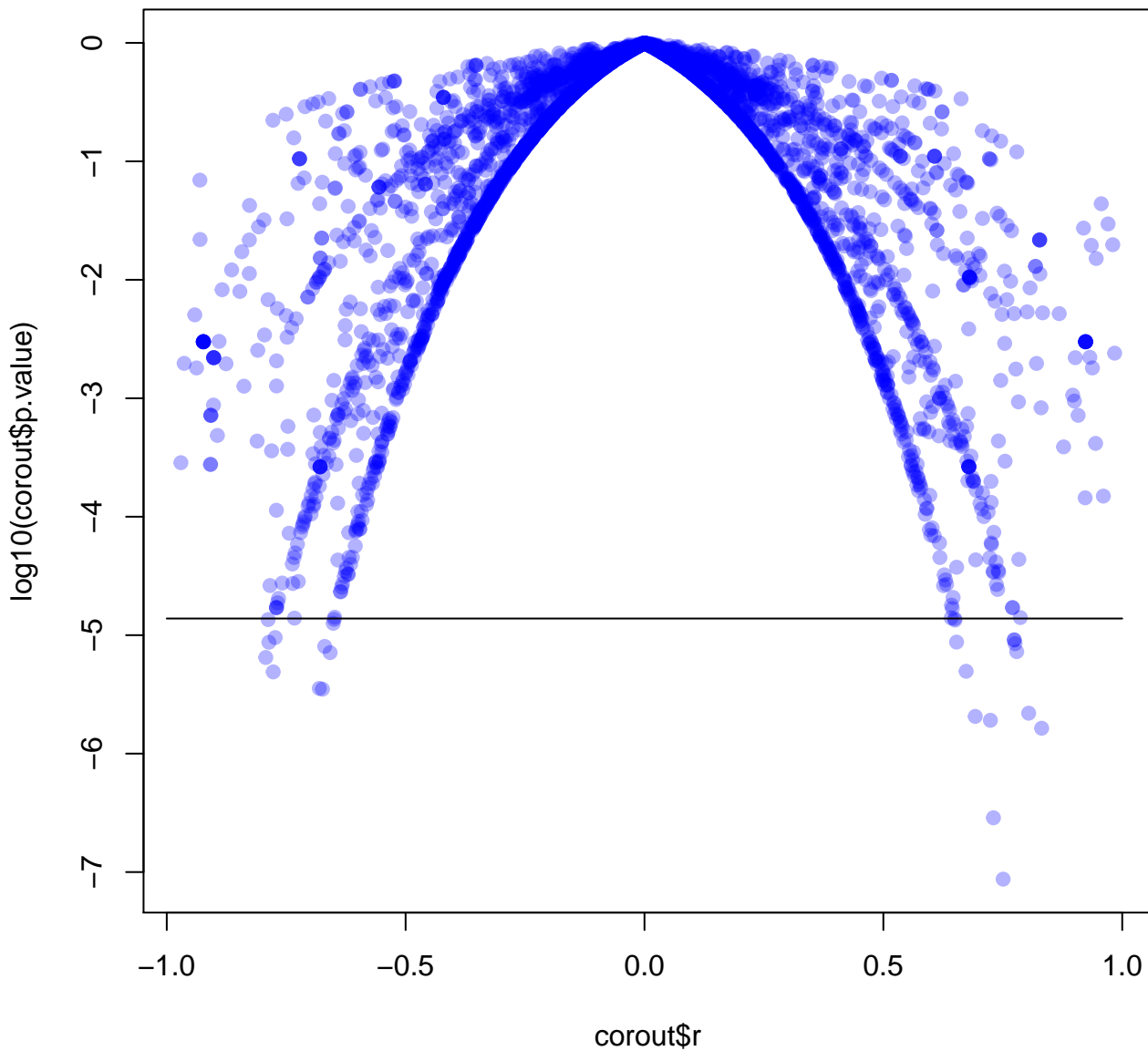


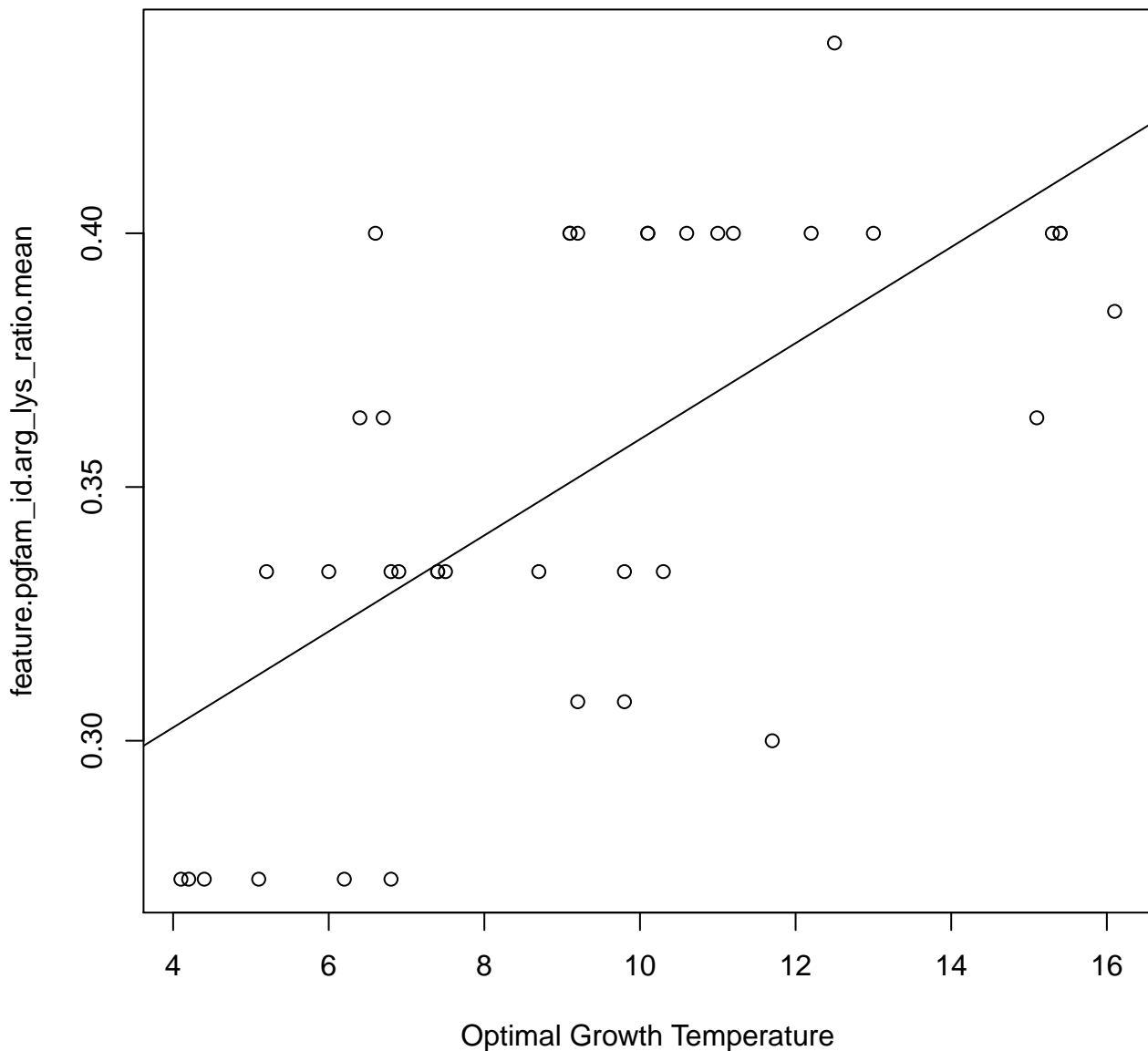
feature.pgfam_id.arg_lys_ratio.mean



feature.pgfam_id.arg_lys_ratio.mean

PGF_00018430

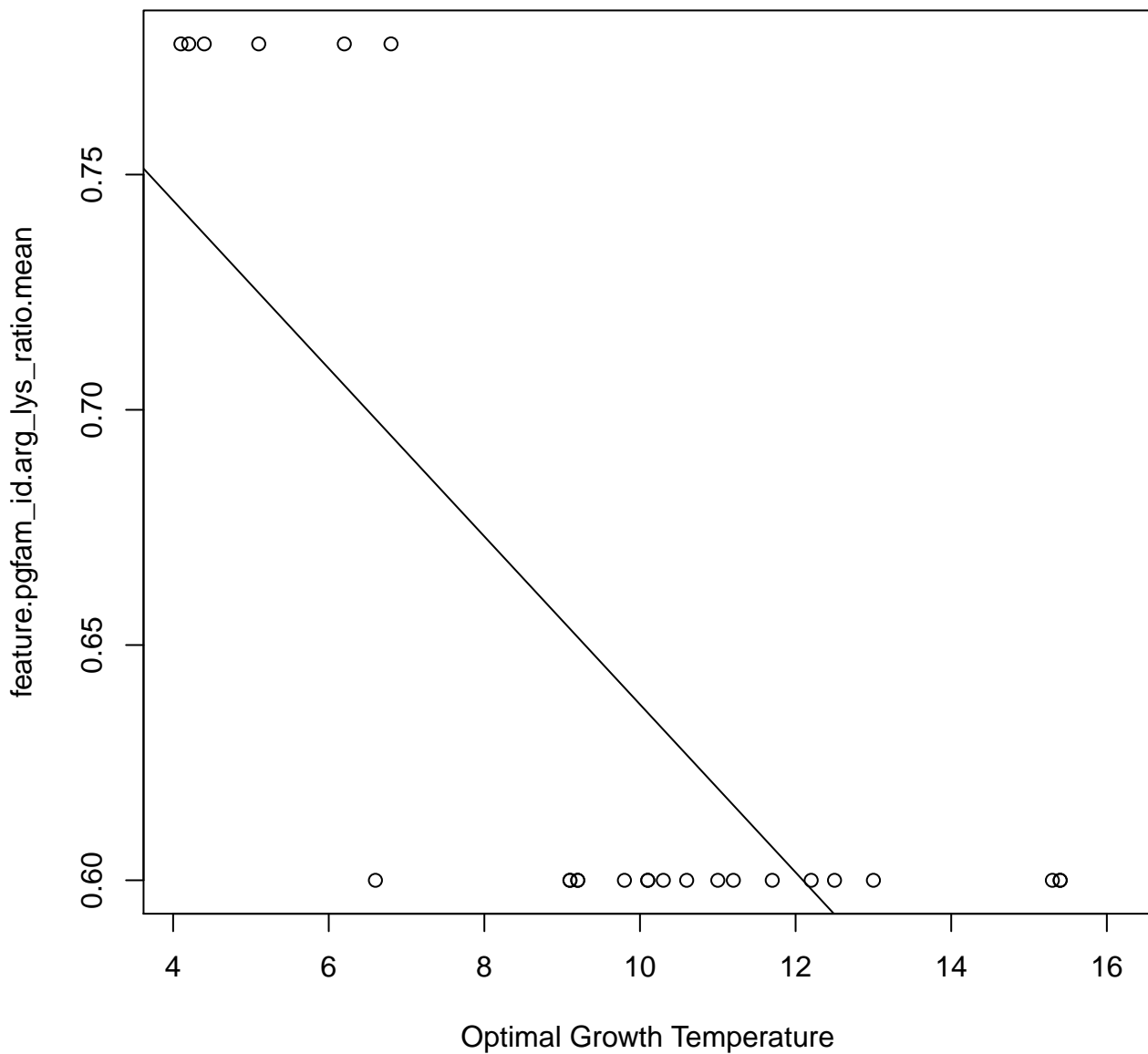
MSHA pilin protein MshB



feature.pgfam_id.arg_lys_ratio.mean

PGF_00044582

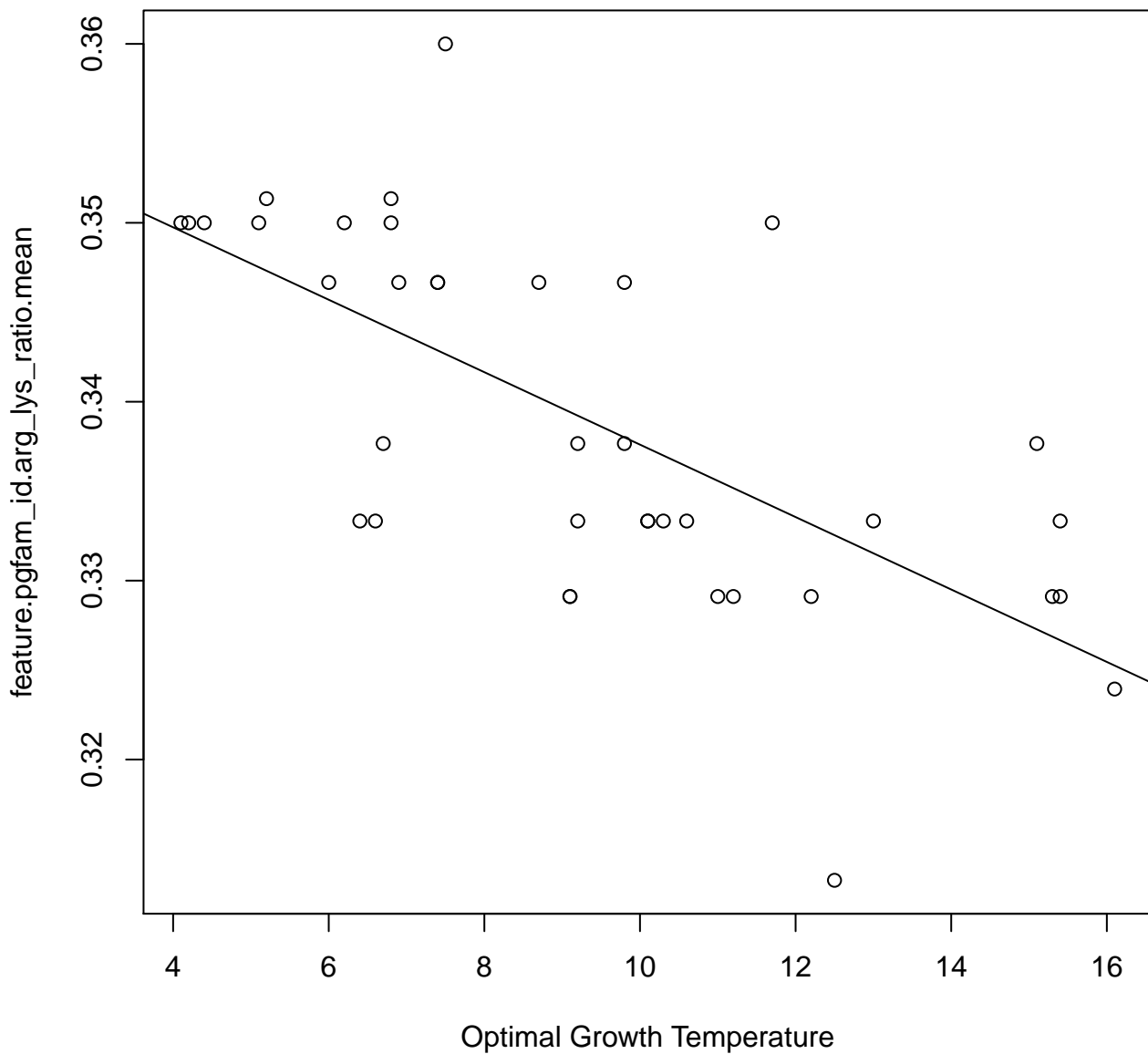
Putative transmembrane protein



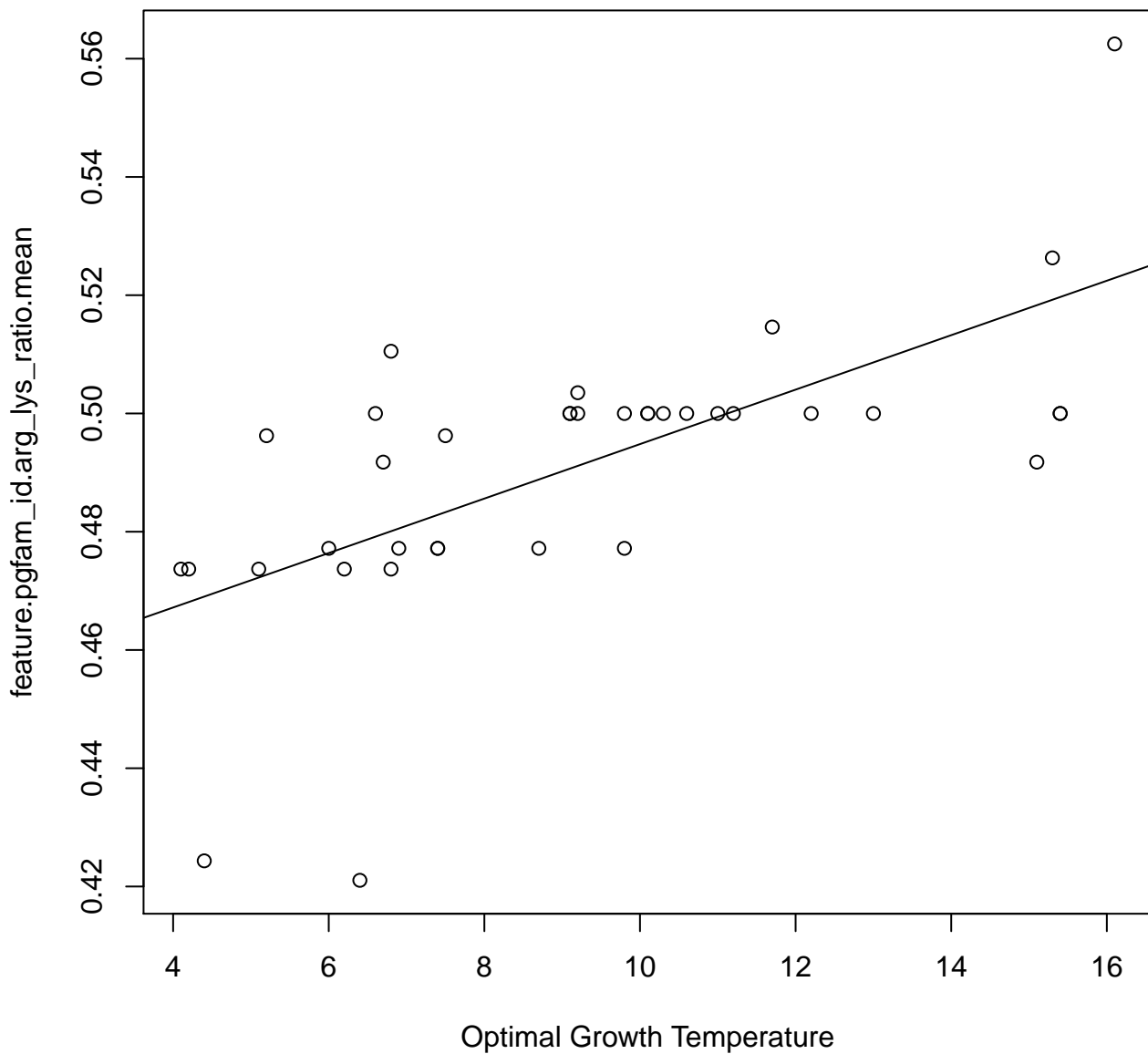
feature.pgfam_id.arg_lys_ratio.mean

PGF_00047484

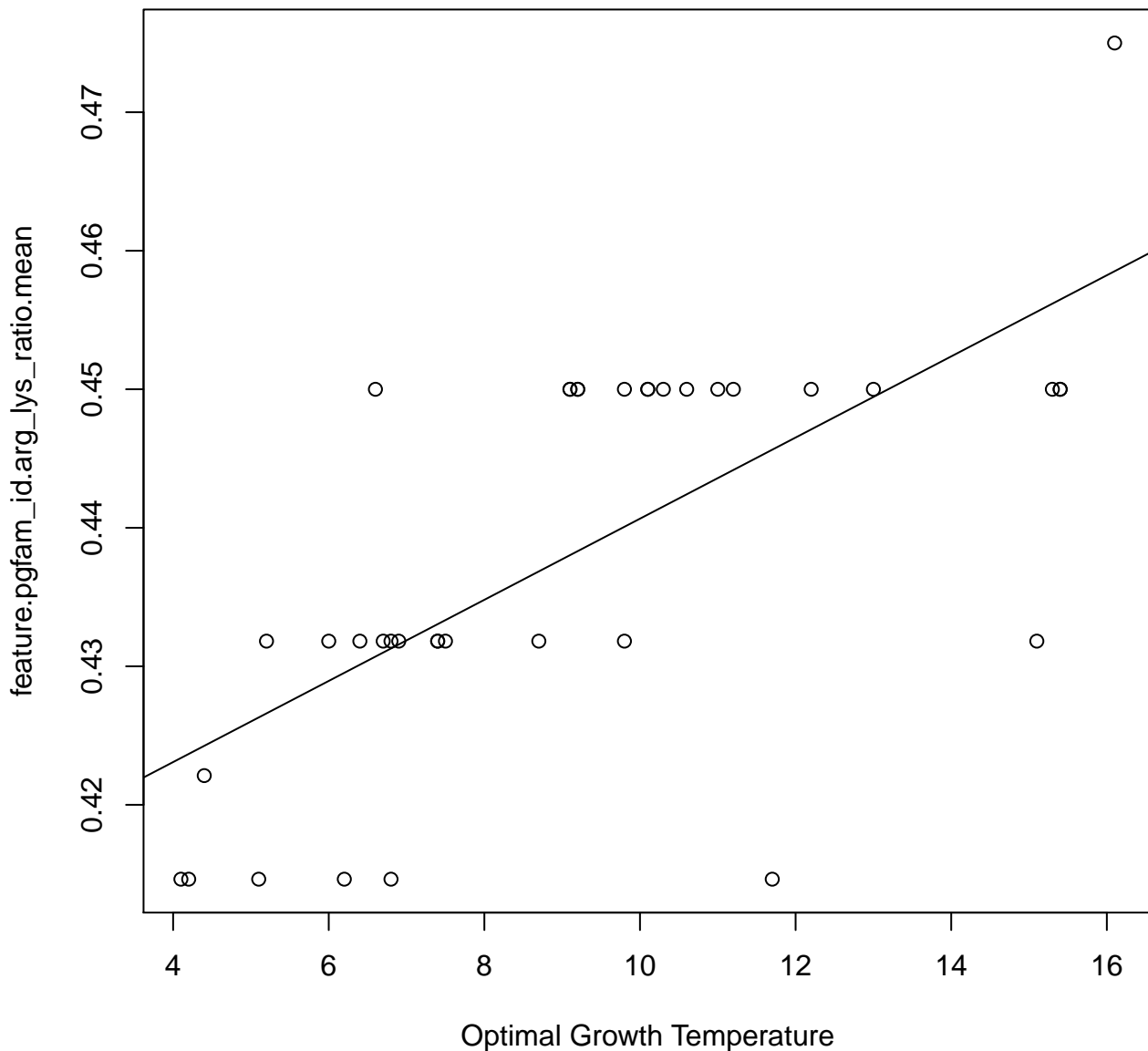
Related to collagenase



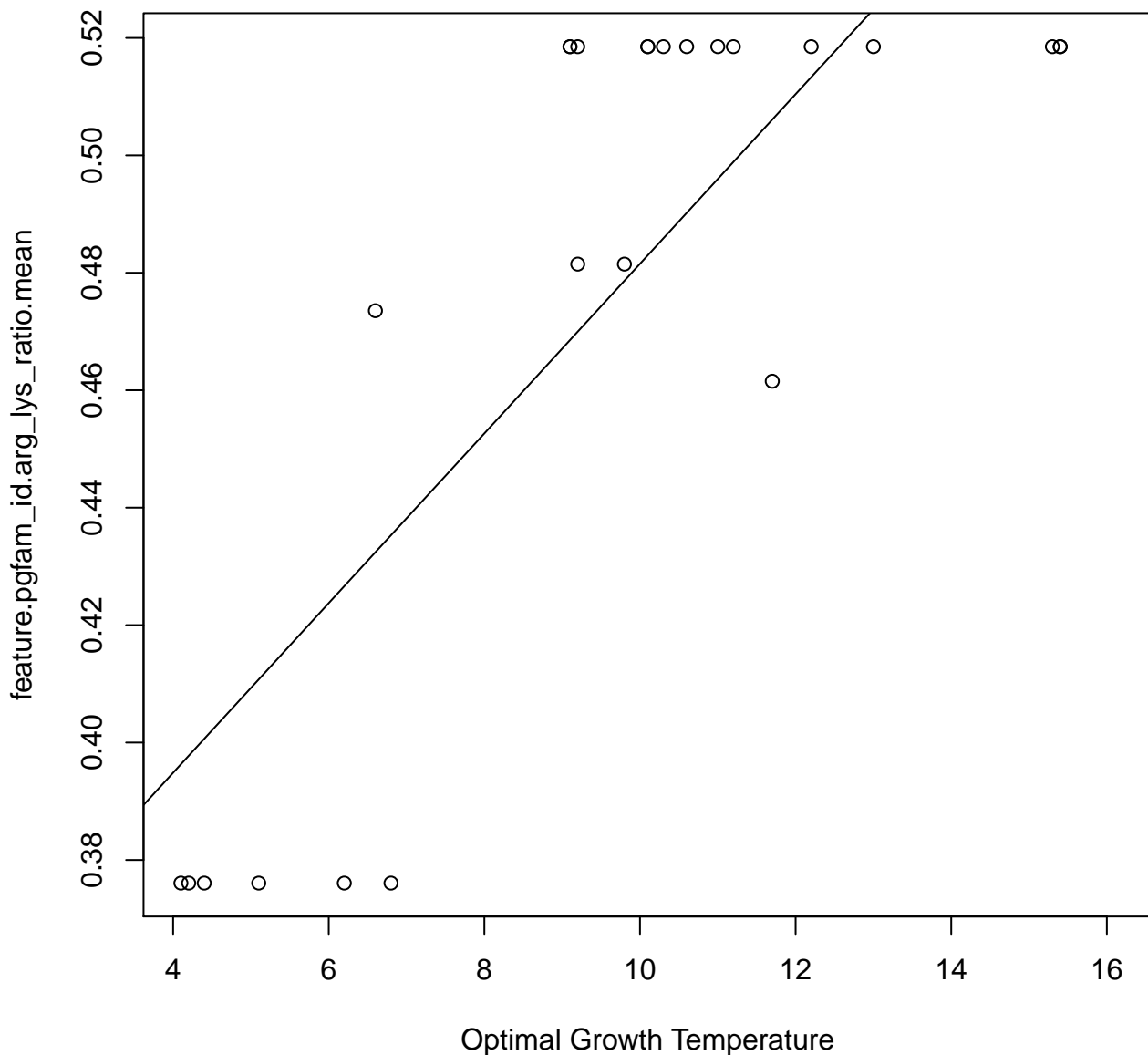
feature.pgfam_id.arg_lys_ratio.mean
PGF_00808195
DNA protection during starvation protein



feature.pgfam_id.arg_lys_ratio.mean
PGF_01137124
Phosphoglucosamine mutase (EC 5.4.2.10)



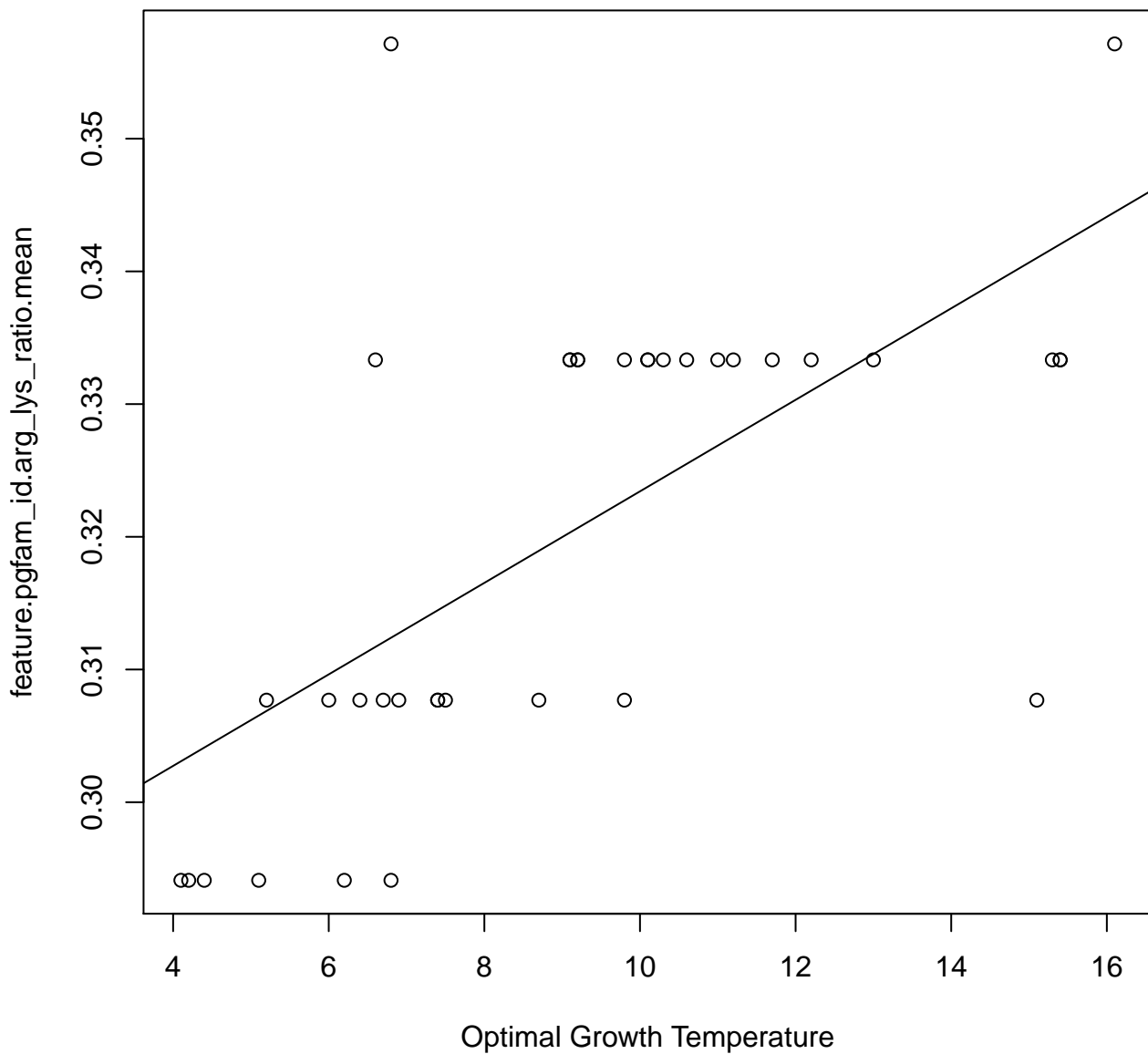
feature.pgfam_id.arg_lys_ratio.mean
PGF_01481272
Chemotaxis protein CheD



feature.pgfam_id.arg_lys_ratio.mean

PGF_02501663

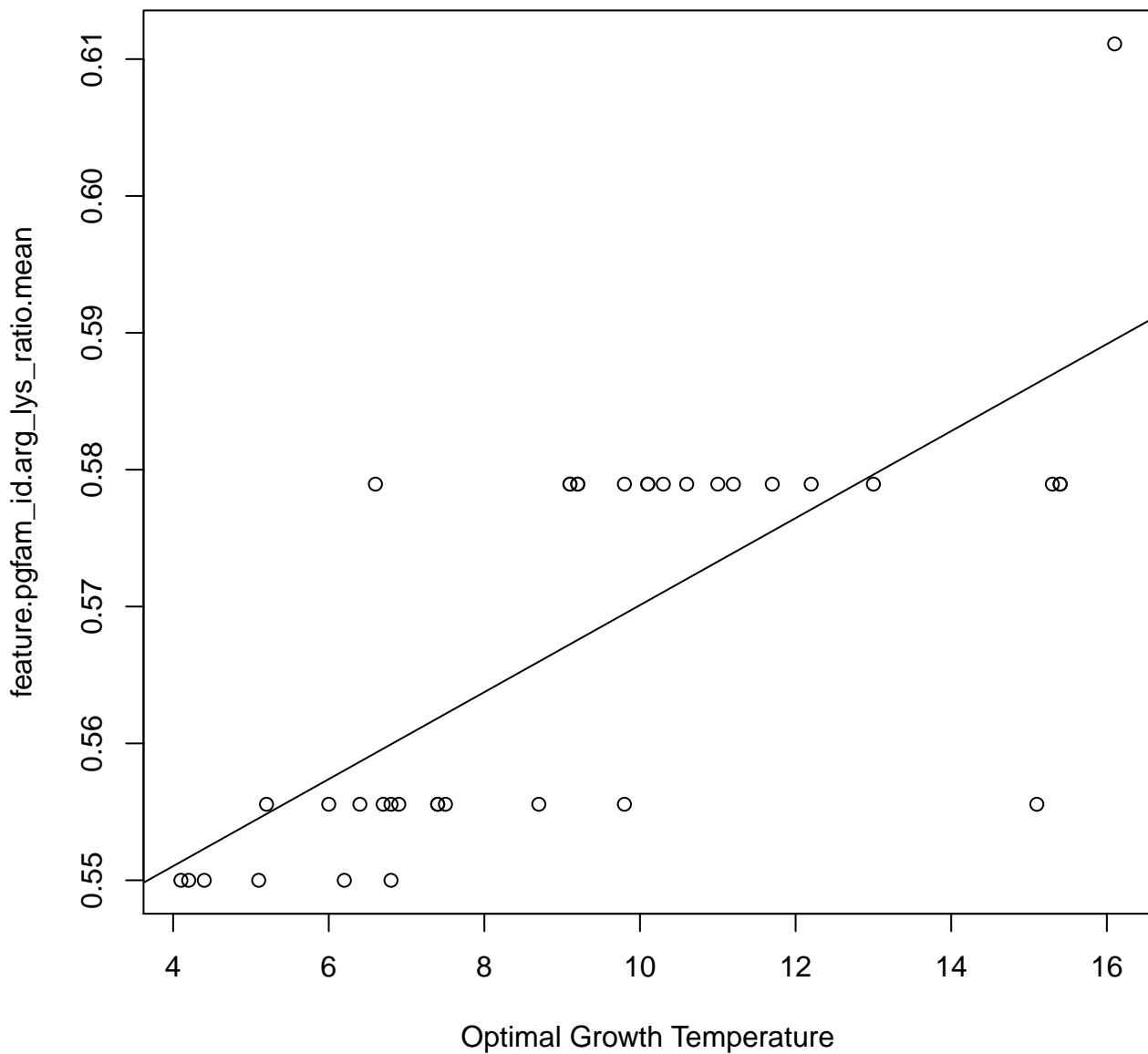
UPF0102 protein YraN



feature.pgfam_id.arg_lys_ratio.mean

PGF_03073036

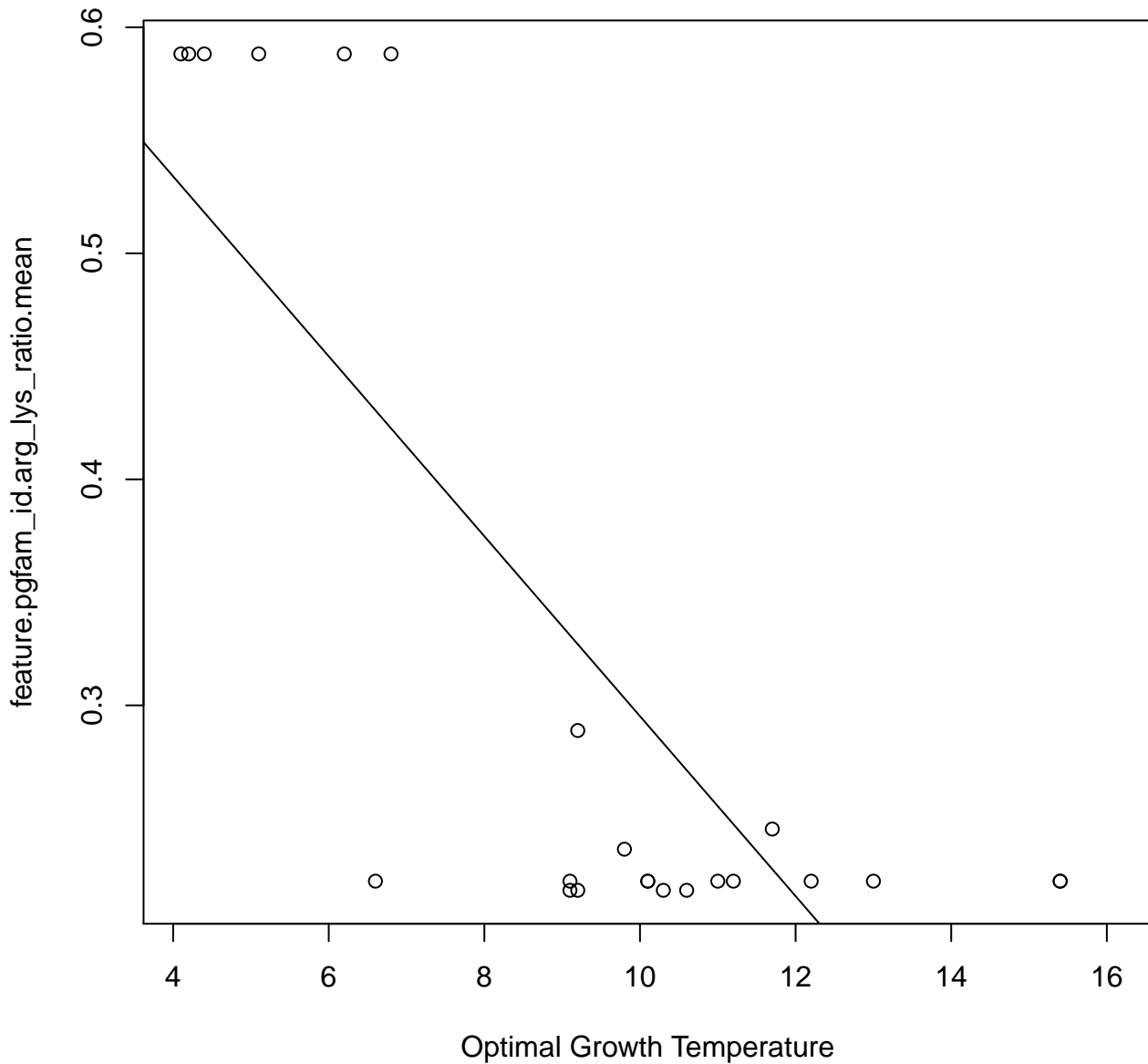
hypothetical protein



feature.pgfam_id.arg_lys_ratio.mean

PGF_03083319

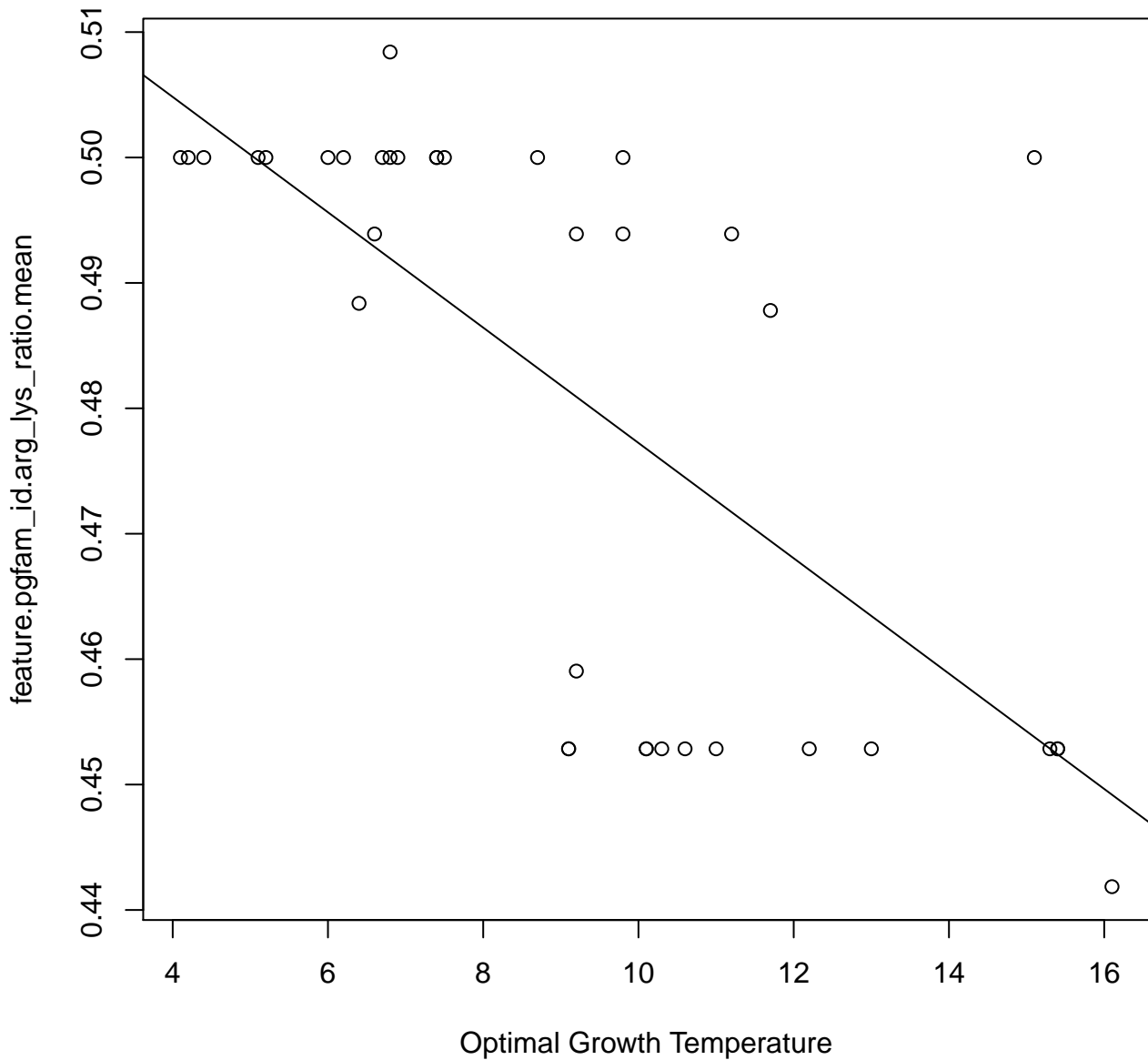
Maltodextrin glucosidase (EC 3.2.1.20)



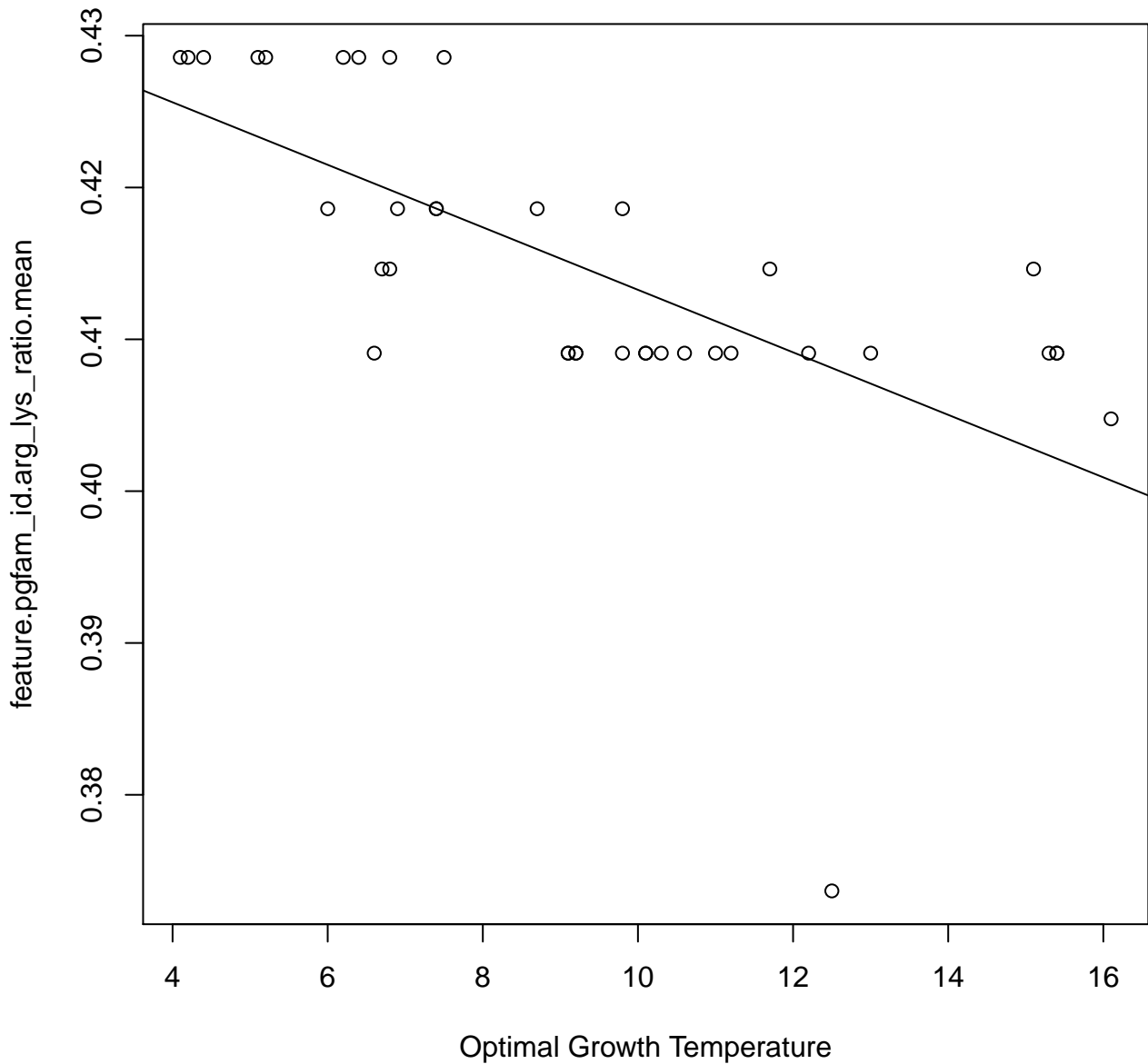
feature.pgfam_id.arg_lys_ratio.mean

PGF_03857575

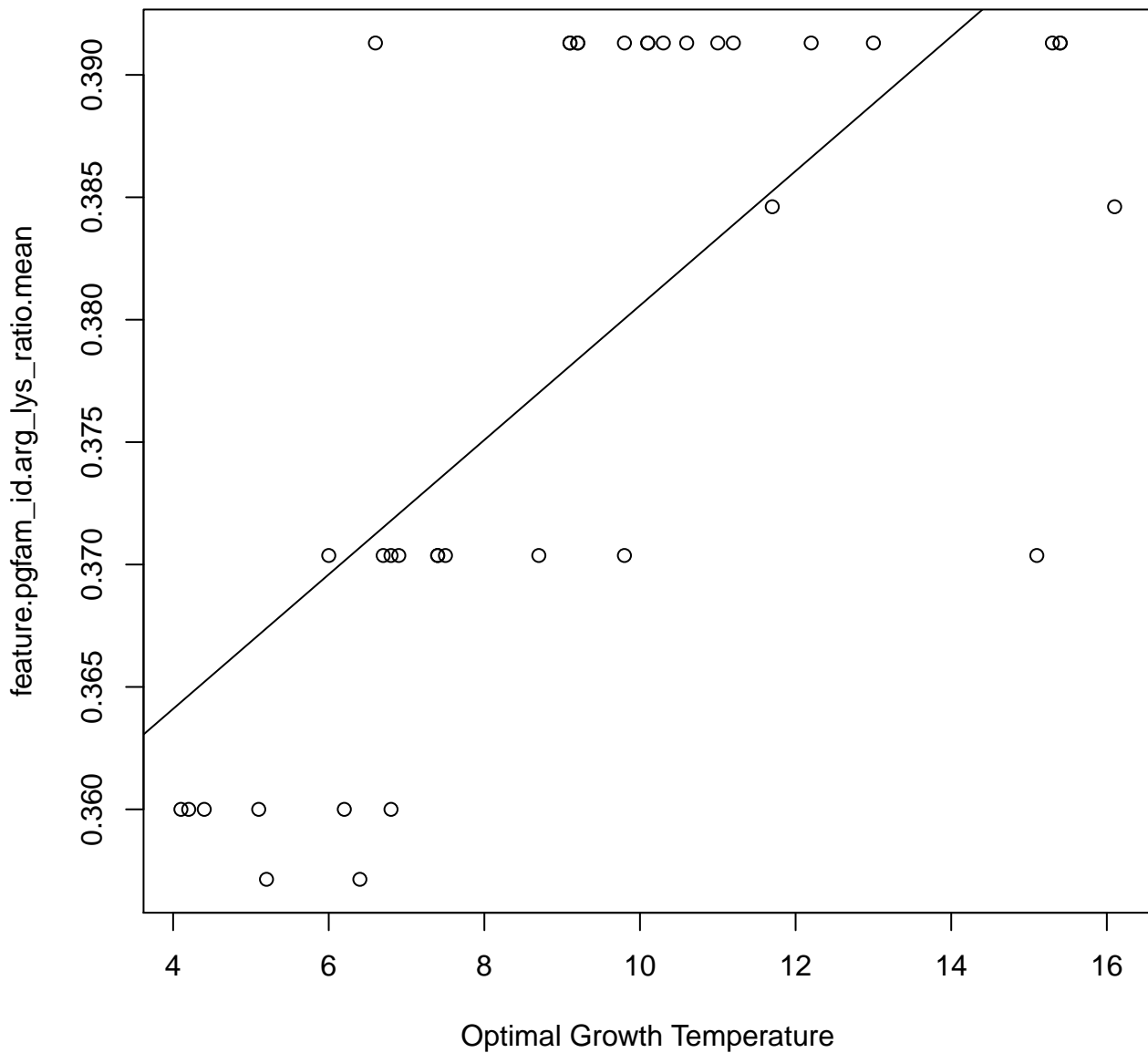
FIG003737: Predicted deacylase



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



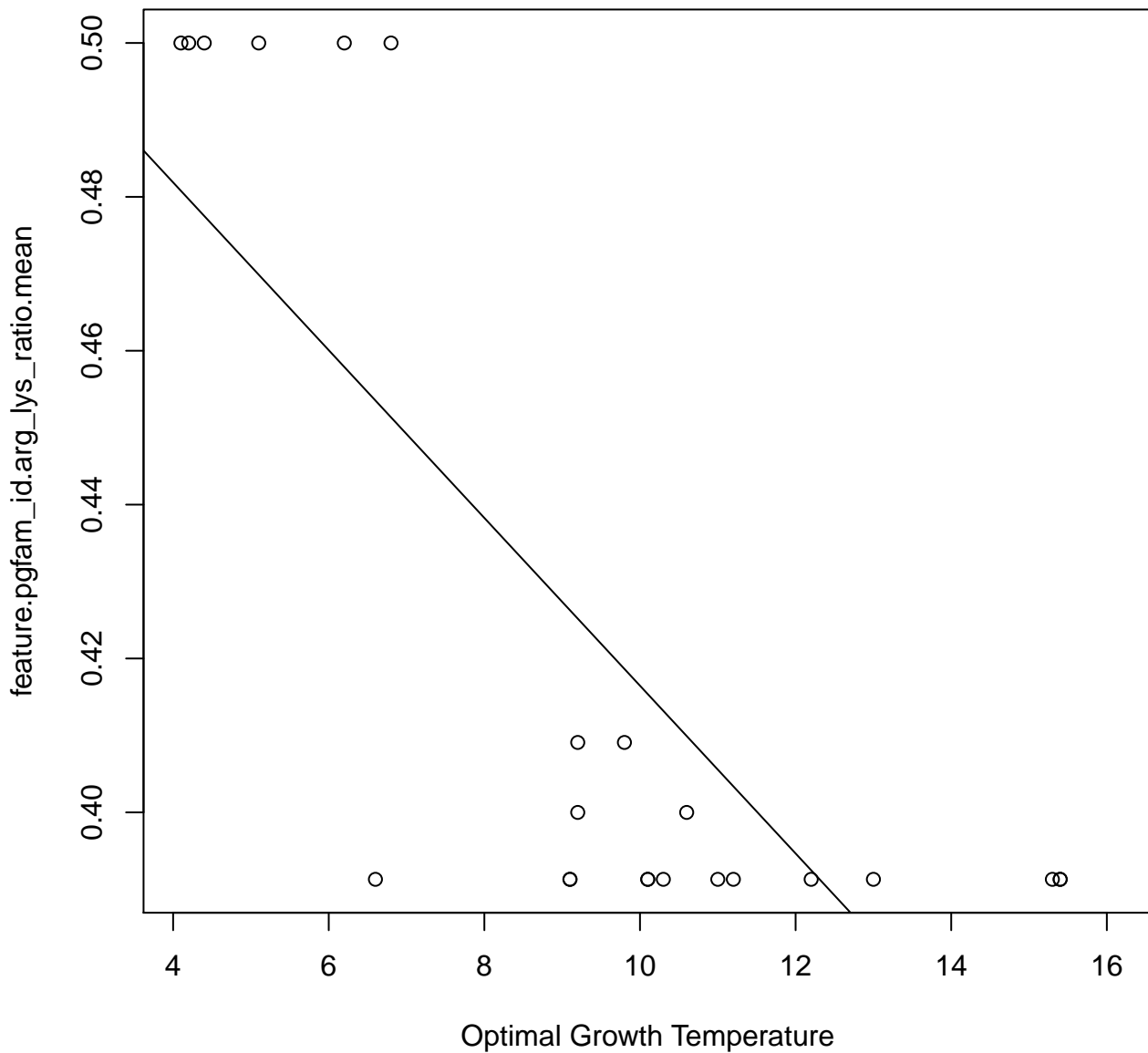
feature.pgfam_id.arg_lys_ratio.mean
PGF_06784545
(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10)



feature.pgfam_id.arg_lys_ratio.mean

PGF_06792096

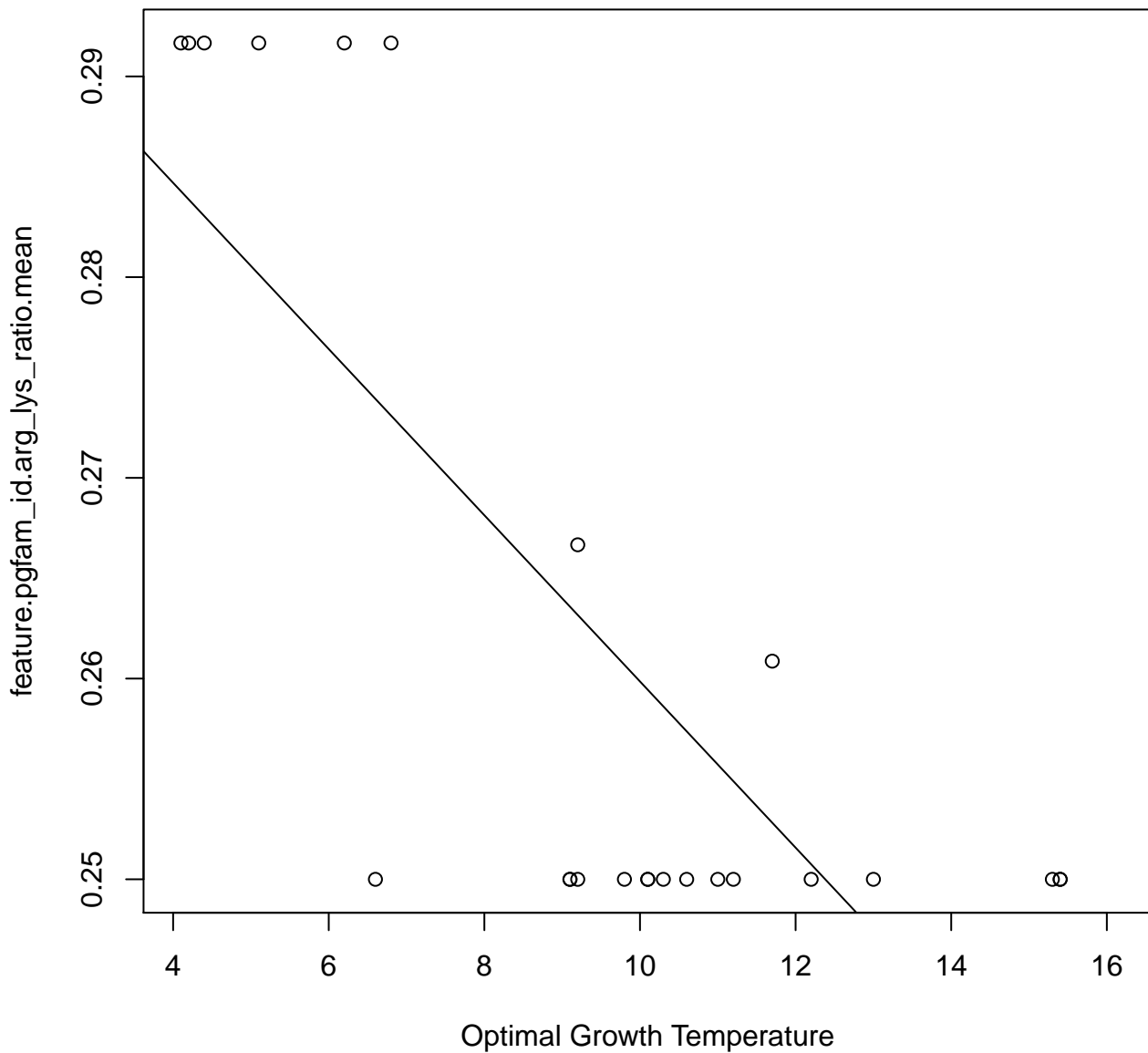
hypothetical protein



feature.pgfam_id.arg_lys_ratio.mean

PGF_07204997

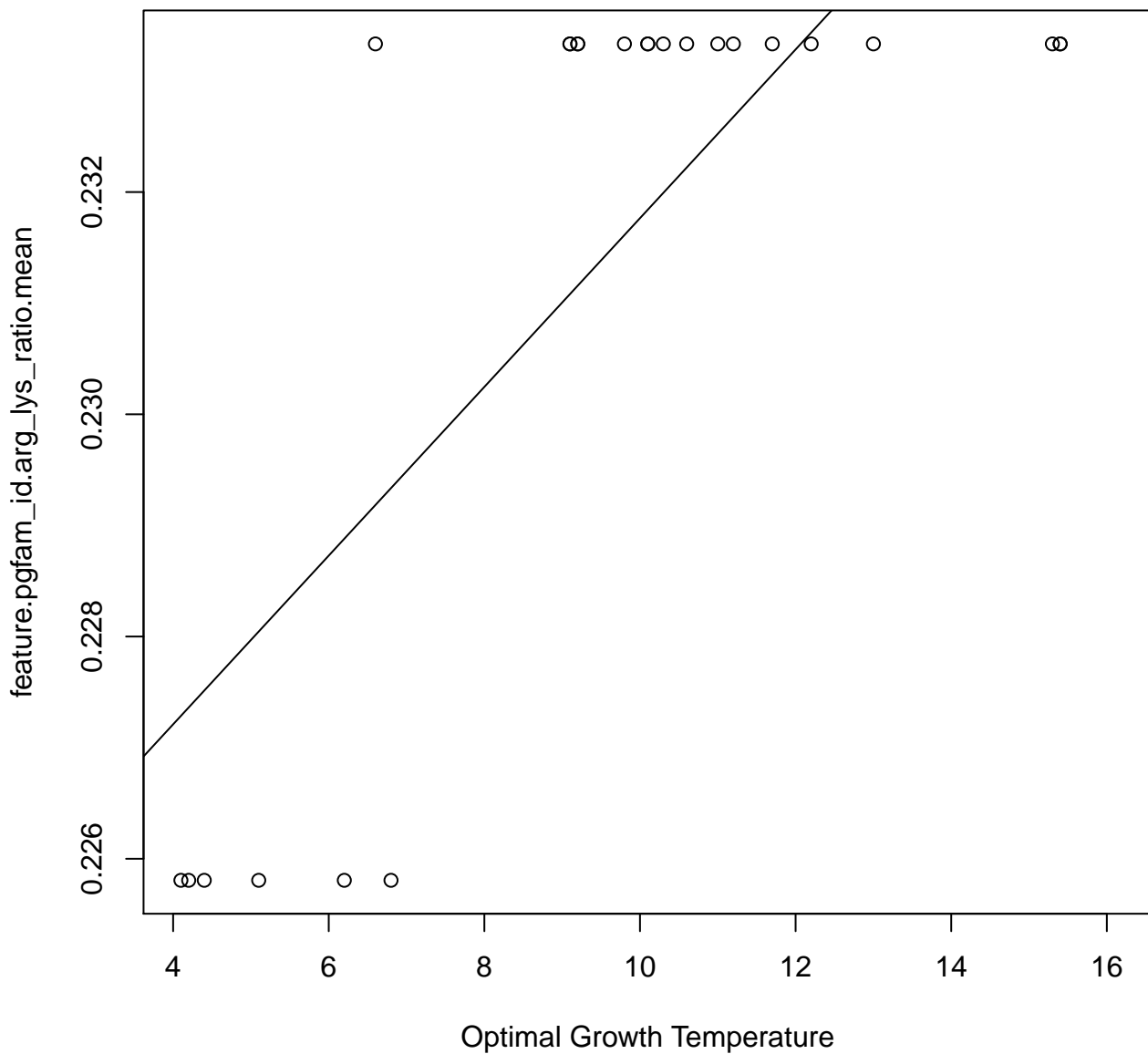
hypothetical protein



feature.pgfam_id.arg_lys_ratio.mean

PGF_07232493

hypothetical protein

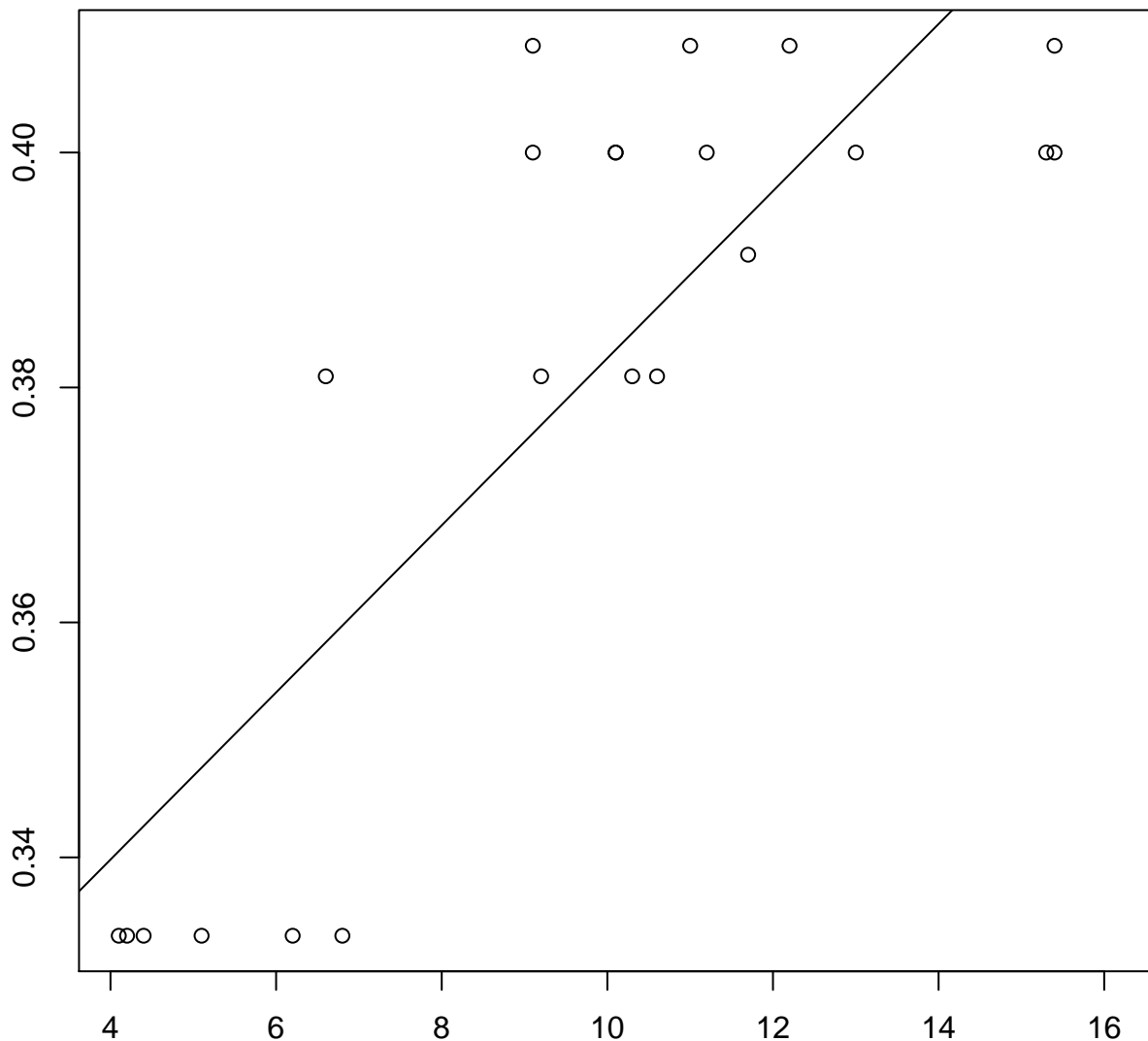


feature.pgfam_id.arg_lys_ratio.mean

PGF_08025863

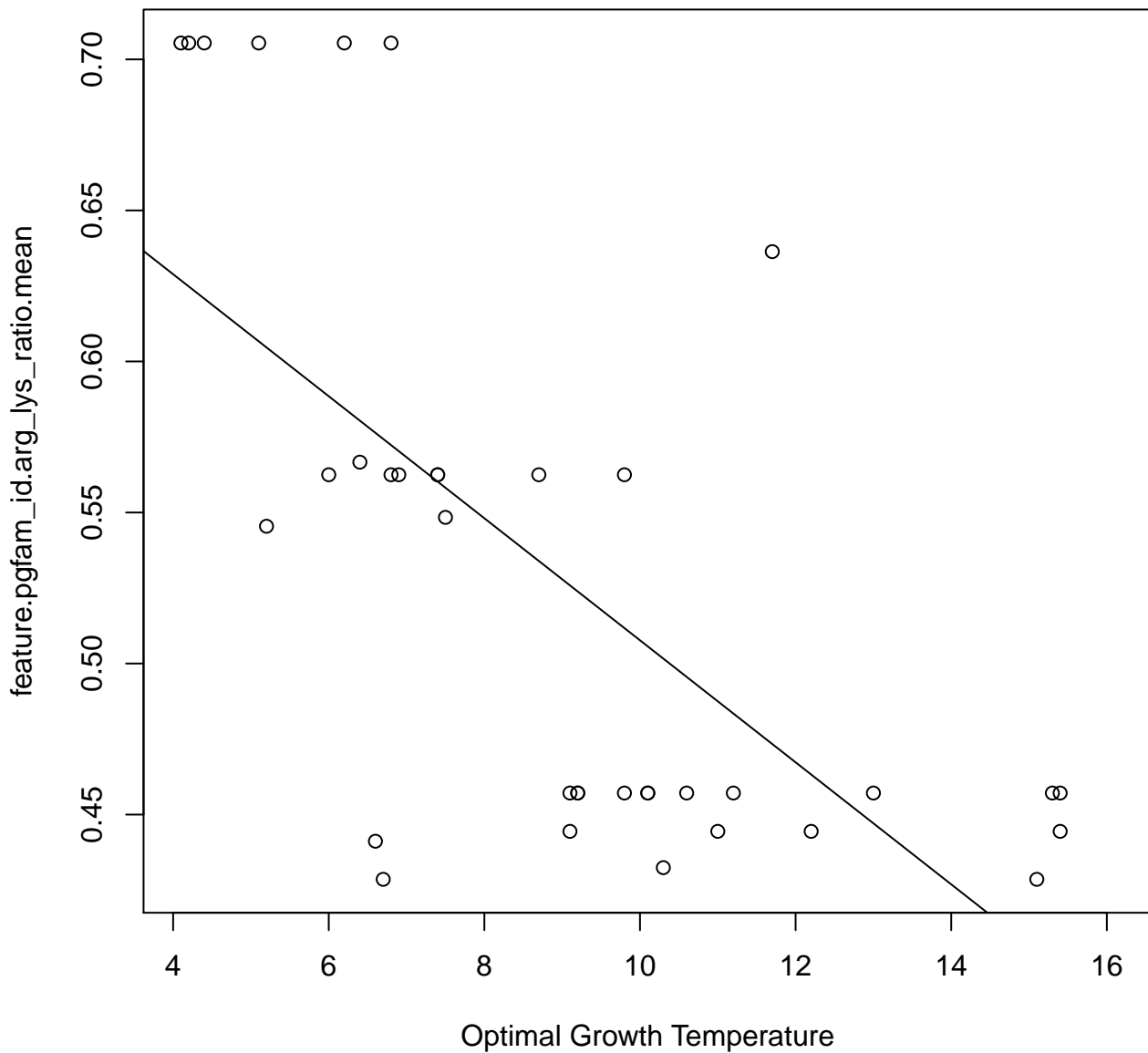
hypothetical protein

feature.pgfam_id.arg_lys_ratio.mean



Optimal Growth Temperature

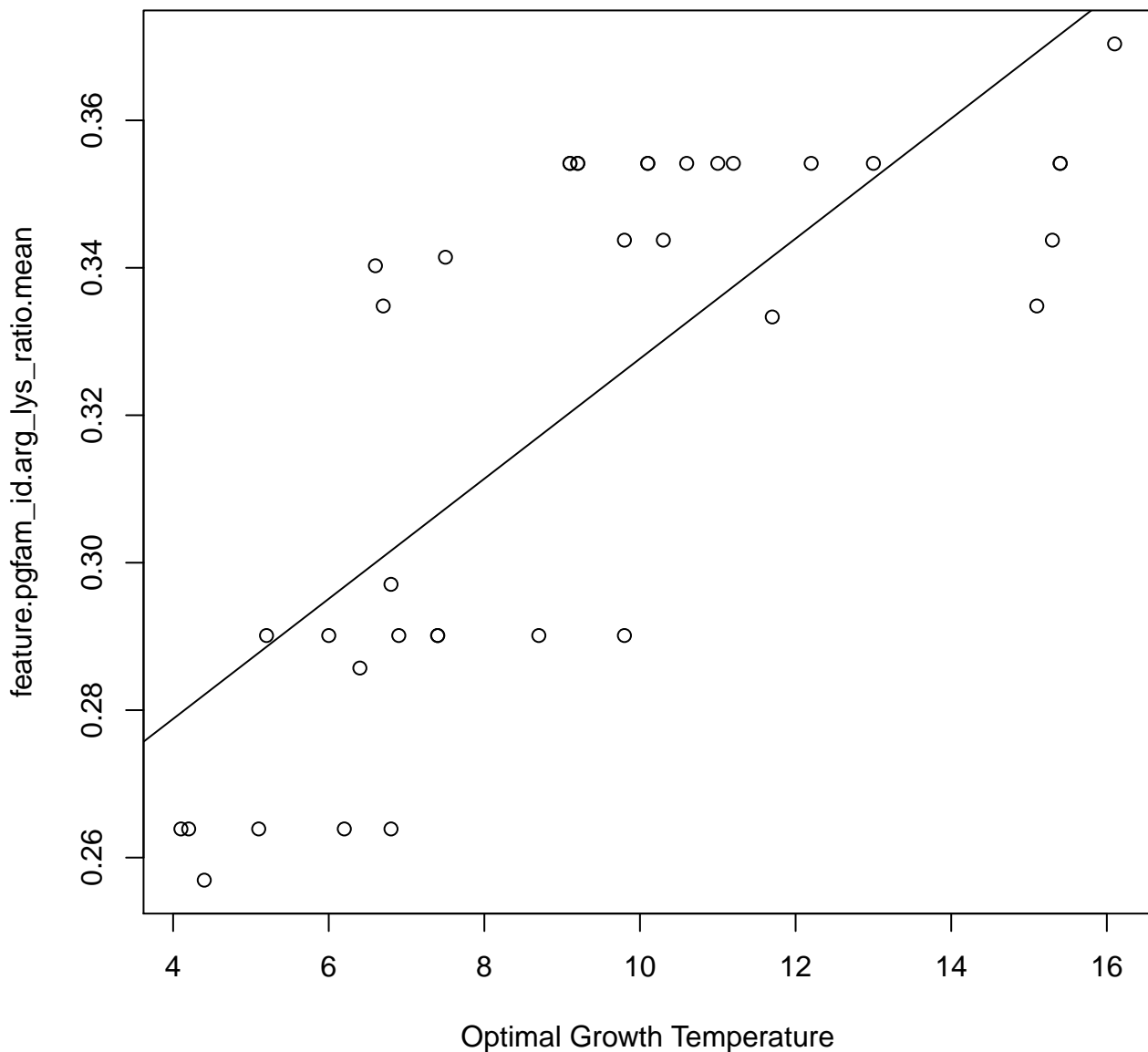
feature.pgfam_id.arg_lys_ratio.mean
PGF_08514768
Glutathione S-transferase, omega (EC 2.5.1.18)



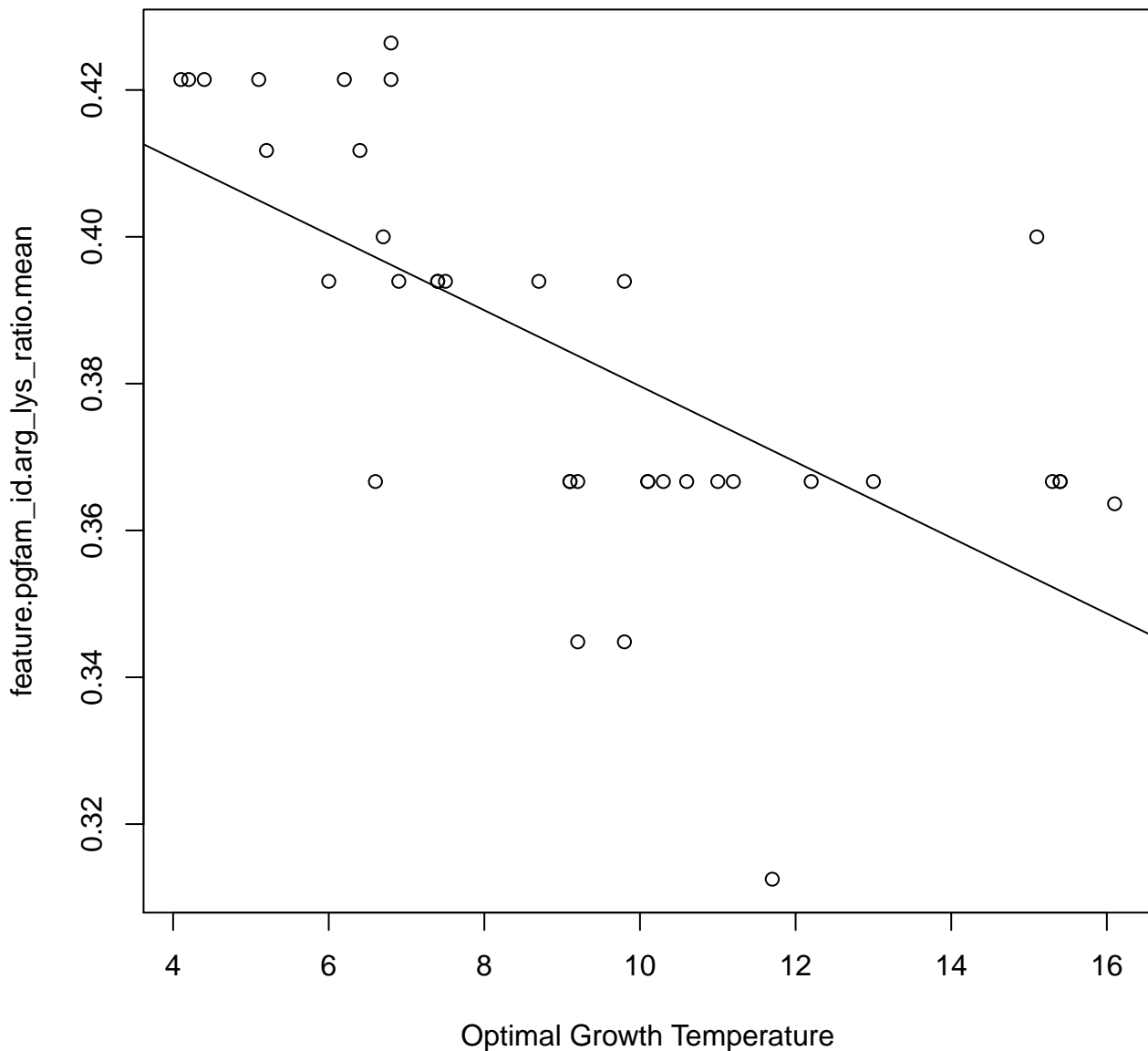
feature.pgfam_id.arg_lys_ratio.mean

PGF_10238627

Chemotaxis regulator – transmits chemoreceptor signals to flagellar motor components CheY



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

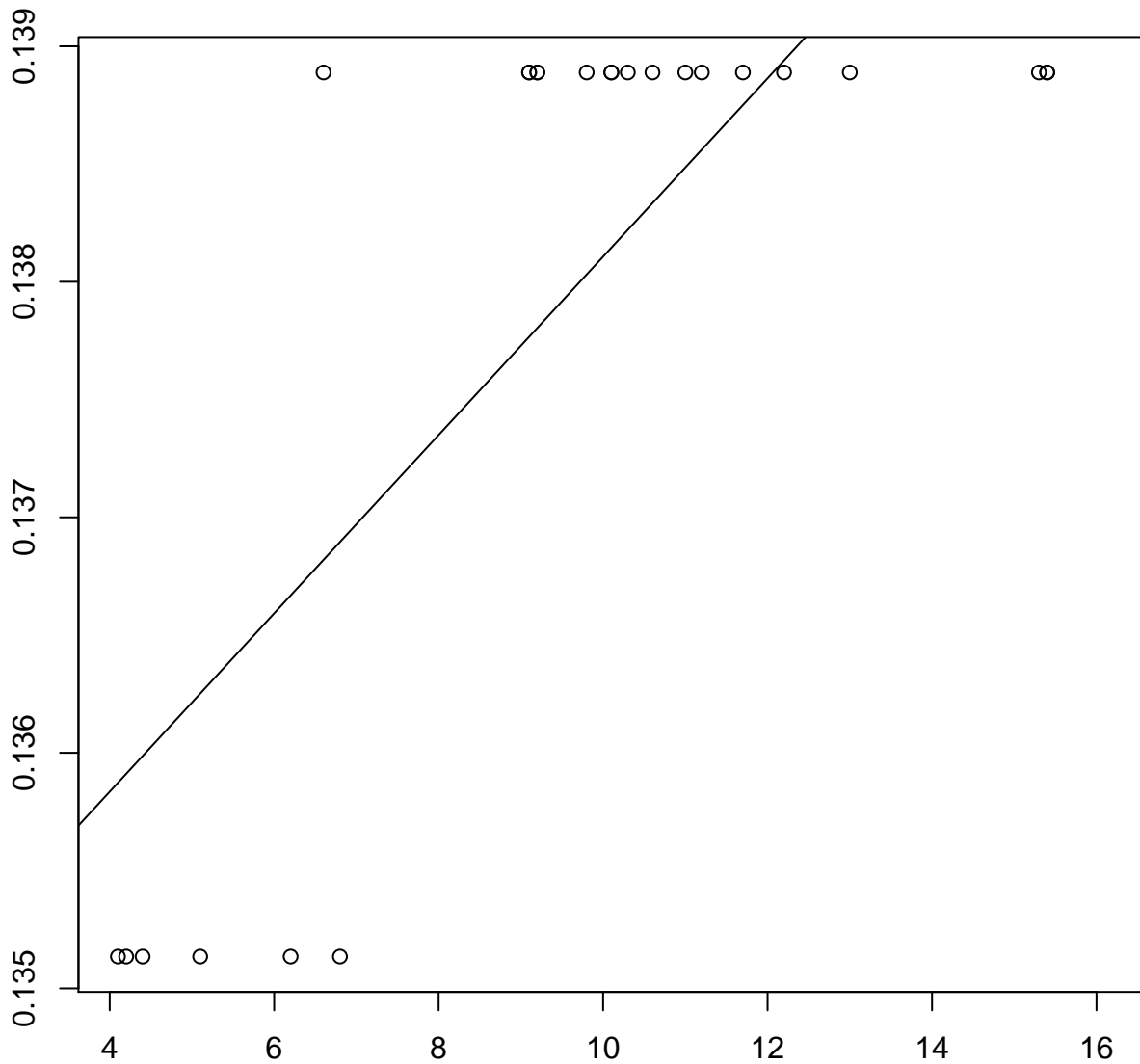


feature.pgfam_id.arg_lys_ratio.mean

PGF_10428899

hypothetical protein

feature.pgfam_id.arg_lys_ratio.mean



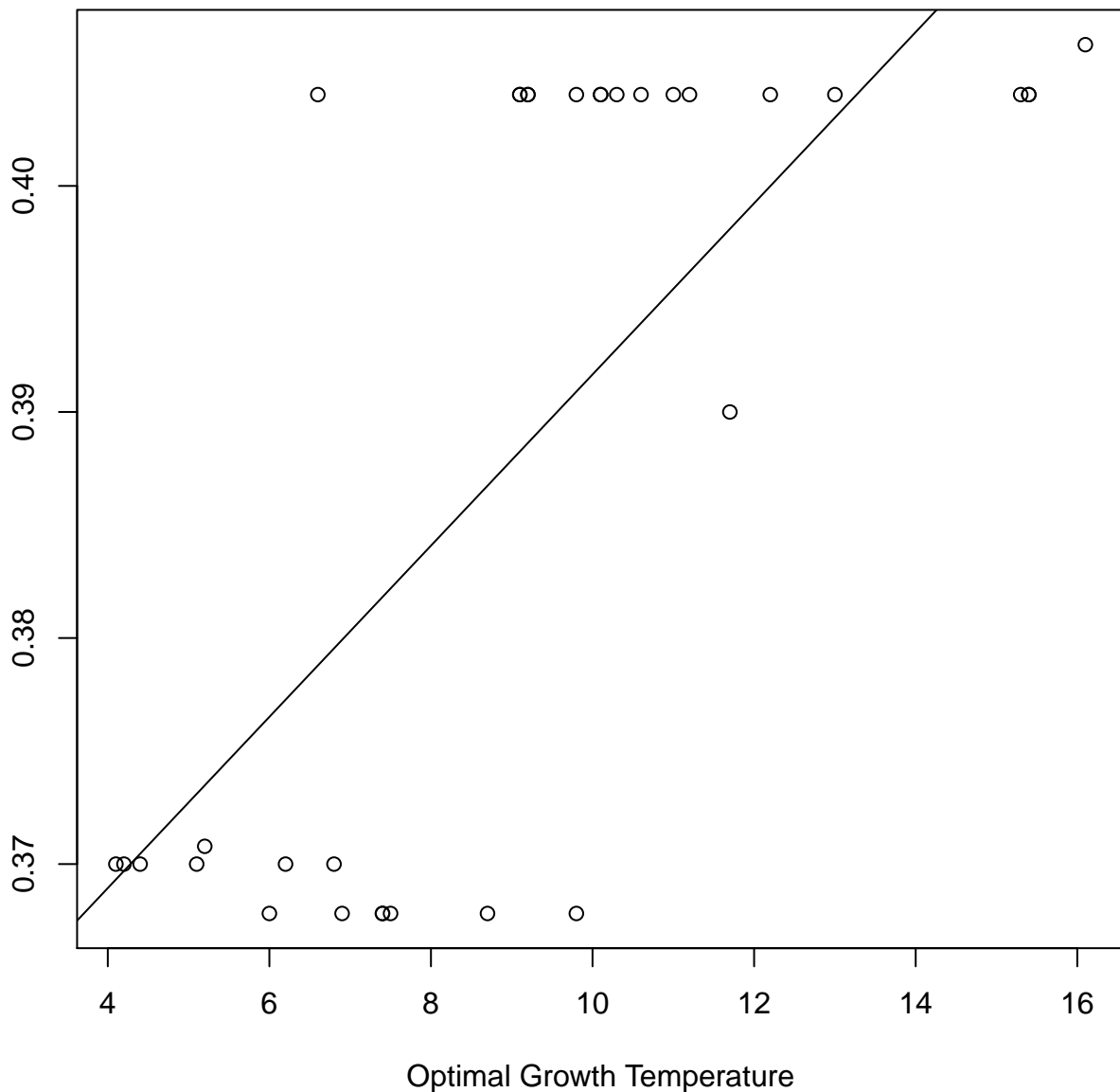
Optimal Growth Temperature

feature.pgfam_id.arg_lys_ratio.mean

PGF_10437481

hypothetical protein

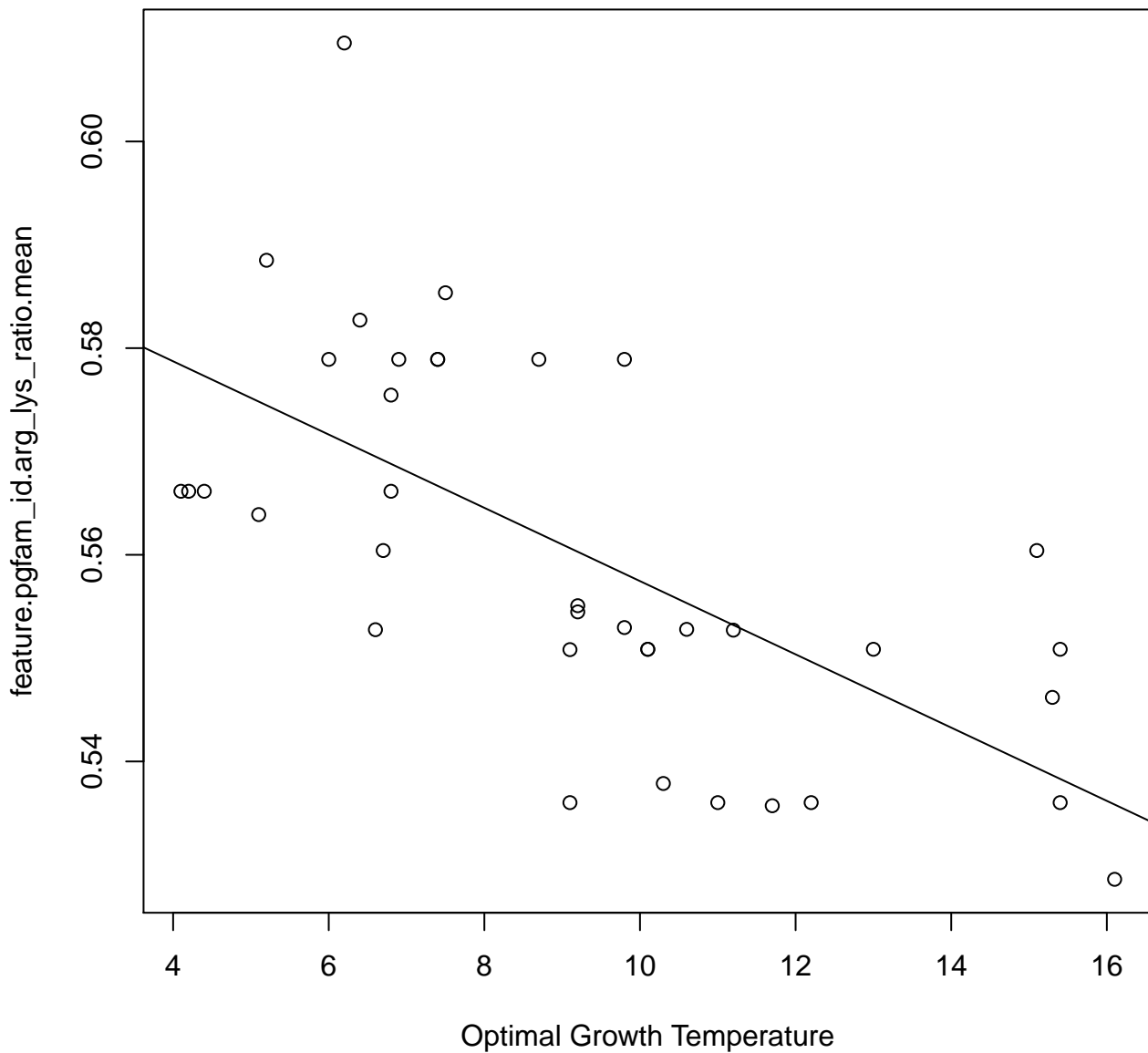
feature.pgfam_id.arg_lys_ratio.mean



feature.pgfam_id.arg_lys_ratio.mean

PGF_10537966

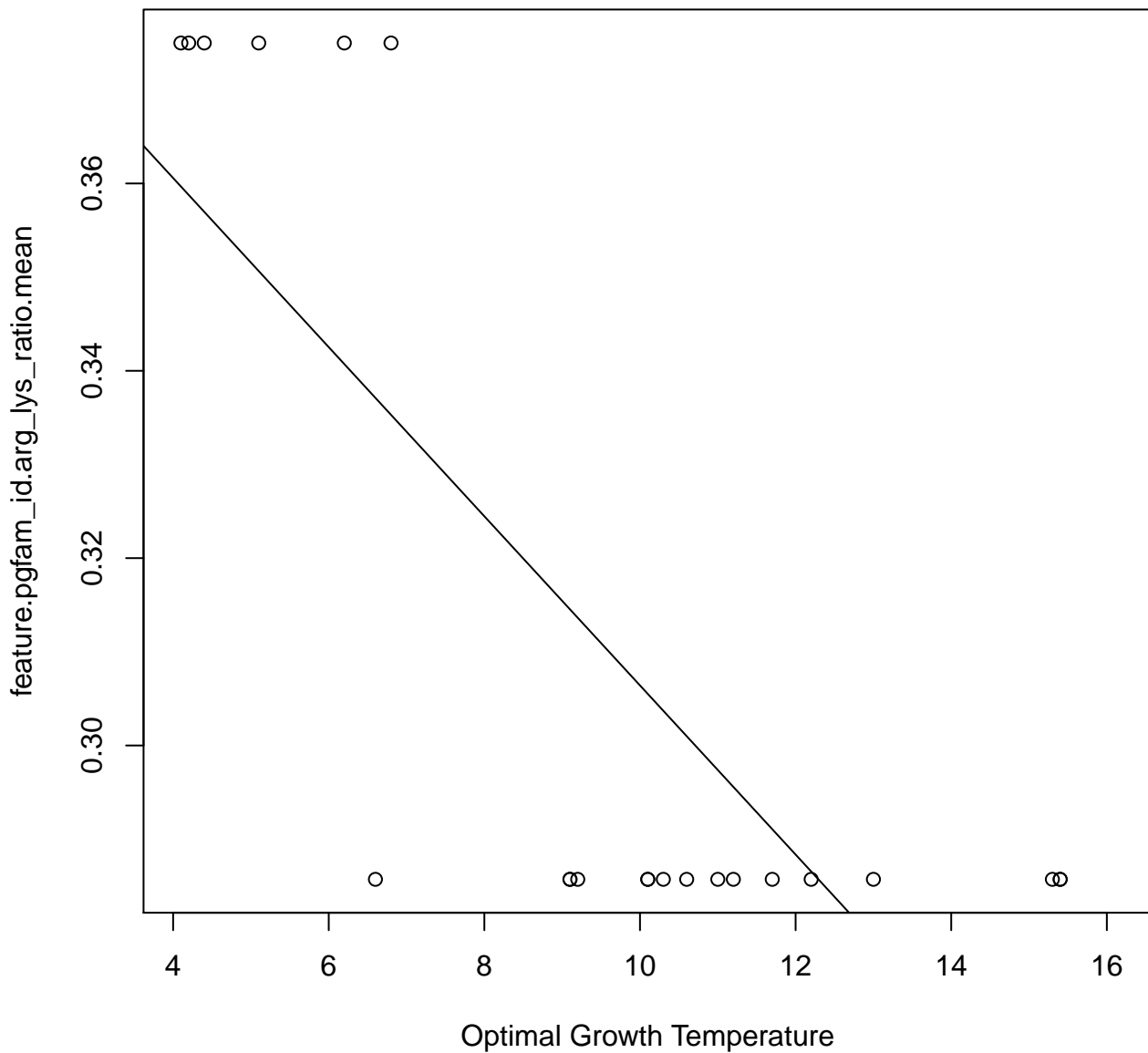
TonB-dependent receptor



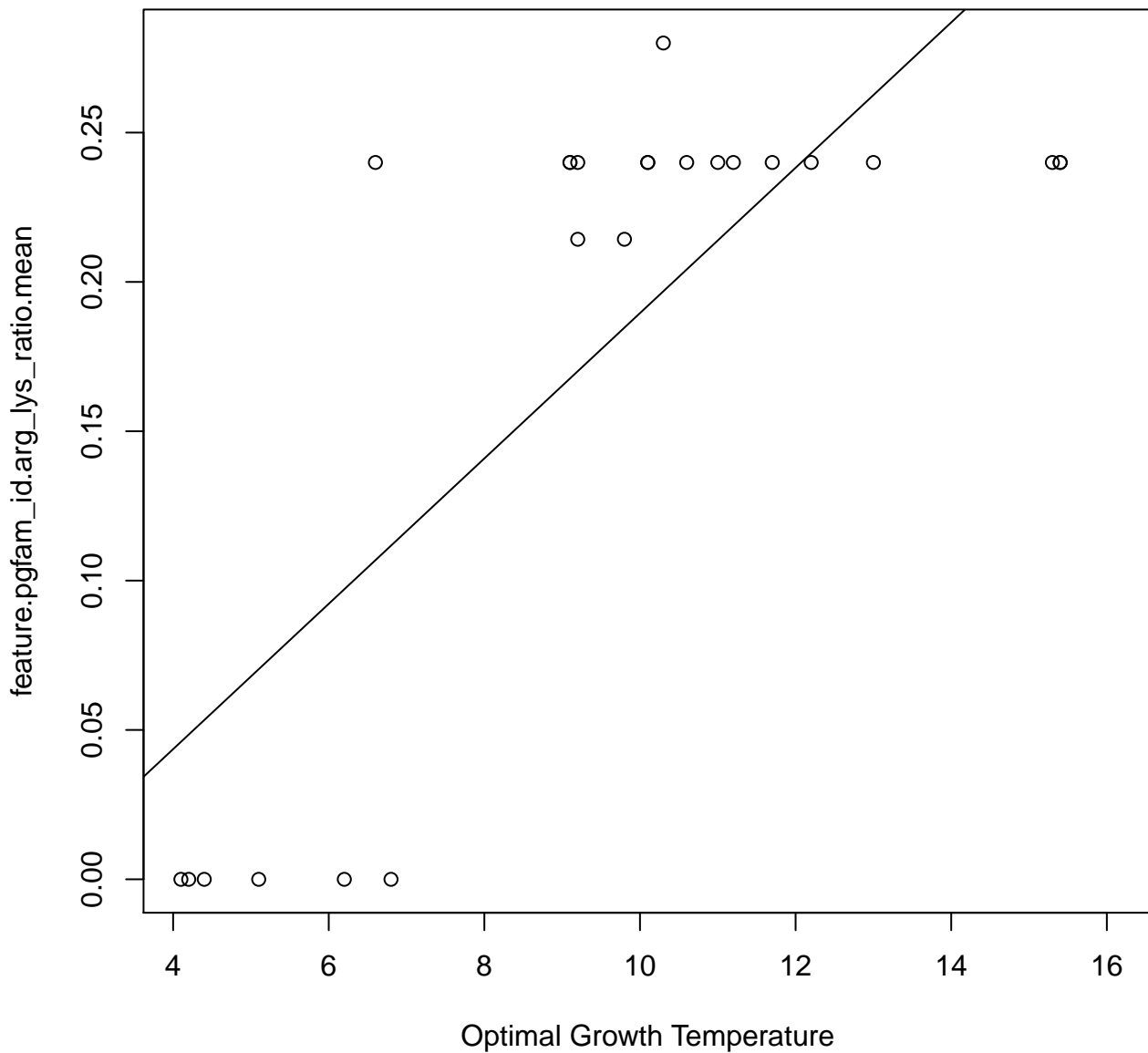
feature.pgfam_id.arg_lys_ratio.mean

PGF_10906072

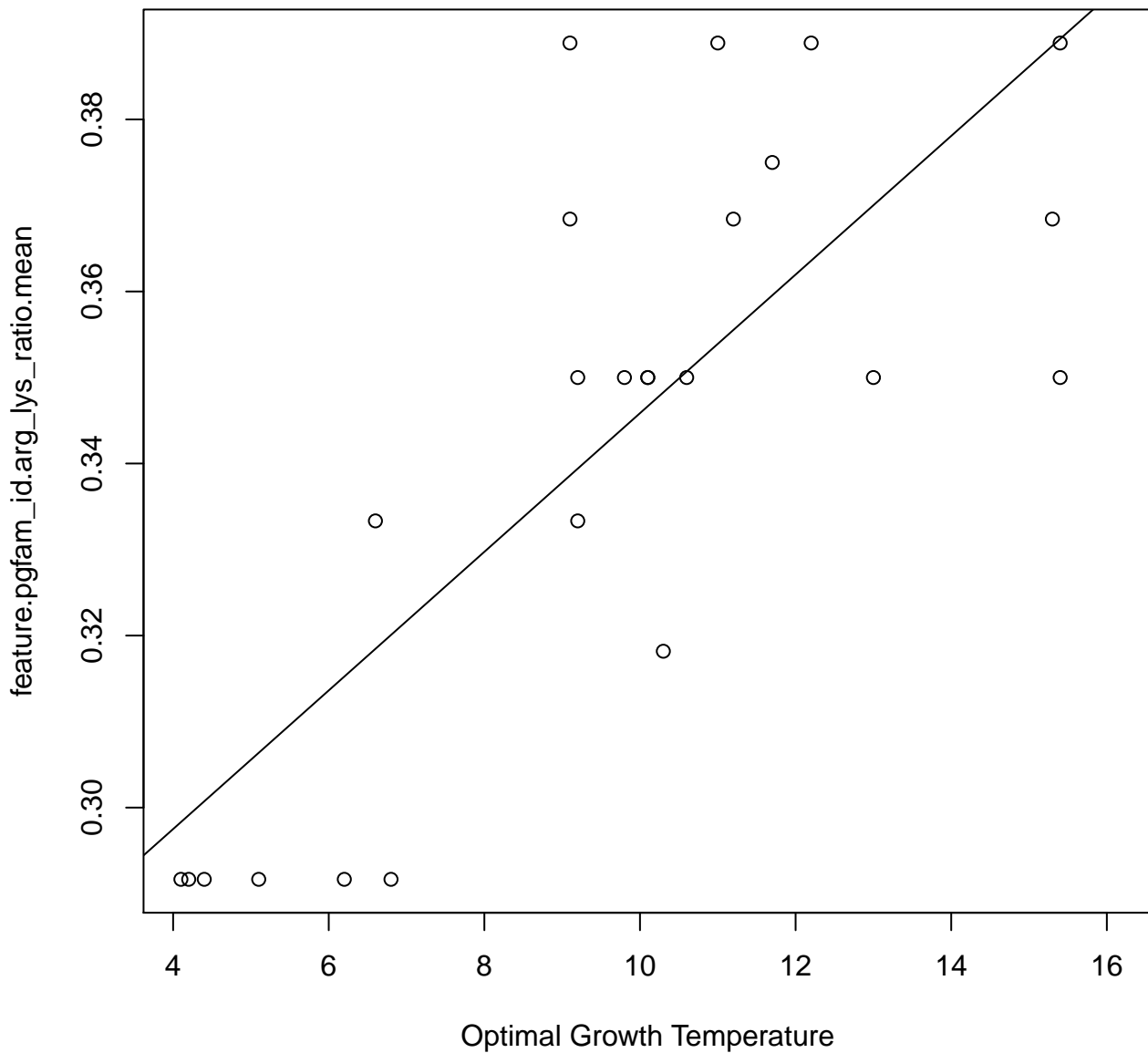
hypothetical protein



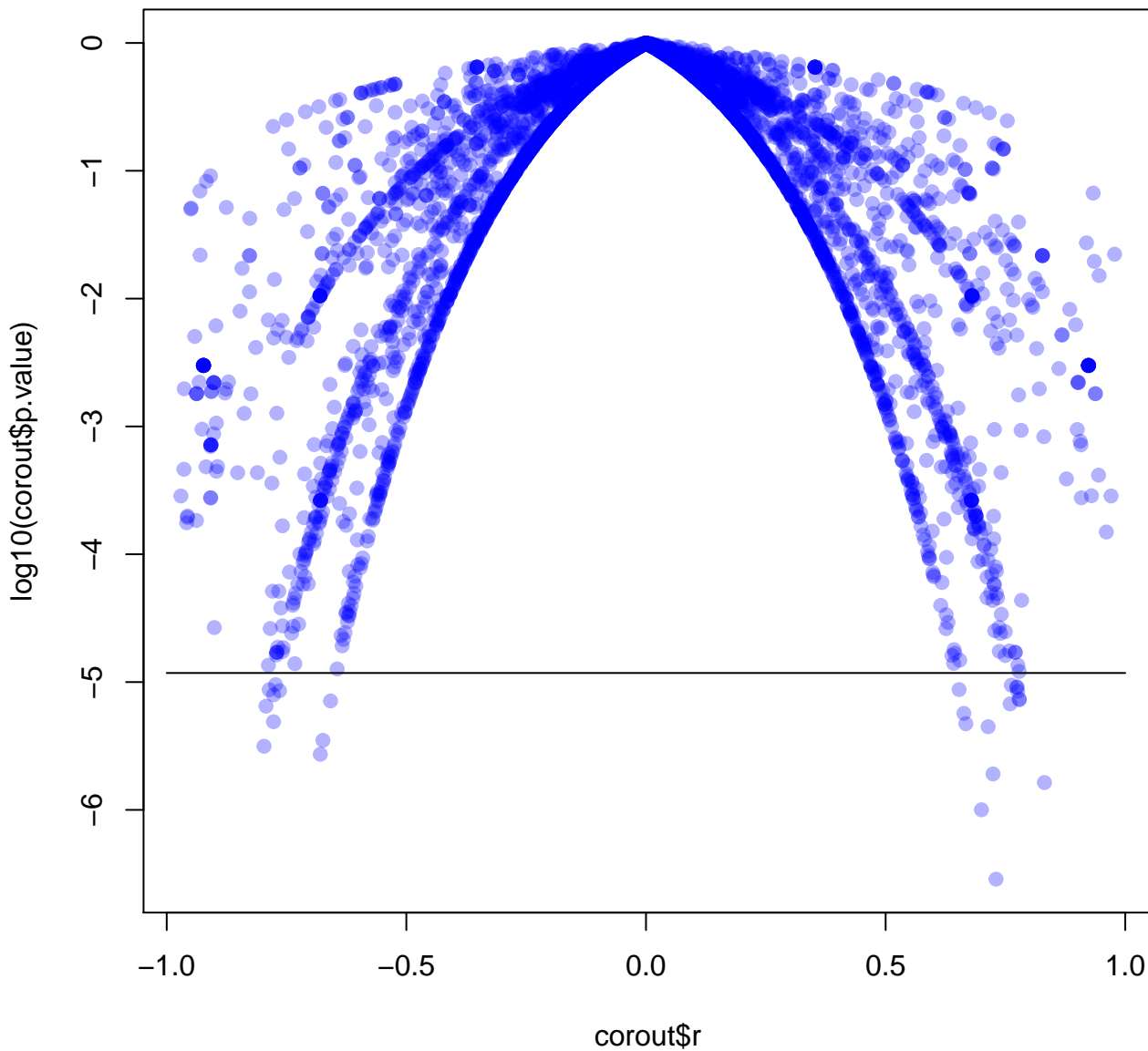
feature.pgfam_id.arg_lys_ratio.mean
PGF_11018774
hypothetical protein



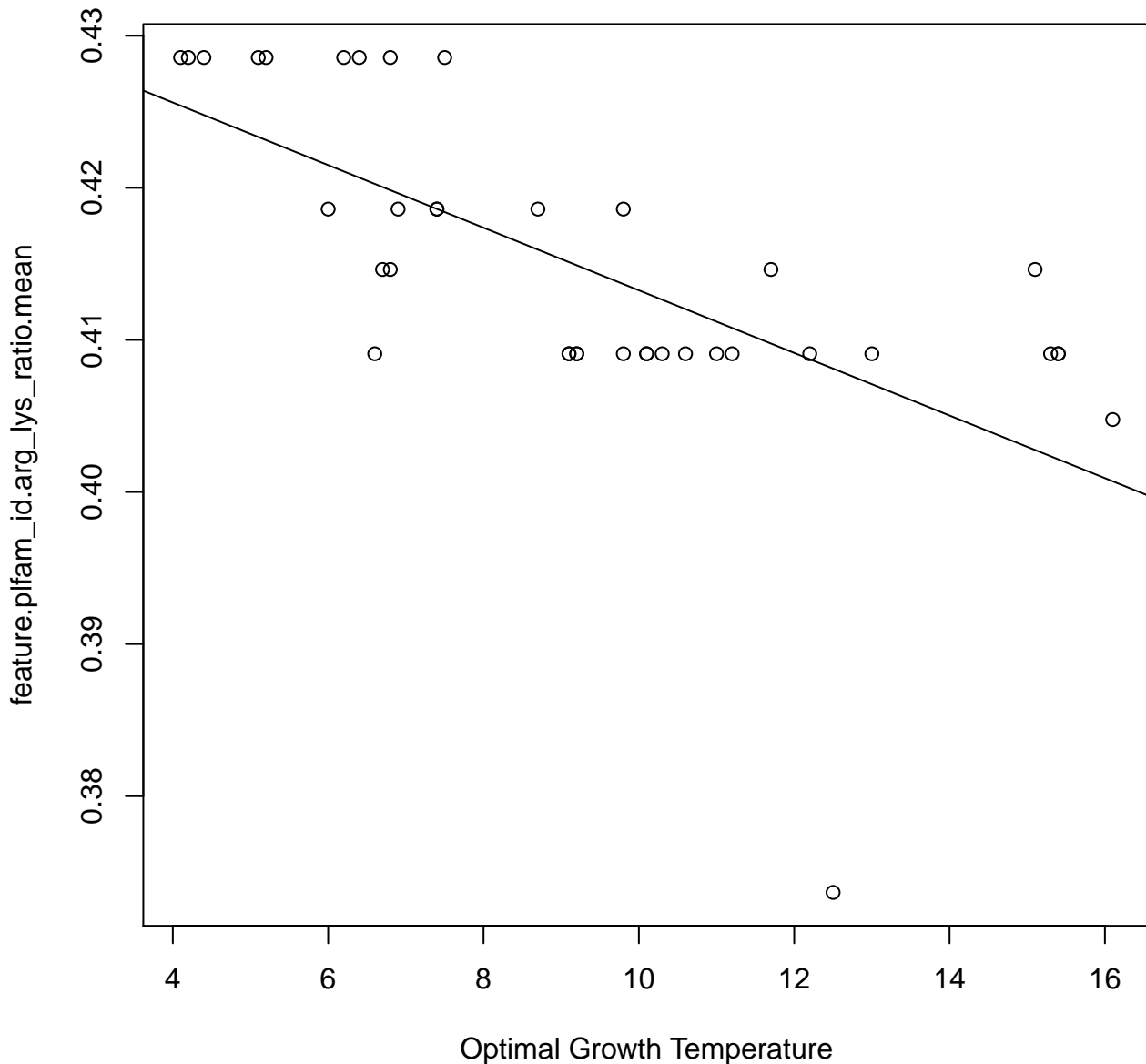
feature.pgfam_id.arg_lys_ratio.mean
PGF_11569208
hypothetical protein



feature.plfam_id.arg_lys_ratio.mean



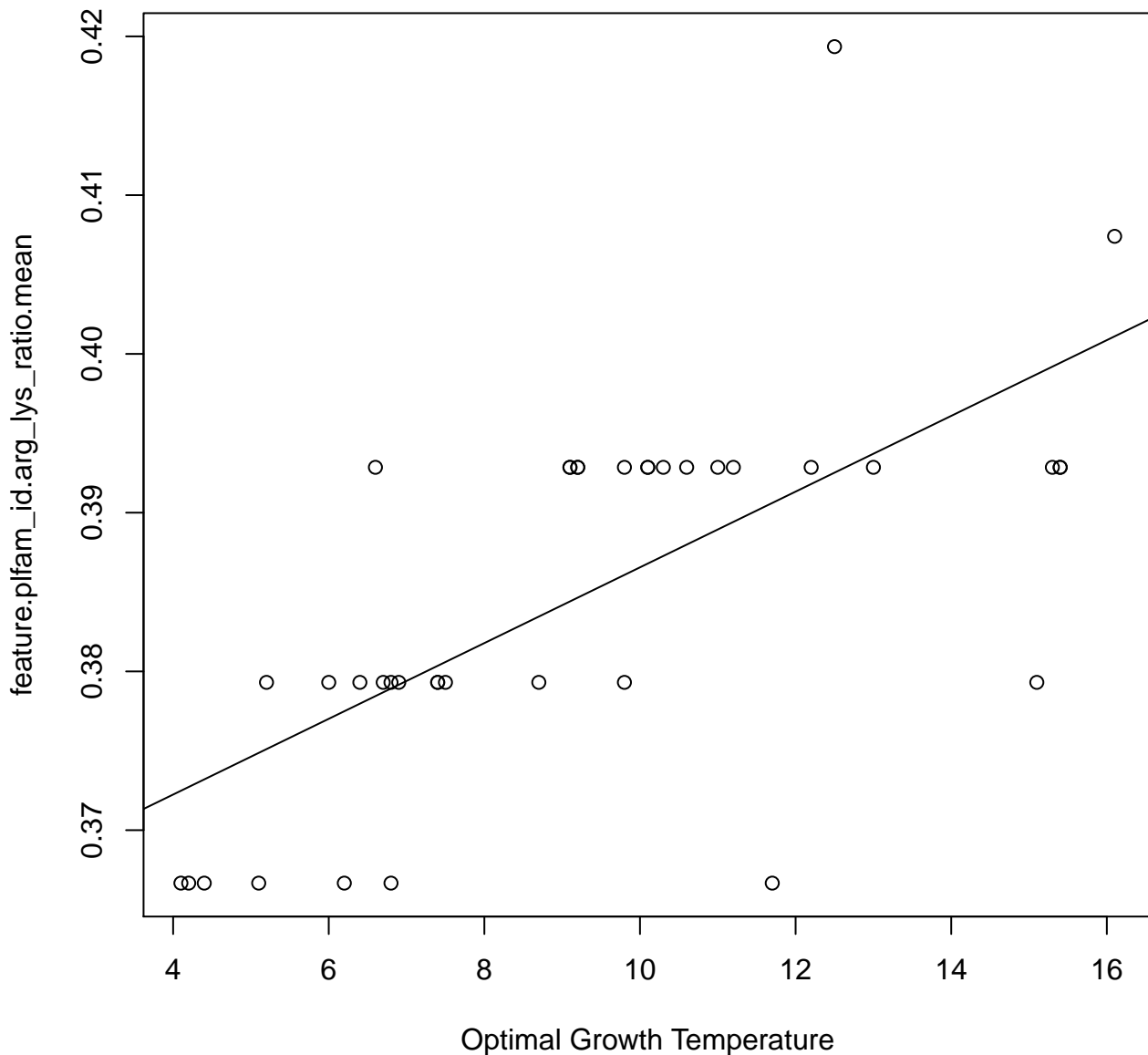
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000010
NADP-dependent malic enzyme (EC 1.1.1.40)



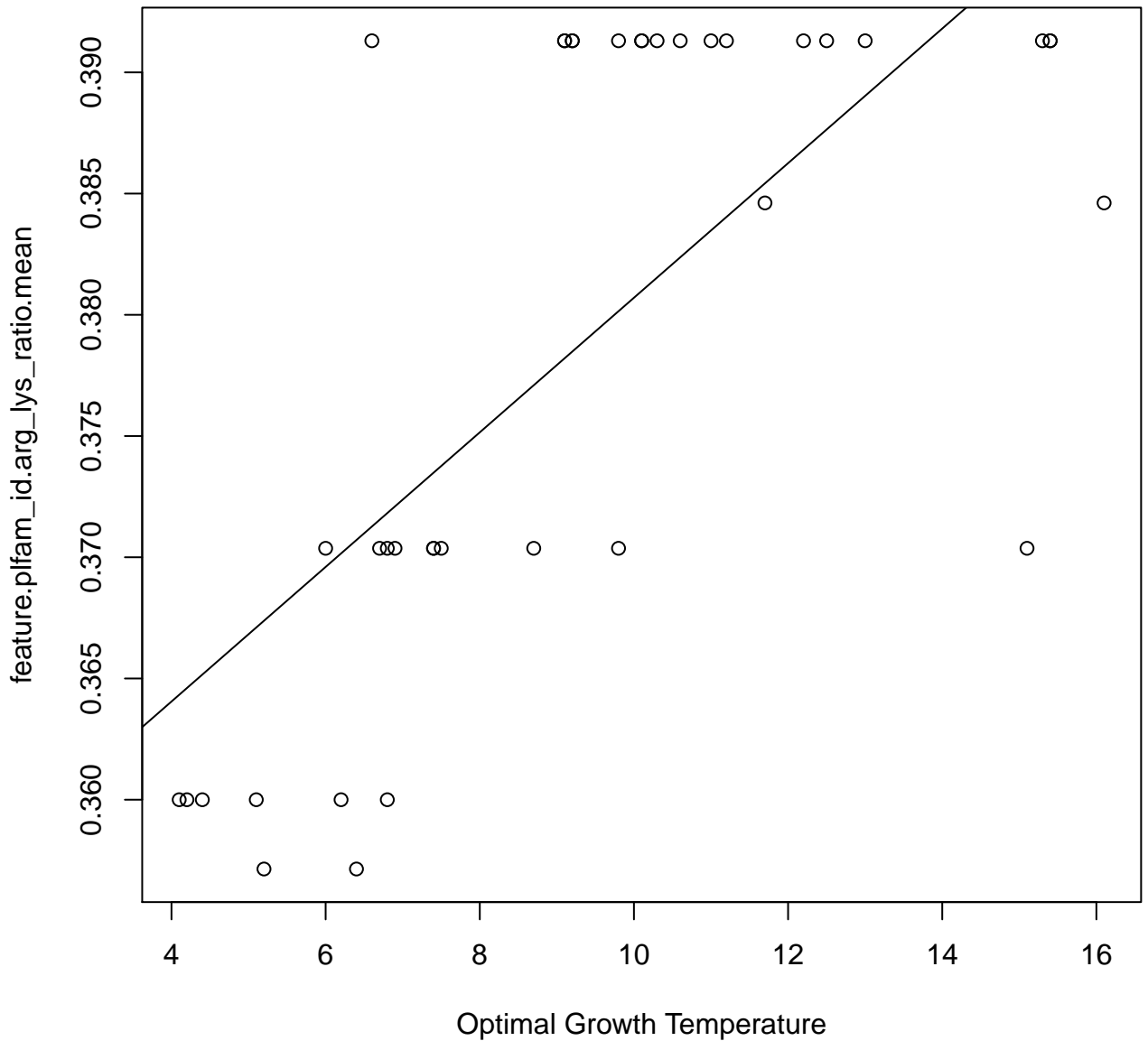
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00000103

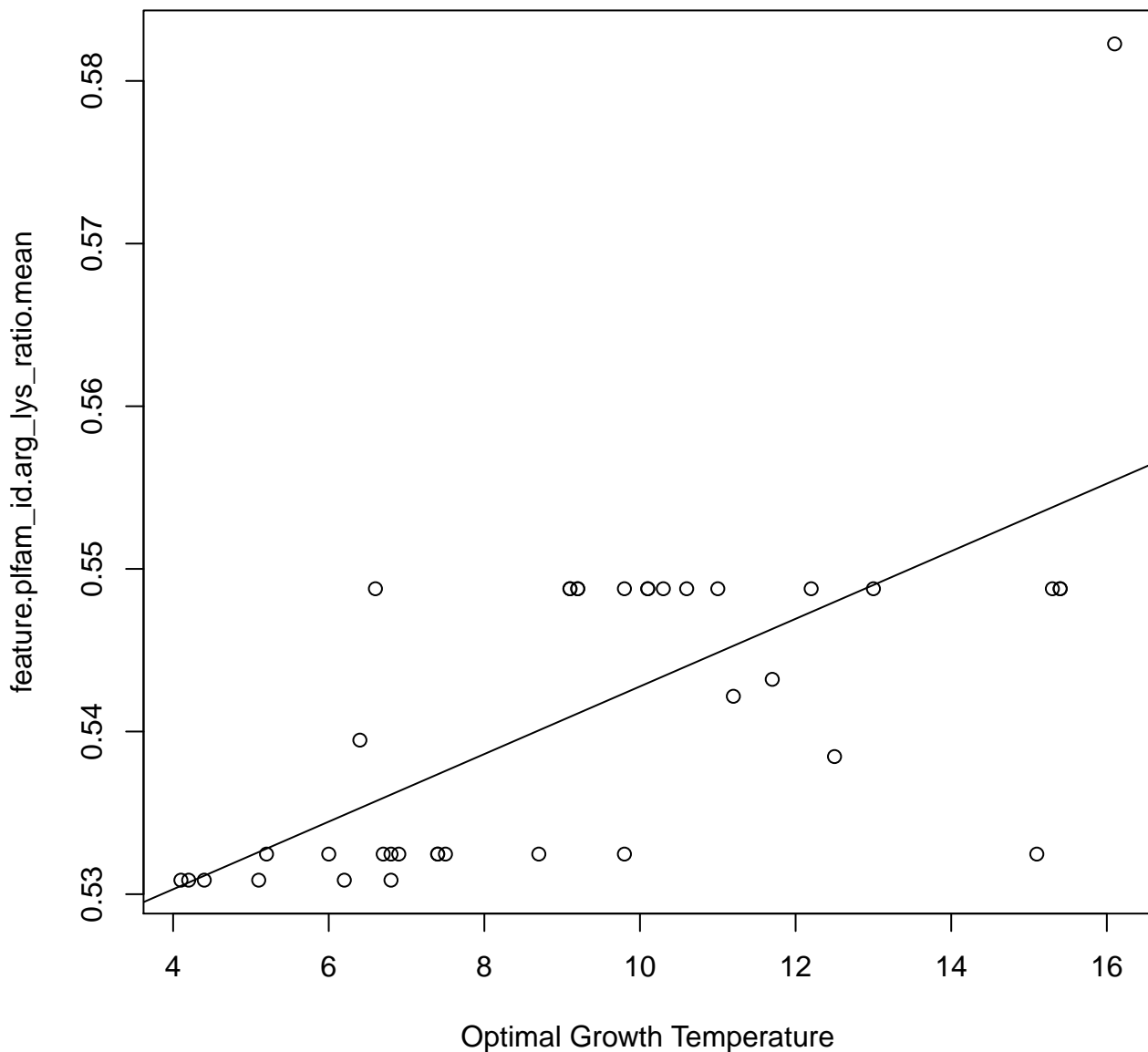
Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / Methylene tetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)



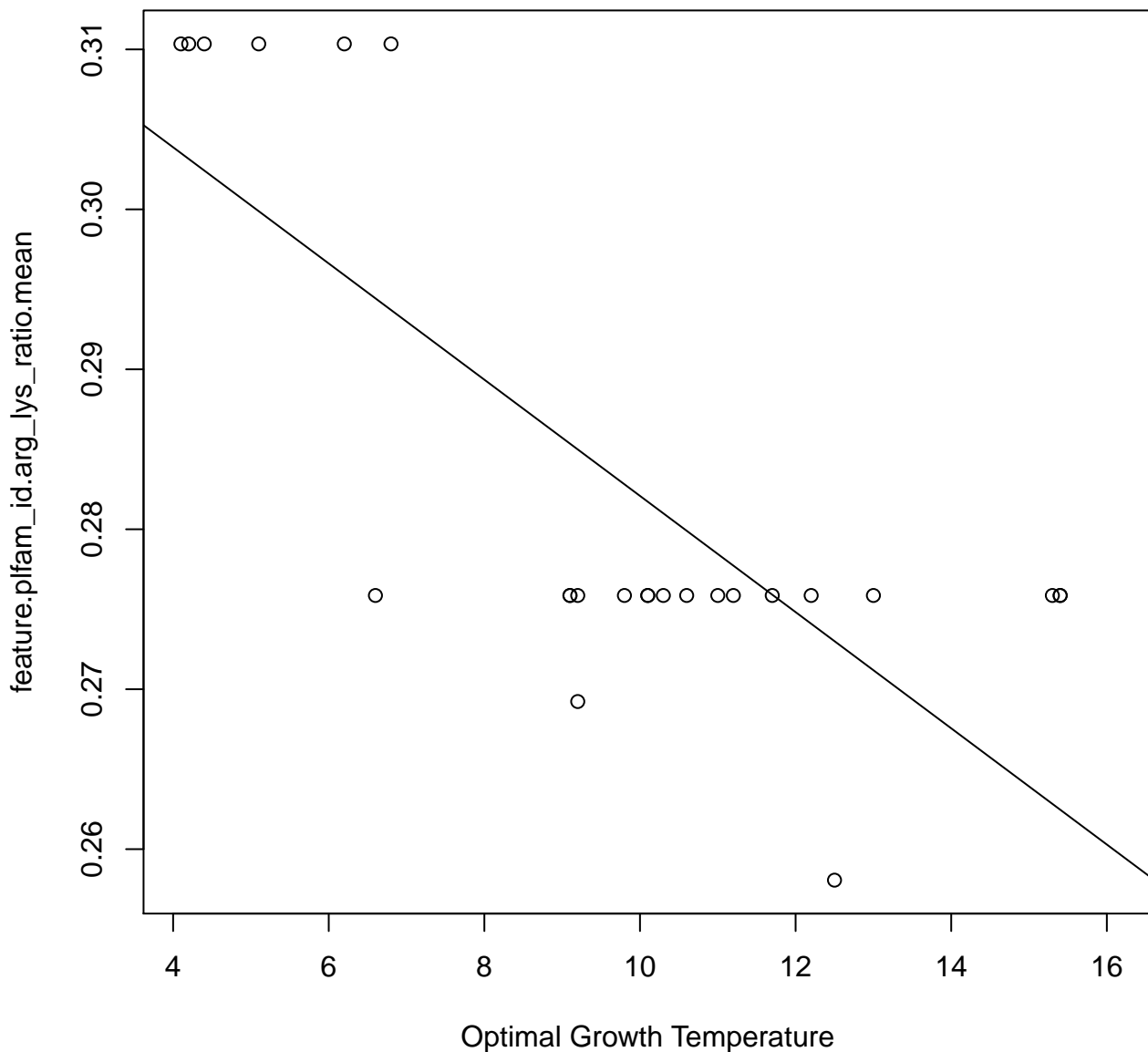
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000179
(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000330
ATP-dependent DNA helicase RecG (EC 3.6.4.12)



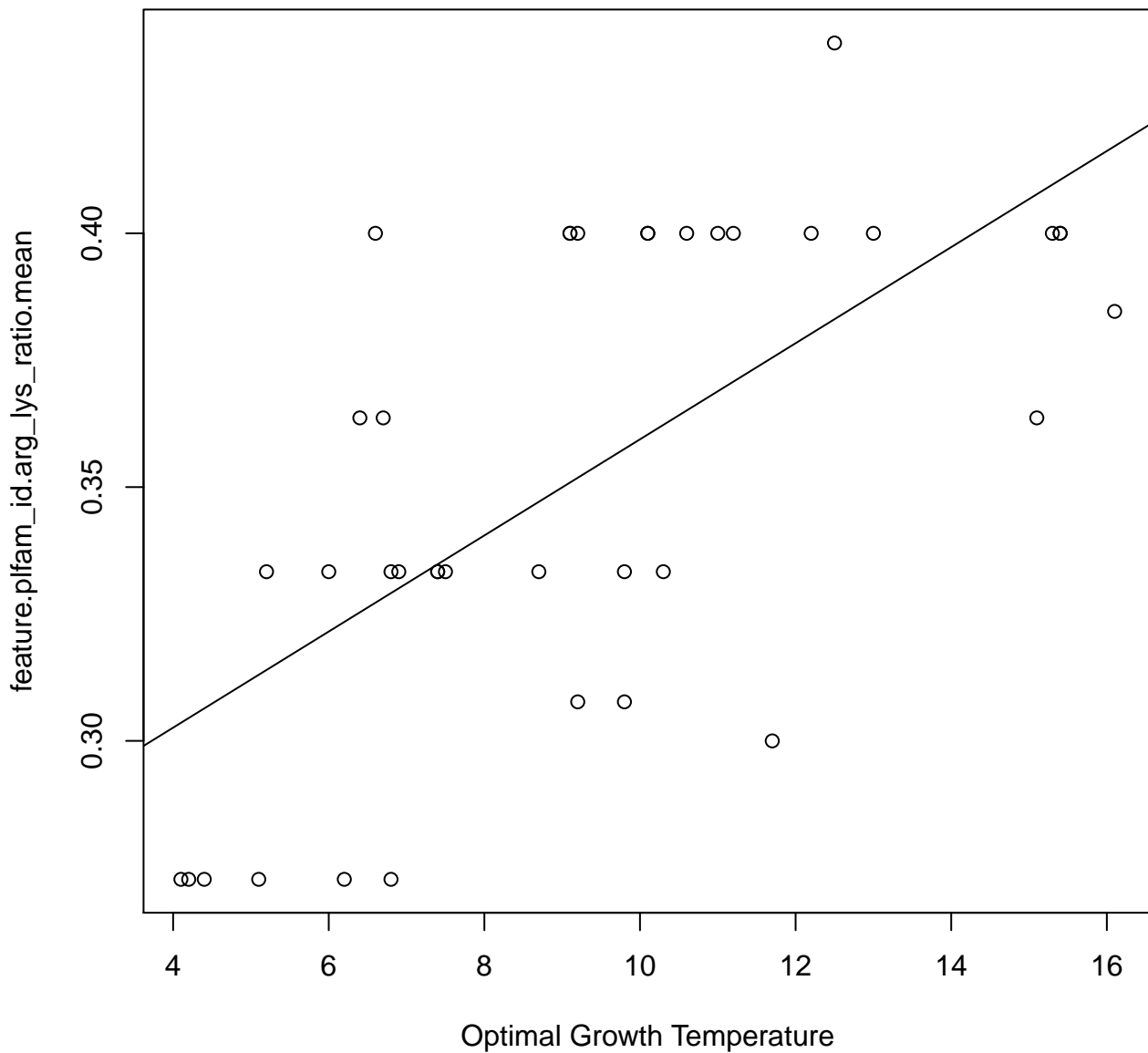
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000396
FIG006045: Sigma factor, ECF subfamily



feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00001718

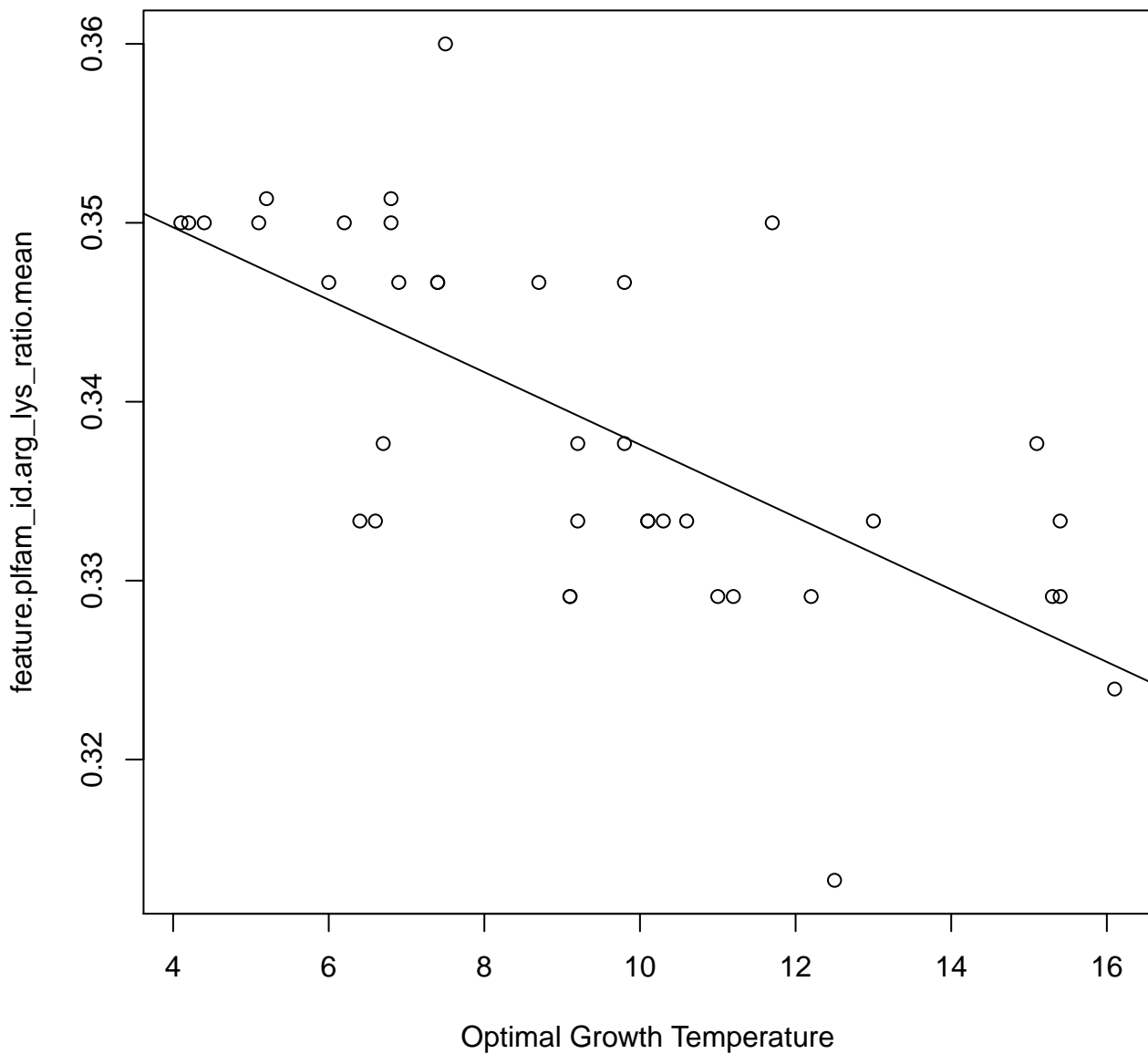
MSHA pilin protein MshB



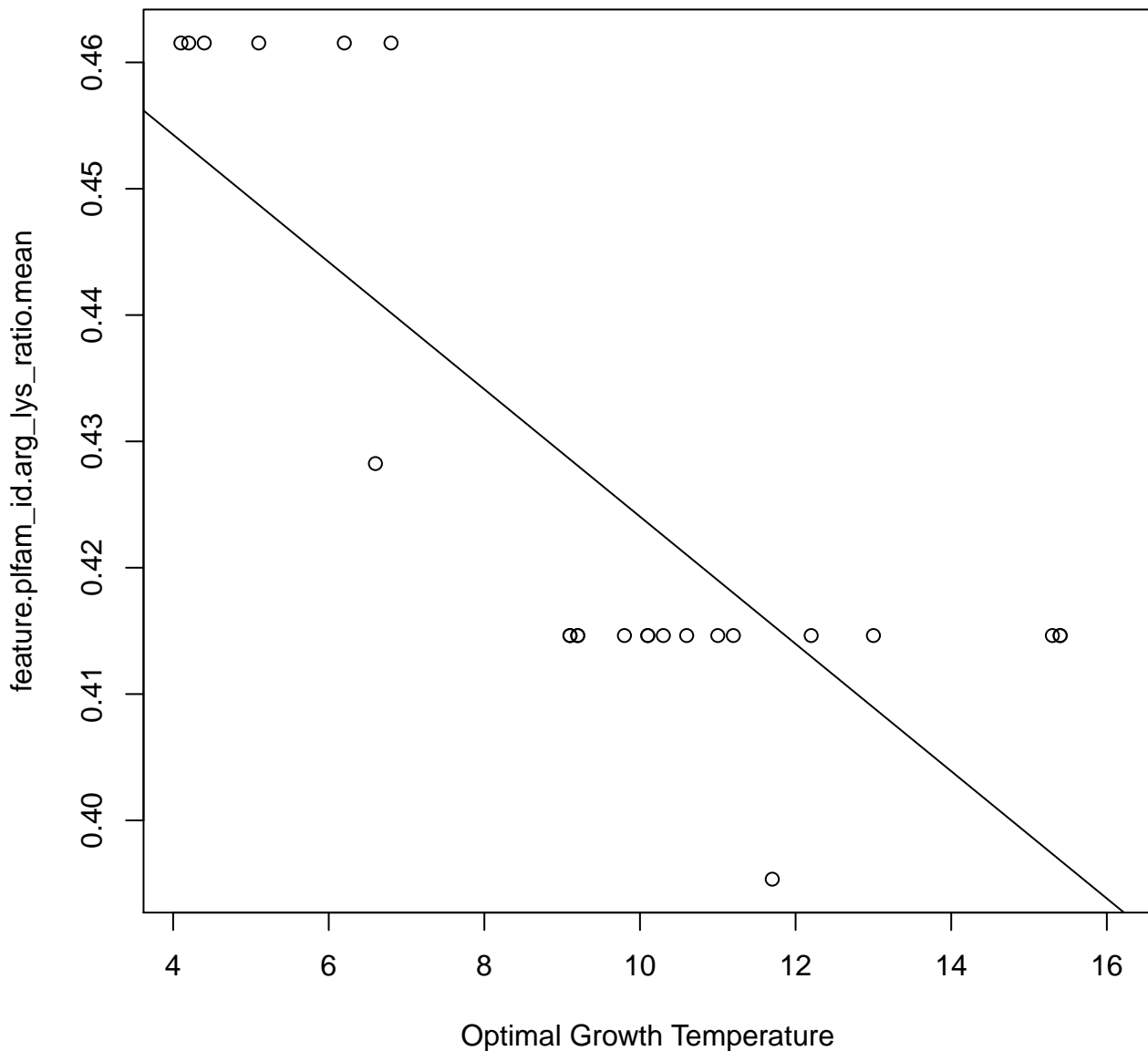
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00002008

Related to collagenase



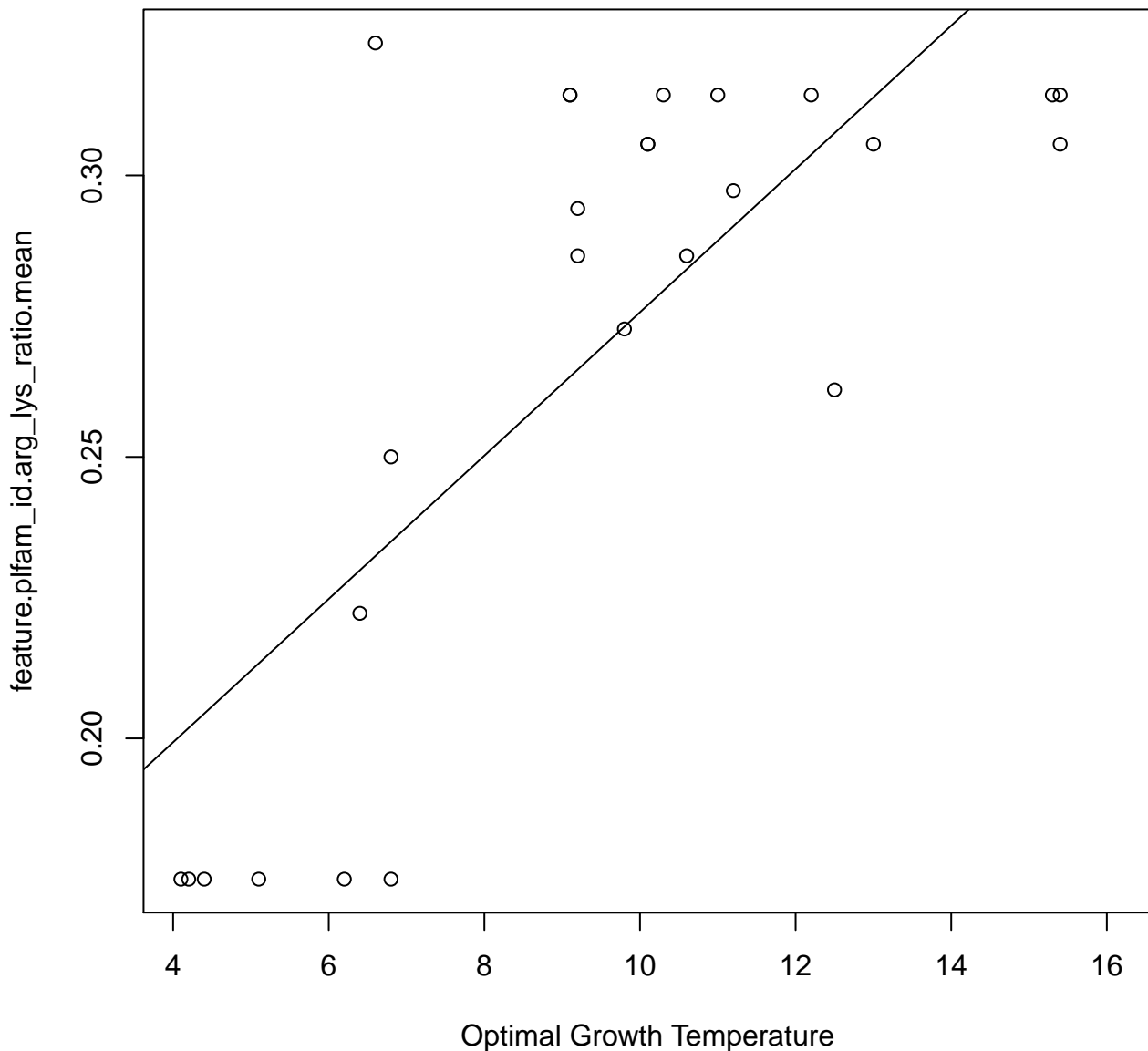
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003282
Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)



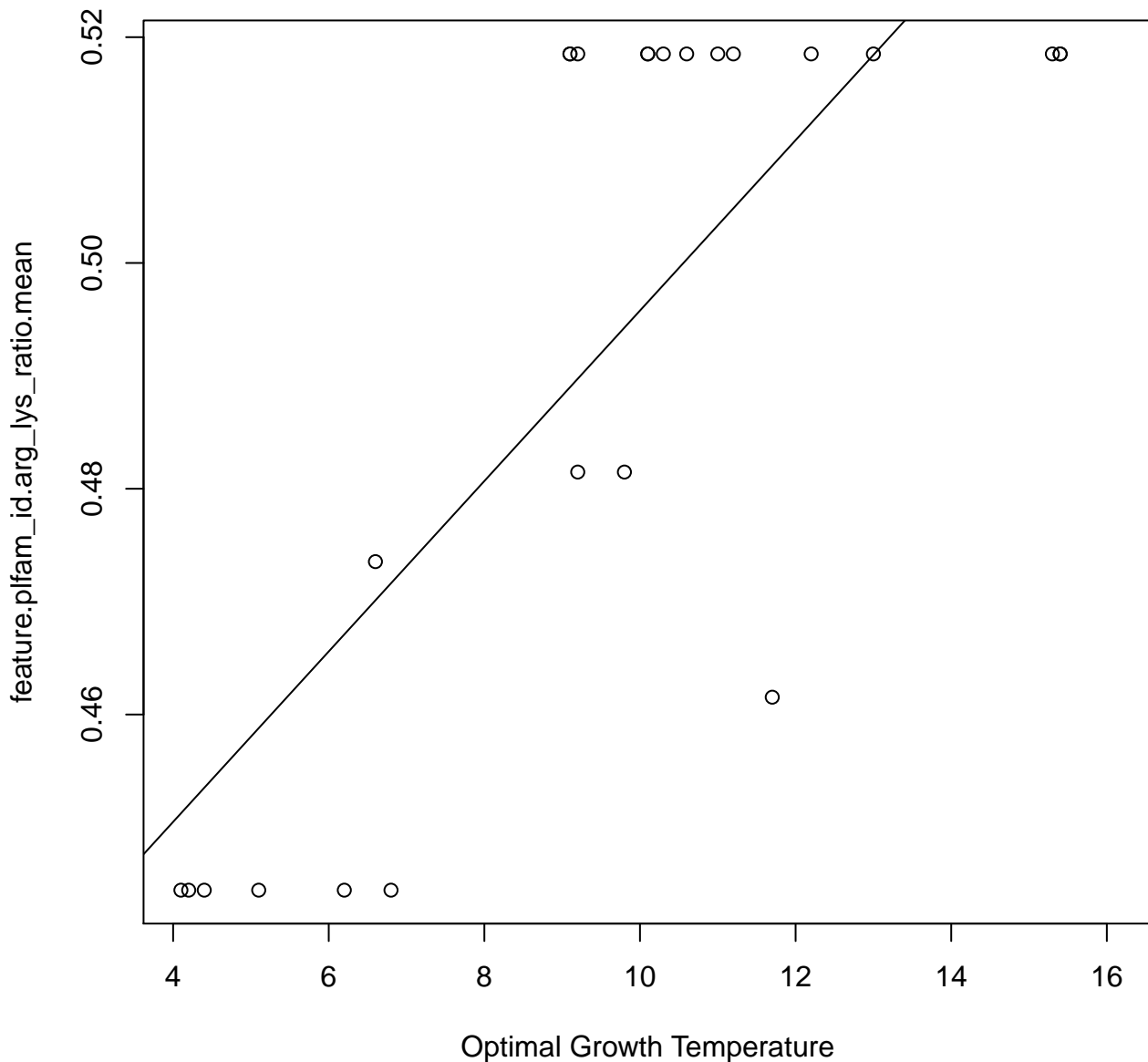
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00003411

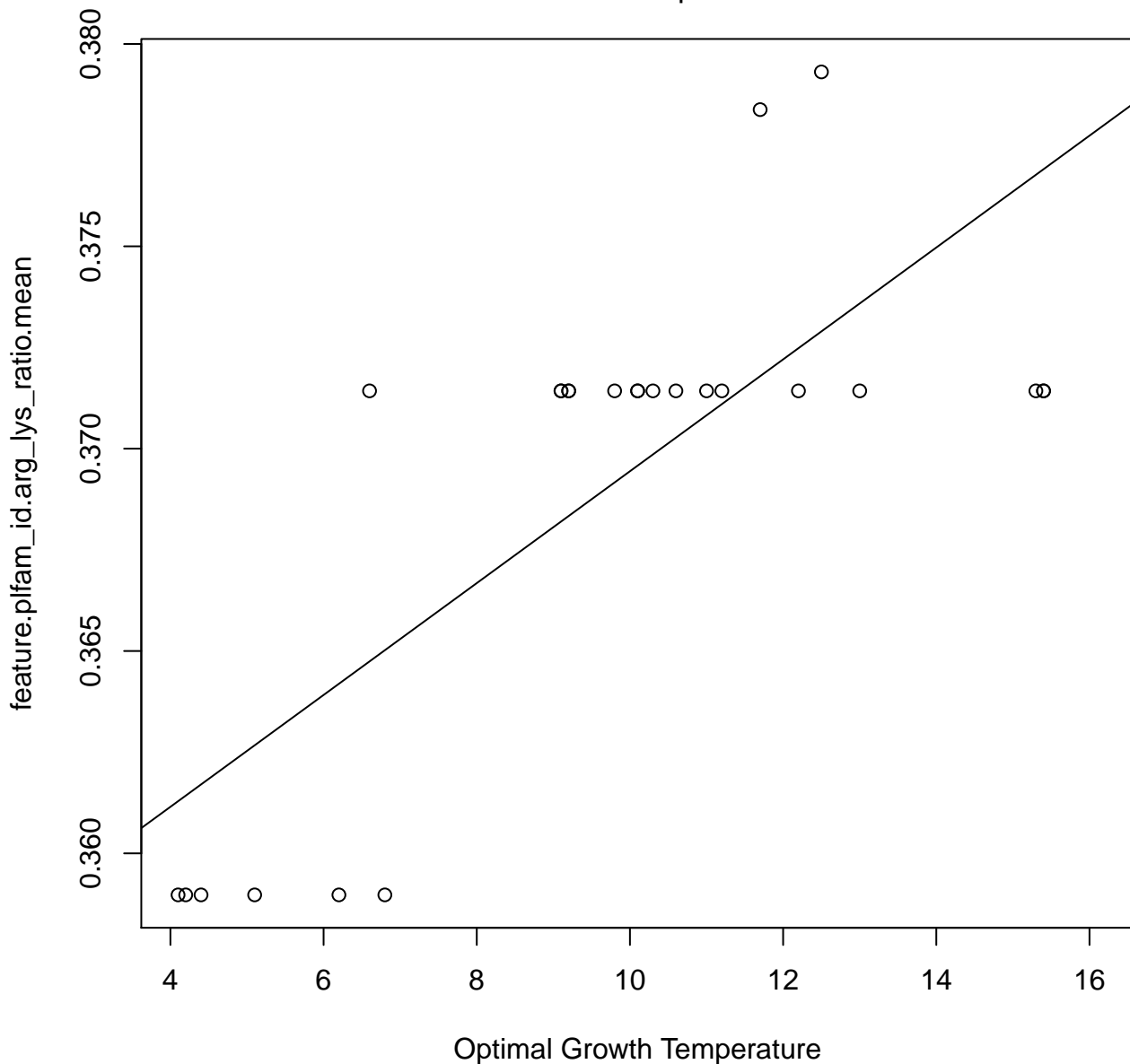
CDP-glycerol: N-acetyl-beta-D-mannosaminyl-1,4-N-acetyl-D-glucosaminyldiphosphoundecaprenyl glycerophosphotransfer



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003412
Chemotaxis protein CheD



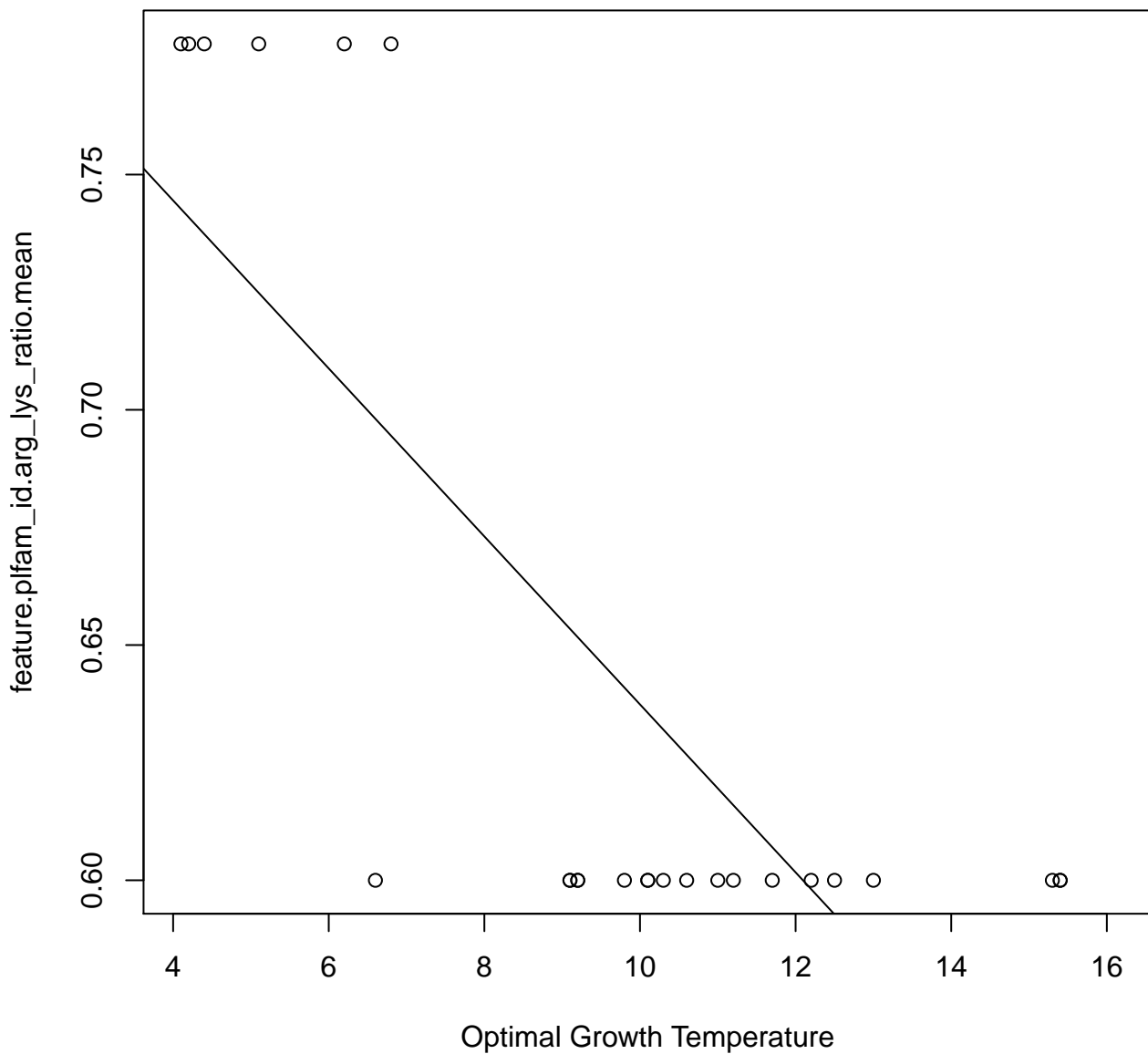
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003454
GGDEF domain protein



feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00003600

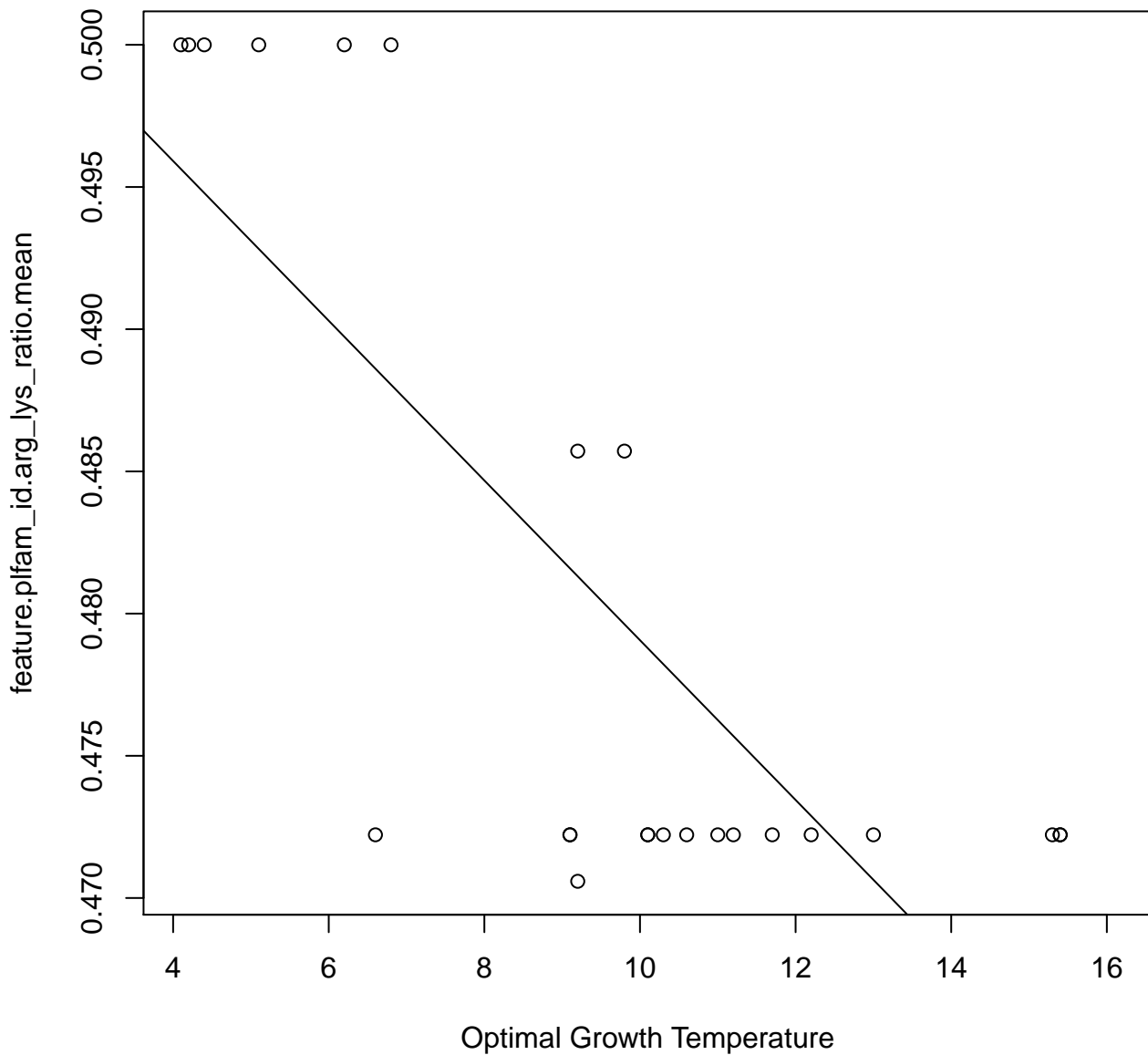
Putative transmembrane protein



feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00005643

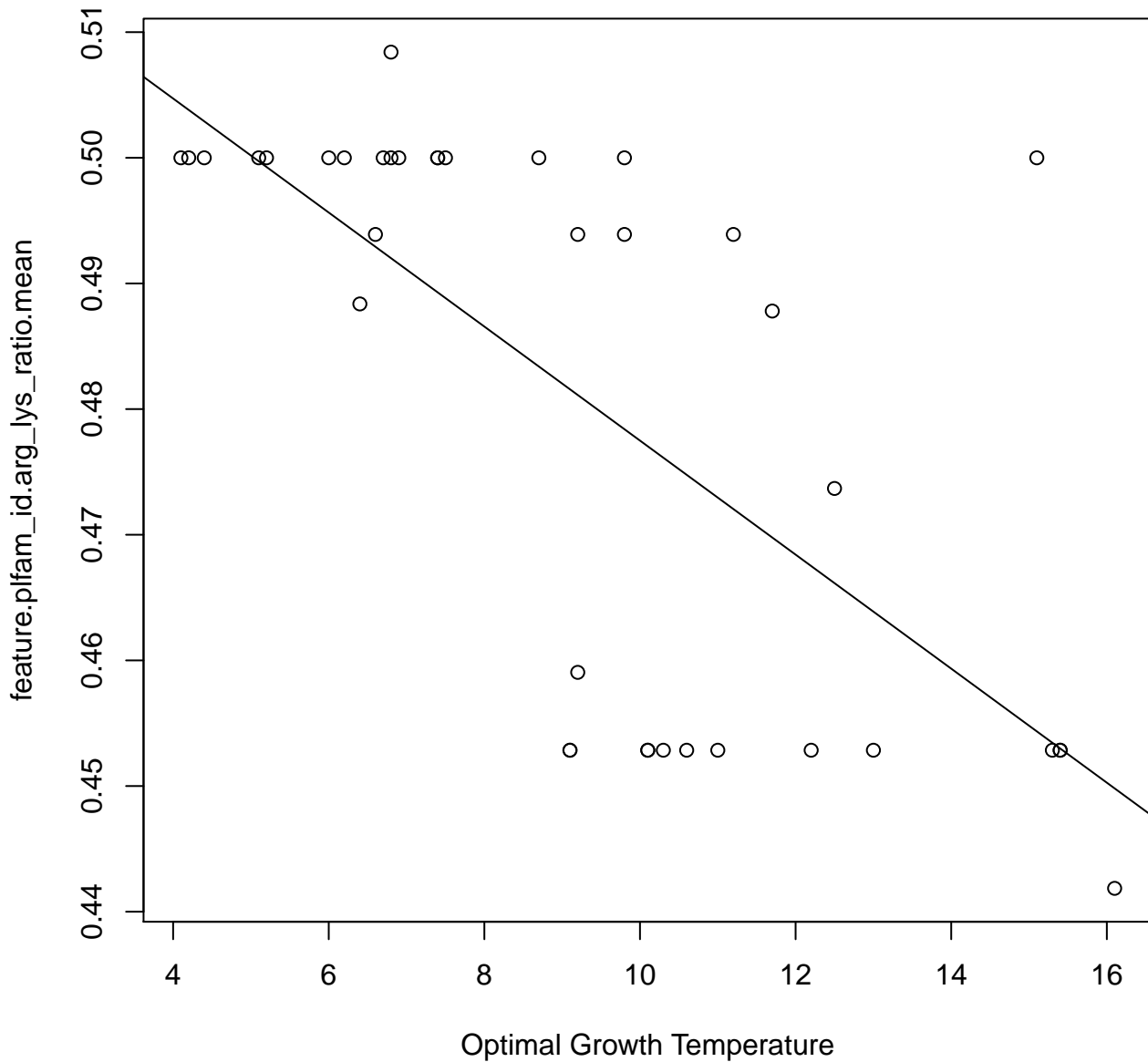
hypothetical protein



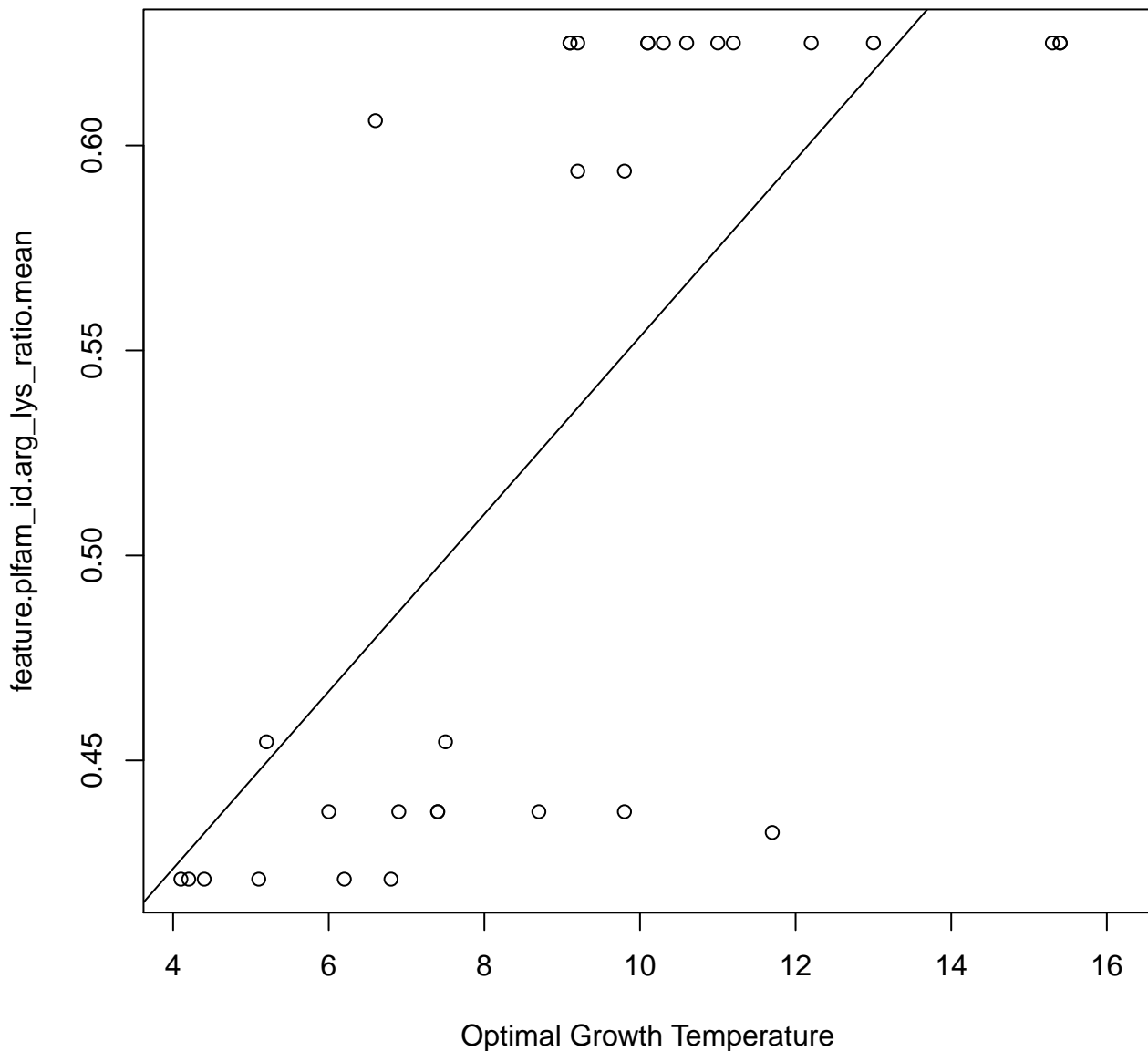
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00006844

