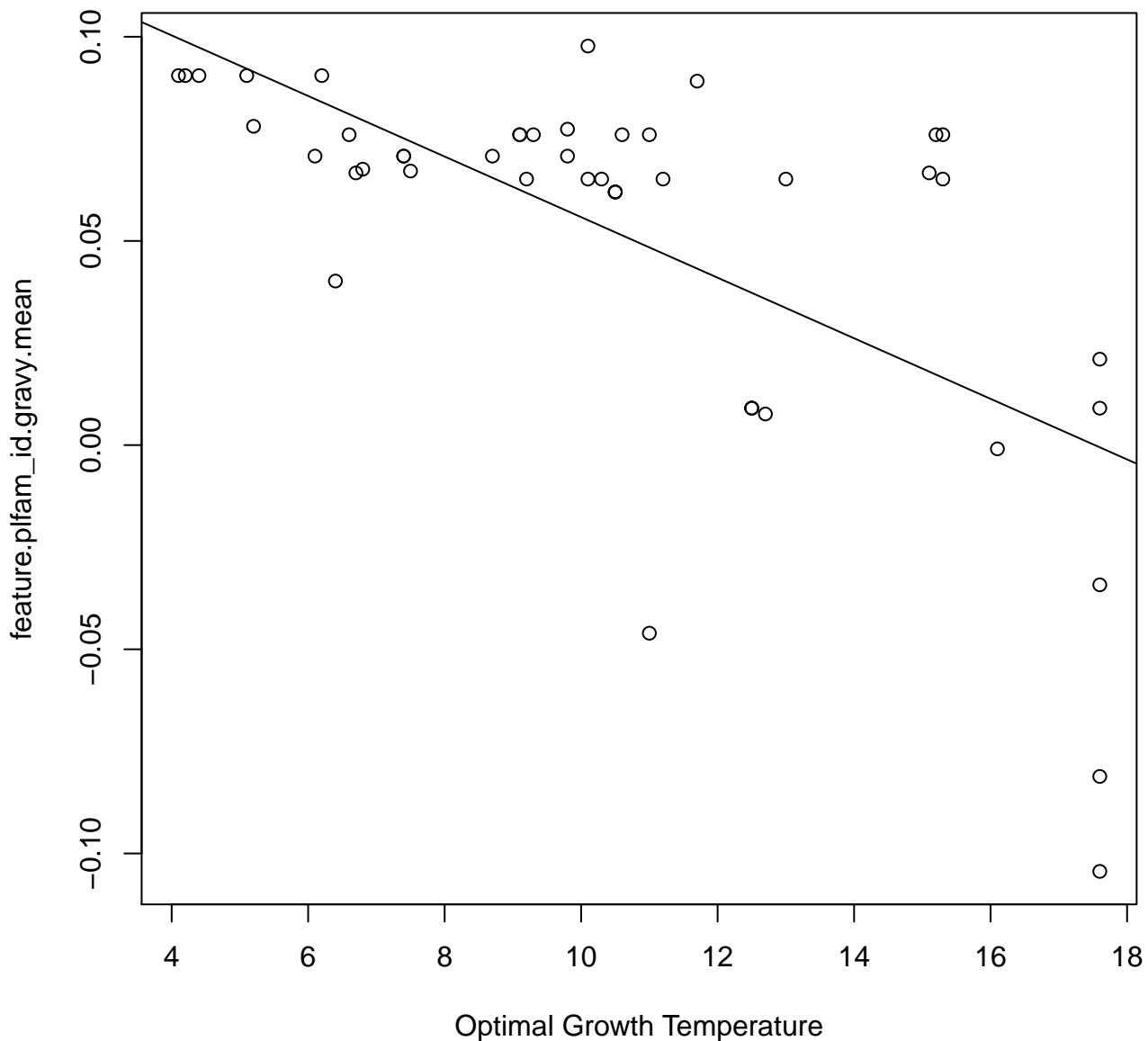
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hypothetical protein



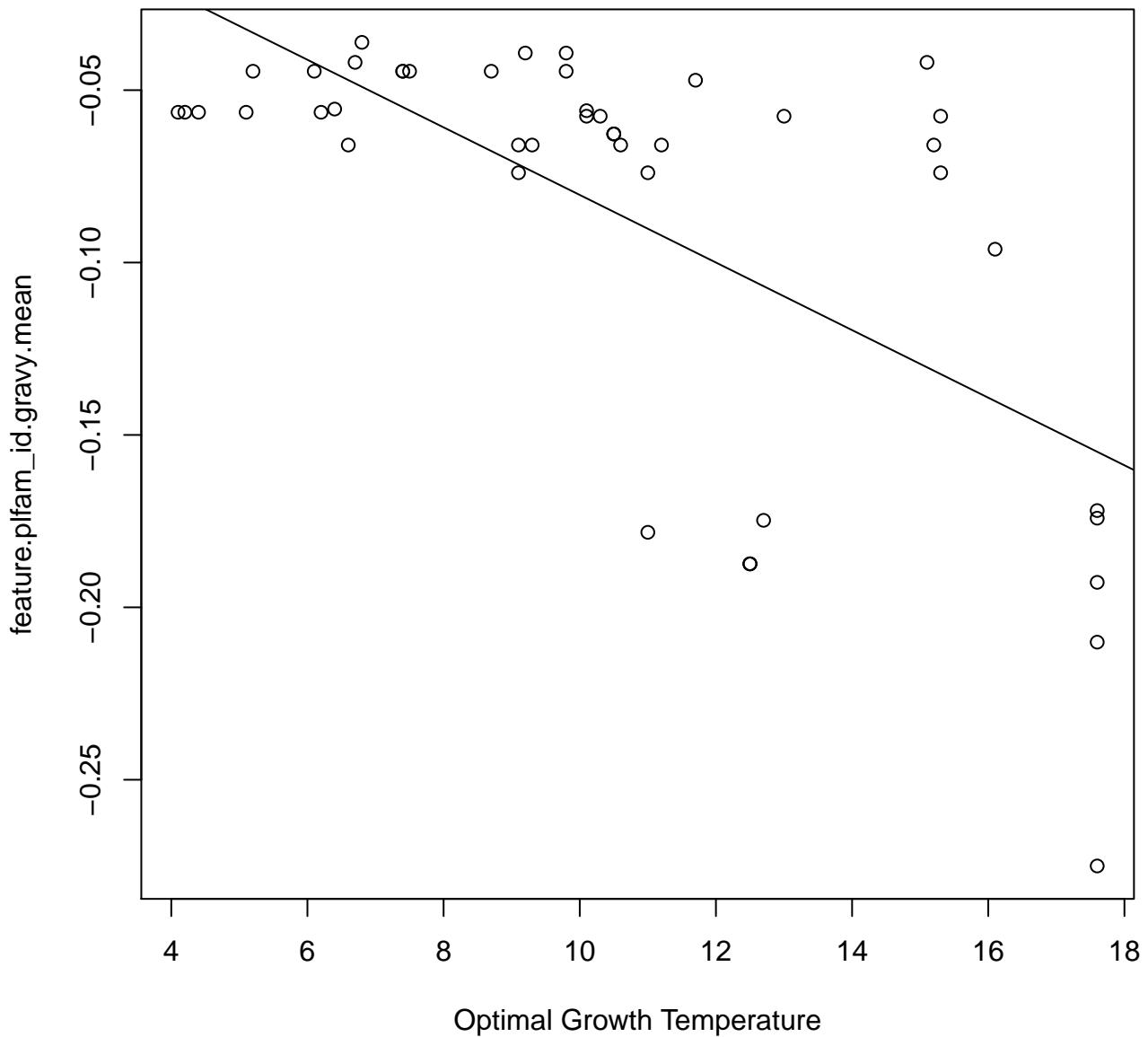
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Dethiobiotin synthase BioD (EC 6.3.3.3)



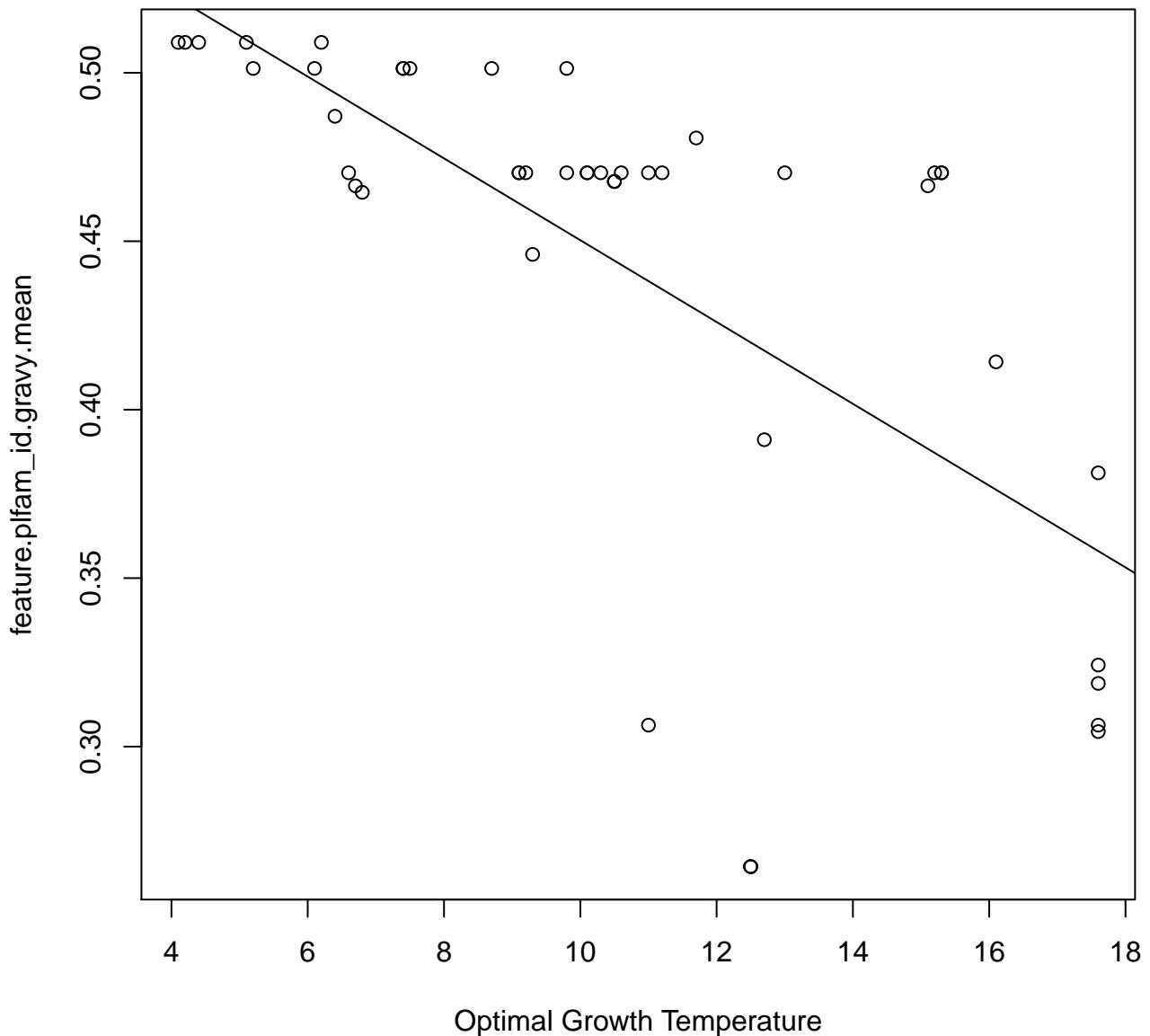
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Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)



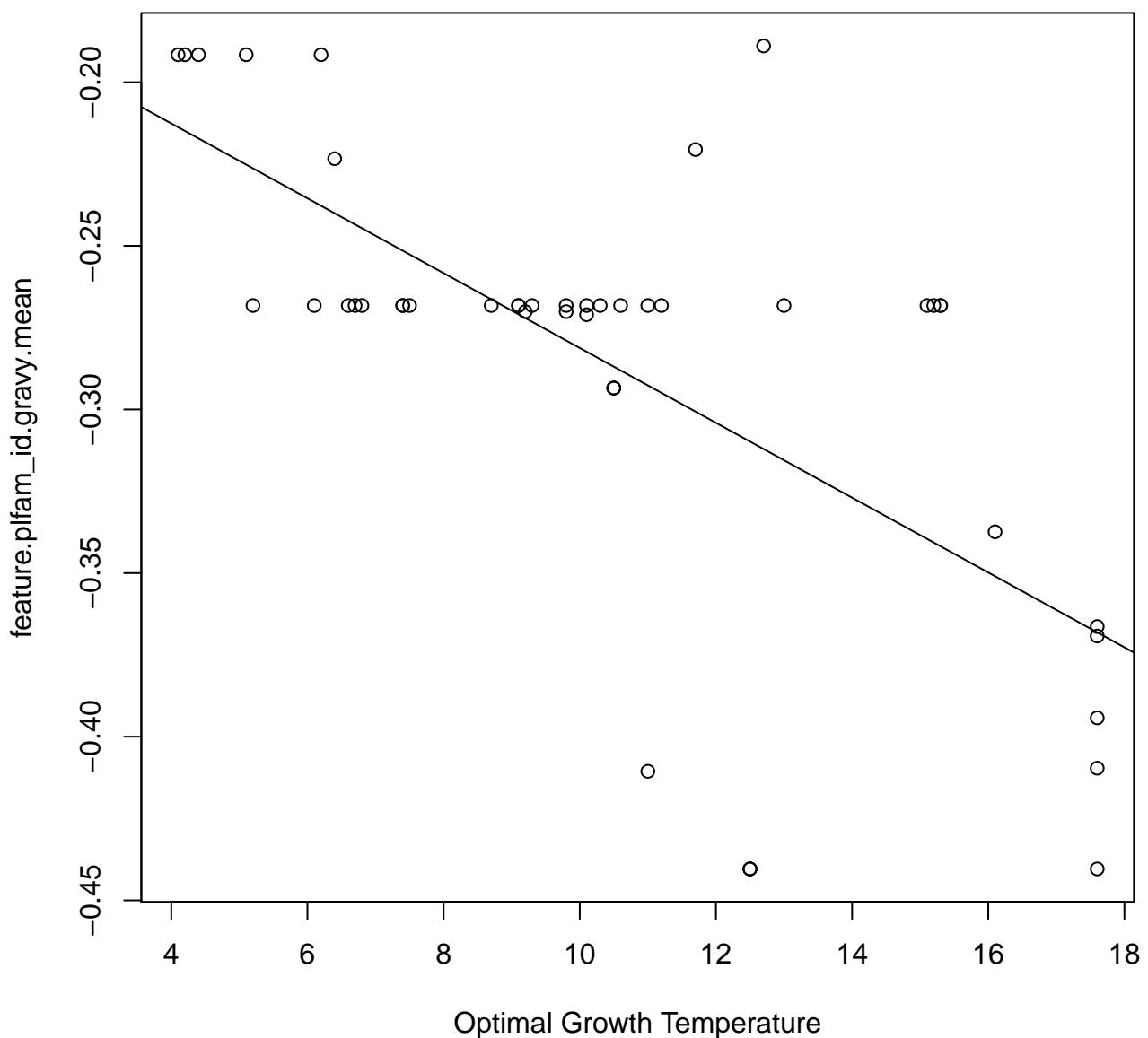
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Porphobilinogen deaminase (EC 2.5.1.61)



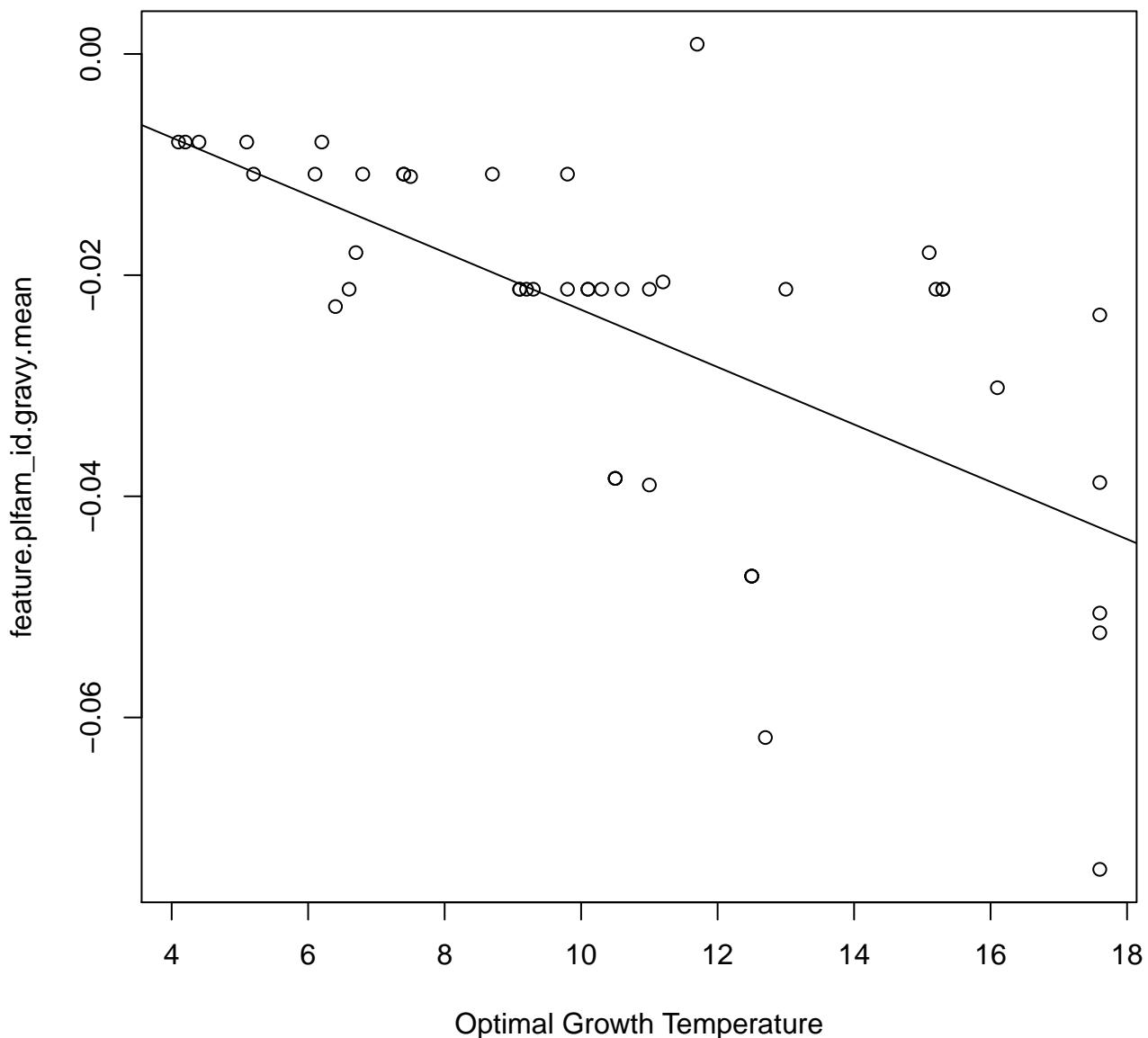
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Phospholipid ABC transporter substrate-binding protein MlaD



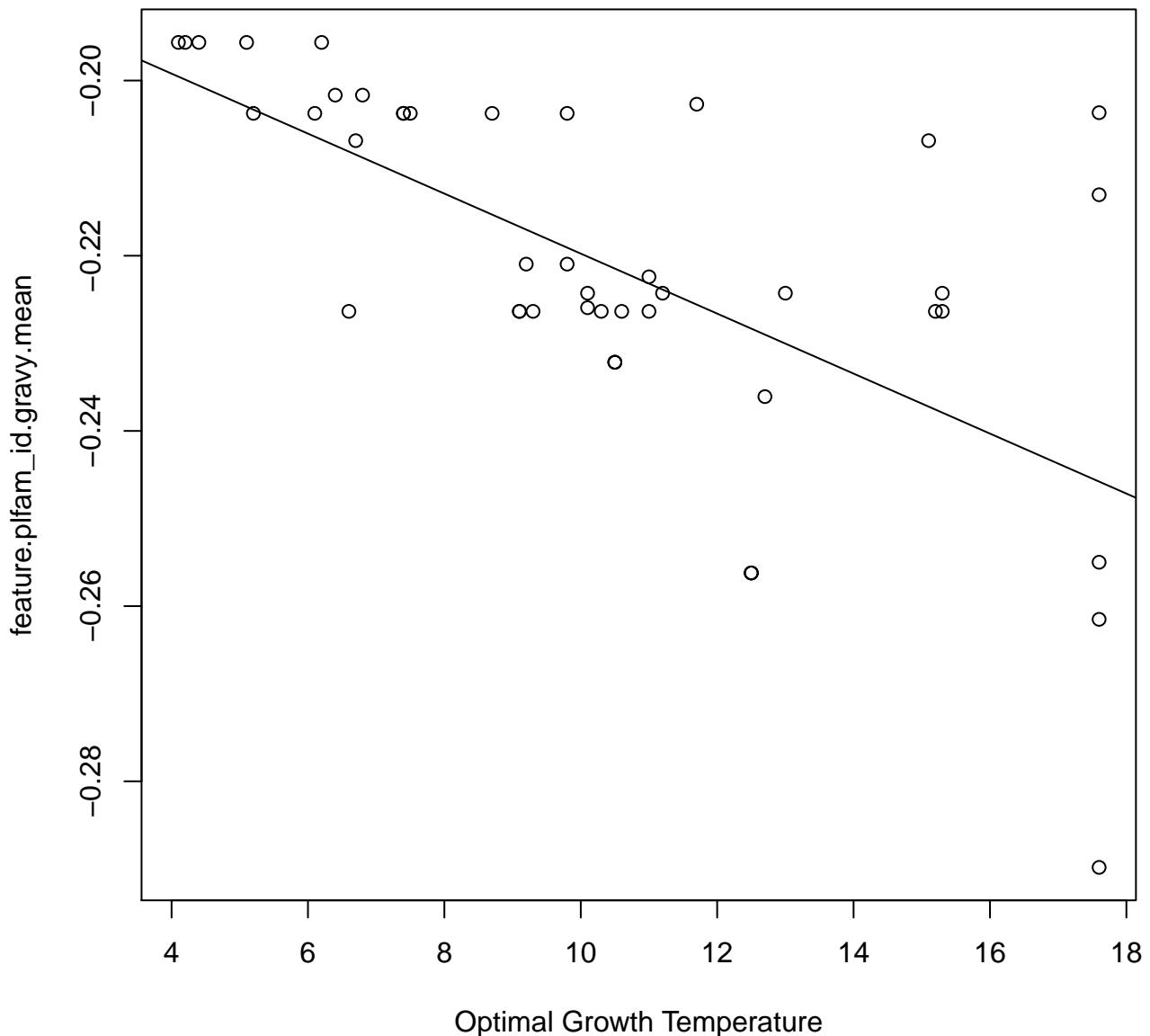
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Cell division protein BolA



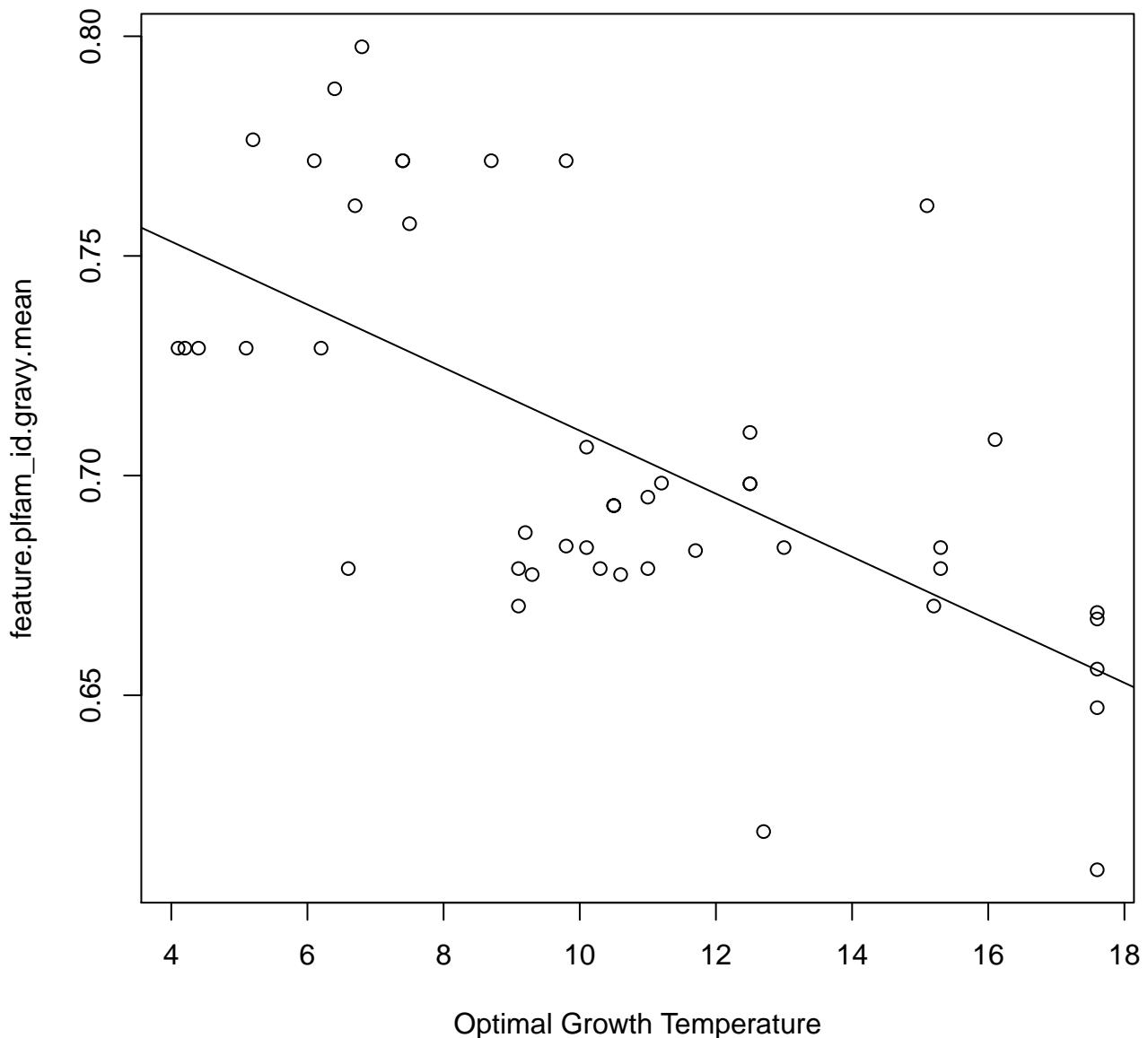
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Flagellum-specific ATP synthase Flil



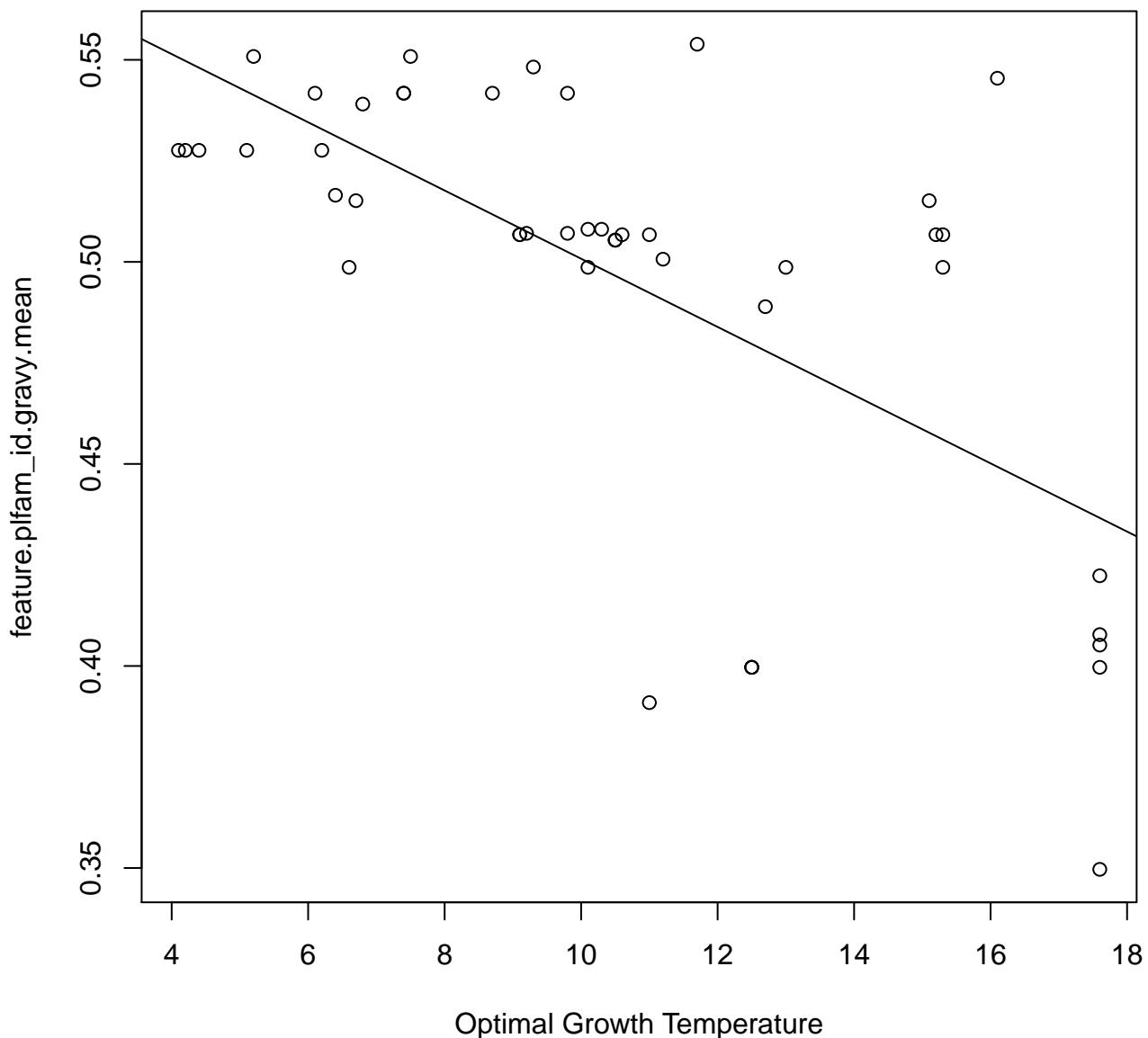
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DNA-binding transcriptional regulator, MocR family / aminotransferase domain



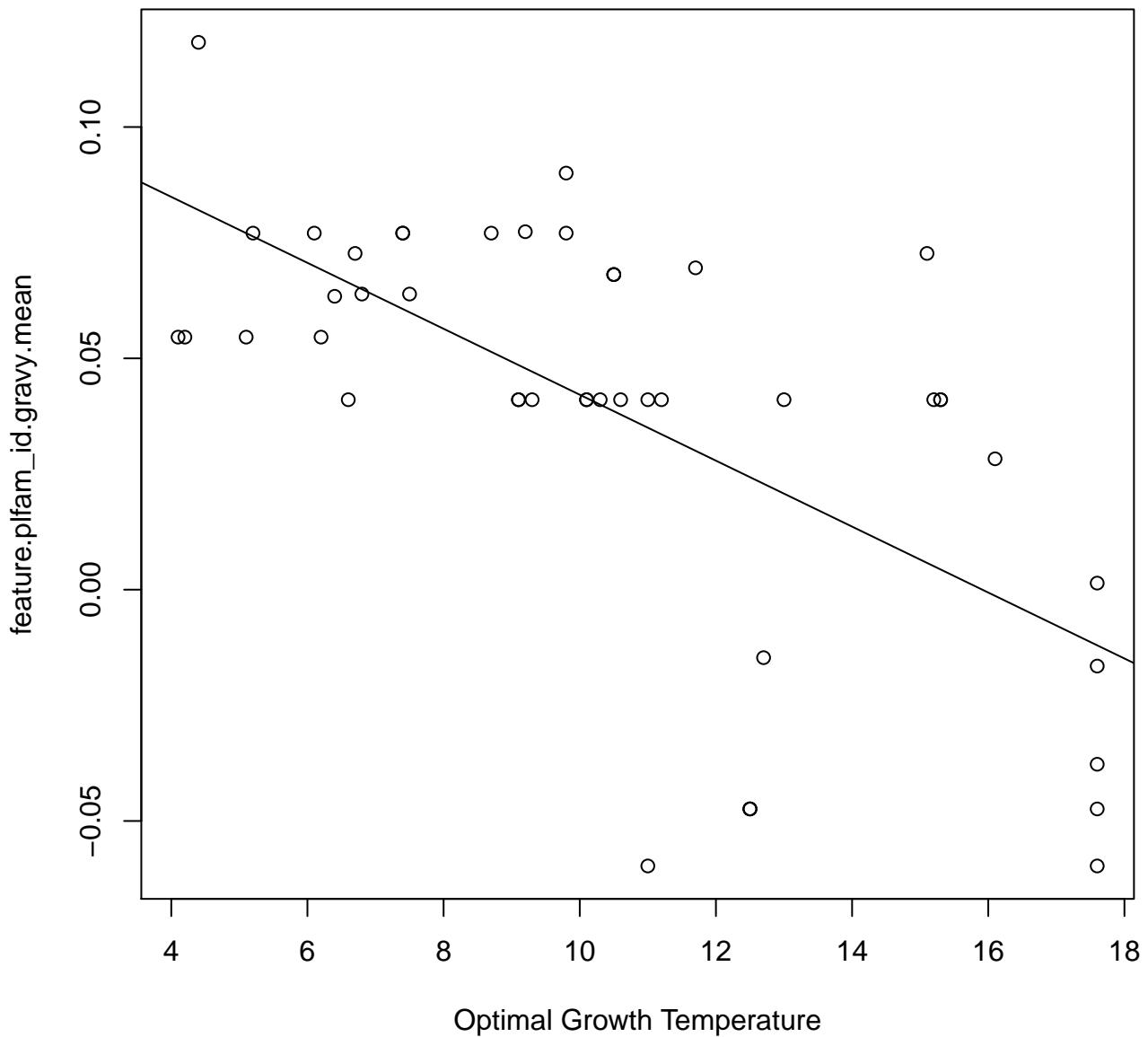
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Leader peptidase (Prephilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-)



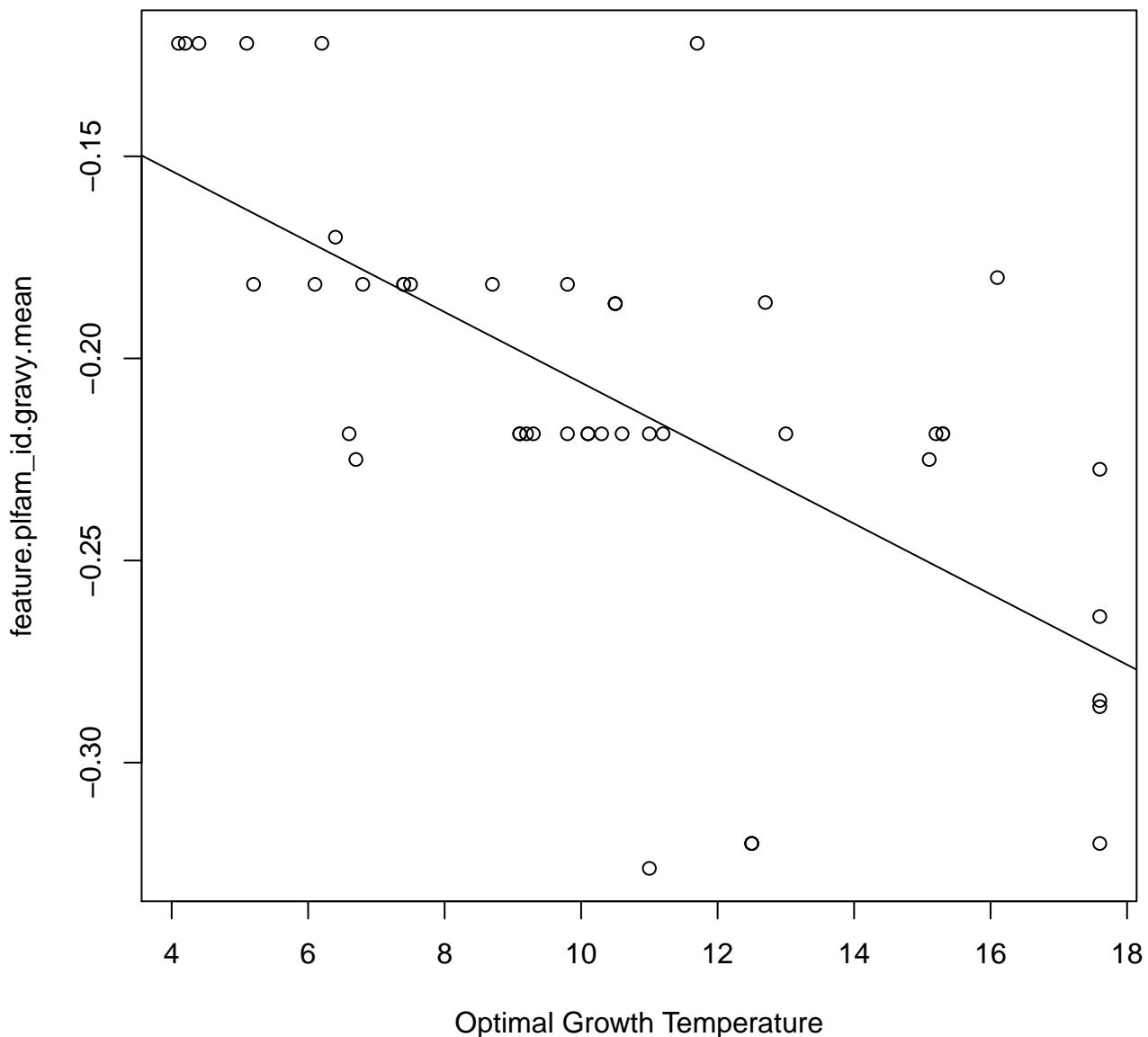
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Mechanosensitive ion channel family protein



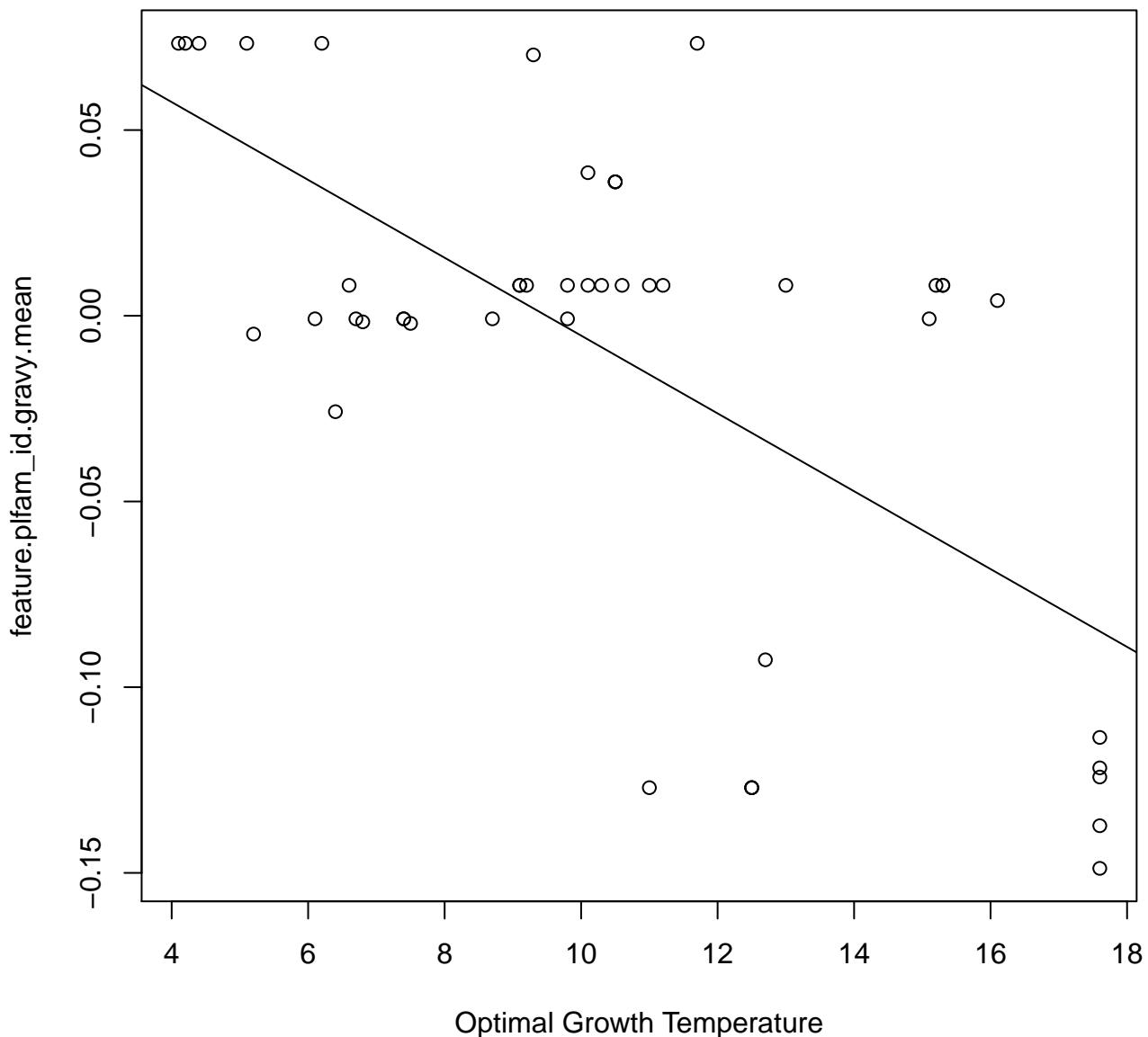
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Holliday junction ATP-dependent DNA helicase RuvA (EC 3.6.4.12)



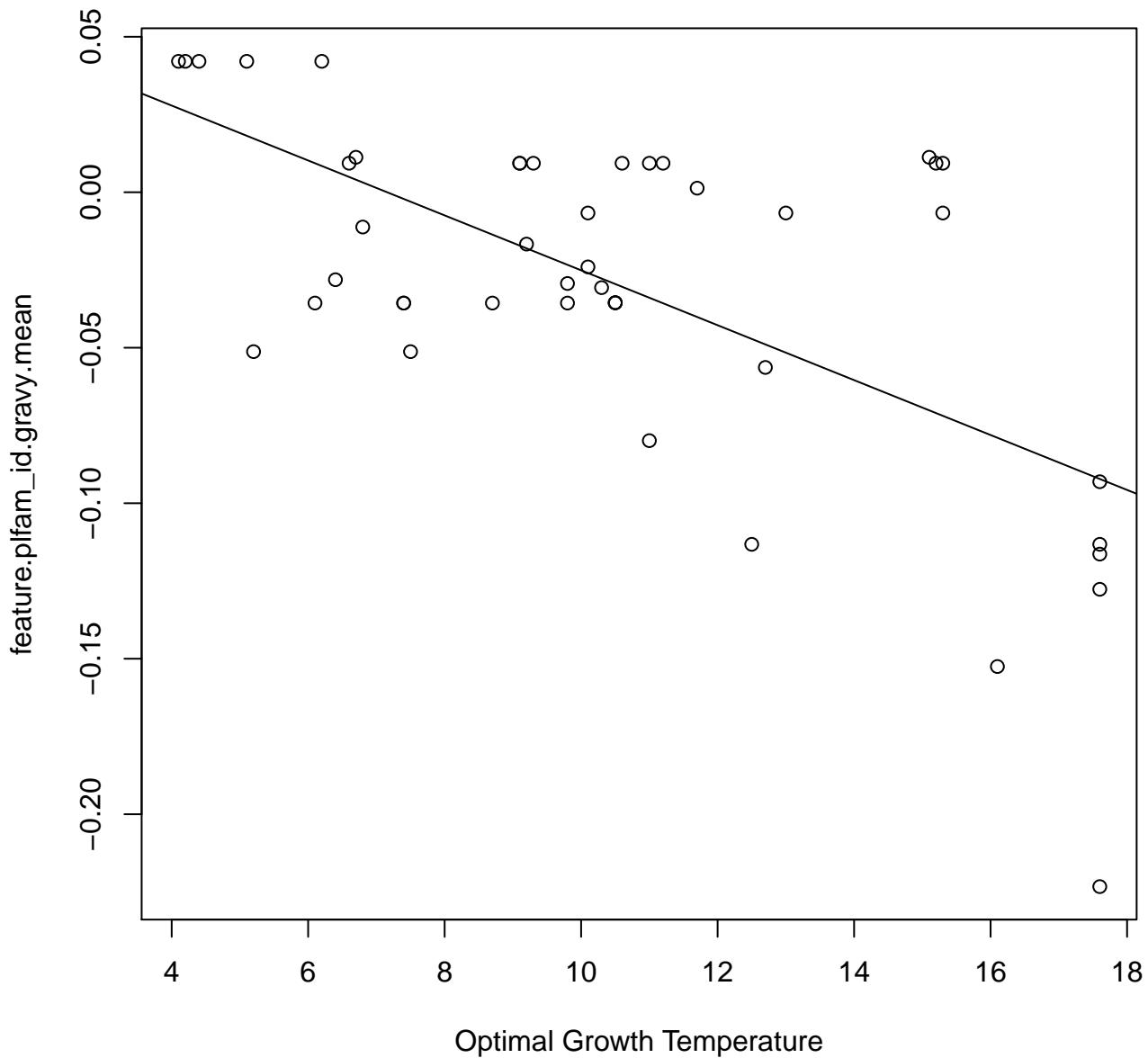
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FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster



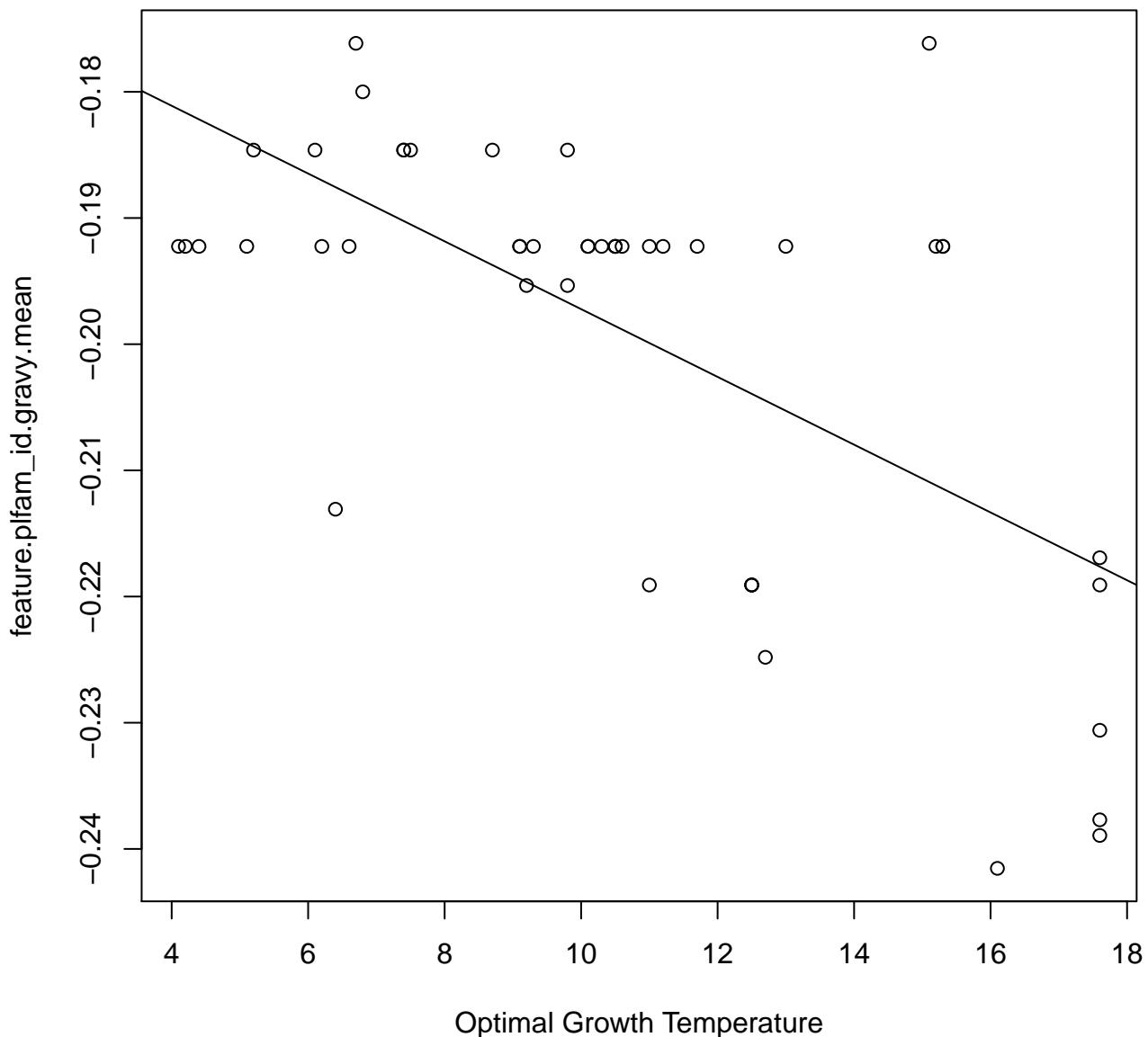
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Carboxy-S-adenosyl-L-methionine synthase



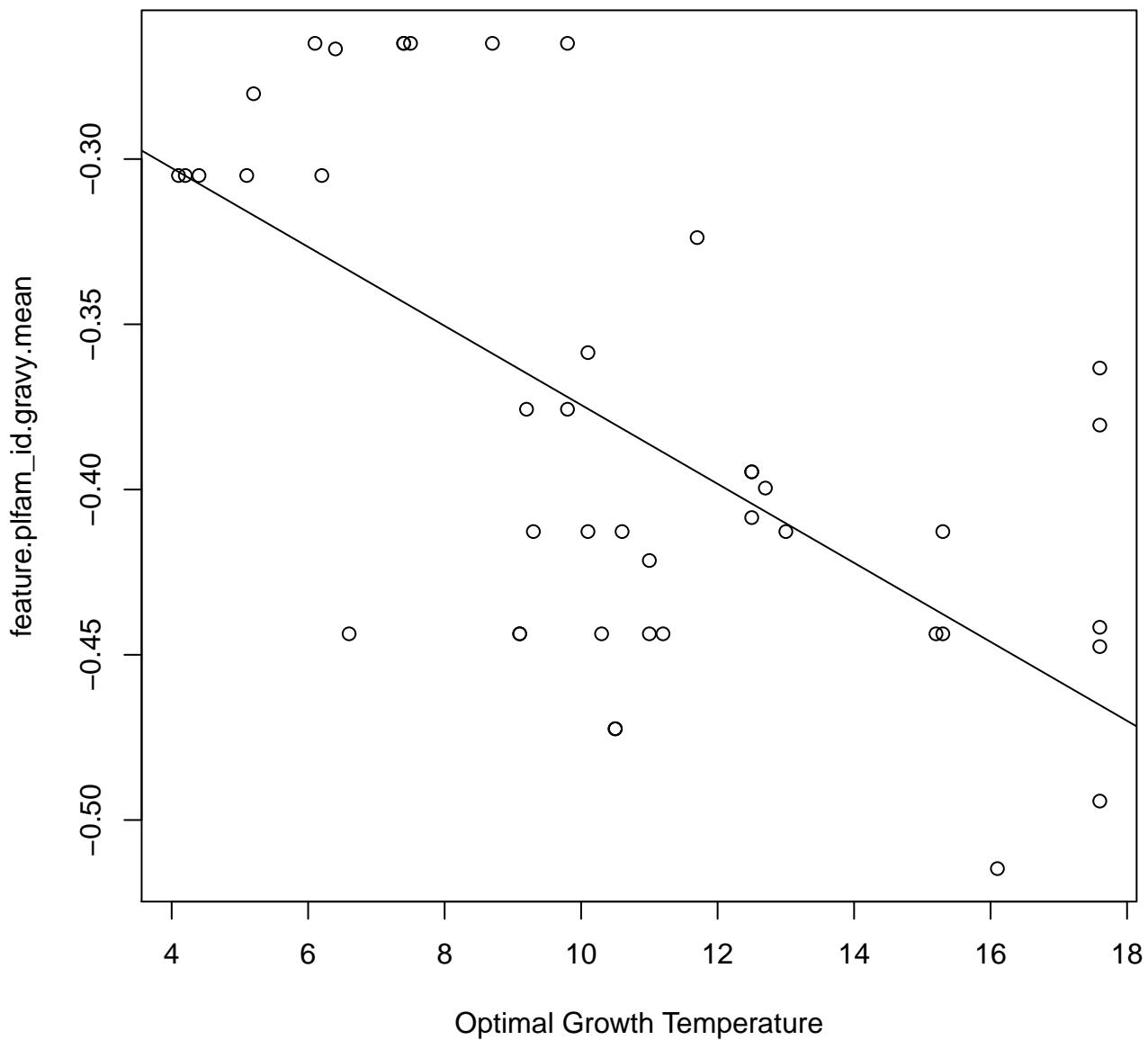
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Stringent starvation protein B



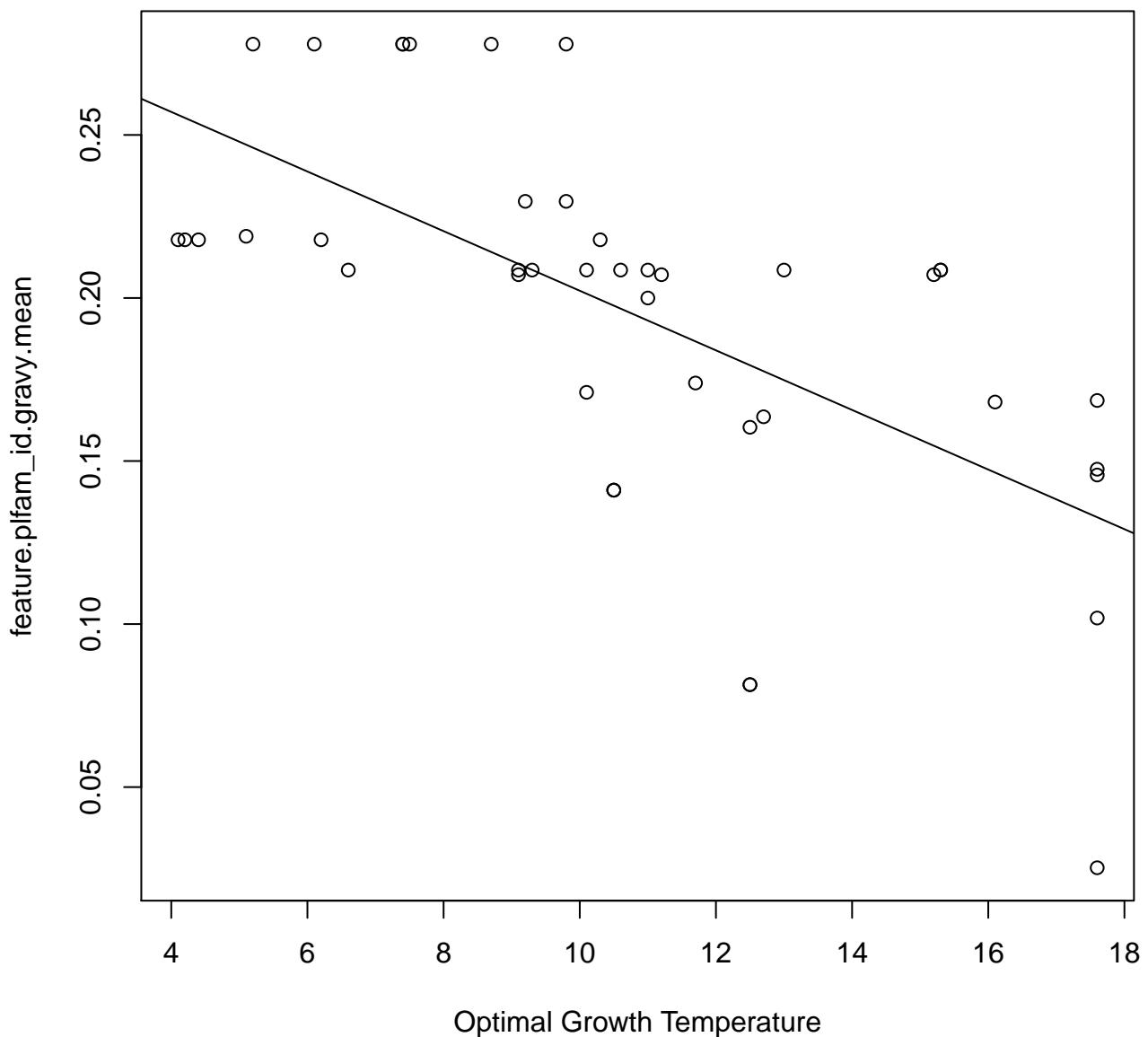
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Flagellar motor switch protein FliN



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PLF_28228_00001927
Potential queD like 2



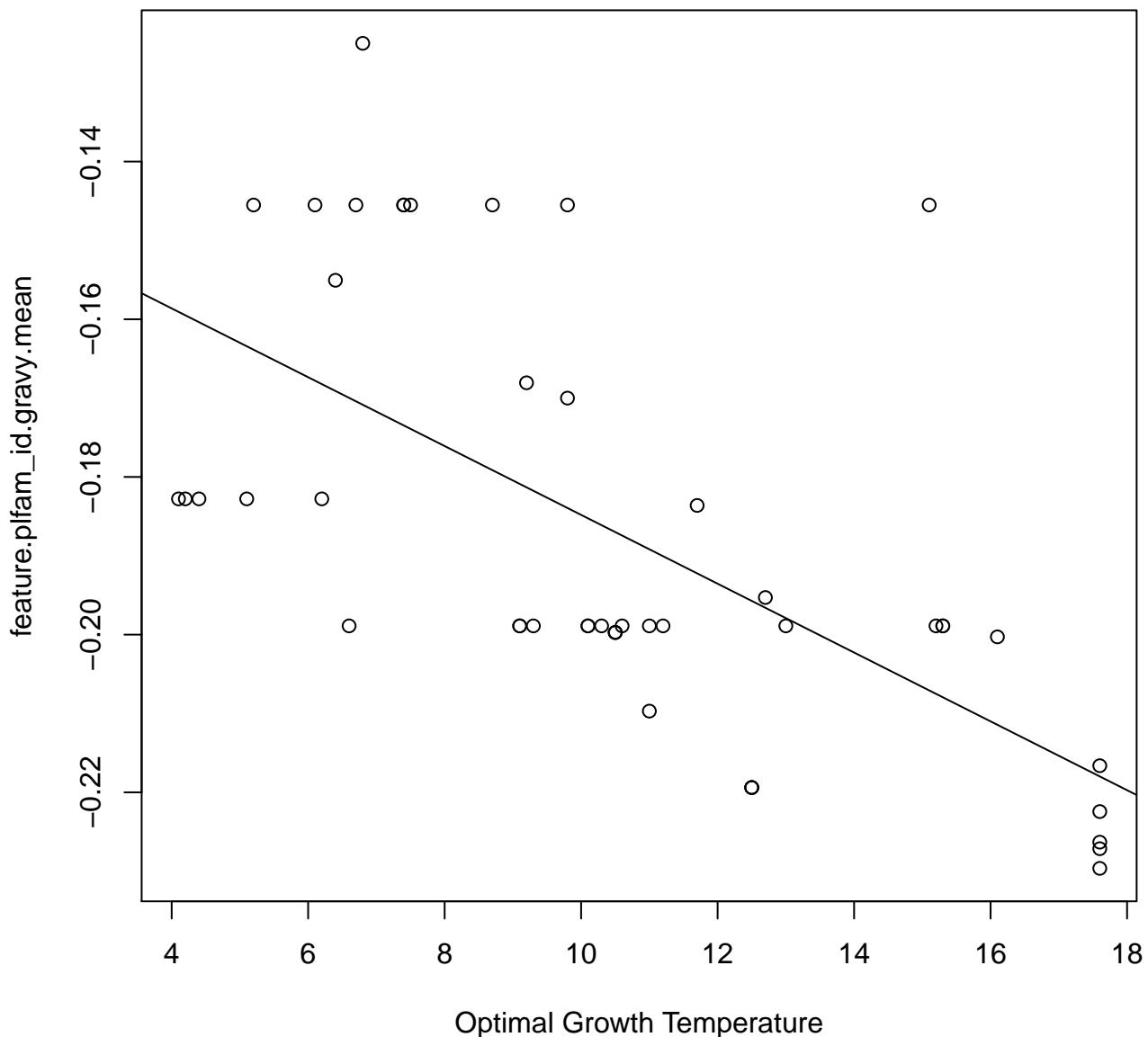
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hypothetical protein



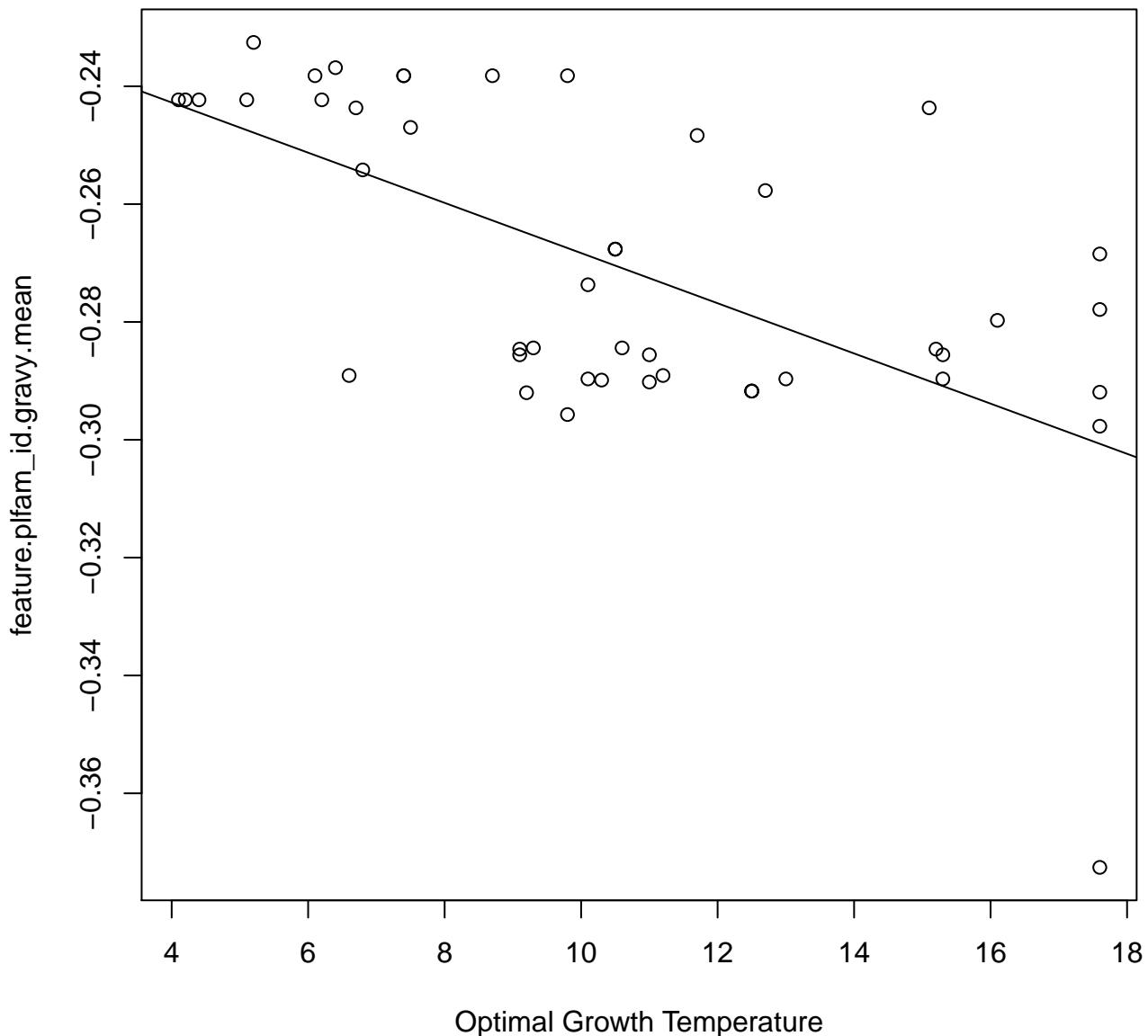
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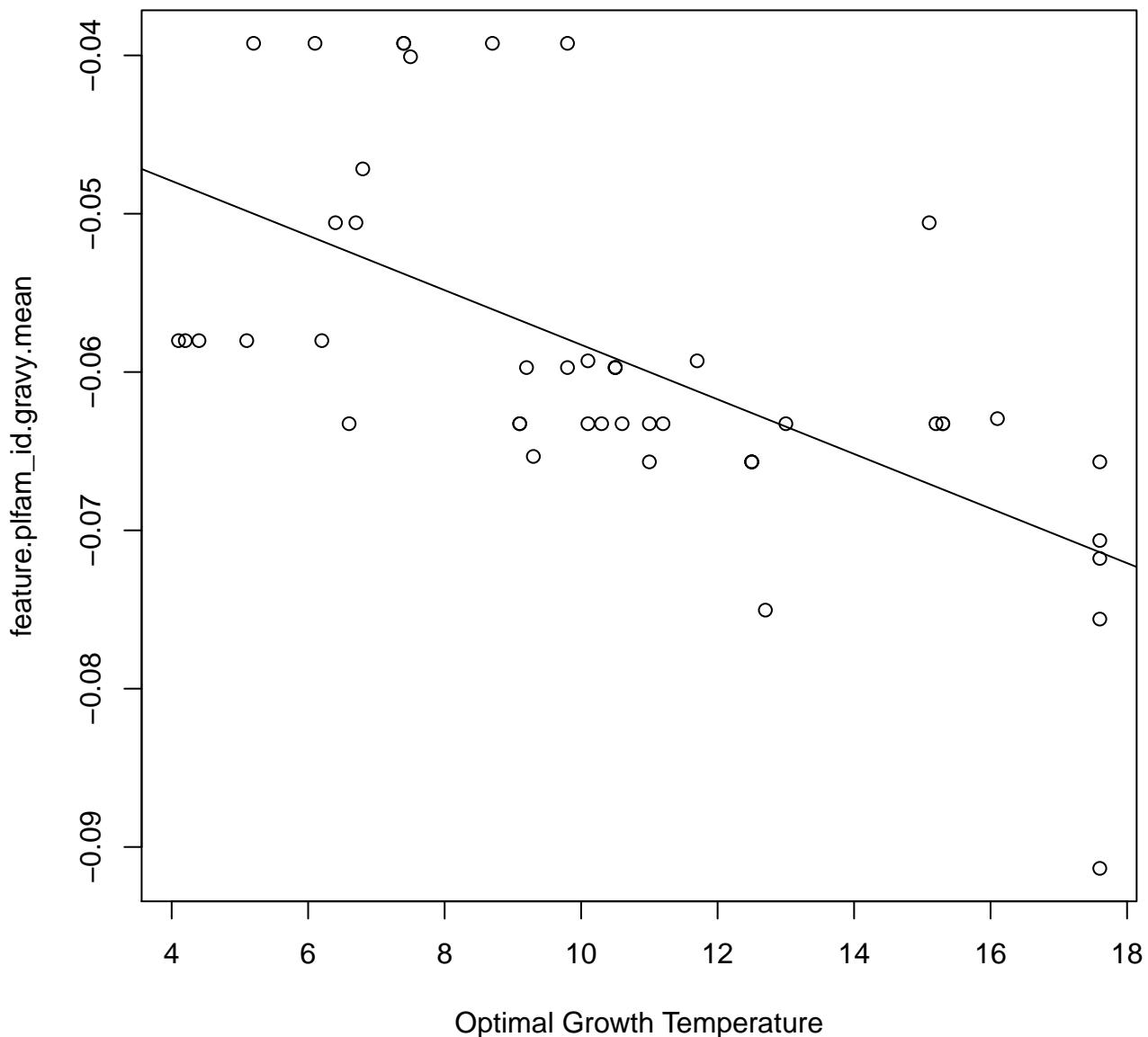
Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)



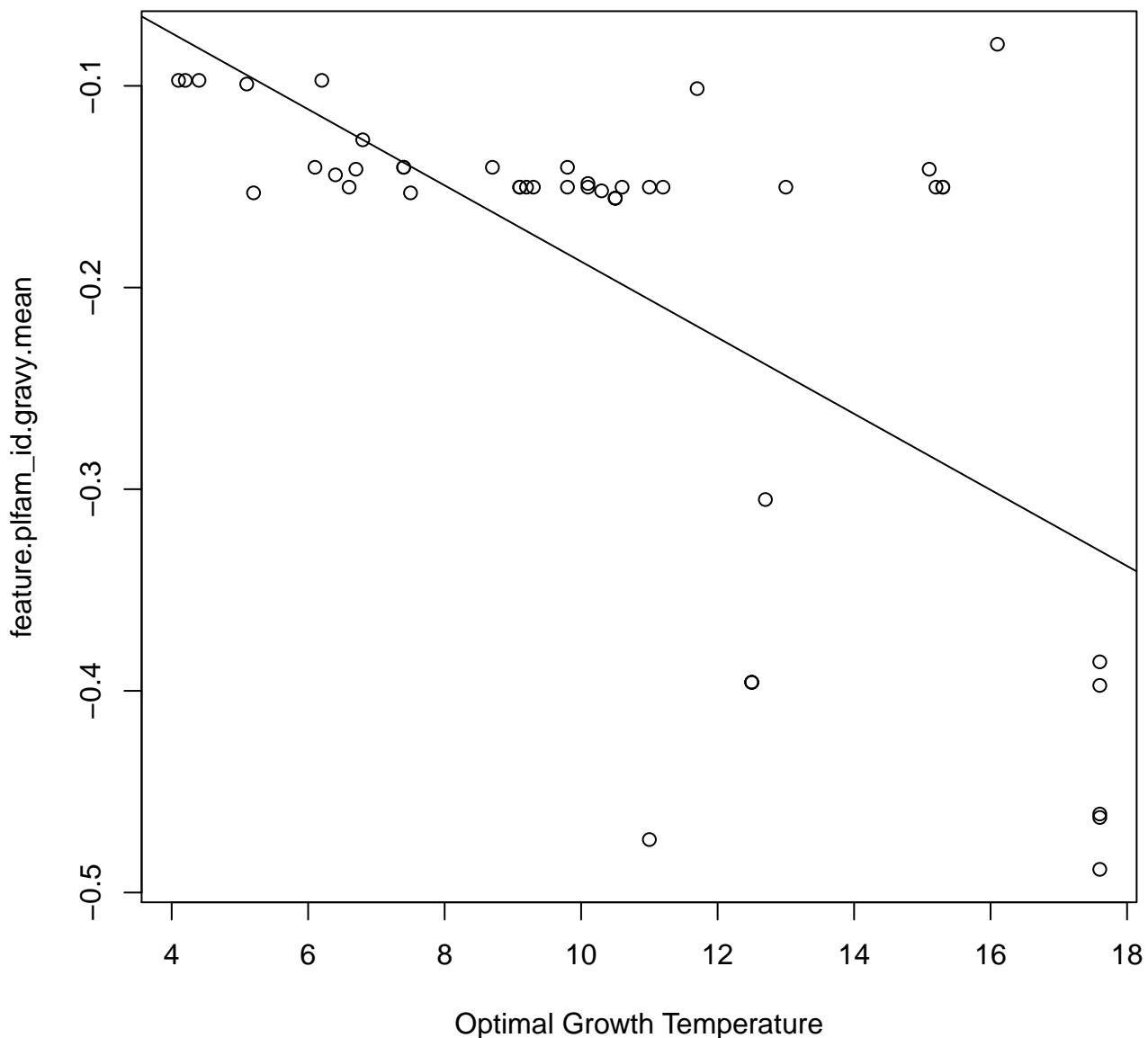
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2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)



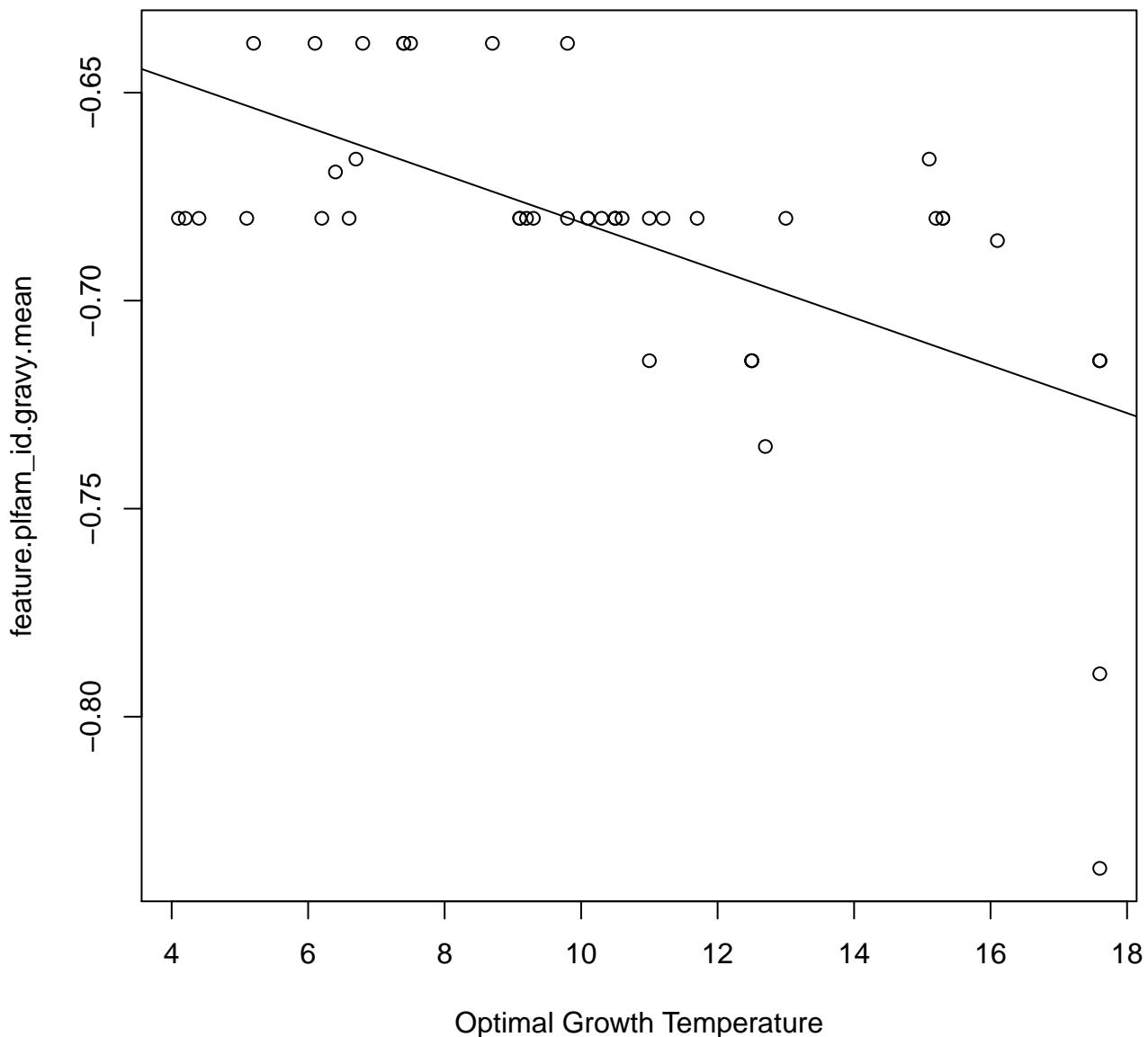
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Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)



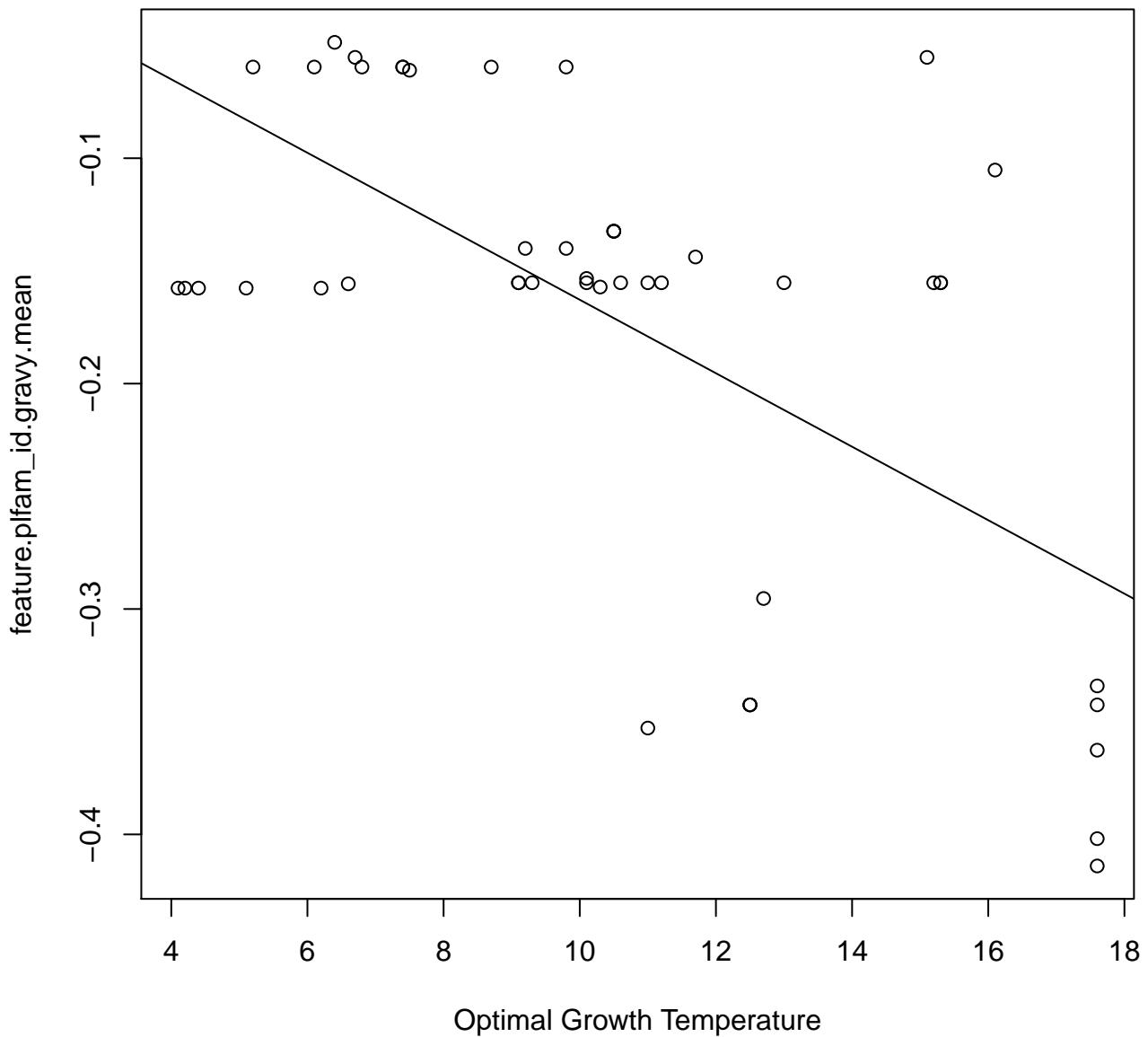
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Electron transport complex protein RnfG



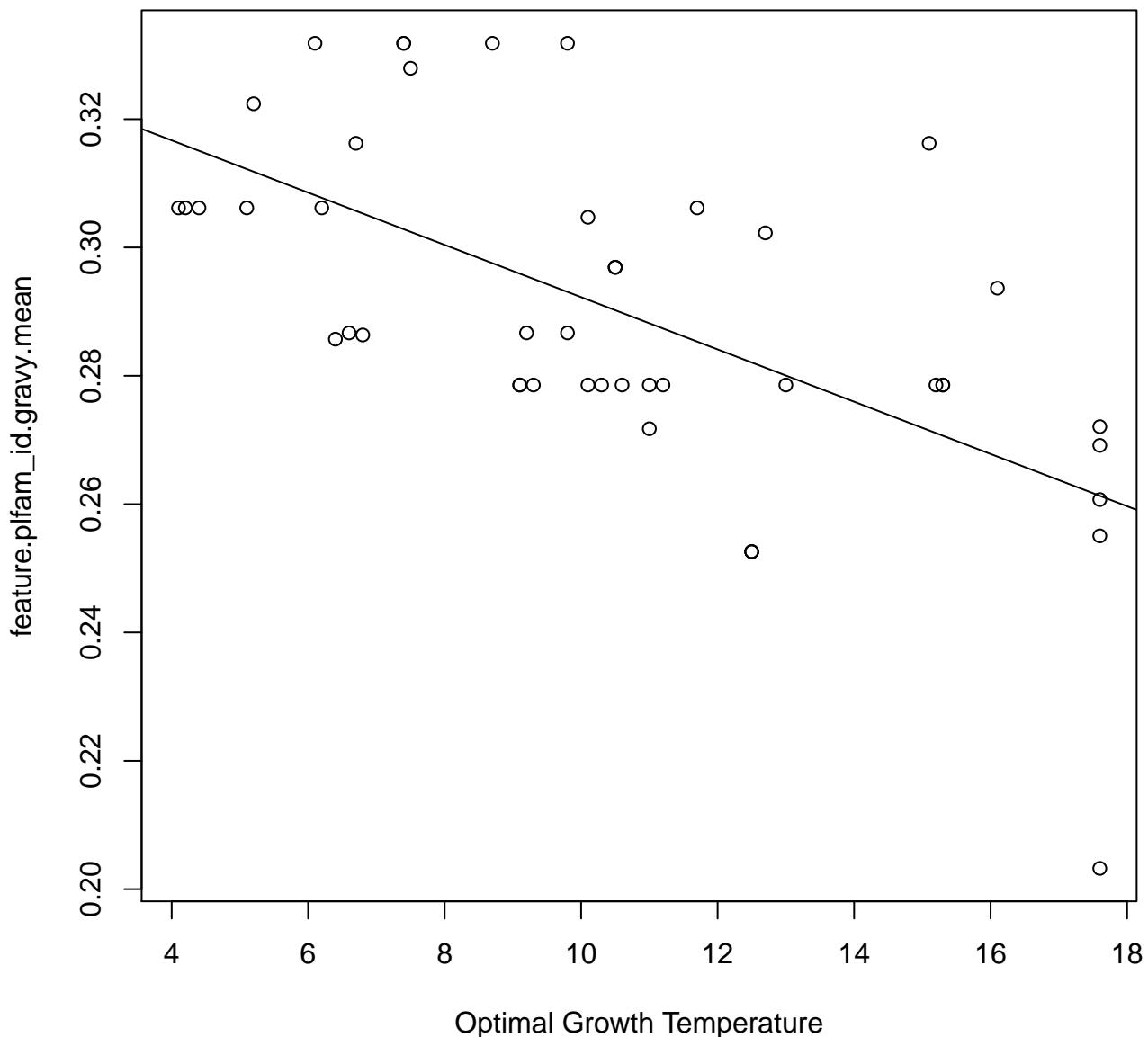
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Integration host factor alpha subunit



feature.plfam_id.gravy.mean
PLF_28228_00000131
Periplasmic thiol:disulfide interchange protein DsbA



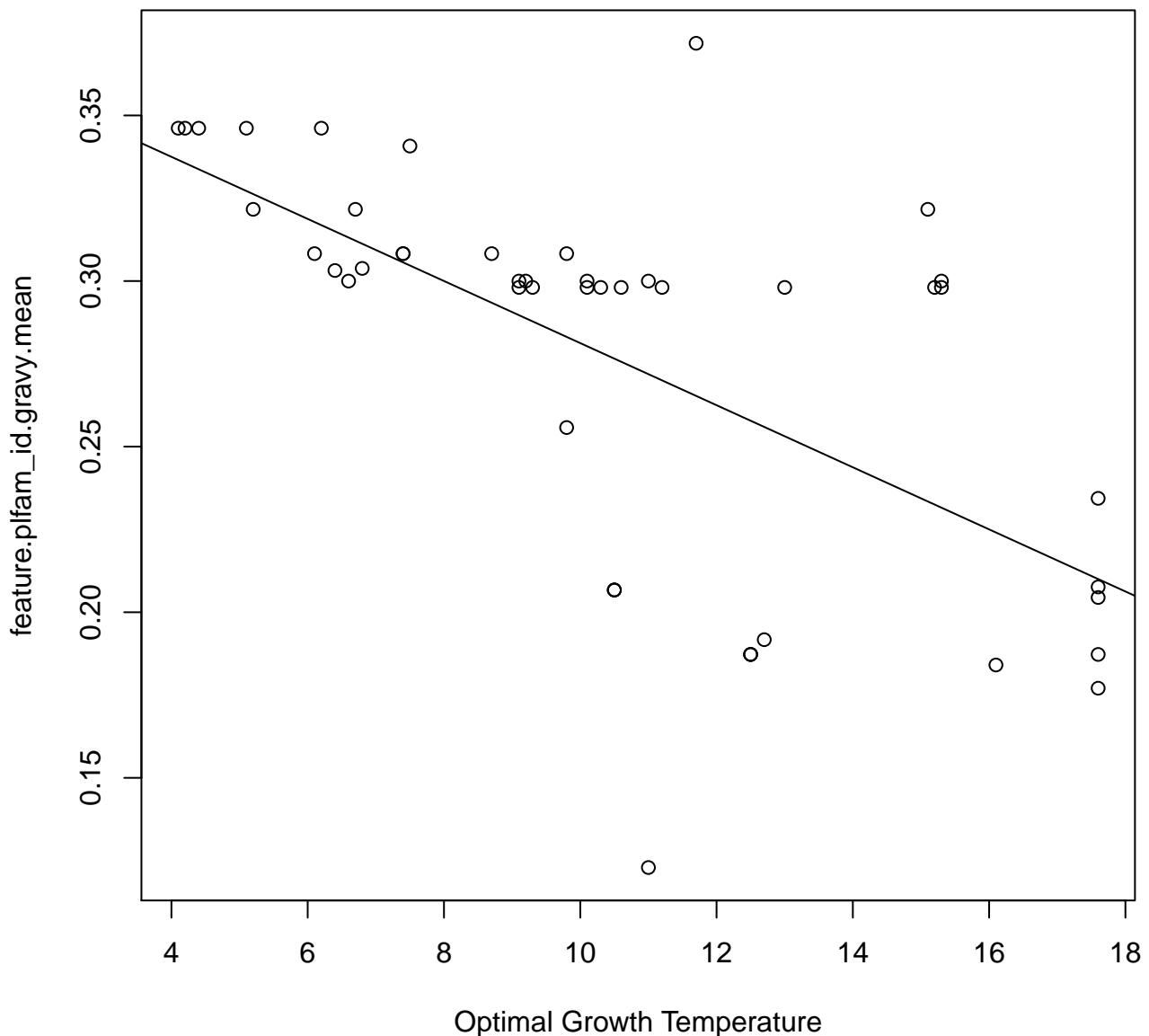
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Electron transfer flavoprotein, alpha subunit



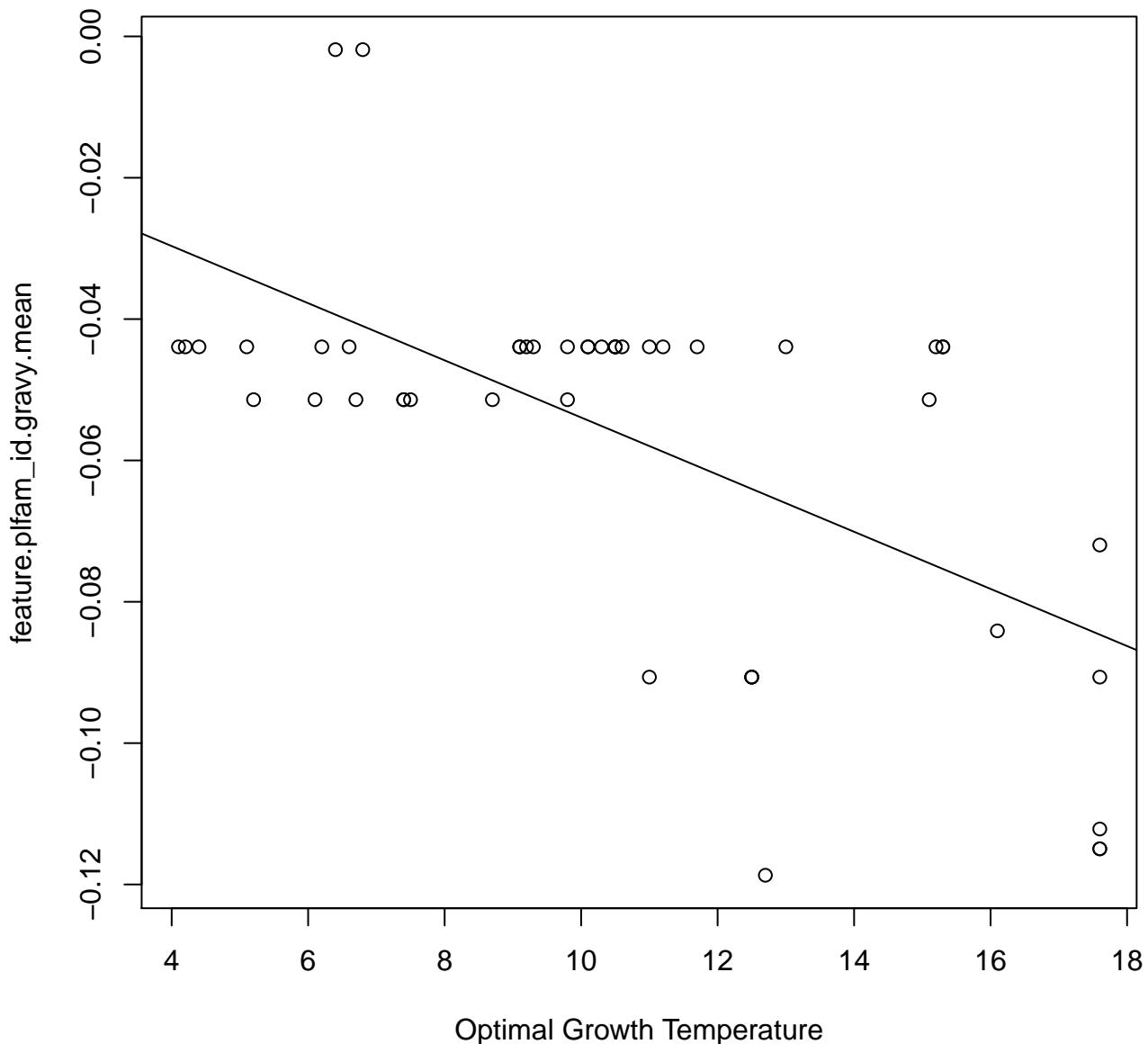
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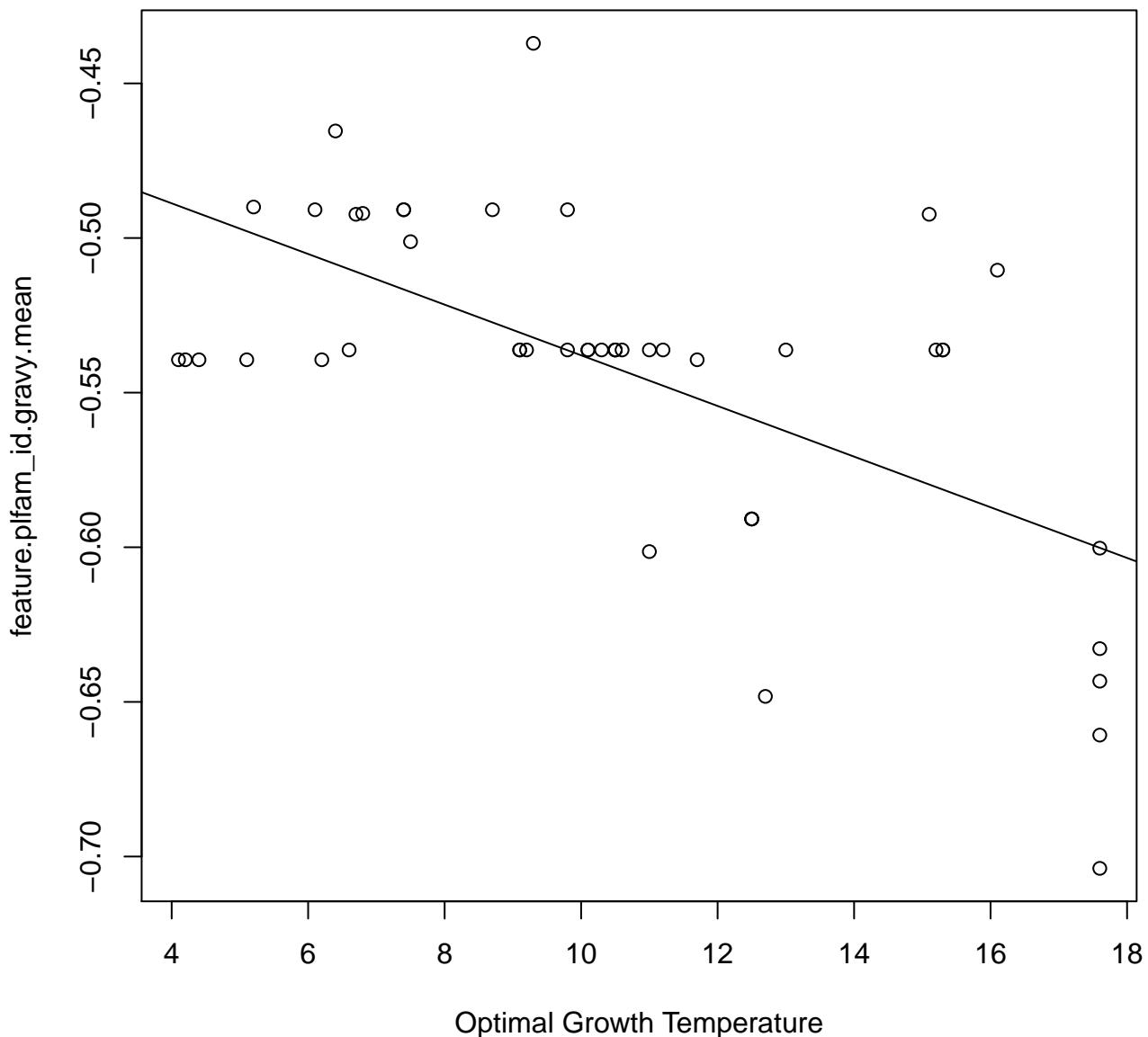
Peptidylprolyl isomerase, FKBP-type (EC 5.2.1.8) / Macrophage infectivity potentiator



feature.pifam_id.gravy.mean
PLF_28228_00000530
Iron-sulfur cluster assembly iron binding protein IscA



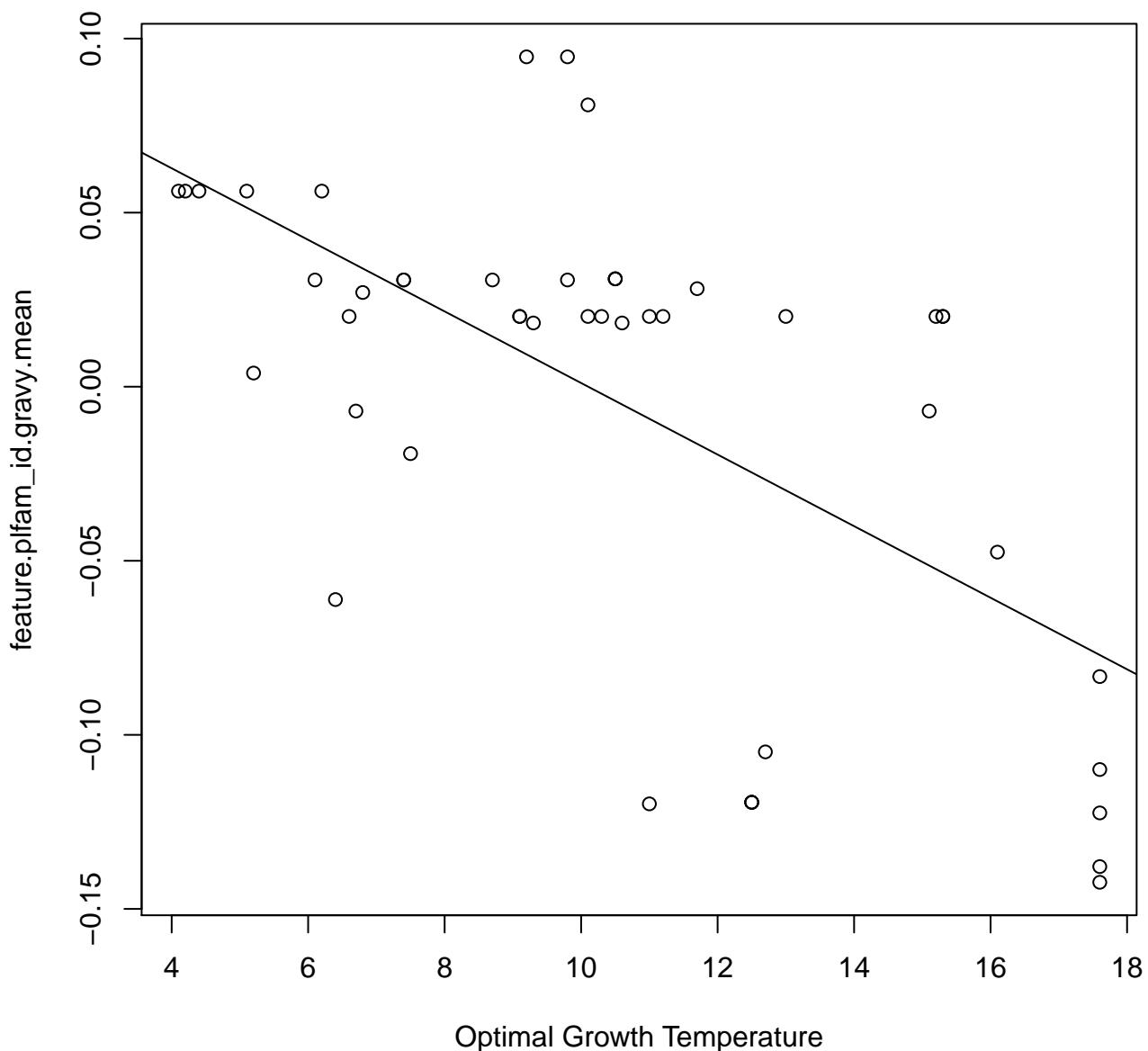
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LSU rRNA pseudouridine(955/2504/2580) synthase (EC 5.4.99.24)



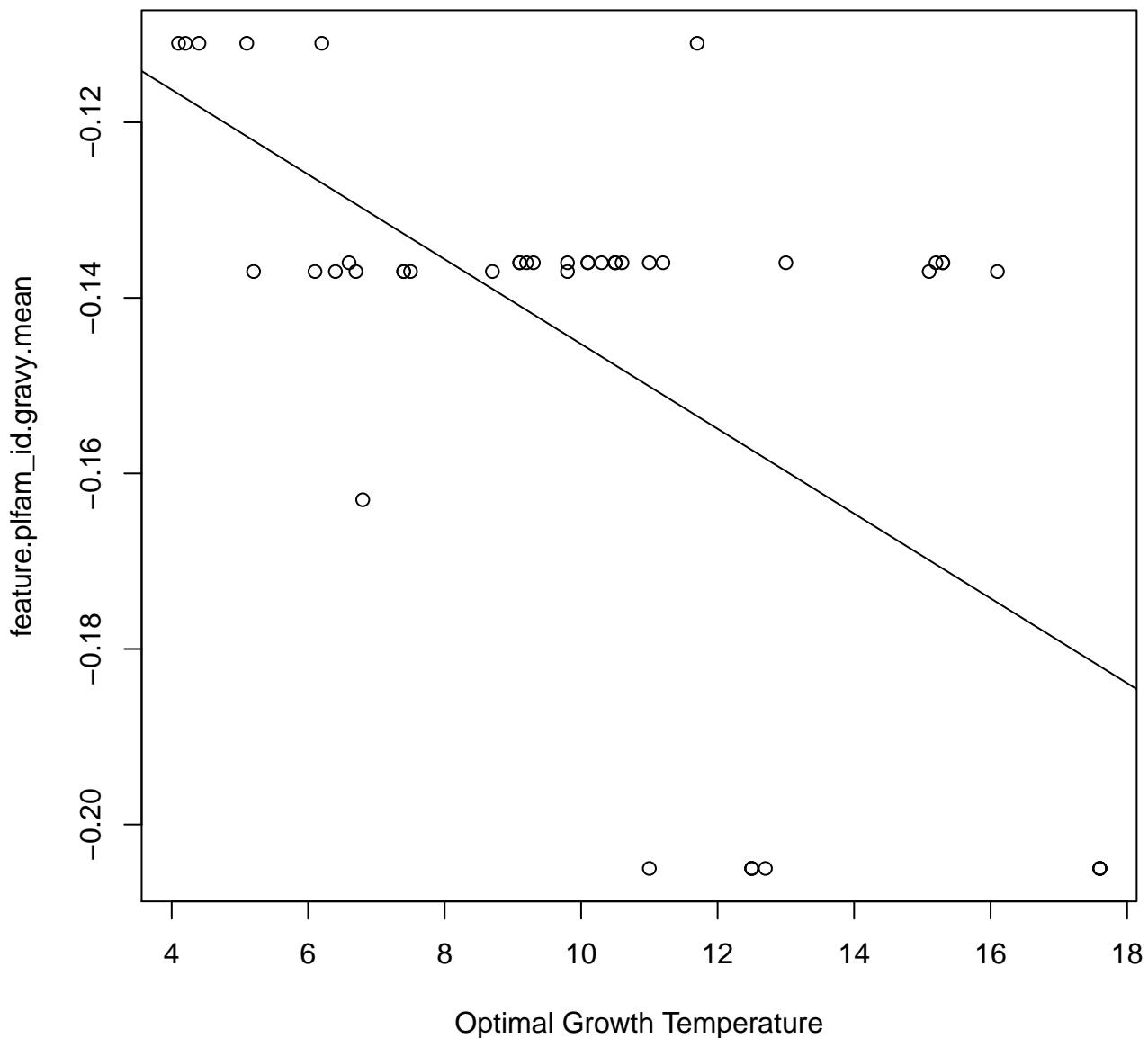
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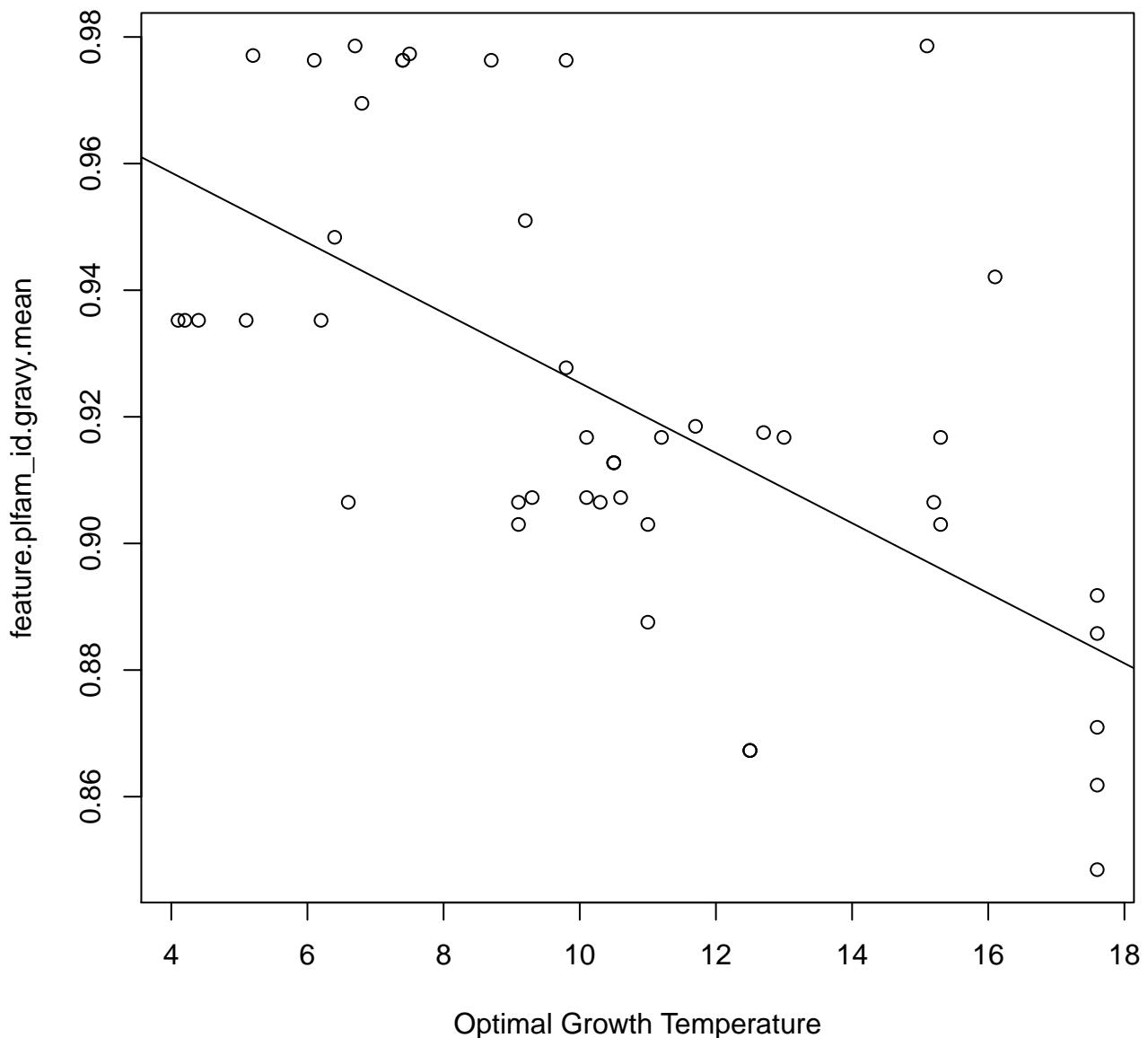
Cytochrome oxidase biogenesis protein Sco1/SenC/PrrC, thiol-disulfide reductase involved in Cu(I) insertion into CoxII Cu(A) ce



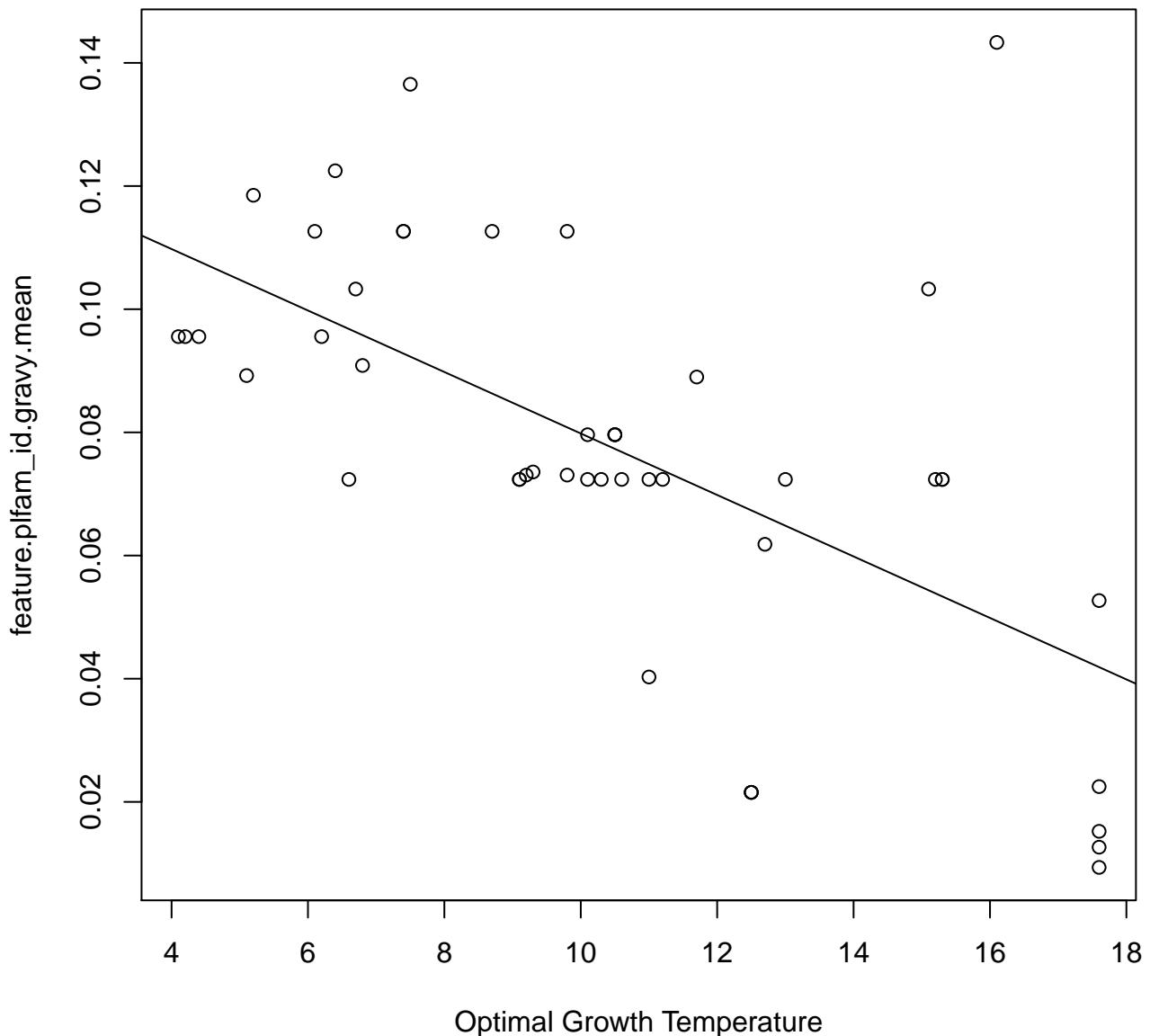
feature.plfam_id.gravy.mean
PLF_28228_00000824
LSU ribosomal protein L23p (L23Ae)



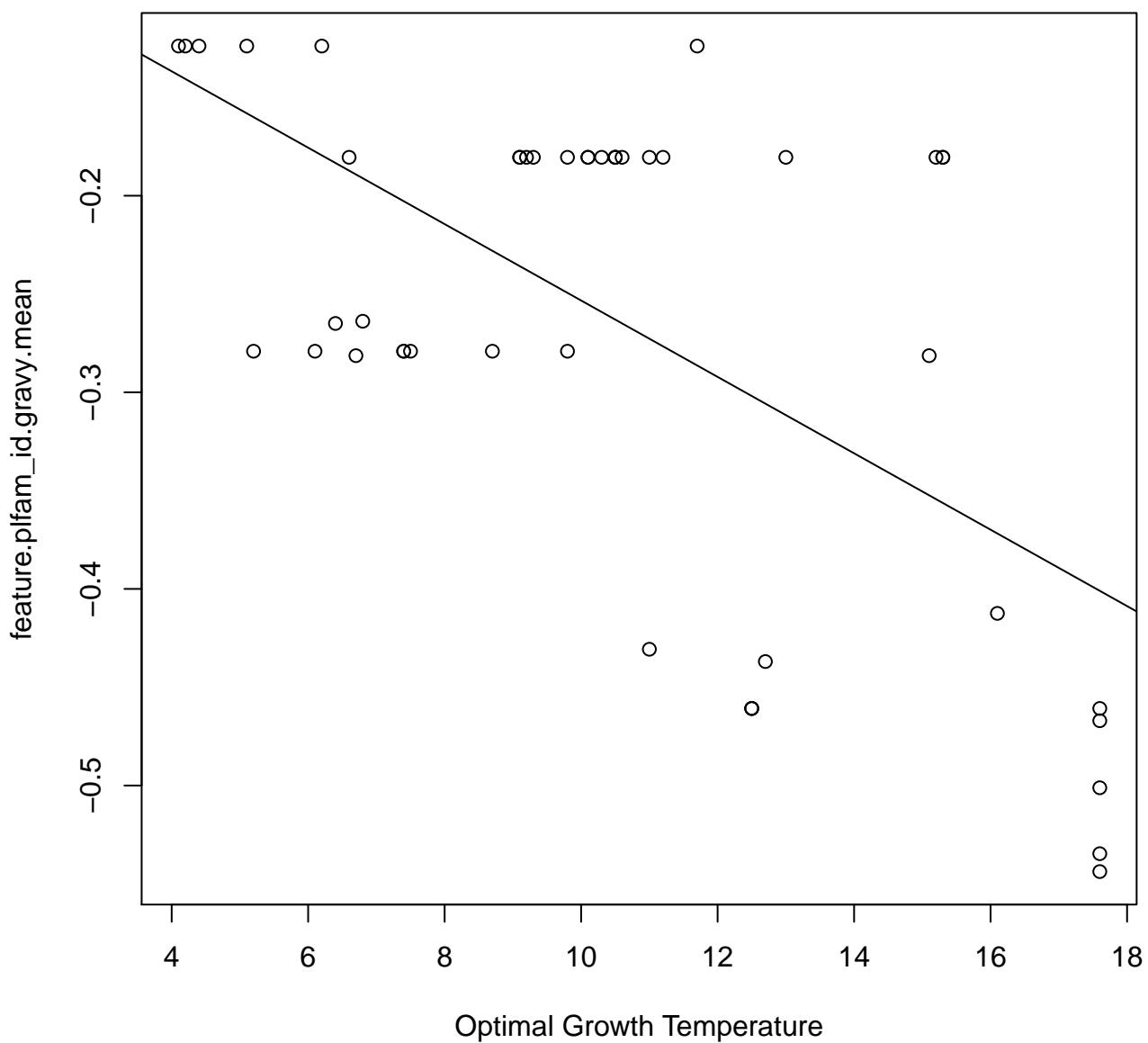
feature.plfam_id.gravy.mean
PLF_28228_00001909
Multidrug resistance transporter, Bcr/CflA family



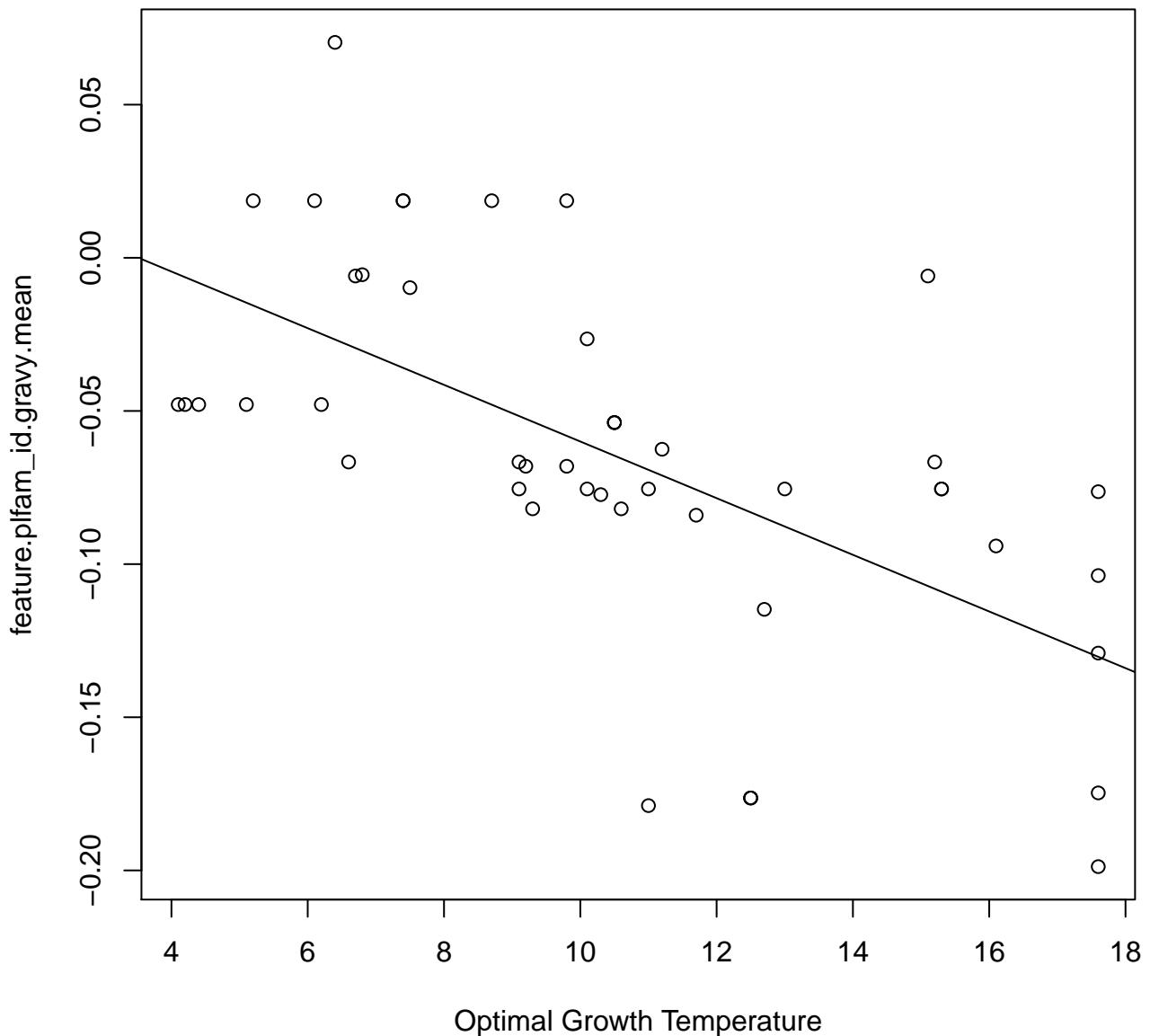
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Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)



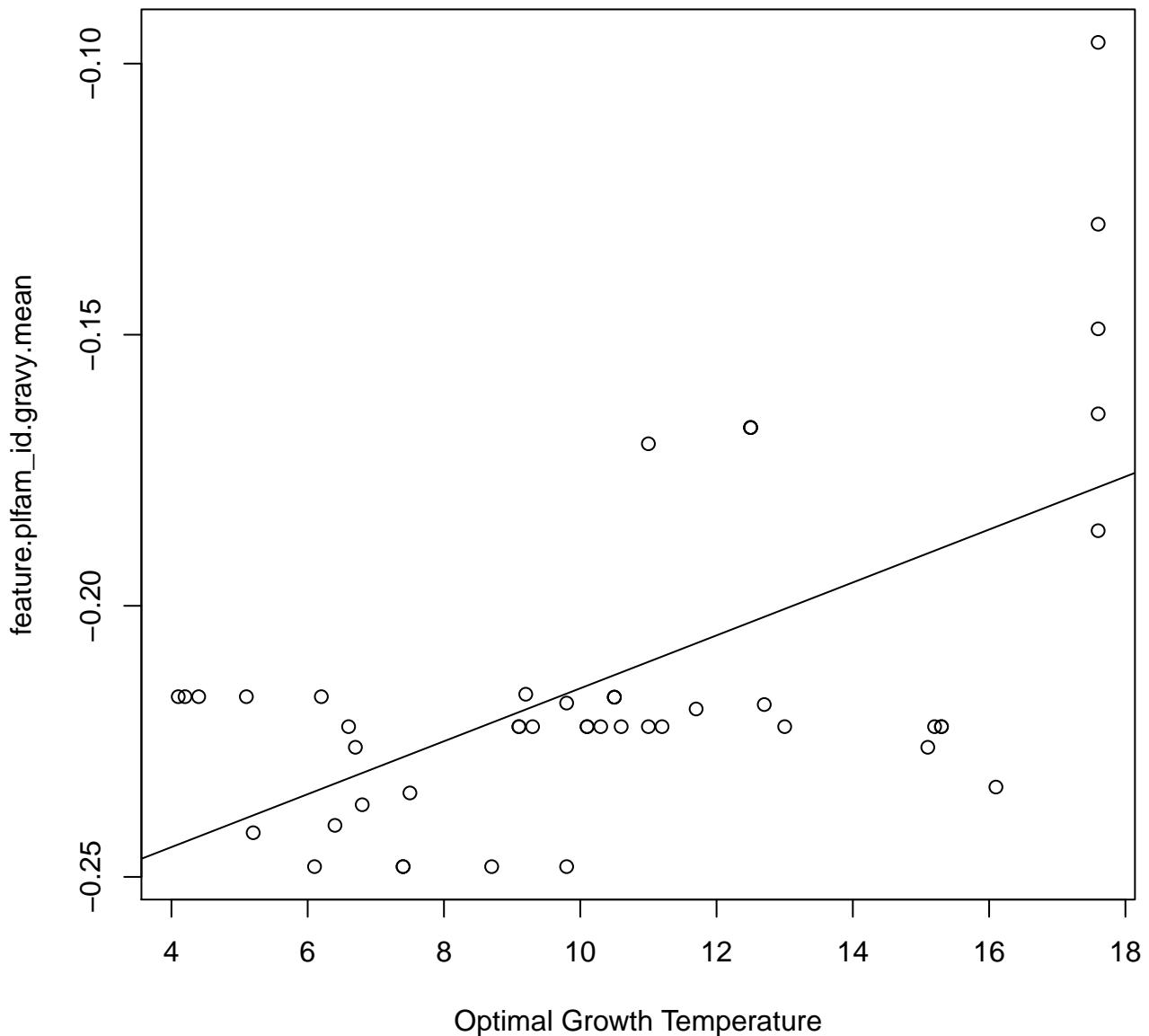
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Glyoxalase family protein



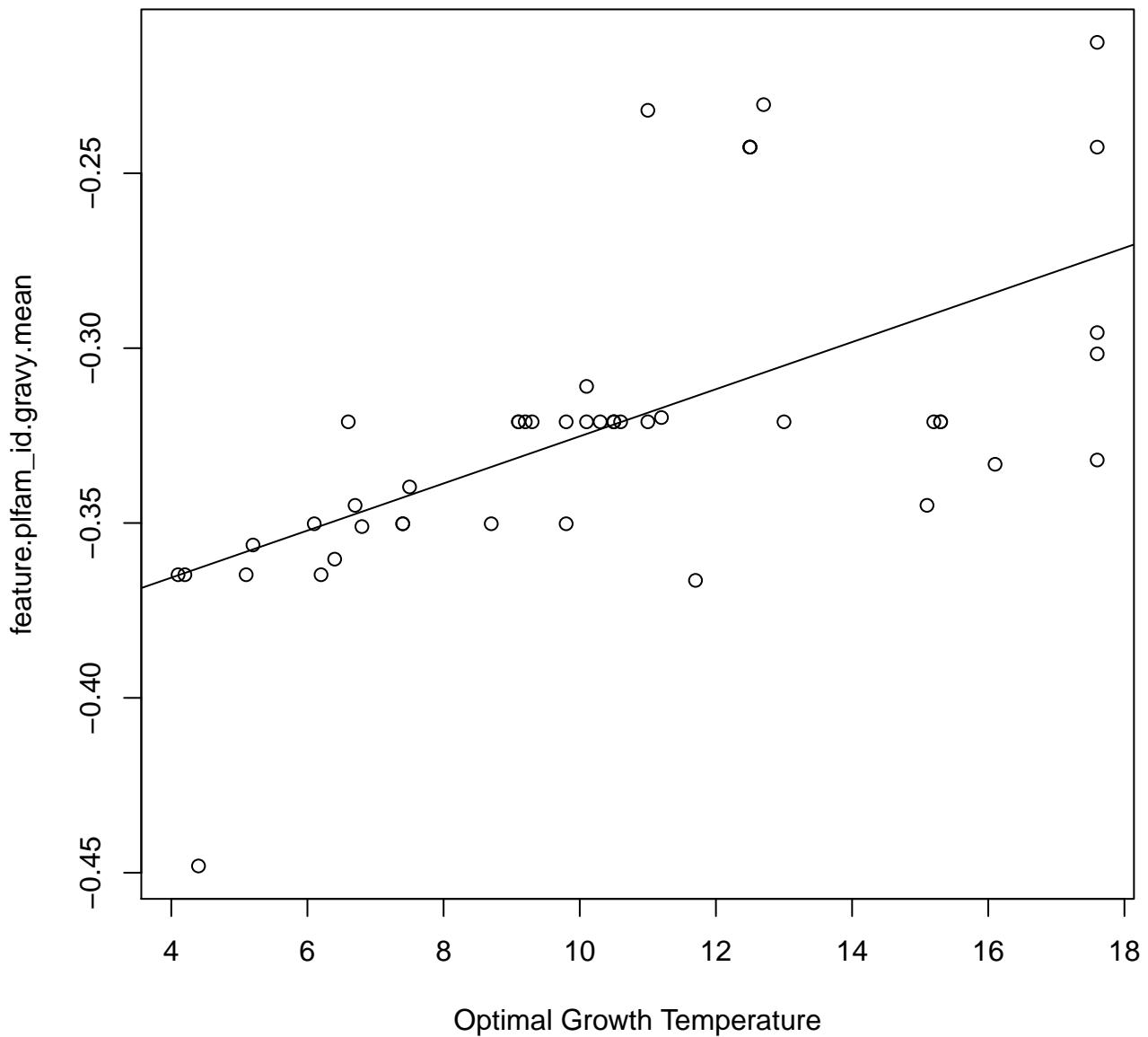
feature.plfam_id.gravy.mean
PLF_28228_00000698
Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)



feature.plfam_id.gravy.mean
PLF_28228_00001315
Arginase/agmatinase/formiminoglutamate hydrolase, arginase family



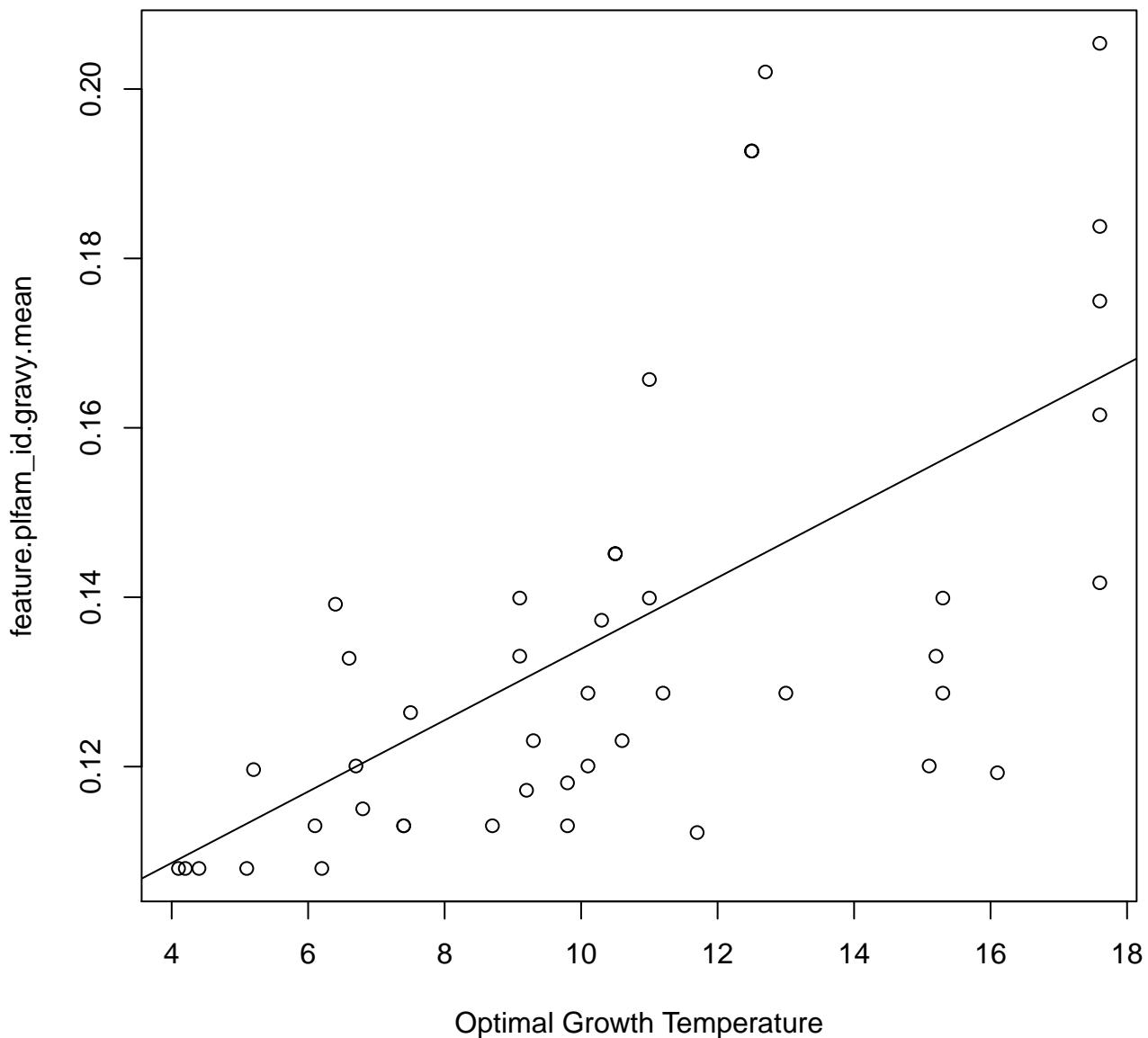
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Flagellar basal-body rod protein FlgF



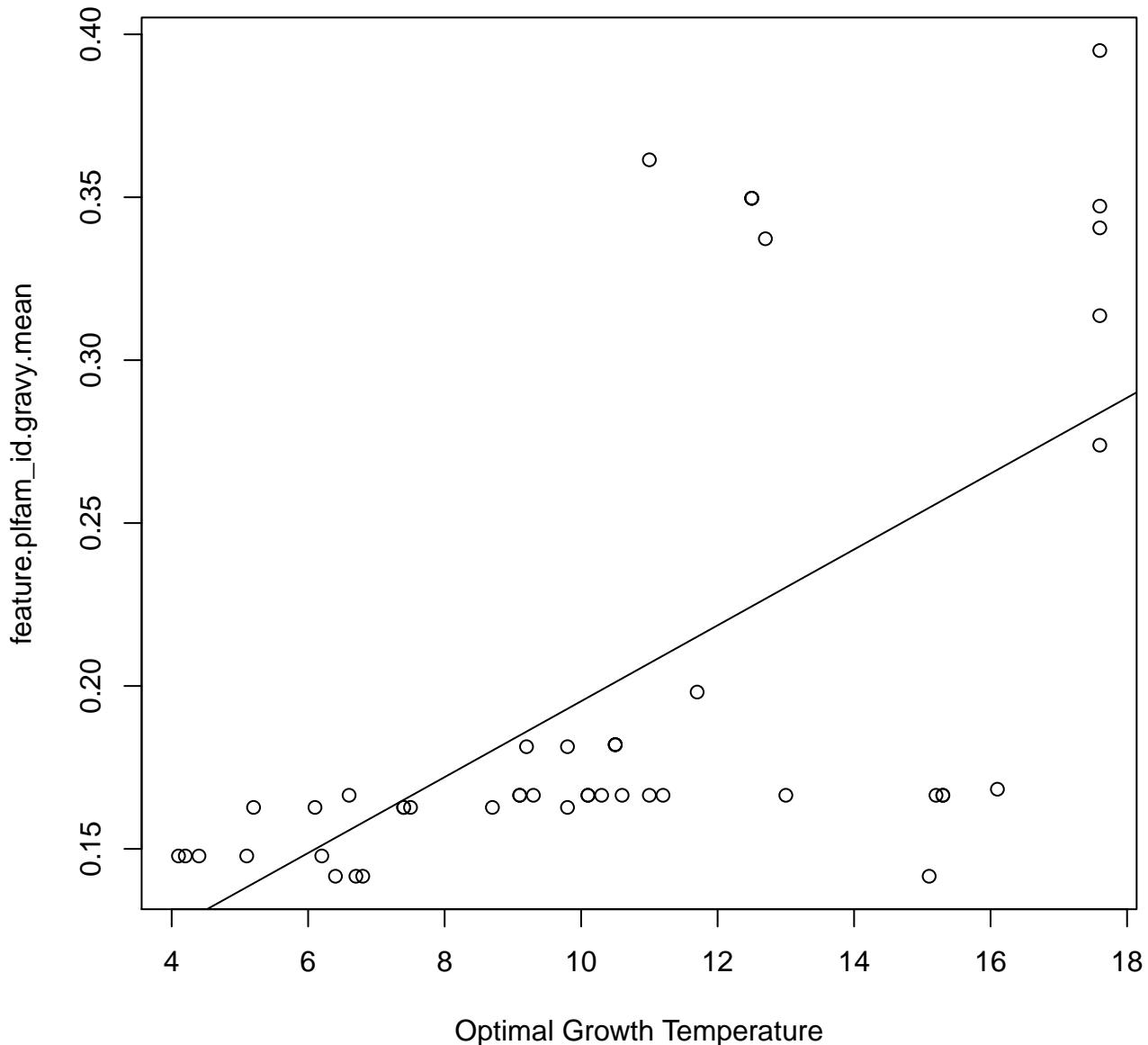
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PLF_28228_00001263

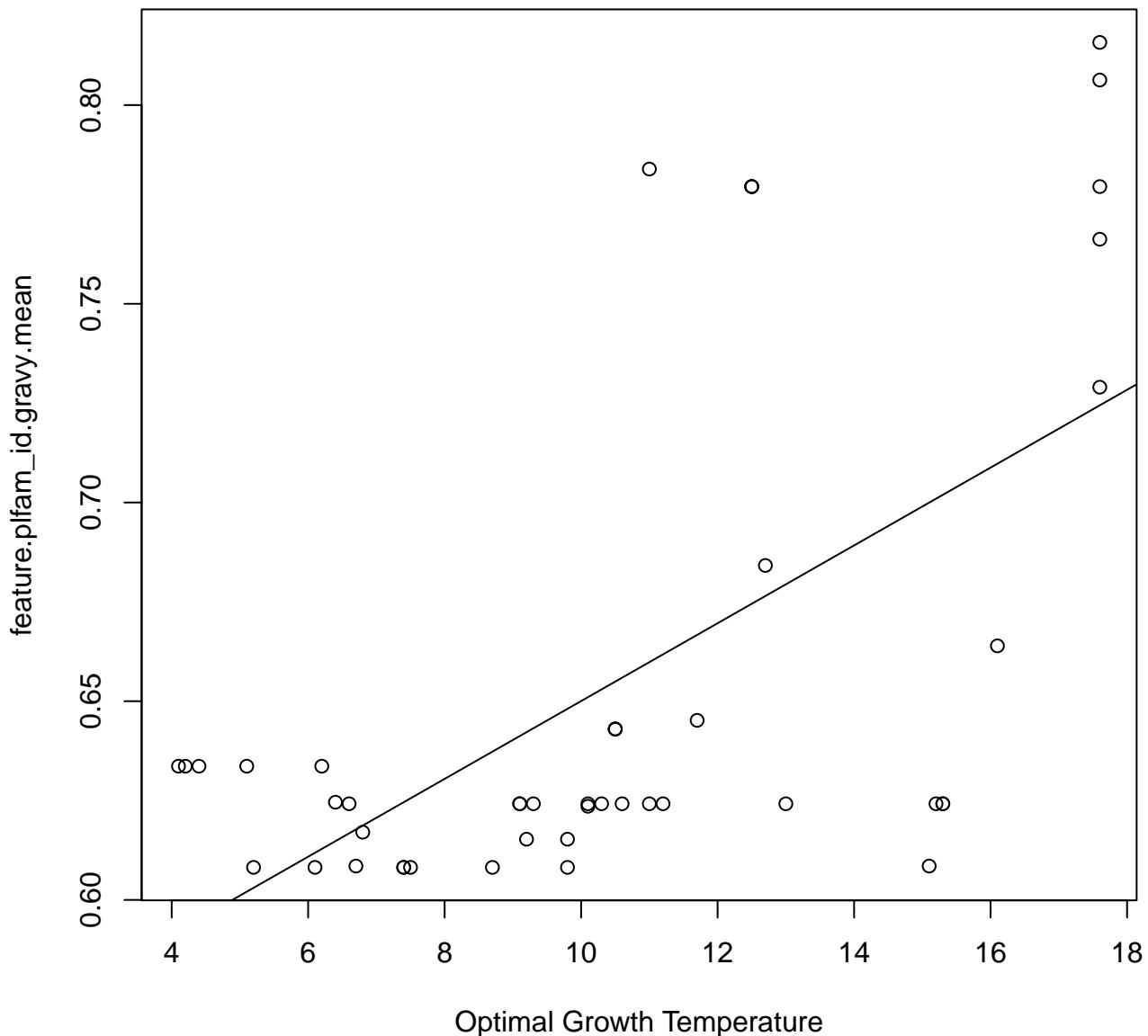
Type cbb3 cytochrome oxidase biogenesis protein Ccol; Copper-translocating P-type ATPase (EC 3.6.3.4)



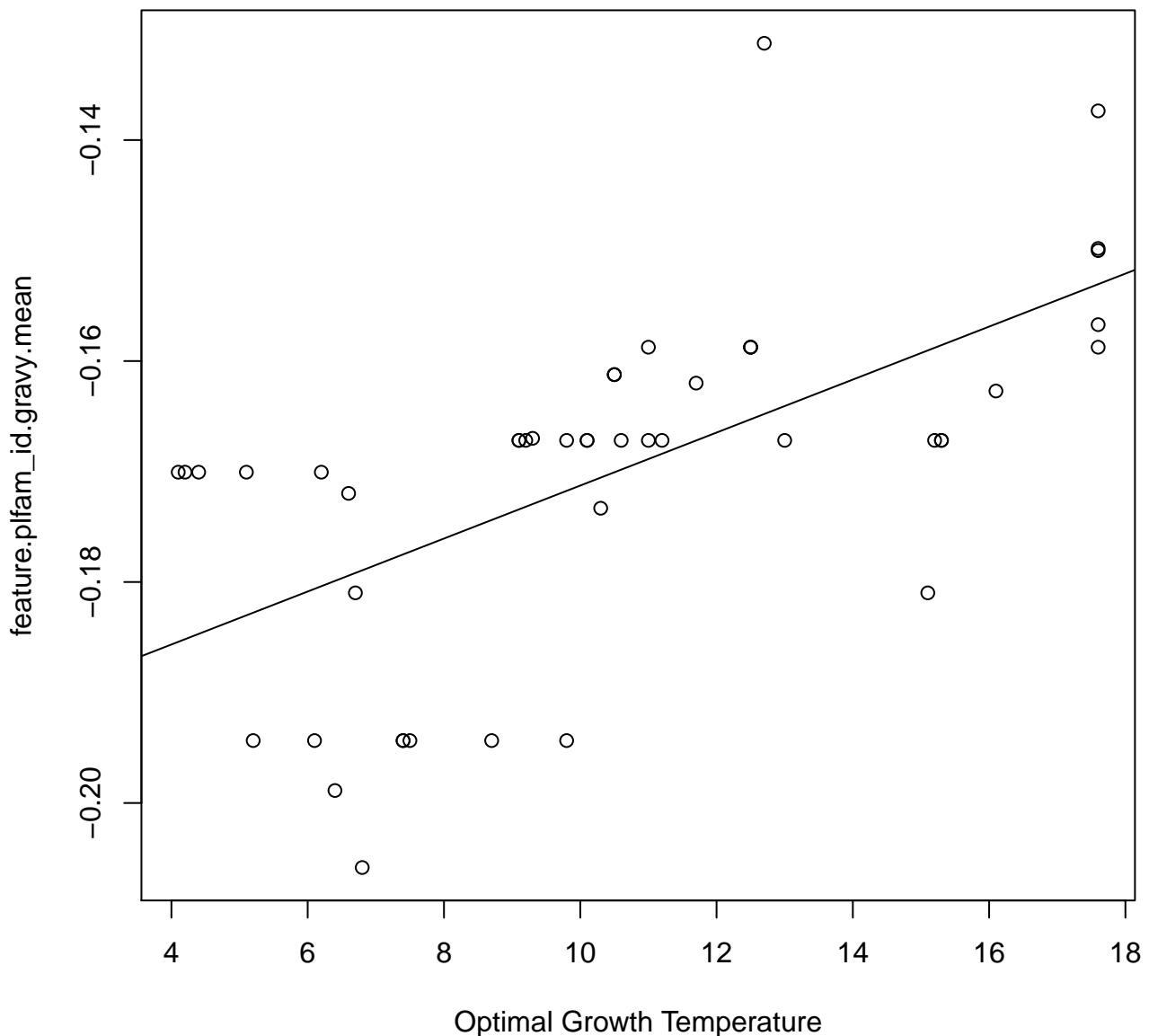
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Ribonuclease E inhibitor RraA



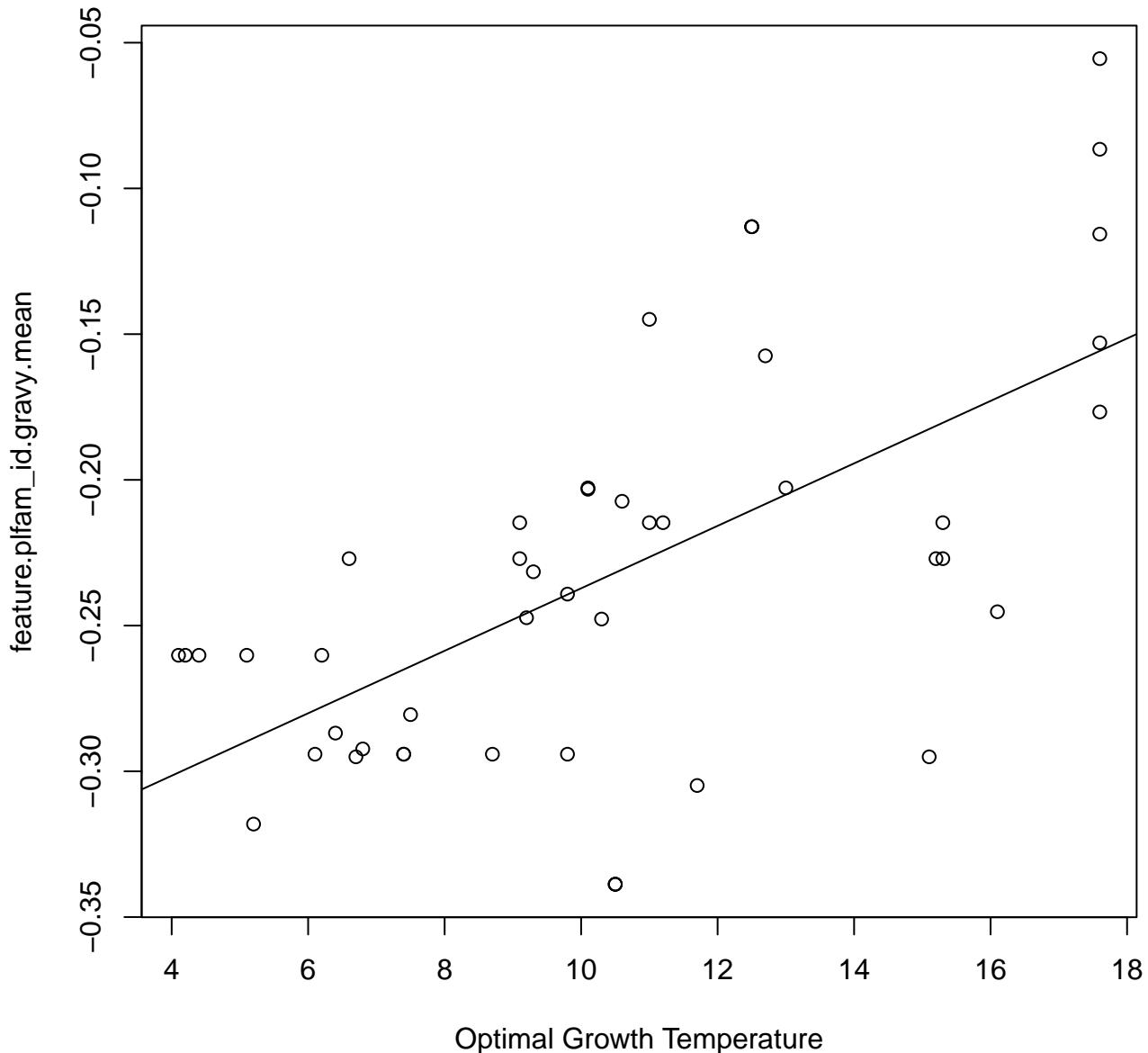
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Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB



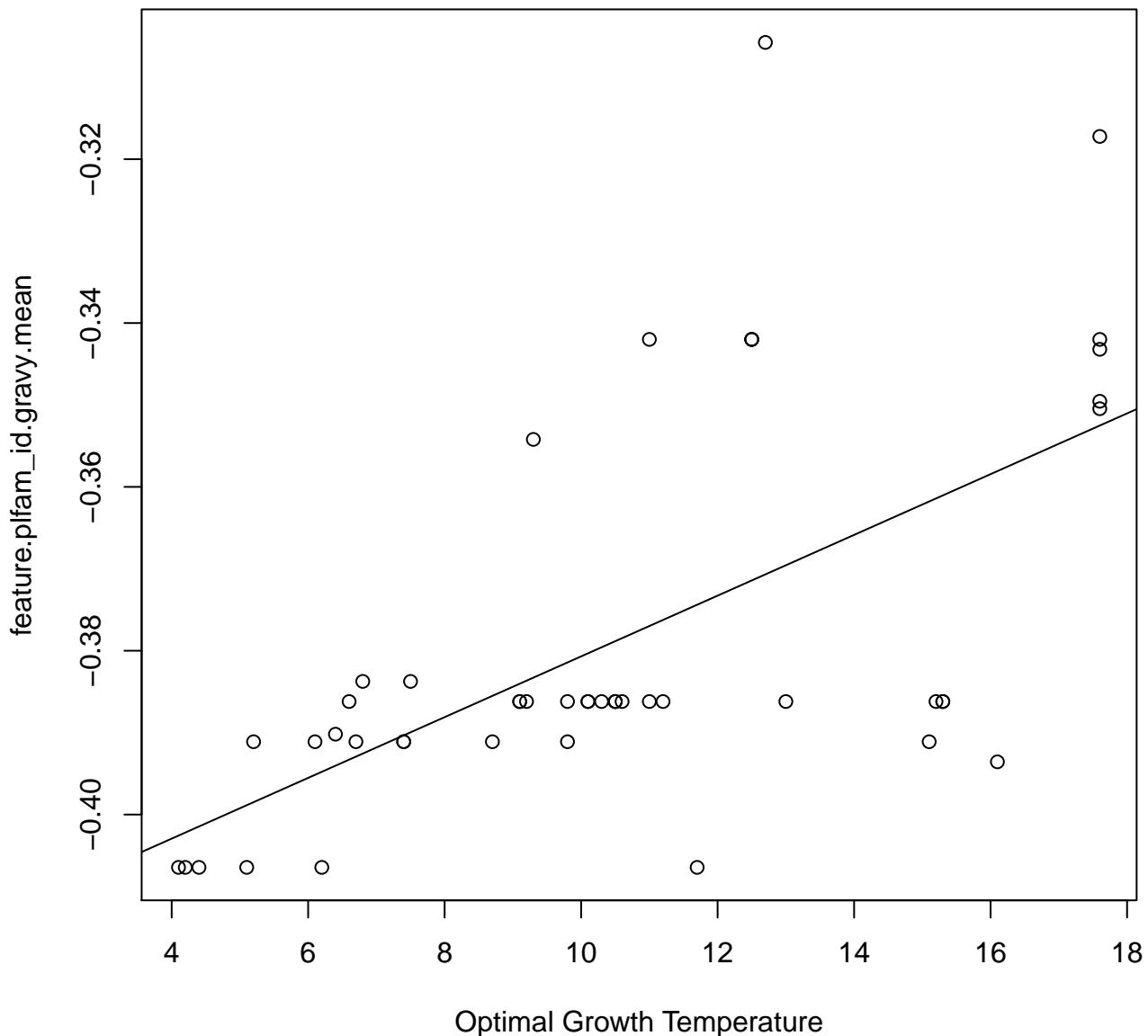
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2-isopropylmalate synthase (EC 2.3.3.13)



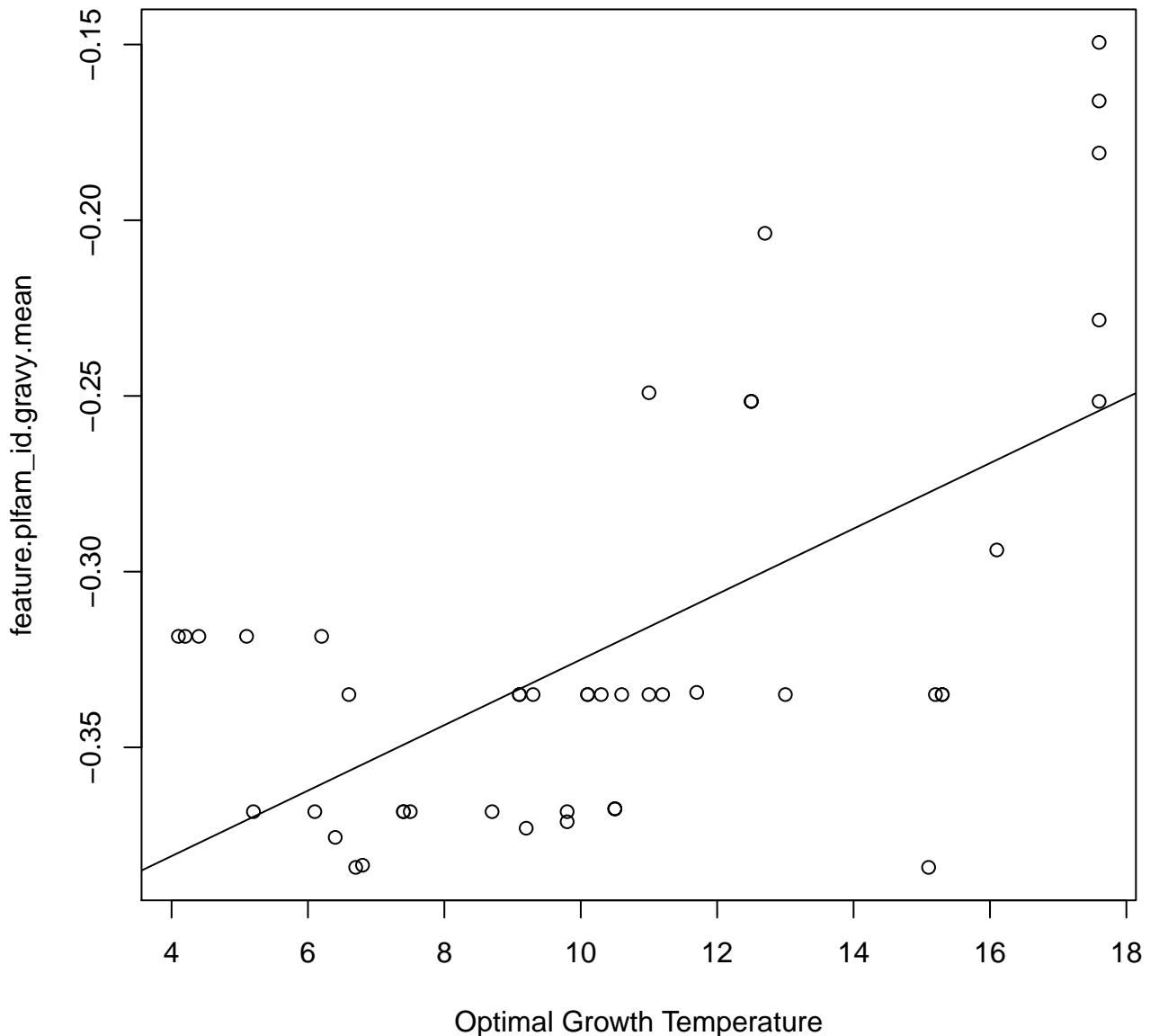
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PLF_28228_00002421
Hydrolase SM_b20688, alpha/beta fold family



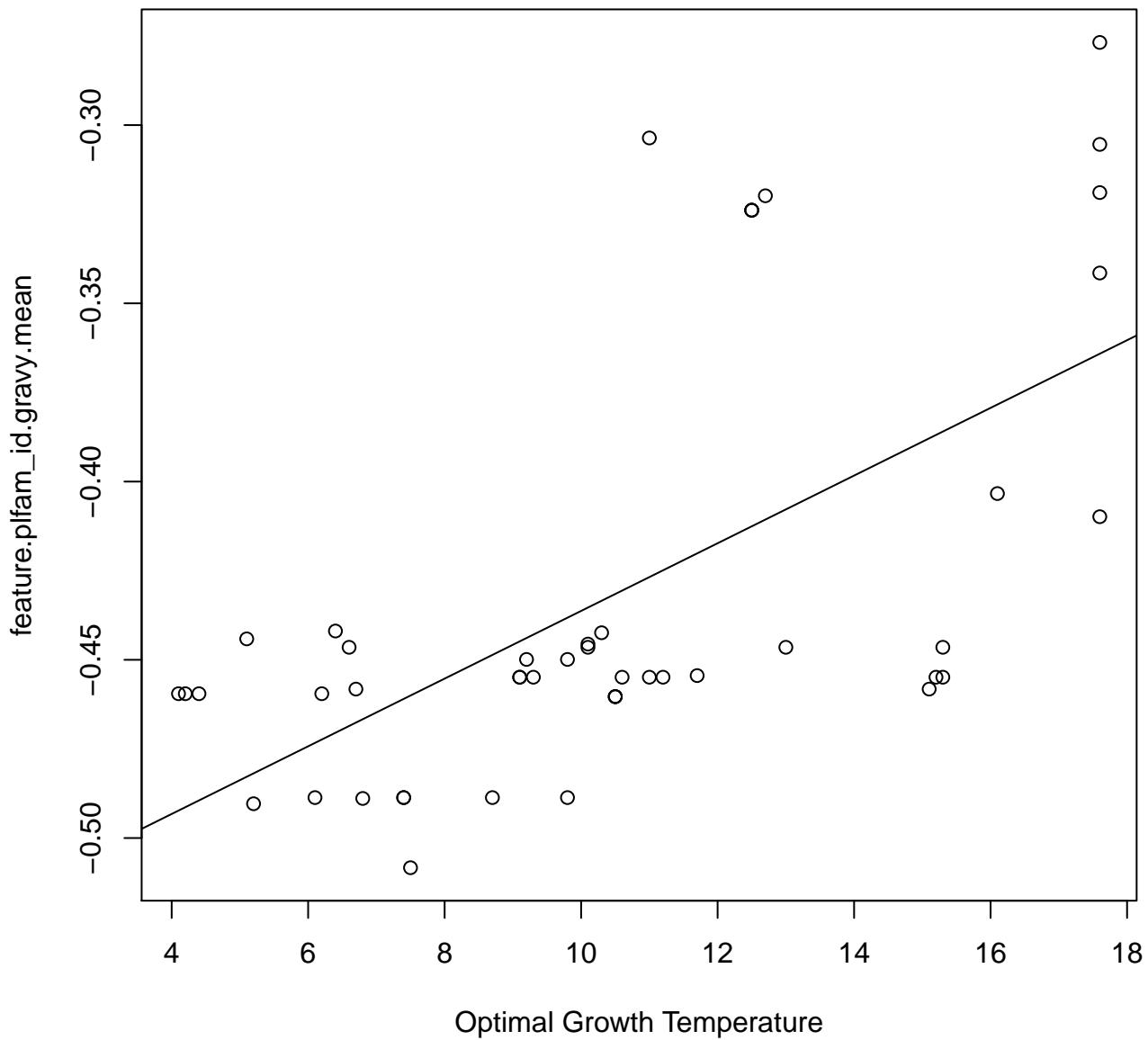
feature.plfam_id.gravy.mean
PLF_28228_00000940
Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)



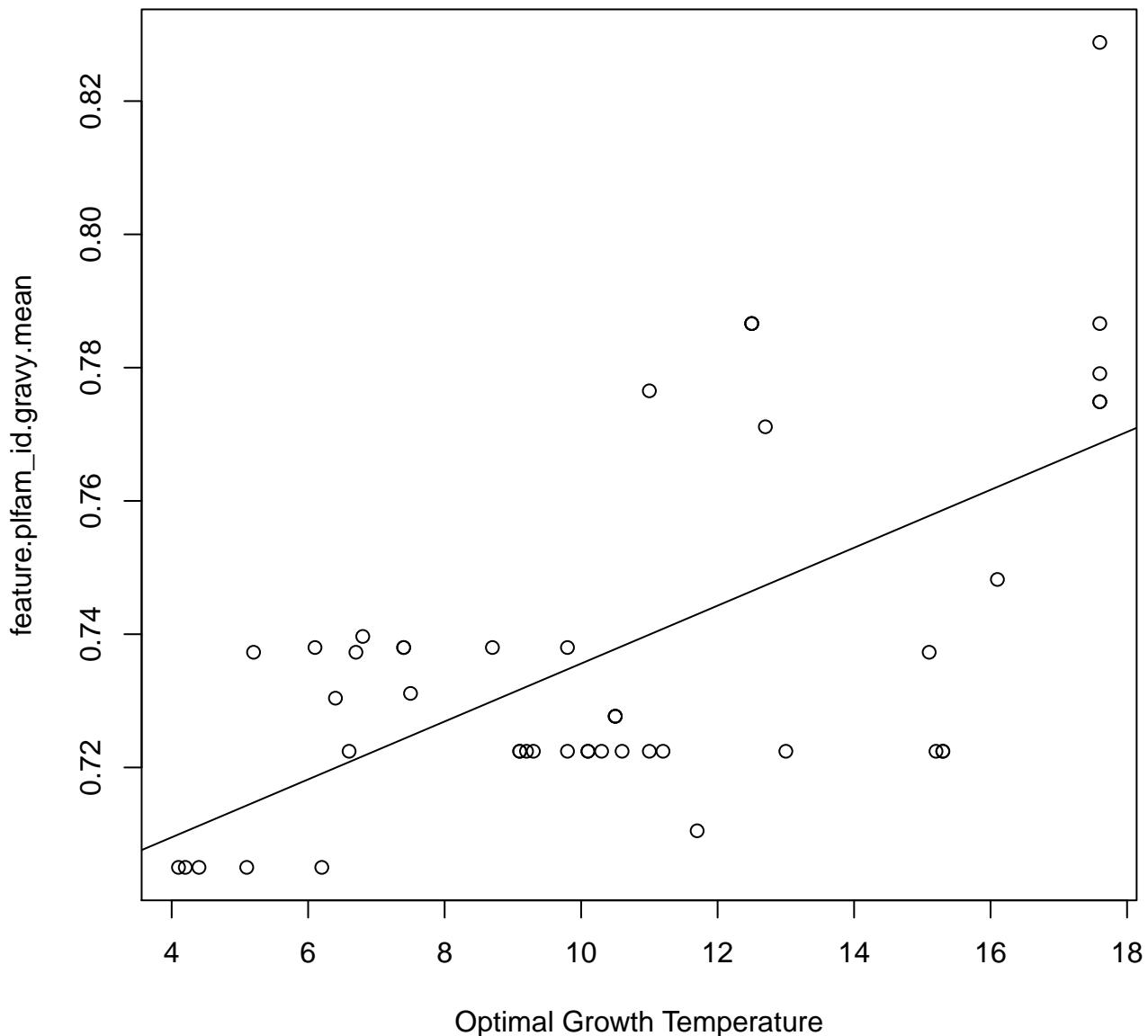
feature.plfam_id.gravy.mean
PLF_28228_00000467
FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)



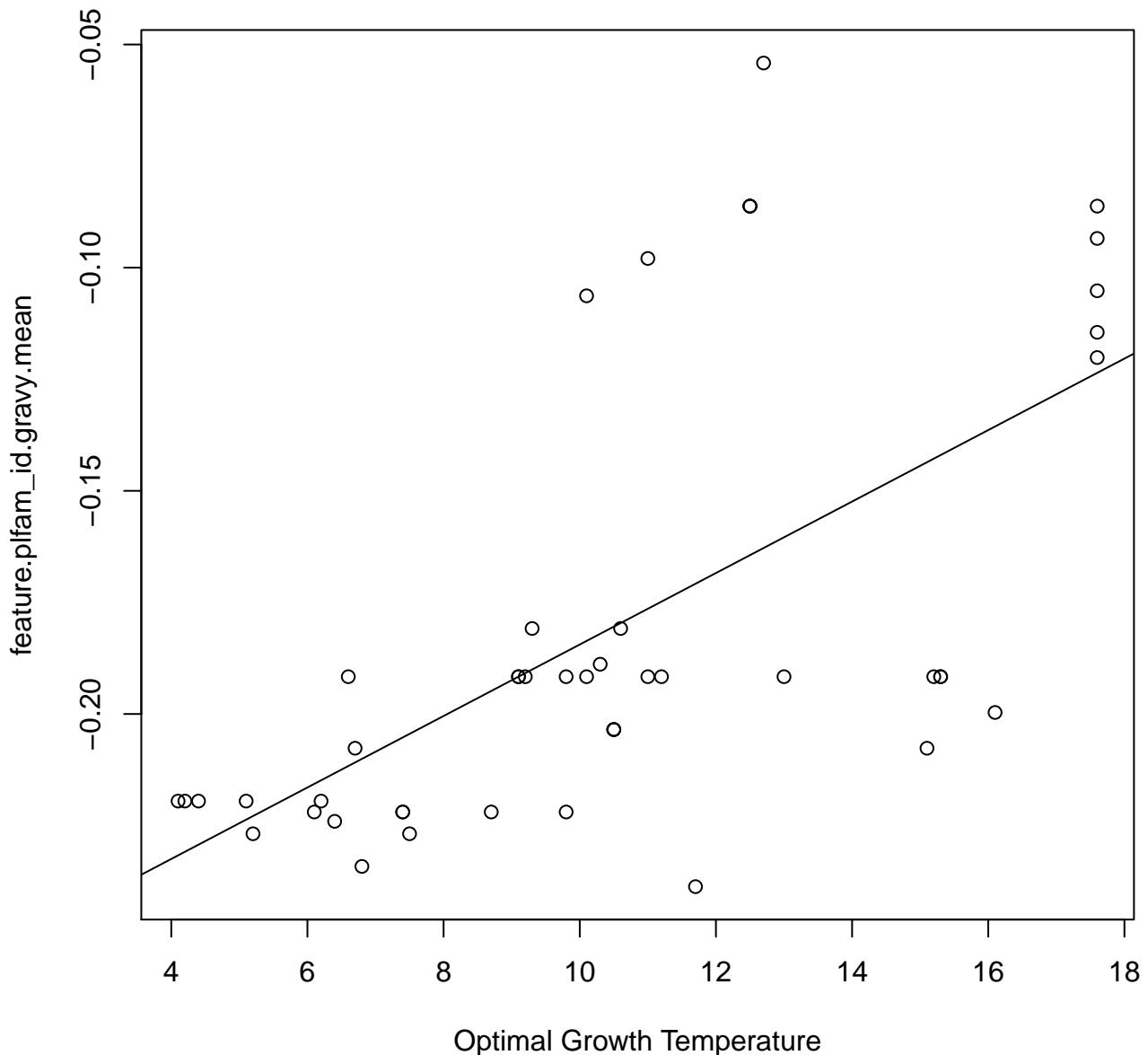
feature.pfam_id.gravy.mean
PLF_28228_00002282
hypothetical protein



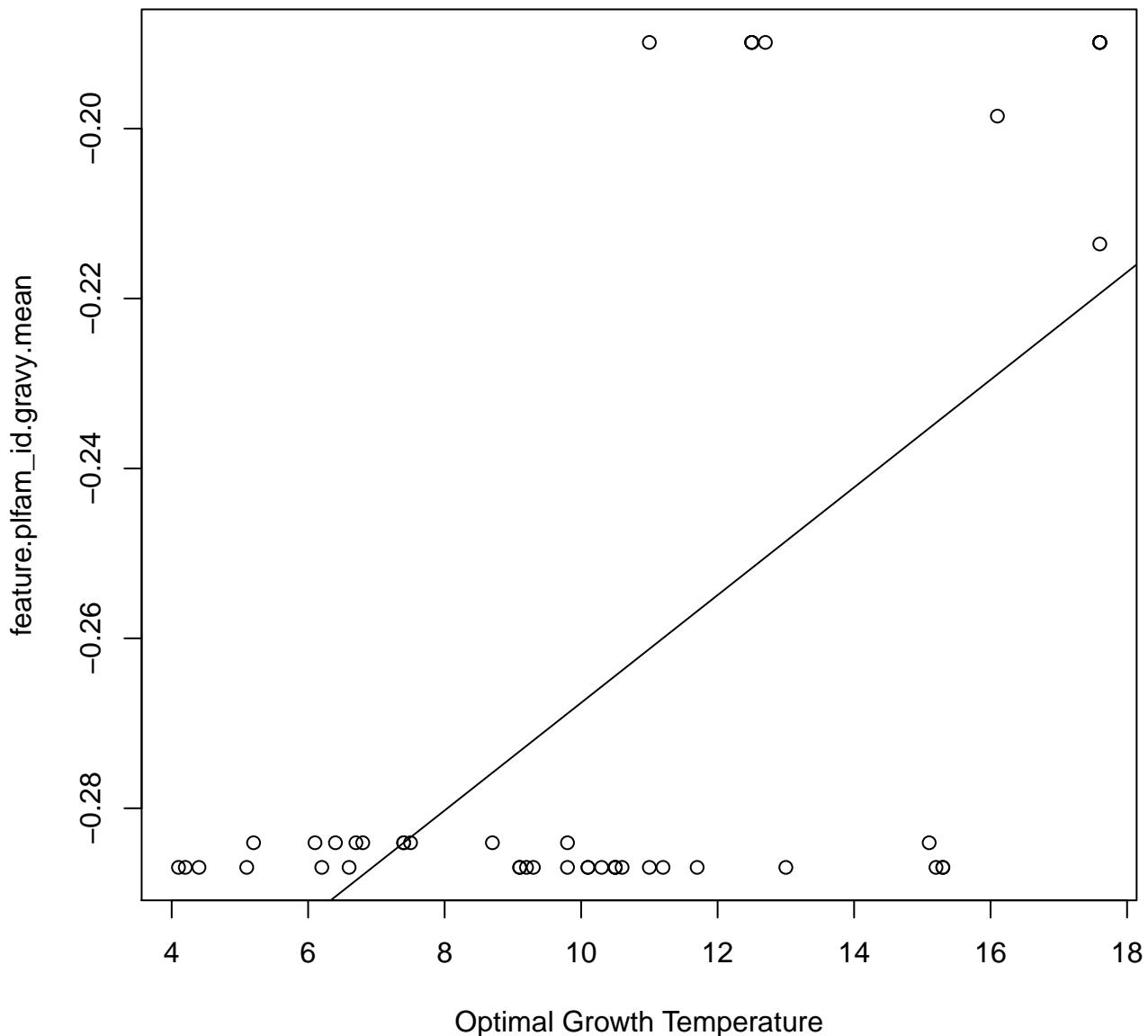
feature.plfam_id.gravy.mean
PLF_28228_00000203
Ammonium transporter



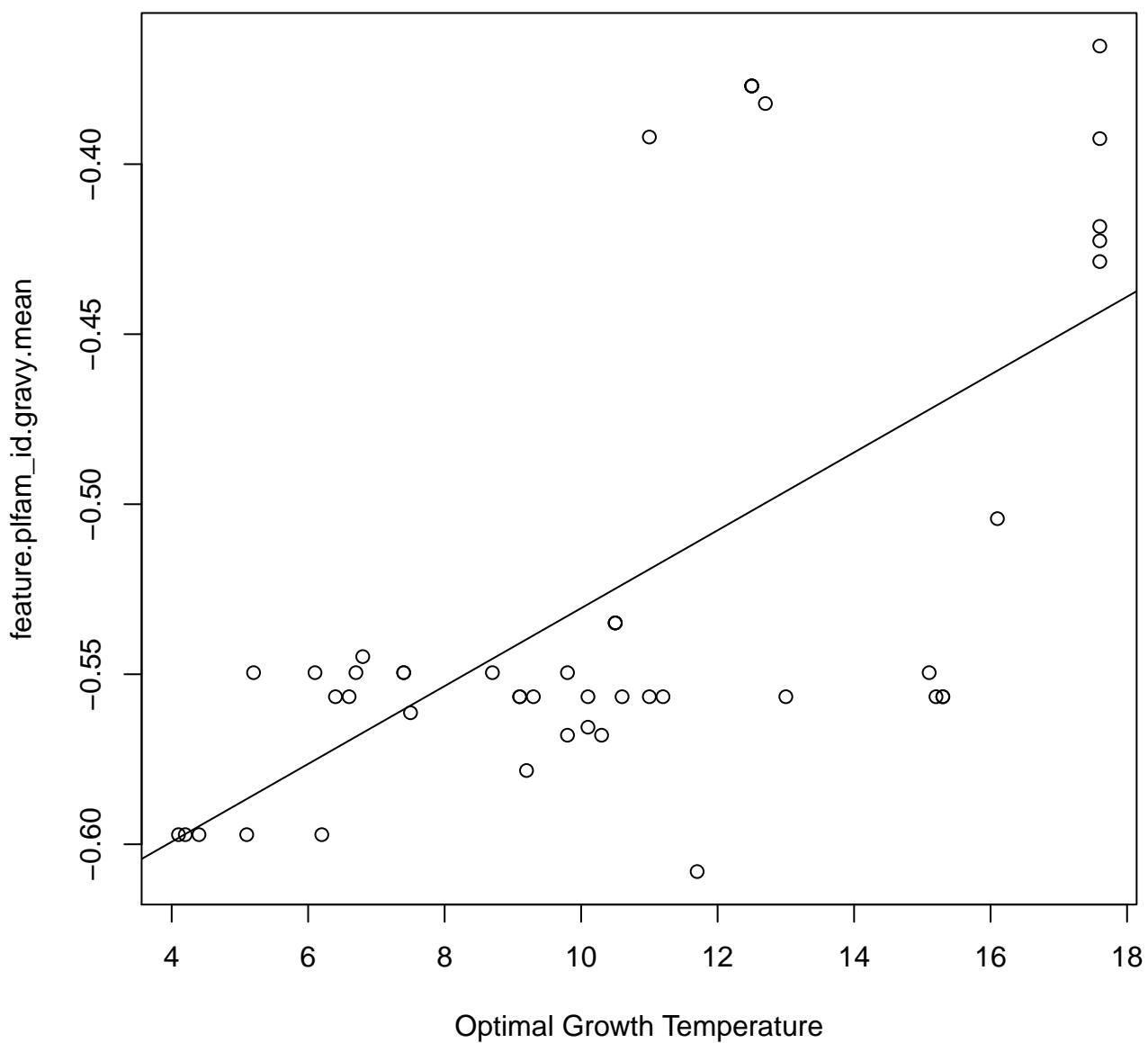
feature.pifam_id.gravy.mean
PLF_28228_00000224
33 kDa chaperonin HsIO



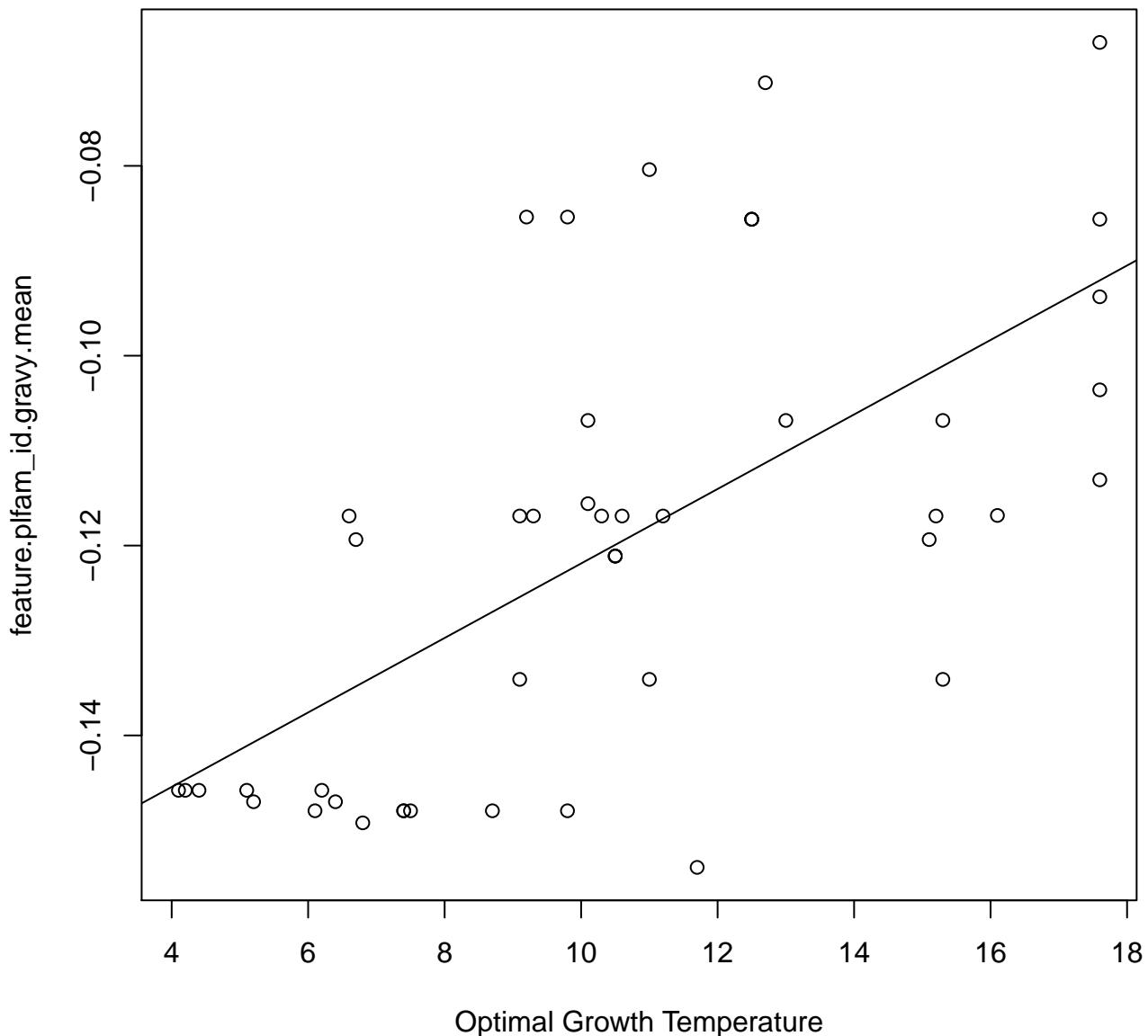
feature.pifam_id.gravy.mean
PLF_28228_00014170
Cold shock protein of CSP family



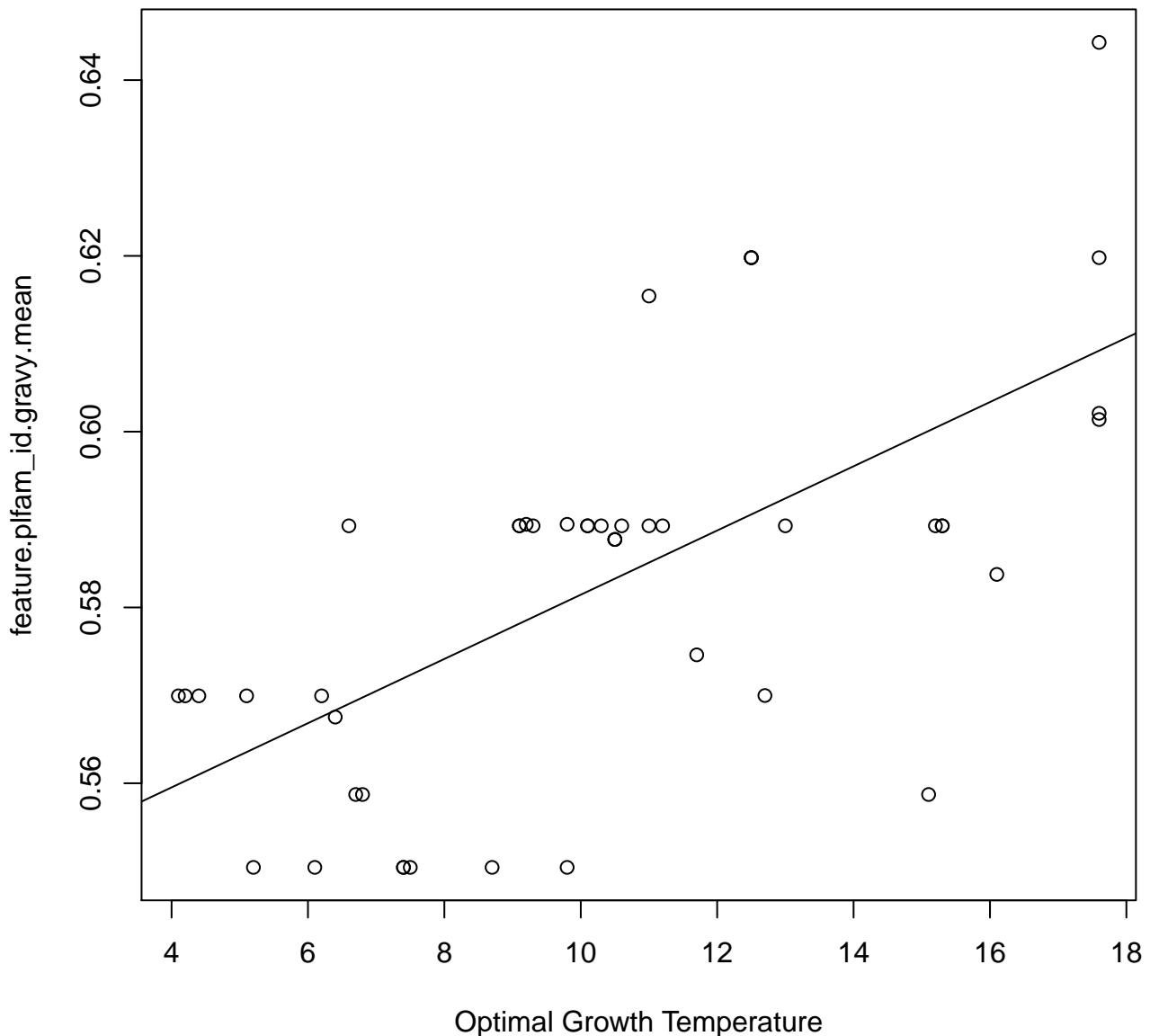
feature.plfam_id.gravy.mean
PLF_28228_00001831
FIG021625: hypothetical protein



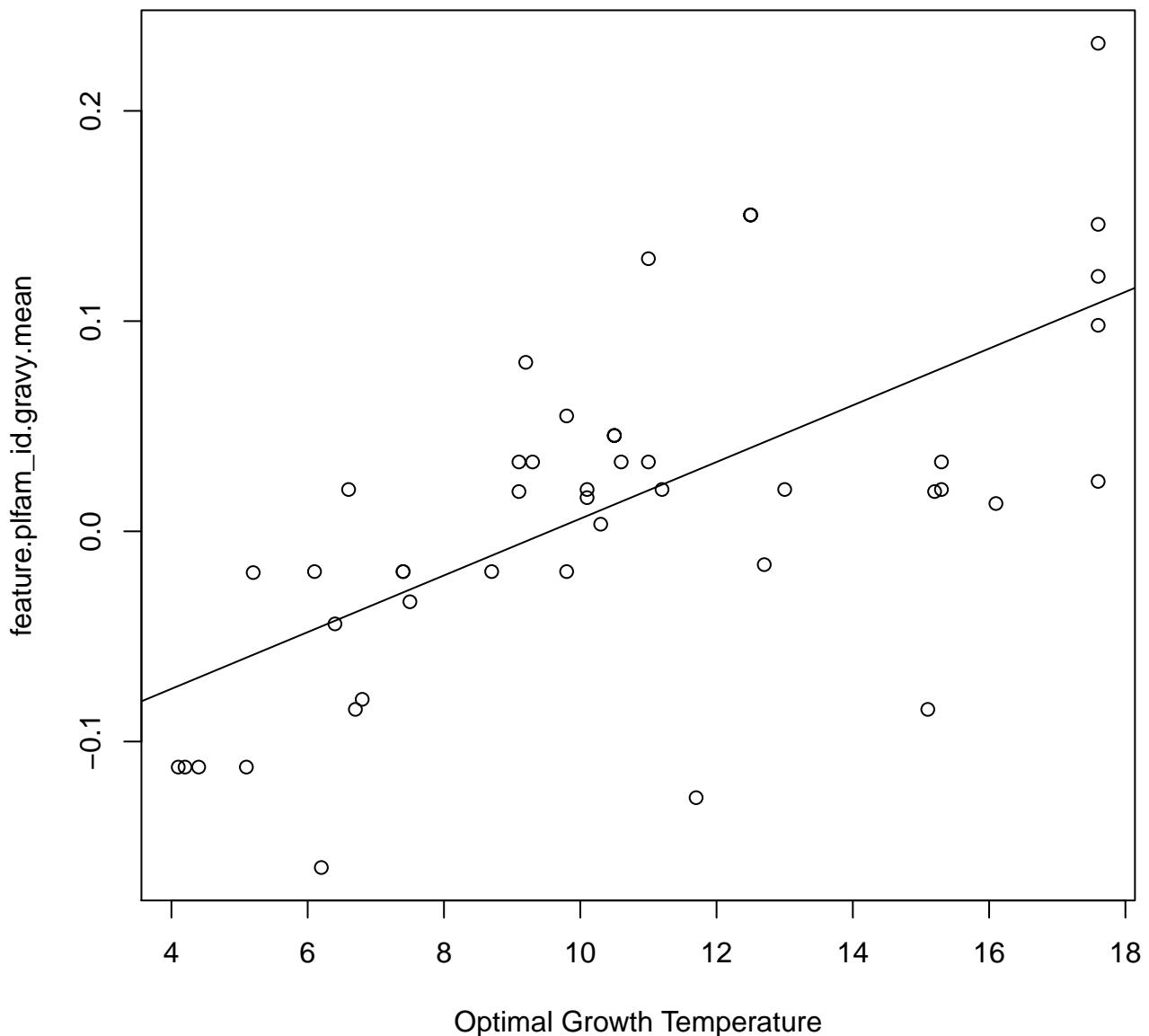
feature.plfam_id.gravy.mean
PLF_28228_00000470
FMN adenylyltransferase (EC 2.7.7.2) / Riboflavin kinase (EC 2.7.1.26)



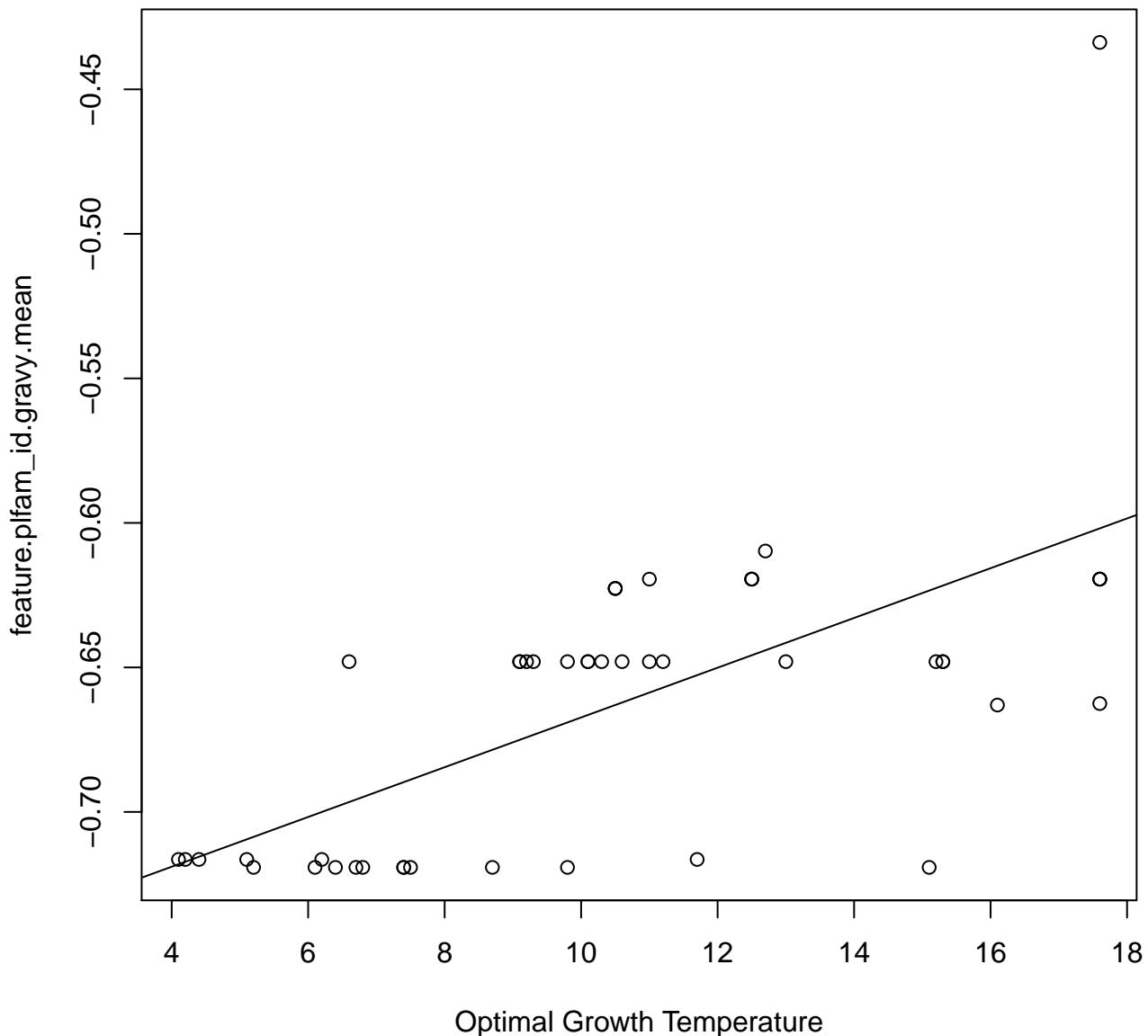
feature.plfam_id.gravy.mean
PLF_28228_00000730
Acetate permease ActP (cation/acetate symporter)



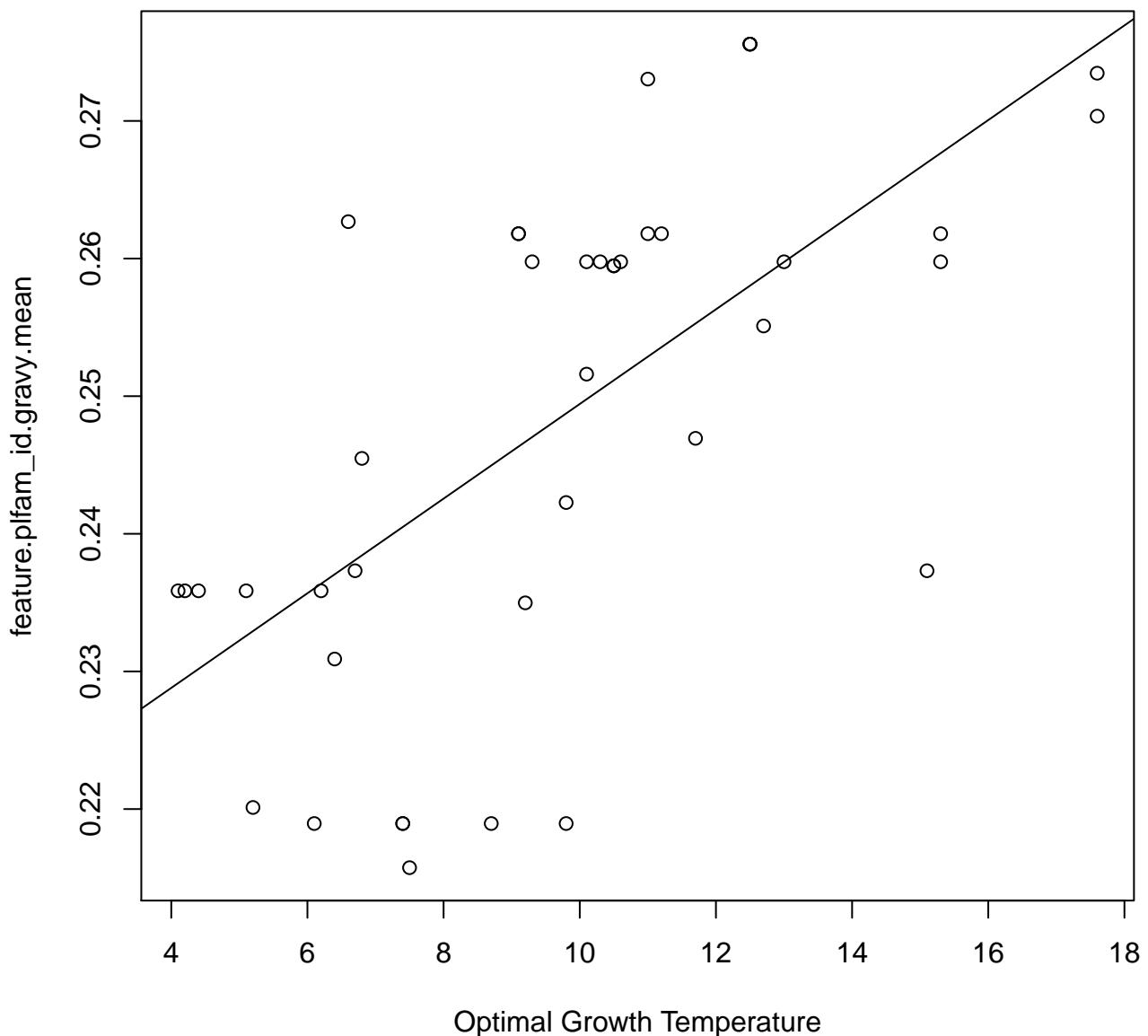
feature.plfam_id.gravy.mean
PLF_28228_00000361
Dephospho-CoA kinase (EC 2.7.1.24)



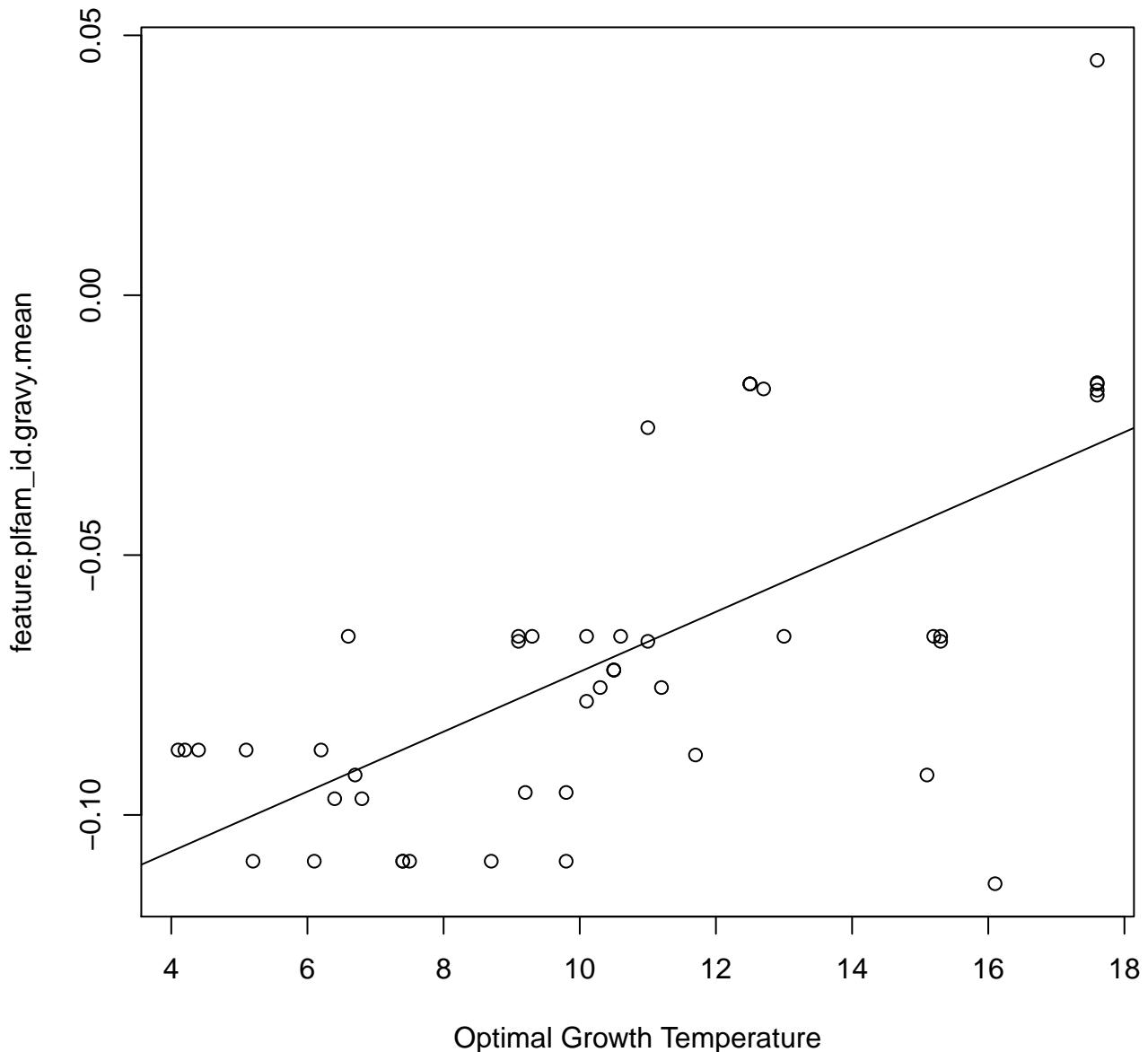
feature.plfam_id.gravy.mean
PLF_28228_00000118
Cold shock protein of CSP family => CspD (naming convention as in E.coli)



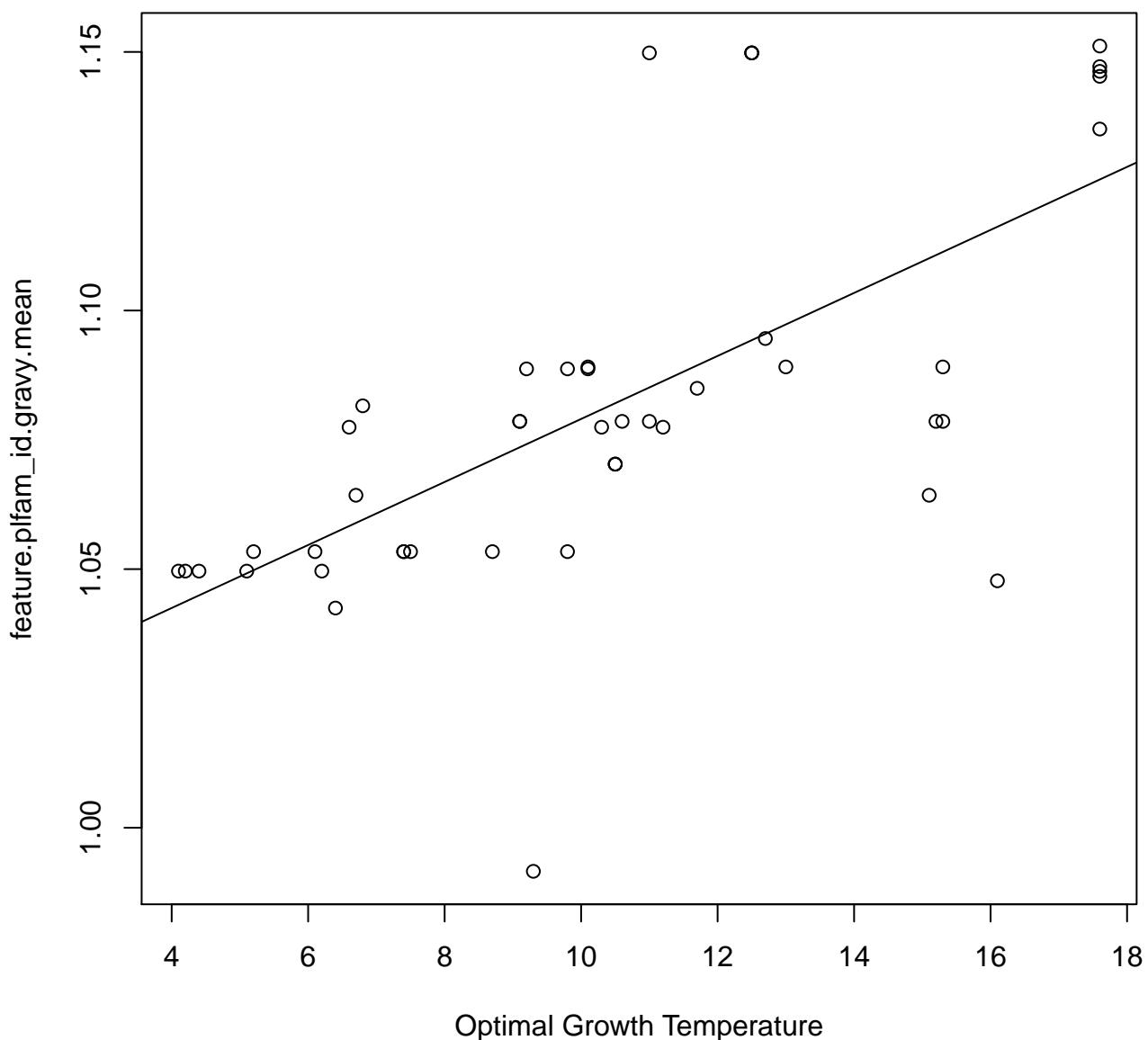
feature.pifam_id.gravy.mean
PLF_28228_00003639
Selenide,water dikinase (EC 2.7.9.3)



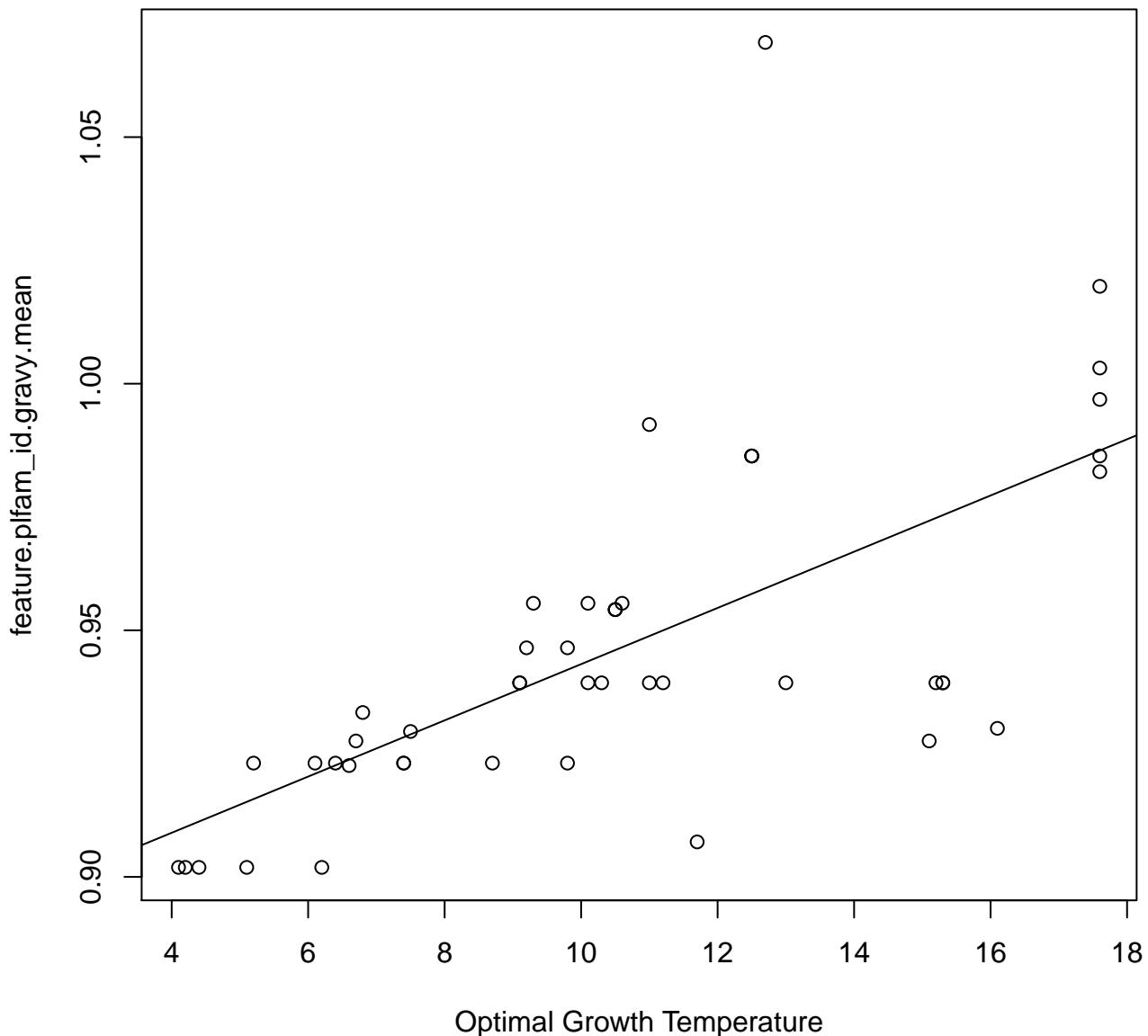
feature.plfam_id.gravy.mean
PLF_28228_00000534
Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)



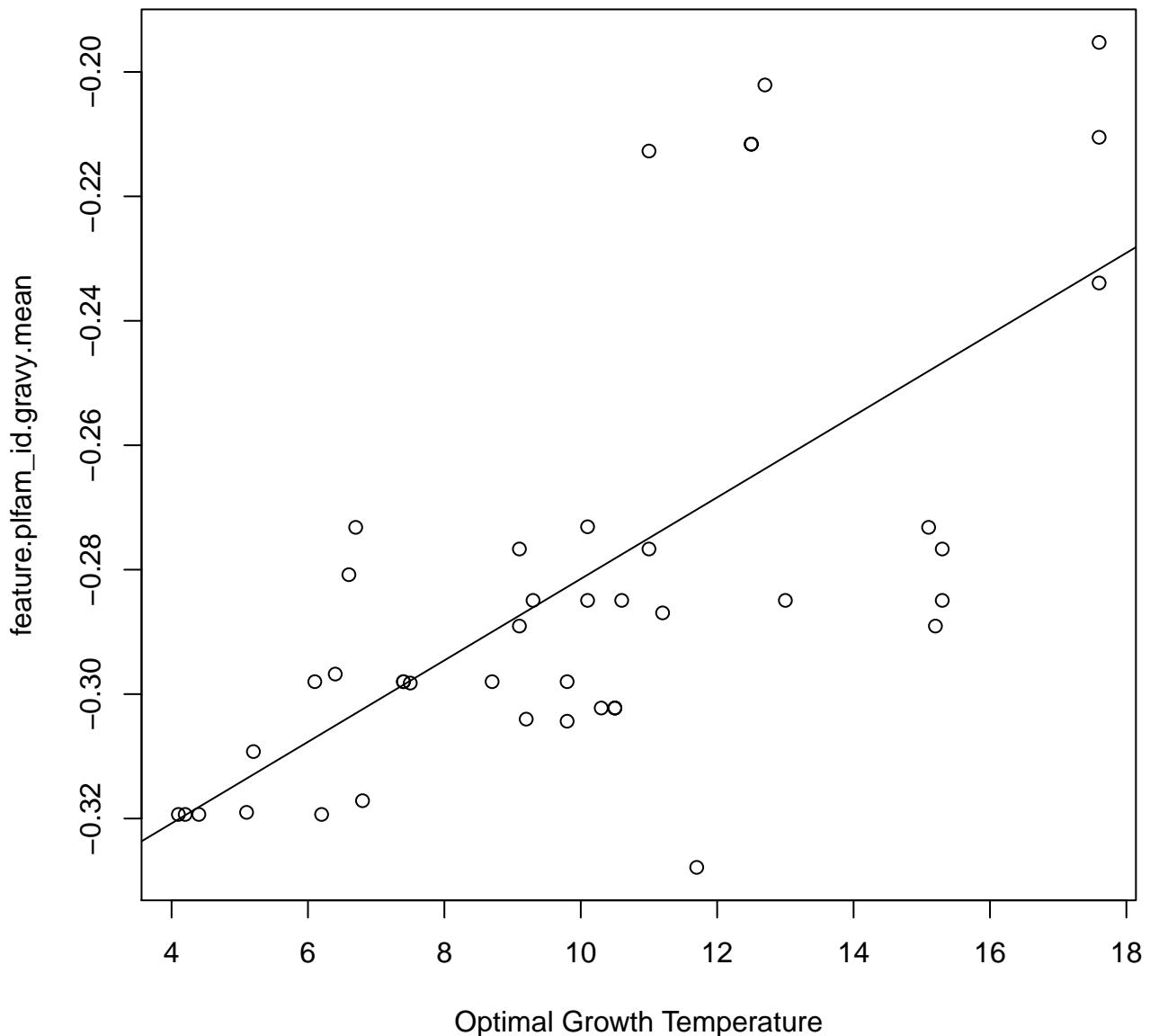
feature.plfam_id.gravy.mean
PLF_28228_00000548
Inner membrane protein YpjD



feature.plfam_id.gravy.mean
PLF_28228_00000132
Phosphatidylglycerophosphatase A (EC 3.1.3.27)



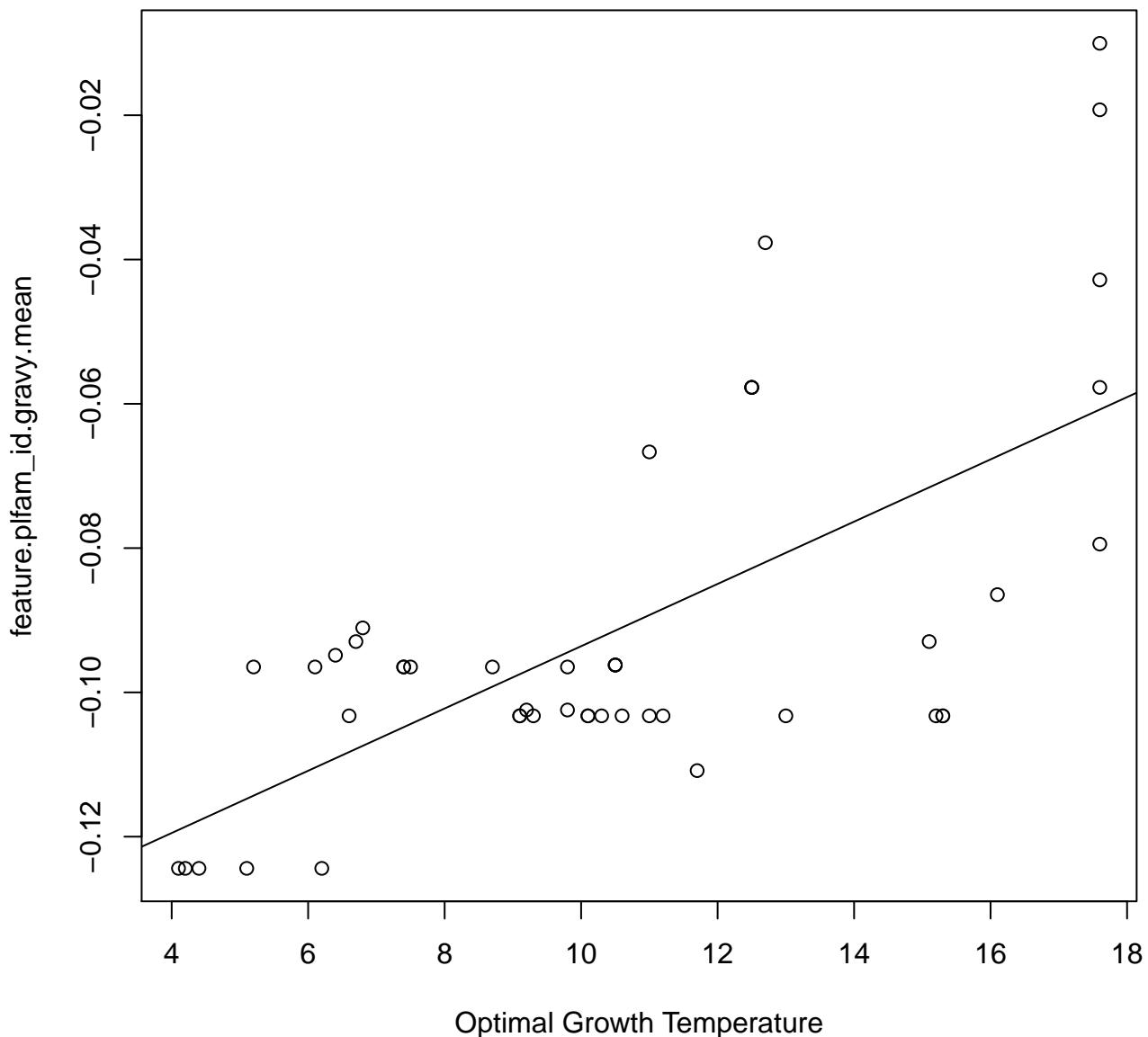
feature.plfam_id.gravy.mean
PLF_28228_00001578
Assimilatory nitrate reductase large subunit (EC 1.7.99.4)



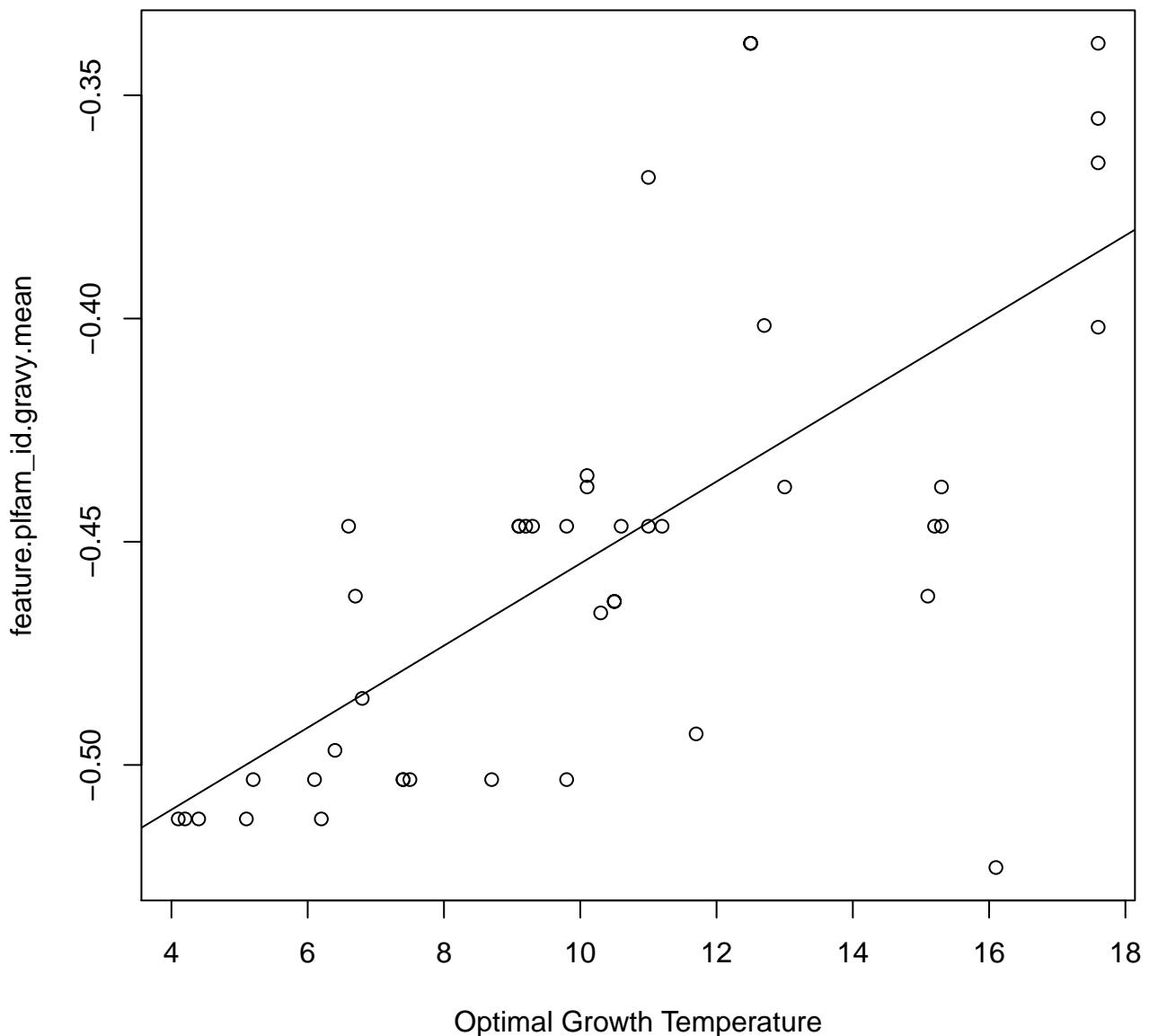
feature.plfam_id.gravy.mean

PLF_28228_00000264

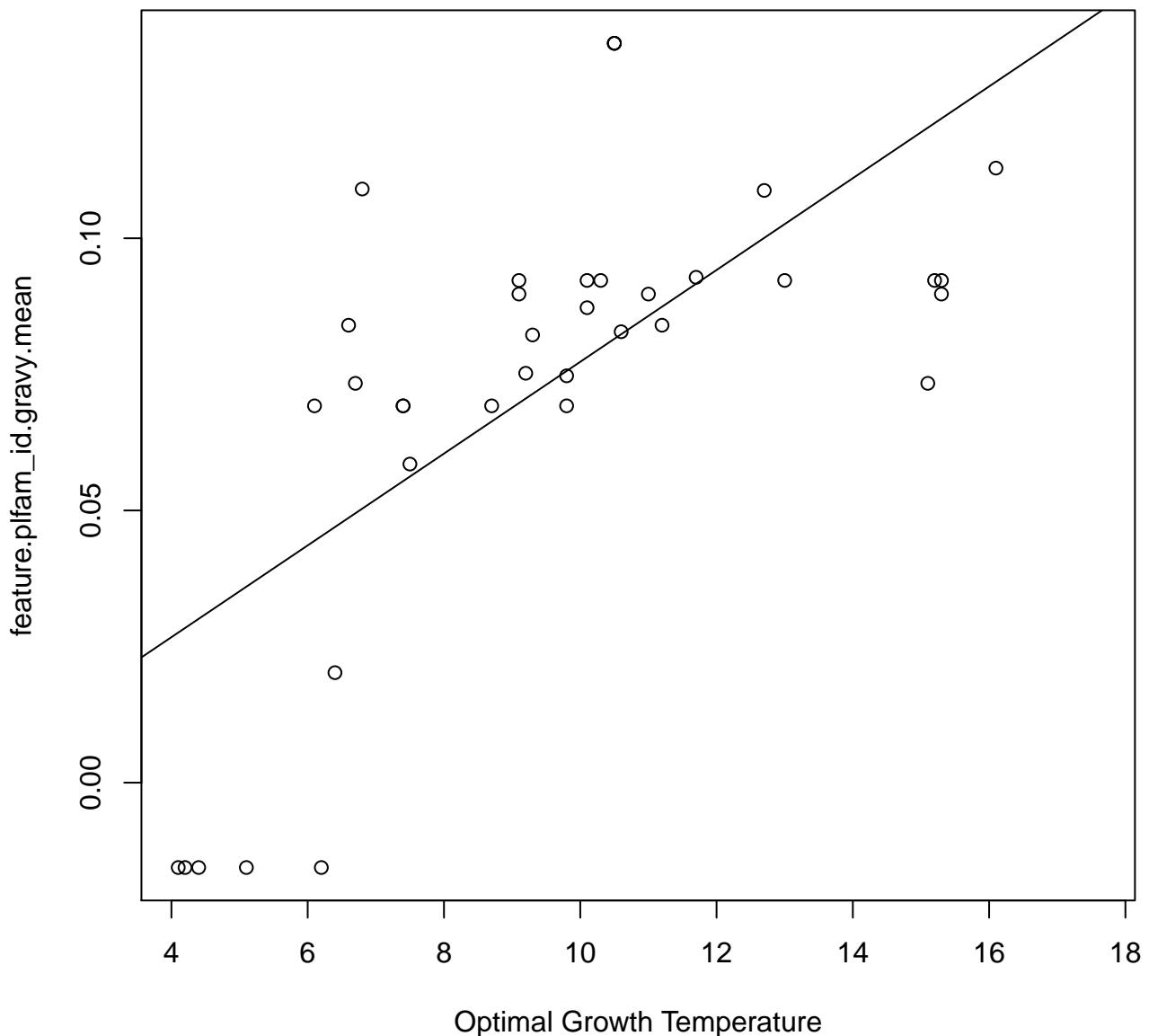
3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12) / GTP cyclohydrolase II (EC 3.5.4.25)



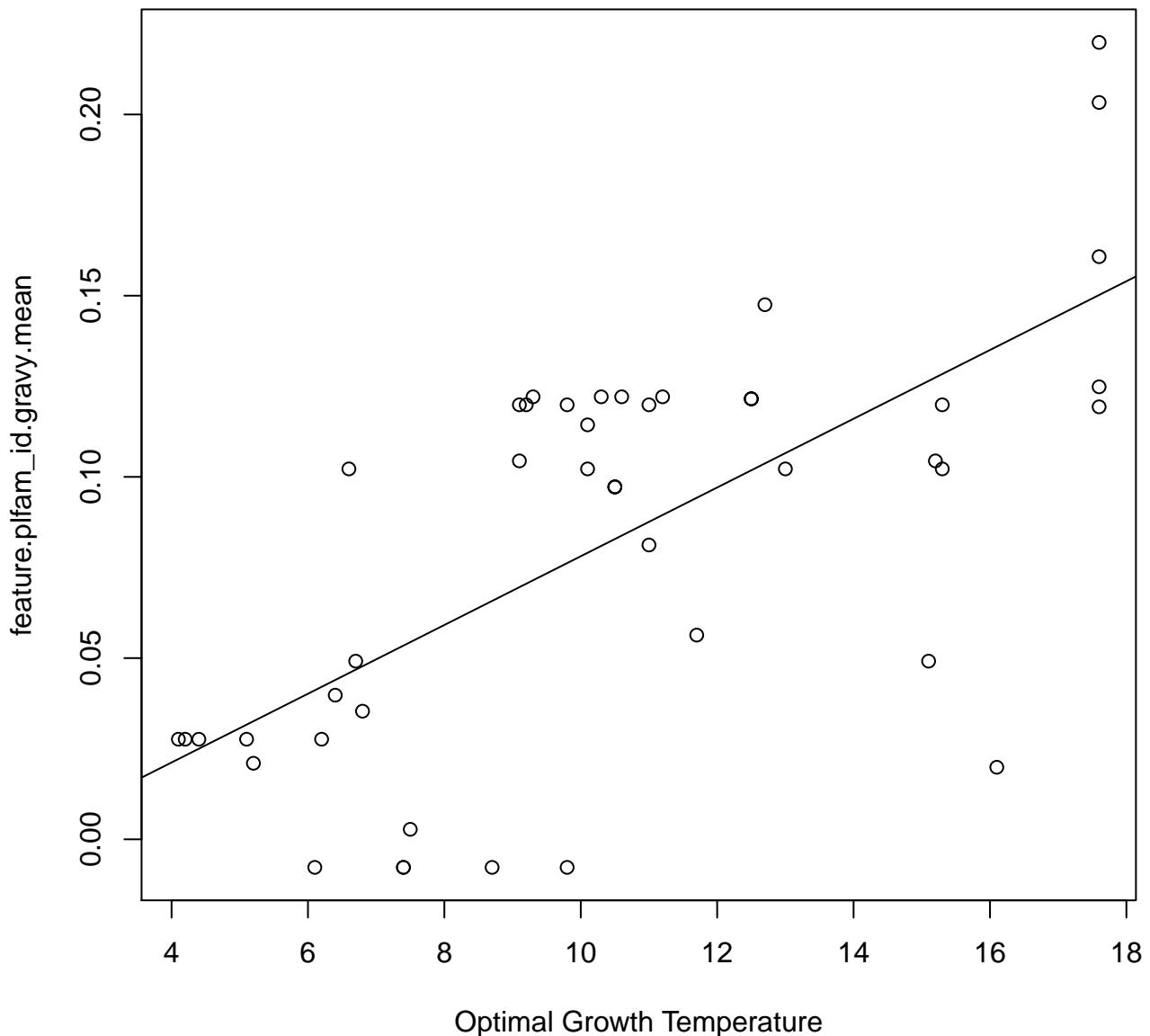
feature.plfam_id.gravy.mean
PLF_28228_00001397
tRNA (guanine(37)-N(1))-methyltransferase (EC 2.1.1.228)



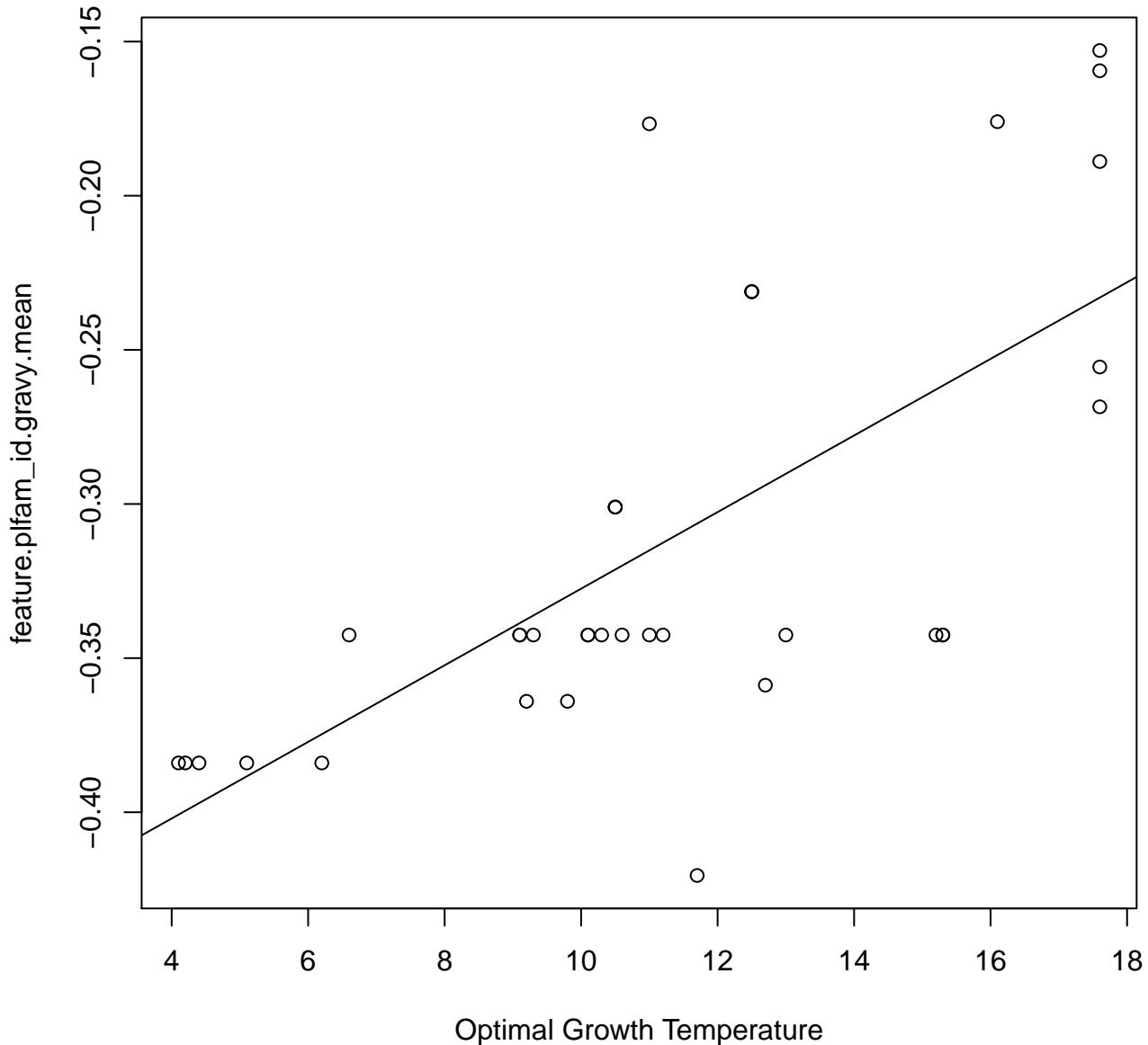
feature.plfam_id.gravy.mean
PLF_28228_00022897
Invasin domain protein



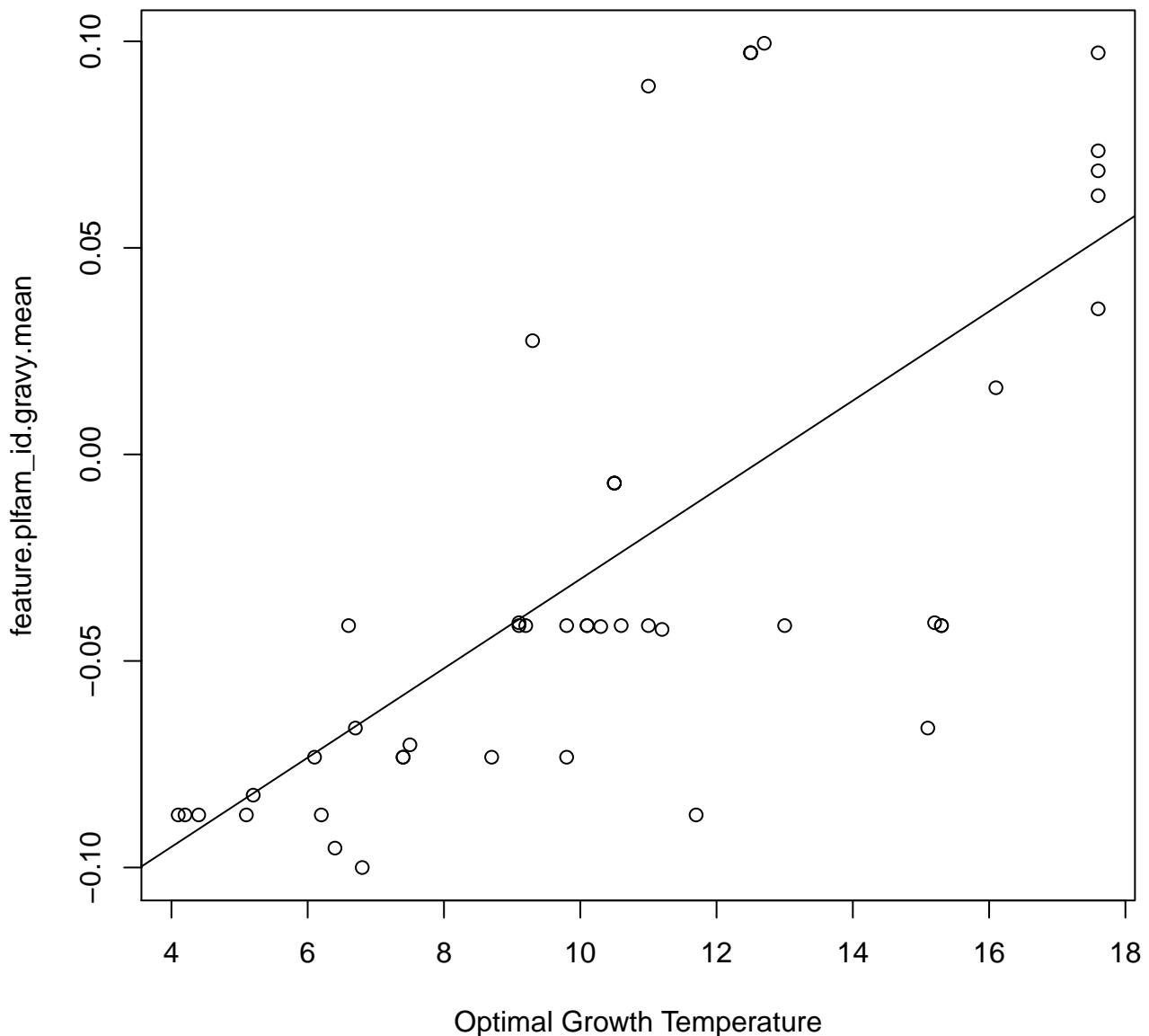
feature.plfam_id.gravy.mean
PLF_28228_00000267
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)



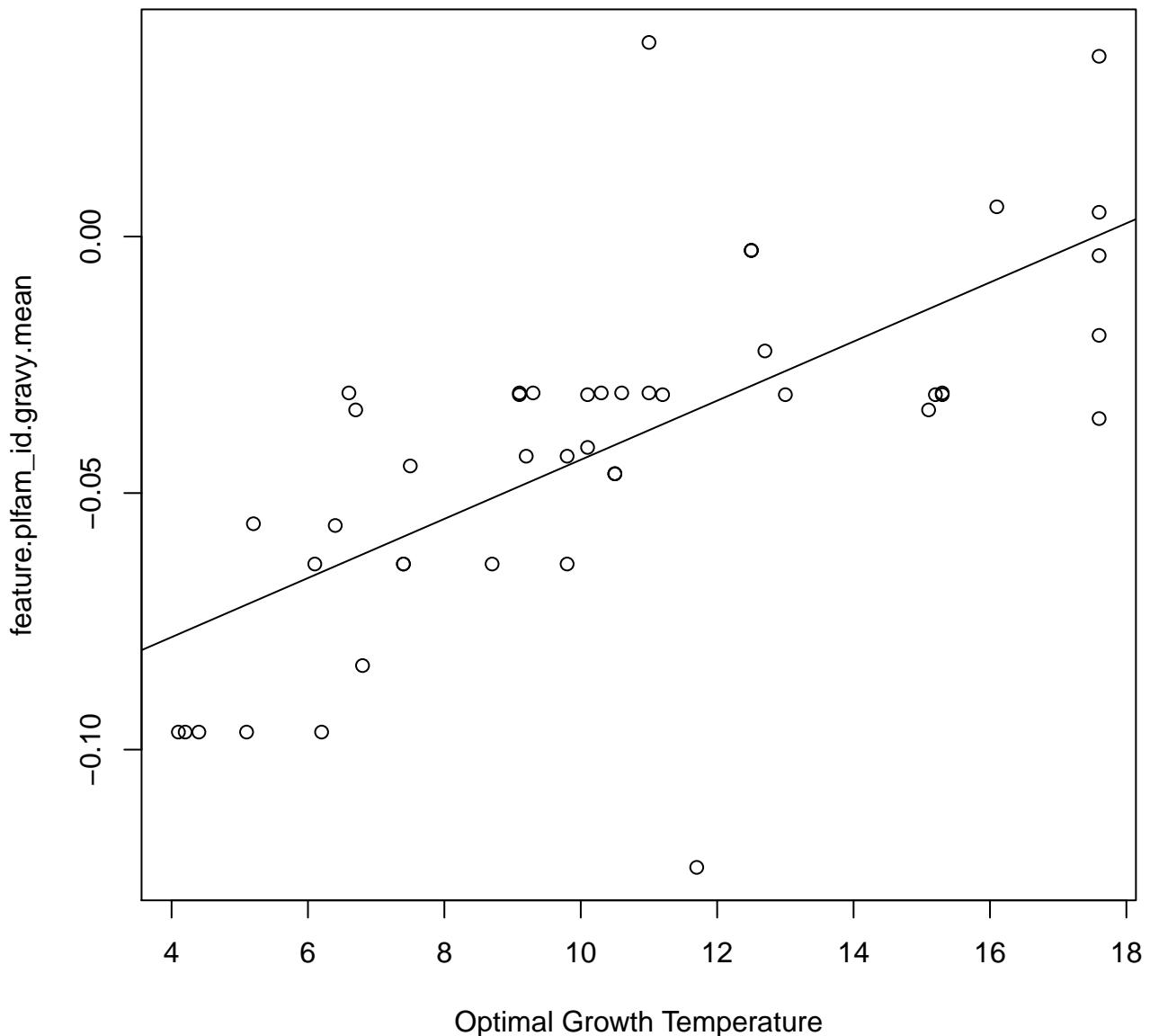
feature.plfam_id.gravy.mean
PLF_28228_00001944
RNA polymerase ECF-type sigma factor



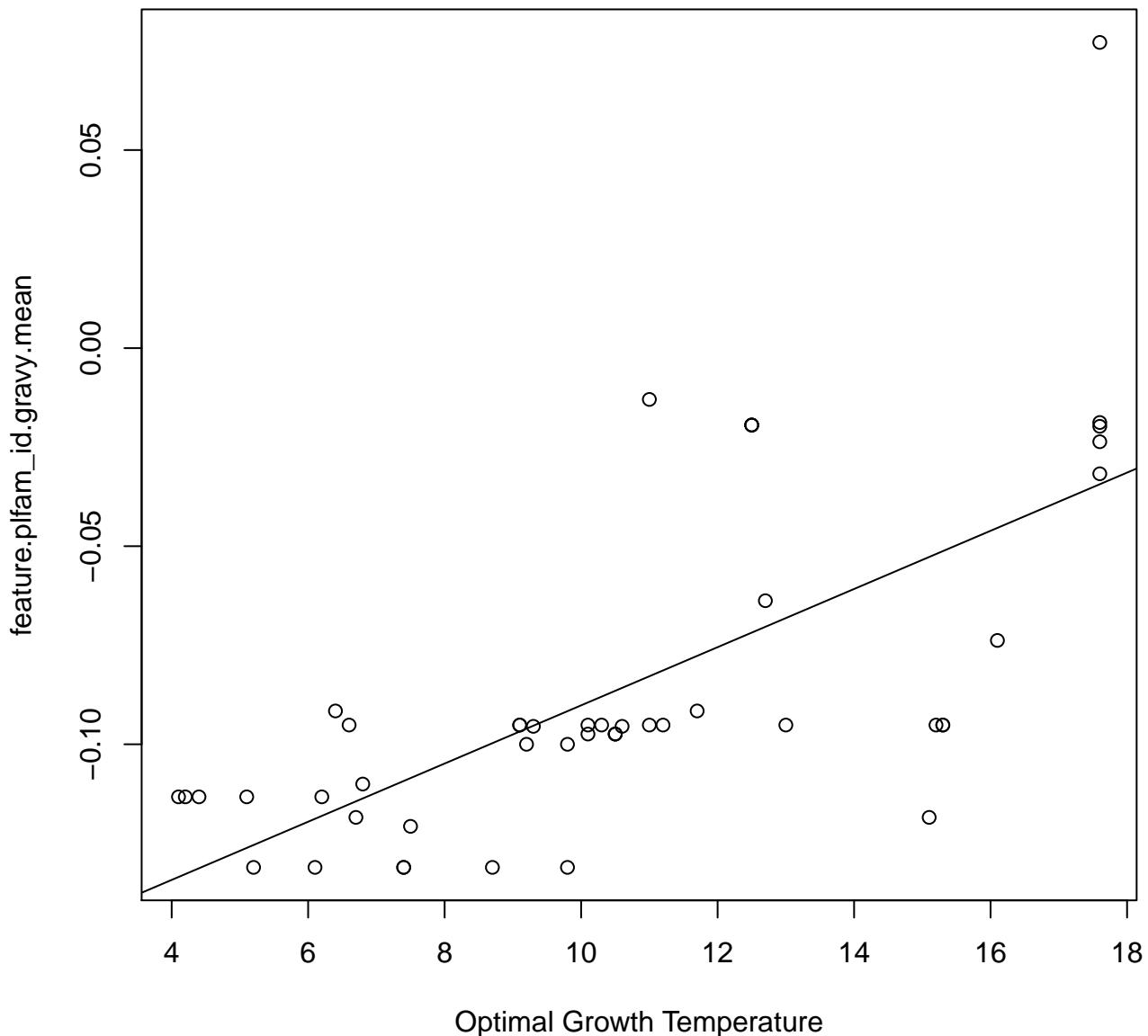
feature.pifam_id.gravy.mean
PLF_28228_00000499
Histidinol dehydrogenase (EC 1.1.1.23)



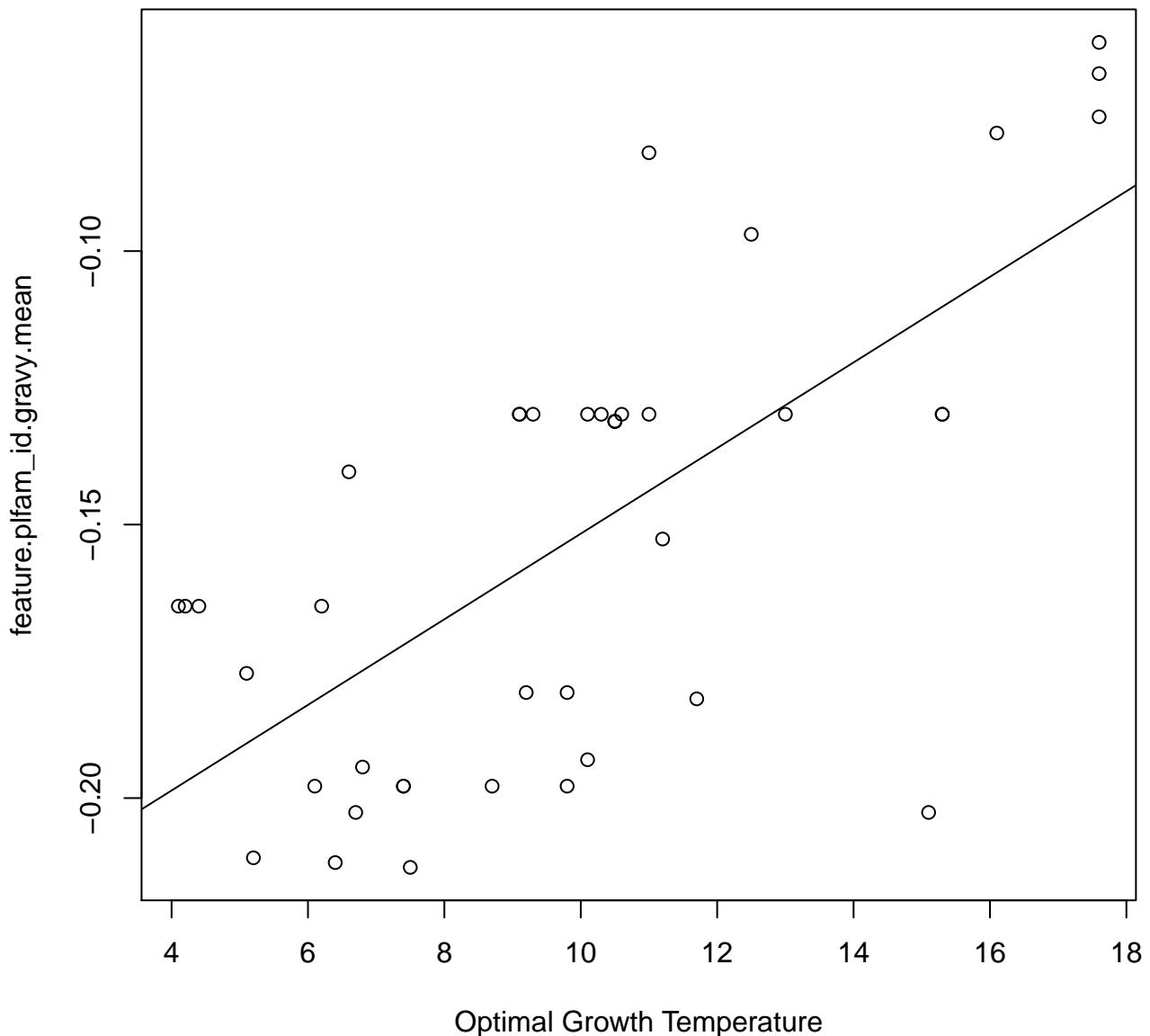
feature.plfam_id.gravy.mean
PLF_28228_00002316
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



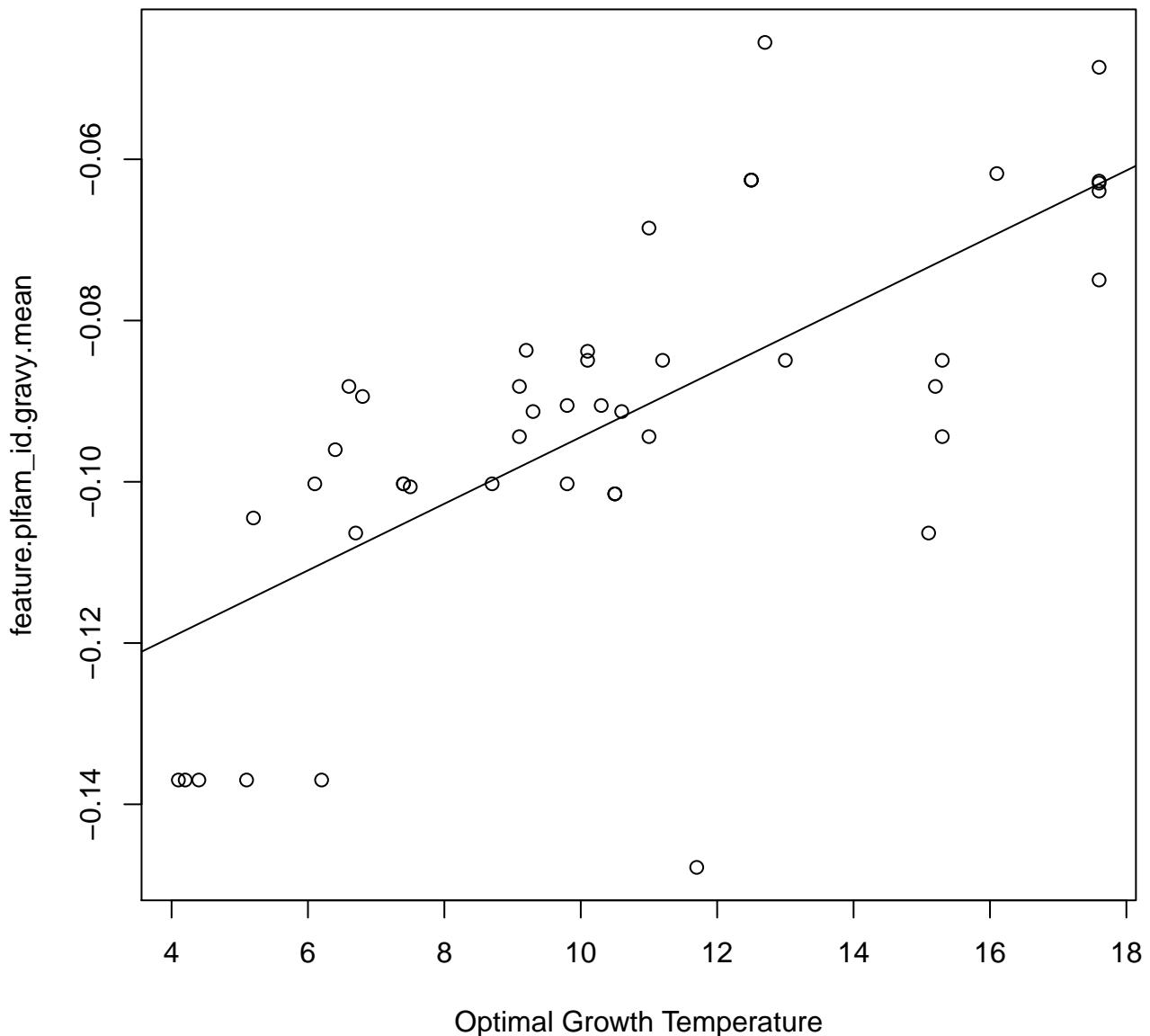
feature.plfam_id.gravy.mean
PLF_28228_00000227
4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.7.4)



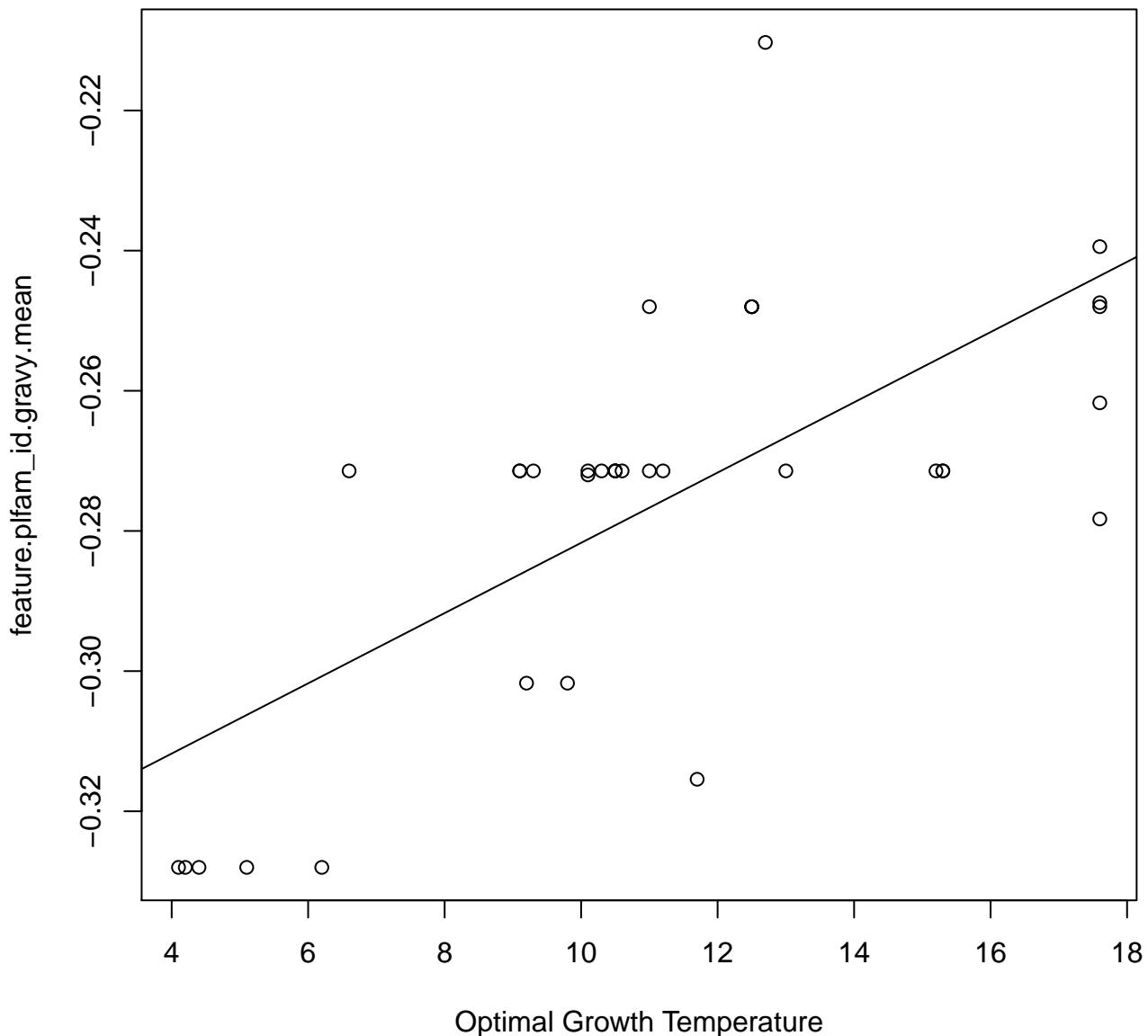
feature.plfam_id.gravy.mean
PLF_28228_00028198
FIG111991: hypothetical protein



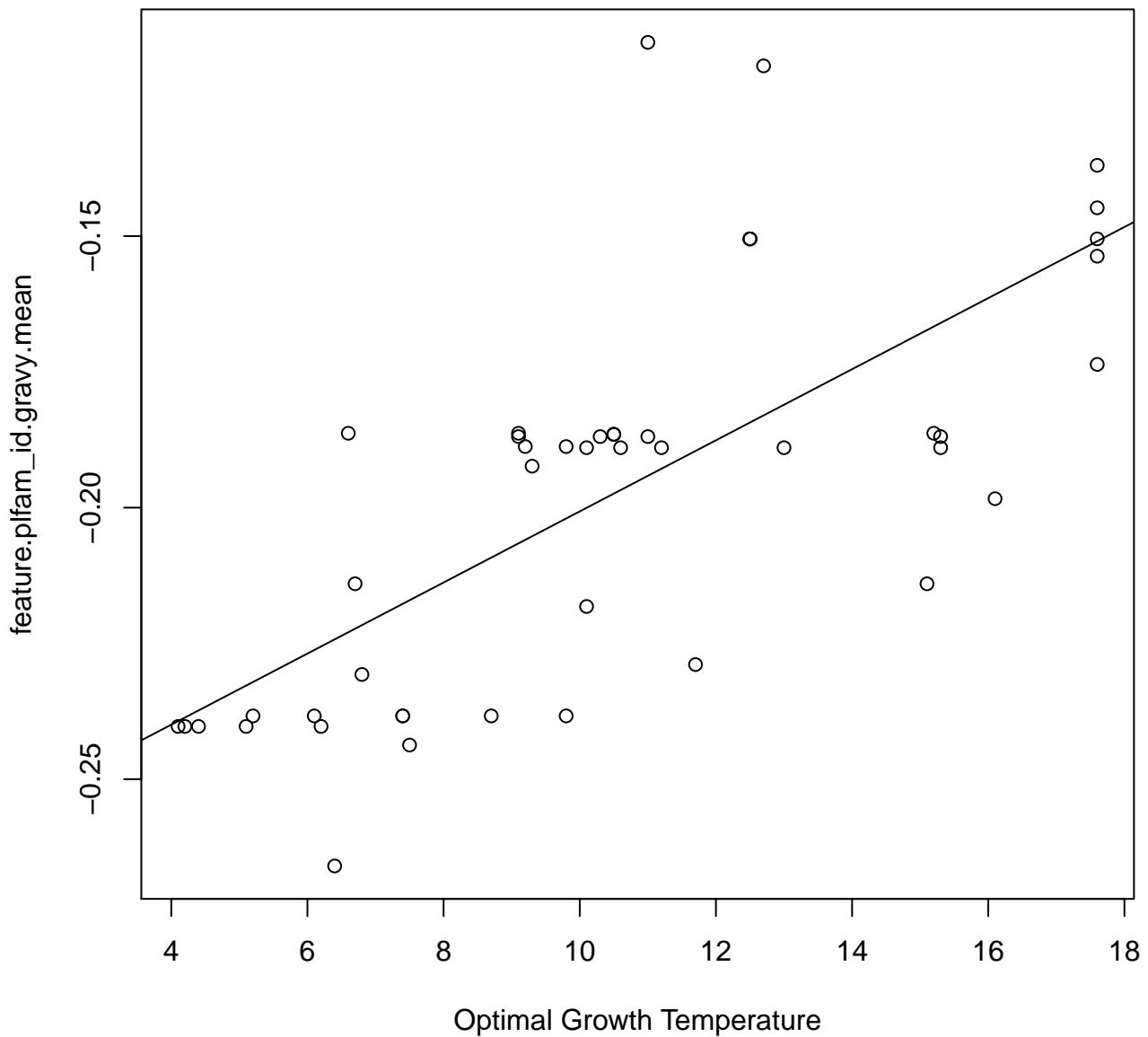
feature.plfam_id.gravy.mean
PLF_28228_00000941
Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)



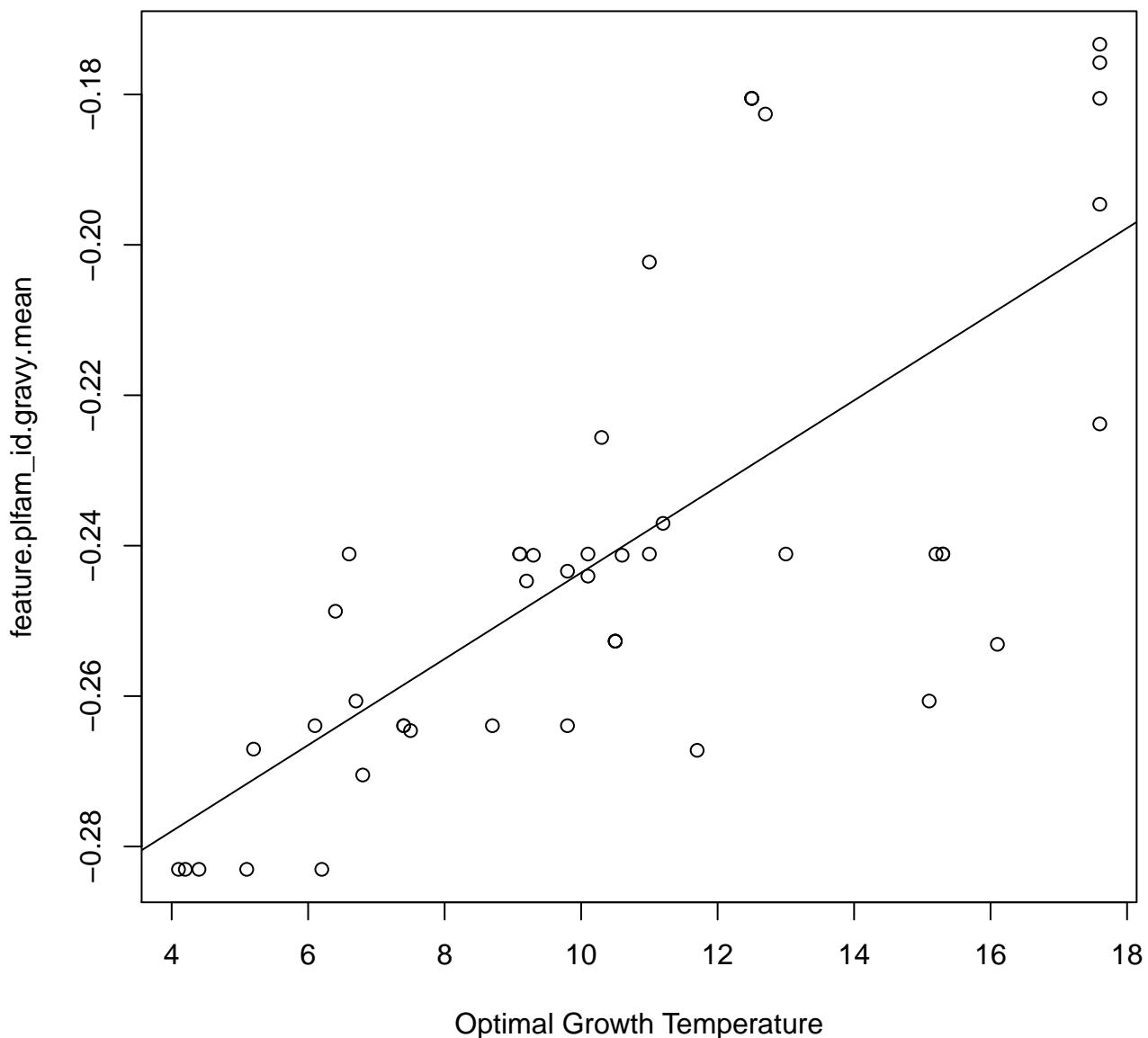
feature.plfam_id.gravy.mean
PLF_28228_00001835
Bacterial non-heme ferritin (EC 1.16.3.2)



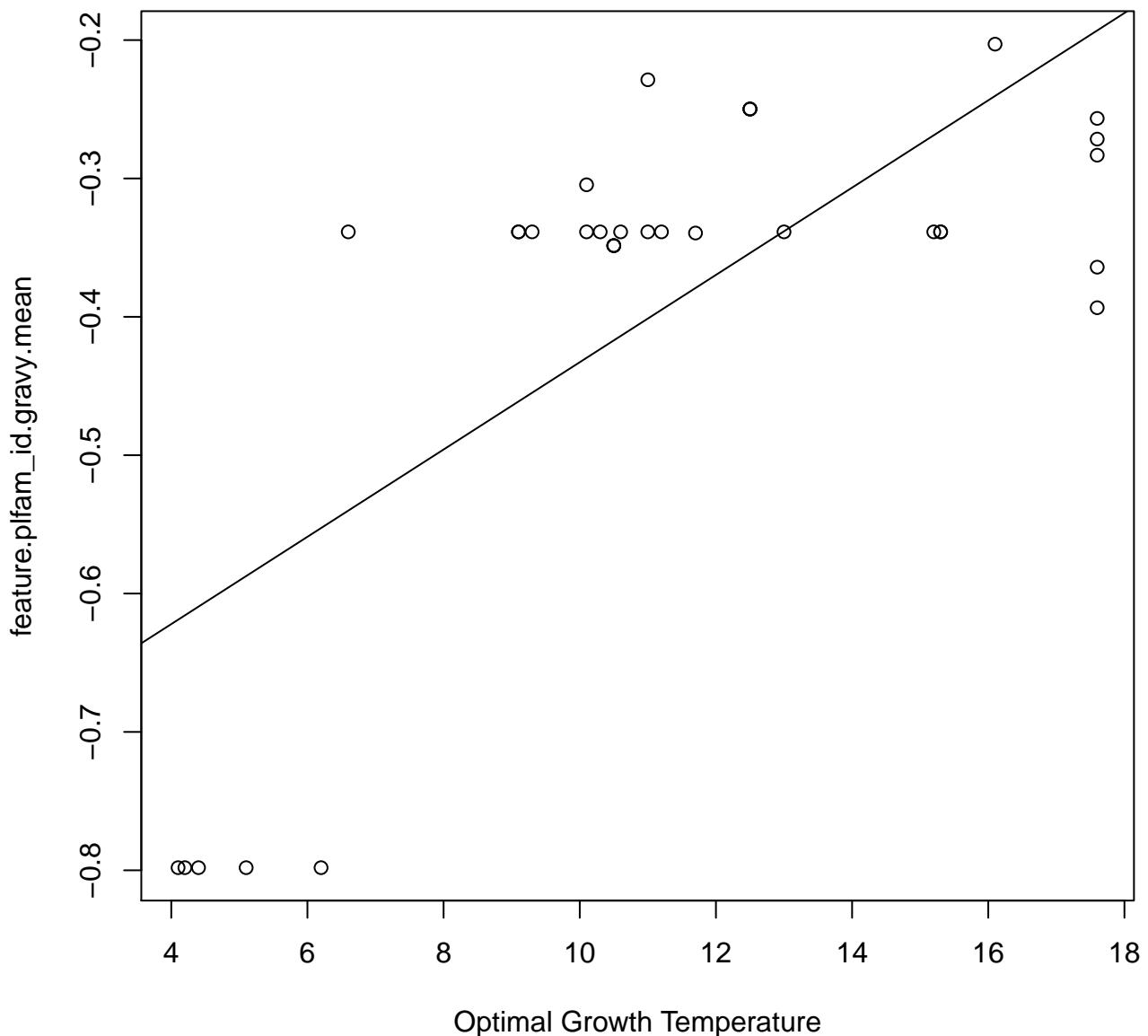
feature.plfam_id.gravy.mean
PLF_28228_00000790
Exported zinc metalloprotease YfgC precursor



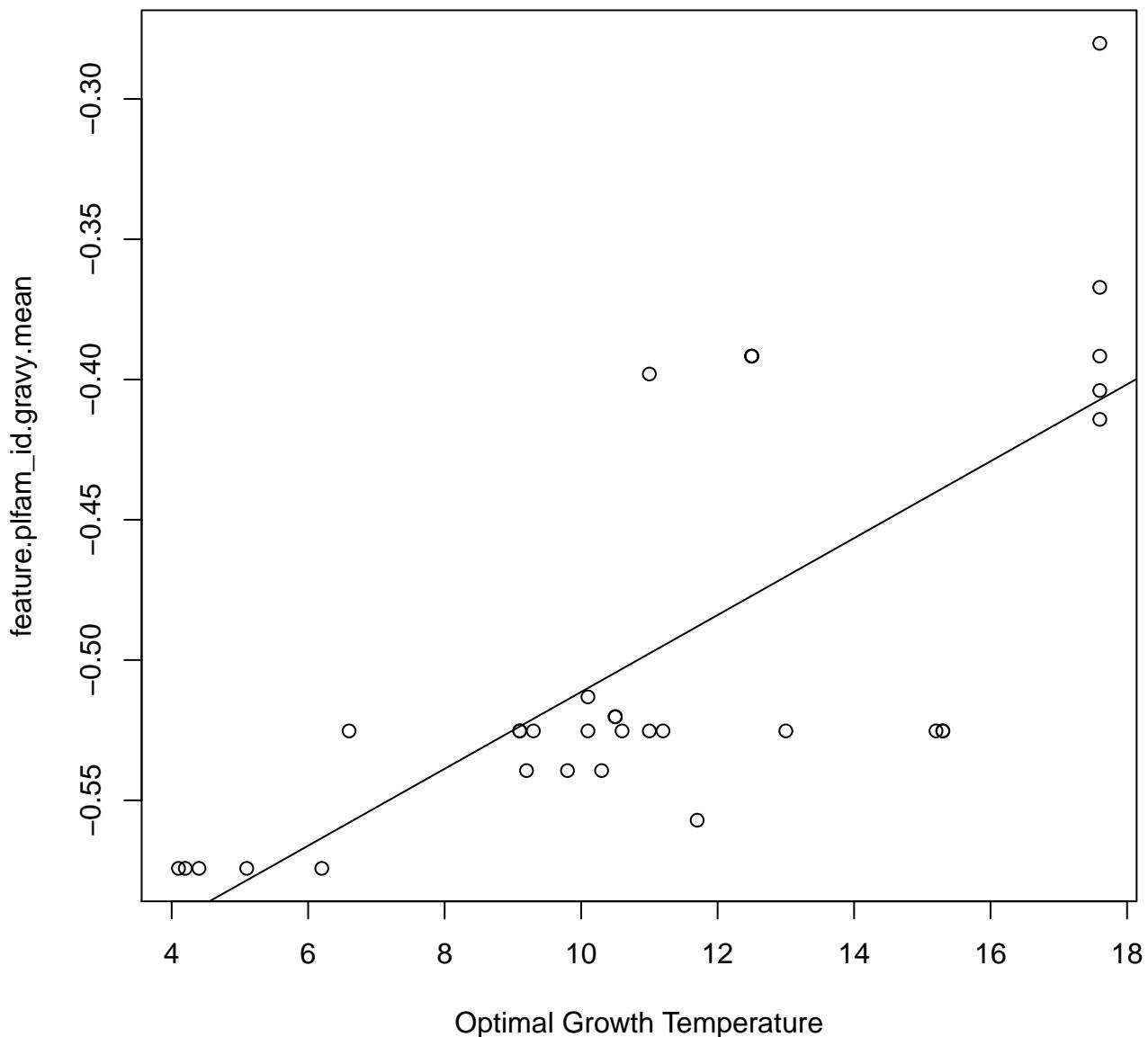
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PLF_28228_00001960
Protein kinase



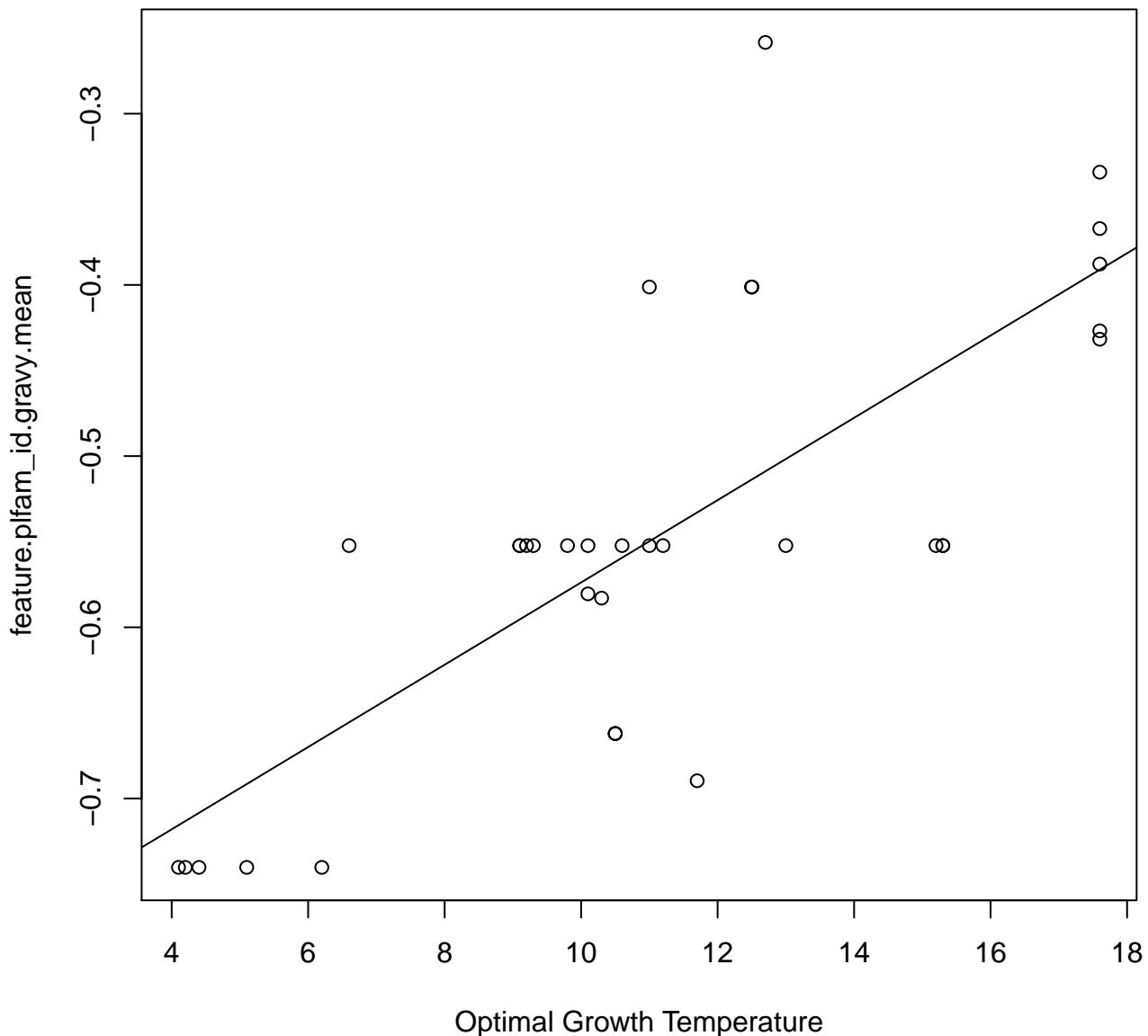
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PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



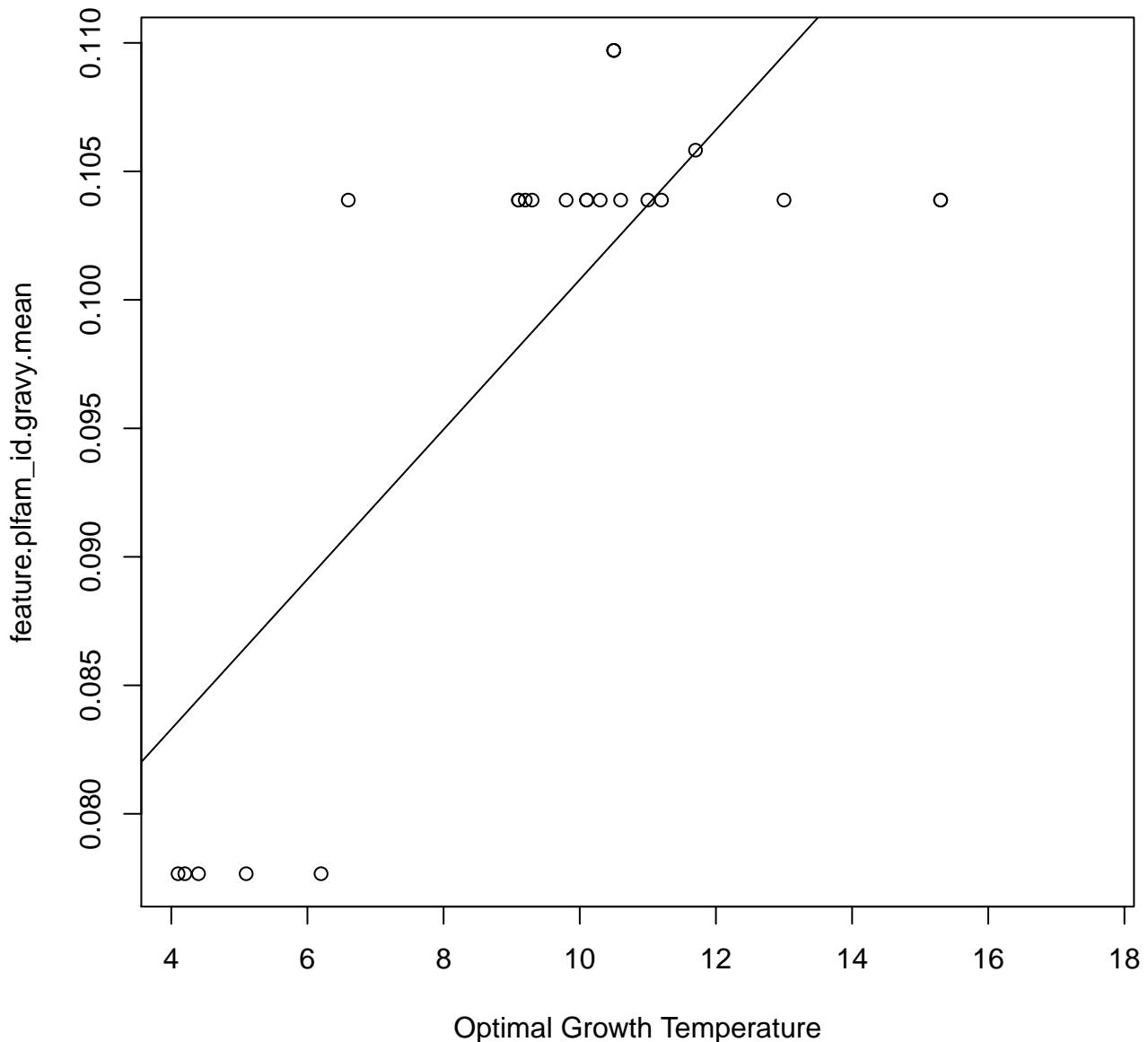
feature.plfam_id.gravy.mean
PLF_28228_00000866
GTP cyclohydrolase II (EC 3.5.4.25)



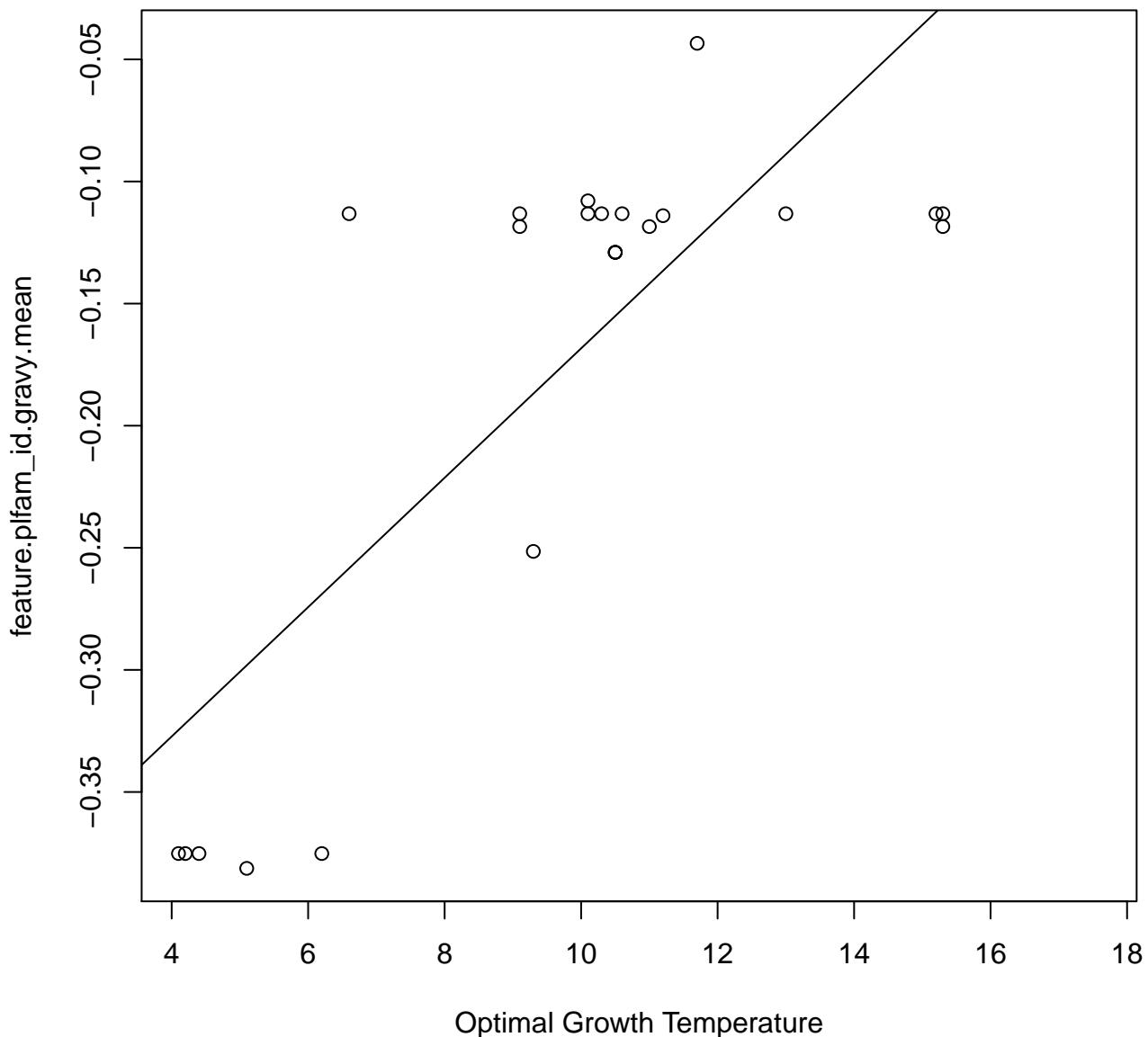
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Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)



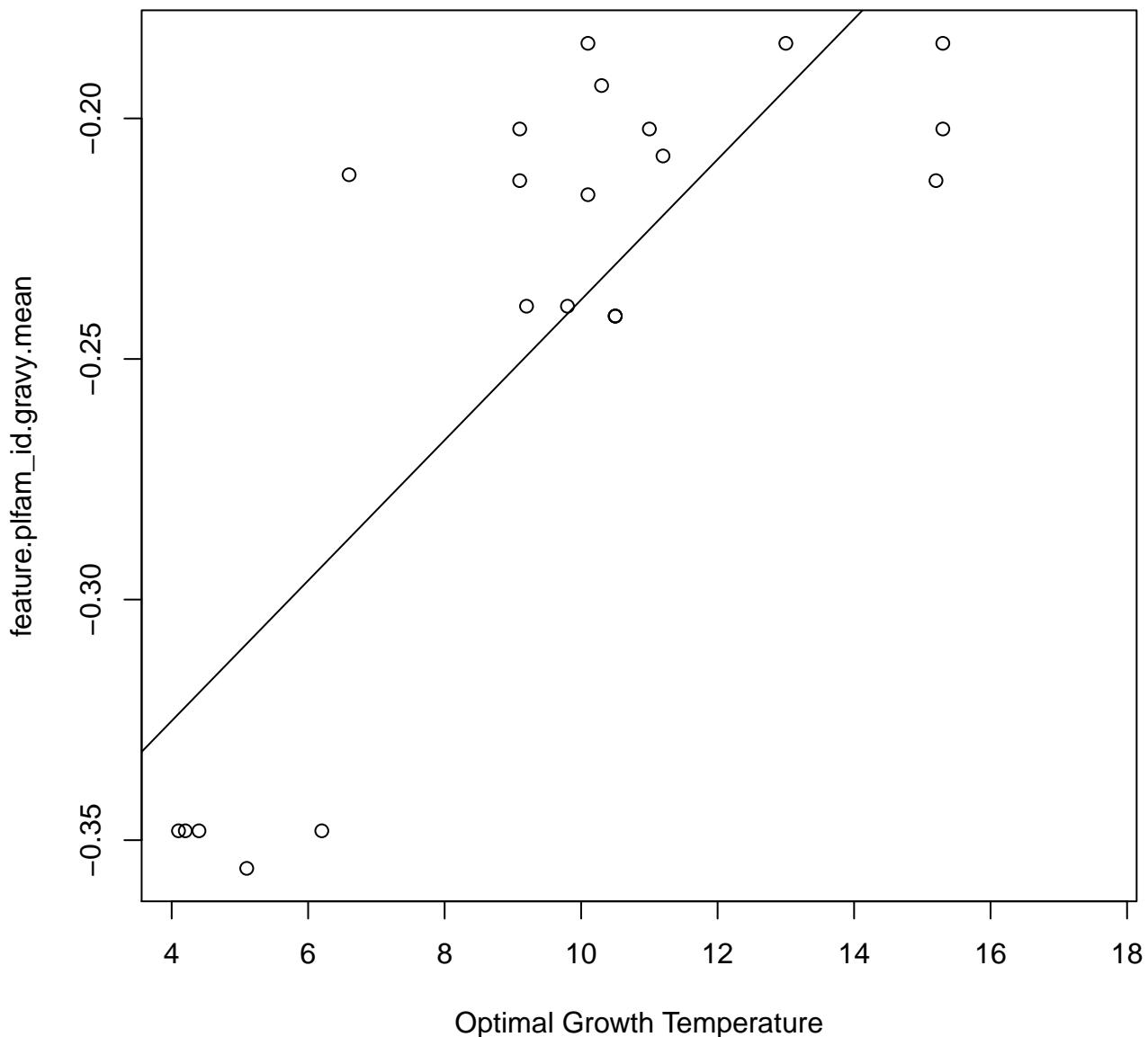
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PLF_28228_00015263
hypothetical protein



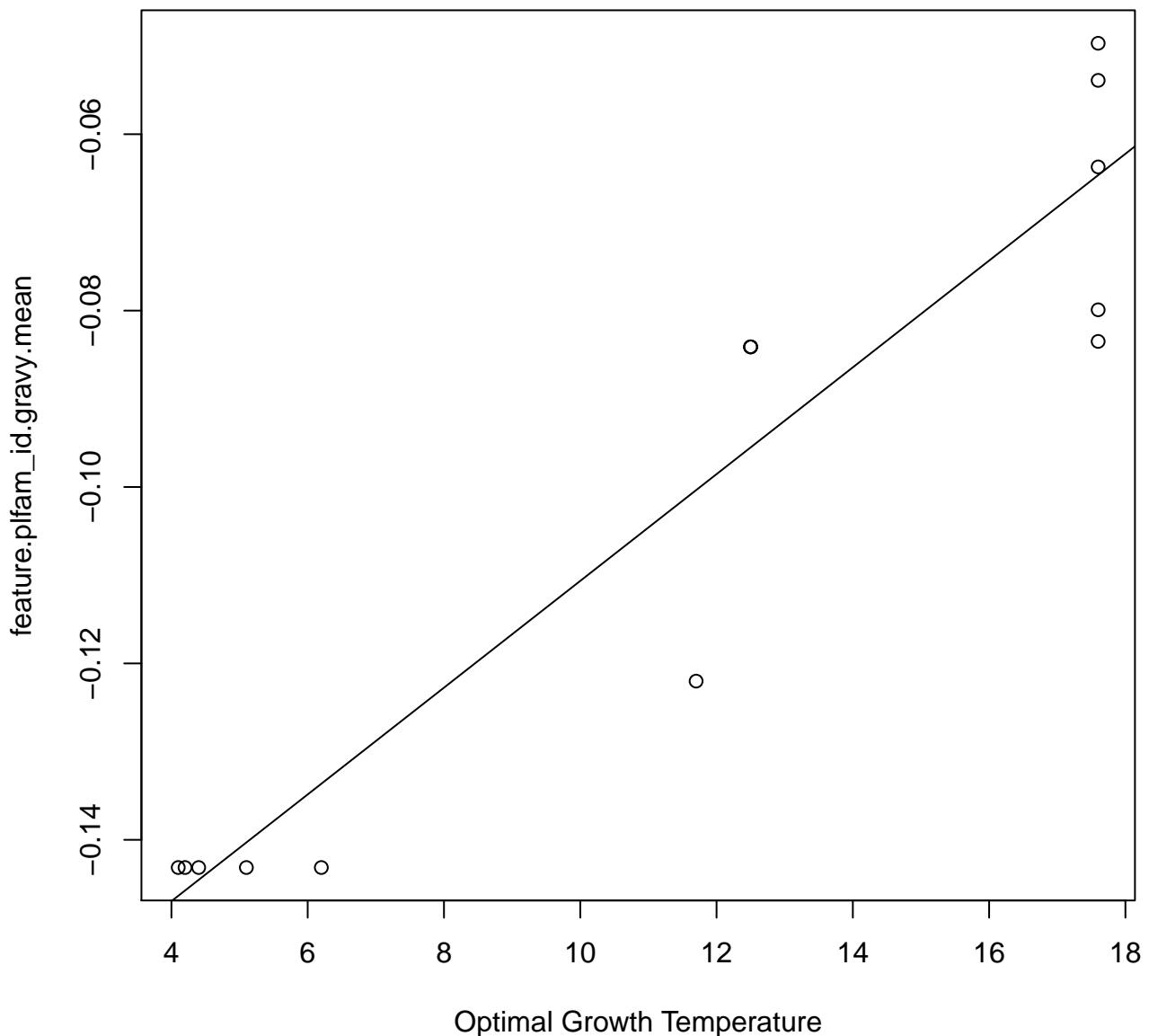
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PLF_28228_00022096
Two-component system sensor histidine kinase



