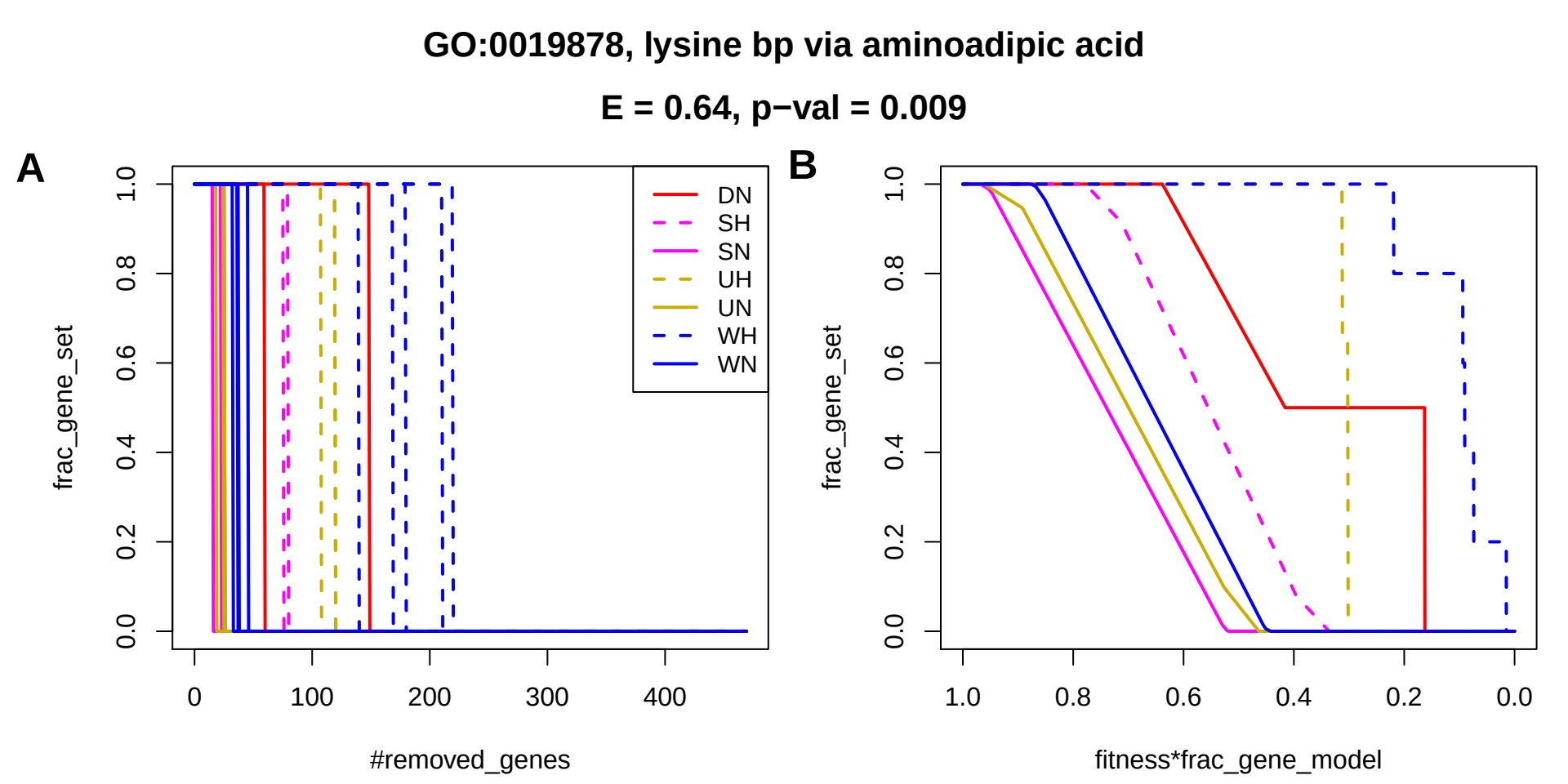
GO:0019878, lysine bp via aminoadipic acid
E = 0.64, p−val = 0.009
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