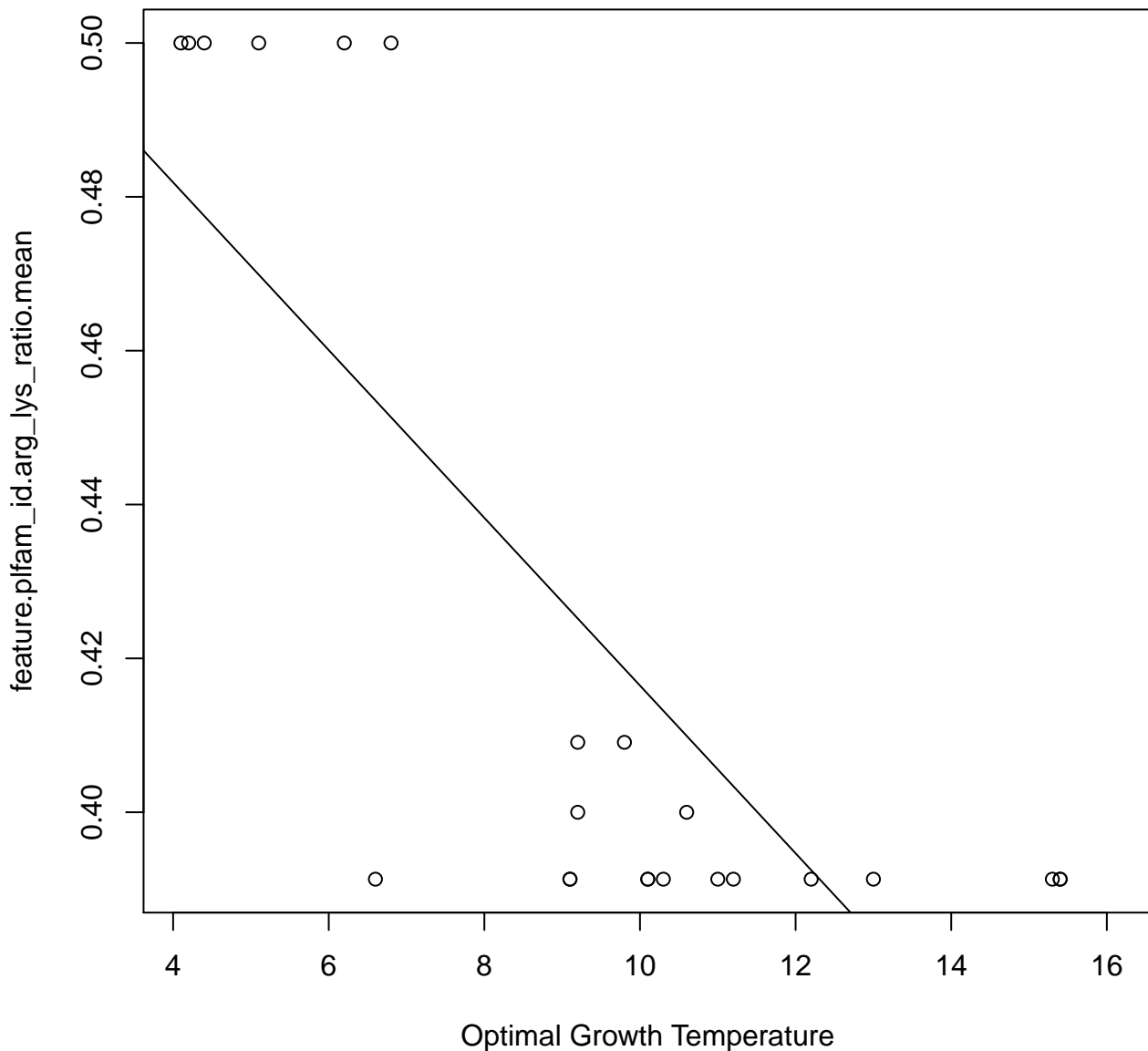
FIG003737: Predicted deacylase



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00013738
hypothetical protein



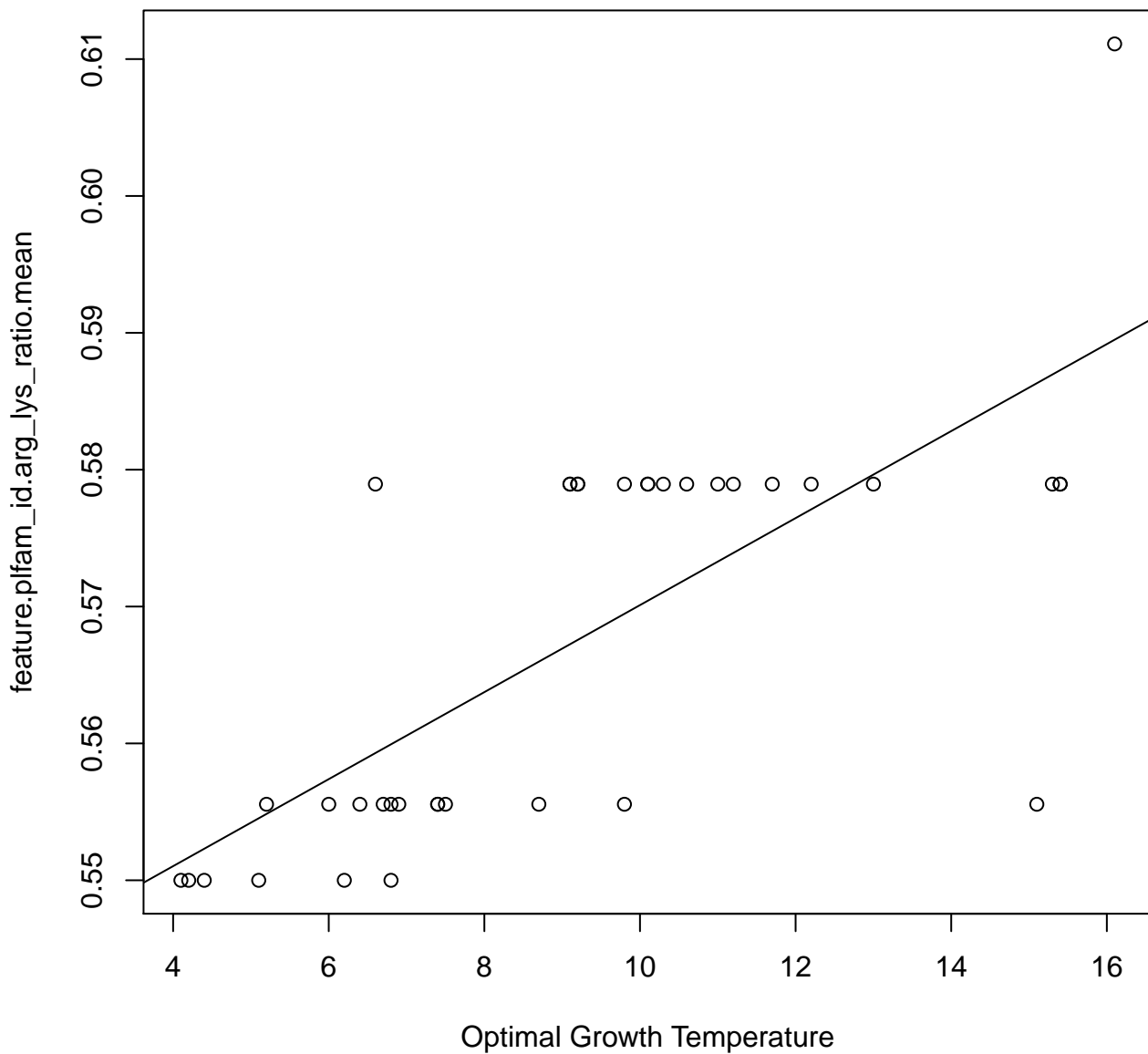
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00014070
hypothetical protein



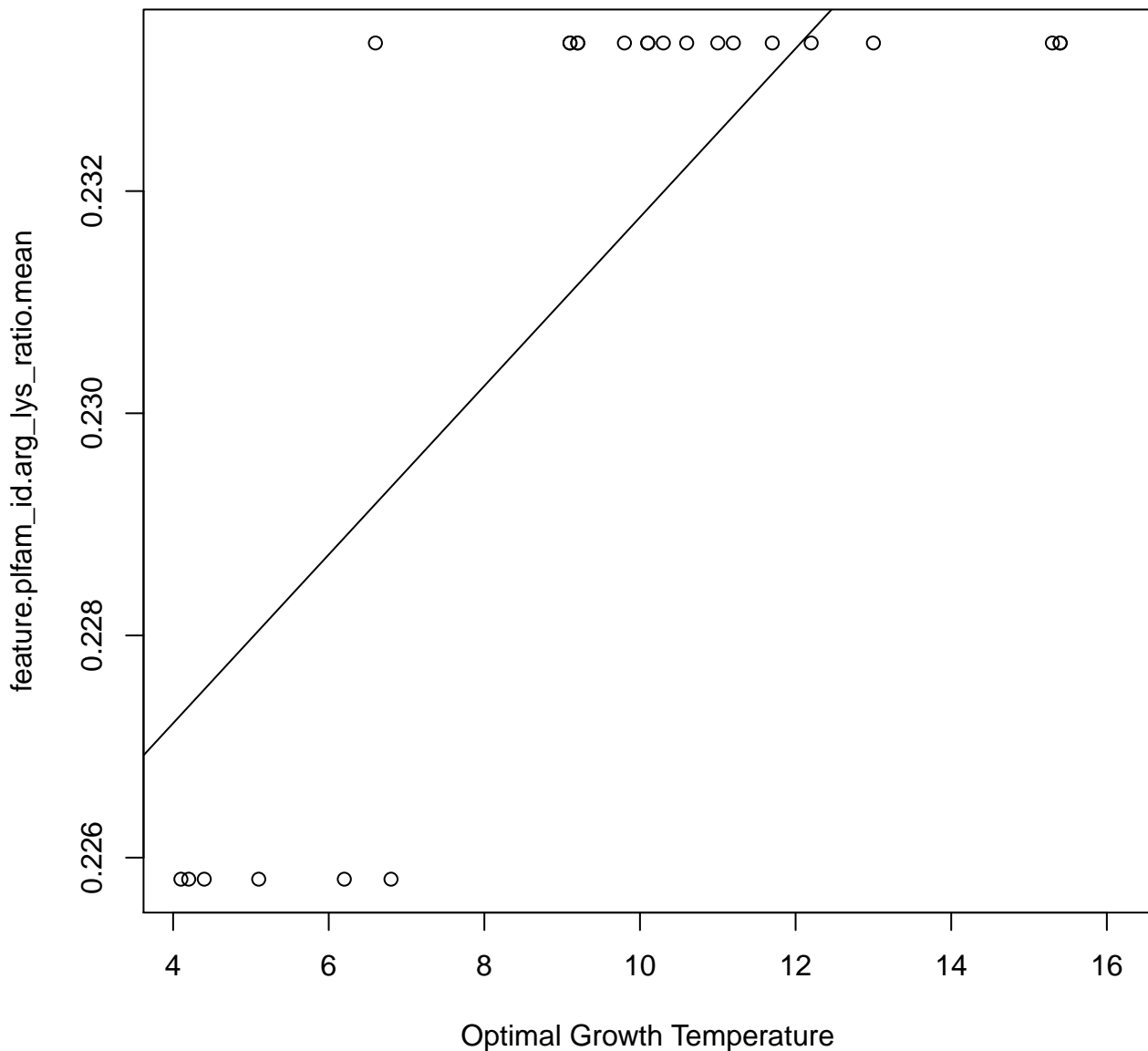
feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00014664

hypothetical protein



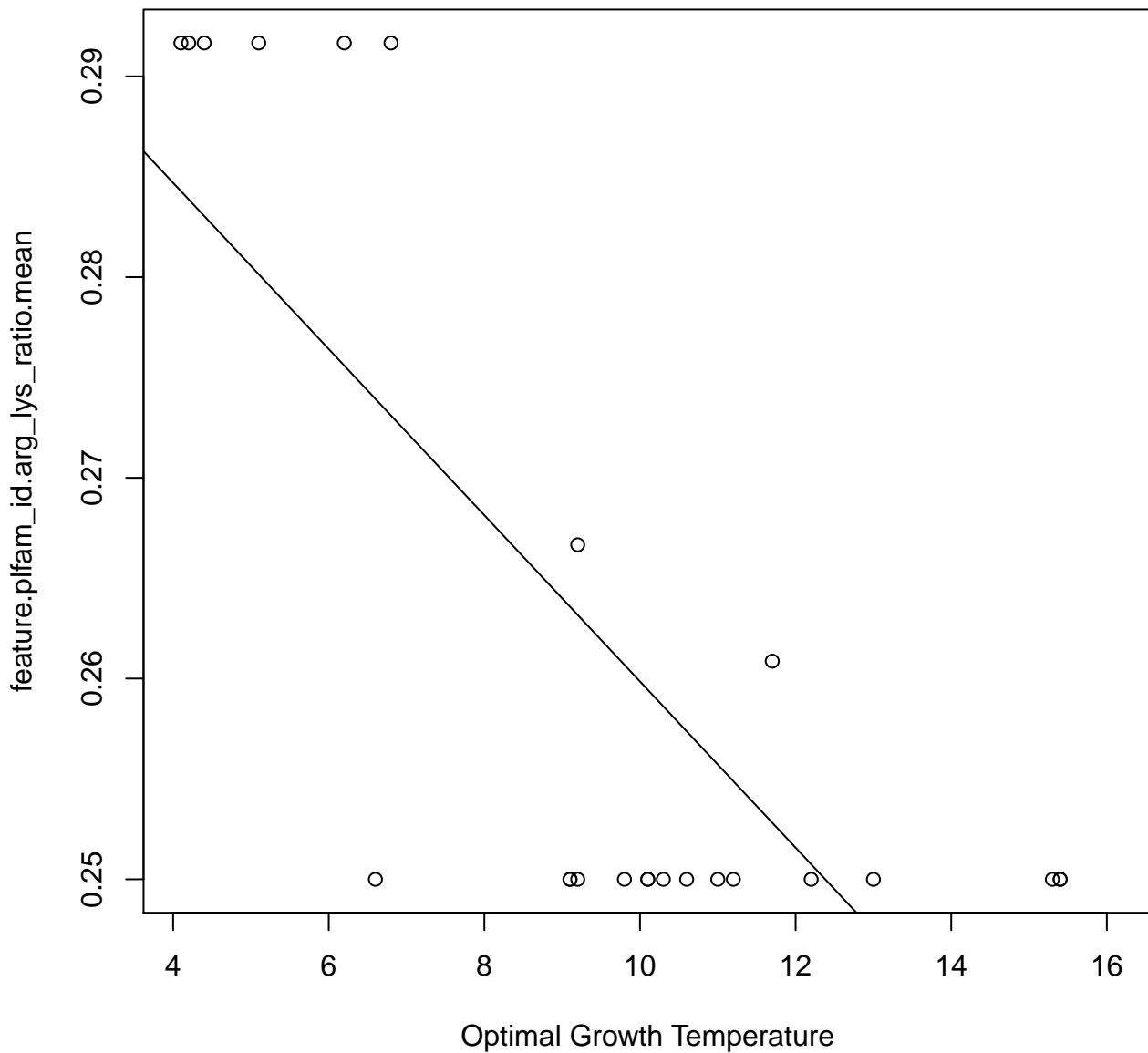
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00015062
hypothetical protein



feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00017041

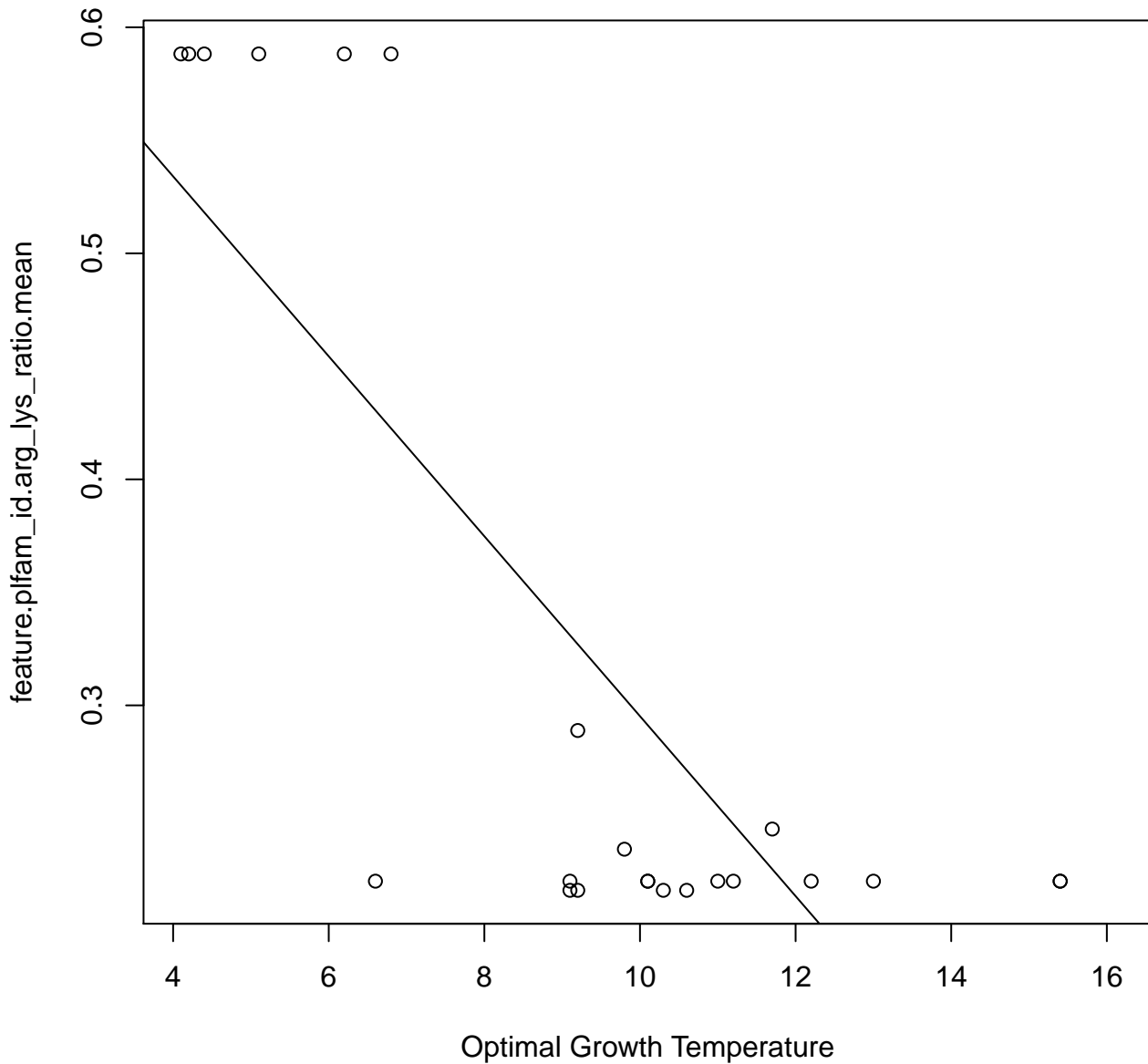
hypothetical protein



feature.plfam_id.arg_lys_ratio.mean

PLF_28228_00017455

Maltodextrin glucosidase (EC 3.2.1.20)

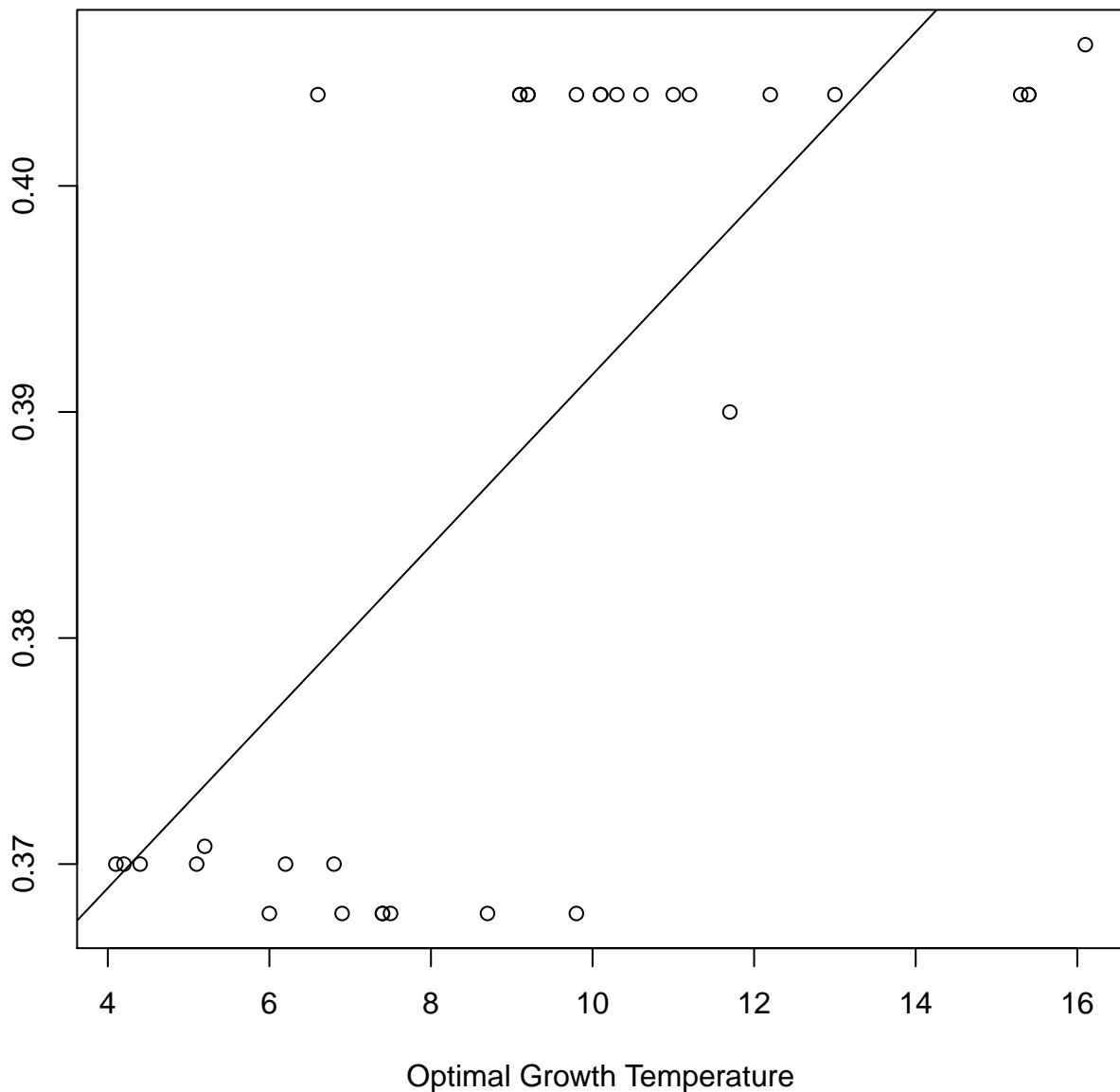


feature.plfam_id.arg_lys_ratio.mean

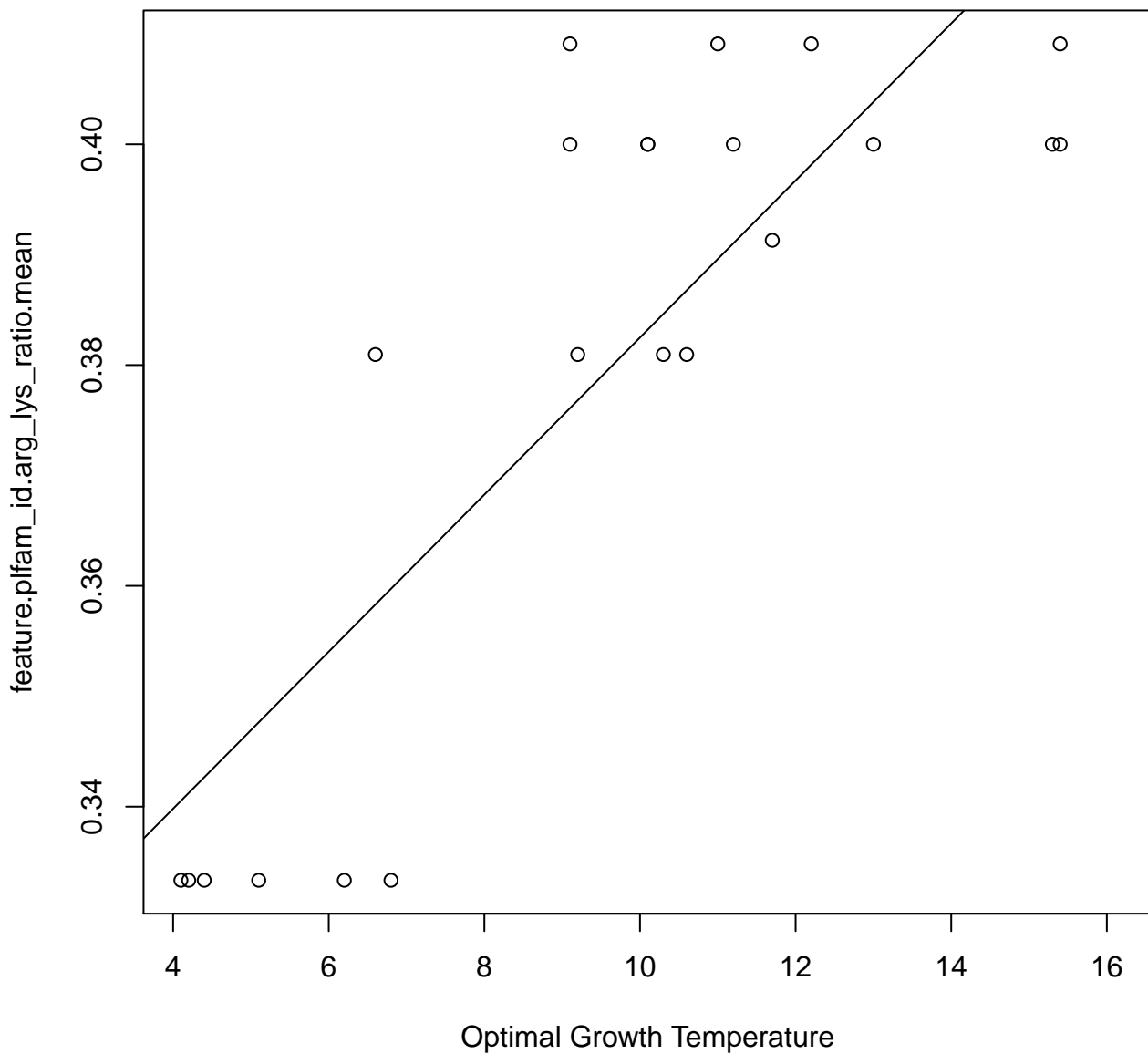
PLF_28228_00018174

hypothetical protein

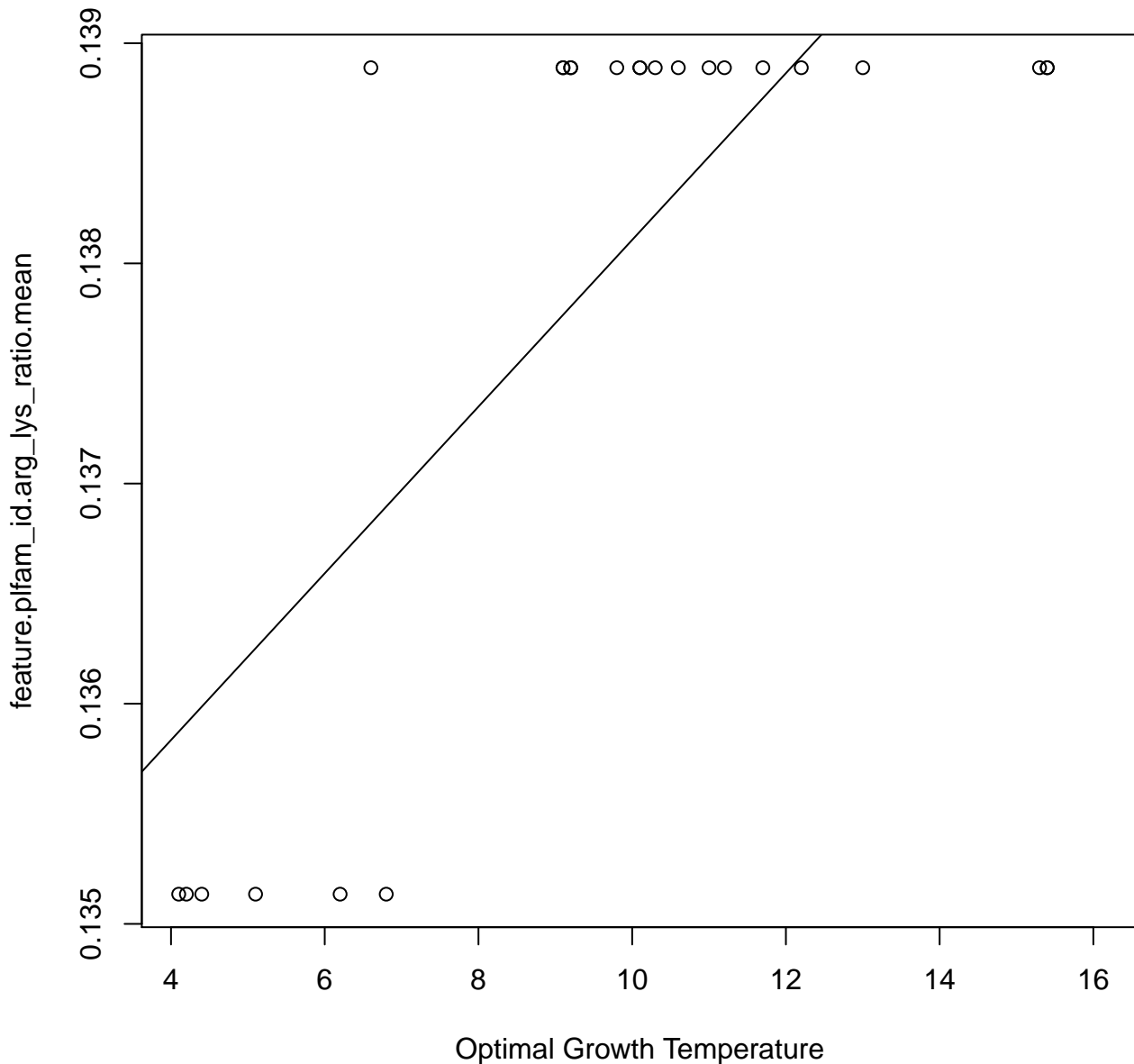
feature.plfam_id.arg_lys_ratio.mean



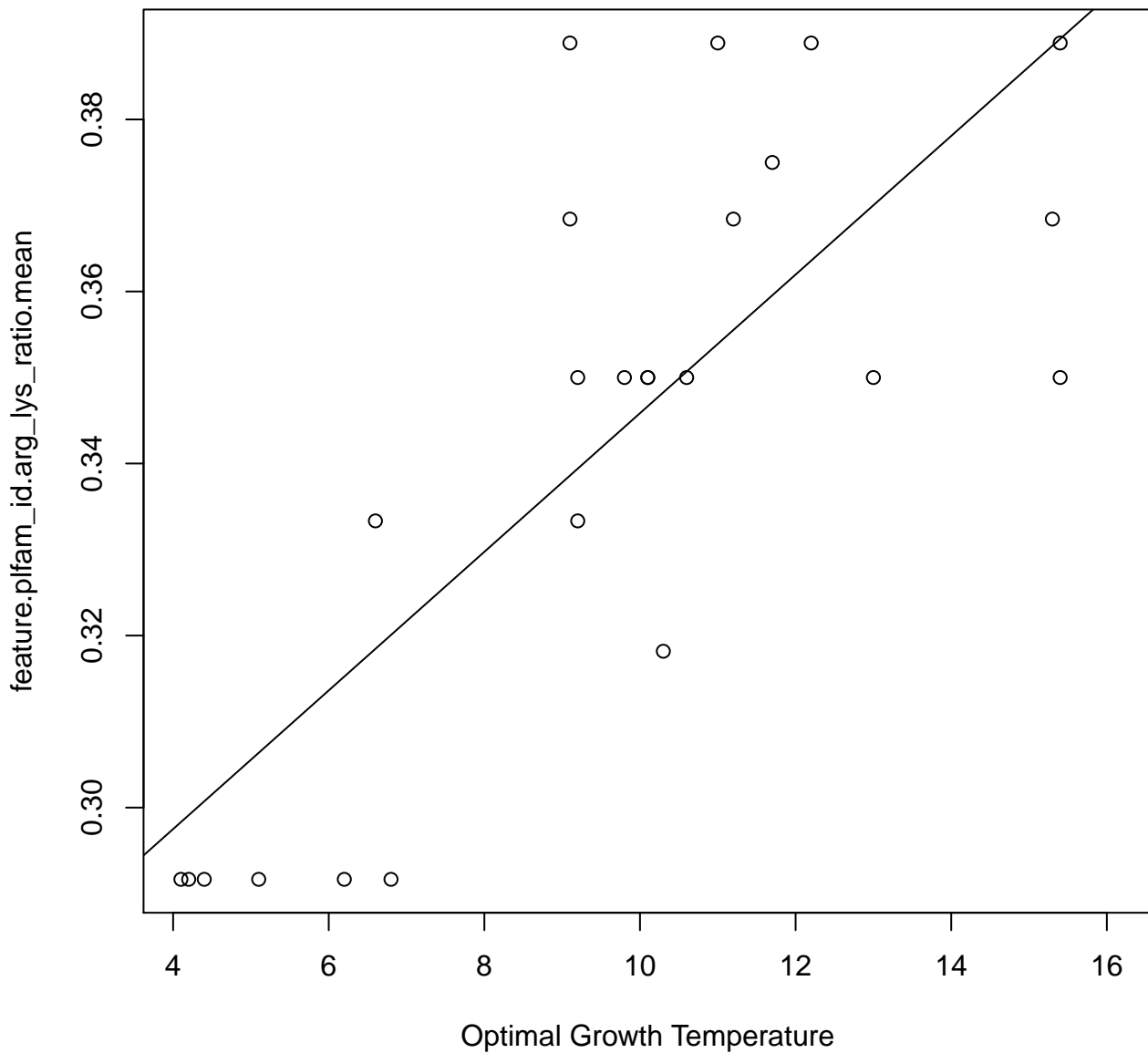
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00020926
hypothetical protein



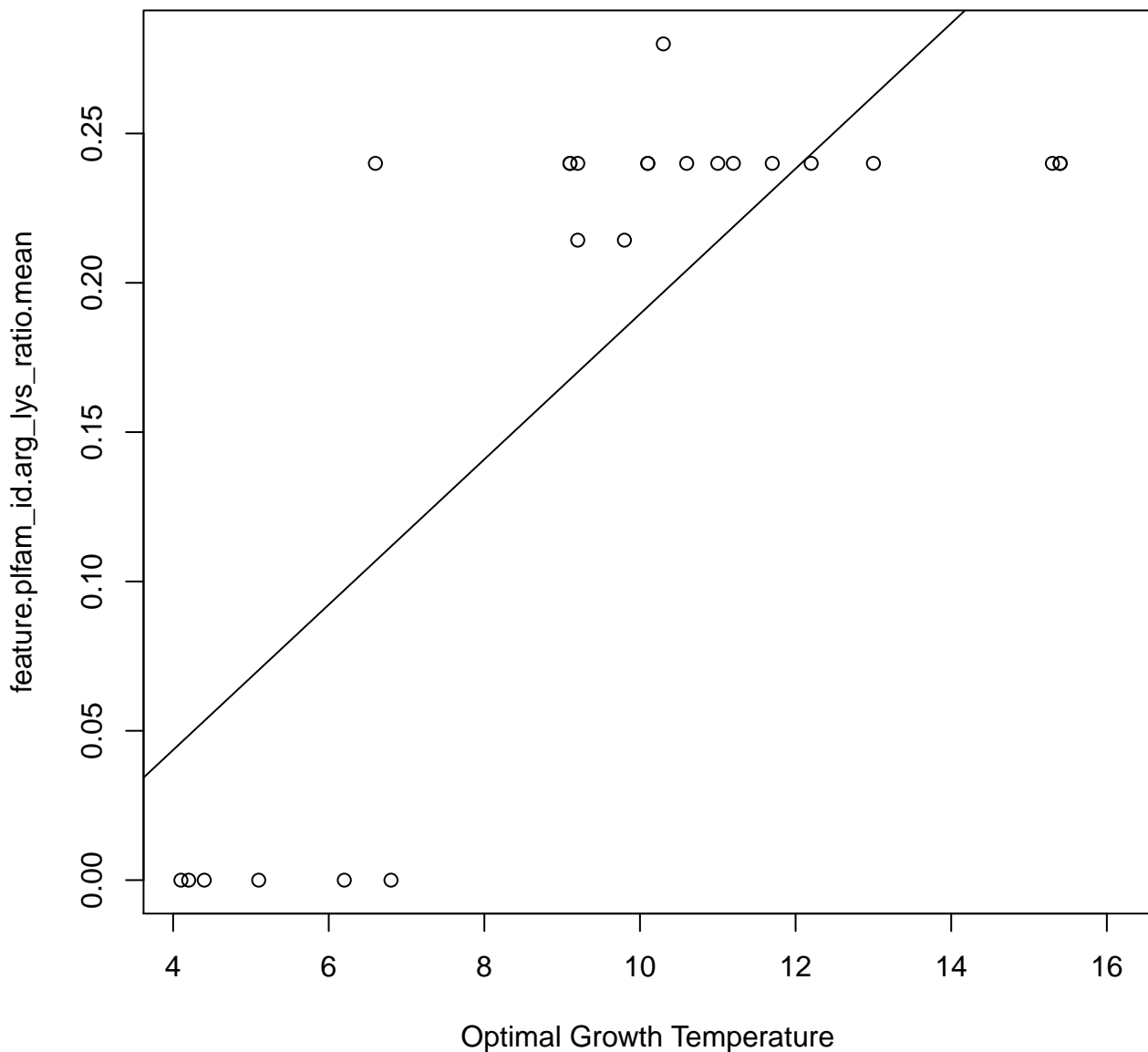
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00023013
hypothetical protein



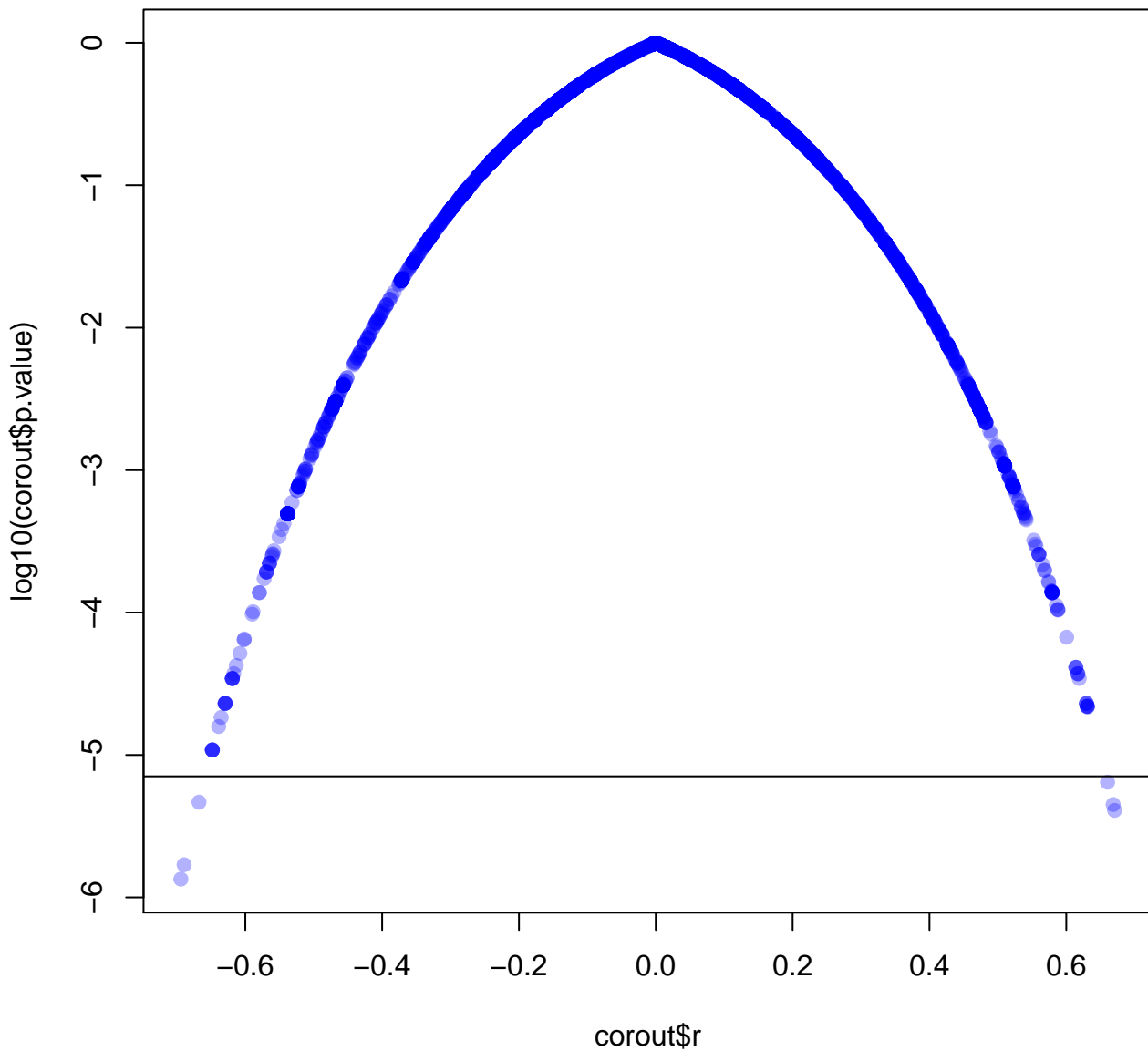
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00030698
hypothetical protein



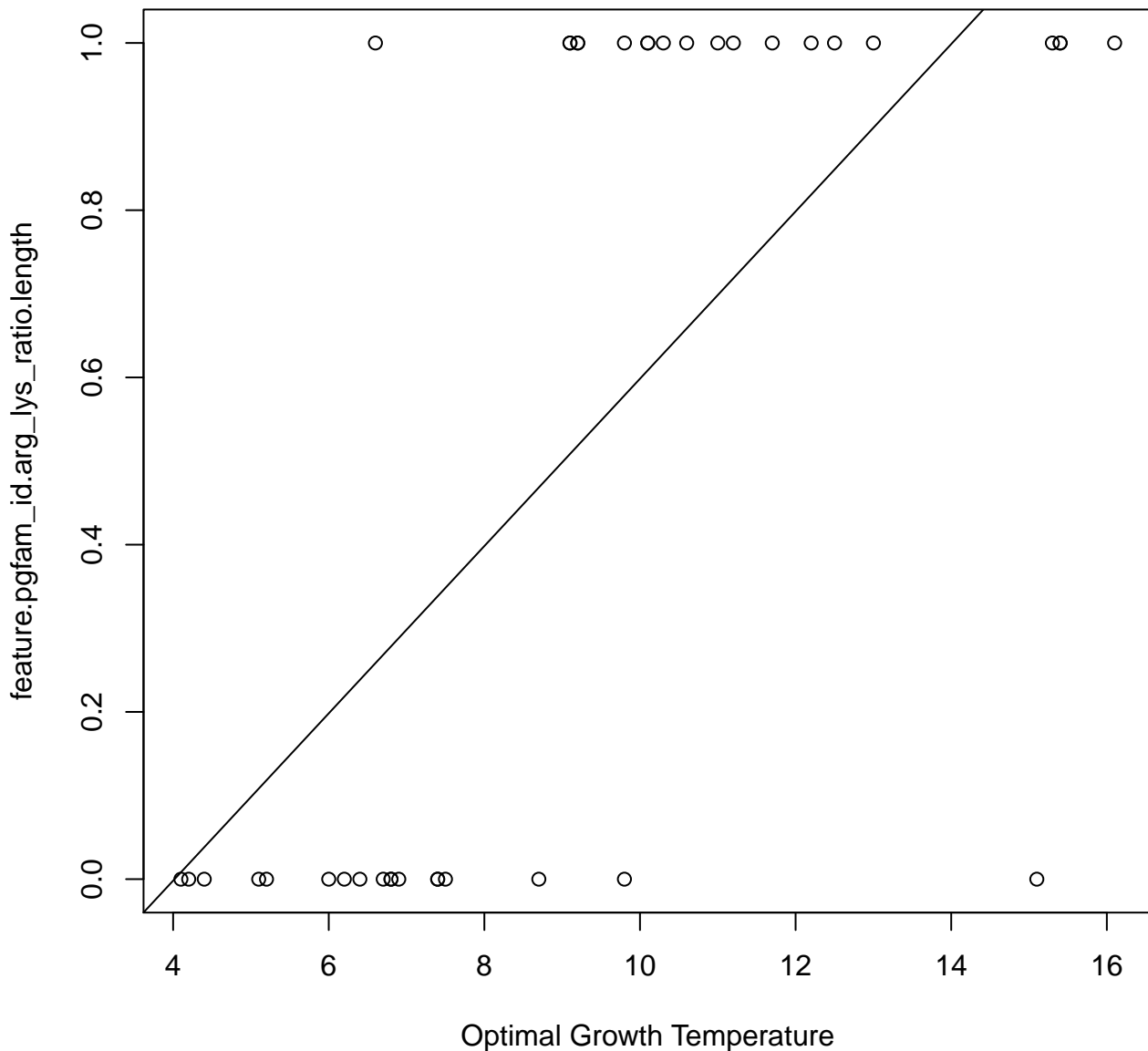
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00031426
hypothetical protein



feature.pgfam_id.arg_lys_ratio.length



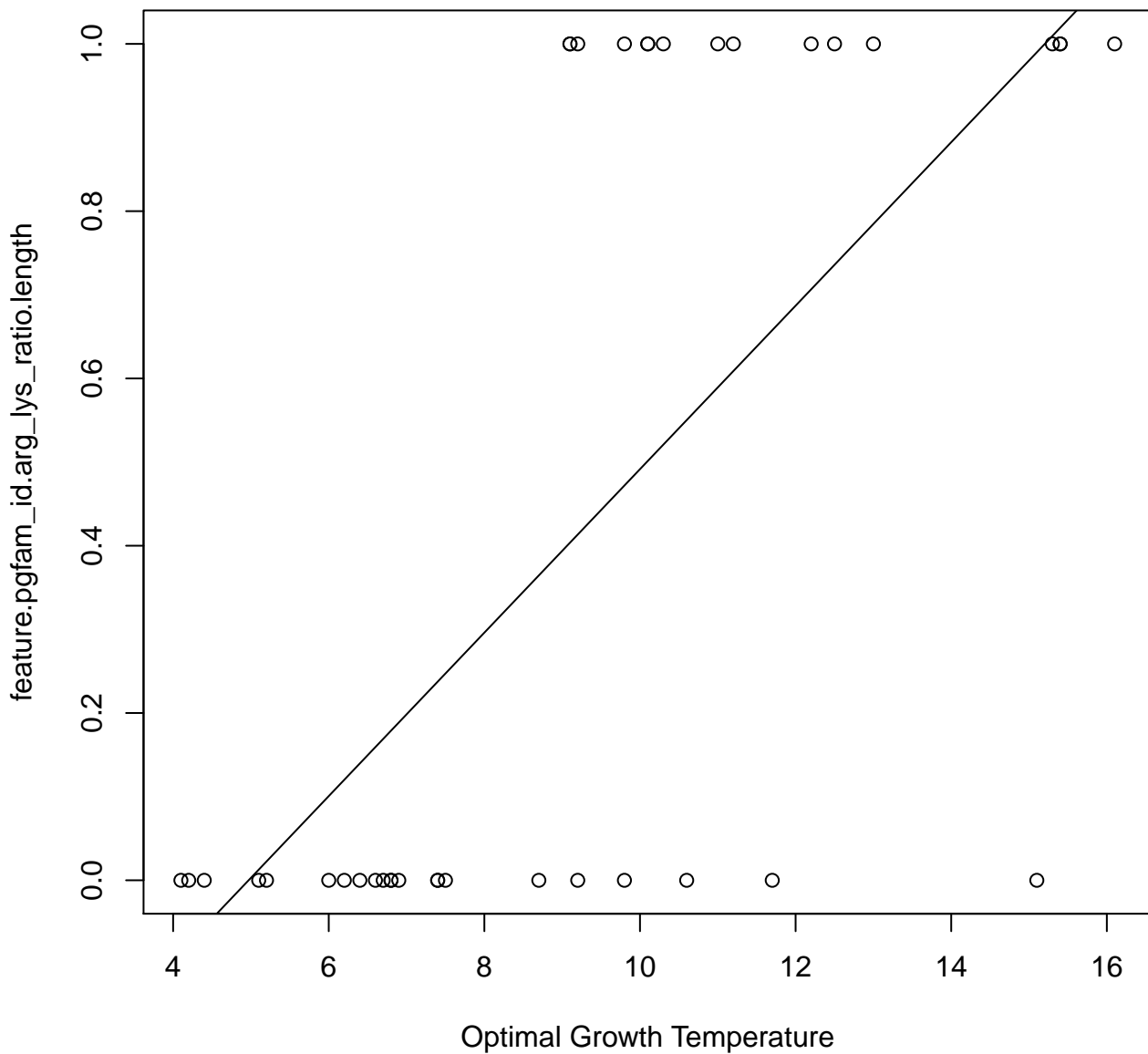
feature.pgfam_id.arg_lys_ratio.length
PGF_00418166
CmpX



feature.pgfam_id.arg_lys_ratio.length

PGF_01917480

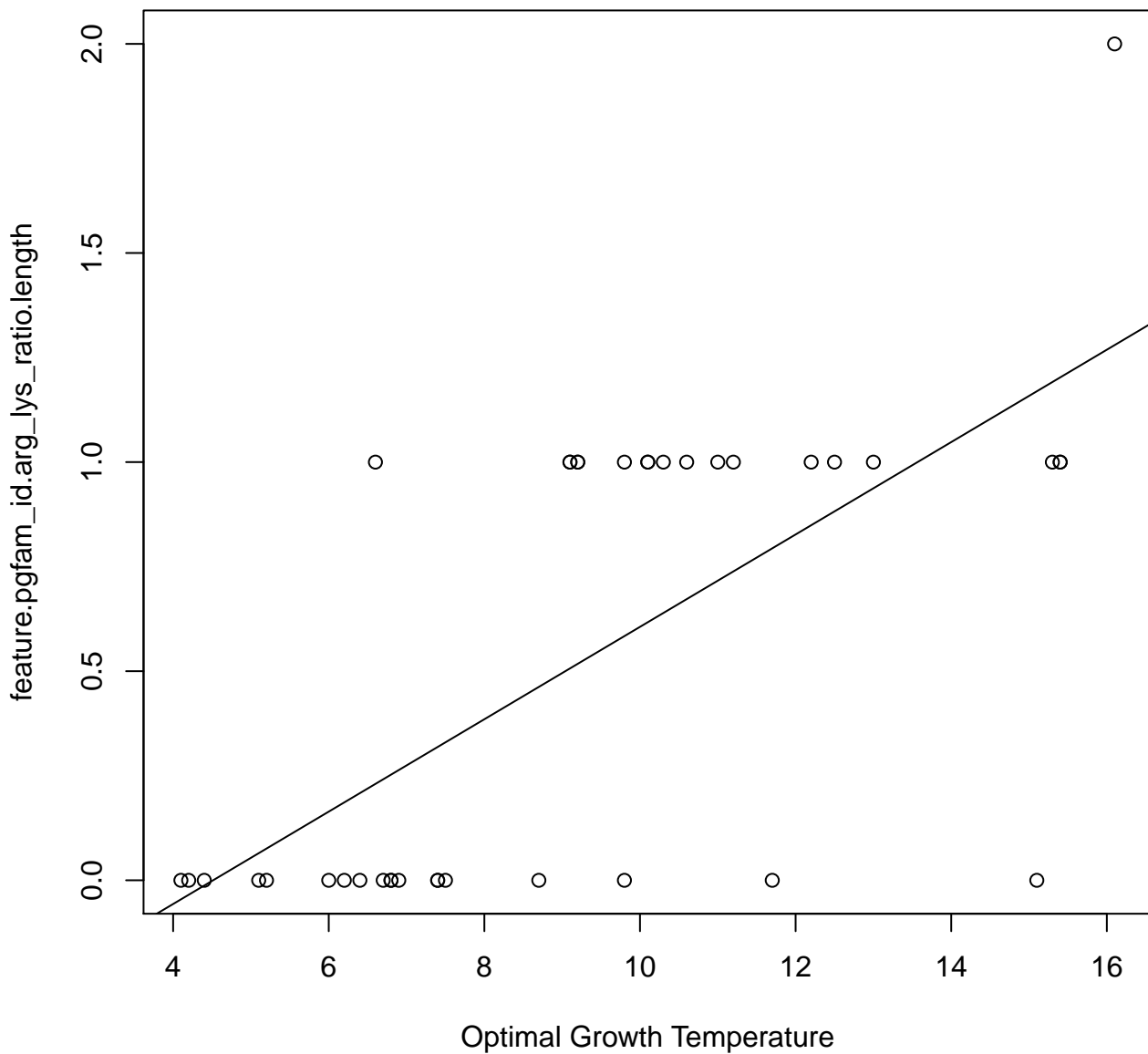
General secretion pathway protein L



feature.pgfam_id.arg_lys_ratio.length

PGF_03687279

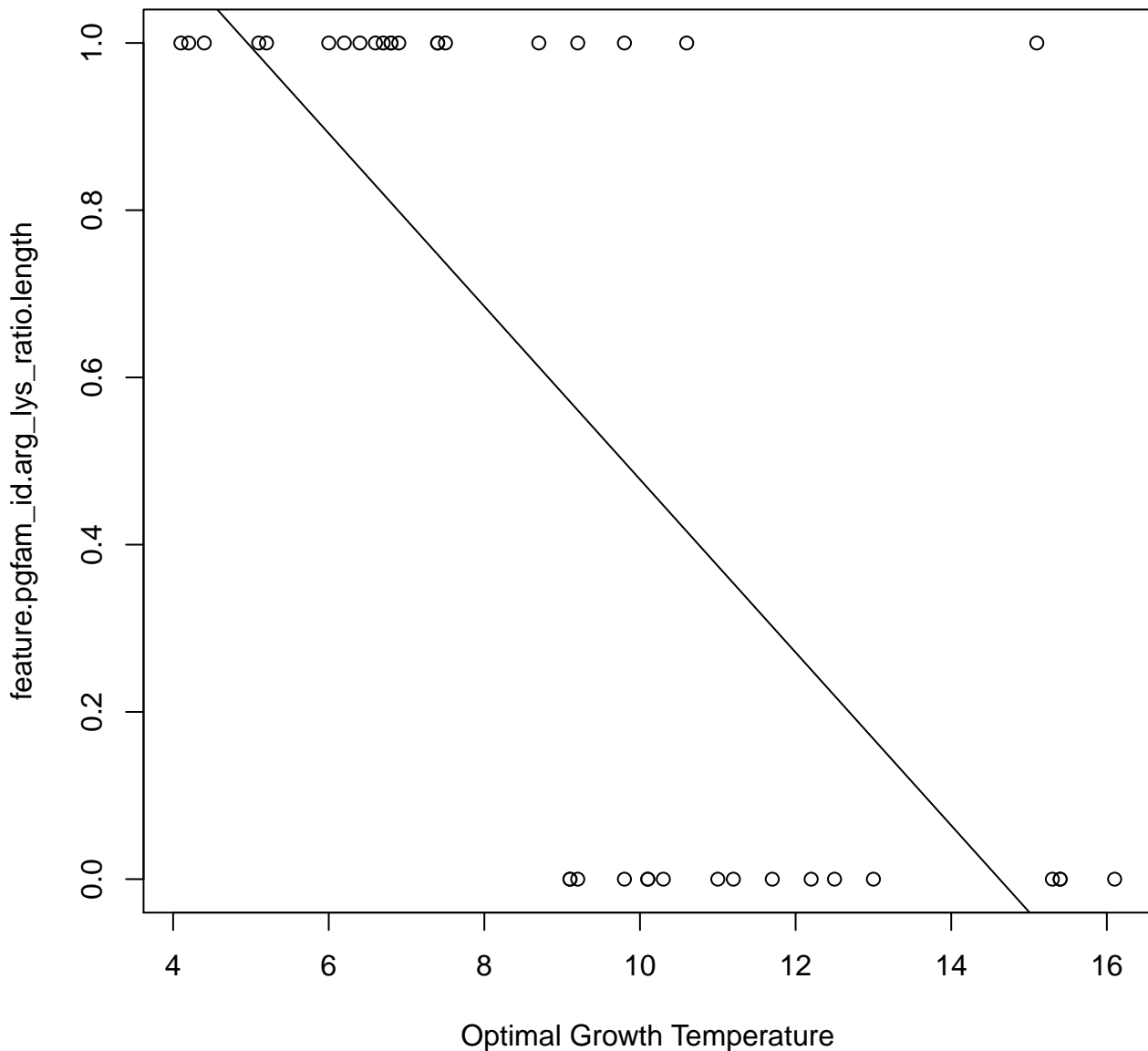
Uncharacterized MFS-type transporter



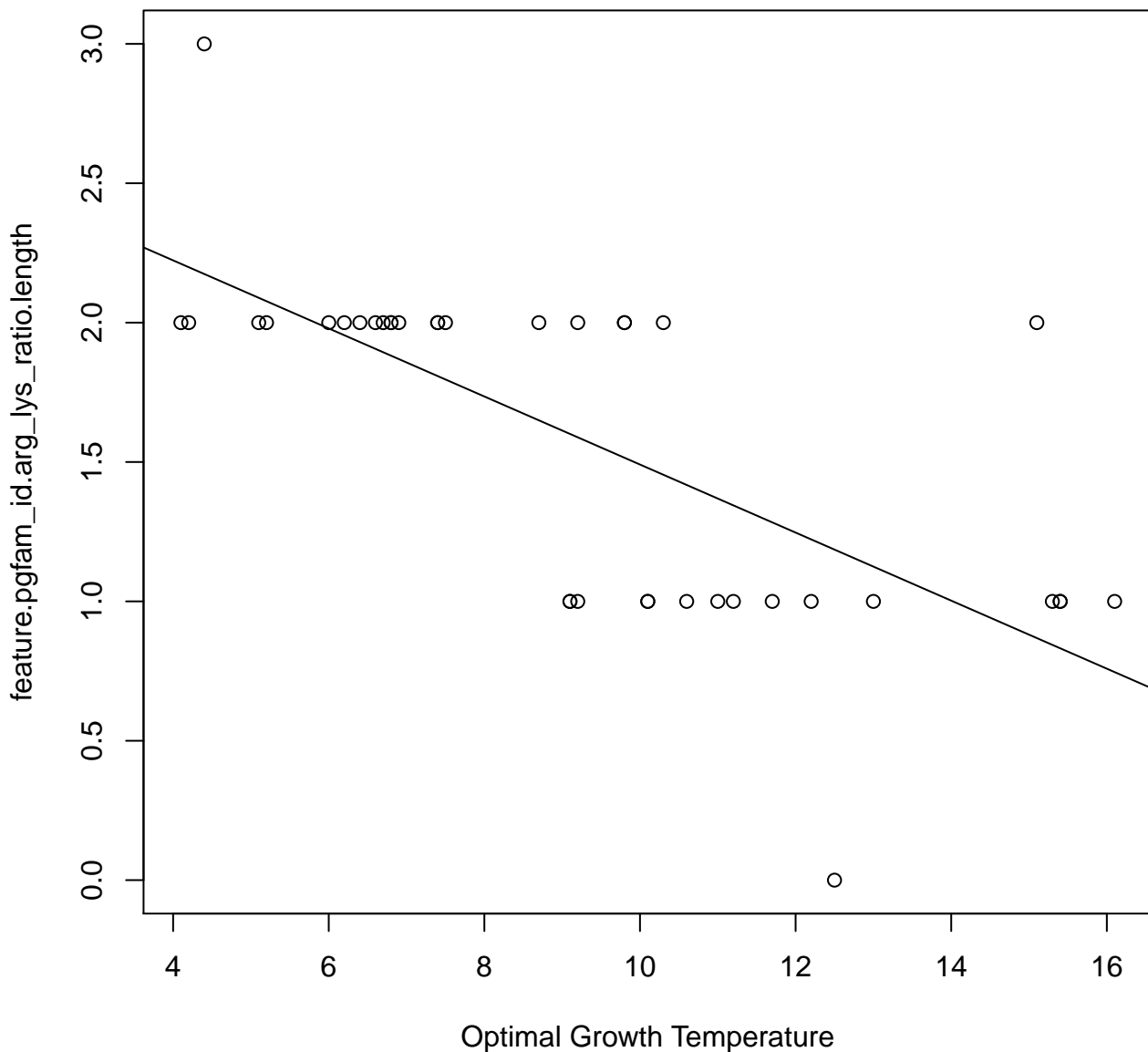
feature.pgfam_id.arg_lys_ratio.length

PGF_07383941

hypothetical protein



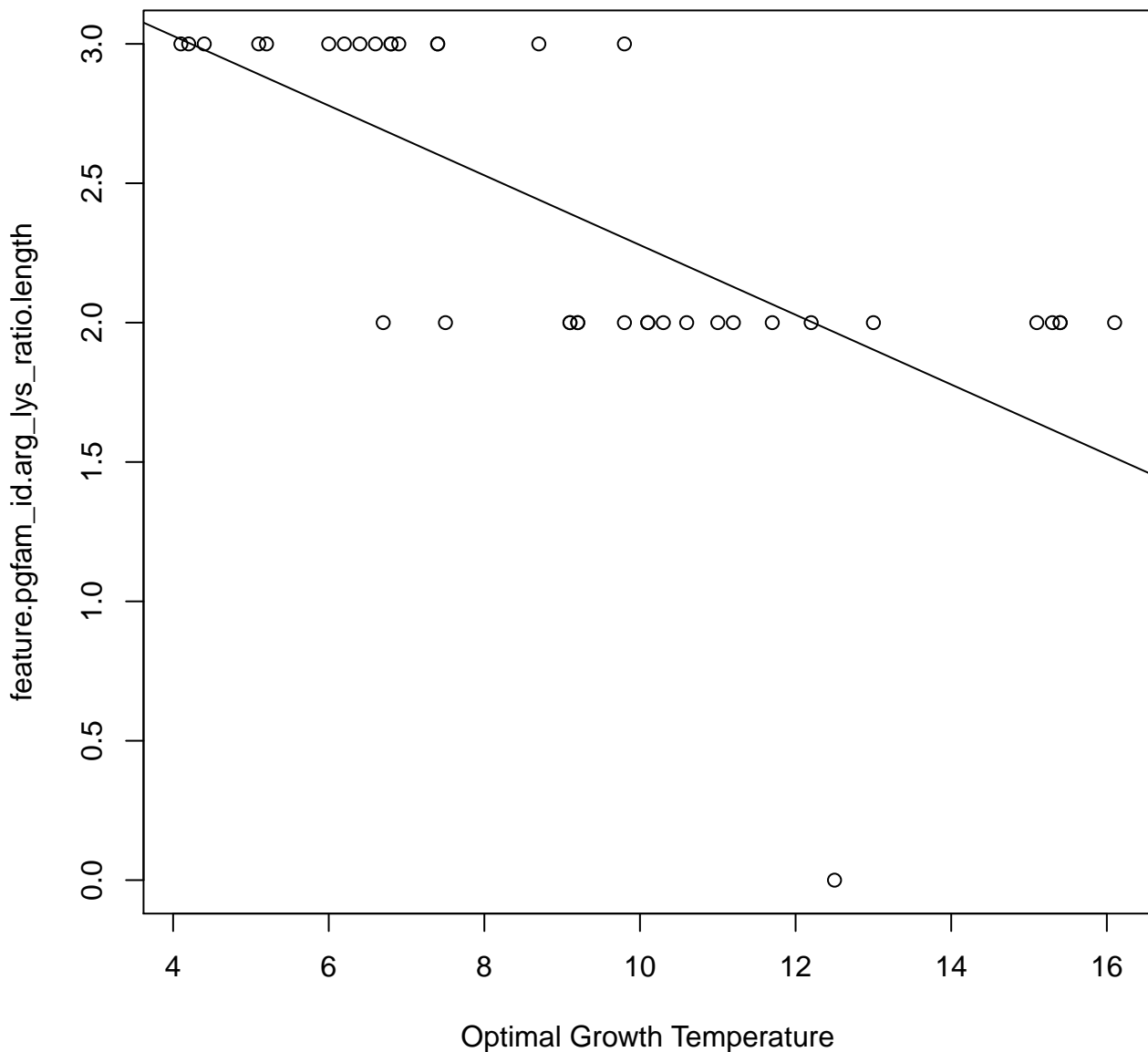
feature.pgfam_id.arg_lys_ratio.length
PGF_07583562
Cysteine desulfurase (EC 2.8.1.7) => SufS



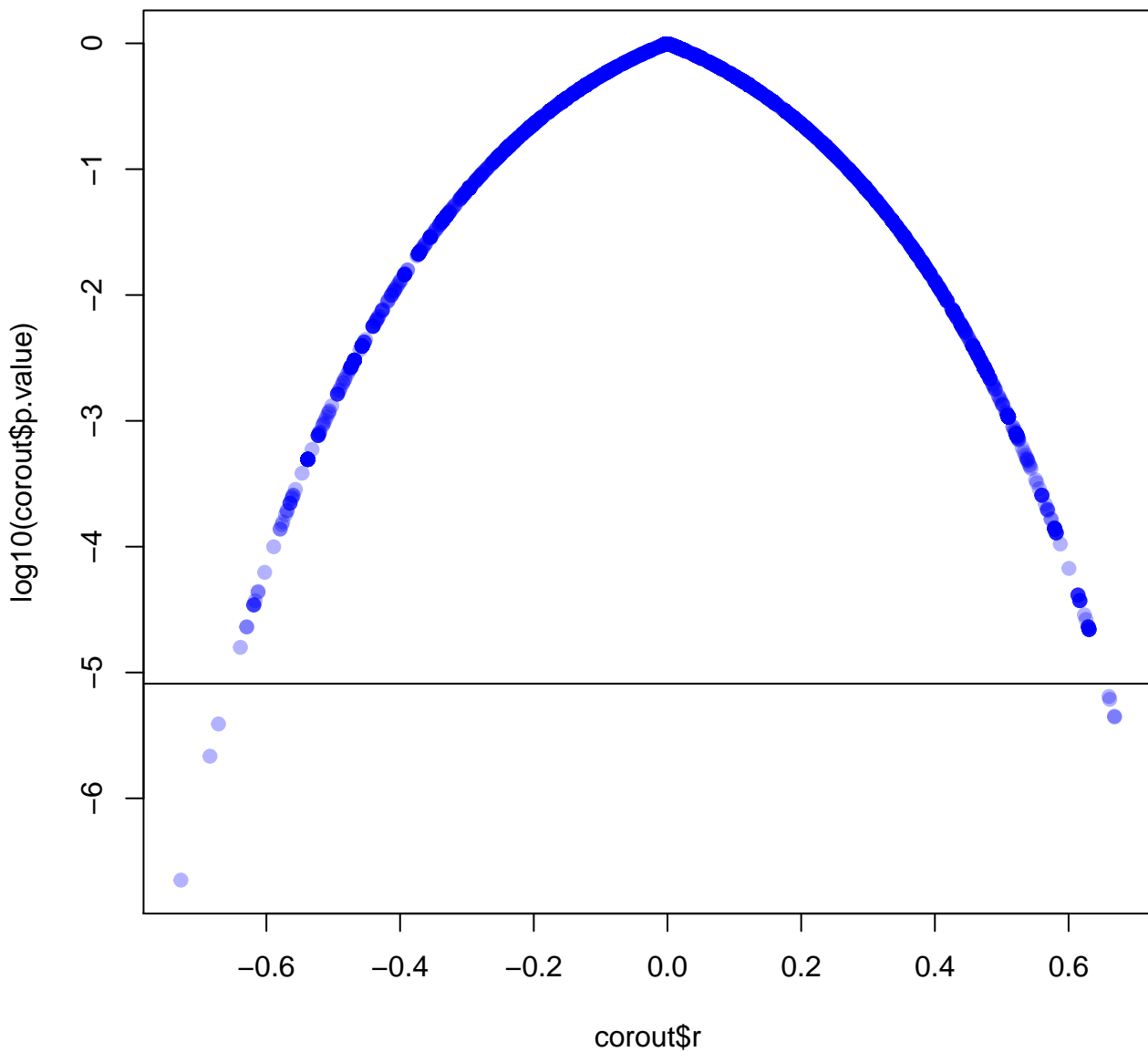
feature.pgfam_id.arg_lys_ratio.length

PGF_10238627

Chemotaxis regulator – transmits chemoreceptor signals to flagellar motor components CheY



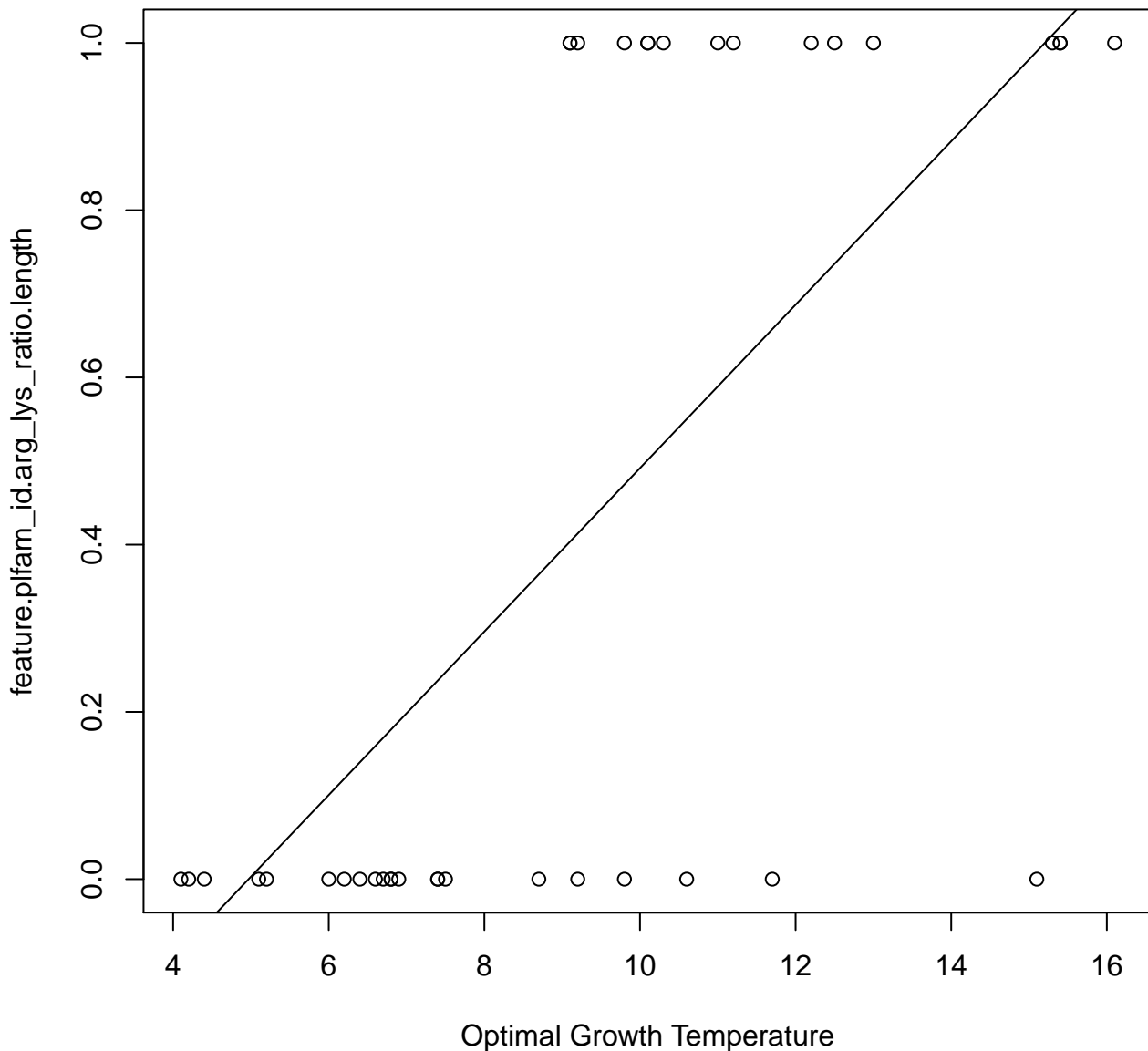
feature.plfam_id.arg_lys_ratio.length



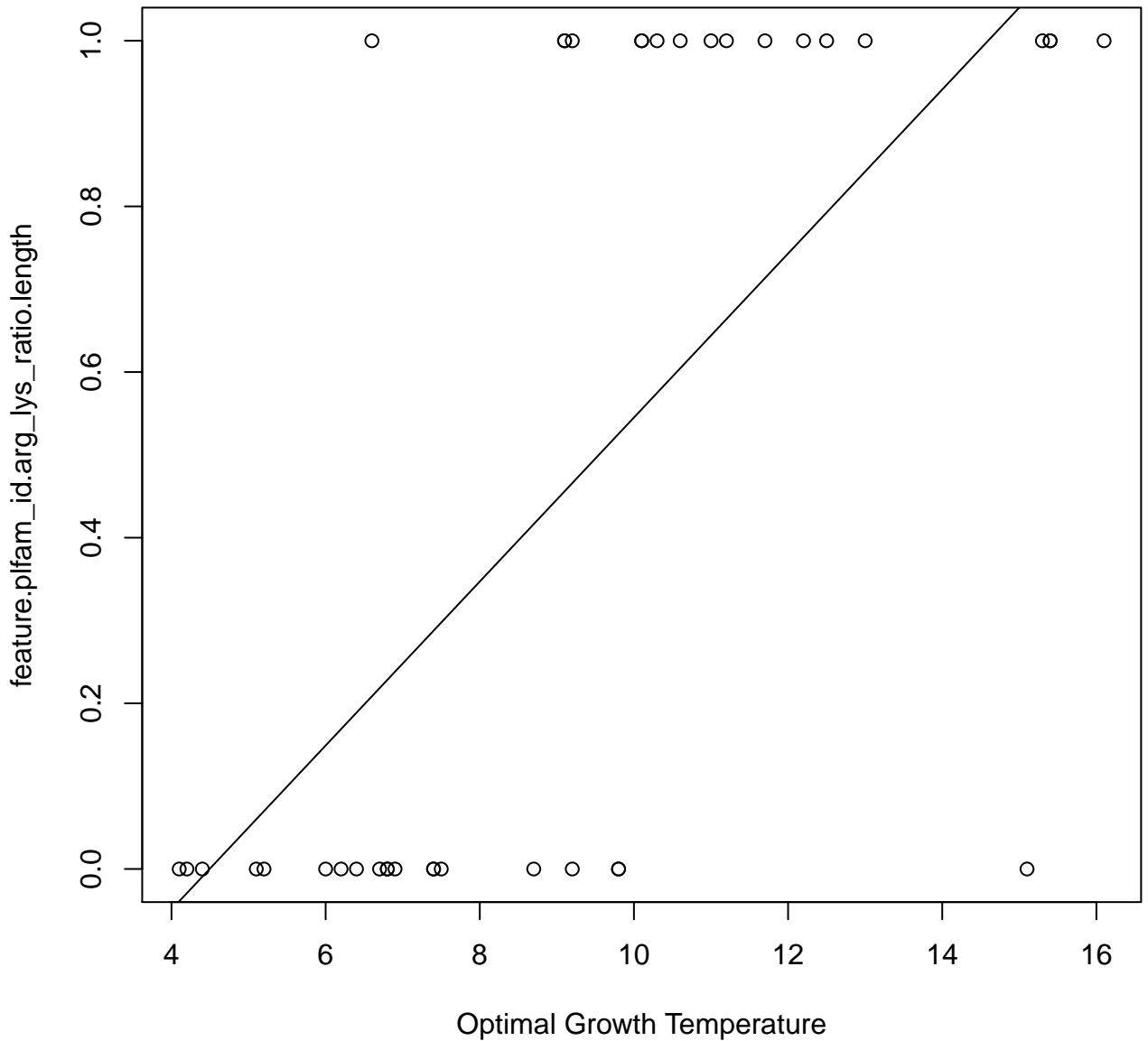
feature.pfam_id.arg_lys_ratio.length

PLF_28228_00000882

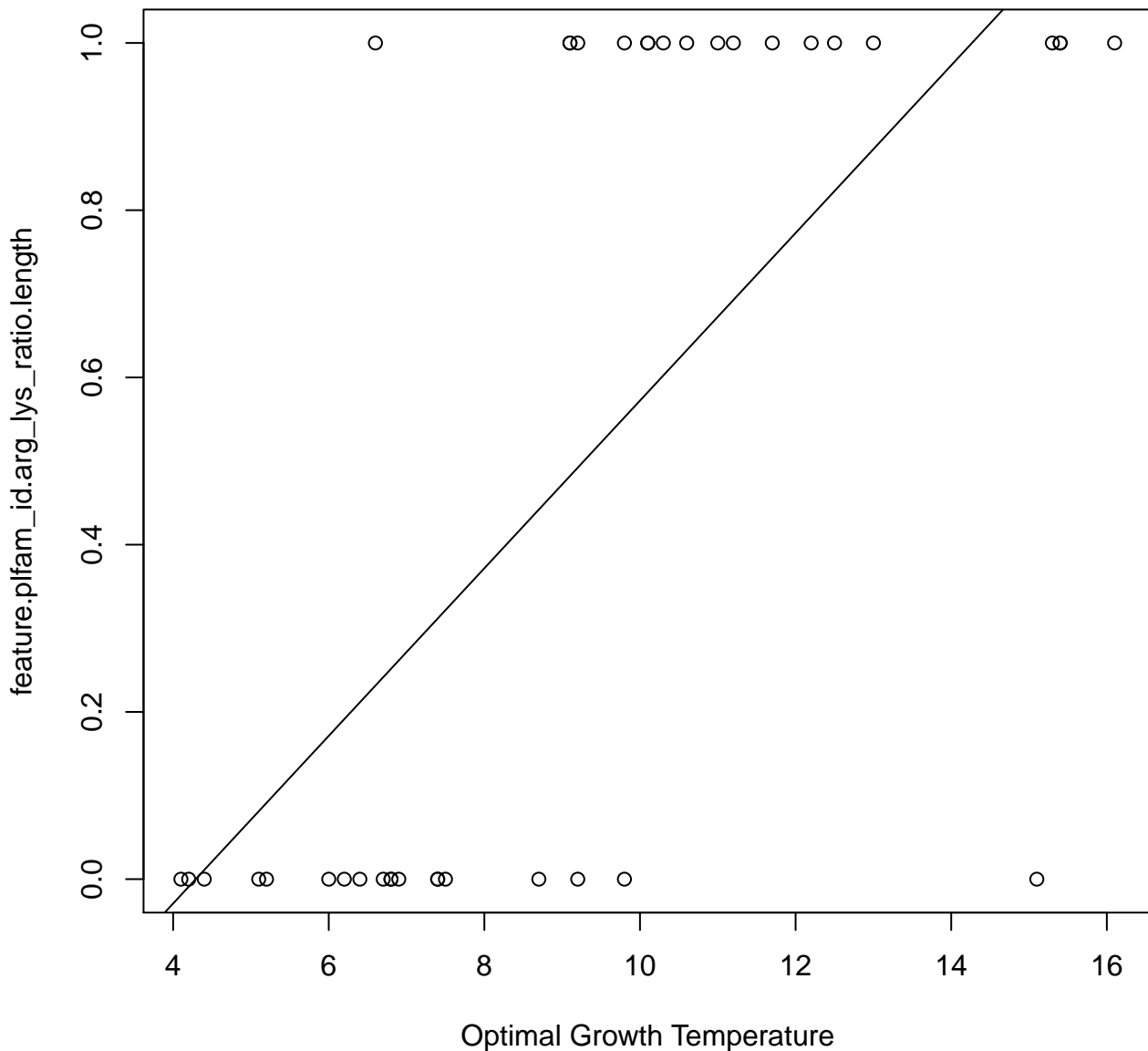
General secretion pathway protein L



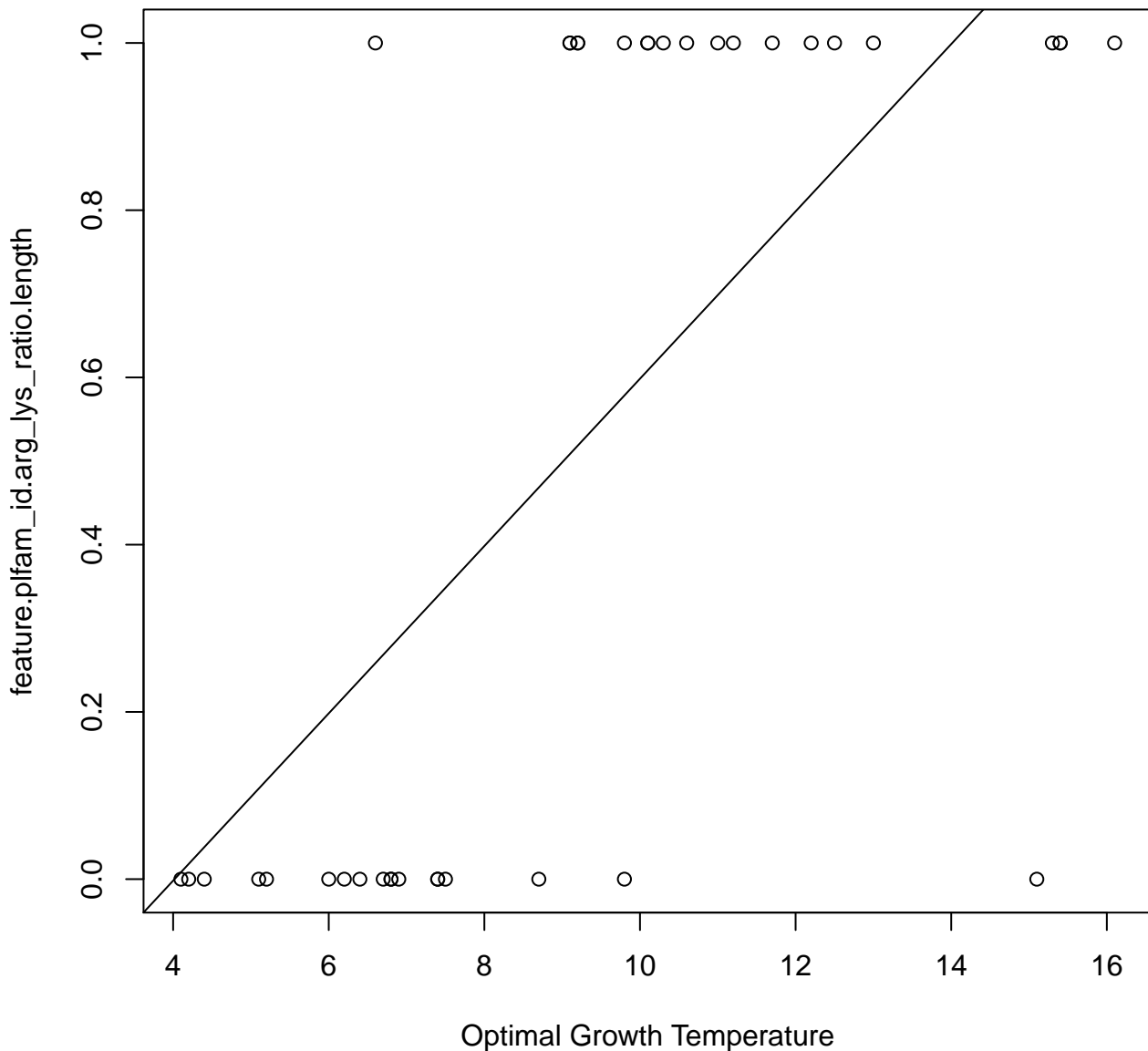
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002716
3-hydroxybutyrate dehydrogenase (EC 1.1.1.30)



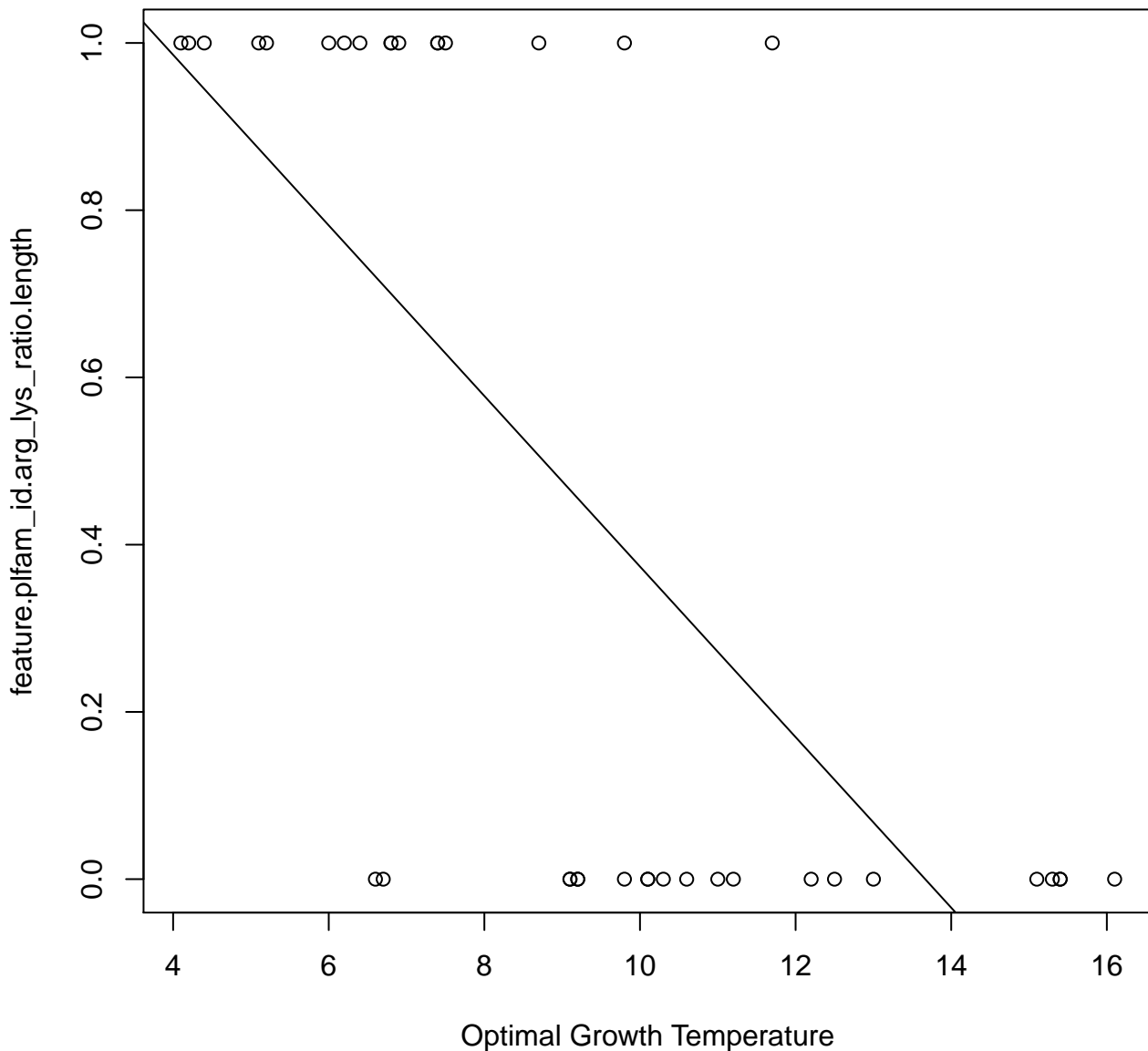
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00002988
hypothetical protein



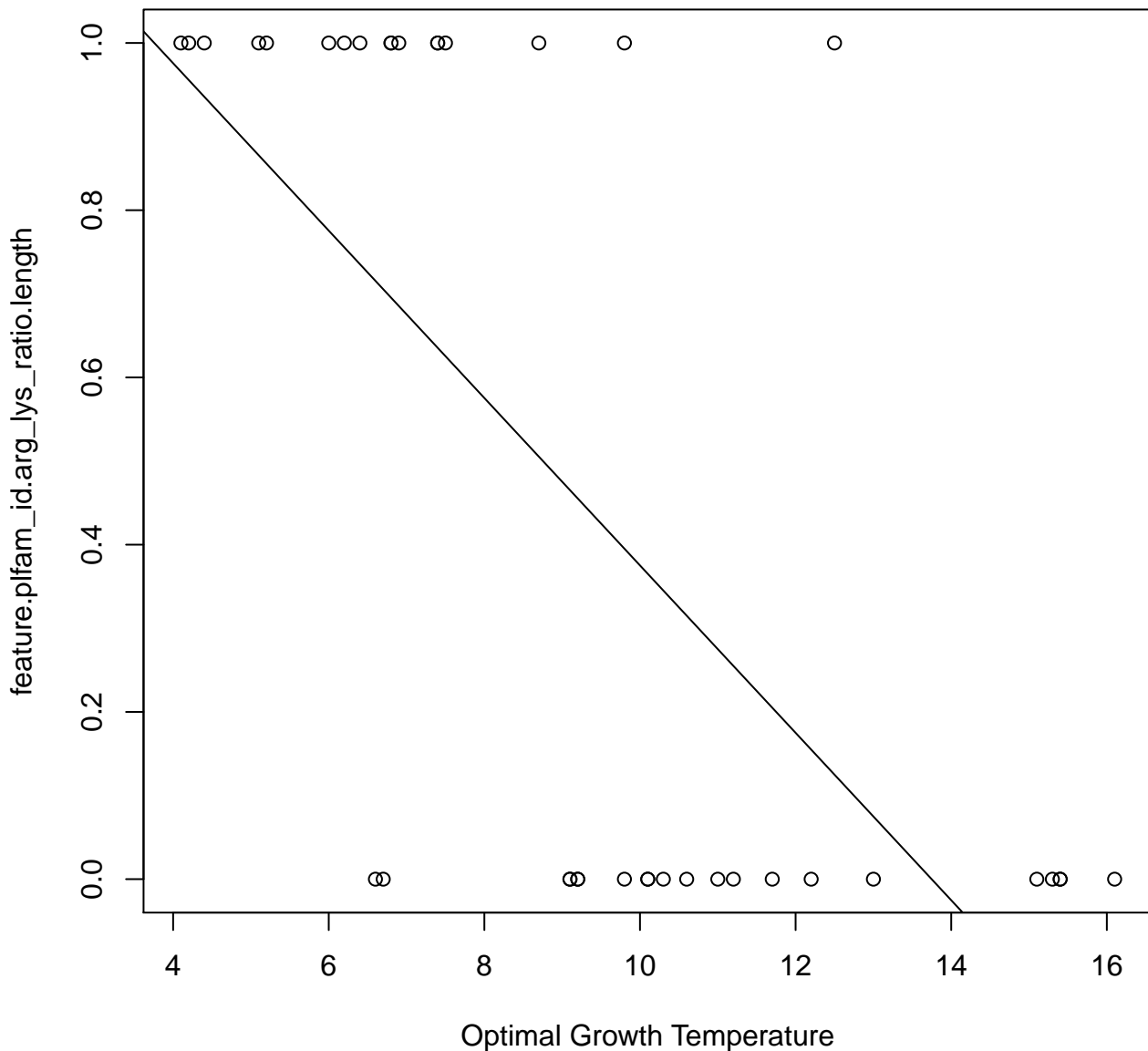
feature.plfam_id.arg_lys_ratio.length
PLF_28228_00003290
CmpX



feature.pfam_id.arg_lys_ratio.length
PLF_28228_00011707
Membrane-bound lytic murein transglycosylase C (EC 3.2.1.n1)



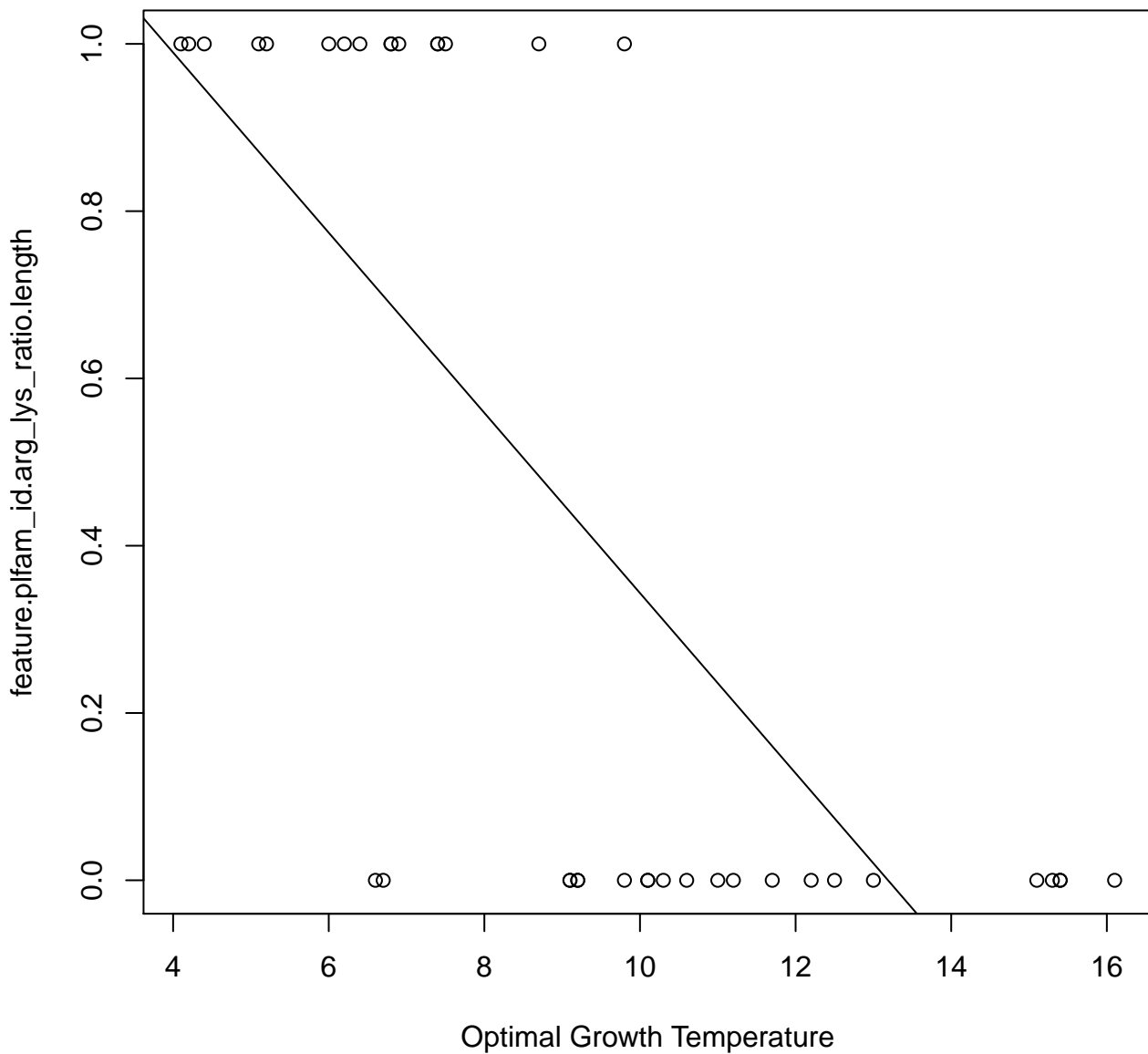
feature.pfam_id.arg_lys_ratio.length
PLF_28228_00014224
FIG006045: Sigma factor, ECF subfamily



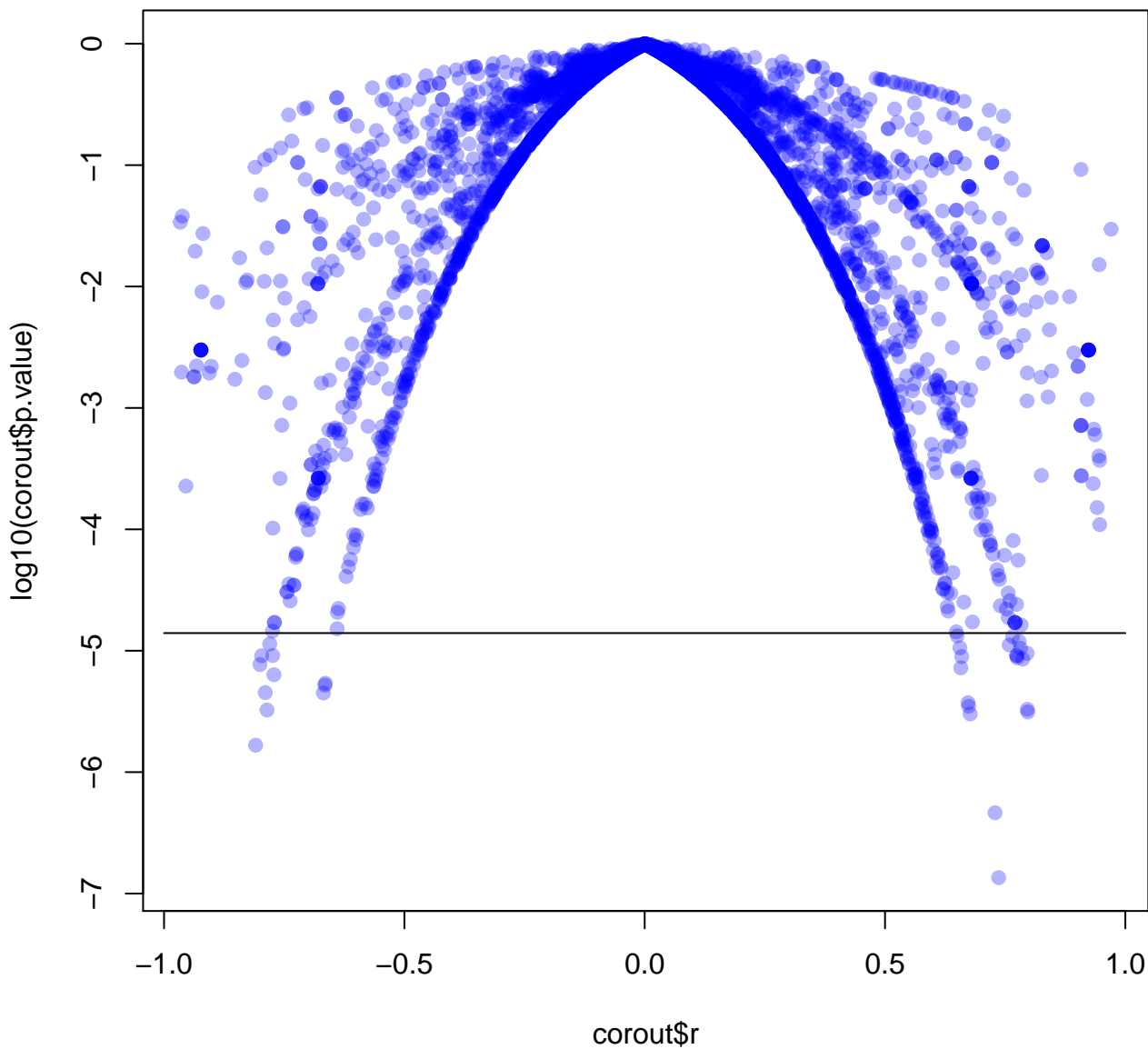
feature.pfam_id.arg_lys_ratio.length

PLF_28228_00028262

Iron siderophore sensor protein



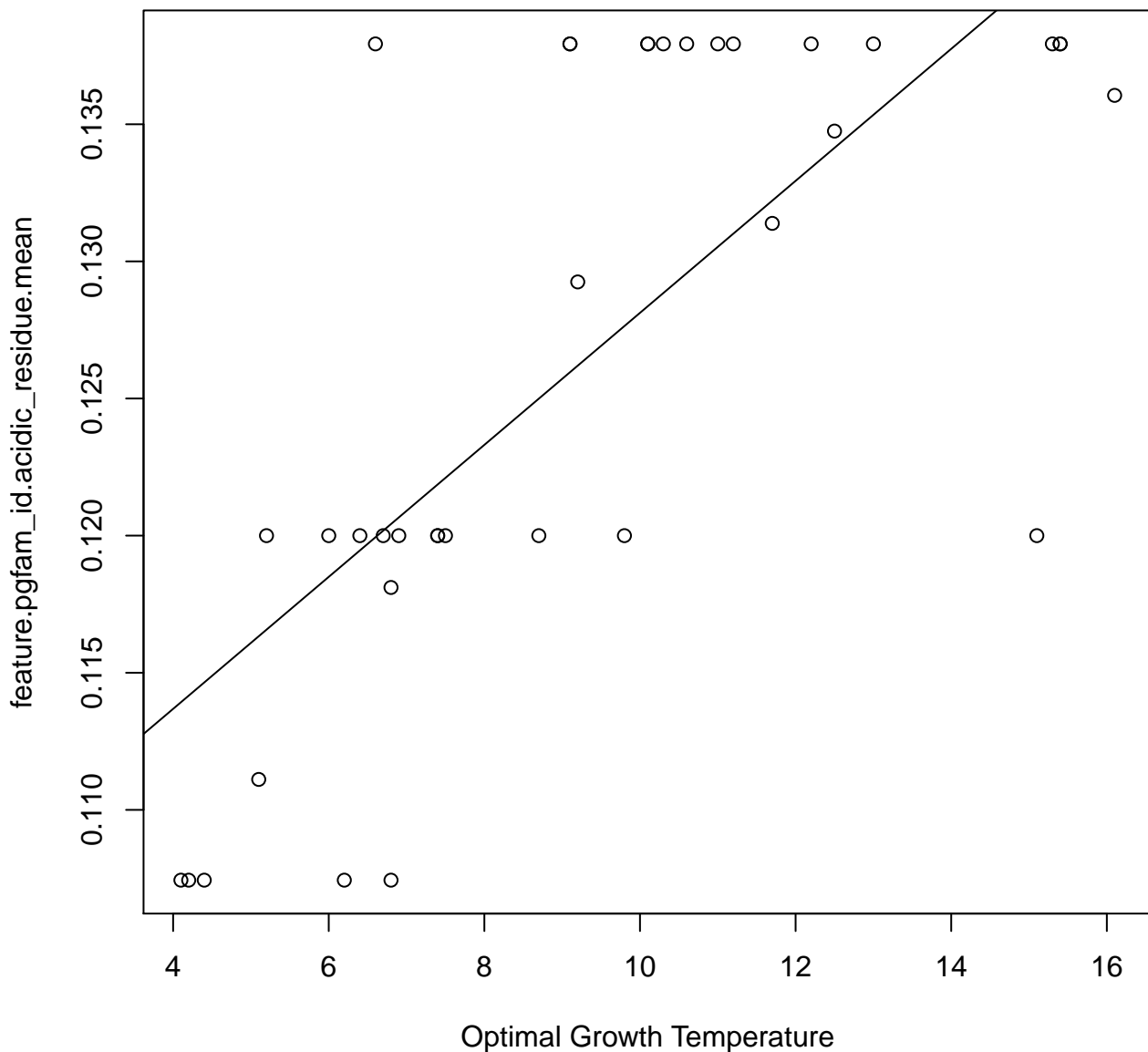
feature.pgfam_id.acidic_residue.mean



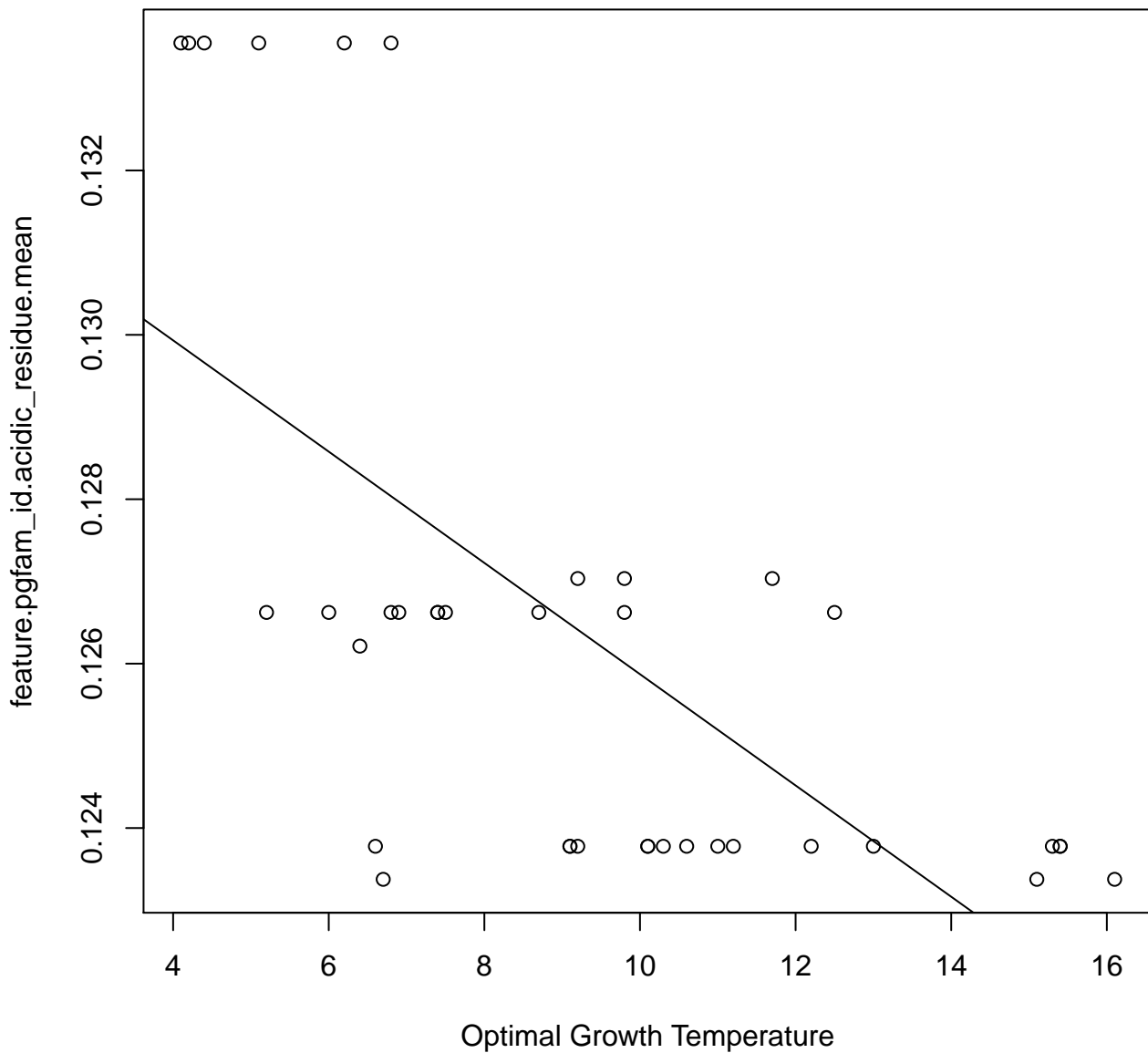
feature.pgfam_id.acidic_residue.mean

PGF_00002863

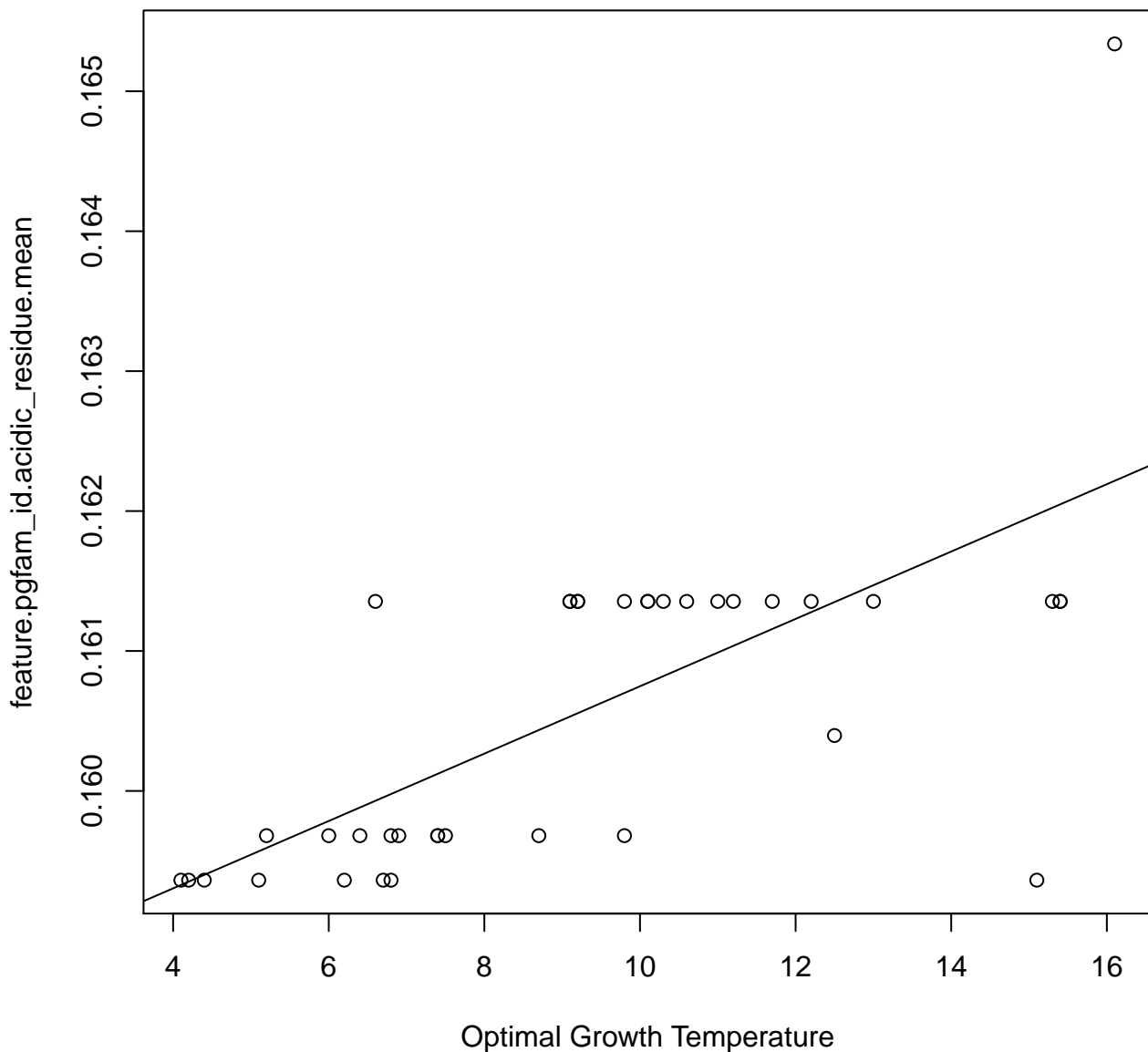
FIG024746: hypothetical protein



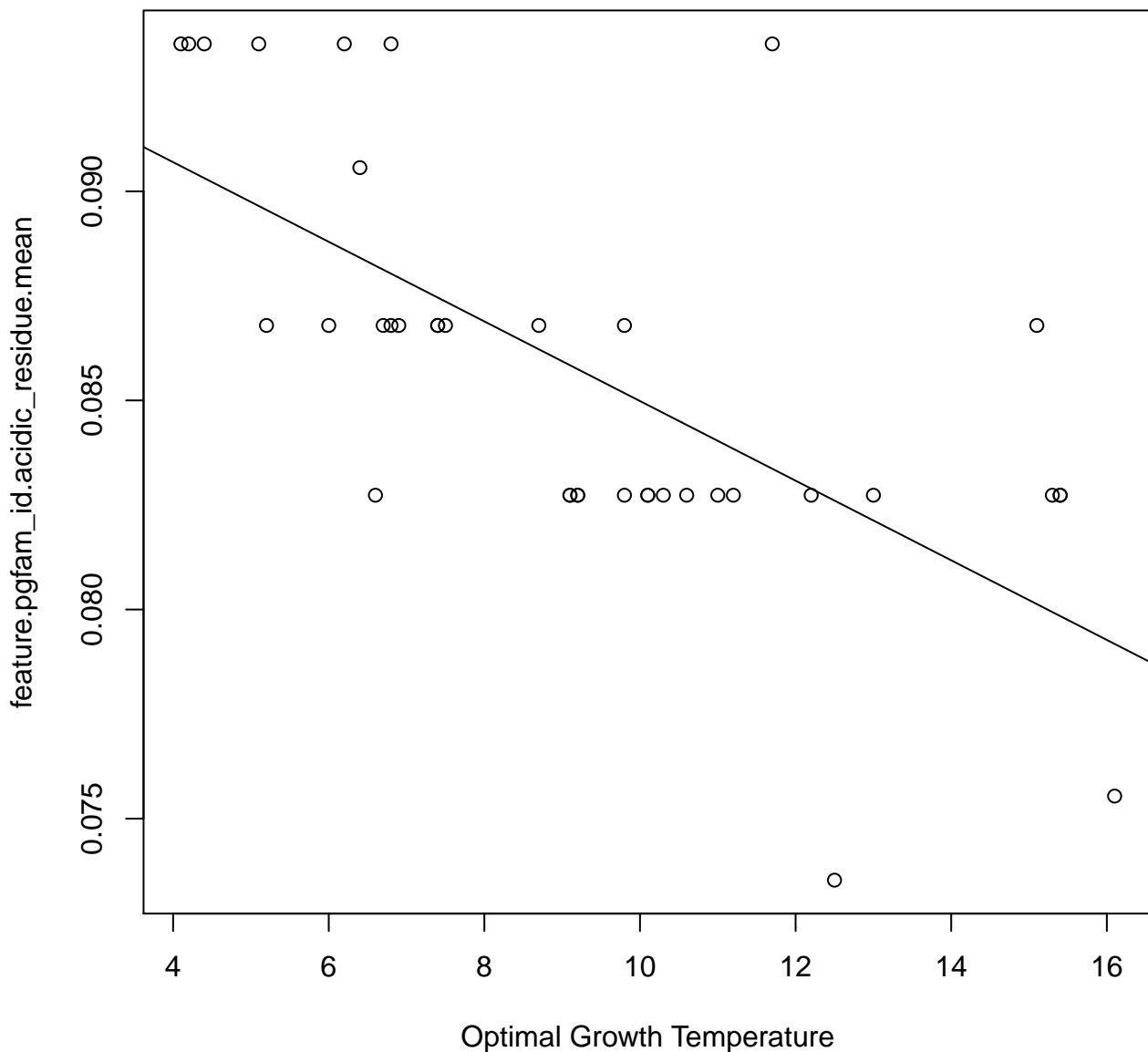
feature.pgfam_id.acidic_residue.mean
PGF_00006983
GTP cyclohydrolase I (EC 3.5.4.16) type 2



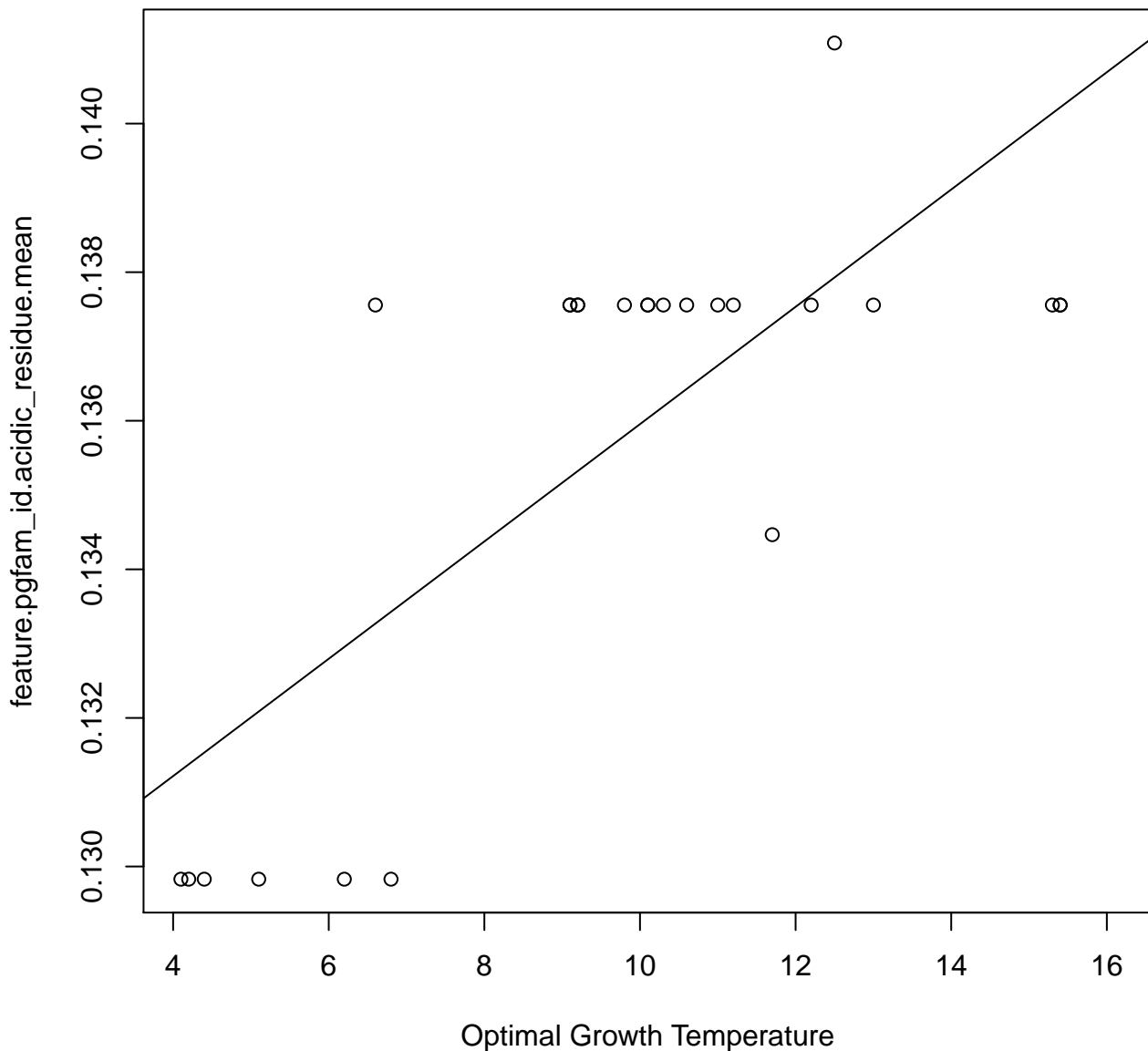
feature.pgfam_id.acidic_residue.mean
PGF_00046403
RNA polymerase sigma-54 factor RpoN



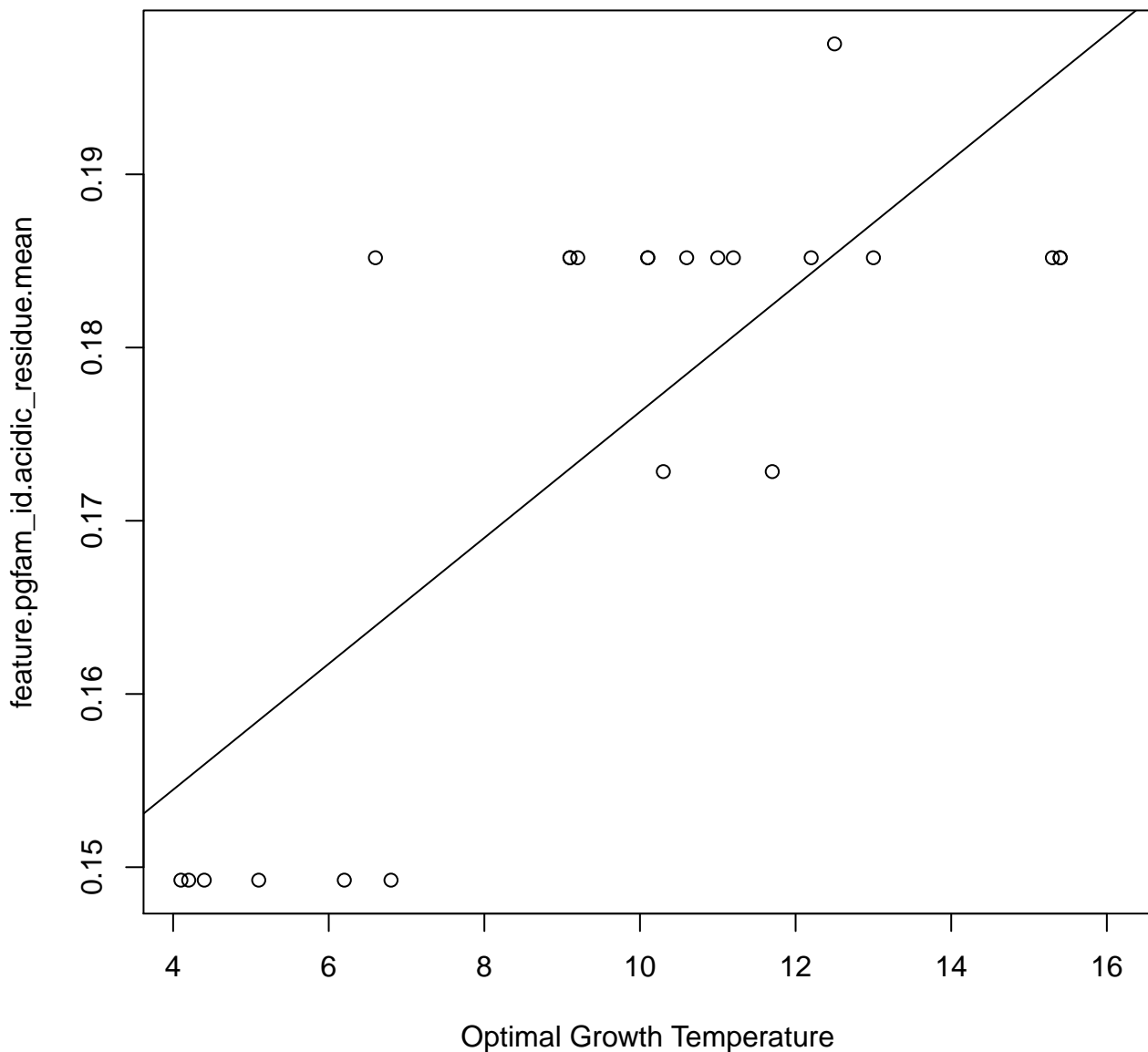
feature.pgfam_id.acidic_residue.mean
PGF_00048554
Caulimovirus viroplasmin / Ribonuclease HI (EC 3.1.26.4)



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



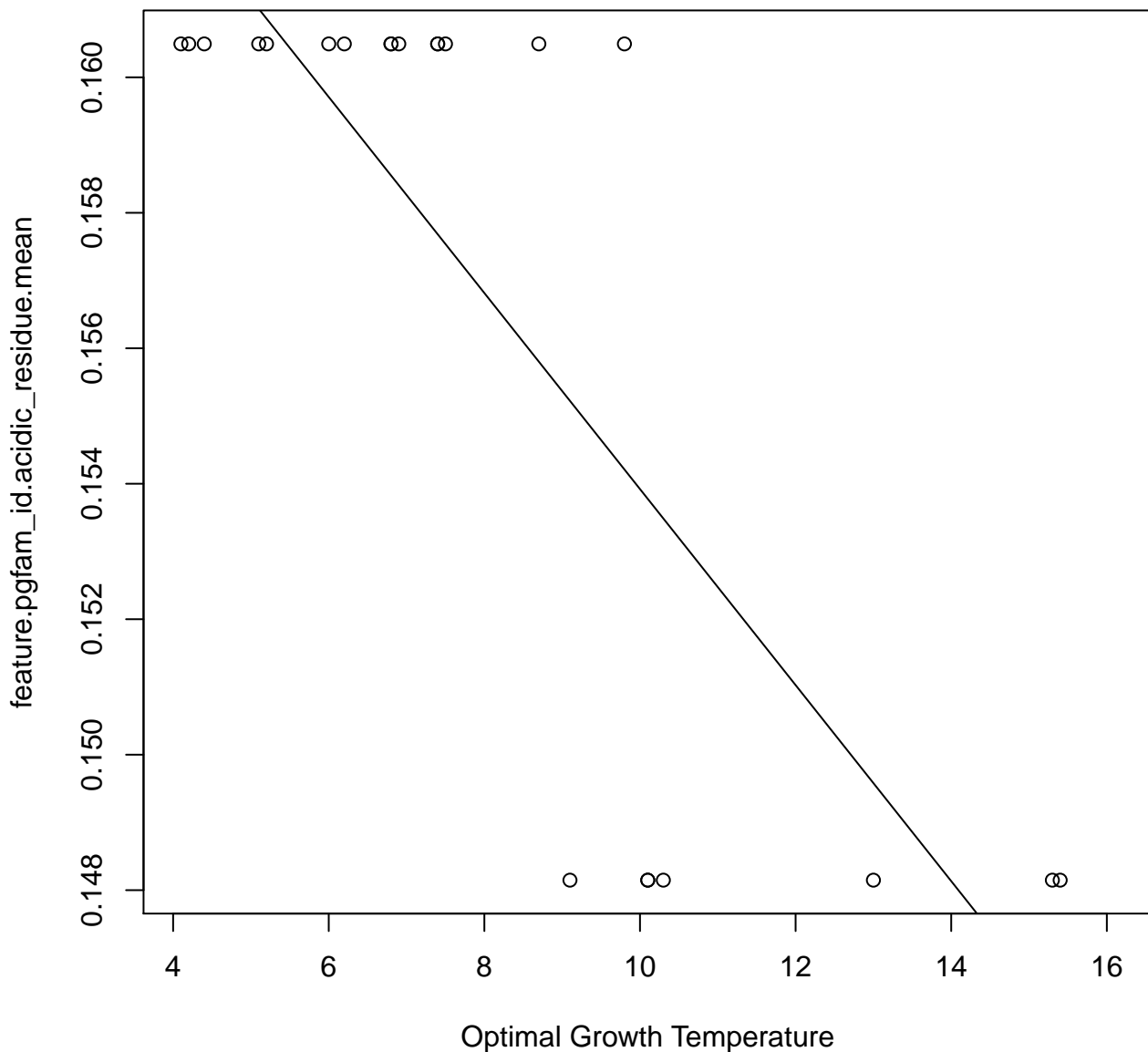
feature.pgfam_id.acidic_residue.mean
PGF_00064685
Uncharacterized ferredoxin-like protein YfhL



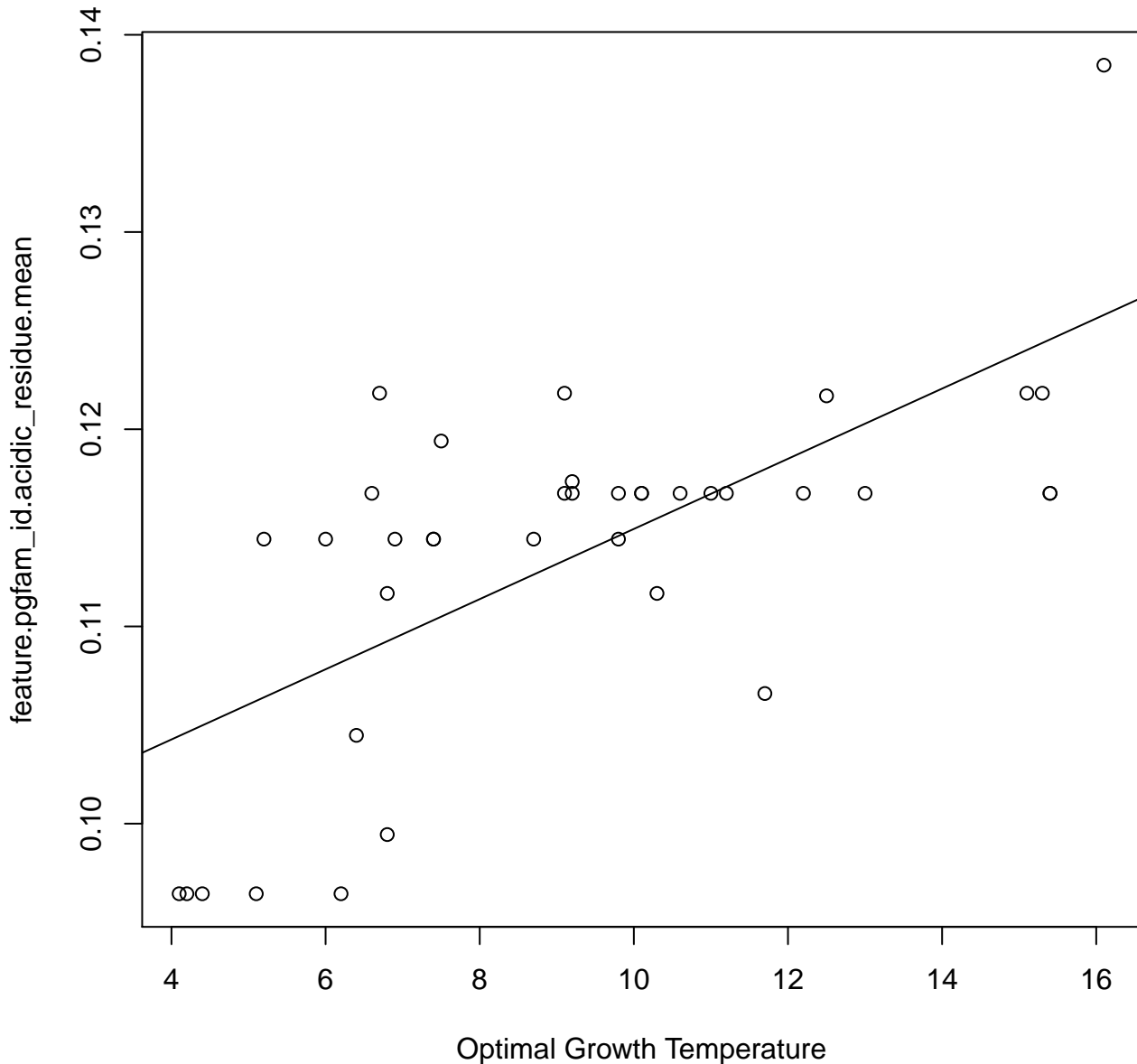
feature.pgfam_id.acidic_residue.mean

PGF_00393434

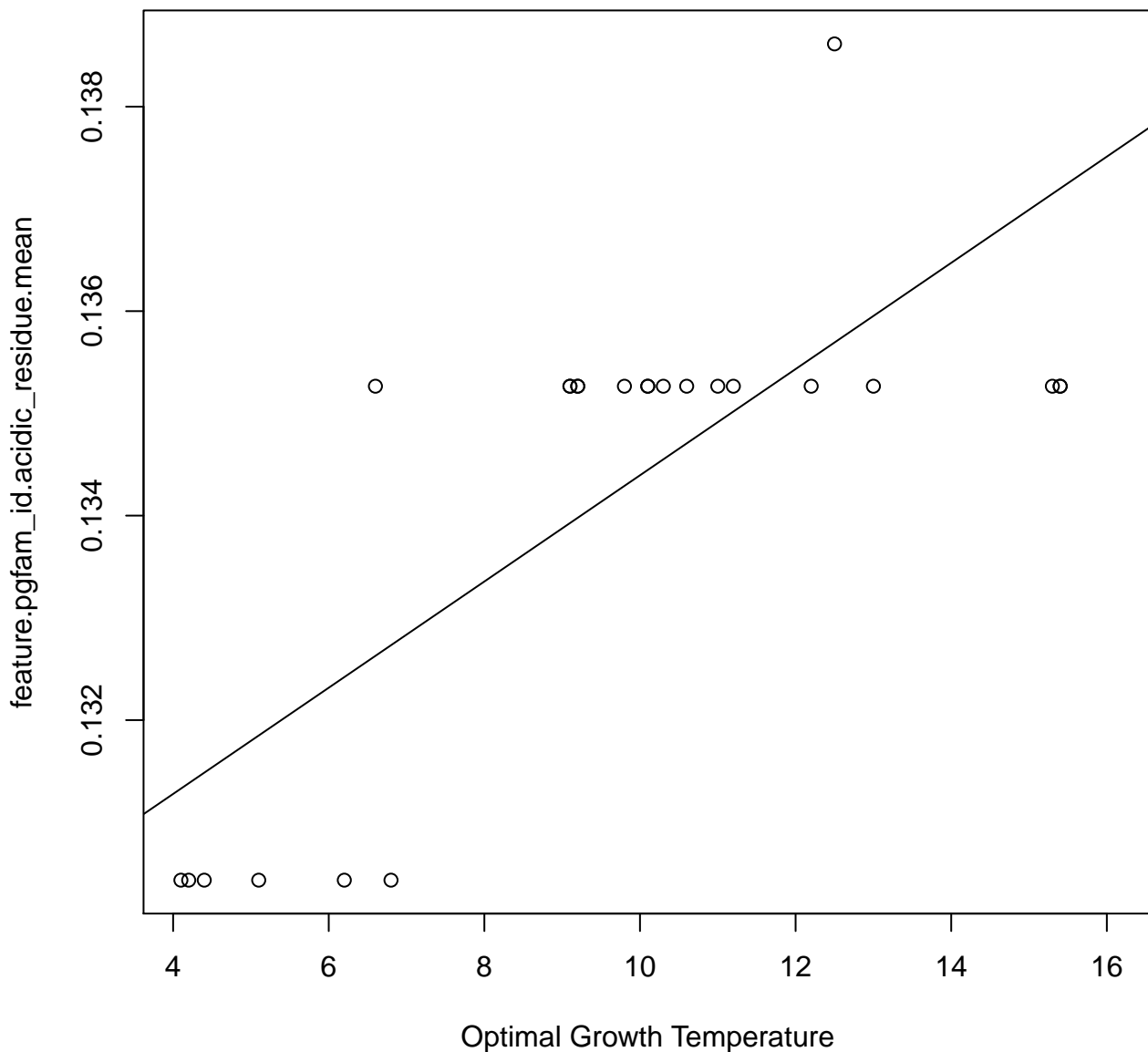
hypothetical protein



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



feature.pgfam_id.acidic_residue.mean
PGF_00717613
Chemotaxis protein CheC -- inhibitor of MCP methylation

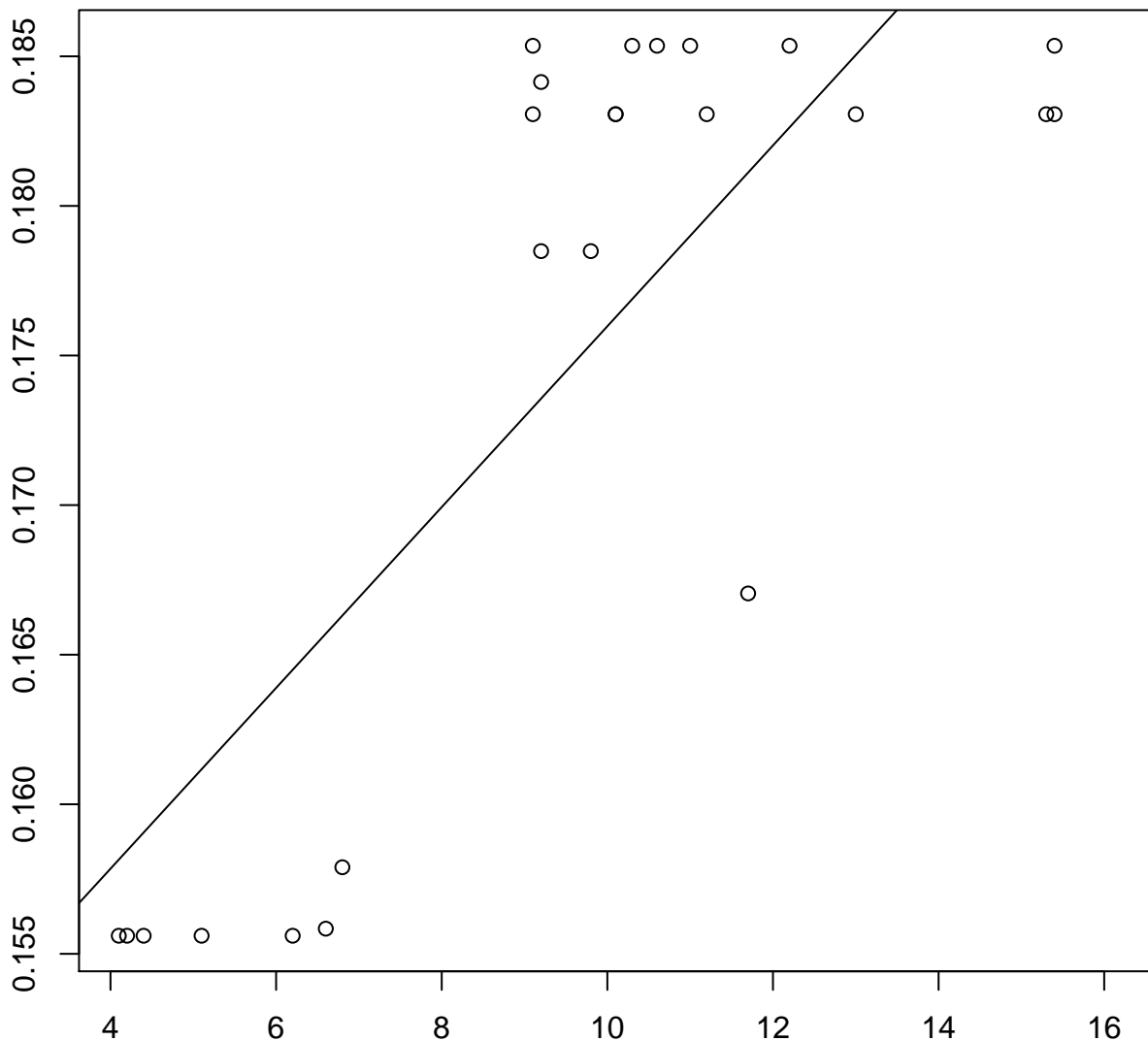


feature.pgfam_id.acidic_residue.mean

PGF_01336976

hypothetical protein

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature

feature.pgfam_id.acidic_residue.mean

PGF_01336977

hypothetical protein

feature.pgfam_id.acidic_residue.mean

0.154
0.156
0.158
0.160

4

6

8

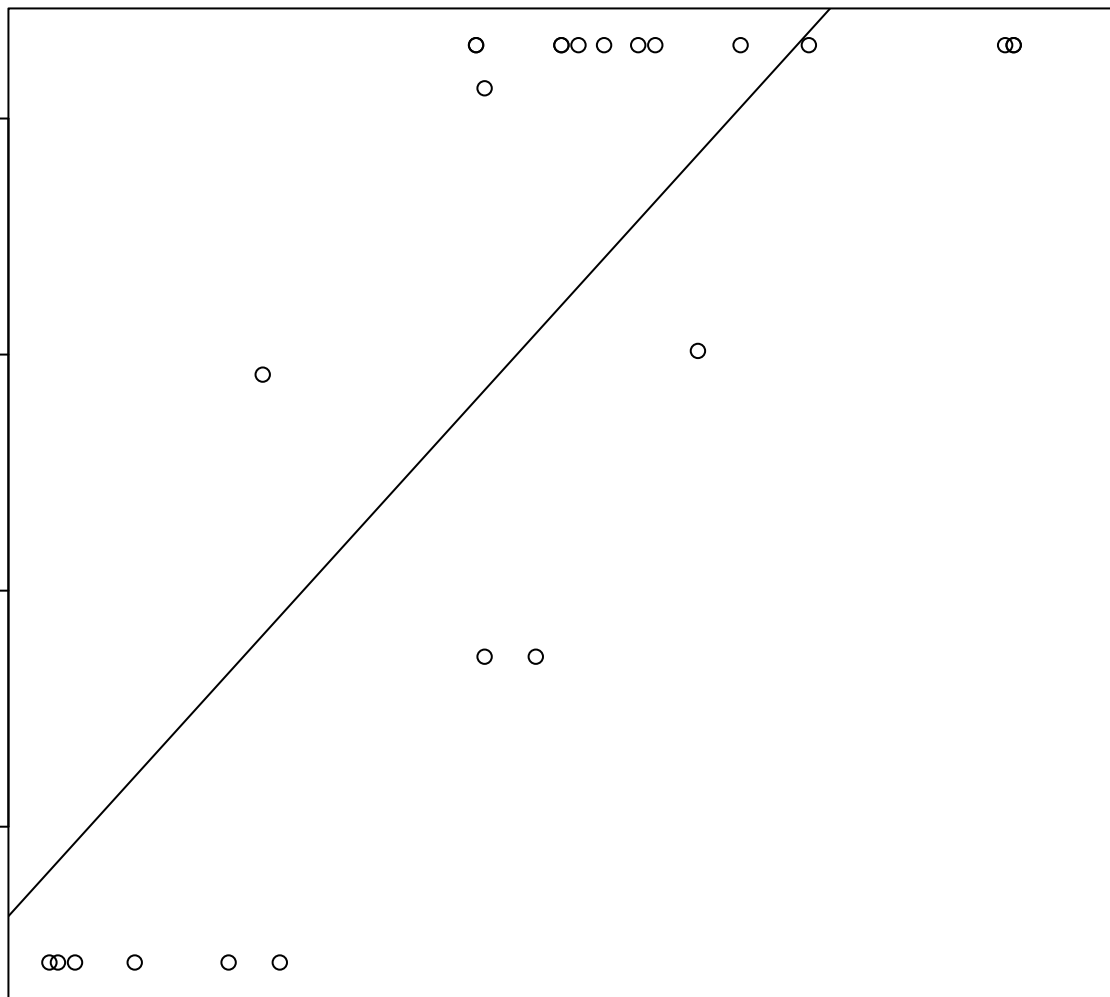
10

12

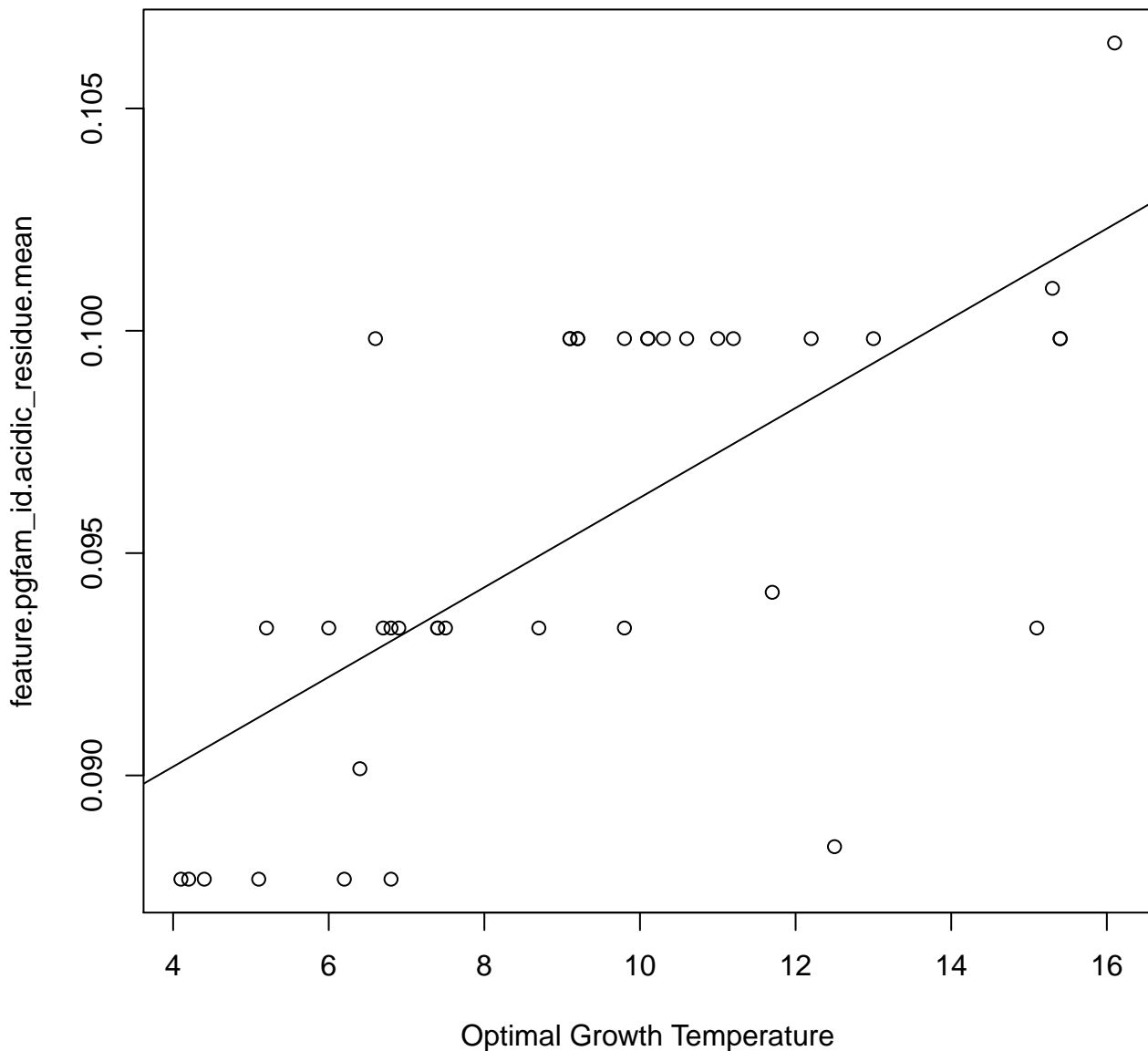
14

16

Optimal Growth Temperature



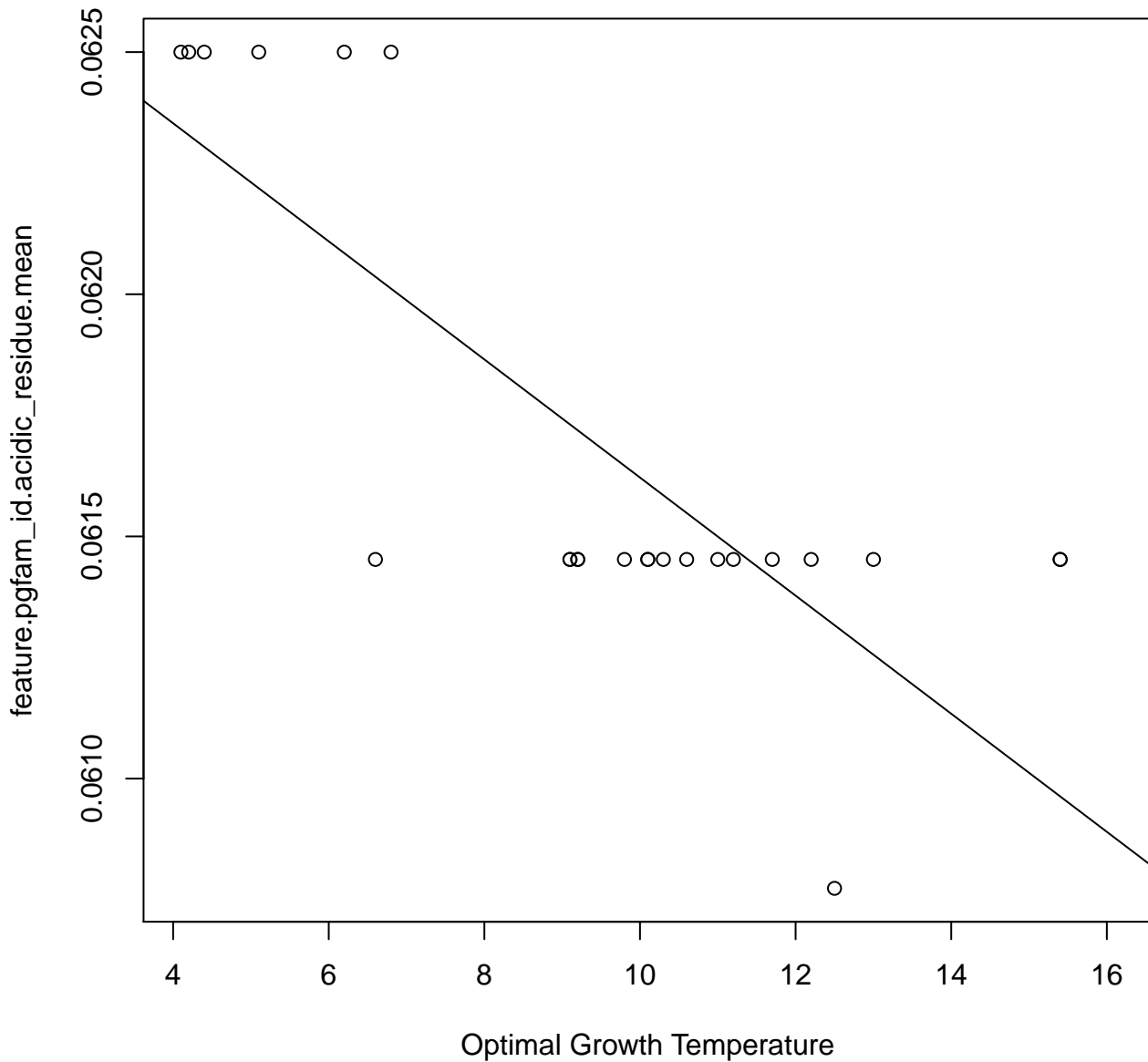
feature.pgfam_id.acidic_residue.mean
PGF_01396822
Uncharacterized aldehyde oxidase, 2Fe-2S subunit



feature.pgfam_id.acidic_residue.mean

PGF_01442793

Putative manganese efflux pump MntP

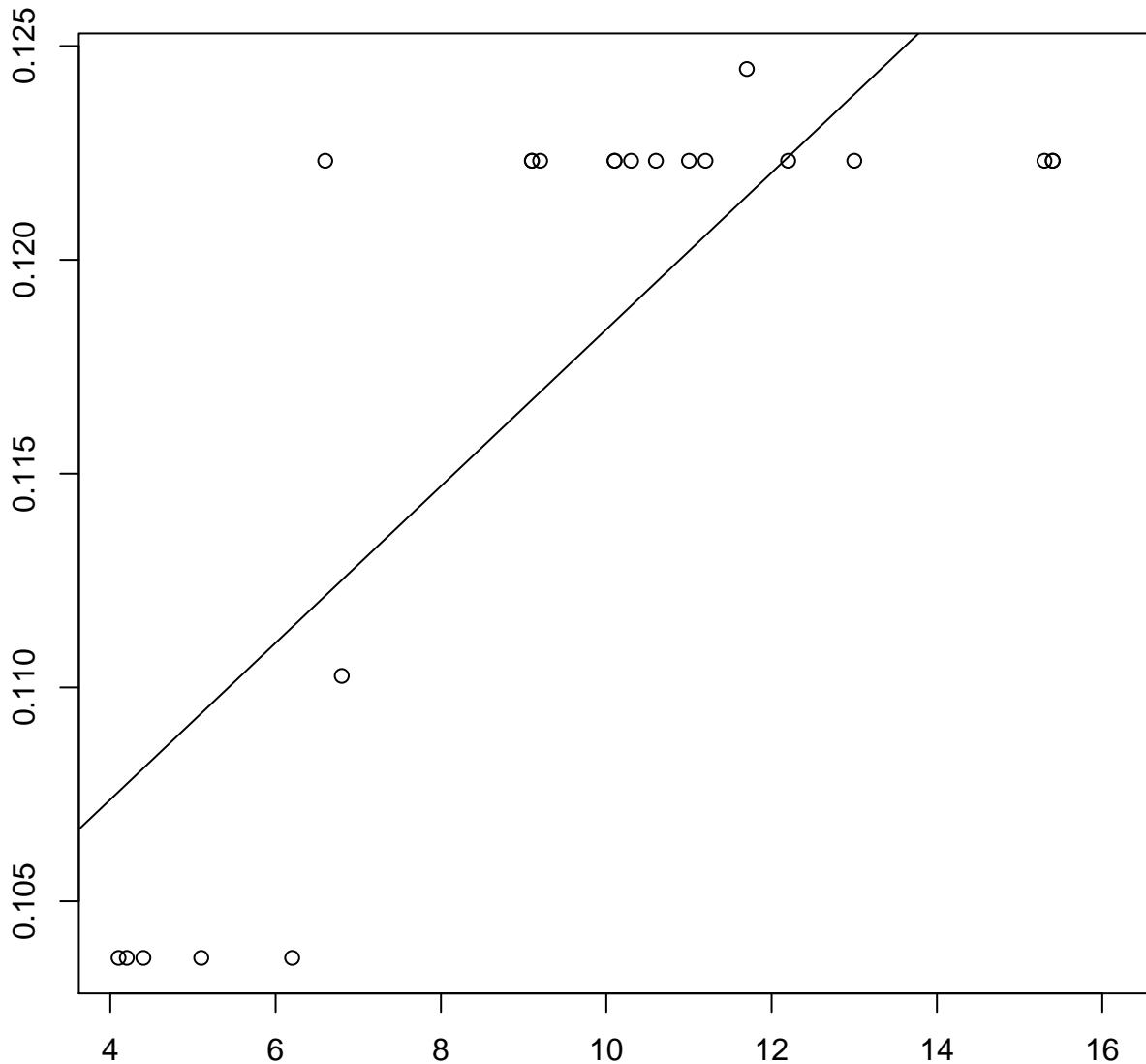


feature.pgfam_id.acidic_residue.mean

PGF_02105064

Uncharacterized protease YegQ

feature.pgfam_id.acidic_residue.mean

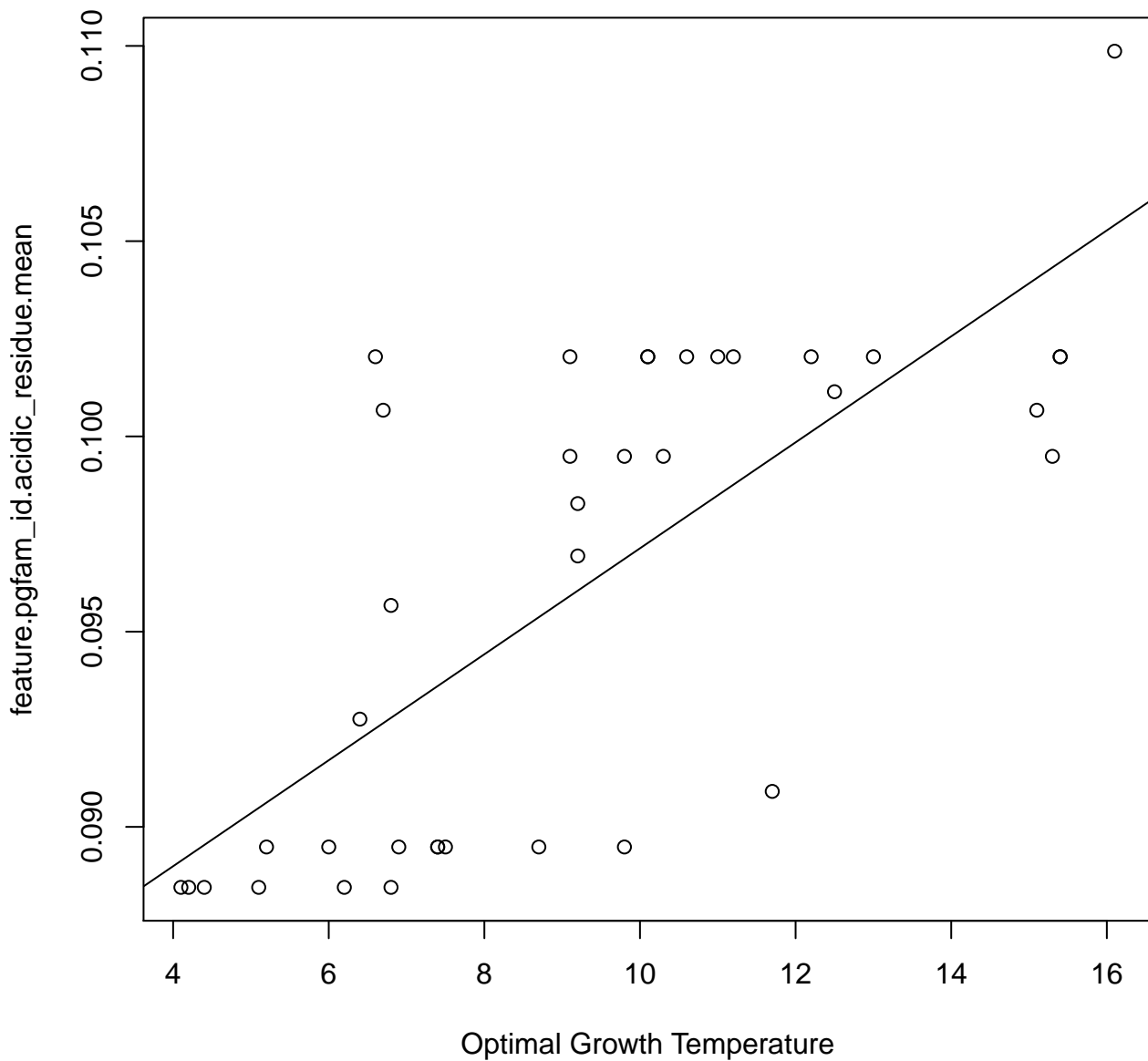


Optimal Growth Temperature

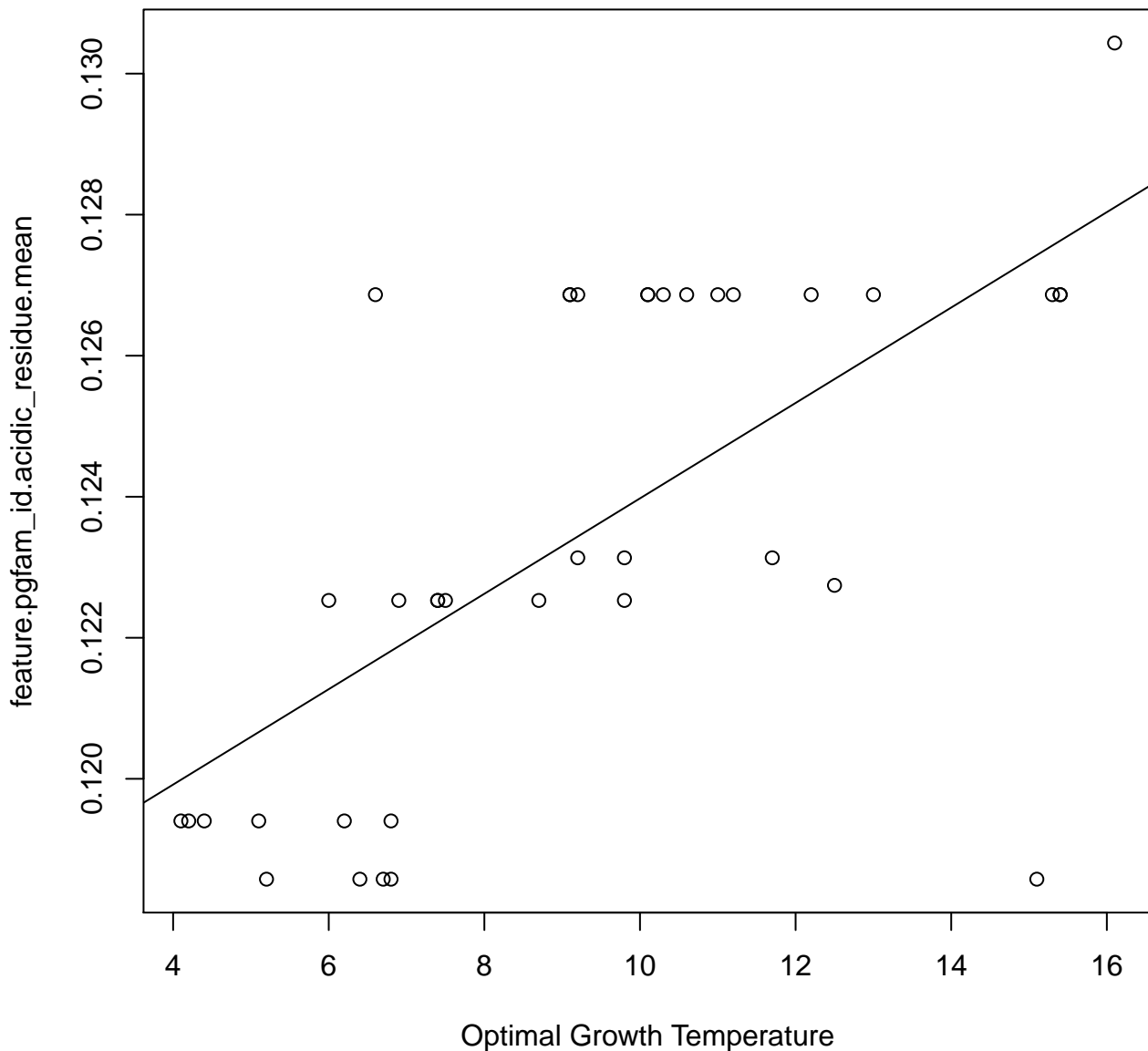
feature.pgfam_id.acidic_residue.mean

PGF_02328856

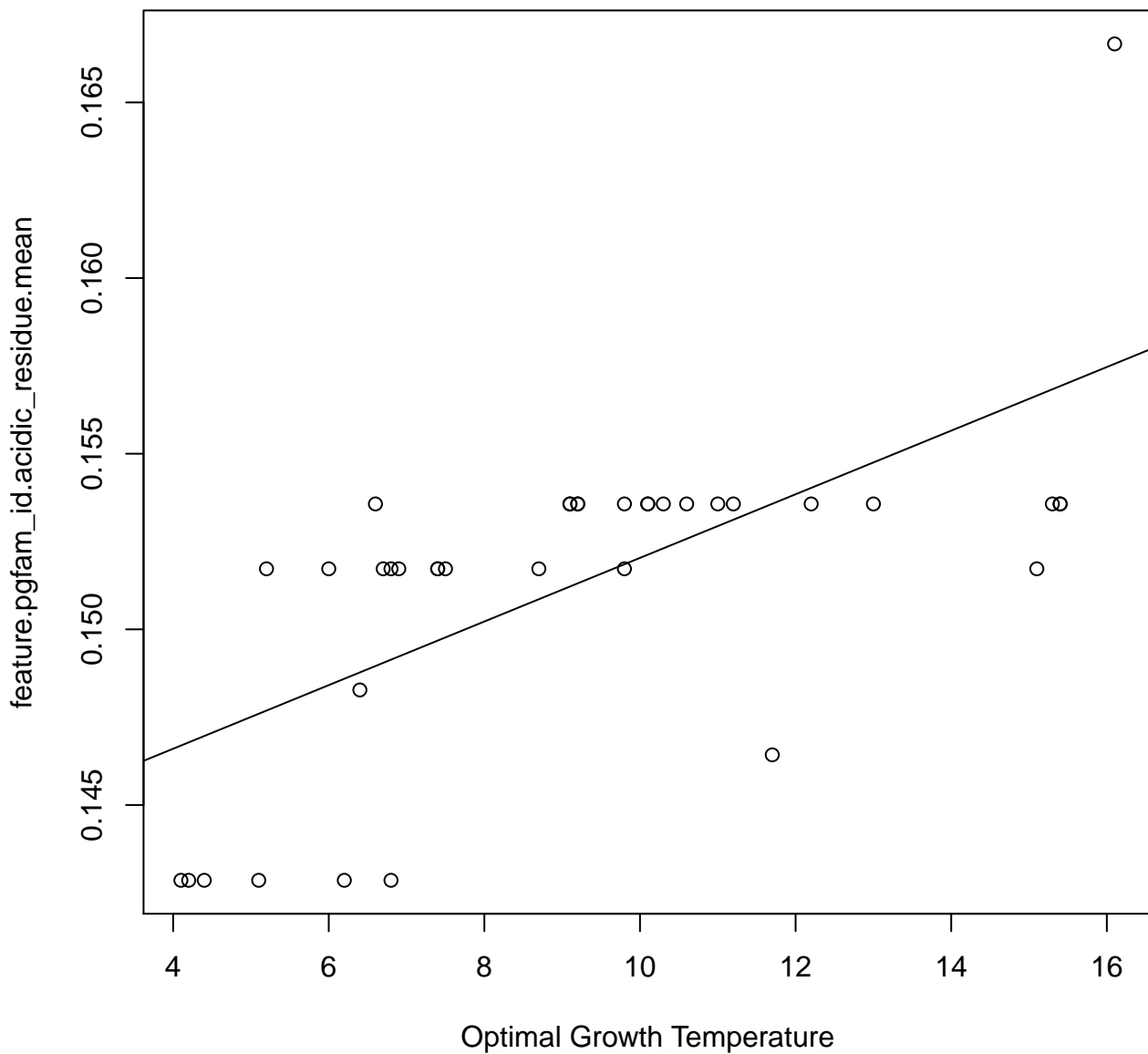
Type IV pilus biogenesis protein PilF



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



feature.pgfam_id.acidic_residue.mean
PGF_02517283
Segregation and condensation protein A