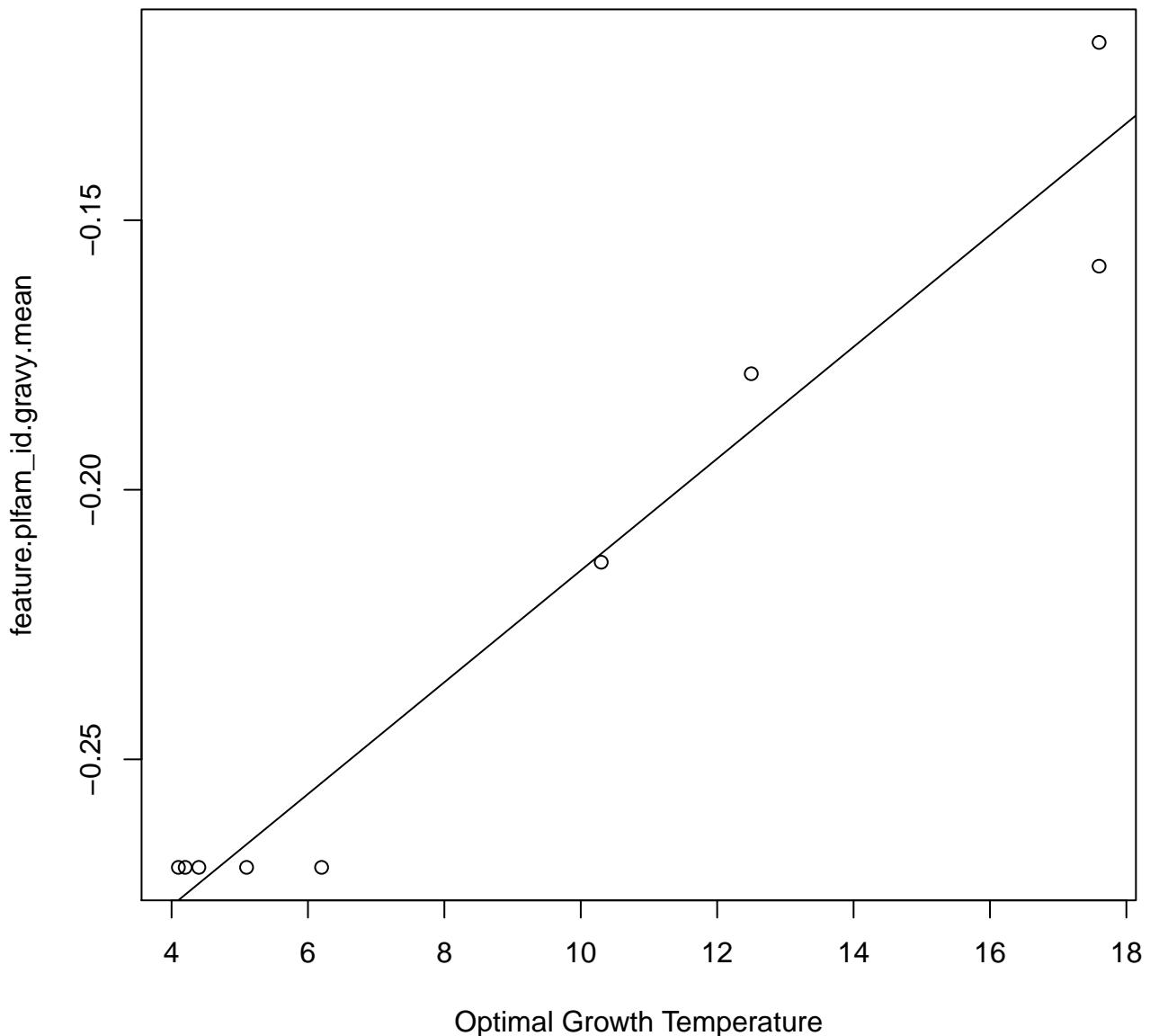
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PLF_28228_00017800
HD domain protein



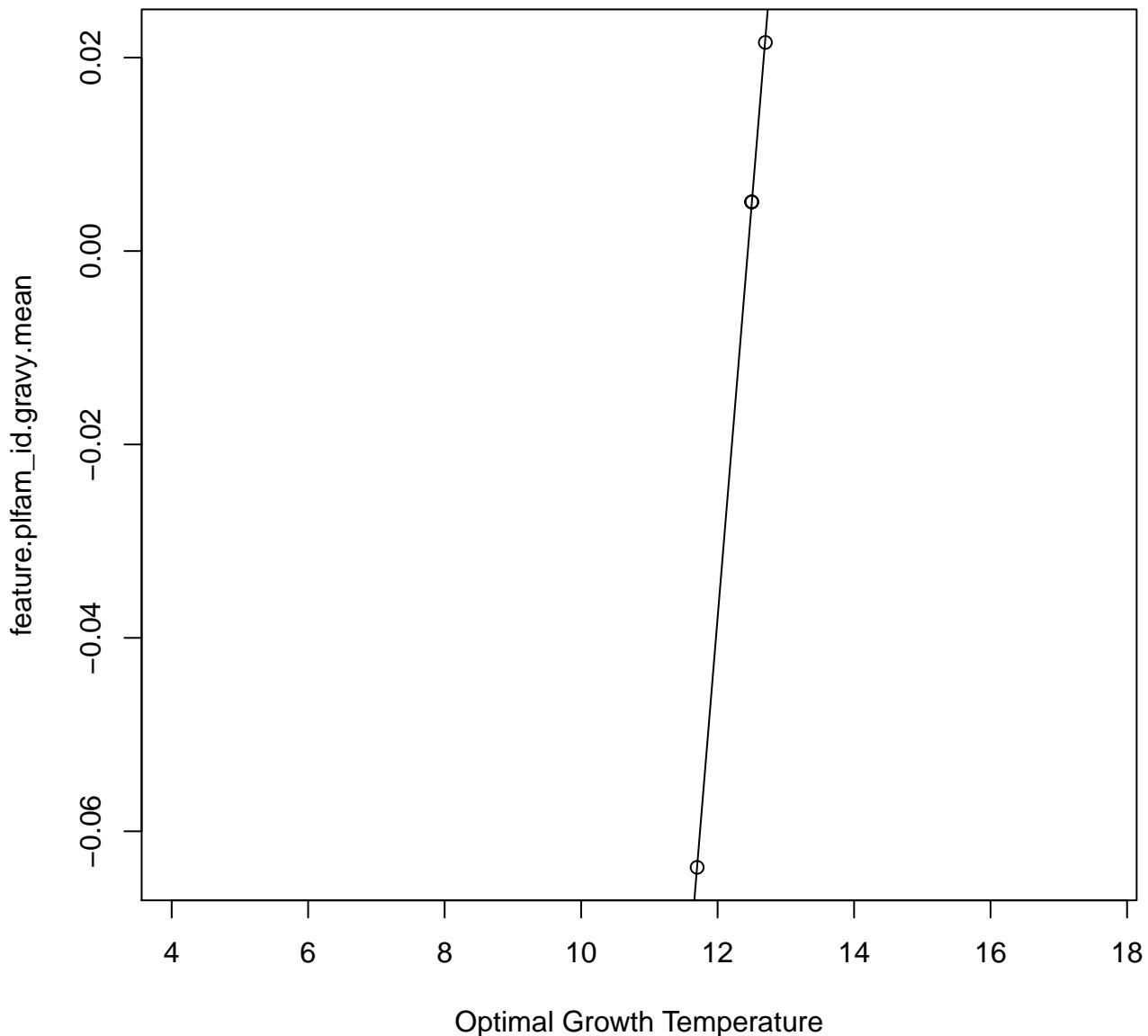
feature.pifam_id.gravy.mean
PLF_28228_00002708
Agglutinin-like sequence 9



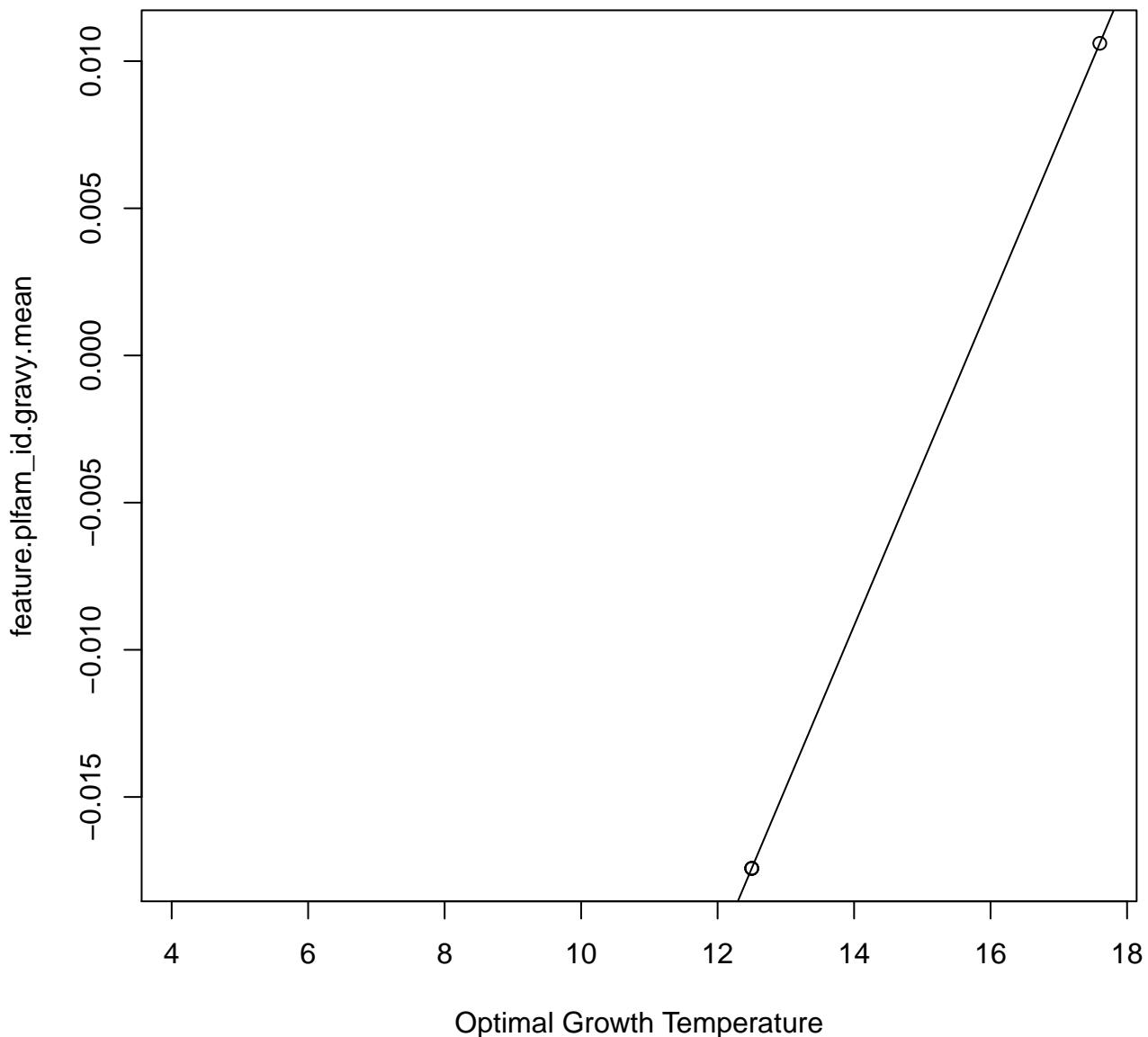
feature.pifam_id.gravy.mean
PLF_28228_00005390
Transcriptional regulator, AraC family



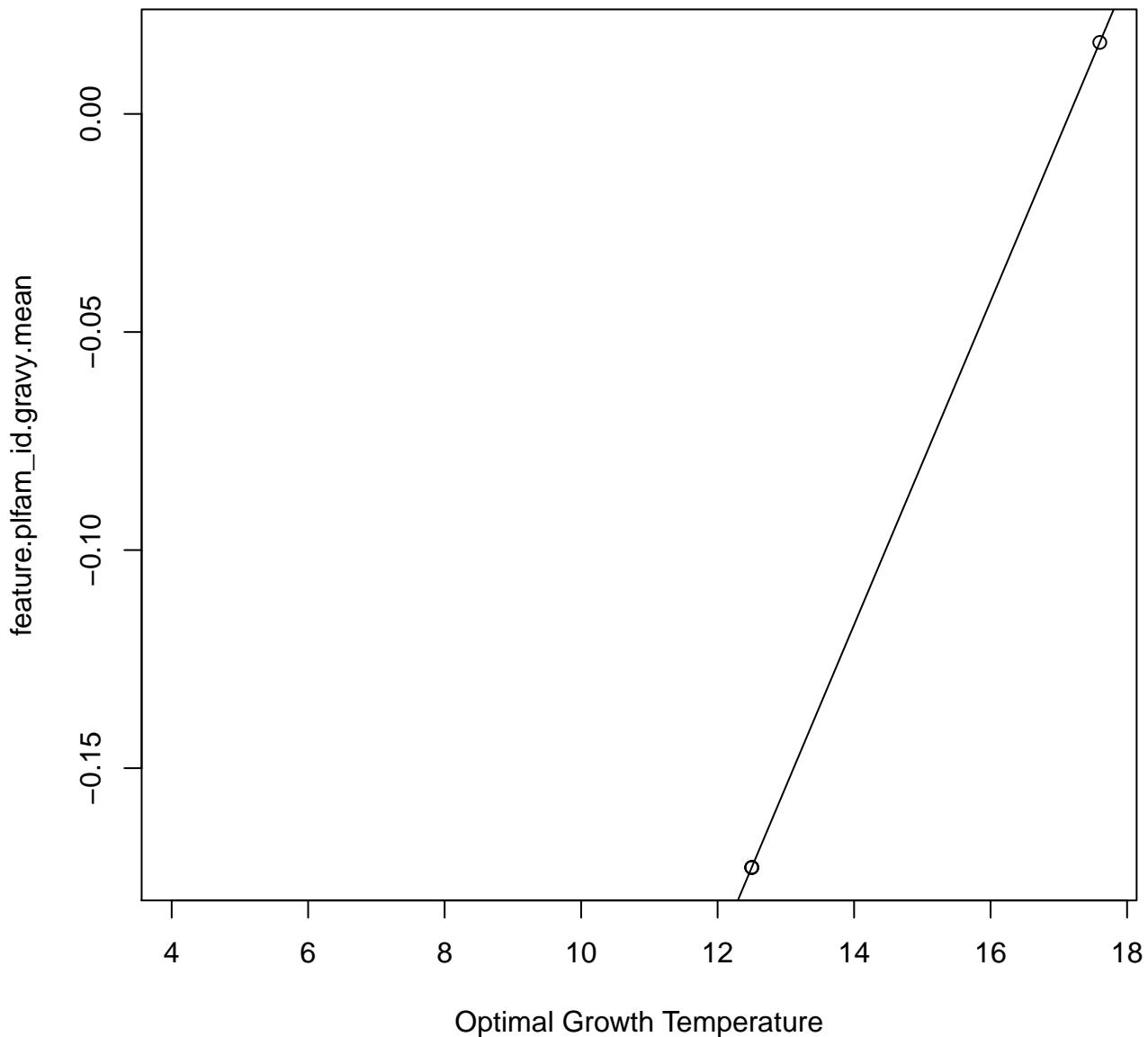
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Probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)



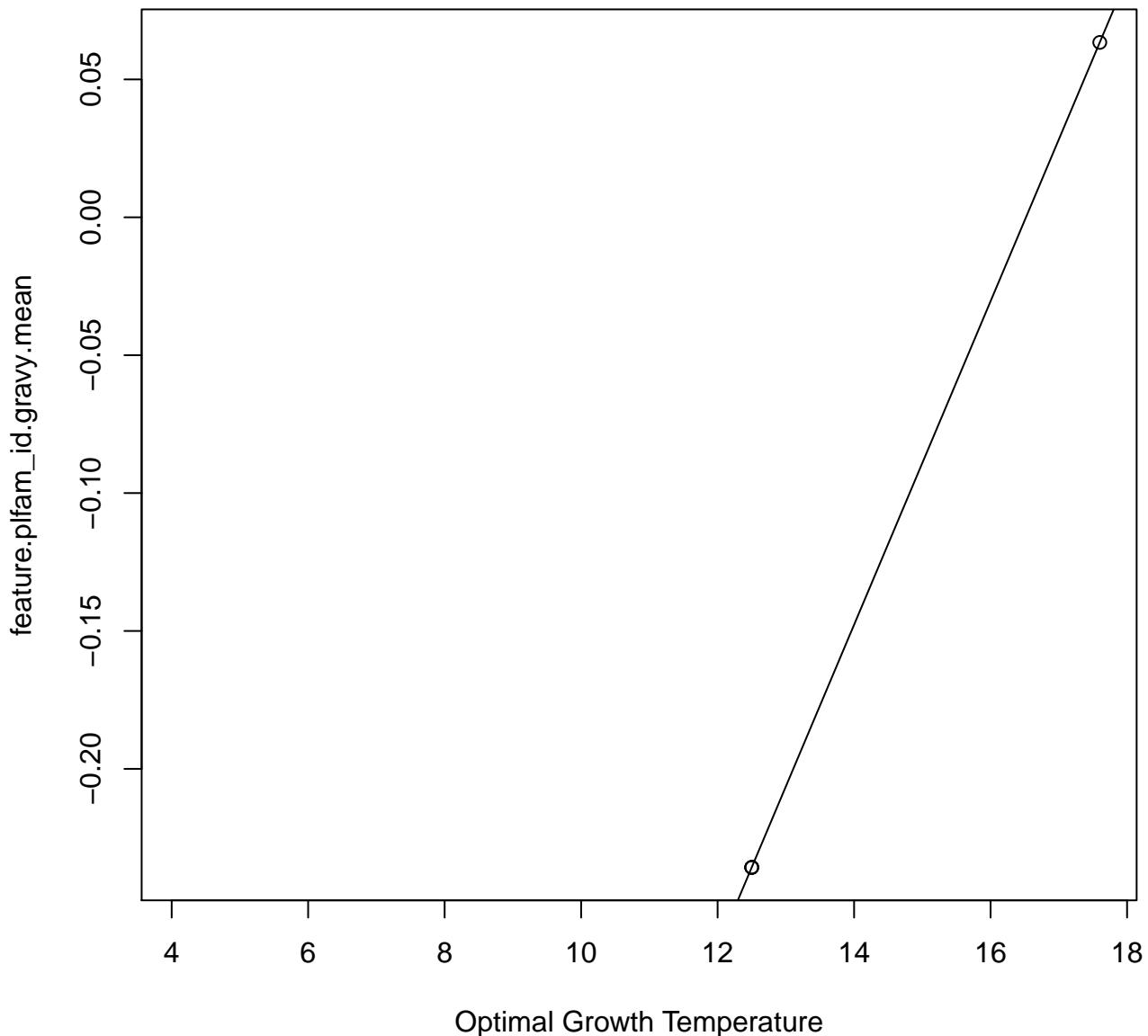
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PLF_28228_00007856
4-carboxymuconolactone decarboxylase (EC 4.1.1.44)



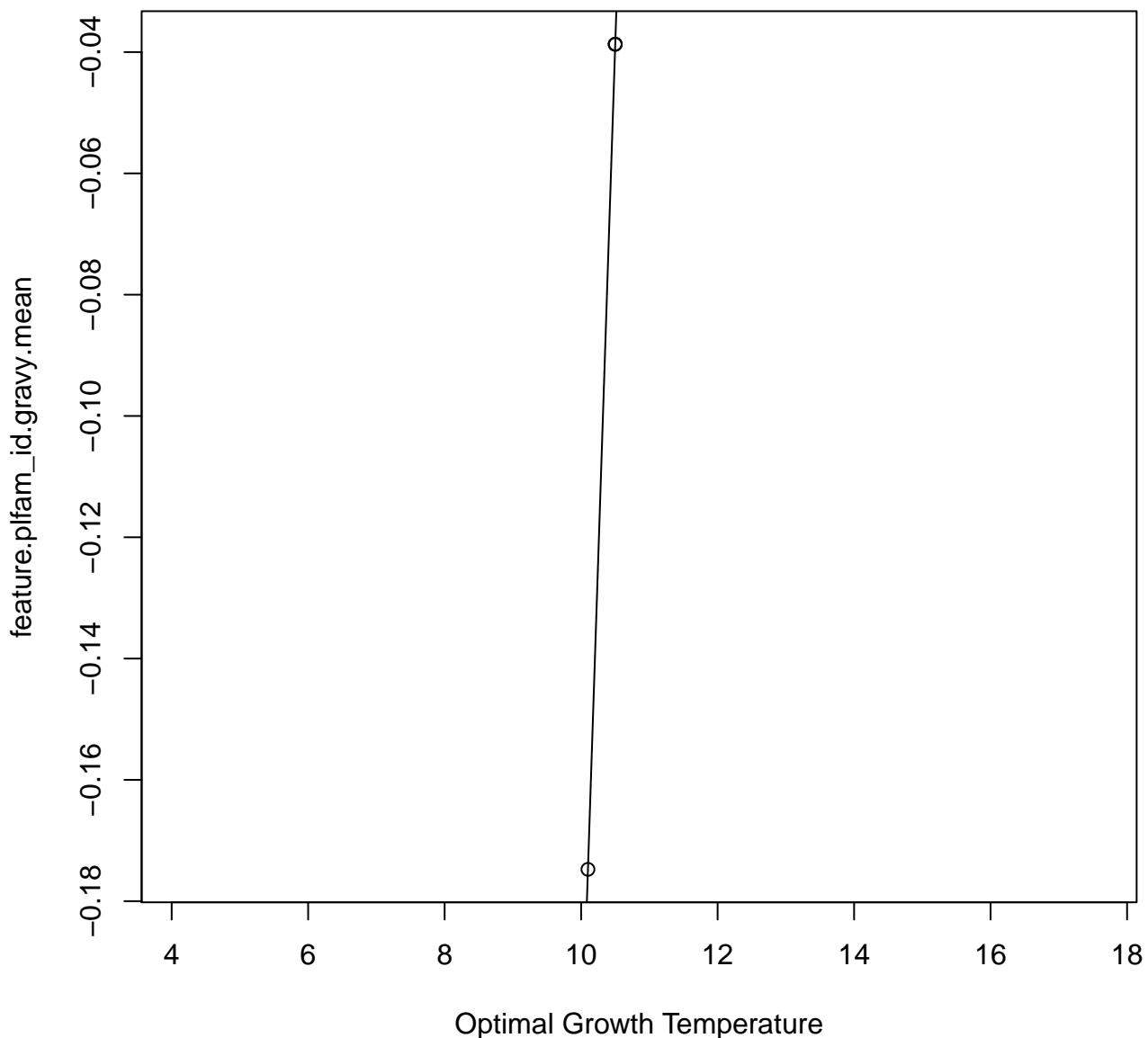
feature.plfam_id.gravy.mean
PLF_28228_00005808
Transcriptional repressor of aga operon



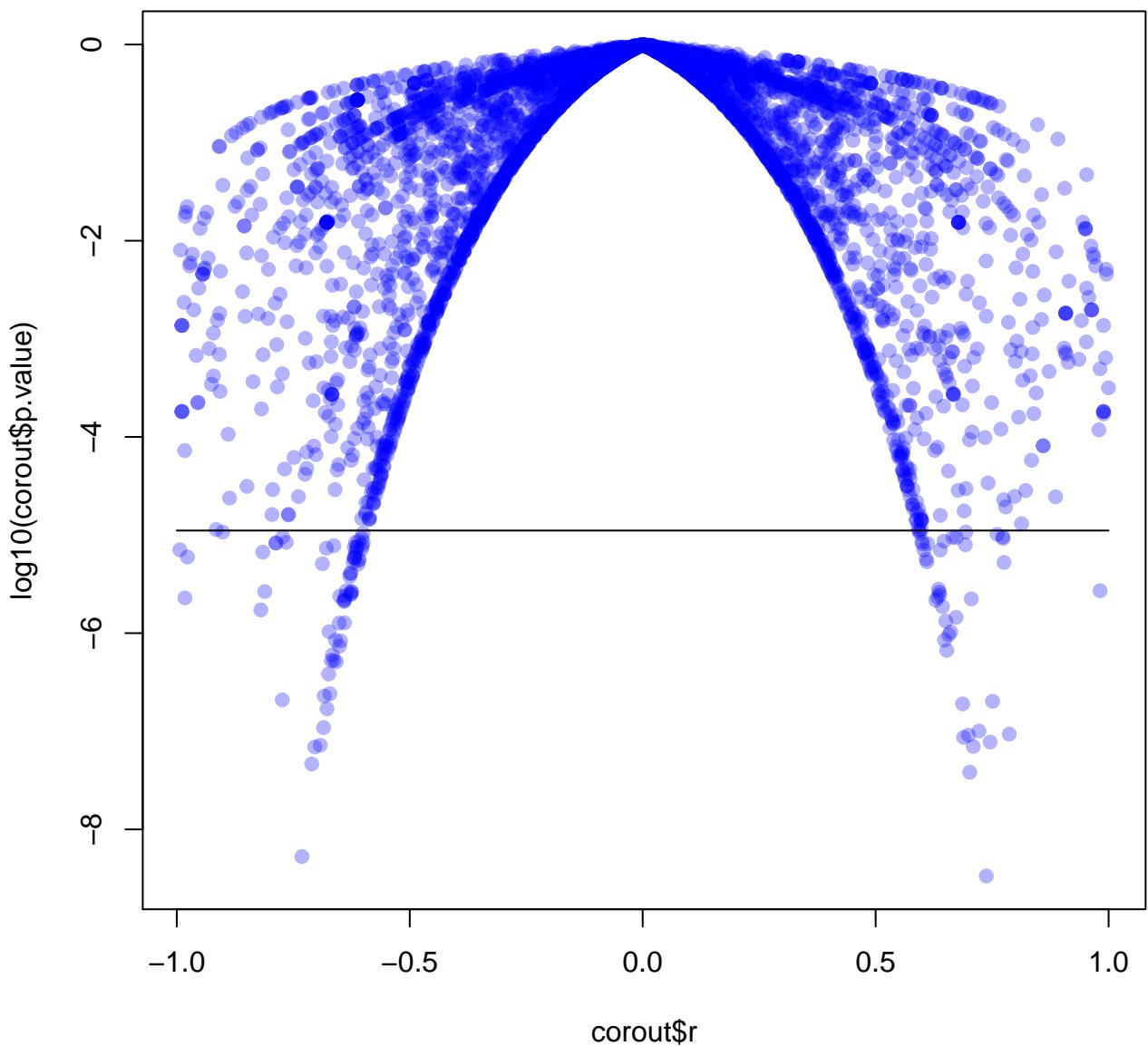
feature.plfam_id.gravy.mean
PLF_28228_00007754
Lipid A phosphoethanolamine transferase, putative



feature.pfam_id.gravy.mean
PLF_28228_00028689
Site-specific tyrosine recombinase



feature.pgfam_id.proline_residue.mean

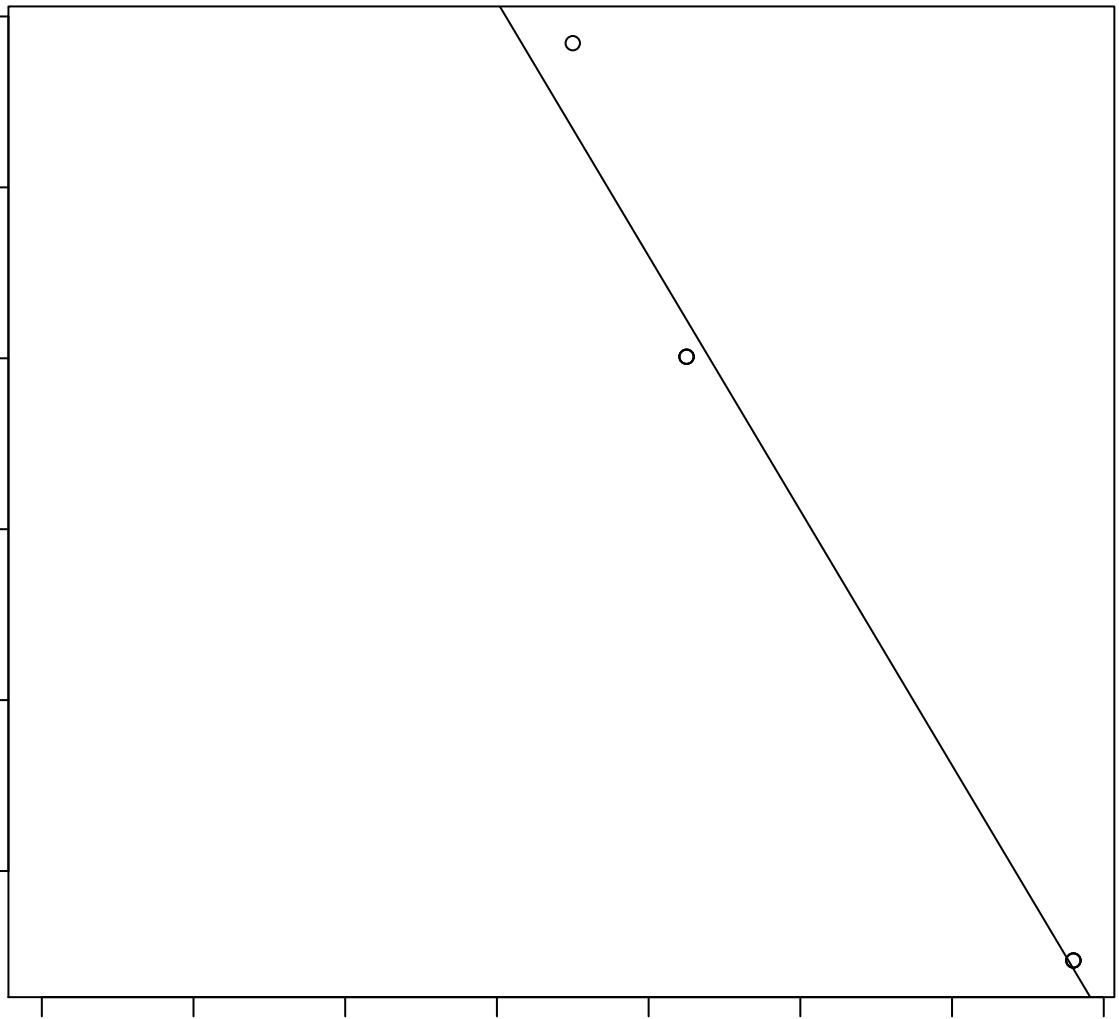


feature.pgfam_id.proline_residue.mean
PGF_01336683
FIG016502: iron uptake protein

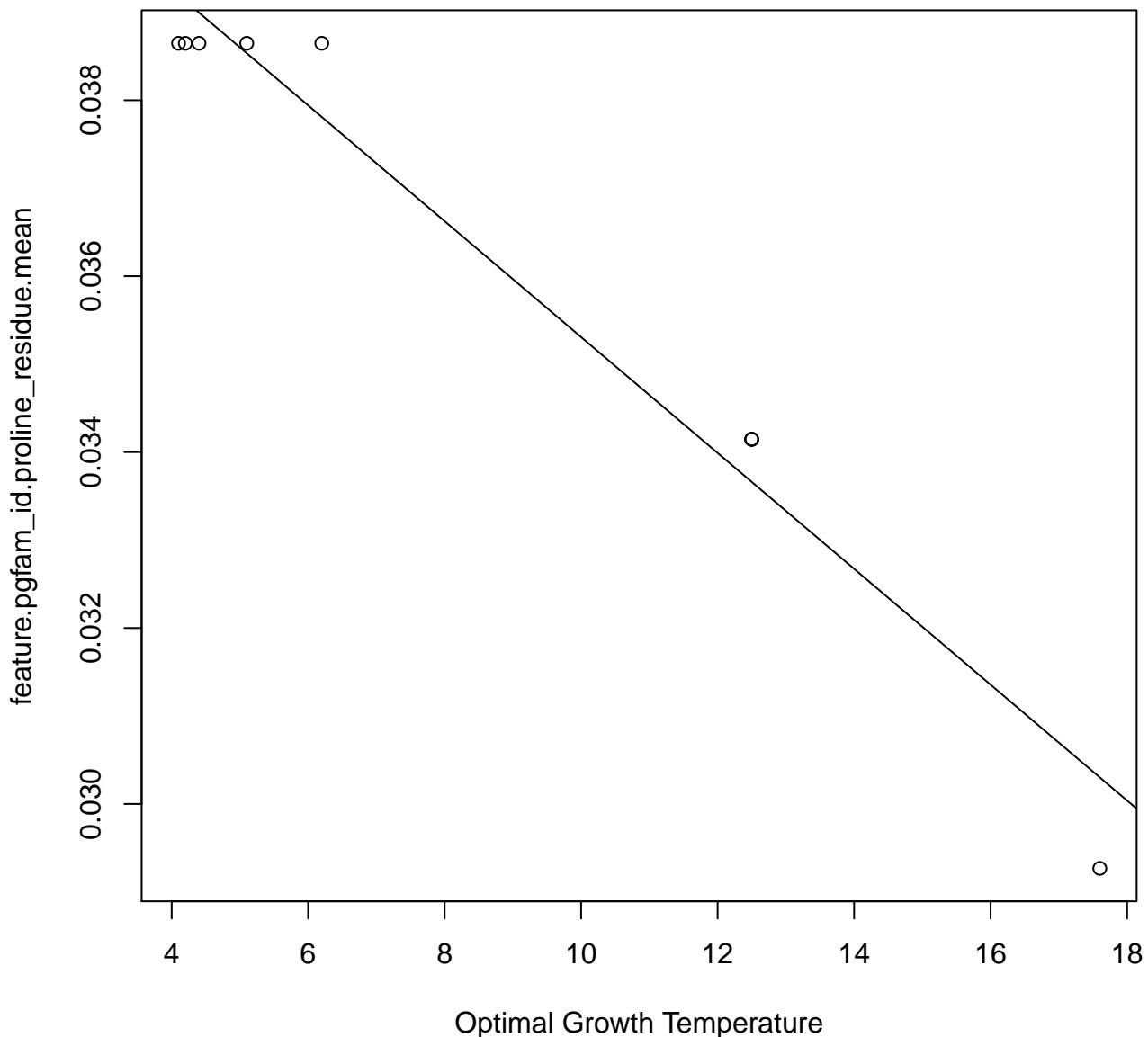
feature.pgfam_id.proline_residue.mean

4 6 8 10 12 14 16 18

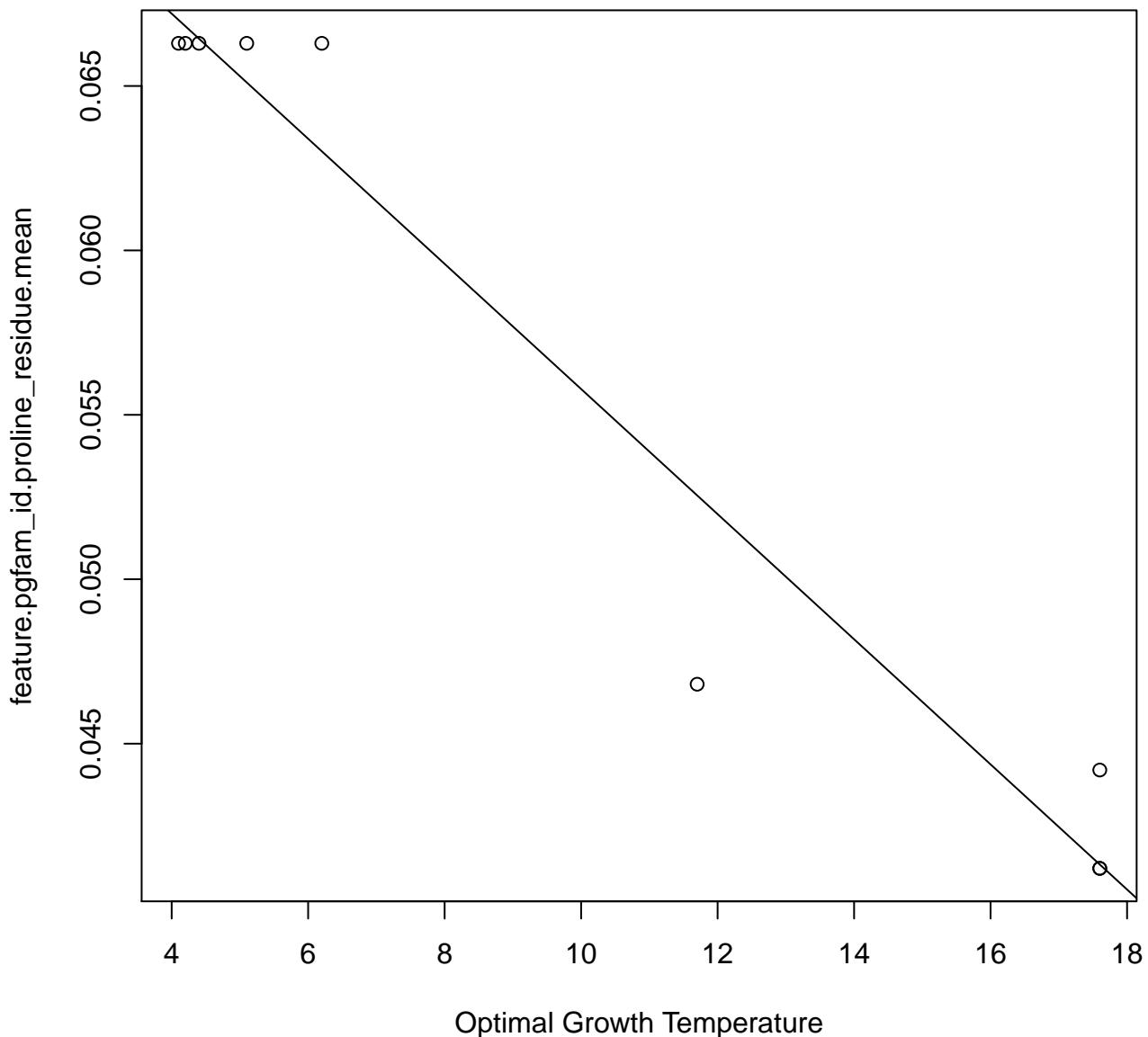
Optimal Growth Temperature



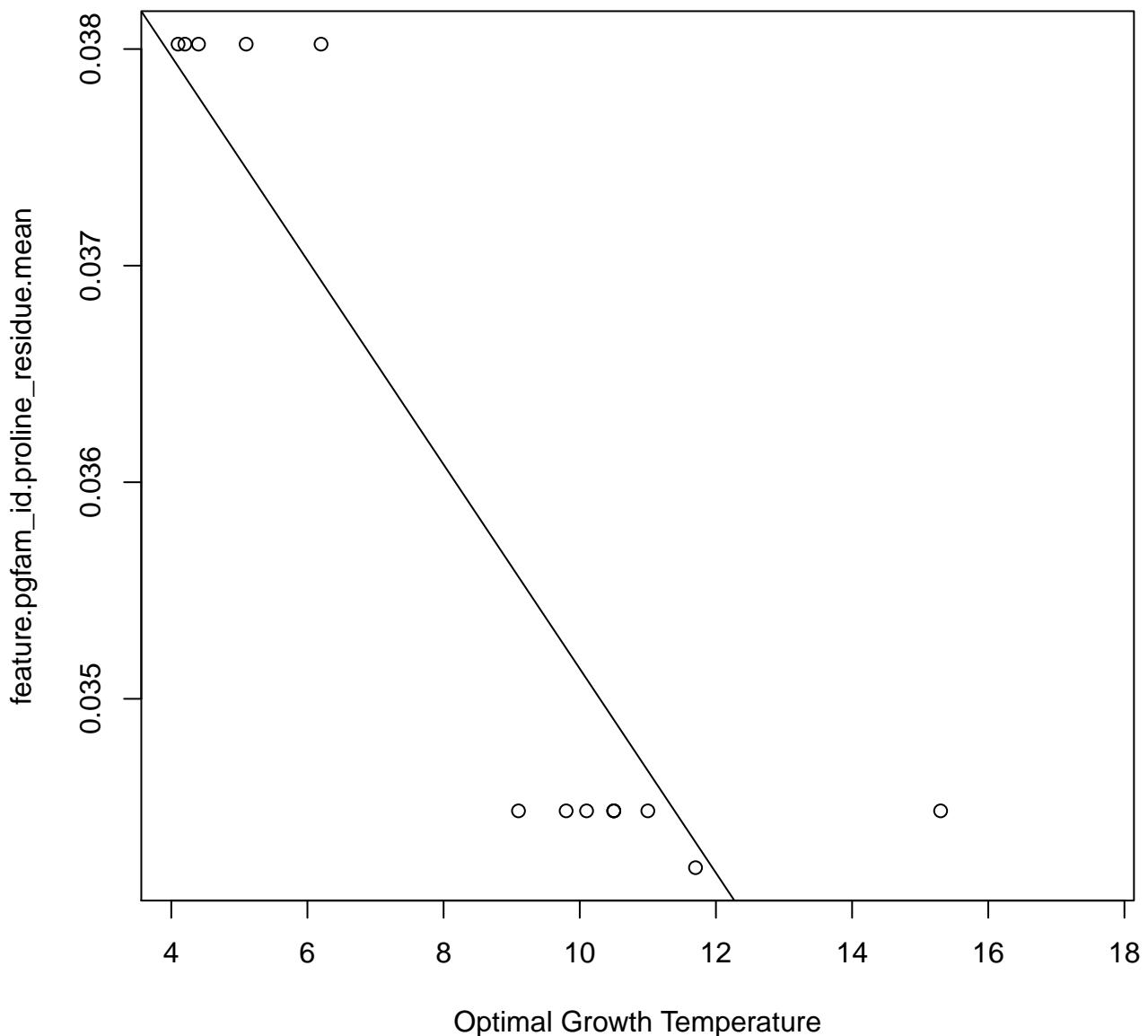
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PGF_01338043
hypothetical protein



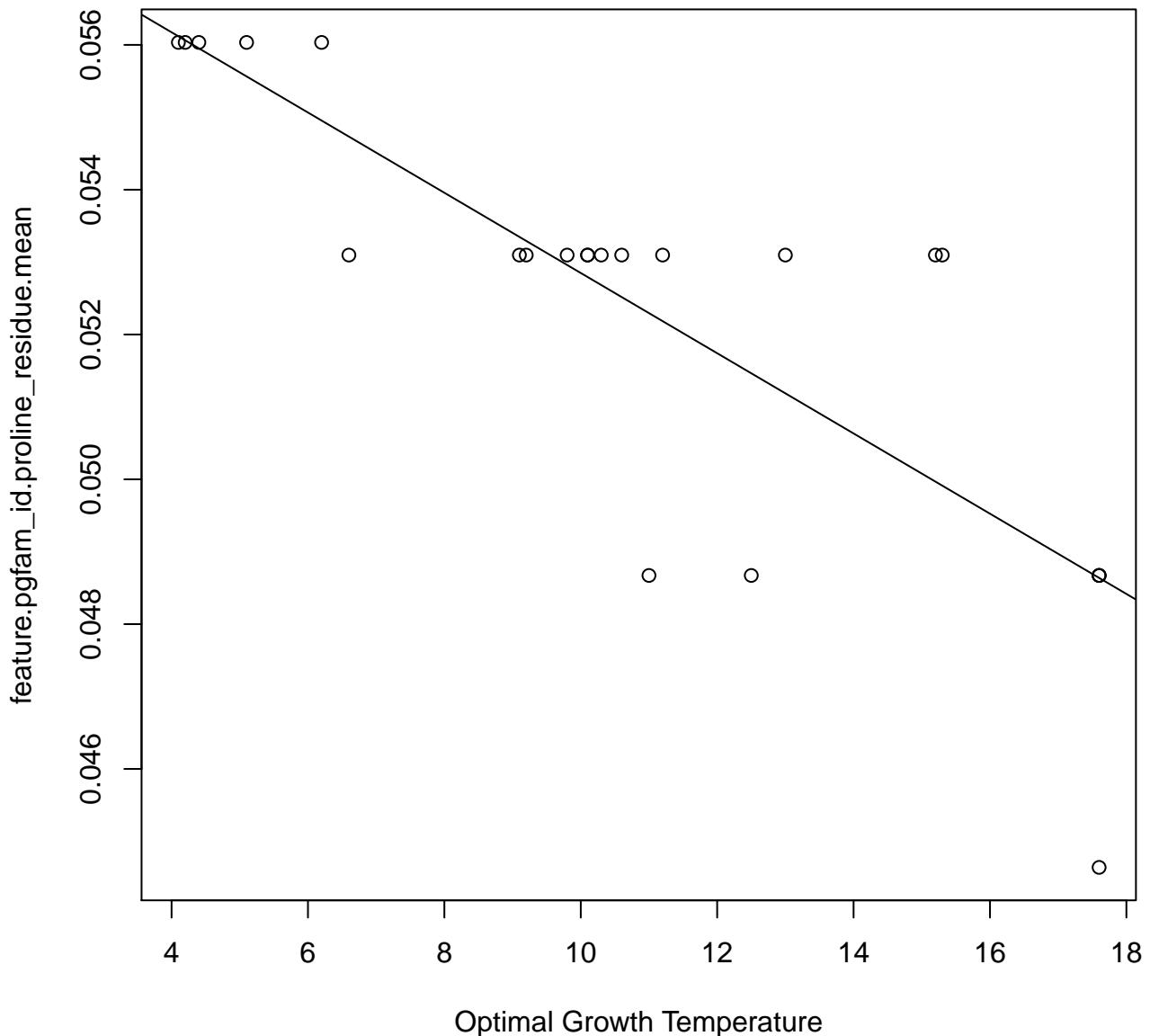
feature.pgfam_id.proline_residue.mean
PGF_03221663
Phage tail collar domain



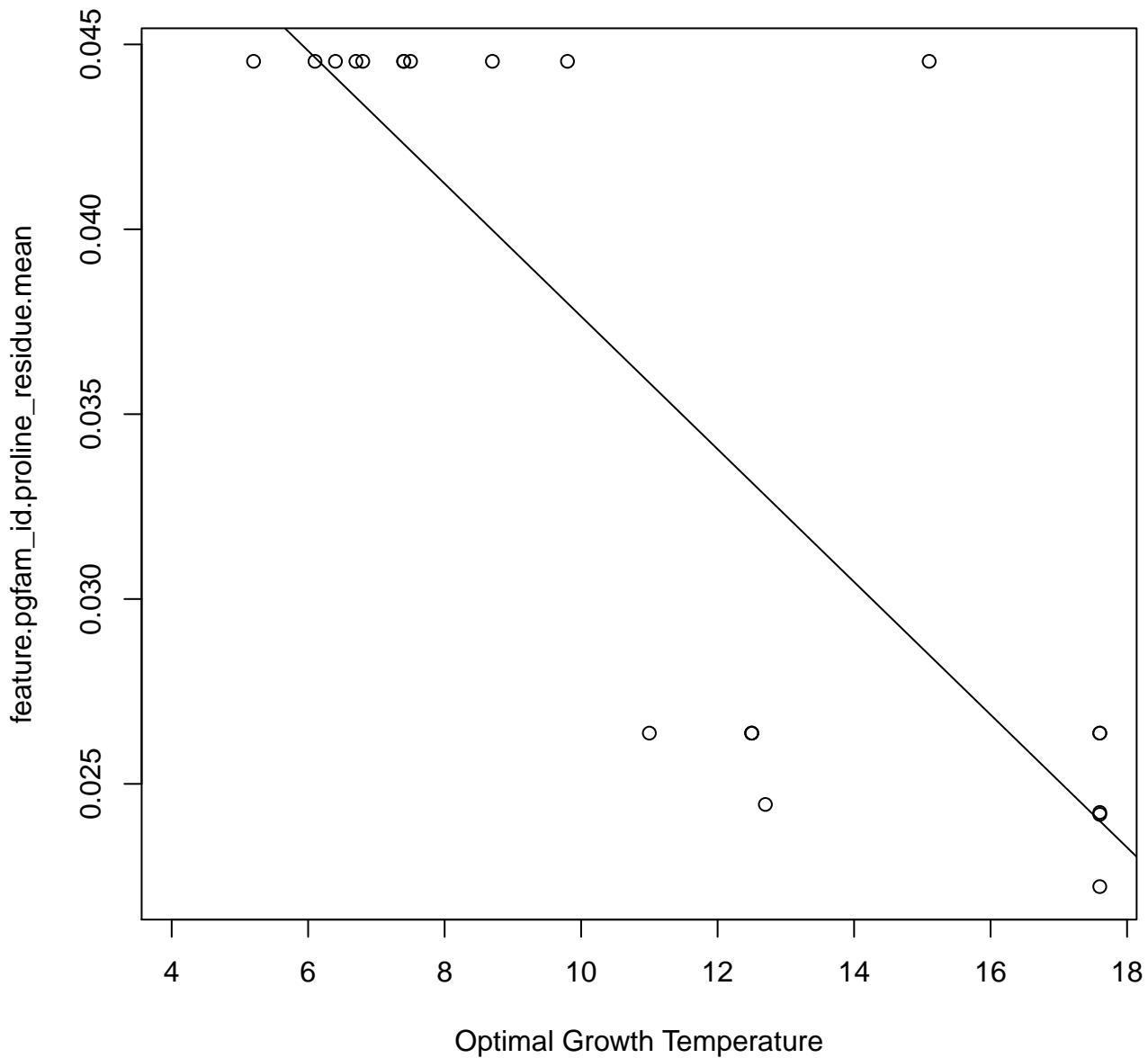
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PGF_10029046
hypothetical protein



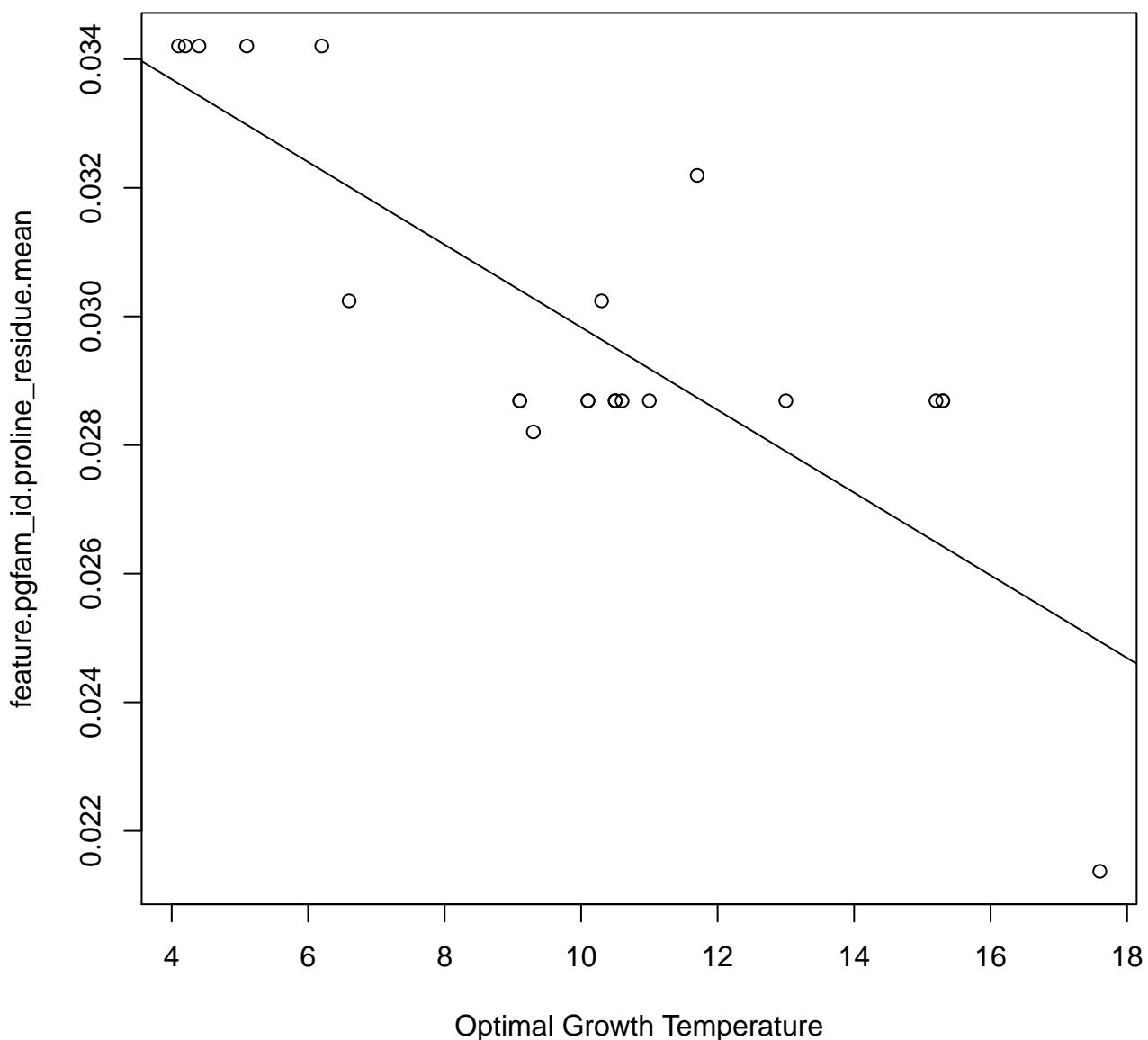
feature.pgfam_id.proline_residue.mean
PGF_08794816
Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)



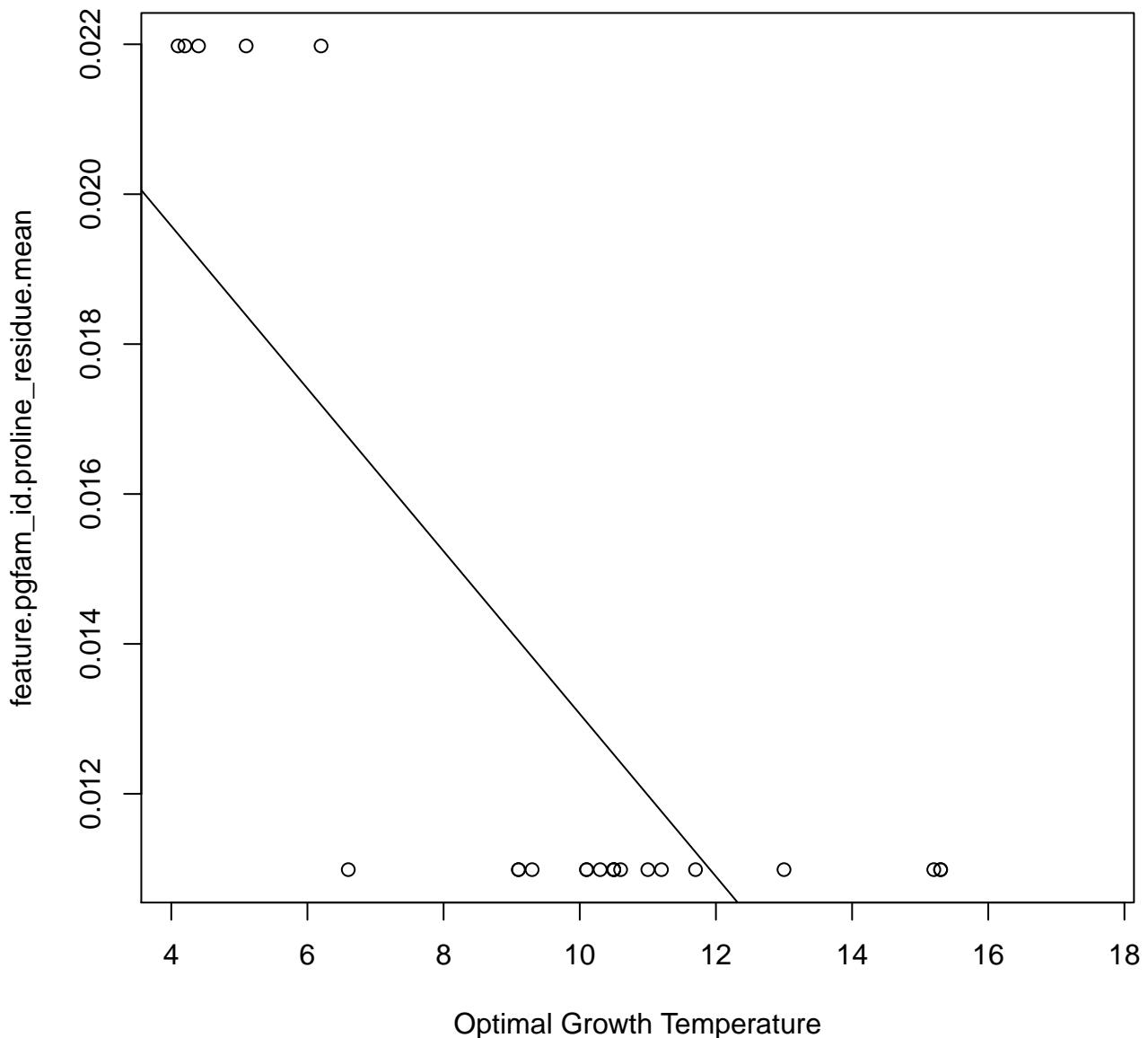
feature.pgfam_id.proline_residue.mean
PGF_00017607
ATP-dependent RNA helicase SO1501



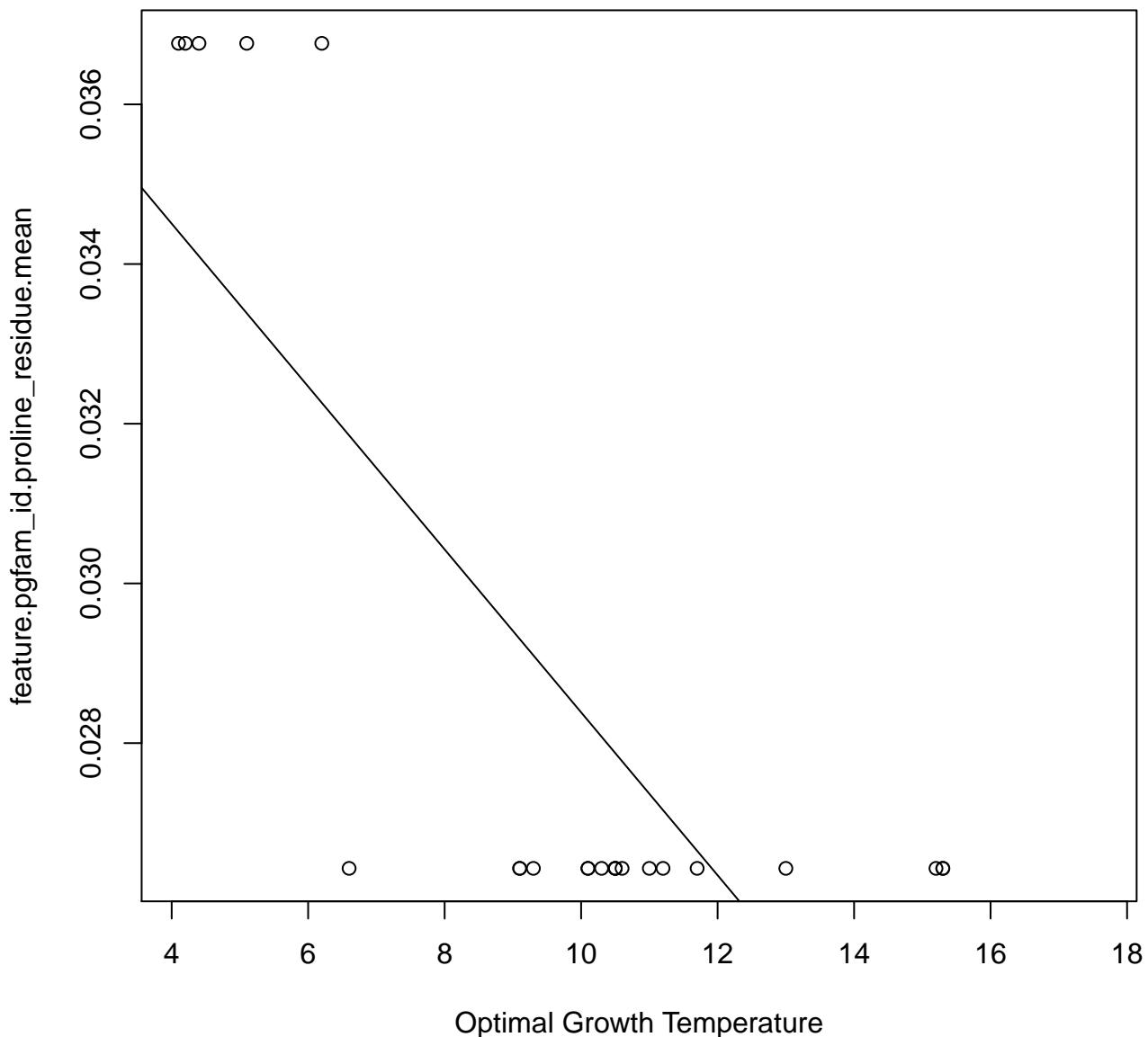
feature.pgfam_id.proline_residue.mean
PGF_02896401
hypothetical protein



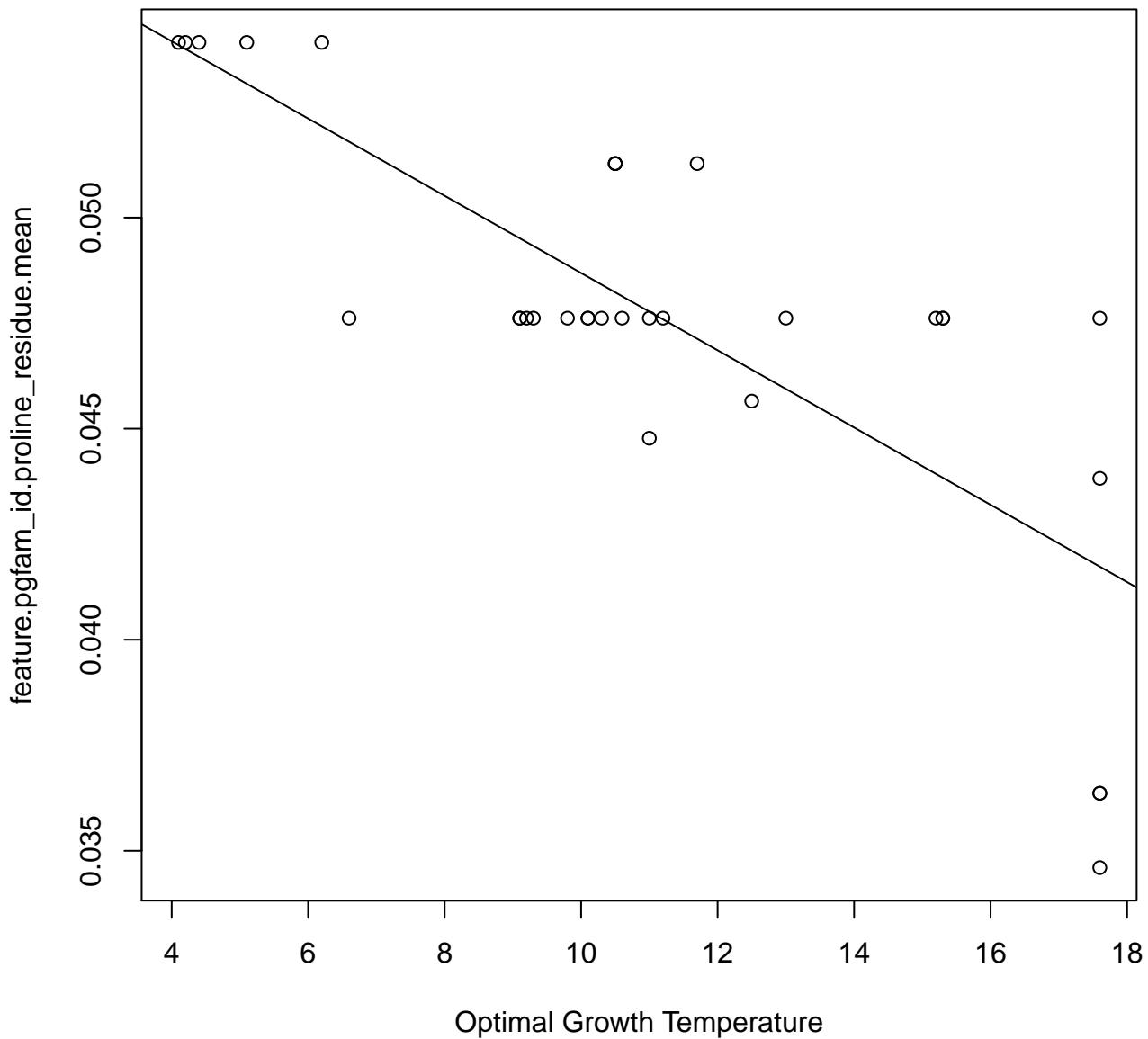
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PGF_10906072
hypothetical protein



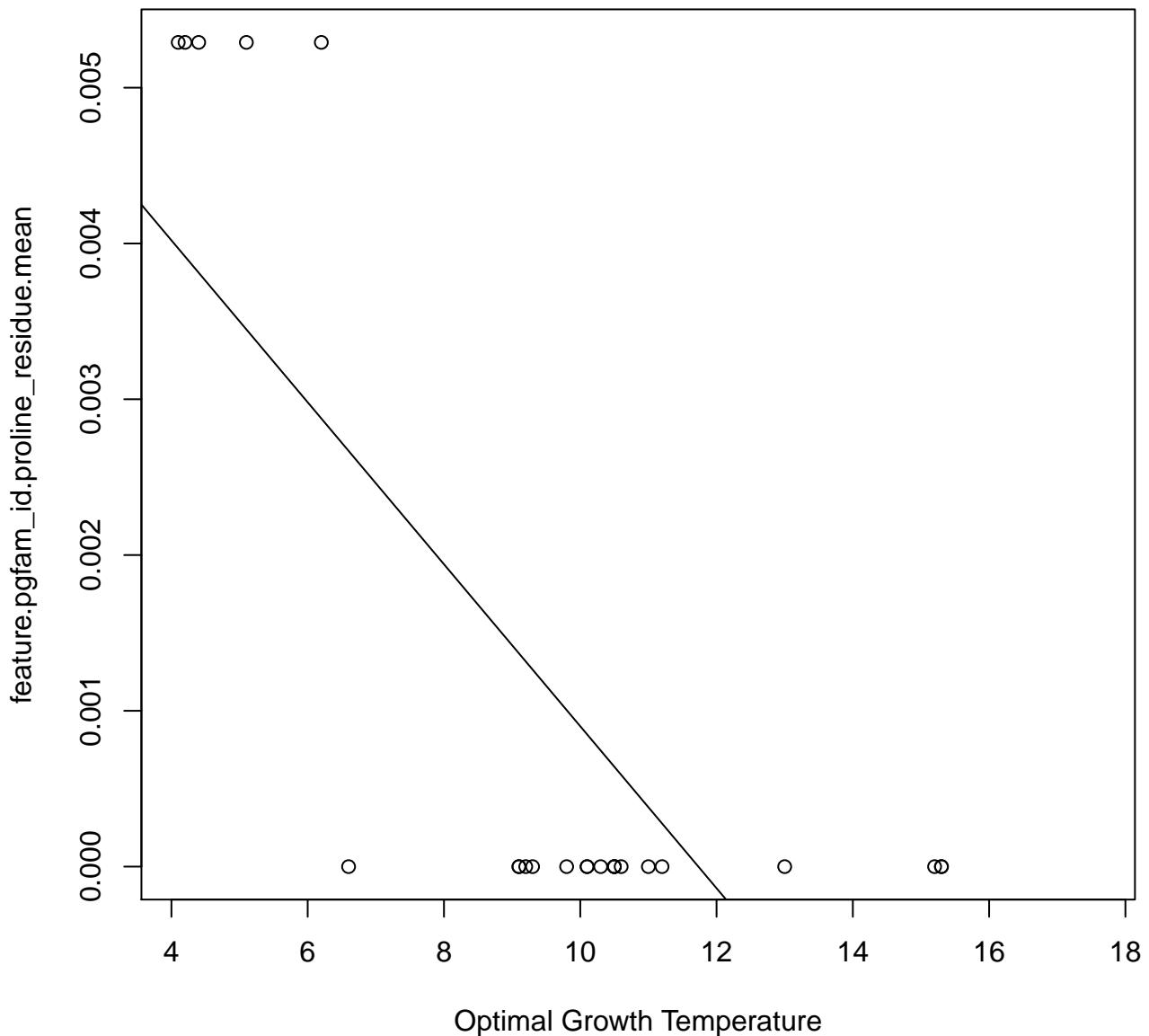
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PGF_11620197
hypothetical protein



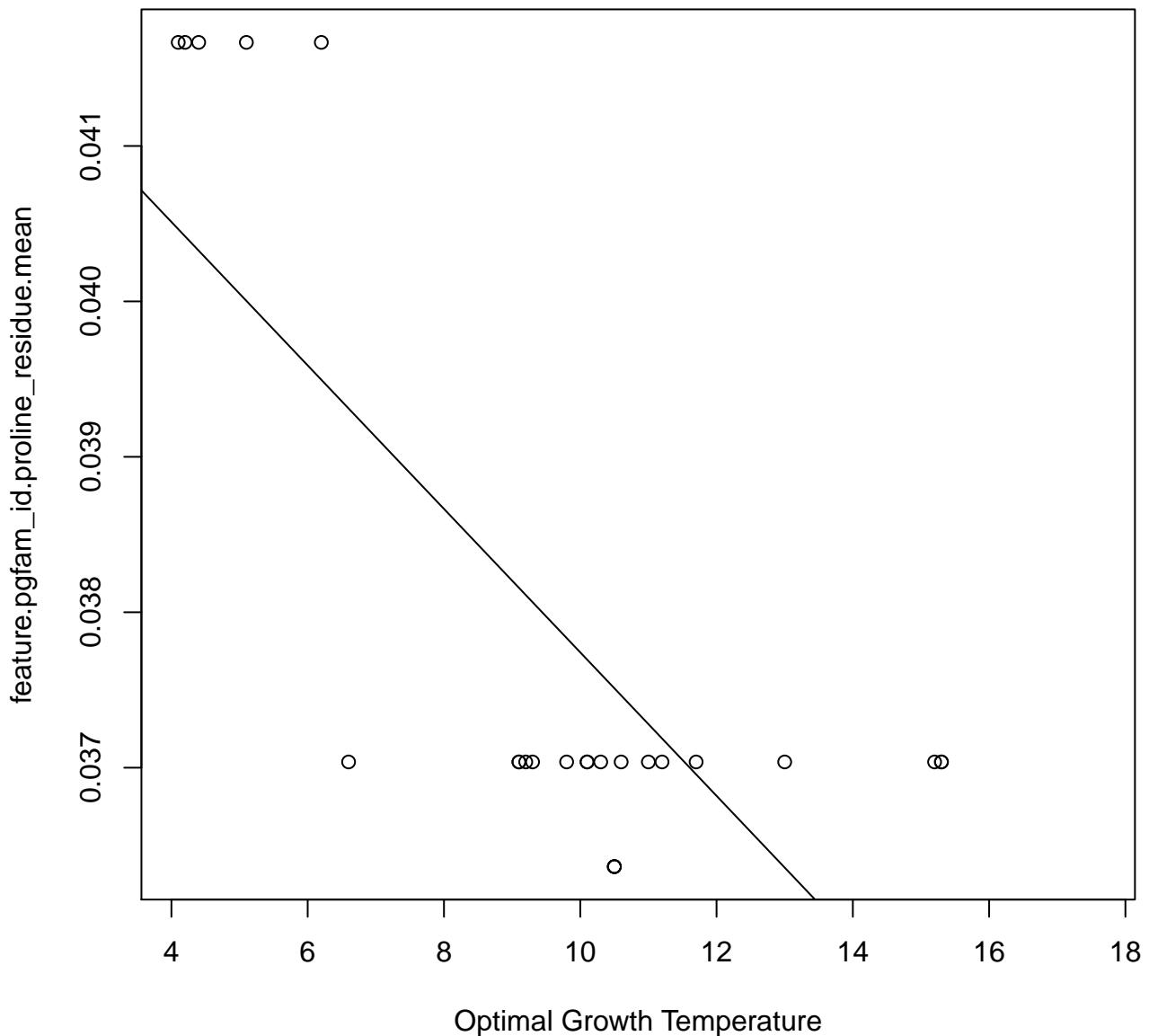
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PGF_10325218
Transcriptional regulator, AraC family



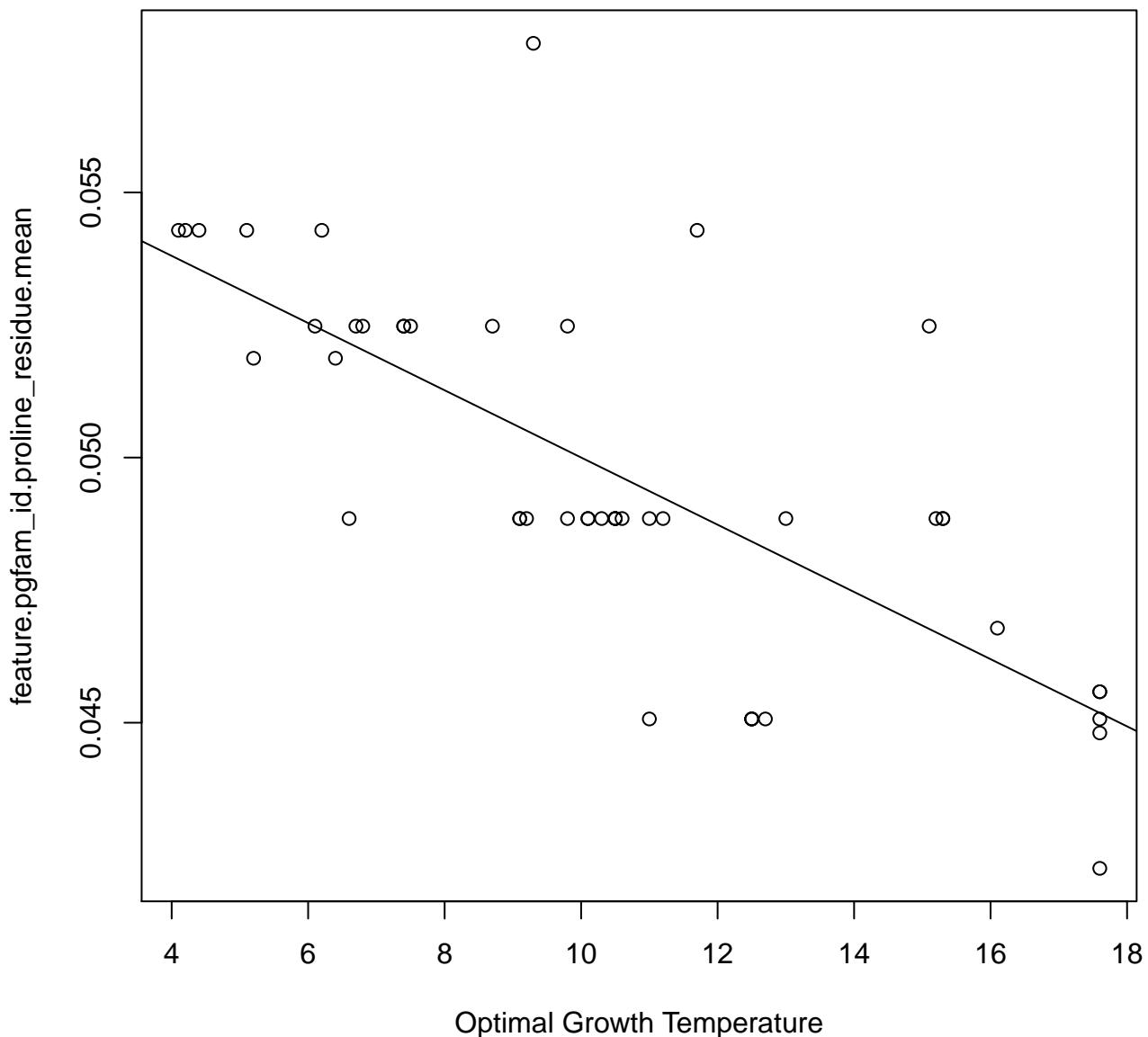
feature.pgfam_id.proline_residue.mean
PGF_12159935
hypothetical protein



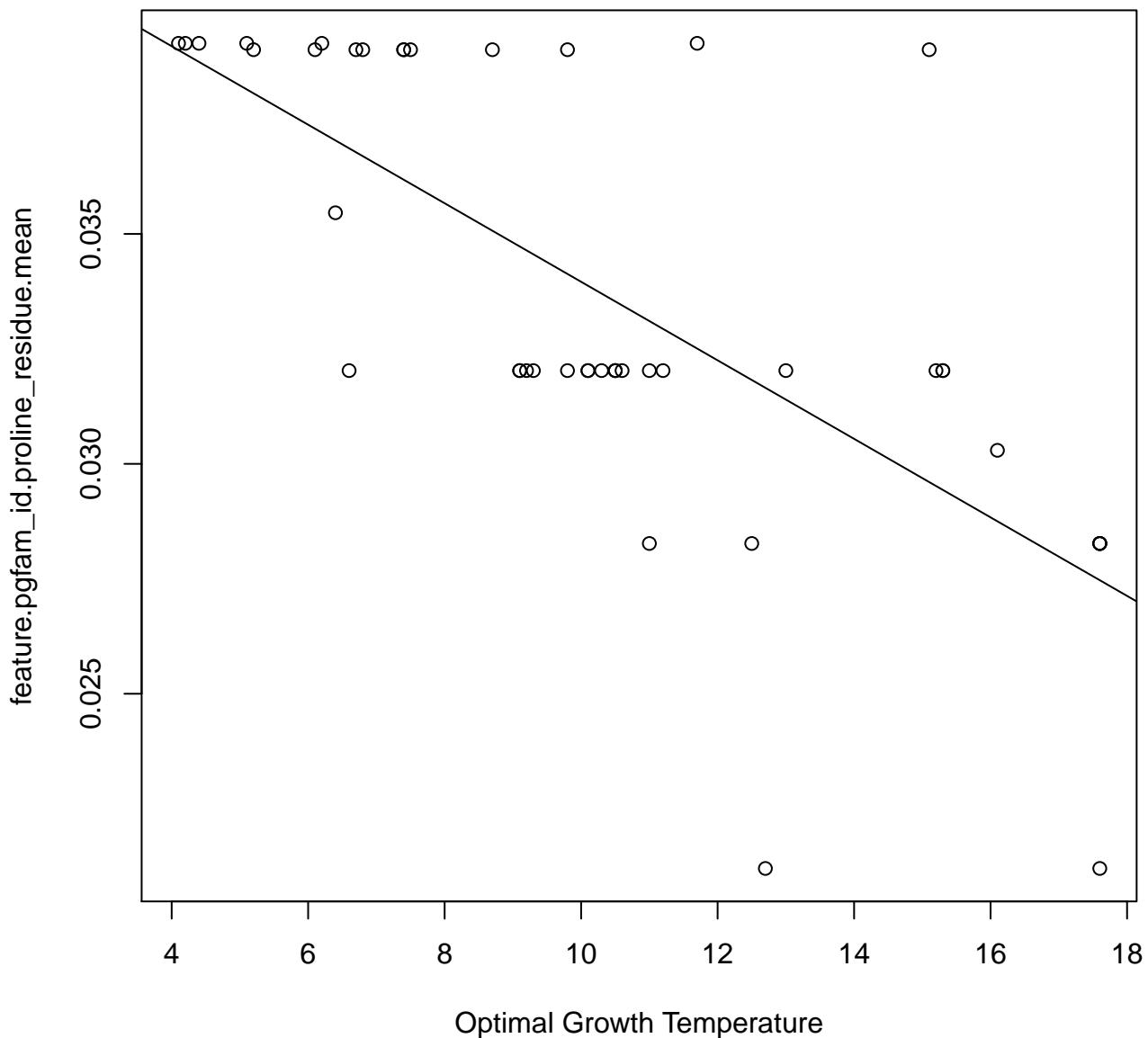
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PGF_11247394
hypothetical protein



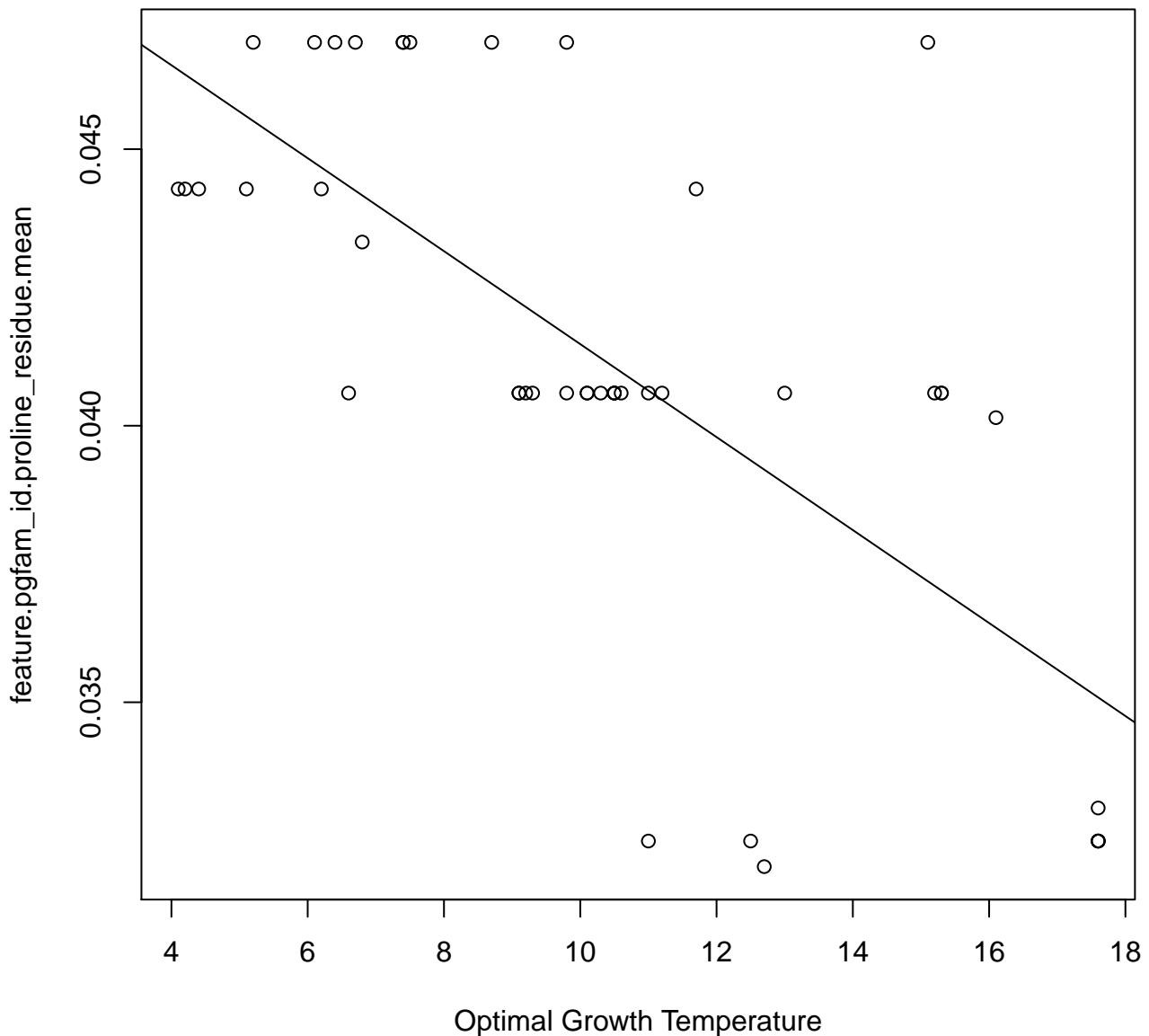
feature.pgfam_id.proline_residue.mean
PGF_00423382
Dihydroorotate (EC 3.5.2.3)



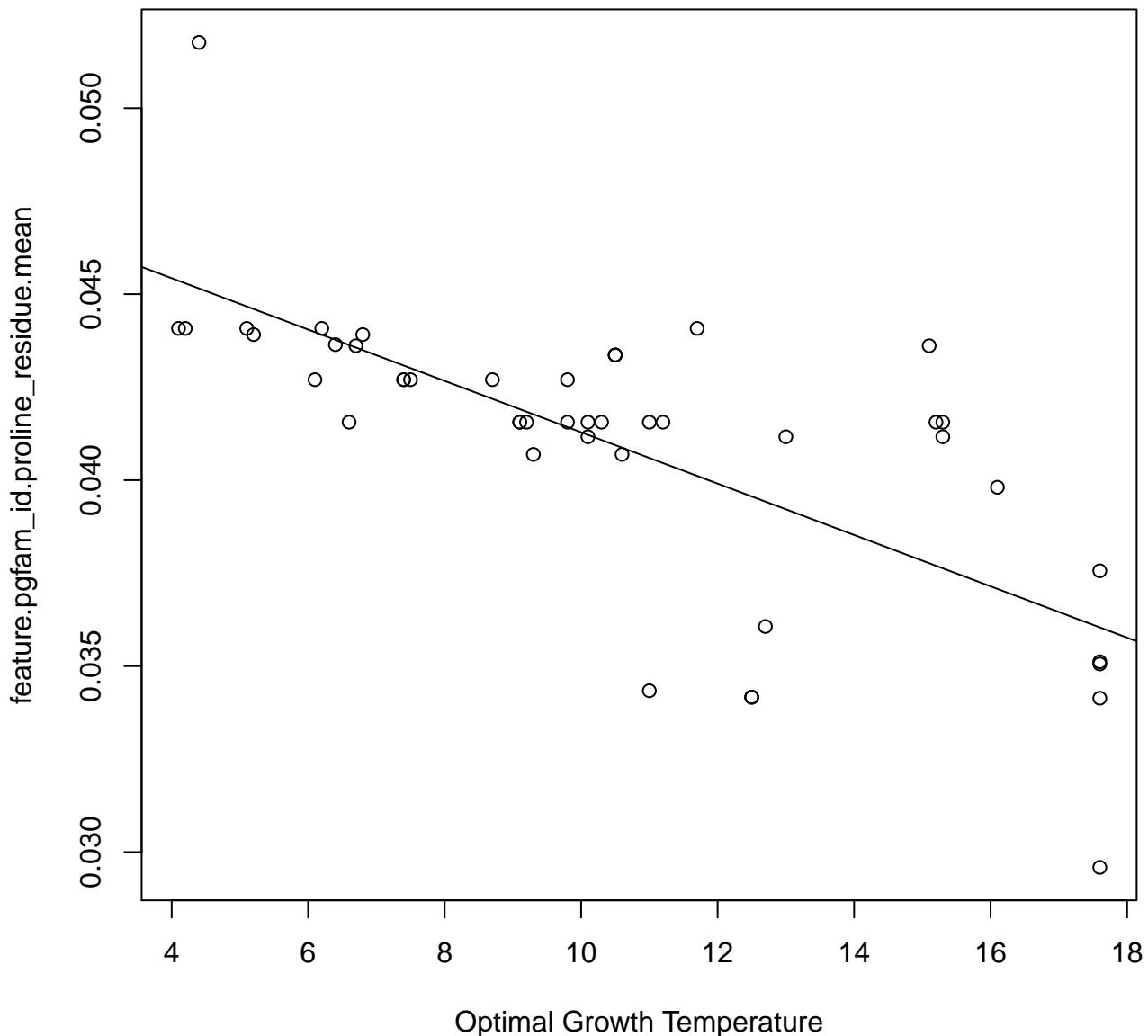
feature.pgfam_id.proline_residue.mean
PGF_00010518
HD domain protein



feature.pgfam_id.proline_residue.mean
PGF_07026465
23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)



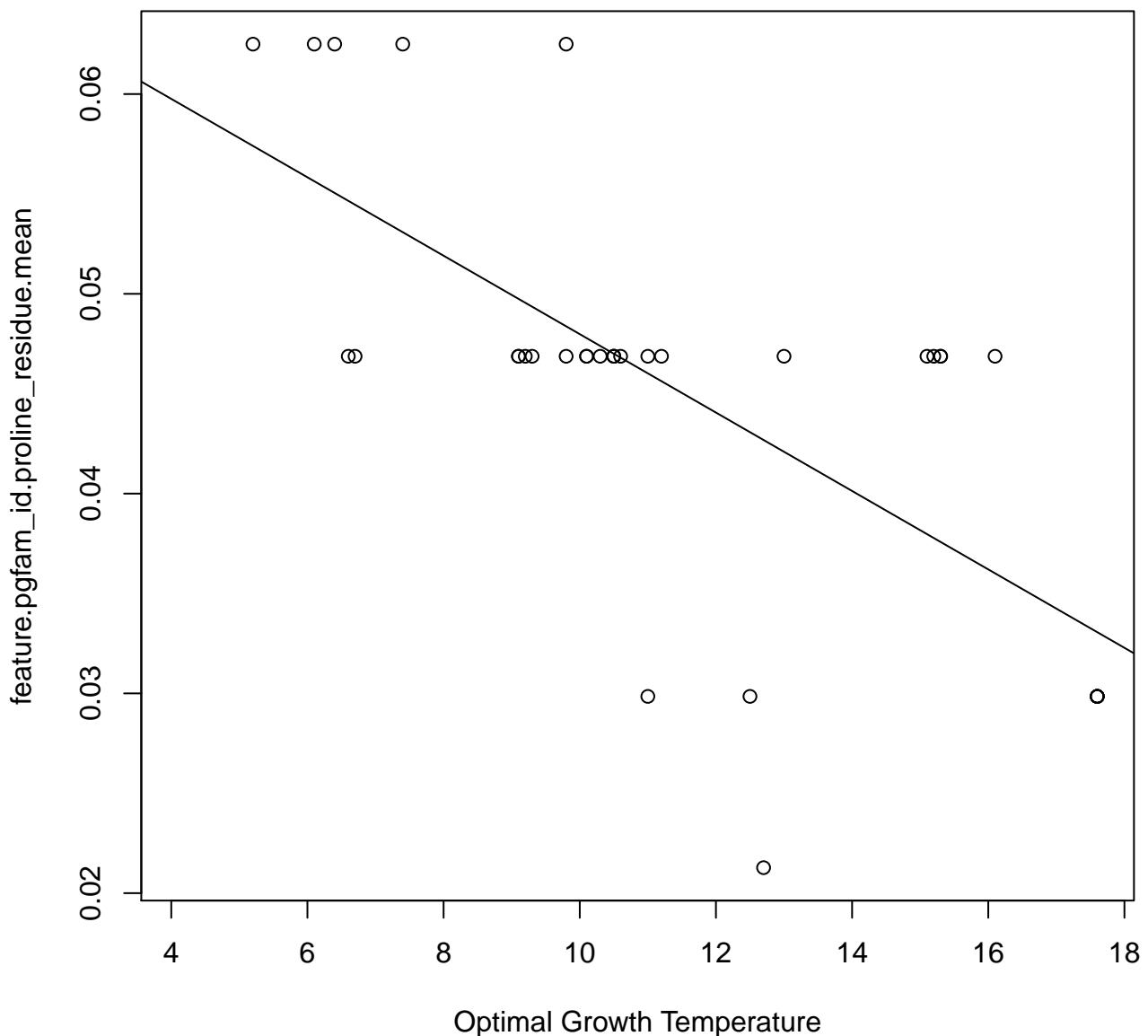
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PGF_00425021
Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)



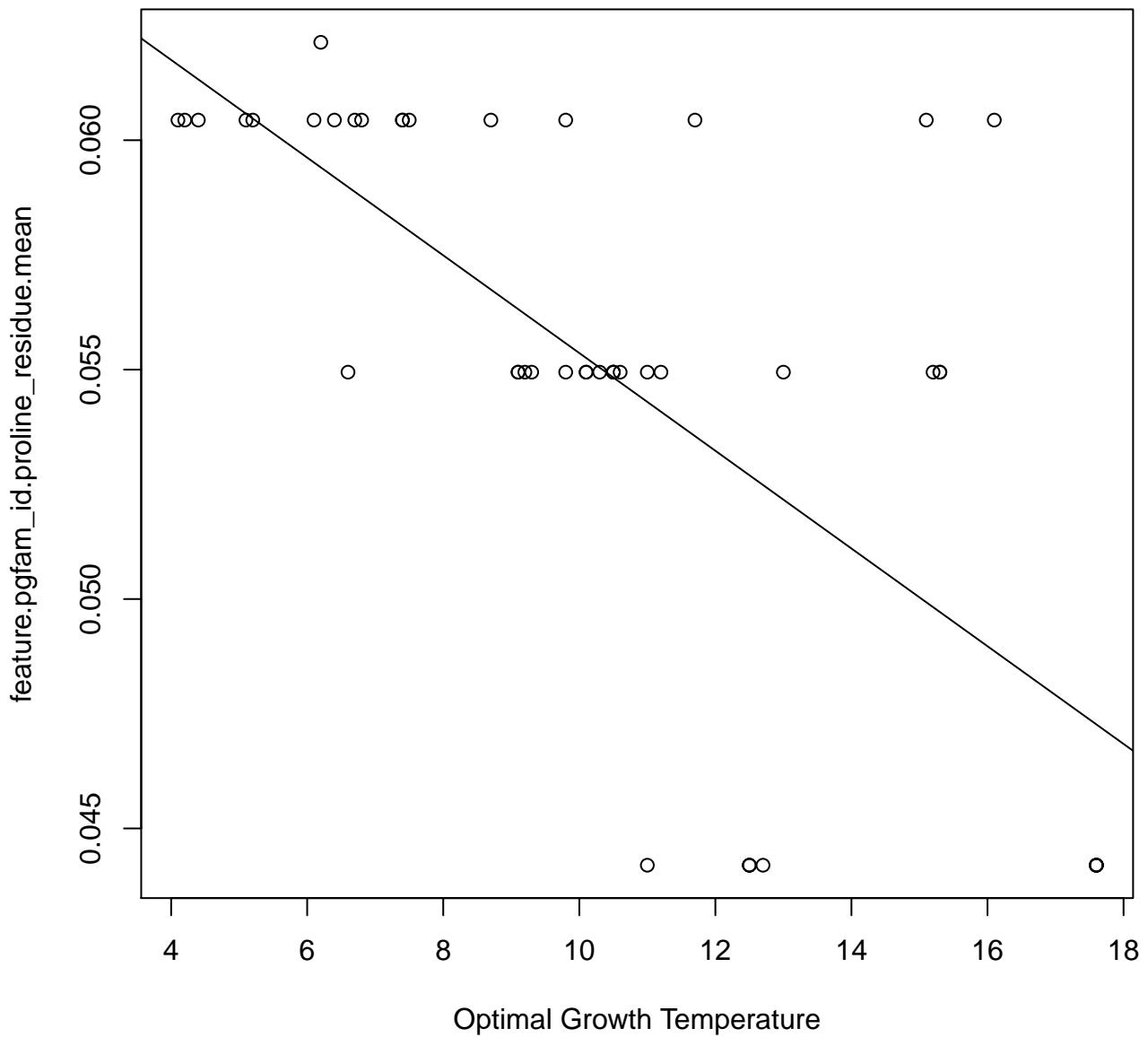
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PGF_01682090

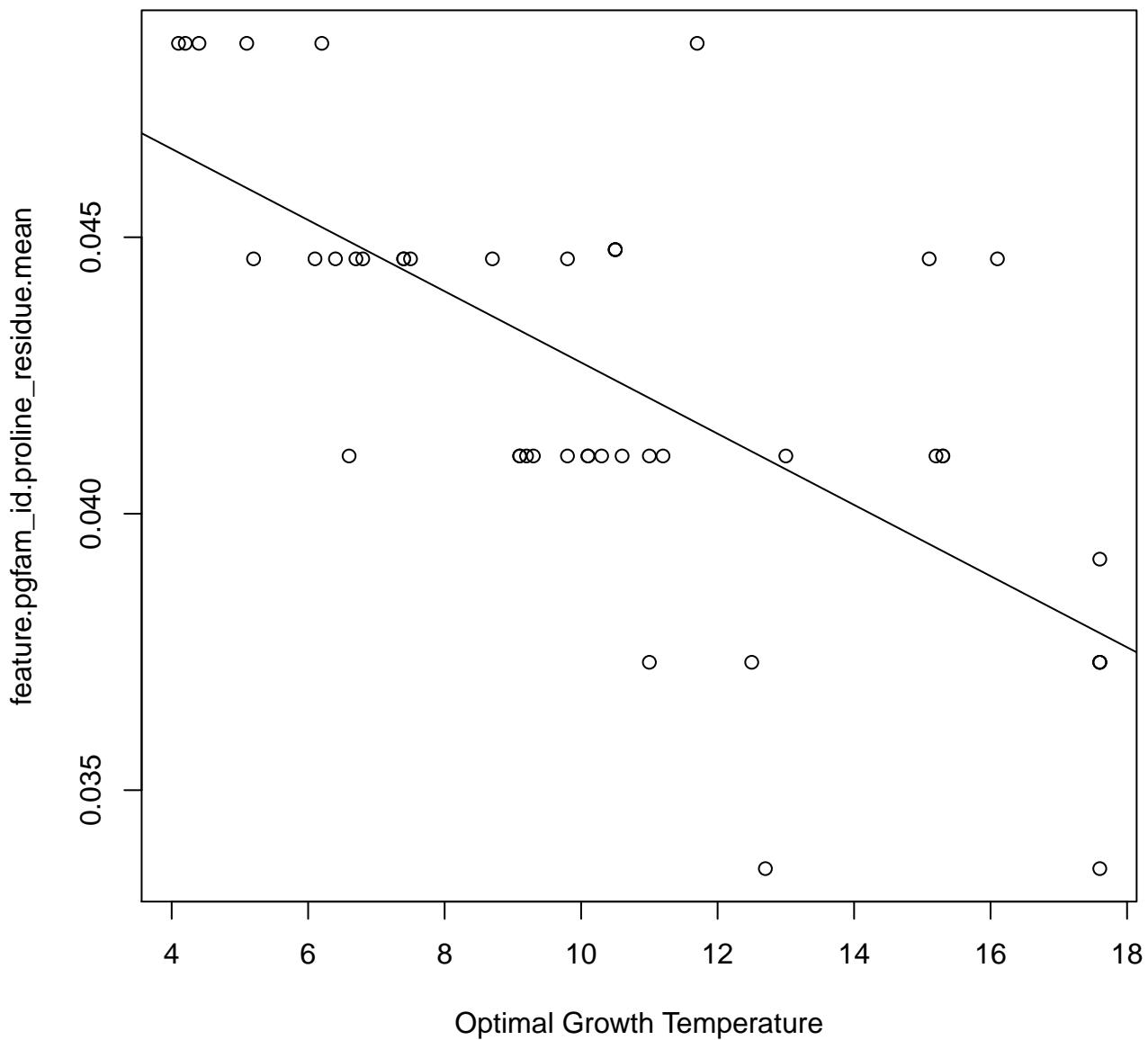
Cytoplasmic protein, probably associated with glutathione-regulated potassium-efflux



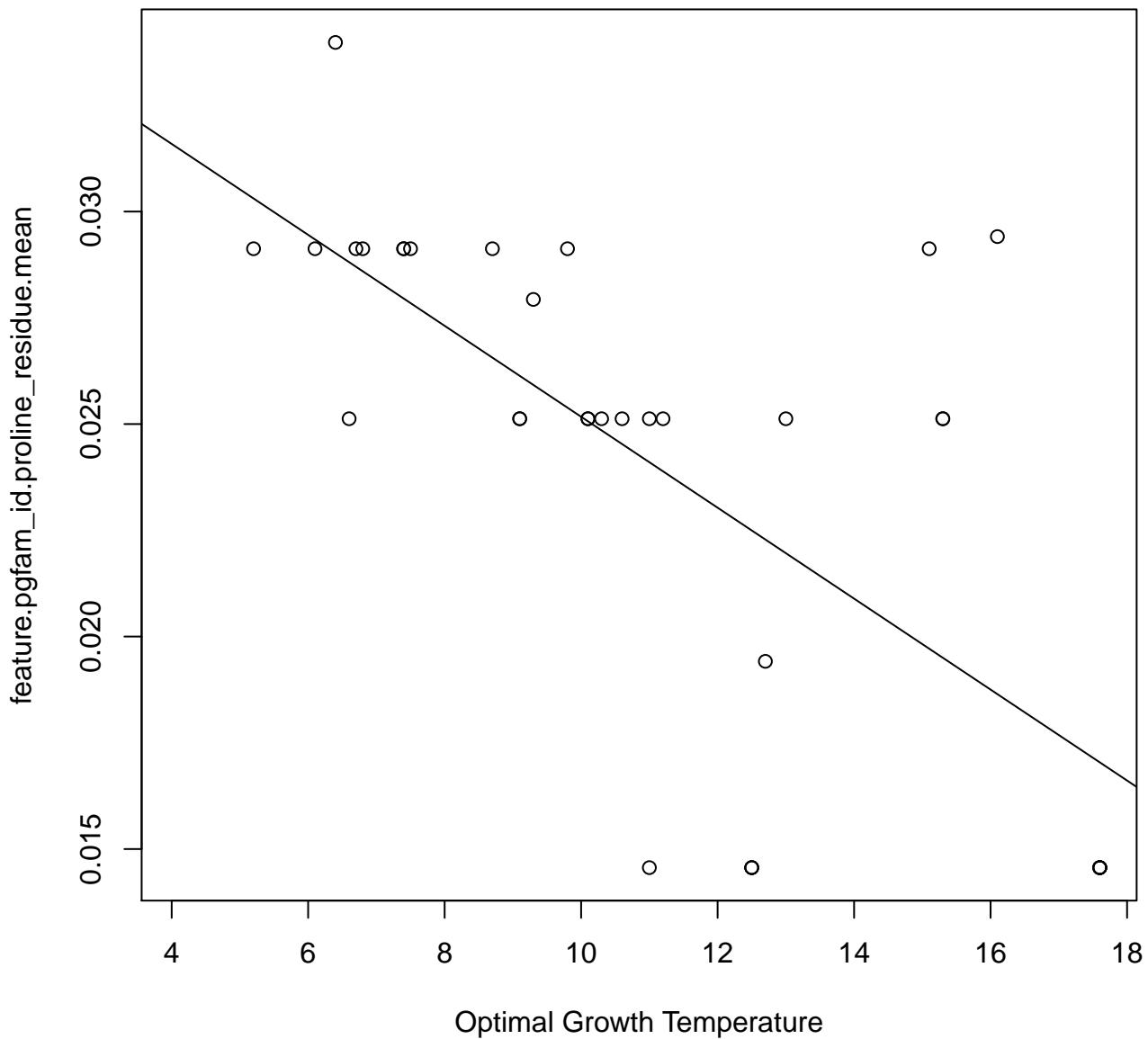
feature.ncbi_id.proline_residue.mean
PGF_03081665
Cell division integral membrane protein, YggT and half-length relatives



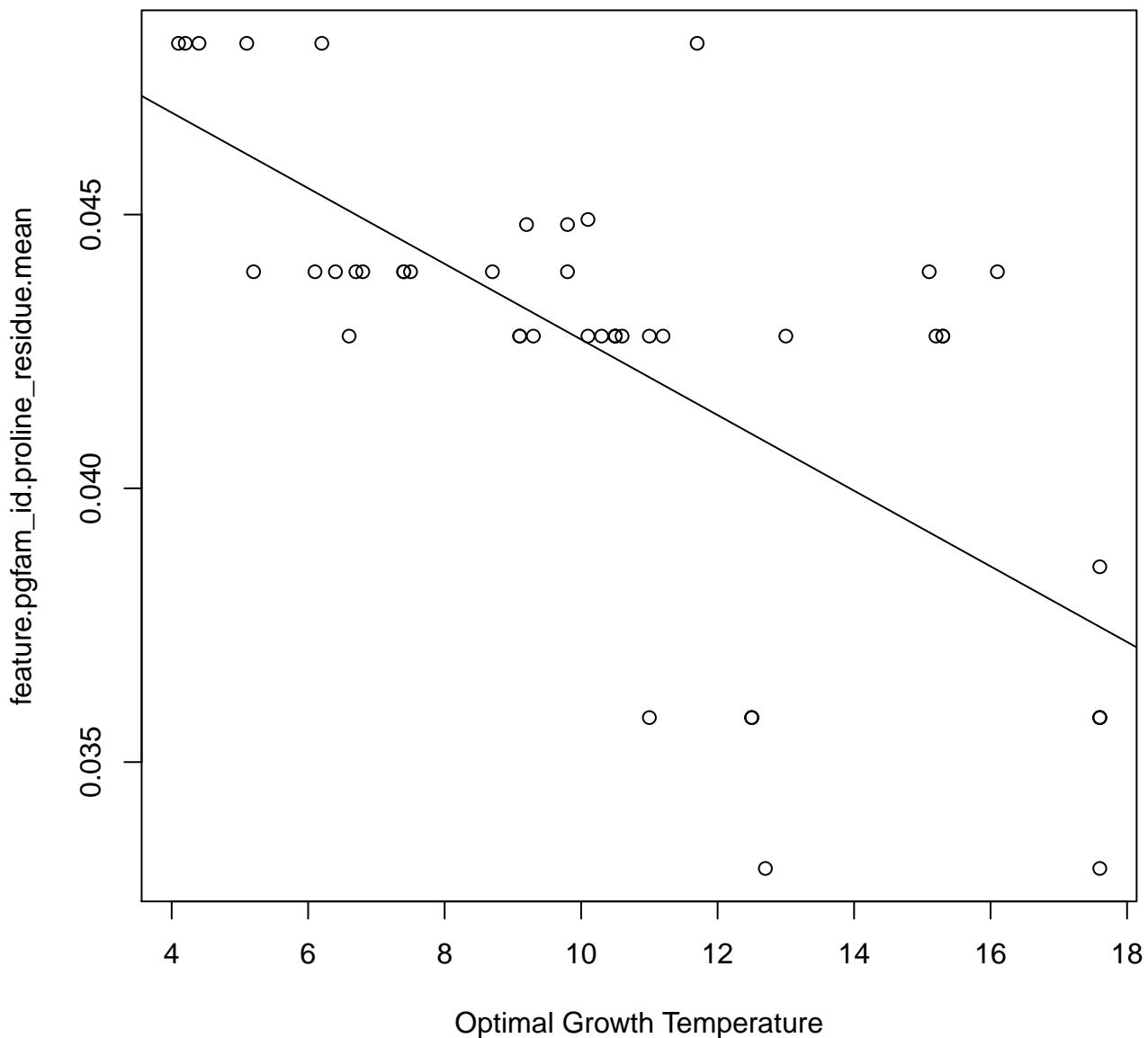
feature.pgfam_id.proline_residue.mean
PGF_07420523
Exodeoxyribonuclease III (EC 3.1.11.2)



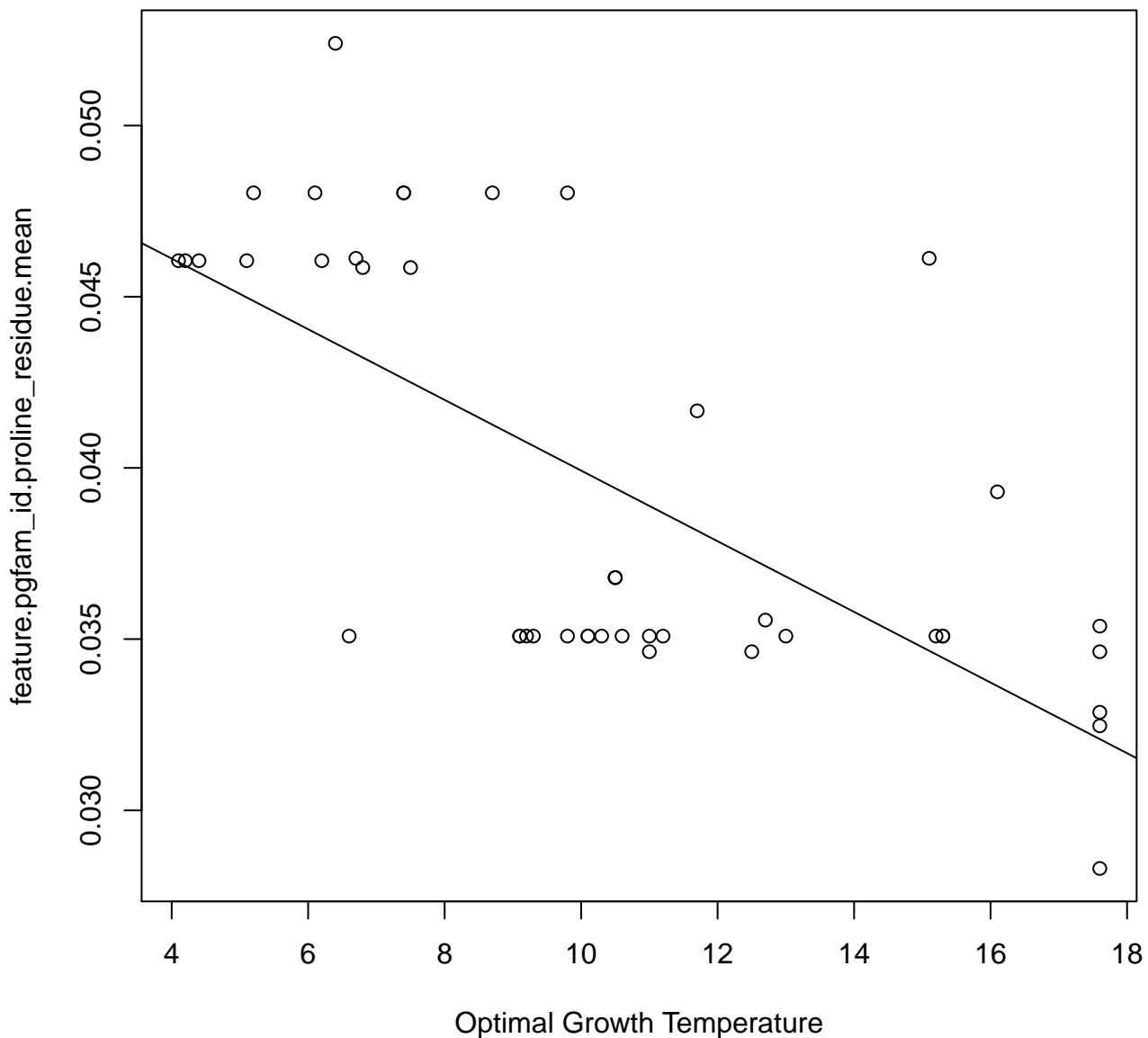
feature.pgfam_id.proline_residue.mean
PGF_03138644
Arginine exporter protein ArgO



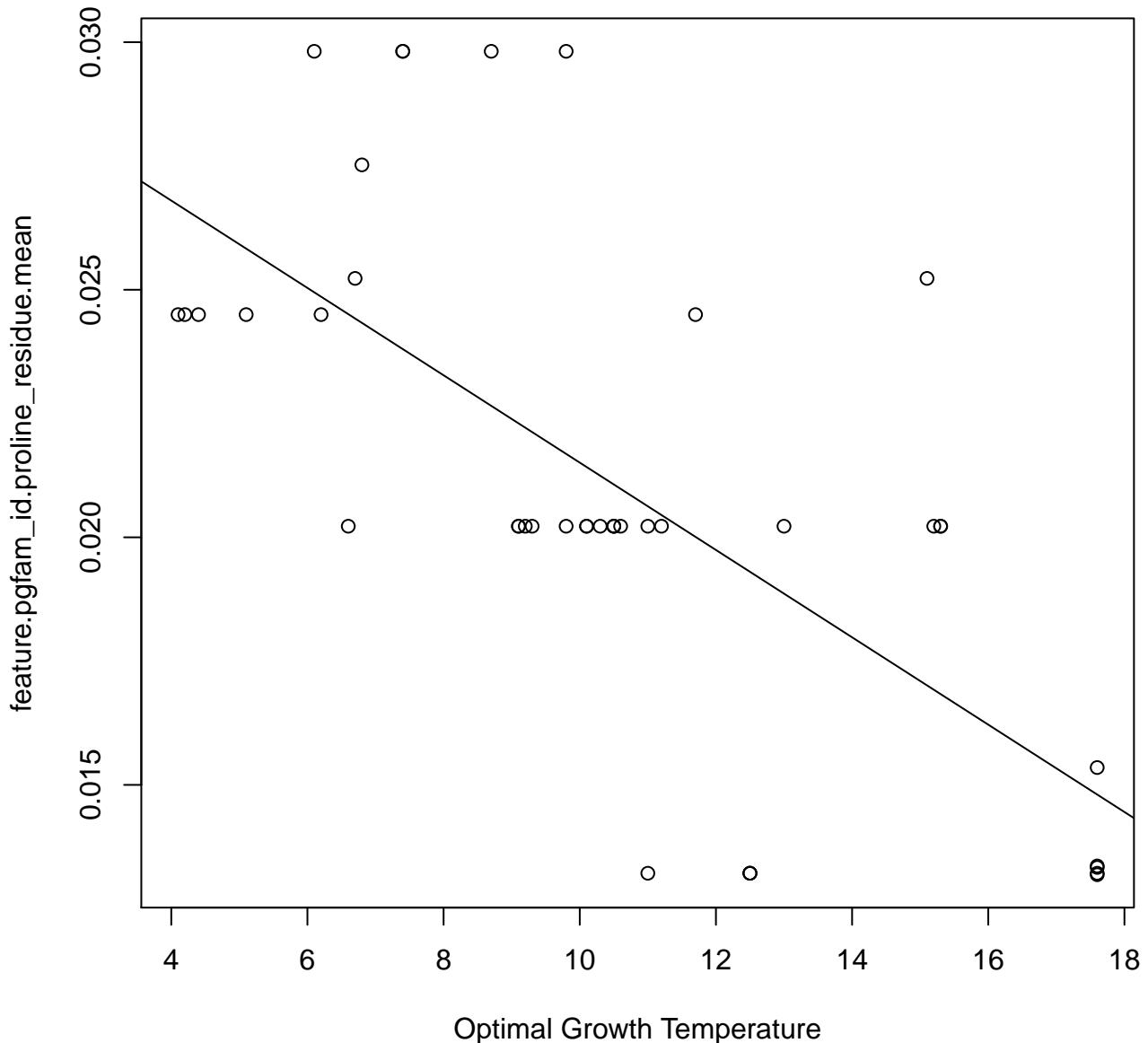
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PGF_00005288
Flagellar P-ring protein Flgl



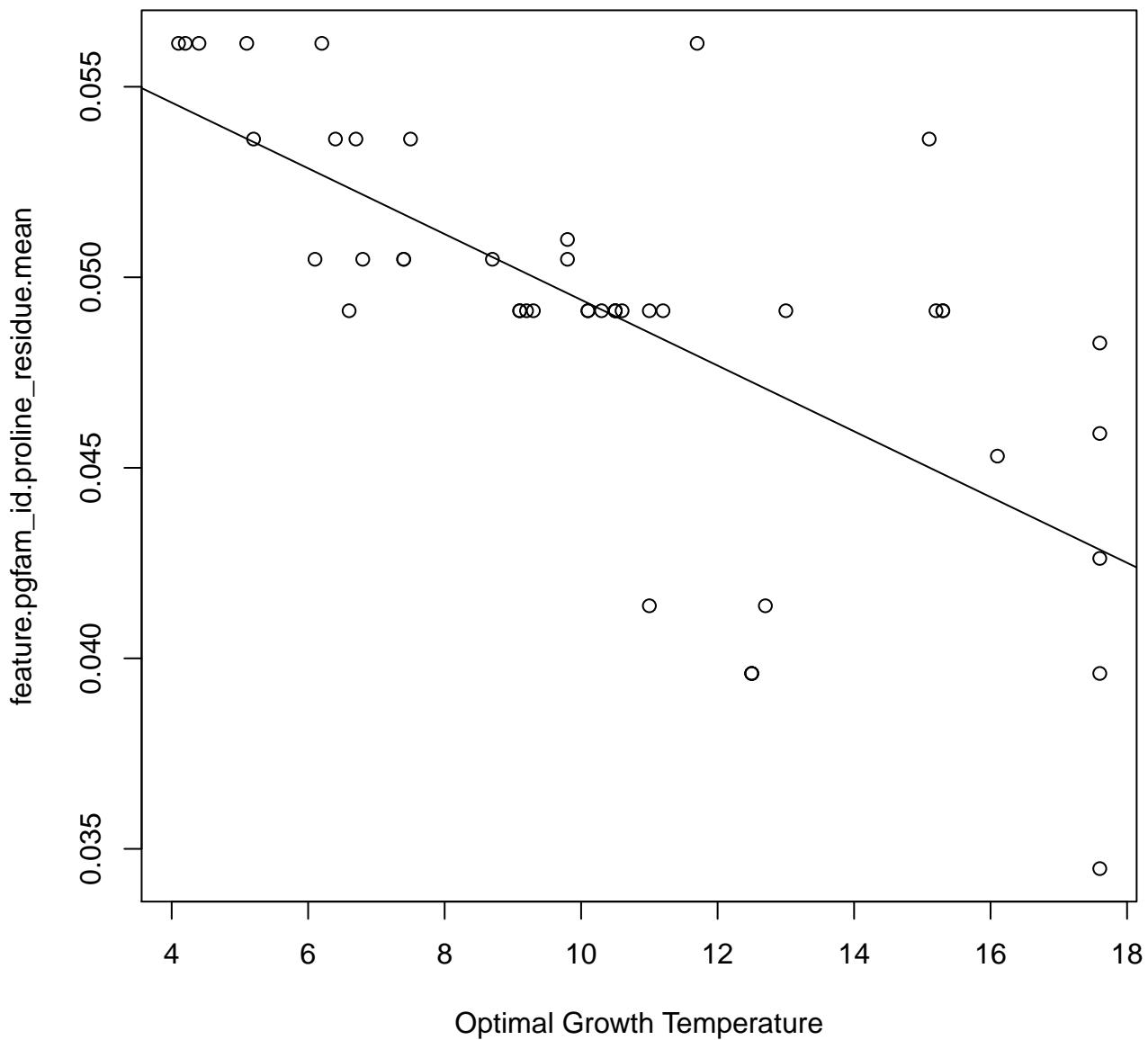
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PGF_09087715
tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)



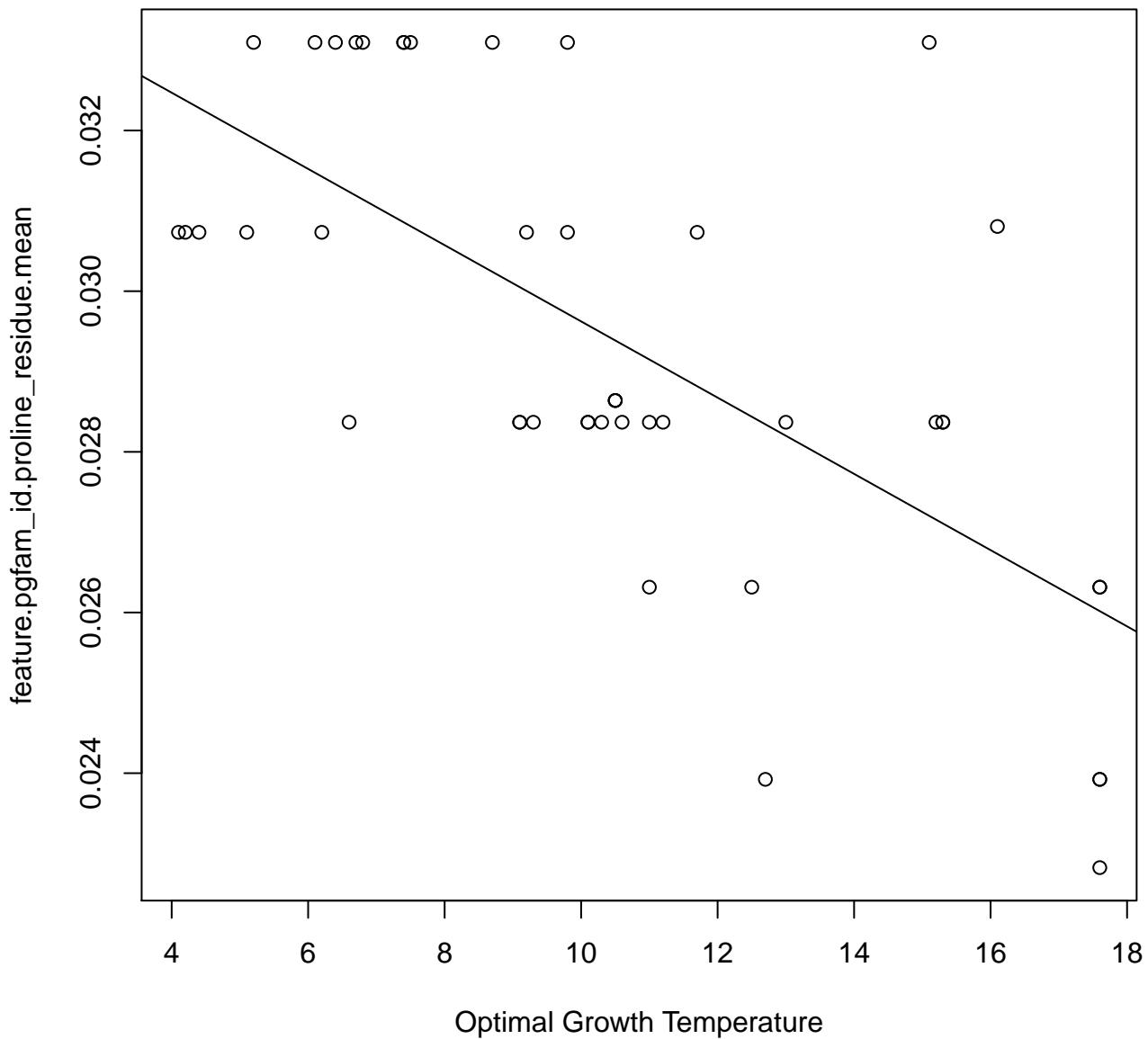
feature.pgfam_id.proline_residue.mean
PGF_00055557
TPR domain protein, putative component of TonB system



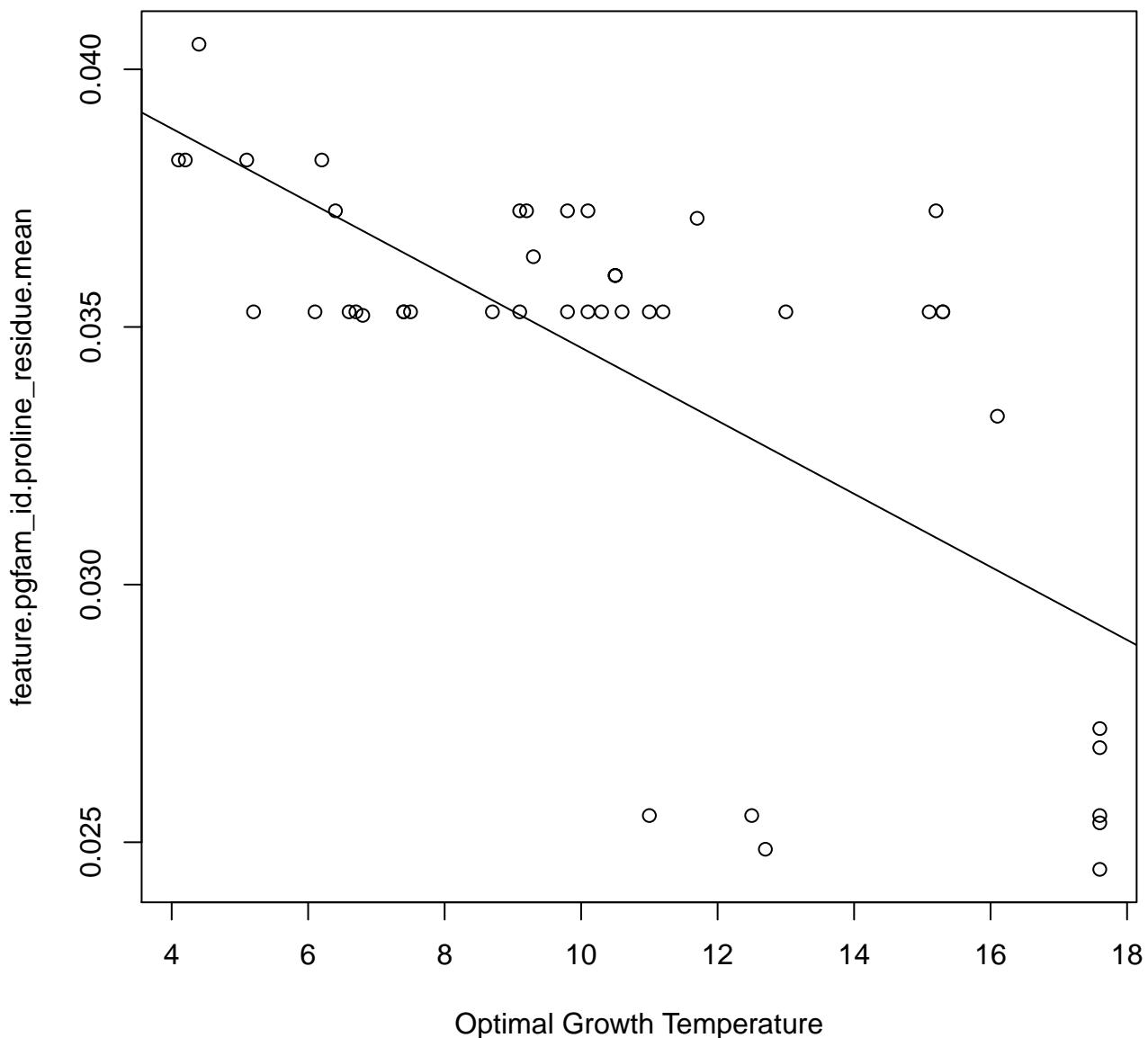
feature.pgfam_id.proline_residue.mean
PGF_00030781
Peptidyl-prolyl cis-trans isomerase



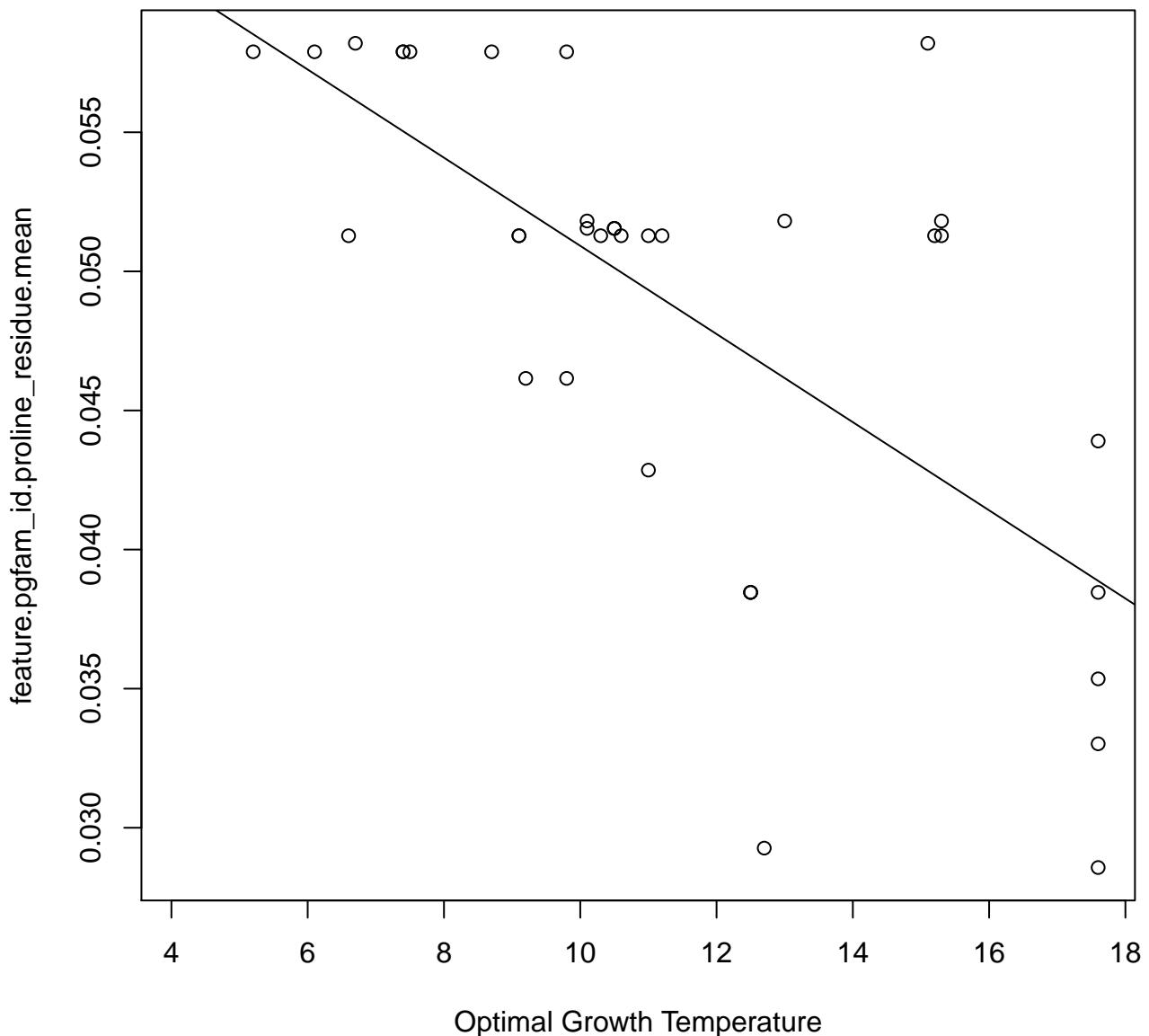
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PGF_05387084
Gamma-glutamyl phosphate reductase (EC 1.2.1.41)



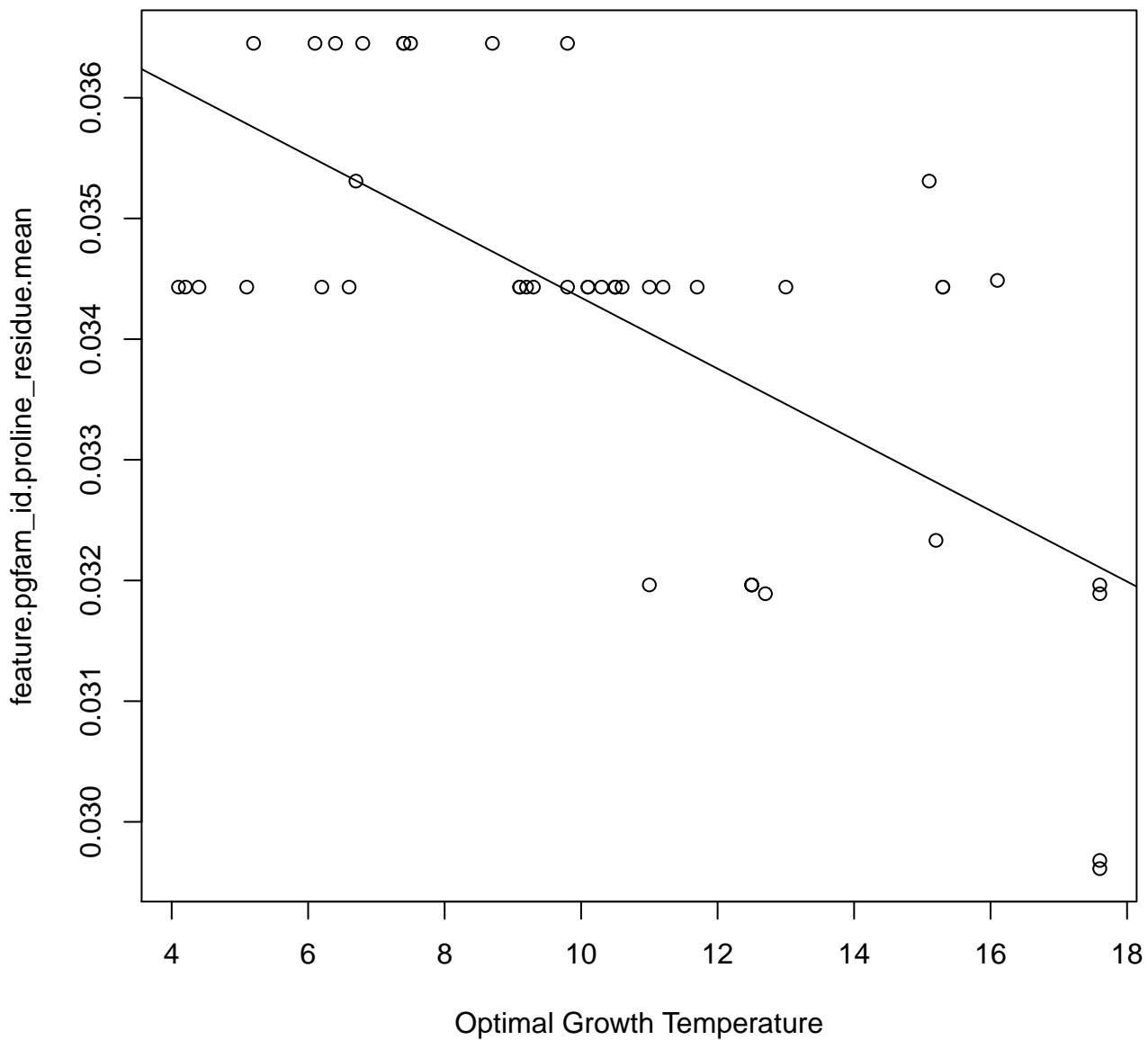
feature.pgfam_id.proline_residue.mean
PGF_02158779
Di-tripeptide/cation symporter



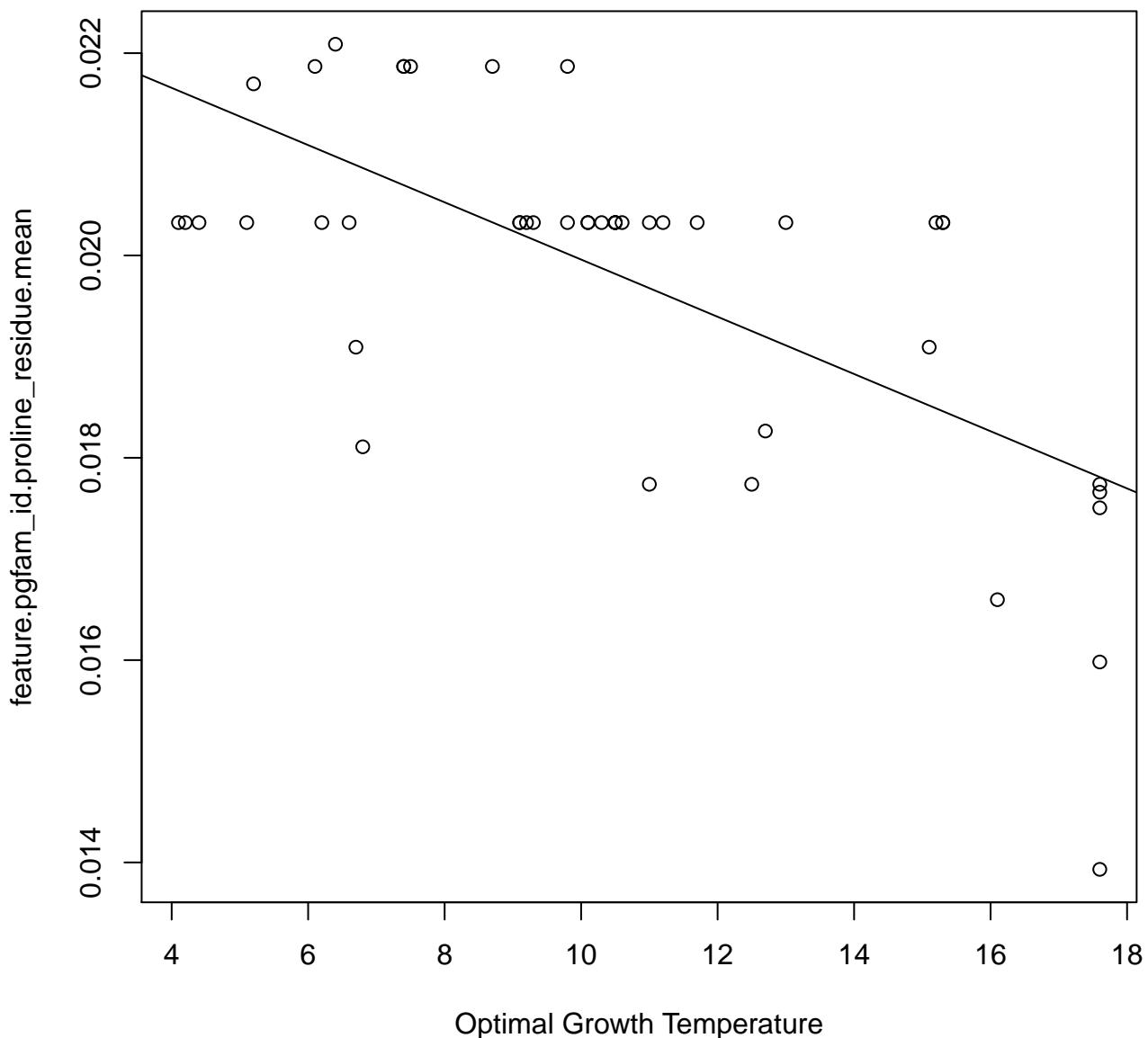
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PGF_00038329
Der GTPase-activating protein Yihl



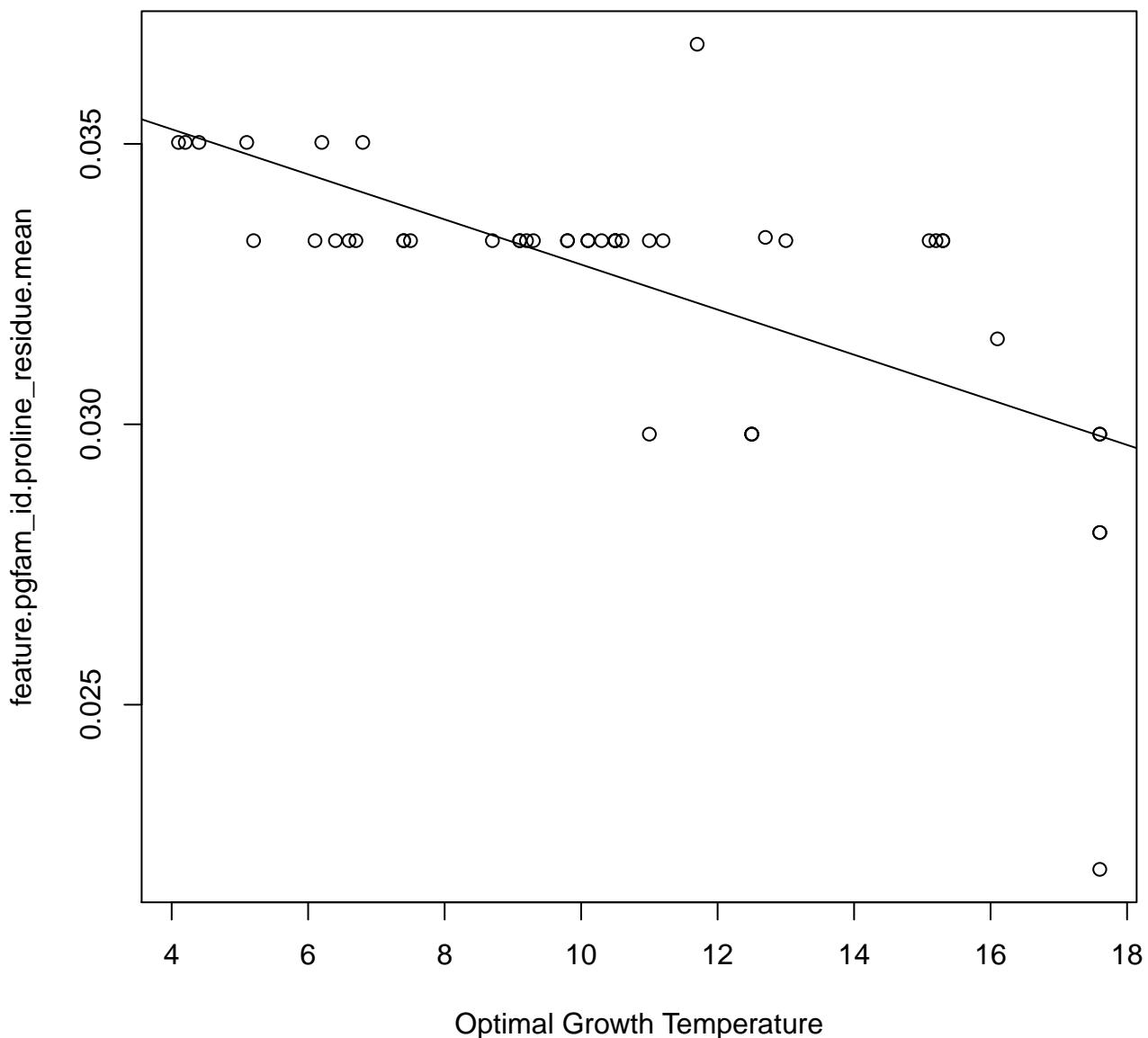
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PGF_00056876
Thymidine phosphorylase (EC 2.4.2.4)



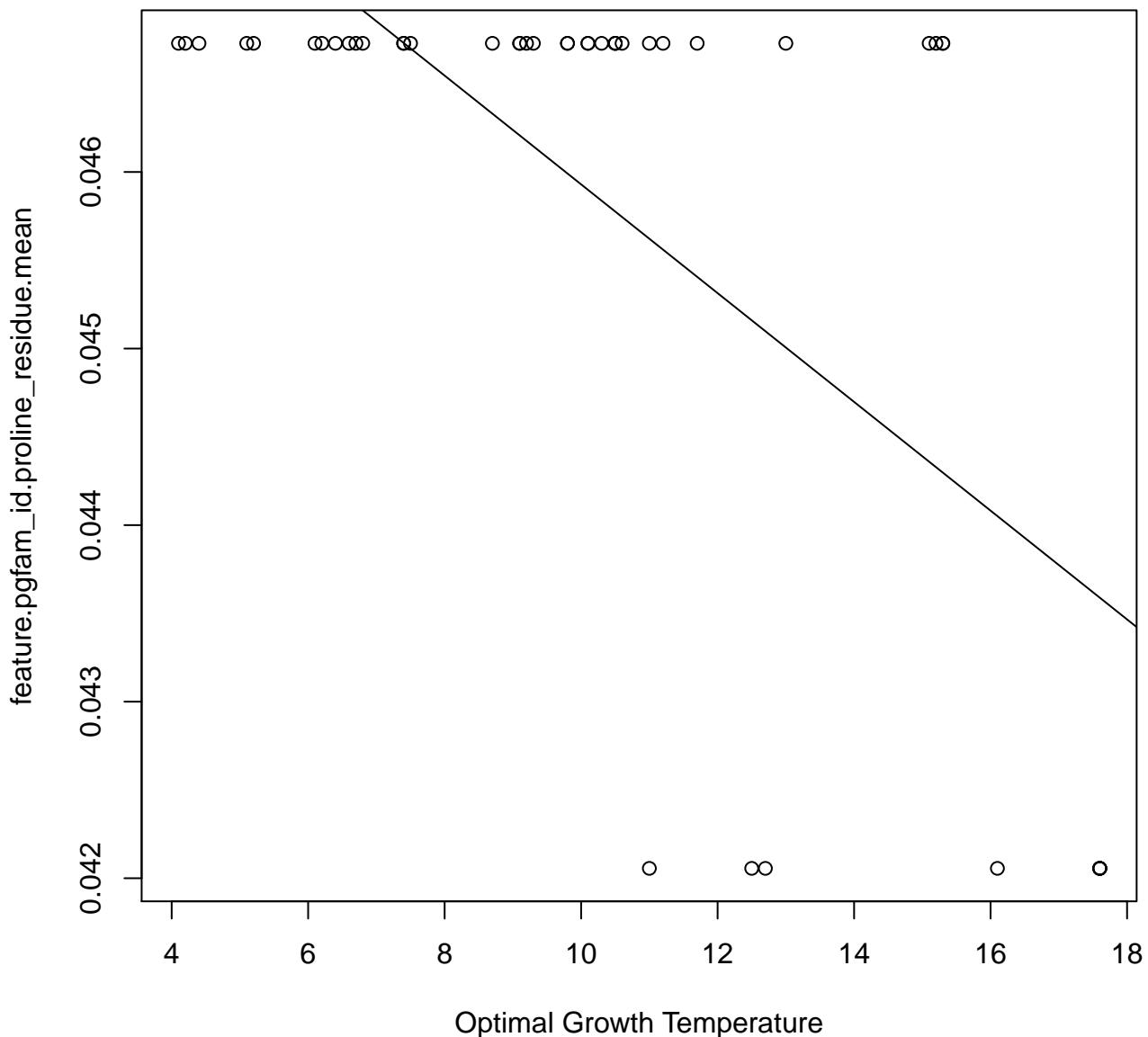
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PGF_10351306
DNA recombination protein RmuC



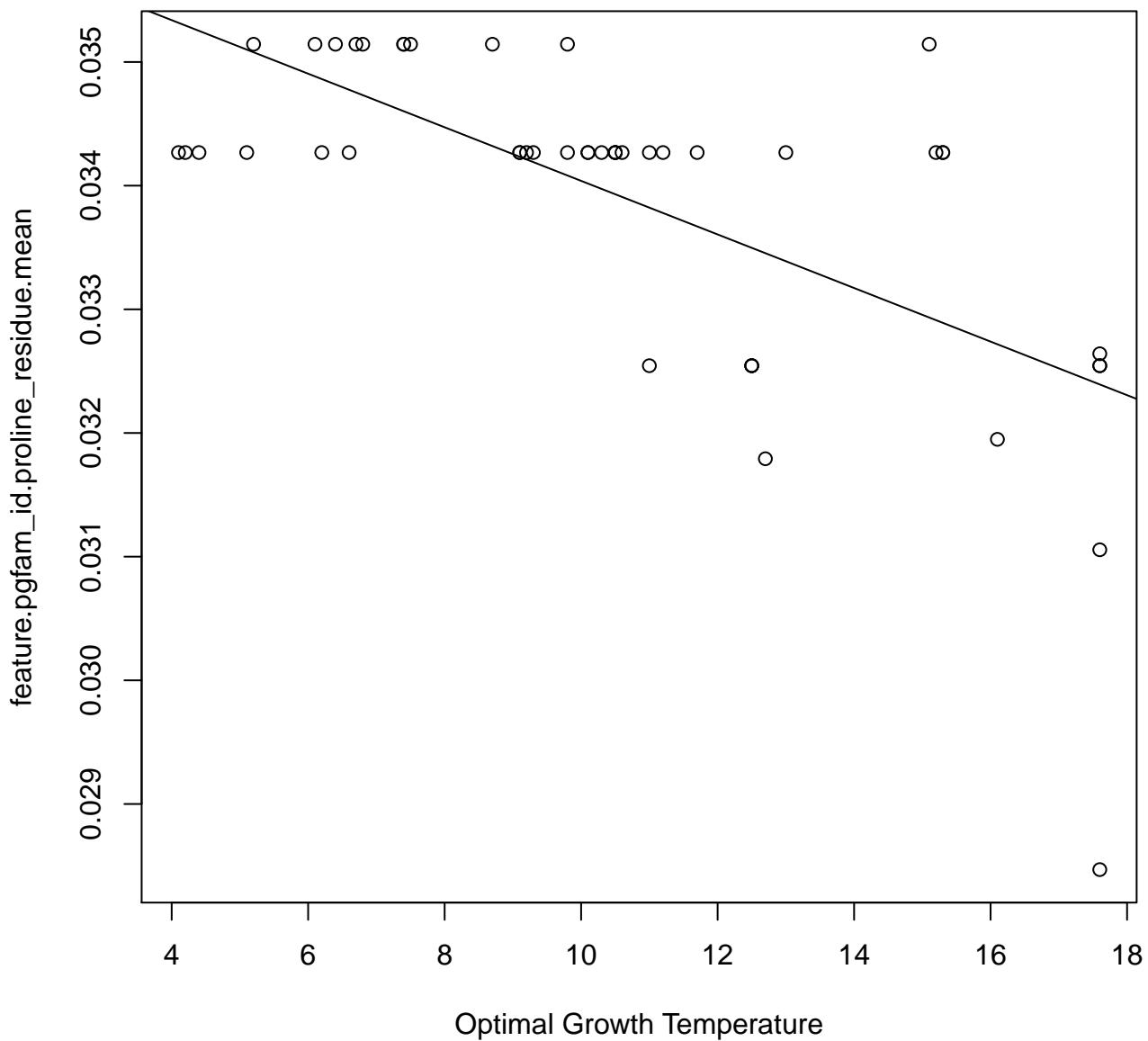
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PGF_00018393
MSHA biogenesis protein MshE



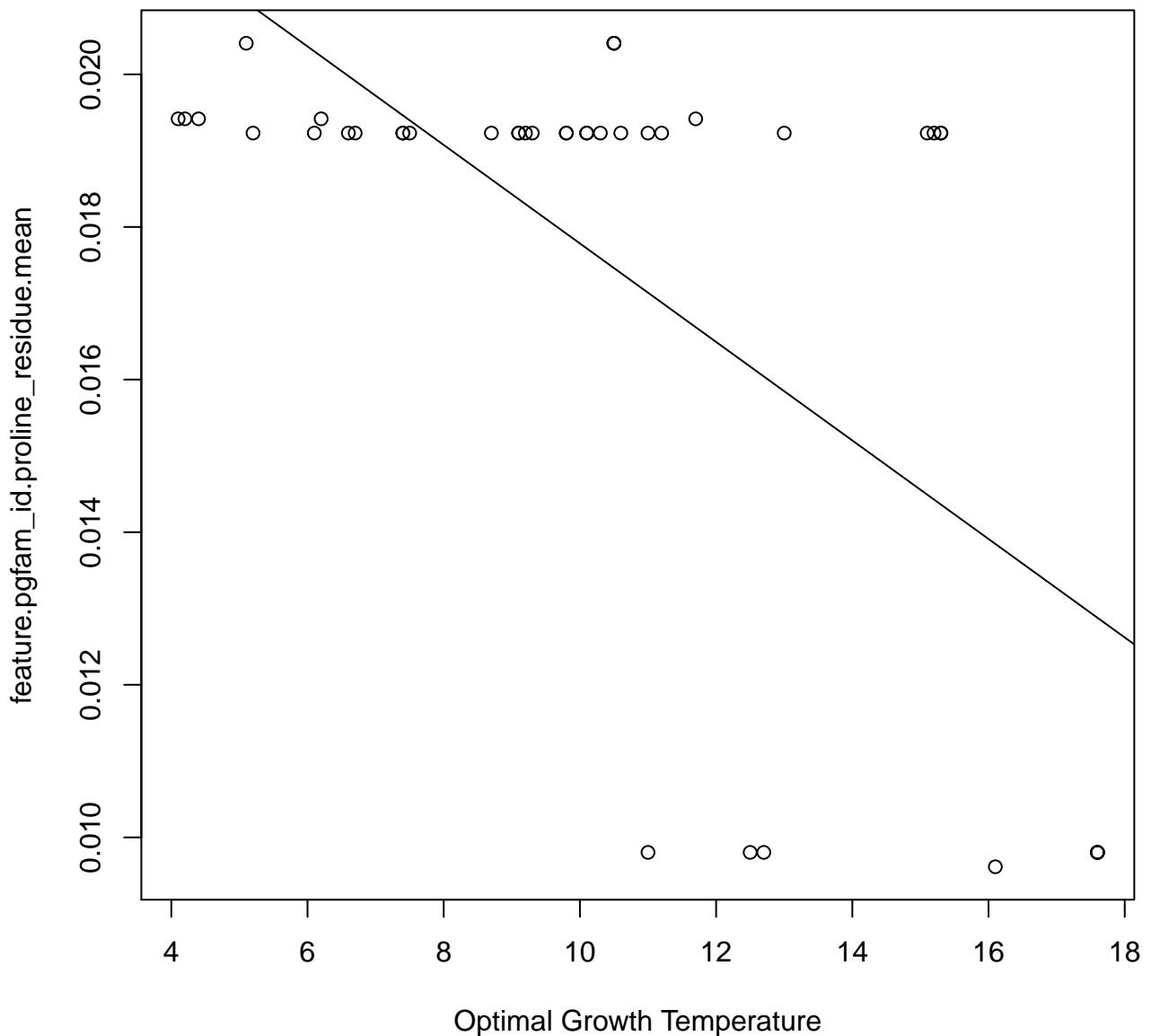
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PGF_04244475
Adenylate kinase (EC 2.7.4.3)



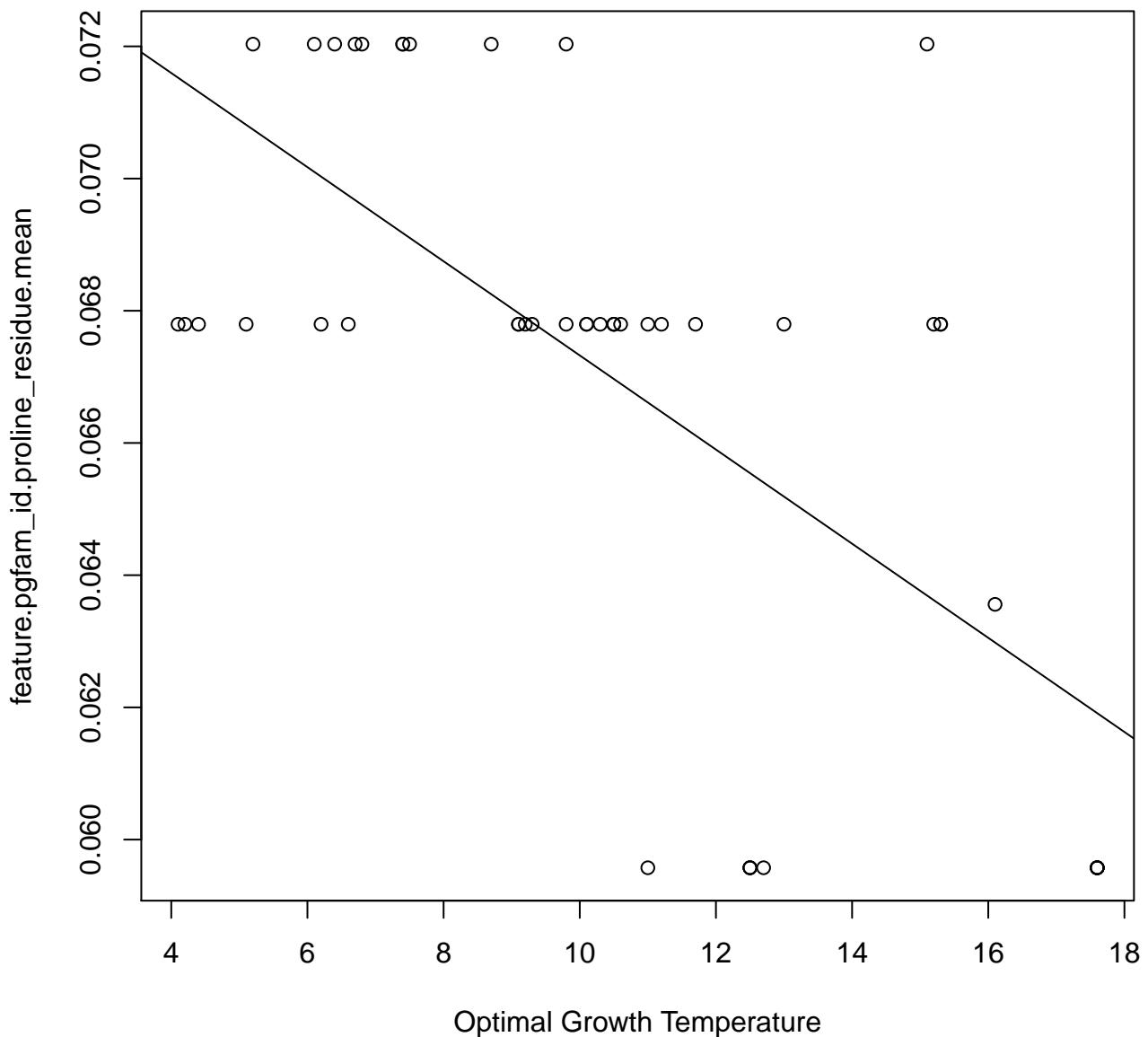
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PGF_00912265
tRNA-dihydrouridine synthase DusB



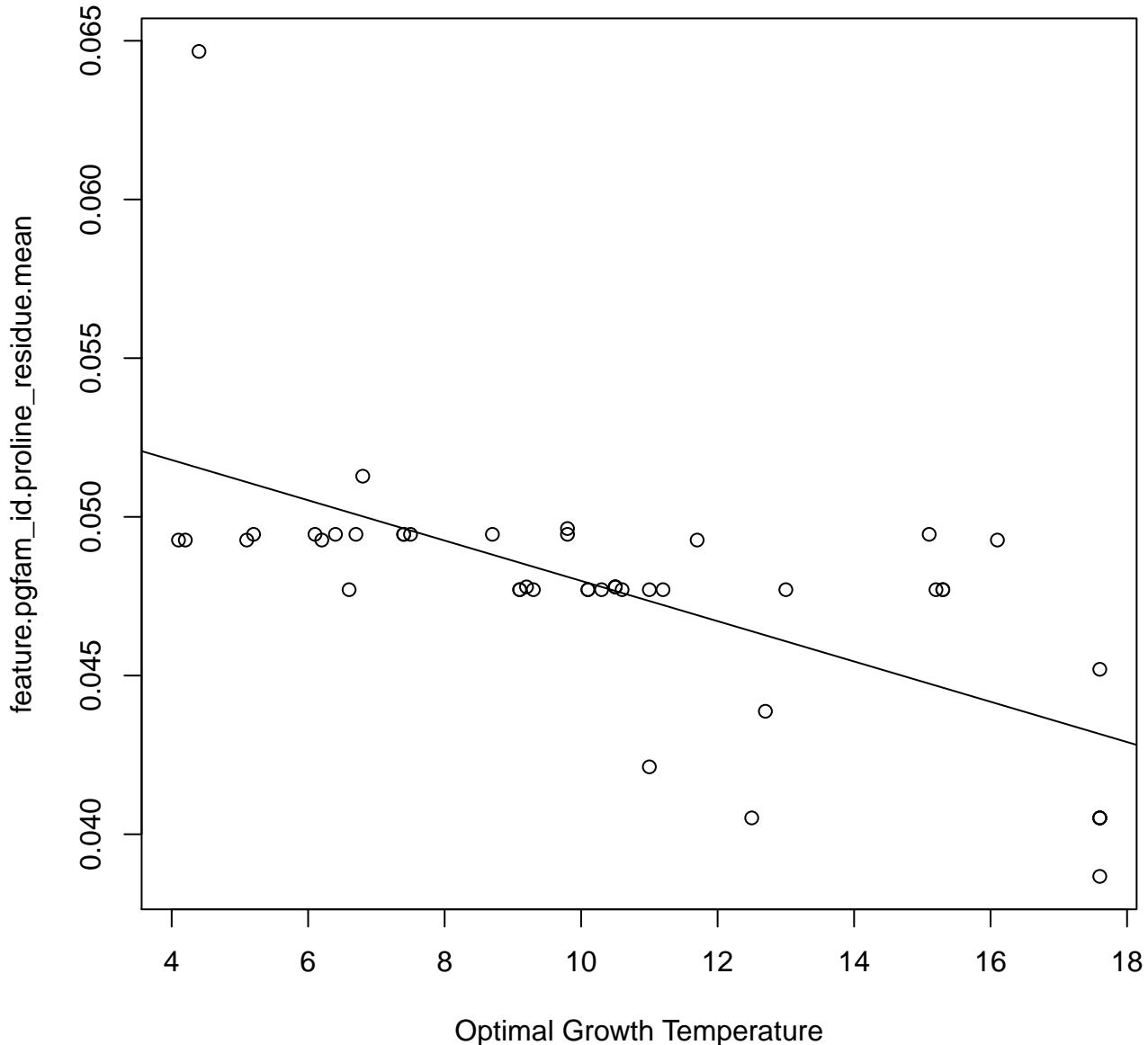
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PGF_01170625
Cell division protein FtsL



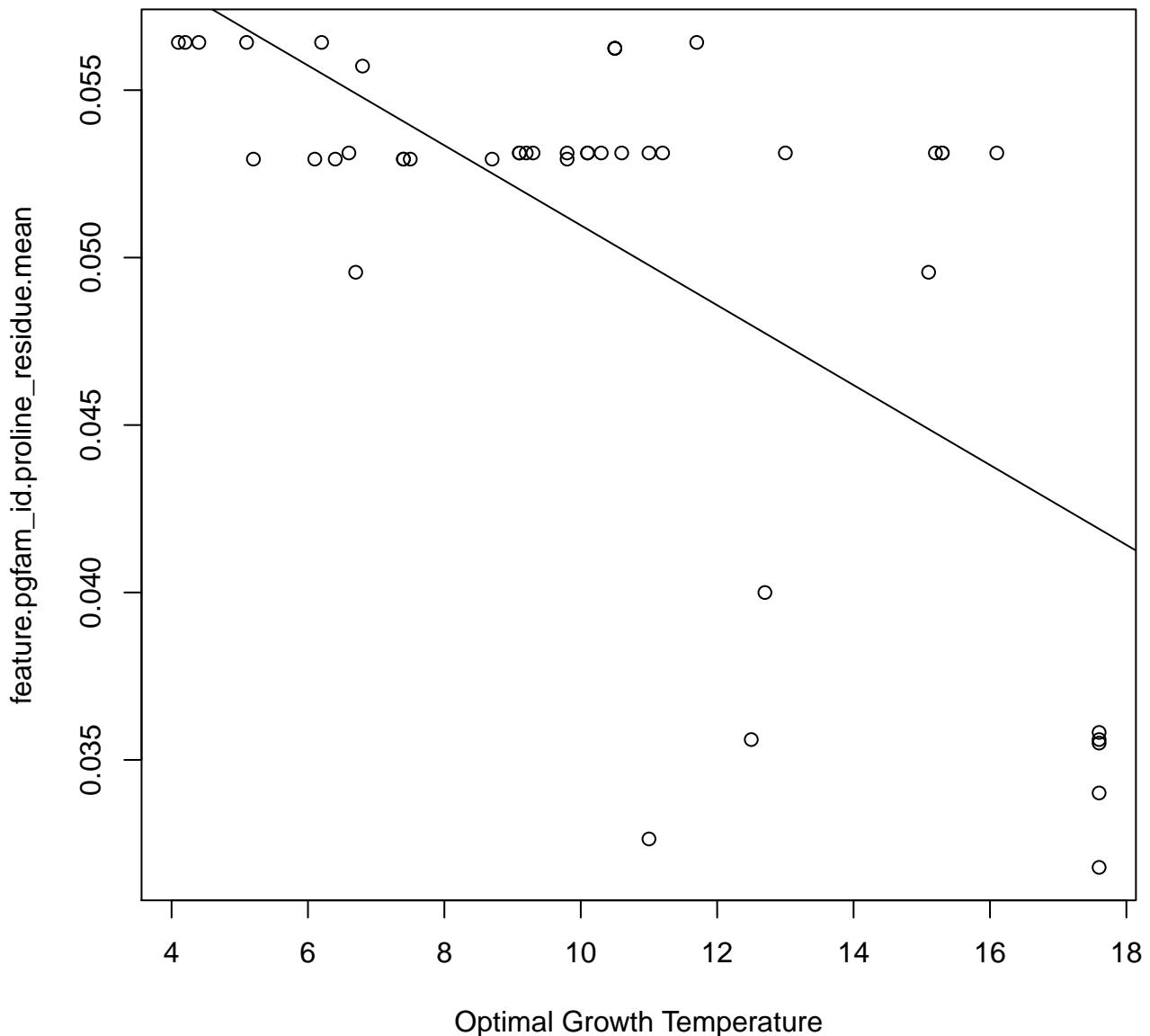
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PGF_00054480
Succinate dehydrogenase iron-sulfur protein (EC 1.3.5.1)



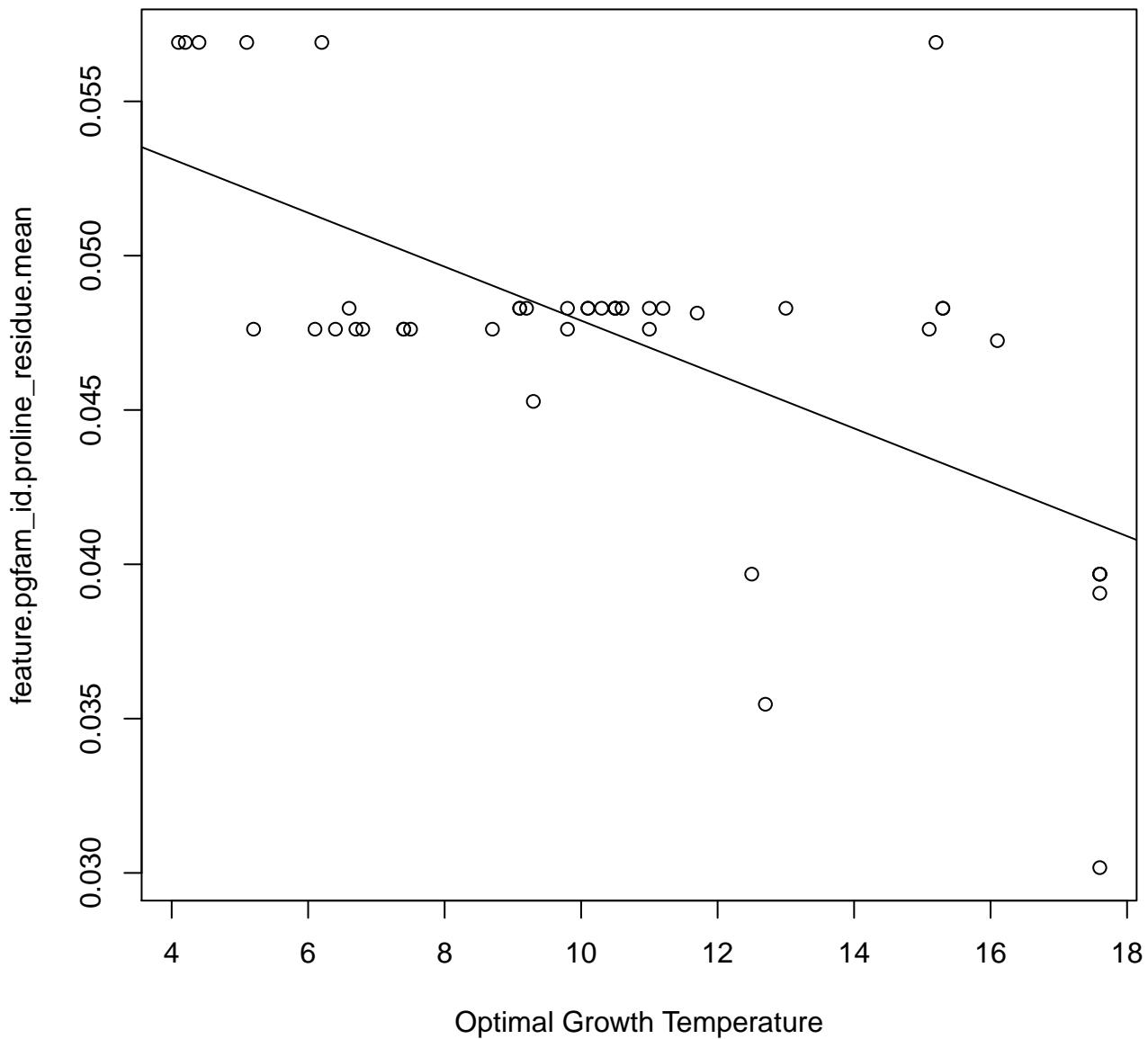
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PGF_03751973
Inner membrane protein translocase and chaperone YidC, long form



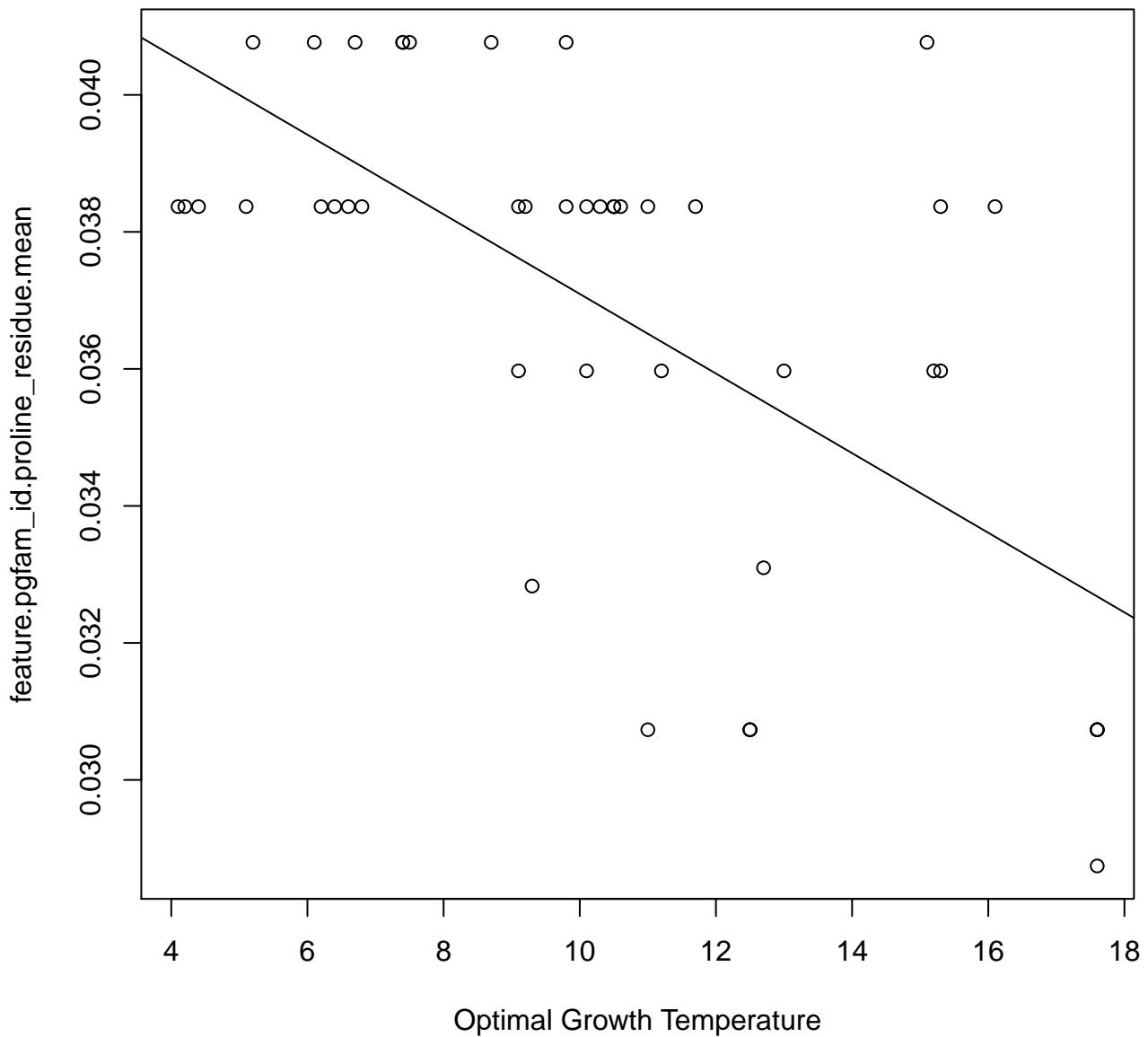
feature.pgfam_id.proline_residue.mean
PGF_00052053
Sigma factor RpoE negative regulatory protein RseB precursor



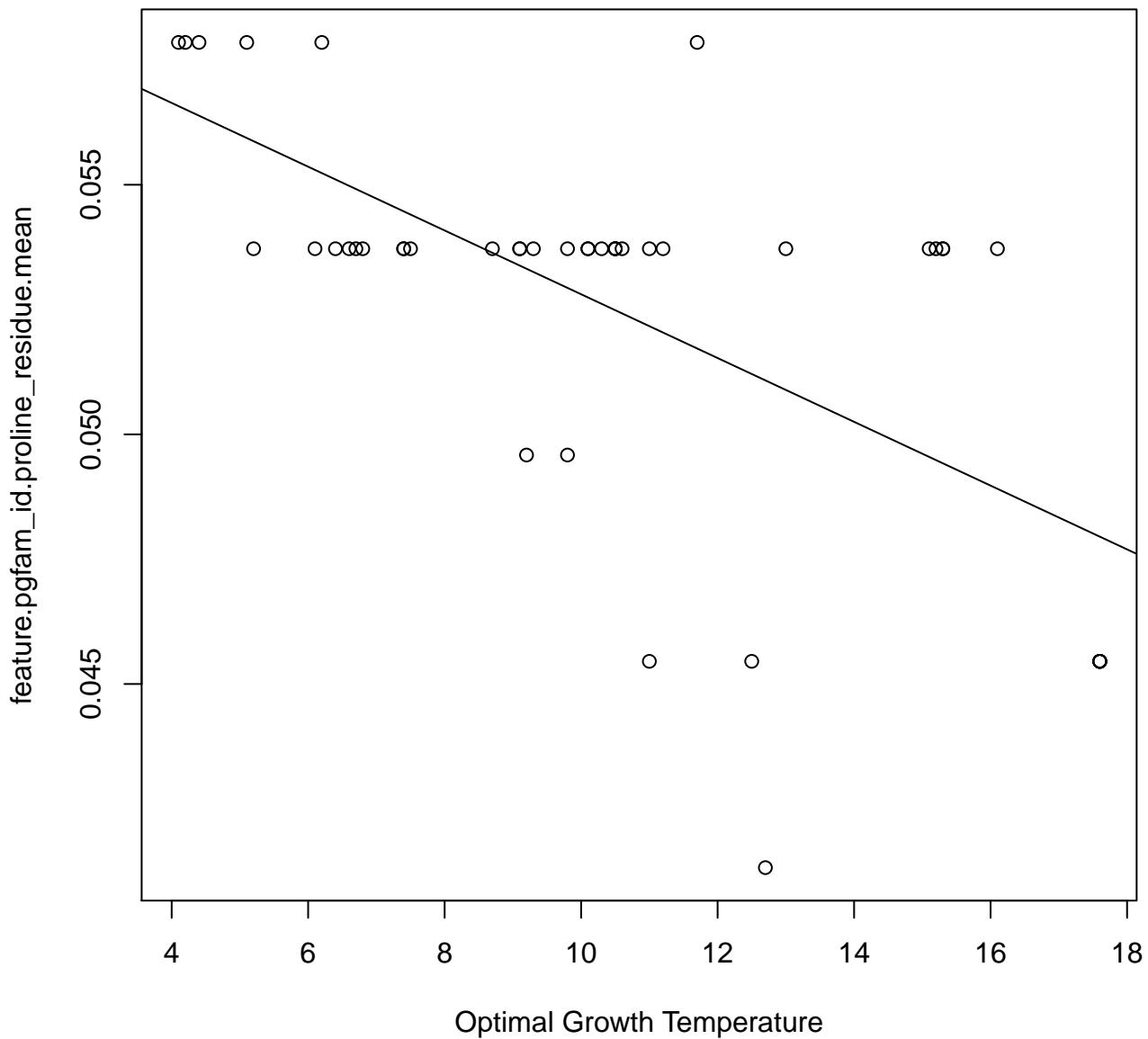
feature.pgfam_id.proline_residue.mean
PGF_06792997
Lactoylglutathione lyase and related lyases



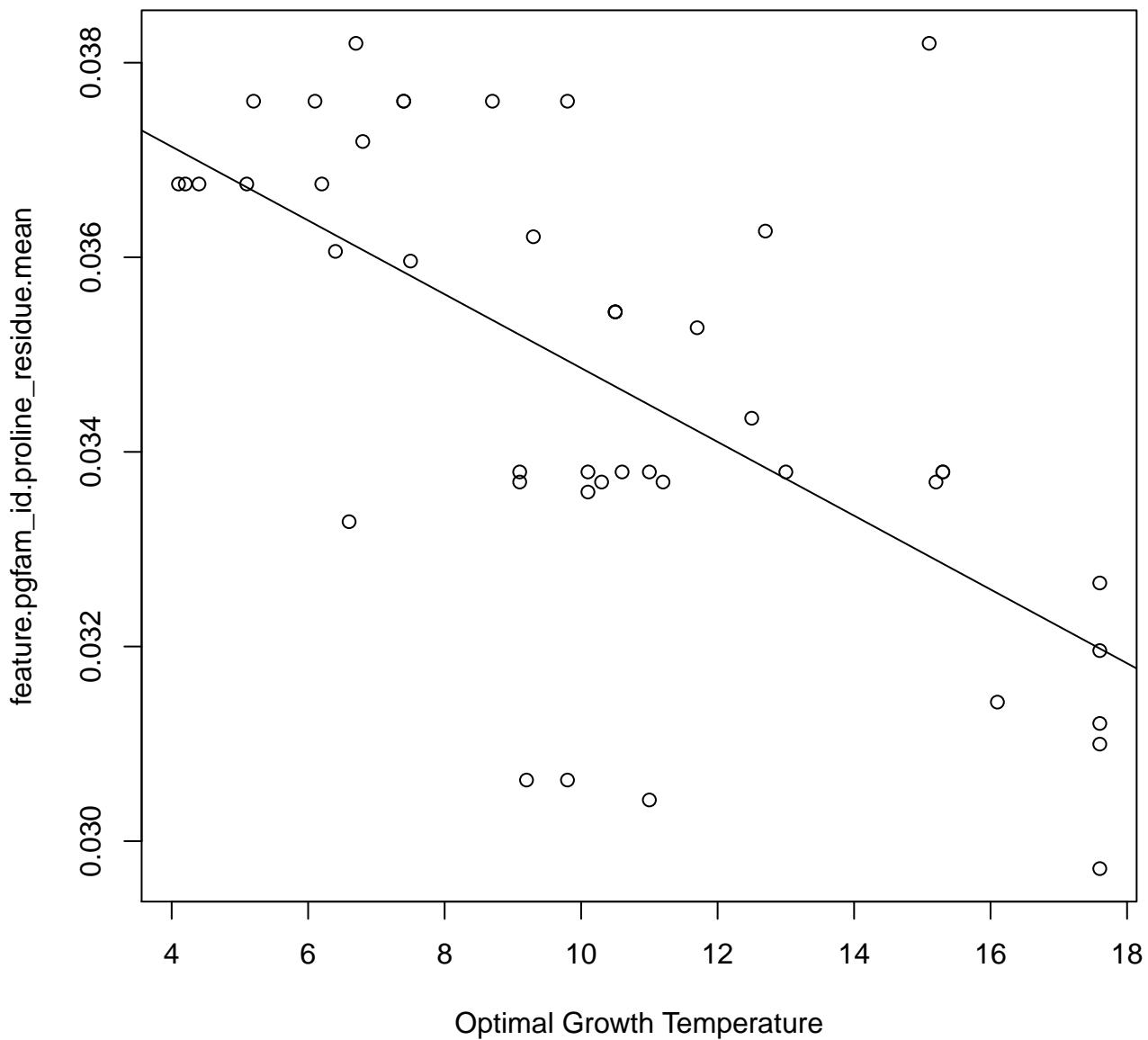
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PGF_03109975
Serine protease precursor MucD/AlgY associated with sigma factor RpoE



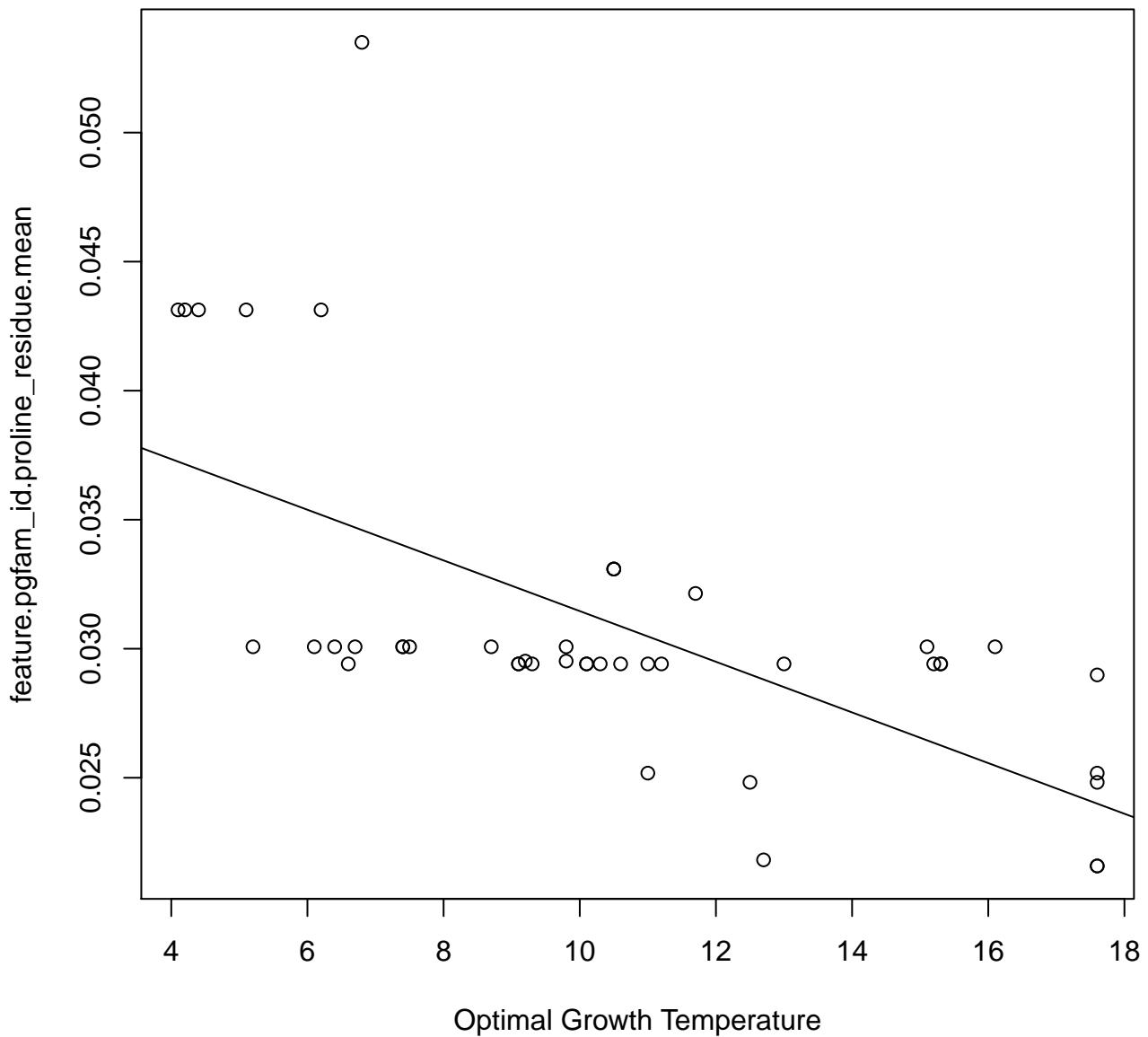
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PGF_00581959
Hybrid peroxiredoxin hyPrx5 (EC 1.11.1.15)



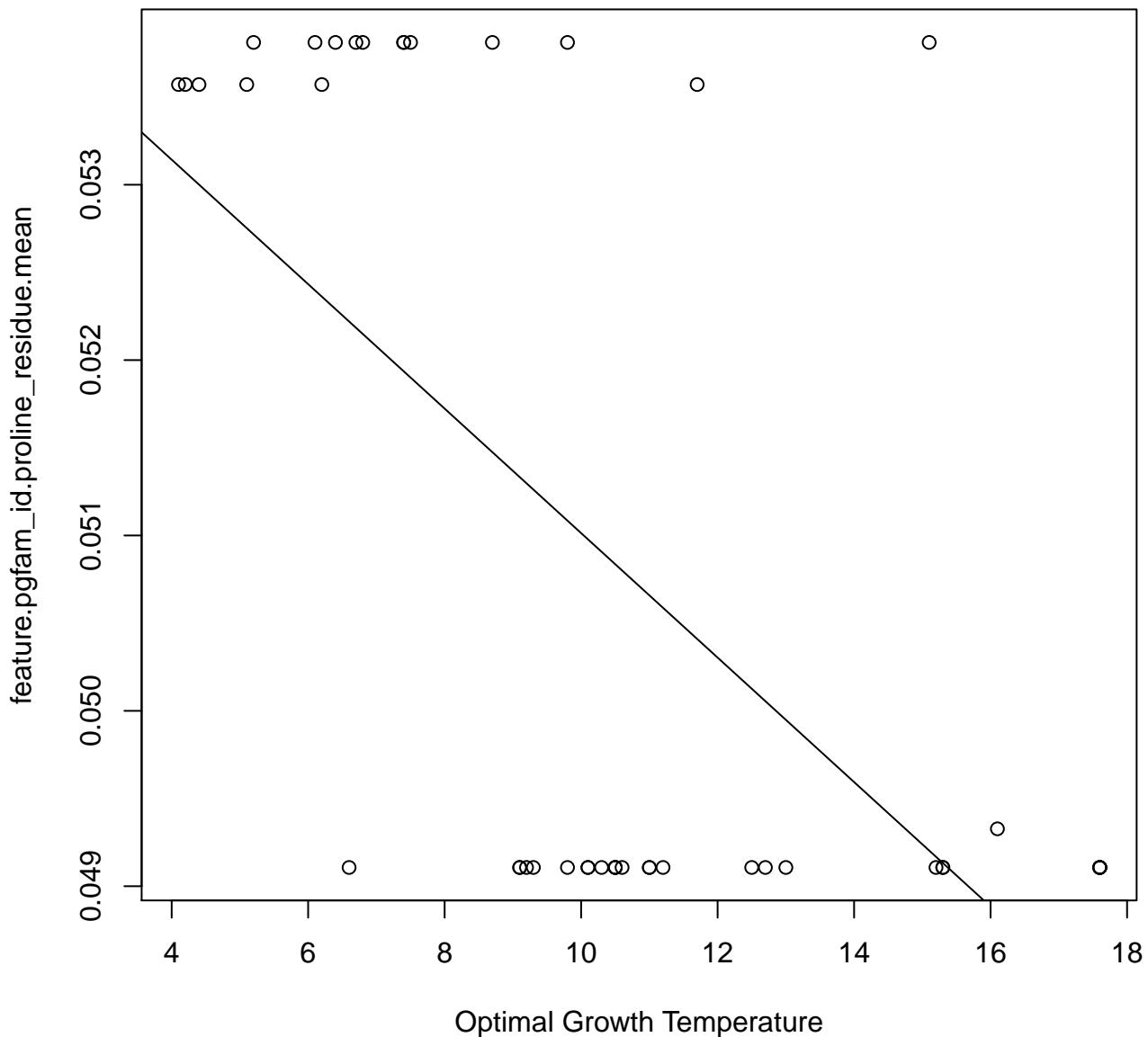
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PGF_00767262
Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)



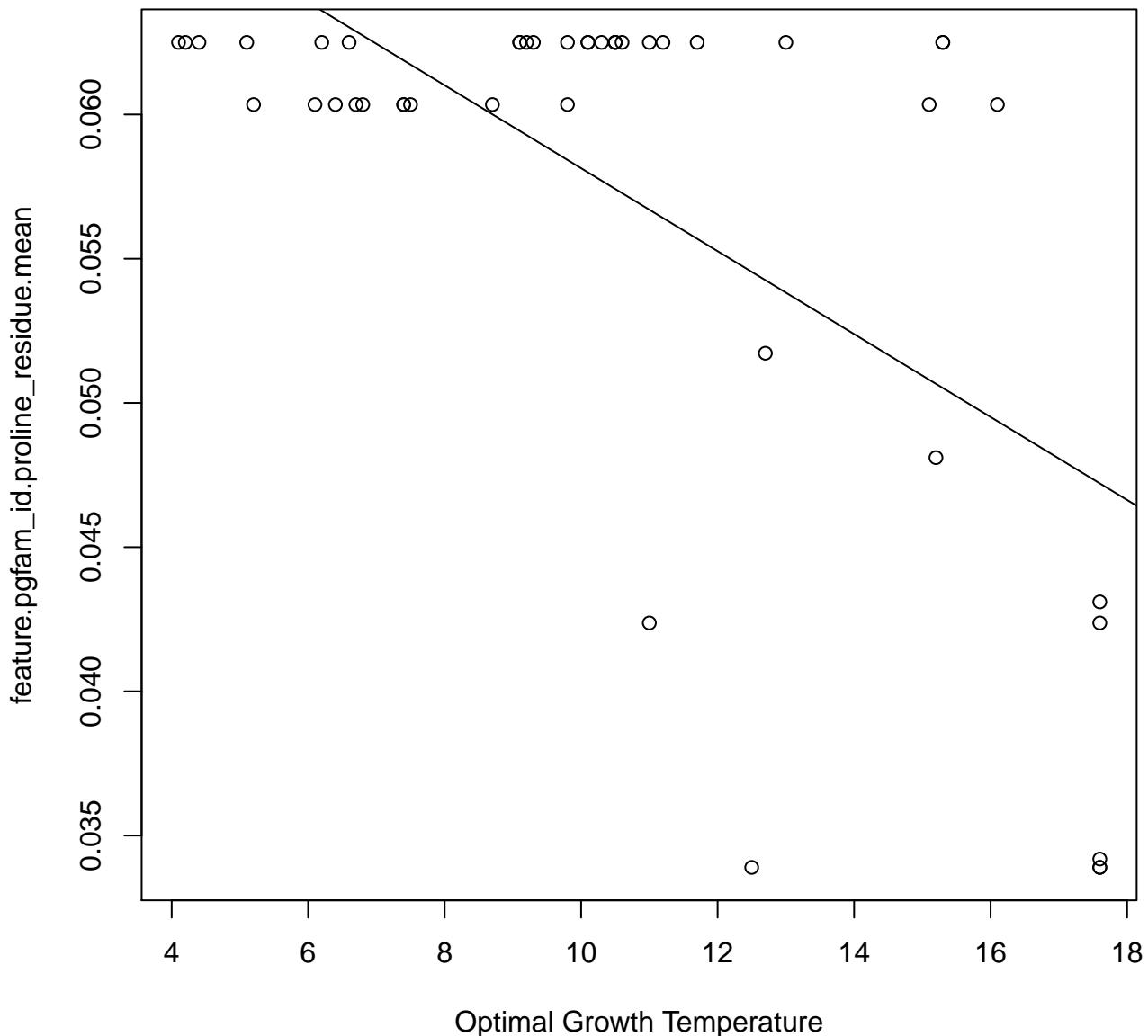
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PGF_10414515
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)



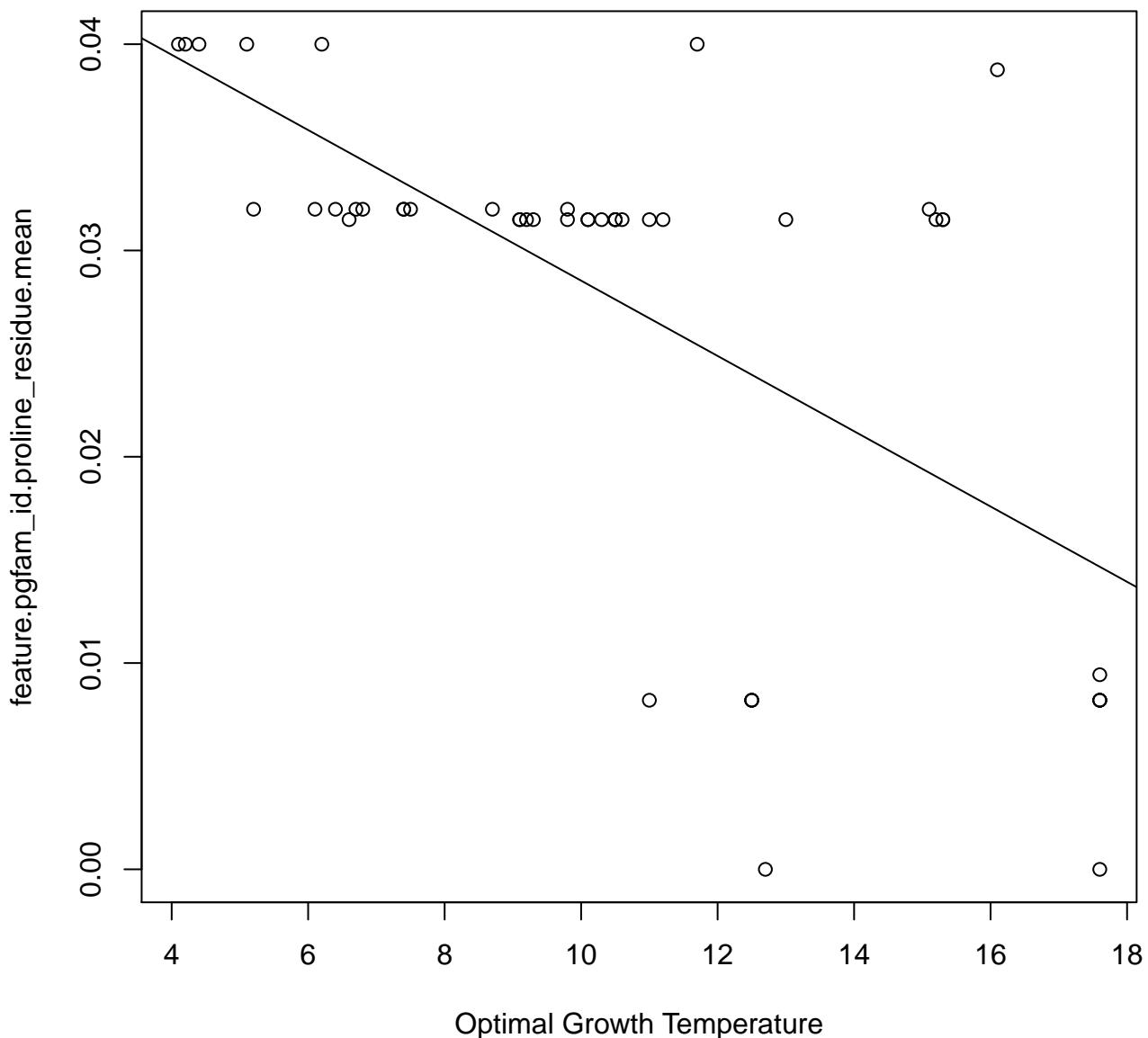
feature.pgfam_id.proline_residue.mean
PGF_10245672
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)



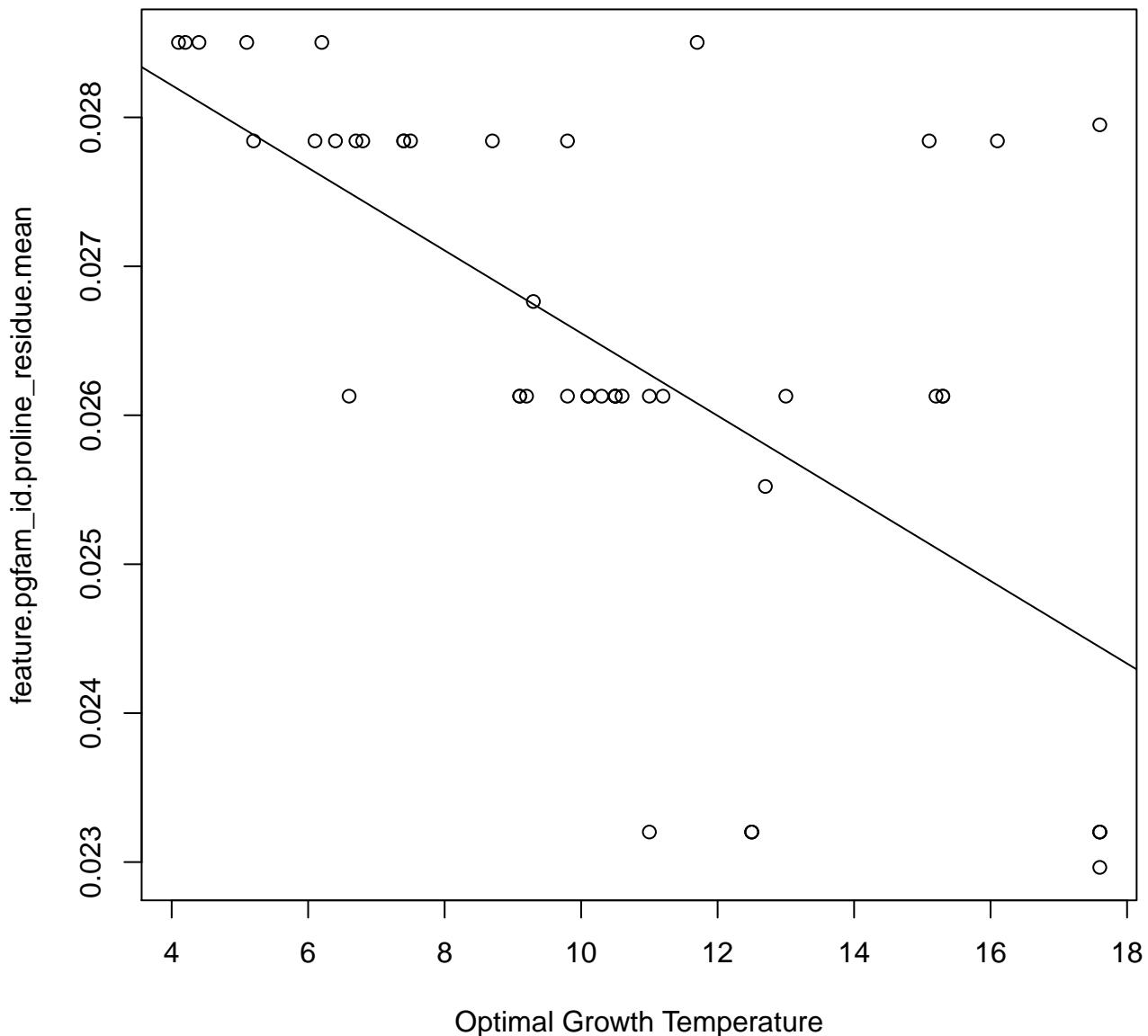
feature.pgfam_id.proline_residue.mean
PGF_09375481
Uncharacterized protein YfgD, not an arsenate reductase



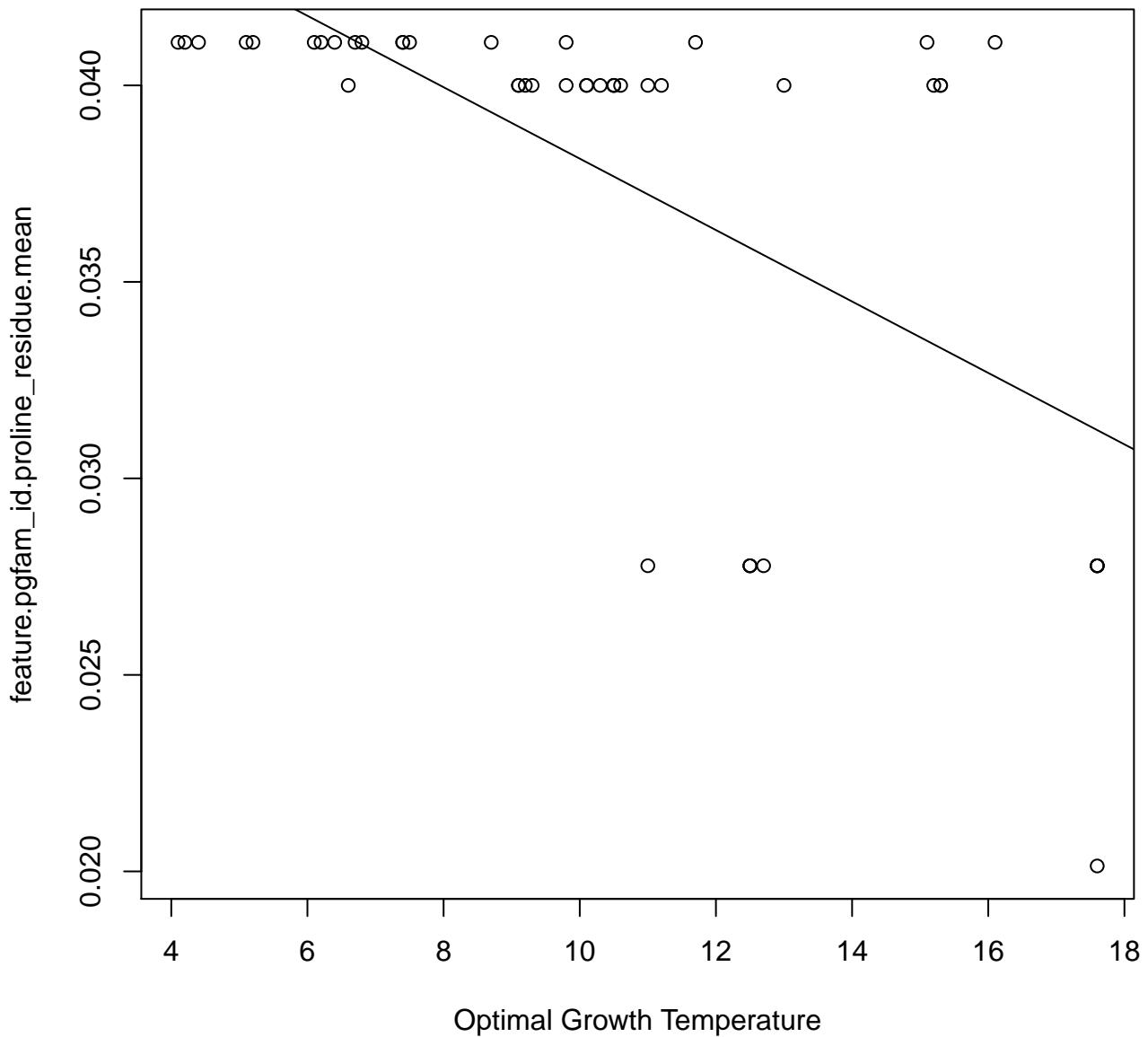
feature.pgfam_id.proline_residue.mean
PGF_01336380
hypothetical protein



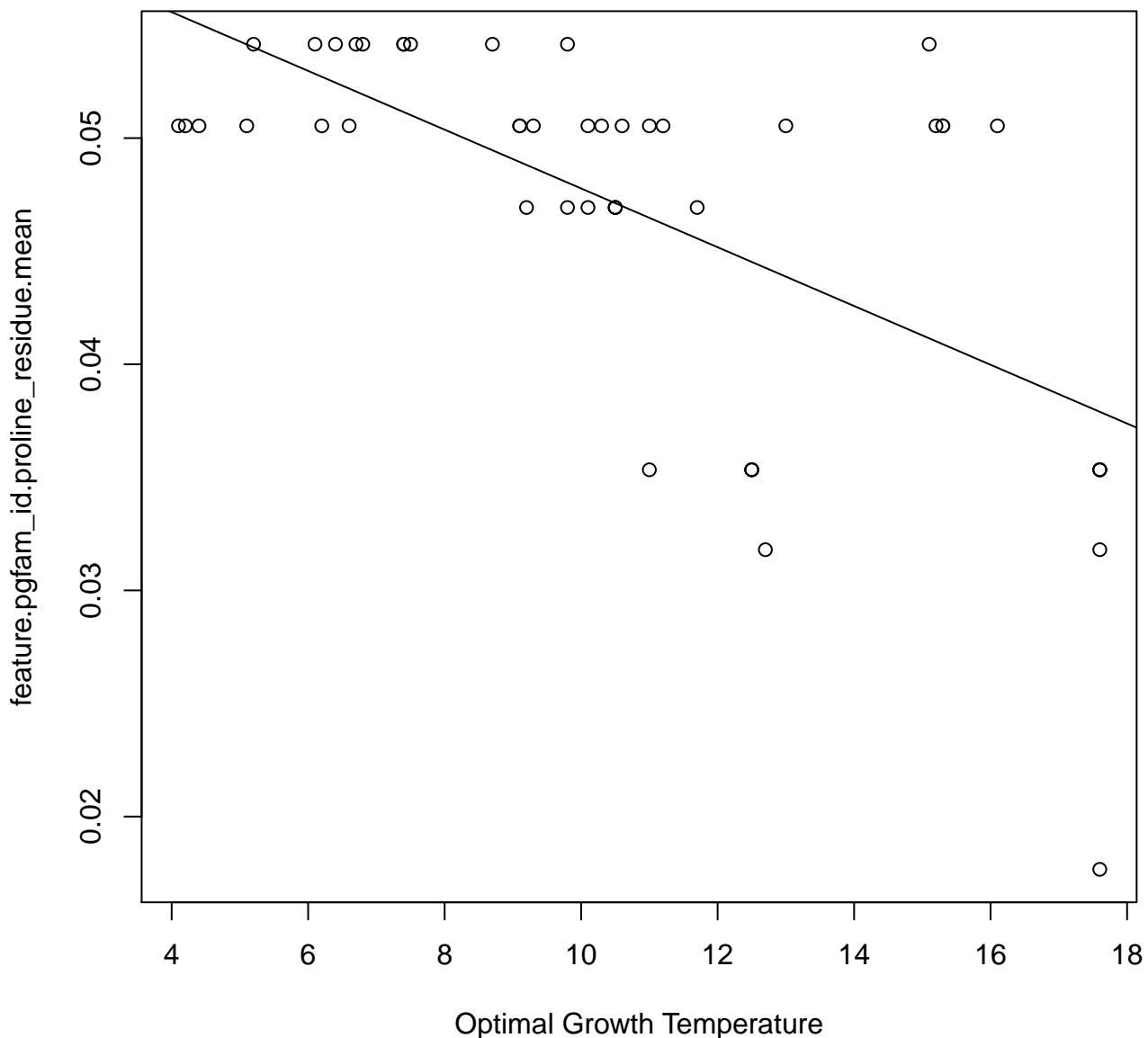
feature.pgfam_id.proline_residue.mean
PGF_00037171
Probable low-affinity inorganic phosphate transporter



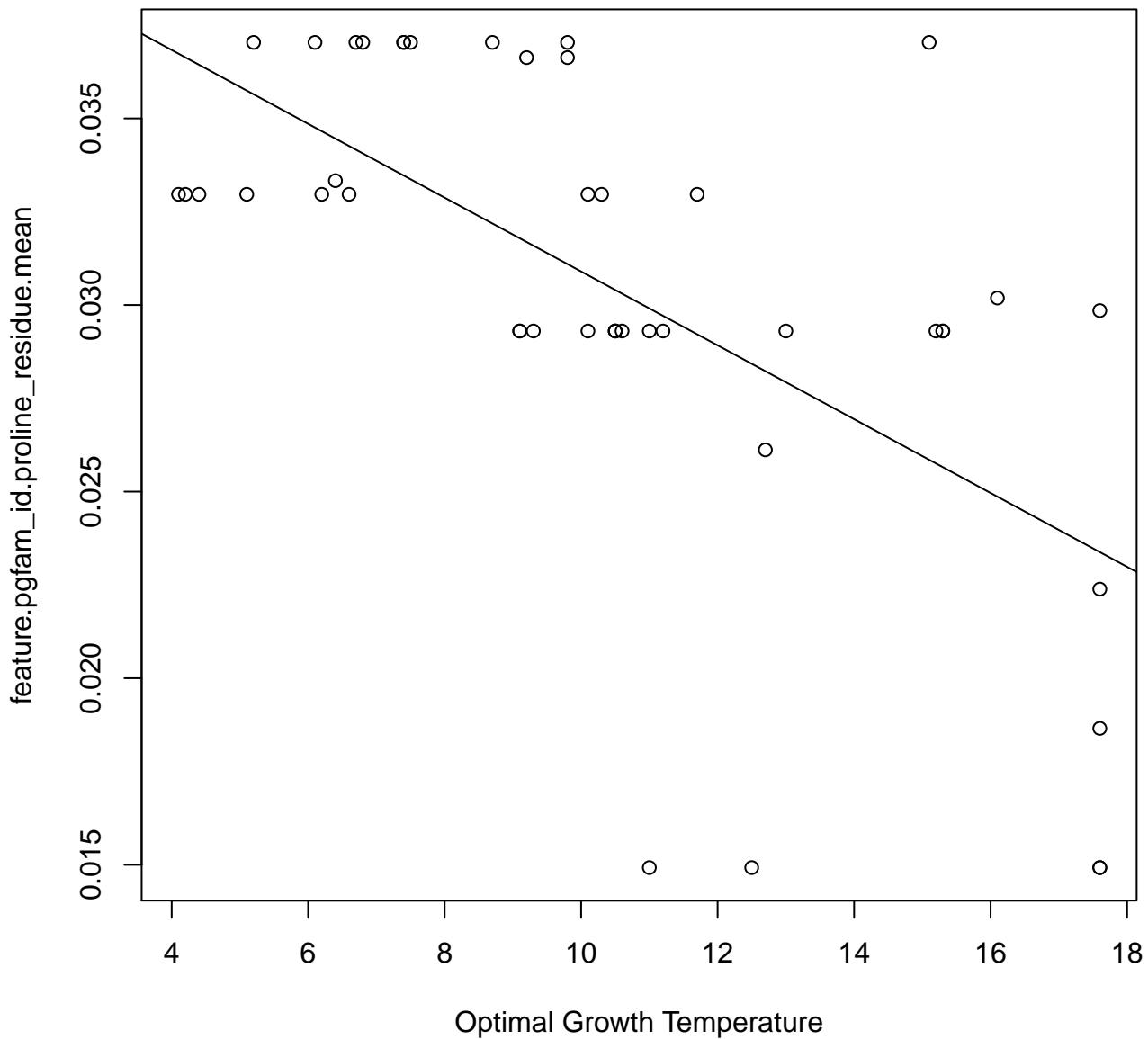
feature.pgfam_id.proline_residue.mean
PGF_00502502
Cold shock protein of CSP family => CspD (naming convention as in E.coli)



feature.pgfam_id.proline_residue.mean
PGF_00056897
Thymidylate synthase (EC 2.1.1.45)



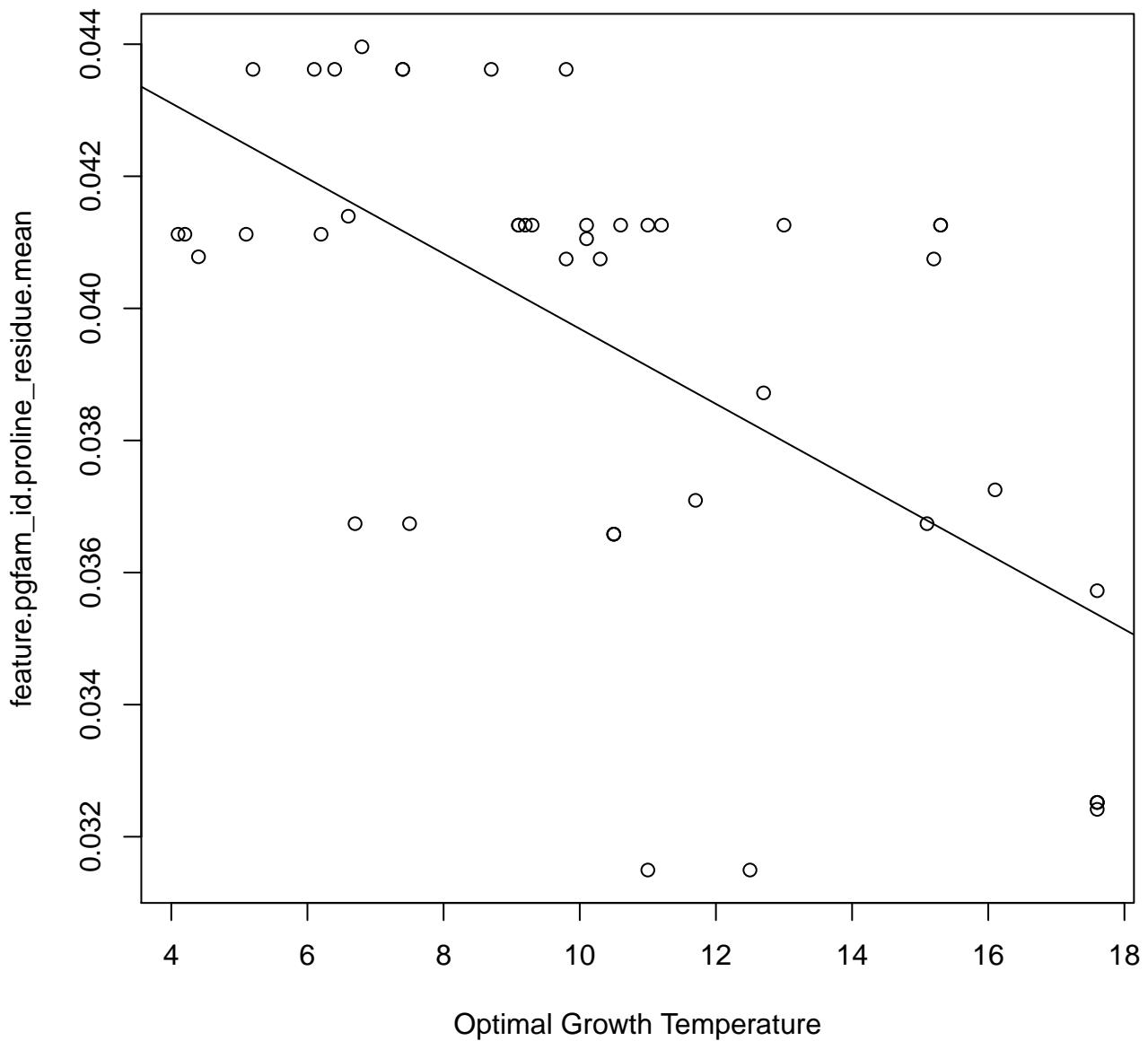
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PGF_09190895
Aminodeoxychorismate lyase (EC 4.1.3.38)



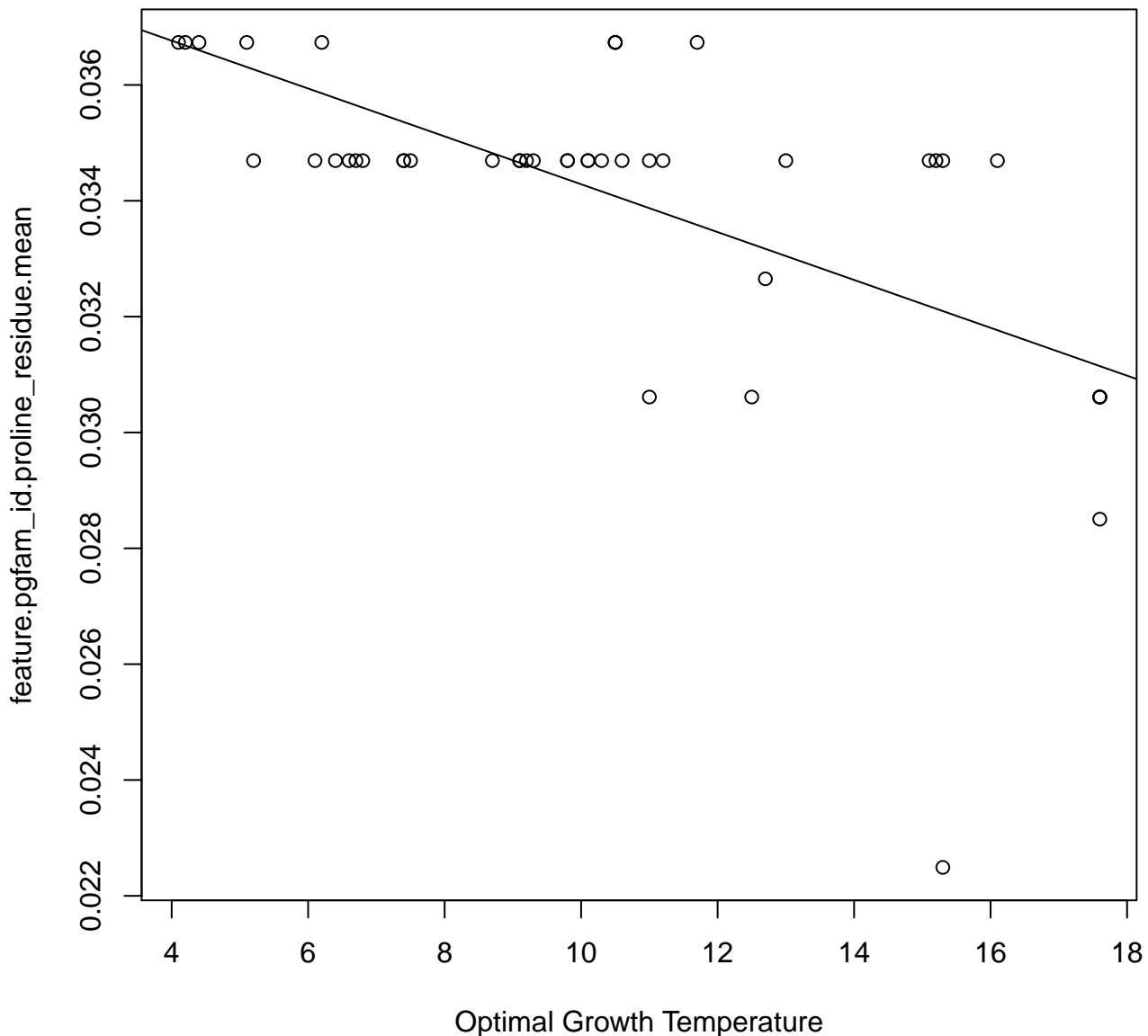
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PGF_10238627

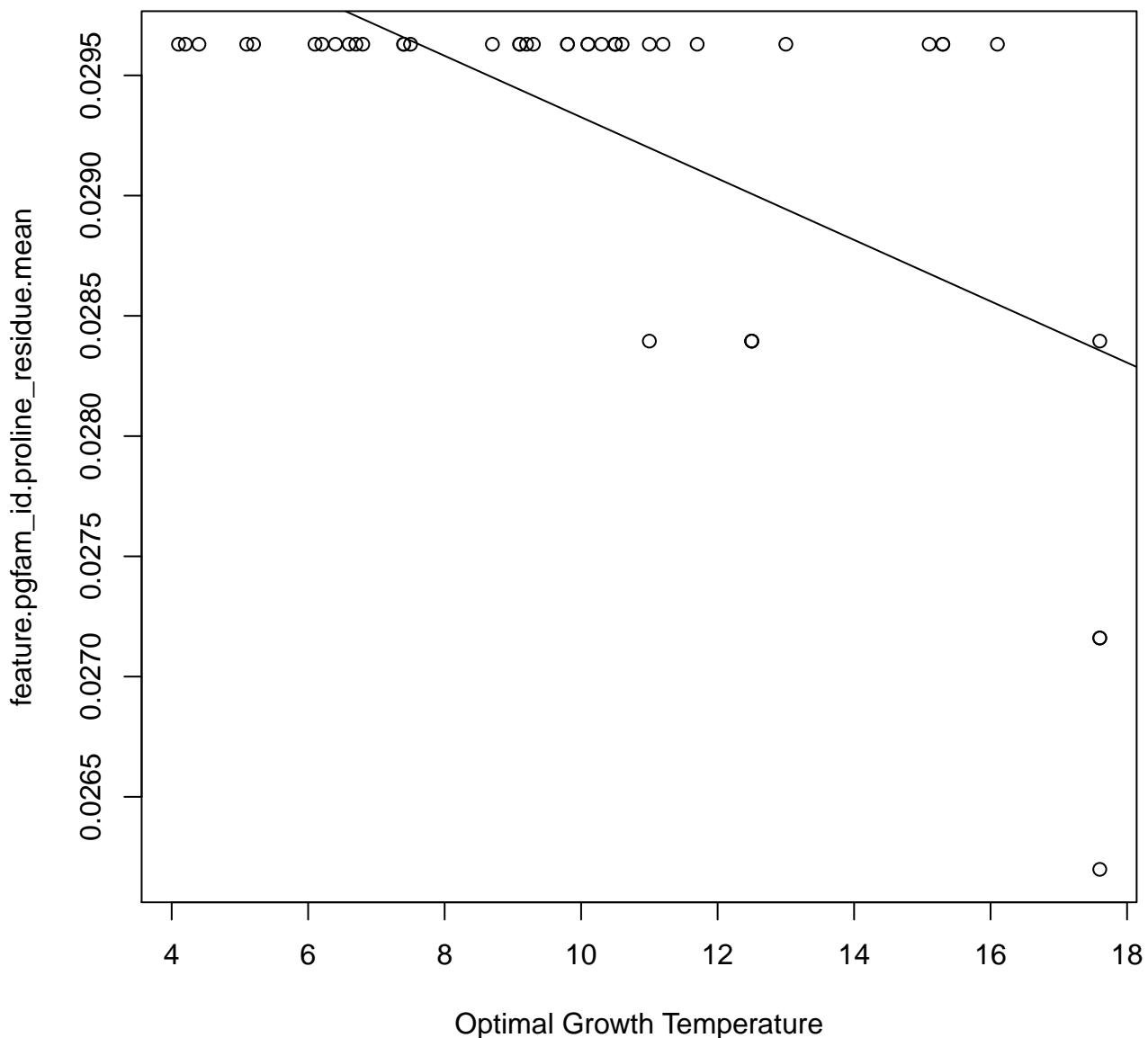
Chemotaxis regulator – transmits chemoreceptor signals to flagellar motor components CheY



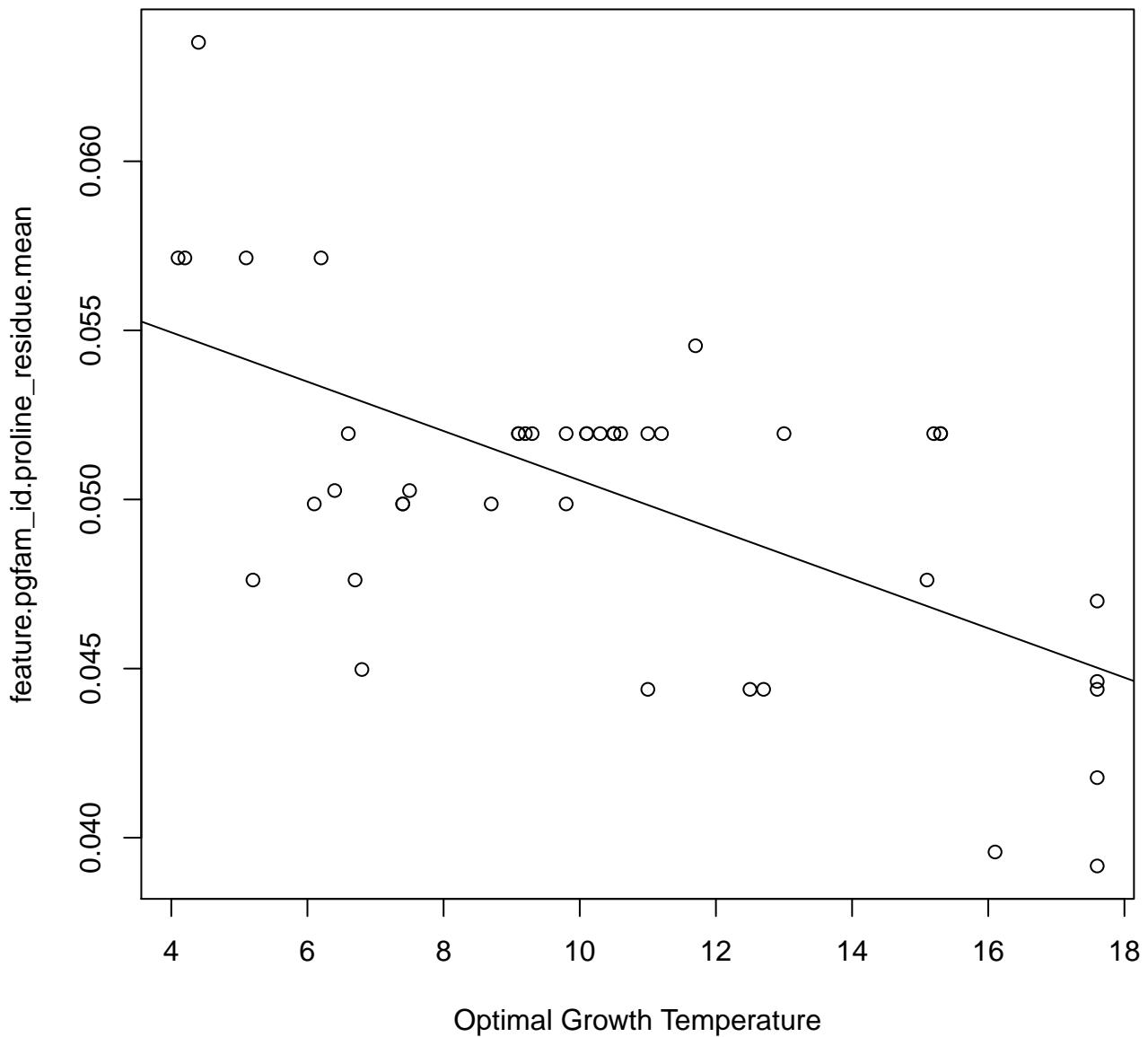
feature.pgfam_id.proline_residue.mean
PGF_10048015
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) / CBS domain



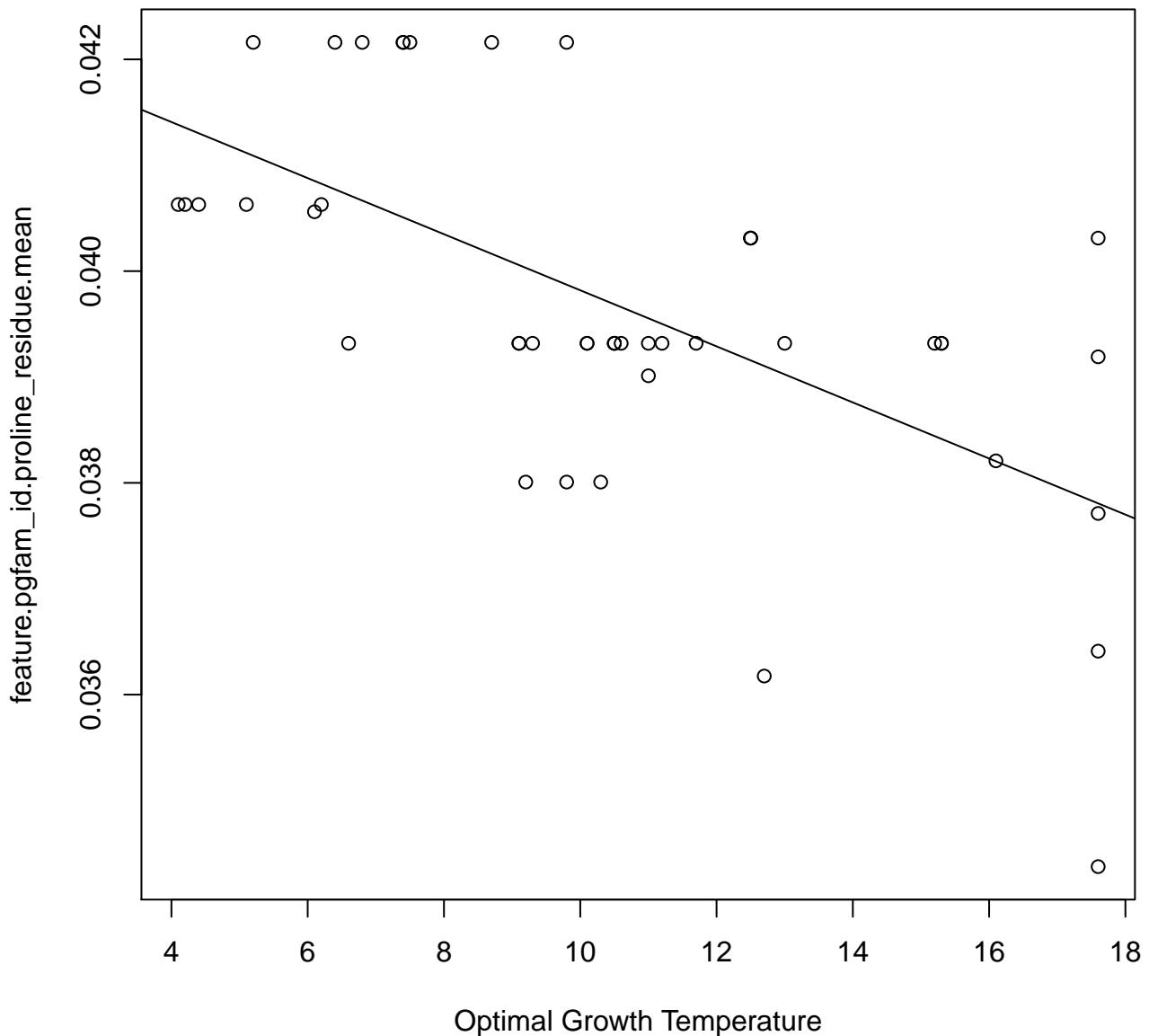
feature.pgfam_id.proline_residue.mean
PGF_00417760
Choline transporter BetT, short form



feature.pgfam_id.proline_residue.mean
PGF_09432500
Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake

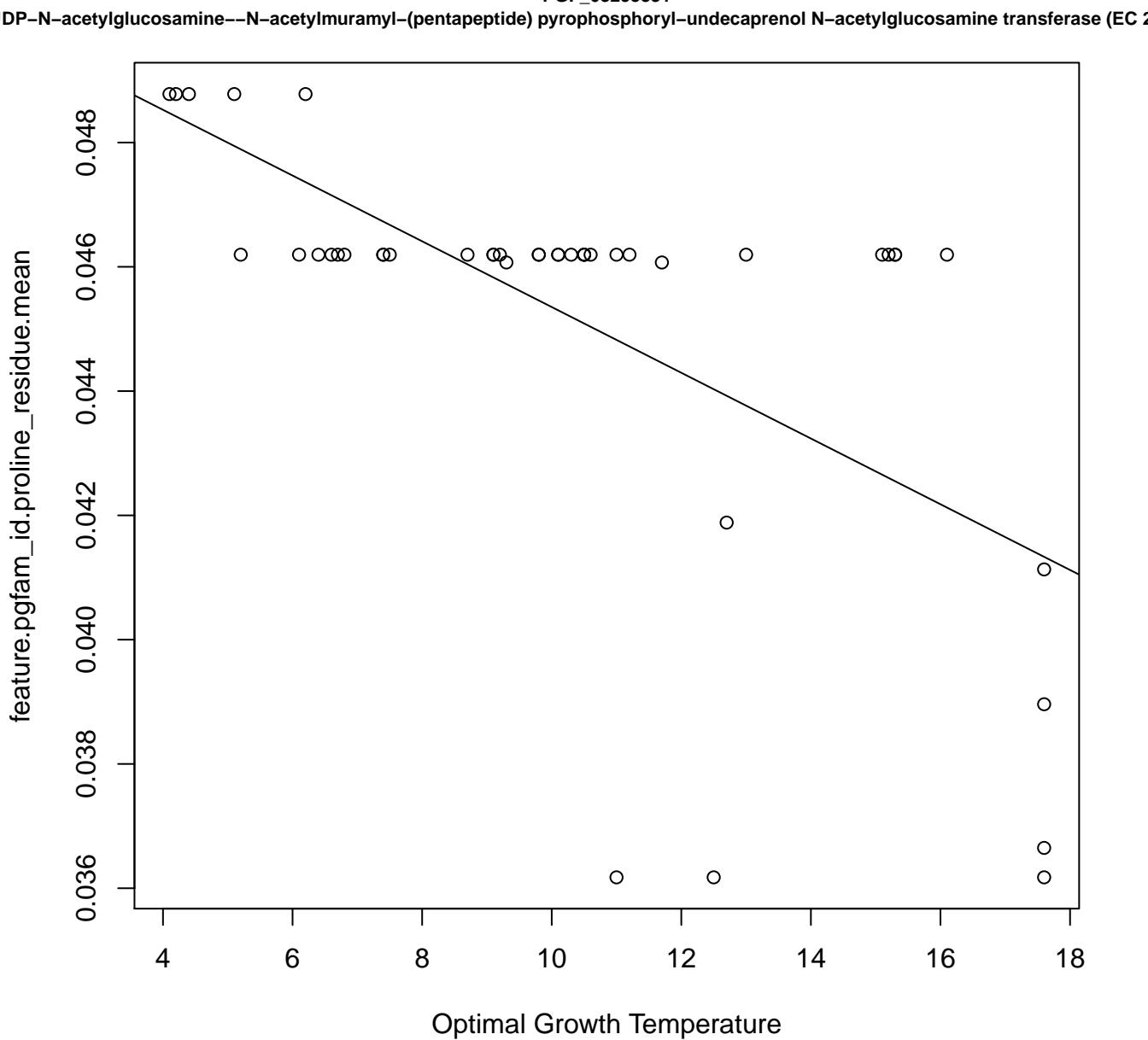


feature.pgfam_id.proline_residue.mean
PGF_06030909
Putative formate dehydrogenase oxidoreductase protein



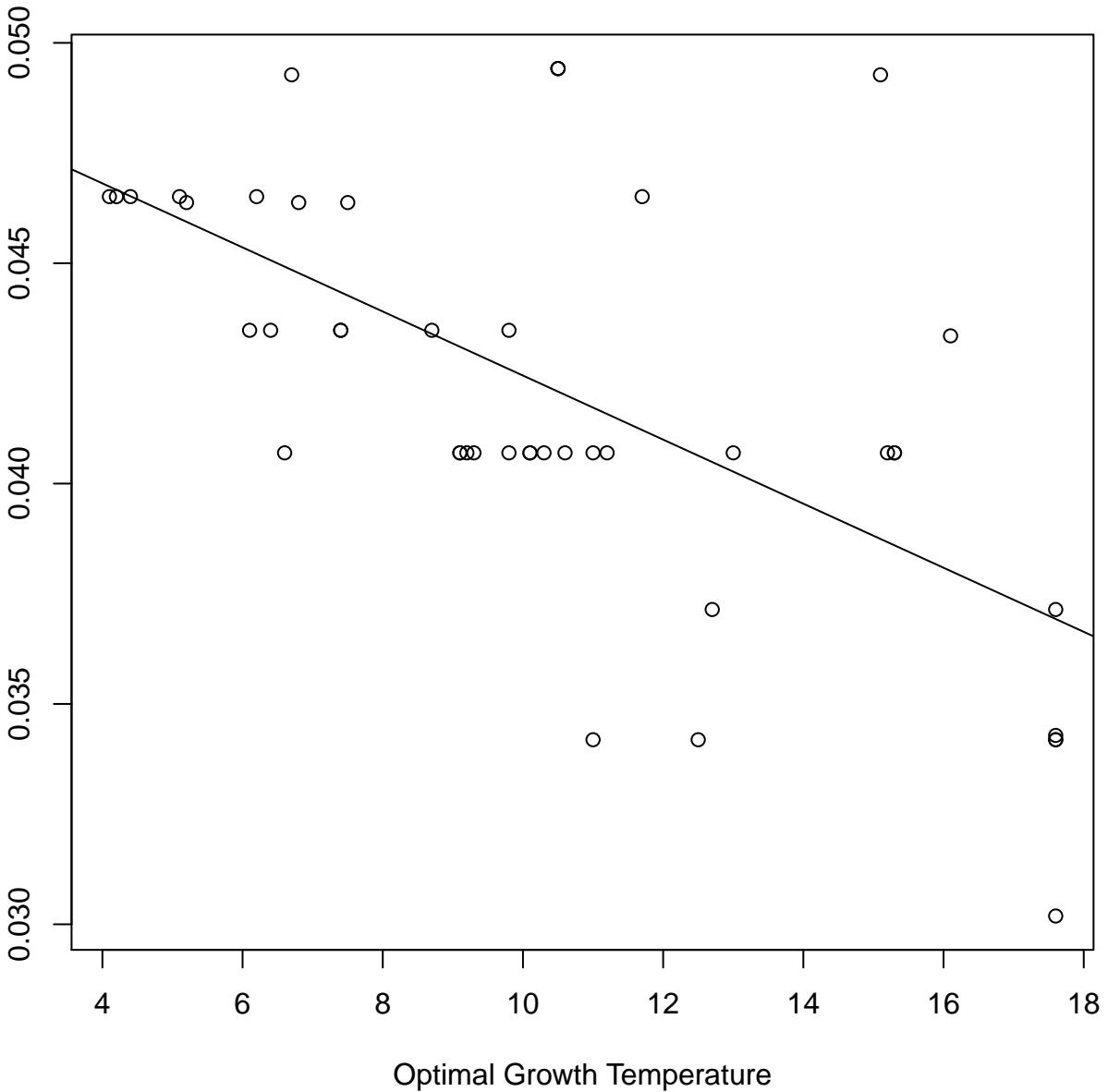
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PGF_03295331

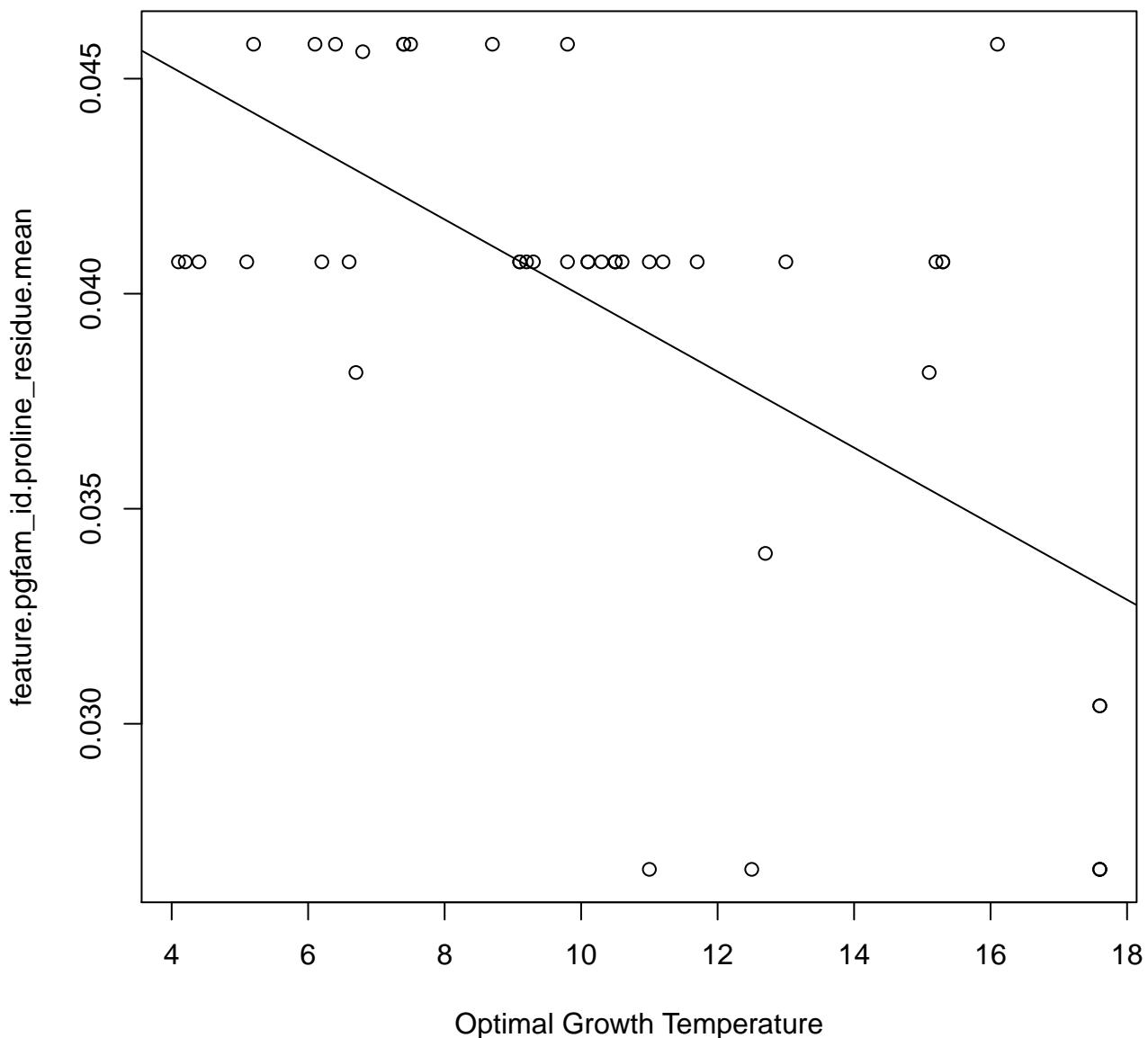


feature.pgfam_id.proline_residue.mean
PGF_07889681
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)

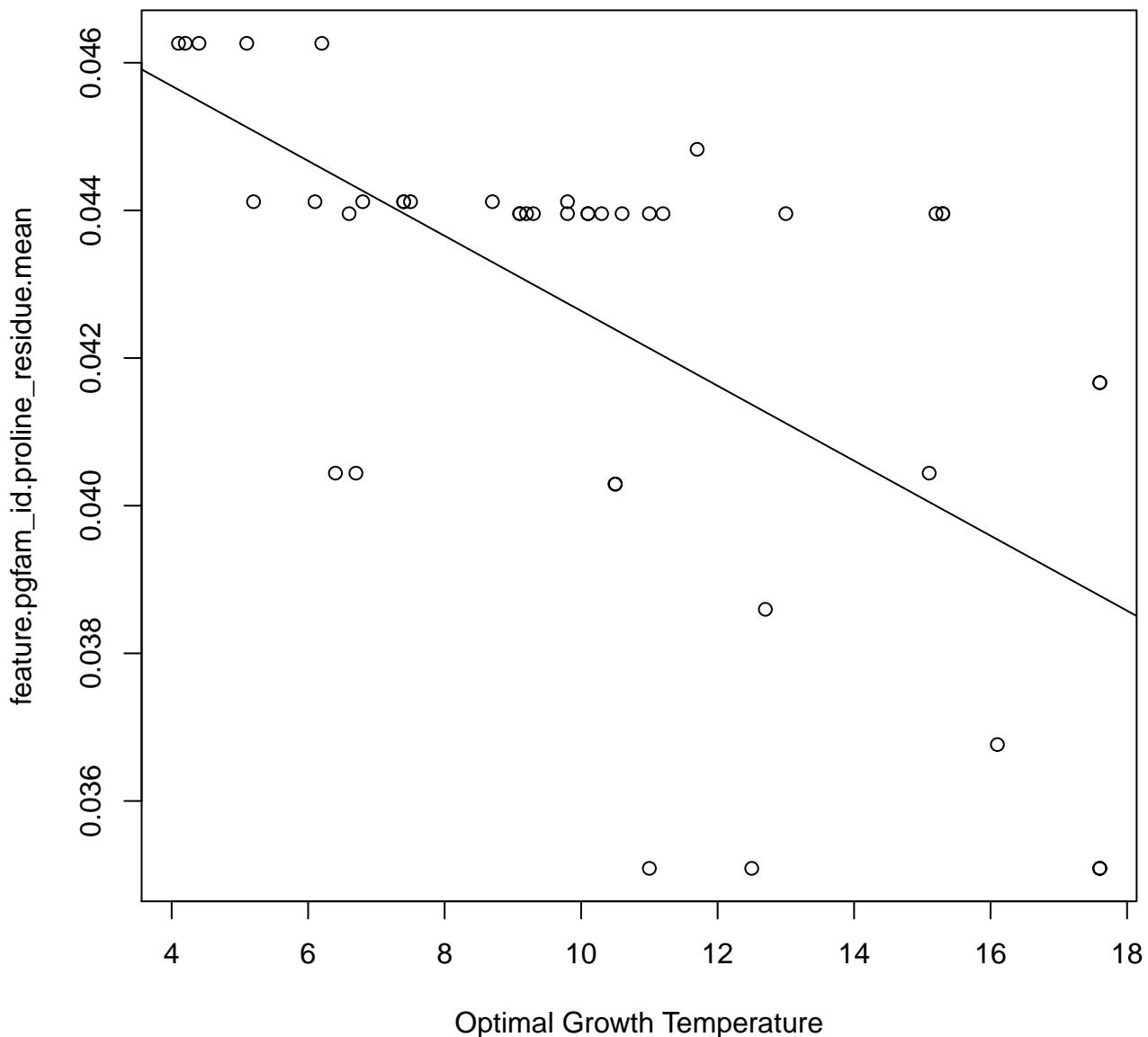
feature.pgfam_id.proline_residue.mean



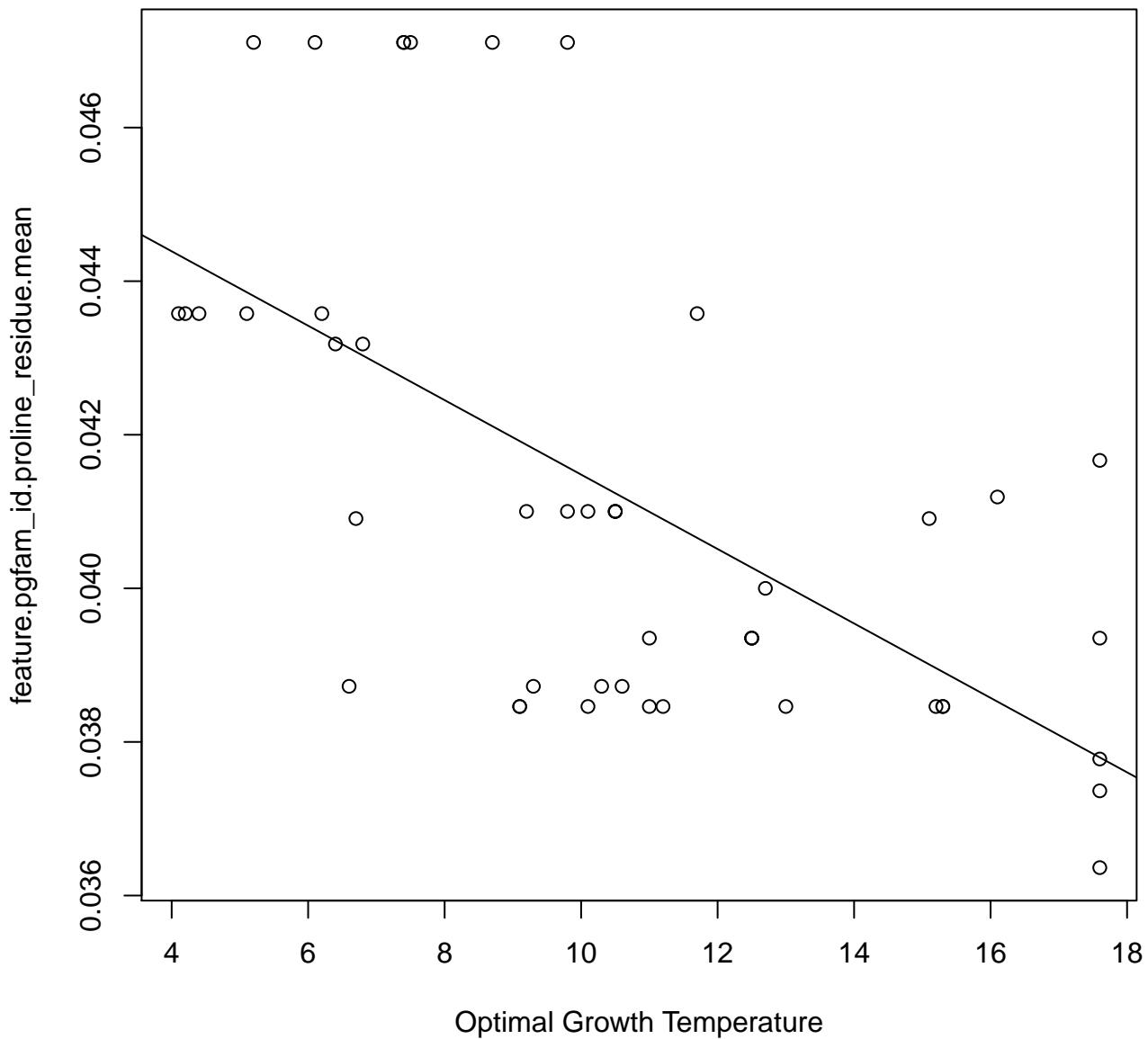
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PGF_01066545
Cell division coordinator CpoB



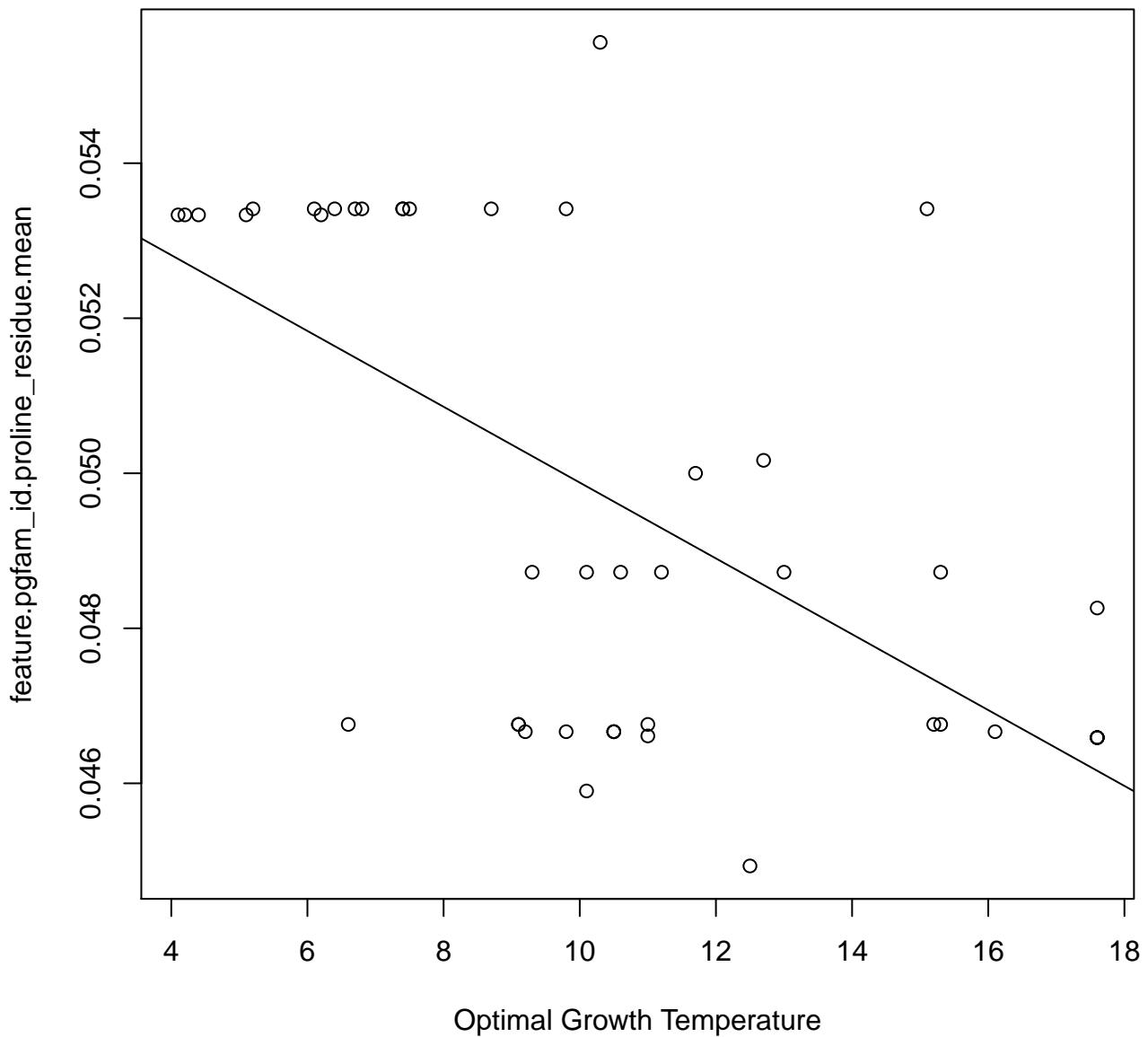
feature.pgfam_id.proline_residue.mean
PGF_07763915
Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)



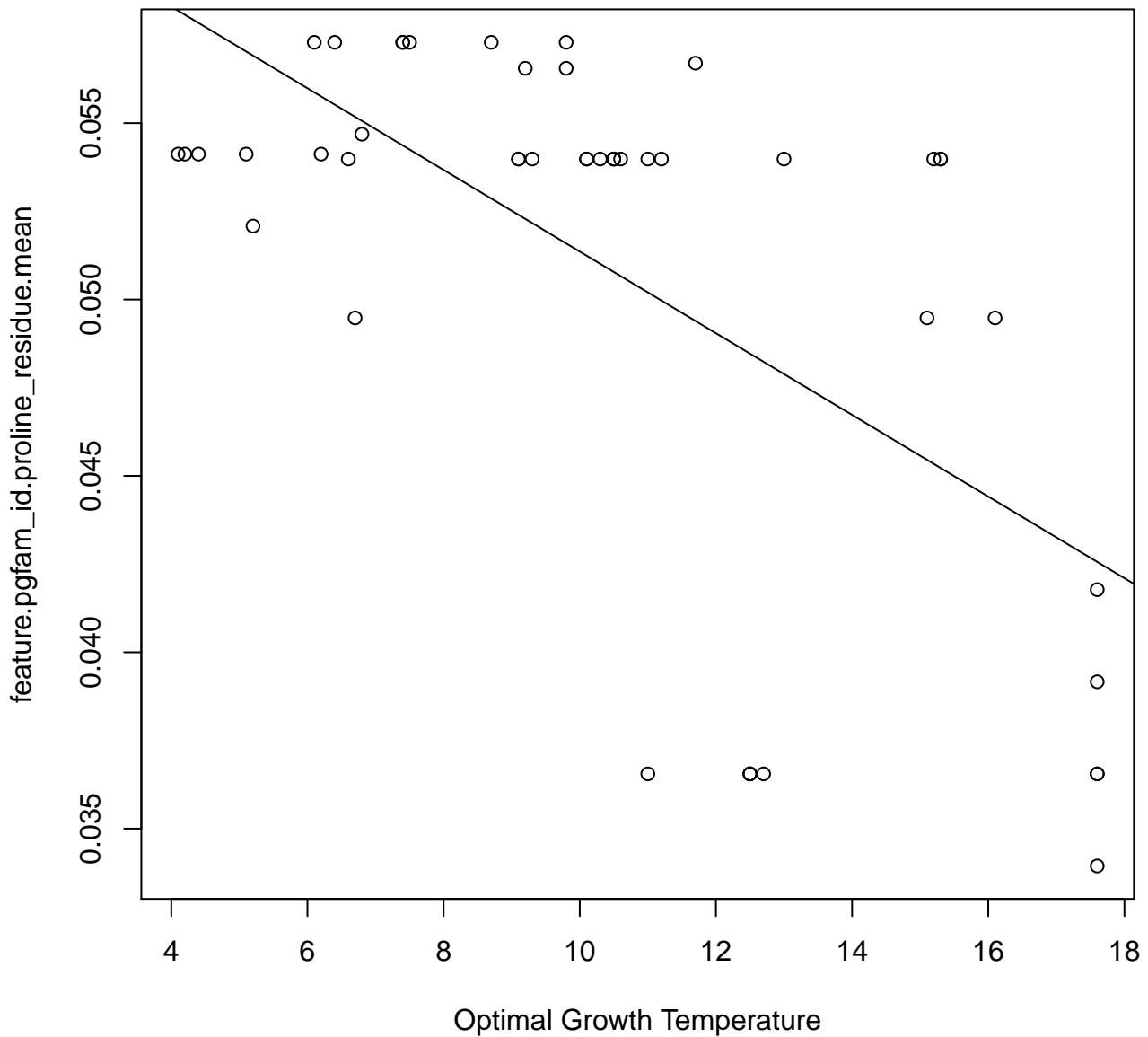
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PGF_00017737
ATP-dependent RNA helicase VF1437



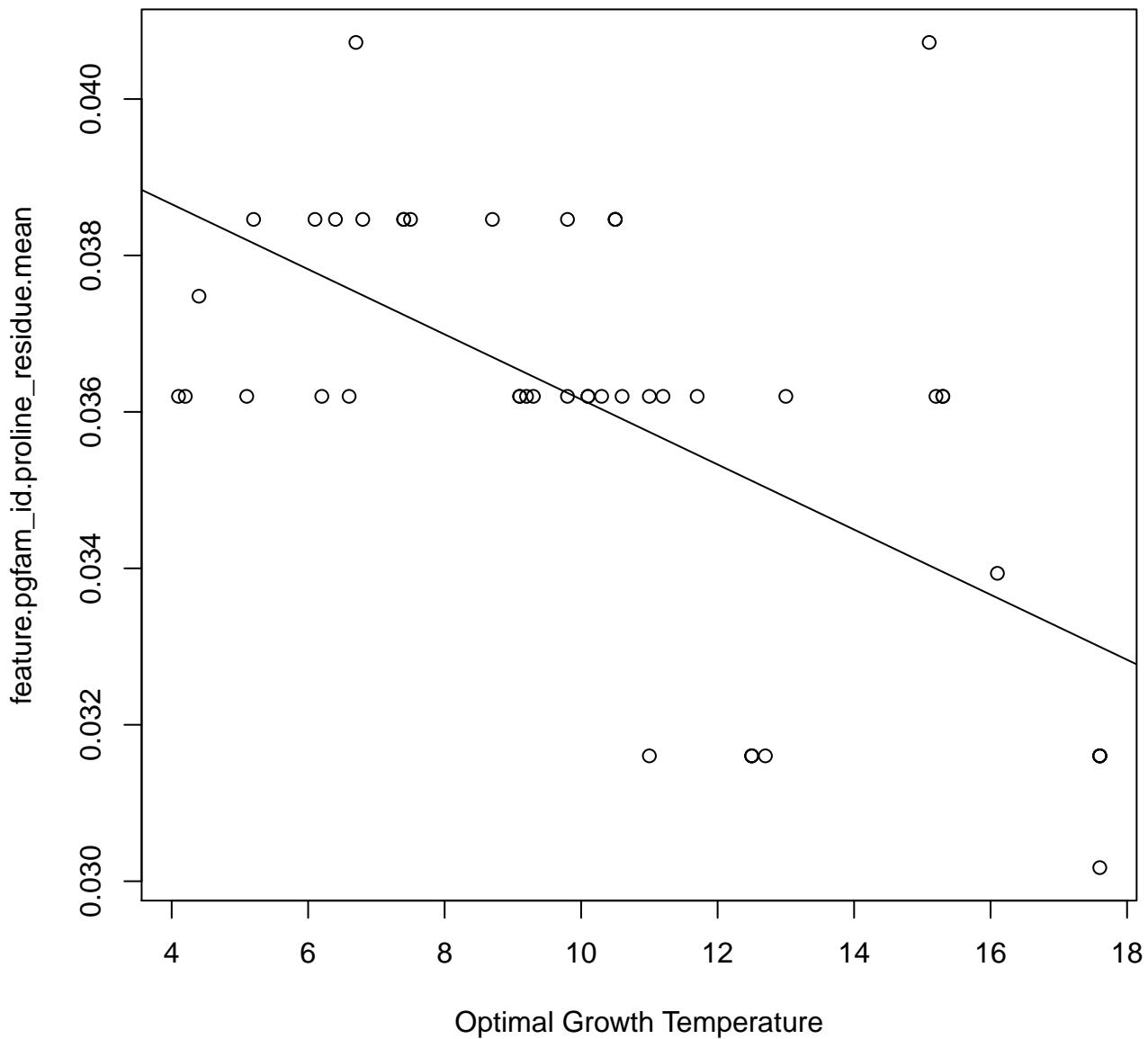
feature.pgfam_id.proline_residue.mean
PGF_05873936
Hydrogen peroxide-inducible genes activator => OxyR



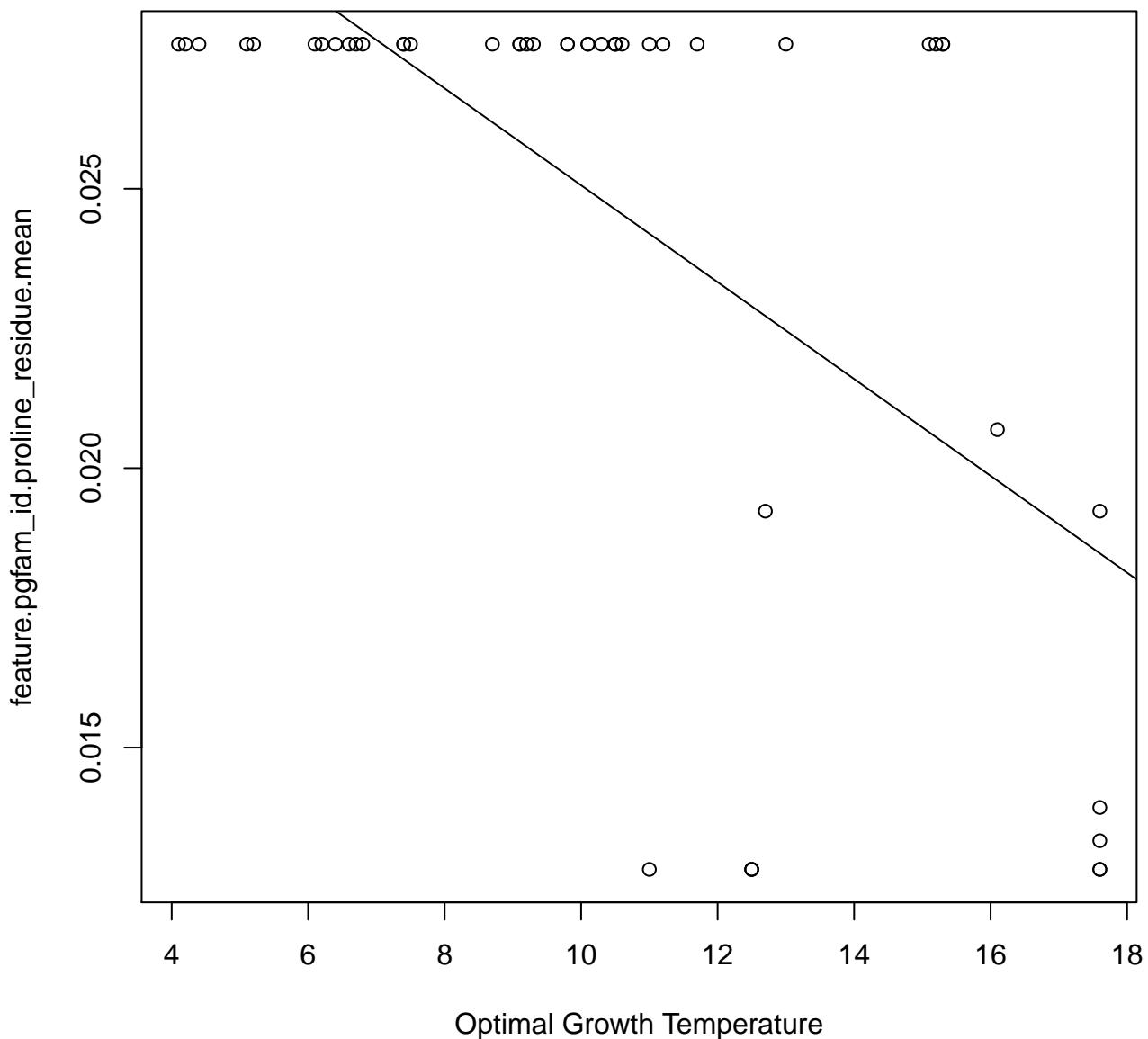
feature.pgfam_id.proline_residue.mean
PGF_00131429
LSU ribosomal protein L16p arginine hydroxylase



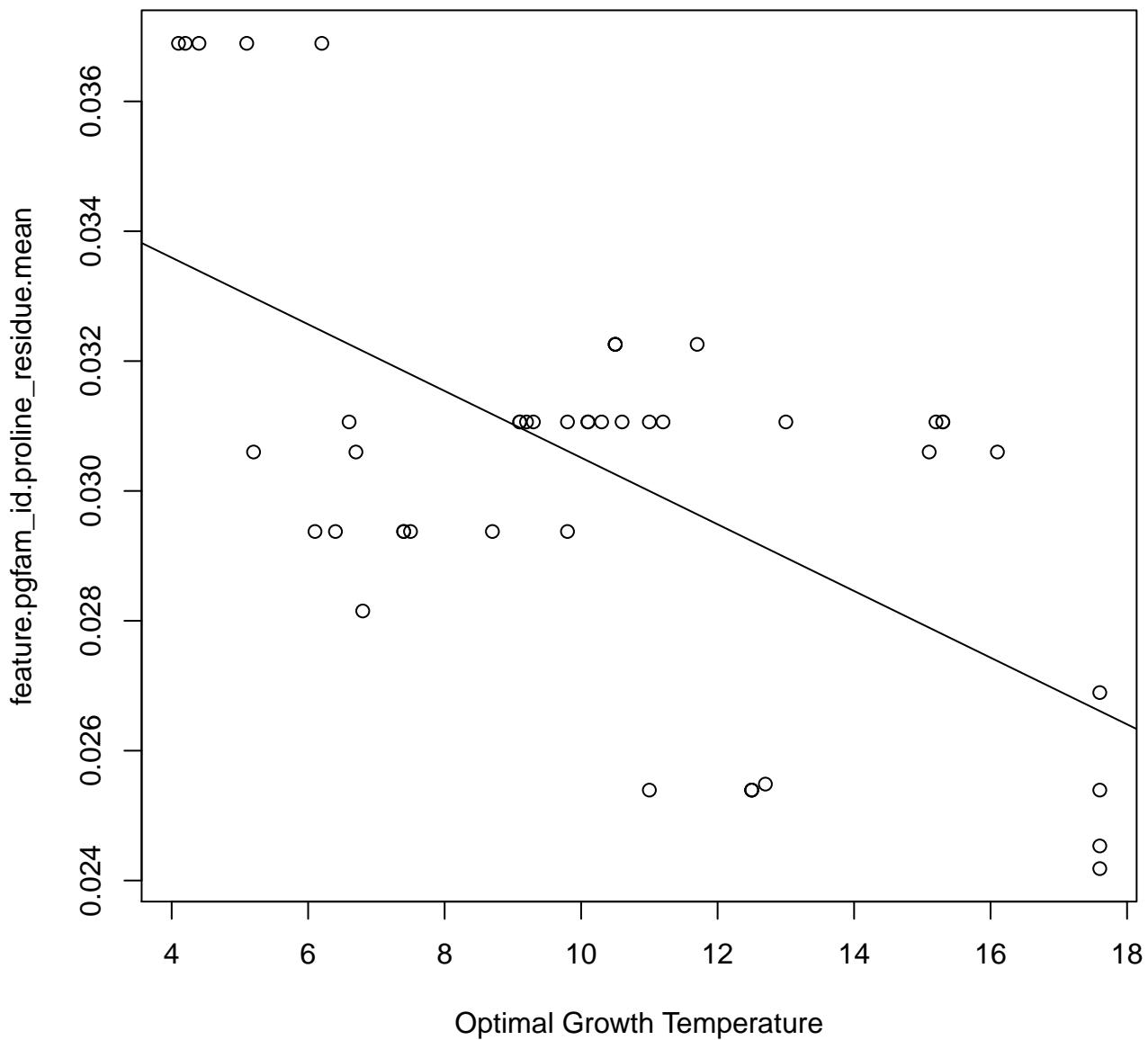
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PGF_00019038
ATP-dependent hsl protease ATP-binding subunit HslU



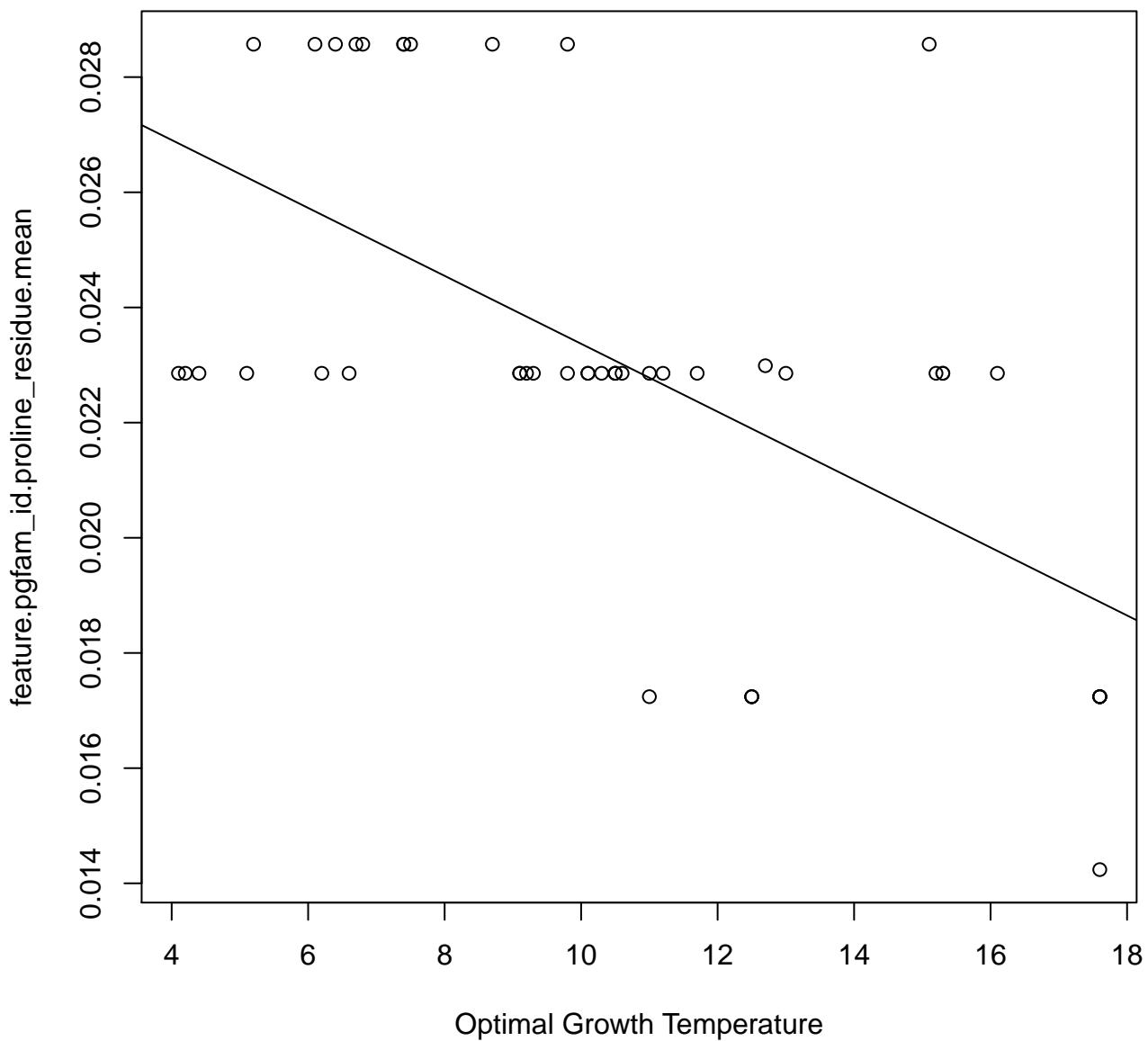
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PGF_03771580
hypothetical protein



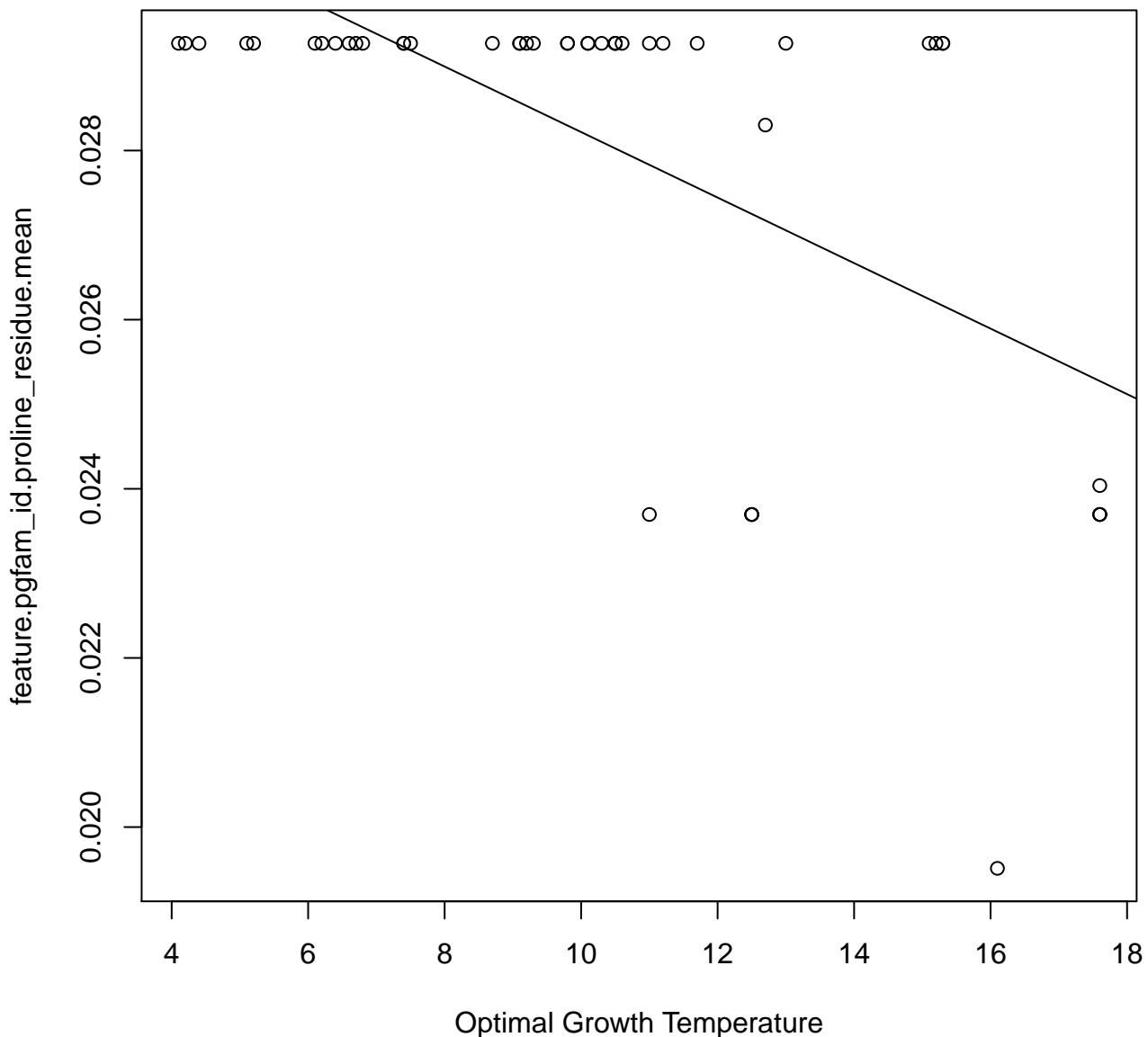
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PGF_00421477
DNA polymerase II (EC 2.7.7.7)



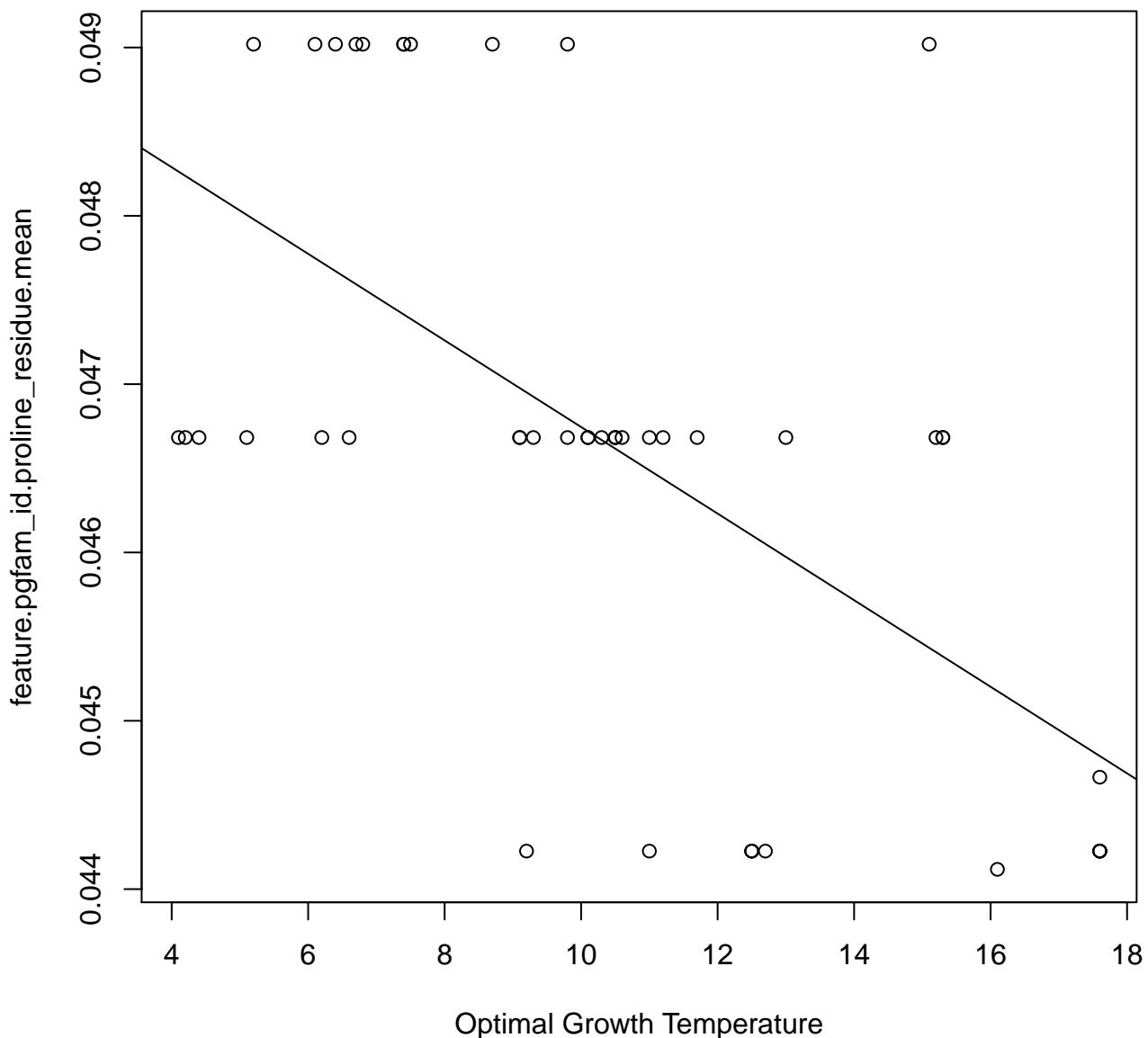
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PGF_00071382
Flavodoxin 1



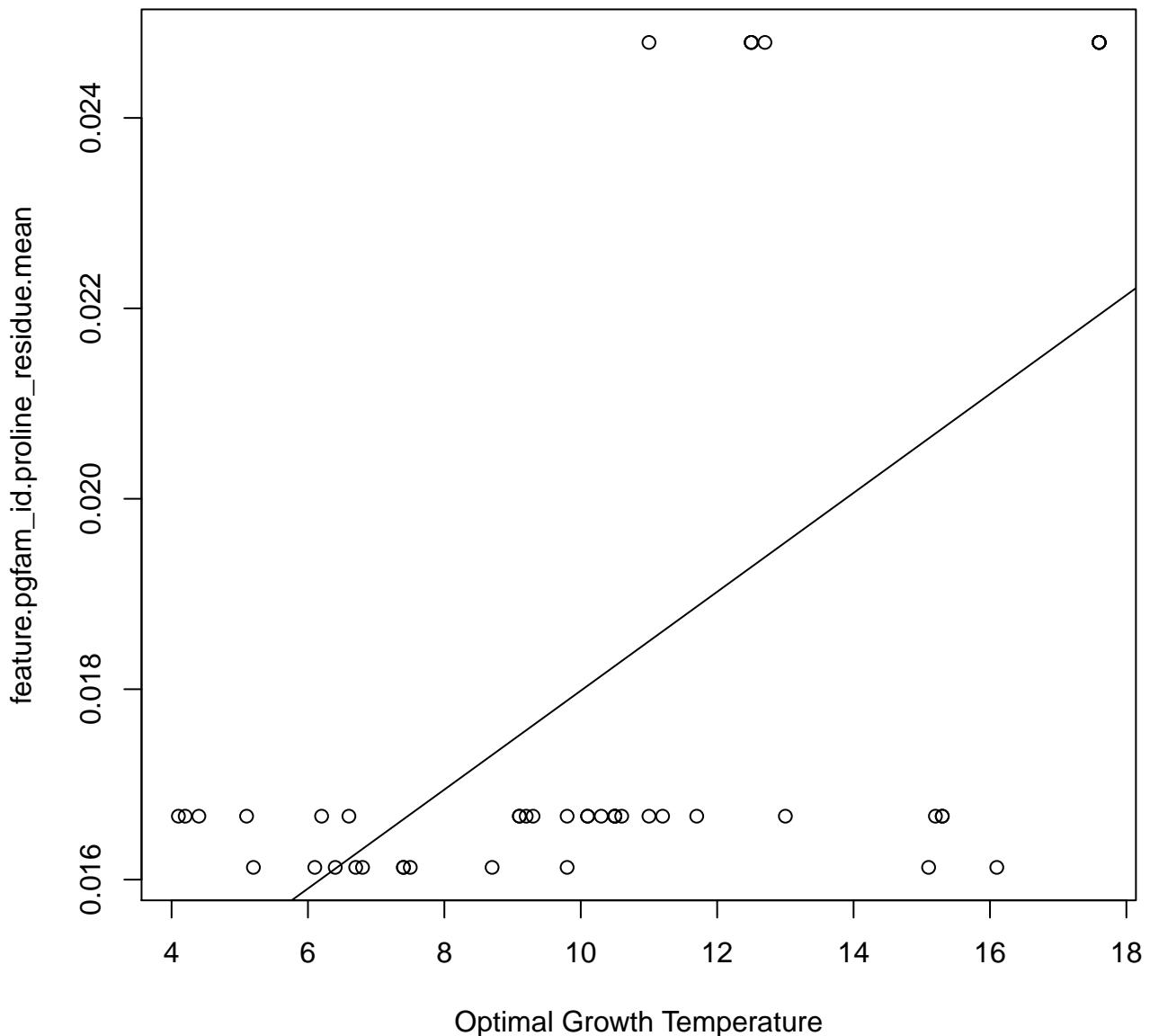
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PGF_00053408
Sodium-type flagellar protein MotX