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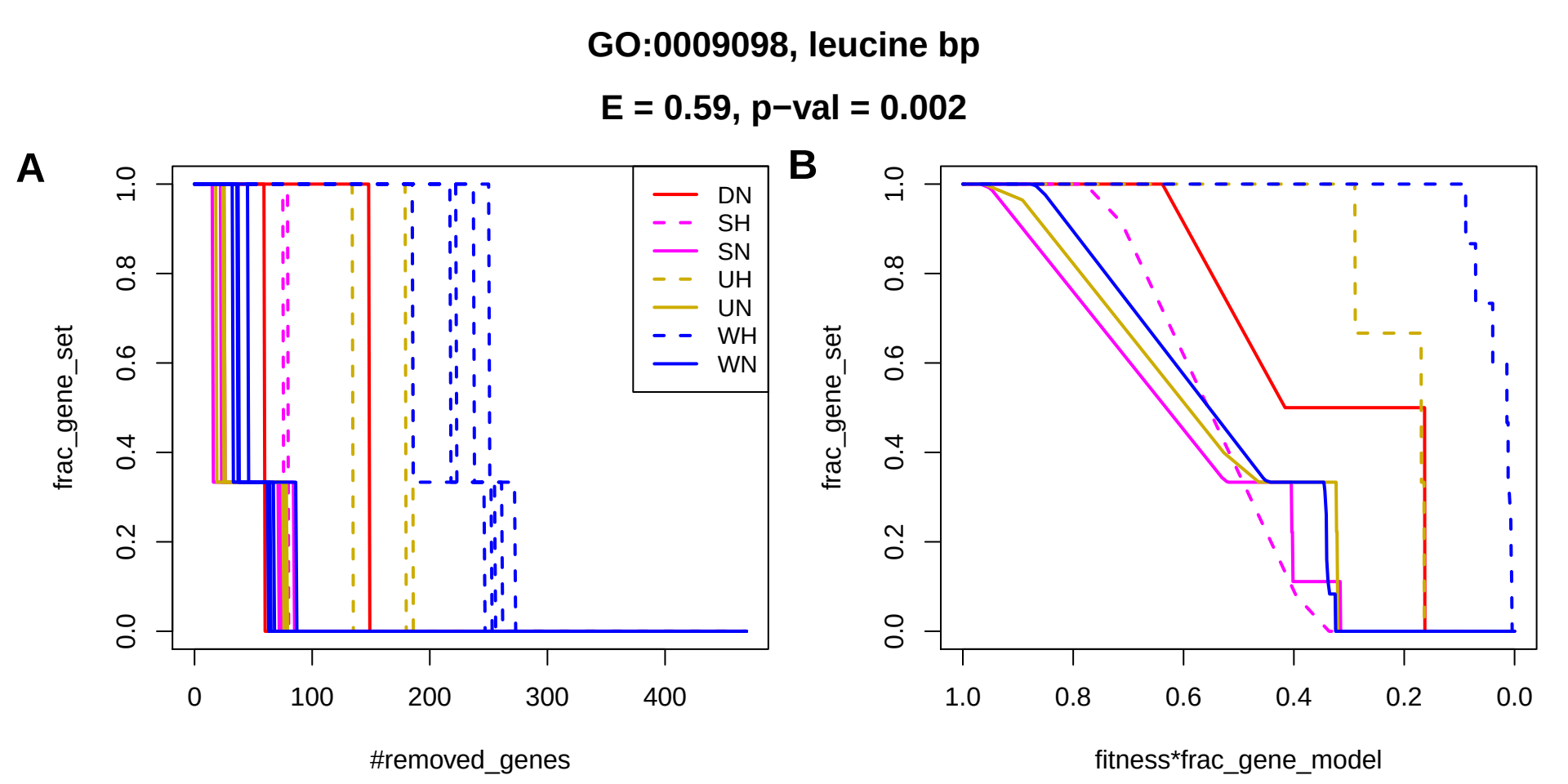
300
400


GO:0009098, leucine bp
E = 0.59, p−val = 0.002