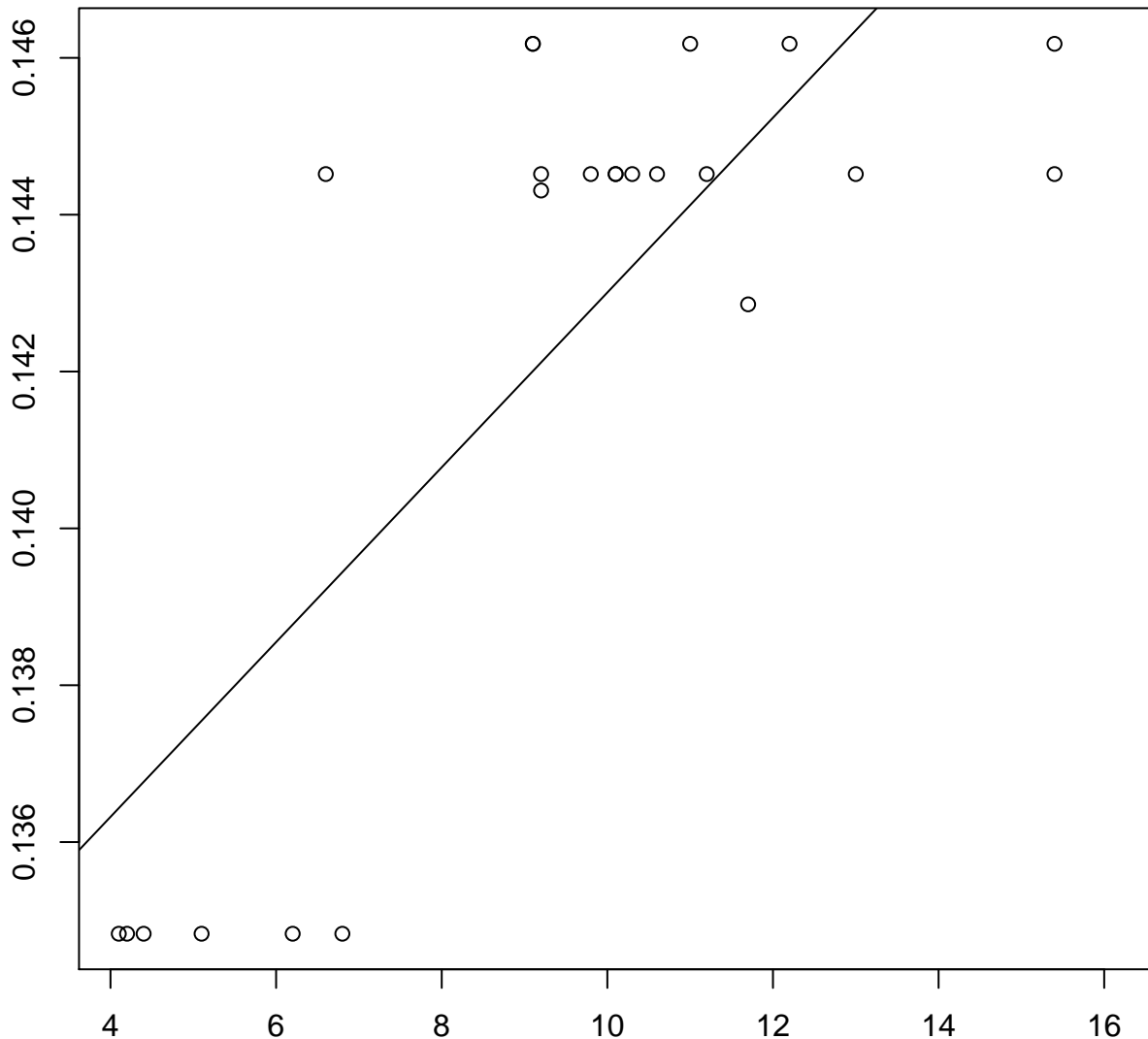


feature.pgfam_id.acidic_residue.mean

PGF_03083319

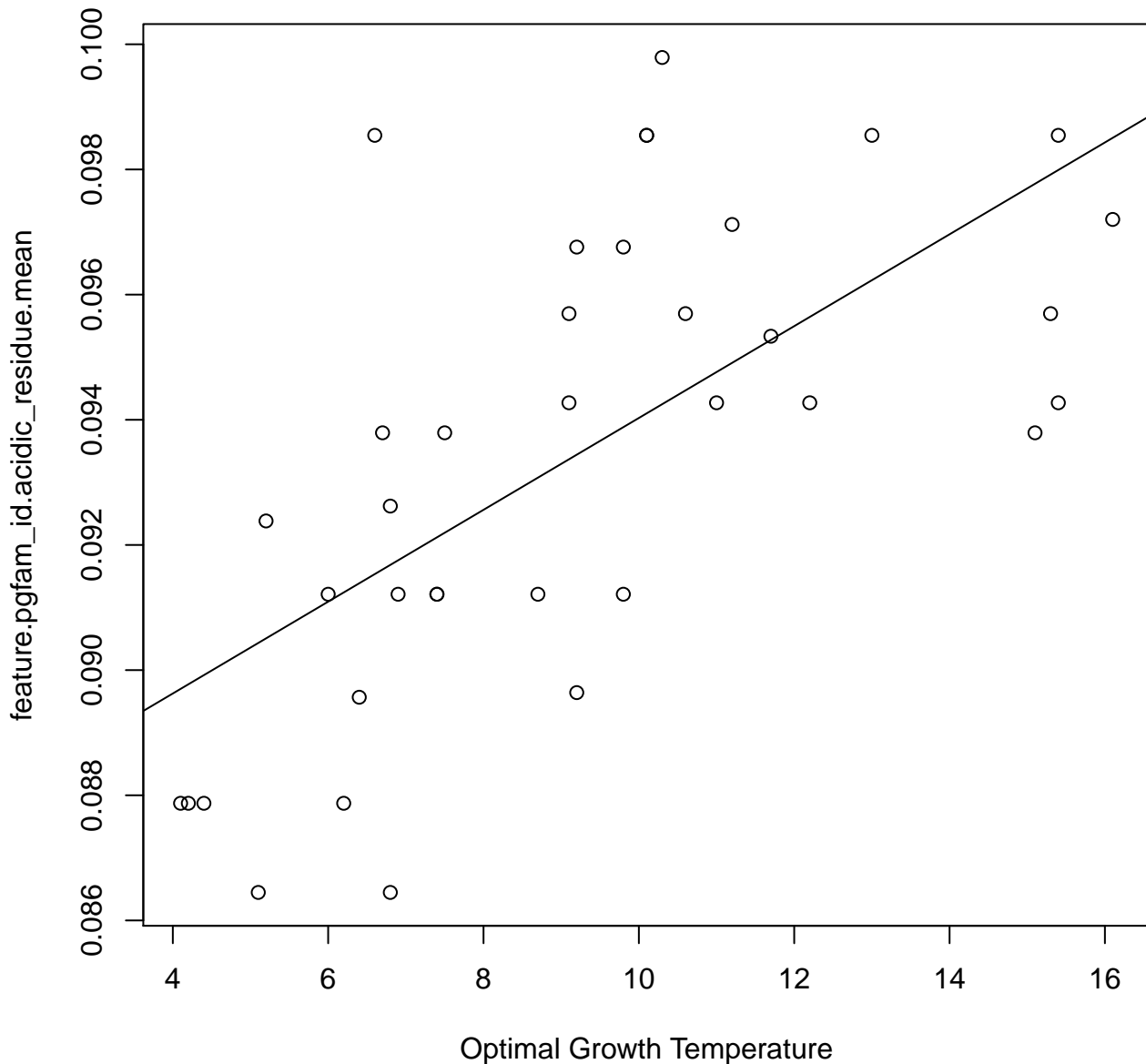
Maltodextrin glucosidase (EC 3.2.1.20)

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature

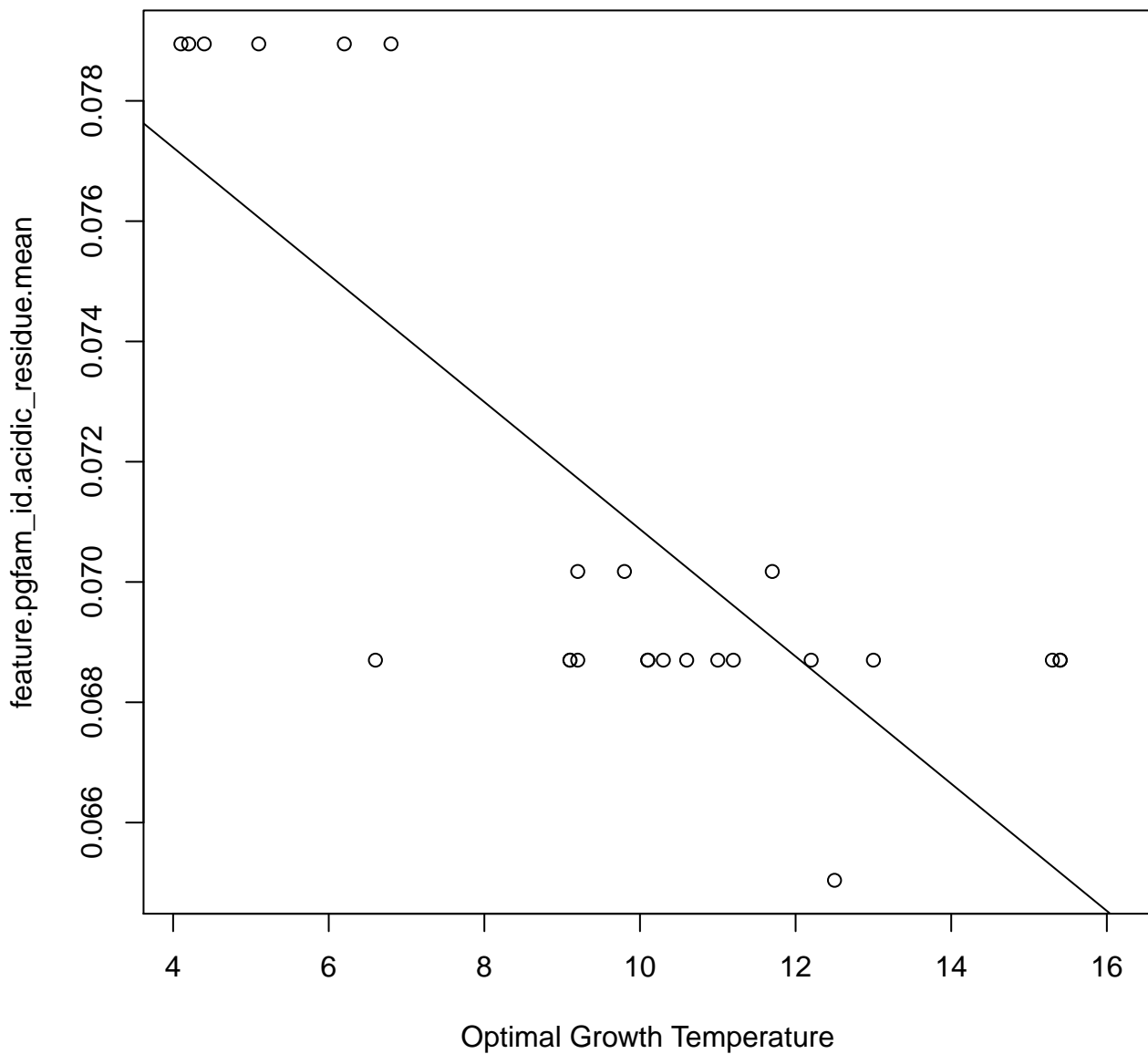
feature.pgfam_id.acidic_residue.mean
PGF_03116630
Membrane-bound lytic murein transglycosylase B



feature.pgfam_id.acidic_residue.mean

PGF_03754184

Na(+) H(+) antiporter subunit C

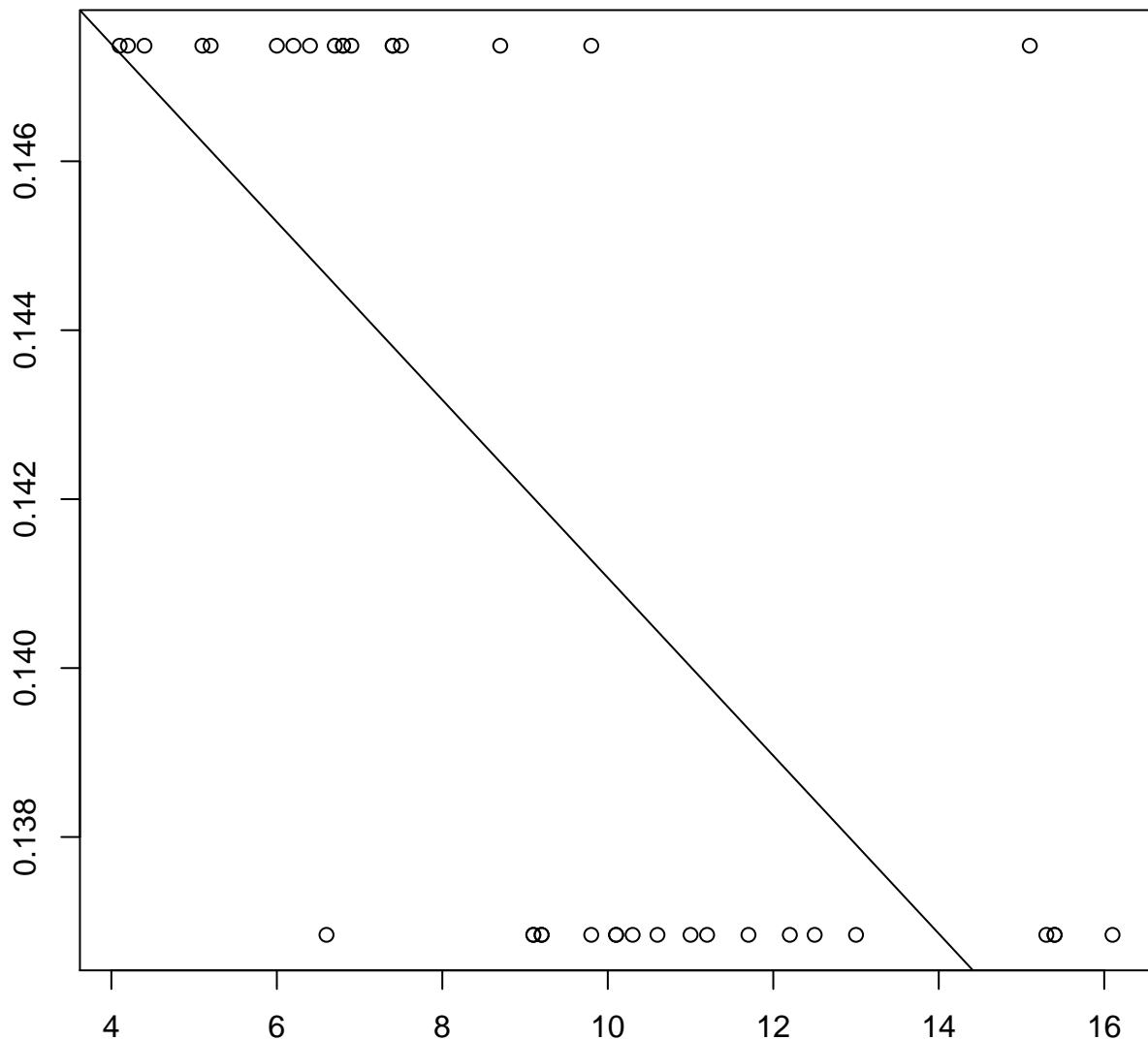


feature.pgfam_id.acidic_residue.mean

PGF_05693577

Integration host factor beta subunit

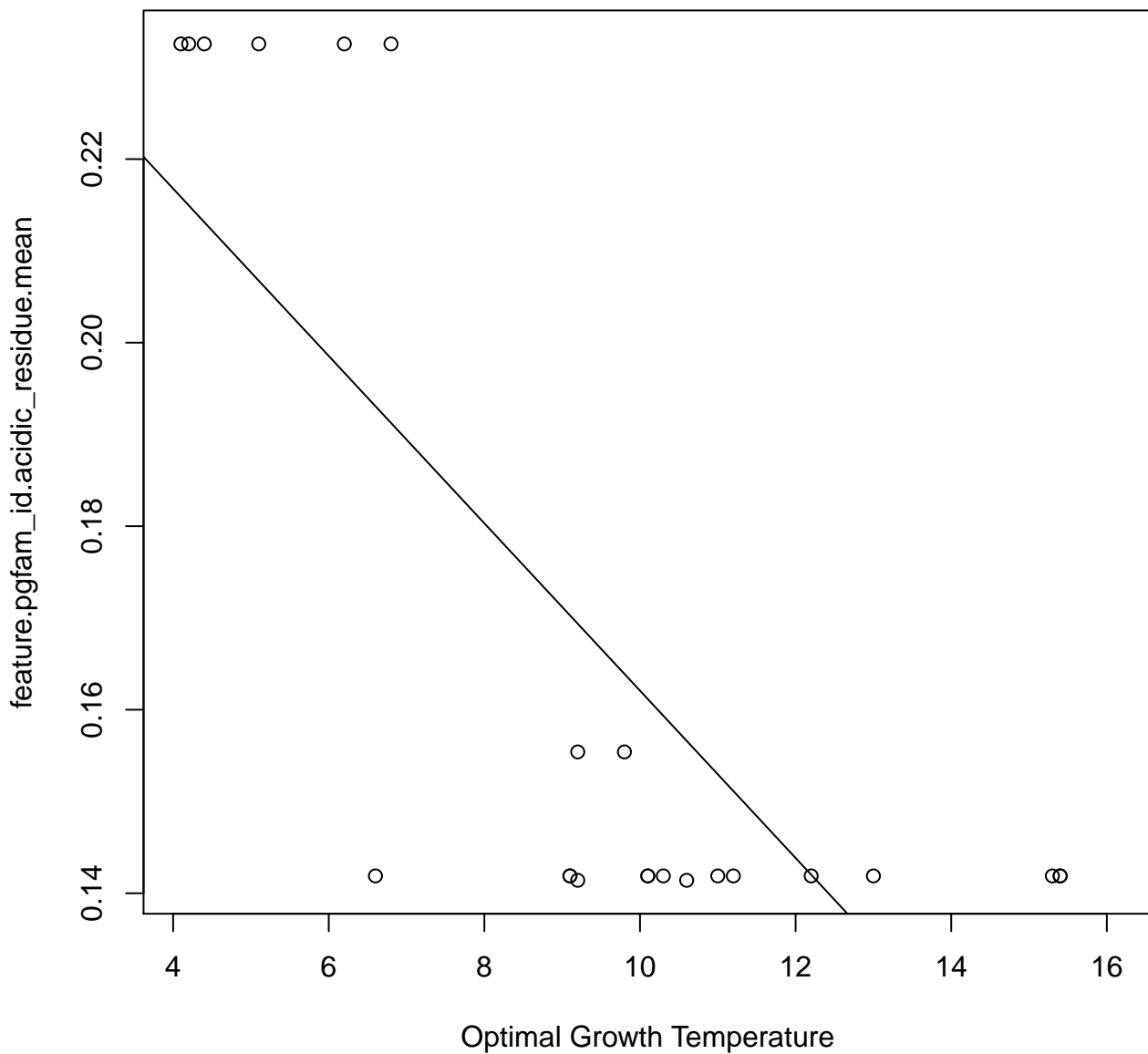
feature.pgfam_id.acidic_residue.mean



feature.pgfam_id.acidic_residue.mean

PGF_06792096

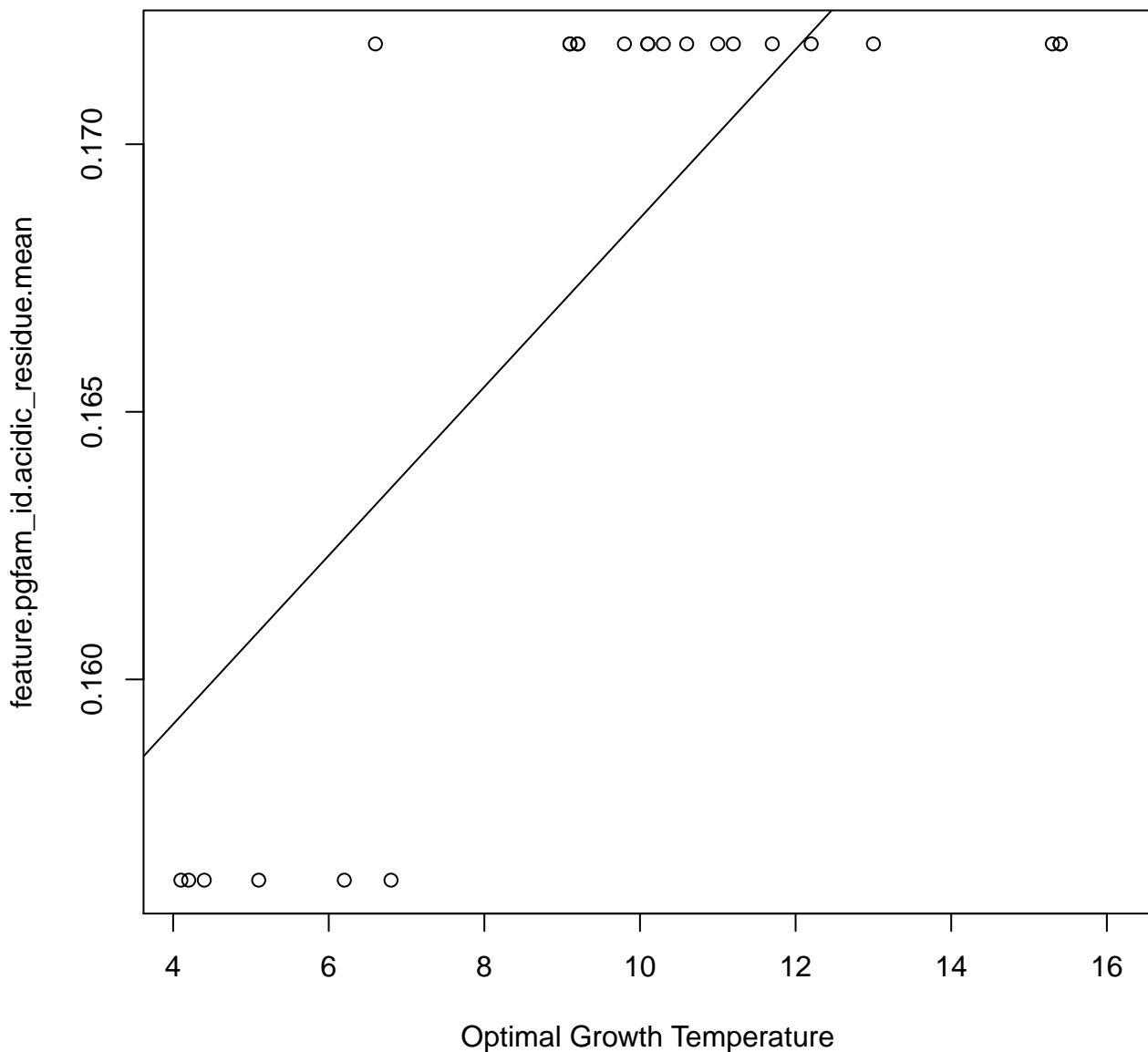
hypothetical protein



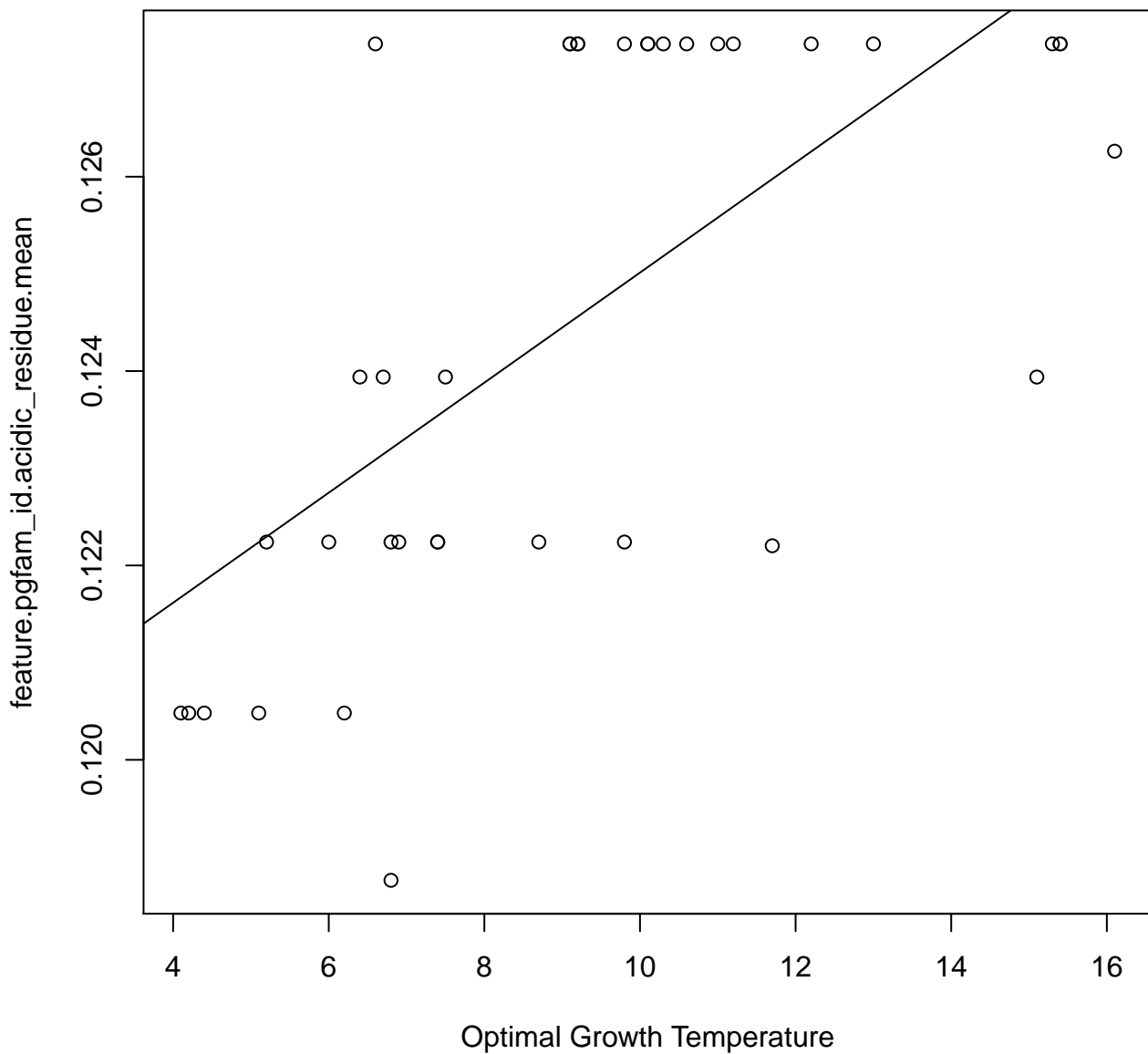
feature.pgfam_id.acidic_residue.mean

PGF_07004481

hypothetical protein



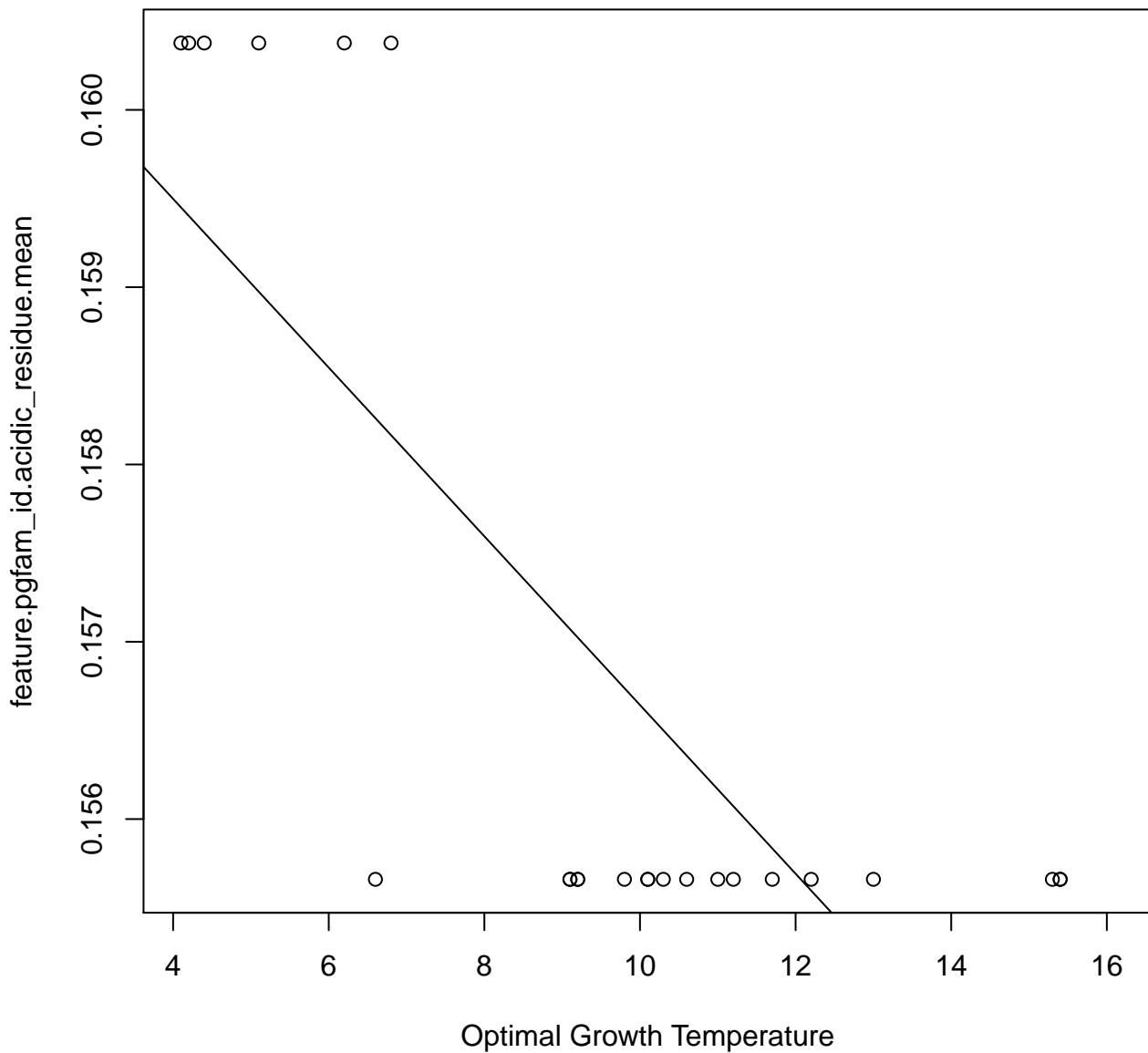
feature.pgfam_id.acidic_residue.mean
PGF_07058357
Single-stranded-DNA-specific exonuclease RecJ



feature.pgfam_id.acidic_residue.mean

PGF_10592448

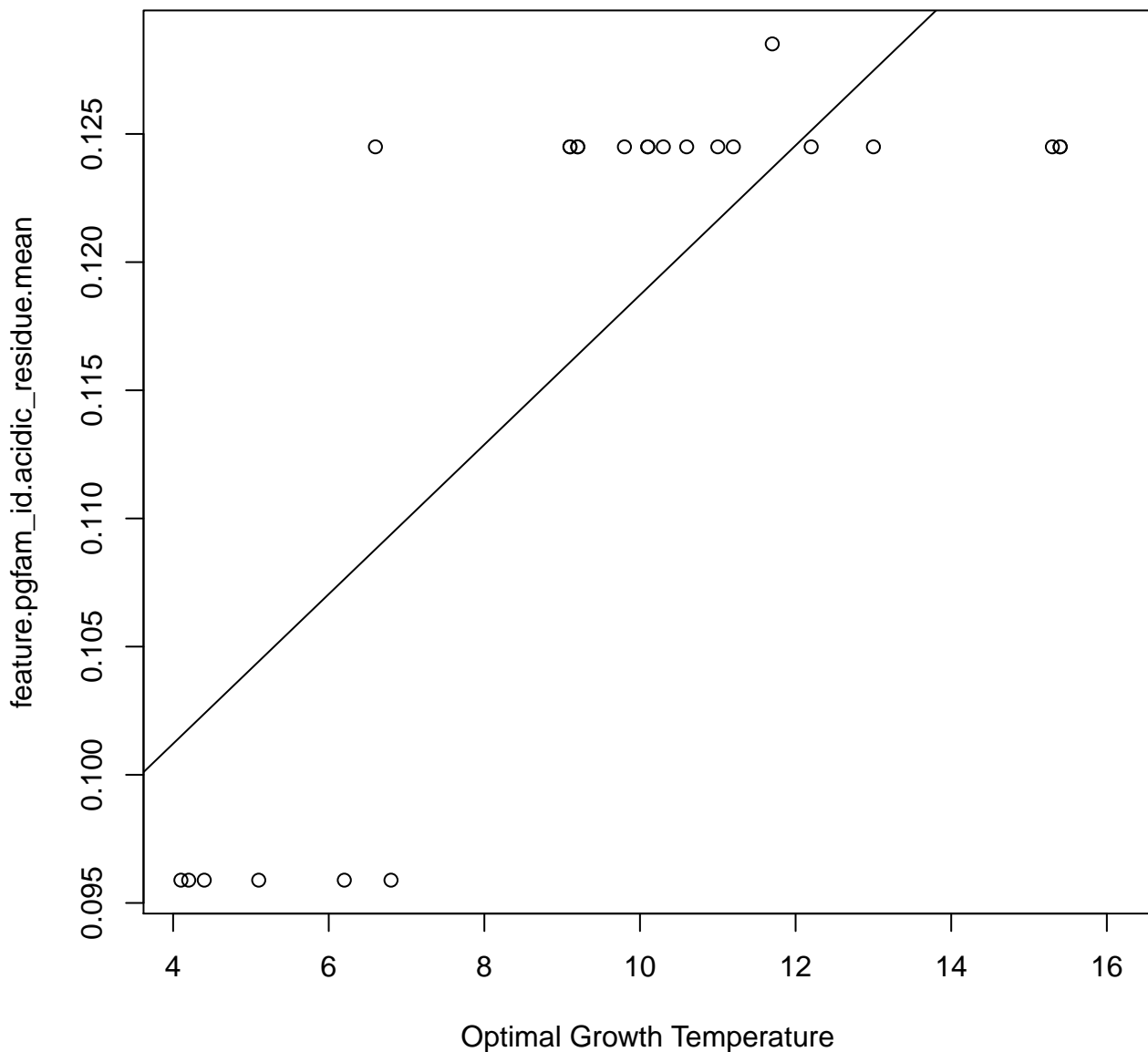
hypothetical protein



feature.pgfam_id.acidic_residue.mean

PGF_11018774

hypothetical protein

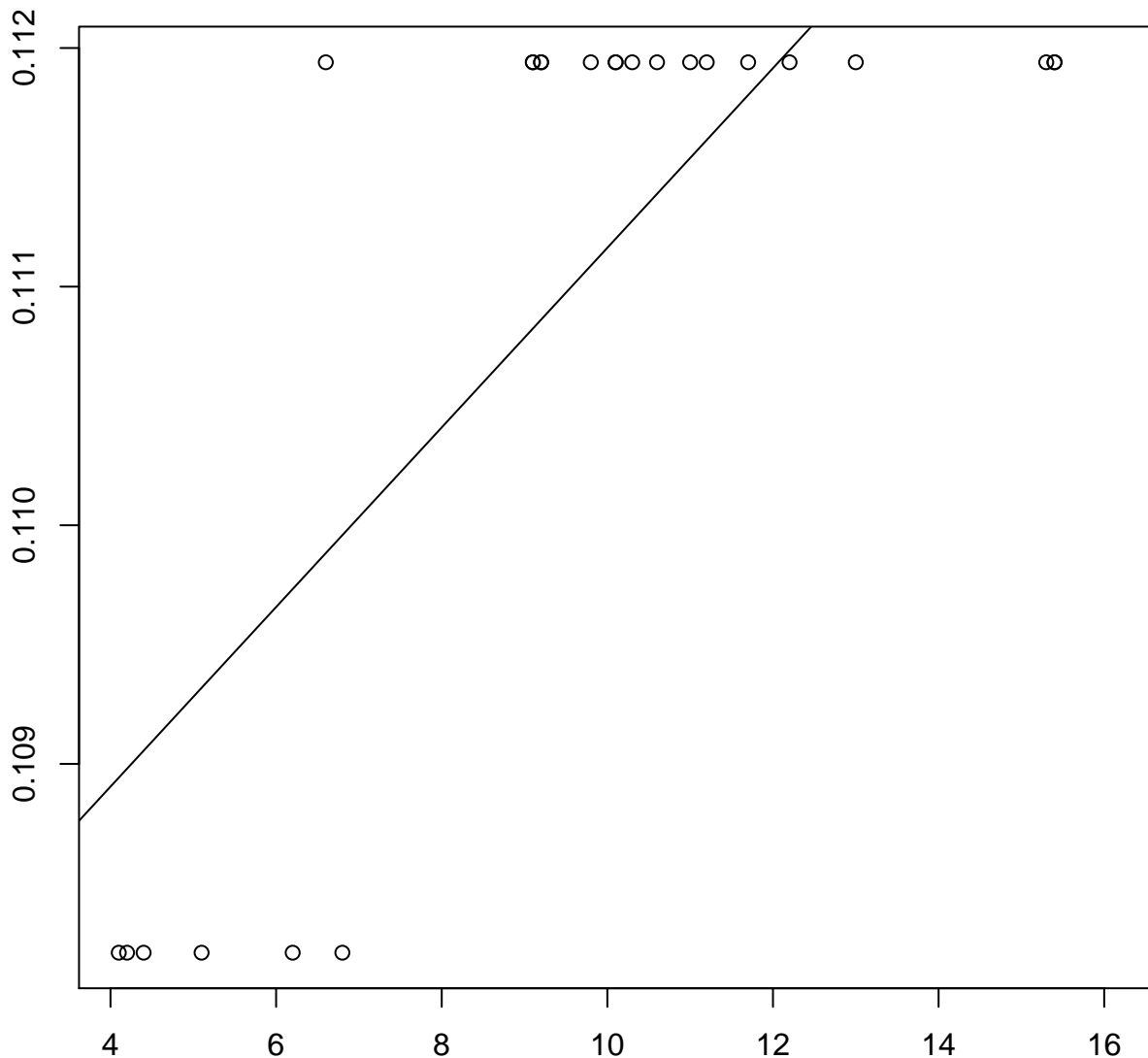


feature.pgfam_id.acidic_residue.mean

PGF_11941604

hypothetical protein

feature.pgfam_id.acidic_residue.mean



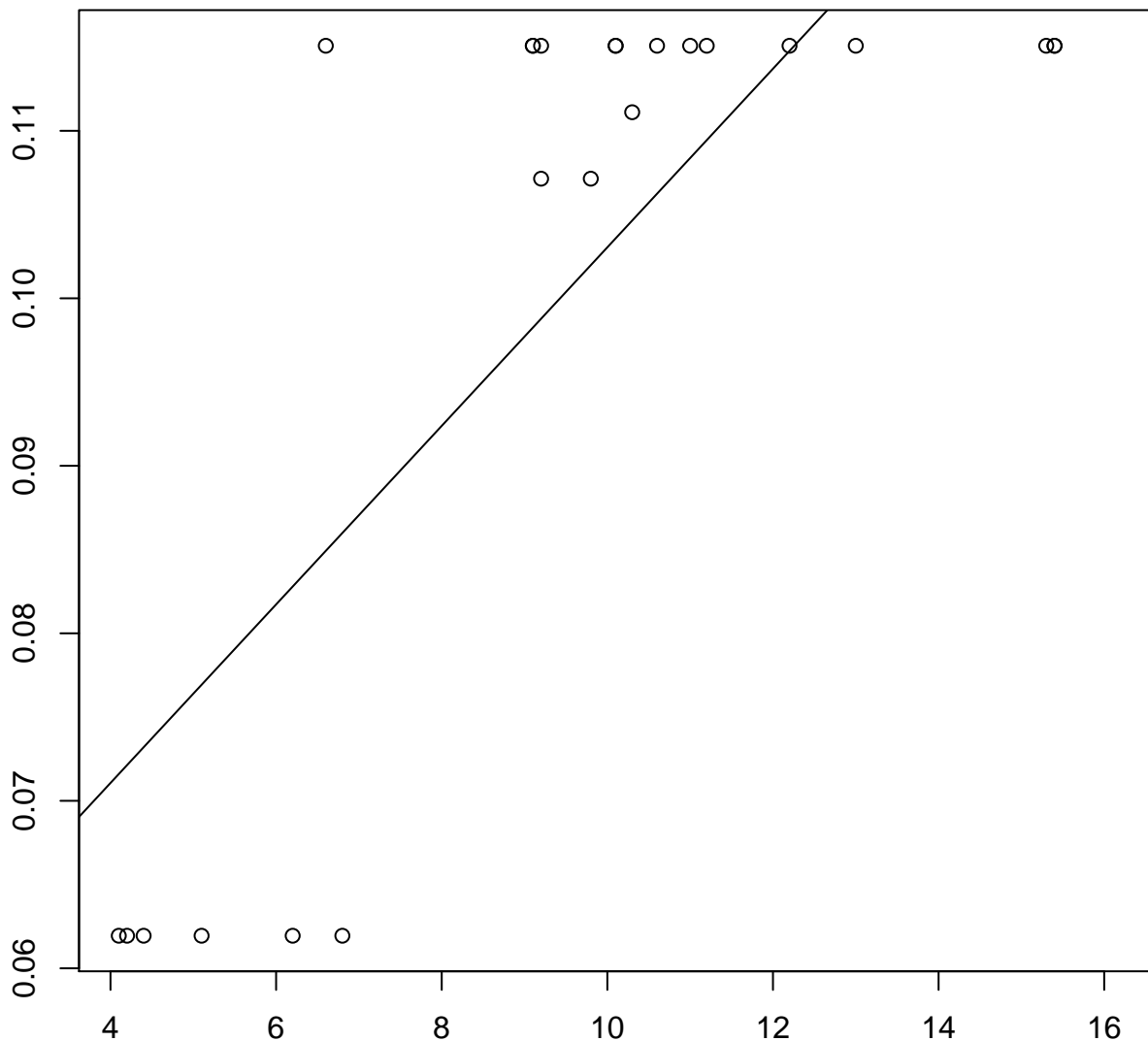
Optimal Growth Temperature

feature.pgfam_id.acidic_residue.mean

PGF_12049070

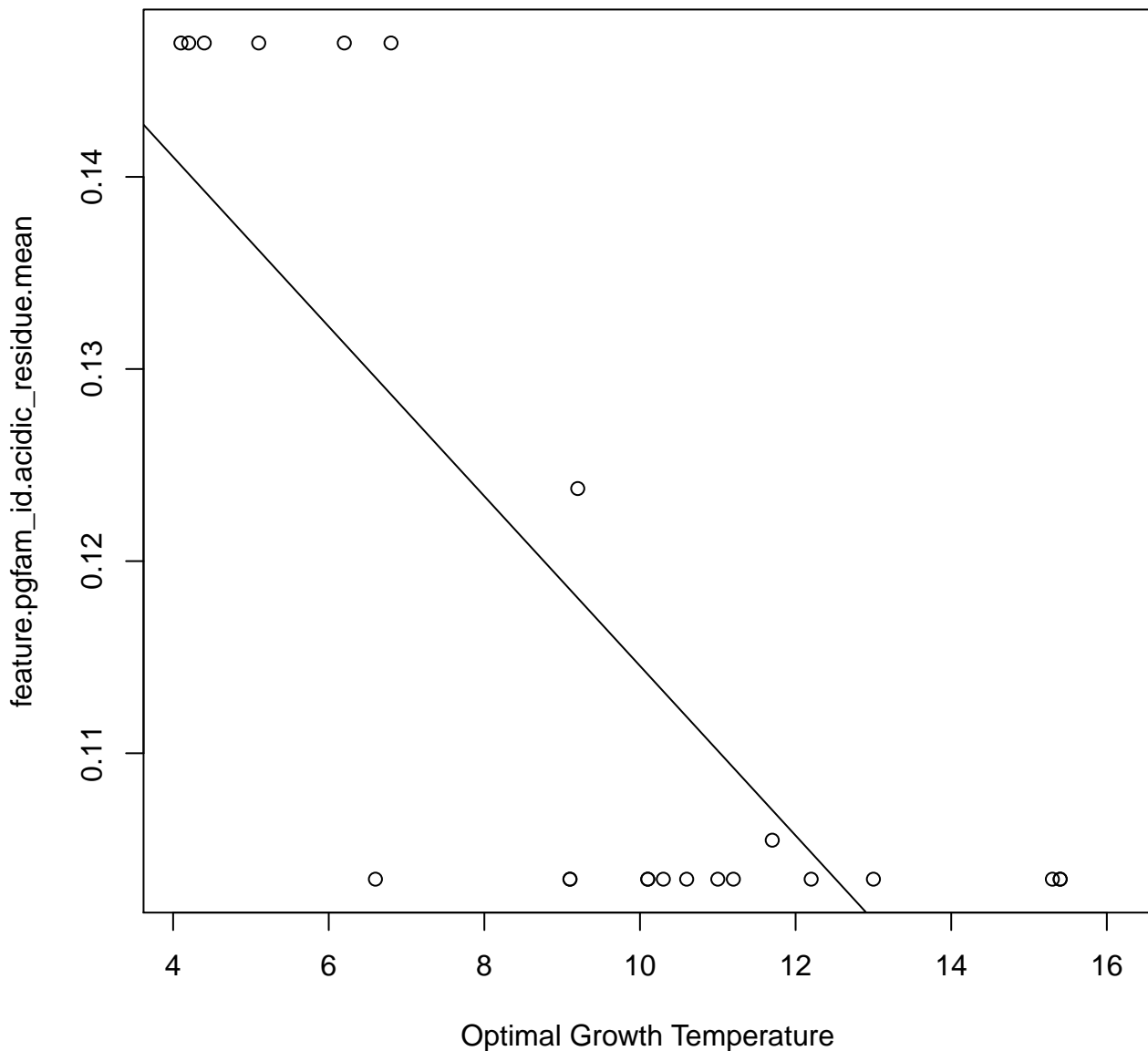
hypothetical protein

feature.pgfam_id.acidic_residue.mean



Optimal Growth Temperature

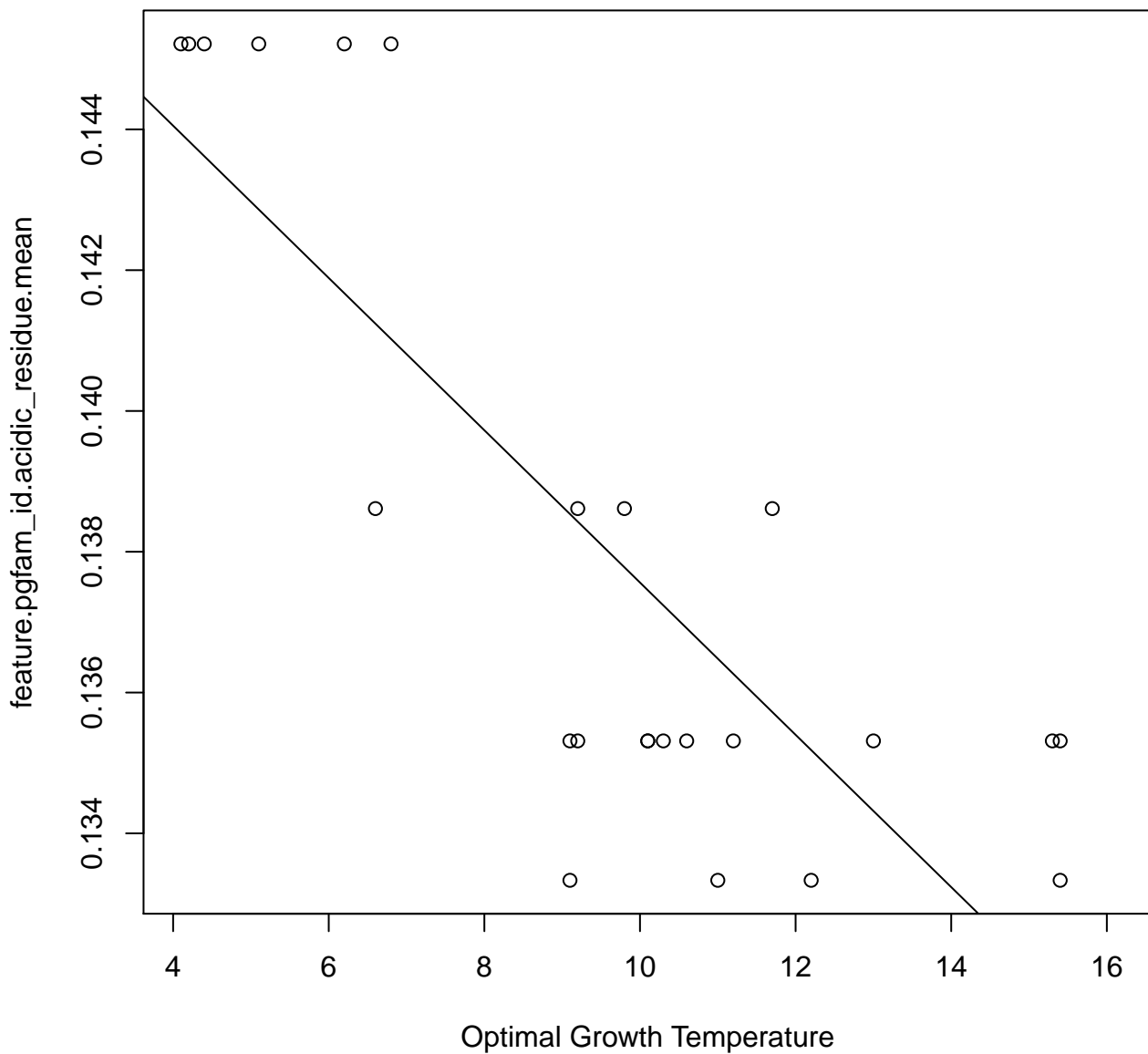
feature.pgfam_id.acidic_residue.mean
PGF_12765299
Two-component system sensor histidine kinase



feature.pgfam_id.acidic_residue.mean

PGF_12817314

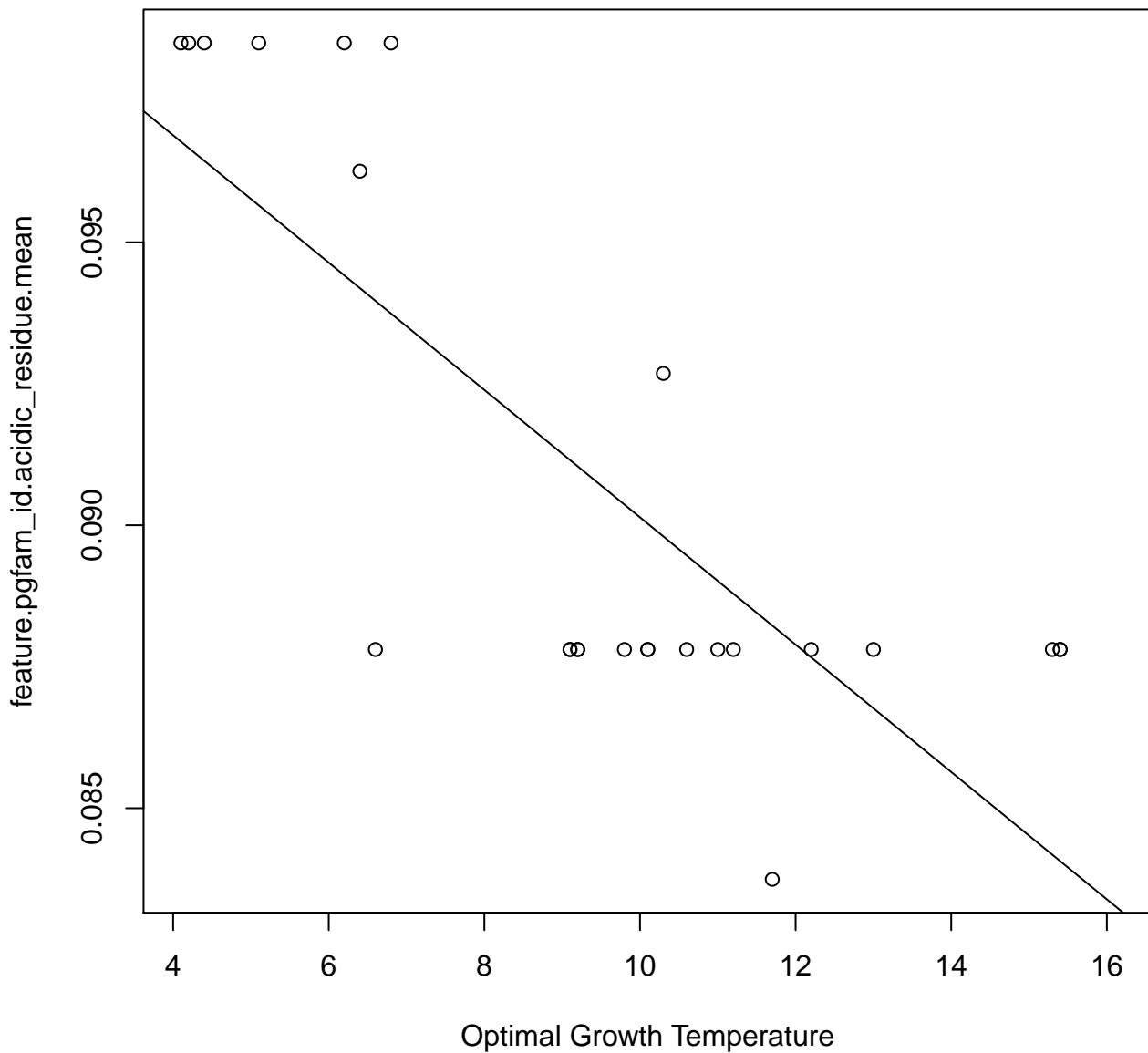
hypothetical protein



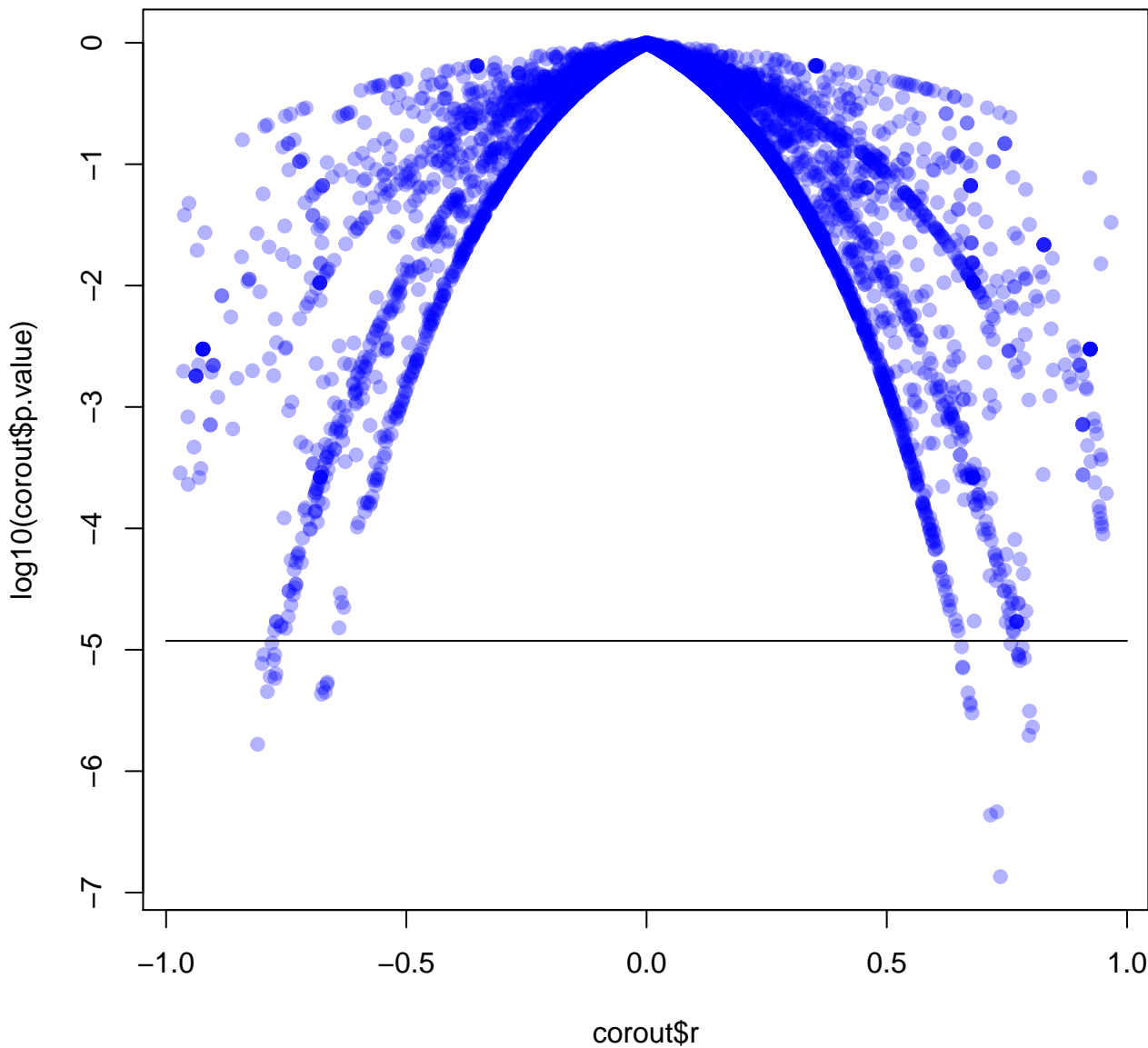
feature.pgfam_id.acidic_residue.mean

PGF_12826297

hypothetical protein



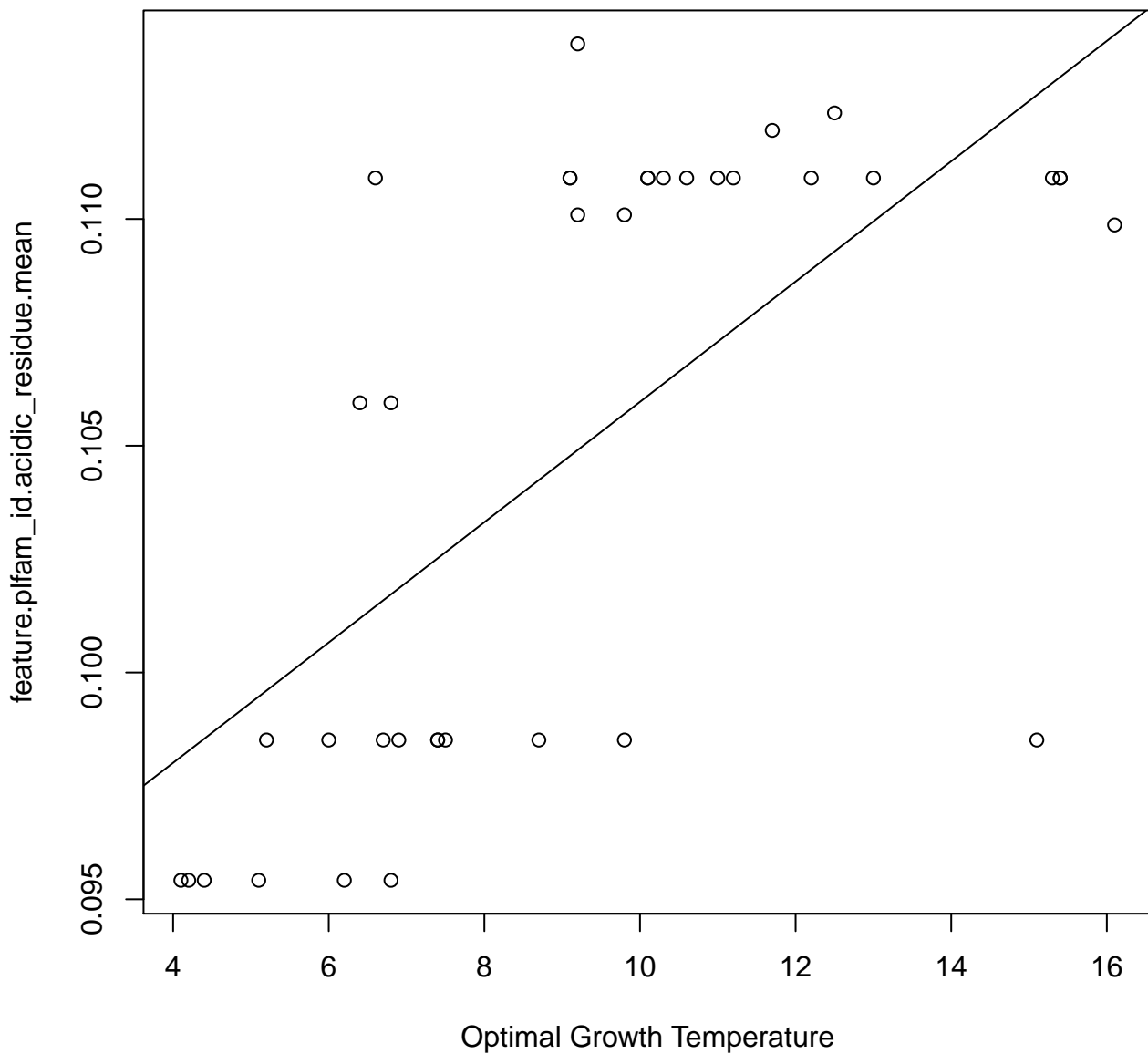
feature.plfam_id.acidic_residue.mean



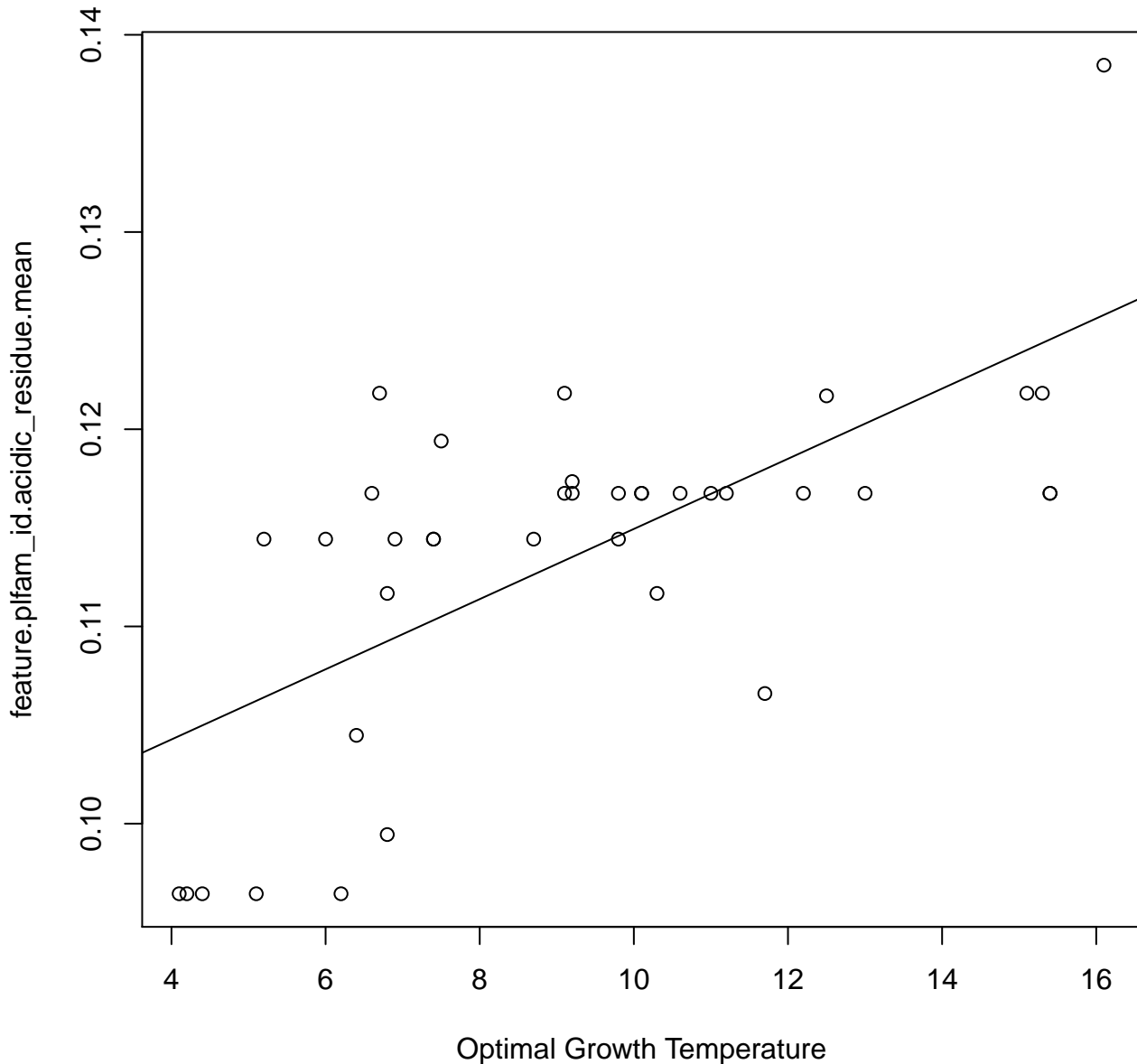
feature.plfam_id.acidic_residue.mean

PLF_28228_00000147

Sensory box histidine kinase



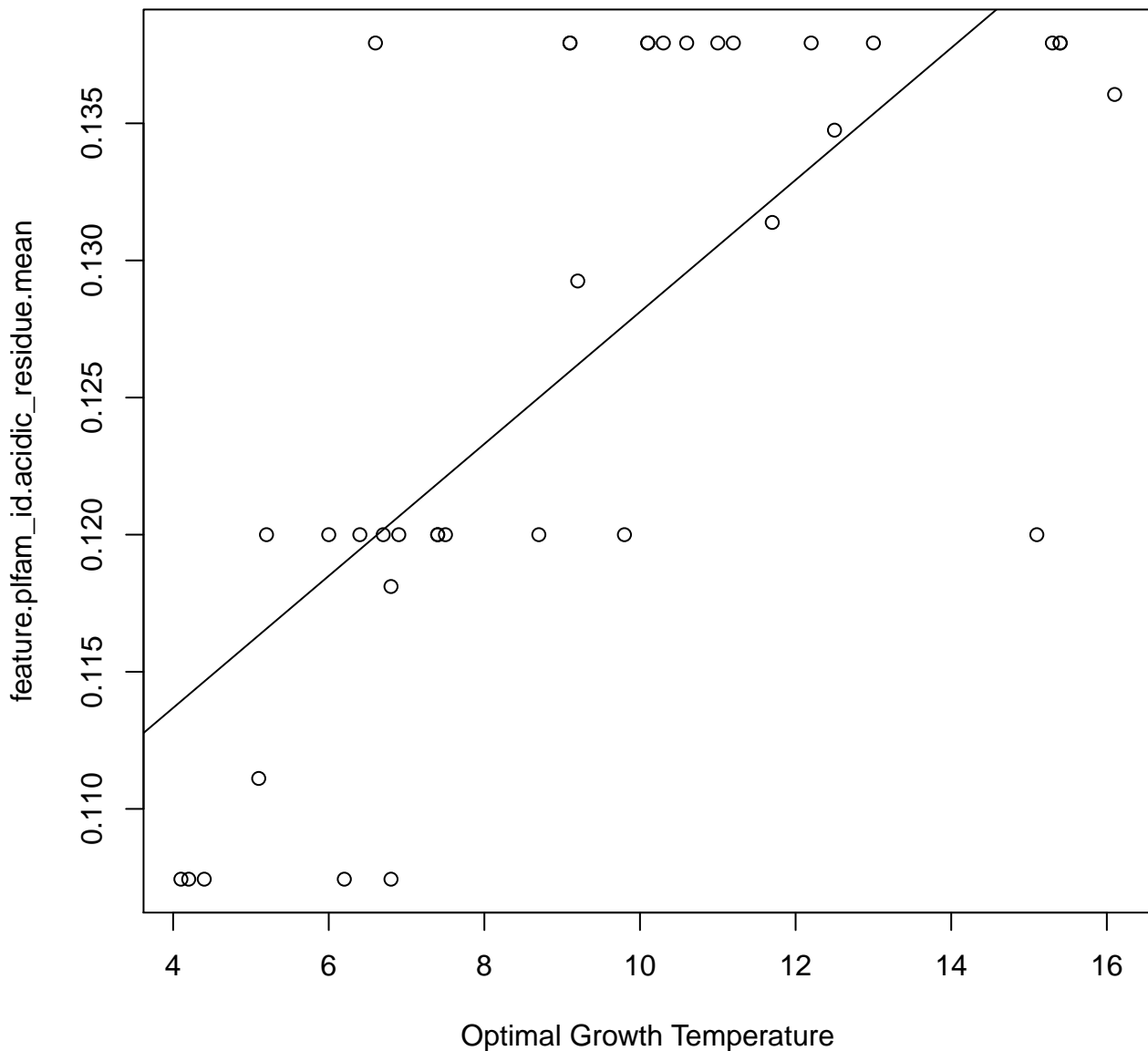
feature.plfam_id.acidic_residue.mean
PLF_28228_00000212
1,6-anhydro-N-acetylmuramyl-L-alanine amidase



feature.plfam_id.acidic_residue.mean

PLF_28228_00000407

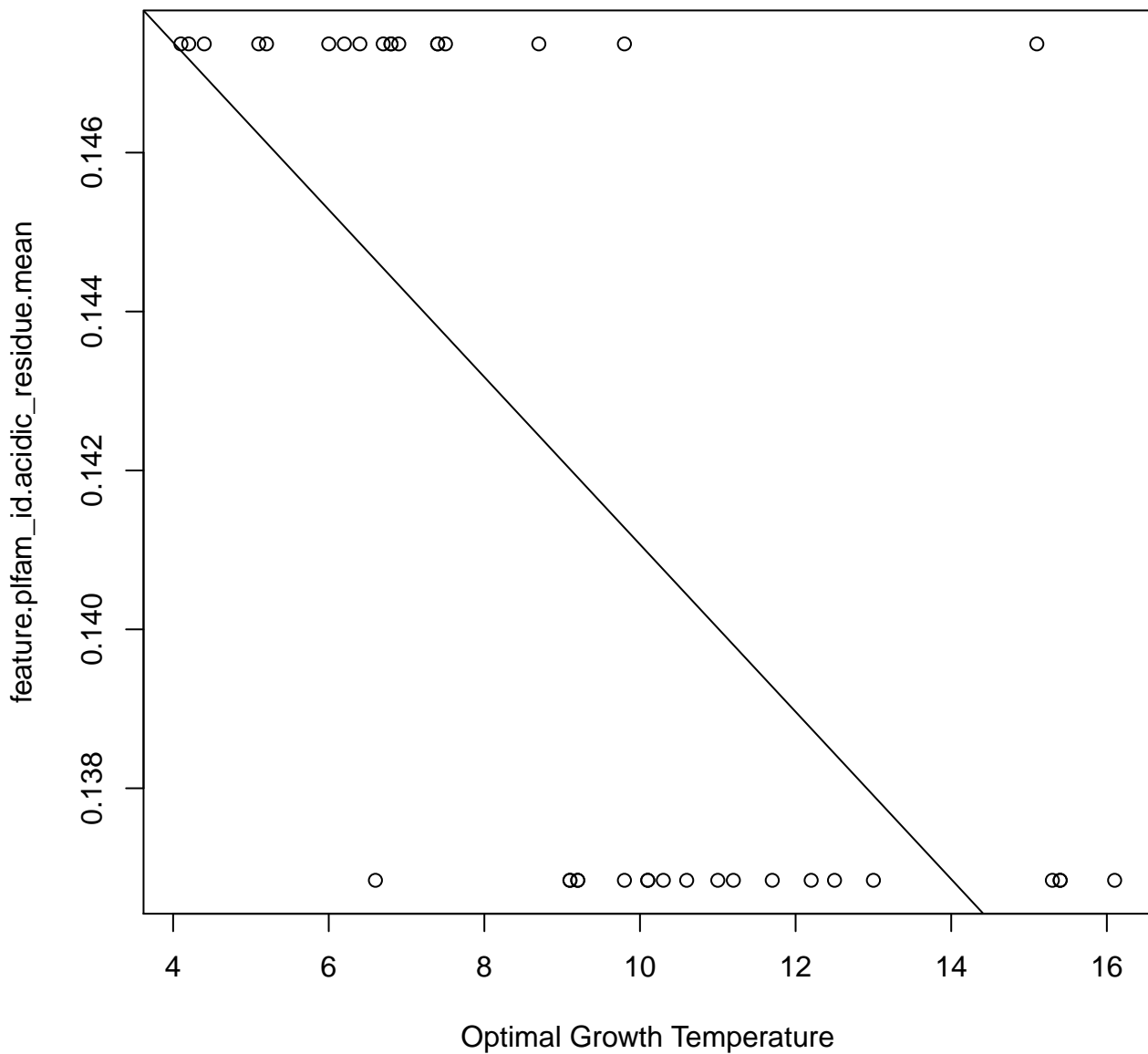
FIG024746: hypothetical protein



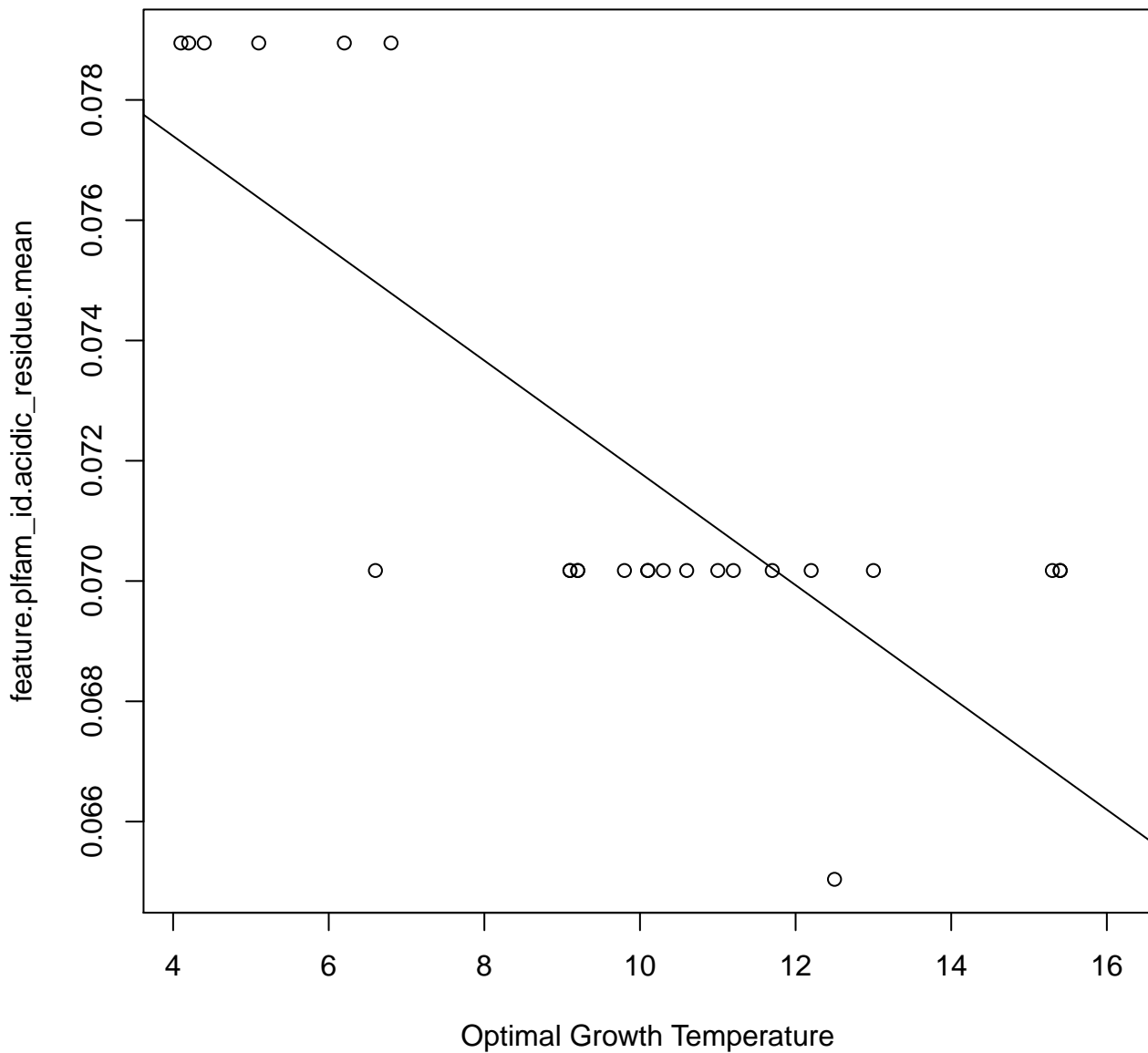
feature.plfam_id.acidic_residue.mean

PLF_28228_00000528

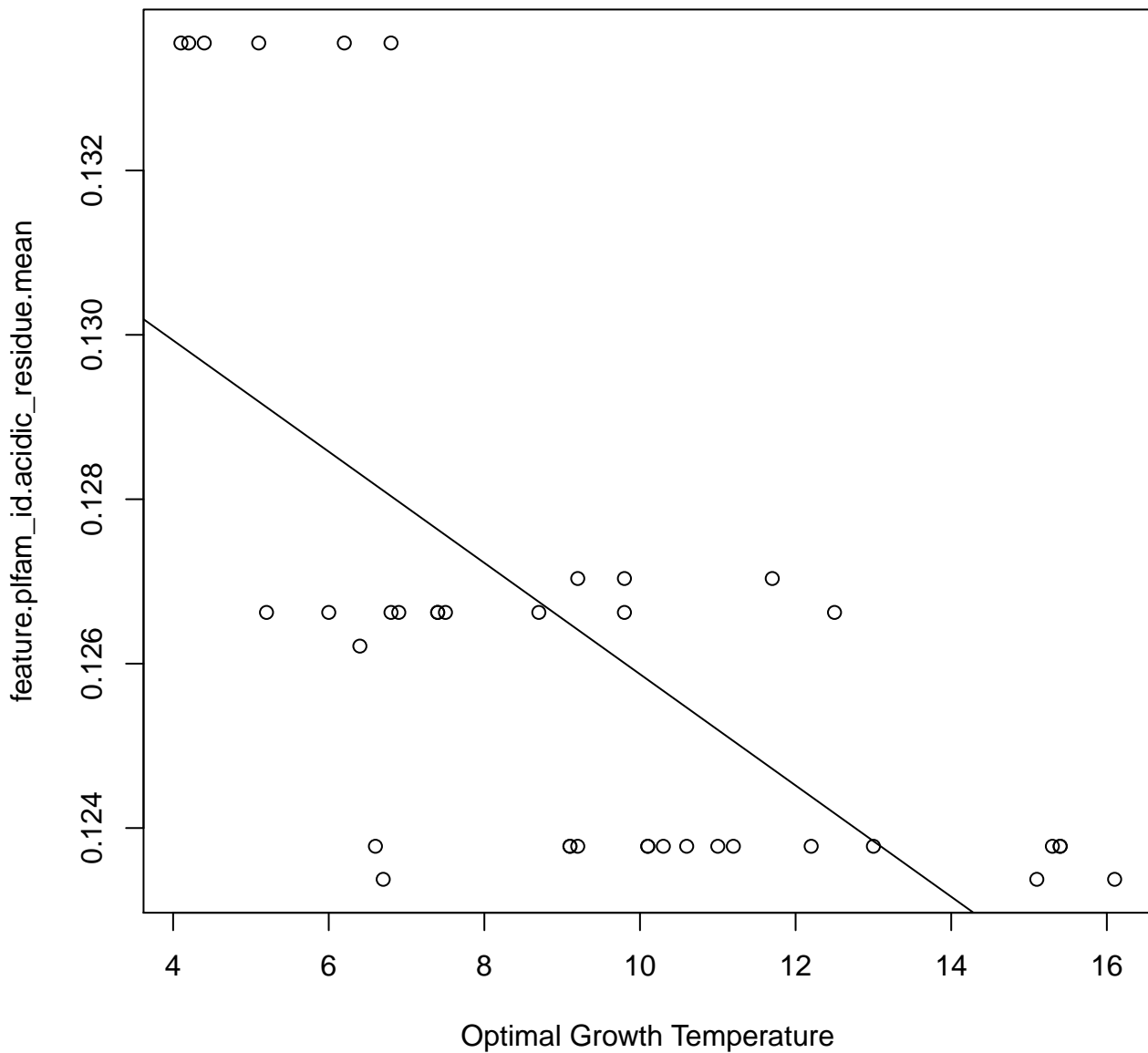
Integration host factor beta subunit



feature.plfam_id.acidic_residue.mean
PLF_28228_00000644
Na(+) H(+) antiporter subunit C



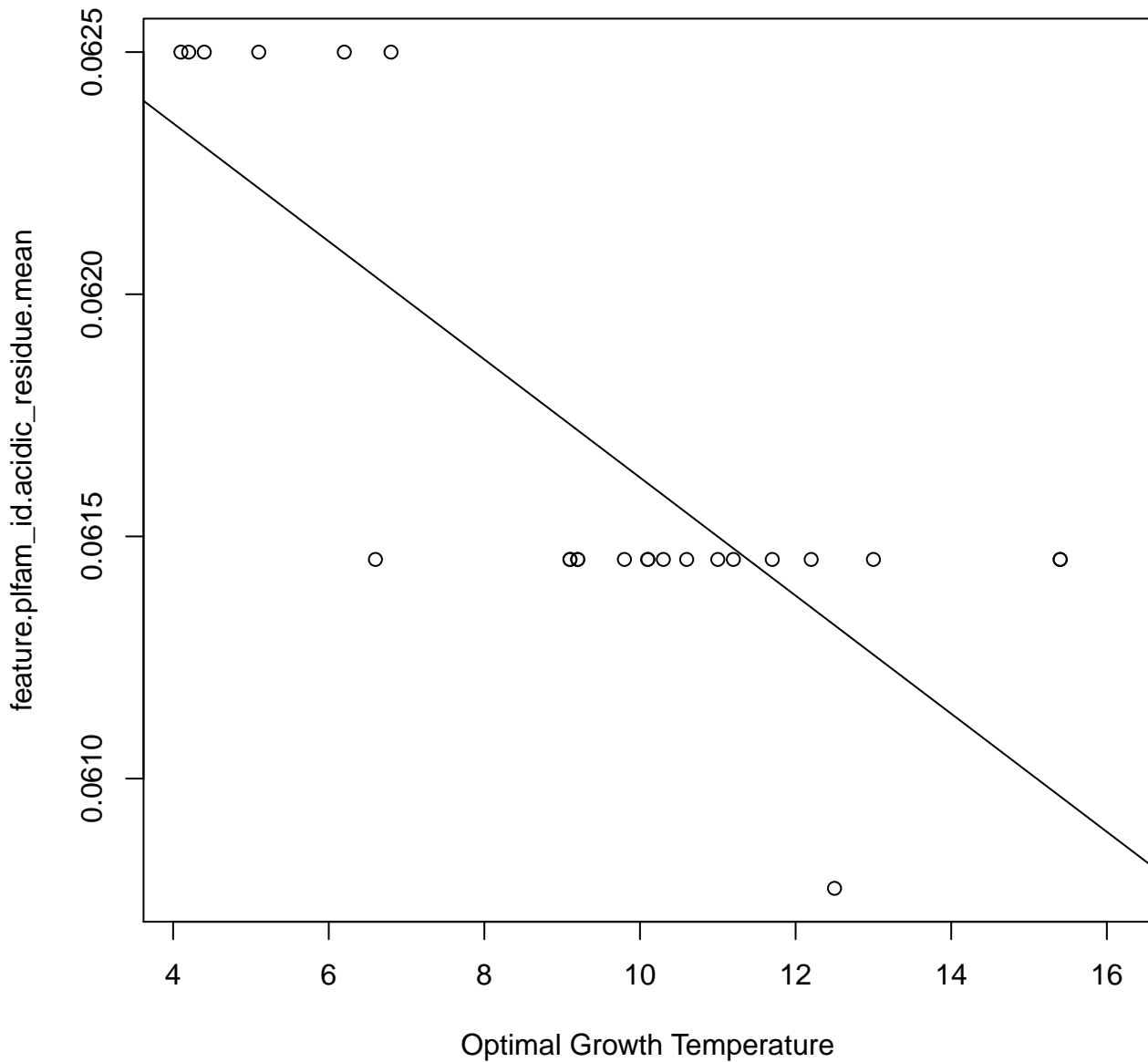
feature.plfam_id.acidic_residue.mean
PLF_28228_00000865
GTP cyclohydrolase I (EC 3.5.4.16) type 2



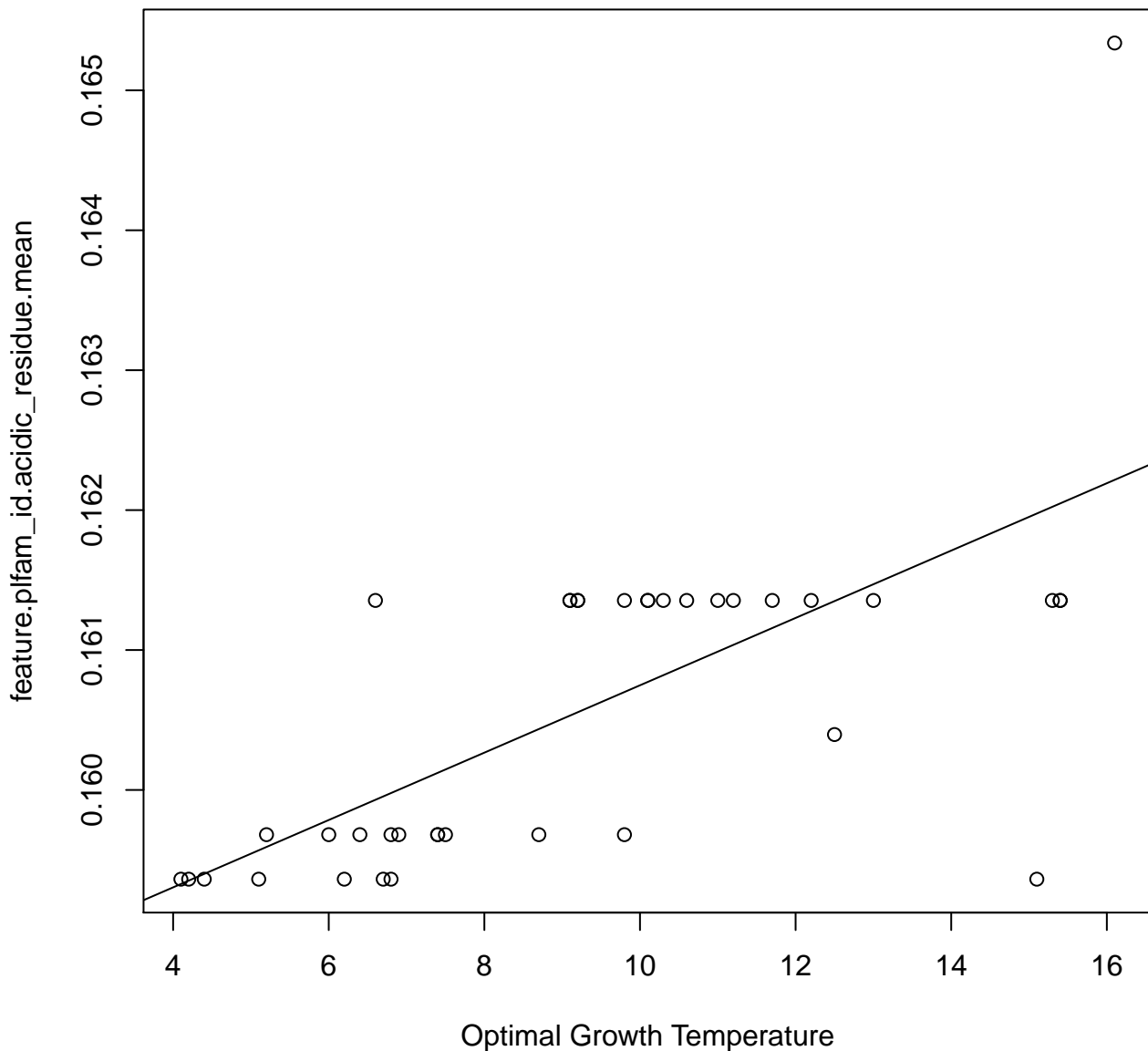
feature.plfam_id.acidic_residue.mean

PLF_28228_00000991

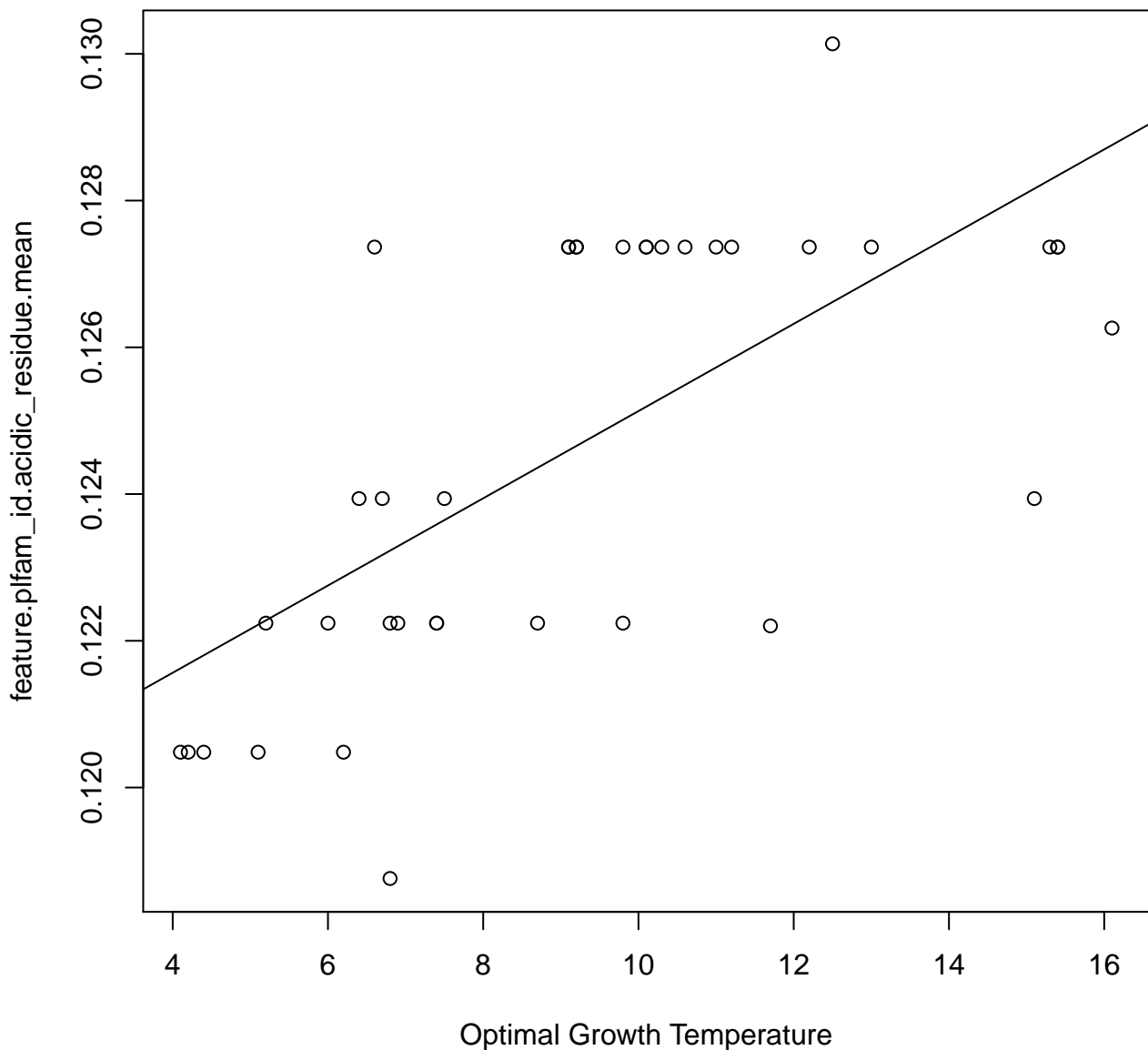
Putative manganese efflux pump MntP



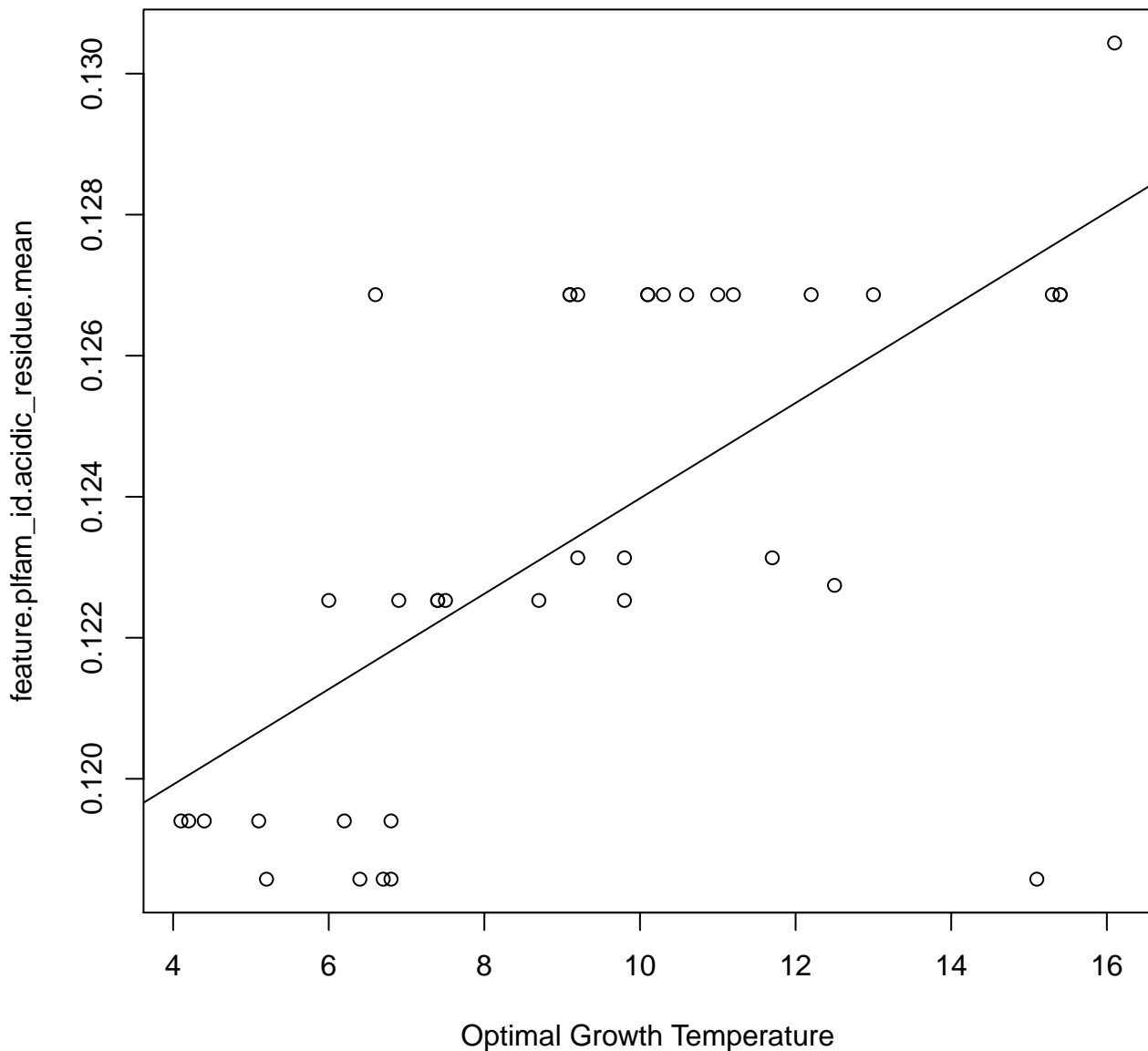
feature.plfam_id.acidic_residue.mean
PLF_28228_00001044
RNA polymerase sigma-54 factor RpoN



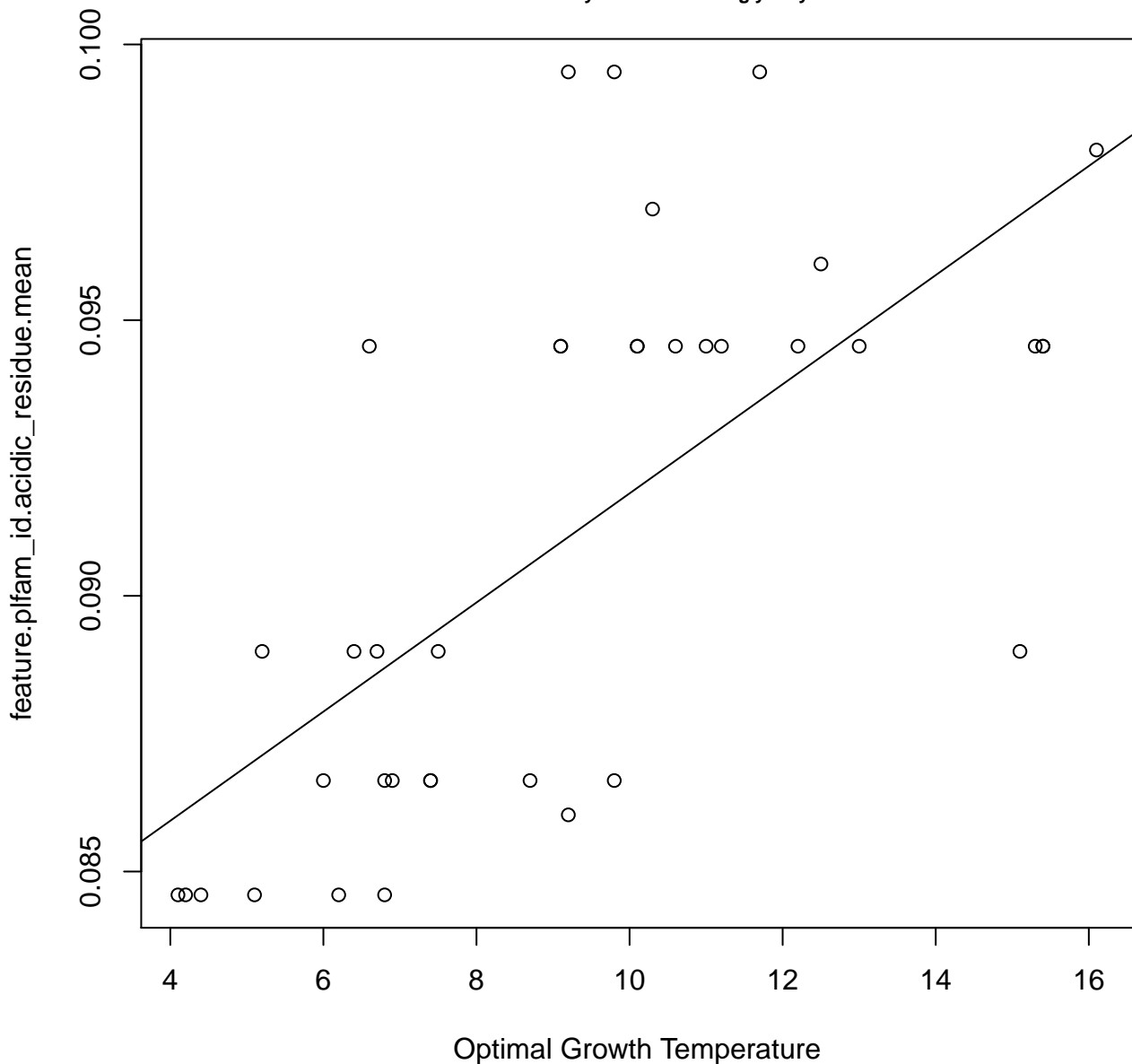
feature.plfam_id.acidic_residue.mean
PLF_28228_00001155
Single-stranded-DNA-specific exonuclease RecJ



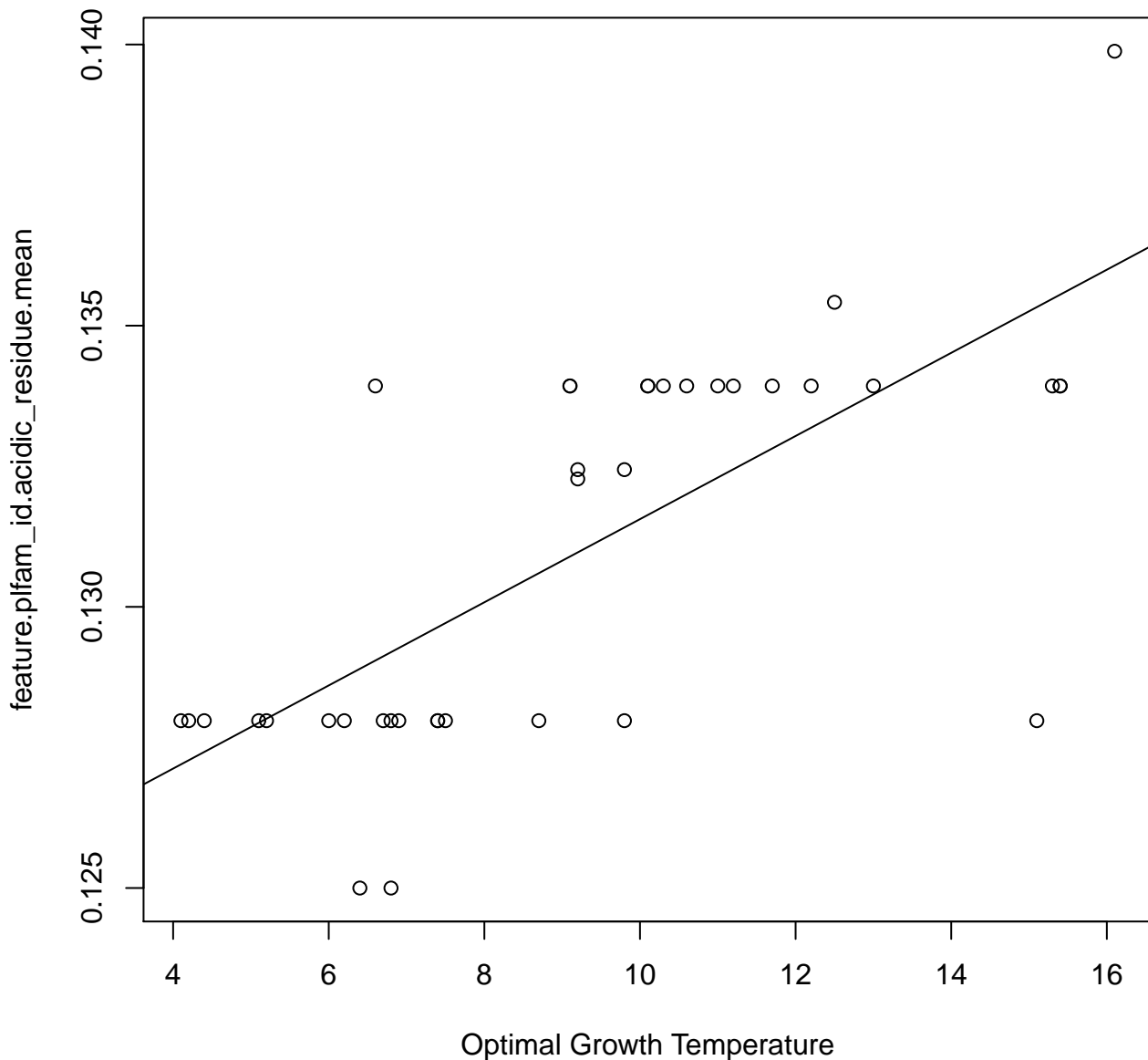
feature.plfam_id.acidic_residue.mean
PLF_28228_00001395
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)



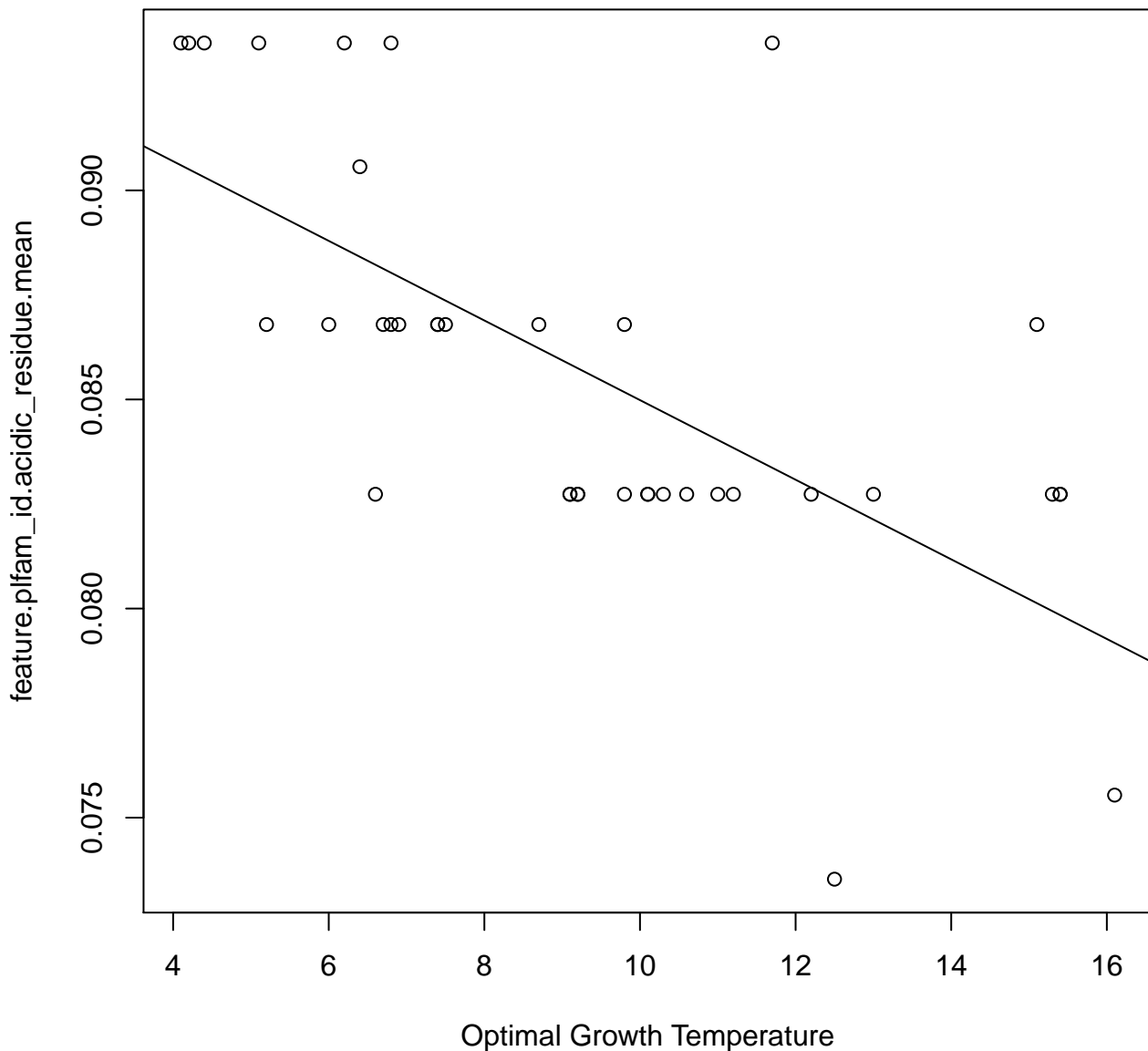
feature.plfam_id.acidic_residue.mean
PLF_28228_00001726
Membrane-bound lytic murein transglycosylase B



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



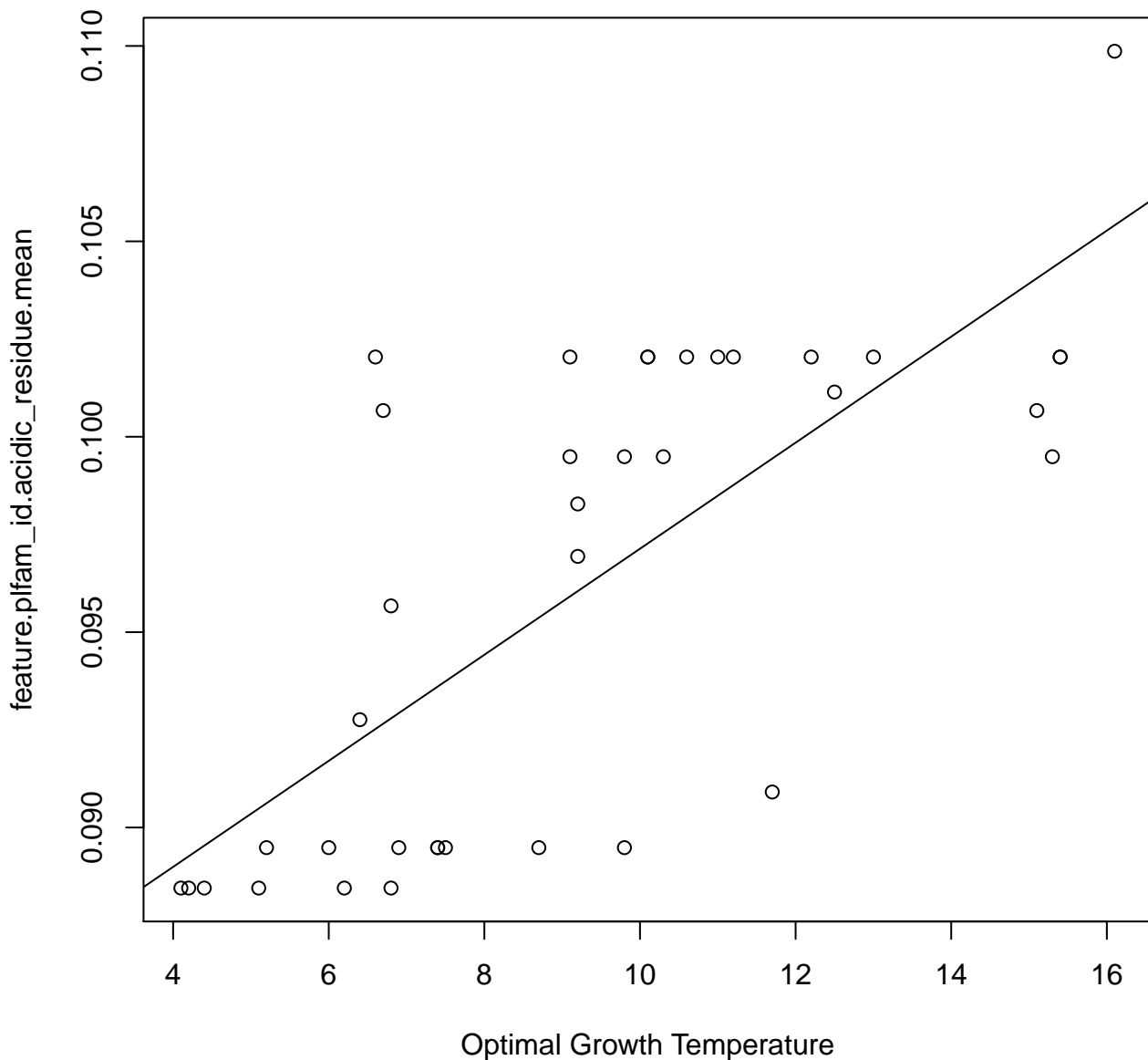
feature.plfam_id.acidic_residue.mean
PLF_28228_00002017
Caulimovirus viroplasm / Ribonuclease HI (EC 3.1.26.4)



feature.plfam_id.acidic_residue.mean

PLF_28228_00002173

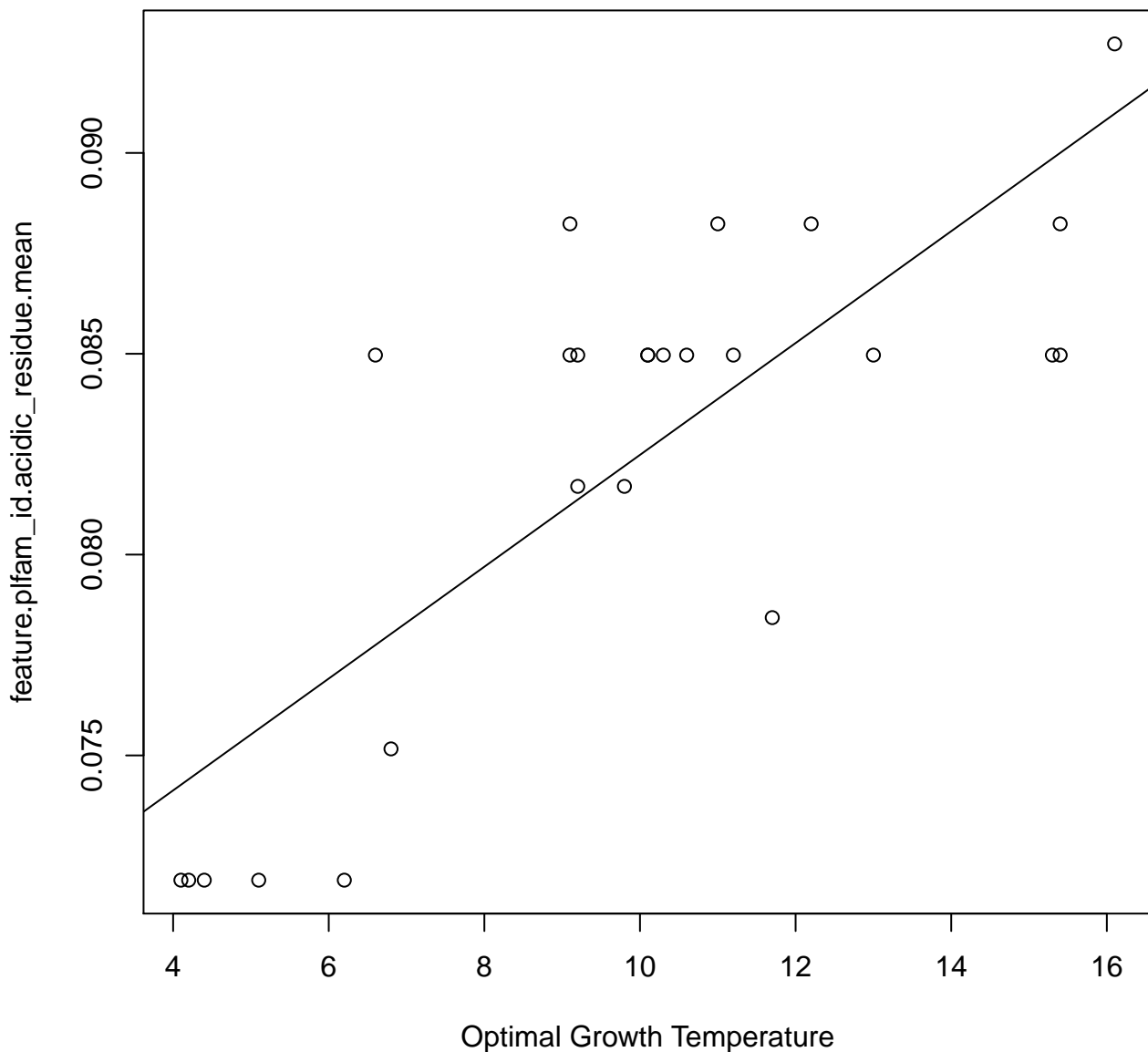
Type IV pilus biogenesis protein PilF



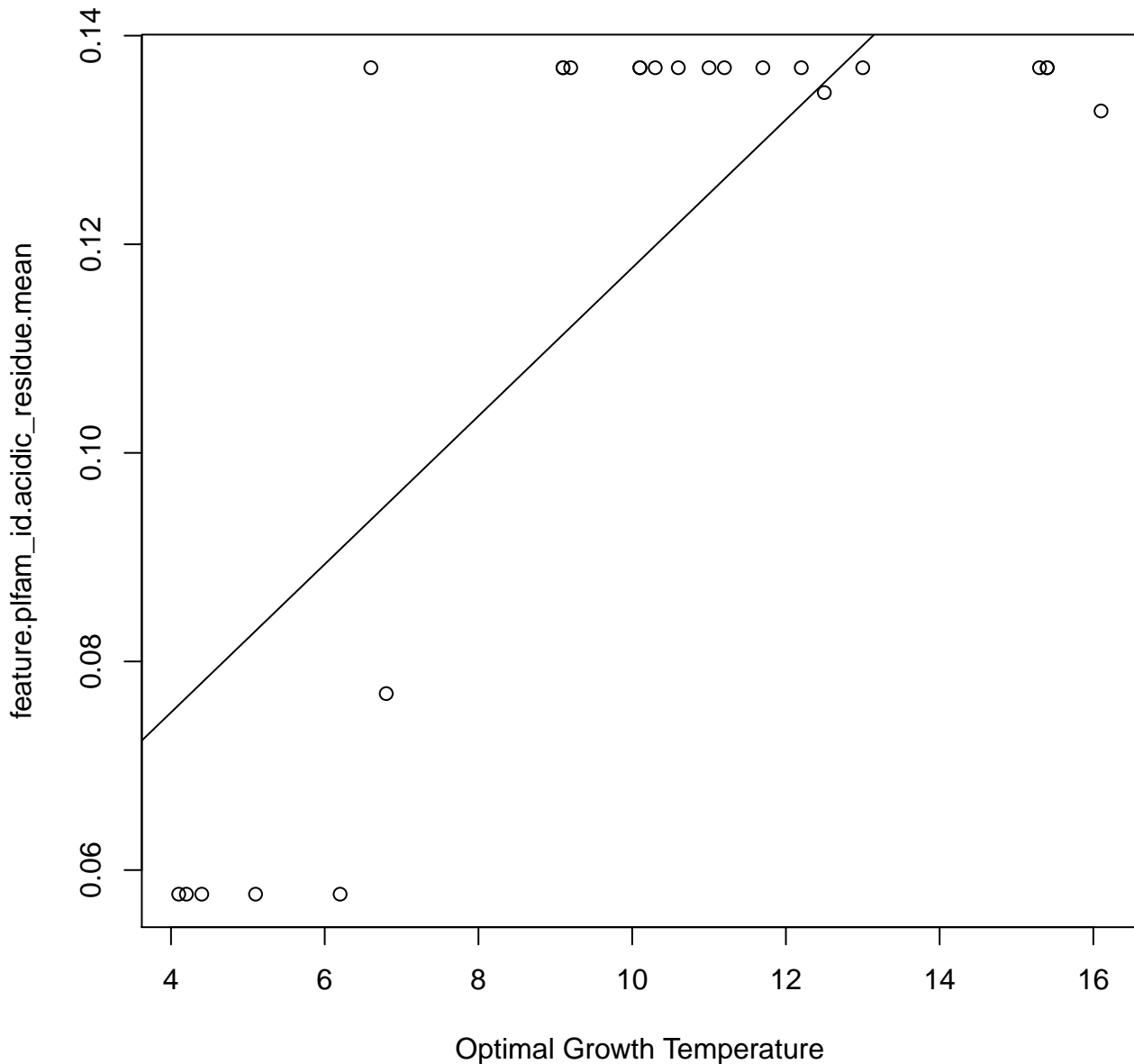
feature.plfam_id.acidic_residue.mean

PLF_28228_00002780

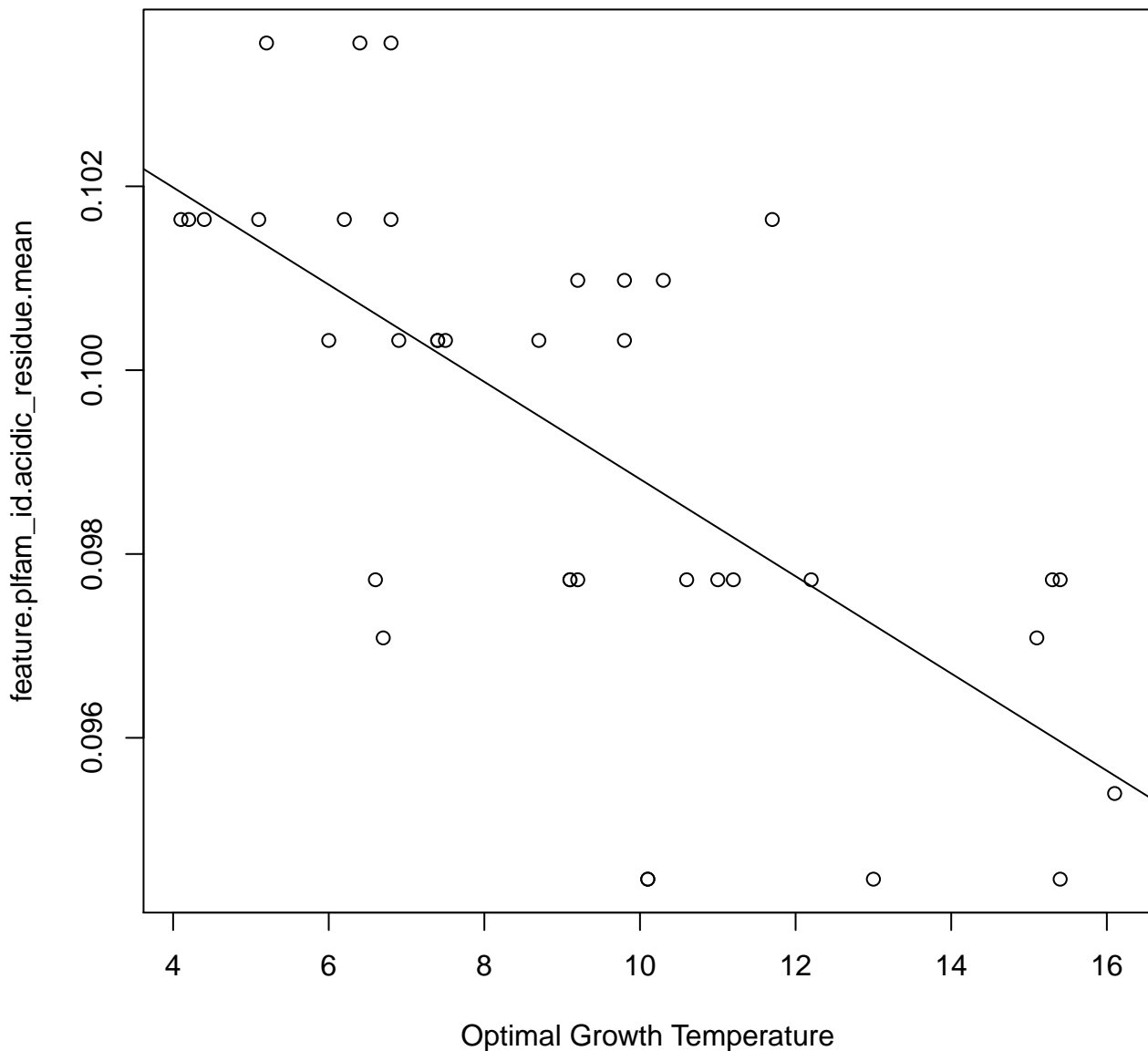
Protein translocase subunit SecF



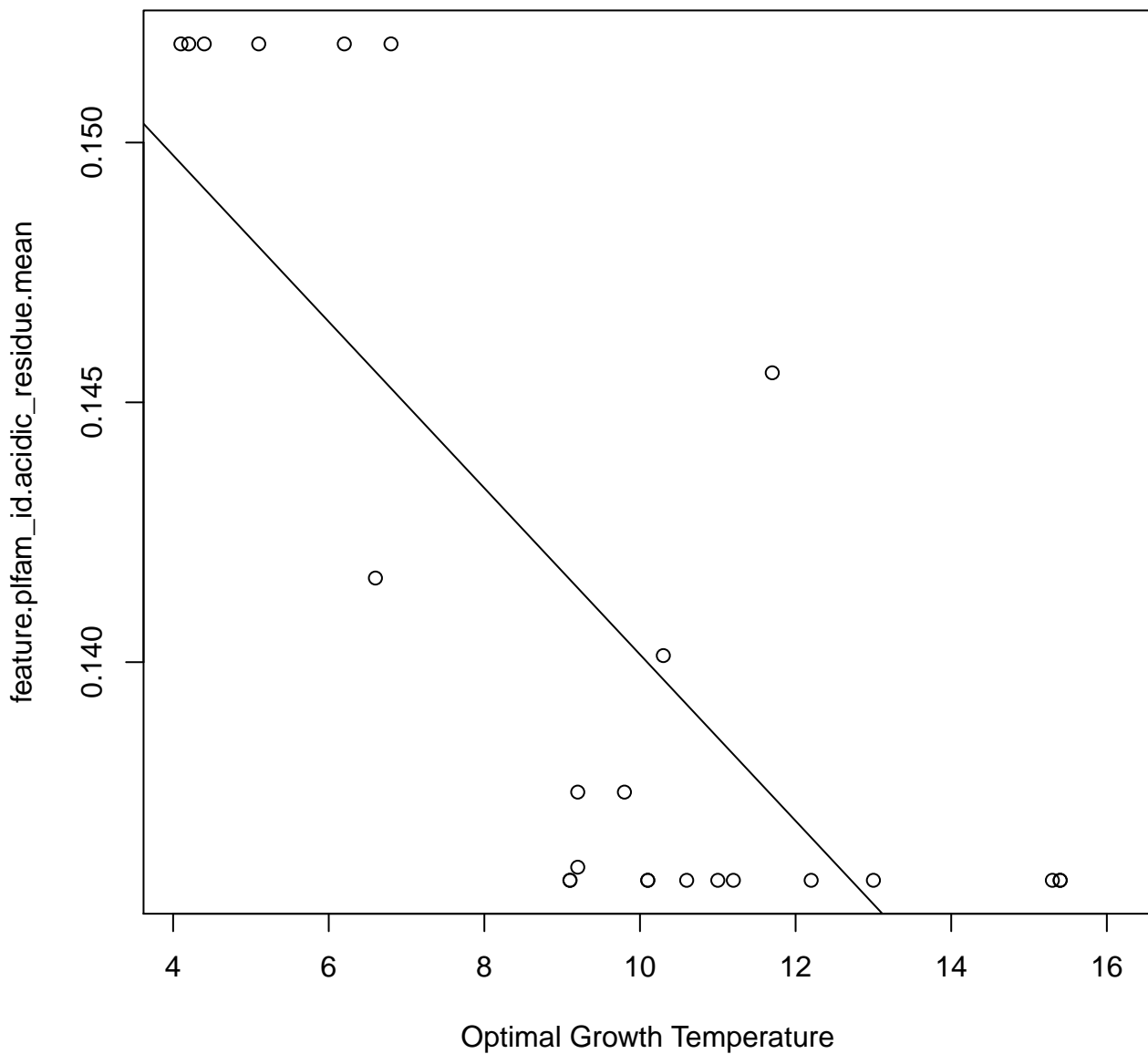
feature.plfam_id.acidic_residue.mean
PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



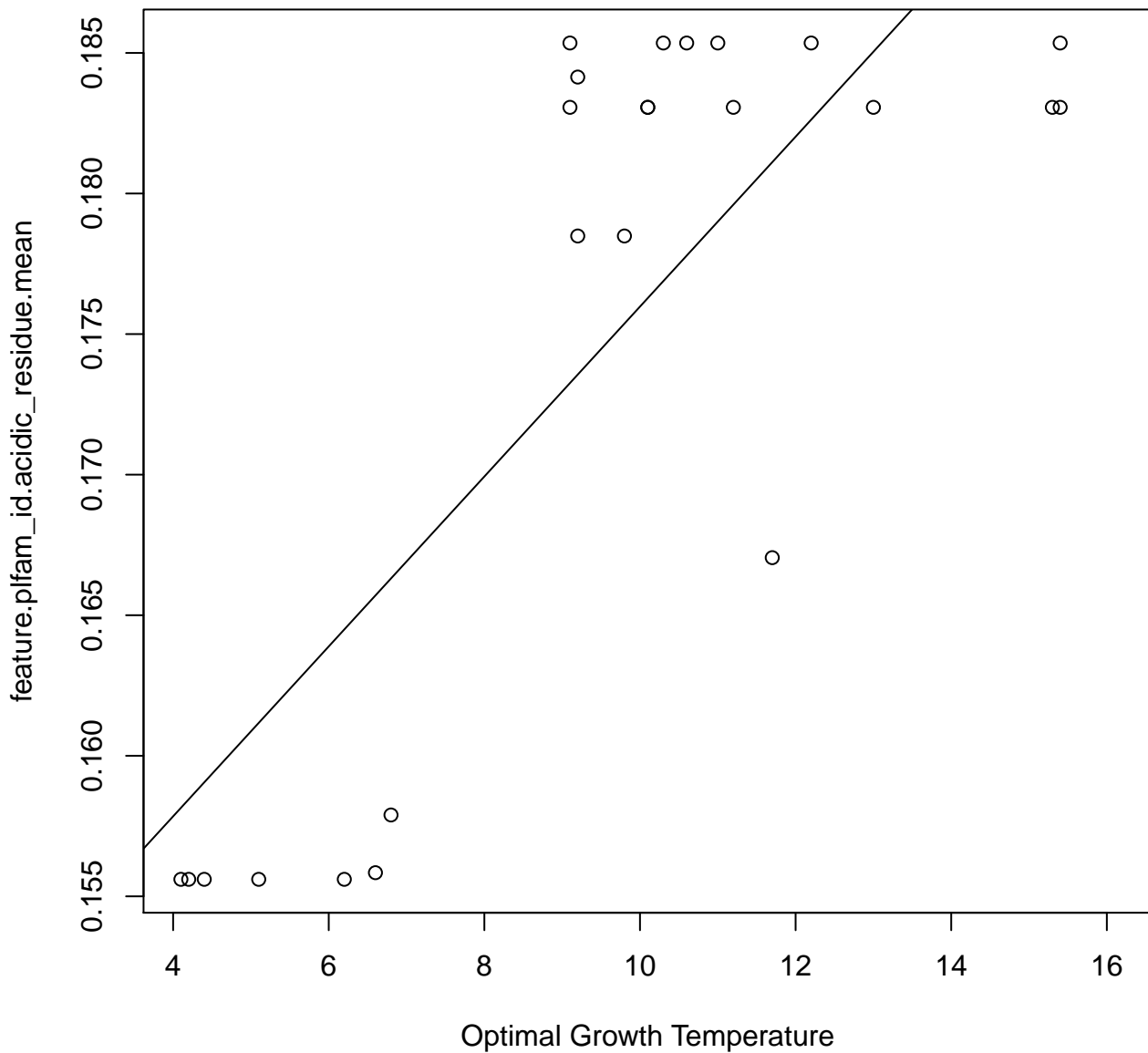
feature.plfam_id.acidic_residue.mean
PLF_28228_00003485
Oxidoreductase, short-chain dehydrogenase/reductase family



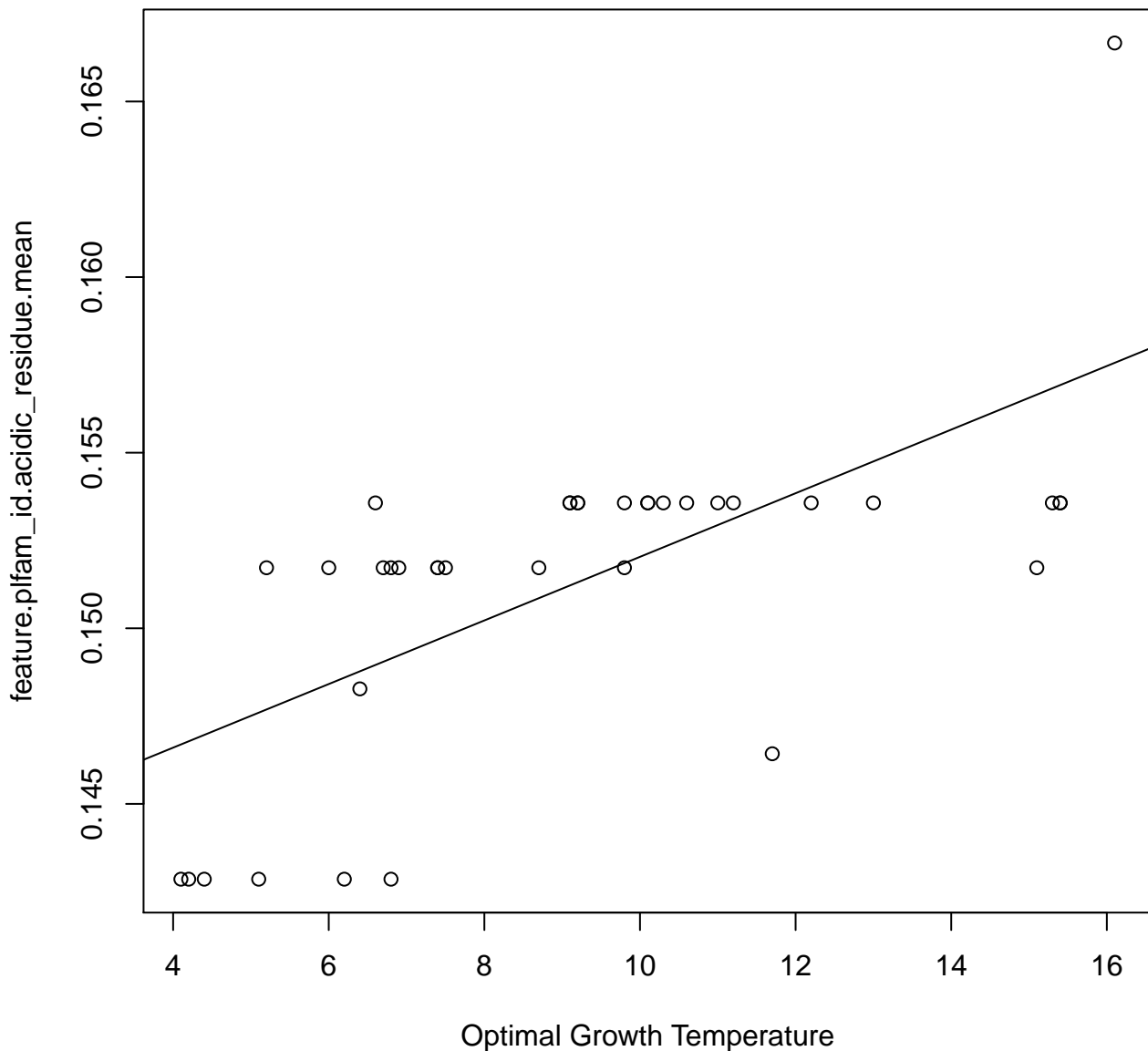
feature.plfam_id.acidic_residue.mean
PLF_28228_00004120
Positive regulator of CheA protein activity (CheW)



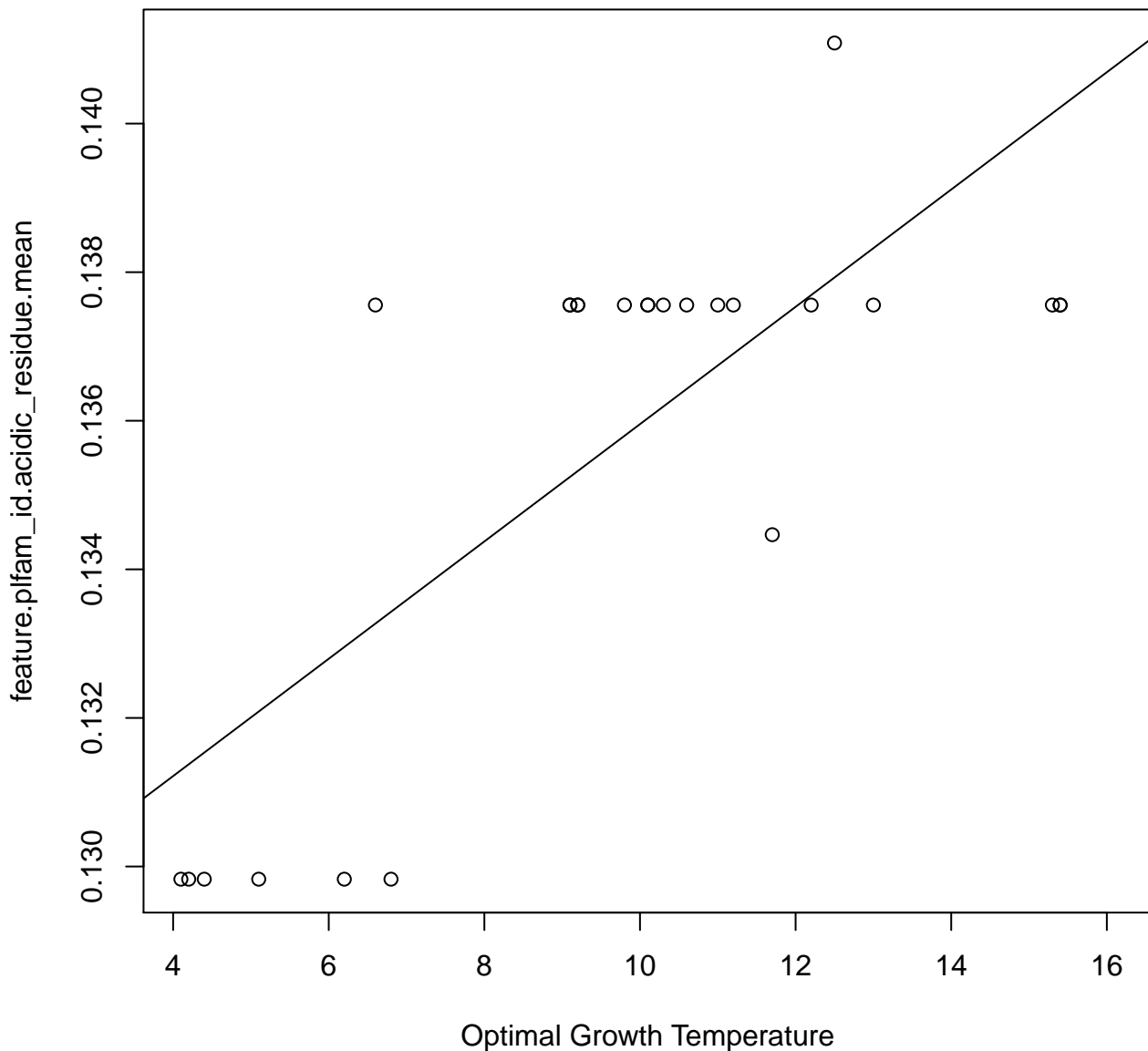
feature.plfam_id.acidic_residue.mean
PLF_28228_00004221
hypothetical protein



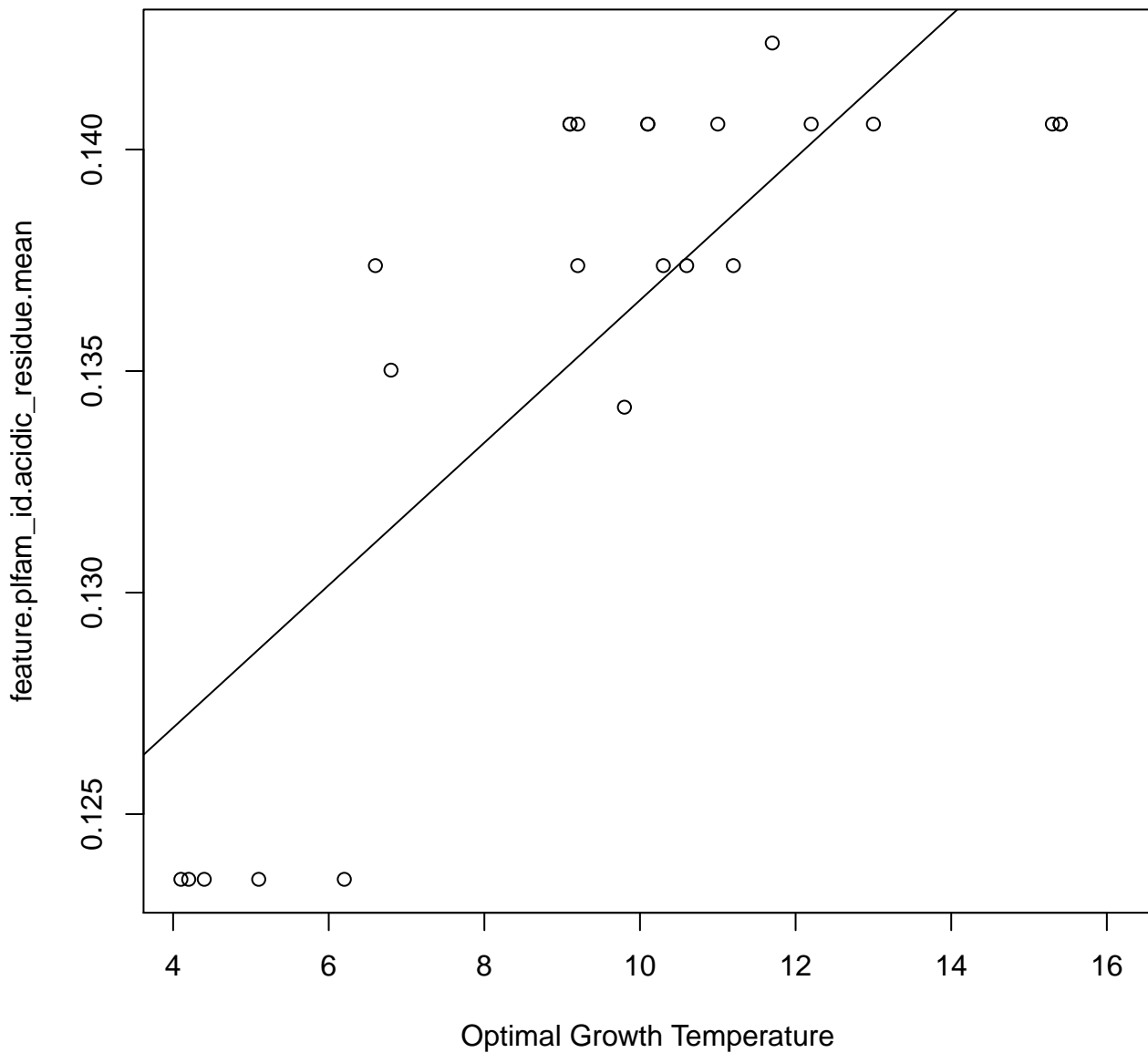
feature.plfam_id.acidic_residue.mean
PLF_28228_00005964
Segregation and condensation protein A



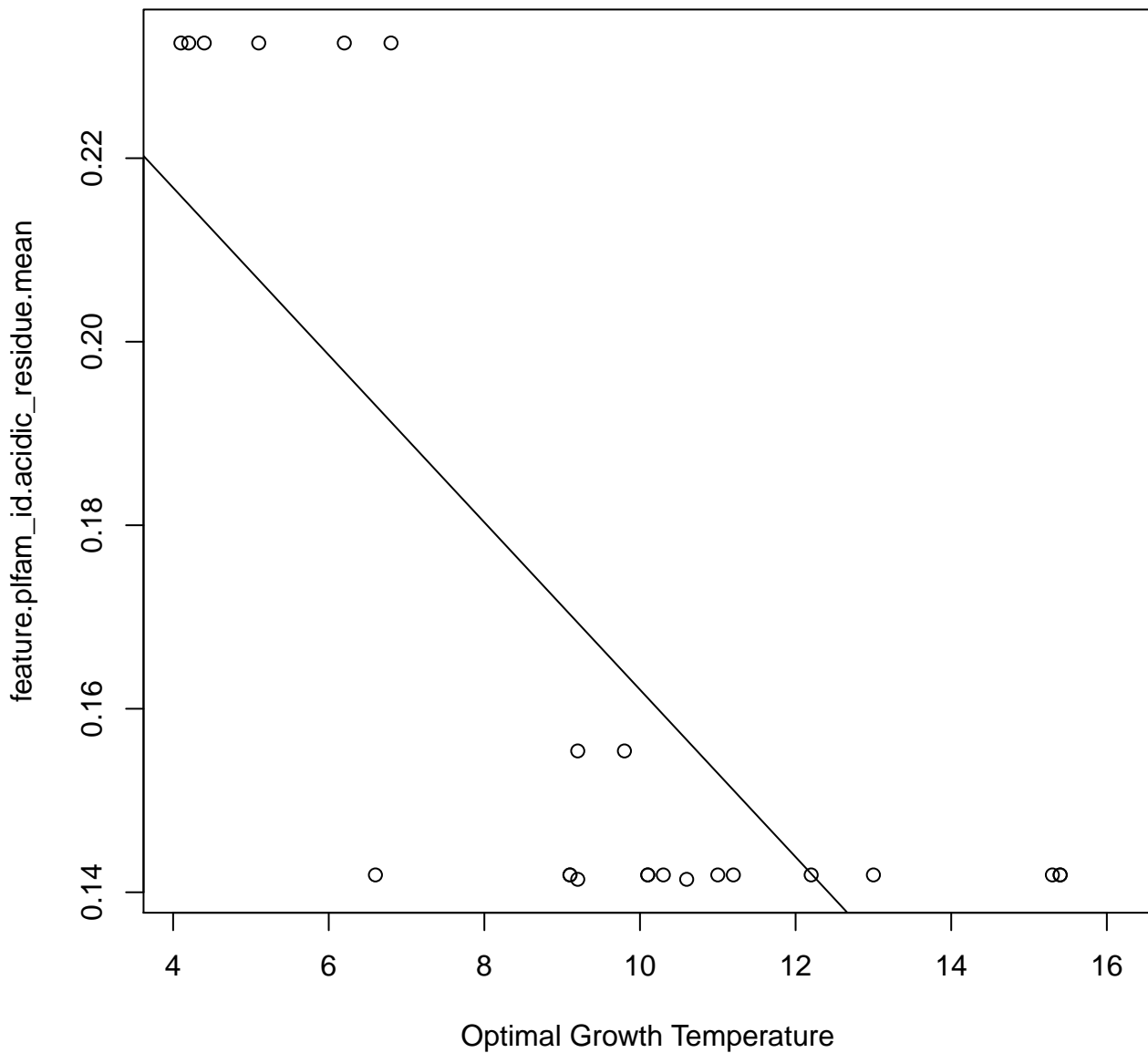
feature.plfam_id.acidic_residue.mean
PLF_28228_00007395
Argininosuccinate lyase (EC 4.3.2.1) / N-acetylglutamate synthase (EC 2.3.1.1)



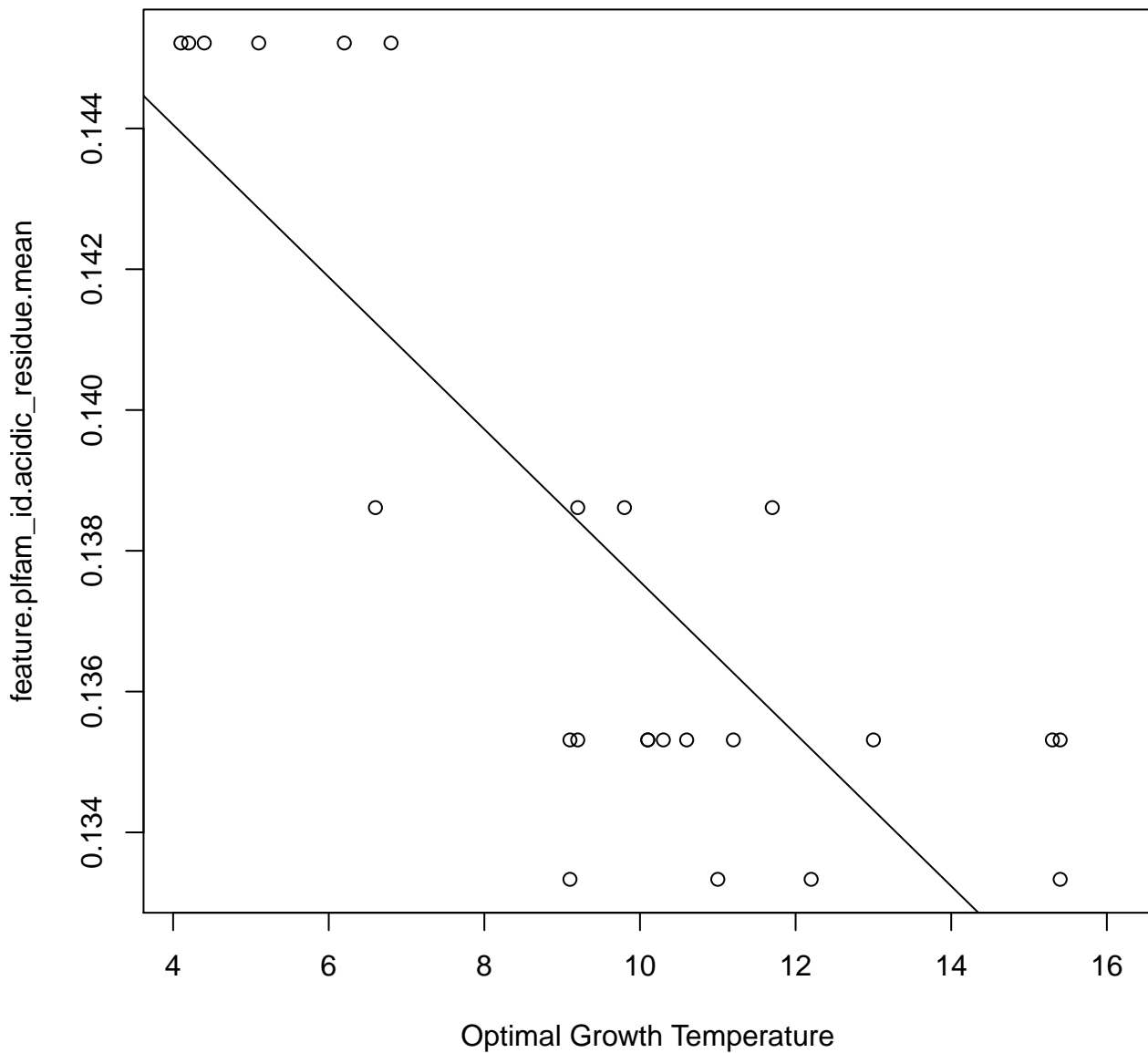
feature.plfam_id.acidic_residue.mean
PLF_28228_00011660
Agmatinase (EC 3.5.3.11)