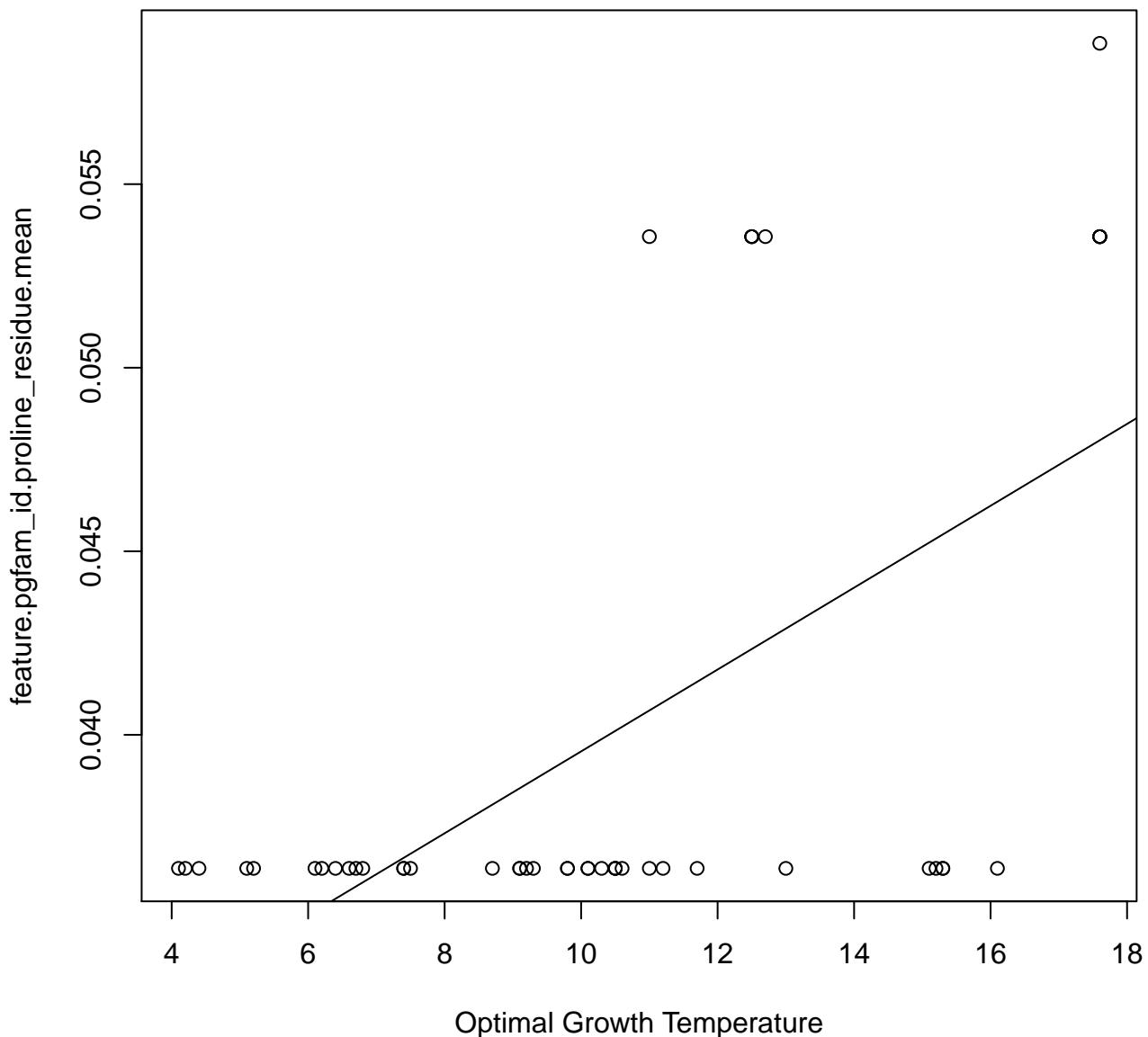
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PGF_00025190
Na(+)–translocating NADH–quinone reductase subunit F (EC 1.6.5.8)



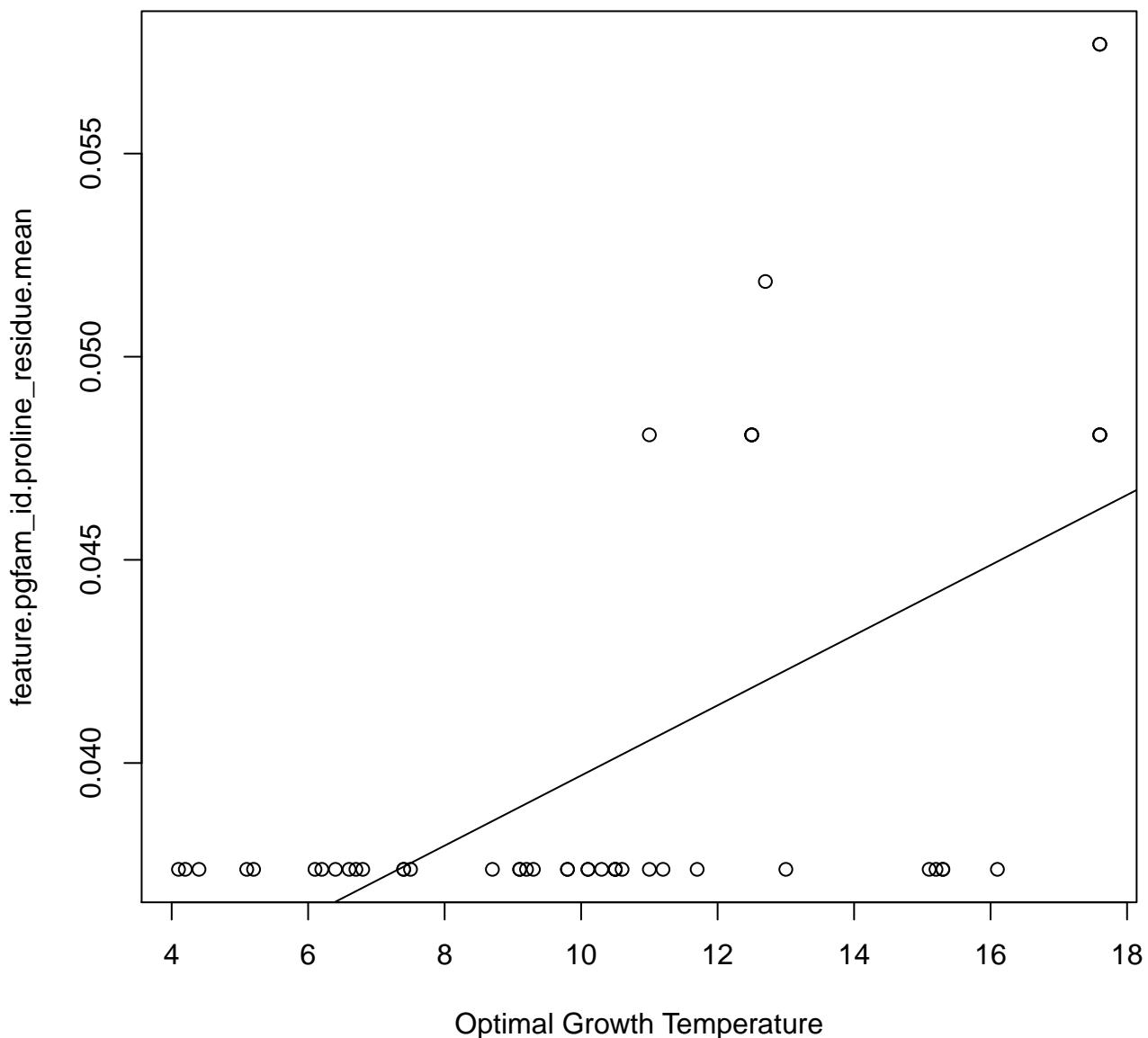
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PGF_00425763
FIG002082: Protein SirB2



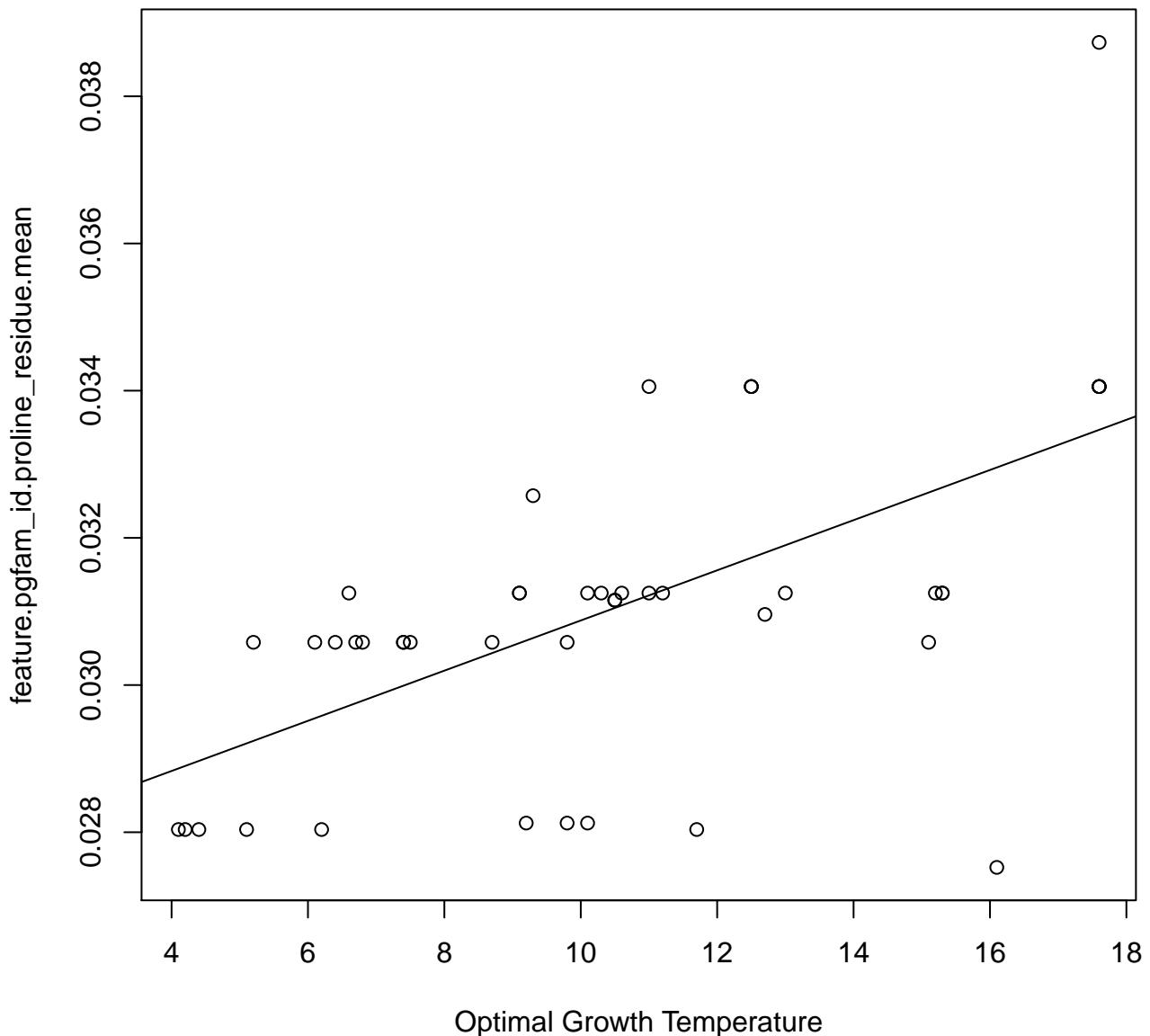
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PGF_00413232
tRNA 2-thiouridine synthesis protein TusE



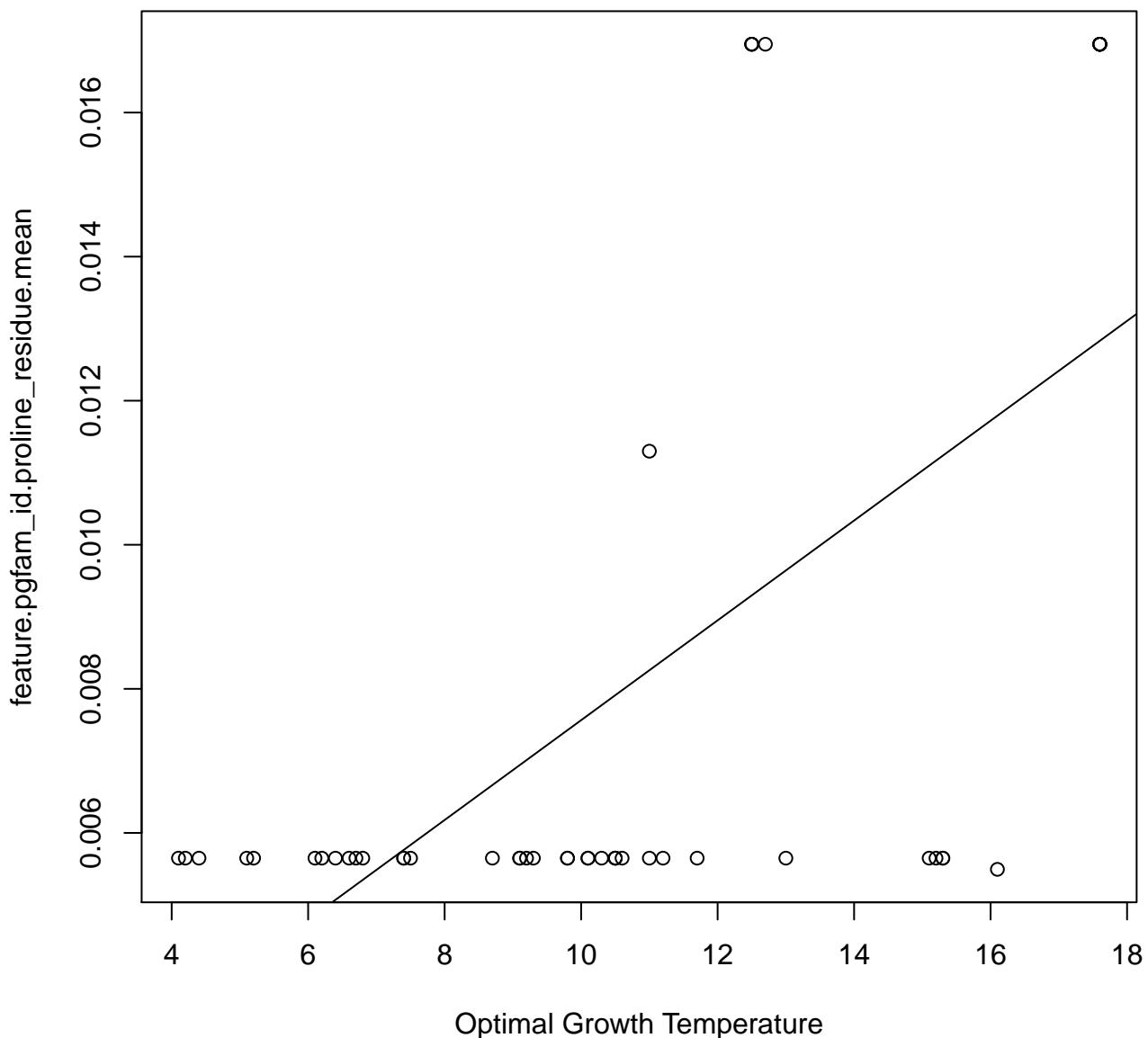
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PGF_00649271
Cell division protein BolA



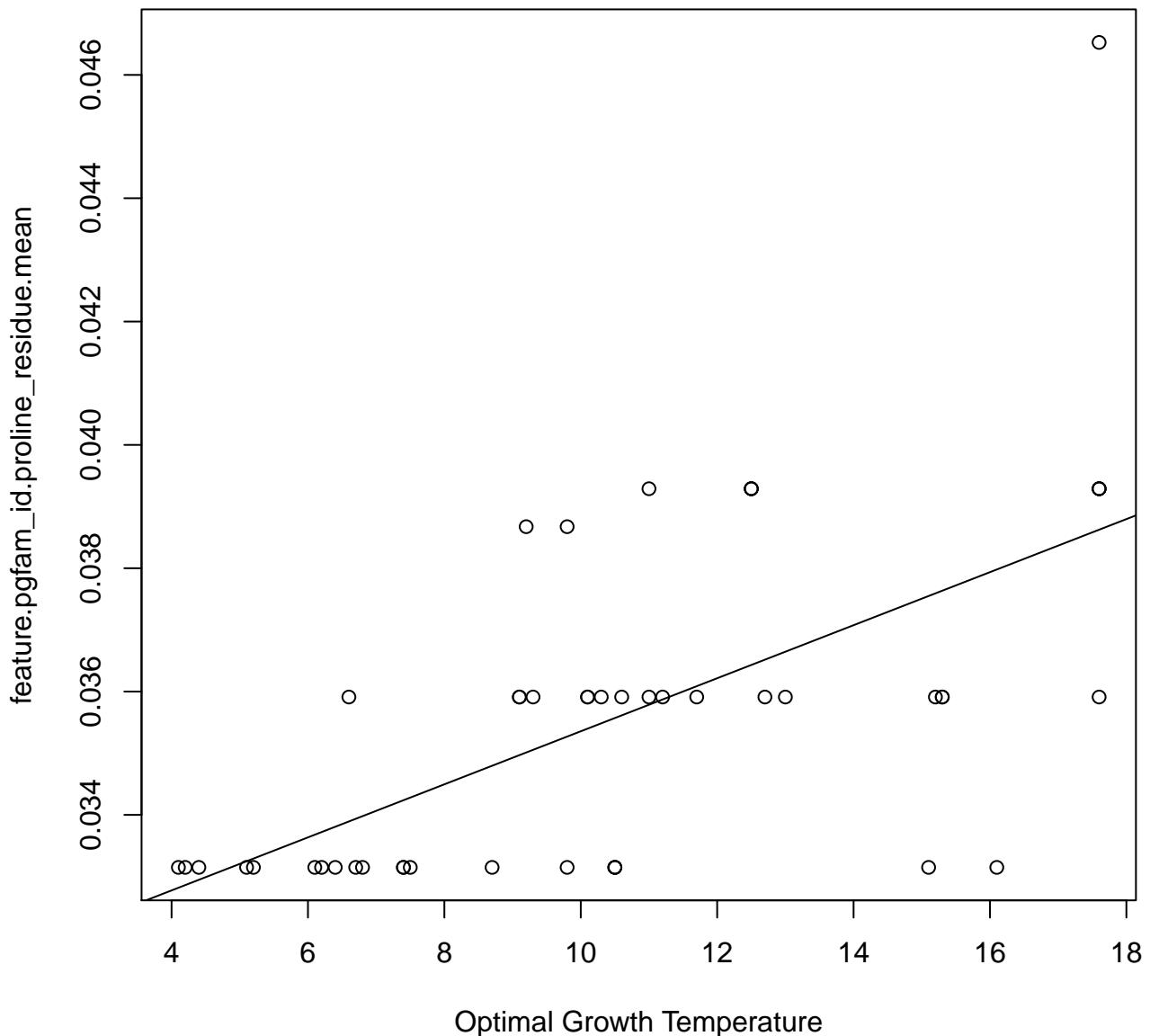
feature.pgfam_id.proline_residue.mean
PGF_03815442
Cytochrome c oxidase (cbb3-type) subunit CcoP (EC 1.9.3.1)



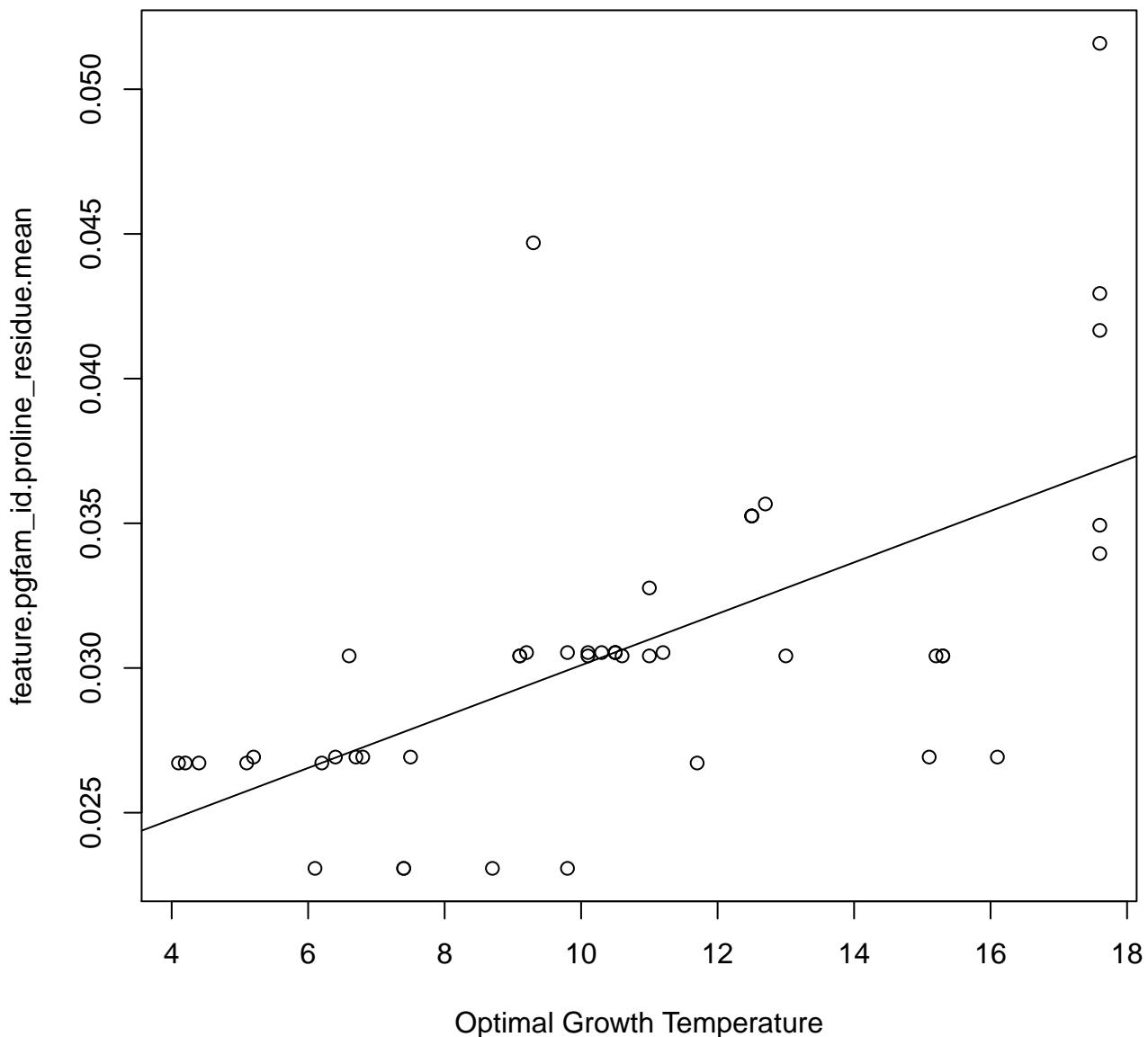
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PGF_00067192
YaeQ protein



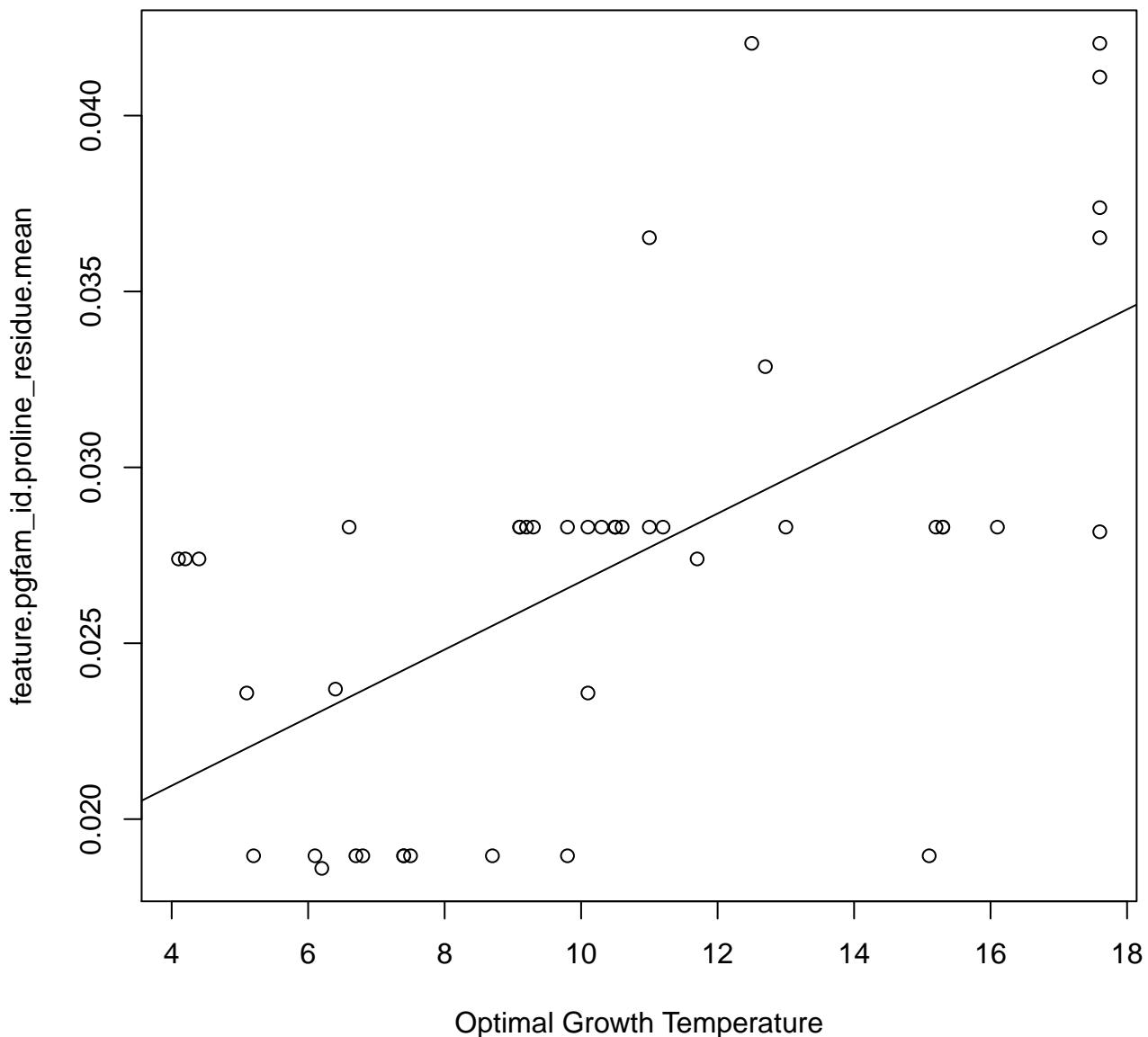
feature.pgfam_id.proline_residue.mean
PGF_00053770
Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)



feature.pgfam_id.proline_residue.mean
PGF_00034157
Phytanoyl-CoA dioxygenase



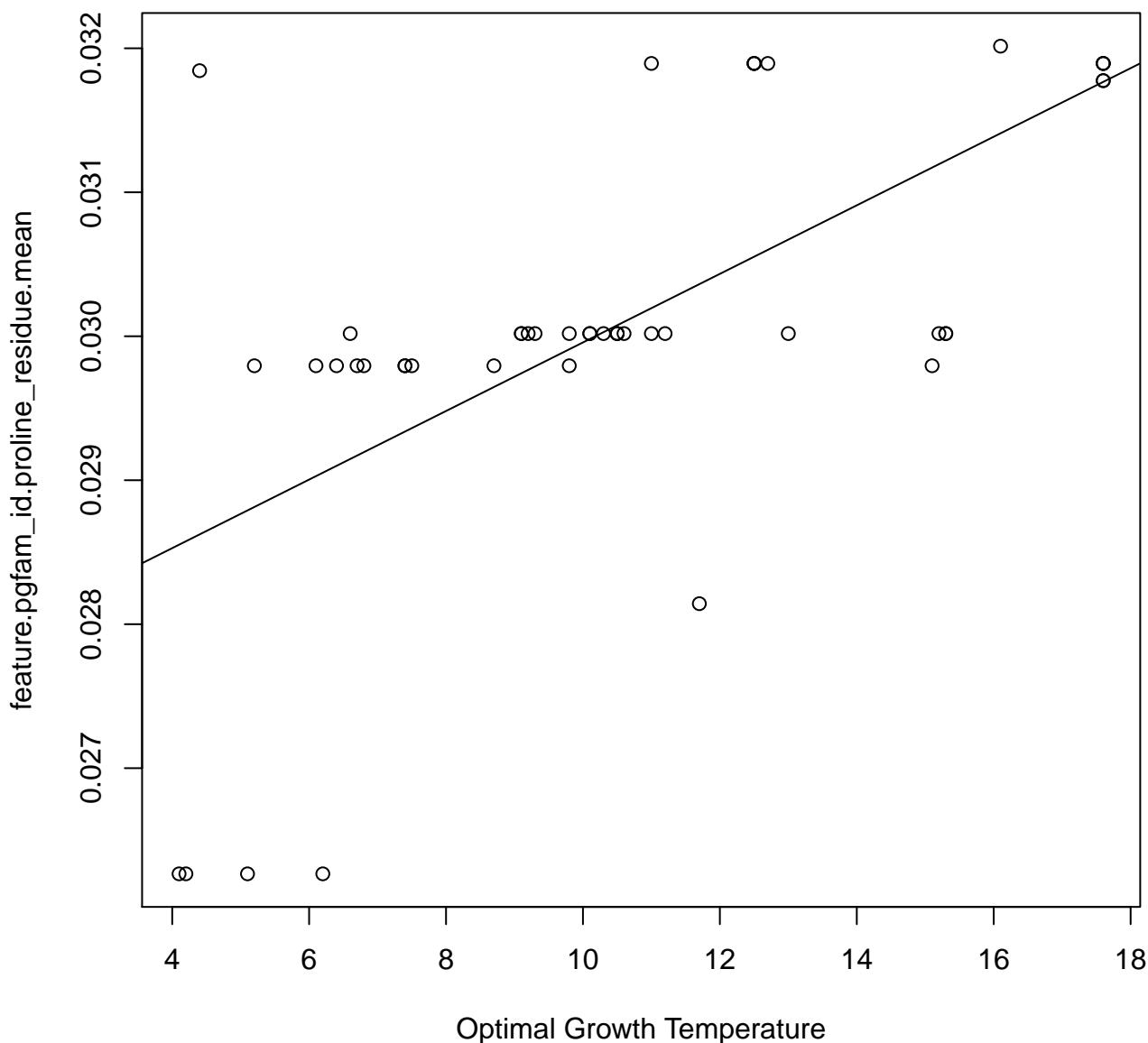
feature.pgfam_id.proline_residue.mean
PGF_07808527
ADP-ribose pyrophosphatase (EC 3.6.1.13)



feature.pgfam_id.proline_residue.mean

PGF_00013509

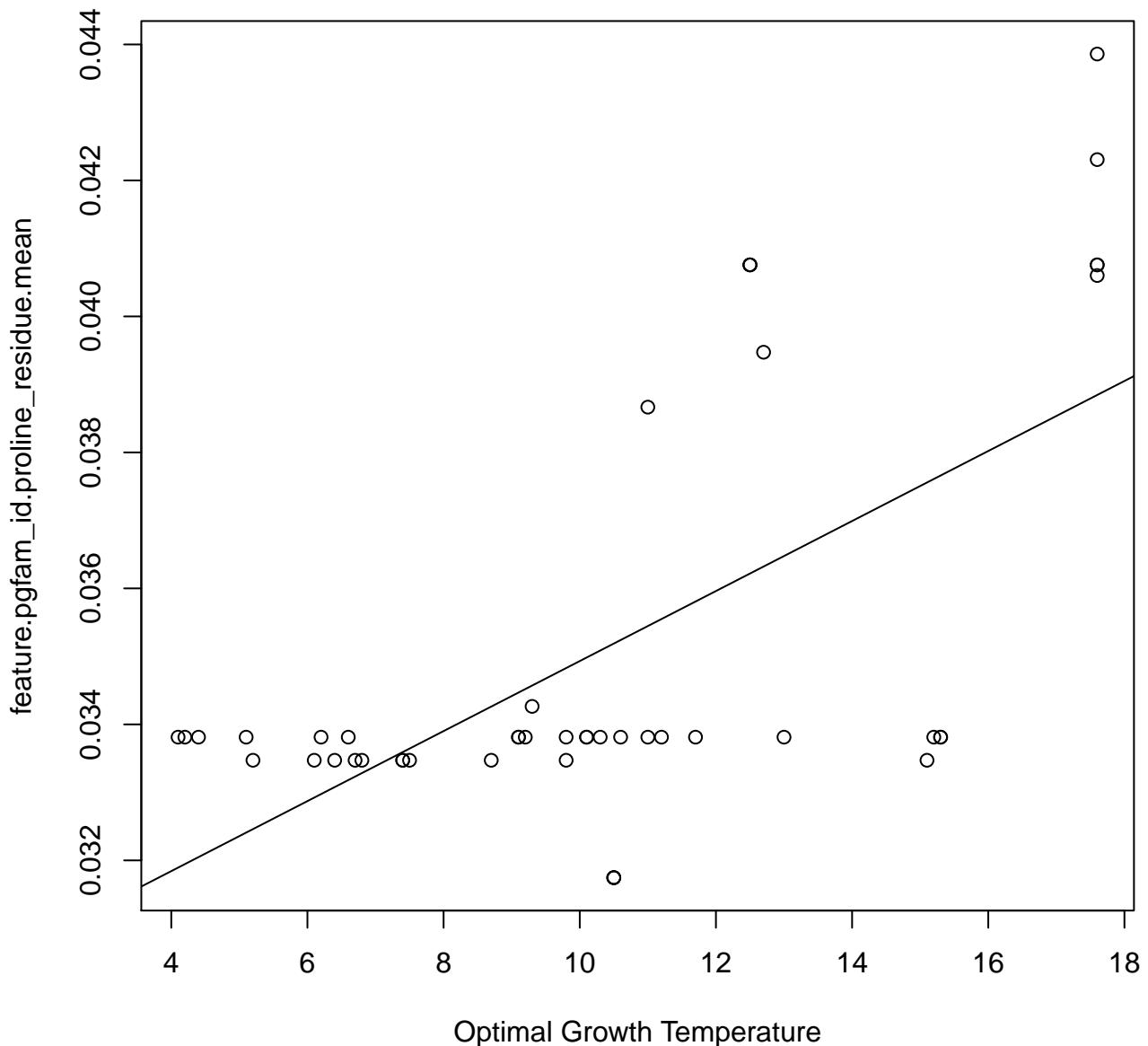
IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)



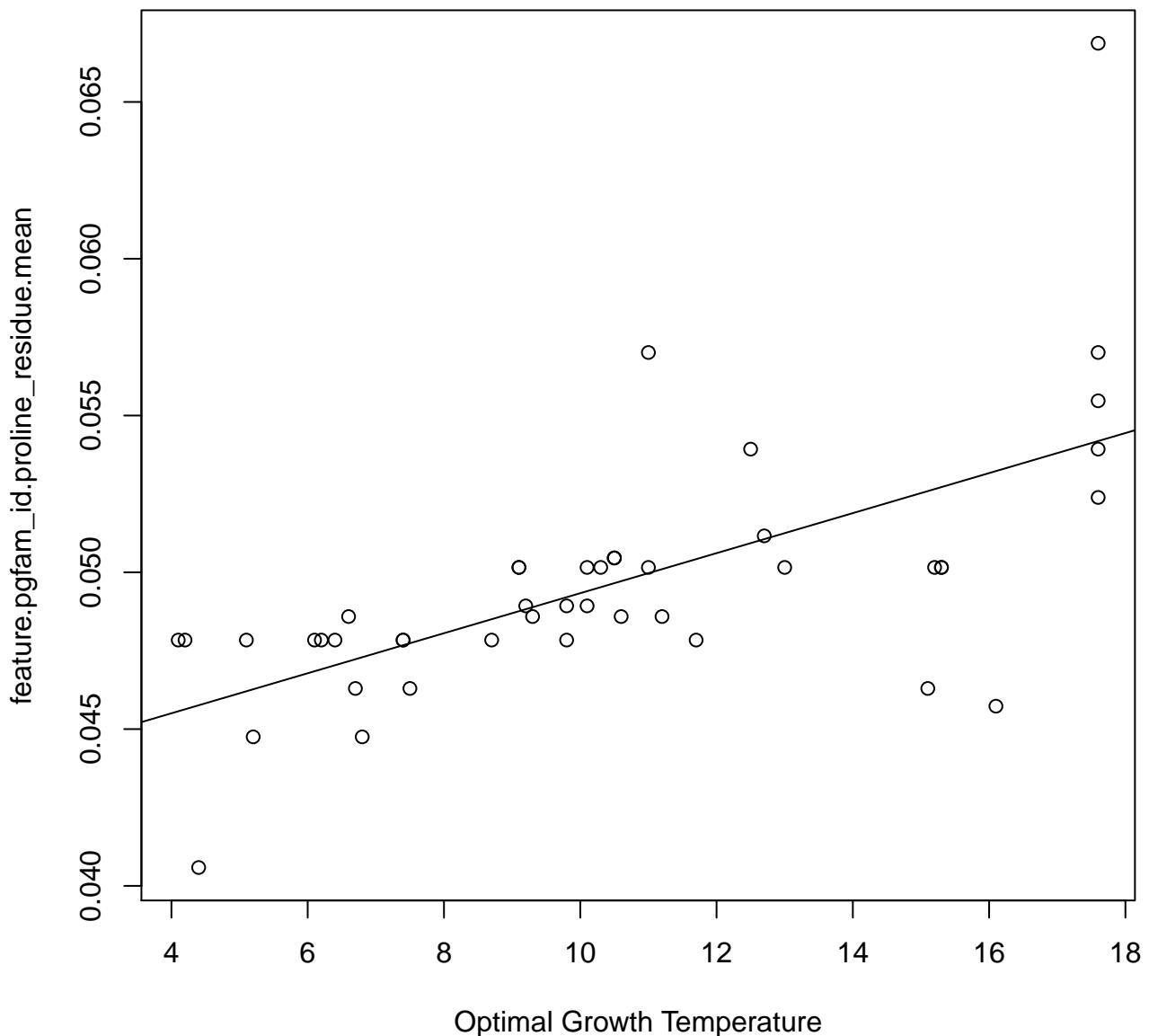
feature.pgfam_id.proline_residue.mean

PGF_06943909

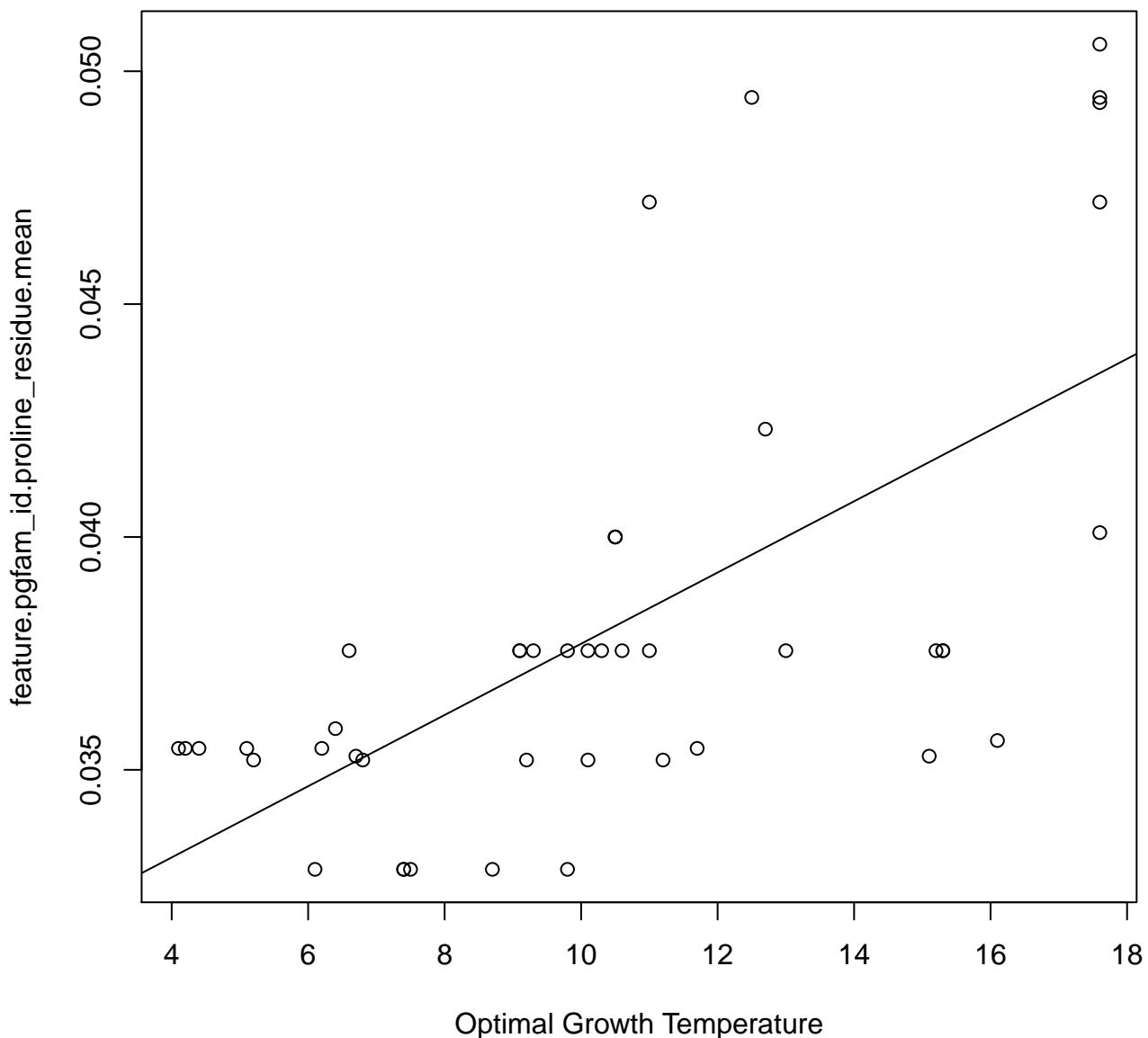
Cytochrome b



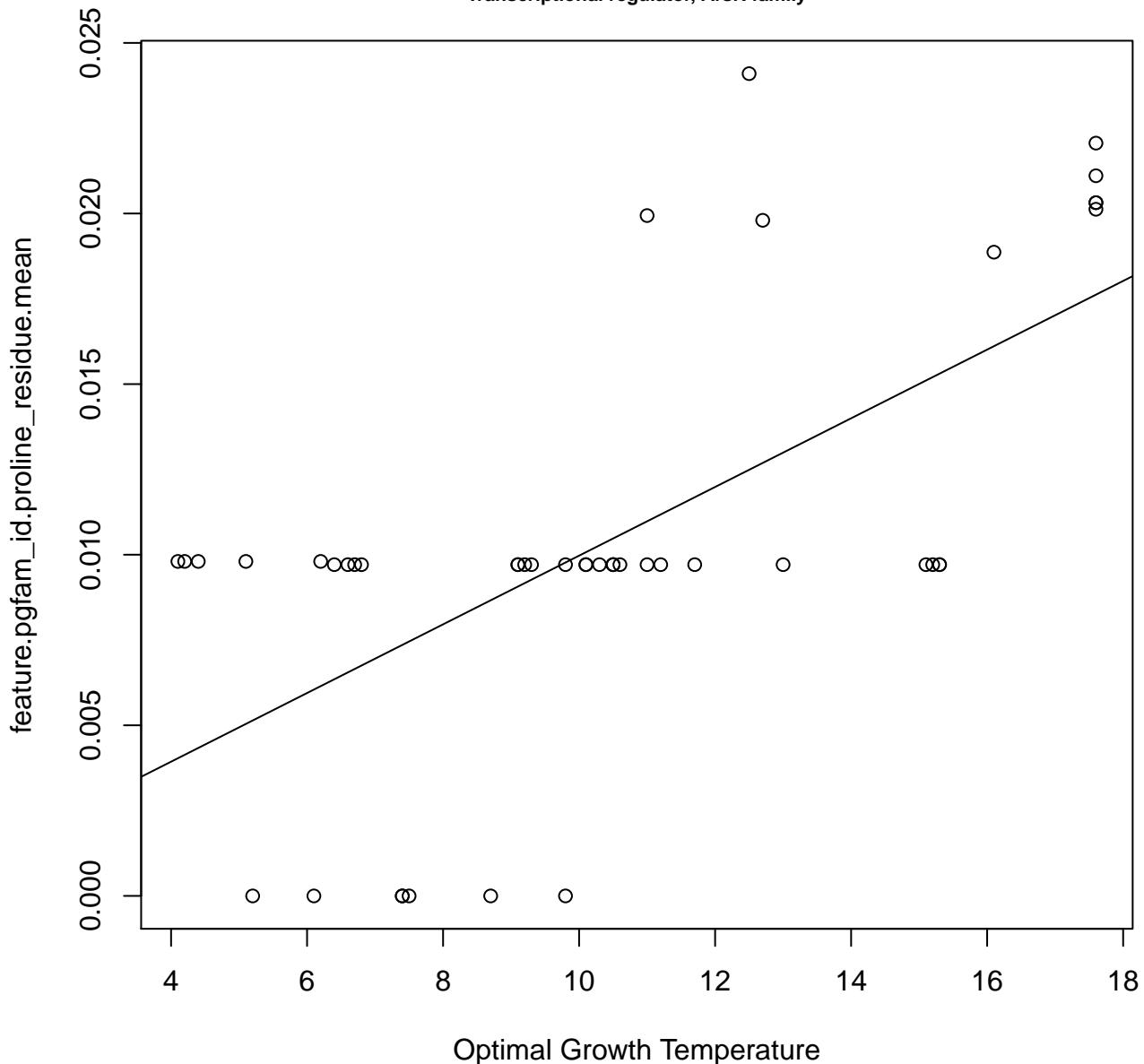
feature.pgfam_id.proline_residue.mean
PGF_10013075
DNA topoisomerase III (EC 5.99.1.2)



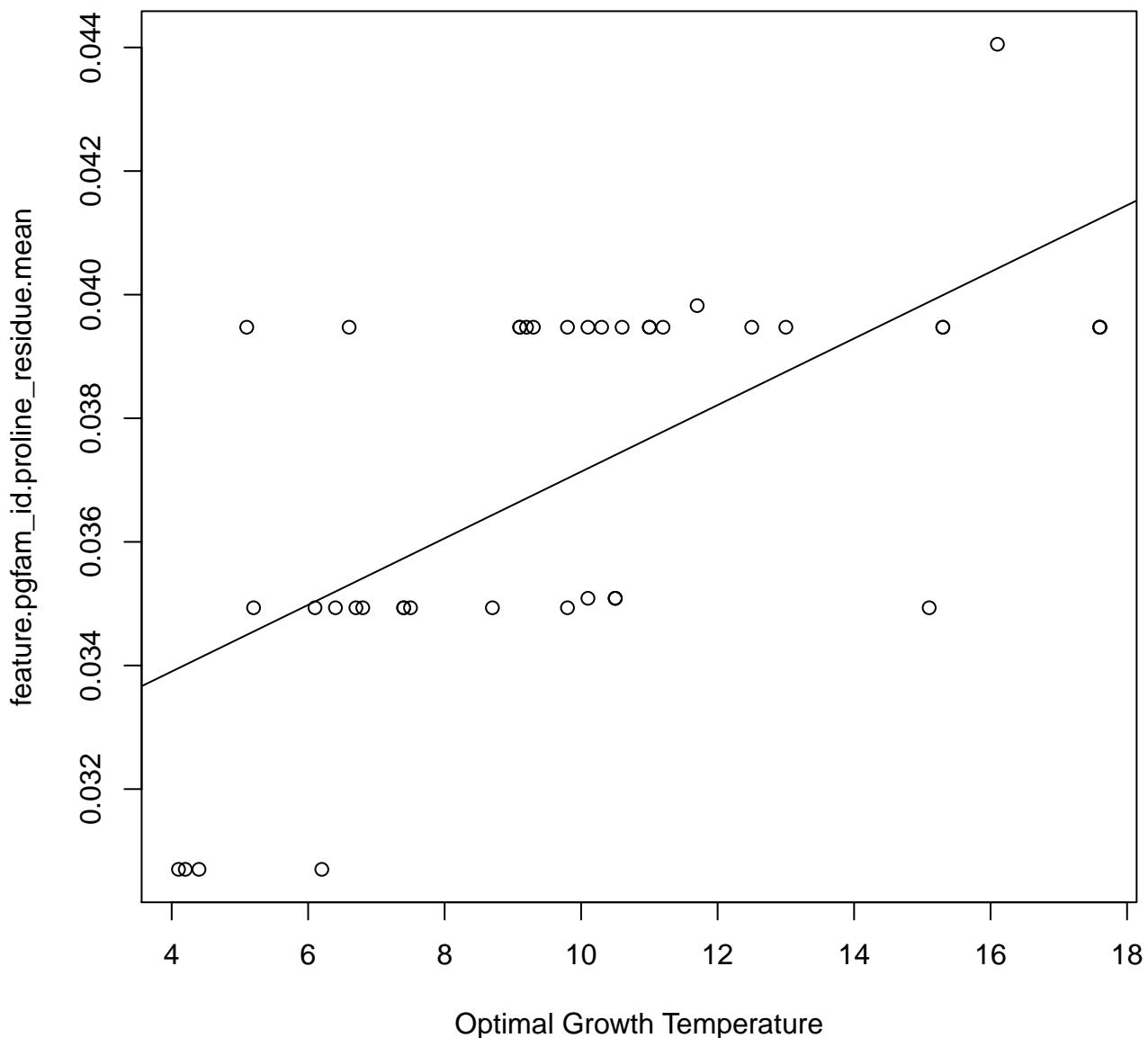
feature.pgfam_id.proline_residue.mean
PGF_08398205
CCA tRNA nucleotidyltransferase (EC 2.7.7.72)



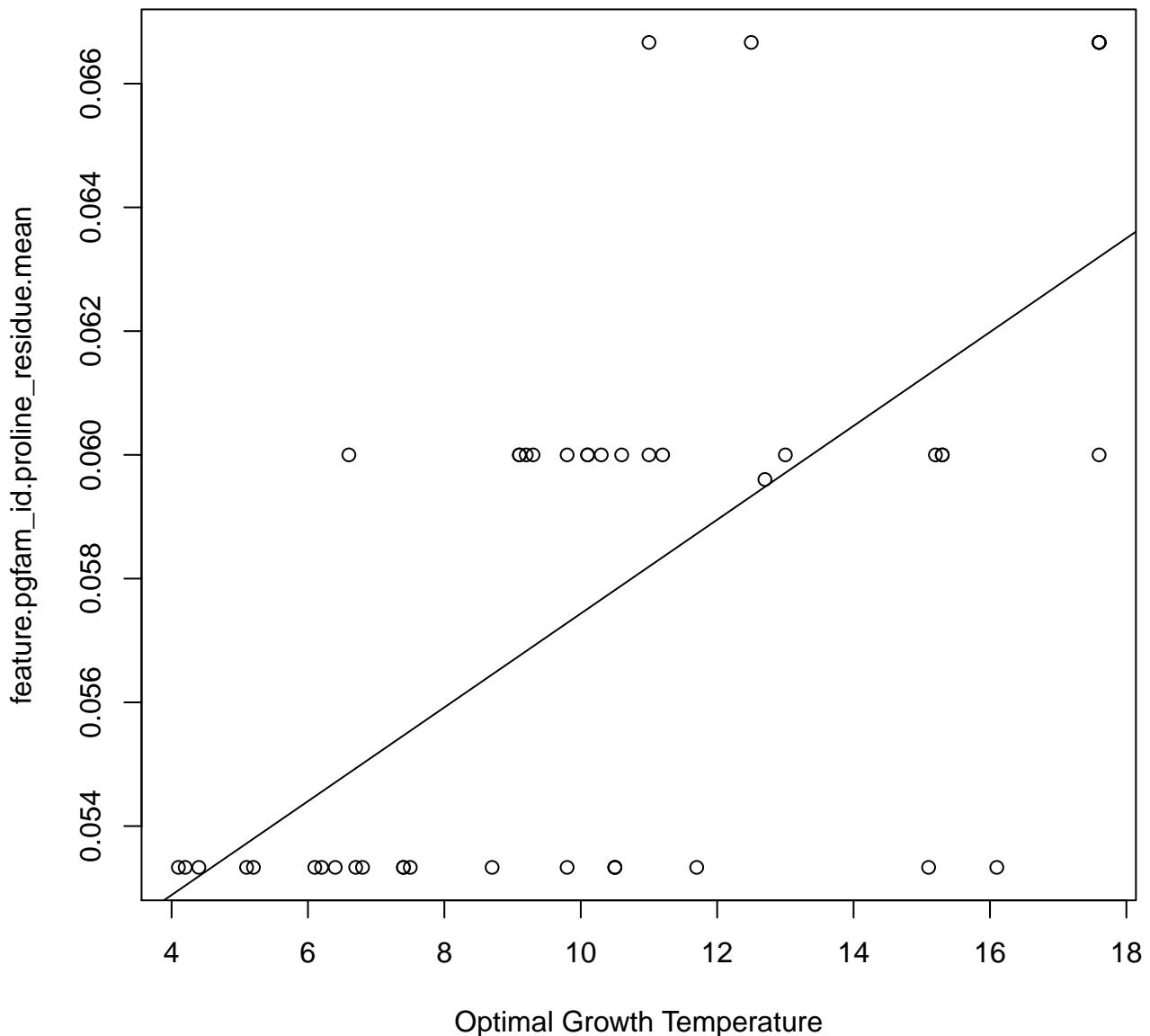
feature.pgfam_id.proline_residue.mean
PGF_08030842
Transcriptional regulator, ArsR family



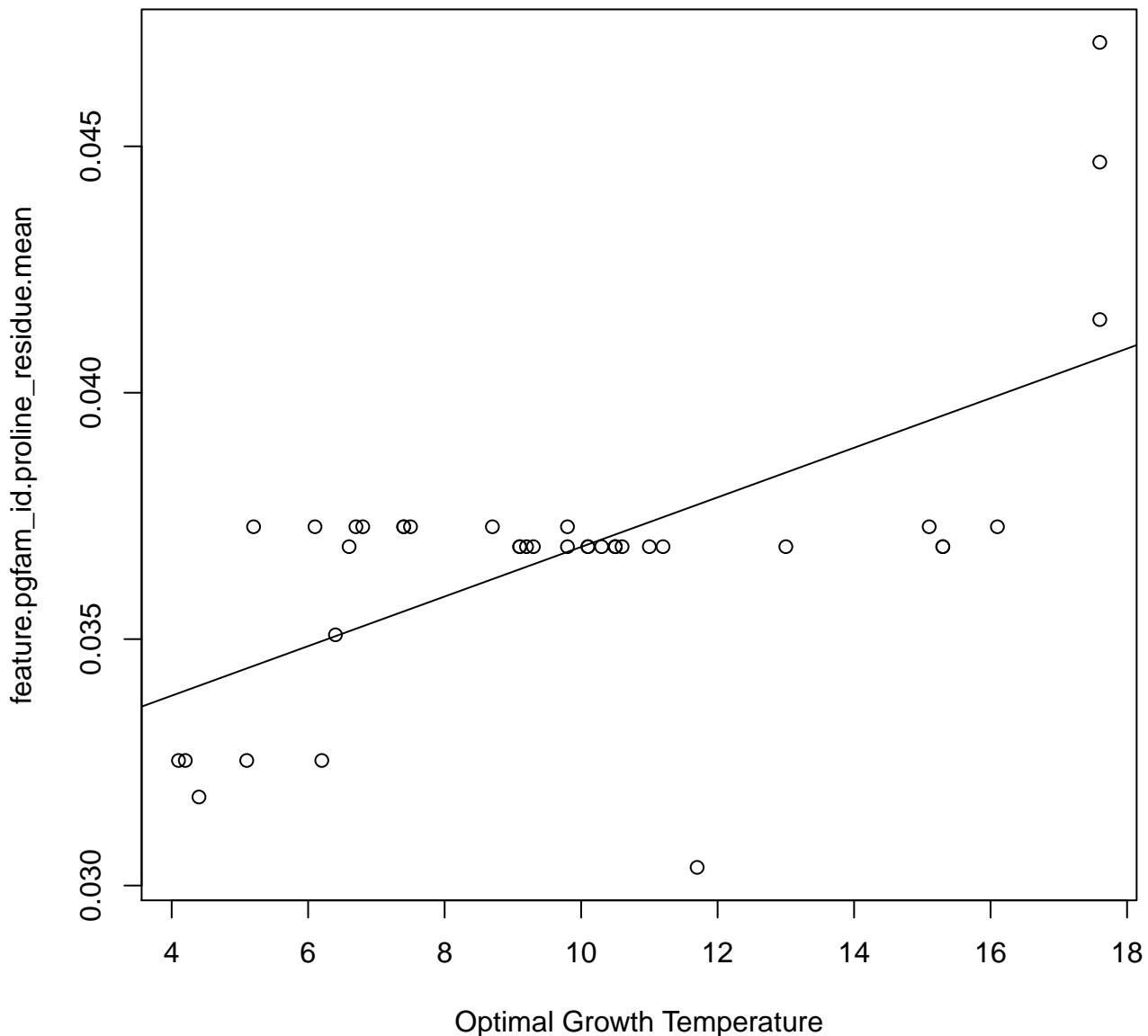
feature.pgfam_id.proline_residue.mean
PGF_03832998
FIG111991: hypothetical protein



feature.pgfam_id.proline_residue.mean
PGF_07504595
3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1.59)



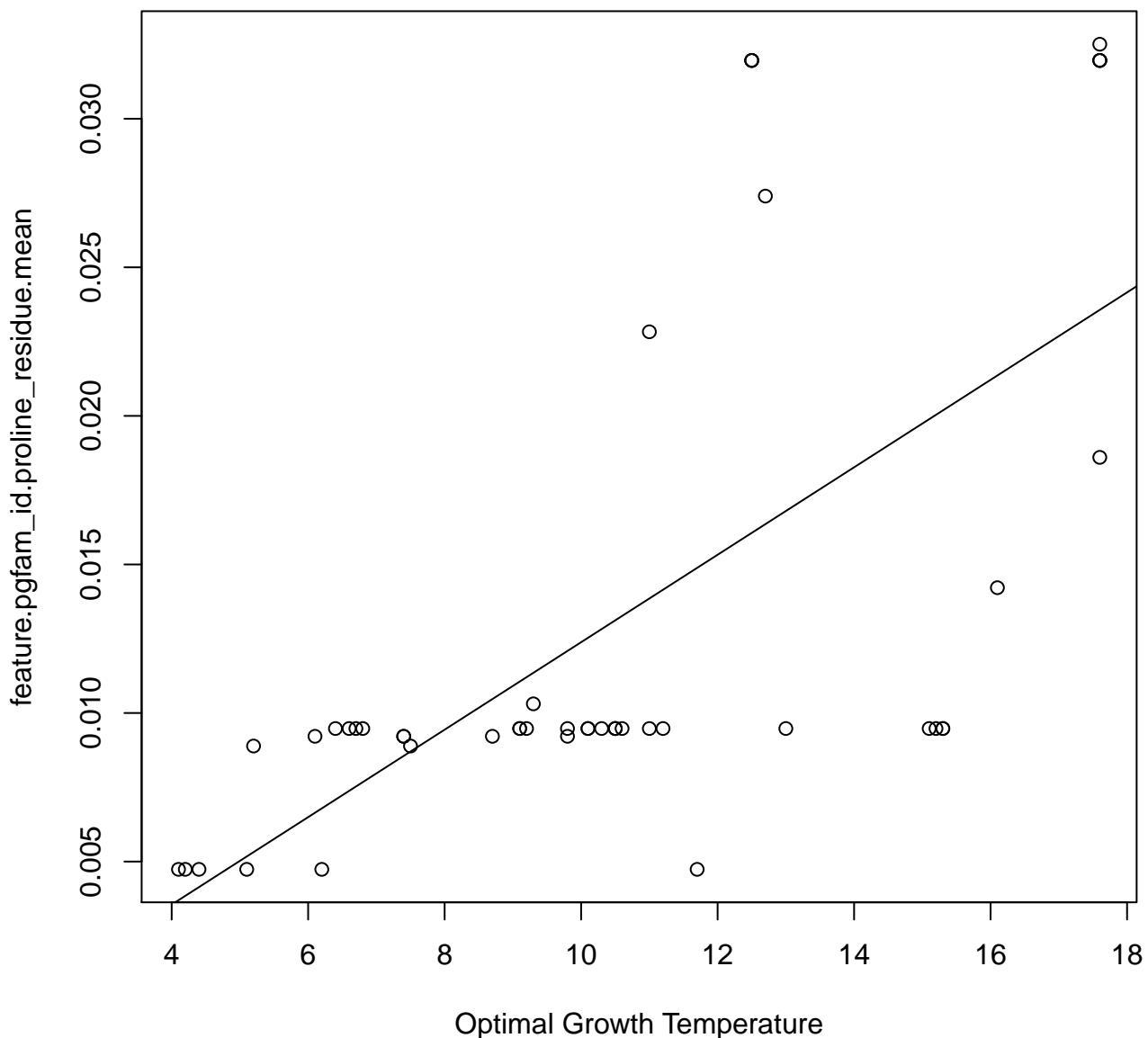
feature.pgfam_id.proline_residue.mean
PGF_00006461
Fumarate hydratase class II (EC 4.2.1.2)



feature.pgfam_id.proline_residue.mean

PGF_00002592

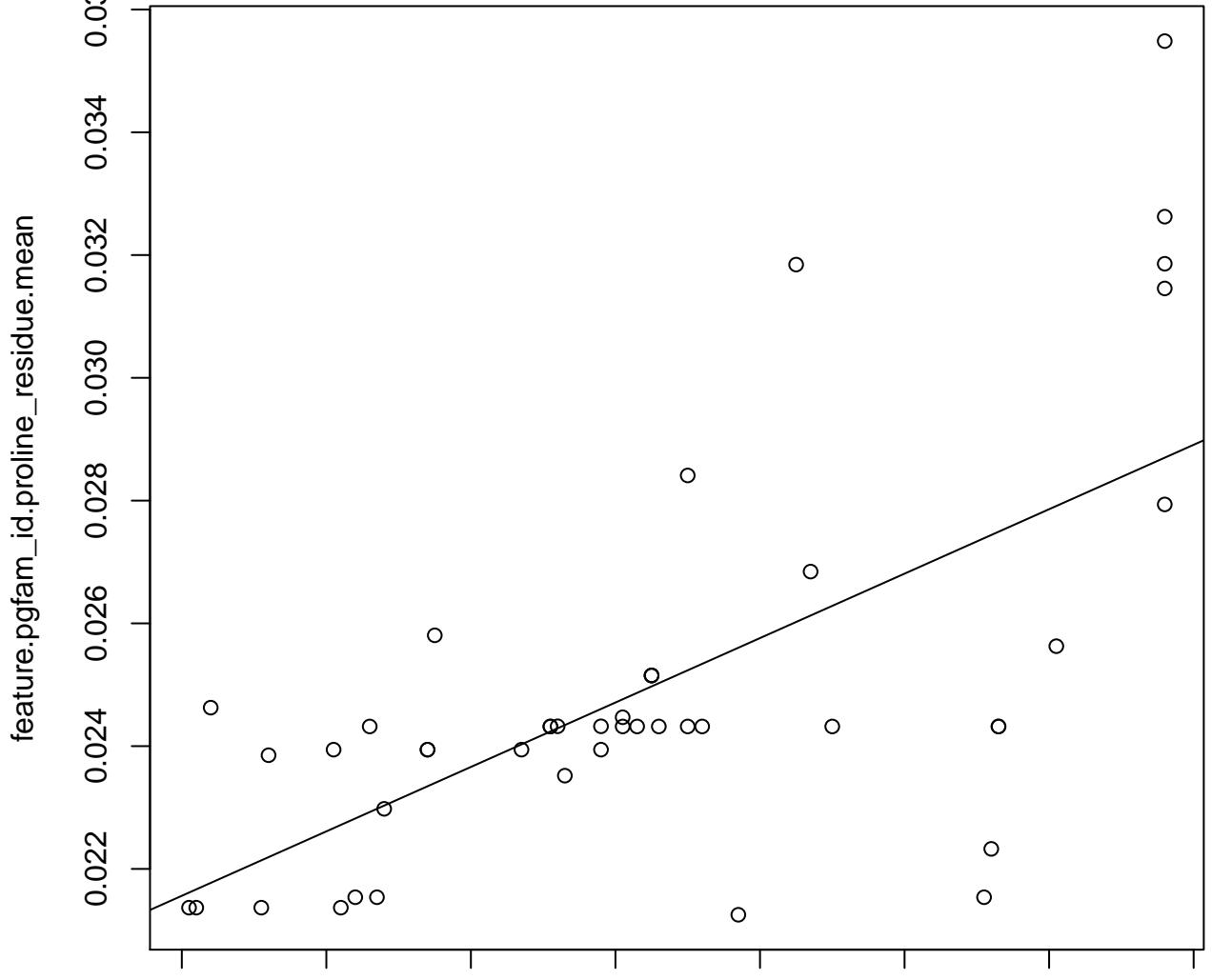
FIG01964566: Predicted membrane protein, hemolysin III homolog



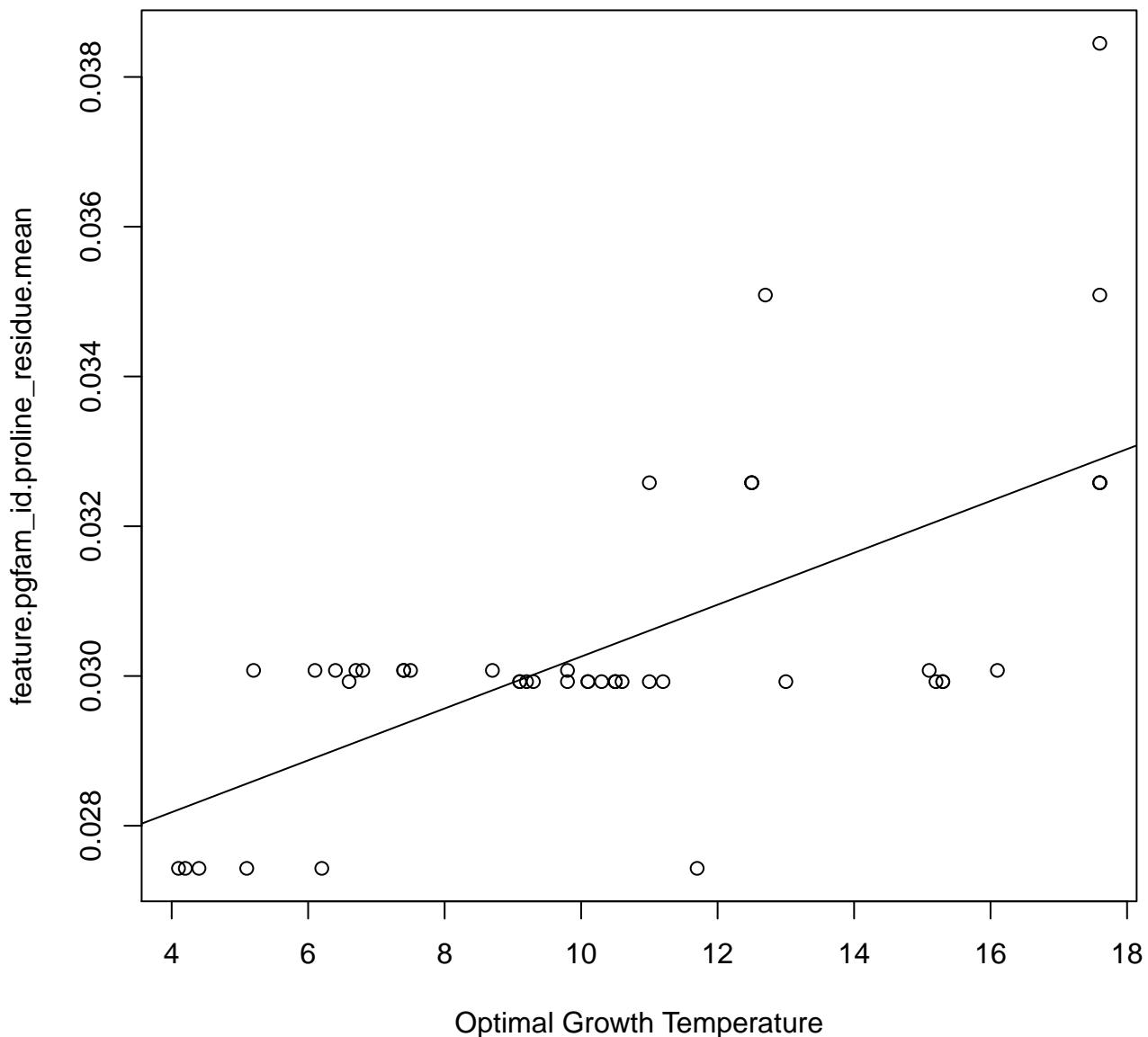
feature.pgfam_id.proline_residue.mean
PGF_07201805
Permease of the drug/metabolite transporter (DMT) superfamily

feature.pgfam_id.proline_residue.mean

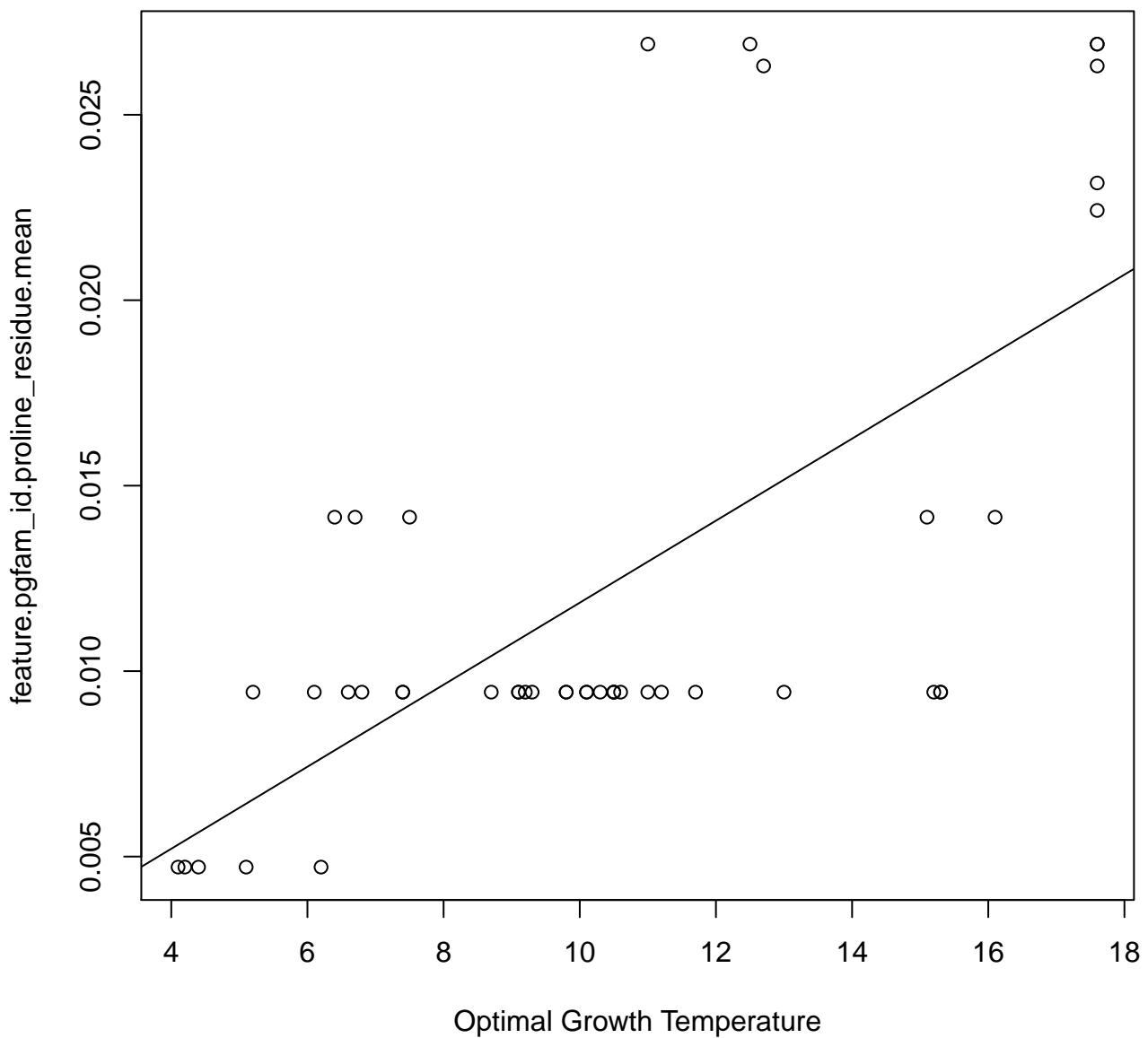
Optimal Growth Temperature



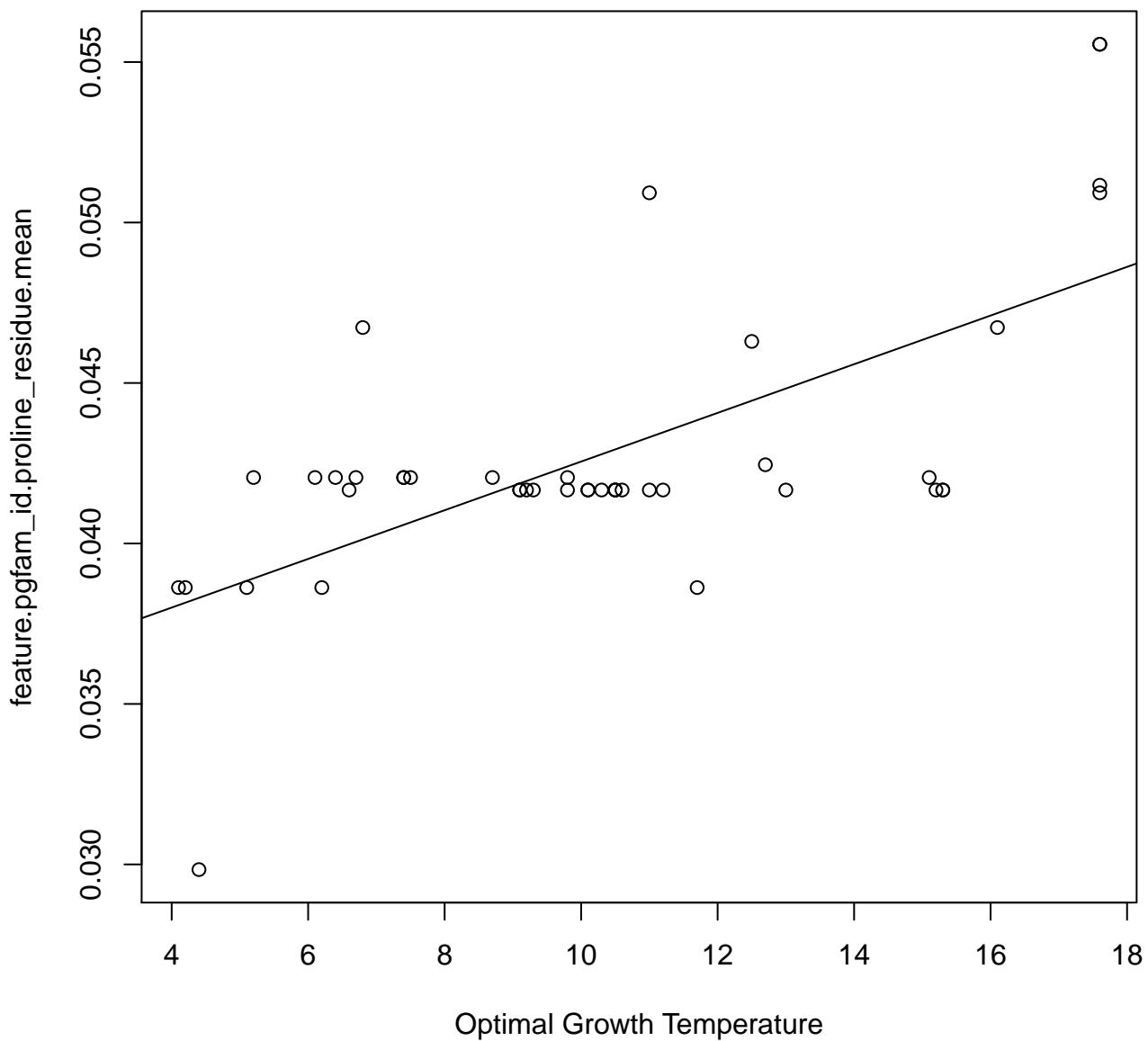
feature.pgfam_id.proline_residue.mean
PGF_00063916
Tyrosyl-tRNA synthetase (EC 6.1.1.1)



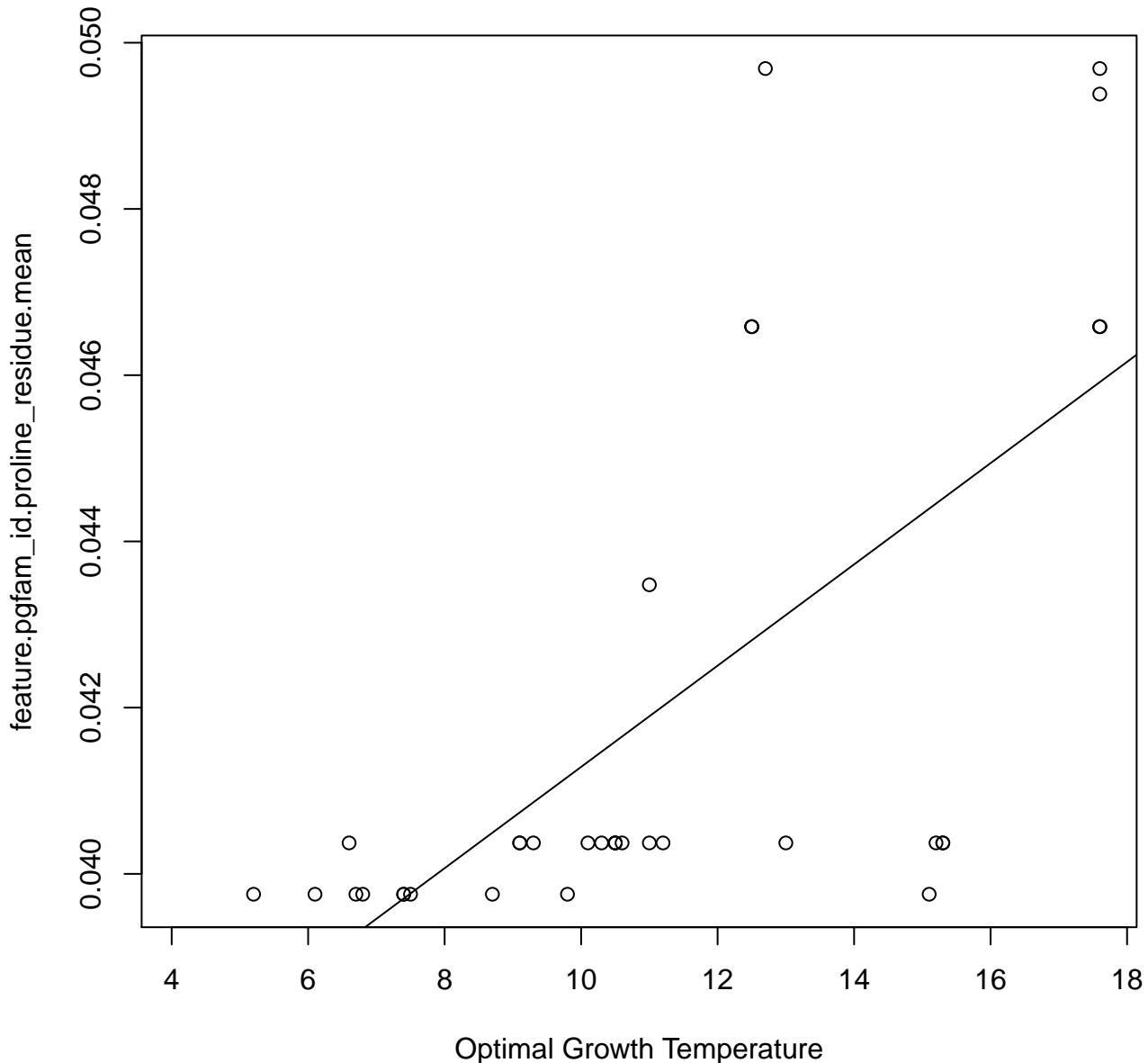
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PGF_07357908
UPF0070 protein YfgM



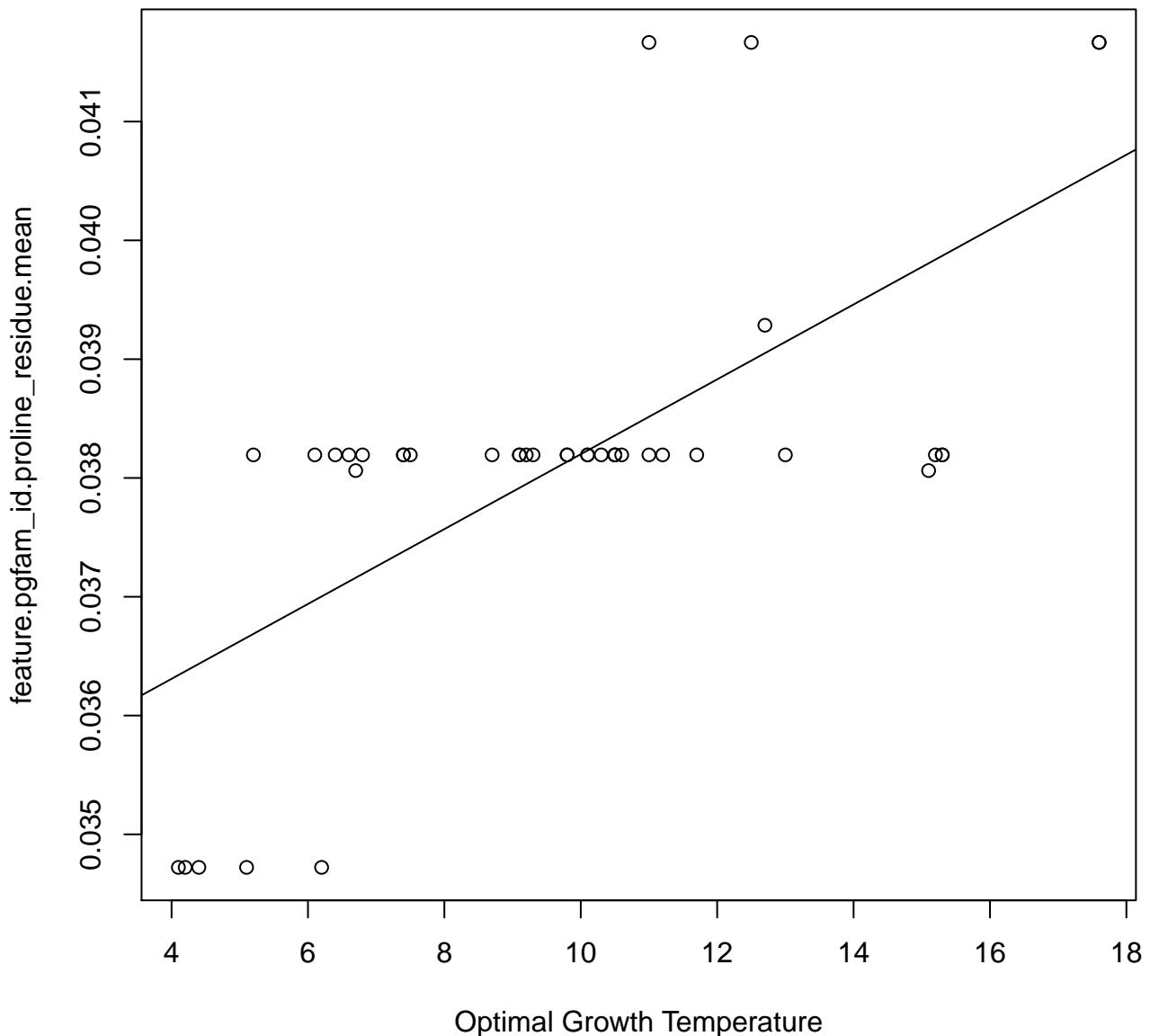
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PGF_01776925
Uridine kinase (EC 2.7.1.48)



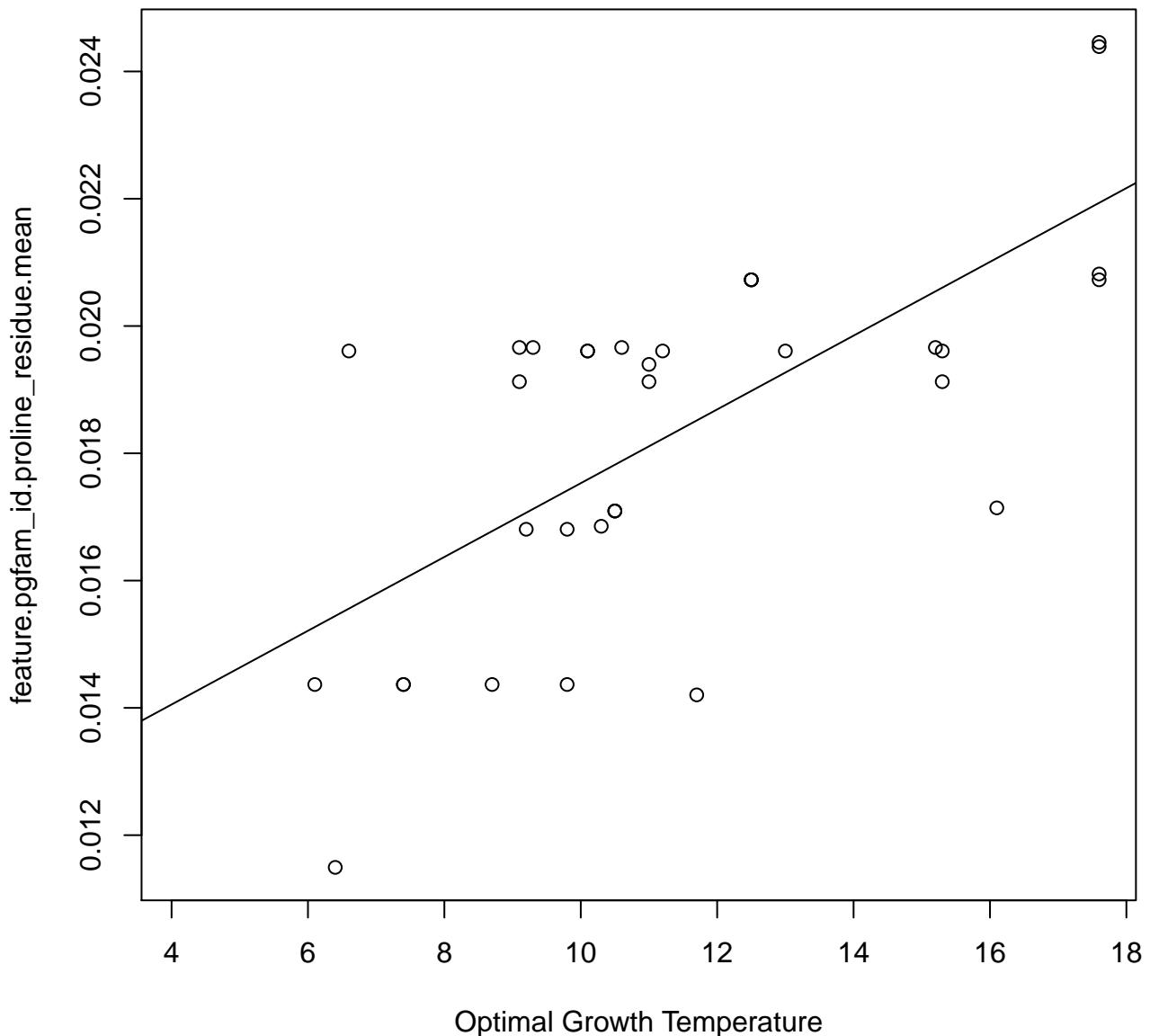
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PGF_03079547
Membrane-fusion protein



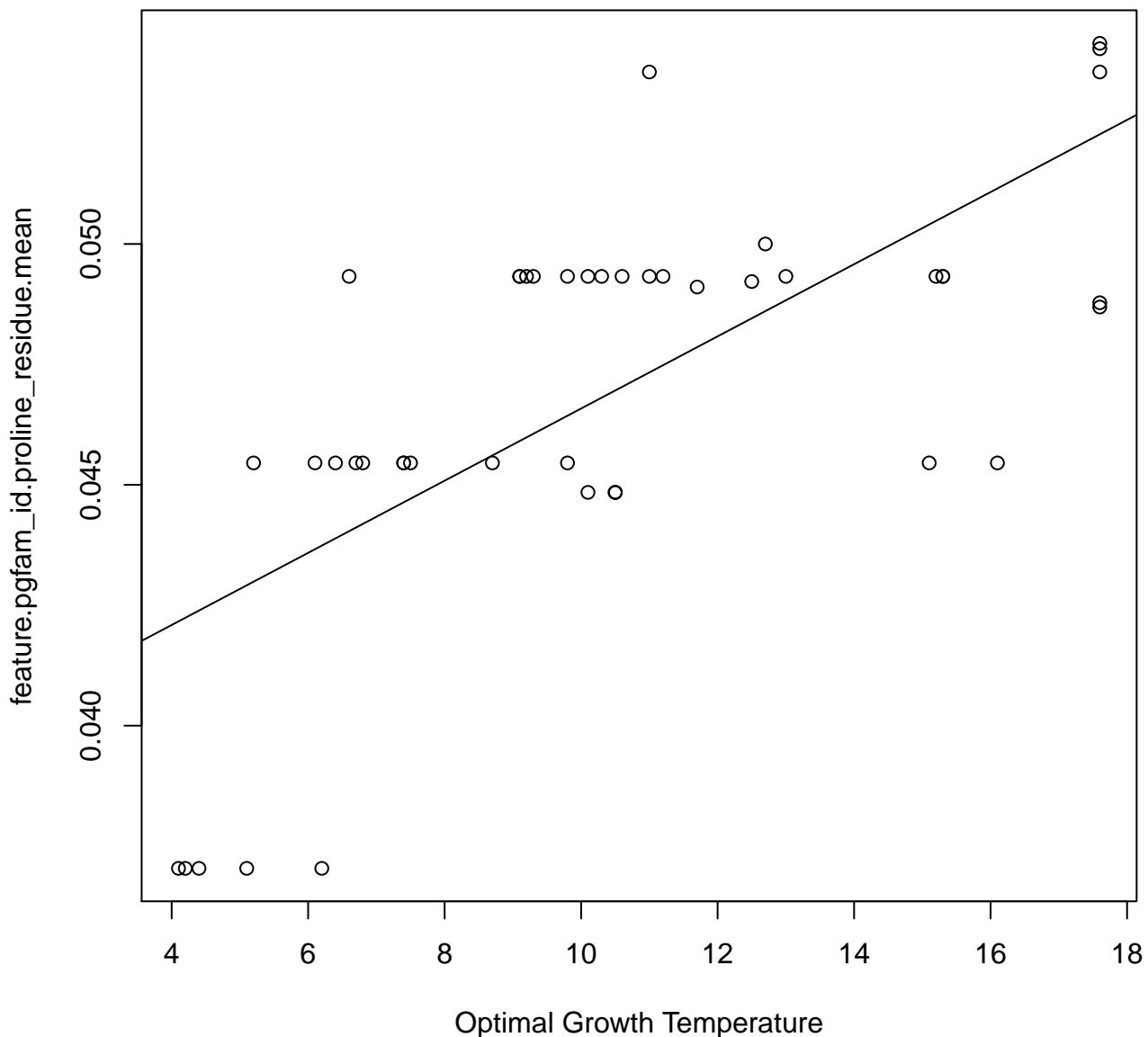
feature.pgfam_id.proline_residue.mean
PGF_01426950
ABC transporter, substrate-binding protein (cluster 12, methionine/phosphonates)



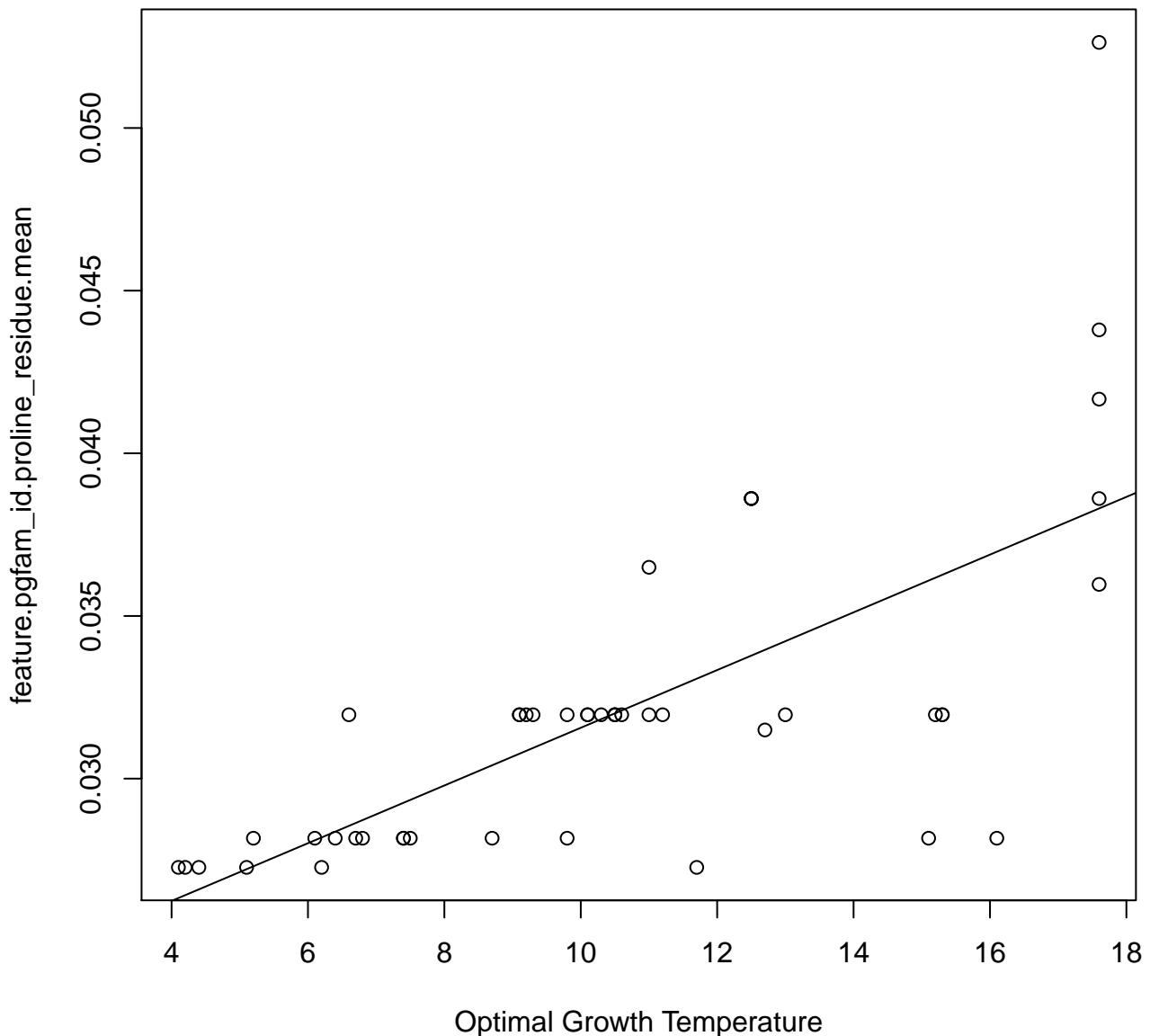
feature.pgfam_id.proline_residue.mean
PGF_01336686
Major porin and structural outer membrane porin OprF



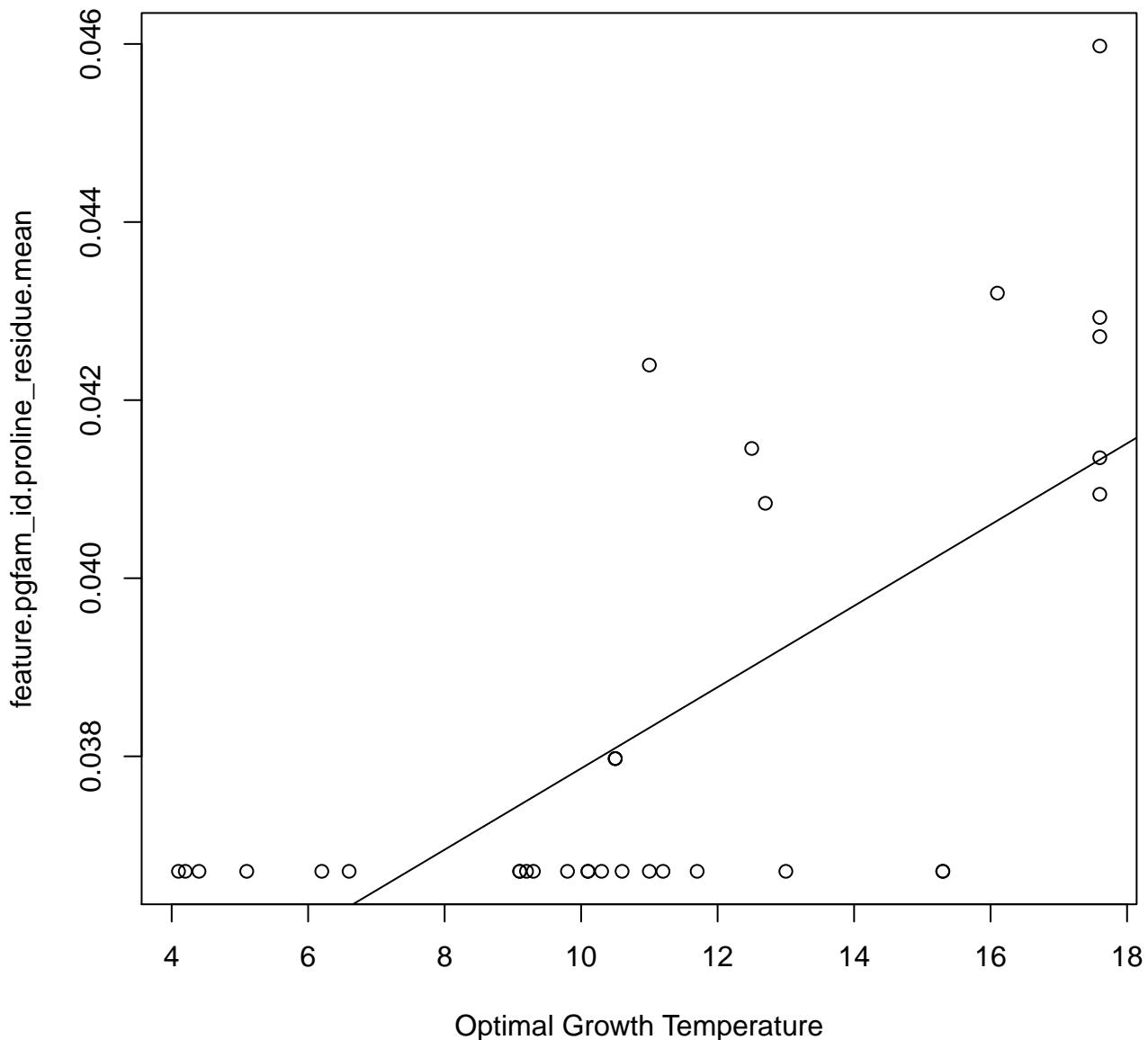
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PGF_04602939
Paraquat-inducible protein A



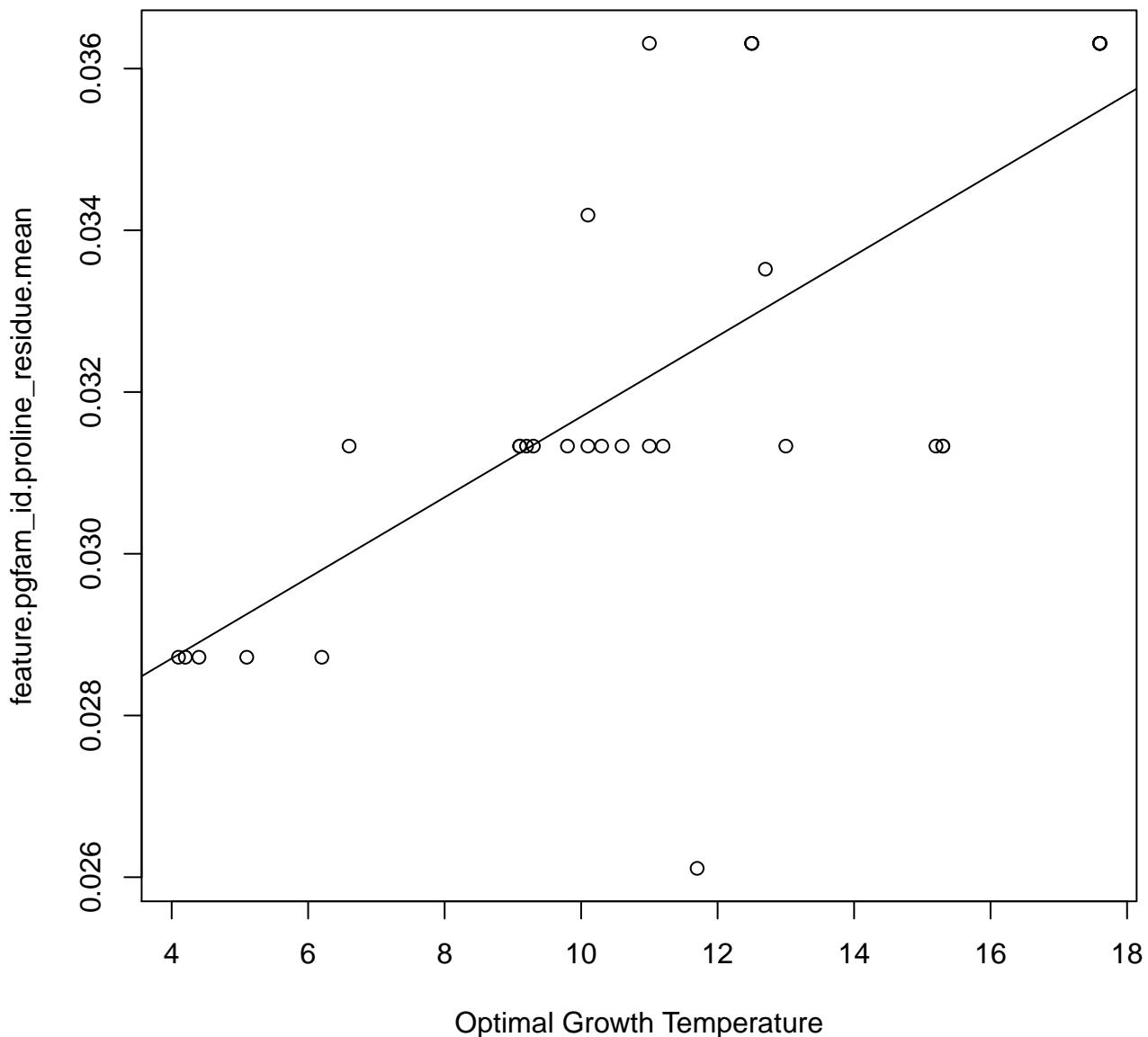
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PGF_01484108
Electron transport complex protein RnfG



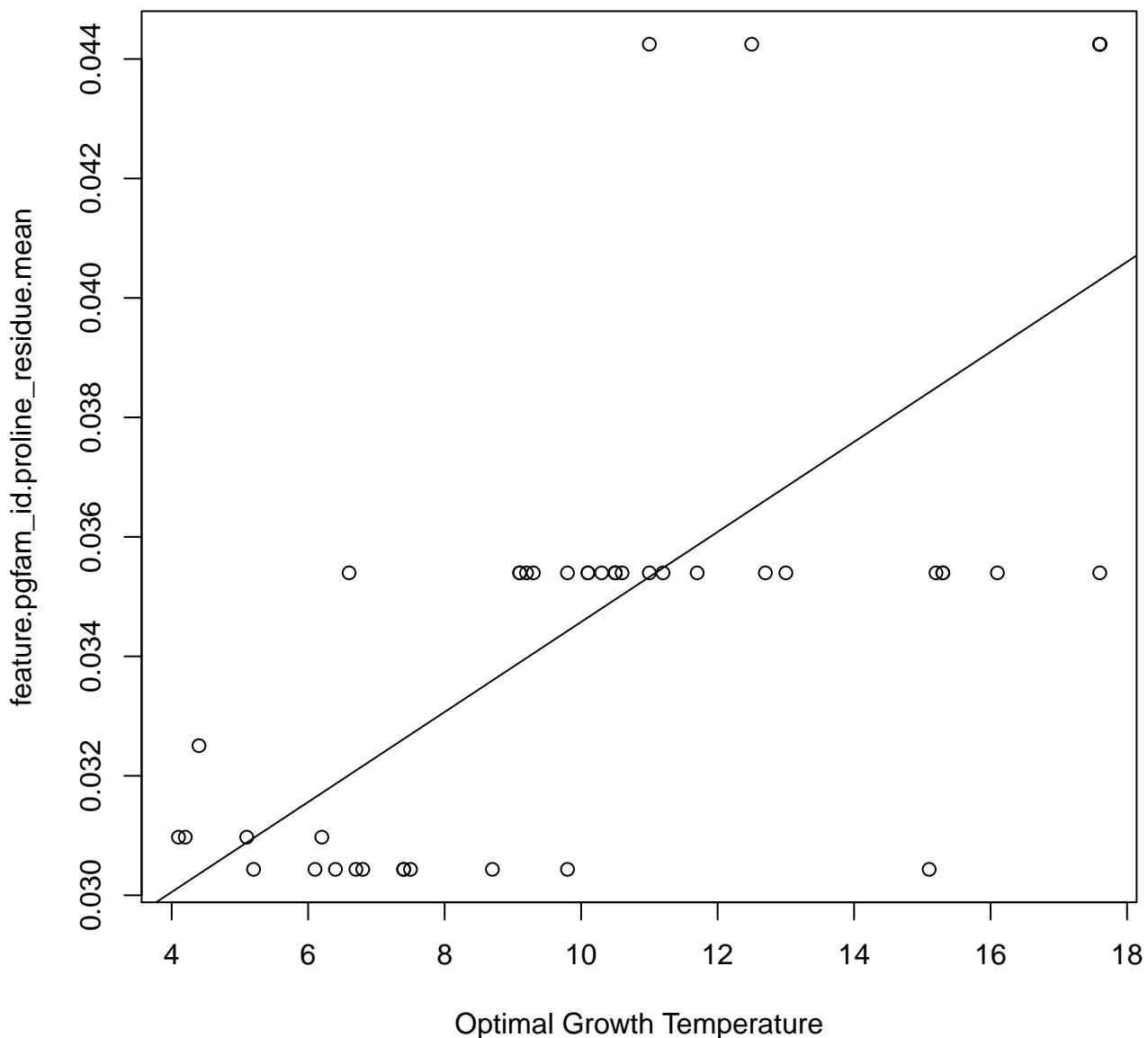
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PGF_10370701
Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)



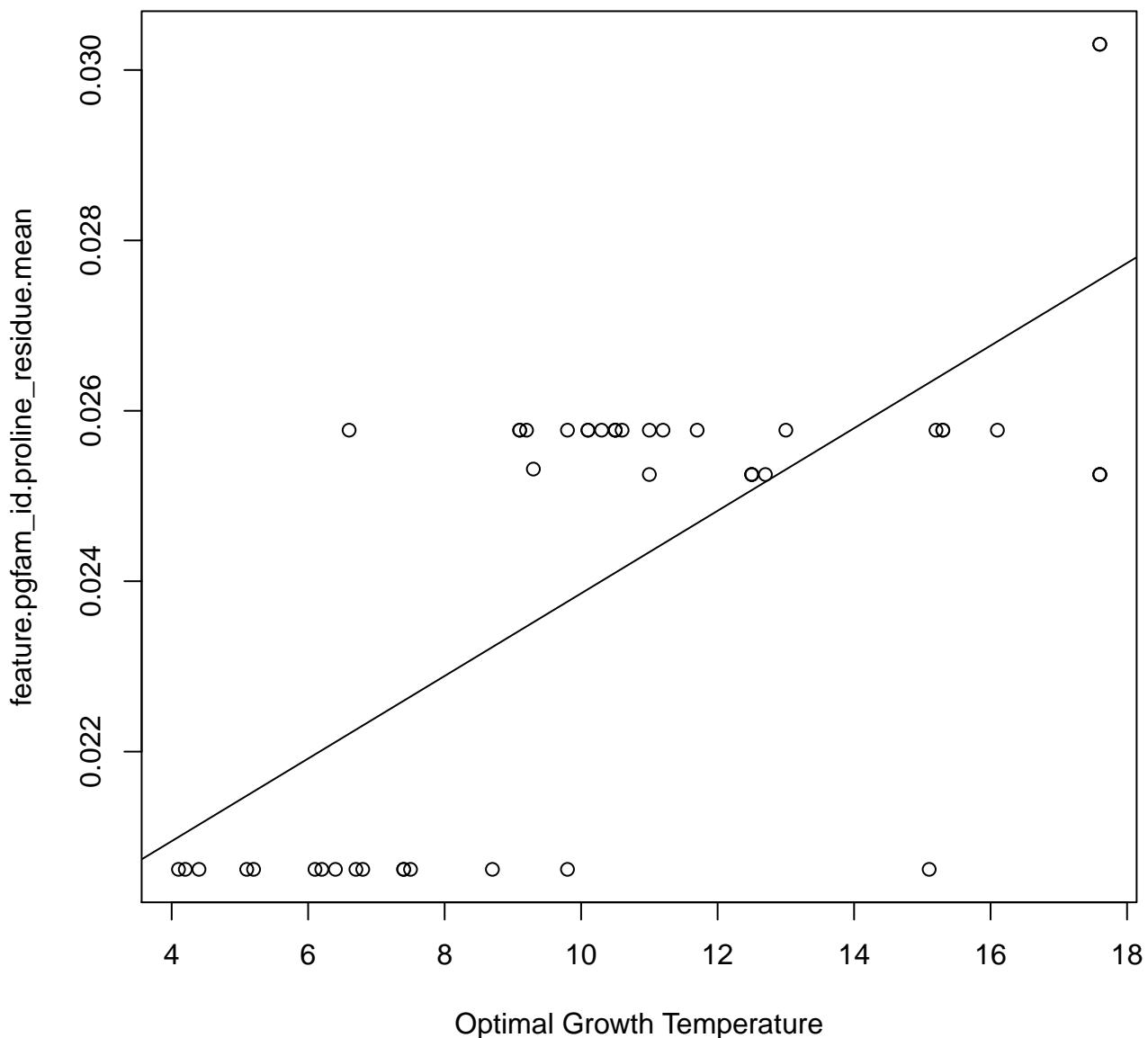
feature.pgfam_id.proline_residue.mean
PGF_00023779
N-acetylglucosamine related transporter, NagX



feature.pgfam_id.proline_residue.mean
PGF_02455692
Cytidylate kinase (EC 2.7.4.25)



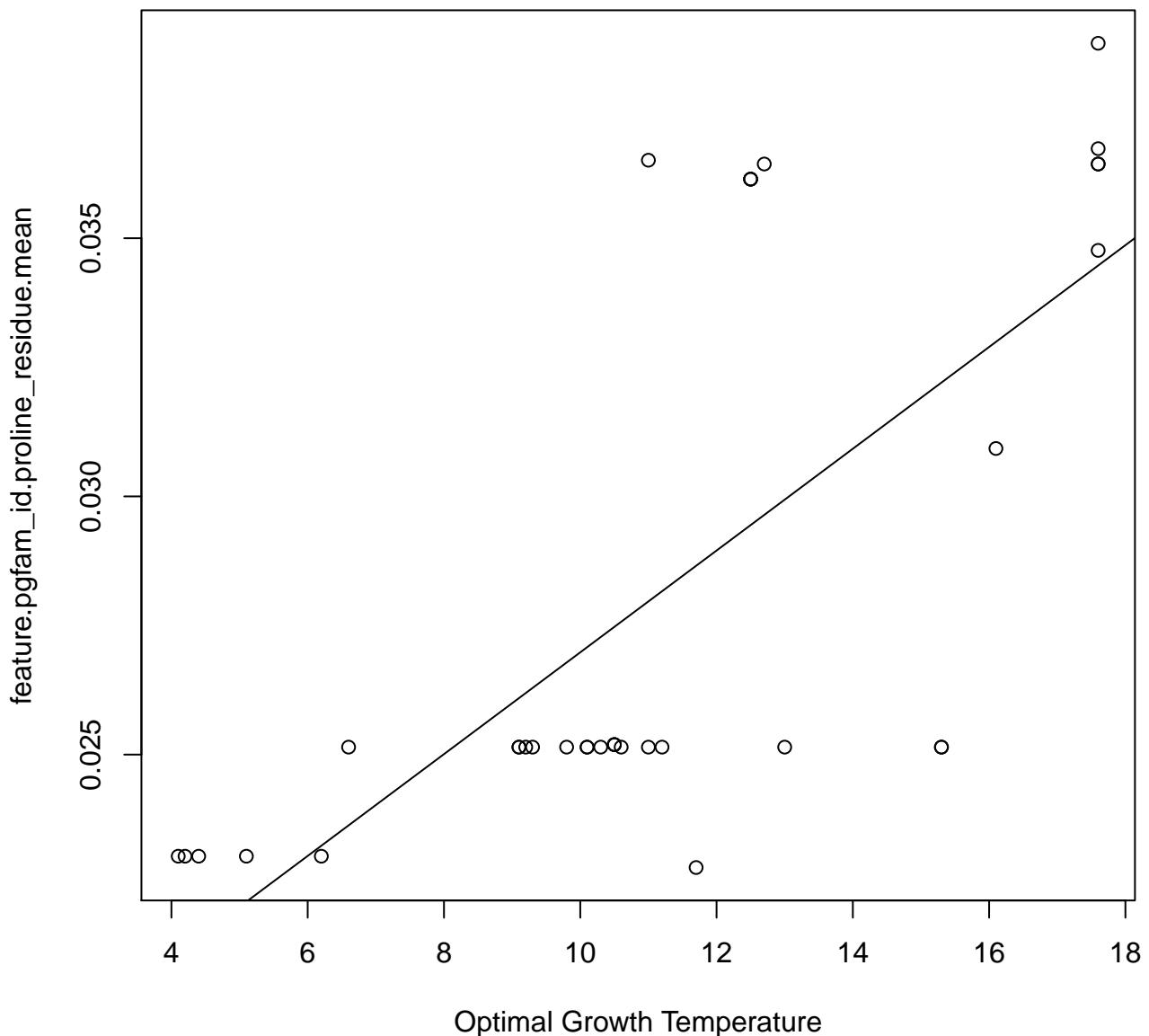
feature.pgfam_id.proline_residue.mean
PGF_00058666
Transcriptional regulator SImA, TetR family



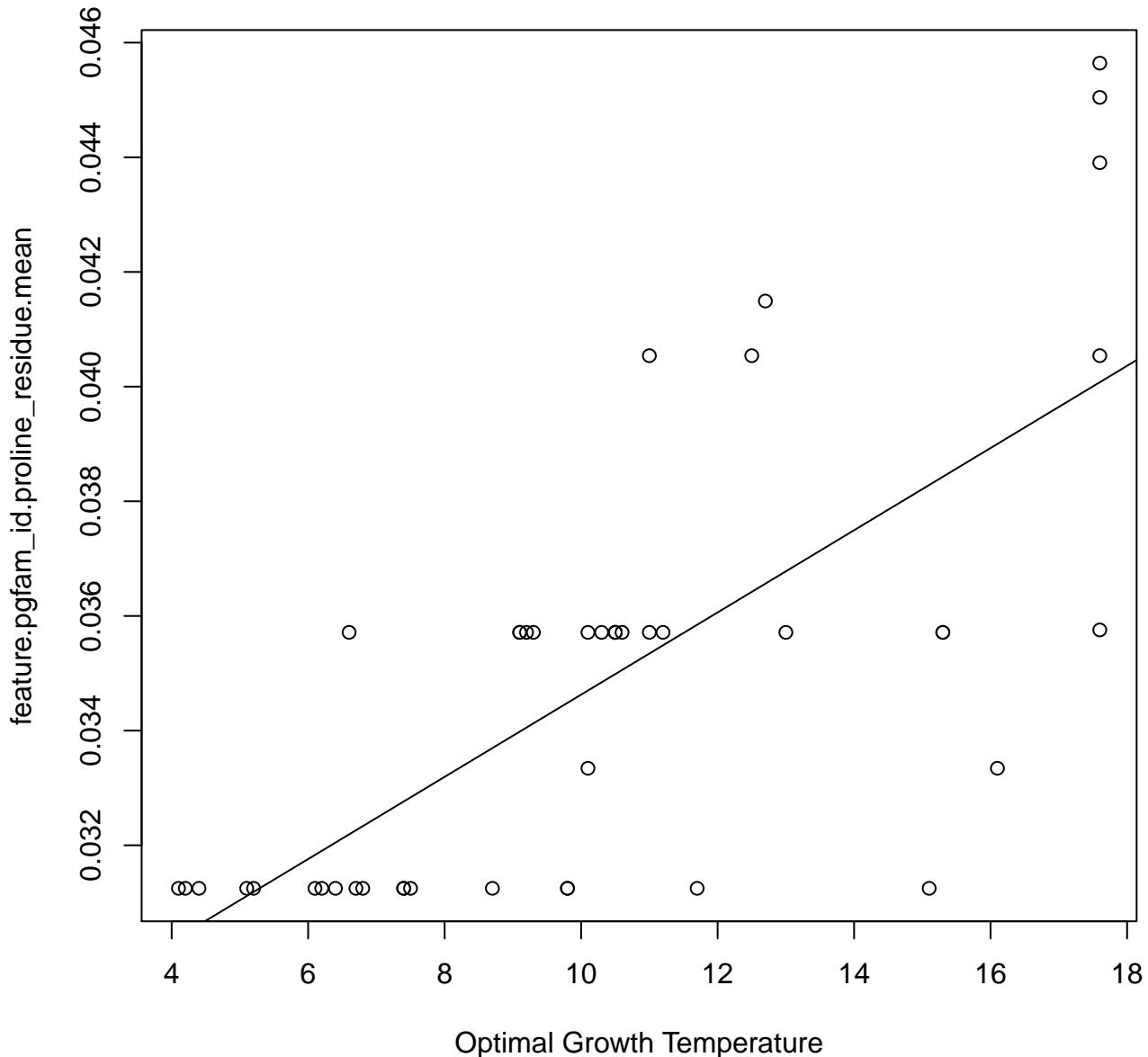
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PGF_04251132

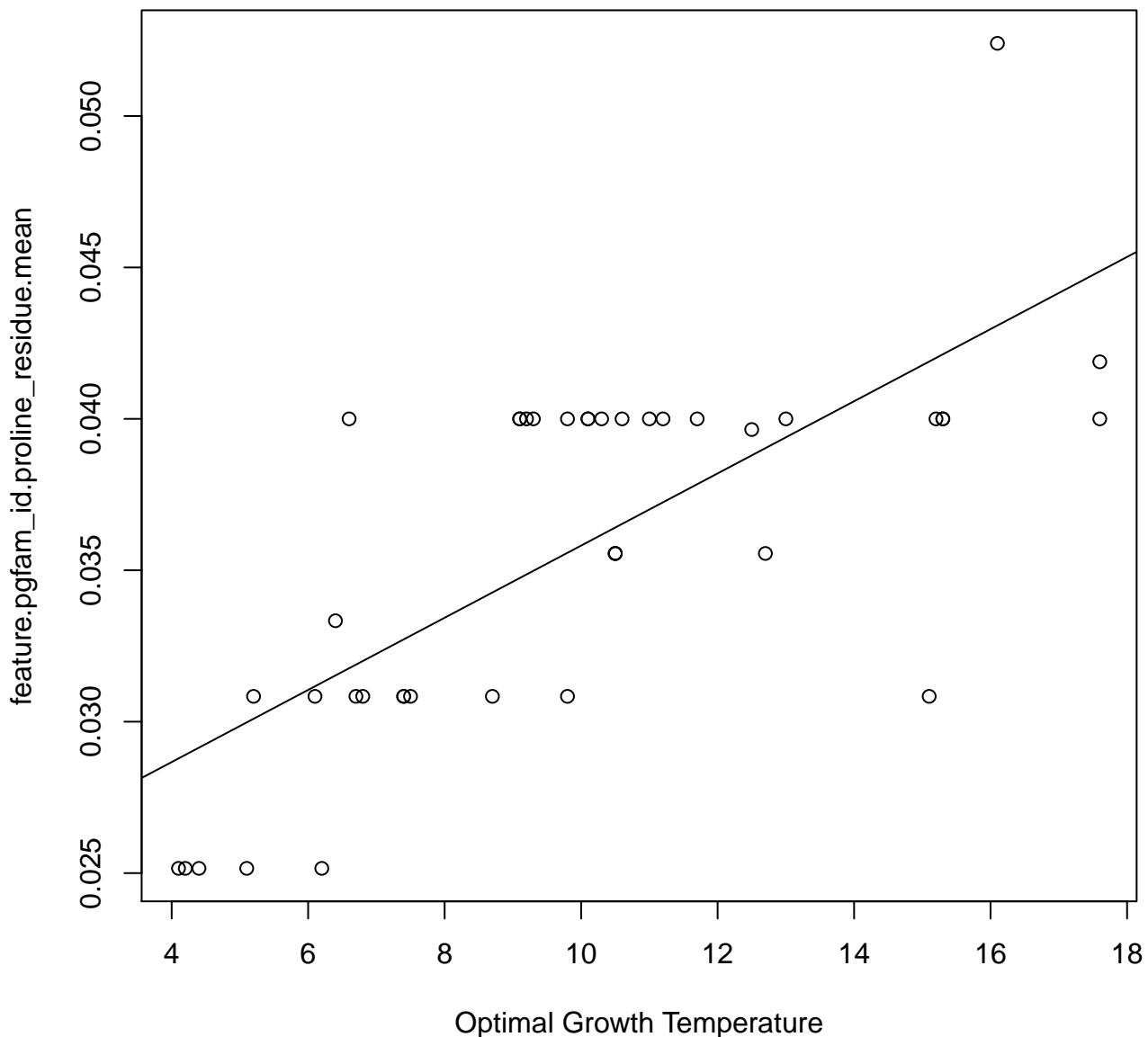
Xanthine dehydrogenase iron–sulfur subunit (EC 1.17.1.4) / Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4)



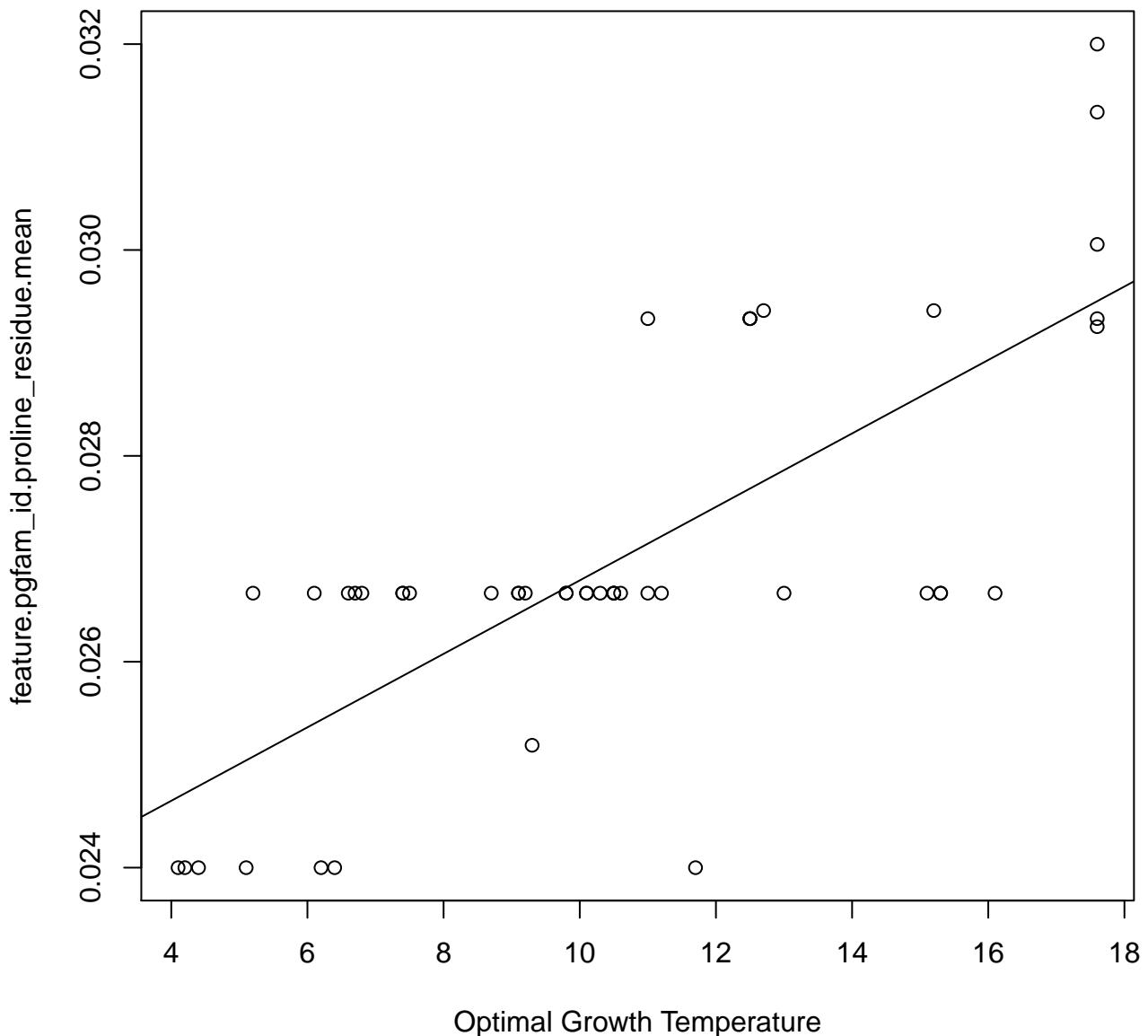
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PGF_02386833
7-carboxy-7-deazaguanine synthase (EC 4.3.99.3)



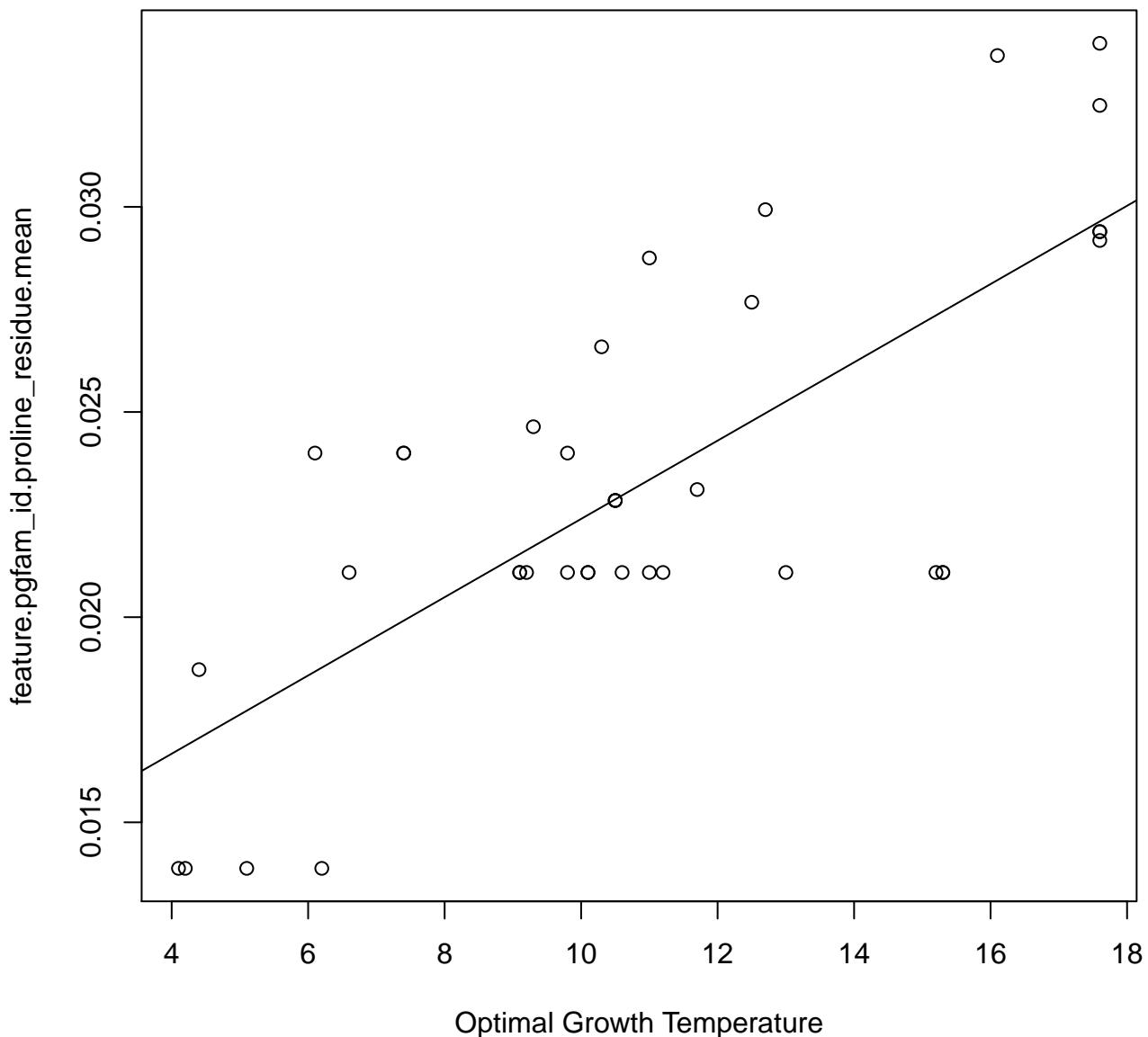
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PGF_02911177
SM-20-related protein



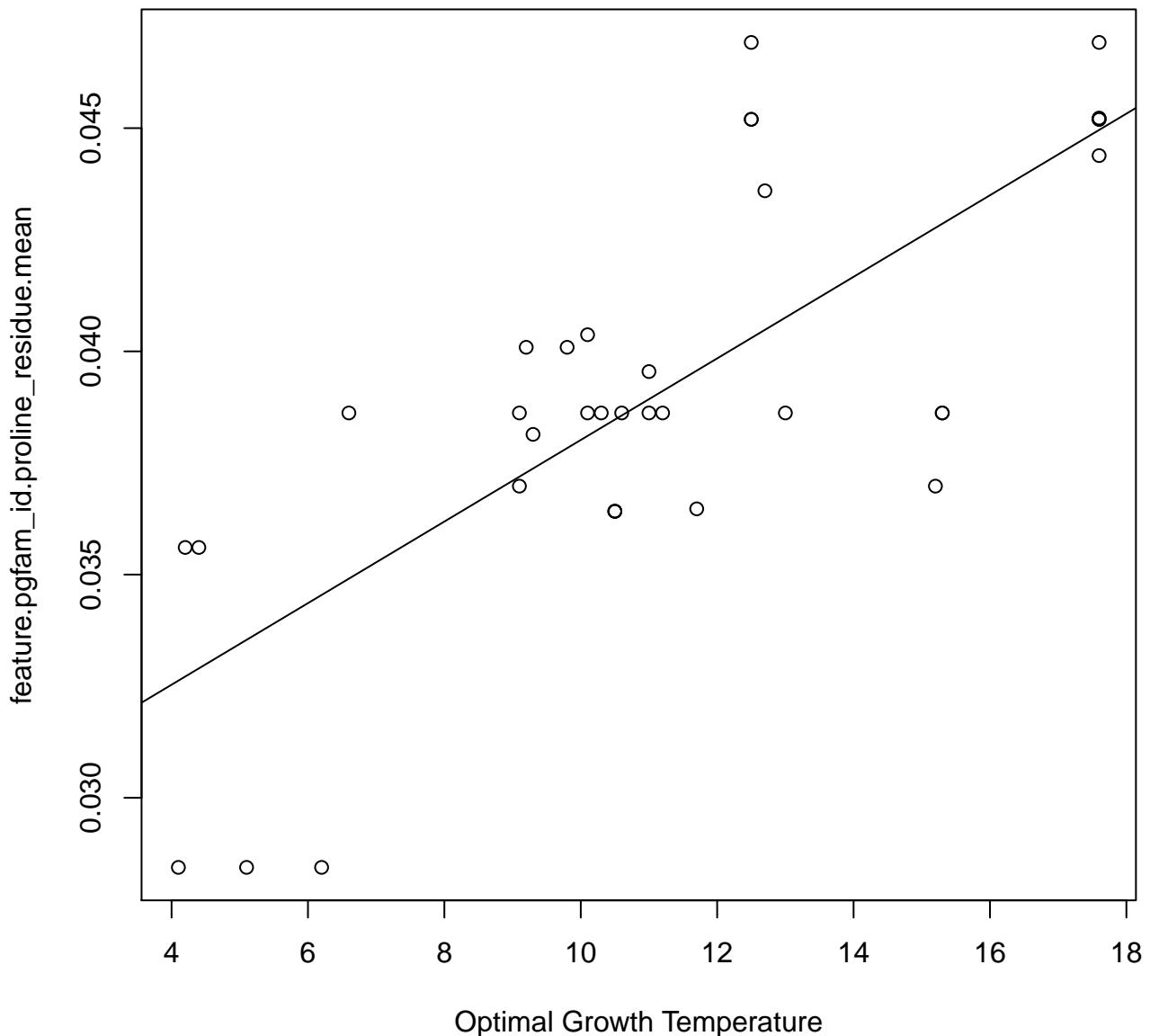
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PGF_00488496
Type IV pilus assembly ATPase component PilU



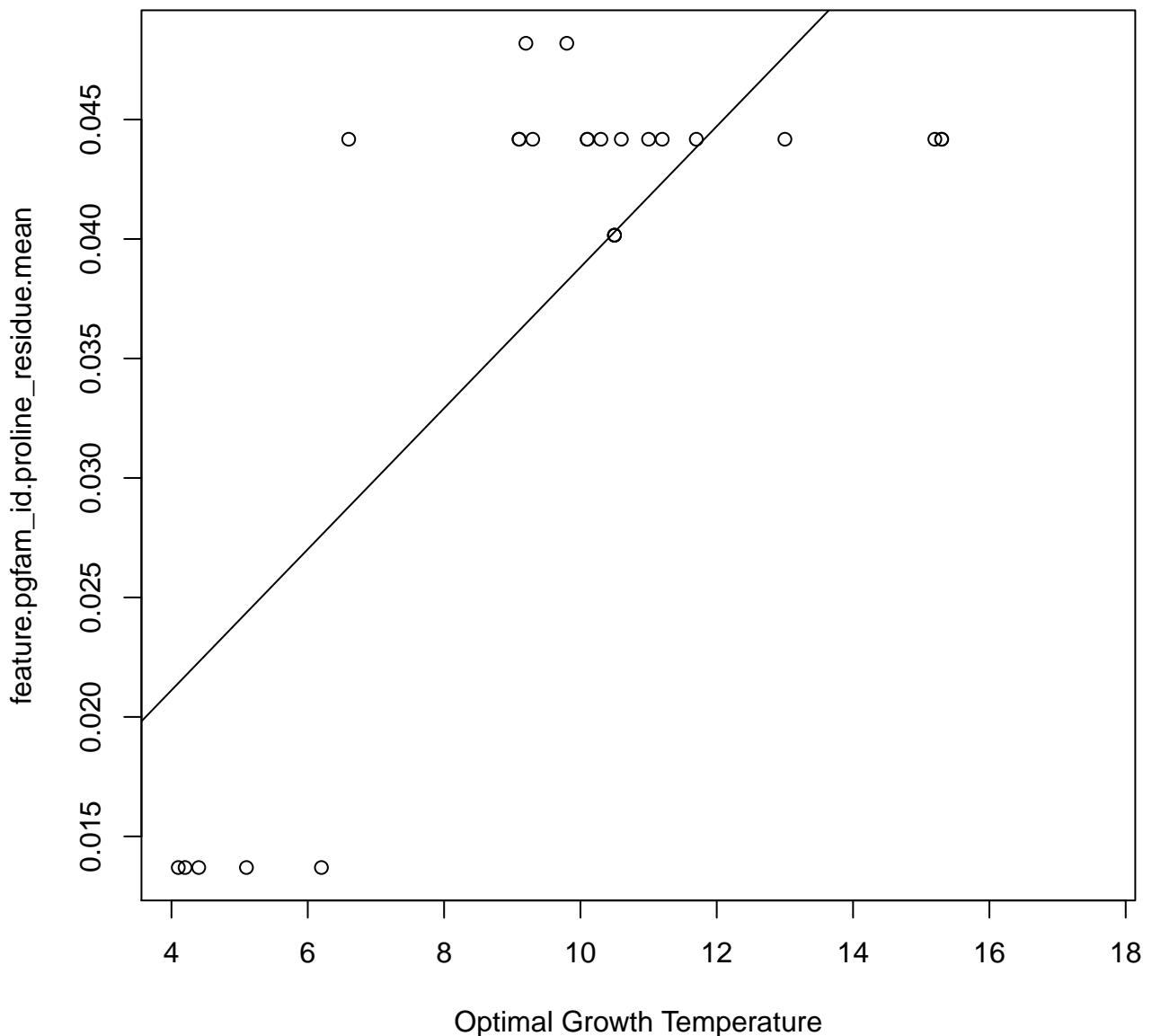
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PGF_07015776



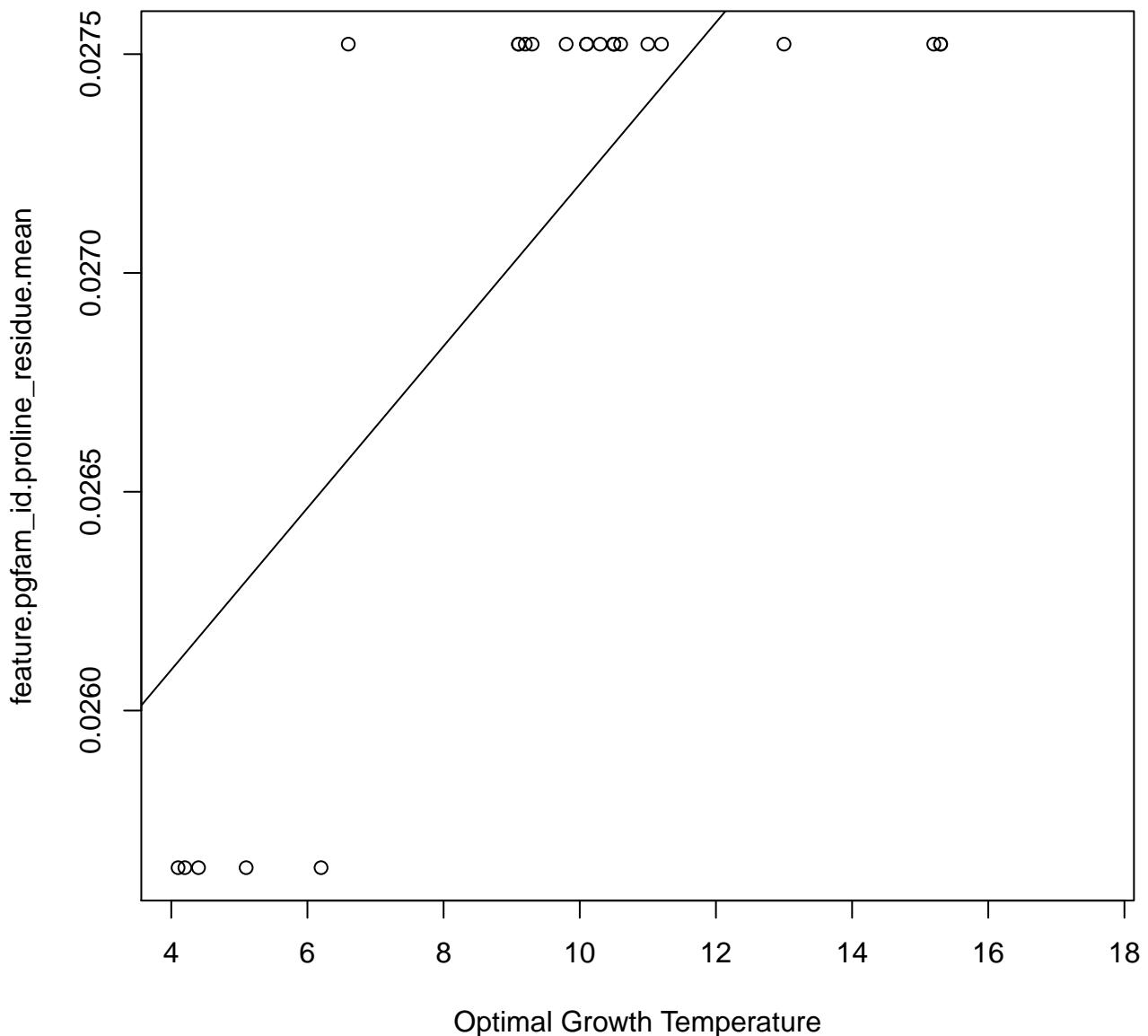
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PGF_00300187
Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) @ Outer membrane phospholipase A



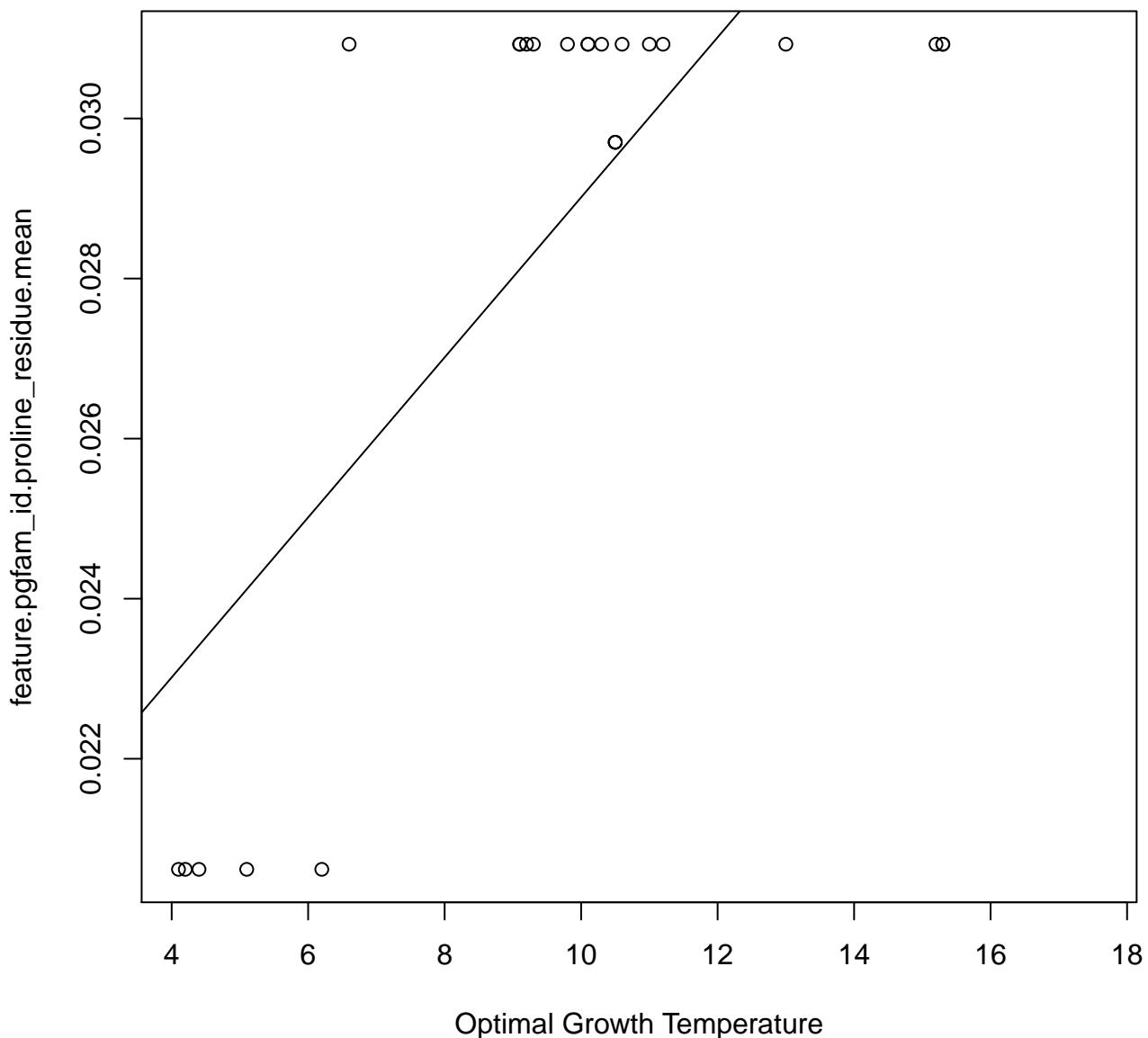
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PGF_11018774
hypothetical protein



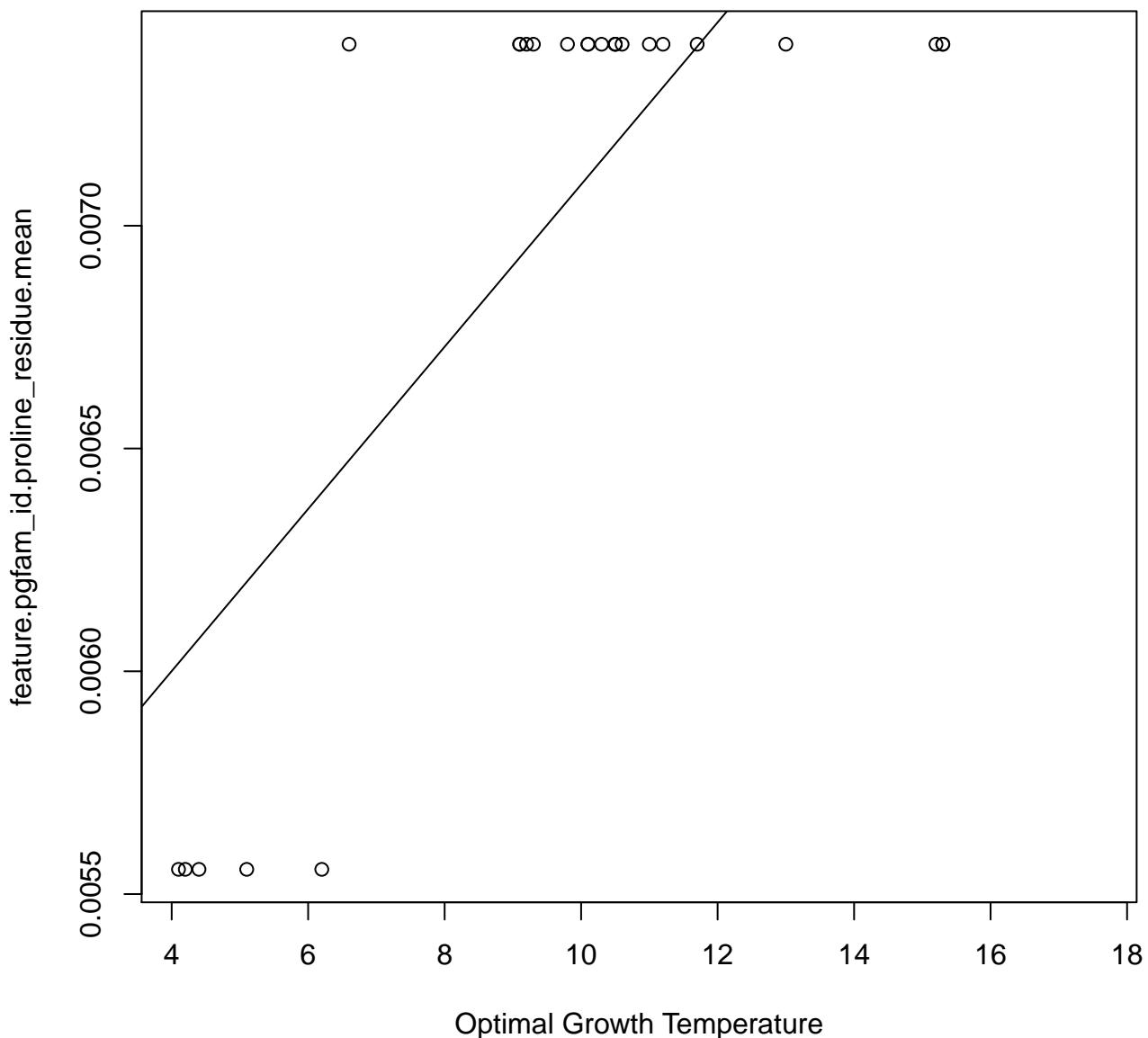
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PGF_11025496
hypothetical protein



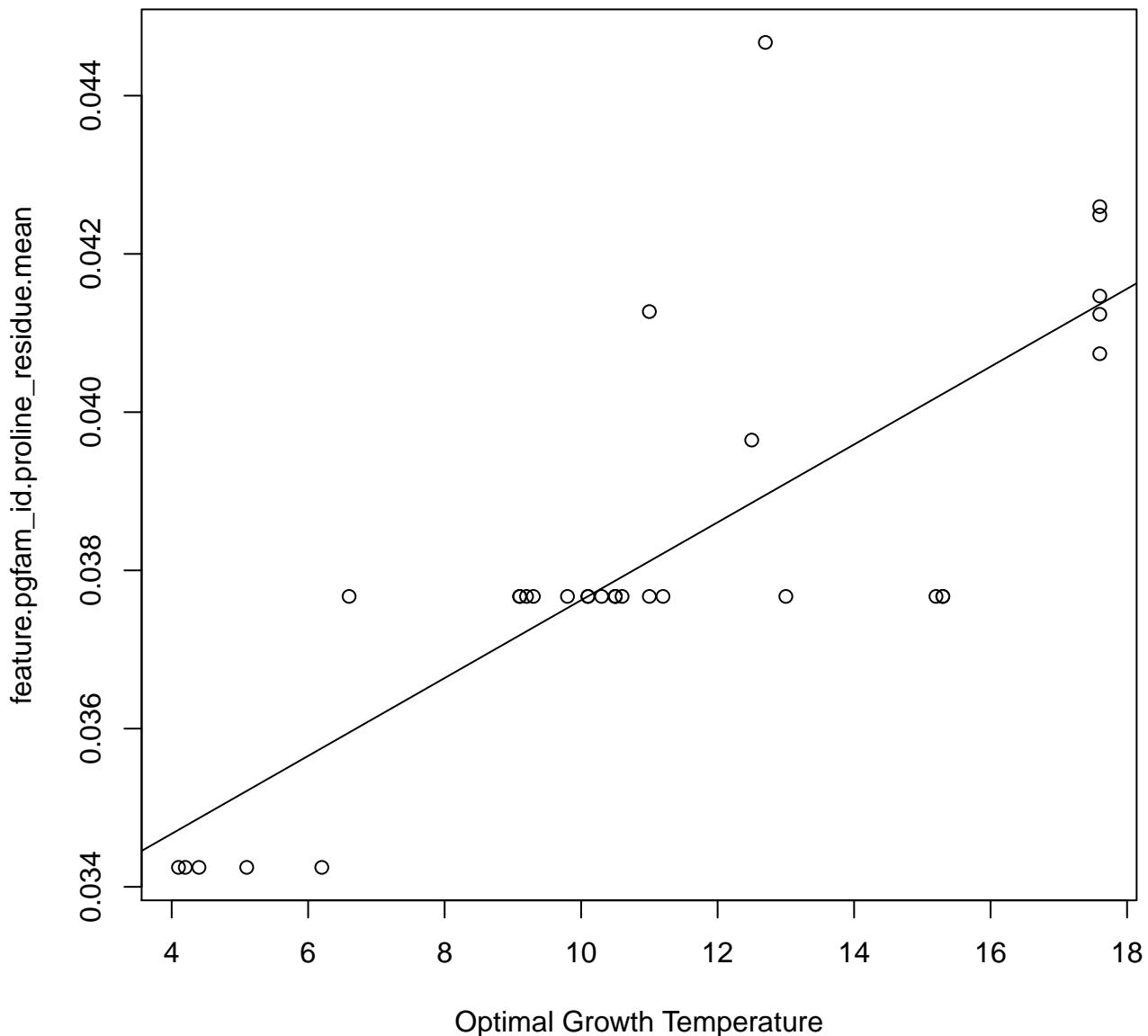
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PGF_11915740
hypothetical protein



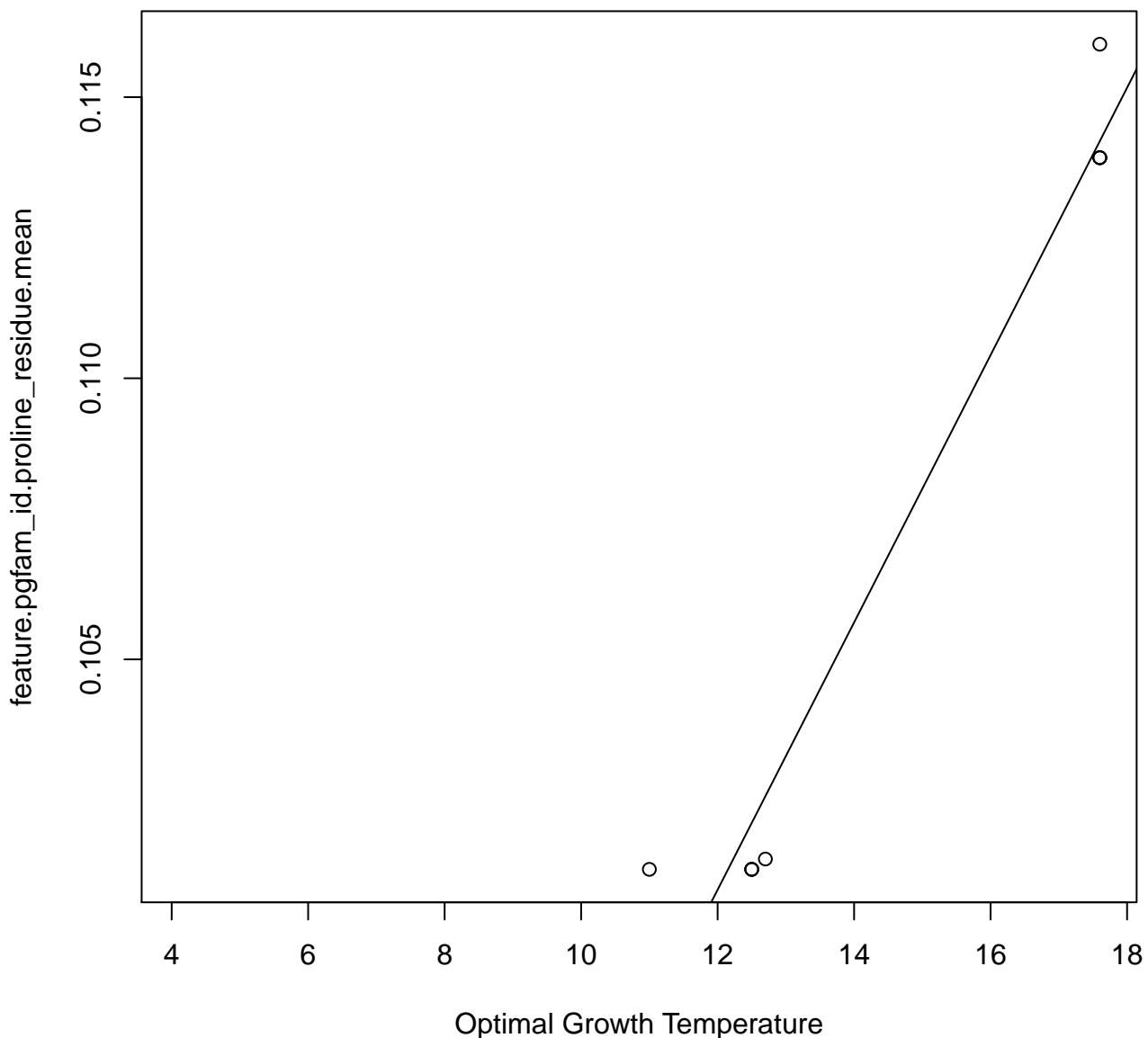
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hypothetical protein



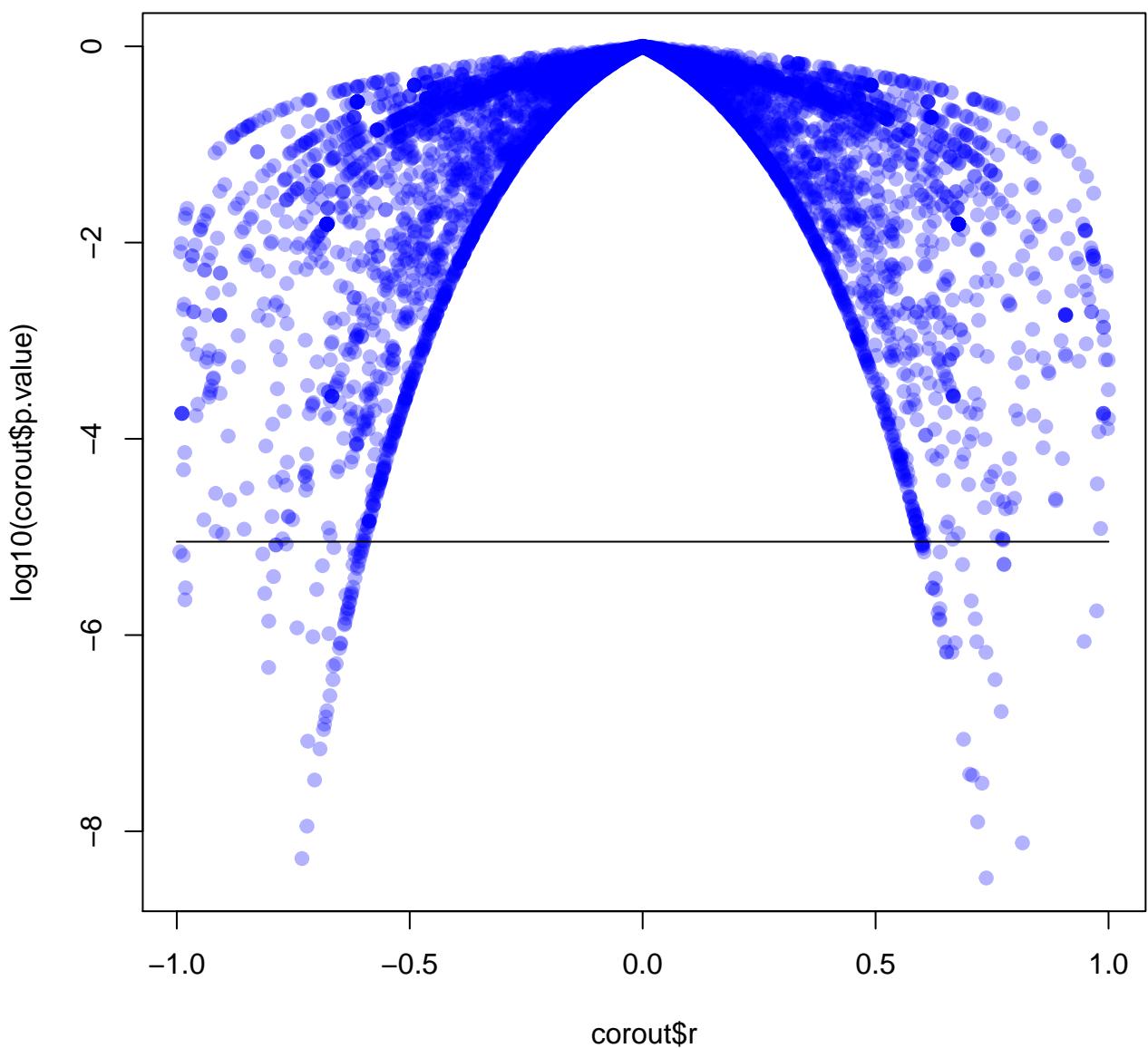
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PGF_00065716
Uncharacterized protein conserved in bacteria, NMA0228-like



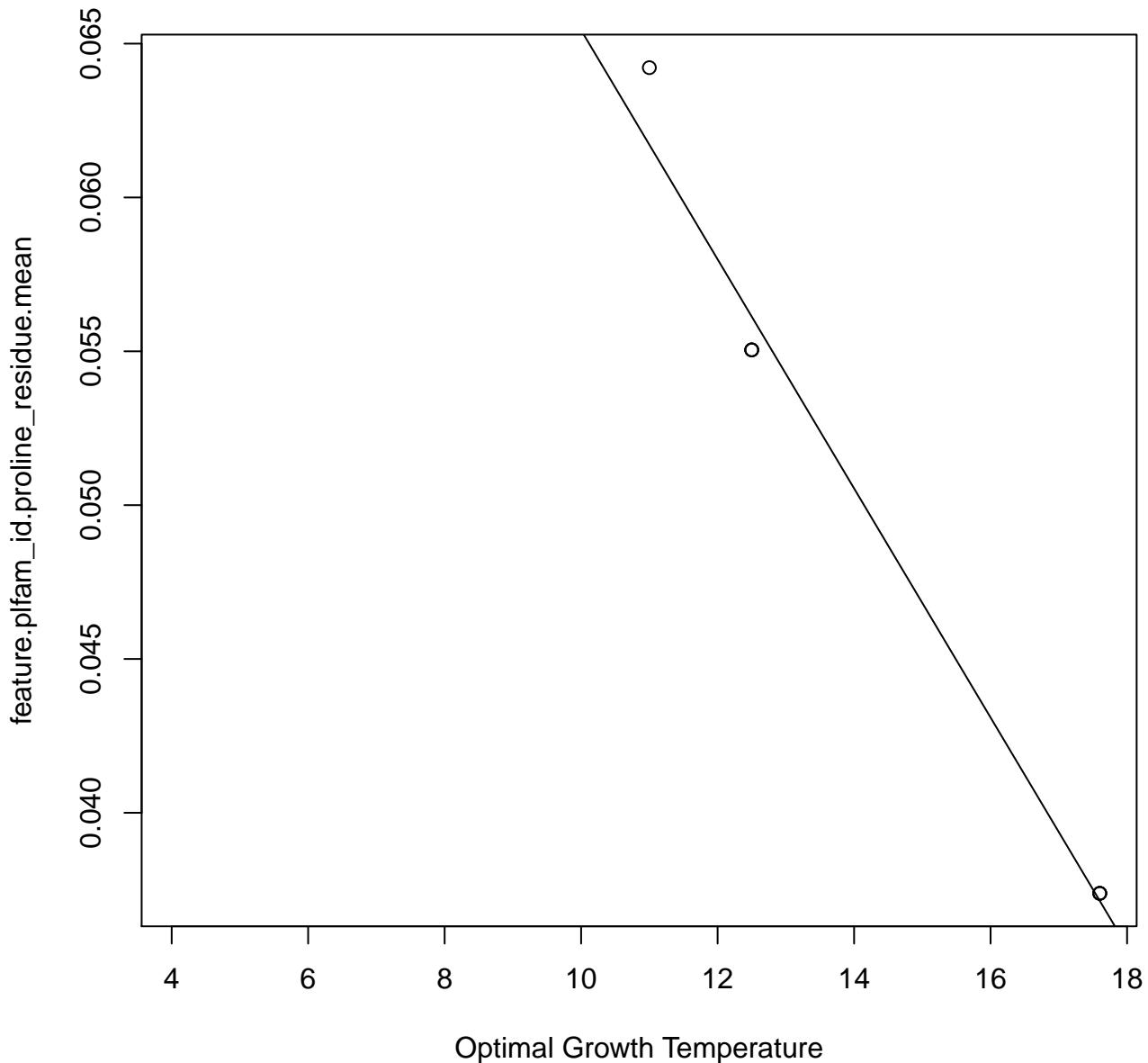
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PGF_01336823
hypothetical protein



feature.plfam_id.proline_residue.mean



feature.plfam_id.proline_residue.mean
PLF_28228_00003280
FIG016502: iron uptake protein

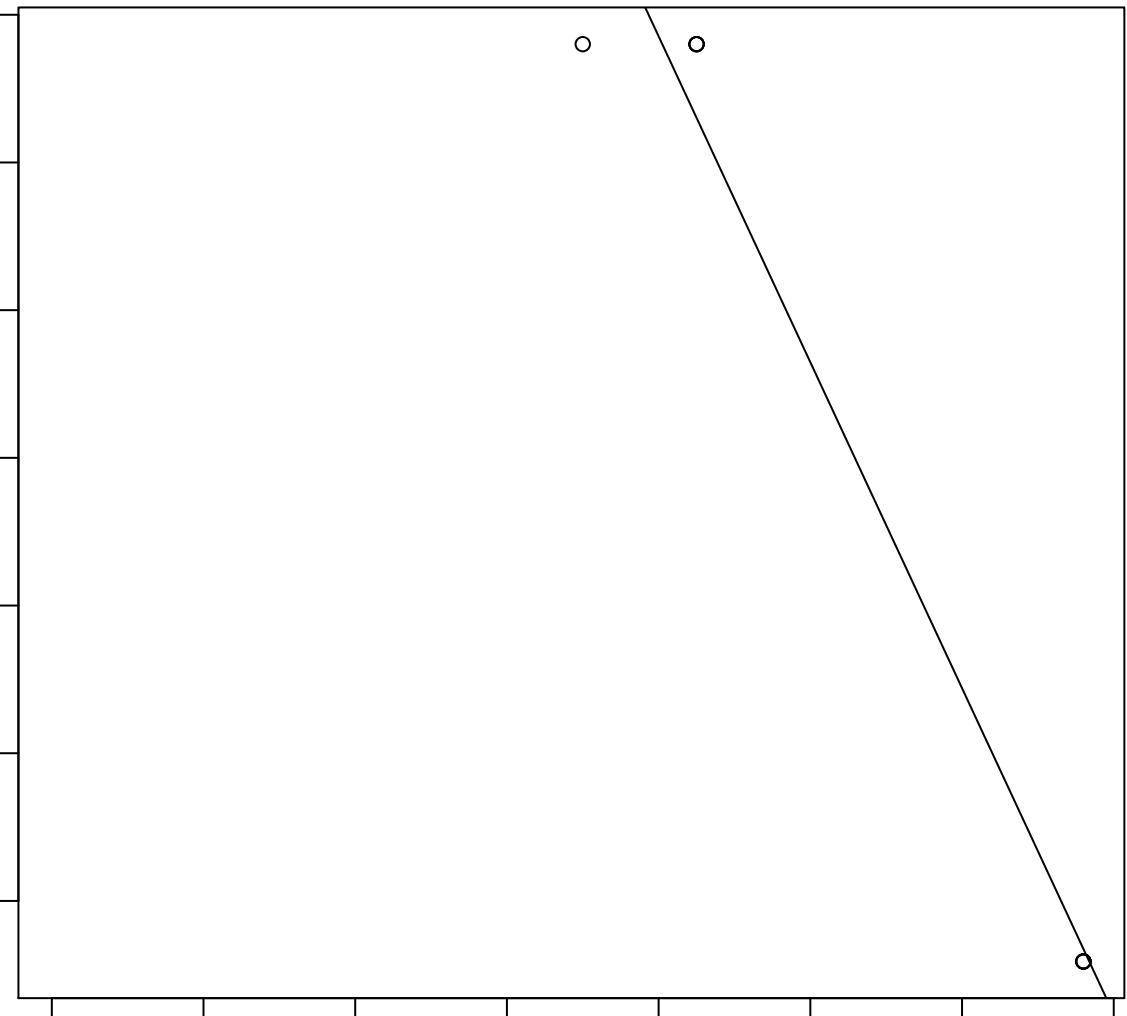


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Permease of the drug/metabolite transporter (DMT) superfamily

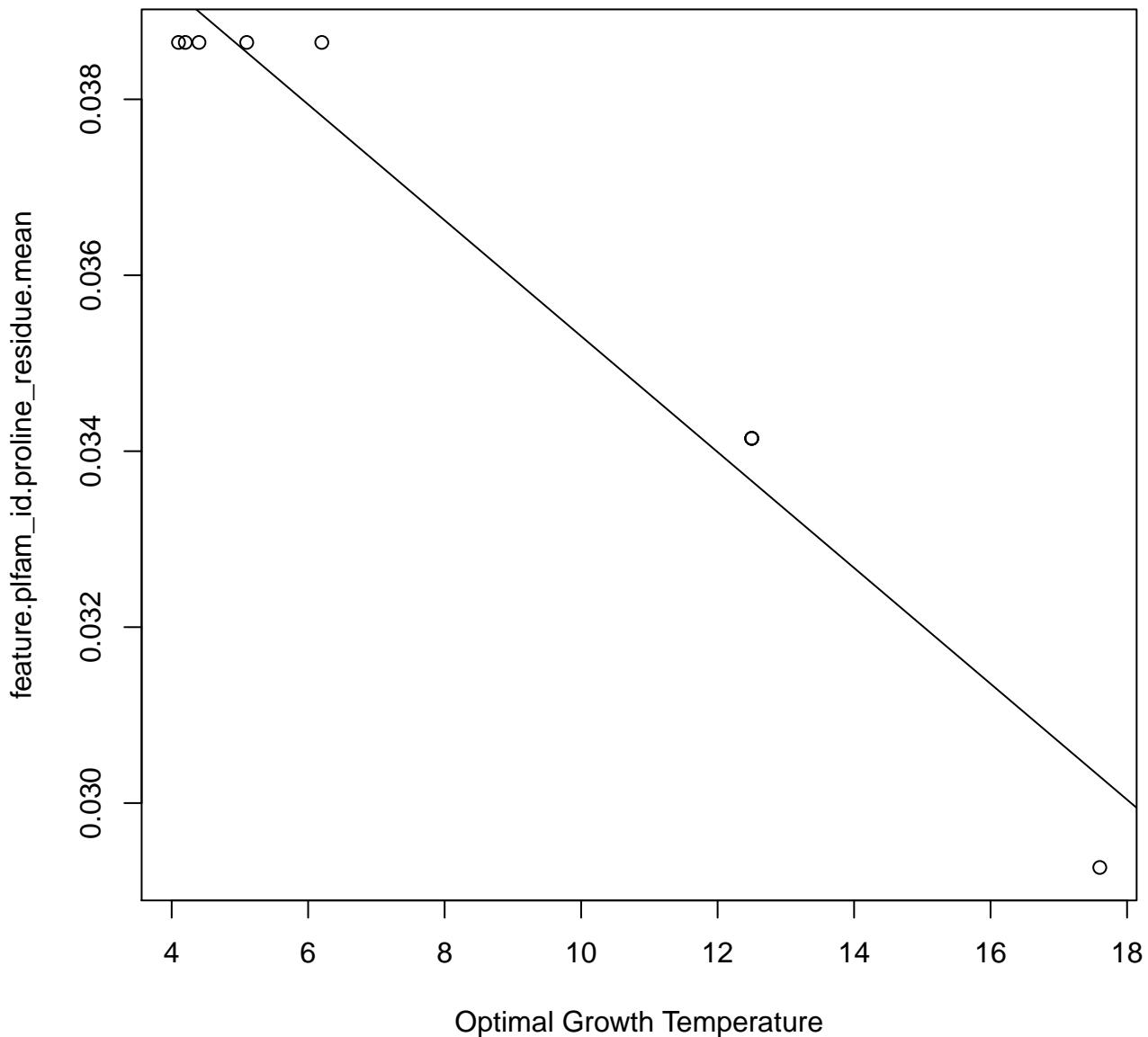
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4 6 8 10 12 14 16 18

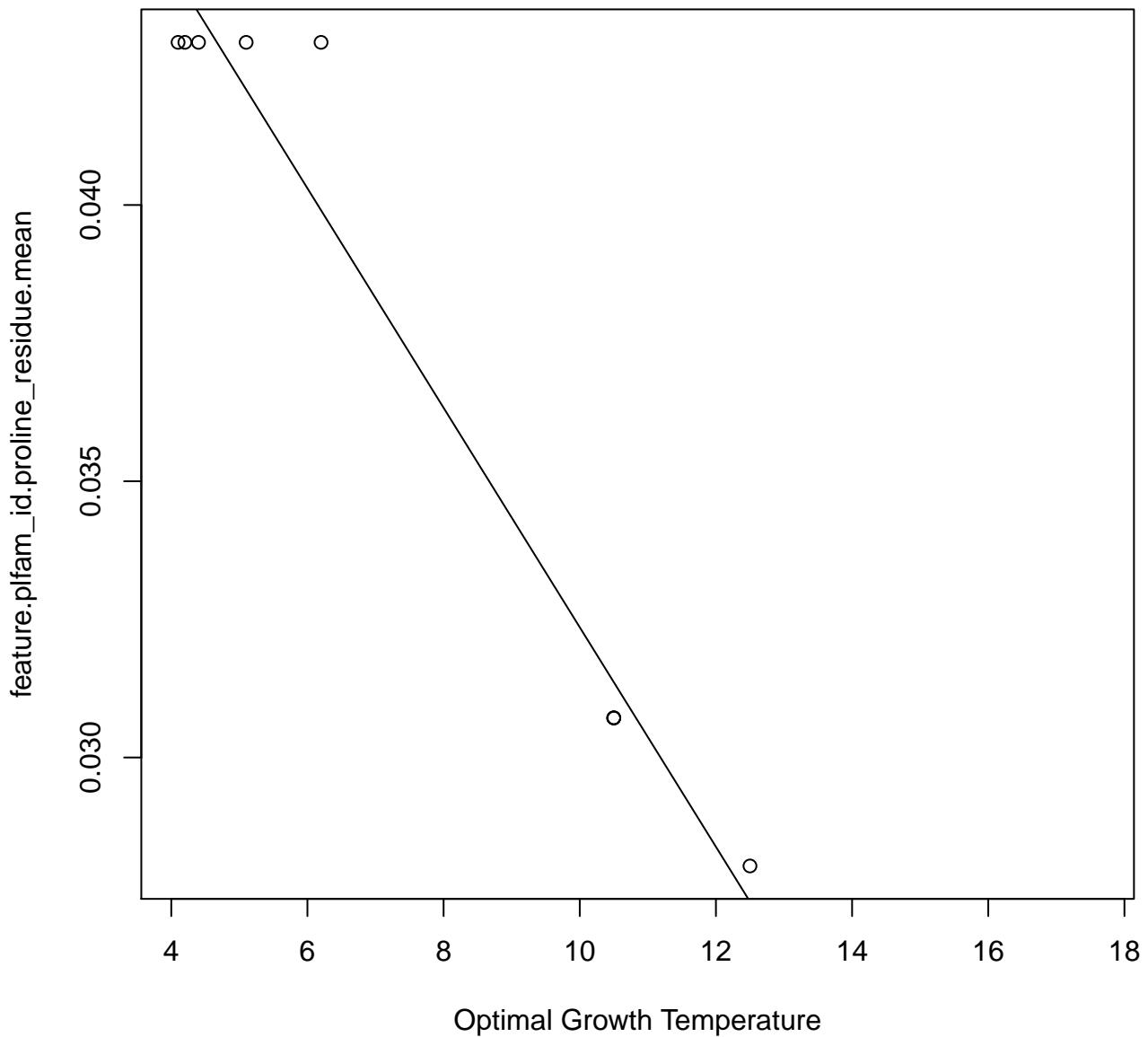
Optimal Growth Temperature



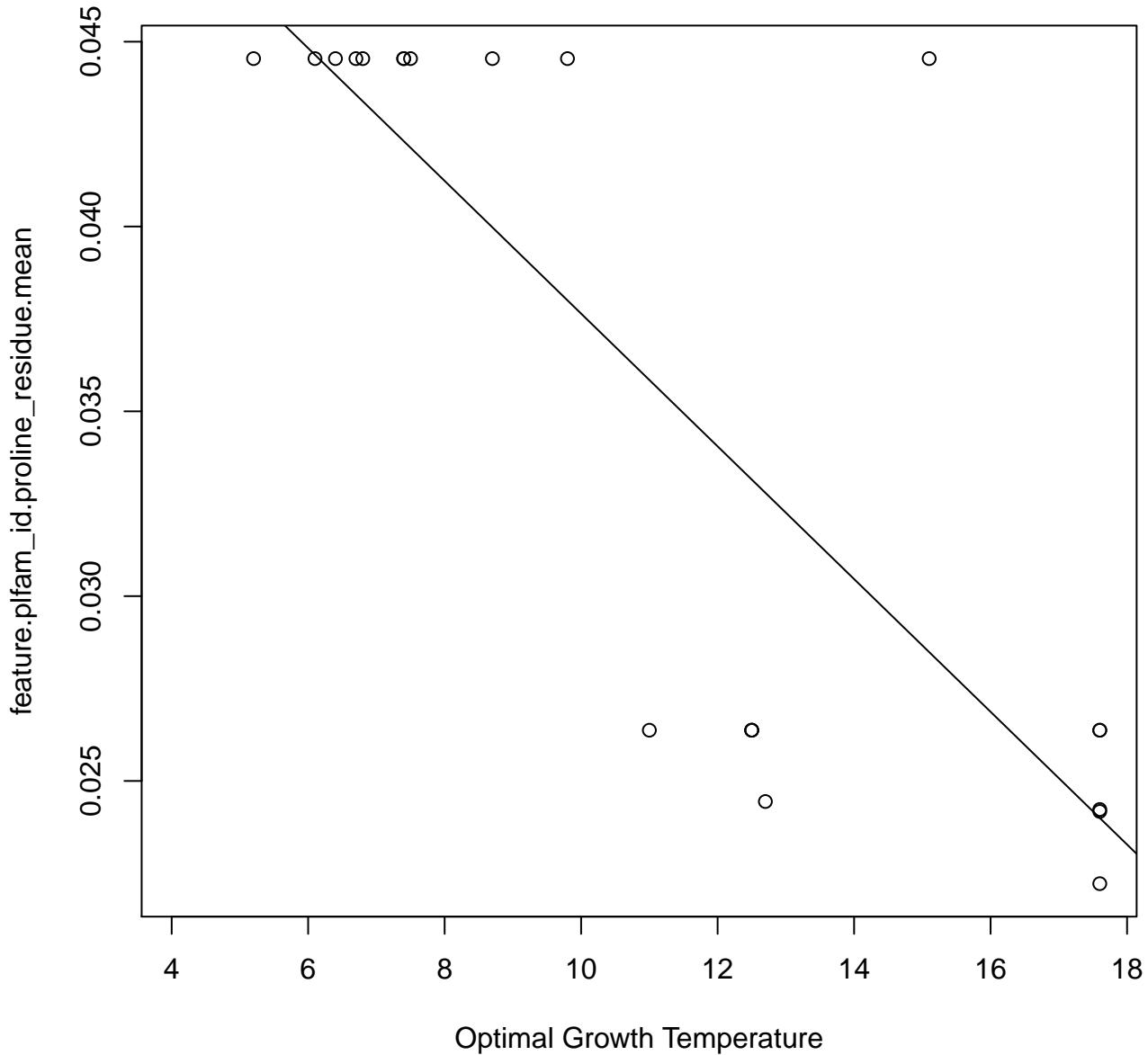
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hypothetical protein



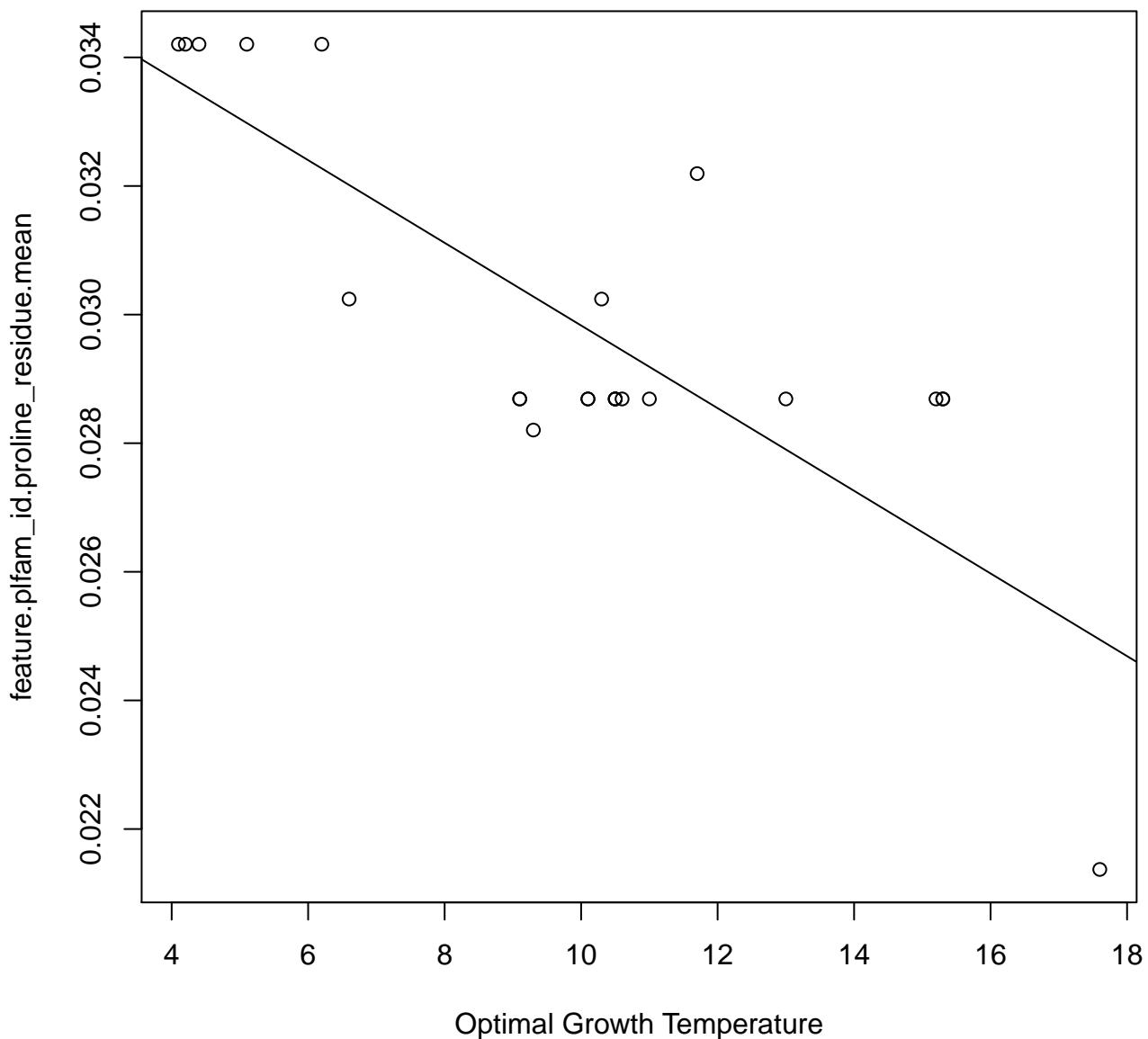
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Mobile element protein



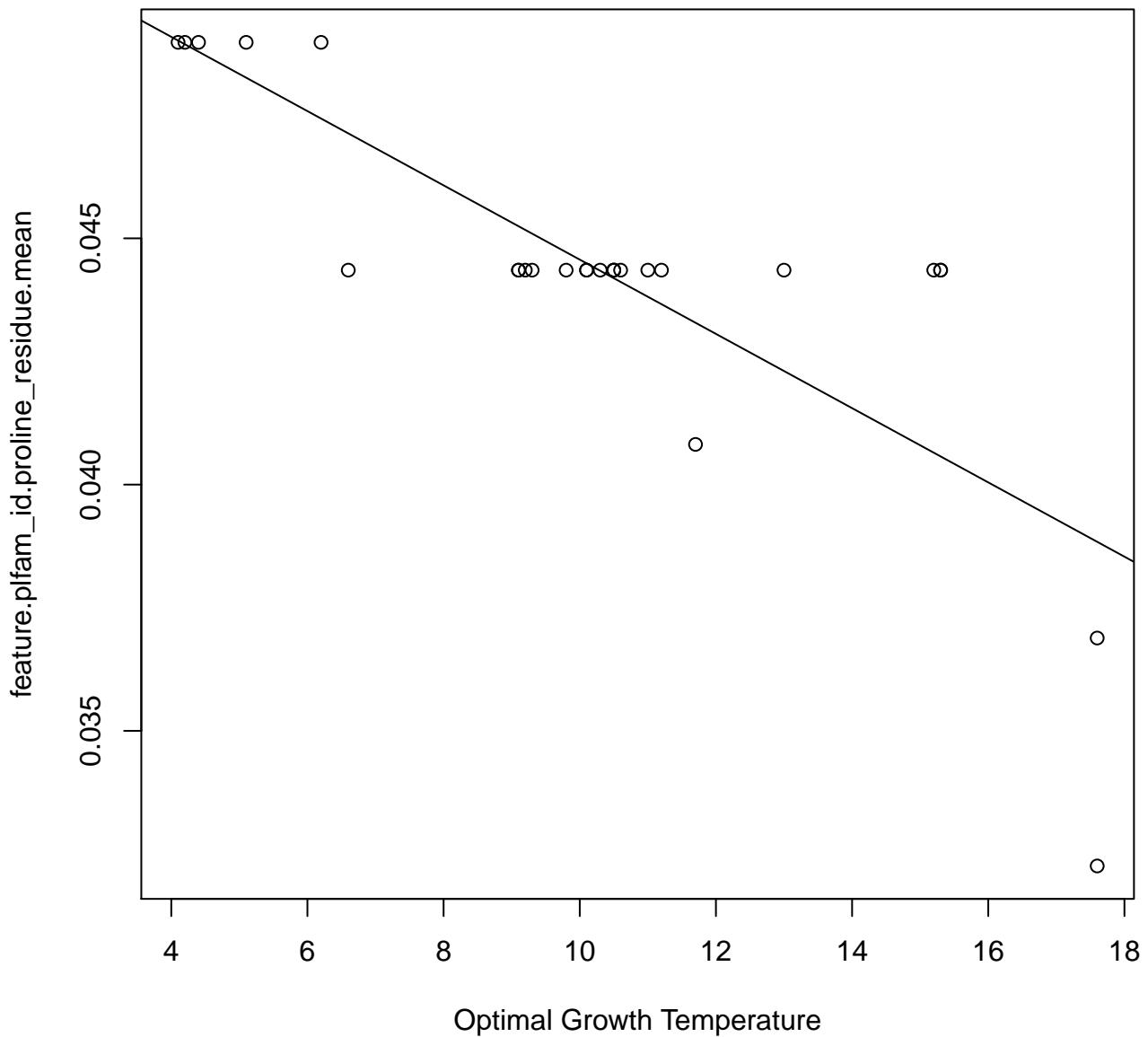
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ATP-dependent RNA helicase SO1501



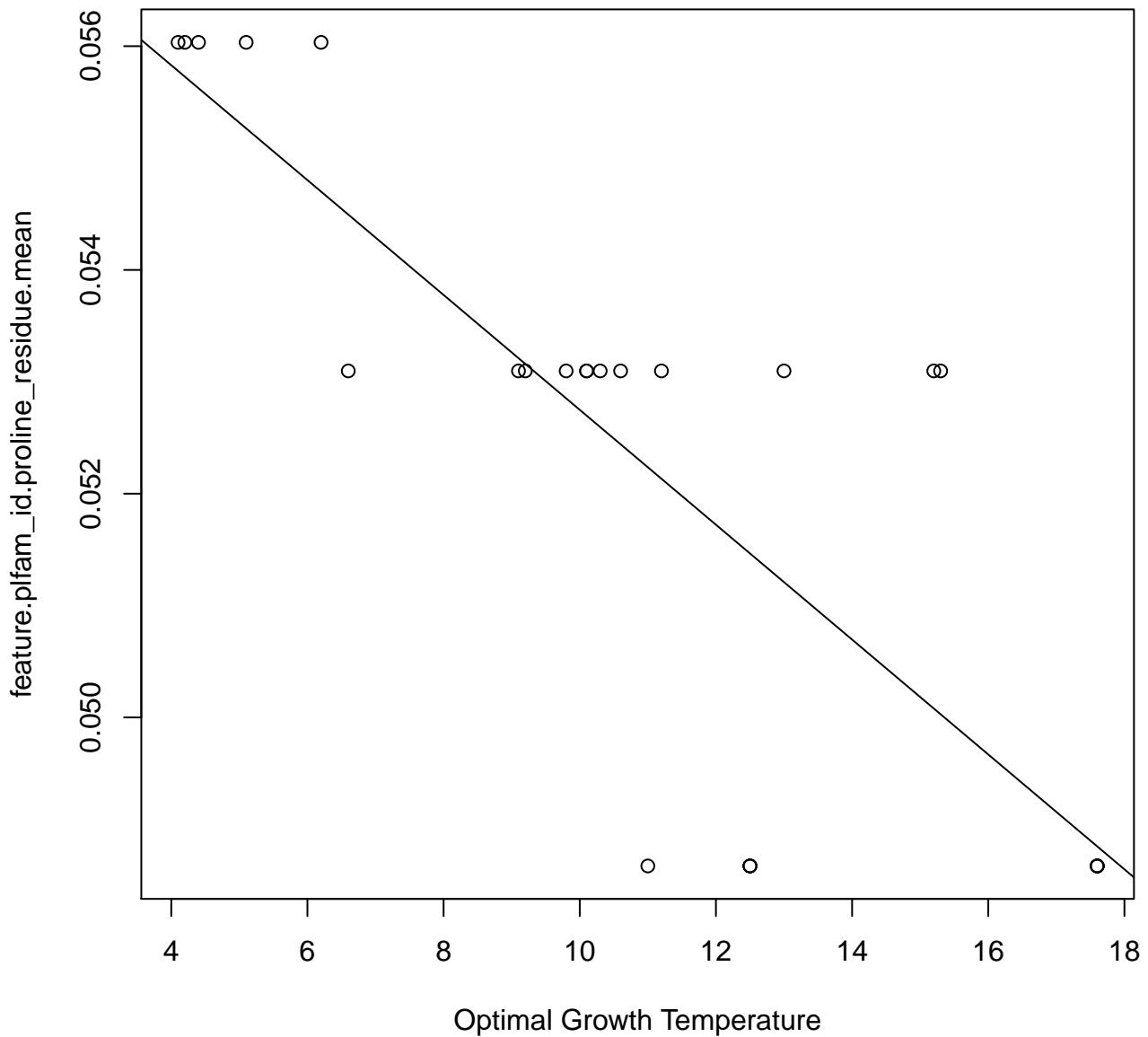
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PLF_28228_00003566
hypothetical protein



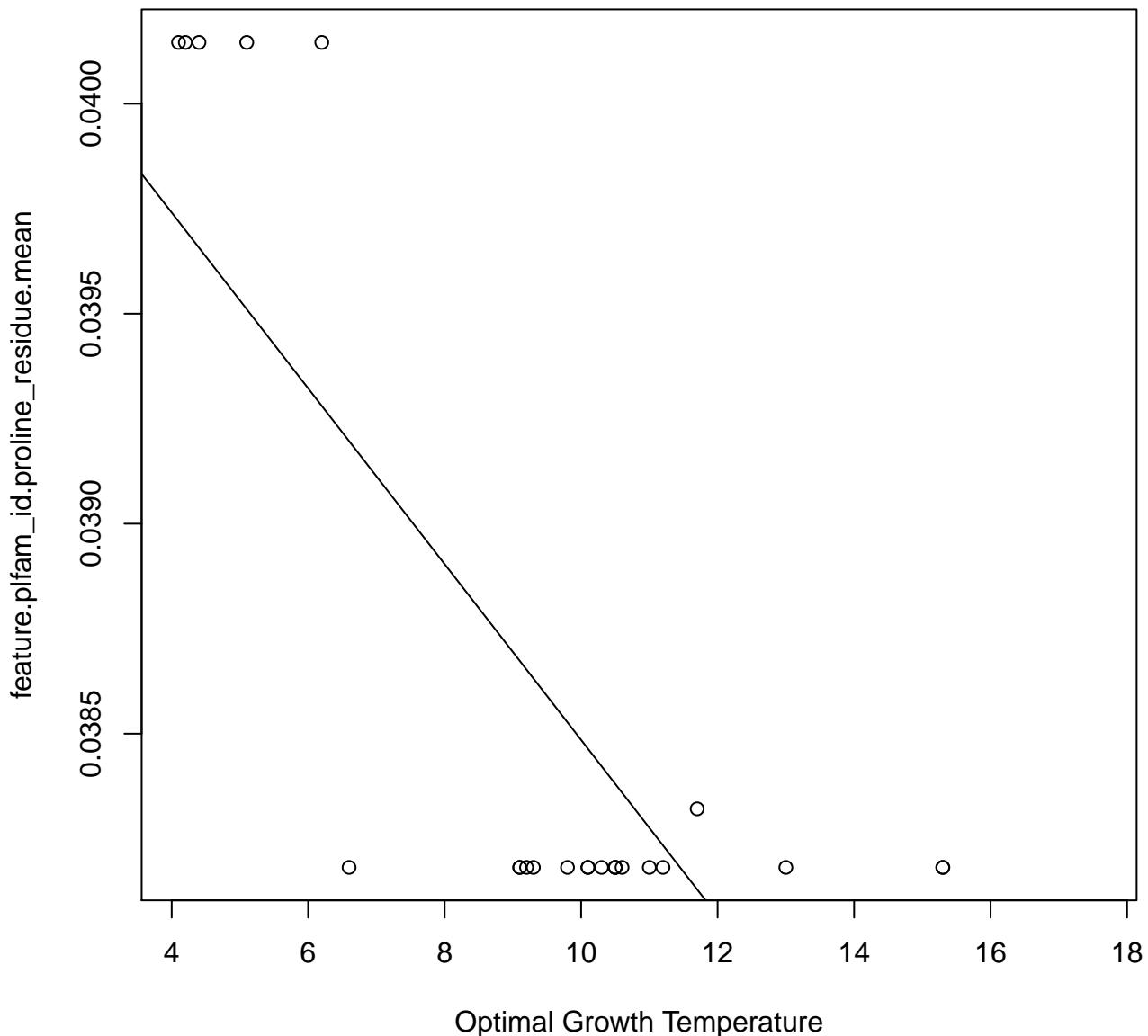
feature.plfam_id.proline_residue.mean
PLF_28228_00003488
Oxidoreductase, short-chain dehydrogenase/reductase family



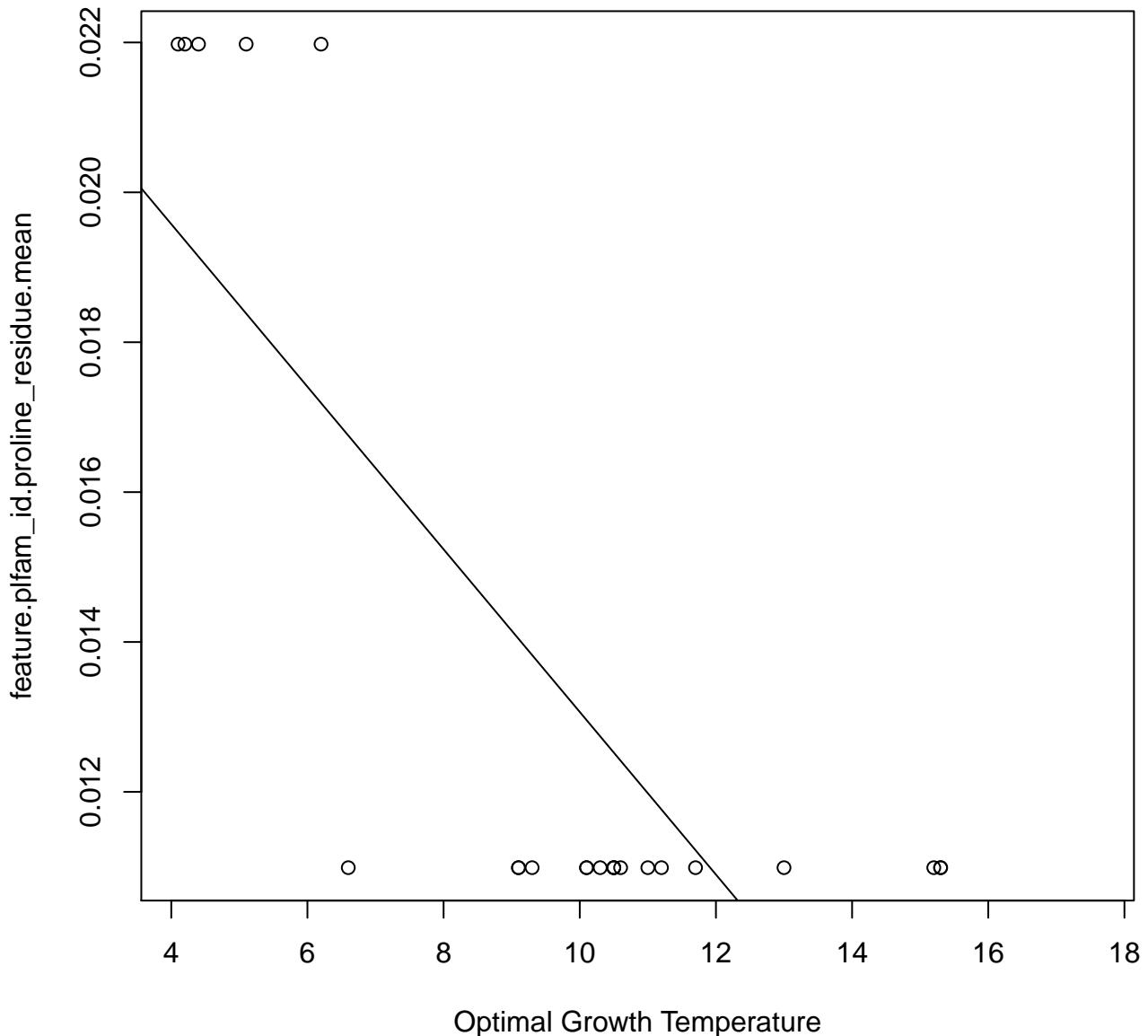
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Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)



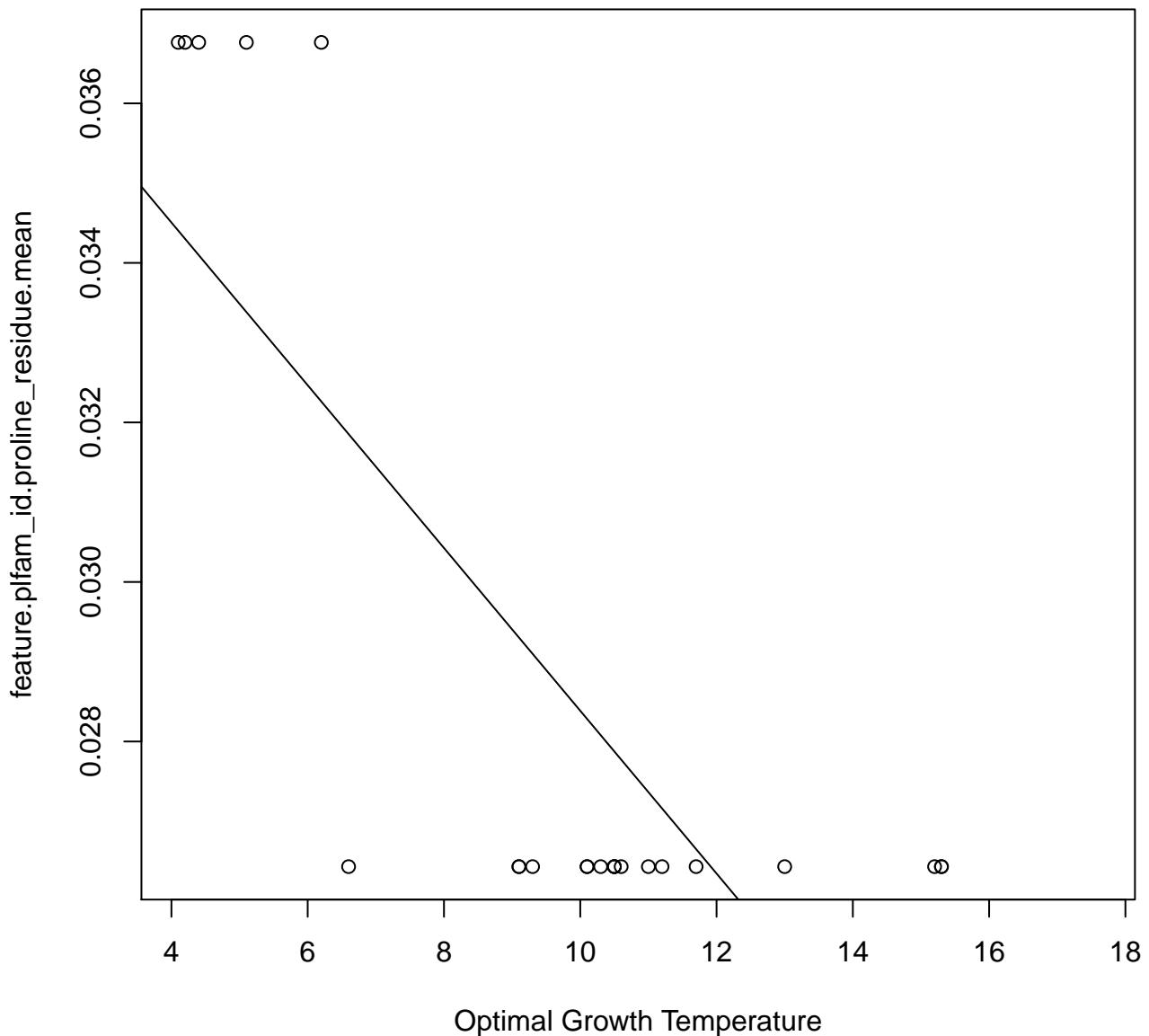
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PLF_28228_00028712
Glucose-6-phosphate isomerase (EC 5.3.1.9)



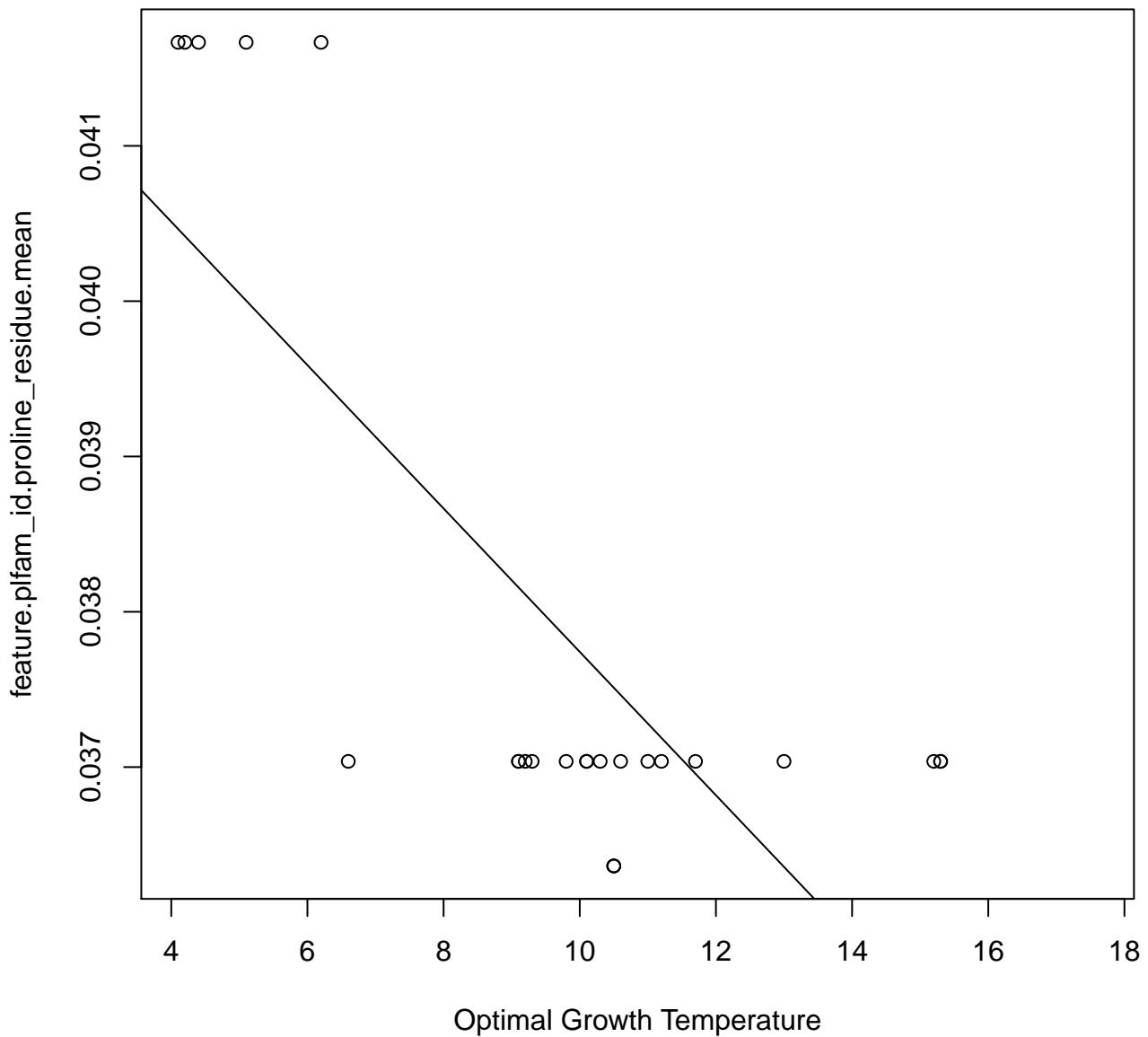
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hypothetical protein



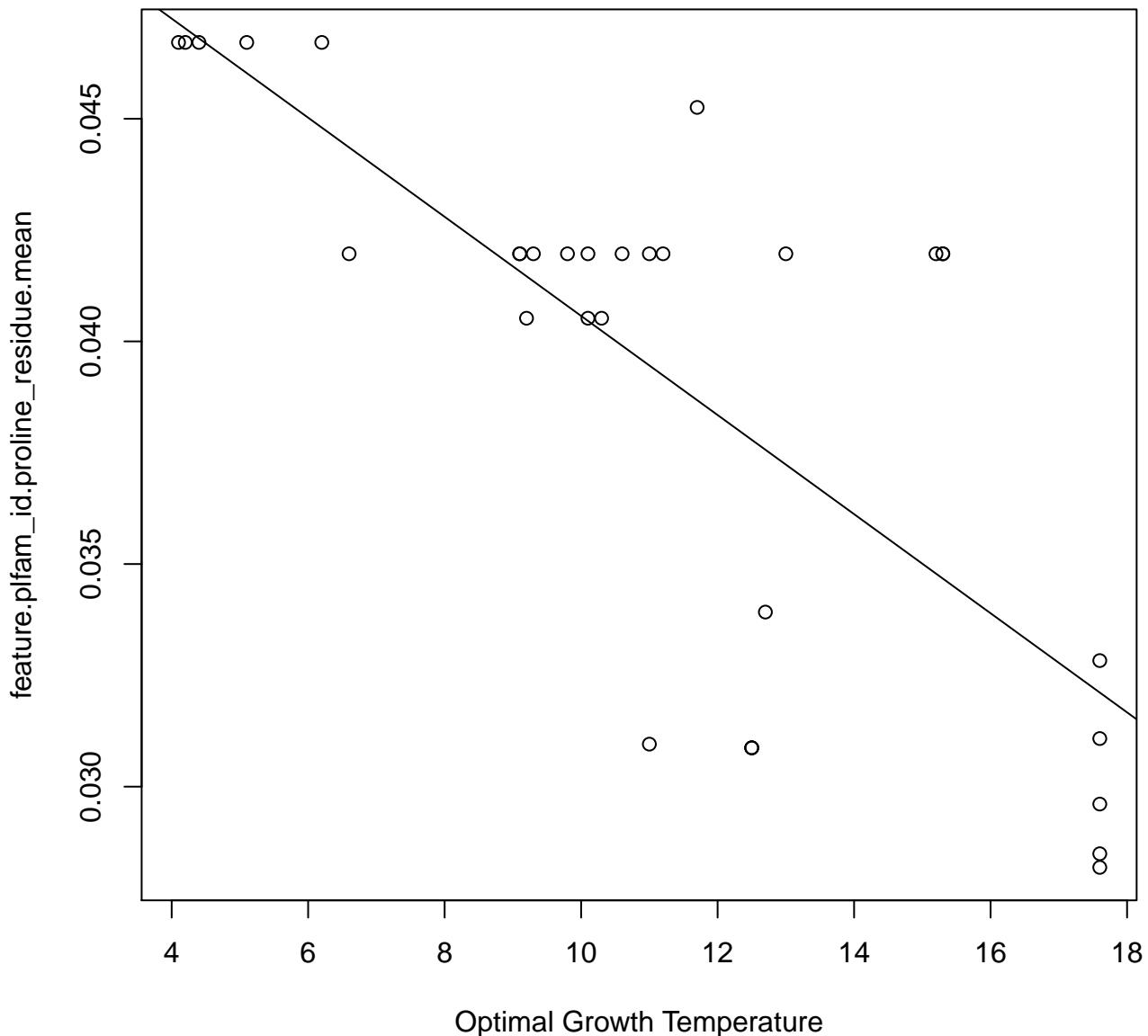
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hypothetical protein



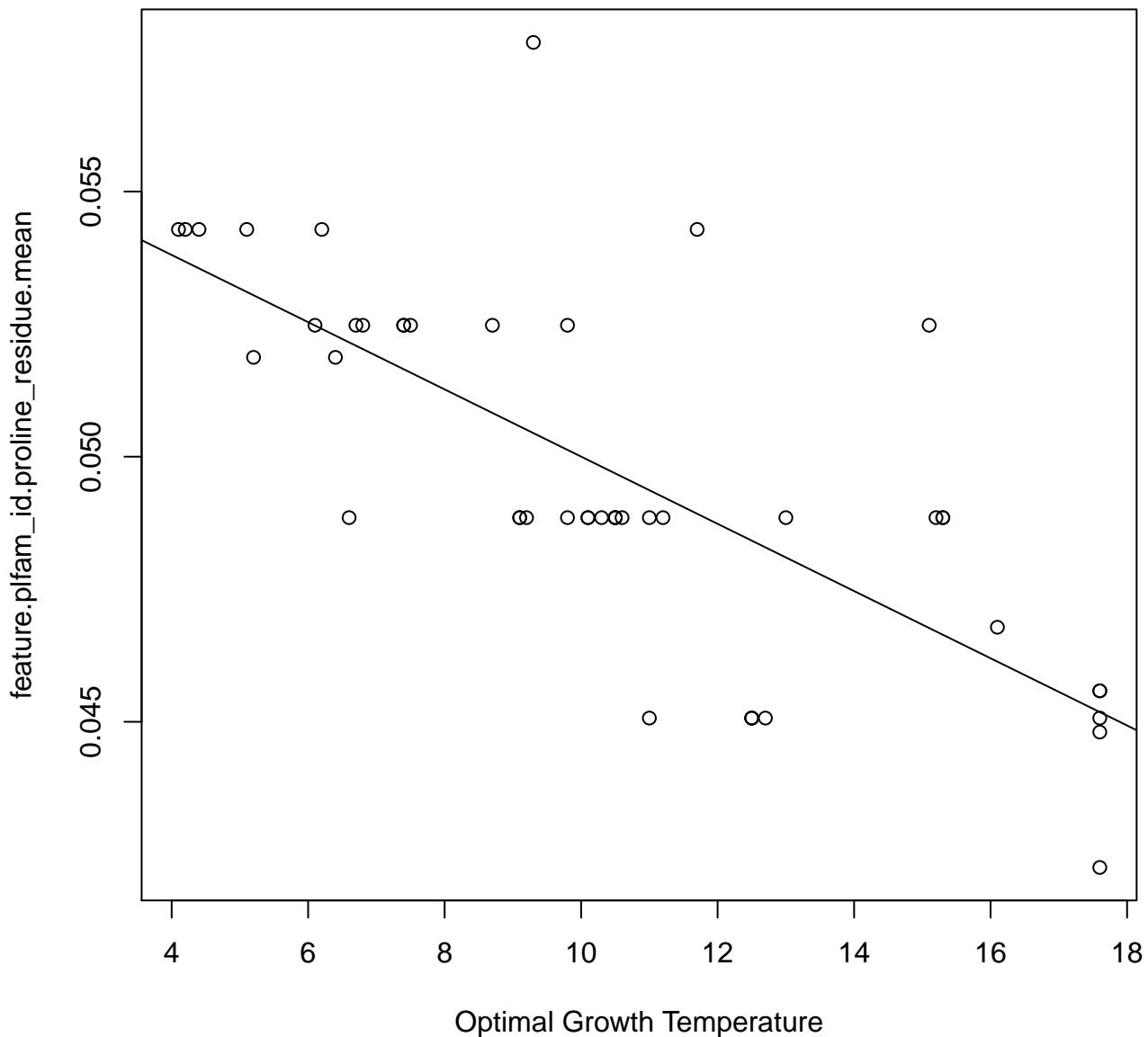
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PLF_28228_00031893
hypothetical protein



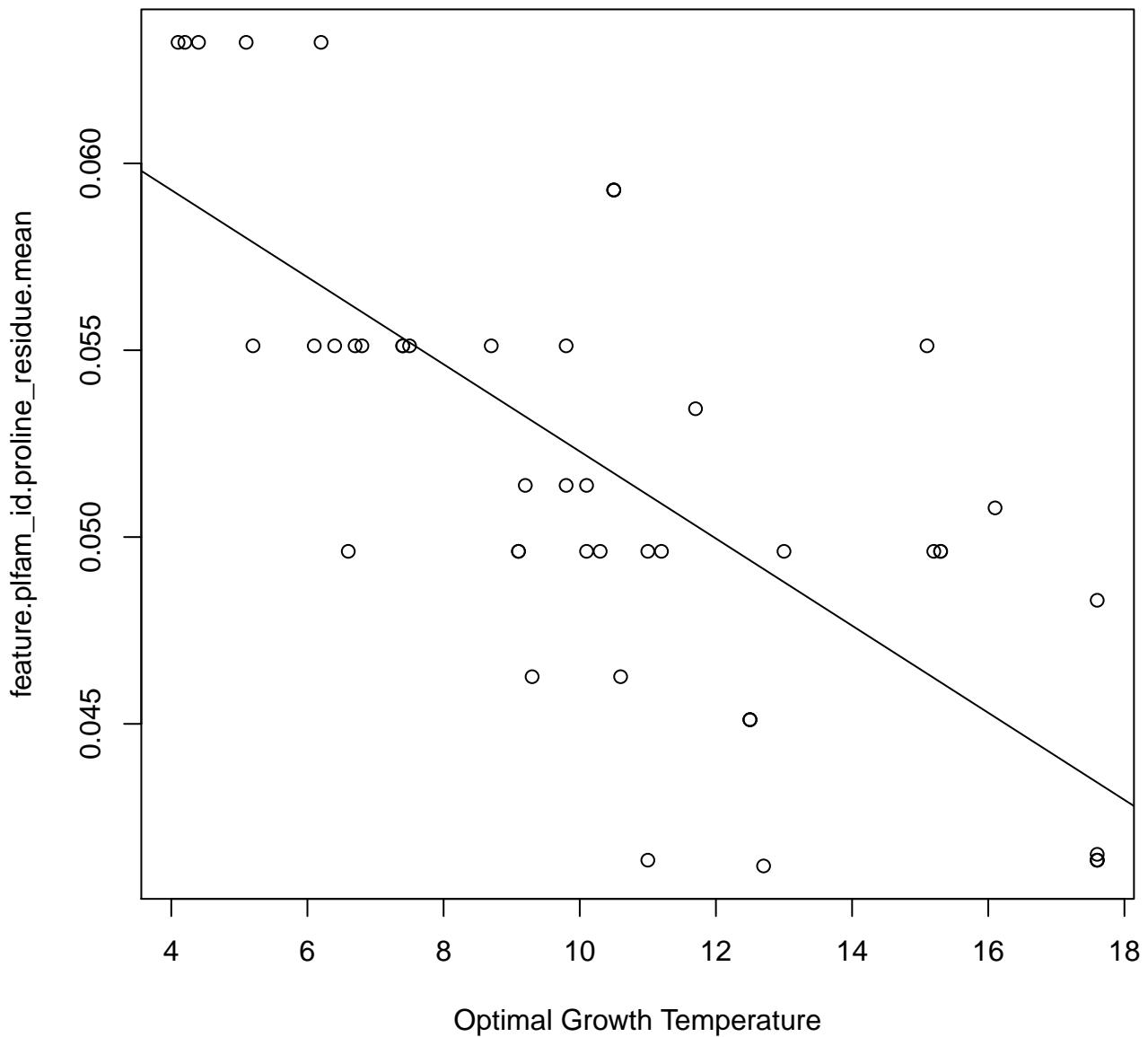
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FIG001454: Transglutaminase-like enzymes, putative cysteine proteases



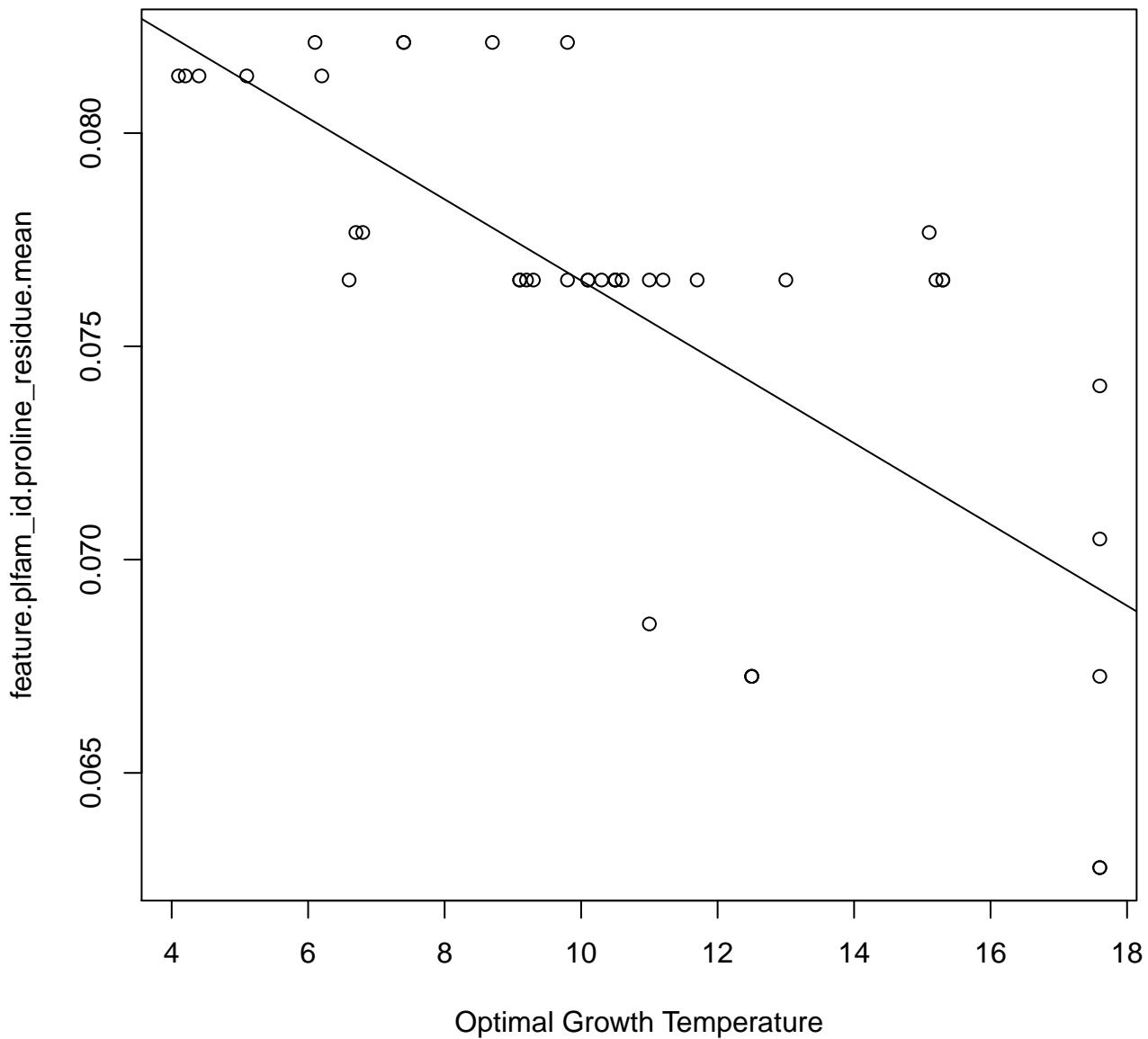
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Dihydroorotate (EC 3.5.2.3)



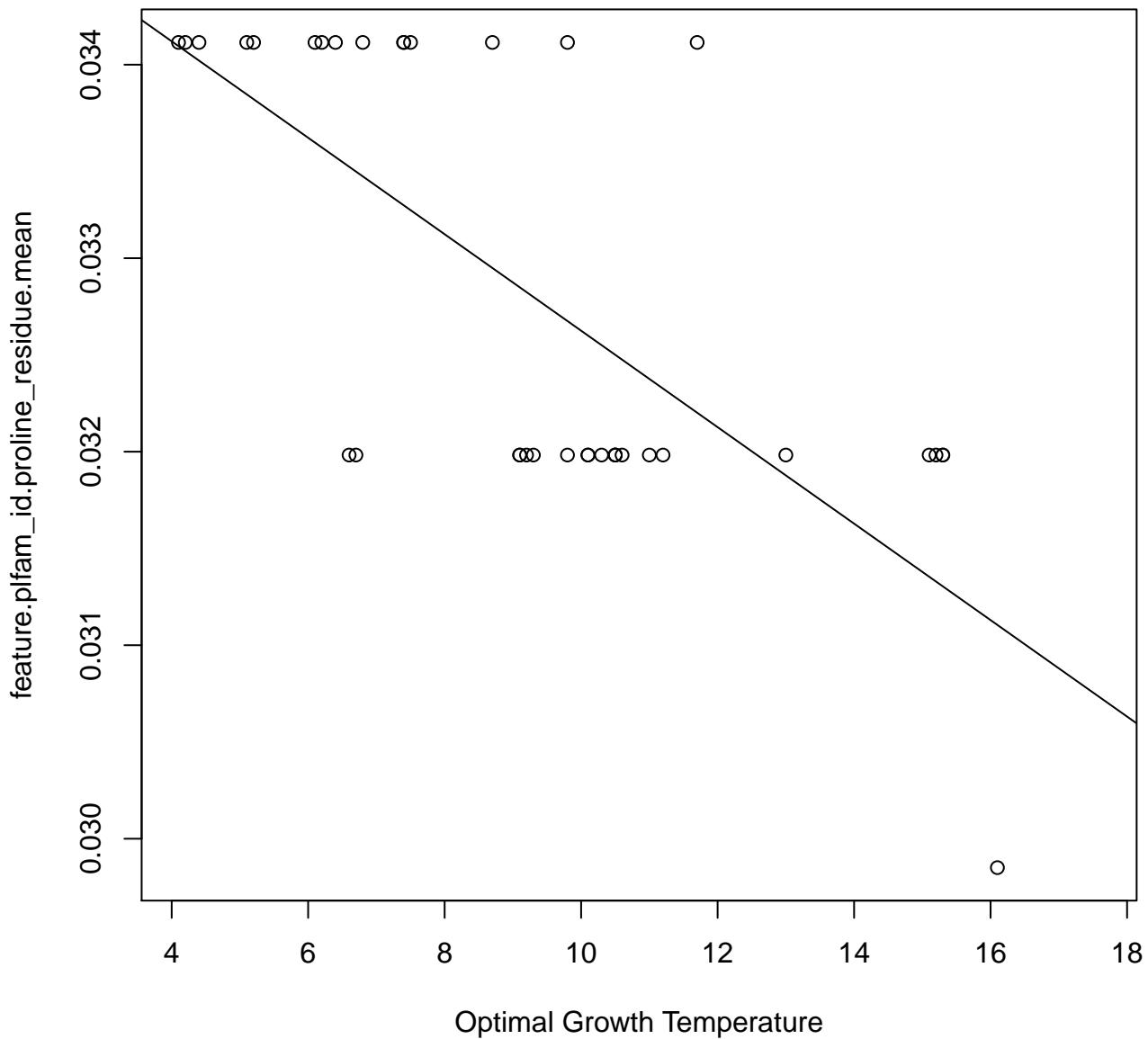
feature.plfam_id.proline_residue.mean
PLF_28228_00001825
Uncharacterized conserved protein YfiP, contains DTW domain



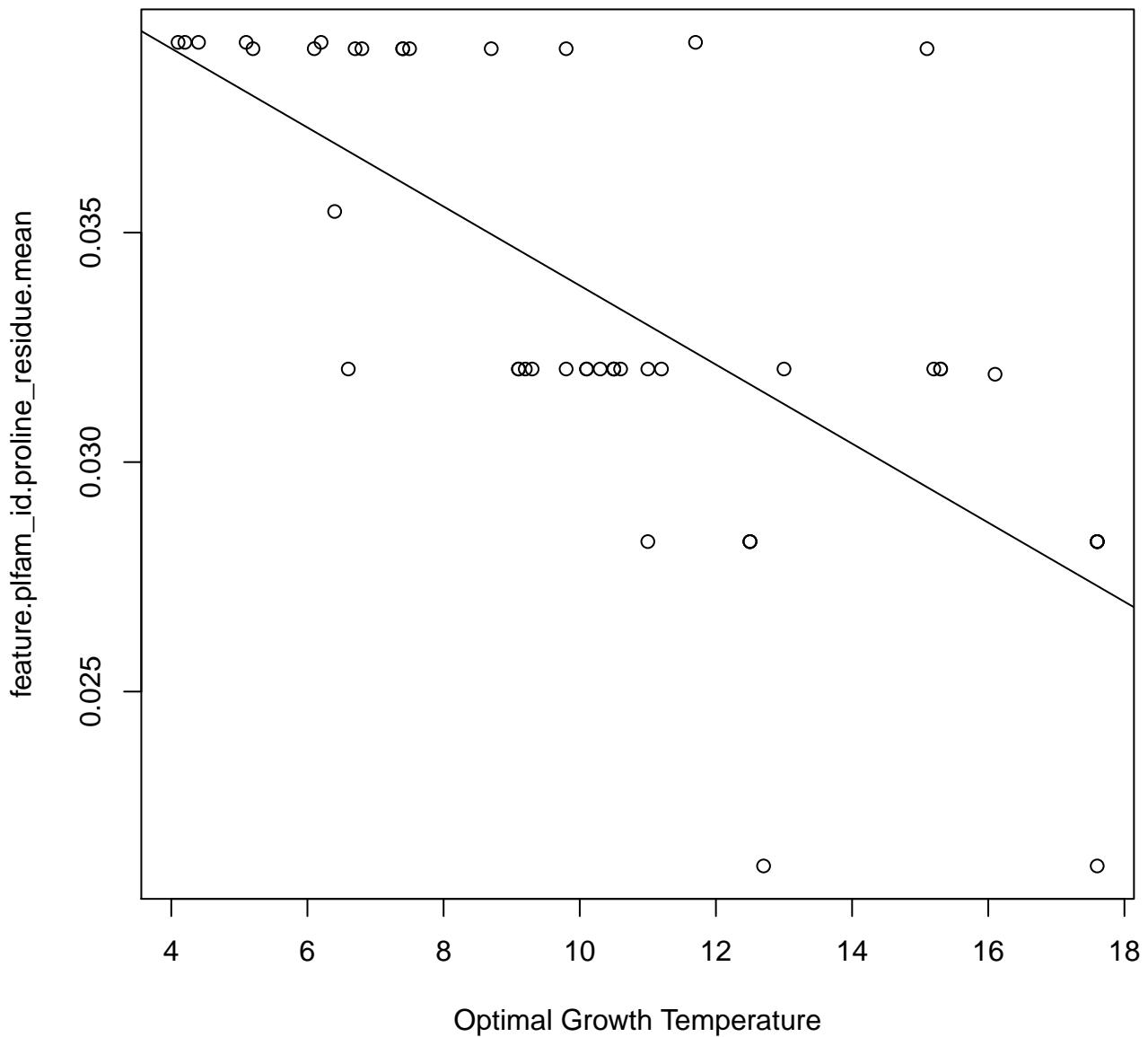
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PLF_28228_00001698
putative TonB-dependent receptor



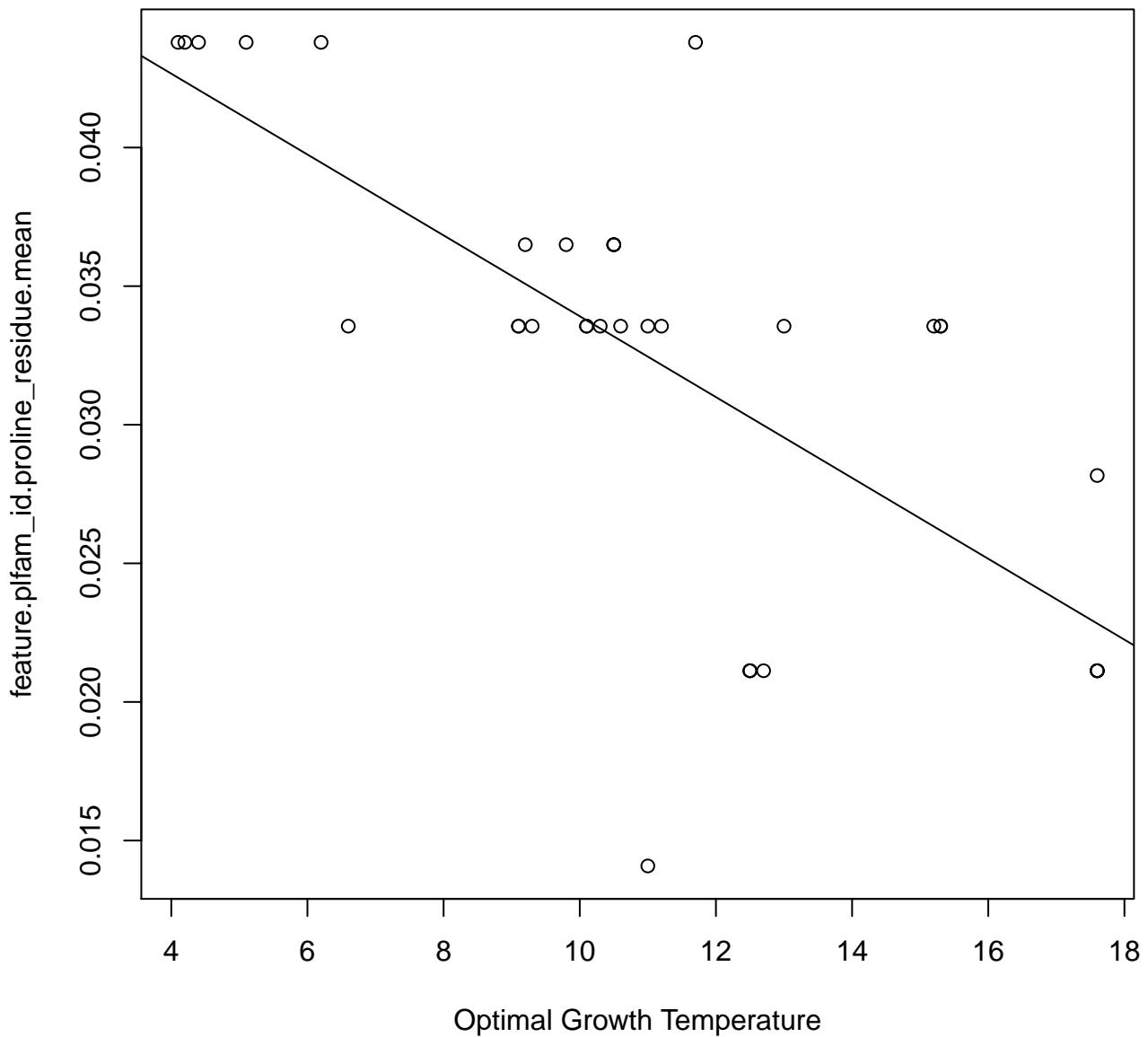
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Aminopeptidase CC_2544



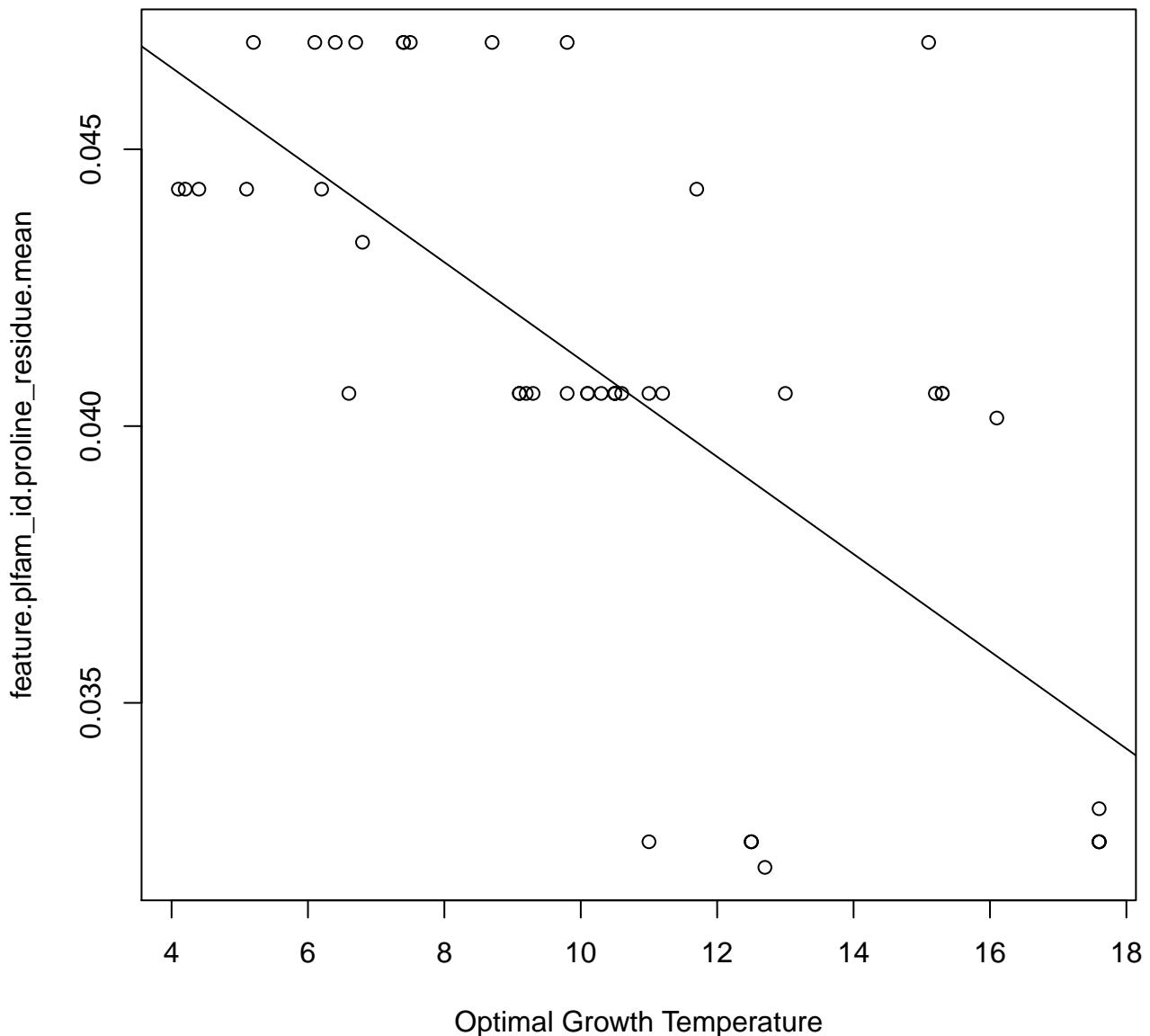
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HD domain protein



feature.plfam_id.proline_residue.mean
PLF_28228_00002482
hypothetical protein



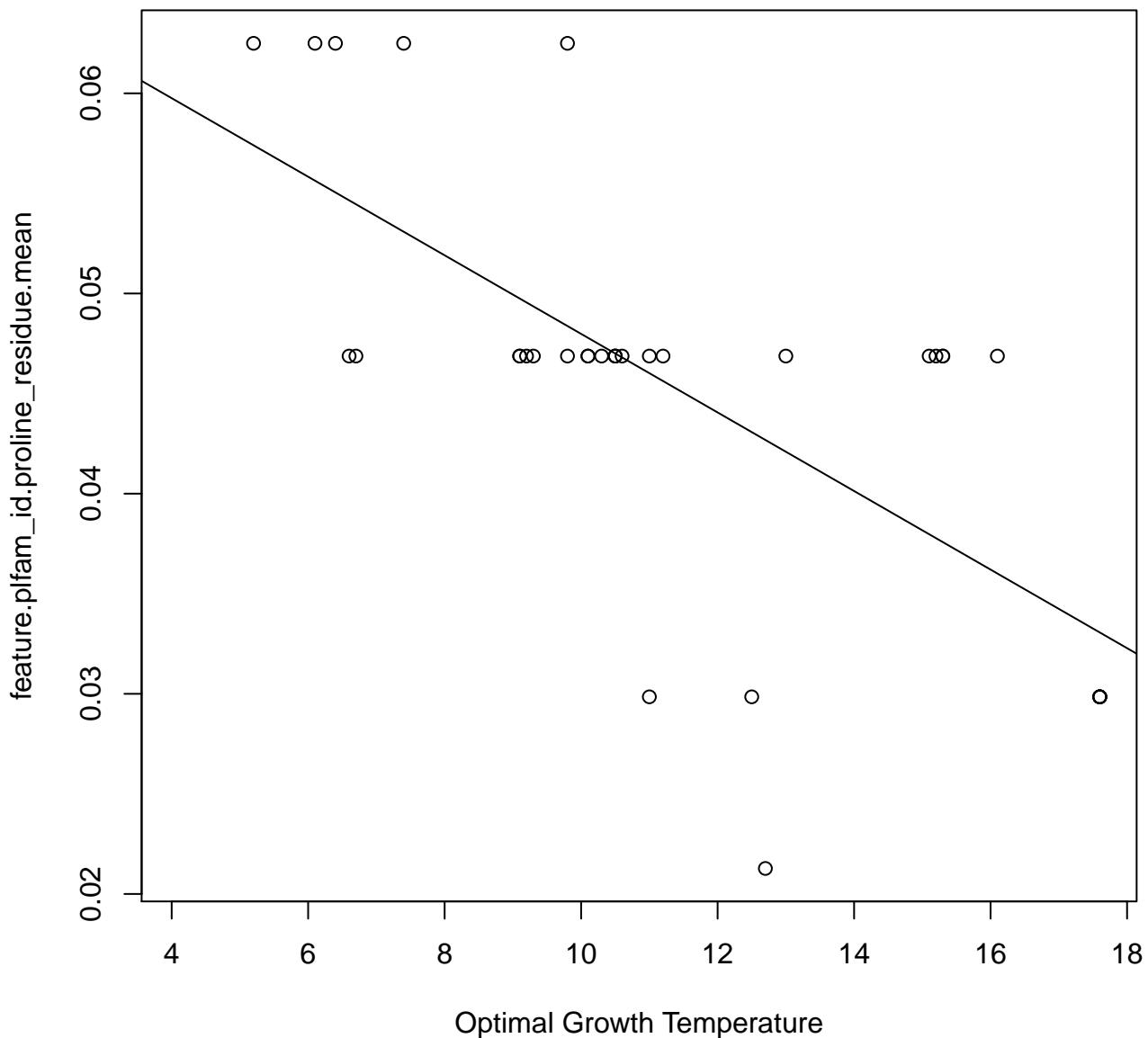
feature.plfam_id.proline_residue.mean
PLF_28228_00001074
23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)



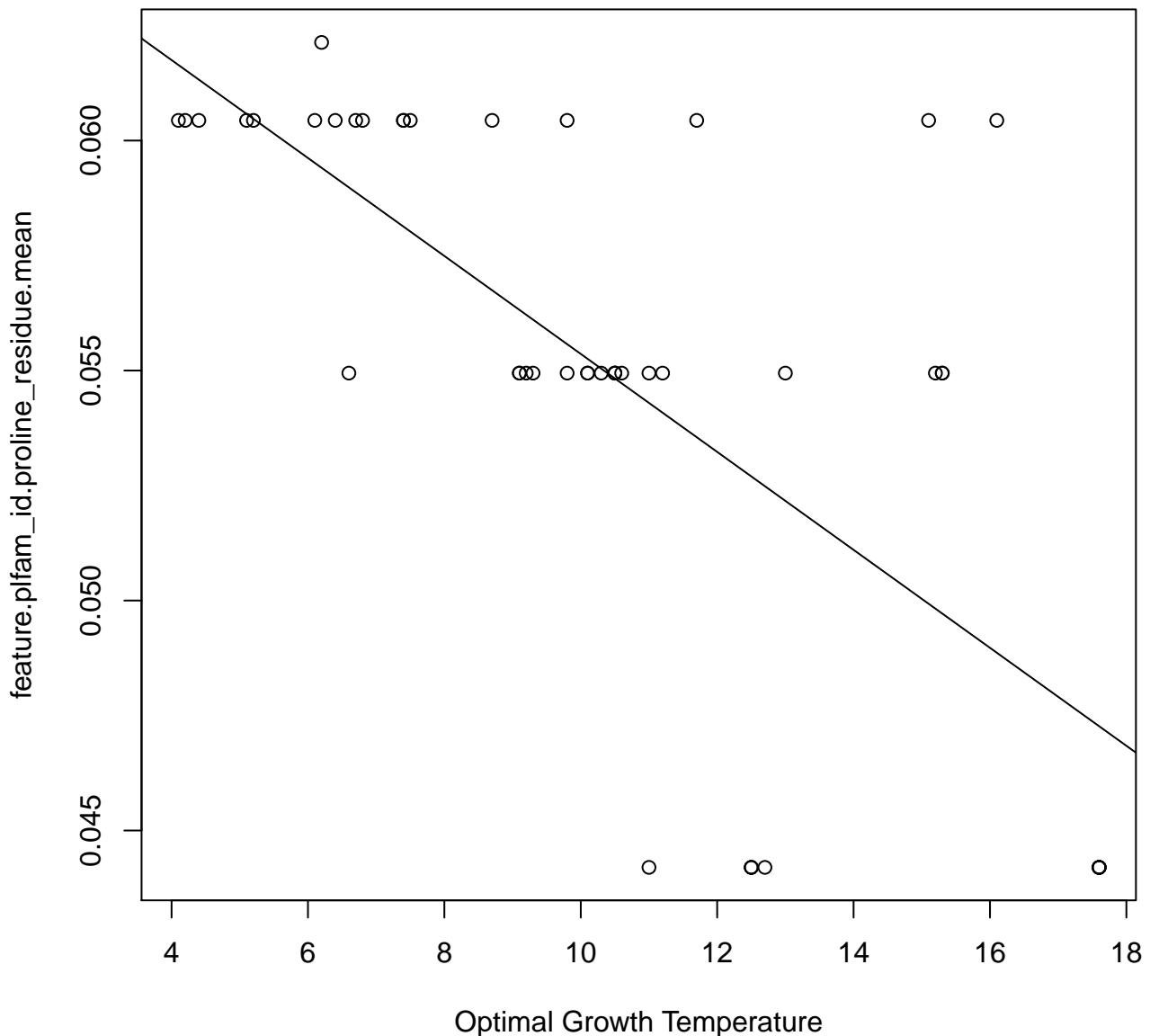
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PLF_28228_00015051

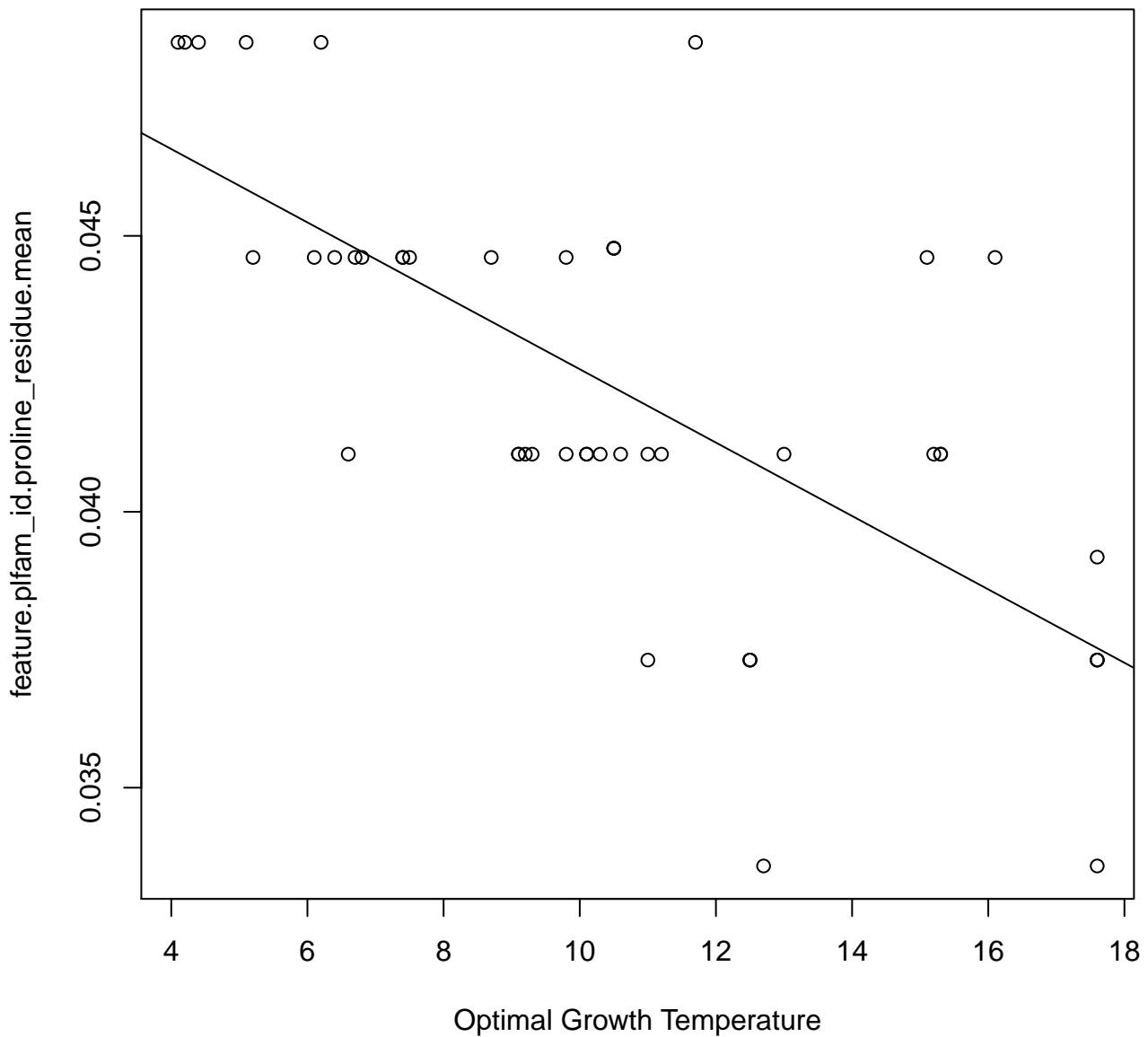
Cytoplasmic protein, probably associated with glutathione-regulated potassium-efflux



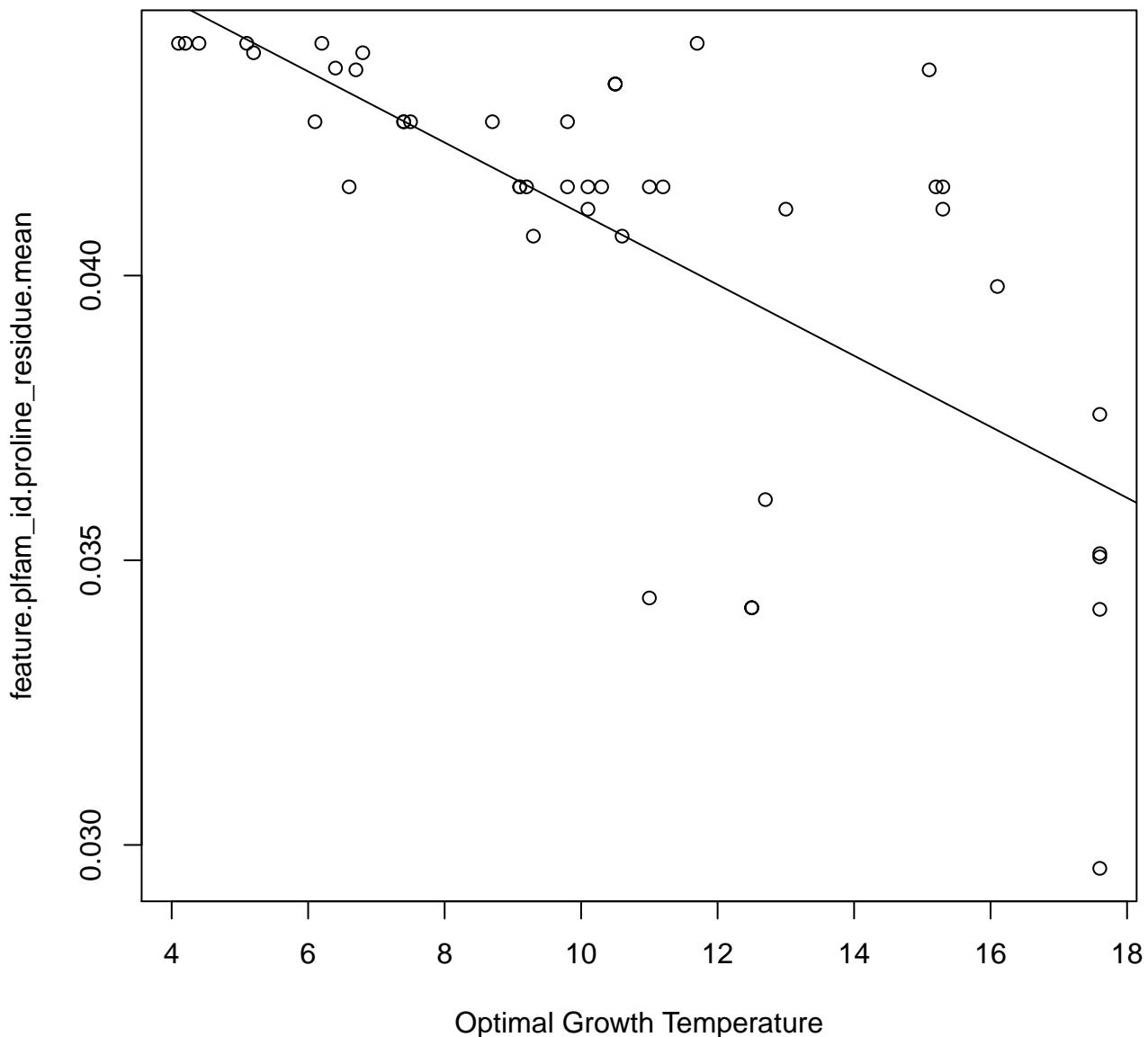
feature.plfam_id.proline_residue.mean
PLF_28228_00001678
Cell division integral membrane protein, YggT and half-length relatives



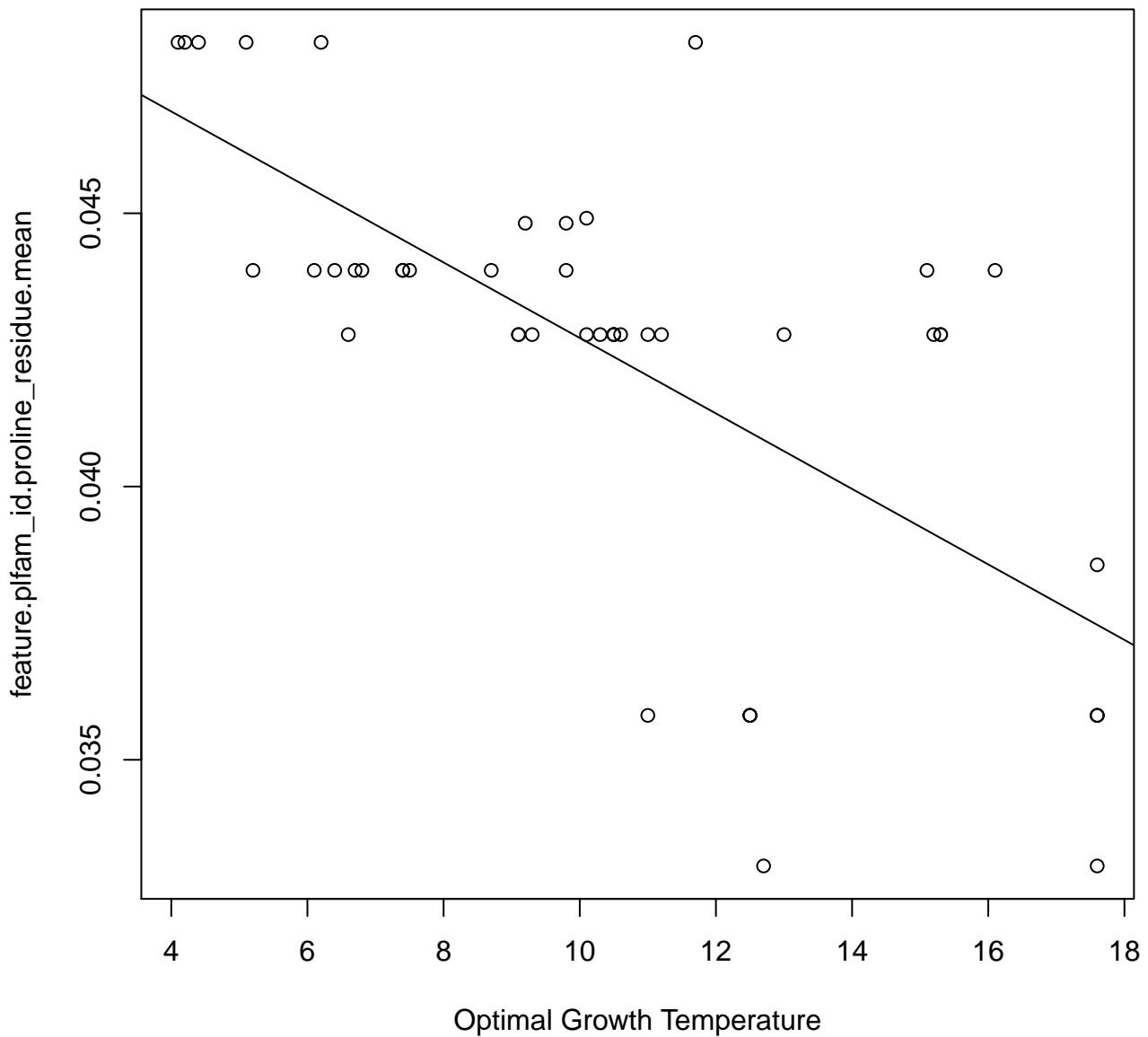
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Exodeoxyribonuclease III (EC 3.1.11.2)



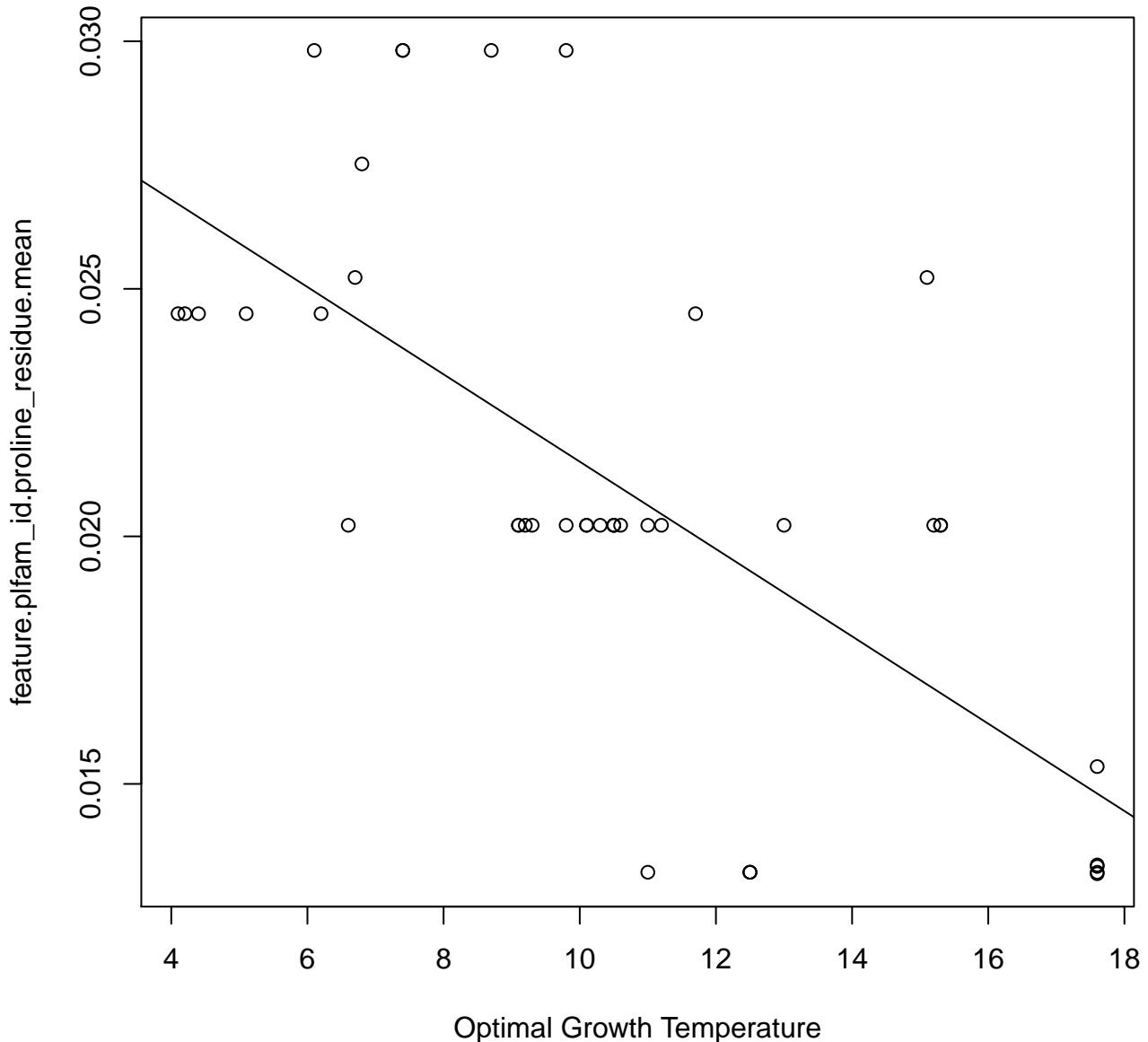
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Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)



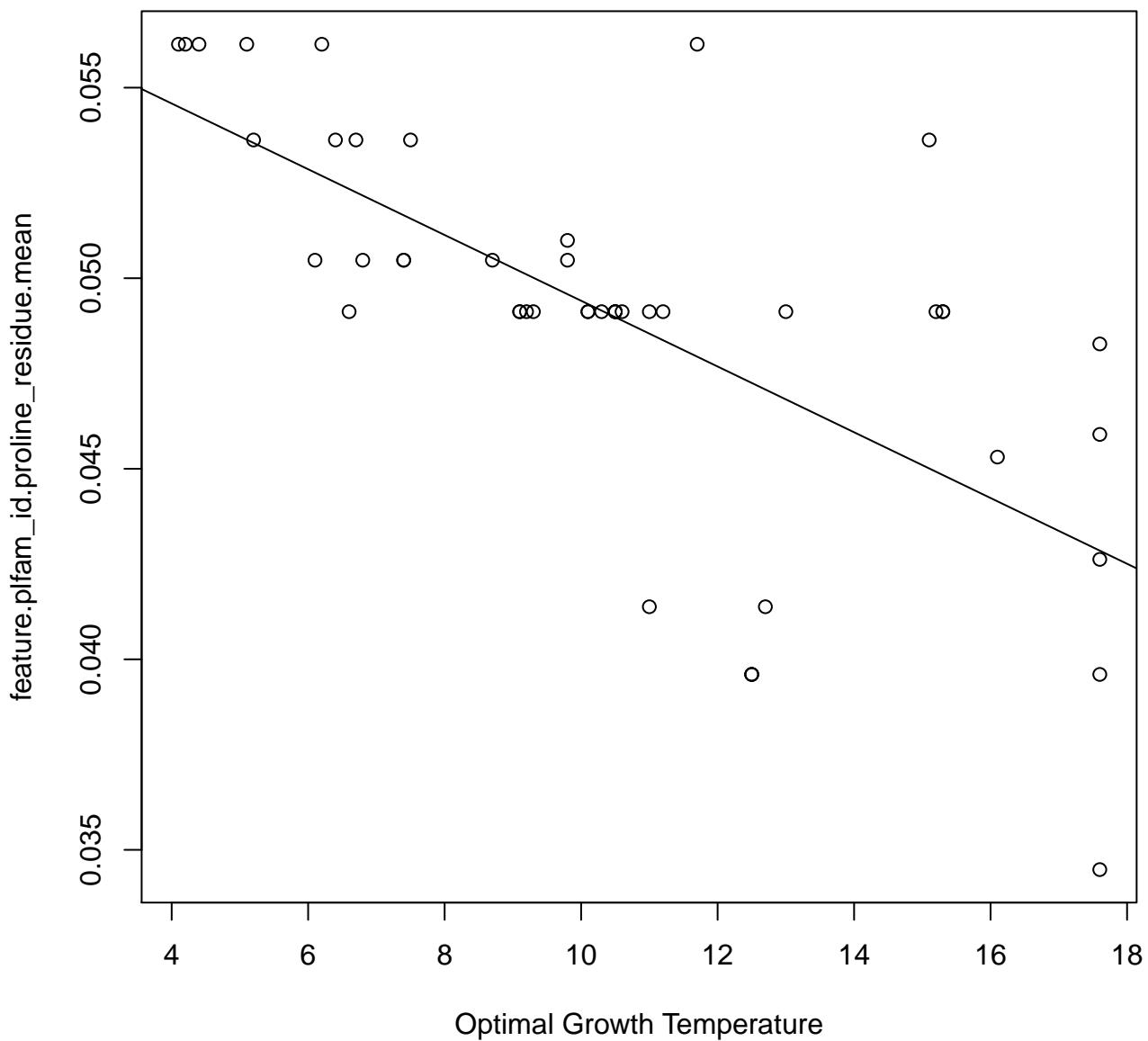
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Flagellar P-ring protein Flgl



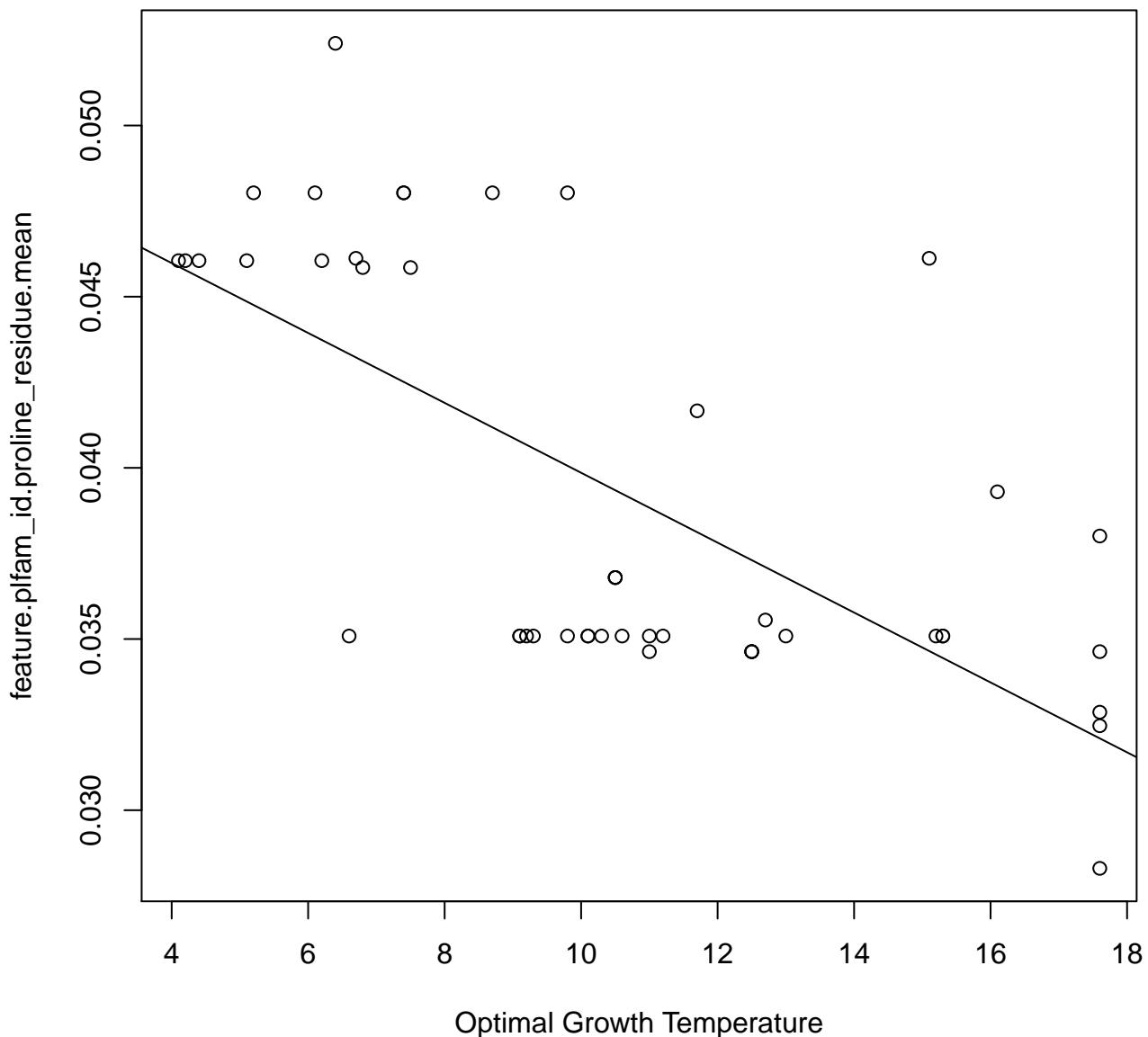
feature.plfam_id.proline_residue.mean
PLF_28228_00004108
TPR domain protein, putative component of TonB system



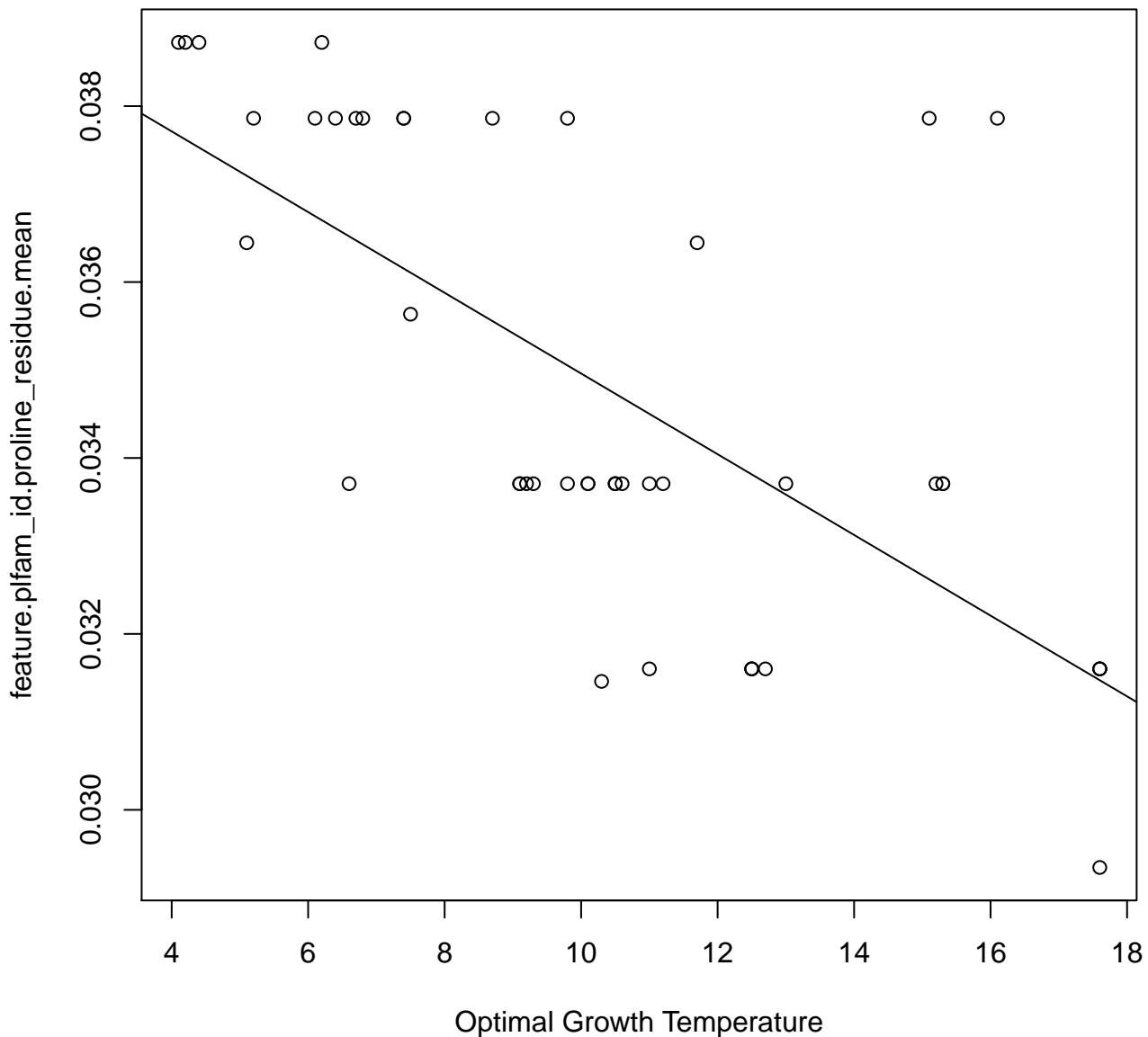
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Peptidyl-prolyl cis-trans isomerase



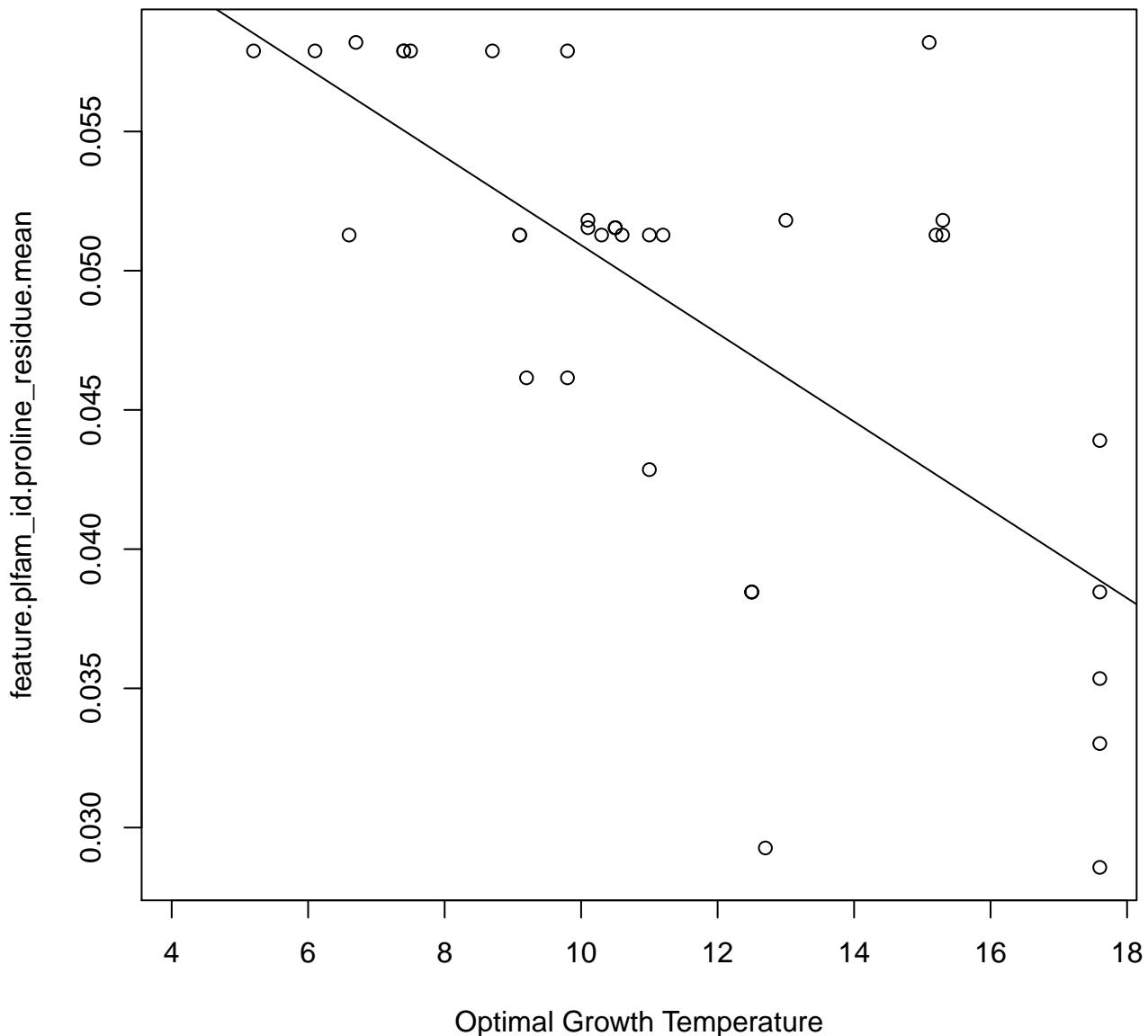
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tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)



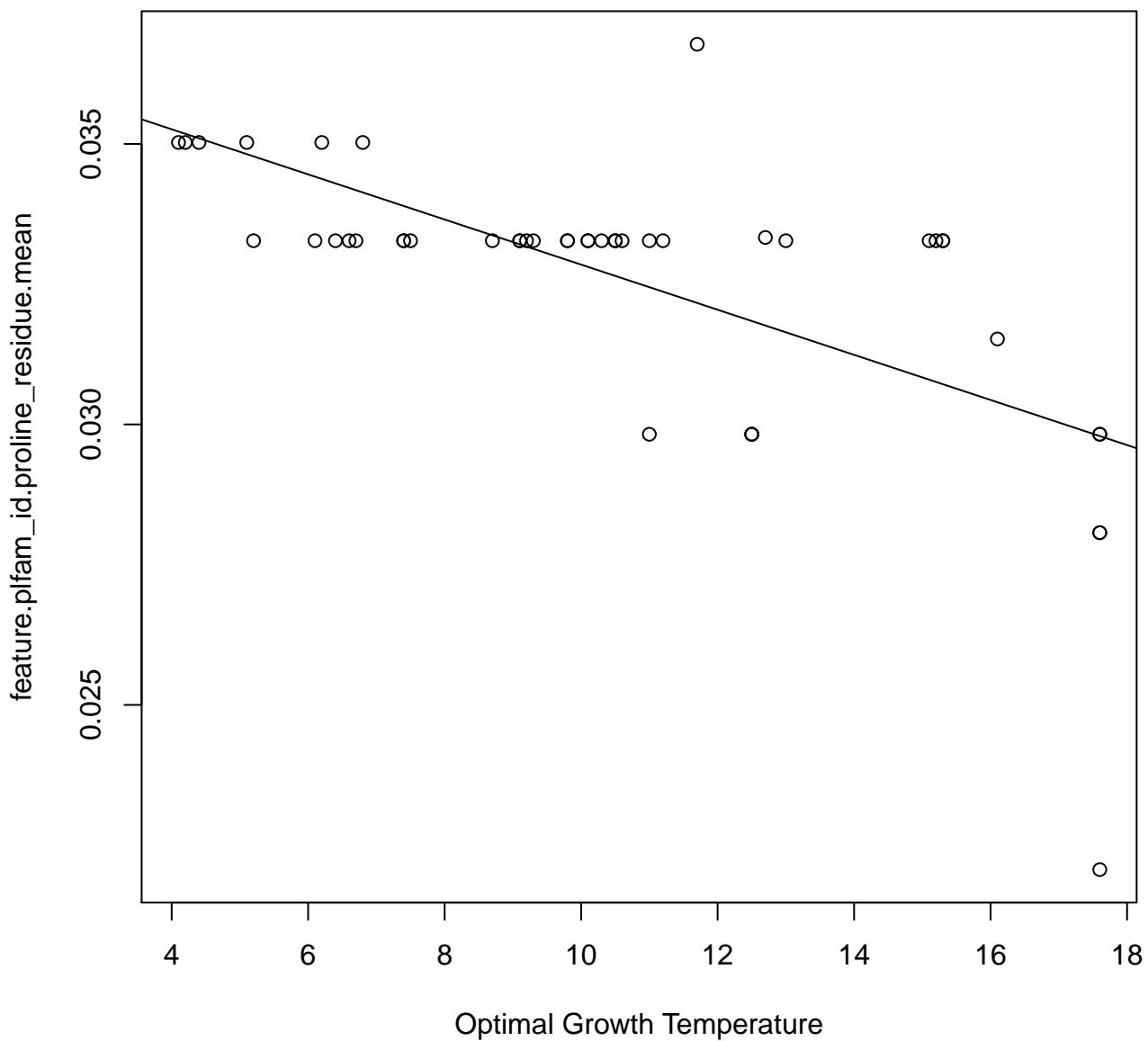
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PLF_28228_00000608
Methionine transporter MetT



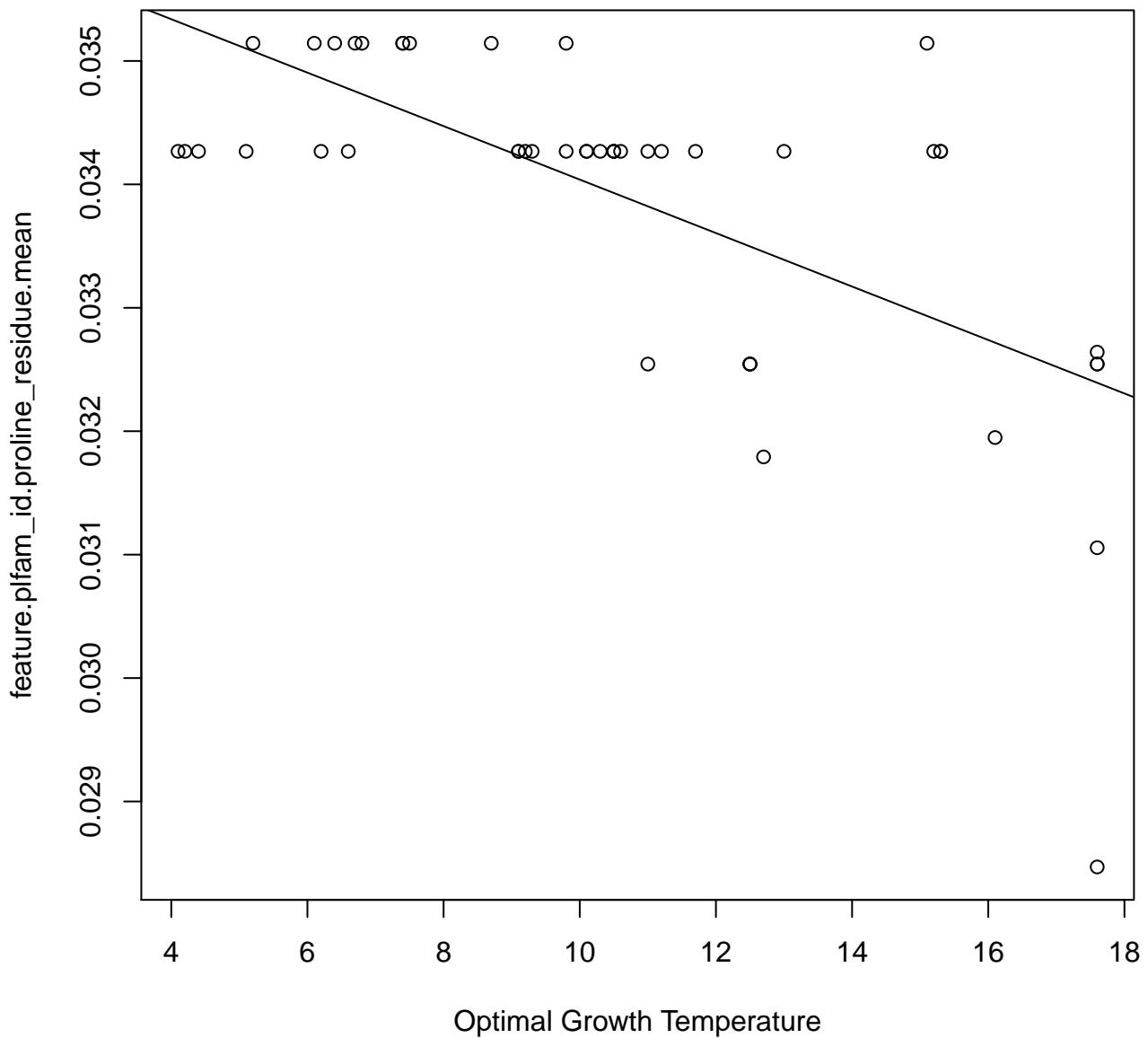
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Der GTPase-activating protein Yihl