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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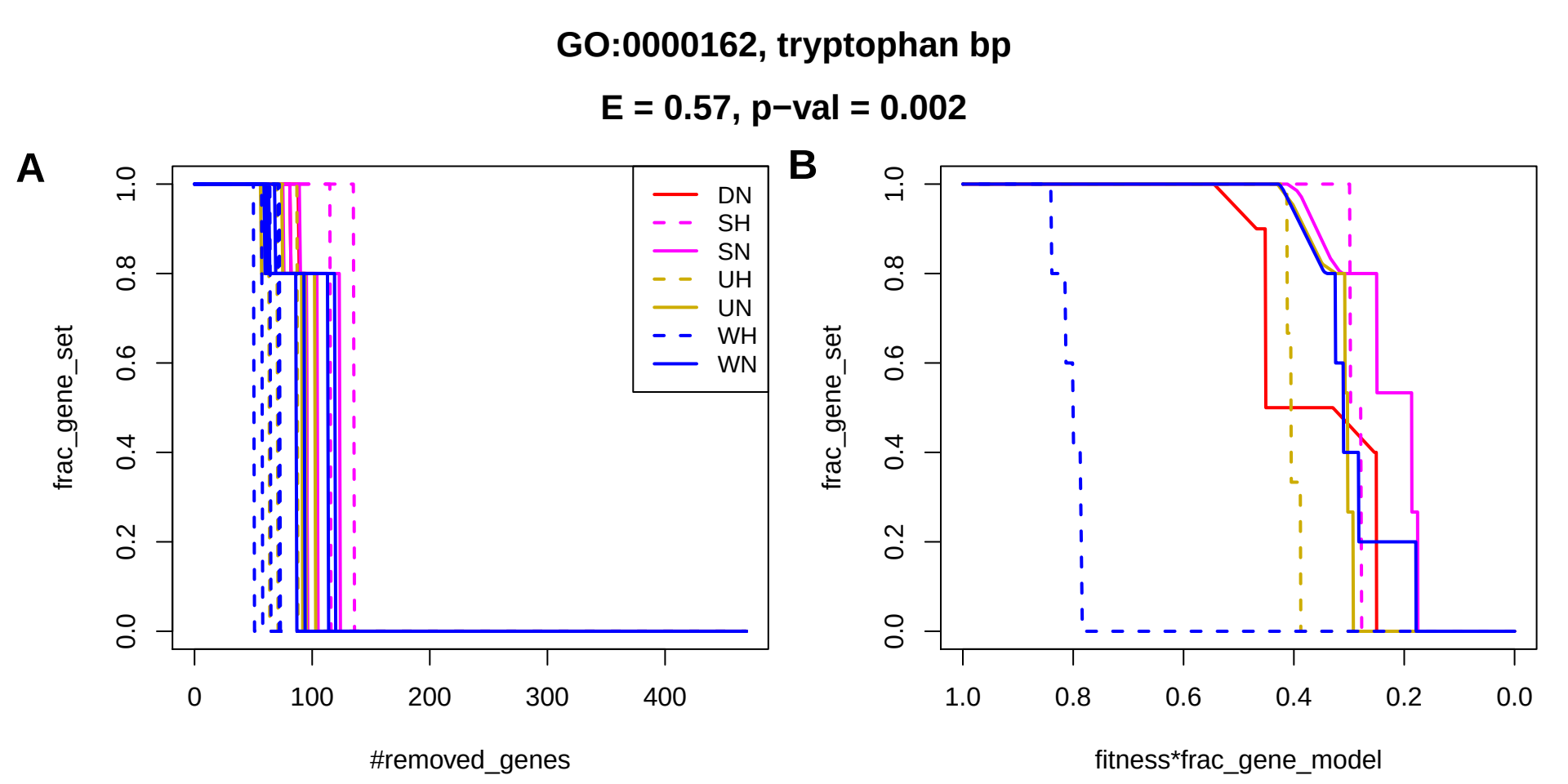
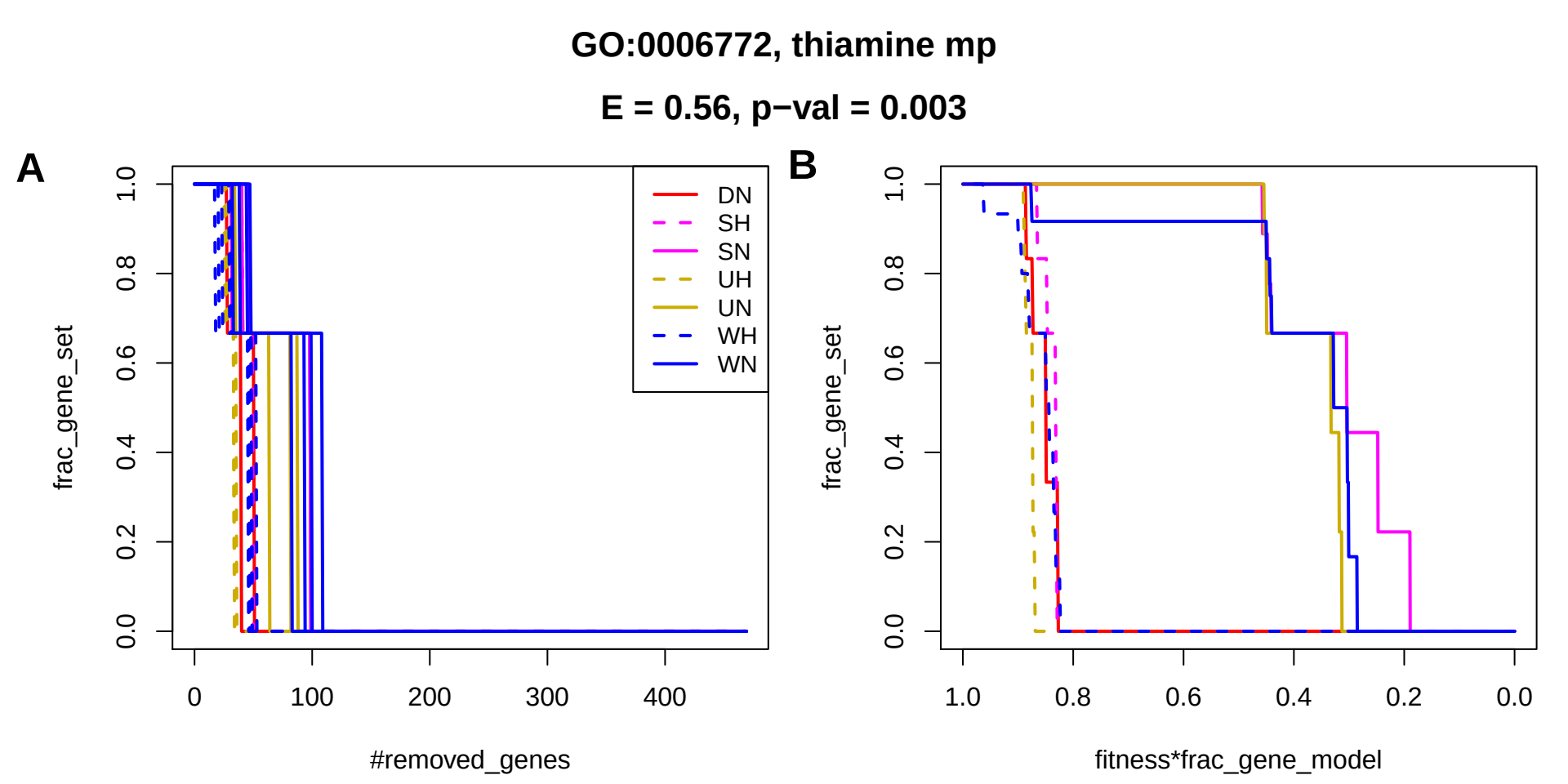