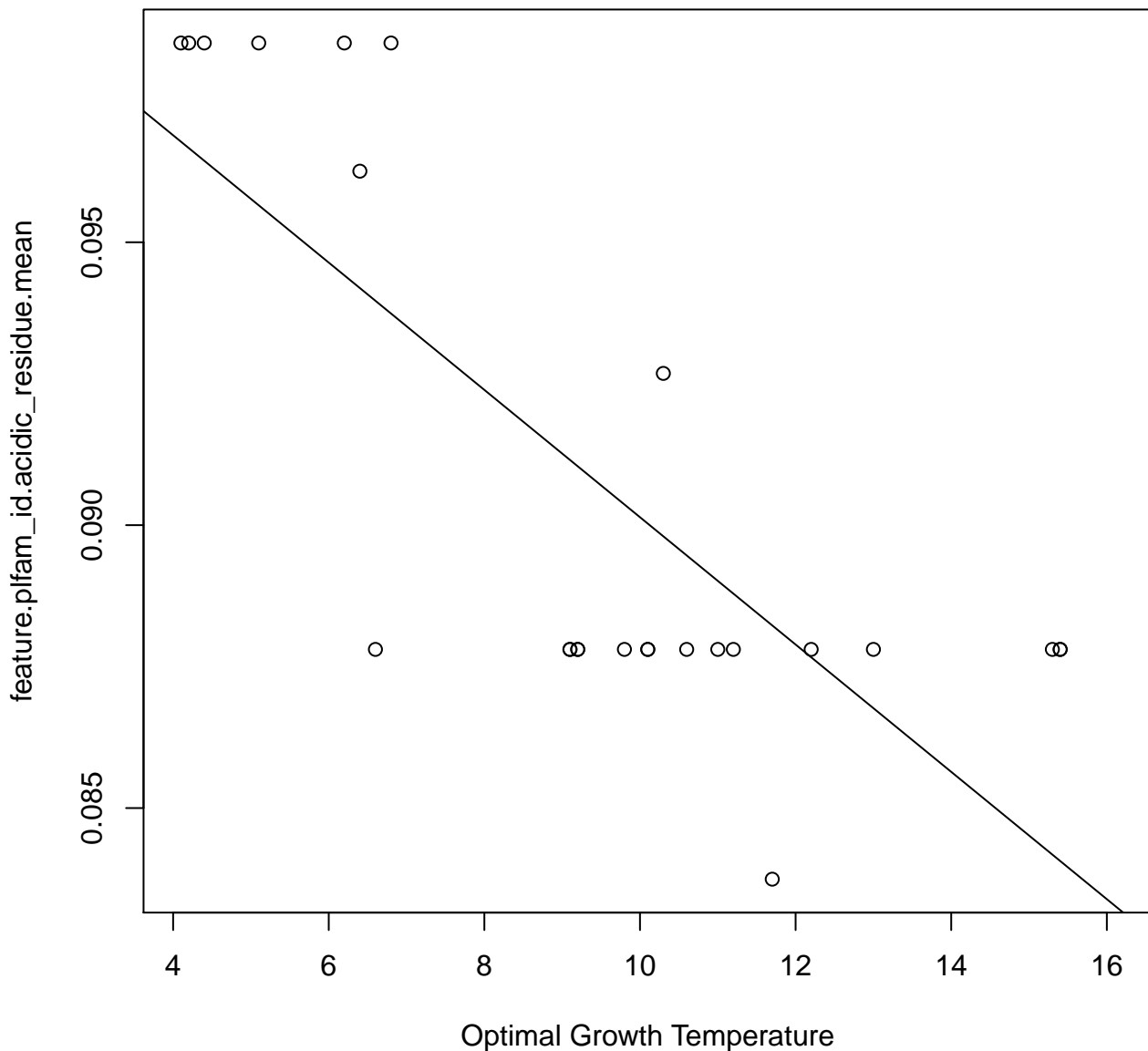
feature.plfam_id.acidic_residue.mean
PLF_28228_00014070
hypothetical protein



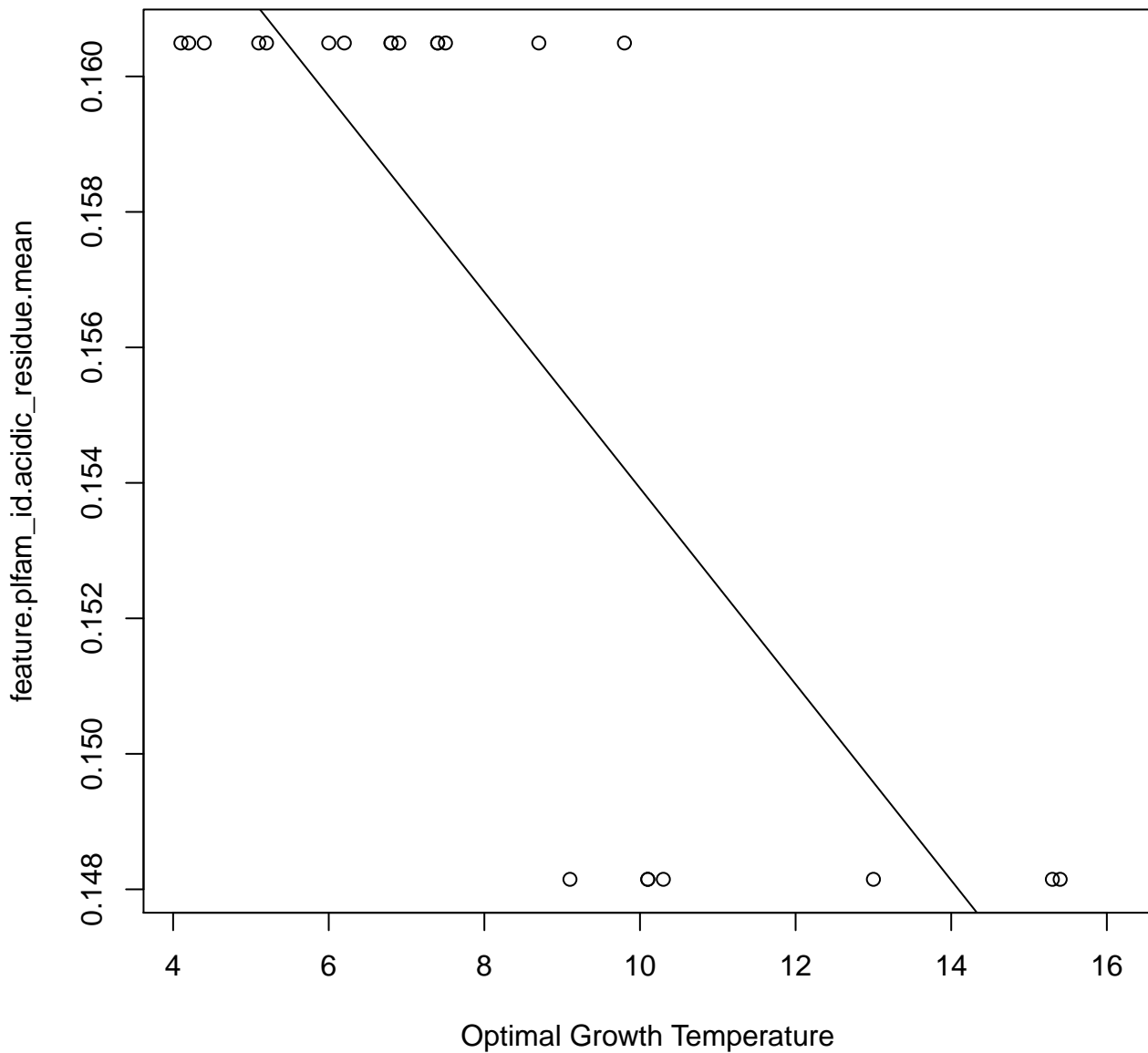
feature.plfam_id.acidic_residue.mean
PLF_28228_00014238
hypothetical protein



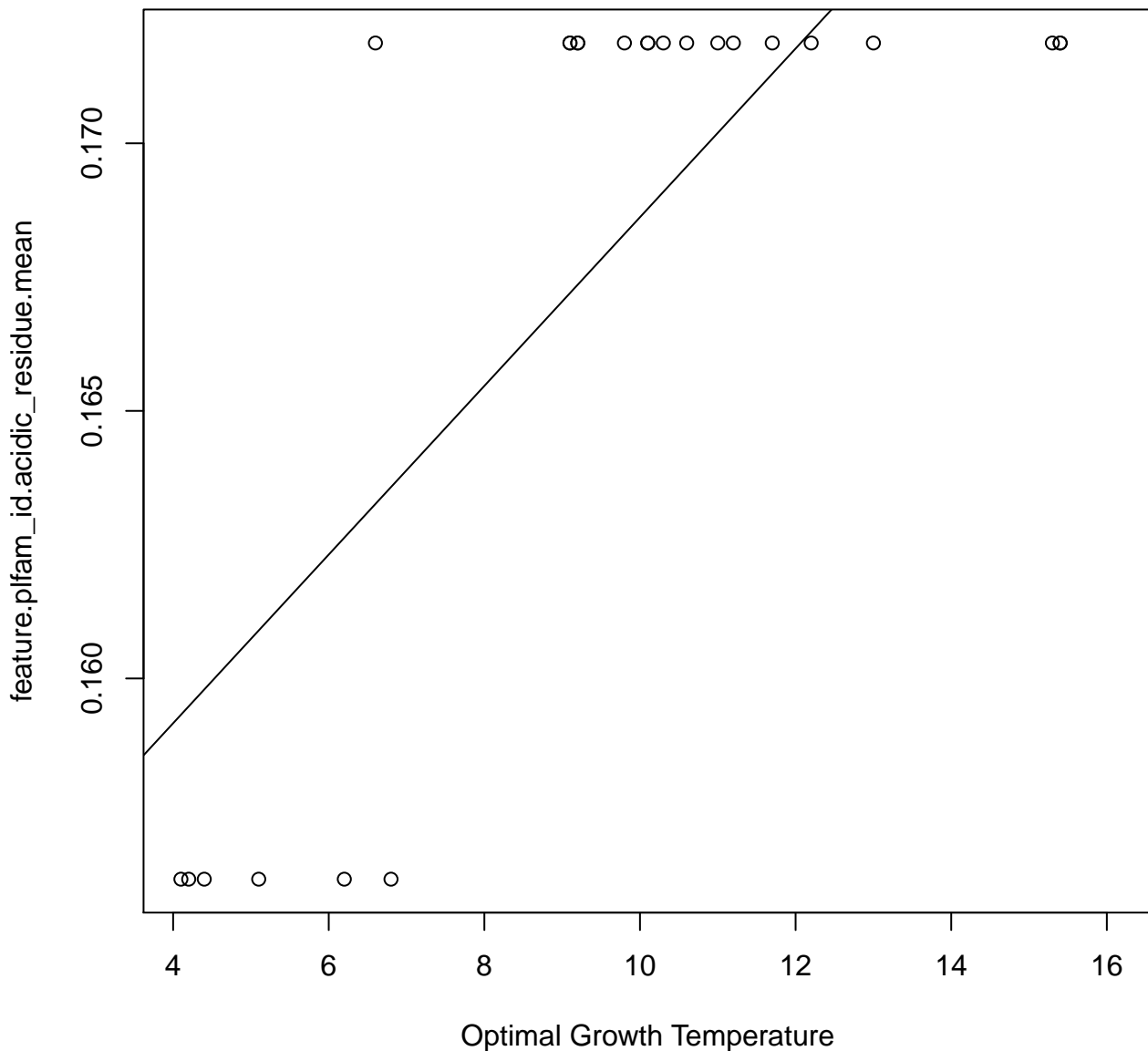
feature.plfam_id.acidic_residue.mean
PLF_28228_00015281
hypothetical protein



feature.plfam_id.acidic_residue.mean
PLF_28228_00016087
hypothetical protein



feature.plfam_id.acidic_residue.mean
PLF_28228_00016786
hypothetical protein

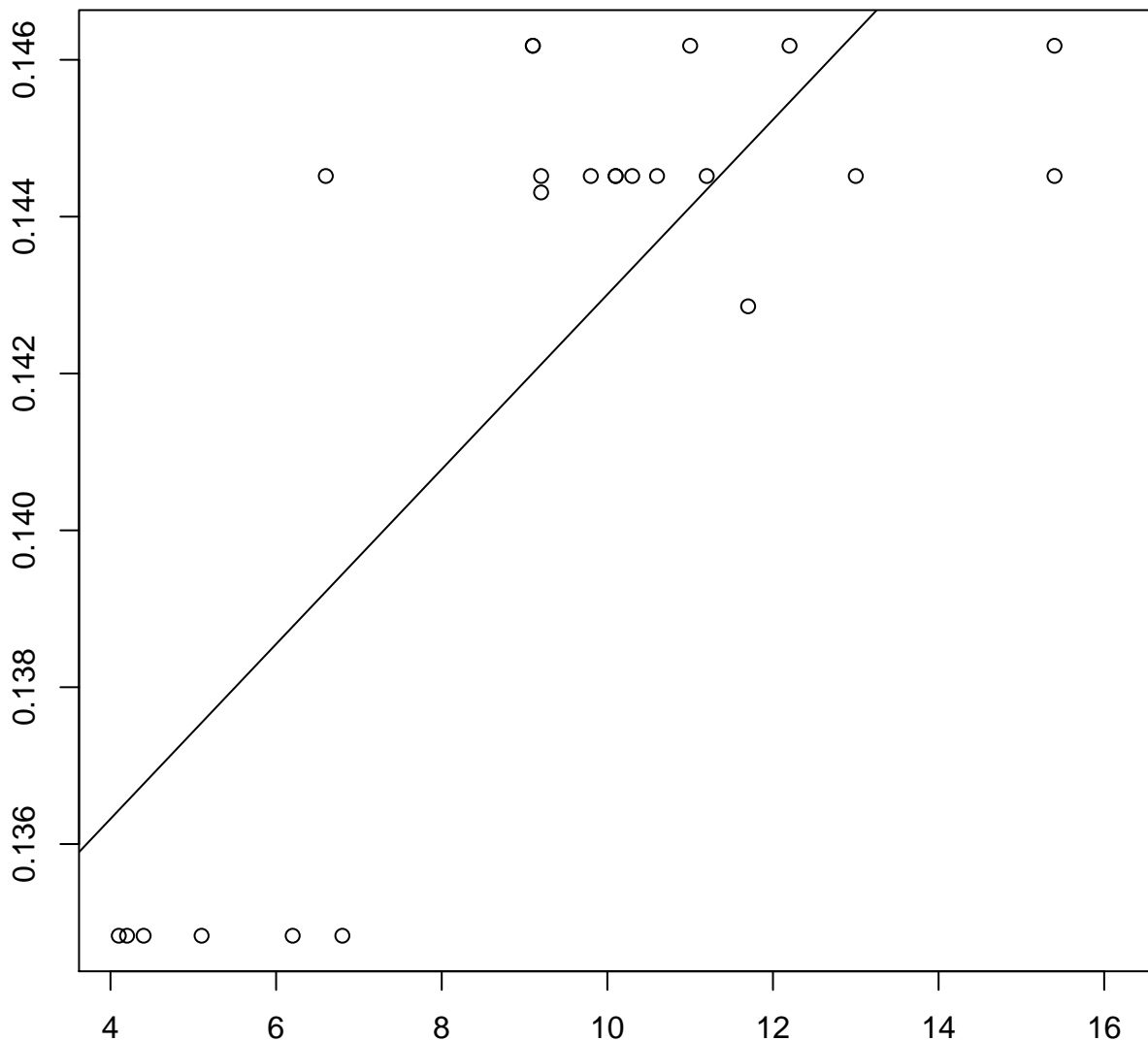


feature.plfam_id.acidic_residue.mean

PLF_28228_00017455

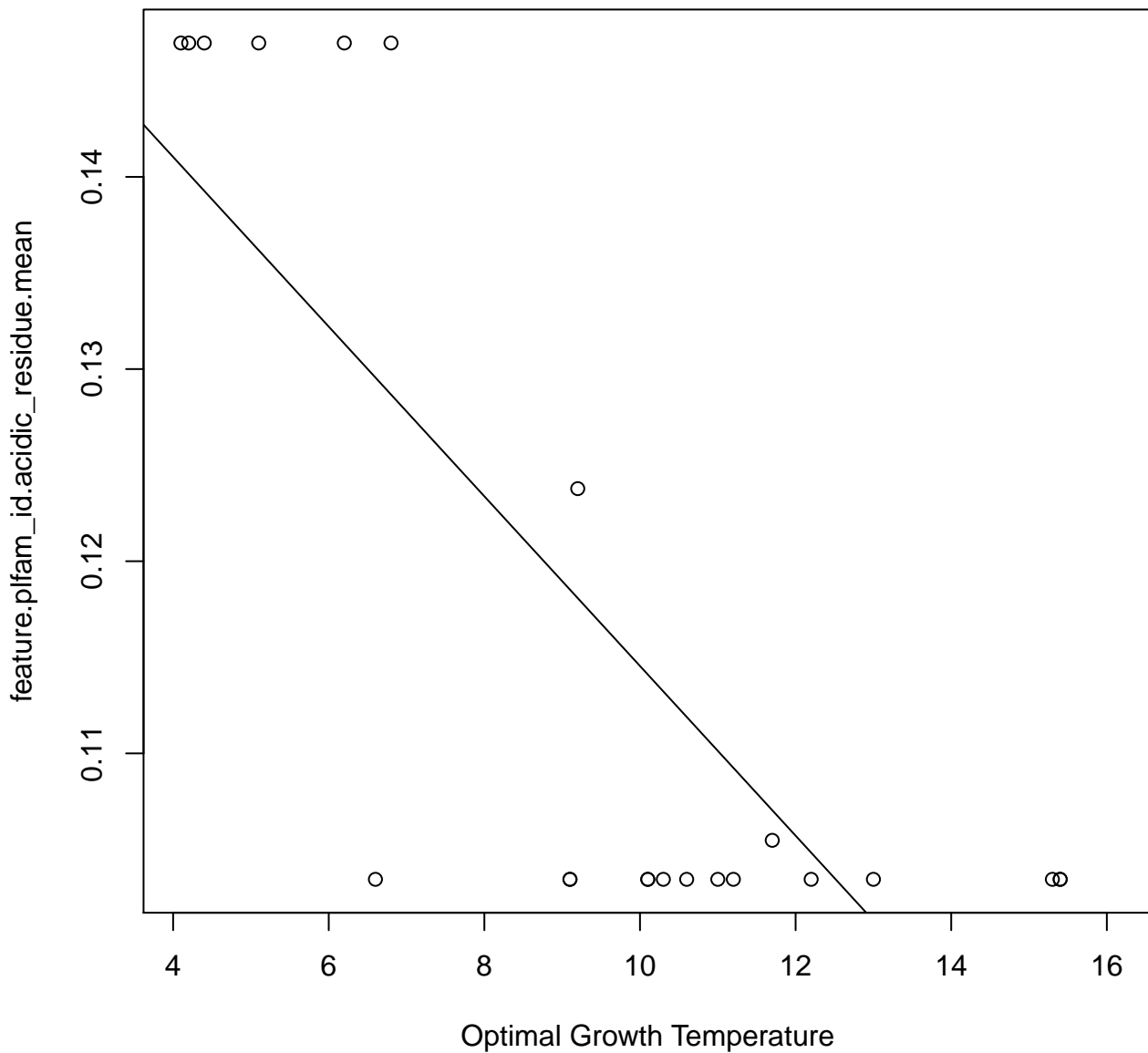
Maltodextrin glucosidase (EC 3.2.1.20)

feature.plfam_id.acidic_residue.mean

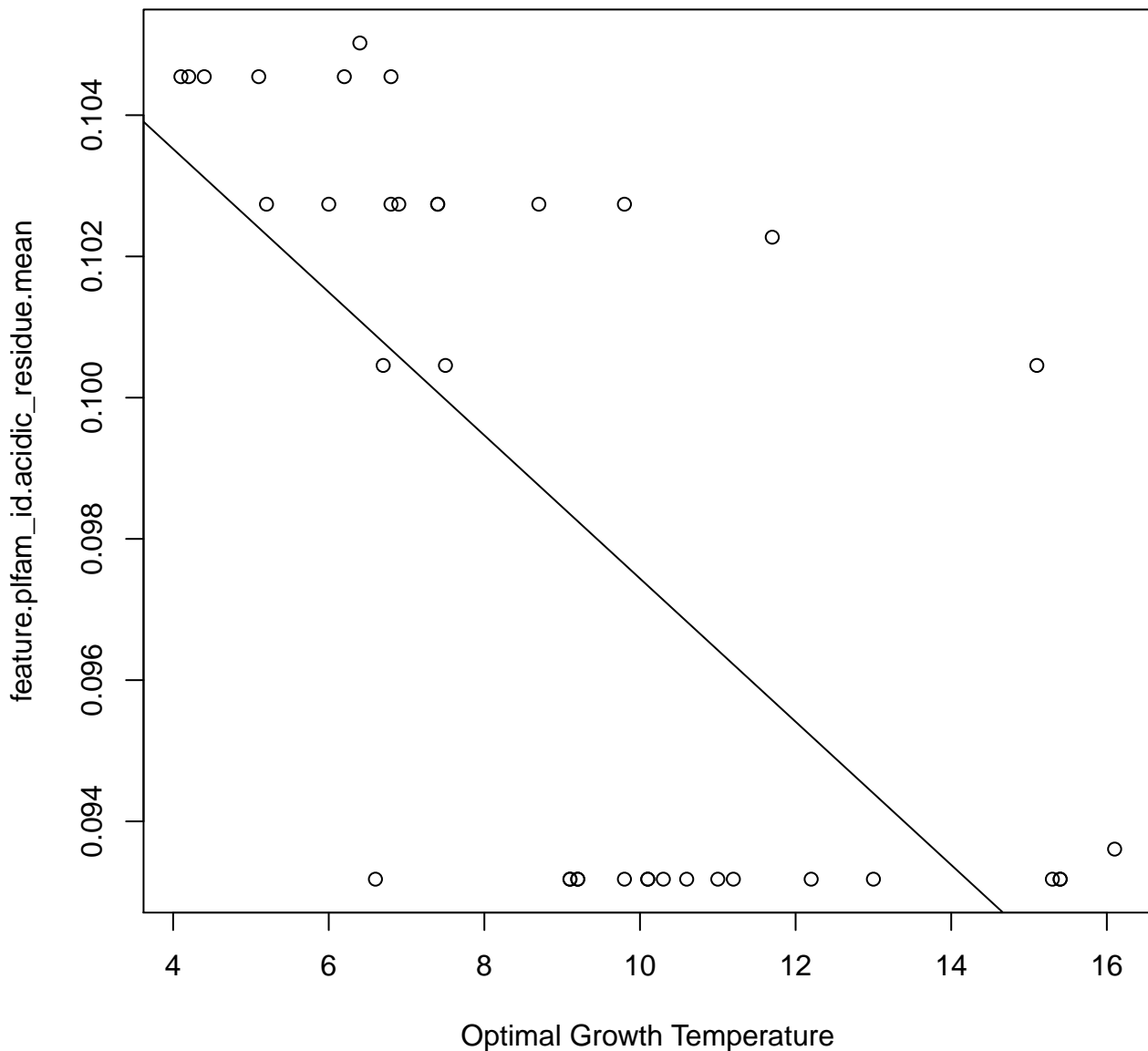


Optimal Growth Temperature

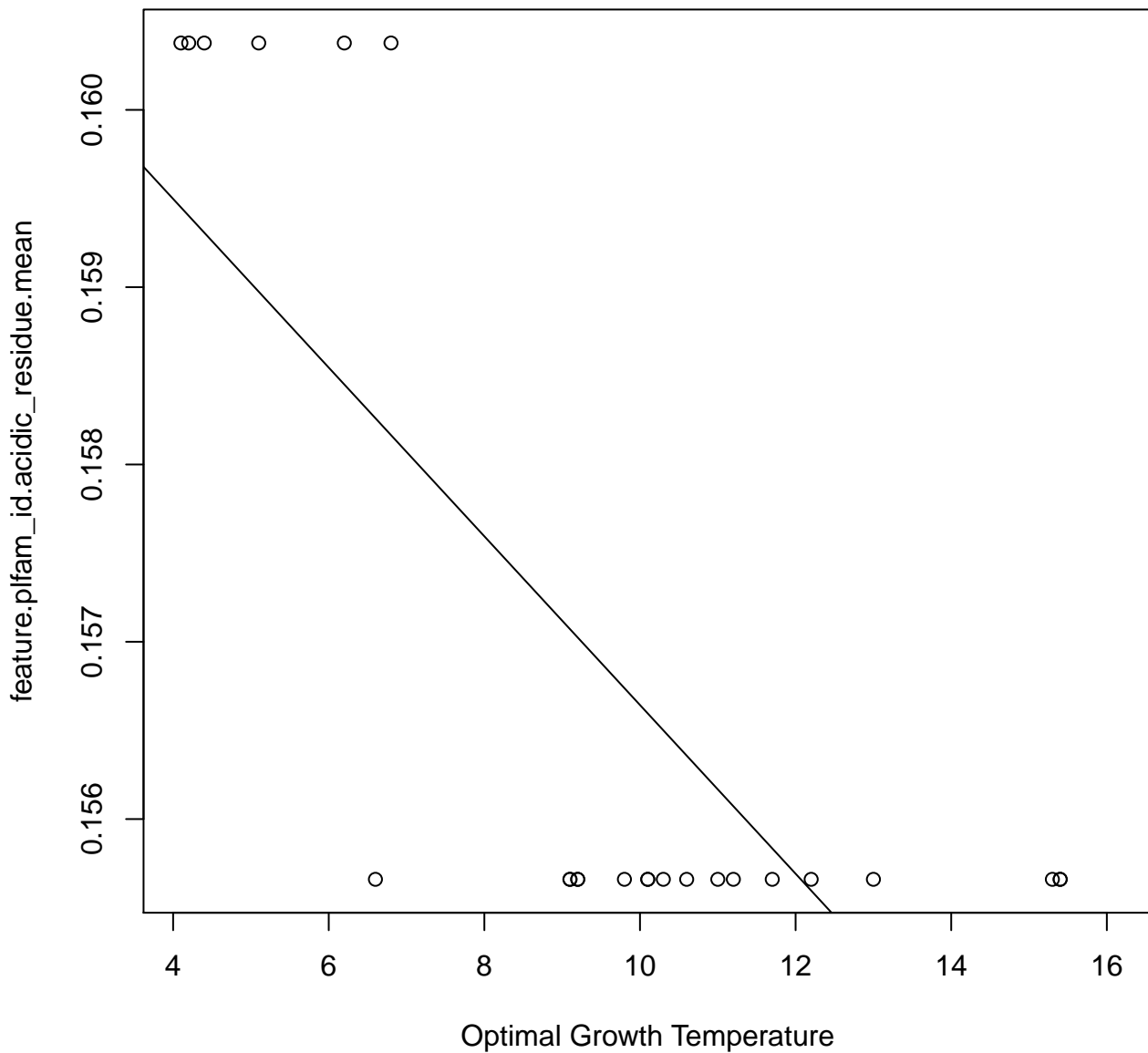
feature.plfam_id.acidic_residue.mean
PLF_28228_00022096
Two-component system sensor histidine kinase



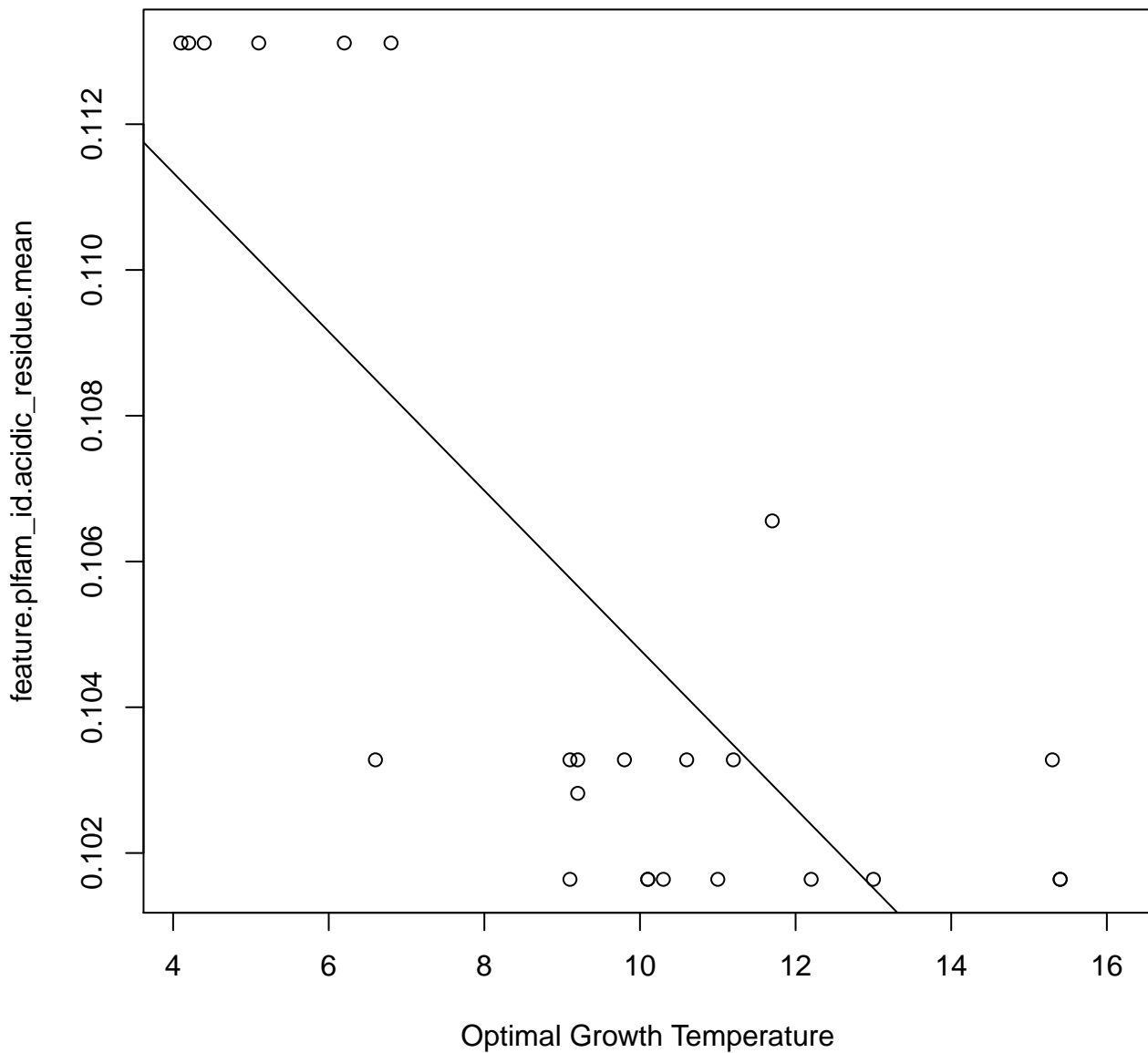
feature.plfam_id.acidic_residue.mean
PLF_28228_00028163
23S rRNA (uracil(1939)-C(5))-methyltransferase (EC 2.1.1.190)



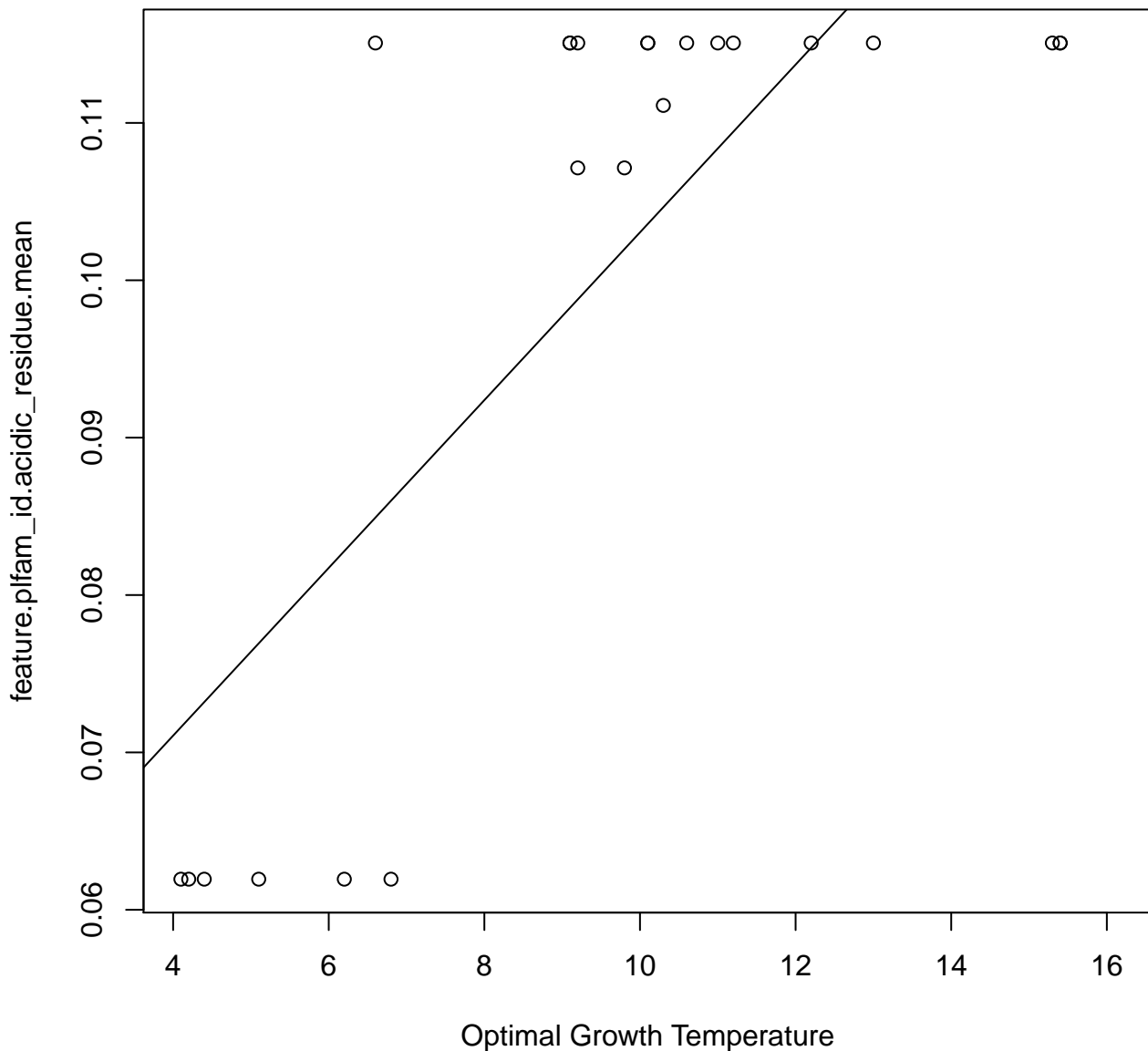
feature.plfam_id.acidic_residue.mean
PLF_28228_00028513
hypothetical protein



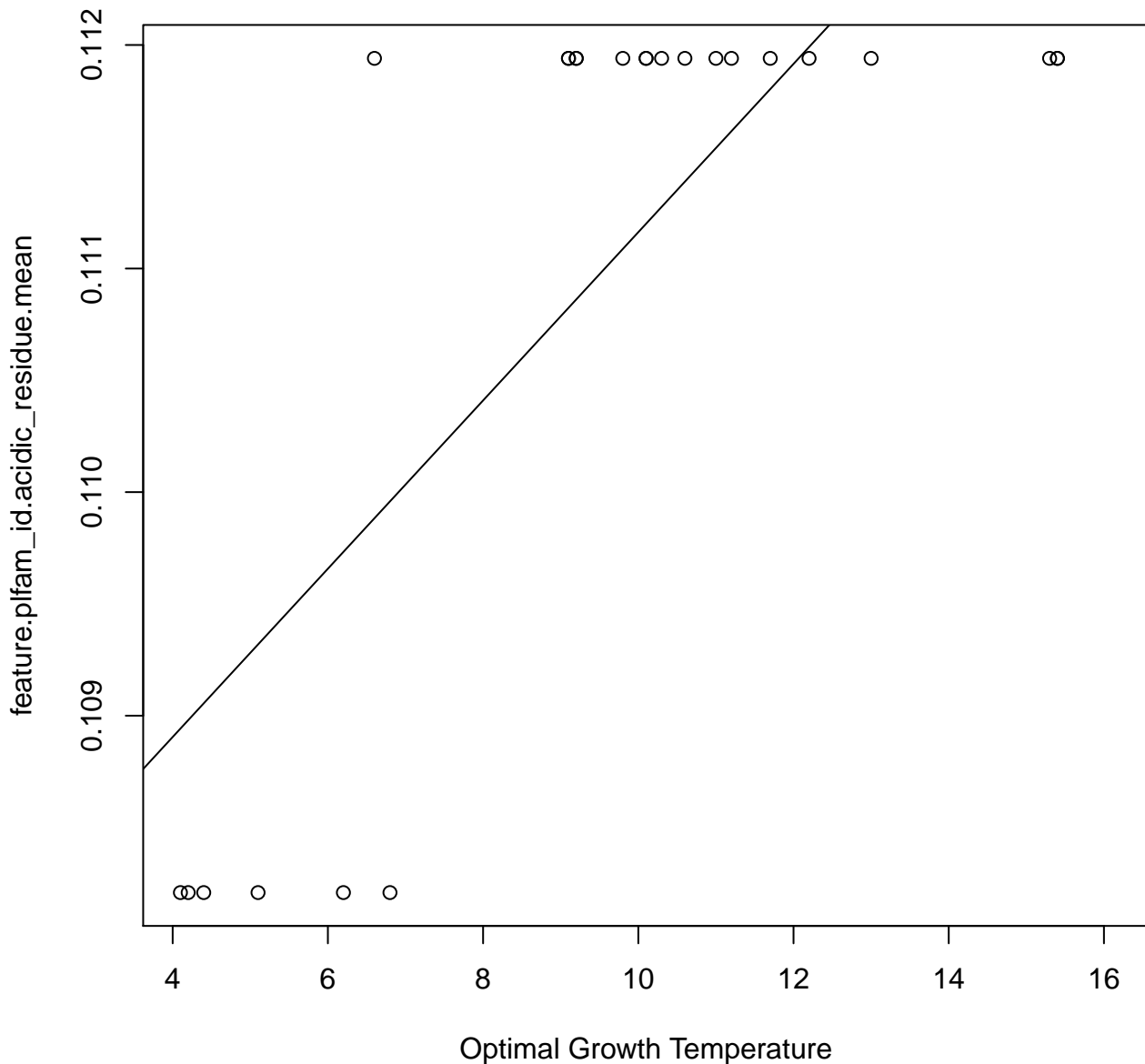
feature.plfam_id.acidic_residue.mean
PLF_28228_00028646
hypothetical protein



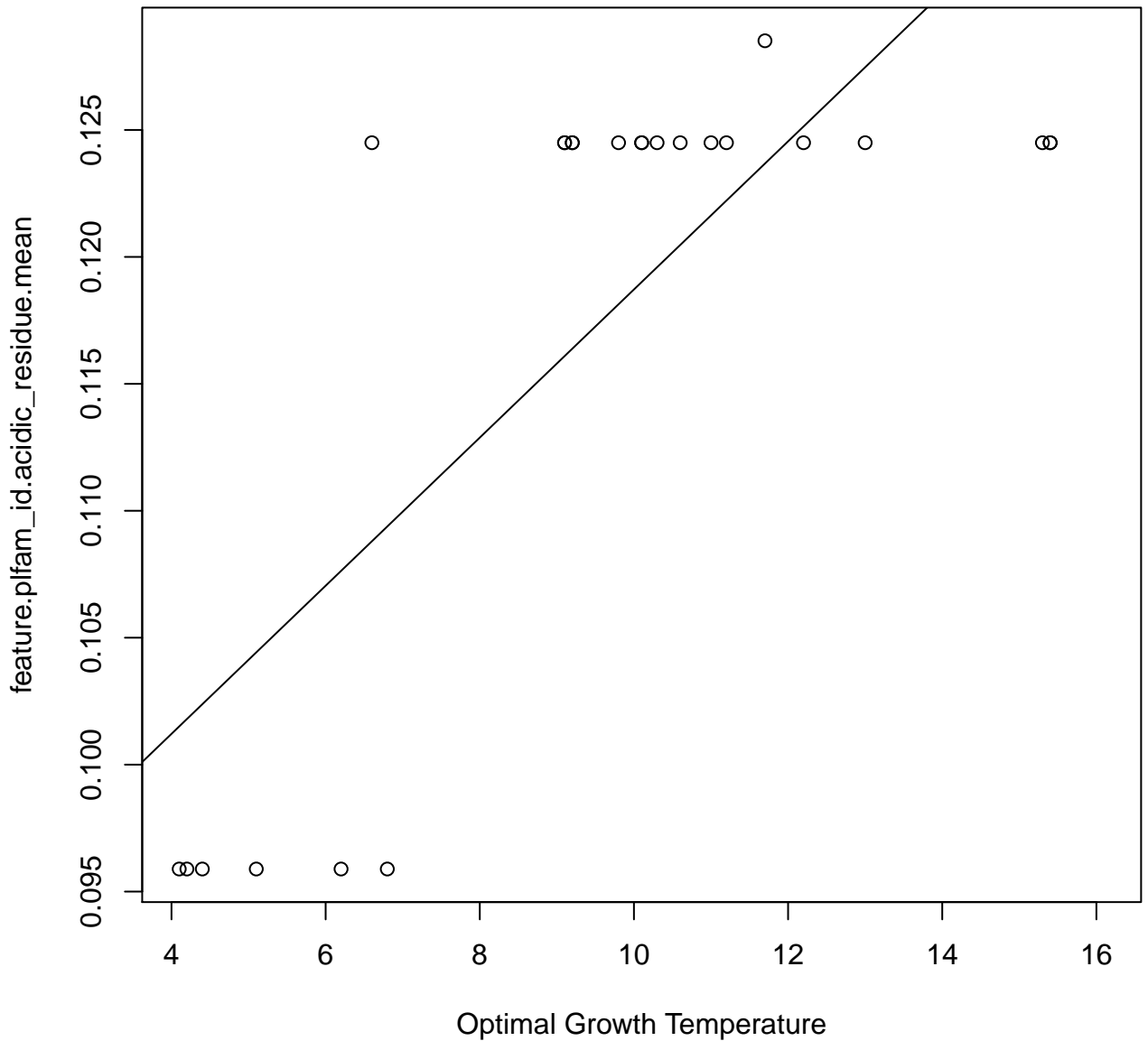
feature.plfam_id.acidic_residue.mean
PLF_28228_00030076
hypothetical protein



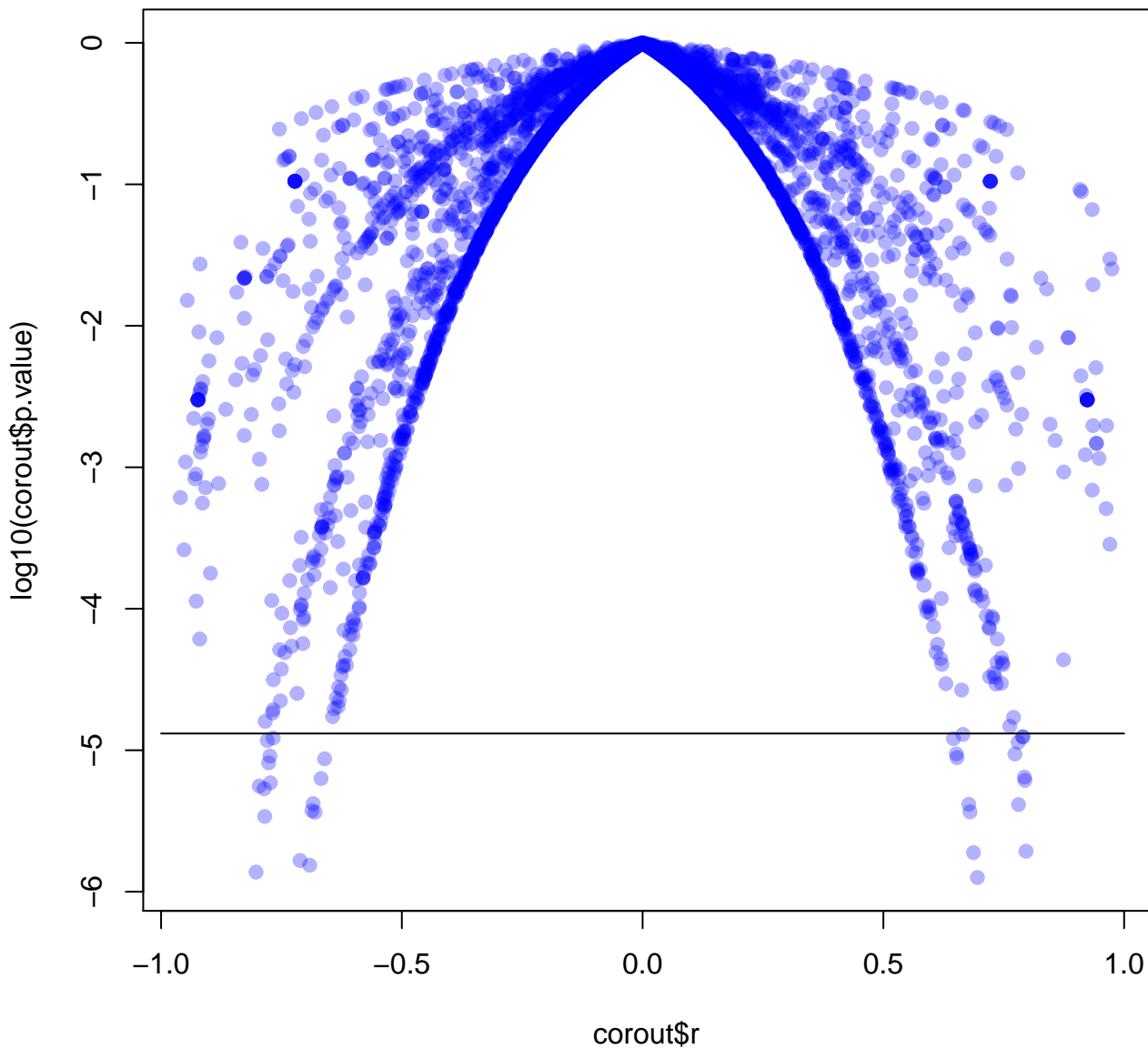
feature.plfam_id.acidic_residue.mean
PLF_28228_00030655
hypothetical protein



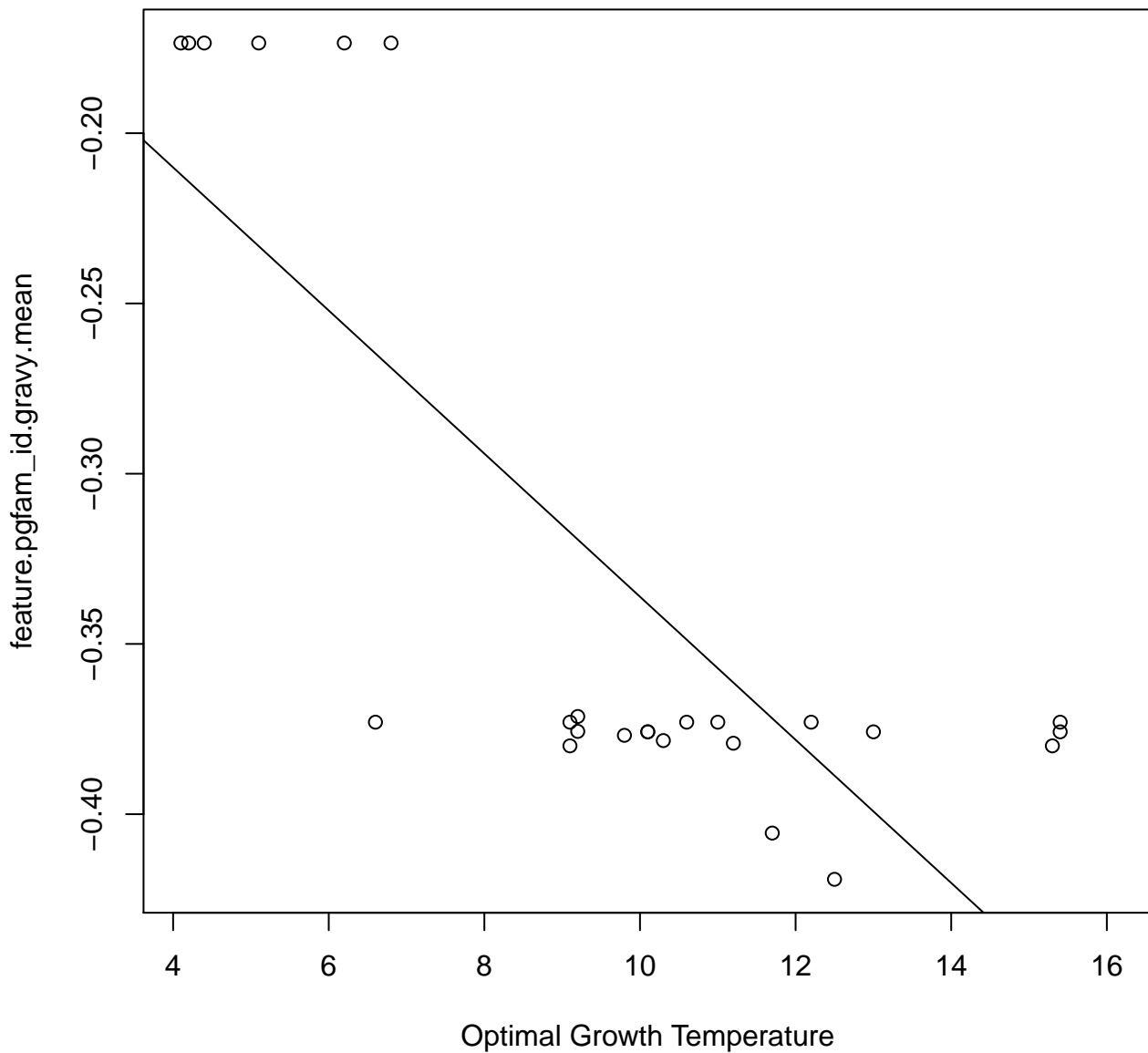
feature.plfam_id.acidic_residue.mean
PLF_28228_00031426
hypothetical protein



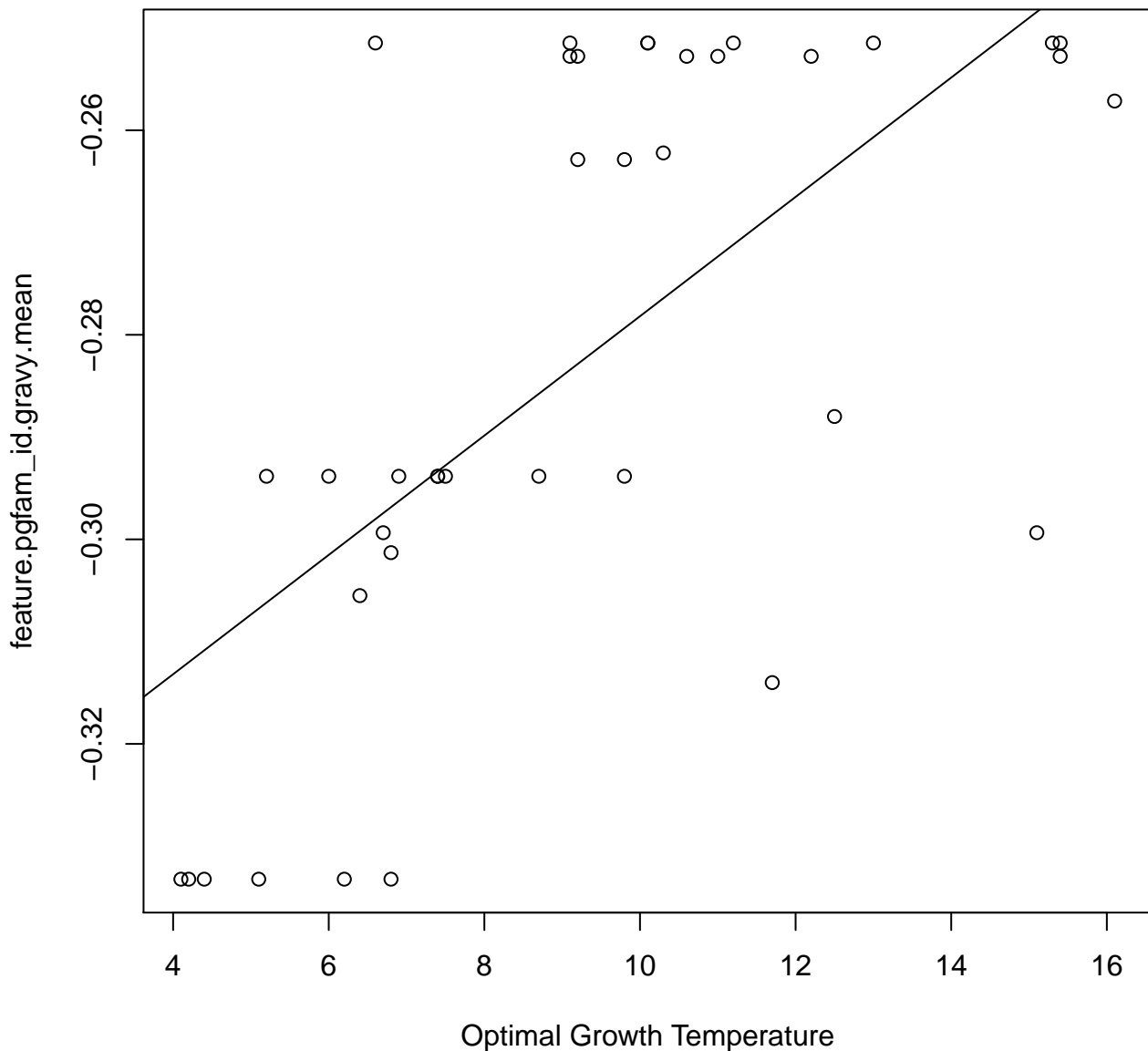
feature.pgfam_id.gravy.mean



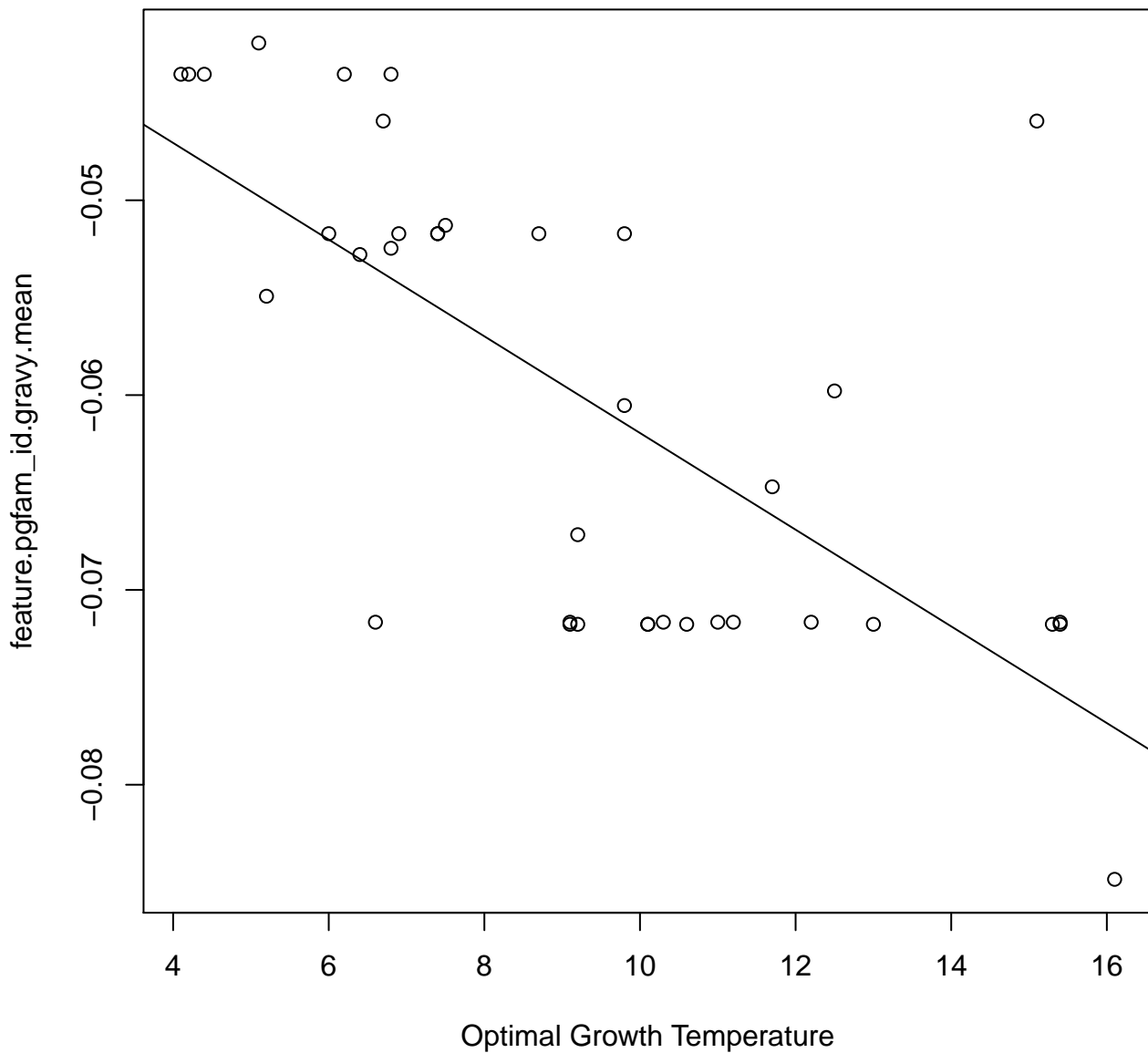
feature.pgfam_id.gravy.mean
PGF_00004056
Fatty acid cis/trans isomerase



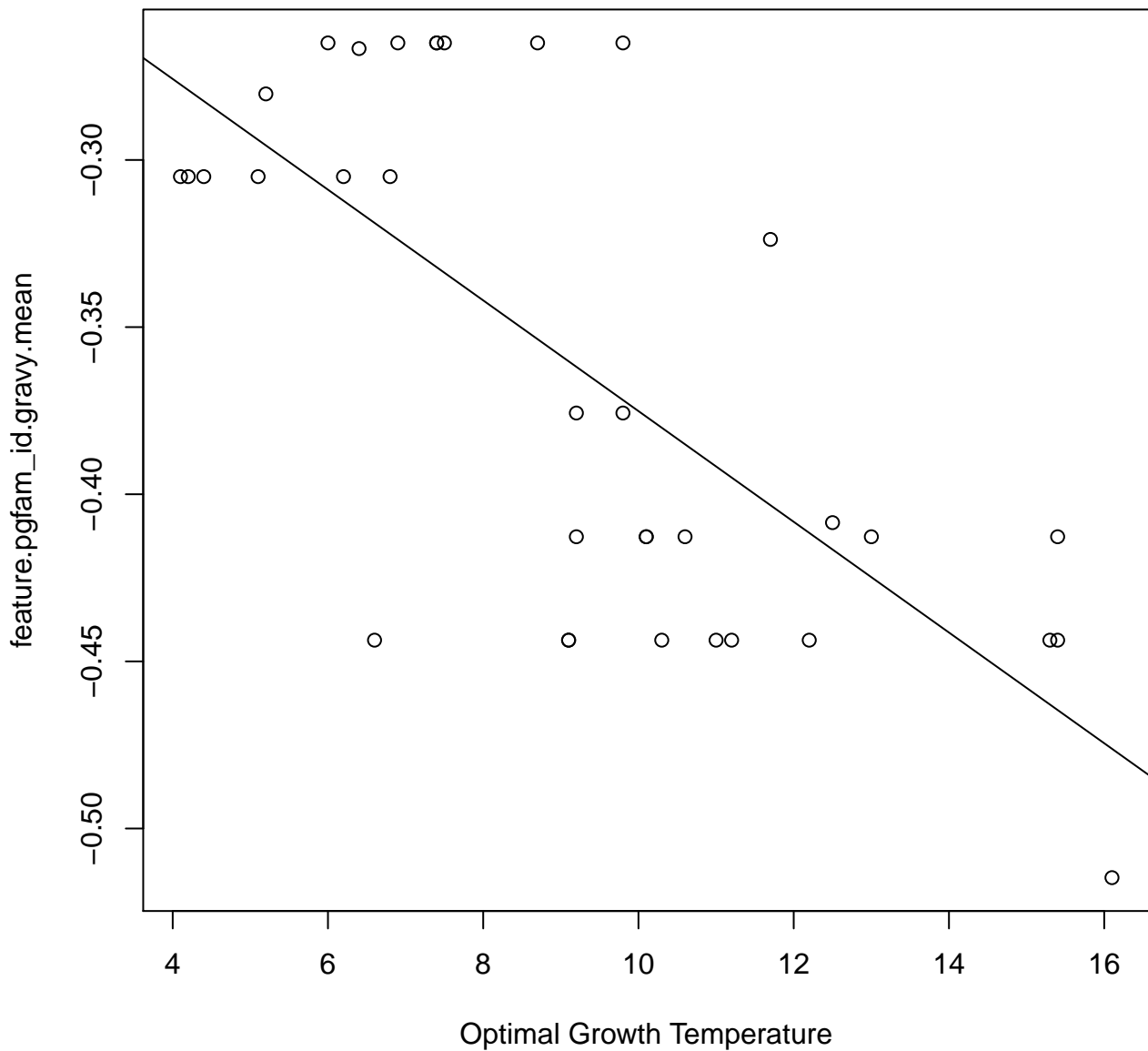
feature.pgfam_id.gravy.mean
PGF_00006983
GTP cyclohydrolase I (EC 3.5.4.16) type 2



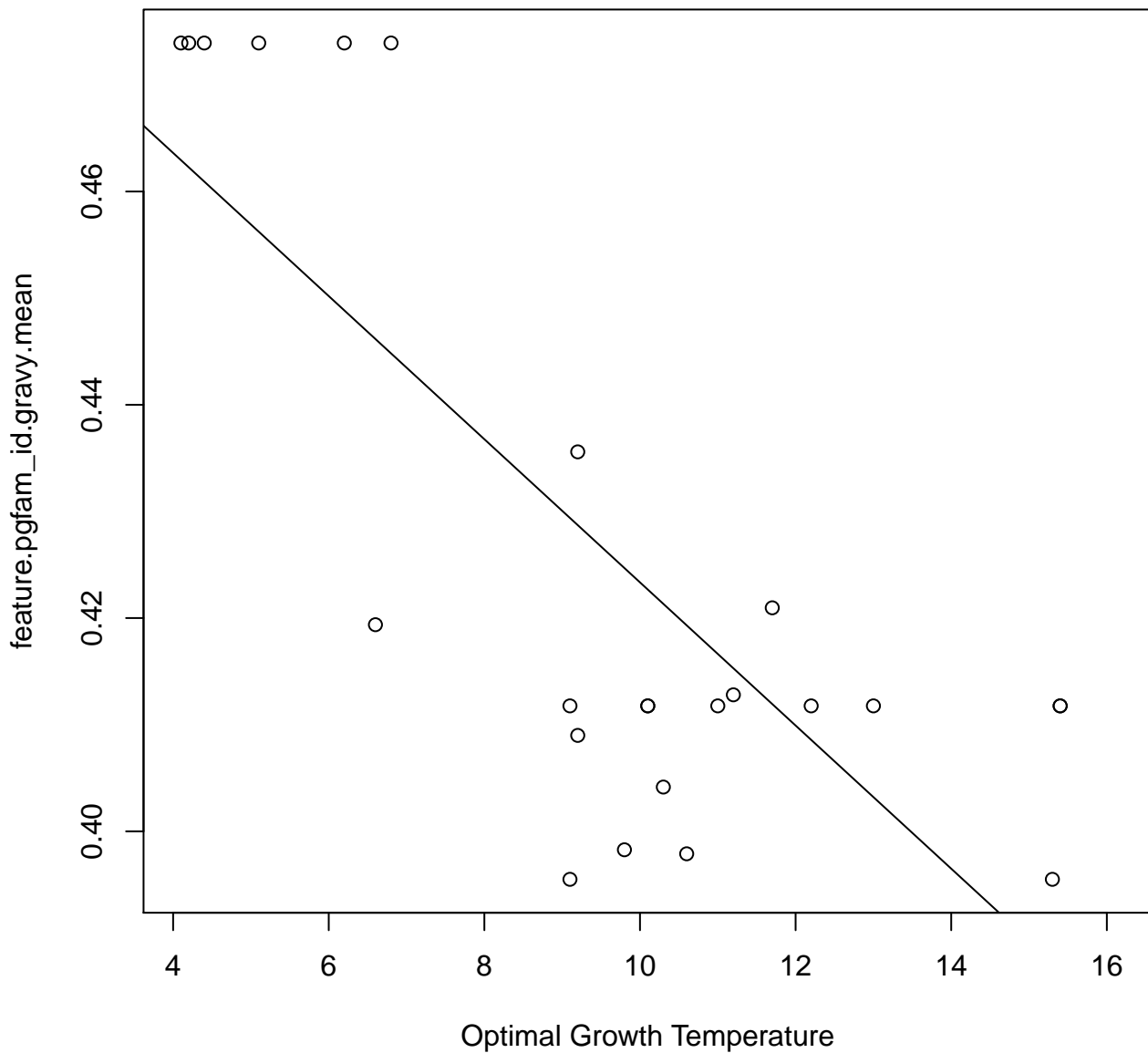
feature.pgfam_id.gravy.mean
PGF_00029286
Aconitate hydratase 2 (EC 4.2.1.3)



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



feature.pgfam_id.gravy.mean
PGF_00048099
Response regulator receiver protein

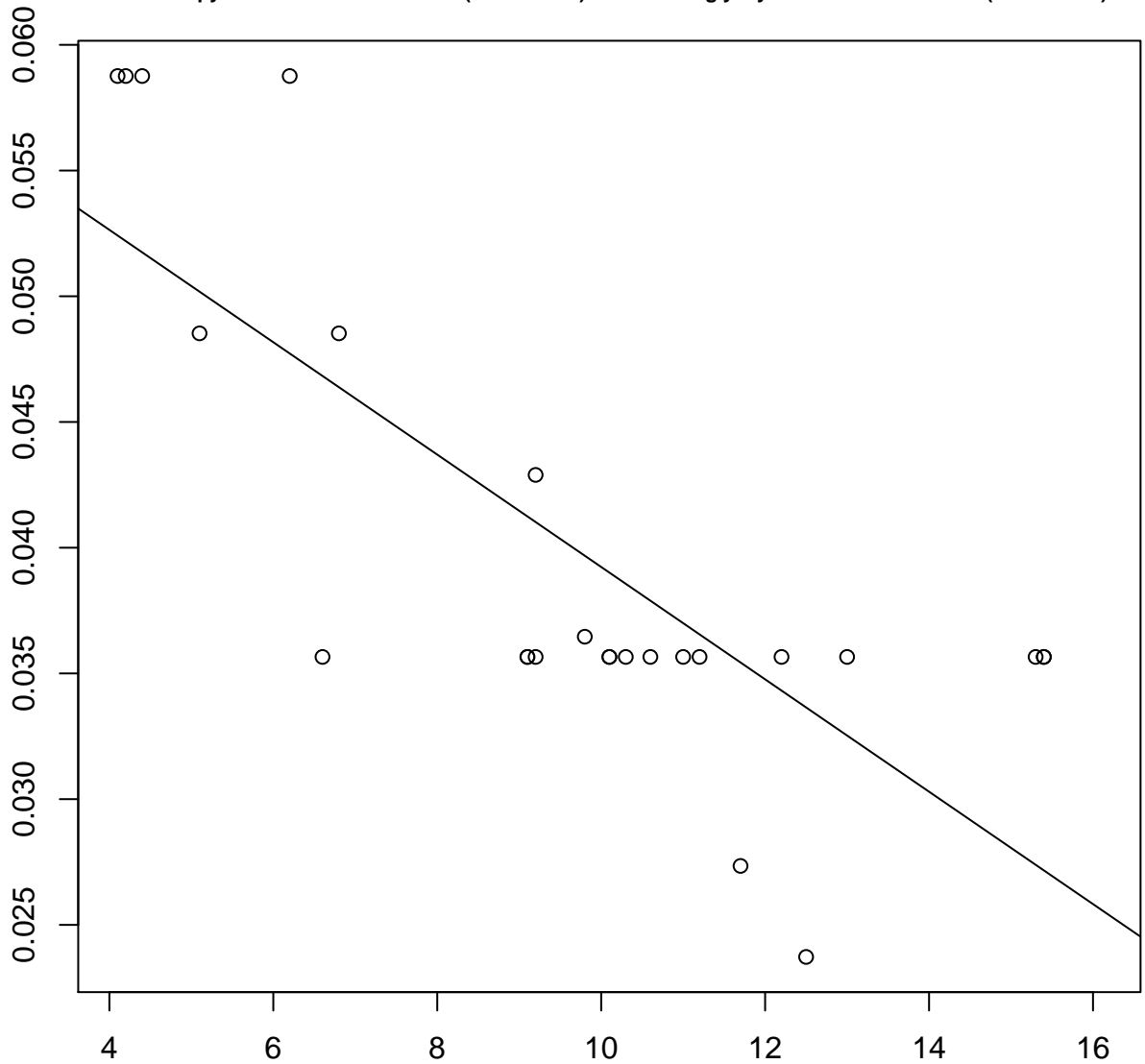


feature.pgfam_id.gravy.mean

PGF_00051334

Serine--pyruvate aminotransferase (EC 2.6.1.51) / L-alanine:glyoxylate aminotransferase (EC 2.6.1.44)

feature.pgfam_id.gravy.mean

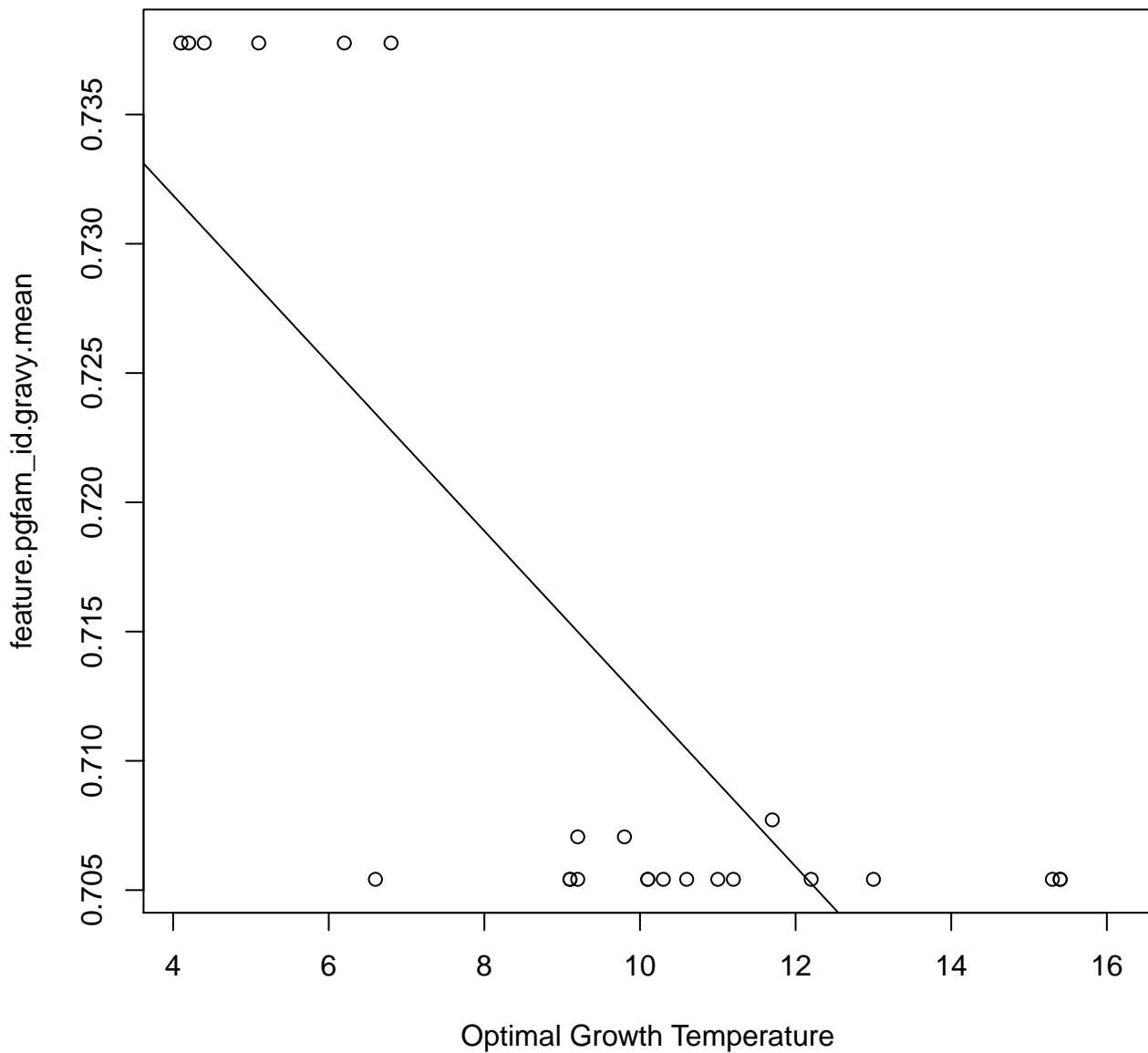


Optimal Growth Temperature

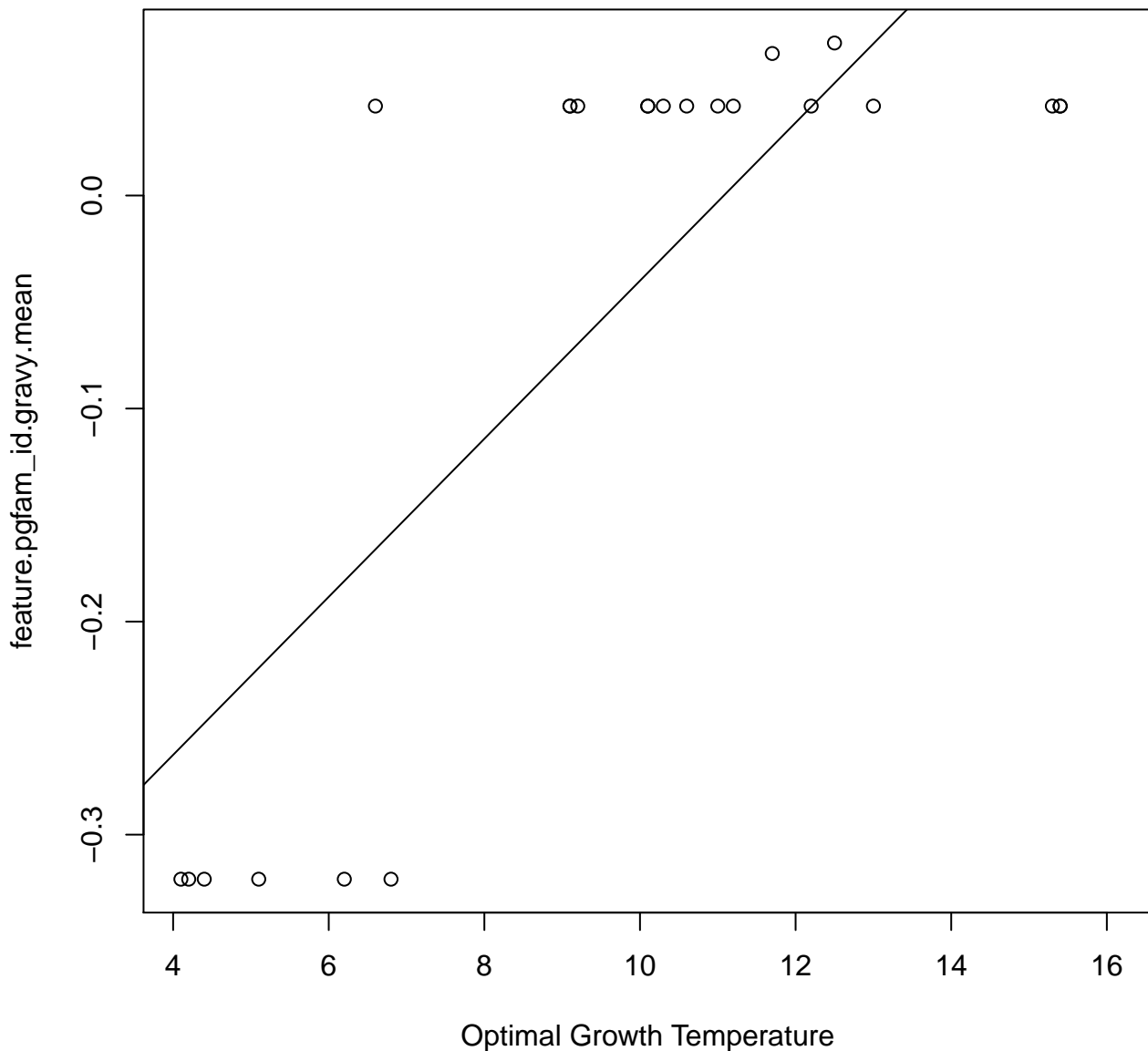
feature.pgfam_id.gravy.mean

PGF_00061953

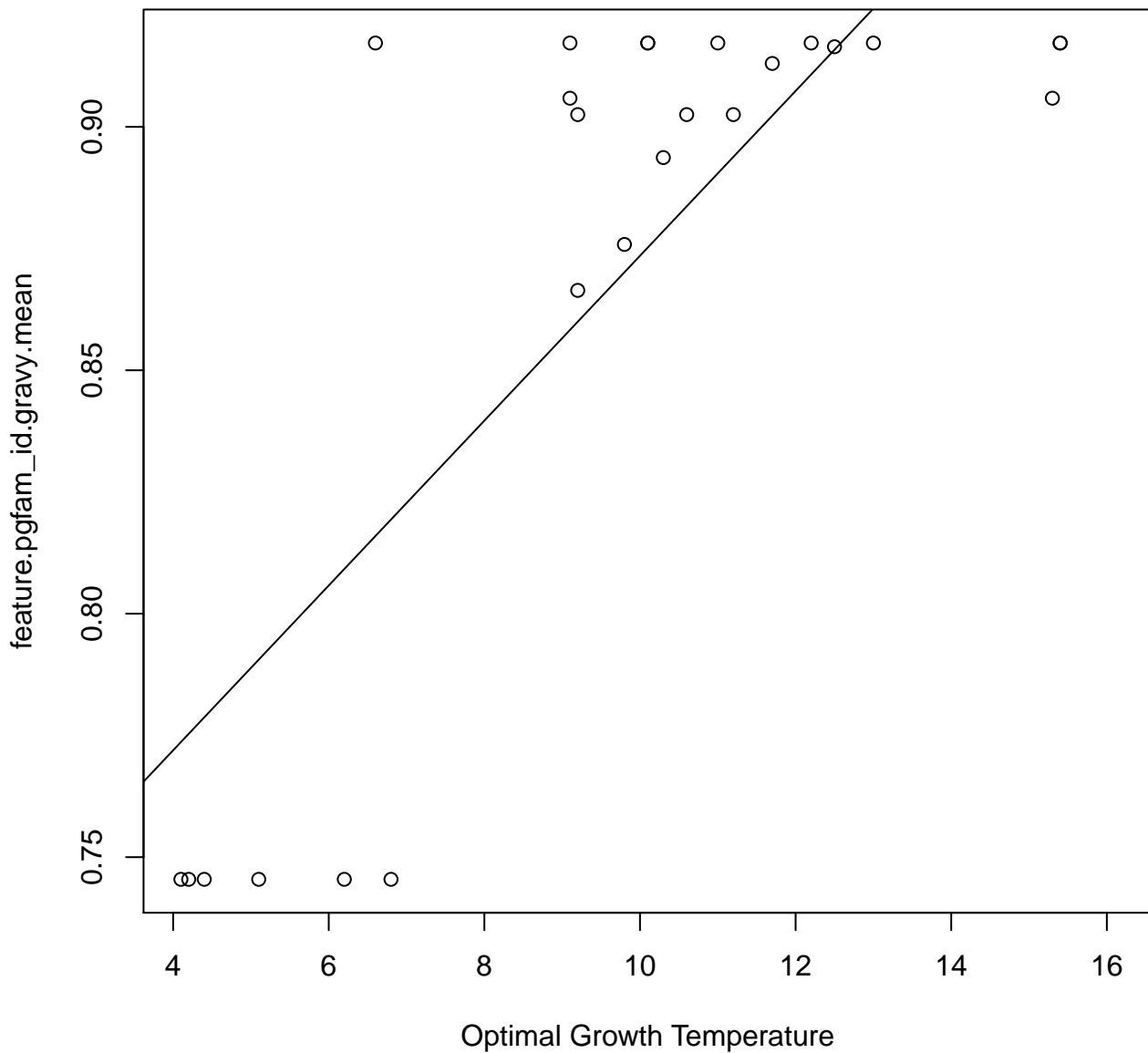
TrkA-C domain protein



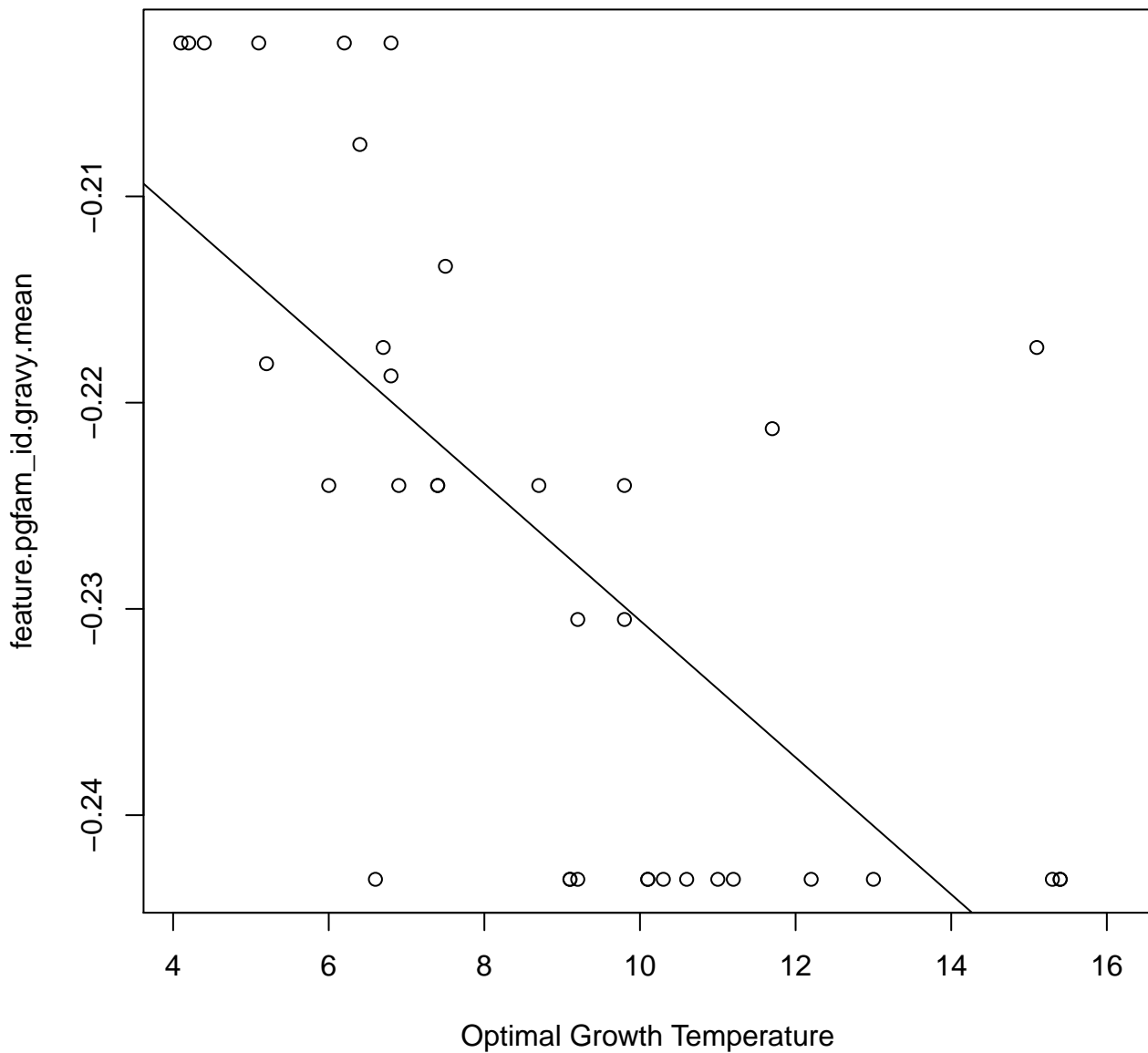
feature.pgfam_id.gravy.mean
PGF_00064685
Uncharacterized ferredoxin-like protein YfhL



feature.pgfam_id.gravy.mean
PGF_00067426
ZIP zinc transporter family protein



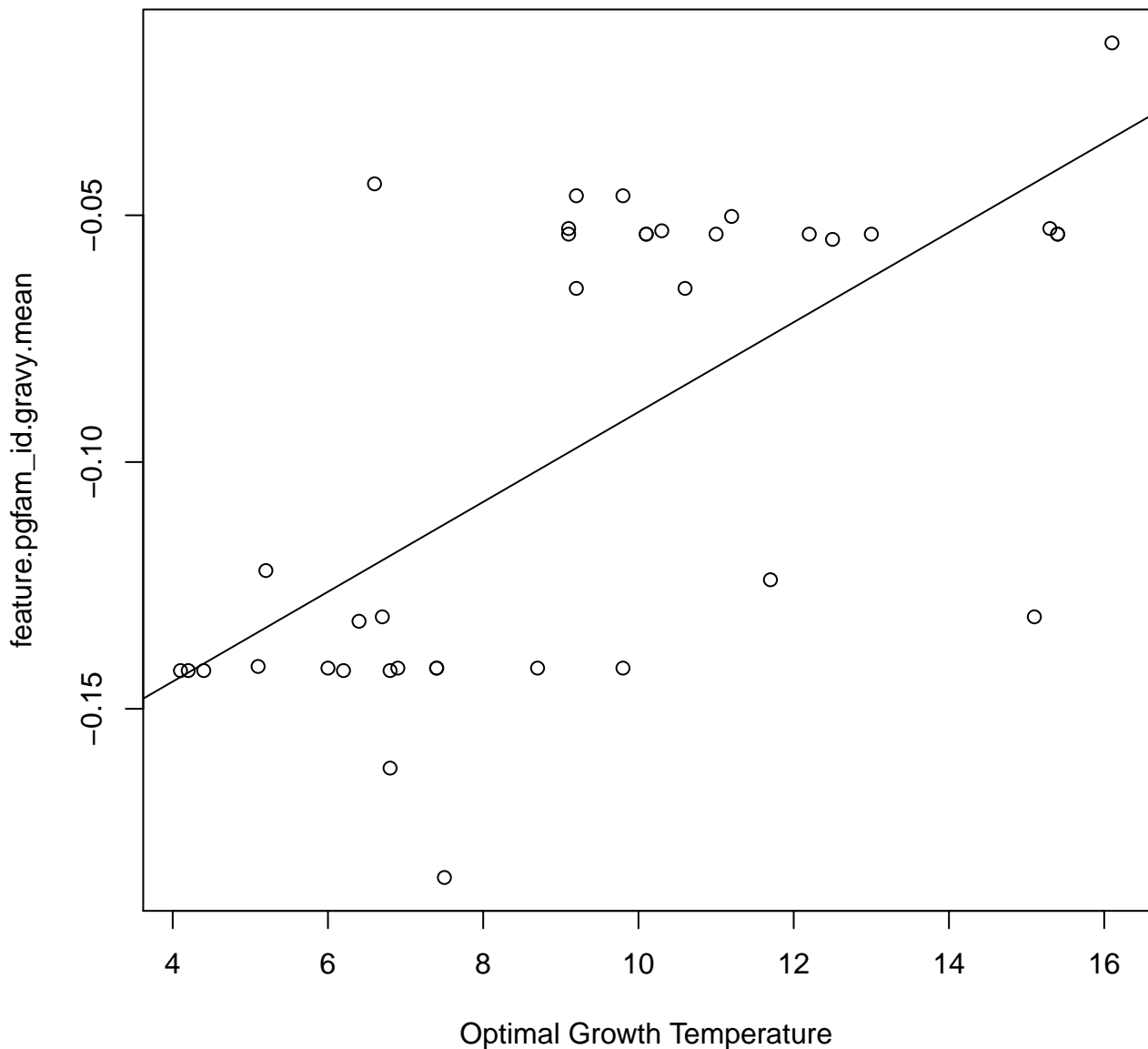
feature.pgfam_id.gravy.mean
PGF_00416513
Carbon-nitrogen hydrolase



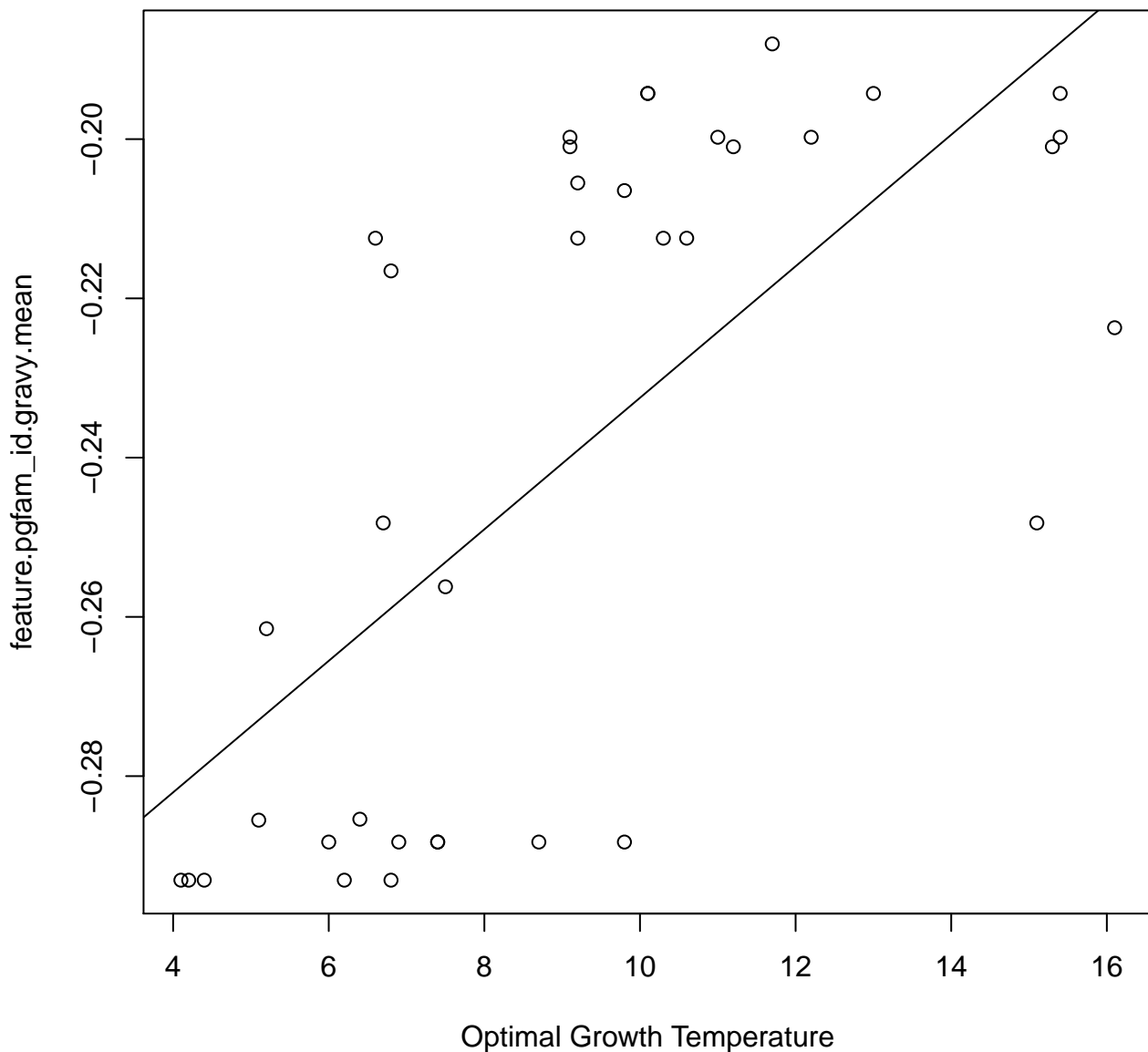
feature.pgfam_id.gravy.mean

PGF_00417755

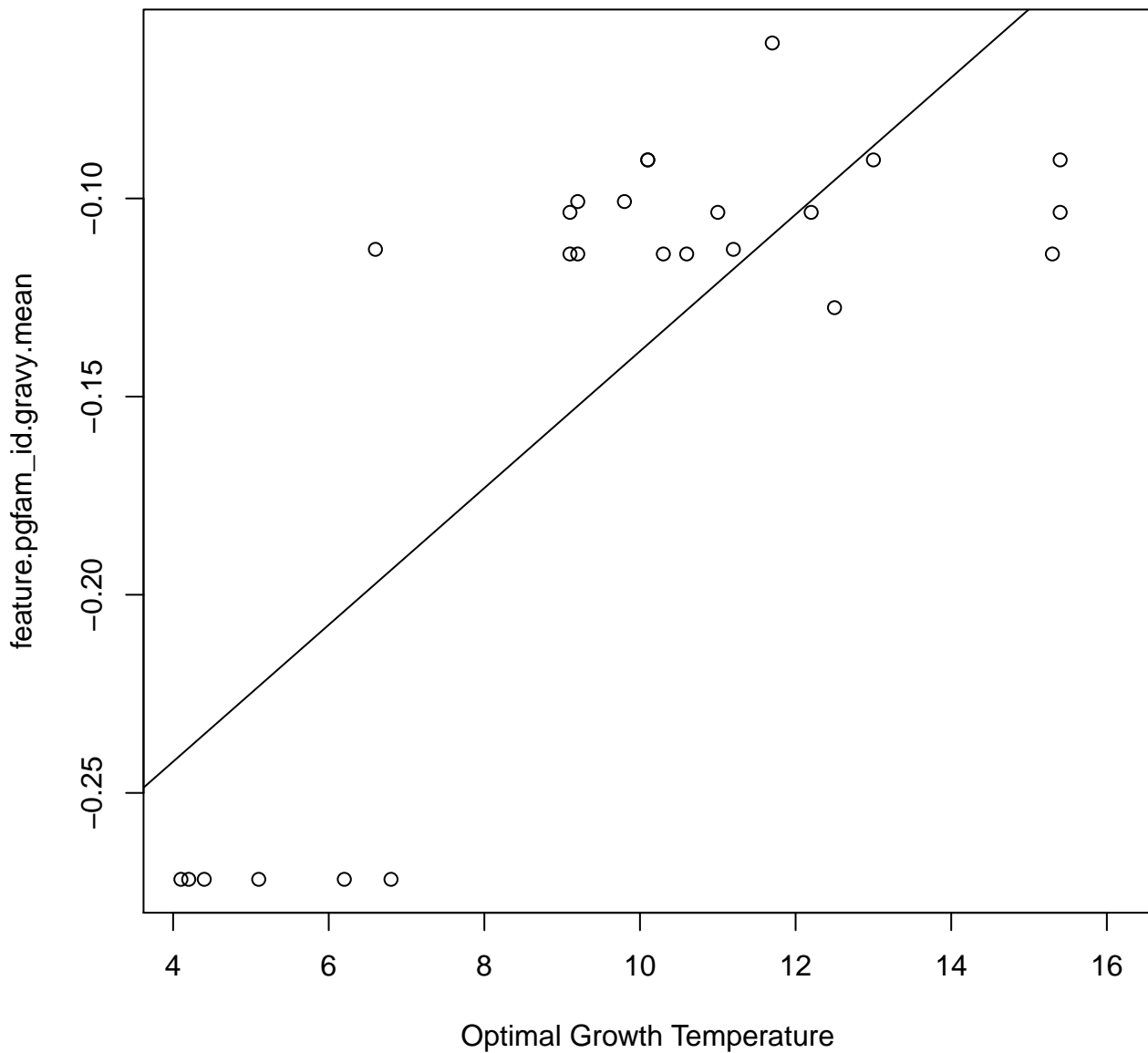
3-demethylubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6-hydroxyphenyl methylase (EC 2.1.1.222)



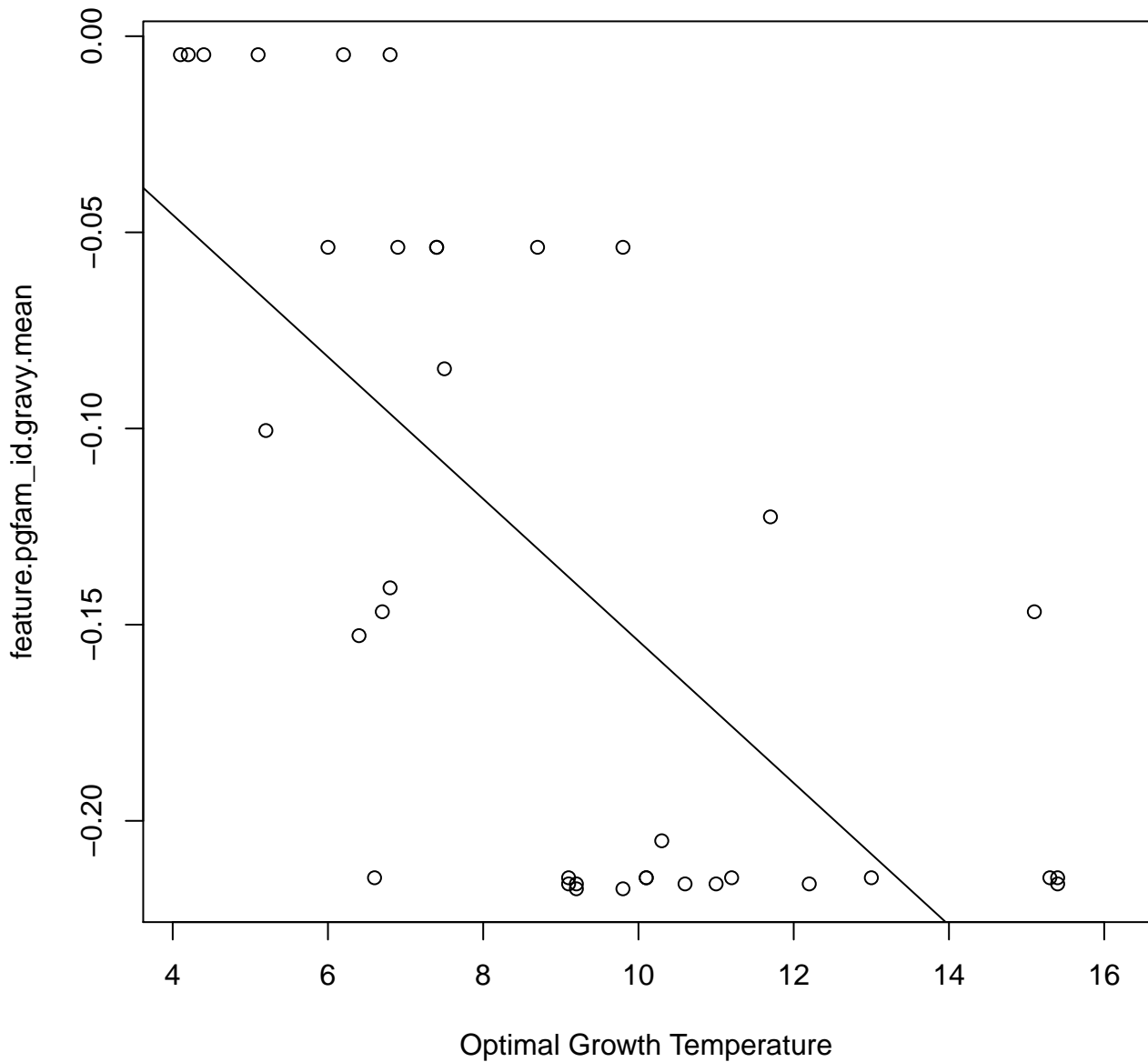
feature.pgfam_id.gravy.mean
PGF_00424726
Error-prone, lesion bypass DNA polymerase V (UmuC)



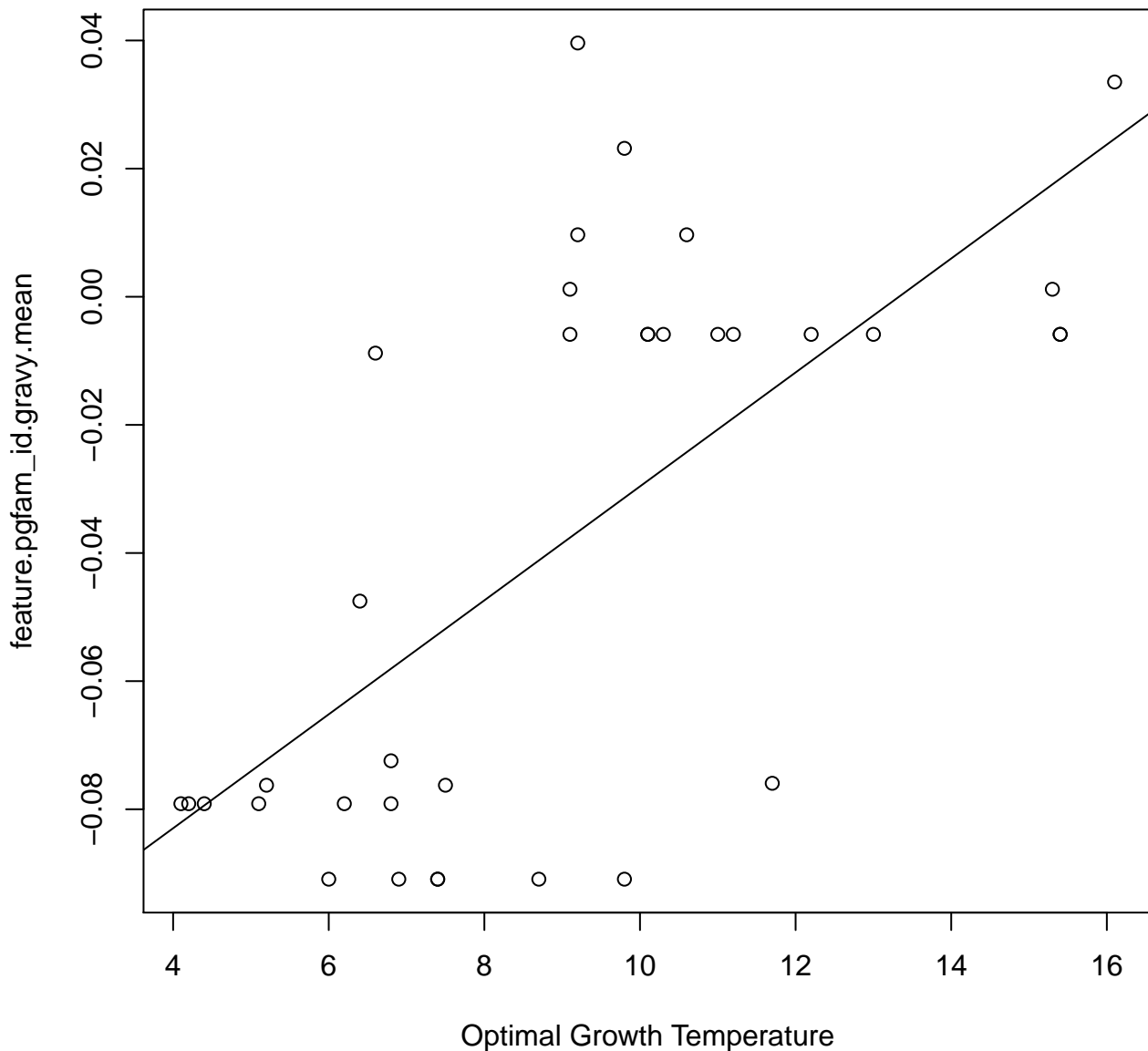
feature.pgfam_id.gravy.mean
PGF_01336501
hypothetical protein



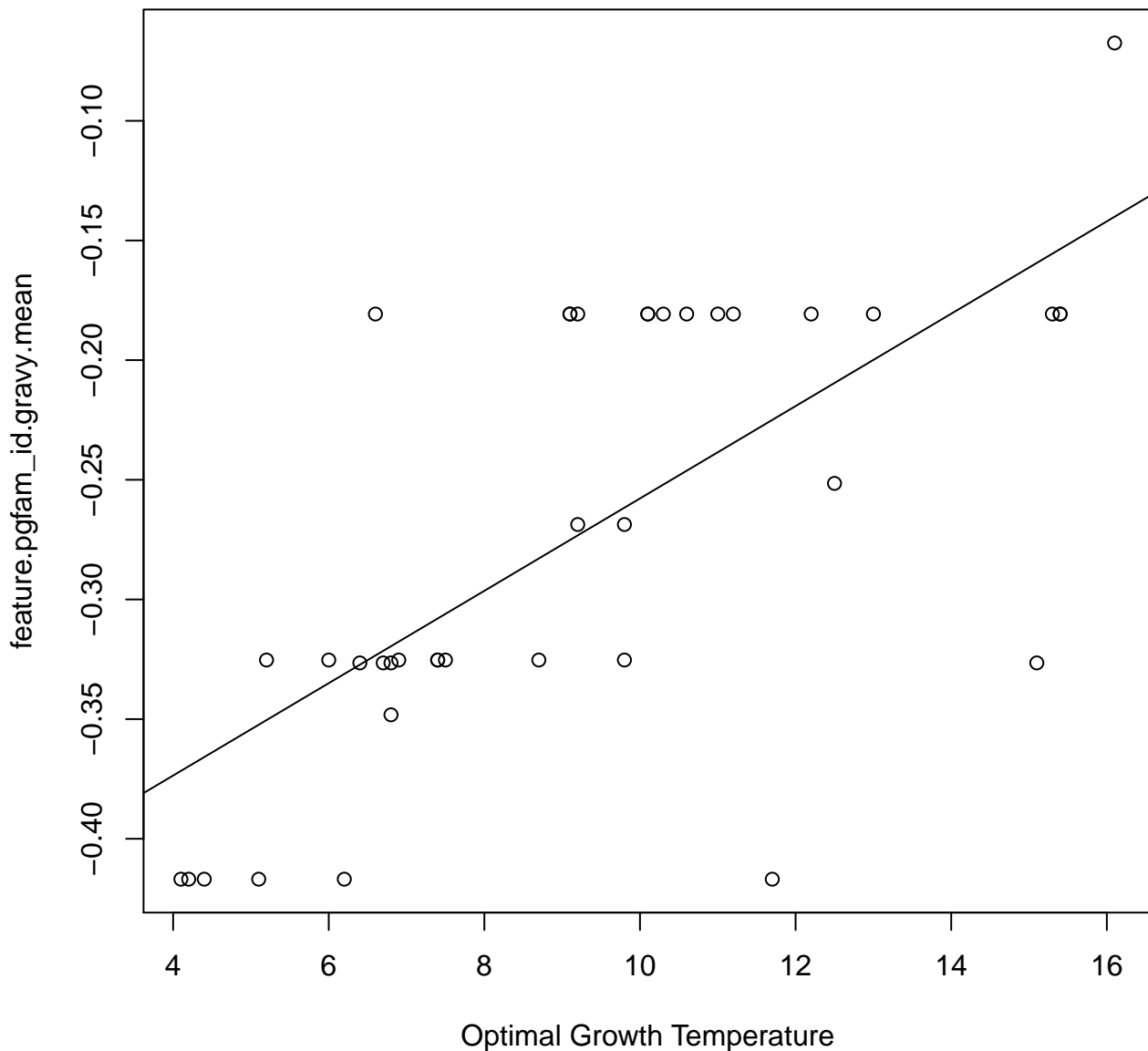
feature.pgfam_id.gravy.mean
PGF_01338555
hypothetical protein



feature.pgfam_id.gravy.mean
PGF_02007855
Zinc-type alcohol dehydrogenase-like protein



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

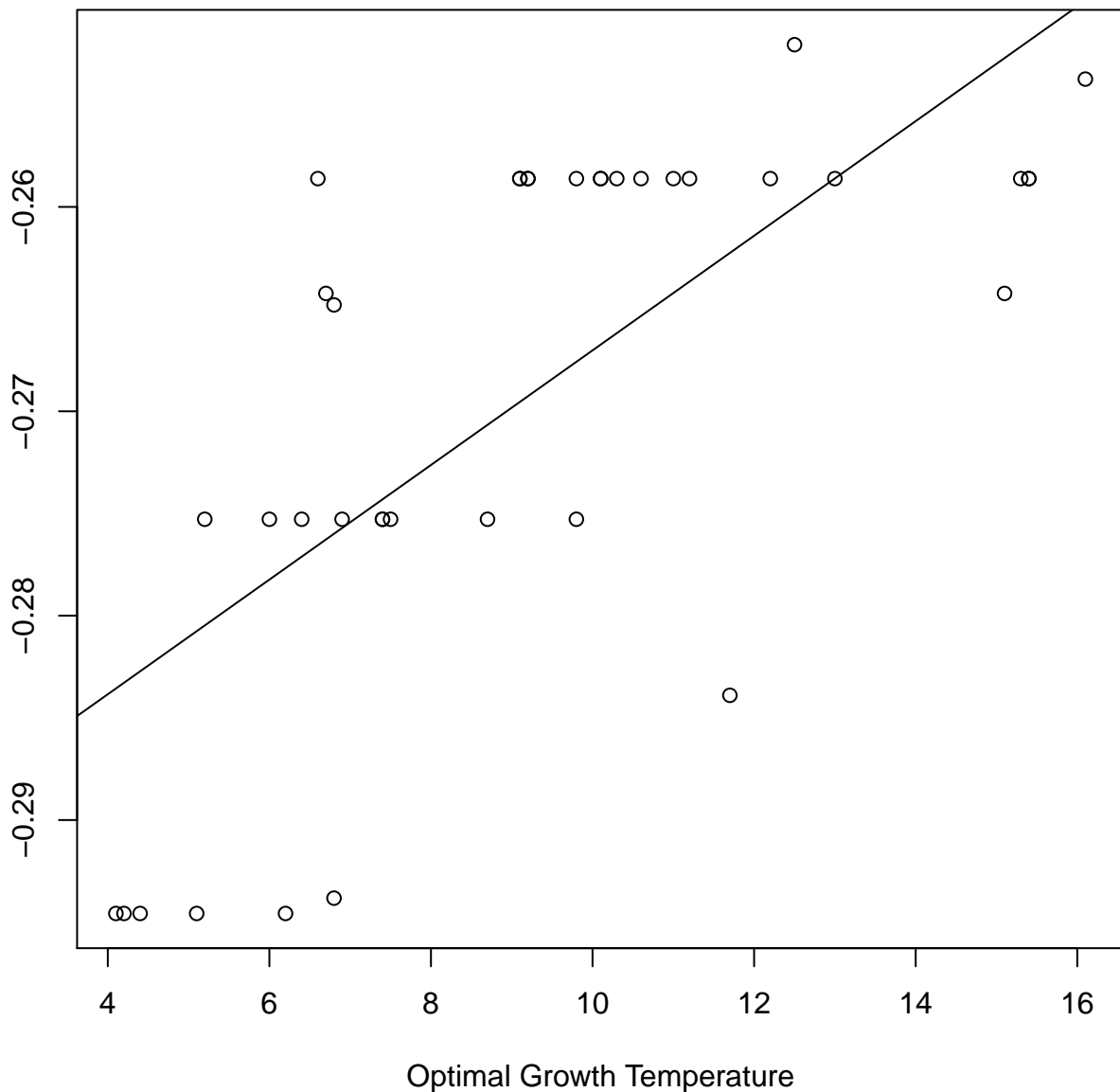


feature.pgfam_id.gravy.mean

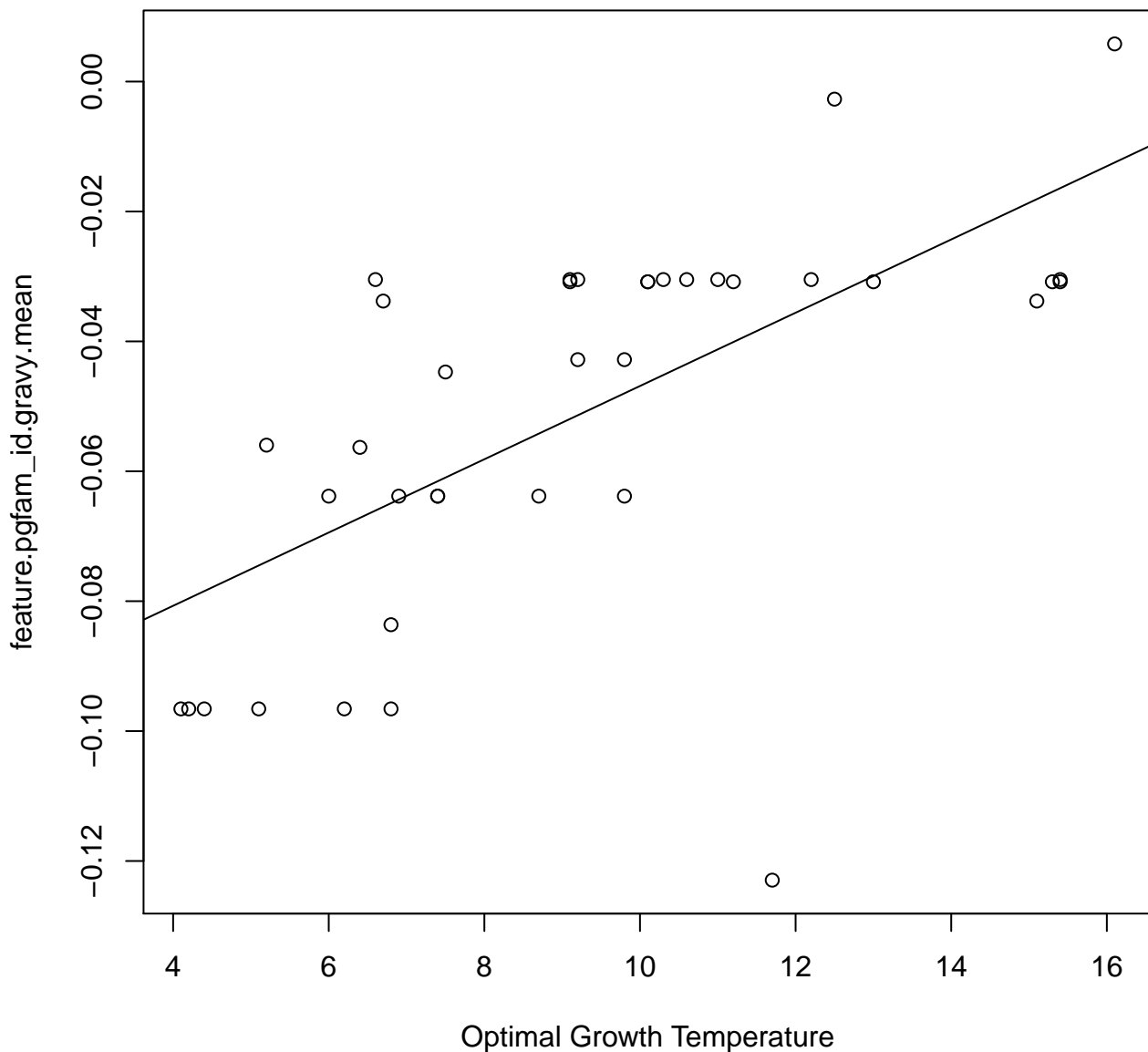
PGF_02903959

Bis-ABC ATPase SO_2525

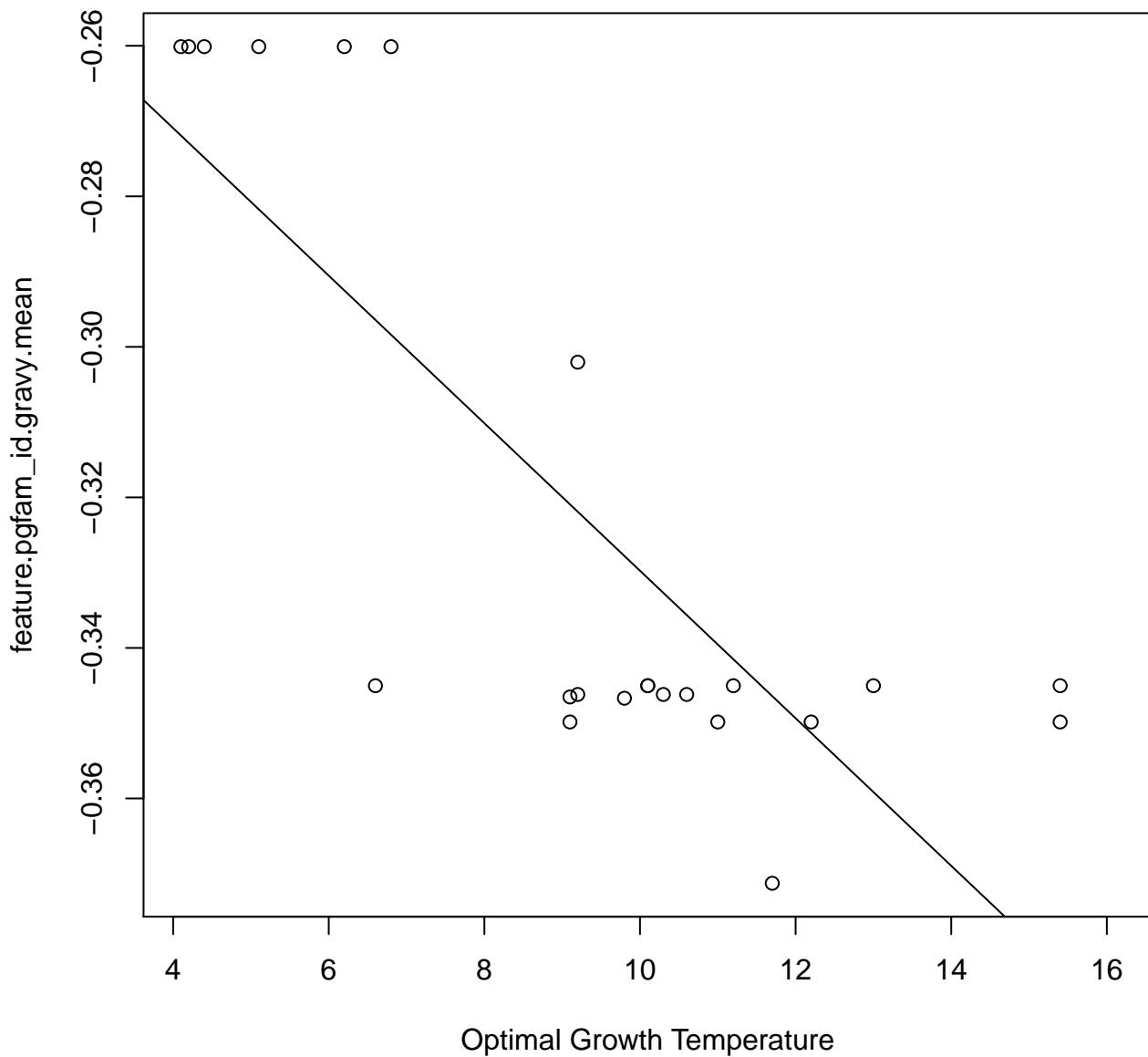
feature.pgfam_id.gravy.mean



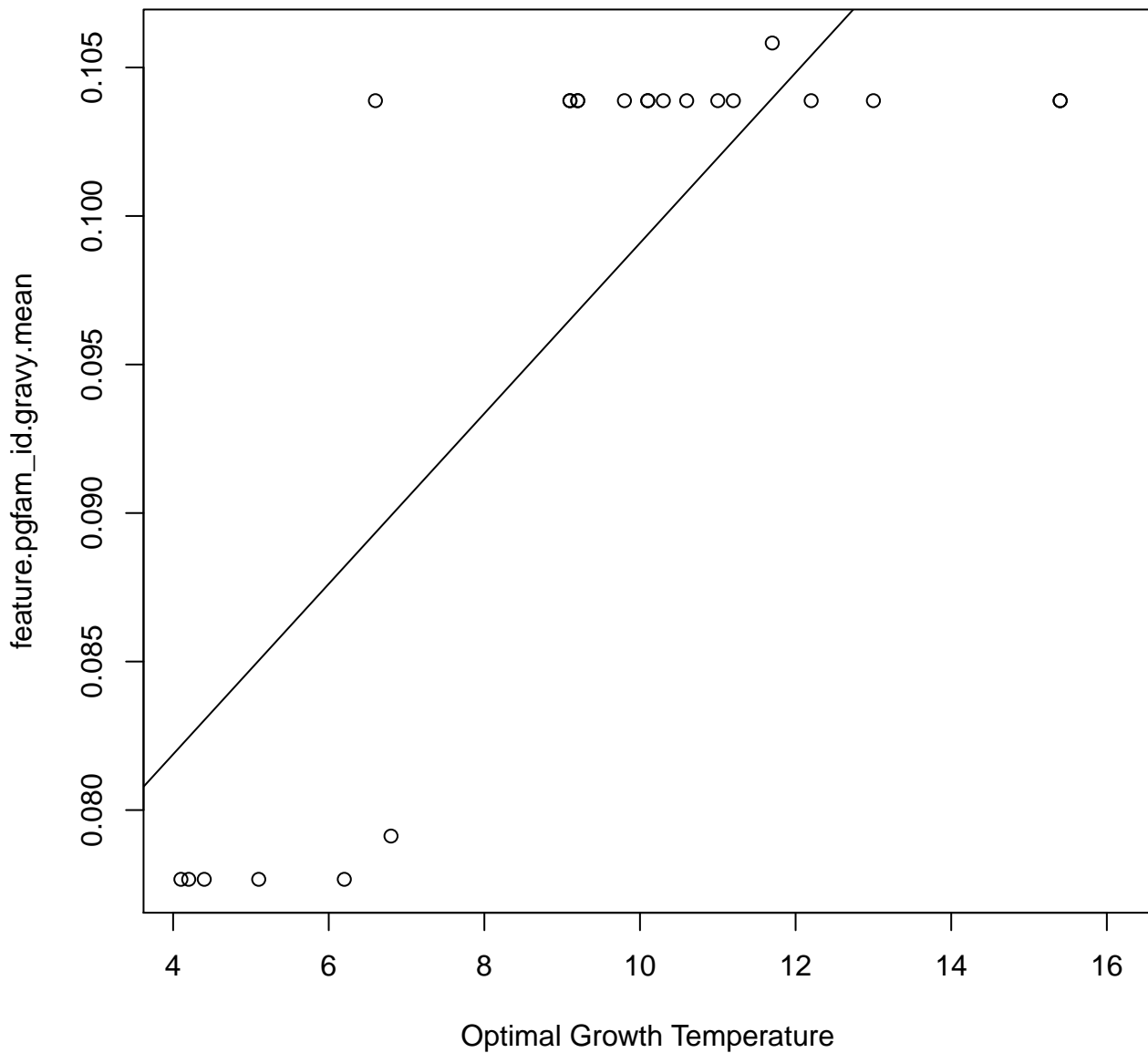
feature.pgfam_id.gravy.mean
PGF_03051420
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



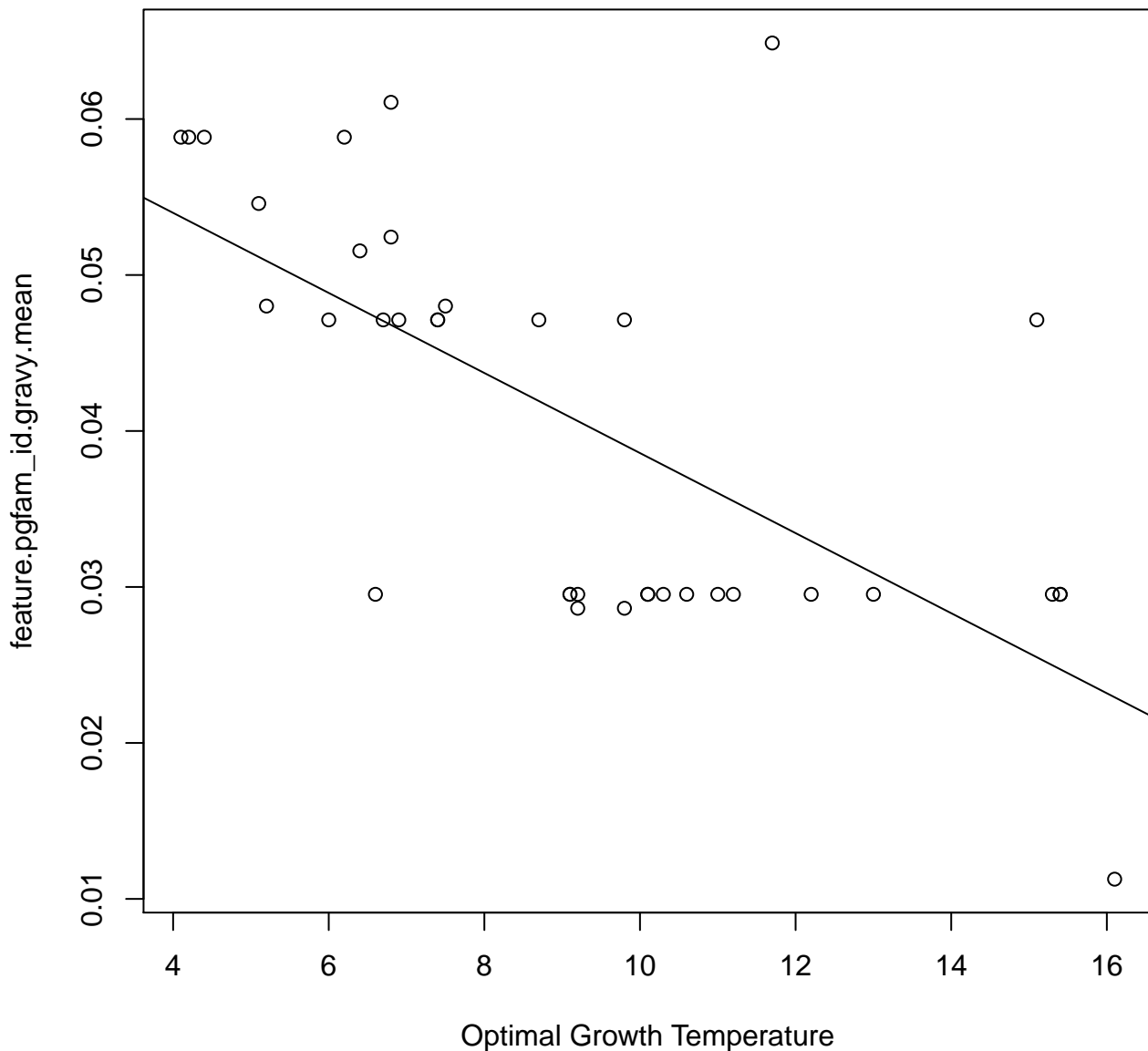
feature.pgfam_id.gravy.mean
PGF_03083319
Maltodextrin glucosidase (EC 3.2.1.20)



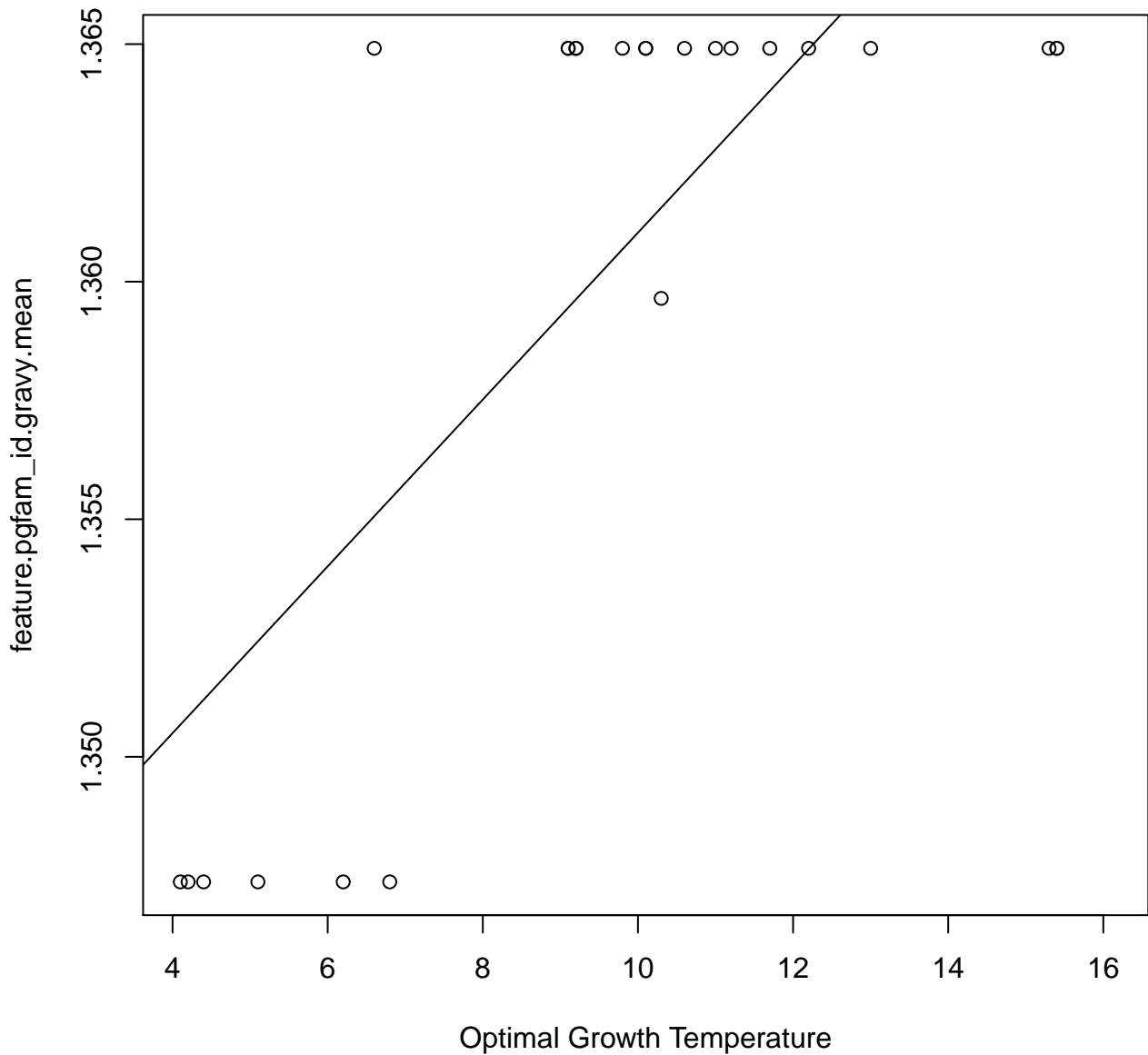
feature.pgfam_id.gravy.mean
PGF_07210740
hypothetical protein



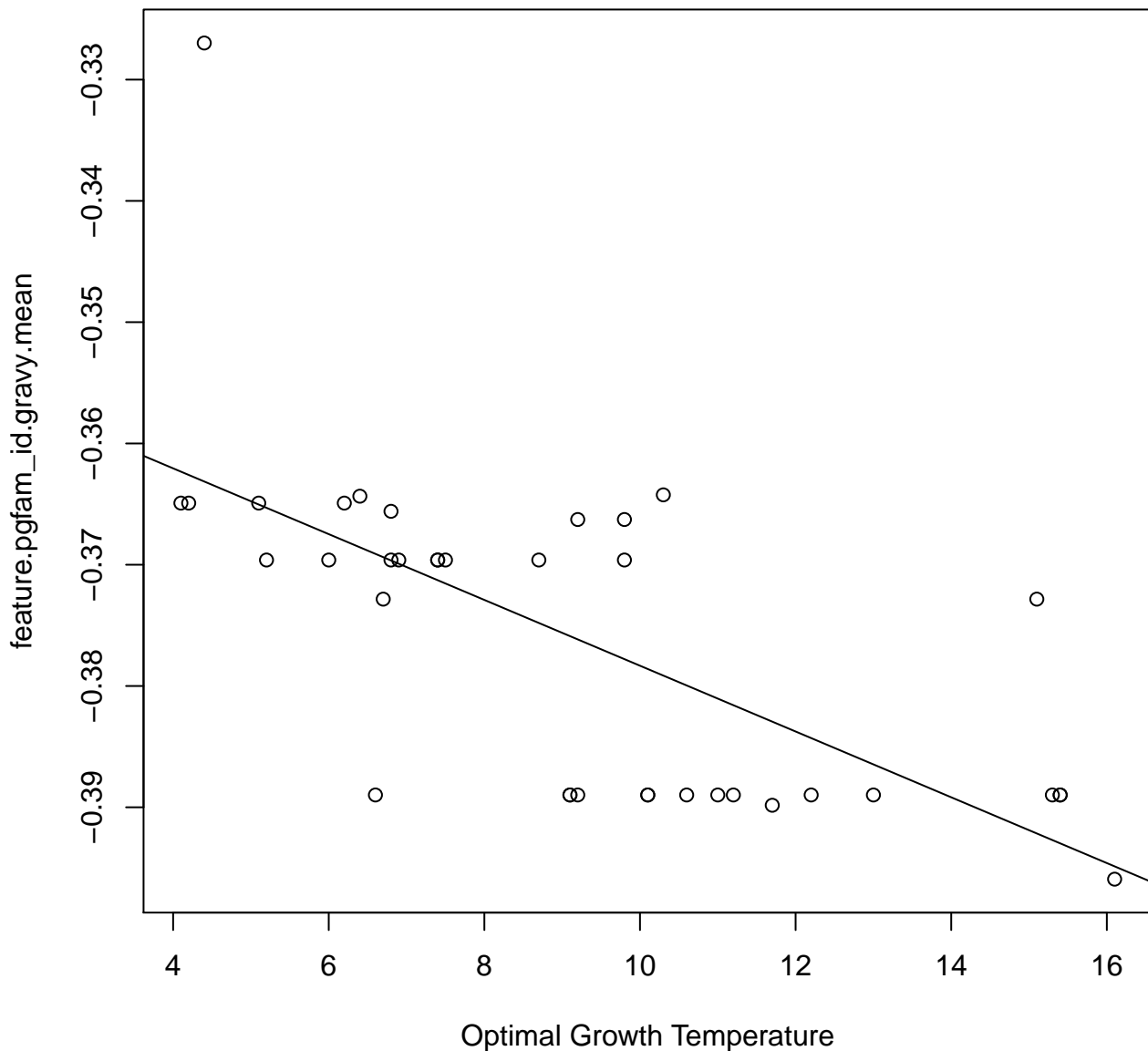
feature.pgfam_id.gravy.mean
PGF_07844318
3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)



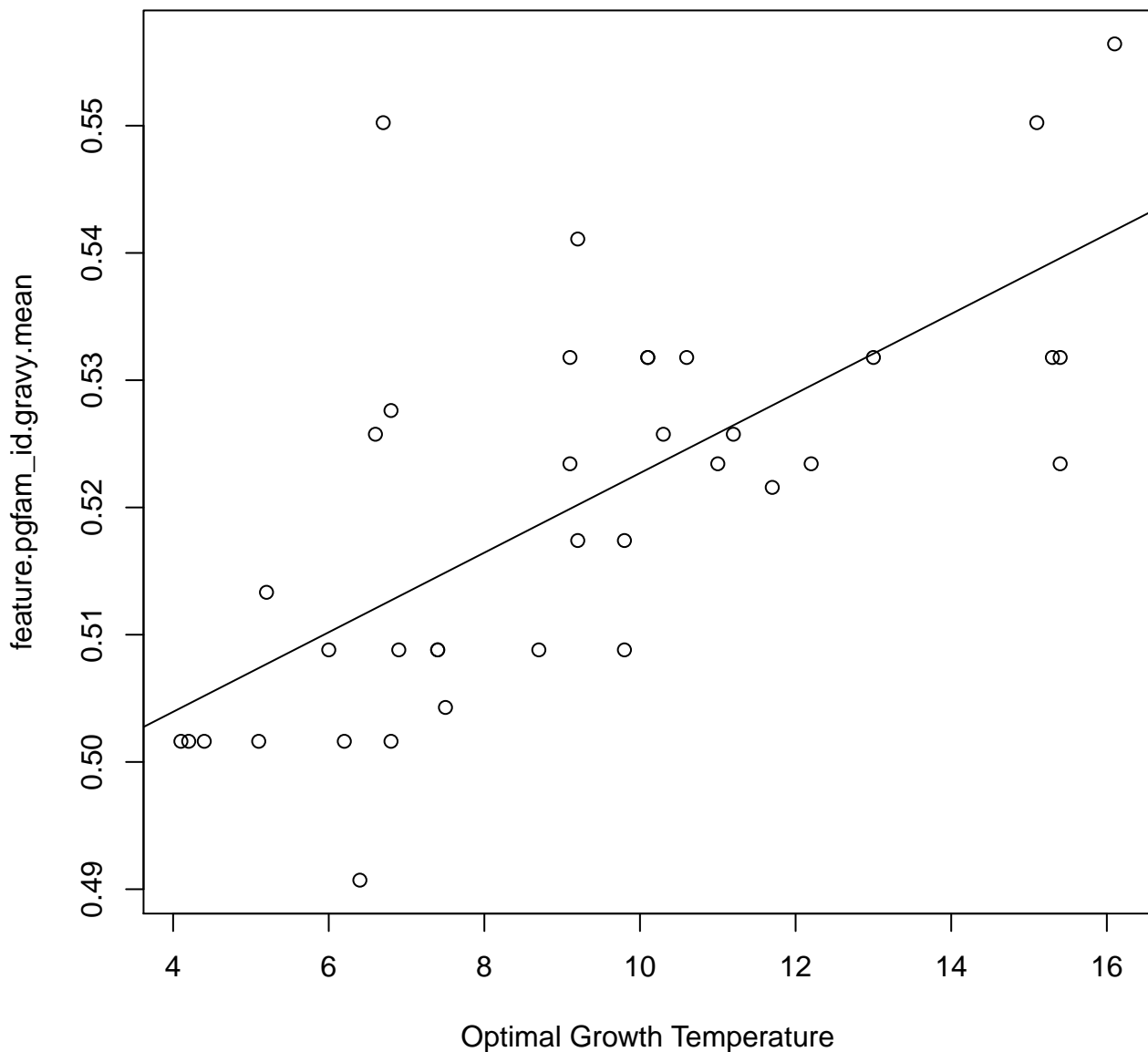
feature.pgfam_id.gravy.mean
PGF_08289417
hypothetical protein



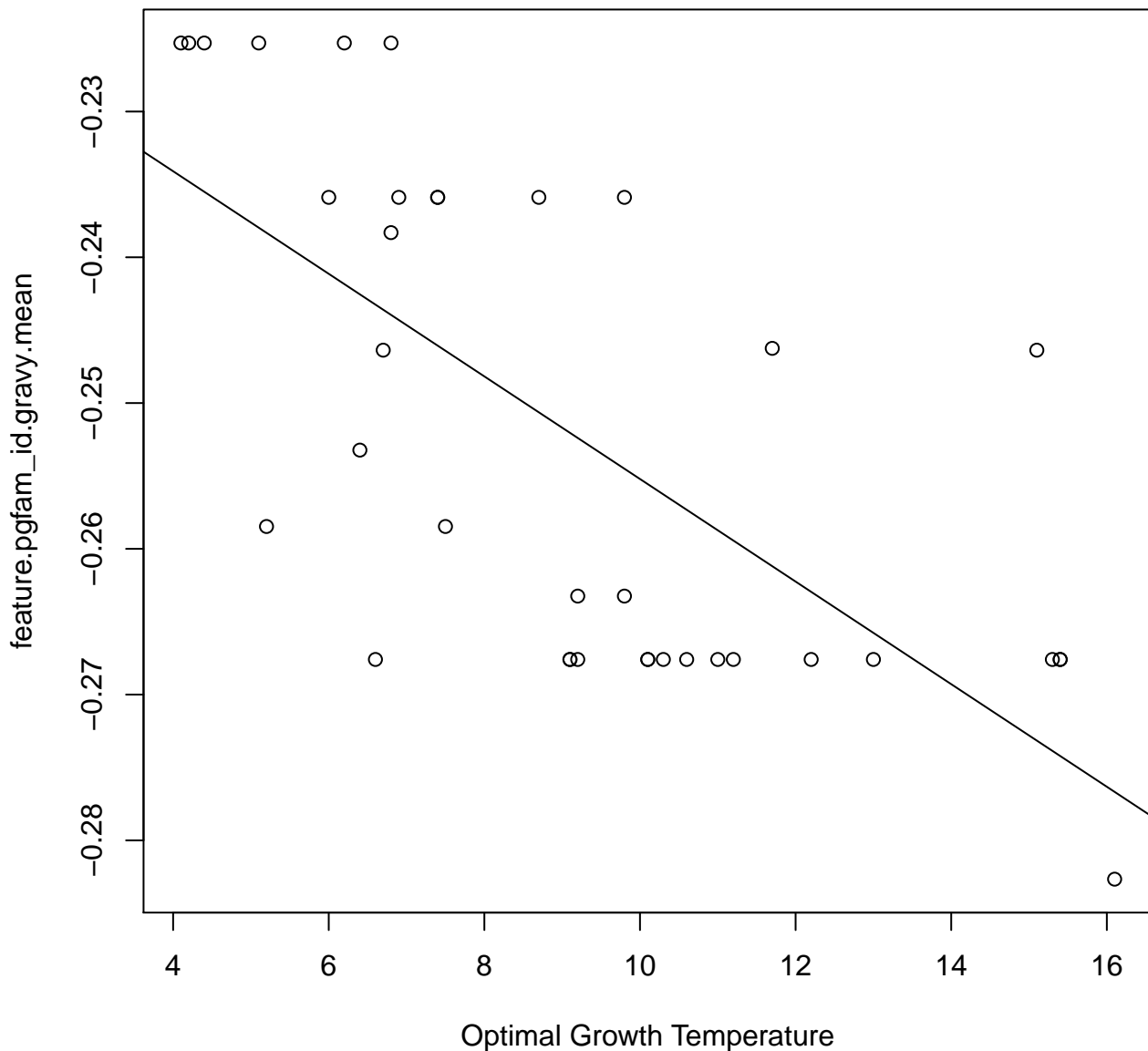
feature.pgfam_id.gravy.mean
PGF_08998238
Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)



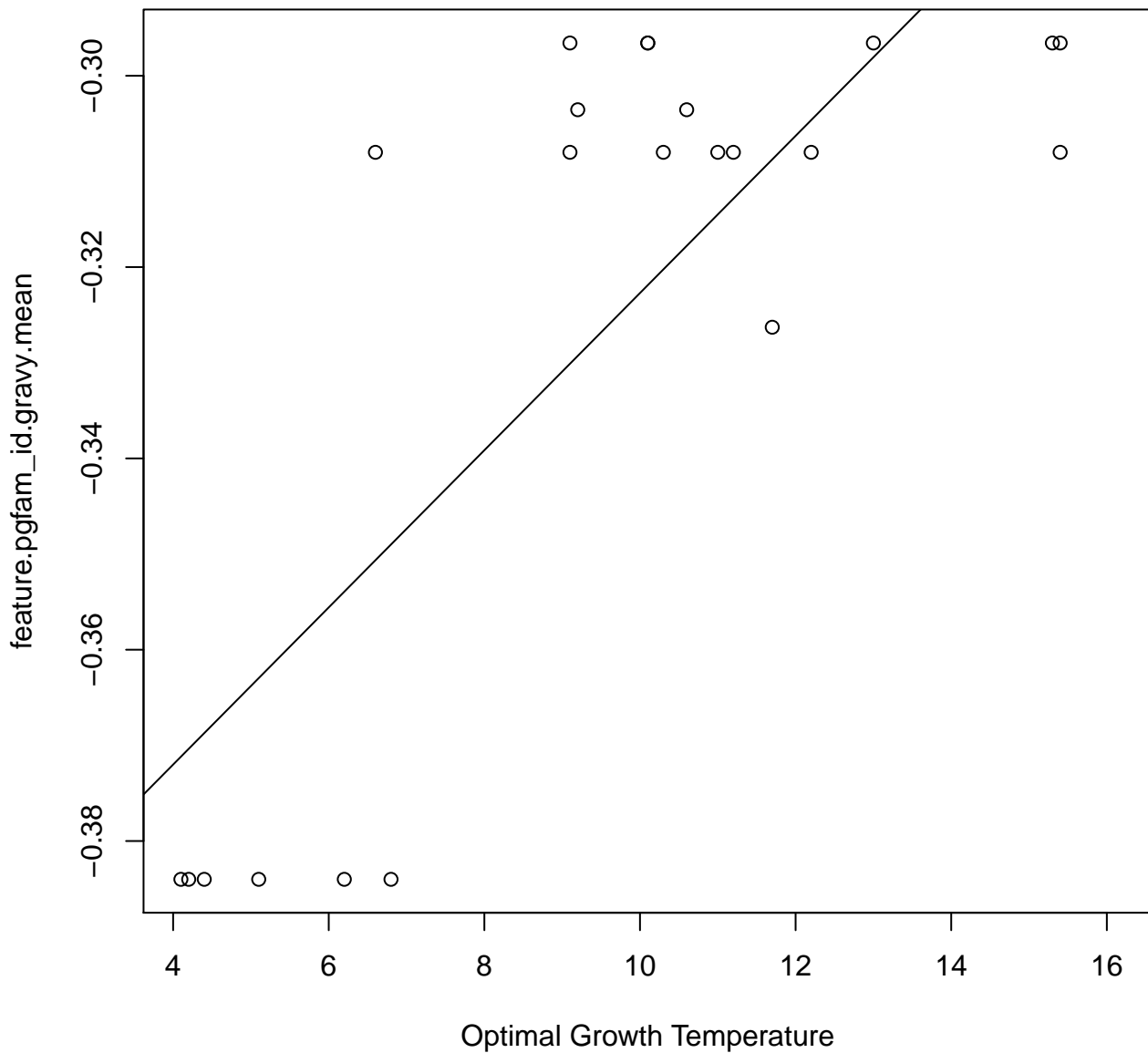
feature.pgfam_id.gravy.mean
PGF_10125426
Peptidoglycan glycosyltransferase FtsW (EC 2.4.1.129)



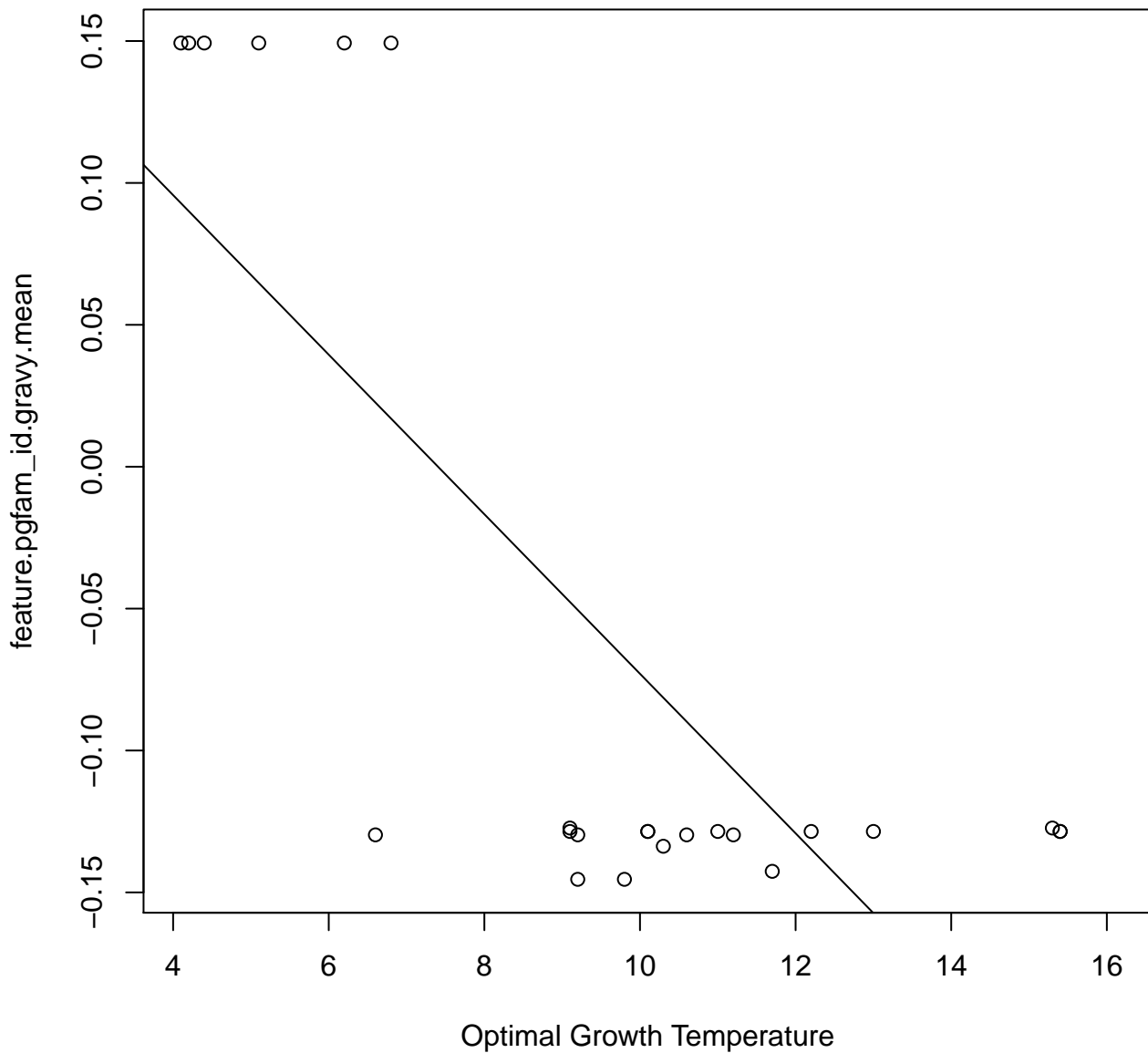
feature.pgfam_id.gravy.mean
PGF_10233208
16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)



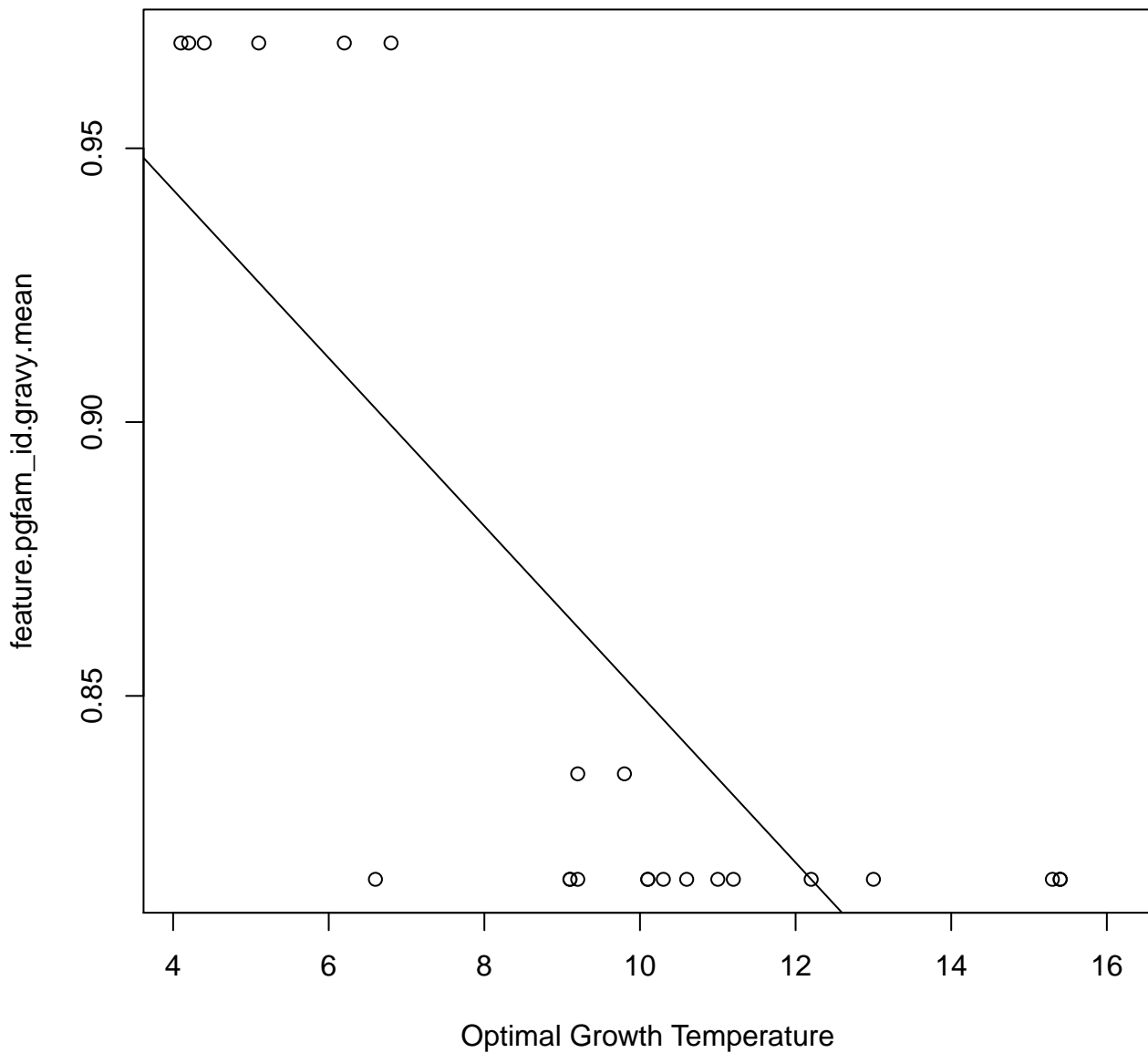
feature.pgfam_id.gravy.mean
PGF_10918576
hypothetical protein



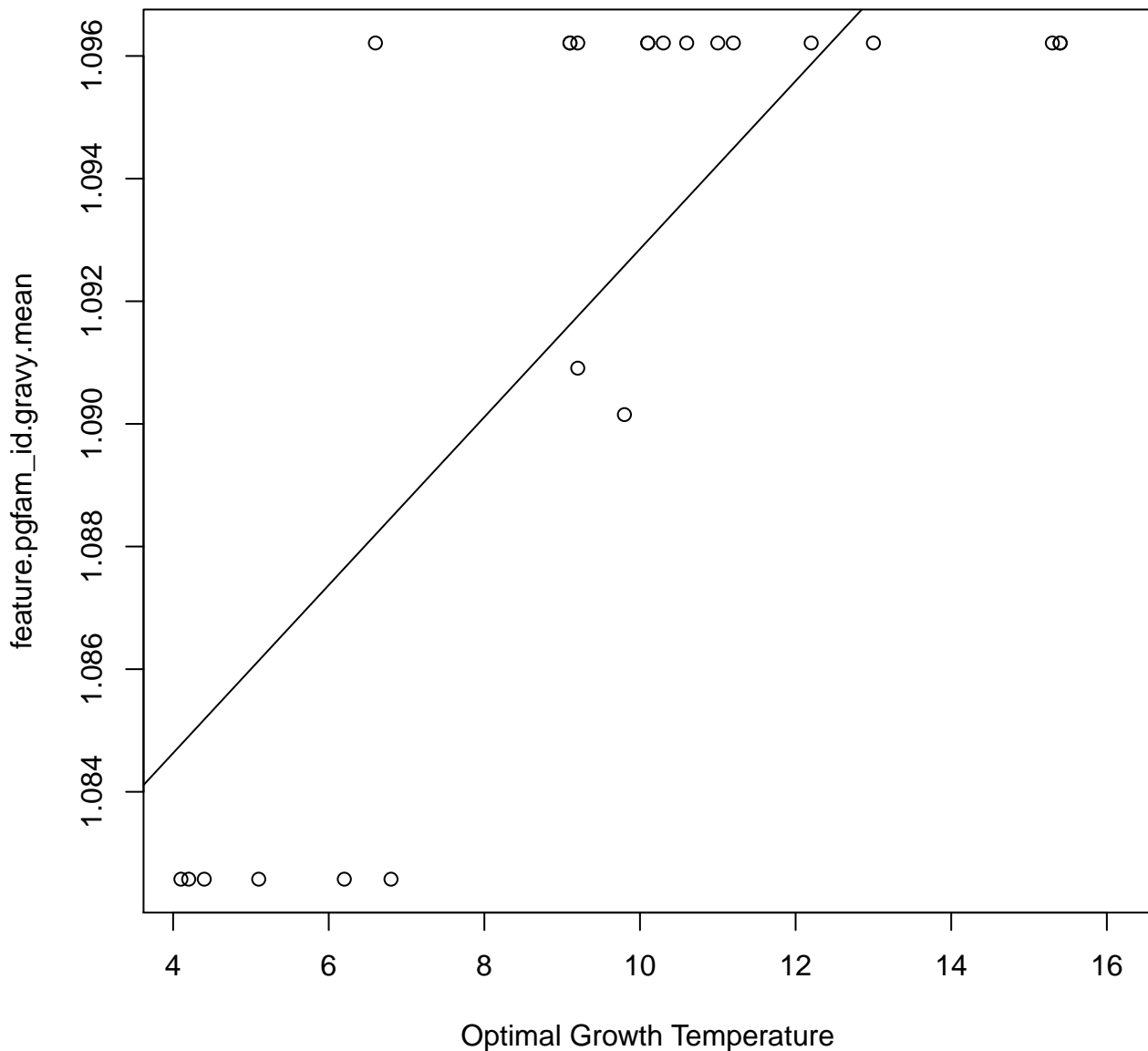
feature.pgfam_id.gravy.mean
PGF_11018774
hypothetical protein



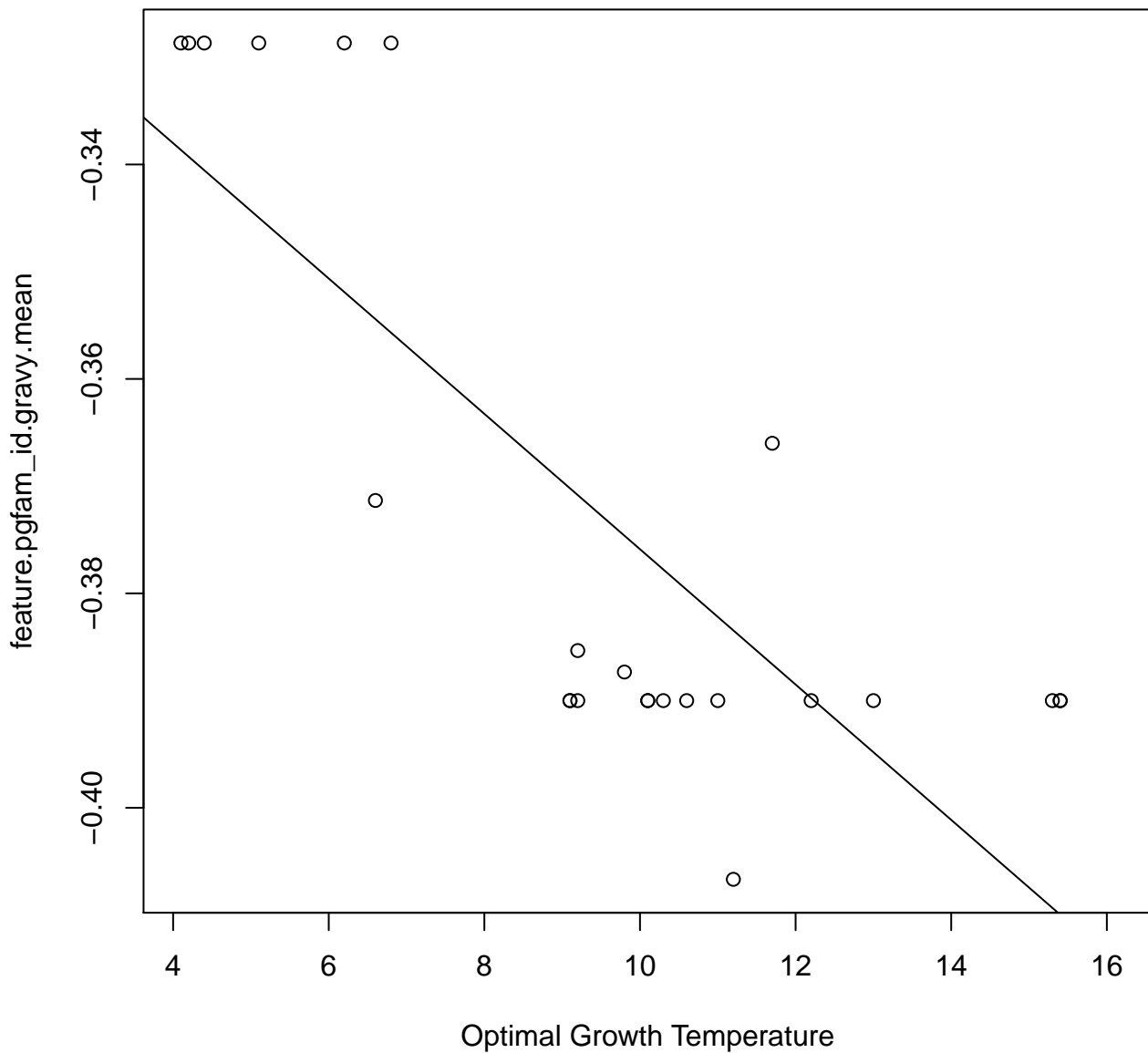
feature.pgfam_id.gravy.mean
PGF_11025496
hypothetical protein