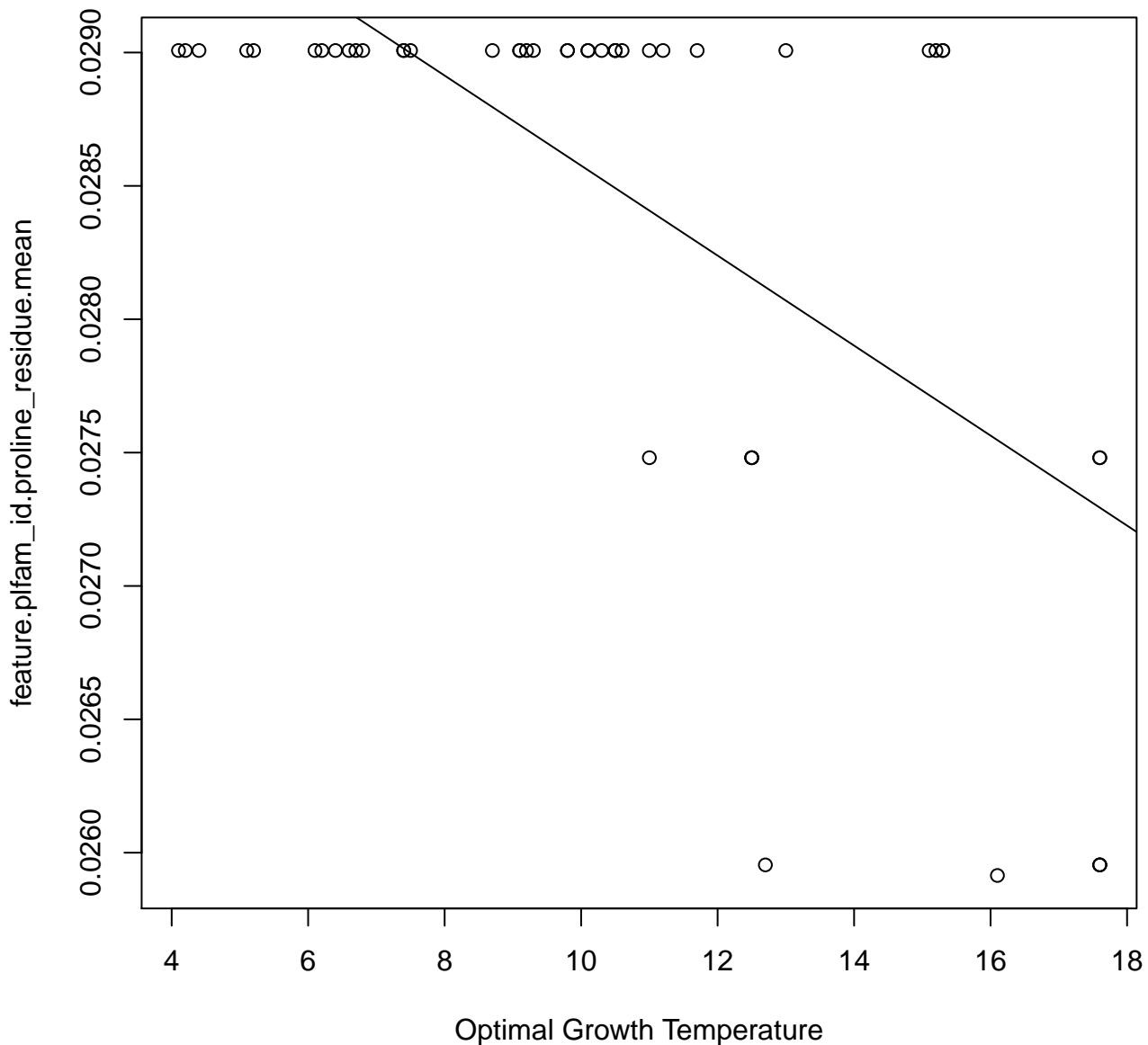
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MSHA biogenesis protein MshE



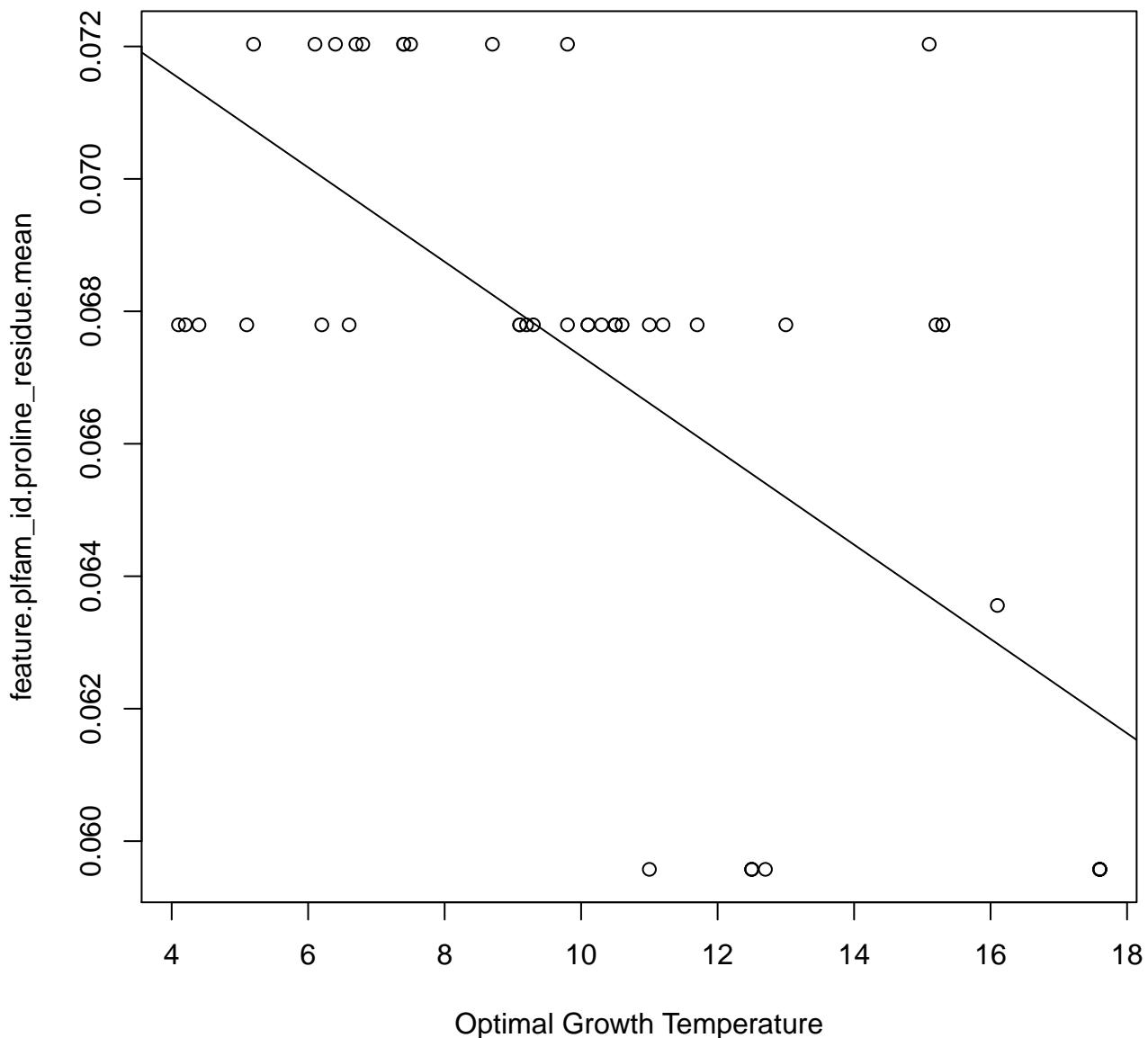
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PLF_28228_00001407
tRNA-dihydrouridine synthase DusB



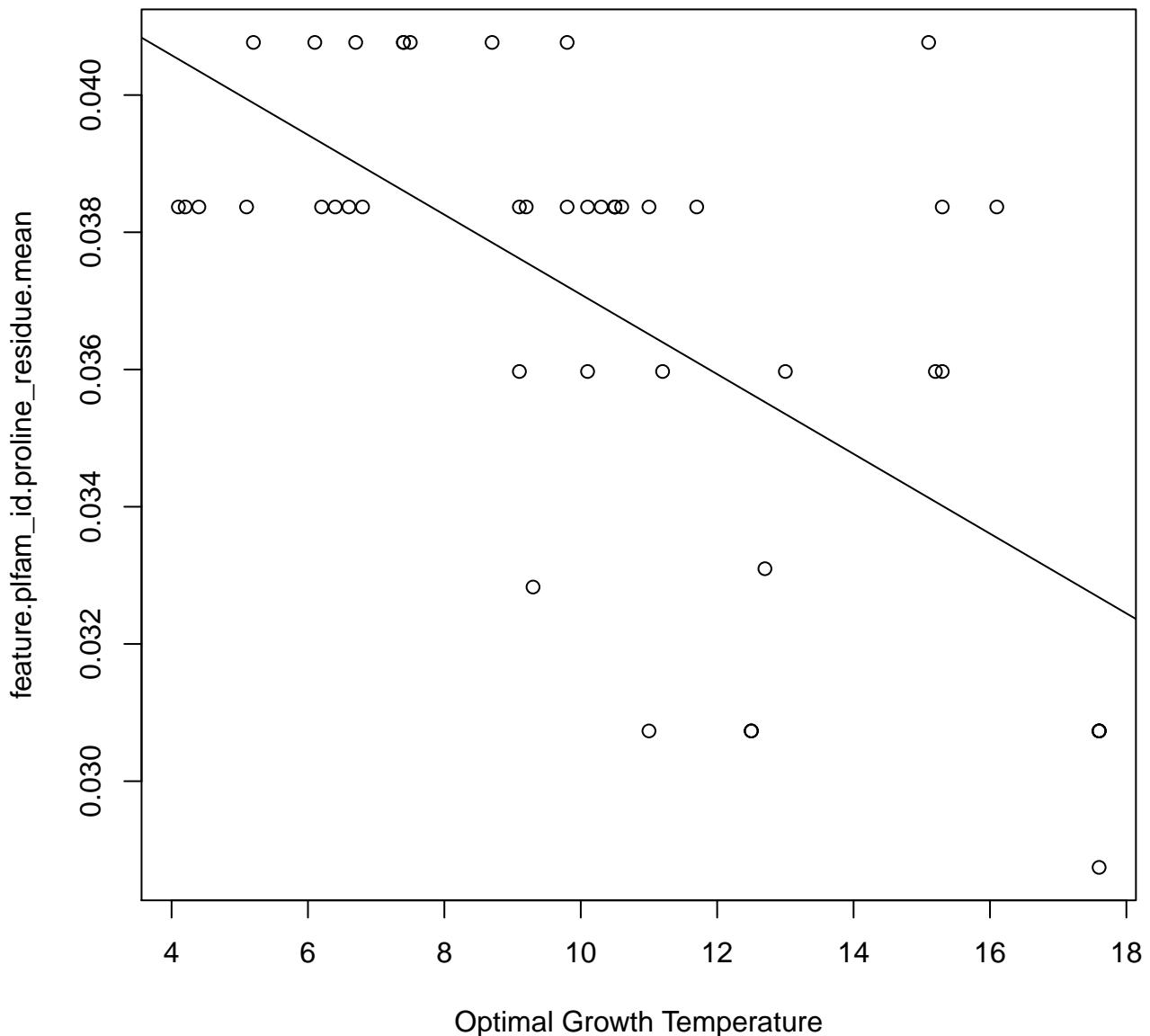
feature.plfam_id.proline_residue.mean
PLF_28228_00001527
Inner membrane protein, KefB/KefC family



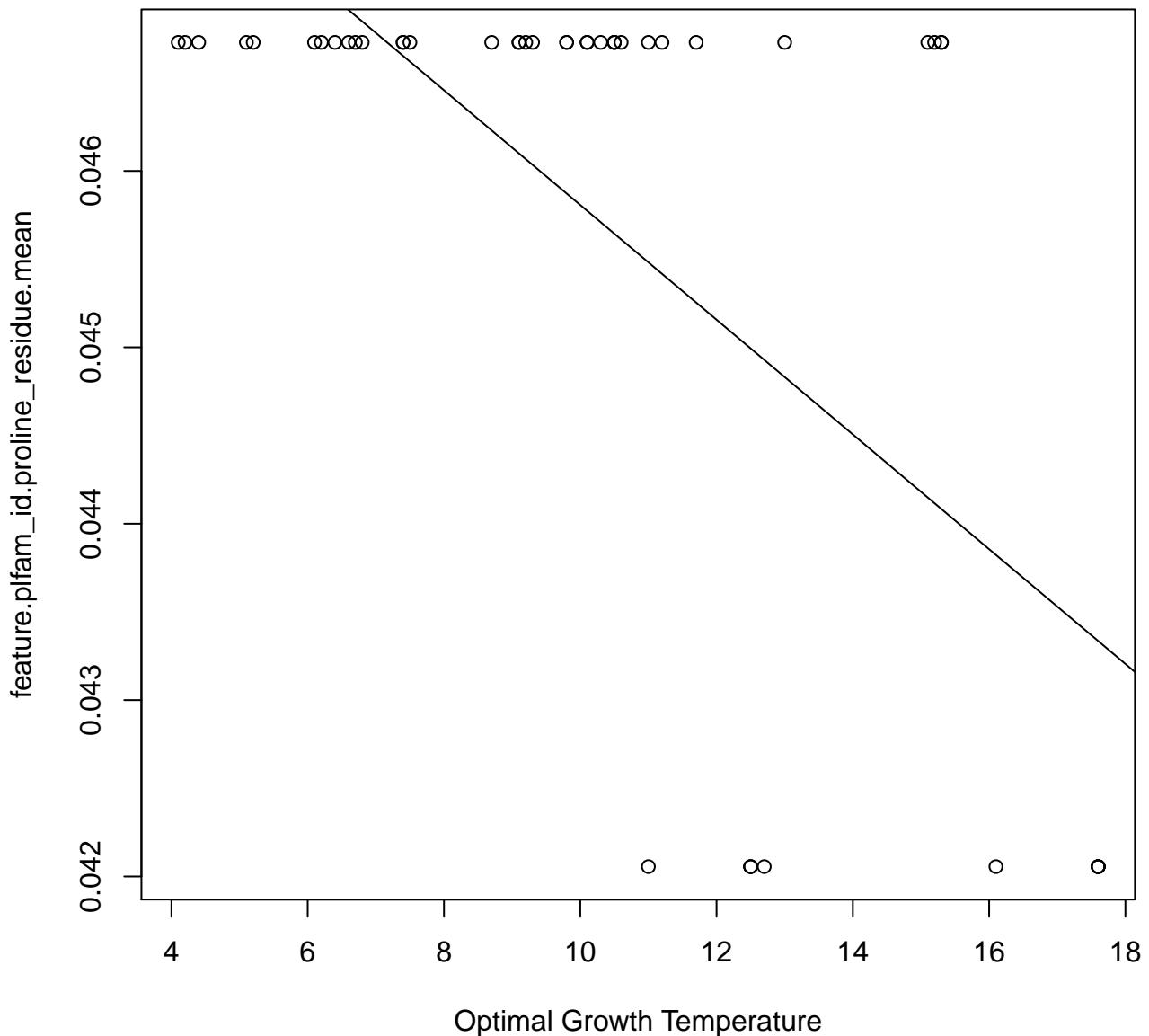
feature.plfam_id.proline_residue.mean
PLF_28228_00001166
Succinate dehydrogenase iron-sulfur protein (EC 1.3.5.1)



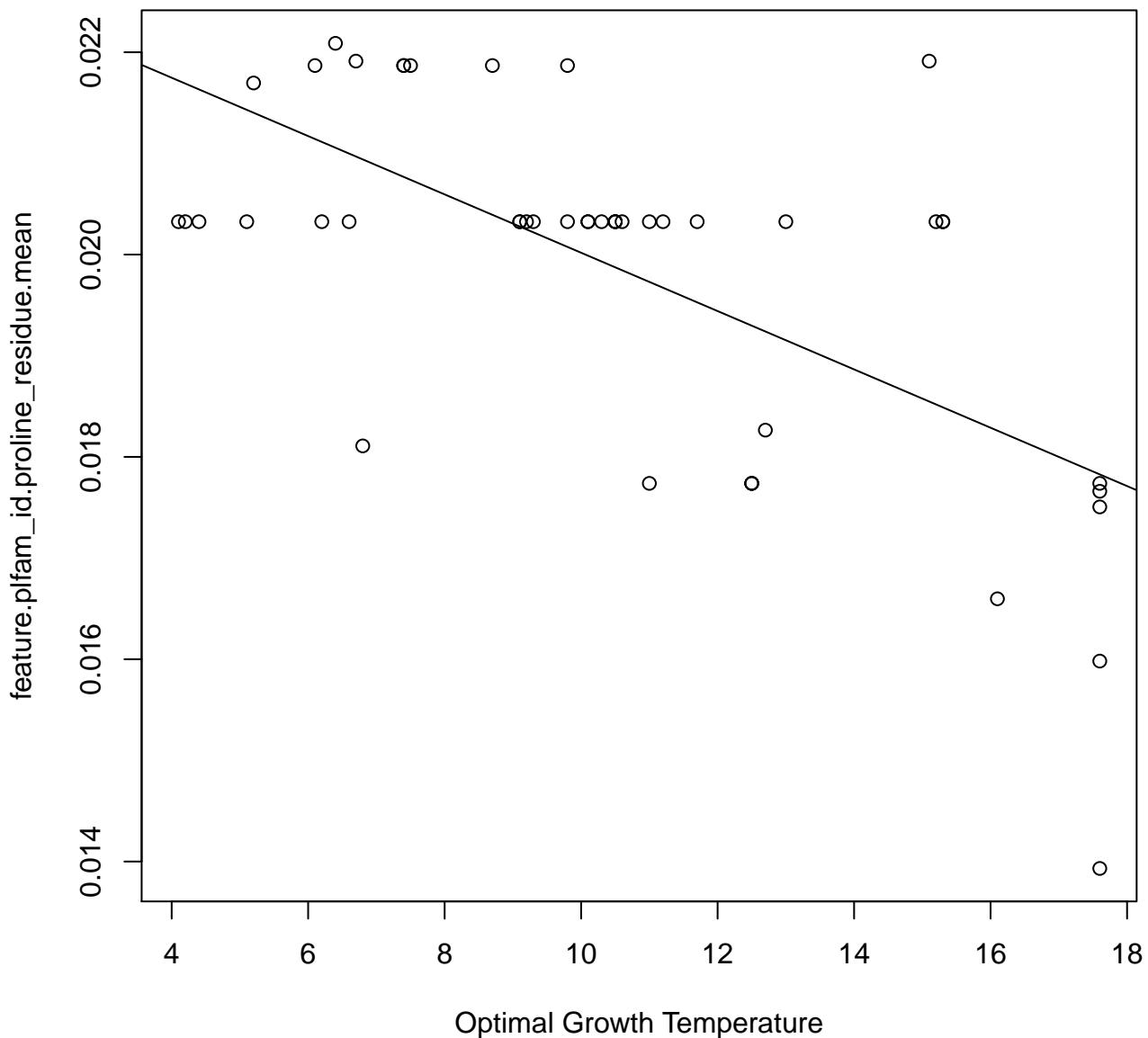
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Serine protease precursor MucD/AlgY associated with sigma factor RpoE



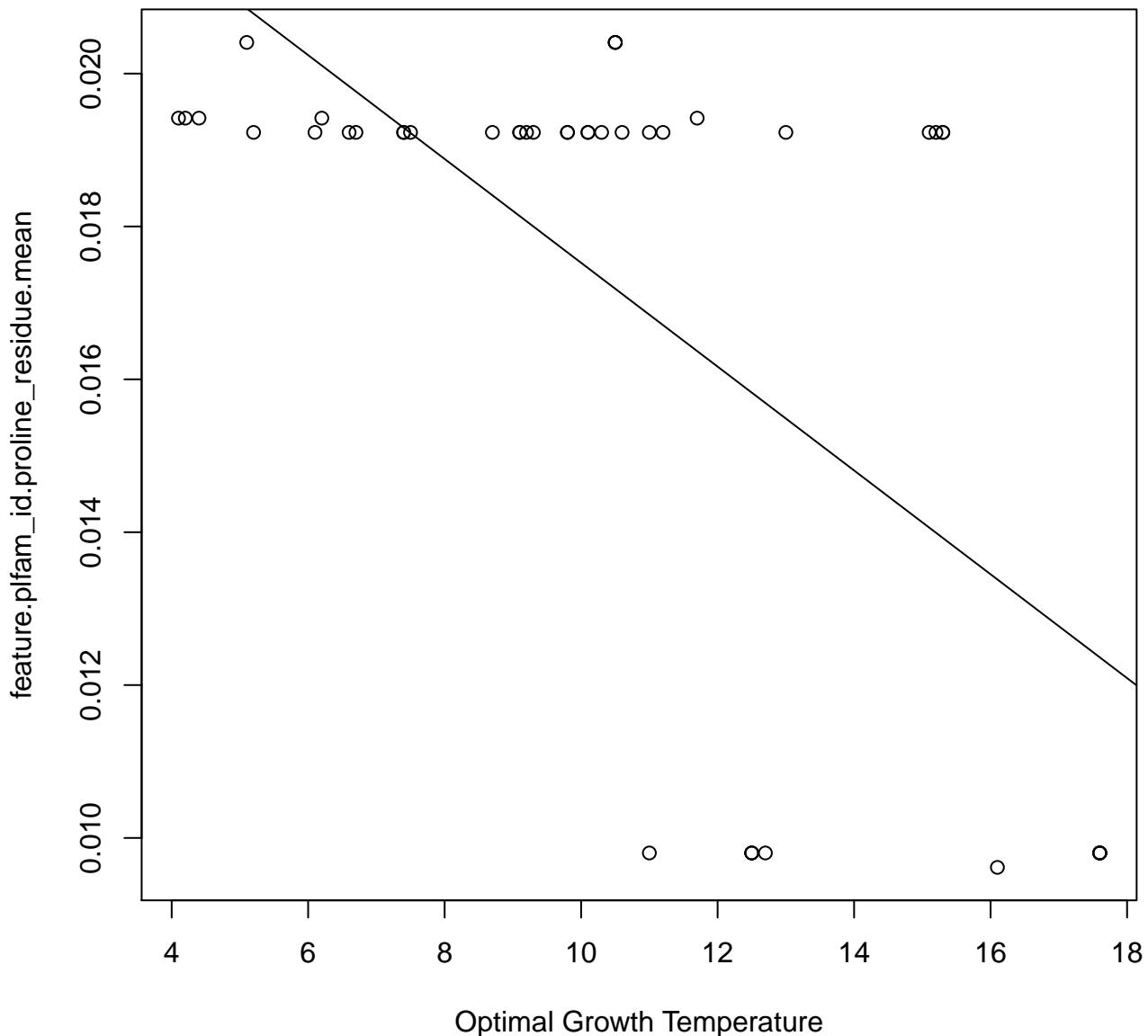
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Adenylate kinase (EC 2.7.4.3)



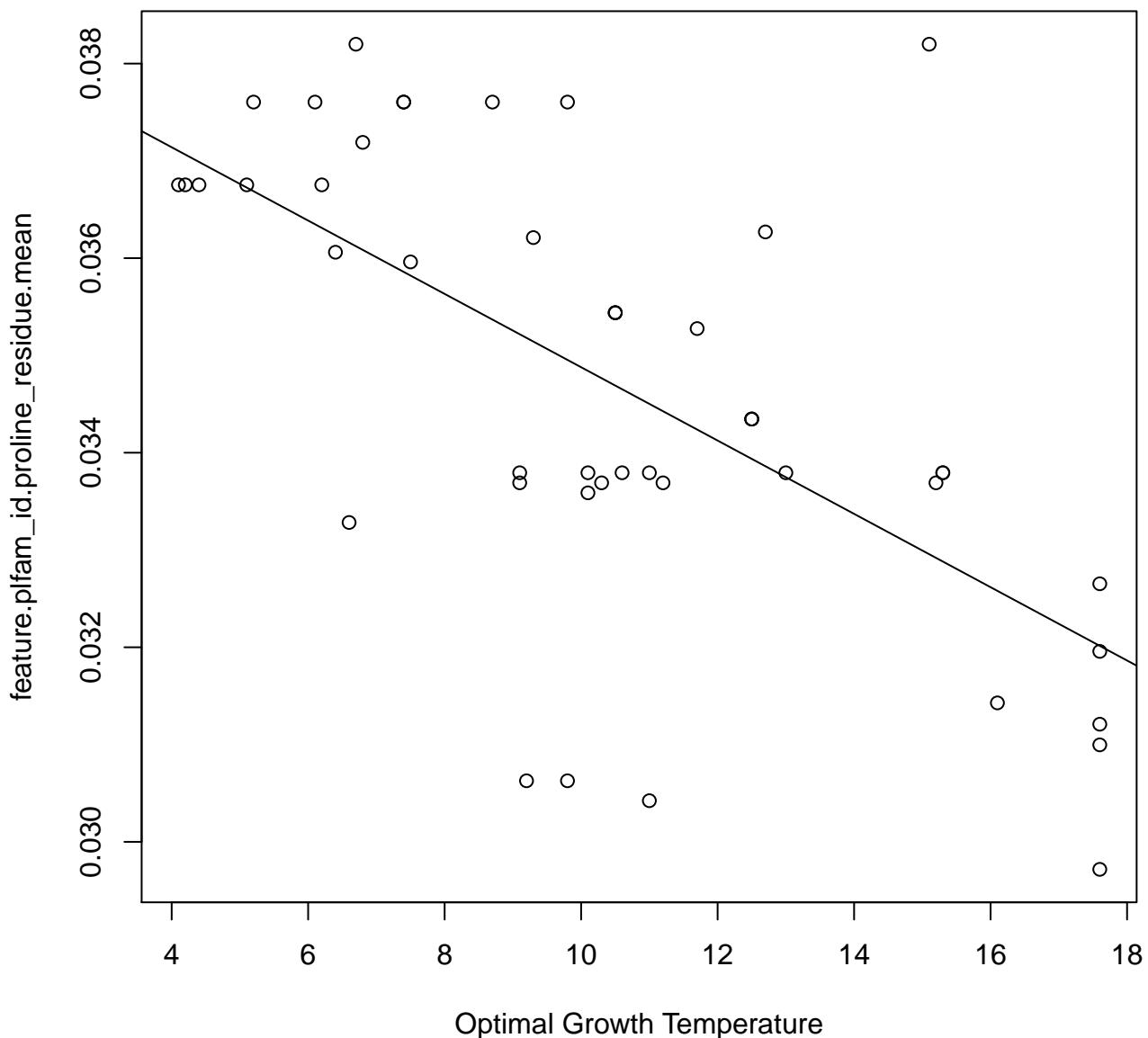
feature.plfam_id.proline_residue.mean
PLF_28228_00001623
DNA recombination protein RmuC



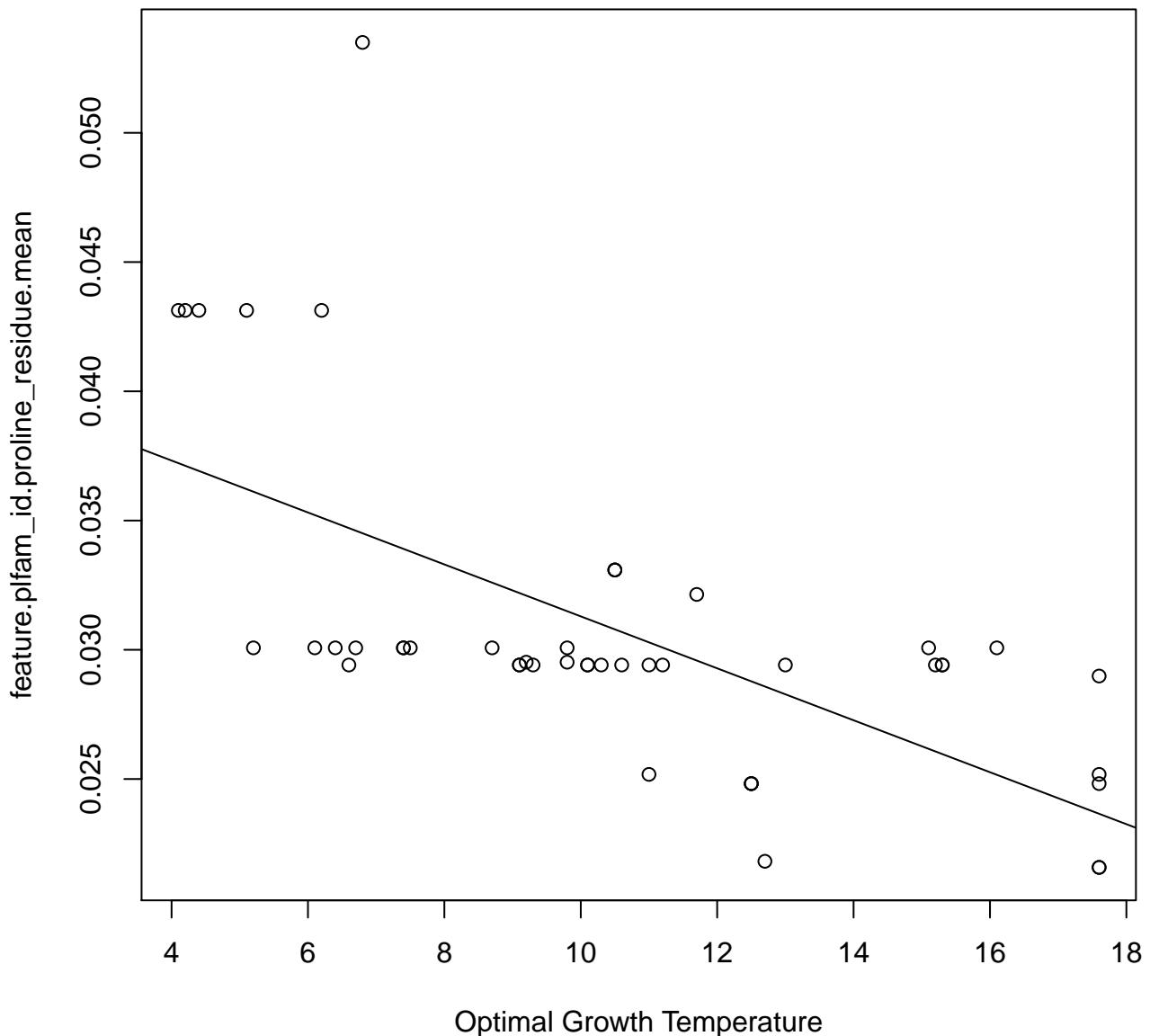
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PLF_28228_00001681
Cell division protein FtsL



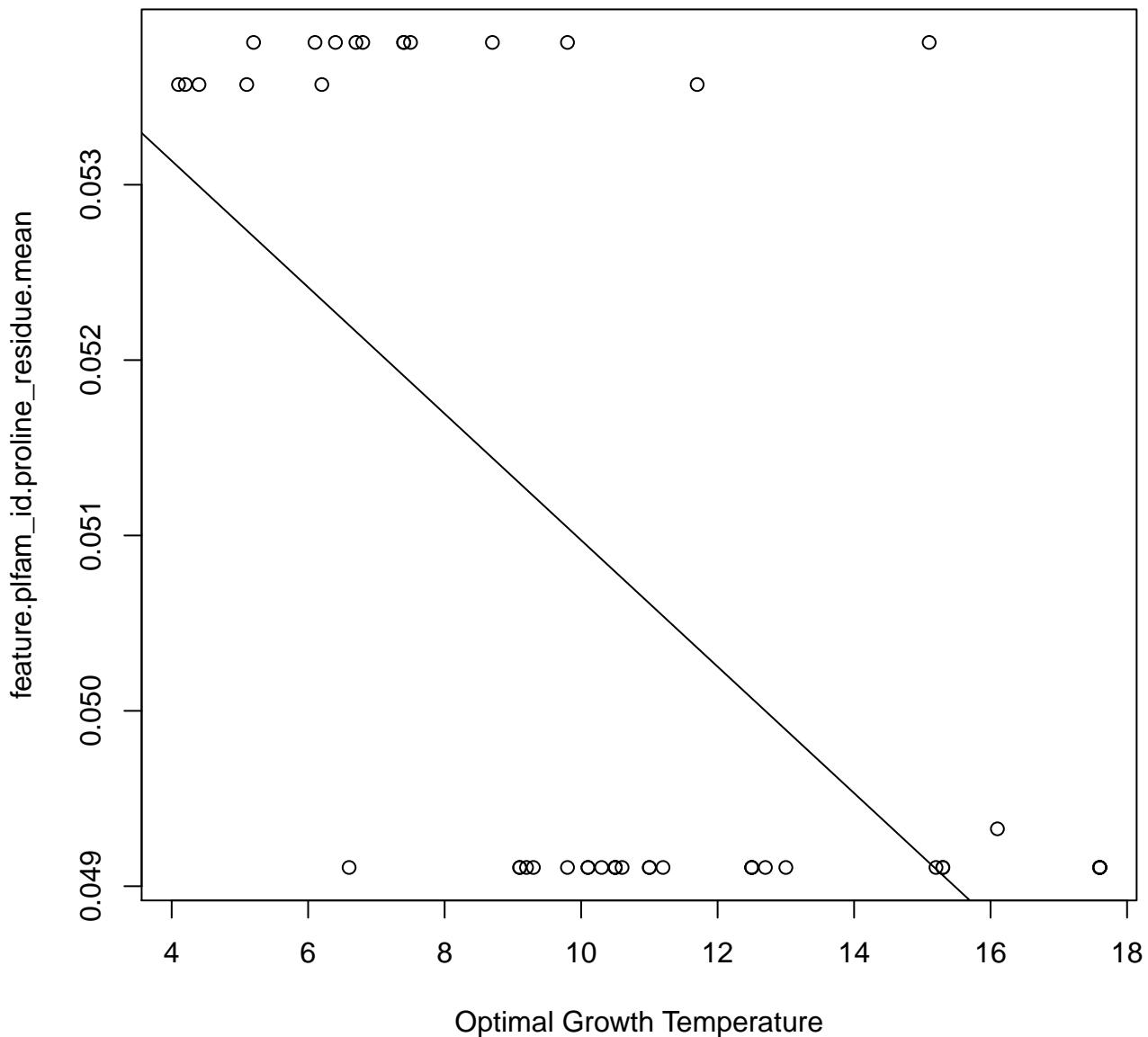
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Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)



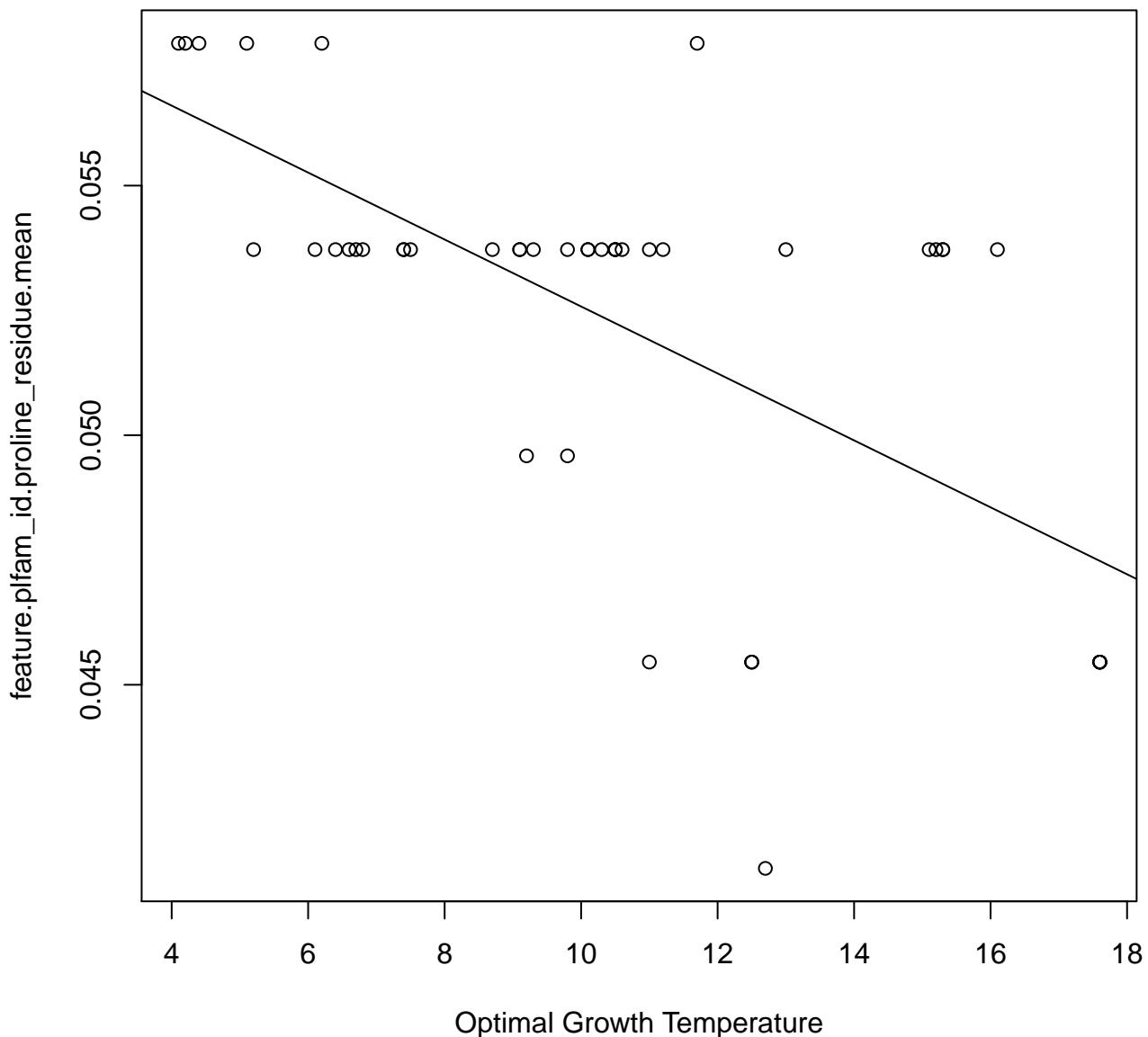
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PLF_28228_00000670
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)



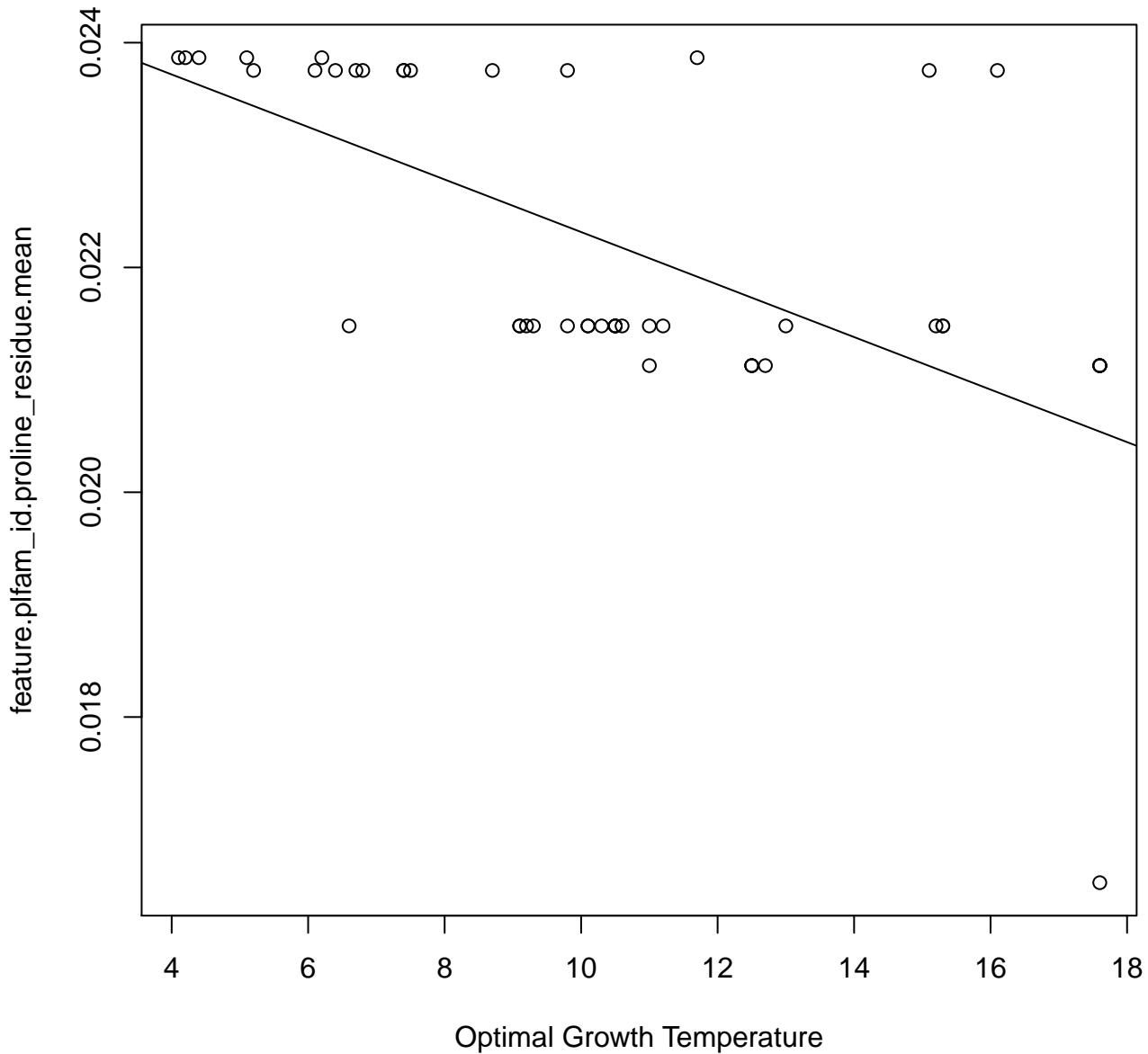
feature.plfam_id.proline_residue.mean
PLF_28228_00001094
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)



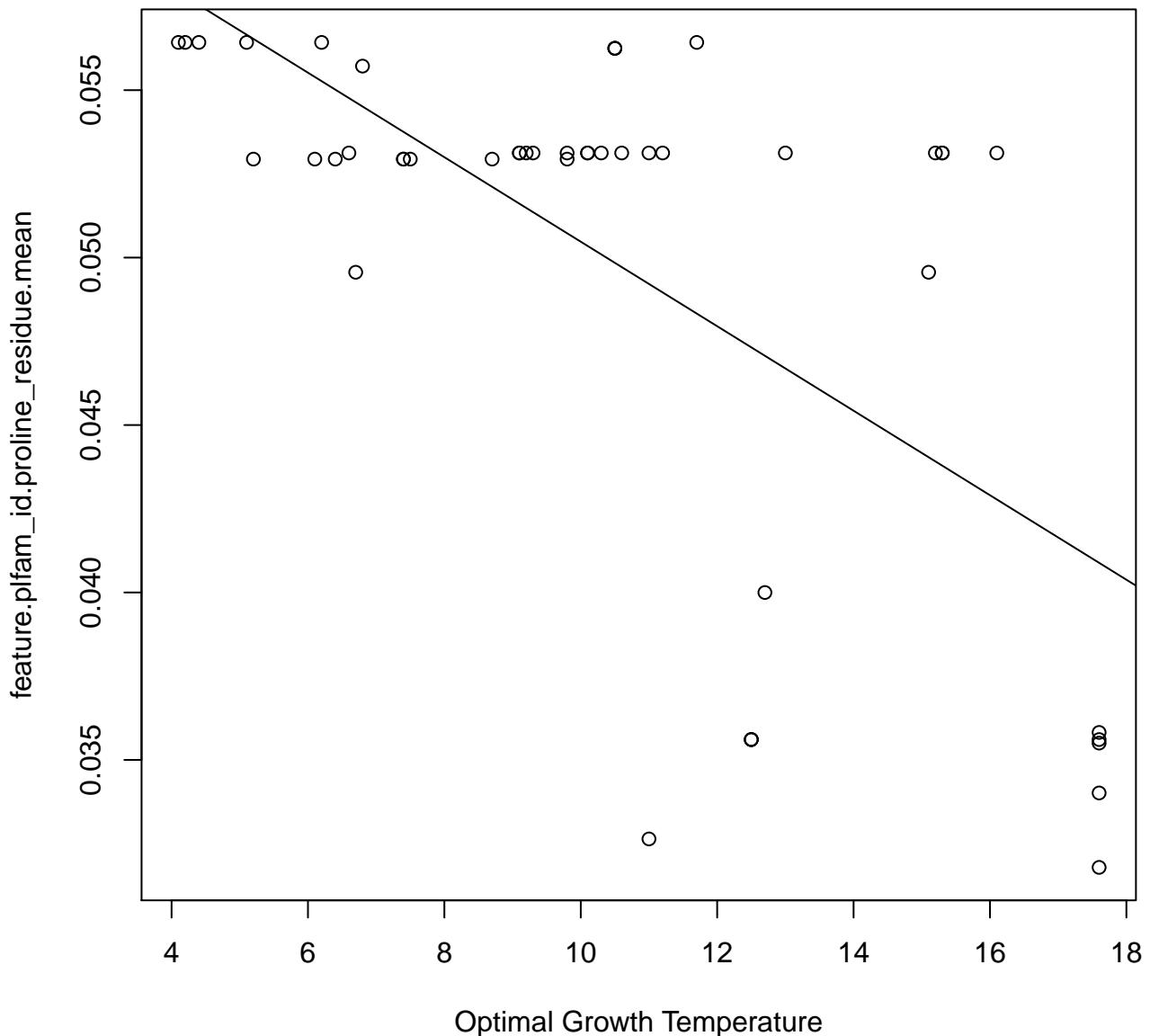
feature.plfam_id.proline_residue.mean
PLF_28228_00000935
Hybrid peroxiredoxin hyPrx5 (EC 1.11.1.15)



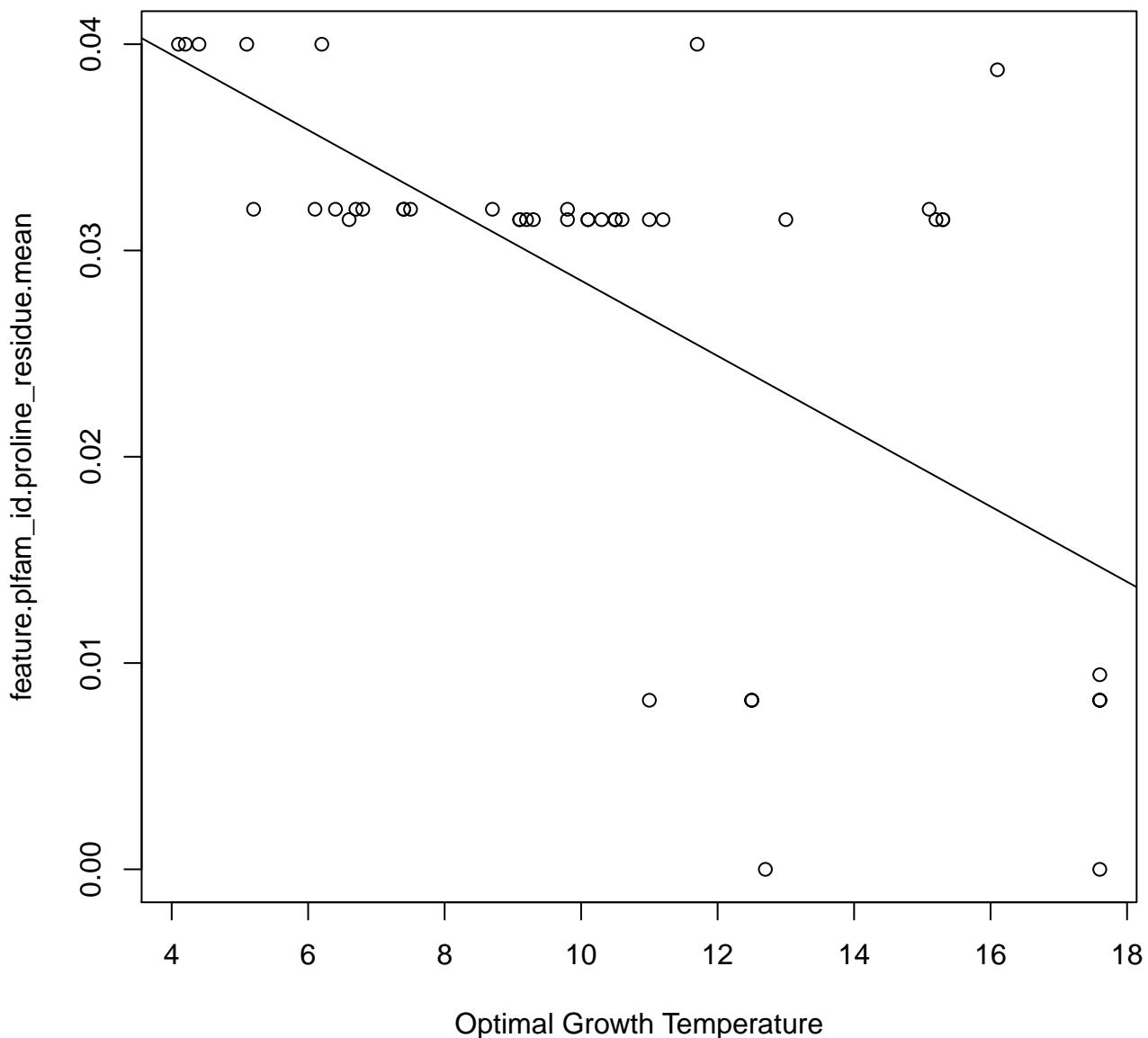
feature.plfam_id.proline_residue.mean
PLF_28228_00000203
Ammonium transporter



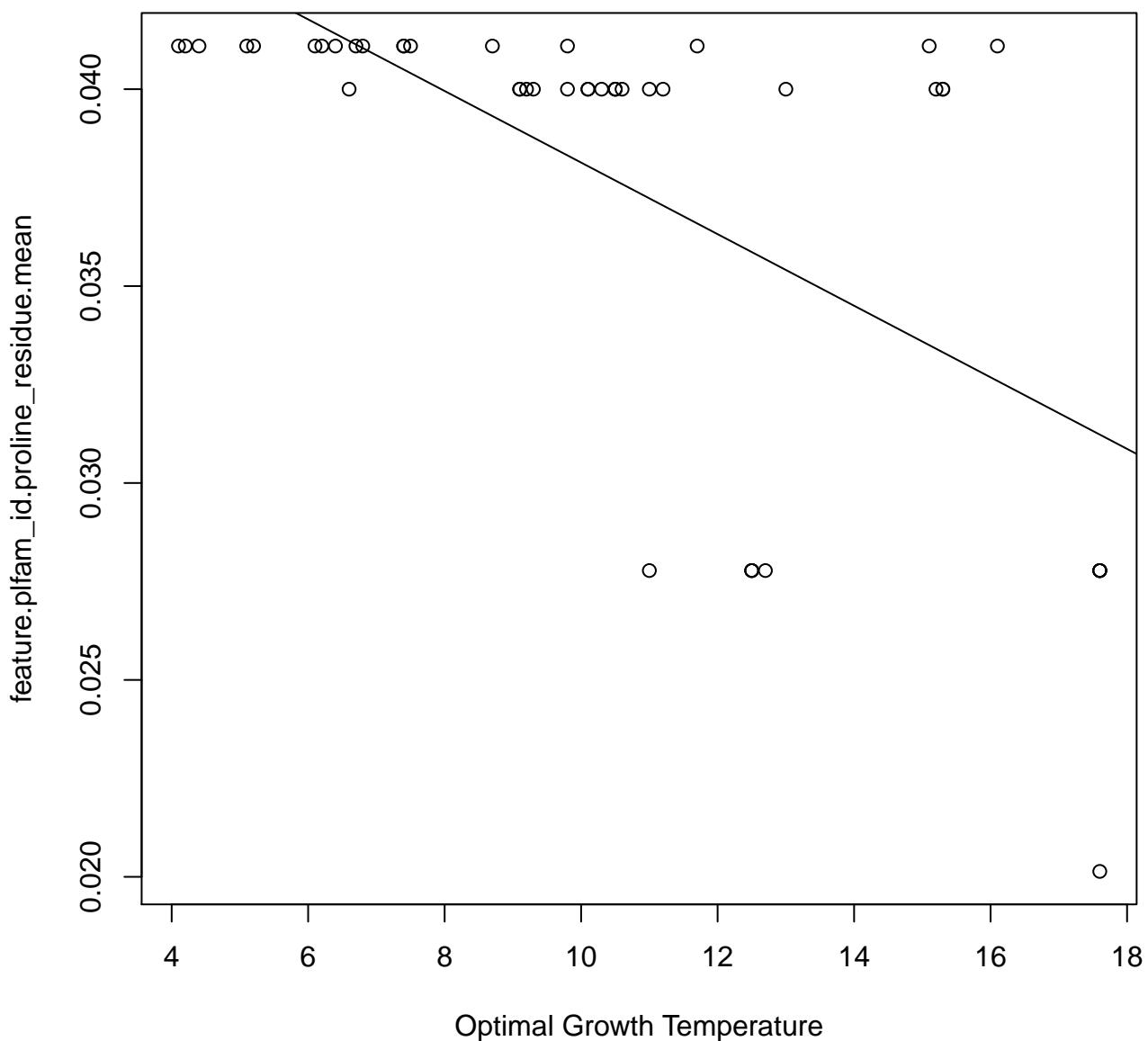
feature.plfam_id.proline_residue.mean
PLF_28228_00002060
Sigma factor RpoE negative regulatory protein RseB precursor



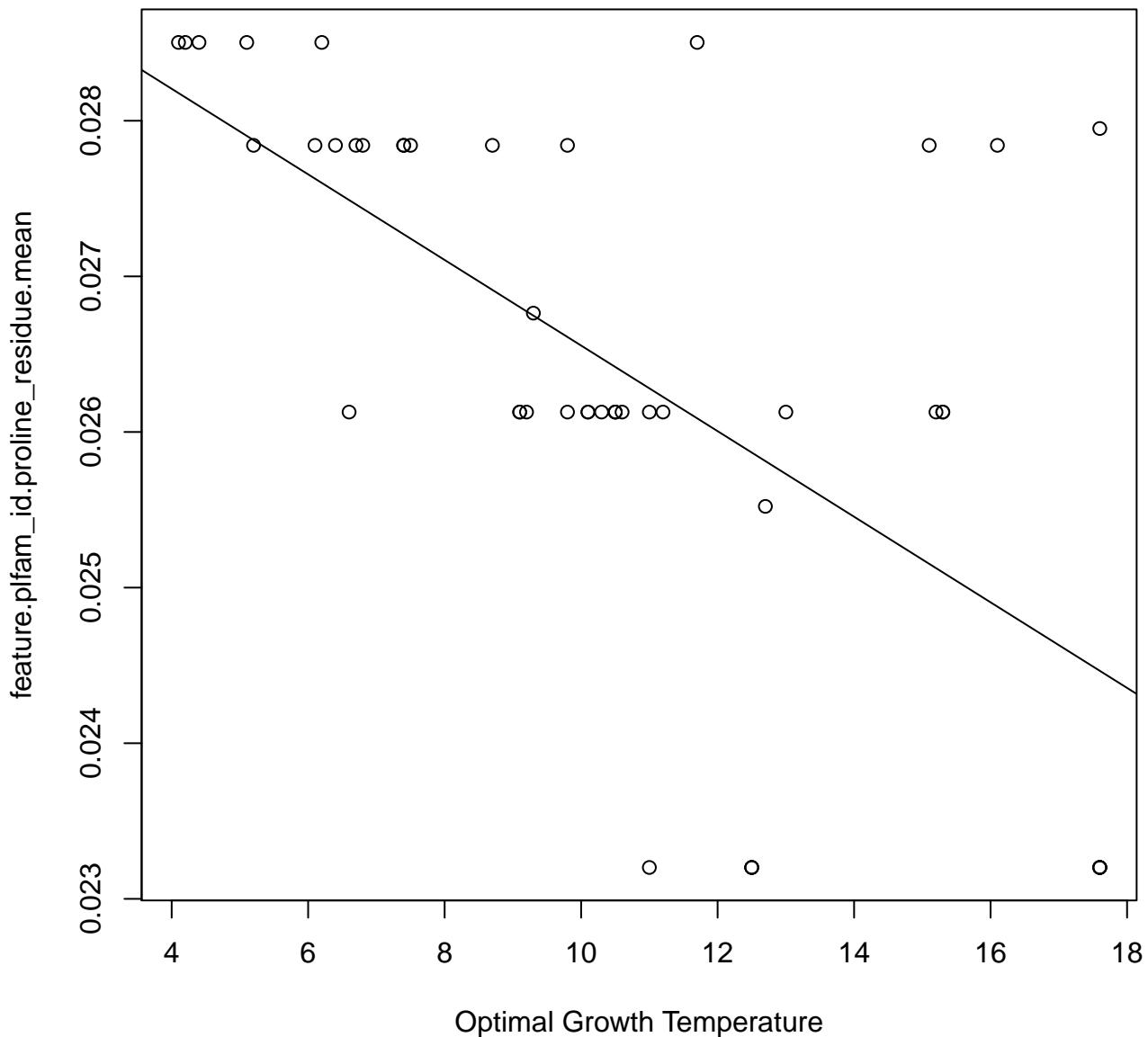
feature.plfam_id.proline_residue.mean
PLF_28228_00002263
hypothetical protein



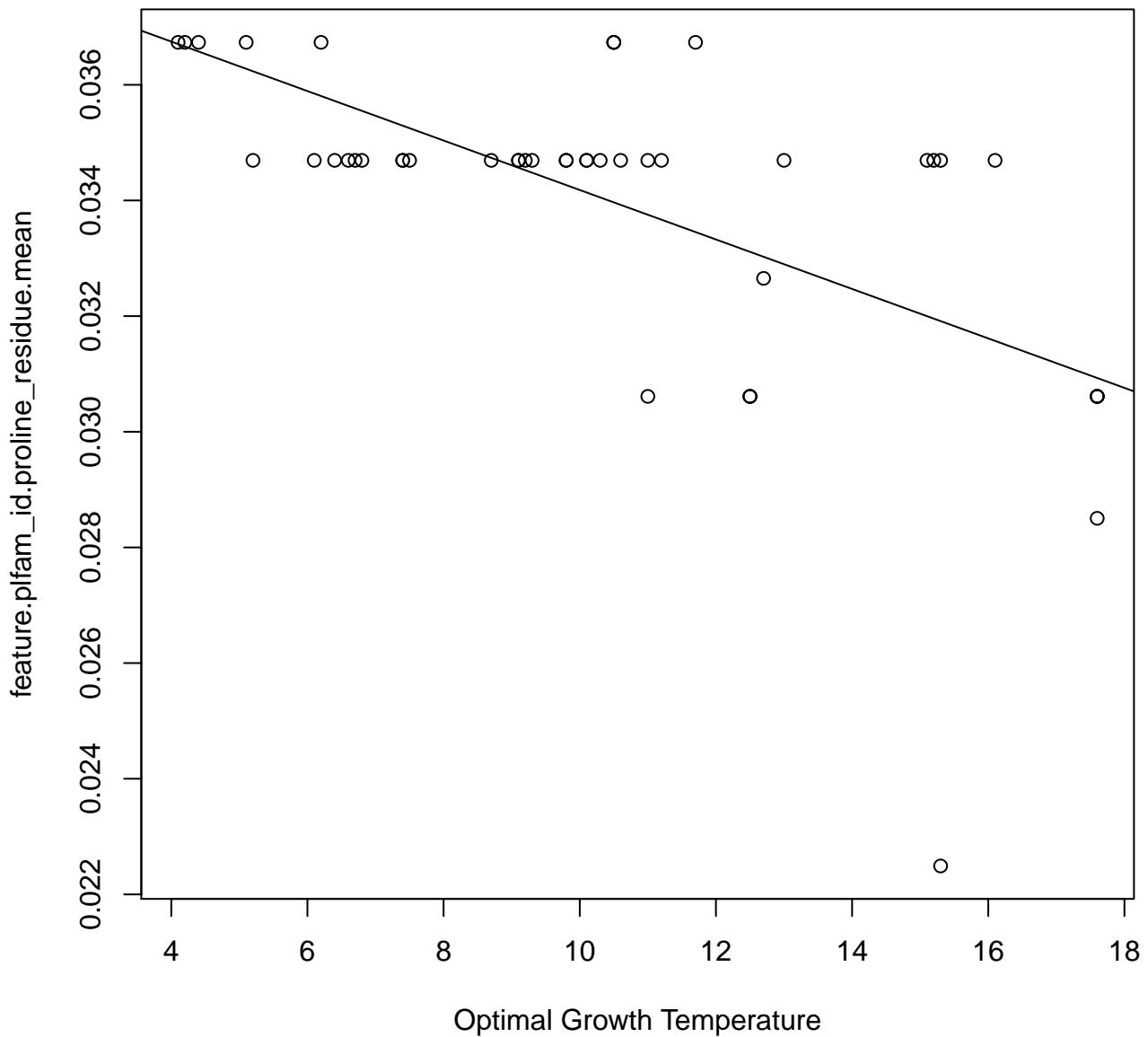
feature.plfam_id.proline_residue.mean
PLF_28228_00000118
Cold shock protein of CSP family => CspD (naming convention as in E.coli)



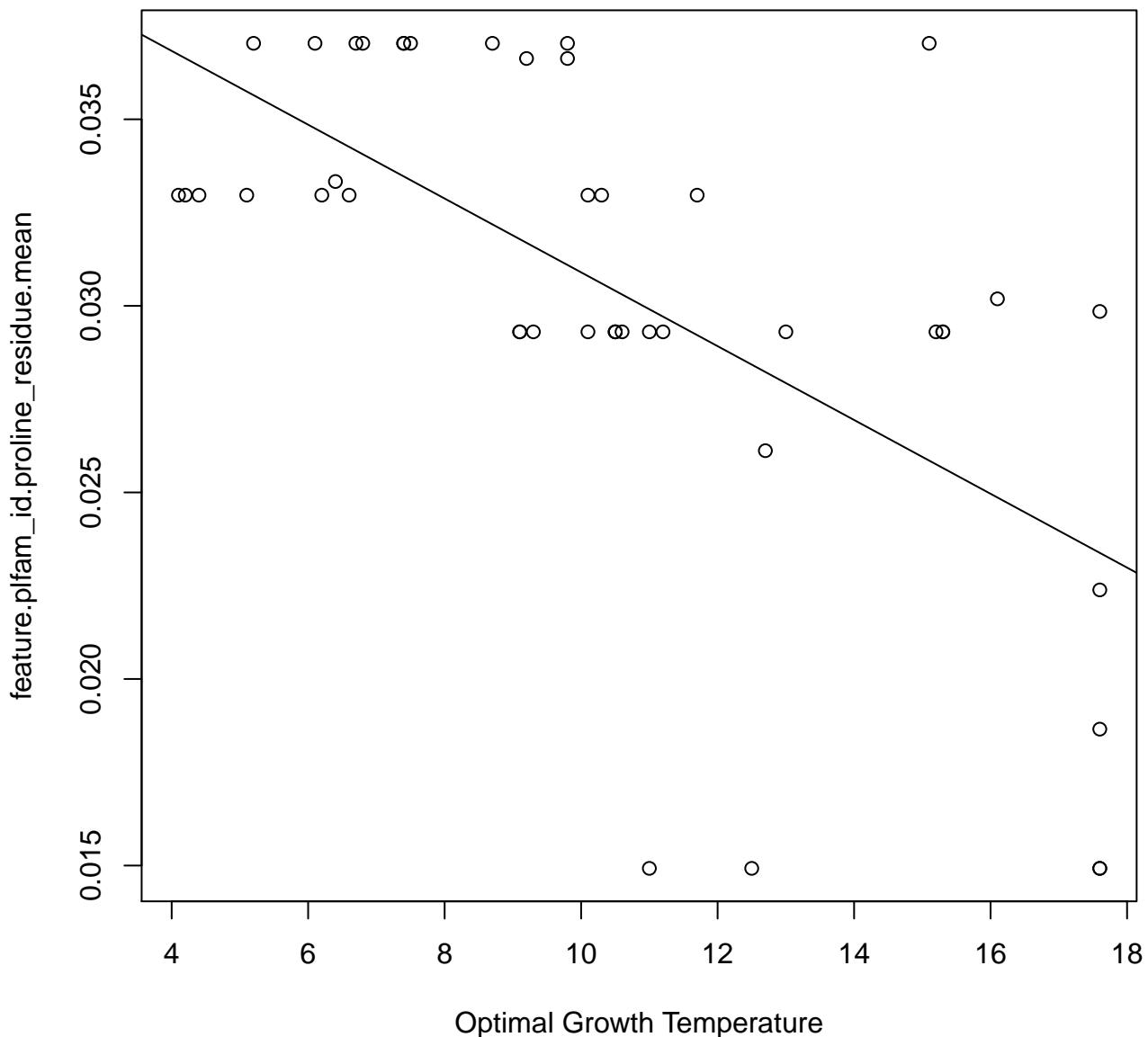
feature.plfam_id.proline_residue.mean
PLF_28228_00000990
Probable low-affinity inorganic phosphate transporter



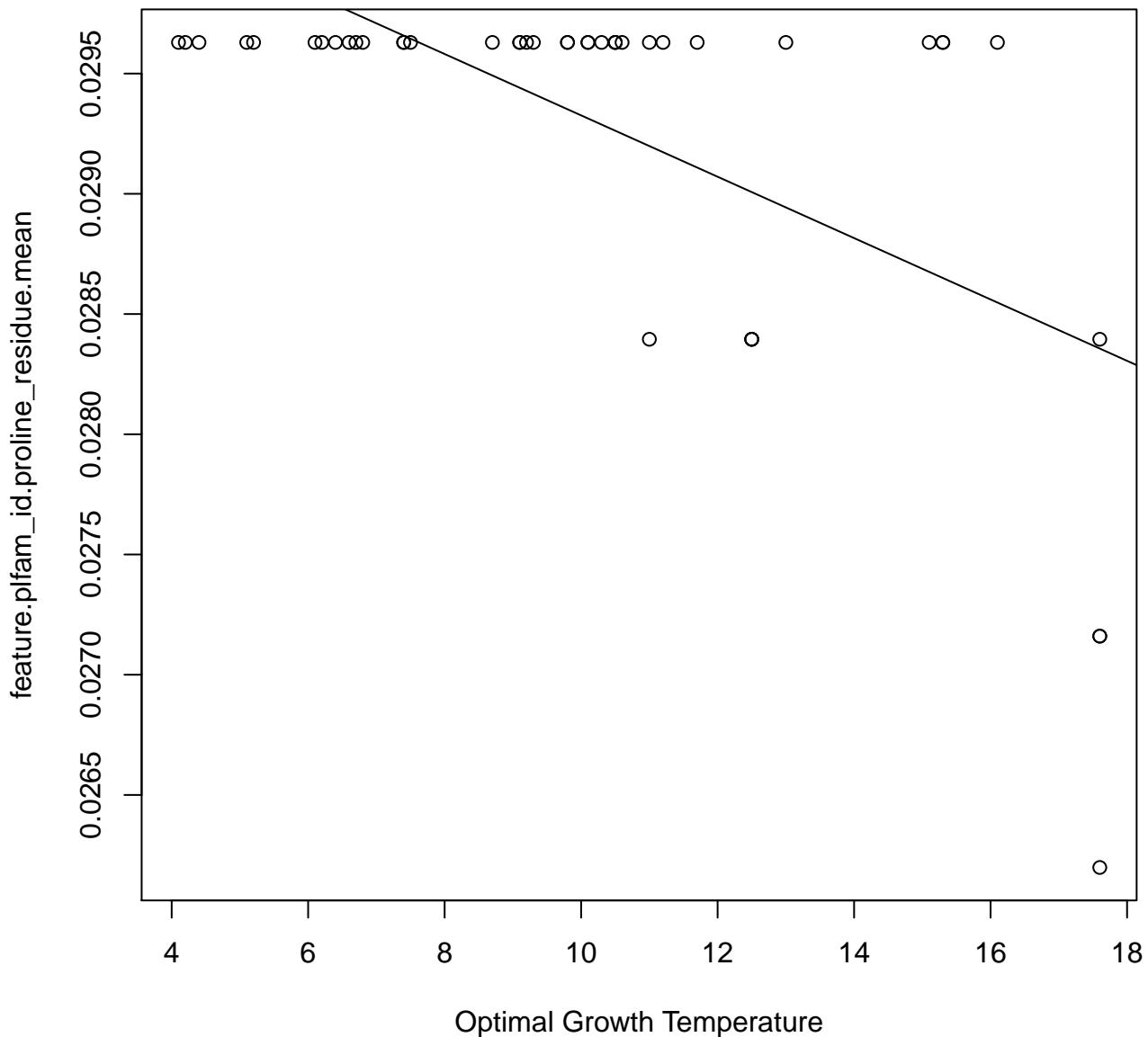
feature.plfam_id.proline_residue.mean
PLF_28228_00000525
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) / CBS domain



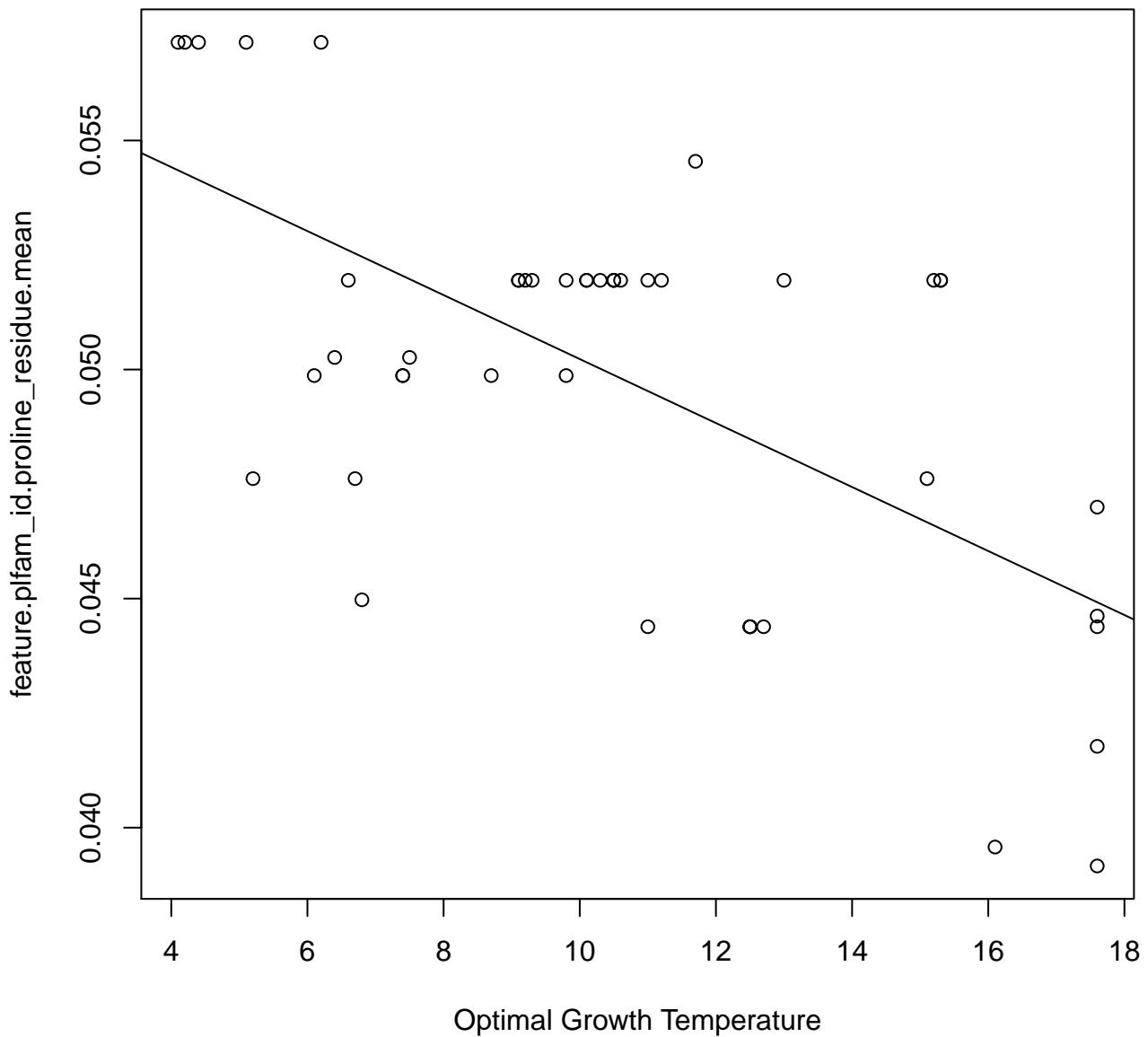
feature.plfam_id.proline_residue.mean
PLF_28228_00018475
Aminodeoxychorismate lyase (EC 4.1.3.38)



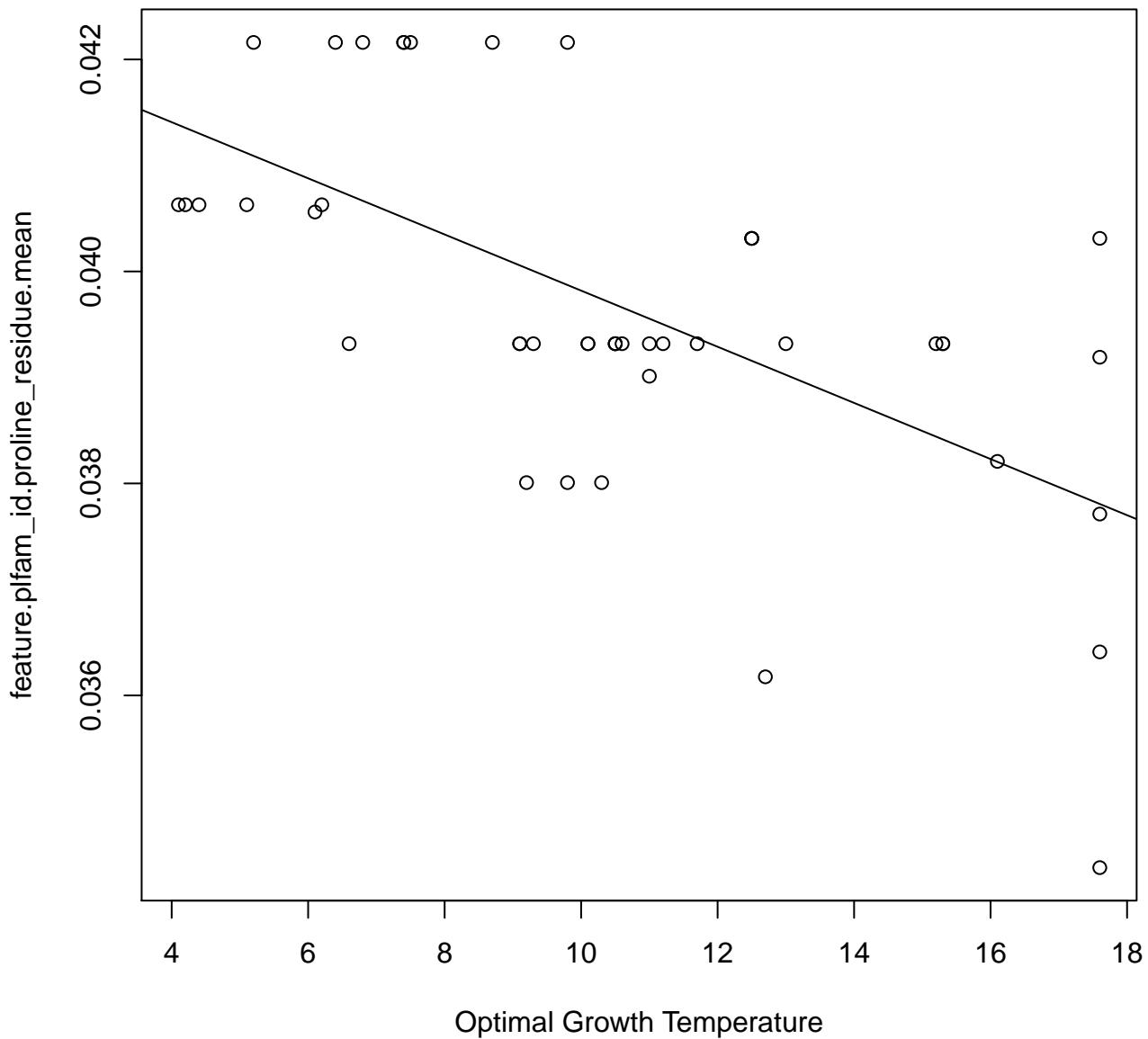
feature.plfam_id.proline_residue.mean
PLF_28228_00001692
Choline transporter BetT, short form



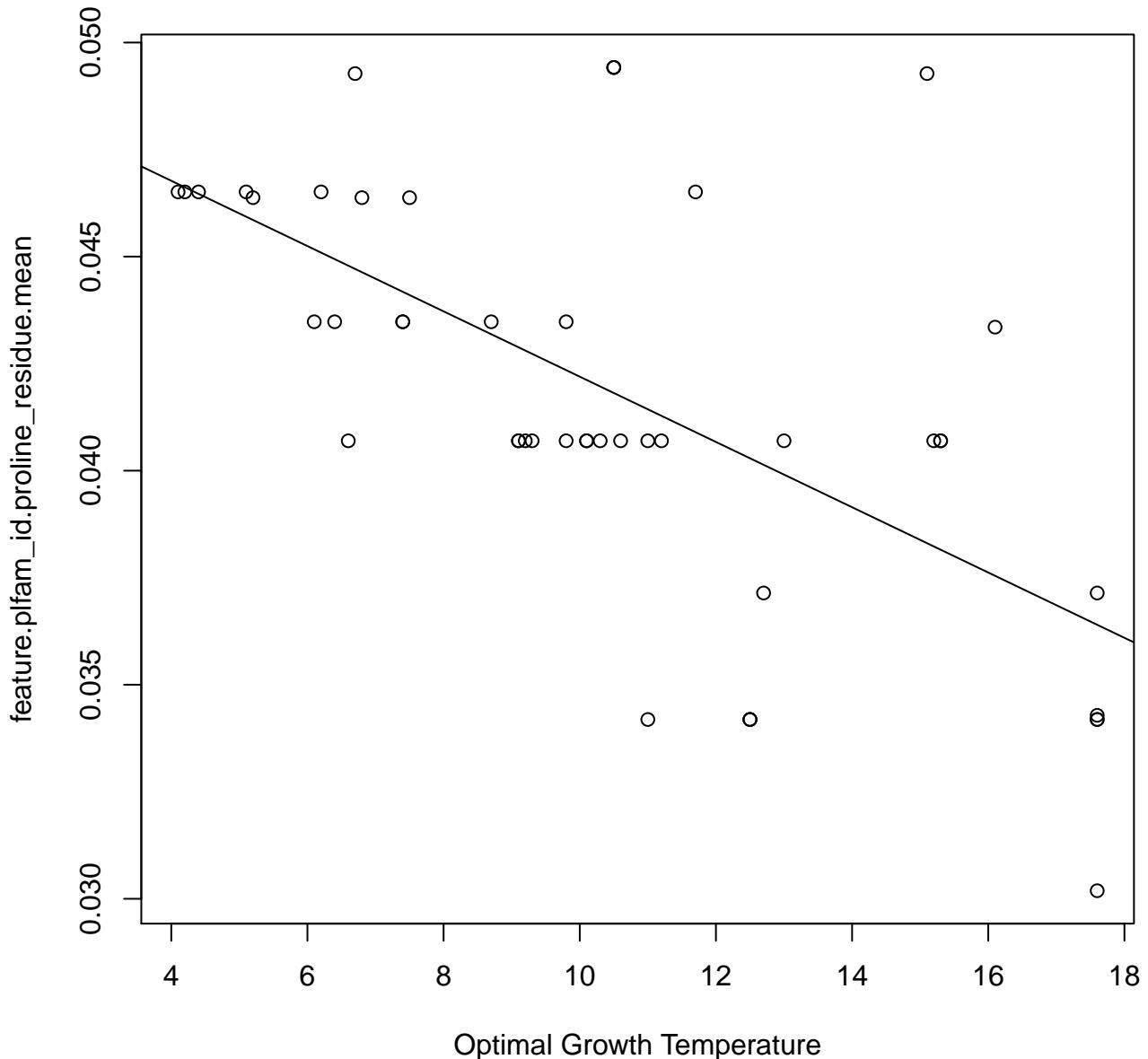
feature.plfam_id.proline_residue.mean
PLF_28228_00001101
Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake



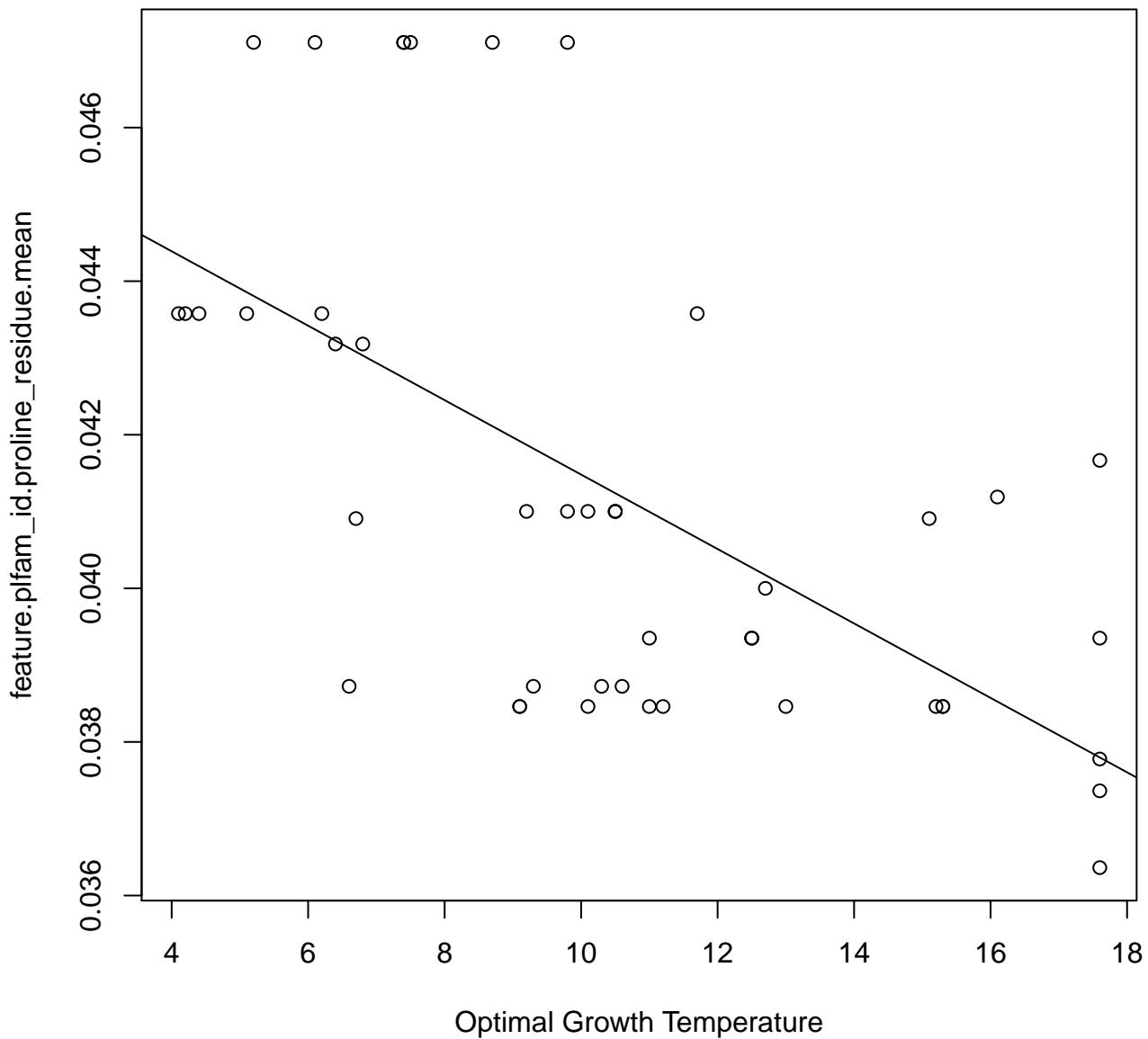
feature.plfam_id.proline_residue.mean
PLF_28228_00003580
Putative formate dehydrogenase oxidoreductase protein



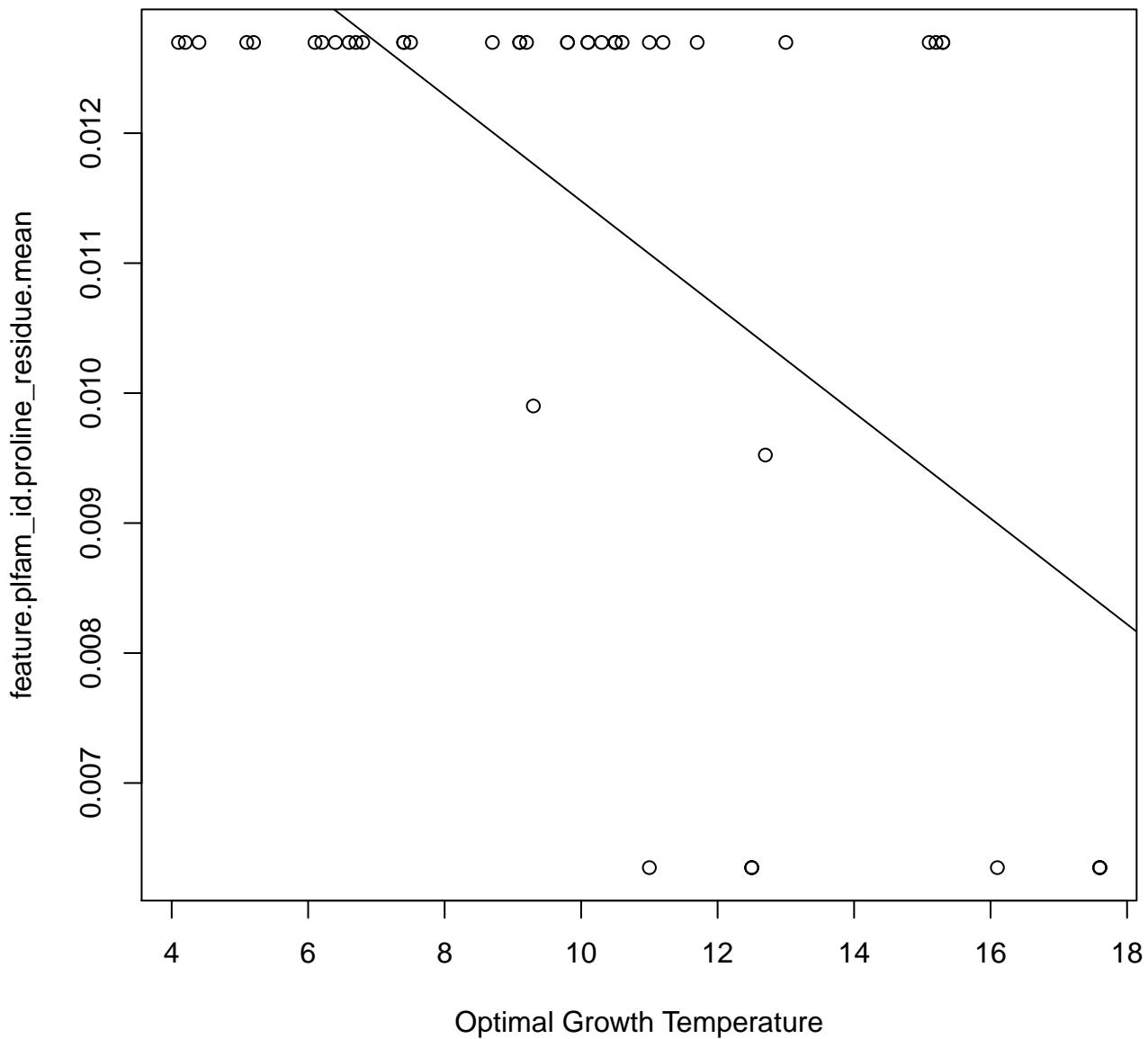
feature.plfam_id.proline_residue.mean
PLF_28228_00000628
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)



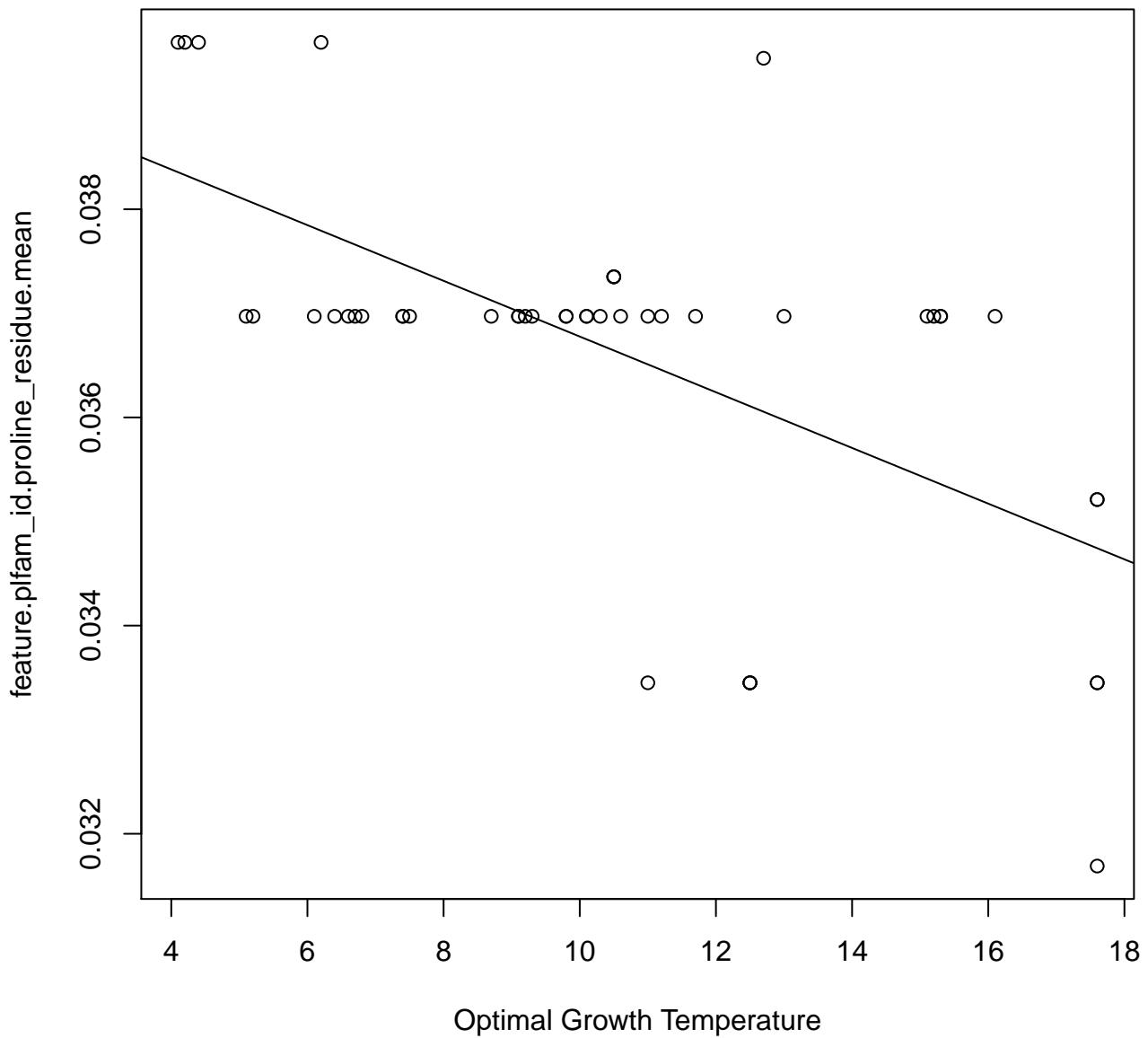
feature.plfam_id.proline_residue.mean
PLF_28228_00000283
ATP-dependent RNA helicase VF1437



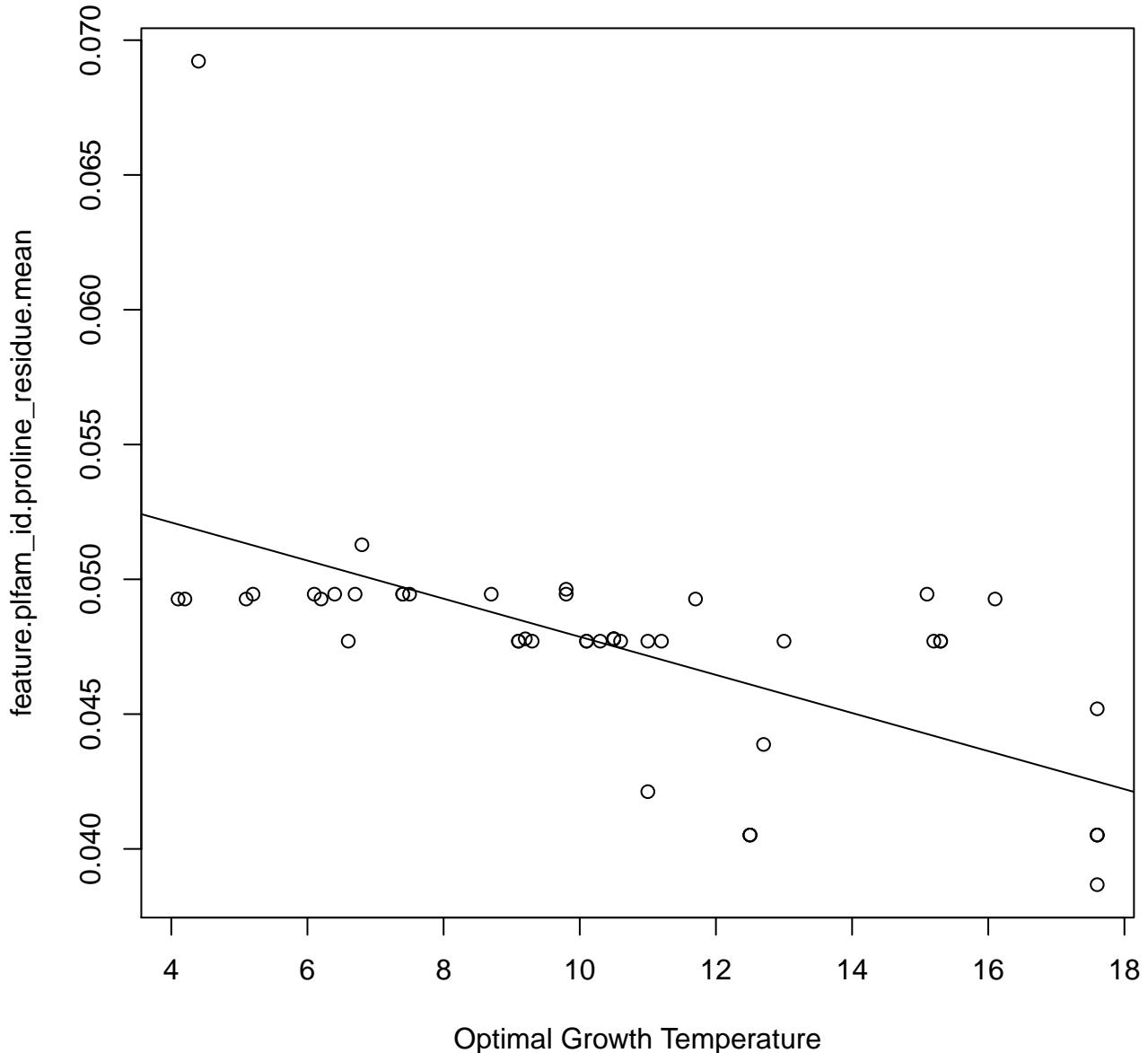
feature.plfam_id.proline_residue.mean
PLF_28228_00001012
Protein translocase subunit SecF



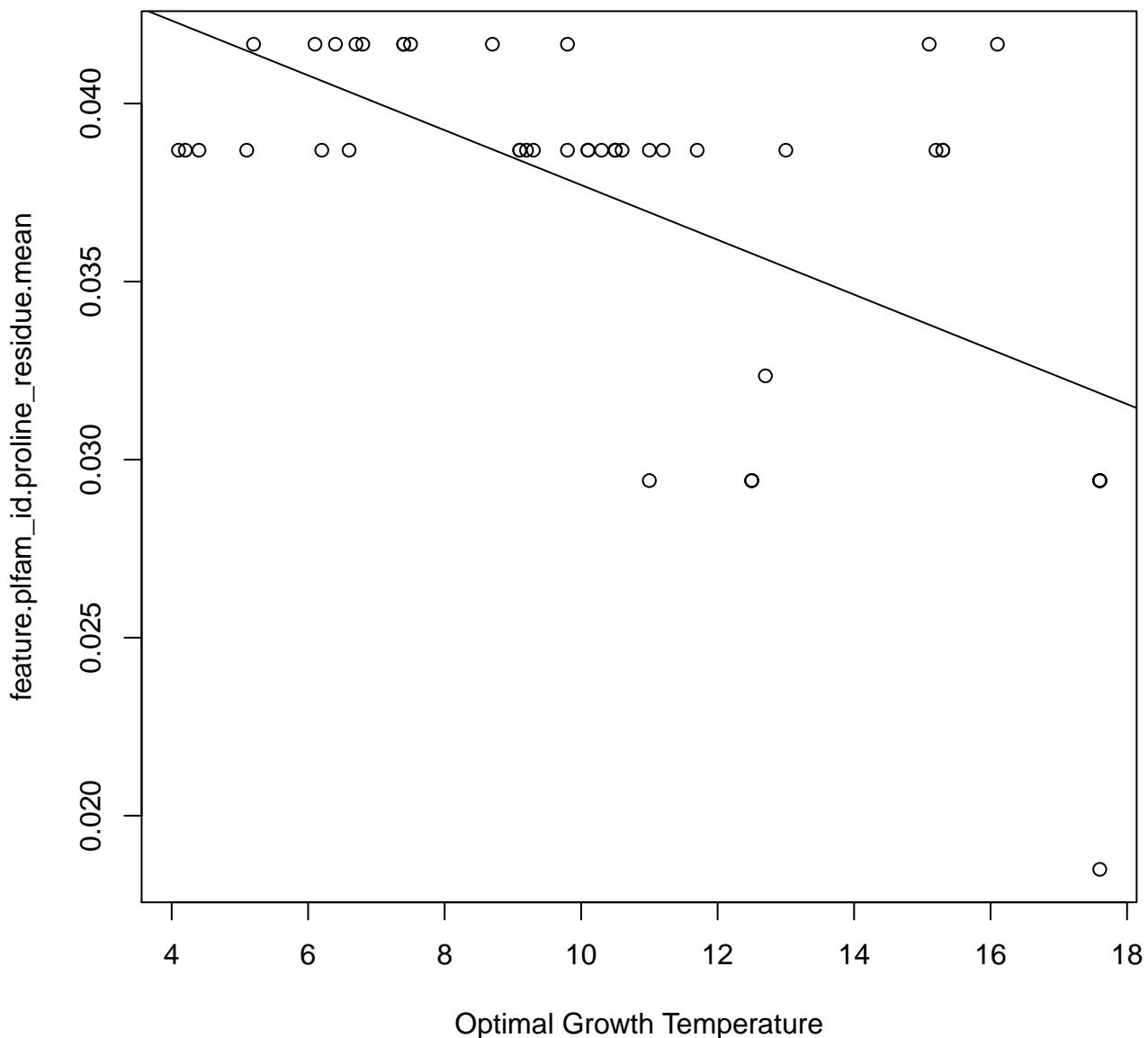
feature.plfam_id.proline_residue.mean
PLF_28228_00001161
Spermidine synthase N-terminal extension / Spermidine synthase (EC 2.5.1.16)



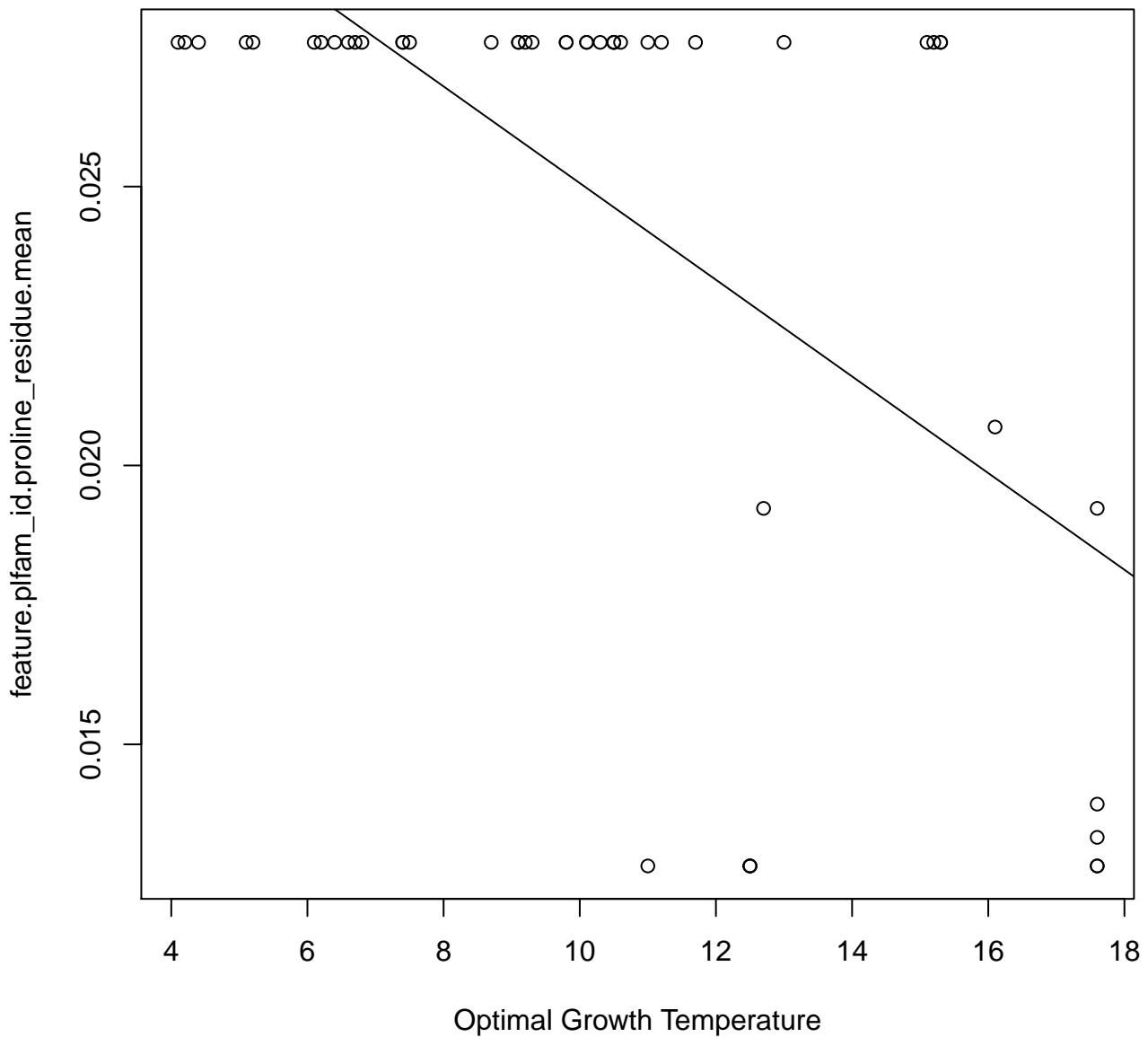
feature.plfam_id.proline_residue.mean
PLF_28228_00000523
Inner membrane protein translocase and chaperone YidC, long form



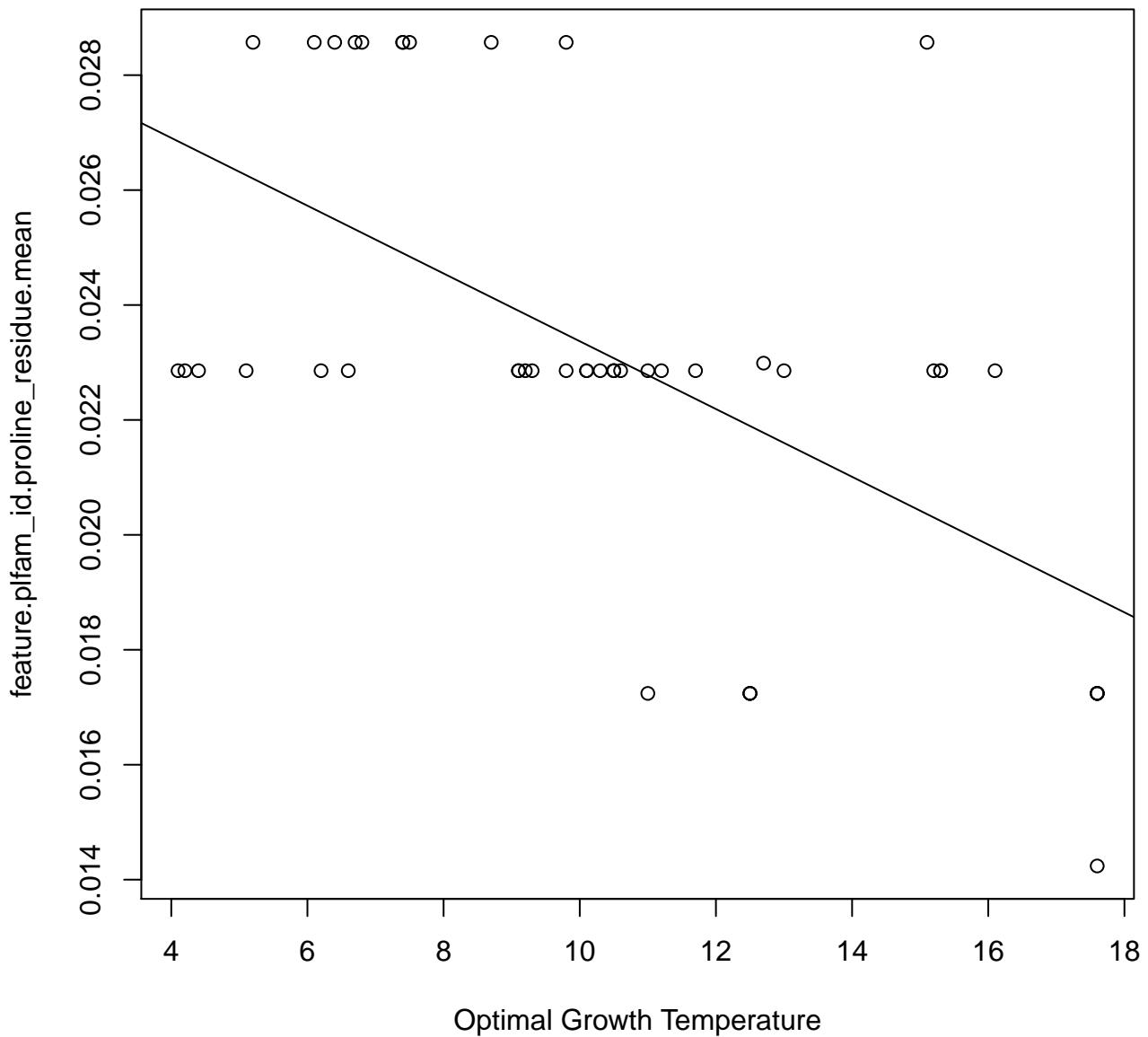
feature.plfam_id.proline_residue.mean
PLF_28228_00001275
UDP-glucose 4-epimerase (EC 5.1.3.2)



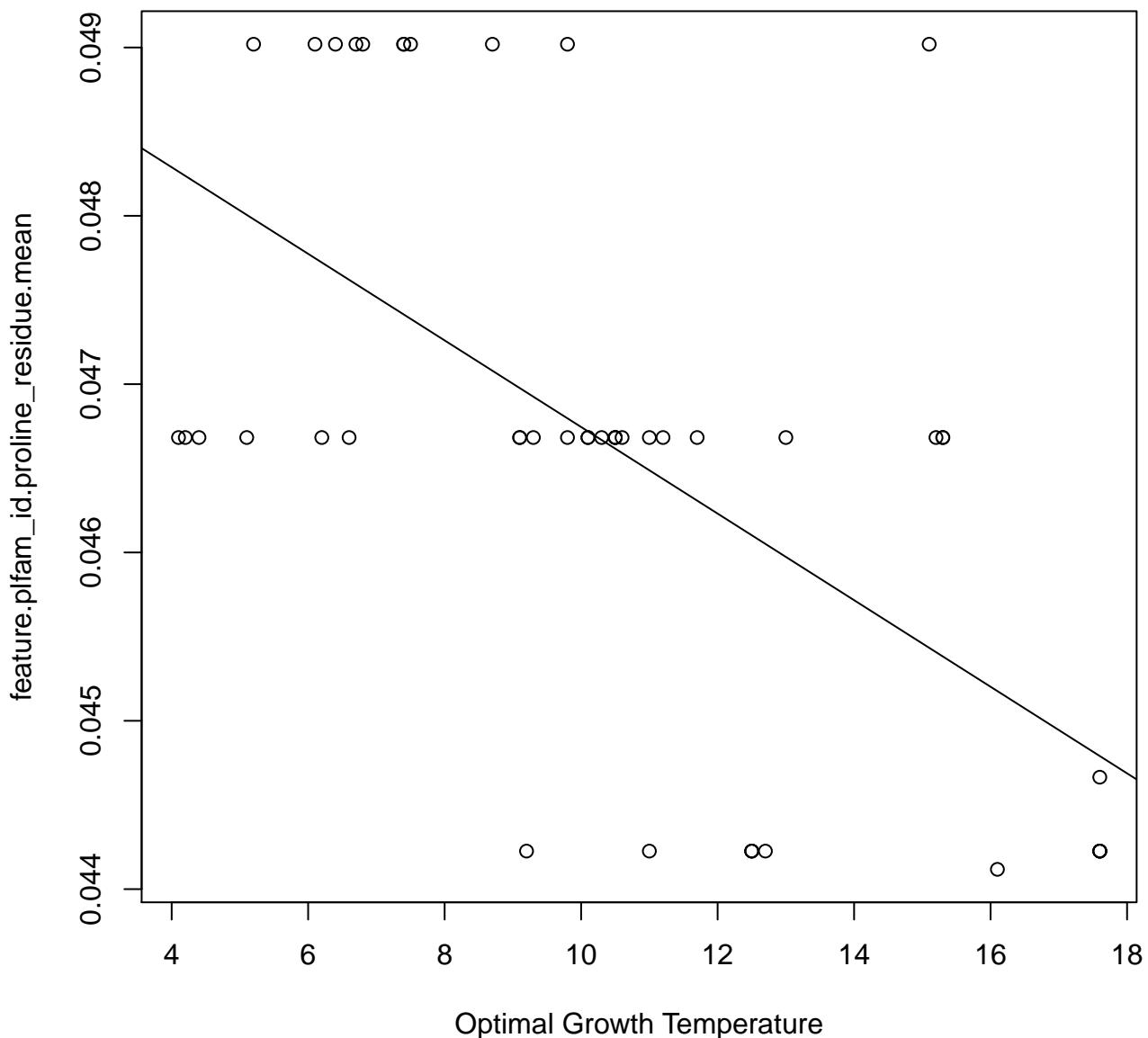
feature.plfam_id.proline_residue.mean
PLF_28228_00002264
hypothetical protein



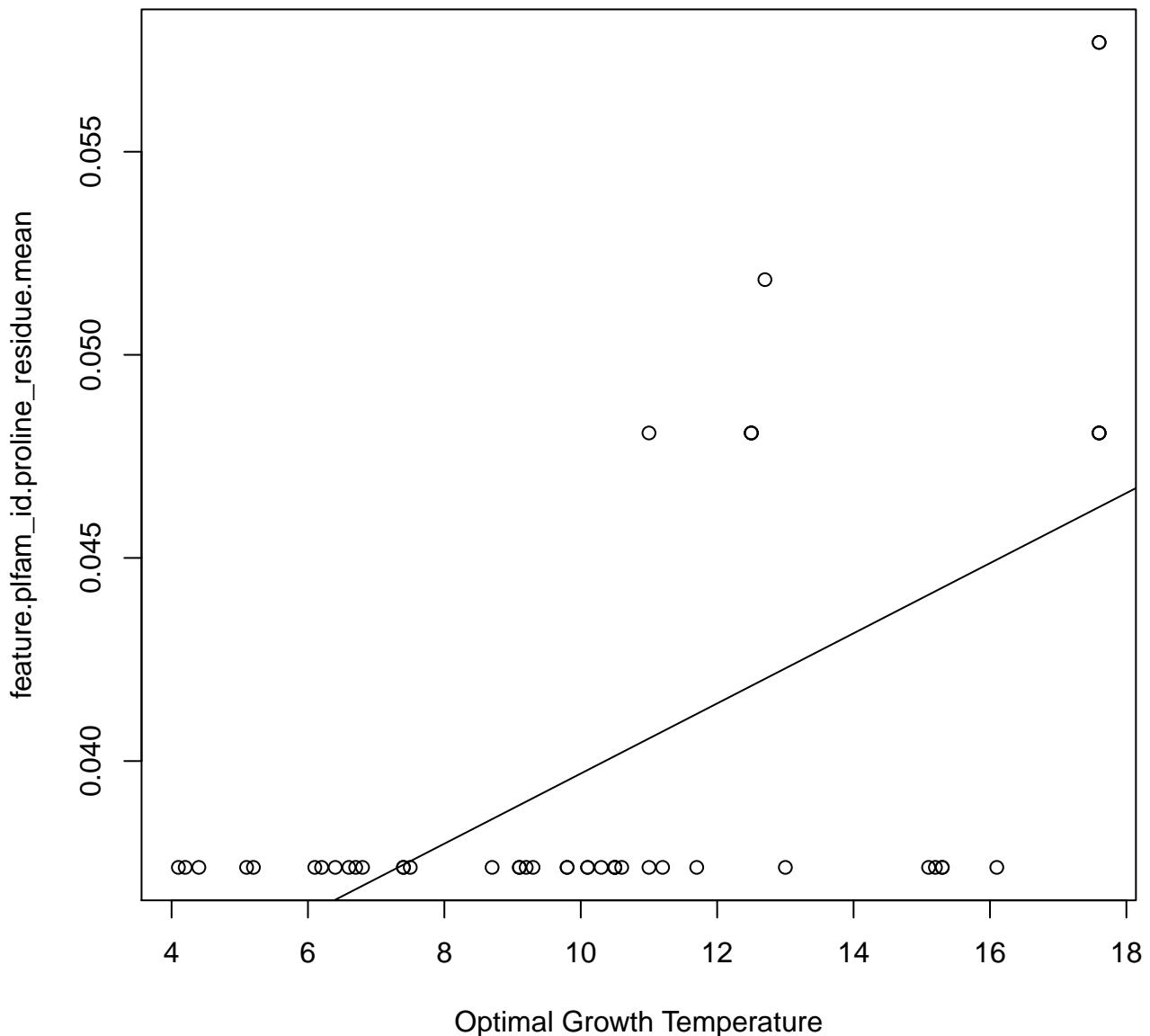
feature.plfam_id.proline_residue.mean
PLF_28228_00000122
Flavodoxin 1



feature.plfam_id.proline_residue.mean
PLF_28228_00000654
Na(+)–translocating NADH–quinone reductase subunit F (EC 1.6.5.8)

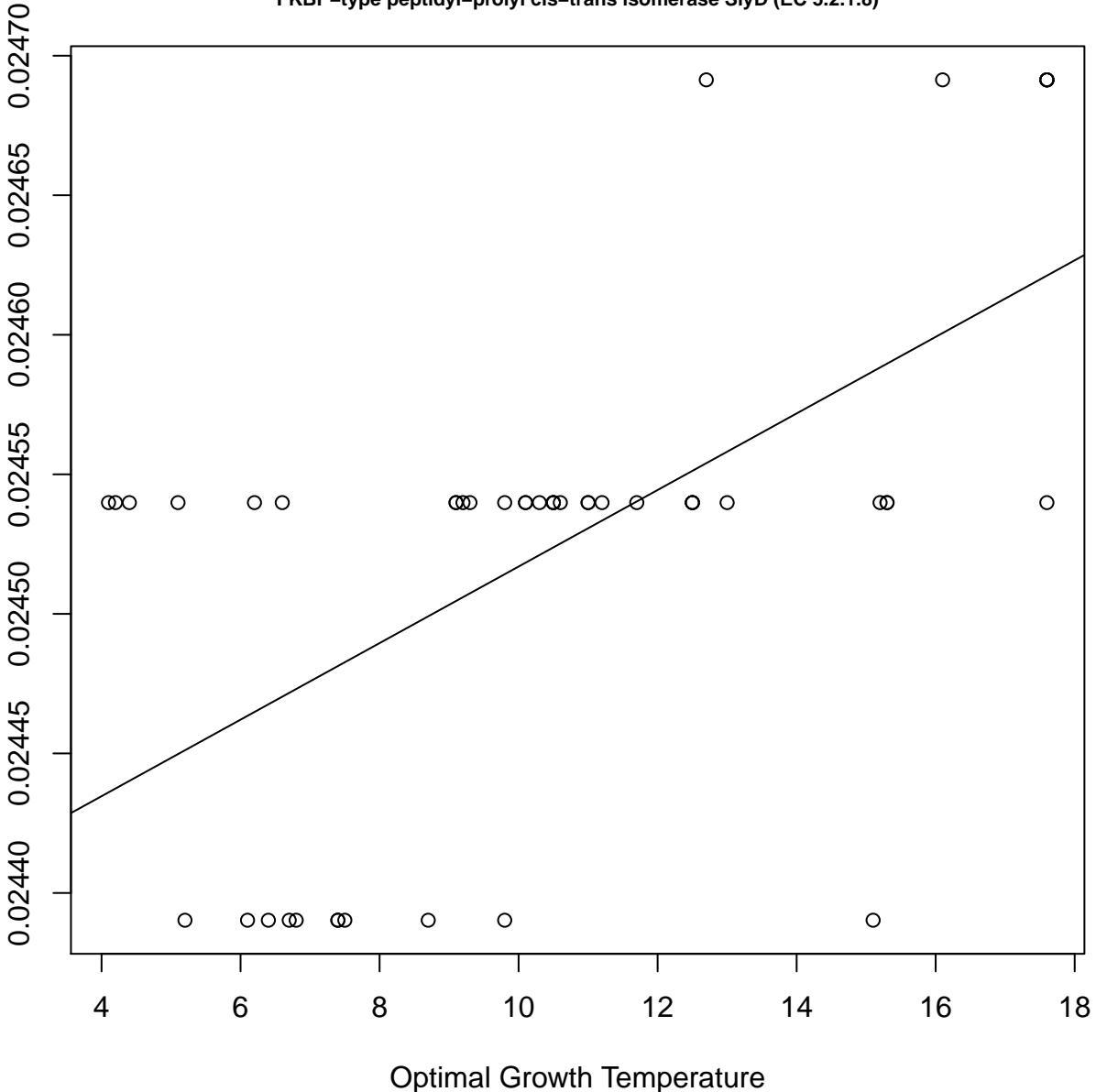


feature.plfam_id.proline_residue.mean
PLF_28228_00001680
Cell division protein BolA



feature.pfam_id.proline_residue.mean
PLF_28228_00000467
FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)

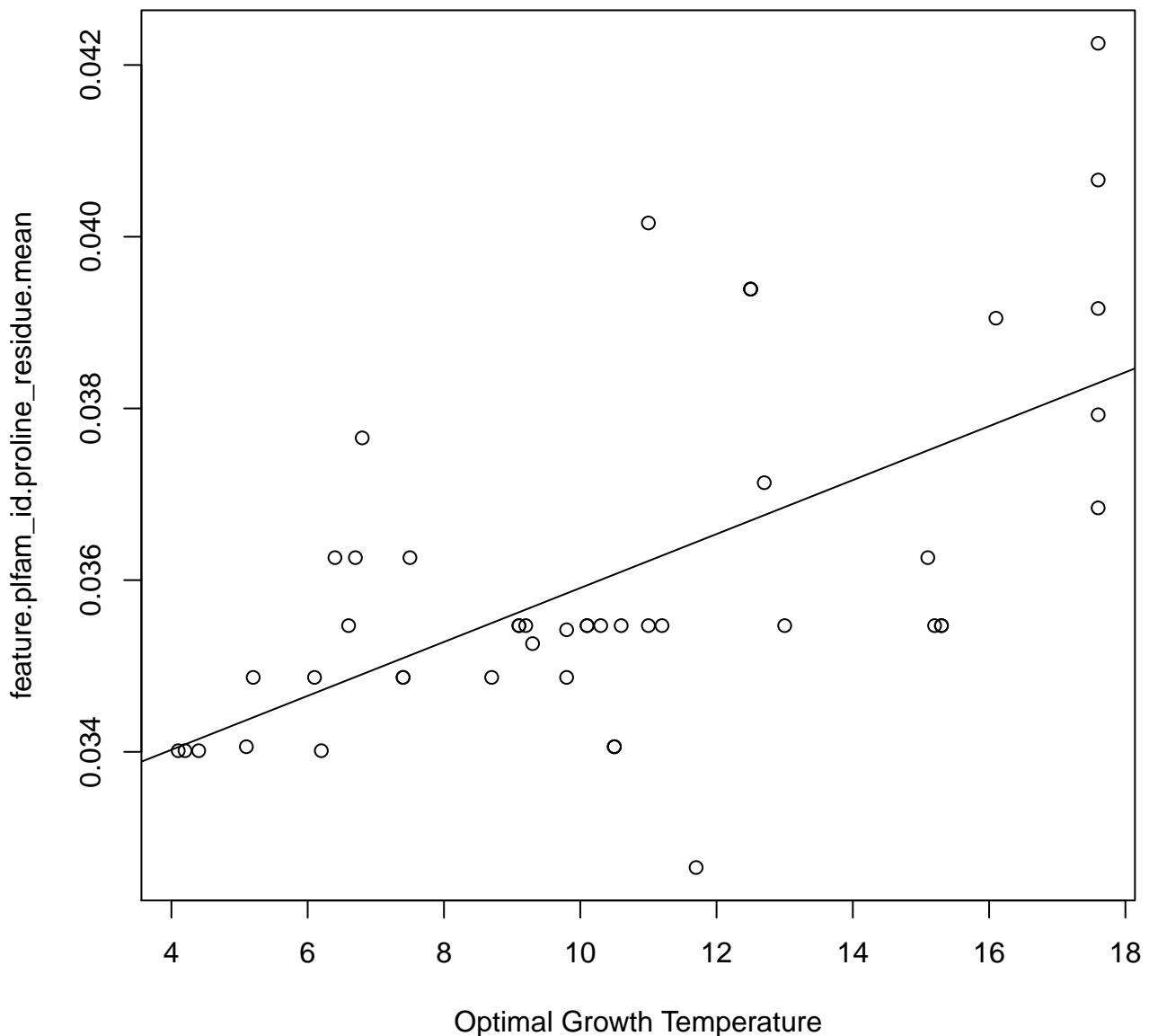
feature.pfam_id.proline_residue.mean



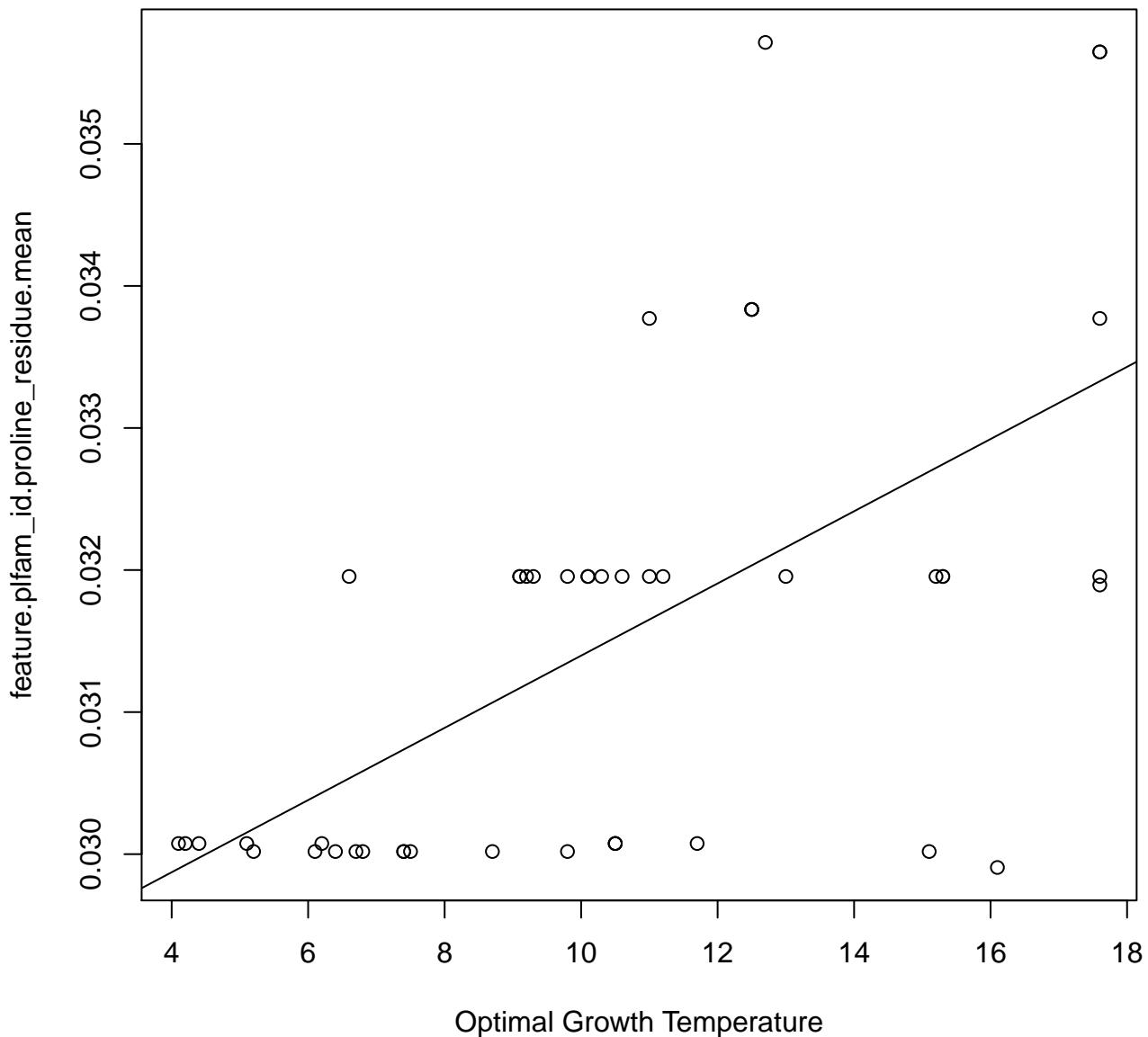
feature.plfam_id.proline_residue.mean

PLF_28228_00000291

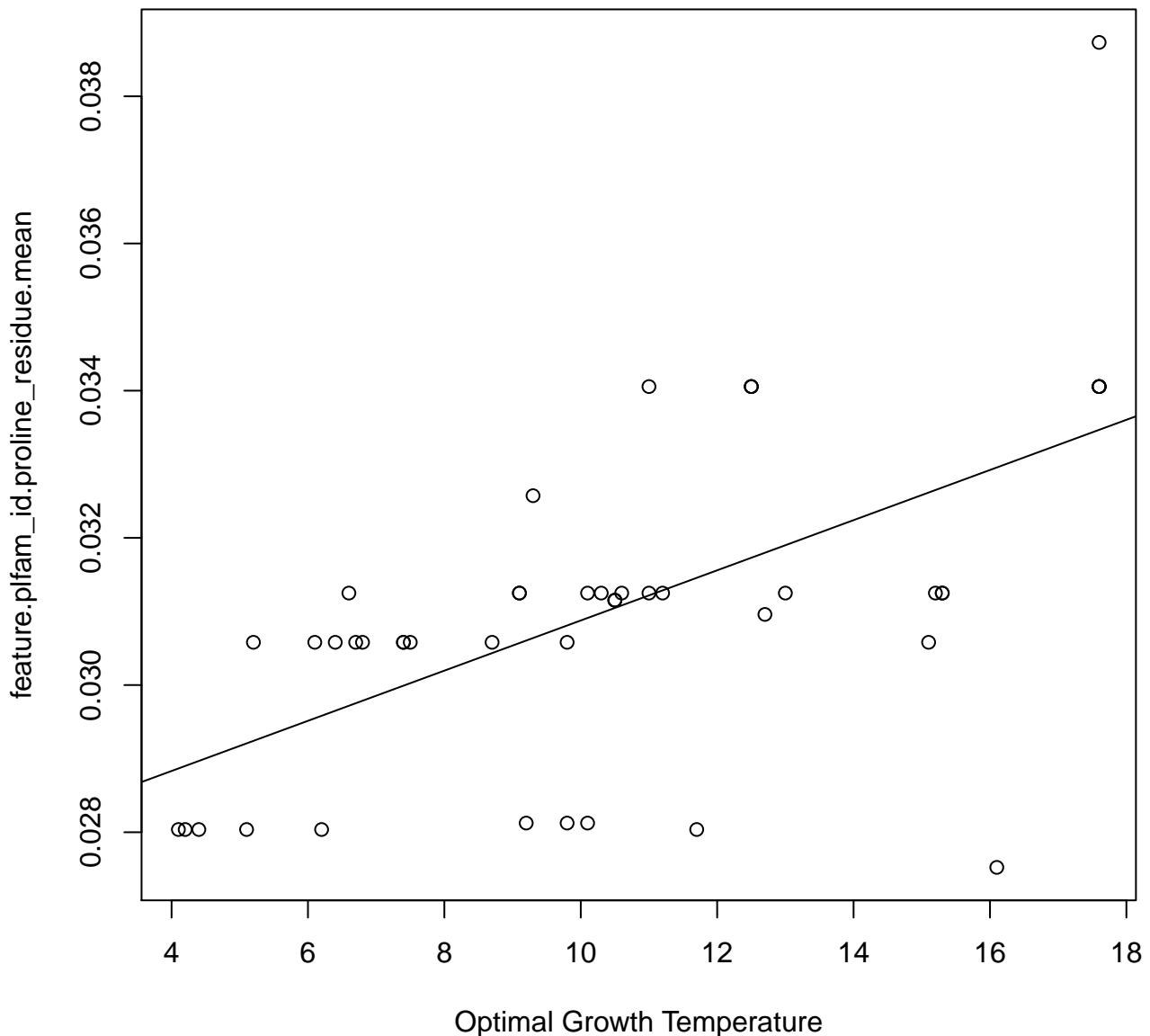
2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxy-



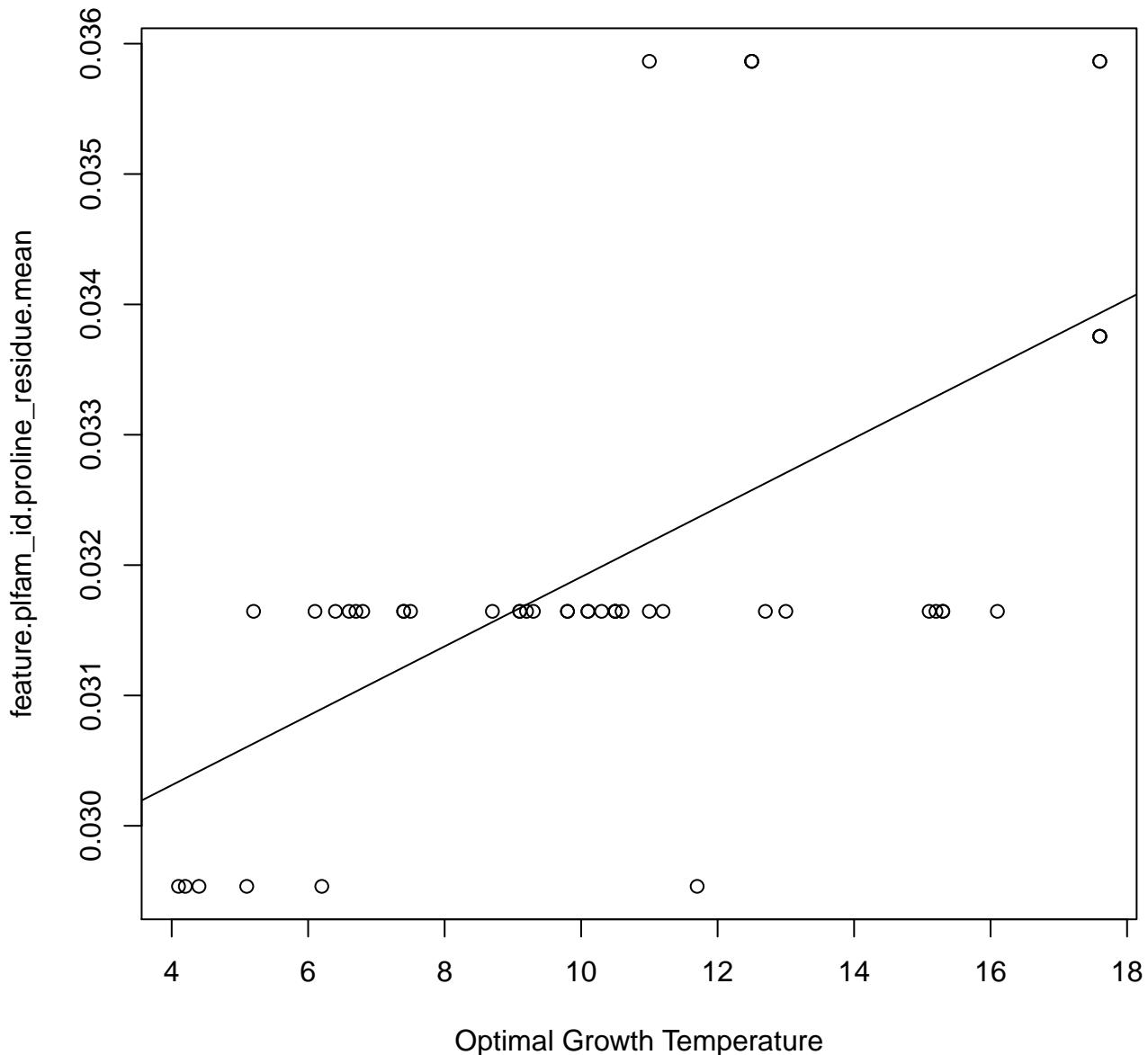
feature.plfam_id.proline_residue.mean
PLF_28228_00000808
L-aspartate oxidase (EC 1.4.3.16)



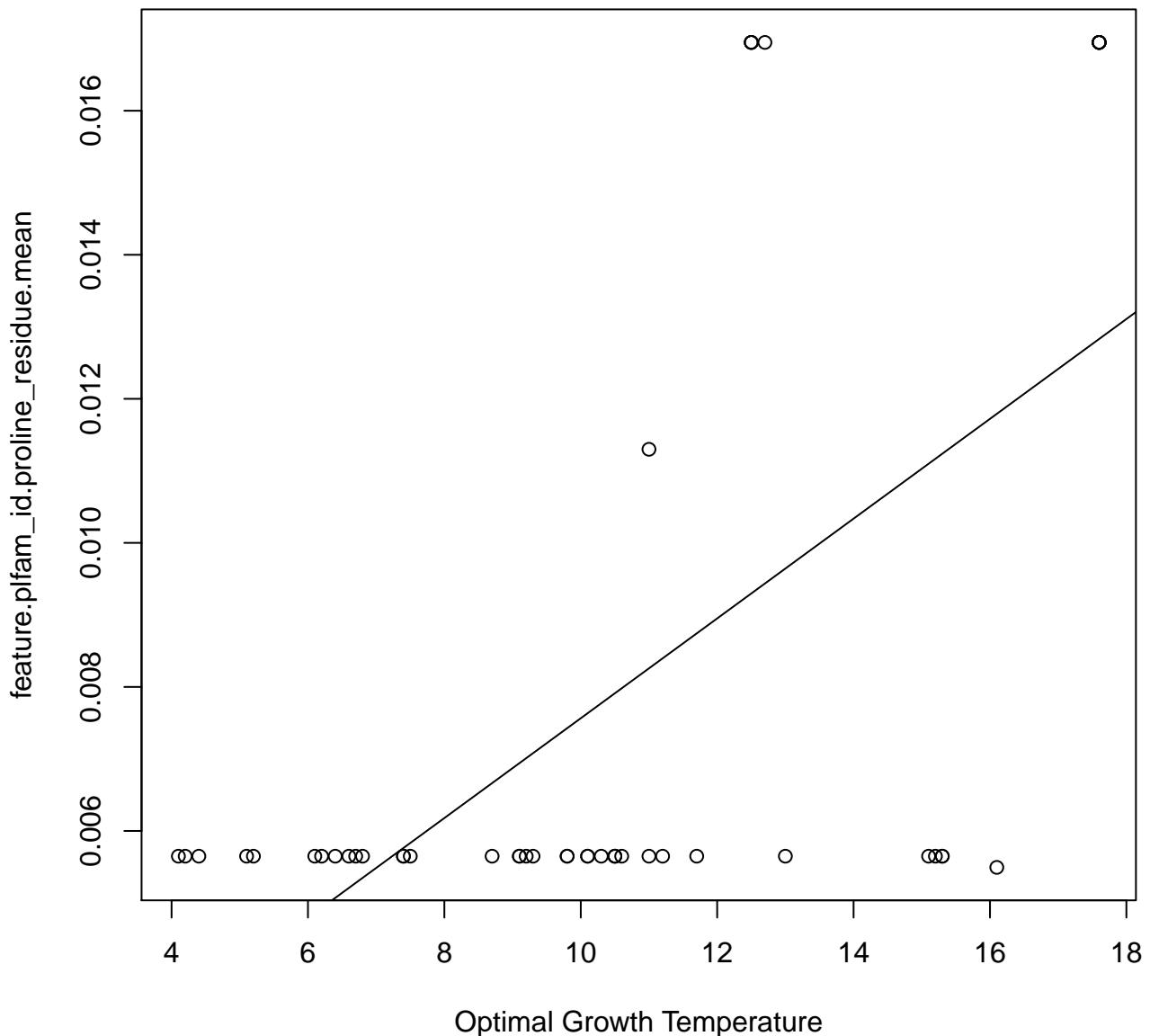
feature.plfam_id.proline_residue.mean
PLF_28228_00000436
Cytochrome c oxidase (cbb3-type) subunit CcoP (EC 1.9.3.1)



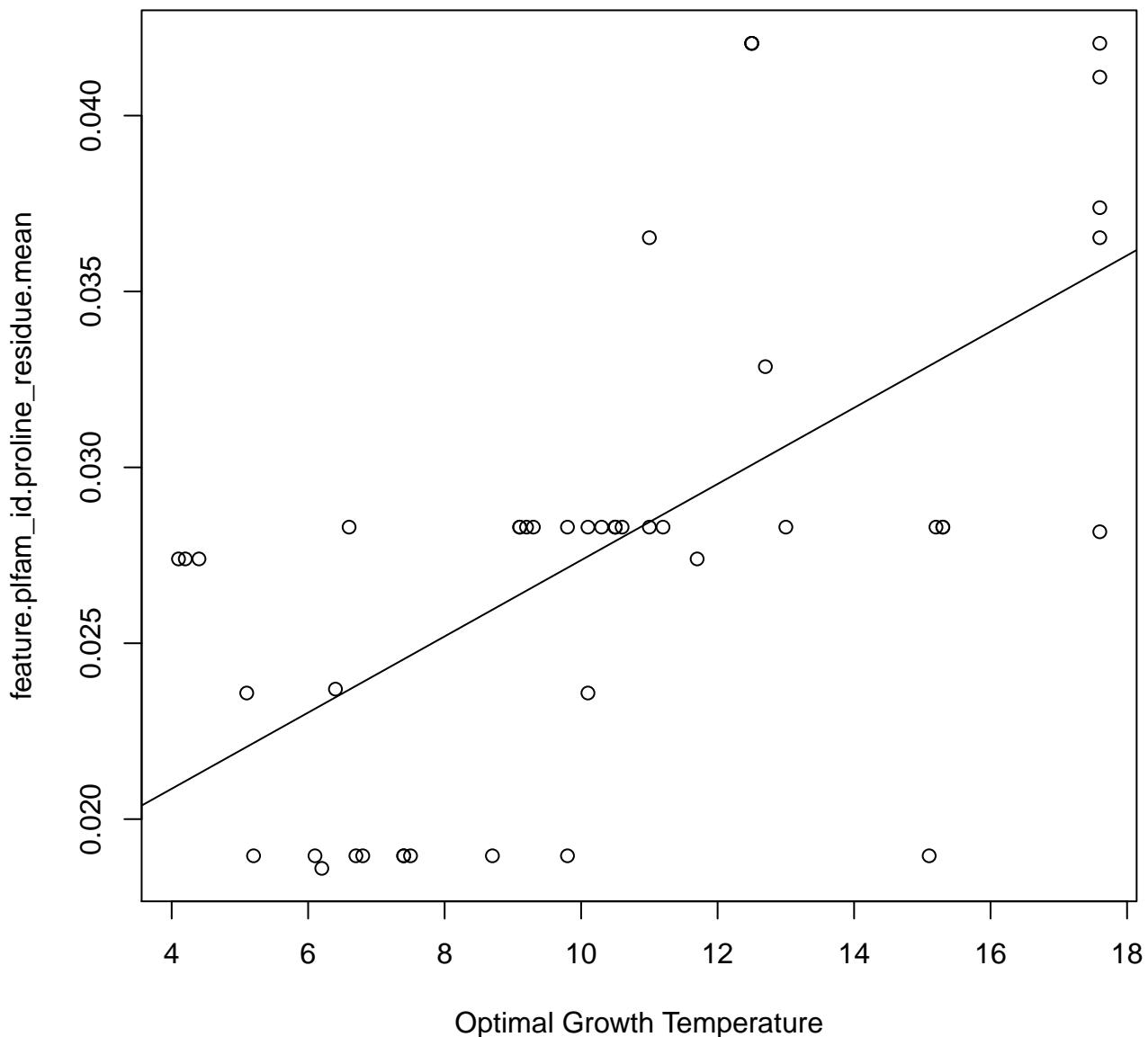
feature.plfam_id.proline_residue.mean
PLF_28228_00002074
Sodium-dependent transporter, SNF family



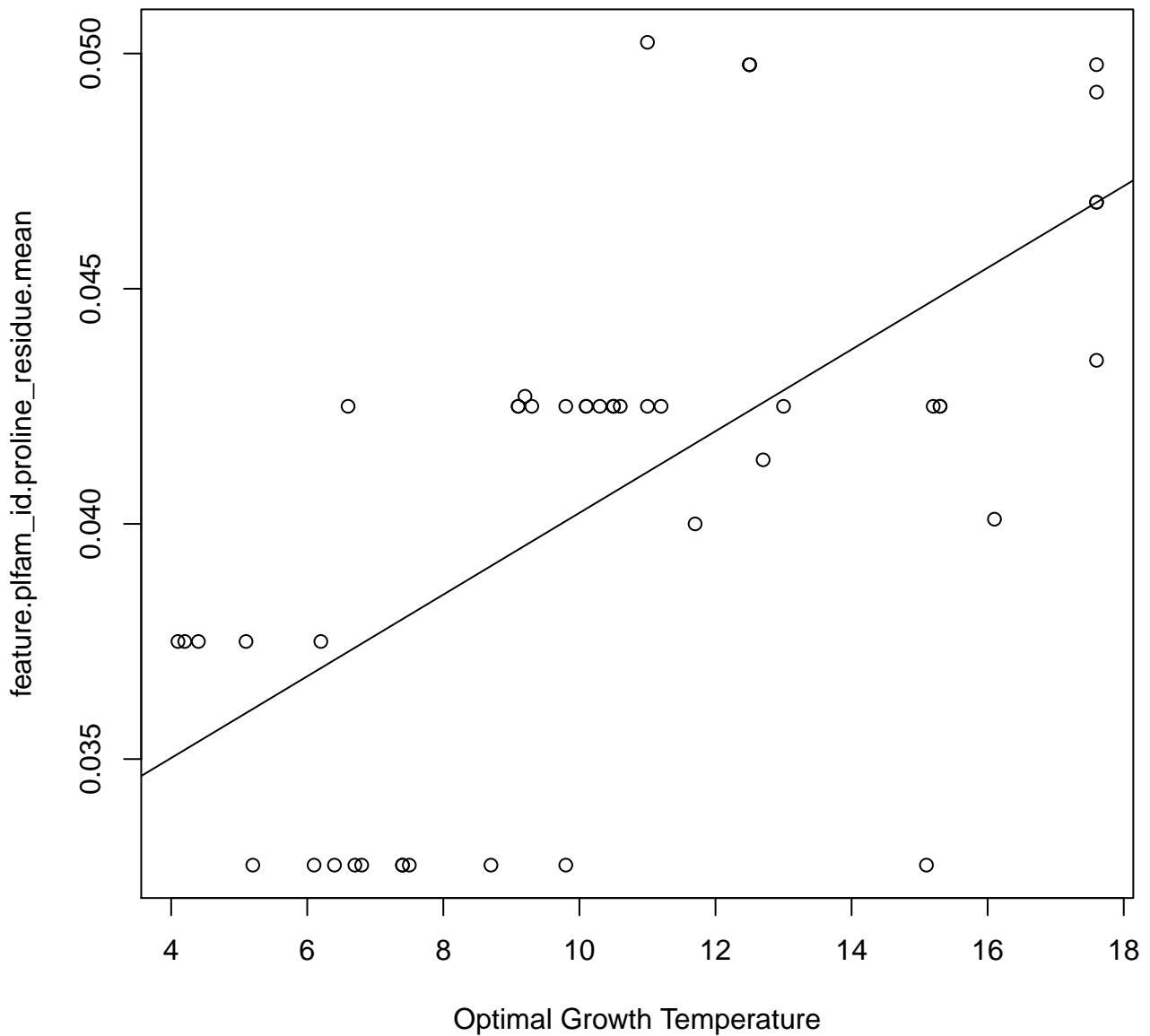
feature.plfam_id.proline_residue.mean
PLF_28228_00001309
YaeQ protein



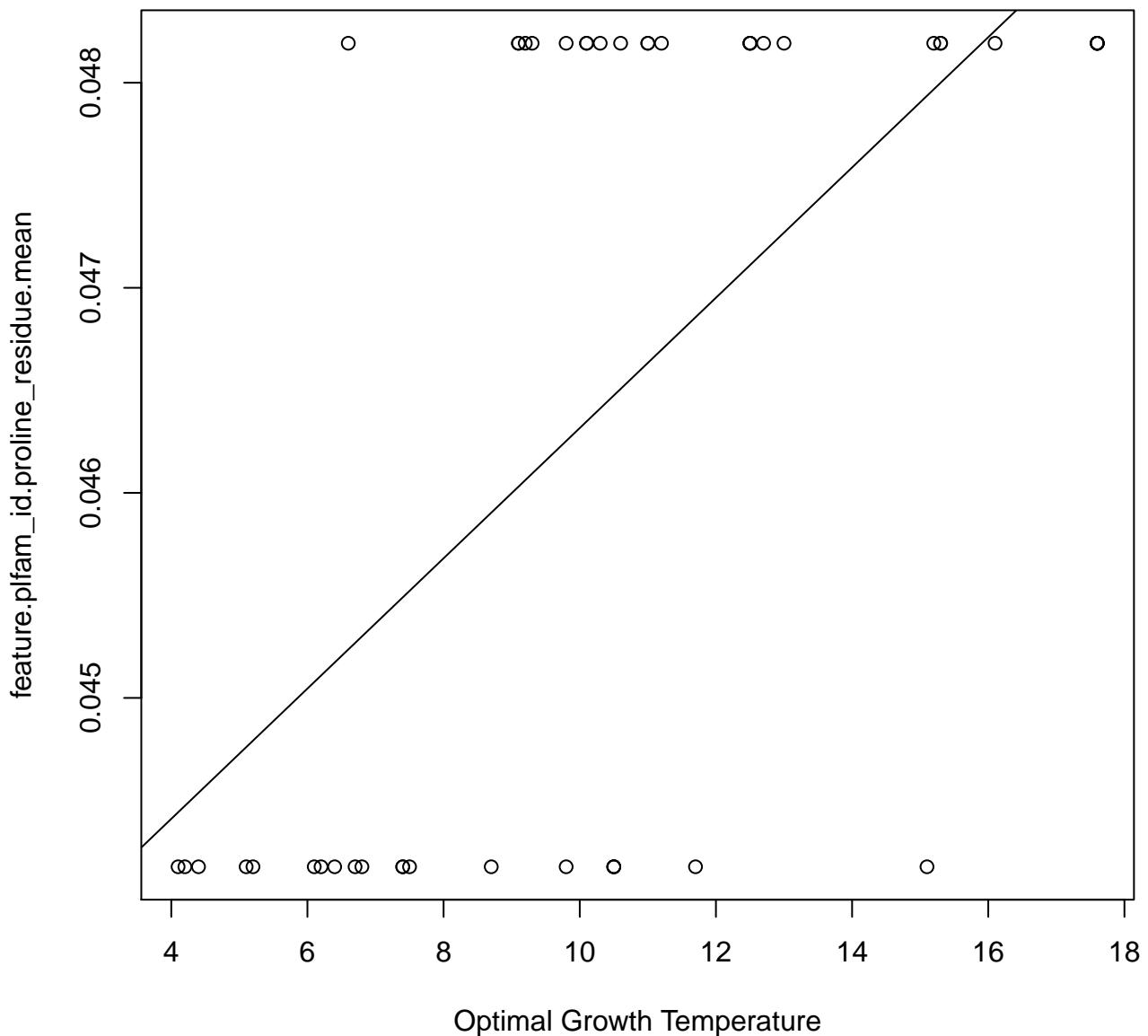
feature.plfam_id.proline_residue.mean
PLF_28228_00004197
ADP-ribose pyrophosphatase (EC 3.6.1.13)



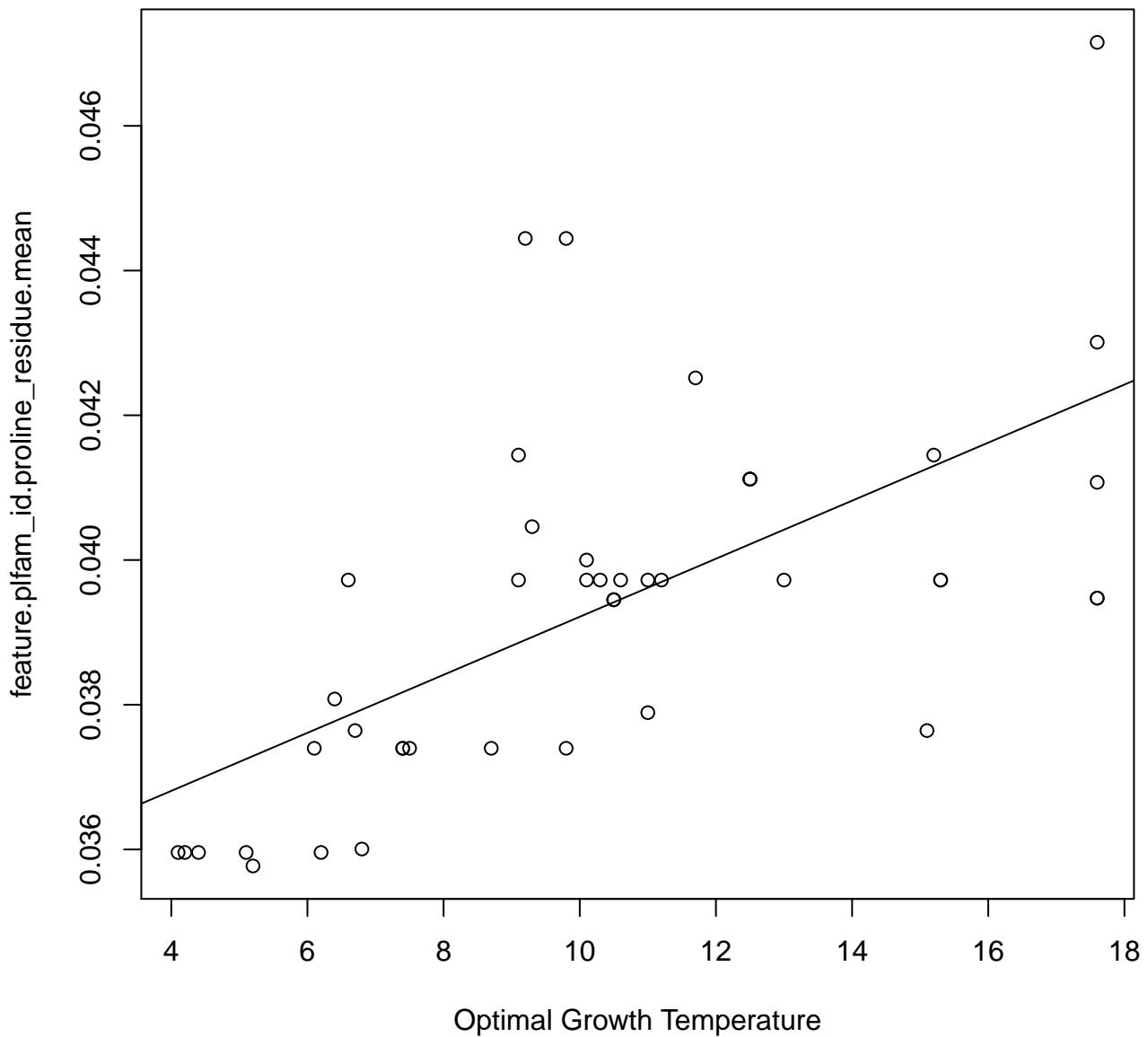
feature.plfam_id.proline_residue.mean
PLF_28228_00001909
Multidrug resistance transporter, Bcr/CfIA family



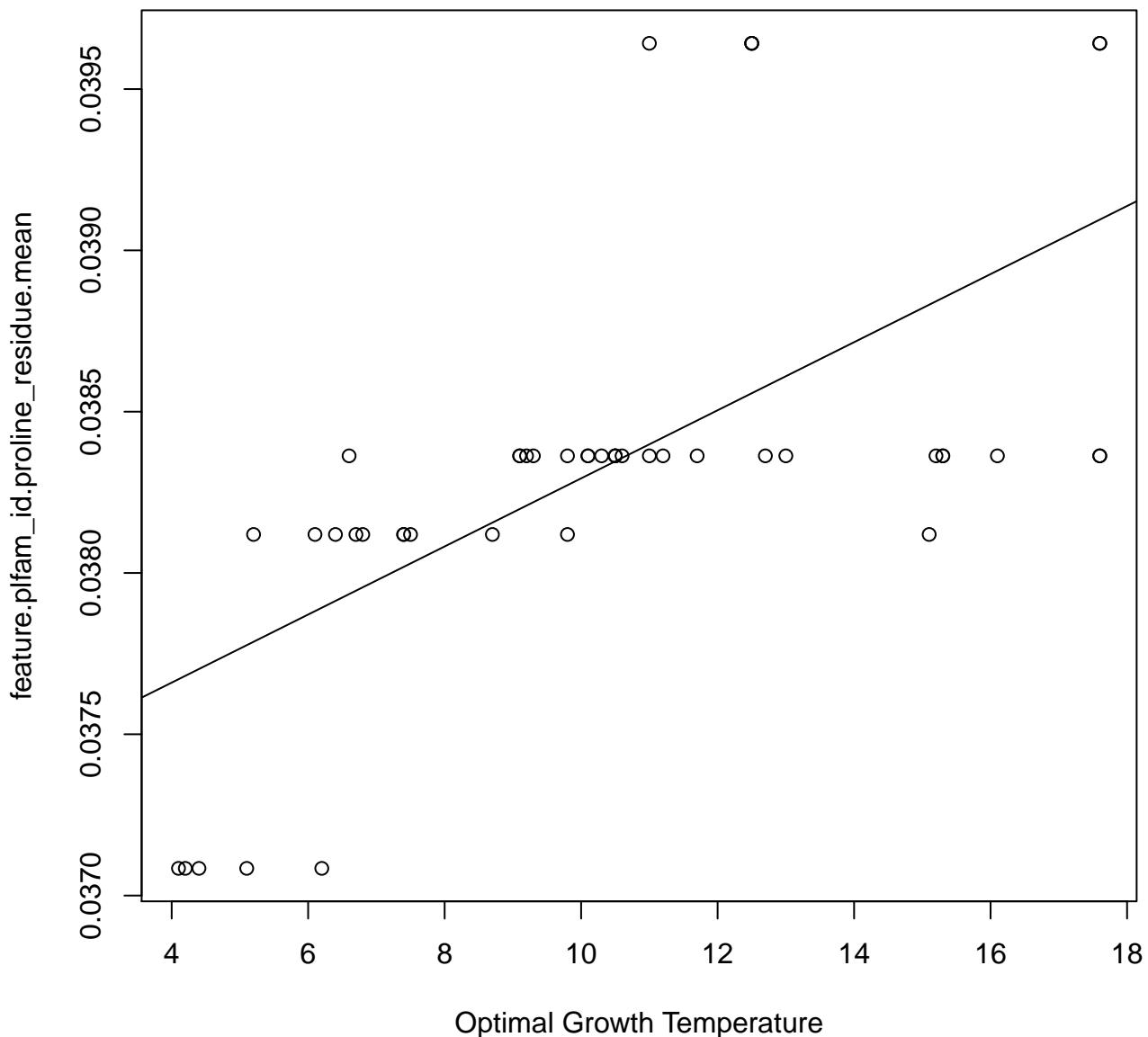
feature.plfam_id.proline_residue.mean
PLF_28228_00000234
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117)



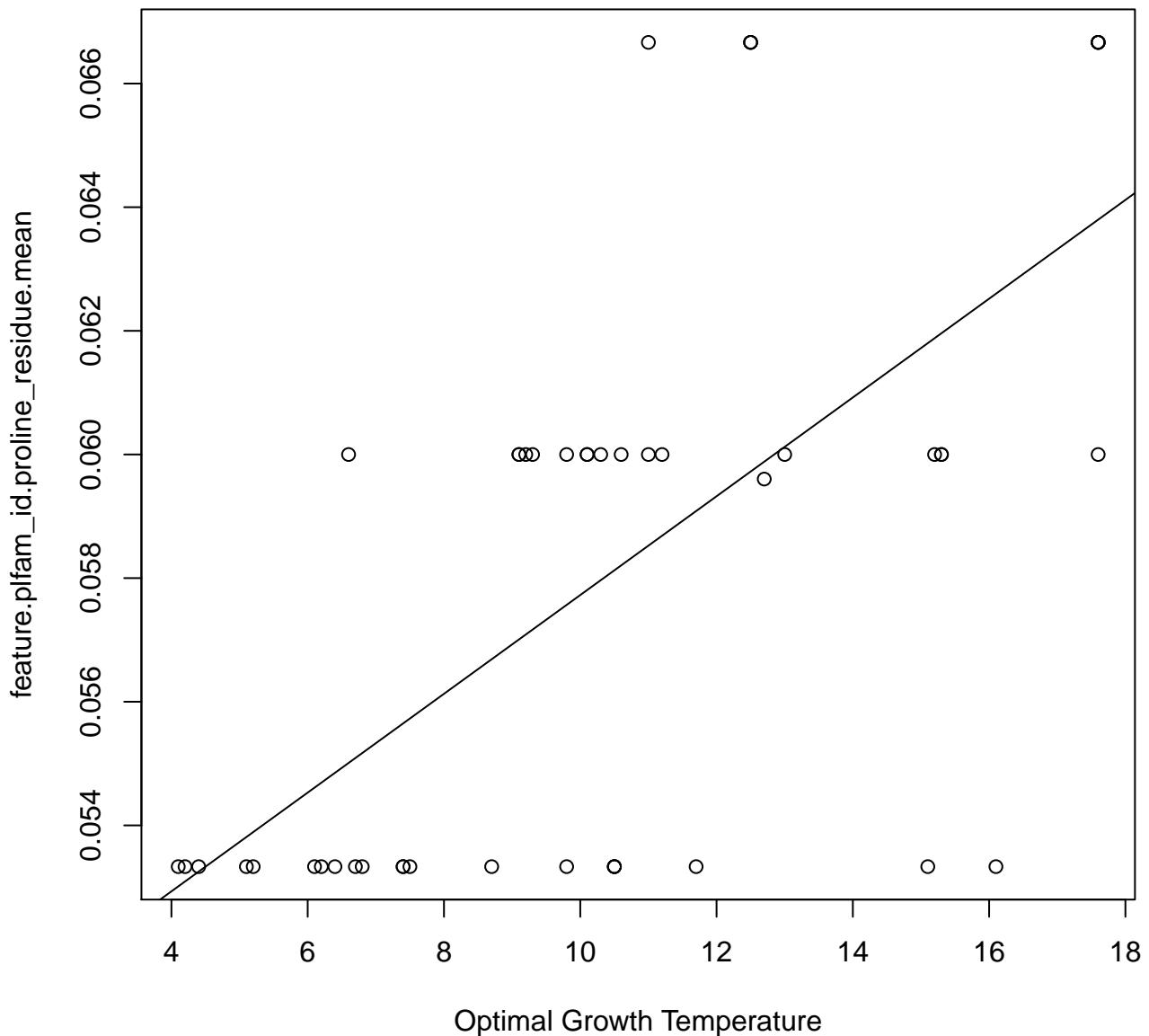
feature.plfam_id.proline_residue.mean
PLF_28228_00002320
hypothetical protein



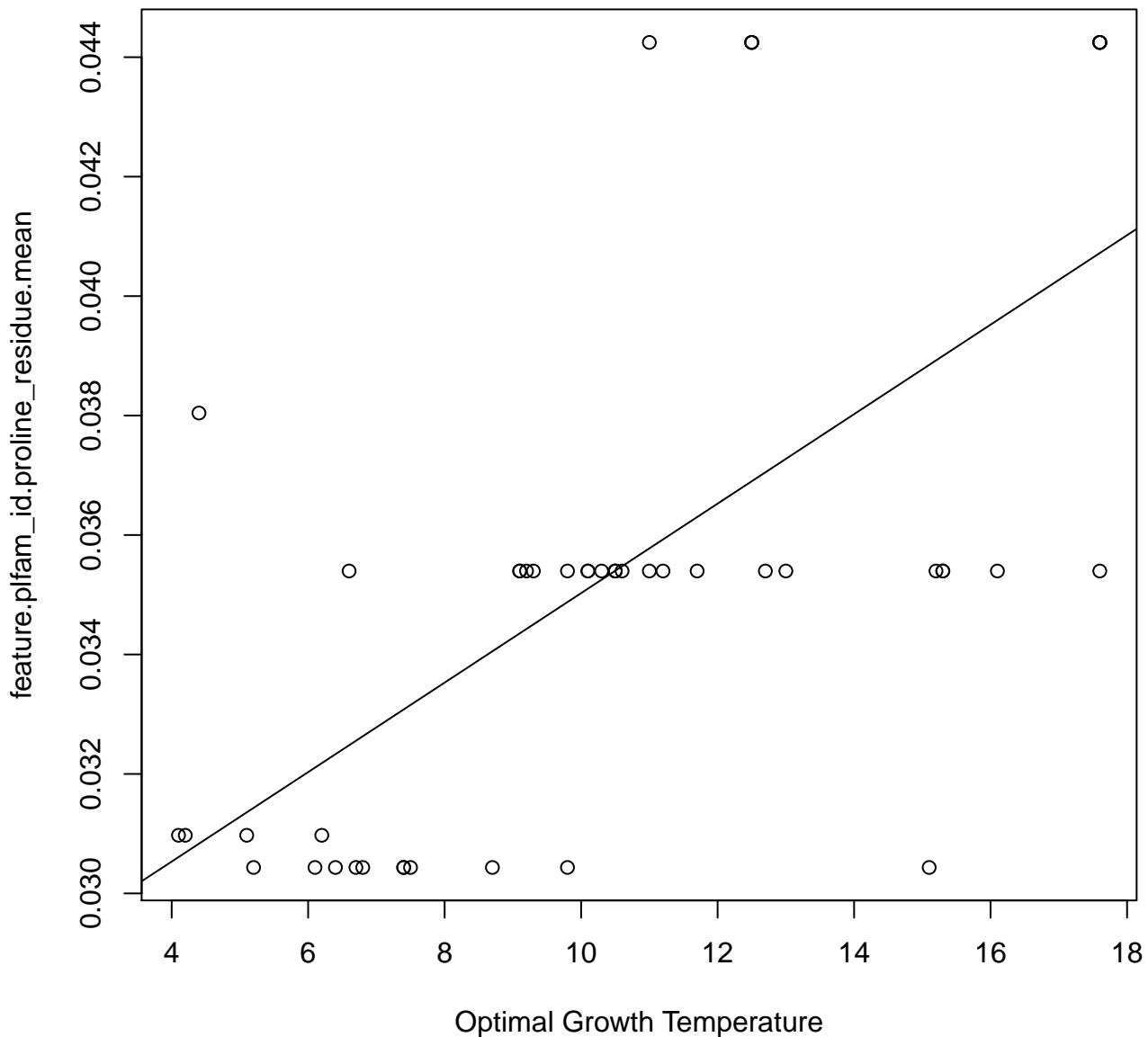
feature.plfam_id.proline_residue.mean
PLF_28228_00000288
ATP-dependent protease La (EC 3.4.21.53) Type I



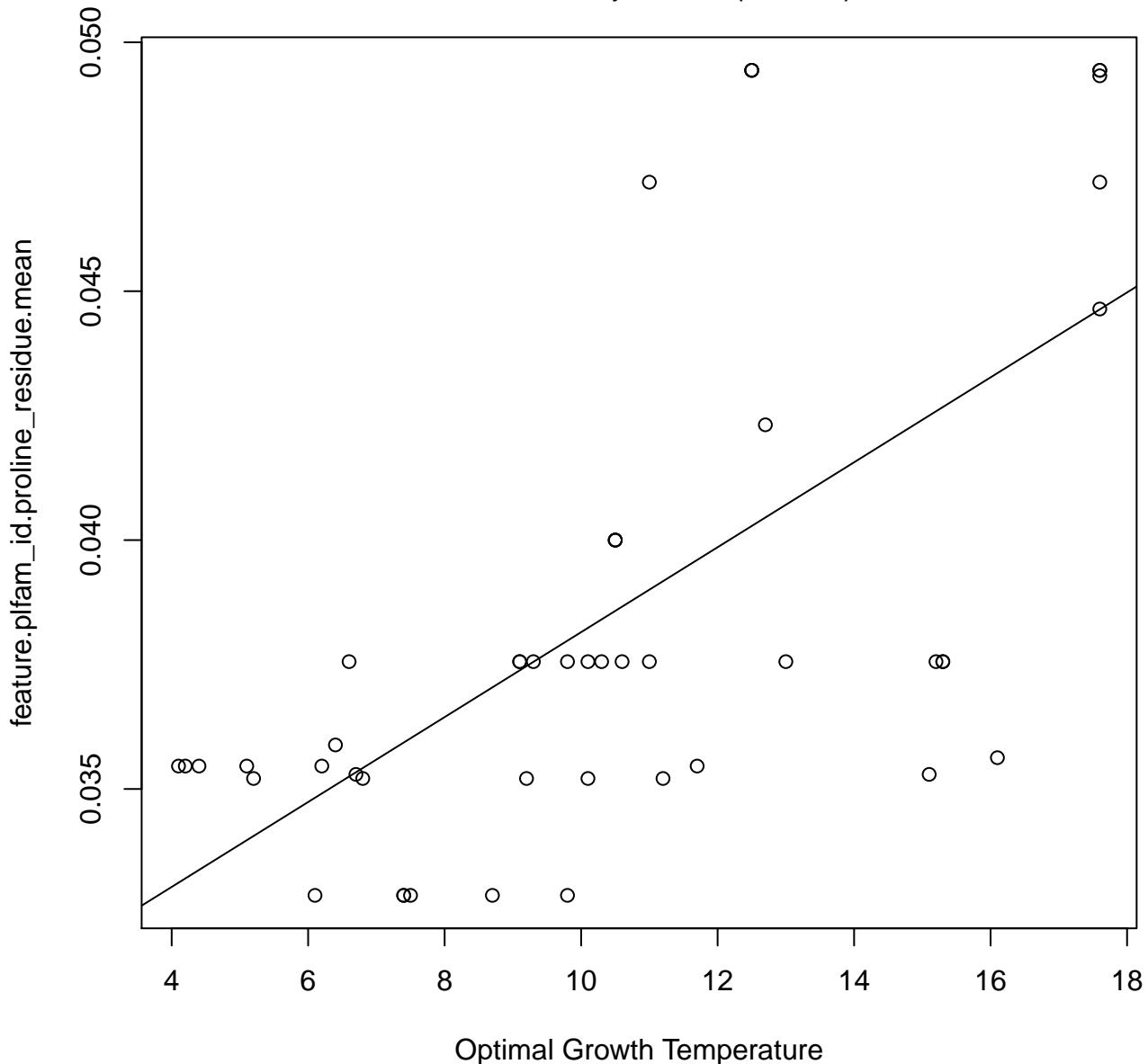
feature.plfam_id.proline_residue.mean
PLF_28228_00000716
3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1.59)



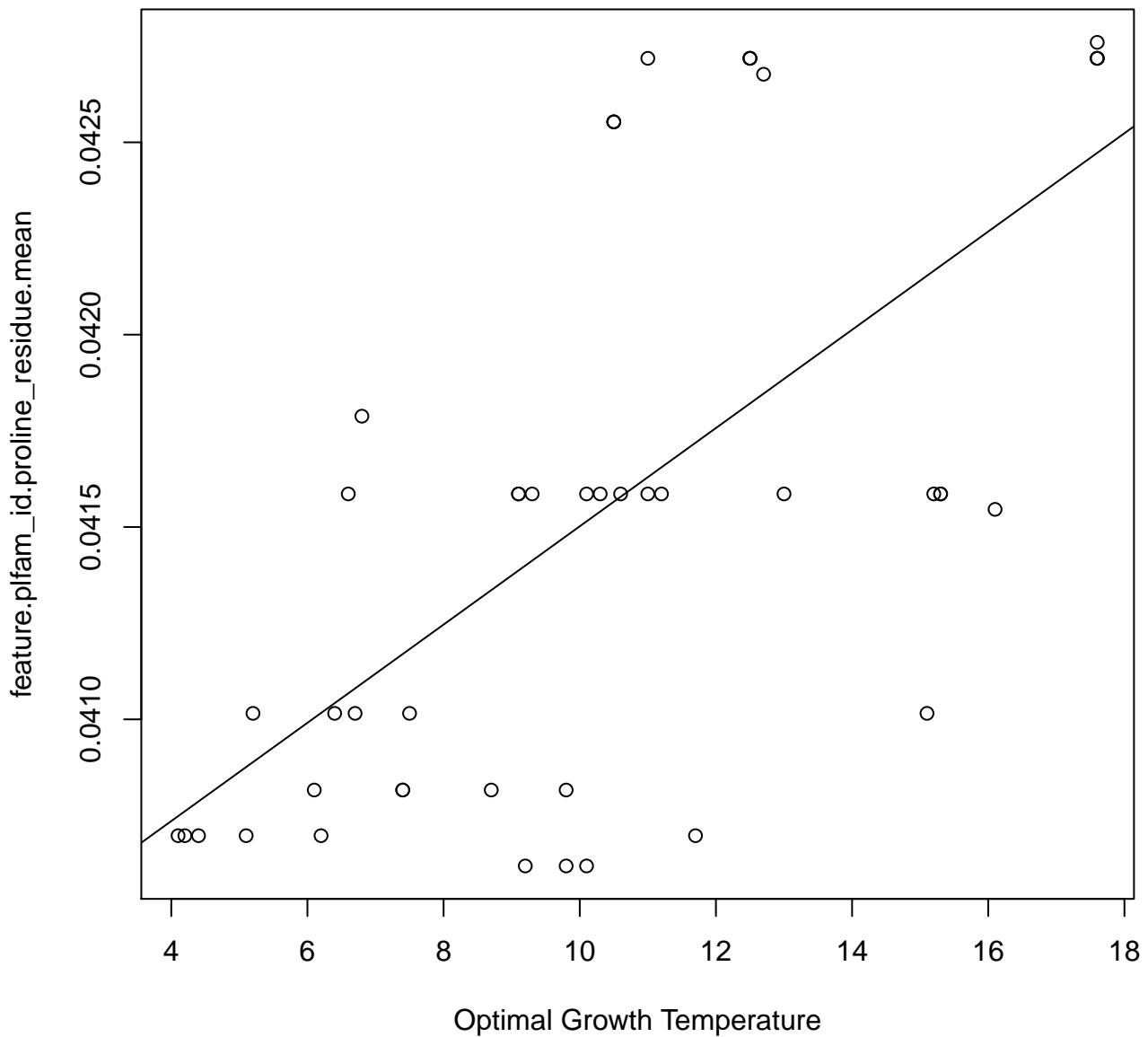
feature.plfam_id.proline_residue.mean
PLF_28228_00000431
Cytidylate kinase (EC 2.7.4.25)



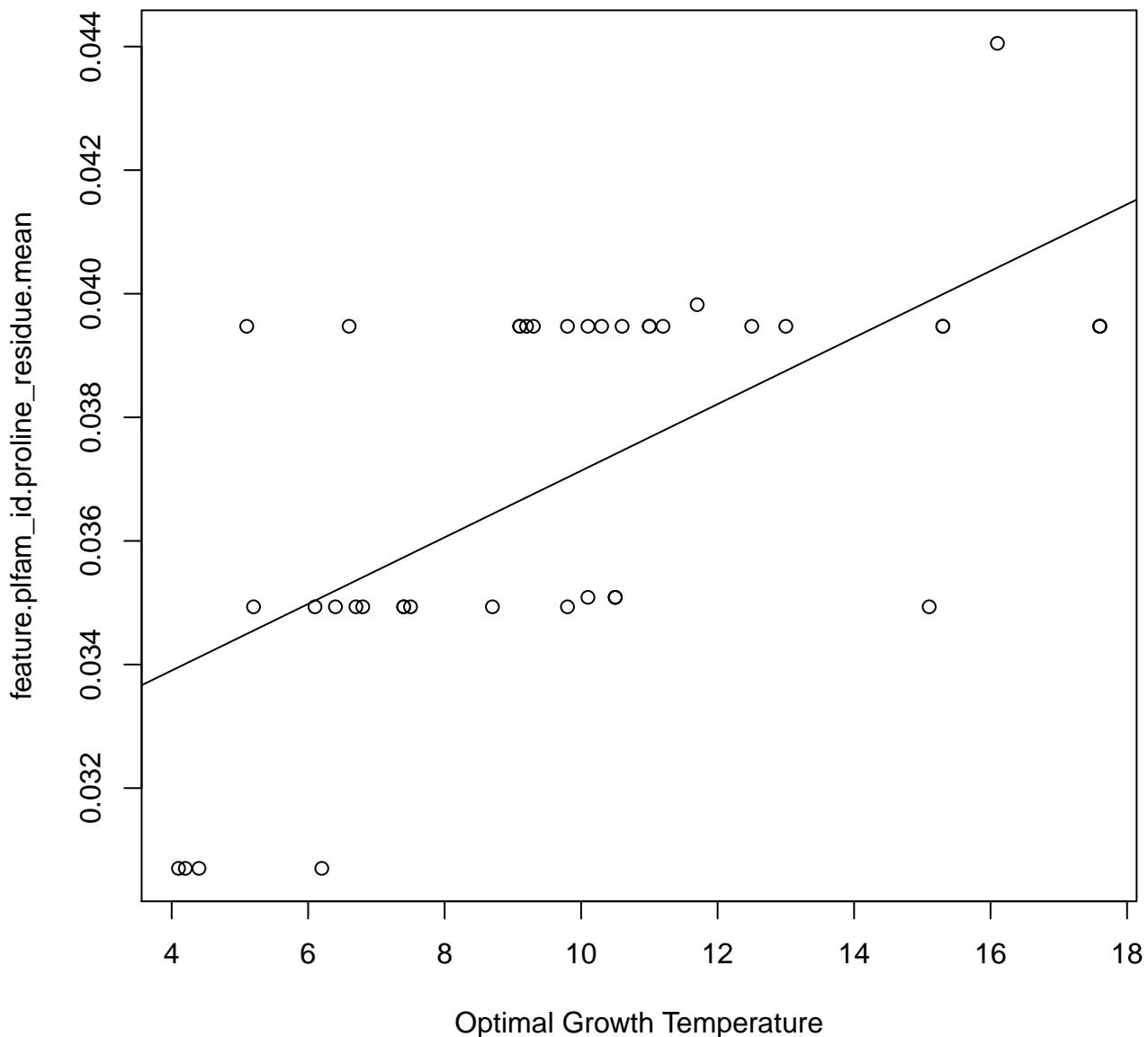
feature.plfam_id.proline_residue.mean
PLF_28228_00001815
CCA tRNA nucleotidyltransferase (EC 2.7.7.72)



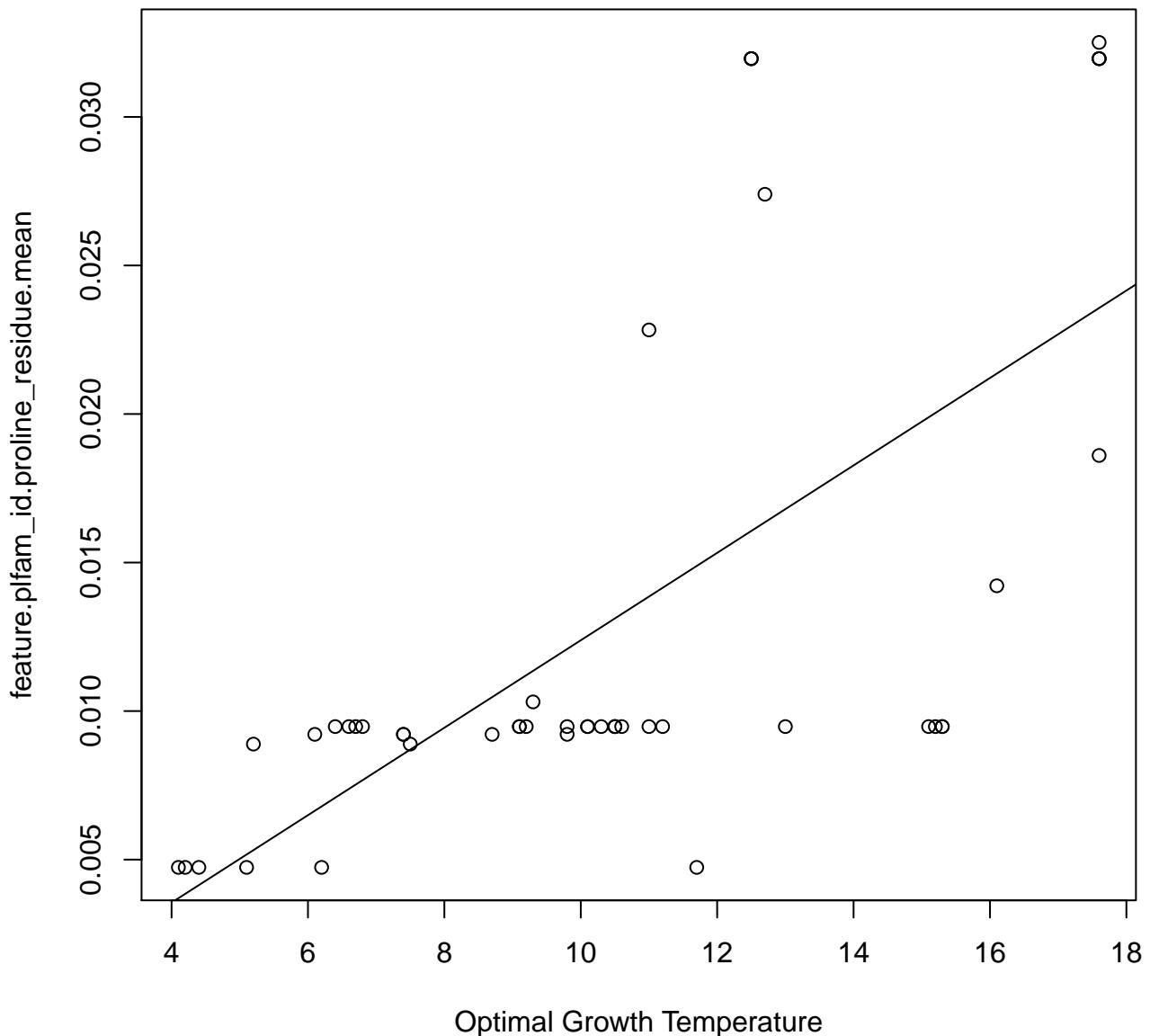
feature.plfam_id.proline_residue.mean
PLF_28228_00002005
RND efflux system, inner membrane transporter



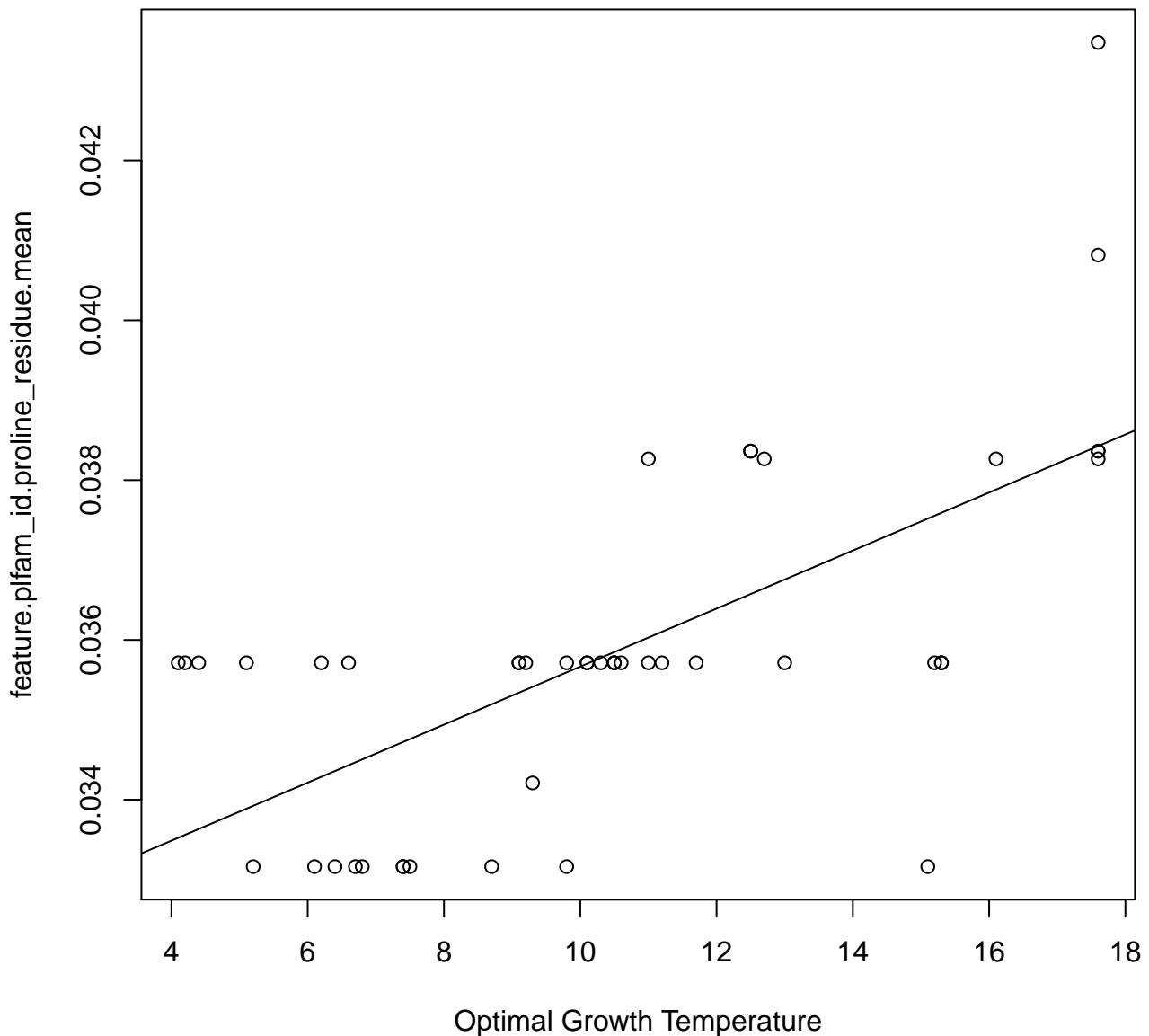
feature.plfam_id.proline_residue.mean
PLF_28228_00028198
FIG111991: hypothetical protein



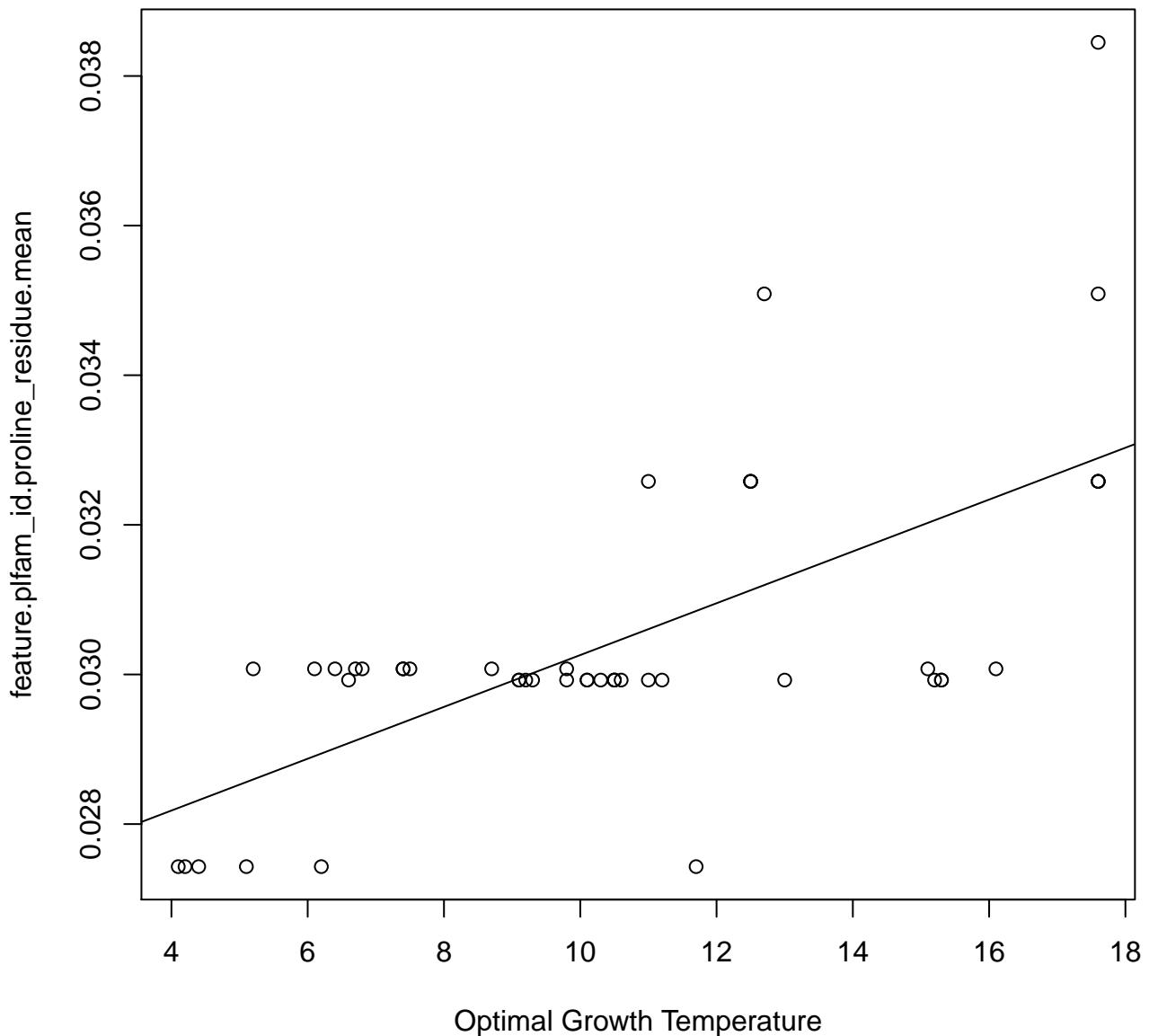
feature.plfam_id.proline_residue.mean
PLF_28228_00000797
FIG01964566: Predicted membrane protein, hemolysin III homolog



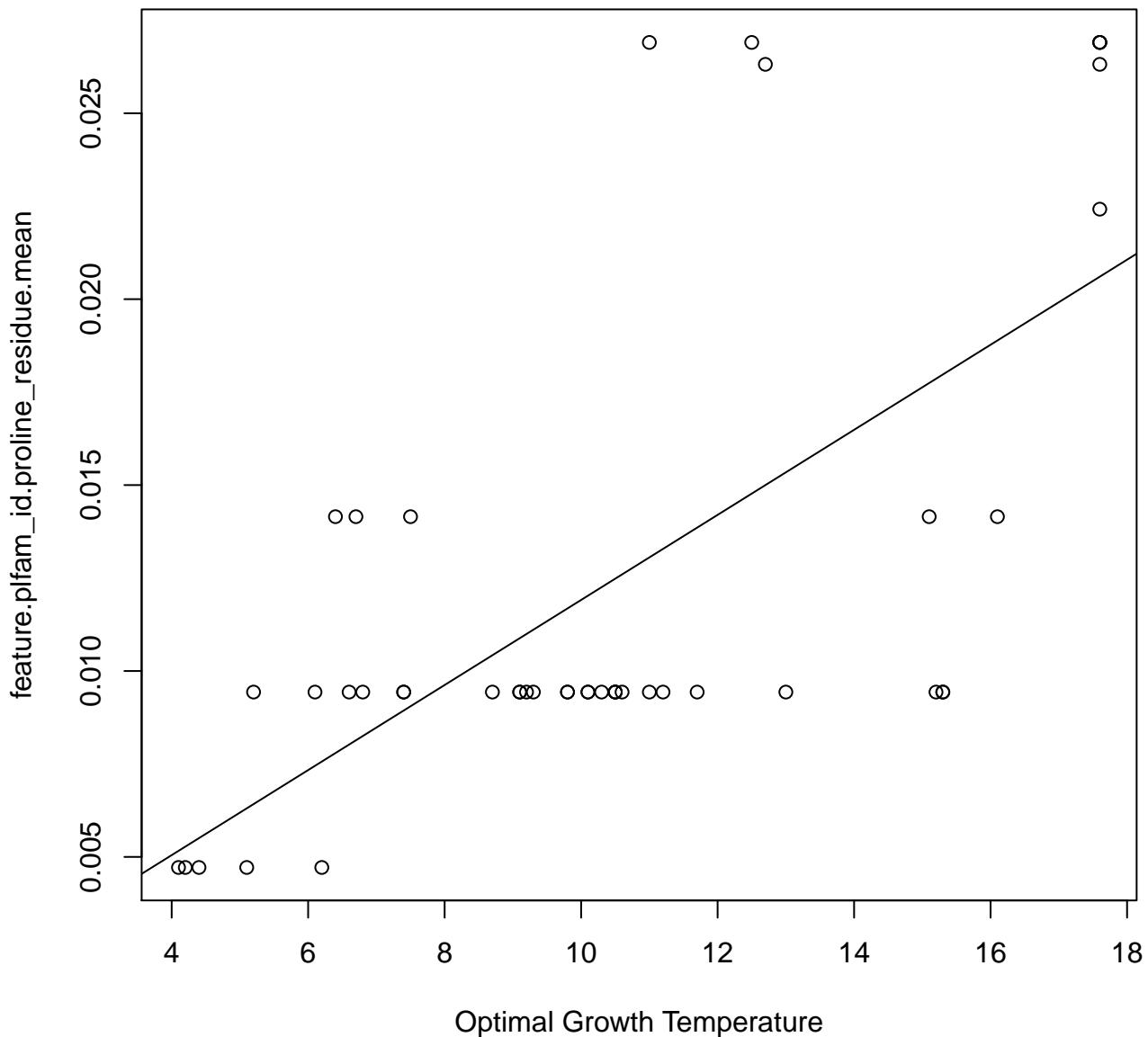
feature.plfam_id.proline_residue.mean
PLF_28228_00000960
Phosphoglycerate kinase (EC 2.7.2.3)



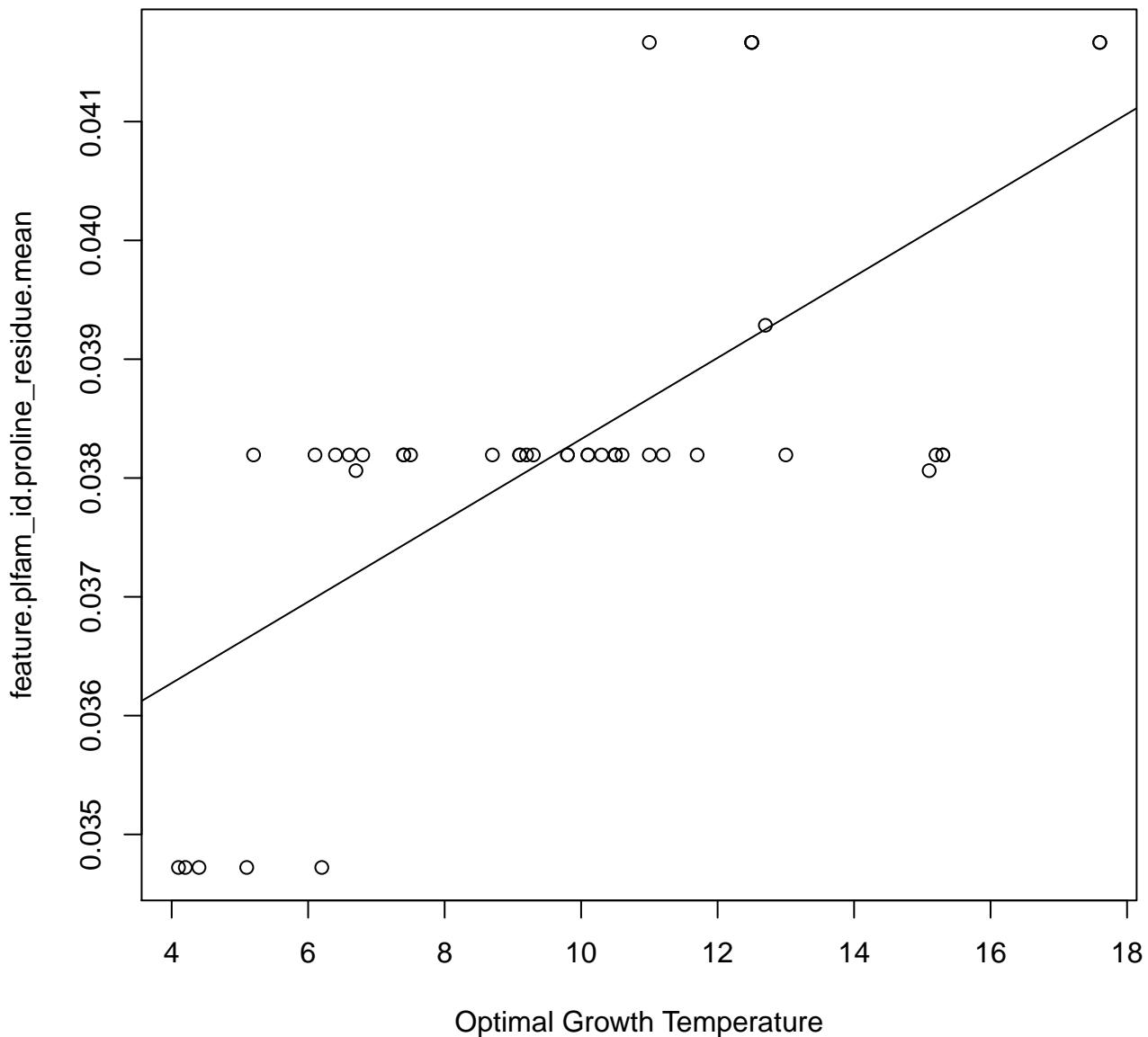
feature.plfam_id.proline_residue.mean
PLF_28228_00001264
Tyrosyl-tRNA synthetase (EC 6.1.1.1)



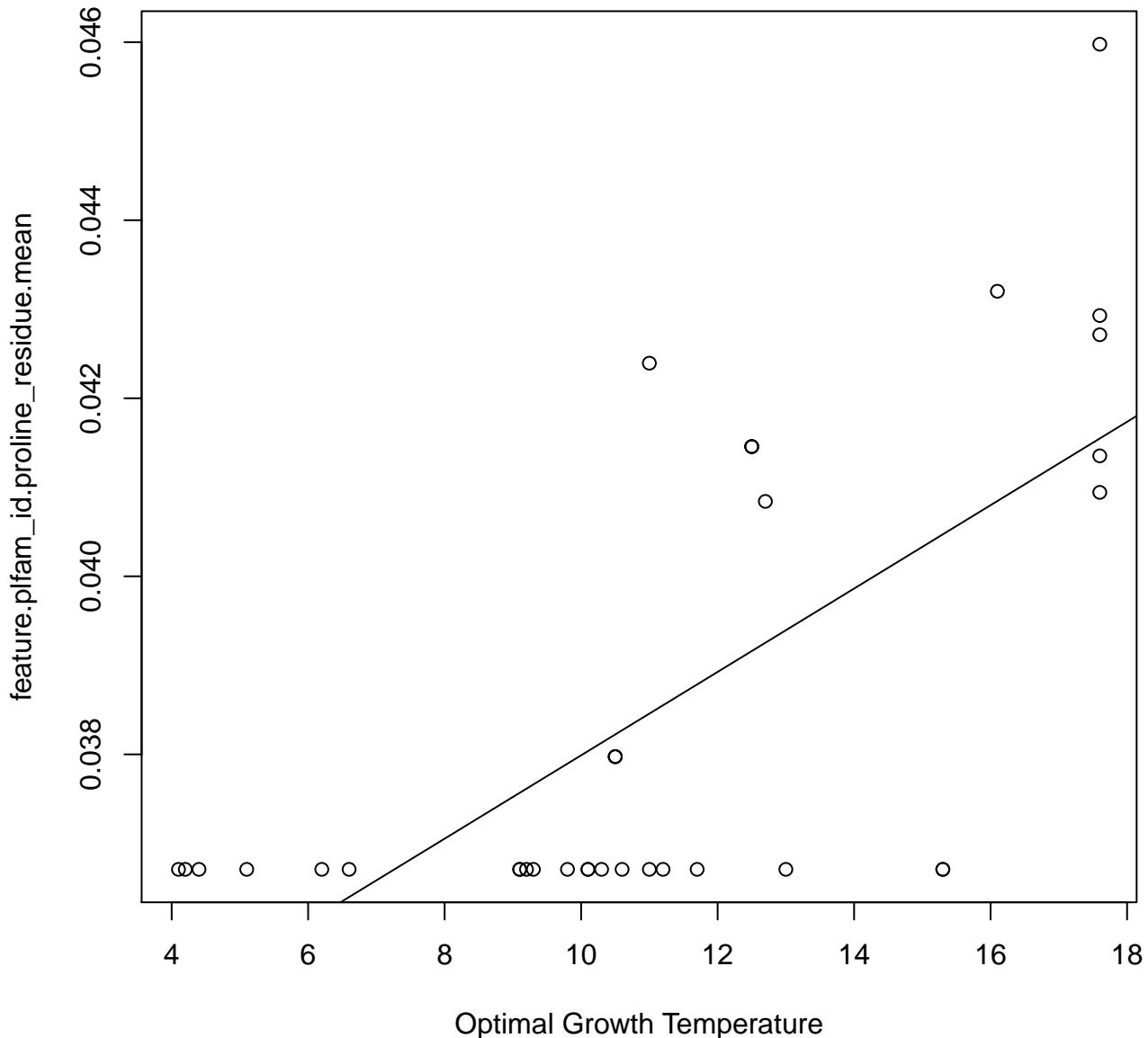
feature.plfam_id.proline_residue.mean
PLF_28228_00028002
UPF0070 protein YfgM



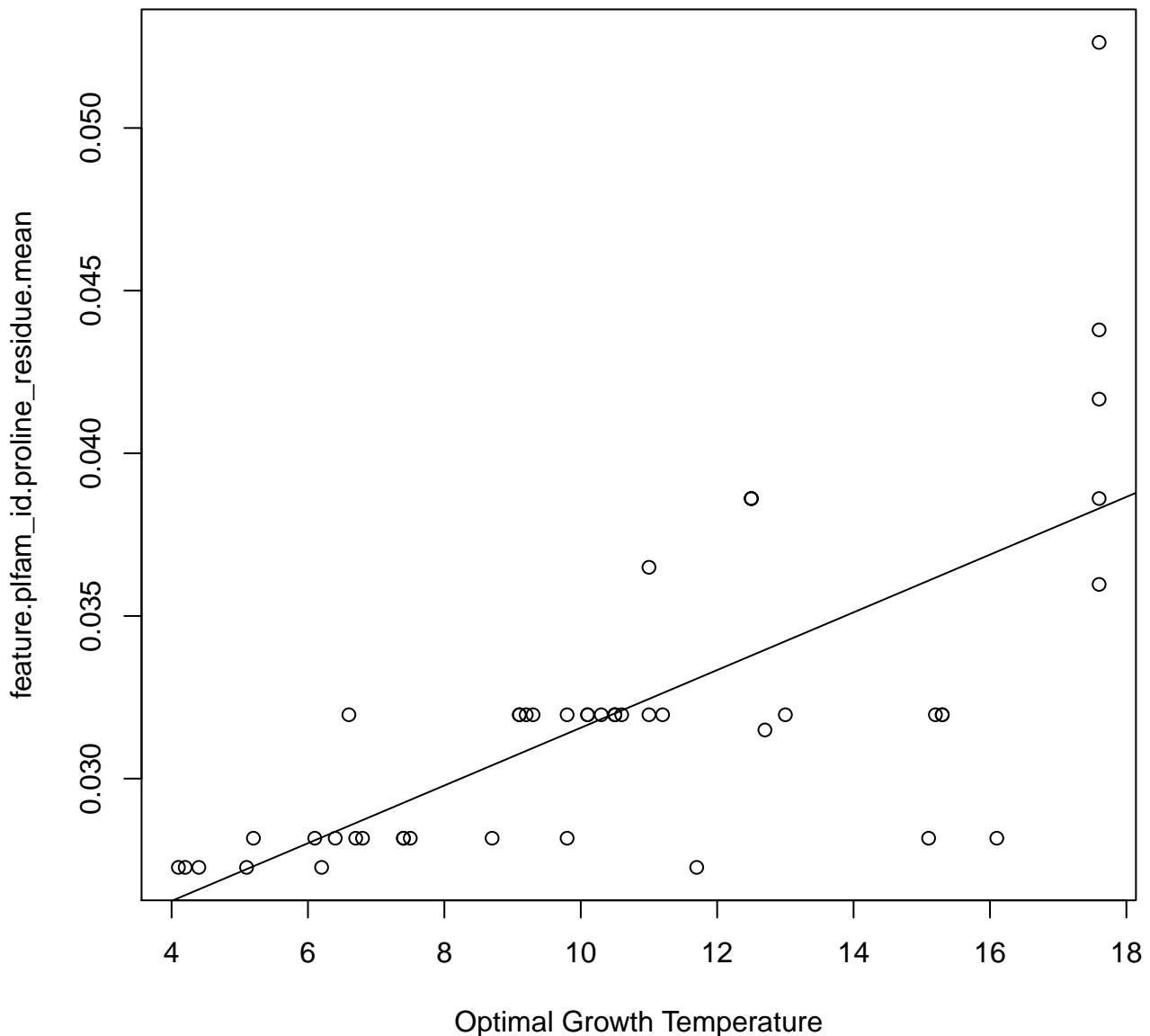
feature.plfam_id.proline_residue.mean
PLF_28228_00003394
ABC transporter, substrate-binding protein (cluster 12, methionine/phosphonates)



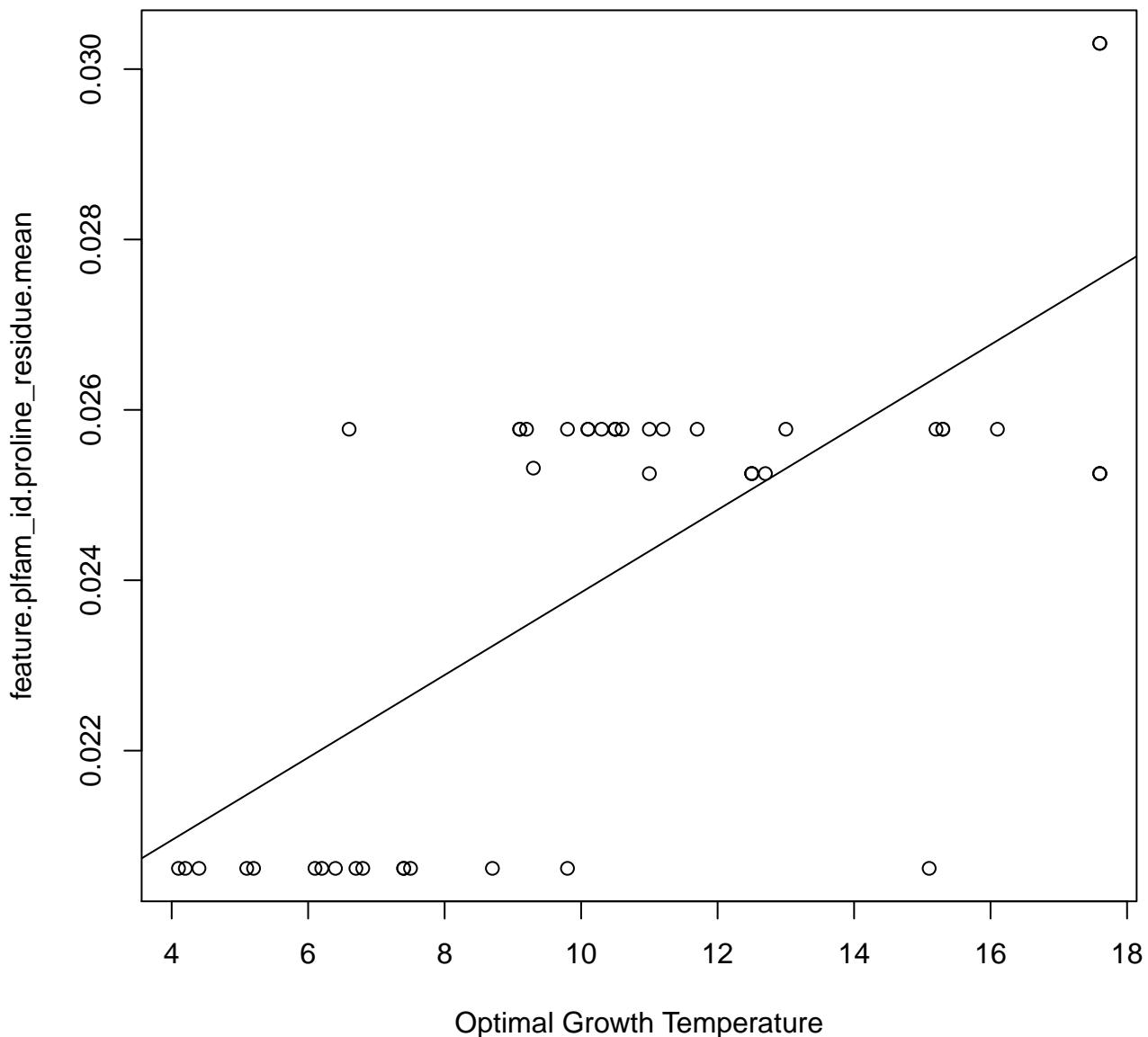
feature.plfam_id.proline_residue.mean
PLF_28228_00002204
Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)



feature.plfam_id.proline_residue.mean
PLF_28228_00000315
Electron transport complex protein RnfG



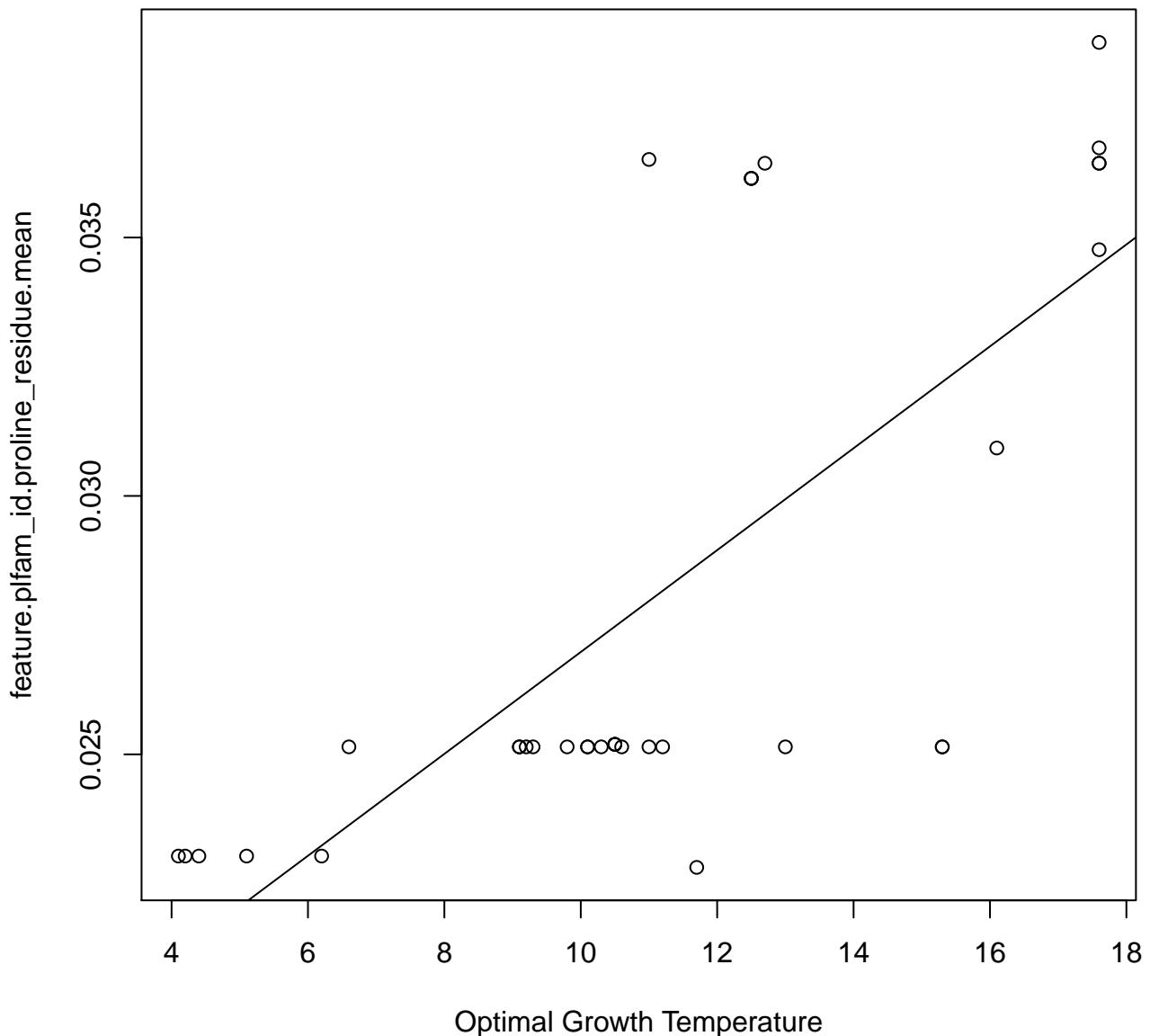
feature.plfam_id.proline_residue.mean
PLF_28228_00001218
Transcriptional regulator SlmA, TetR family



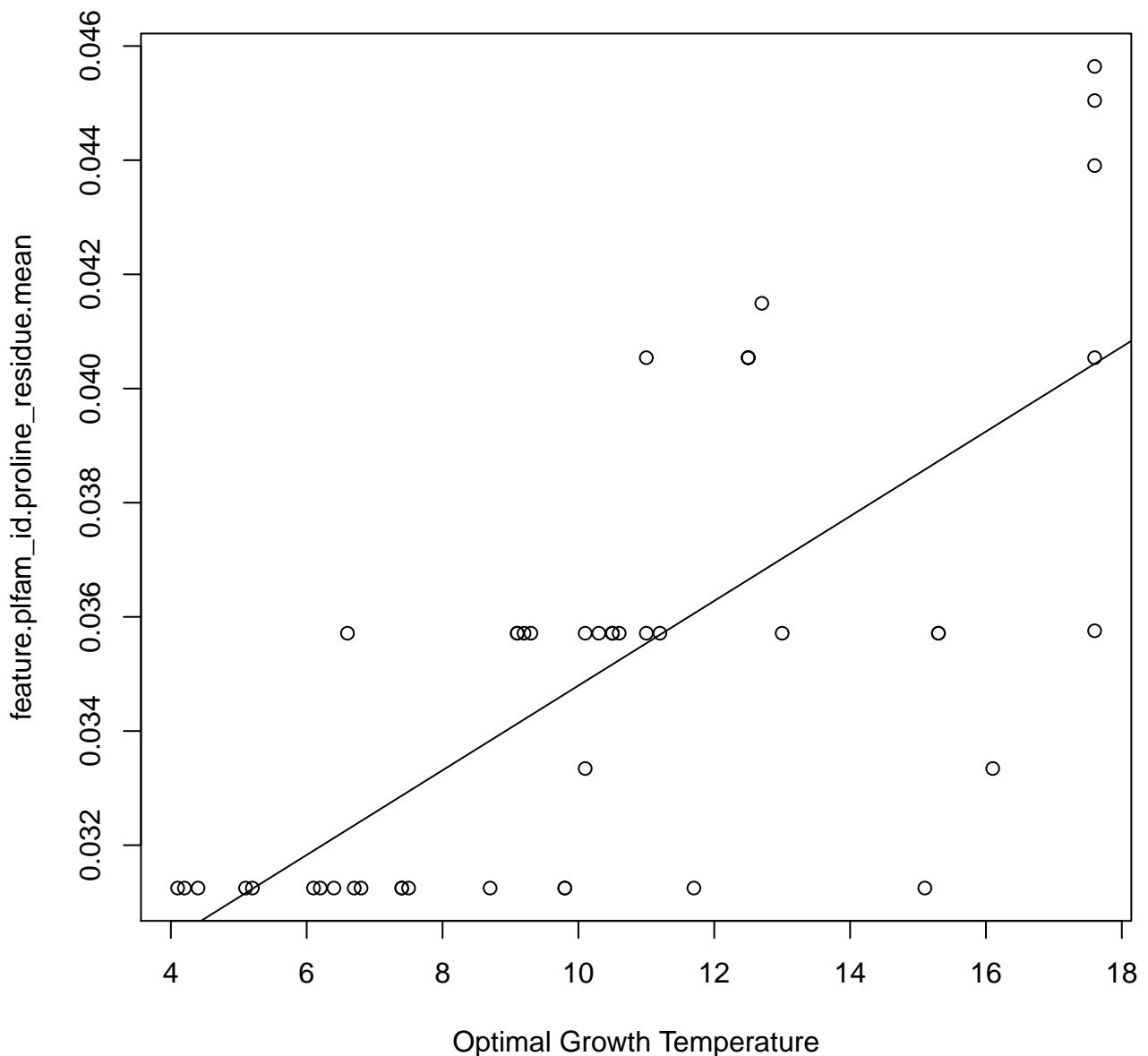
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PLF_28228_00002203

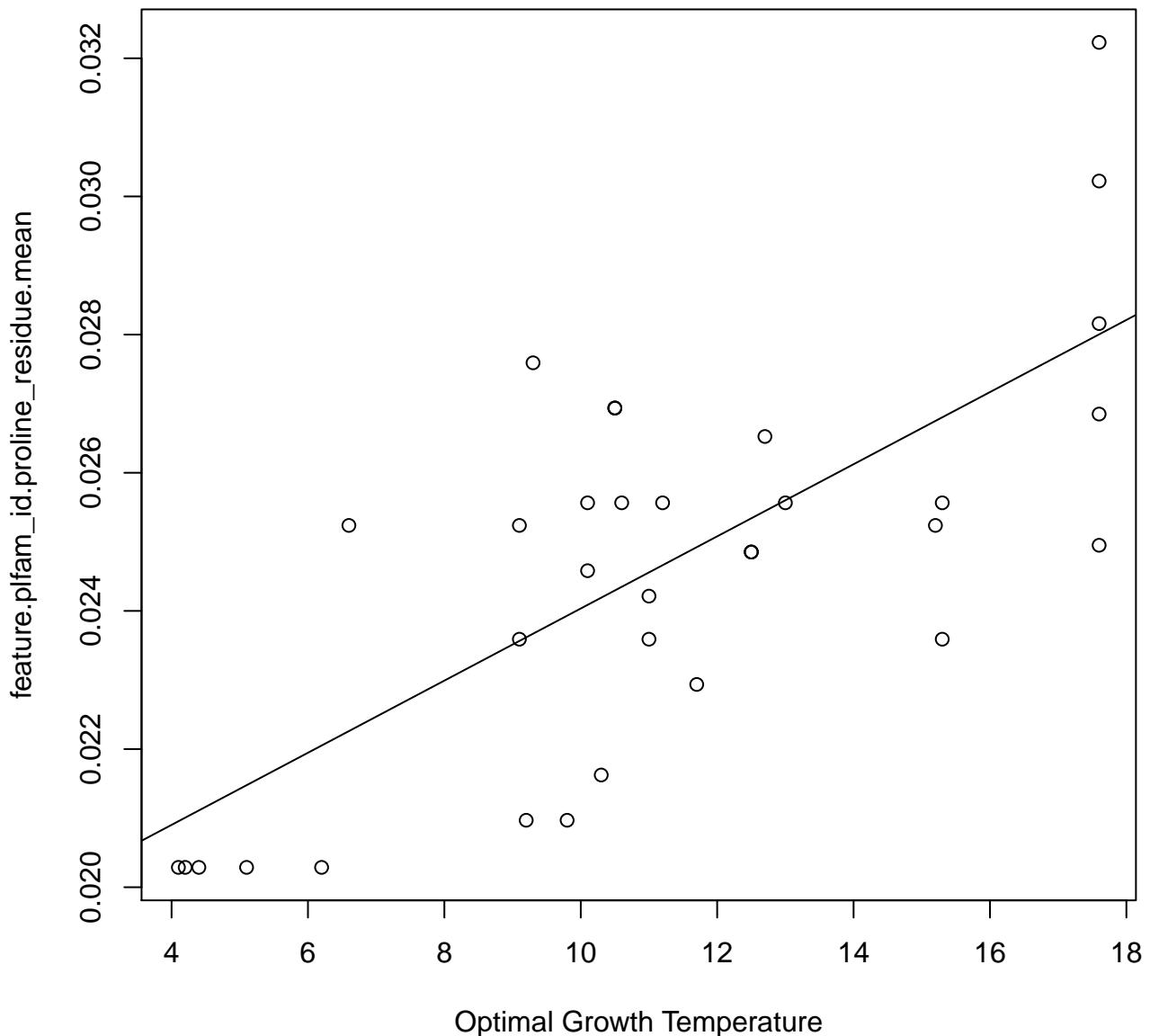
Xanthine dehydrogenase iron–sulfur subunit (EC 1.17.1.4) / Xanthine dehydrogenase, FAD binding subunit (EC 1.17.1.4)



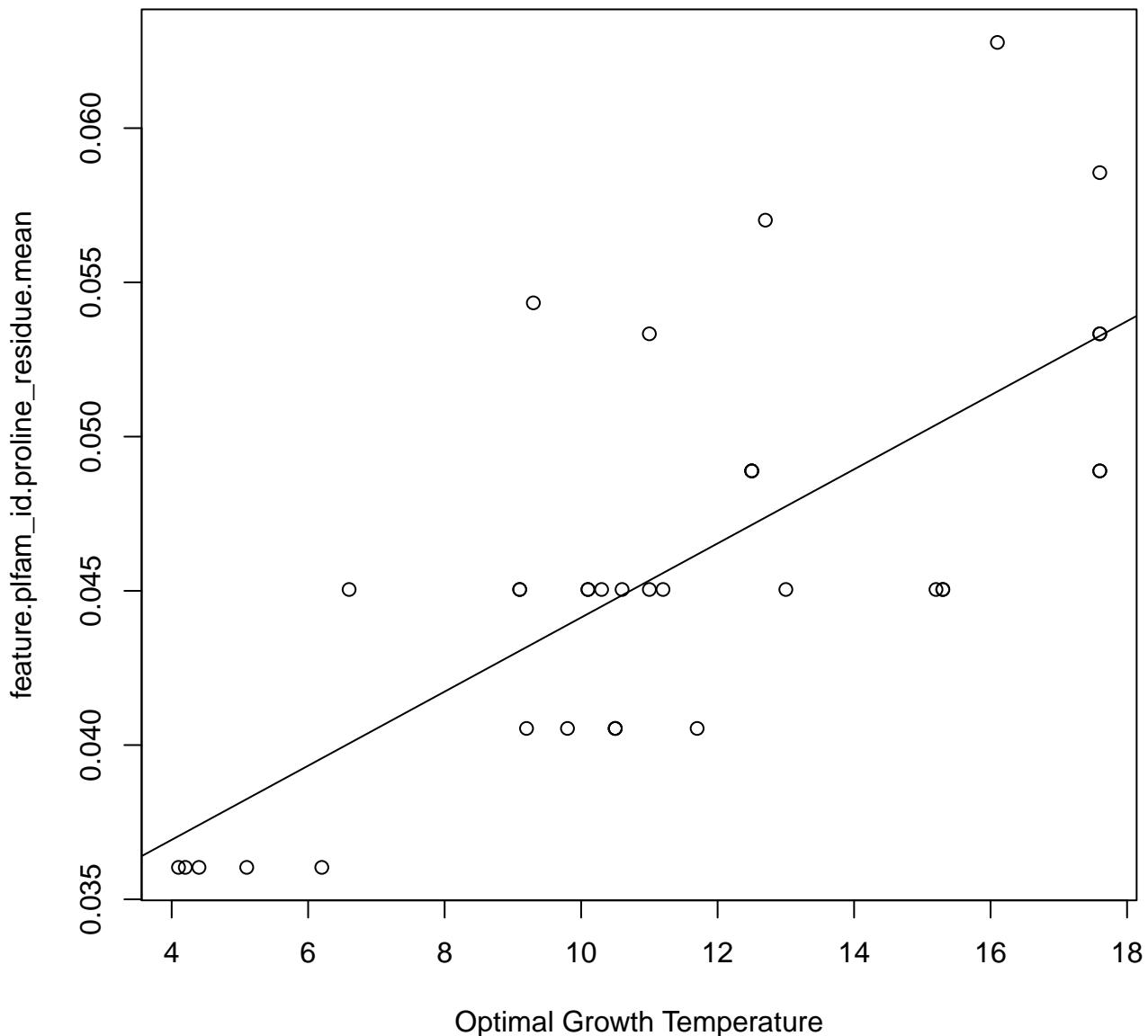
feature.plfam_id.proline_residue.mean
PLF_28228_00000140
7-carboxy-7-deazaguanine synthase (EC 4.3.99.3)



feature.plfam_id.proline_residue.mean
PLF_28228_00002039
Sensory box protein



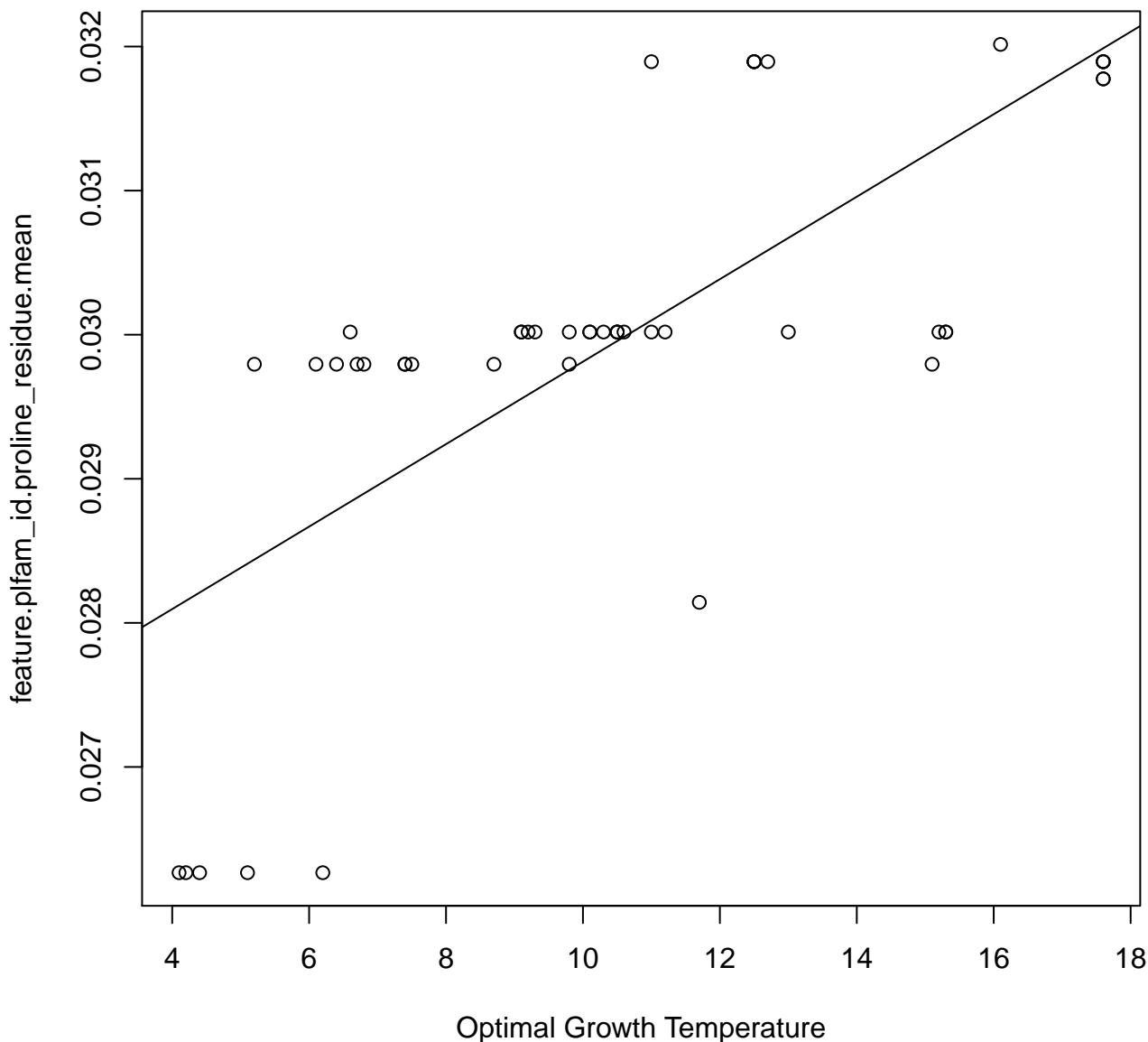
feature.plfam_id.proline_residue.mean
PLF_28228_00001354
hypothetical protein



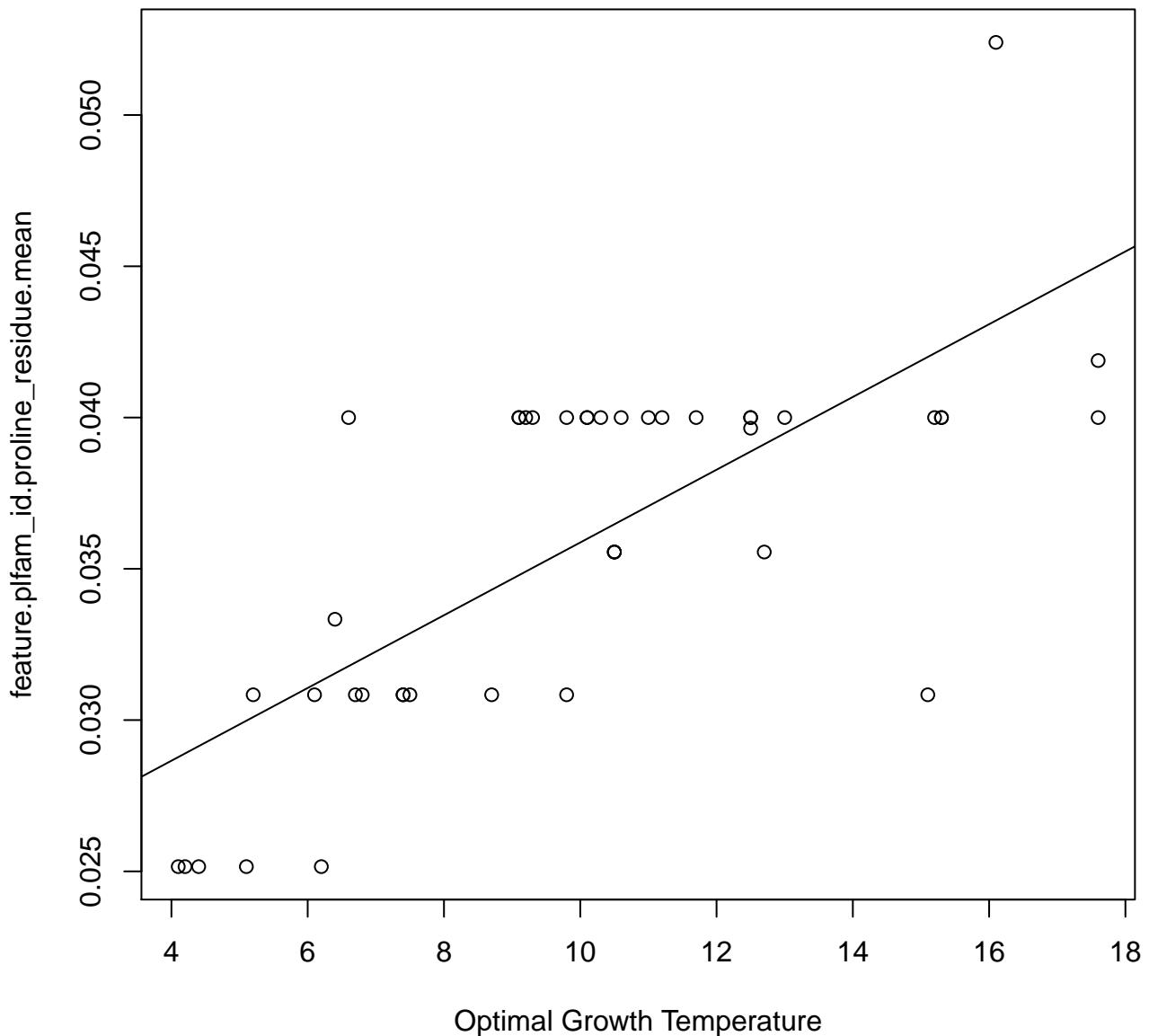
feature.plfam_id.proline_residue.mean

PLF_28228_00000516

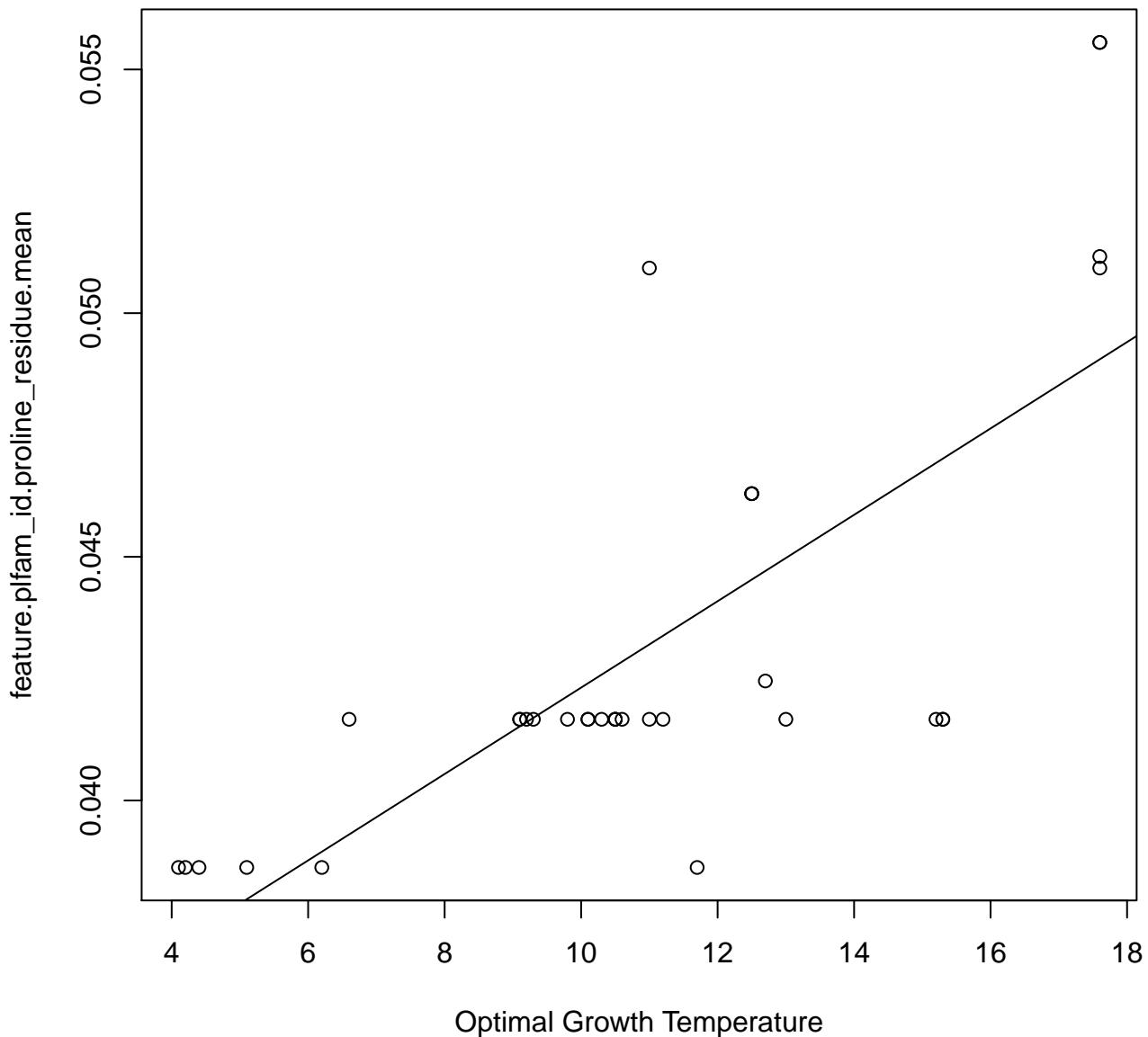
IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)



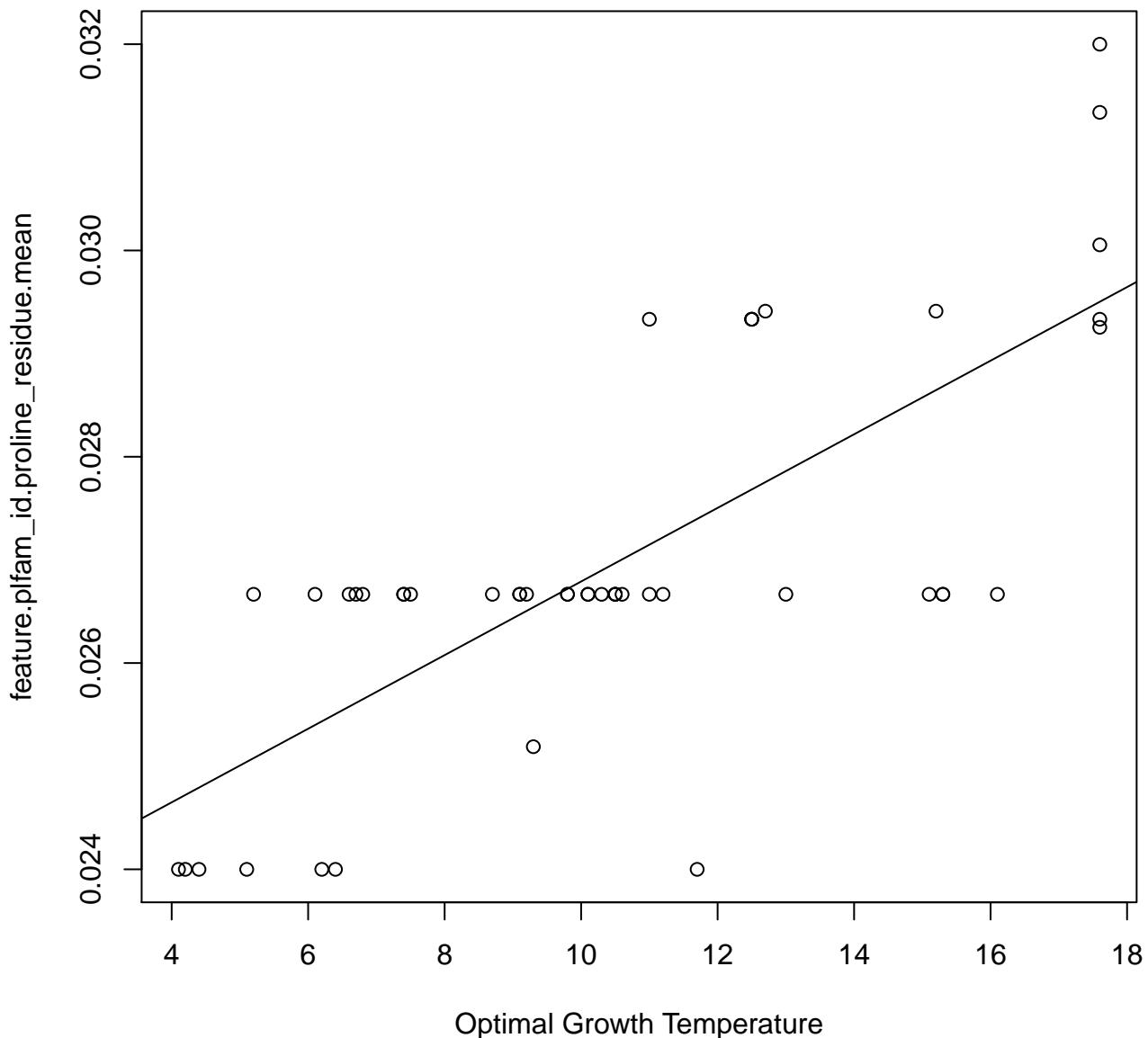
feature.plfam_id.proline_residue.mean
PLF_28228_00002803
SM-20-related protein



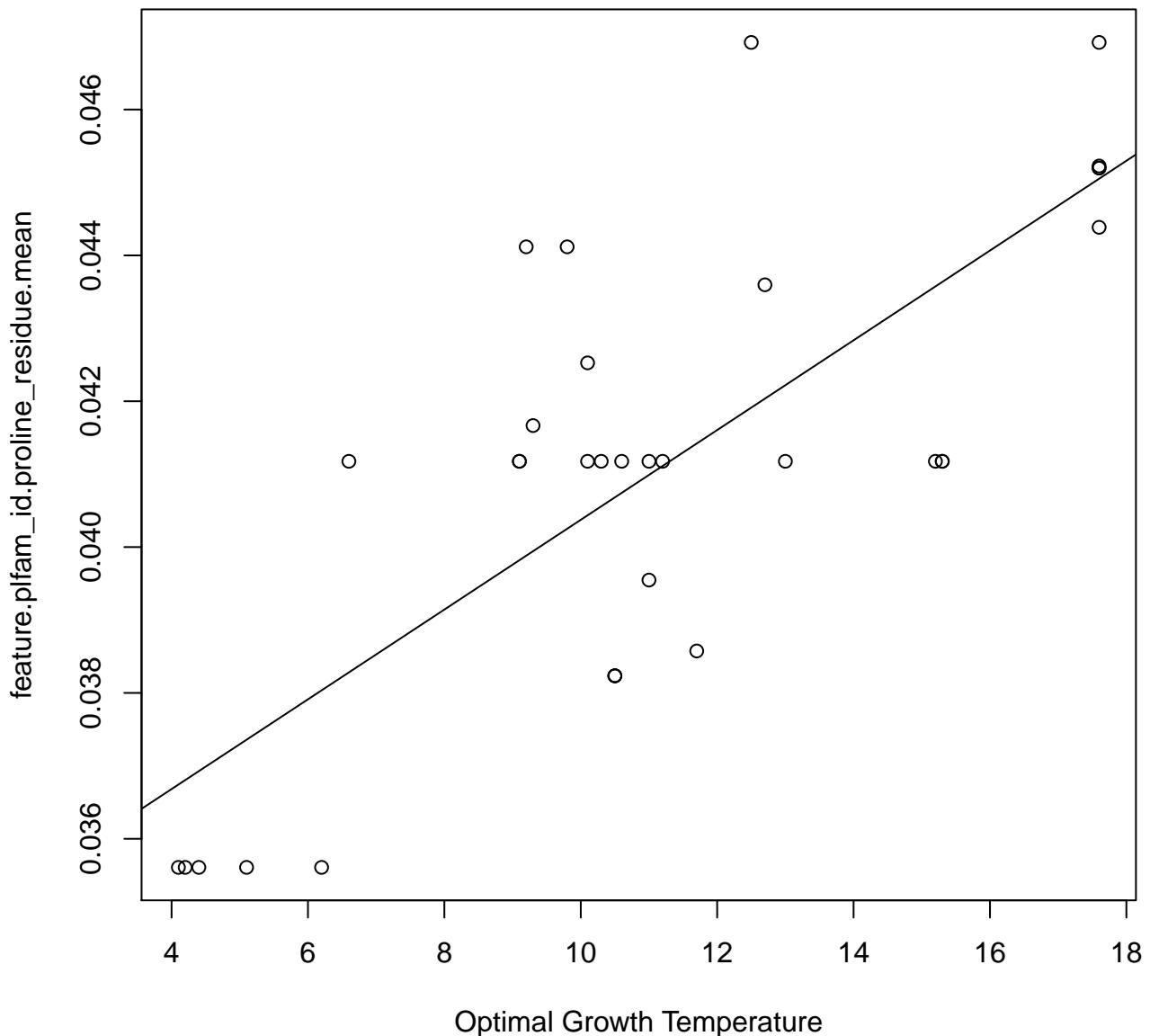
feature.plfam_id.proline_residue.mean
PLF_28228_00001302
Uridine kinase (EC 2.7.1.48)



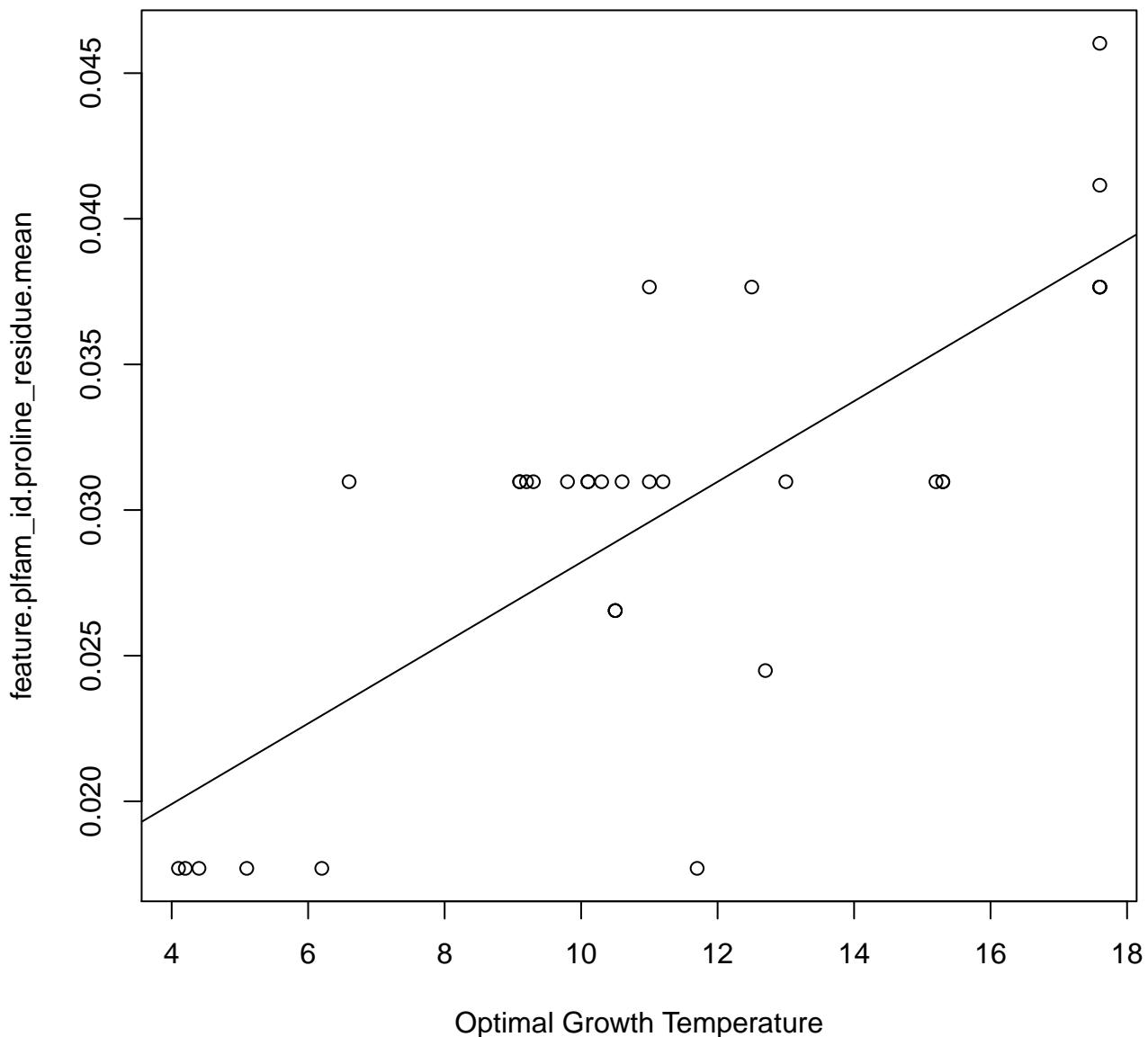
feature.plfam_id.proline_residue.mean
PLF_28228_00001256
Type IV pilus assembly ATPase component PilU



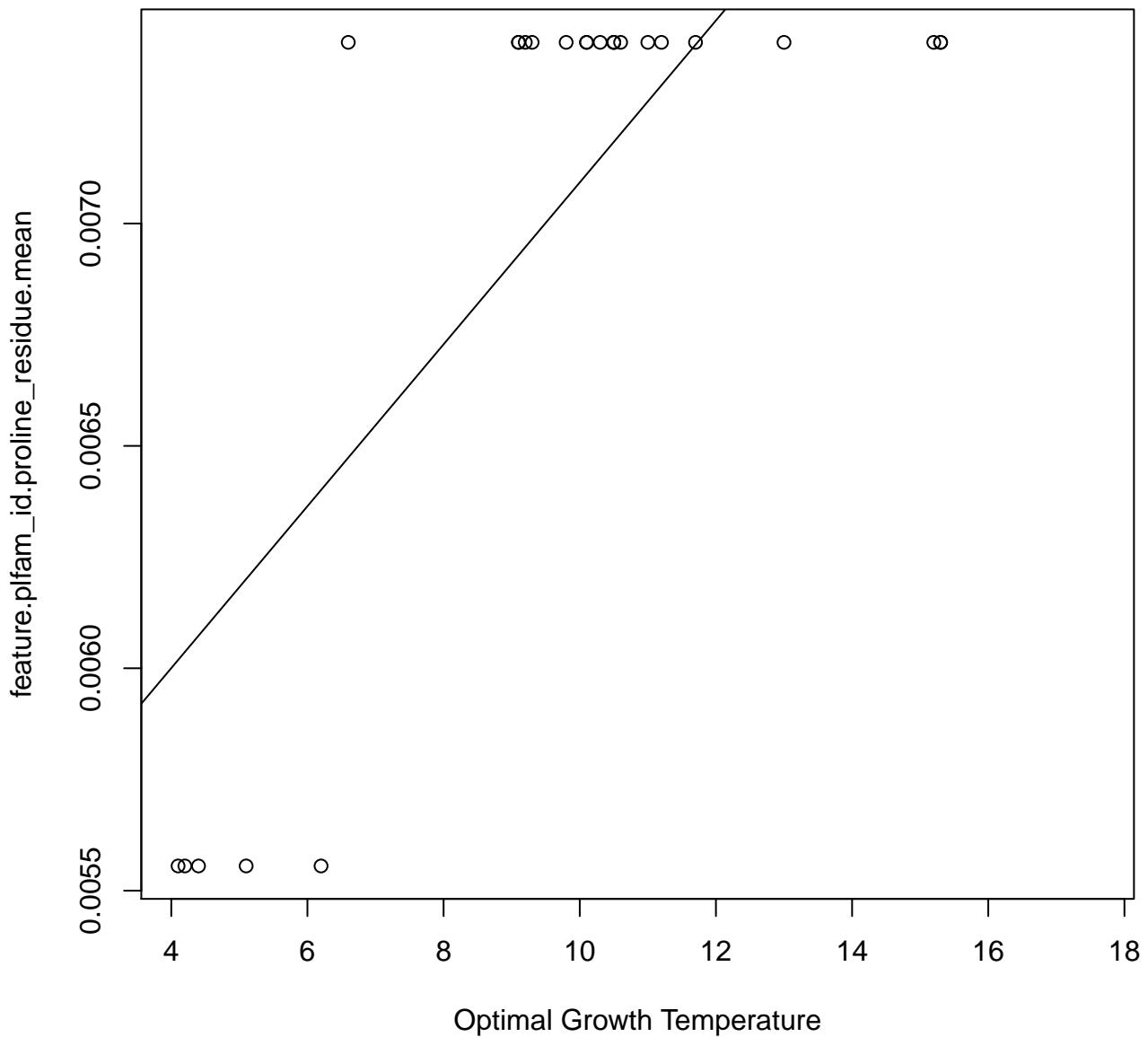
feature.plfam_id.proline_residue.mean
PLF_28228_00027970
Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) @ Outer membrane phospholipase A



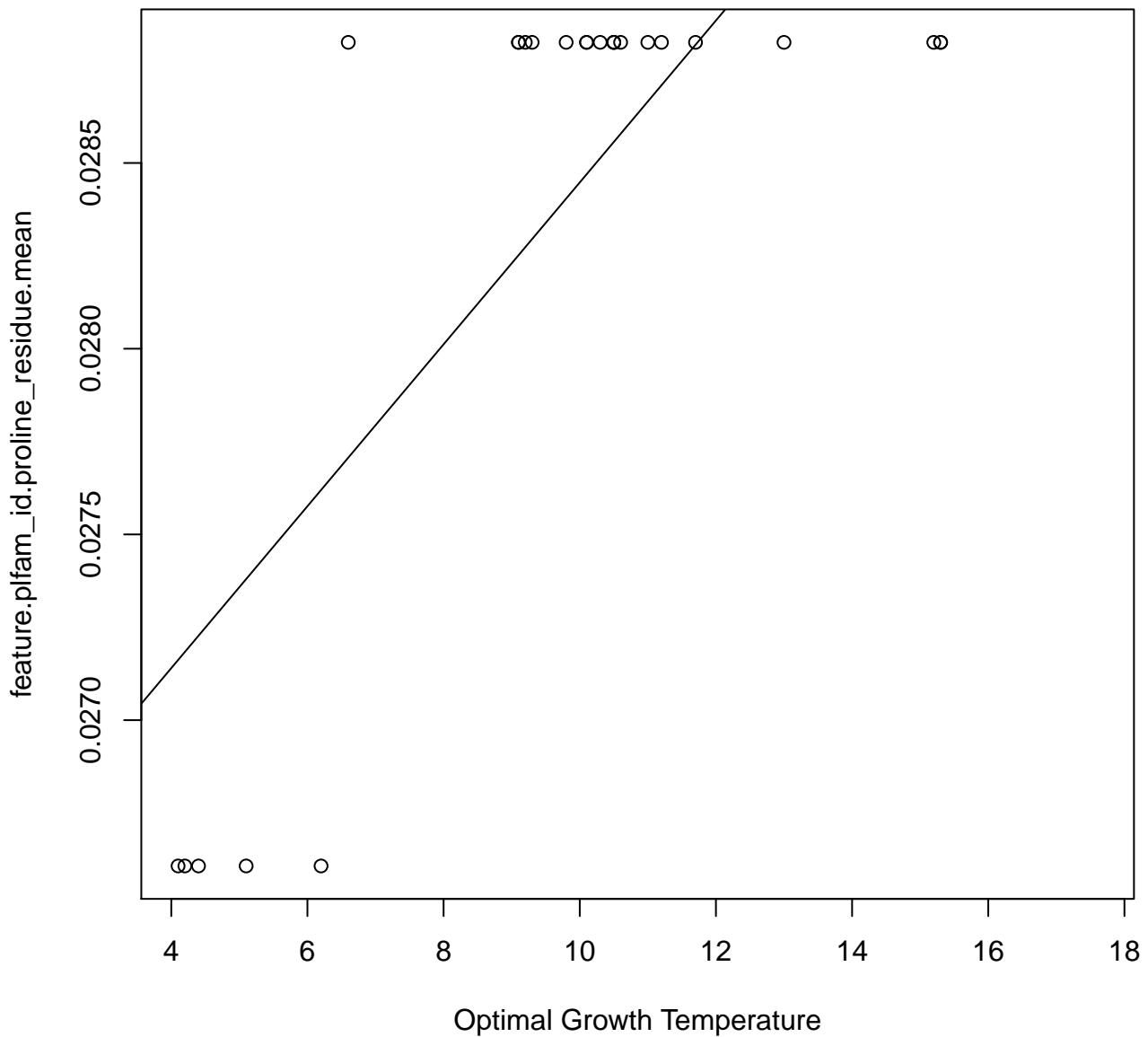
feature.plfam_id.proline_residue.mean
PLF_28228_00014865
Pyridoxal phosphate-containing protein YggS



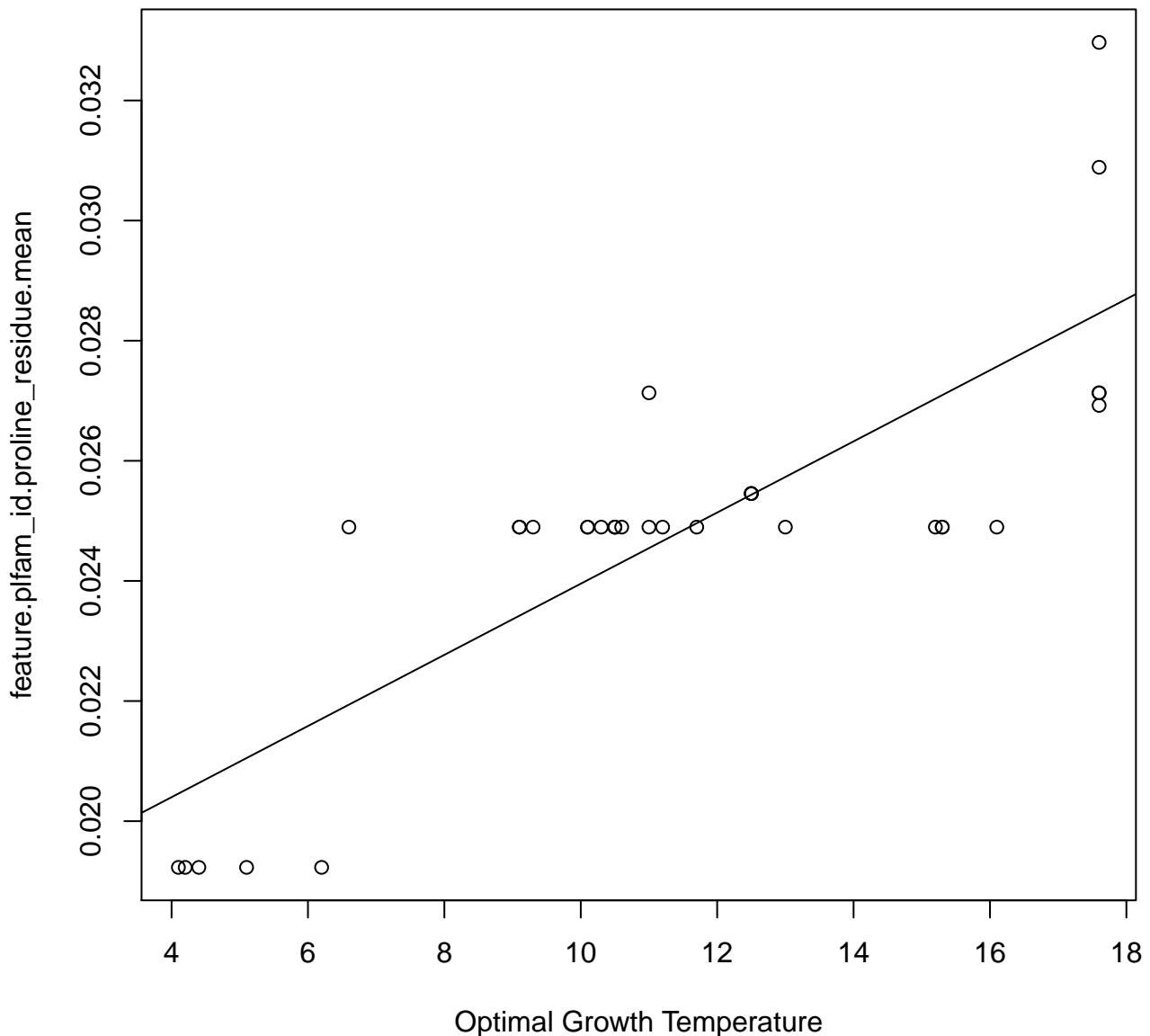
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PLF_28228_00028208
hypothetical protein



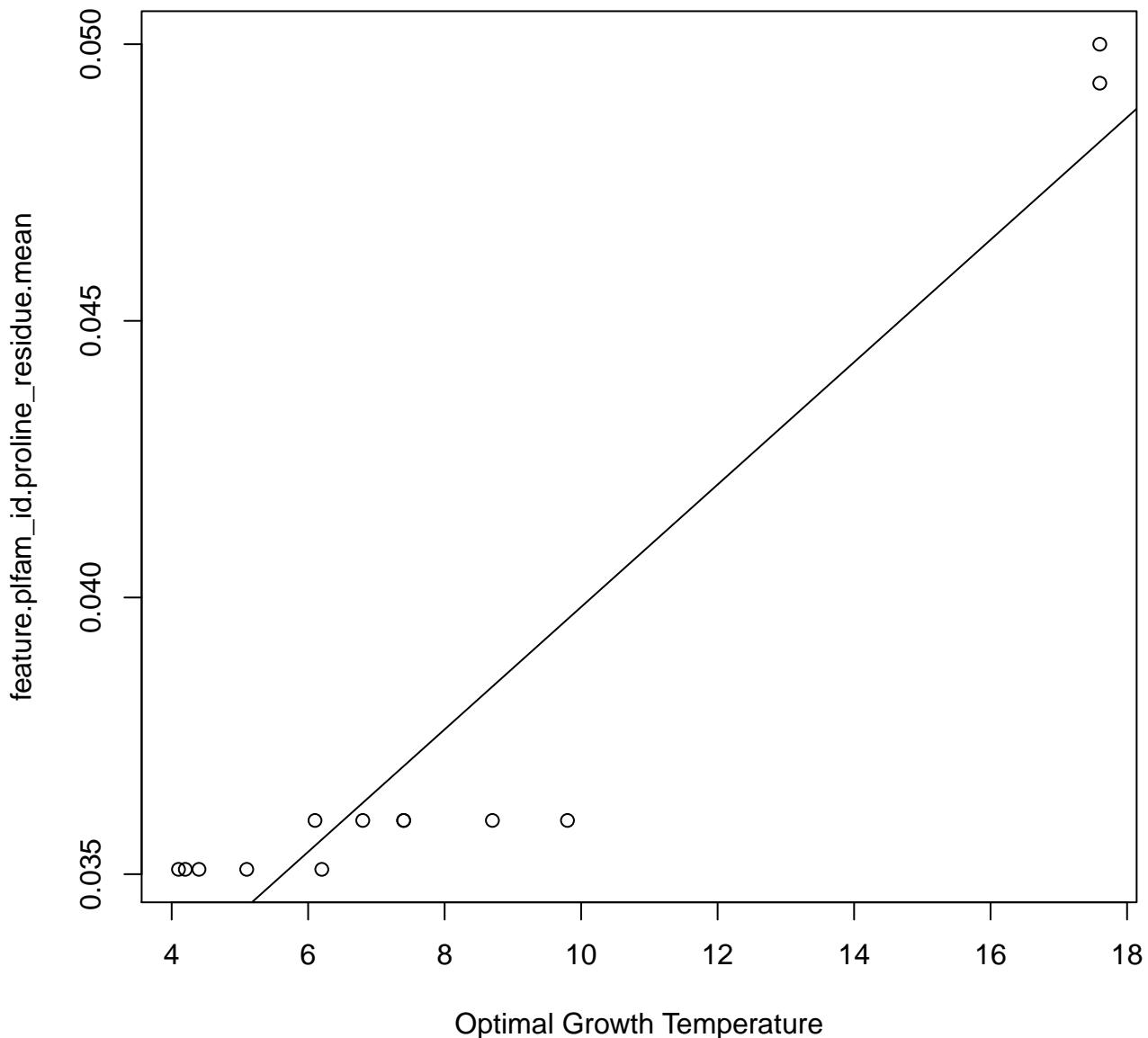
feature.plfam_id.proline_residue.mean
PLF_28228_00028633
Mg/Co/Ni transporter MgtE, CBS domain-containing



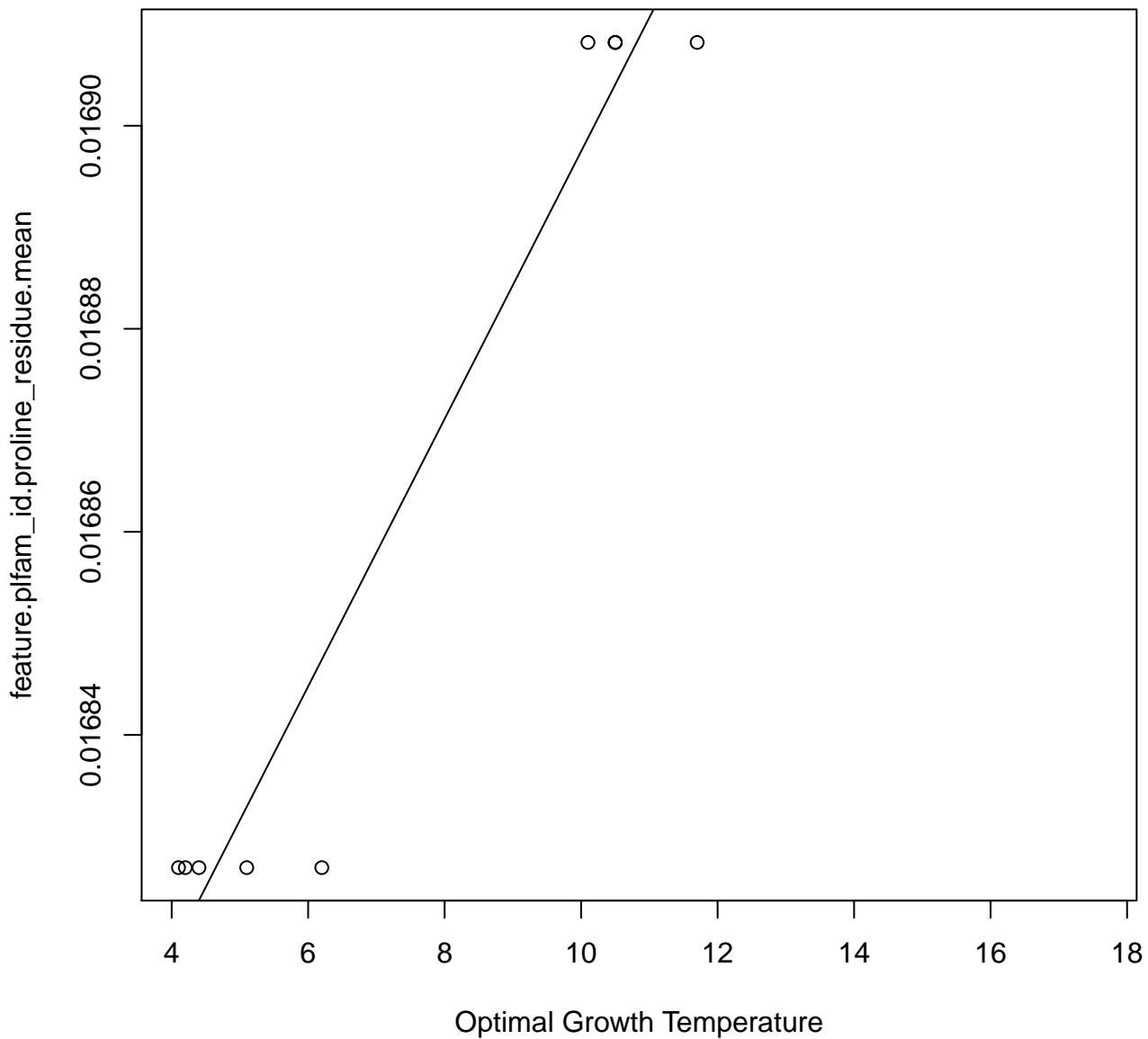
feature.plfam_id.proline_residue.mean
PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



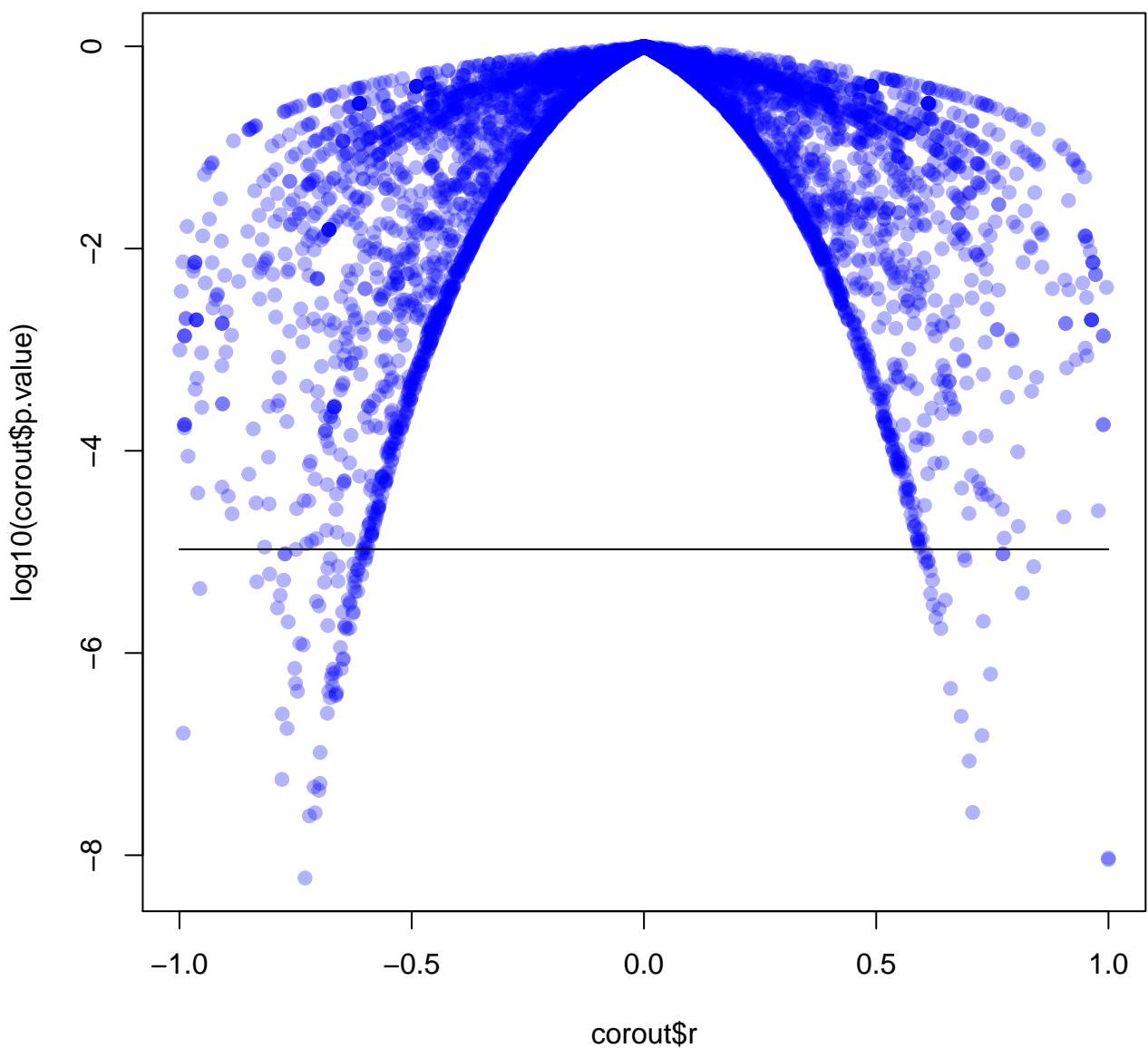
feature.plfam_id.proline_residue.mean
PLF_28228_00007776
hypothetical protein



feature.plfam_id.proline_residue.mean
PLF_28228_00011513
hypothetical protein



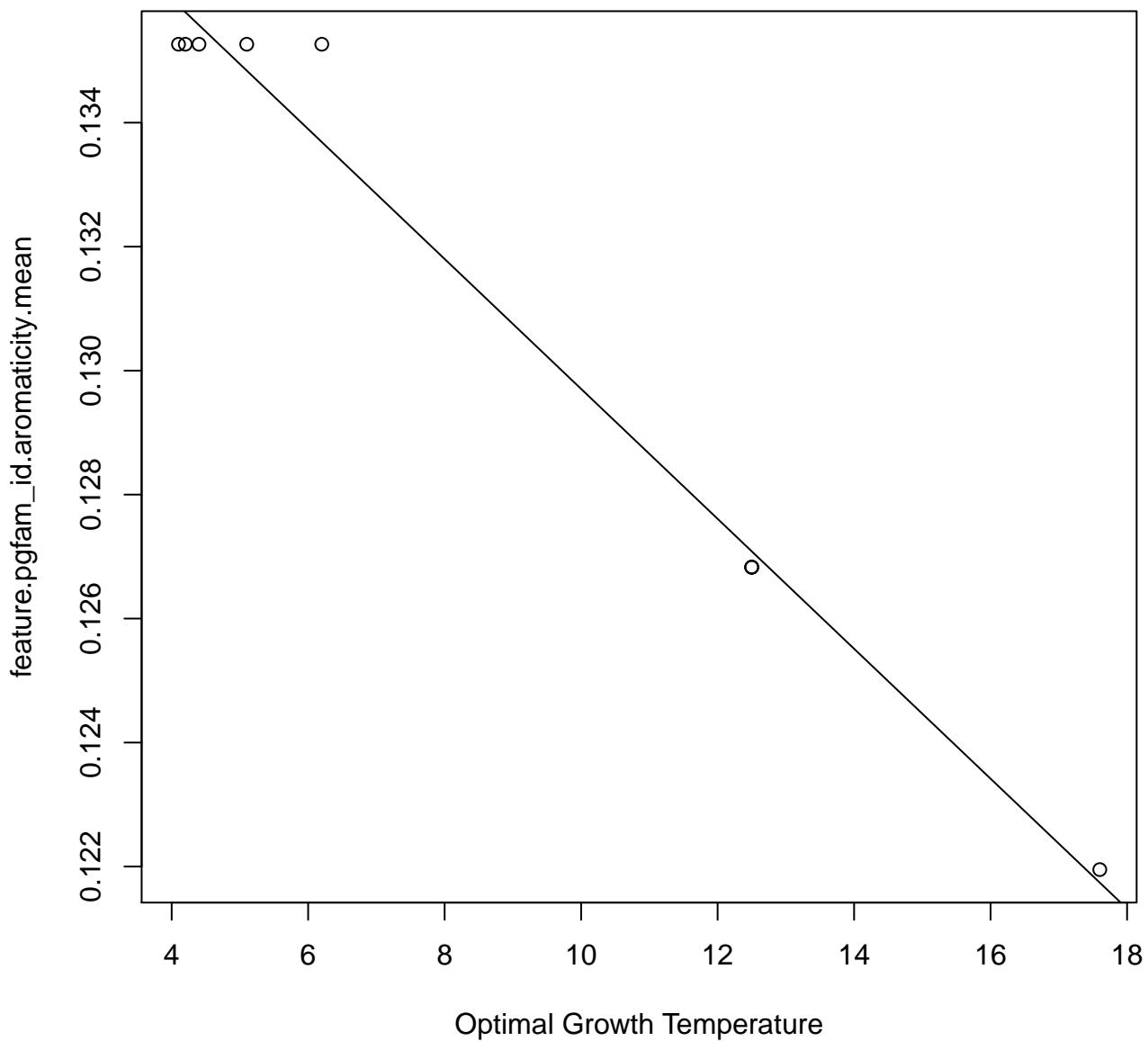
feature.pgfam_id.aromaticity.mean



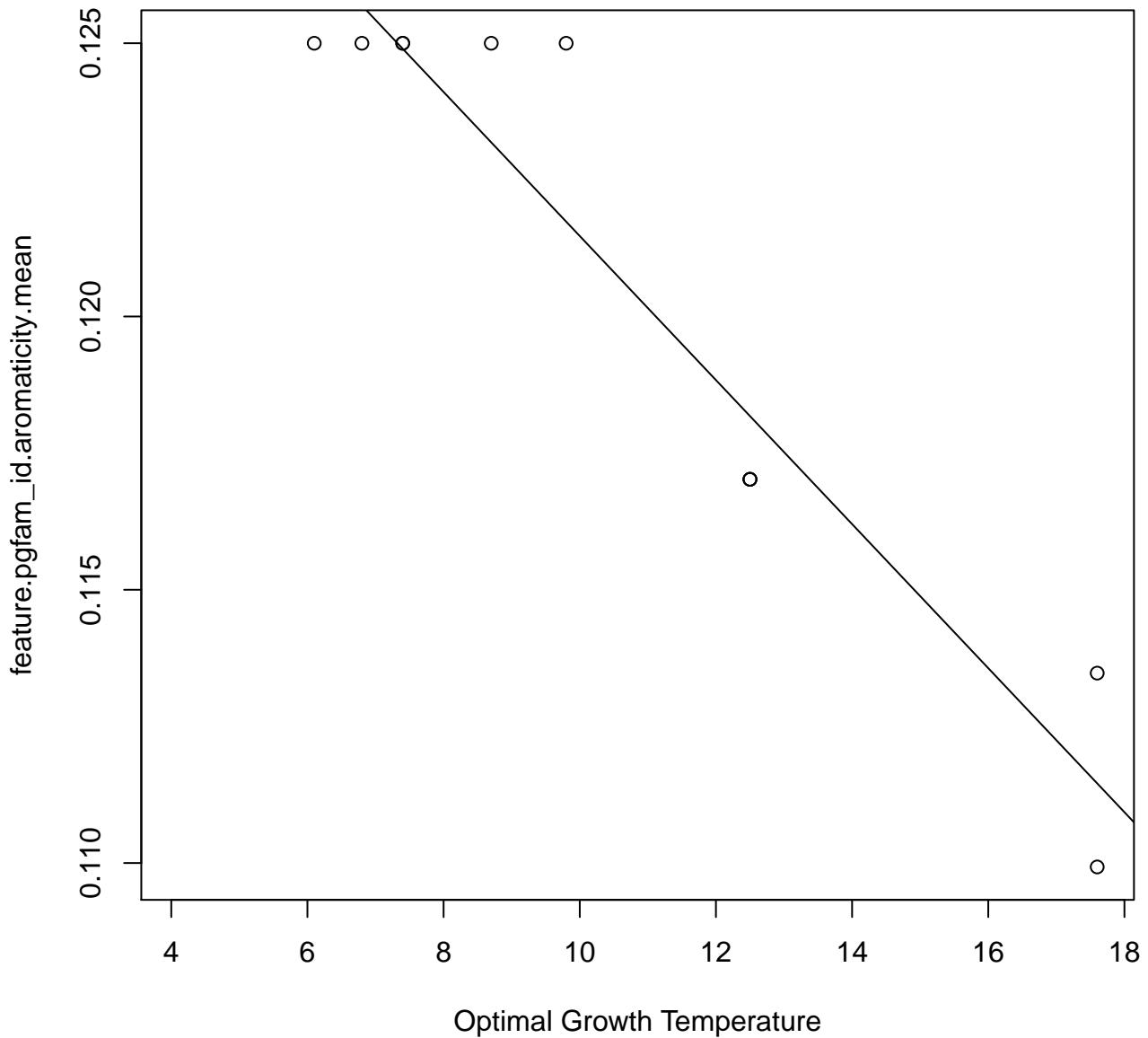
feature.pgfam_id.aromaticity.mean

PGF_01338043

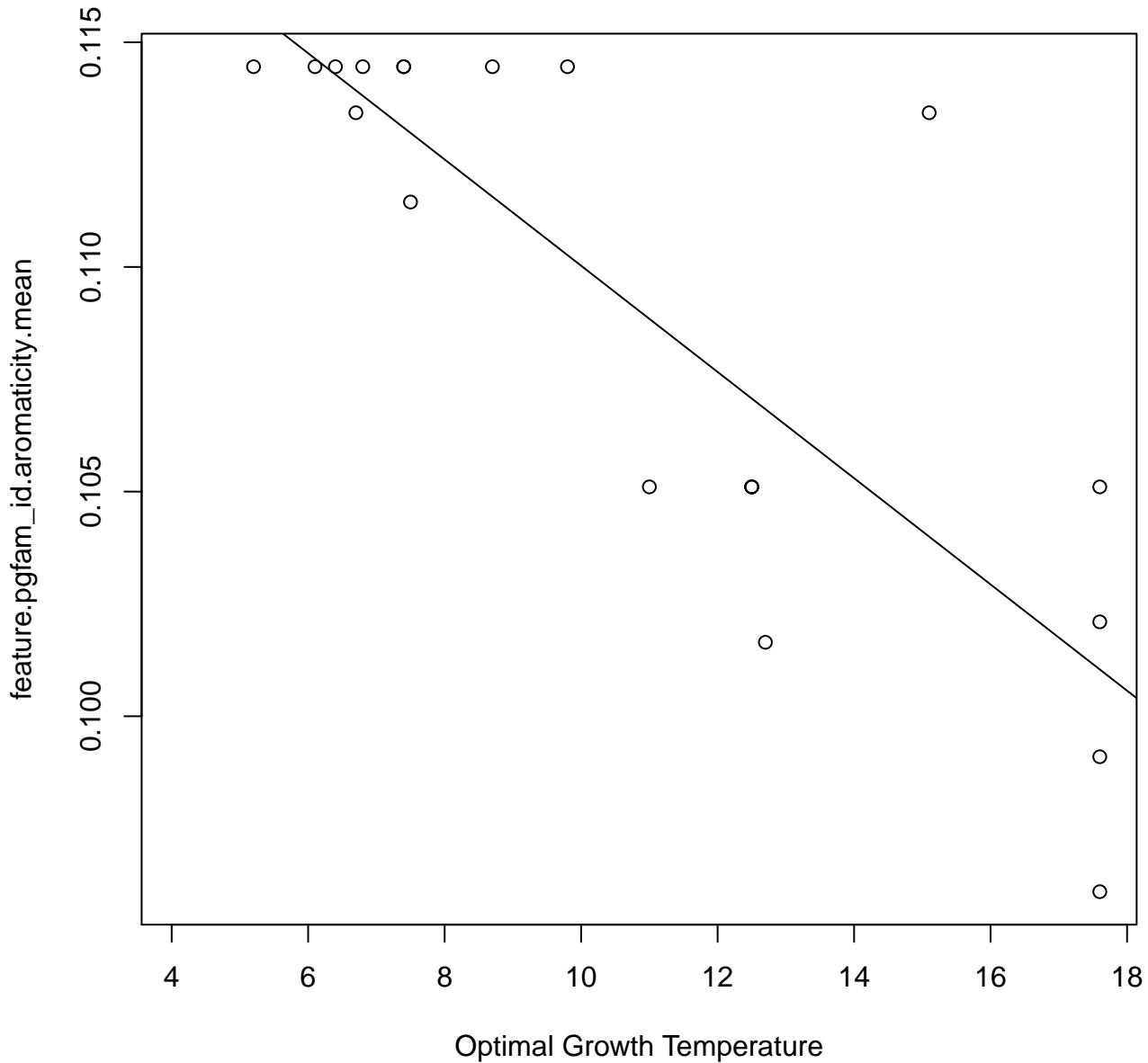
hypothetical protein



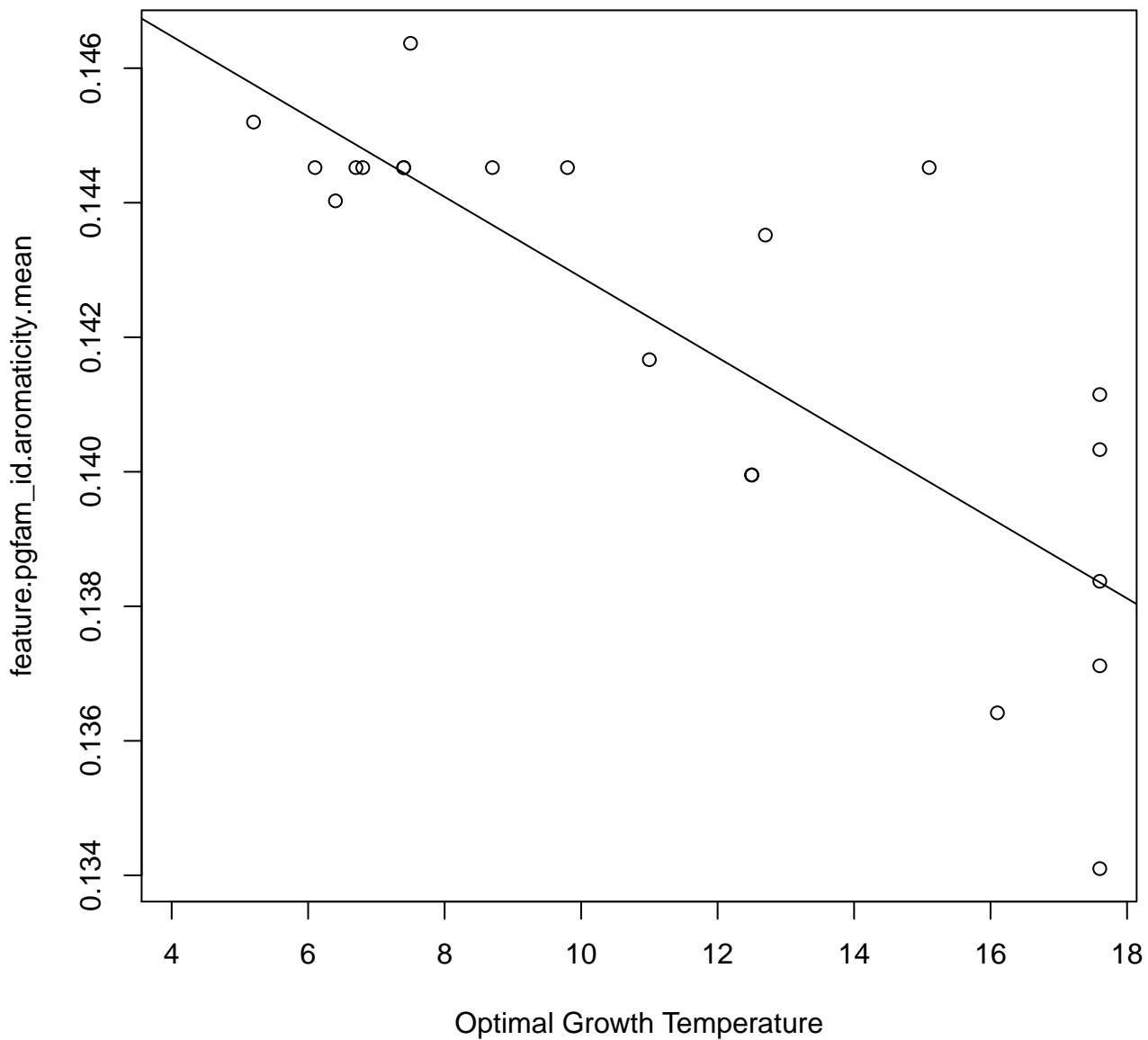
feature.pgfam_id.aromaticity.mean
PGF_01338003
Membrane-associated methyl-accepting chemotaxis protein with HAMP domain



feature.pgfam_id.aromaticity.mean
PGF_00058771
Transcriptional regulator of beta-glucosides utilization, LacI family