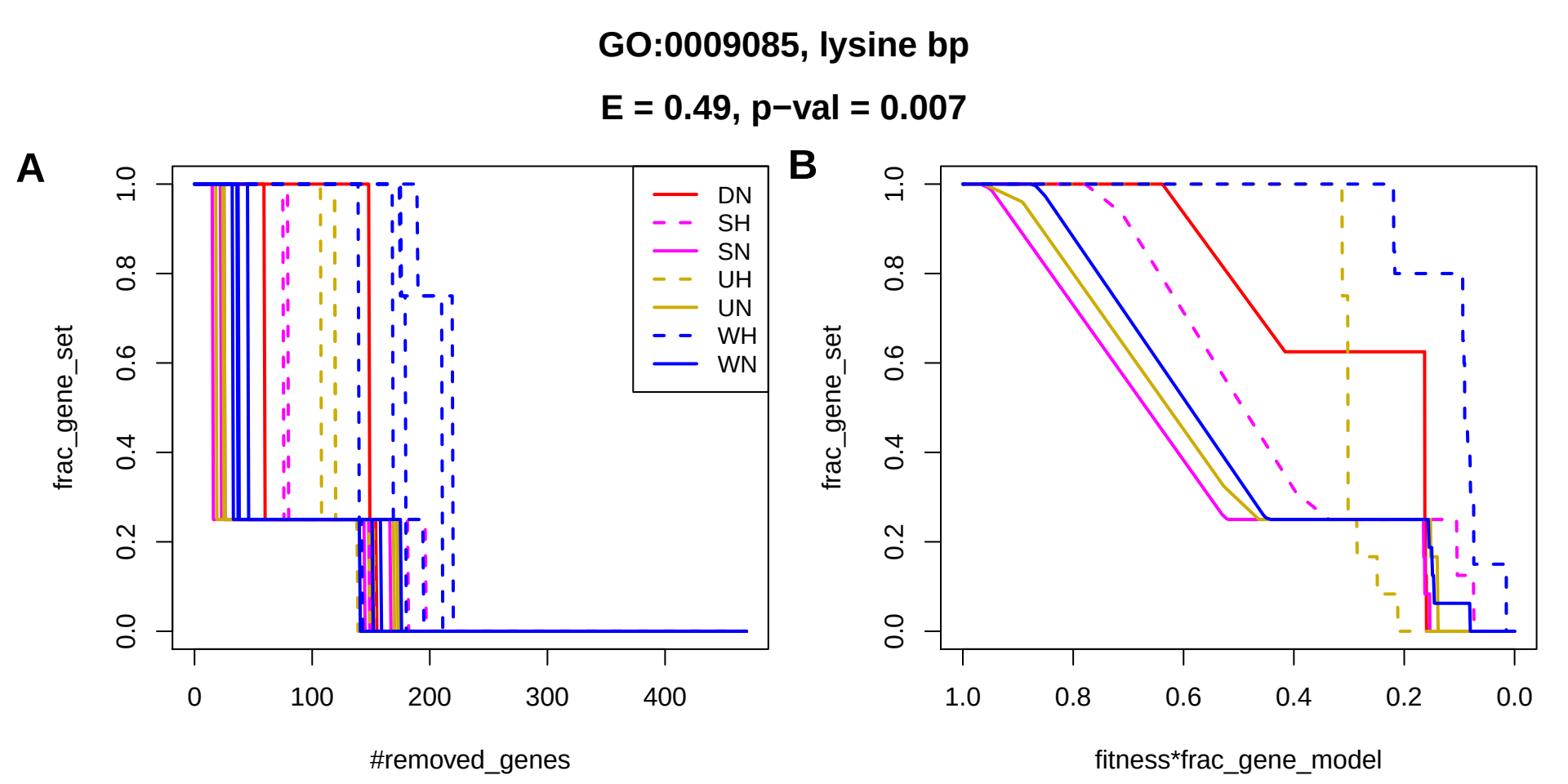
300
400


GO:0000162, tryptophan bp
E = 0.57, p−val = 0.002
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006772, thiamine mp