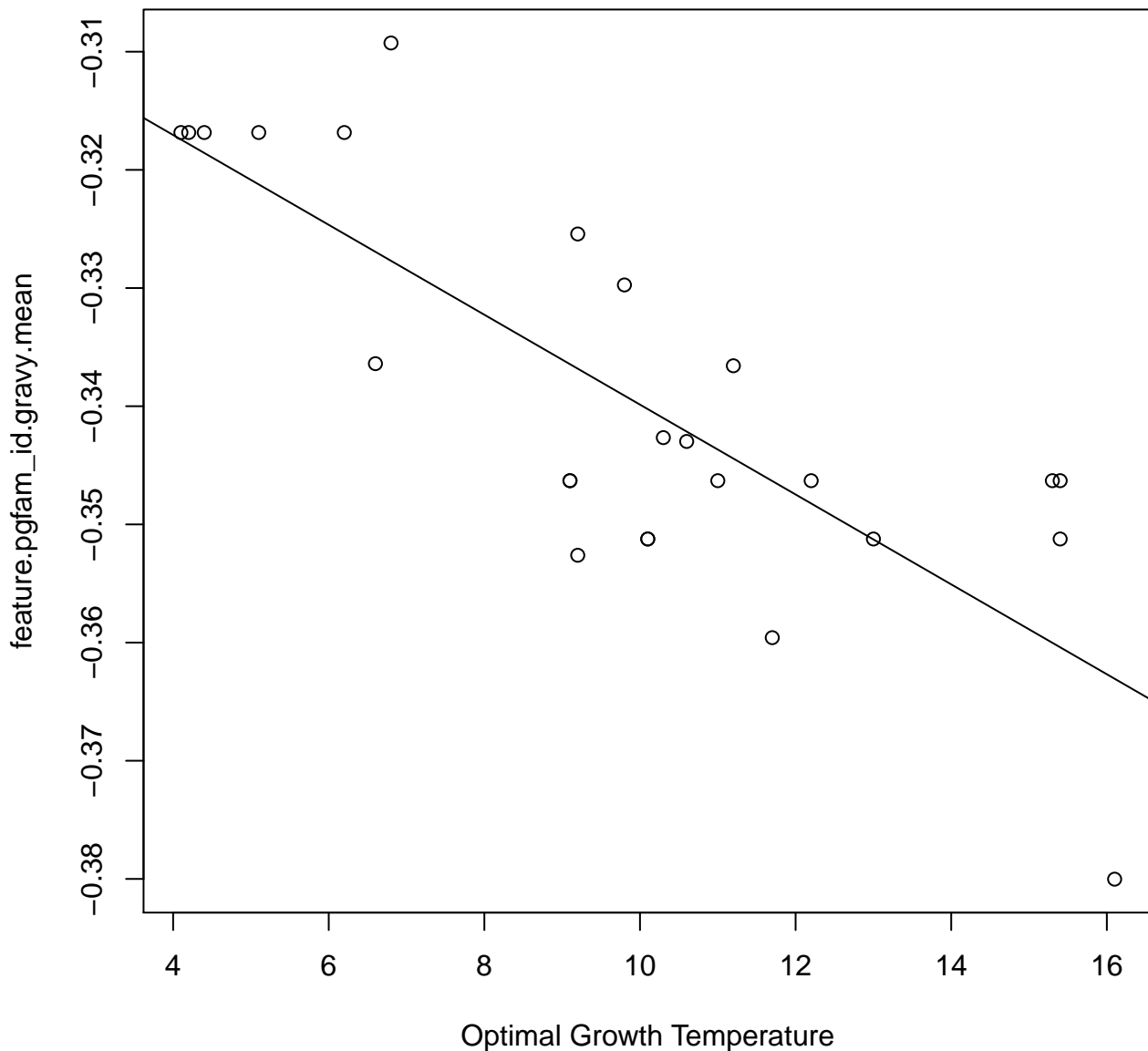
feature.pgfam_id.gravy.mean
PGF_11600935
hypothetical protein



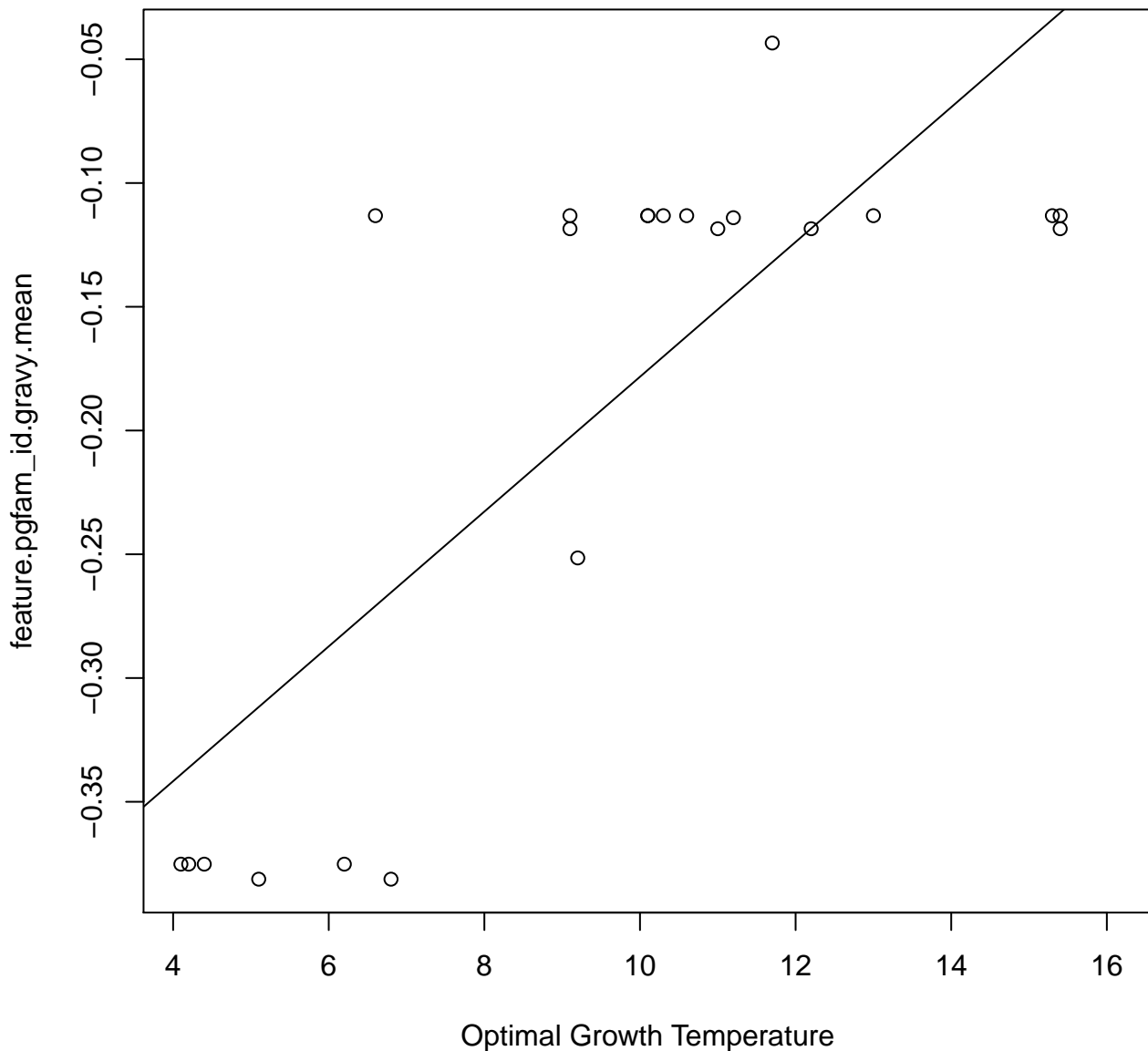
feature.pgfam_id.gravy.mean
PGF_11796071
hypothetical protein



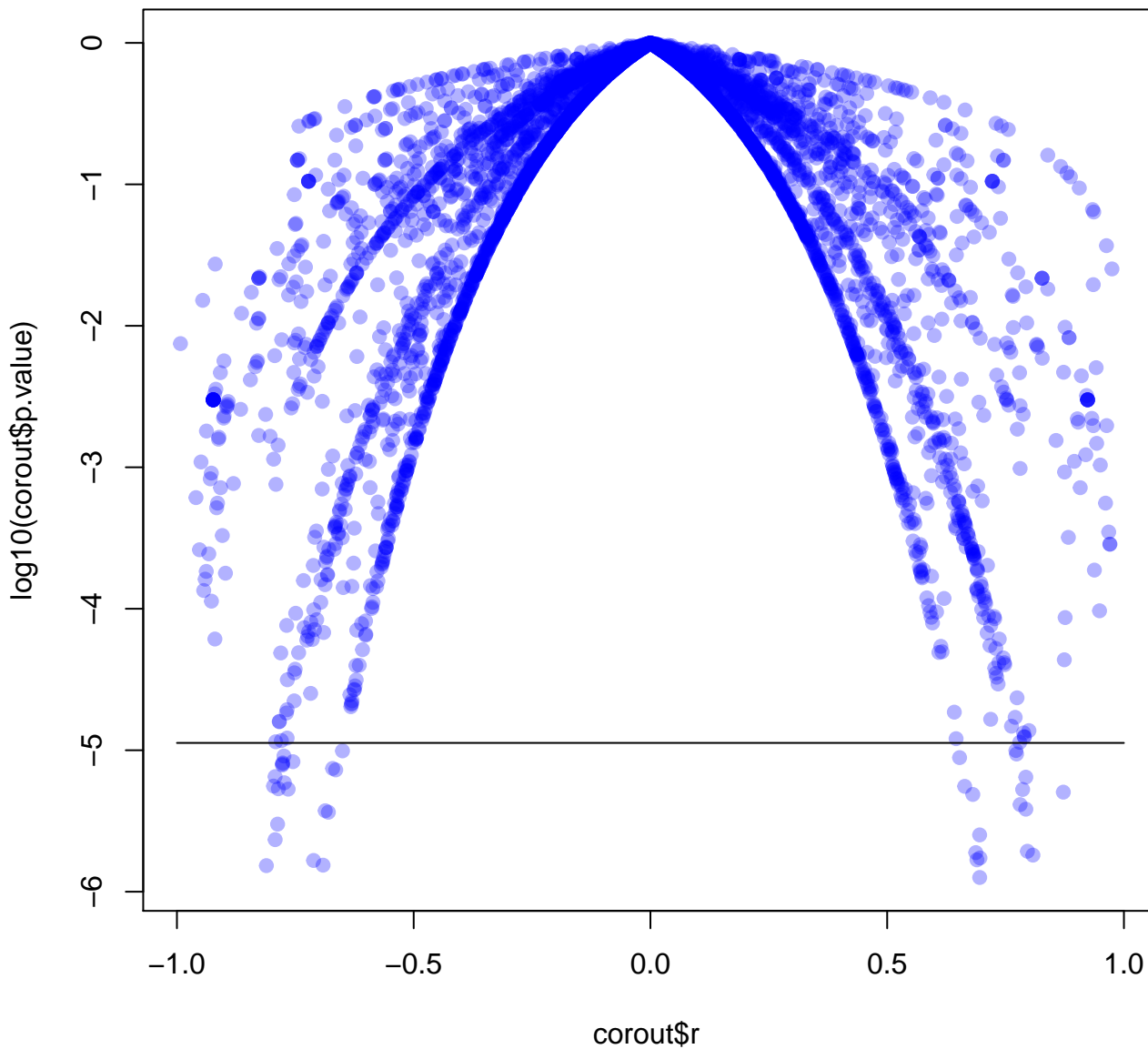
feature.pgfam_id.gravy.mean
PGF_12728693
Two-component system sensor histidine kinase/response regulator hybrid



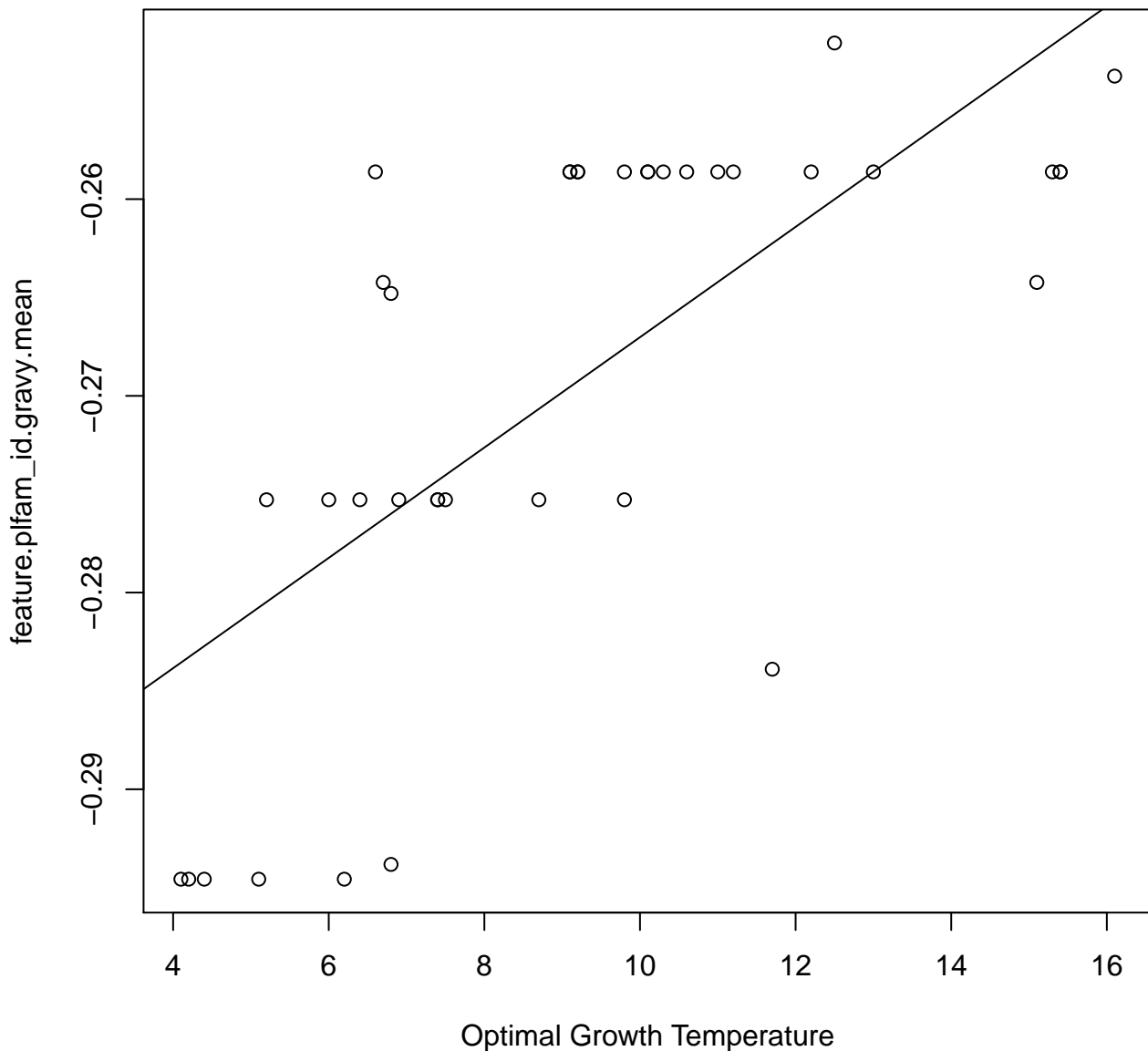
feature.pgfam_id.gravy.mean
PGF_12765299
Two-component system sensor histidine kinase



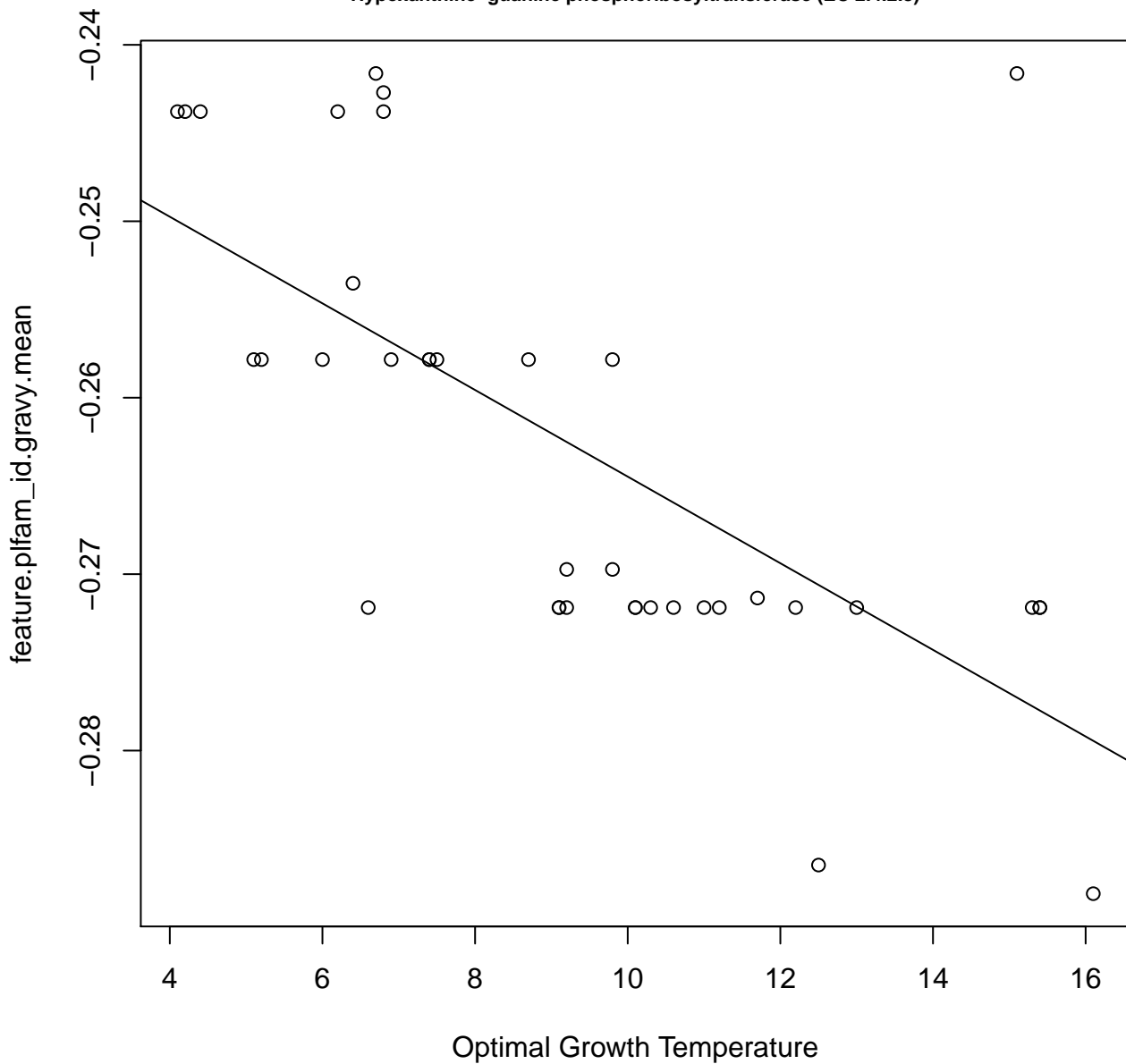
feature.plfam_id.gravy.mean



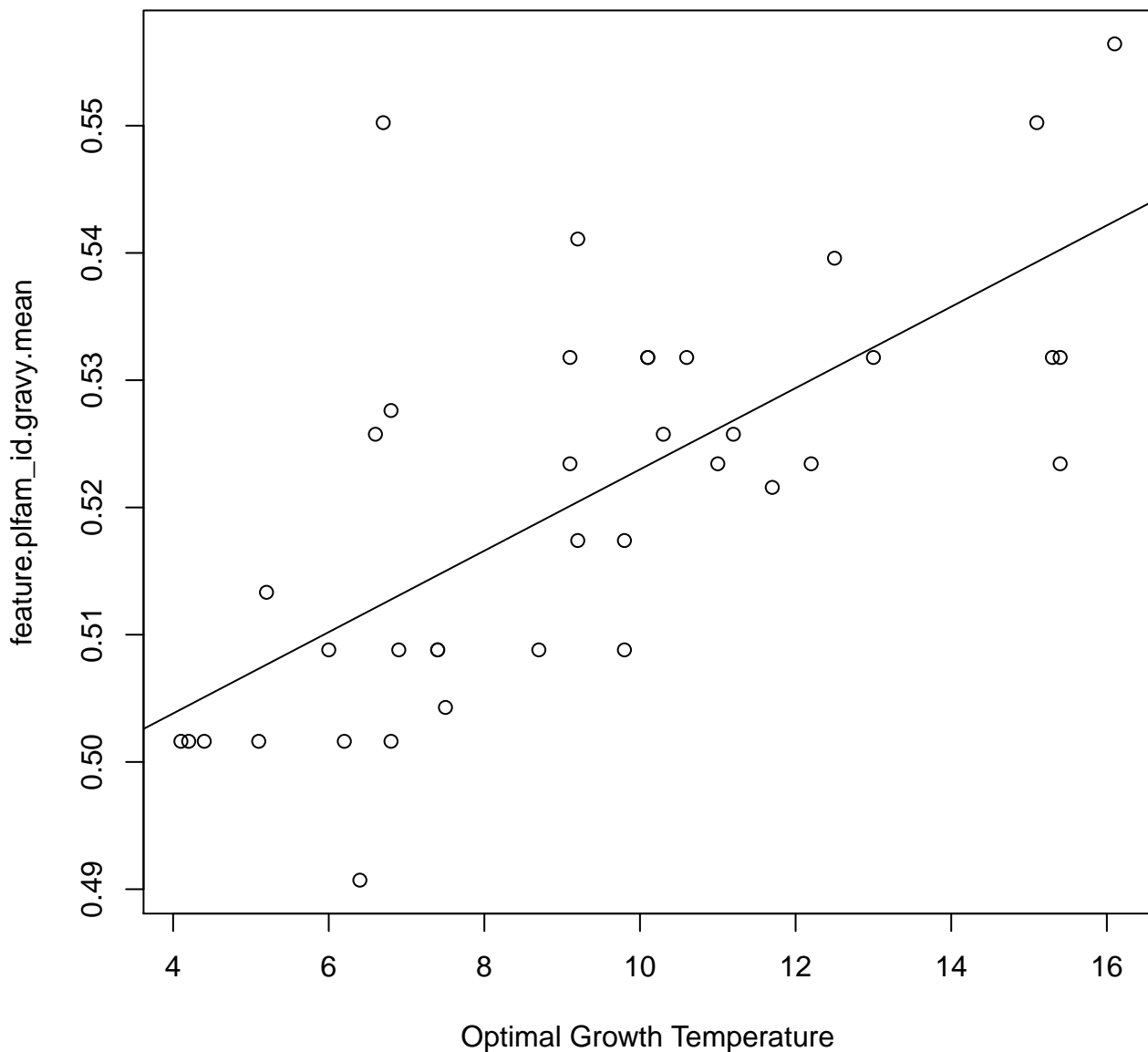
feature.plfam_id.gravy.mean
PLF_28228_00000078
Bis-ABC ATPase SO_2525



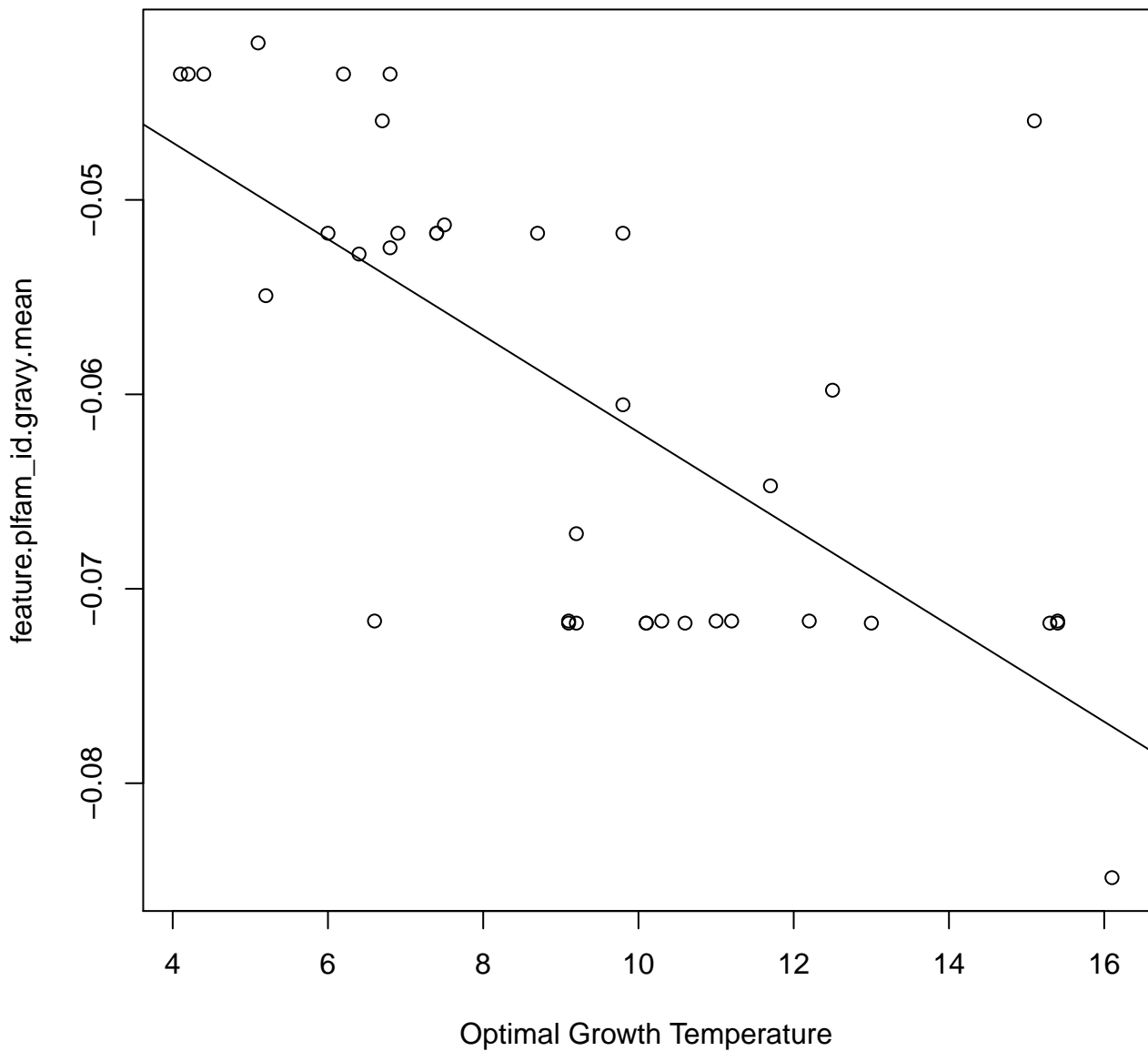
feature.plfam_id.gravy.mean
PLF_28228_00000515
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)



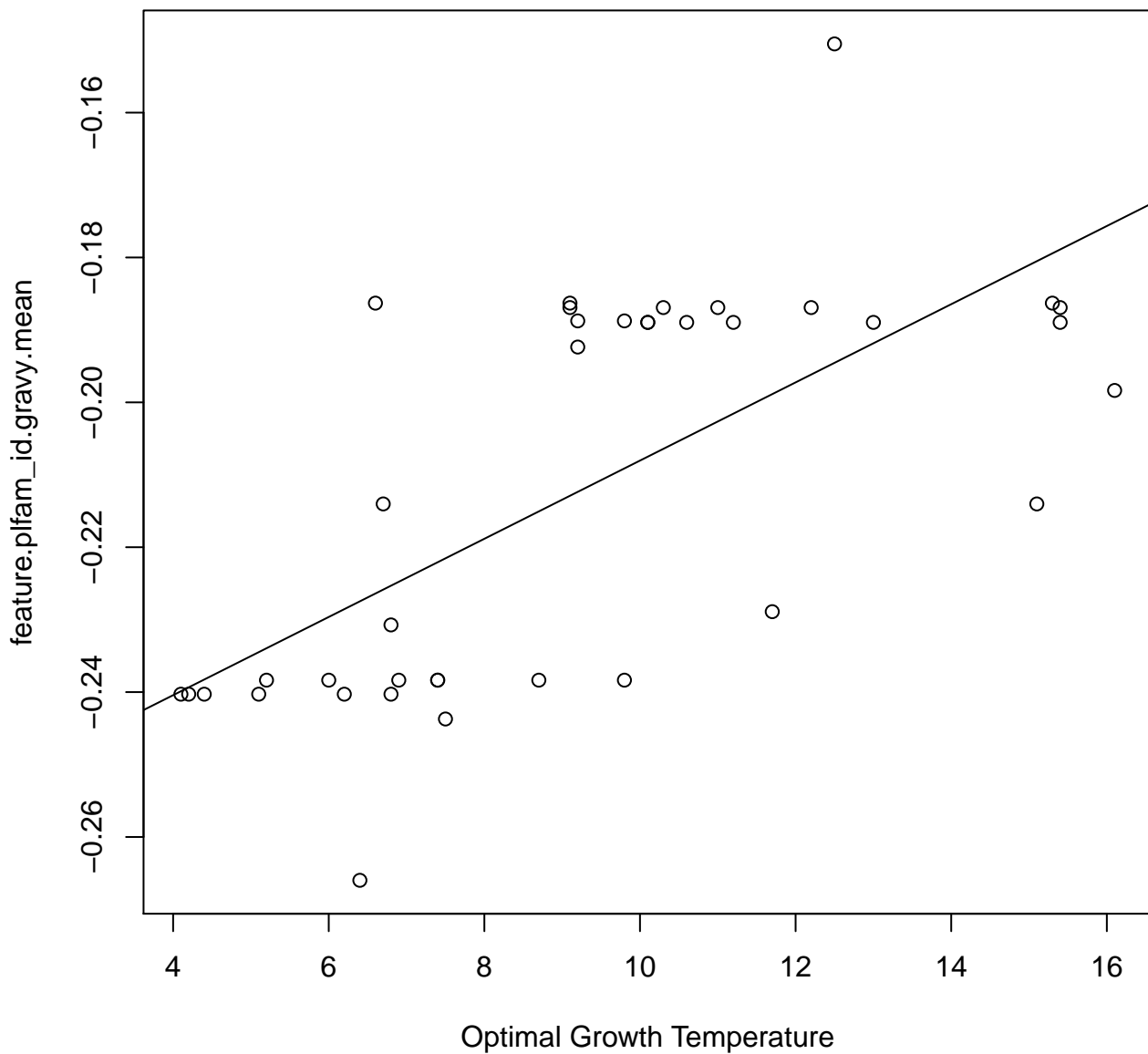
feature.plfam_id.gravy.mean
PLF_28228_00000553
Peptidoglycan glycosyltransferase FtsW (EC 2.4.1.129)



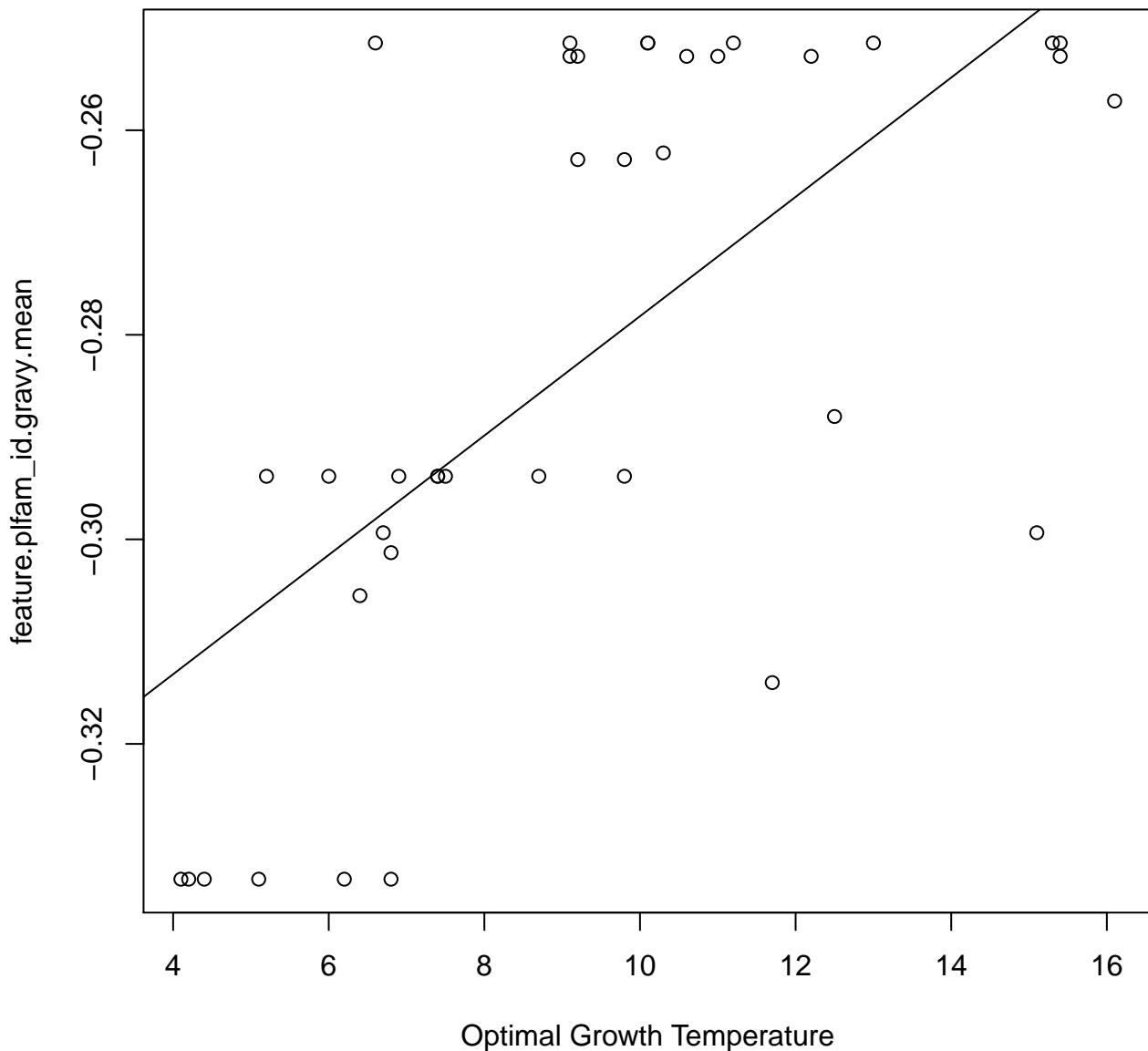
feature.plfam_id.gravy.mean
PLF_28228_00000733
Aconitate hydratase 2 (EC 4.2.1.3)



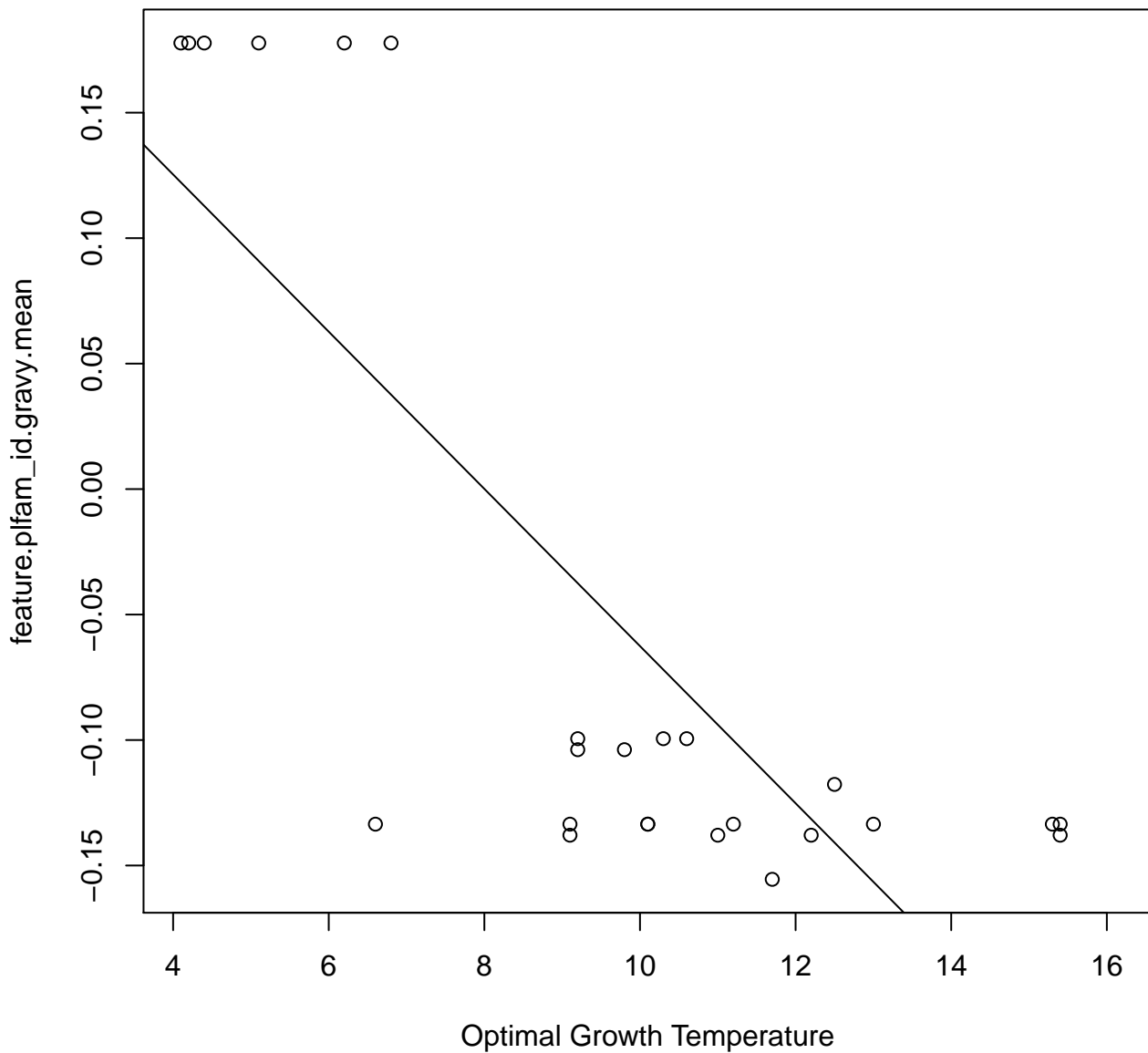
feature.plfam_id.gravy.mean
PLF_28228_00000790
Exported zinc metalloprotease YfgC precursor



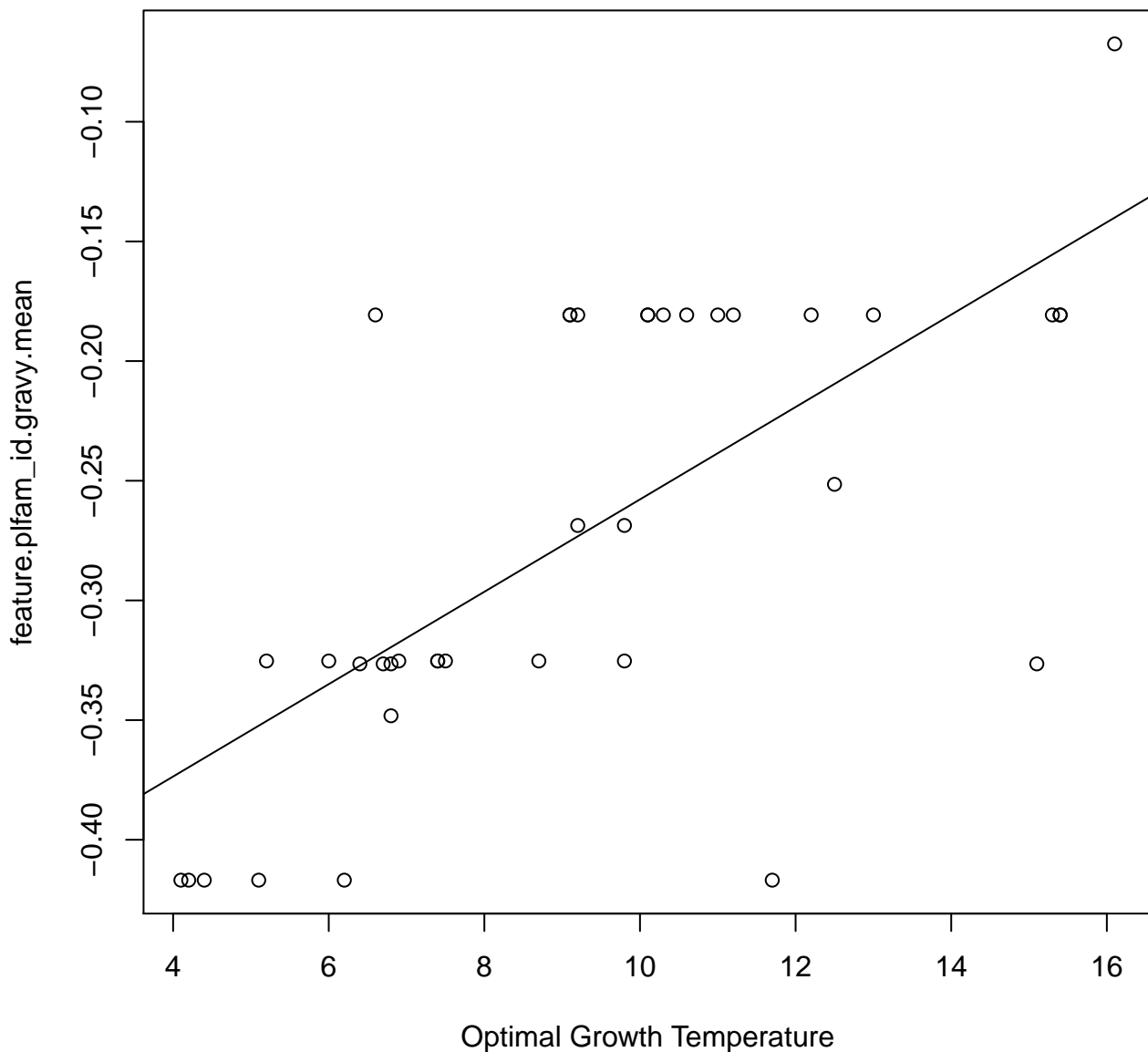
feature.plfam_id.gravy.mean
PLF_28228_00000865
GTP cyclohydrolase I (EC 3.5.4.16) type 2



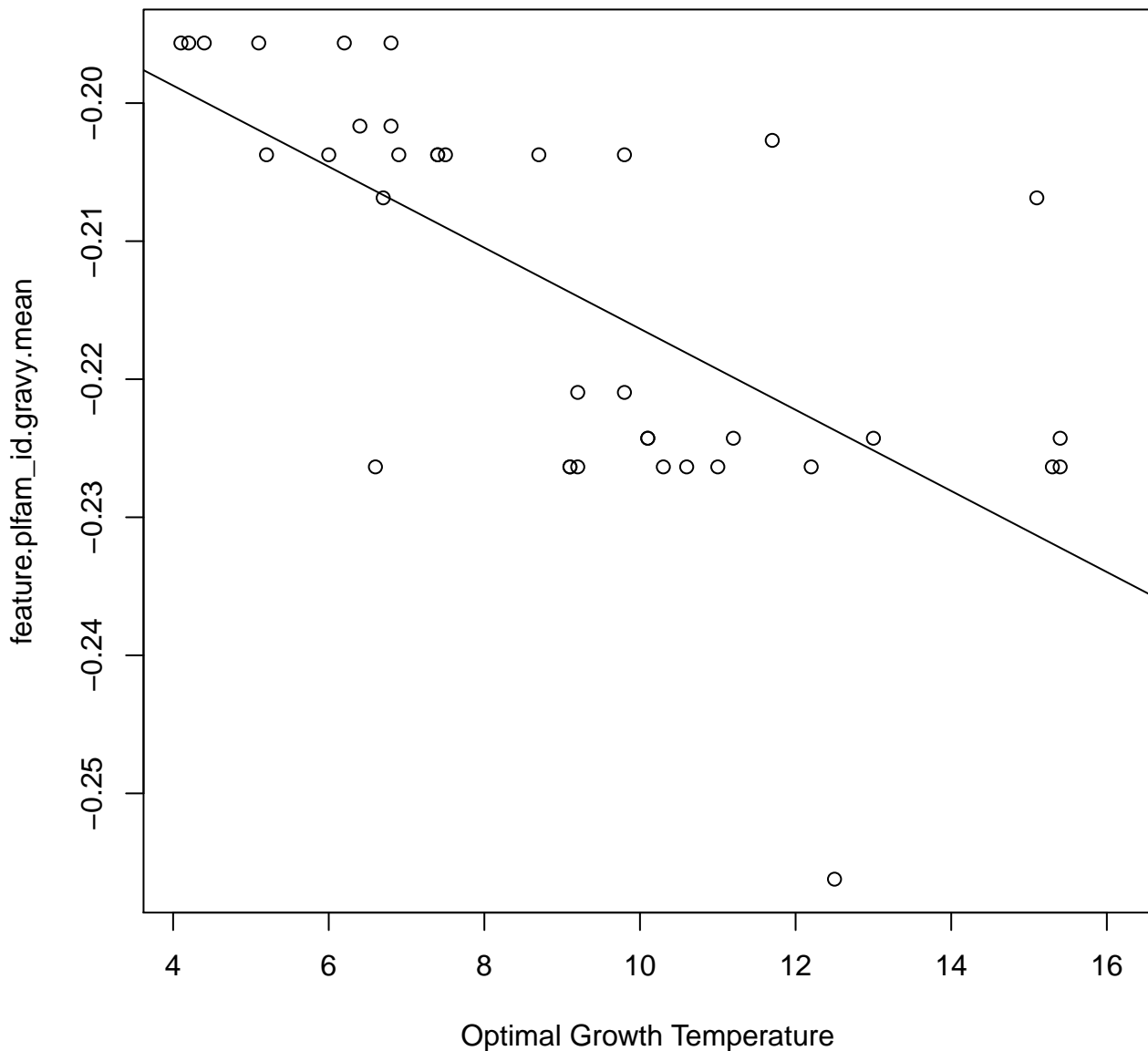
feature.plfam_id.gravy.mean
PLF_28228_00001024
Putative NAD(P)H nitroreductase YdjA



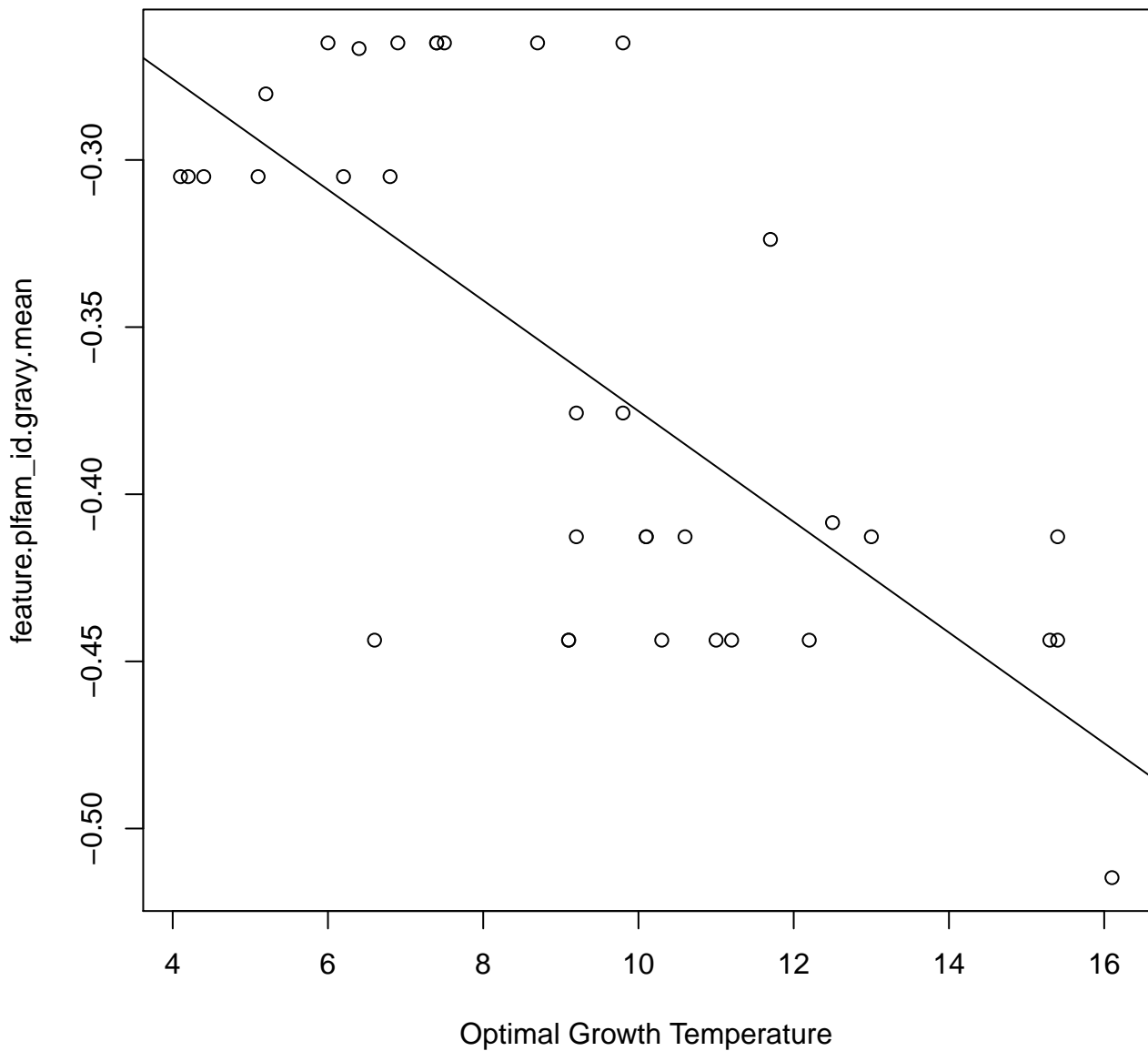
feature.plfam_id.gravy.mean
PLF_28228_00001310
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin



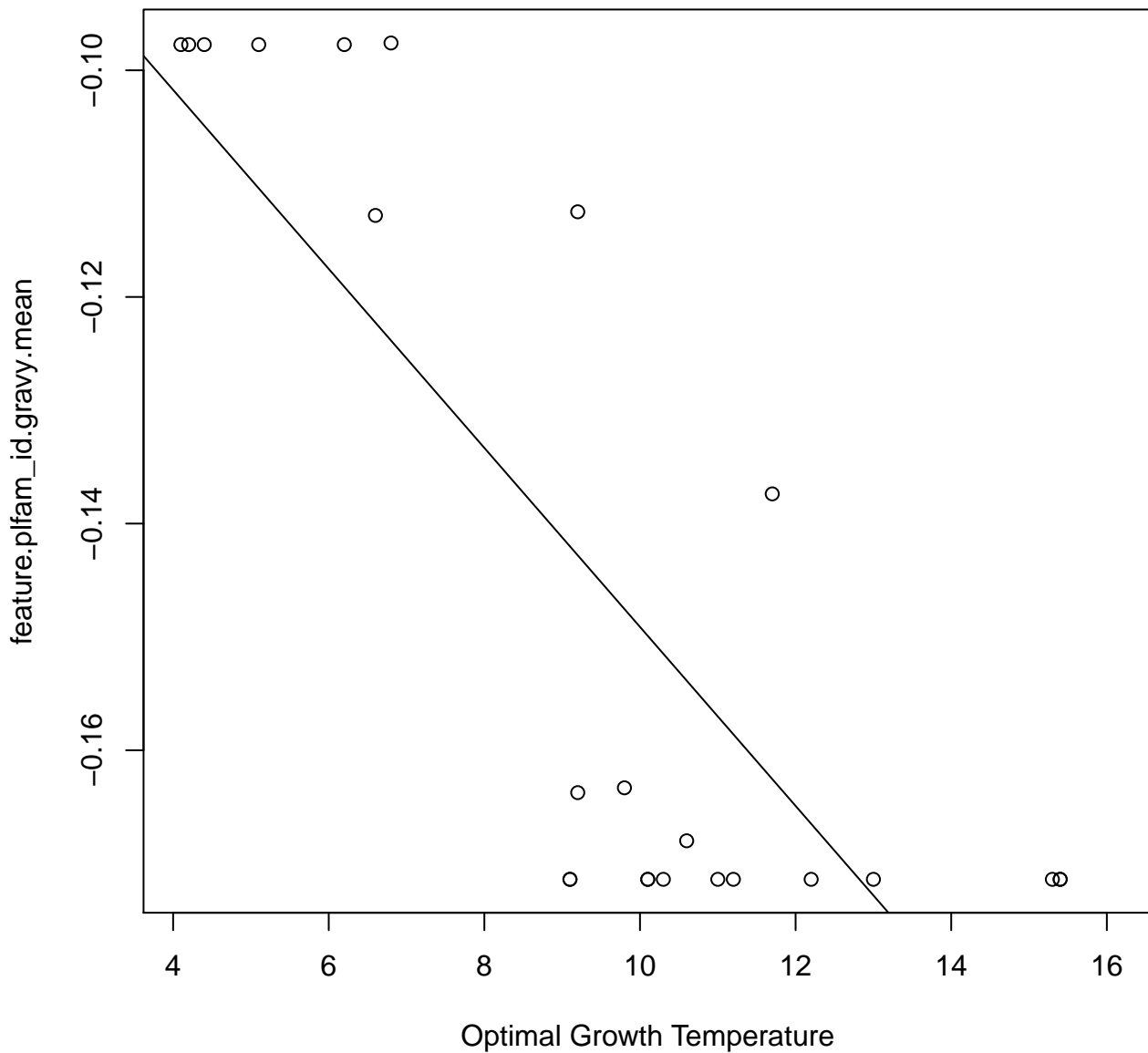
feature.plfam_id.gravy.mean
PLF_28228_00001635
DNA-binding transcriptional regulator, MocR family / aminotransferase domain



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



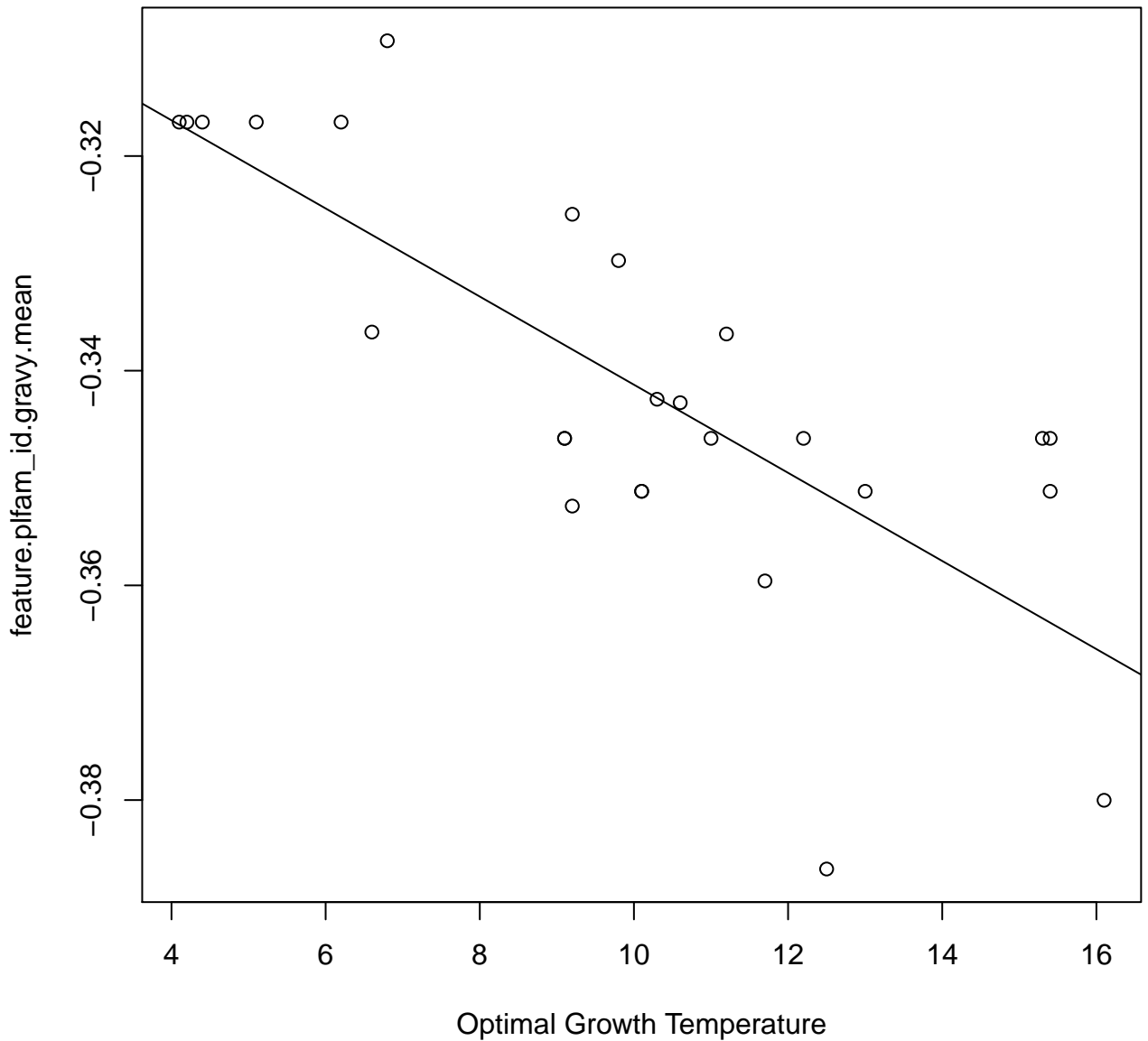
feature.plfam_id.gravy.mean
PLF_28228_00002064
Signal transduction histidine kinase CheA



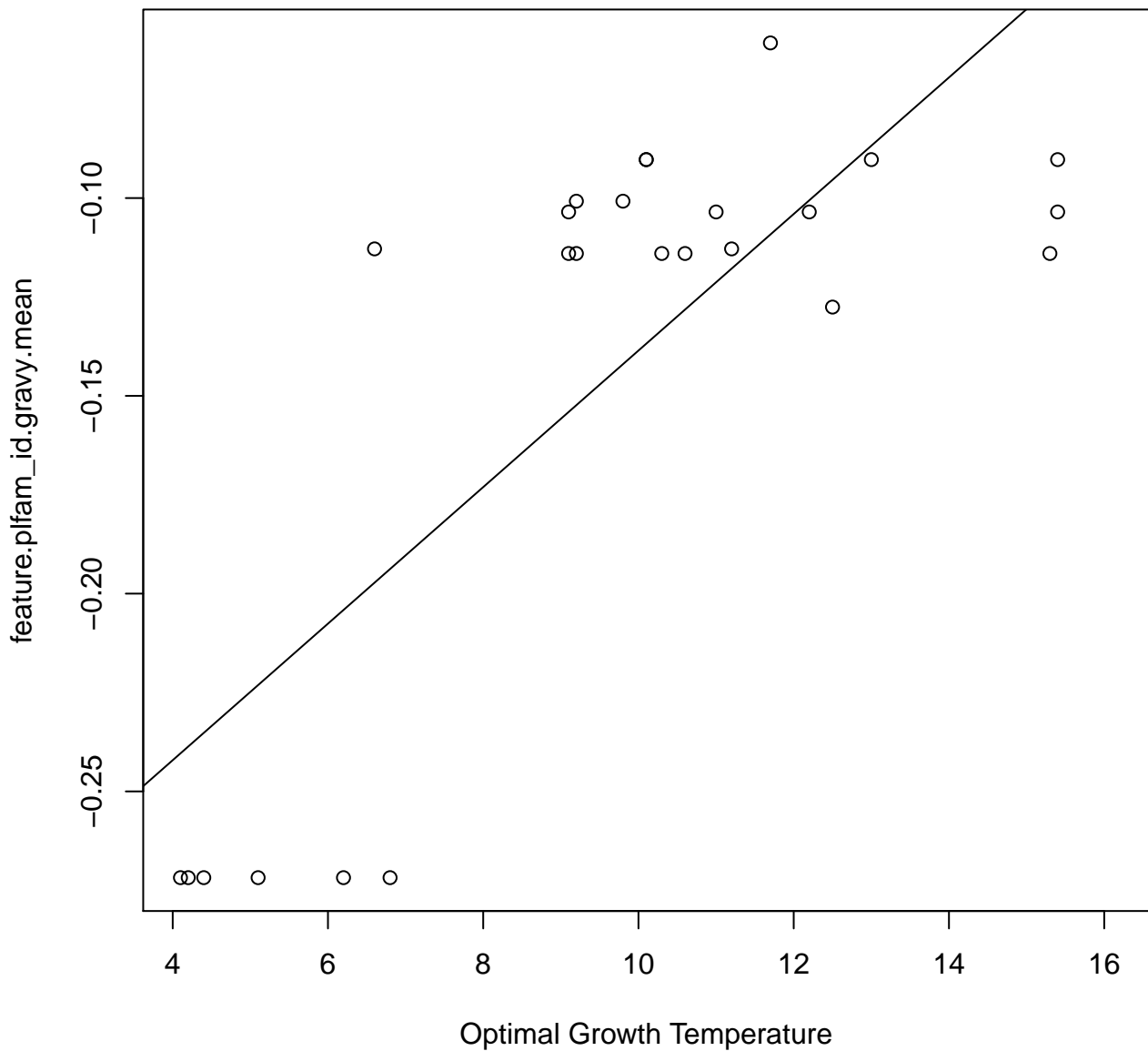
feature.plfam_id.gravy.mean

PLF_28228_00002160

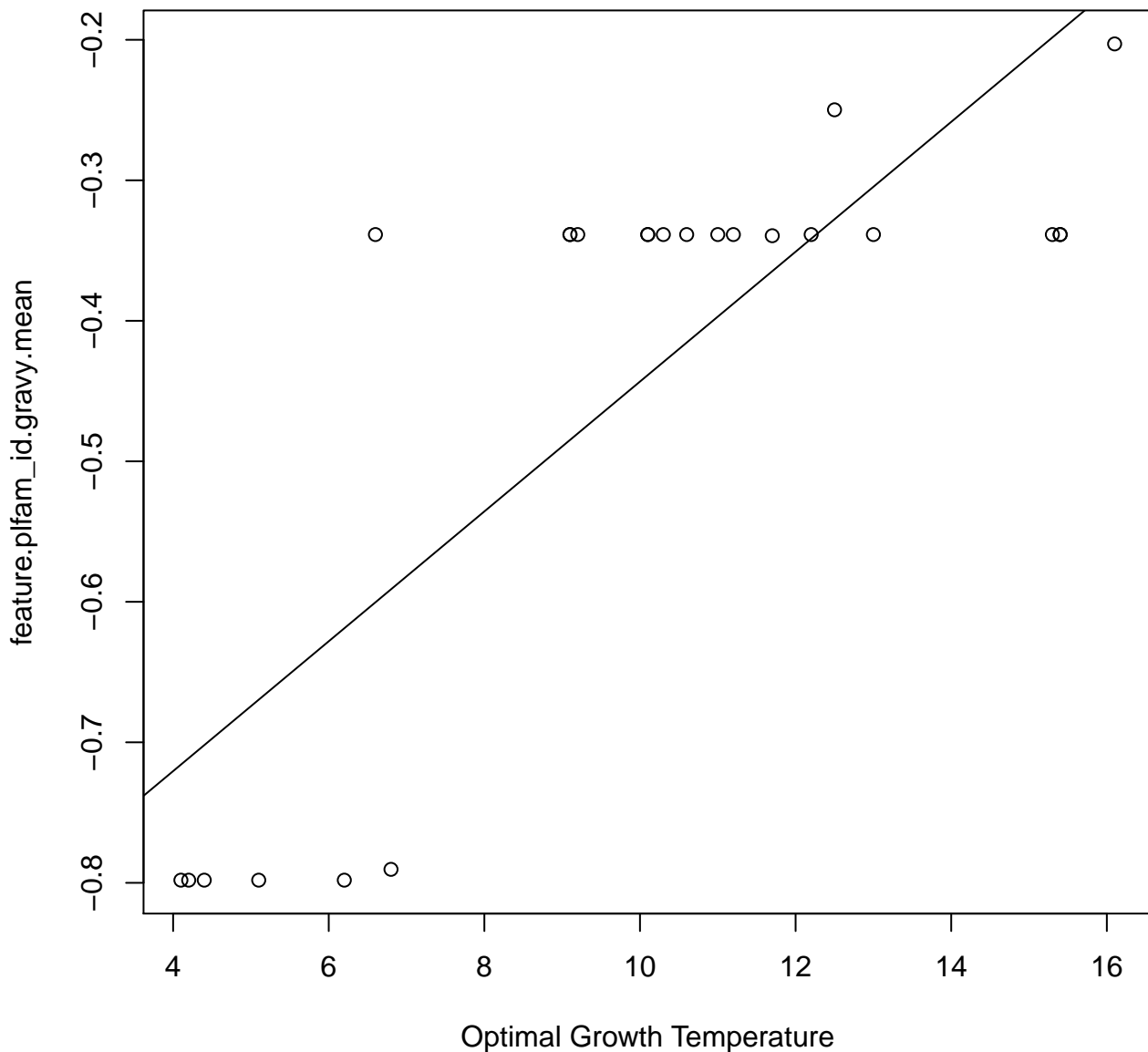
Two-component system sensor histidine kinase/response regulator hybrid



feature.plfam_id.gravy.mean
PLF_28228_00002434
hypothetical protein



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

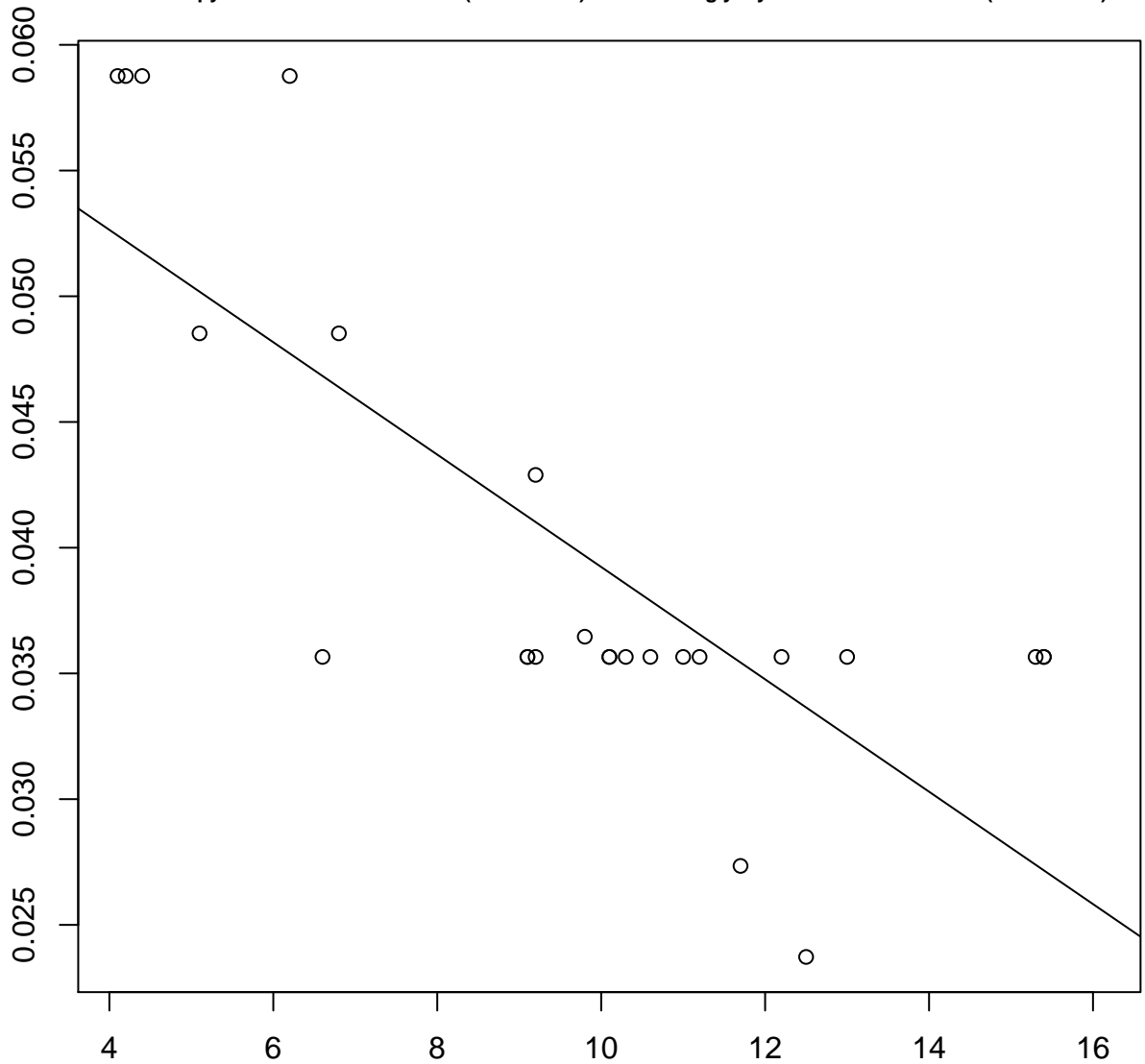


feature.plfam_id.gravy.mean

PLF_28228_00002818

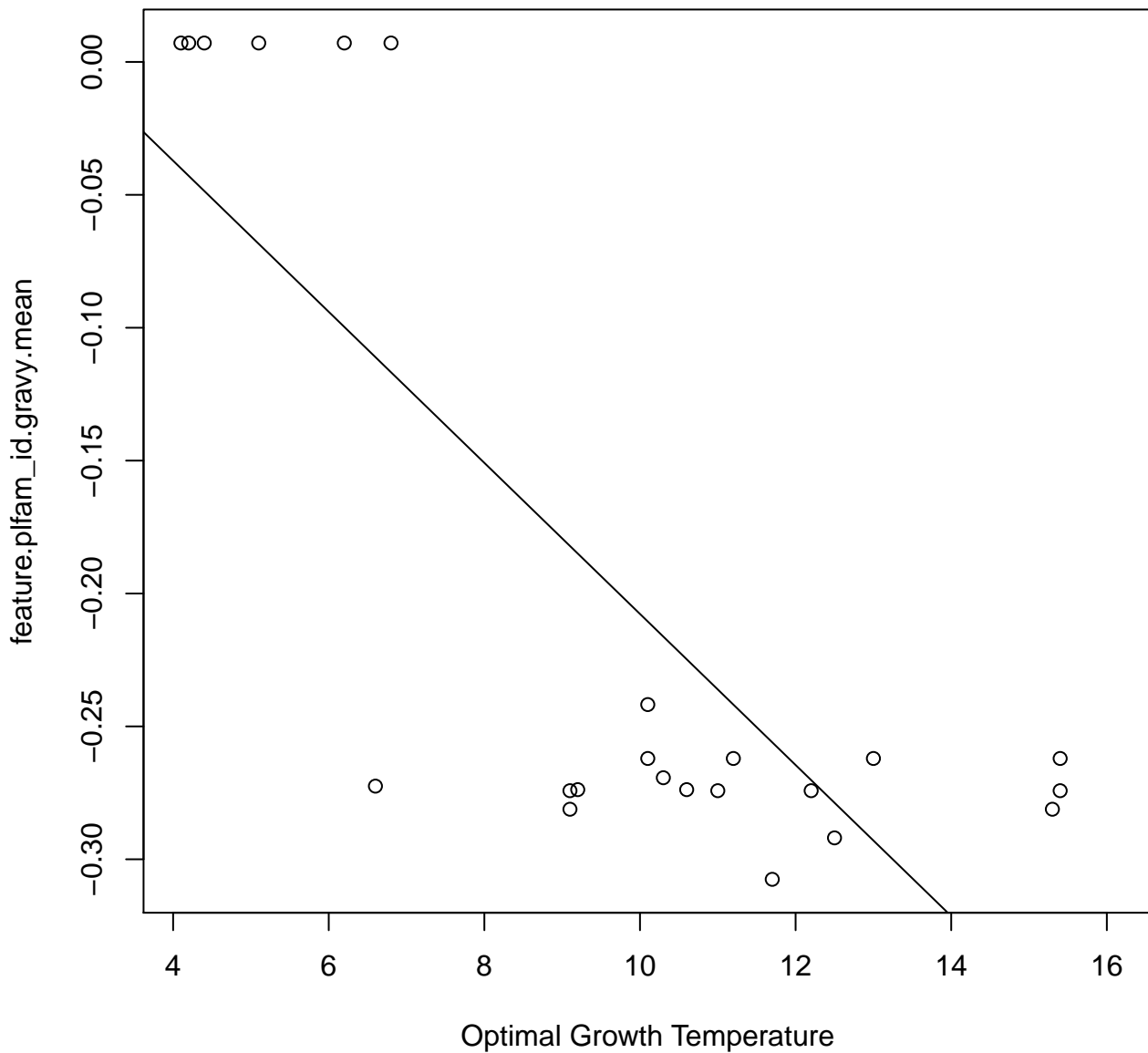
Serine--pyruvate aminotransferase (EC 2.6.1.51) / L-alanine:glyoxylate aminotransferase (EC 2.6.1.44)

feature.plfam_id.gravy.mean

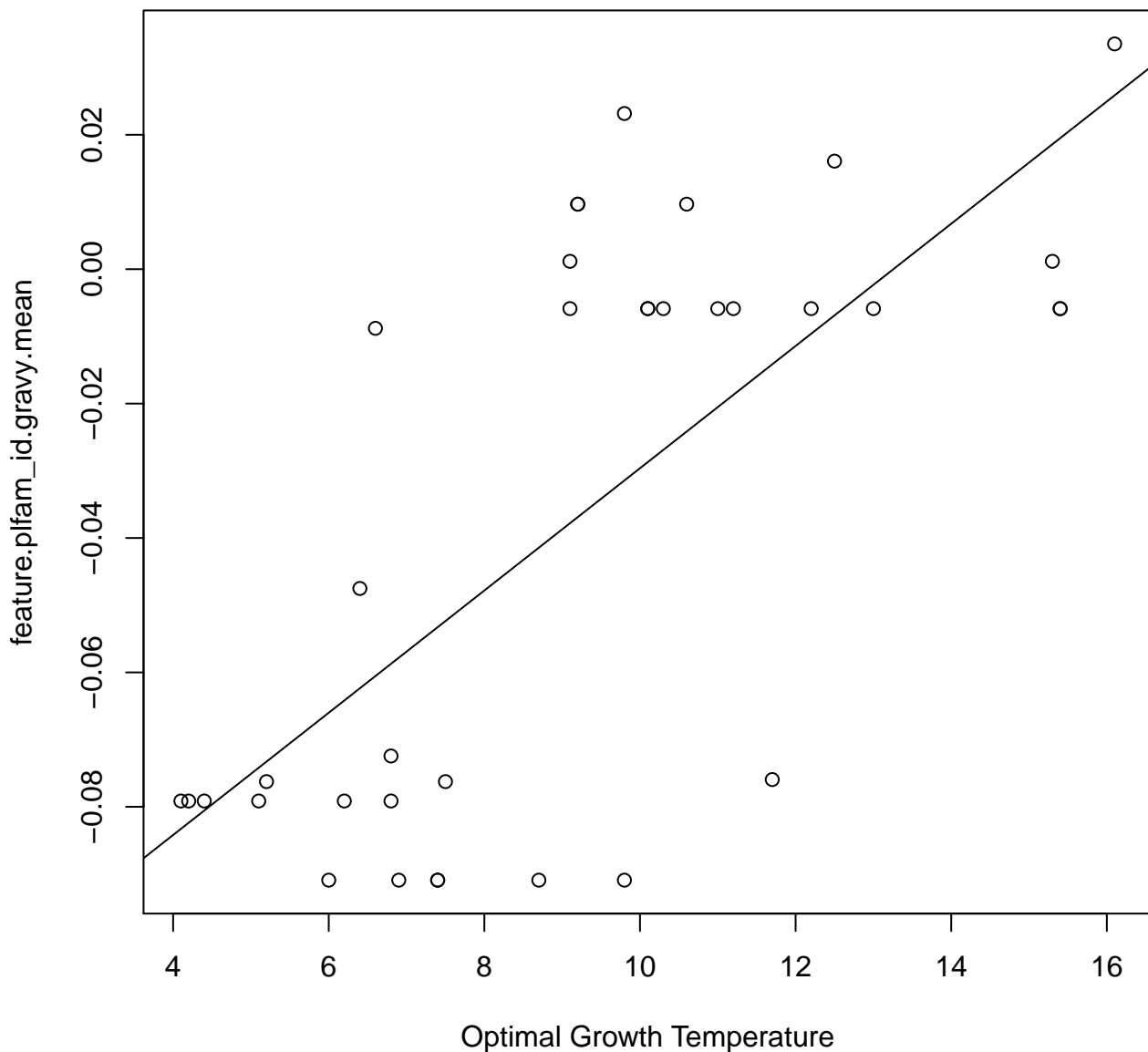


Optimal Growth Temperature

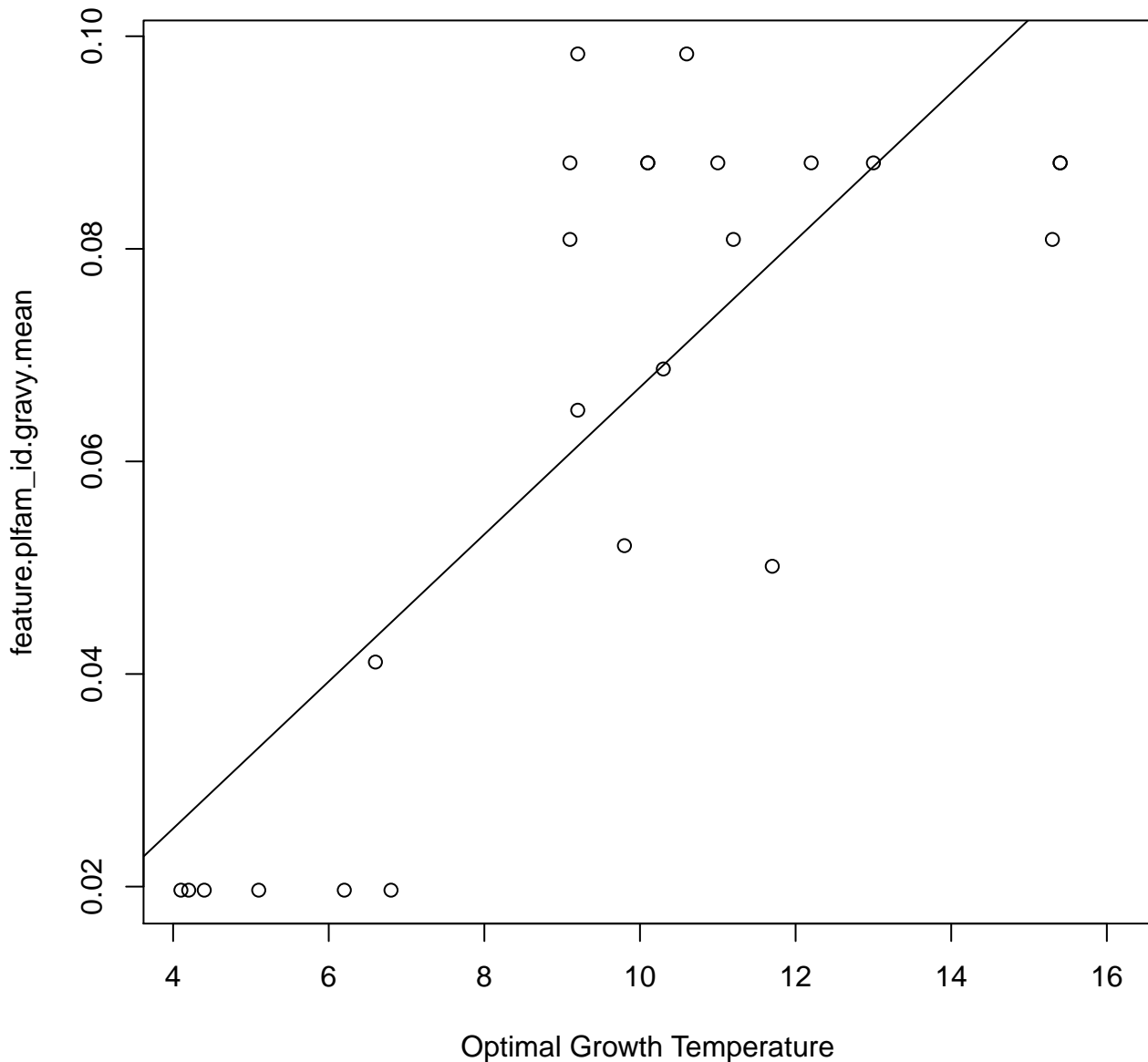
feature.plfam_id.gravy.mean
PLF_28228_00002829
TonB-dependent receptor



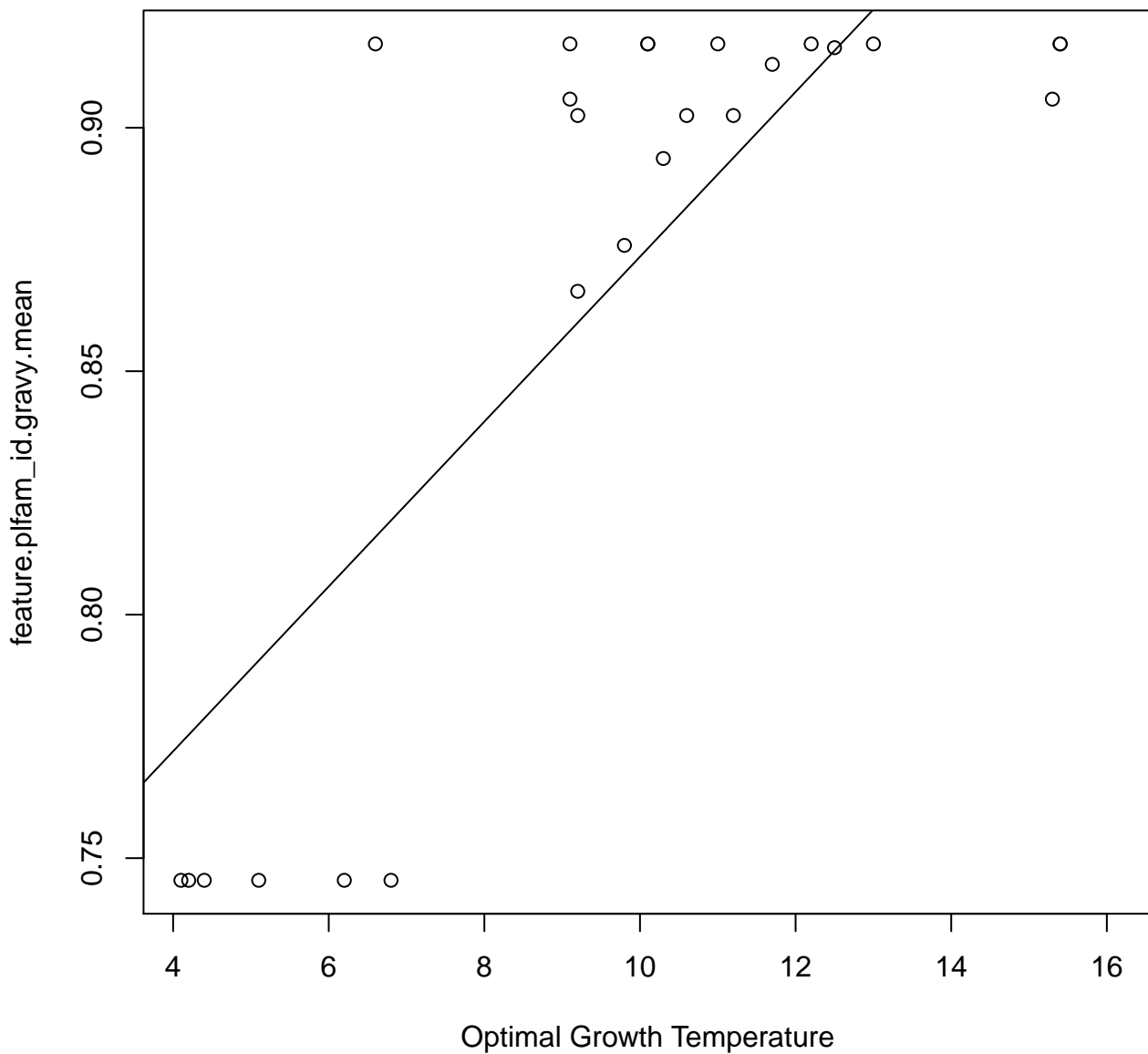
feature.plfam_id.gravy.mean
PLF_28228_00003170
Zinc-type alcohol dehydrogenase-like protein



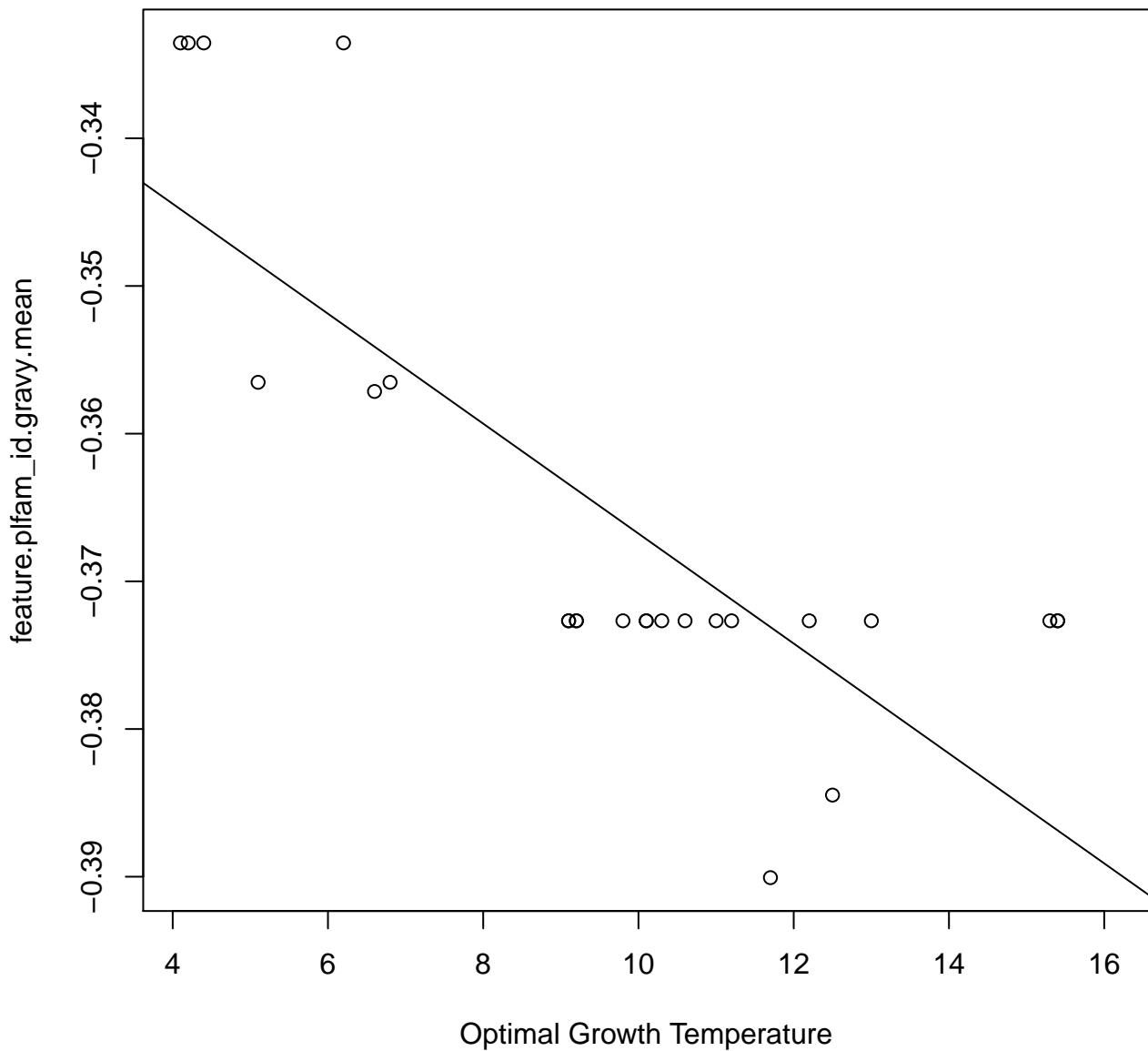
feature.plfam_id.gravy.mean
PLF_28228_00003565
Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)



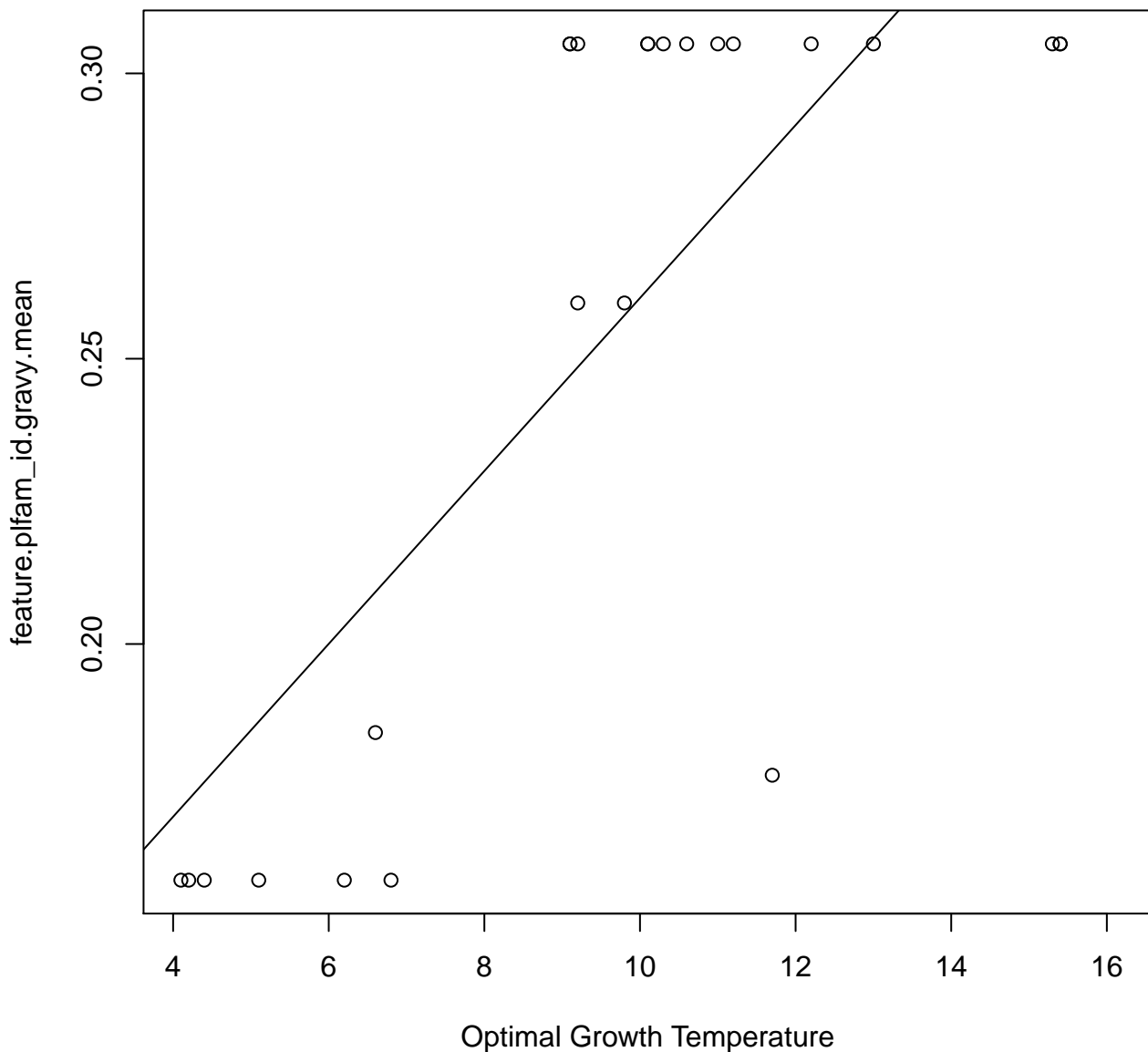
feature.plfam_id.gravy.mean
PLF_28228_00003803
ZIP zinc transporter family protein



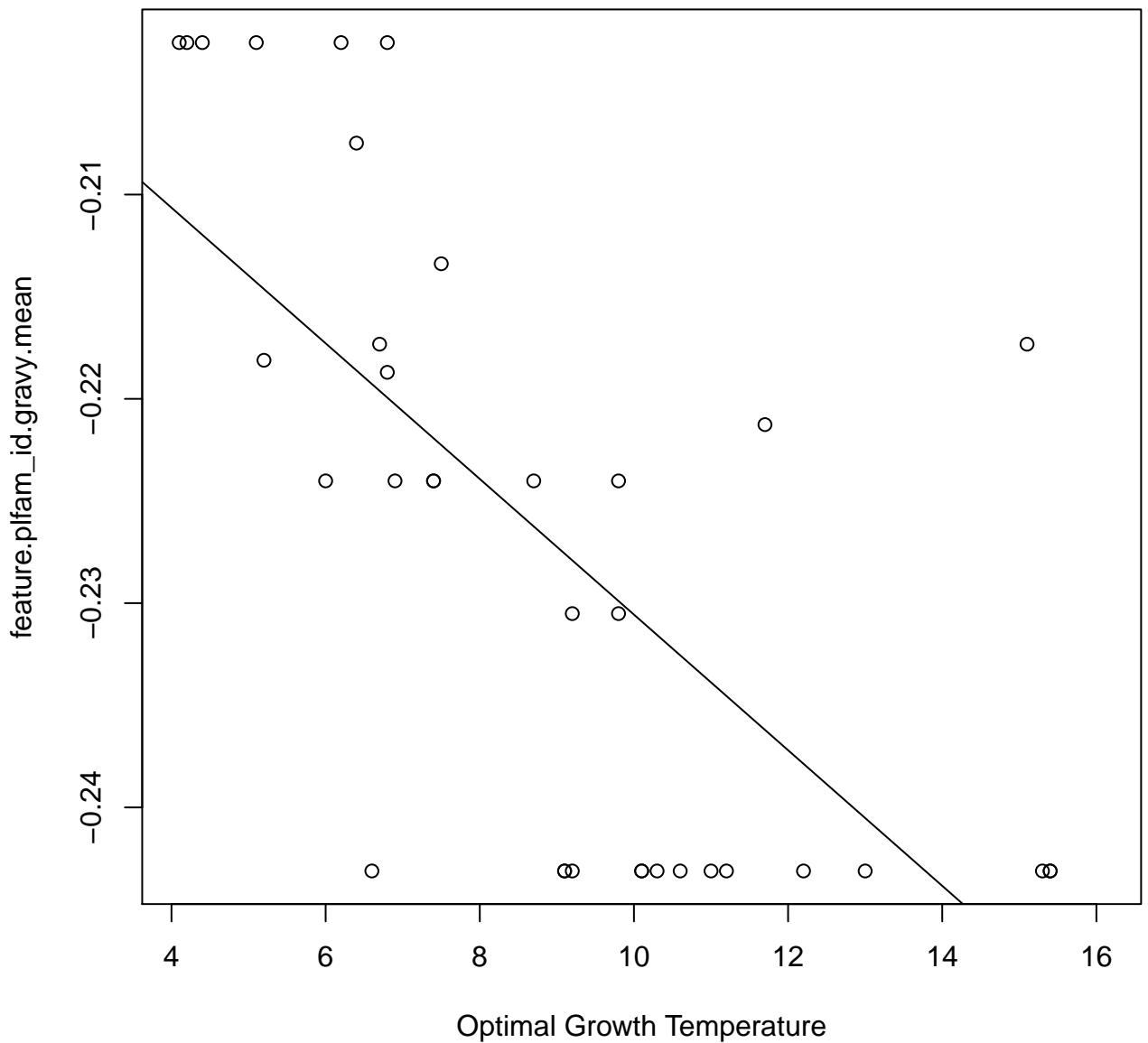
feature.plfam_id.gravy.mean
PLF_28228_00003922
hypothetical protein



feature.plfam_id.gravy.mean
PLF_28228_00005496
Positive regulator of CheA protein activity (CheW)



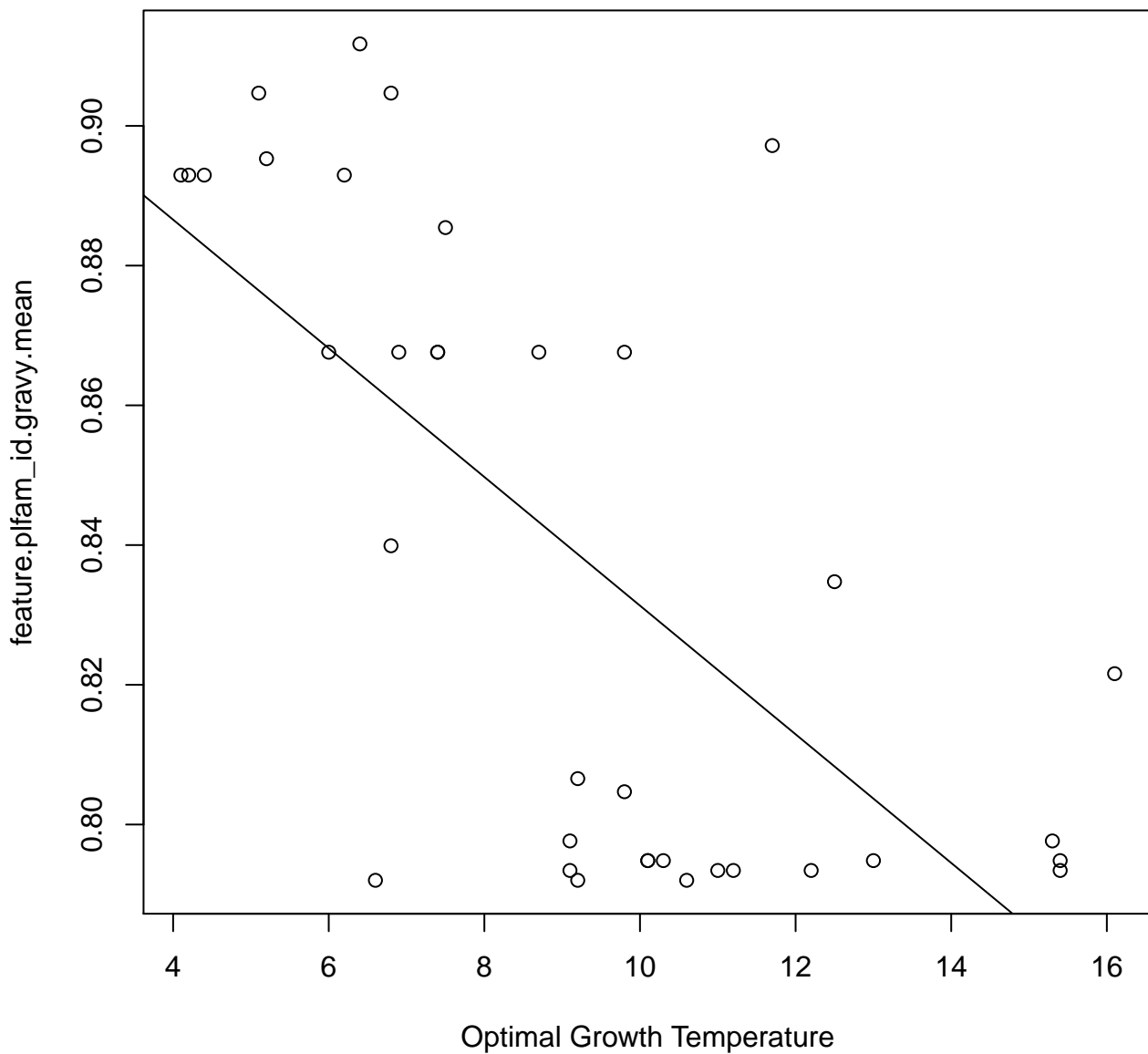
feature.plfam_id.gravy.mean
PLF_28228_00006965
Carbon-nitrogen hydrolase



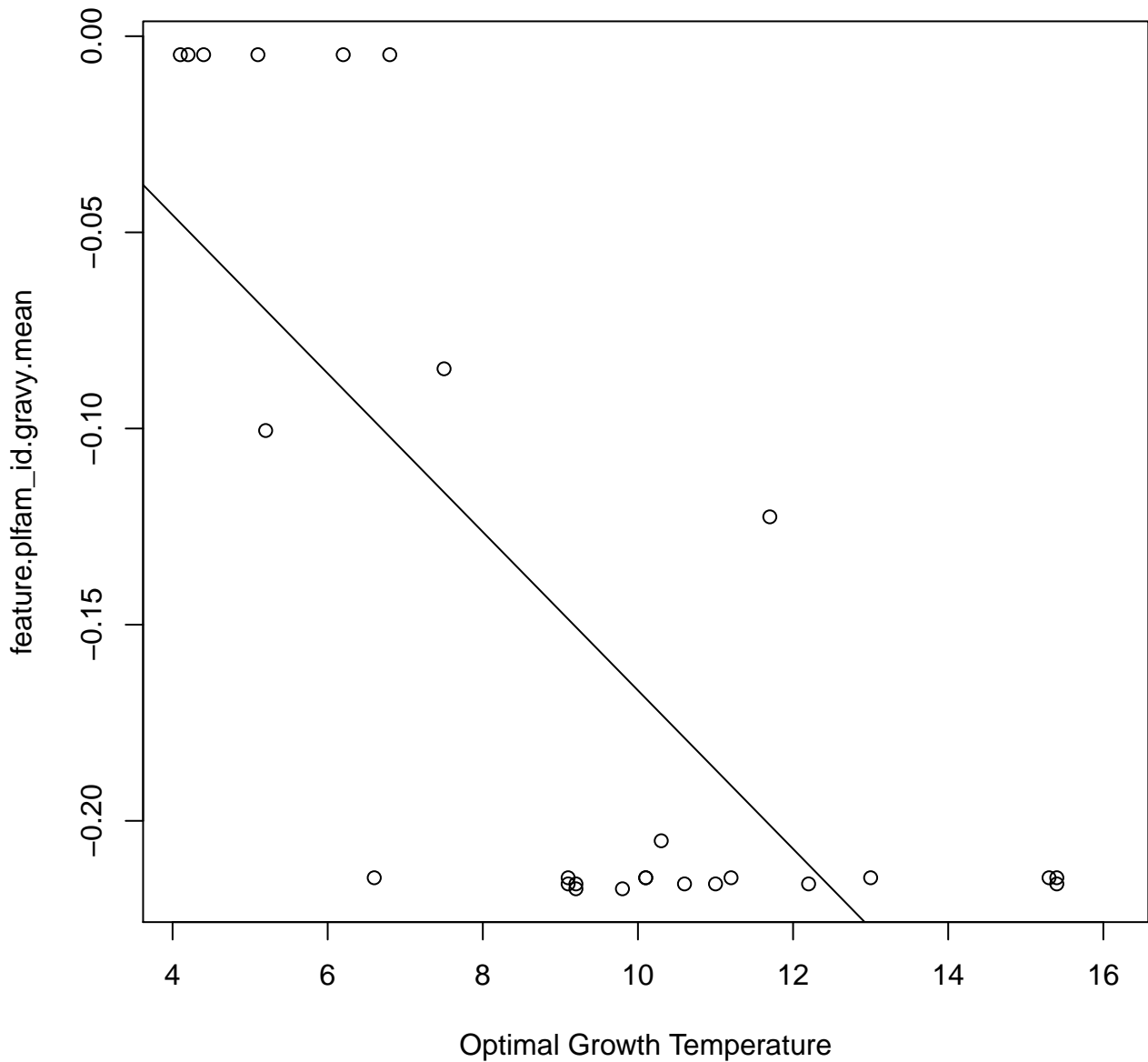
feature.plfam_id.gravy.mean

PLF_28228_00007491

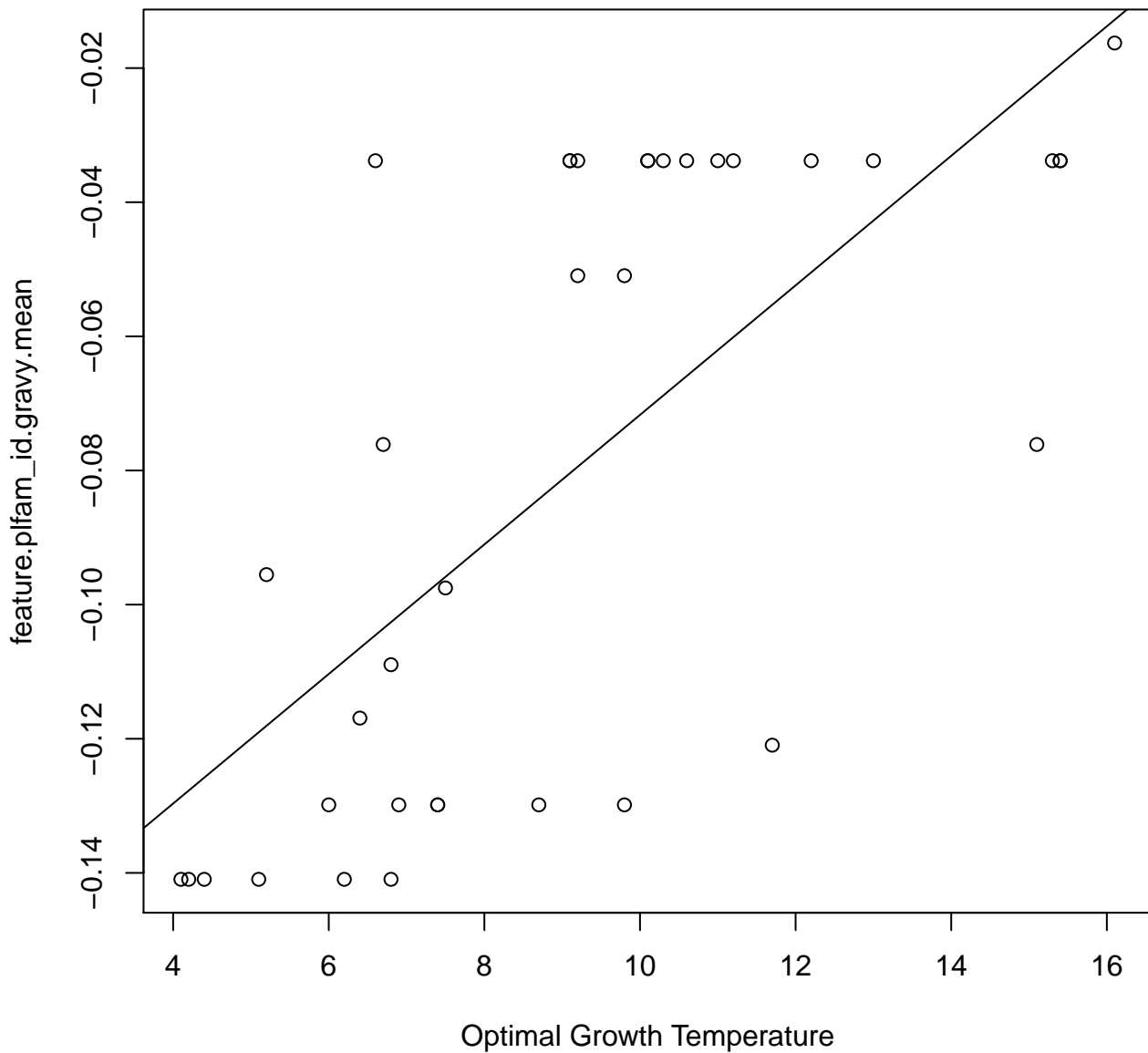
Threonine efflux protein



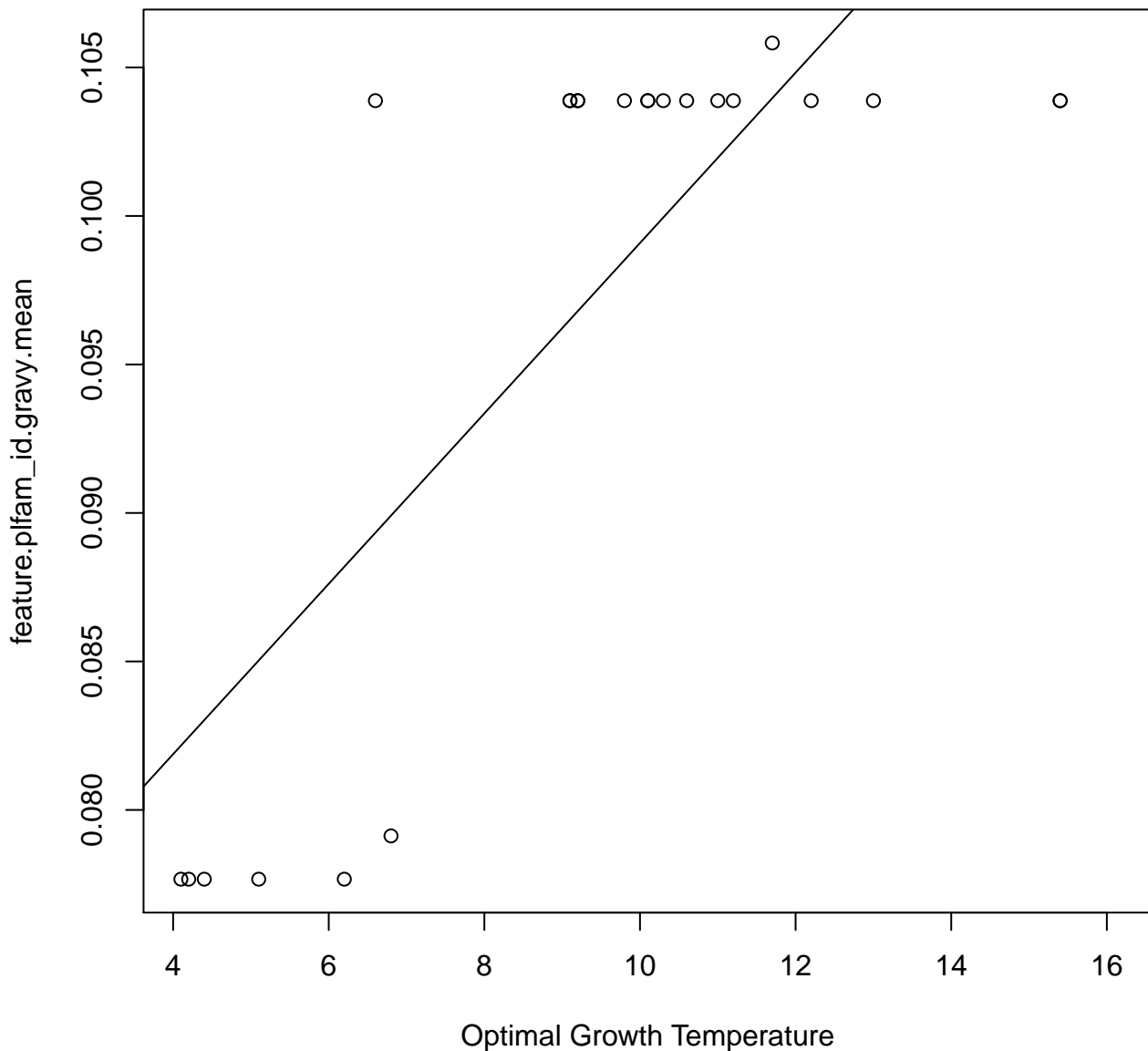
feature.plfam_id.gravy.mean
PLF_28228_00008631
hypothetical protein



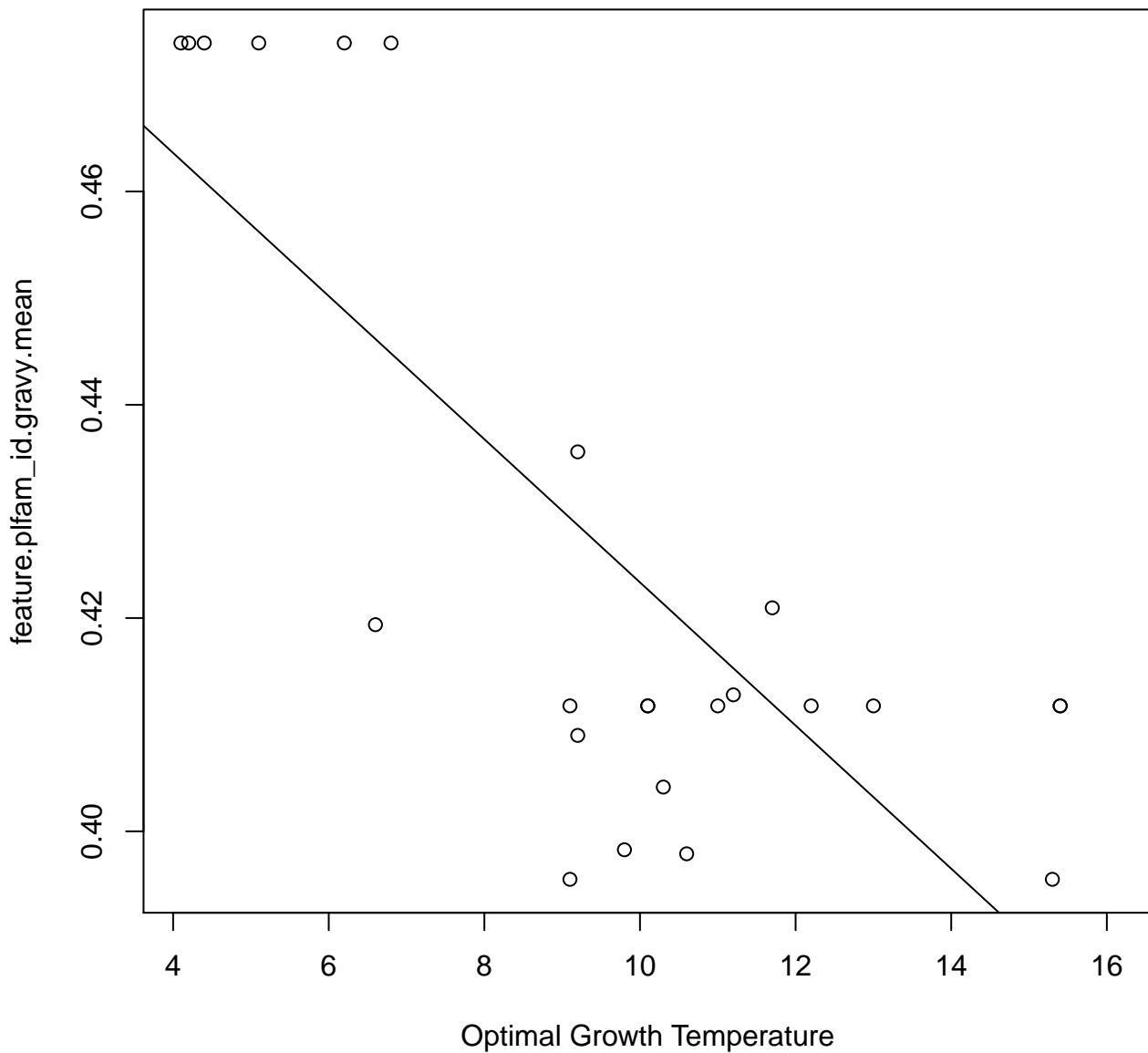
feature.plfam_id.gravy.mean
PLF_28228_00011313
hypothetical protein



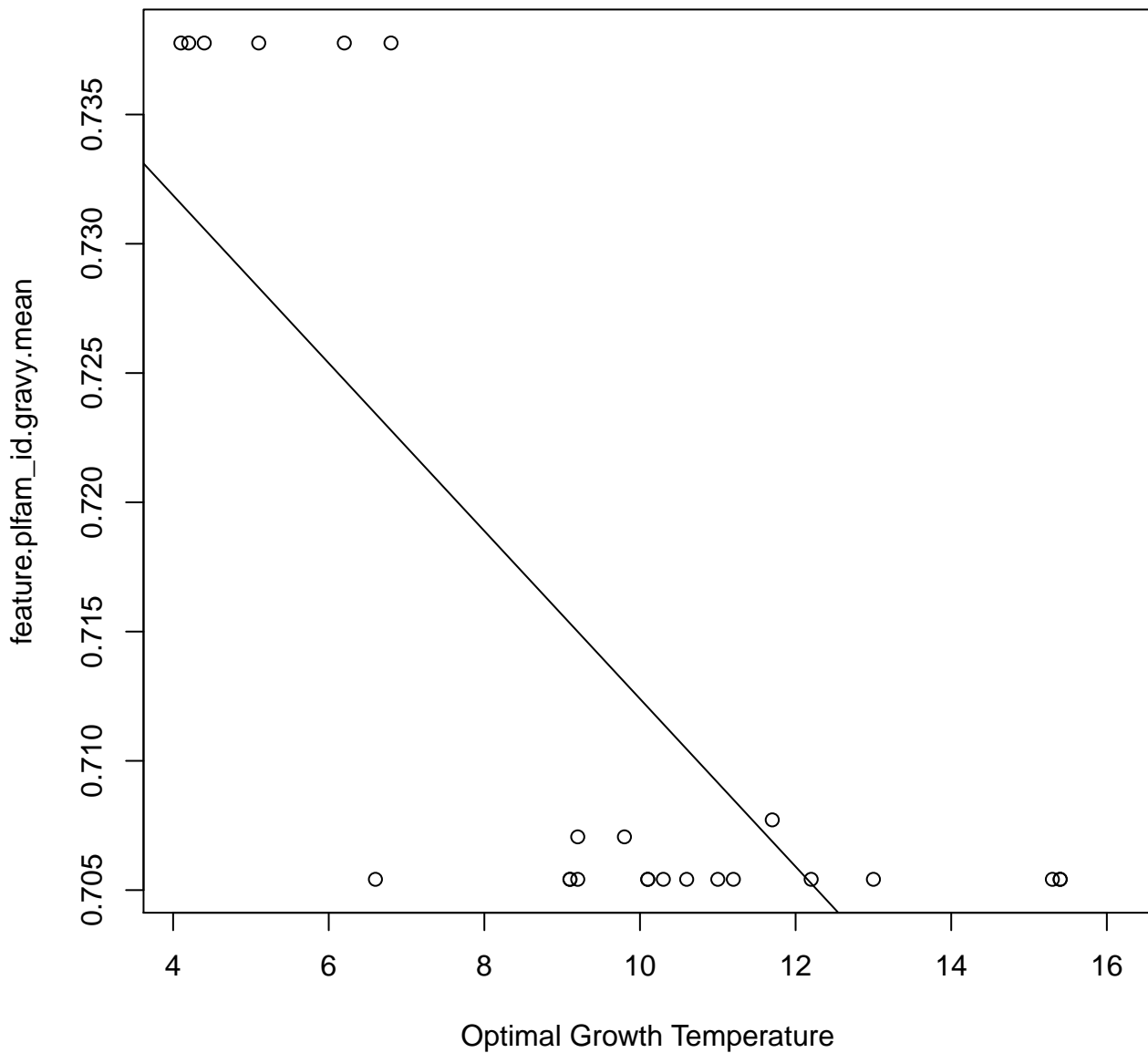
feature.plfam_id.gravy.mean
PLF_28228_00015263
hypothetical protein



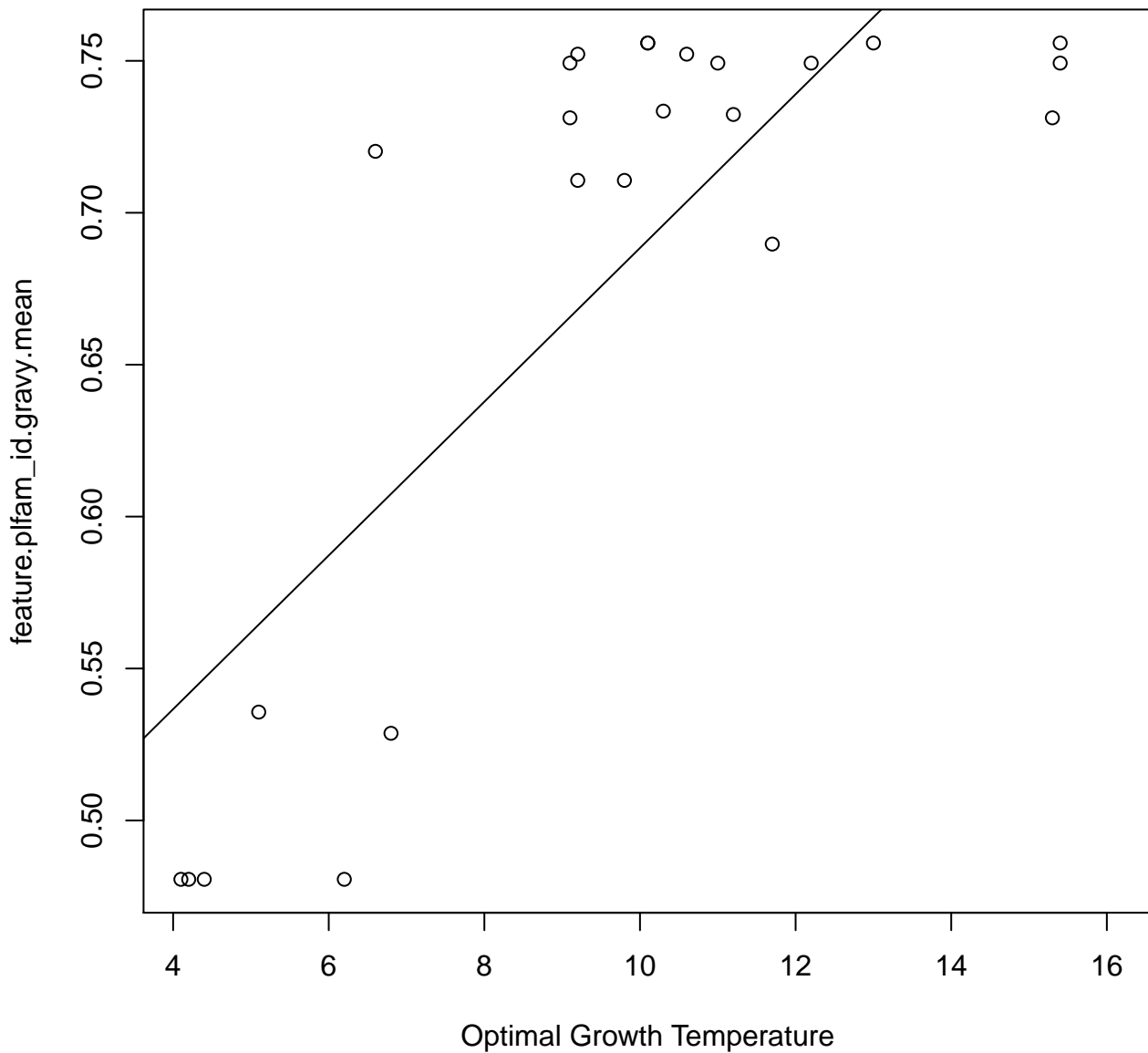
feature.plfam_id.gravy.mean
PLF_28228_00016239
Response regulator receiver protein



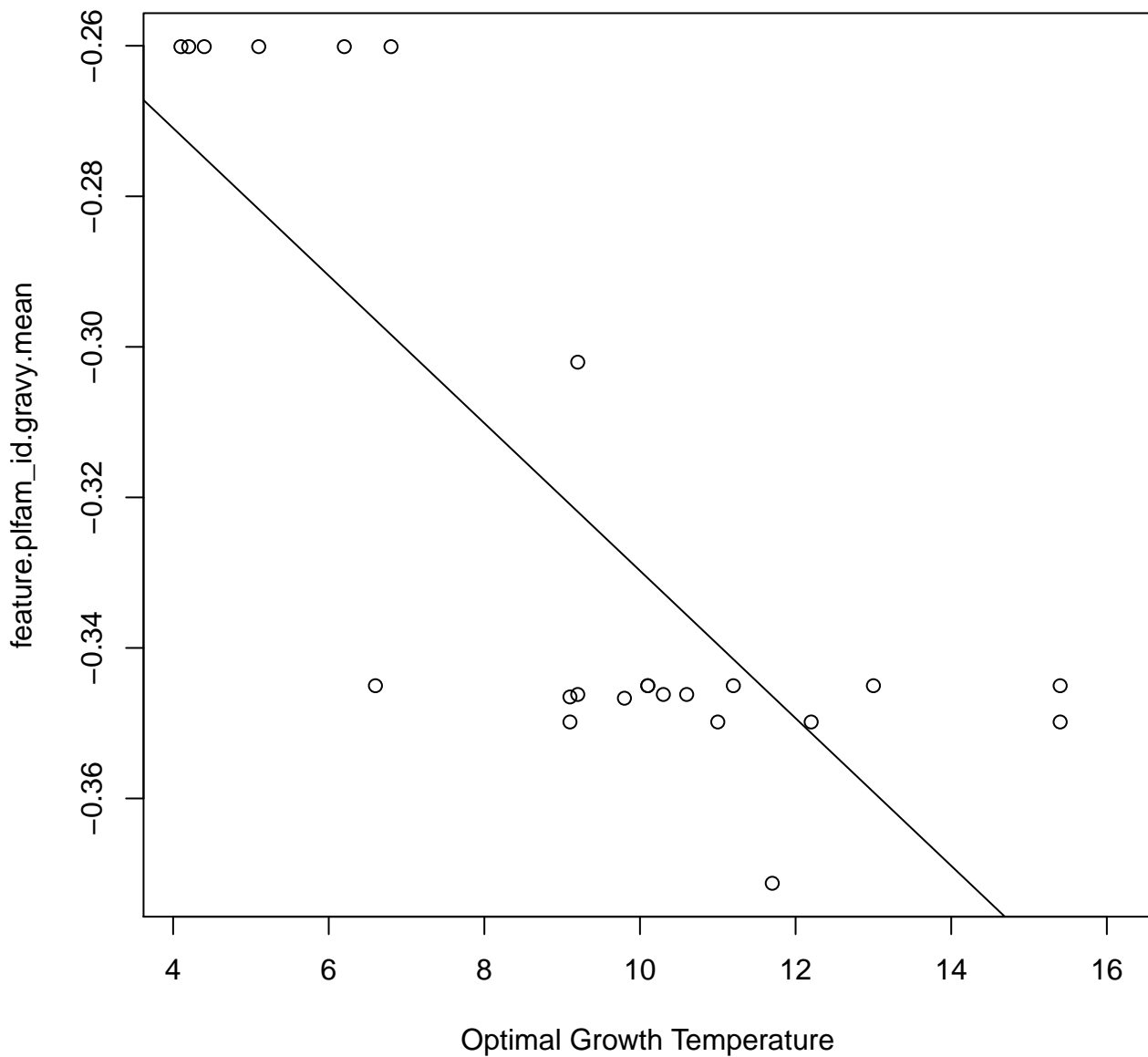
feature.plfam_id.gravy.mean
PLF_28228_00016373
TrkA-C domain protein



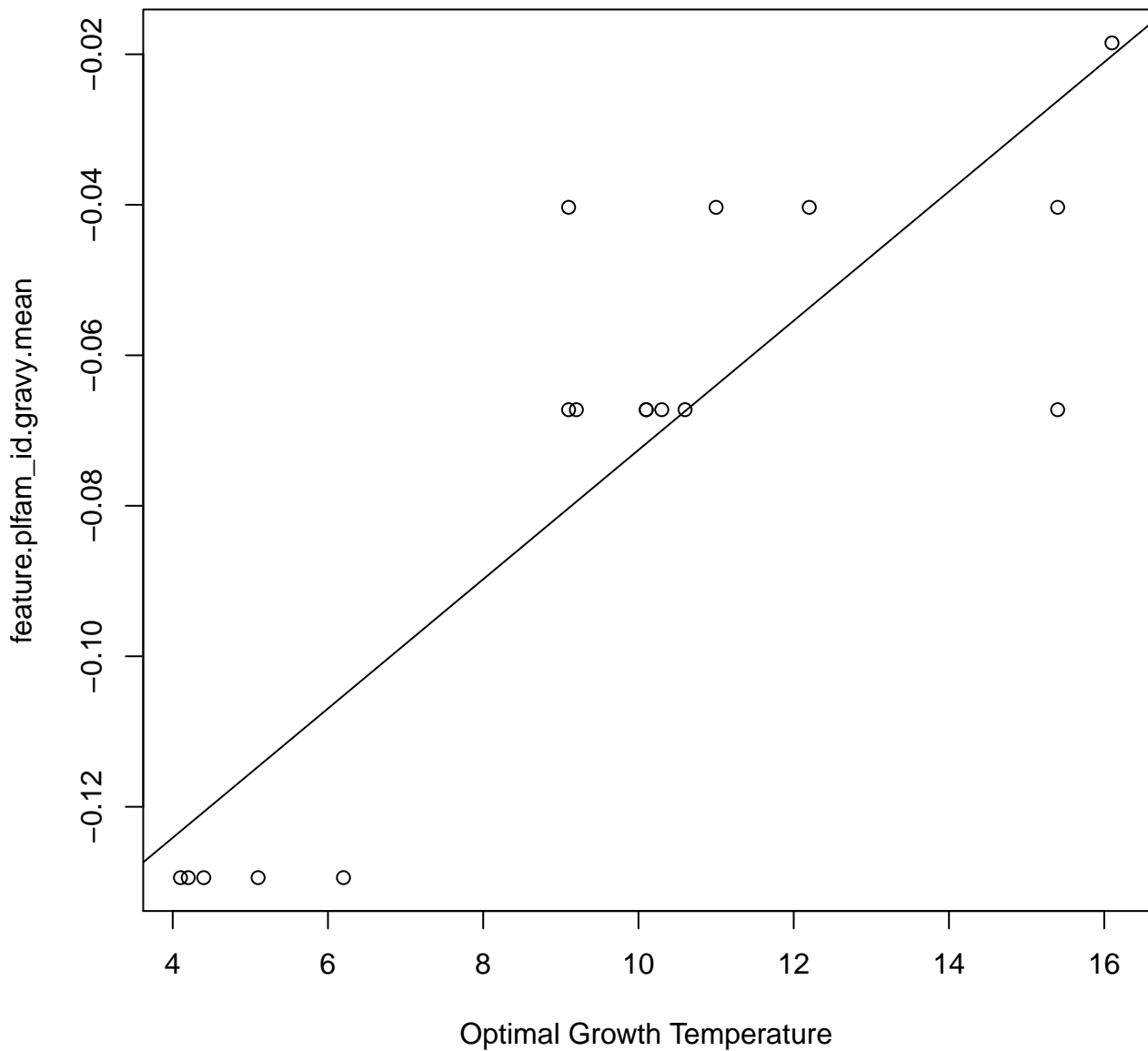
feature.plfam_id.gravy.mean
PLF_28228_00016648
hypothetical protein



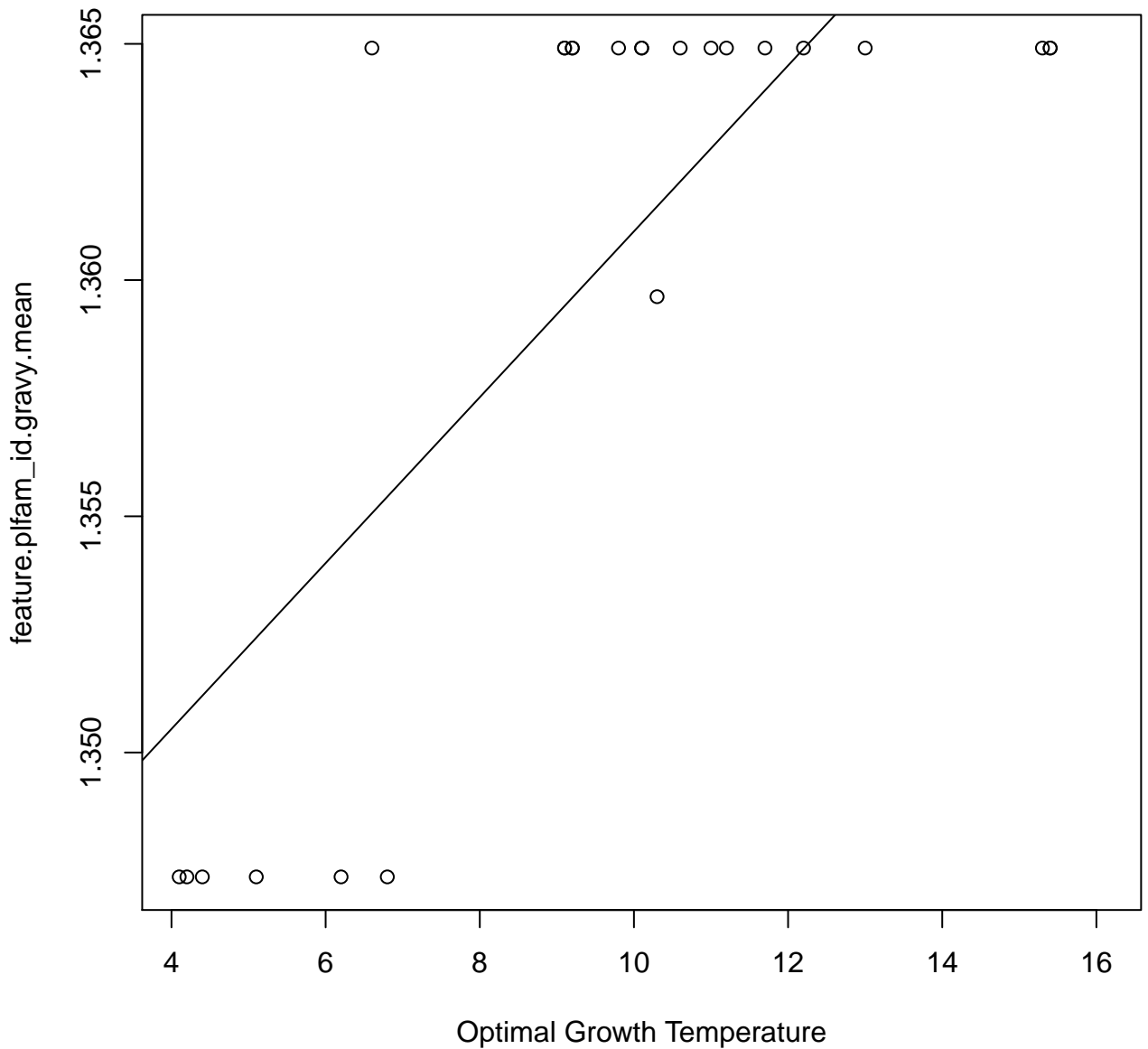
feature.plfam_id.gravy.mean
PLF_28228_00017455
Maltodextrin glucosidase (EC 3.2.1.20)



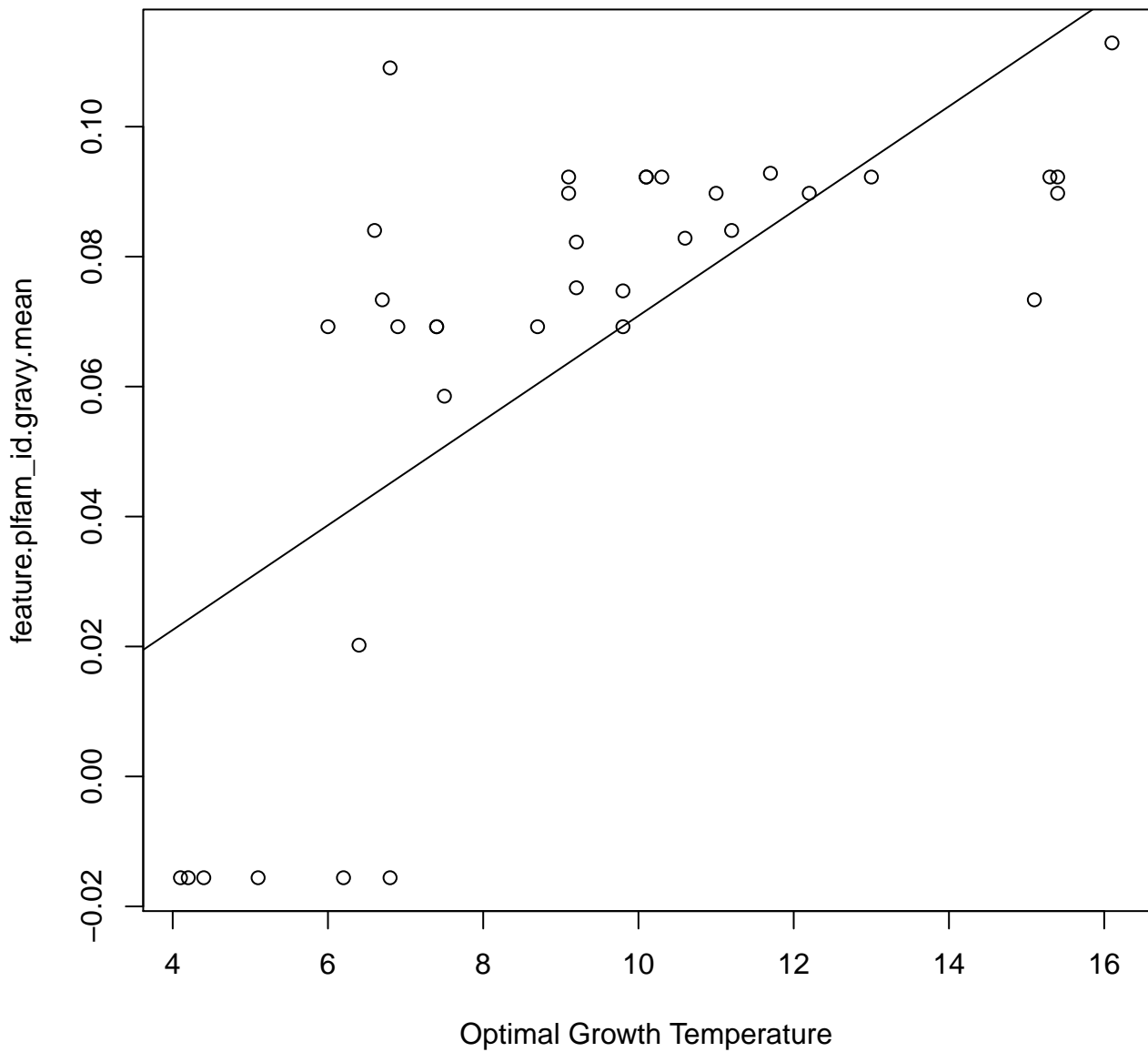
feature.plfam_id.gravy.mean
PLF_28228_00018861
Glyoxalase family protein



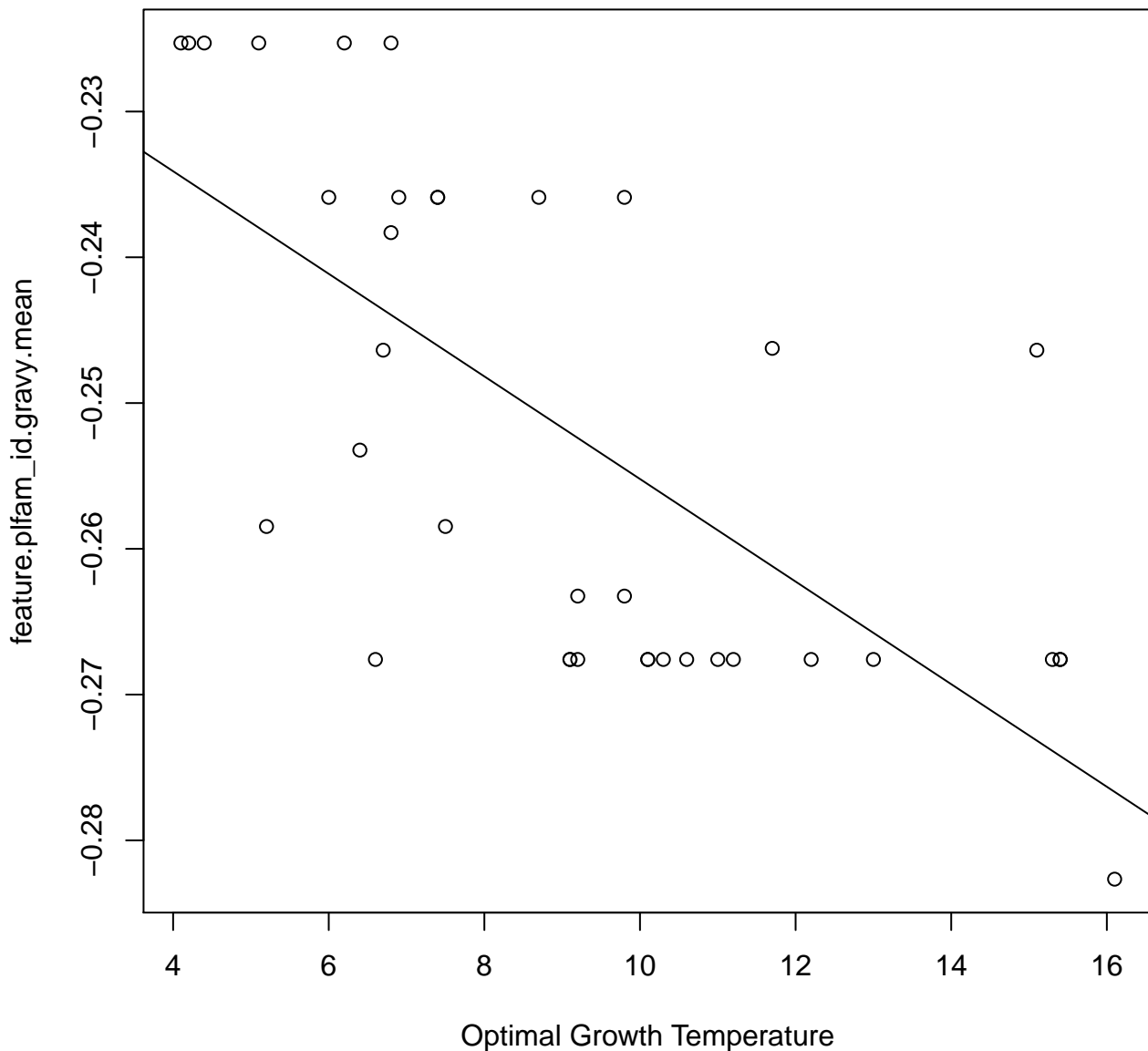
feature.plfam_id.gravy.mean
PLF_28228_00022617
hypothetical protein



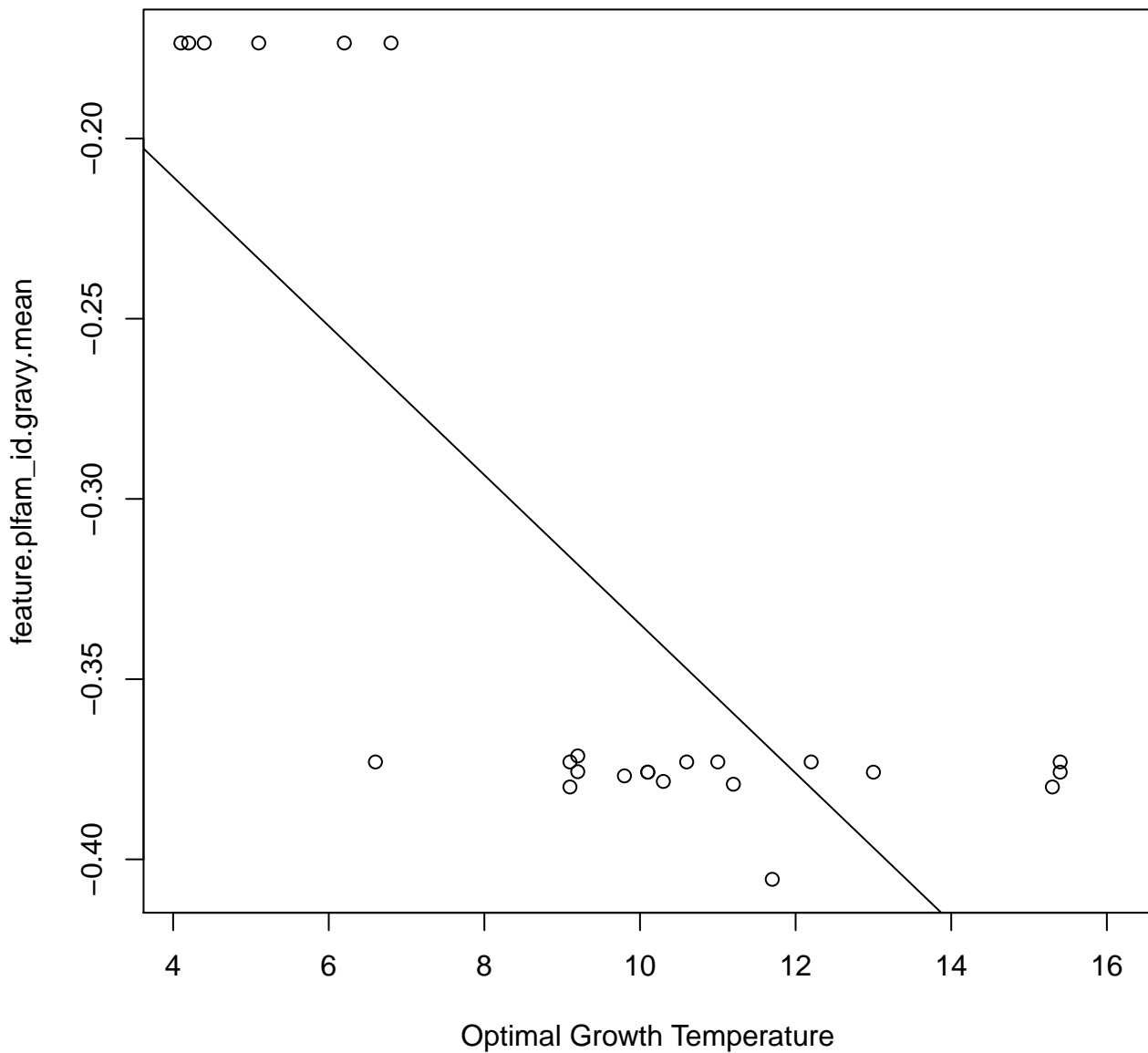
feature.plfam_id.gravy.mean
PLF_28228_00022897
Invasin domain protein



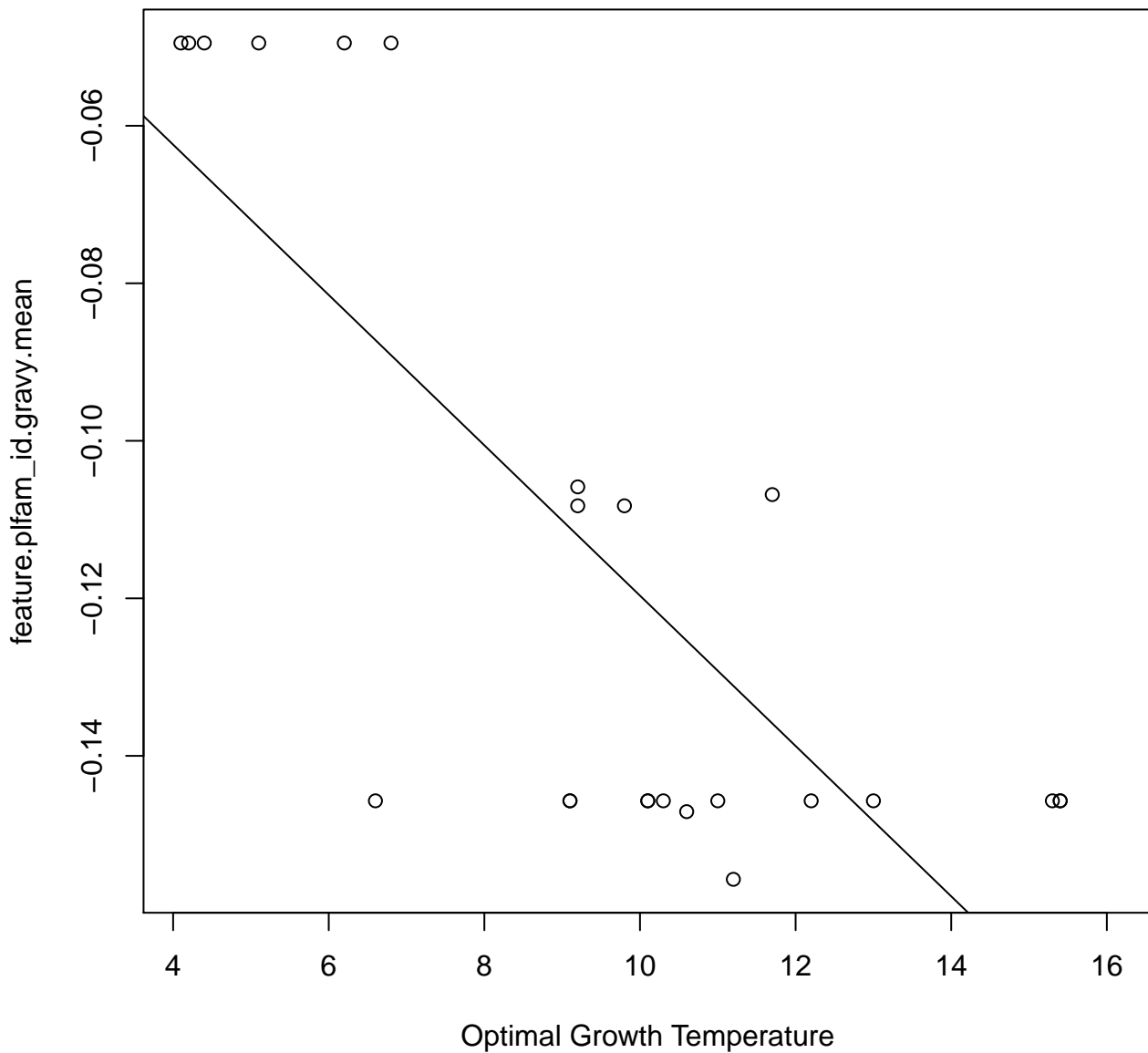
feature.plfam_id.gravy.mean
PLF_28228_00027836
16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)



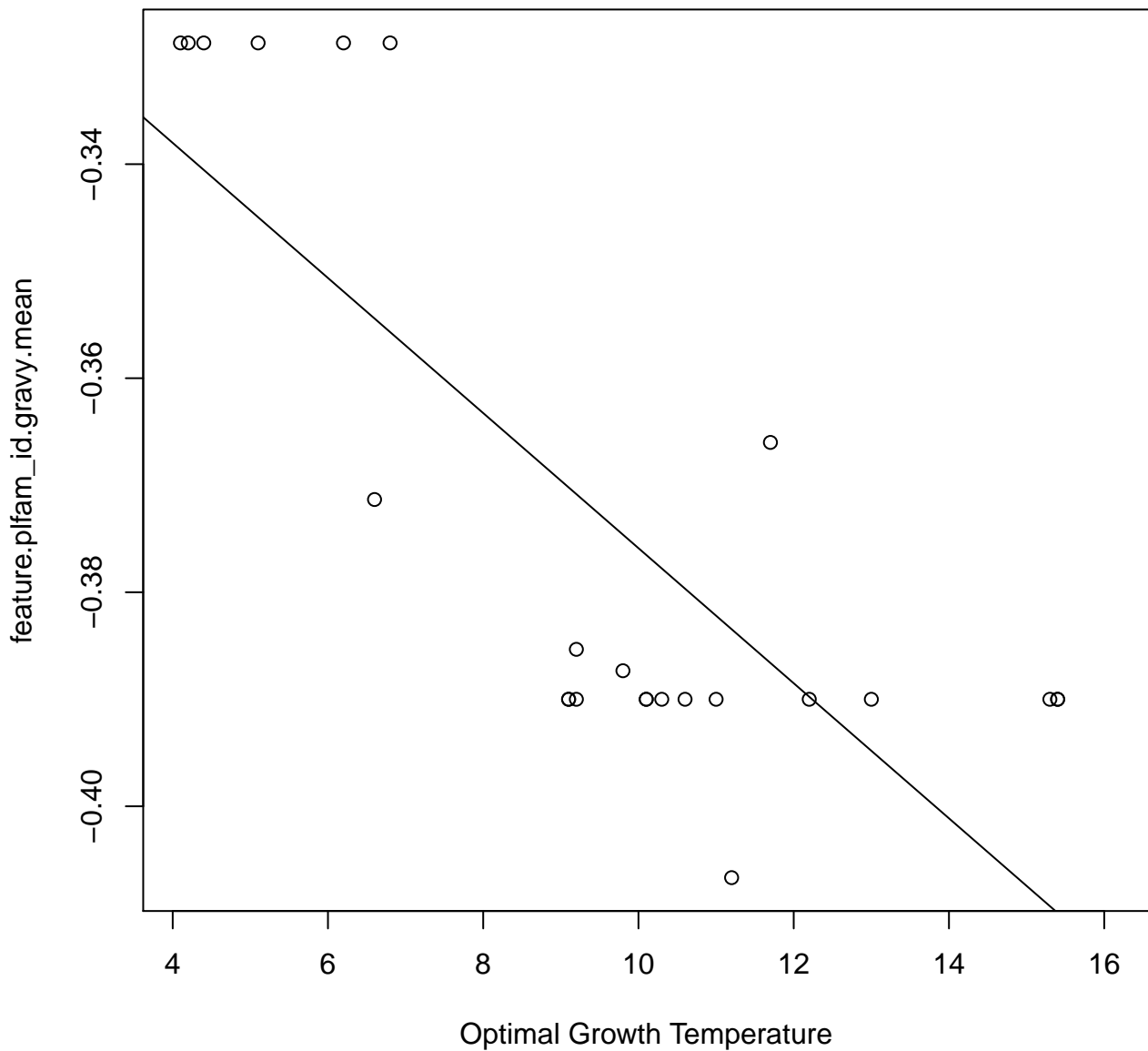
feature.plfam_id.gravy.mean
PLF_28228_00028047
Fatty acid cis/trans isomerase