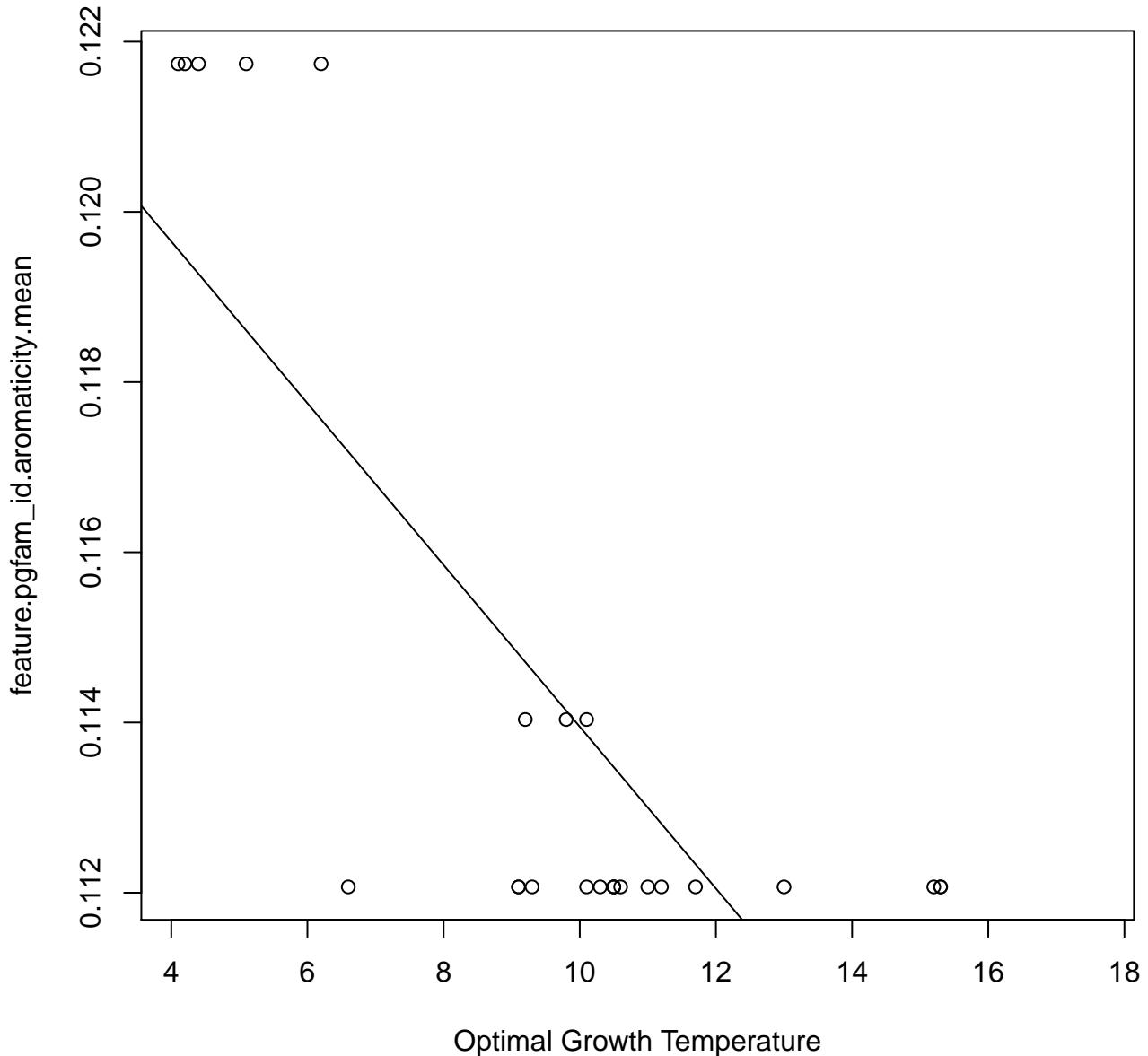
feature.pgfam_id.aromaticity.mean
PGF_00027102
Oligosaccharide 4-alpha-D-glucosyltransferase (EC 2.4.1.161)



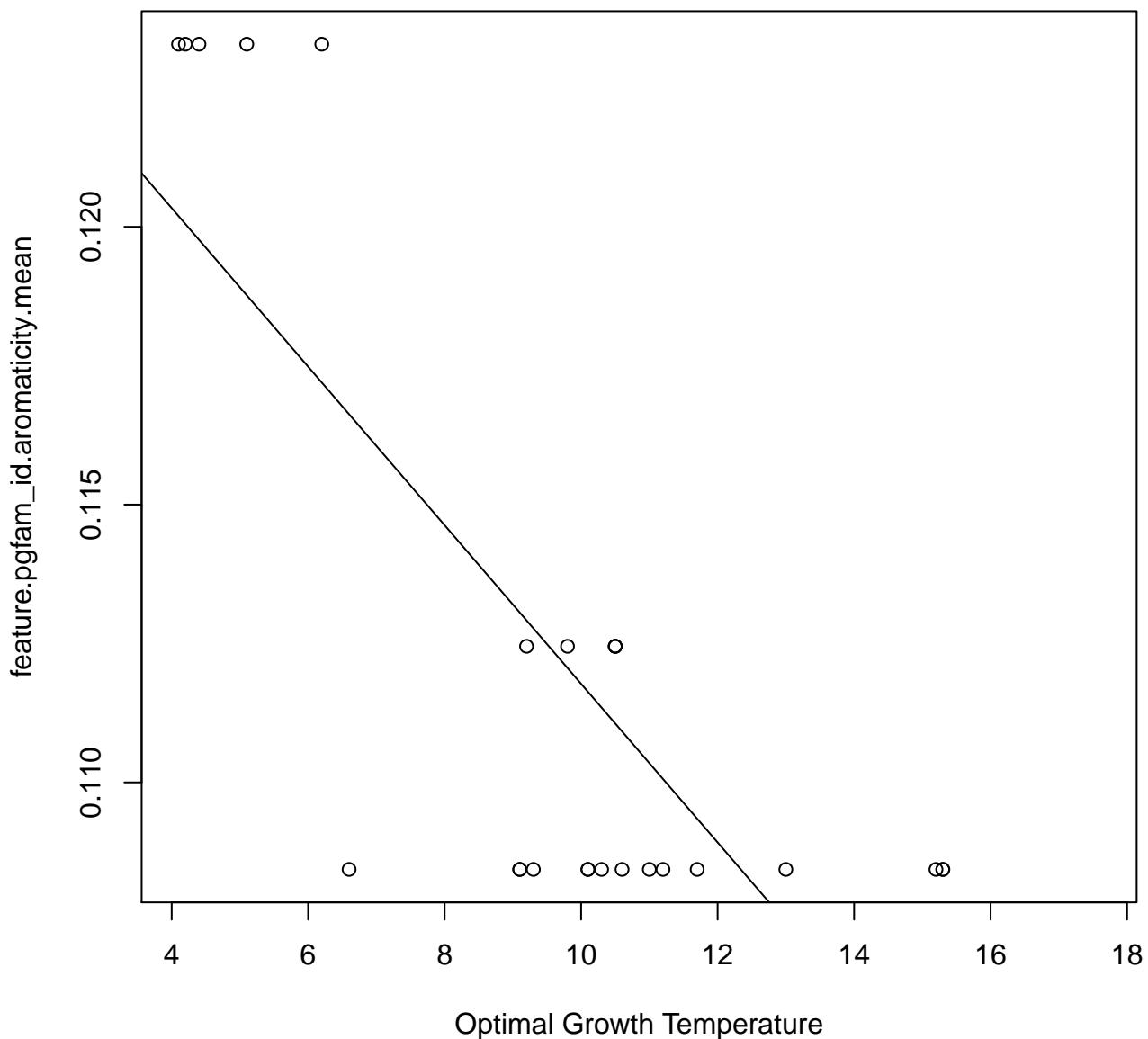
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PGF_07361149

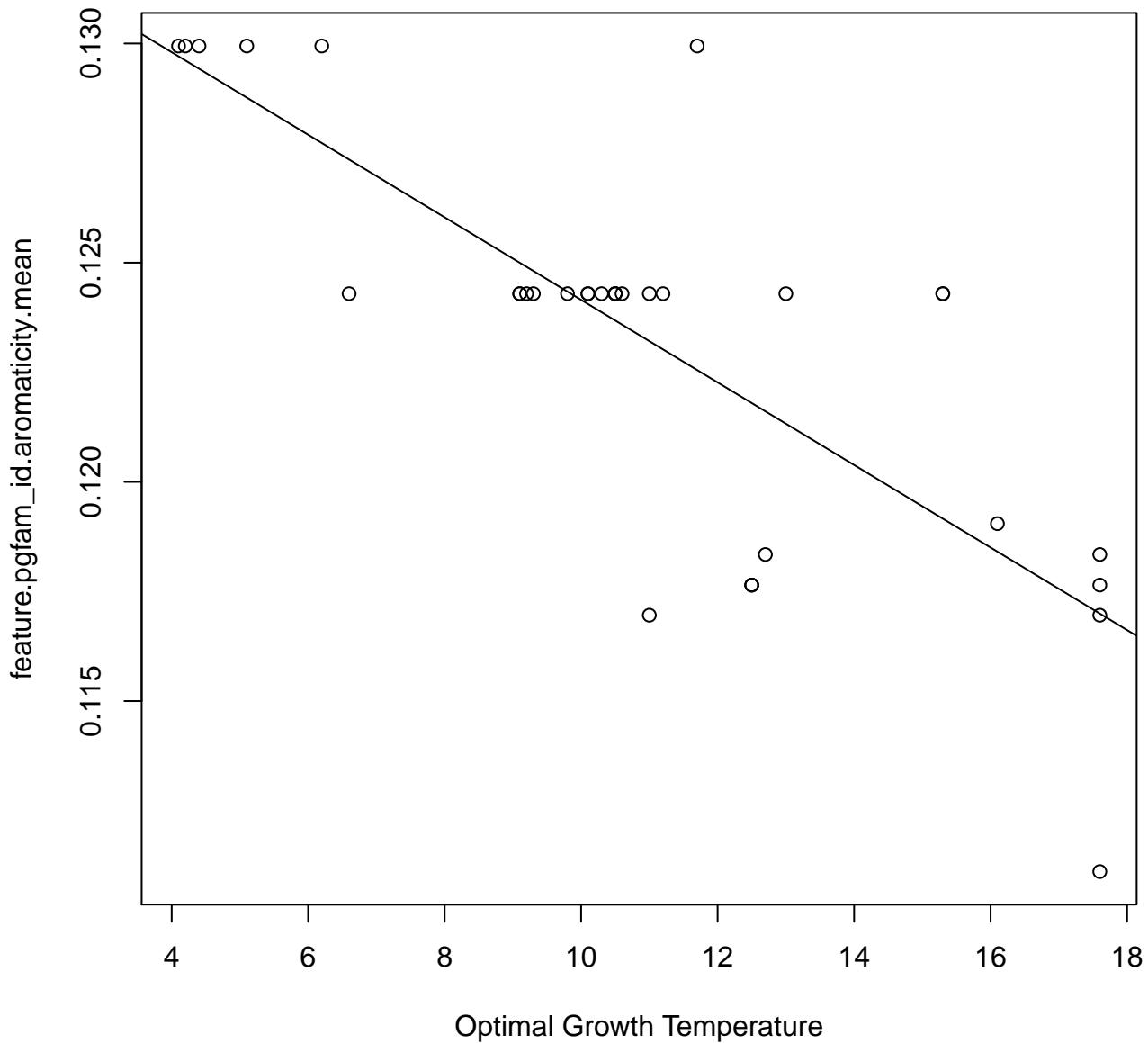
hypothetical protein



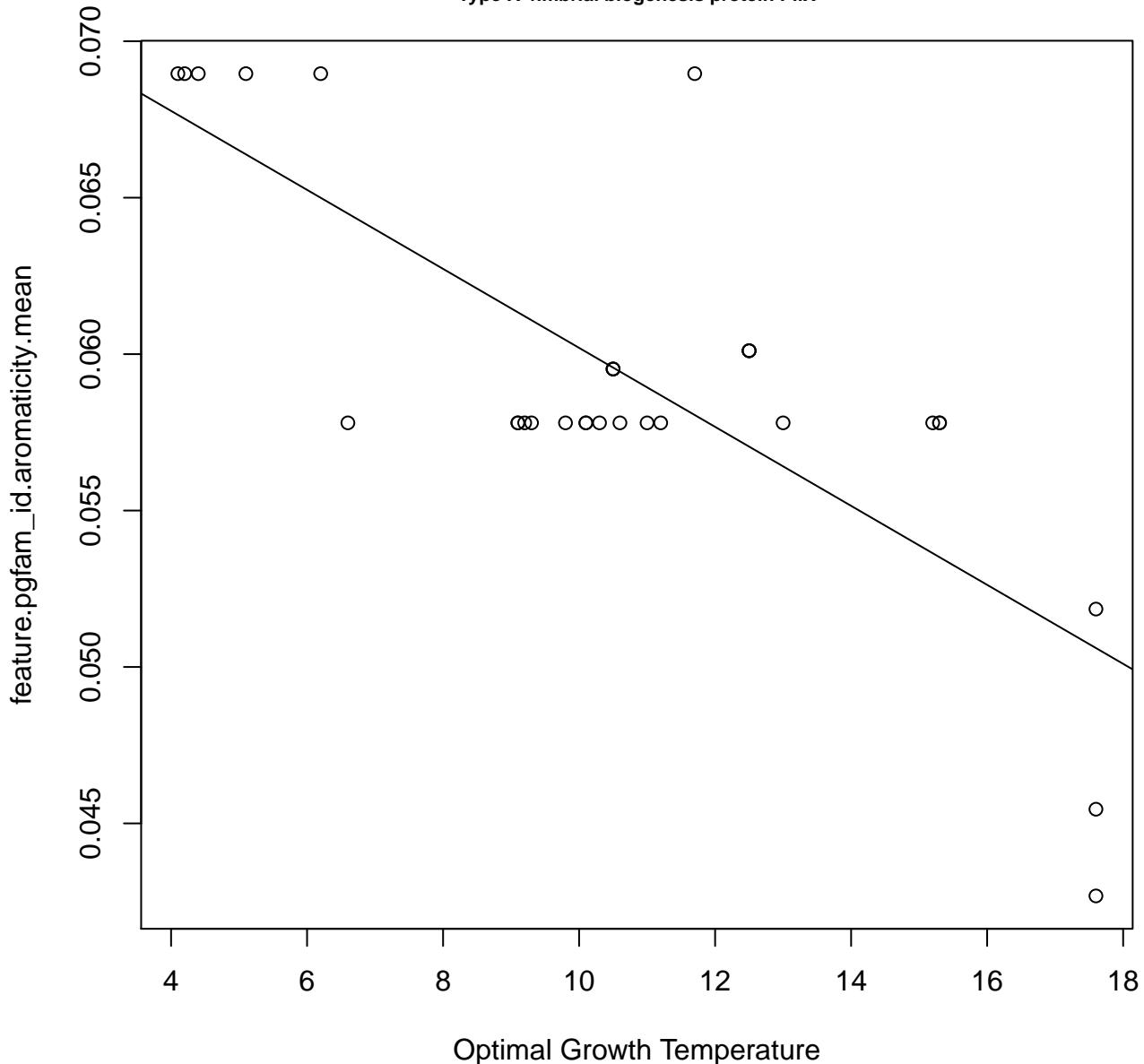
feature.pgfam_id.aromaticity.mean
PGF_11018774
hypothetical protein



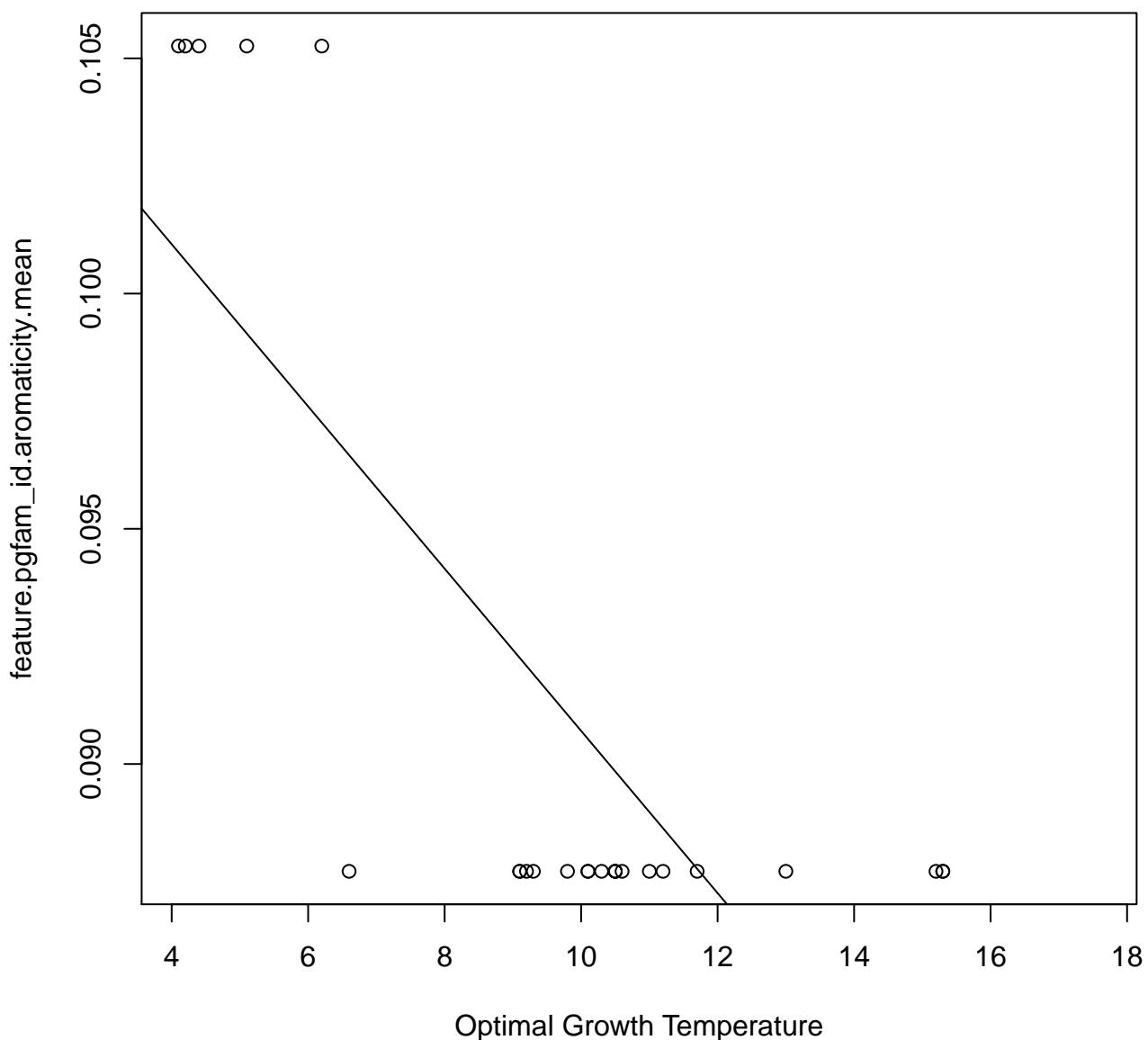
feature.pgfam_id.aromaticity.mean
PGF_03021302
Ureidoglycolate lyase (EC 4.3.2.3)



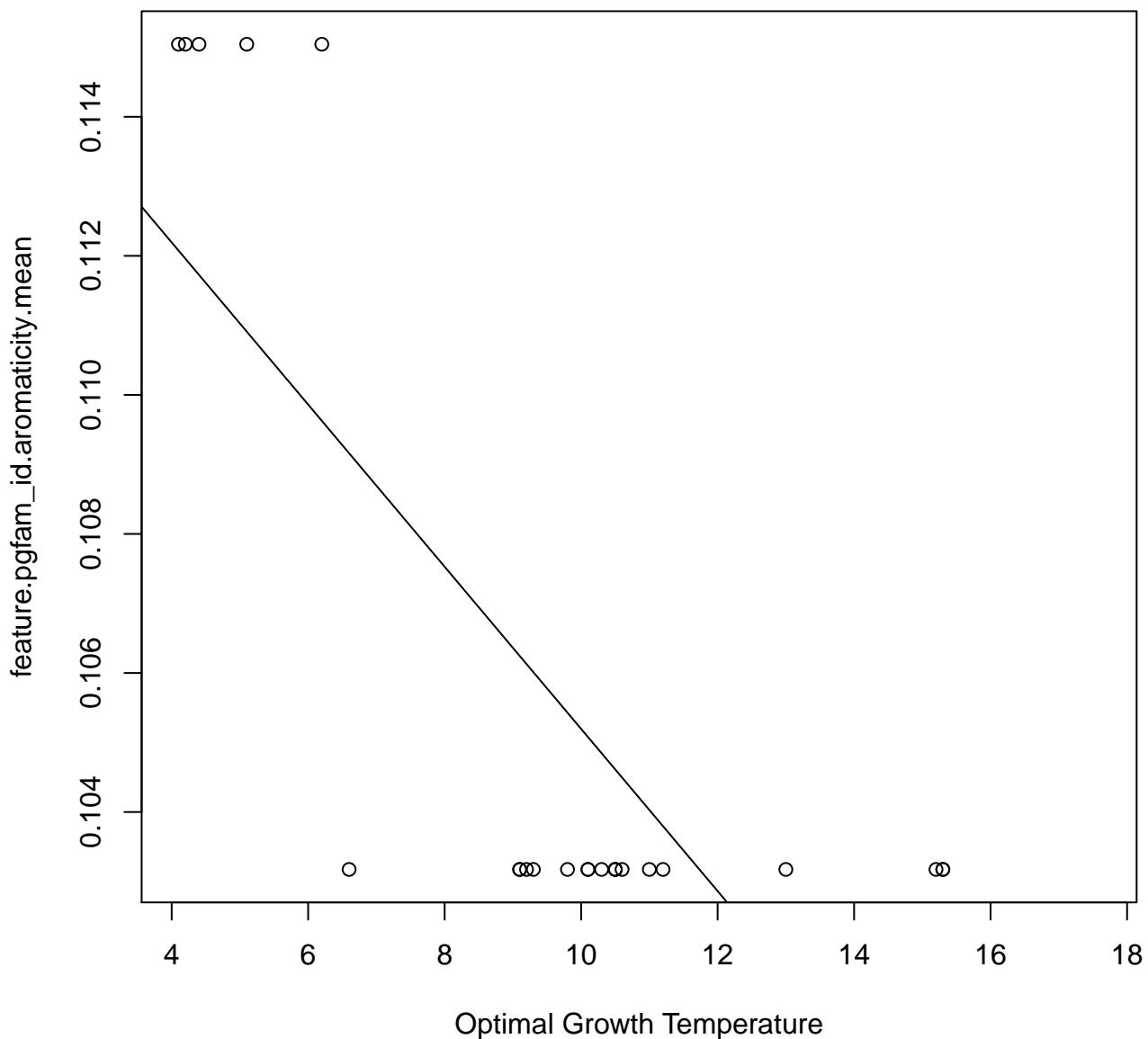
feature.pgfam_id.aromaticity.mean
PGF_01064051
Type IV fimbrial biogenesis protein PilX



feature.pgfam_id.aromaticity.mean
PGF_08289417
hypothetical protein



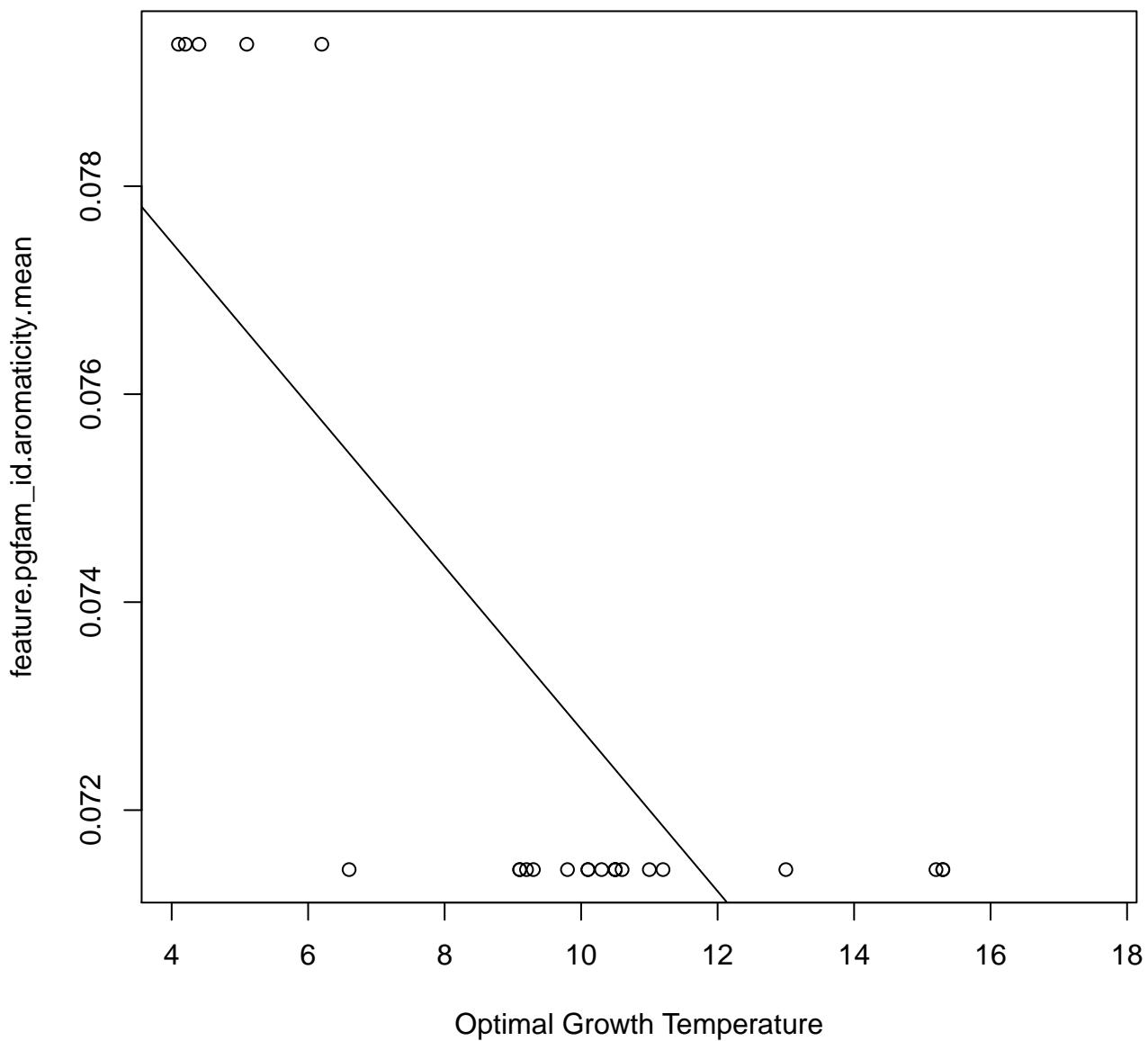
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PGF_12049070
hypothetical protein



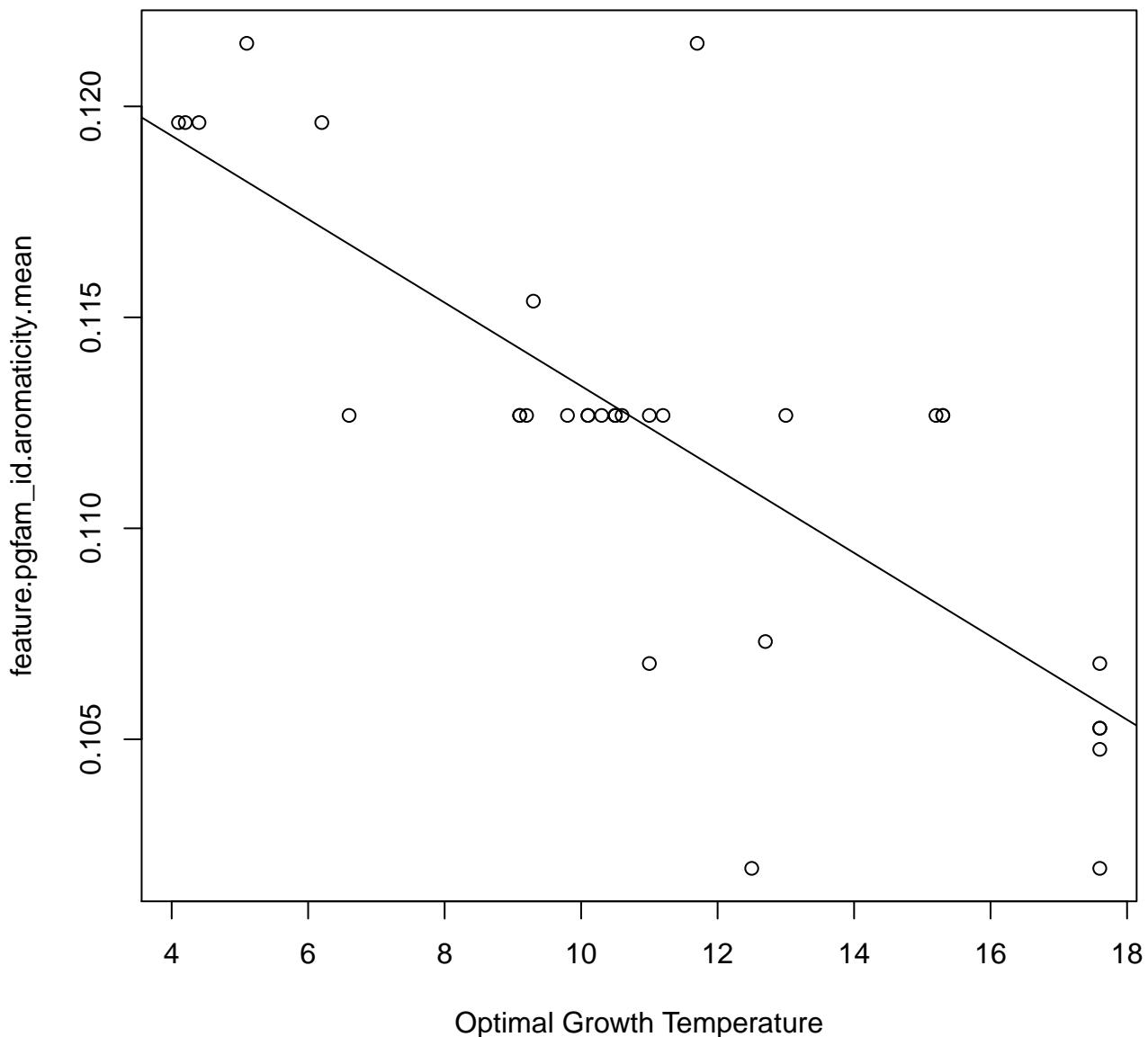
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PGF_12288710

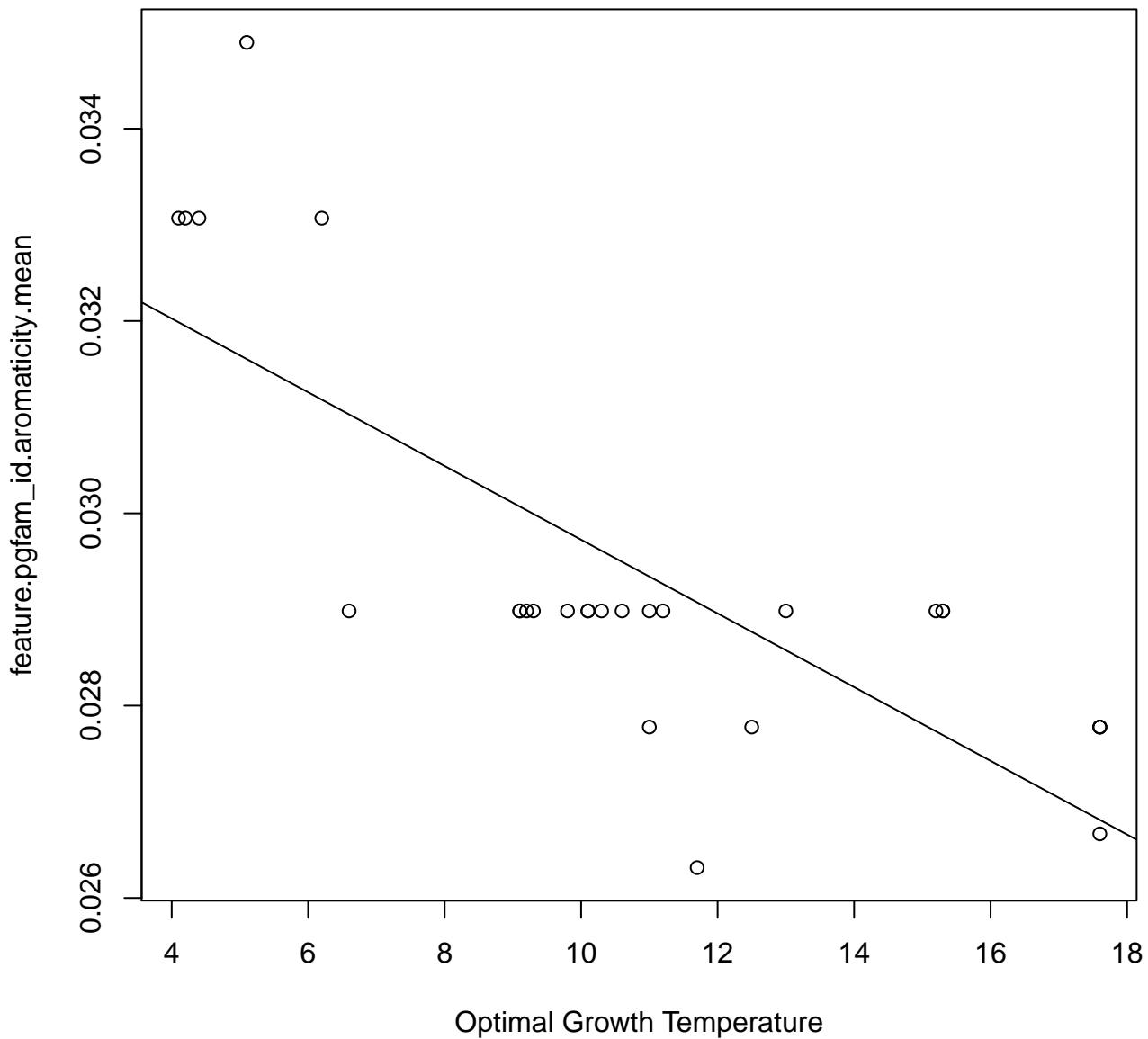
hypothetical protein



feature.pgfam_id.aromaticity.mean
PGF_03324420
General secretion pathway protein H



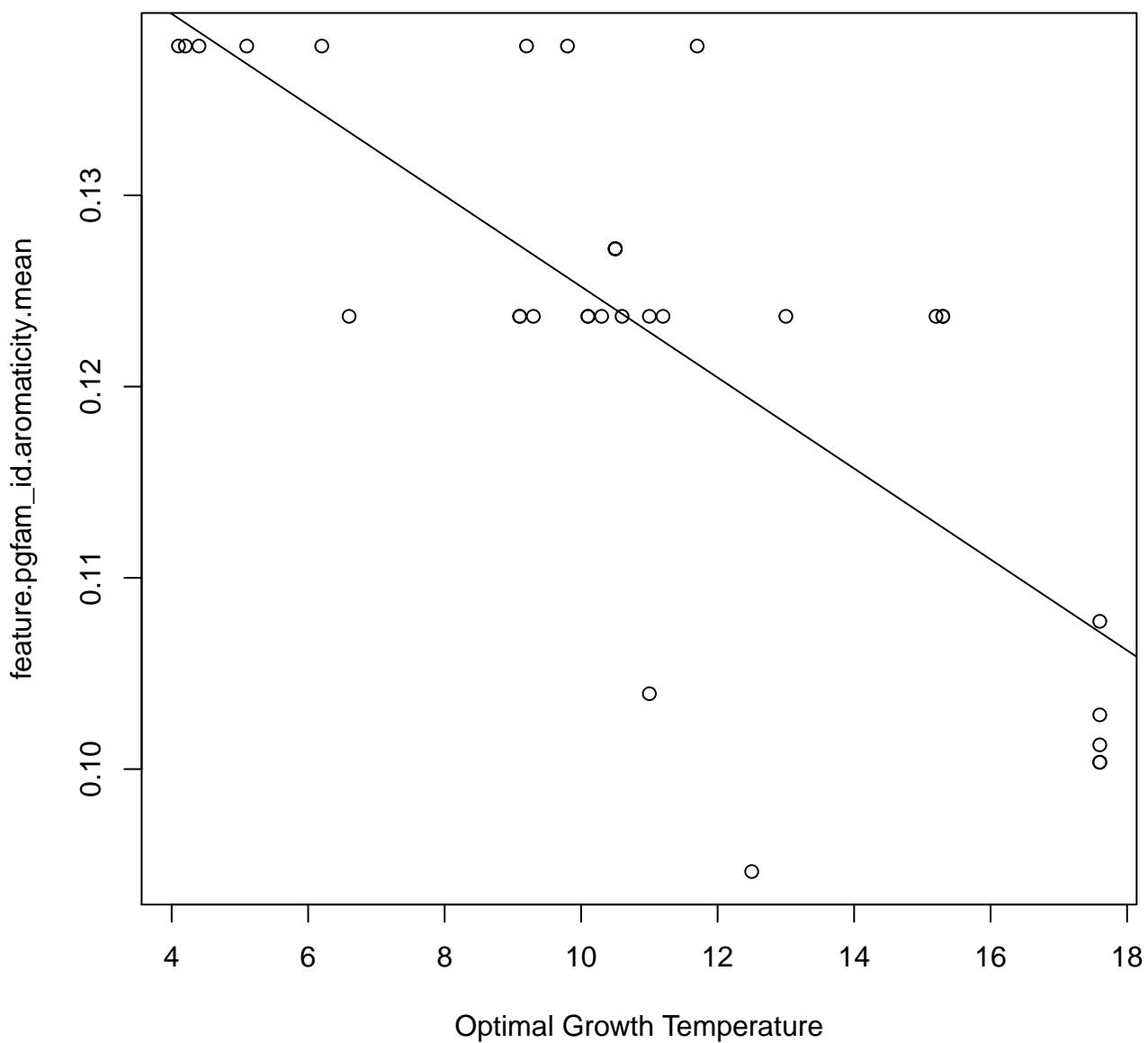
feature.pgfam_id.aromaticity.mean
PGF_04743045
Uncharacterized transcriptional regulator YozG, Cro/Cl family



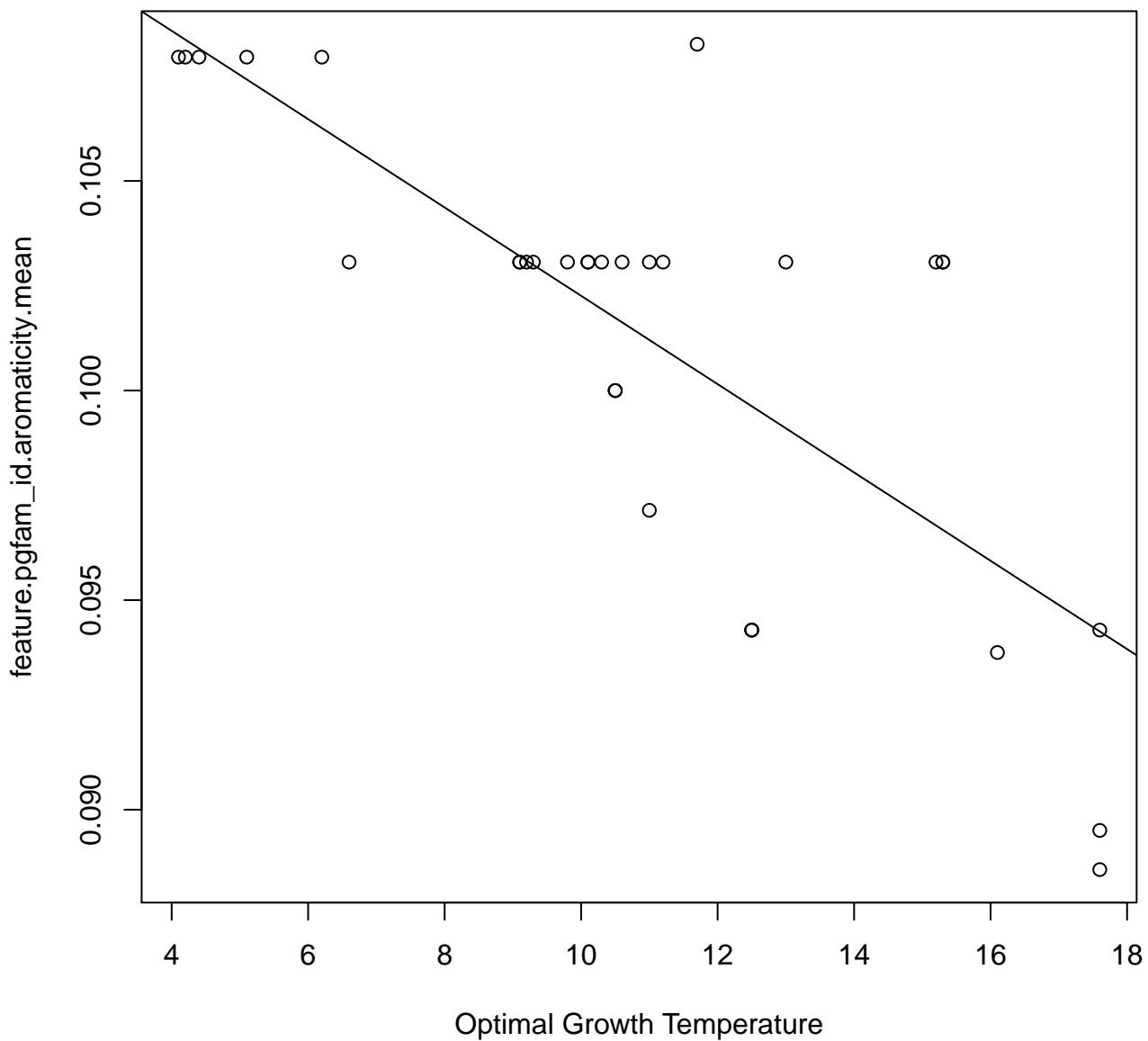
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PGF_03965214

hypothetical protein



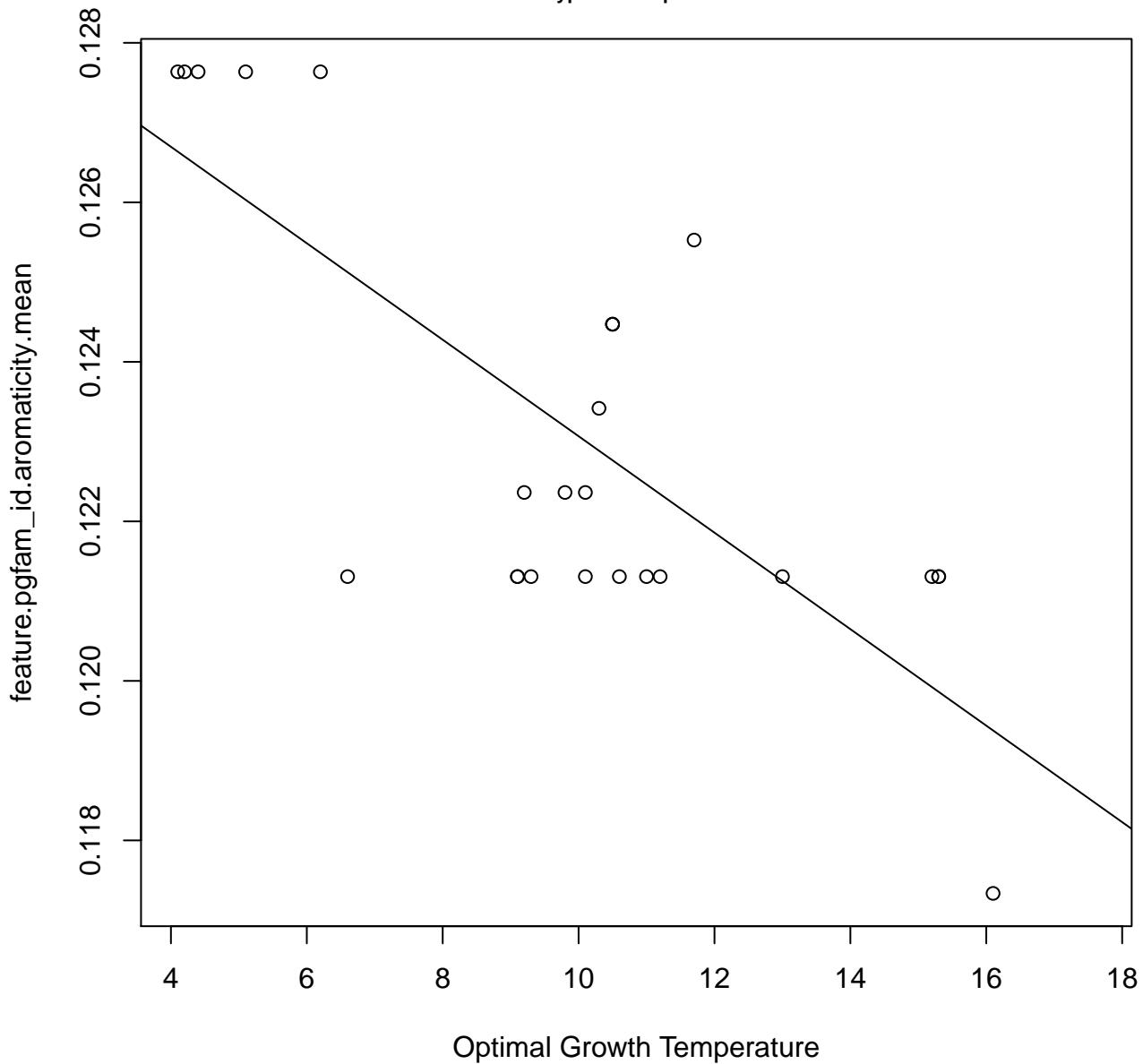
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PGF_07448574
hypothetical protein



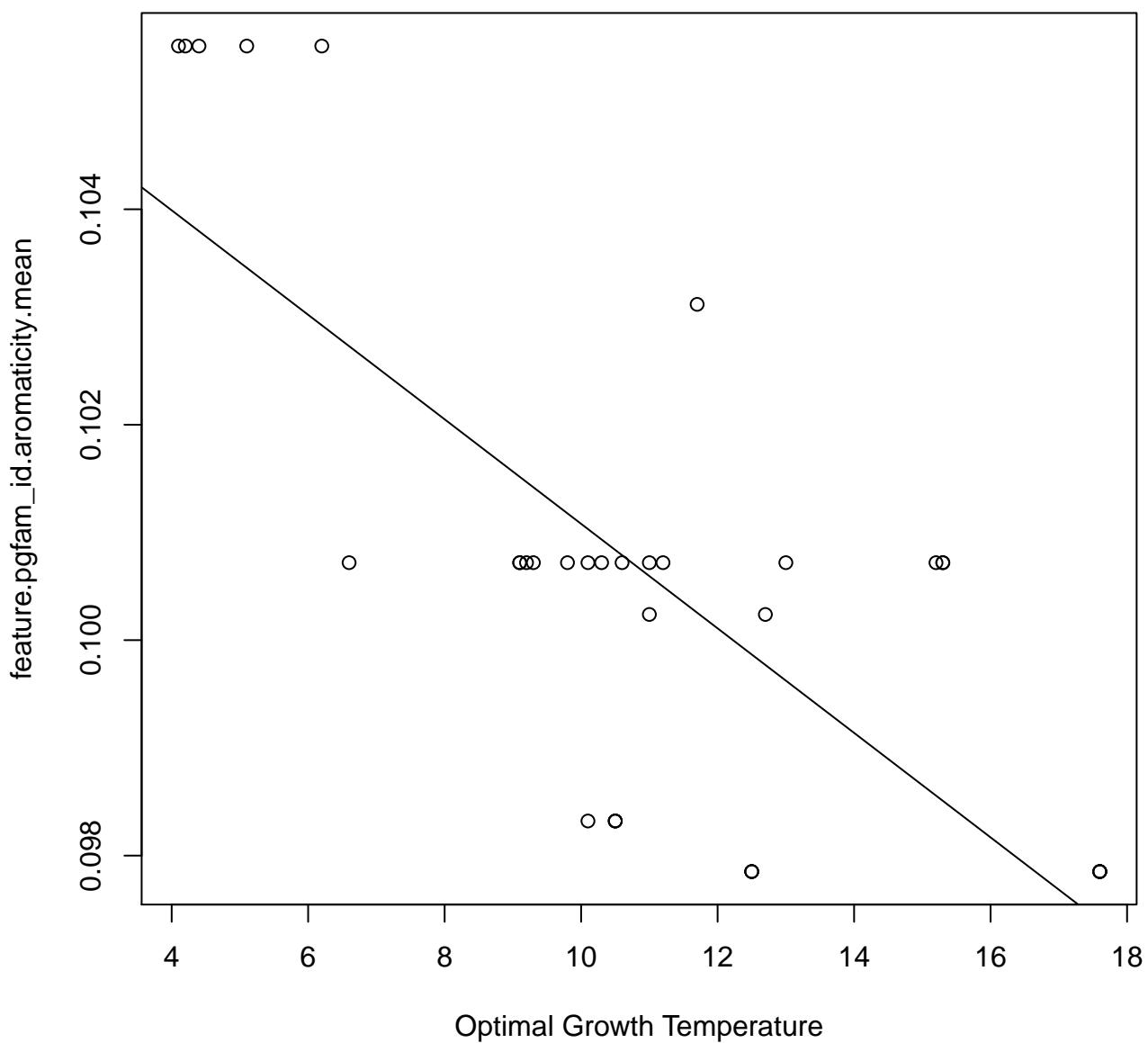
feature.pgfam_id.aromaticity.mean

PGF_04802662

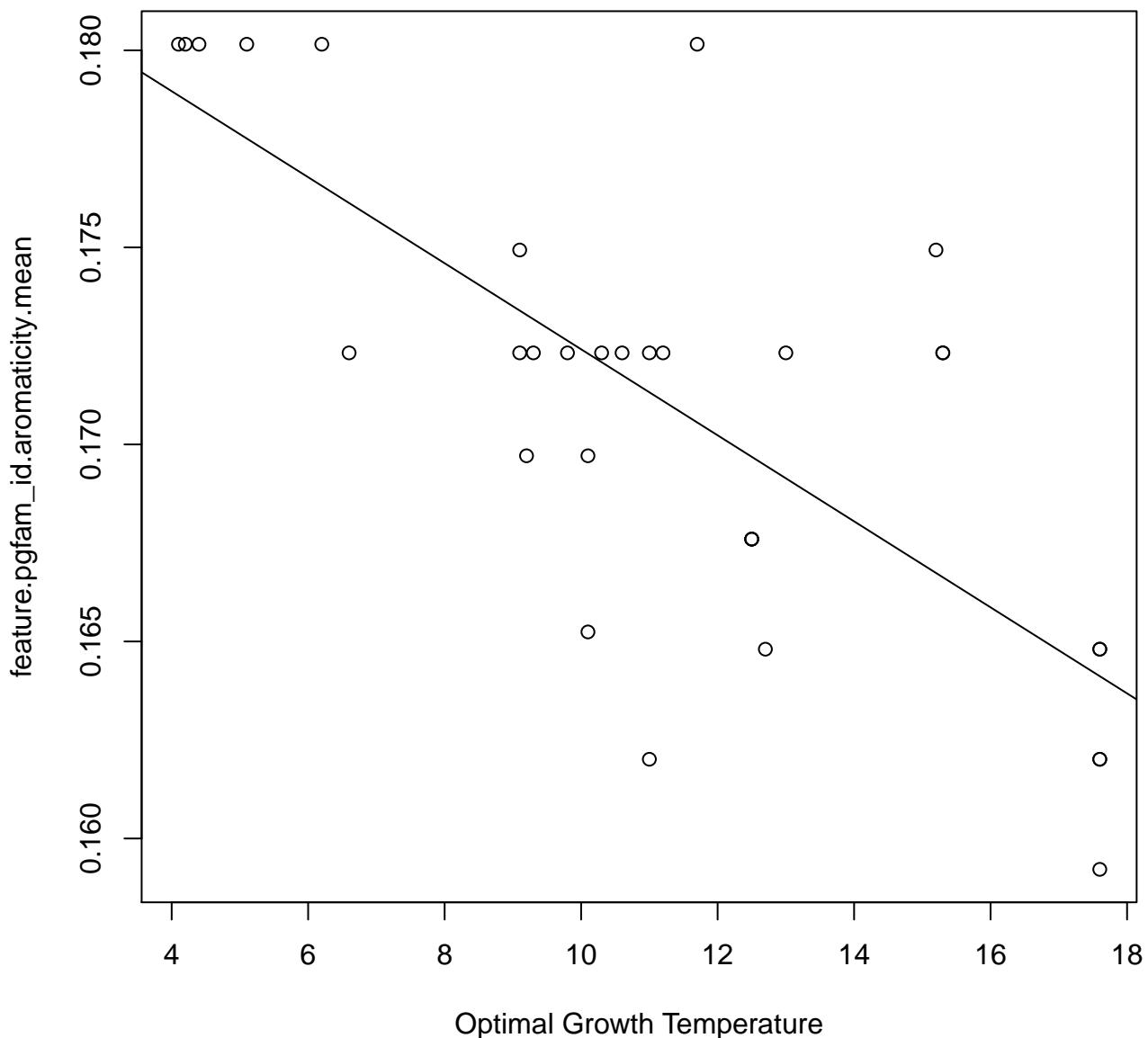
hypothetical protein



feature.pgfam_id.aromaticity.mean
PGF_01336341
Transcriptional regulator

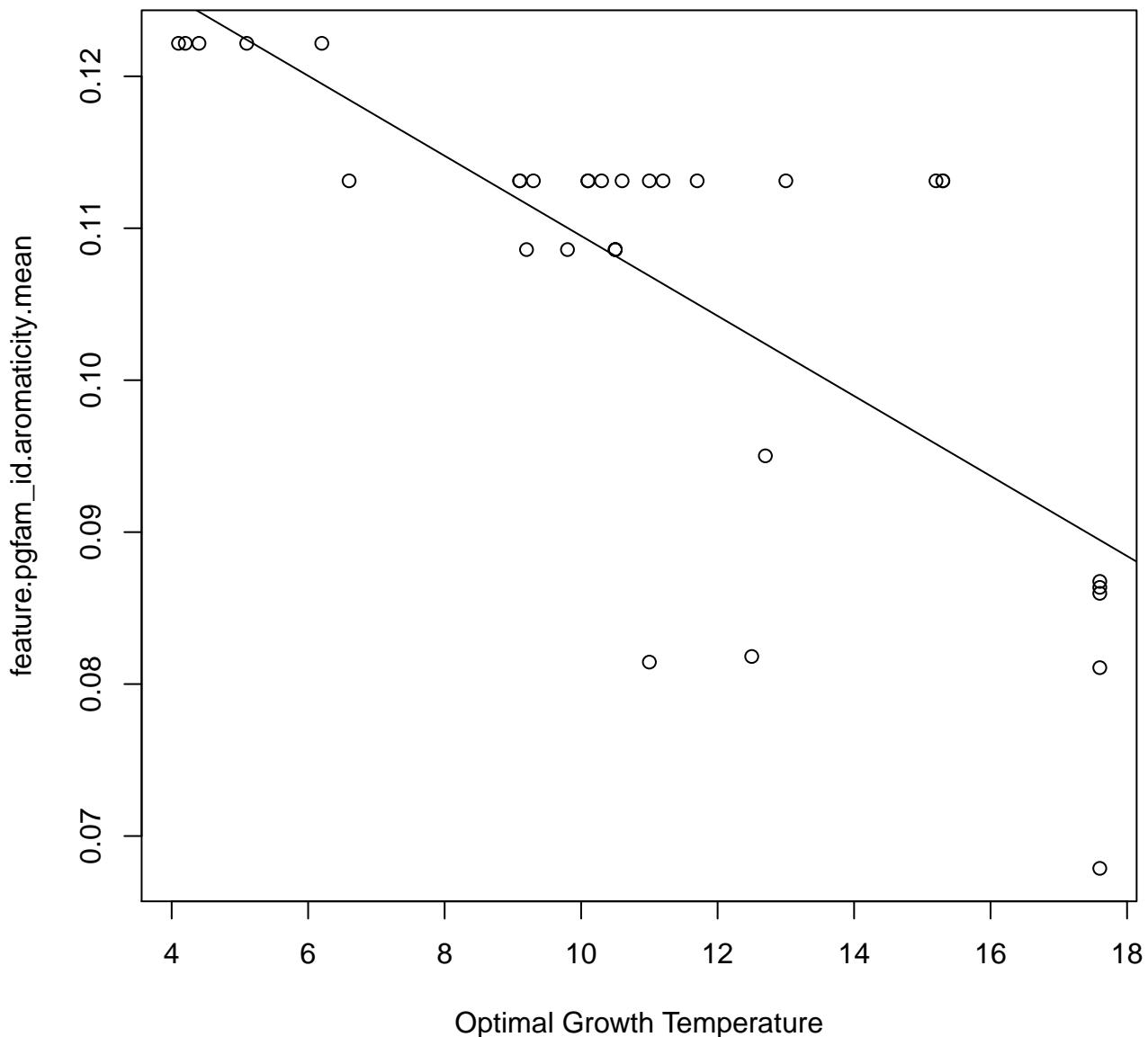


feature.pgfam_id.aromaticity.mean
PGF_00023779
N-acetylglucosamine related transporter, NagX

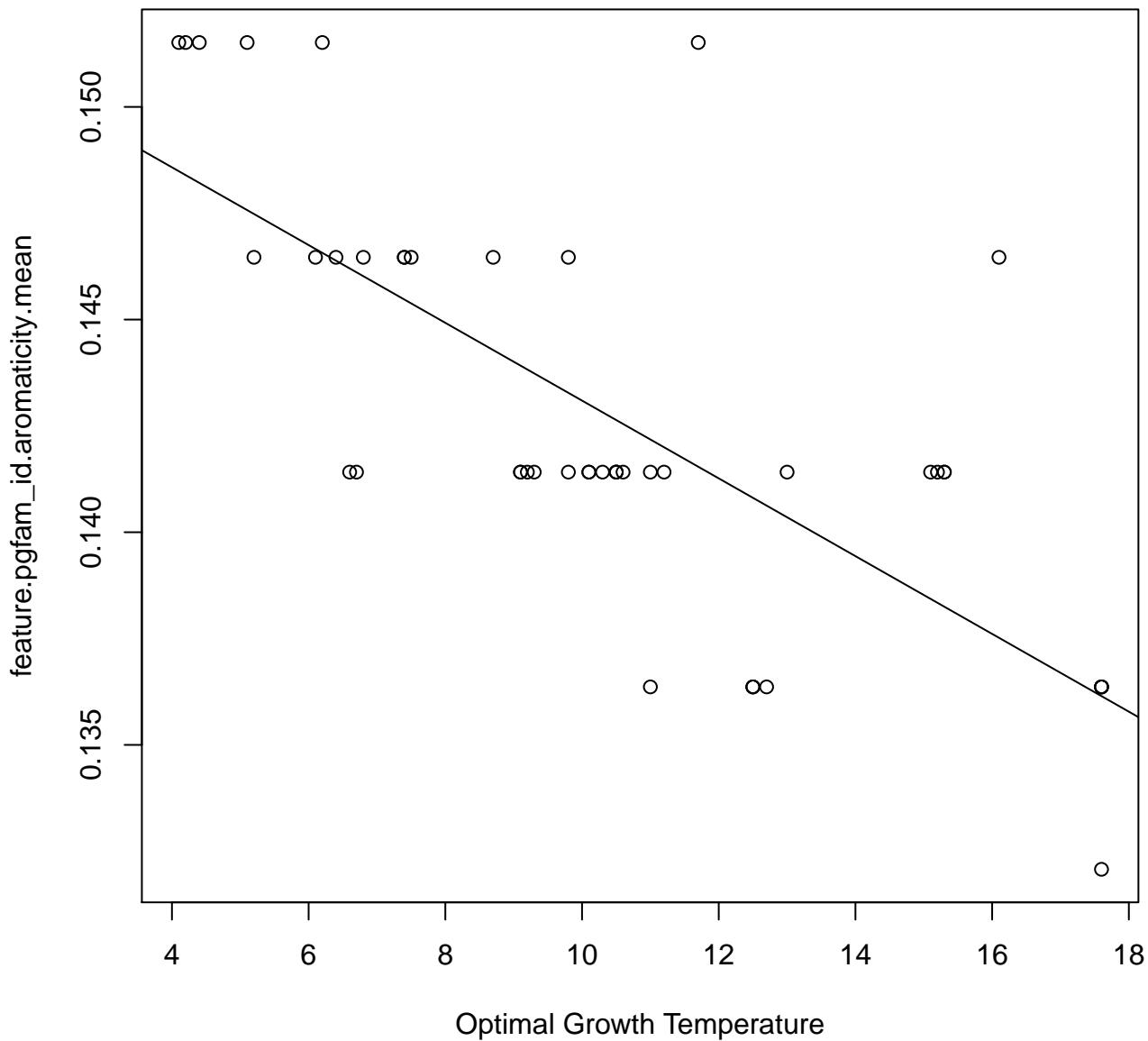


feature.pgfam_id.aromaticity.mean
PGF_07191133

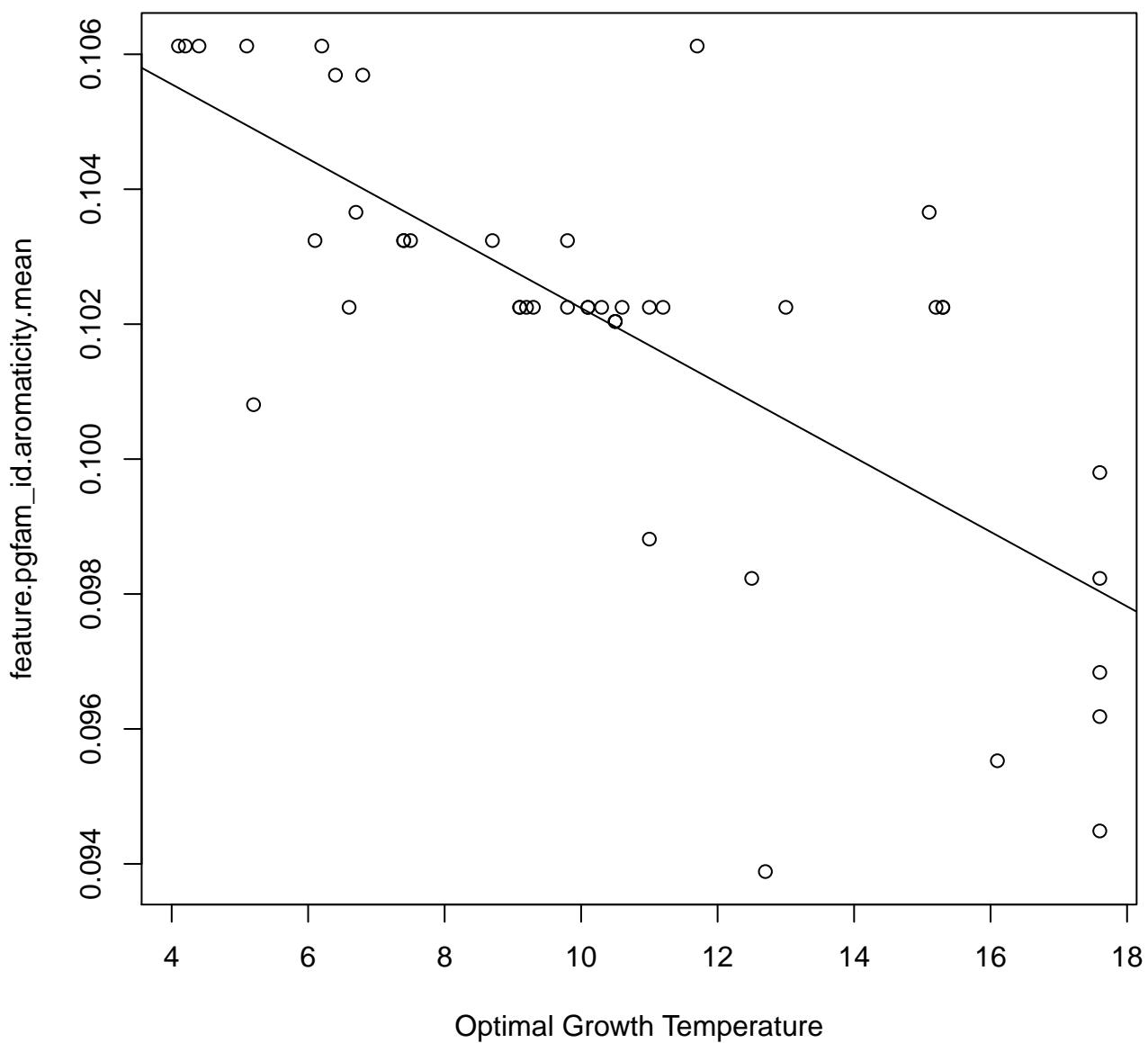
Similar to phosphoglycolate phosphatase, clustered with ribosomal large subunit pseudouridine synthase C



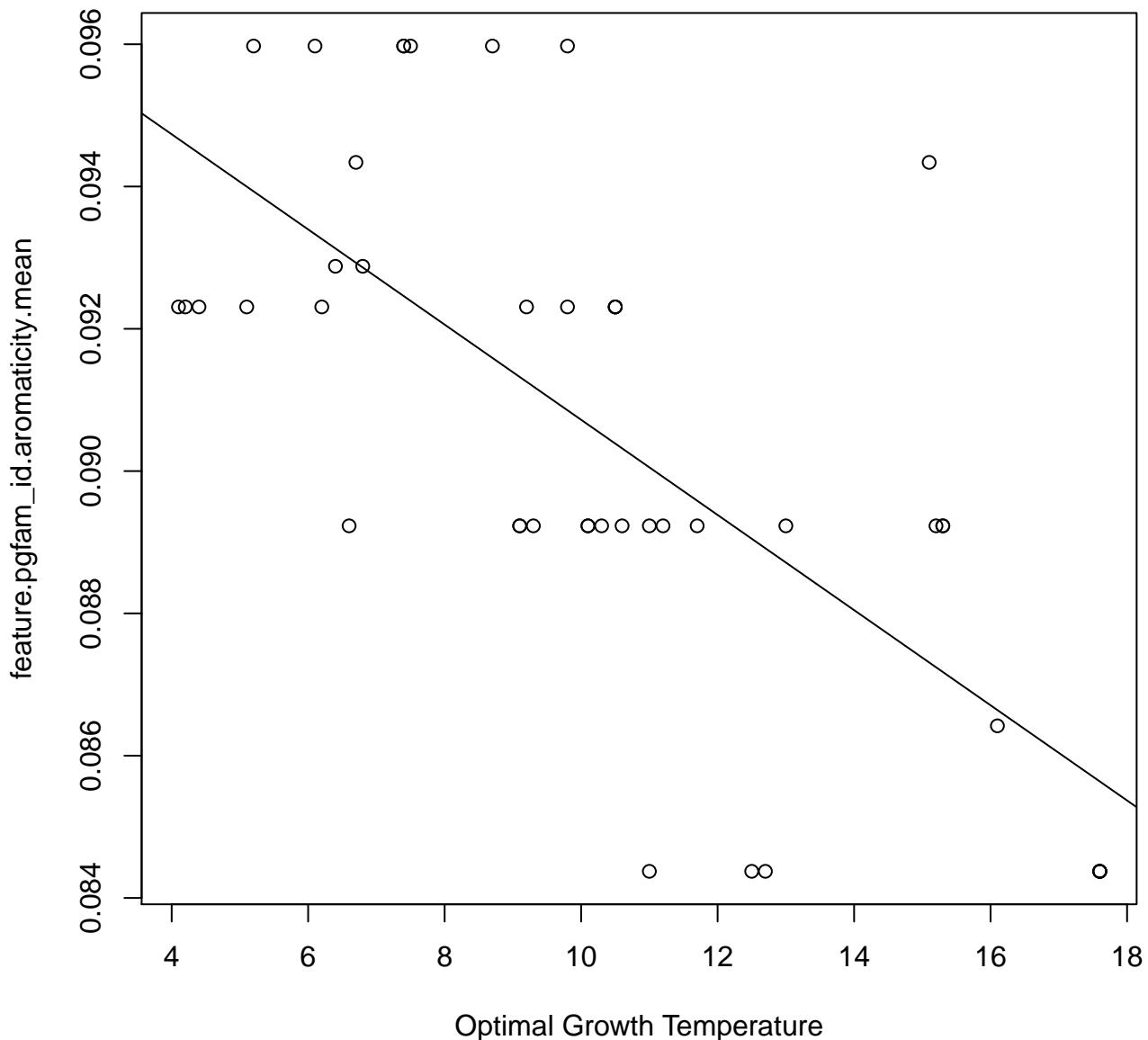
feature.pgfam_id.aromaticity.mean
PGF_06660812
3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)



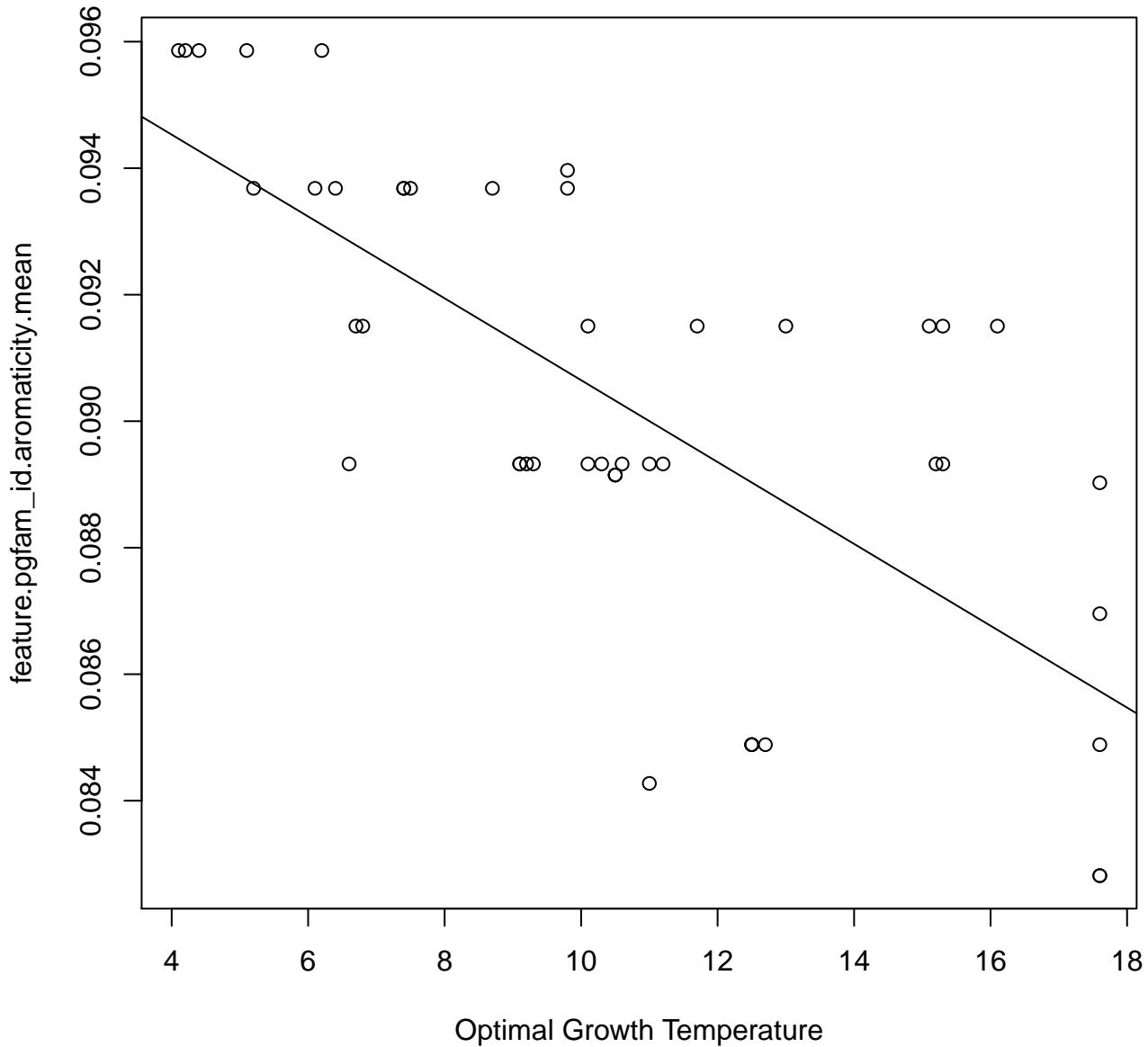
feature.pgfam_id.aromaticity.mean
PGF_06261512
Flagellar regulatory protein FleQ



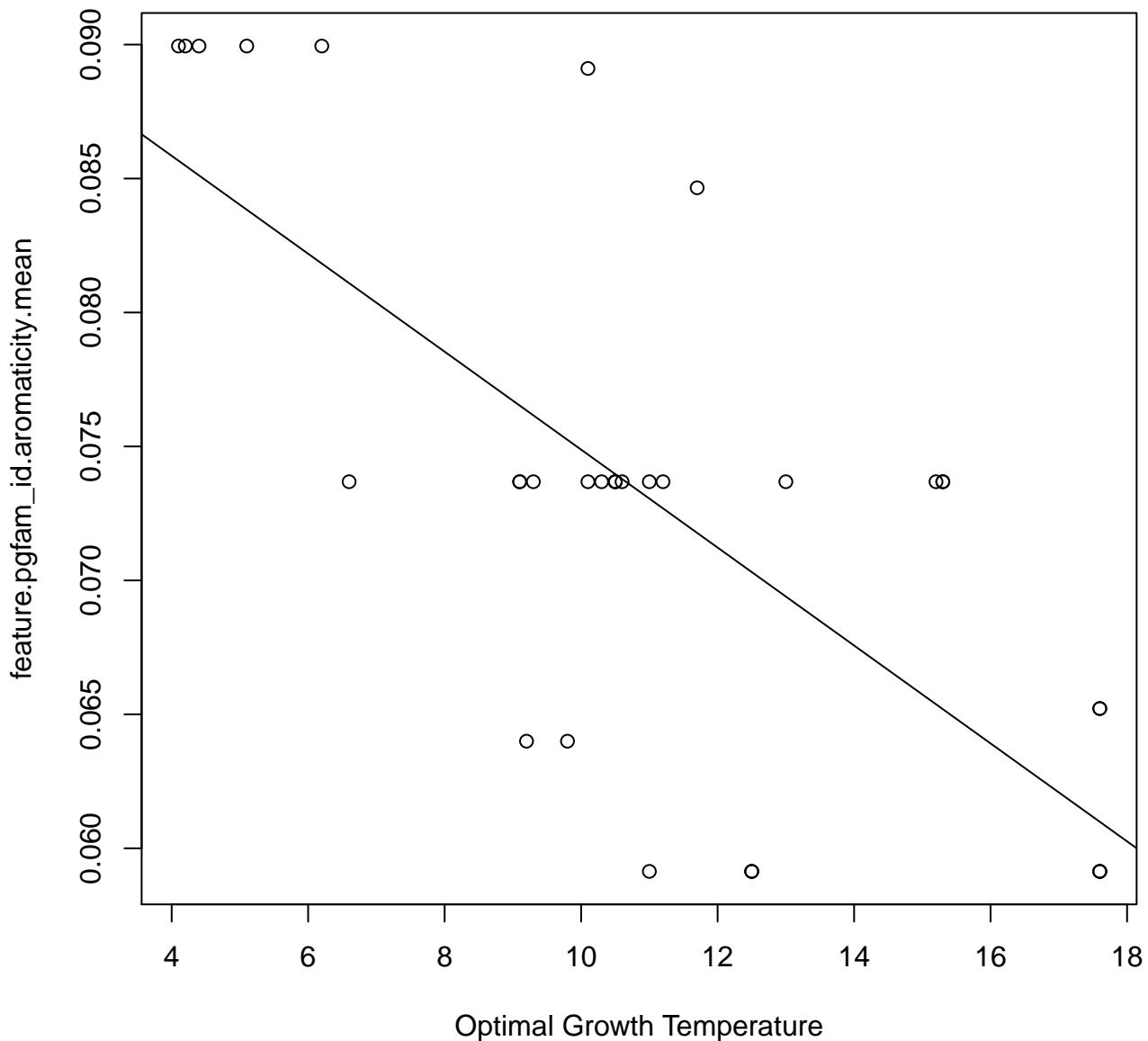
feature.pgfam_id.aromaticity.mean
PGF_02191019
Thiamine-monophosphate kinase (EC 2.7.4.16)



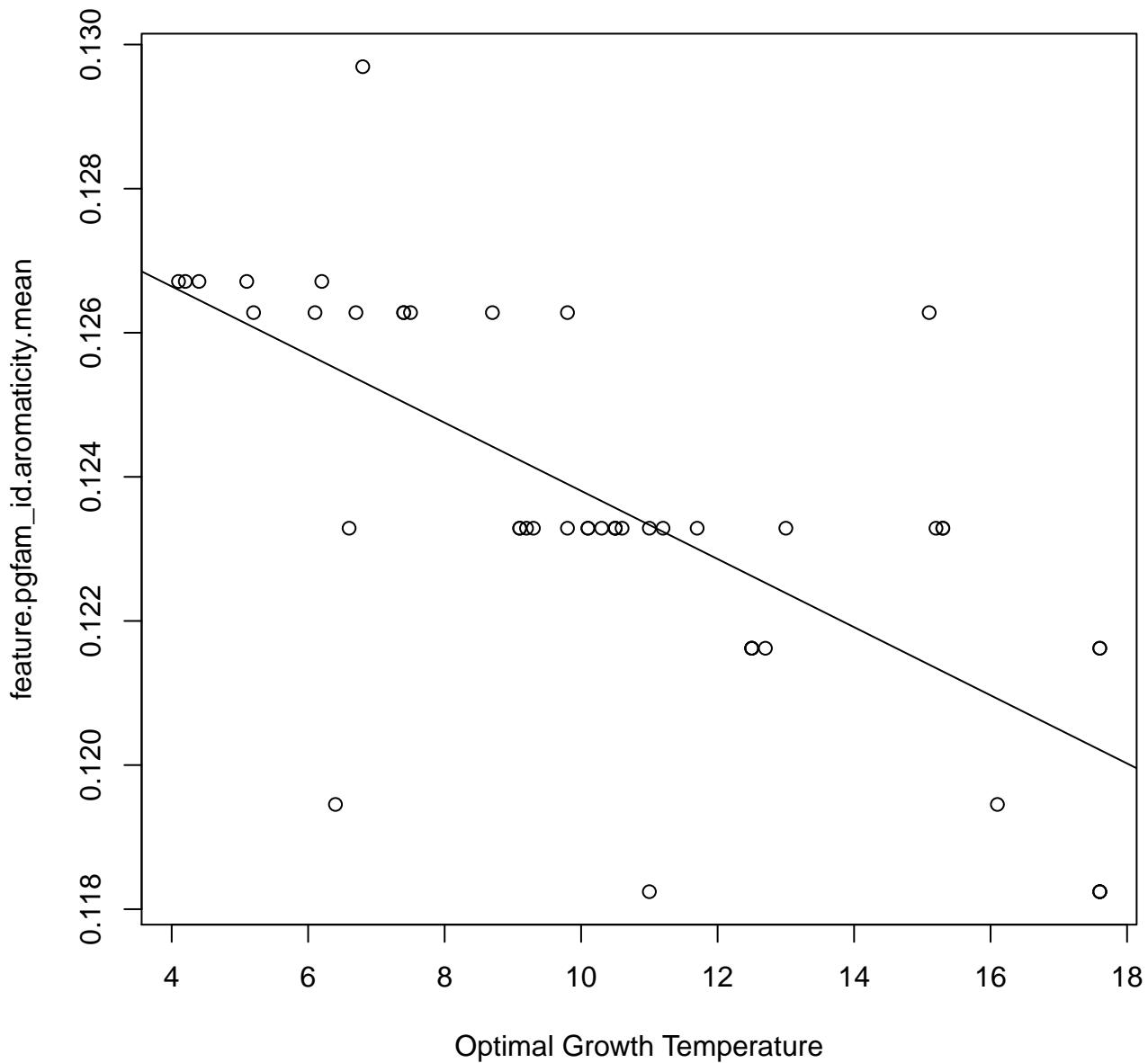
feature.pgfam_id.aromaticity.mean
PGF_06051594
Predicted ATPase related to phosphate starvation-inducible protein PhoH



feature.pgfam_id.aromaticity.mean
PGF_00423668
Dna binding response regulator PrrA (RegA)



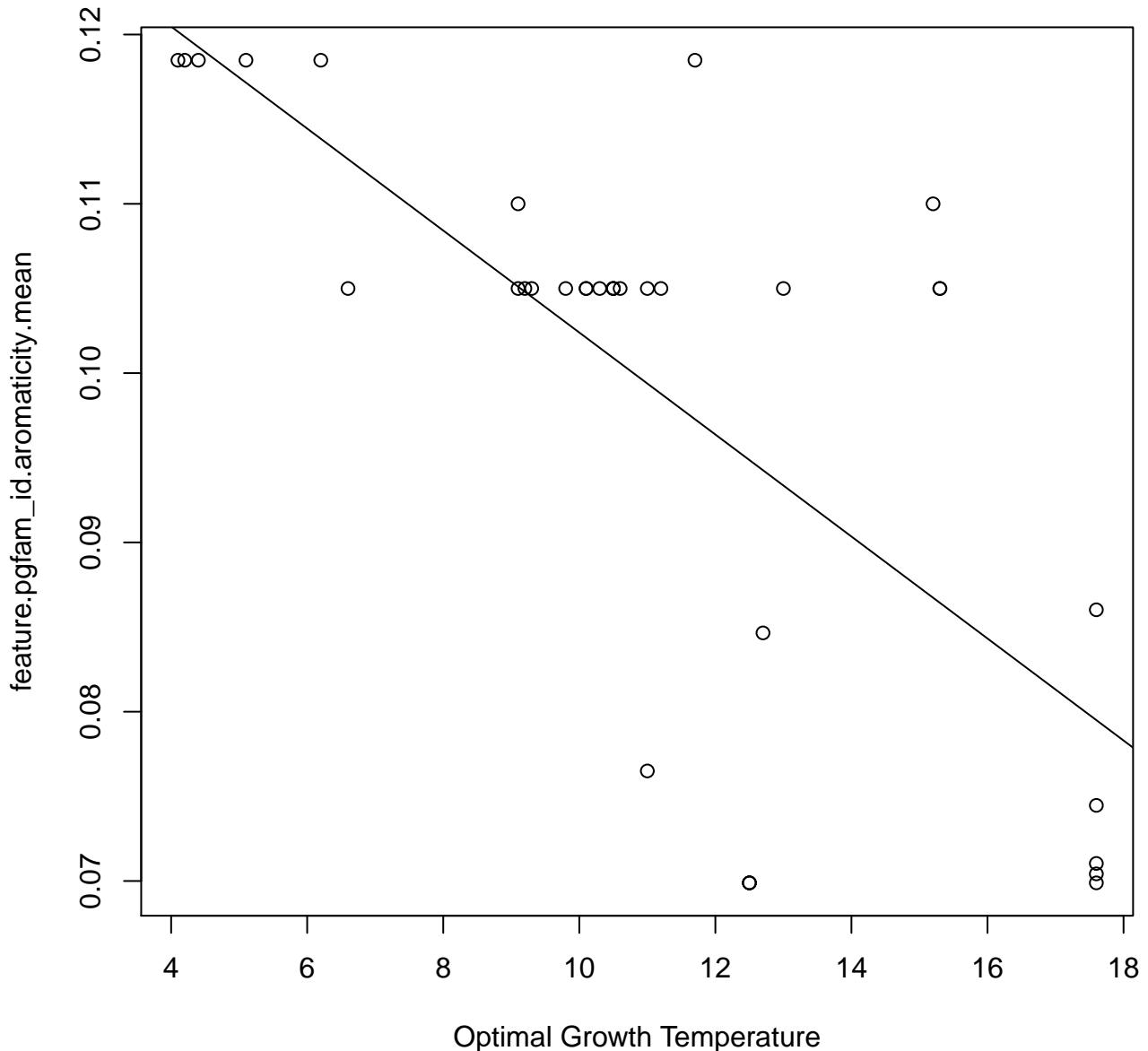
feature.pgfam_id.aromaticity.mean
PGF_03051420
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



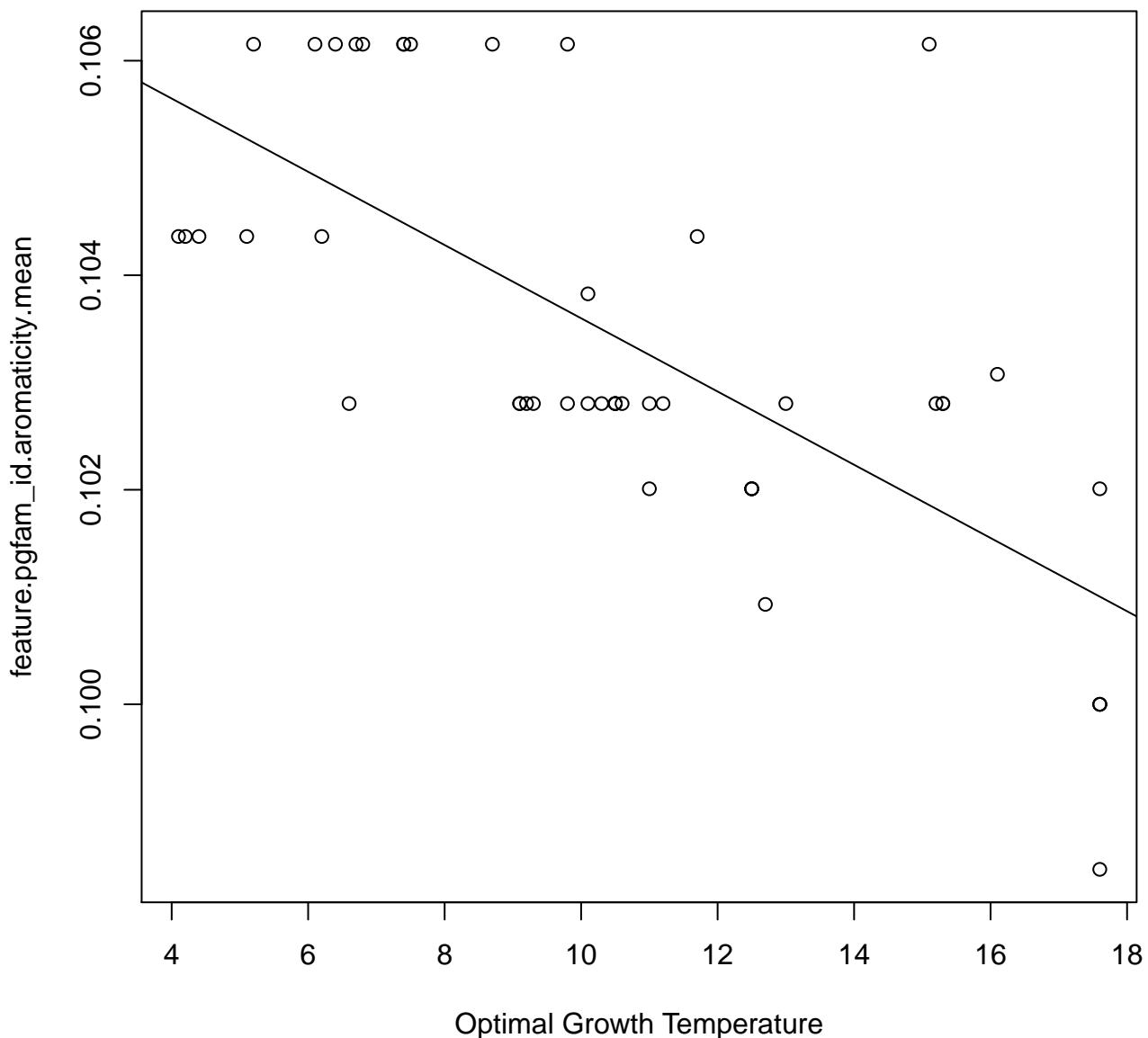
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PGF_02790700

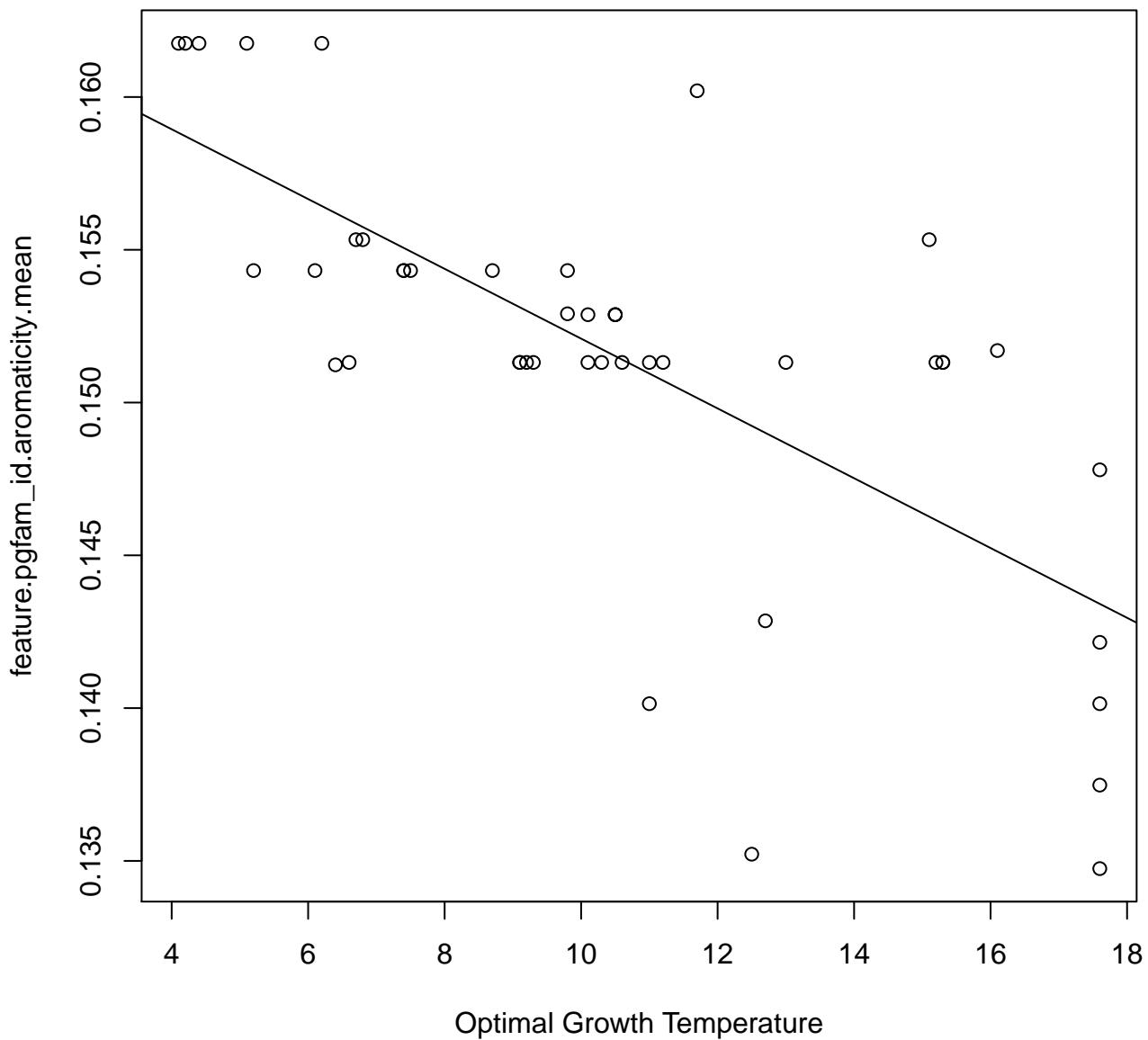
Adenosylcobinamide kinase (EC 2.7.1.156) / Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)



feature.pgfam_id.aromaticity.mean
PGF_00423472
DinG family ATP-dependent helicase YoaA



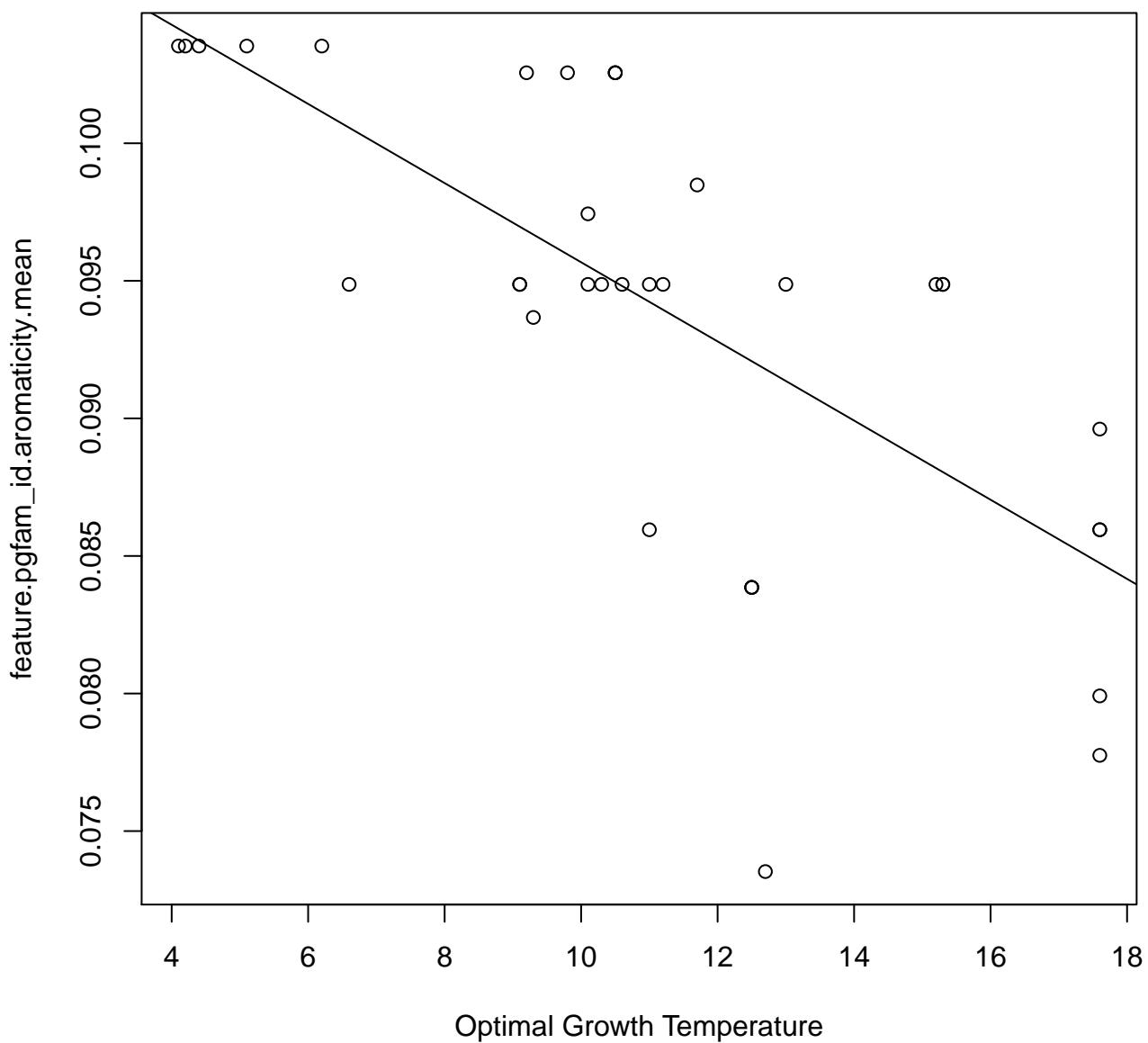
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PGF_07780089
Proline iminopeptidase (EC 3.4.11.5)



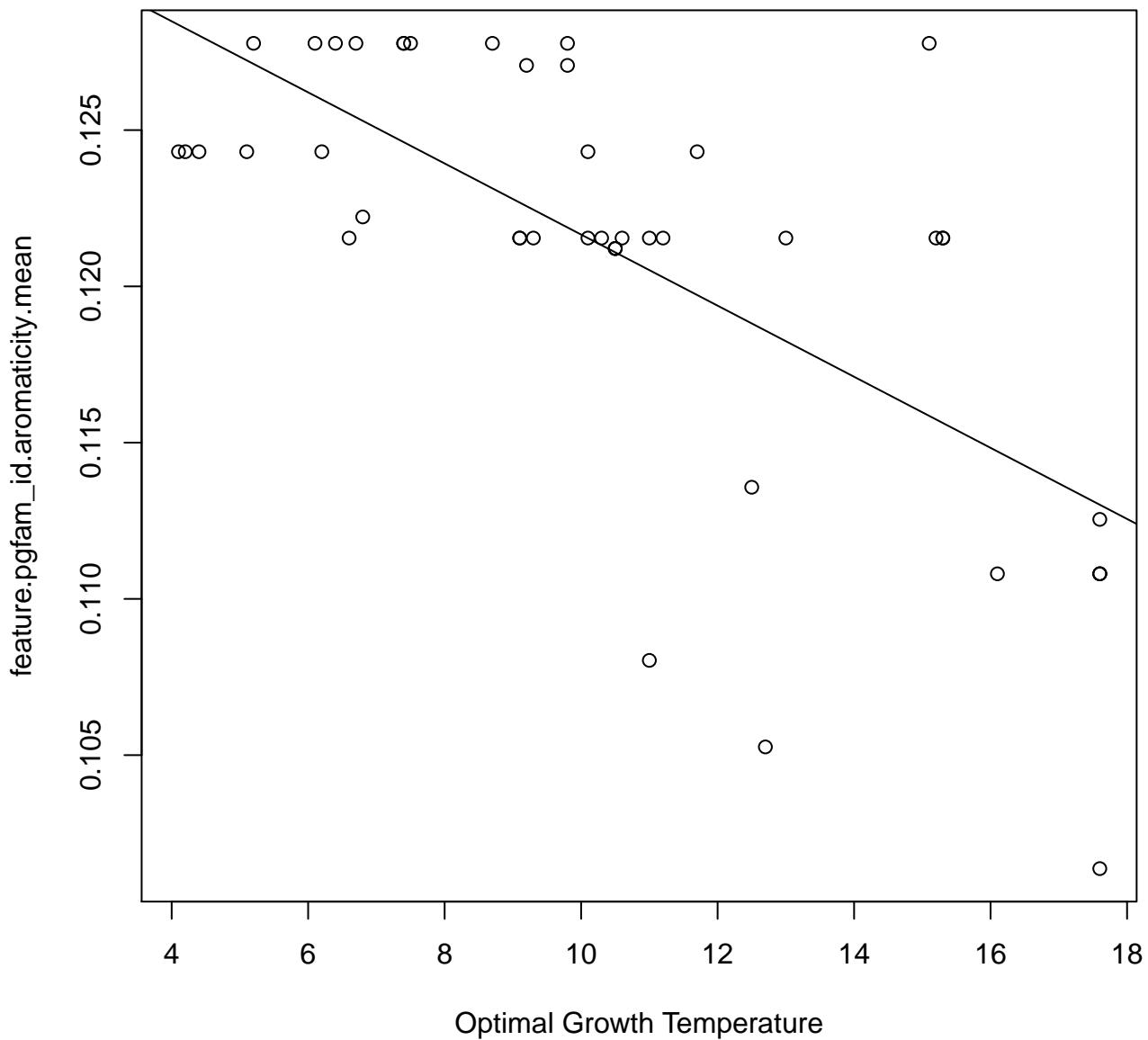
feature.pgfam_id.aromaticity.mean

PGF_01336373

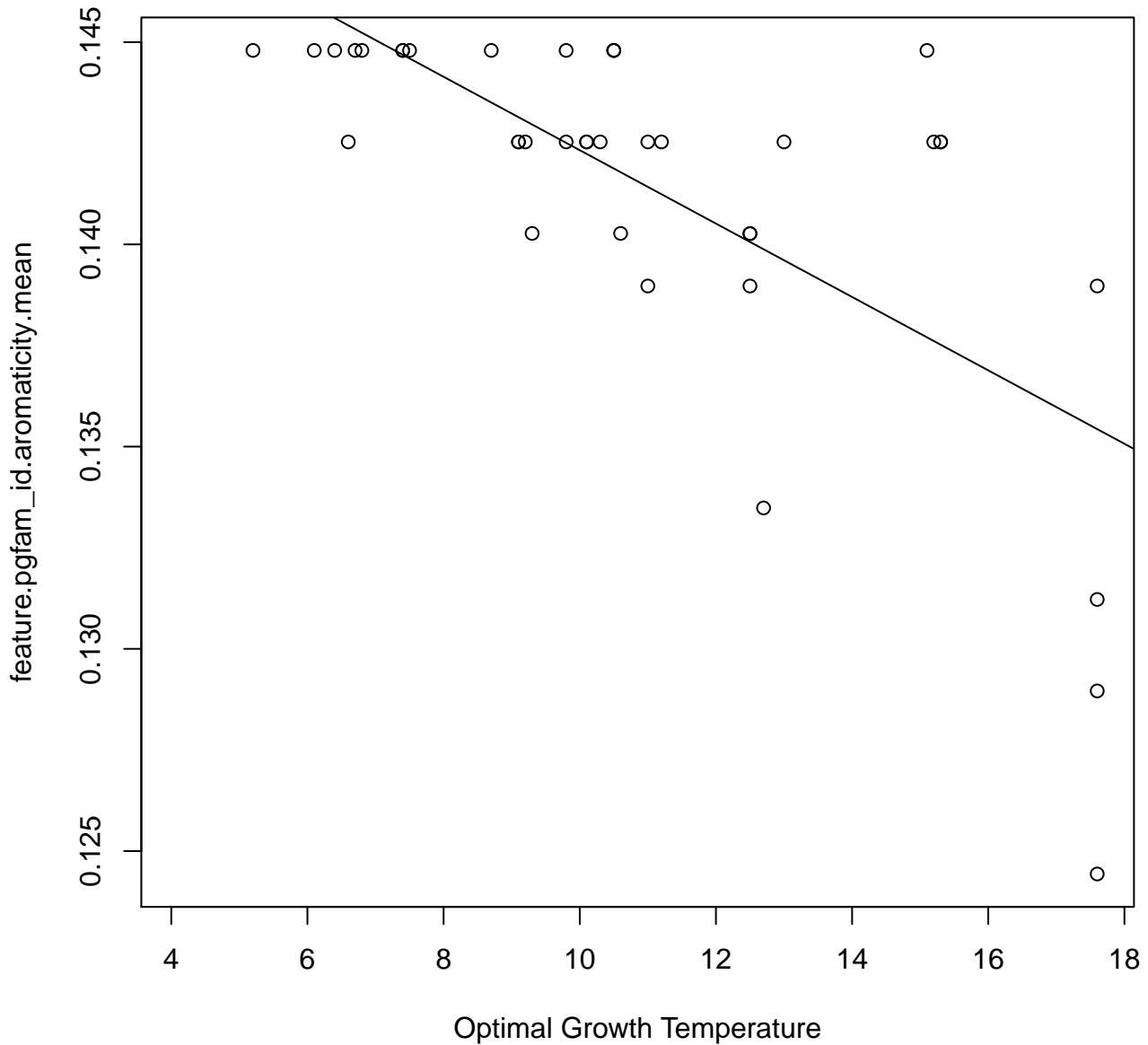
hypothetical protein



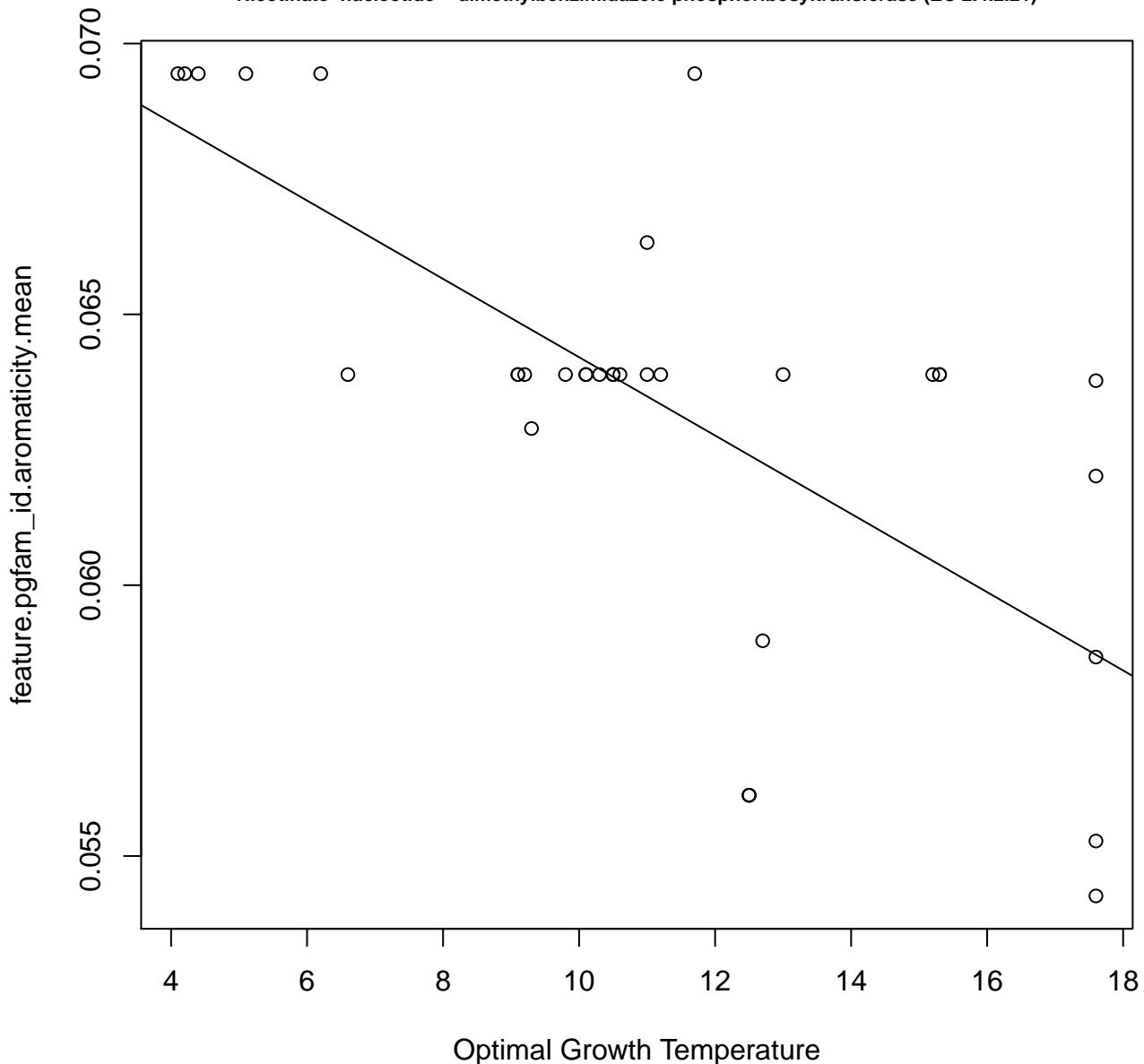
feature.pgfam_id.aromaticity.mean
PGF_04477253
Phosphoserine aminotransferase (EC 2.6.1.52)



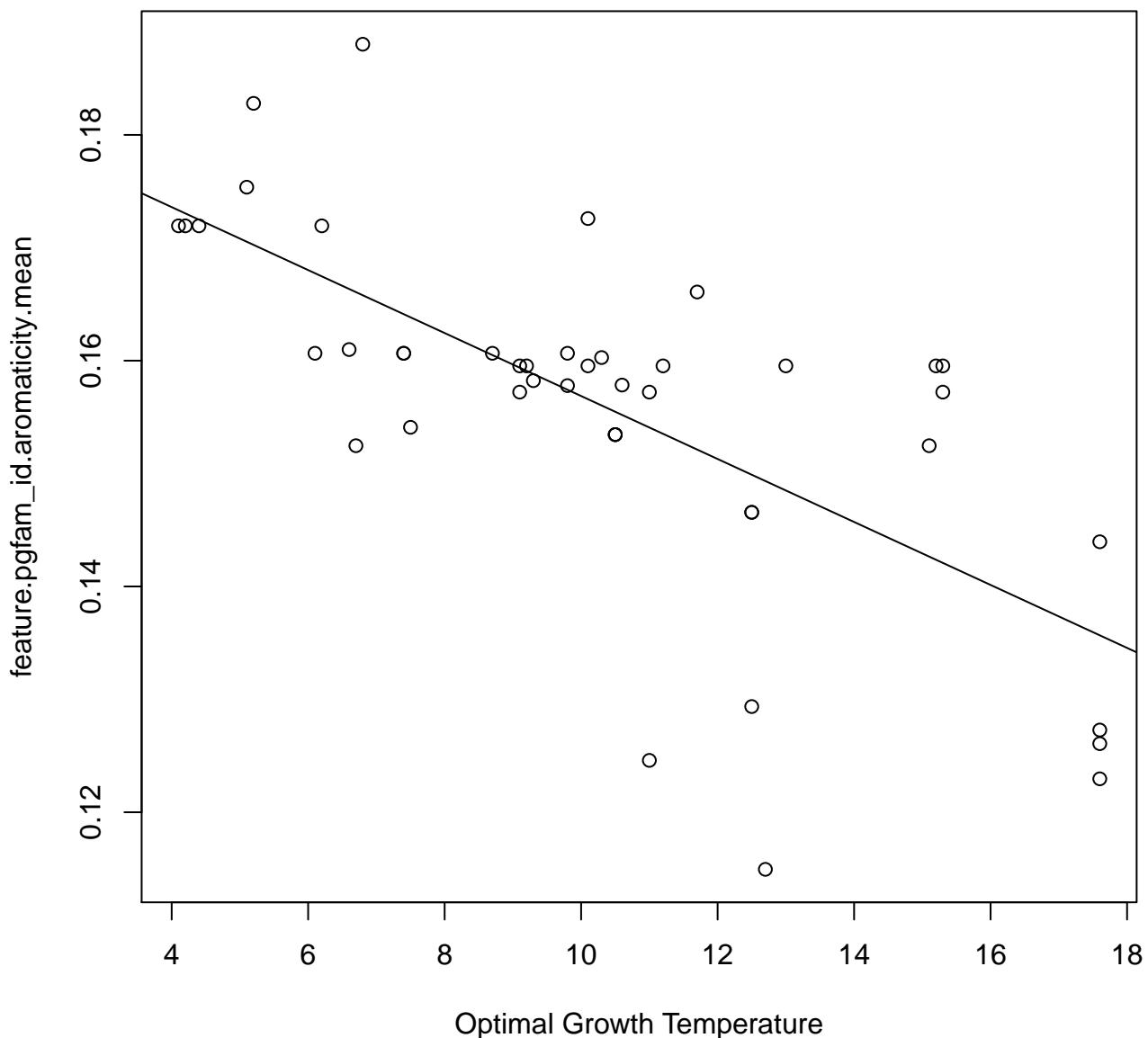
feature.pgfam_id.aromaticity.mean
PGF_00035718
Predicted beta-glucoside transporter, GPH family



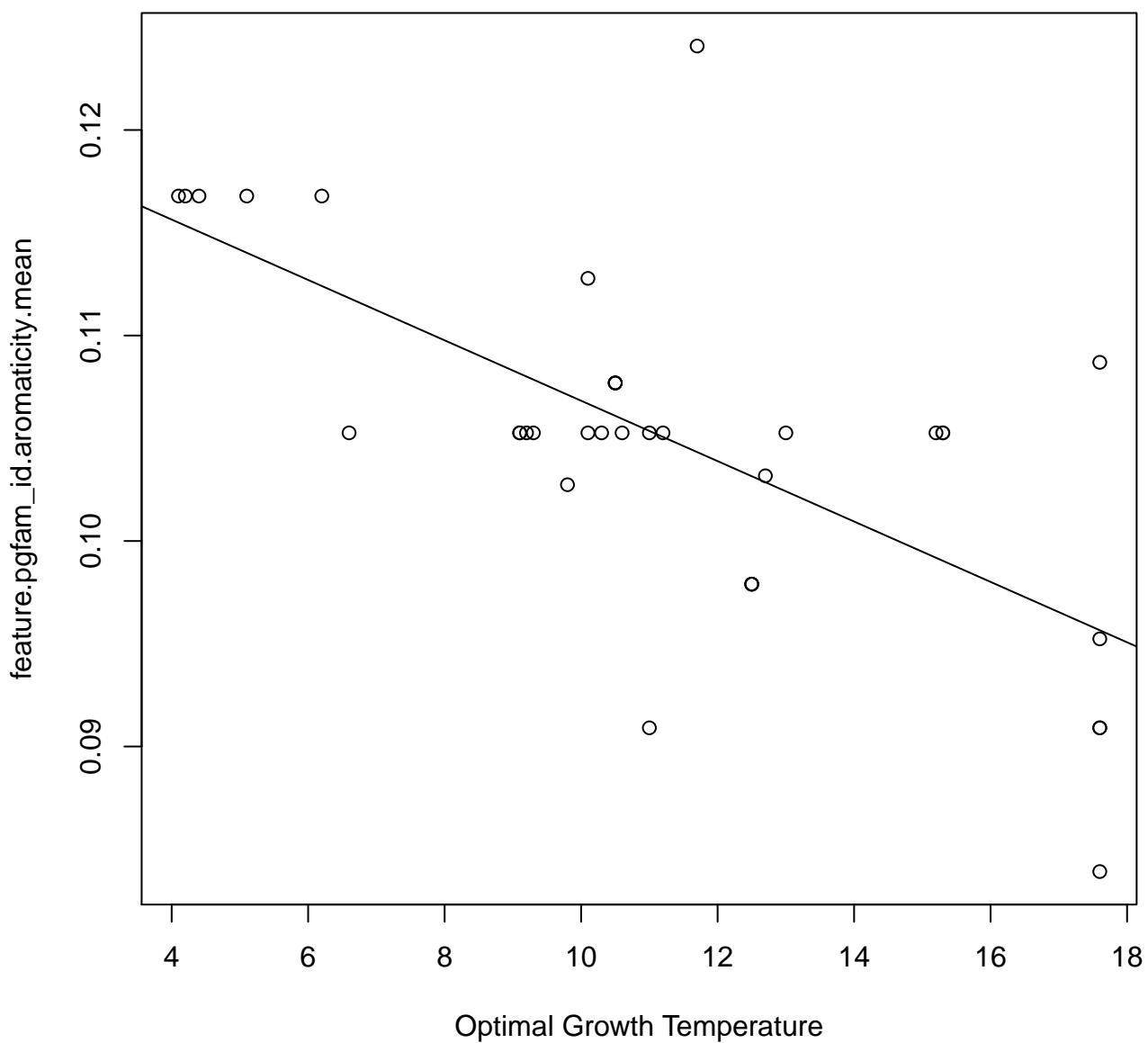
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PGF_00025623
Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)



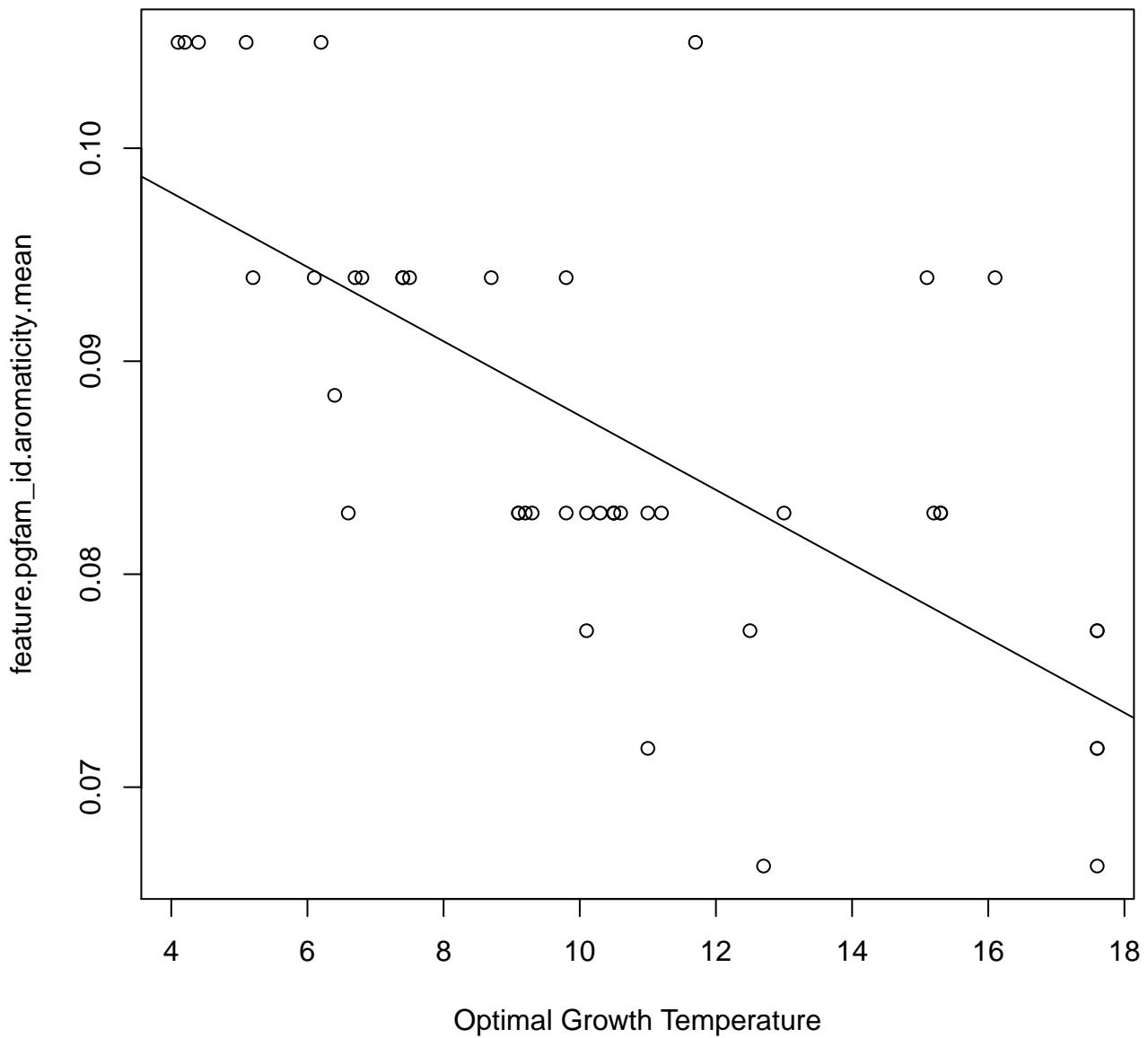
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PGF_01336427
hypothetical protein



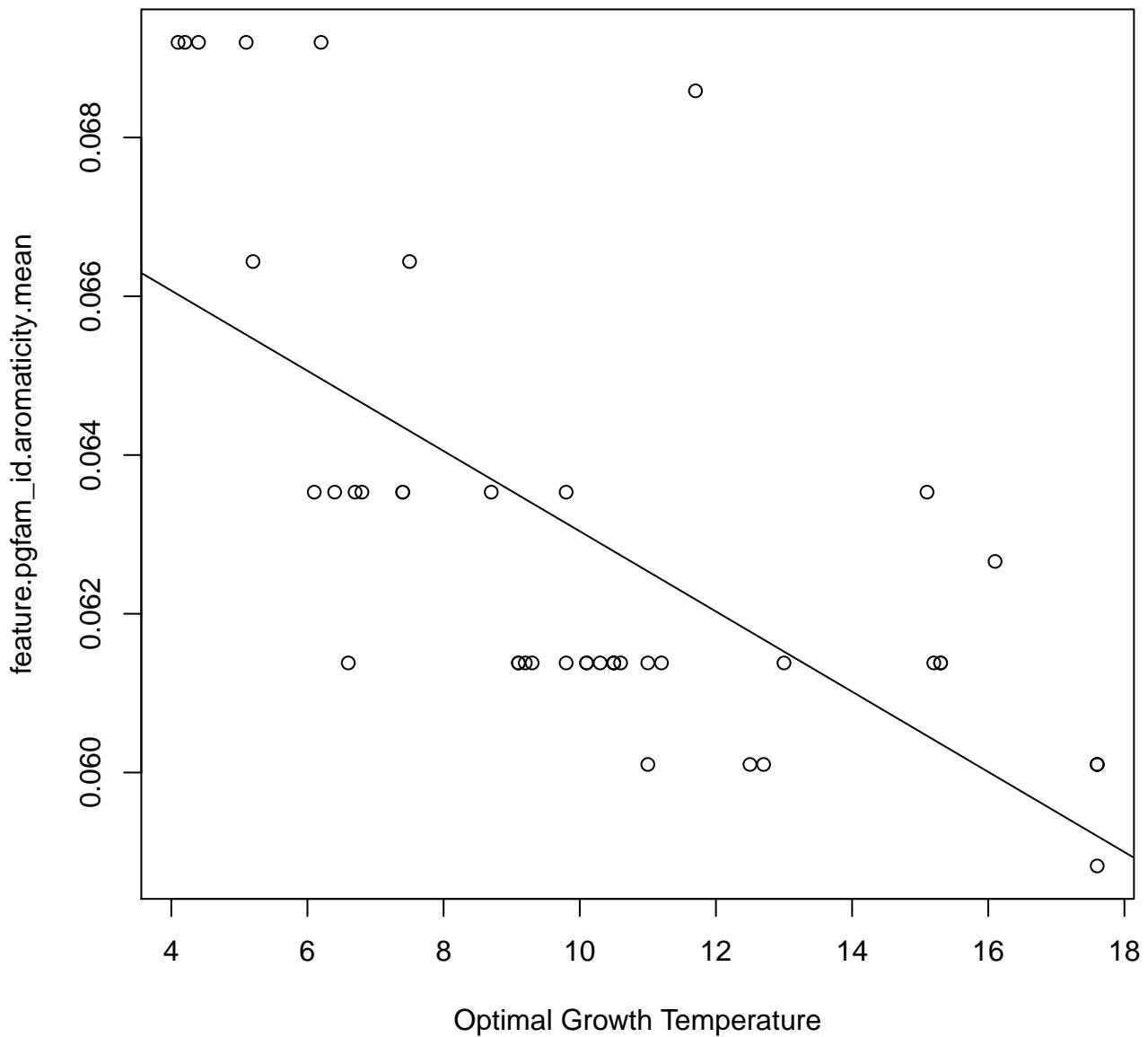
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PGF_01336430
hypothetical protein



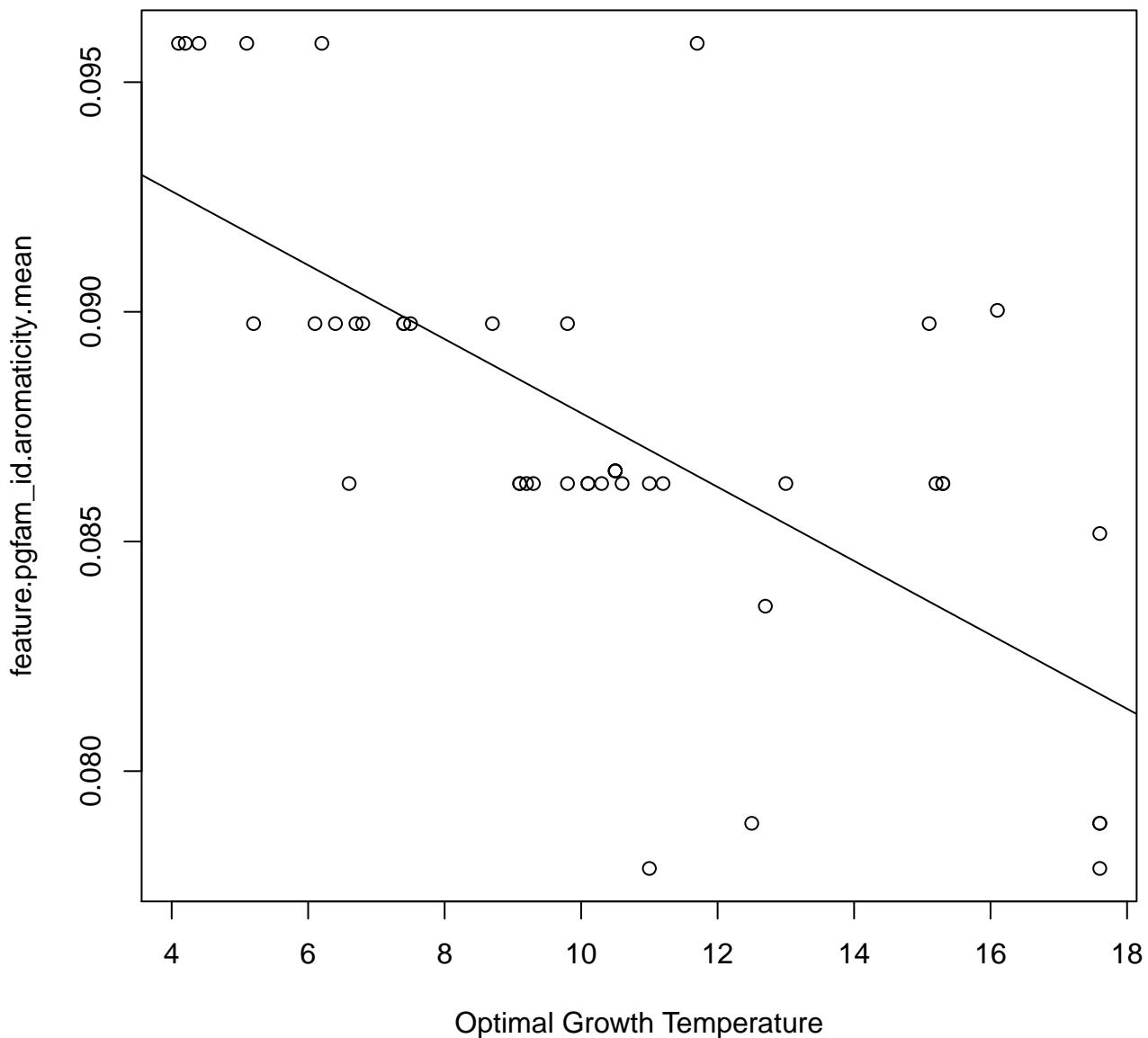
feature.pgfam_id.aromaticity.mean
PGF_06894101
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)



feature.pgfam_id.aromaticity.mean
PGF_04438983
ATP-dependent protease La (EC 3.4.21.53) Type I



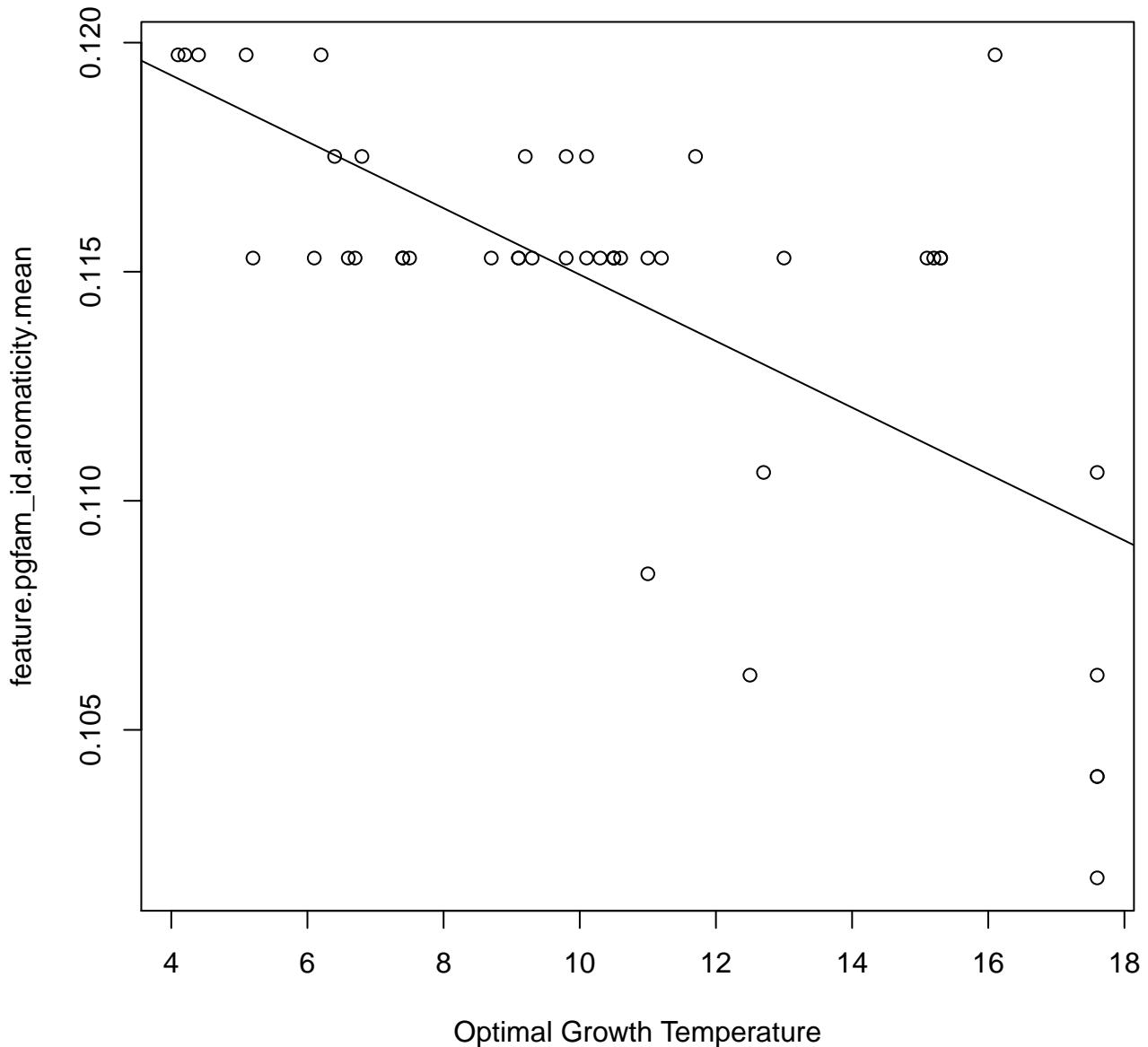
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D-alanine--D-alanine ligase (EC 6.3.2.4)



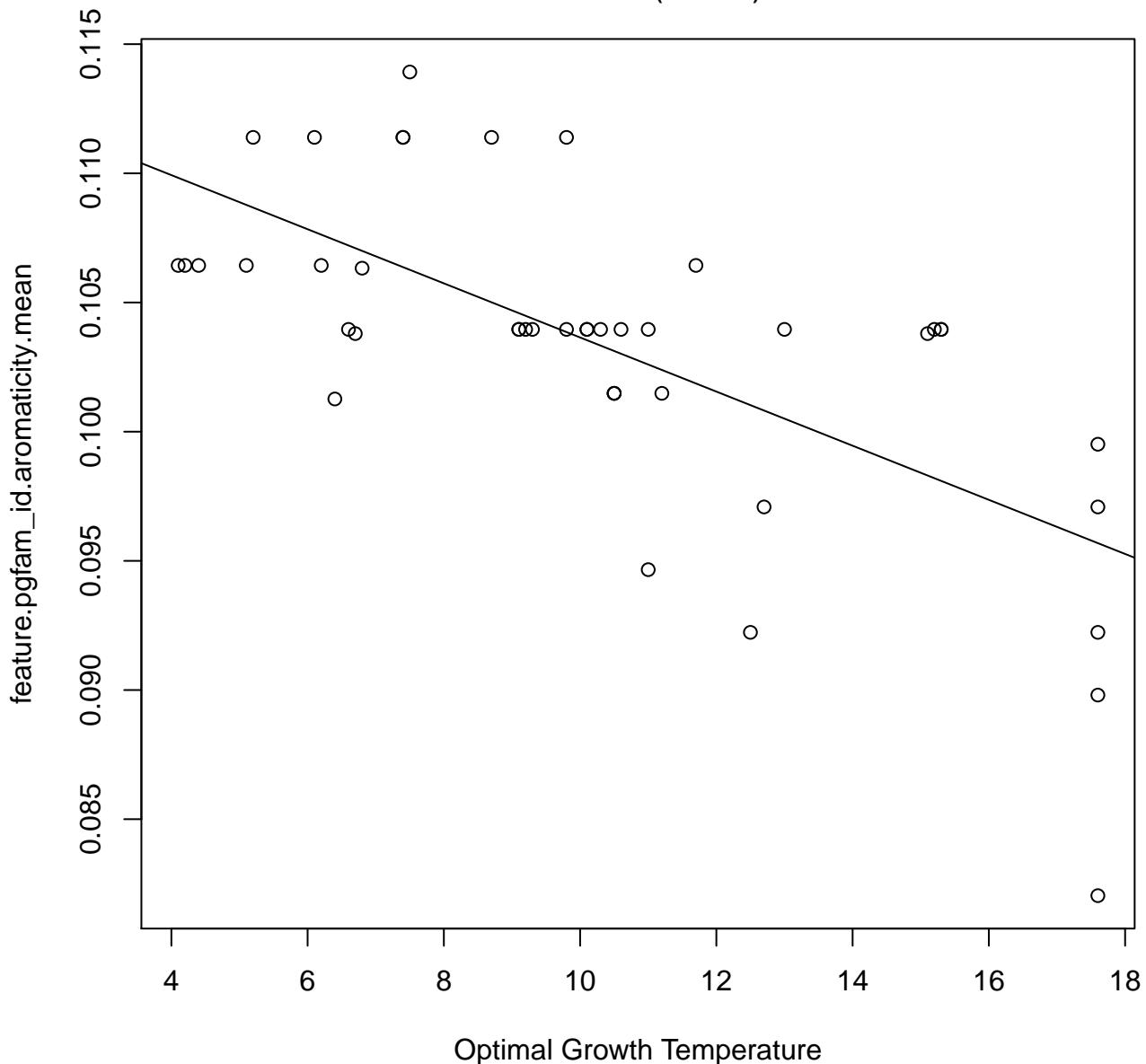
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PGF_03752718

Intramembrane protease RasP/YIuC, implicated in cell division based on FtsL cleavage



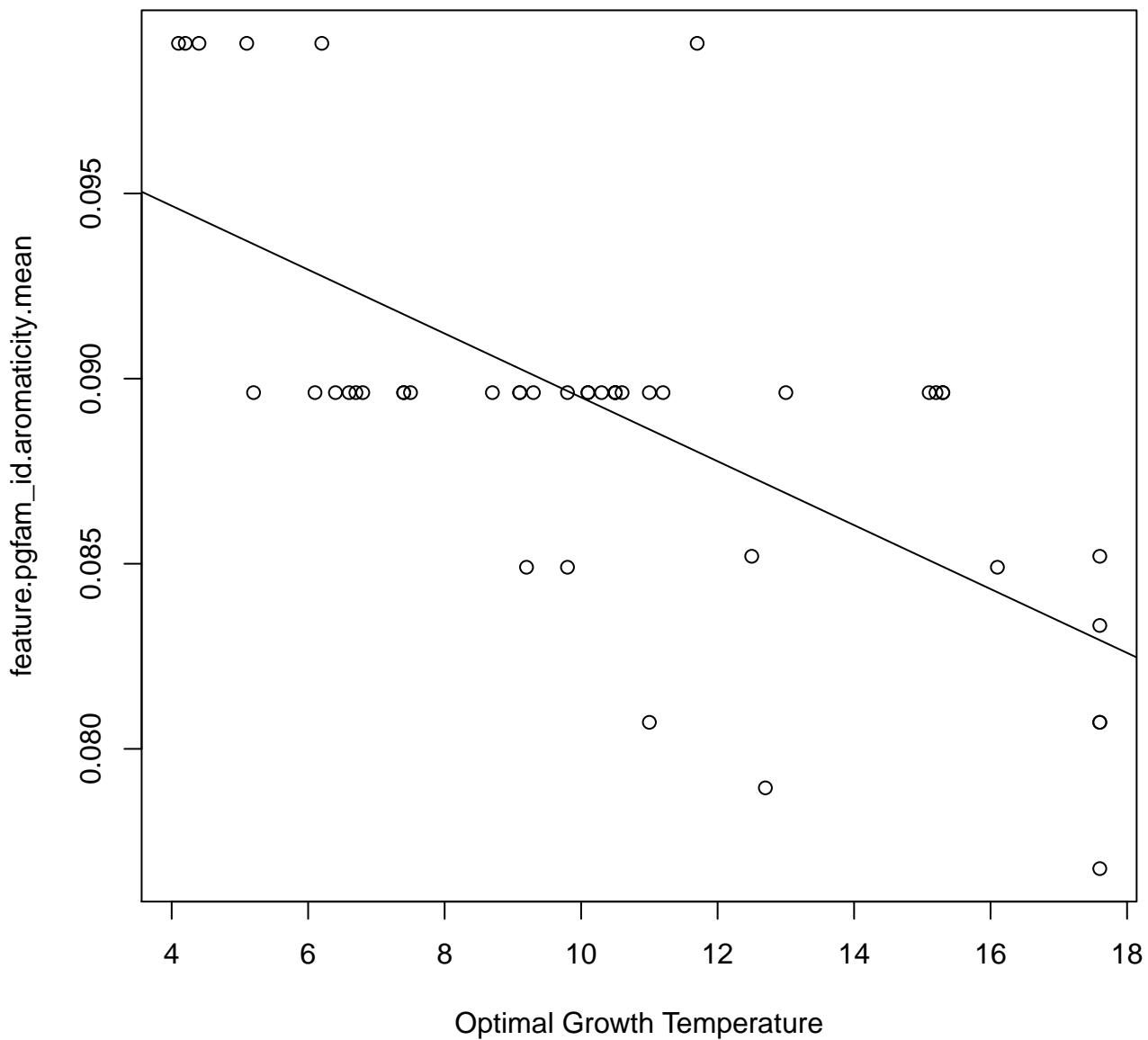
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Acetate kinase (EC 2.7.2.1)



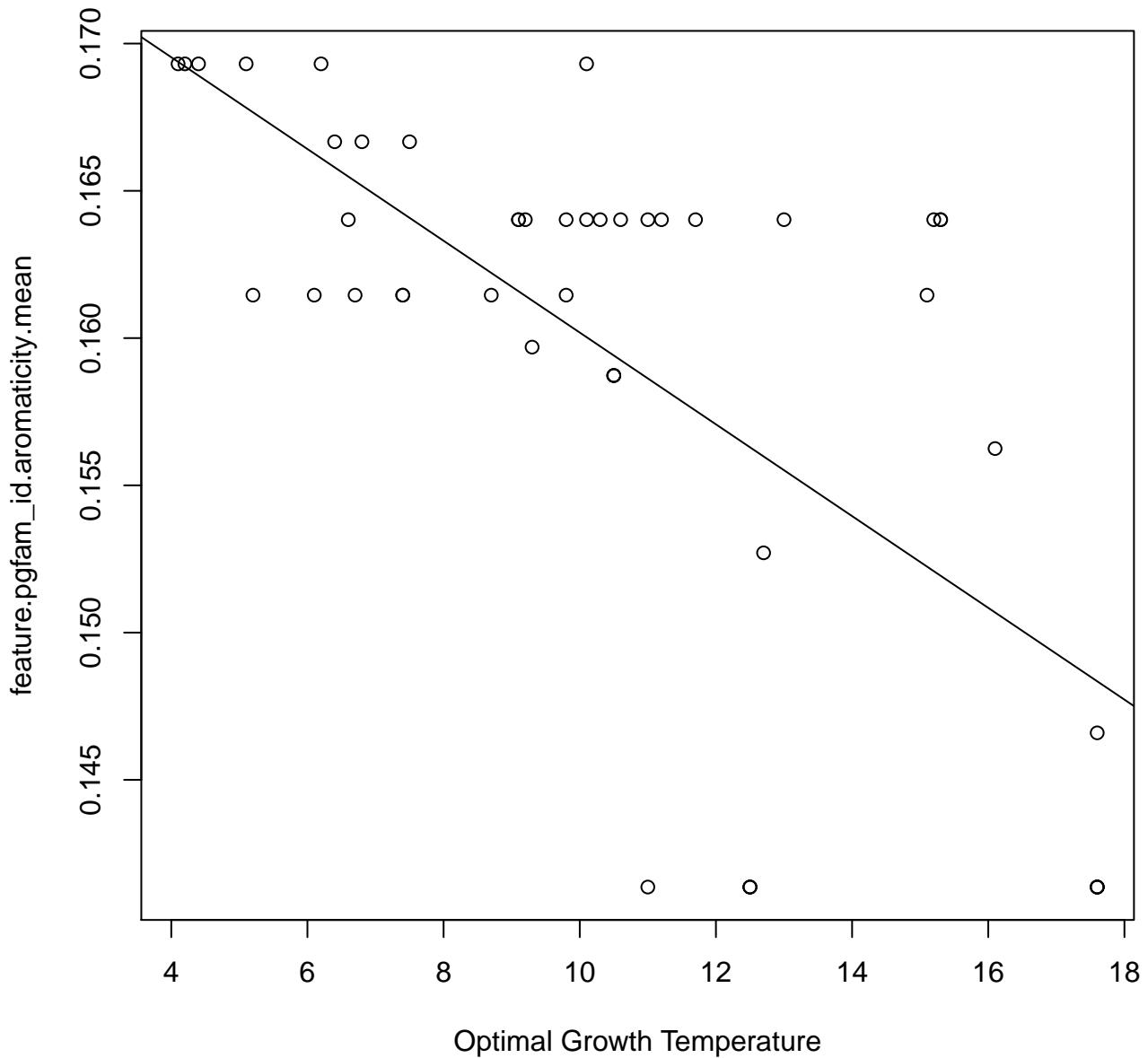
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PGF 07357908

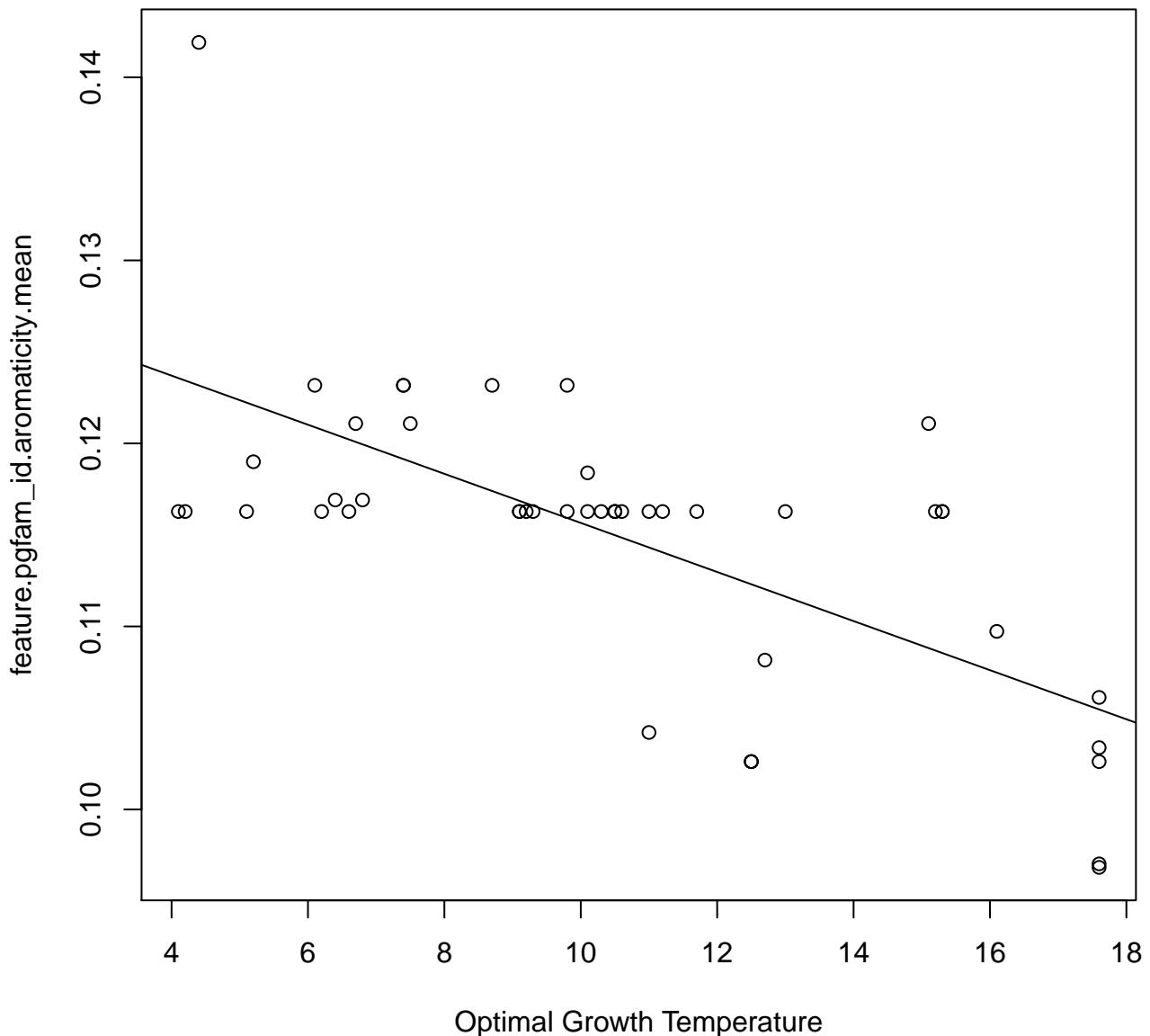
UPF0070 protein YfgM



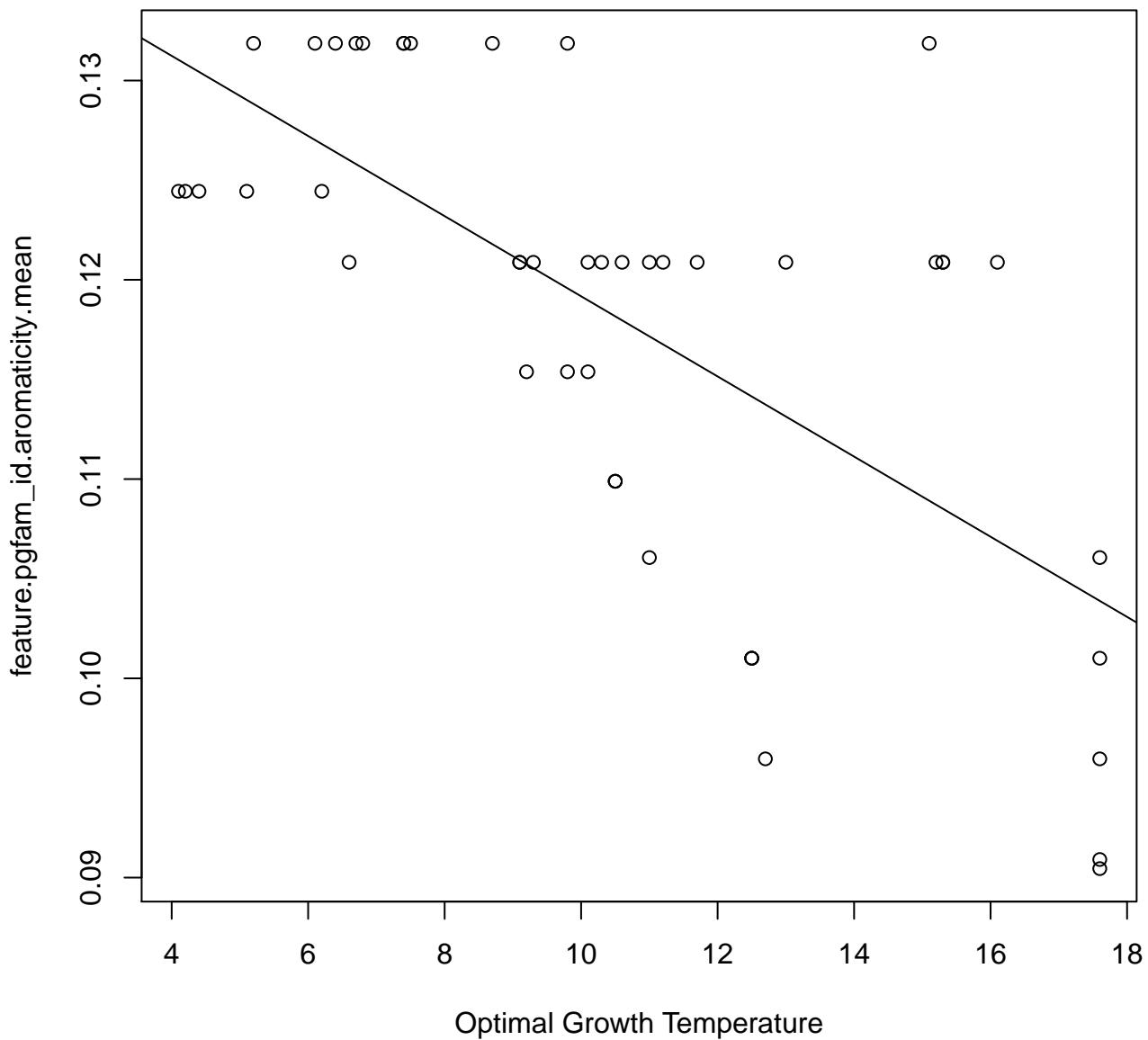
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PGF_02489591
Uncharacterized Nudix hydrolase NudL



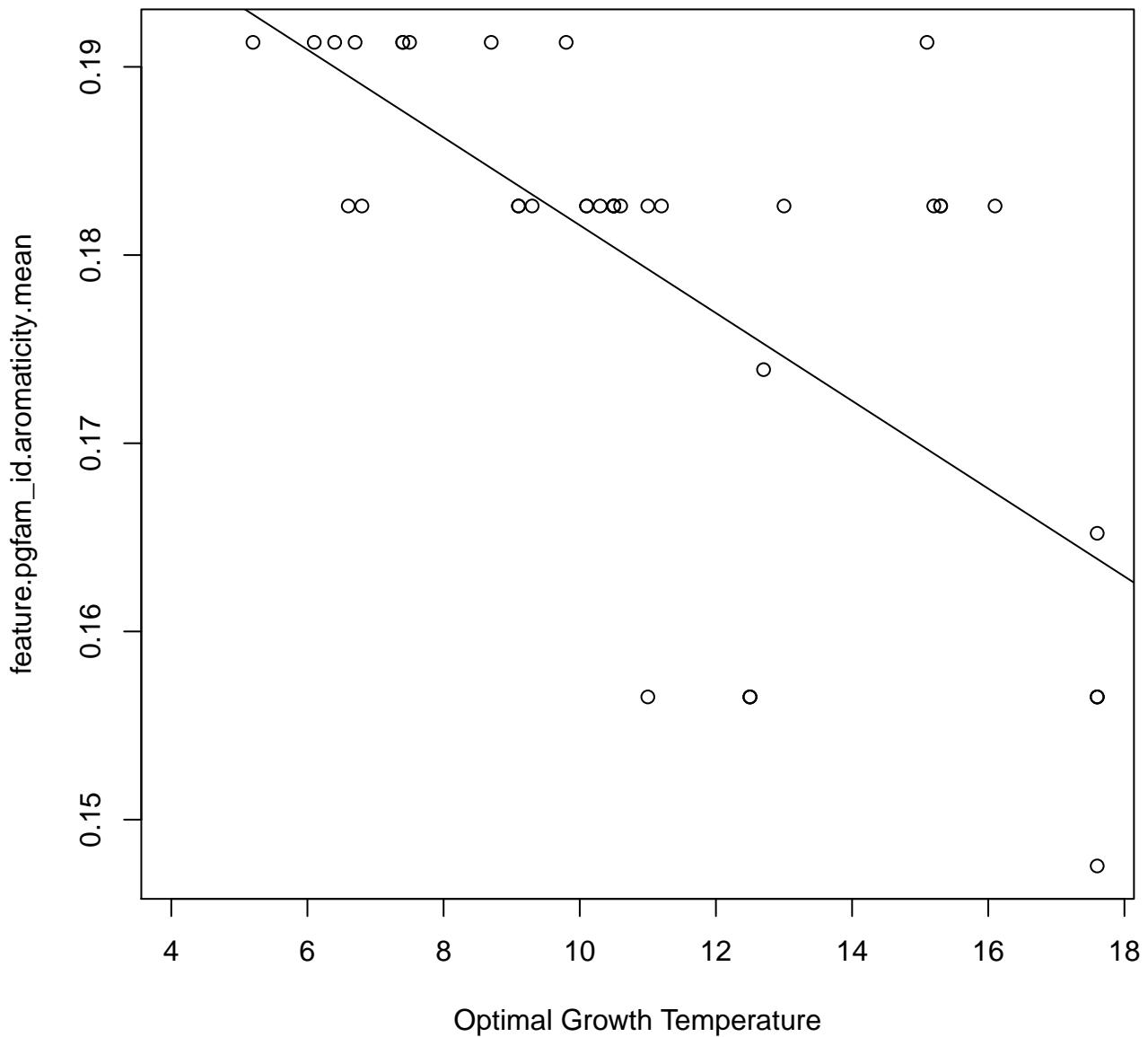
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PGF_01174807
Para-aminobenzoate synthase, aminase component (EC 2.6.1.85)



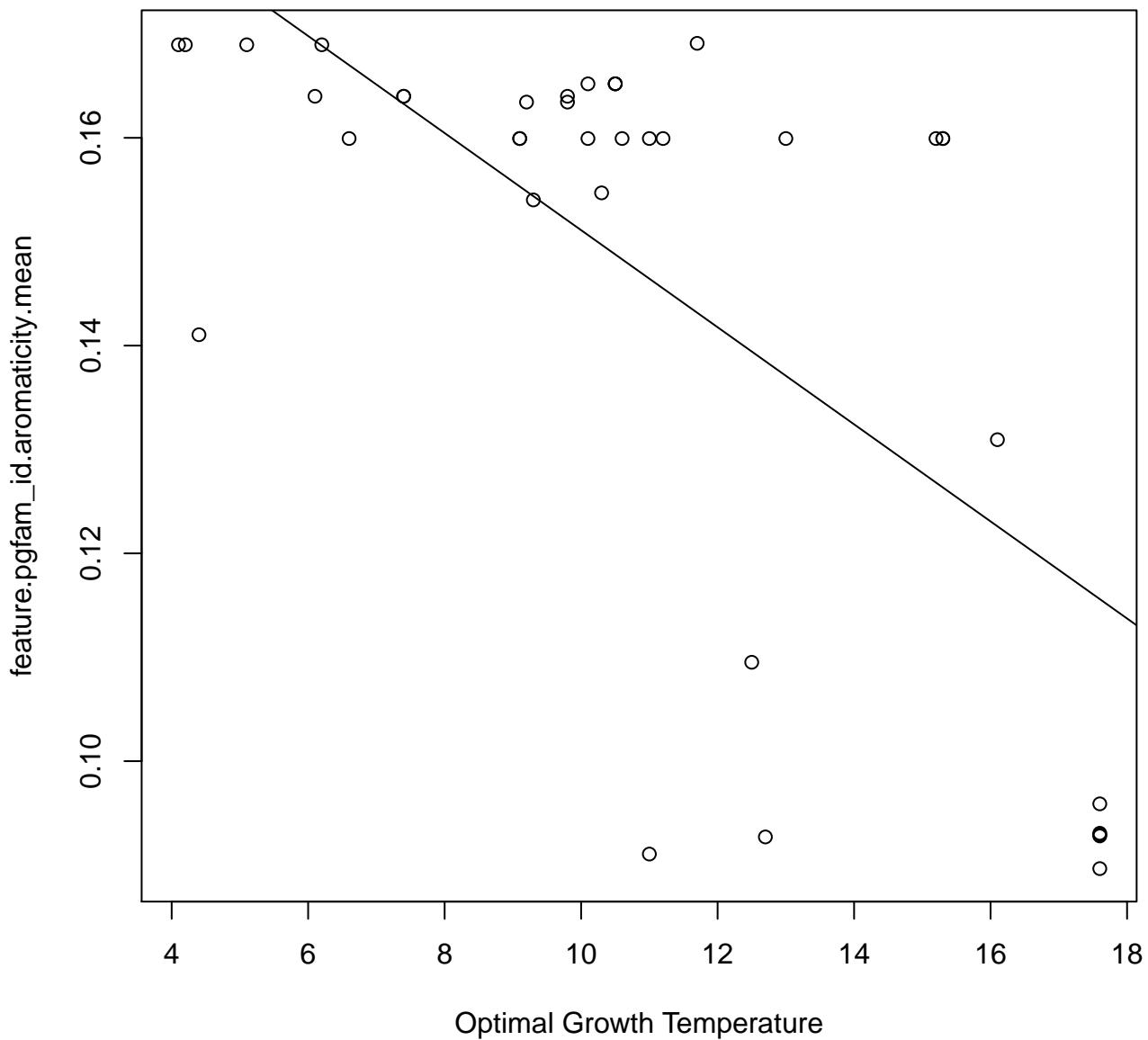
feature.pgfam_id.aromaticity.mean
PGF_00039503
Putative NAD(P)H nitroreductase YdjA



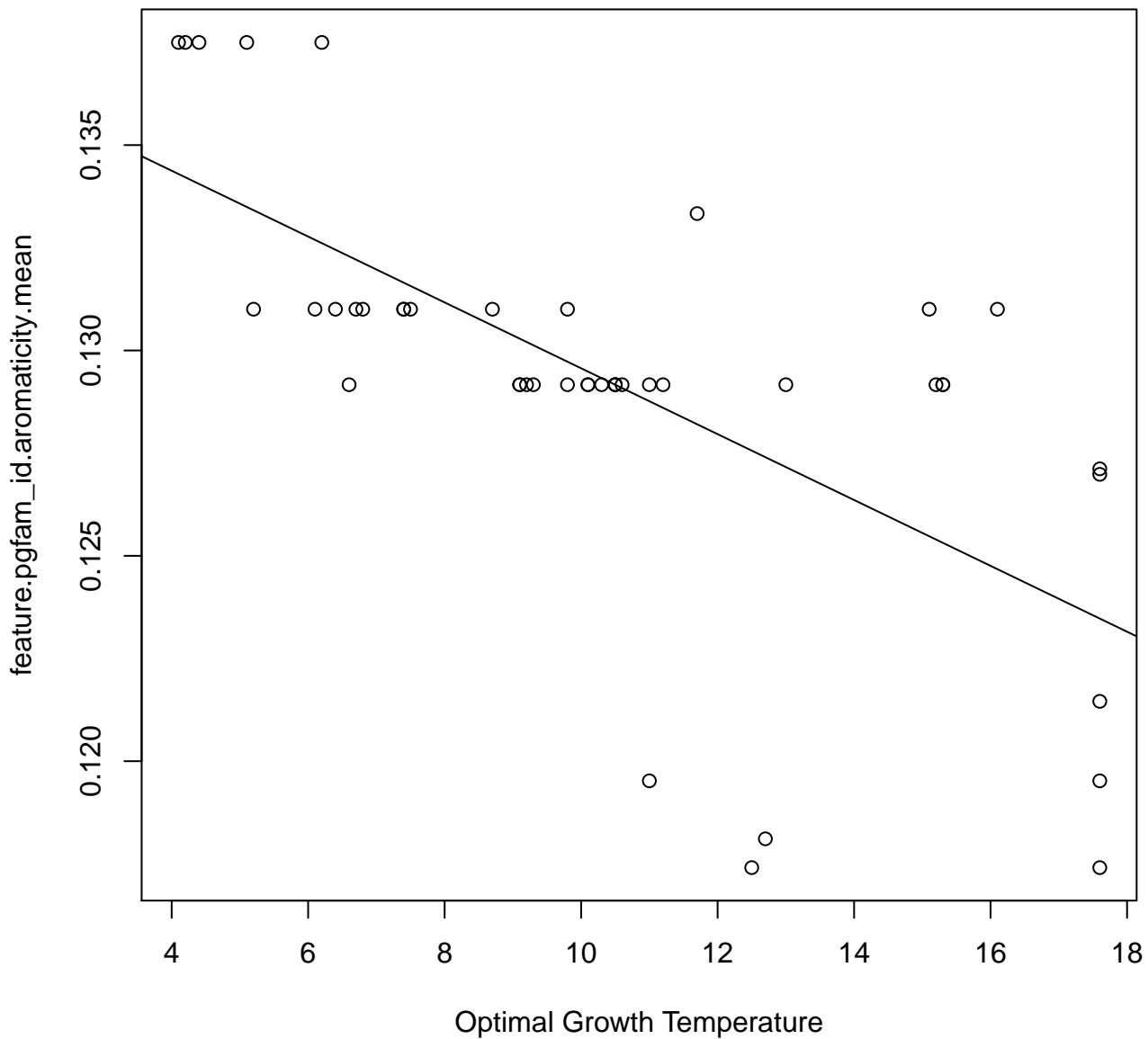
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PGF_00054476
Succinate dehydrogenase hydrophobic membrane anchor protein



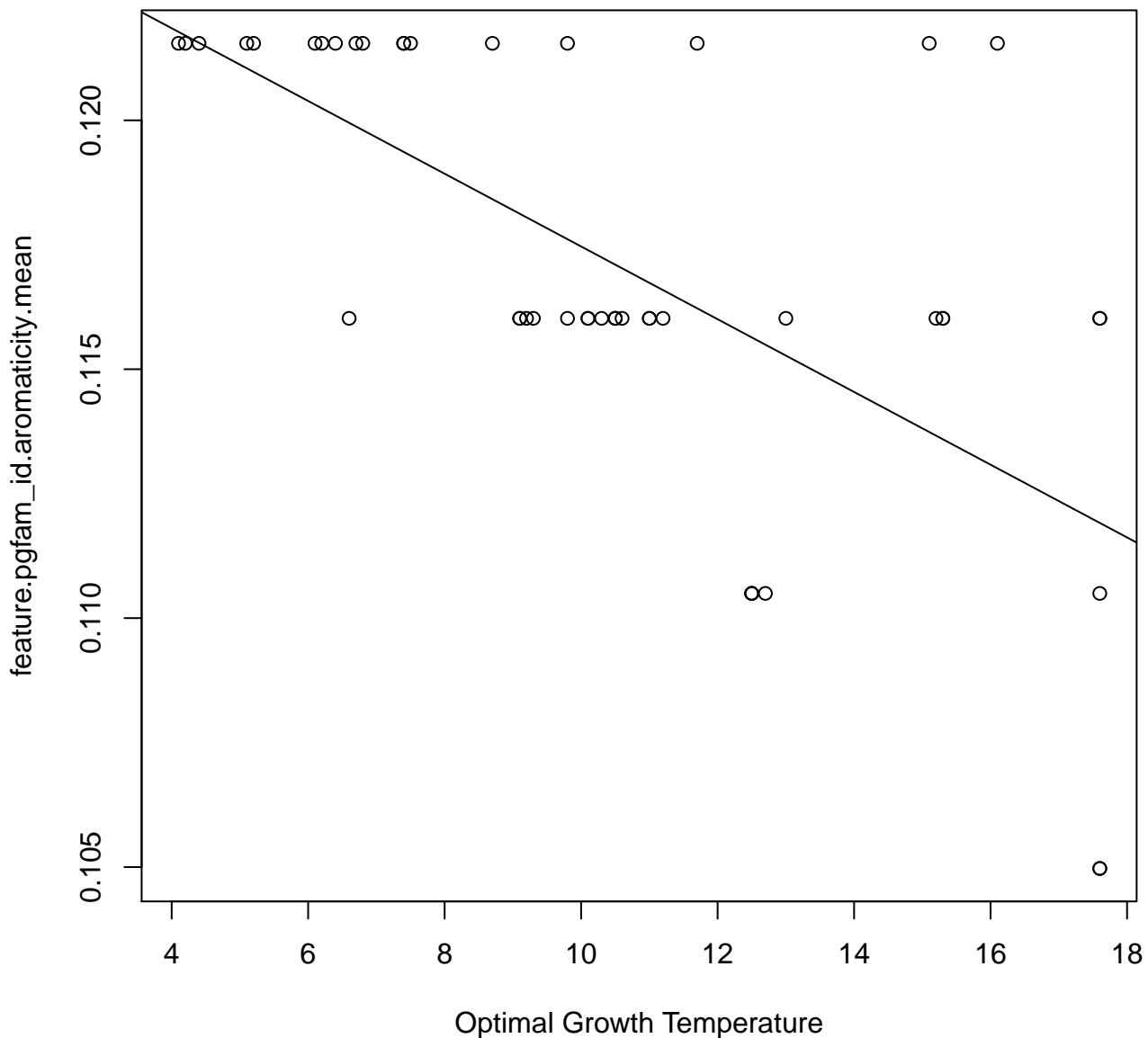
feature.pgfam_id.aromaticity.mean
PGF_07015776
Small-conductance mechanosensitive channel



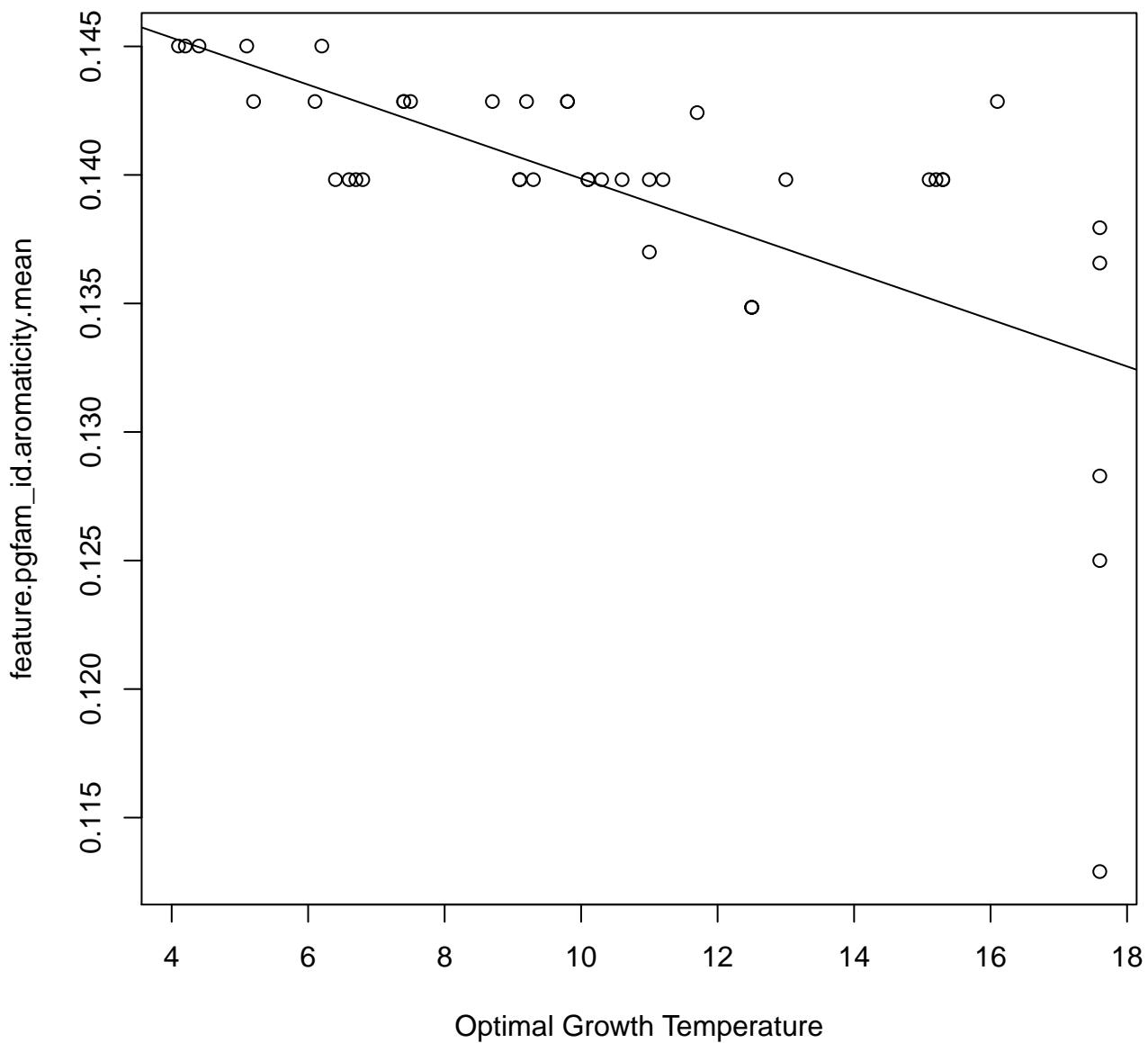
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PGF_01776806
predicted S-adenosylmethionine-dependent tRNA (guanine-N(7)-)methyltransferase



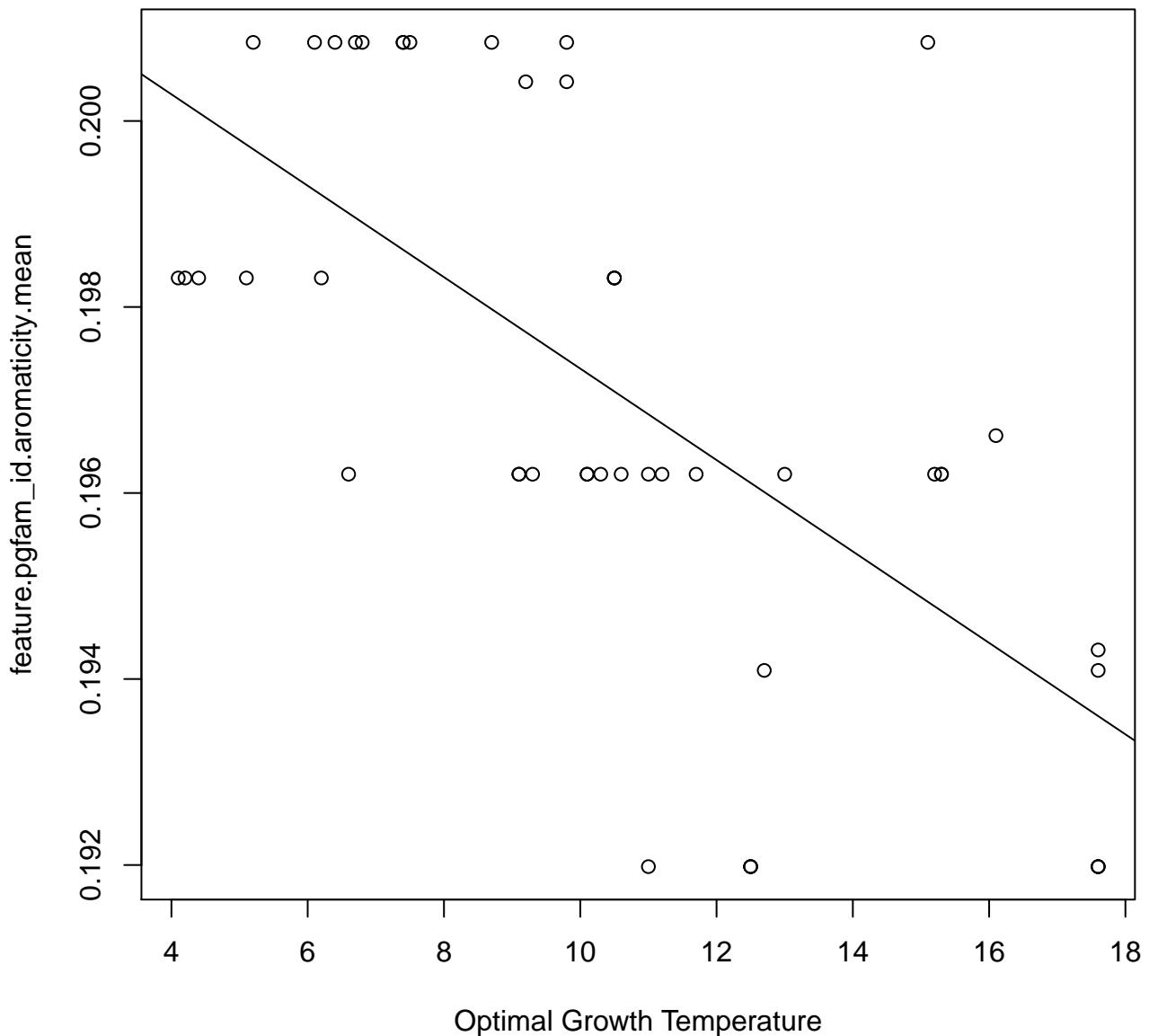
feature.pgfam_id.aromaticity.mean
PGF_00416576
3'-to-5' oligoribonuclease (orn)



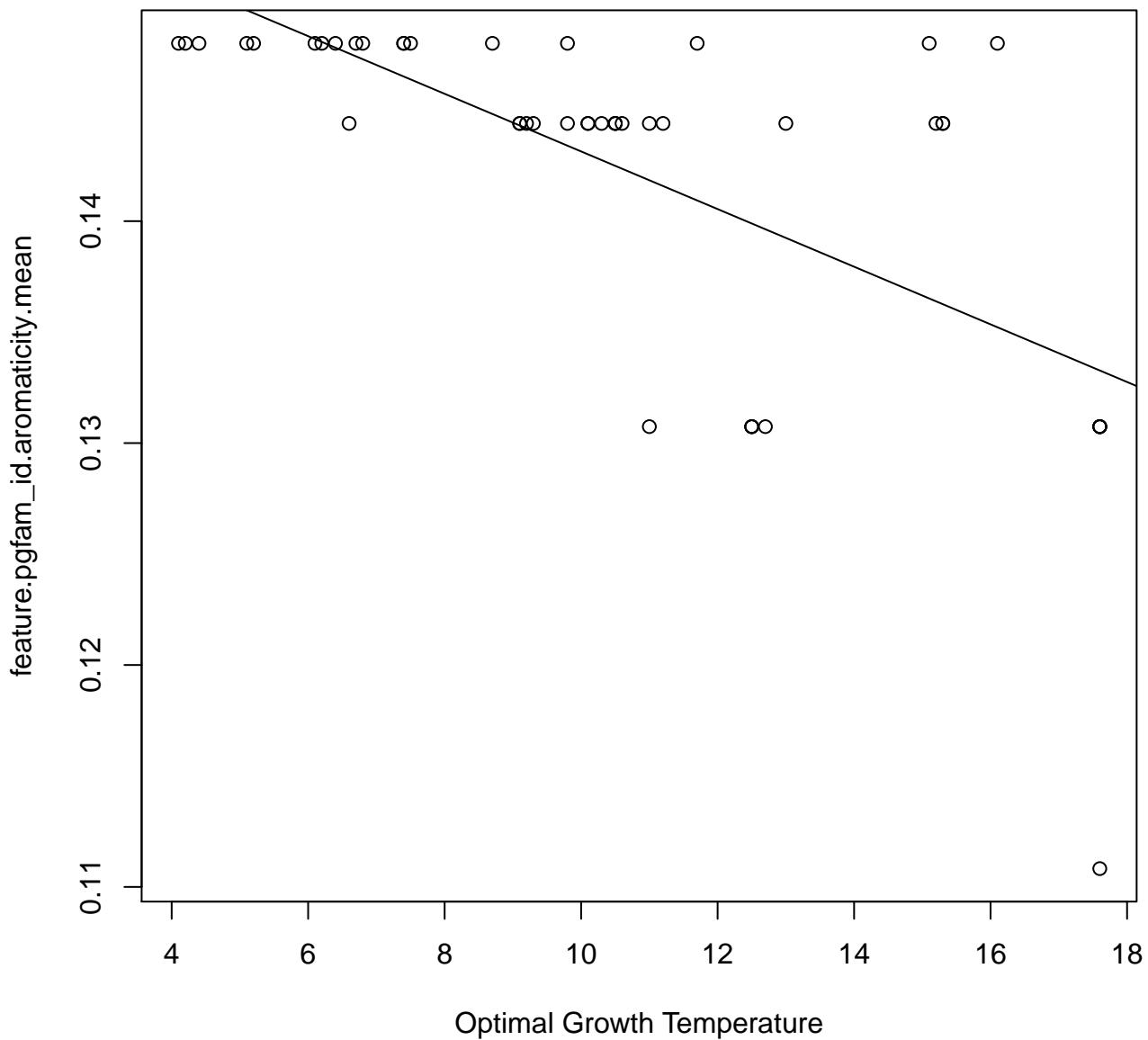
feature.pgfam_id.aromaticity.mean
PGF_03342342
Uncharacterized membrane protein, YraQ family



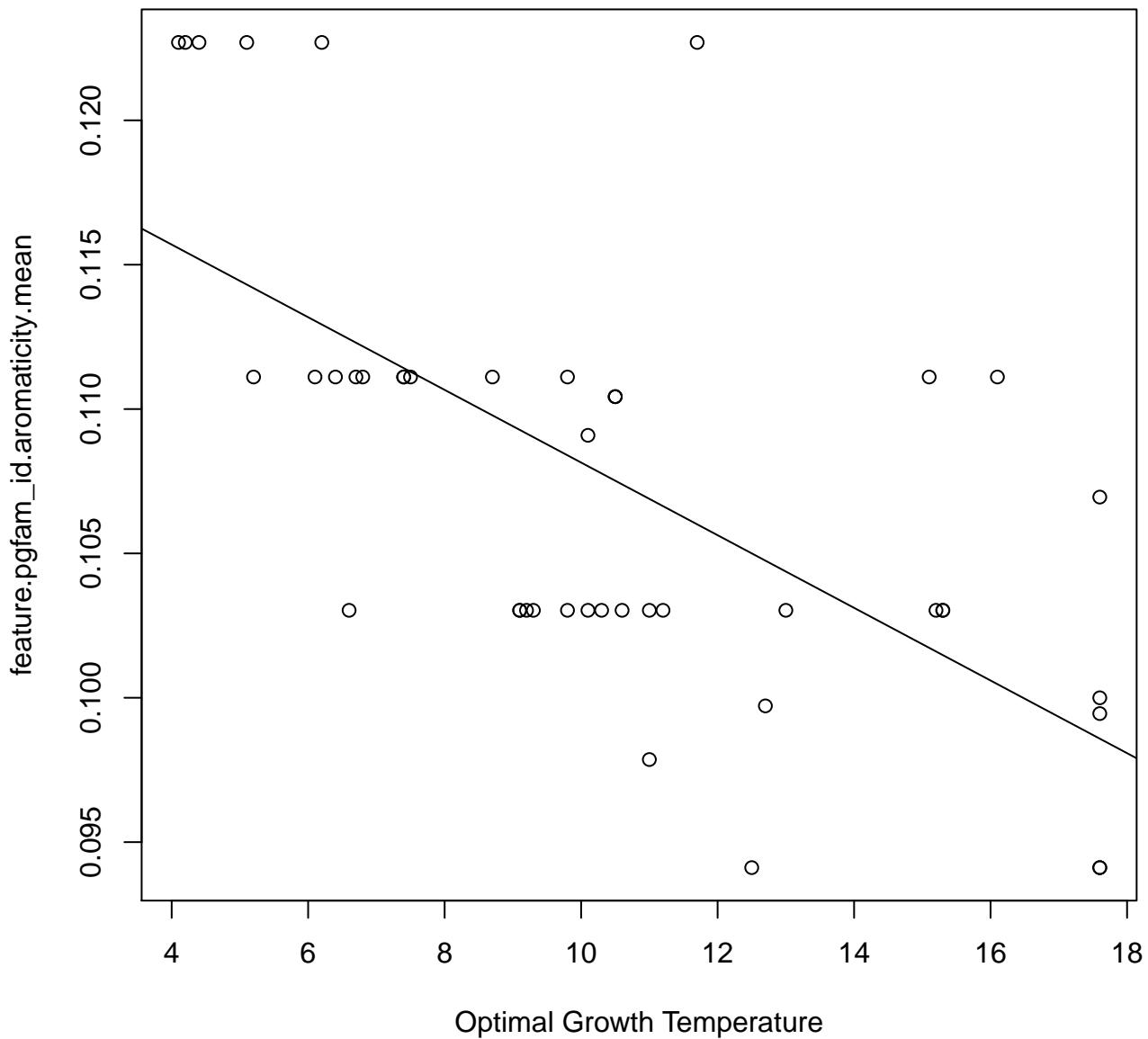
feature.pgfam_id.aromaticity.mean
PGF_00420358
Cytochrome c oxidase (cbb3-type) subunit CcoN (EC 1.9.3.1)



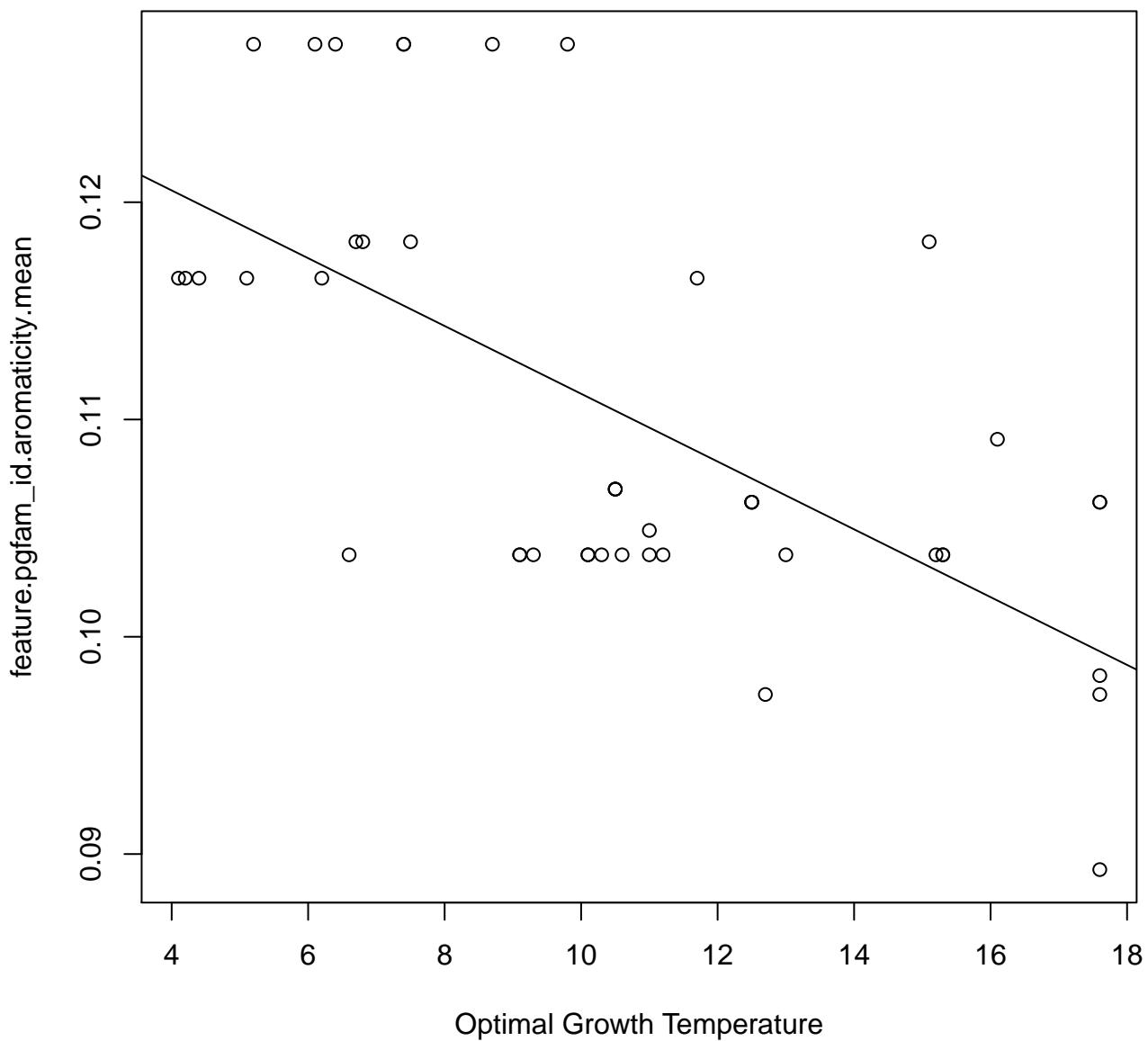
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PGF_00056897
Thymidylate synthase (EC 2.1.1.45)



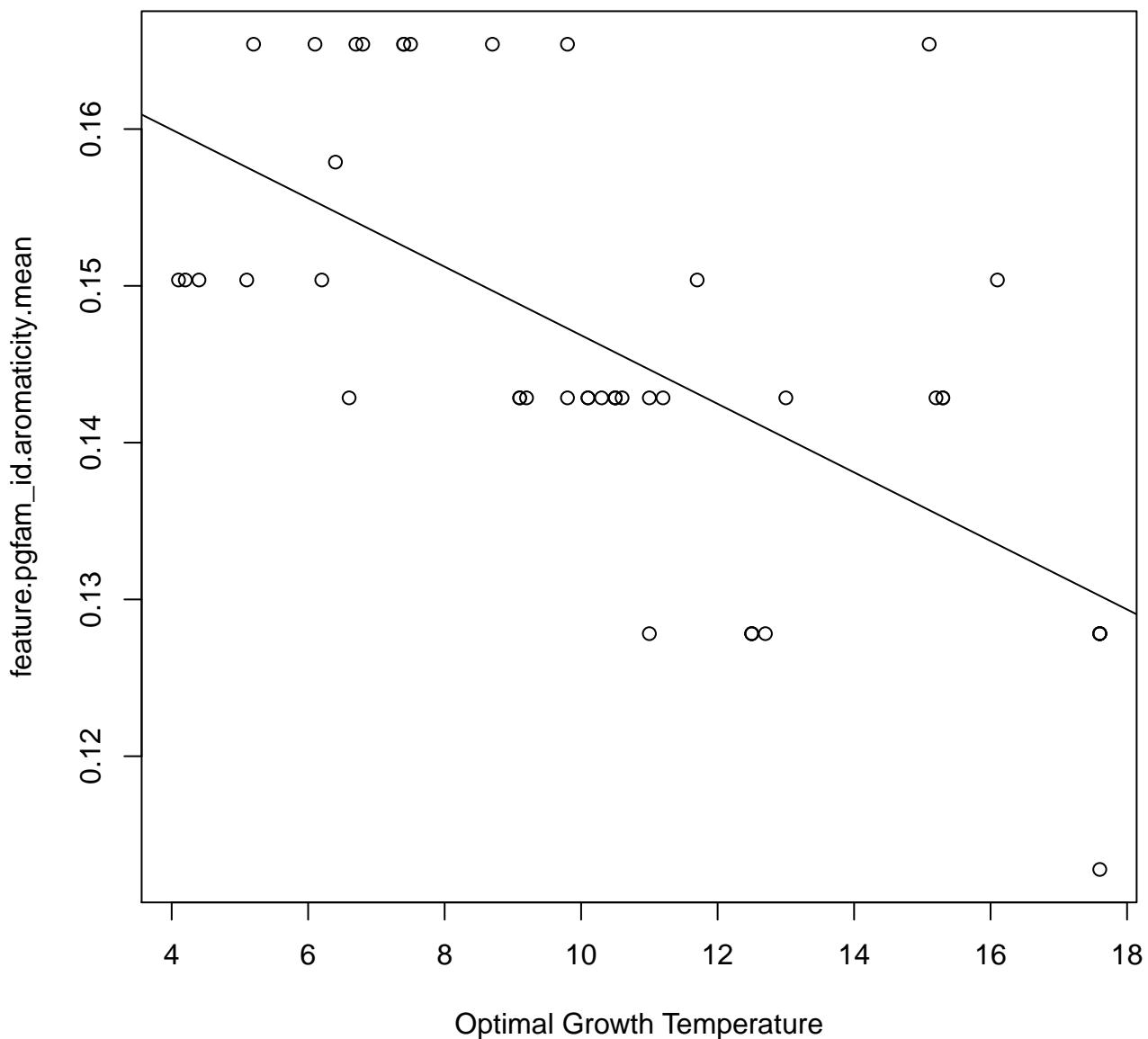
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Dihydrofolate reductase (EC 1.5.1.3)



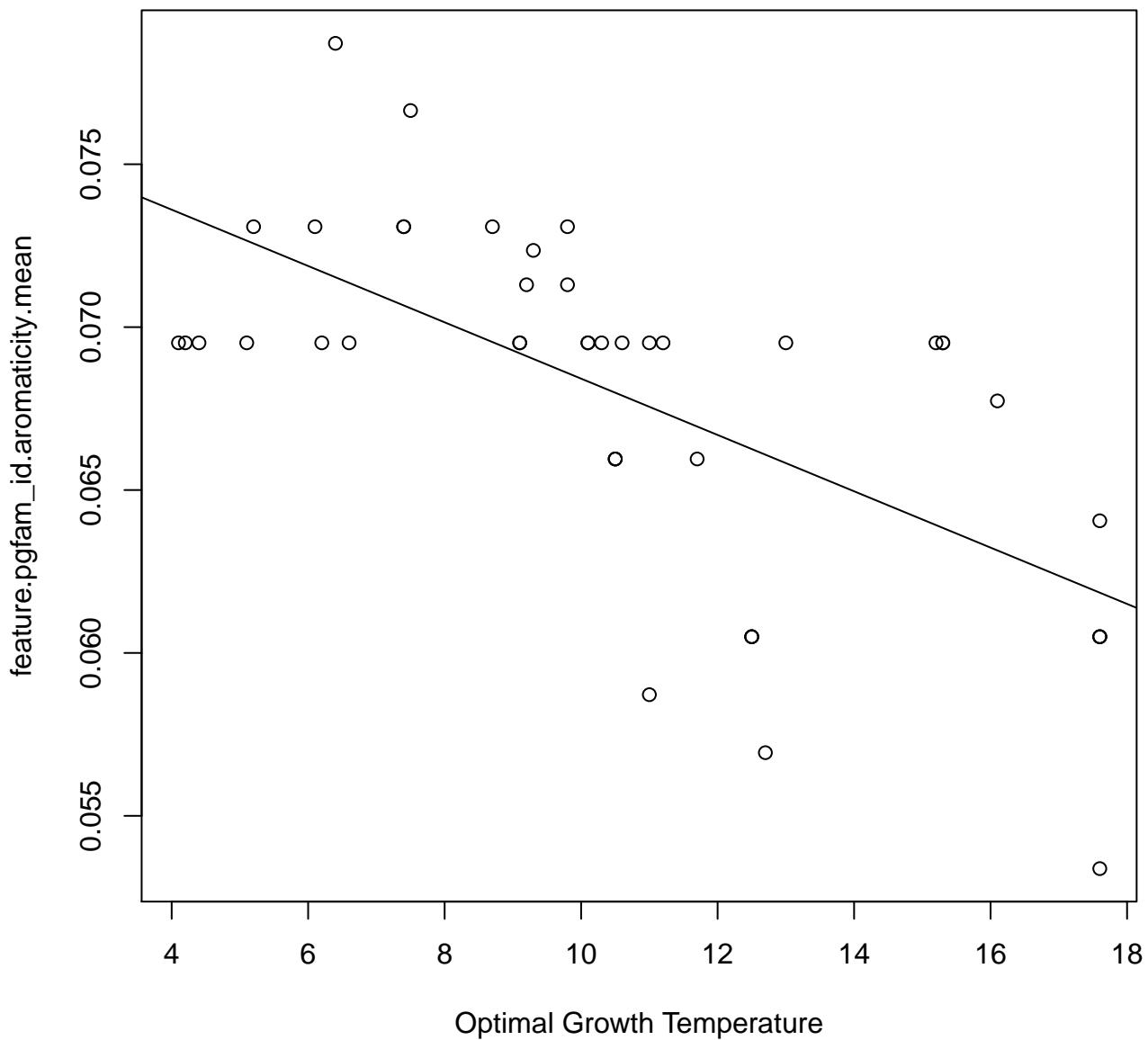
feature.pgfam_id.aromaticity.mean
PGF_01336507
hypothetical protein



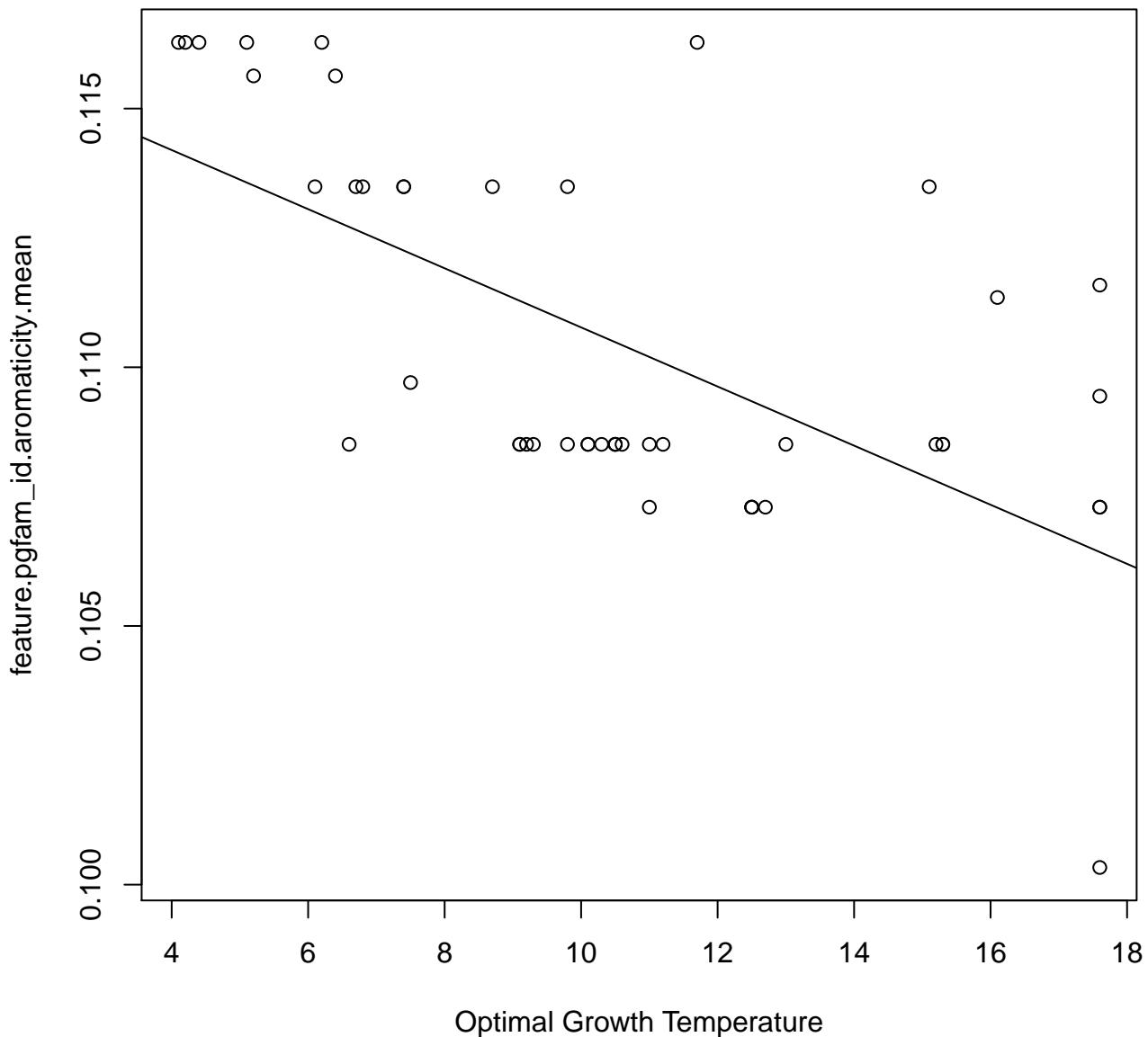
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PGF_06545170
Fluoride ion transporter CrcB



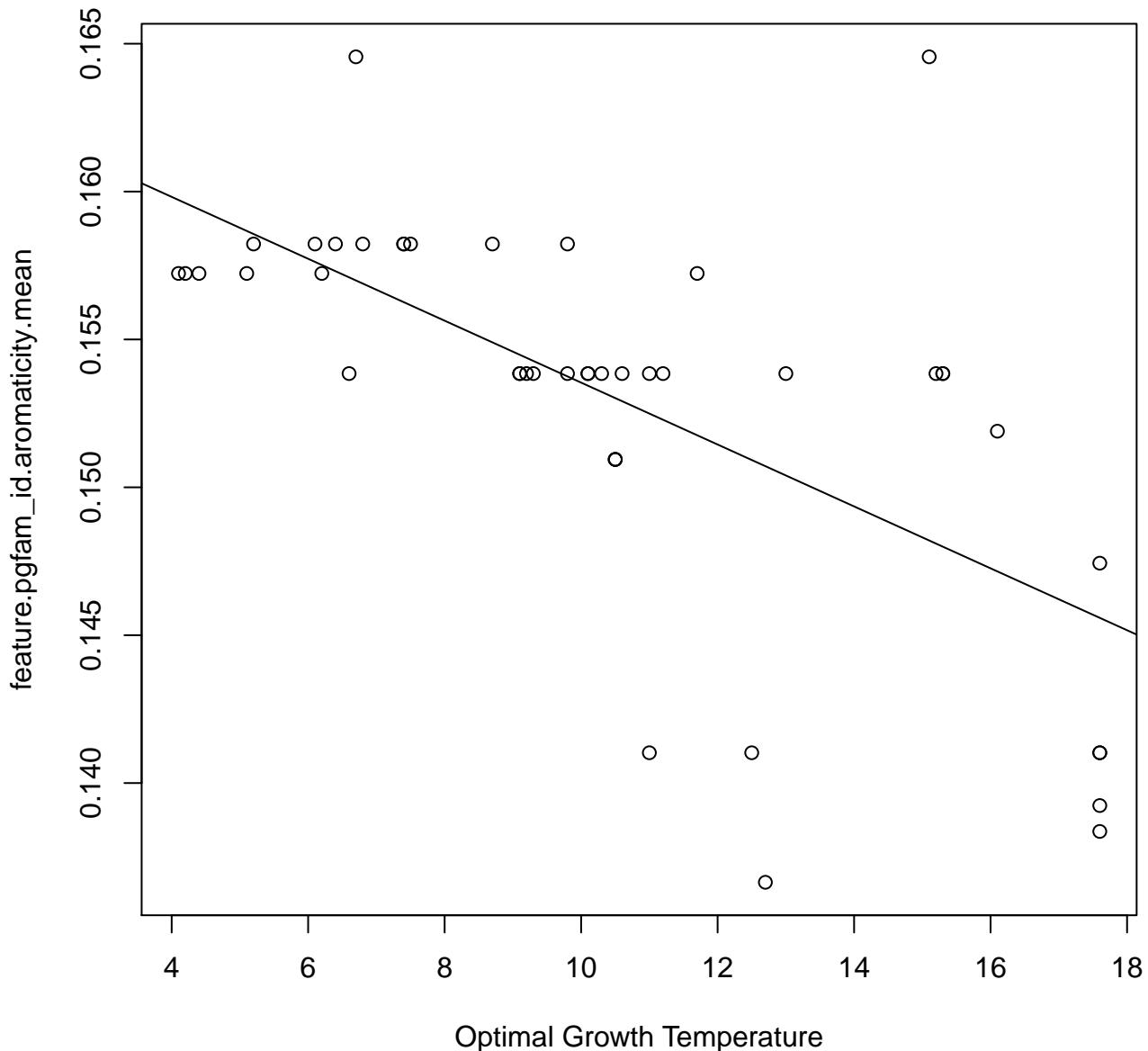
feature.pgfam_id.aromaticity.mean
PGF_01336311
Protein of unknown function DUF342



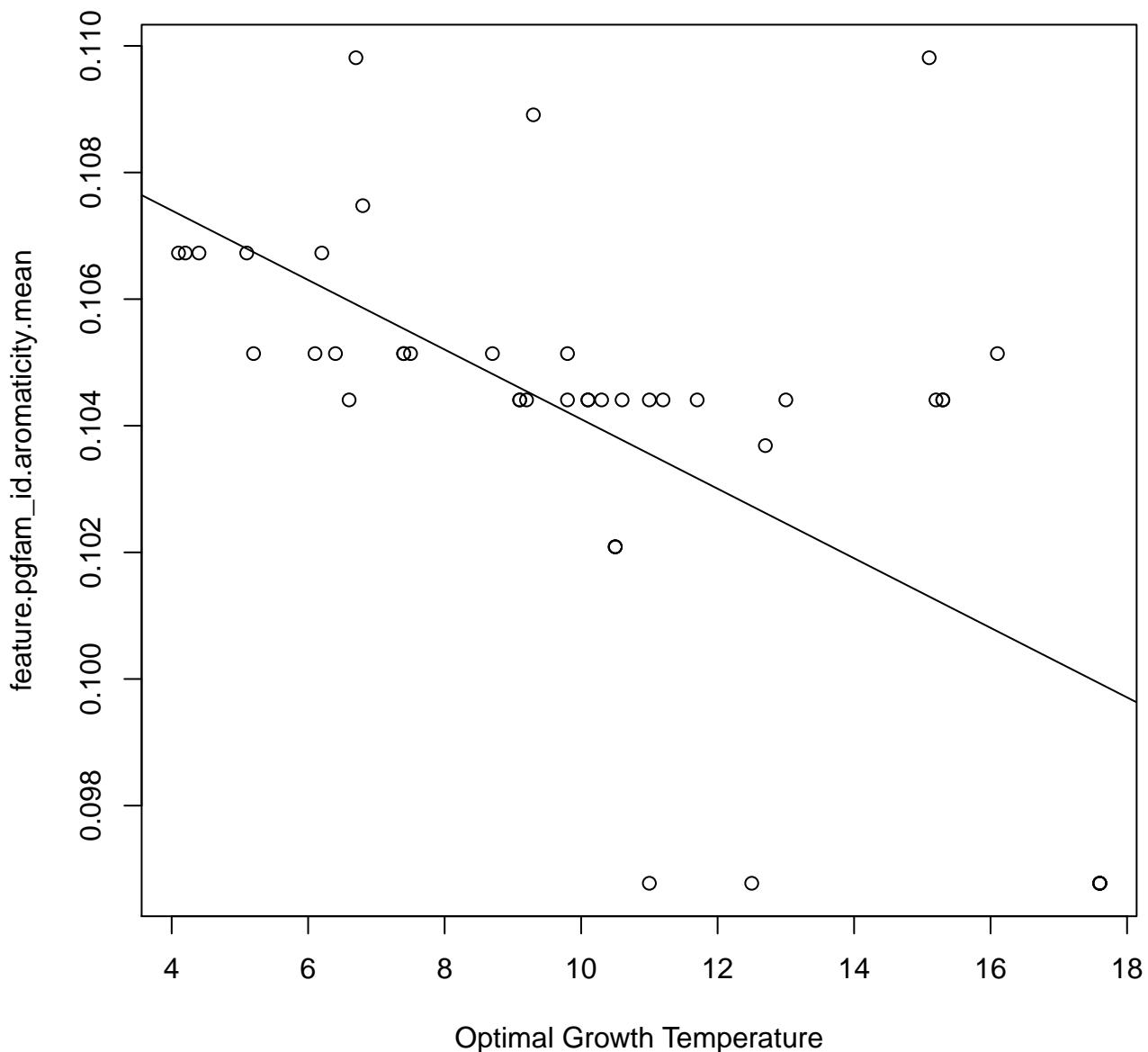
feature.pgfam_id.aromaticity.mean
PGF_00054959
Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)



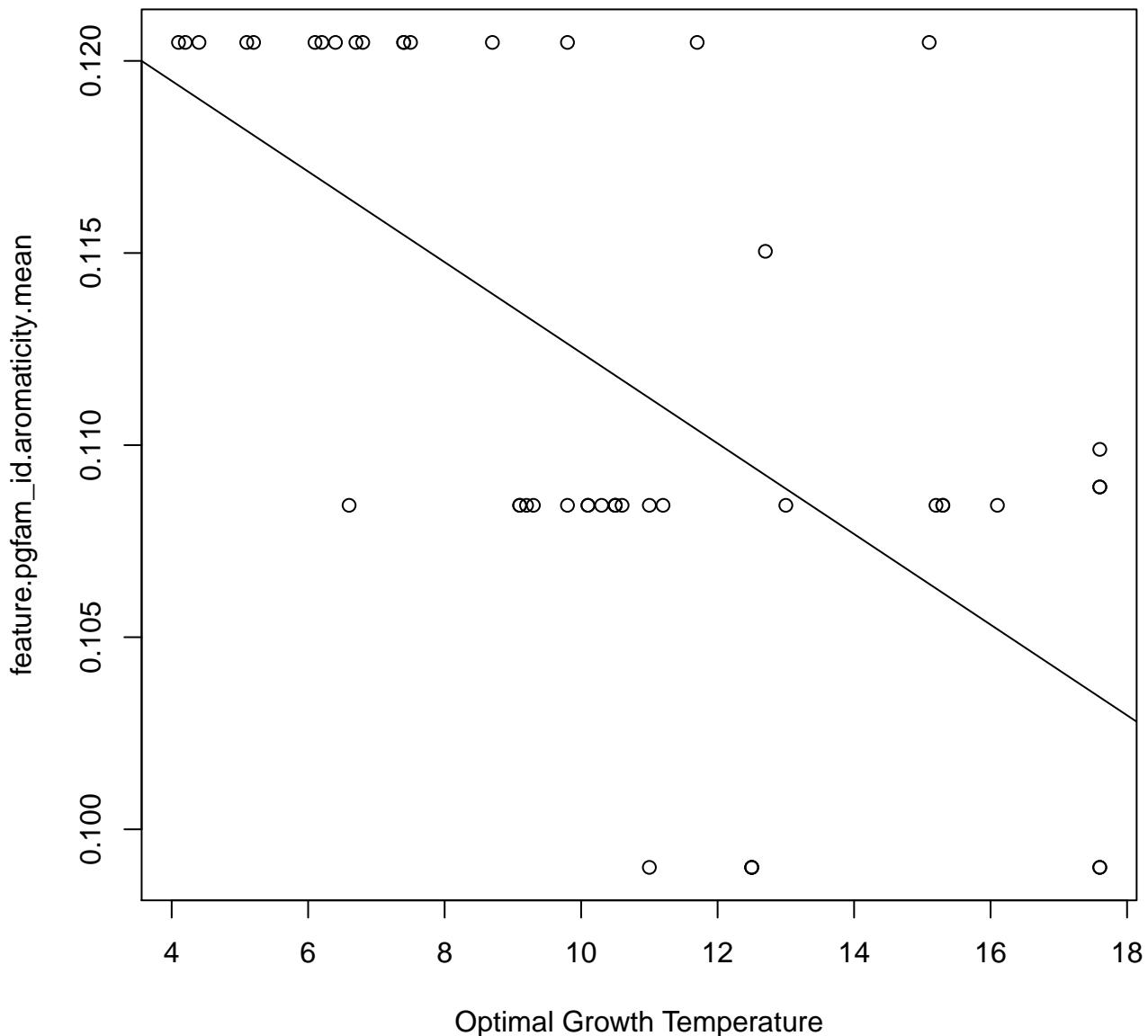
feature.pgfam_id.aromaticity.mean
PGF_00645831
DNA polymerase III chi subunit (EC 2.7.7.7)



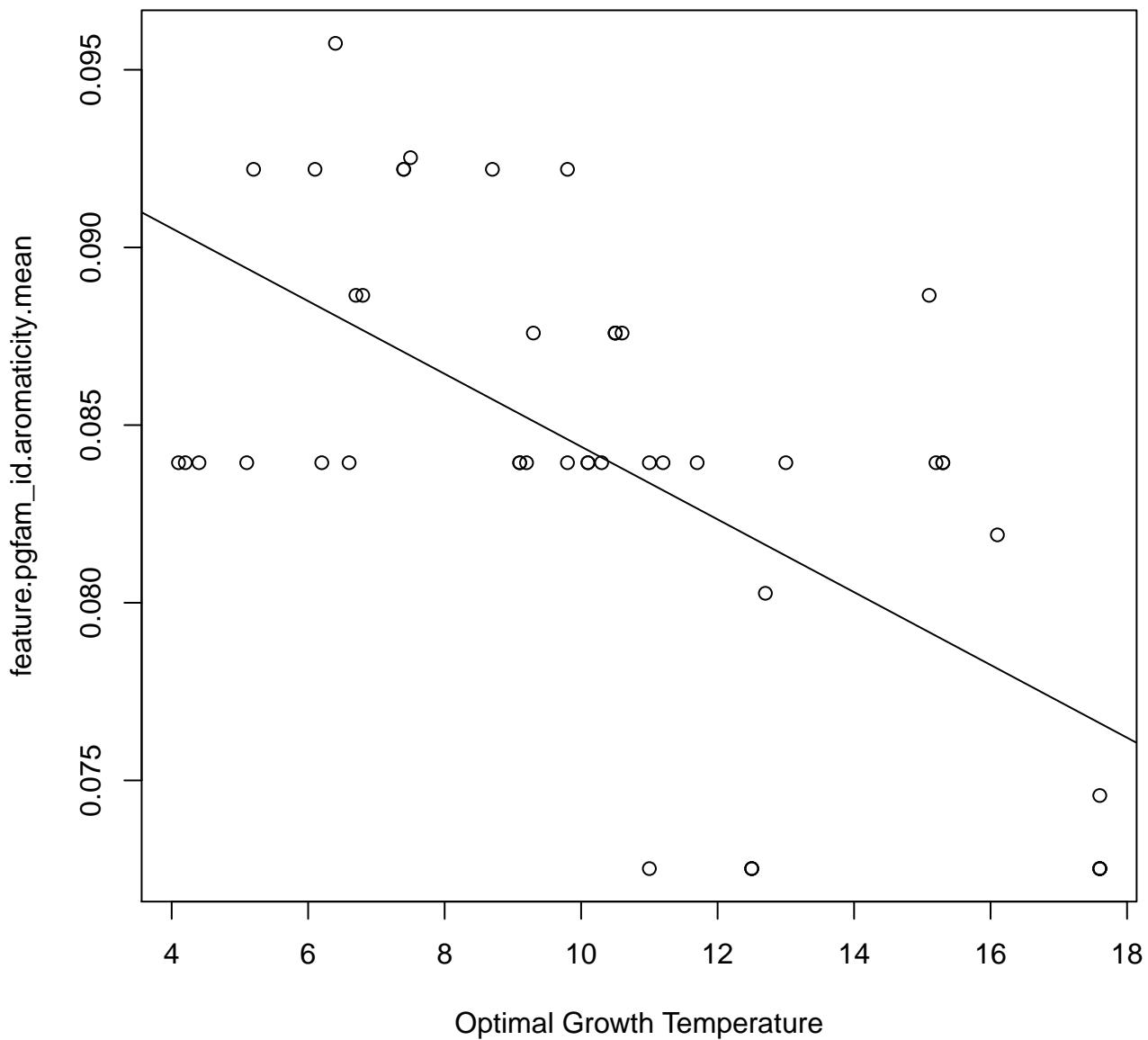
feature.pgfam_id.aromaticity.mean
PGF_03316046
Threonine synthase (EC 4.2.3.1)



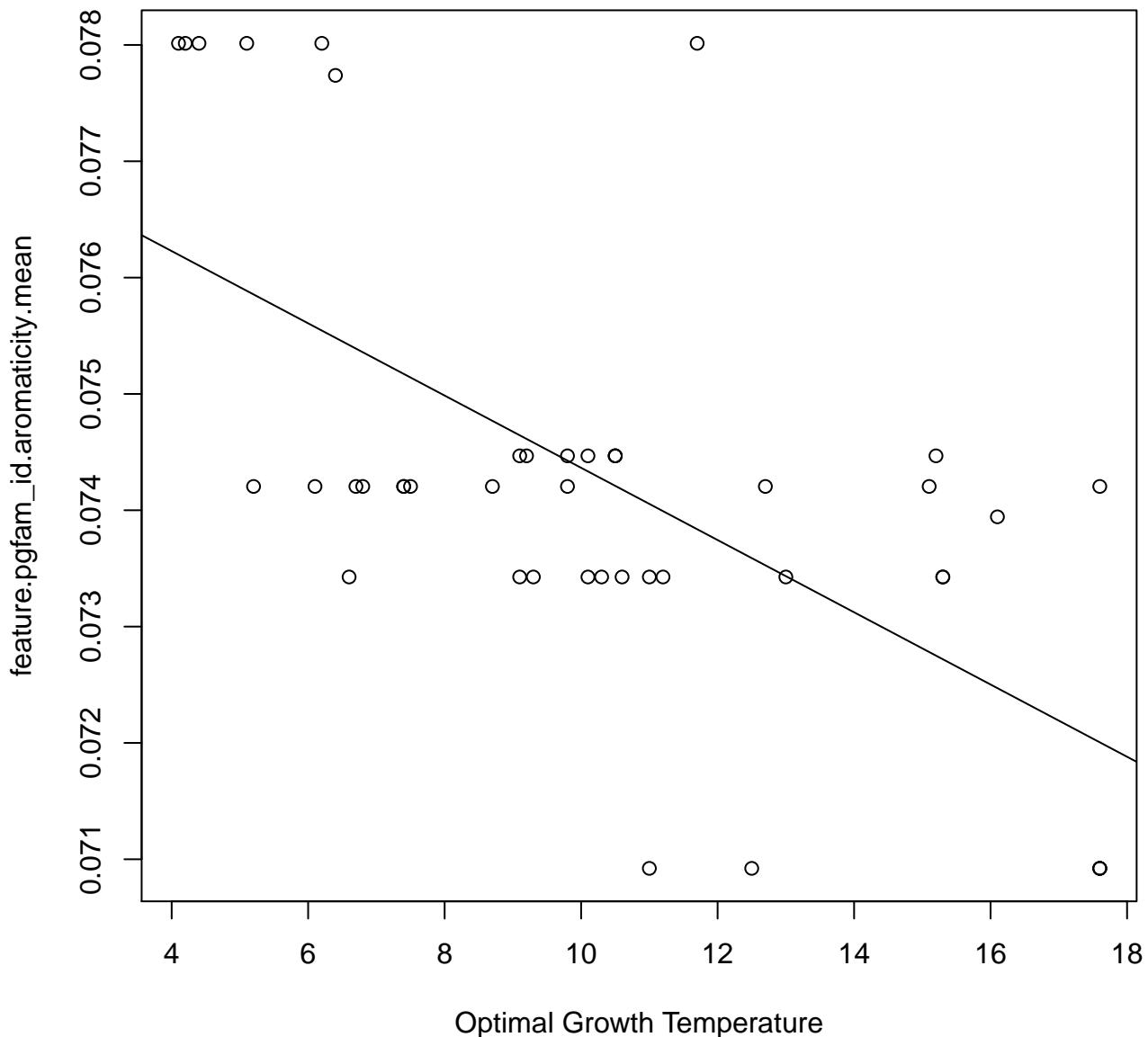
feature.pgfam_id.aromaticity.mean
PGF_02069837
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin



feature.pgfam_id.aromaticity.mean
PGF_00943546
Methylglutaconyl-CoA hydratase (EC 4.2.1.18)



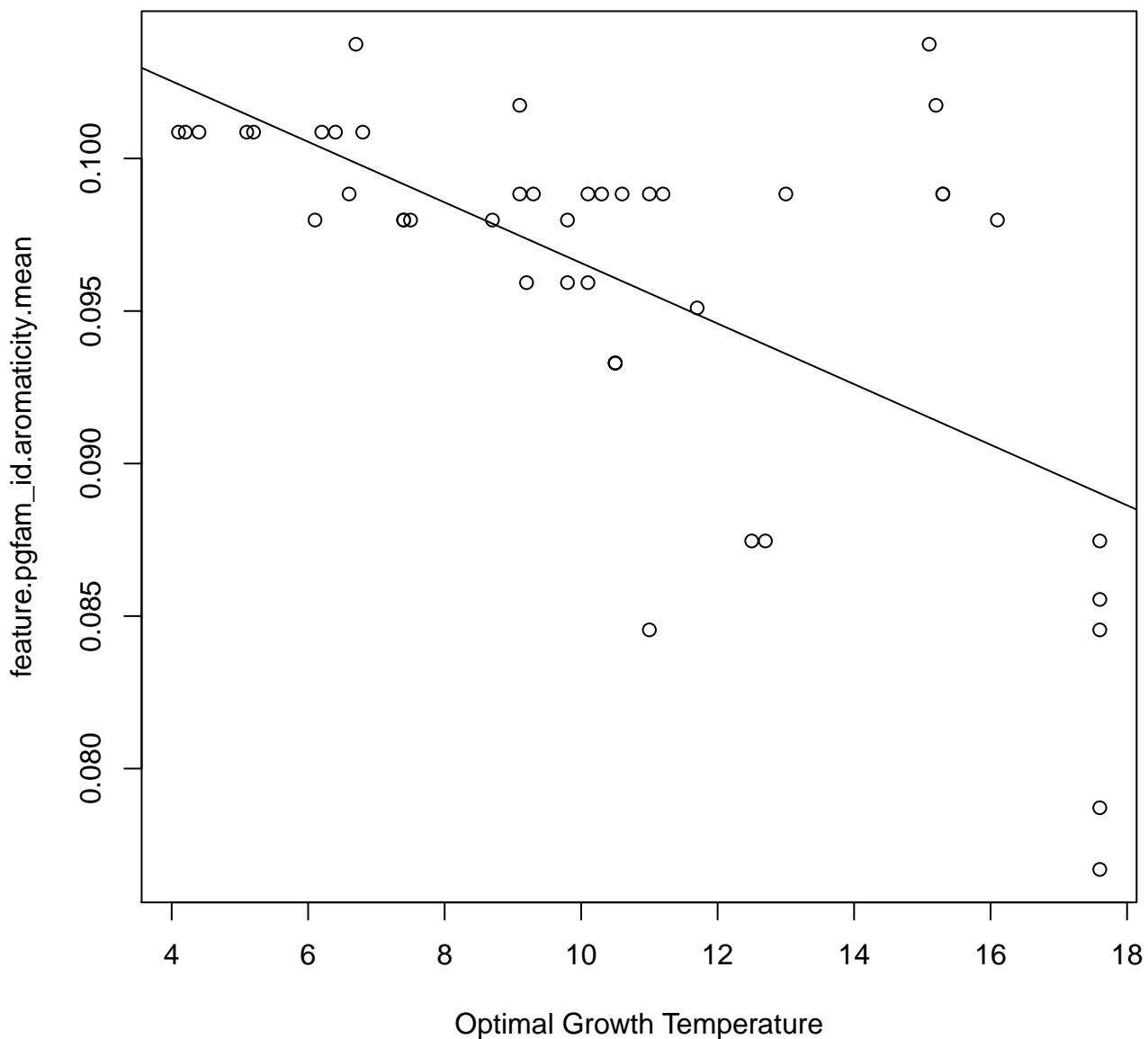
feature.pgfam_id.aromaticity.mean
PGF_03215471
16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)



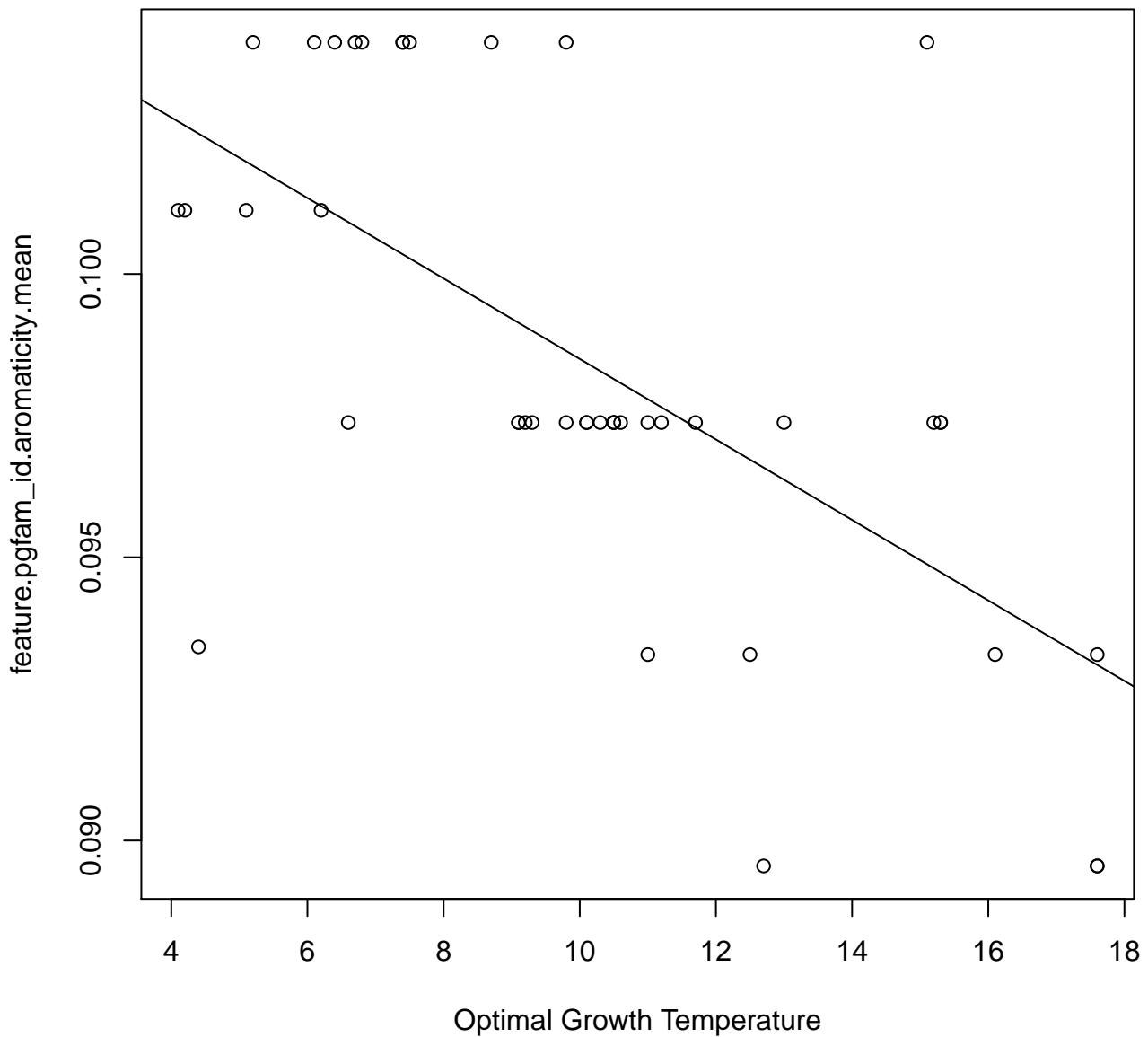
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PGF_10439576

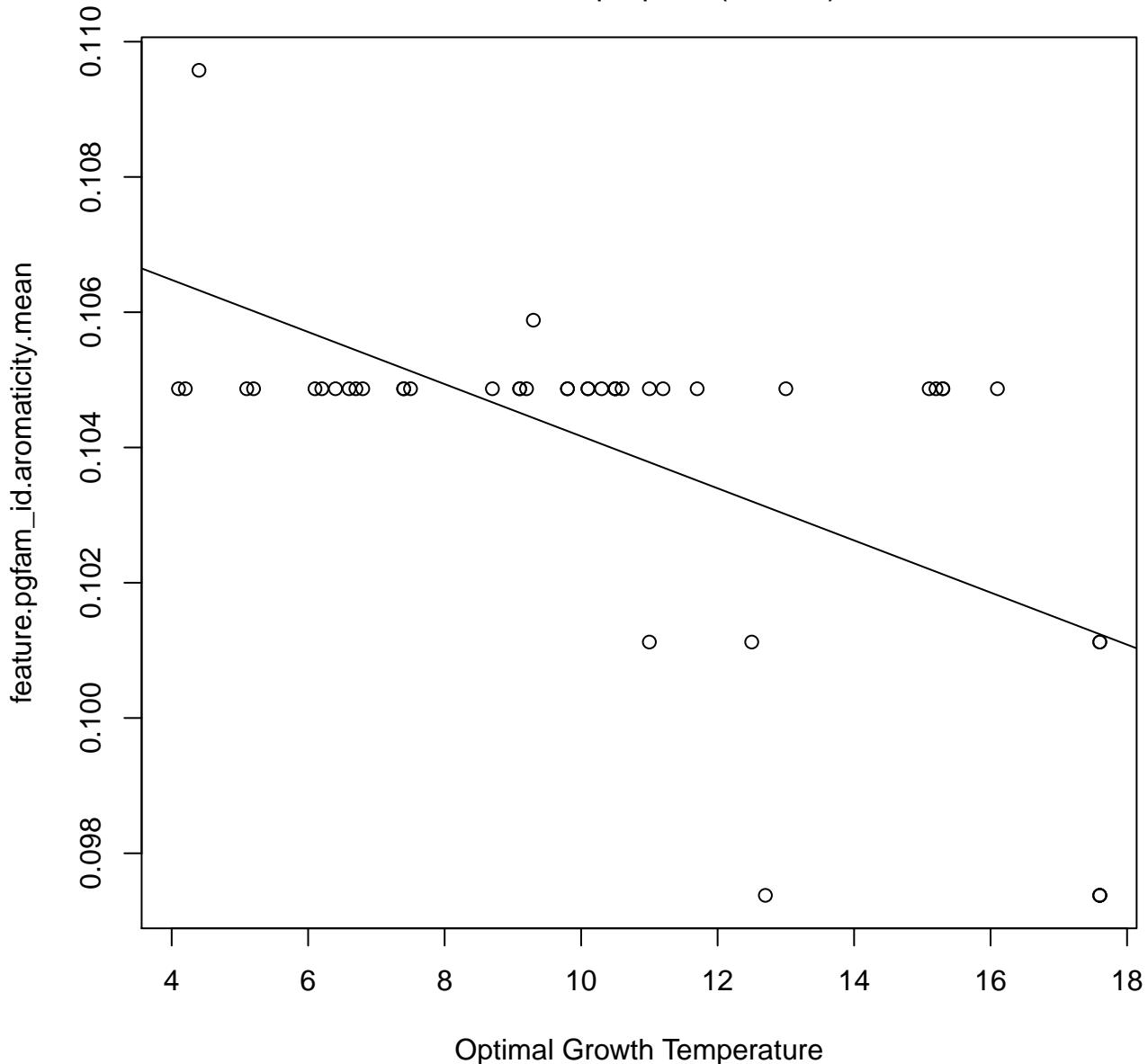
FAD:protein FMN transferase (EC 2.7.1.180) @ FAD:protein FMN transferase (EC 2.7.1.180), NqrBC-associated



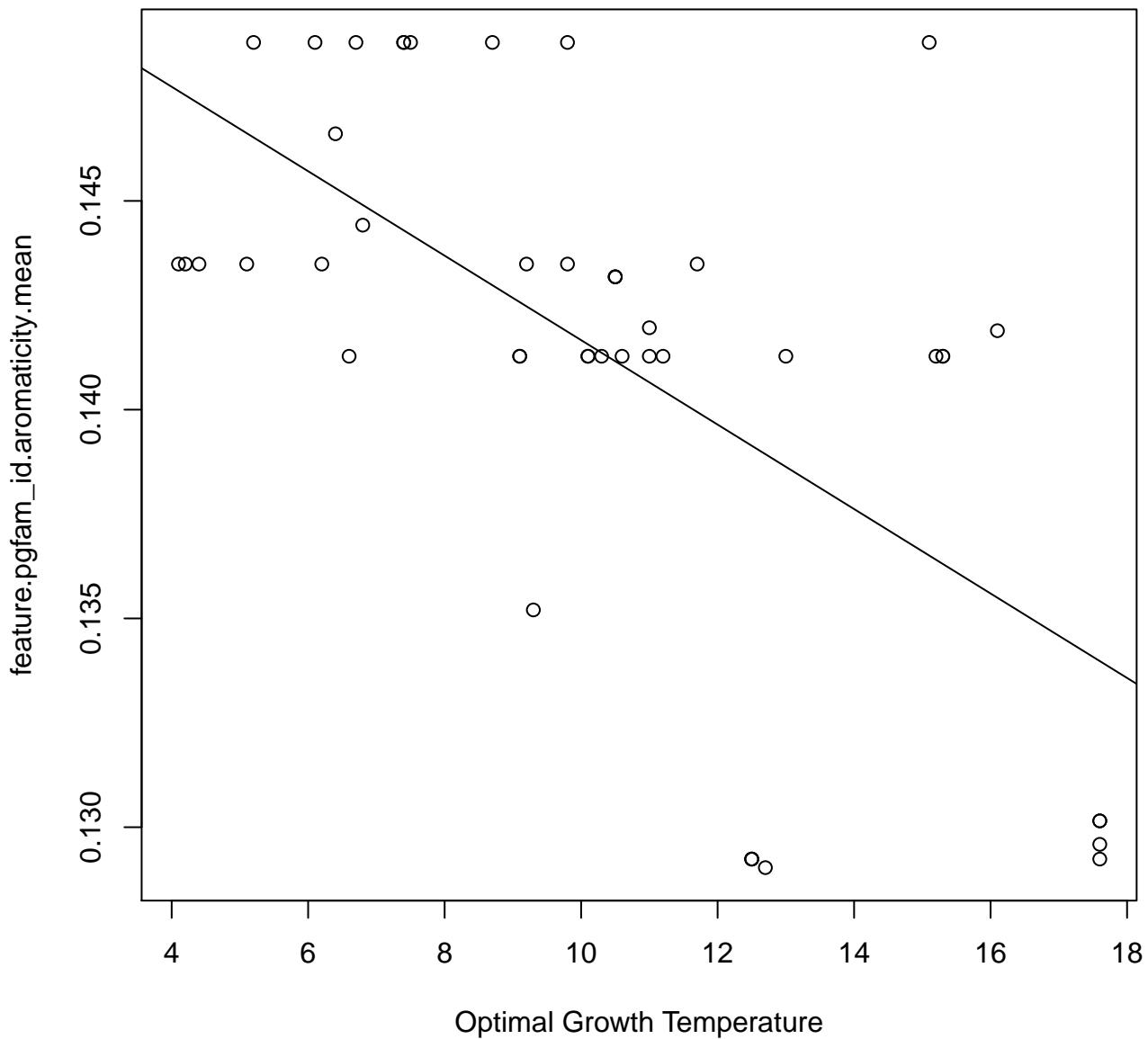
feature.pgfam_id.aromaticity.mean
PGF_01176589
4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)



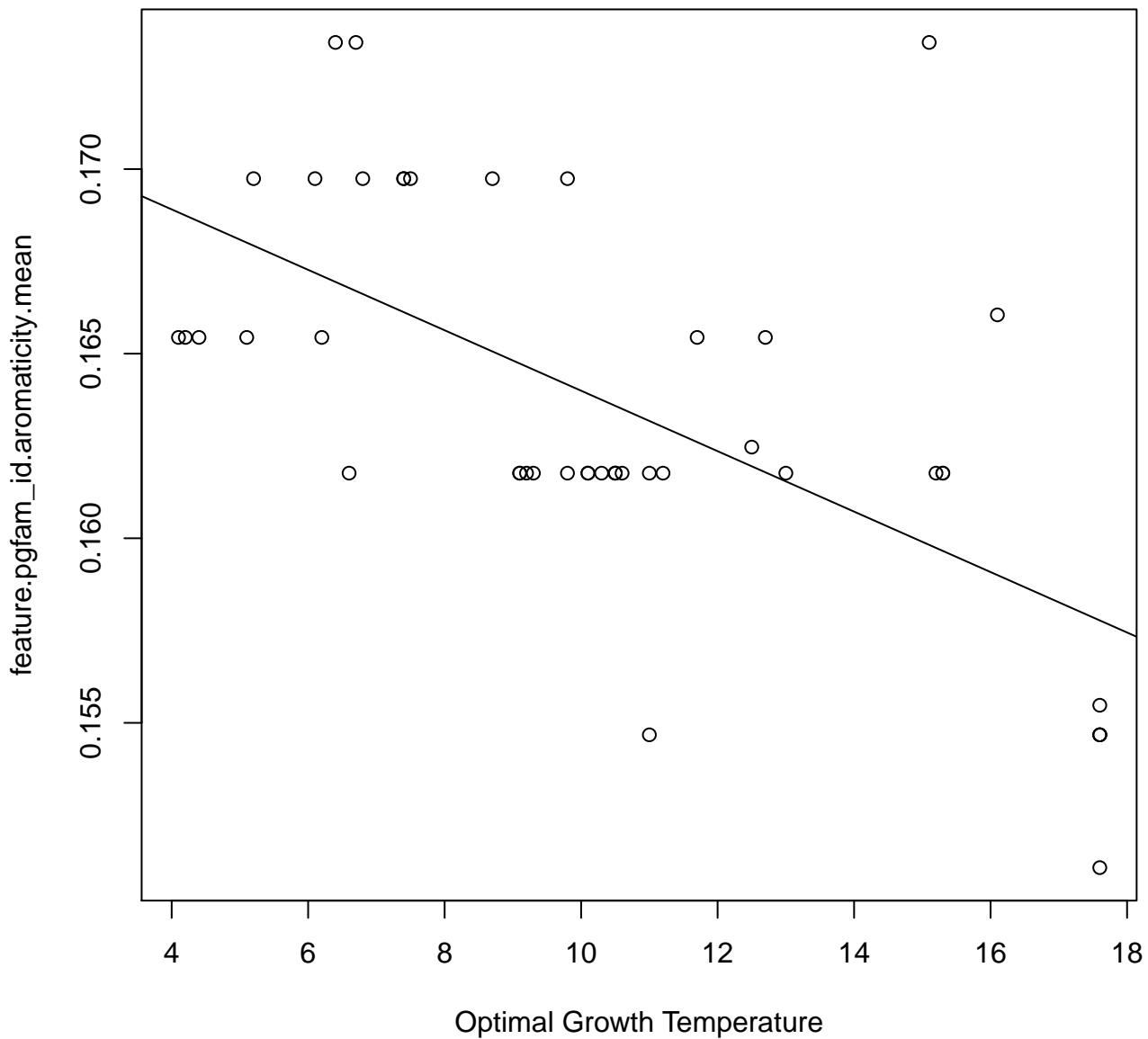
feature.pgfam_id.aromaticity.mean
PGF_10300175
Inositol-1-monophosphatase (EC 3.1.3.25)



feature.pgfam_id.aromaticity.mean
PGF_00401551
Multidrug efflux transporter MdtK/NorM (MATE family)



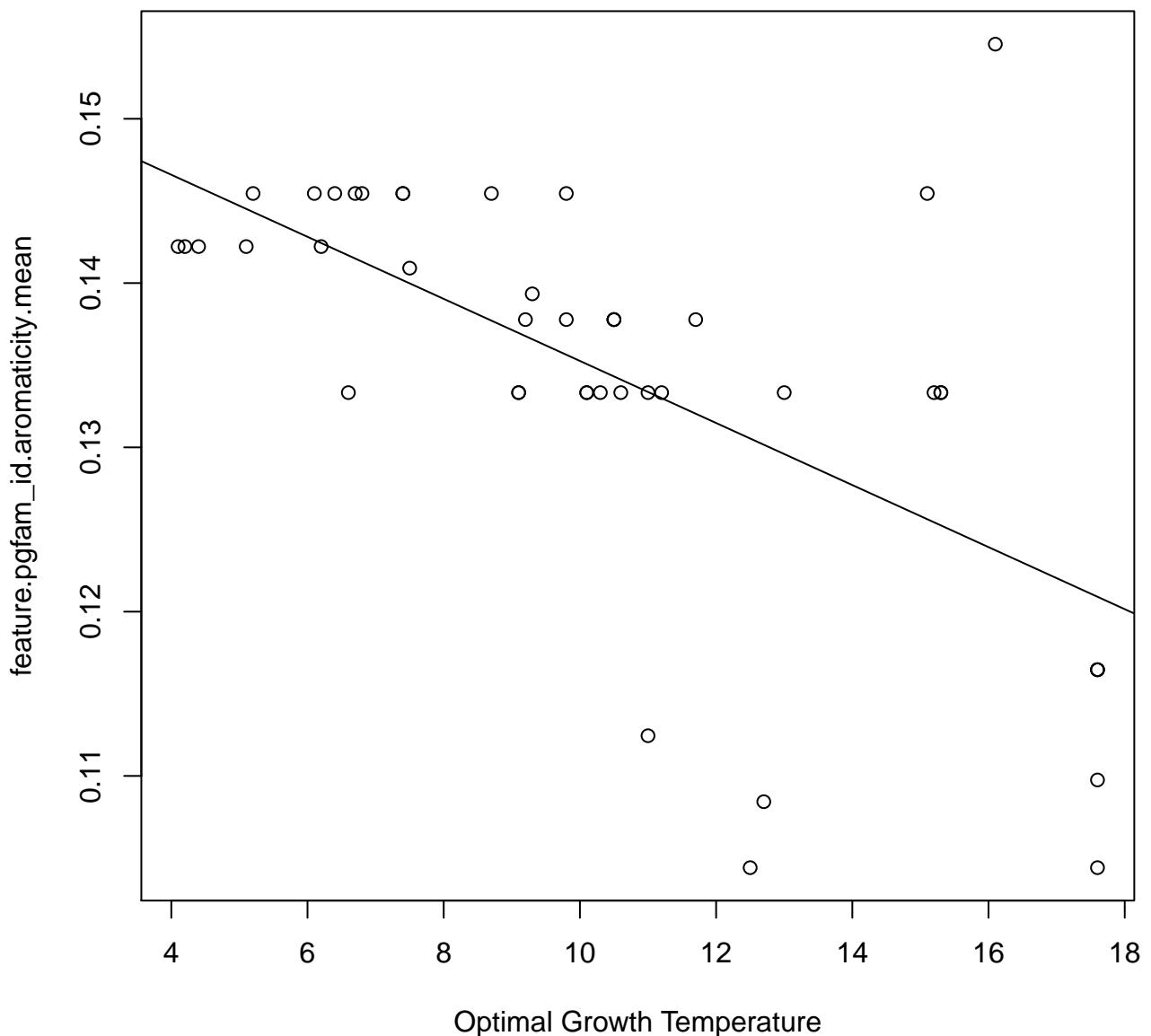
feature.pgfam_id.aromaticity.mean
PGF_12867503
Methyl-directed repair DNA adenine methylase (EC 2.1.1.72)



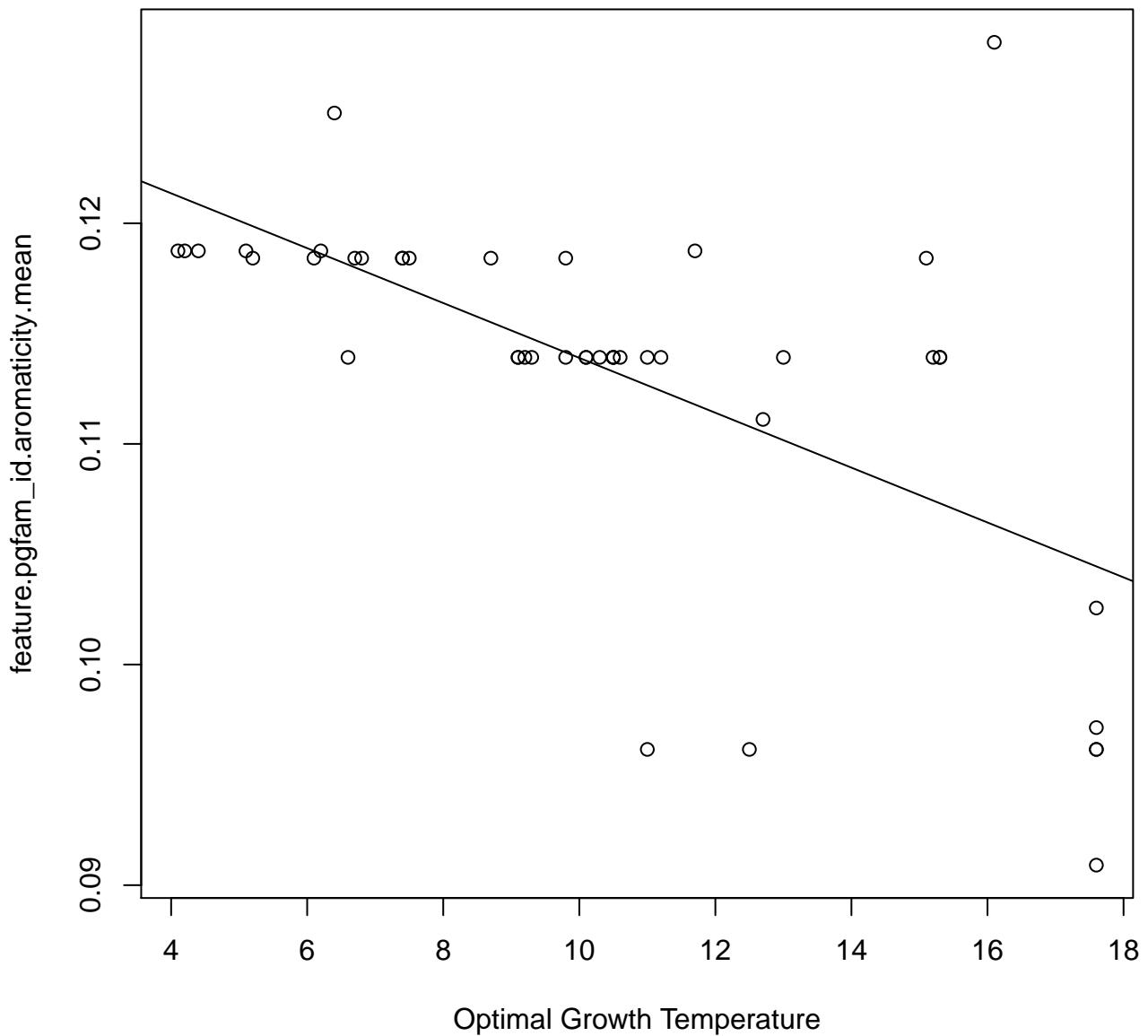
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PGF_00344969

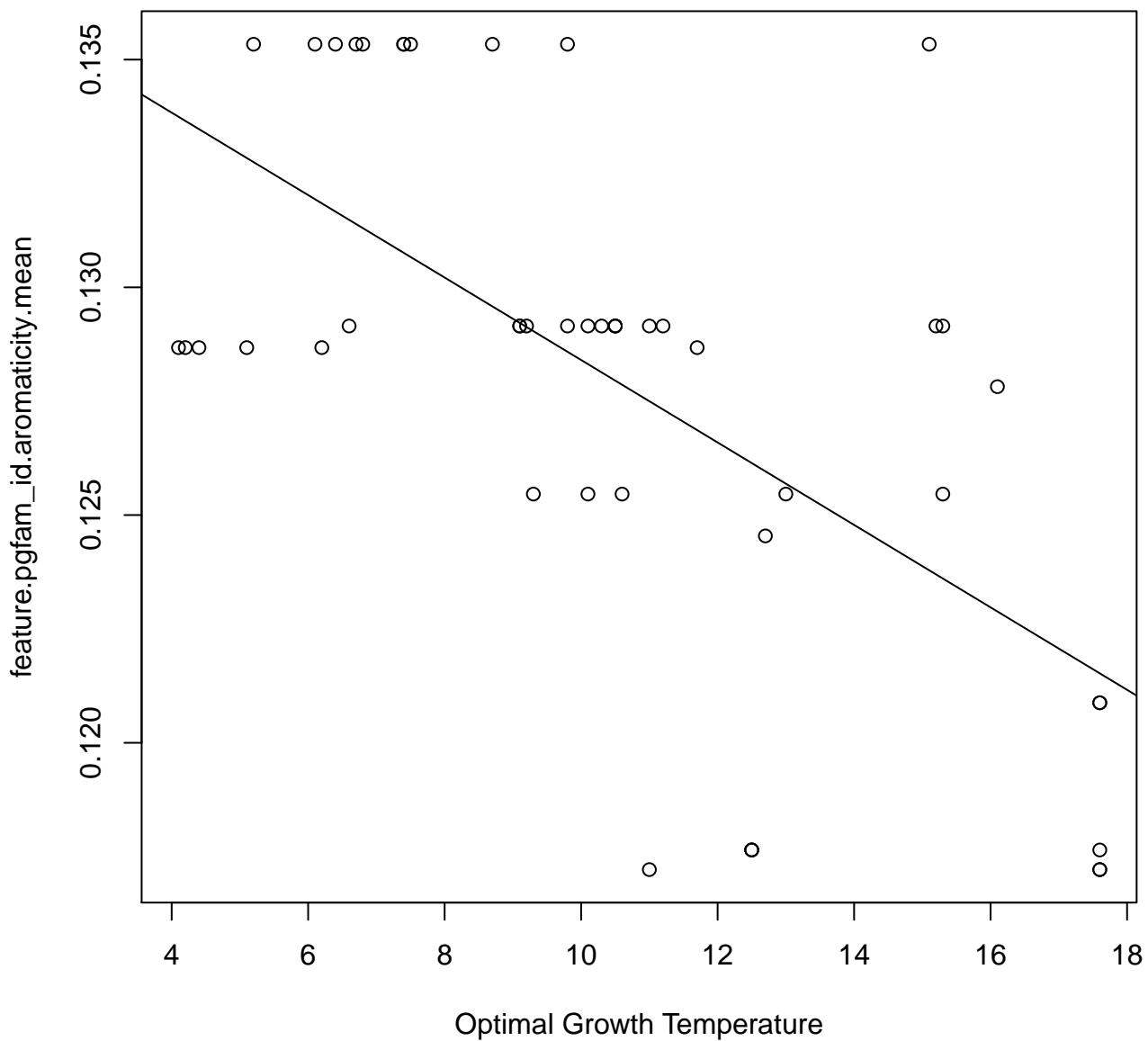
metal-associated domain (N-terminus) and membrane–bounded cytochrome biogenesis cycZ-like domain, possible membrane copper



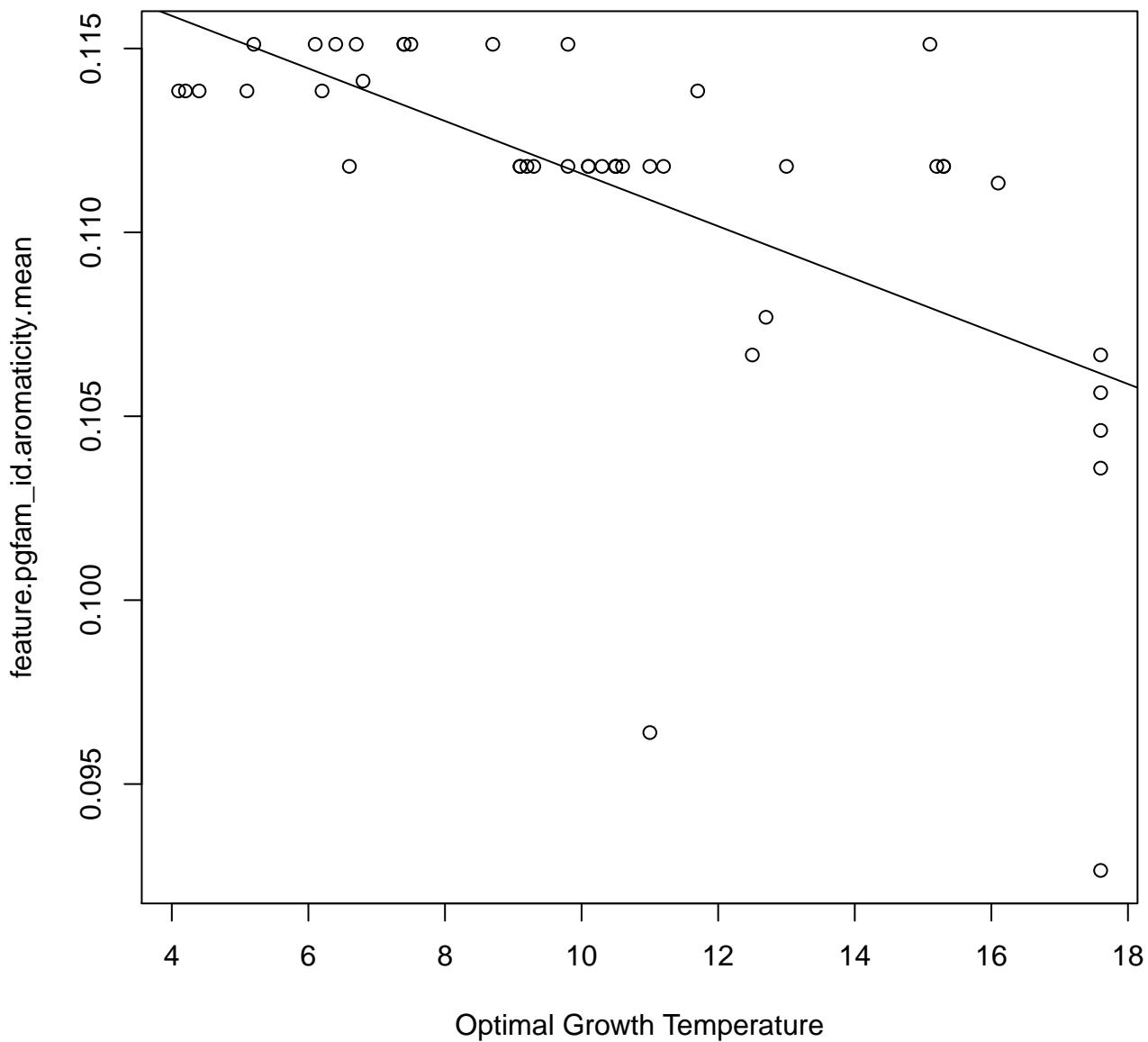
feature.pgfam_id.aromaticity.mean
PGF_00022550
Molybdopterin synthase catalytic subunit MoaE (EC 2.8.1.12)



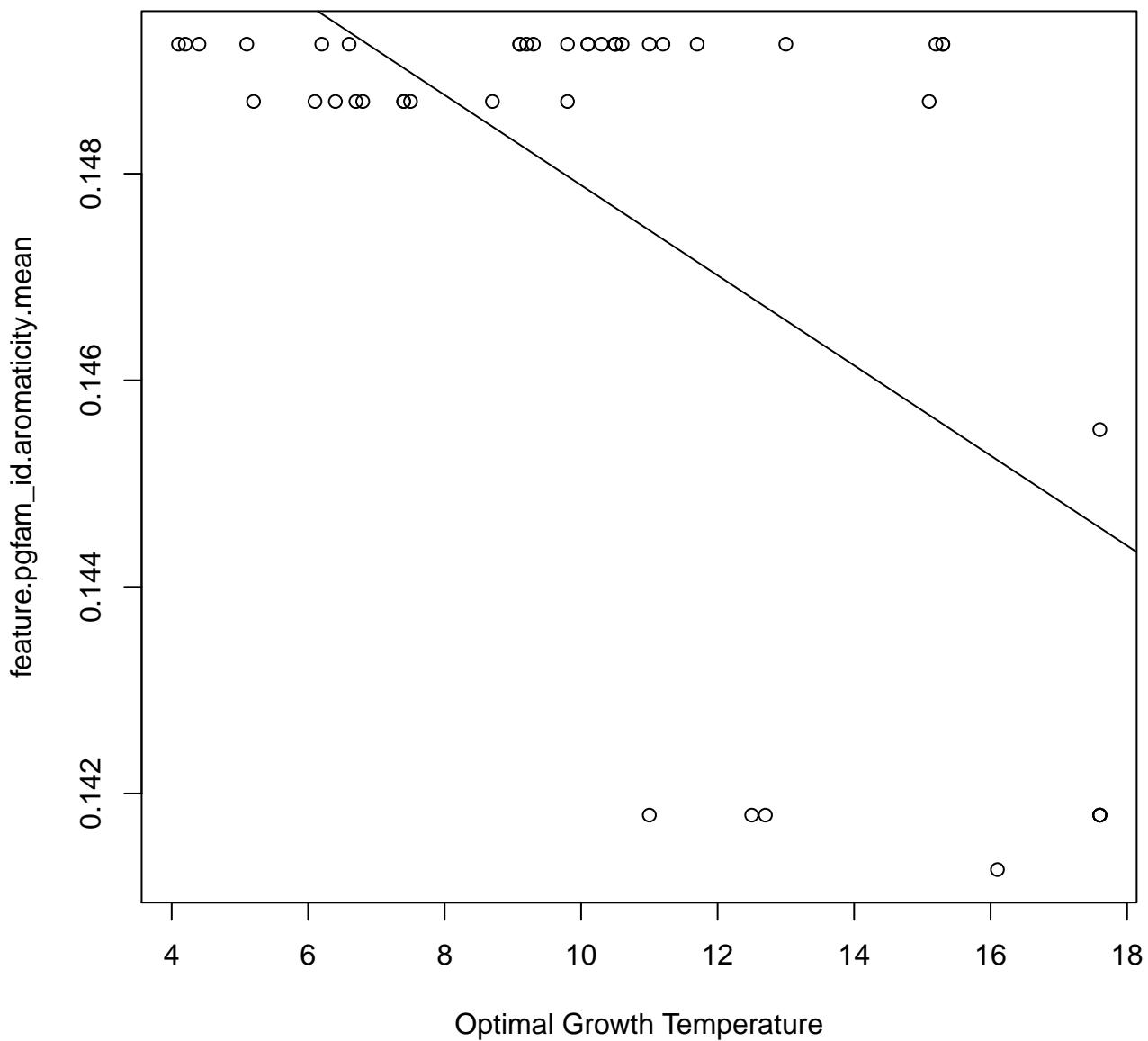
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Undecaprenyl-diphosphatase (EC 3.6.1.27)



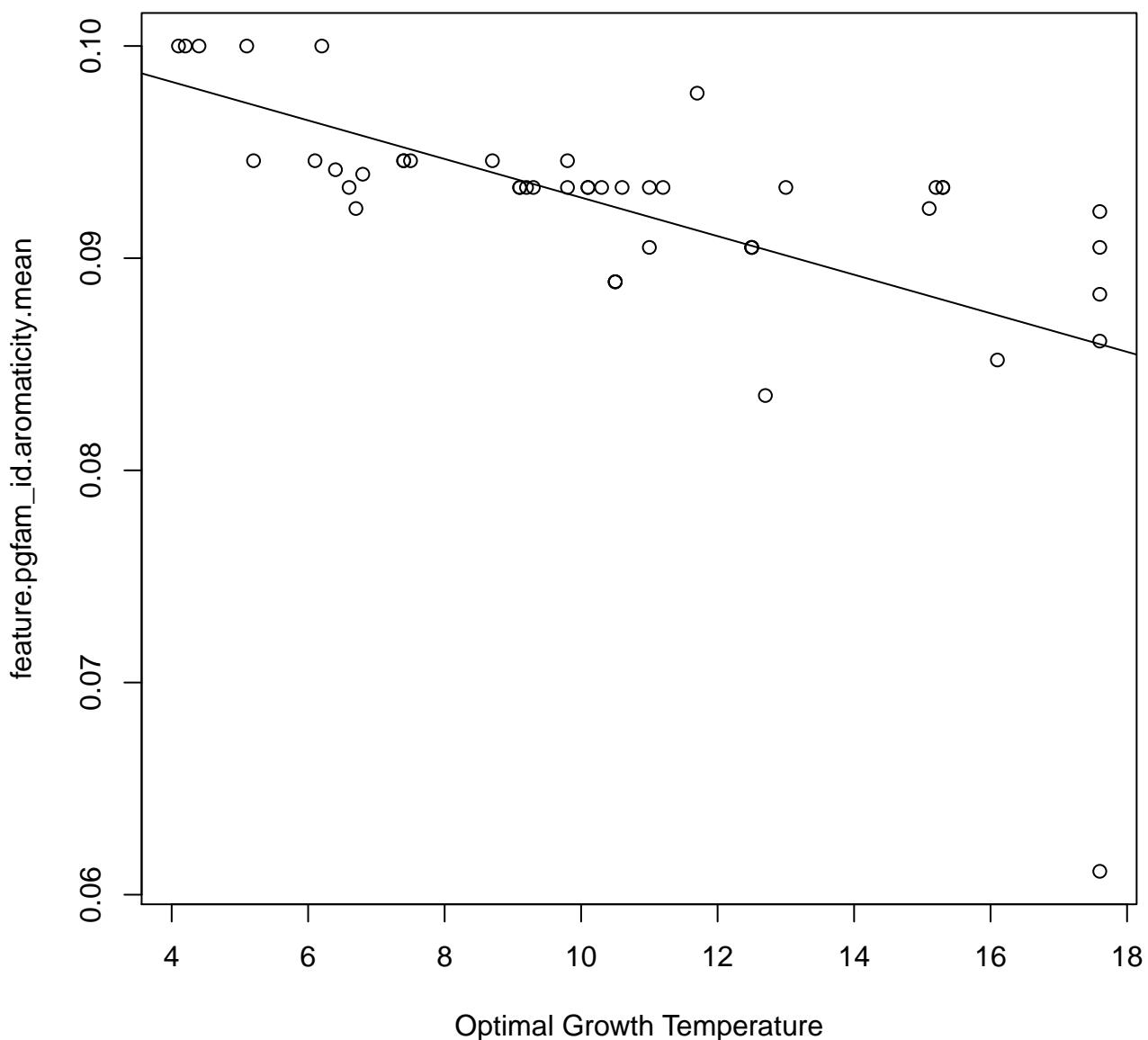
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RNA polymerase associated protein RapA



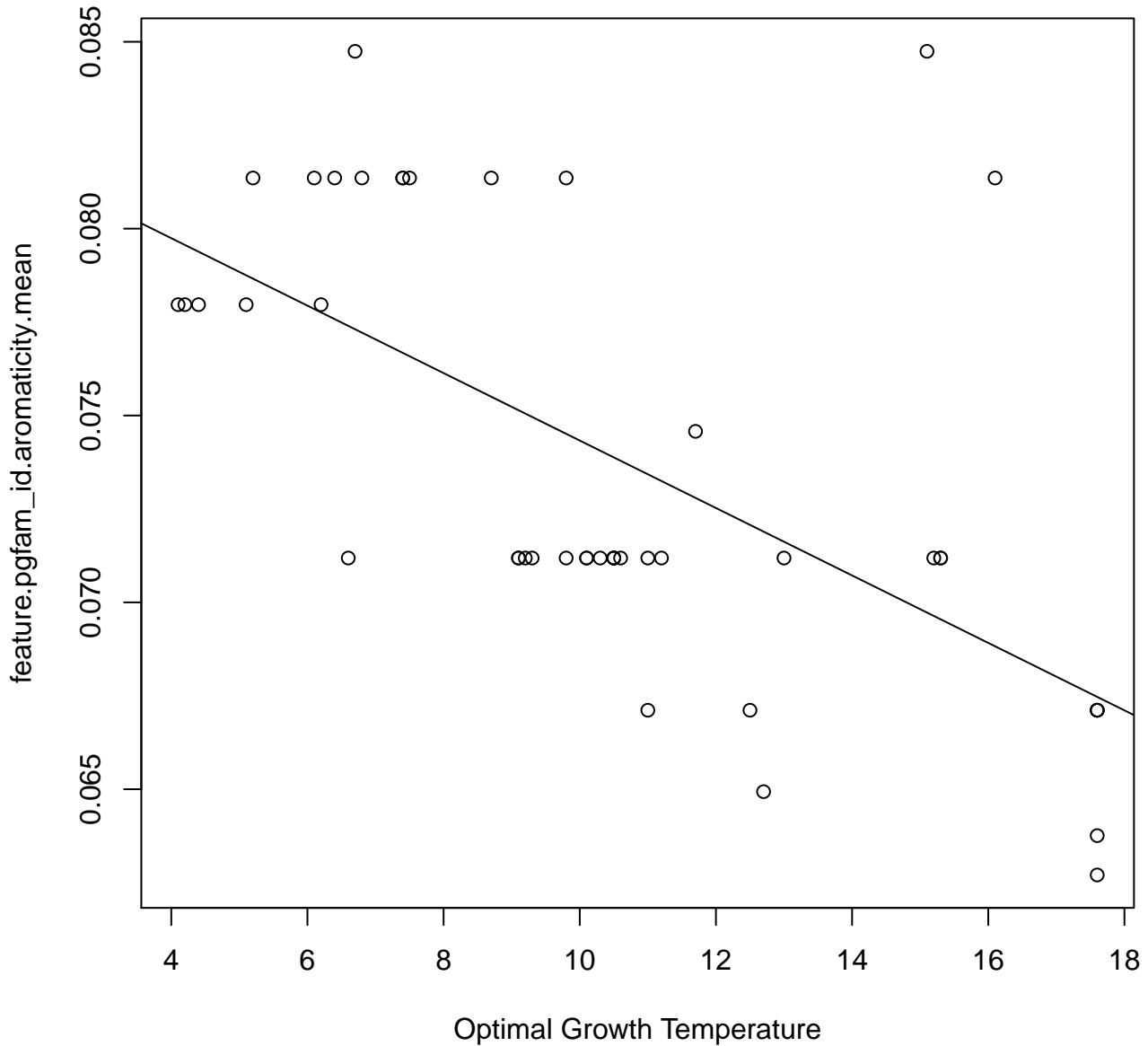
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Exodeoxyribonuclease III (EC 3.1.11.2)



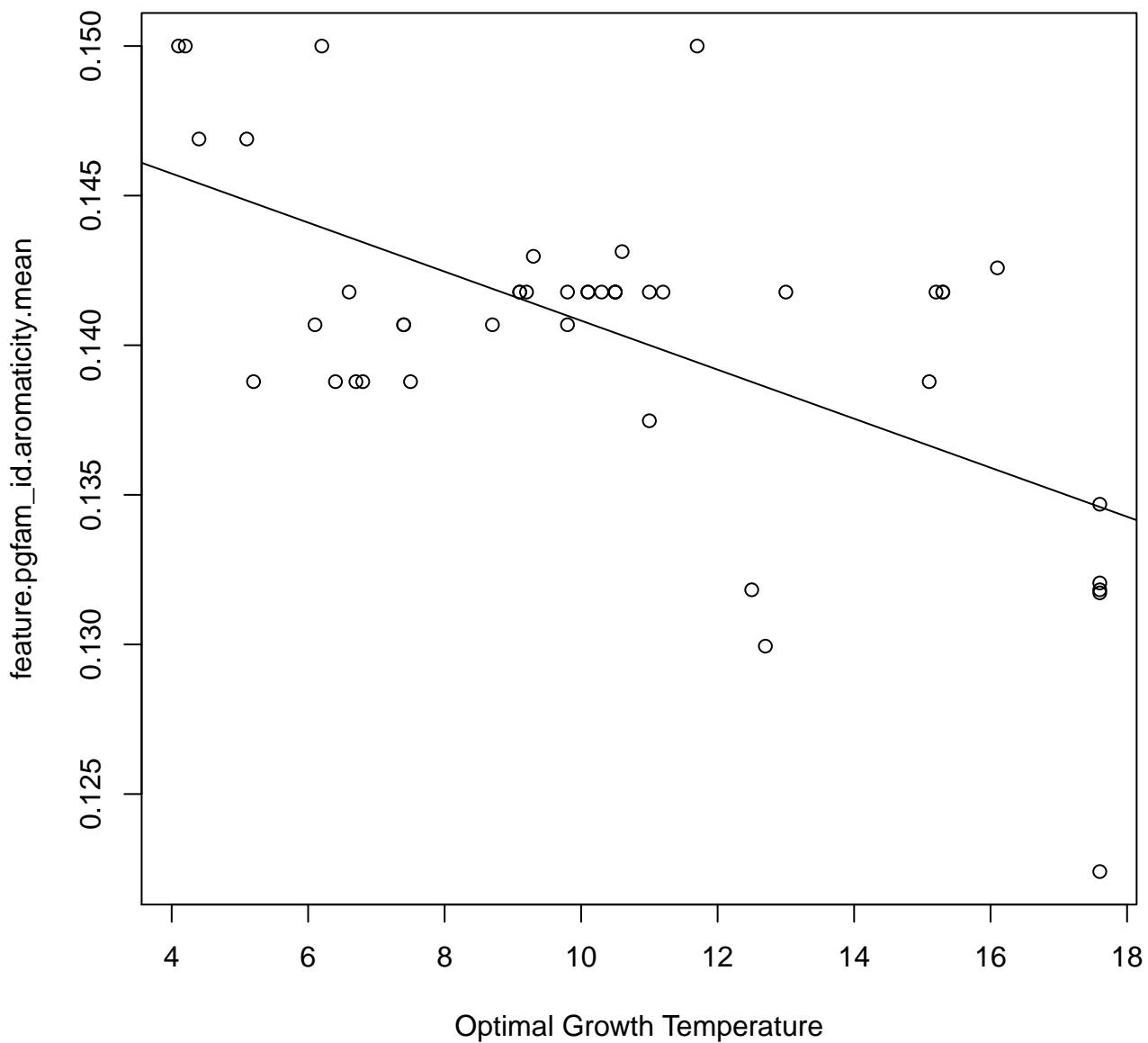
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PGF_00583021
Proton/glutamate symporter



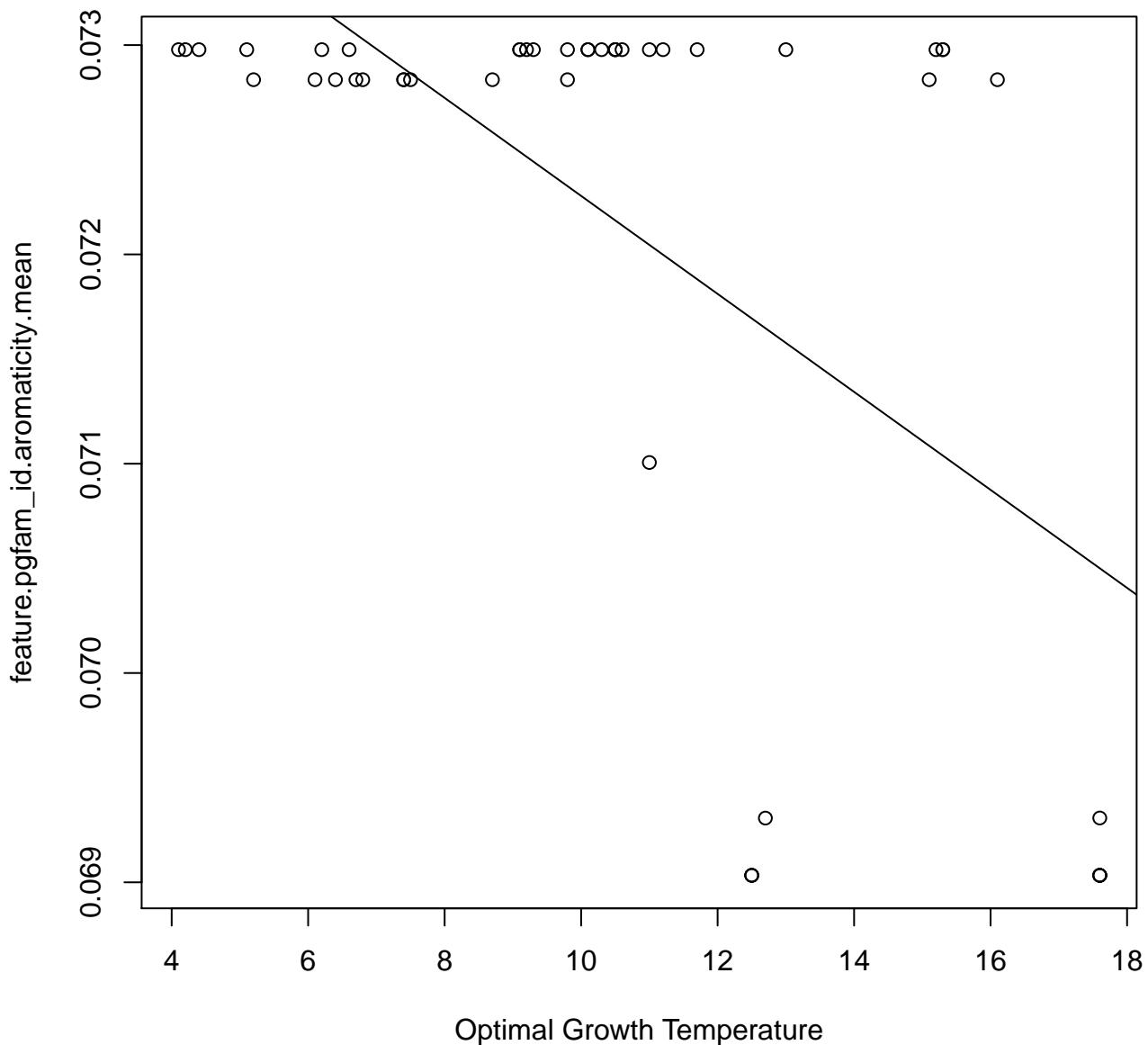
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PGF_04828114
Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)



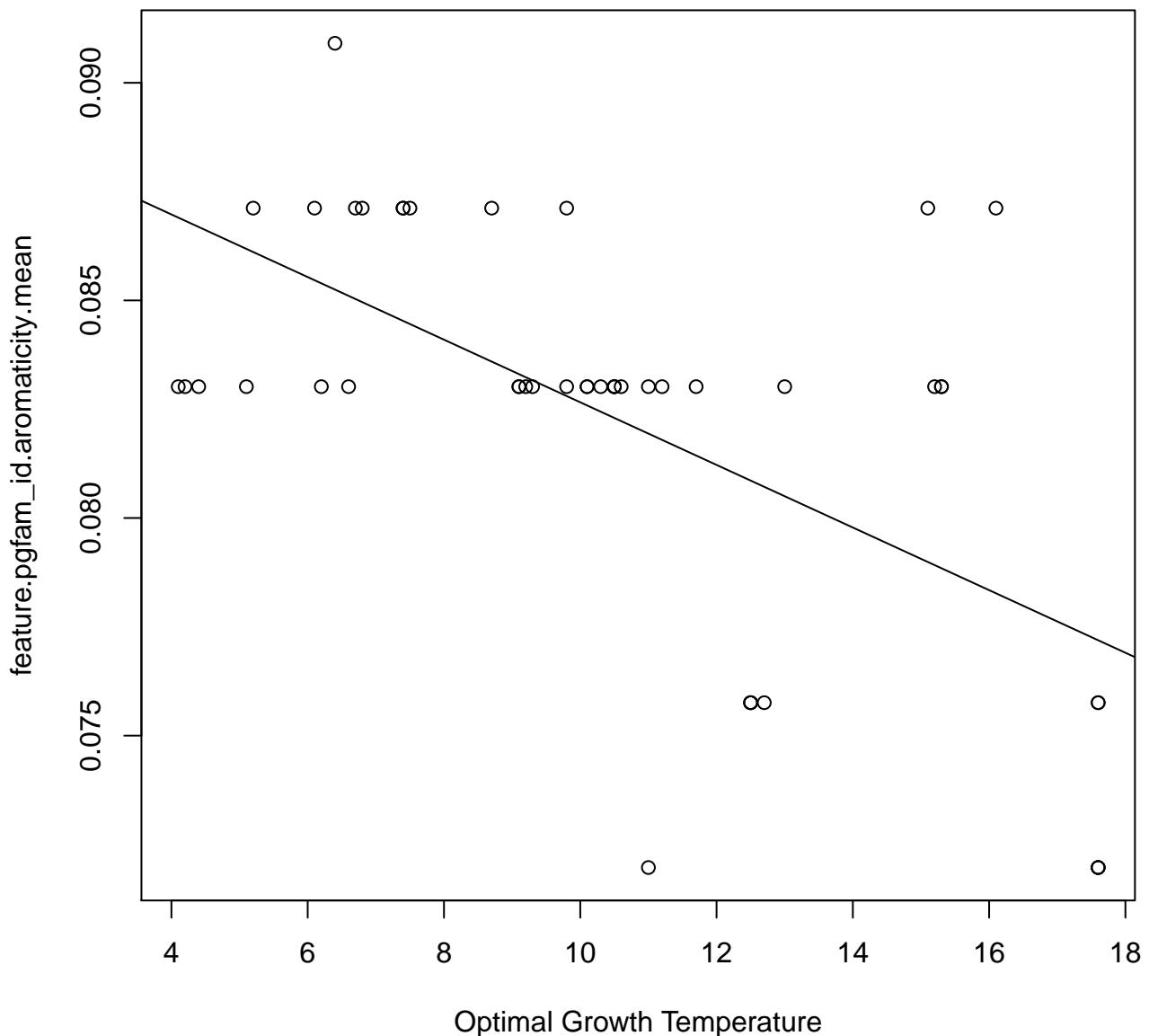
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Peptidoglycan lipid II flippase MurJ



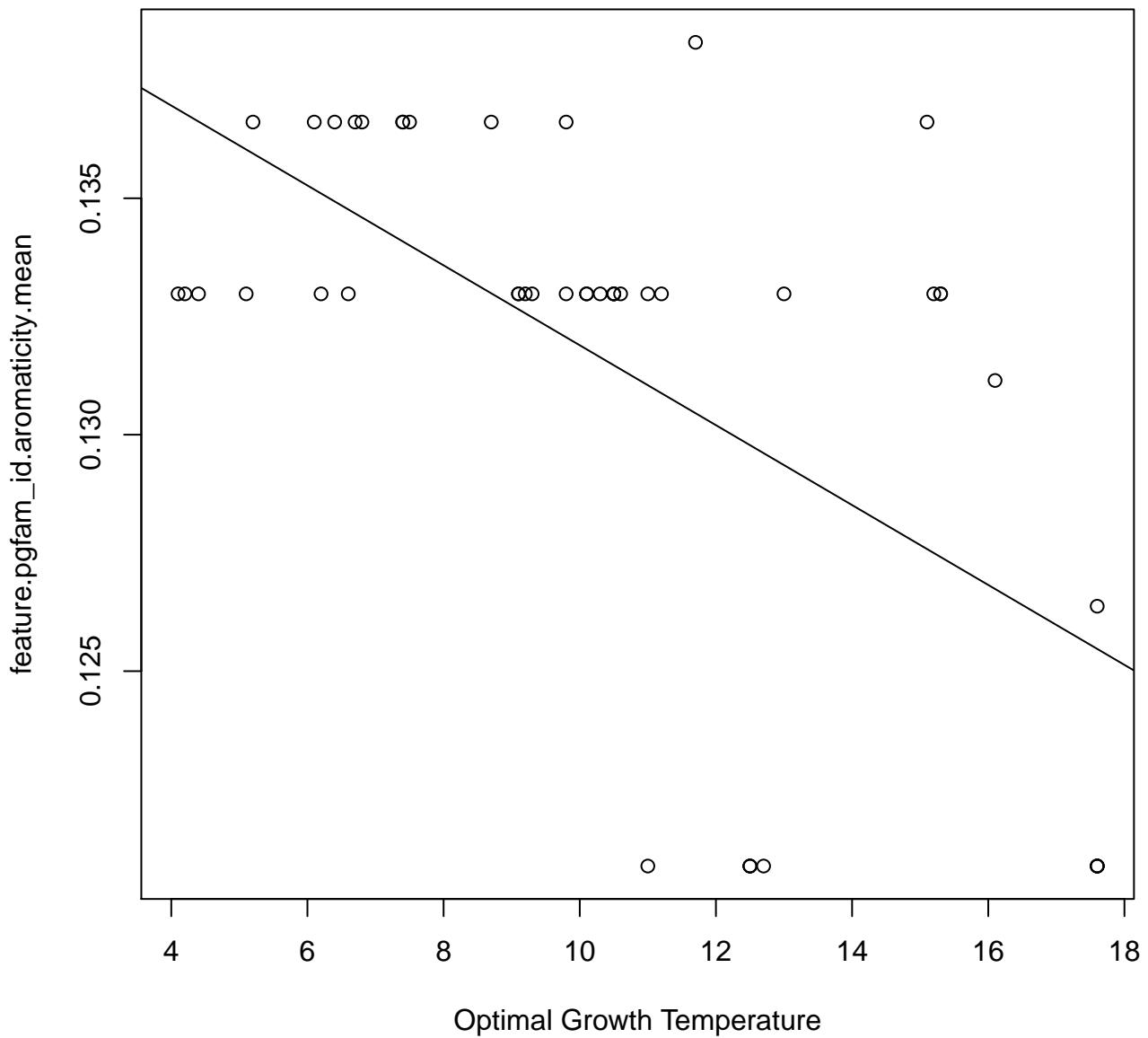
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Fumarate hydratase class I, aerobic (EC 4.2.1.2)