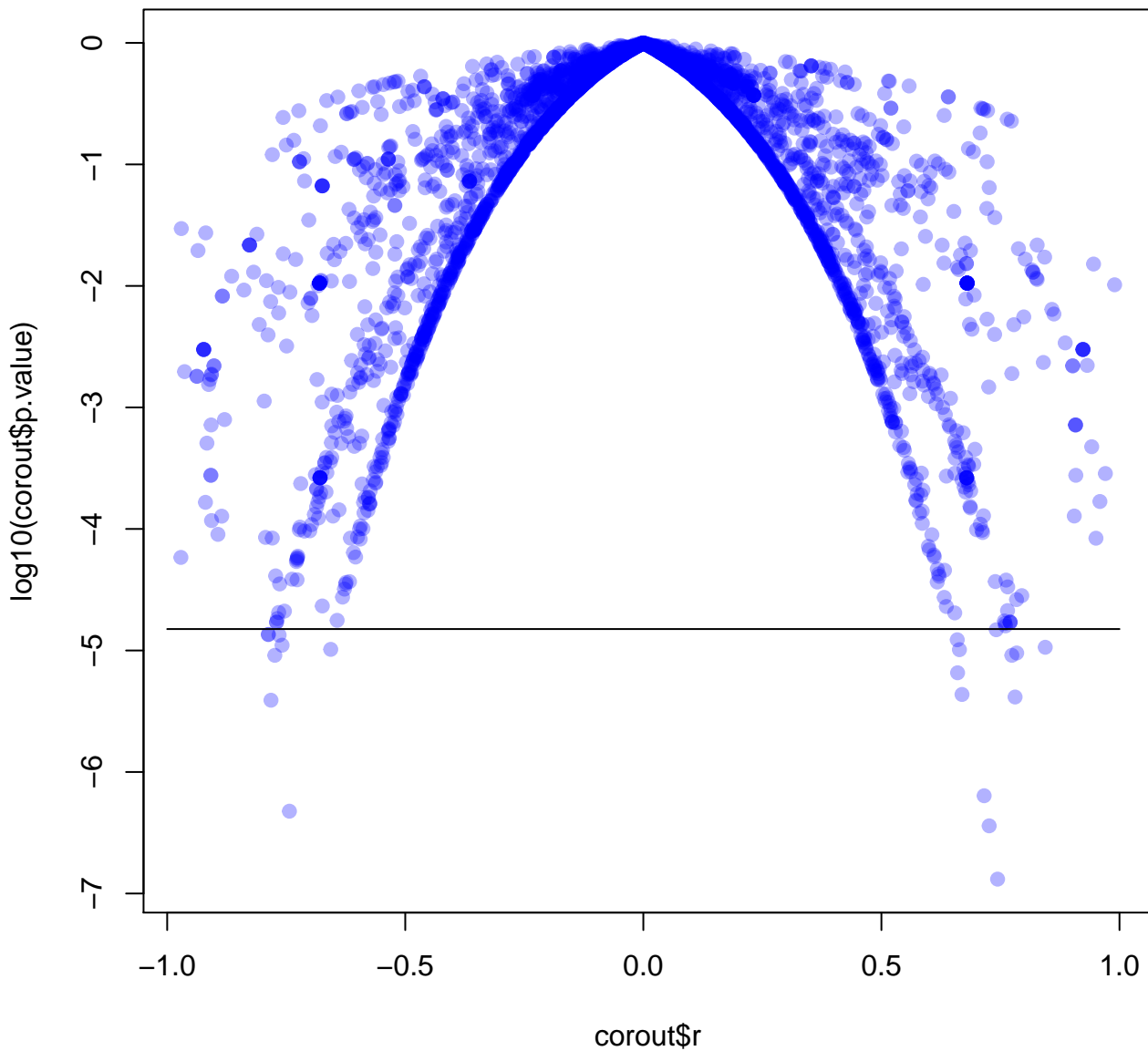
feature.plfam_id.gravy.mean
PLF_28228_00028713
Transcriptional regulator VCA1020, LysR family



feature.plfam_id.gravy.mean
PLF_28228_00030040
hypothetical protein



feature.pgfam_id.proline_residue.mean

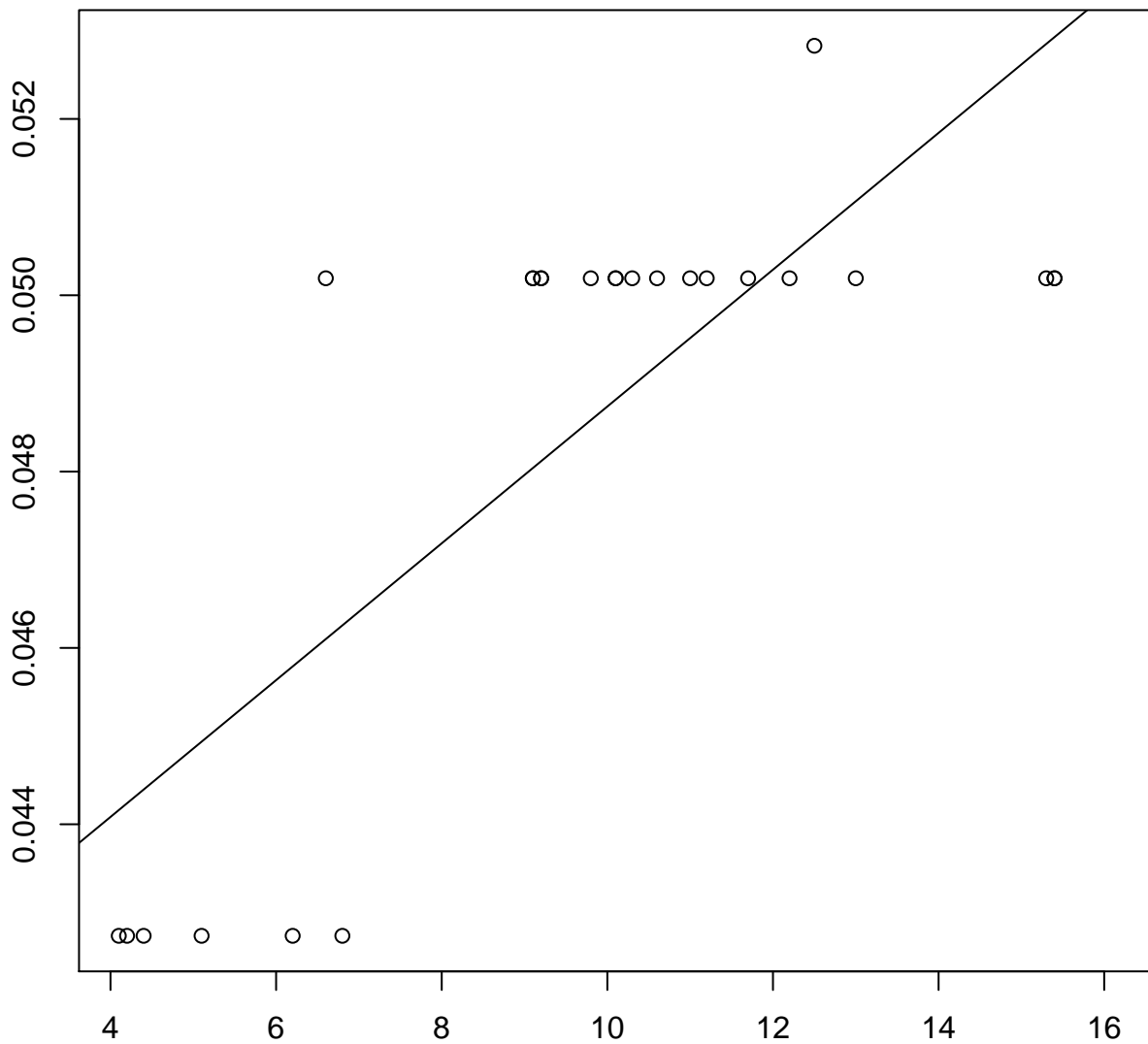


feature.pgfam_id.proline_residue.mean

PGF_00004056

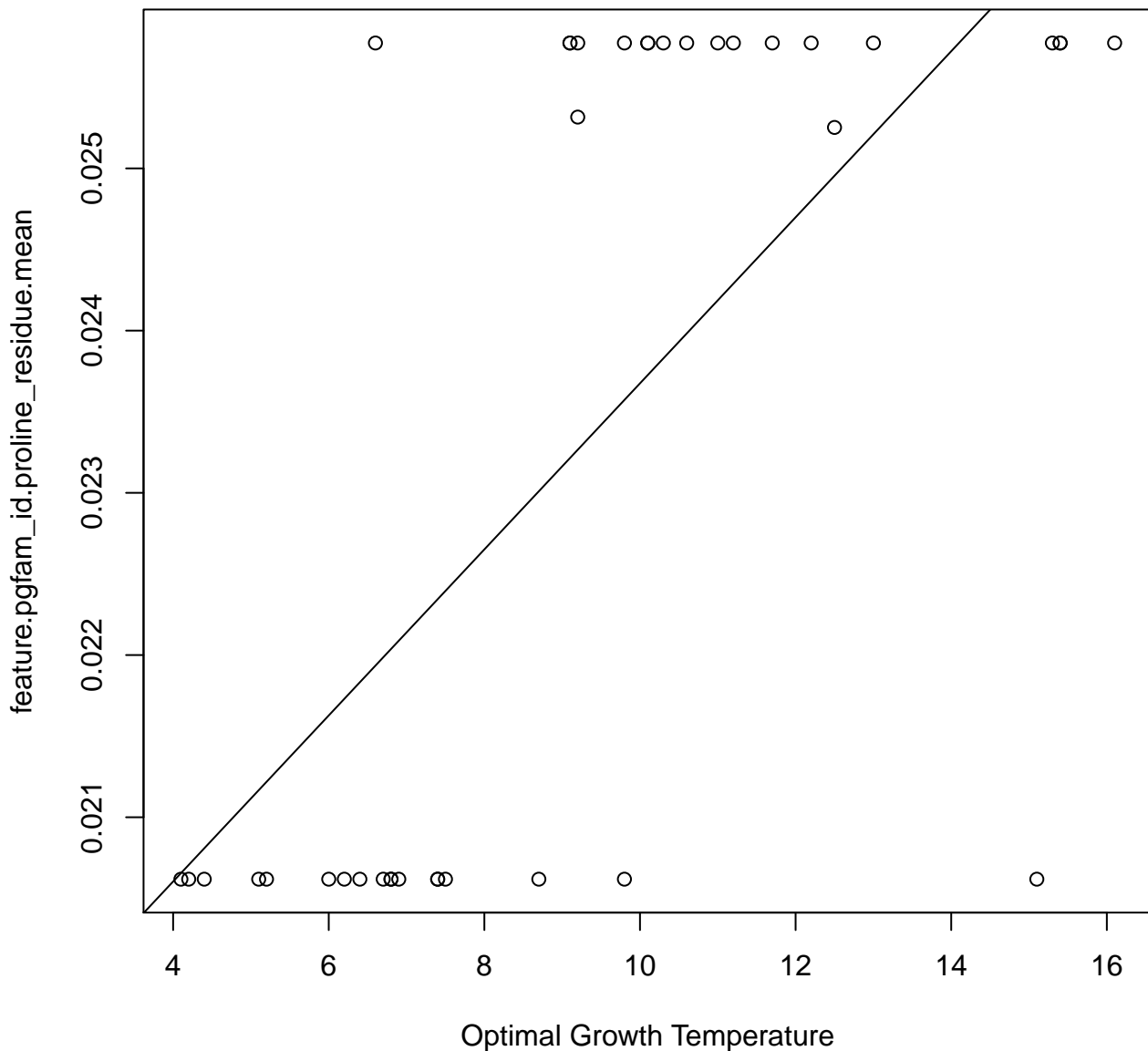
Fatty acid cis/trans isomerase

feature.pgfam_id.proline_residue.mean

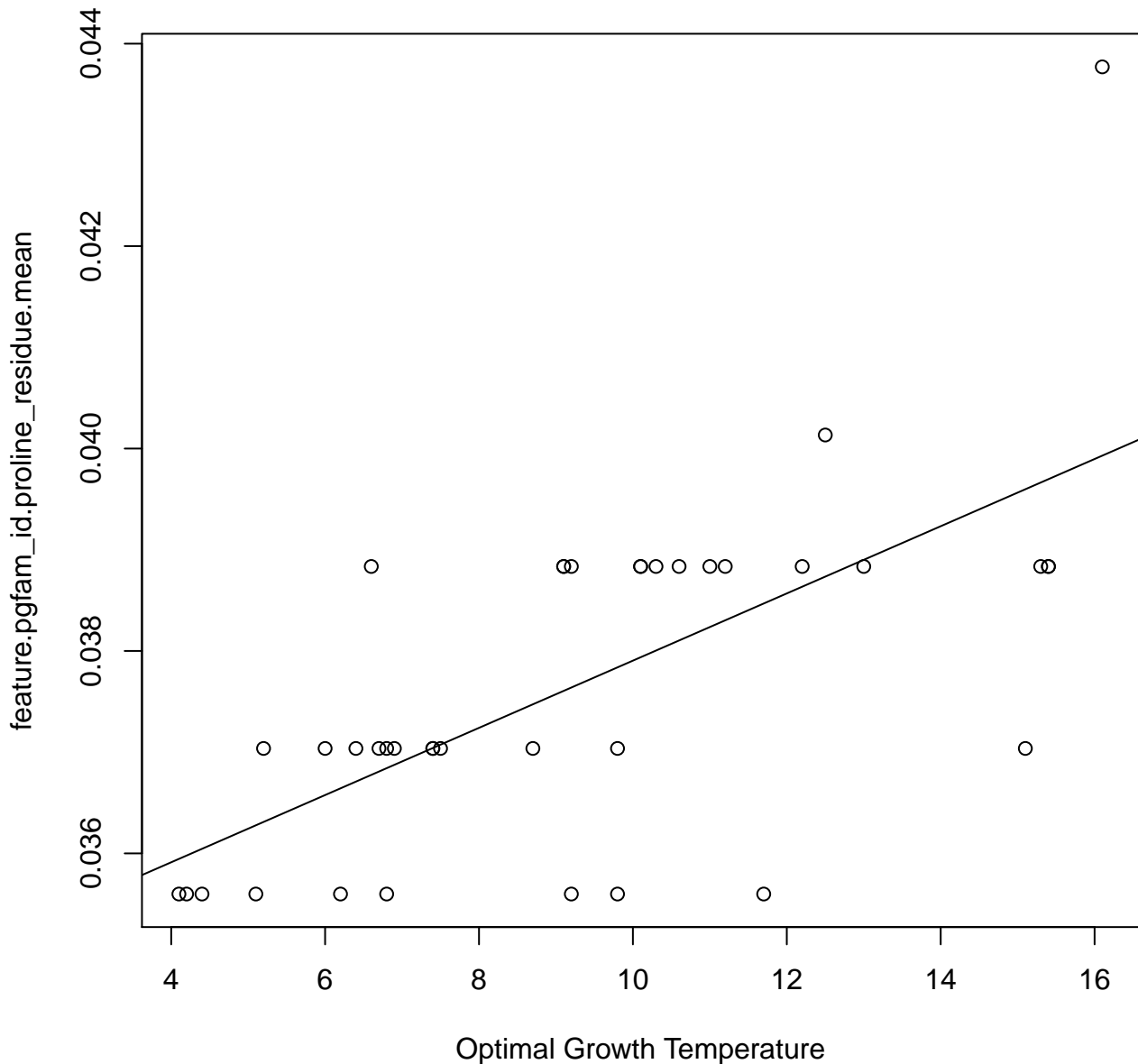


Optimal Growth Temperature

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



feature.pgfam_id.proline_residue.mean
PGF_00064827
Uncharacterized methyltransferase PA1407

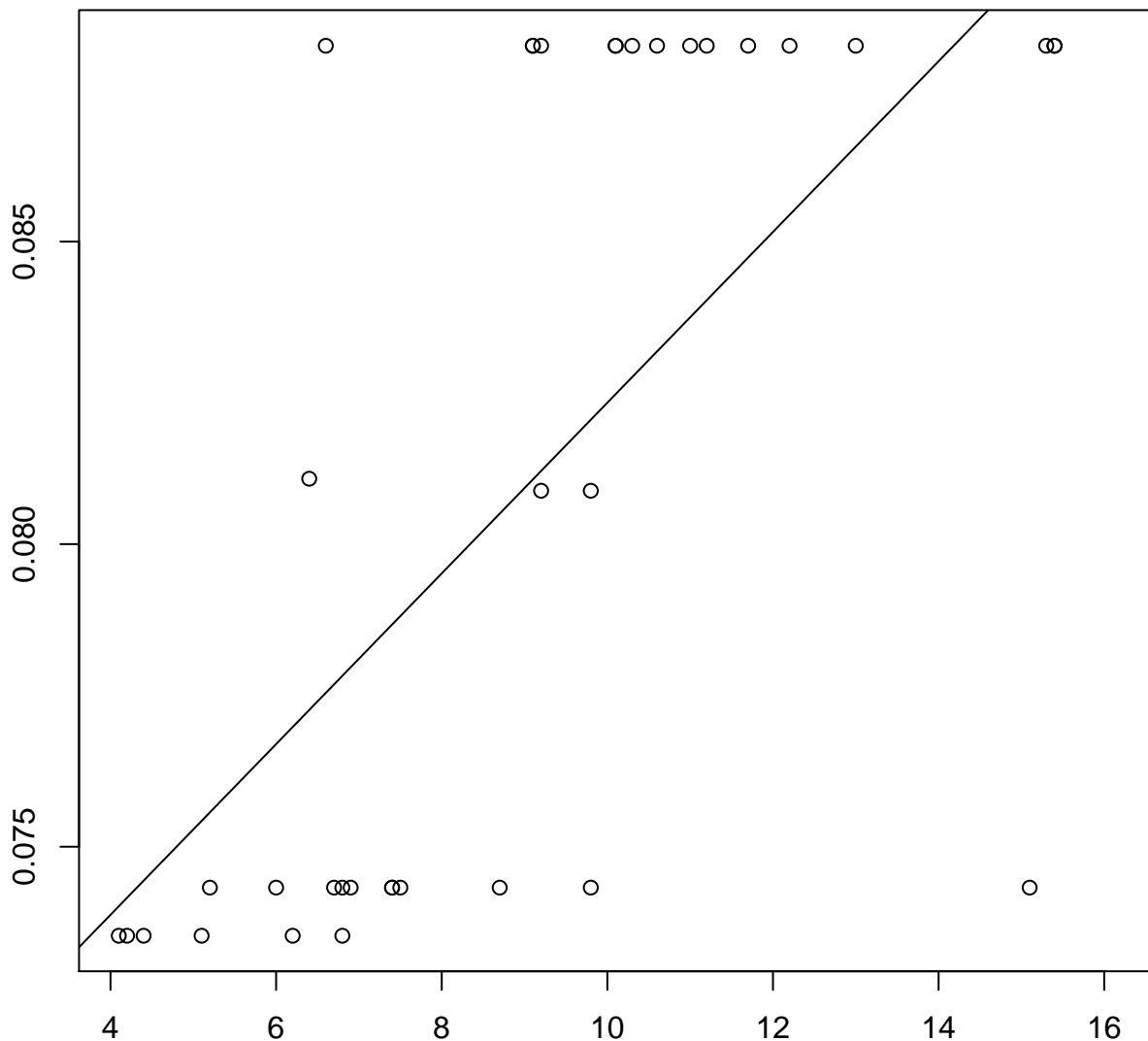


feature.pgfam_id.proline_residue.mean

PGF_00391487

hypothetical protein

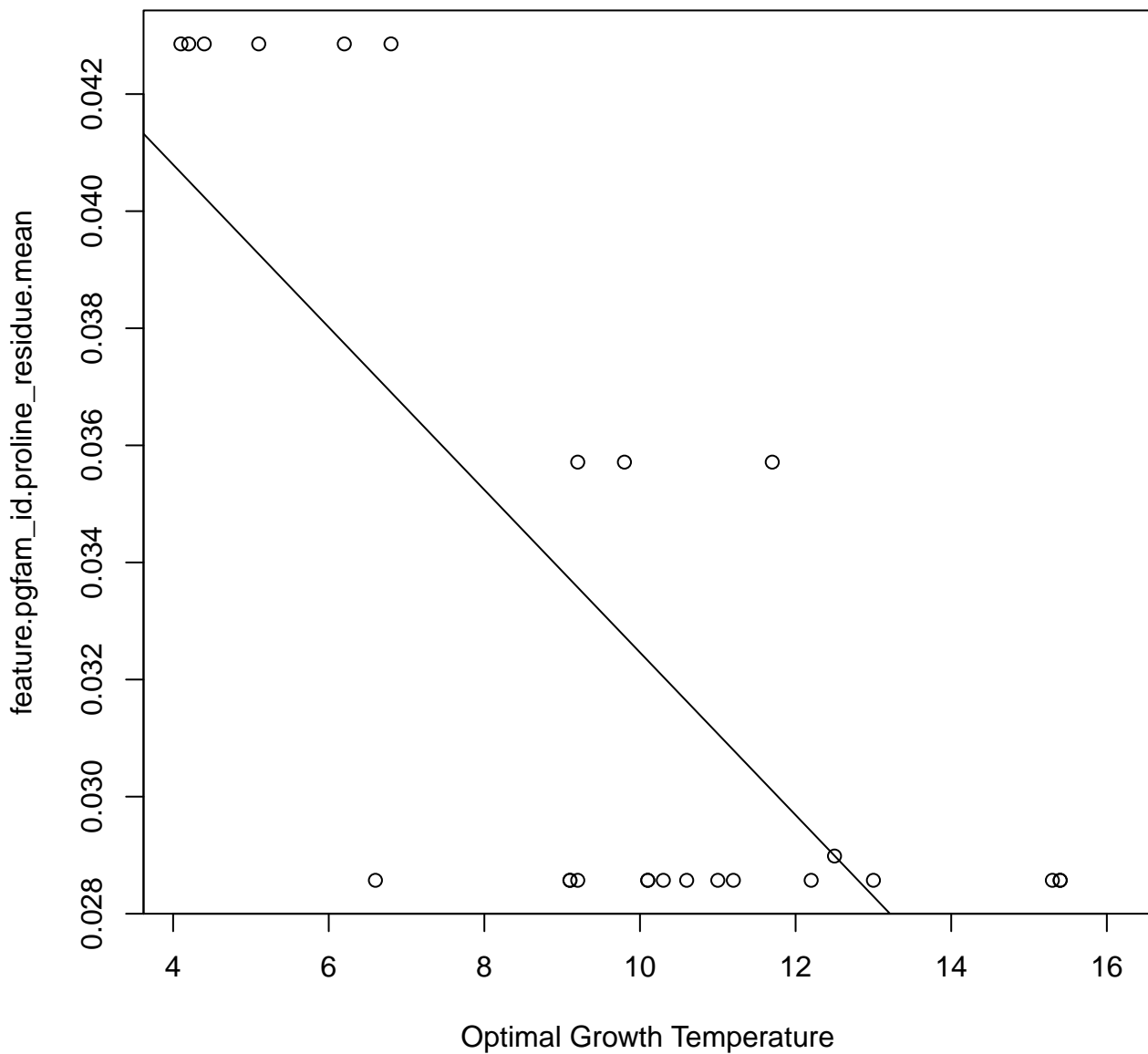
feature.pgfam_id.proline_residue.mean



feature.pgfam_id.proline_residue.mean

PGF_01009507

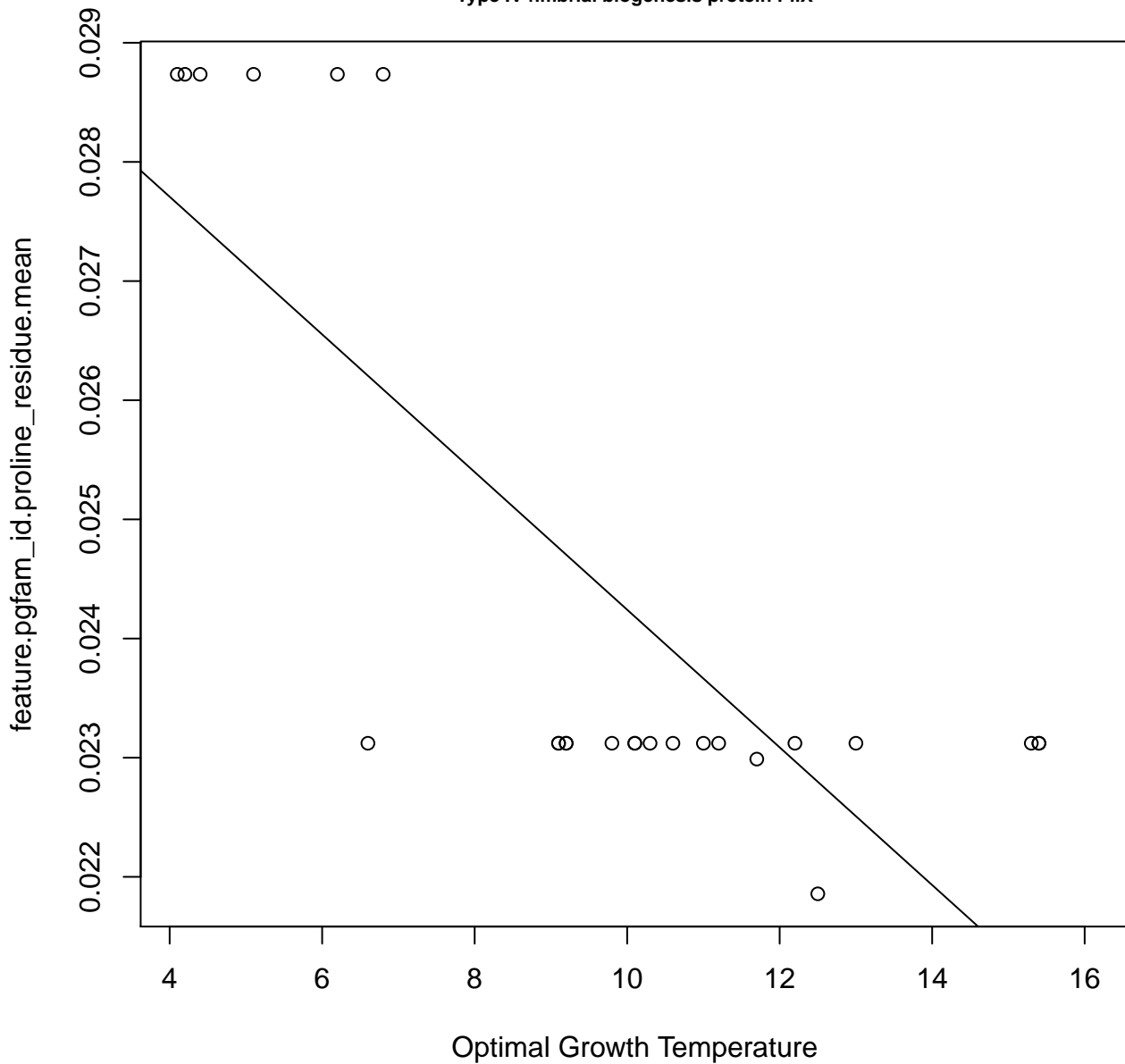
Glyoxalase family protein



feature.pgfam_id.proline_residue.mean

PGF_01064051

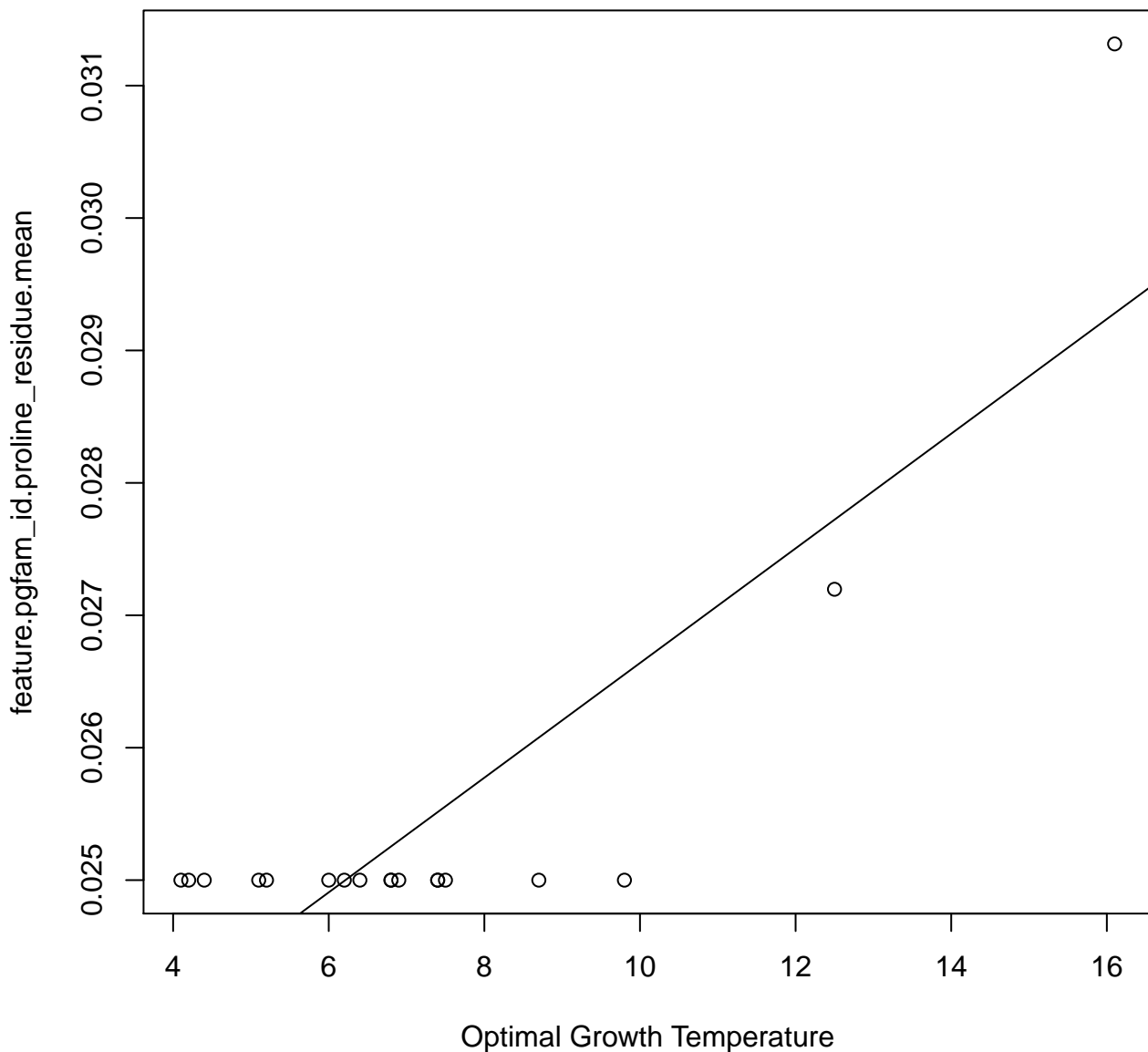
Type IV fimbrial biogenesis protein PilX



feature.pgfam_id.proline_residue.mean

PGF_02732386

Glucose/mannose:H⁺ symporter GlcP

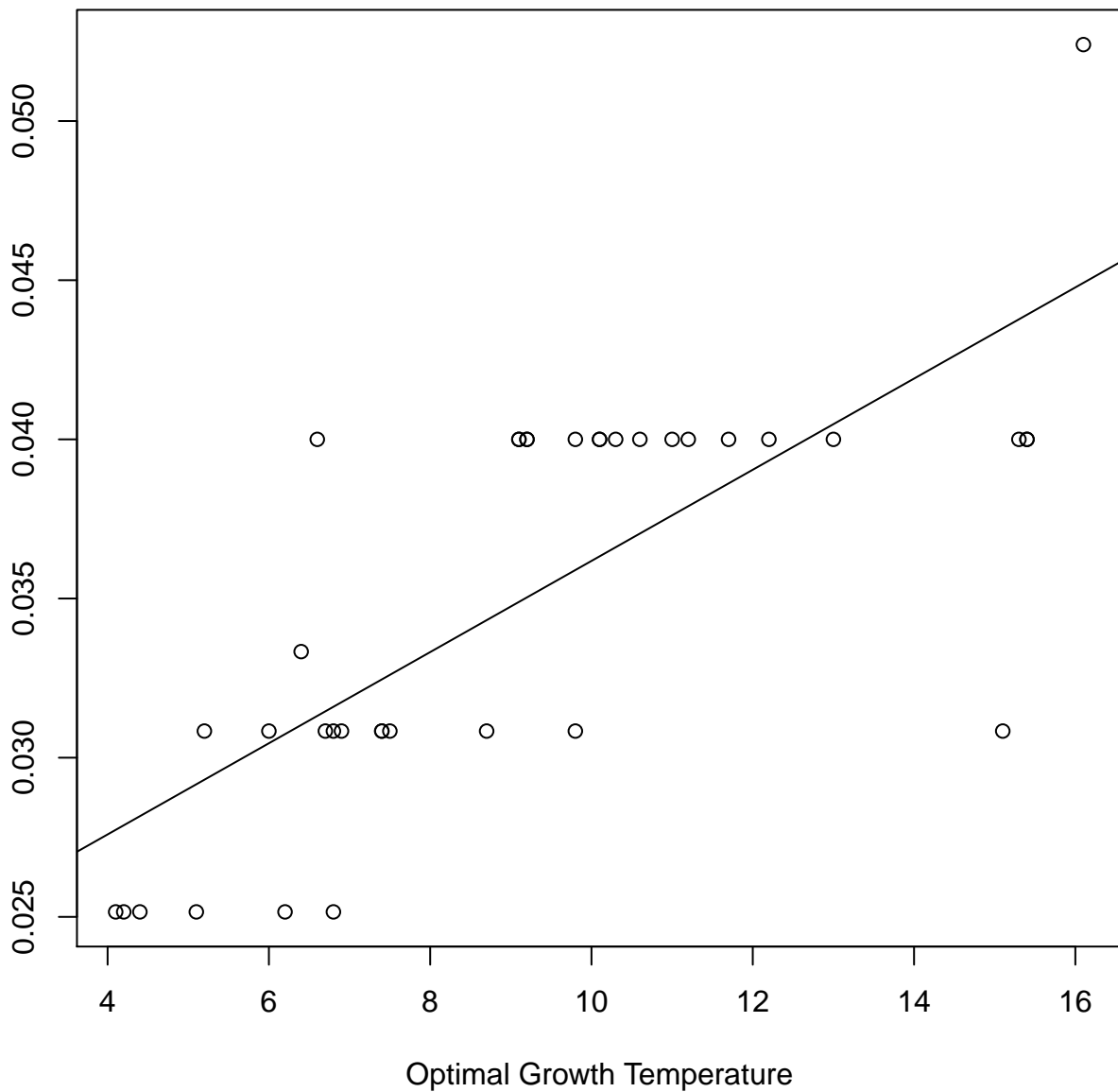


feature.pgfam_id.proline_residue.mean

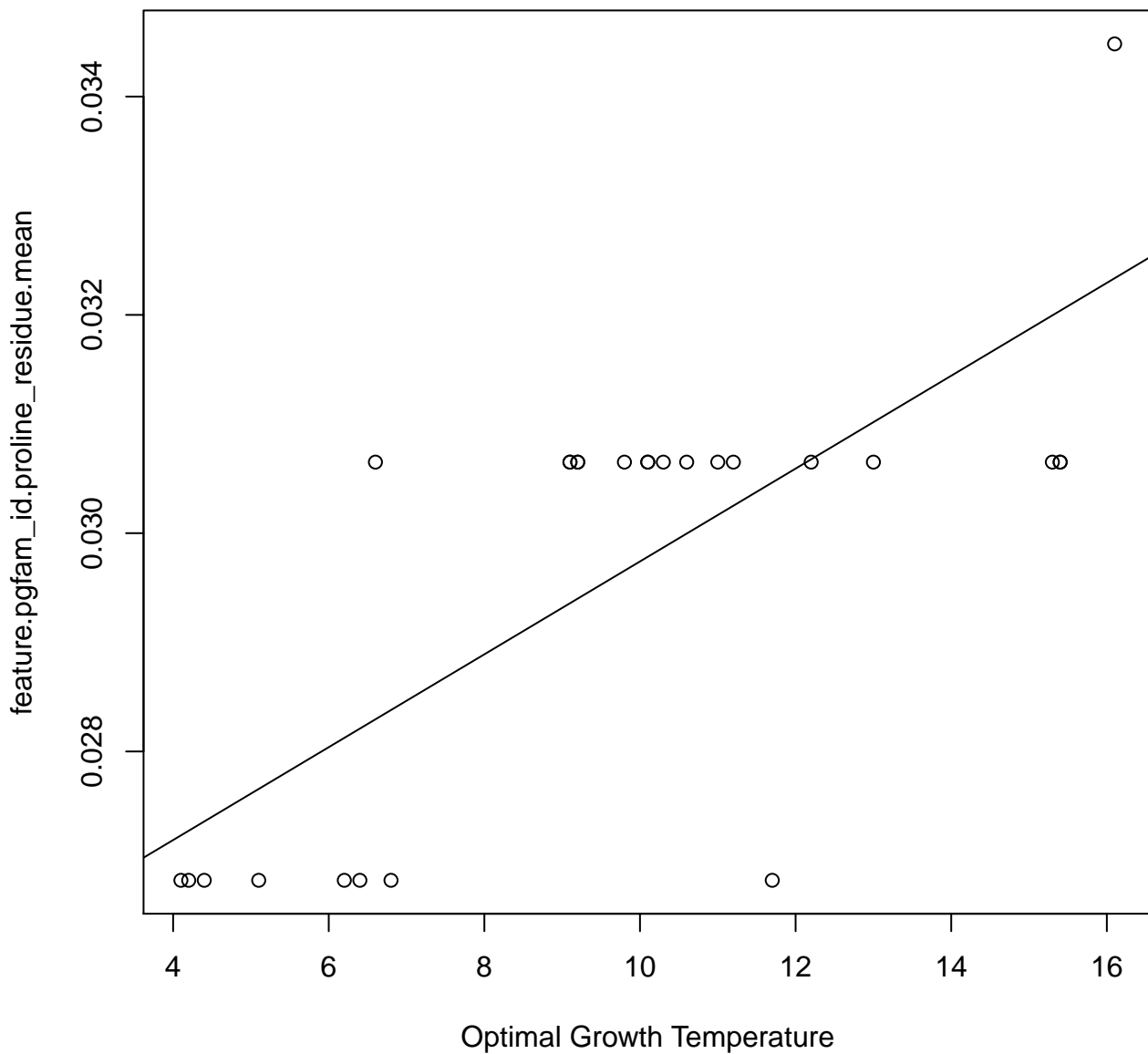
PGF_02911177

SM-20-related protein

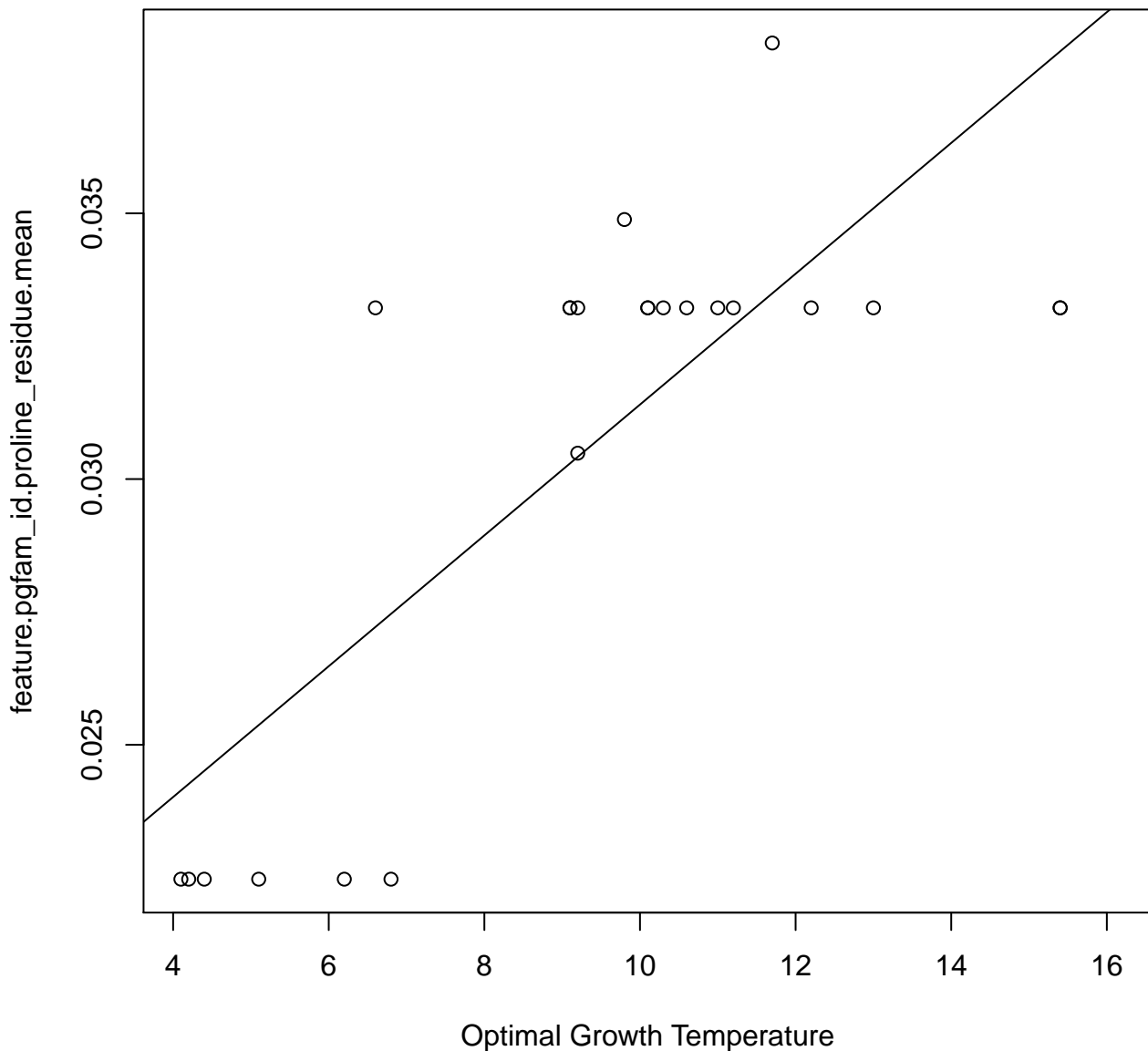
feature.pgfam_id.proline_residue.mean



feature.pgfam_id.proline_residue.mean
PGF_02931312
Malonyl-[acyl-carrier protein] O-methyltransferase (EC 2.1.1.197)



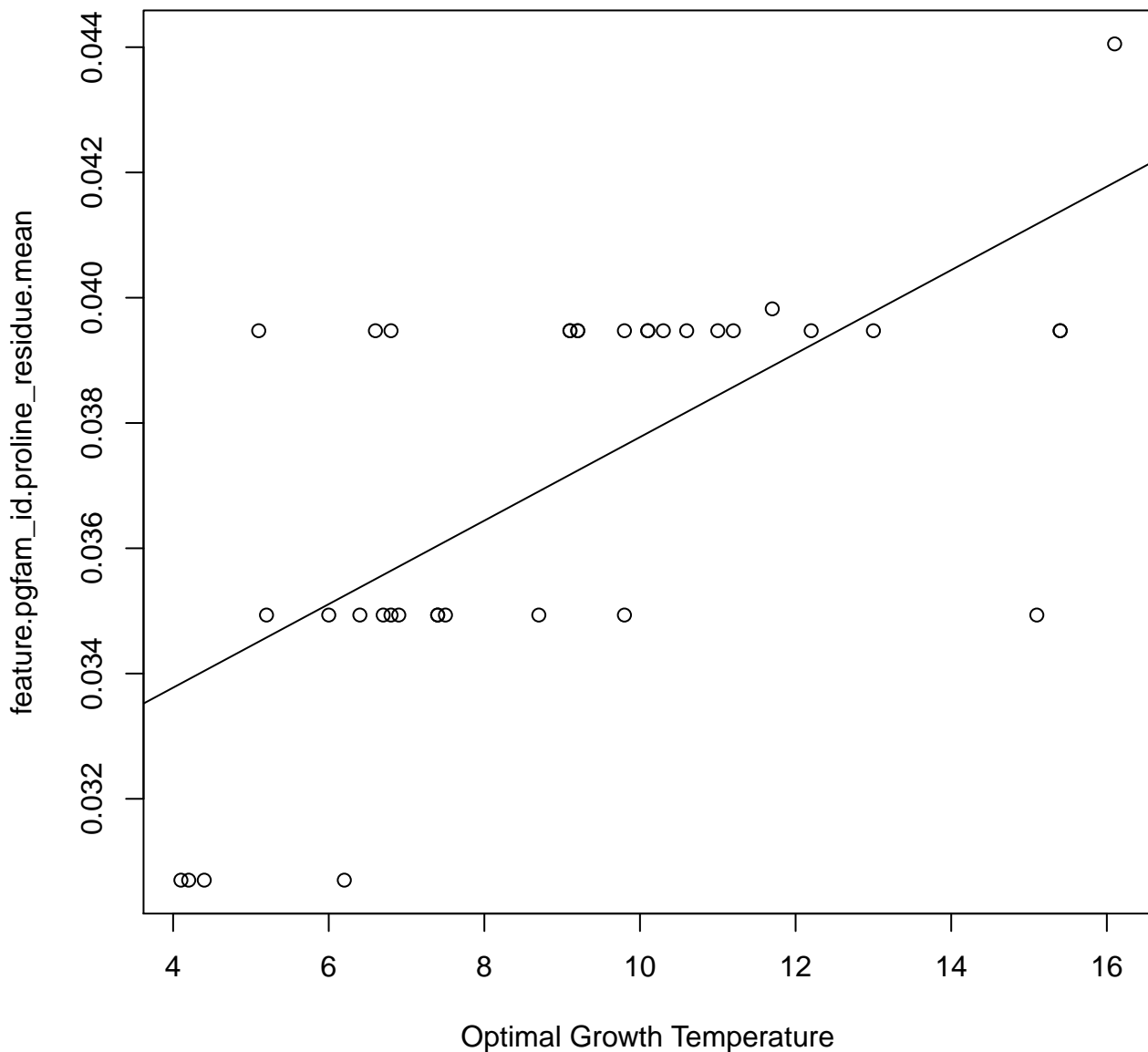
feature.pgfam_id.proline_residue.mean
PGF_03083319
Maltodextrin glucosidase (EC 3.2.1.20)



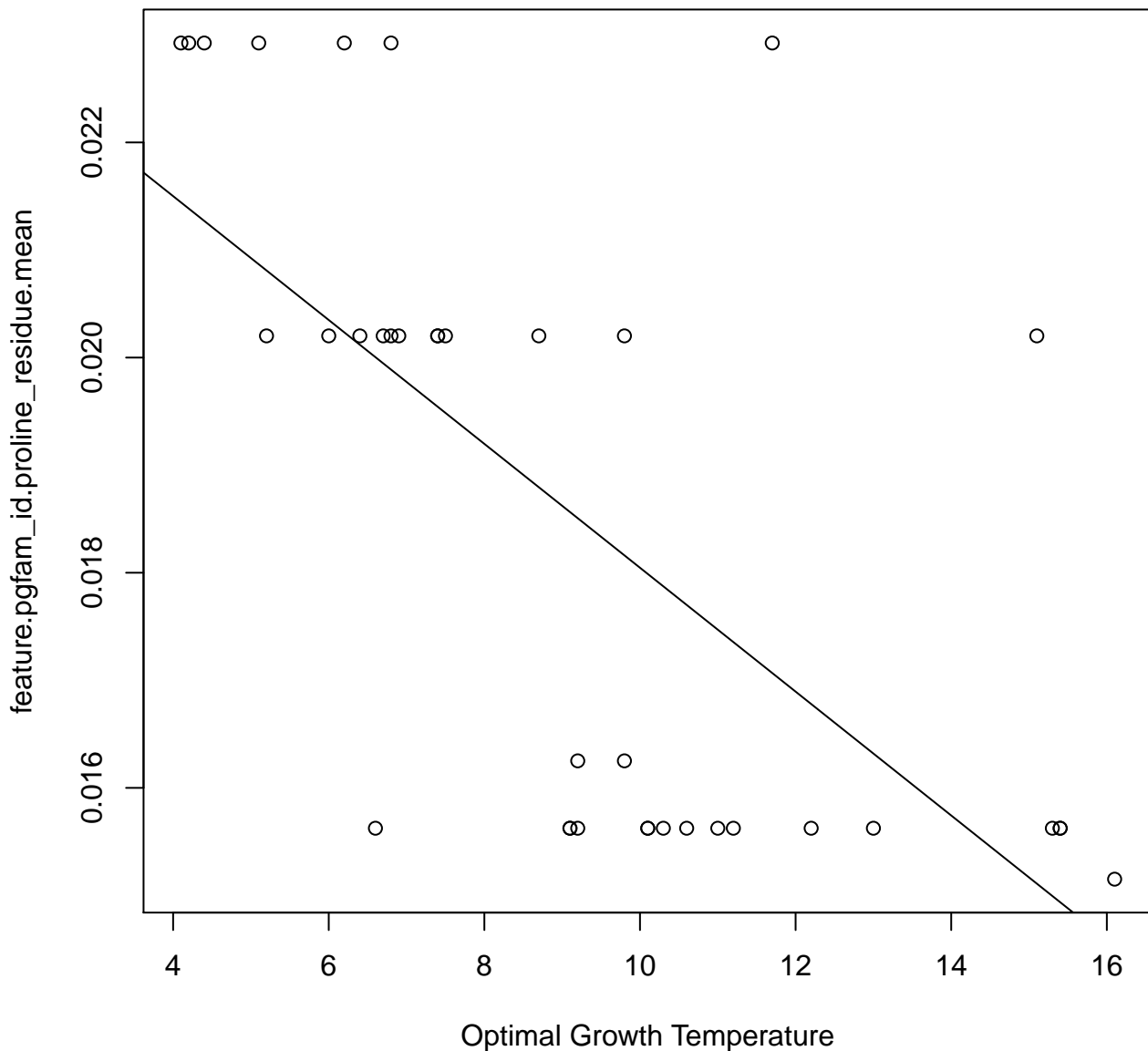
feature.pgfam_id.proline_residue.mean

PGF_03832998

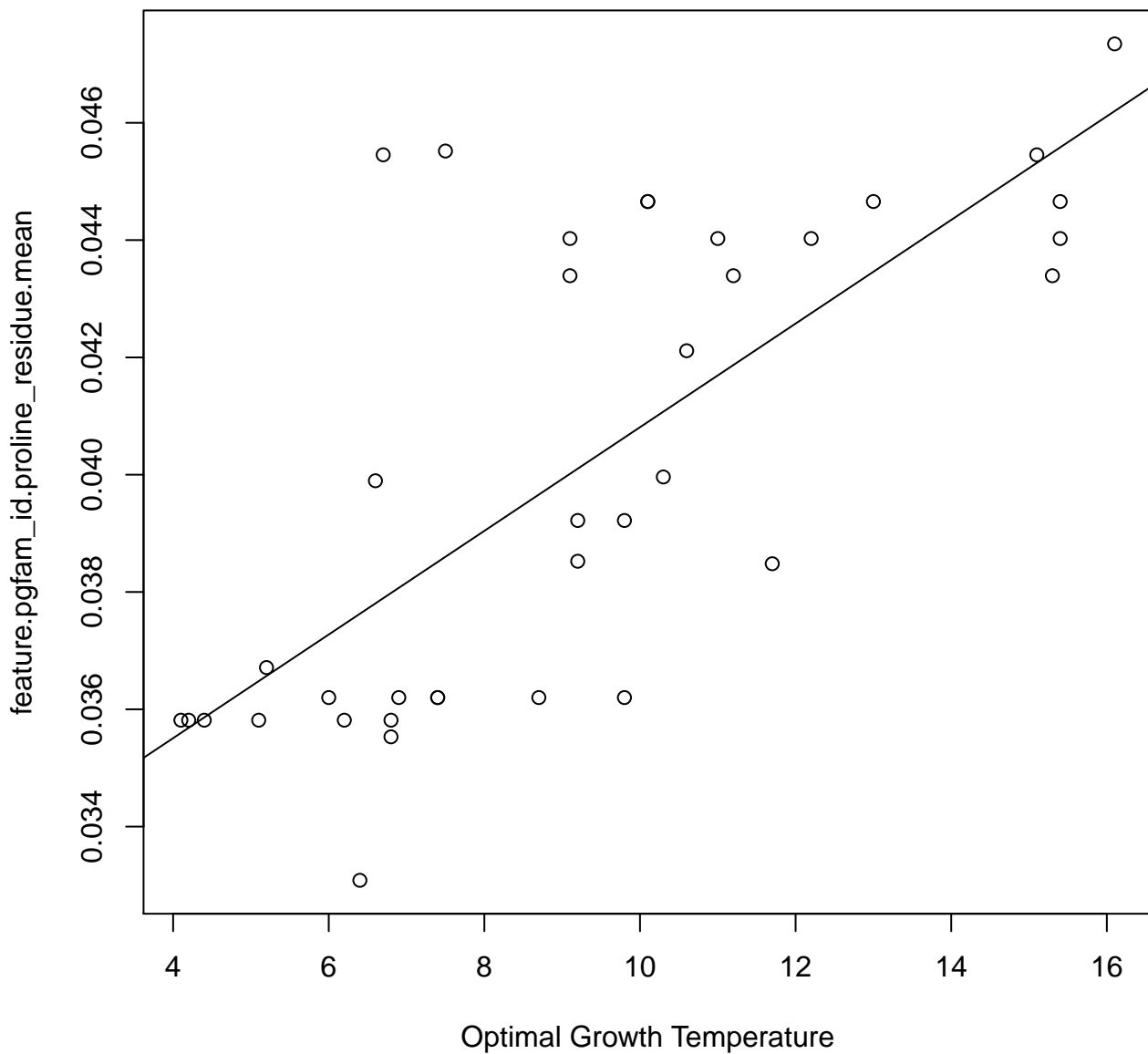
FIG111991: hypothetical protein



feature.pgfam_id.proline_residue.mean
PGF_05357708
DNA-3-methyladenine glycosylase (EC 3.2.2.20)



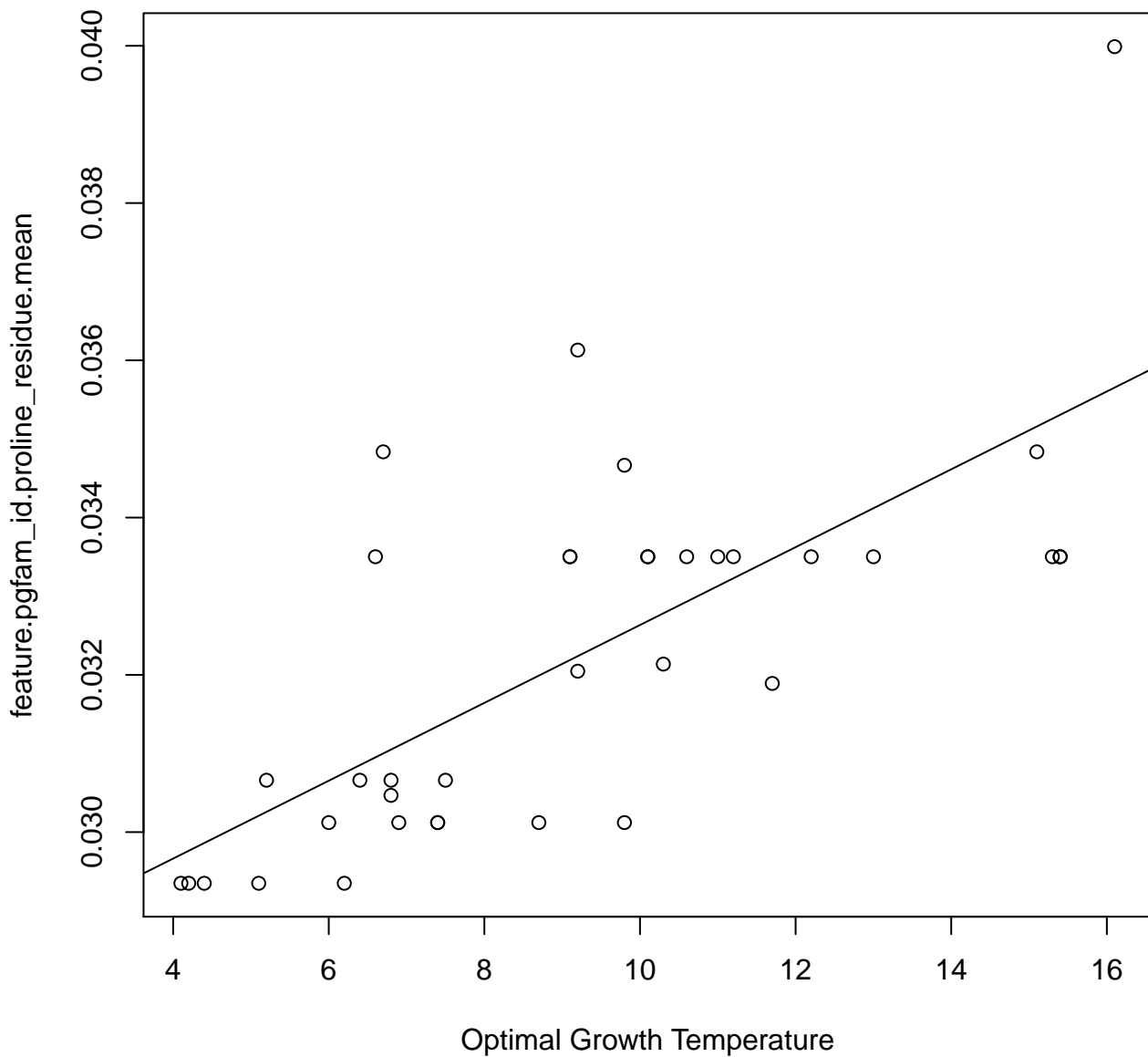
feature.pgfam_id.proline_residue.mean
PGF_08121553
Signal transduction histidine kinase CheA



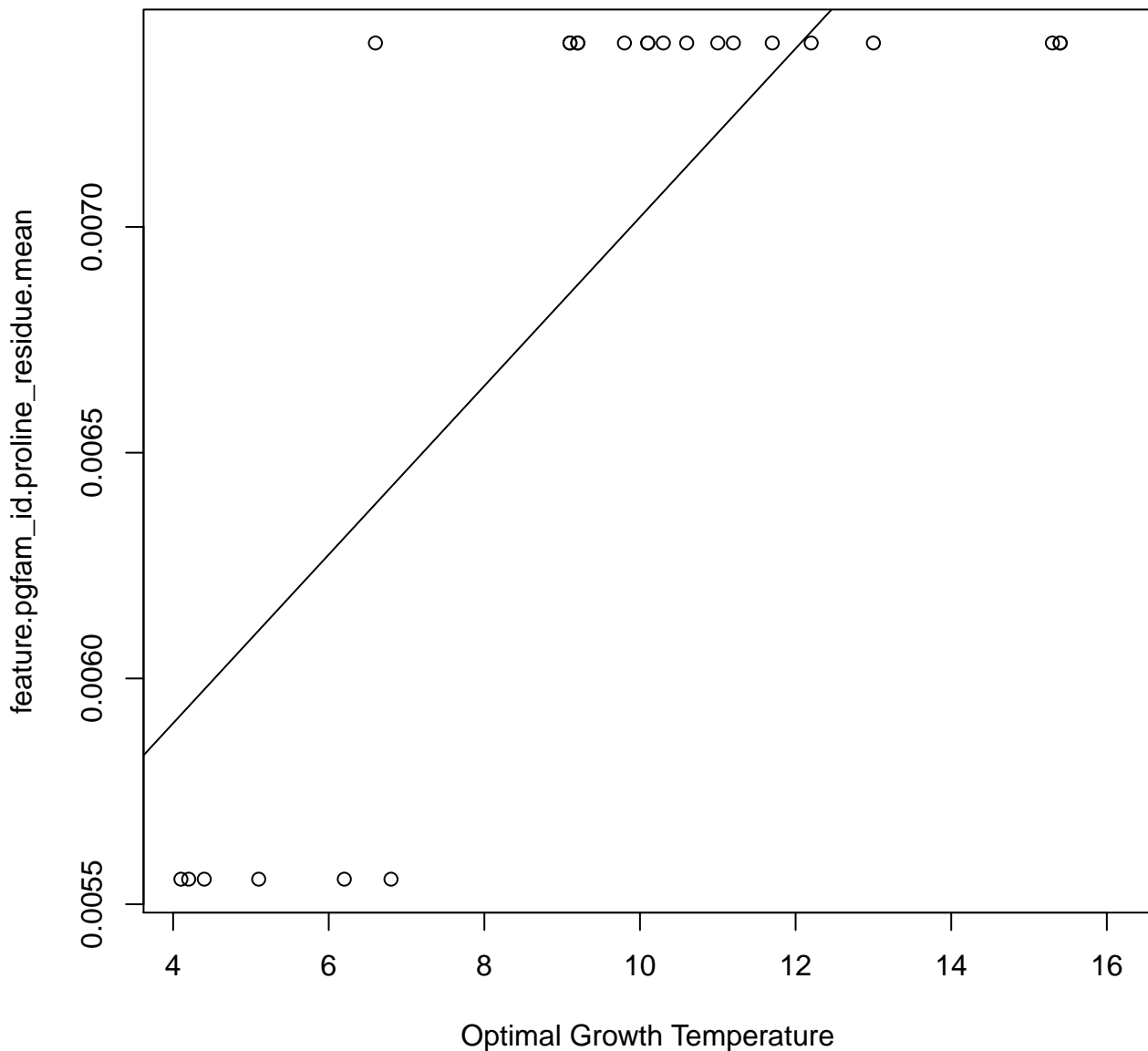
feature.pgfam_id.proline_residue.mean

PGF_10425579

ABC transporter, ATP-binding protein



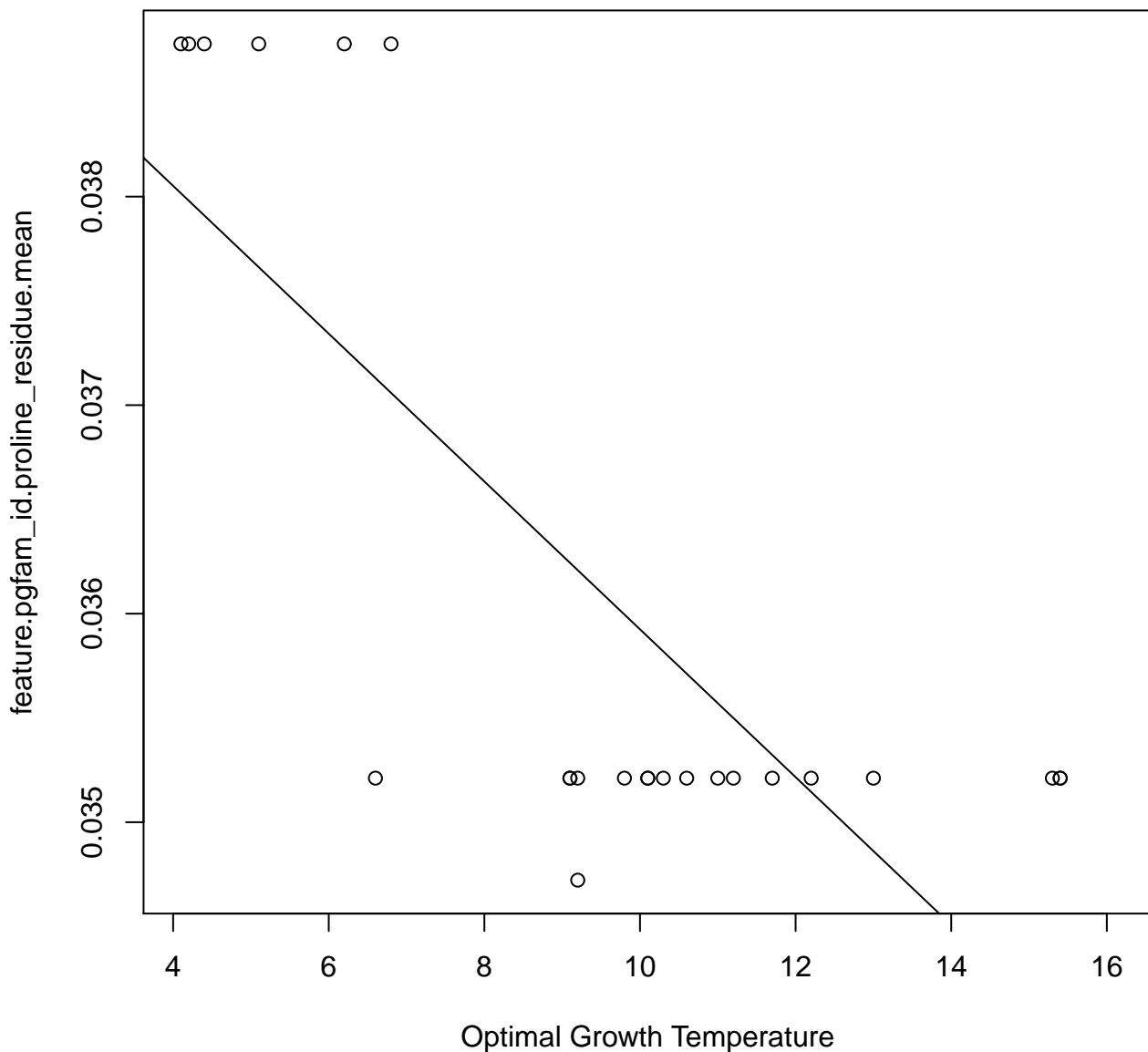
feature.pgfam_id.proline_residue.mean
PGF_10494566
hypothetical protein



feature.pgfam_id.proline_residue.mean

PGF_10866927

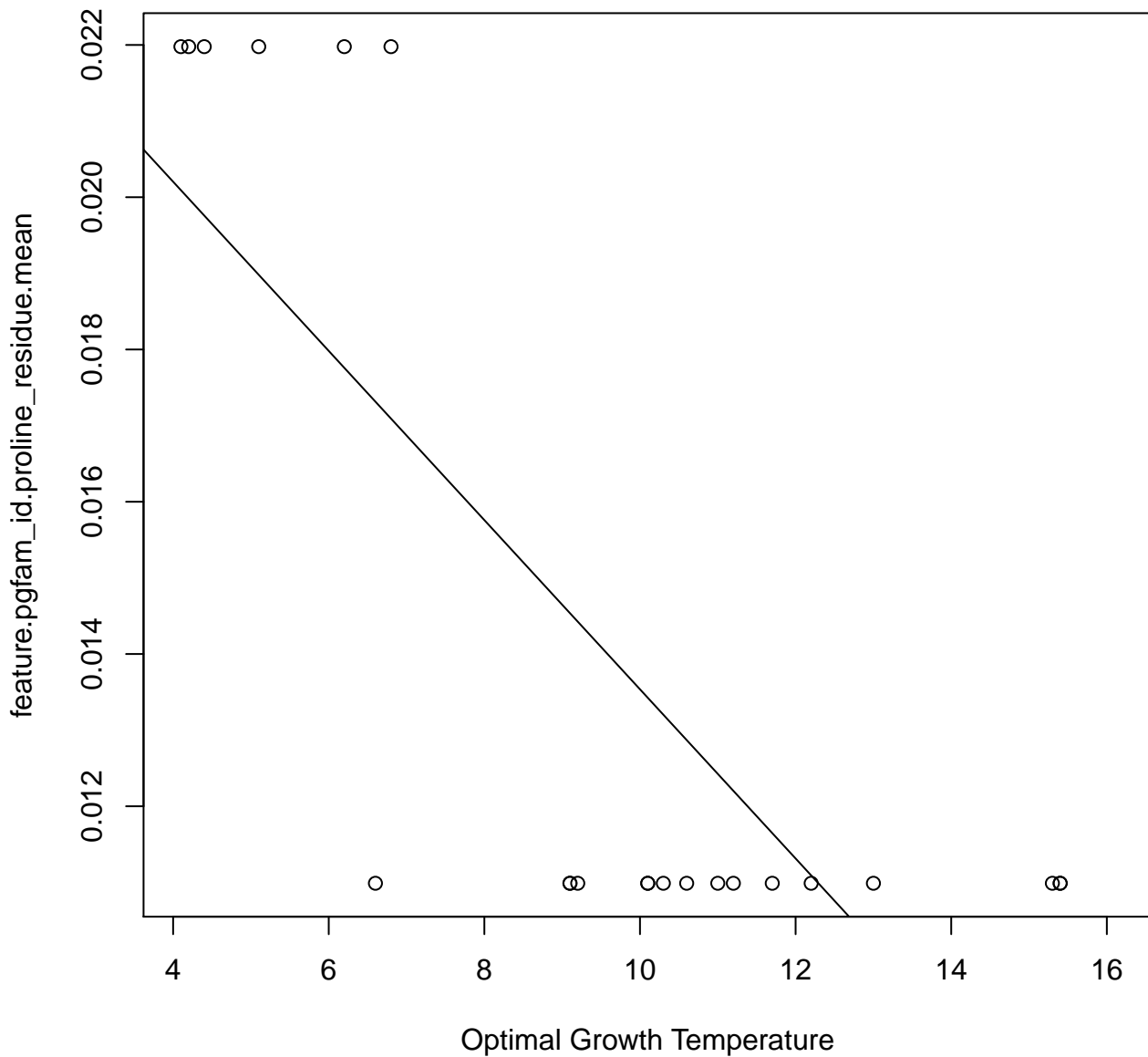
hypothetical protein



feature.pgfam_id.proline_residue.mean

PGF_10906072

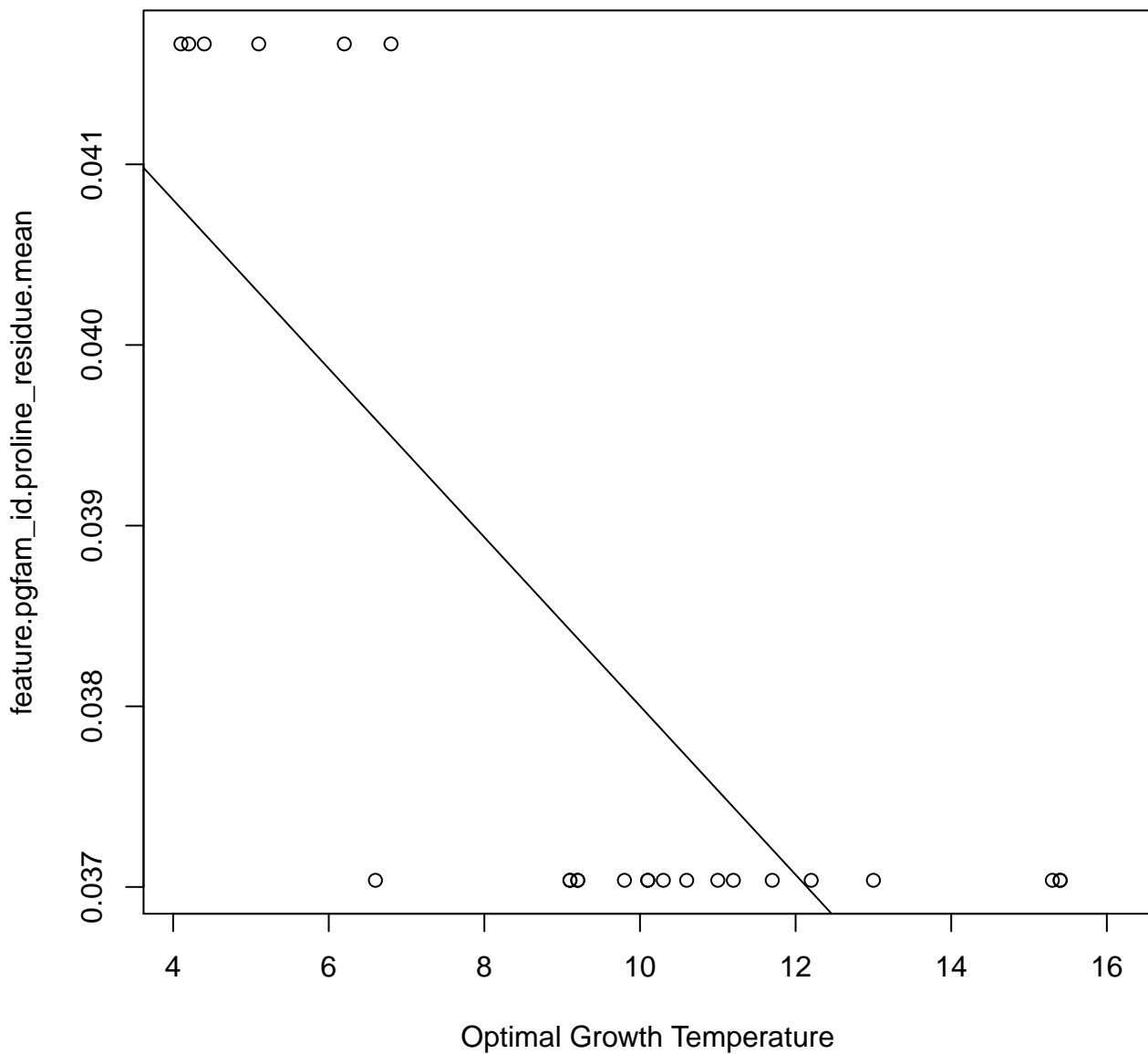
hypothetical protein



feature.pgfam_id.proline_residue.mean

PGF_11247394

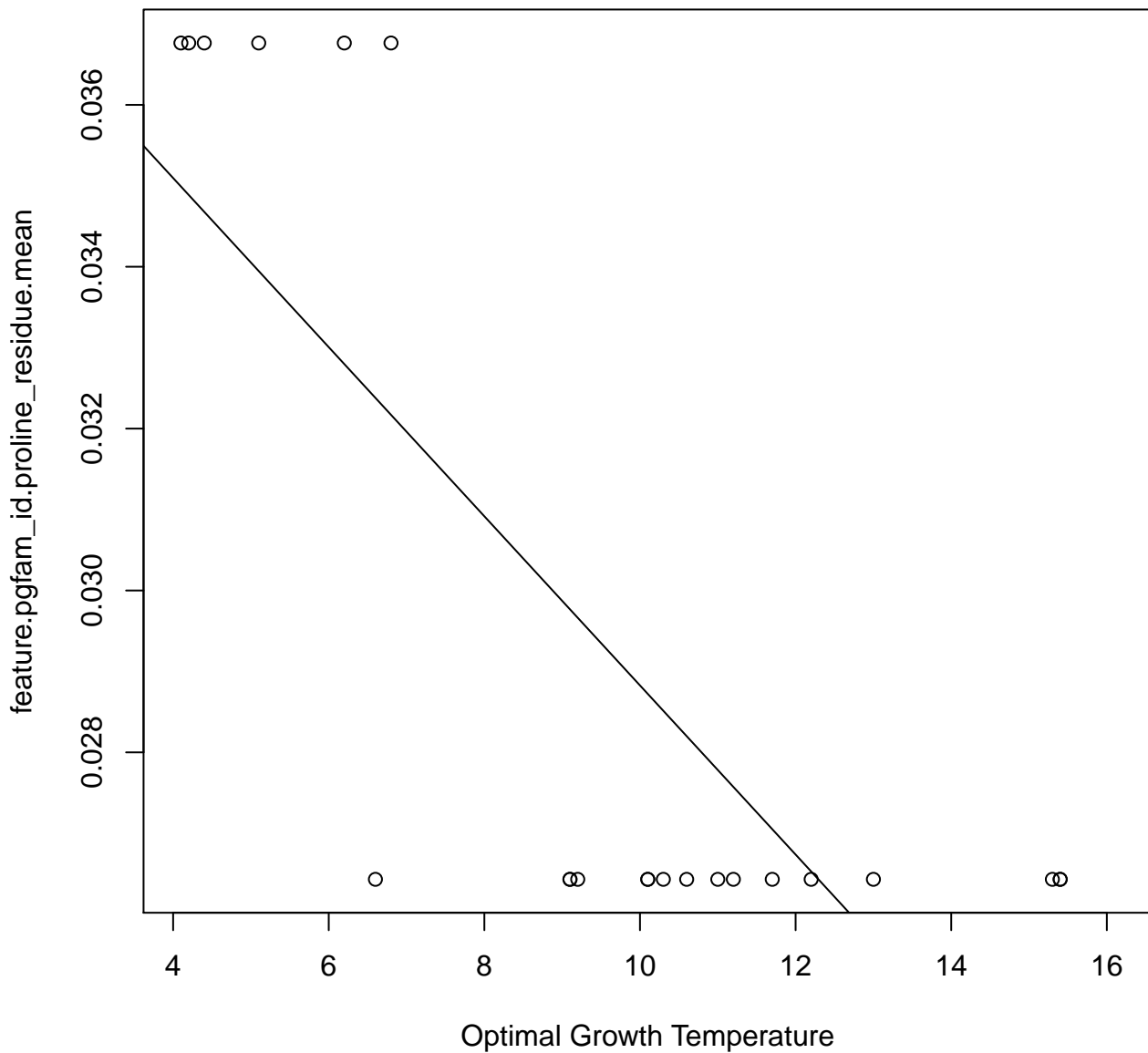
hypothetical protein



feature.pgfam_id.proline_residue.mean

PGF_11620197

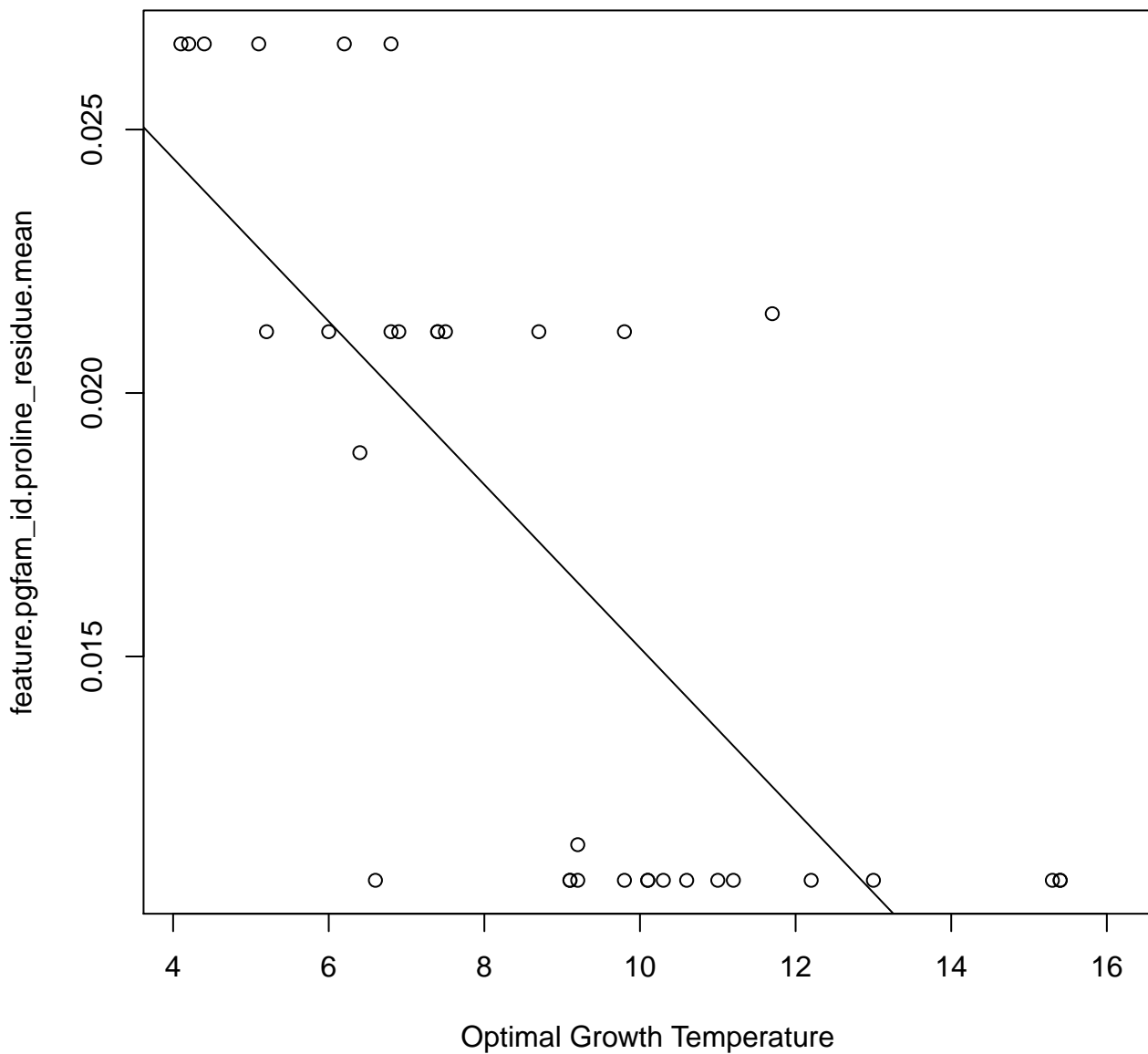
hypothetical protein



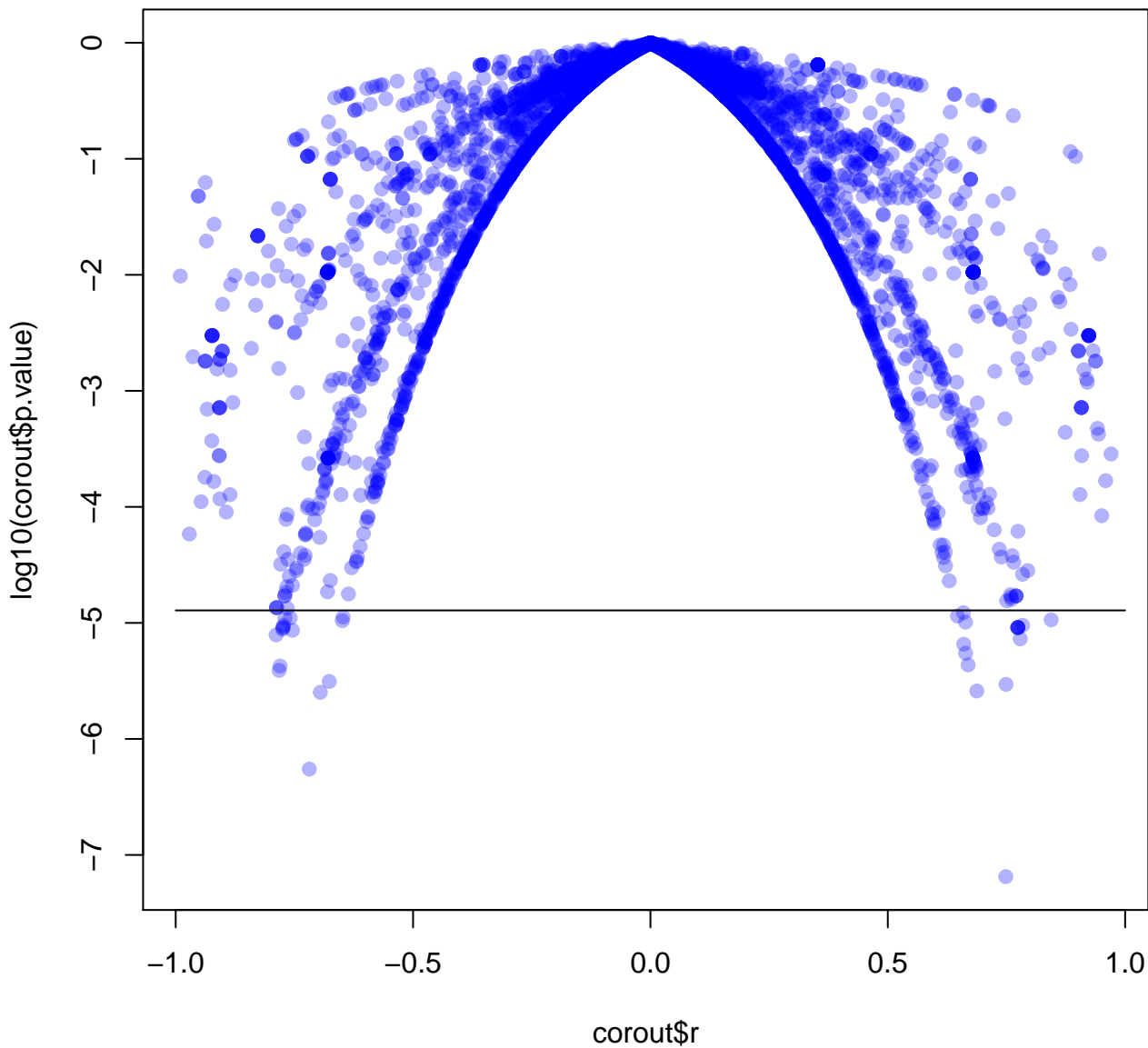
feature.pgfam_id.proline_residue.mean

PGF_12669666

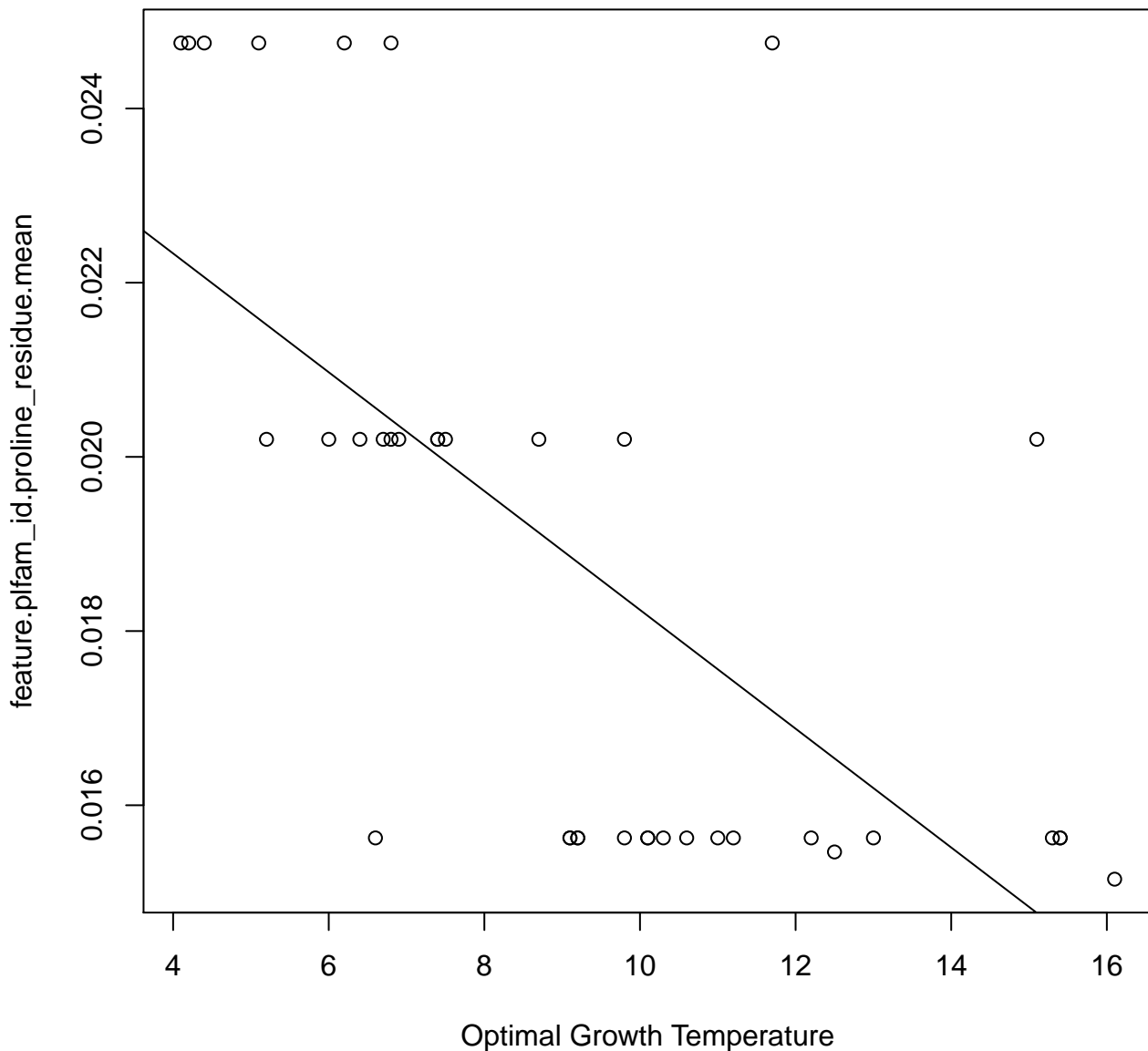
FIG006045: Sigma factor, ECF subfamily



feature.plfam_id.proline_residue.mean



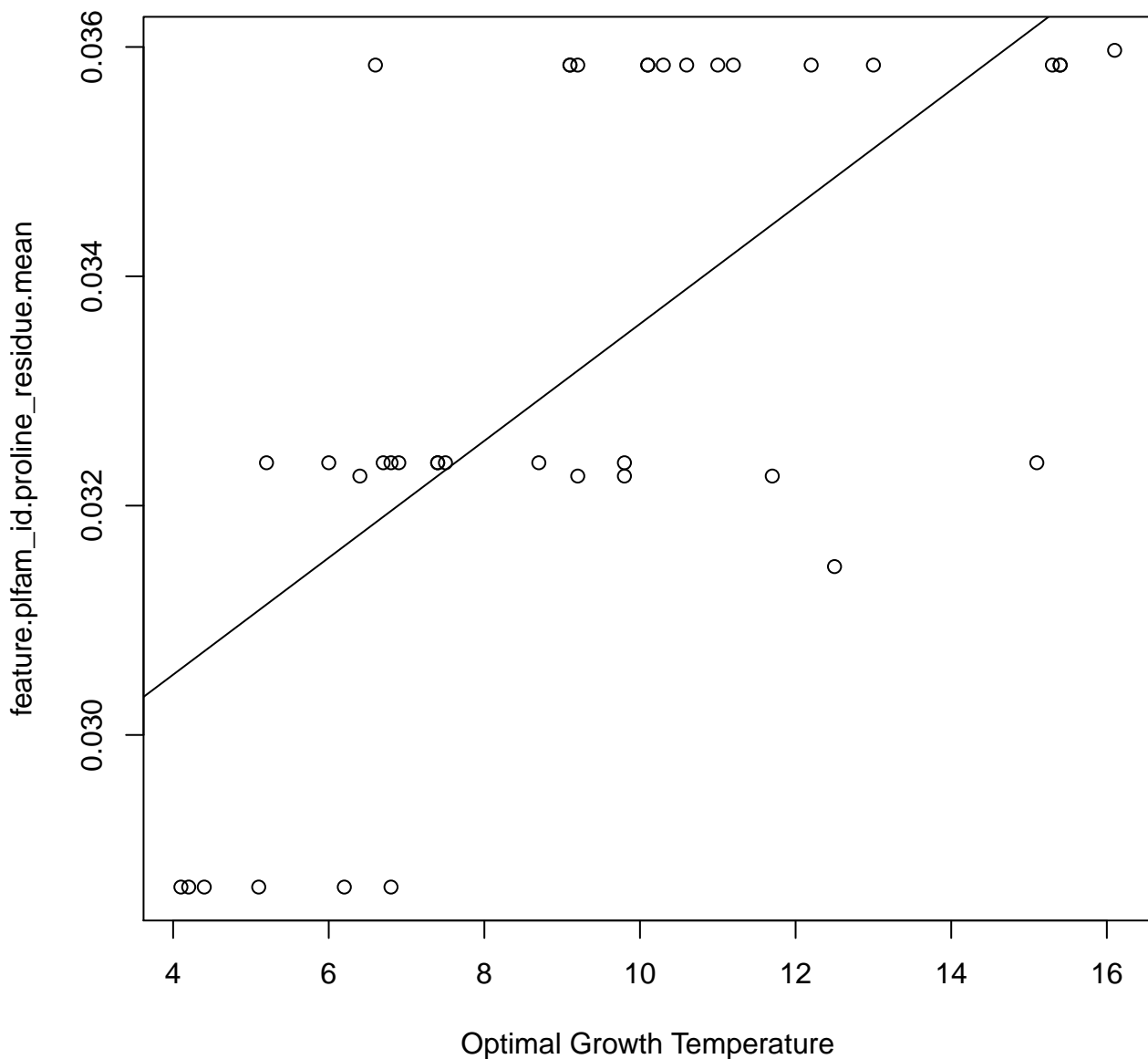
feature.plfam_id.proline_residue.mean
PLF_28228_00000187
DNA-3-methyladenine glycosylase (EC 3.2.2.20)



feature.plfam_id.proline_residue.mean

PLF_28228_00000236

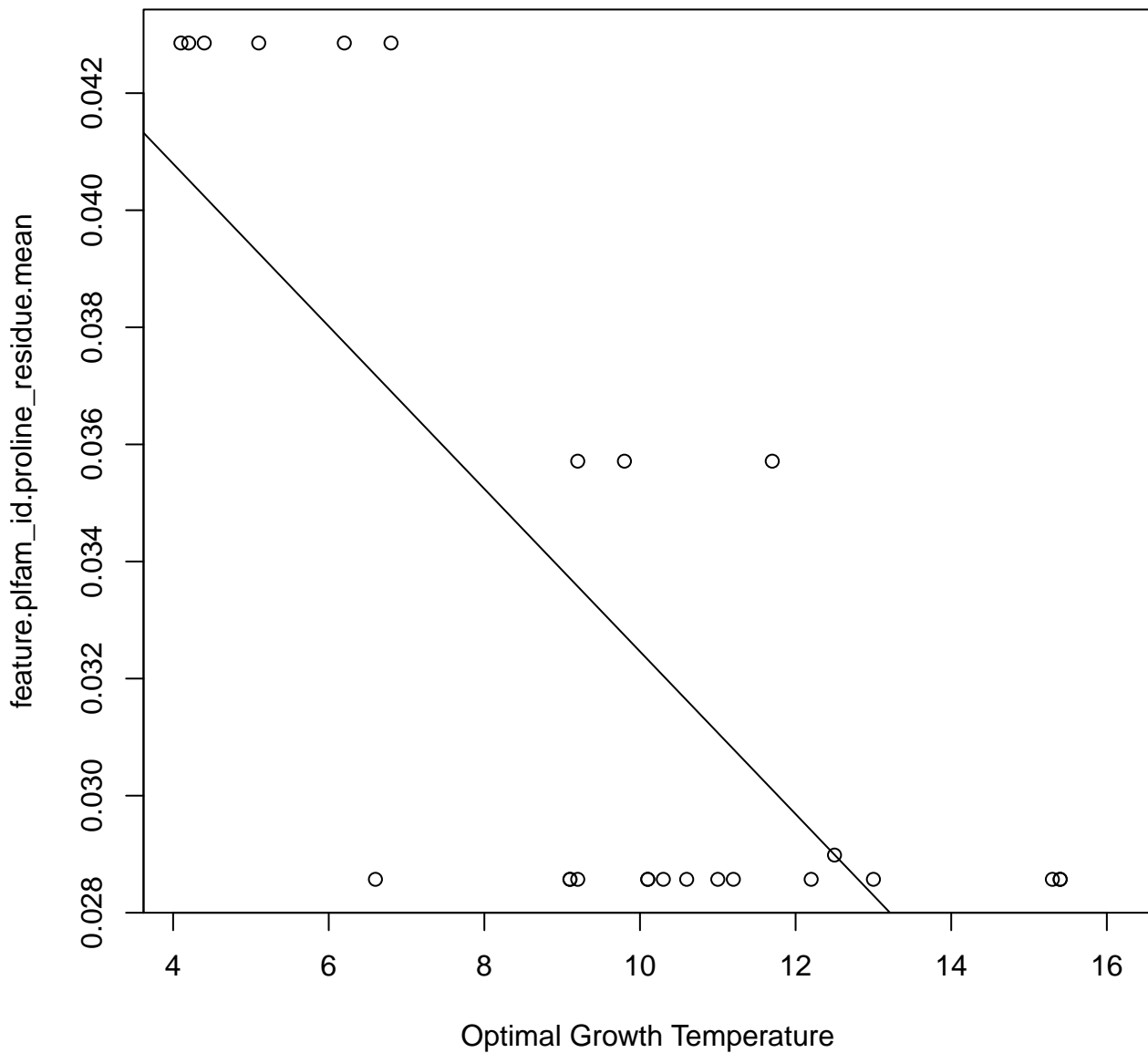
Dihydropteroate synthase (EC 2.5.1.15)



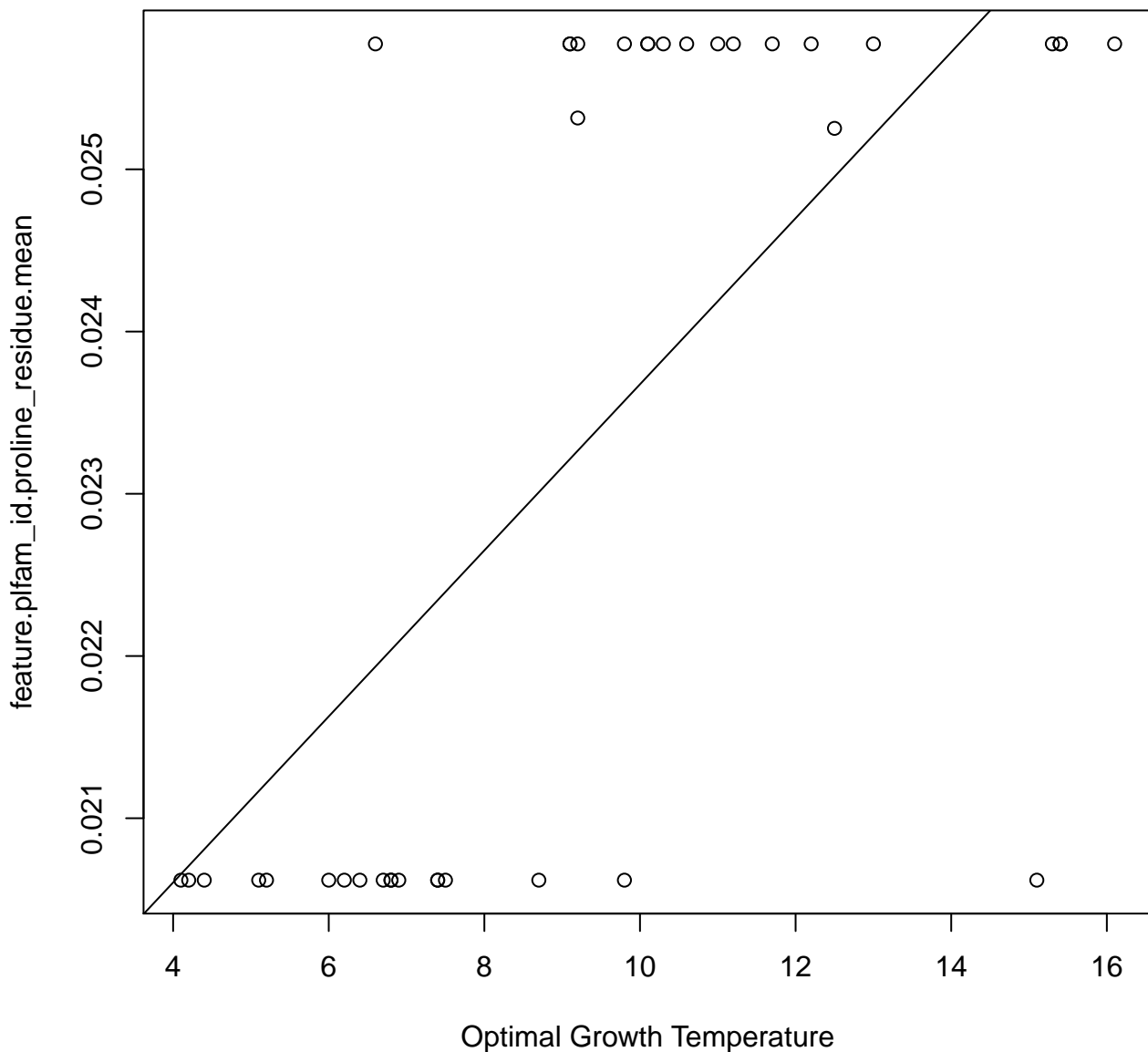
feature.plfam_id.proline_residue.mean

PLF_28228_00000478

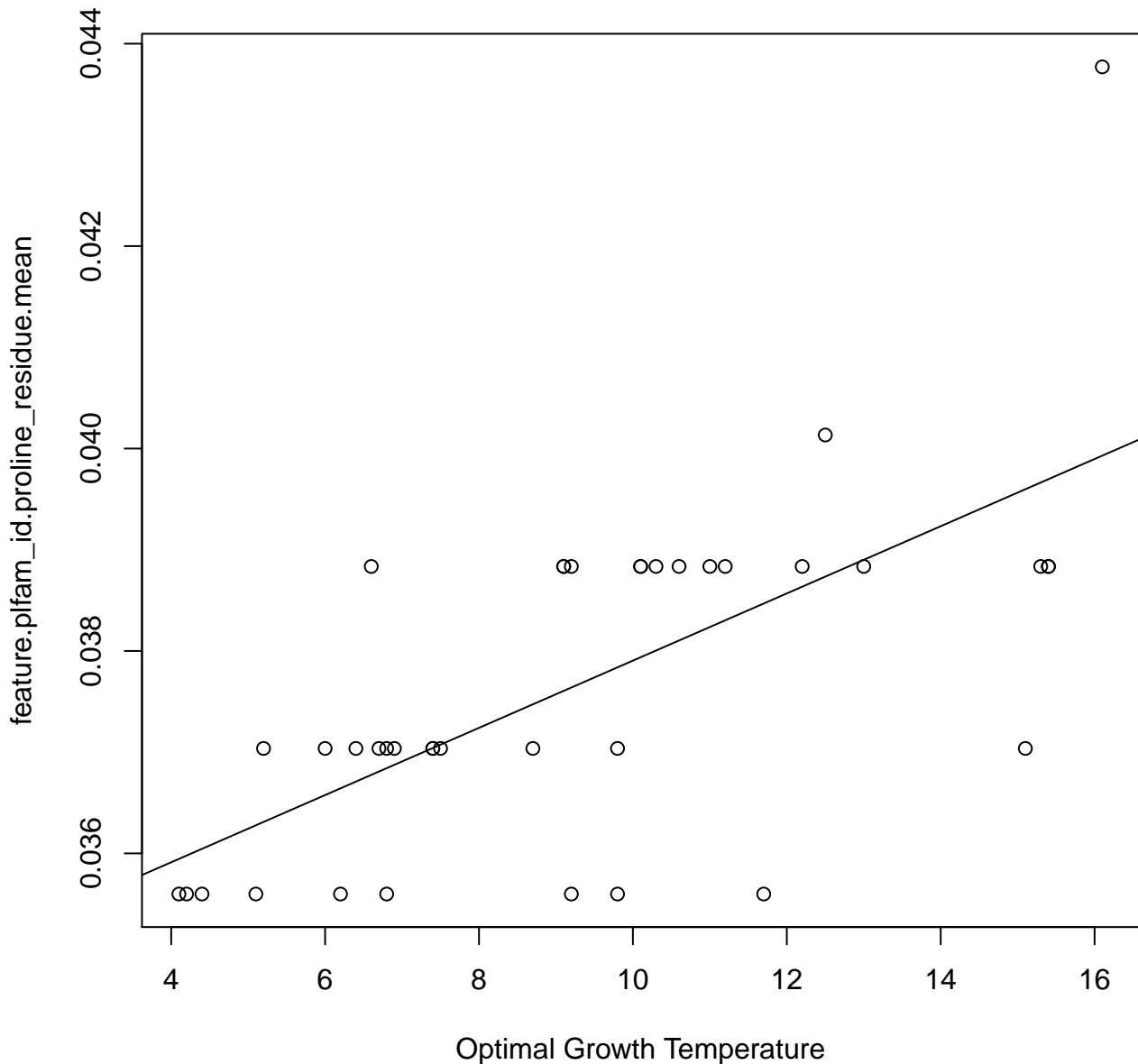
Glyoxalase family protein



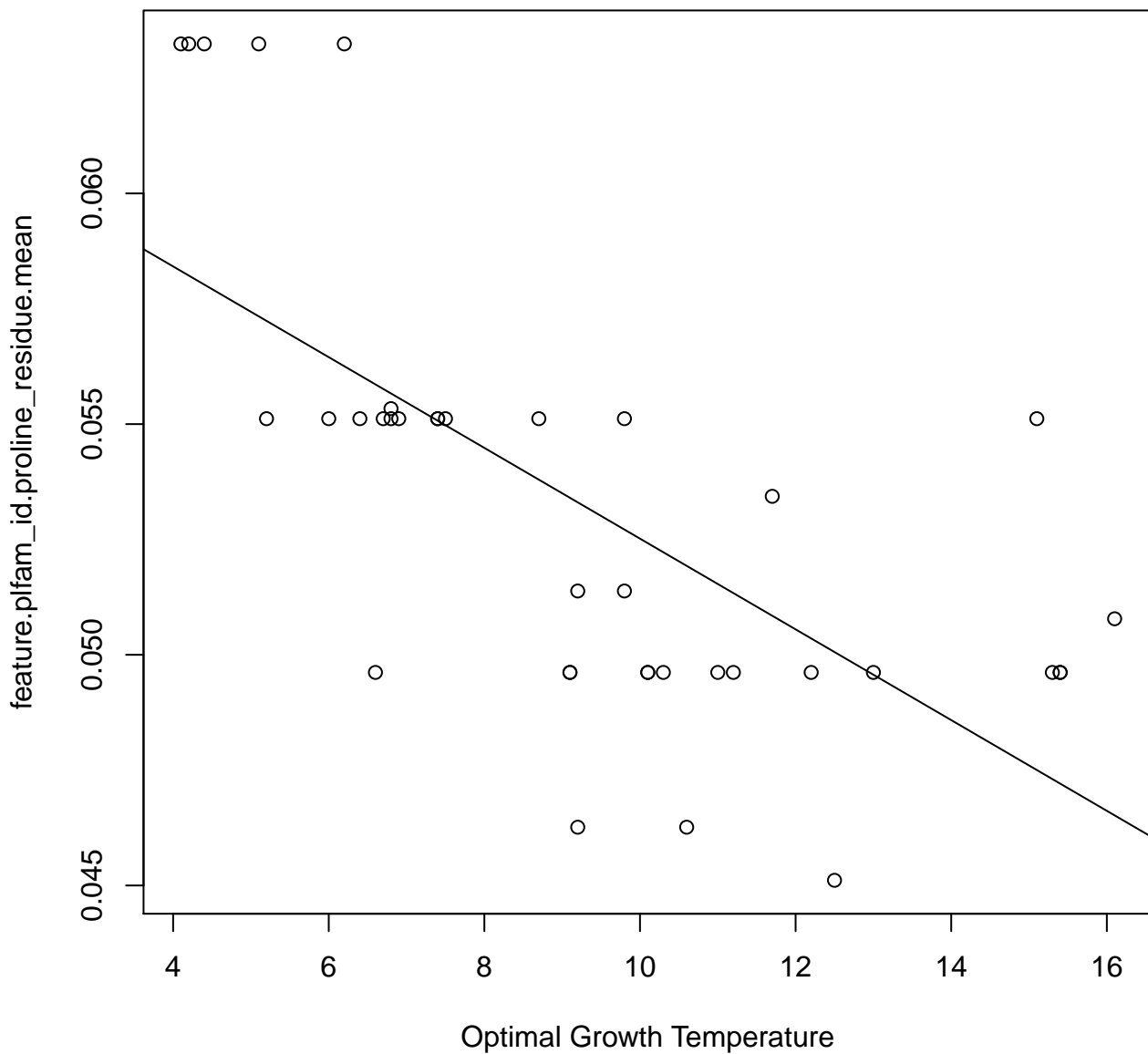
feature.plfam_id.proline_residue.mean
PLF_28228_00001218
Transcriptional regulator SlmA, TetR family



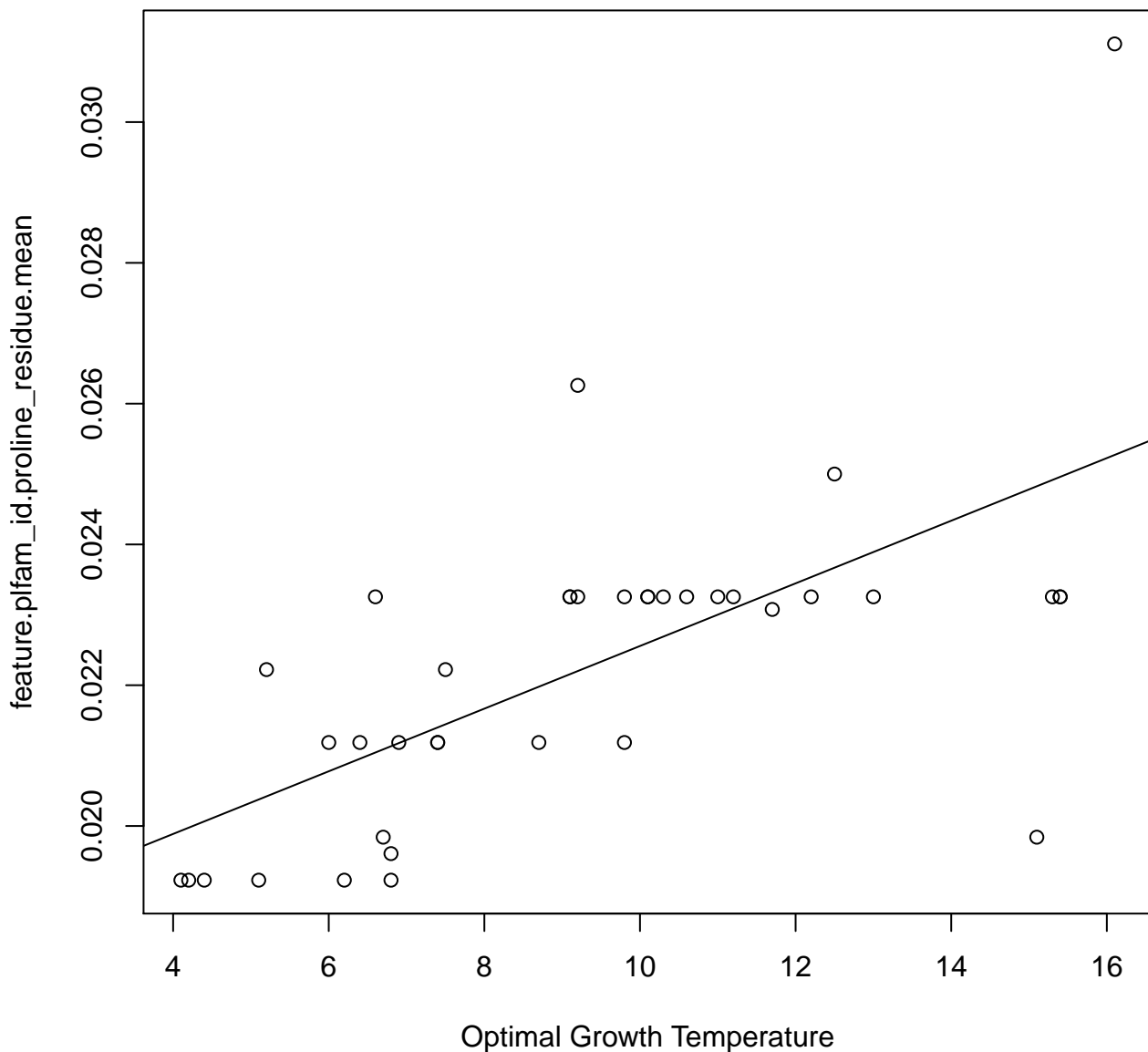
feature.plfam_id.proline_residue.mean
PLF_28228_00001288
Uncharacterized methyltransferase PA1407



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



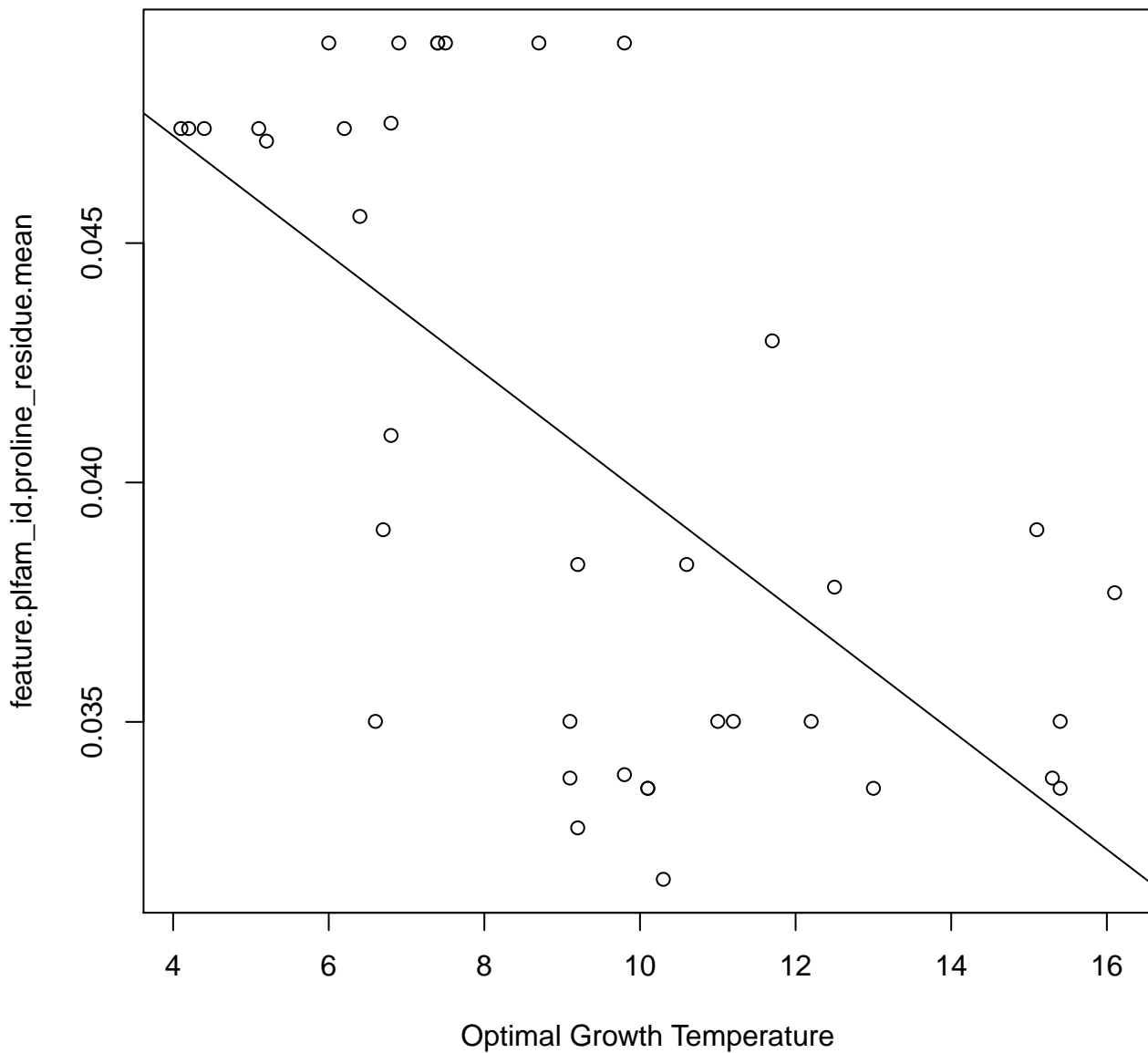
feature.plfam_id.proline_residue.mean
PLF_28228_00002021
SSU rRNA pseudouridine(516) synthase (EC 5.4.99.19)



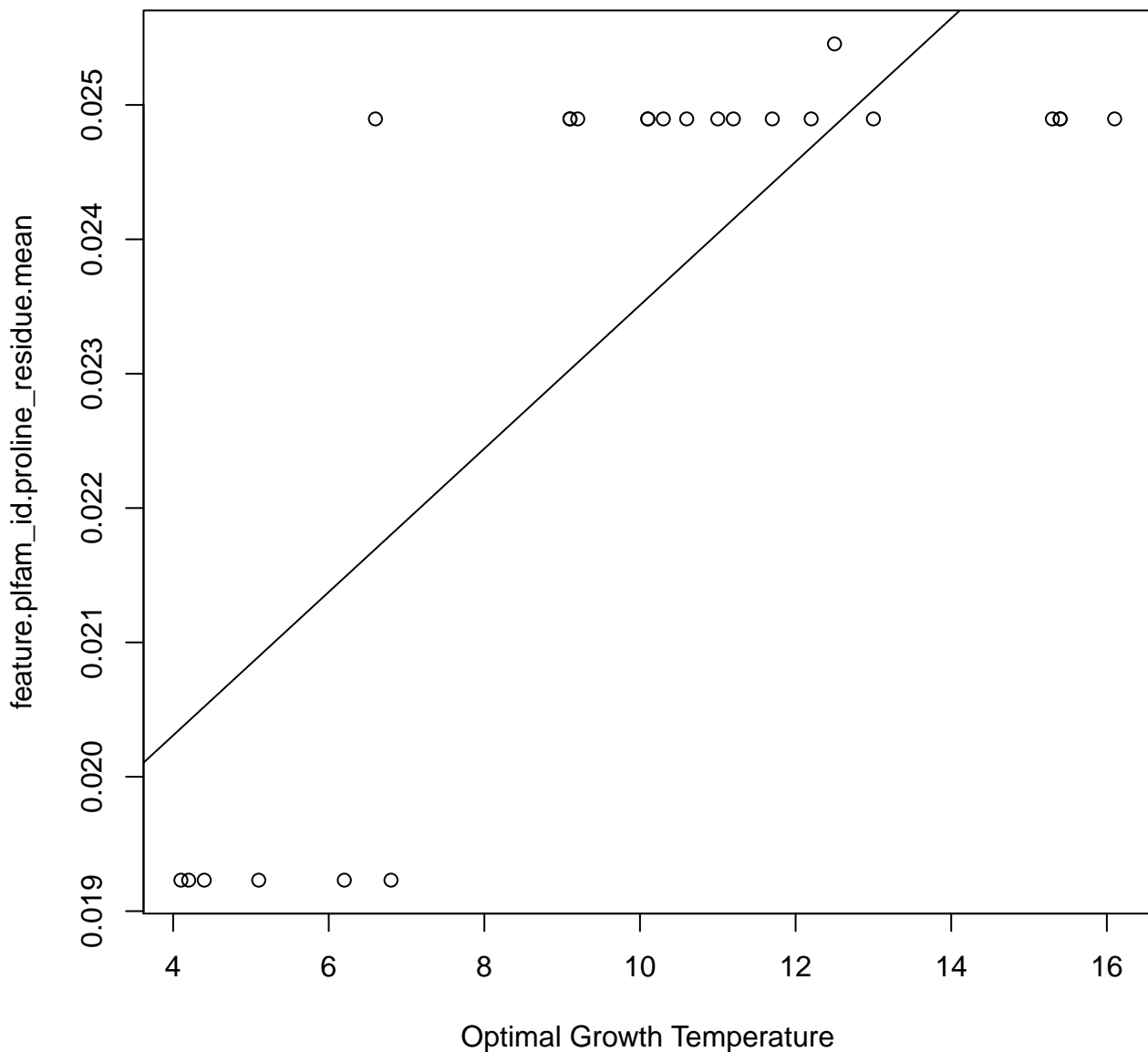
feature.plfam_id.proline_residue.mean

PLF_28228_00002525

hypothetical protein



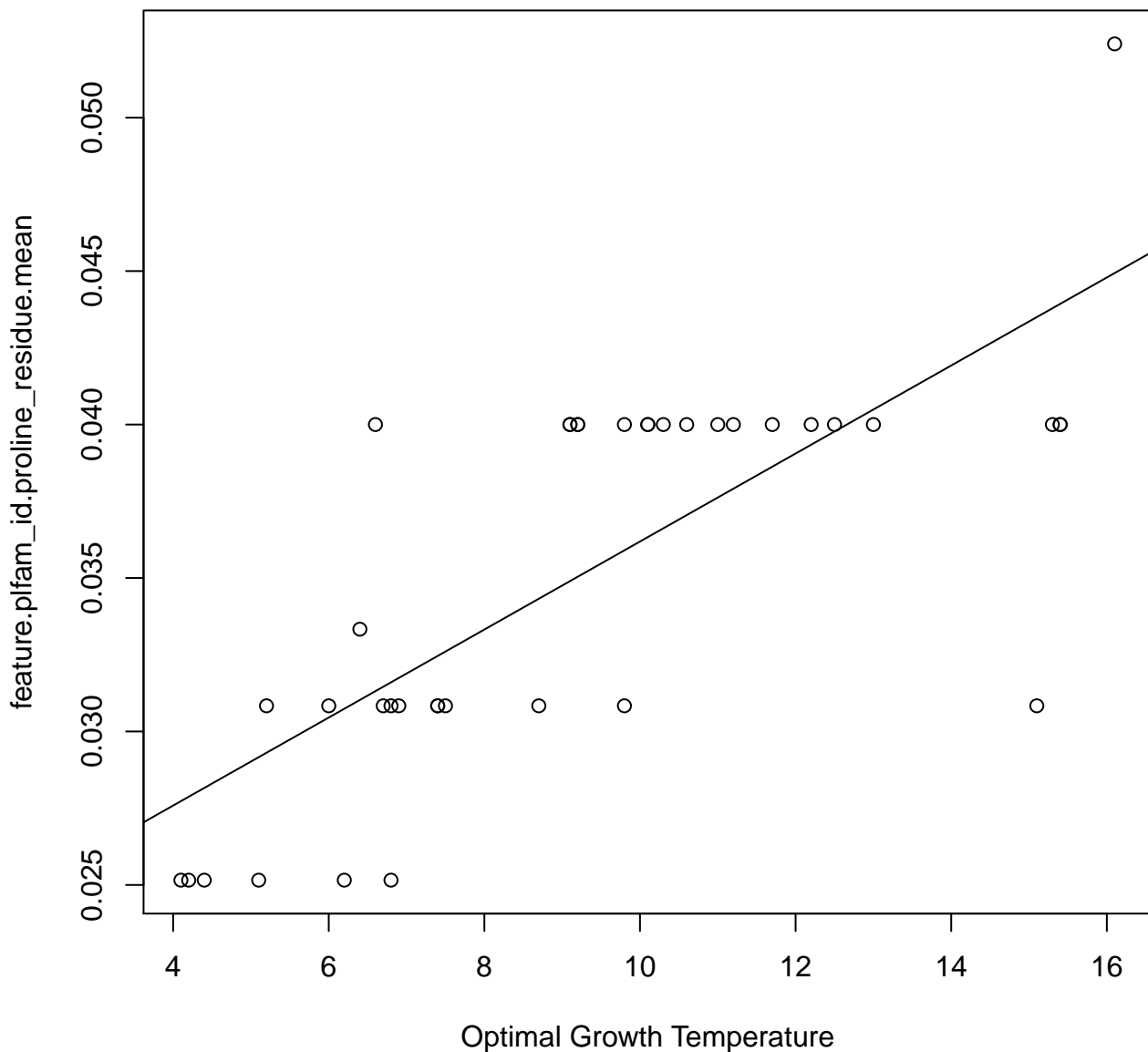
feature.plfam_id.proline_residue.mean
PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



feature.plfam_id.proline_residue.mean

PLF_28228_00002803

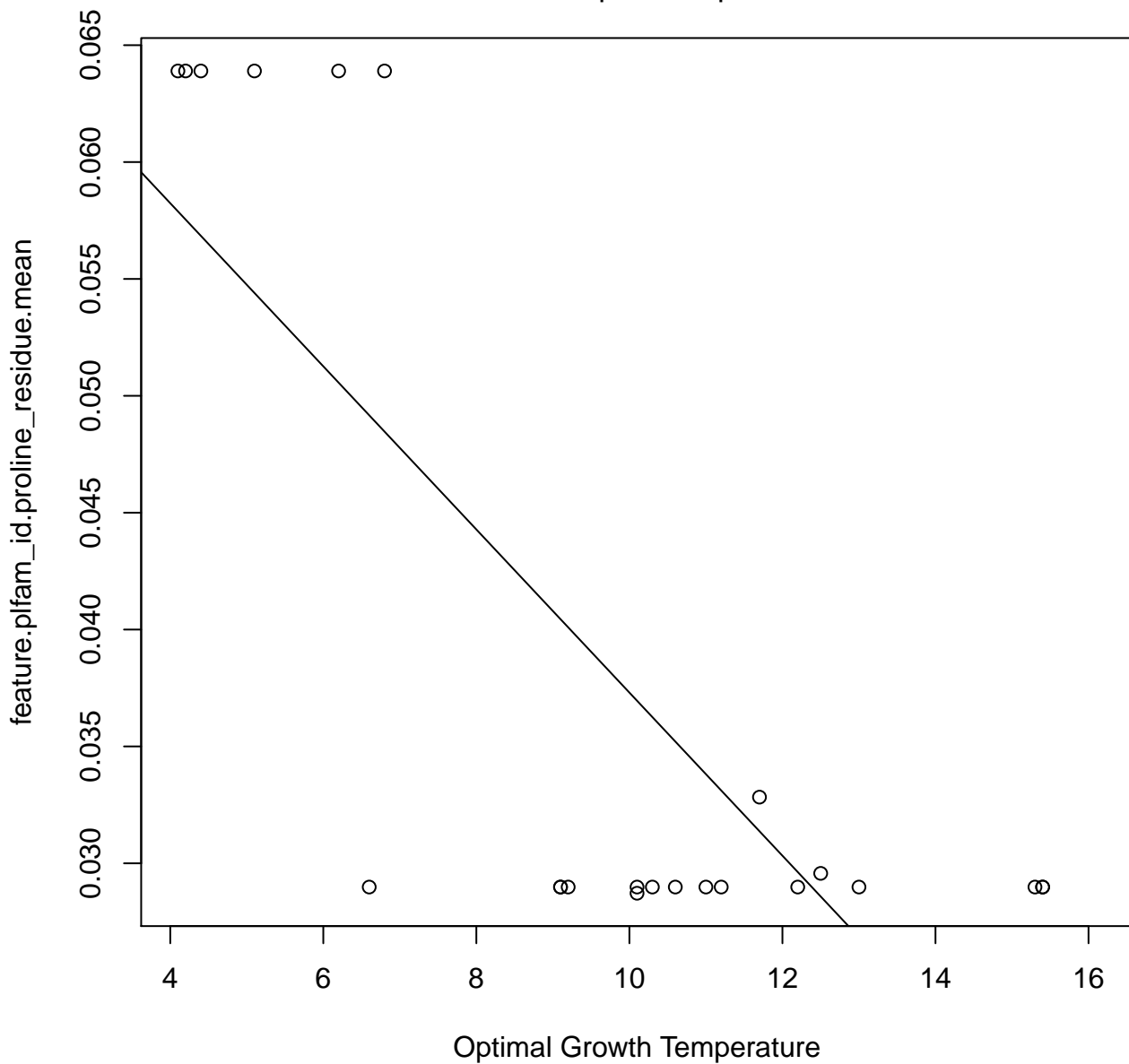
SM-20-related protein



feature.plfam_id.proline_residue.mean

PLF_28228_00002829

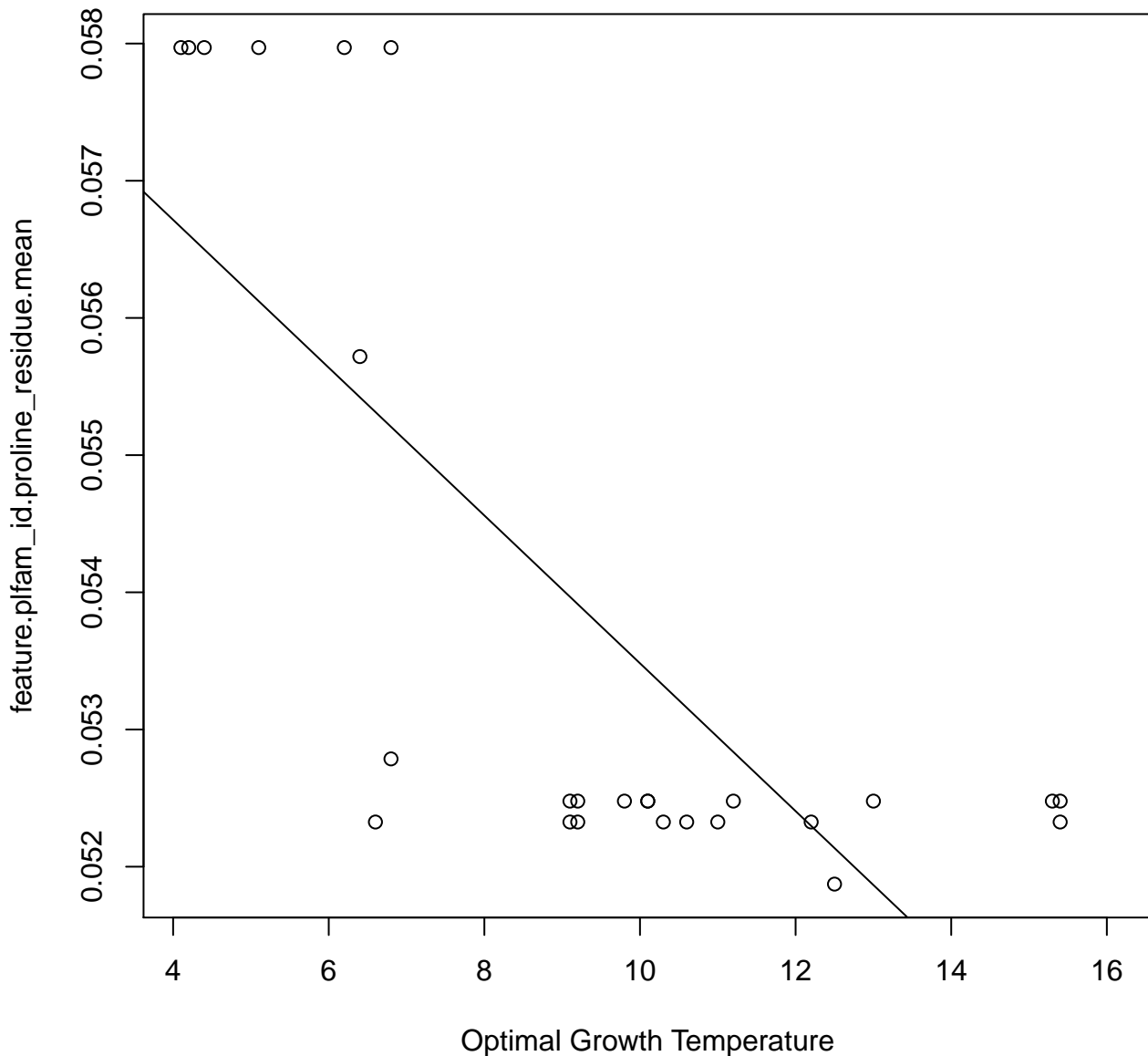
TonB-dependent receptor



feature.plfam_id.proline_residue.mean

PLF_28228_00003411

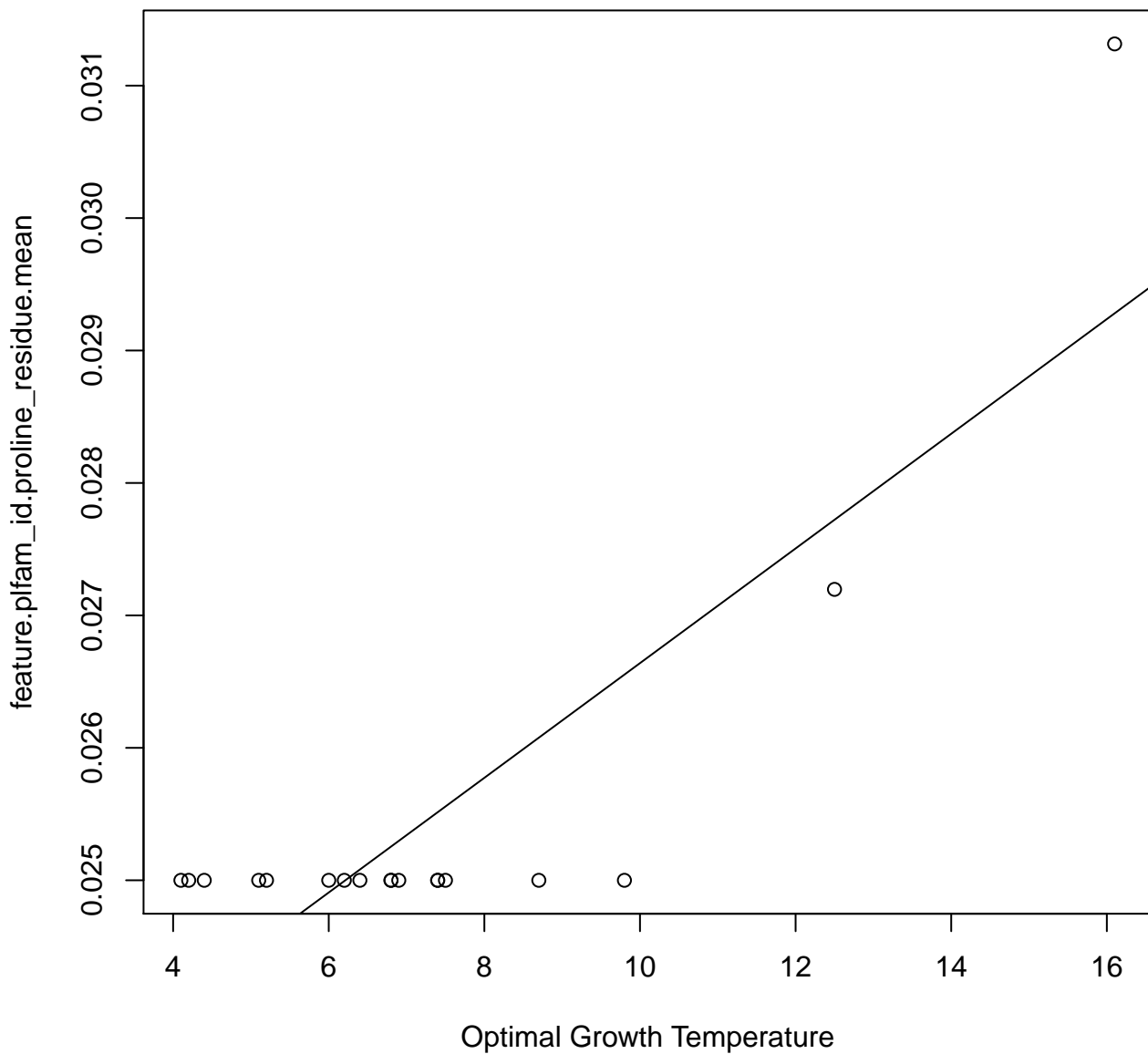
CDP-glycerol: N-acetyl-beta-D-mannosaminy-1,4-N-acetyl-D-glucosaminyldiphosphoundecaprenyl glycerophosphotransfer



feature.plfam_id.proline_residue.mean

PLF_28228_00003471

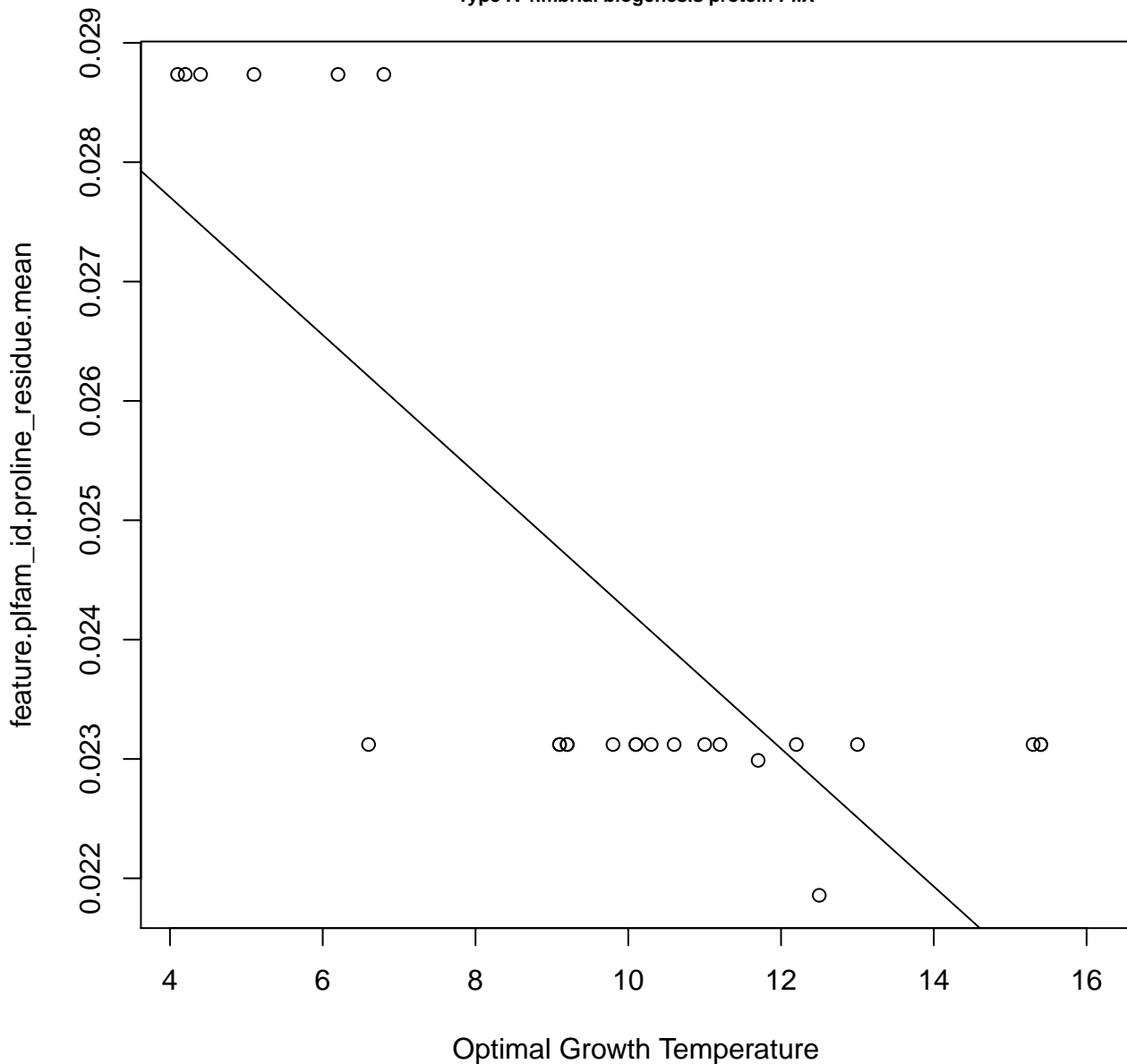
Glucose/mannose:H⁺ symporter GlcP



feature.plfam_id.proline_residue.mean

PLF_28228_00003777

Type IV fimbrial biogenesis protein PilX

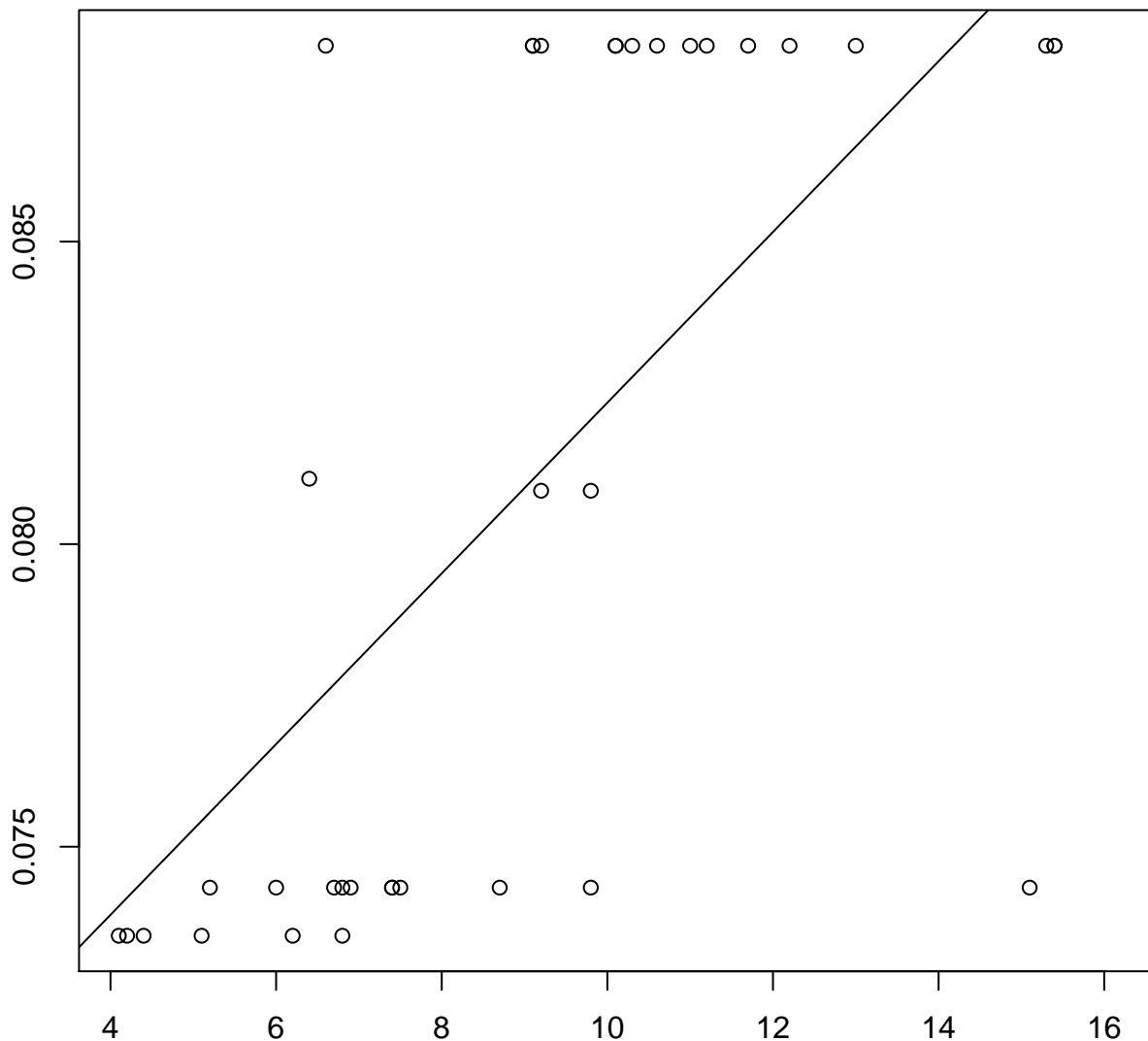


feature.plfam_id.proline_residue.mean

PLF_28228_00006228

hypothetical protein

feature.plfam_id.proline_residue.mean

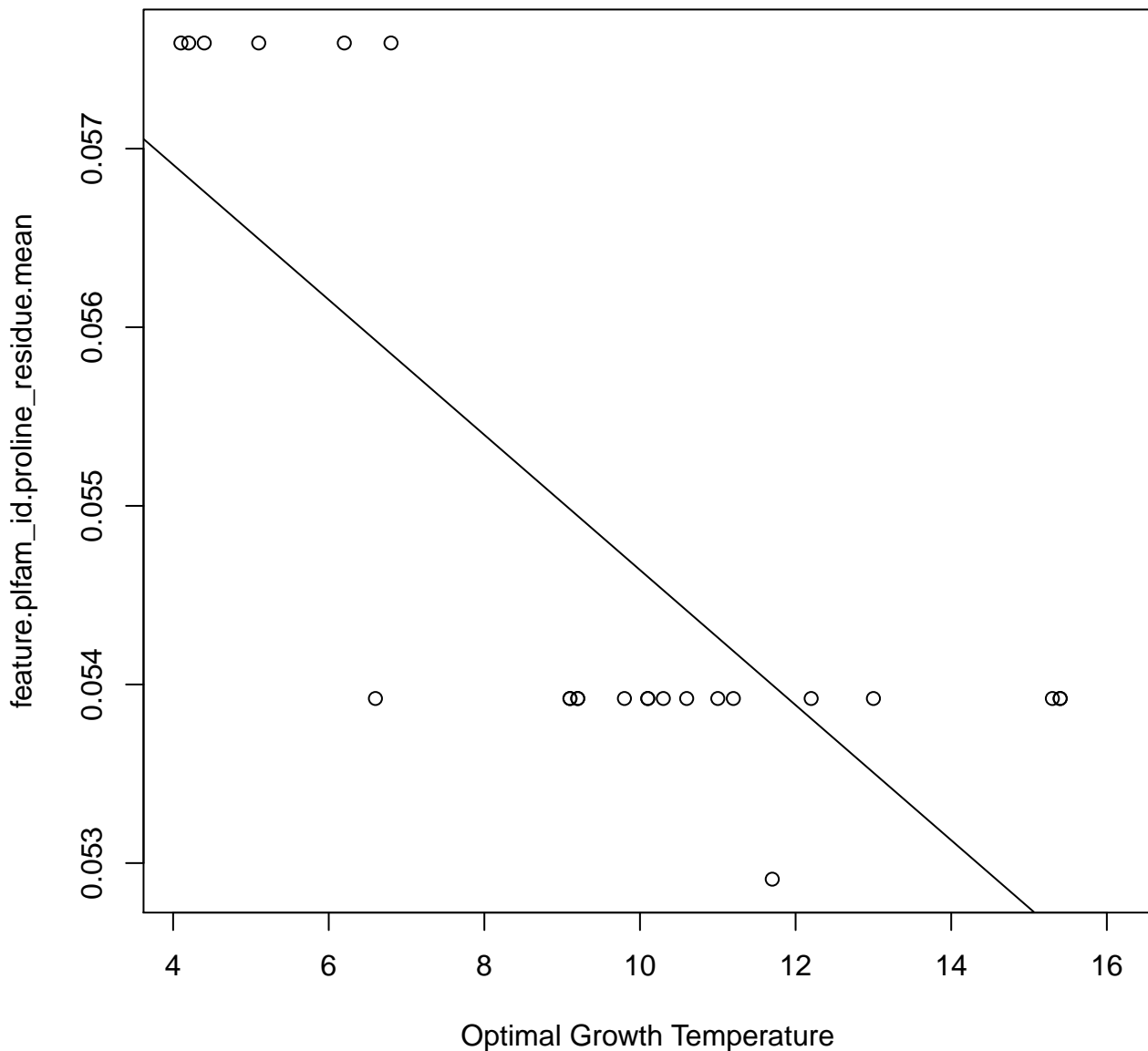


Optimal Growth Temperature

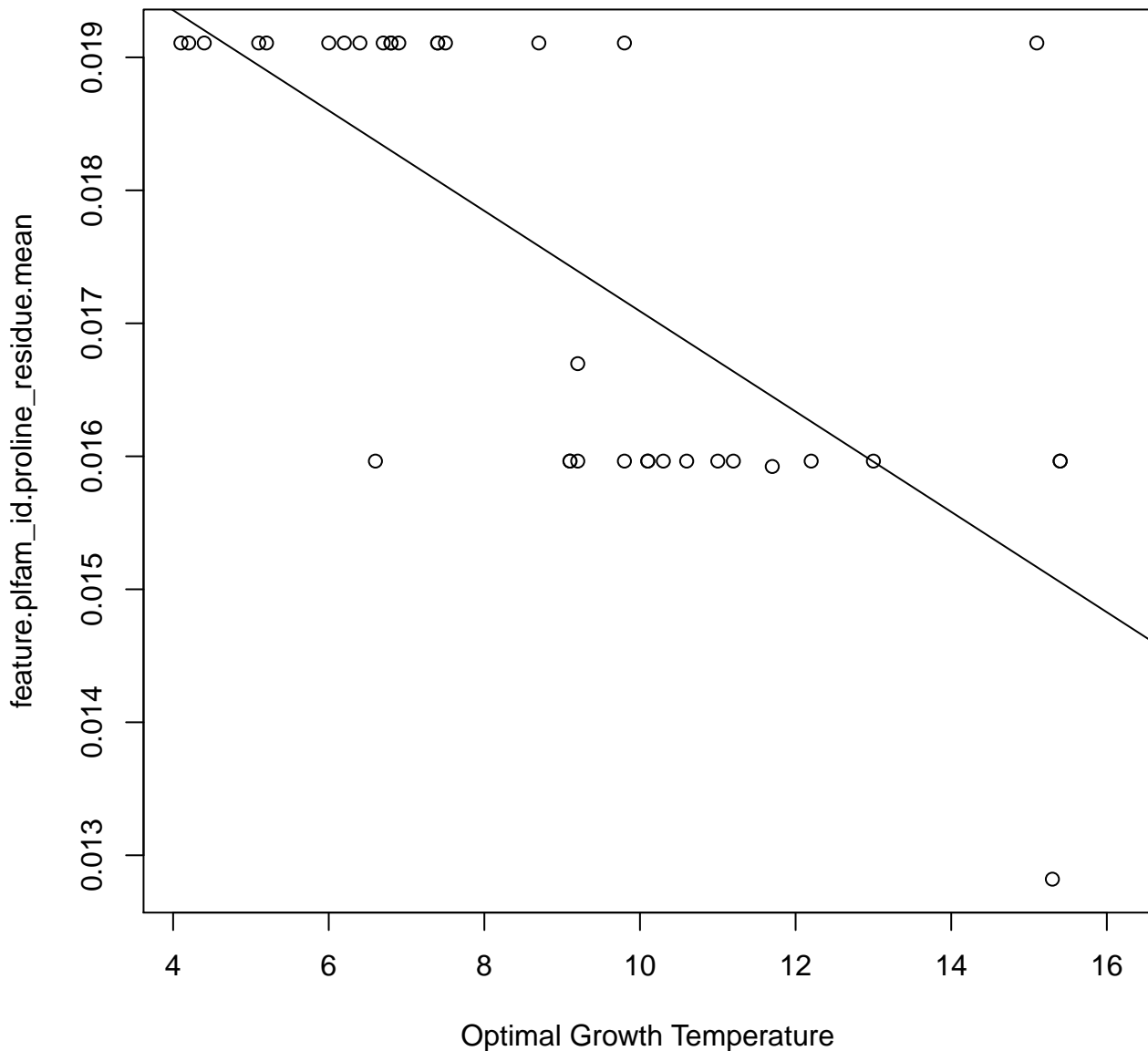
feature.plfam_id.proline_residue.mean

PLF_28228_00007320

Arylesterase precursor (EC 3.1.1.2)



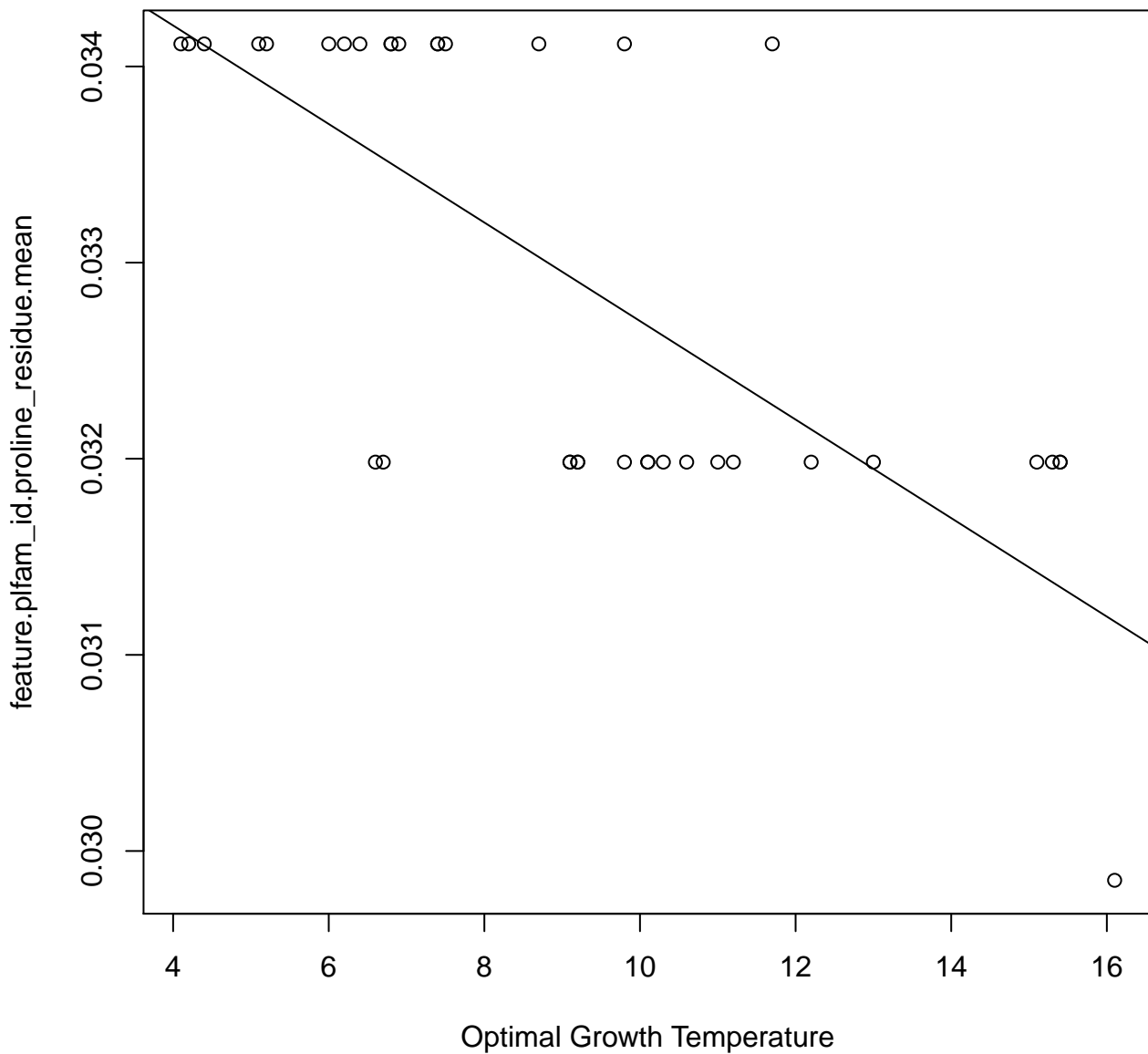
feature.plfam_id.proline_residue.mean
PLF_28228_00010807
DNA protection during starvation protein



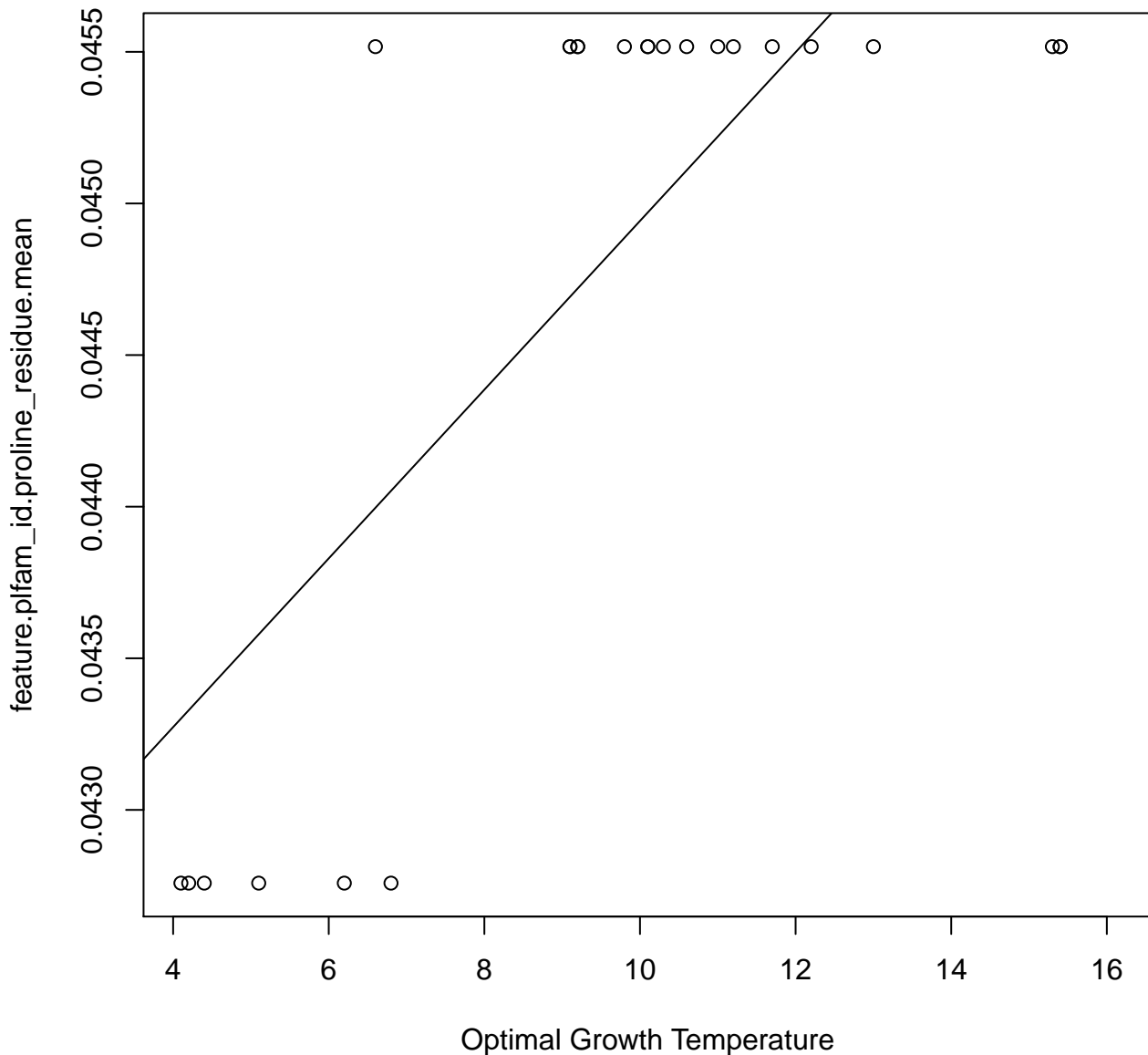
feature.plfam_id.proline_residue.mean

PLF_28228_00014301

Aminopeptidase CC_2544



feature.plfam_id.proline_residue.mean
PLF_28228_00014473
Uncharacterized aldehyde oxidase, molybdopterin-binding subunit

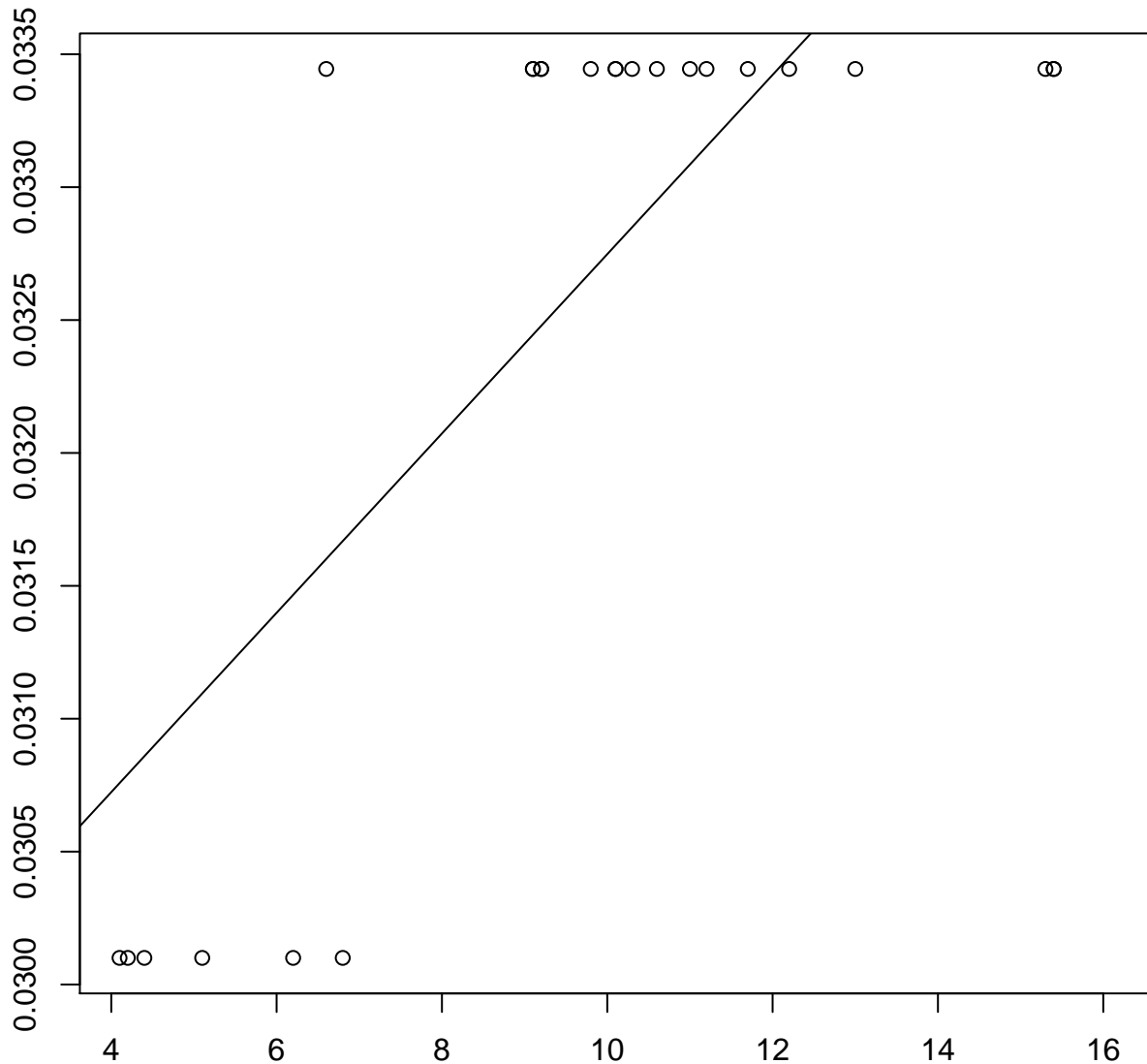


feature.plfam_id.proline_residue.mean

PLF_28228_00016148

hypothetical protein

feature.plfam_id.proline_residue.mean

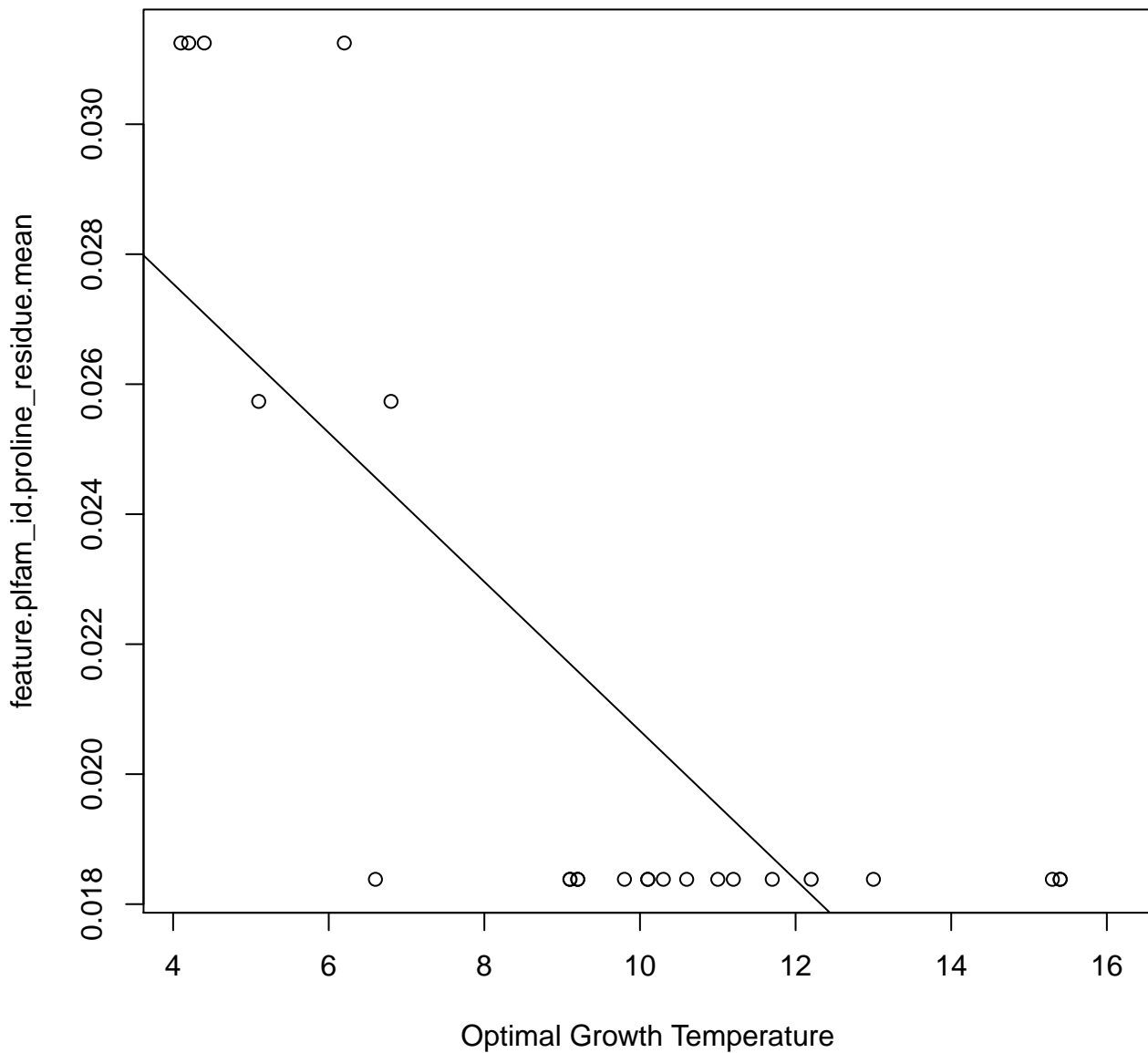


Optimal Growth Temperature

feature.plfam_id.proline_residue.mean

PLF_28228_00016648

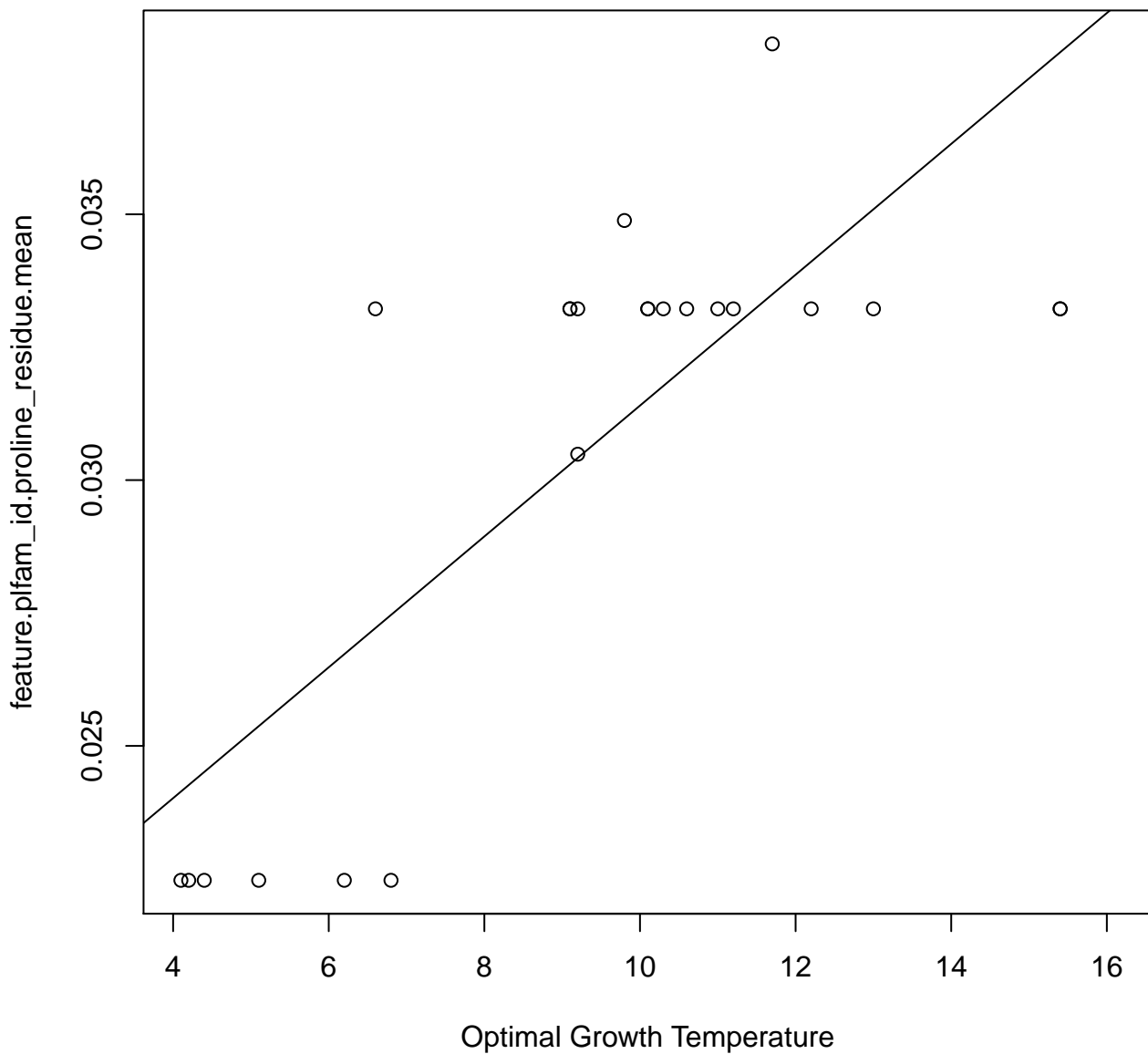
hypothetical protein



feature.plfam_id.proline_residue.mean

PLF_28228_00017455

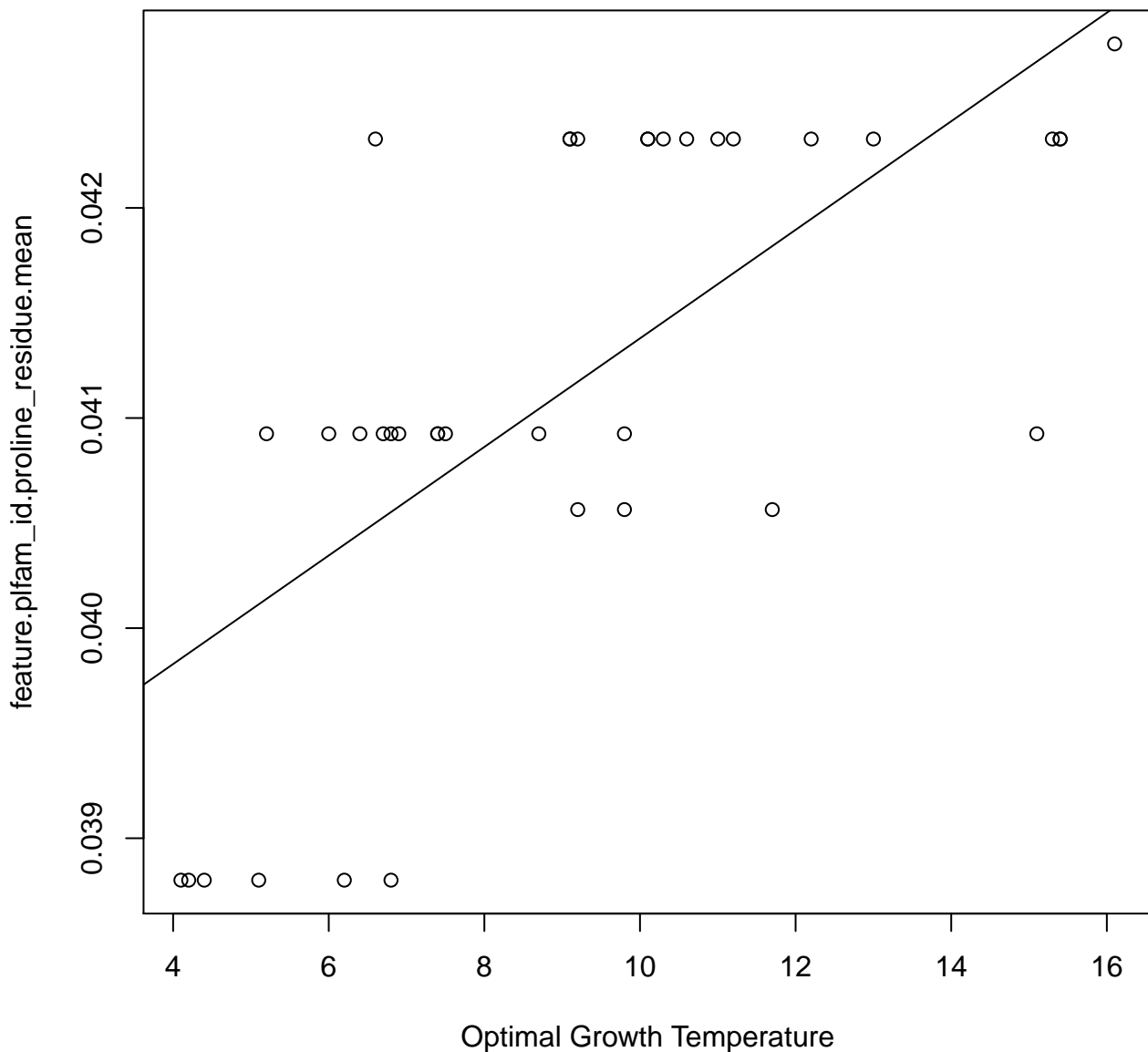
Maltodextrin glucosidase (EC 3.2.1.20)



feature.plfam_id.proline_residue.mean

PLF_28228_00018483

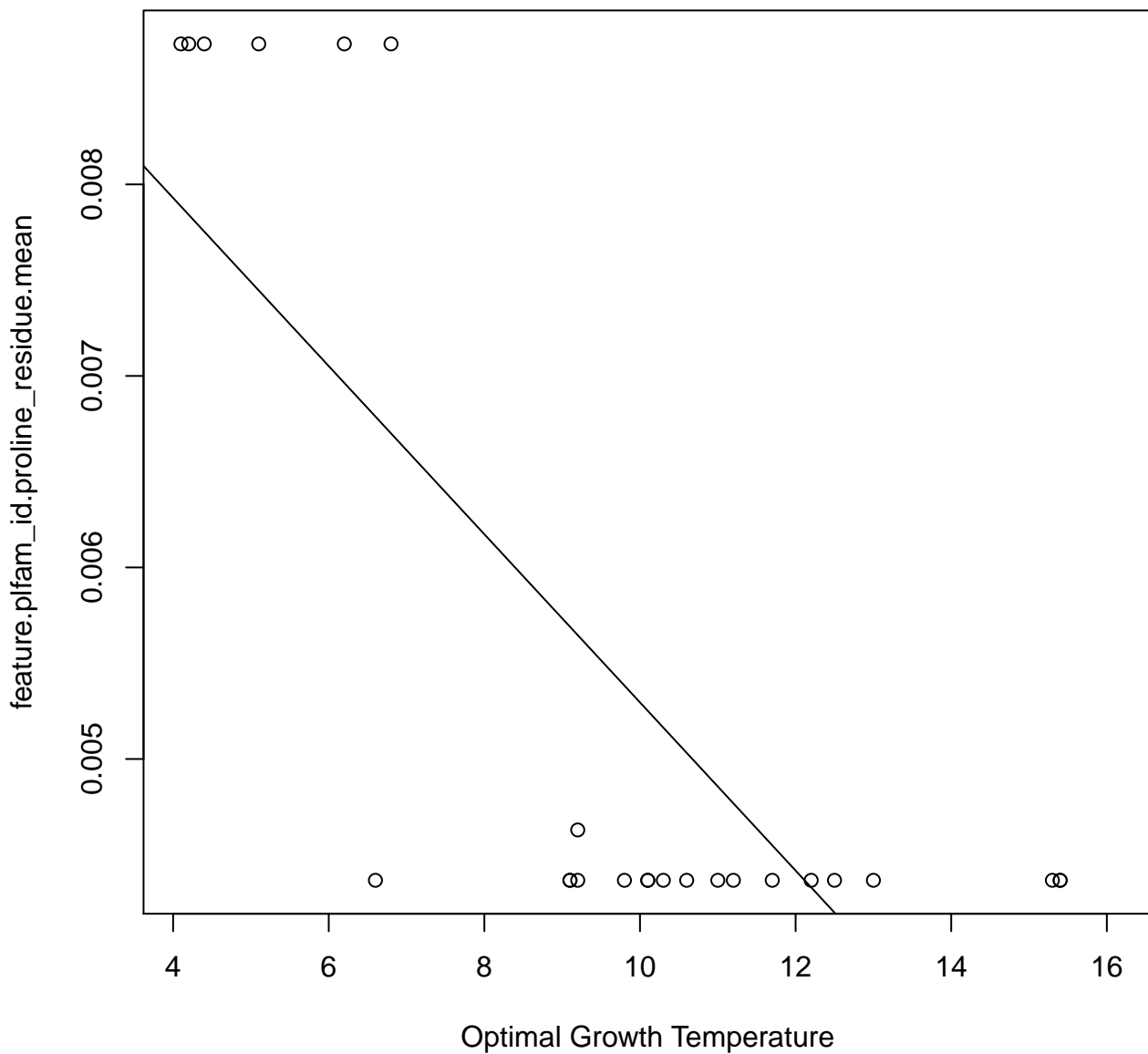
Chloride channel protein EriC



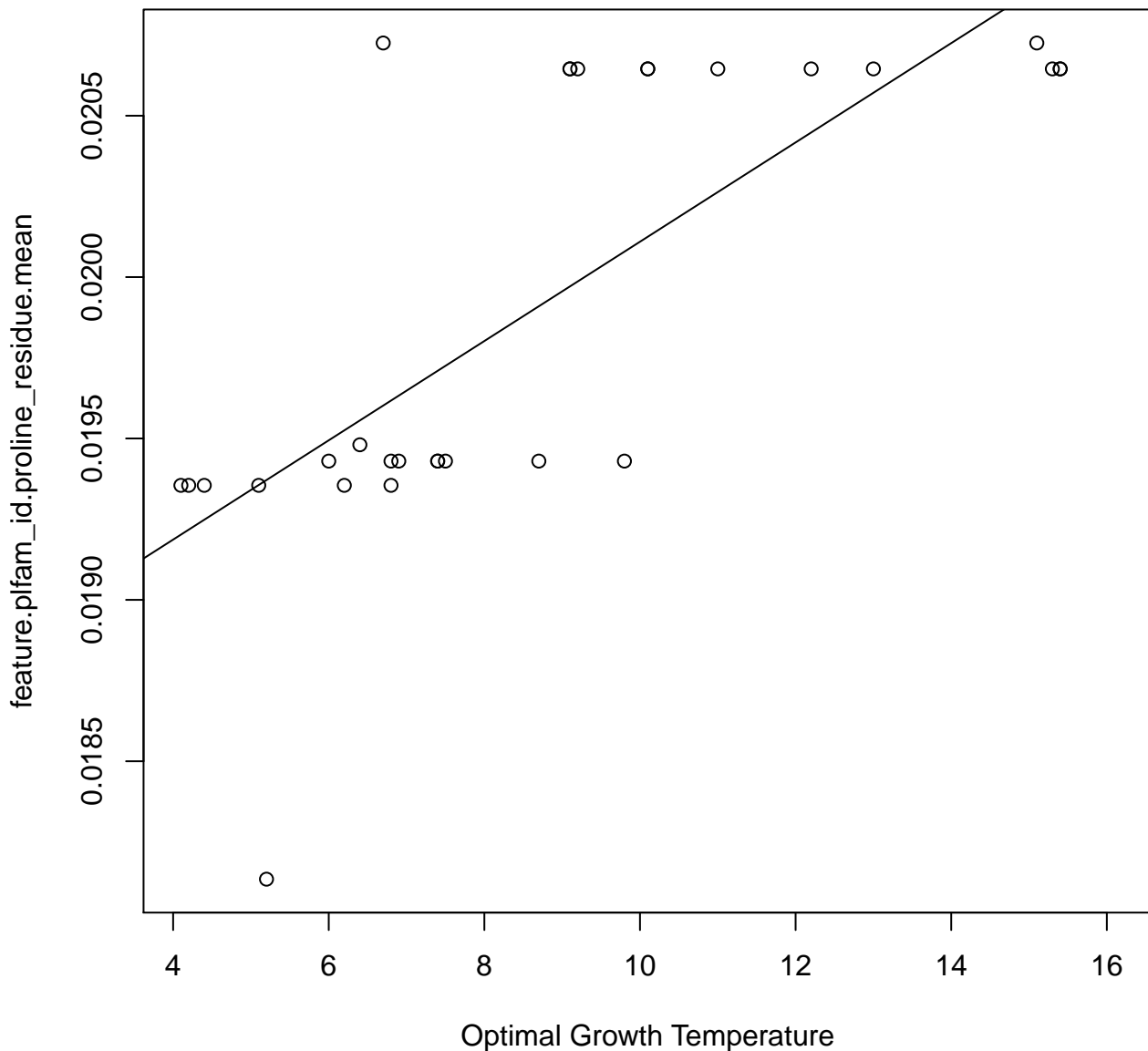
feature.plfam_id.proline_residue.mean

PLF_28228_00018510

Conserved hypothetical protein 2001



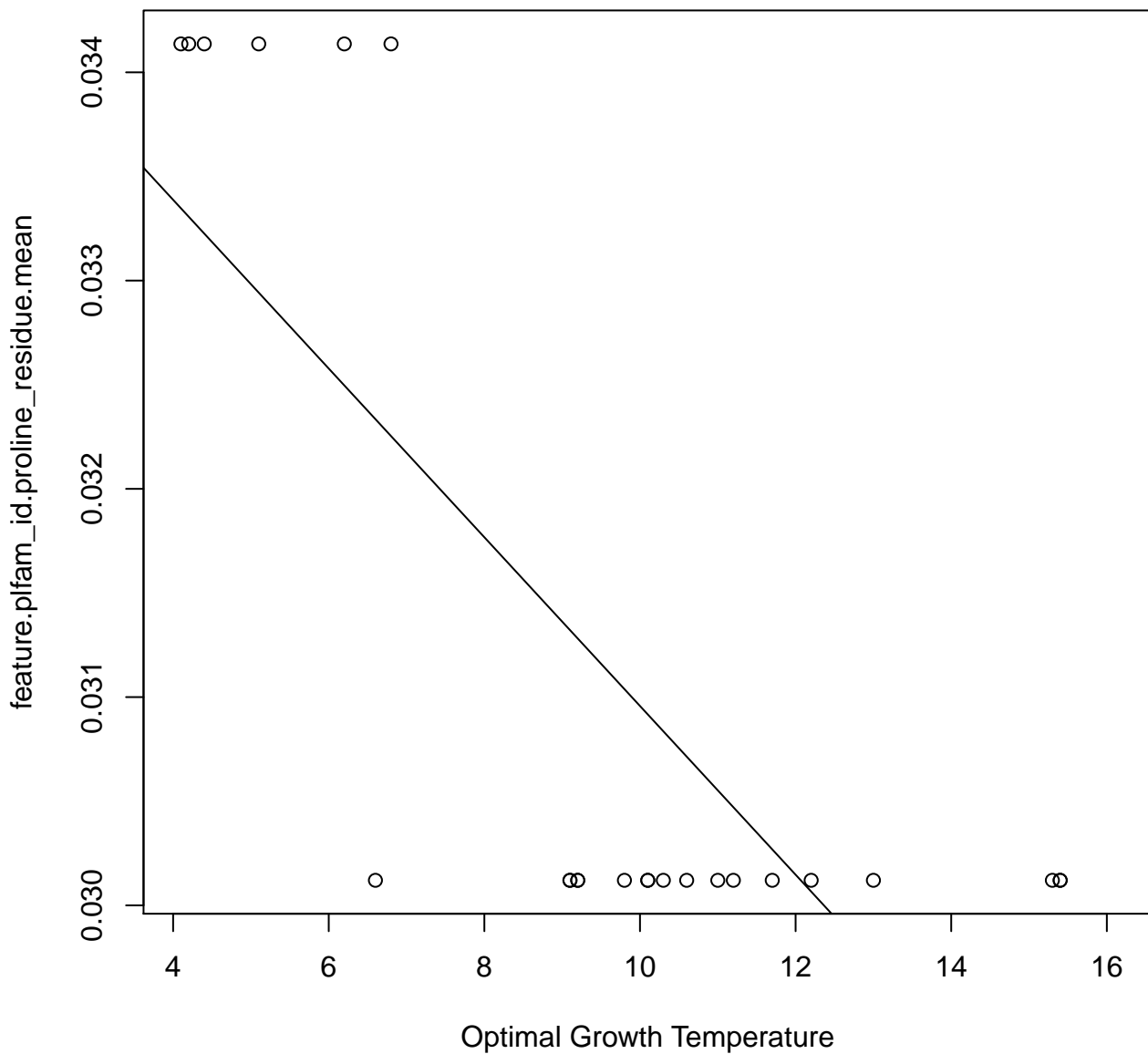
feature.plfam_id.proline_residue.mean
PLF_28228_00021199
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)



feature.plfam_id.proline_residue.mean

PLF_28228_00027931

Inorganic triphosphatase (EC 3.6.1.25)



feature.plfam_id.proline_residue.mean

PLF_28228_00028047

Fatty acid cis/trans isomerase

feature.plfam_id.proline_residue.mean

0.050
0.048
0.046
0.044

4

6

8

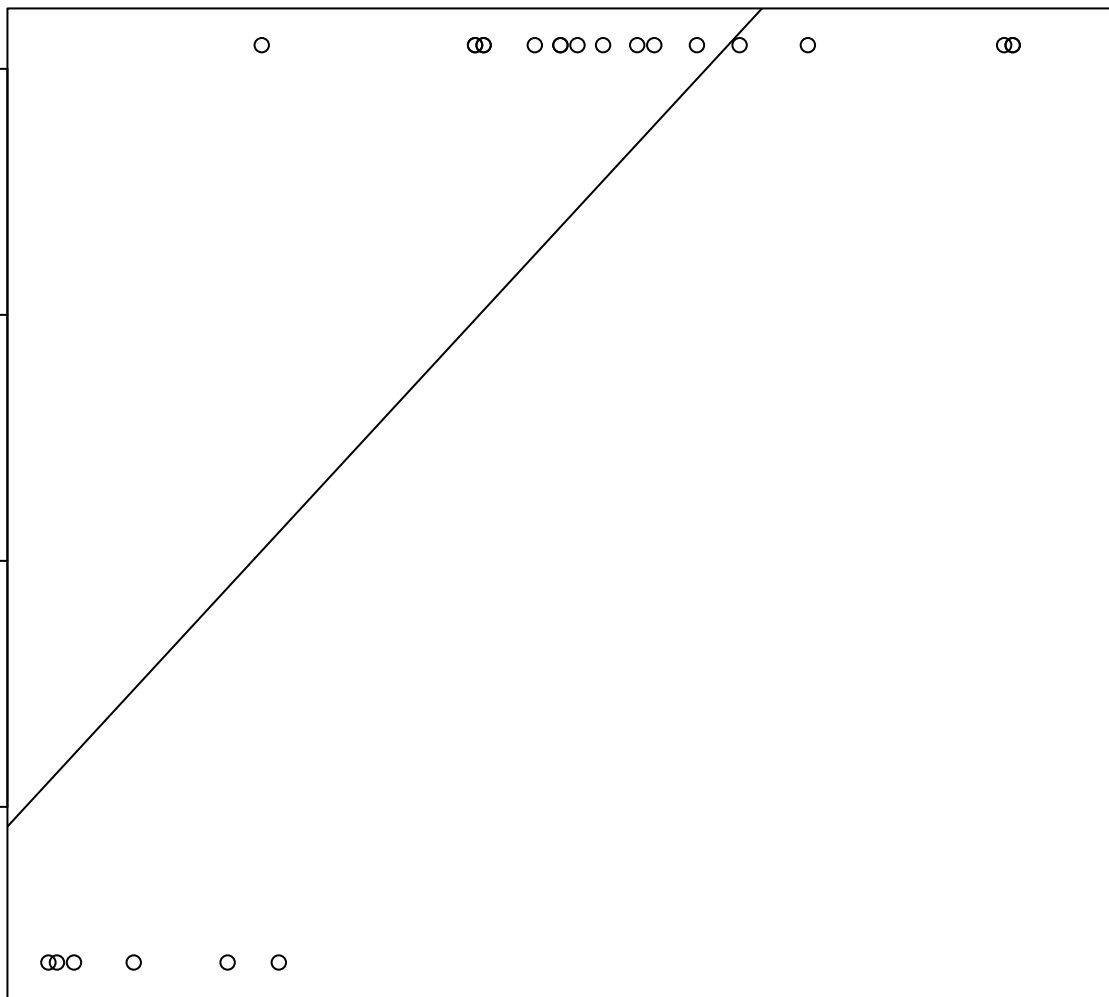
10

12

14

16

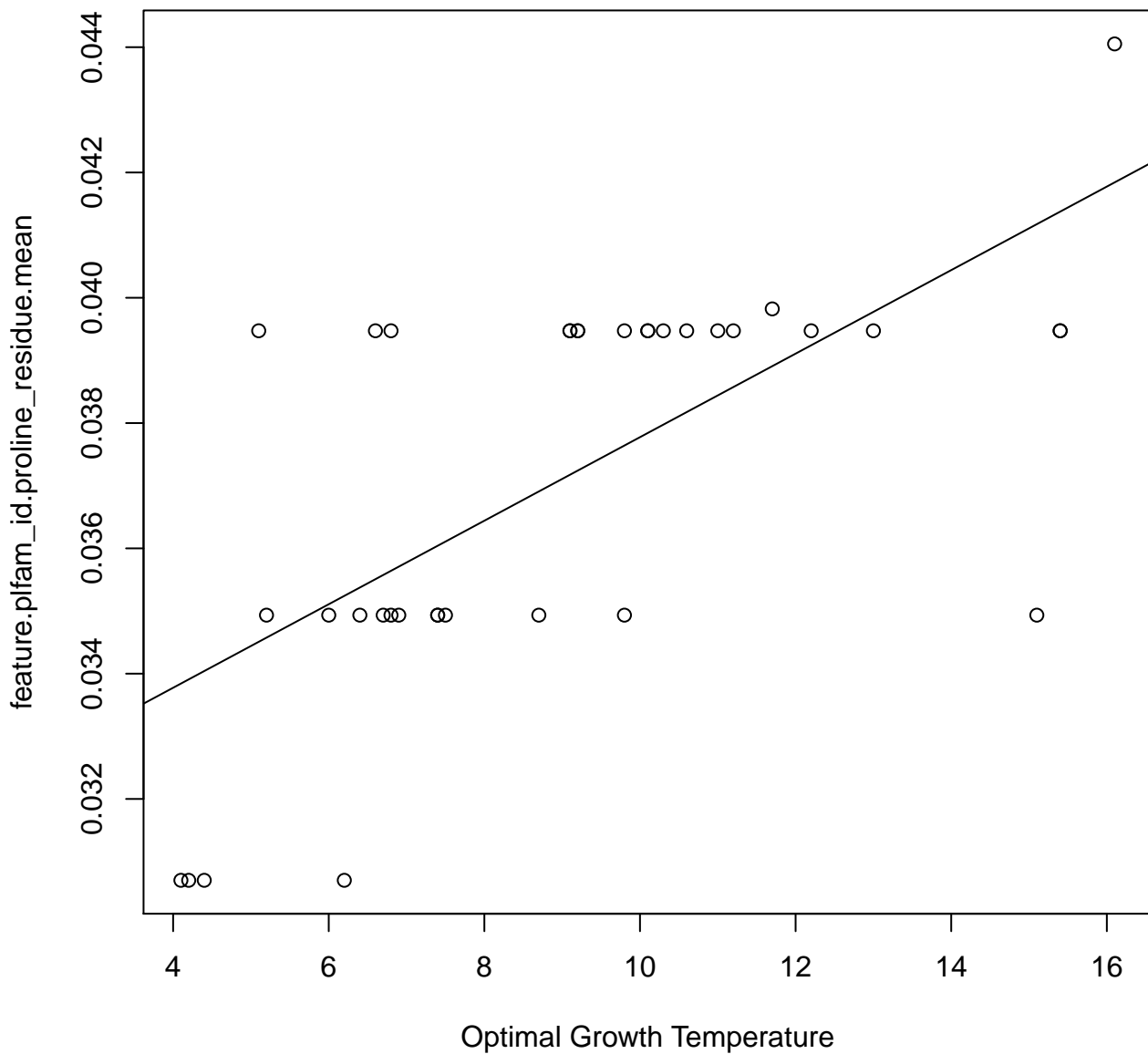
Optimal Growth Temperature



feature.plfam_id.proline_residue.mean

PLF_28228_00028198

FIG111991: hypothetical protein

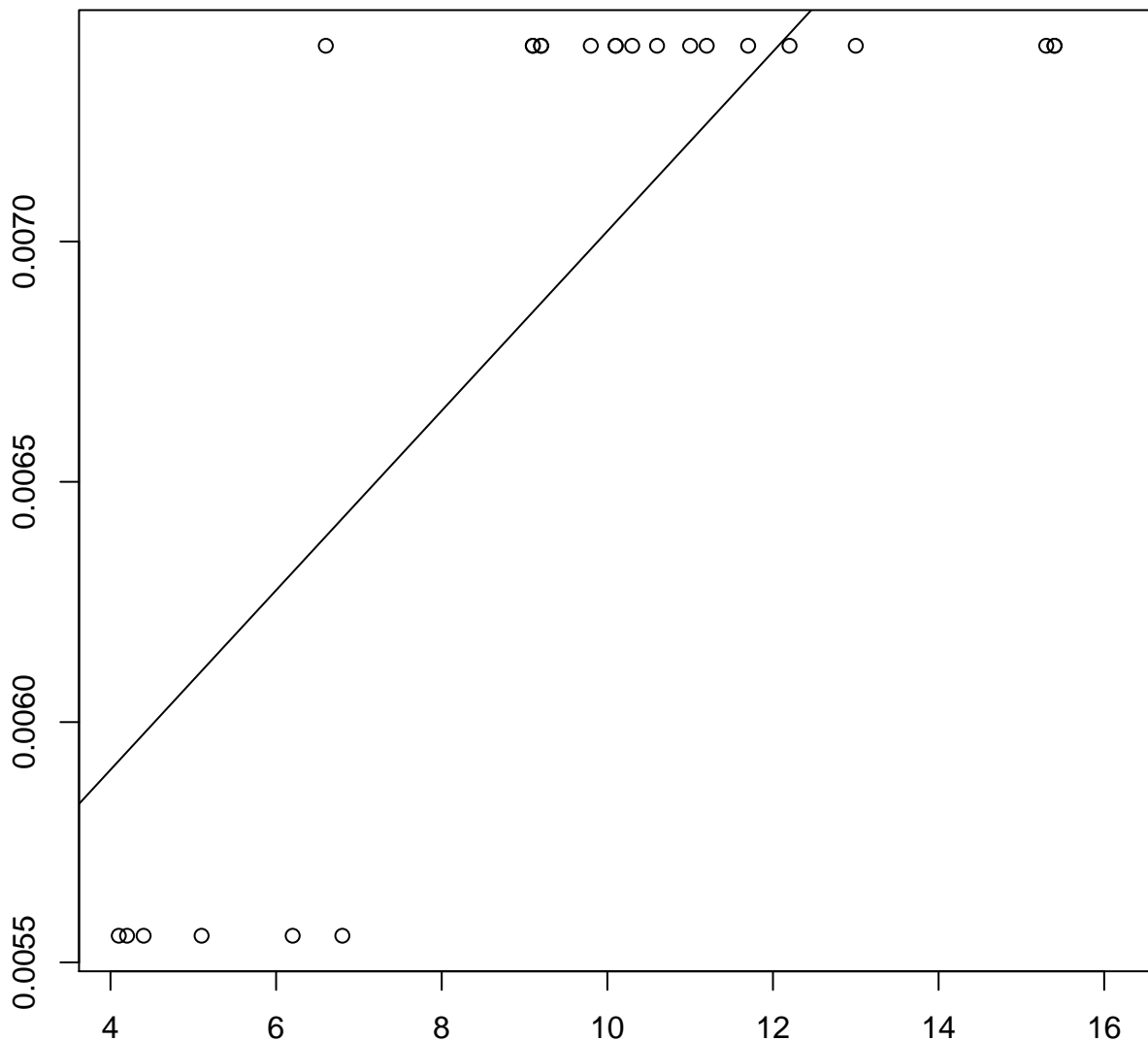


feature.plfam_id.proline_residue.mean

PLF_28228_00028208

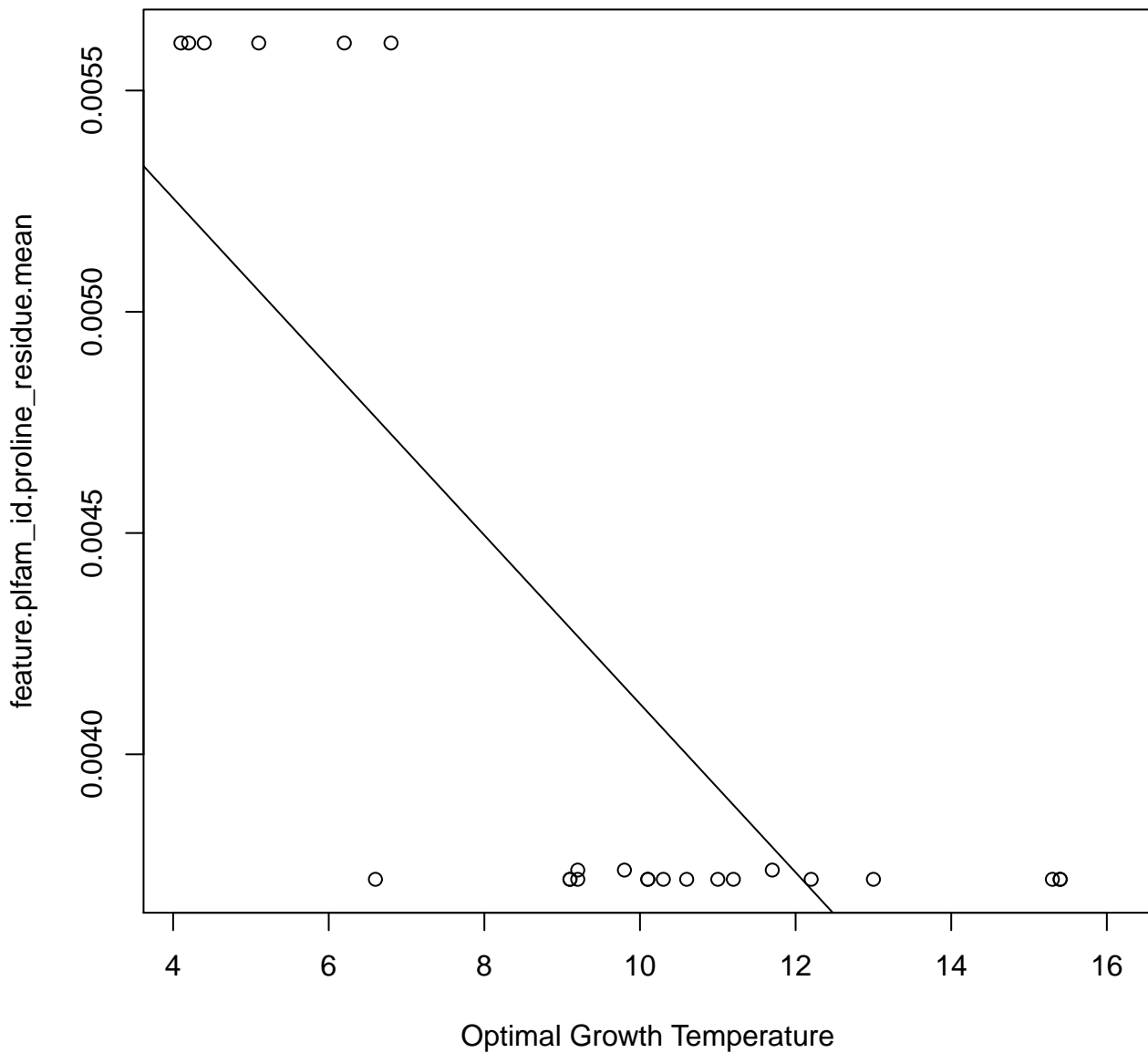
hypothetical protein

feature.plfam_id.proline_residue.mean

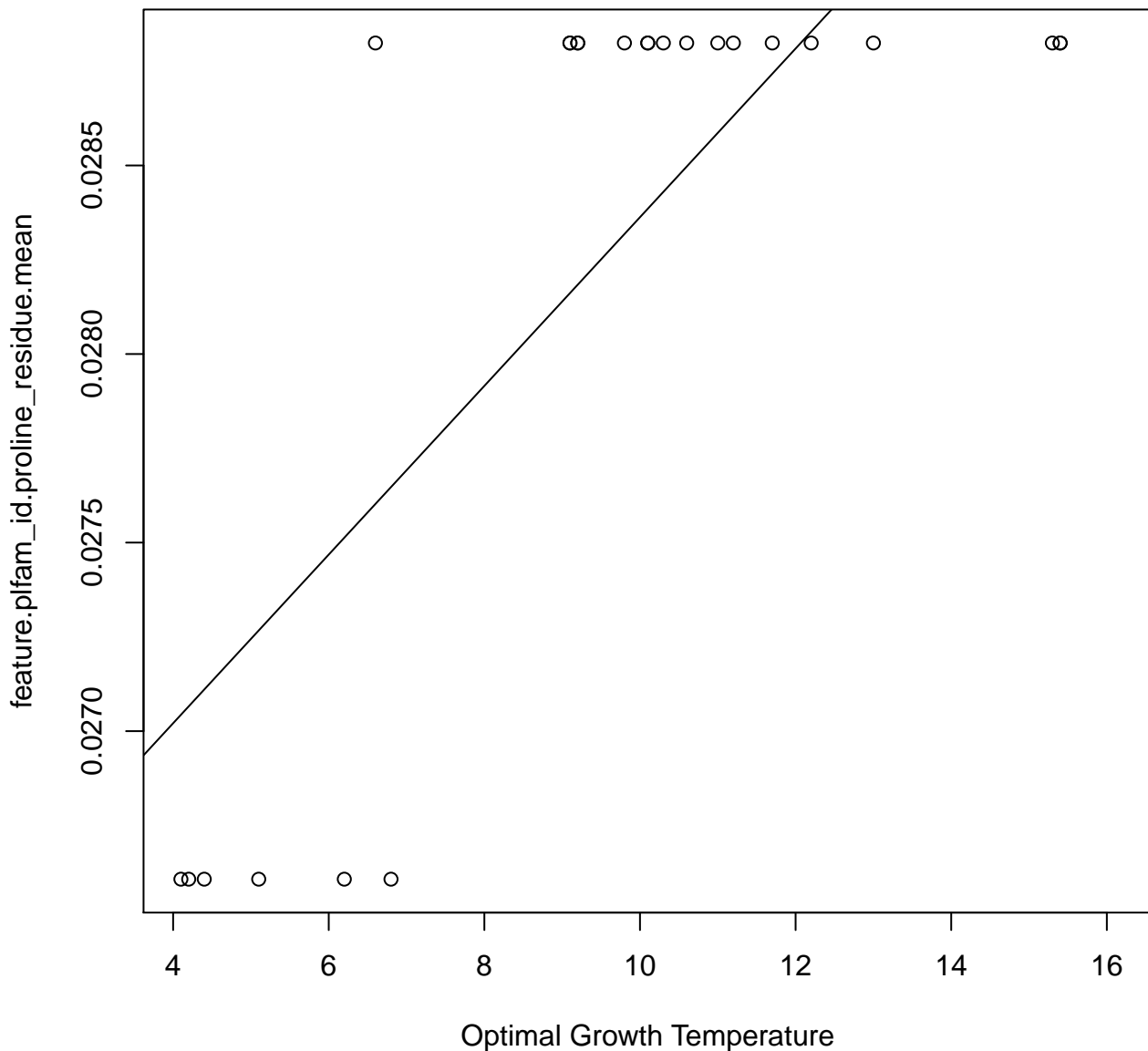


Optimal Growth Temperature

feature.plfam_id.proline_residue.mean
PLF_28228_00028320
Methyl-accepting chemotaxis sensor/transducer protein



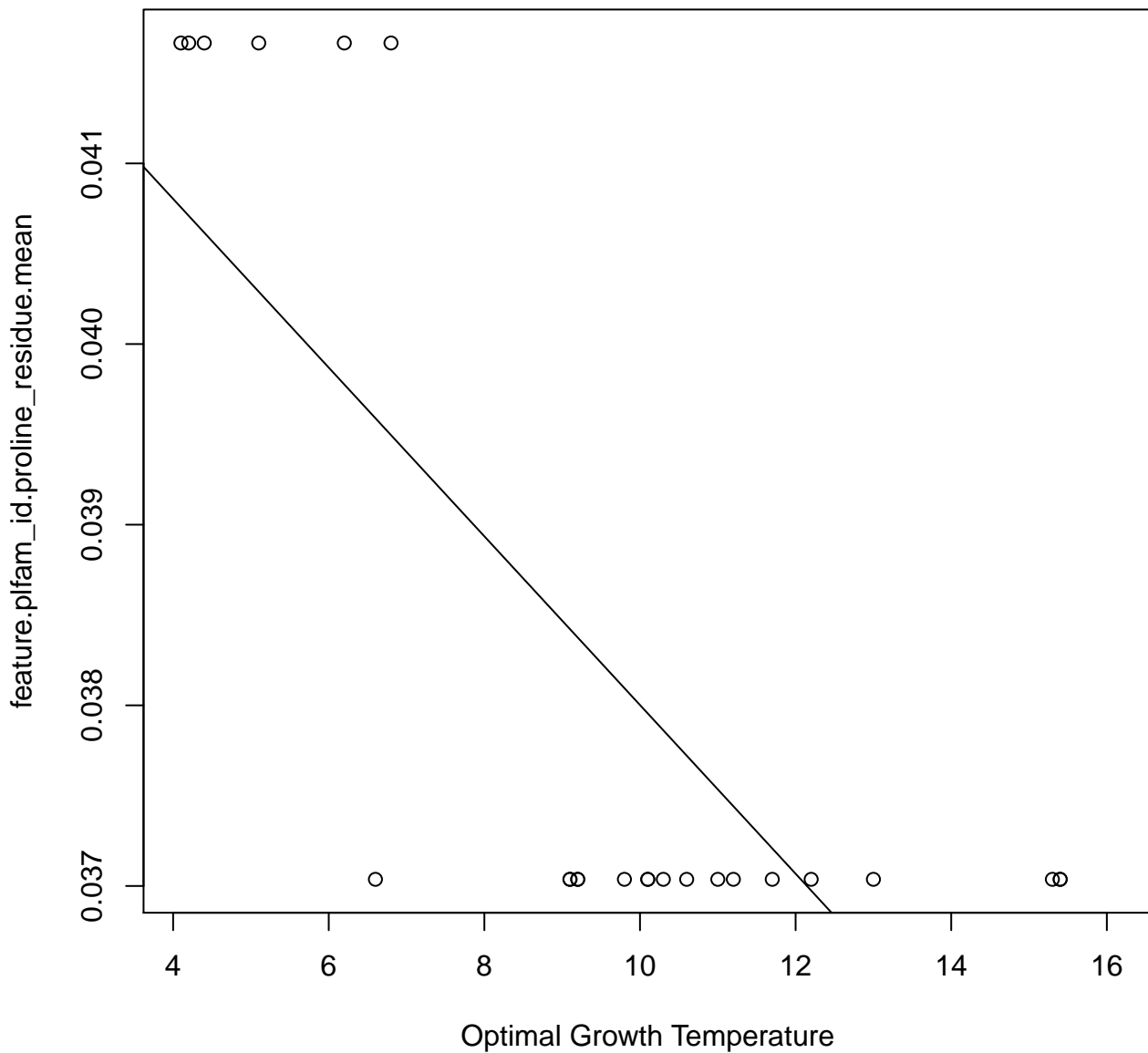
feature.plfam_id.proline_residue.mean
PLF_28228_00028633
Mg/Co/Ni transporter MgtE, CBS domain-containing



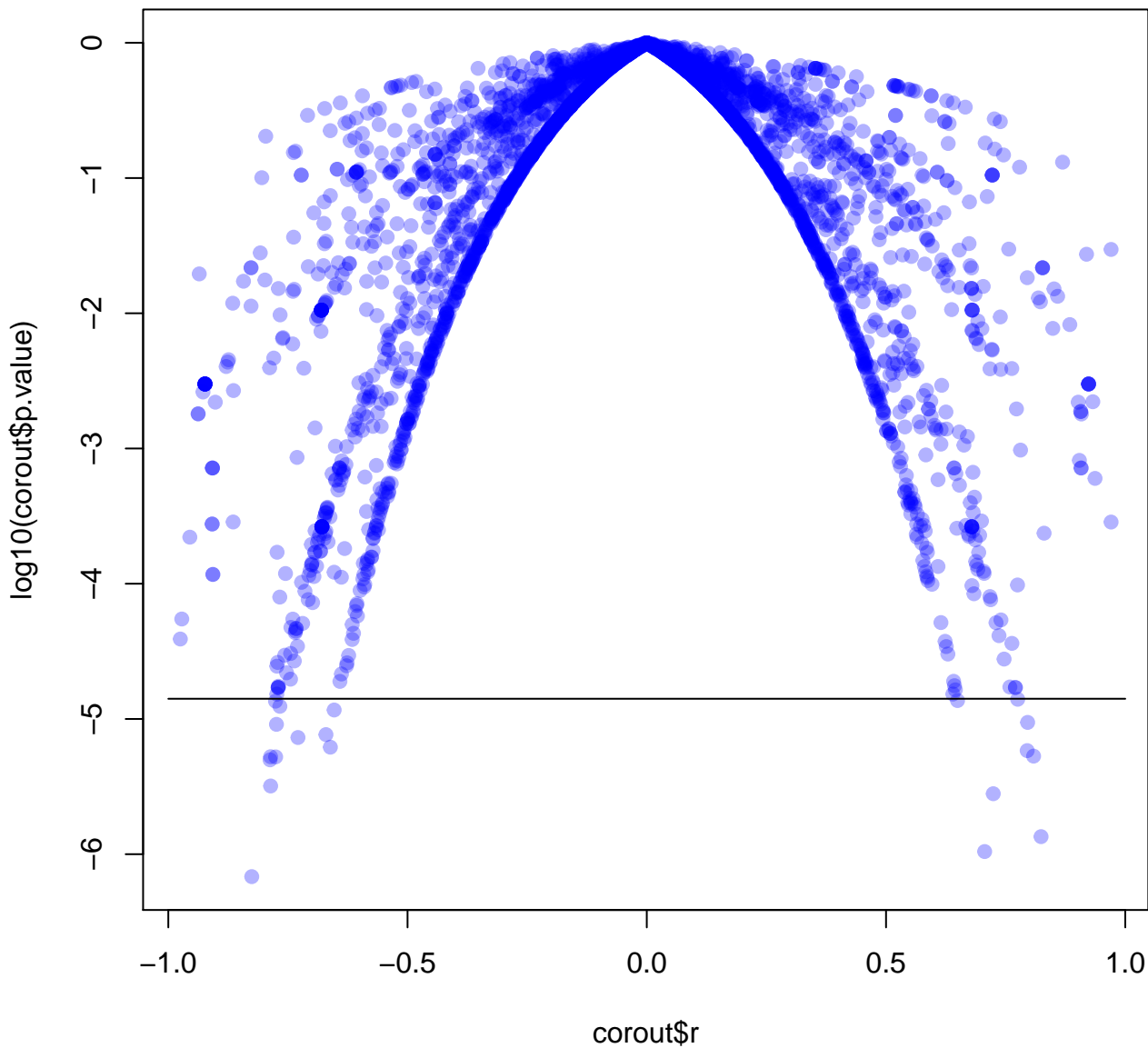
feature.plfam_id.proline_residue.mean

PLF_28228_00031893

hypothetical protein



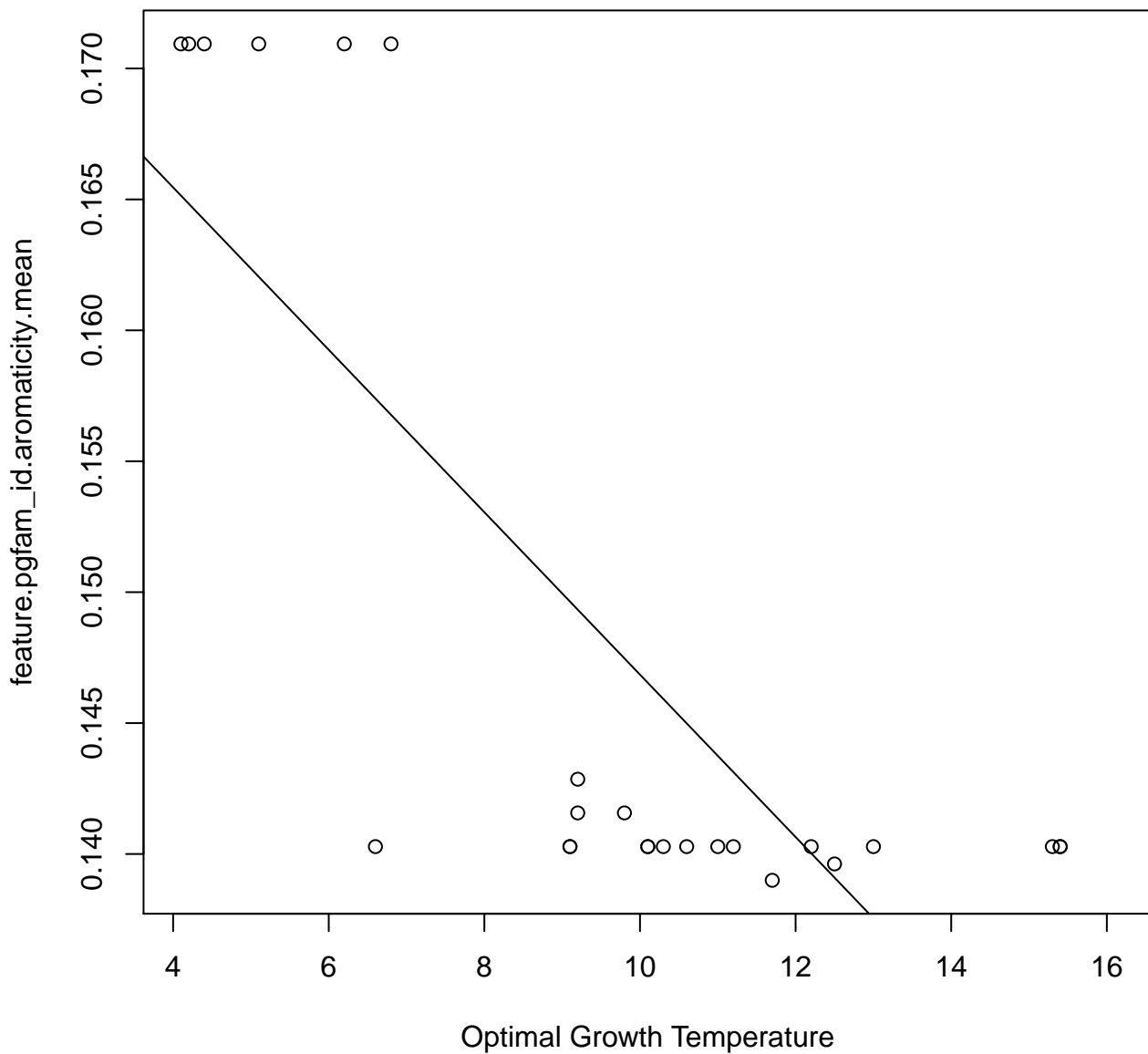
feature.pgfam_id.aromaticity.mean



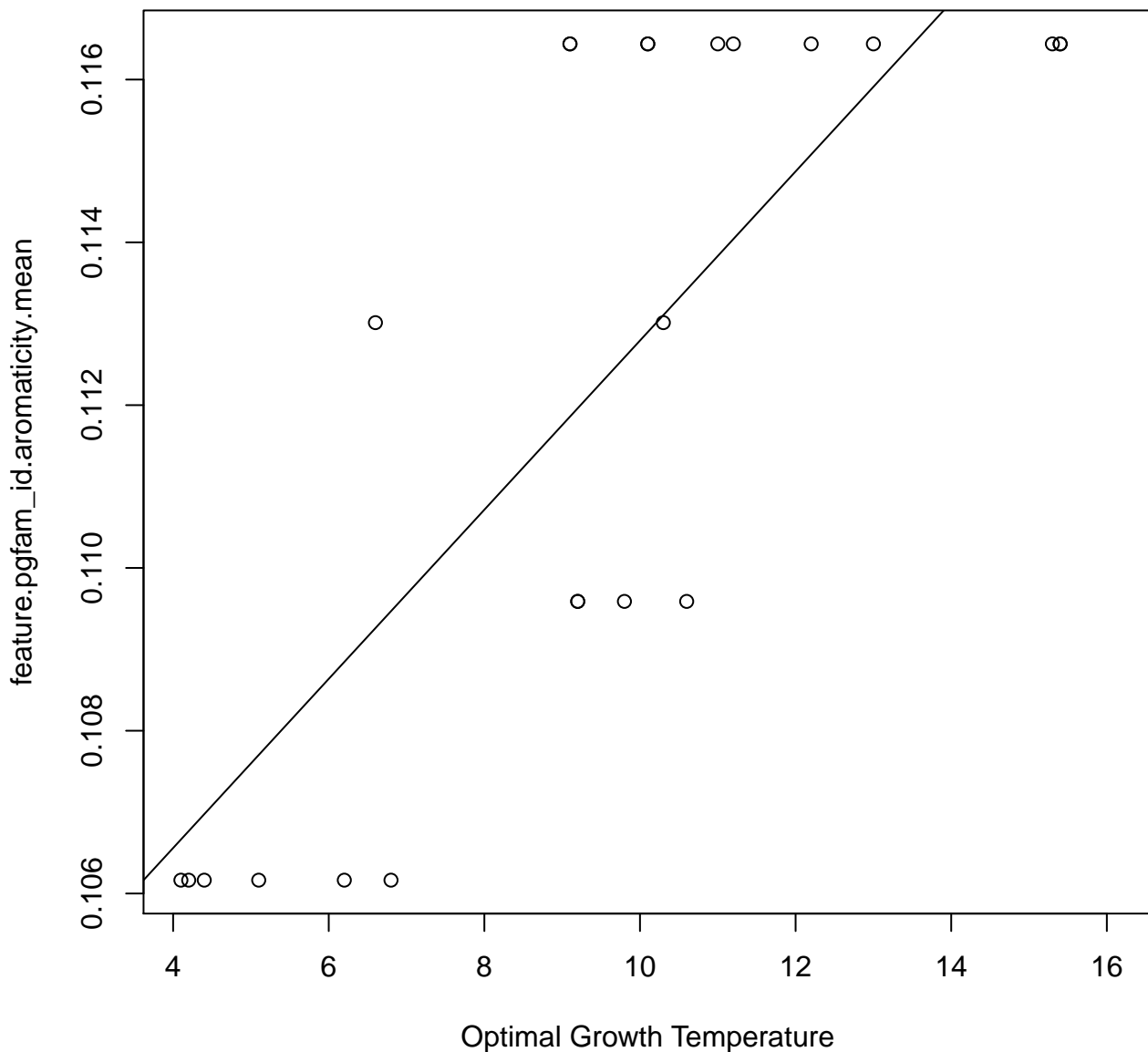
feature.pgfam_id.aromaticity.mean

PGF_00004056

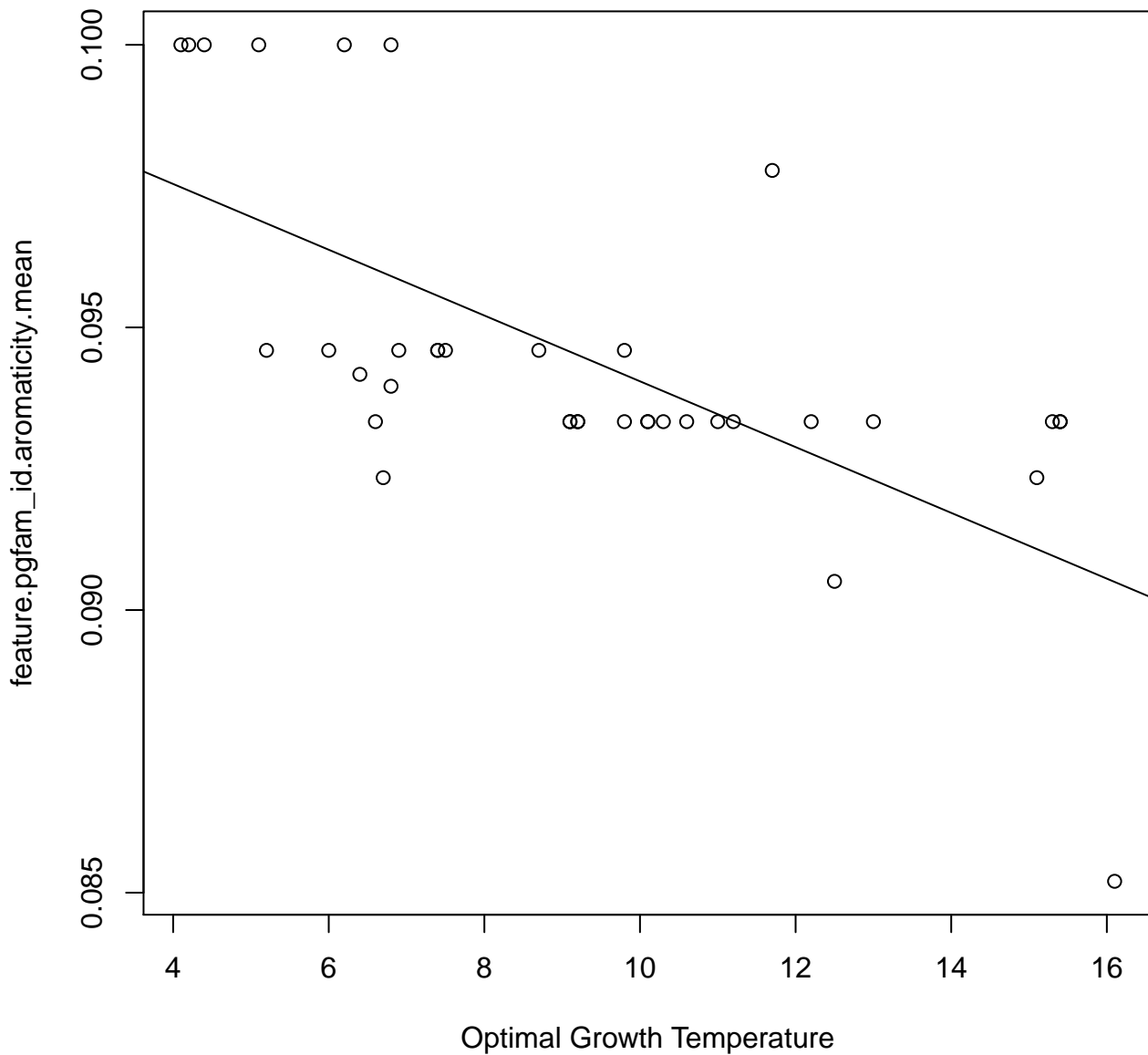
Fatty acid cis/trans isomerase



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



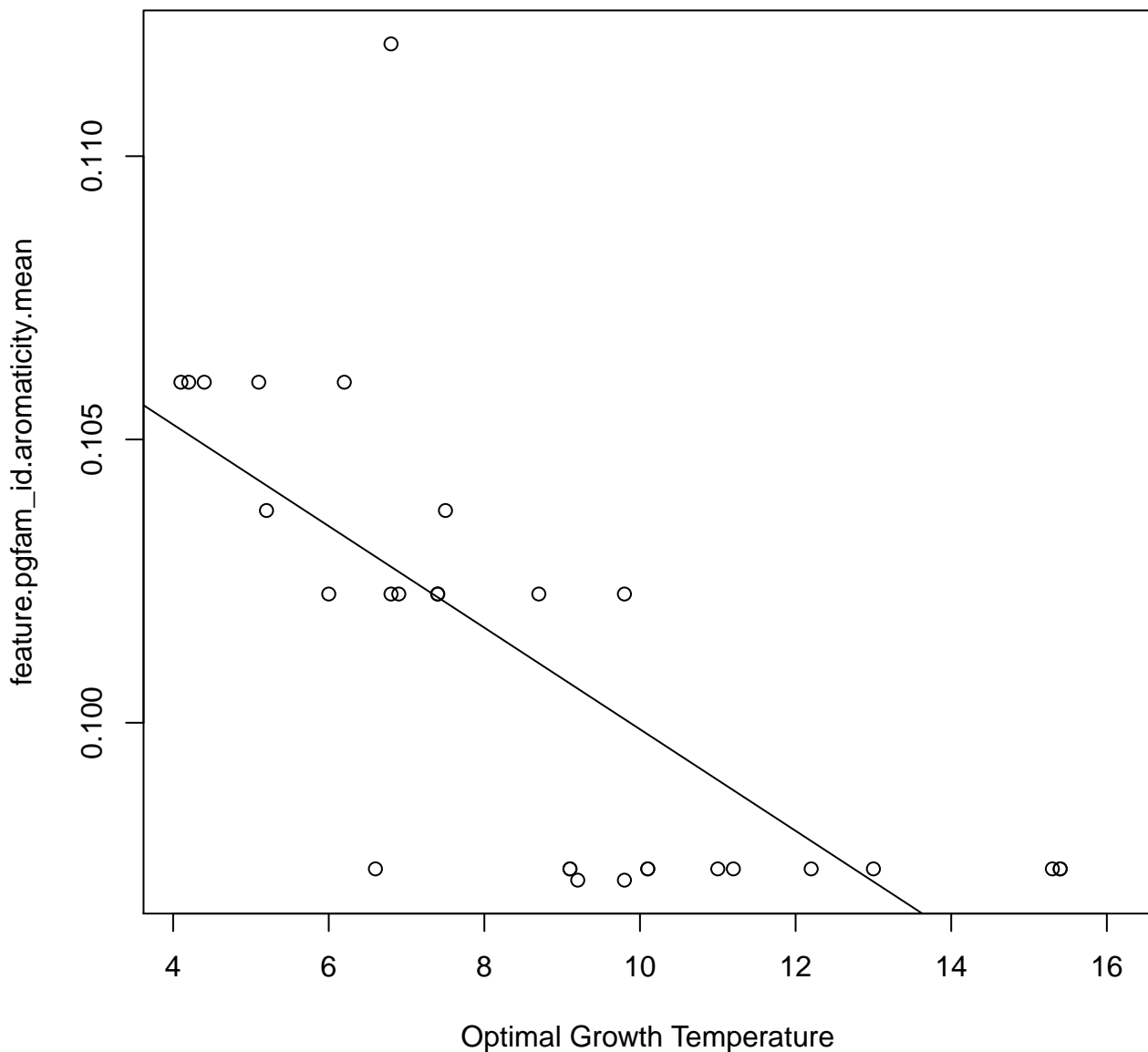
feature.pgfam_id.aromaticity.mean
PGF_00583021
Proton/glutamate symporter



feature.pgfam_id.aromaticity.mean

PGF_01219411

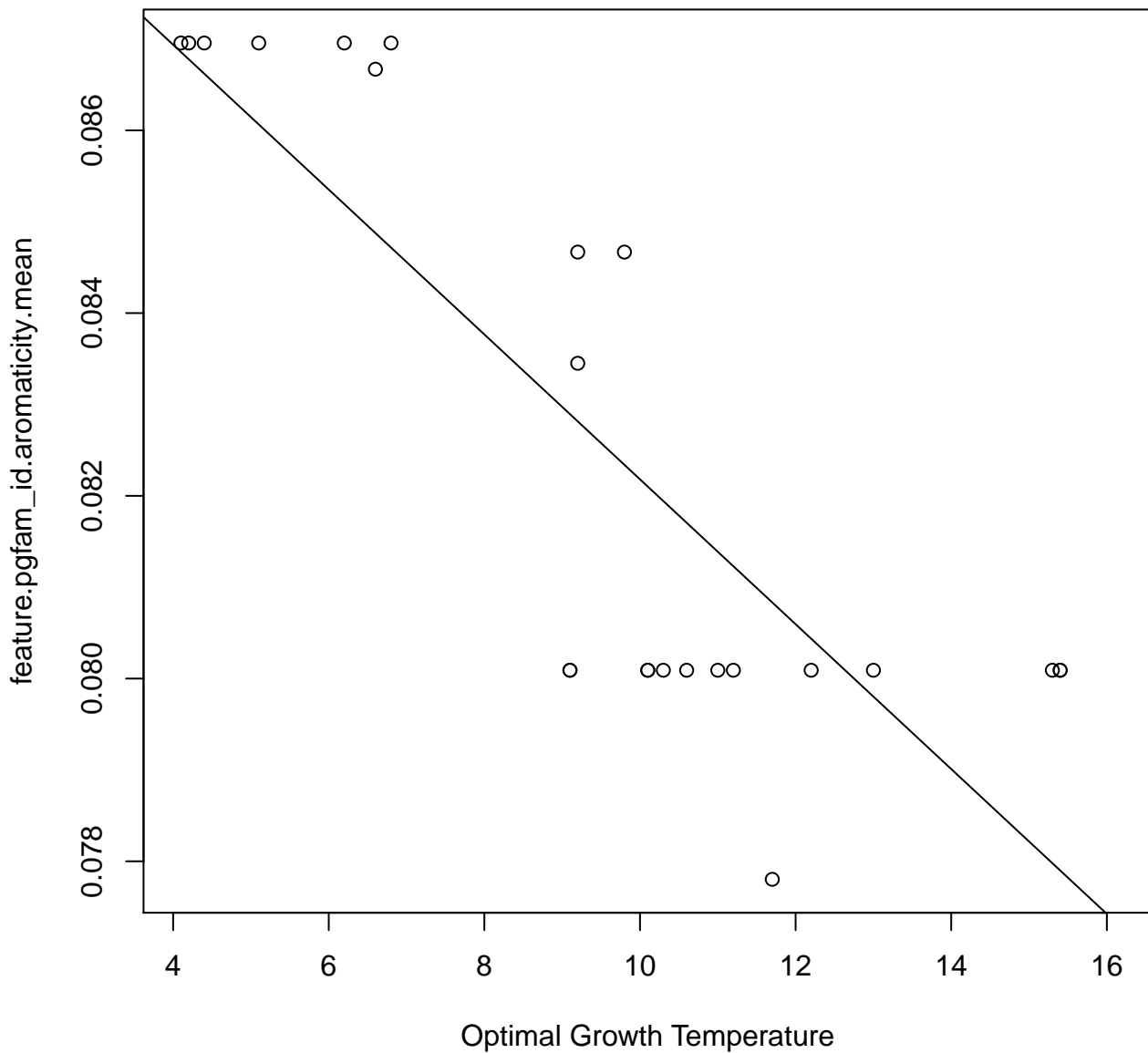
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14)



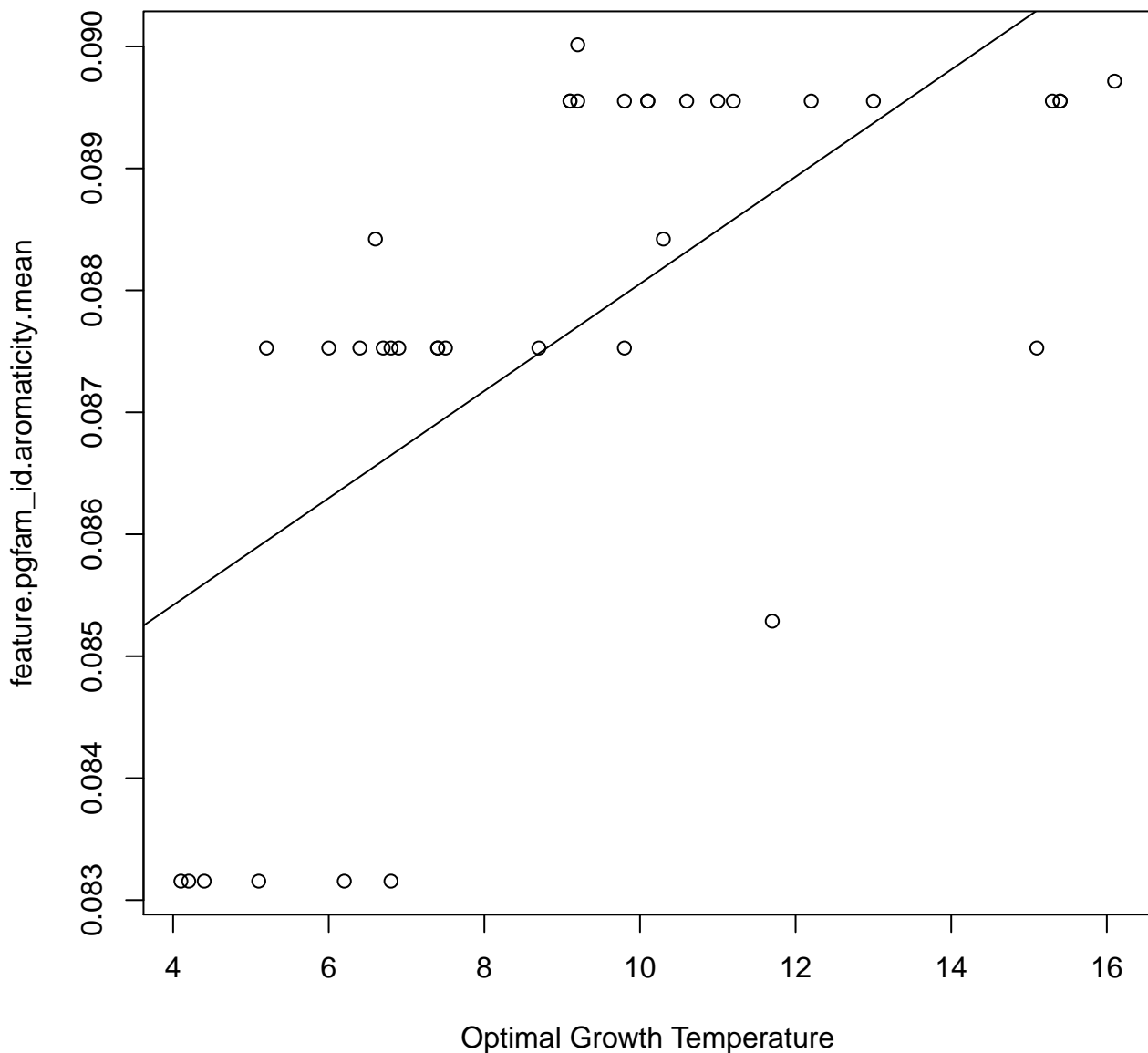
feature.pgfam_id.aromaticity.mean

PGF_01336976

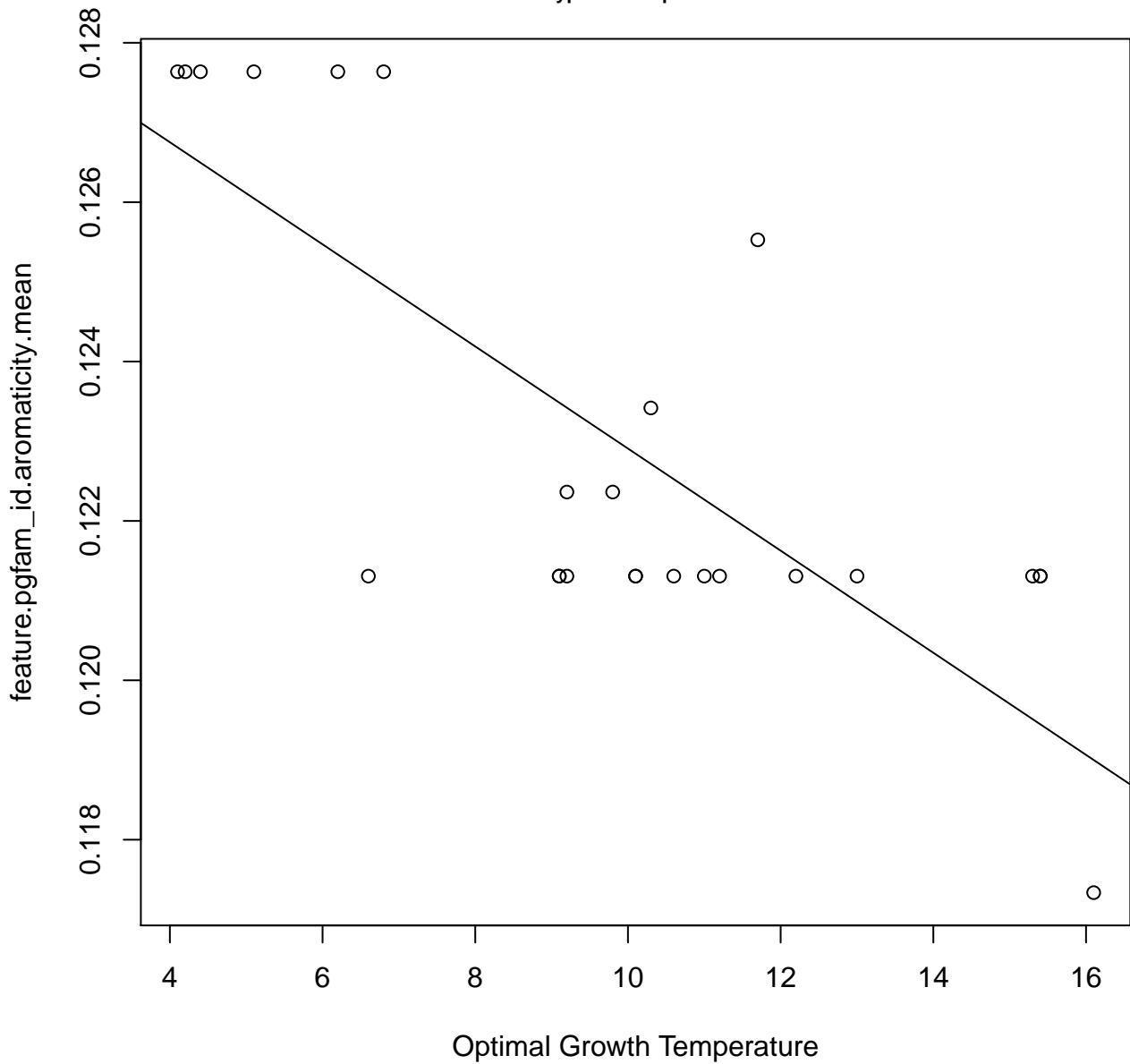
hypothetical protein



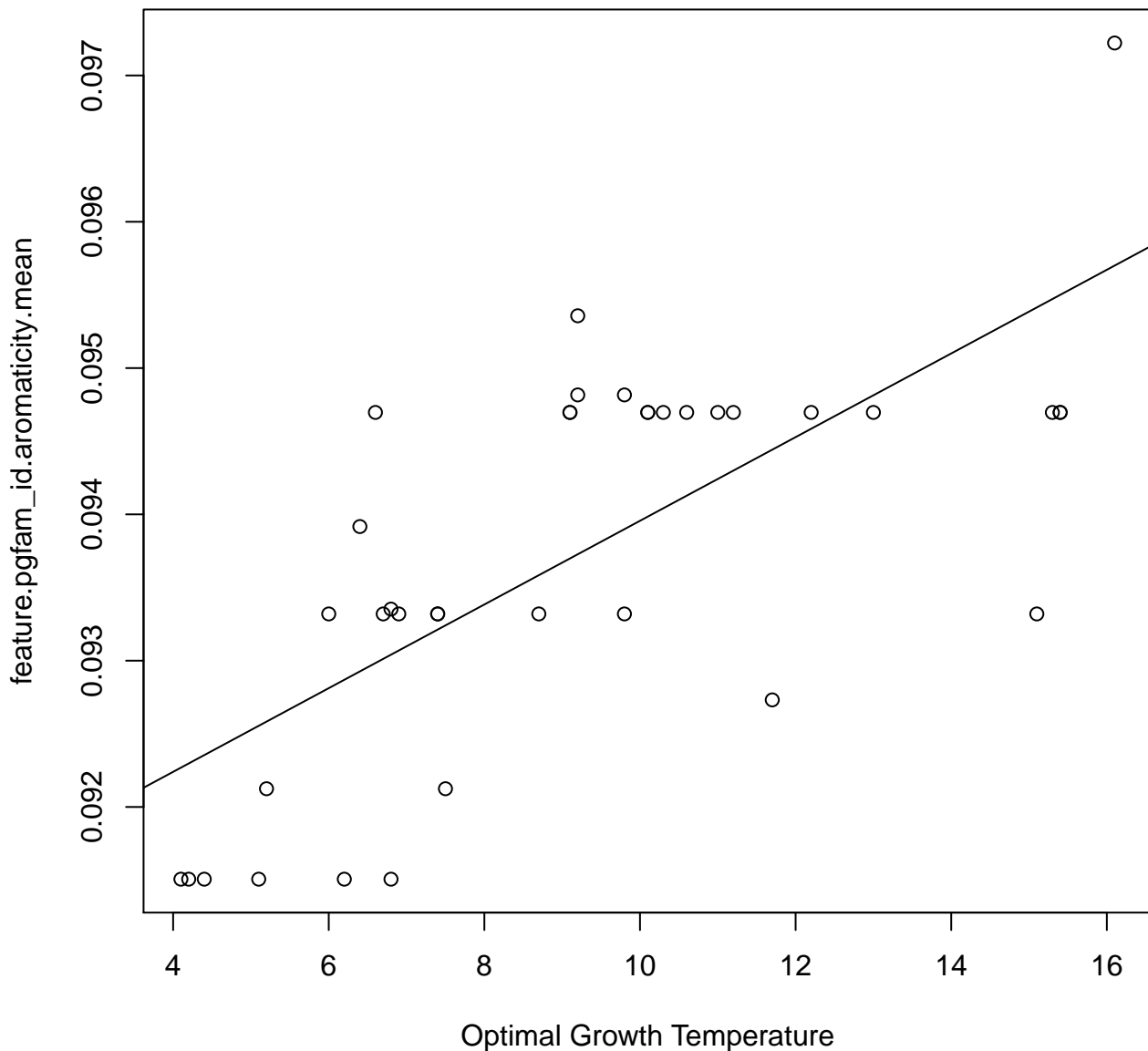
feature.pgfam_id.aromaticity.mean
PGF_03232027
Transcriptional response regulatory protein GlrR



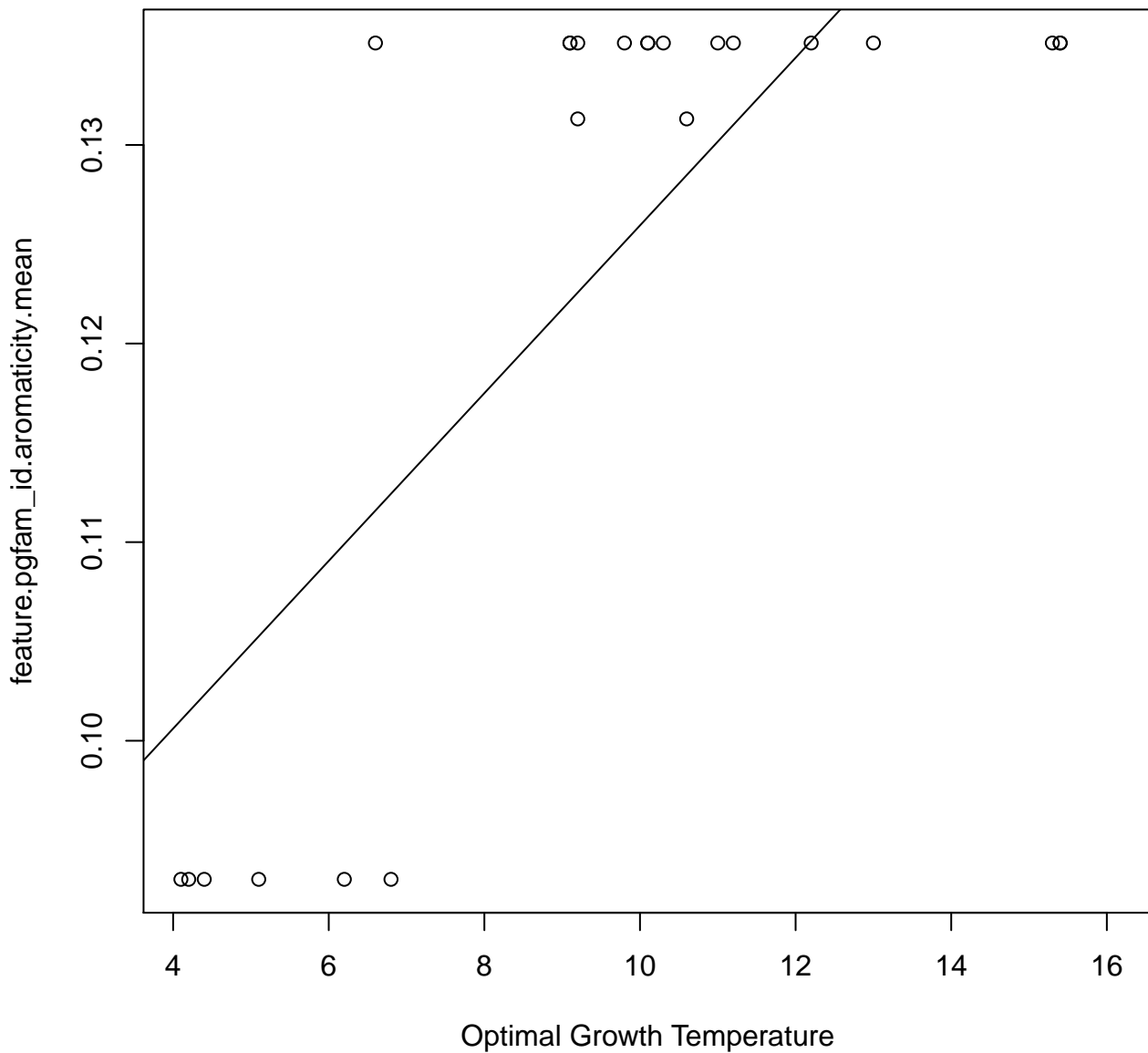
feature.pgfam_id.aromaticity.mean
PGF_04802662
hypothetical protein



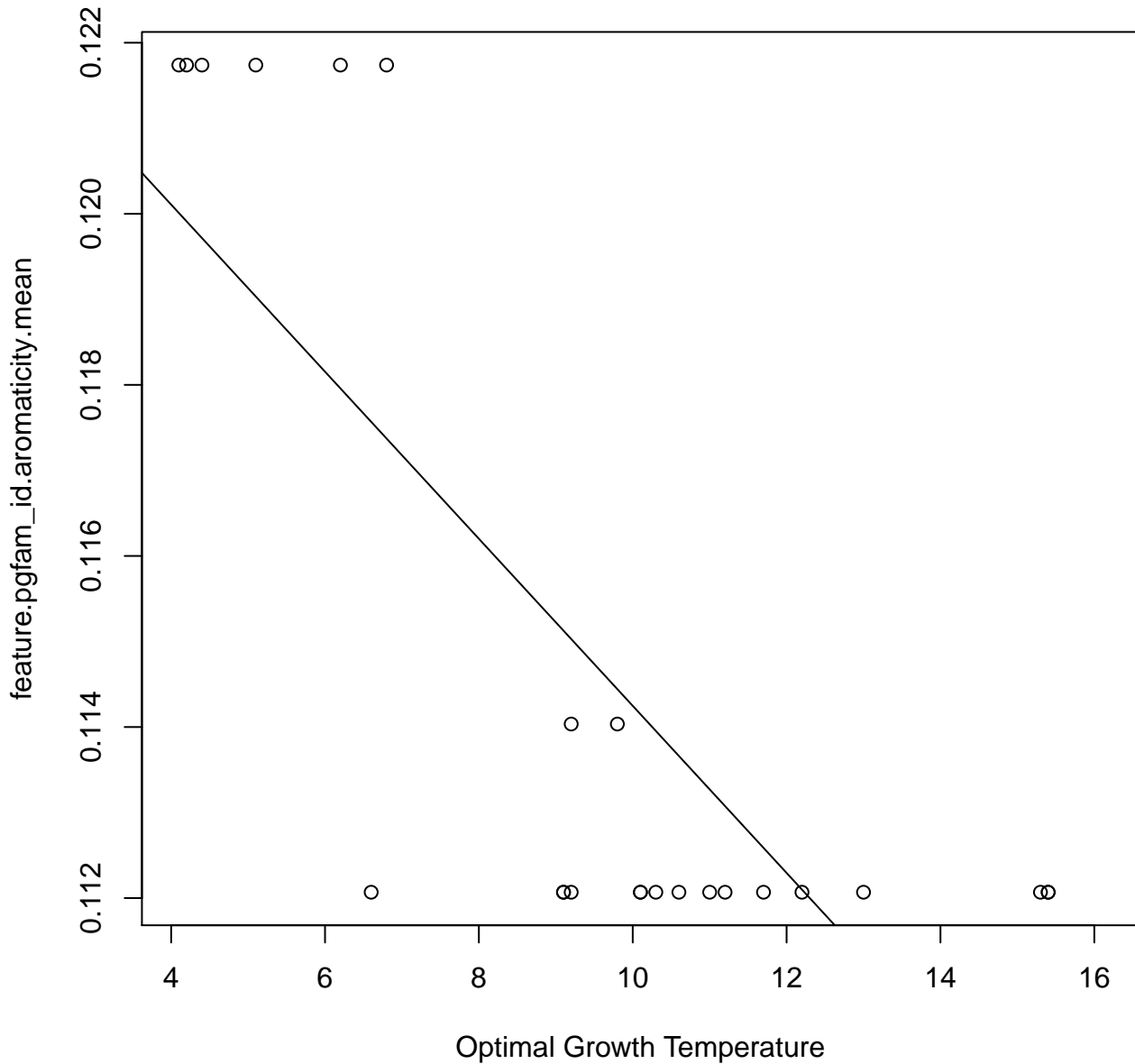
feature.pgfam_id.aromaticity.mean
PGF_05438553
Phosphoenolpyruvate synthase (EC 2.7.9.2)



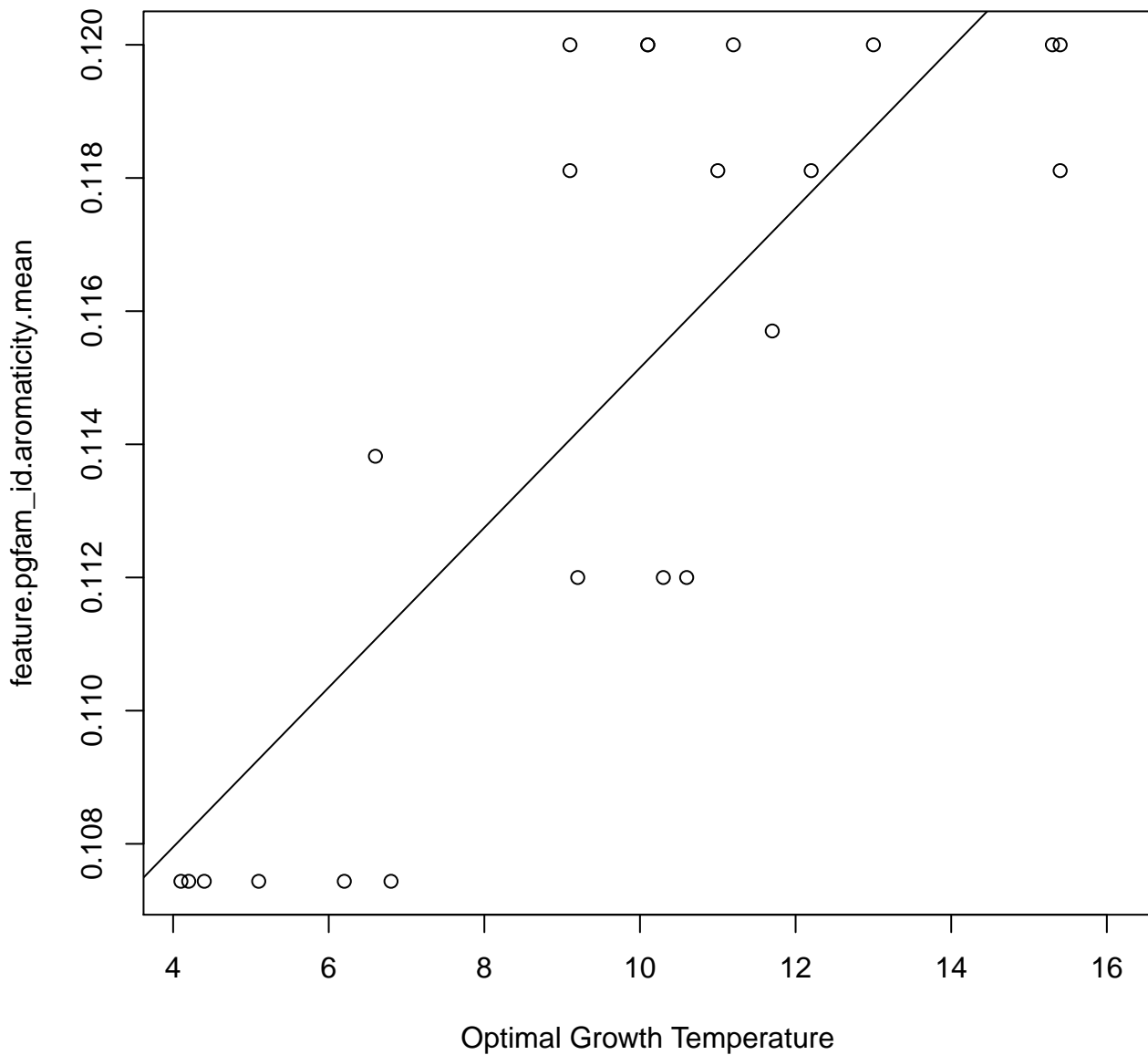
feature.pgfam_id.aromaticity.mean
PGF_06792096
hypothetical protein



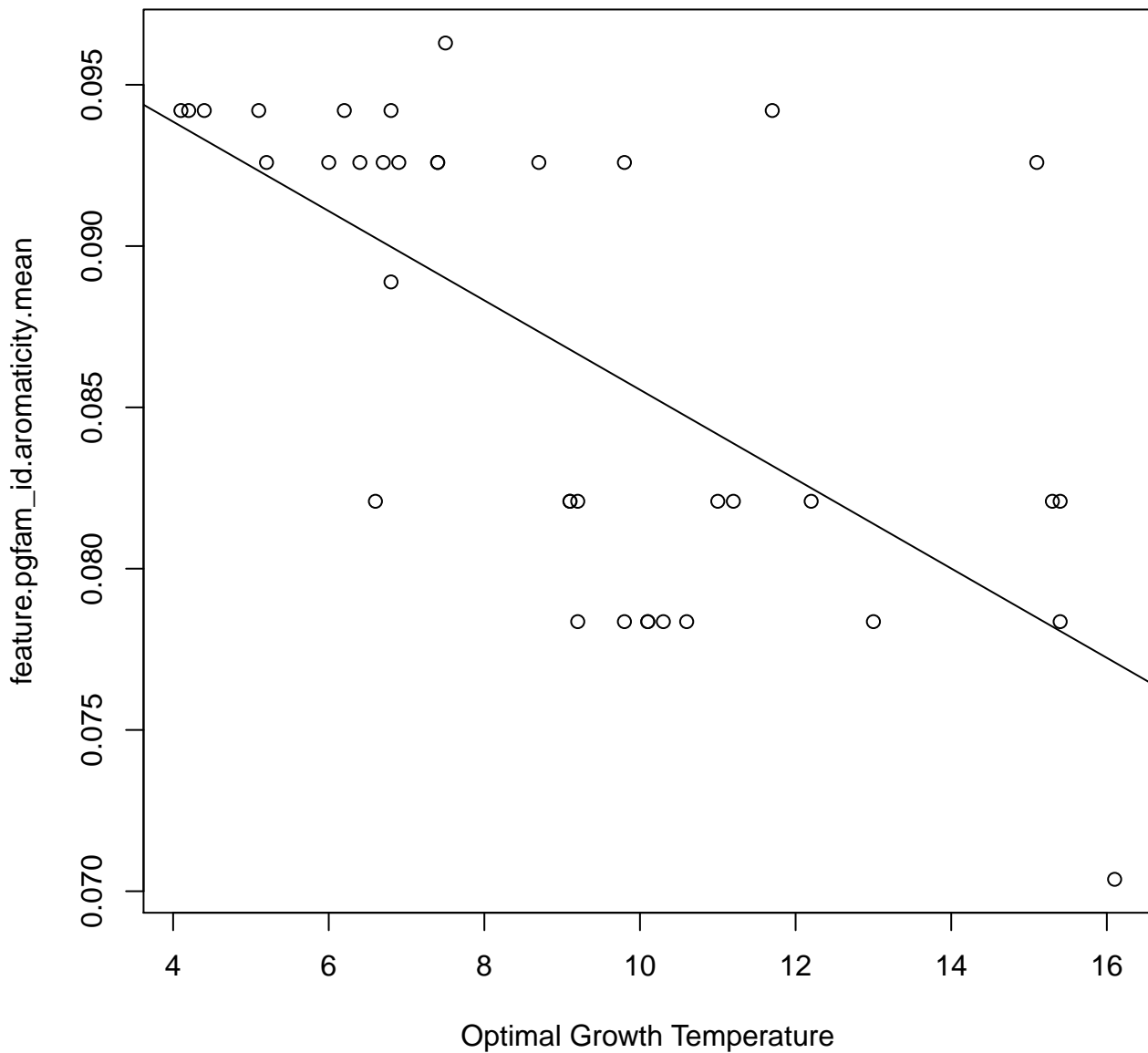
feature.pgfam_id.aromaticity.mean
PGF_07361149
hypothetical protein



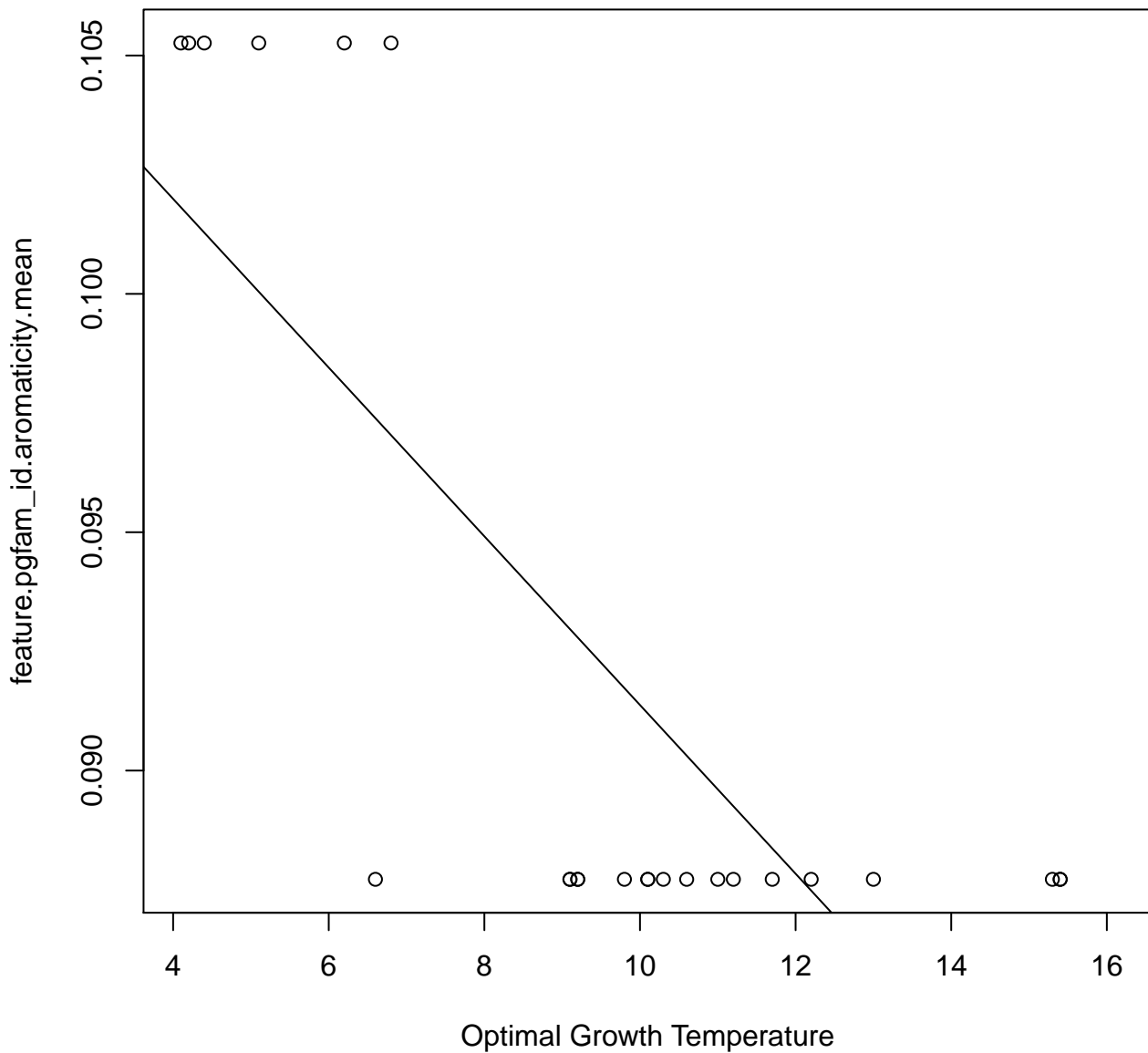
feature.pgfam_id.aromaticity.mean
PGF_08025863
hypothetical protein



feature.pgfam_id.aromaticity.mean
PGF_08181546
Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)



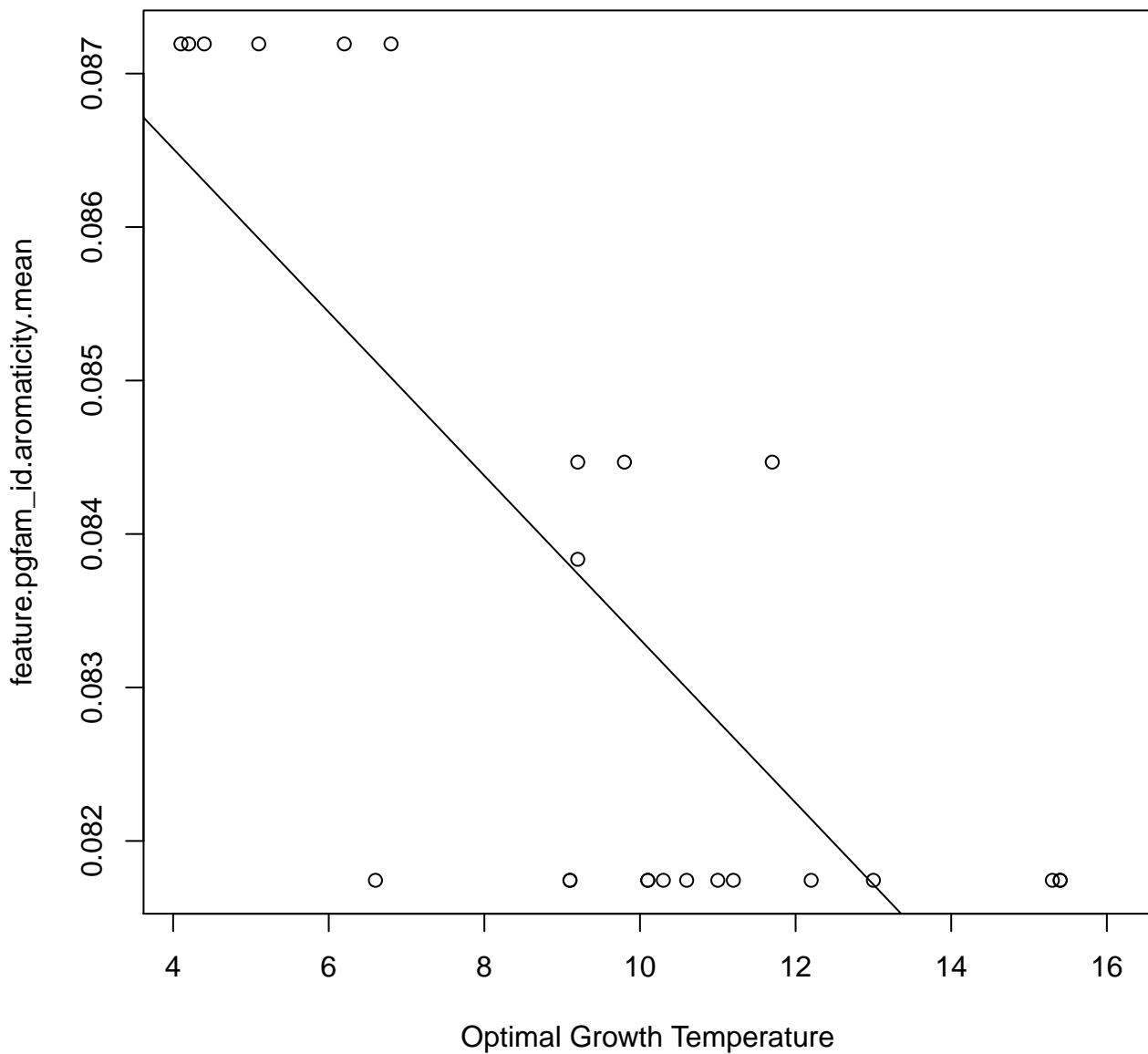
feature.pgfam_id.aromaticity.mean
PGF_08289417
hypothetical protein



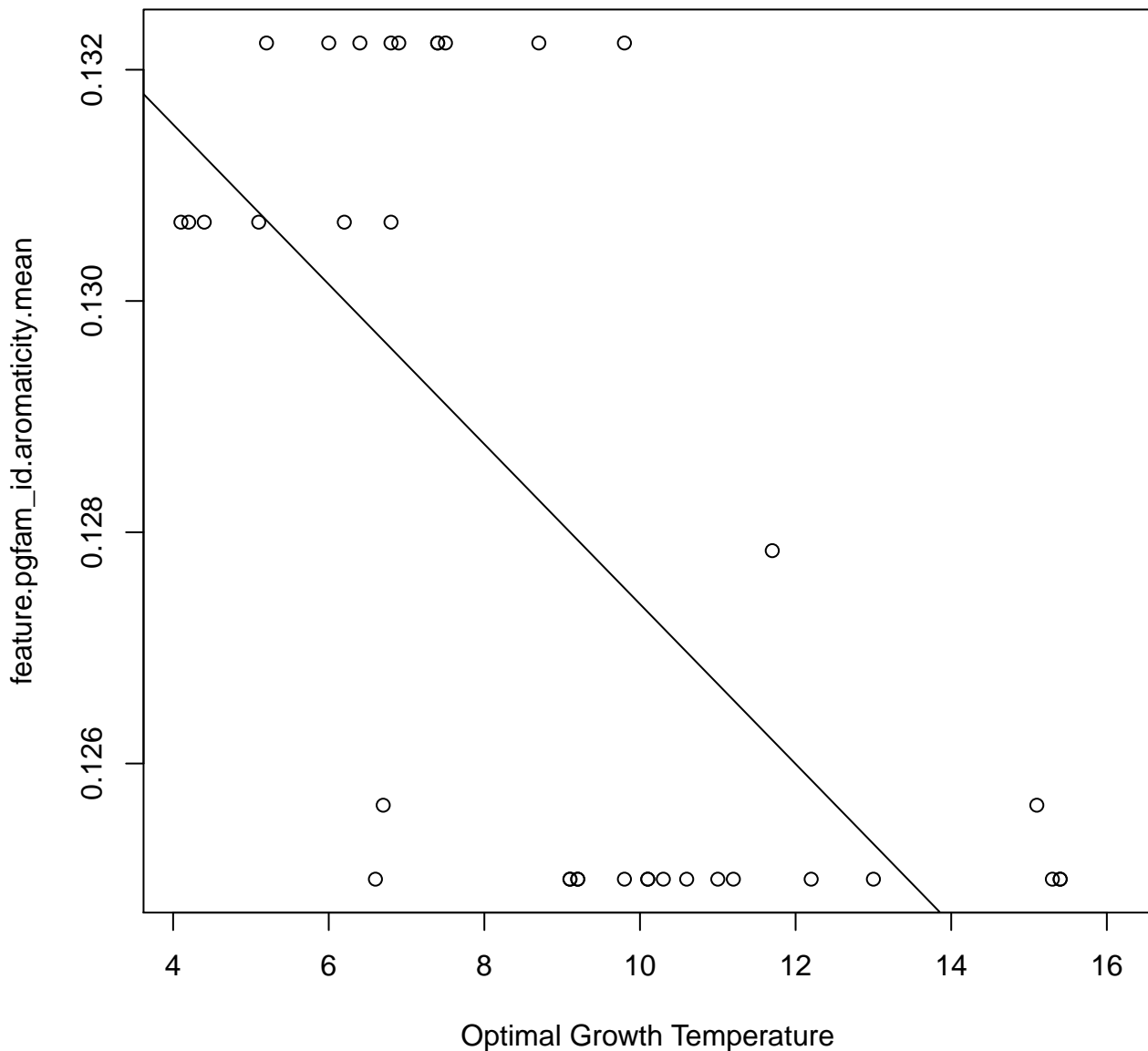
feature.pgfam_id.aromaticity.mean

PGF_09674332

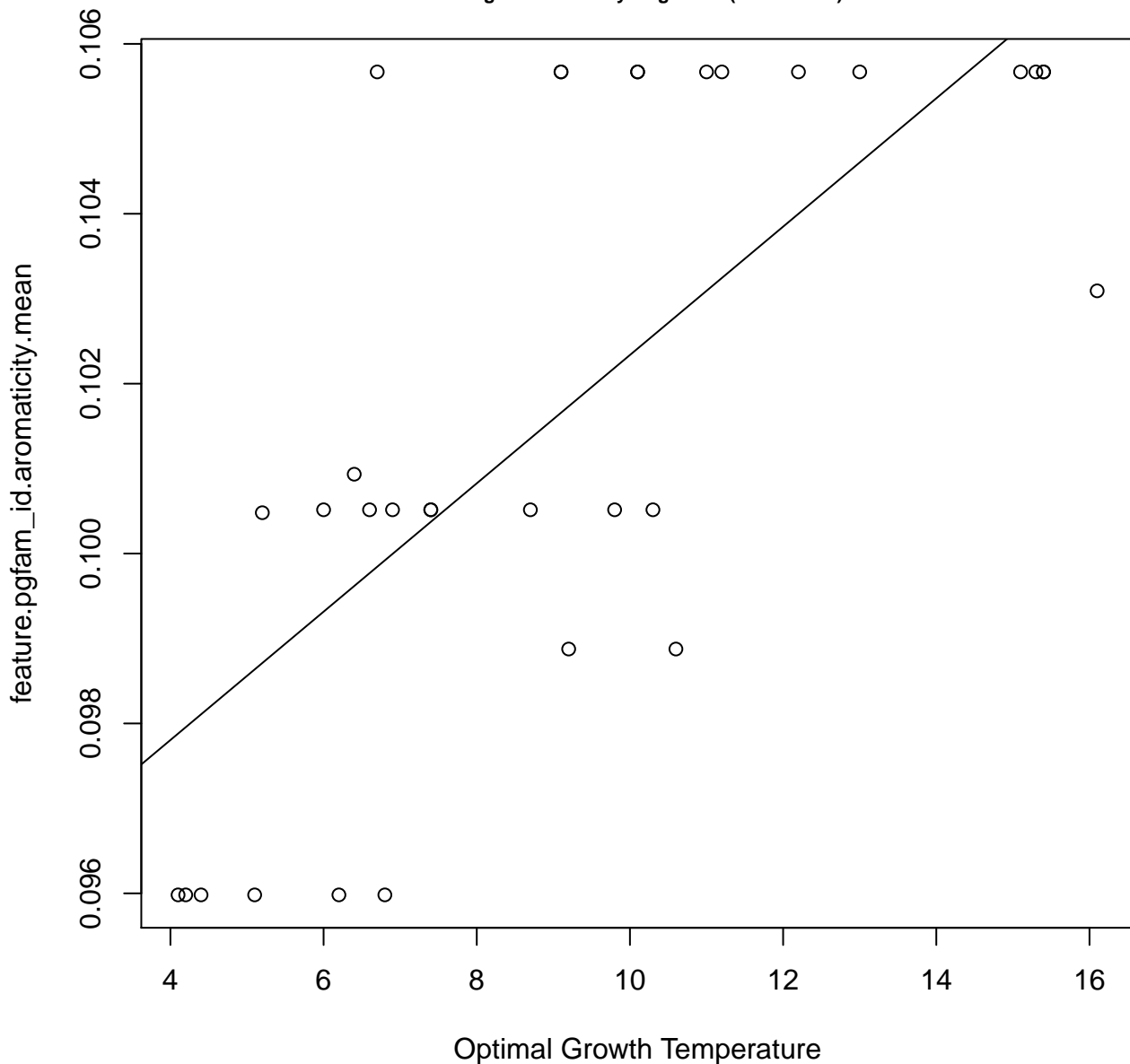
hypothetical protein



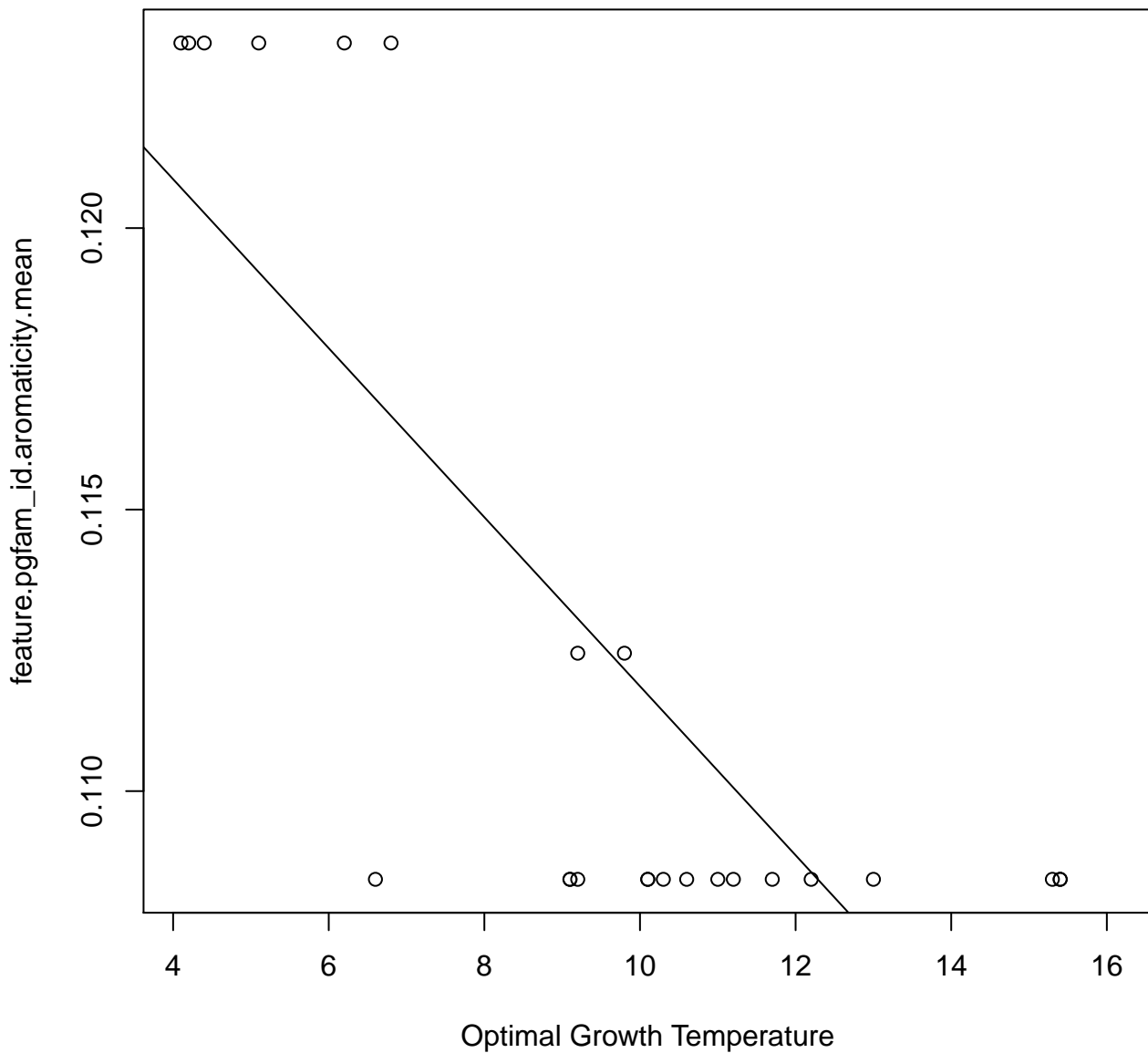
feature.pgfam_id.aromaticity.mean
PGF_09996125
NADH:flavin oxidoreductases, Old Yellow Enzyme family



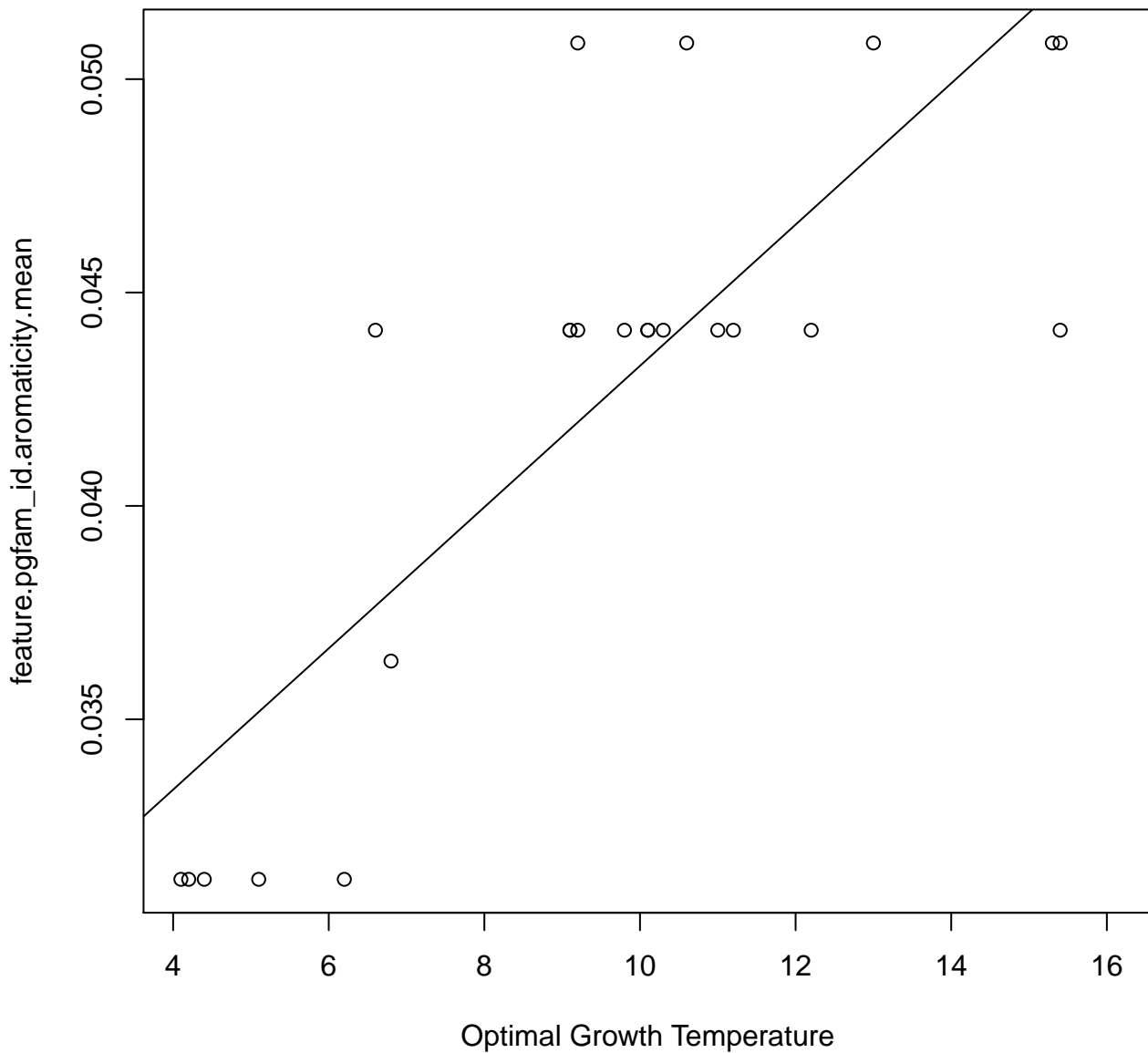
feature.pgfam_id.aromaticity.mean
PGF_10410292
UDP-glucose 6-dehydrogenase (EC 1.1.1.22)



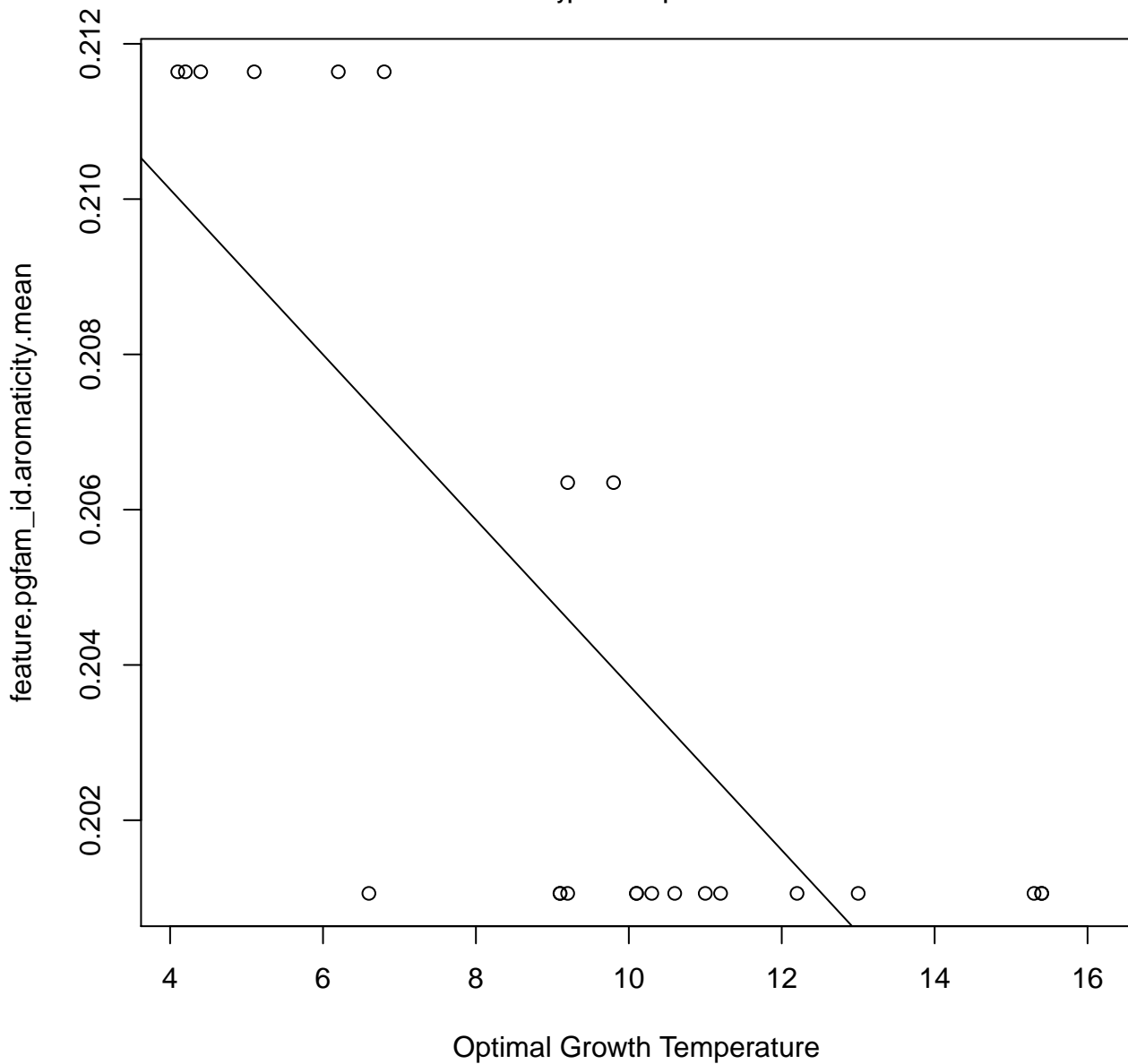
feature.pgfam_id.aromaticity.mean
PGF_11018774
hypothetical protein



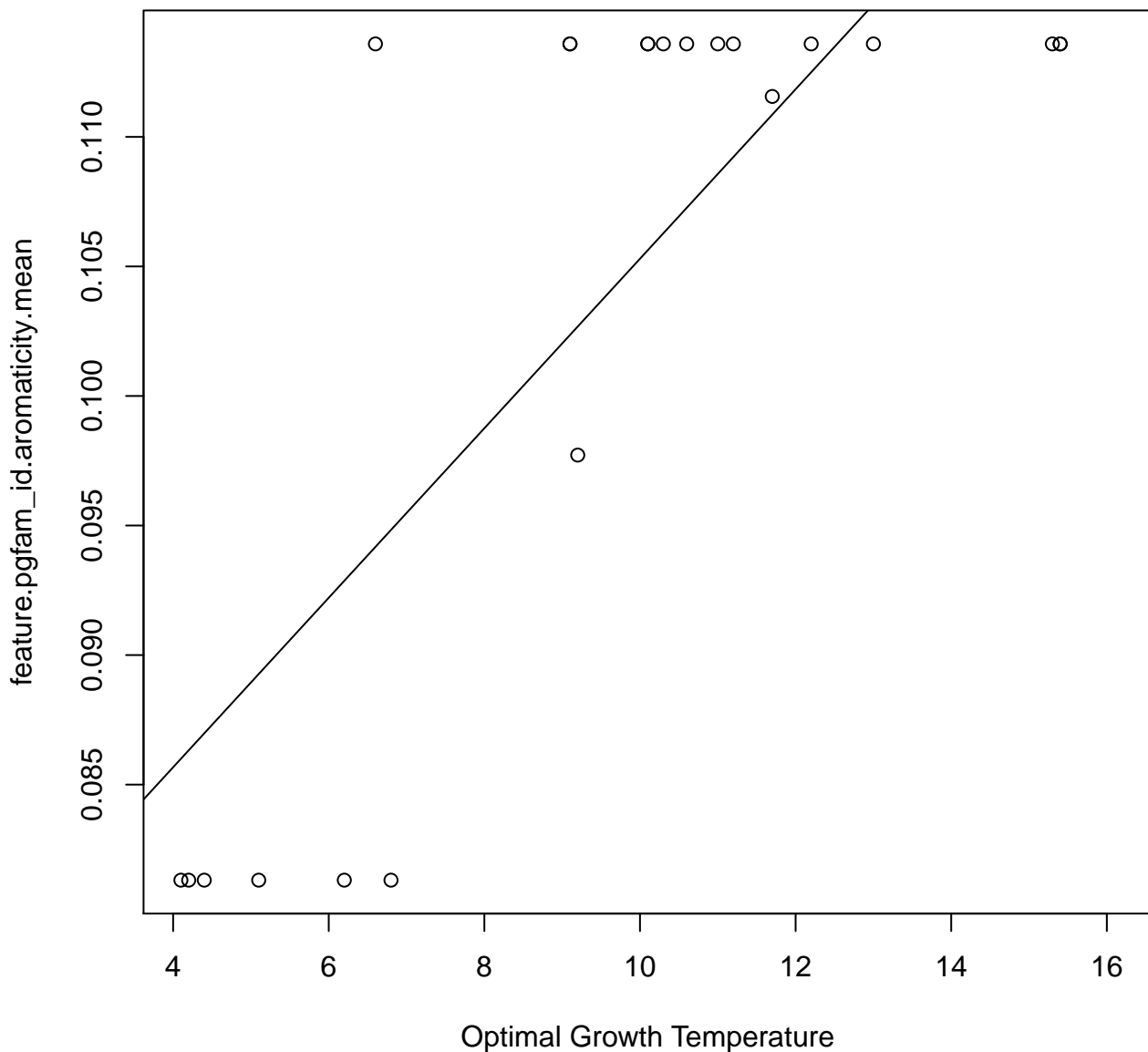
feature.pgfam_id.aromaticity.mean
PGF_11038859
hypothetical protein



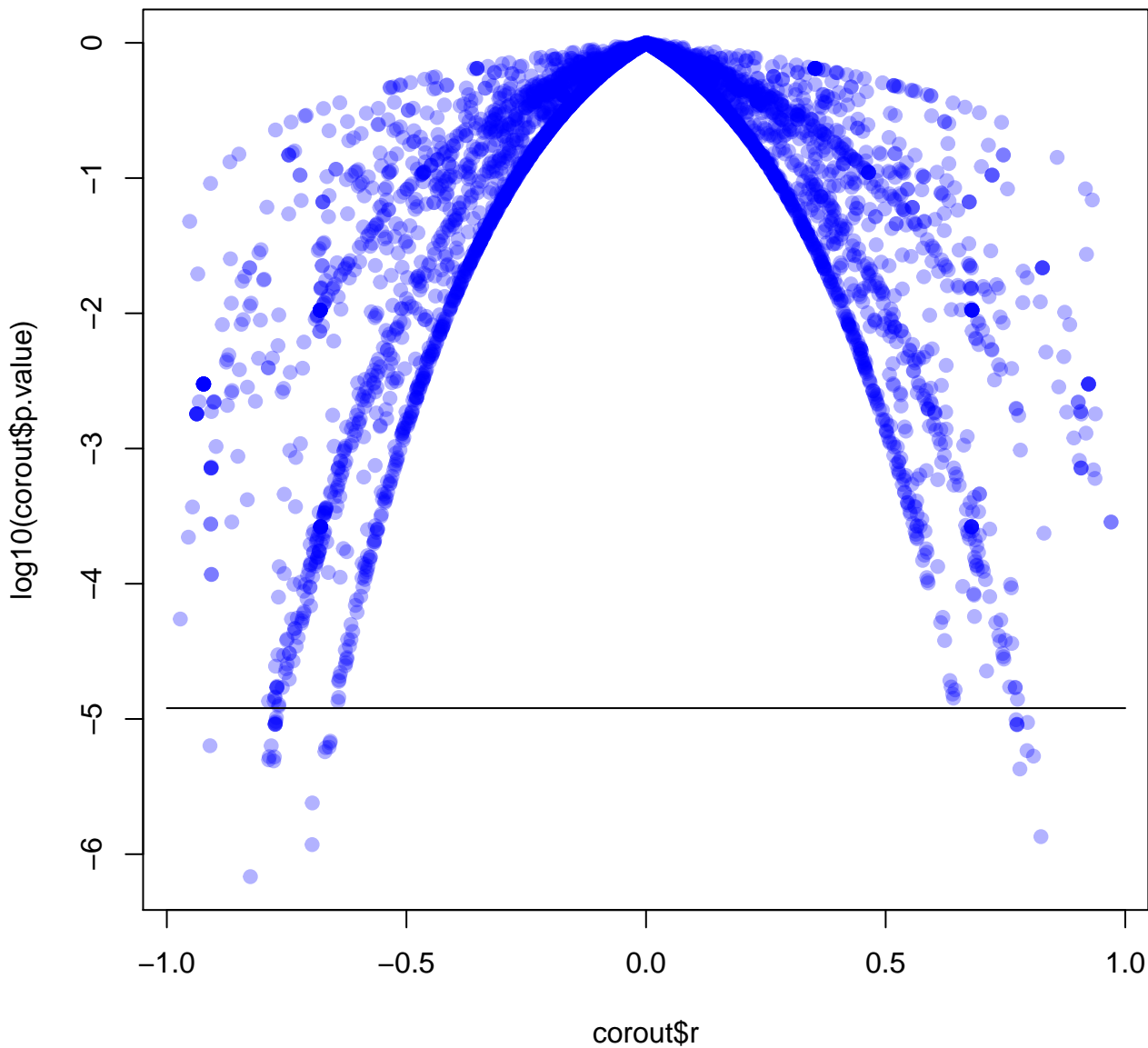
feature.pgfam_id.aromaticity.mean
PGF_12159935
hypothetical protein



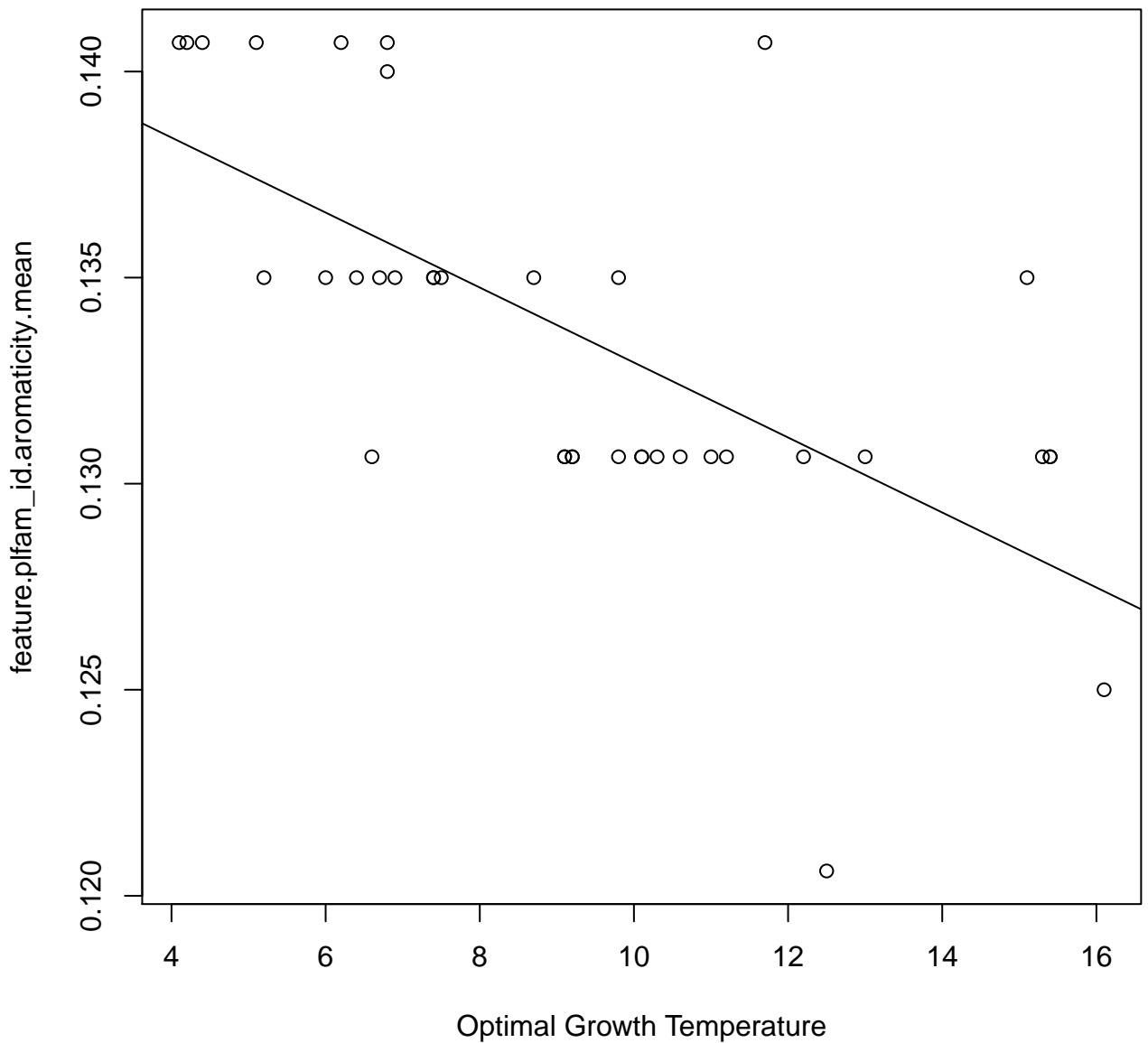
feature.pgfam_id.aromaticity.mean
PGF_12765299
Two-component system sensor histidine kinase



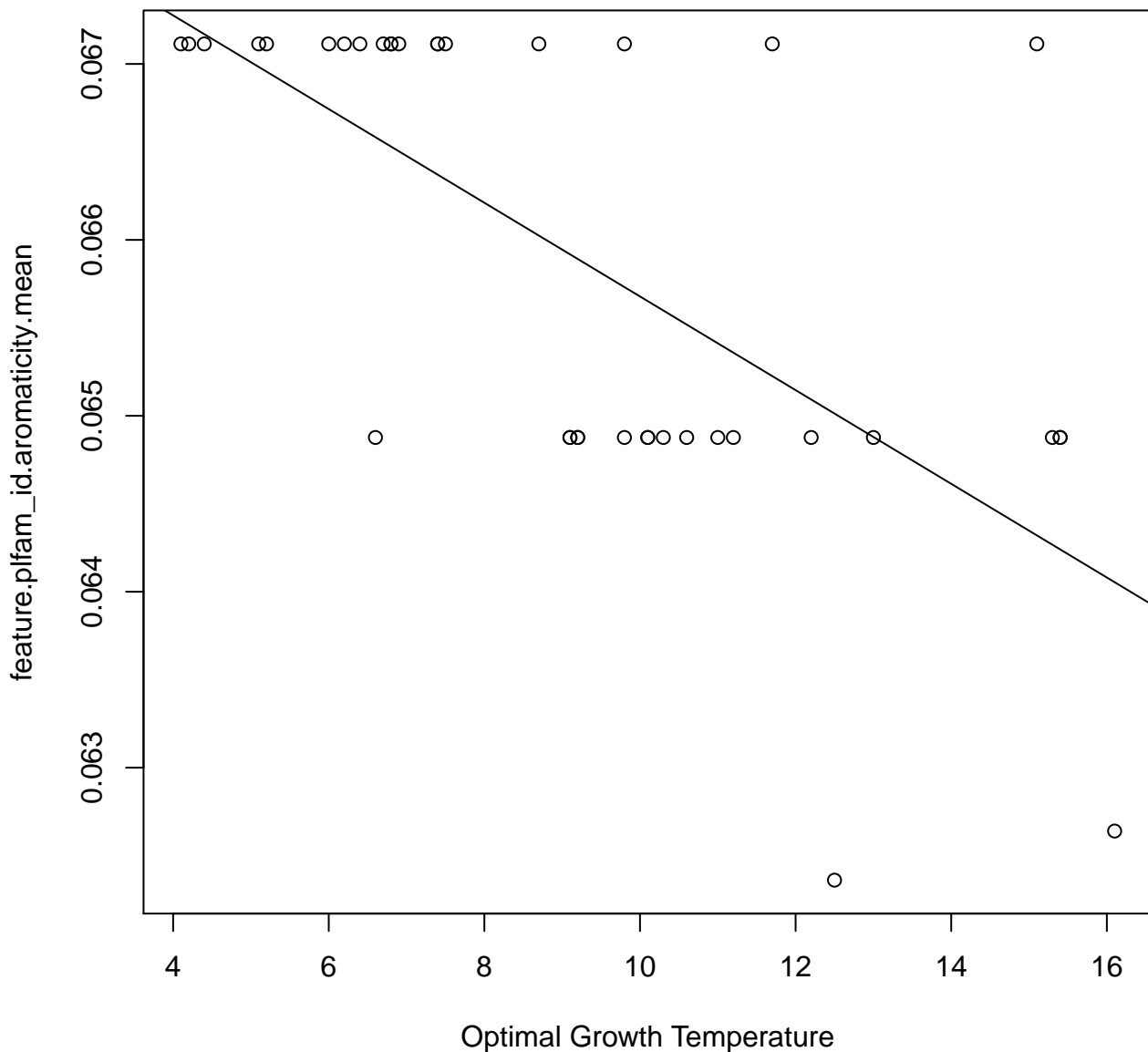
feature.plfam_id.aromaticity.mean



feature.plfam_id.aromaticity.mean
PLF_28228_00000546
Carbonic anhydrase, beta class (EC 4.2.1.1)



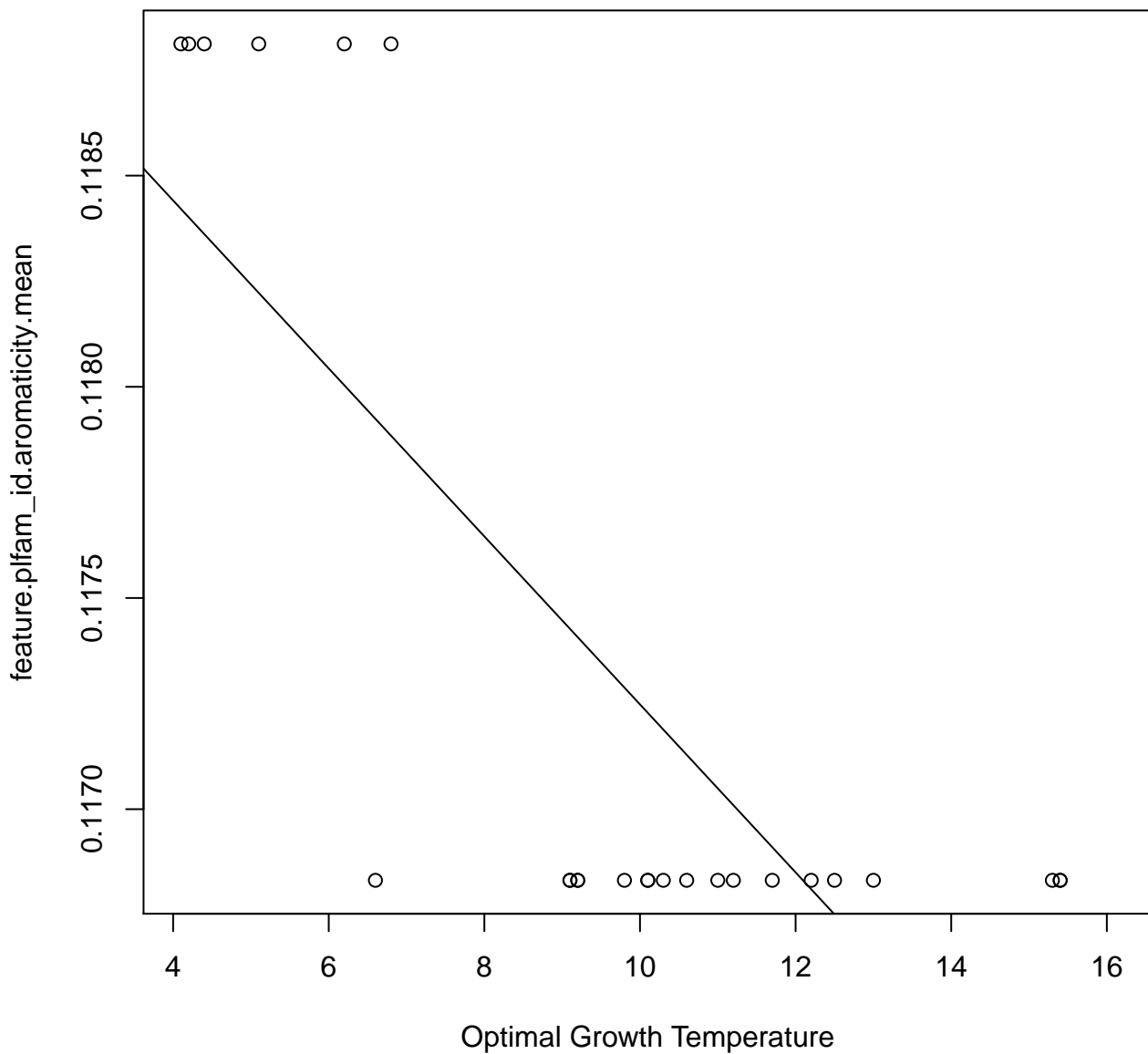
feature.plfam_id.aromaticity.mean
PLF_28228_00000622
MotA/TolQ/ExbB proton channel family protein



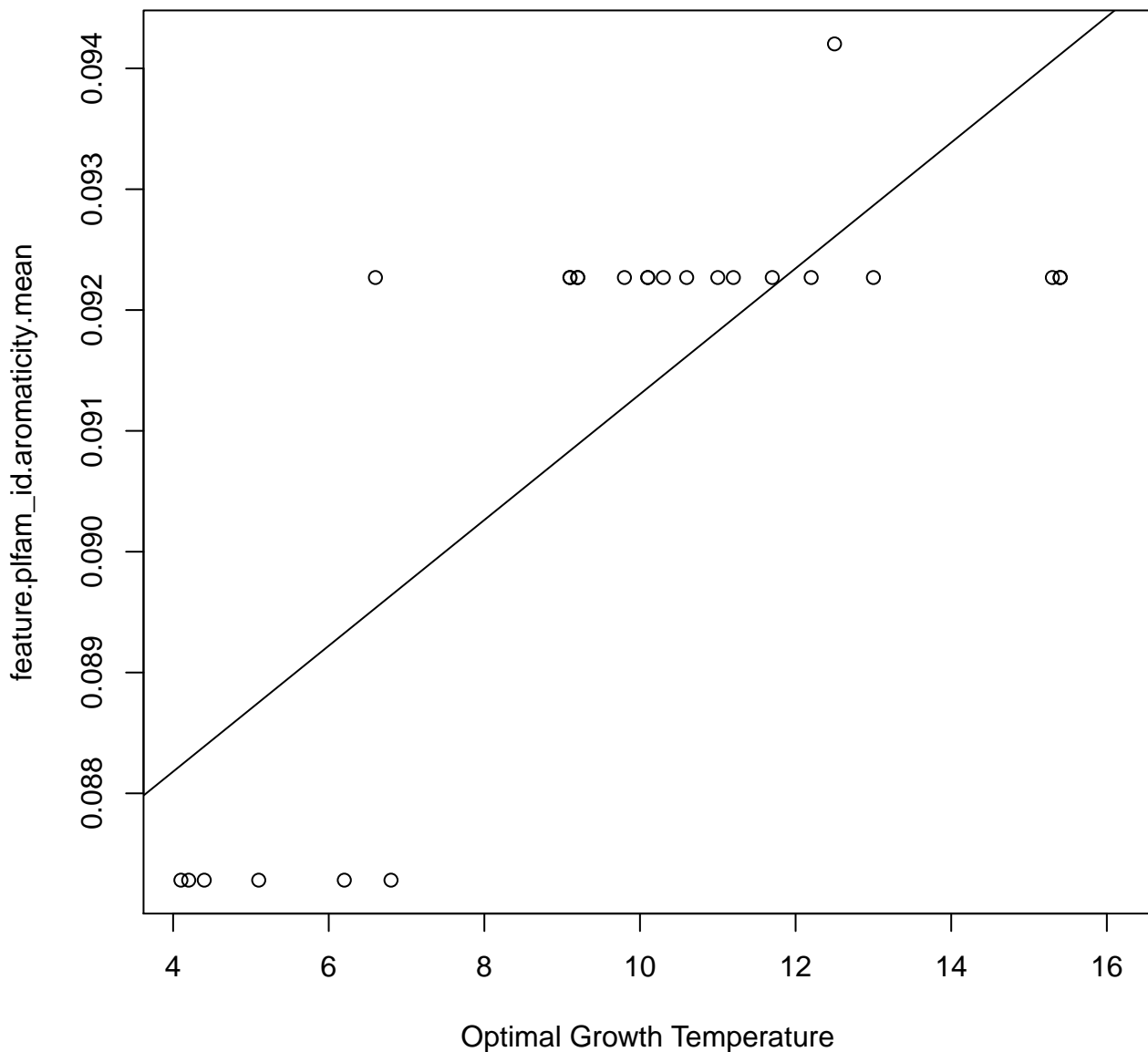
feature.plfam_id.aromaticity.mean

PLF_28228_00000645

Na(+) H(+) antiporter subunit D



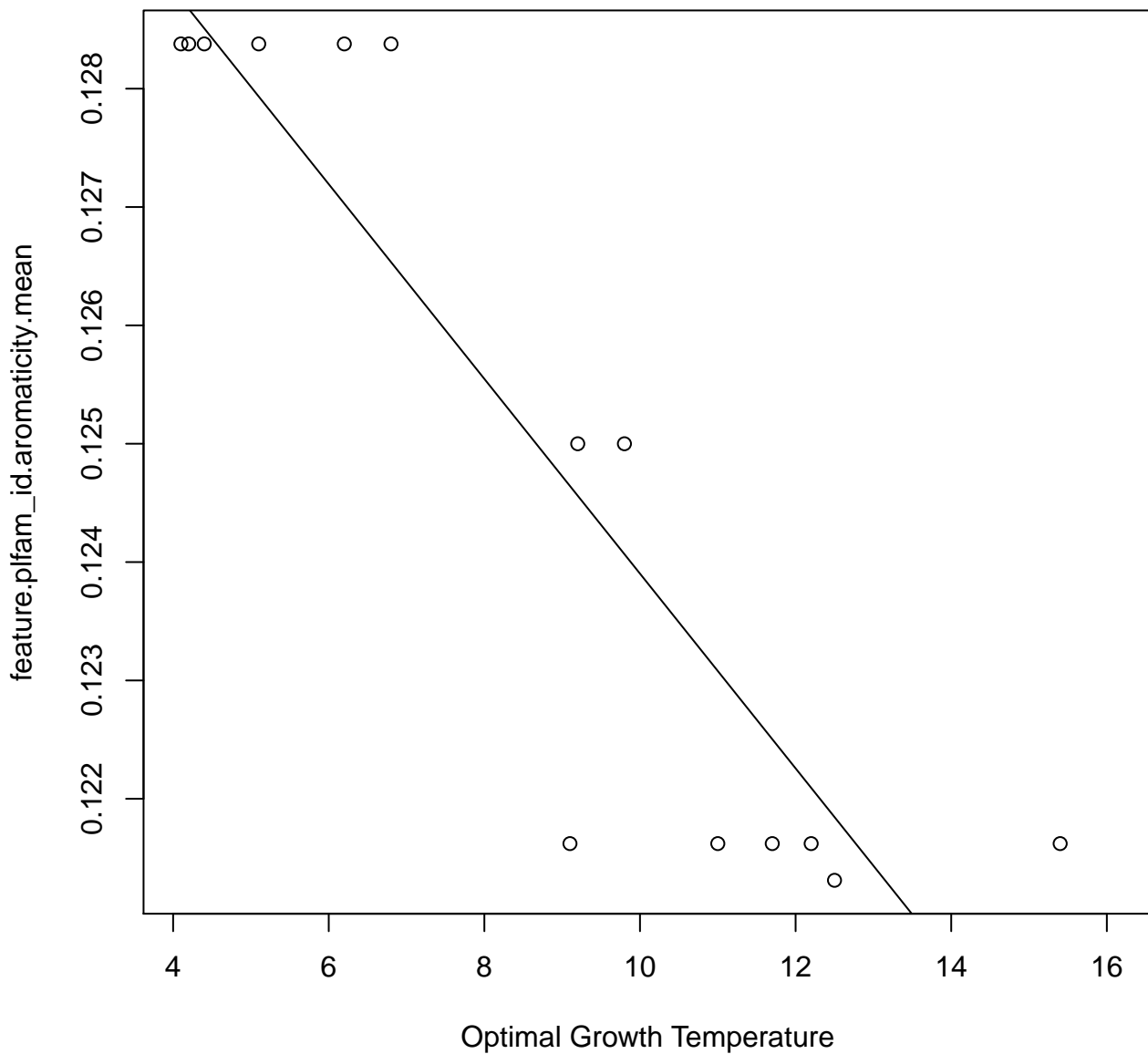
feature.plfam_id.aromaticity.mean
PLF_28228_00000683
Outer membrane beta-barrel assembly protein BamB



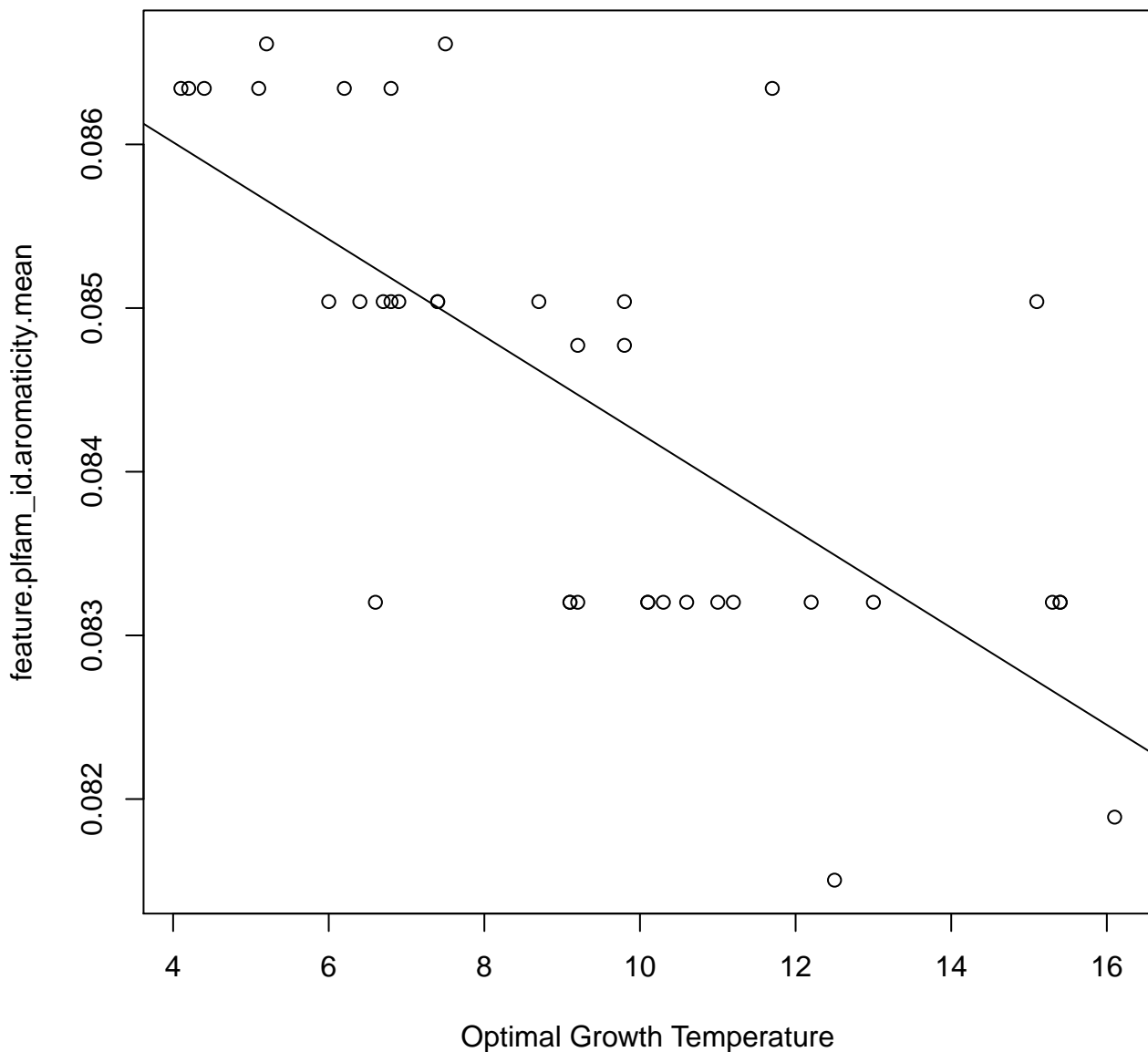
feature.plfam_id.aromaticity.mean

PLF_28228_00001856

GGDEF domain protein



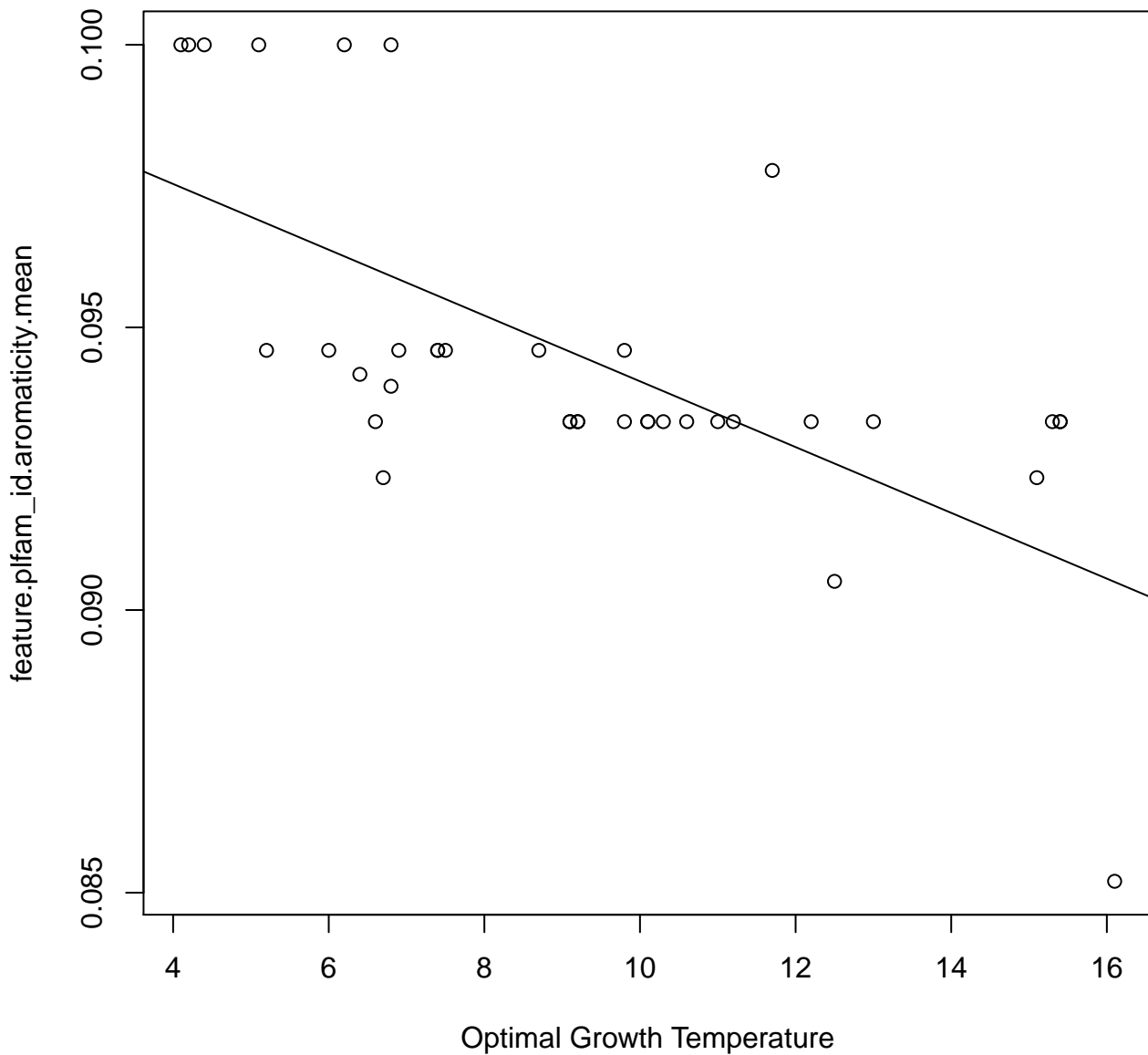
feature.plfam_id.aromaticity.mean
PLF_28228_00001900
Peptidyl-prolyl cis-trans isomerase PpiD (EC 5.2.1.8)