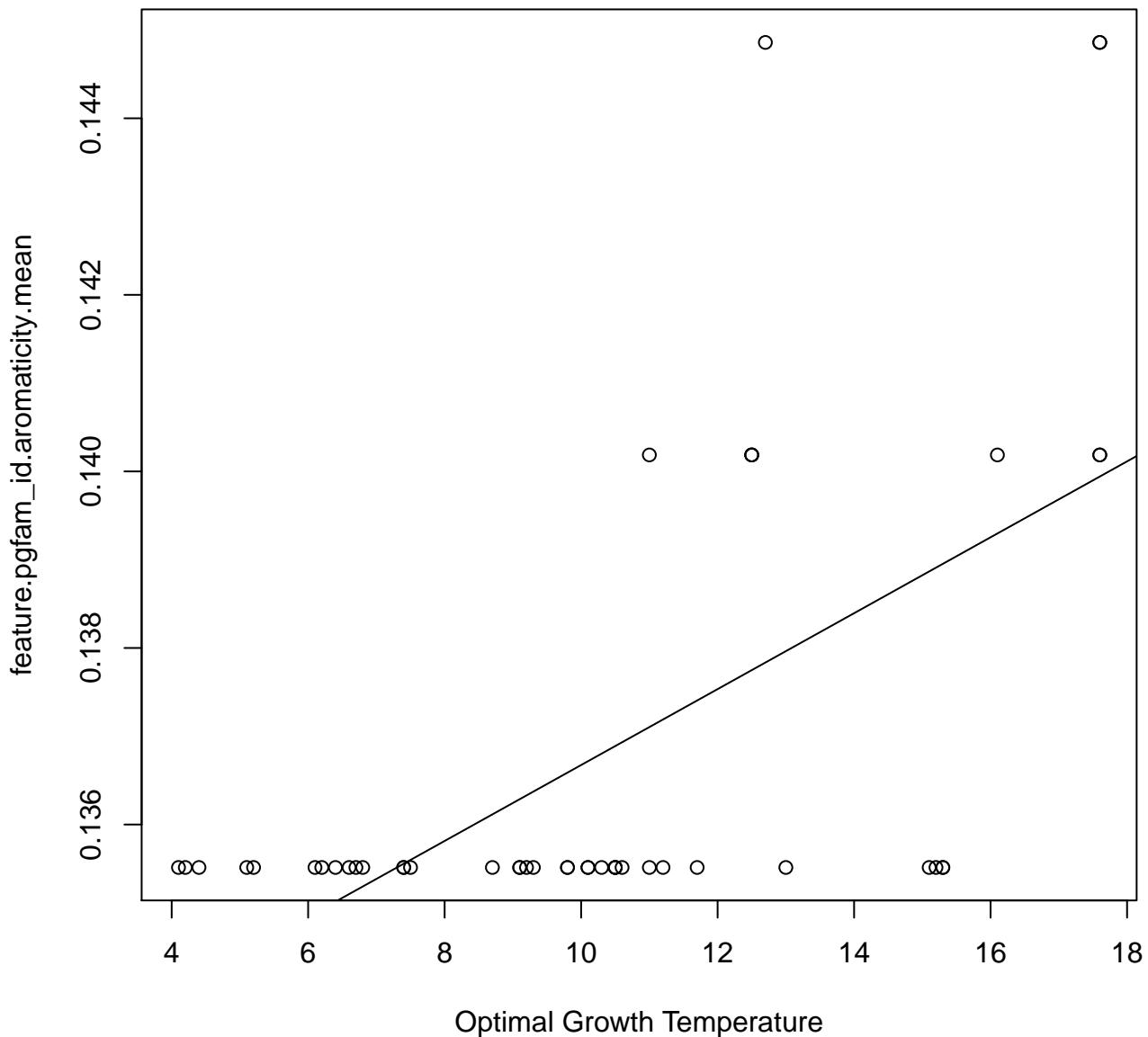
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3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)



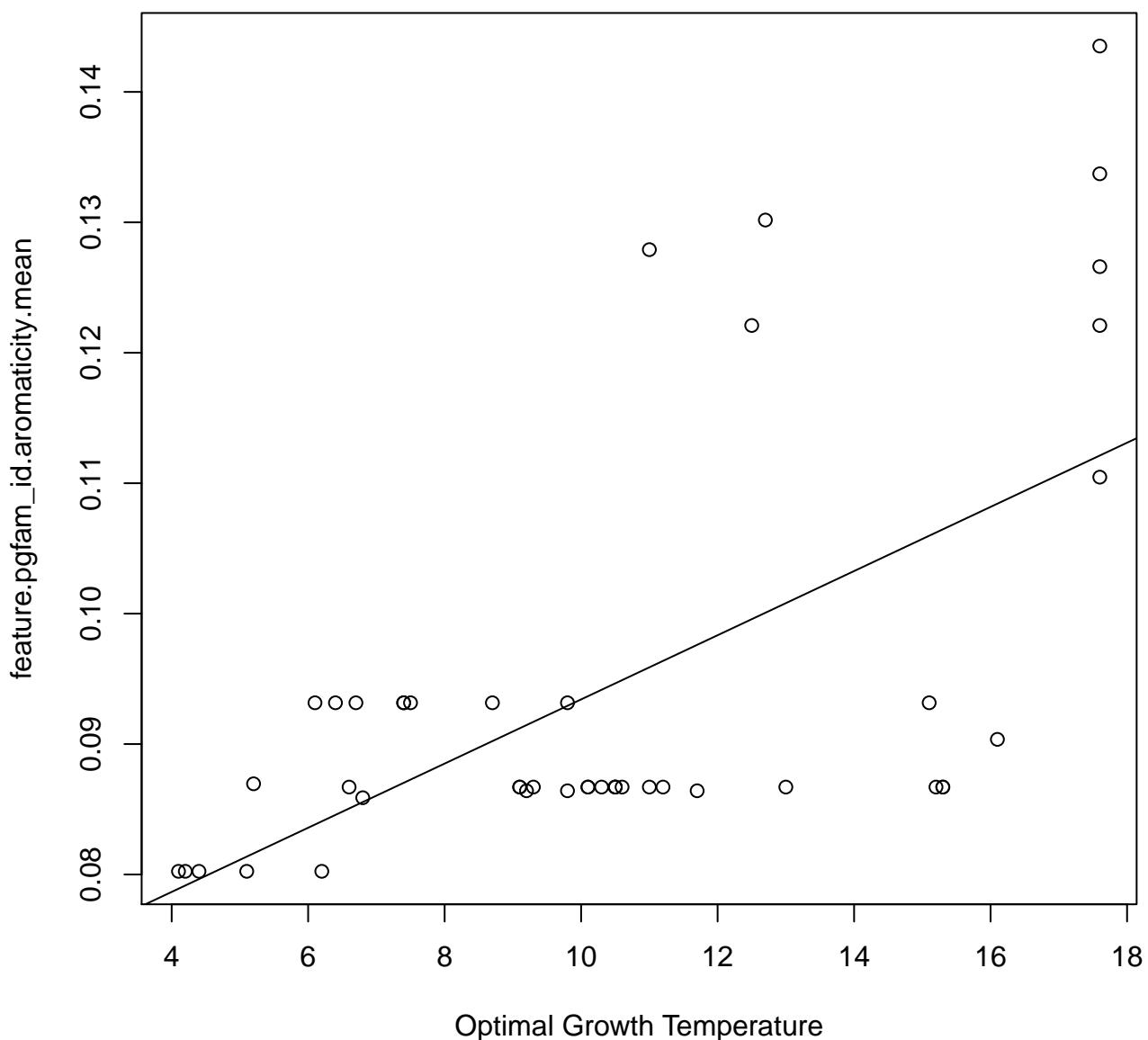
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Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase



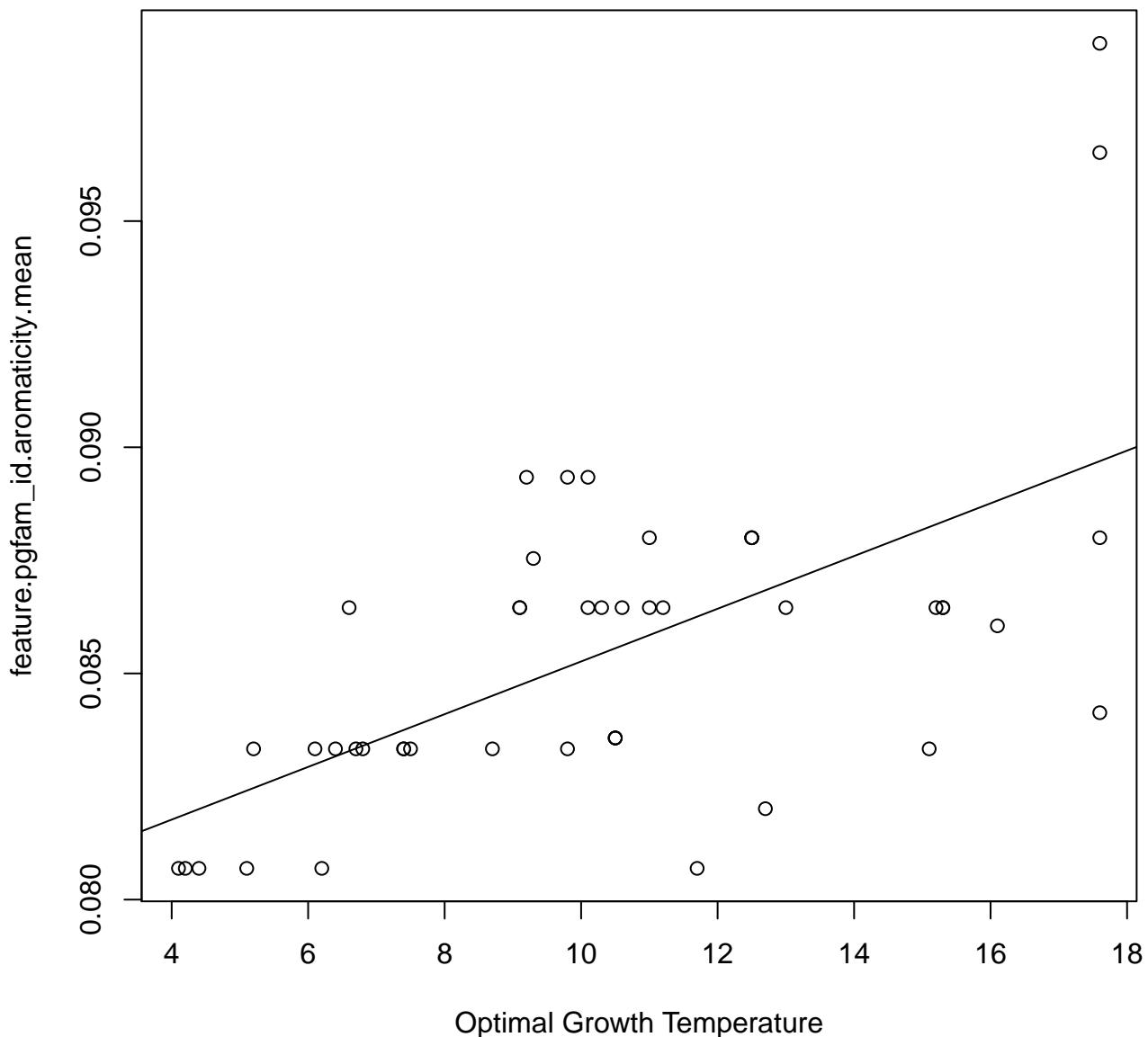
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Cytochrome c oxidase (cbb3-type) subunit CcoO (EC 1.9.3.1)



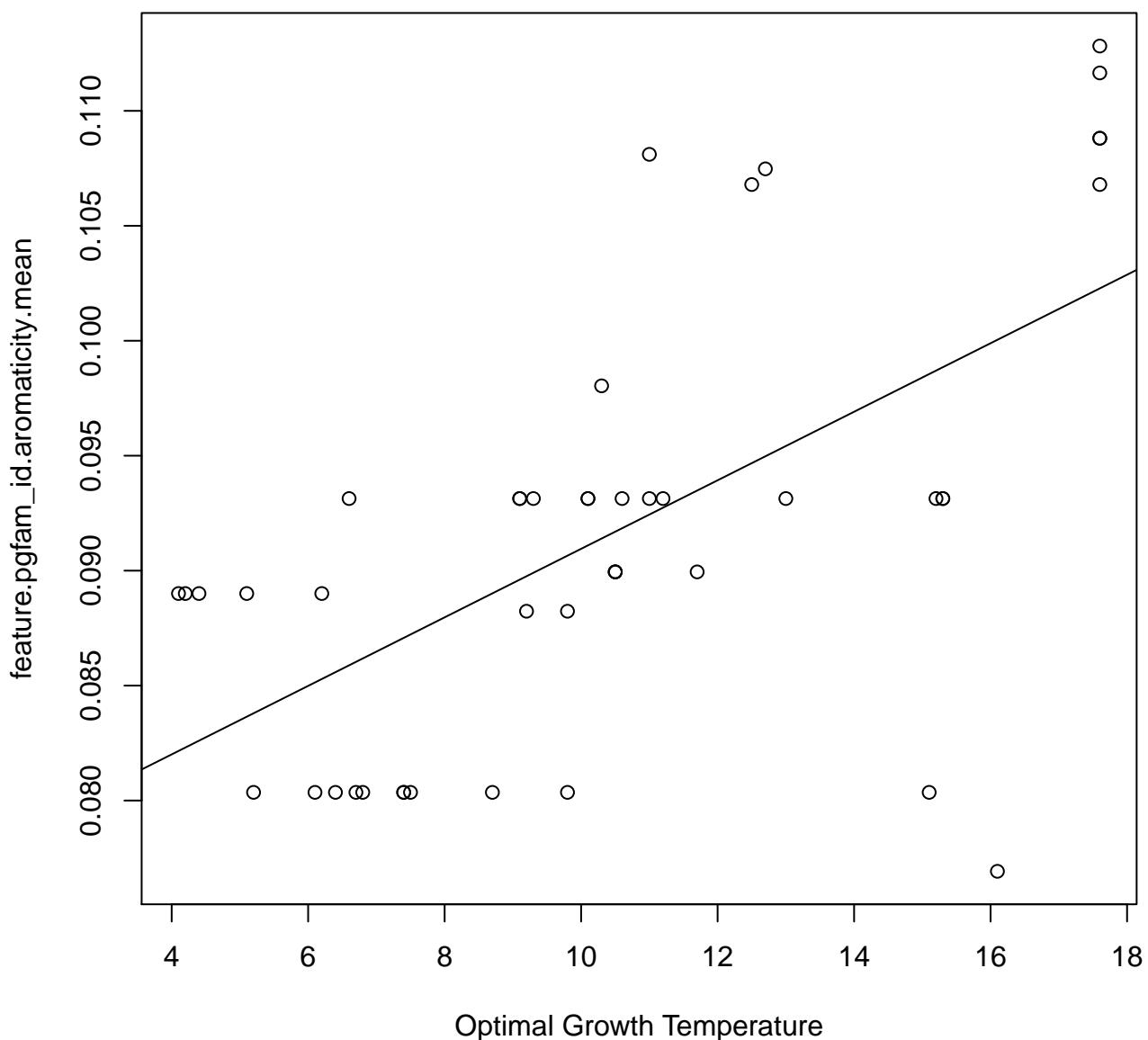
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PGF_05239055
hypothetical protein



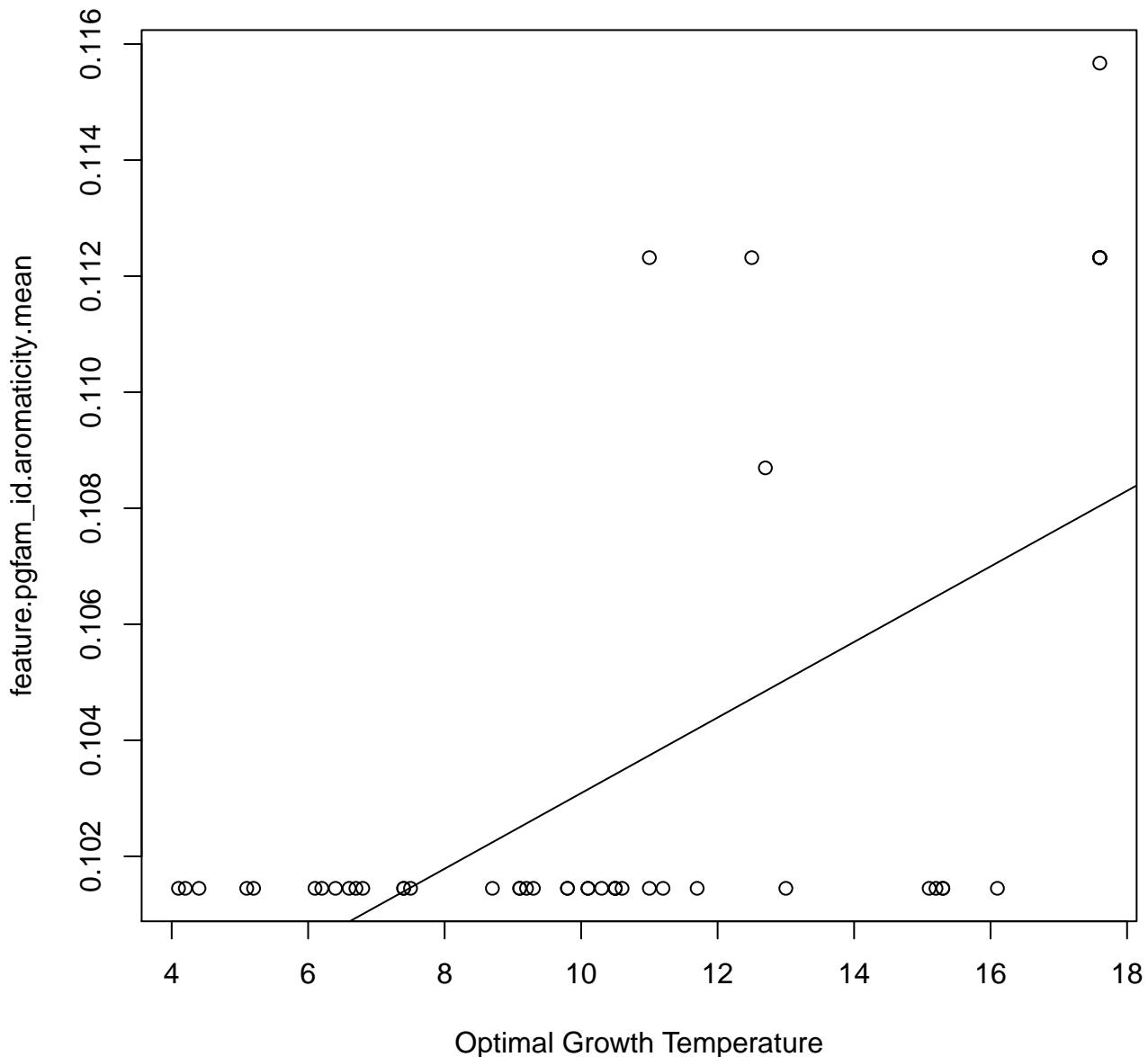
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PGF_00019974
Membrane protein YcjF



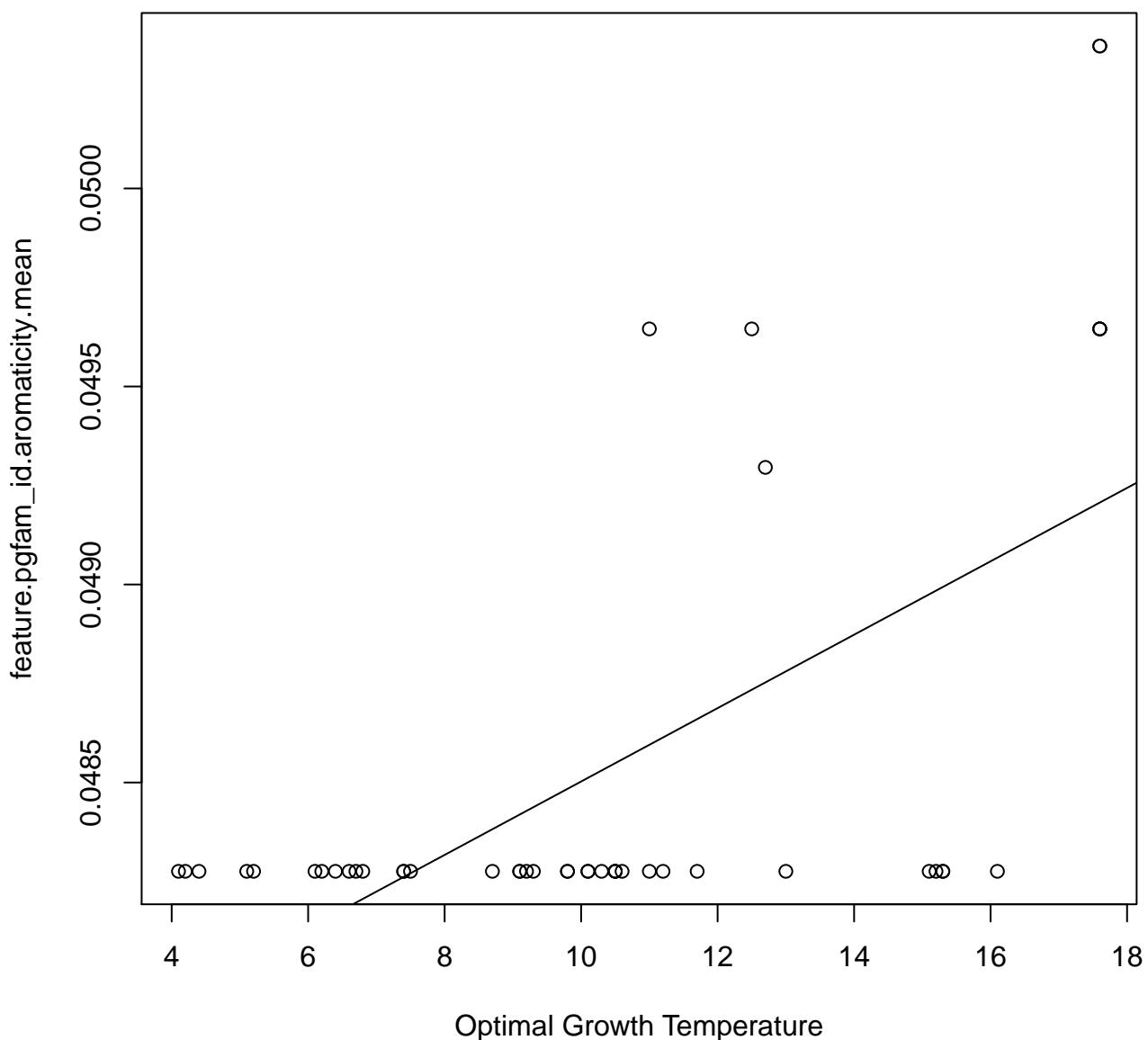
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Arylesterase precursor (EC 3.1.1.2)



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Diaminopimelate epimerase (EC 5.1.1.7)



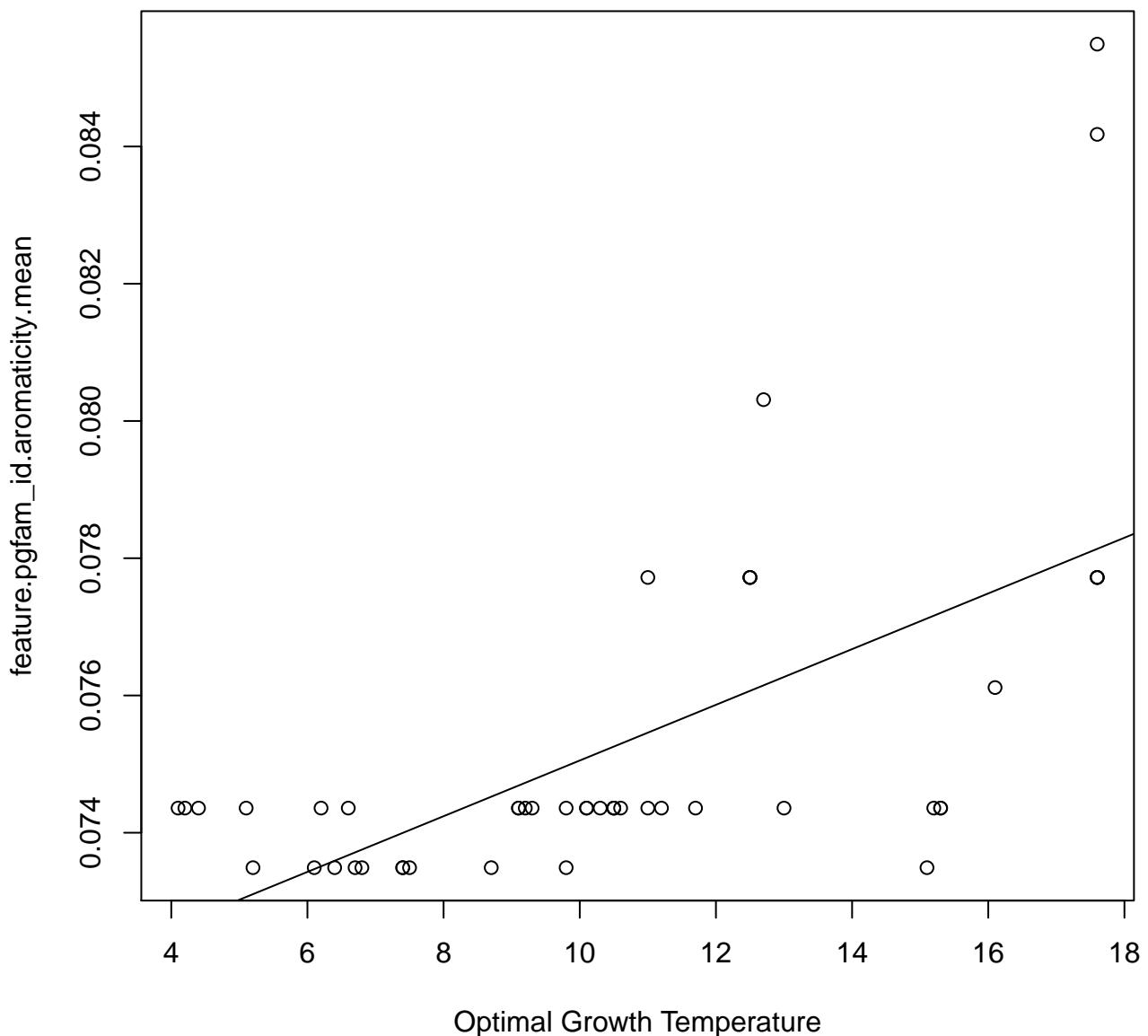
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Translation elongation factor Ts



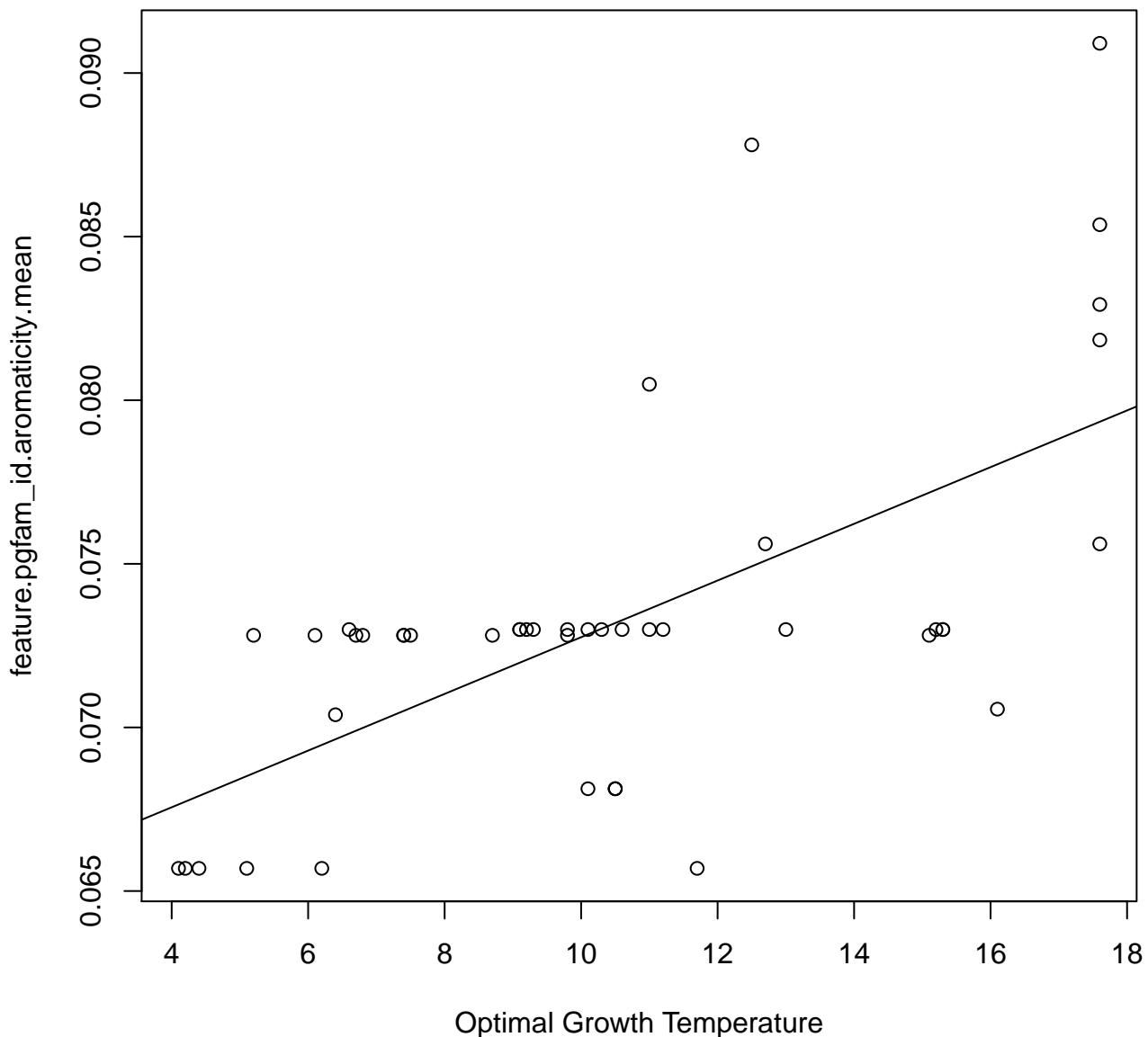
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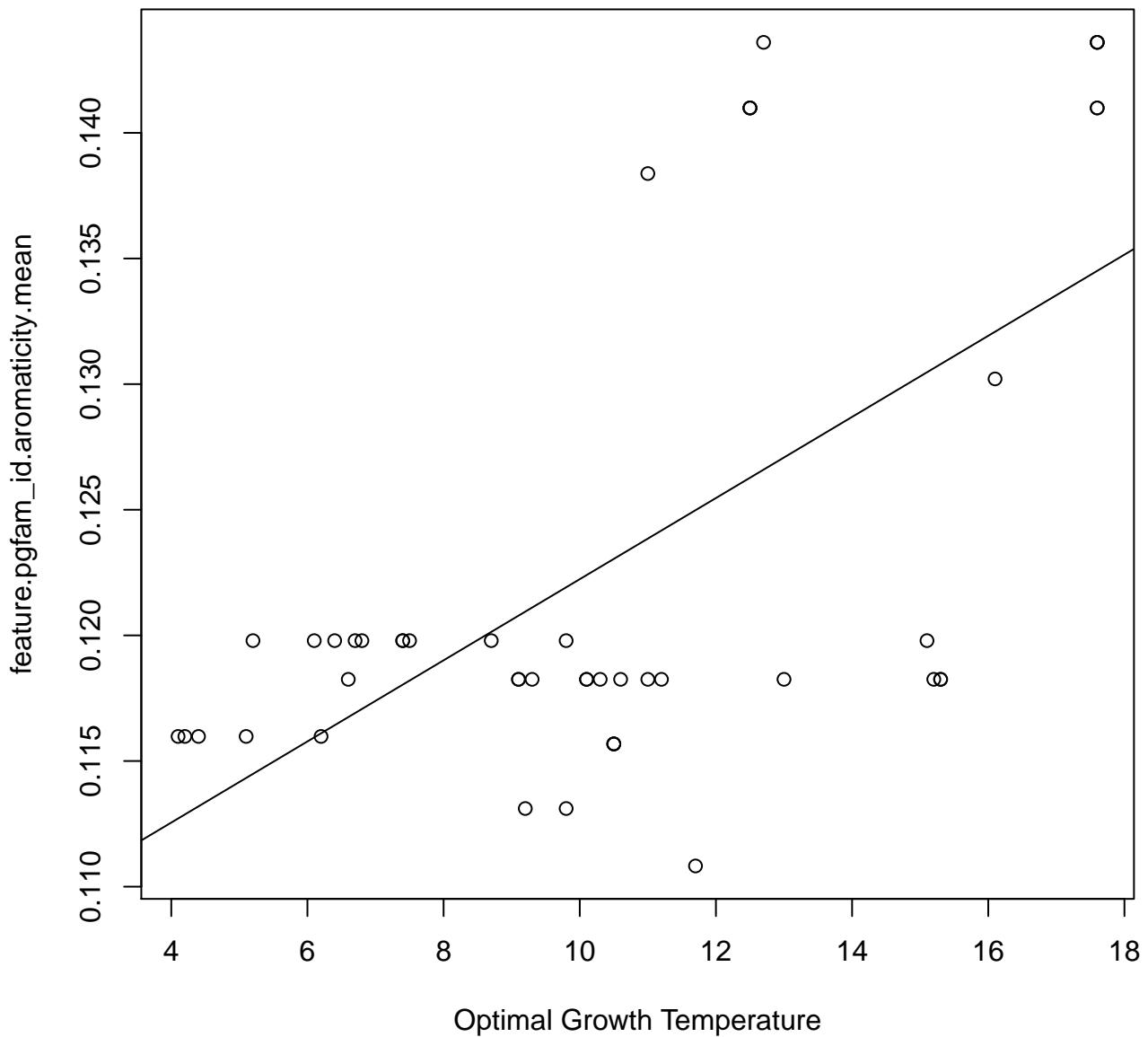
23S rRNA (adenine(2503)-C(2))-methyltransferase @ tRNA (adenine(37)-C(2))-methyltransferase (EC 2.1.1.192)



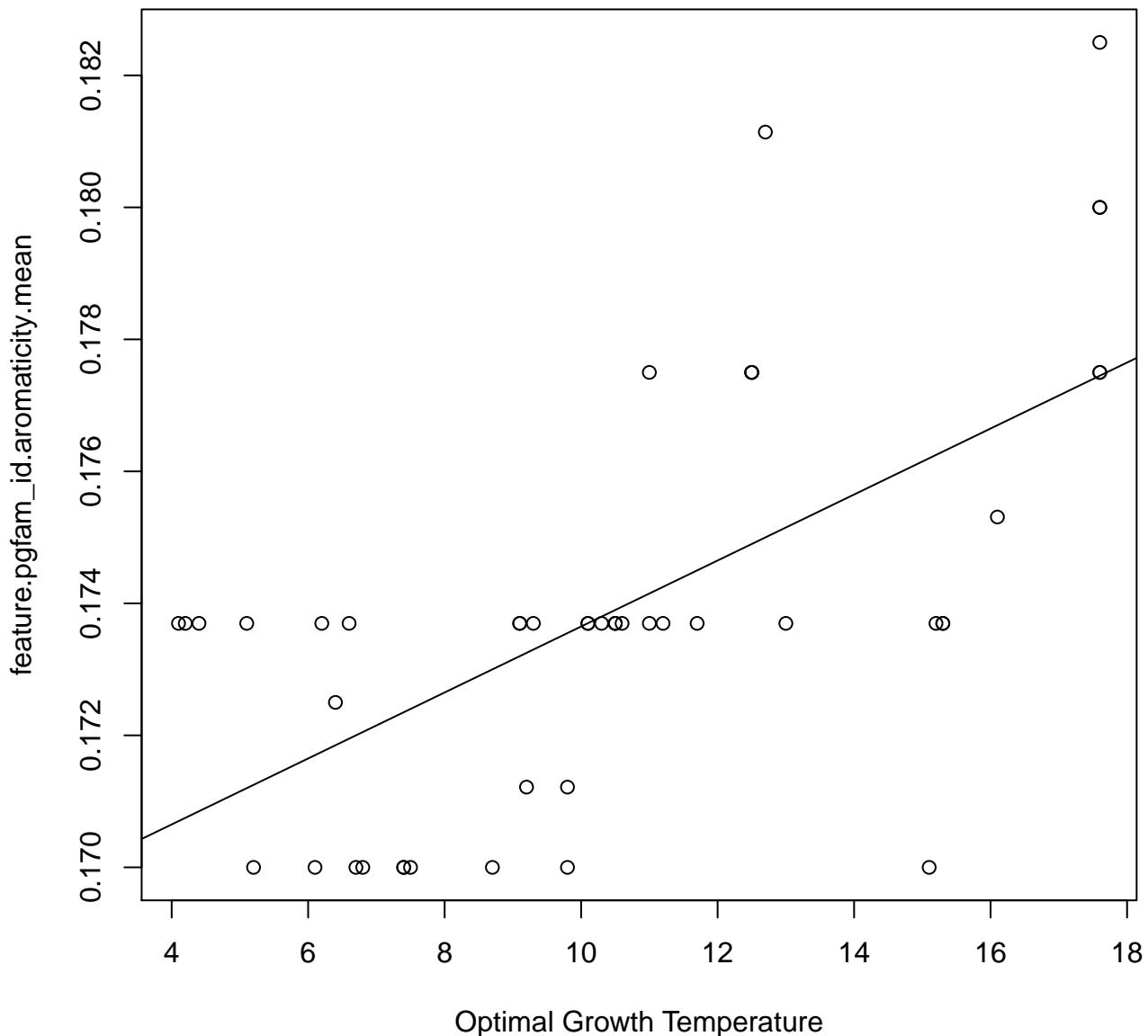
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Molybdopterin molybdenumtransferase (EC 2.10.1.1)



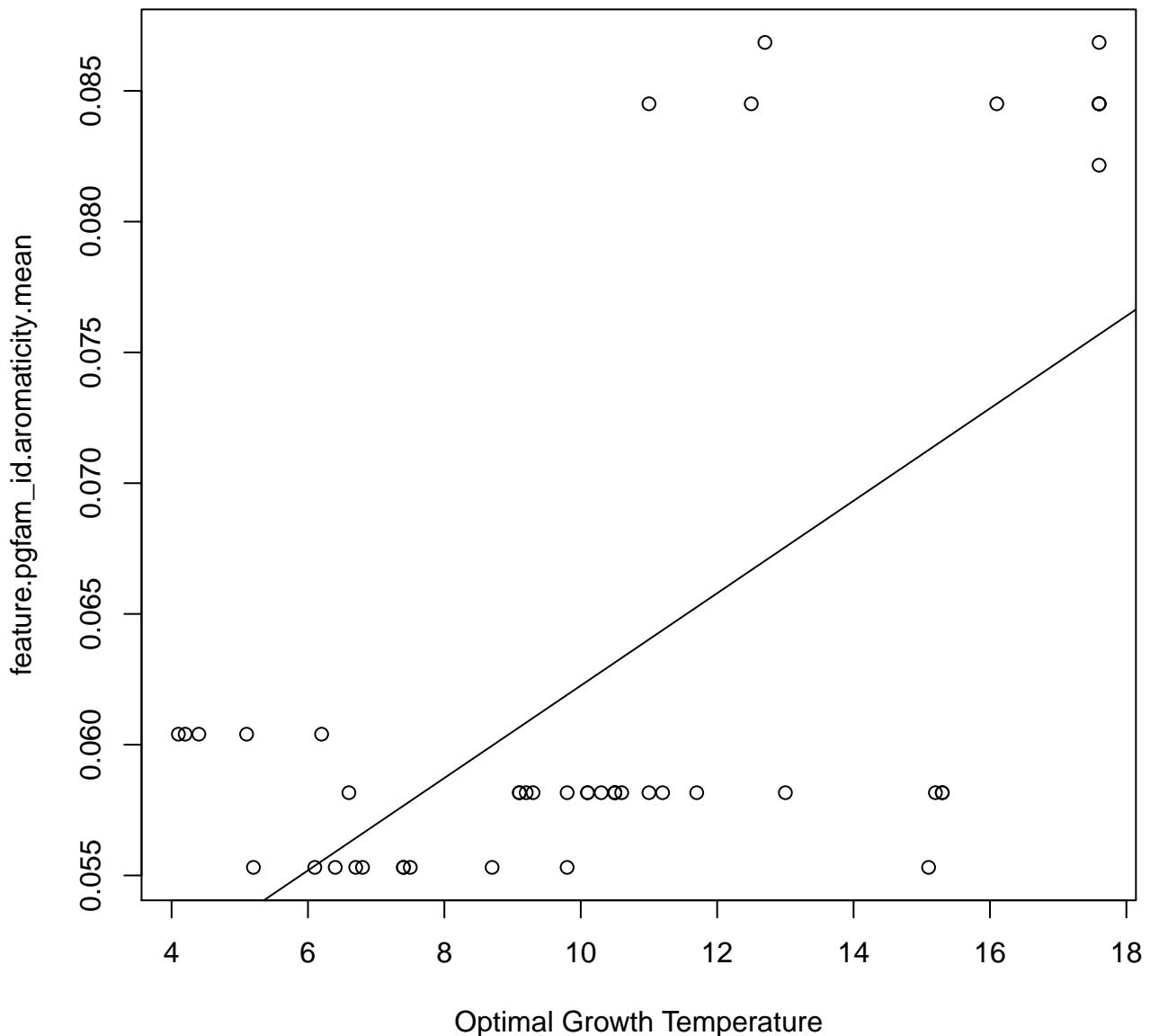
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PGF_00131429
LSU ribosomal protein L16p arginine hydroxylase



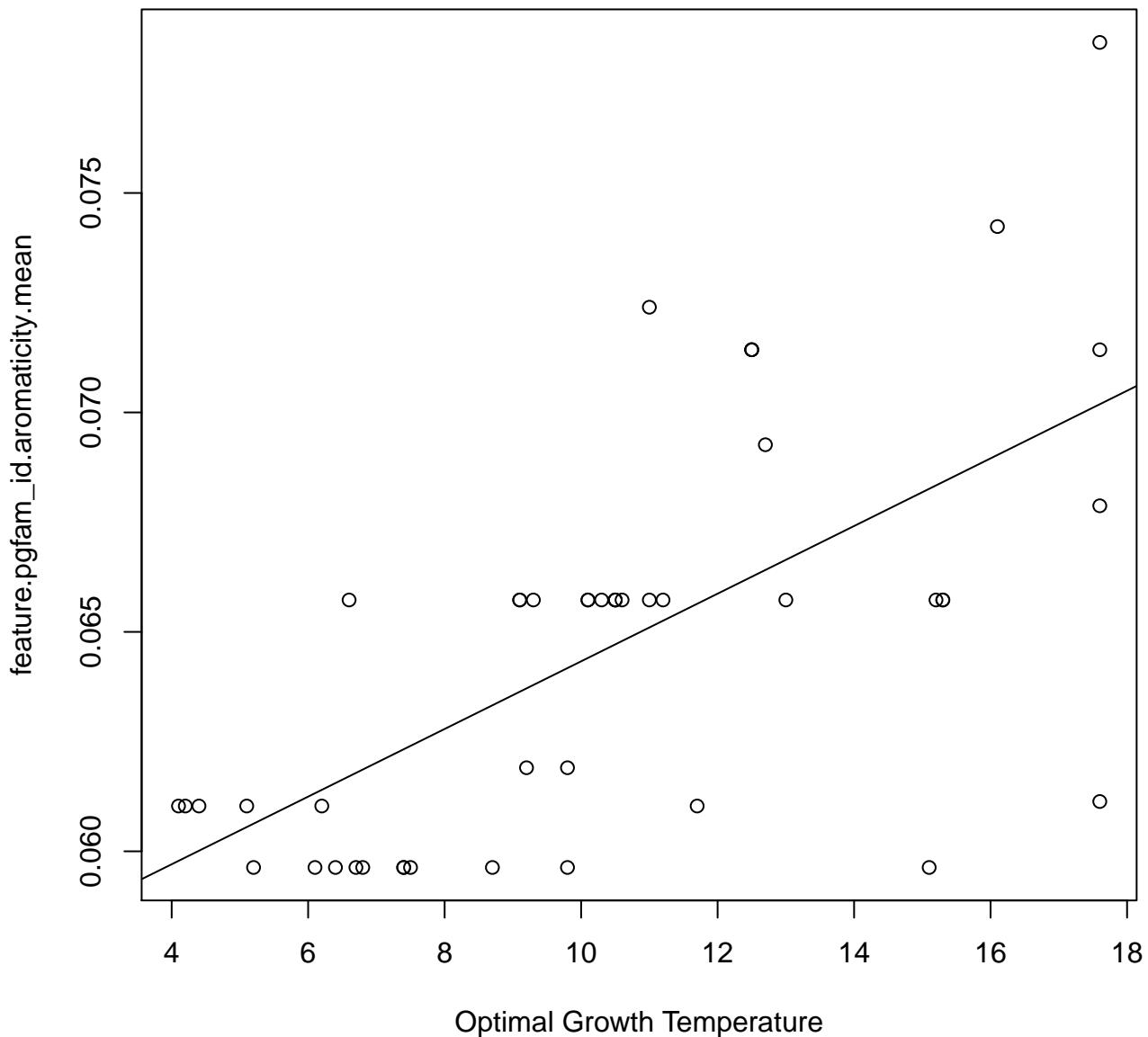
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Na(+)–translocating NADH–quinone reductase subunit B (EC 1.6.5.8)



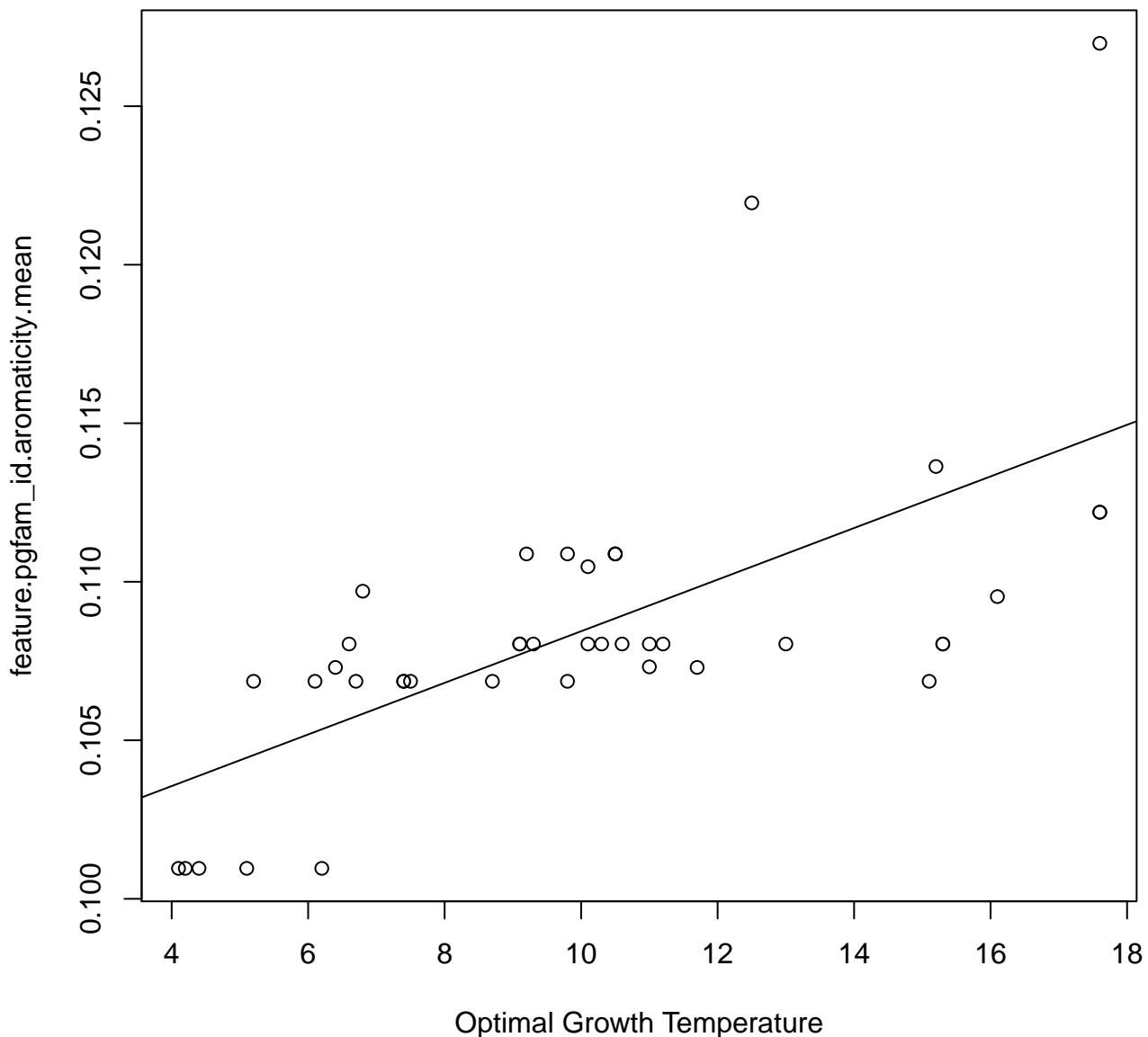
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3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)



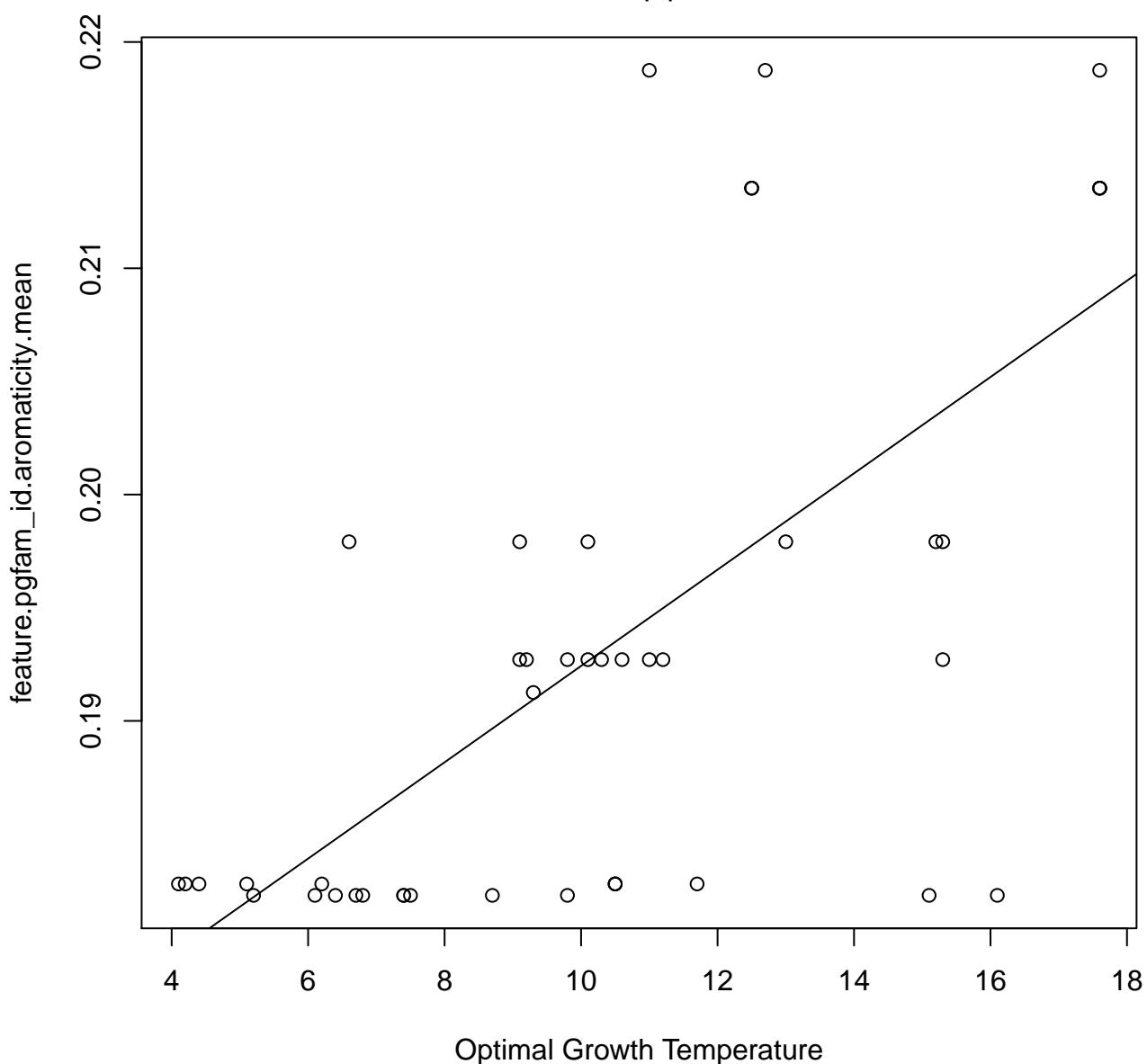
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GTP-binding protein EngB



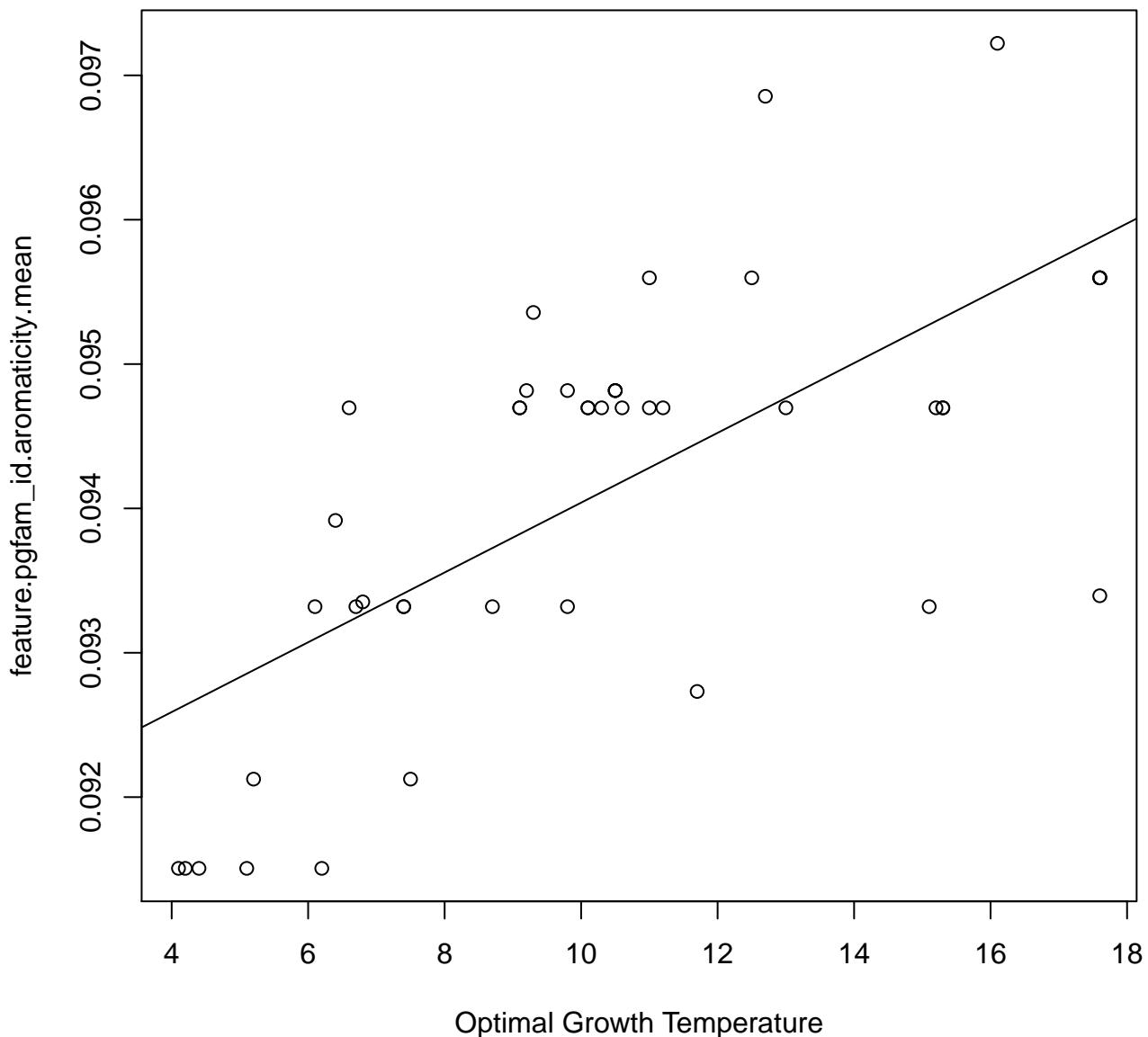
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PGF_07370053
RNA polymerase sigma-70 factor



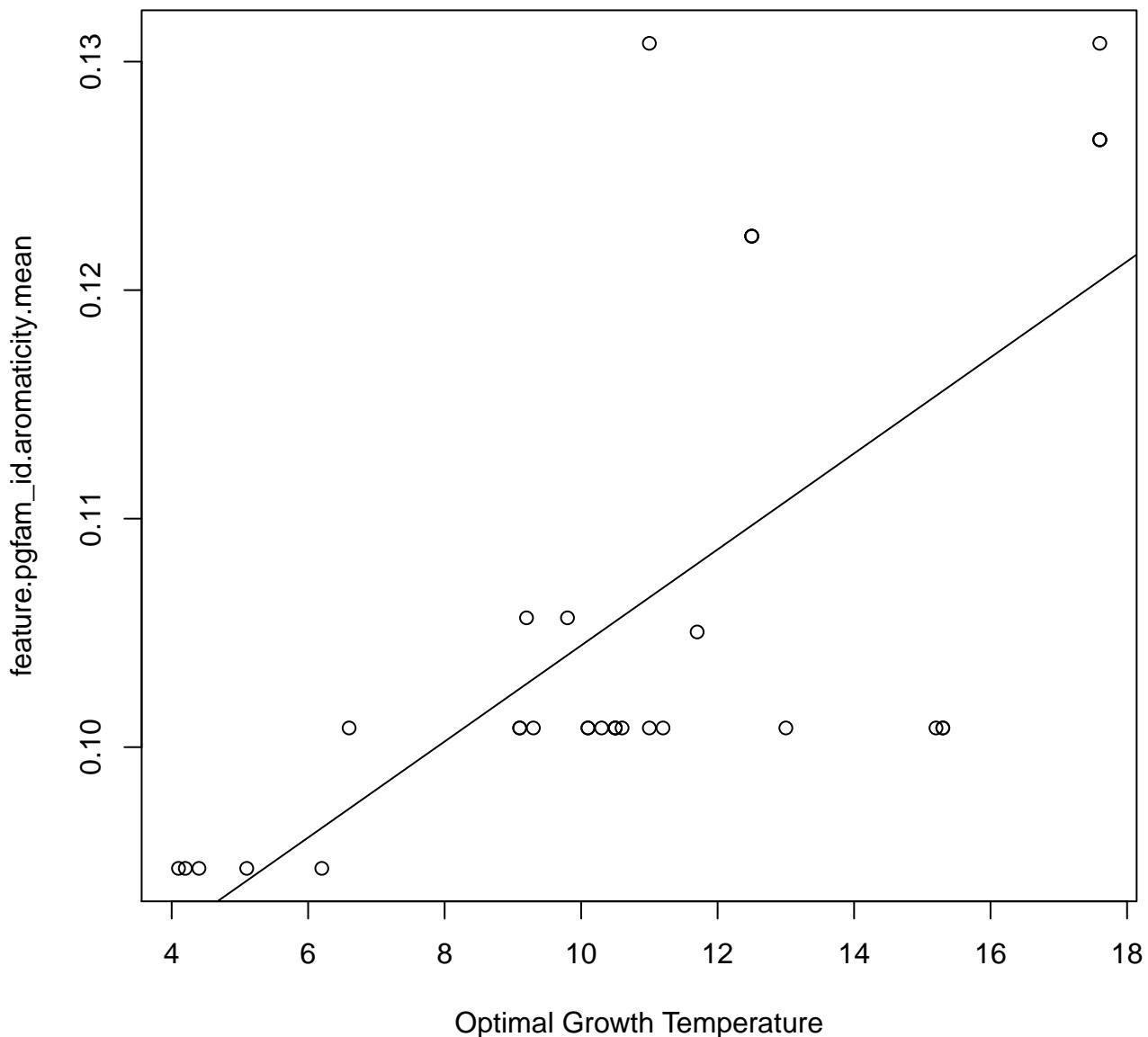
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PGF_00706032
FIG139438: lipoprotein B



feature.pgfam_id.aromaticity.mean
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Phosphoenolpyruvate synthase (EC 2.7.9.2)



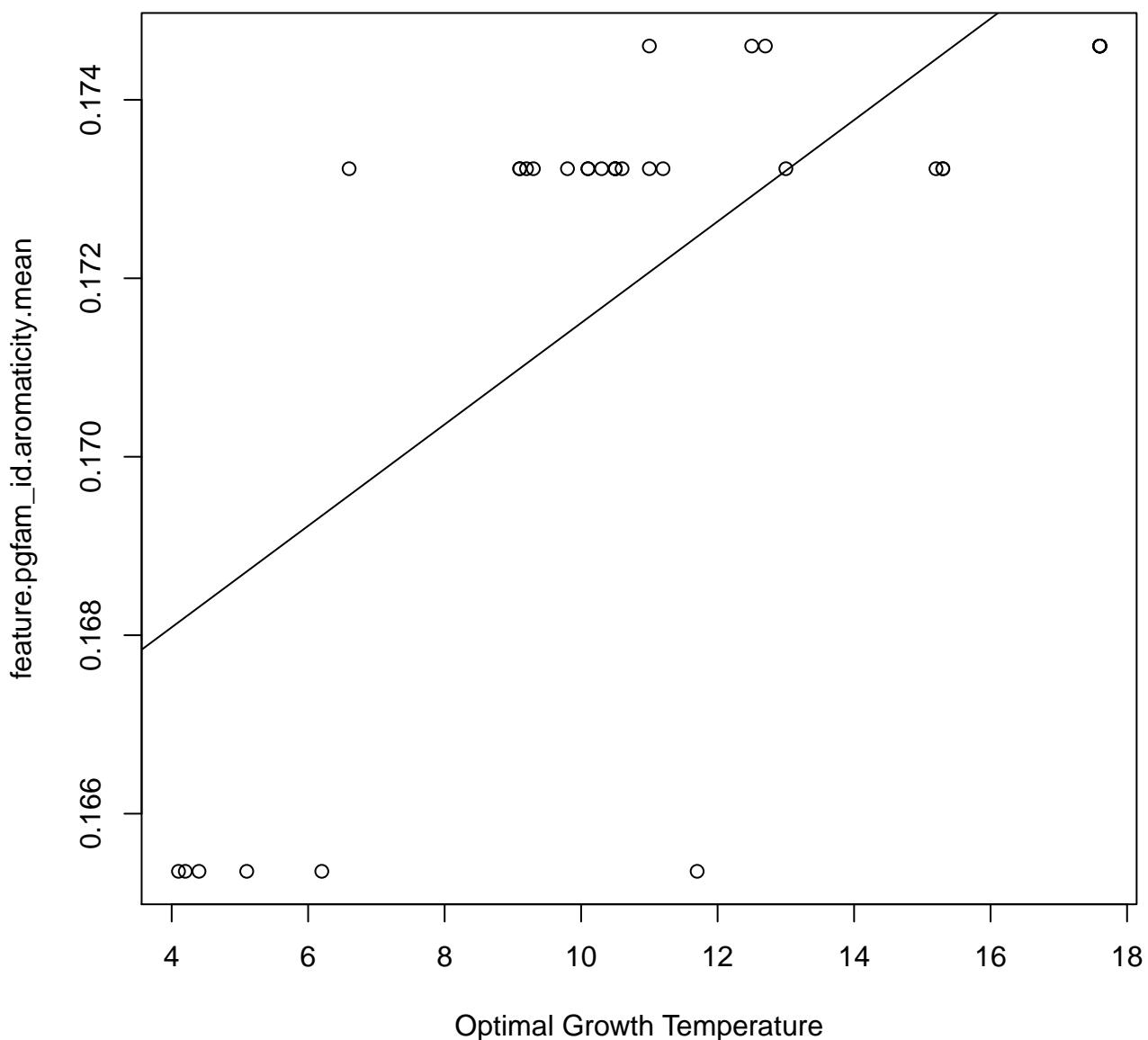
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PGF_00067426
ZIP zinc transporter family protein



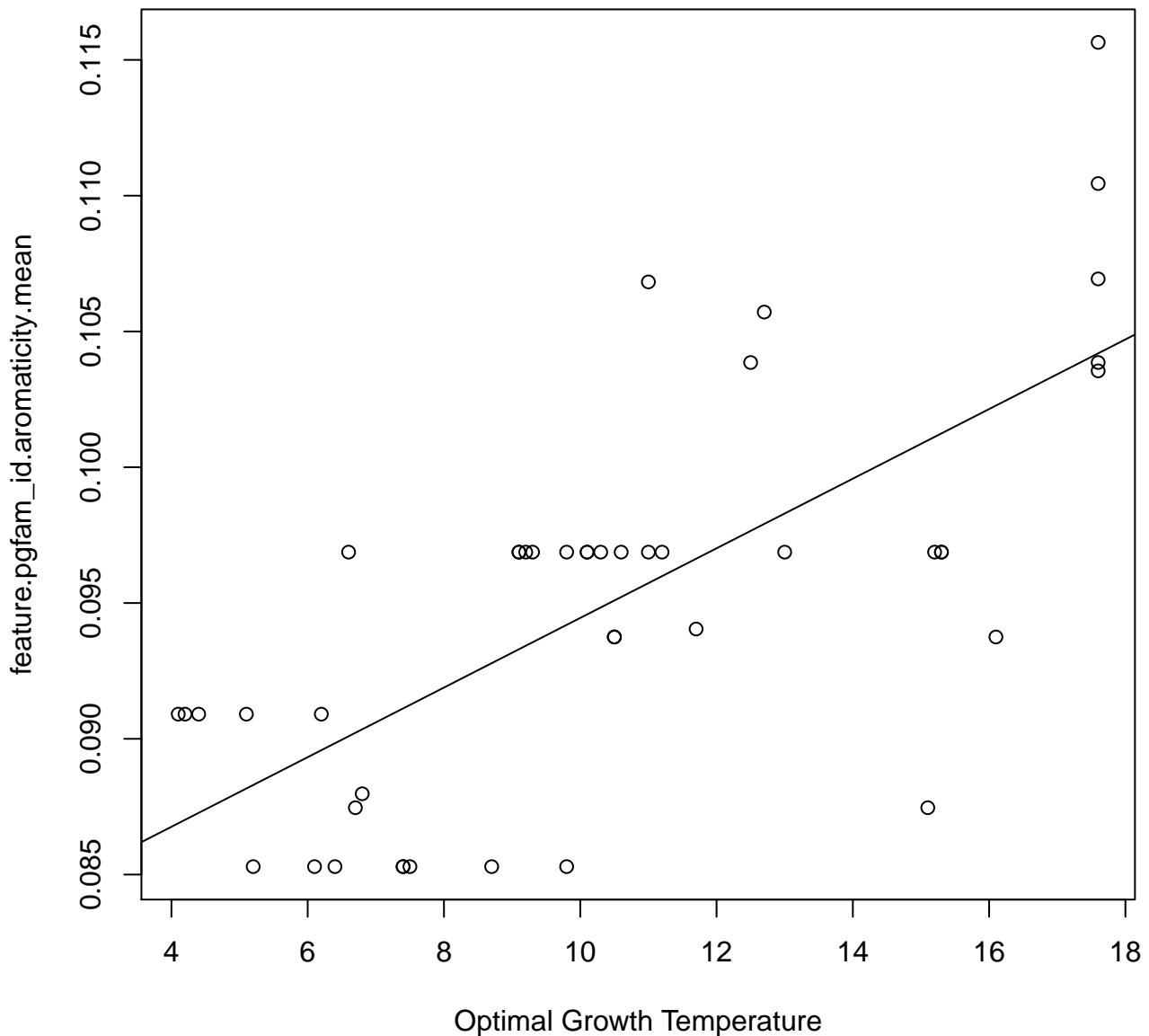
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PGF_03072985

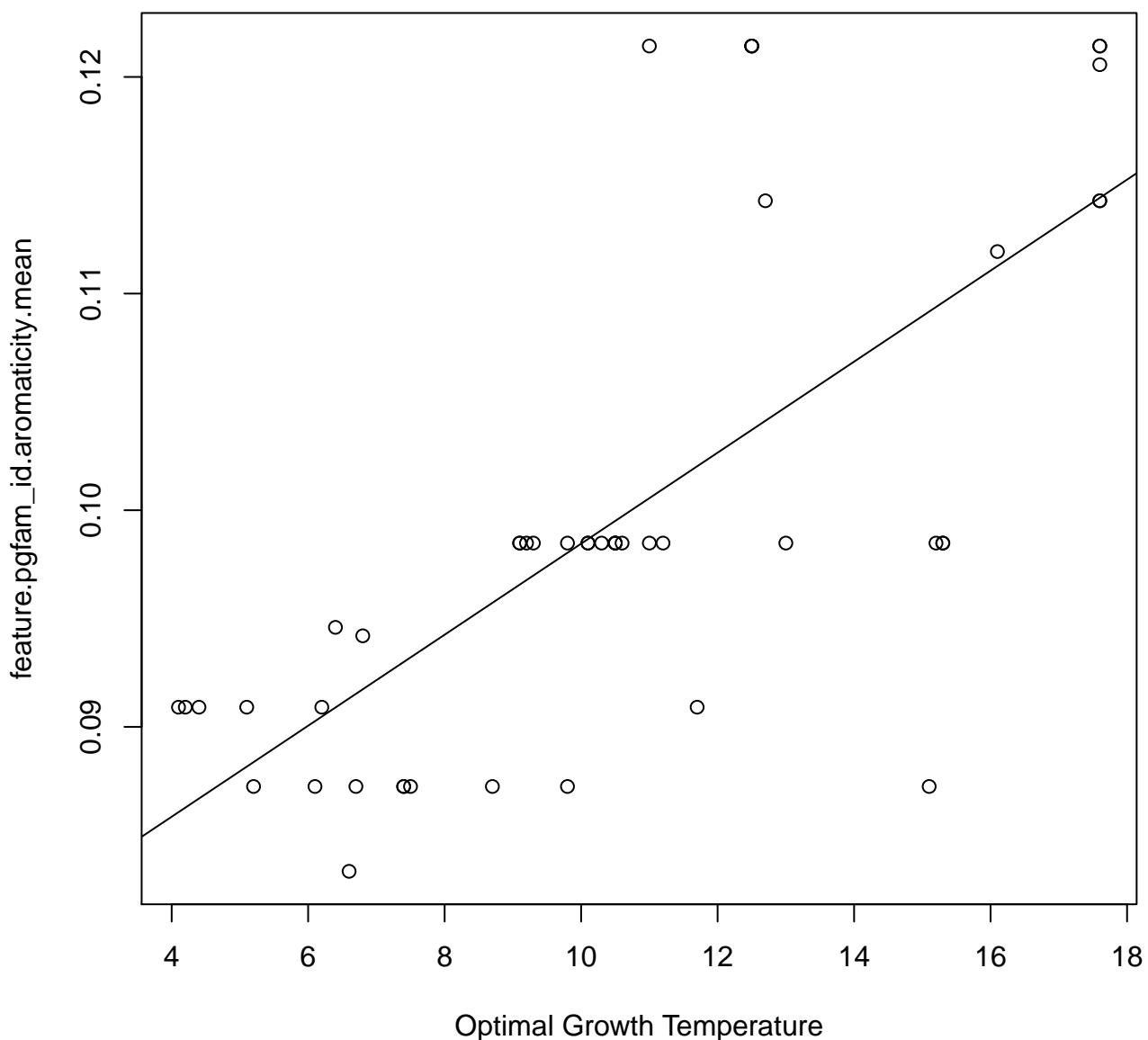
hypothetical protein



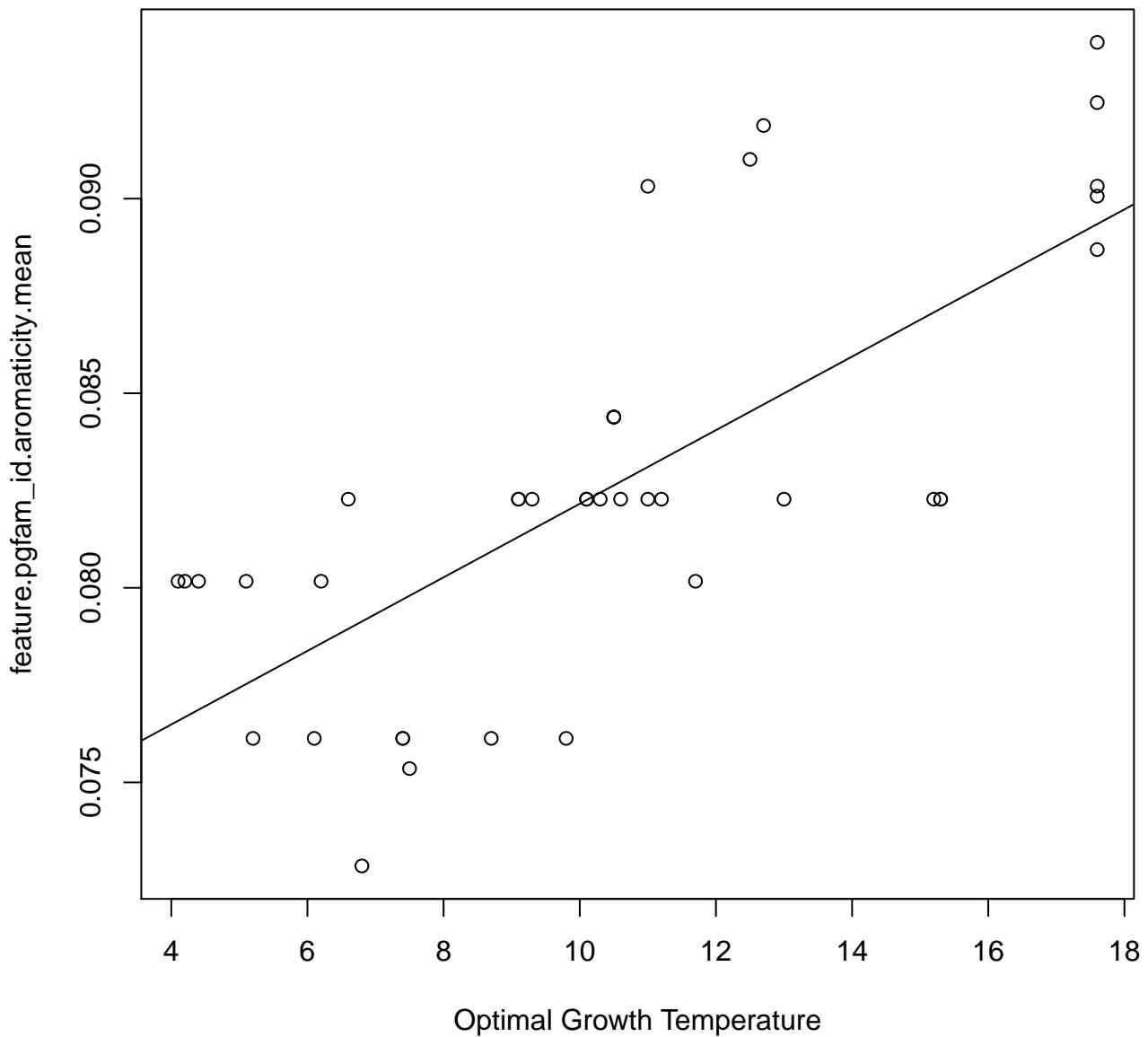
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PGF_00052053
Sigma factor RpoE negative regulatory protein RseB precursor



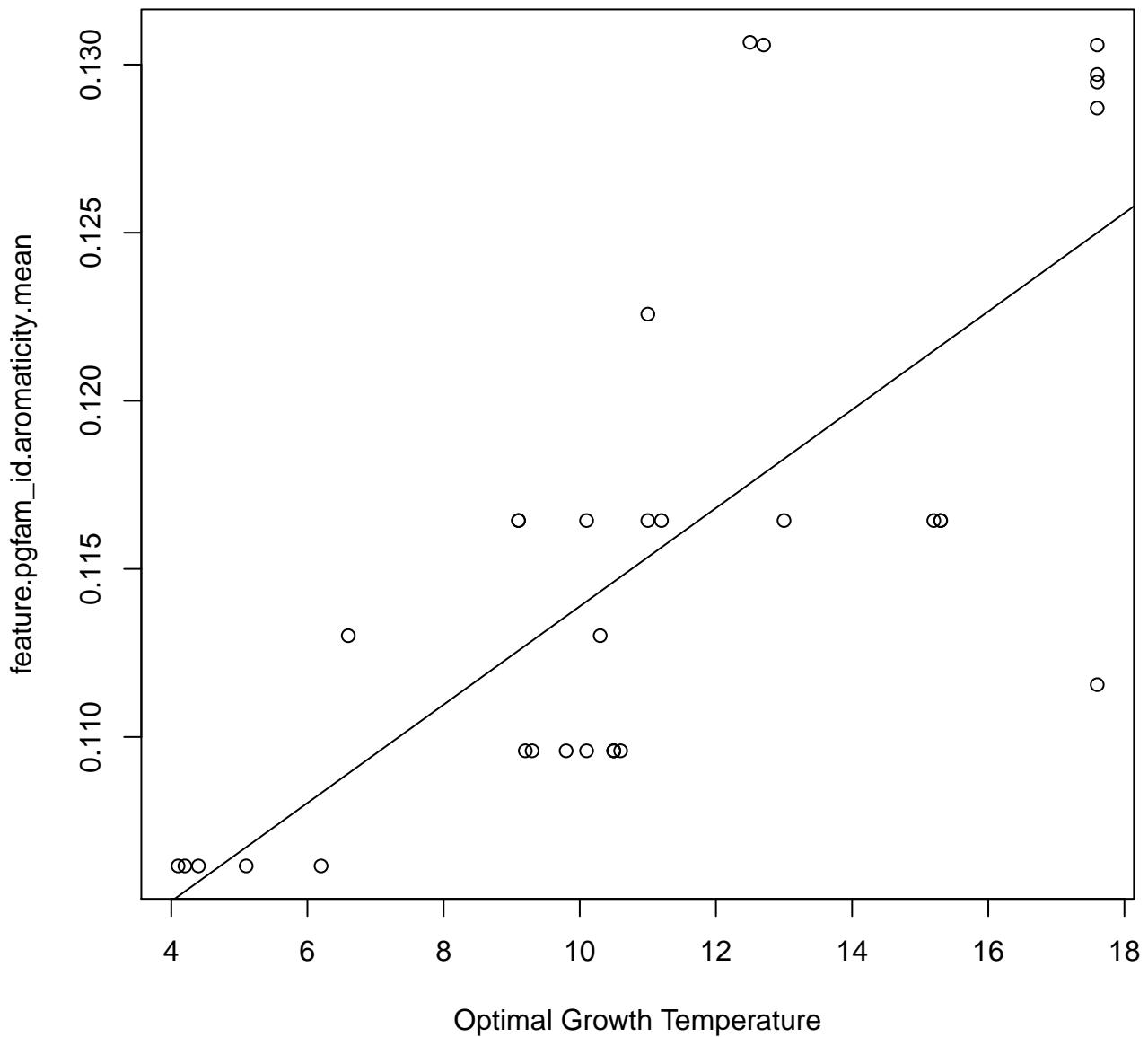
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PGF_00422096
DNA-binding protein, CopG family



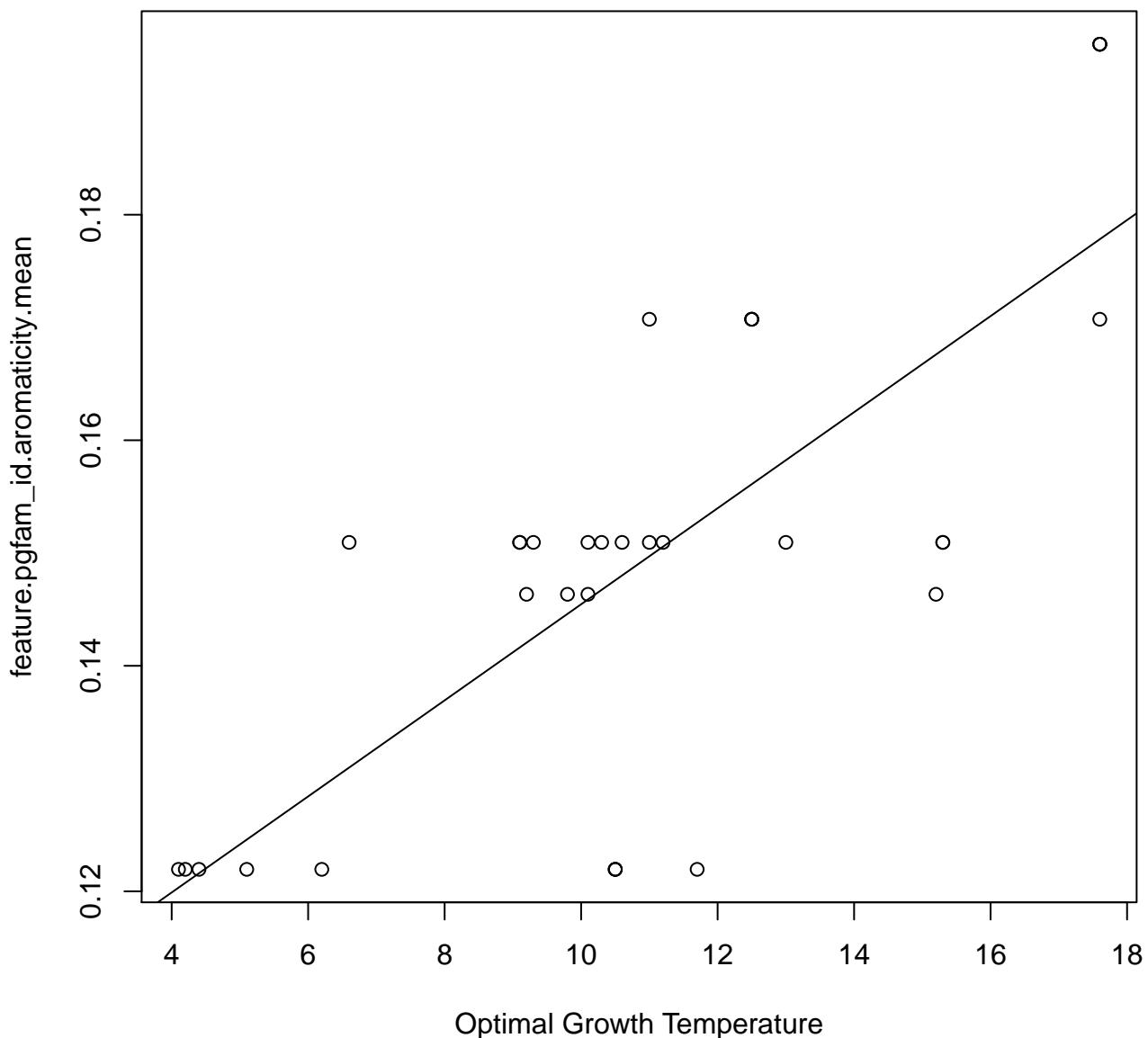
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PGF_06982509
Efflux transport system, outer membrane factor (OMF) lipoprotein



feature.pgfam_id.aromaticity.mean
PGF_00065716
Uncharacterized protein conserved in bacteria, NMA0228-like



feature.pgfam_id.aromaticity.mean
PGF_01336904
nr0040.cl00013



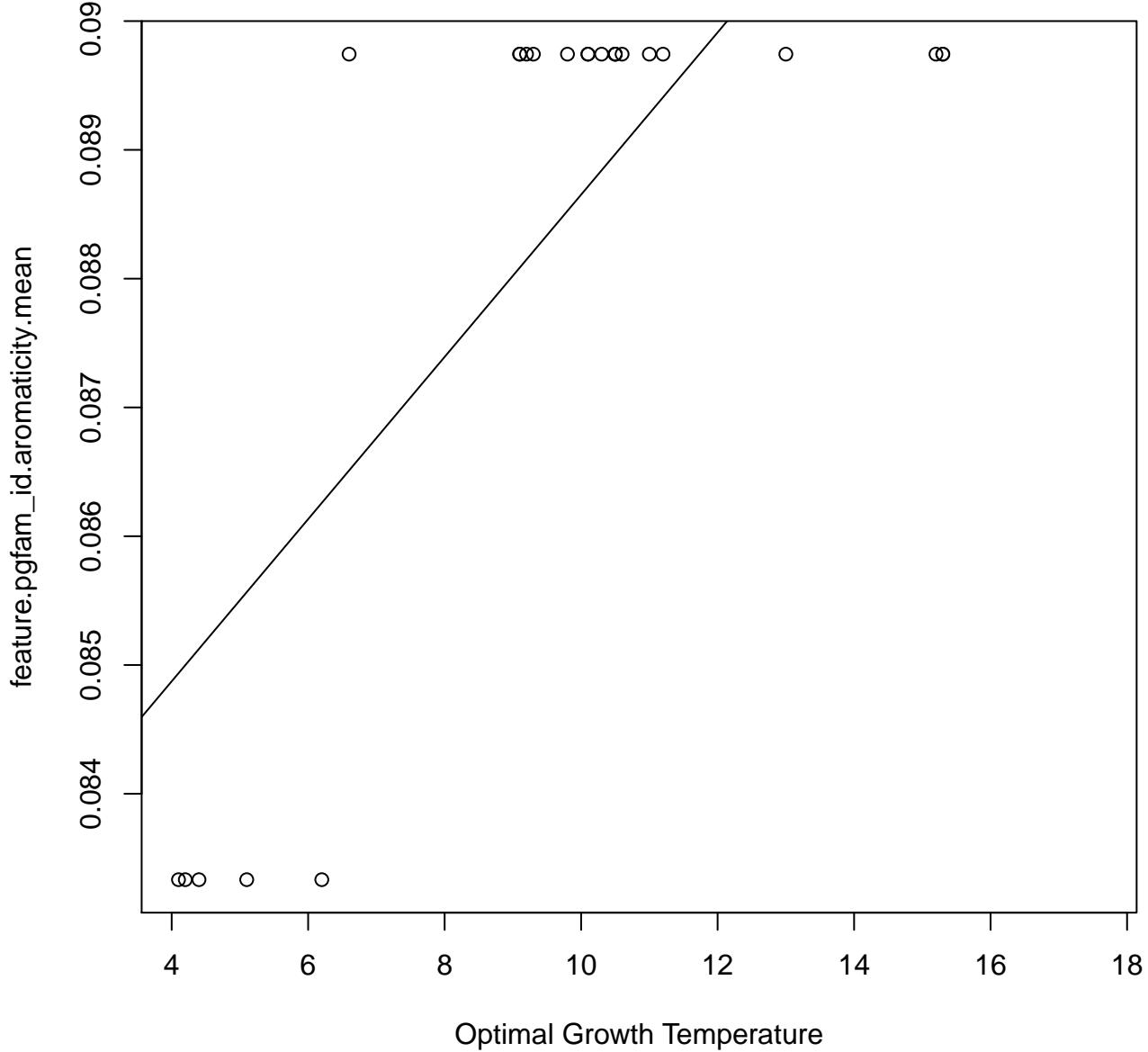
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PGF_04213500

hypothetical protein

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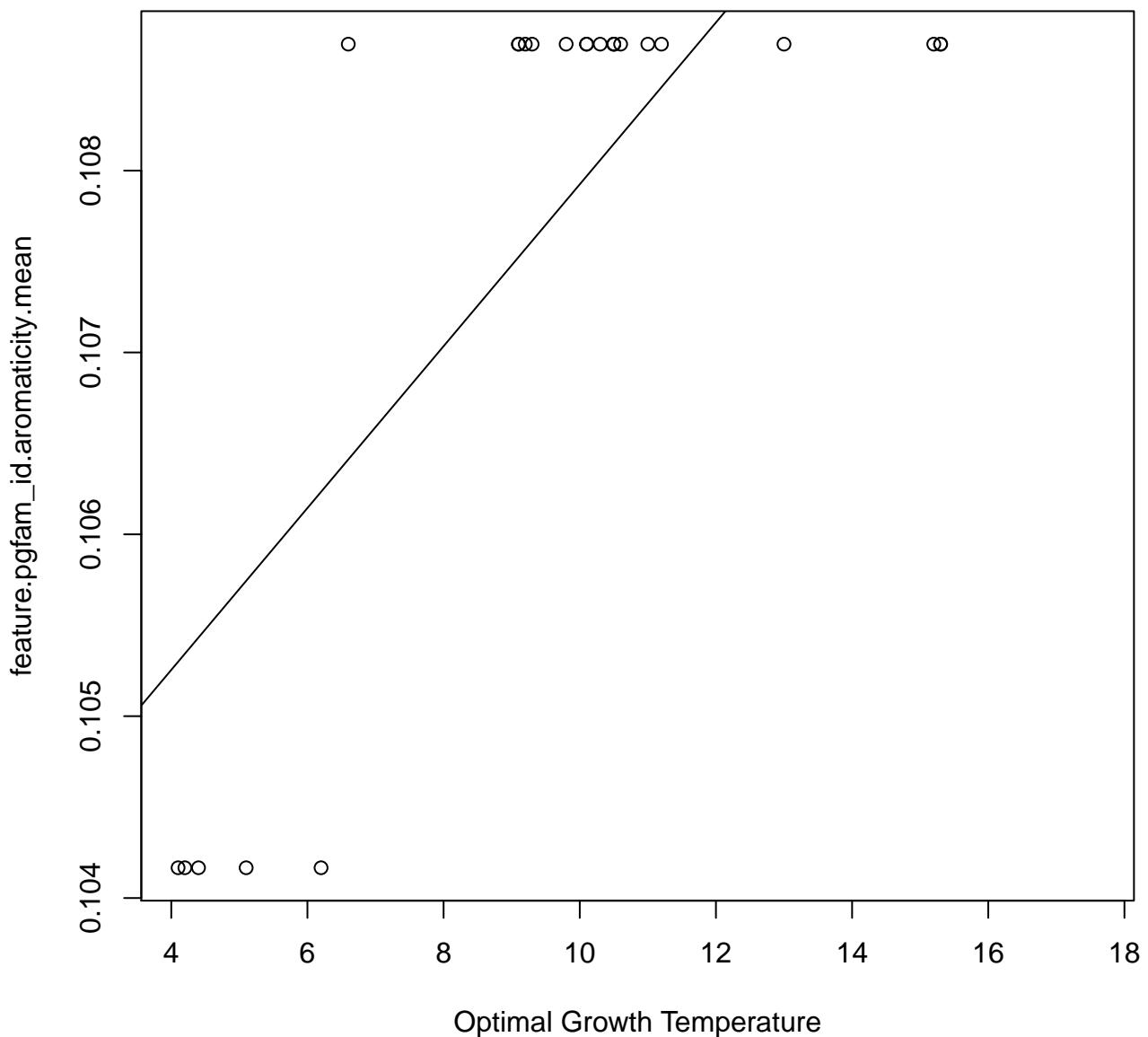
Optimal Growth Temperature



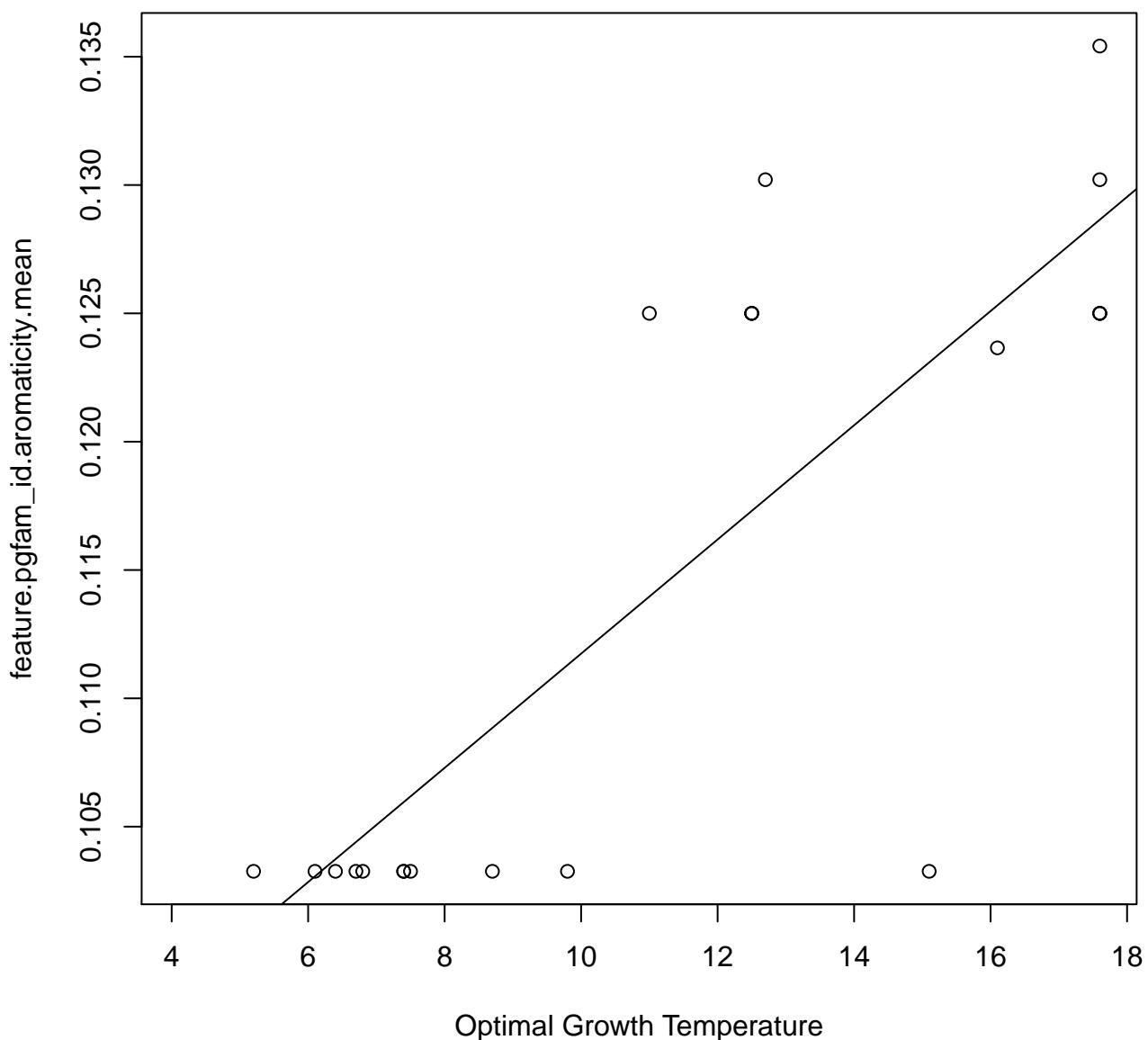
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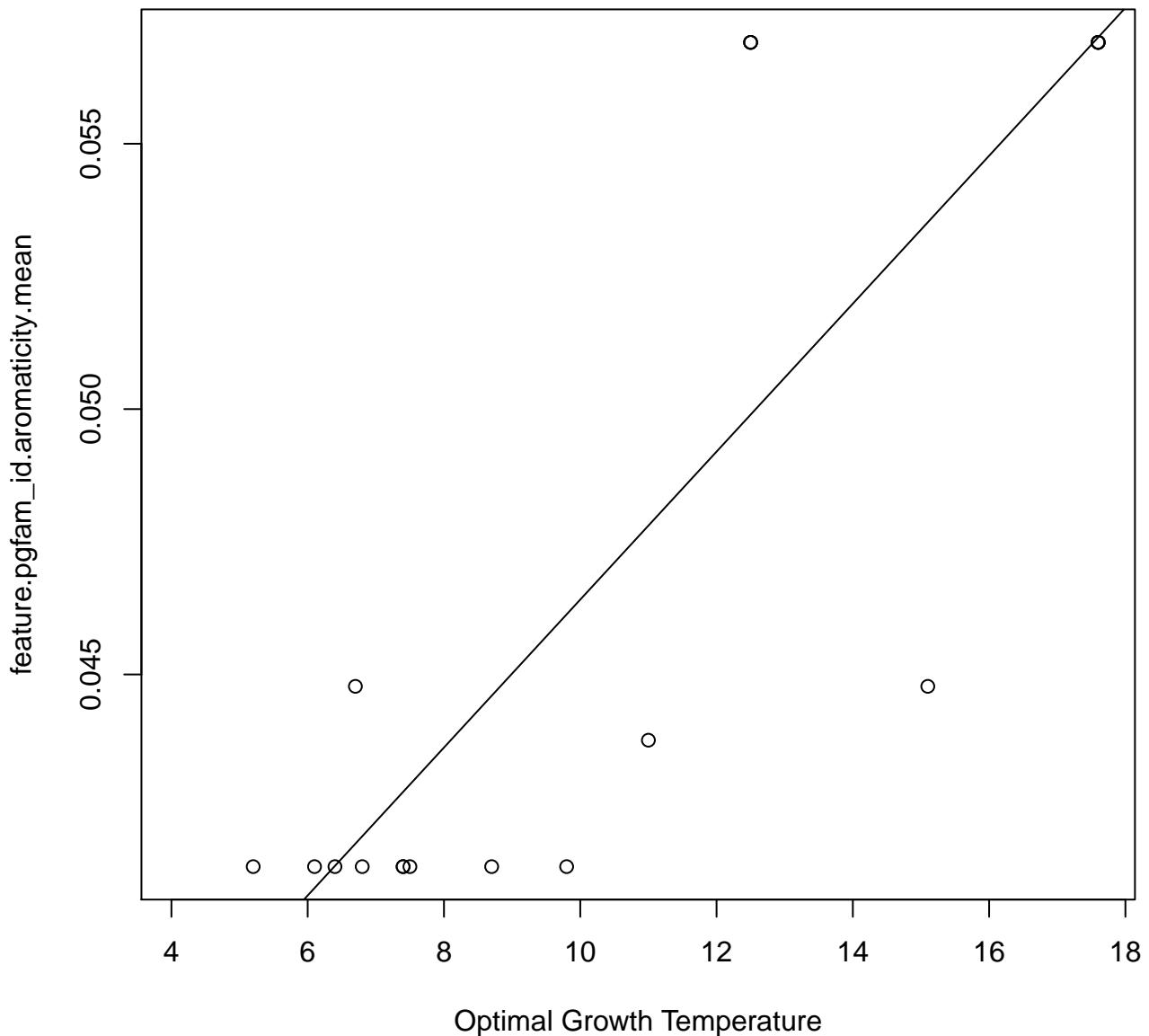
hypothetical protein



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PGF_00408280
putative lipoprotein



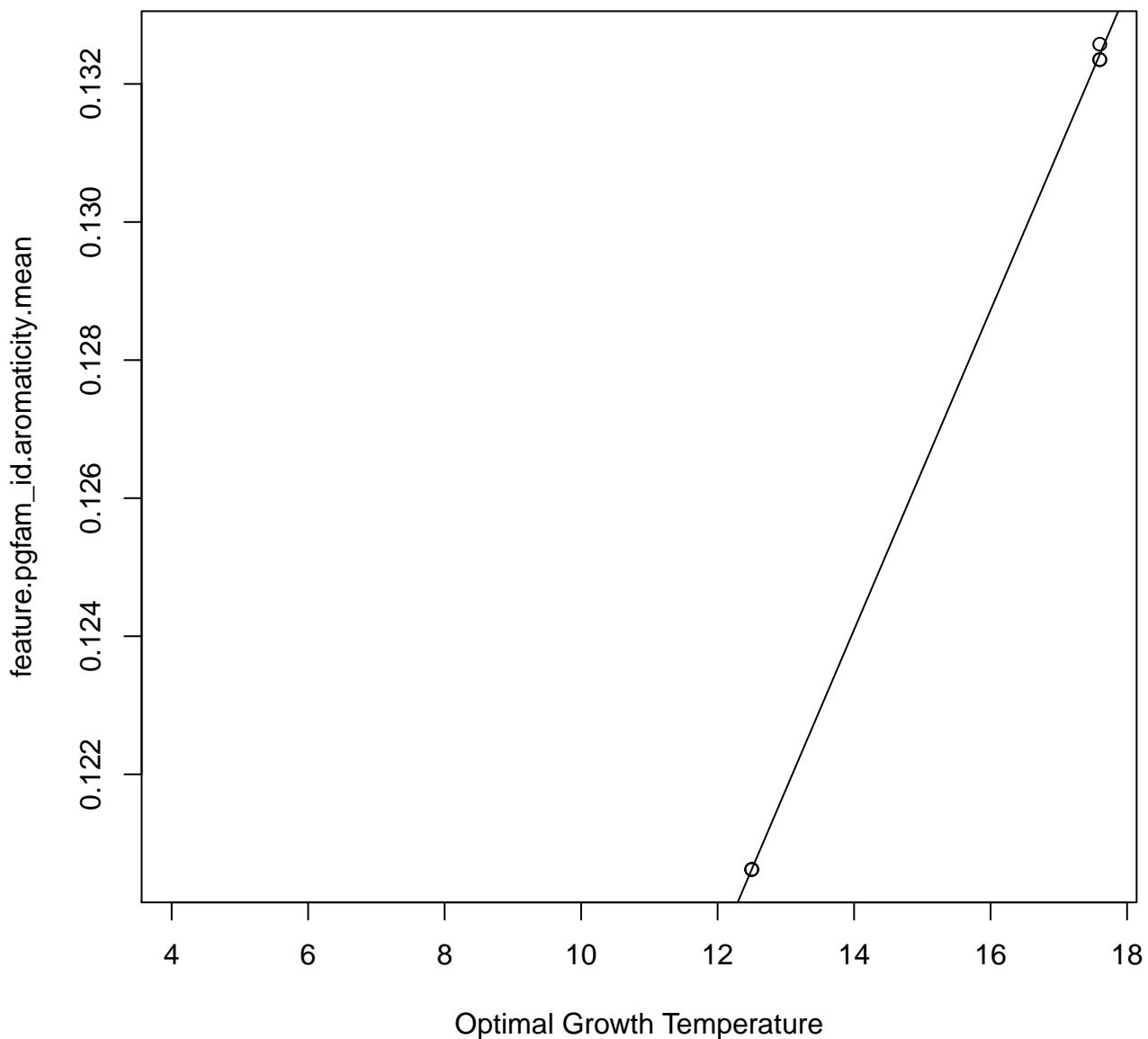
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PGF_00407225
putative granule-associated protein



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PGF_01336907

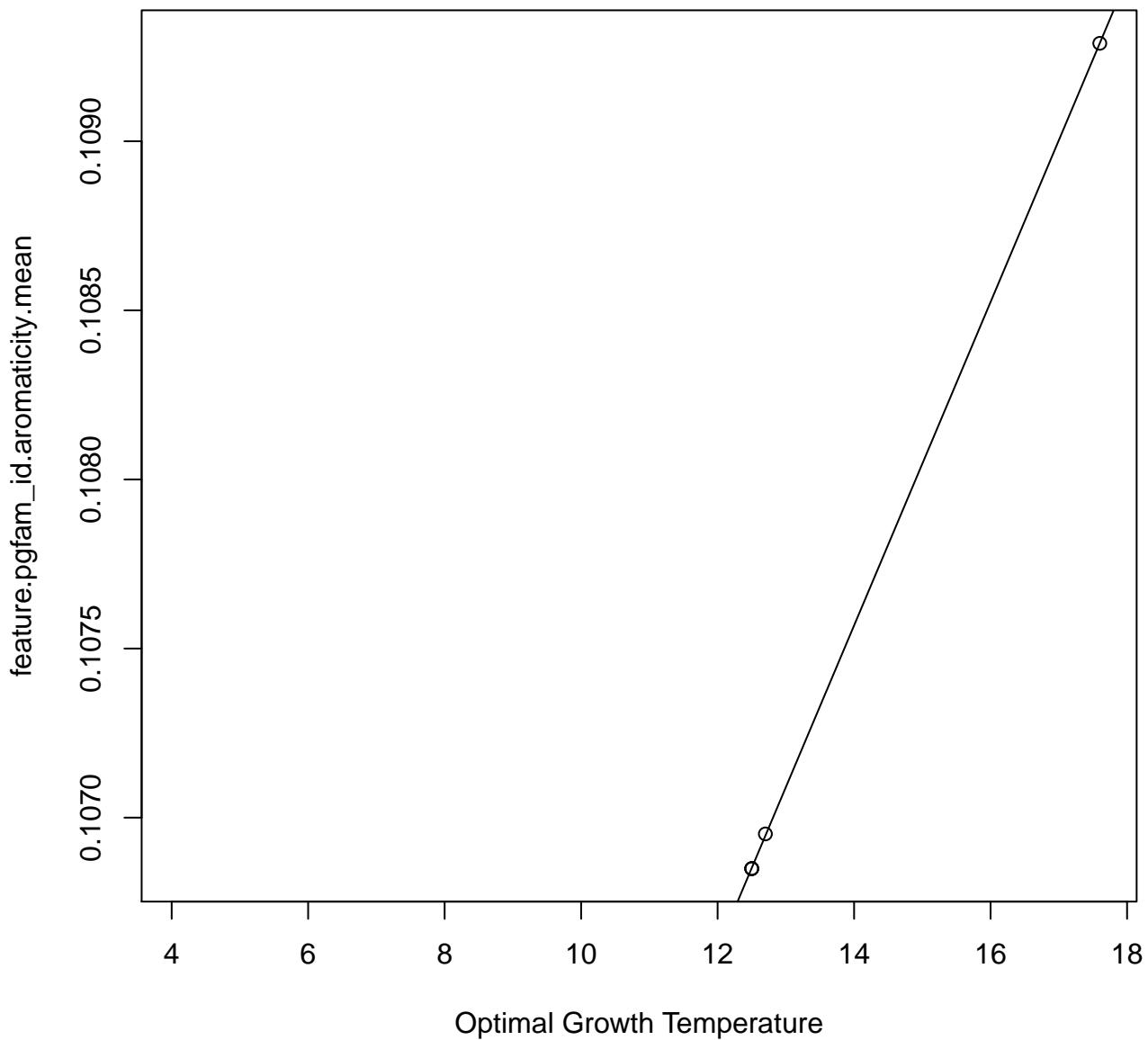
hypothetical protein



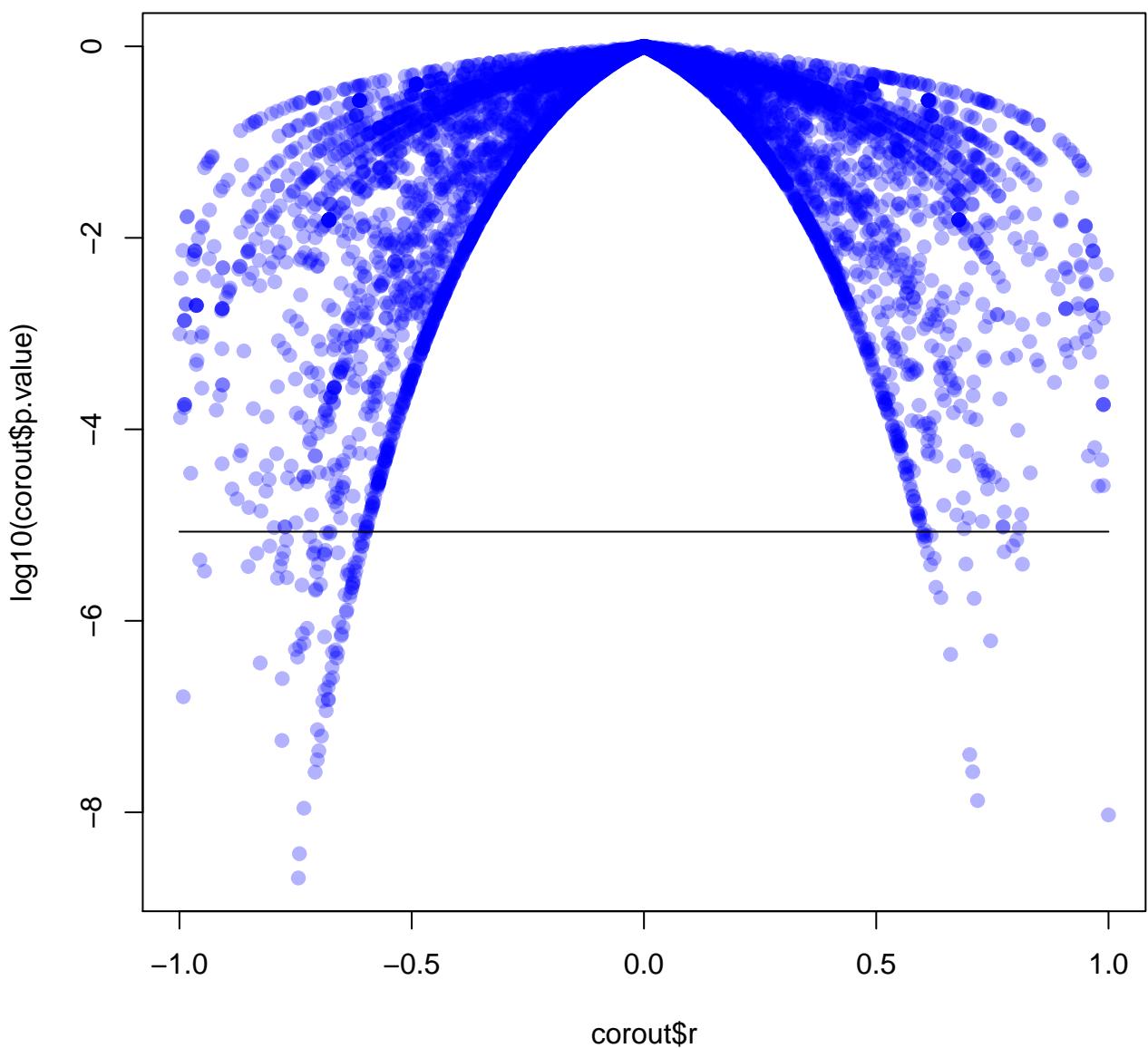
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PGF_00275103

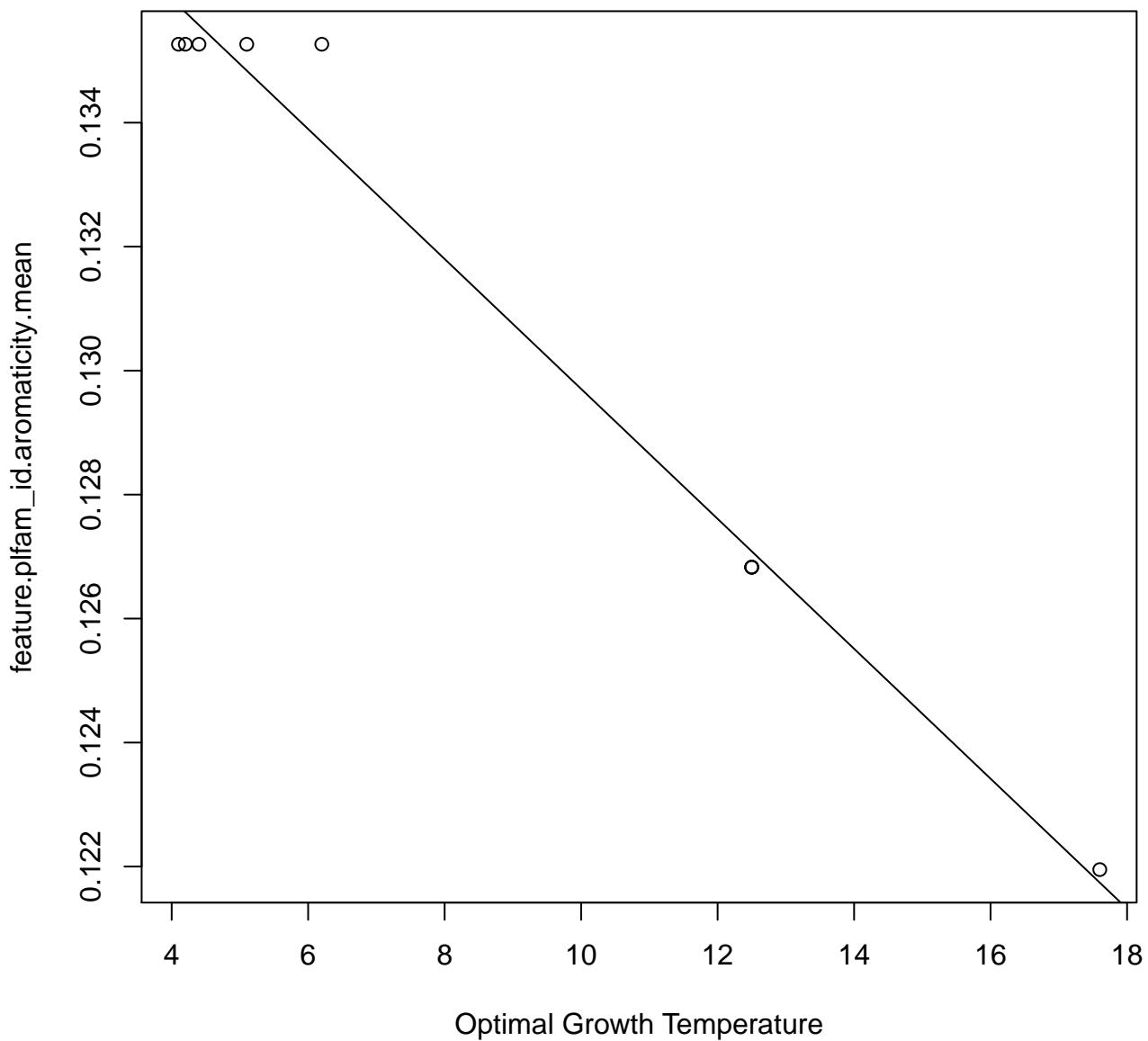
hypothetical protein



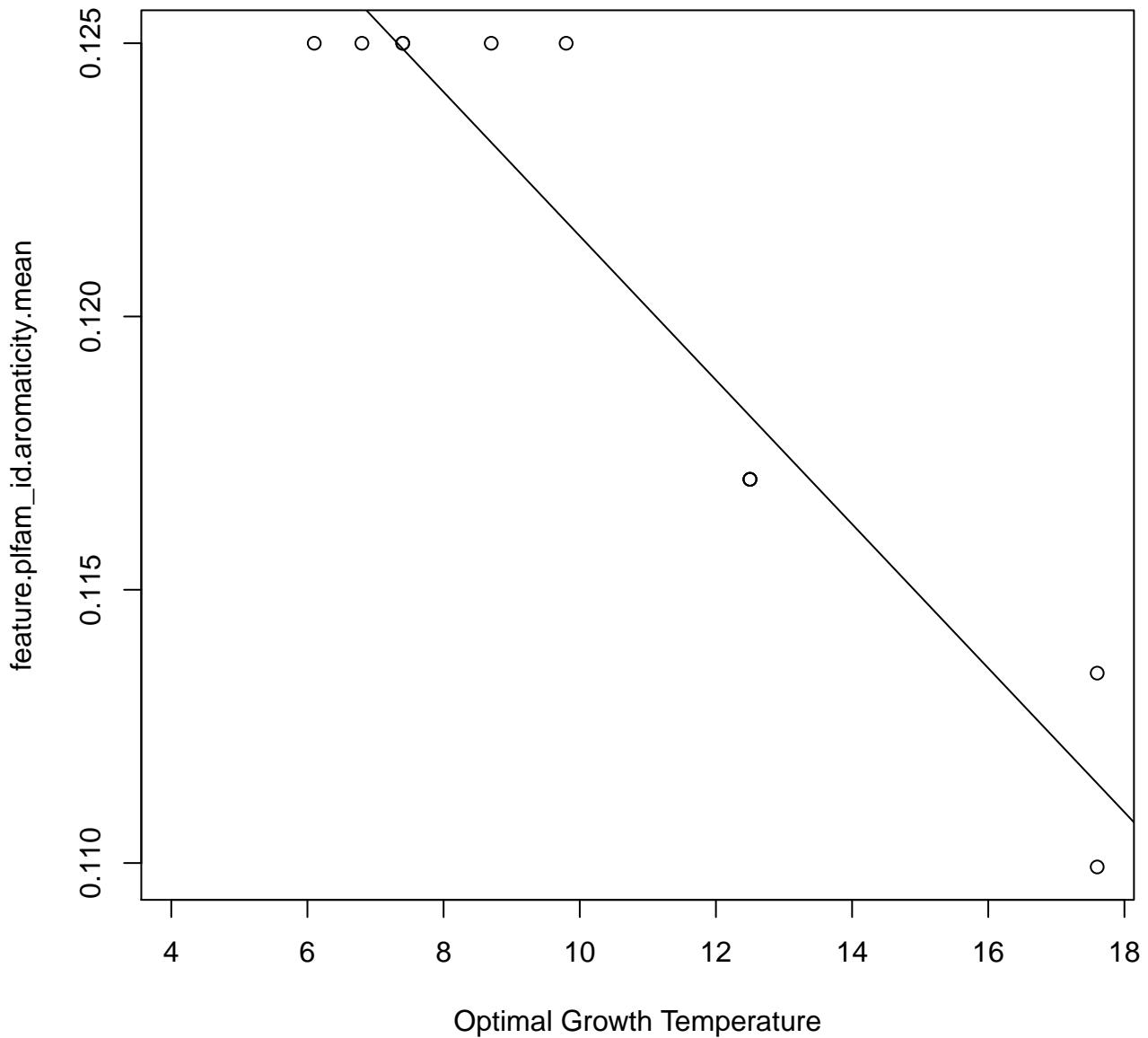
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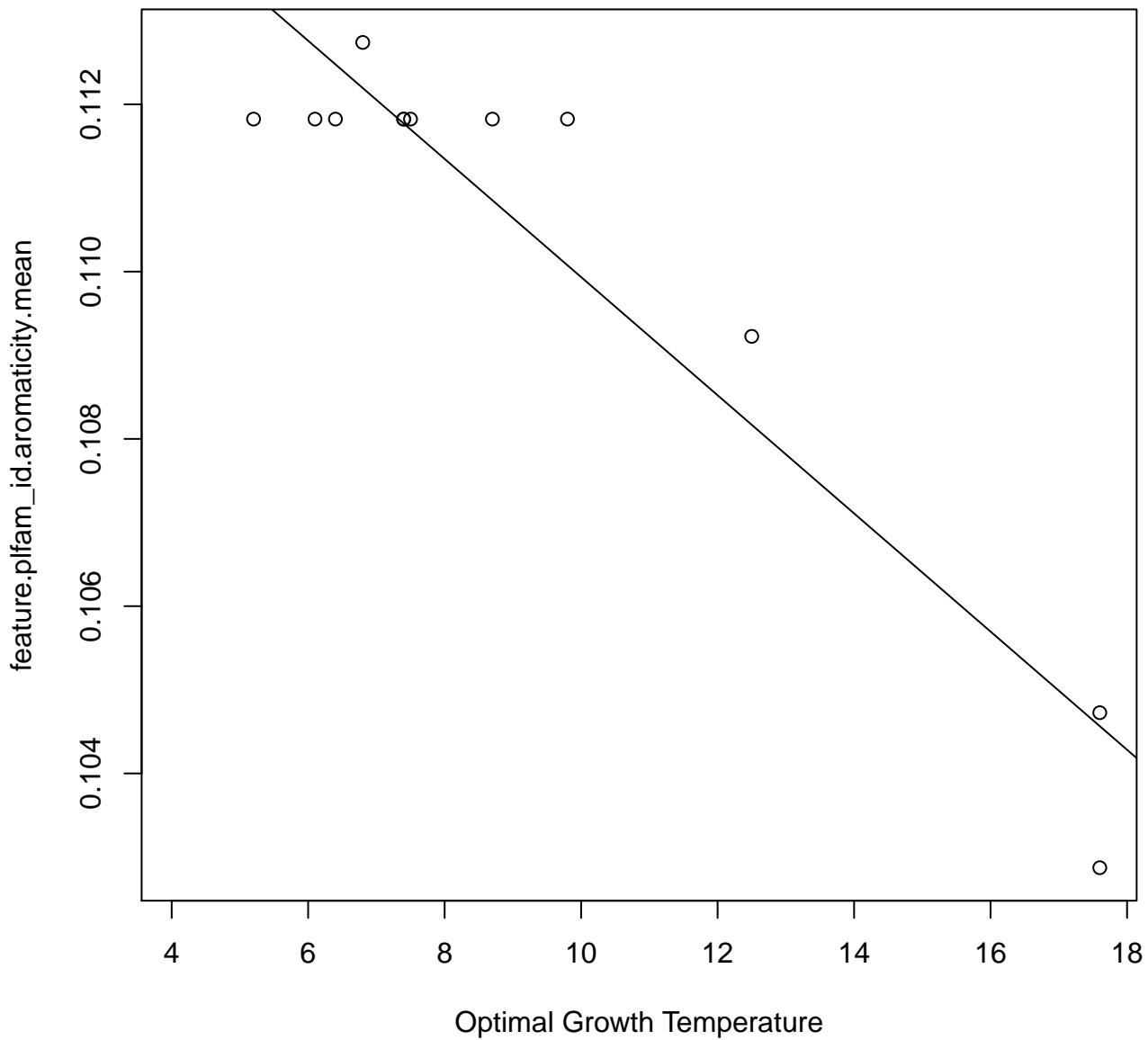
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hypothetical protein



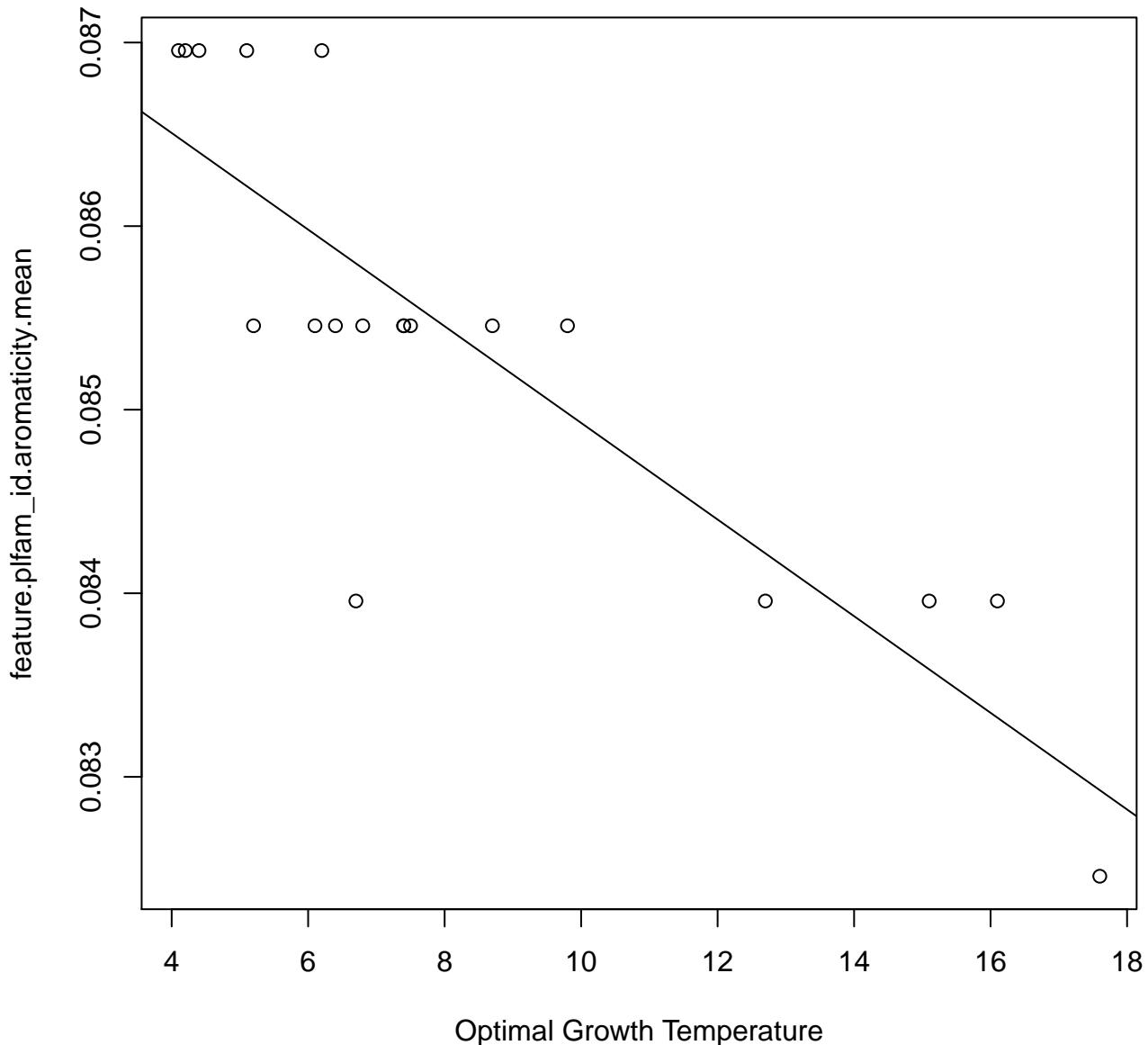
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Membrane-associated methyl-accepting chemotaxis protein with HAMP domain



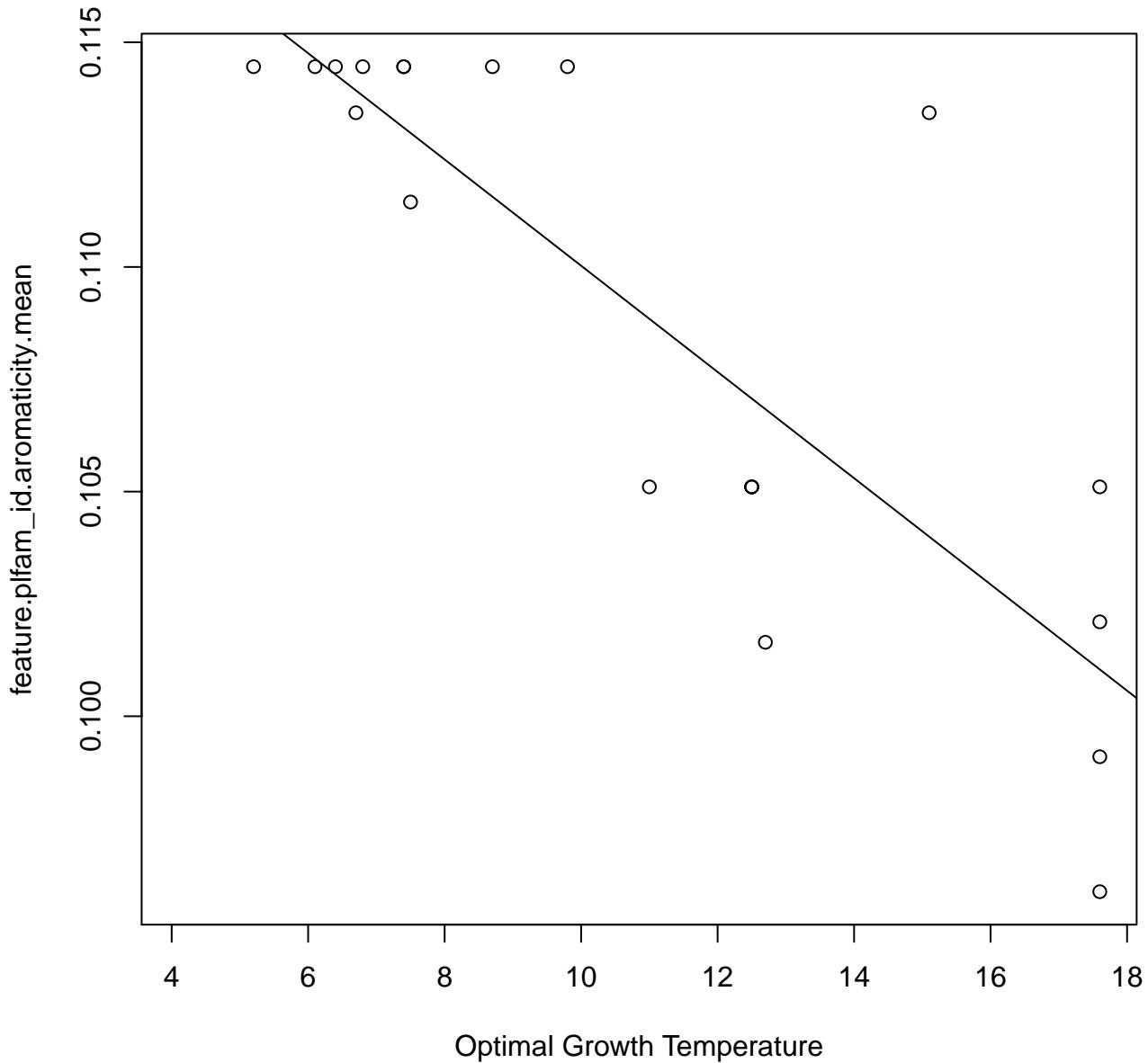
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TonB-dependent receptor



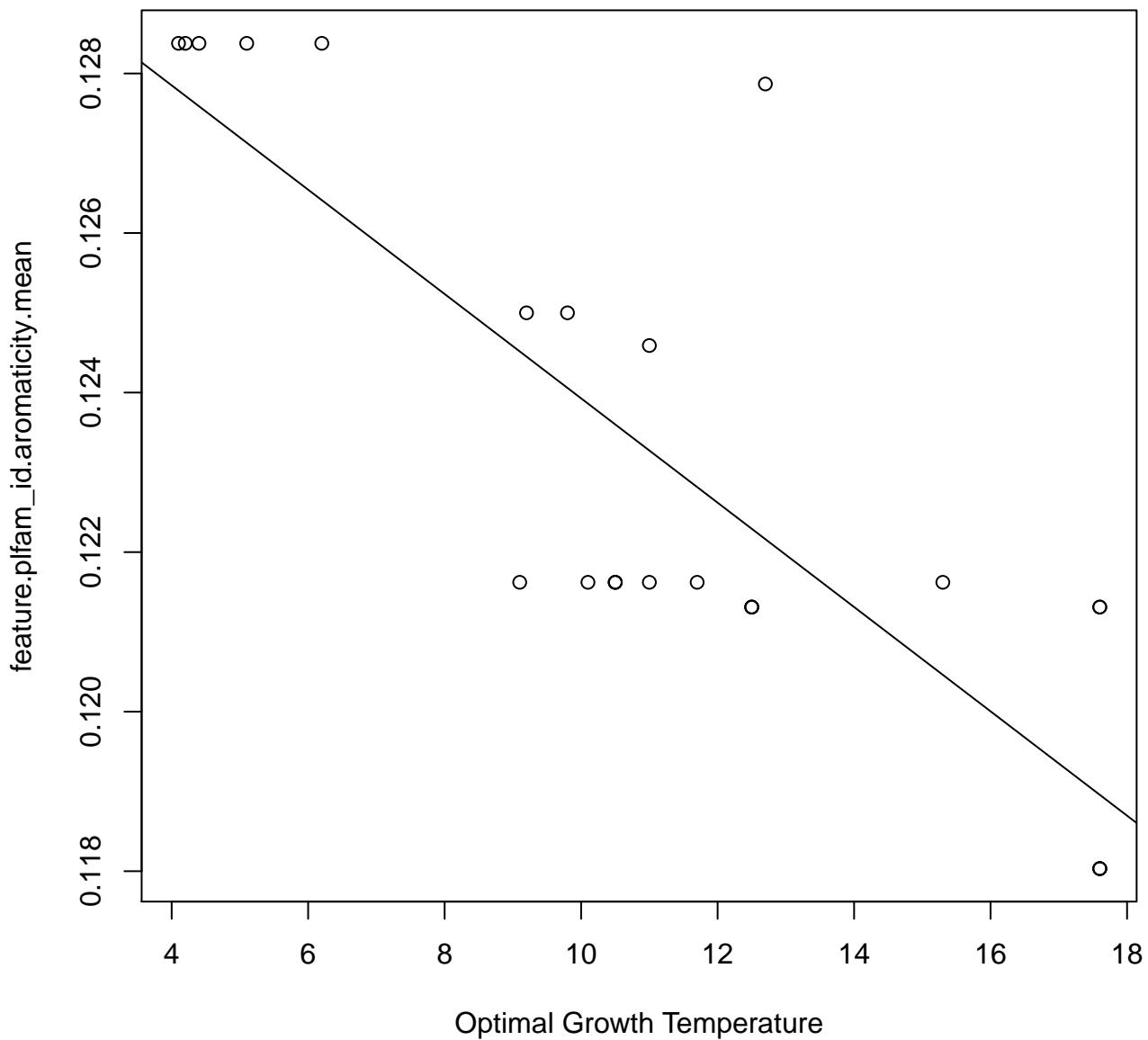
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Methyl-accepting chemotaxis protein



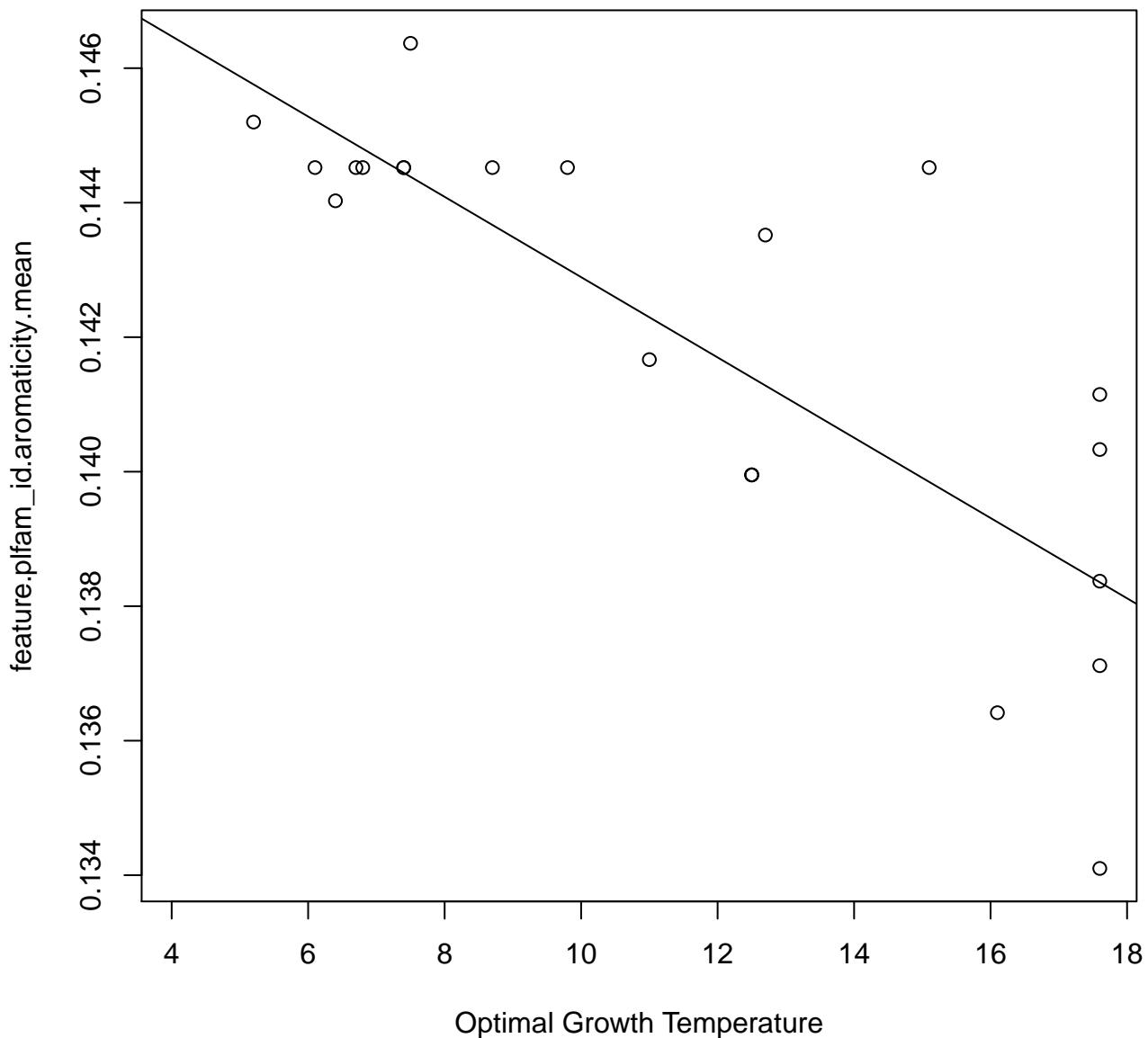
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Transcriptional regulator of beta-glucosides utilization, LacI family



feature.plfam_id.aromaticity.mean
PLF_28228_00001856
GGDEF domain protein



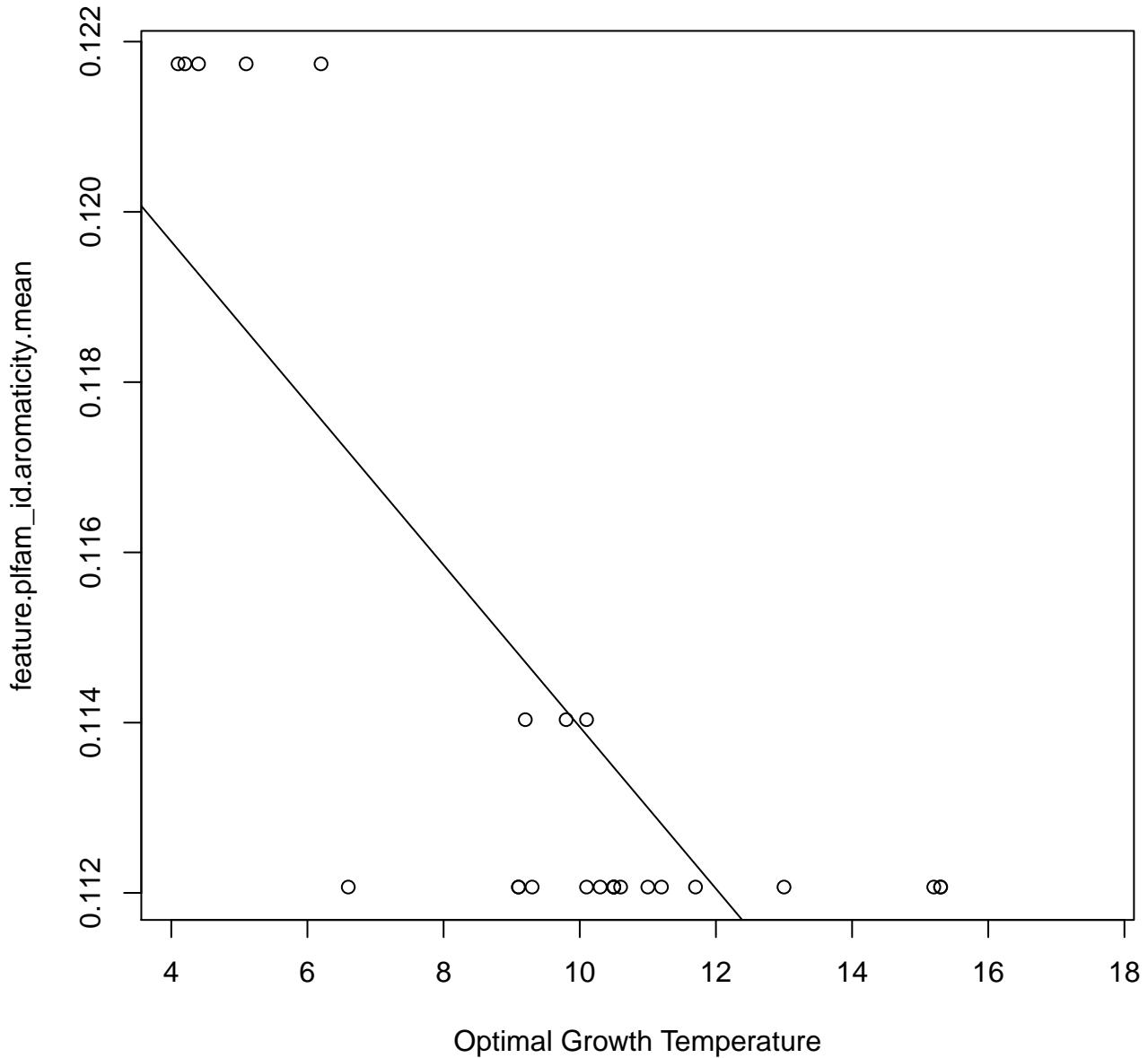
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Oligosaccharide 4-alpha-D-glucosyltransferase (EC 2.4.1.161)



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PLF_28228_00016319

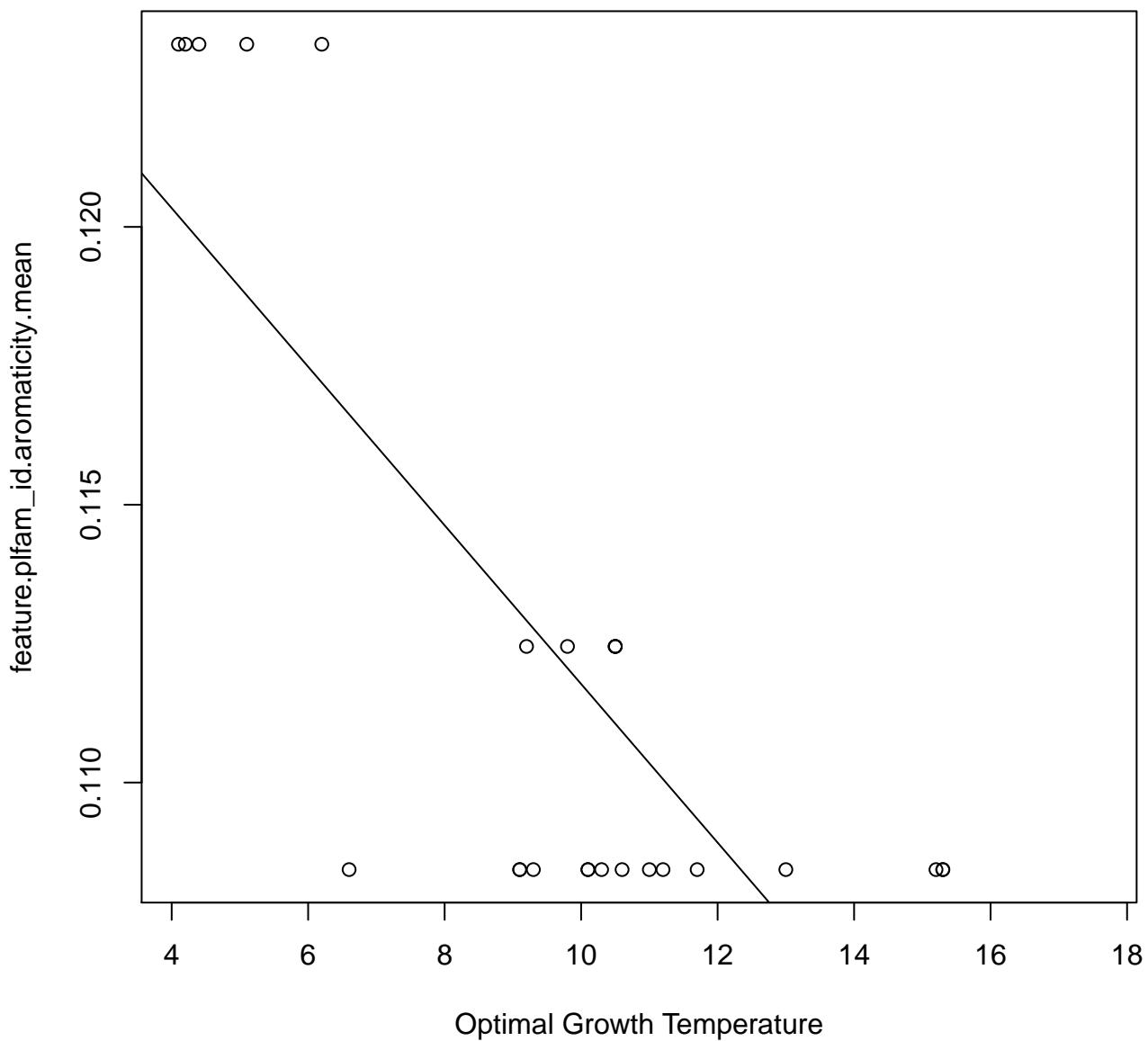
hypothetical protein



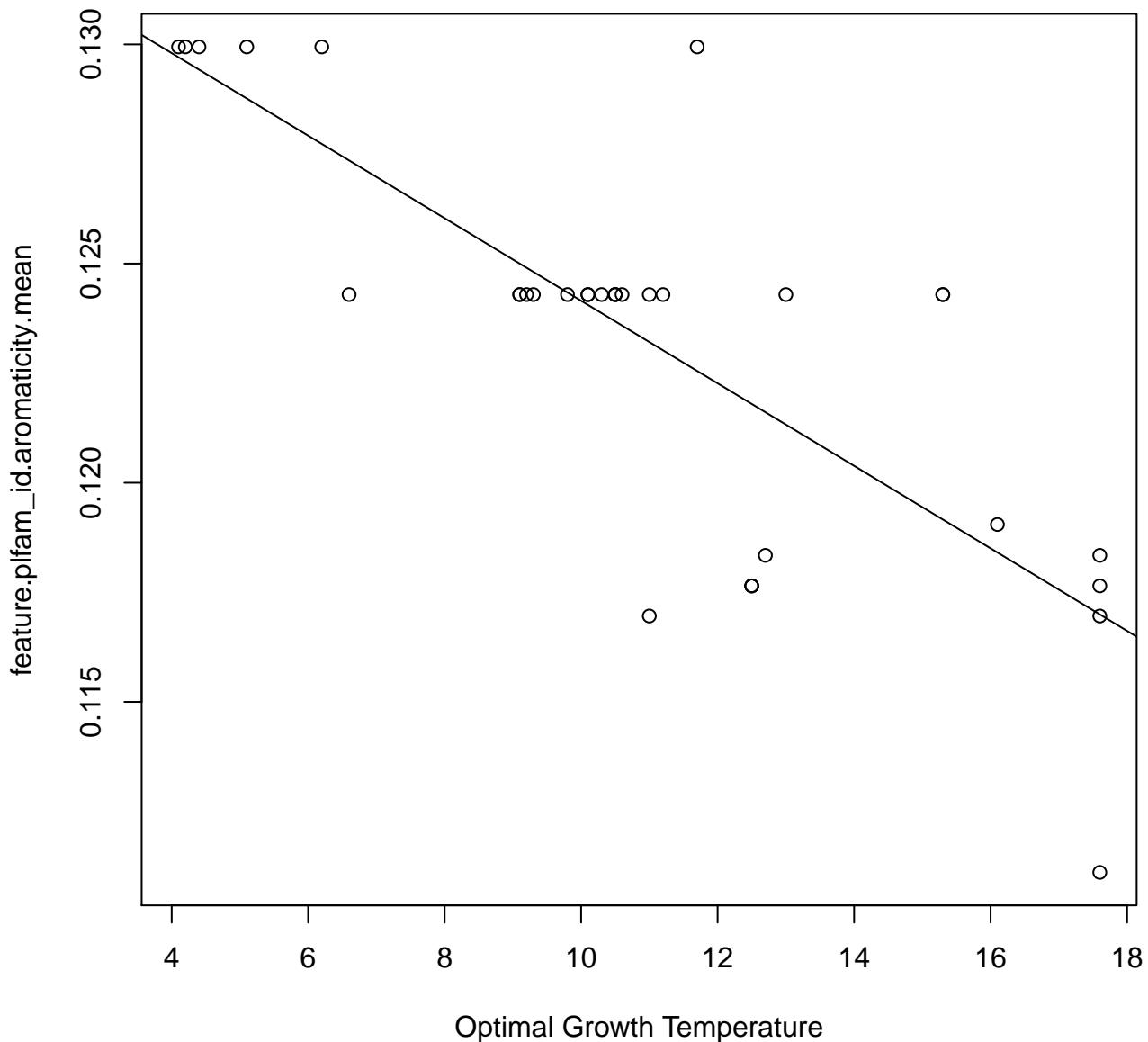
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PLF_28228_00031426

hypothetical protein



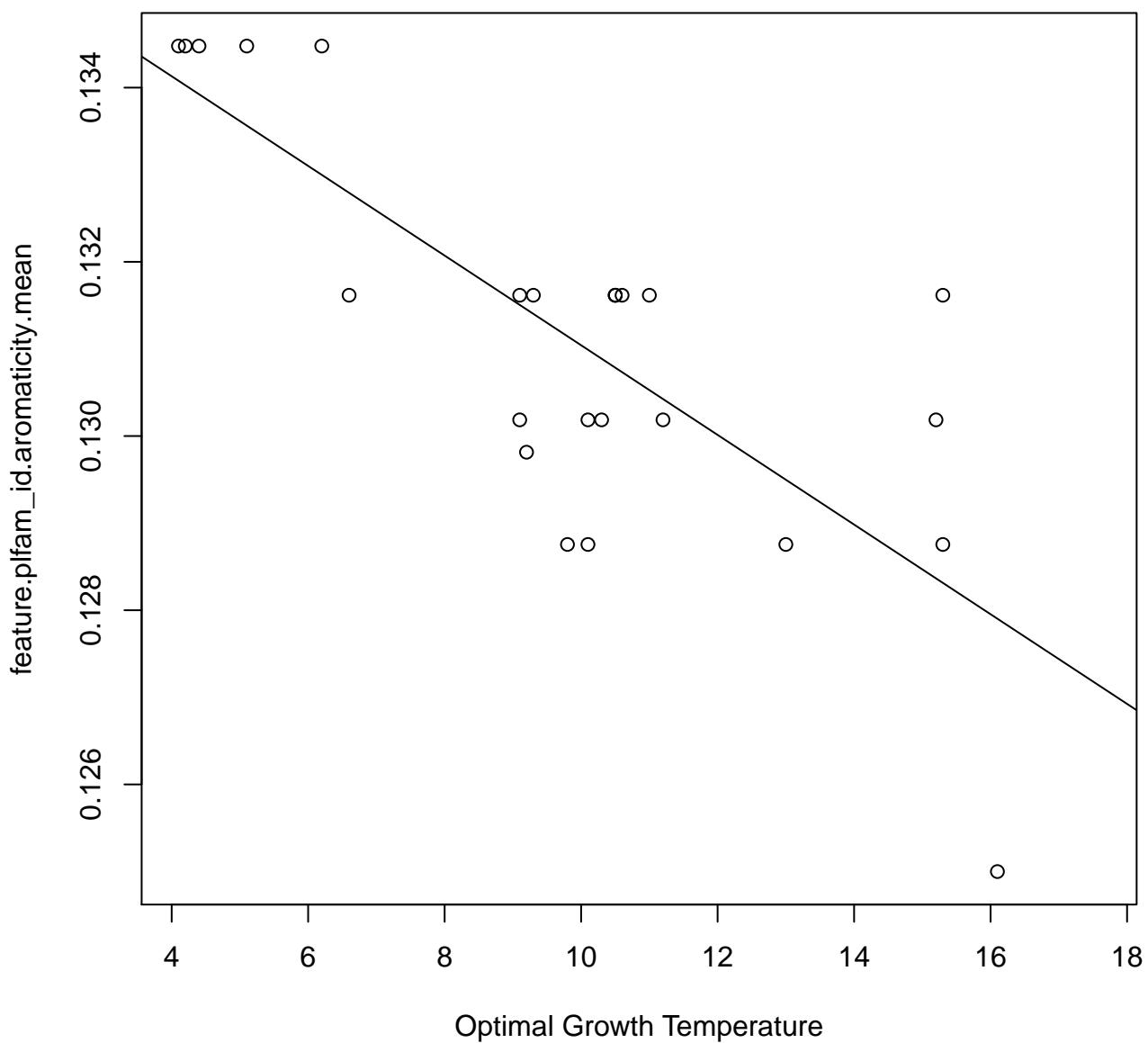
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Ureidoglycolate lyase (EC 4.3.2.3)



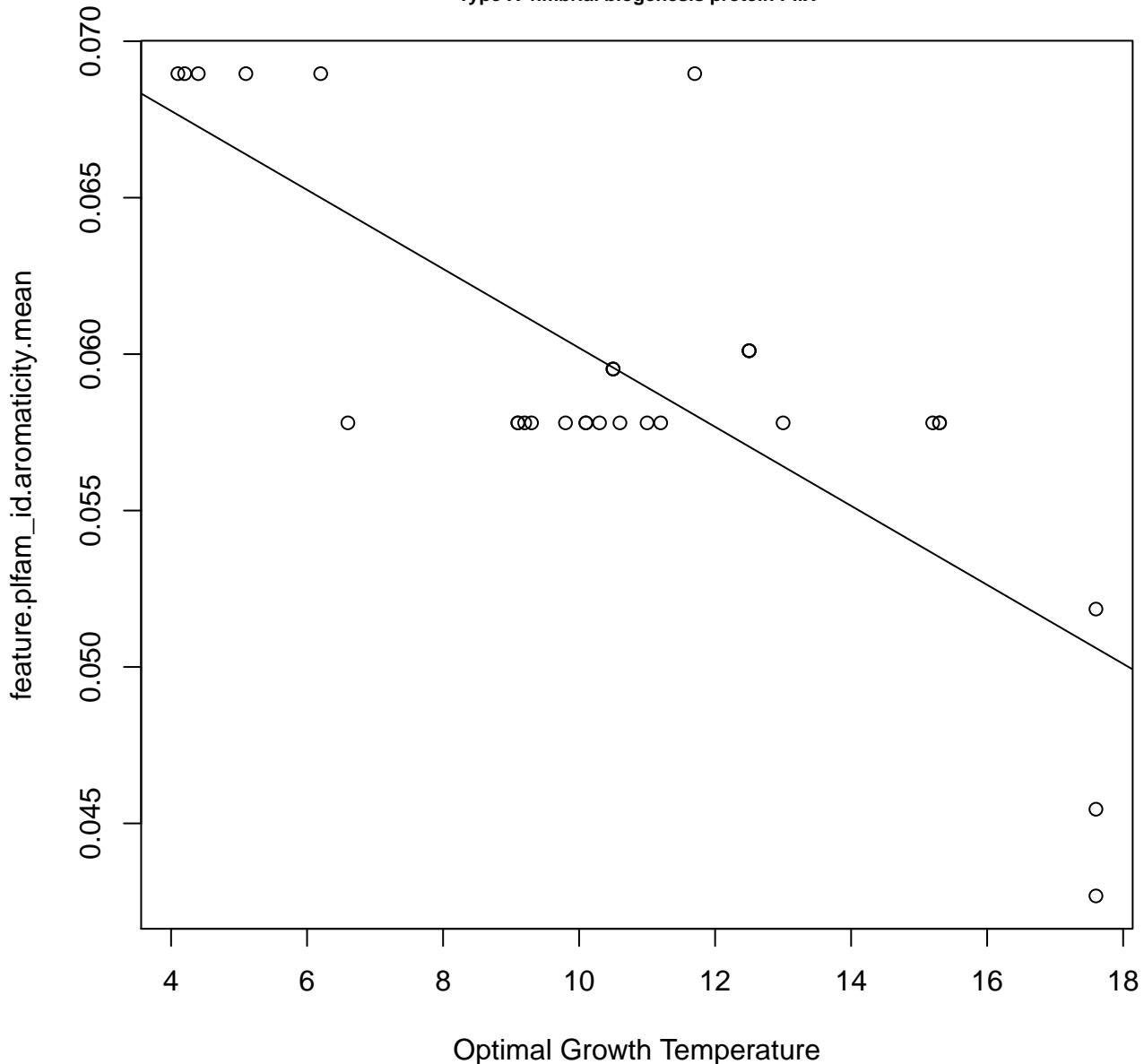
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PLF_28228_00016855

hypothetical protein



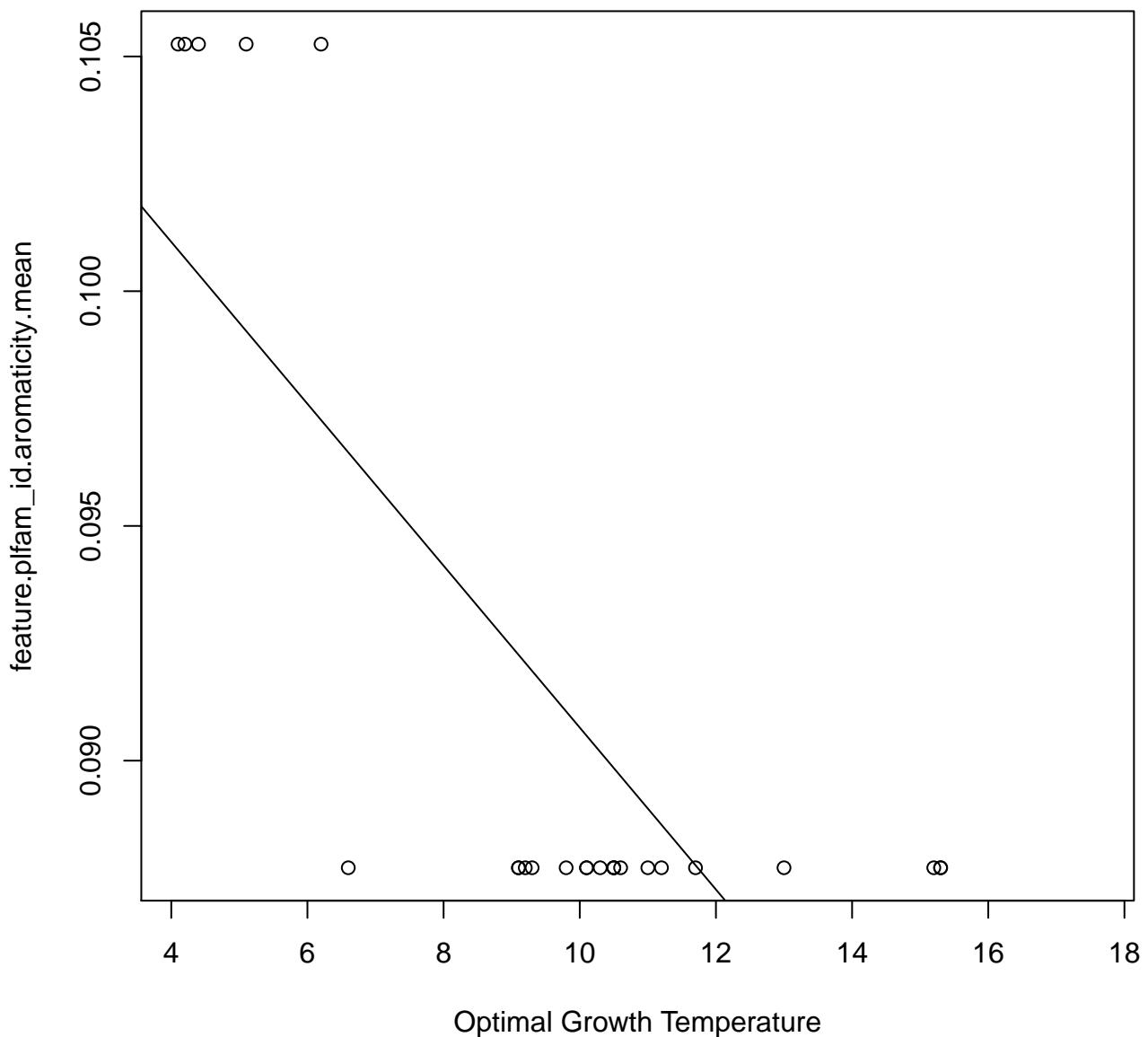
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Type IV fimbrial biogenesis protein PilX



feature.plfam_id.aromaticity.mean

PLF_28228_00022617

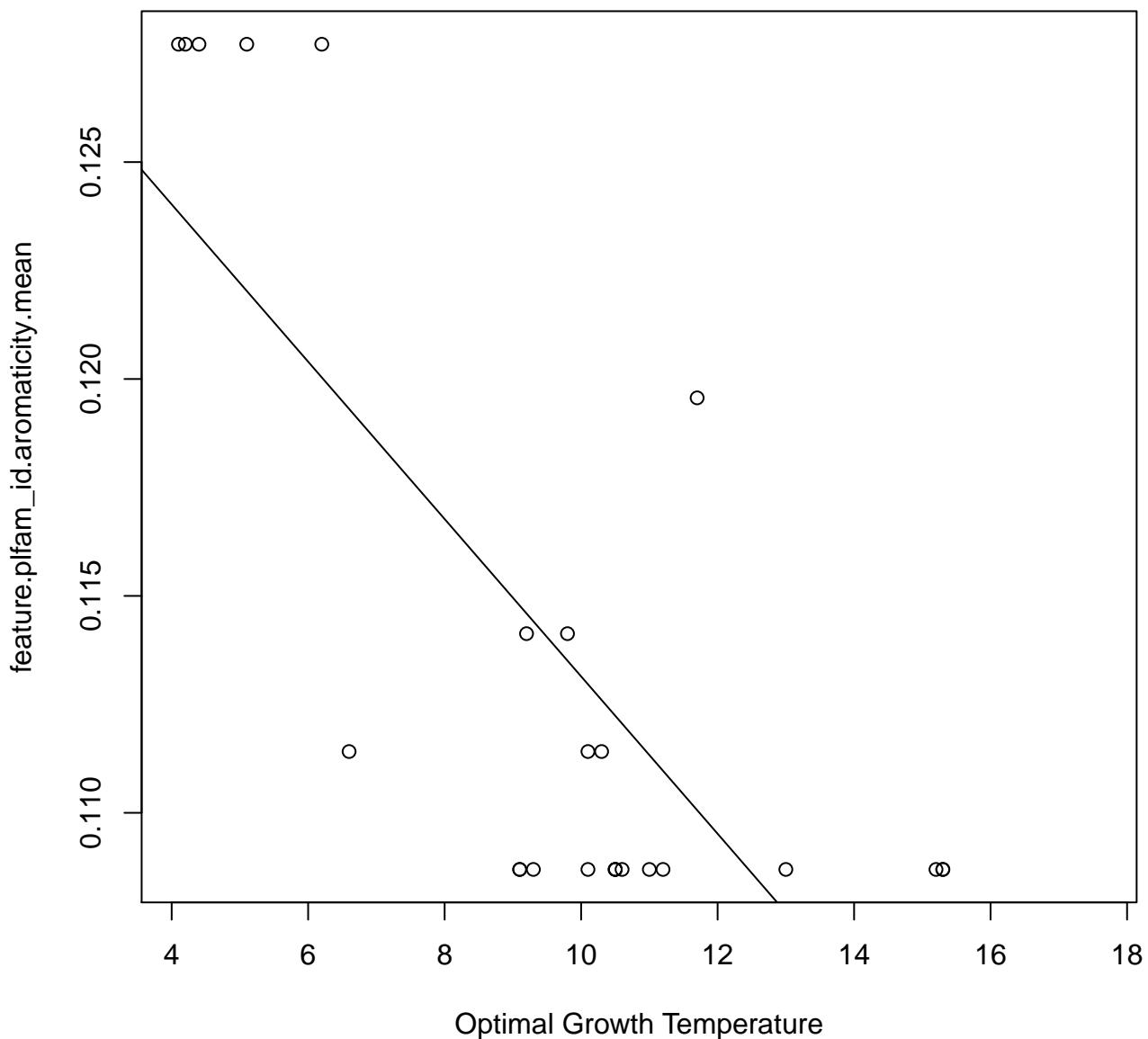
hypothetical protein



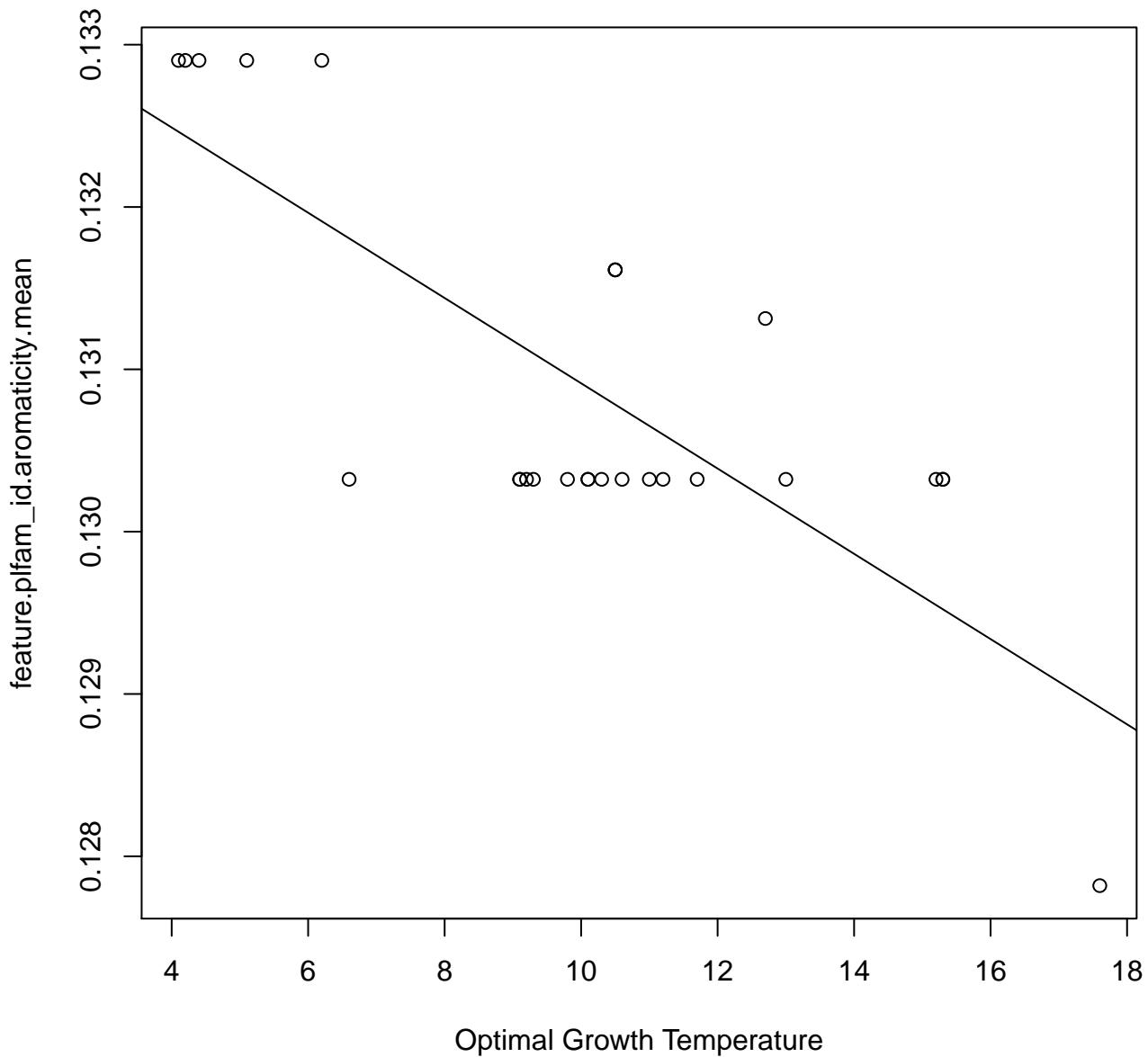
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PLF_28228_00032200

hypothetical protein



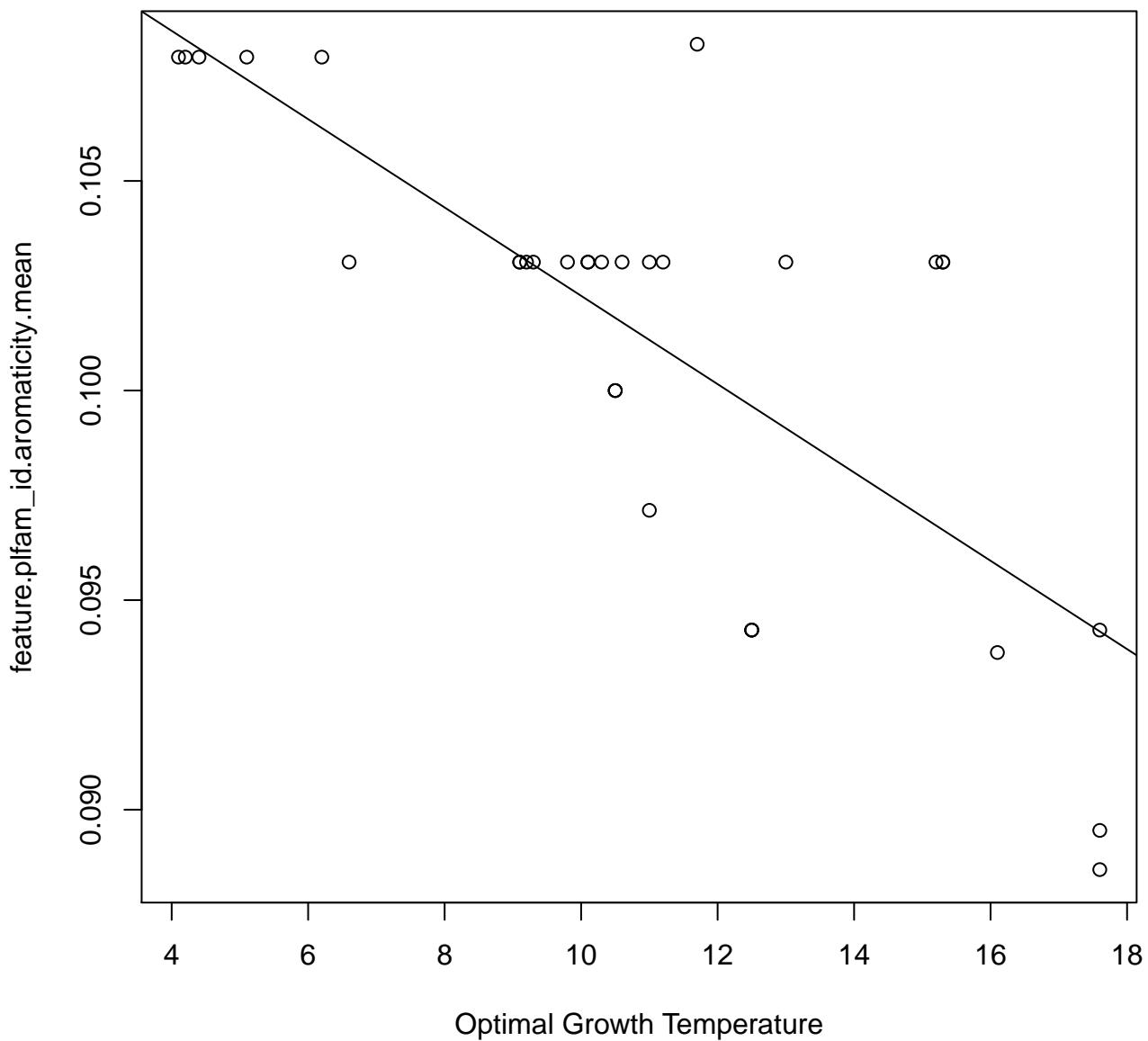
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Dipeptidyl peptidase IV



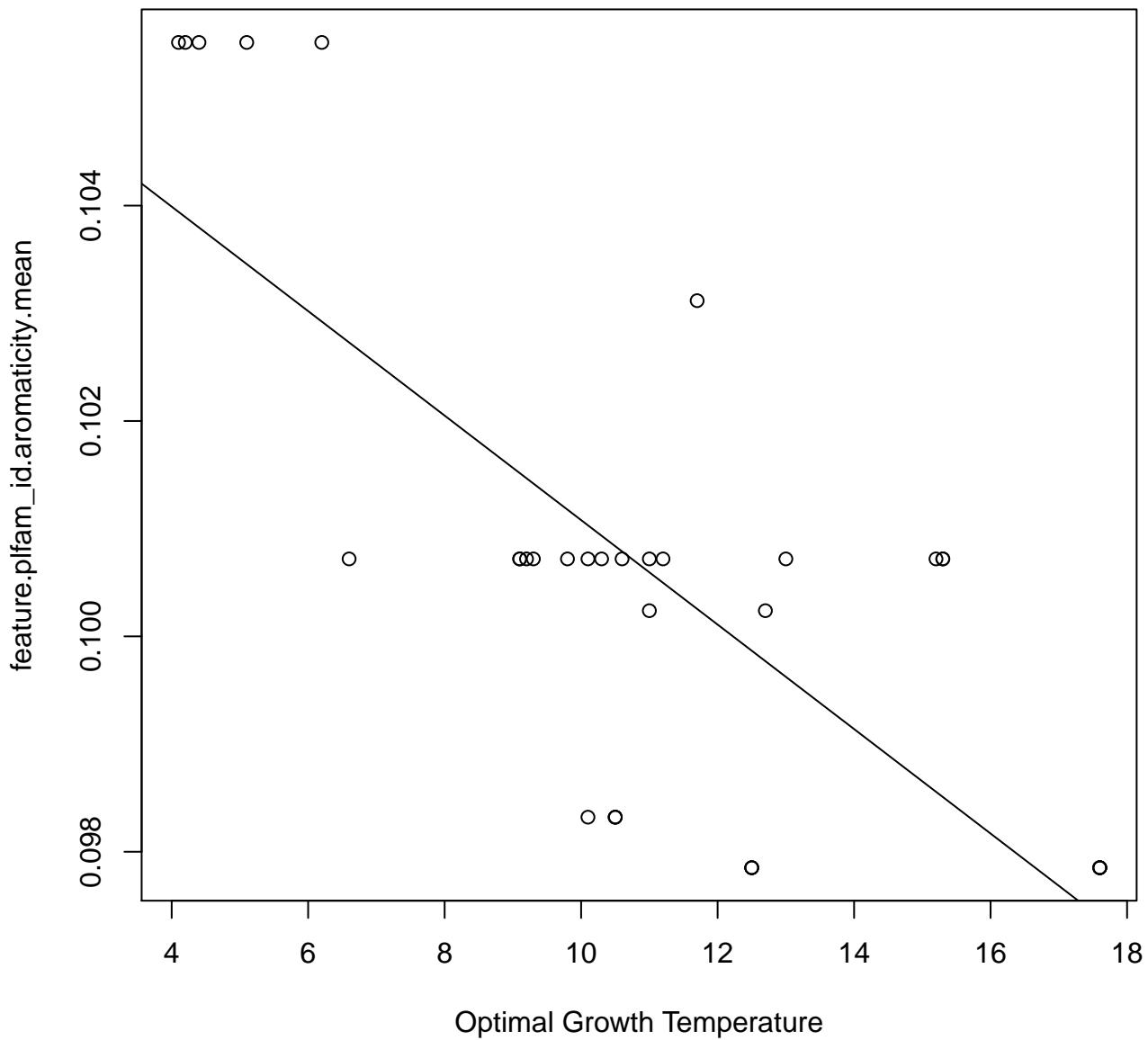
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PLF_28228_00003903

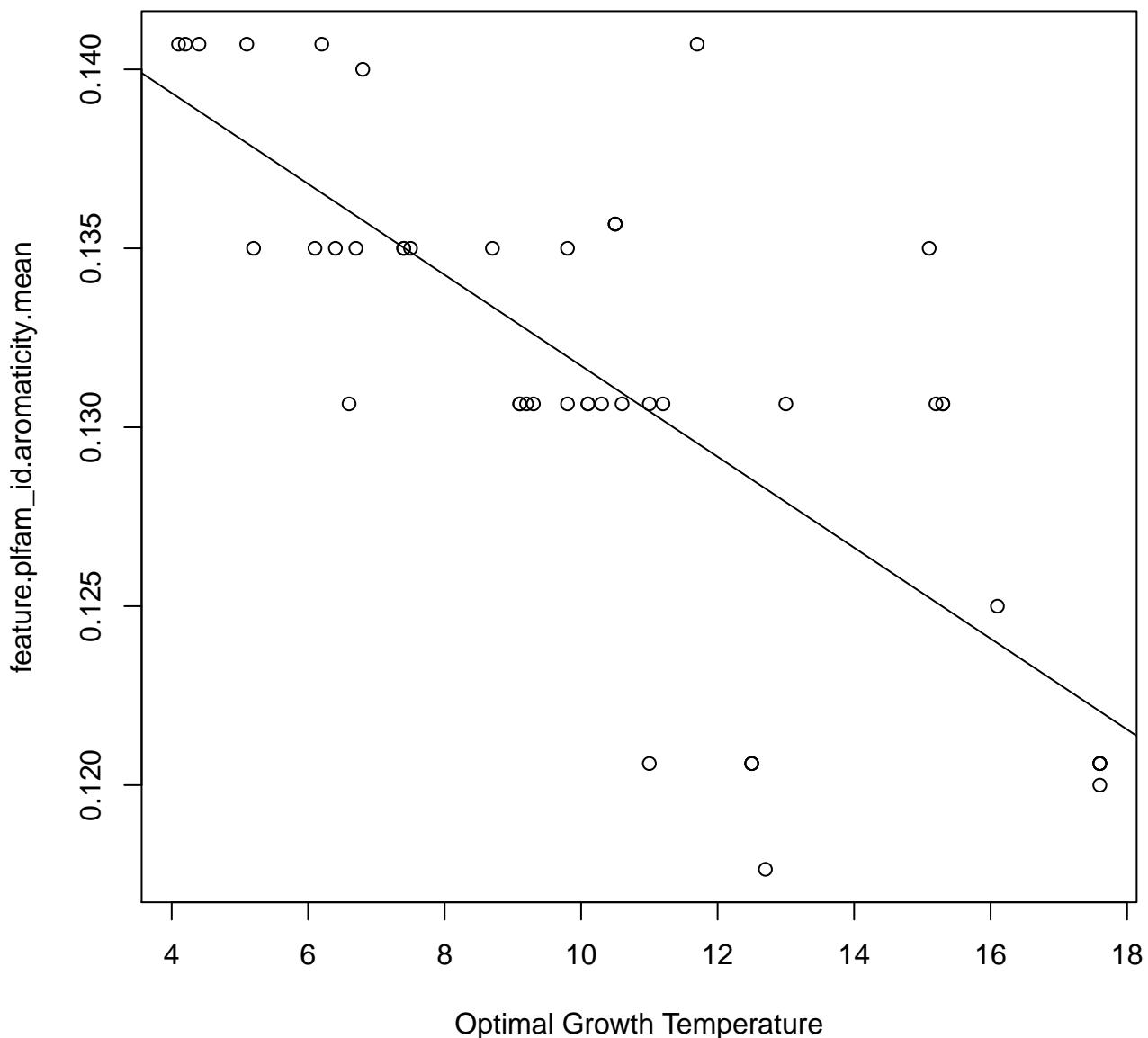
hypothetical protein



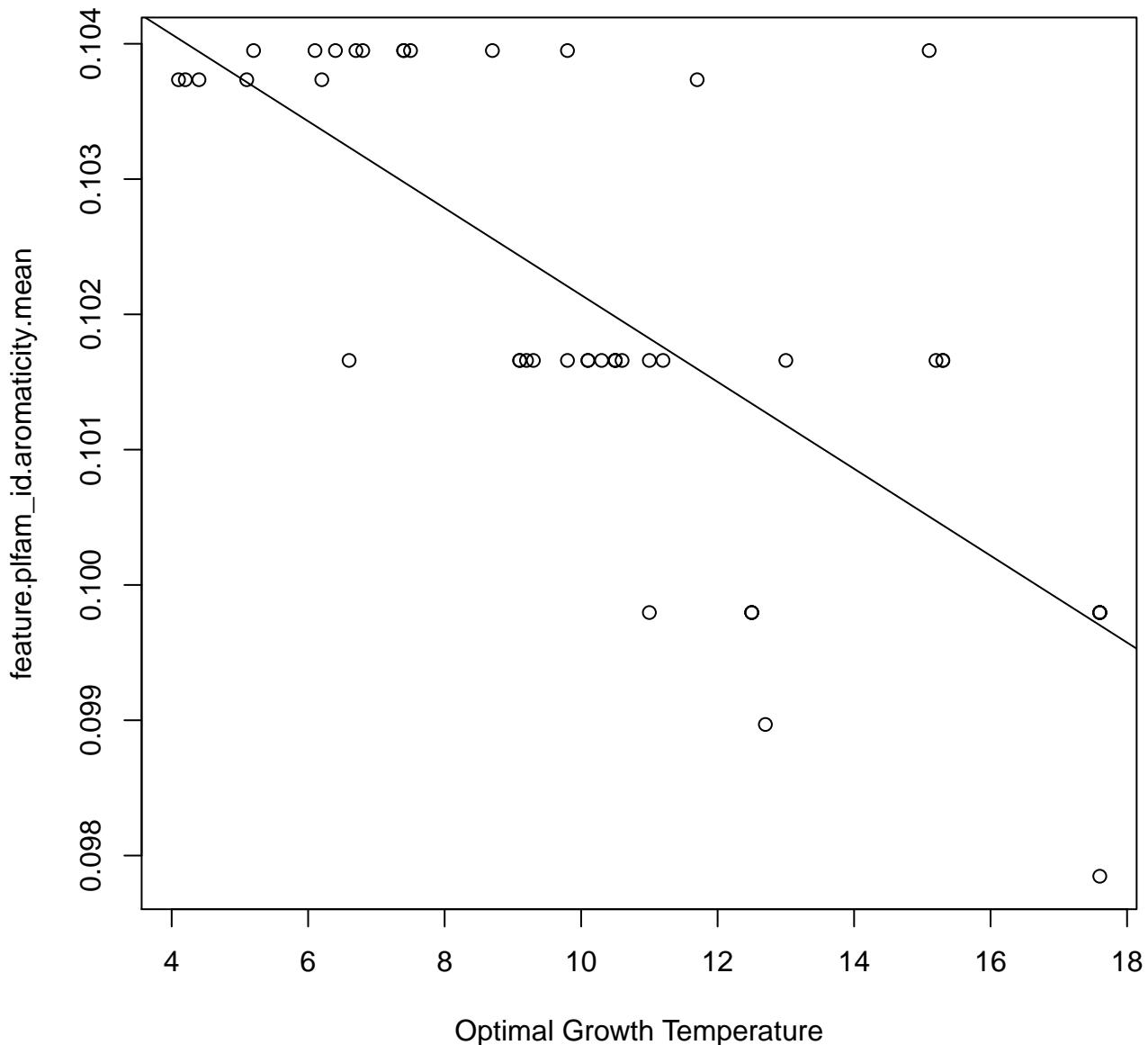
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Transcriptional regulator



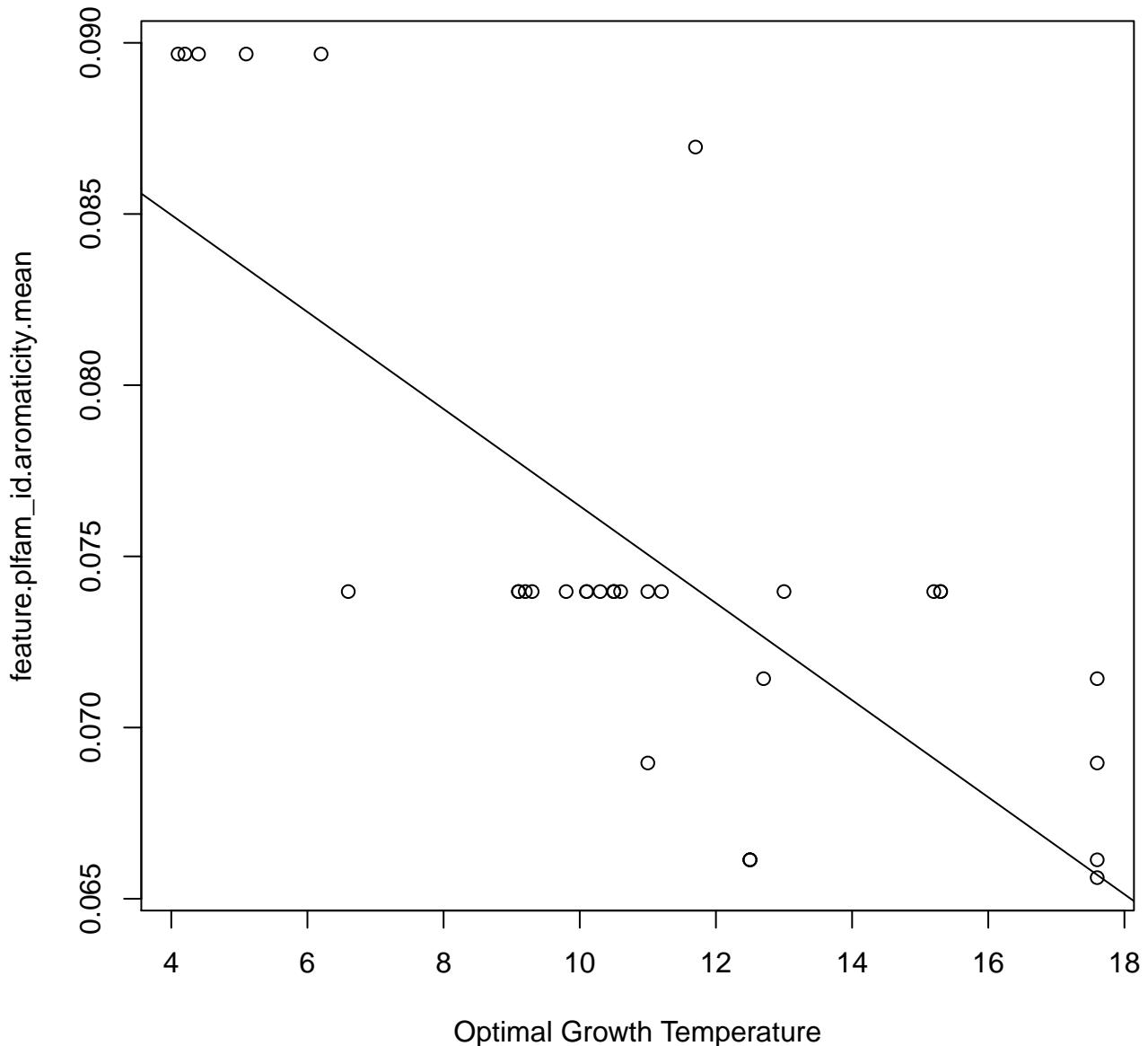
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Carbonic anhydrase, beta class (EC 4.2.1.1)



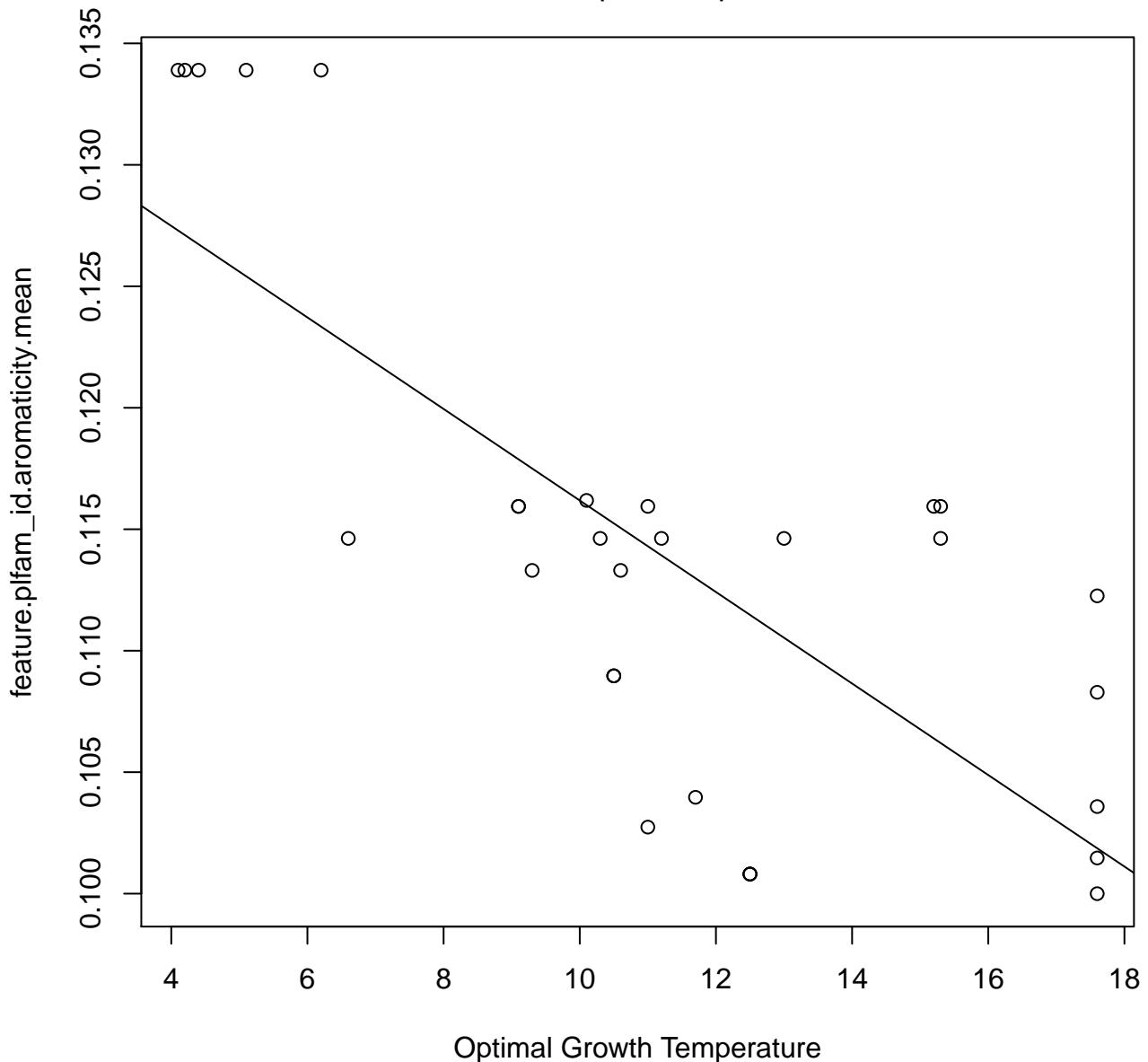
feature.plfam_id.aromaticity.mean
PLF_28228_00001635
DNA-binding transcriptional regulator, MocR family / aminotransferase domain



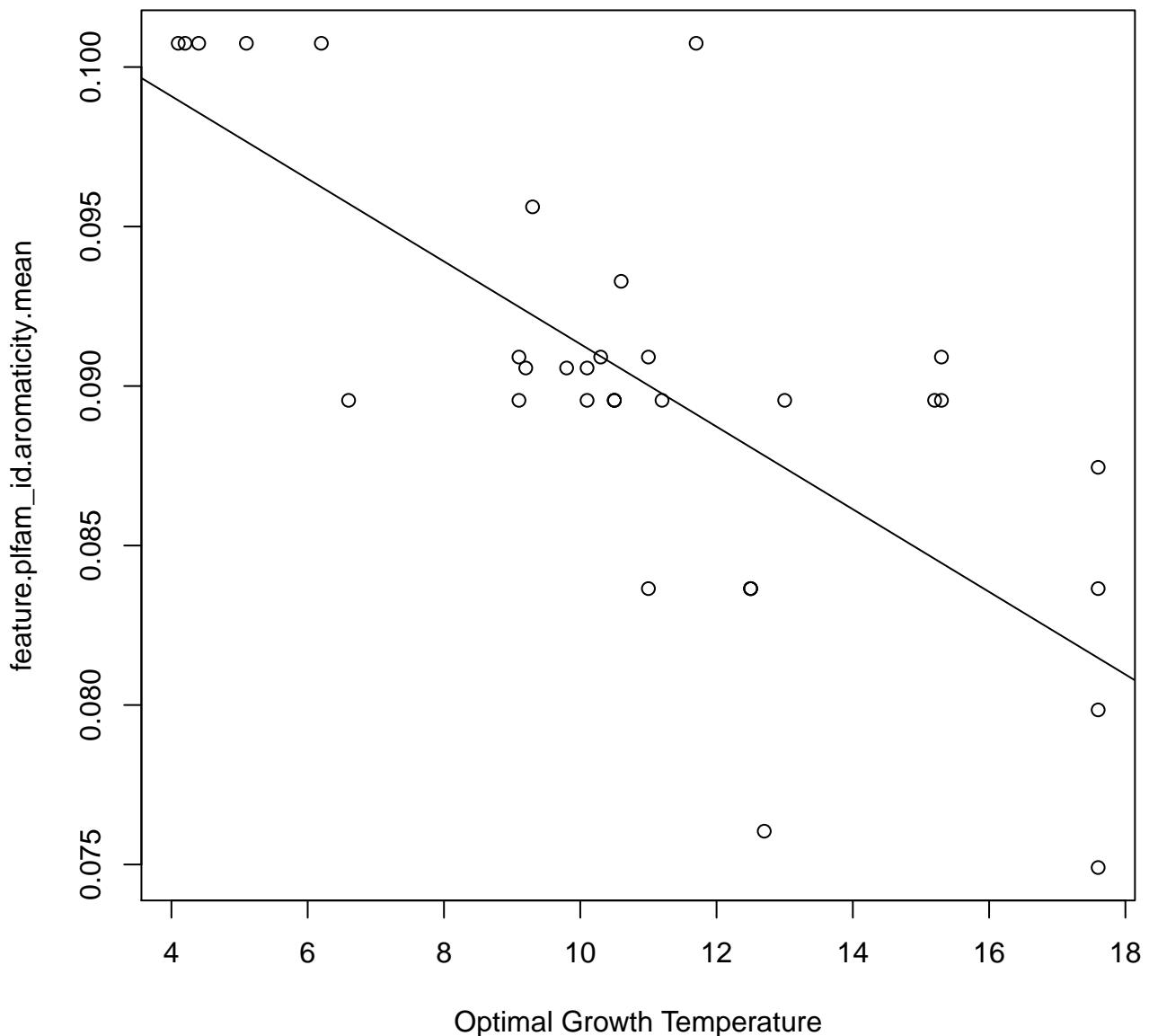
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CzcABC family efflux RND transporter, membrane fusion protein



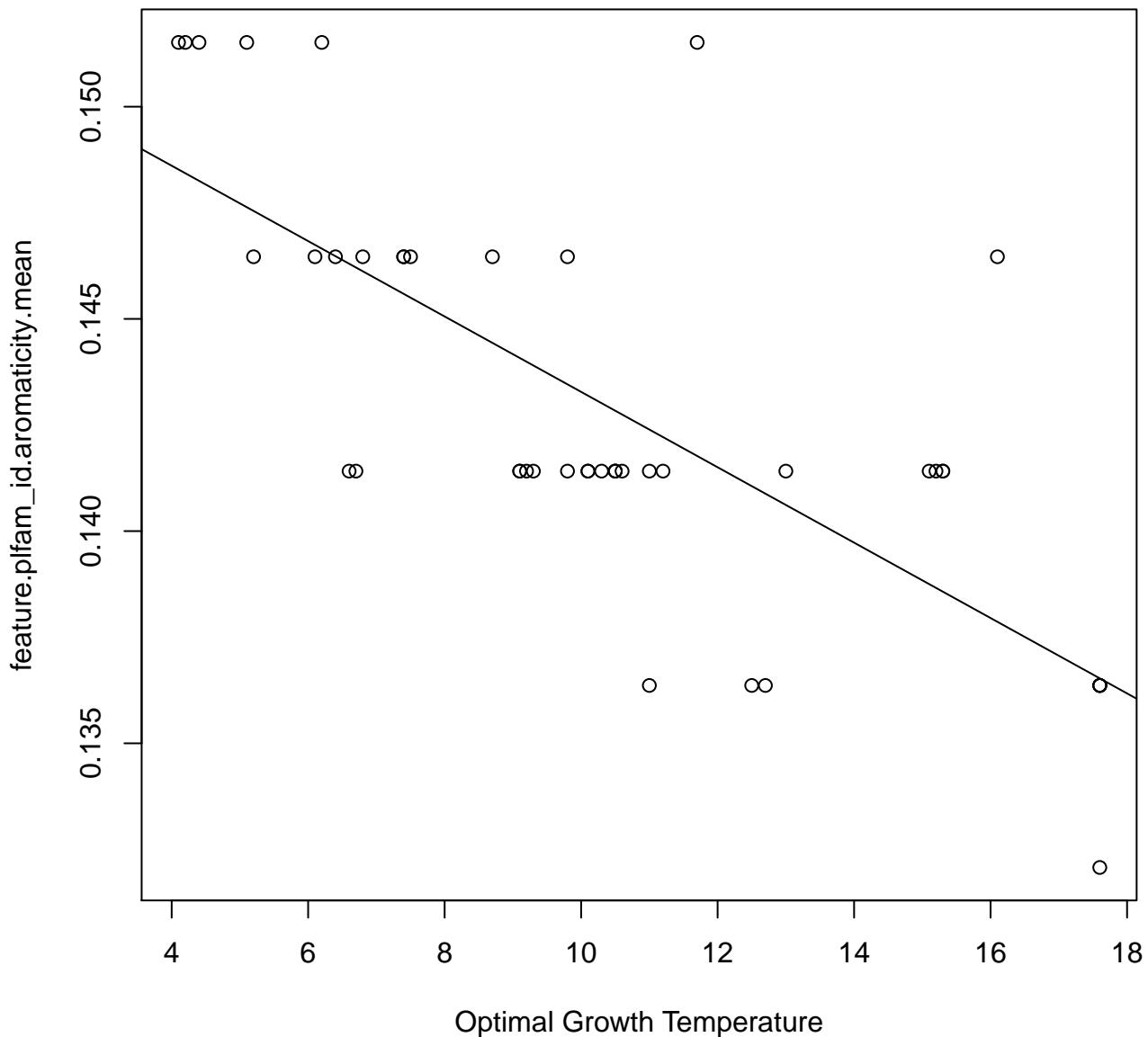
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TonB-dependent receptor



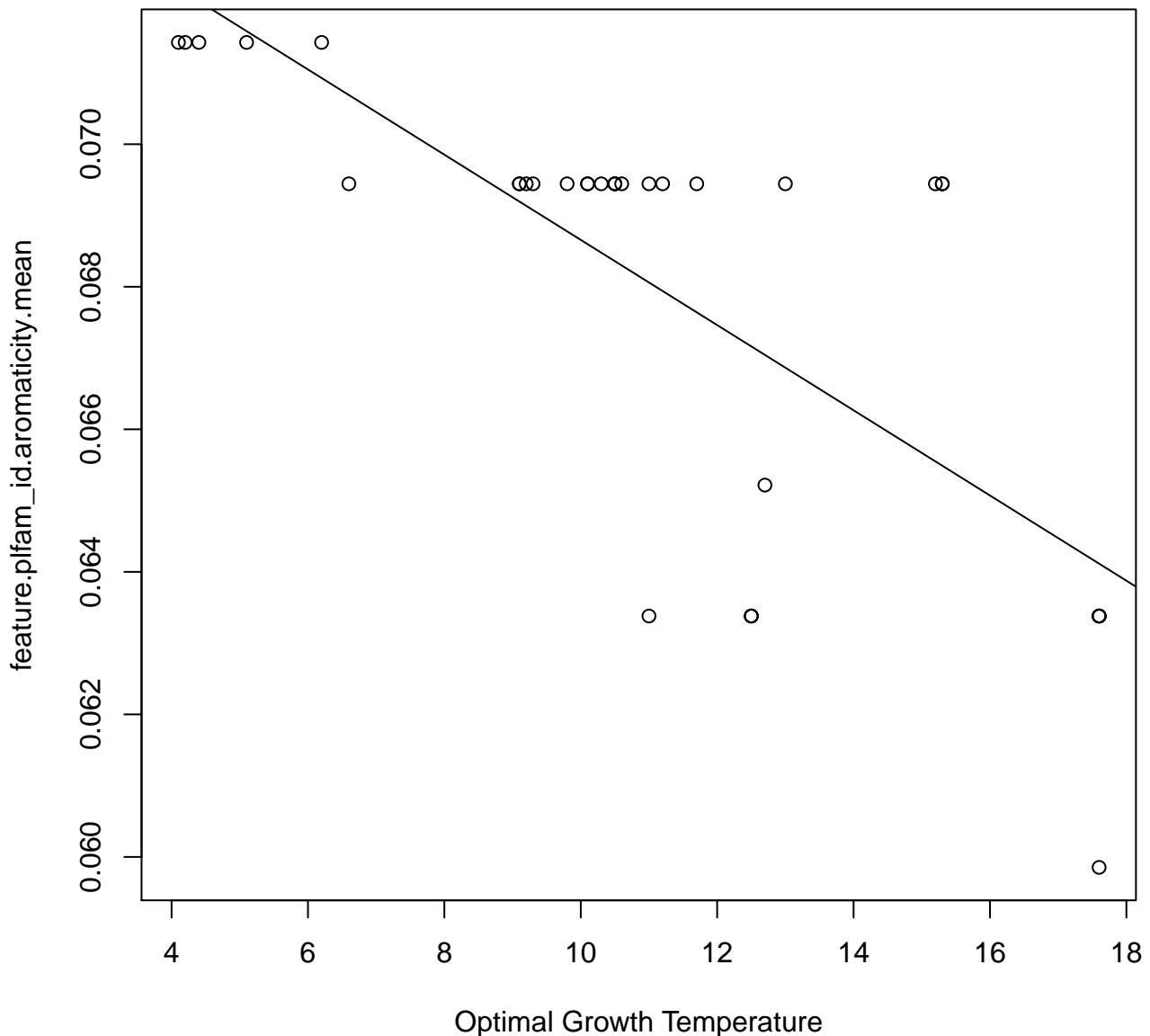
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Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)



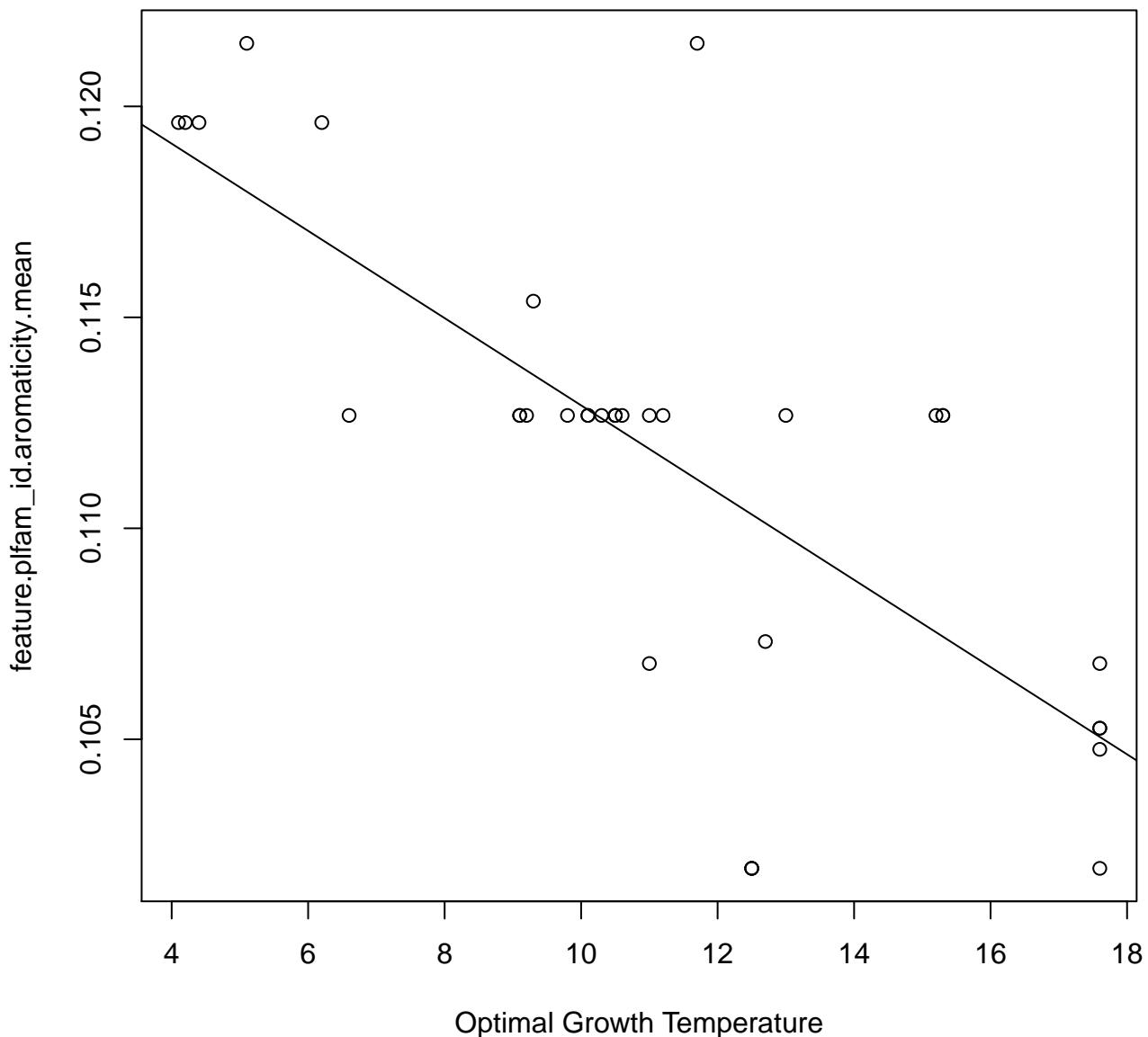
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3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)



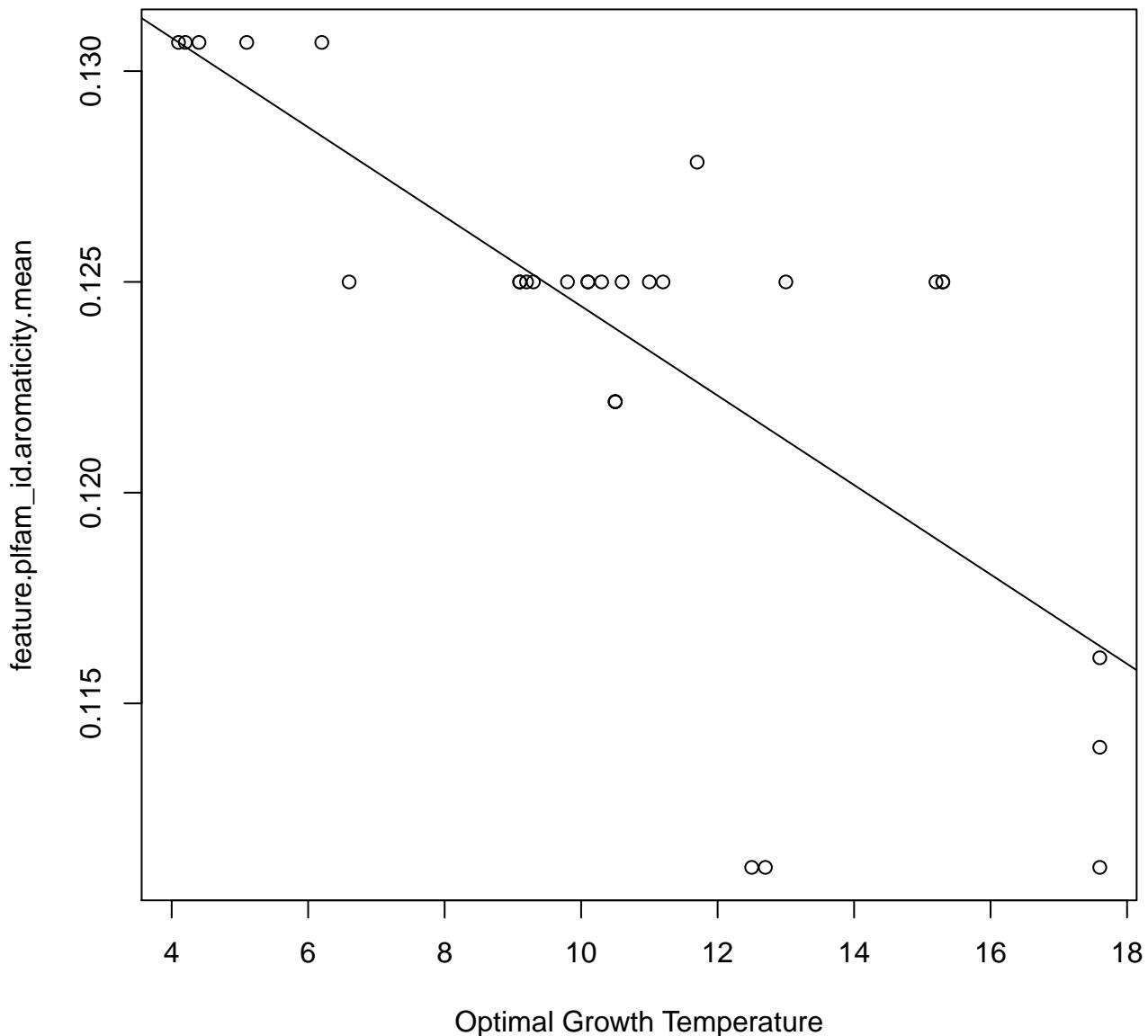
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Ribosome-binding factor A



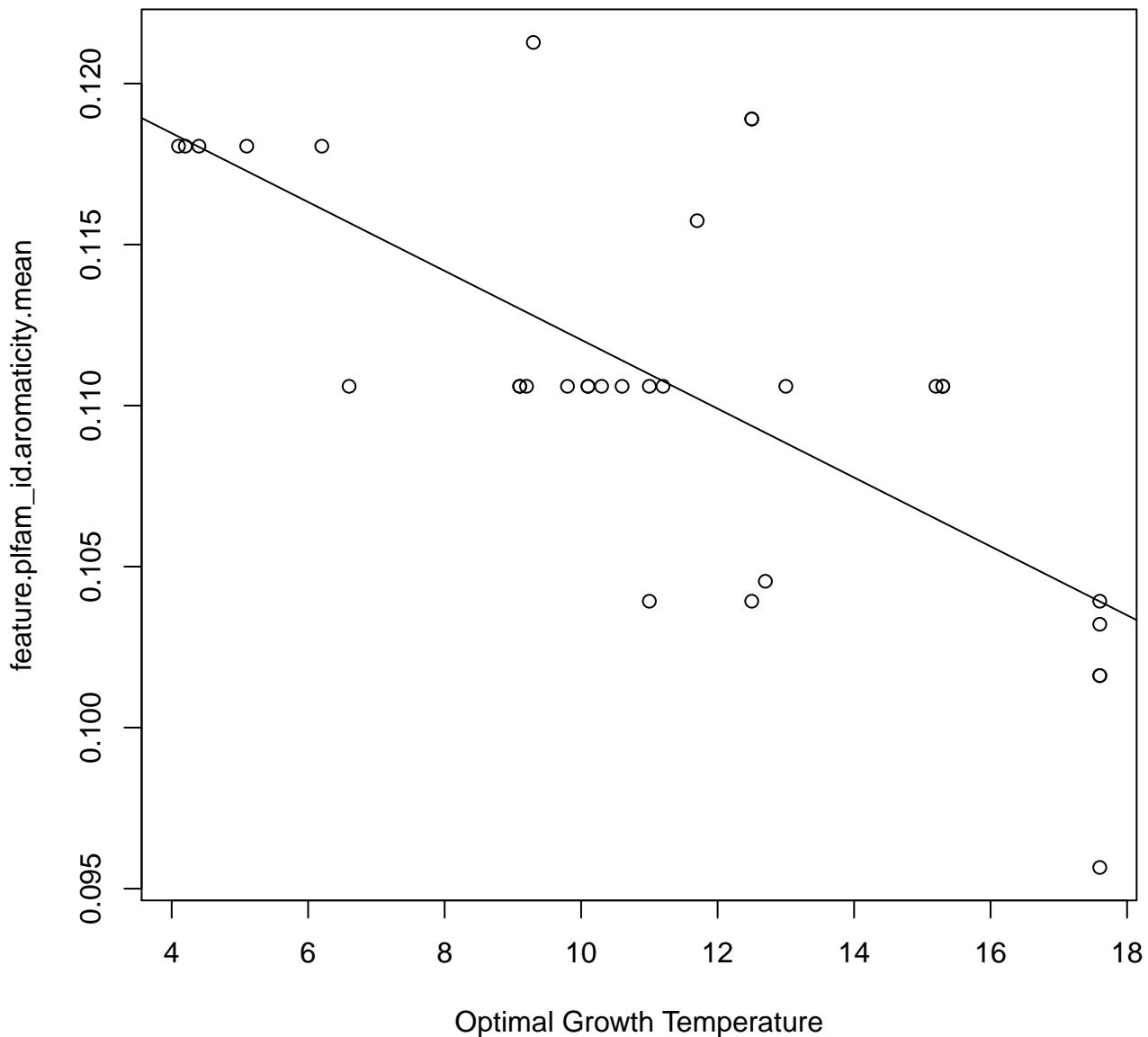
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PLF_28228_00001865
General secretion pathway protein H



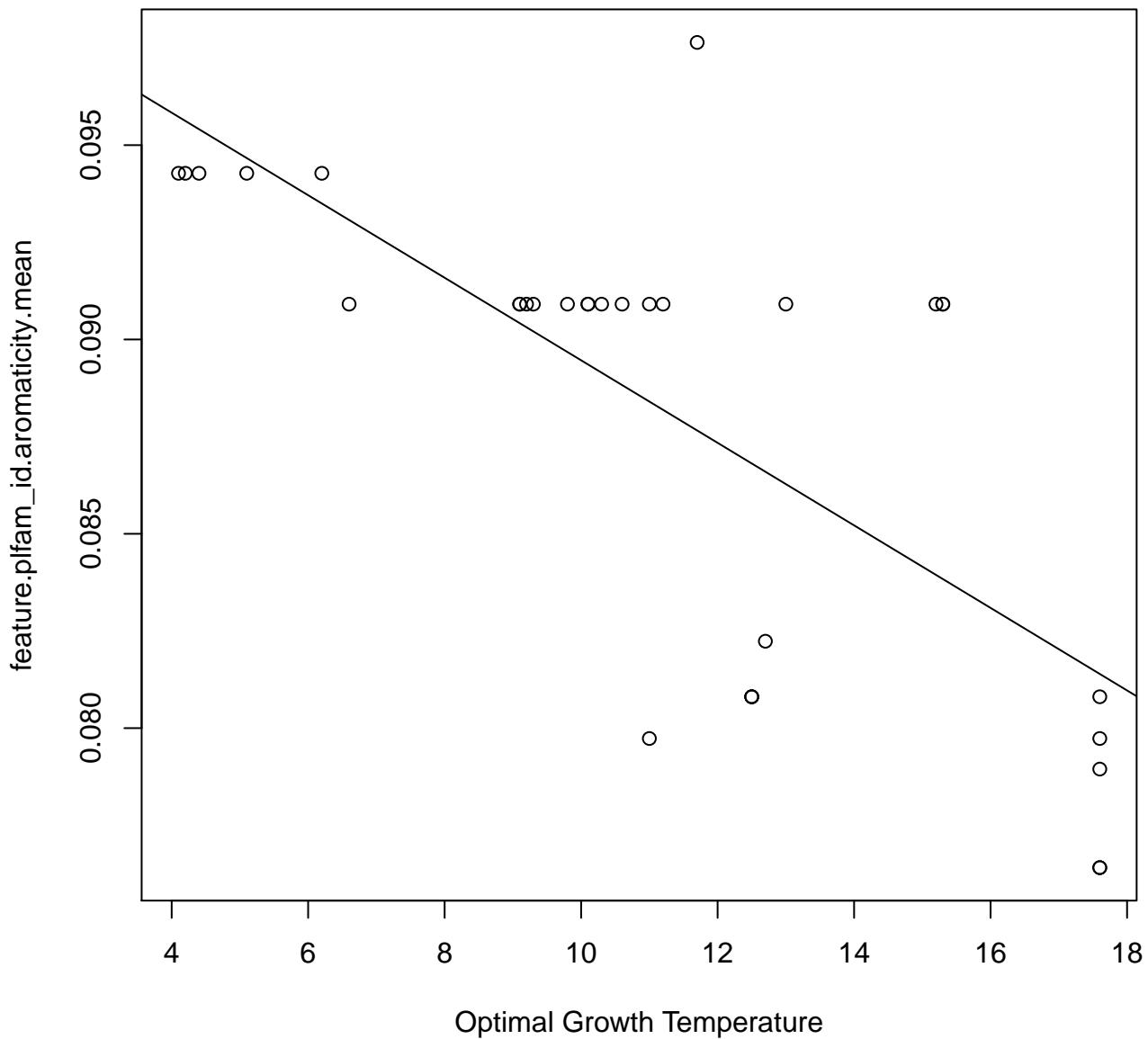
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PLF_28228_00007209
NADH:flavin oxidoreductases, Old Yellow Enzyme family



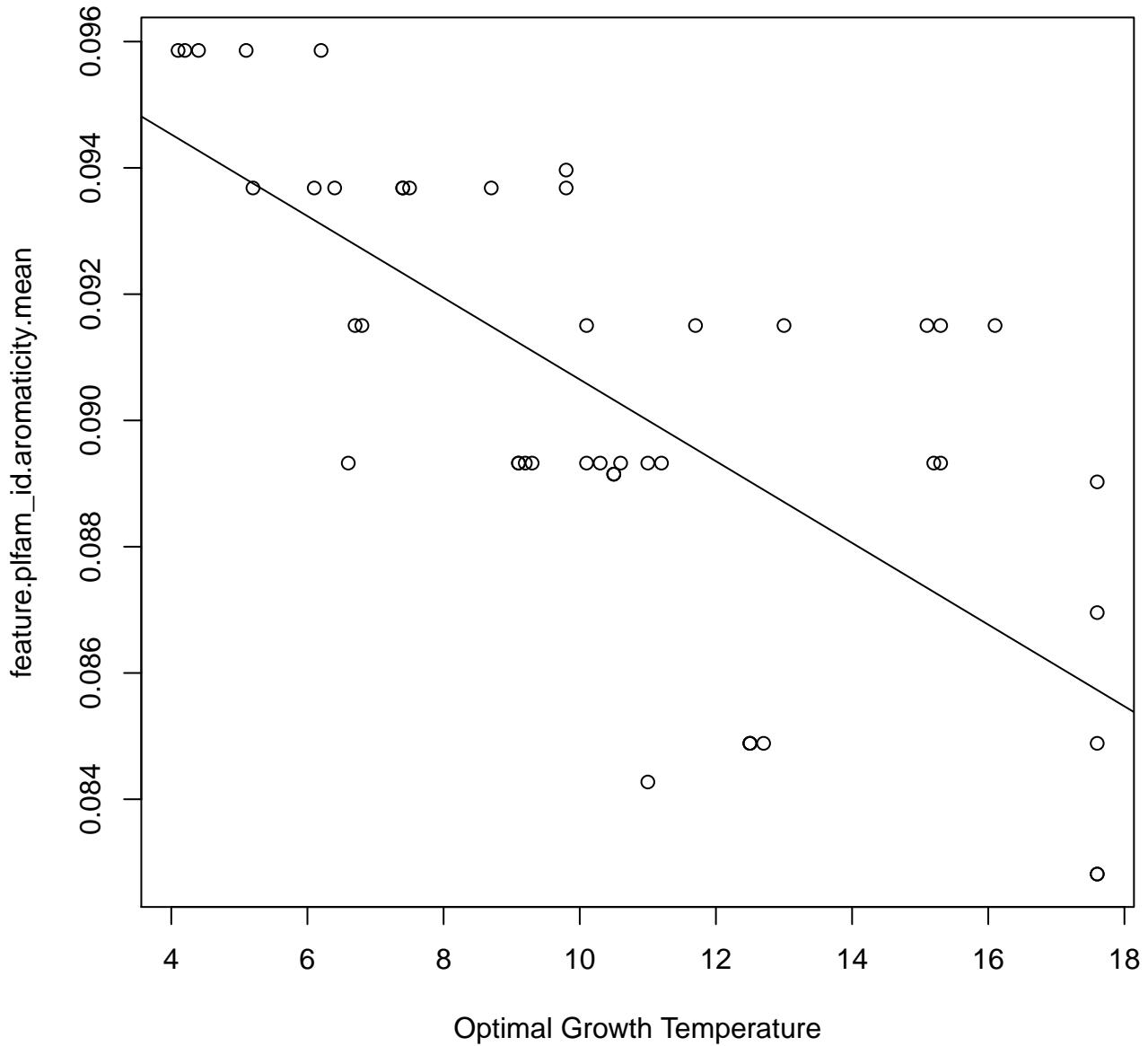
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PLF_28228_00000107
N-acetyl glucosamine transporter, NagP



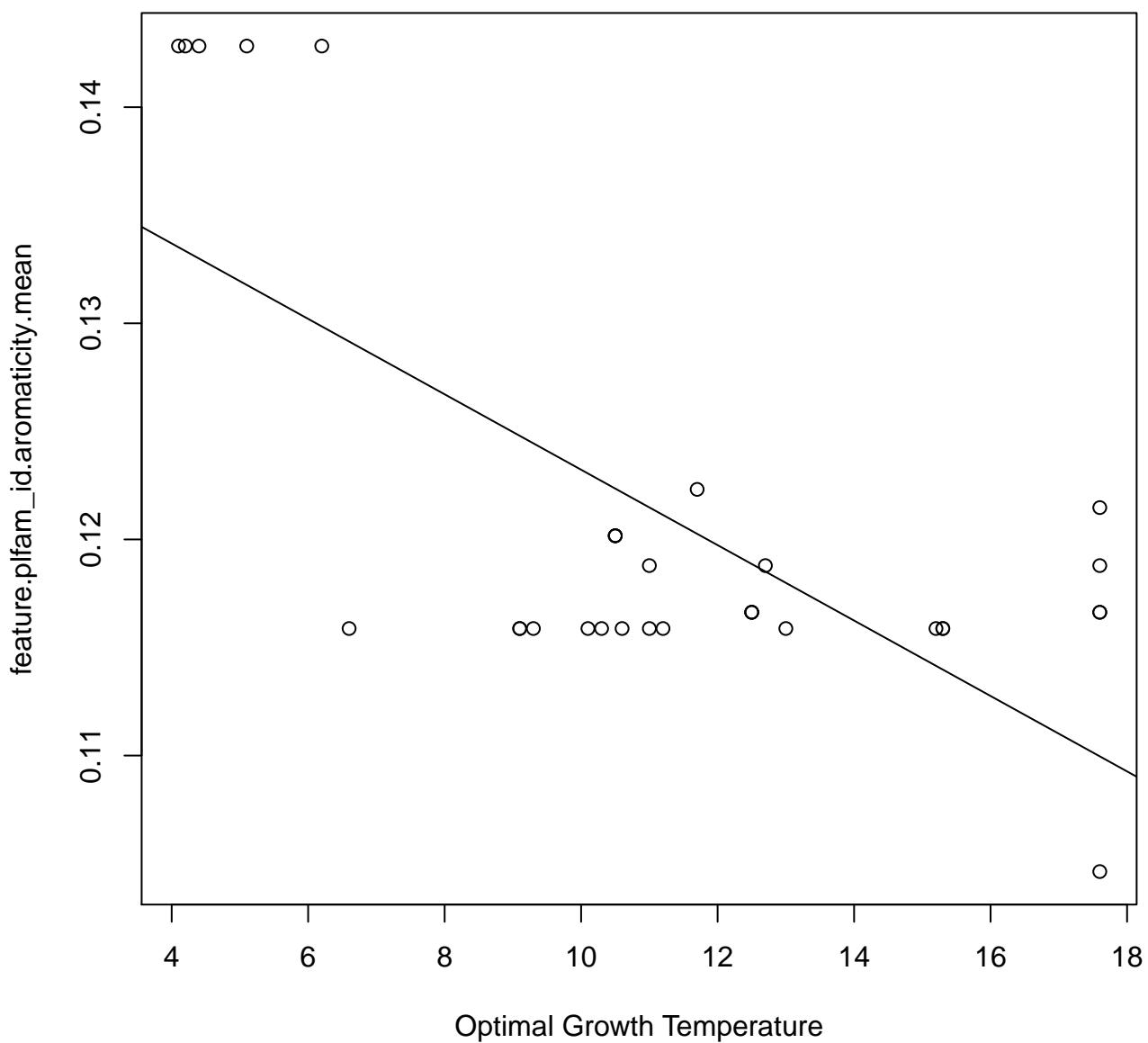
feature.plfam_id.aromaticity.mean
PLF_28228_00000629
N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)



feature.plfam_id.aromaticity.mean
PLF_28228_00000981
Predicted ATPase related to phosphate starvation-inducible protein PhoH



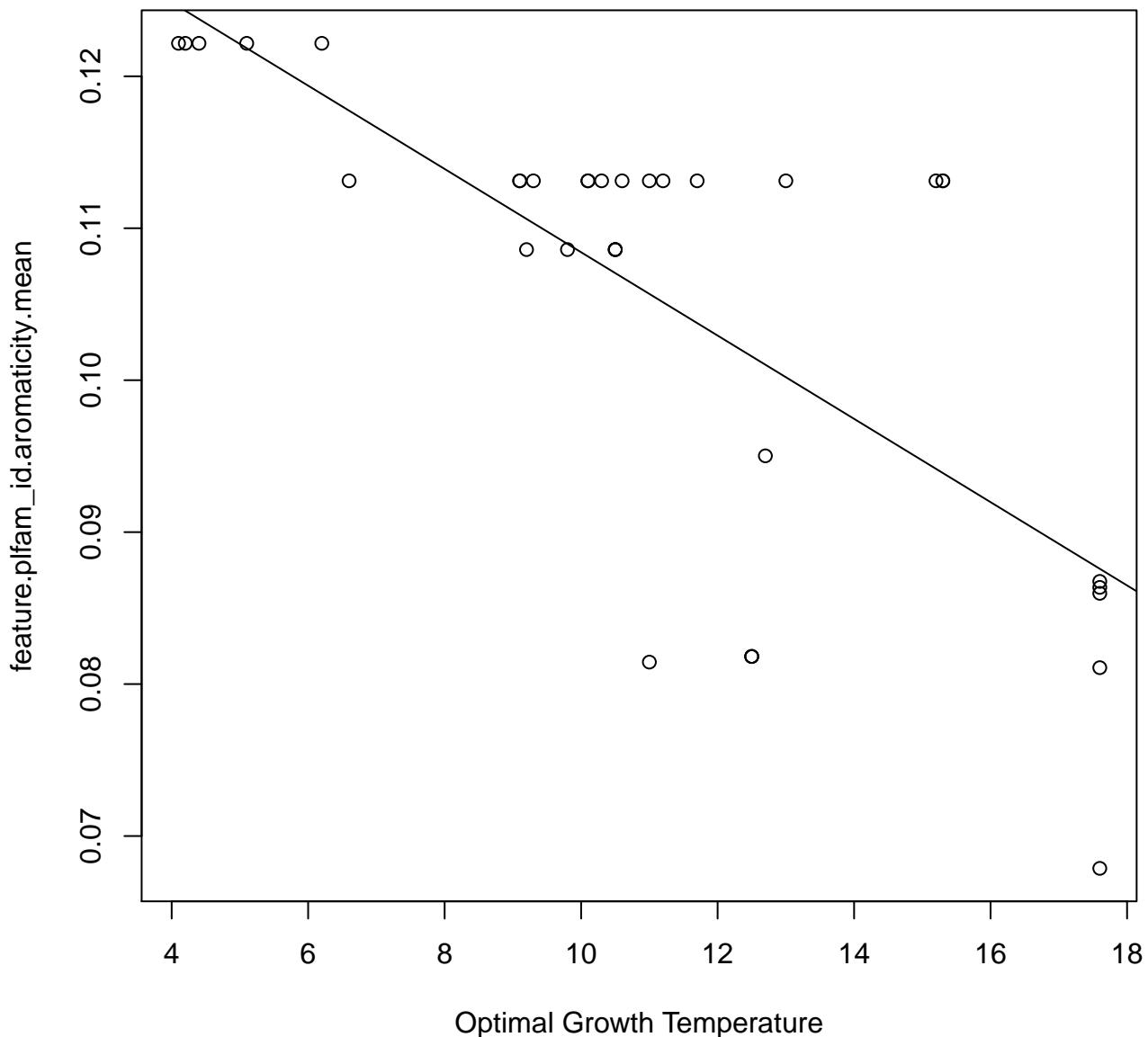
feature.pfam_id.aromaticity.mean
PLF_28228_00001289
Uncharacterized protease YegQ



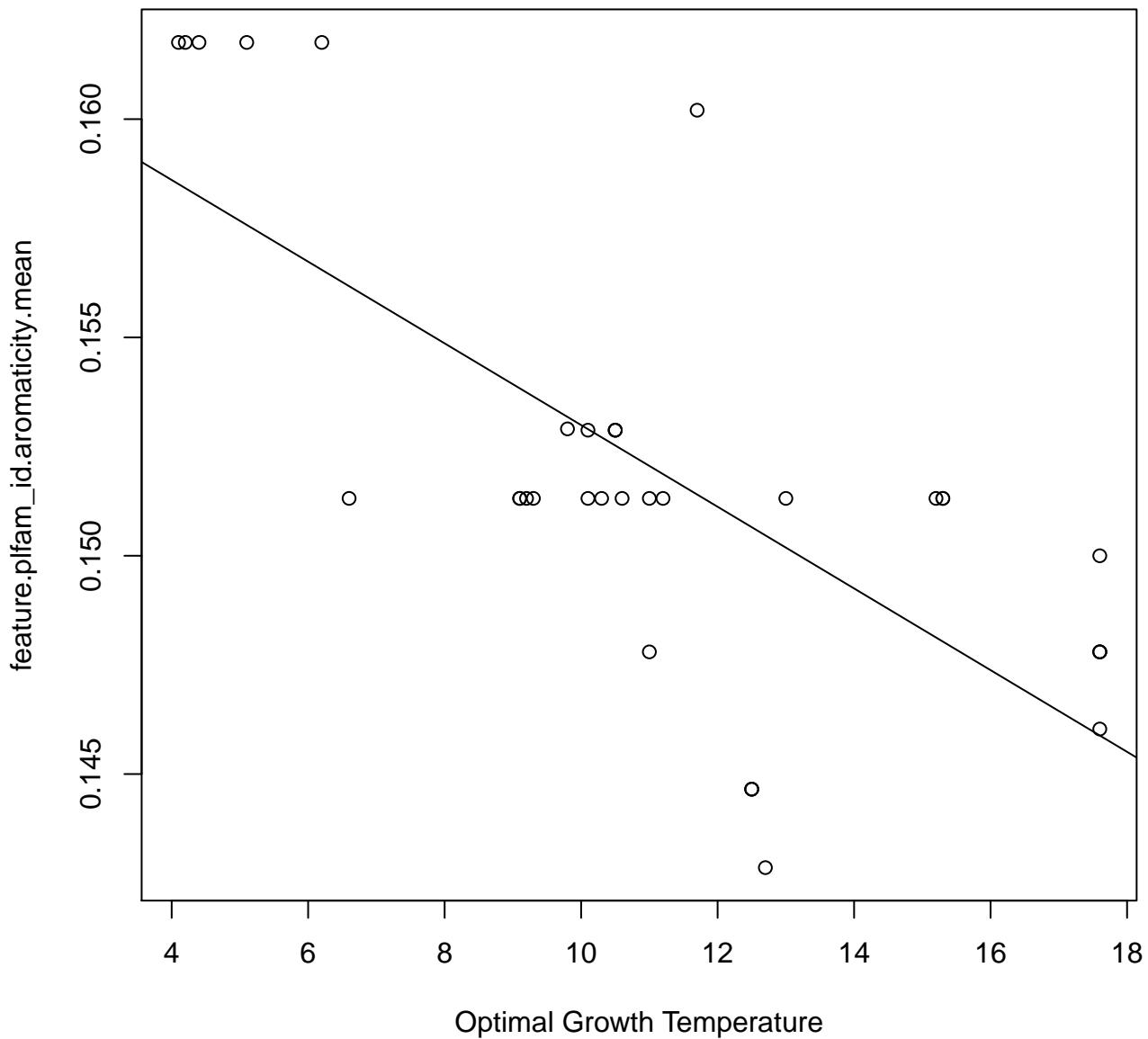
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PLF_28228_00001153

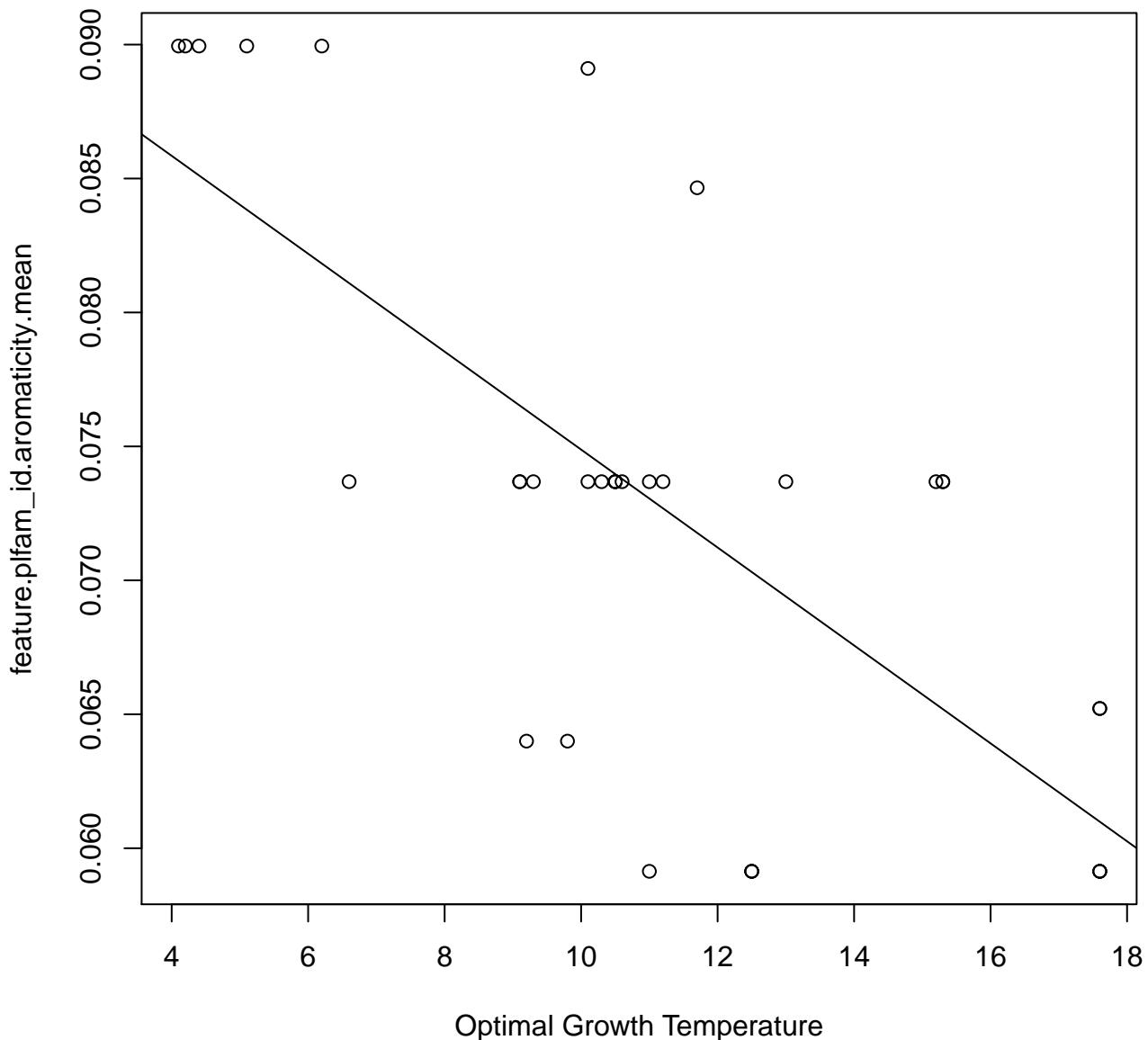
Similar to phosphoglycolate phosphatase, clustered with ribosomal large subunit pseudouridine synthase C



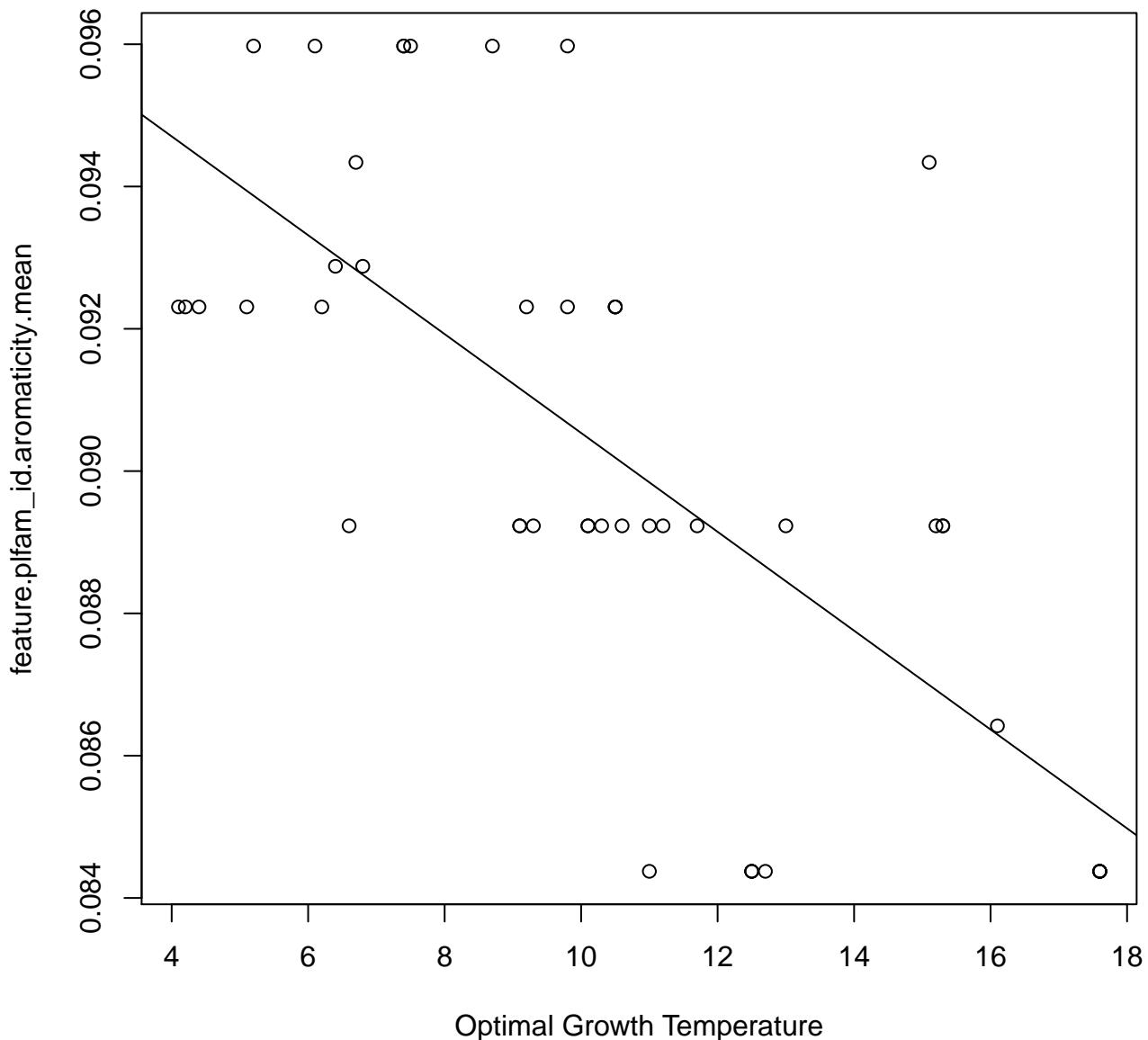
feature.plfam_id.aromaticity.mean
PLF_28228_00001949
Proline iminopeptidase (EC 3.4.11.5)



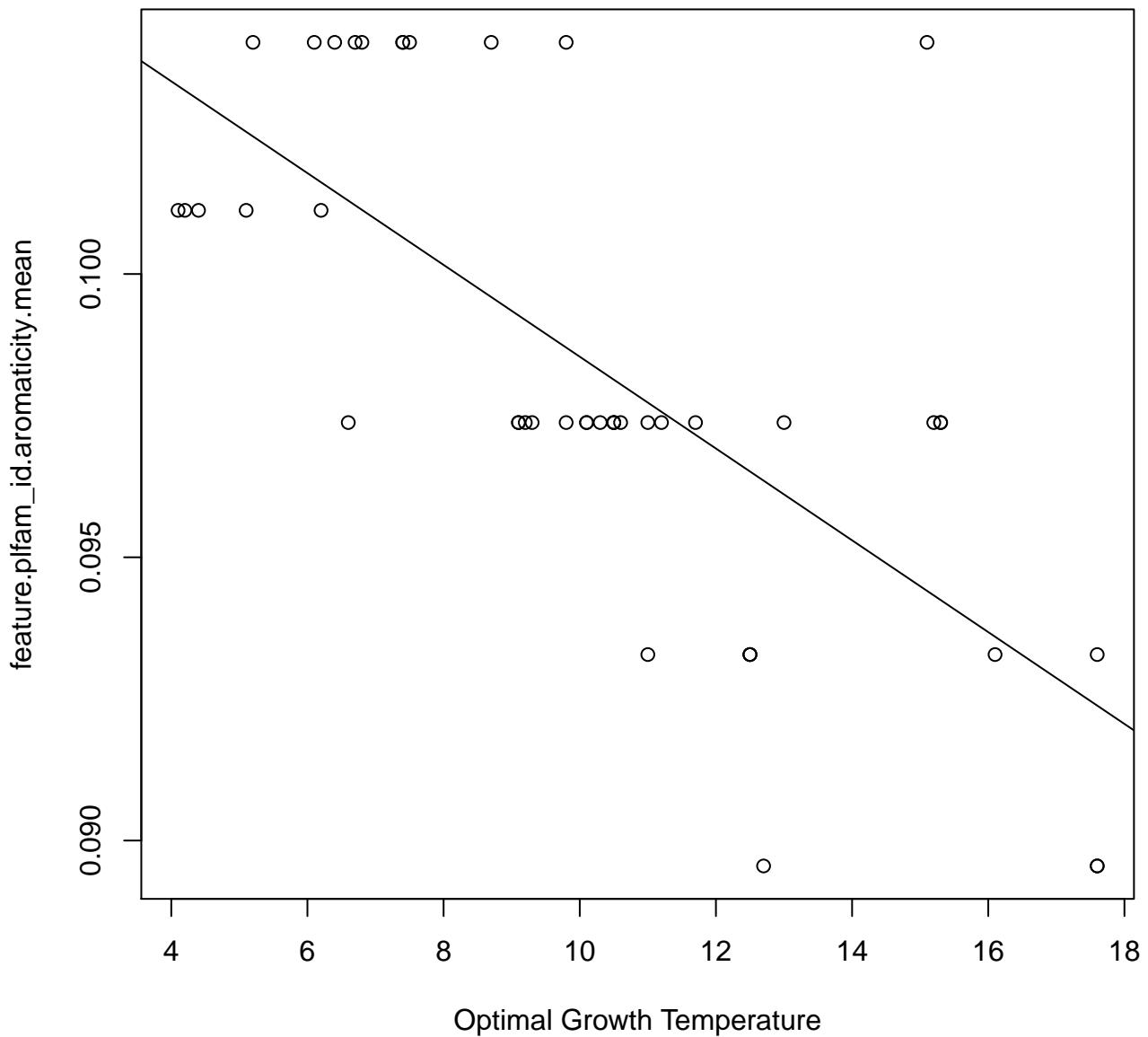
feature.plfam_id.aromaticity.mean
PLF_28228_00001484
Dna binding response regulator PrrA (RegA)



feature.plfam_id.aromaticity.mean
PLF_28228_00001186
Thiamine-monophosphate kinase (EC 2.7.4.16)



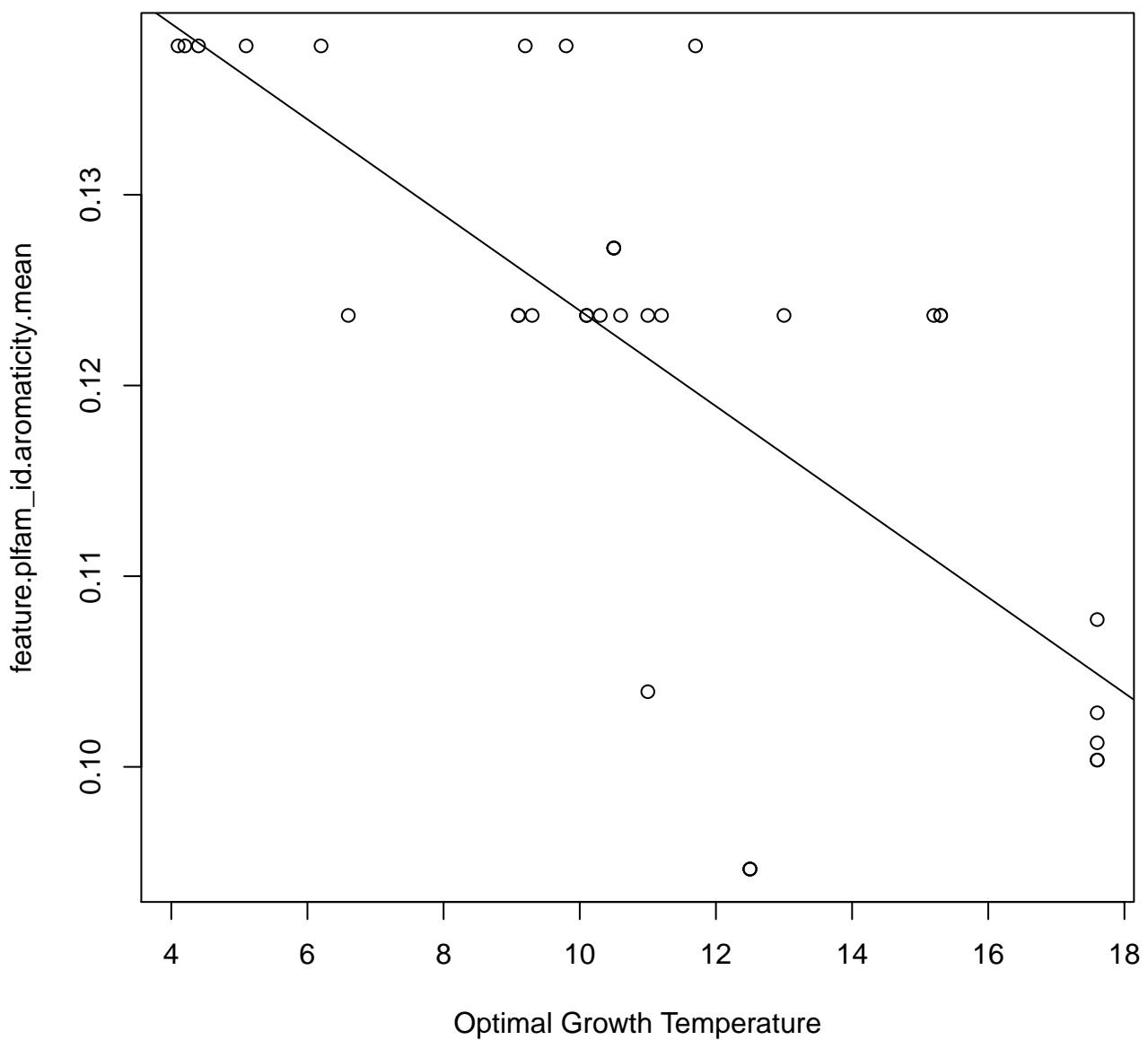
feature.plfam_id.aromaticity.mean
PLF_28228_00000719
4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)



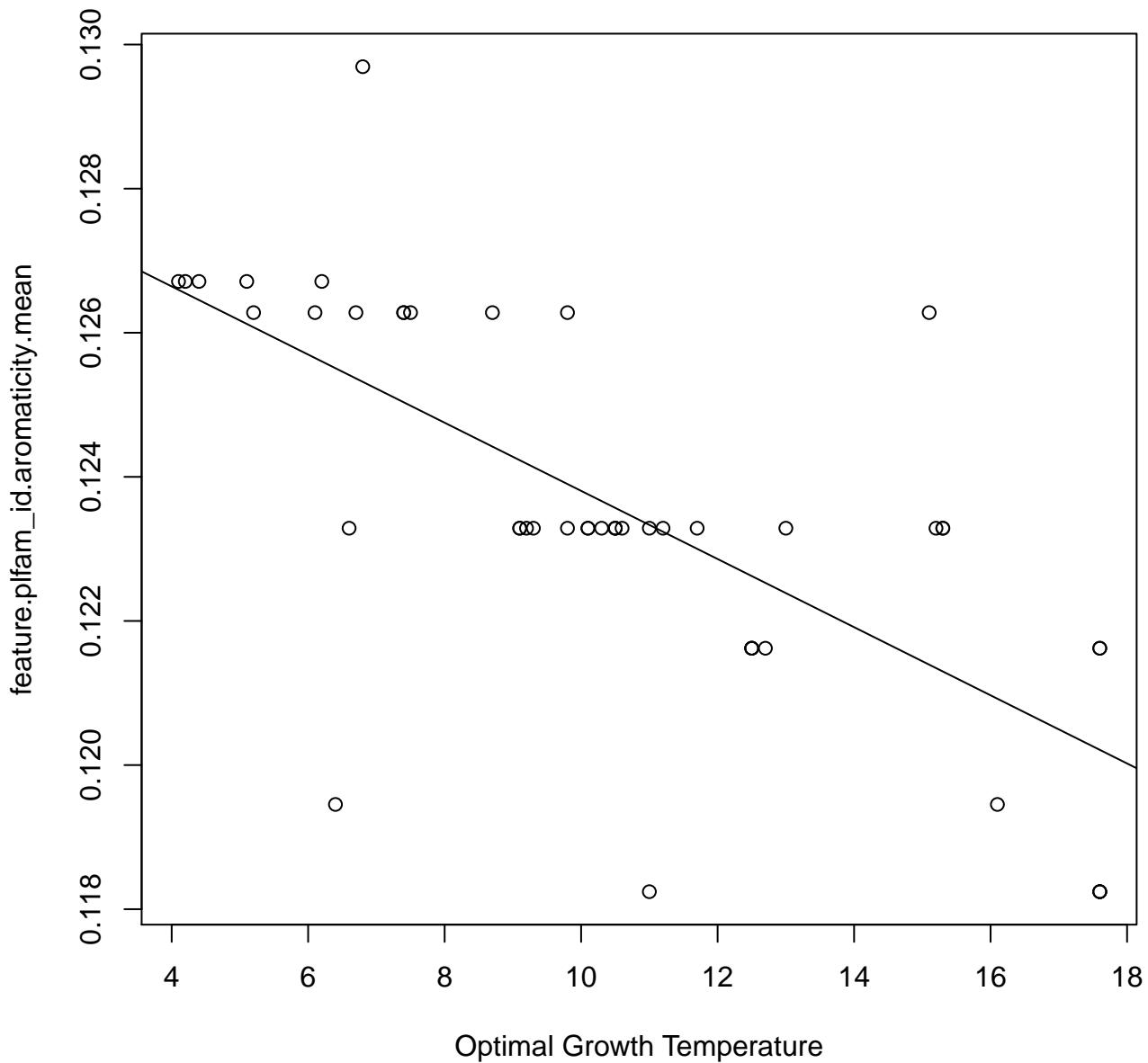
feature.pfam_id.aromaticity.mean

PLF_28228_00002949

hypothetical protein



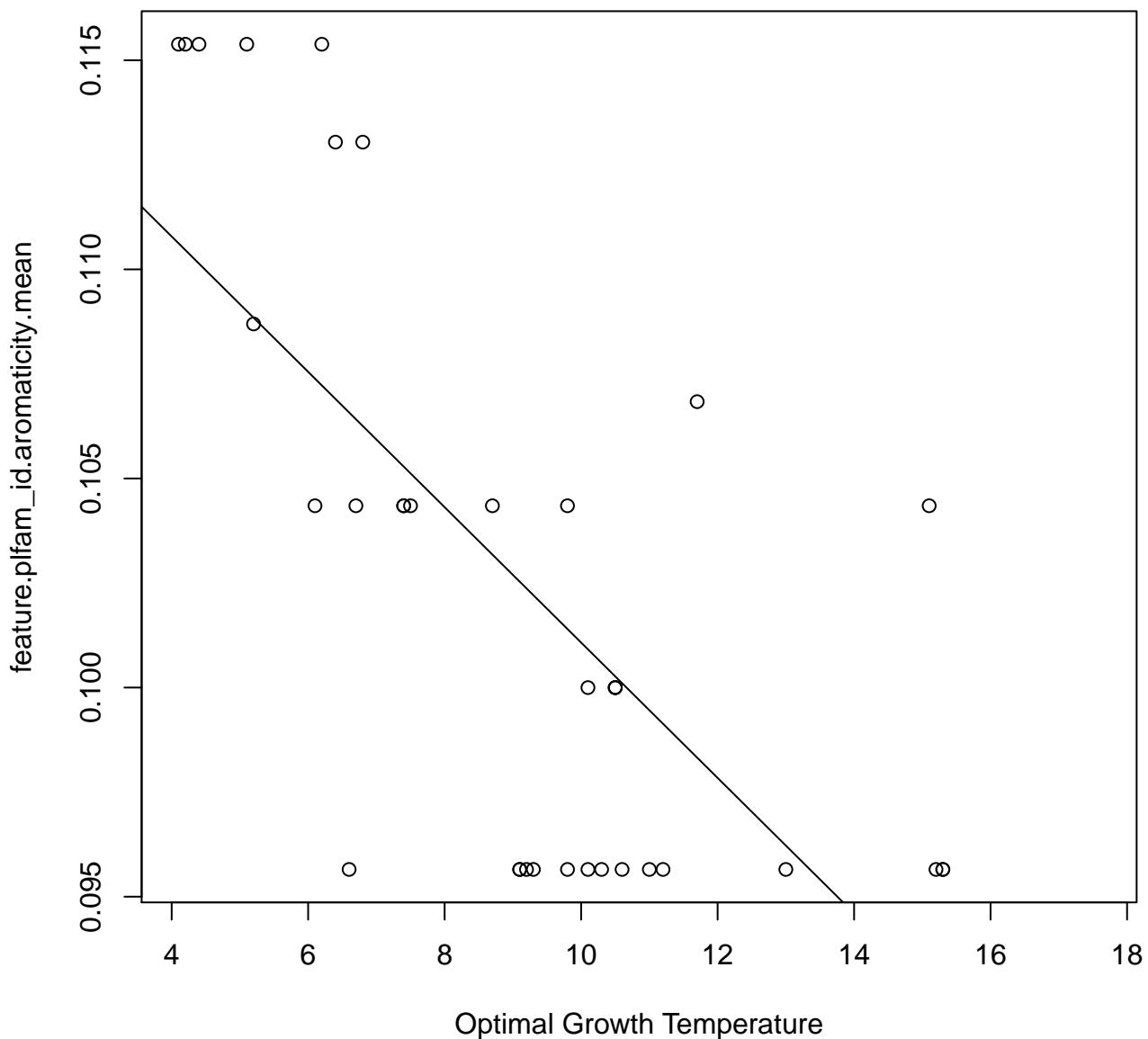
feature.plfam_id.aromaticity.mean
PLF_28228_00002316
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



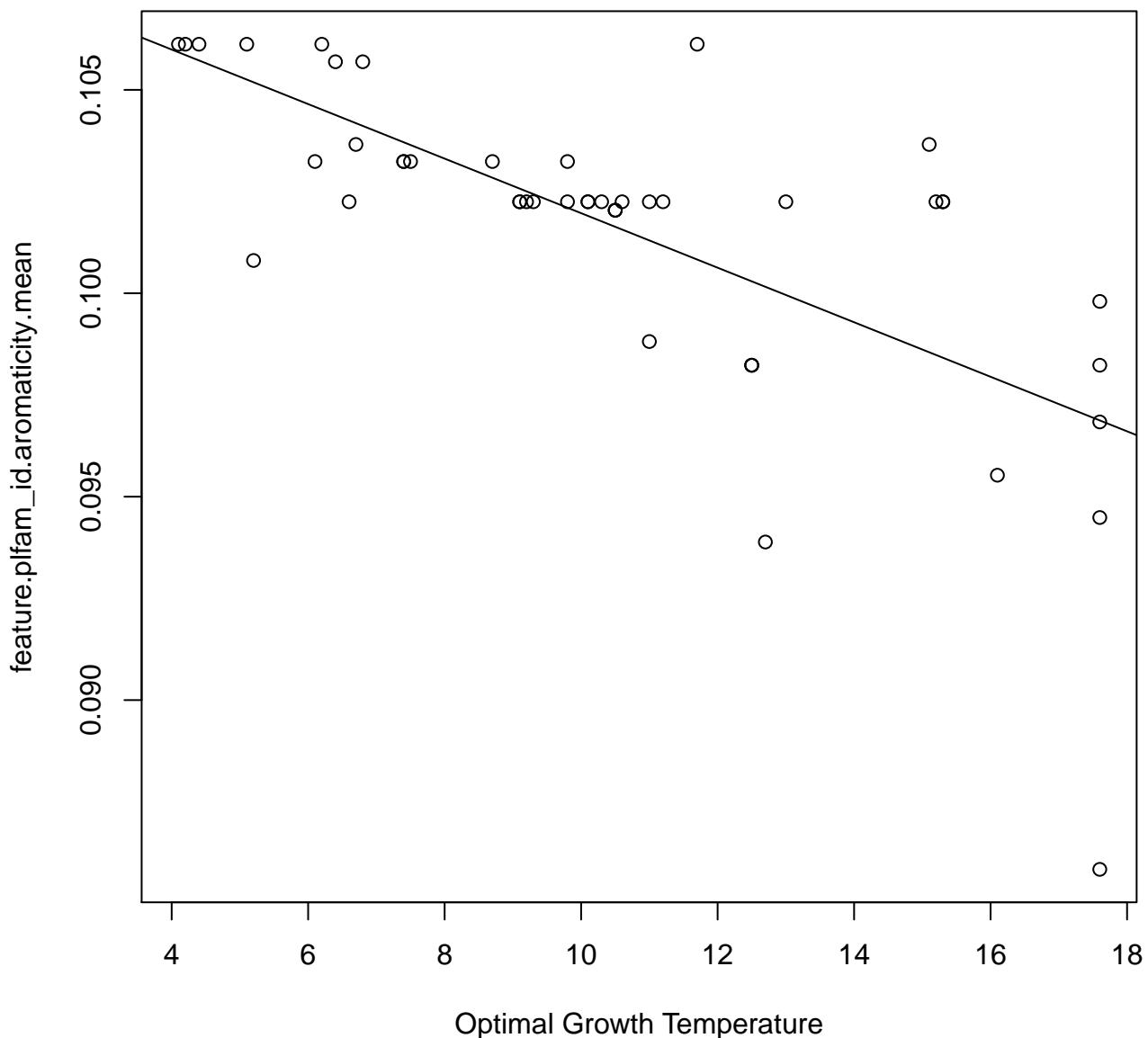
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PLF_28228_00006398

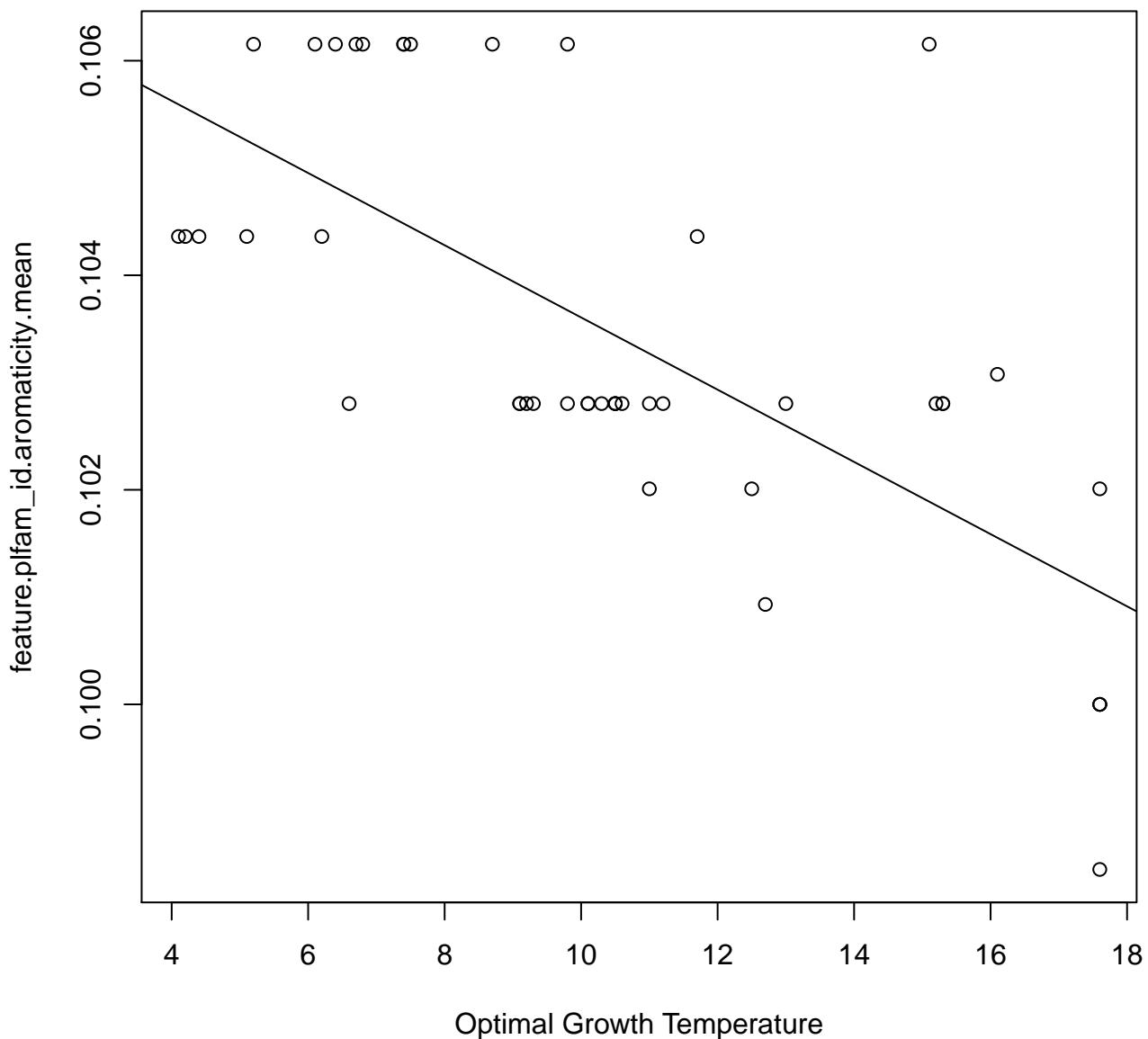
hypothetical protein



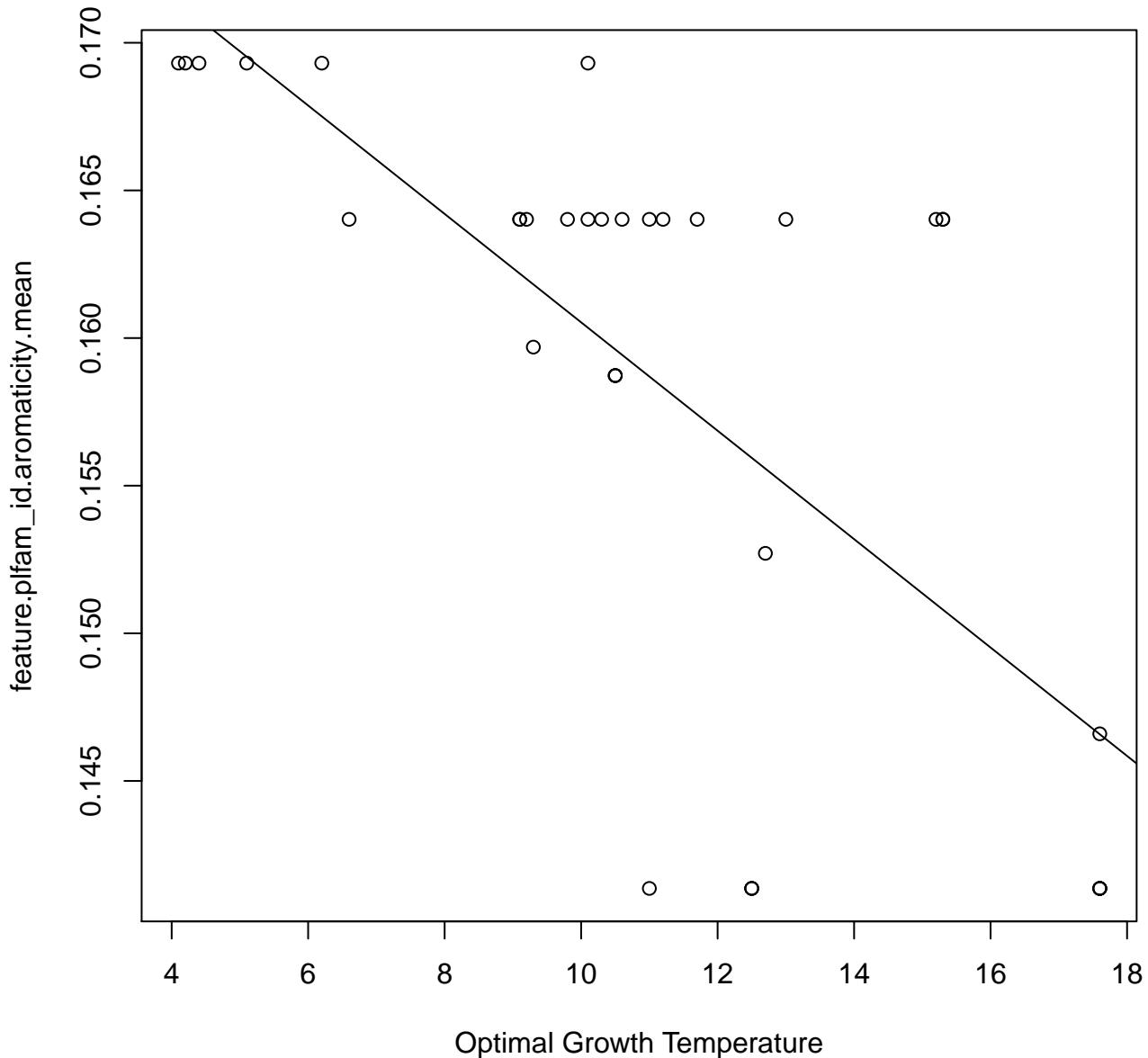
feature.pfam_id.aromaticity.mean
PLF_28228_00000848
Flagellar regulatory protein FleQ



feature.plfam_id.aromaticity.mean
PLF_28228_00028153
DinG family ATP-dependent helicase YoaA



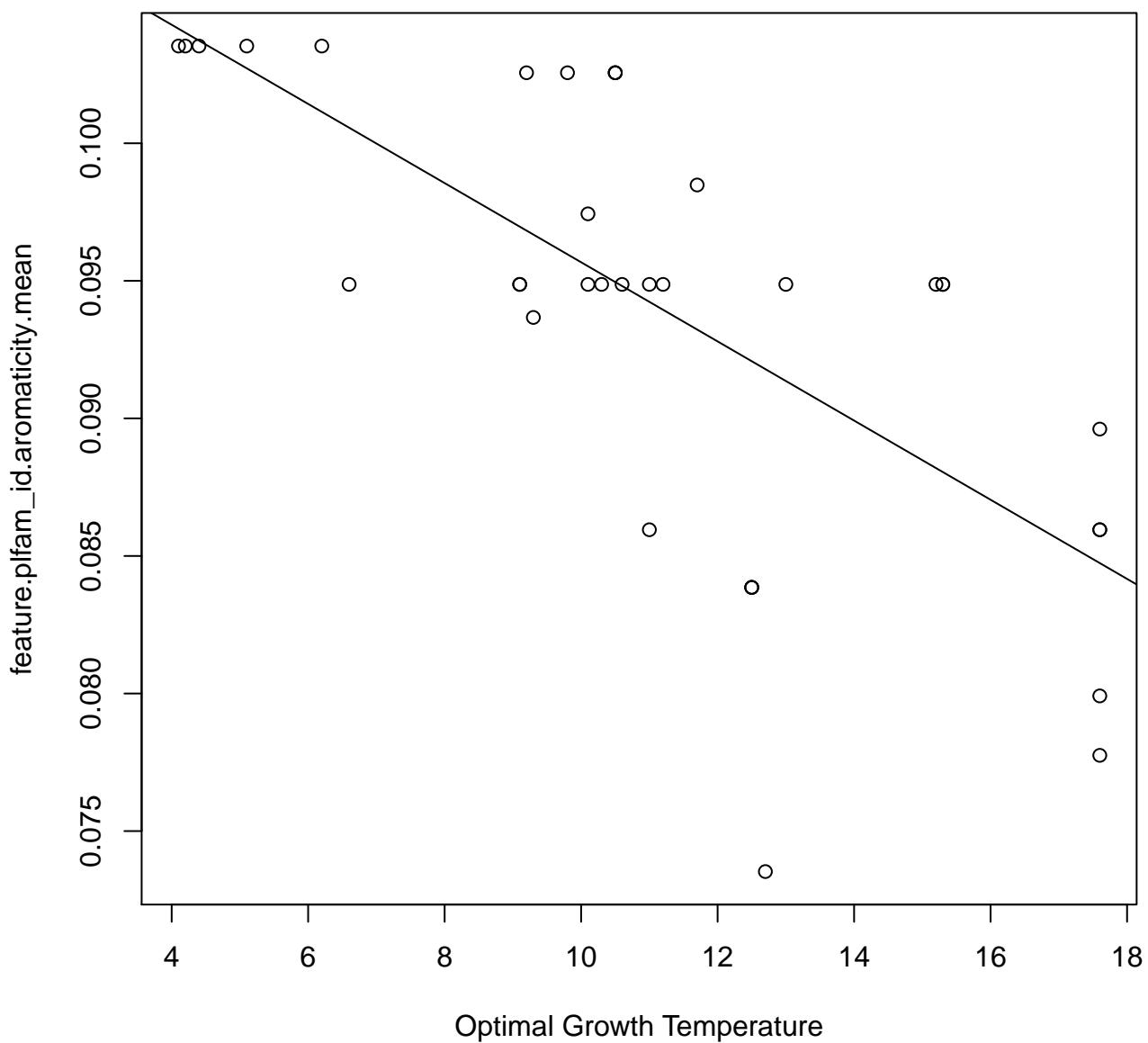
feature.pfam_id.aromaticity.mean
PLF_28228_00002187
Uncharacterized Nudix hydrolase NudL



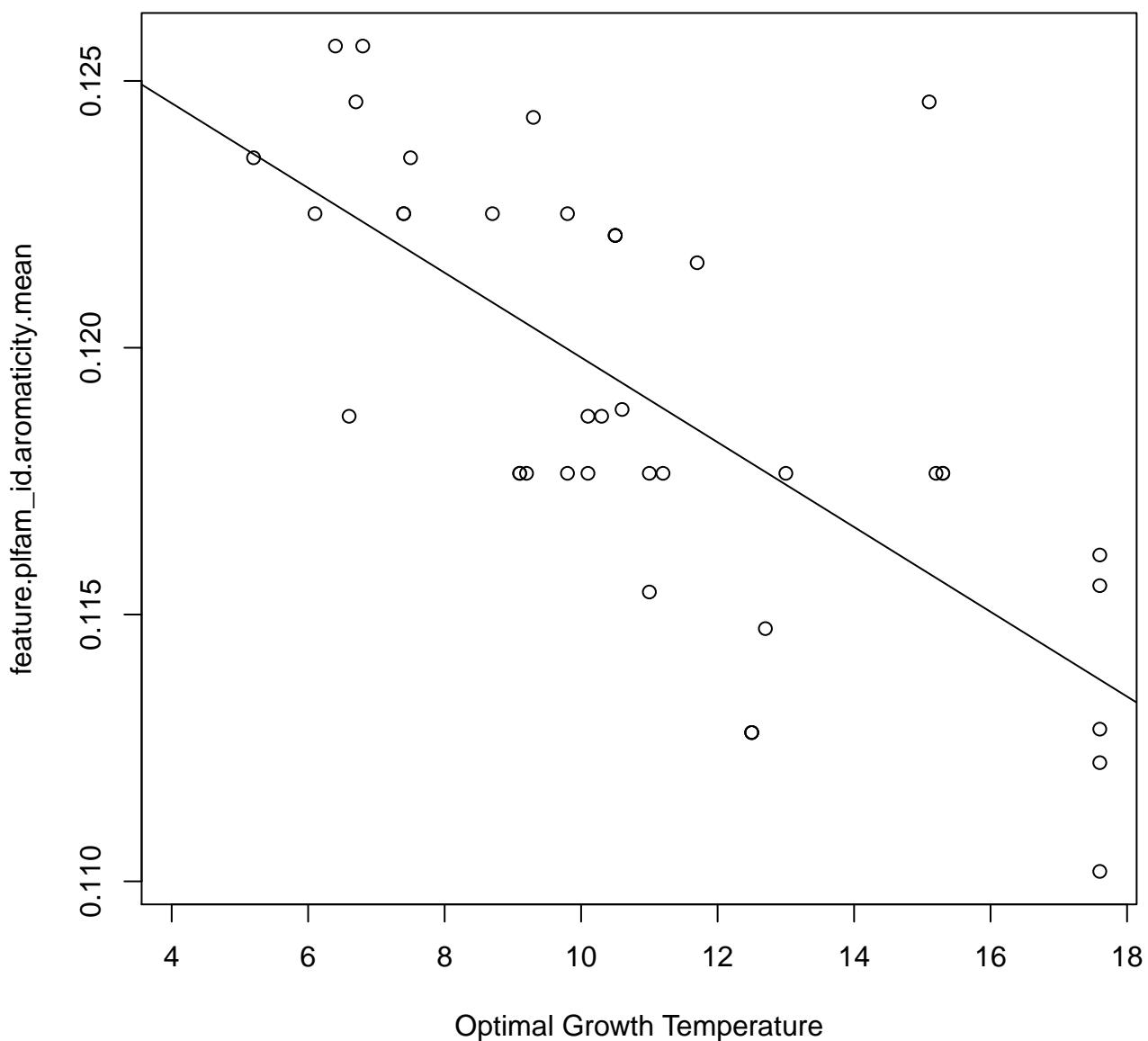
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PLF_28228_00002255

hypothetical protein



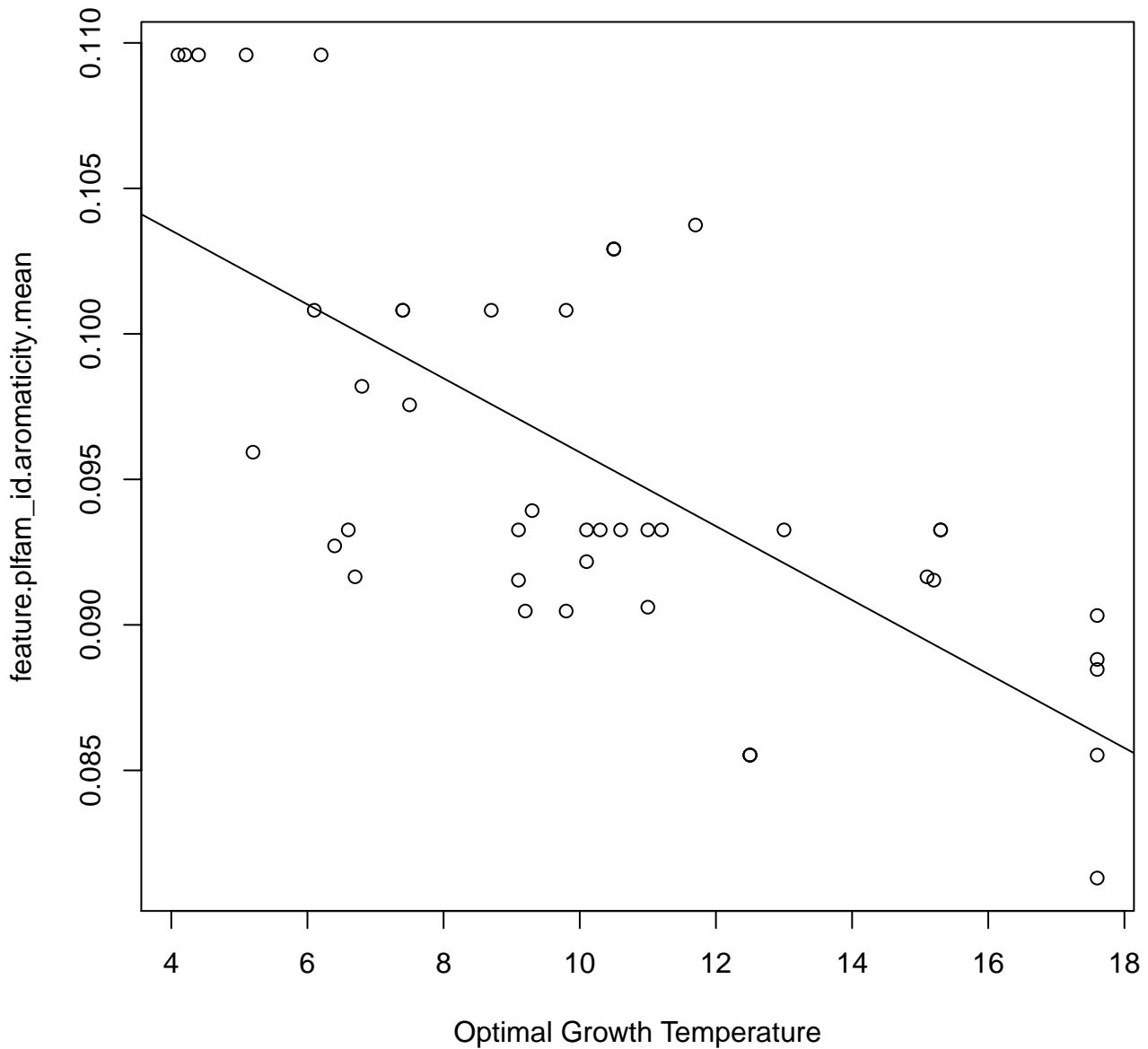
feature.pfam_id.aromaticity.mean
PLF_28228_00002166
Pullulanase (EC 3.2.1.41)



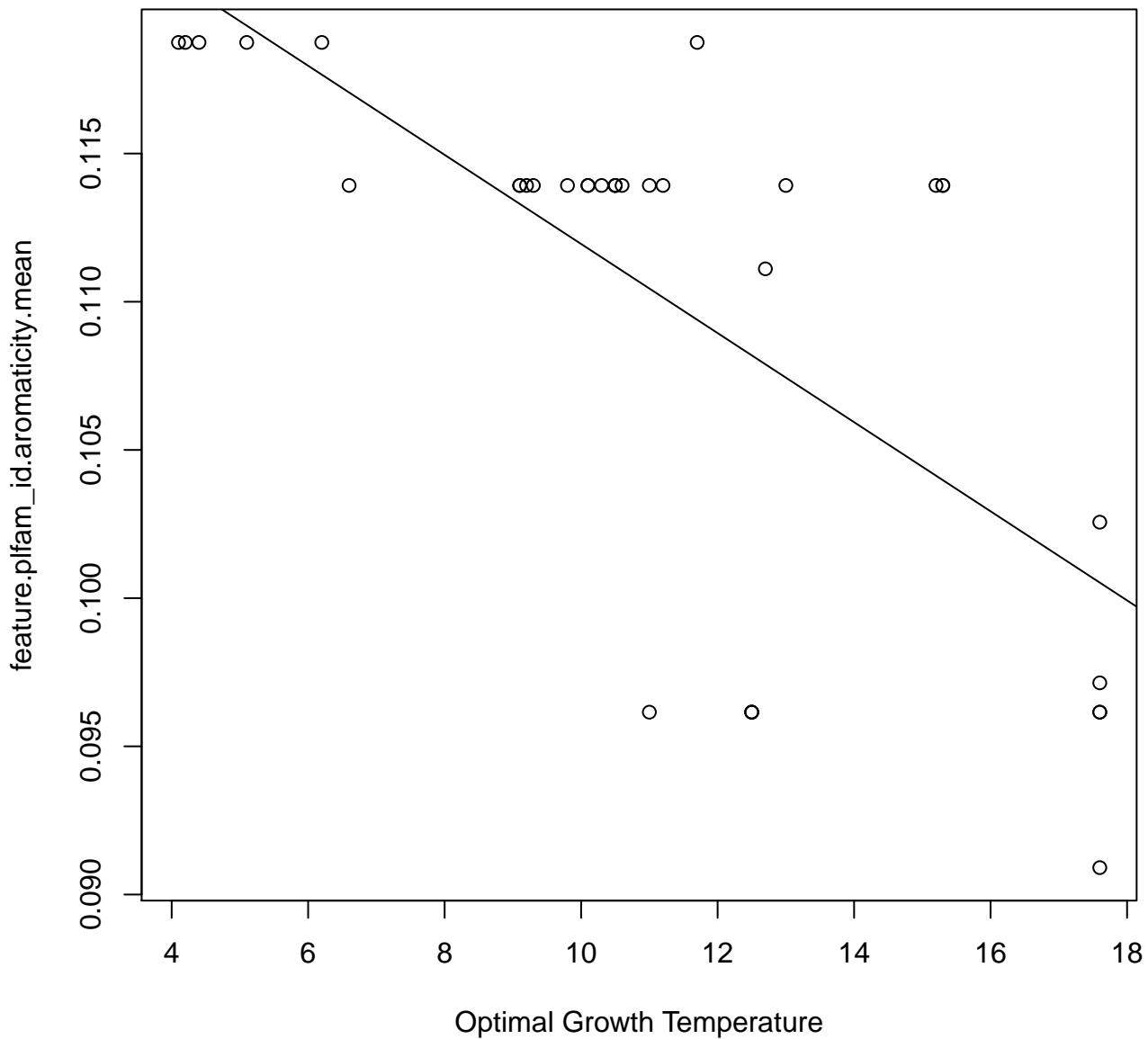
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PLF_28228_00002320