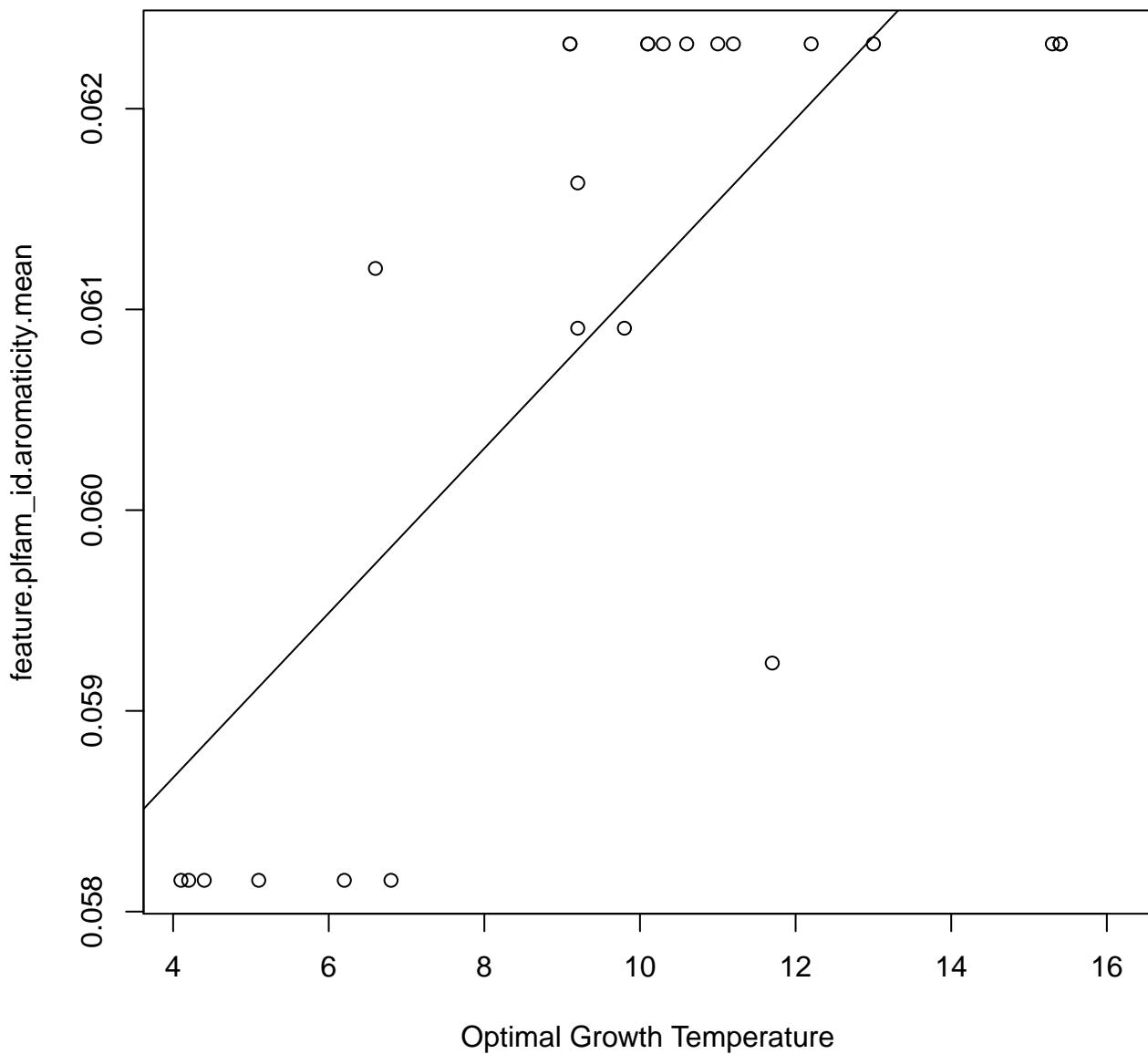
feature.plfam_id.aromaticity.mean

PLF_28228_00001972

Proton/glutamate symporter



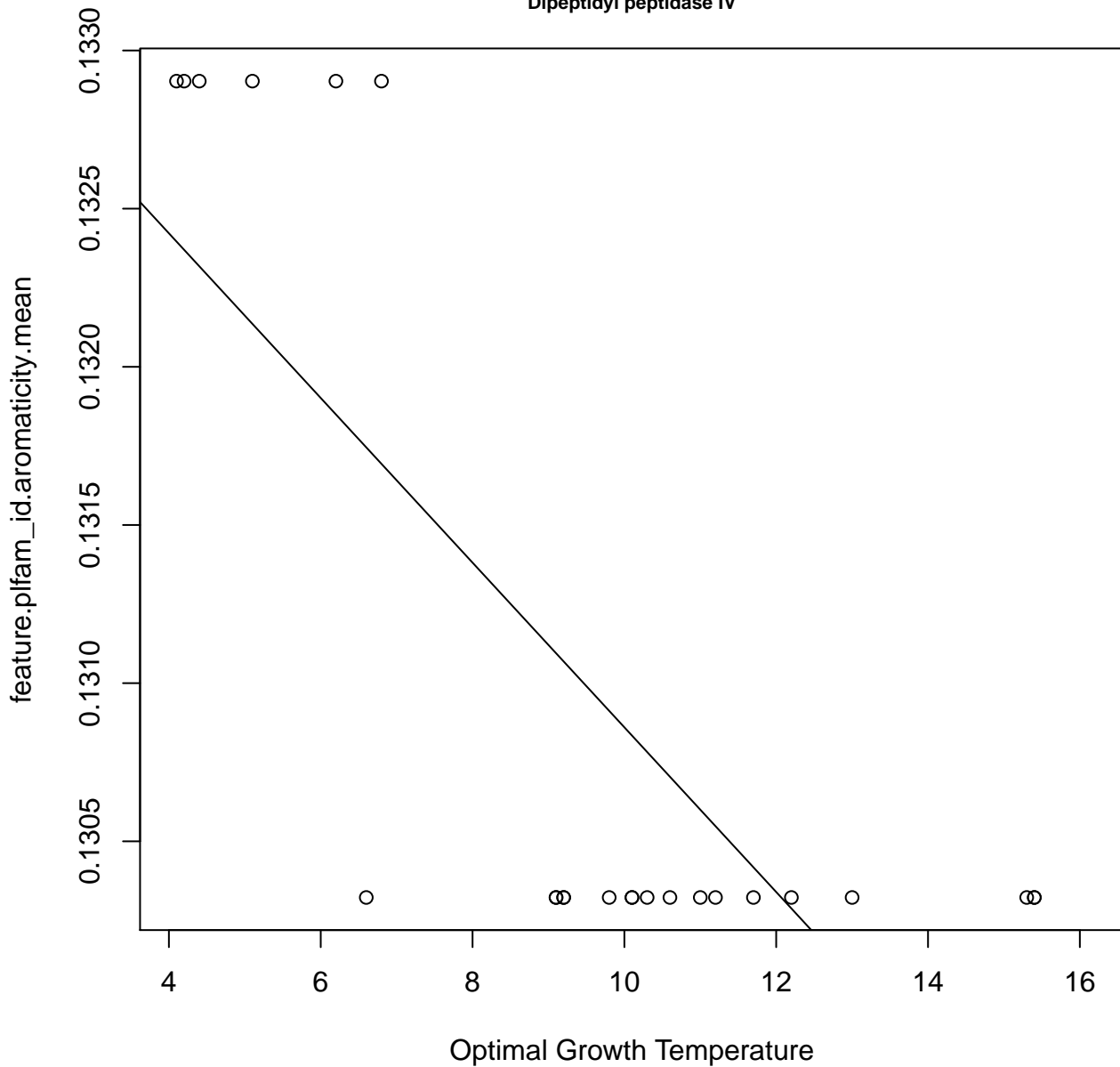
feature.plfam_id.aromaticity.mean
PLF_28228_00002064
Signal transduction histidine kinase CheA



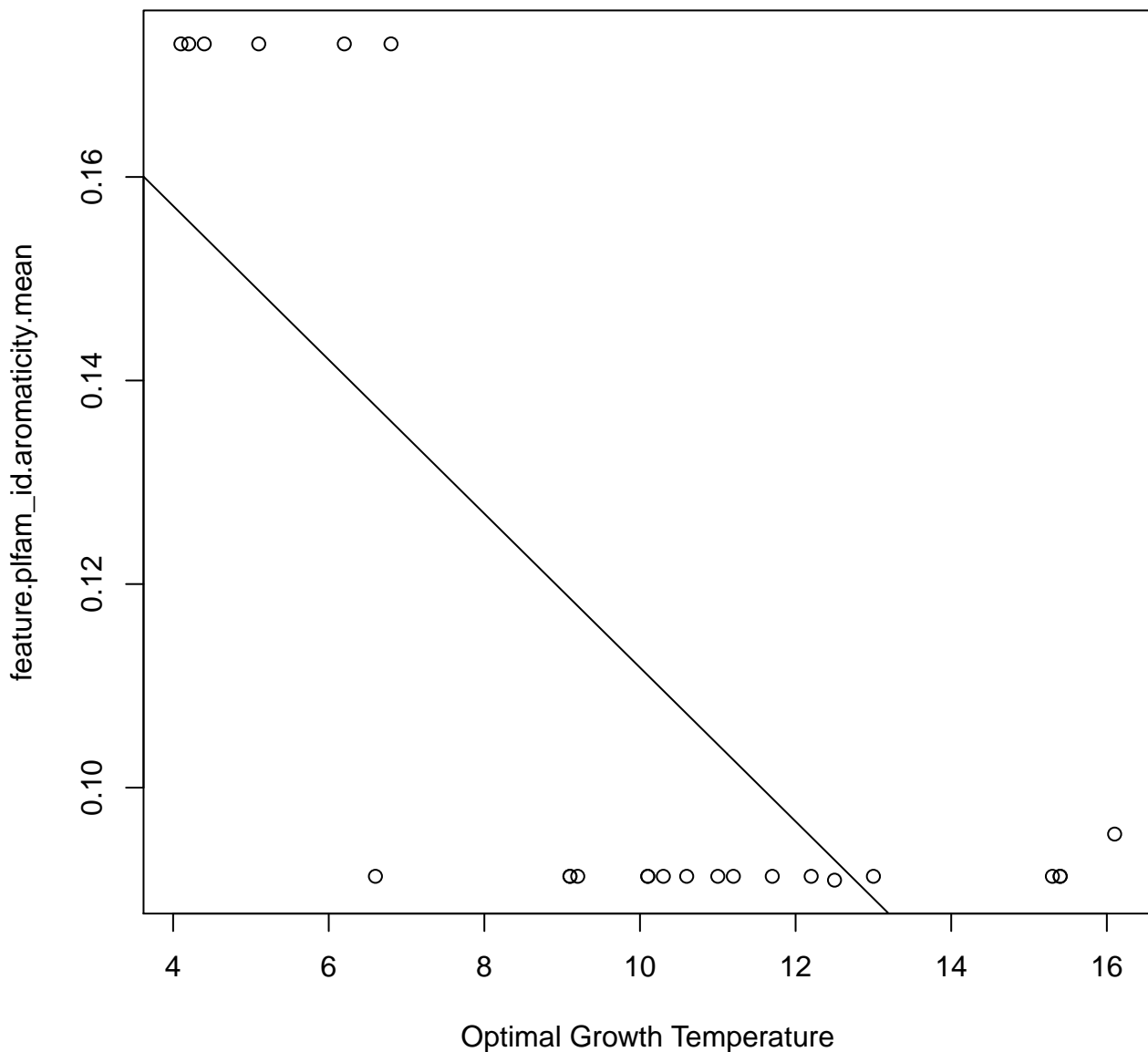
feature.plfam_id.aromaticity.mean

PLF_28228_00002575

Dipeptidyl peptidase IV



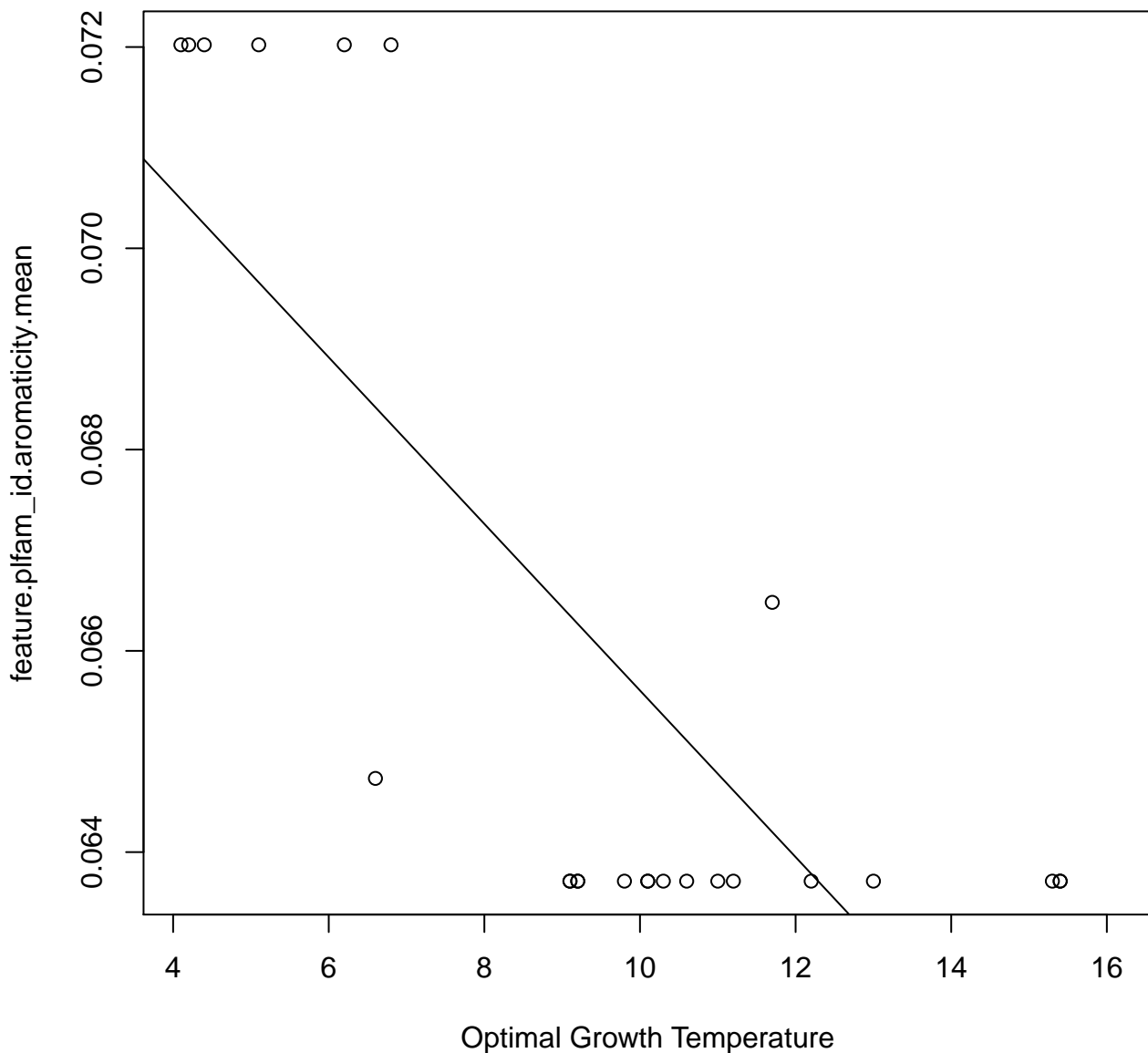
feature.plfam_id.aromaticity.mean
PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



feature.plfam_id.aromaticity.mean

PLF_28228_00003565

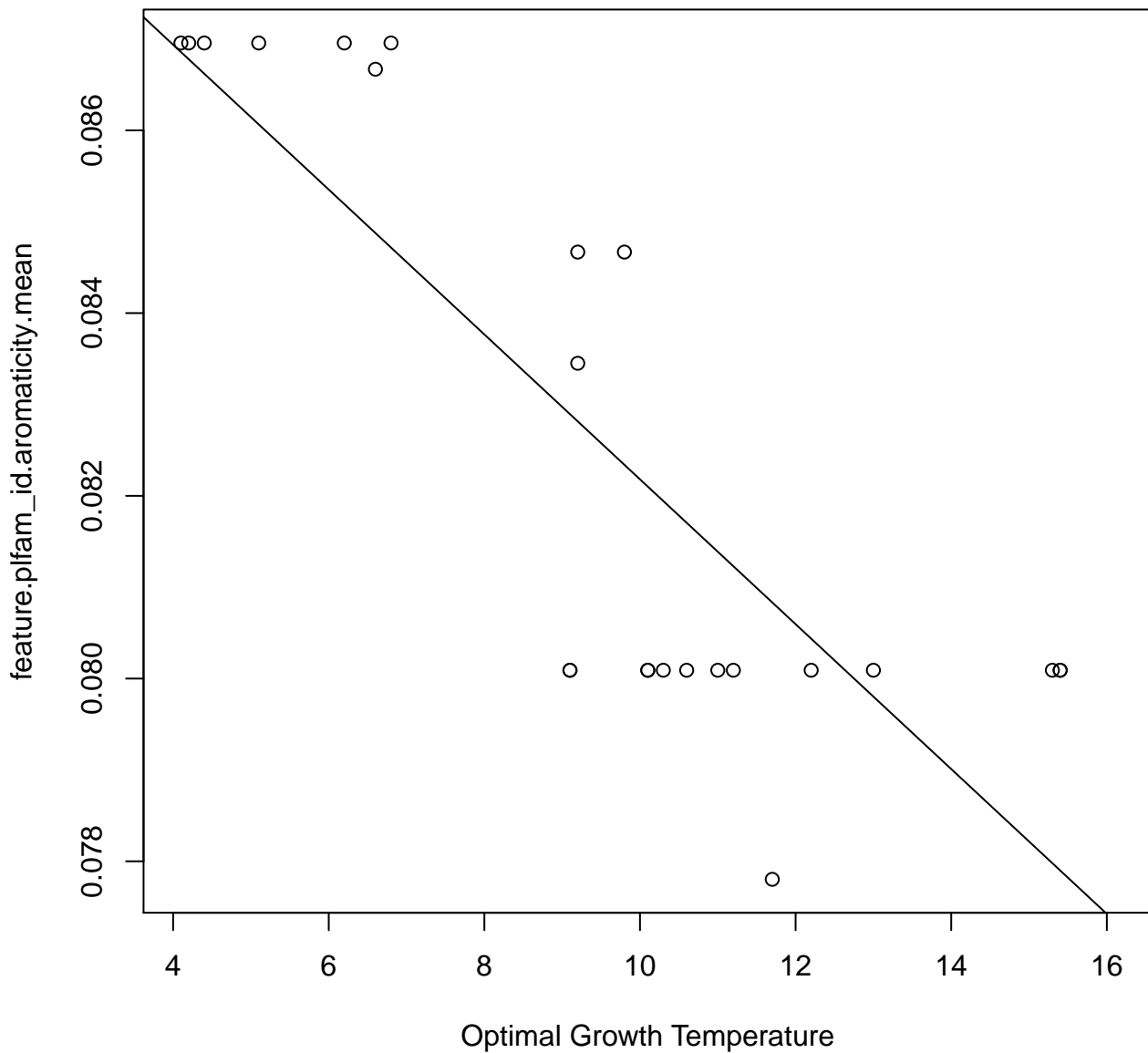
Chemotaxis response regulator–glutamate methylesterase CheB (EC 3.1.1.61)



feature.plfam_id.aromaticity.mean

PLF_28228_00004221

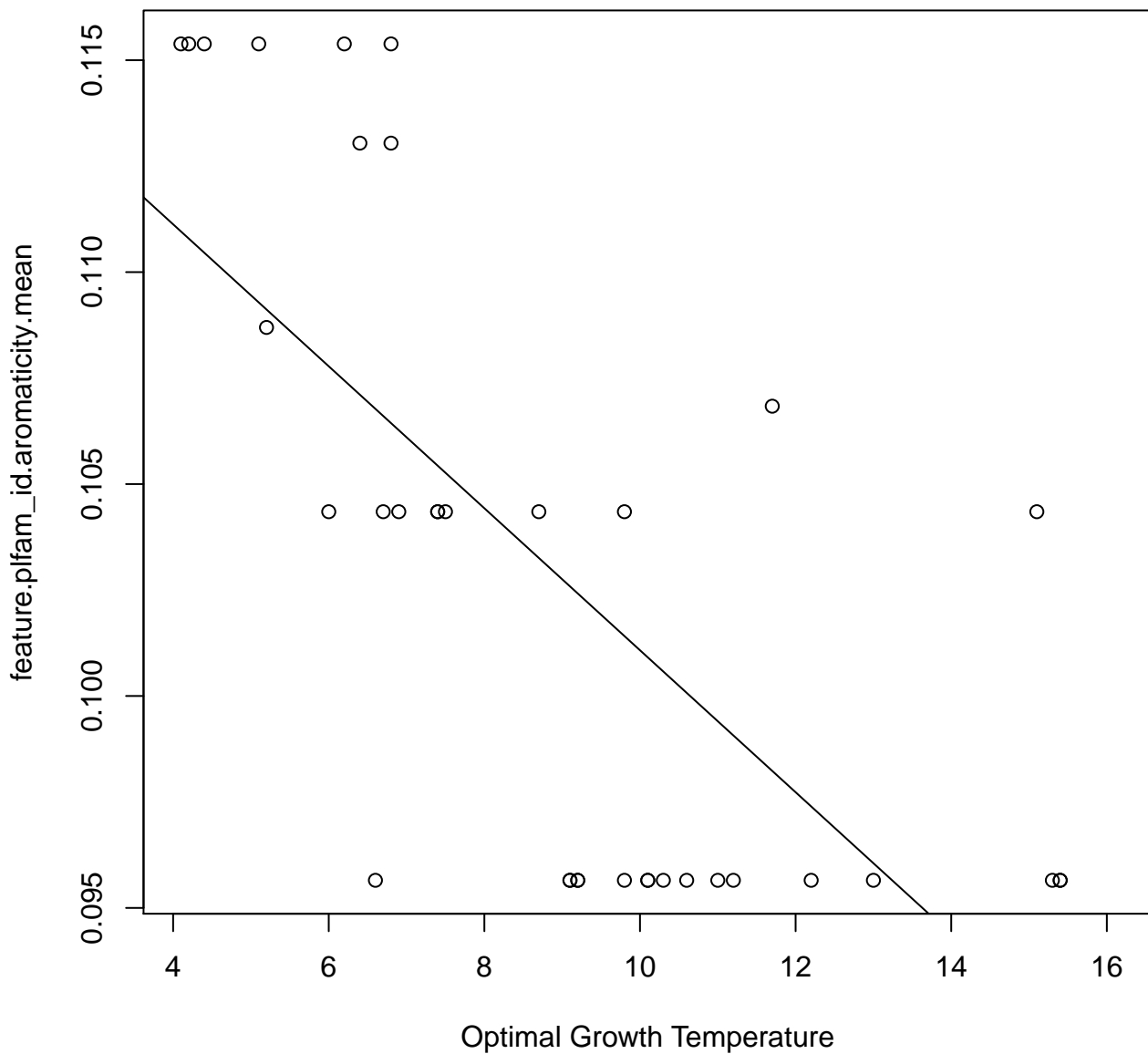
hypothetical protein



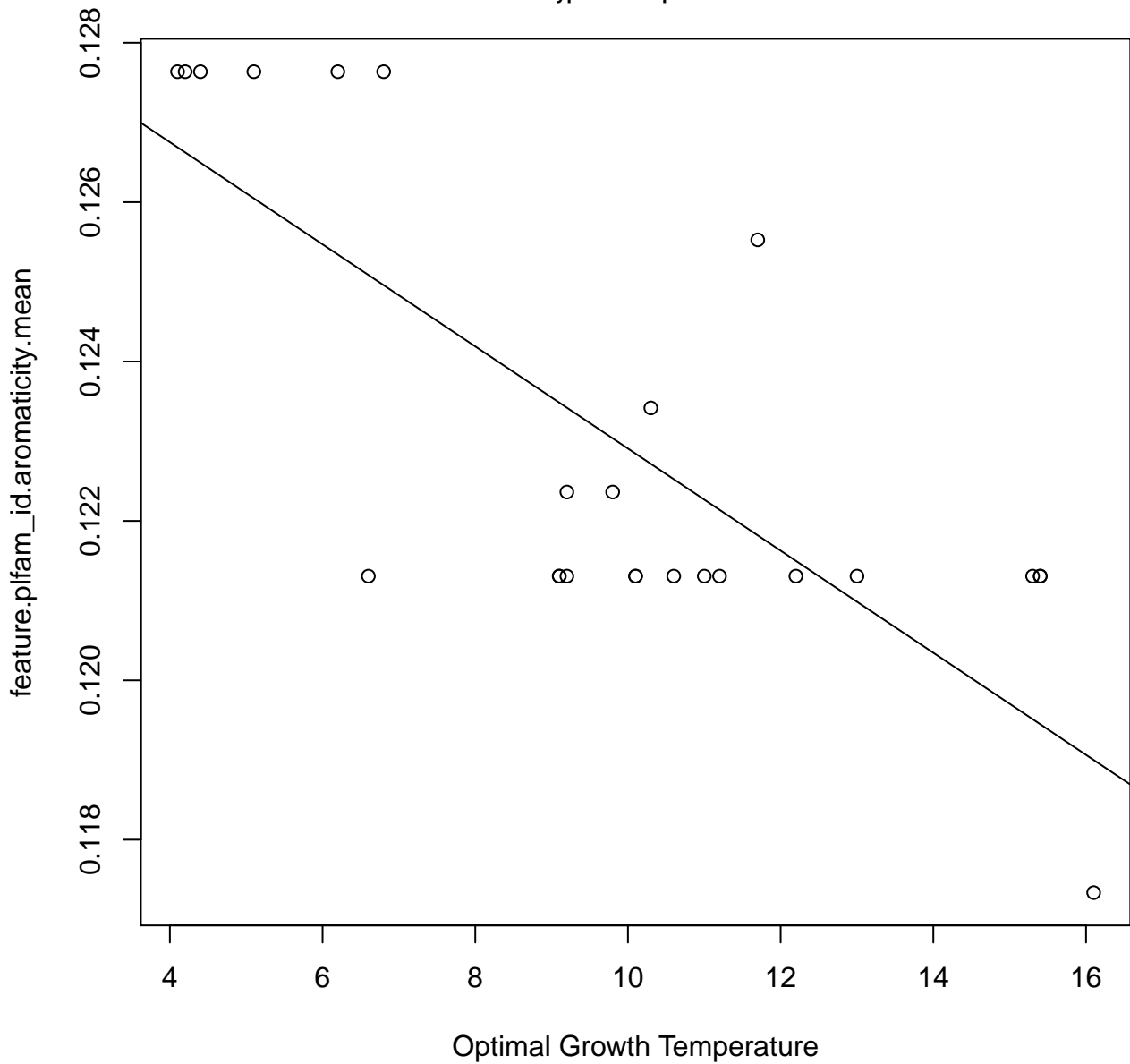
feature.plfam_id.aromaticity.mean

PLF_28228_00006398

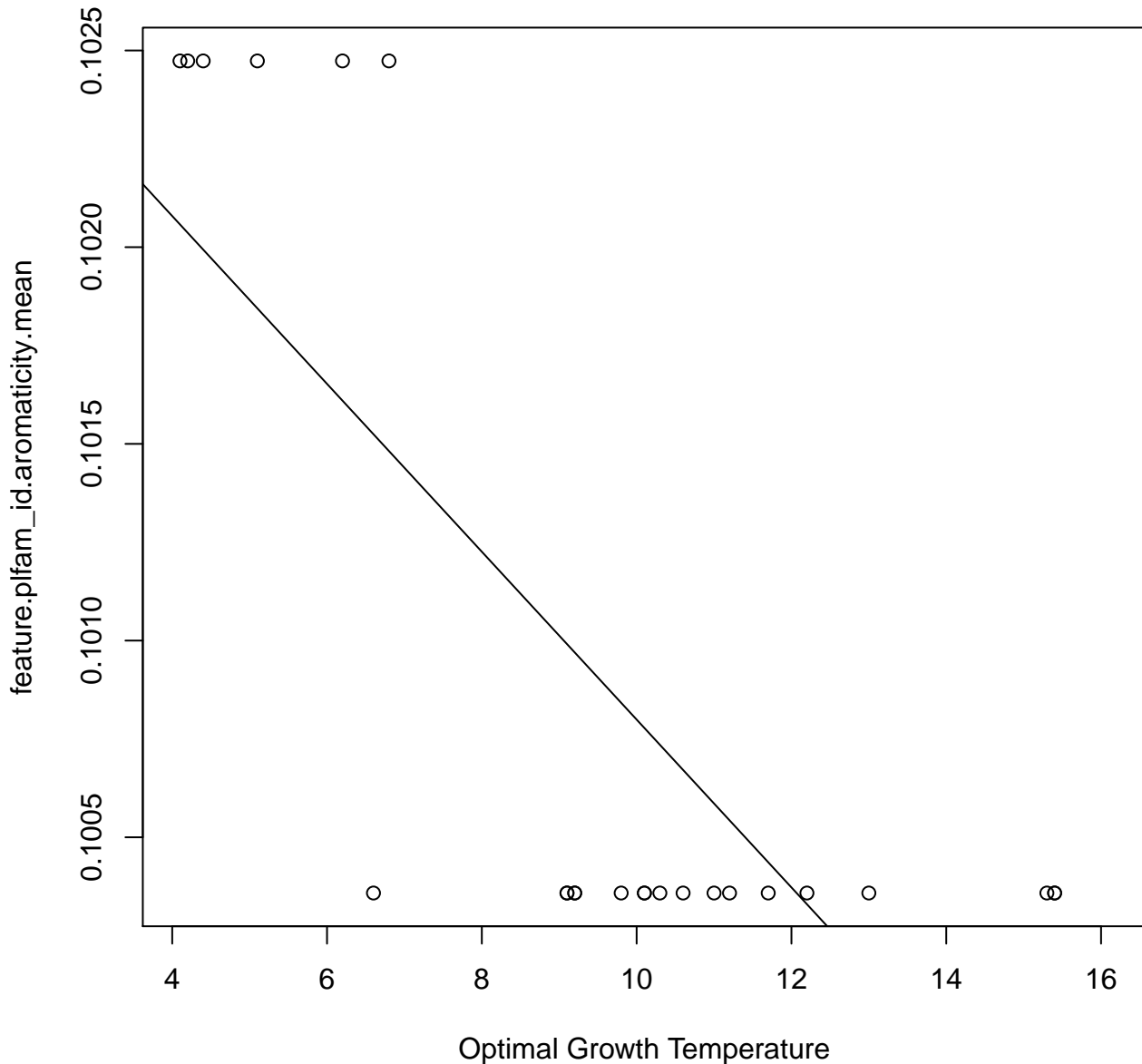
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00013222
hypothetical protein



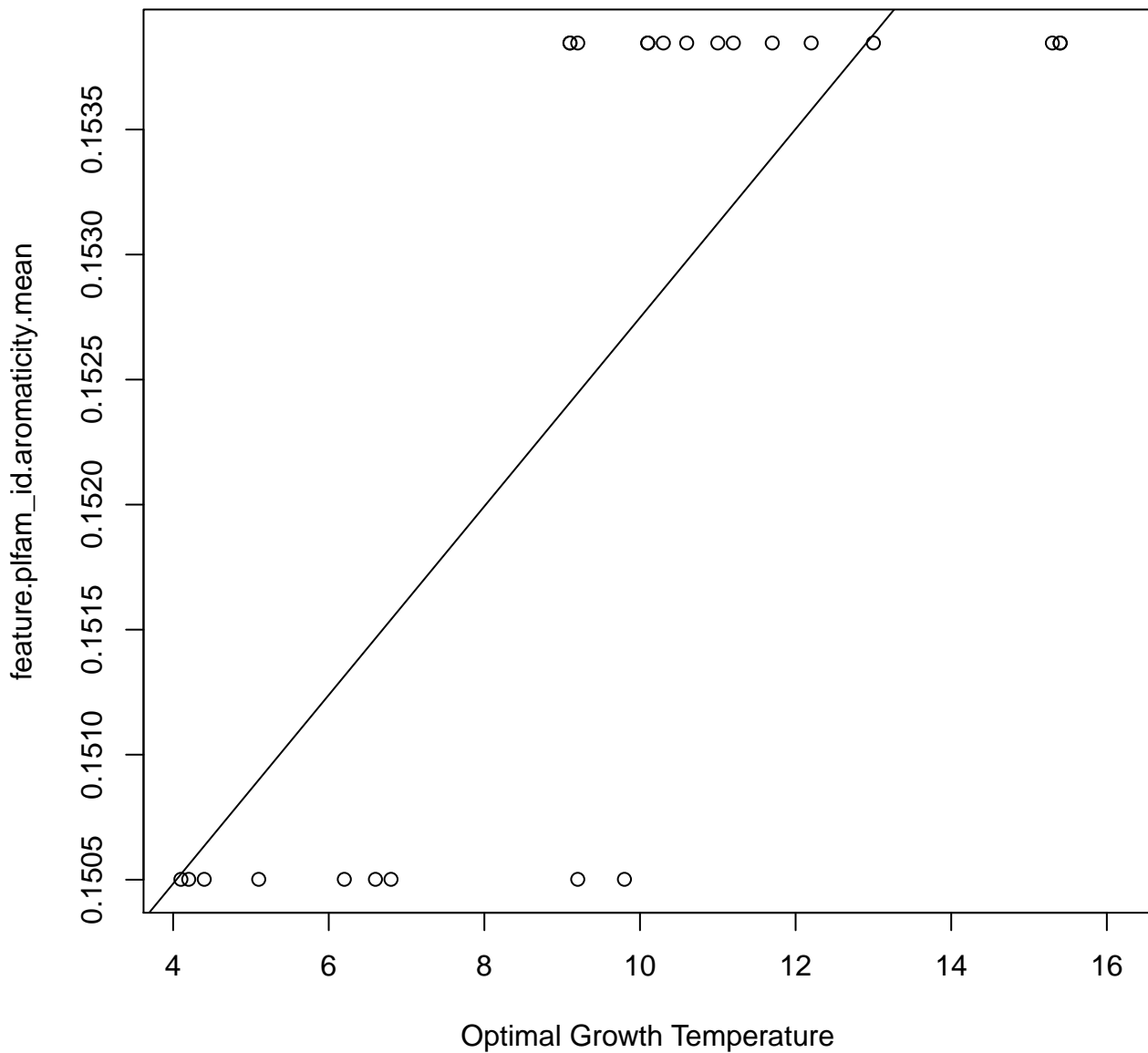
feature.plfam_id.aromaticity.mean
PLF_28228_00014476
Vitamin B12 ABC transporter, substrate-binding protein BtuF



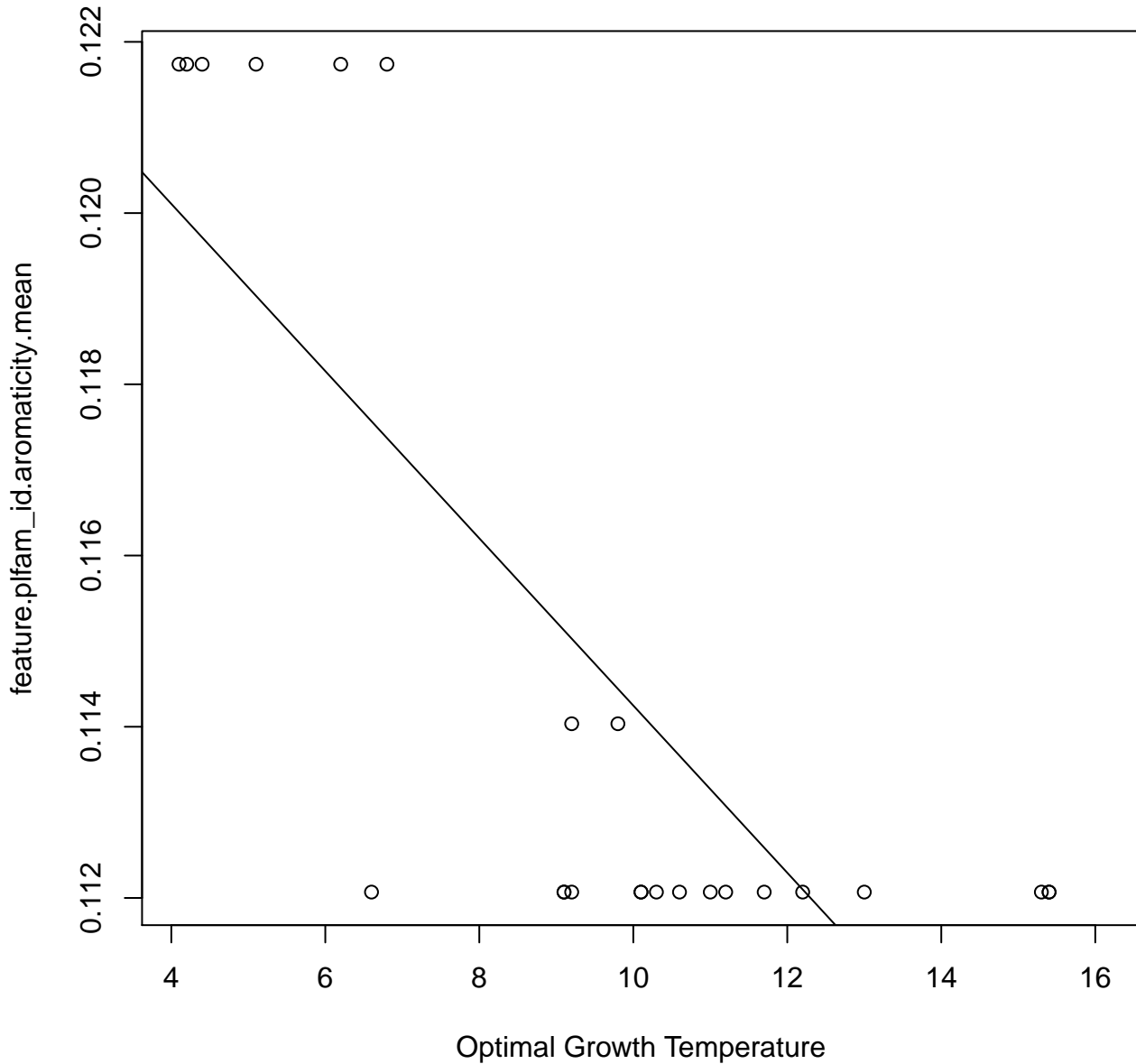
feature.plfam_id.aromaticity.mean

PLF_28228_00016148

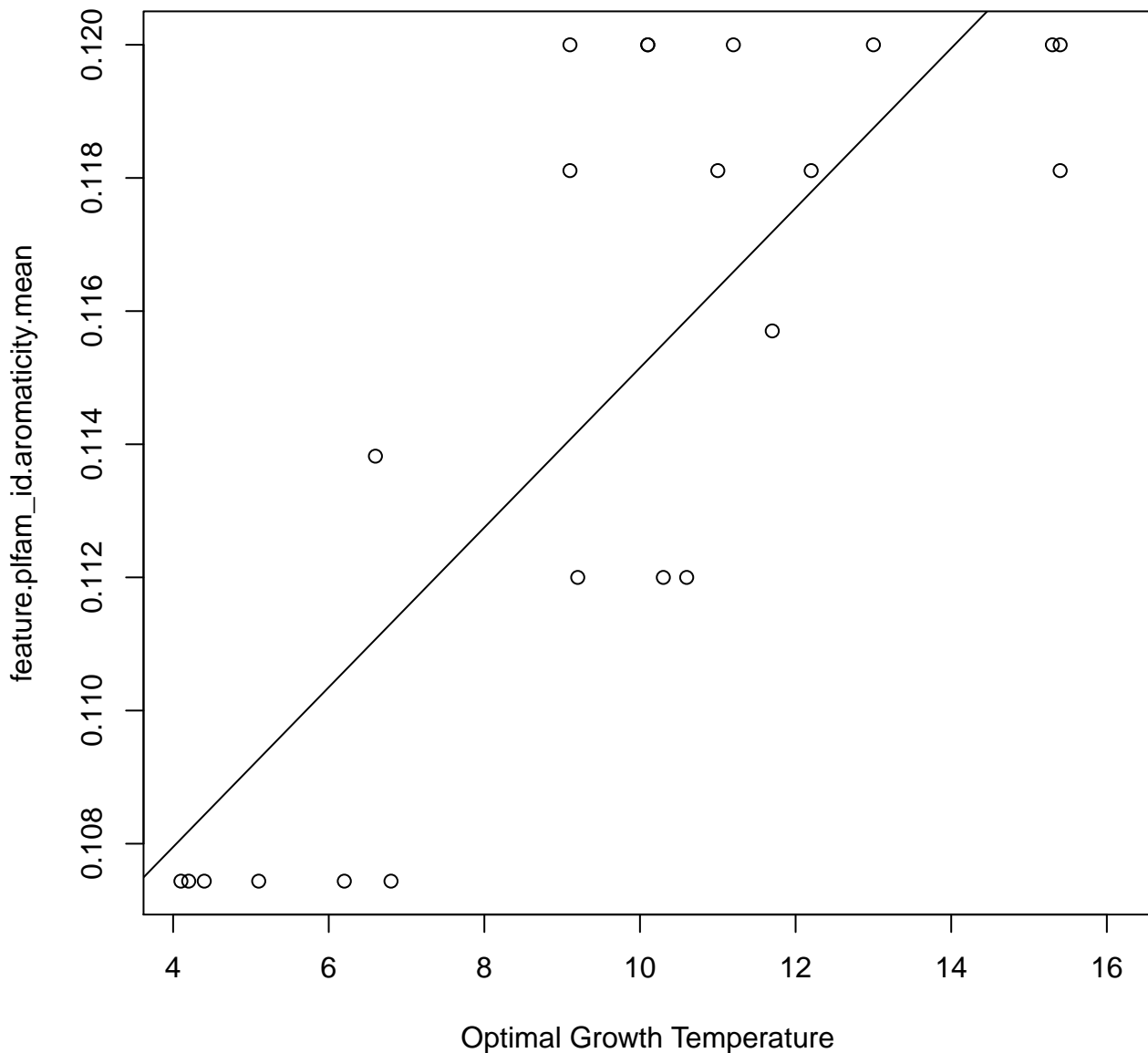
hypothetical protein



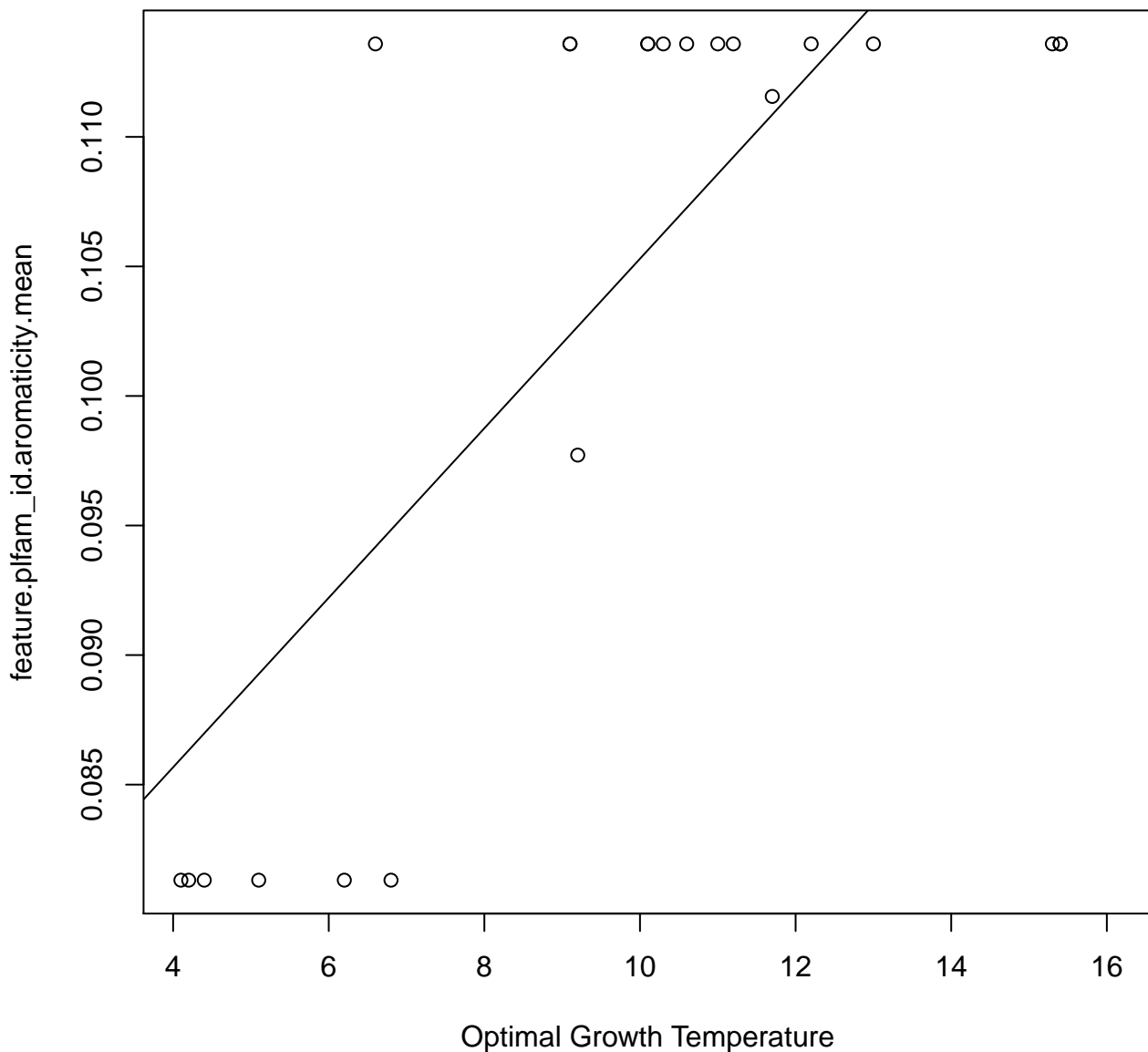
feature.plfam_id.aromaticity.mean
PLF_28228_00016319
hypothetical protein



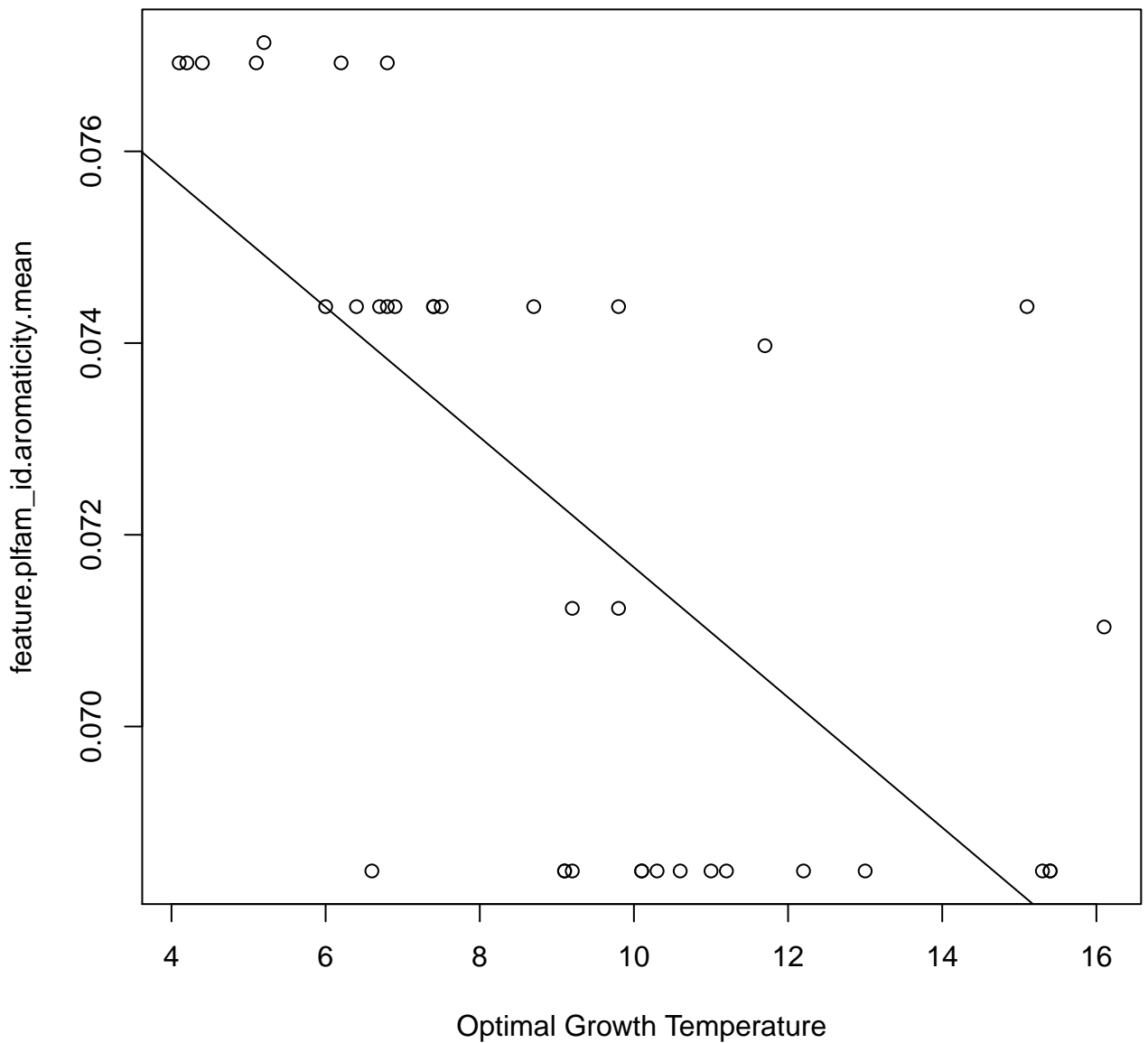
feature.plfam_id.aromaticity.mean
PLF_28228_00020926
hypothetical protein



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



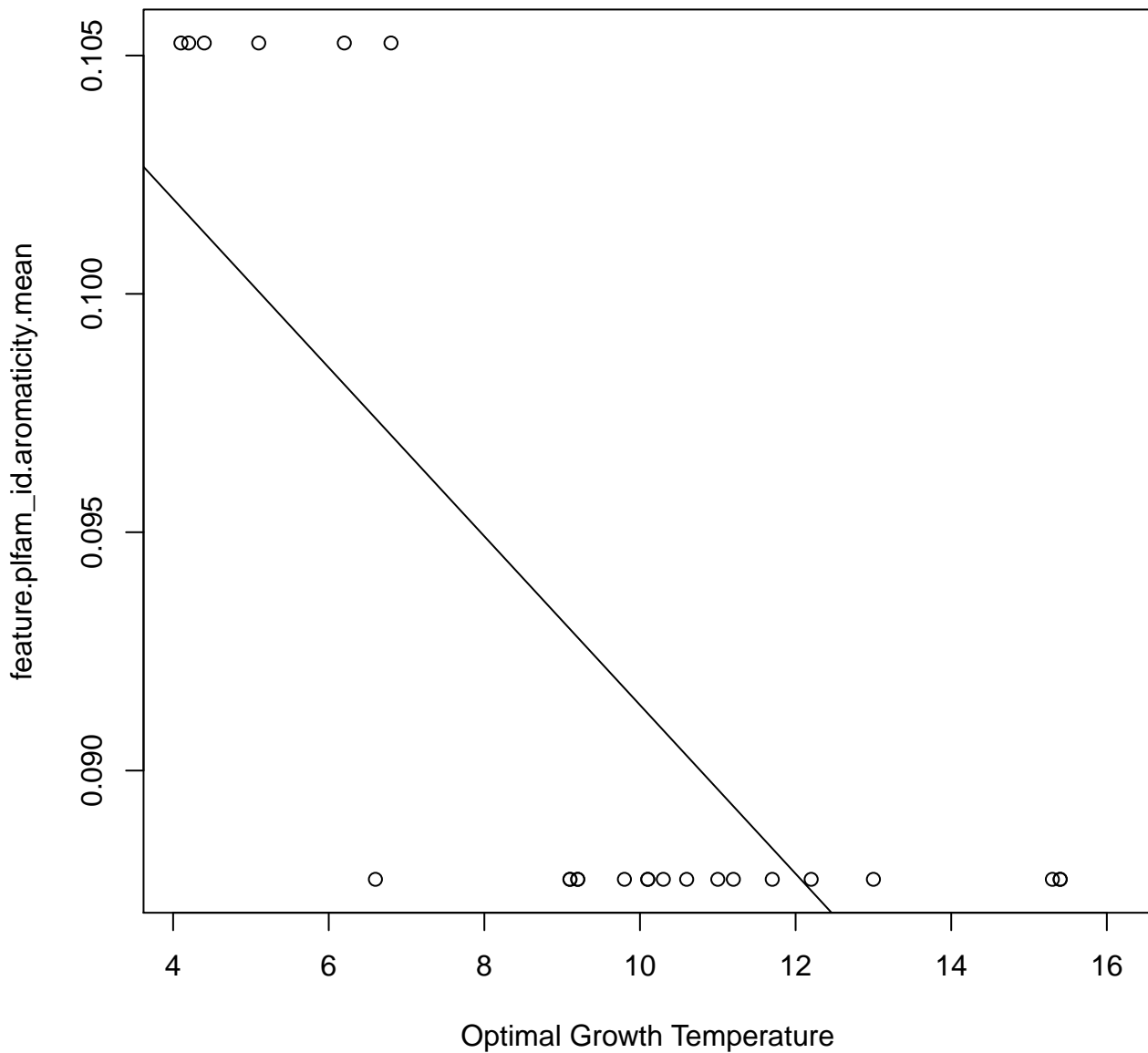
feature.plfam_id.aromaticity.mean
PLF_28228_00022166
[4Fe-4S] cluster assembly scaffold protein Mrp (=ApcC)



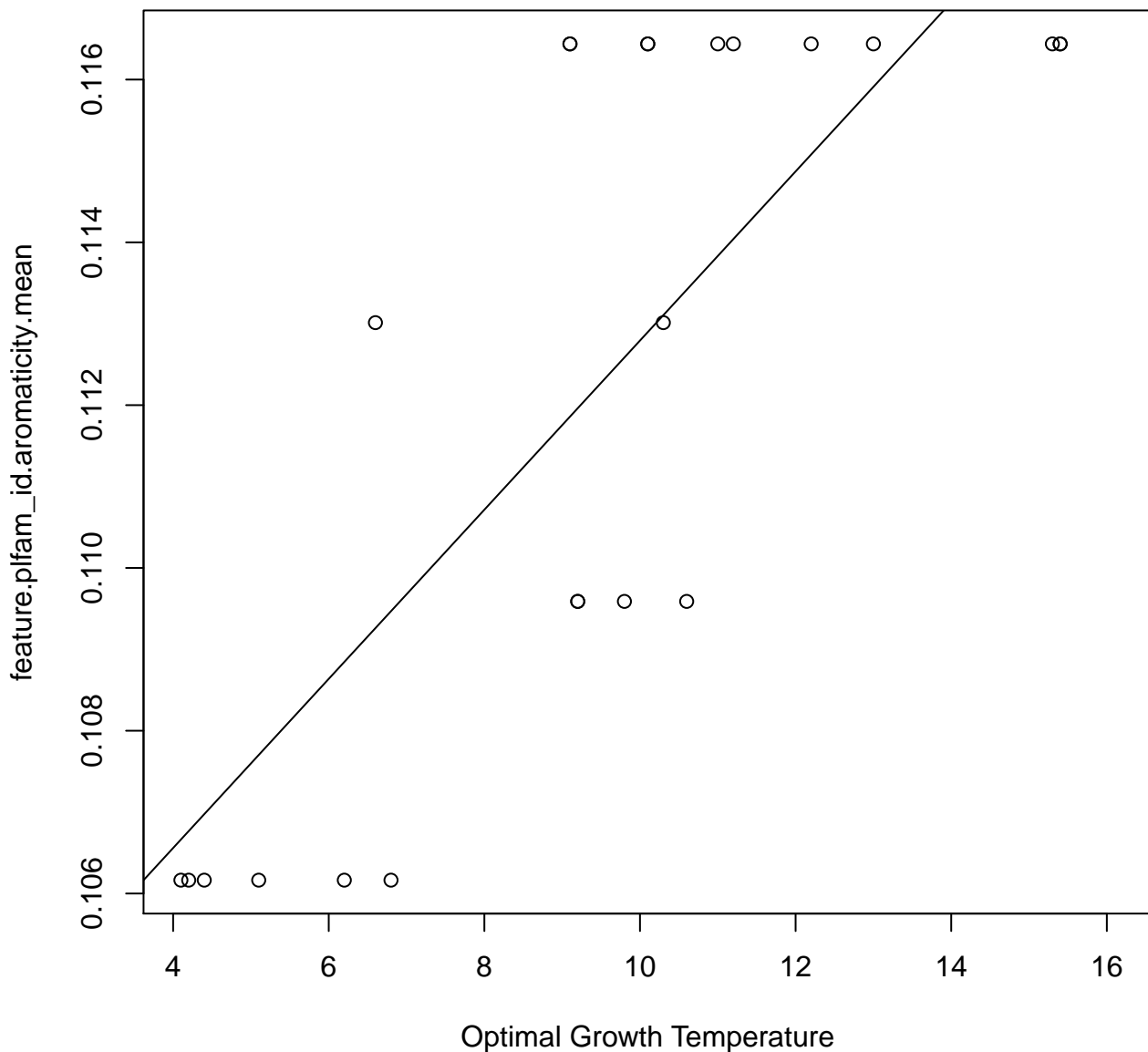
feature.plfam_id.aromaticity.mean

PLF_28228_00022617

hypothetical protein



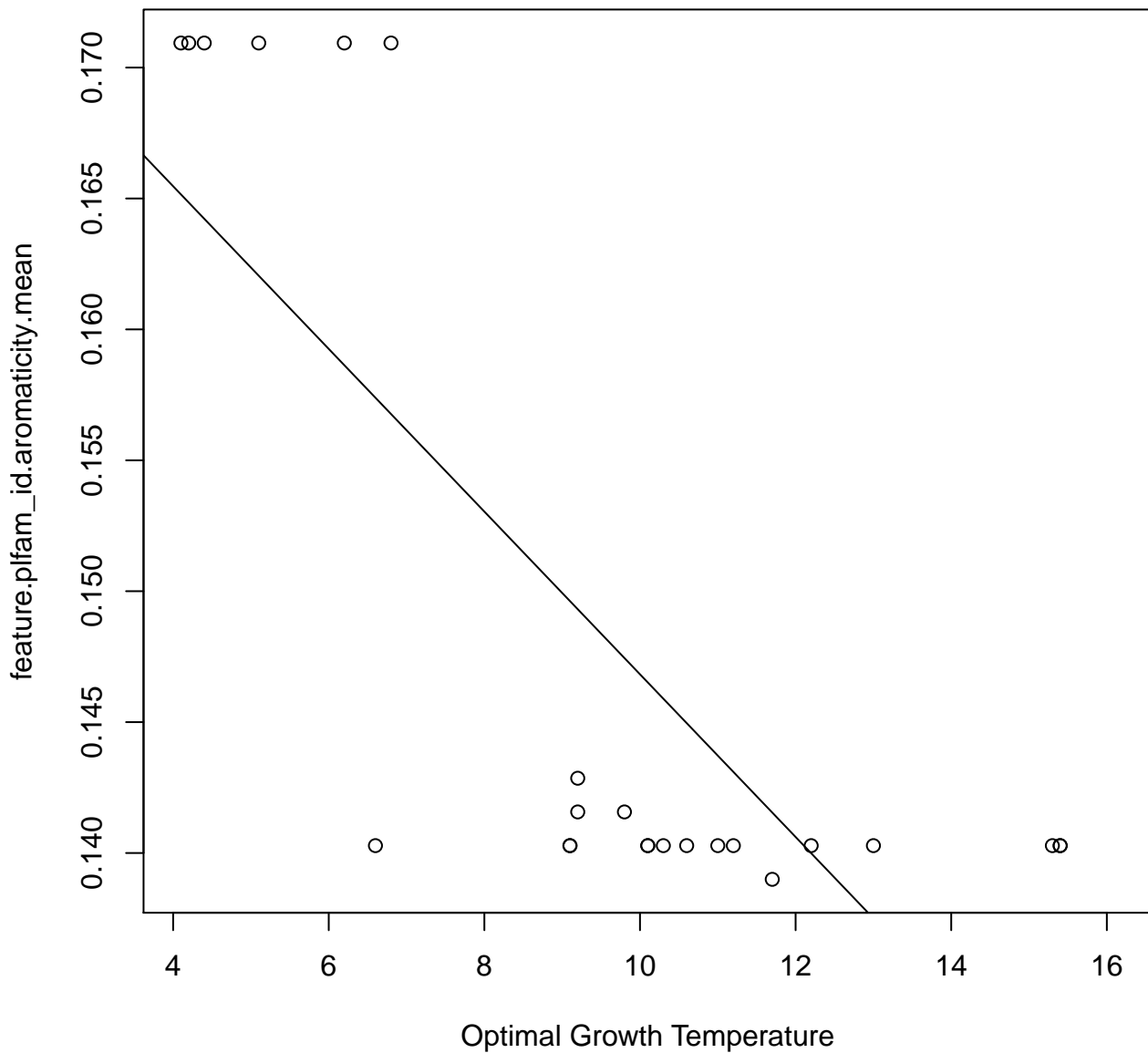
feature.plfam_id.aromaticity.mean
PLF_28228_00023267
Uncharacterized protein conserved in bacteria, NMA0228-like



feature.plfam_id.aromaticity.mean

PLF_28228_00028047

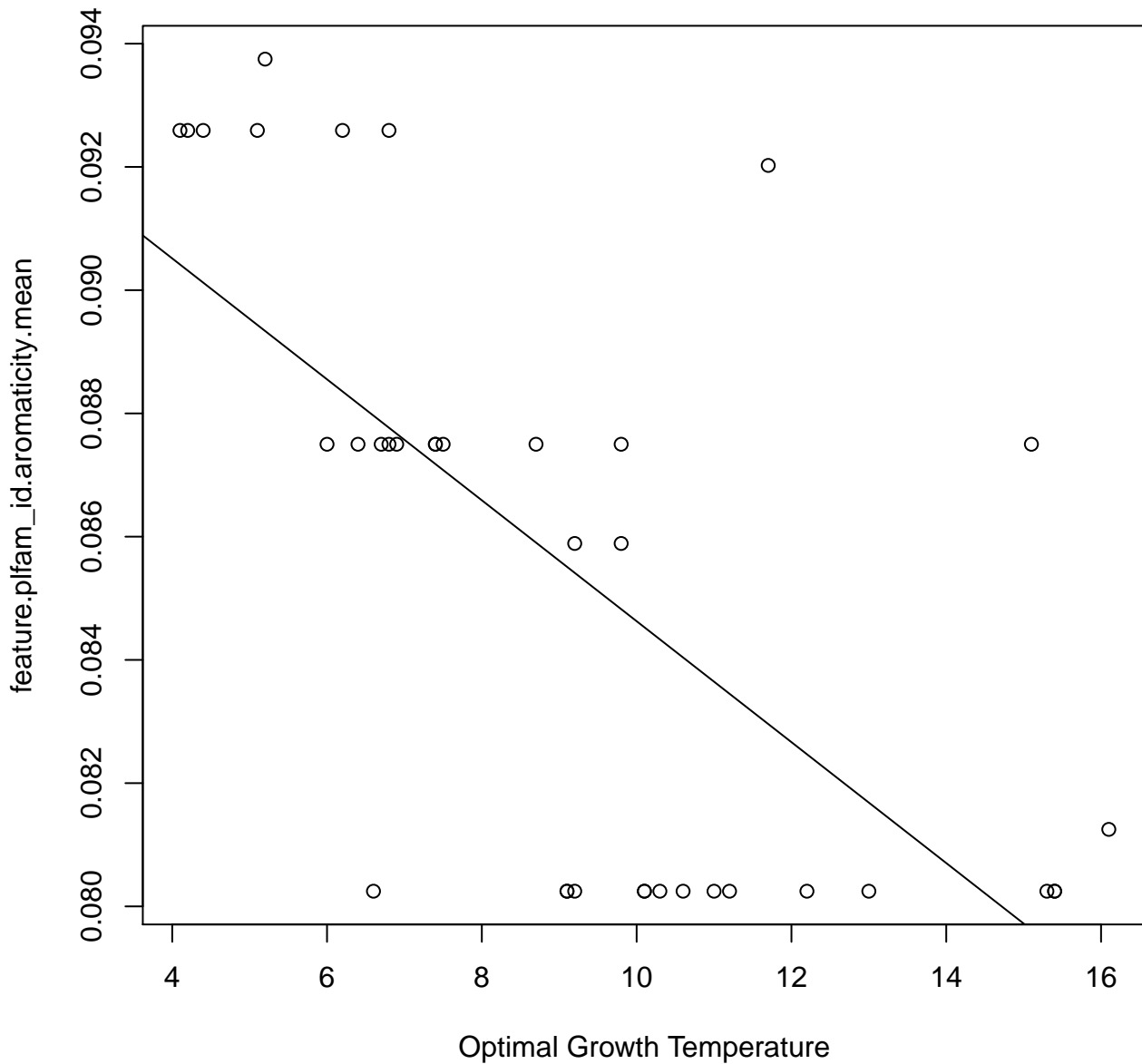
Fatty acid cis/trans isomerase



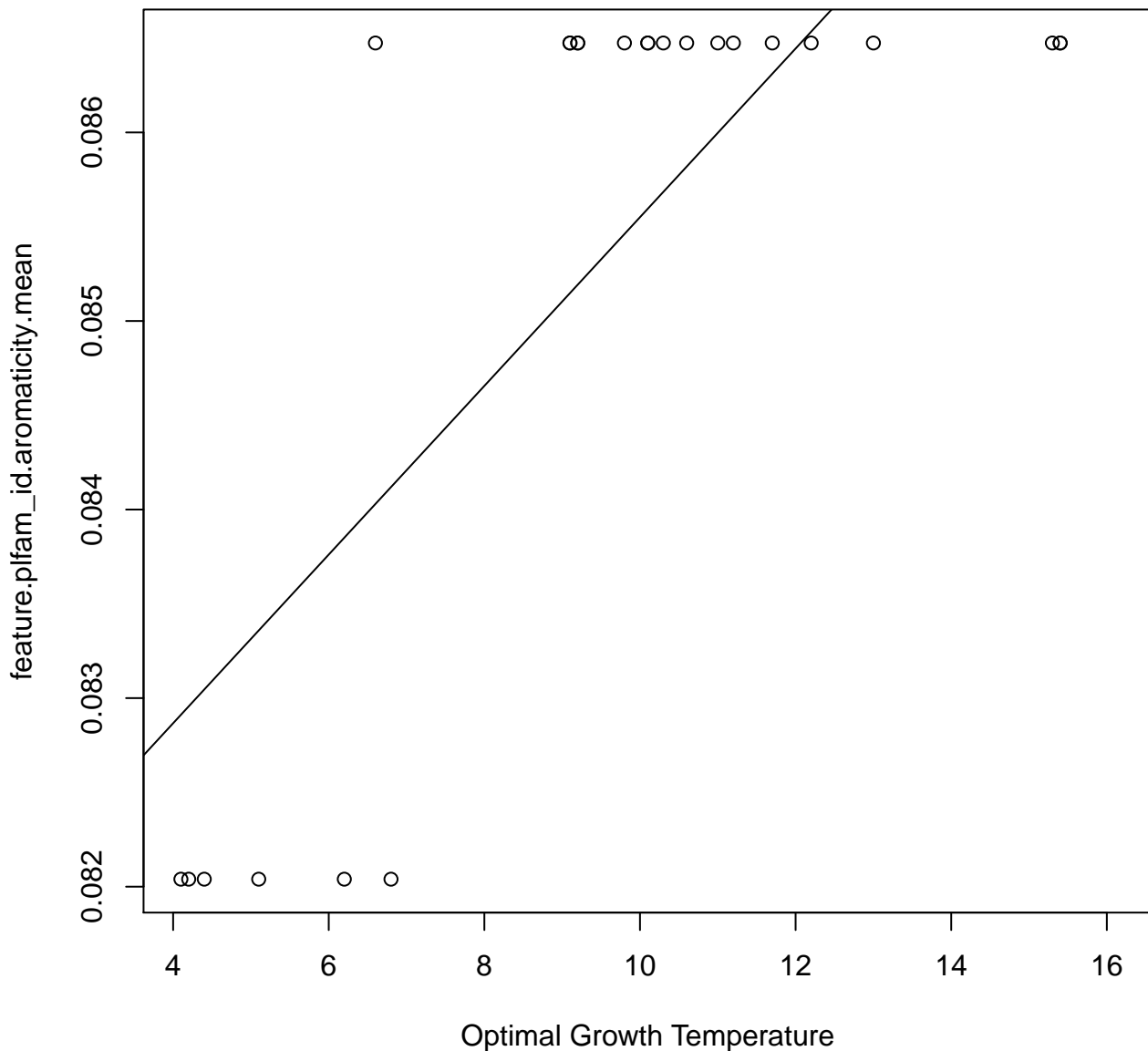
feature.plfam_id.aromaticity.mean

PLF_28228_00028100

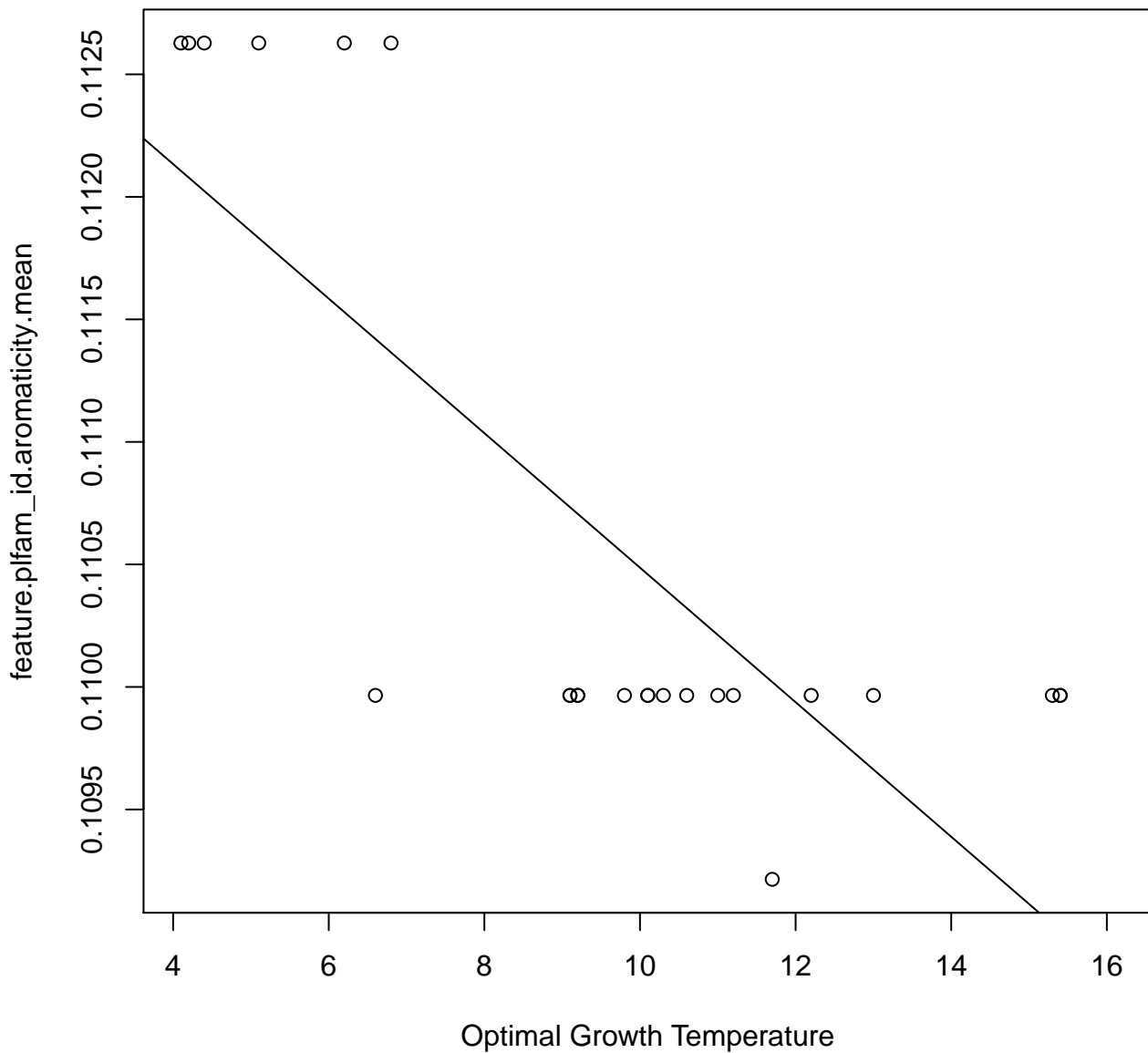
Ribonuclease E inhibitor RraA



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



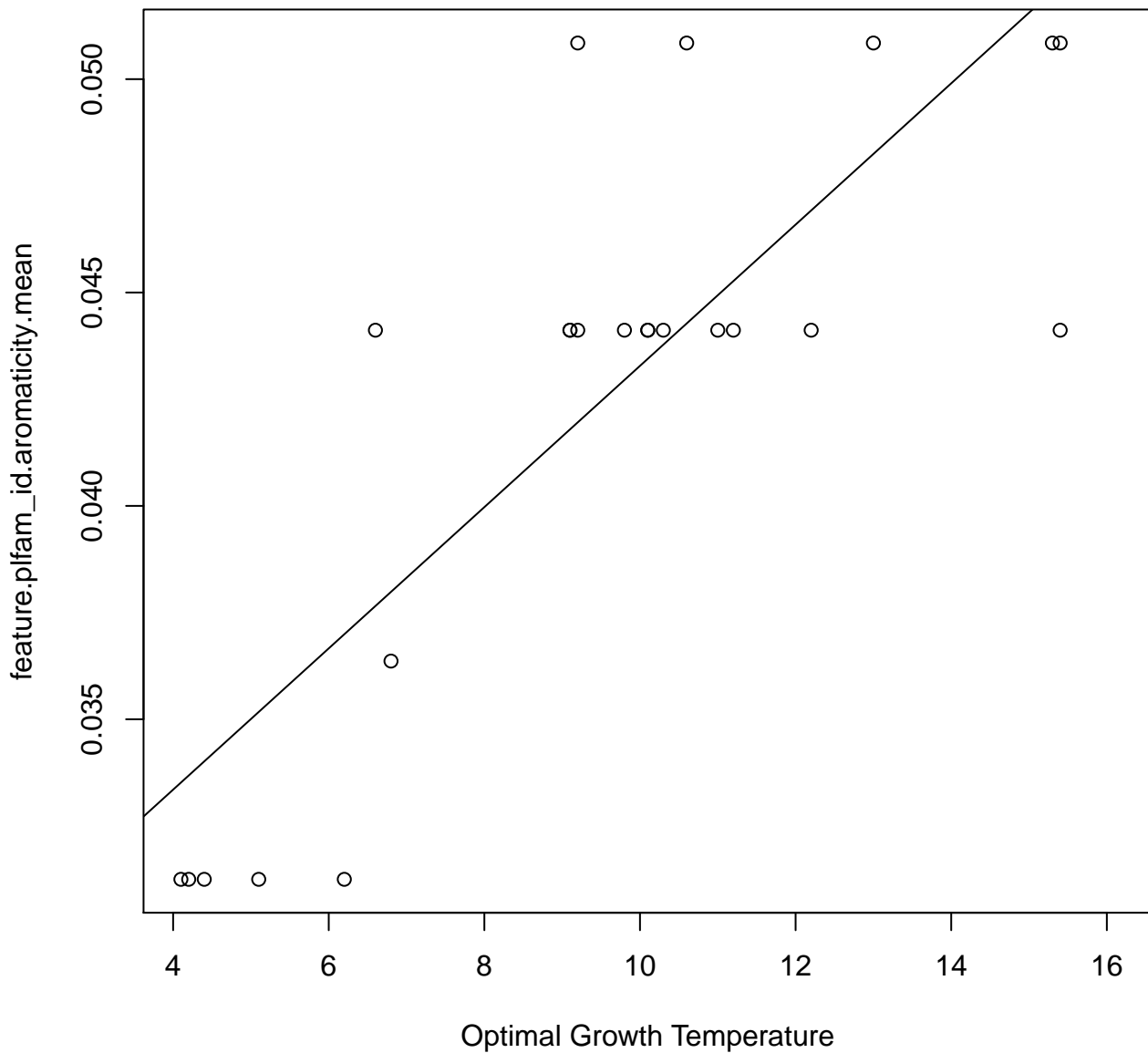
feature.plfam_id.aromaticity.mean
PLF_28228_00028713
Transcriptional regulator VCA1020, LysR family



feature.plfam_id.aromaticity.mean

PLF_28228_00029456

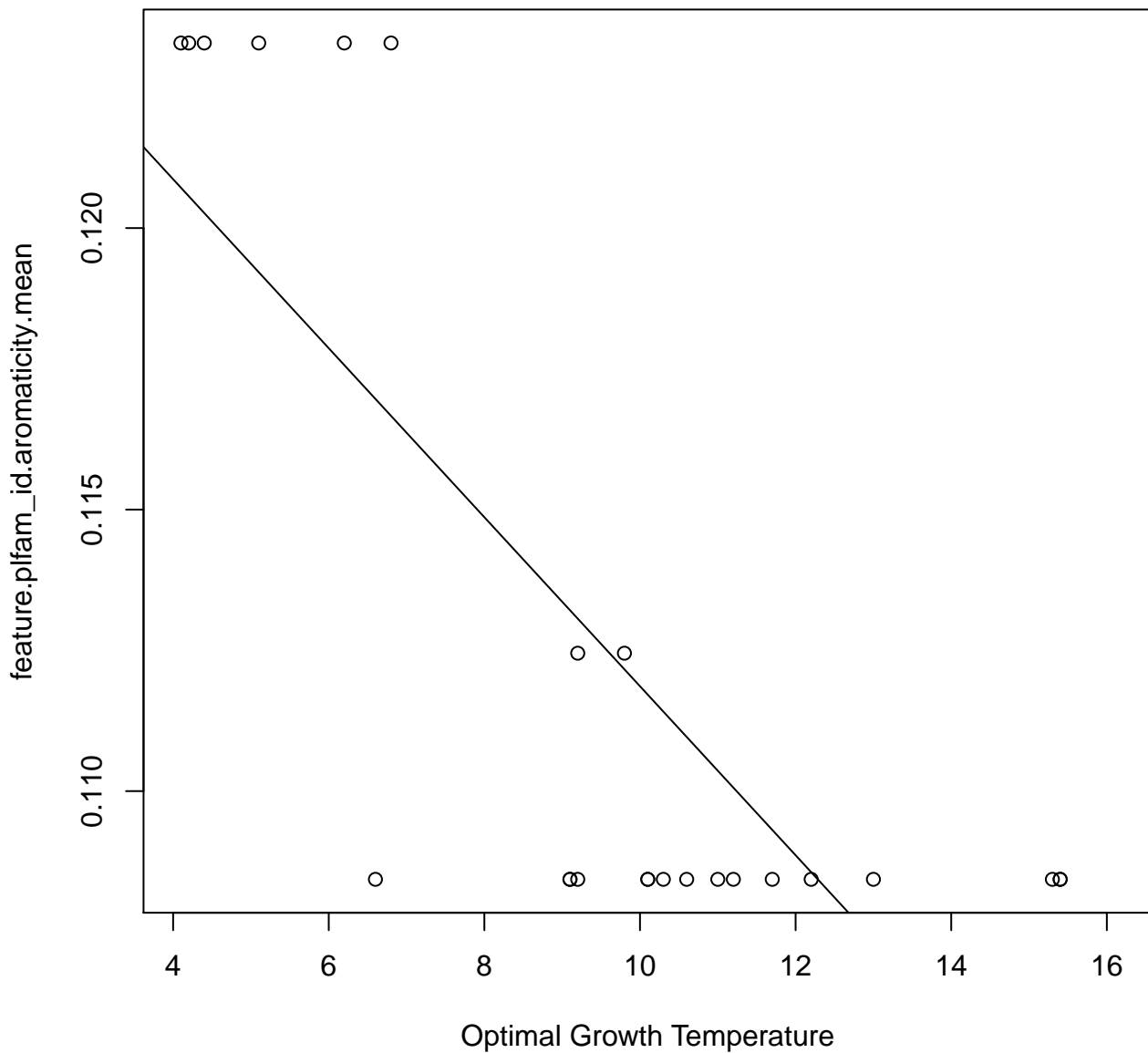
hypothetical protein



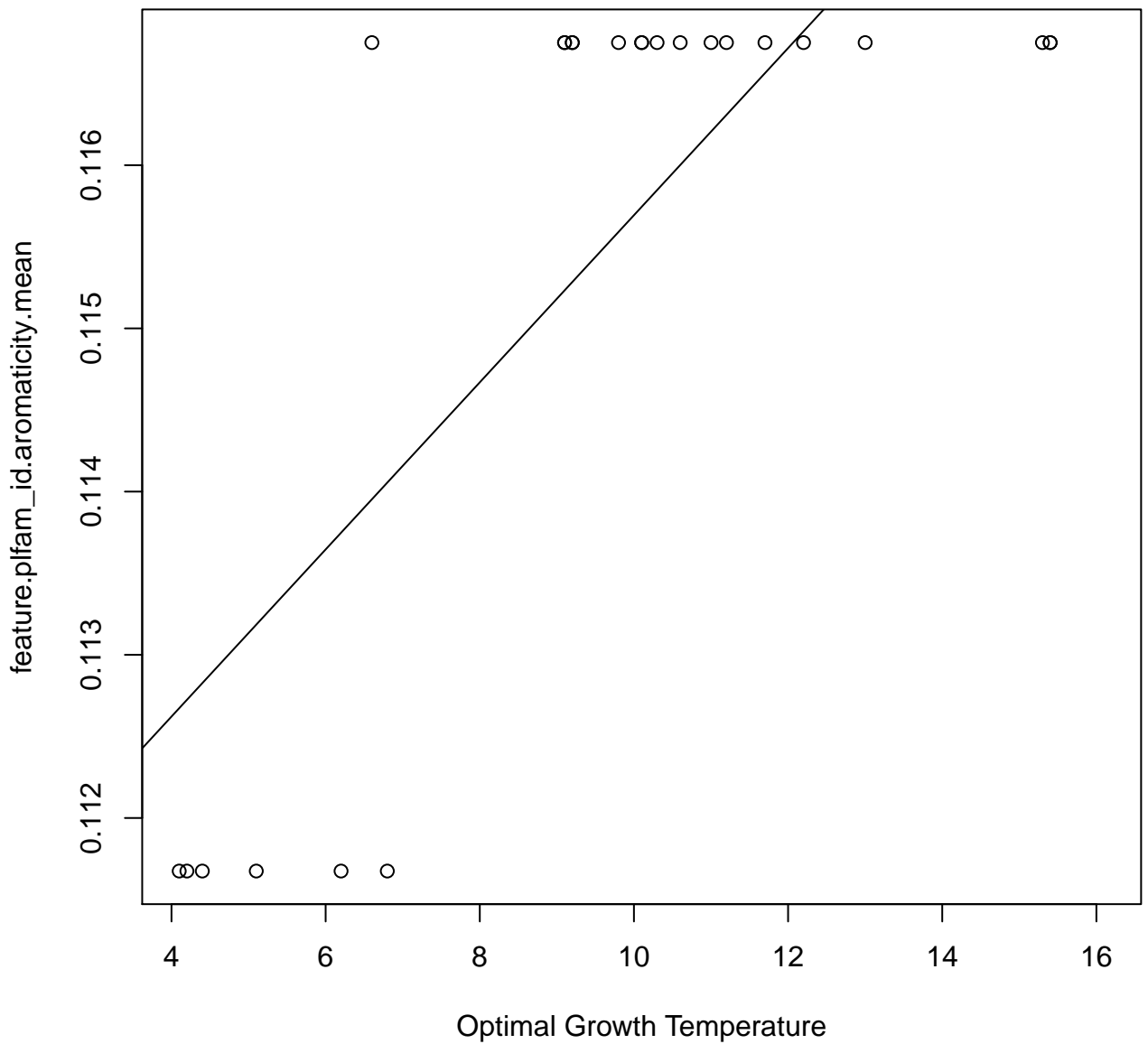
feature.plfam_id.aromaticity.mean

PLF_28228_00031426

hypothetical protein



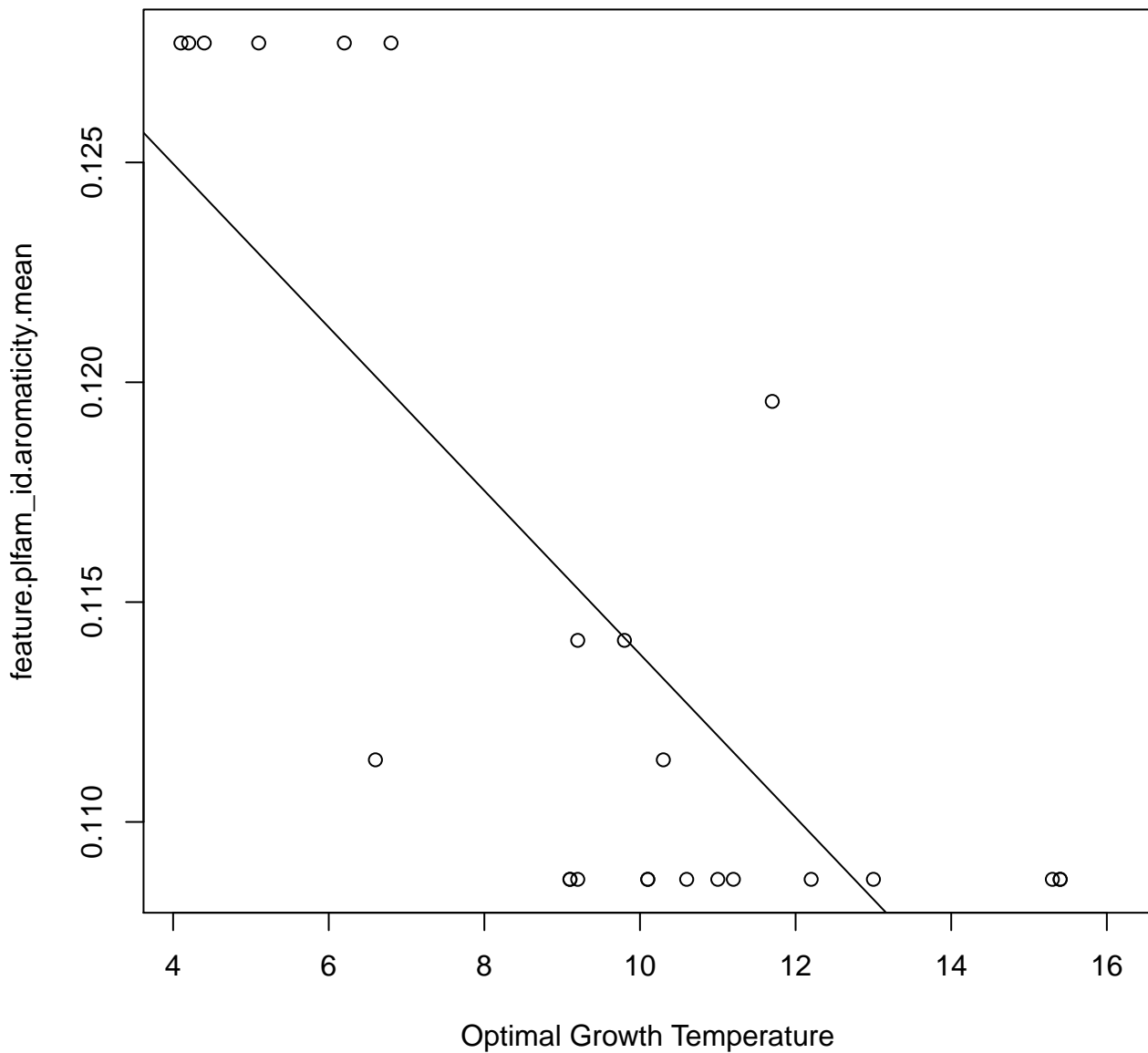
feature.plfam_id.aromaticity.mean
PLF_28228_00032199
Uncharacterized hydrolase DSY2054



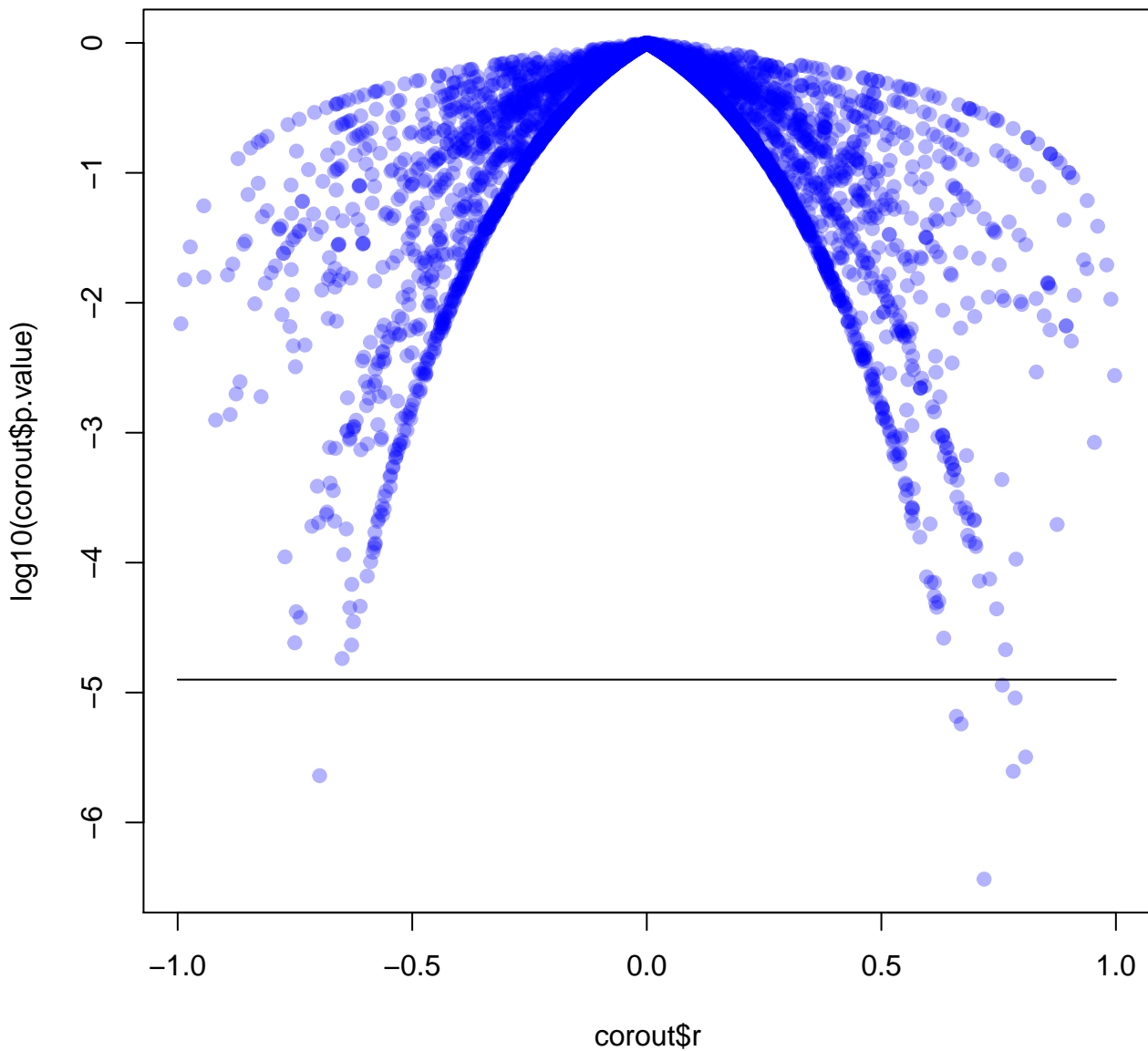
feature.plfam_id.aromaticity.mean

PLF_28228_00032200

hypothetical protein



feature.pgfam_id.aliphatic_index.mean

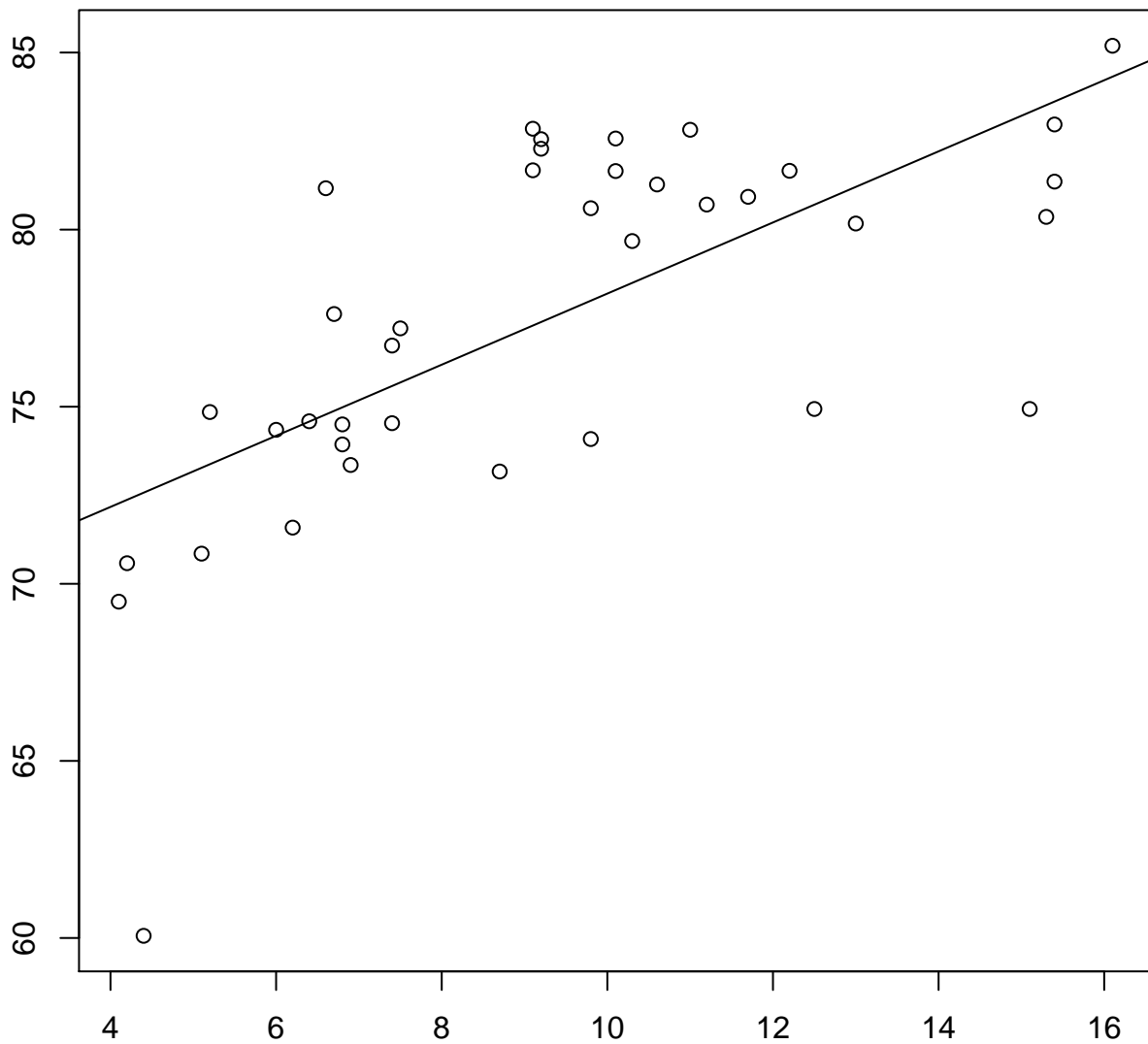


feature.pgfam_id.aliphatic_index.mean

PGF_00011634

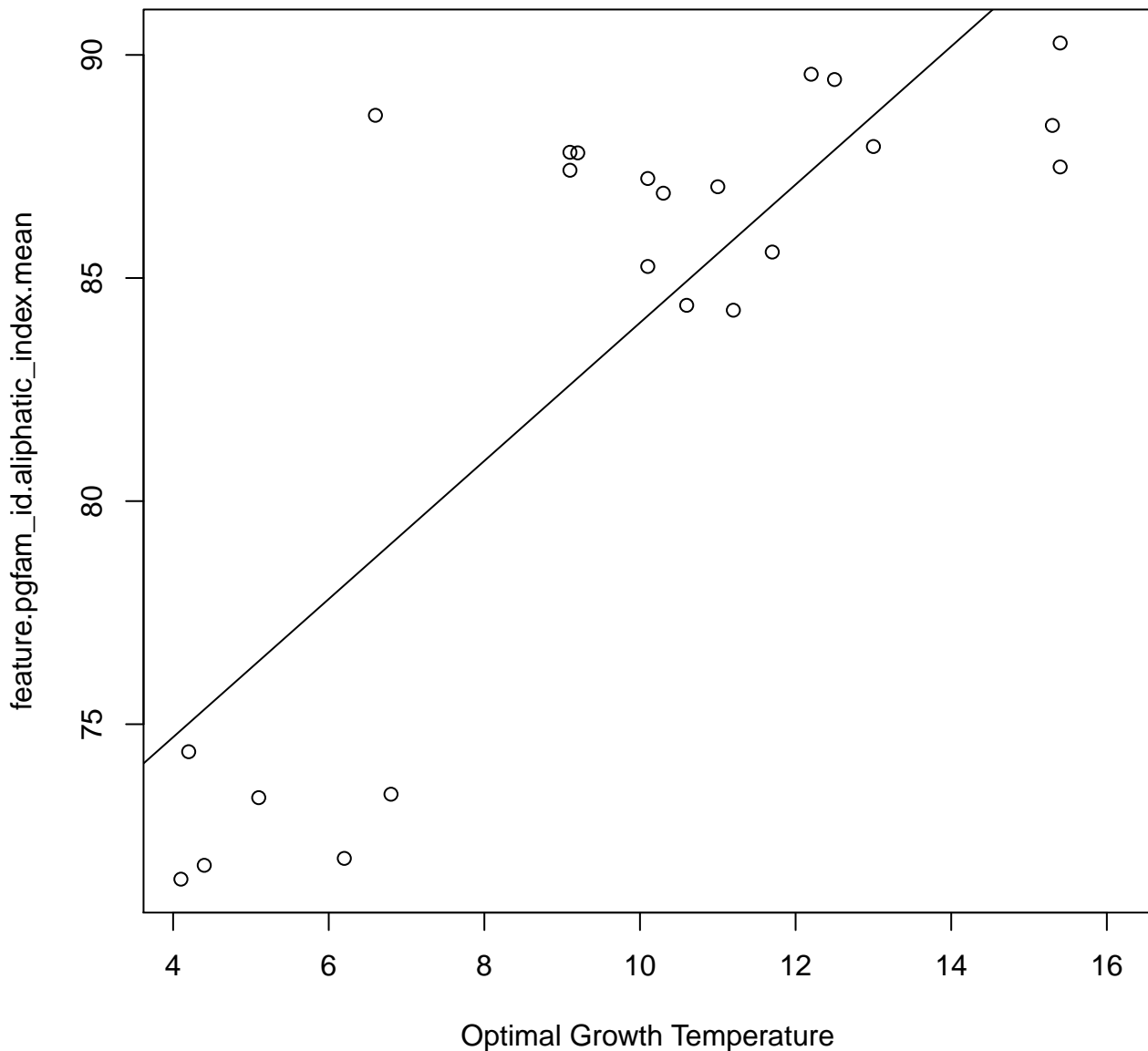
HflK protein

feature.pgfam_id.aliphatic_index.mean



Optimal Growth Temperature

feature.pgfam_id.aliphatic_index.mean
PGF_00064685
Uncharacterized ferredoxin-like protein YfhL

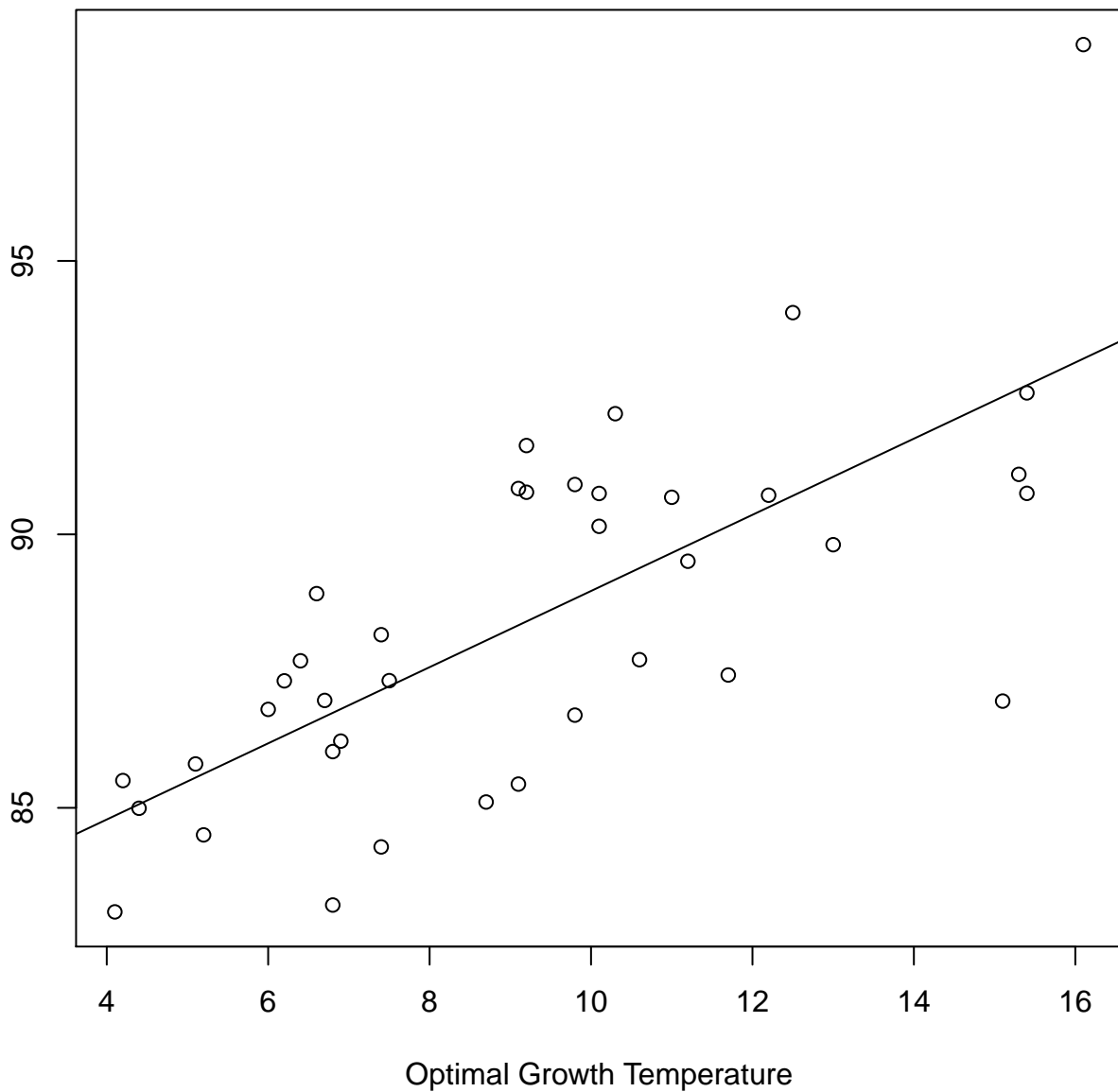


feature.pgfam_id.aliphatic_index.mean

PGF_01337968

hypothetical protein

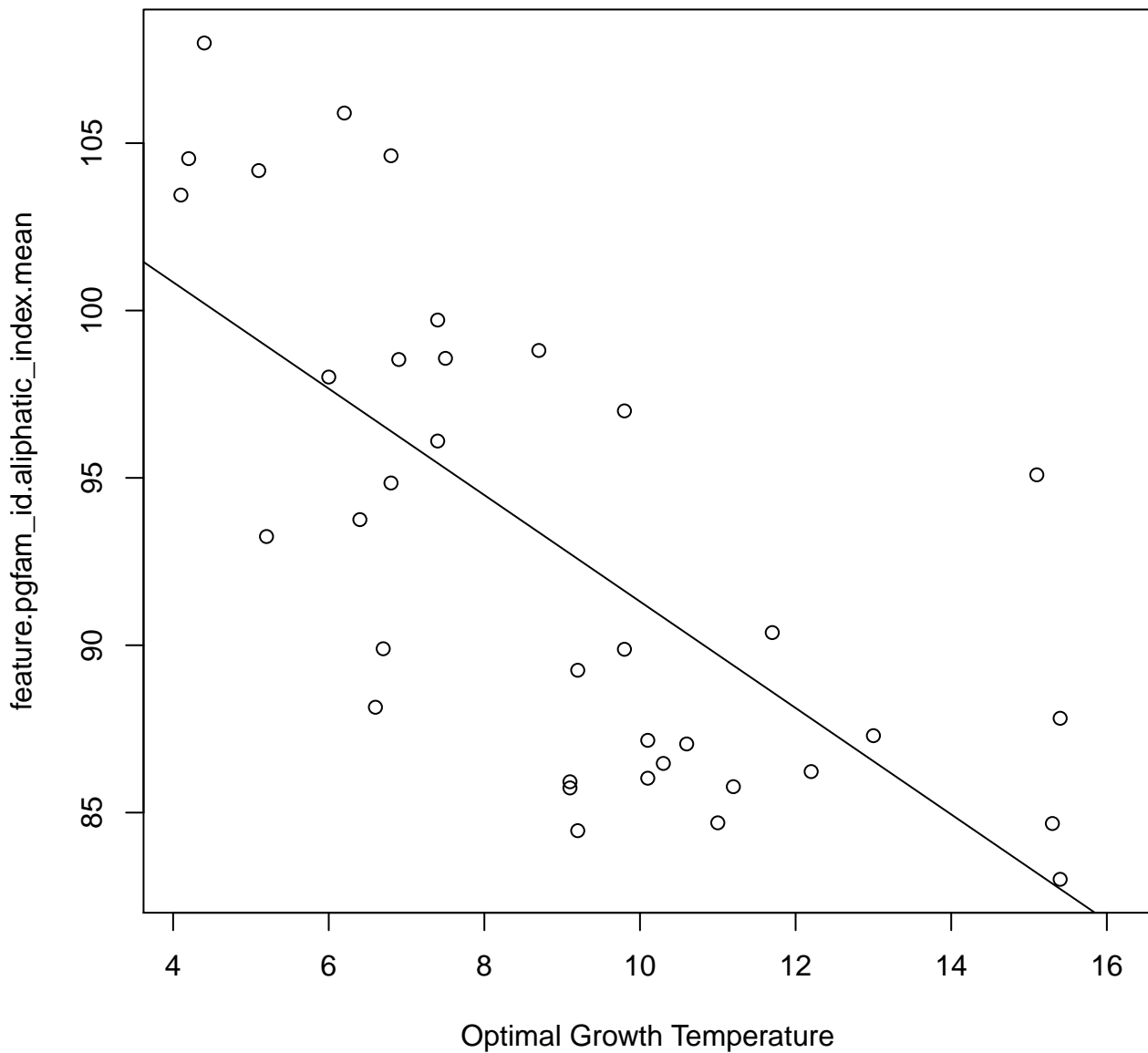
feature.pgfam_id.aliphatic_index.mean



feature.pgfam_id.aliphatic_index.mean

PGF_01338555

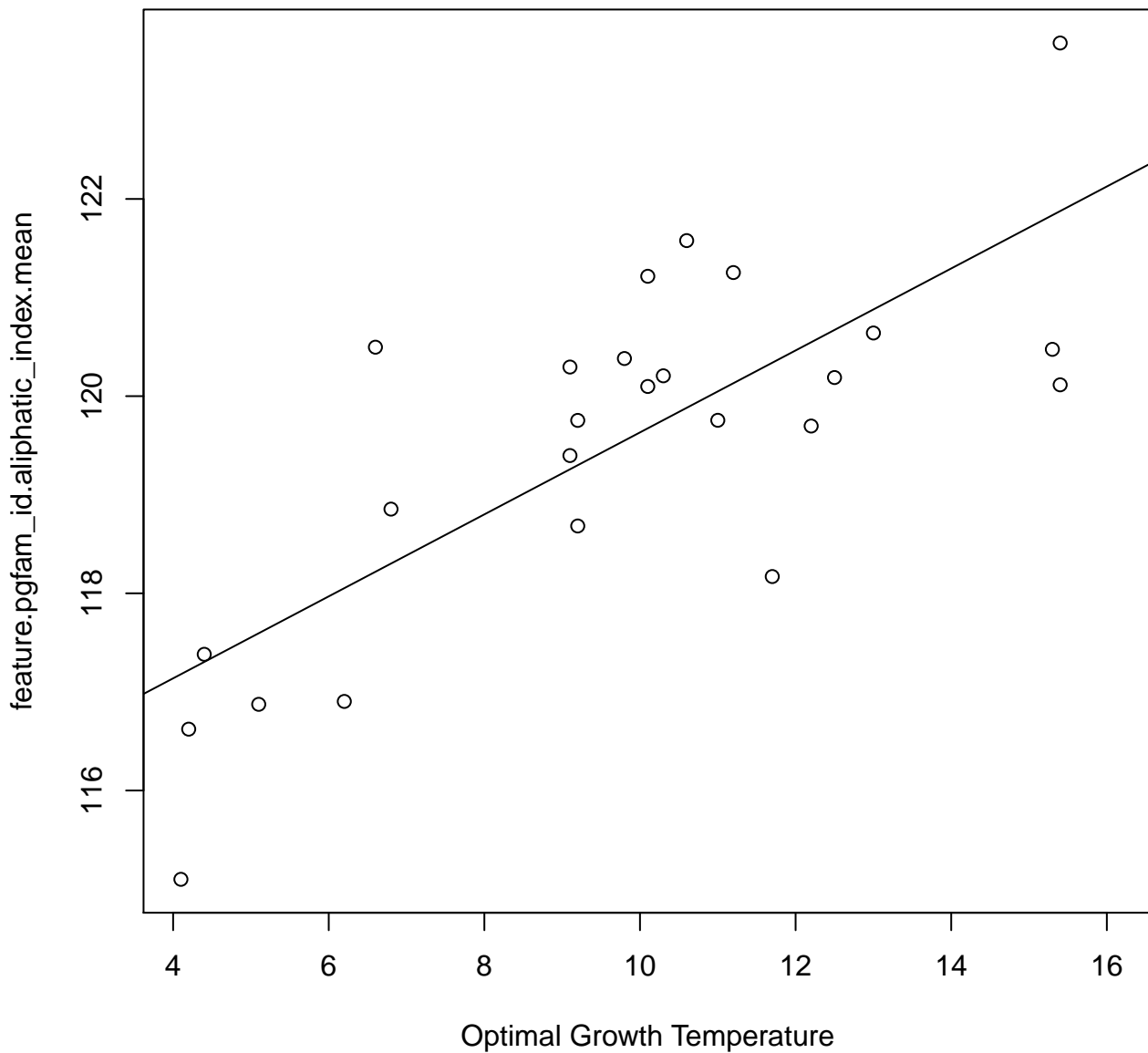
hypothetical protein



feature.pgfam_id.aliphatic_index.mean

PGF_03754184

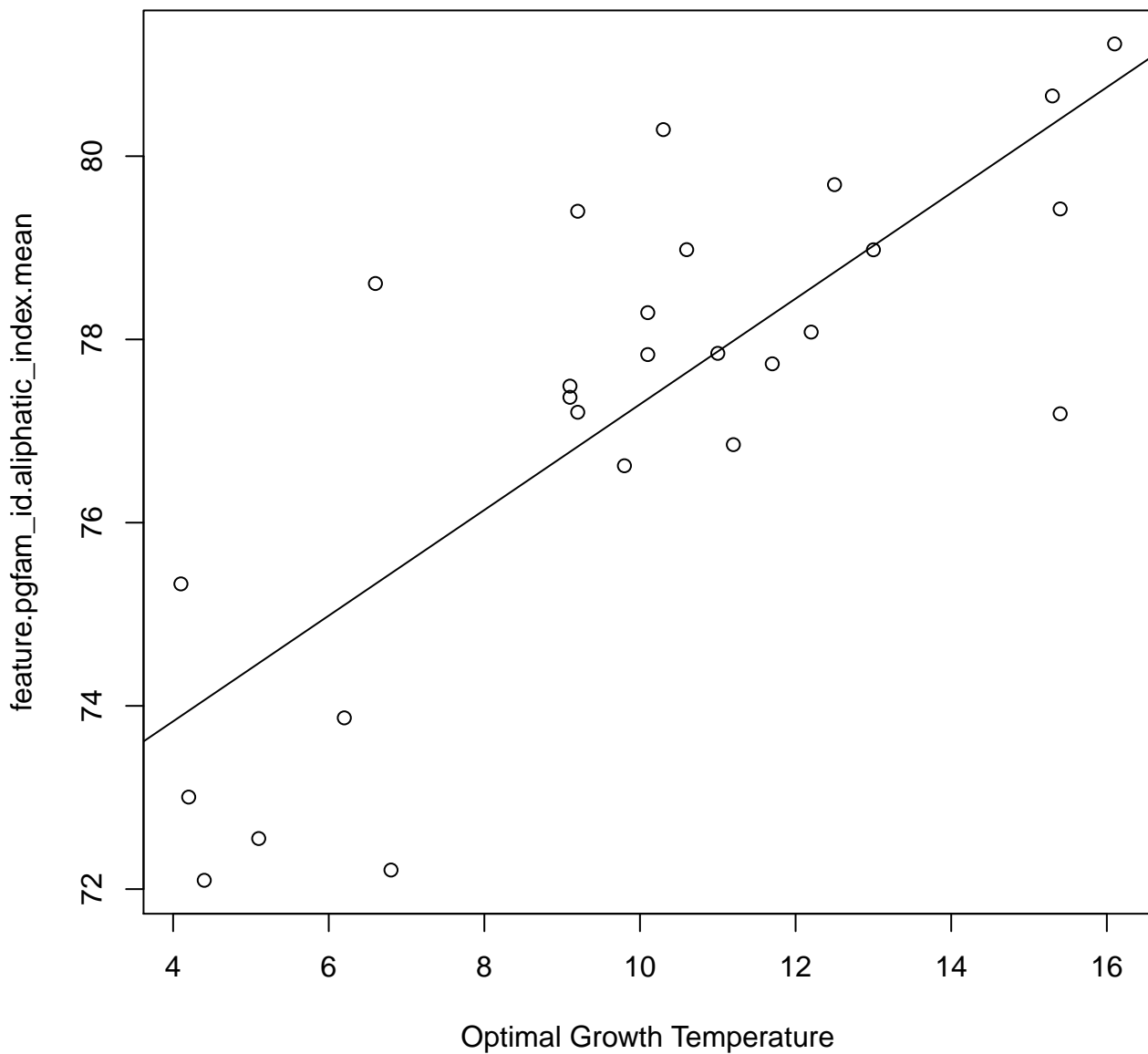
Na(+) H(+) antiporter subunit C



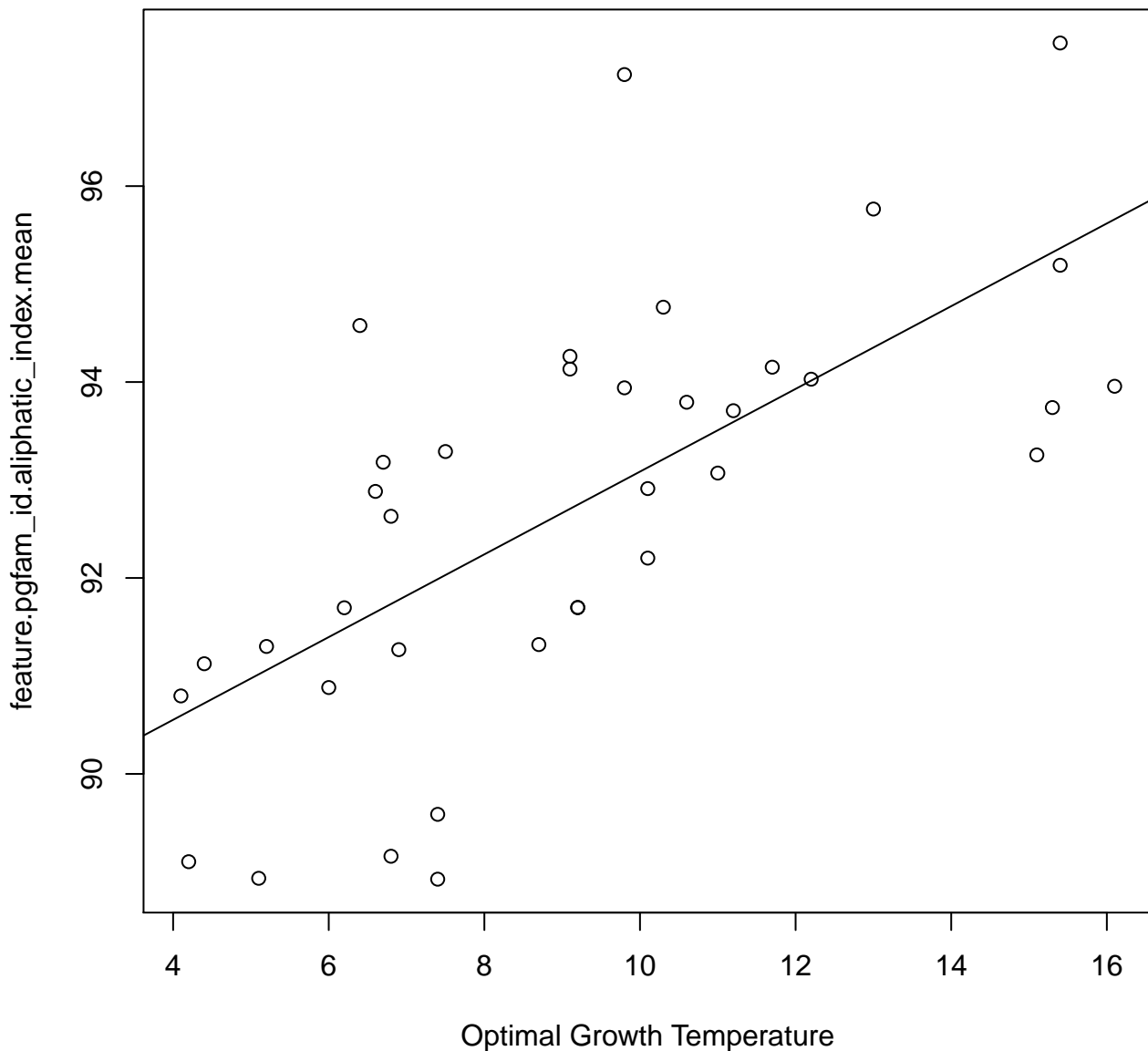
feature.pgfam_id.aliphatic_index.mean

PGF_07675395

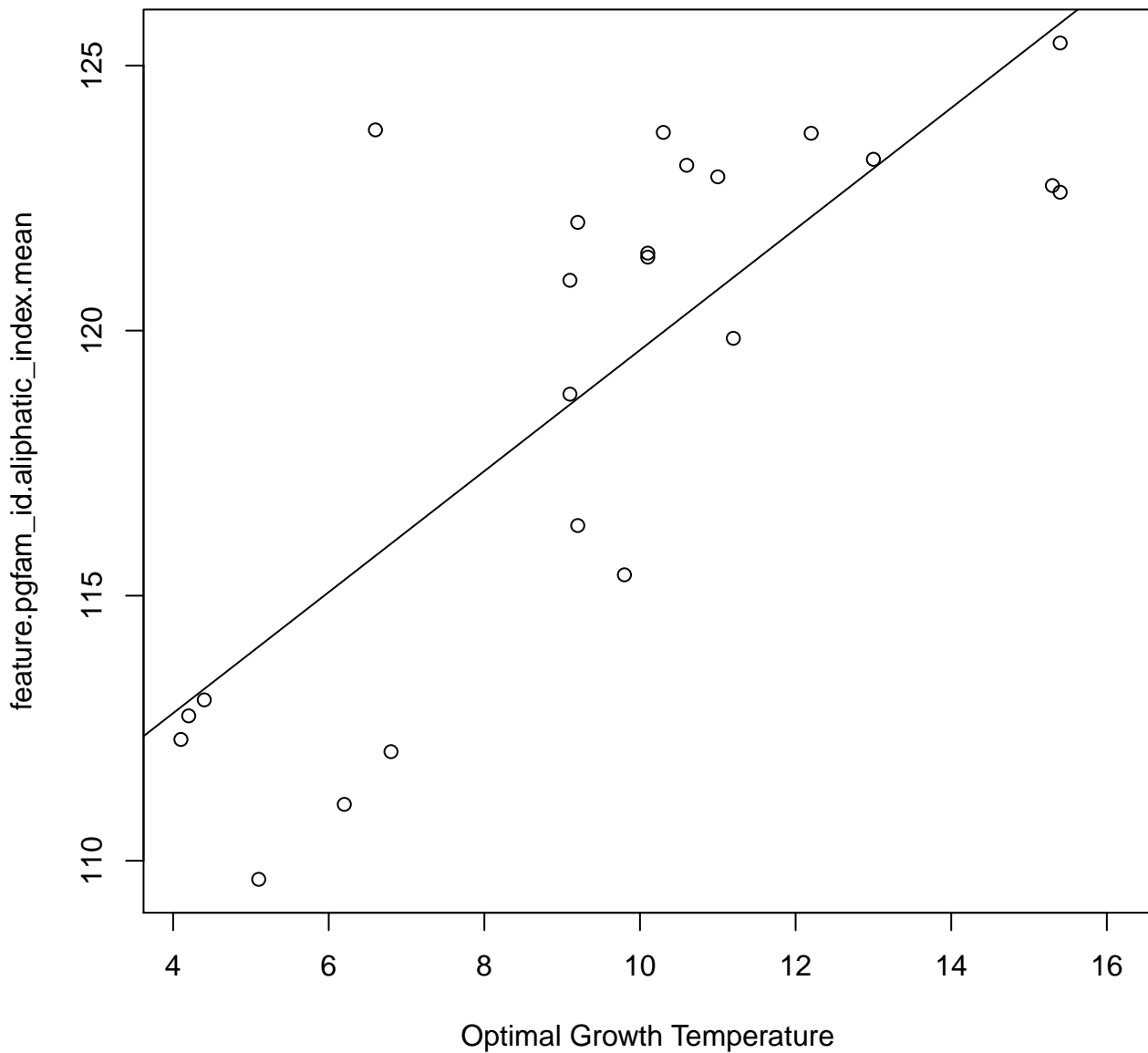
Flagellar protein FliJ



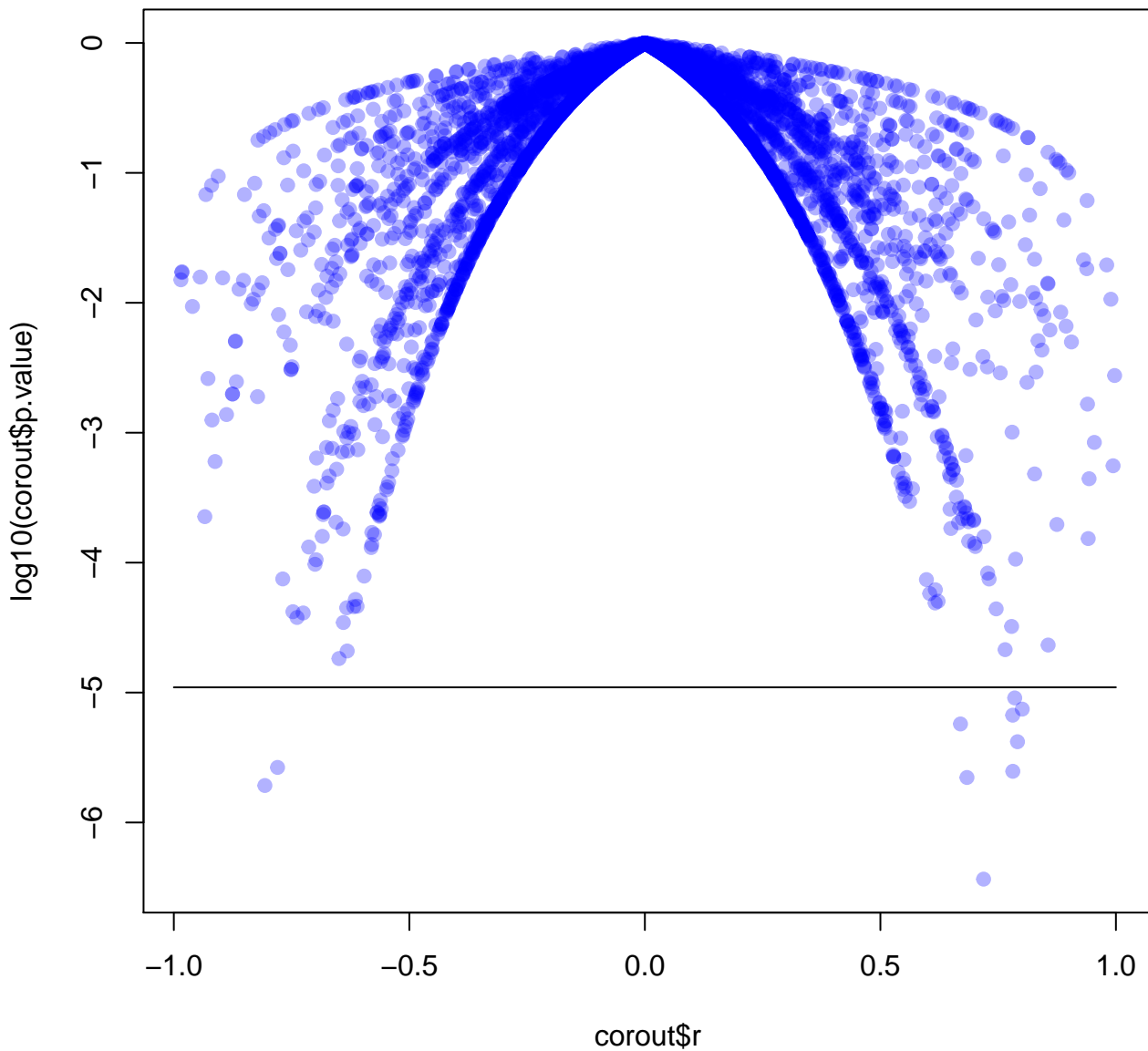
feature.pgfam_id.aliphatic_index.mean
PGF_10373609
CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)



feature.pgfam_id.aliphatic_index.mean
PGF_11600935
hypothetical protein



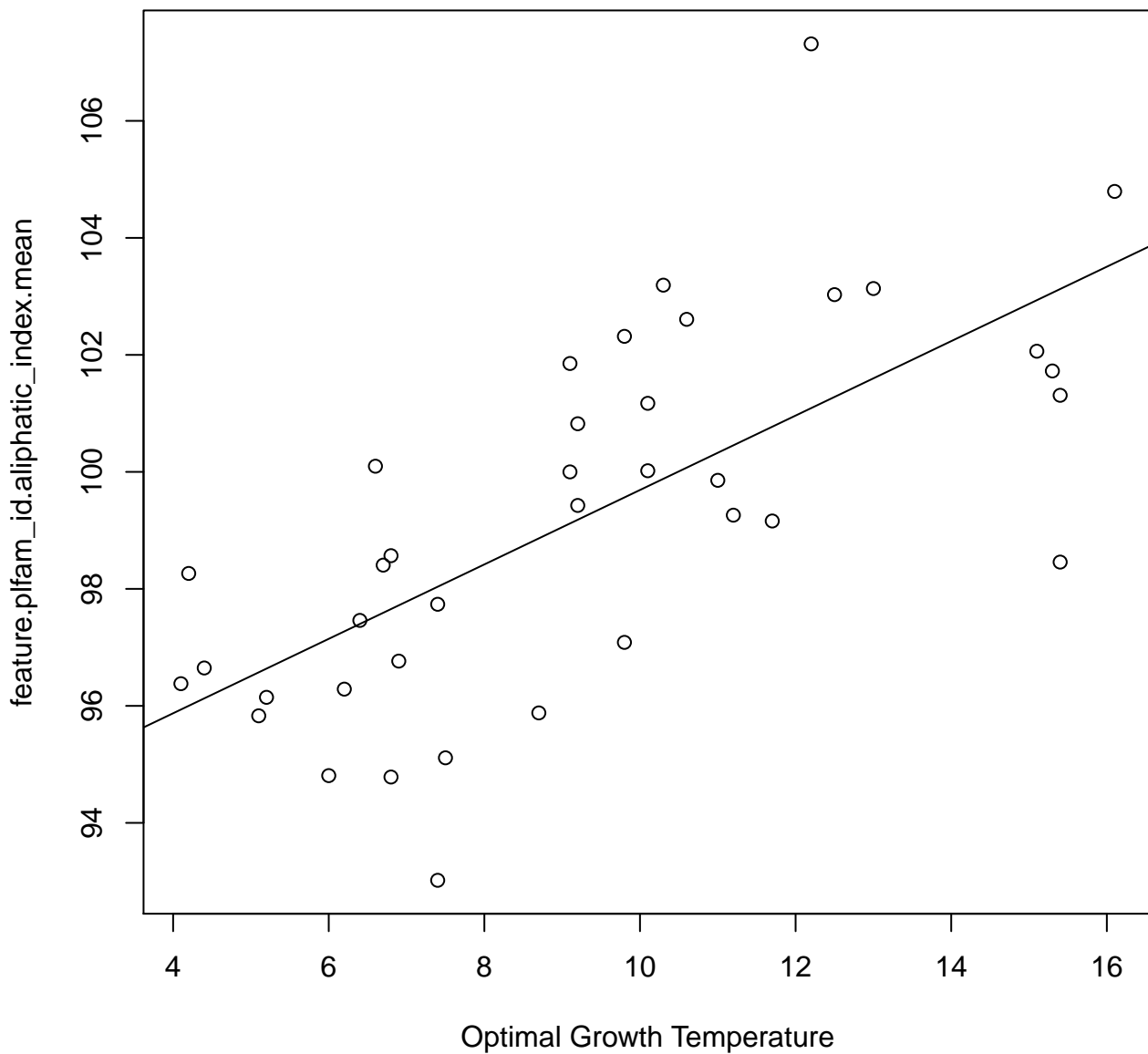
feature.plfam_id.aliphatic_index.mean



feature.plfam_id.aliphatic_index.mean

PLF_28228_00000039

UPF0758 family protein

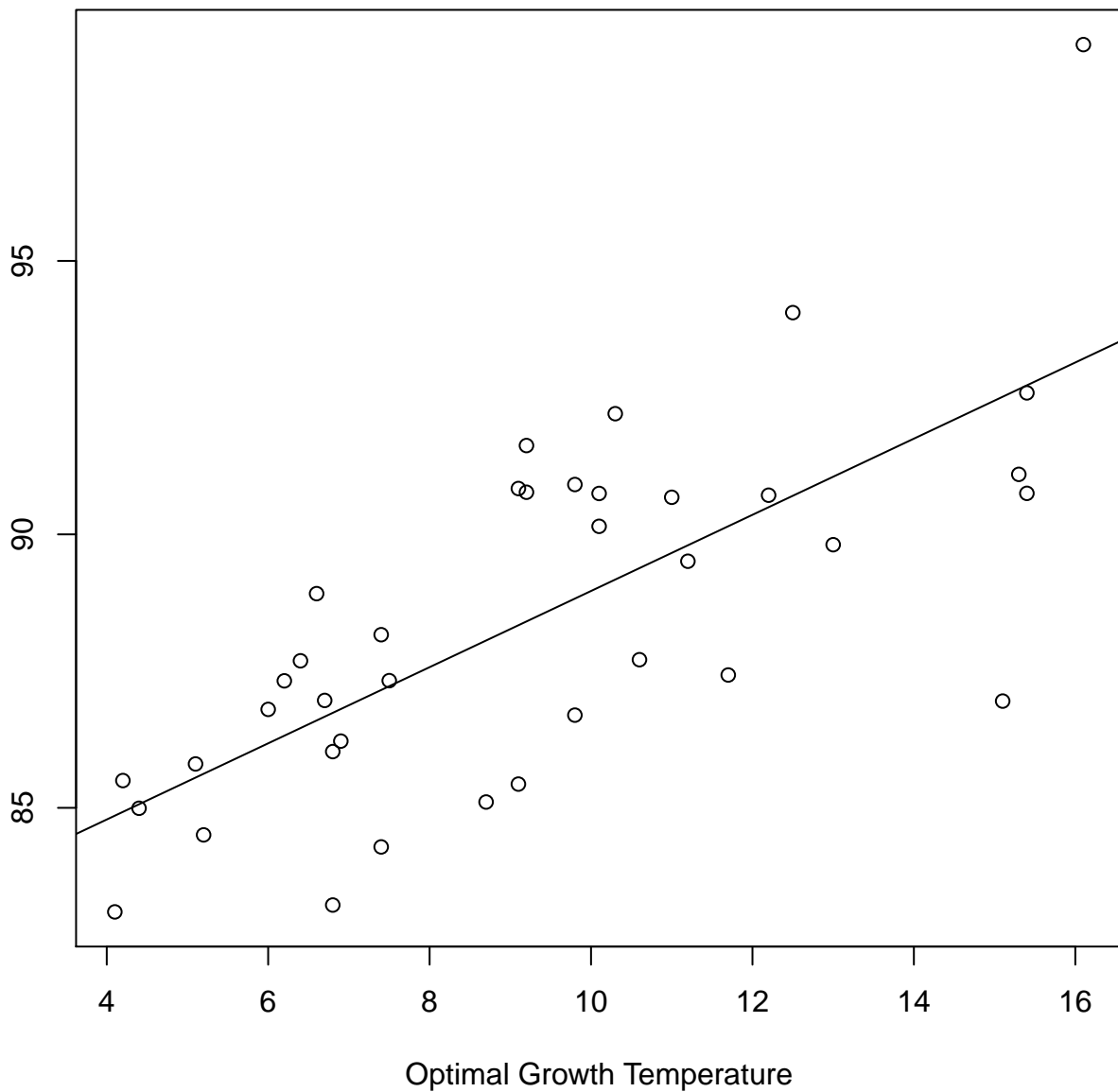


feature.plfam_id.aliphatic_index.mean

PLF_28228_00000063

hypothetical protein

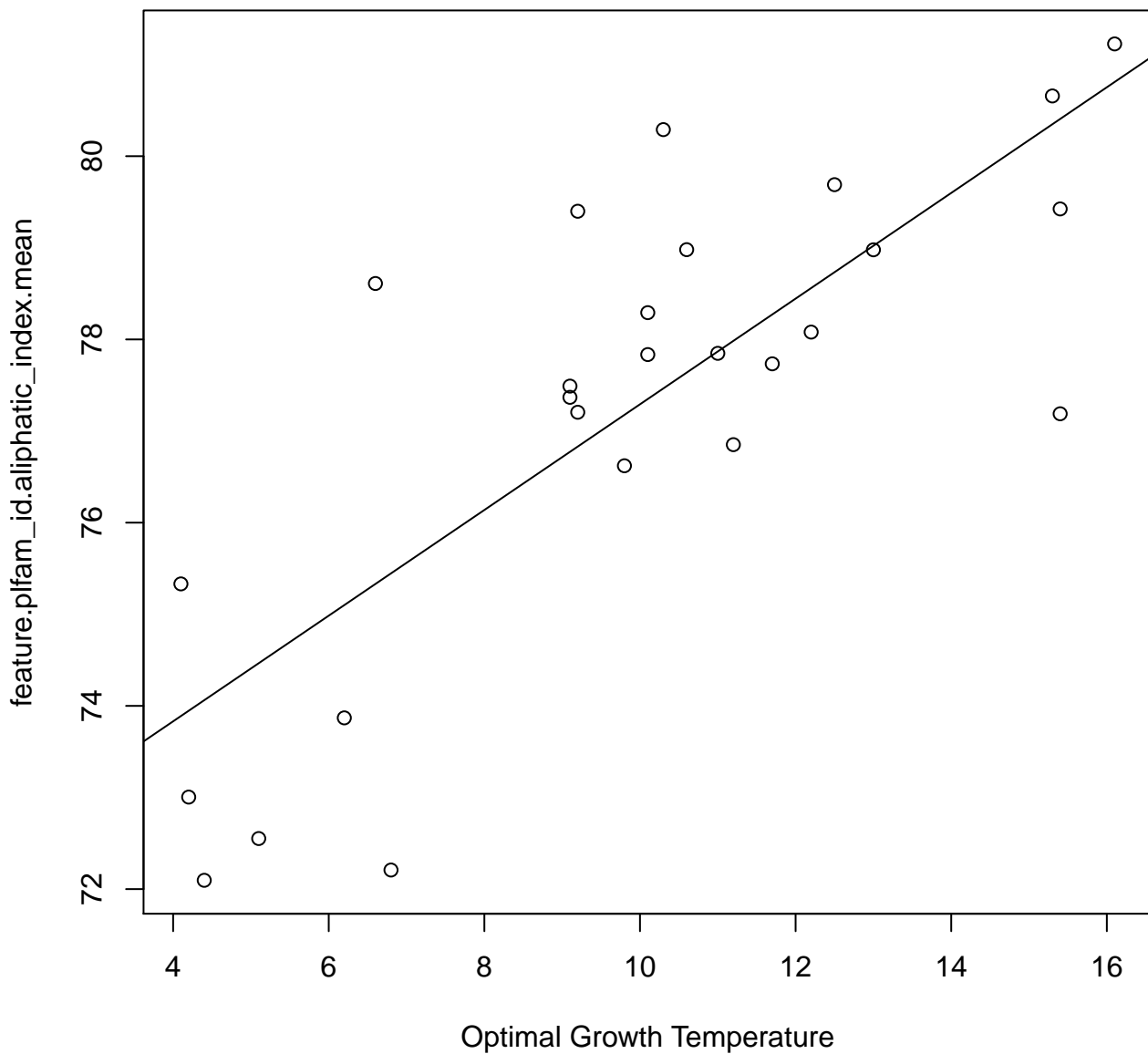
feature.plfam_id.aliphatic_index.mean



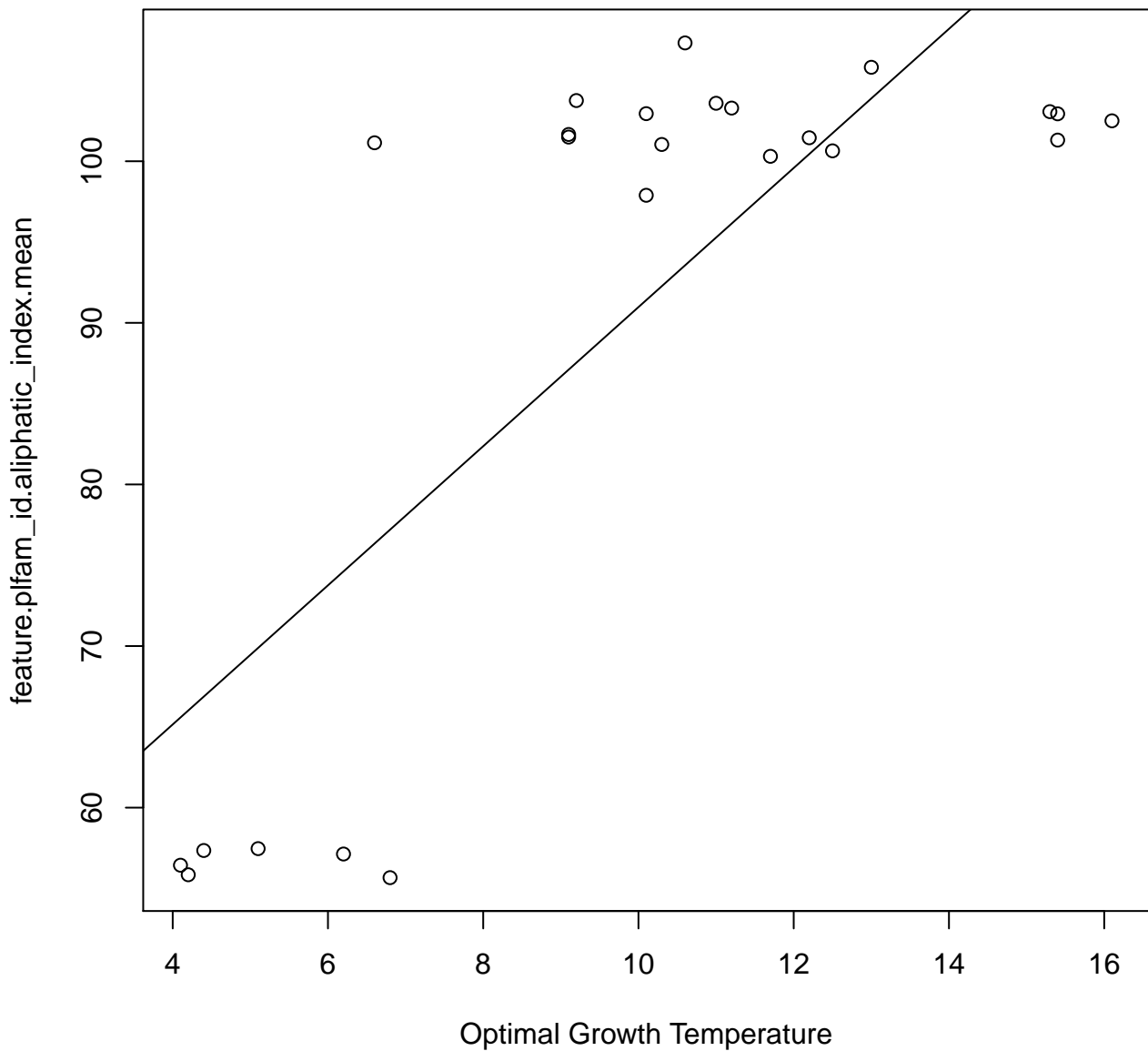
feature.plfam_id.aliphatic_index.mean

PLF_28228_00001844

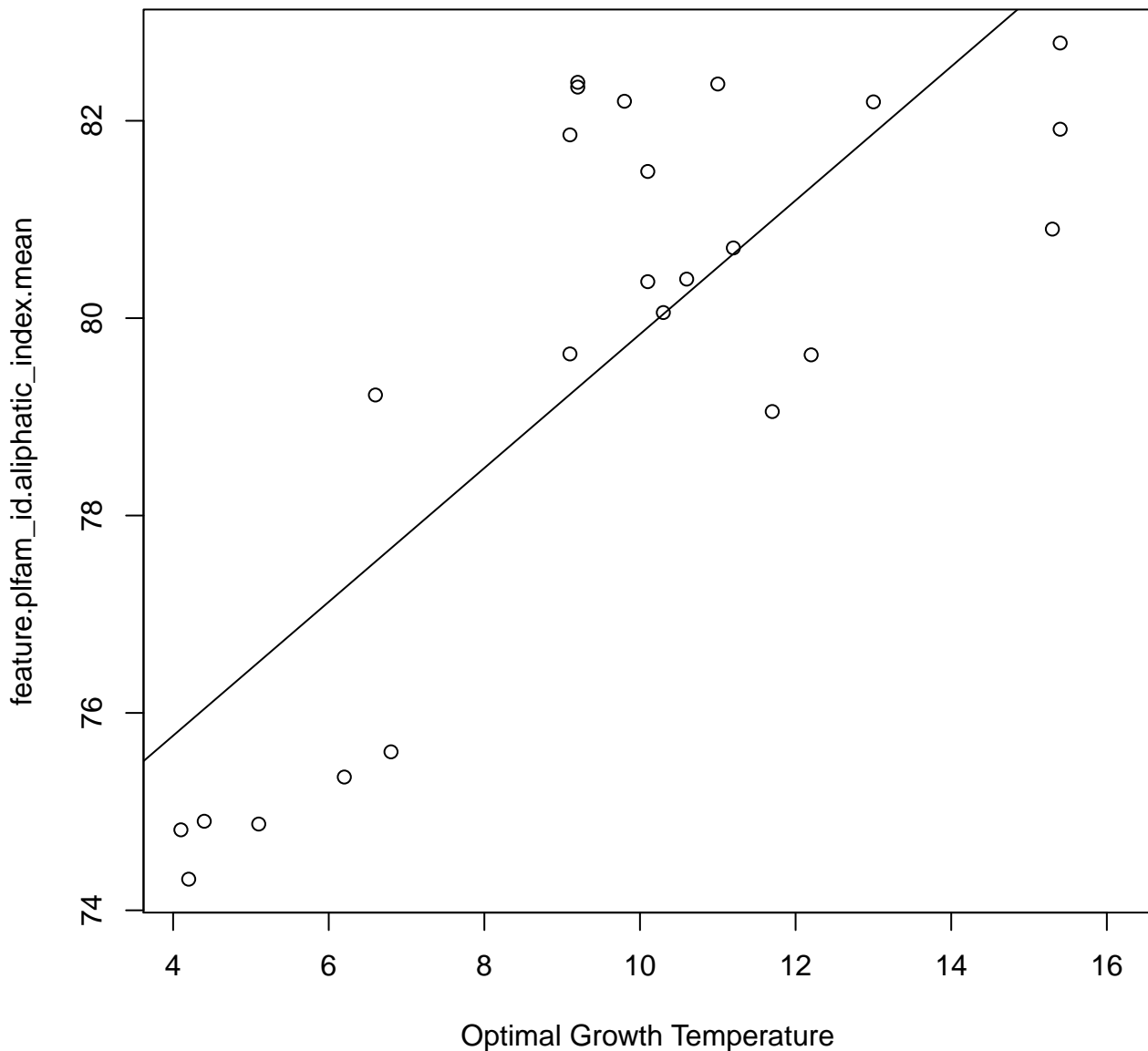
Flagellar protein FliJ



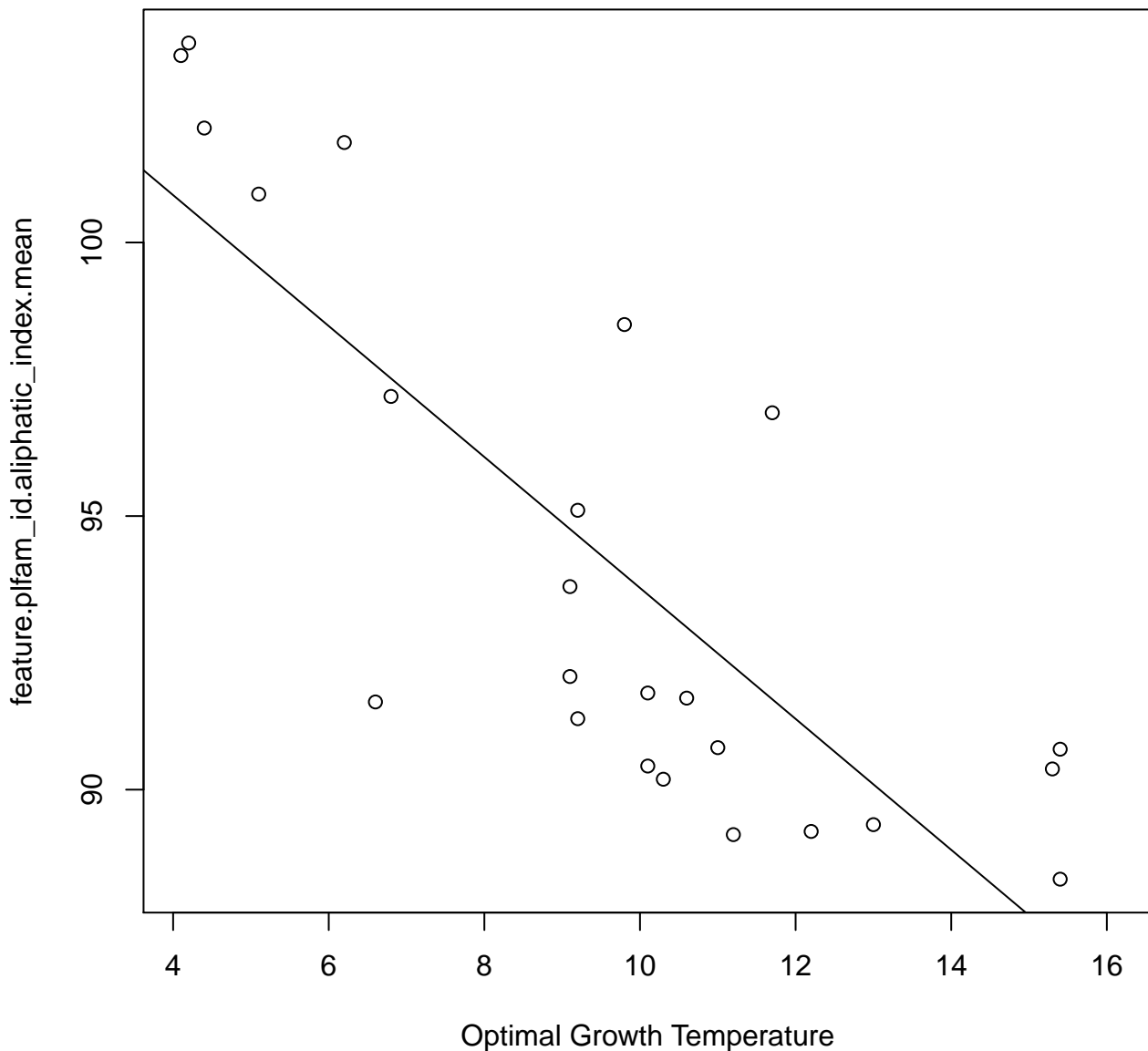
feature.plfam_id.aliphatic_index.mean
PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



feature.plfam_id.aliphatic_index.mean
PLF_28228_00003999
hypothetical protein



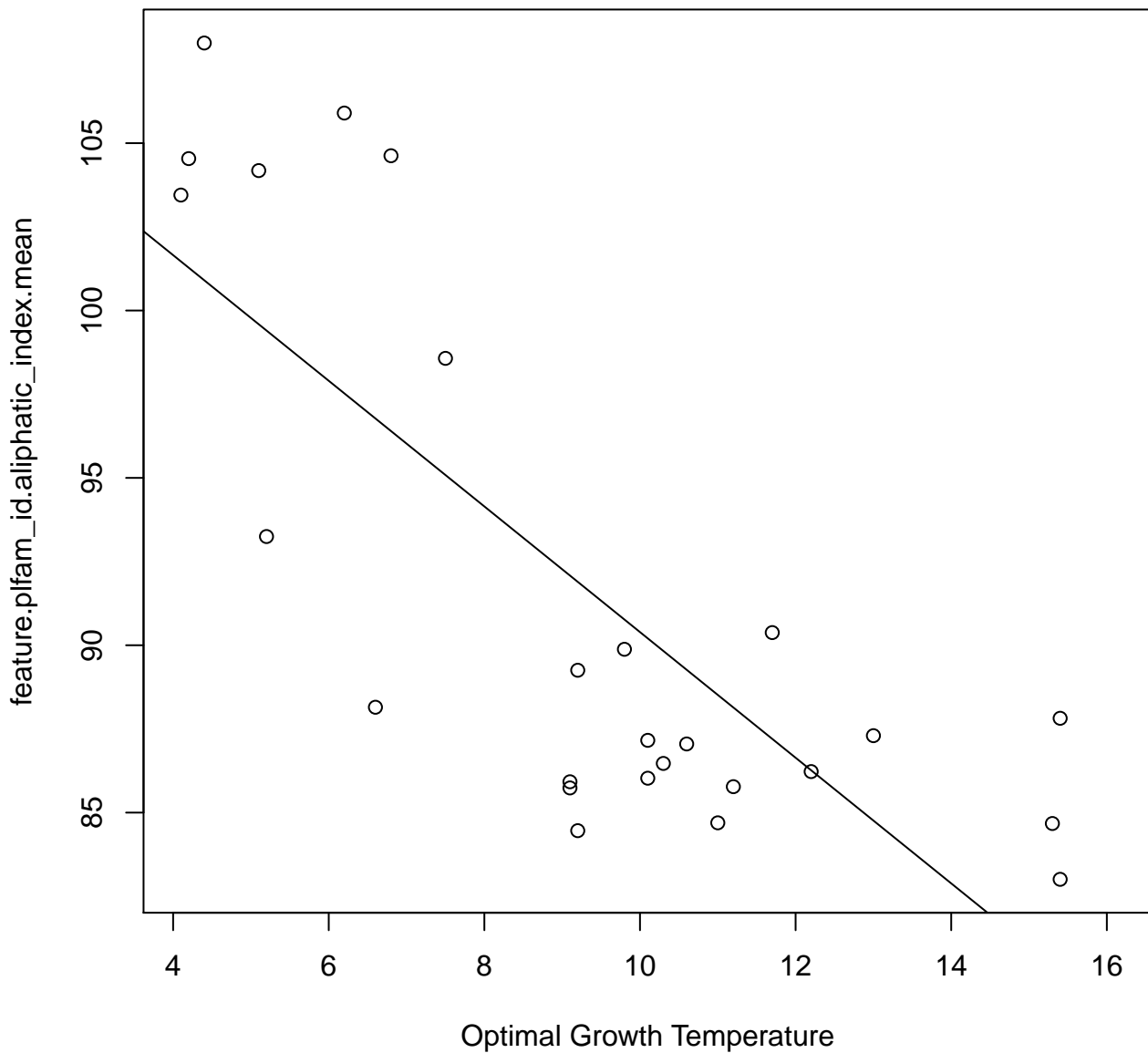
feature.plfam_id.aliphatic_index.mean
PLF_28228_00004488
hypothetical protein



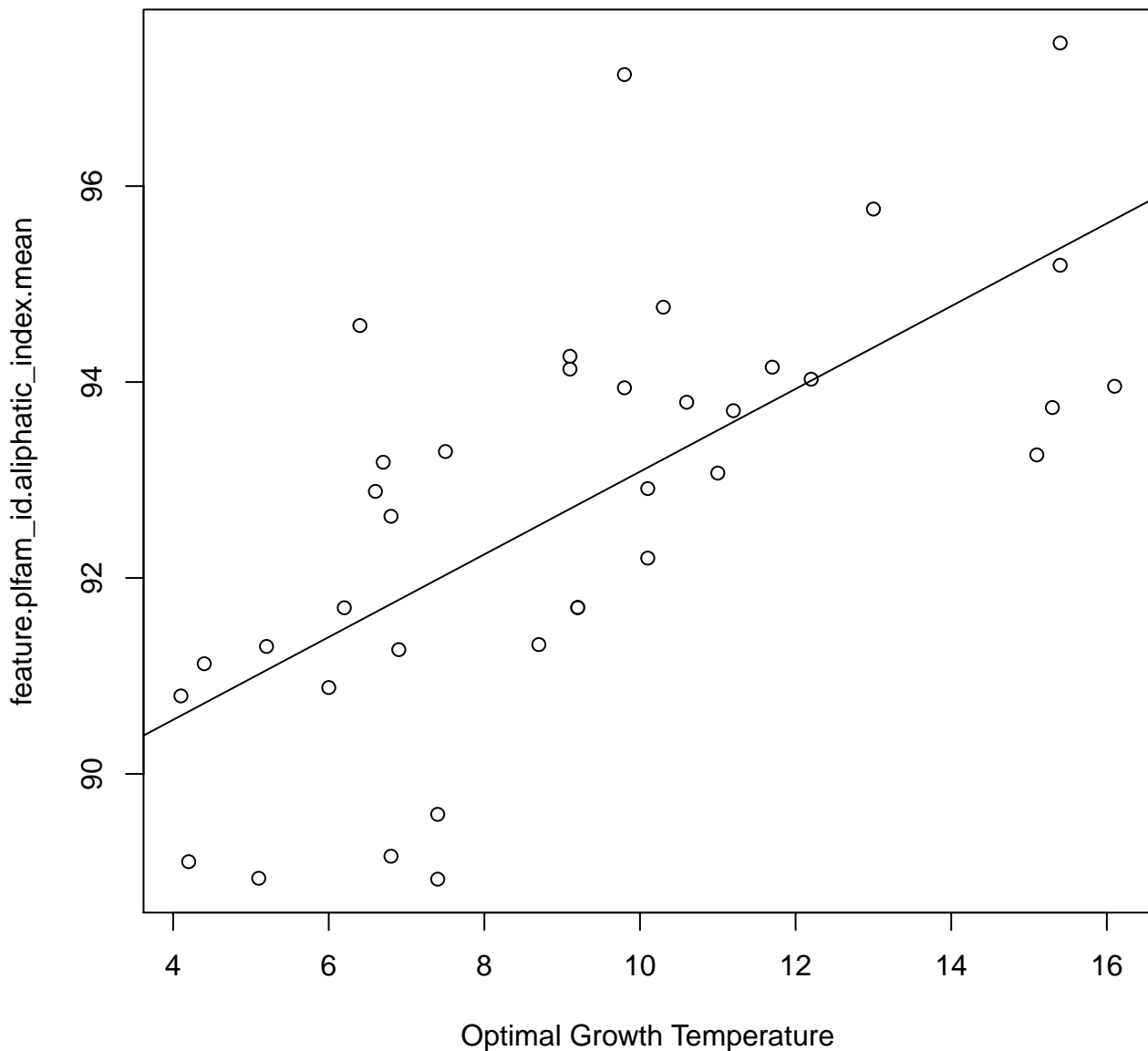
feature.plfam_id.aliphatic_index.mean

PLF_28228_00008631

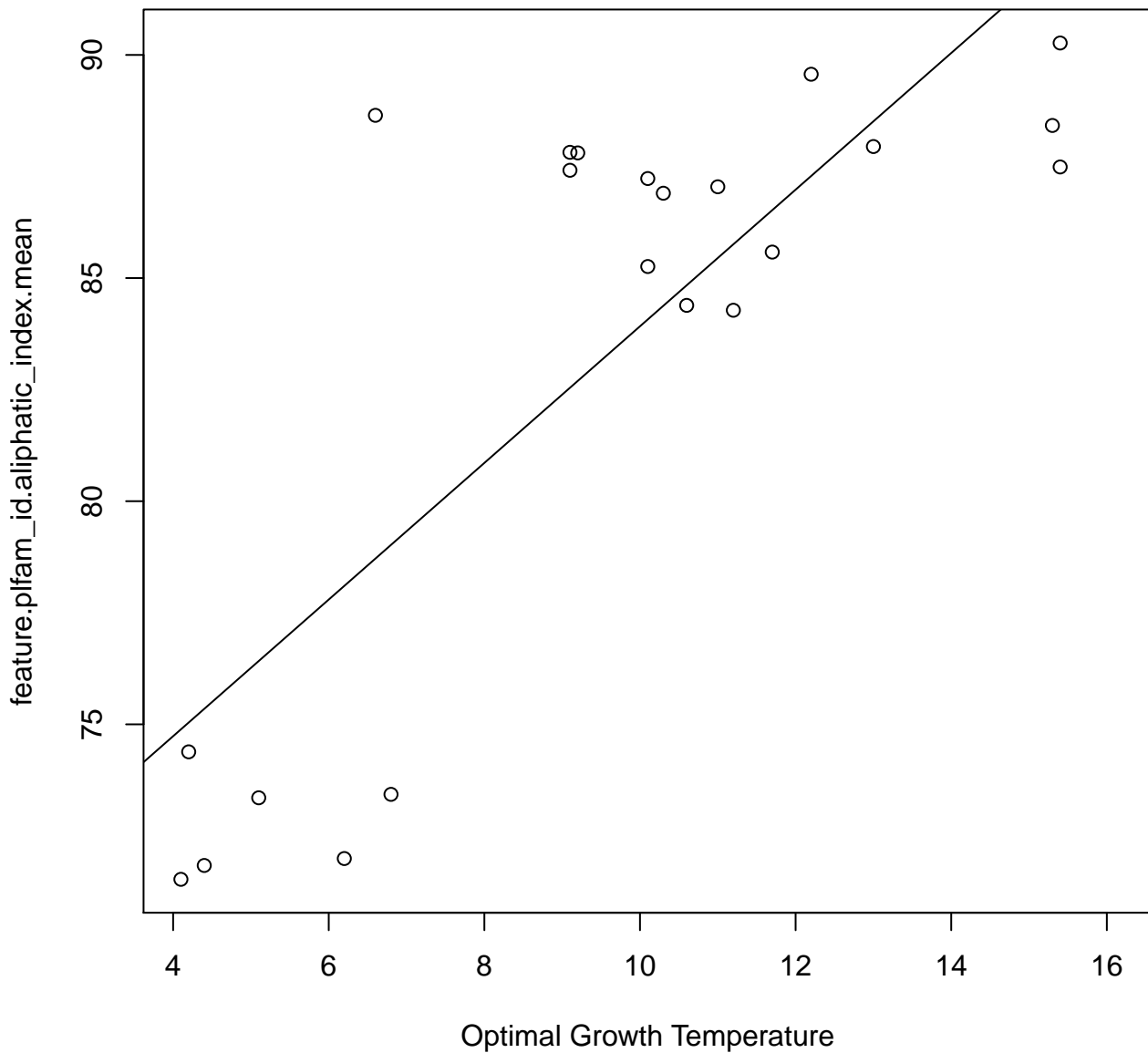
hypothetical protein



feature.plfam_id.aliphatic_index.mean
PLF_28228_00014025
CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)



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



feature.plfam_id.aliphatic_index.mean
PLF_28228_00030864
hypothetical protein