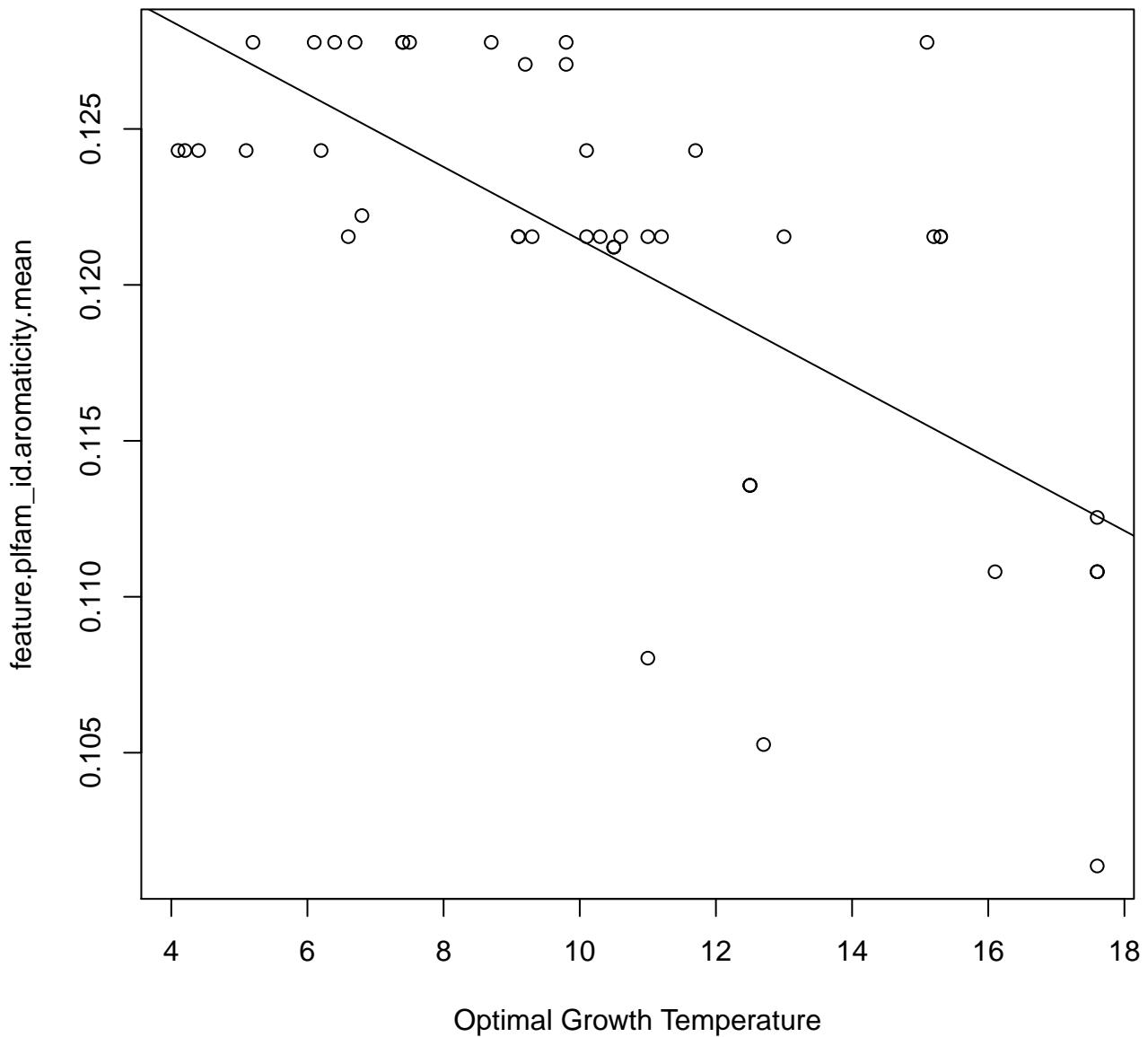
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00001748
Molybdopterin synthase catalytic subunit MoaE (EC 2.8.1.12)



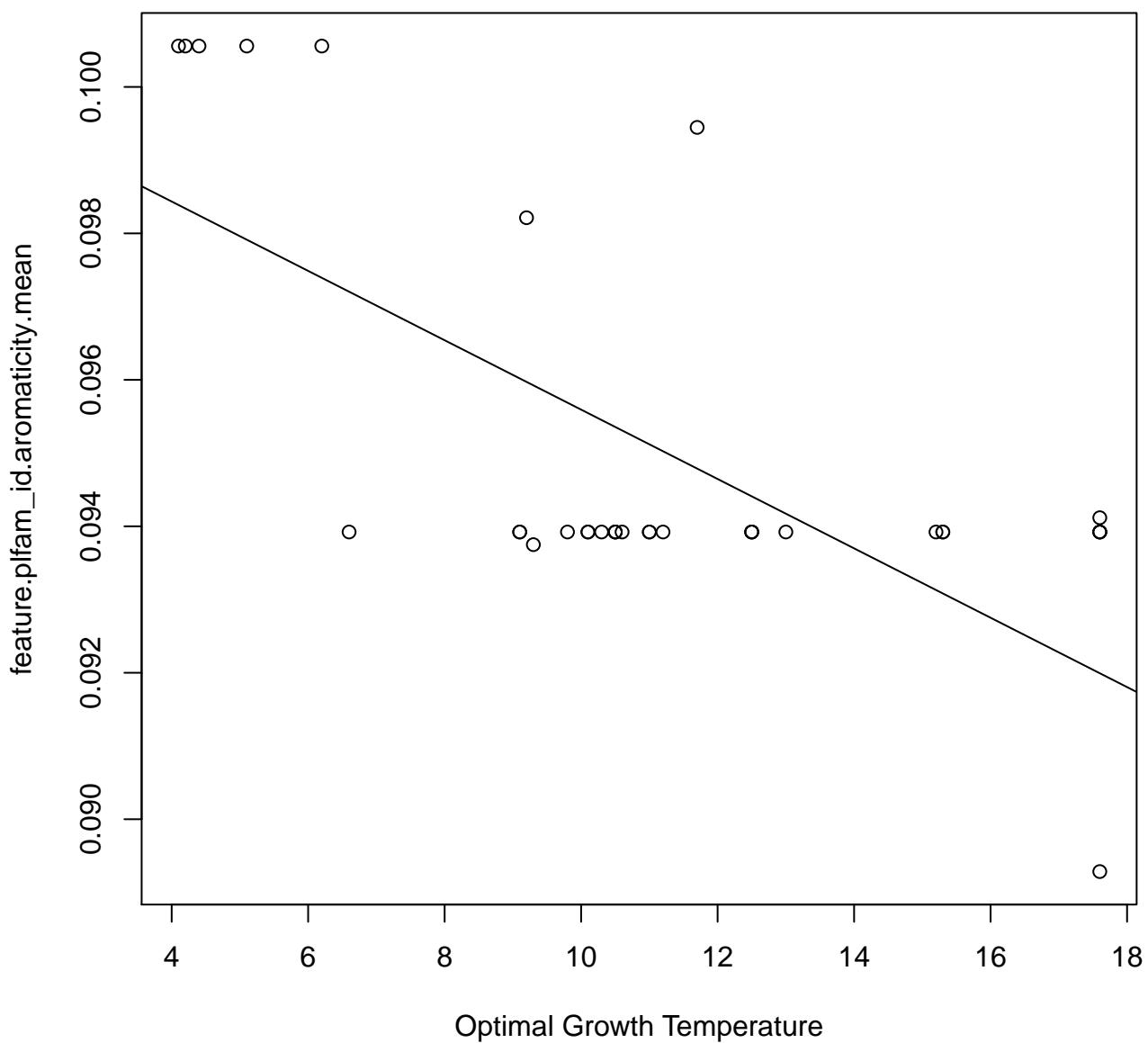
feature.plfam_id.aromaticity.mean
PLF_28228_00000973
Phosphoserine aminotransferase (EC 2.6.1.52)



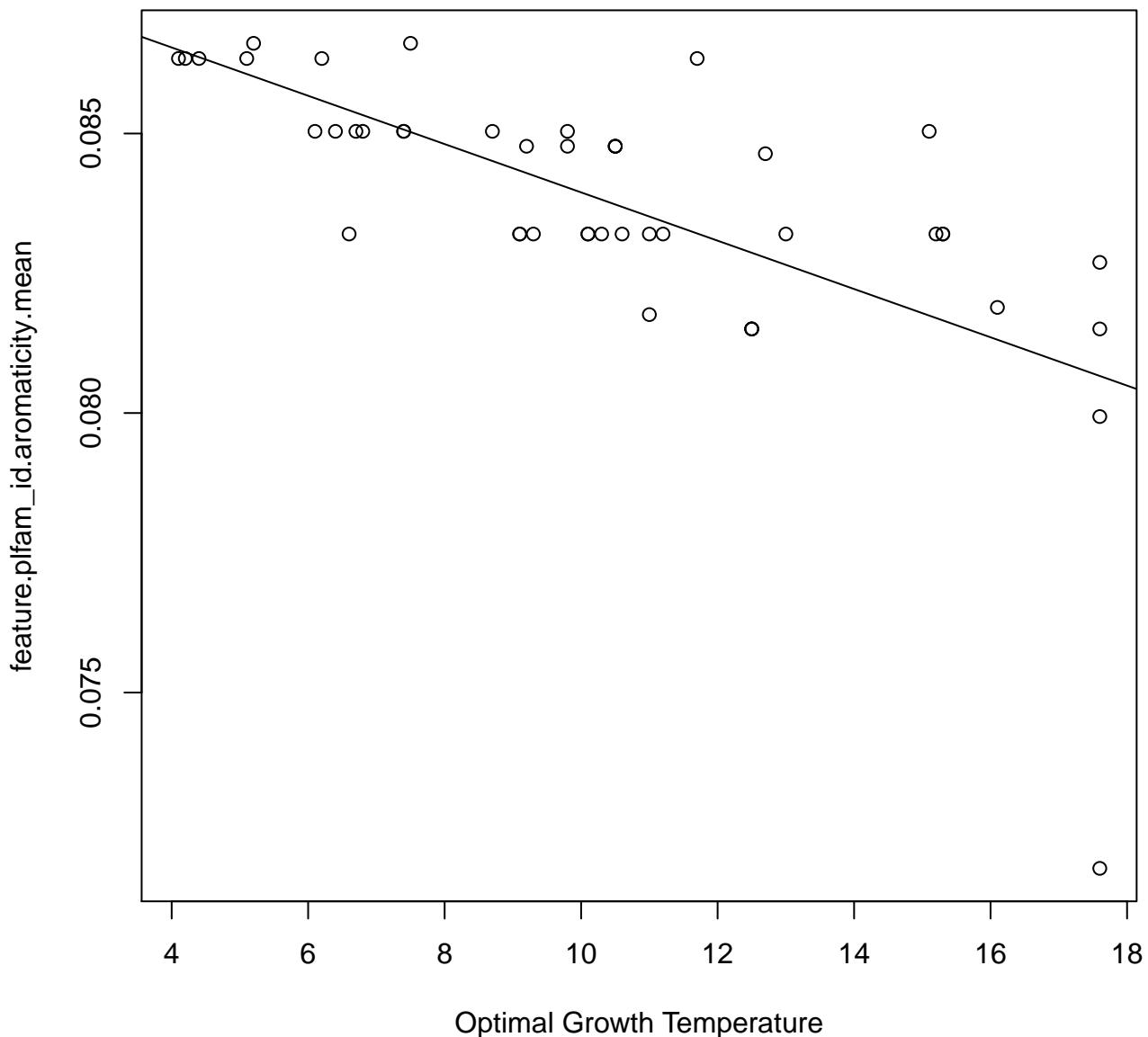
feature.pifam_id.aromaticity.mean

PLF_28228_00002946

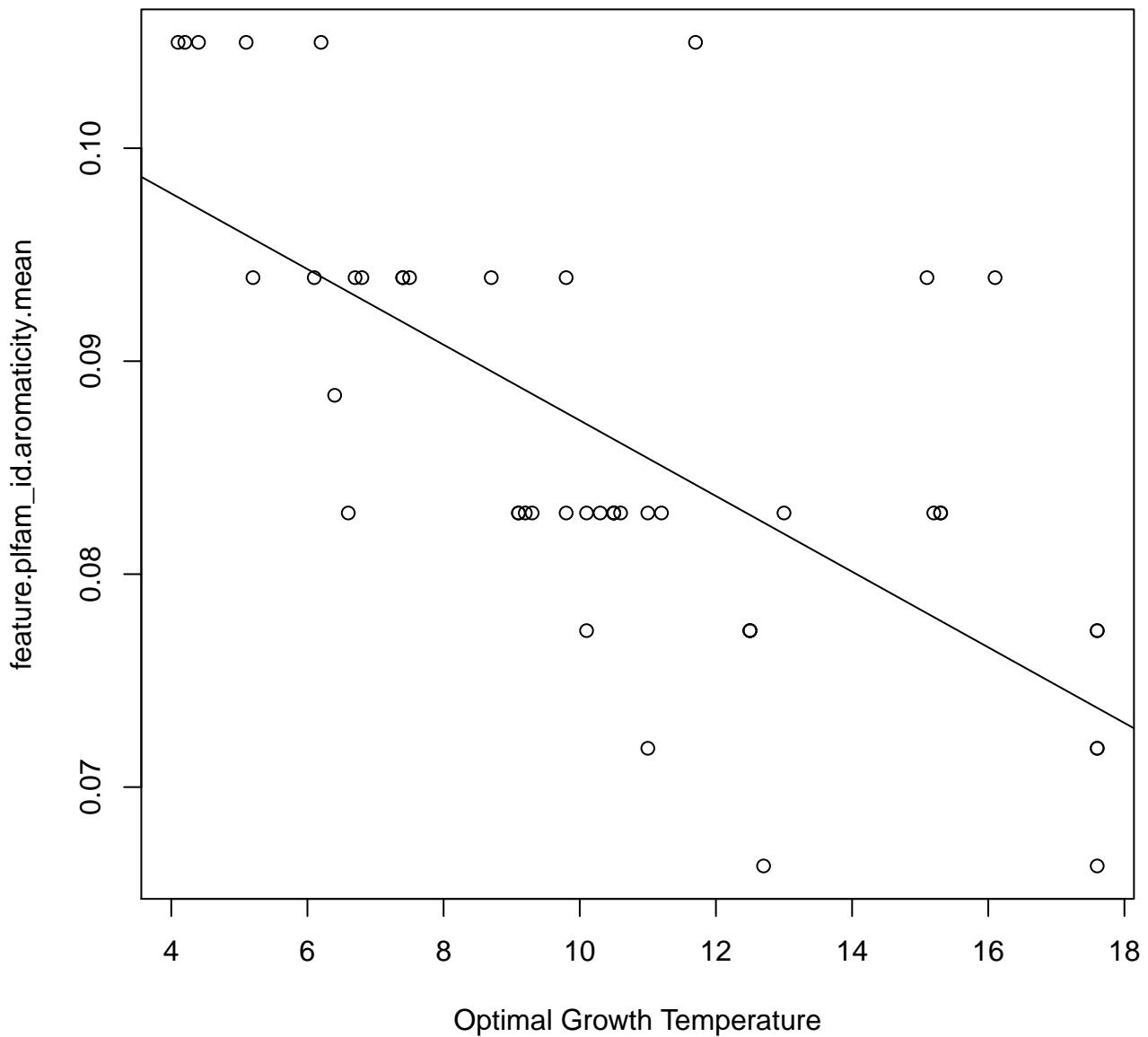
hypothetical protein



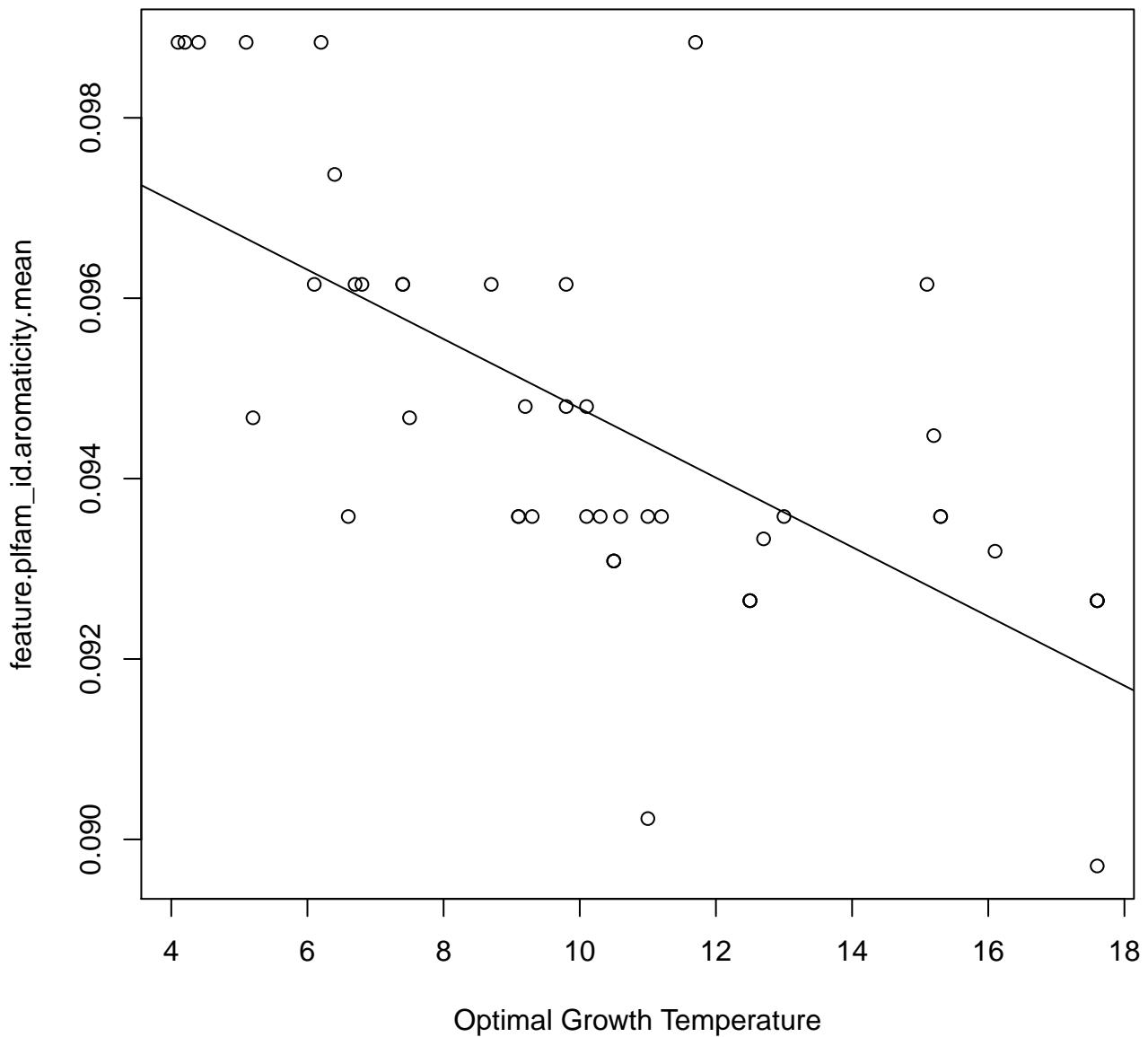
feature.plfam_id.aromaticity.mean
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Peptidyl-prolyl cis-trans isomerase PpiD (EC 5.2.1.8)



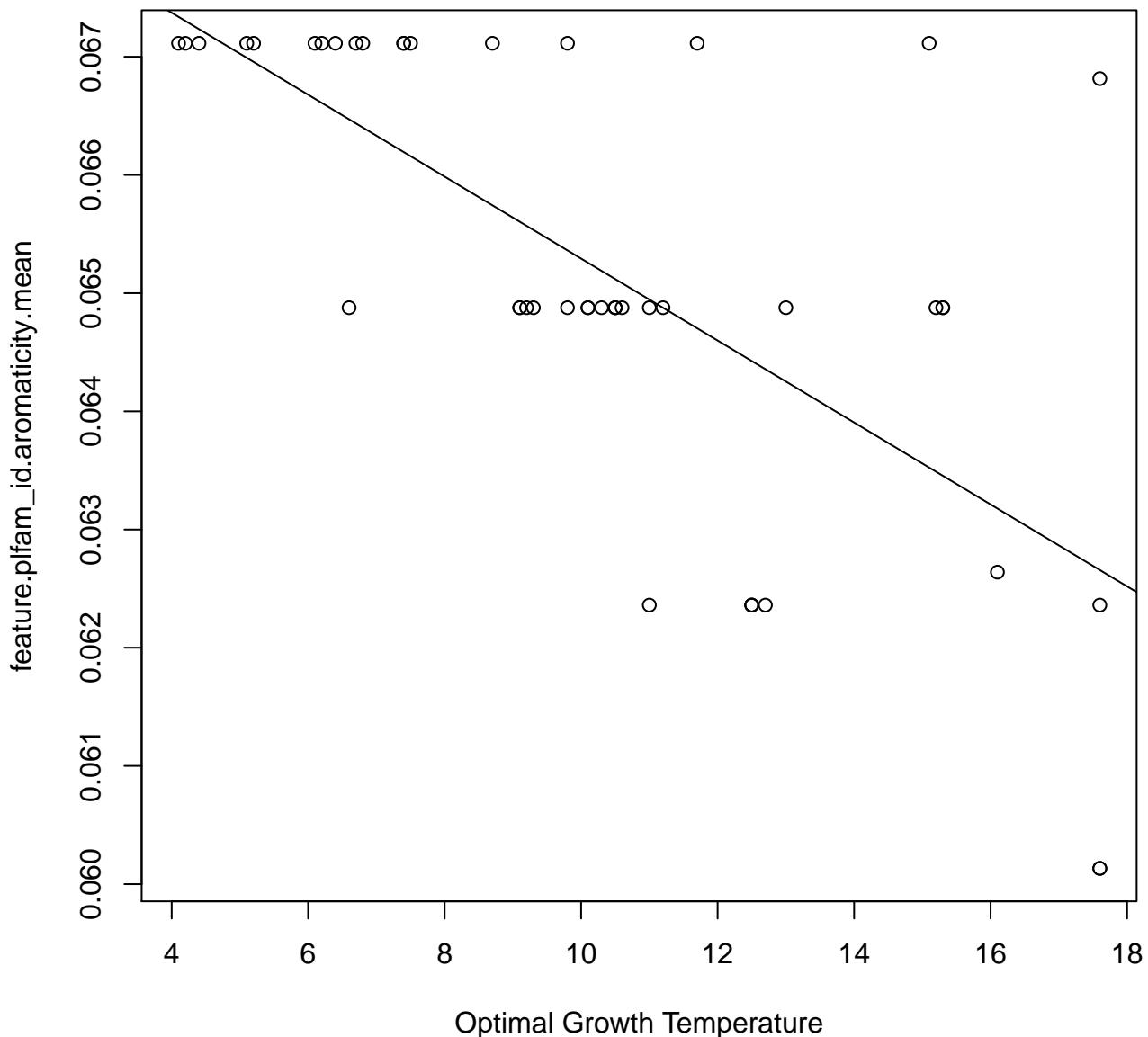
feature.plfam_id.aromaticity.mean
PLF_28228_00000267
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)



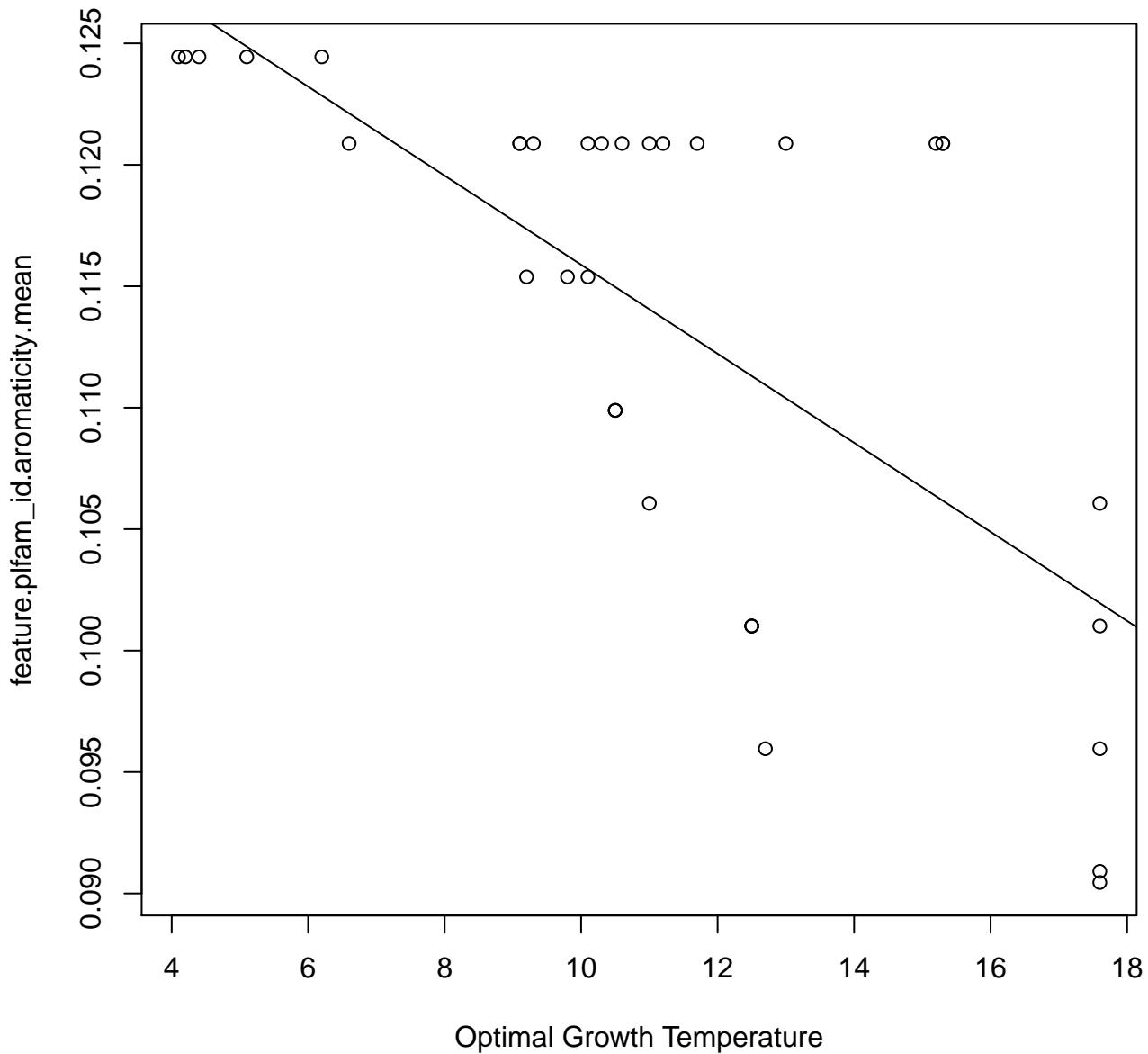
feature.plfam_id.aromaticity.mean
PLF_28228_00000071
2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)



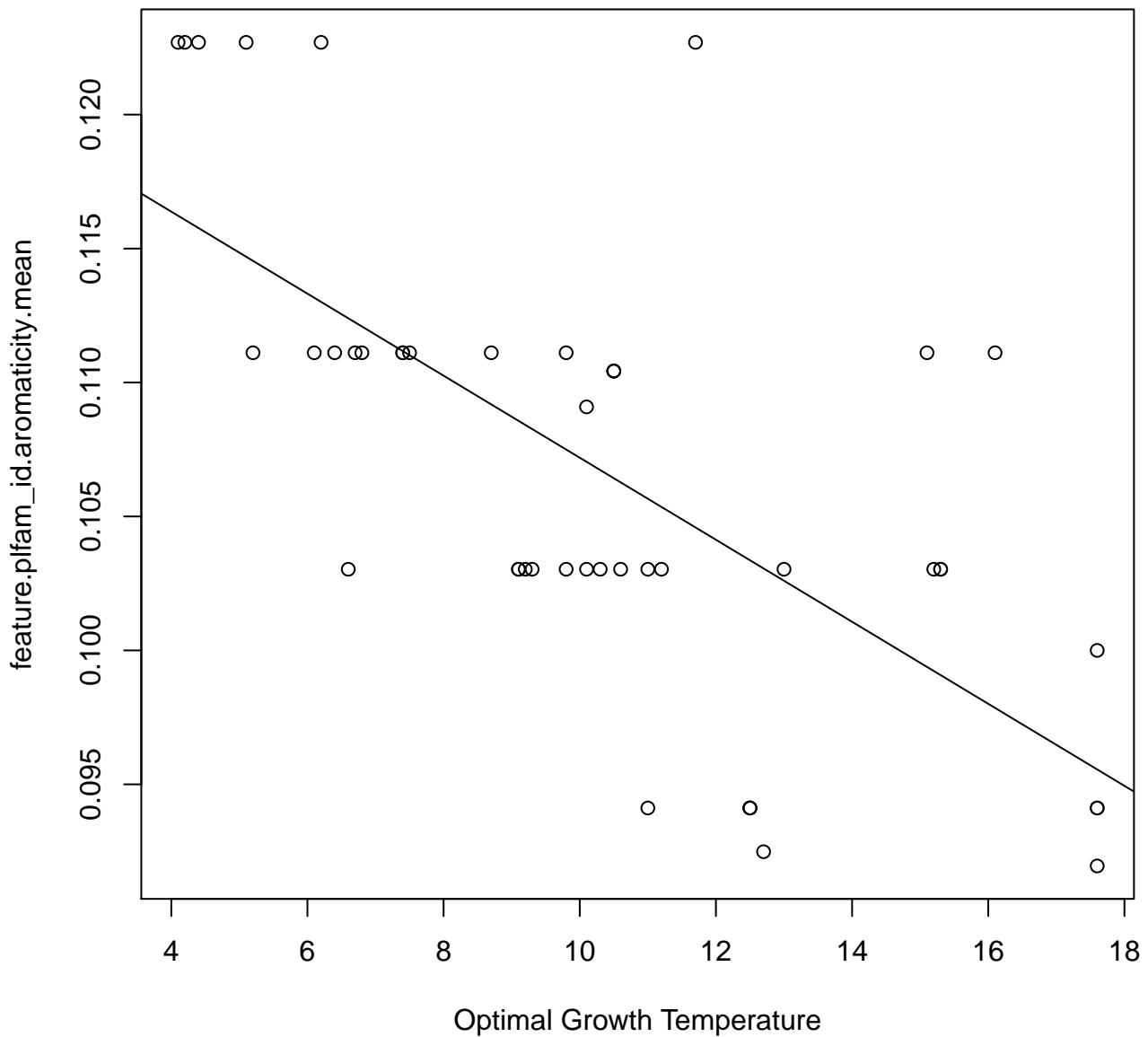
feature.plfam_id.aromaticity.mean
PLF_28228_00000622
MotA/ToIQ/ExbB proton channel family protein



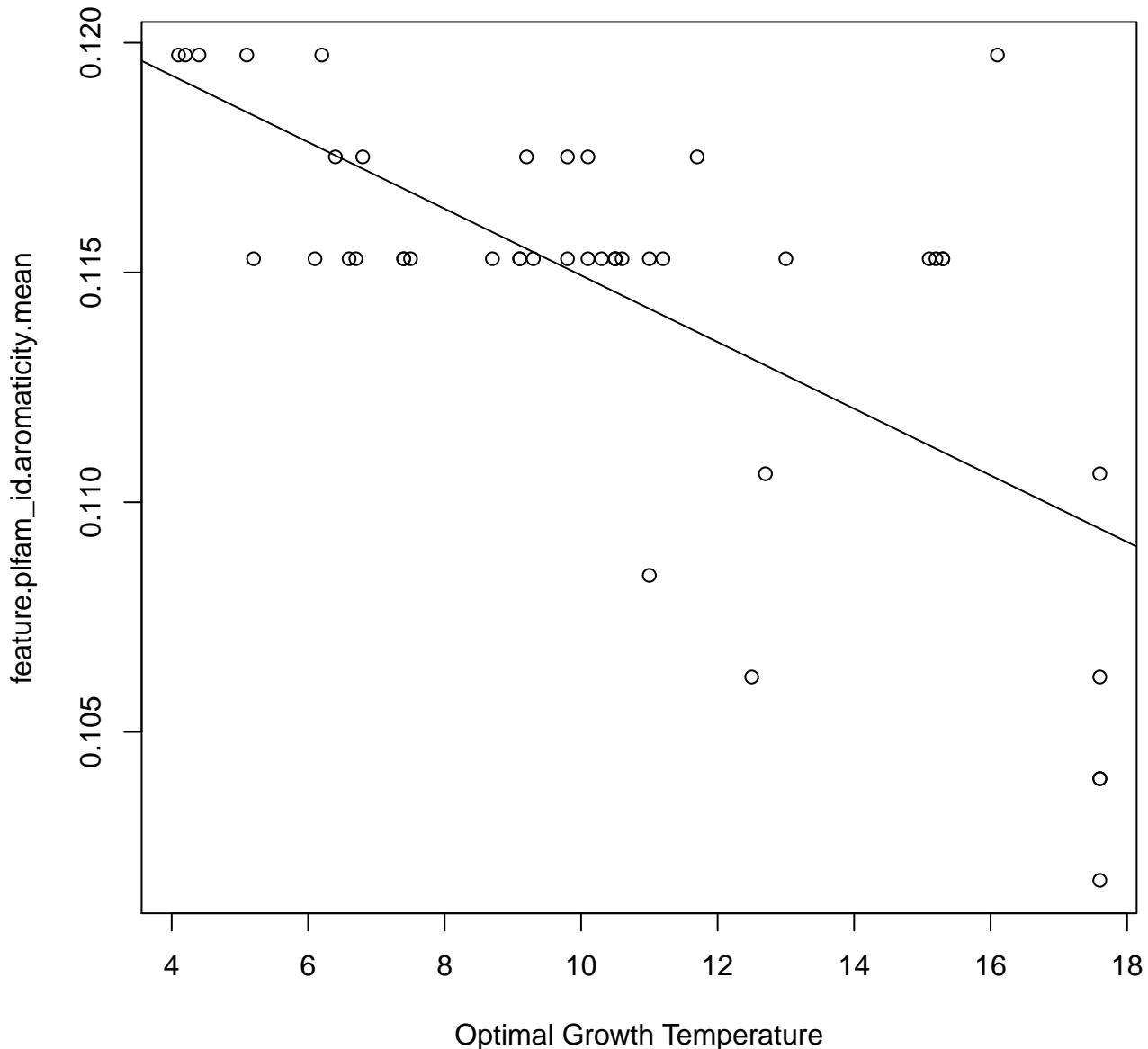
feature.pfam_id.aromaticity.mean
PLF_28228_00001024
Putative NAD(P)H nitroreductase YdjA



feature.pfam_id.aromaticity.mean
PLF_28228_00000781
Dihydrofolate reductase (EC 1.5.1.3)



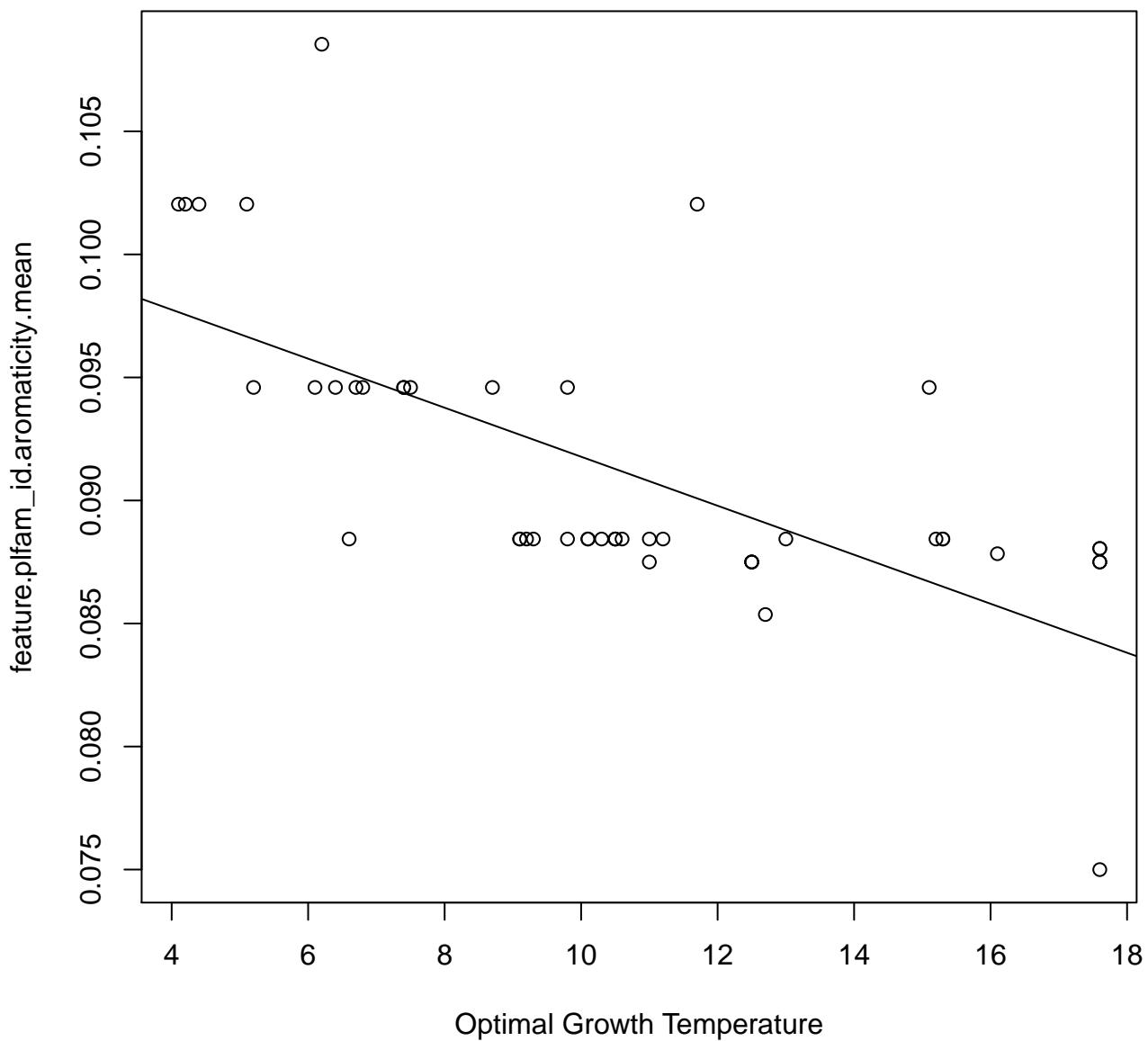
feature.plfam_id.aromaticity.mean
PLF_28228_00022122
Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage



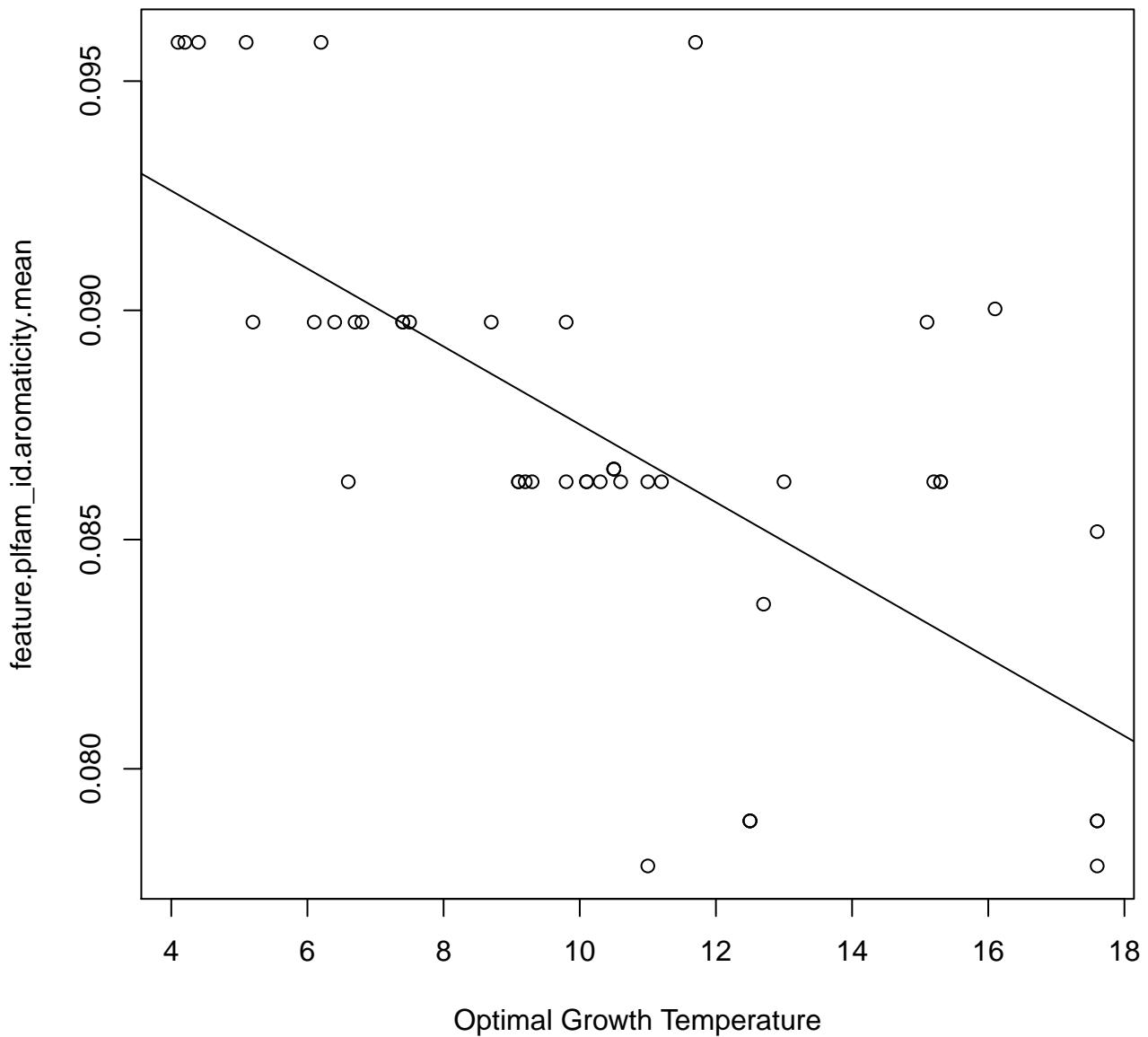
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PLF_28228_00001047

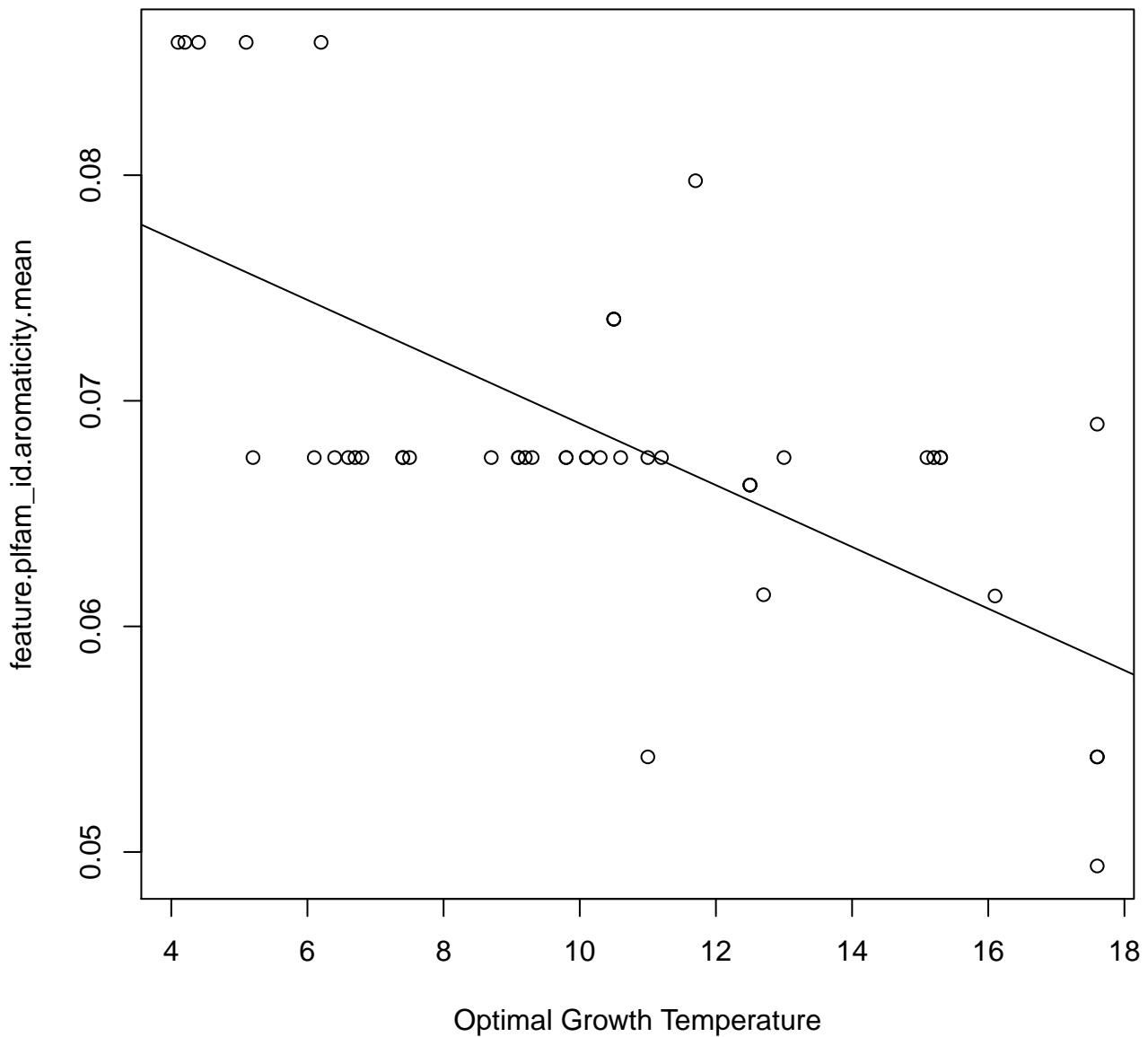
RNA-binding protein



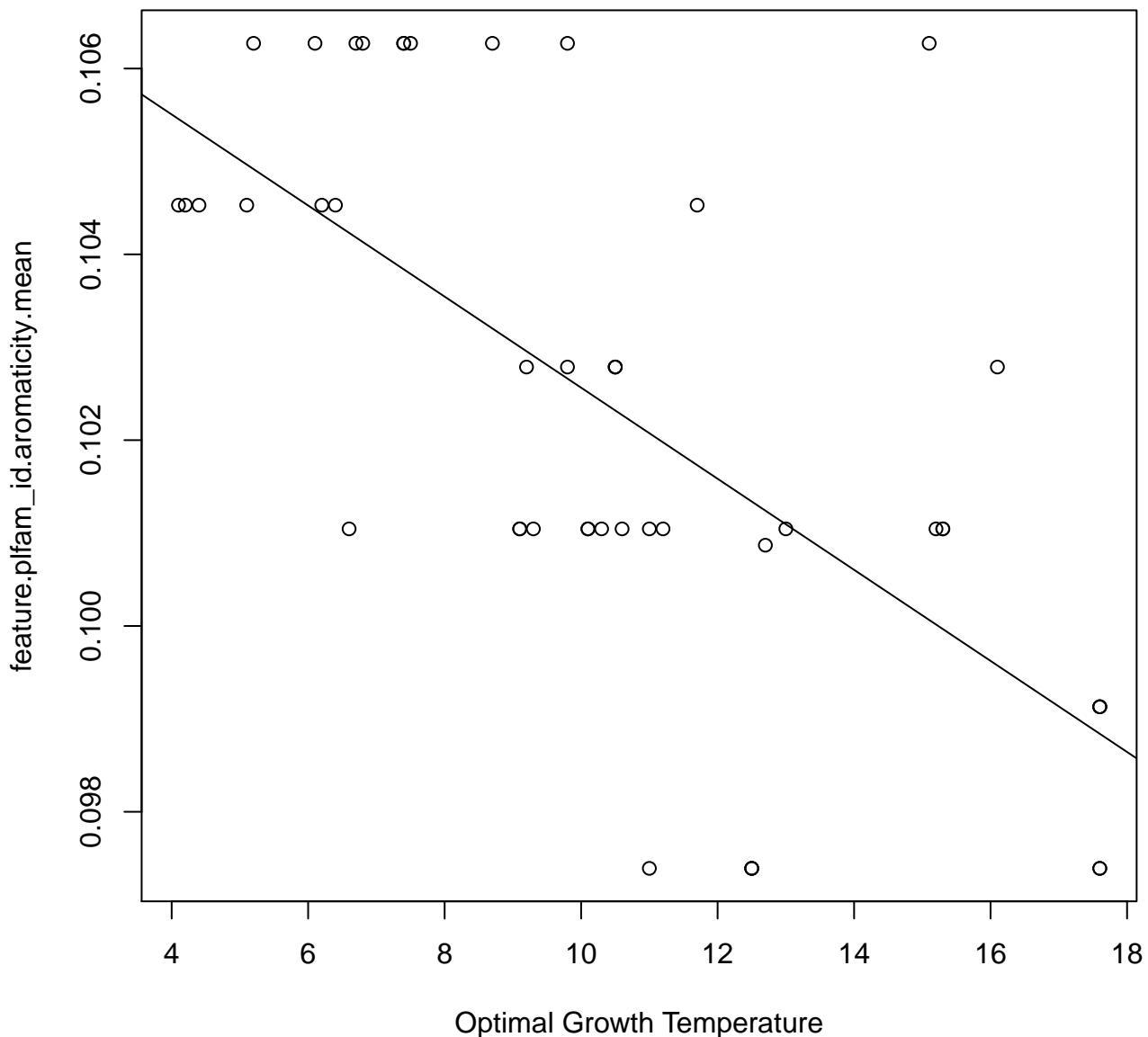
feature.plfam_id.aromaticity.mean
PLF_28228_00000770
D-alanine--D-alanine ligase (EC 6.3.2.4)



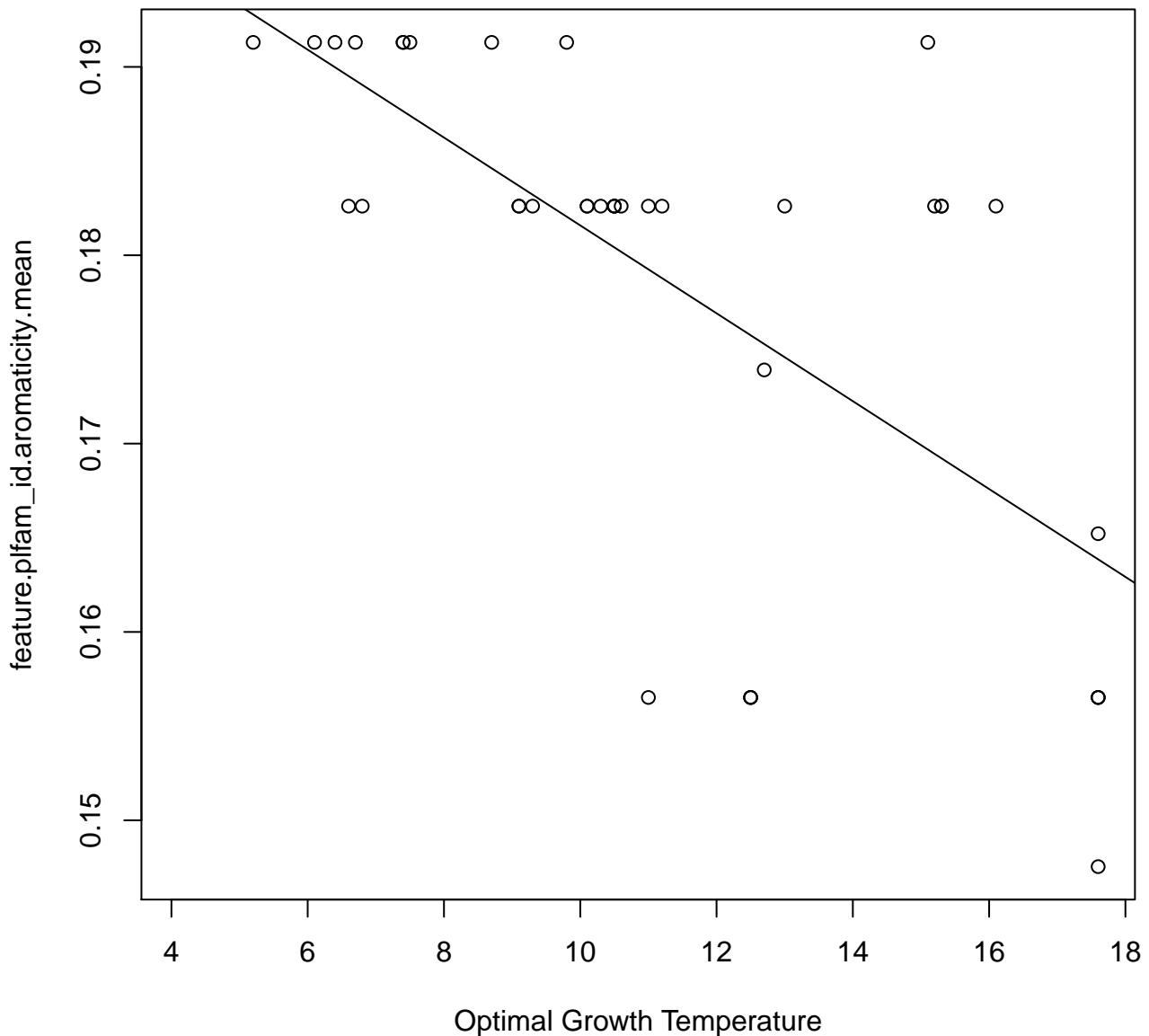
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2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase (EC 2.7.6.3)



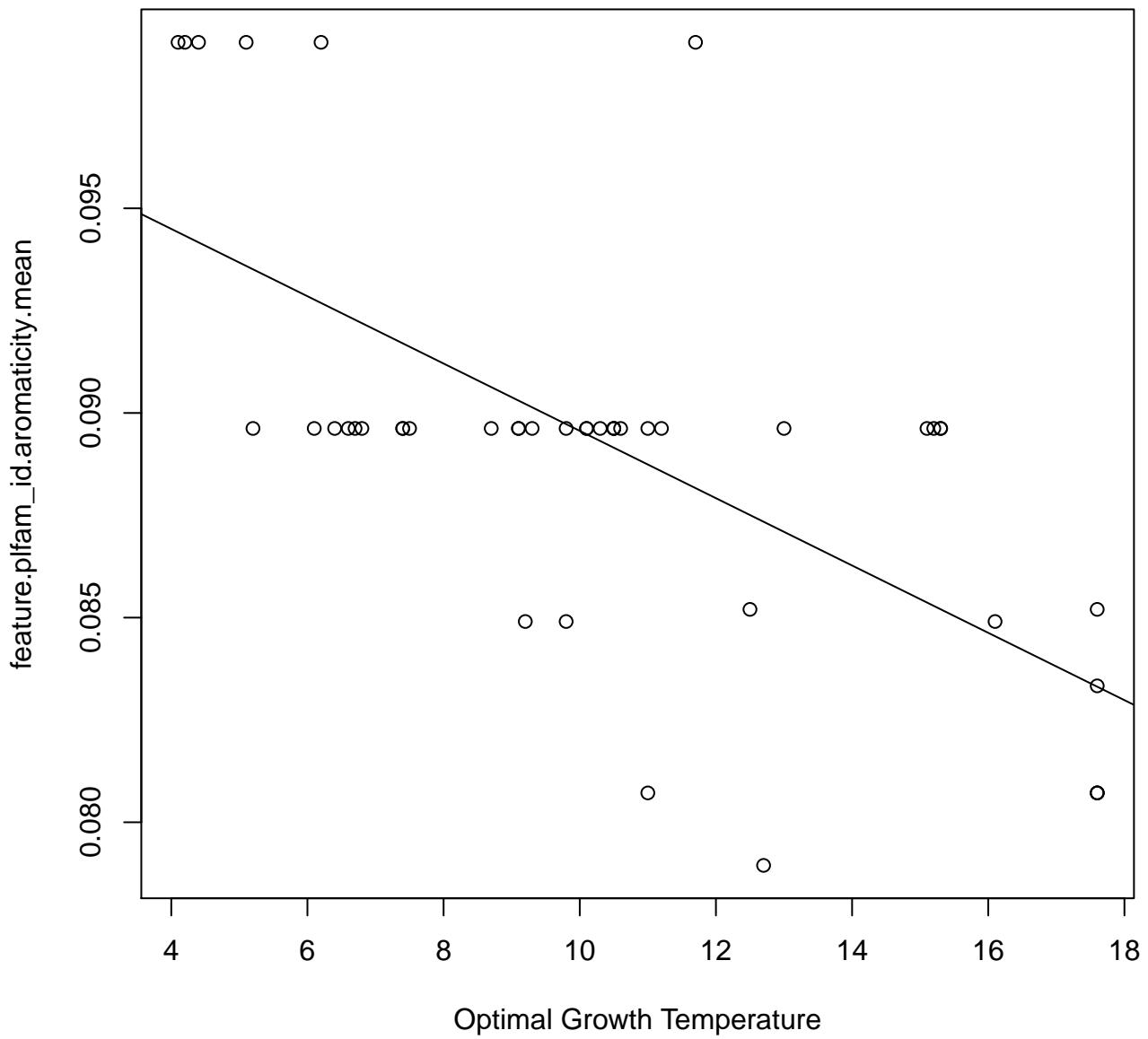
feature.plfam_id.aromaticity.mean
PLF_28228_00000731
Acetolactate synthase large subunit (EC 2.2.1.6)



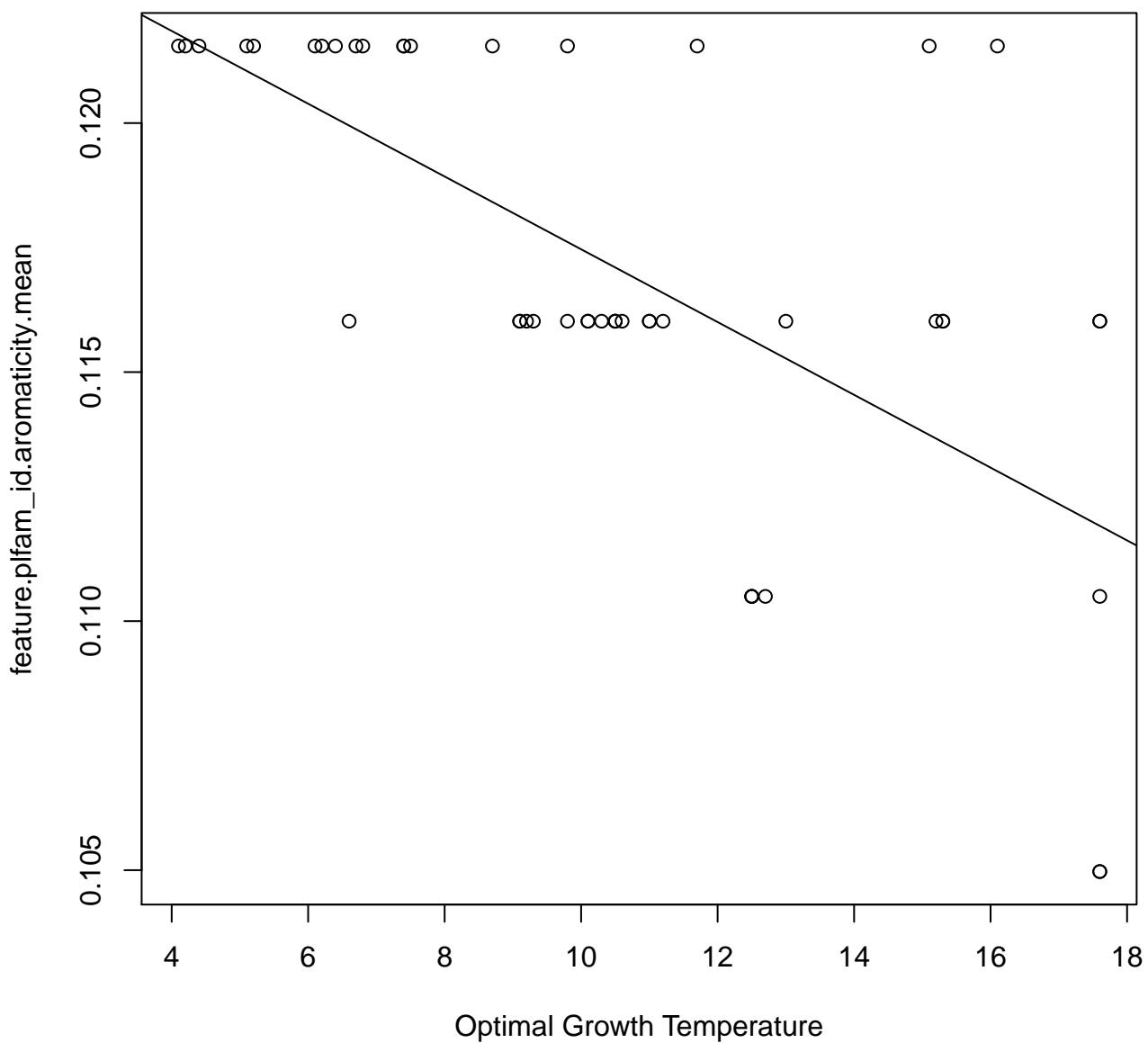
feature.plfam_id.aromaticity.mean
PLF_28228_00002083
Succinate dehydrogenase hydrophobic membrane anchor protein



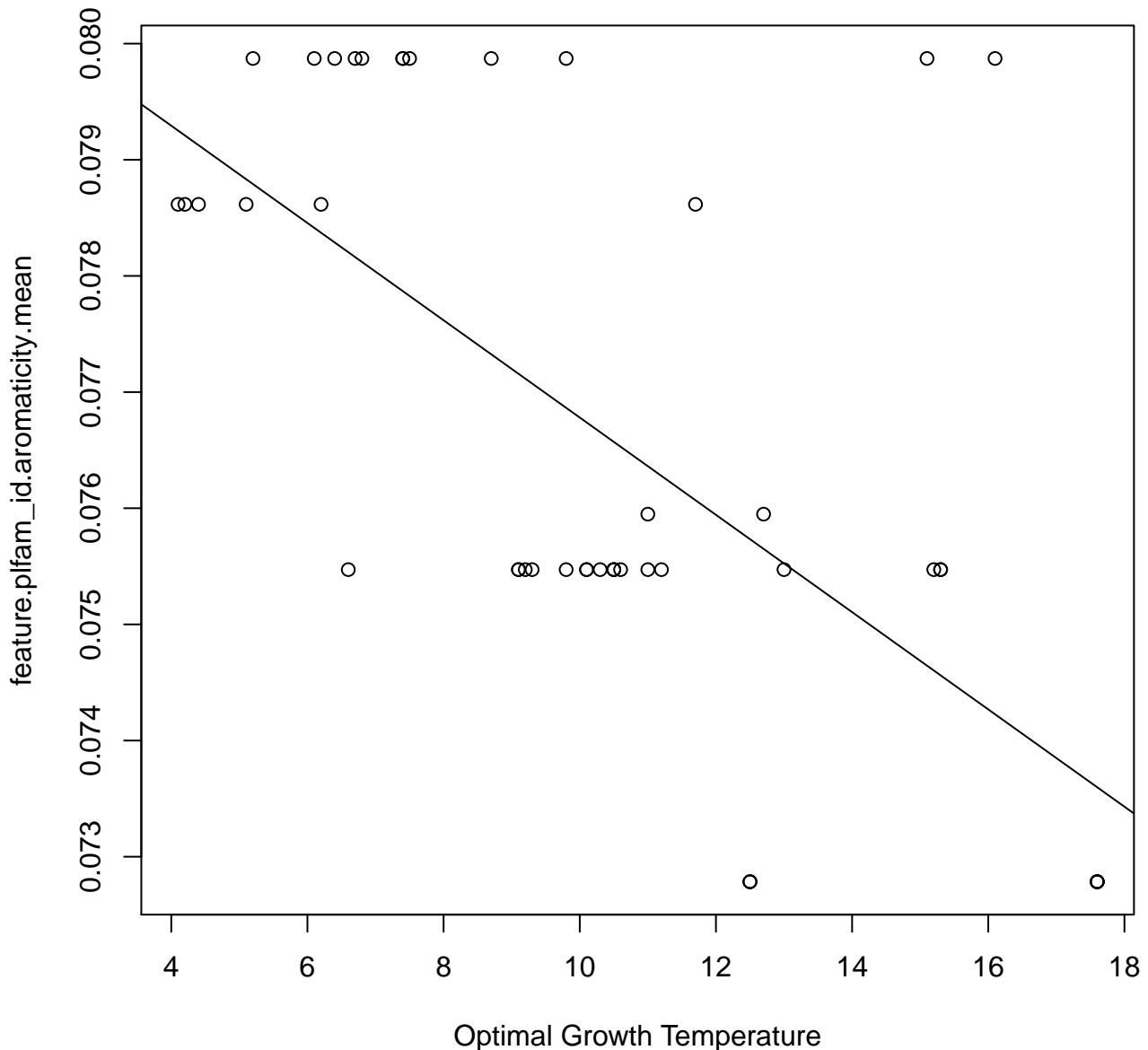
feature.plfam_id.aromaticity.mean
PLF_28228_00028002
UPF0070 protein YfgM



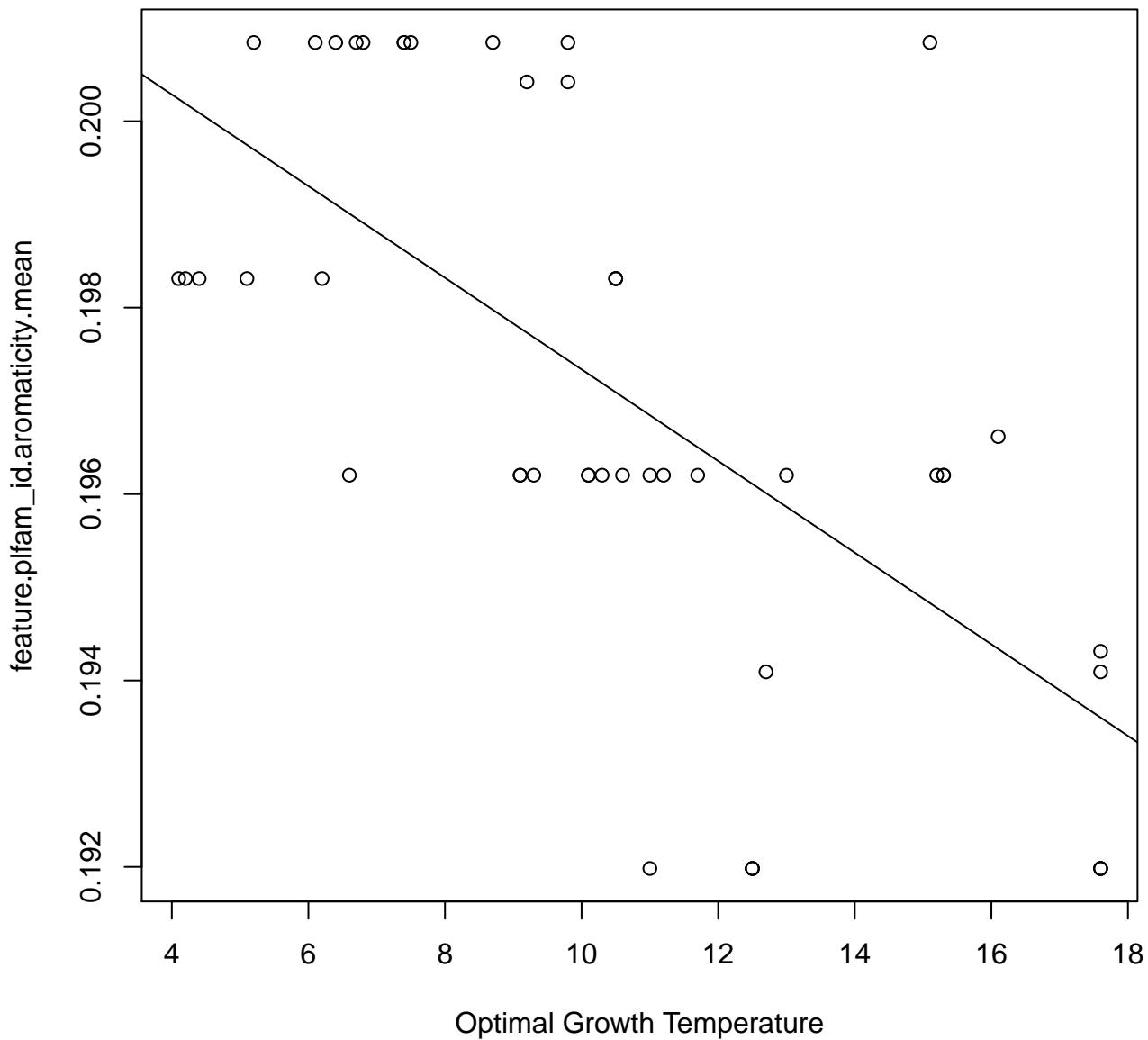
feature.plfam_id.aromaticity.mean
PLF_28228_00000263
3'-to-5' oligoribonuclease (orn)



feature.pfam_id.aromaticity.mean
PLF_28228_00000217
16S rRNA (cytosine(1402)-N(4))-methyltransferase (EC 2.1.1.199)



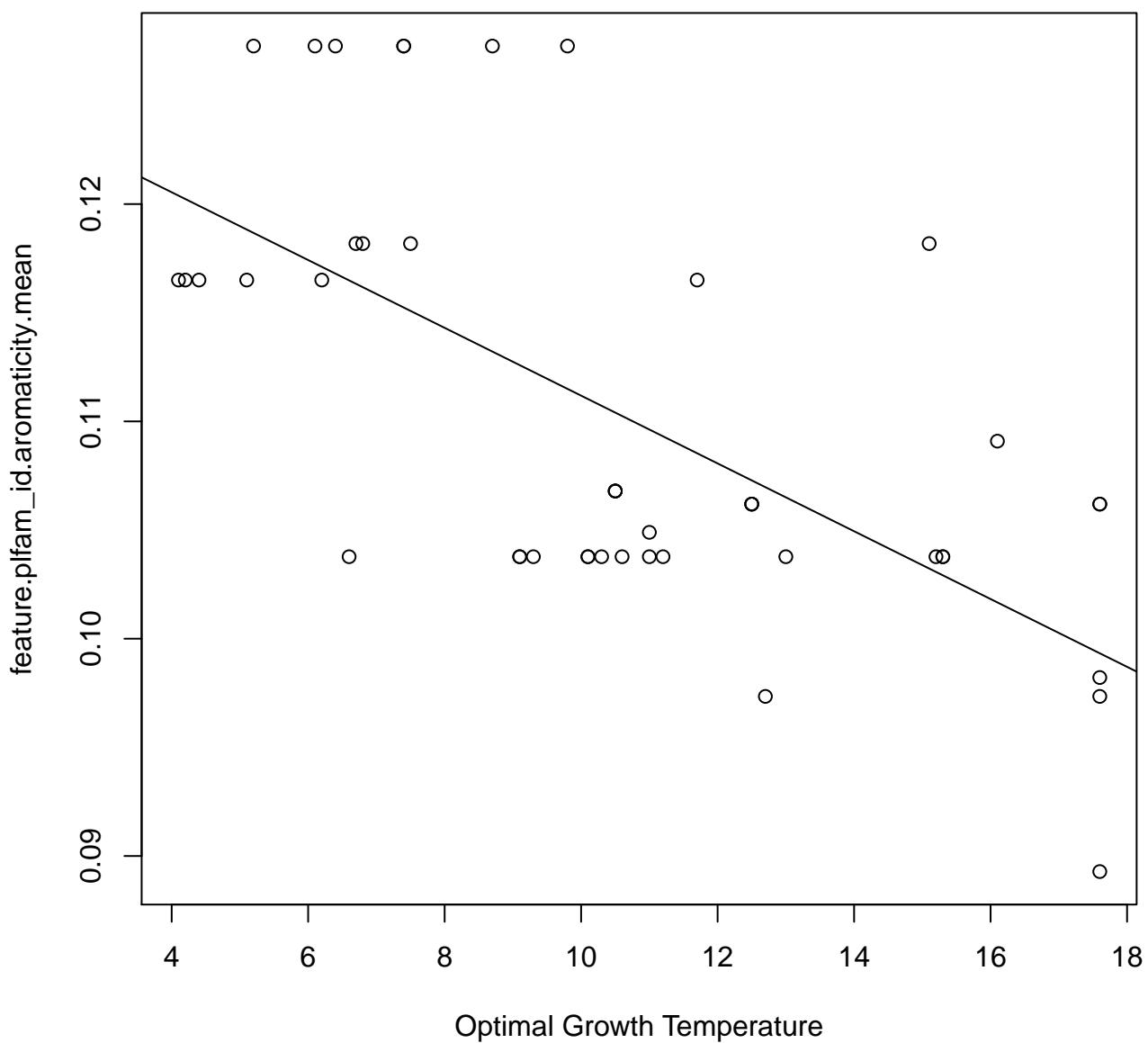
feature.plfam_id.aromaticity.mean
PLF_28228_00000433
Cytochrome c oxidase (cbb3-type) subunit CcoN (EC 1.9.3.1)



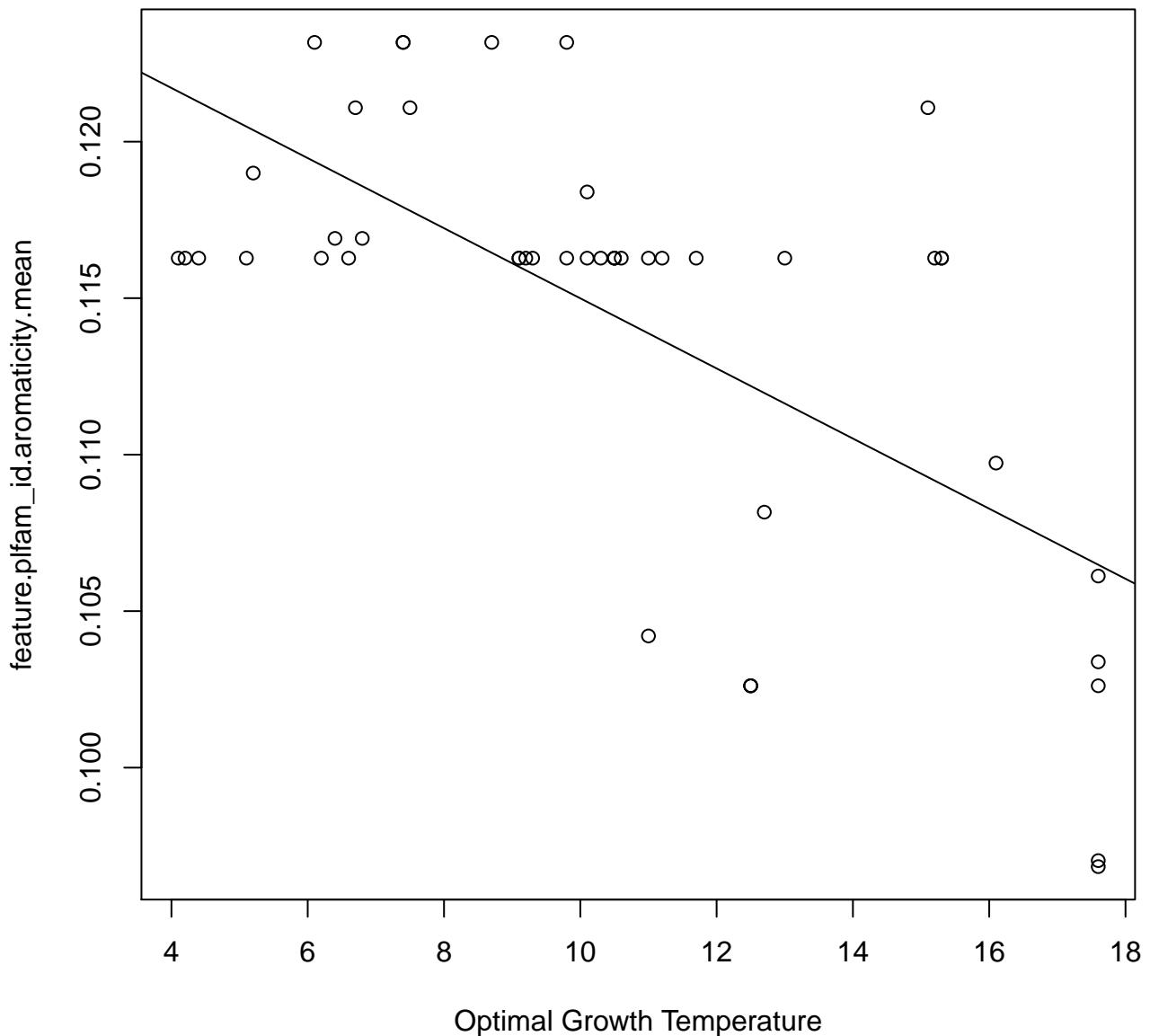
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PLF_28228_00002444

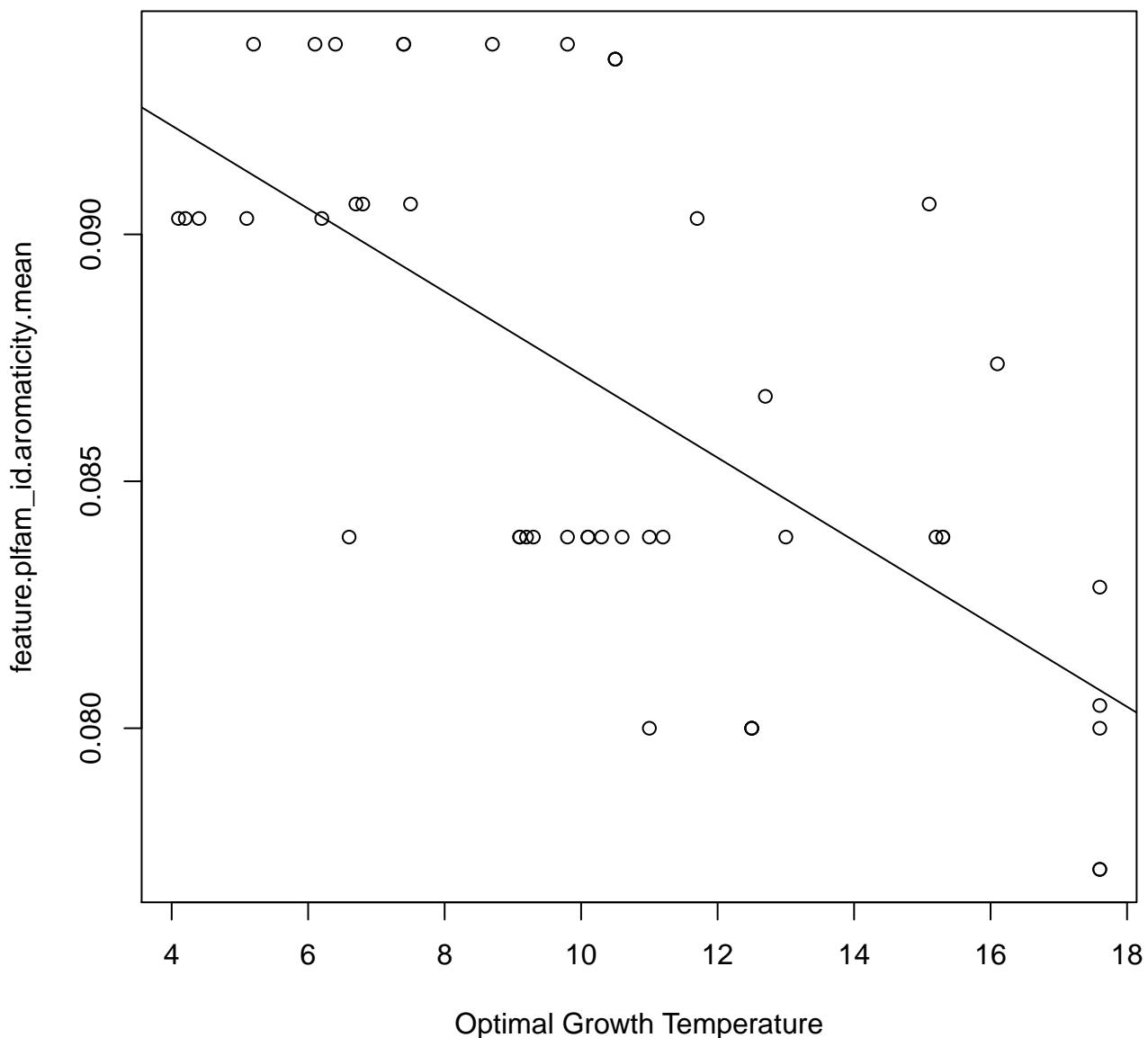
hypothetical protein



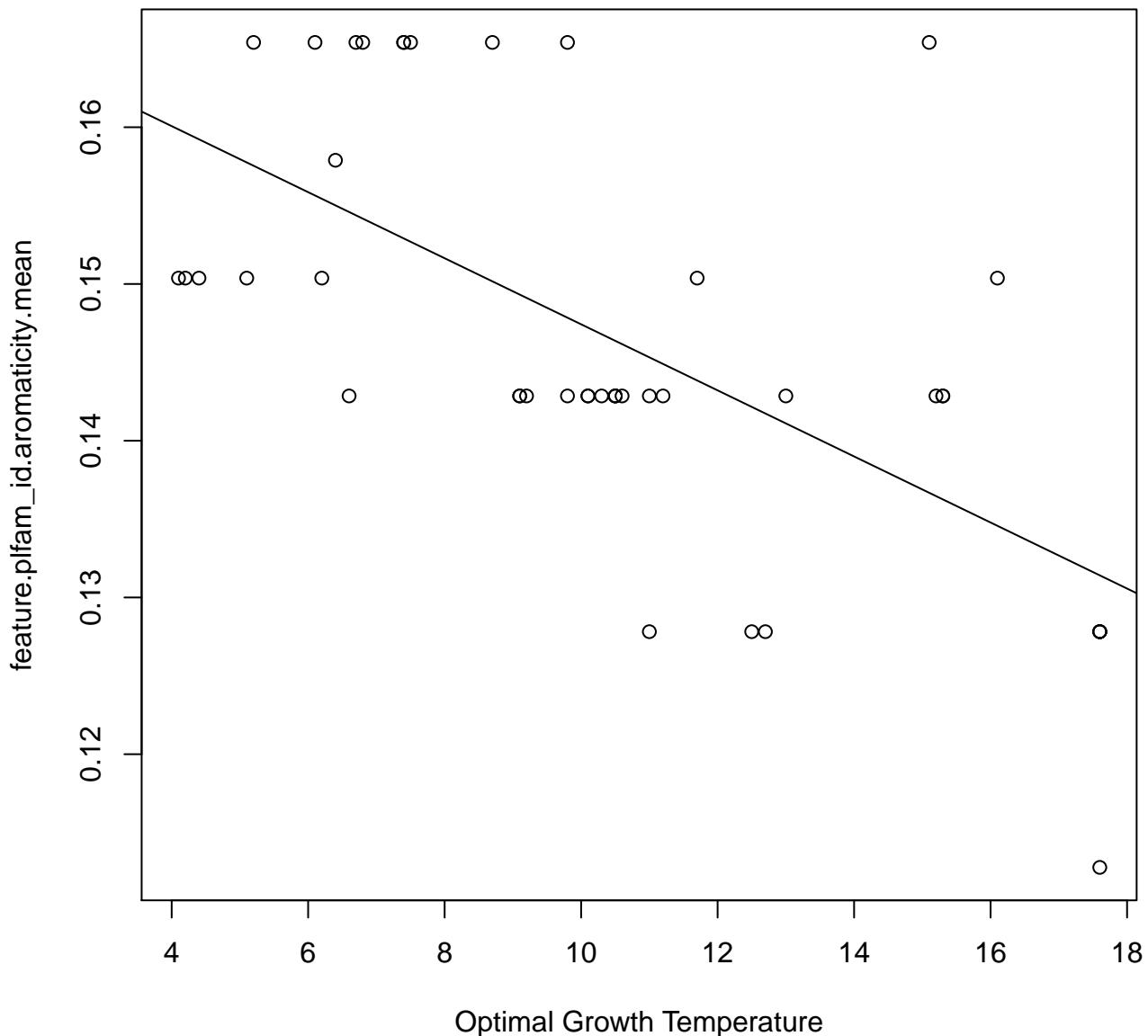
feature.plfam_id.aromaticity.mean
PLF_28228_00000911
Para-aminobenzoate synthase, aminase component (EC 2.6.1.85)



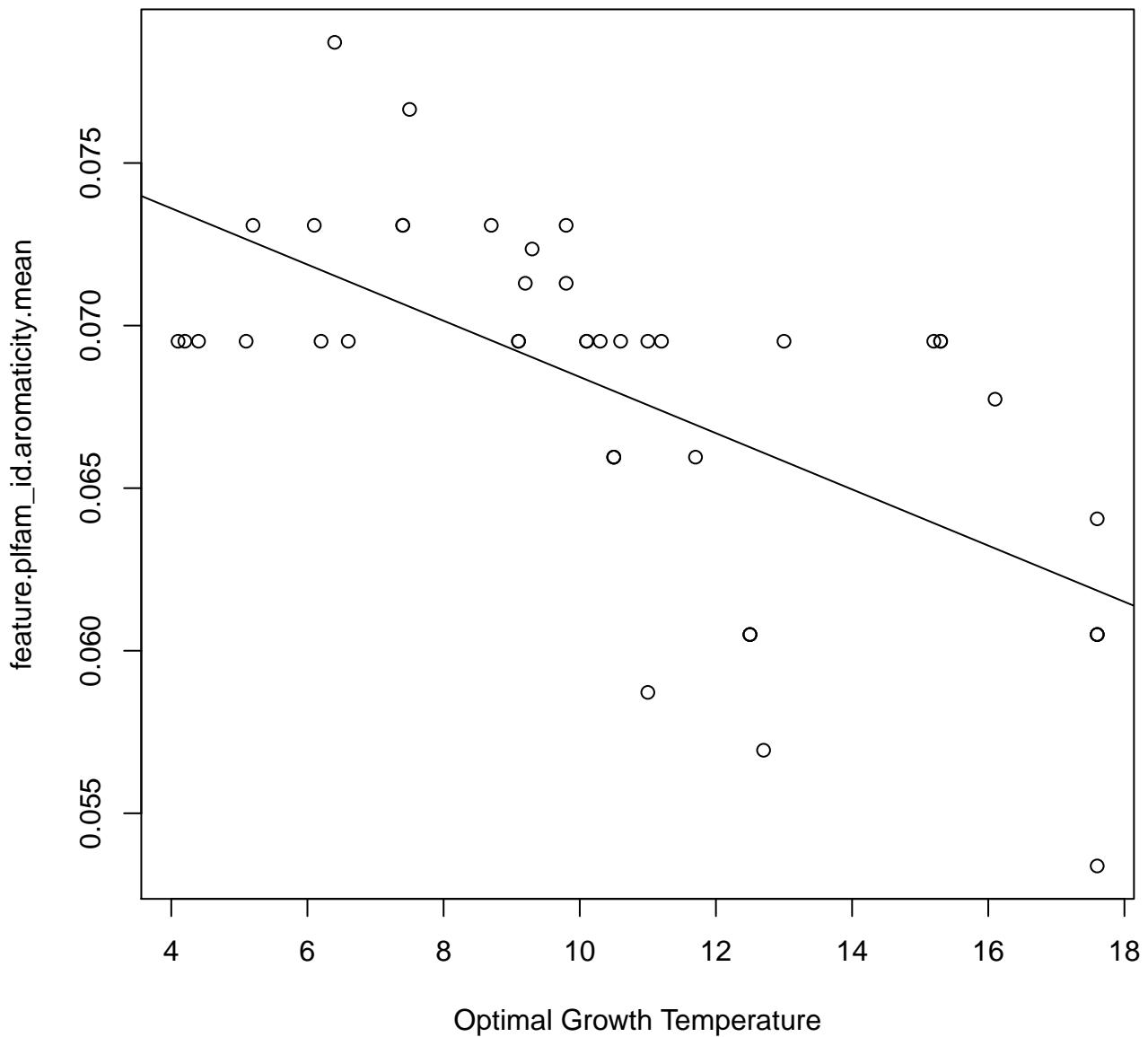
feature.plfam_id.aromaticity.mean
PLF_28228_00000569
FIG022979: MoxR-like ATPases



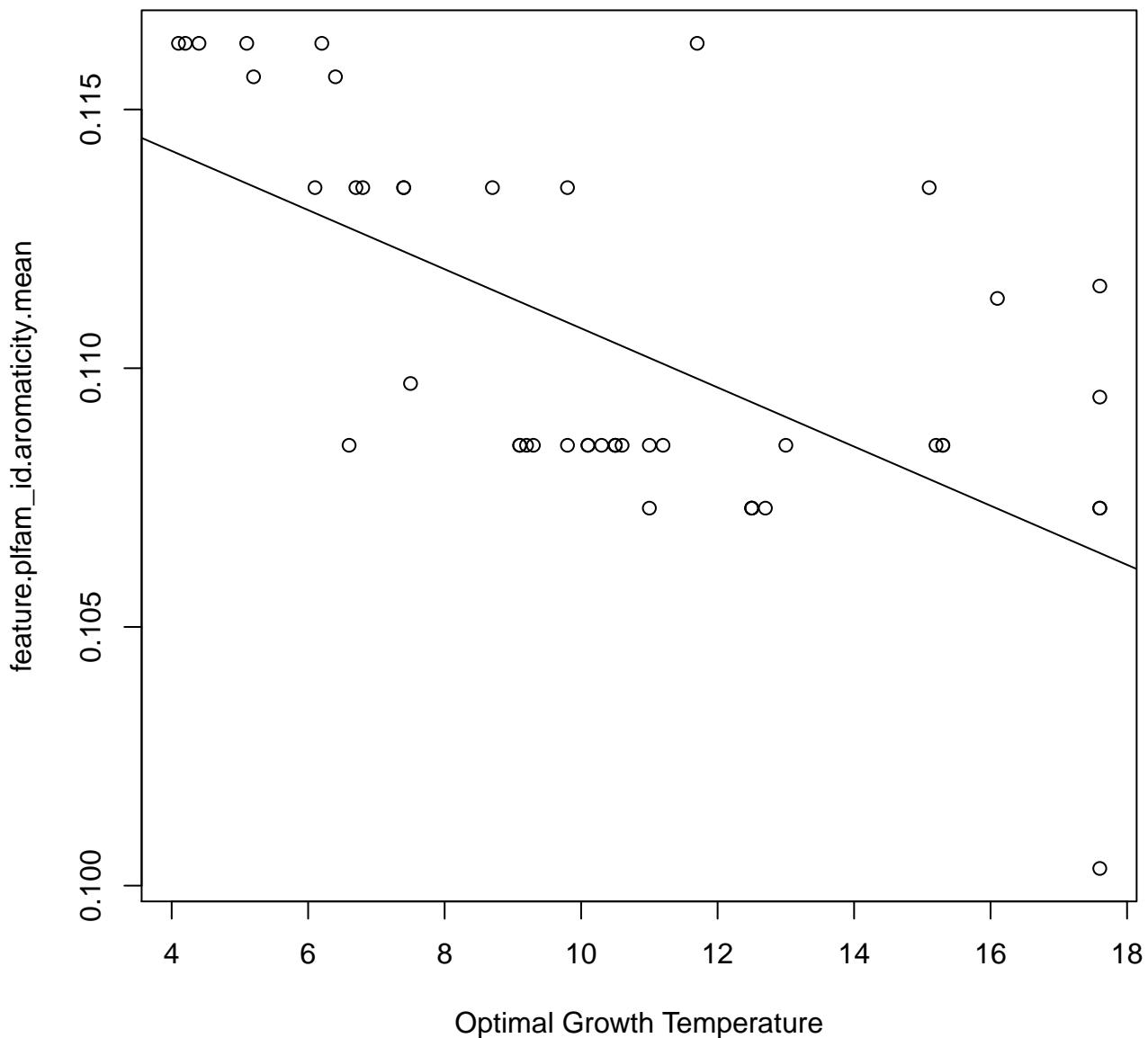
feature.pfam_id.aromaticity.mean
PLF_28228_00028103
Fluoride ion transporter CrcB



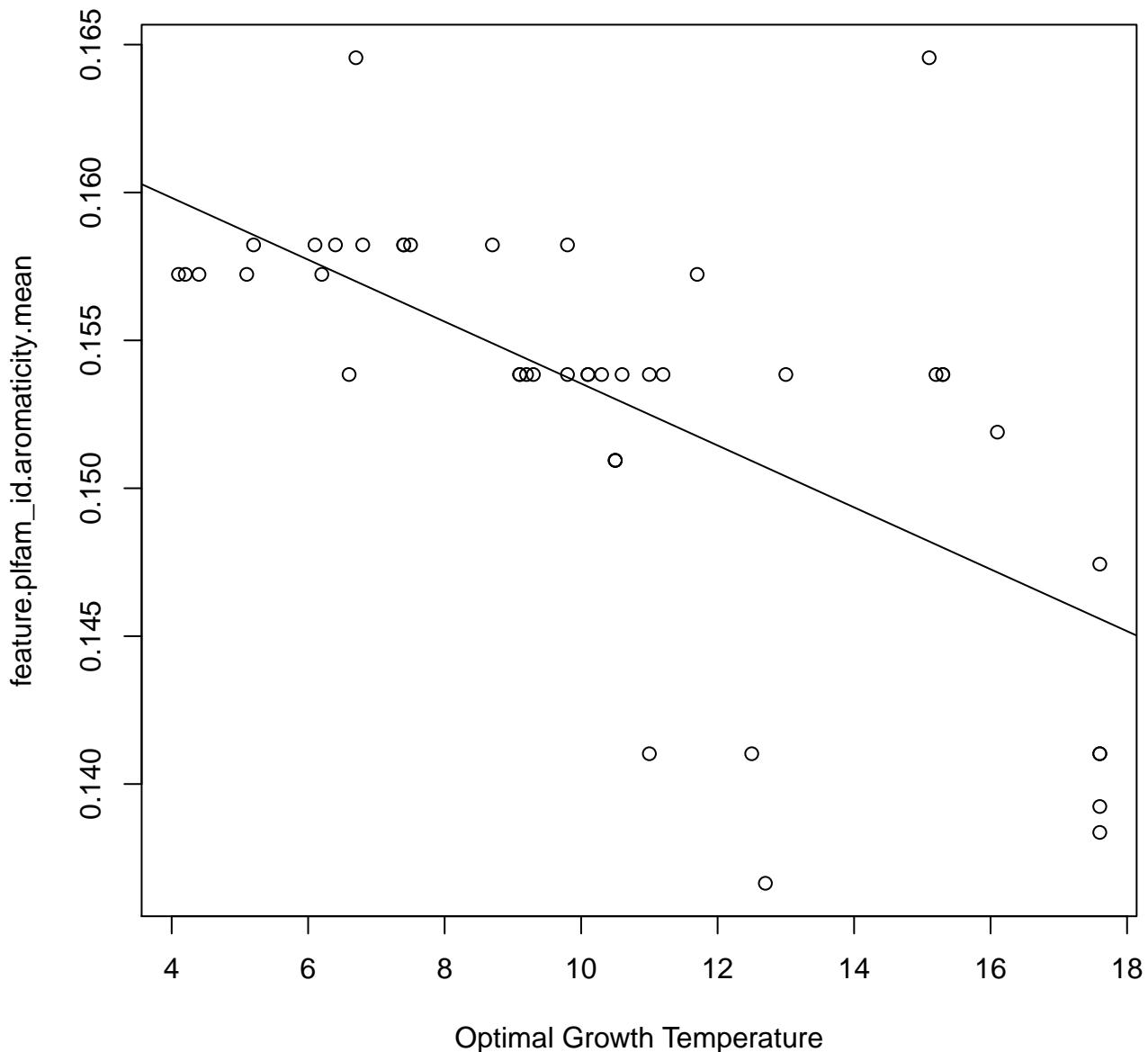
feature.plfam_id.aromaticity.mean
PLF_28228_00001964
Protein of unknown function DUF342



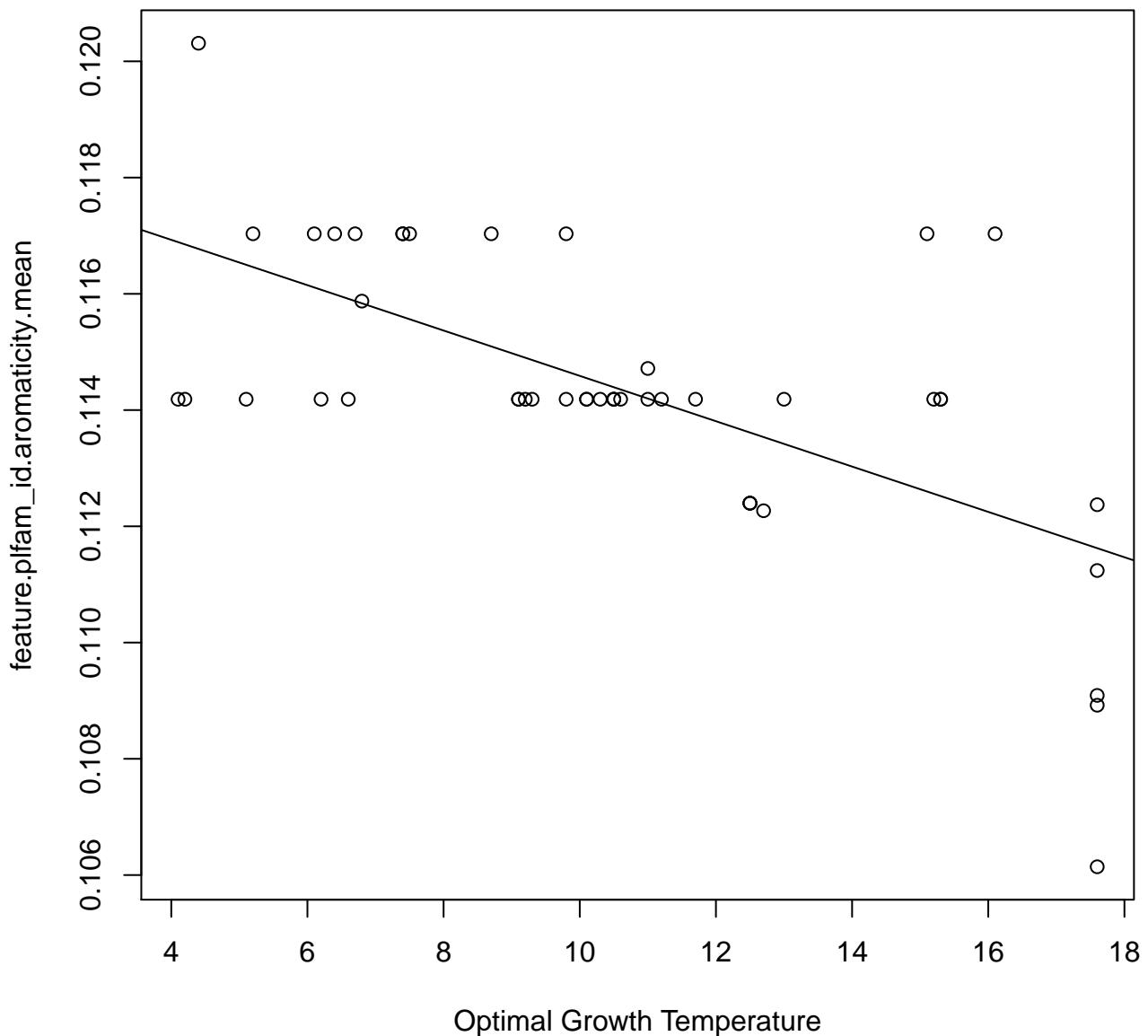
feature.plfam_id.aromaticity.mean
PLF_28228_00001172
Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)



feature.pifam_id.aromaticity.mean
PLF_28228_00016412
DNA polymerase III chi subunit (EC 2.7.7.7)



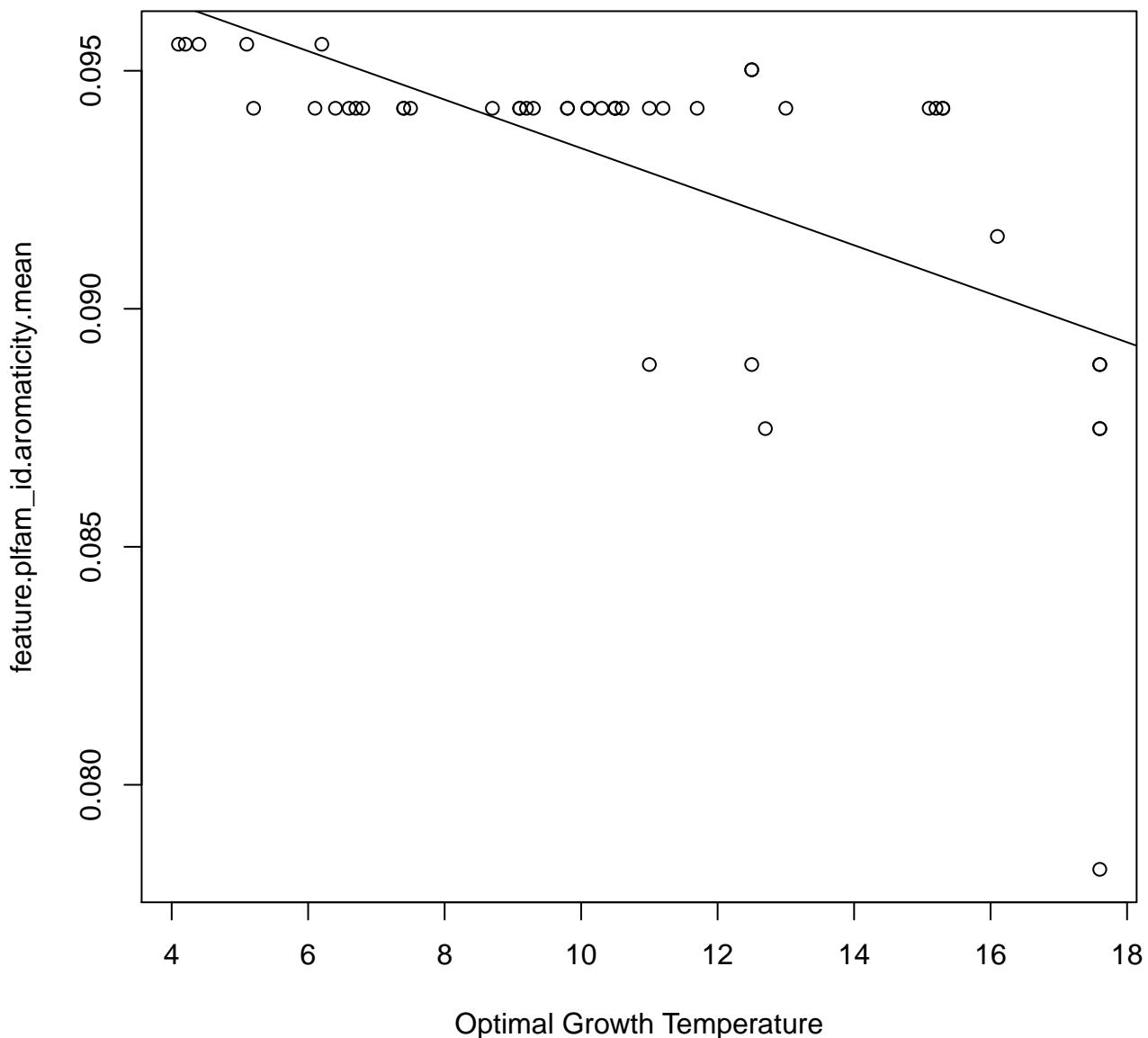
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PLF_28228_00000697
Leucyl-tRNA synthetase (EC 6.1.1.4)



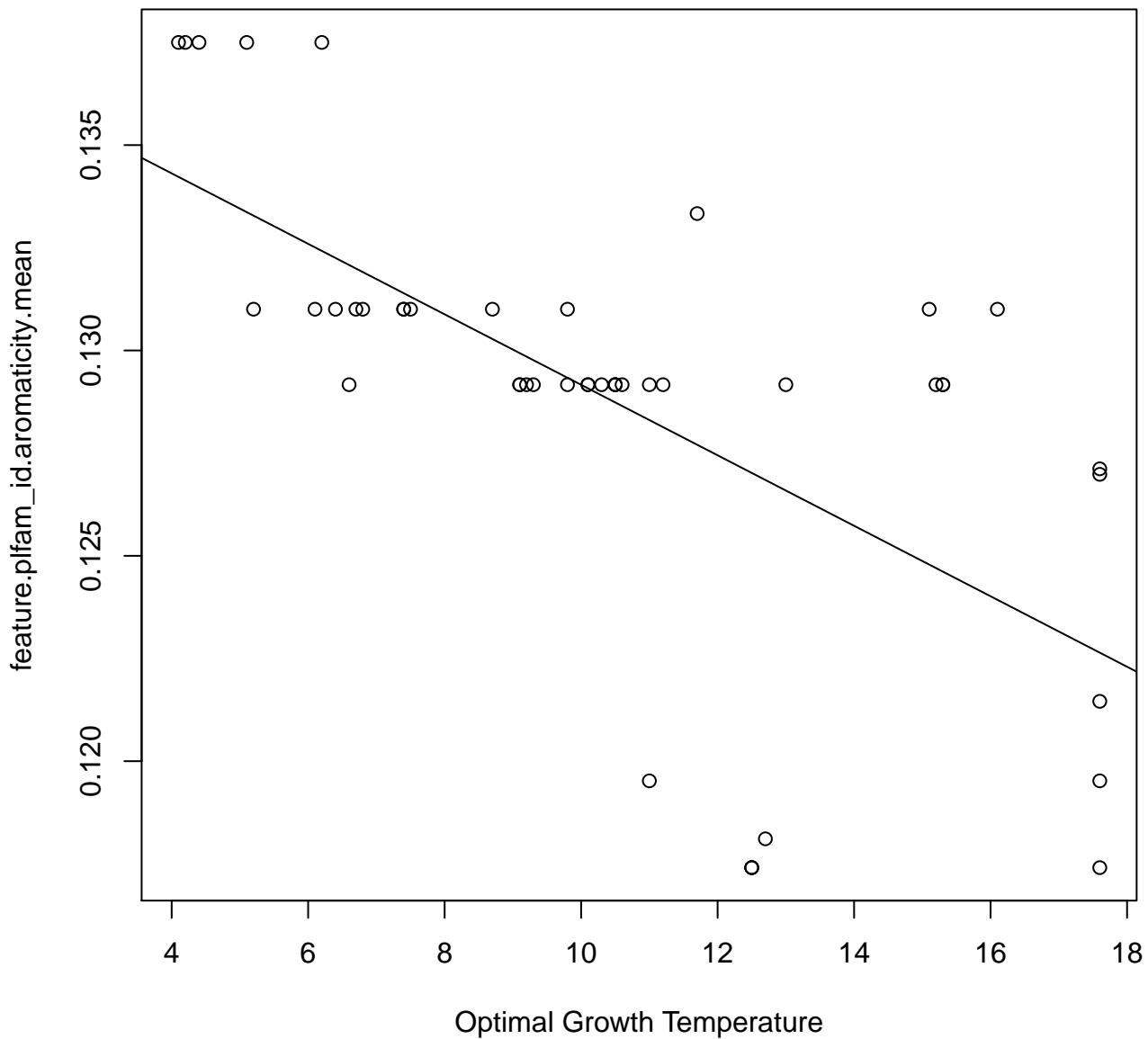
feature.plfam_id.aromaticity.mean

PLF_28228_00000535

Isocitrate dehydrogenase [NADP] (EC 1.1.1.42); Monomeric isocitrate dehydrogenase [NADP] (EC 1.1.1.42)



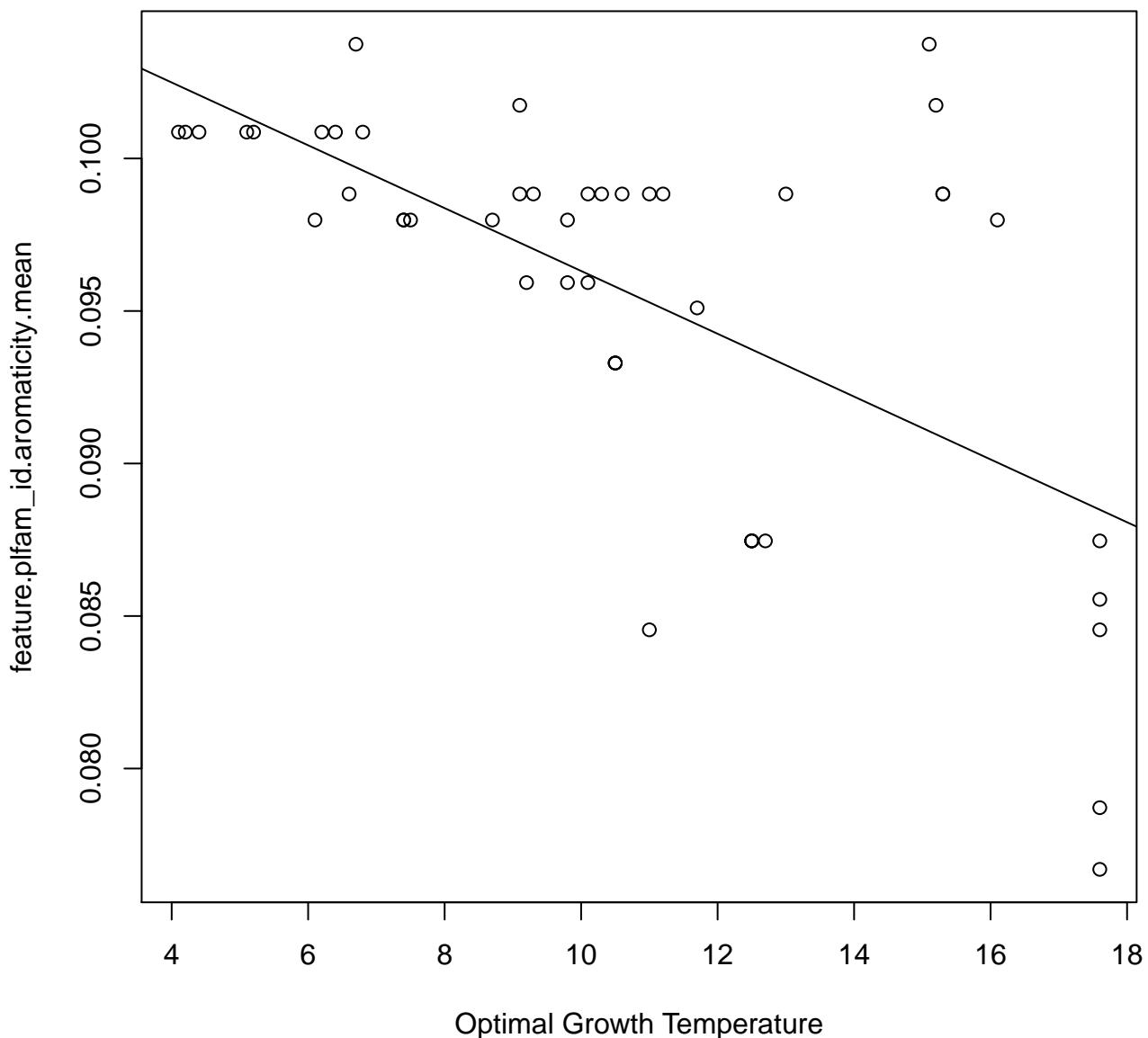
feature.plfam_id.aromaticity.mean
PLF_28228_00002384
predicted S-adenosylmethionine-dependent tRNA (guanine-N(7)-)methyltransferase



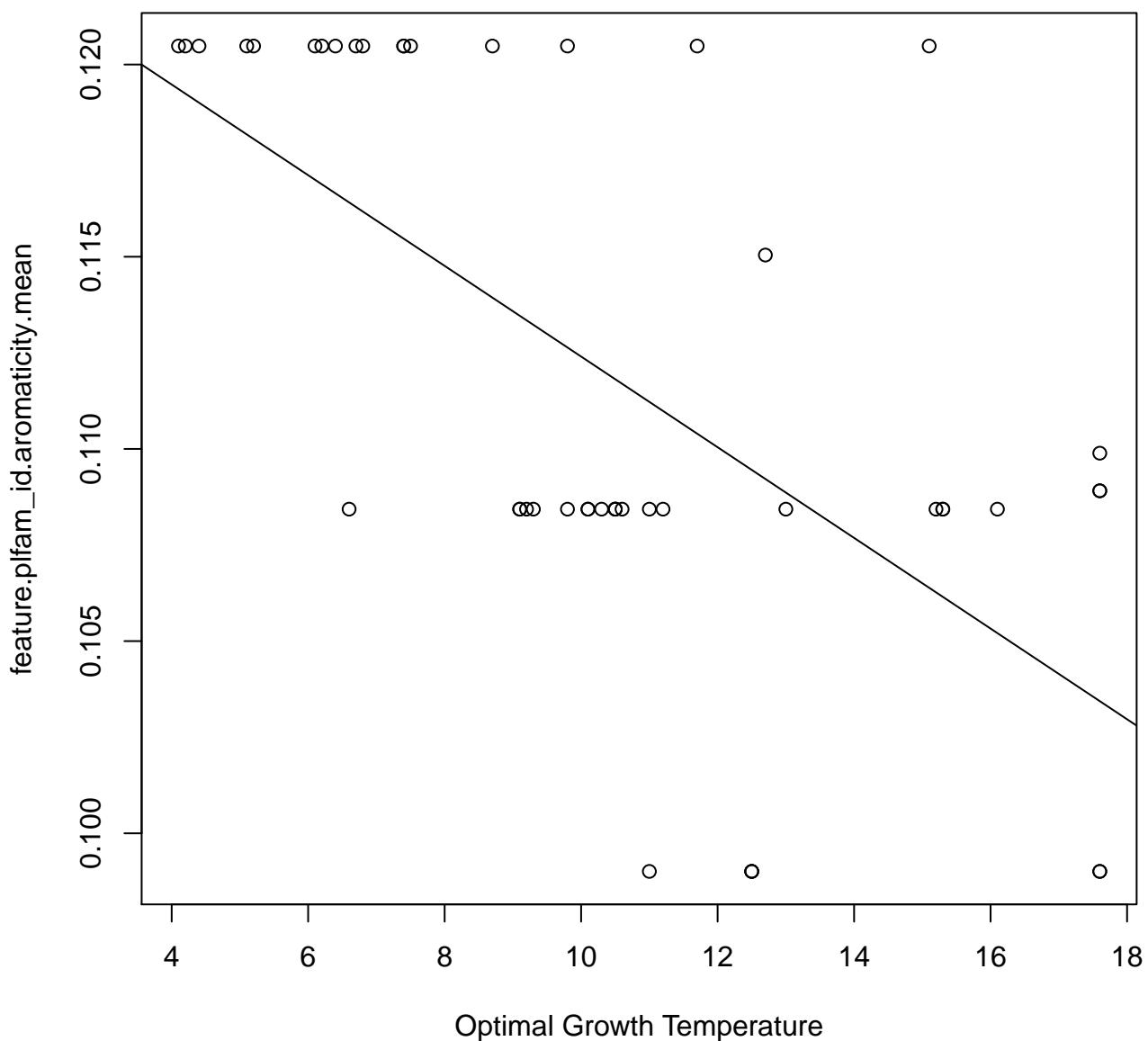
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PLF_28228_00001828

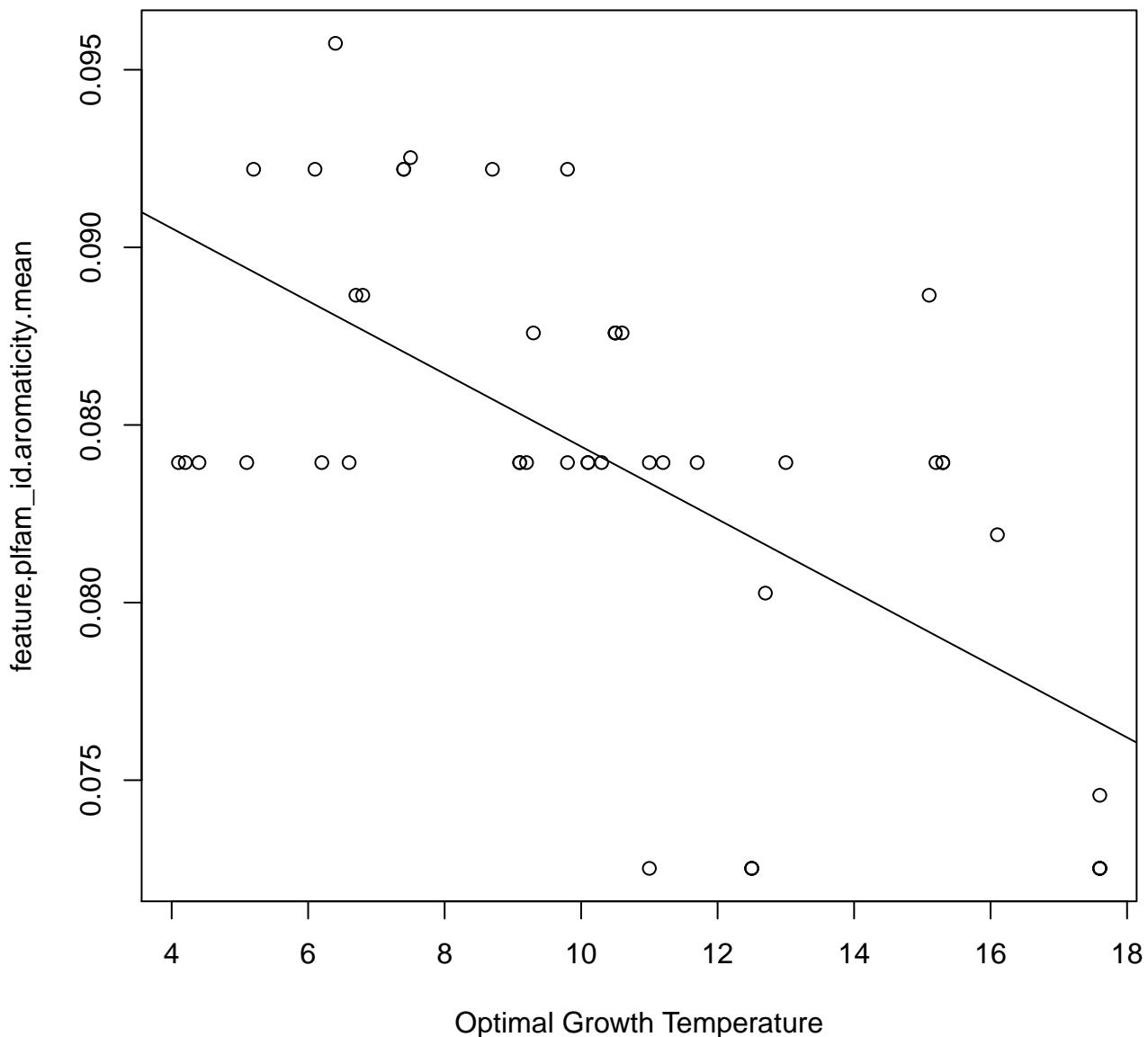
FAD:protein FMN transferase (EC 2.7.1.180) @ FAD:protein FMN transferase (EC 2.7.1.180), NqrBC-associated



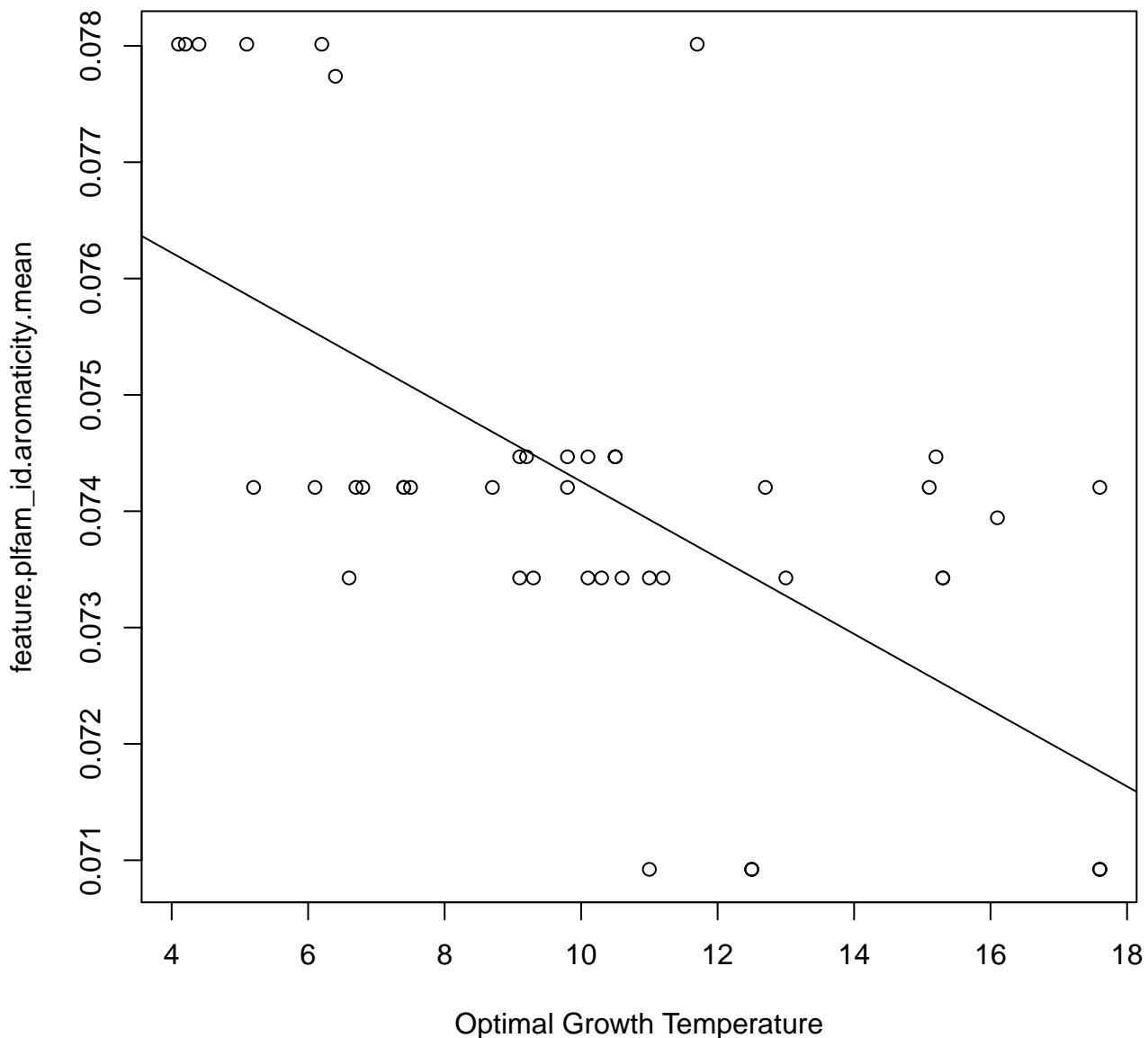
feature.plfam_id.aromaticity.mean
PLF_28228_00001310
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin



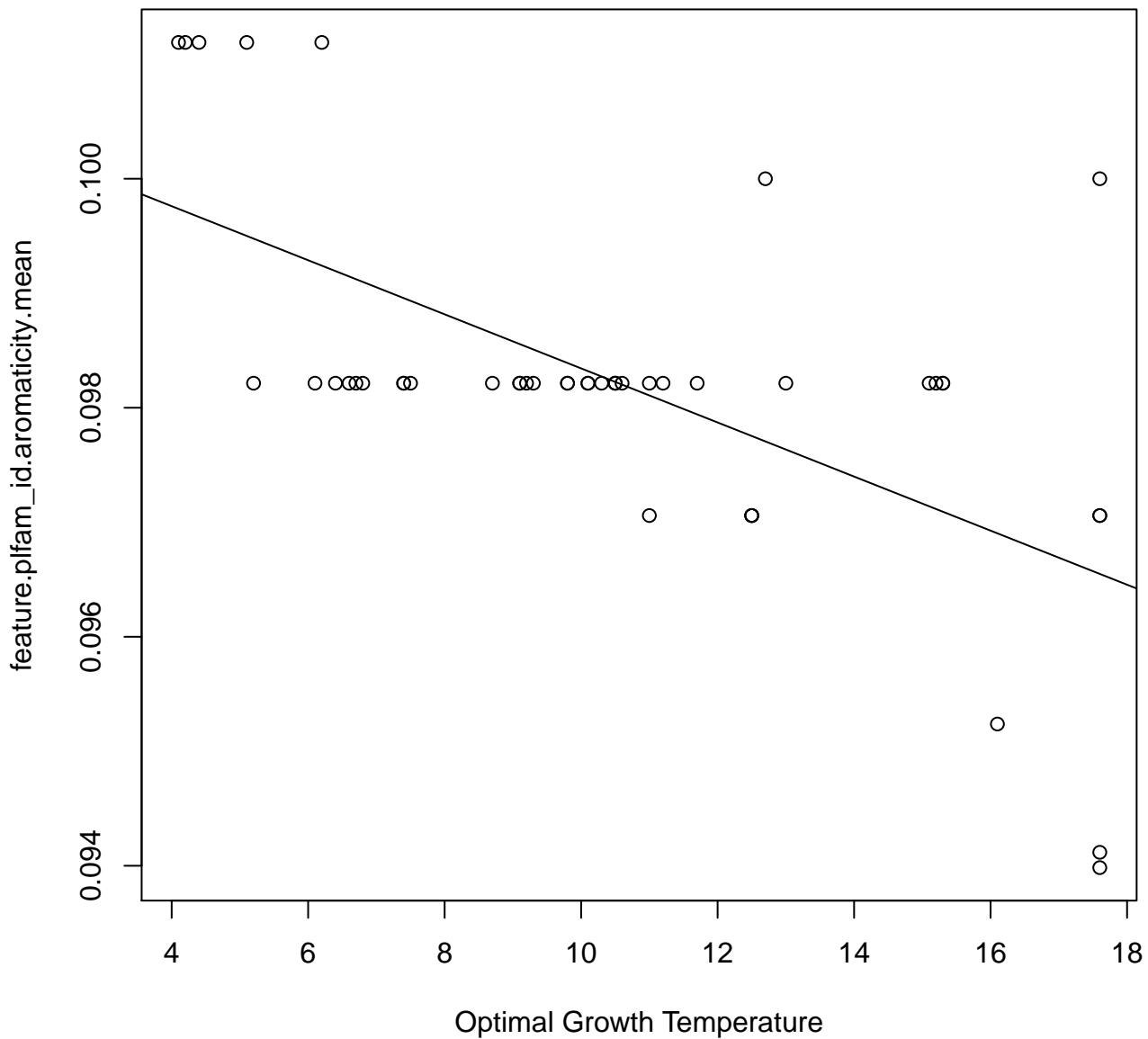
feature.plfam_id.aromaticity.mean
PLF_28228_00000616
Methylglutaconyl-CoA hydratase (EC 4.2.1.18)



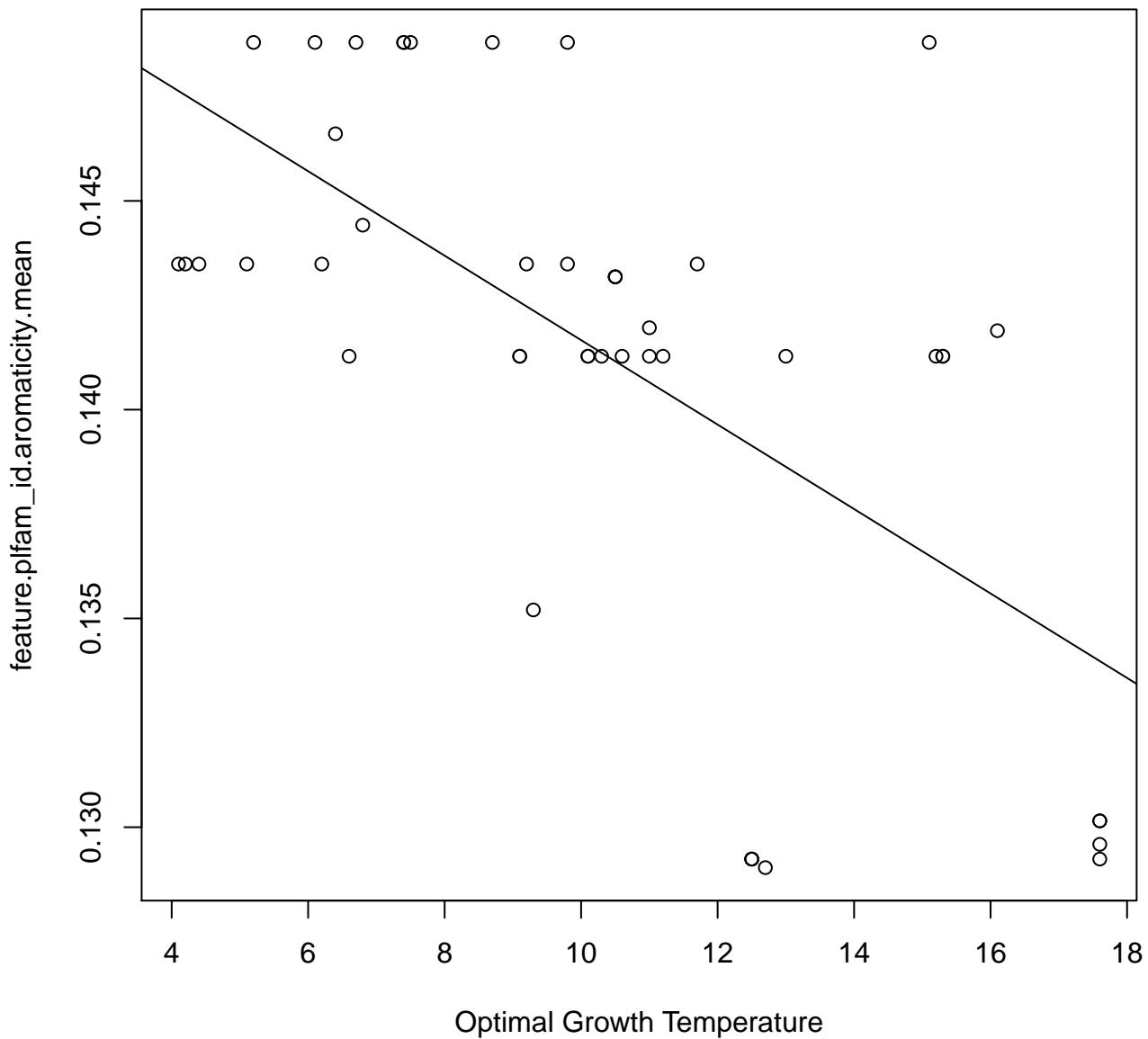
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PLF_28228_00000702
16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)



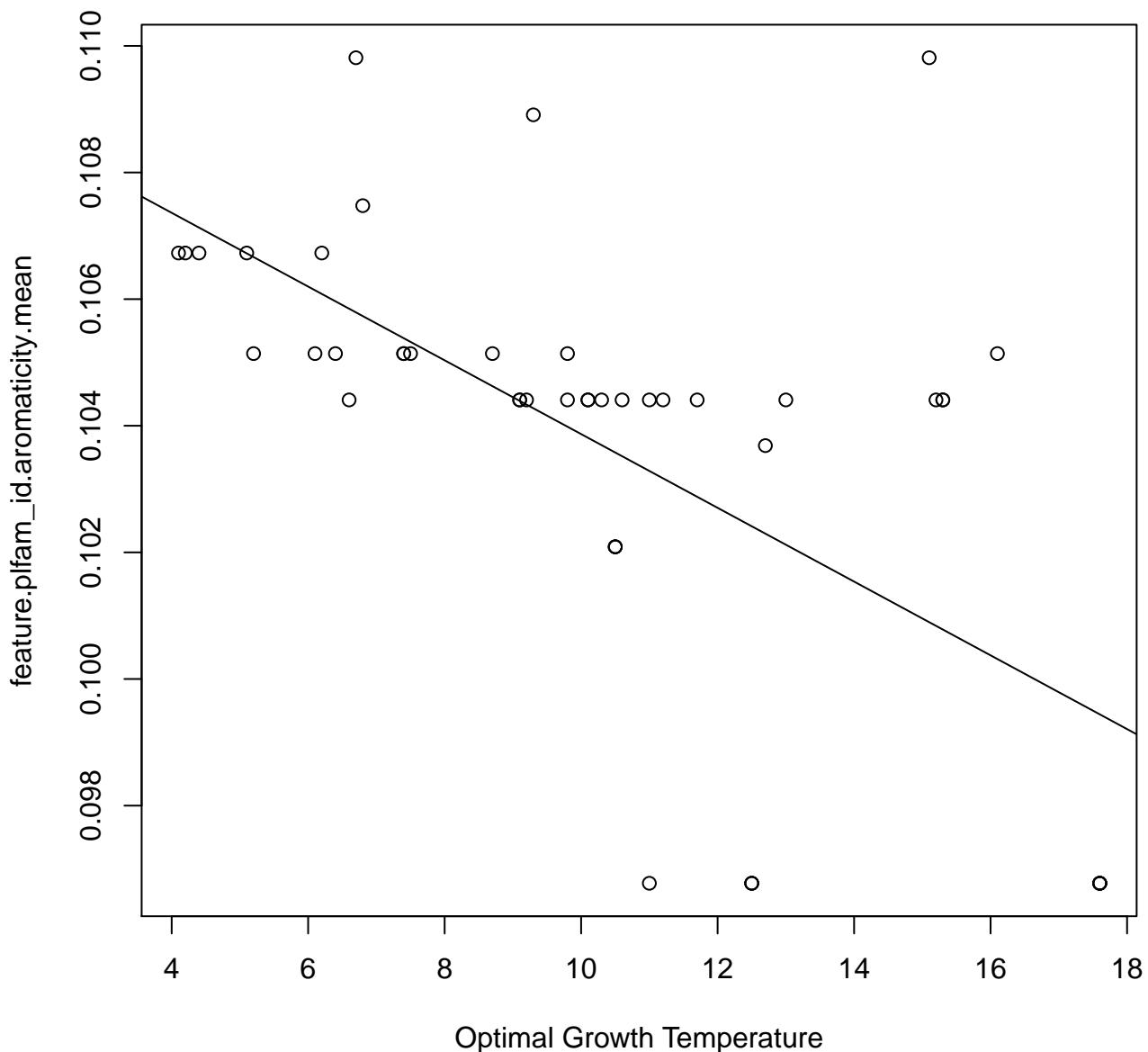
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UDP-glucose 4-epimerase (EC 5.1.3.2)



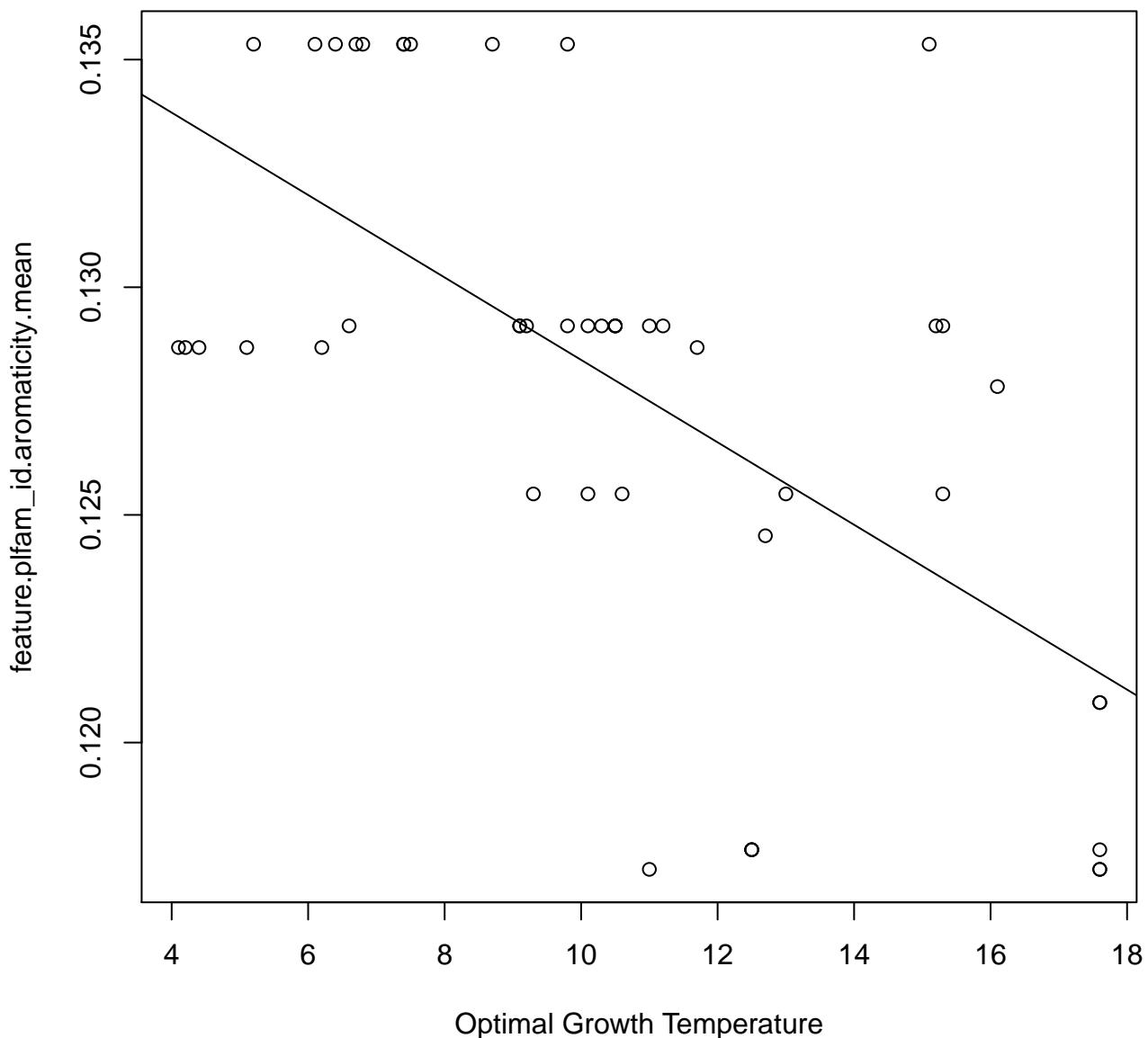
feature.plfam_id.aromaticity.mean
PLF_28228_00003558
Multidrug efflux transporter MdtK/NorM (MATE family)



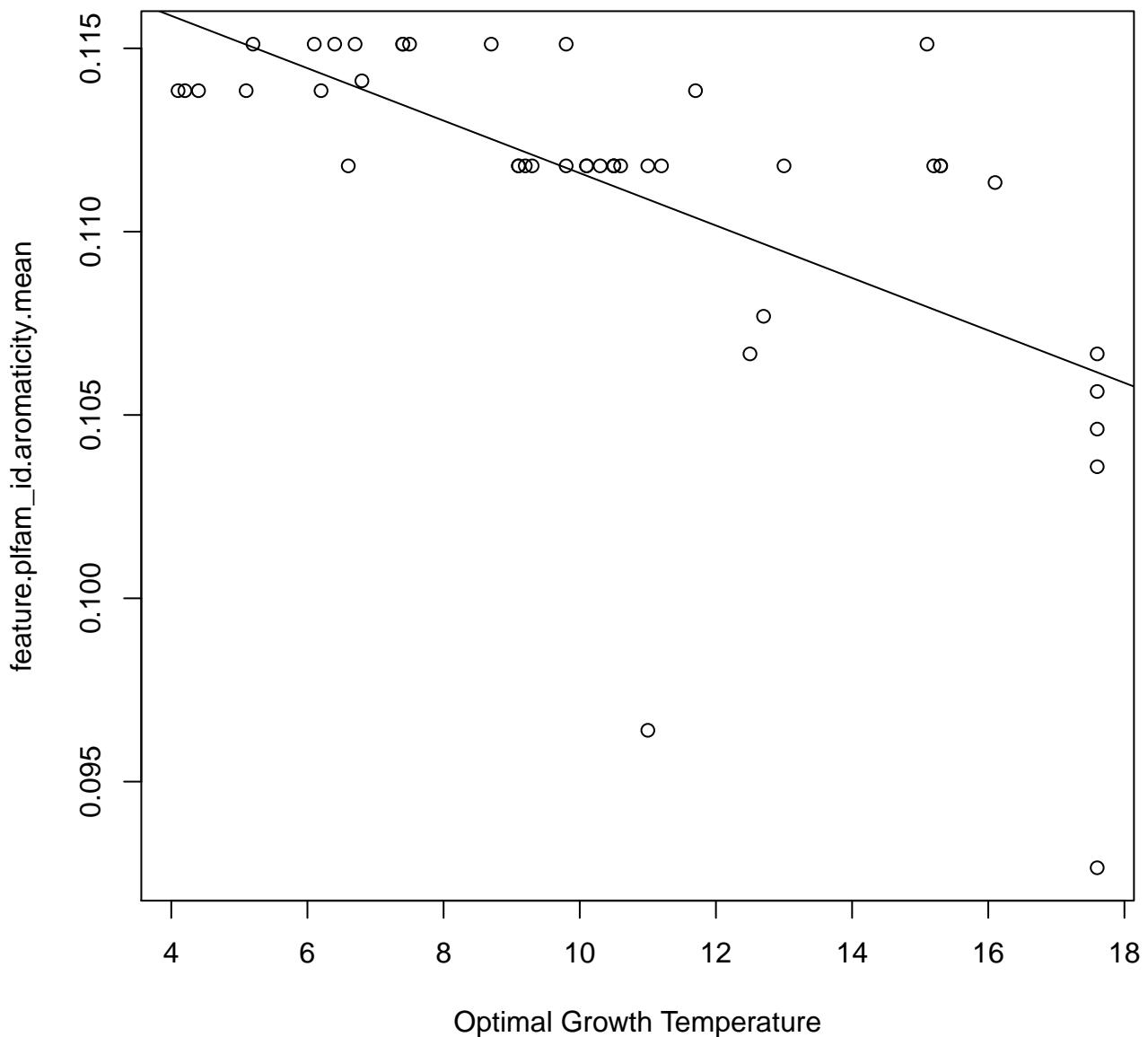
feature.plfam_id.aromaticity.mean
PLF_28228_00001195
Threonine synthase (EC 4.2.3.1)



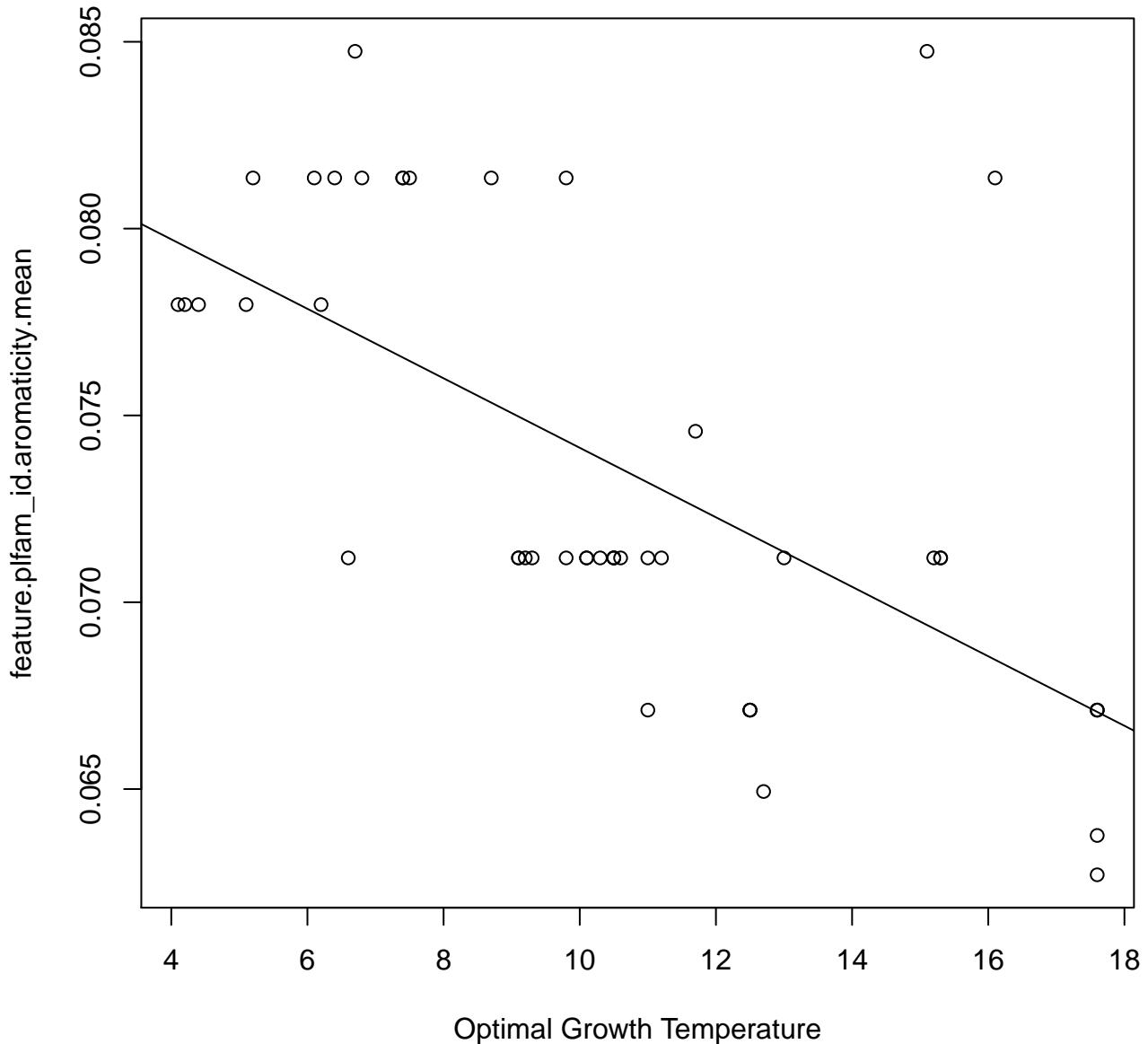
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Undecaprenyl-diphosphatase (EC 3.6.1.27)



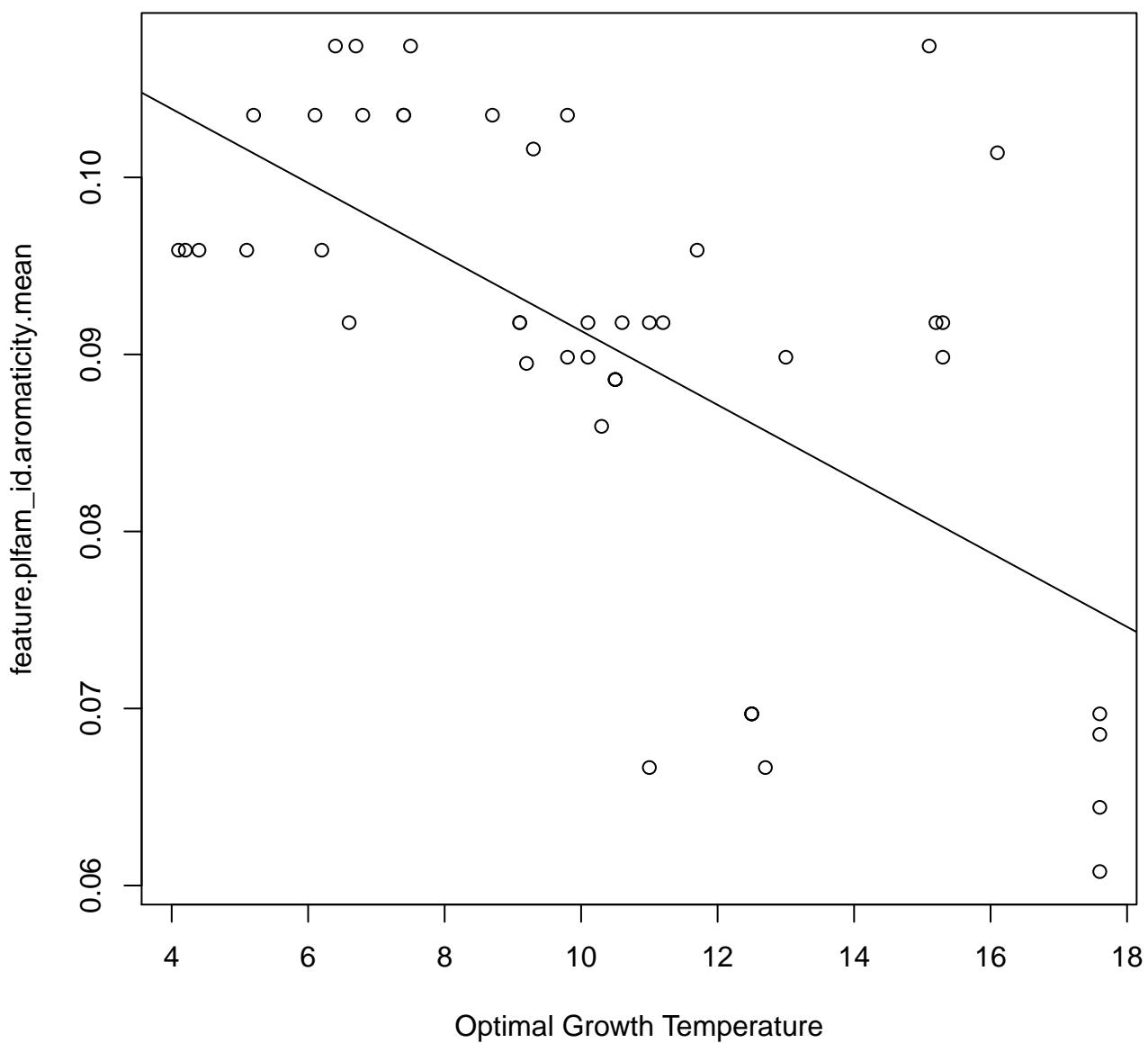
feature.plfam_id.aromaticity.mean
PLF_28228_00028230
RNA polymerase associated protein RapA



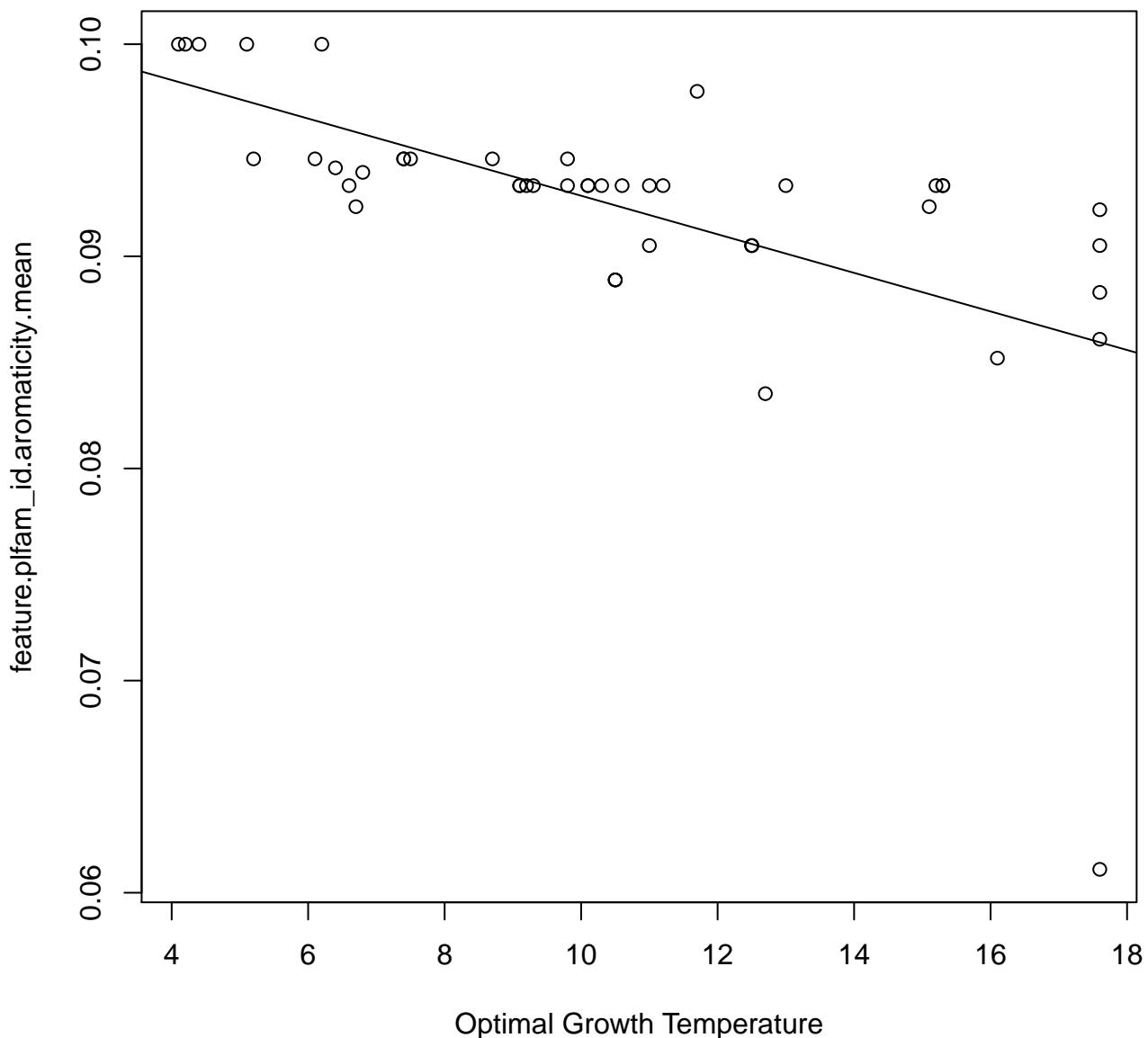
feature.plfam_id.aromaticity.mean
PLF_28228_00001035
Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)



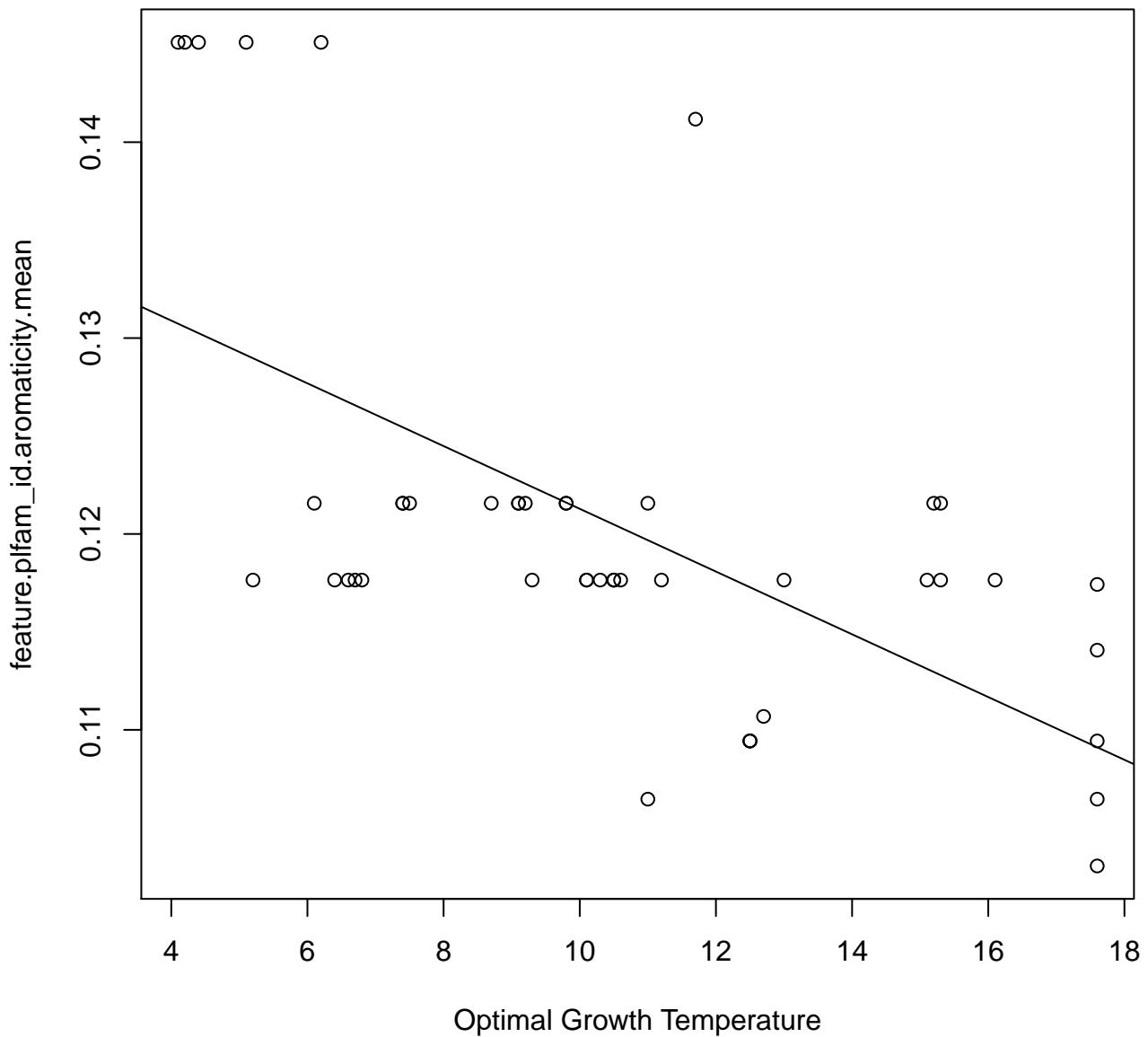
feature.pfam_id.aromaticity.mean
PLF_28228_00001525
Exopolyphosphatase (EC 3.6.1.11)



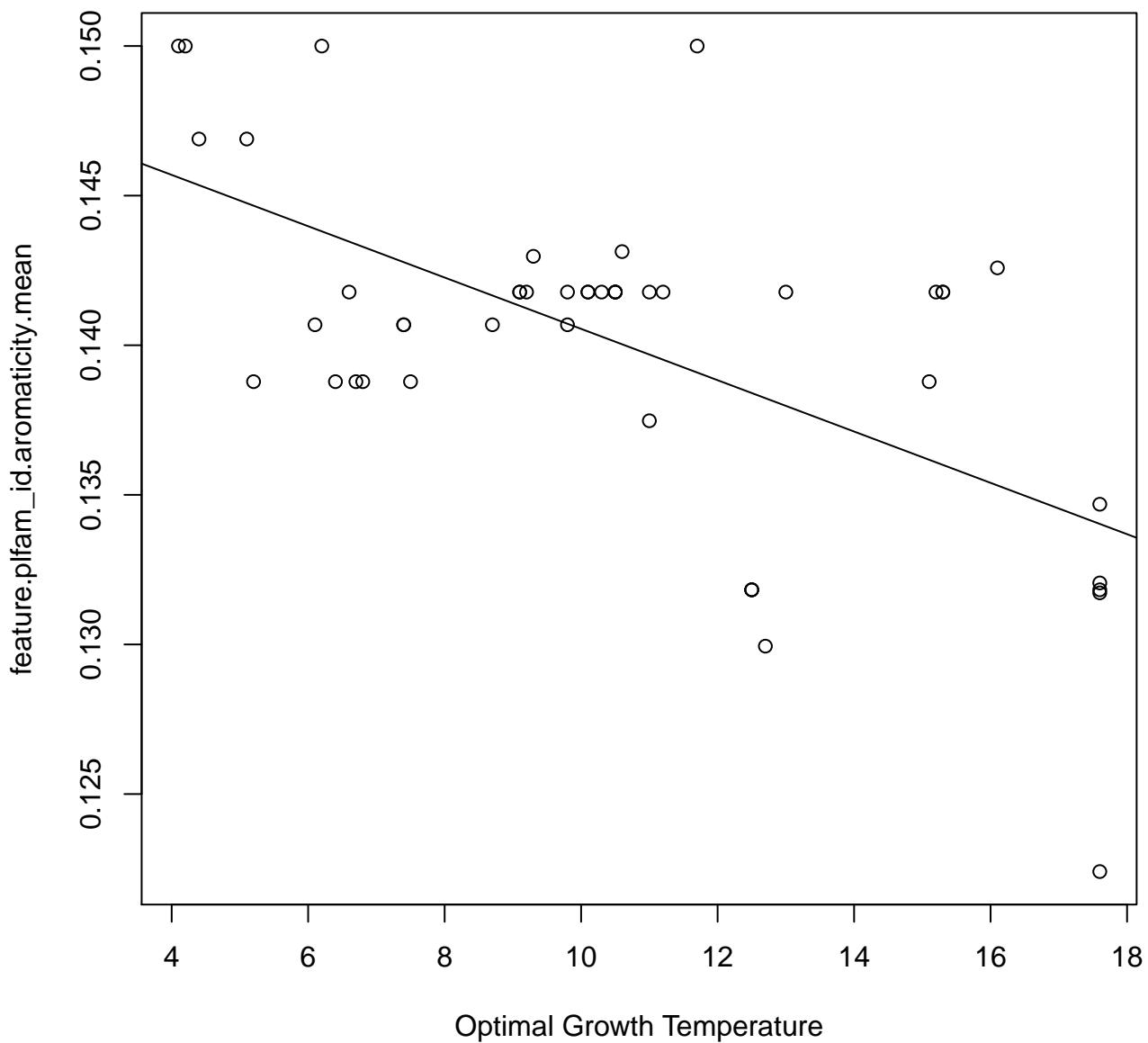
feature.pifam_id.aromaticity.mean
PLF_28228_00001972
Proton/glutamate symporter



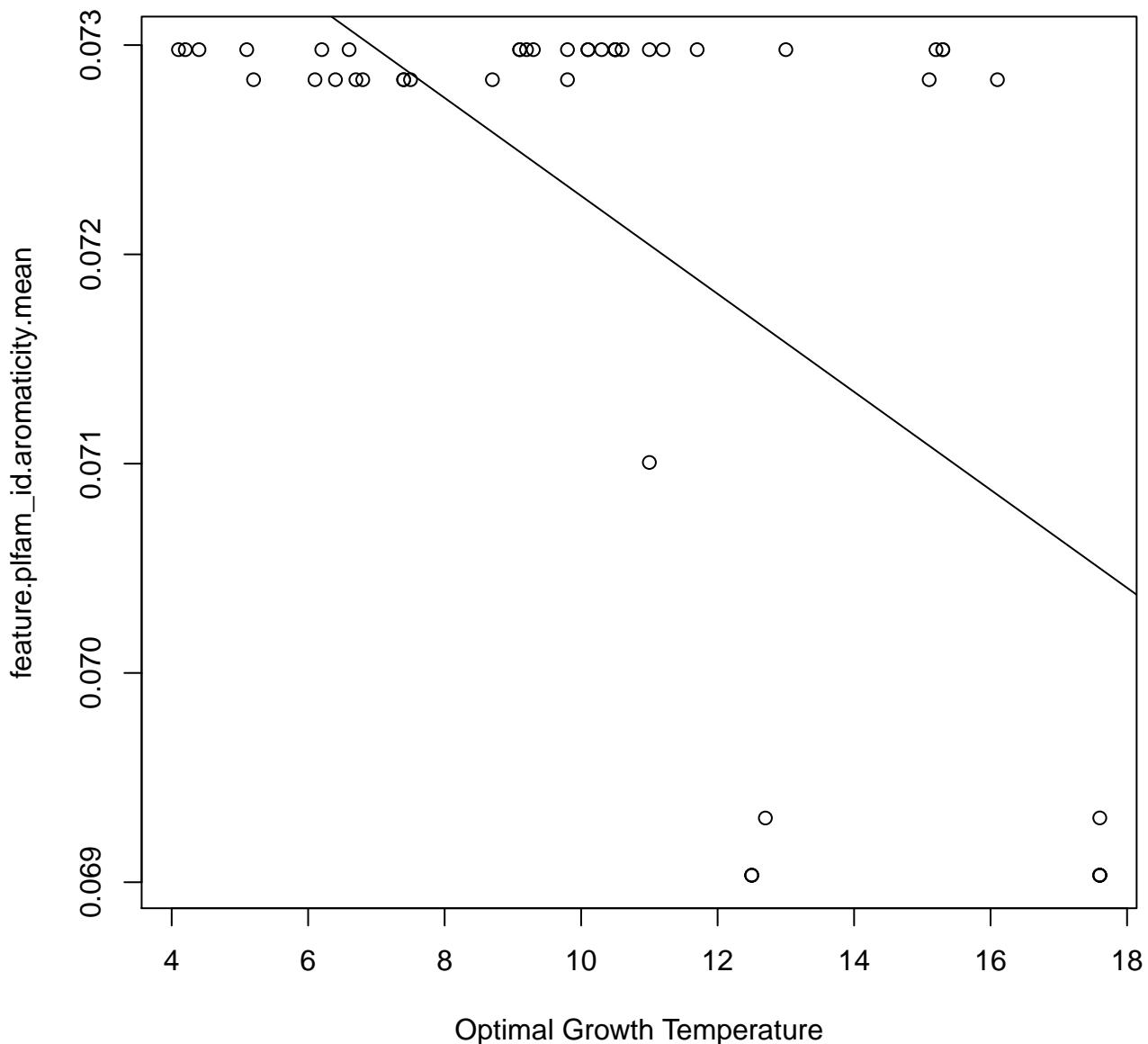
feature.plfam_id.aromaticity.mean
PLF_28228_00000786
Esterase ybfF (EC 3.1.-.-)



feature.plfam_id.aromaticity.mean
PLF_28228_00001001
Peptidoglycan lipid II flippase MurJ



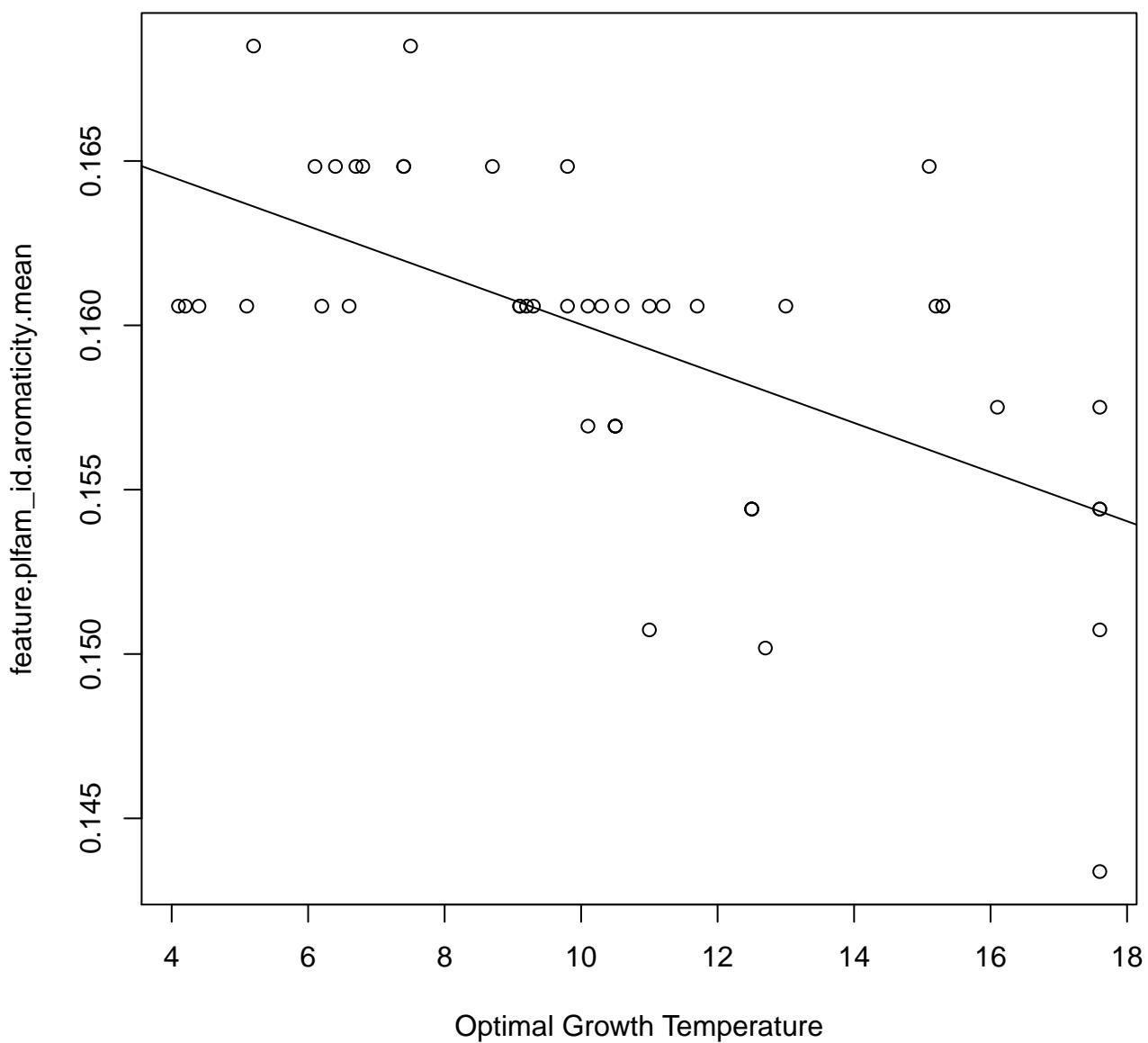
feature.plfam_id.aromaticity.mean
PLF_28228_00000861
Fumarate hydratase class I, aerobic (EC 4.2.1.2)



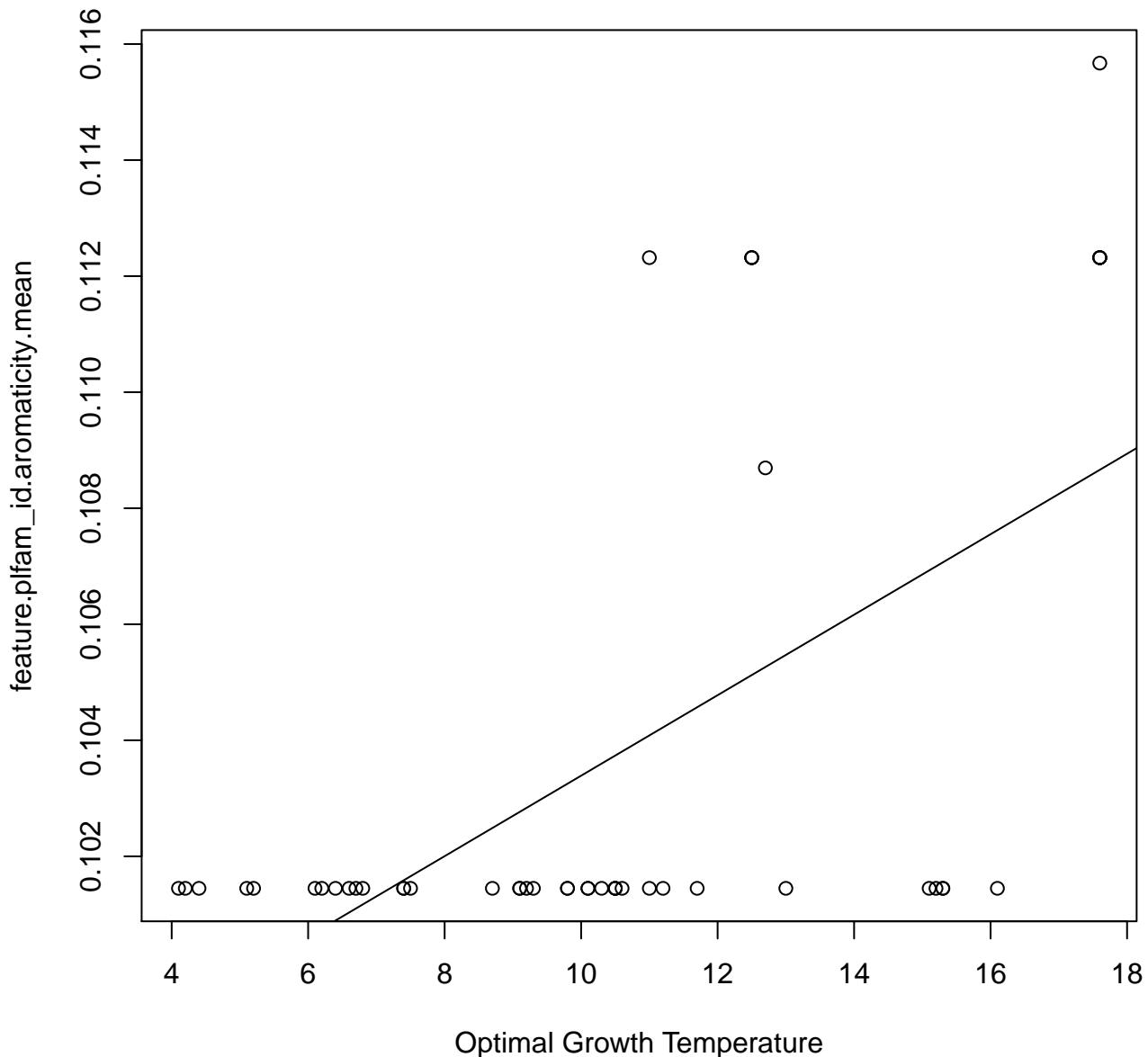
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PLF_28228_00001351

hypothetical protein



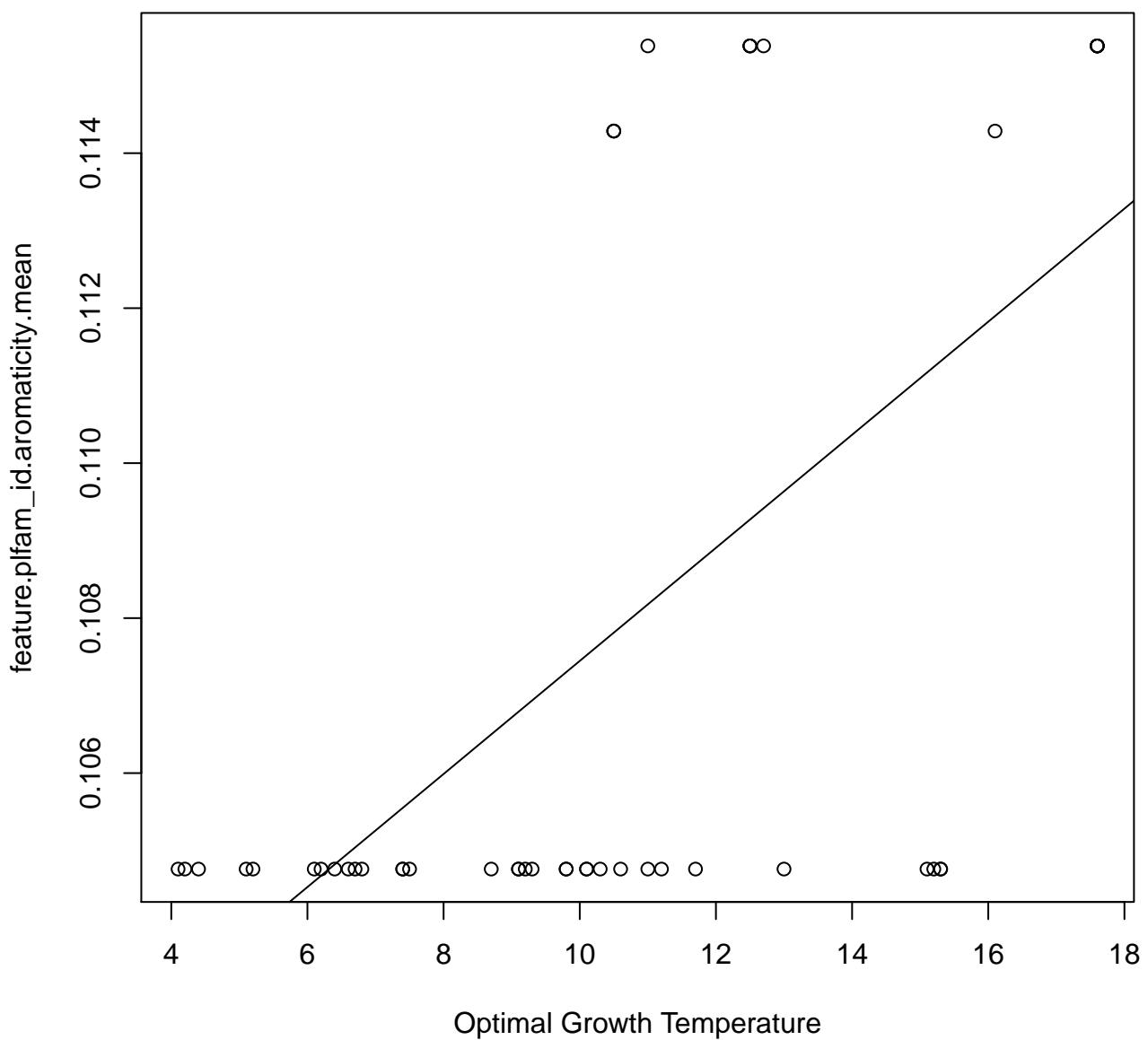
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PLF_28228_00000364
Diaminopimelate epimerase (EC 5.1.1.7)



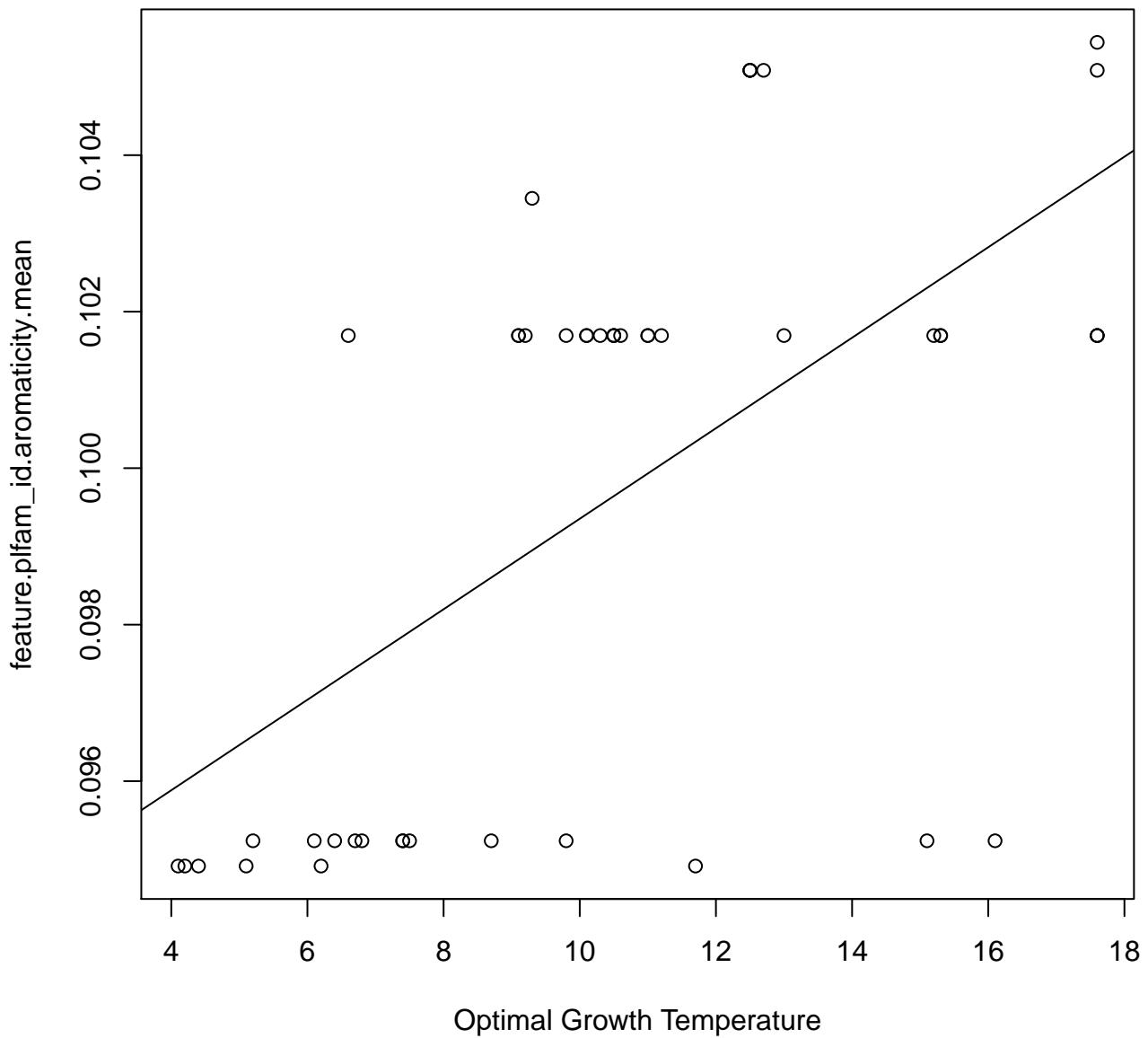
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PLF_28228_00001324

hypothetical protein



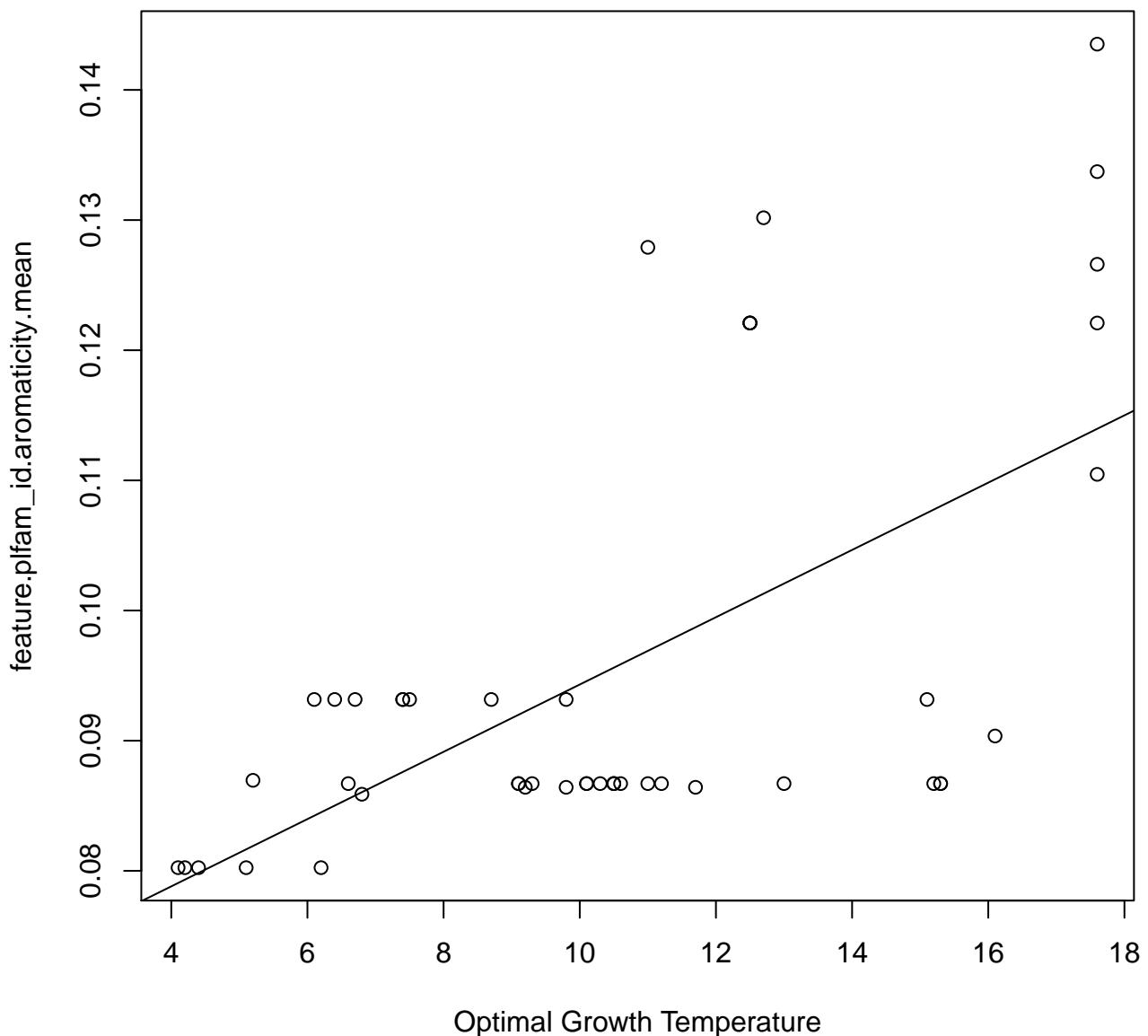
feature.pfam_id.aromaticity.mean
PLF_28228_00000094
HfIC protein



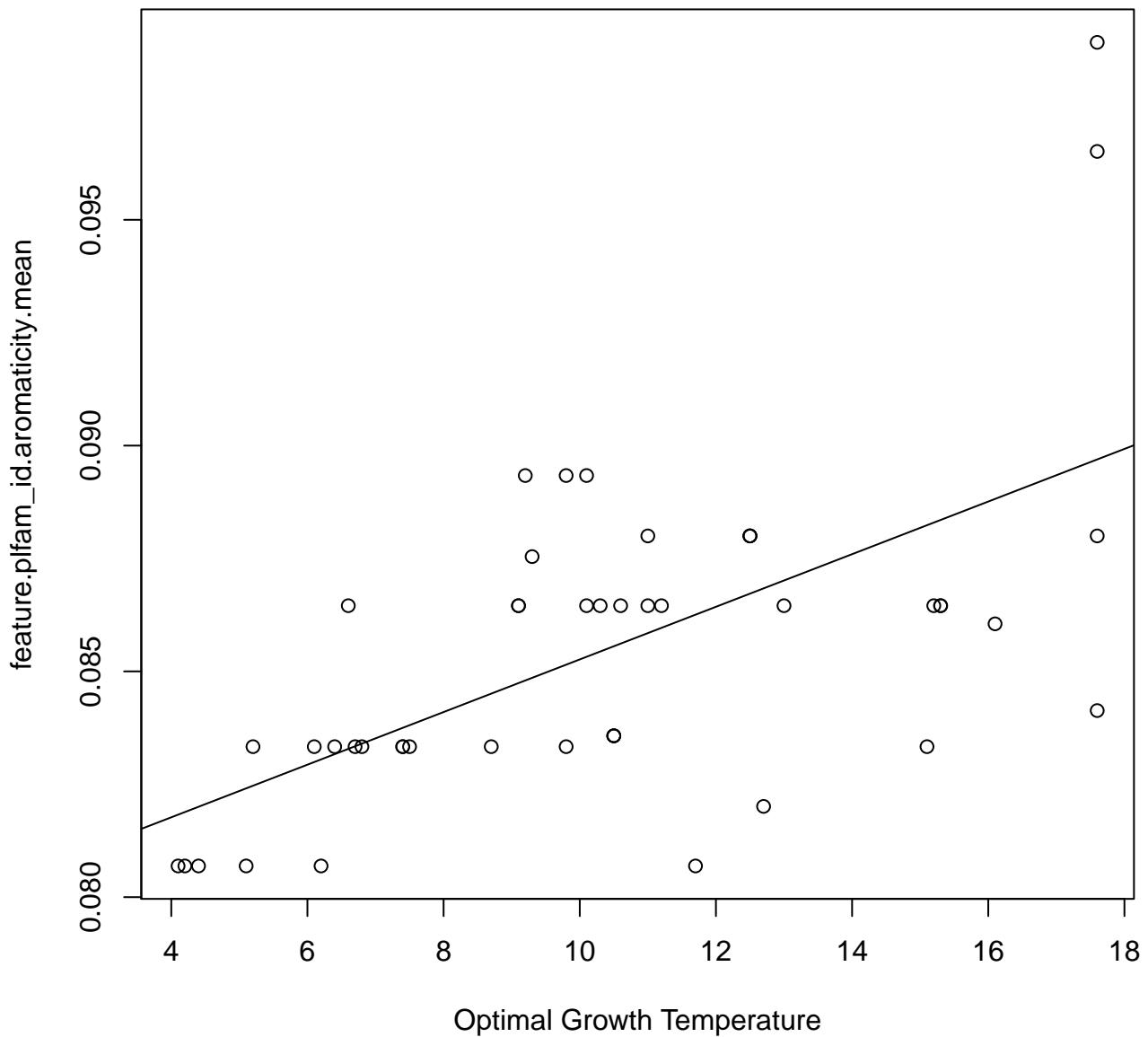
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PLF_28228_00002363

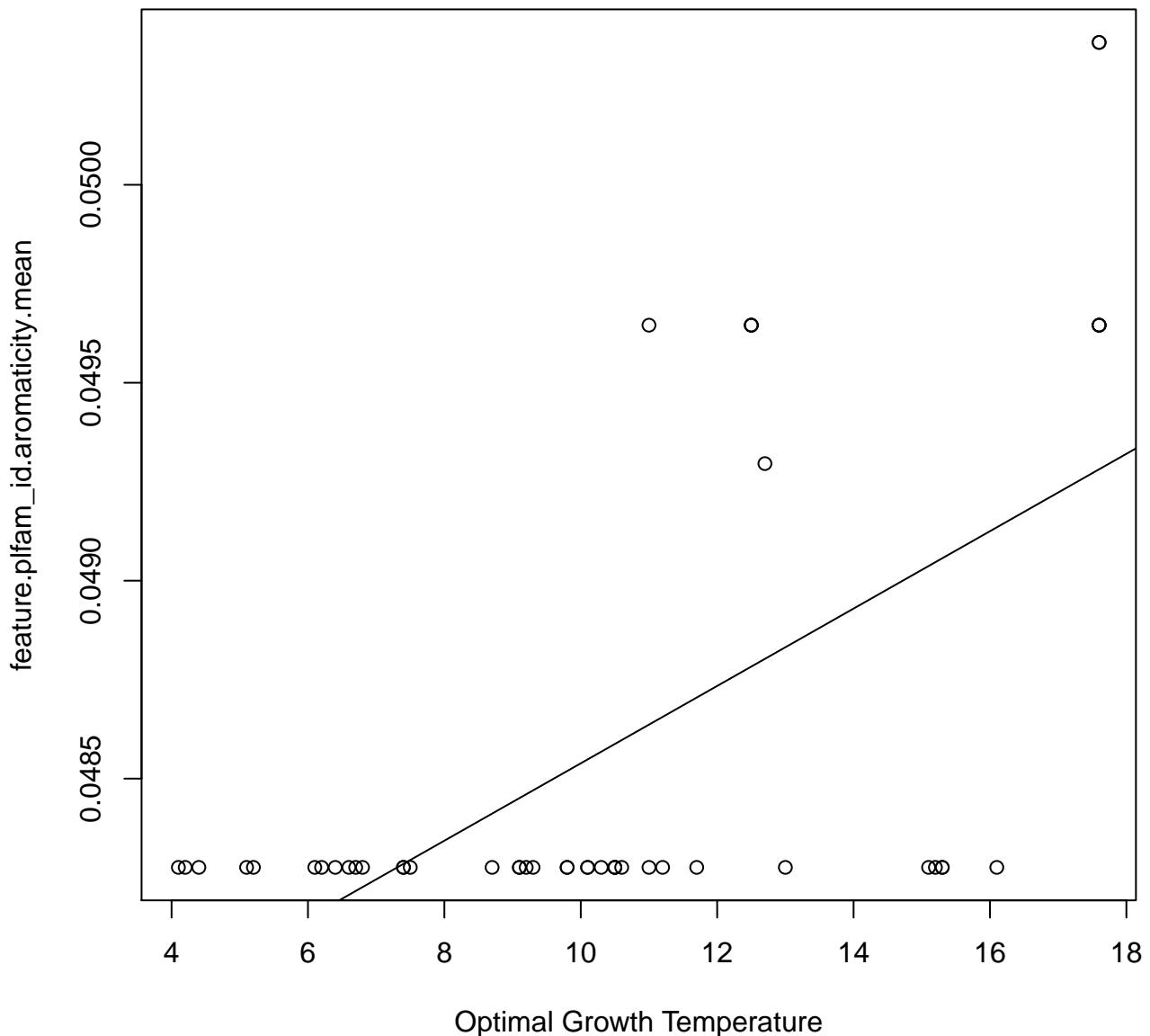
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00001723
Membrane protein YcjF



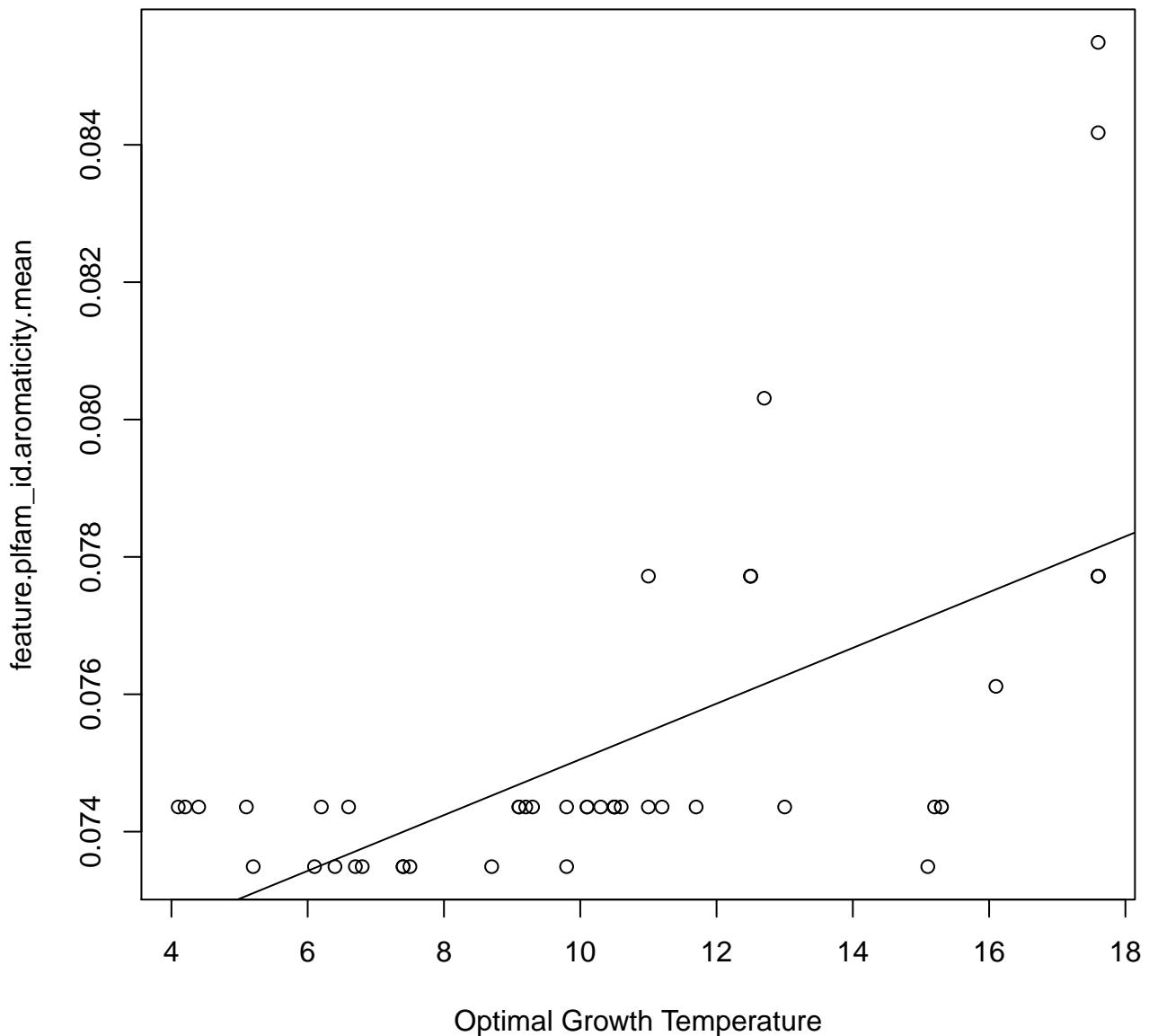
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PLF_28228_00001237
Translation elongation factor Ts



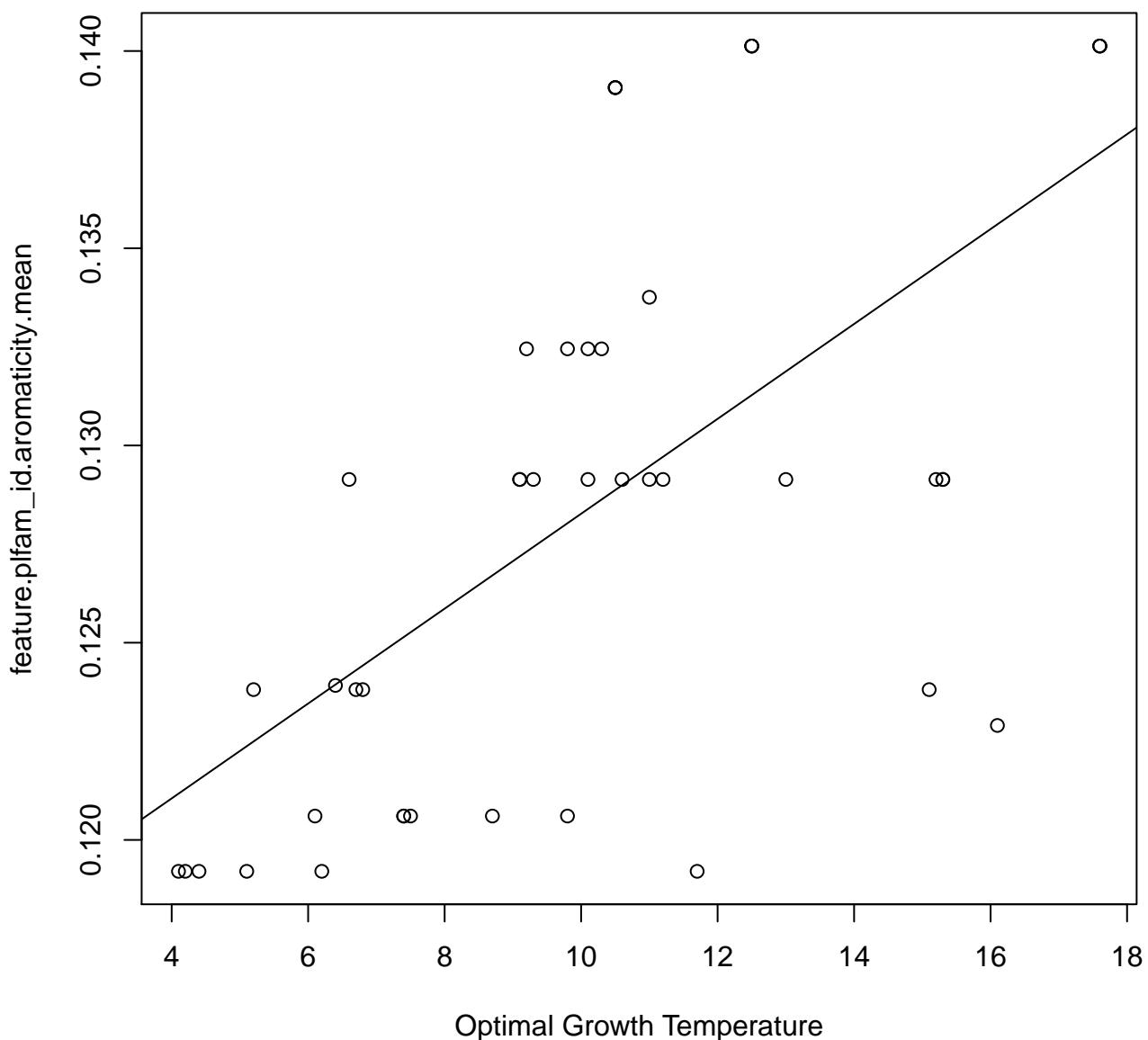
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PLF_28228_00000254

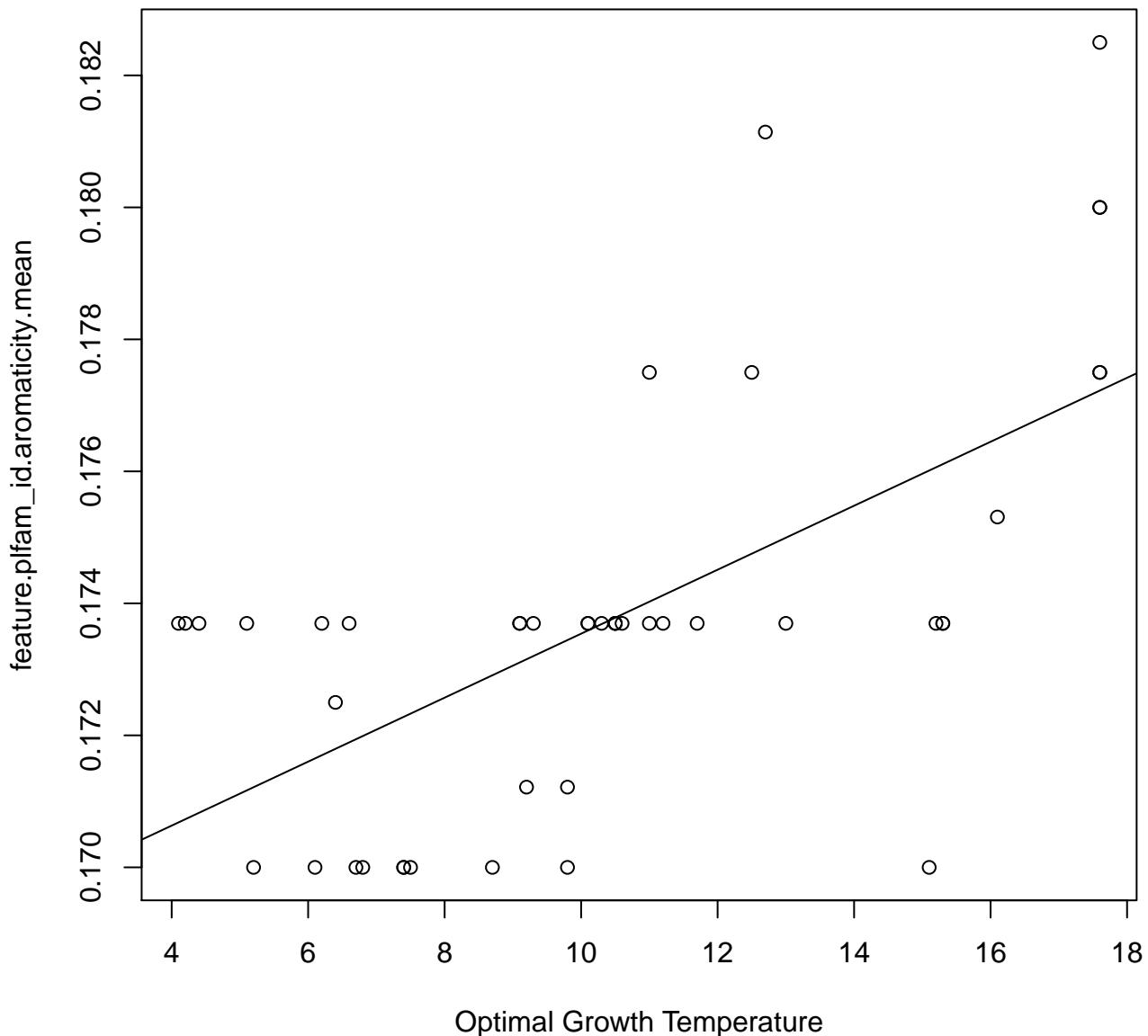
23S rRNA (adenine(2503)-C(2))-methyltransferase @ tRNA (adenine(37)-C(2))-methyltransferase (EC 2.1.1.192)



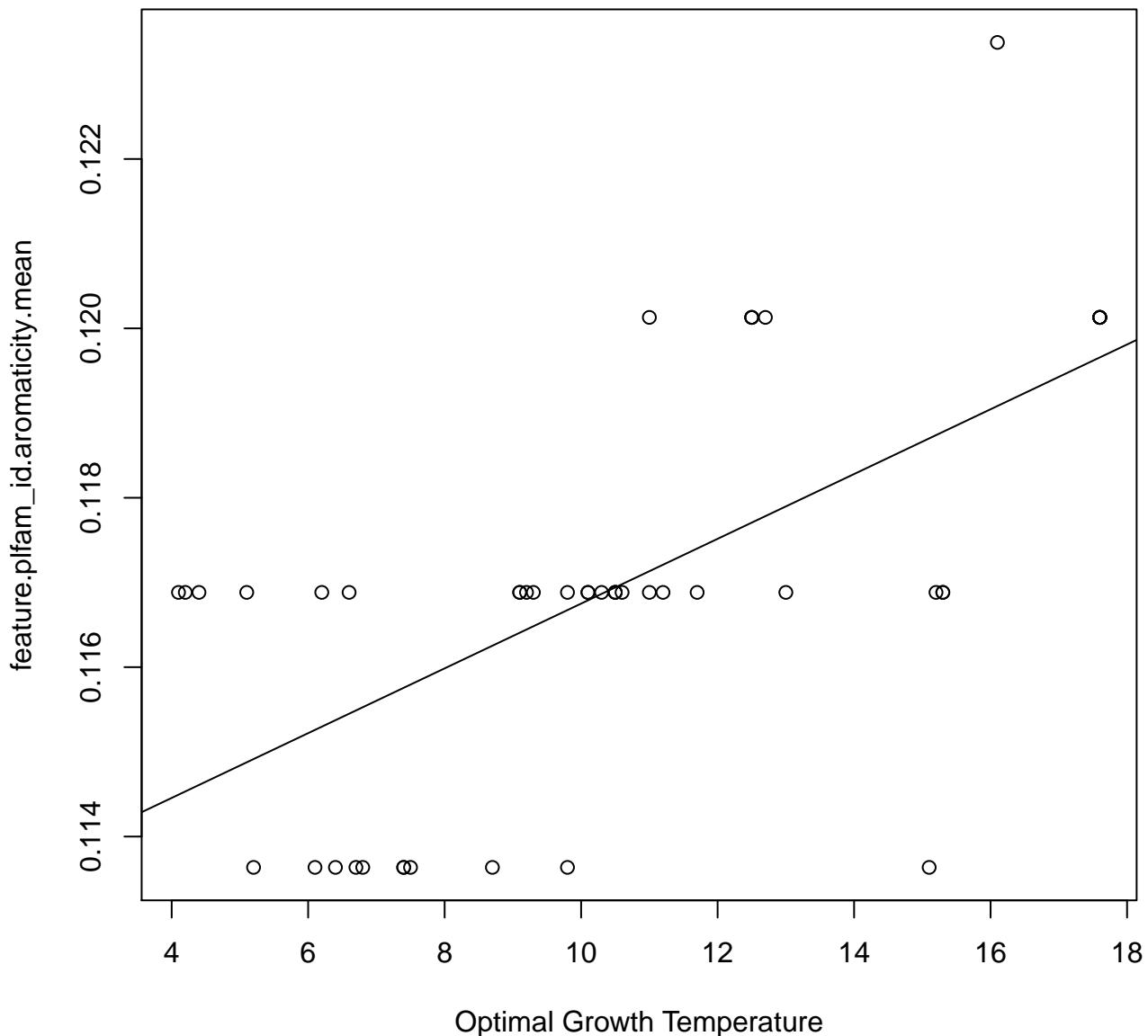
feature.plfam_id.aromaticity.mean
PLF_28228_00002622
Cytochrome c family protein



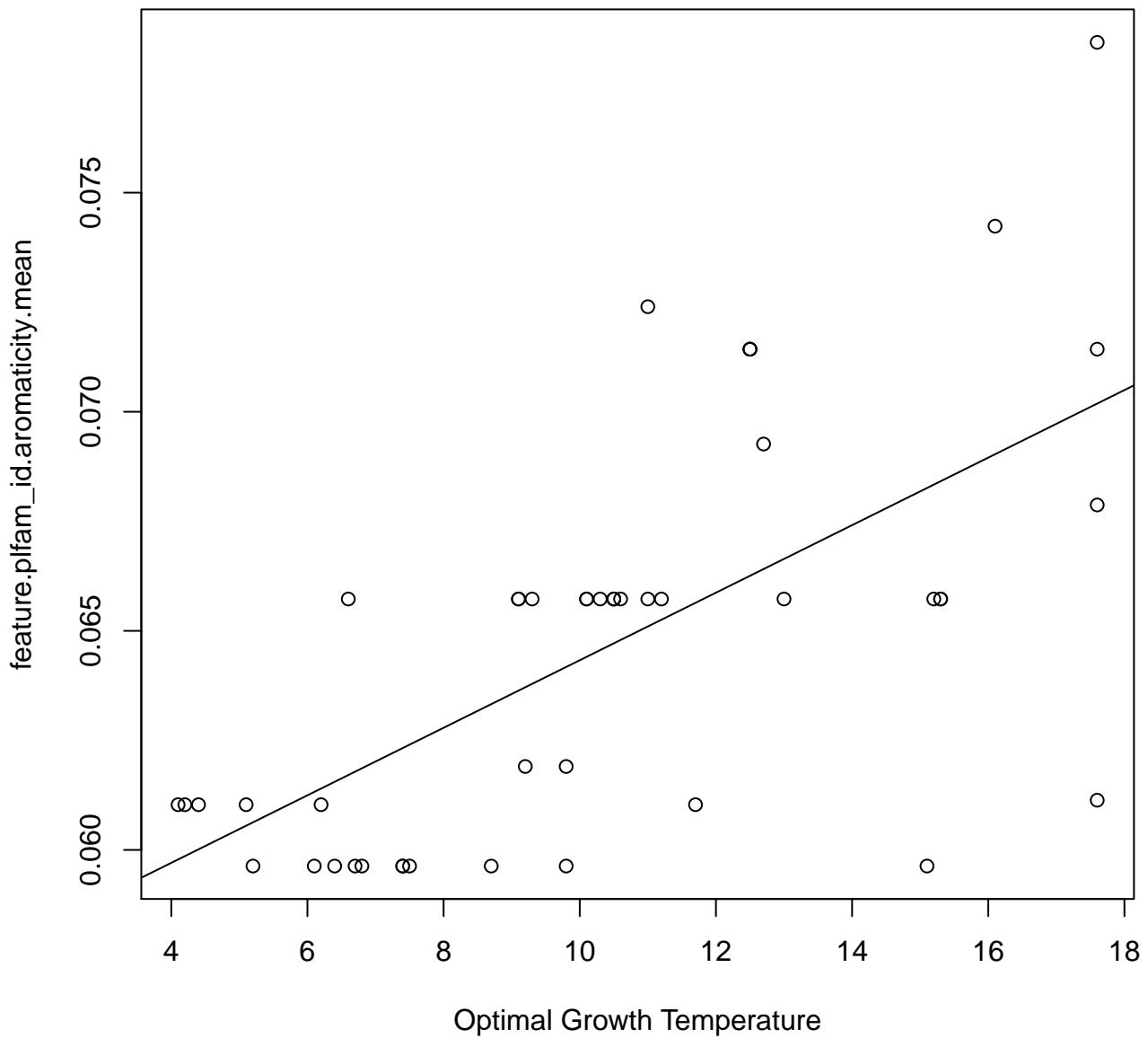
feature.plfam_id.aromaticity.mean
PLF_28228_00028079
Na(+)–translocating NADH–quinone reductase subunit B (EC 1.6.5.8)



feature.plfam_id.aromaticity.mean
PLF_28228_00001574
Branched-chain amino acid aminotransferase (EC 2.6.1.42)



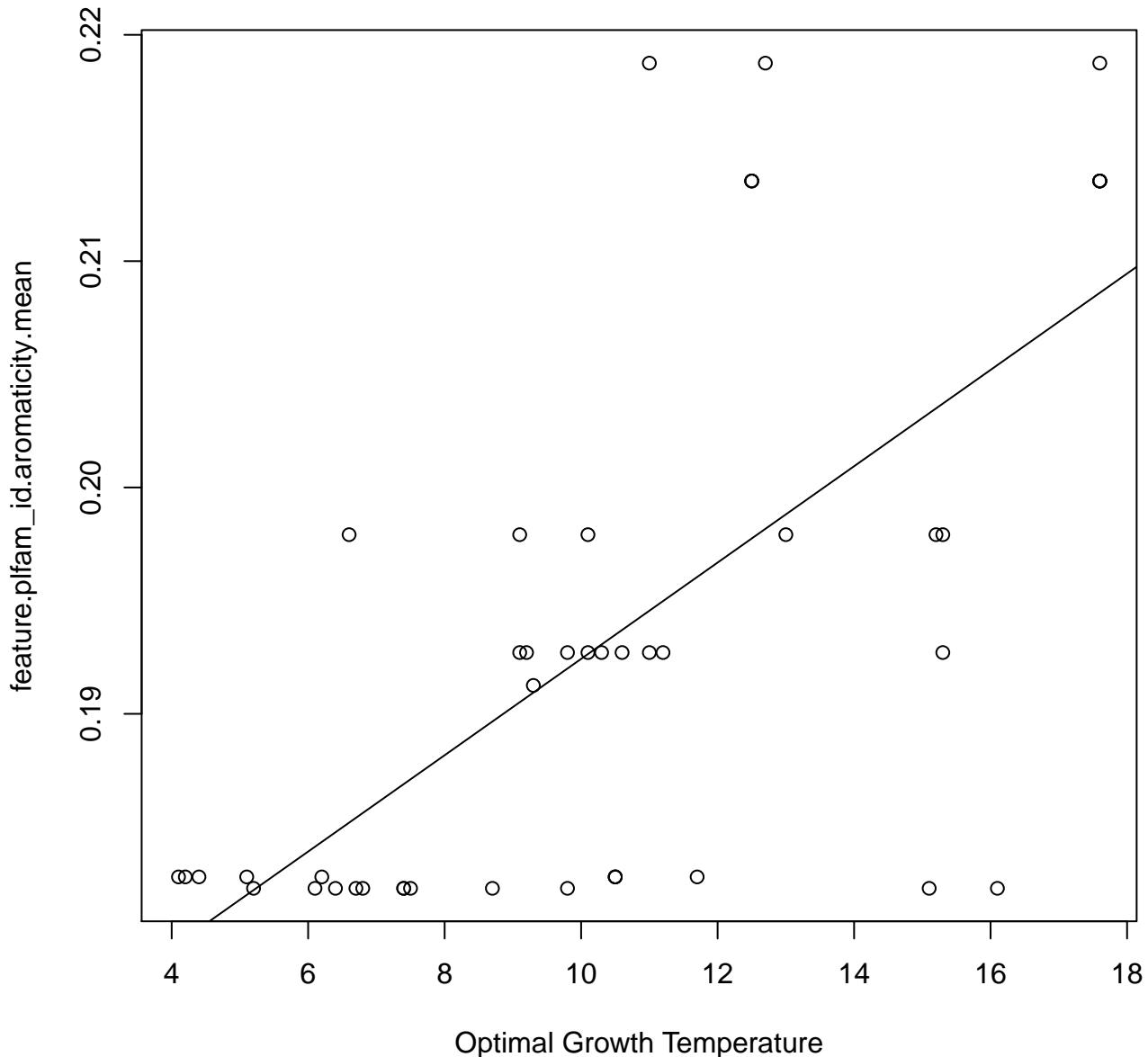
feature.plfam_id.aromaticity.mean
PLF_28228_00000869
GTP-binding protein EngB



feature.plfam_id.aromaticity.mean

PLF 28228 00000446

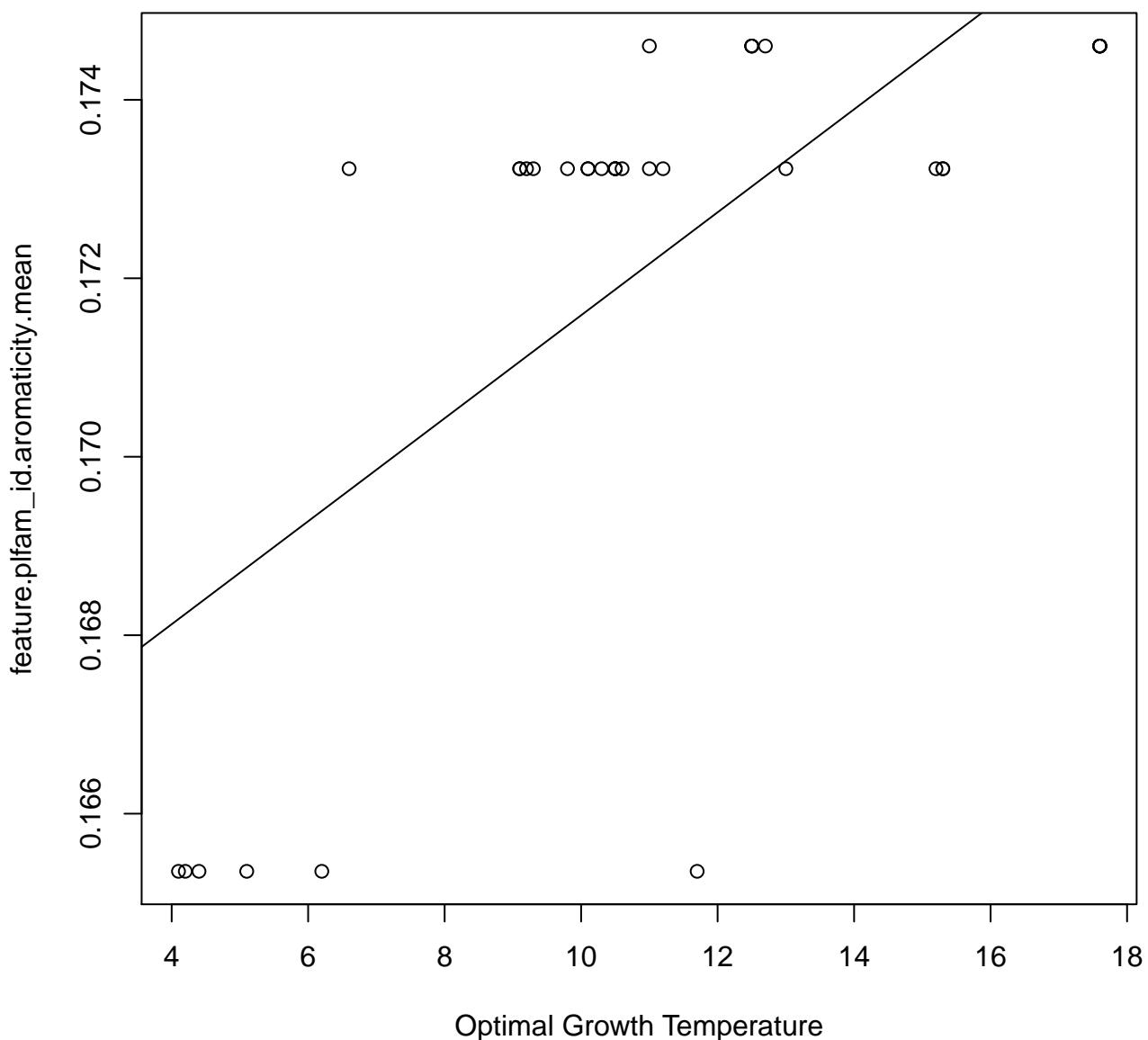
FIG139438: lipoprotein E



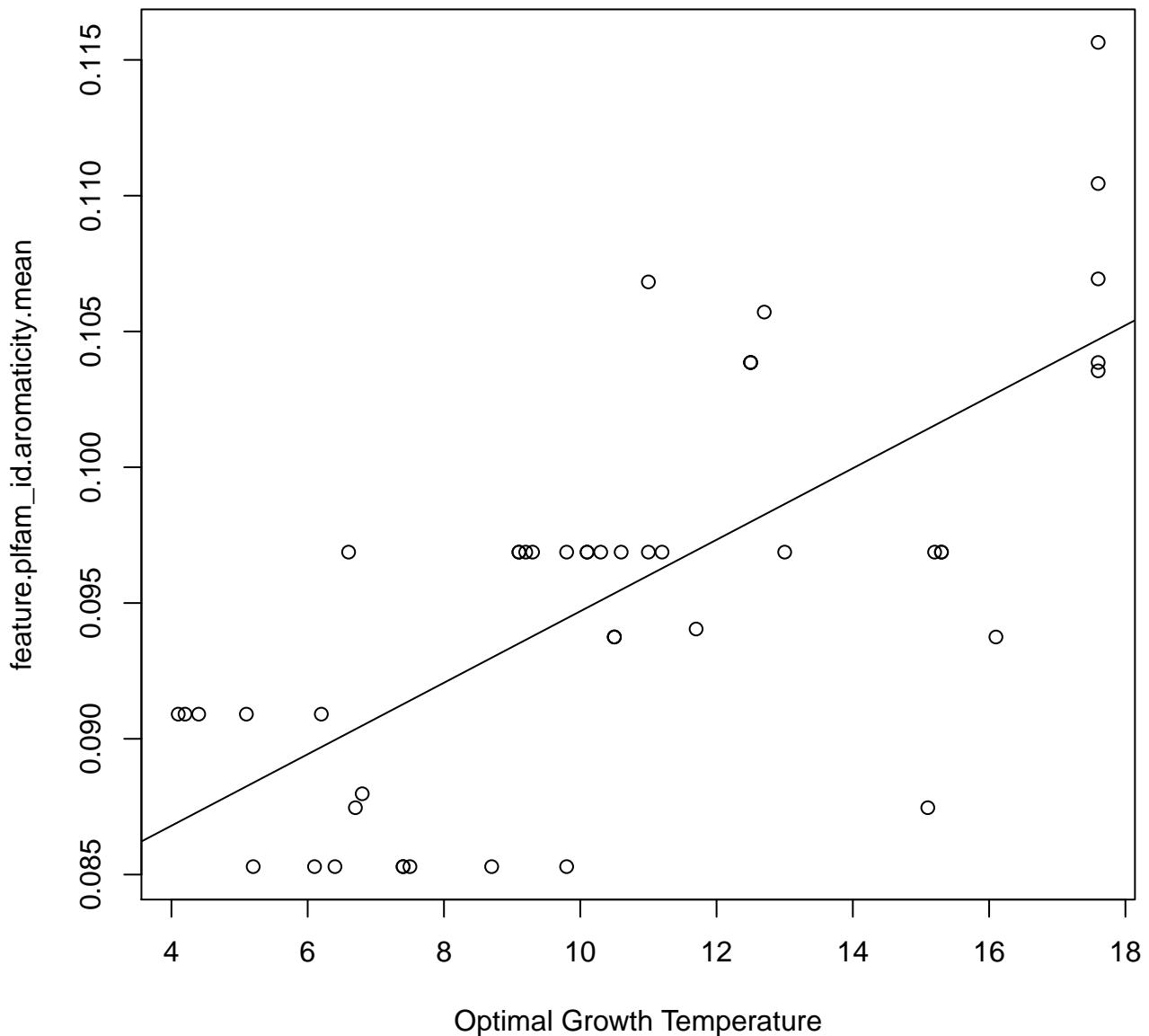
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PLF_28228_00002252

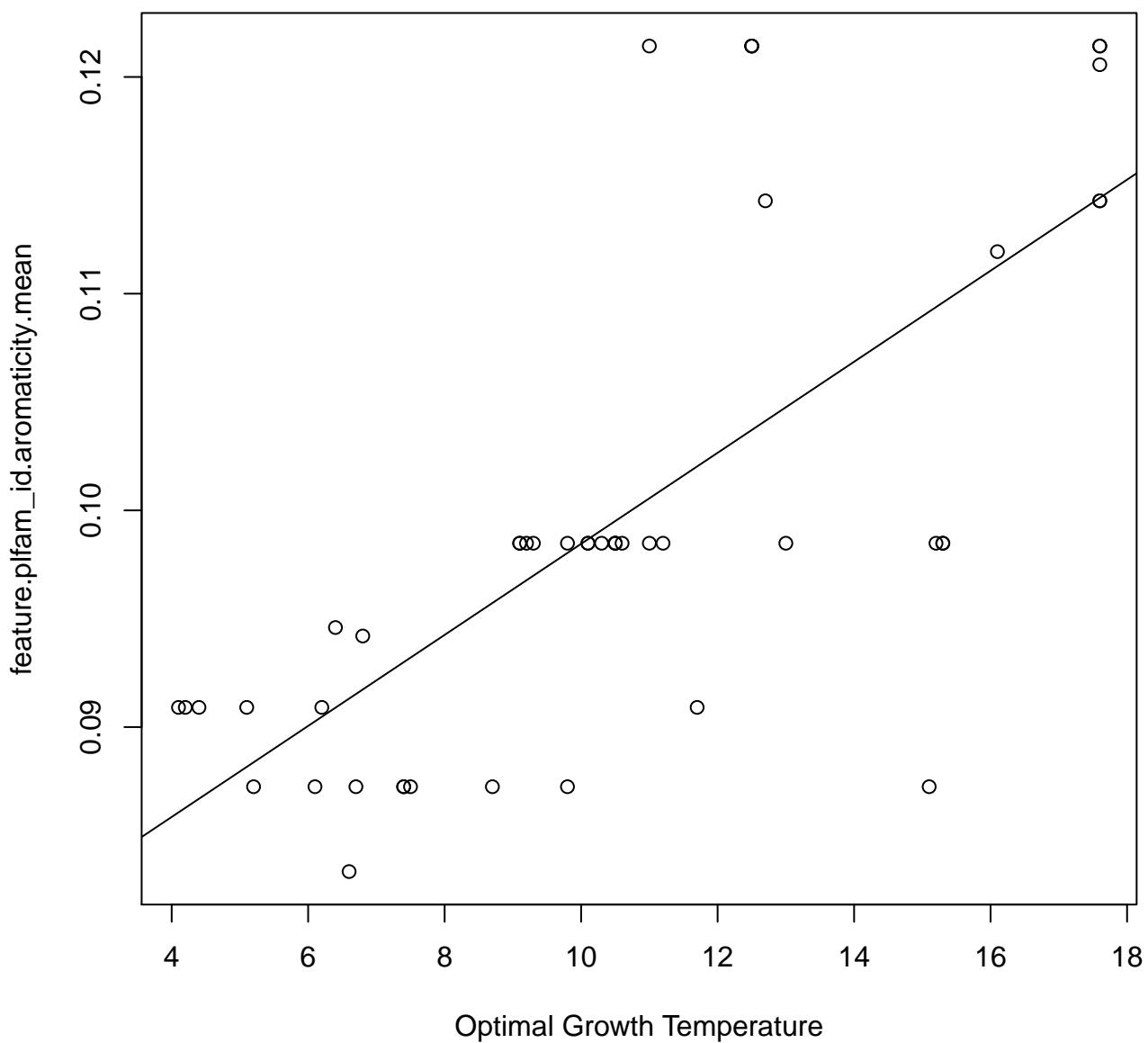
hypothetical protein



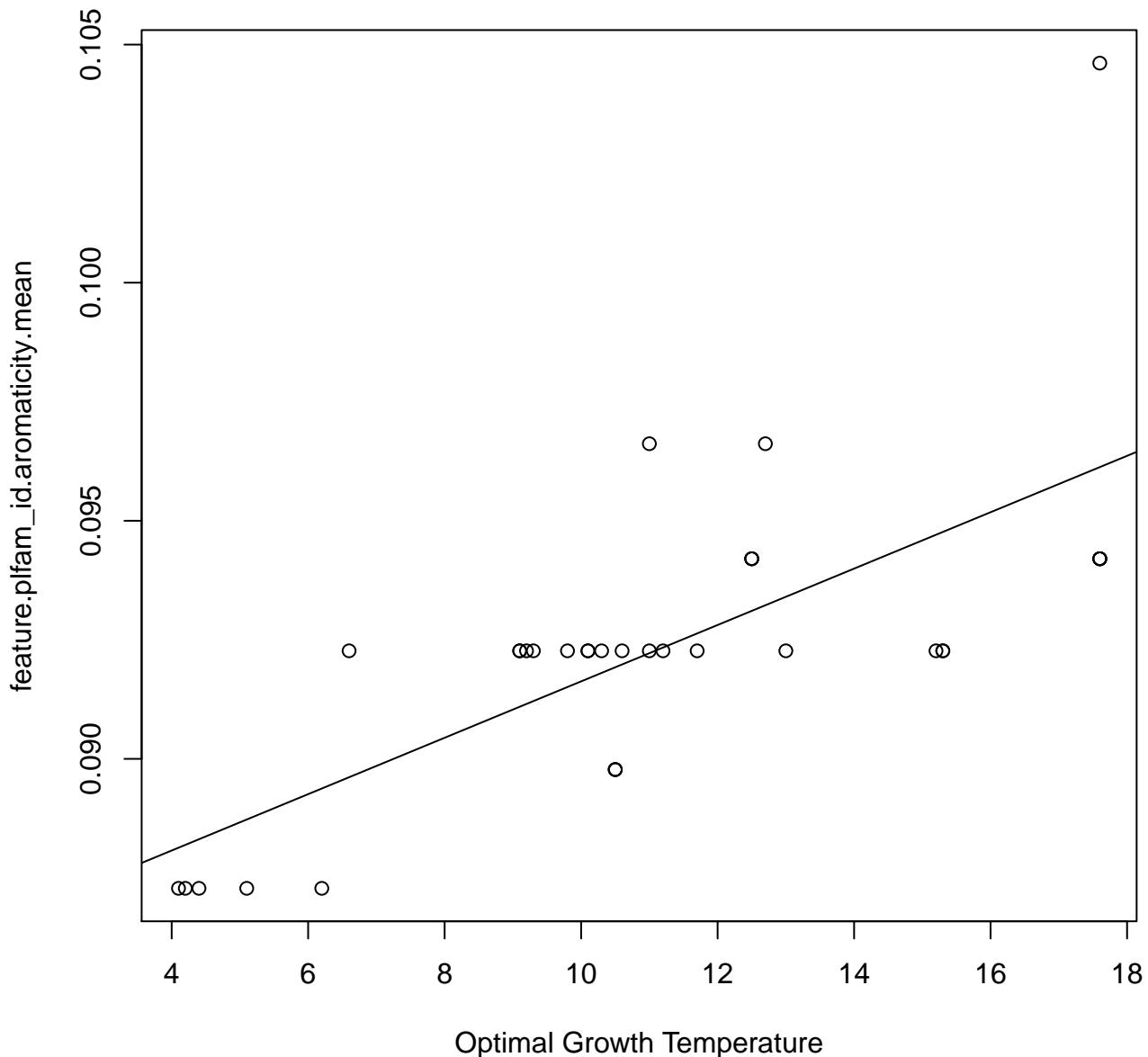
feature.plfam_id.aromaticity.mean
PLF_28228_00002060
Sigma factor RpoE negative regulatory protein RseB precursor



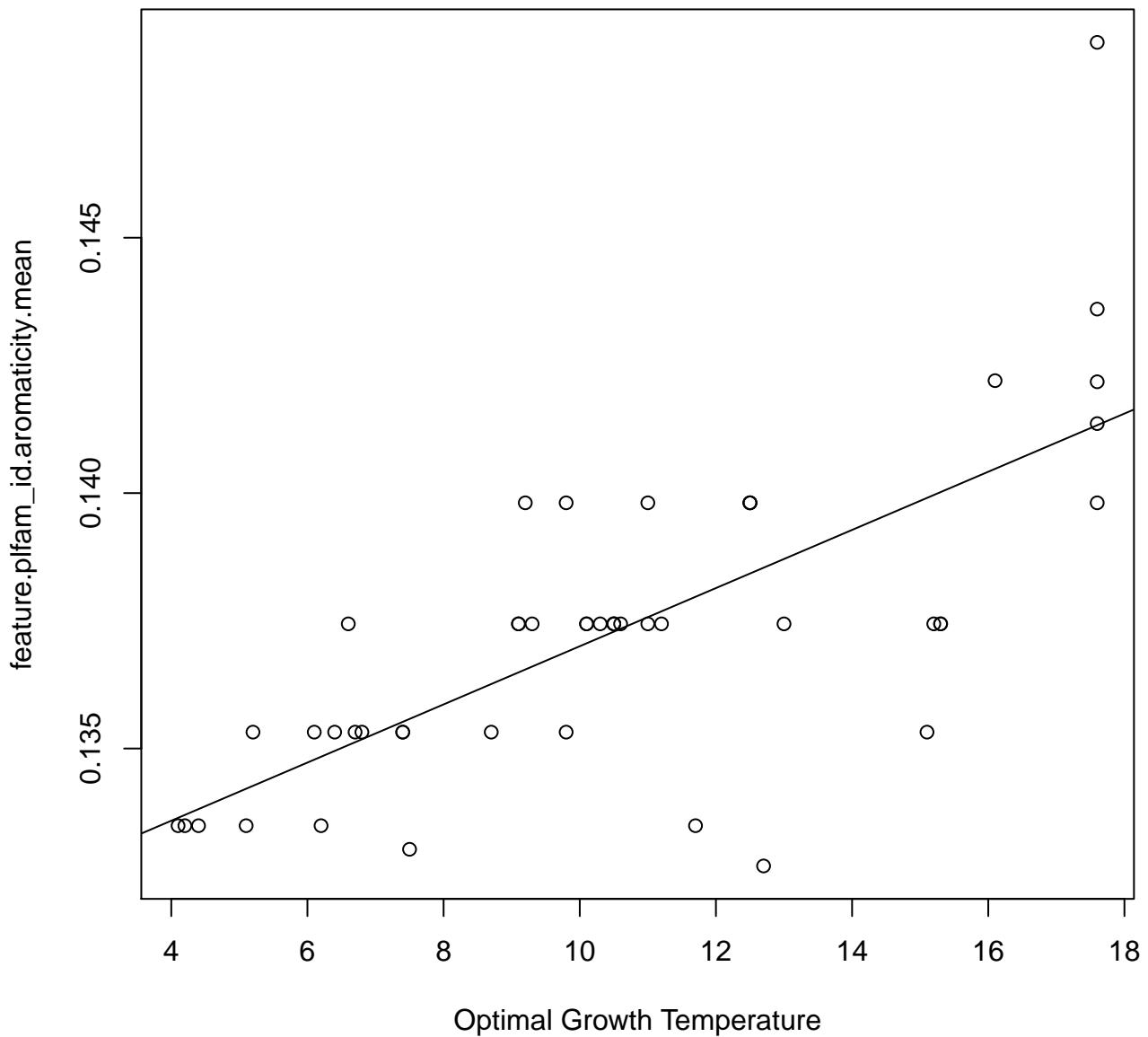
feature.plfam_id.aromaticity.mean
PLF_28228_00001543
DNA-binding protein, CopG family



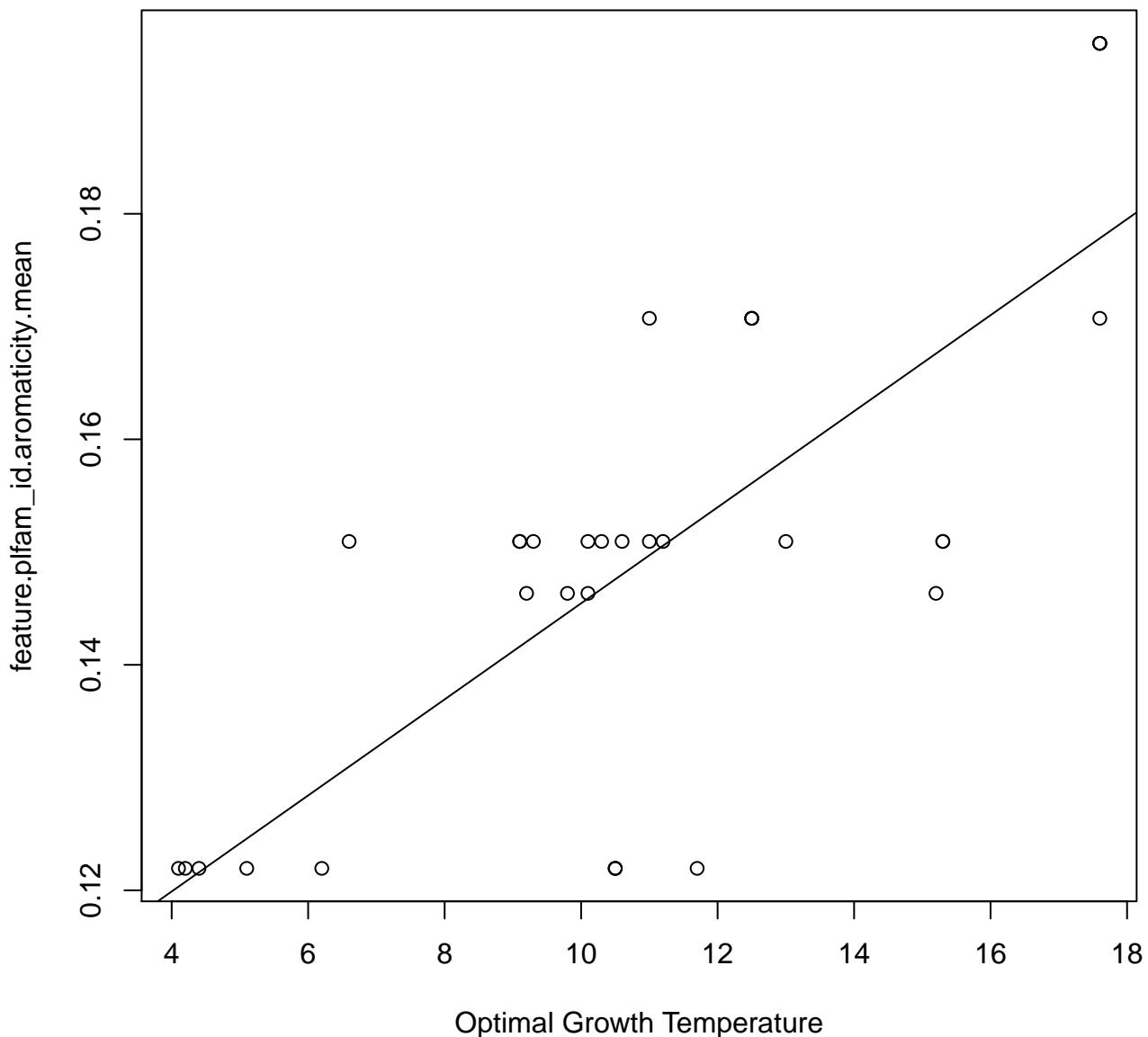
feature.plfam_id.aromaticity.mean
PLF_28228_00000683
Outer membrane beta-barrel assembly protein BamB



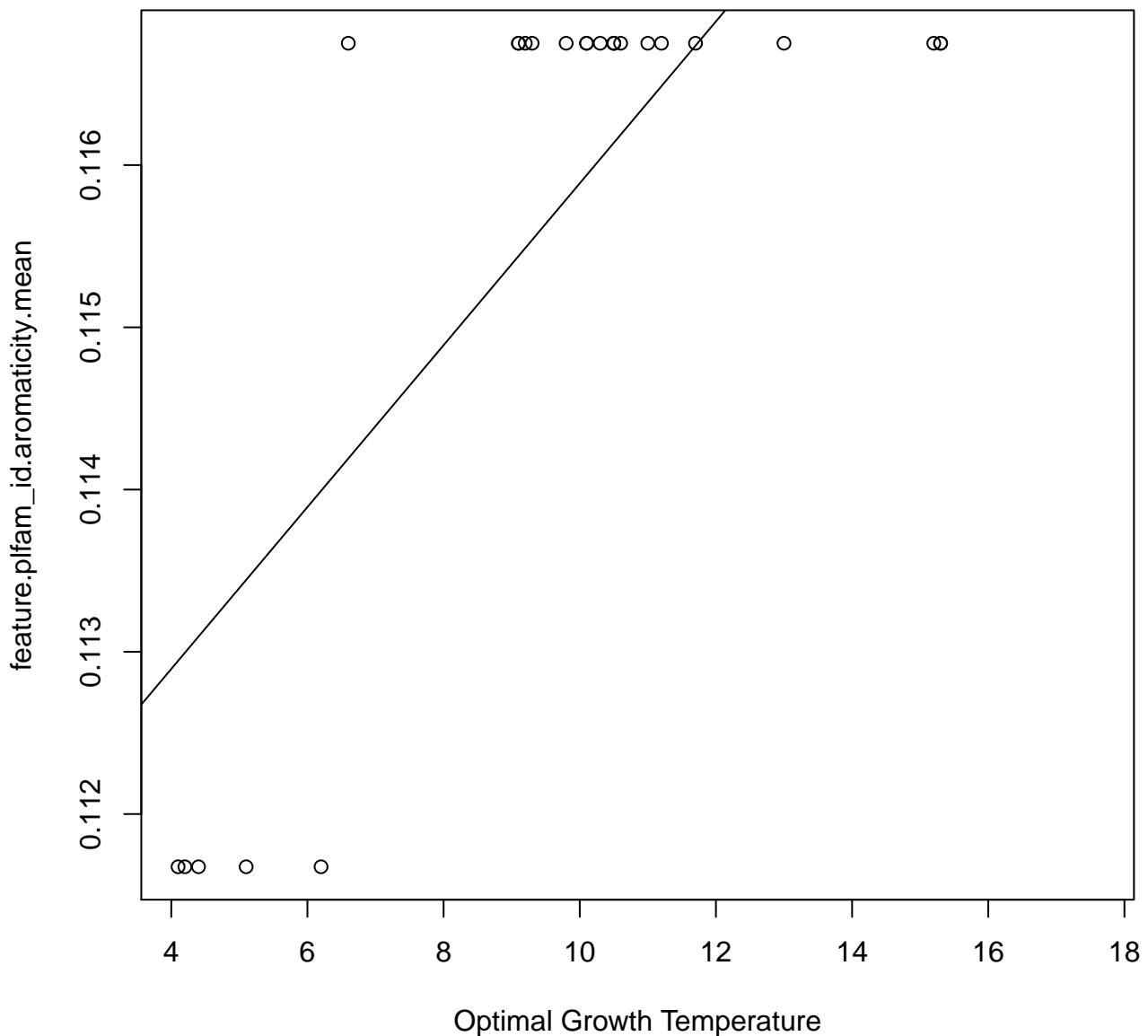
feature.plfam_id.aromaticity.mean
PLF_28228_00002535
Uncharacterized MFS-type transporter



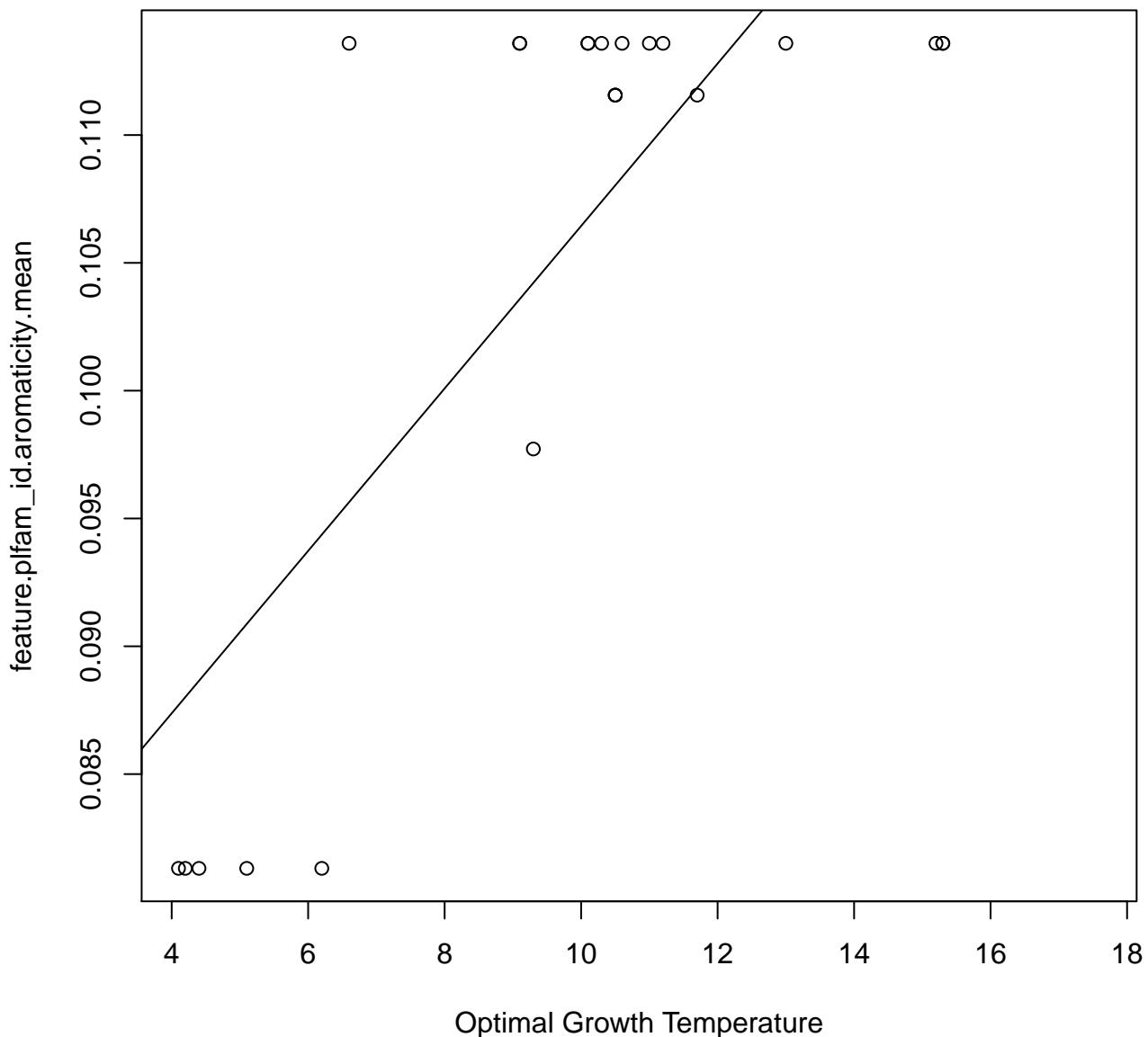
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PLF_28228_00018539
nr0040.cl00013



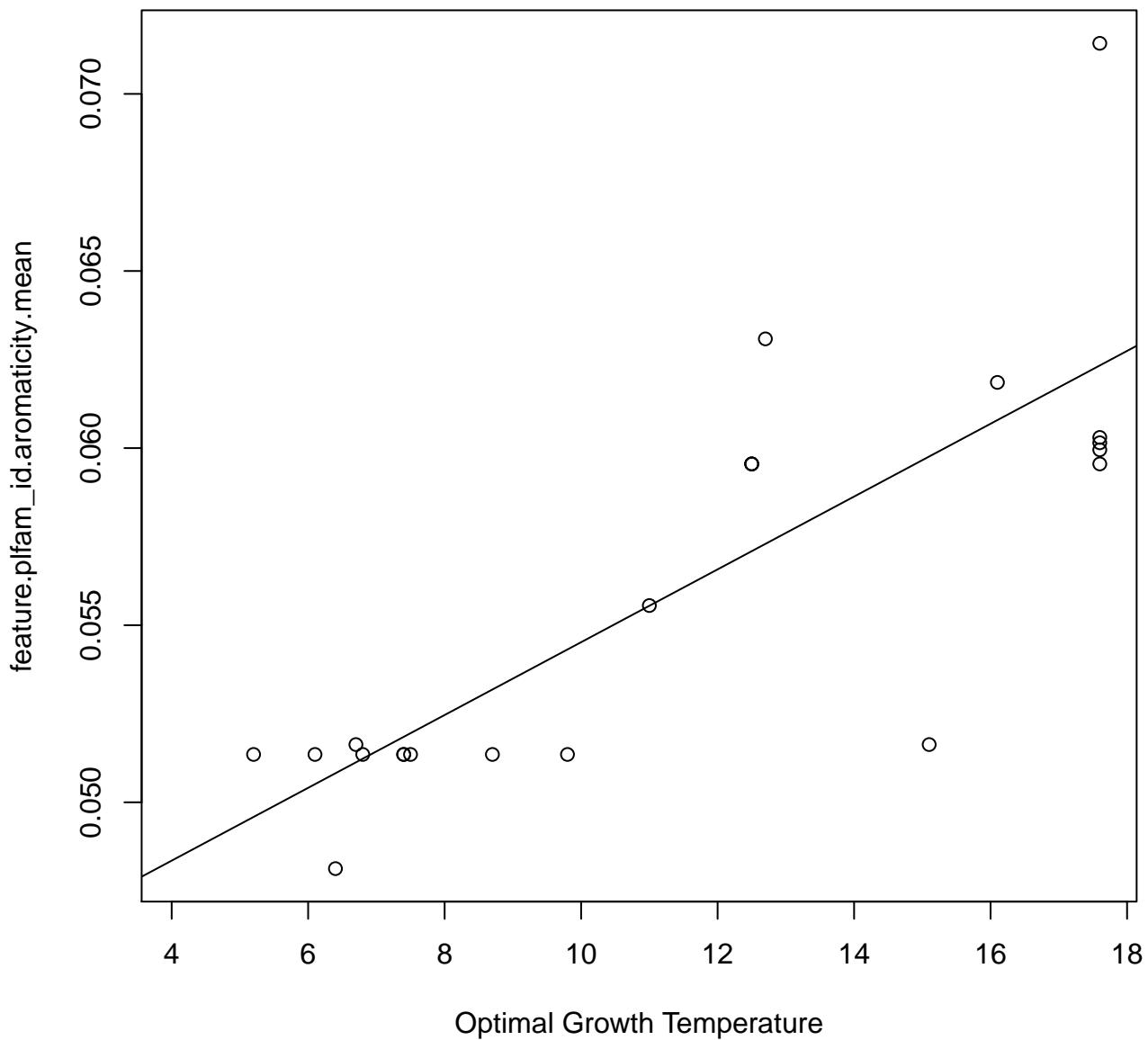
feature.plfam_id.aromaticity.mean
PLF_28228_00032199
Uncharacterized hydrolase DSY2054



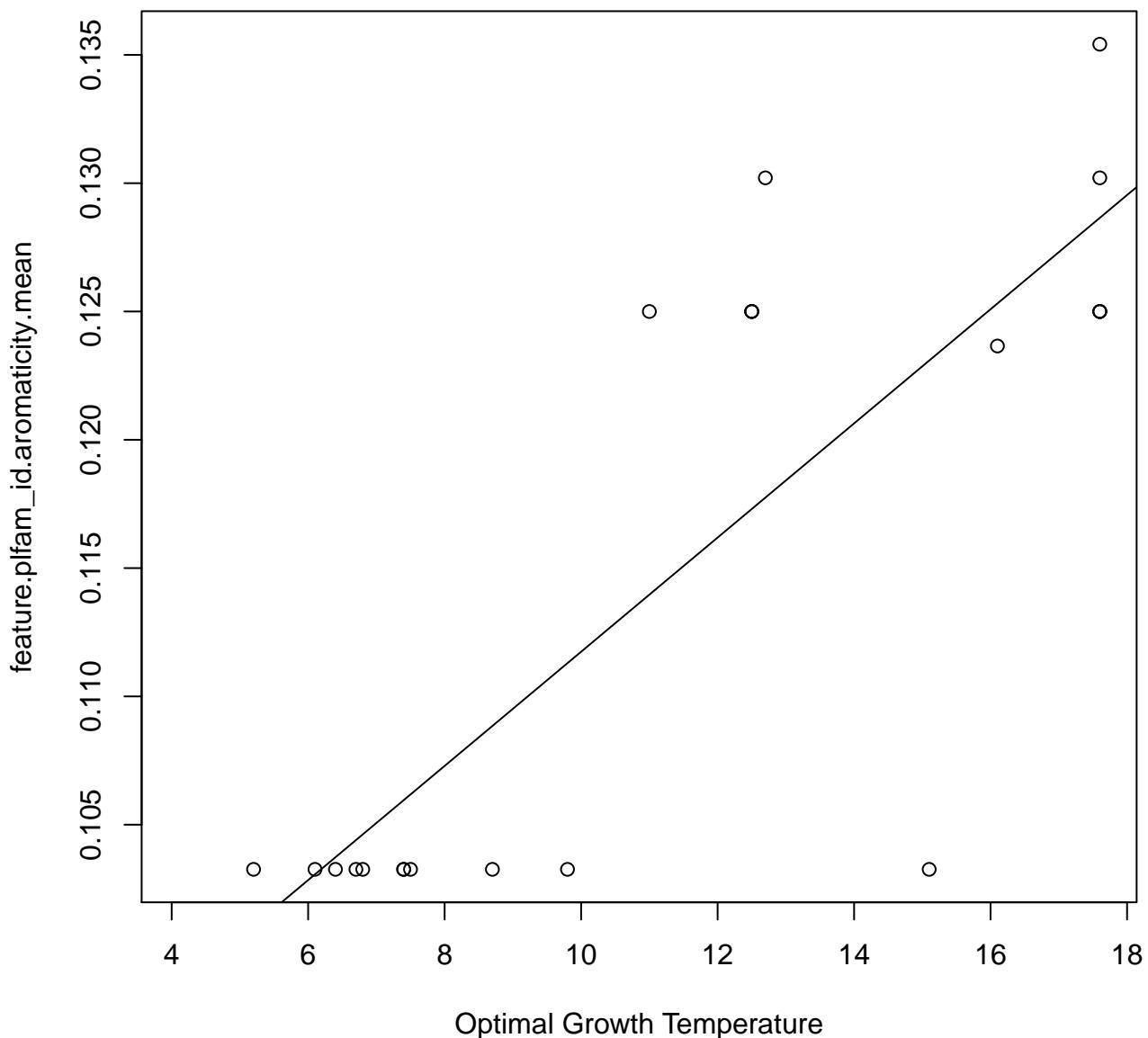
feature.plfam_id.aromaticity.mean
PLF_28228_00022096
Two-component system sensor histidine kinase



feature.pfam_id.aromaticity.mean
PLF_28228_00022176
MSHA biogenesis protein MshN



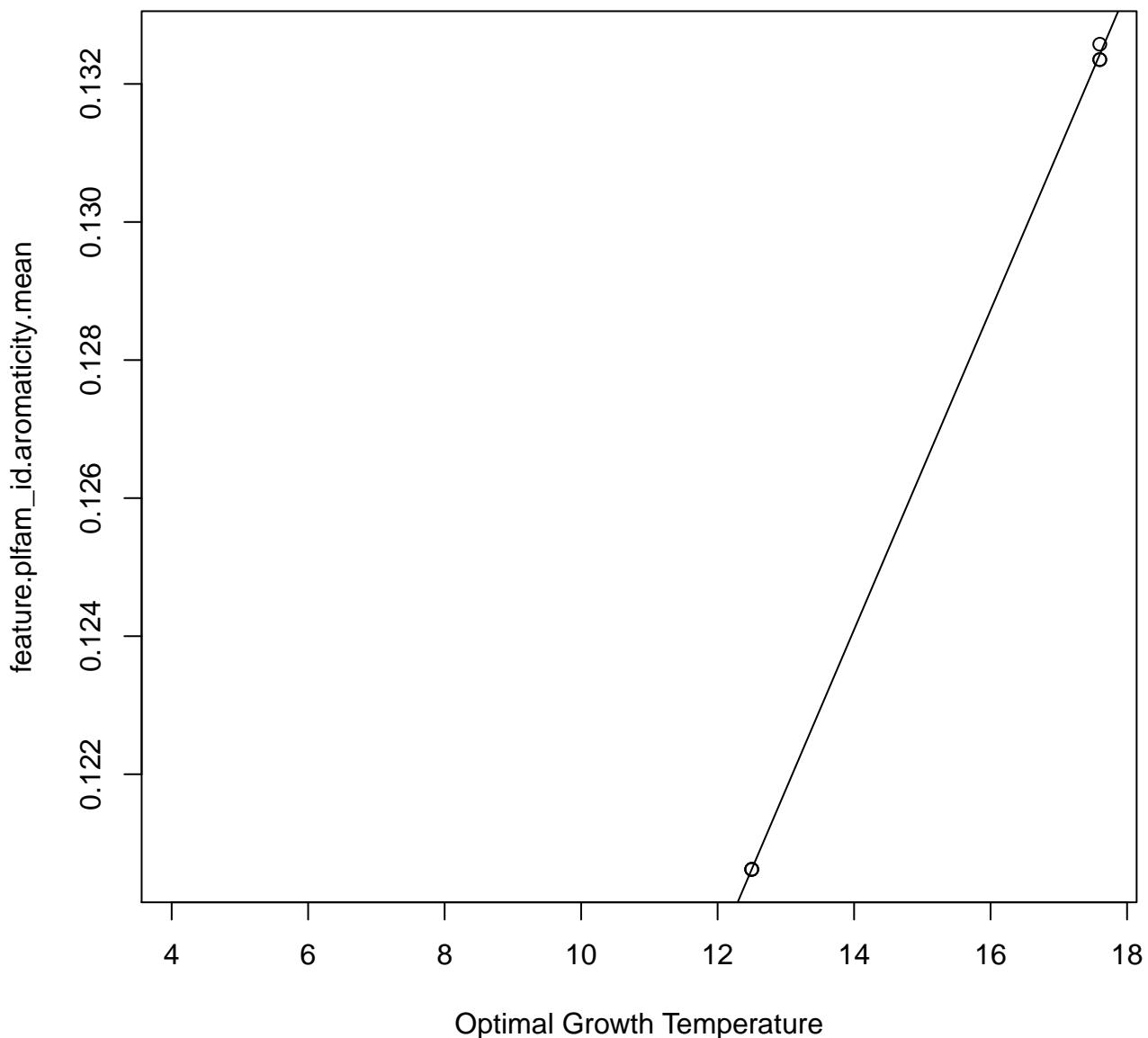
feature.pfam_id.aromaticity.mean
PLF_28228_00002527
putative lipoprotein



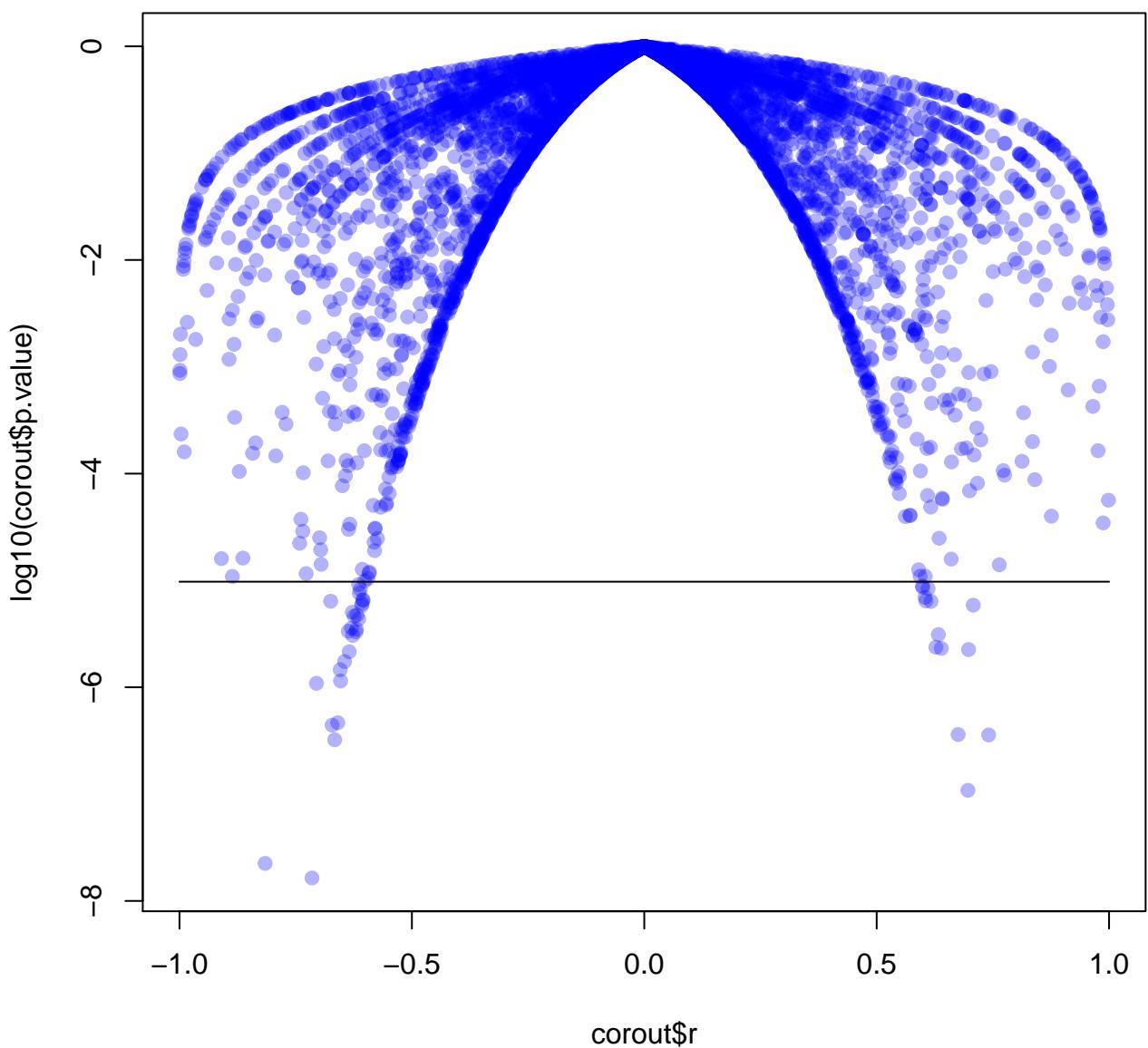
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PLF_28228_00018366

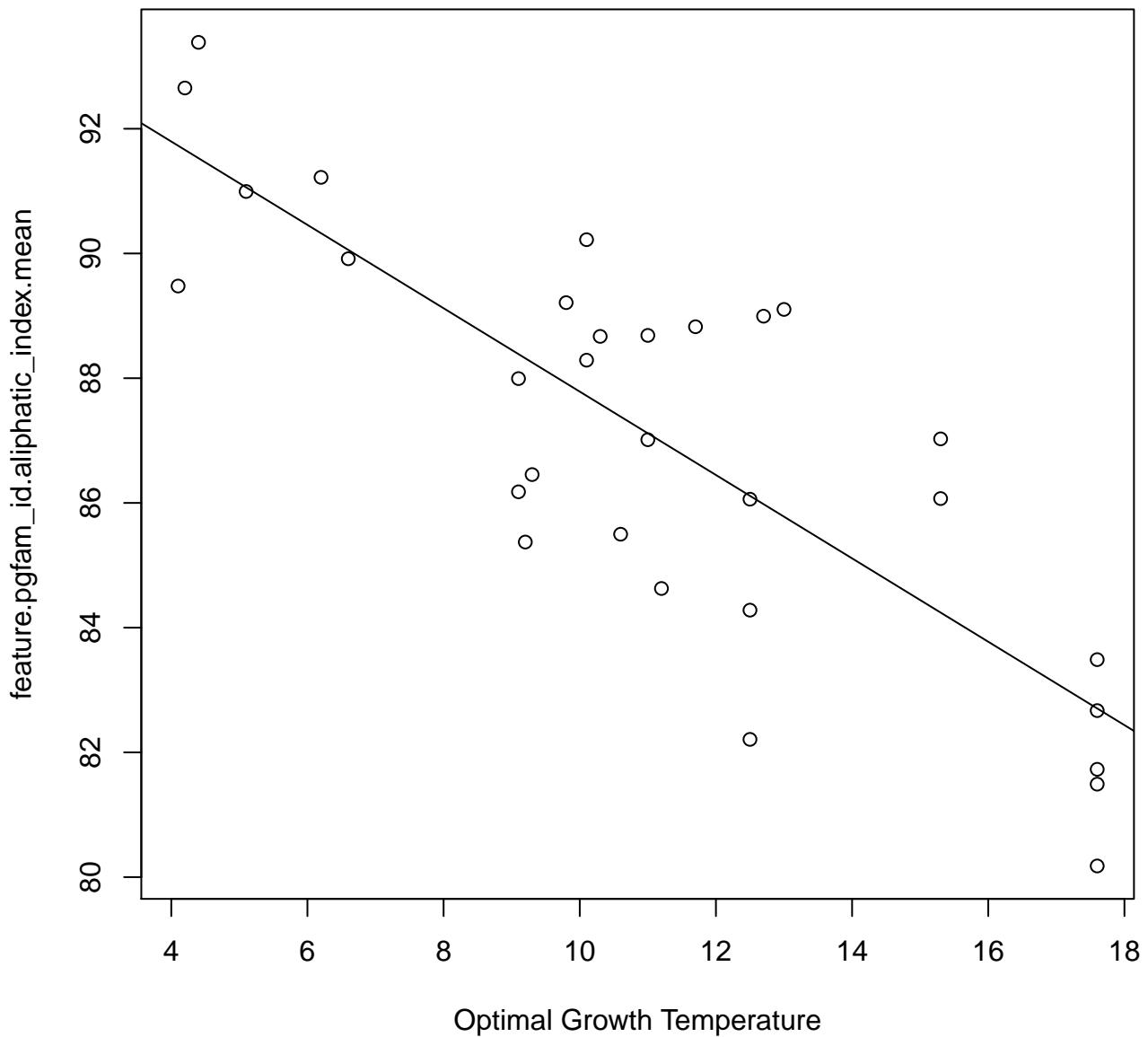
hypothetical protein



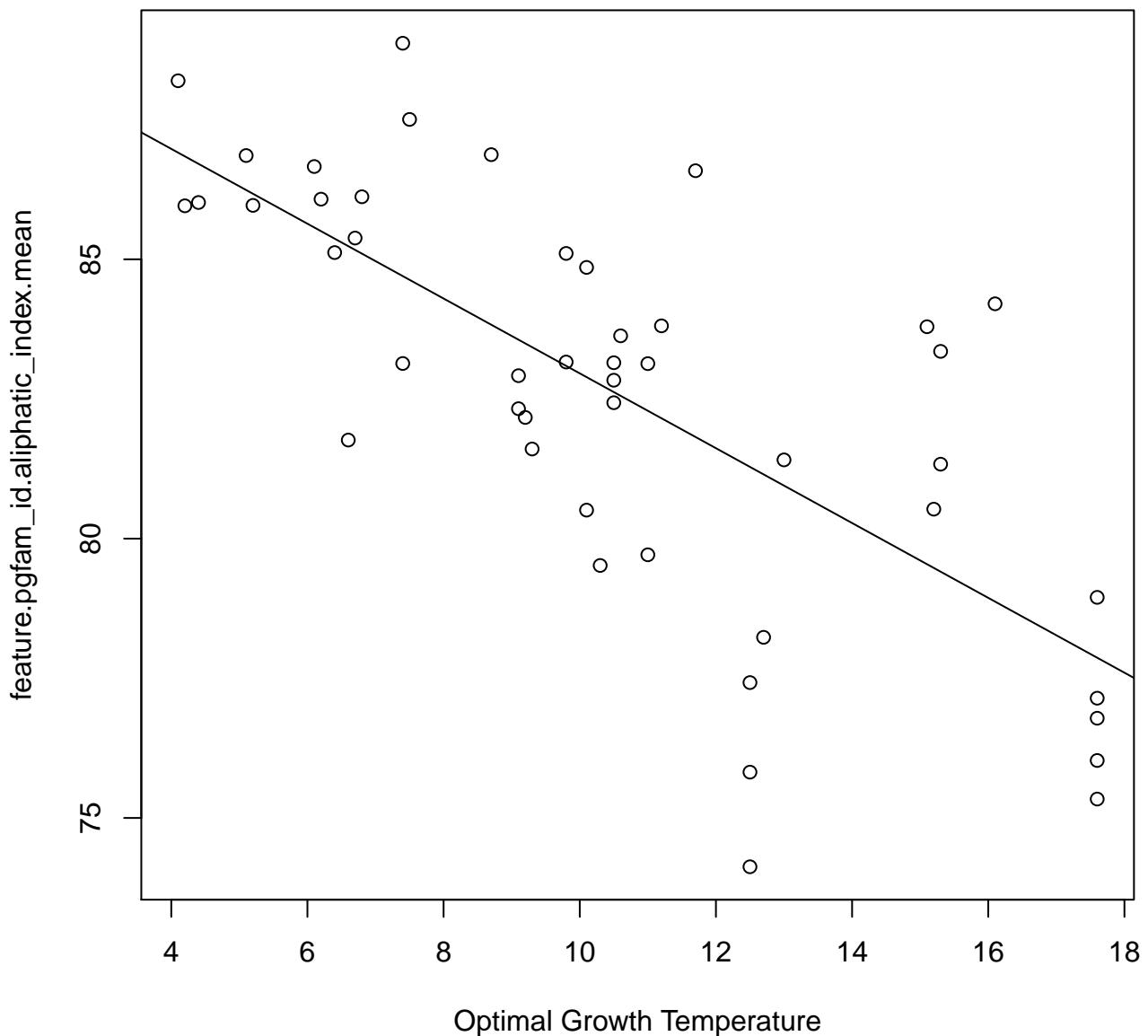
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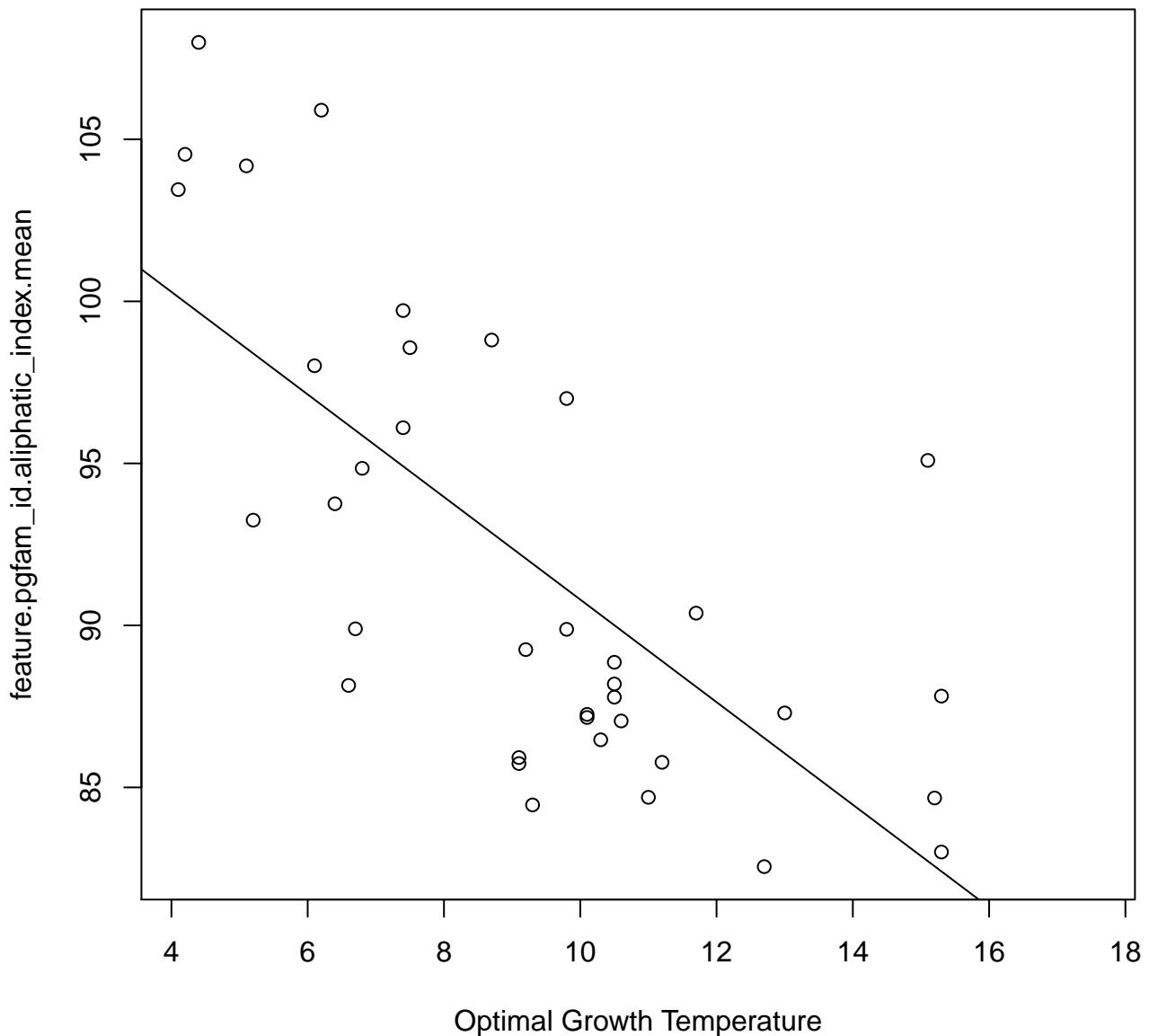
feature.pgfam_id.aliphatic_index.mean
PGF_03940803
Alkylated DNA repair protein



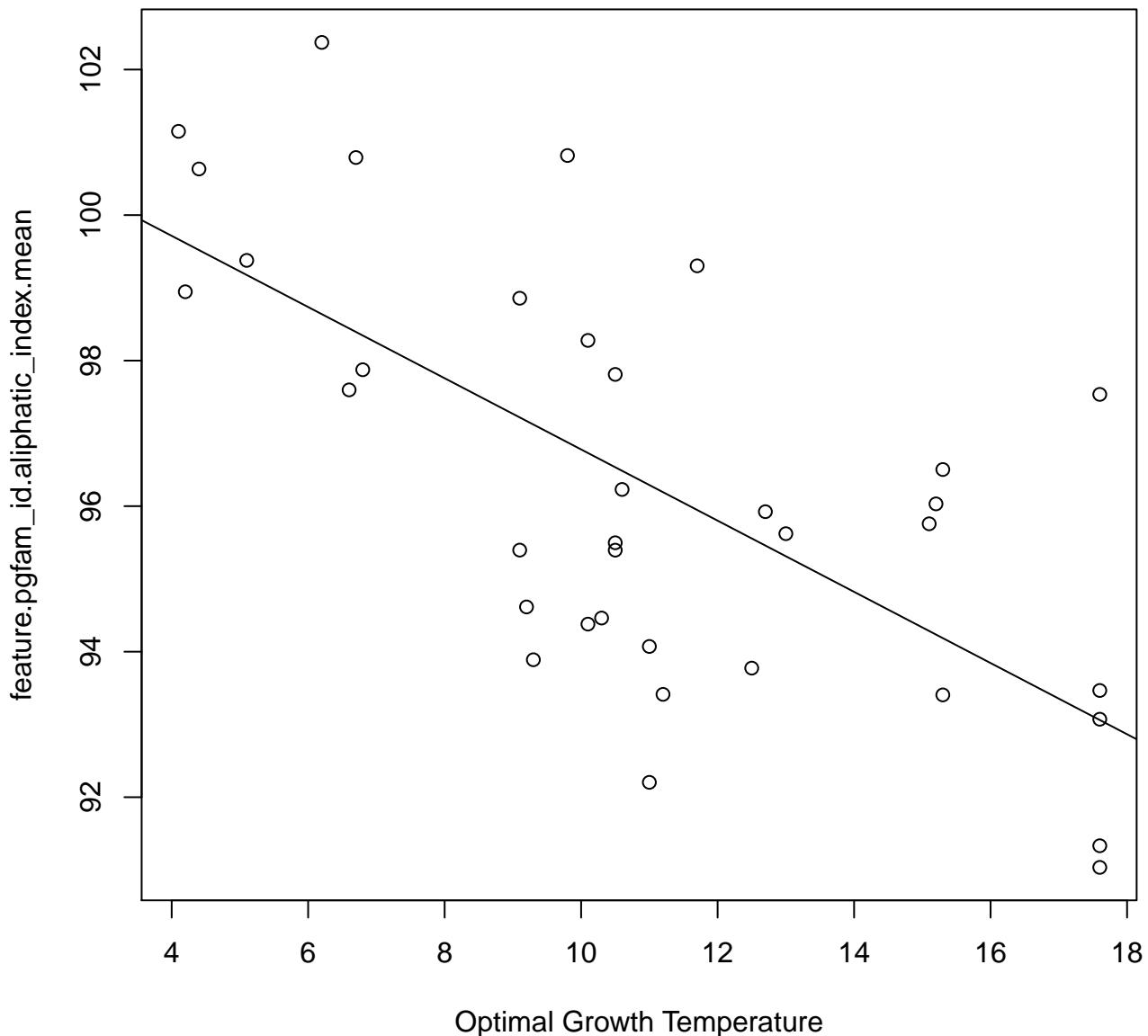
feature.pgfam_id.aliphatic_index.mean
PGF_02473279
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)



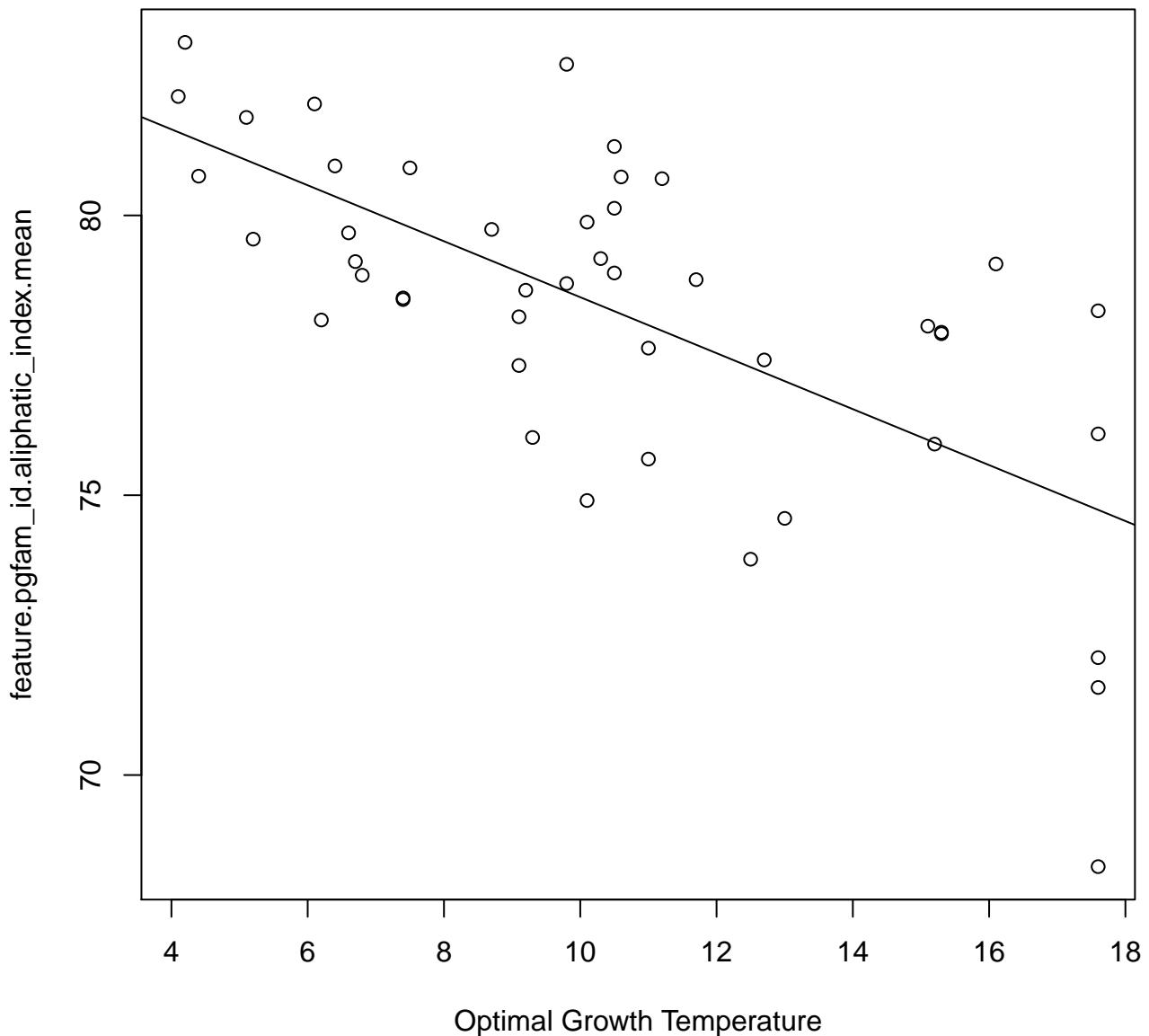
feature.pgfam_id.aliphatic_index.mean
PGF_01338555
hypothetical protein



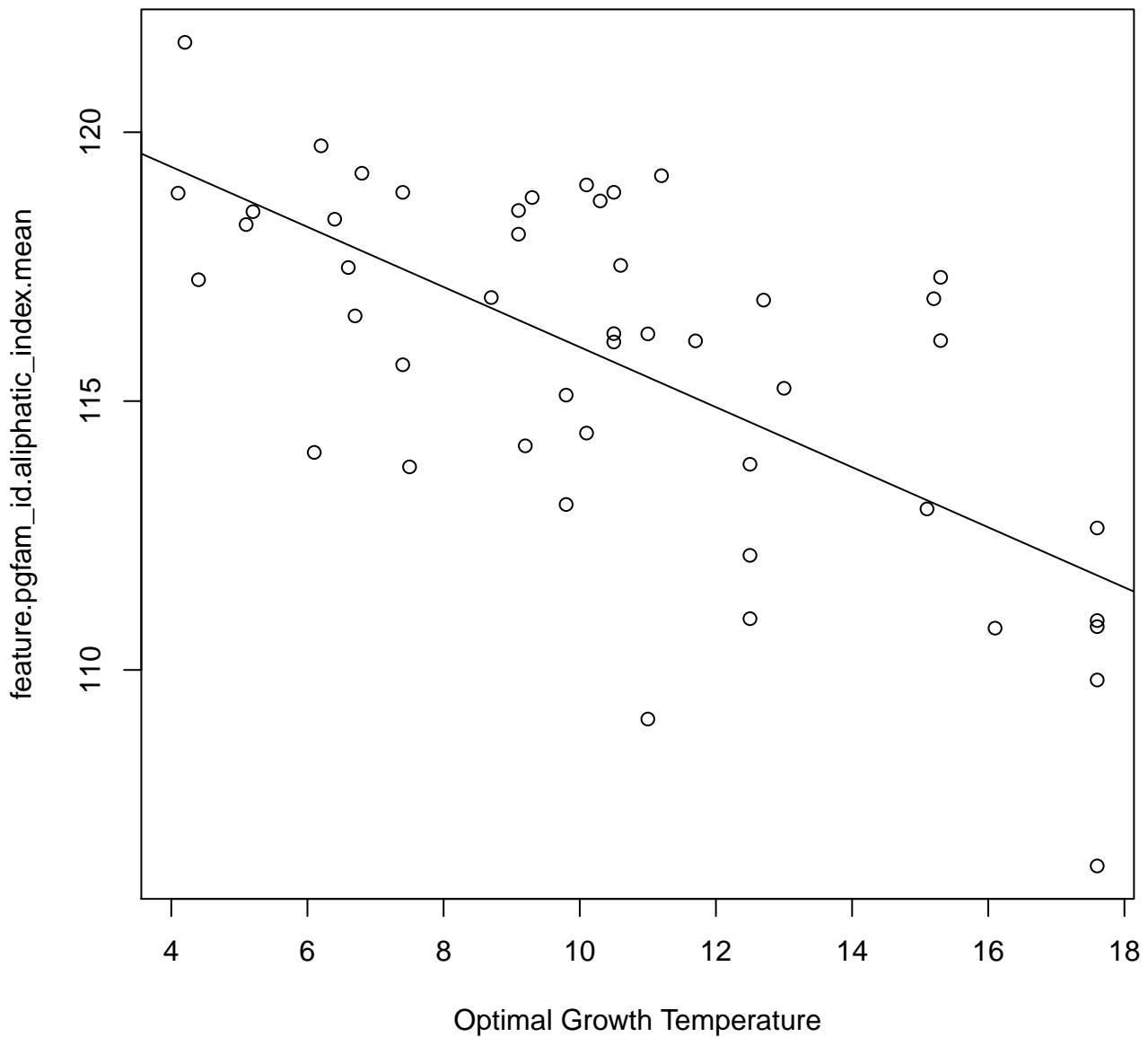
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PGF_05554840
Cobyric acid synthase (EC 6.3.5.10)



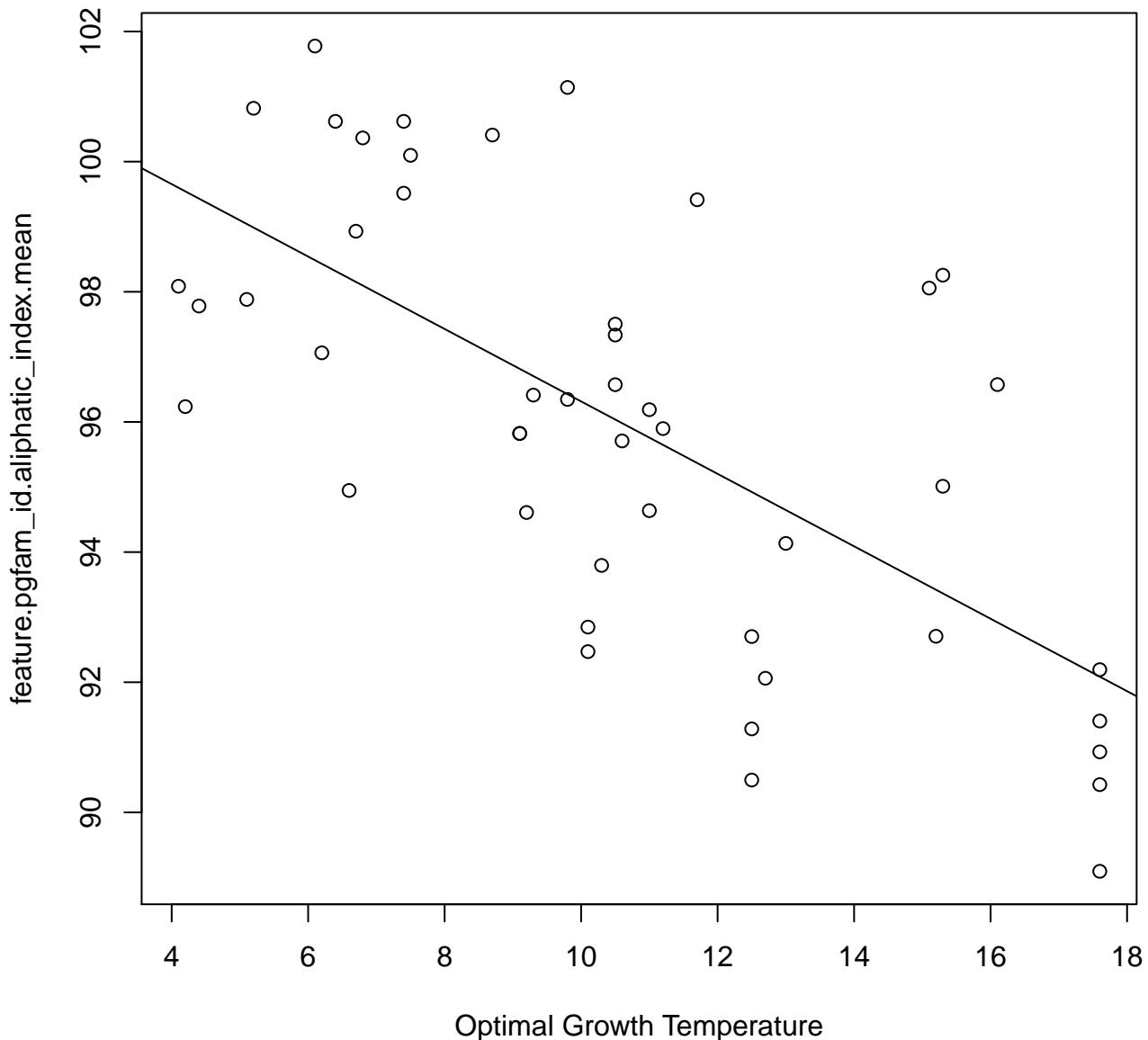
feature.pgfam_id.aliphatic_index.mean
PGF_07026465
23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)



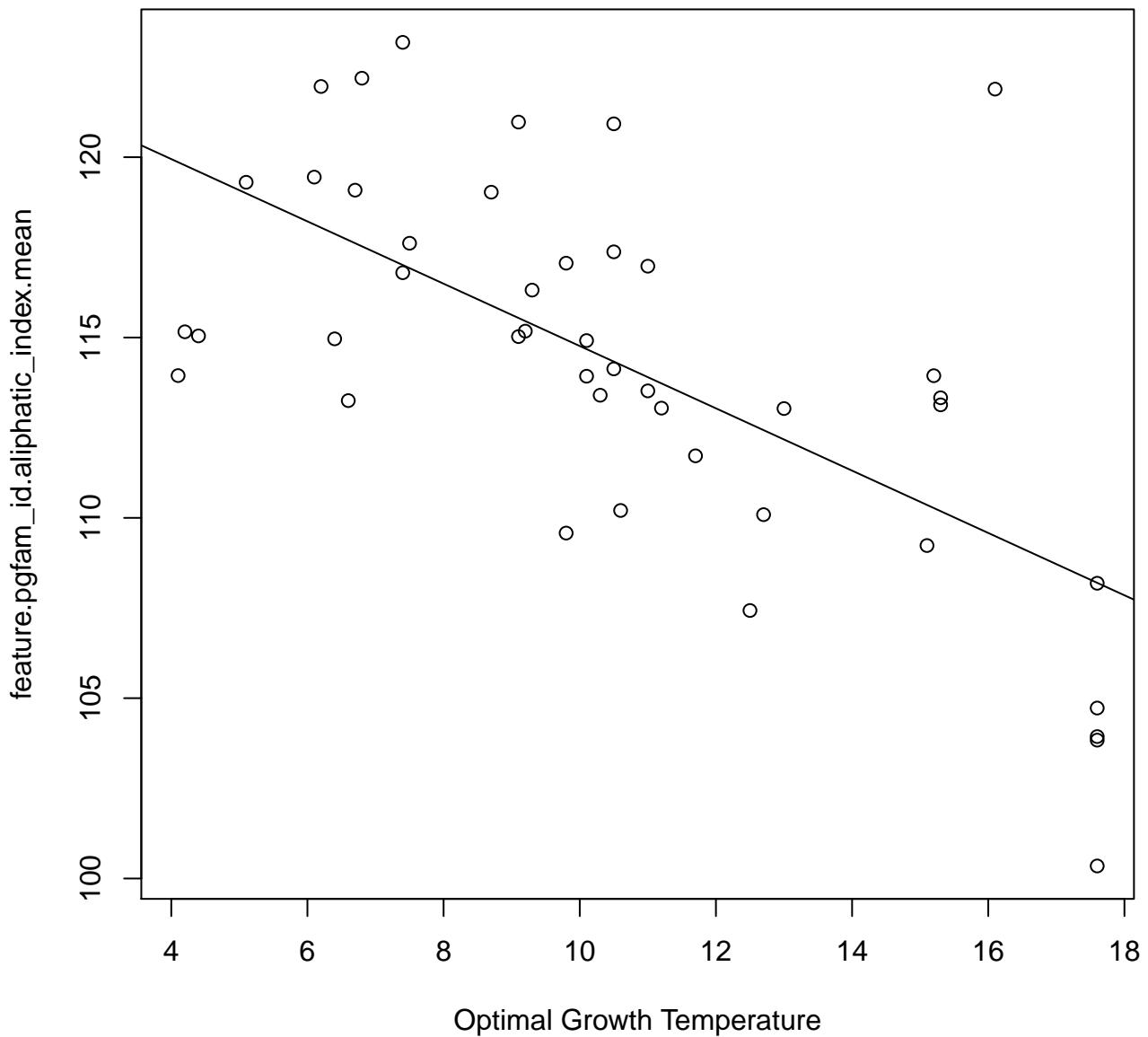
feature.pgfam_id.aliphatic_index.mean
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Twin-arginine translocation protein TatC



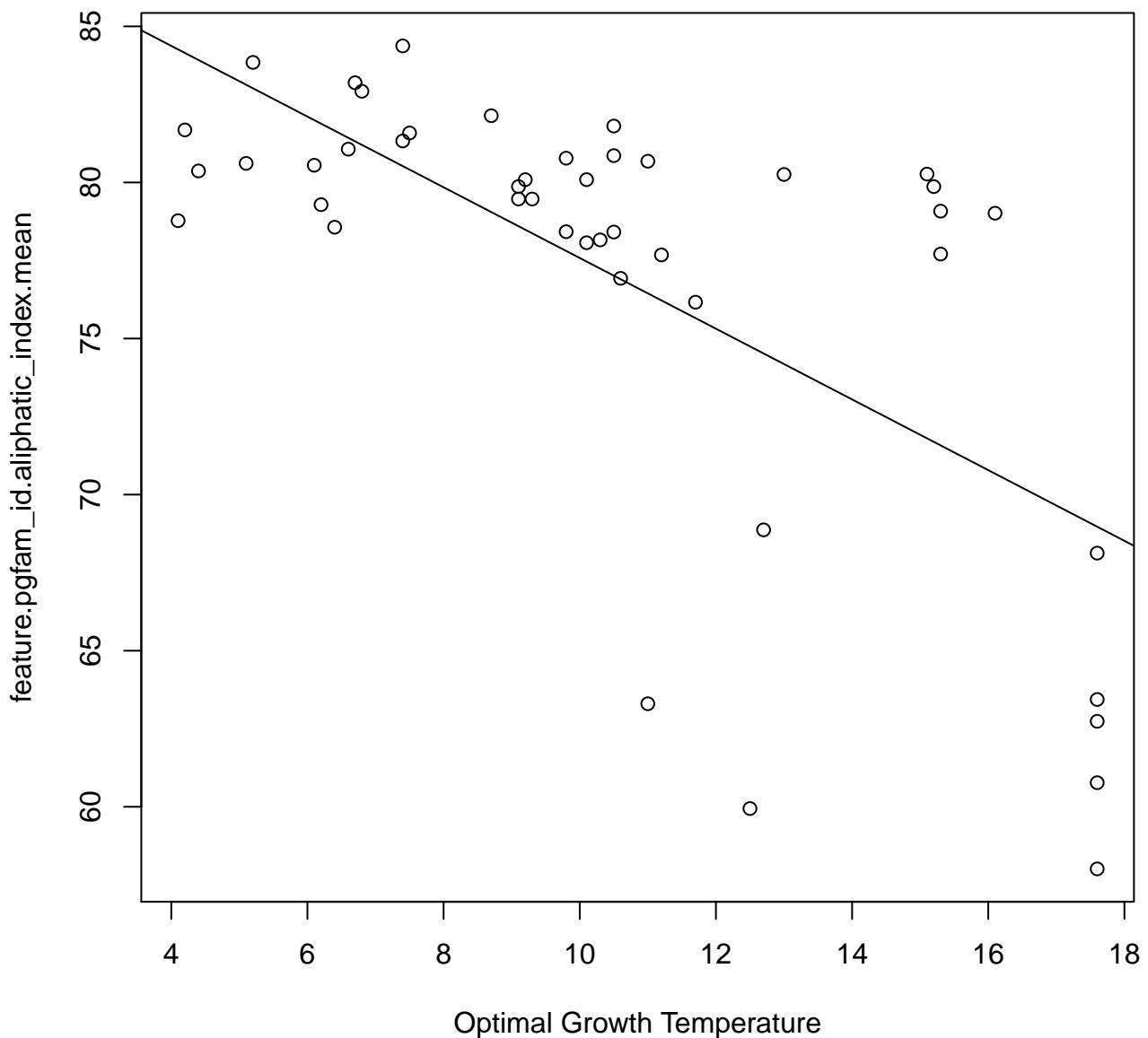
feature.pgfam_id.aliphatic_index.mean
PGF_04630848
Cytochrome c-type biogenesis protein CcmE, heme chaperone



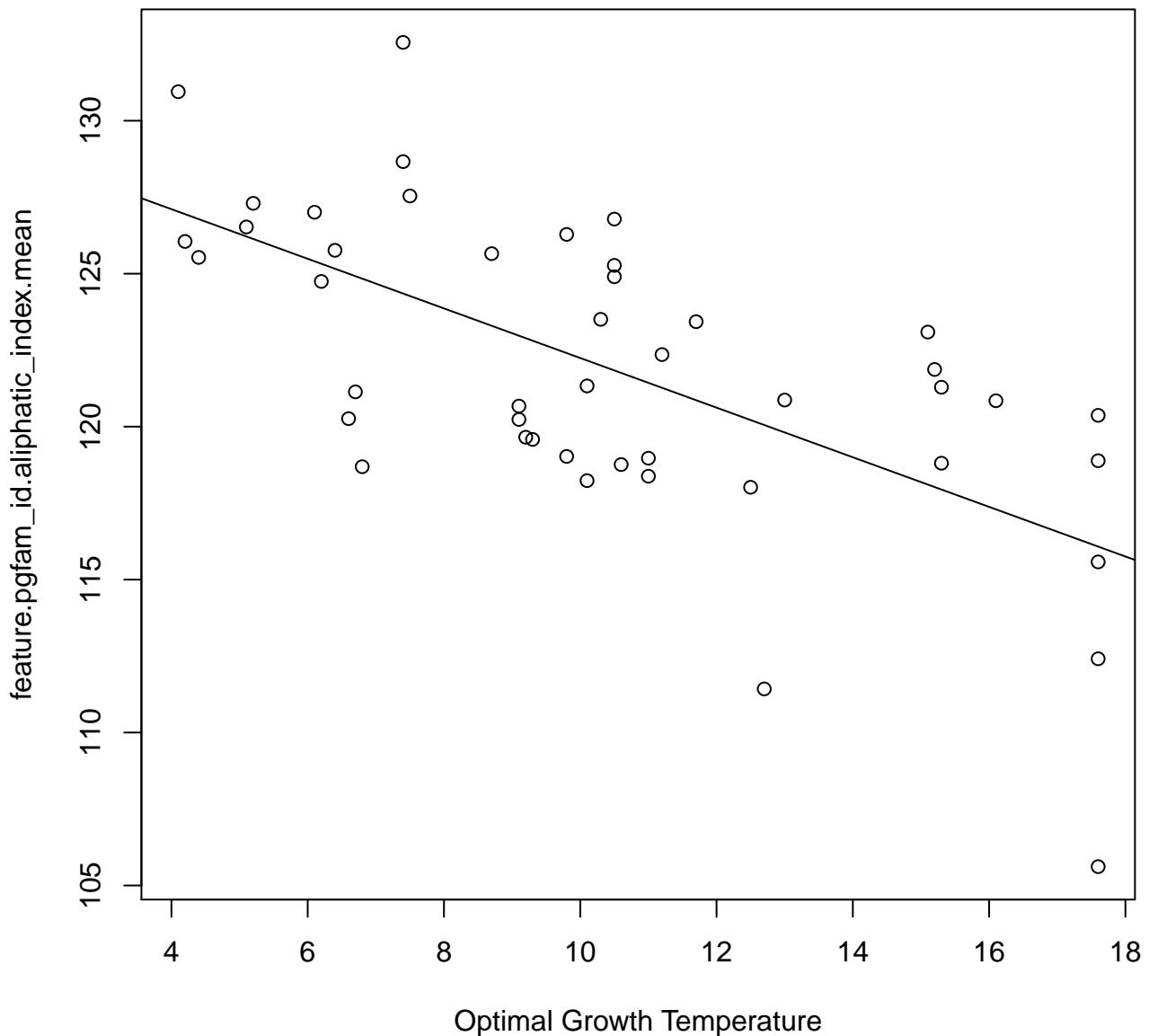
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PGF_00335891
hypothetical protein



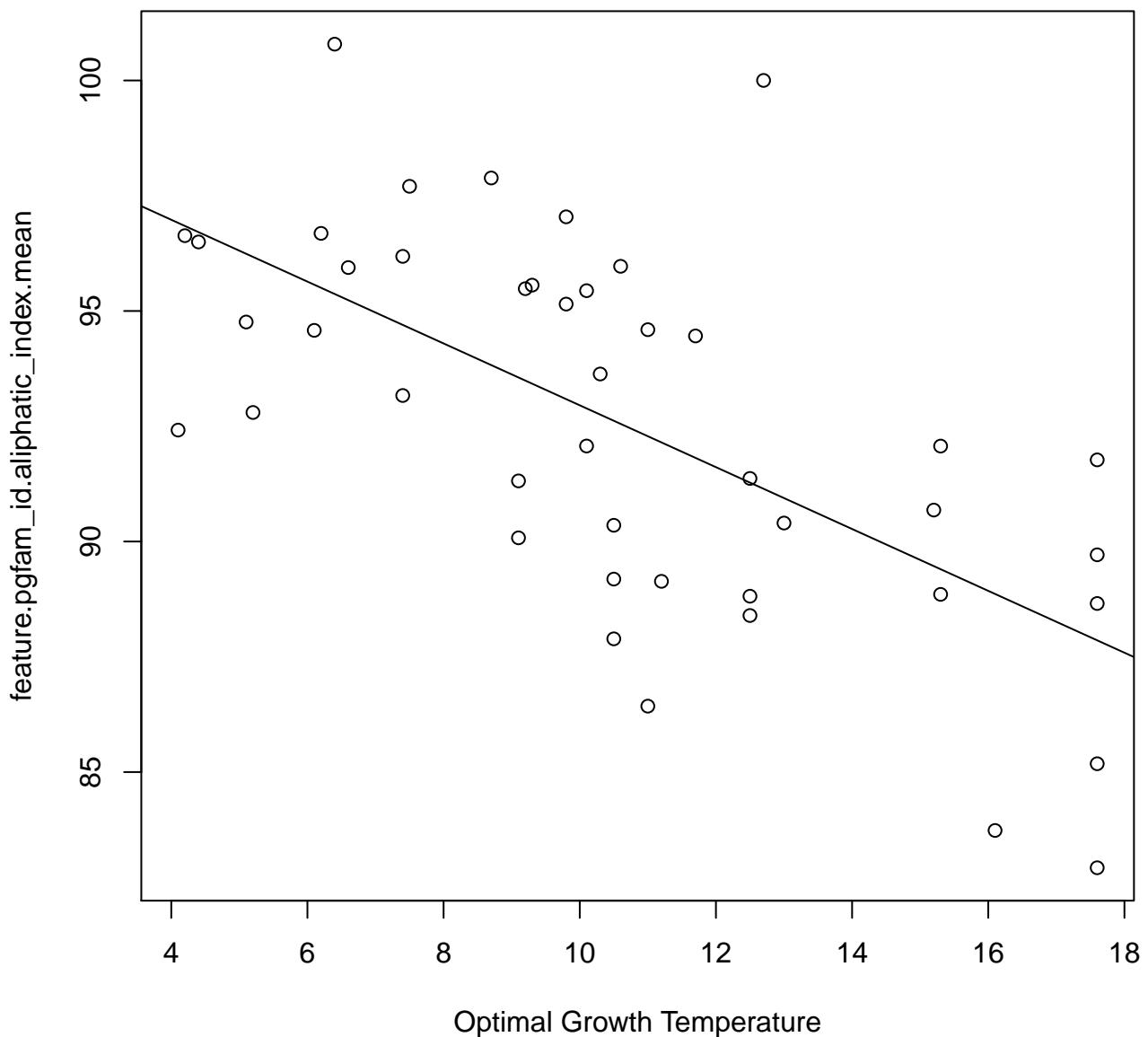
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PGF_10080321
hypothetical protein



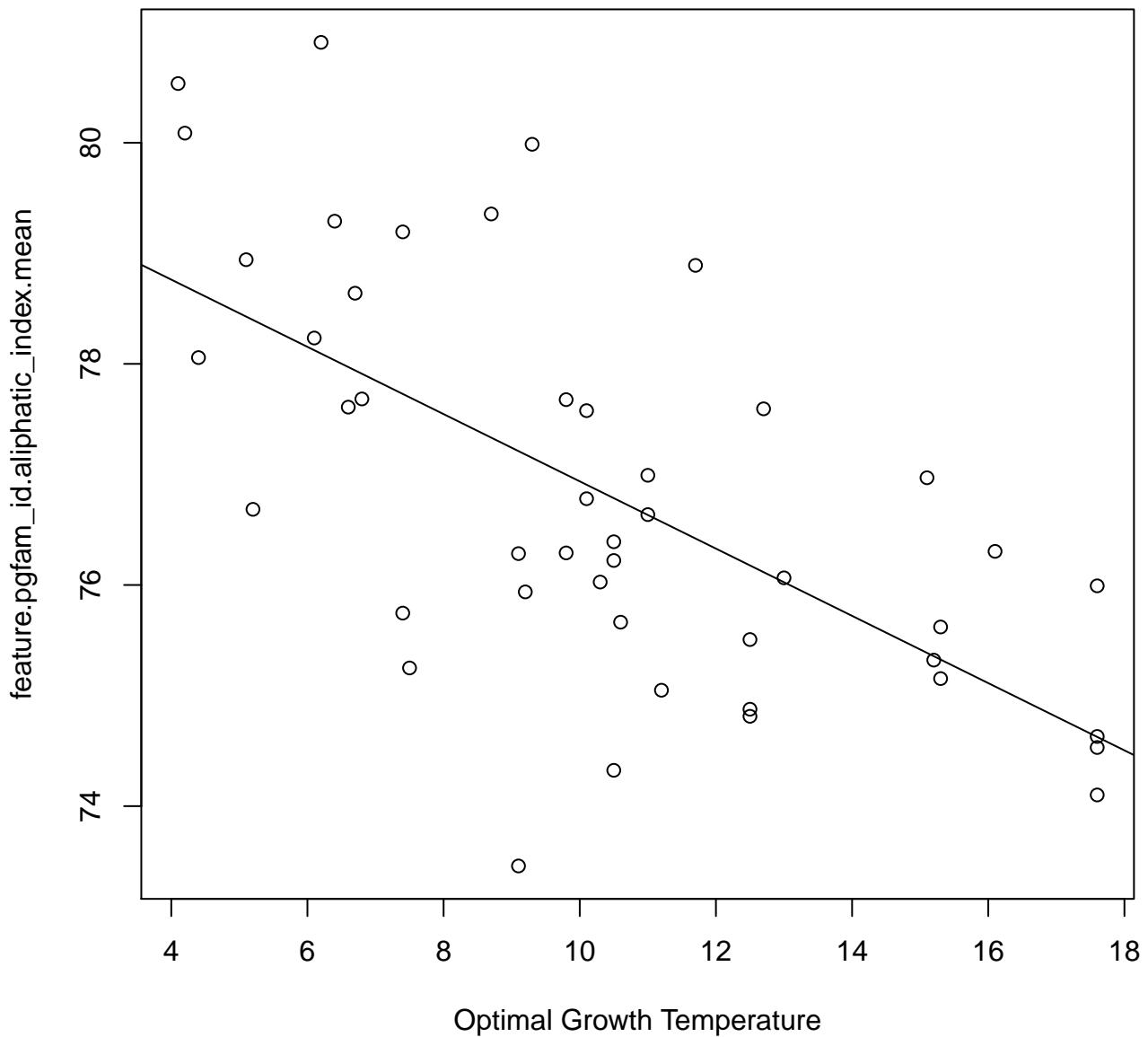
feature.pgfam_id.aliphatic_index.mean
PGF_03950680
Transporter, LysE family



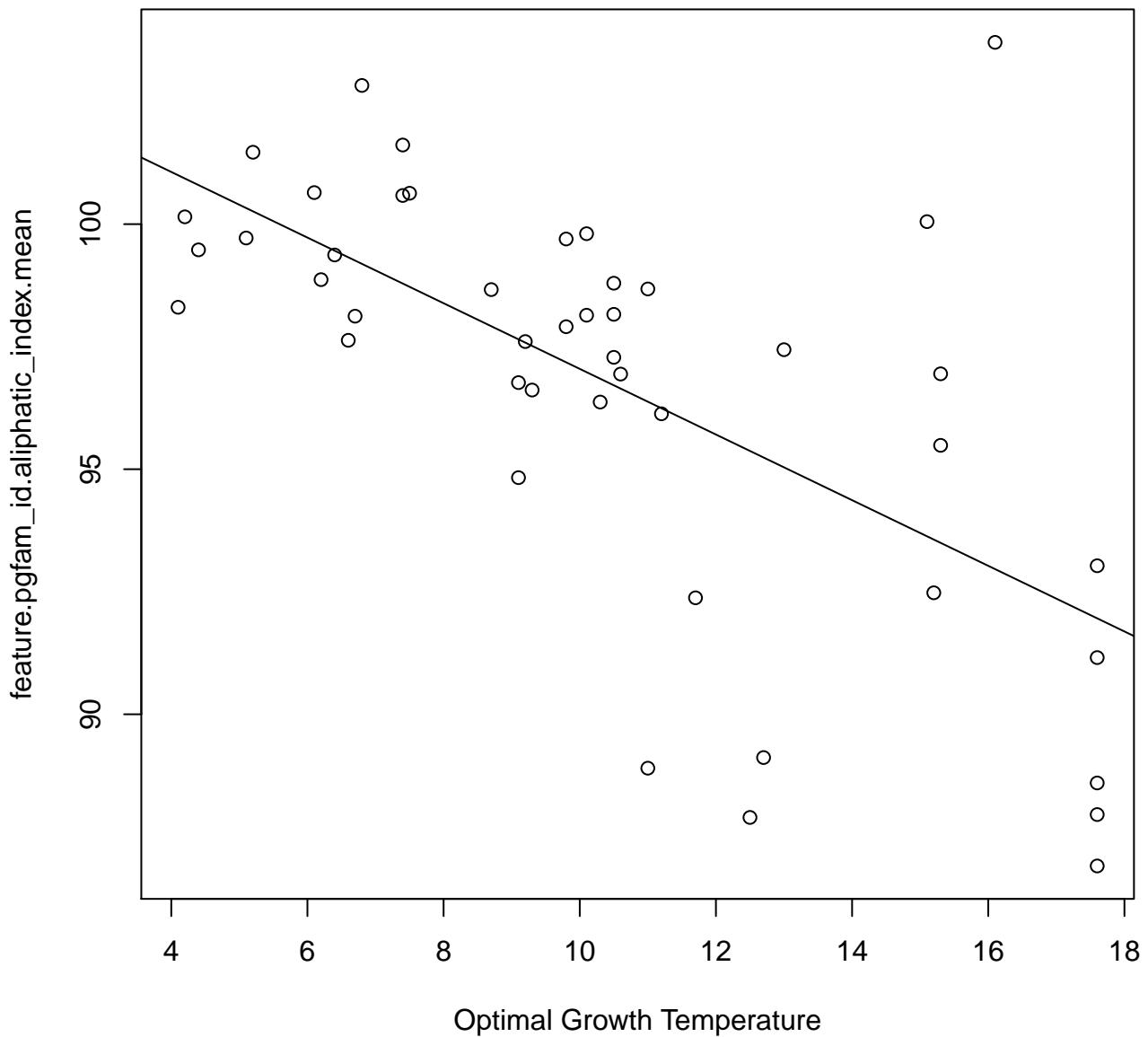
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PGF_00035421
Potential queD like 2



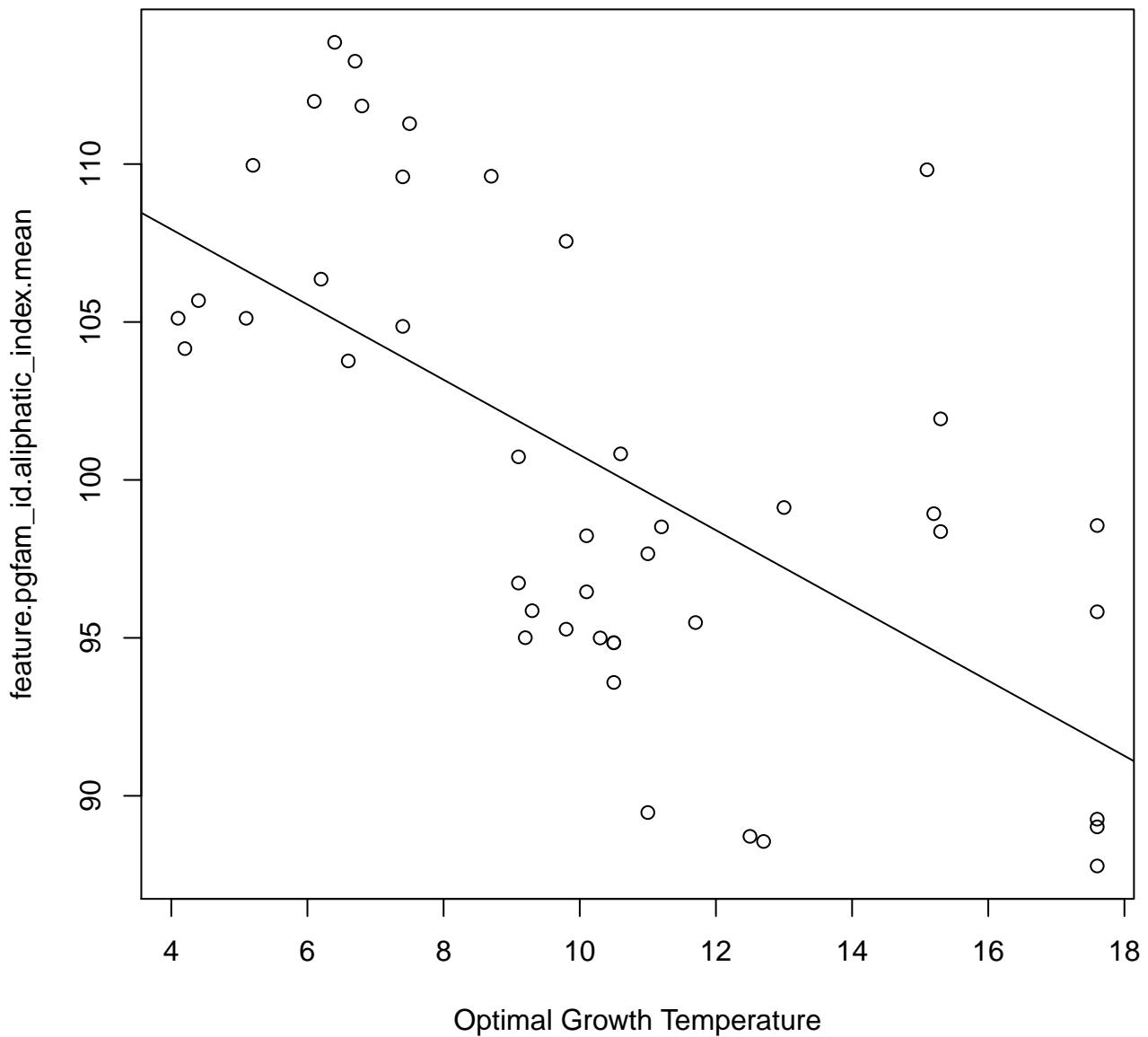
feature.pgfam_id.aliphatic_index.mean
PGF_00016431
LSU ribosomal protein L3p (L3e)



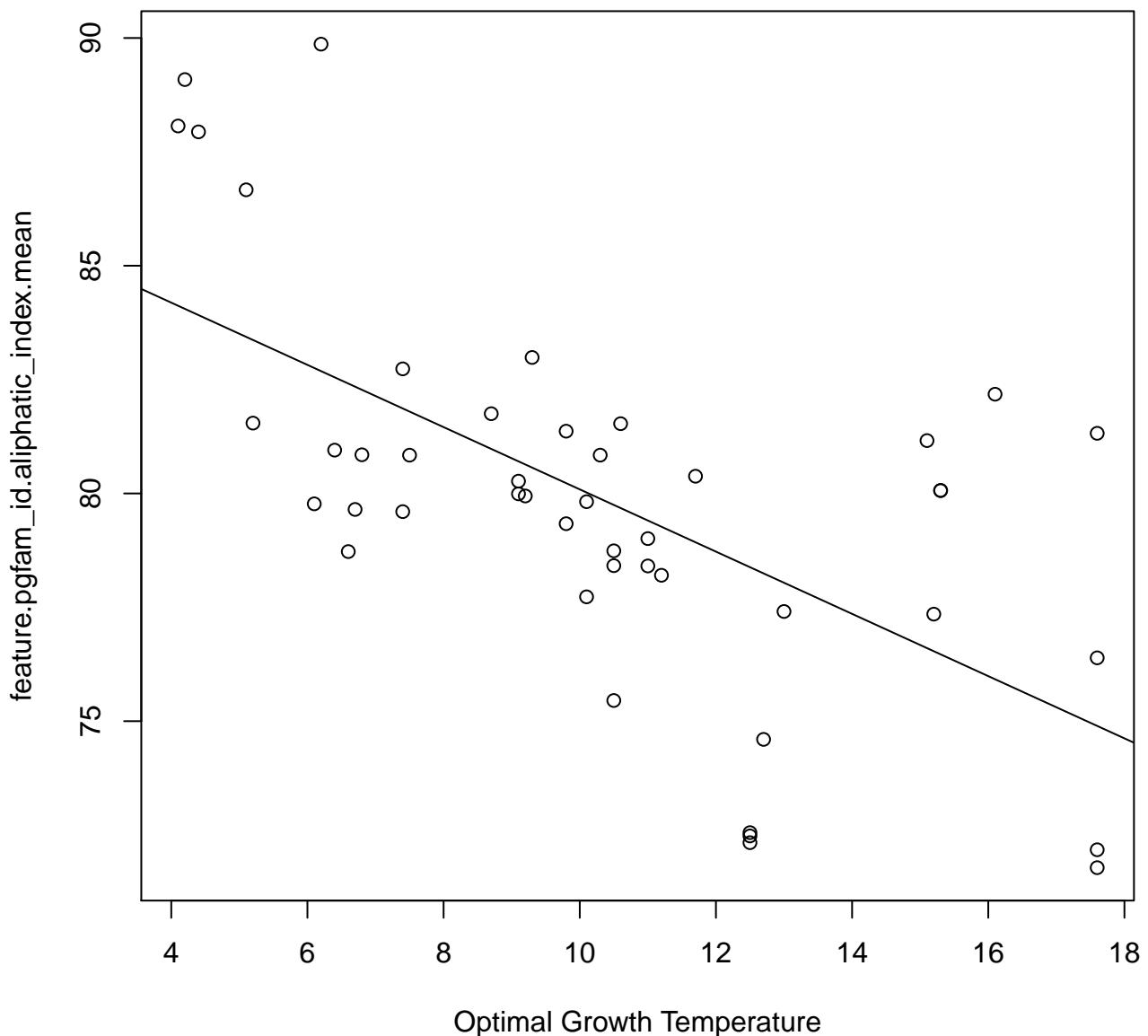
feature.pgfam_id.aliphatic_index.mean
PGF_03751076
Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)



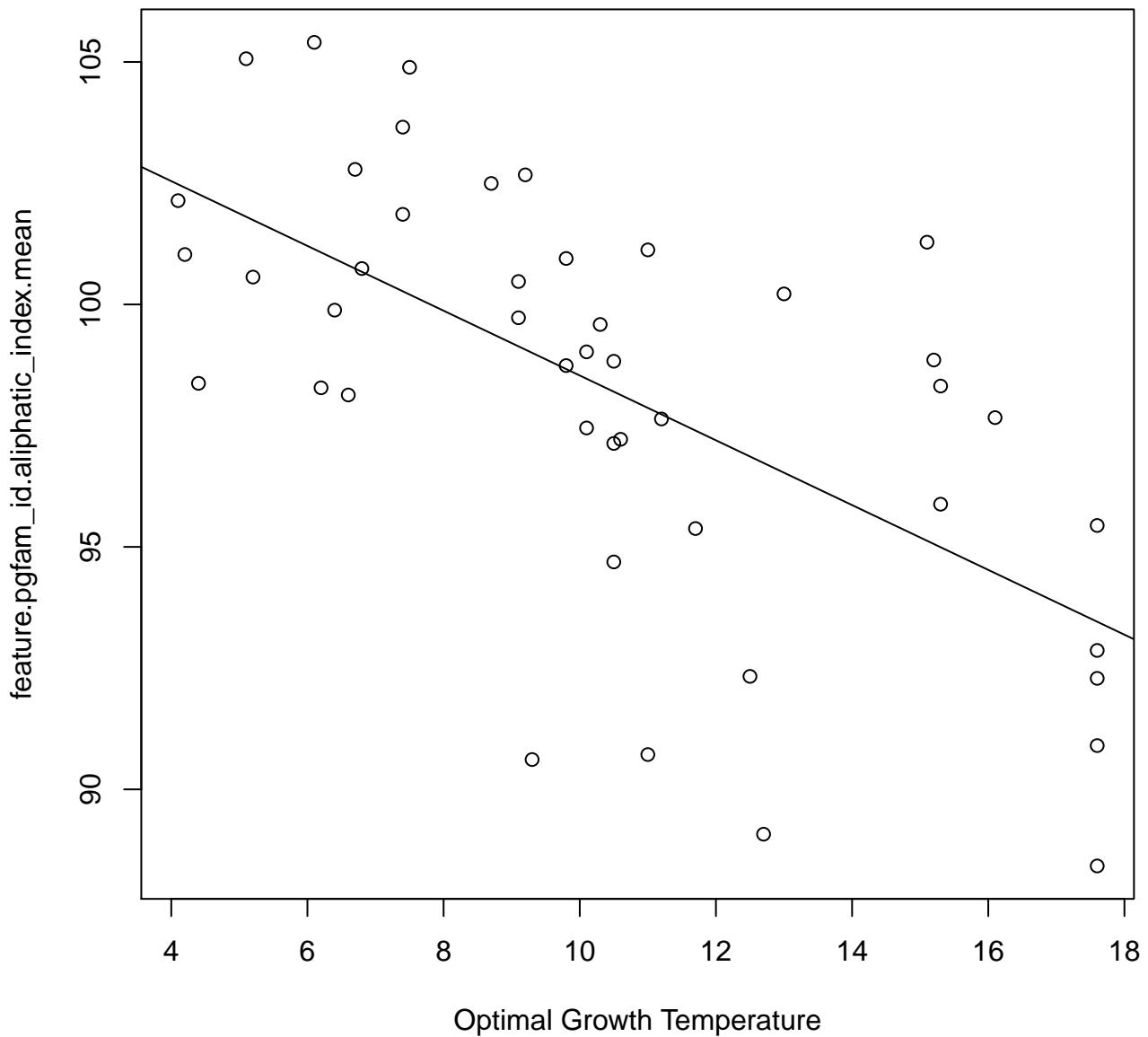
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PGF_00707140
Cys-tRNA(Pro) deacylase YbaK



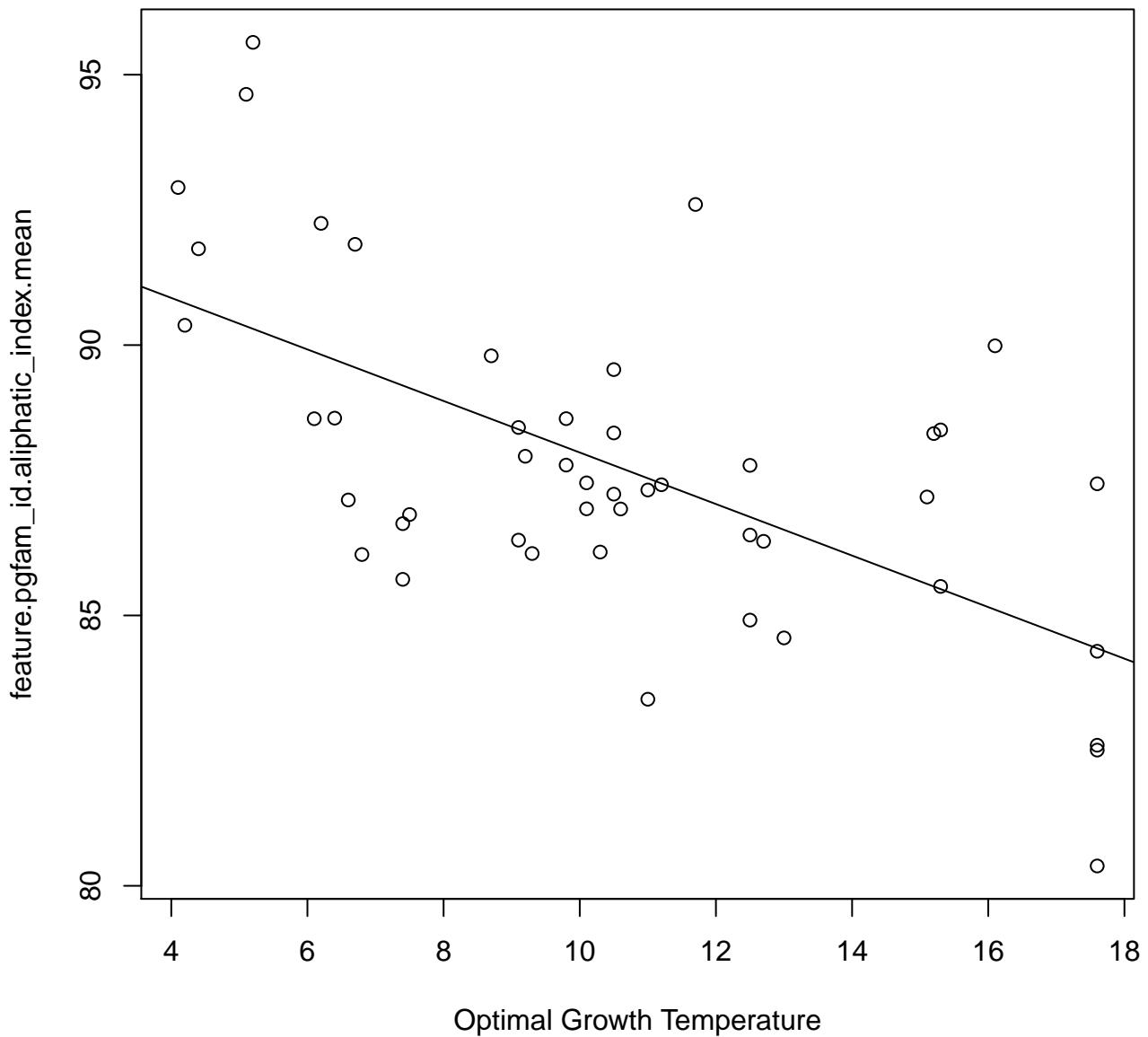
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PGF_01782190
3-deoxy-D-manno-octulose-2'-acid kinase (EC 2.7.1.166)



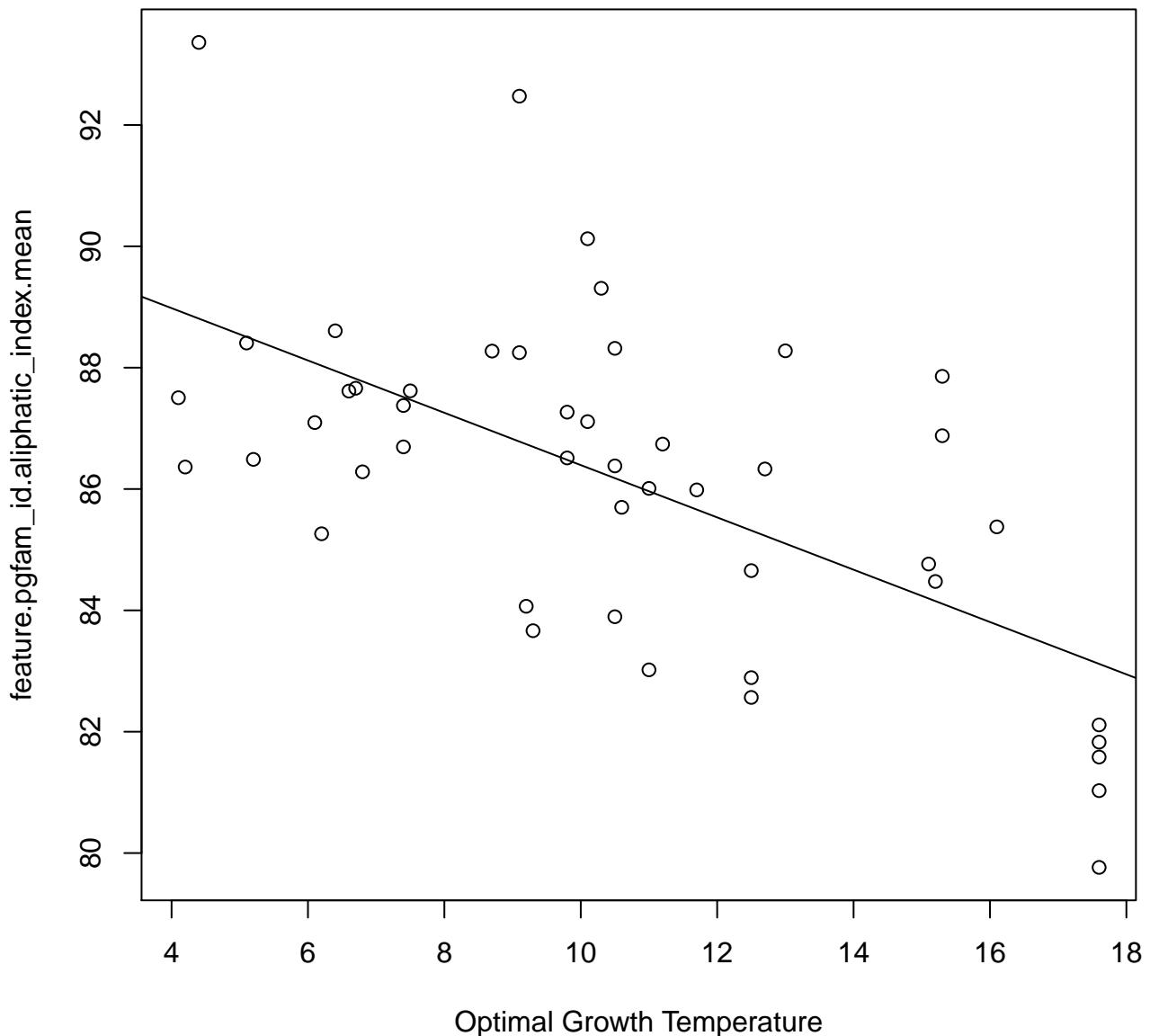
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PGF_10369954
Rod shape-determining protein MreC



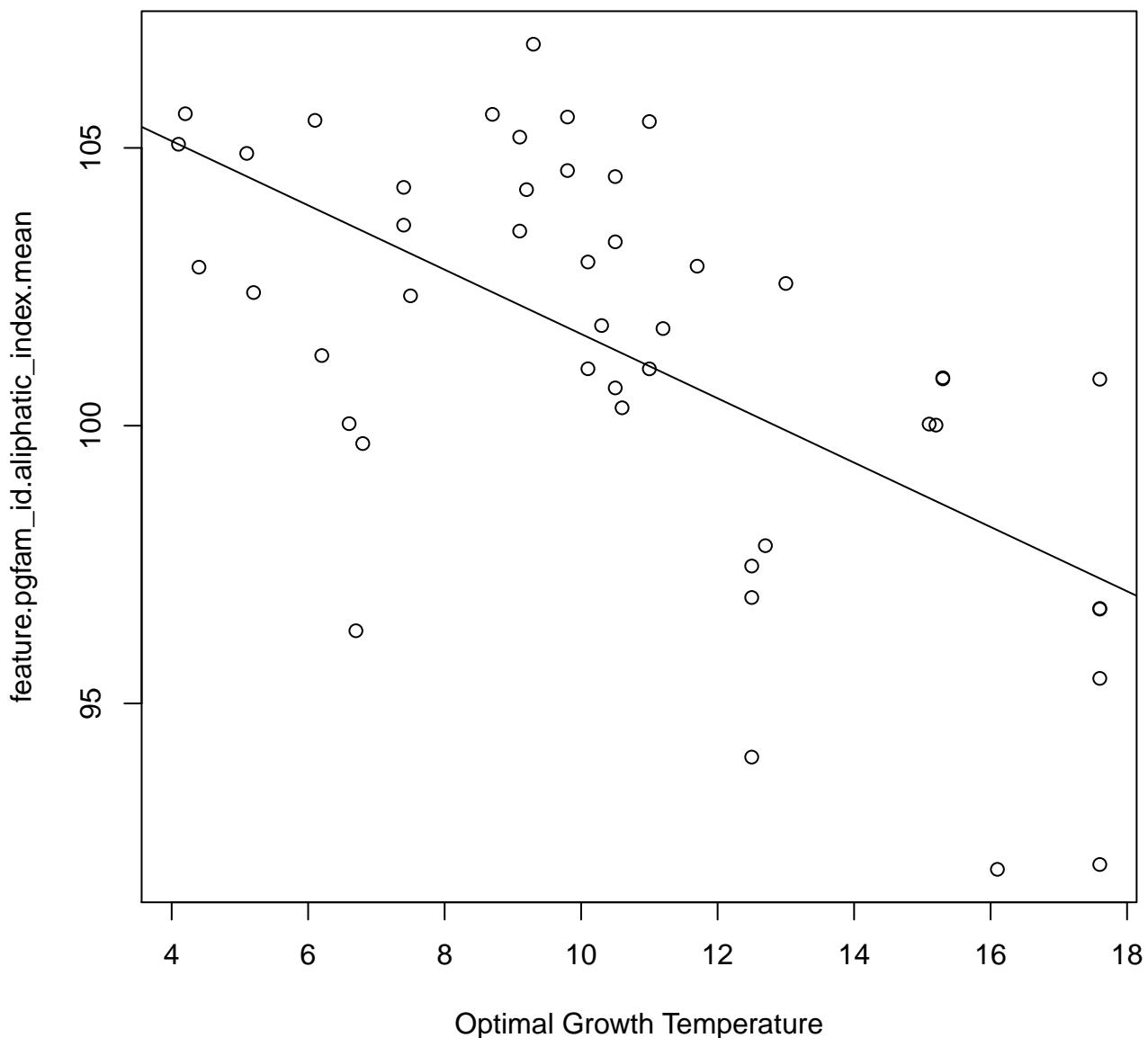
feature.pgfam_id.aliphatic_index.mean
PGF_00131429
LSU ribosomal protein L16p arginine hydroxylase



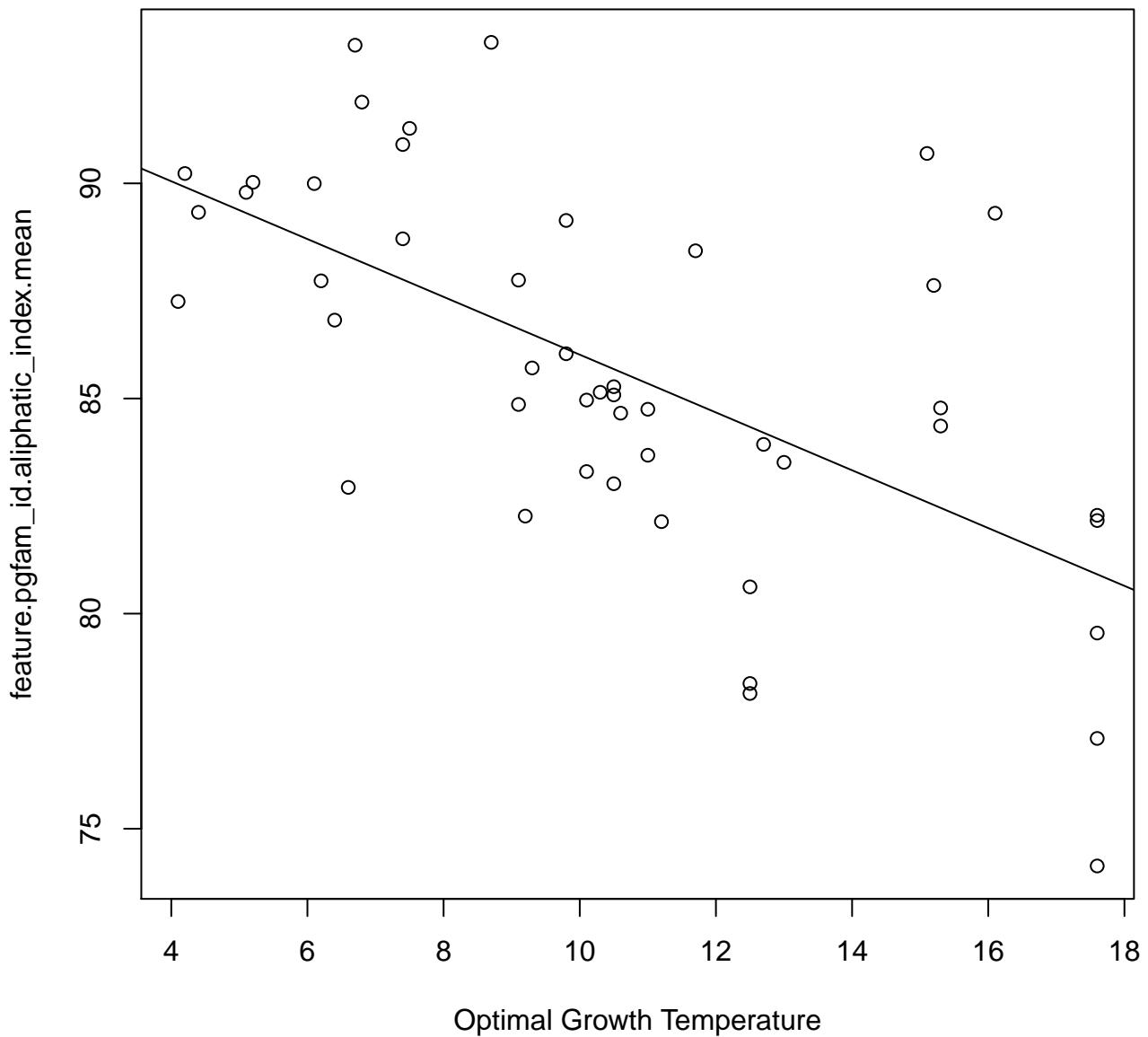
feature.pgfam_id.aliphatic_index.mean
PGF_00415346
23S rRNA (cytosine(1962)-C(5))-methyltransferase (EC 2.1.1.191)



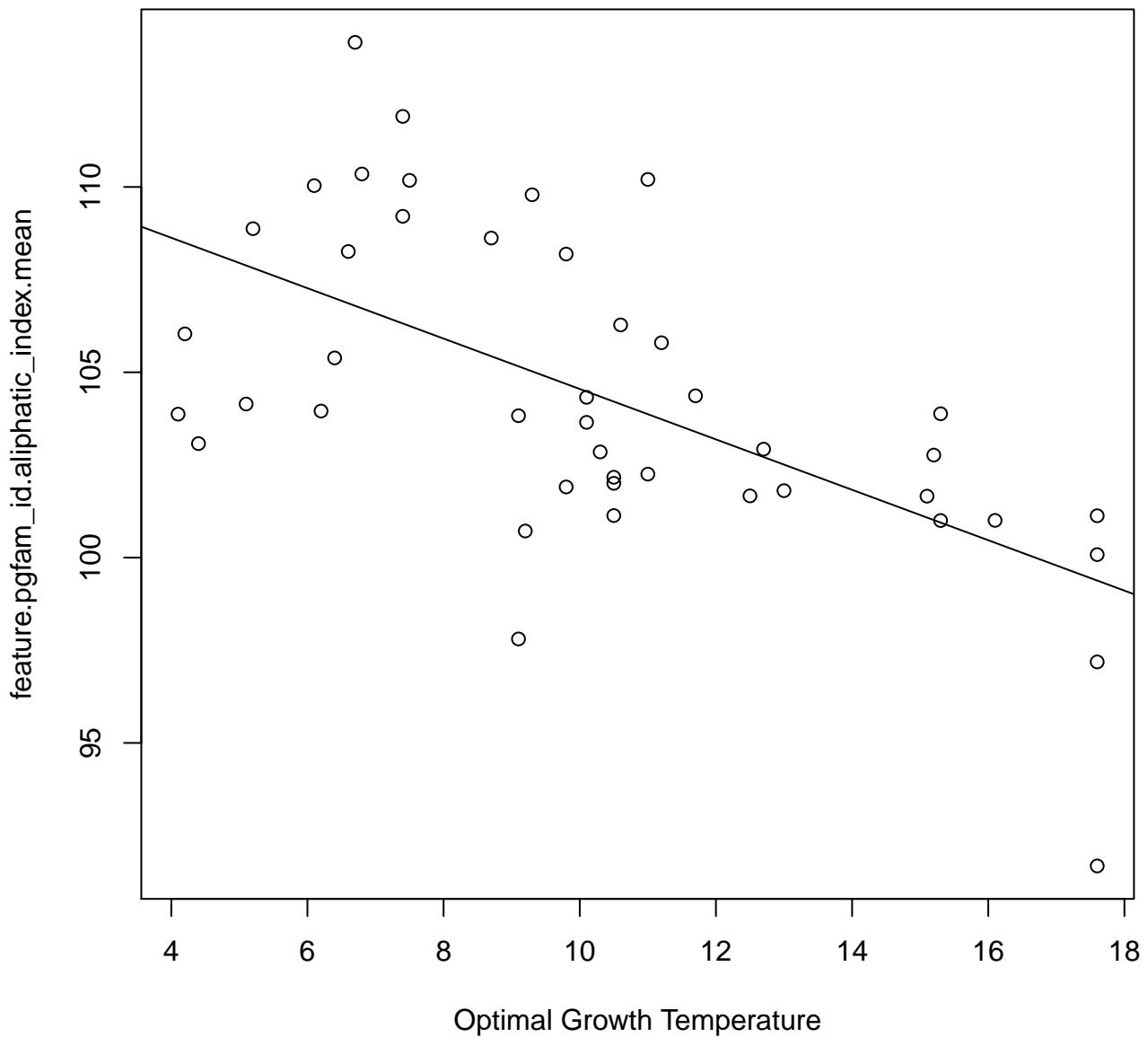
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PGF_01336291
hypothetical protein



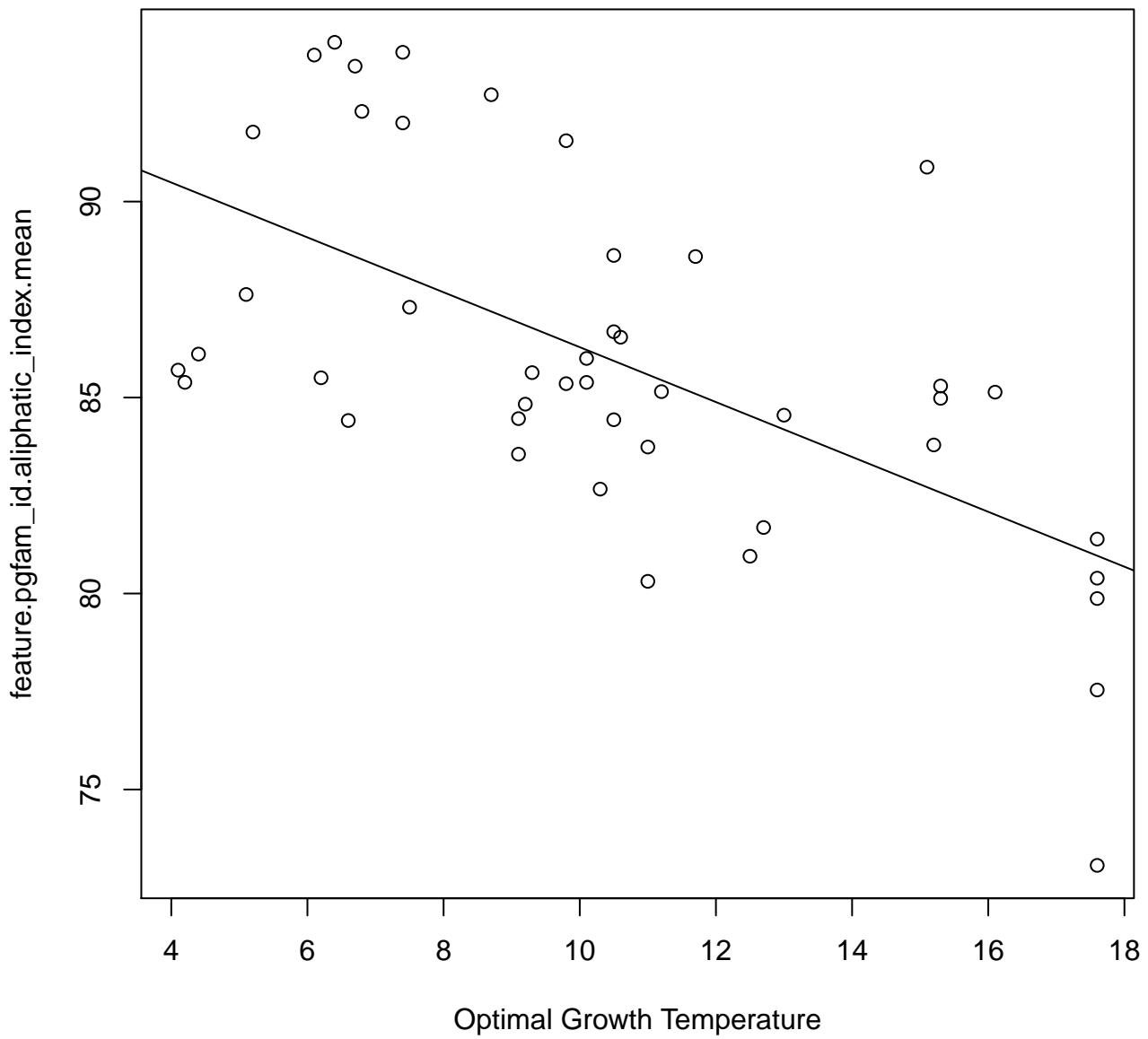
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PGF_00064199
UPF0115 protein YfcN



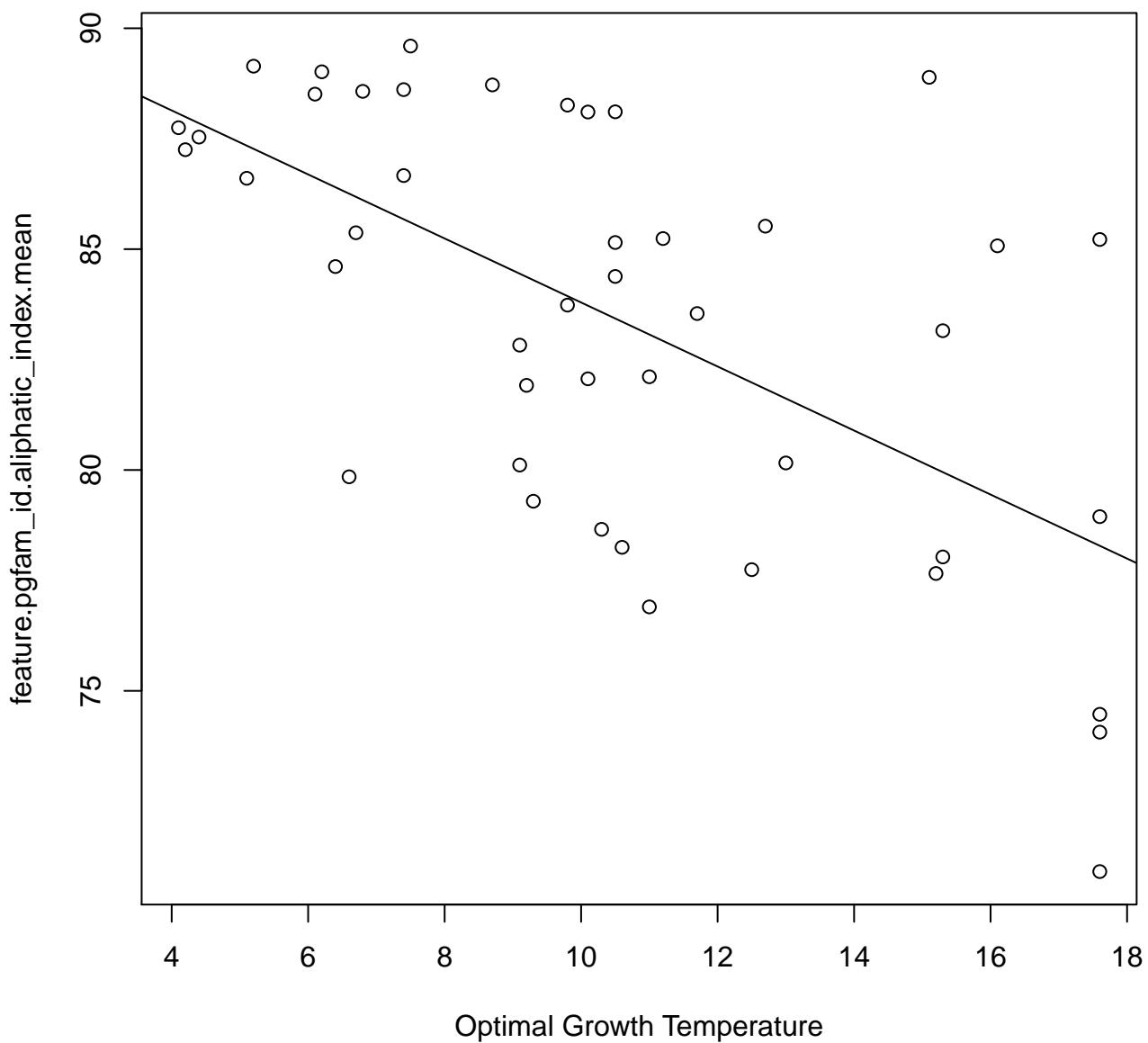
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PGF_03948315
DEDDh 3'-5' exonuclease domain of the epsilon subunit of DNA polymerase III



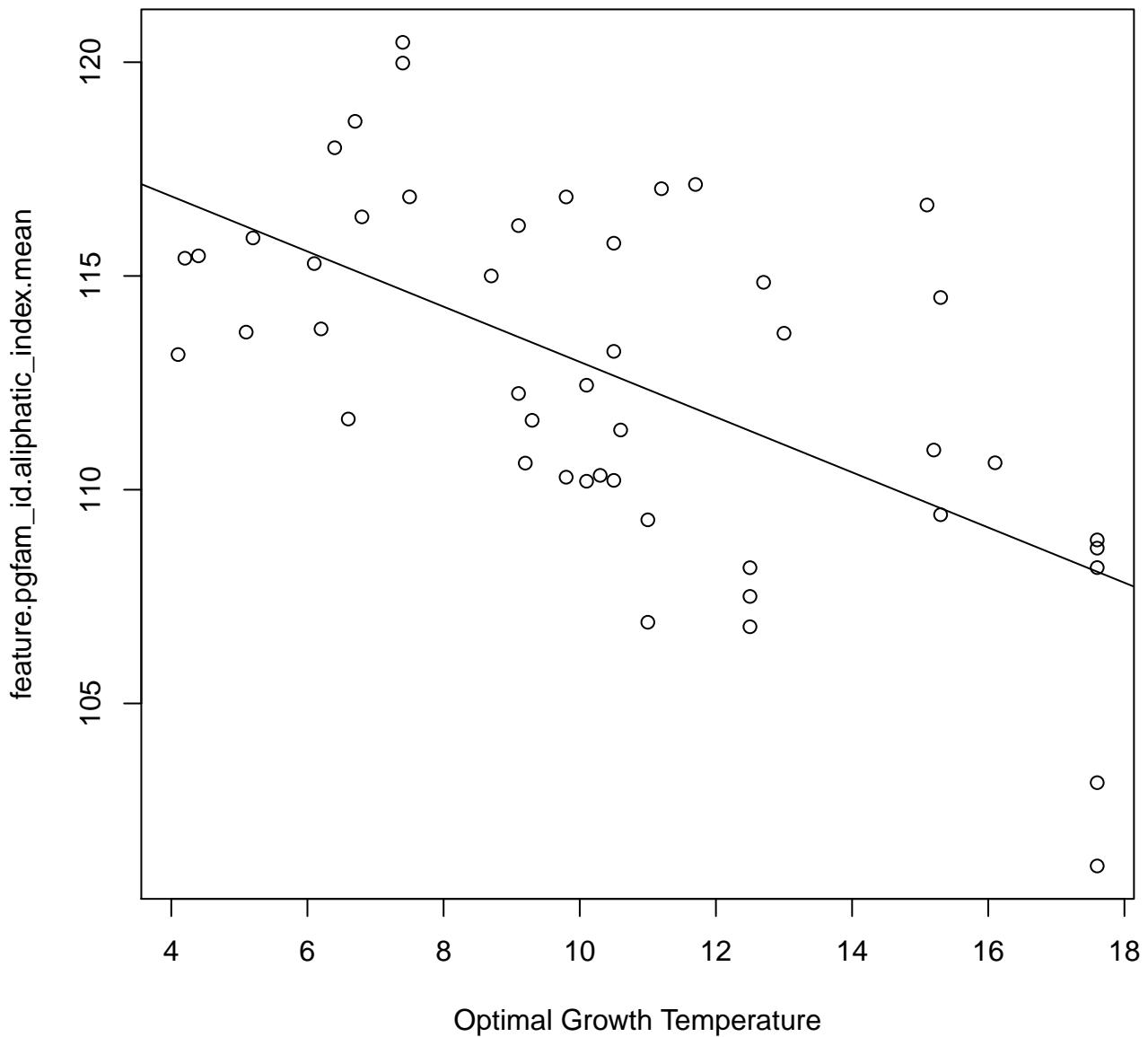
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PGF_07460808
hypothetical protein PA3071



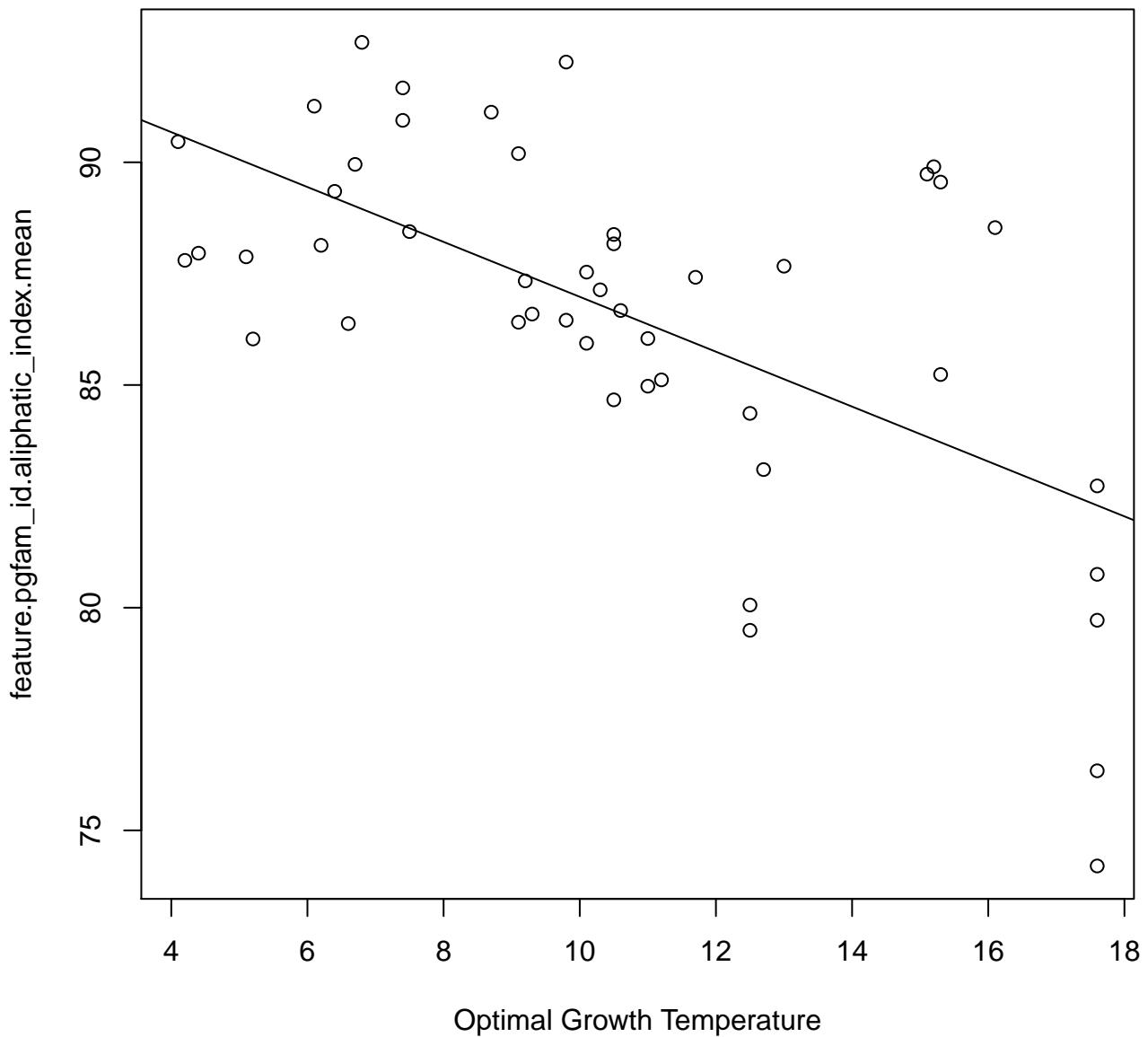
feature.pgfam_id.aliphatic_index.mean
PGF_09515854
Low molecular weight protein tyrosine phosphatase (EC 3.1.3.48)



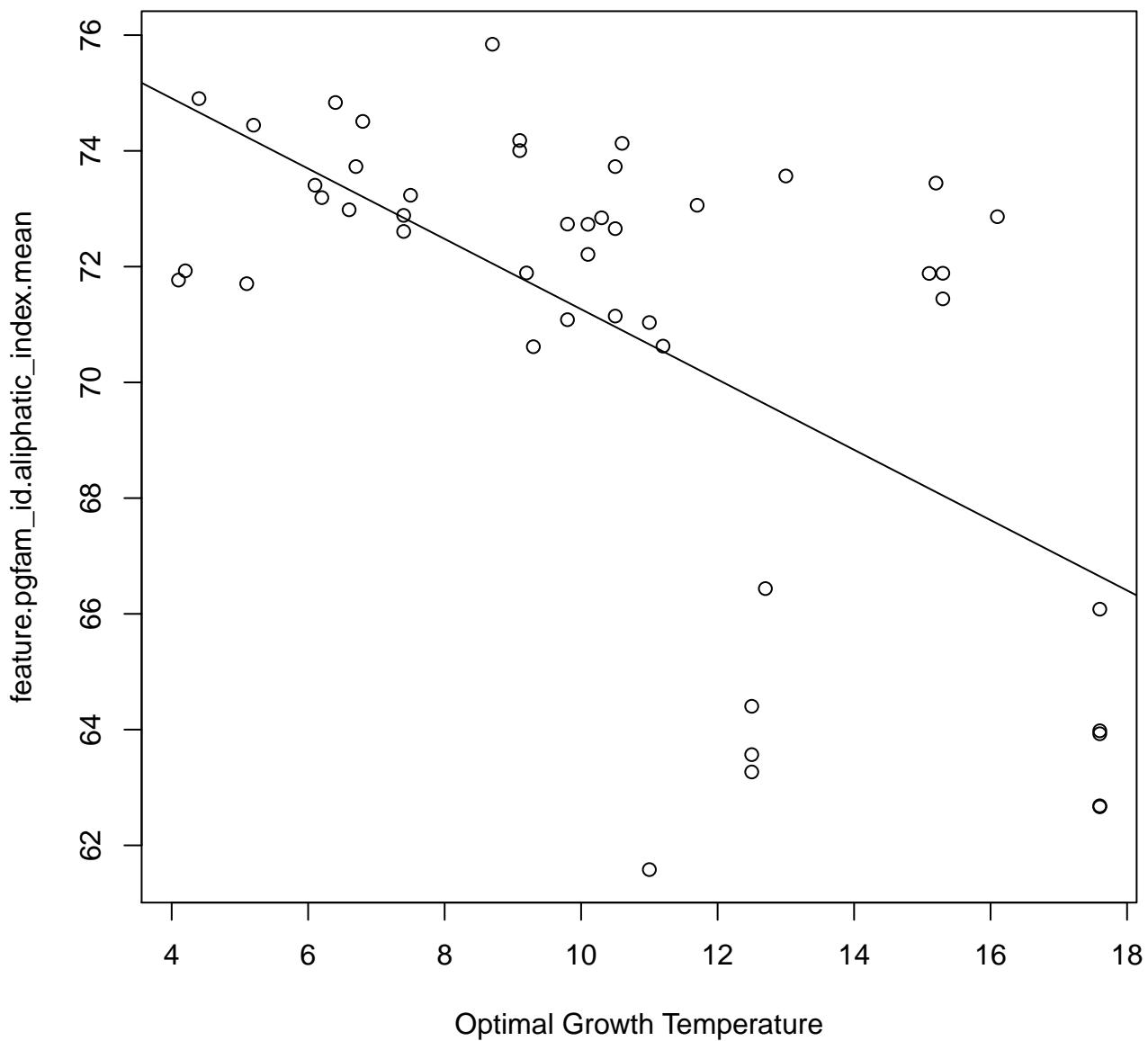
feature.pgfam_id.aliphatic_index.mean
PGF_00973394
Phospholipid ABC transporter substrate-binding protein MlaD



feature.pgfam_id.aliphatic_index.mean
PGF_03063012
Chaperone protein HscB



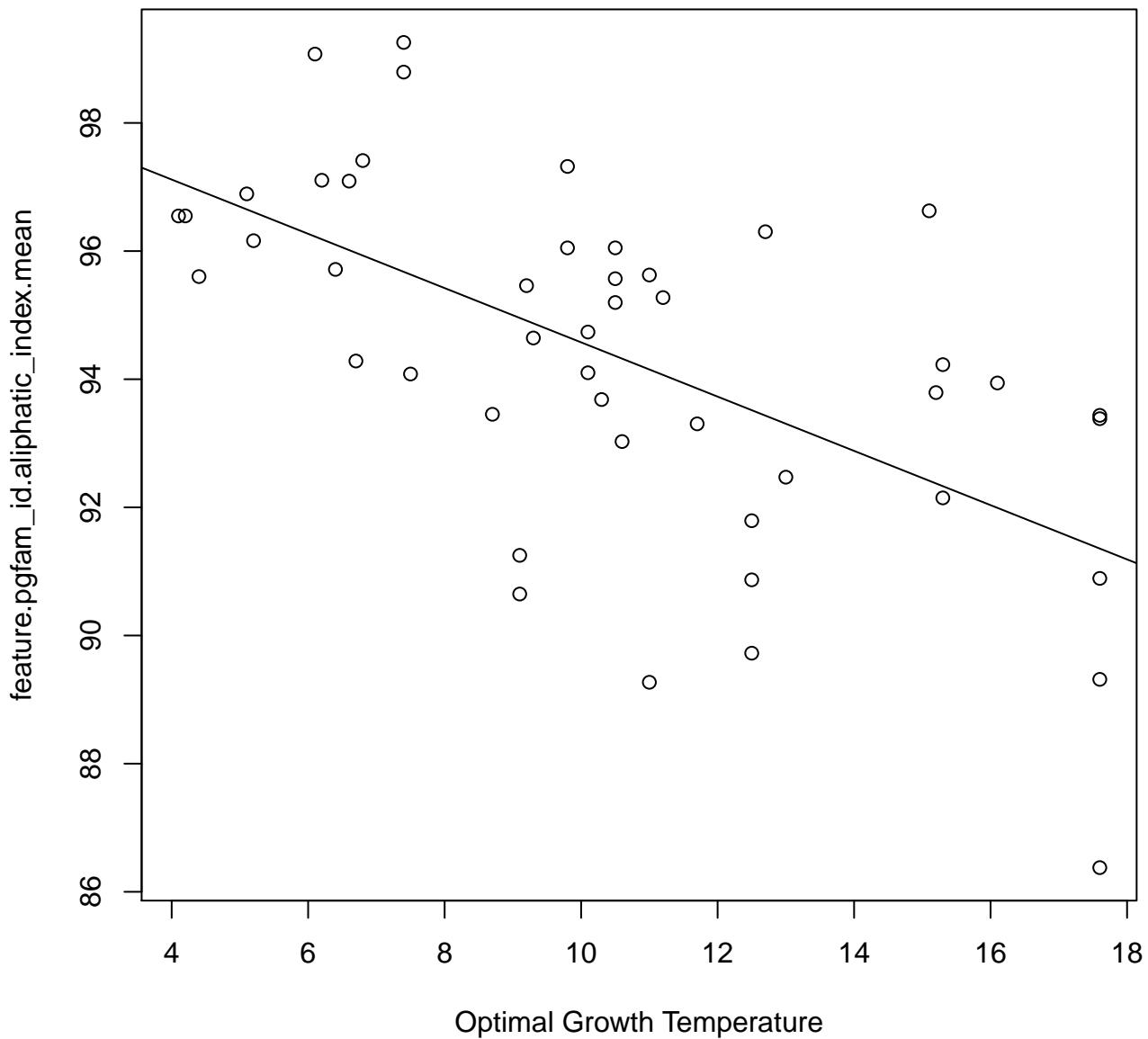
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PGF_00048829
LSU rRNA pseudouridine(2605) synthase (EC 5.4.99.22)



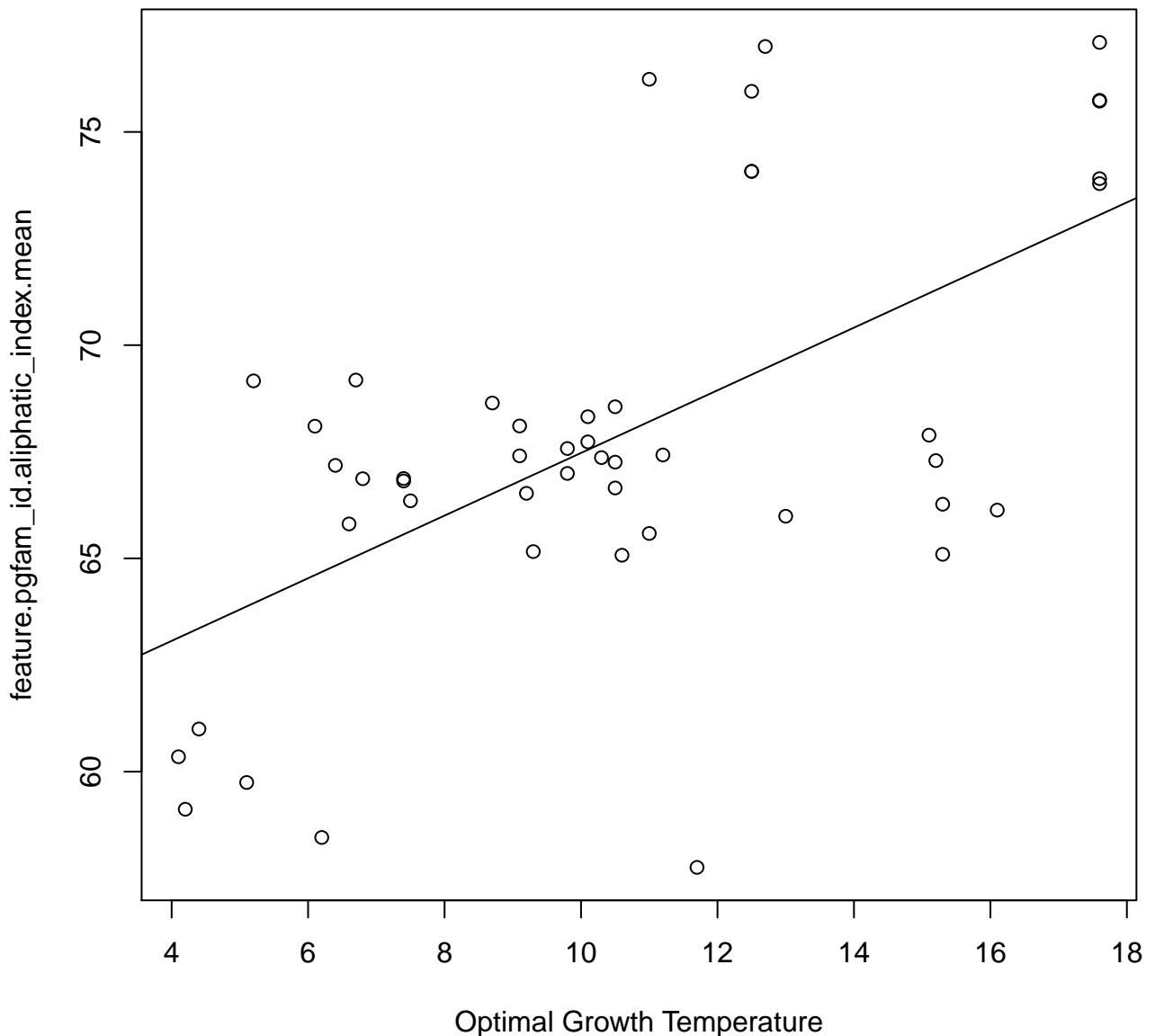
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PGF_00417831

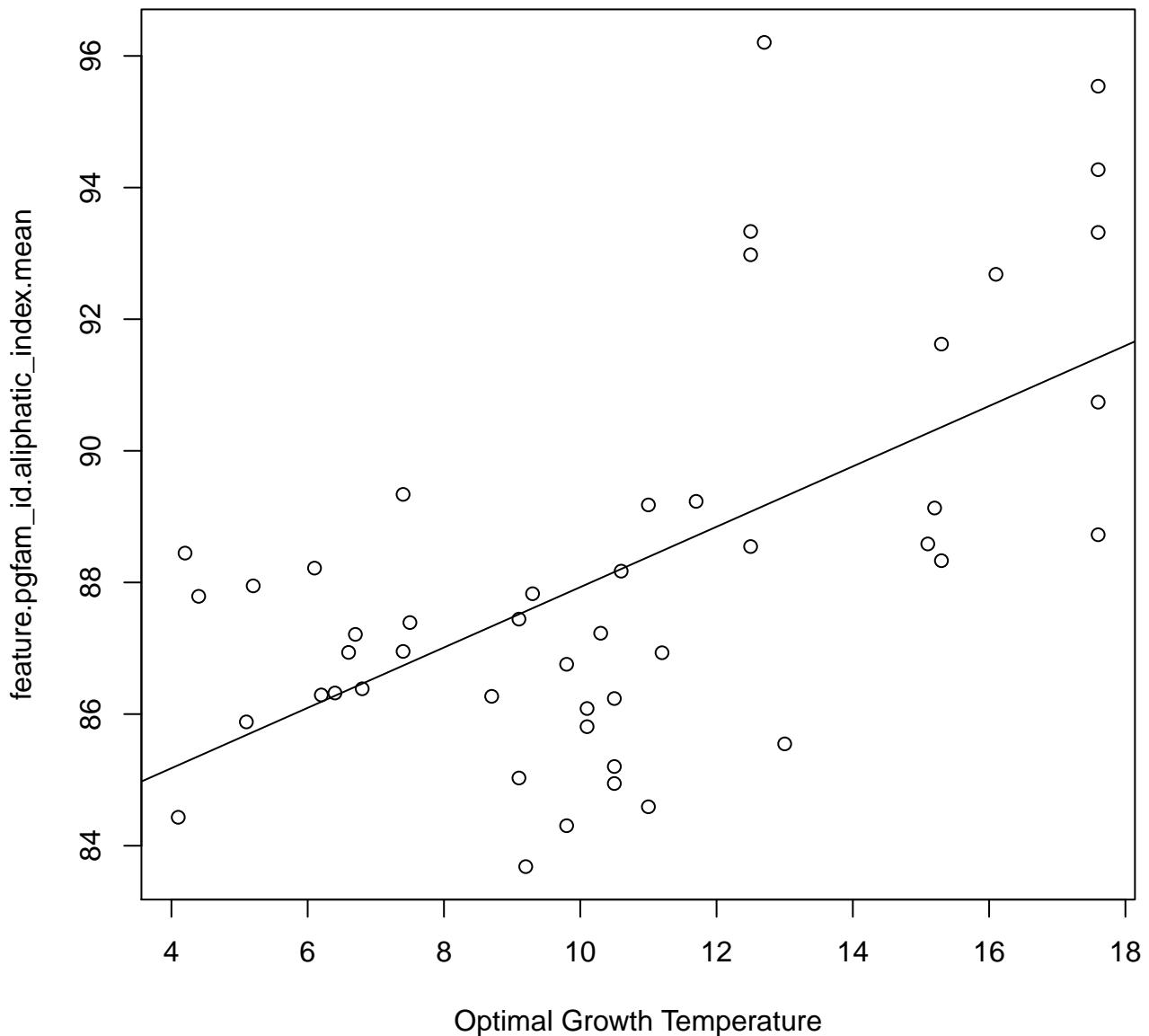
Chorismate mutase I (EC 5.4.99.5) / Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC 1.3.1.43)



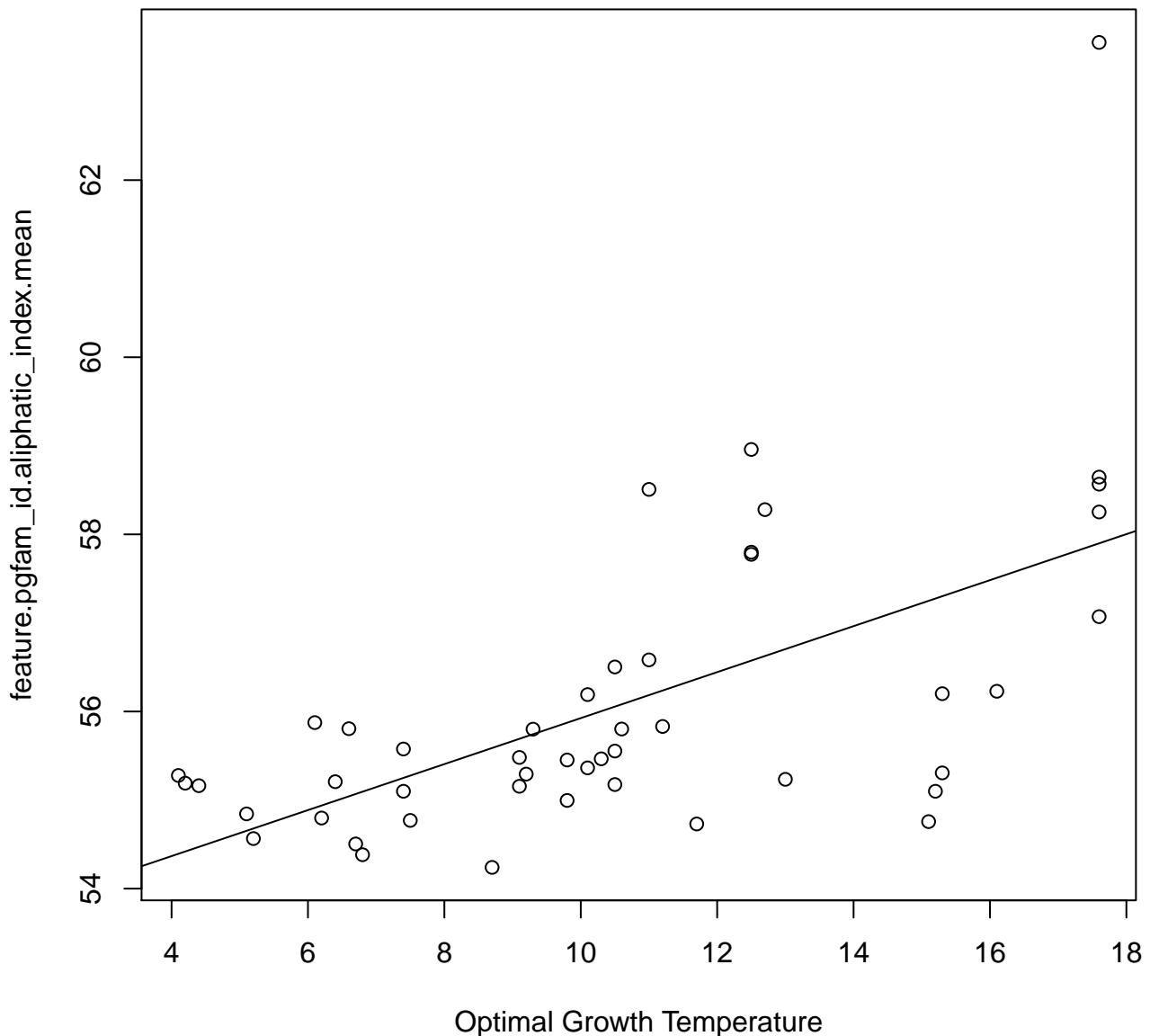
feature.pgfam_id.aliphatic_index.mean
PGF_02744871
Flagellar hook–basal body complex protein FliE



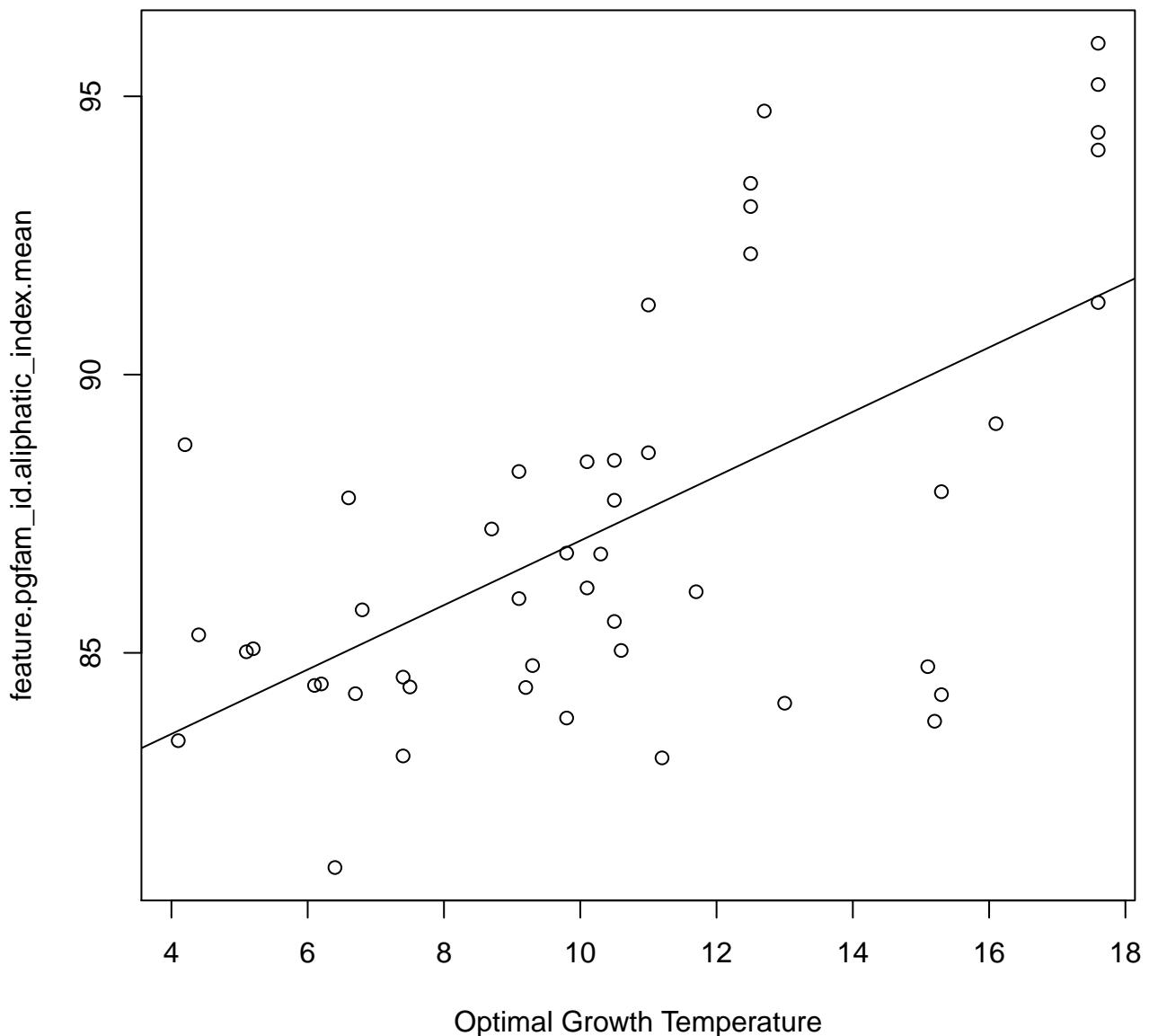
feature.pgfam_id.aliphatic_index.mean
PGF_05255412
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62)



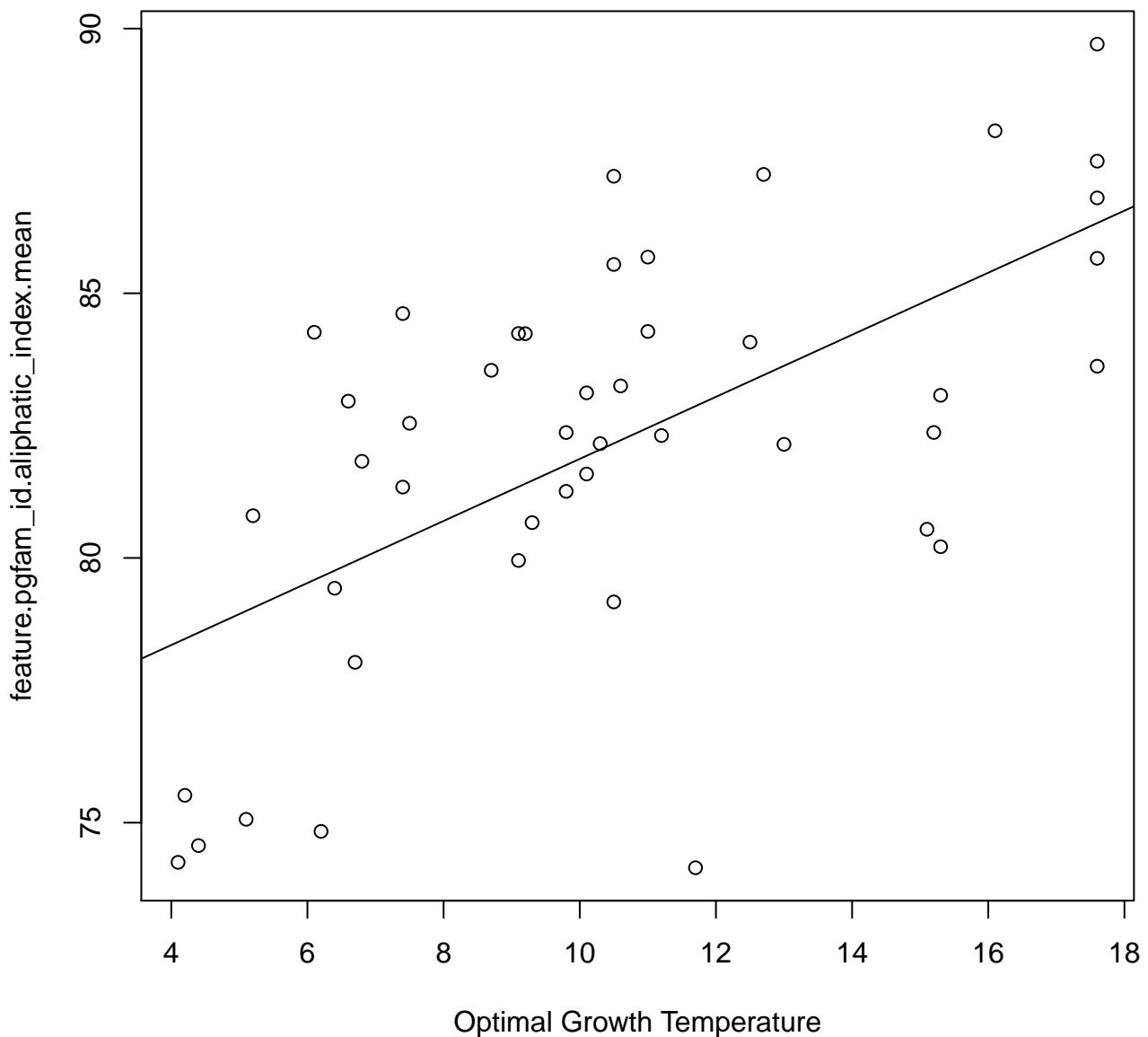
feature.pgfam_id.aliphatic_index.mean
PGF_02049468
Cold shock protein of CSP family



feature.pgfam_id.aliphatic_index.mean
PGF_06120144
Ribosome association toxin RatA



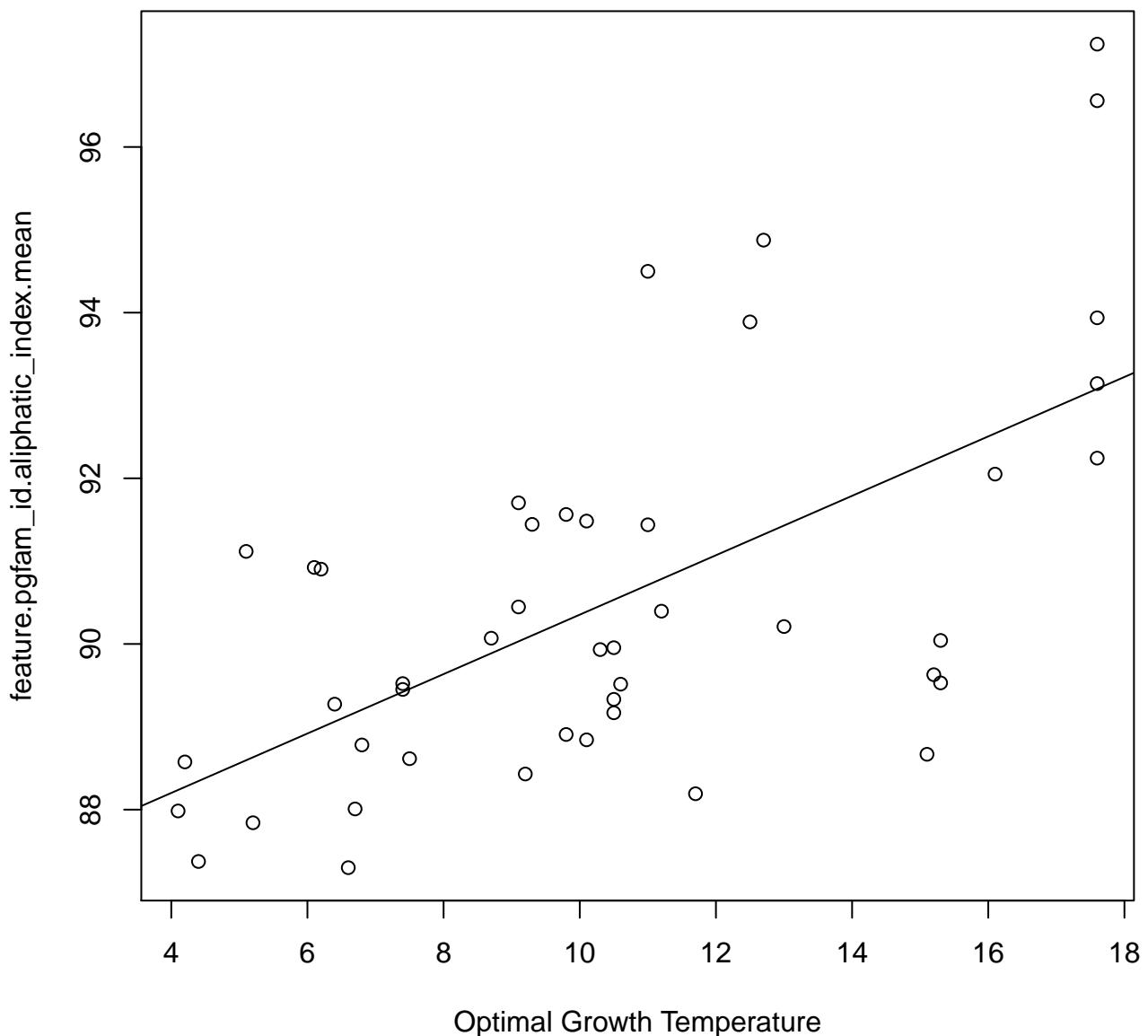
feature.pgfam_id.aliphatic_index.mean
PGF_07357908
UPF0070 protein YfgM



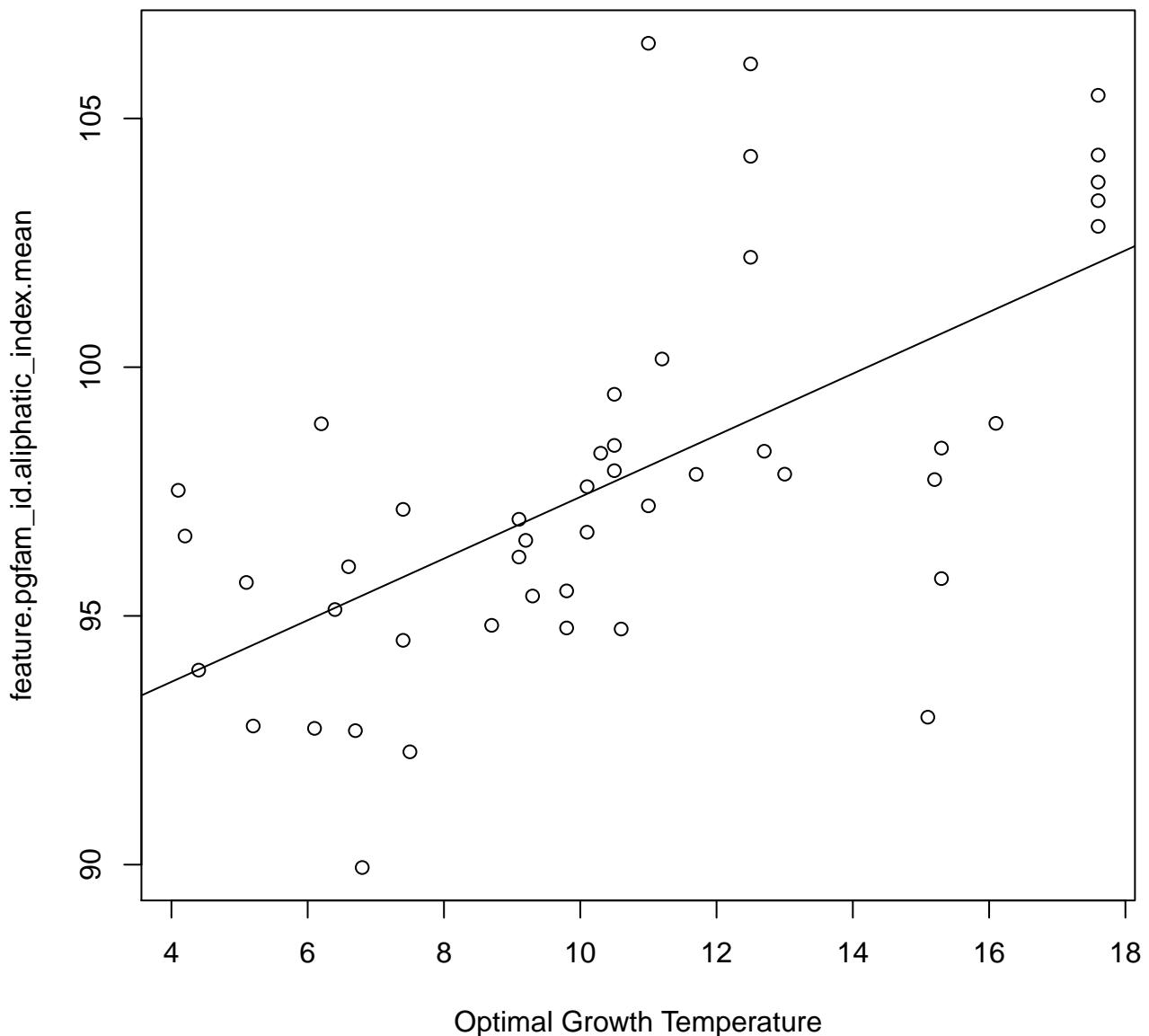
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PGF_12698553

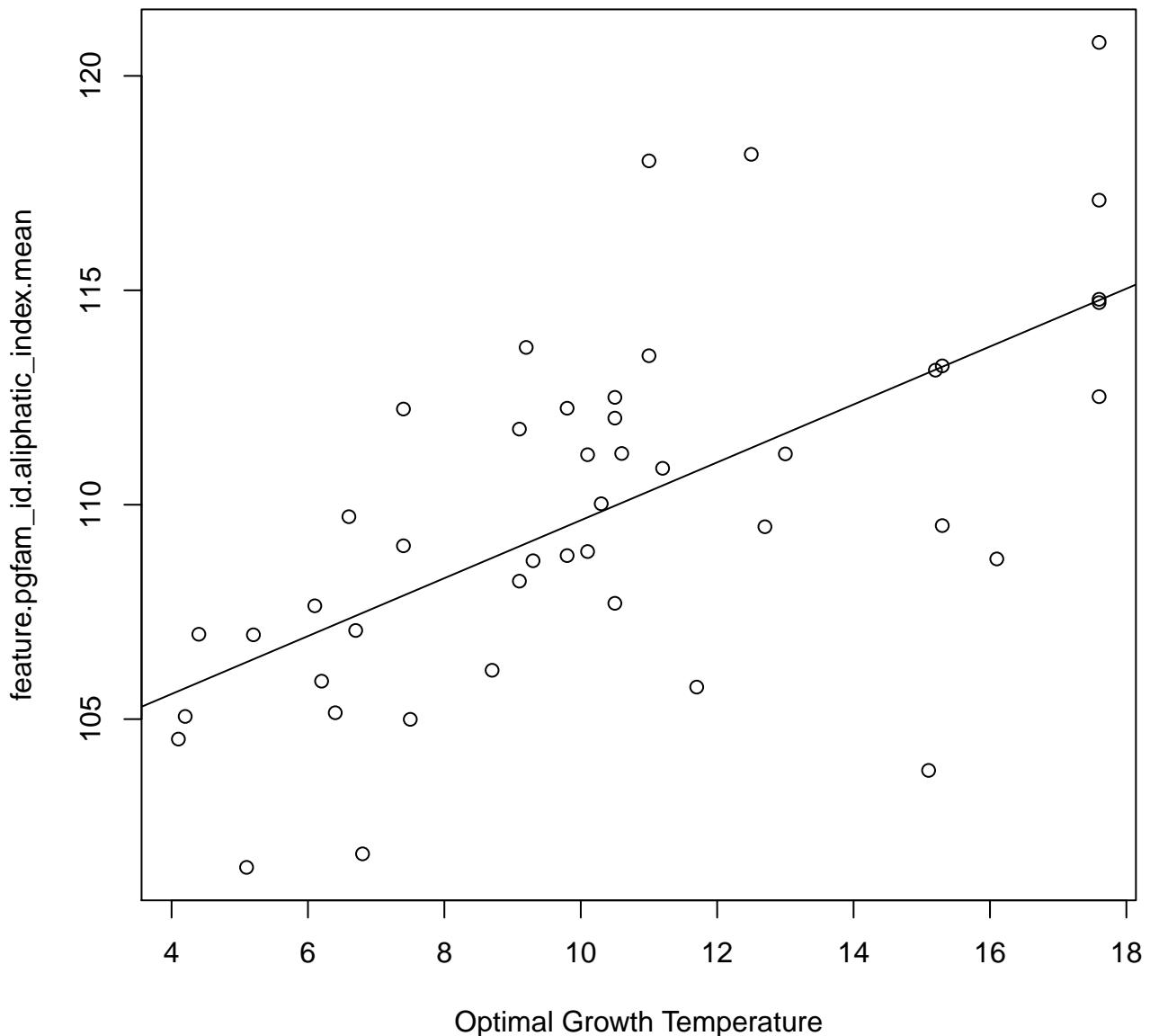
Protein kinase



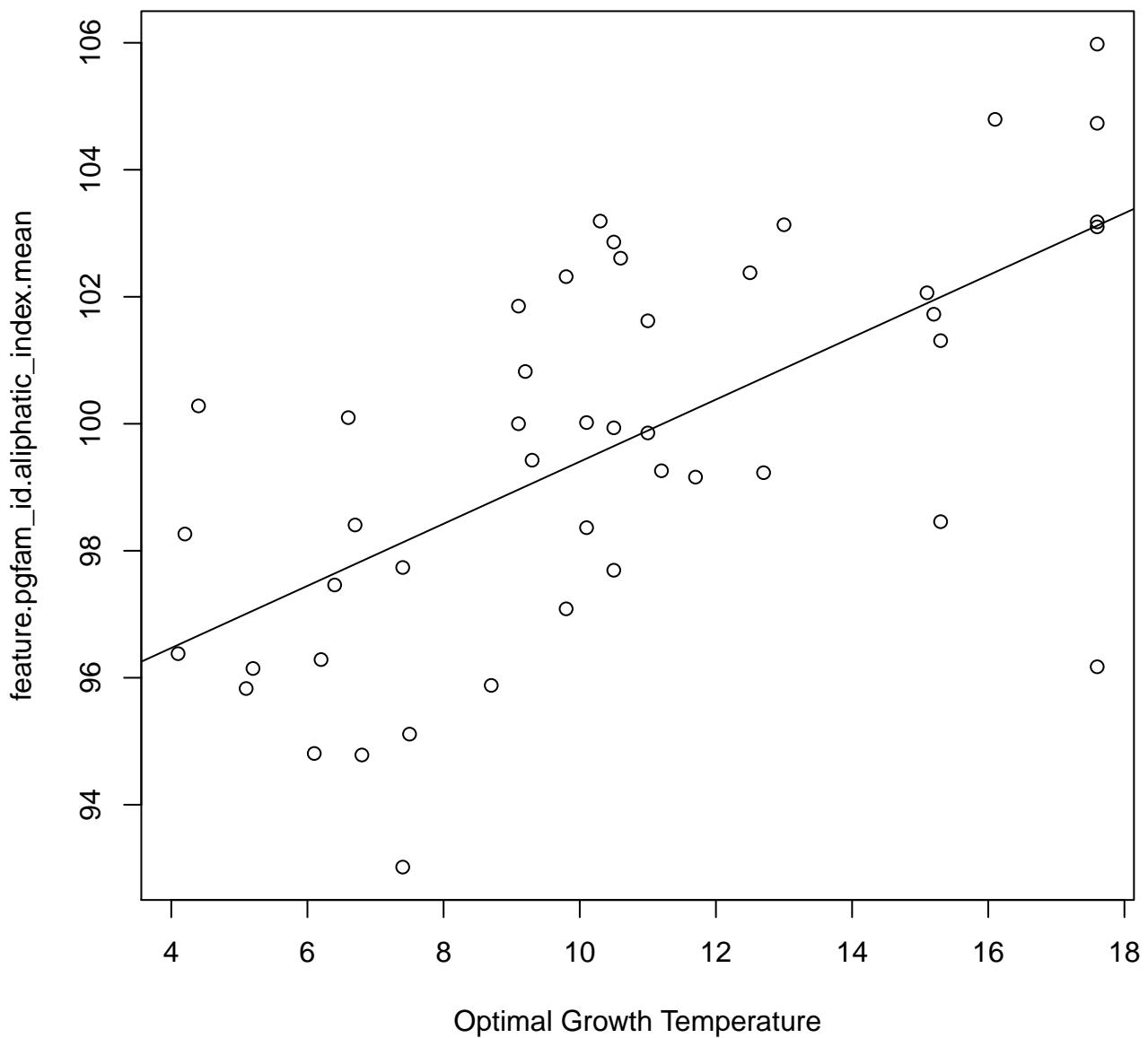
feature.pgfam_id.aliphatic_index.mean
PGF_03051420
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



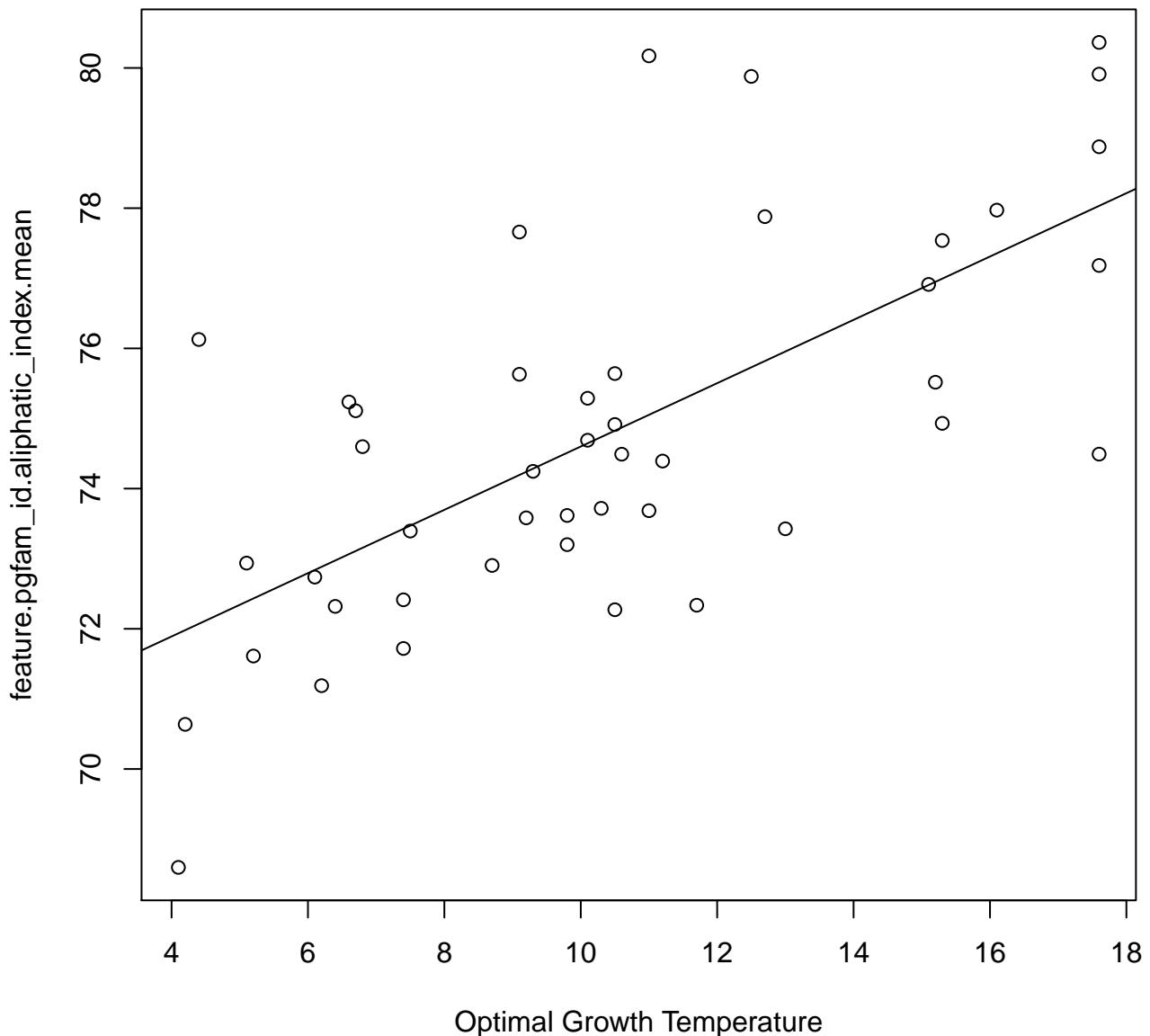
feature.pgfam_id.aliphatic_index.mean
PGF_03824105
UPF0352 protein YejL



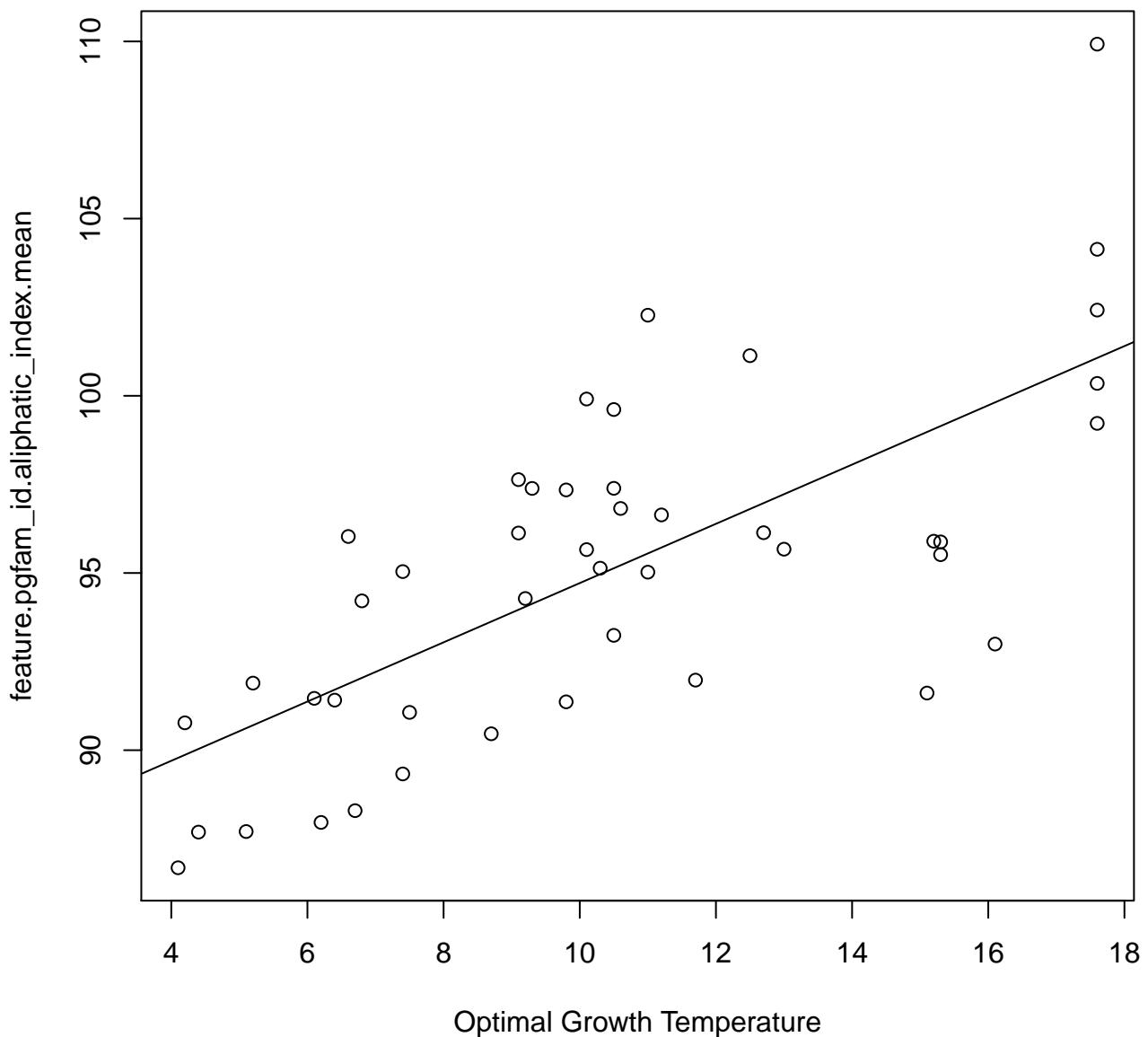
feature.pgfam_id.aliphatic_index.mean
PGF_10454652
UPF0758 family protein



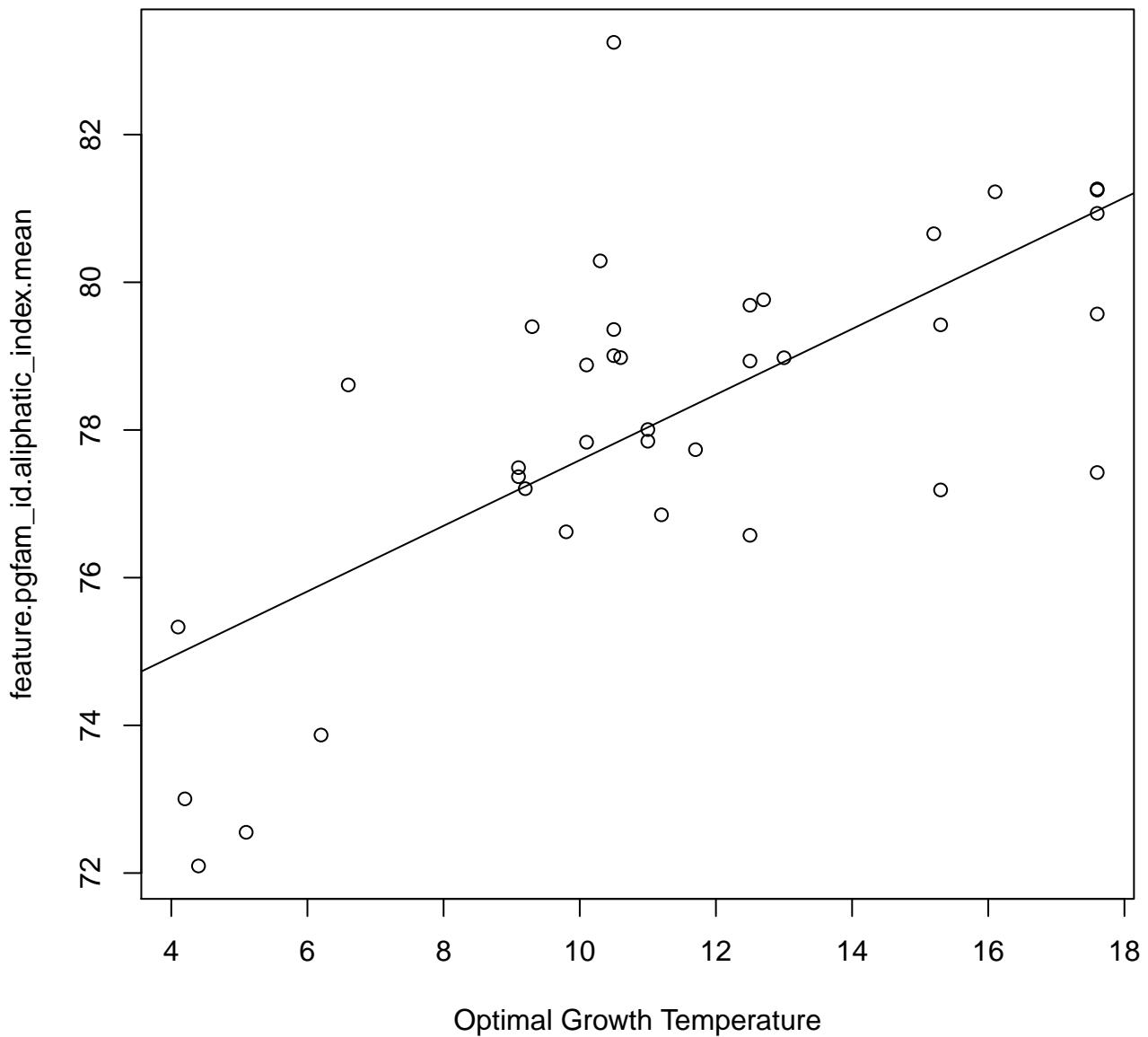
feature.pgfam_id.aliphatic_index.mean
PGF_07179577
Flagellar basal-body rod protein FlgF



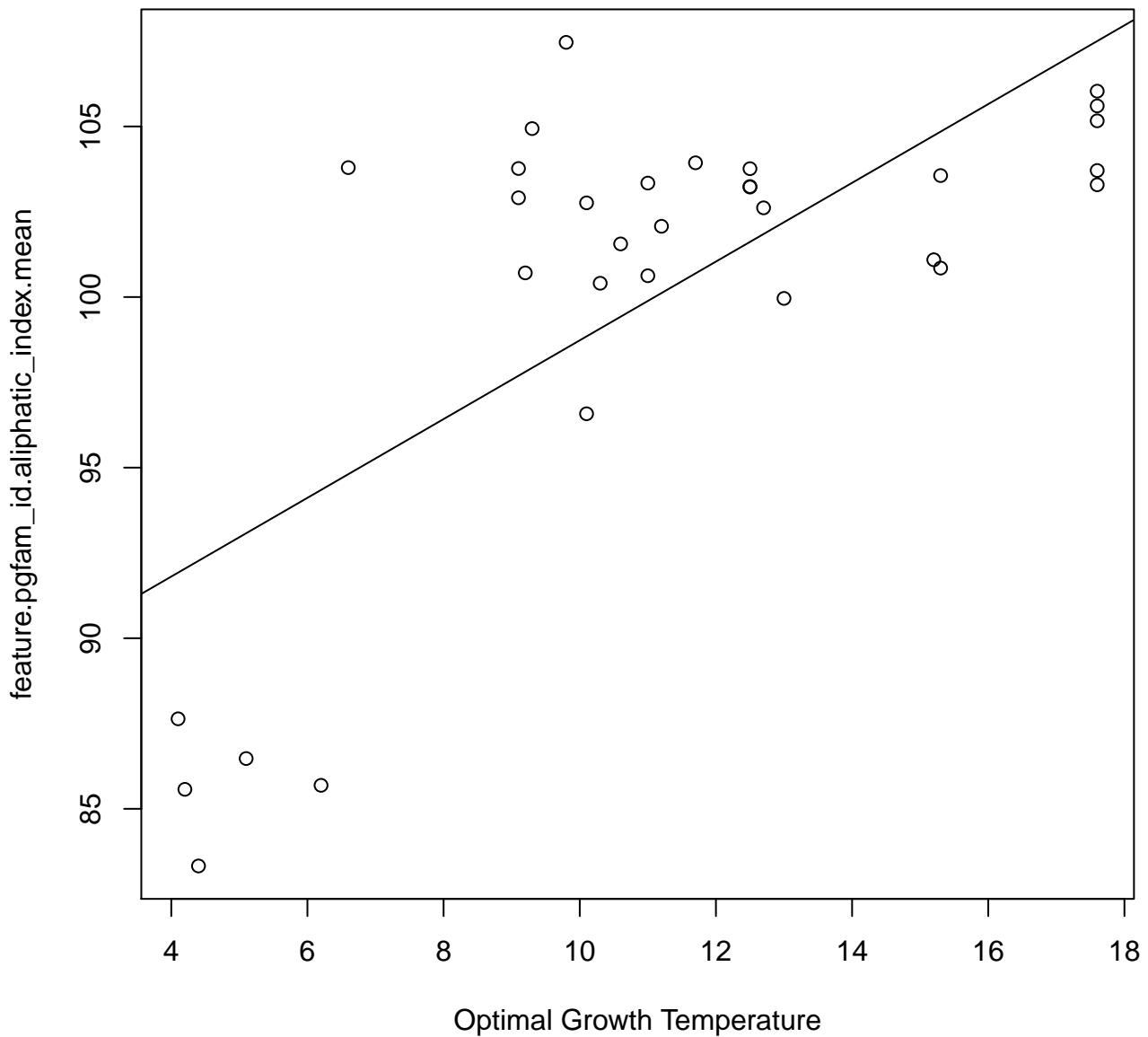
feature.pgfam_id.aliphatic_index.mean
PGF_06250778
Esterase ybfF (EC 3.1.-.-)



feature.pgfam_id.aliphatic_index.mean
PGF_07675395
Flagellar protein FliJ



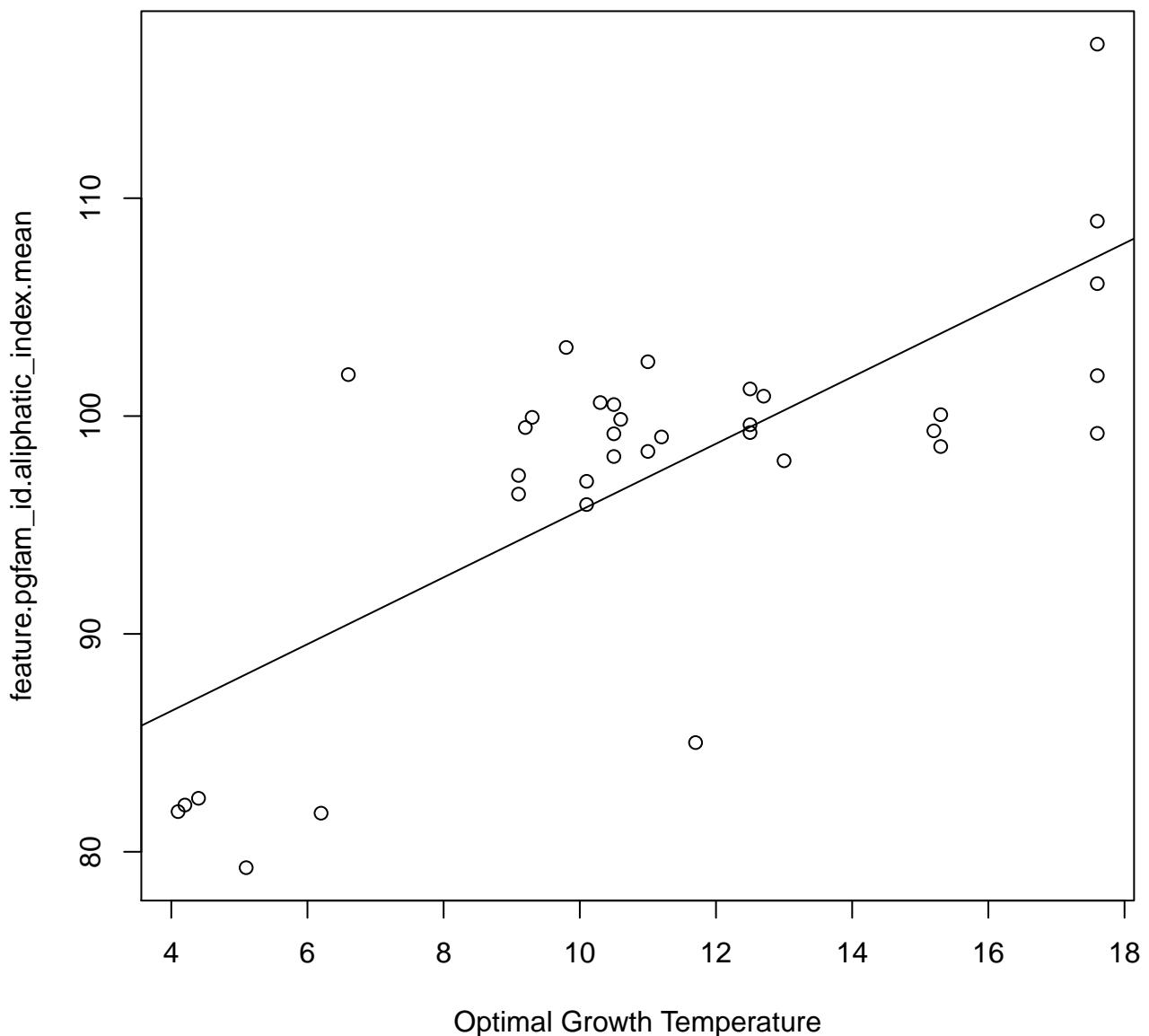
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PGF_01336501
hypothetical protein



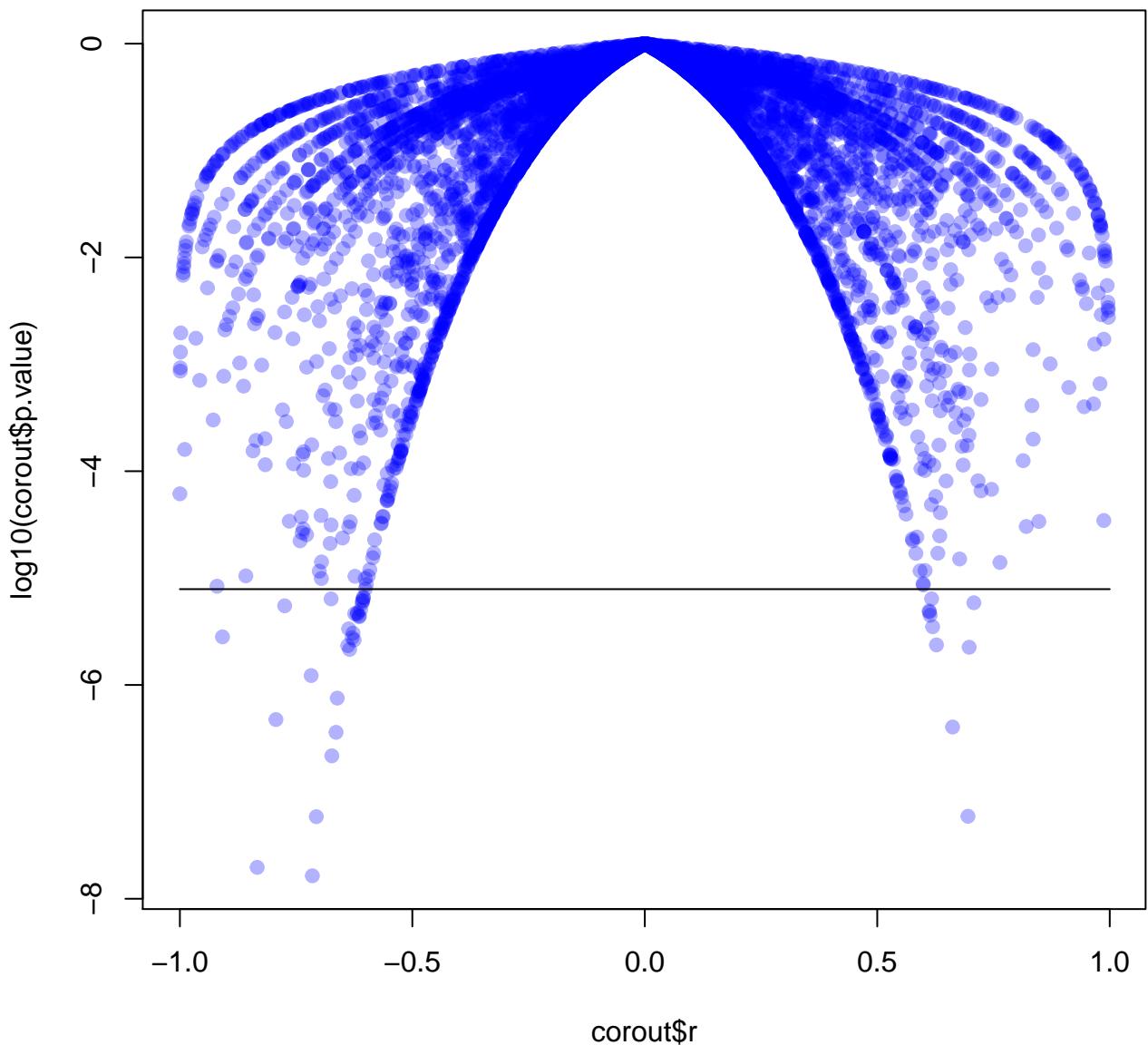
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PGF_02790700

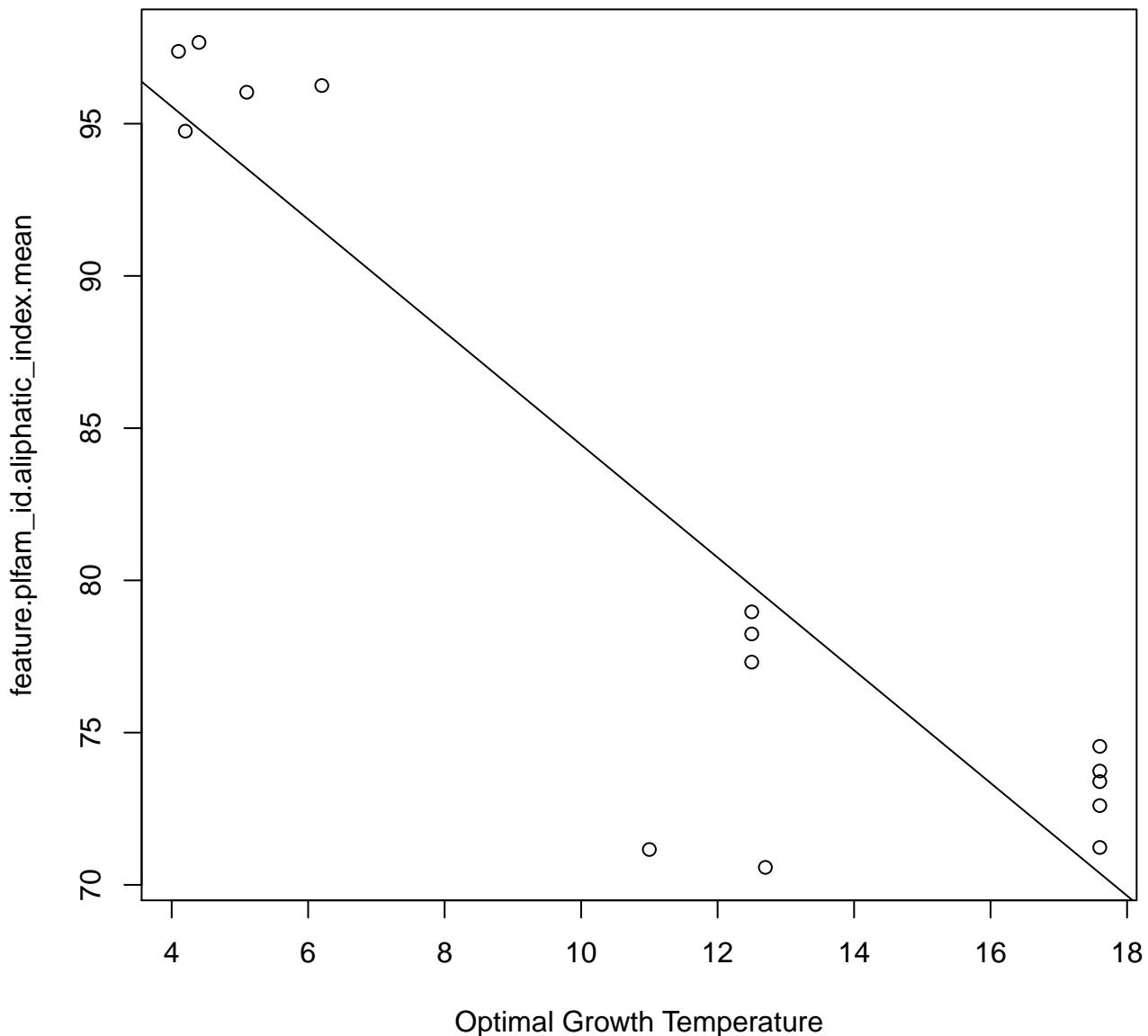
Adenosylcobinamide kinase (EC 2.7.1.156) / Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)



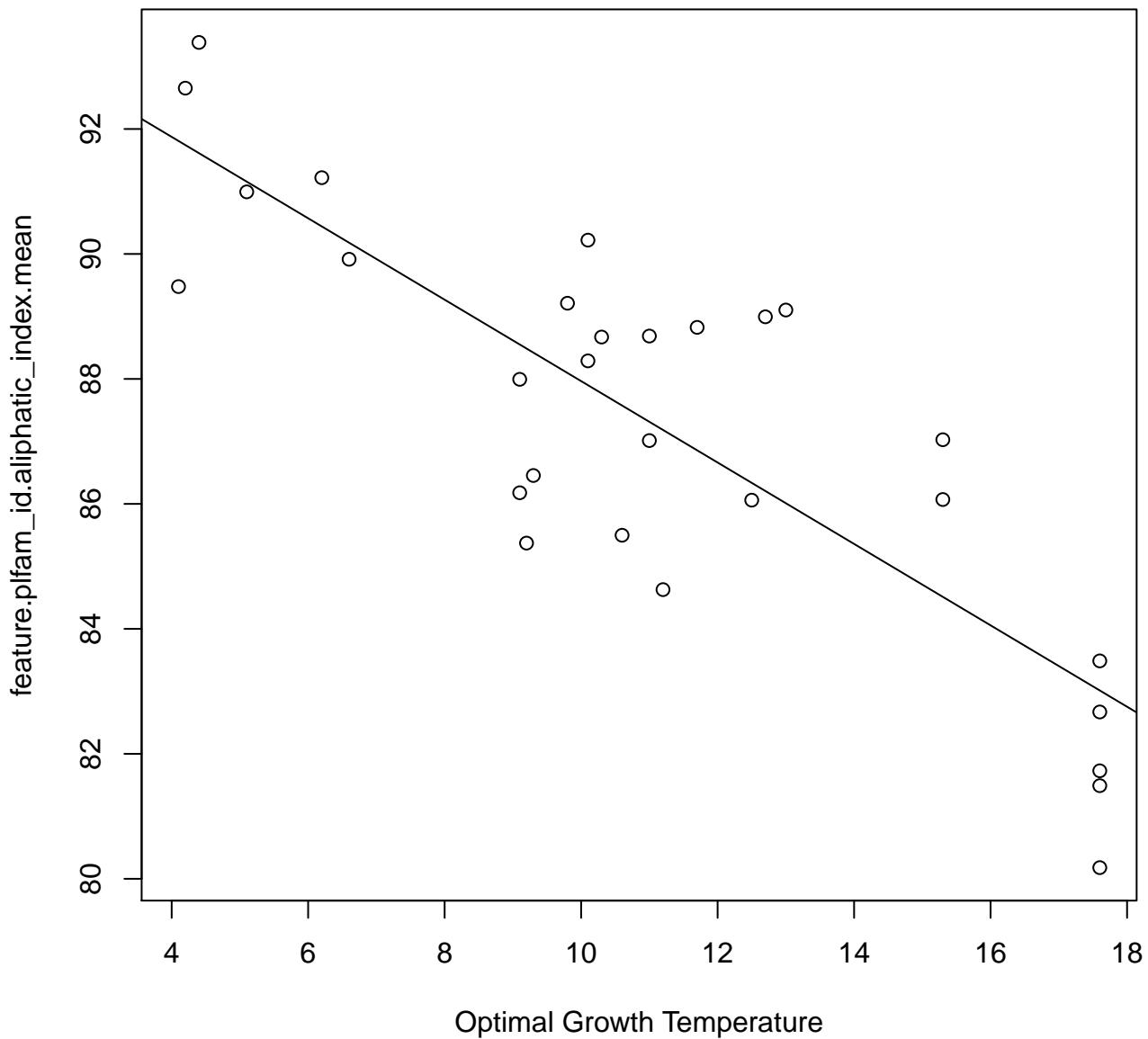
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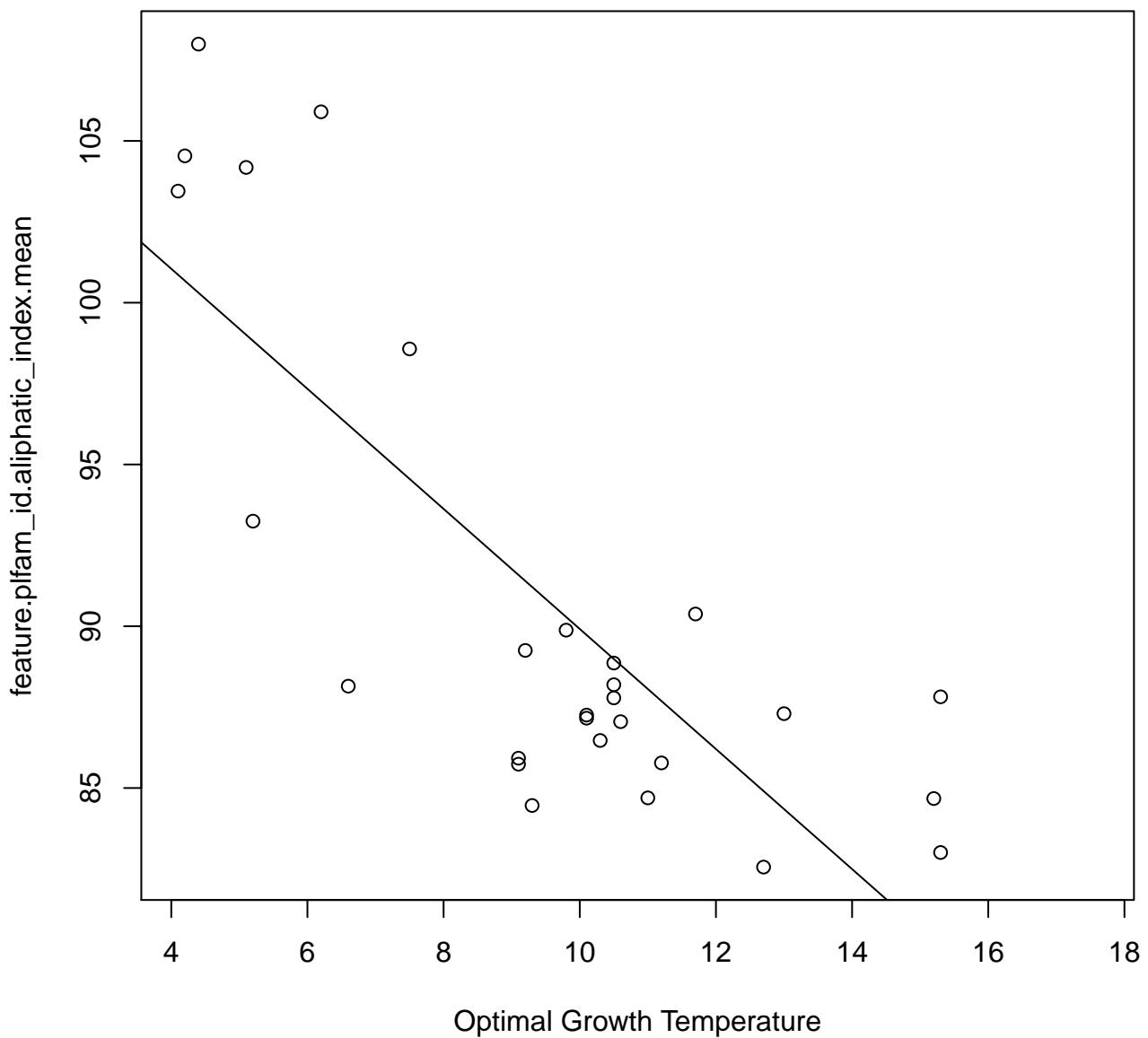
feature.plfam_id.aliphatic_index.mean
PLF_28228_00001794
Outer membrane beta-barrel assembly protein BamE



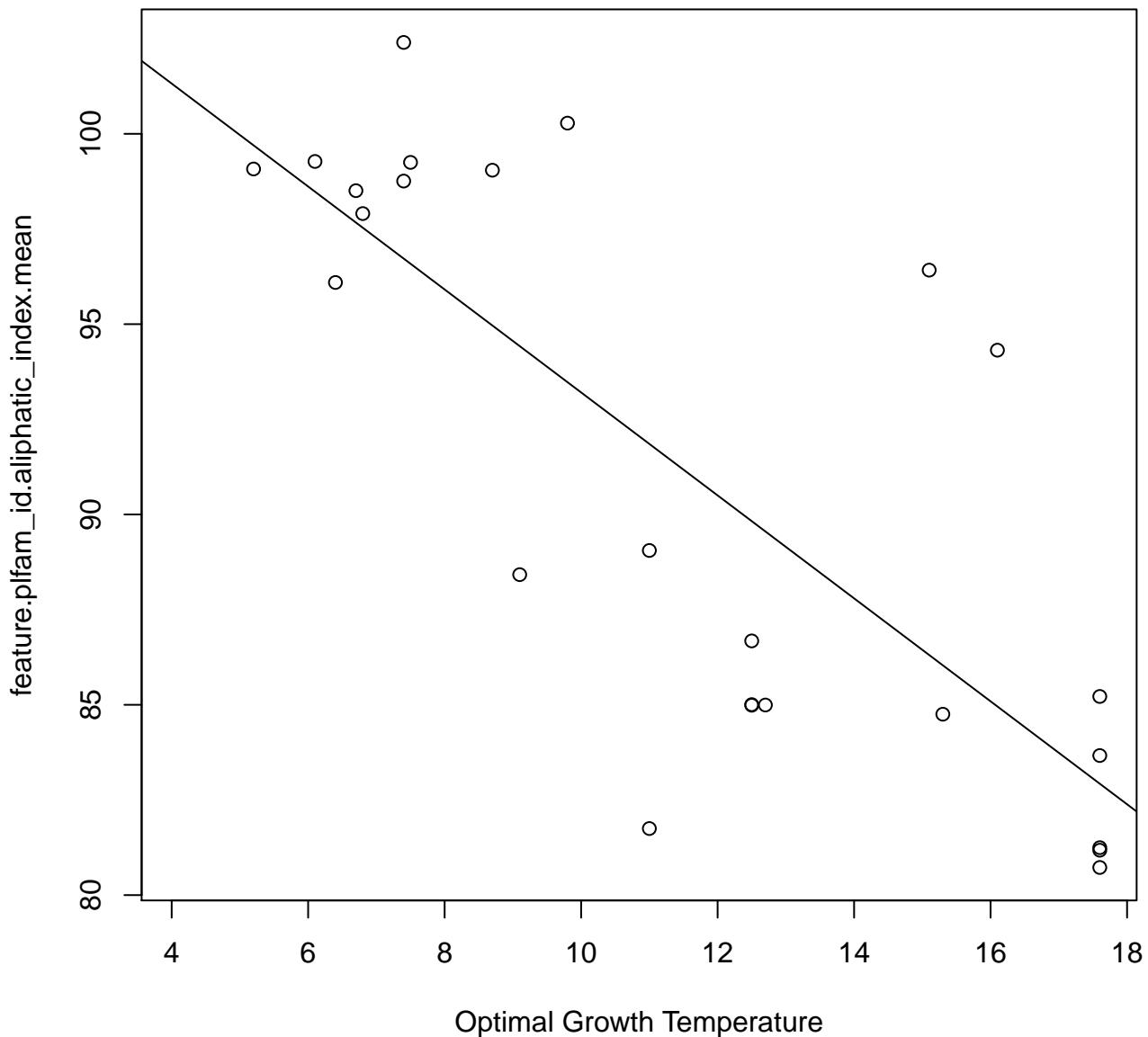
feature.plfam_id.aliphatic_index.mean
PLF_28228_00017084
Alkylated DNA repair protein



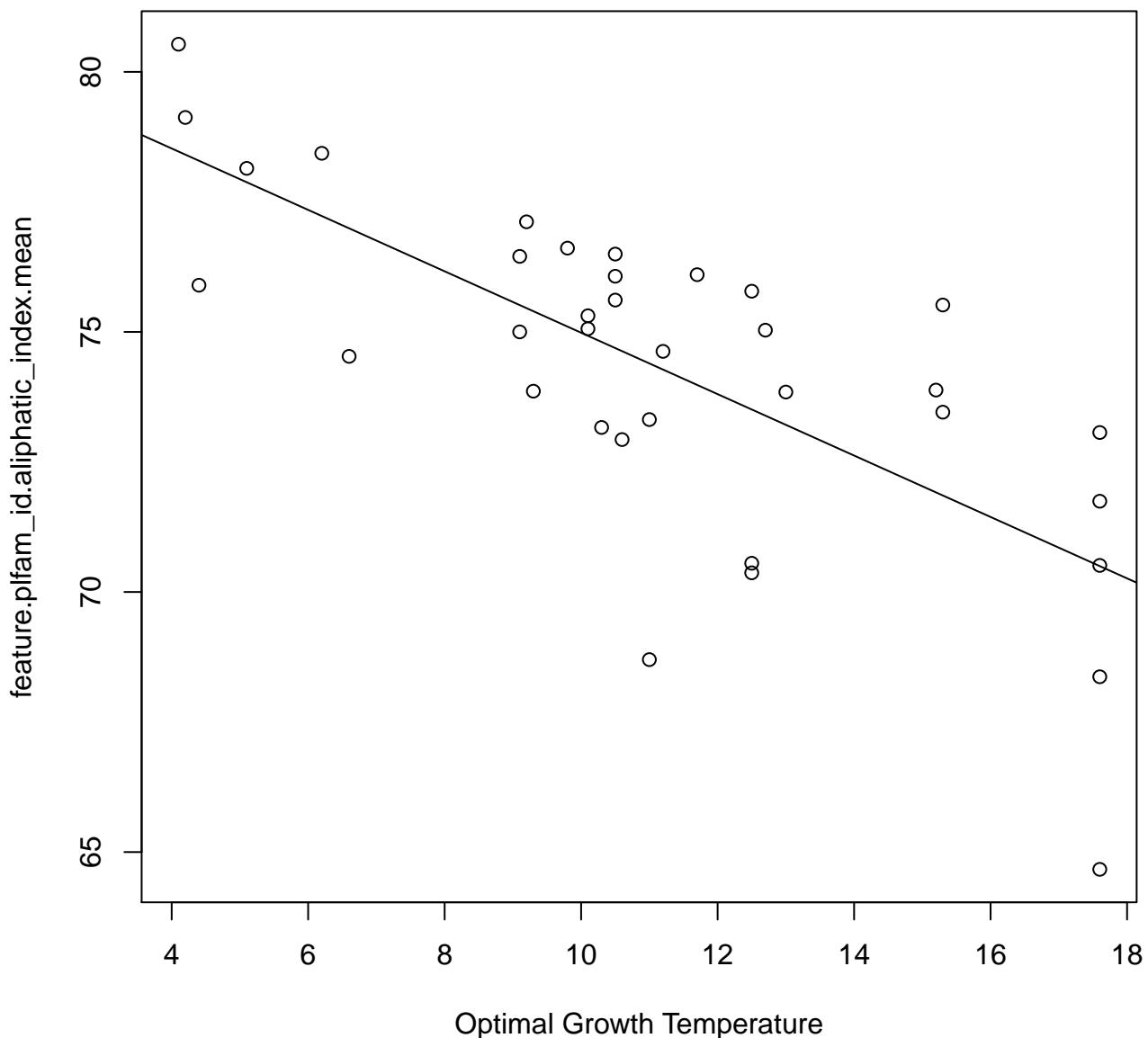
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hypothetical protein



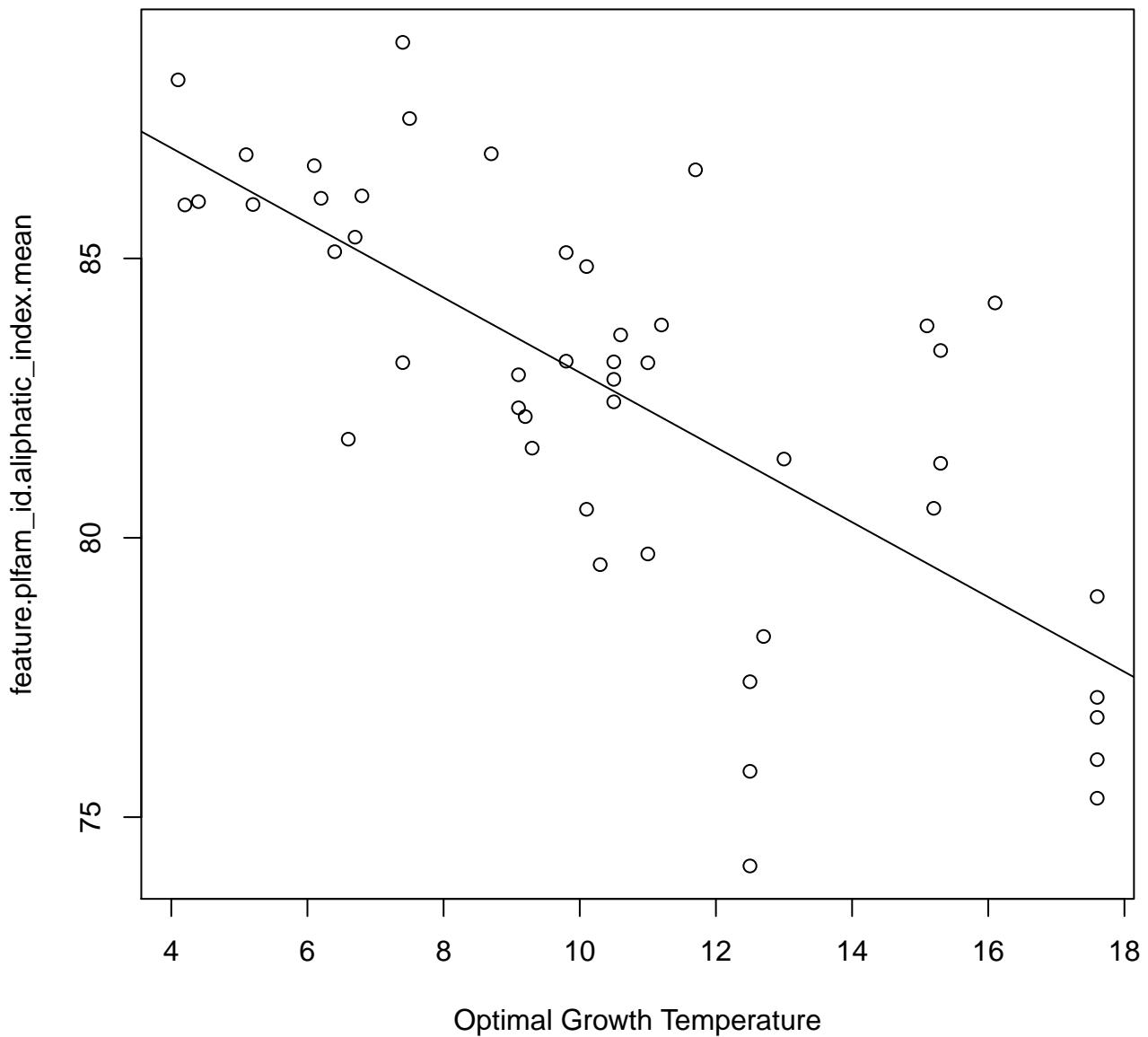
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Peptidyl-tRNA hydrolase ArfB (EC 3.1.1.29)



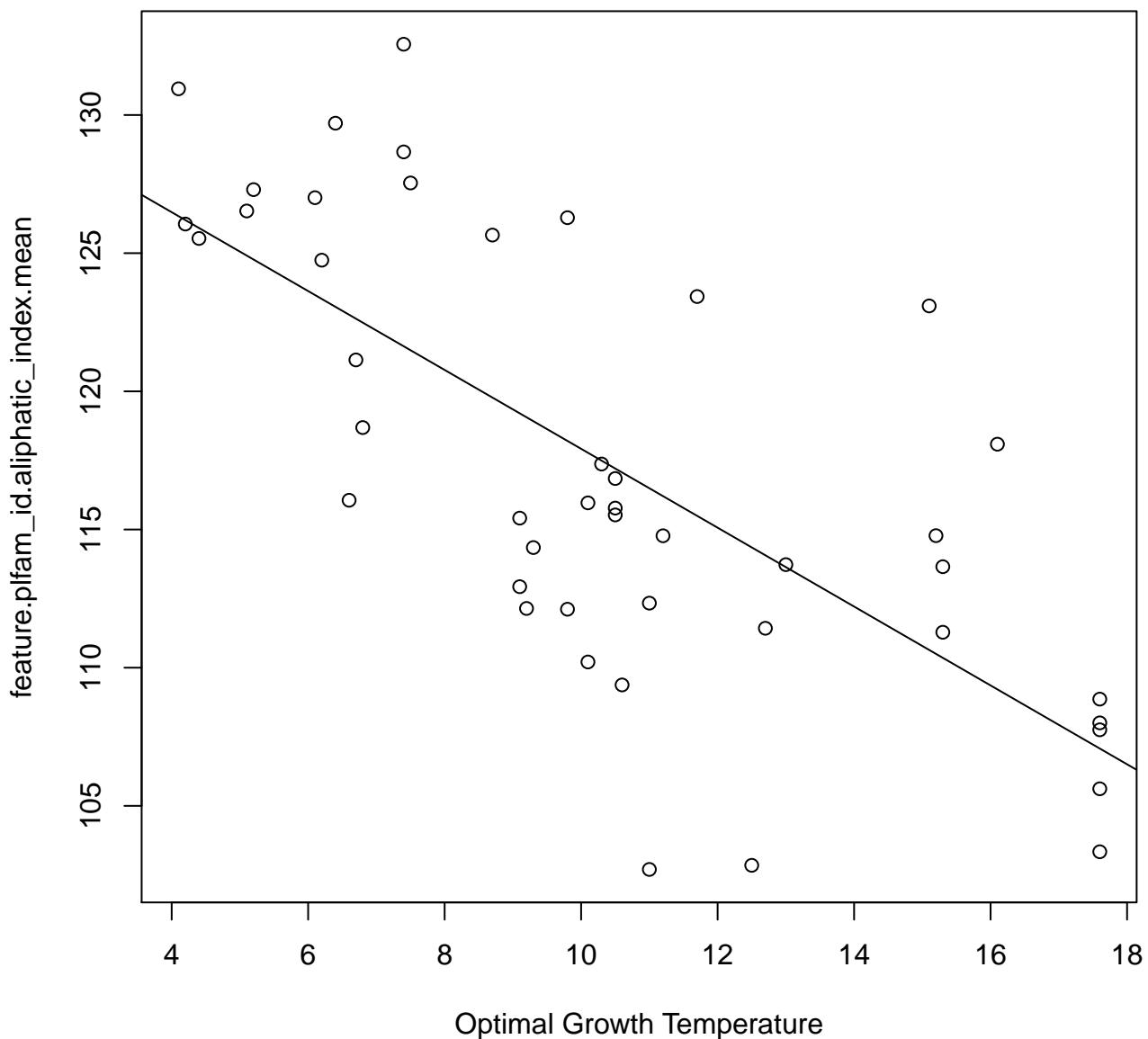
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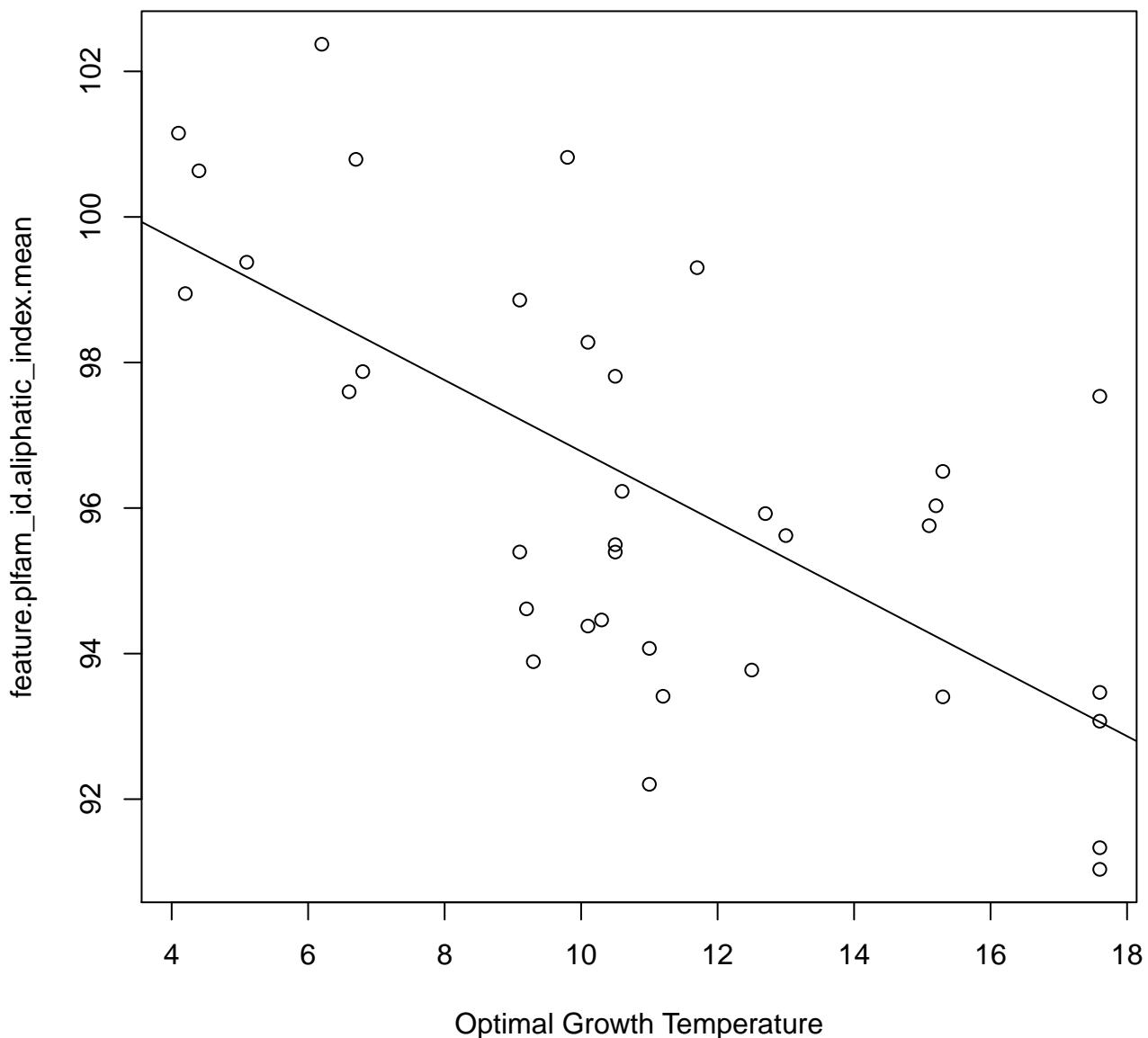
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tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)



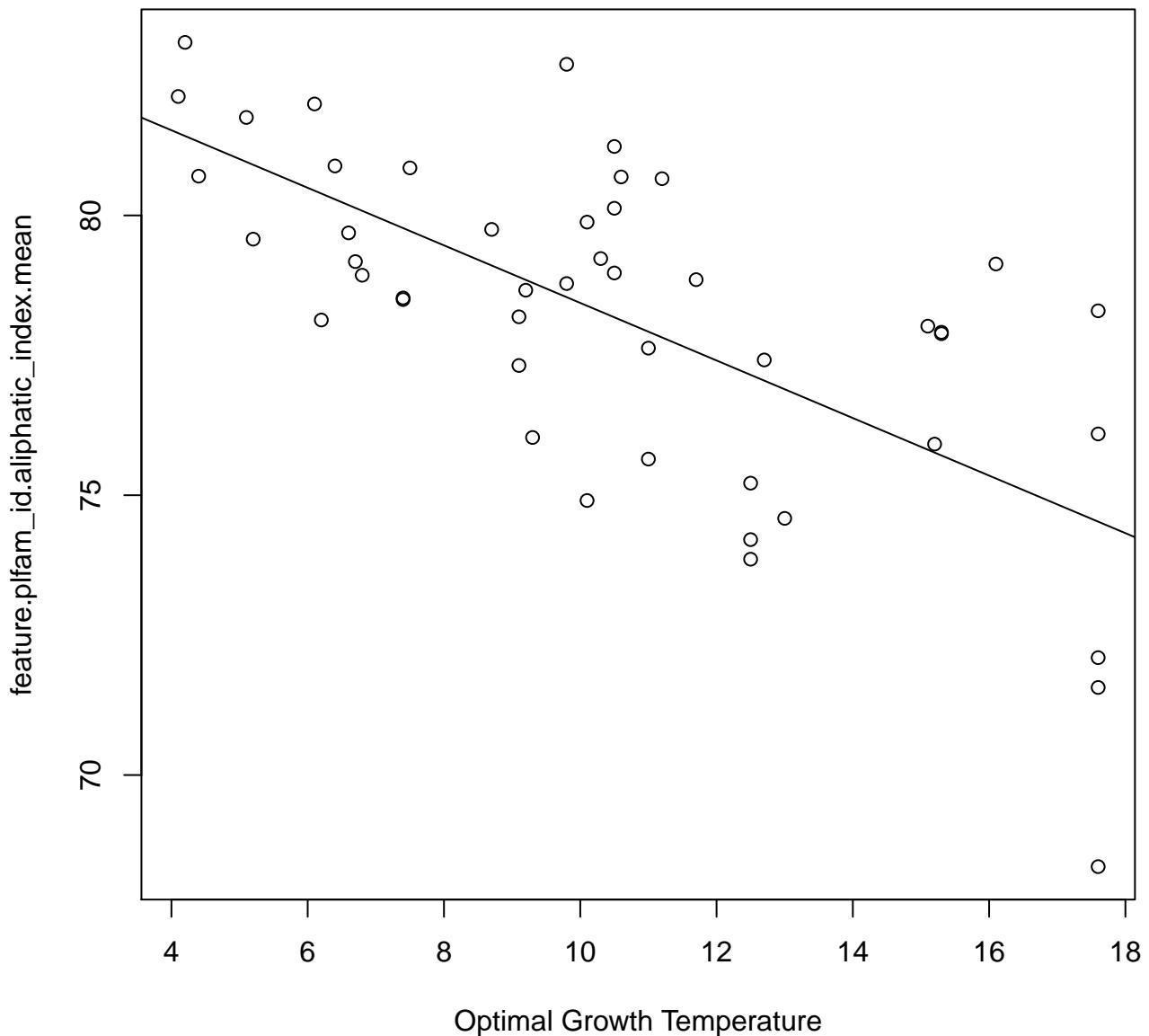
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Transporter, LysE family



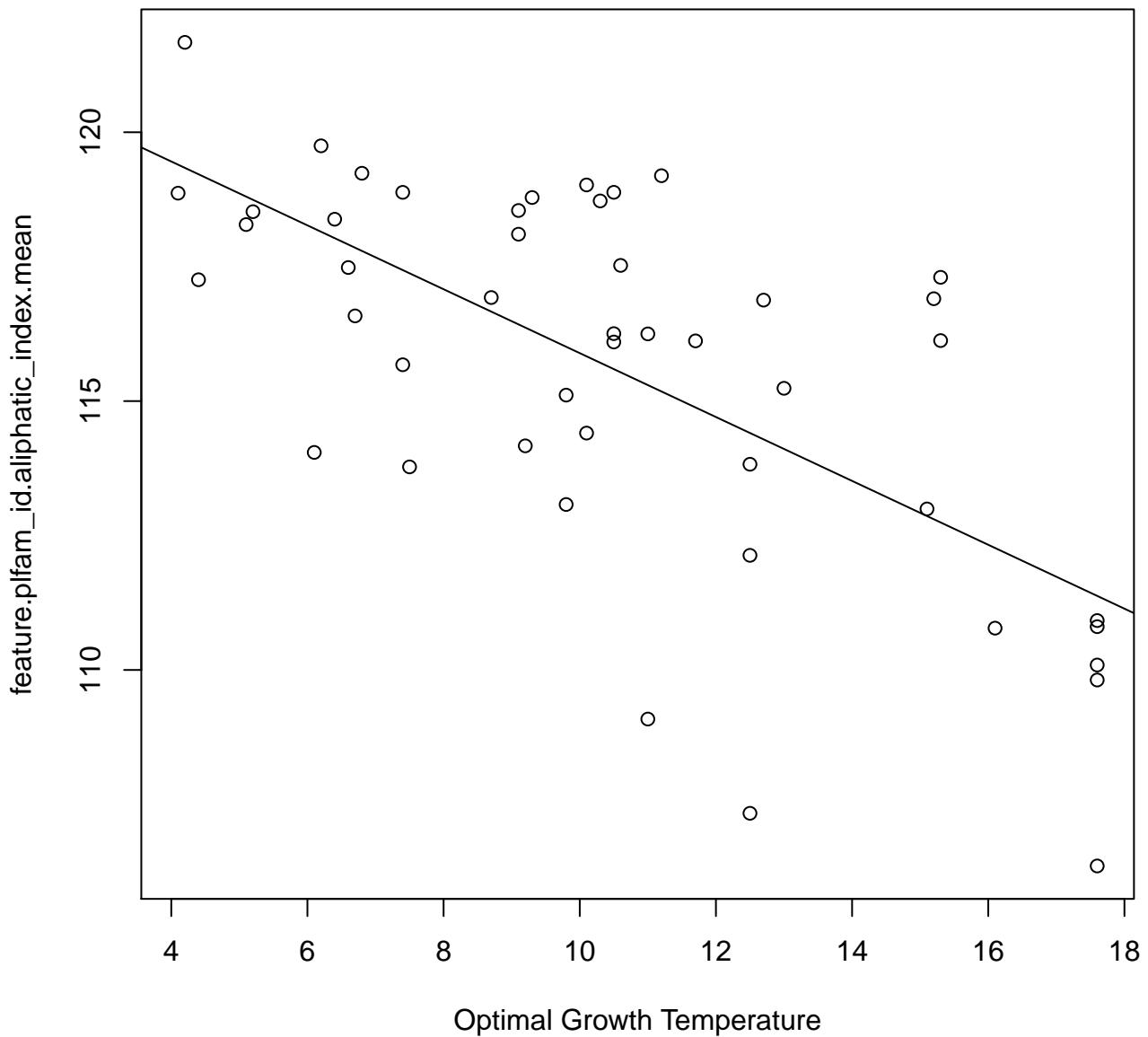
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Cobyric acid synthase (EC 6.3.5.10)



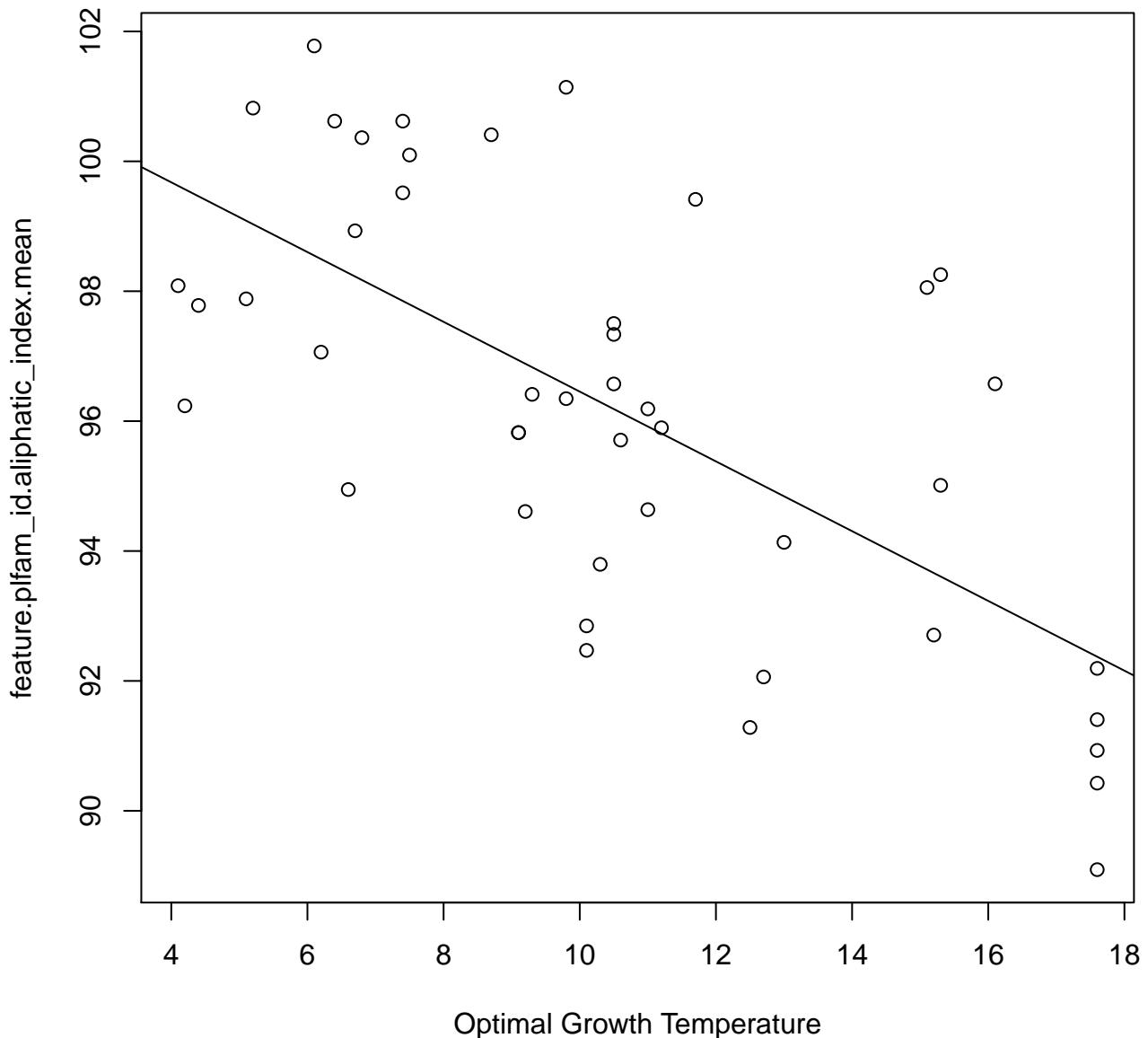
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23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)



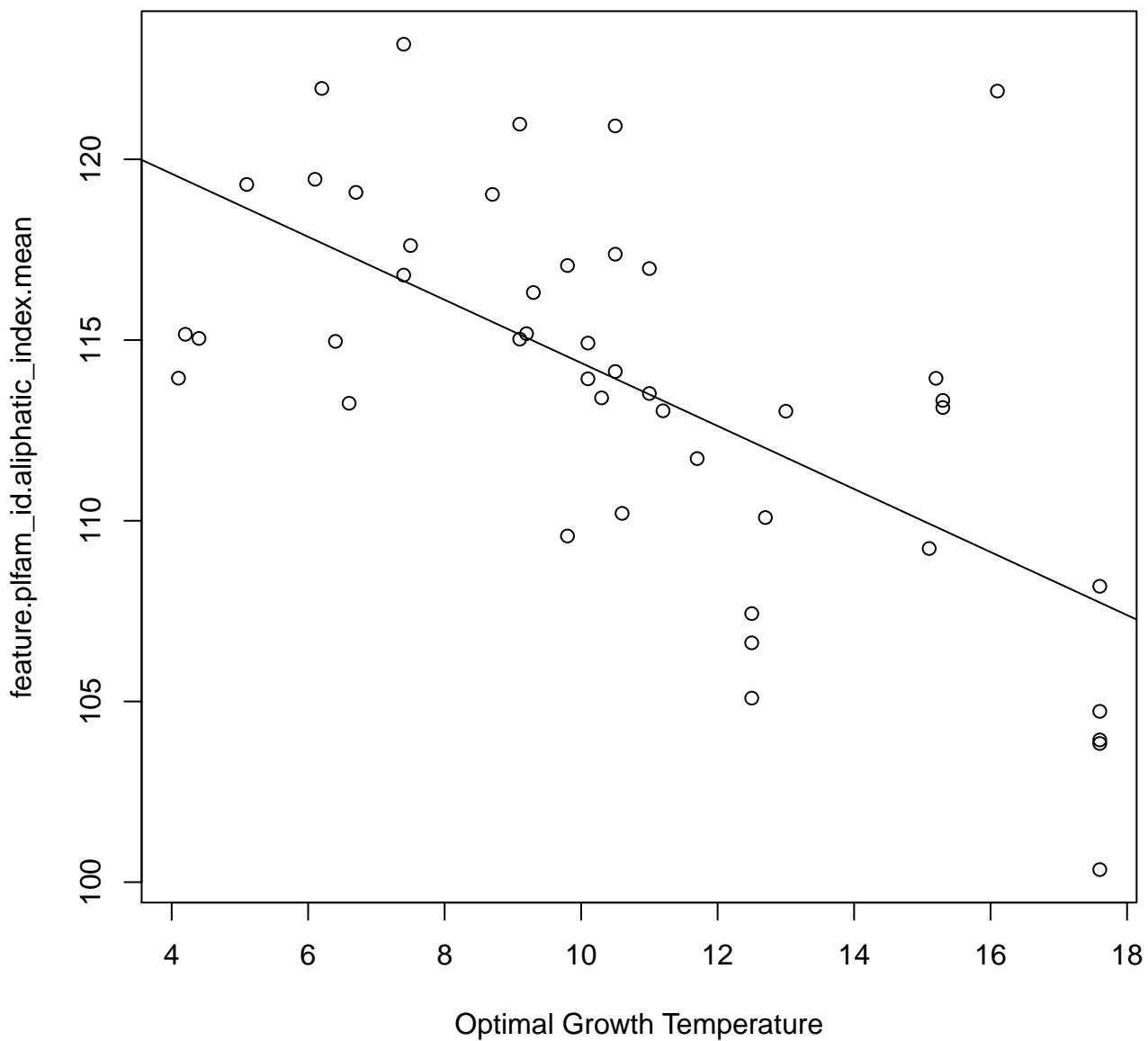
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Twin-arginine translocation protein TatC



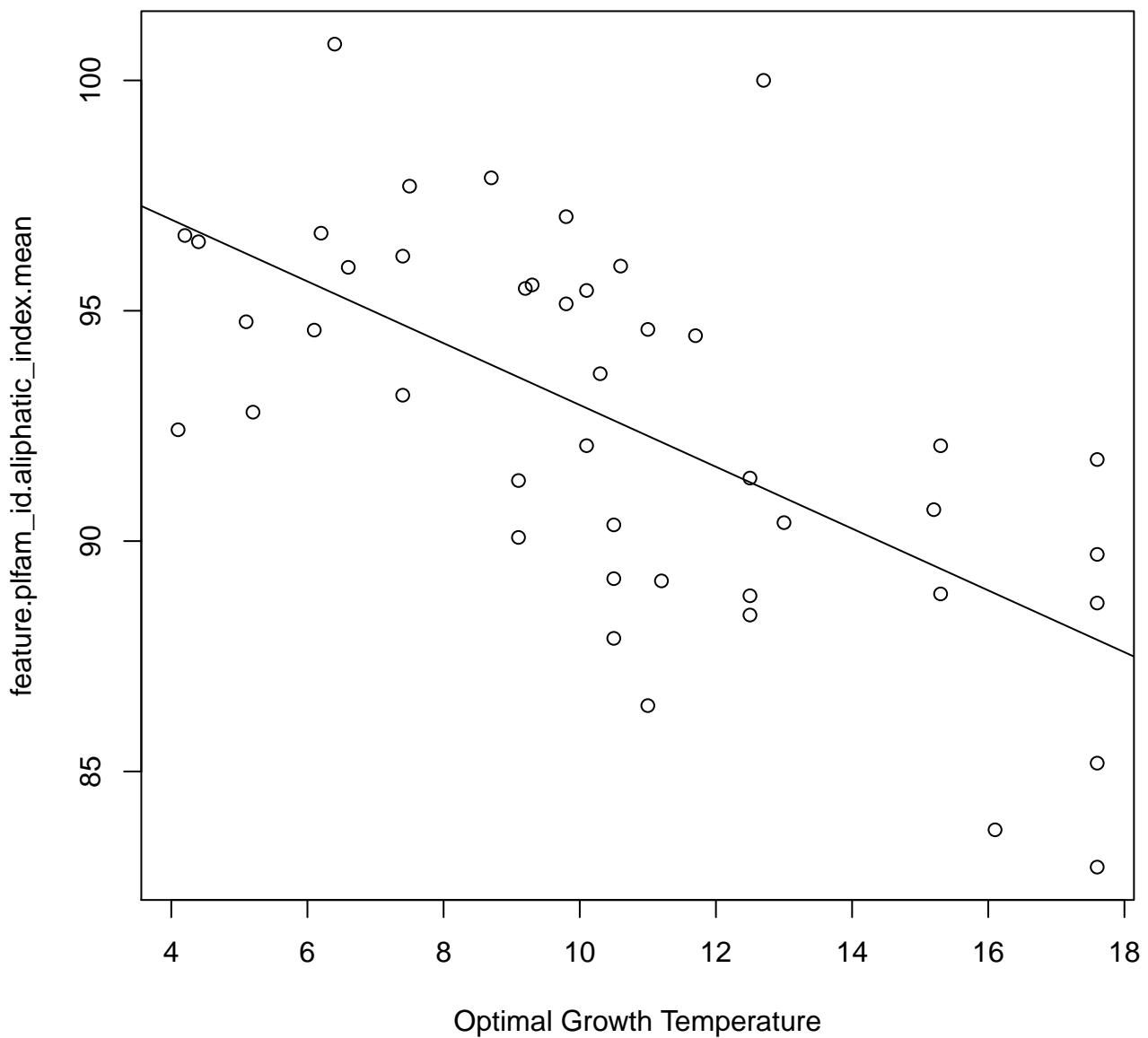
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Cytochrome c-type biogenesis protein CcmE, heme chaperone



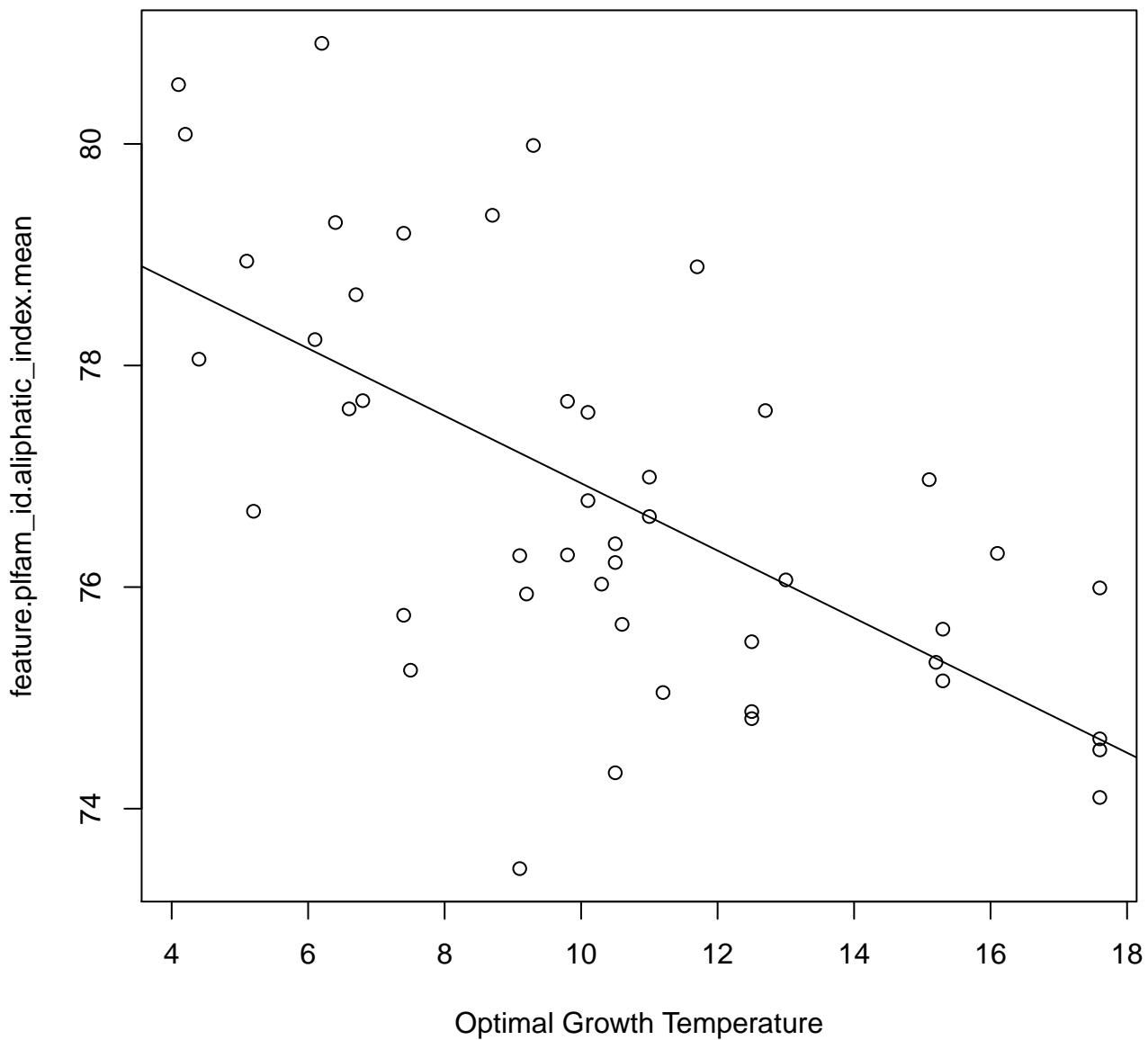
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hypothetical protein



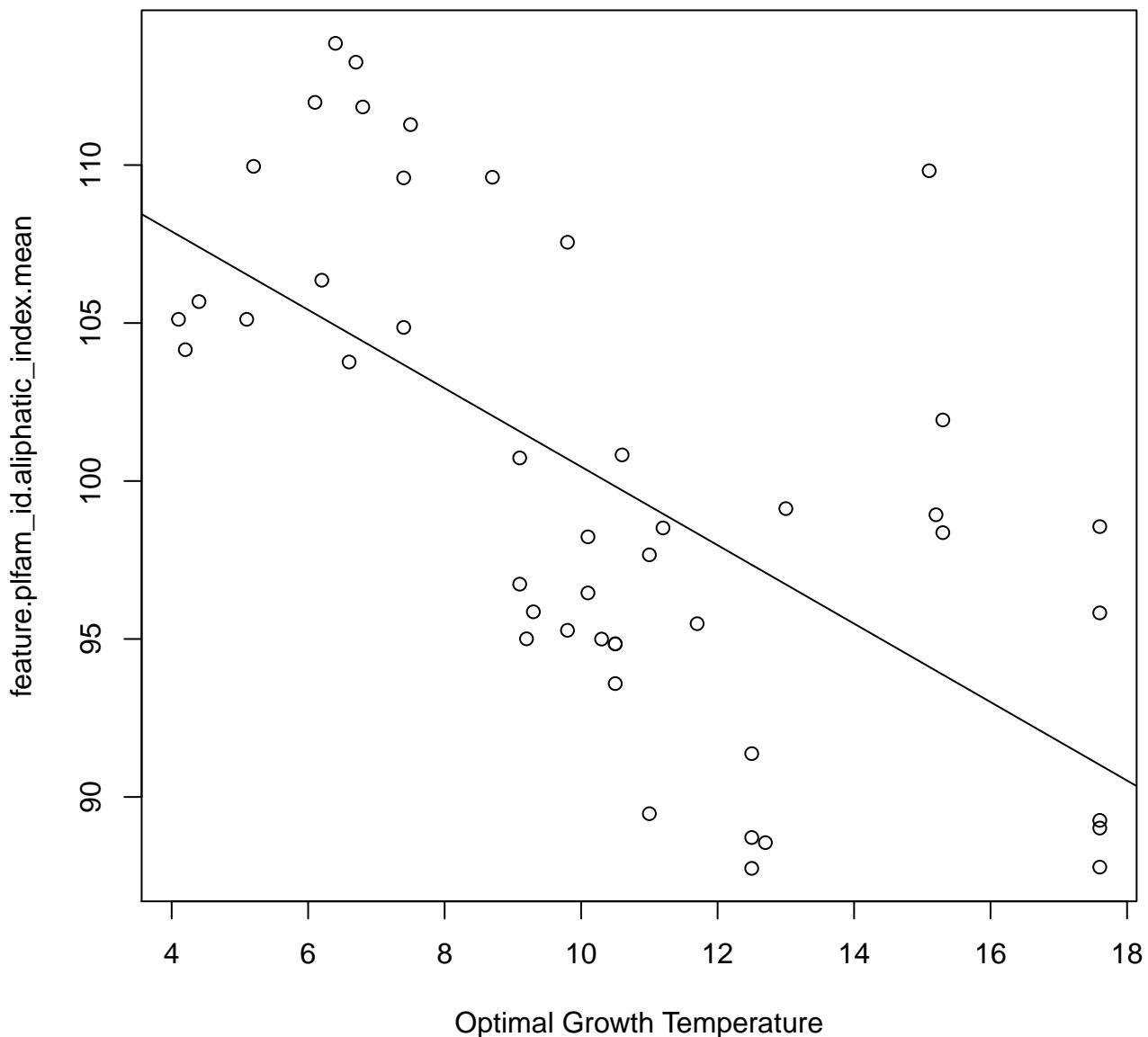
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Potential queD like 2



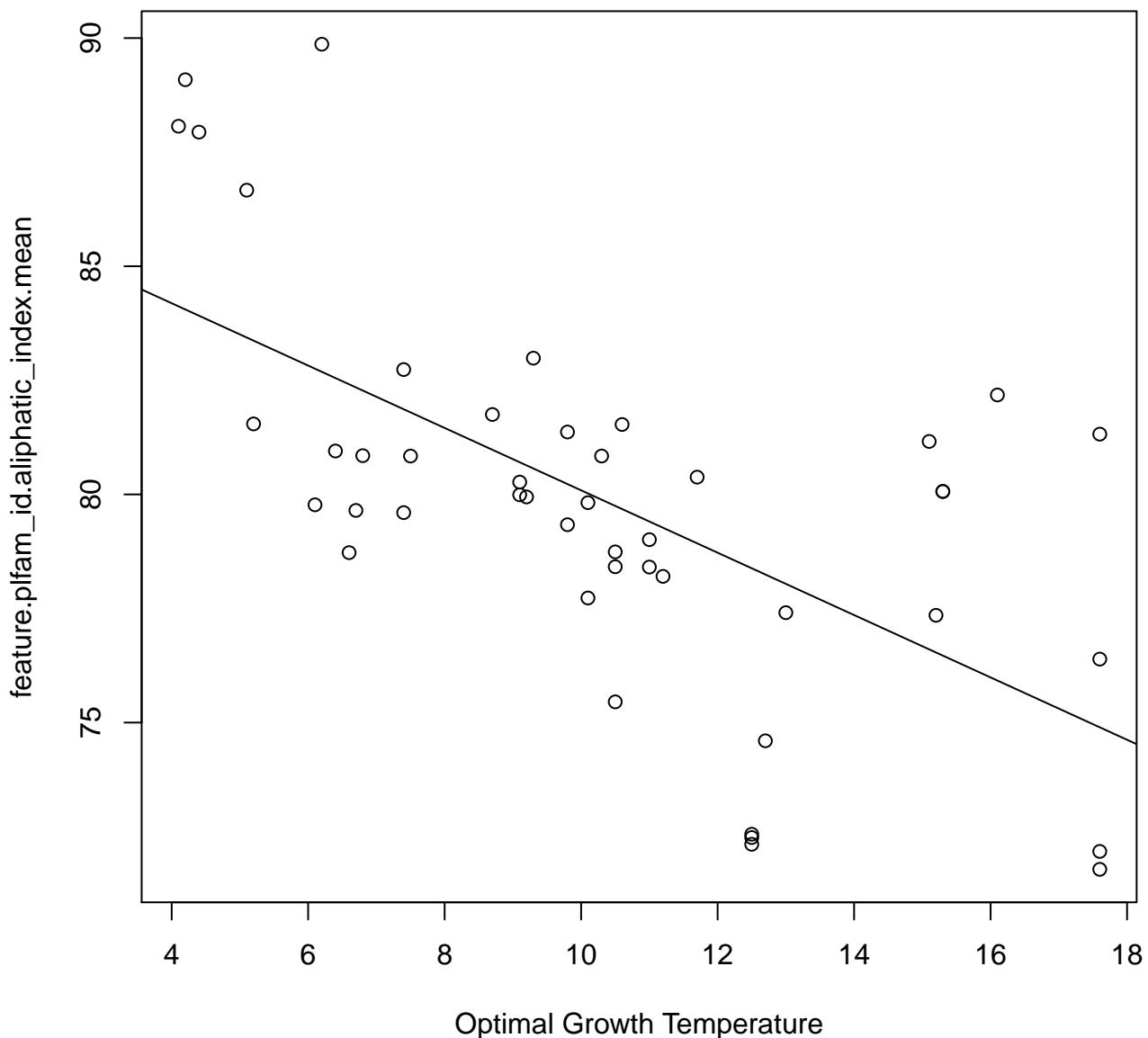
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LSU ribosomal protein L3p (L3e)



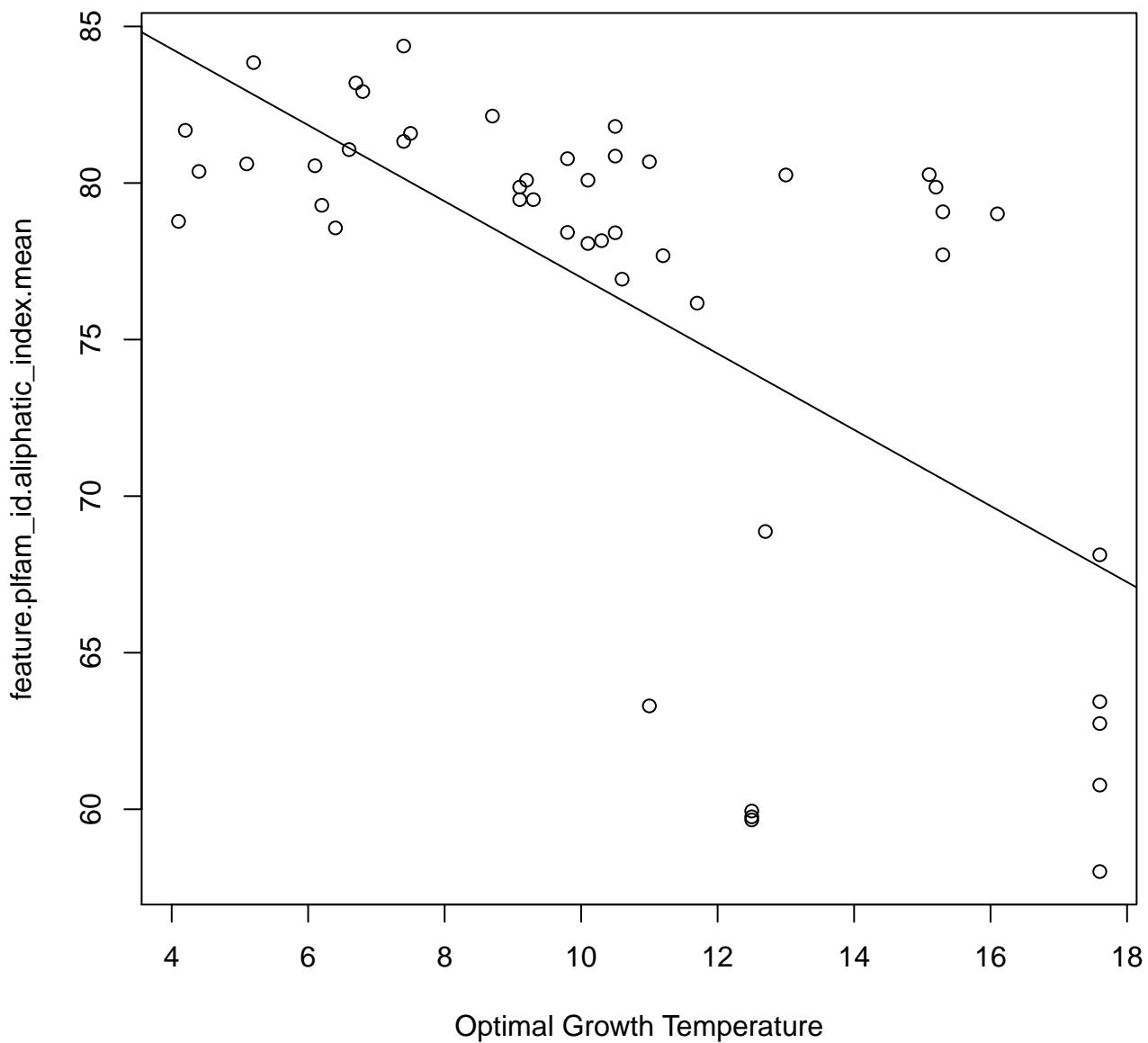
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Cys-tRNA(Pro) deacylase YbaK



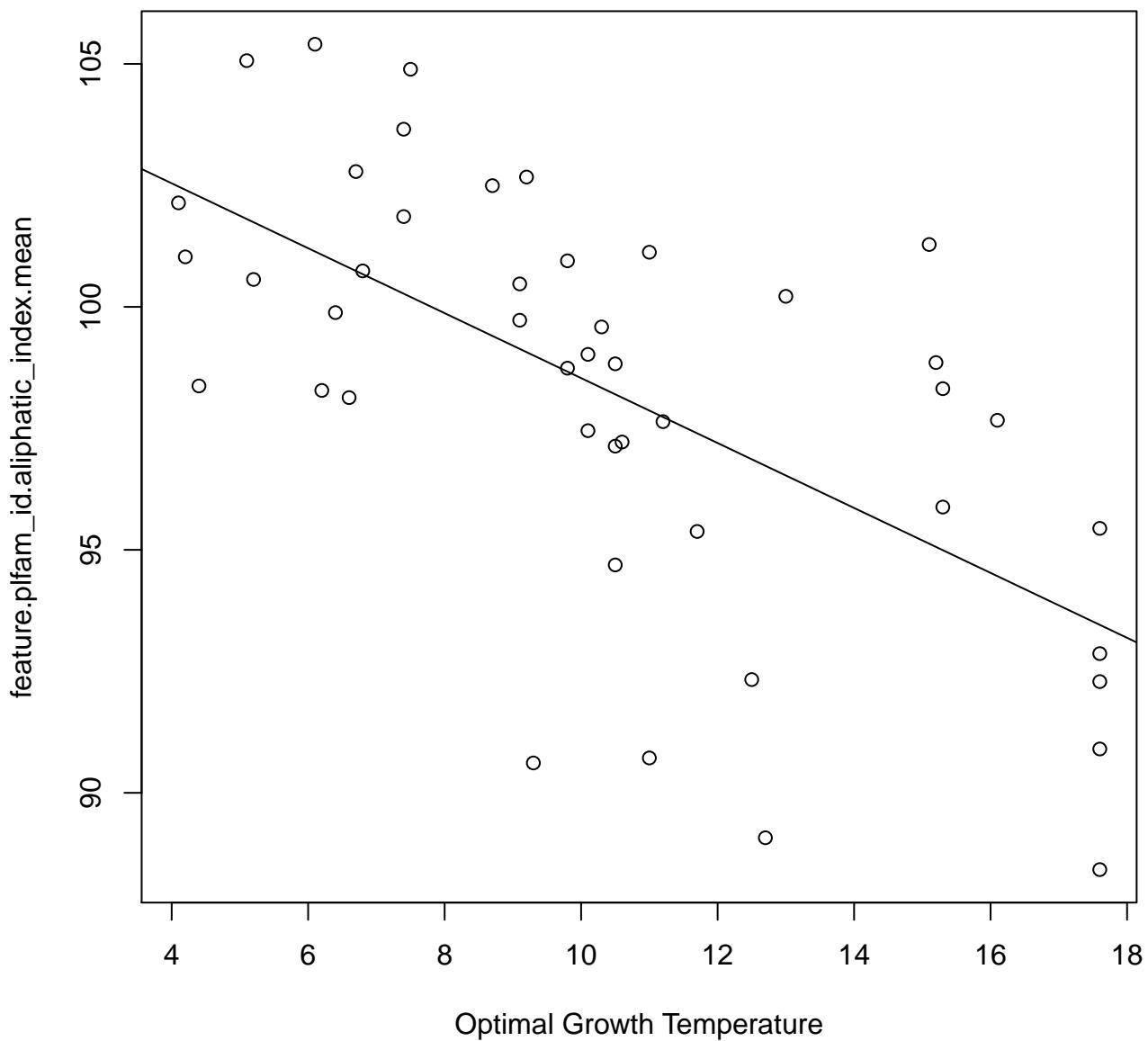
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3-deoxy-D-manno-octulose-2'-phosphate kinase (EC 2.7.1.166)



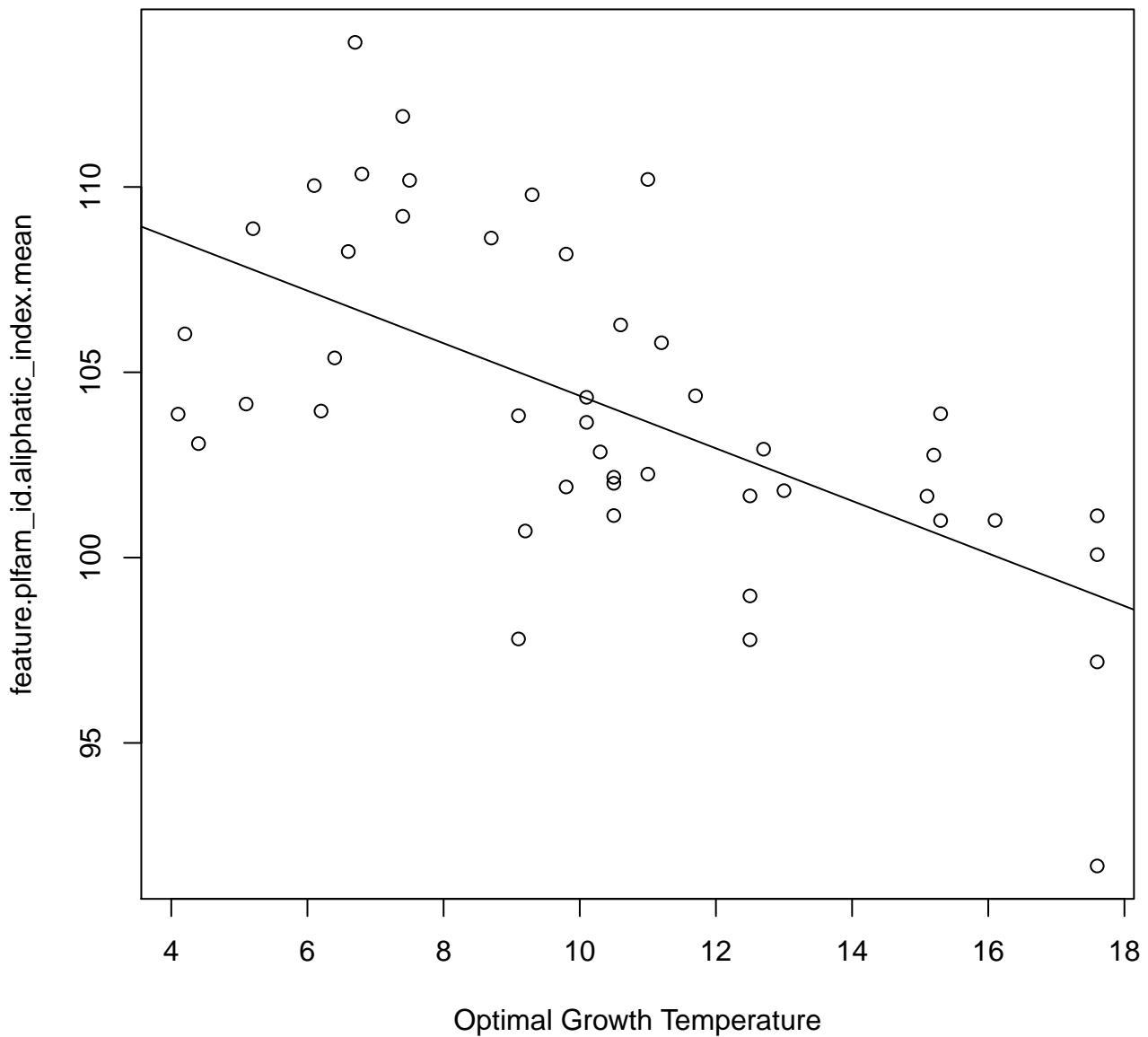
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PLF_28228_00001347
hypothetical protein



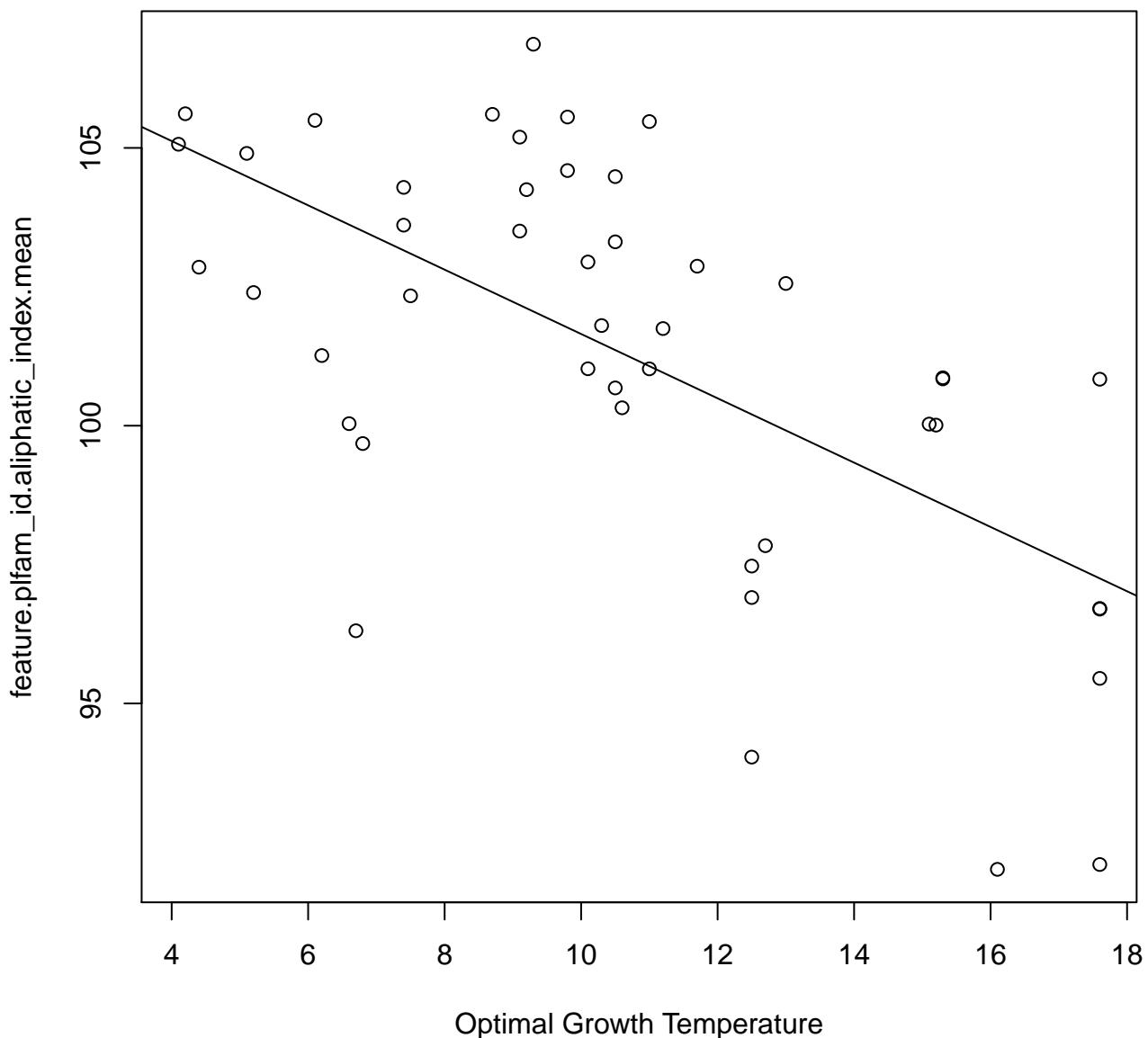
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Rod shape-determining protein MreC



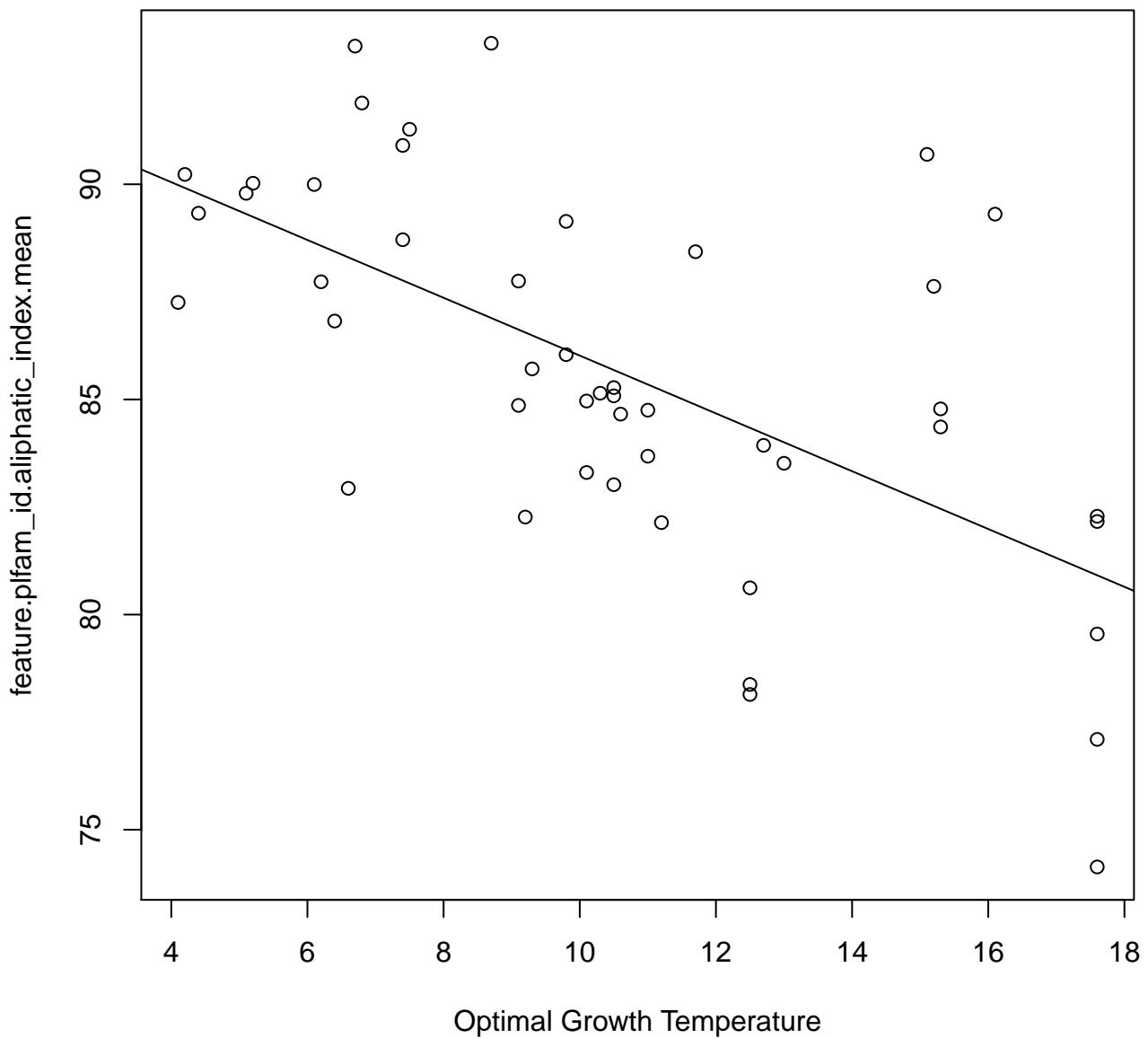
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DEDDh 3'-5' exonuclease domain of the epsilon subunit of DNA polymerase III



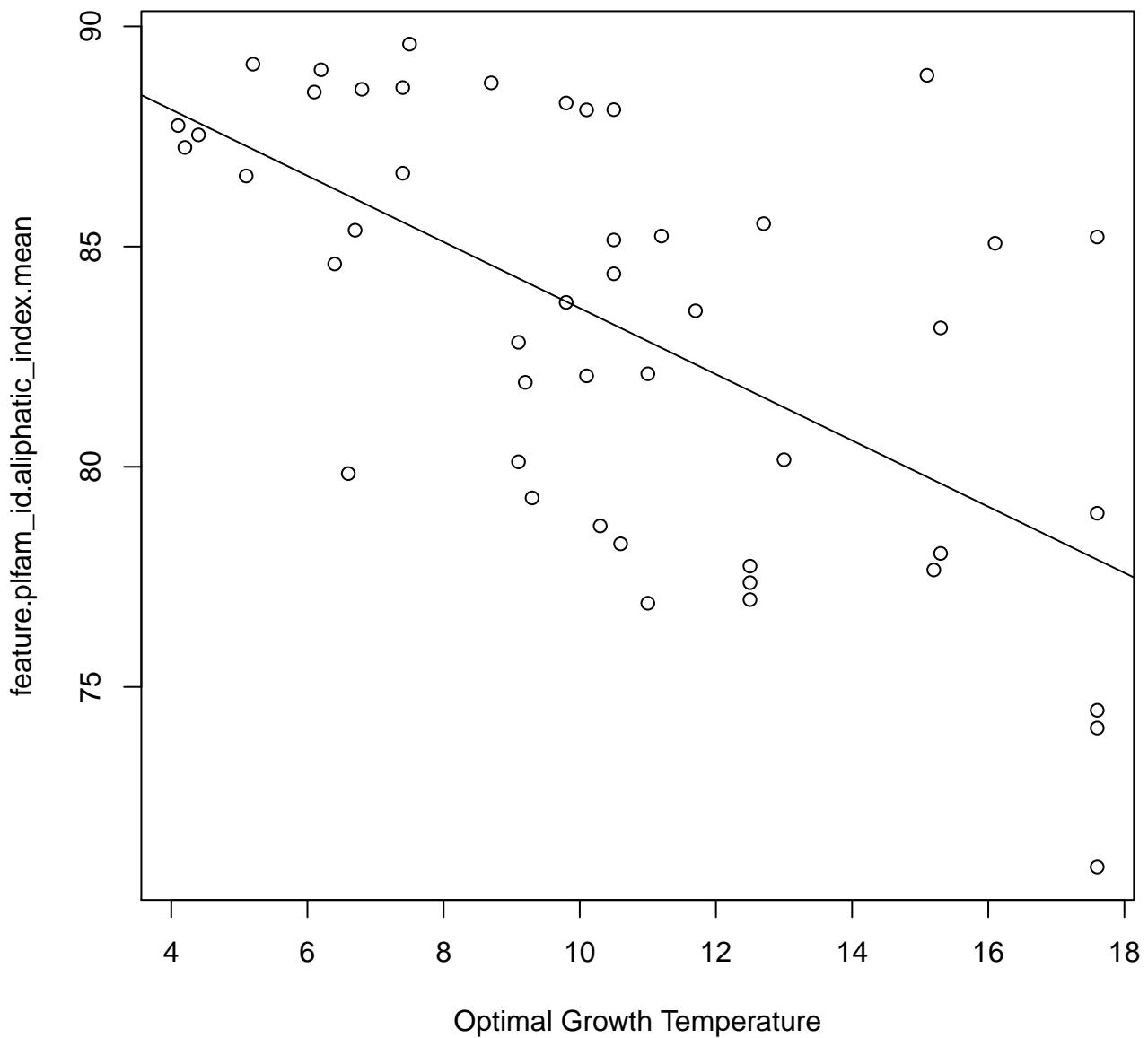
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PLF_28228_00001822
hypothetical protein



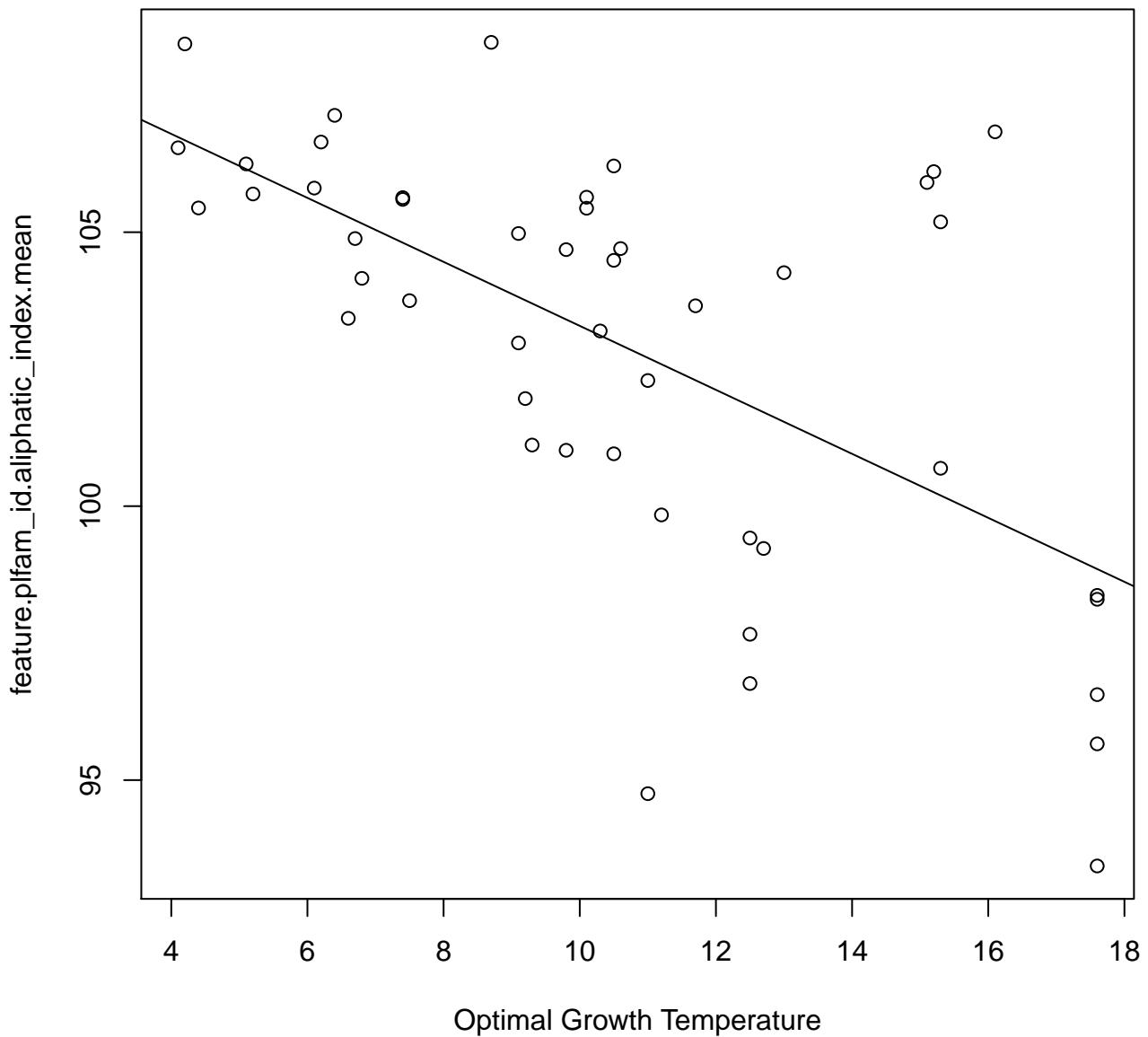
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UPF0115 protein YfcN



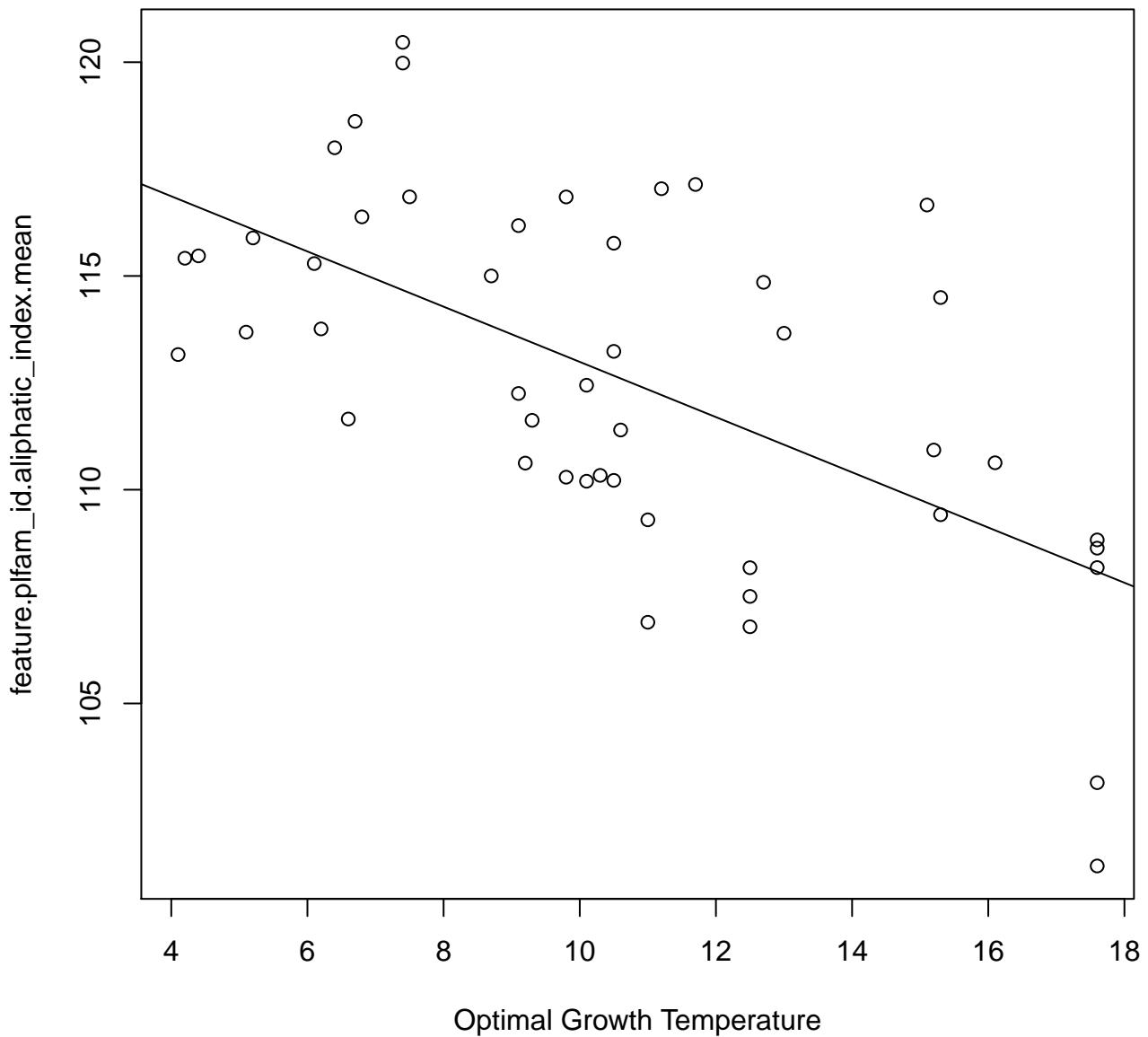
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Low molecular weight protein tyrosine phosphatase (EC 3.1.3.48)



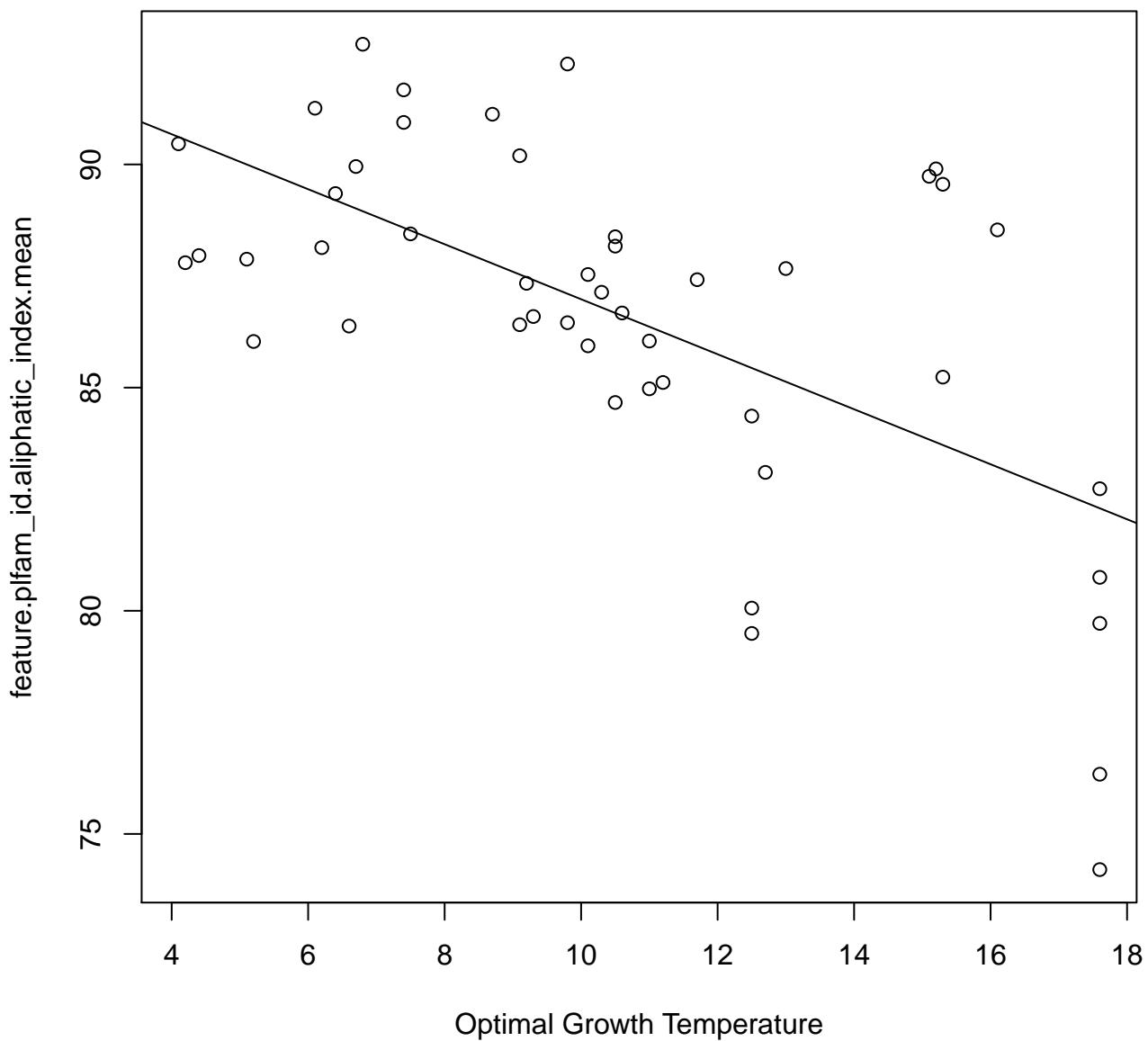
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4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)



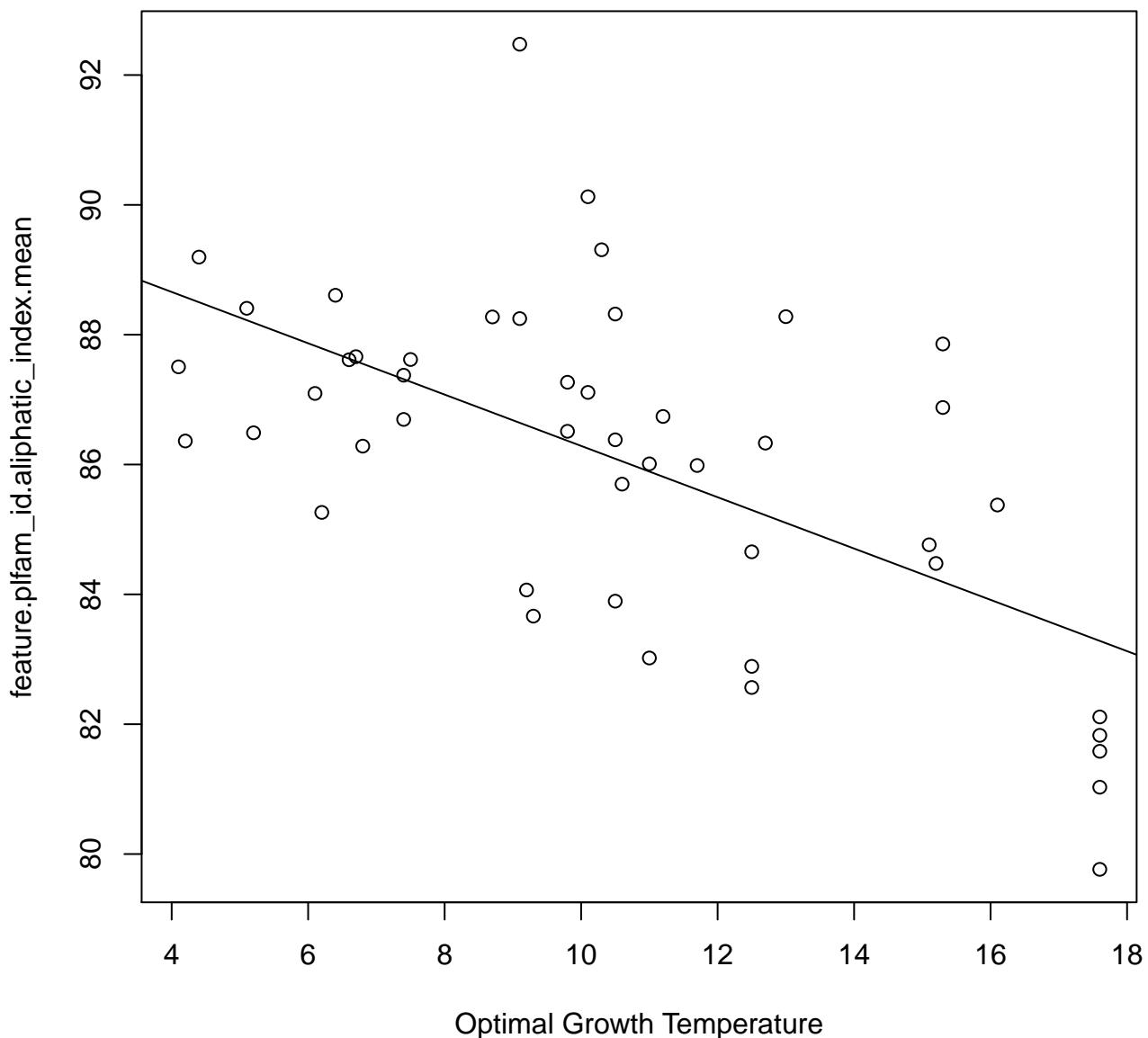
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Phospholipid ABC transporter substrate-binding protein MlaD



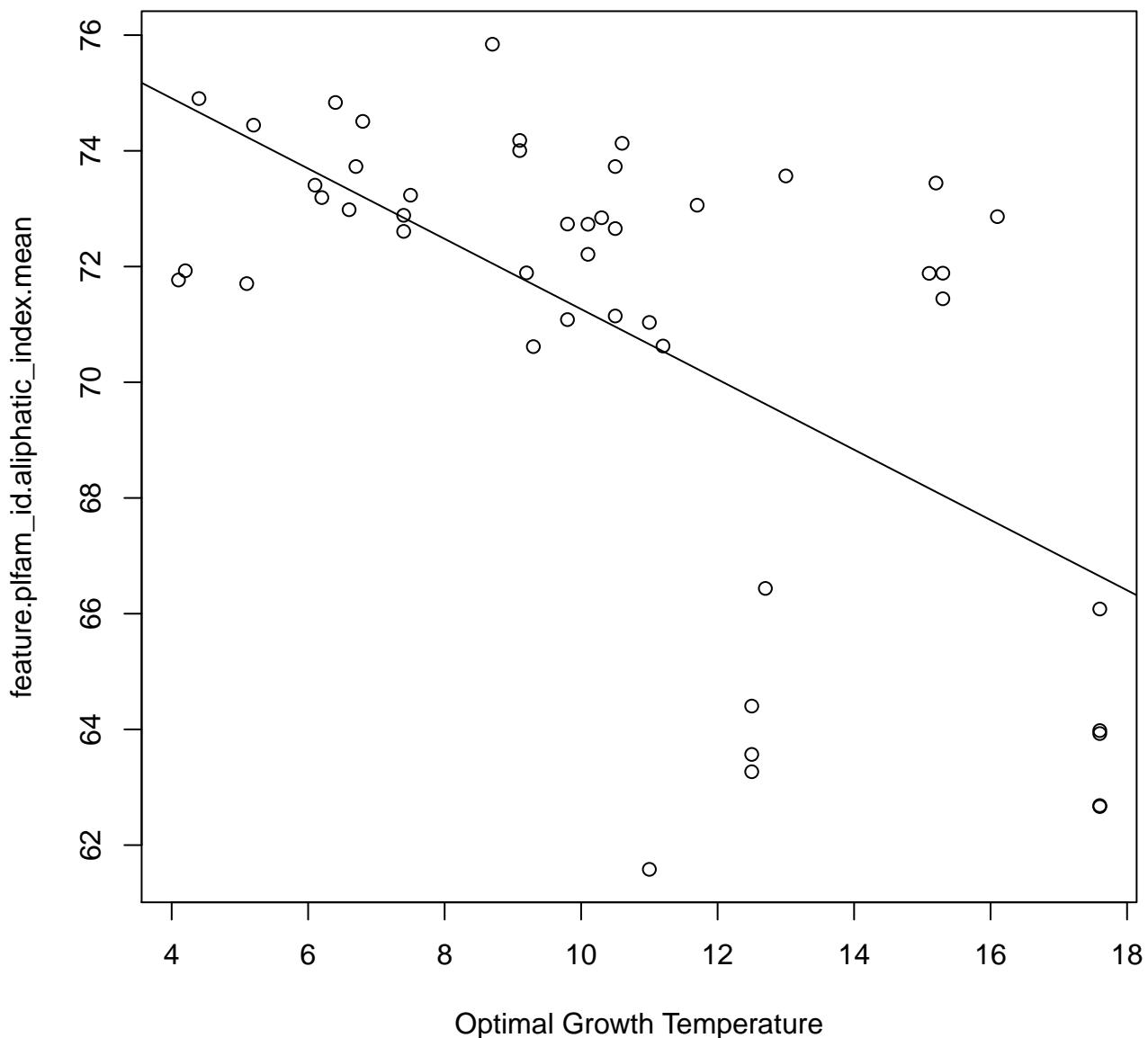
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Chaperone protein HscB



feature.plfam_id.aliphatic_index.mean
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23S rRNA (cytosine(1962)-C(5))-methyltransferase (EC 2.1.1.191)



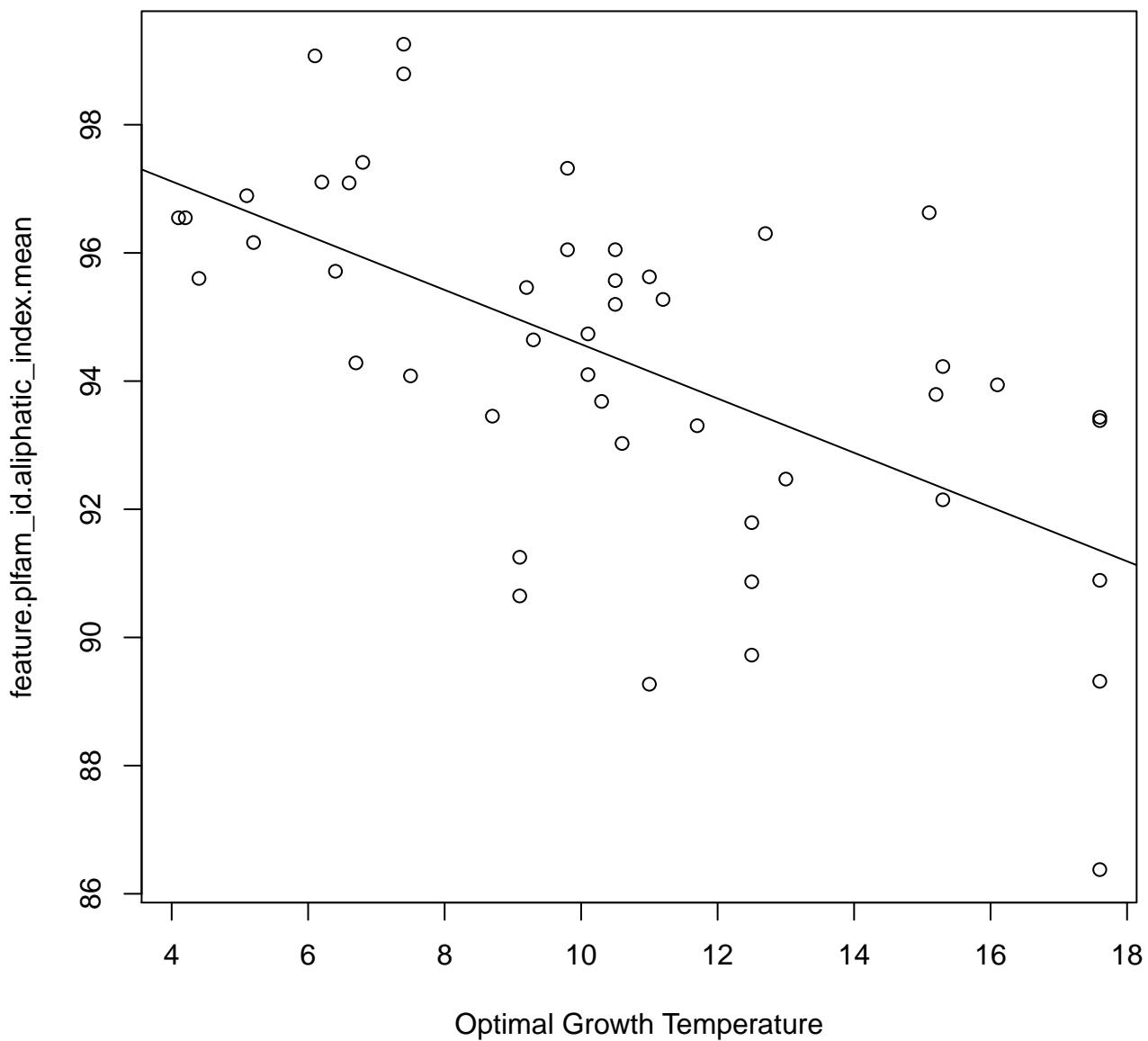
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LSU rRNA pseudouridine(2605) synthase (EC 5.4.99.22)



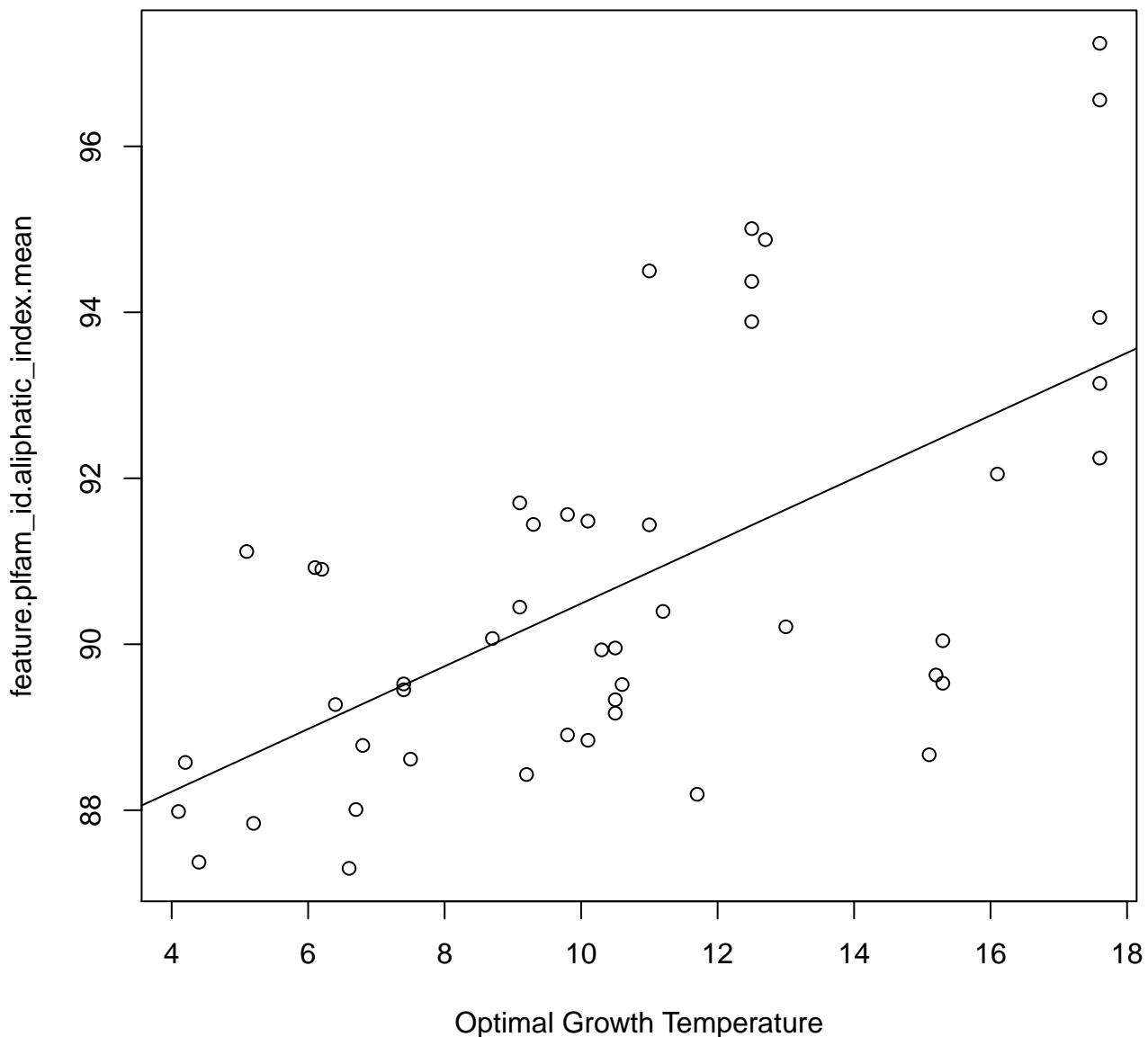
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PLF_28228_00000565

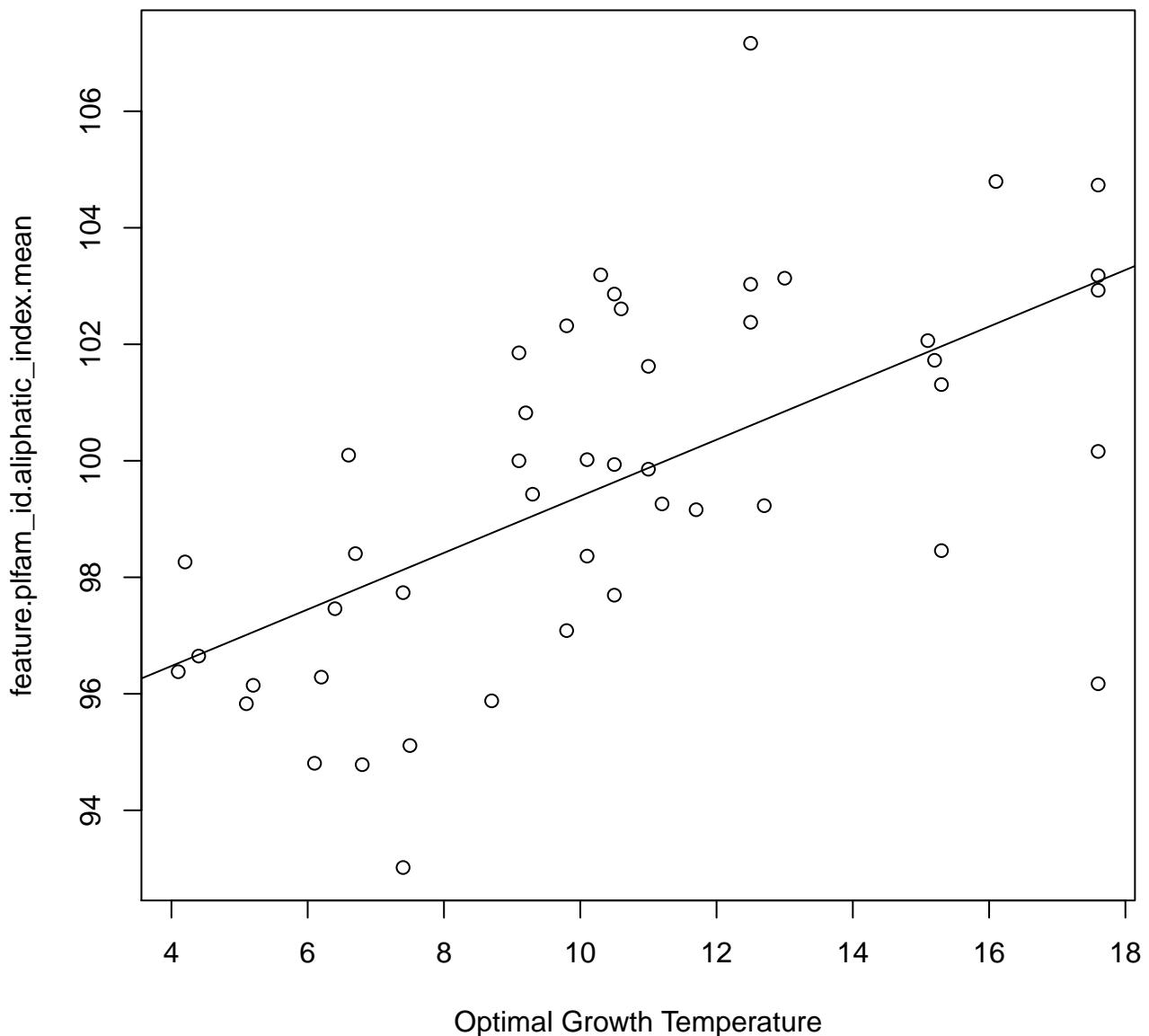
Chorismate mutase I (EC 5.4.99.5) / Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC 1.3.1.43)



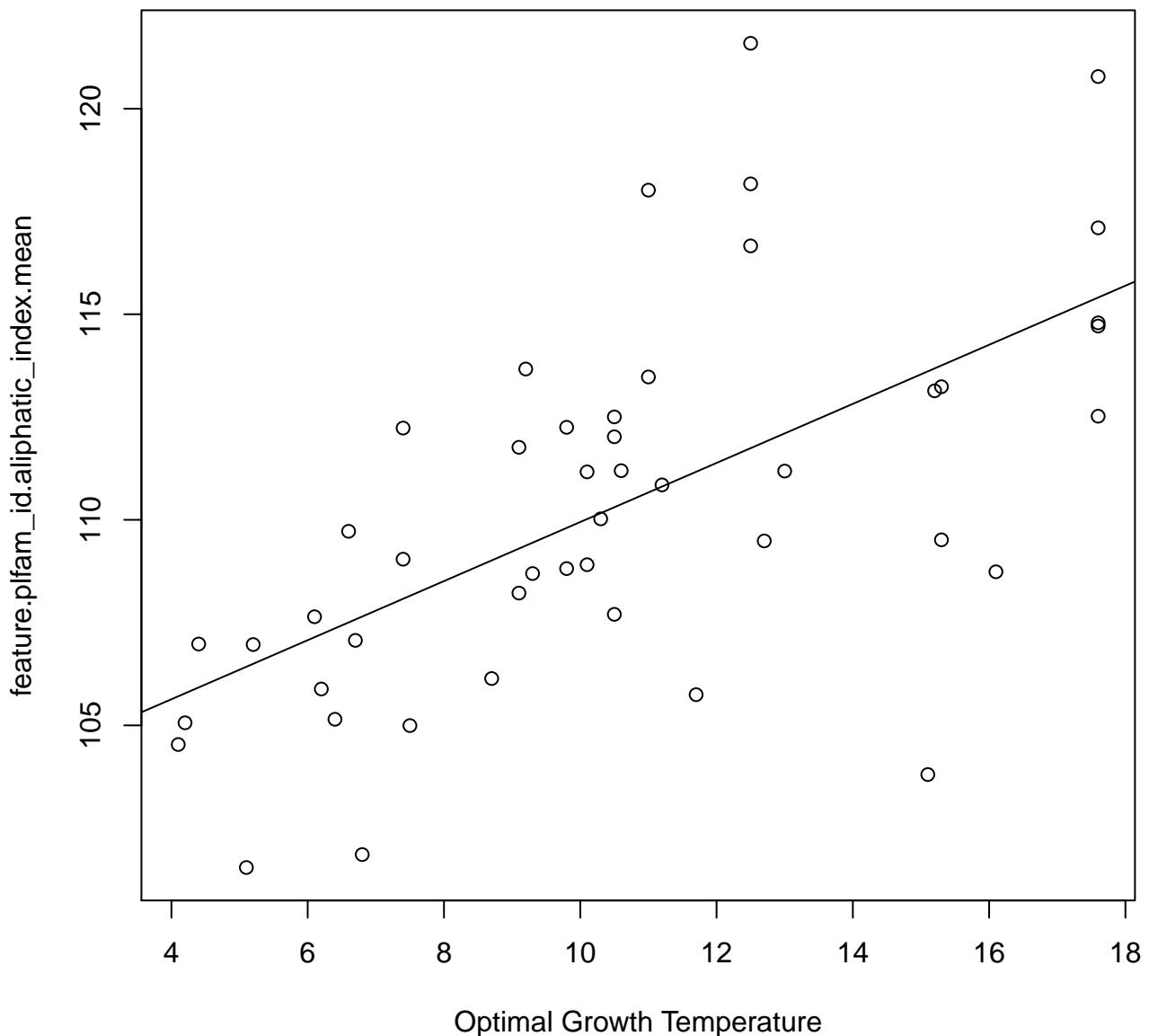
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Protein kinase



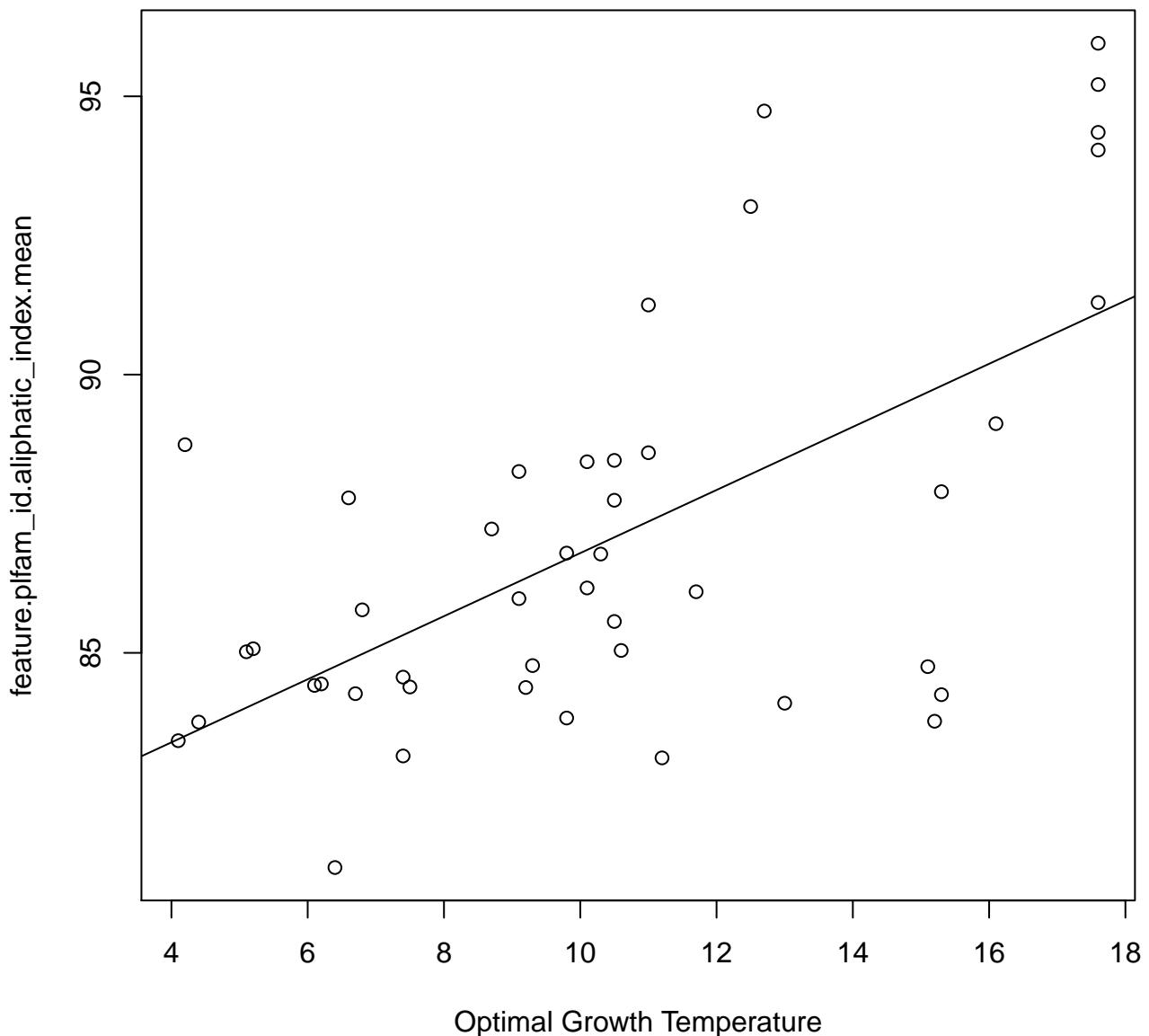
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UPF0758 family protein



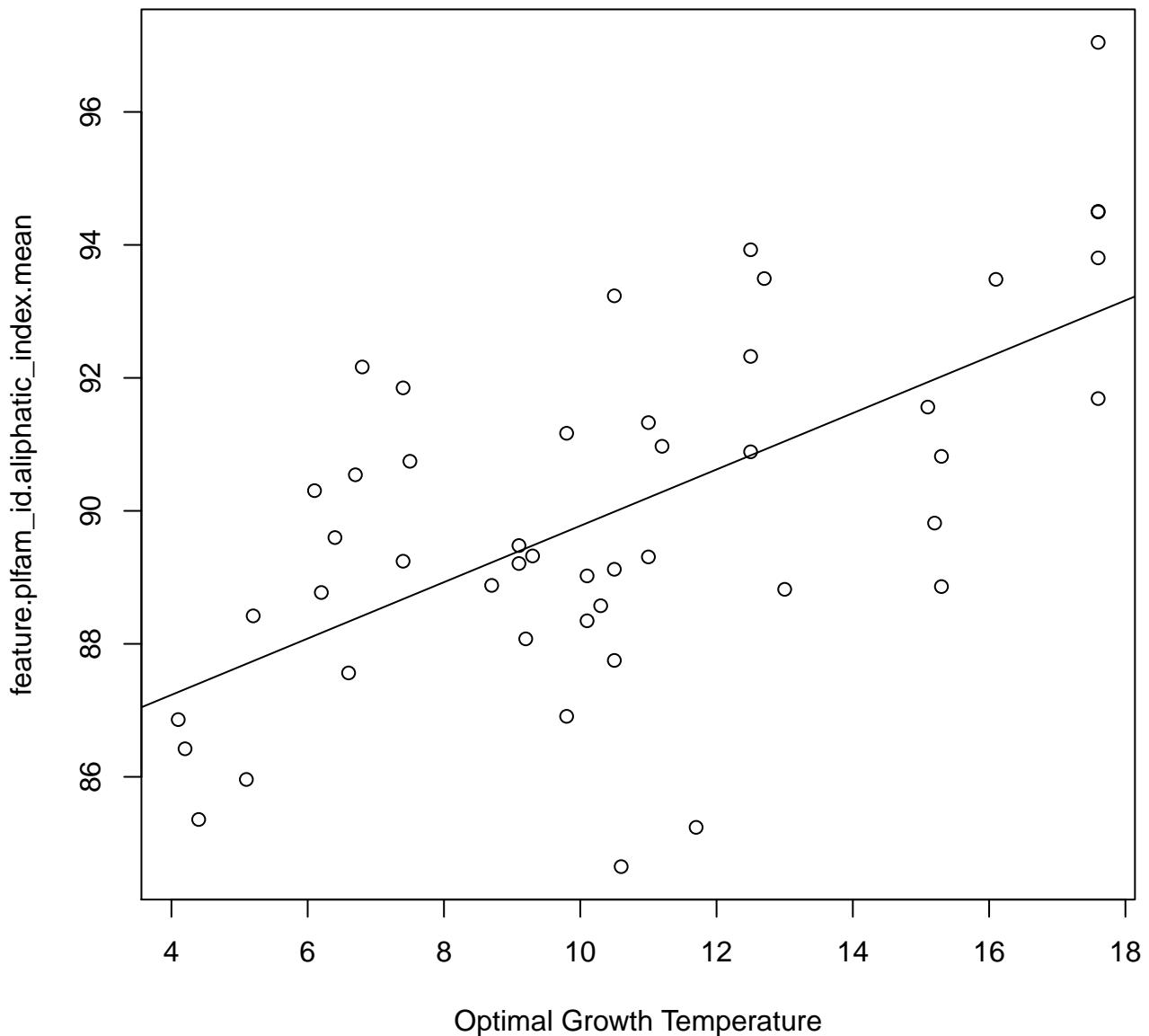
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UPF0352 protein YejL



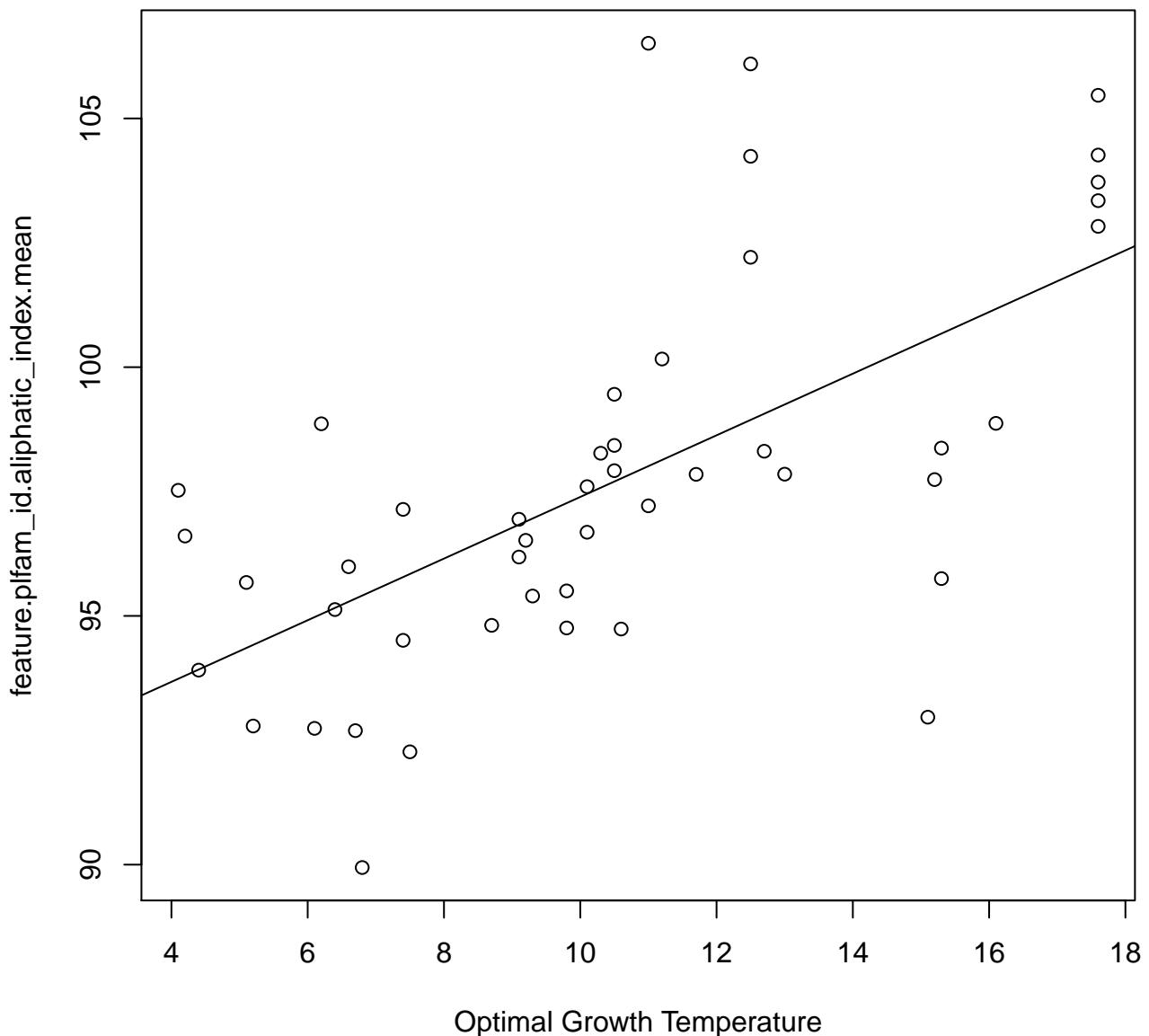
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PLF_28228_00028000
Ribosome association toxin RatA



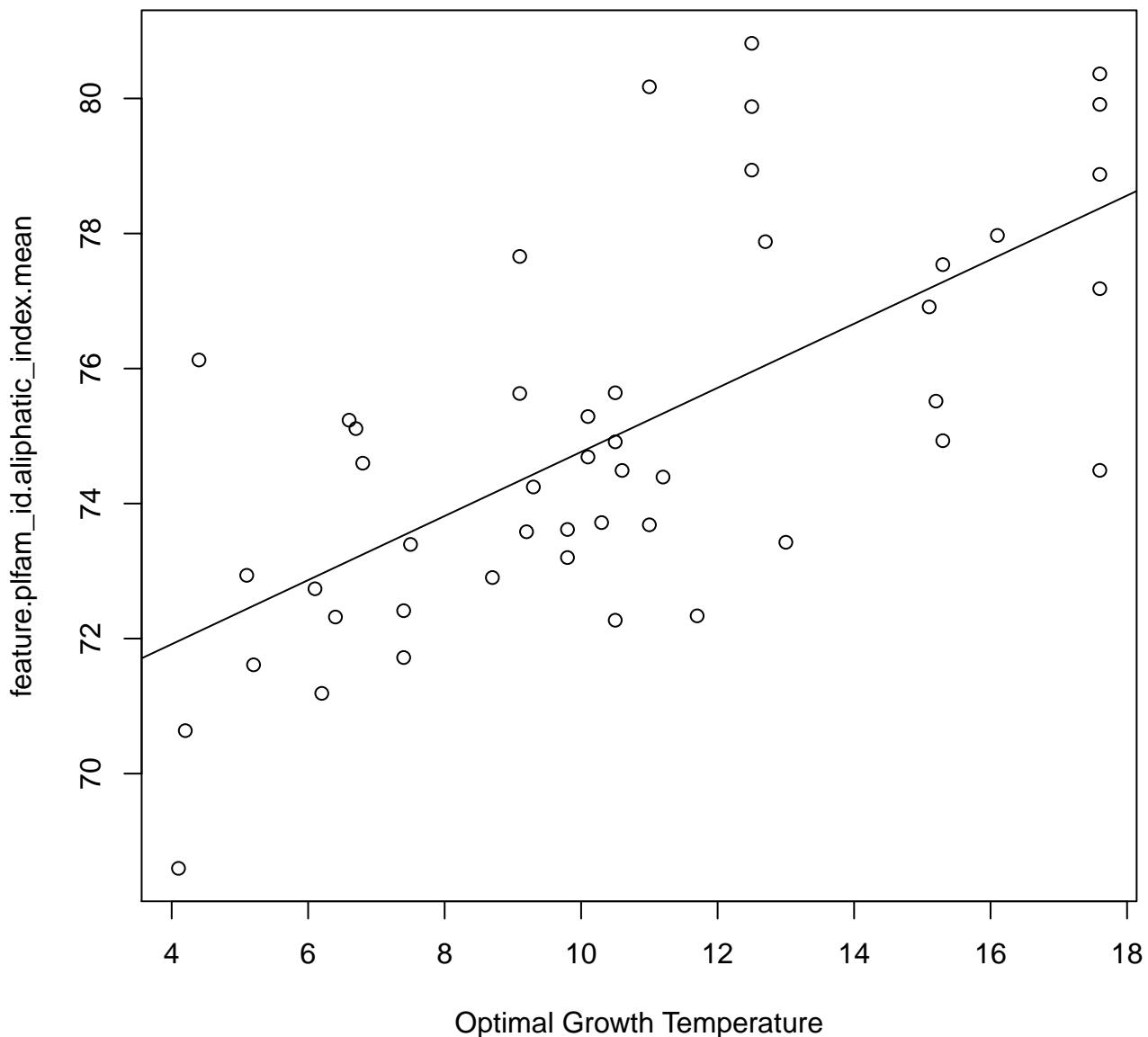
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PLF_28228_00001095
RidA/YER057c/UK114 superfamily protein



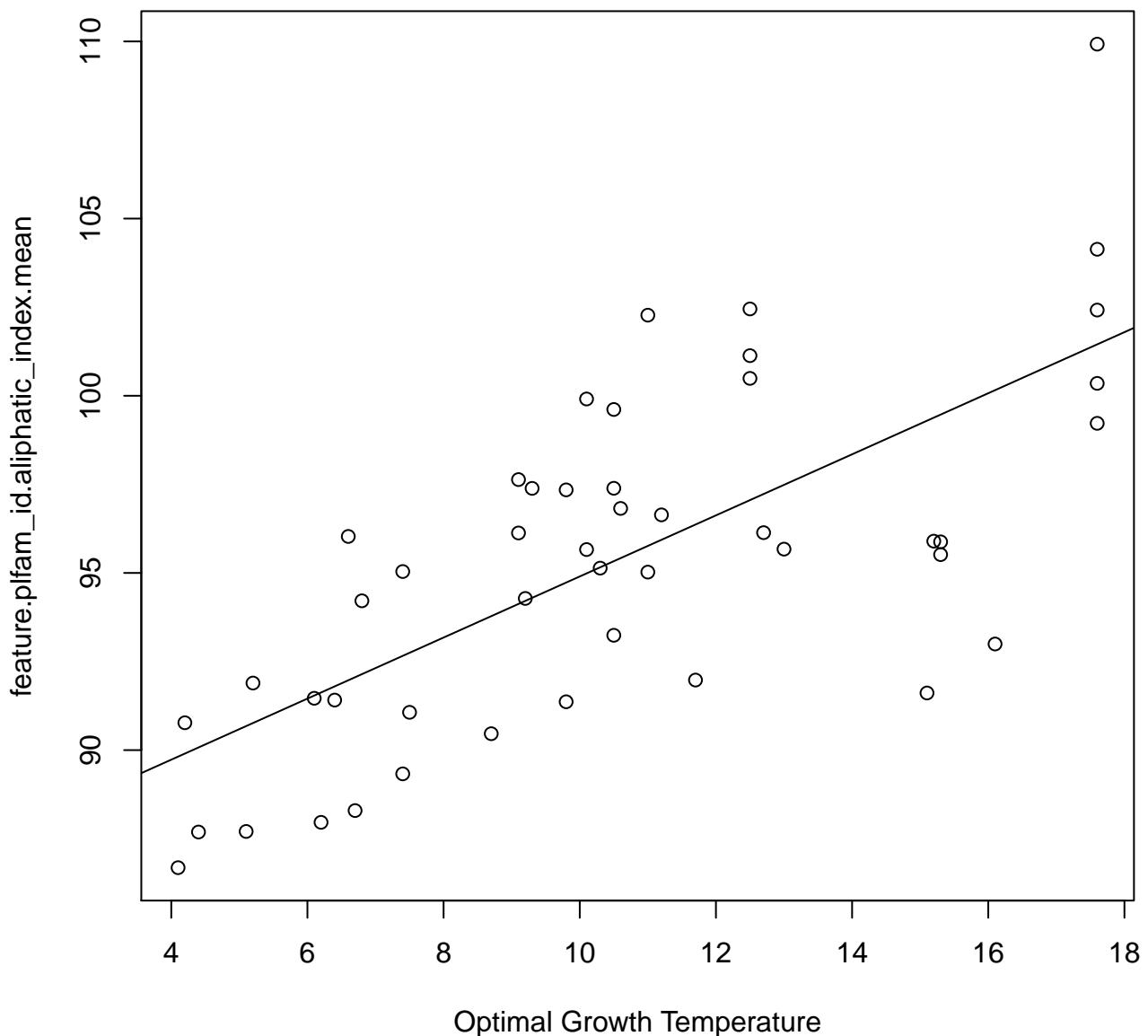
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6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



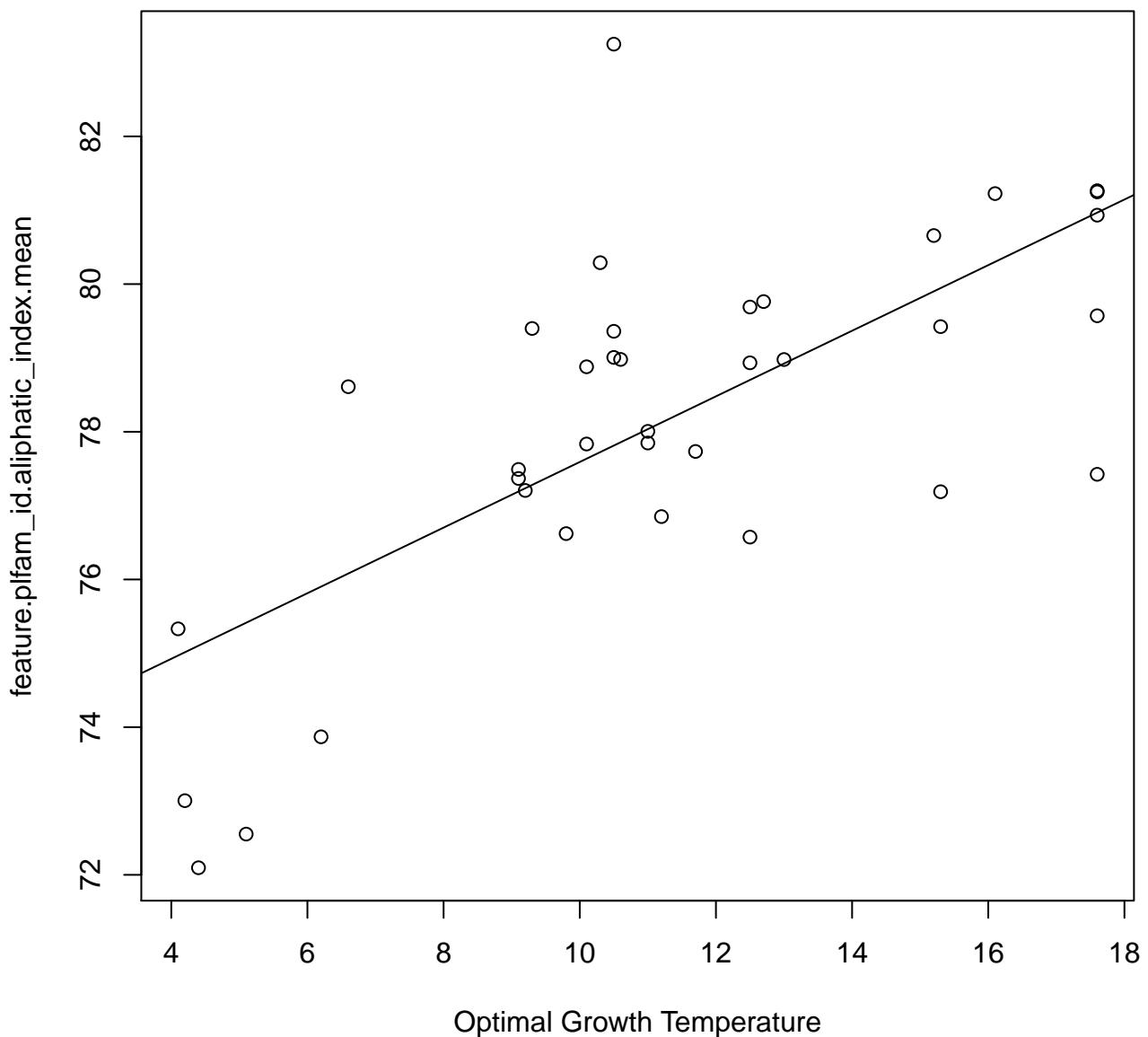
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PLF_28228_00000483
Flagellar basal-body rod protein FlgF



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PLF_28228_00000786
Esterase ybfF (EC 3.1.-.-)



feature.plfam_id.aliphatic_index.mean
PLF_28228_00001844
Flagellar protein FliJ



feature.plfam_id.aliphatic_index.mean
PLF_28228_00002434
hypothetical protein