E = 0.56, p−val = 0.003
A
B
DN
SH
SN
UH
UN
WH
WN
frac_gene_set
#removed_genes
fitness*frac_gene_model
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009085, lysine bp
E = 0.49, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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100
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300
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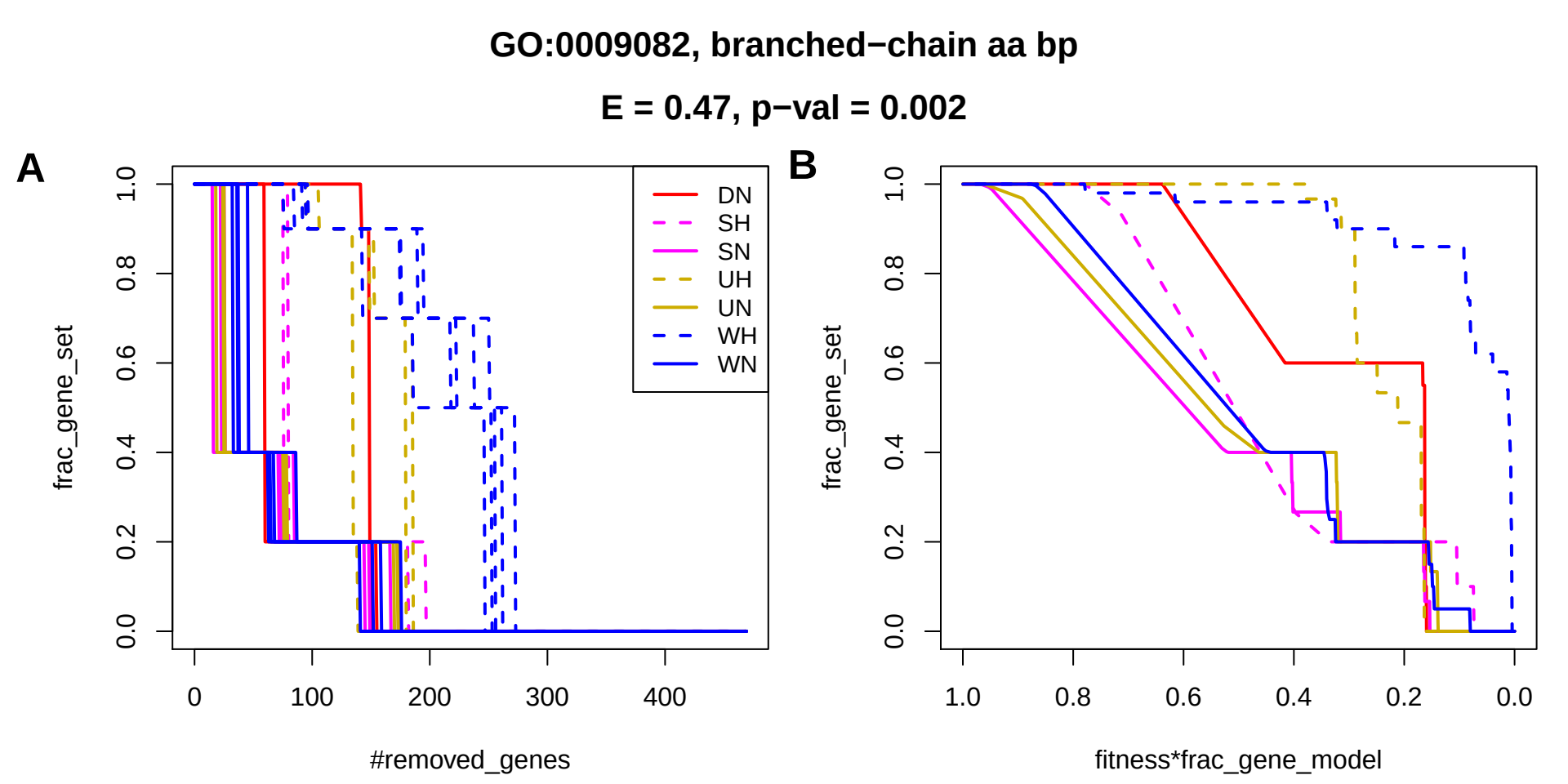
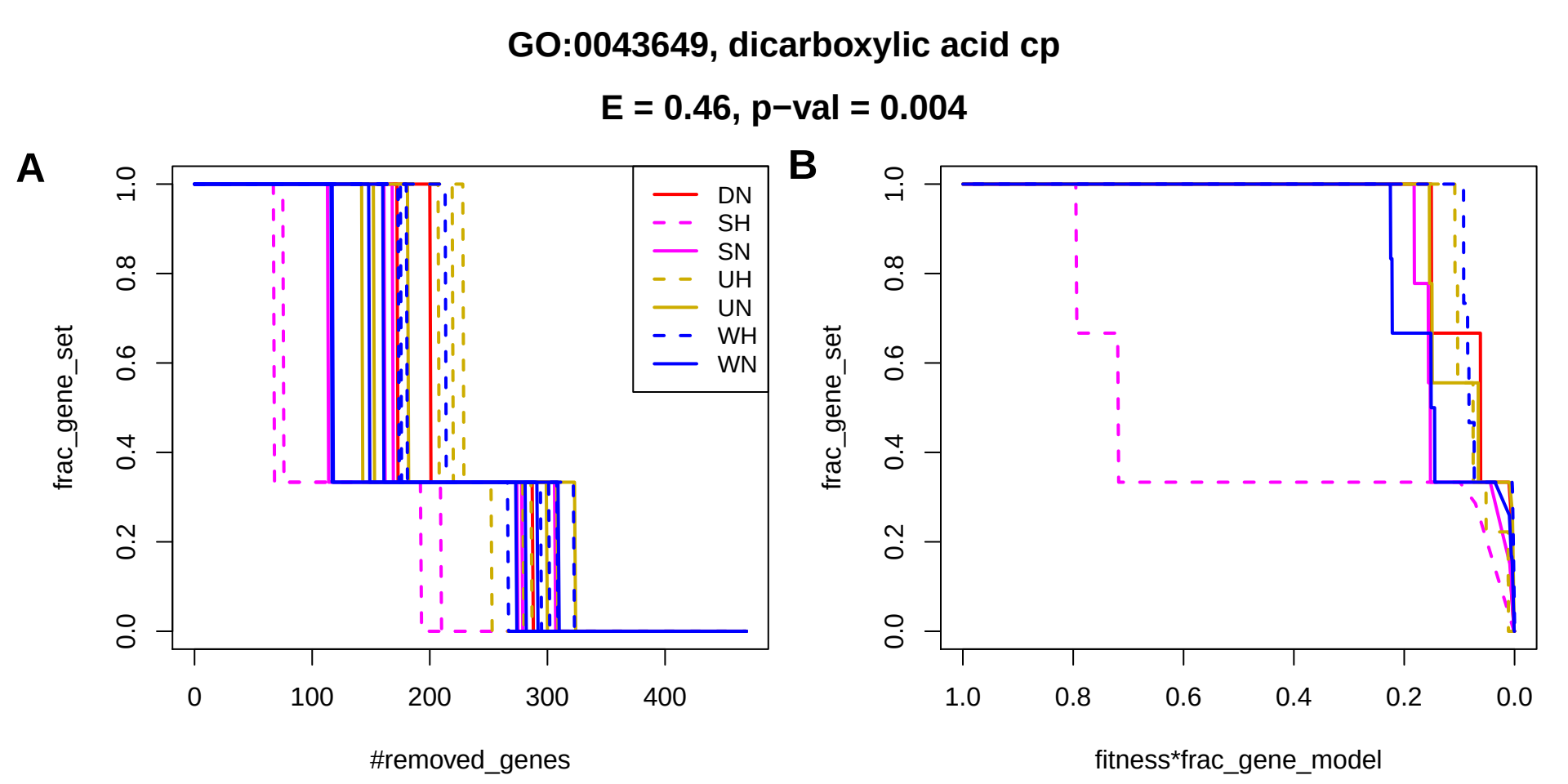
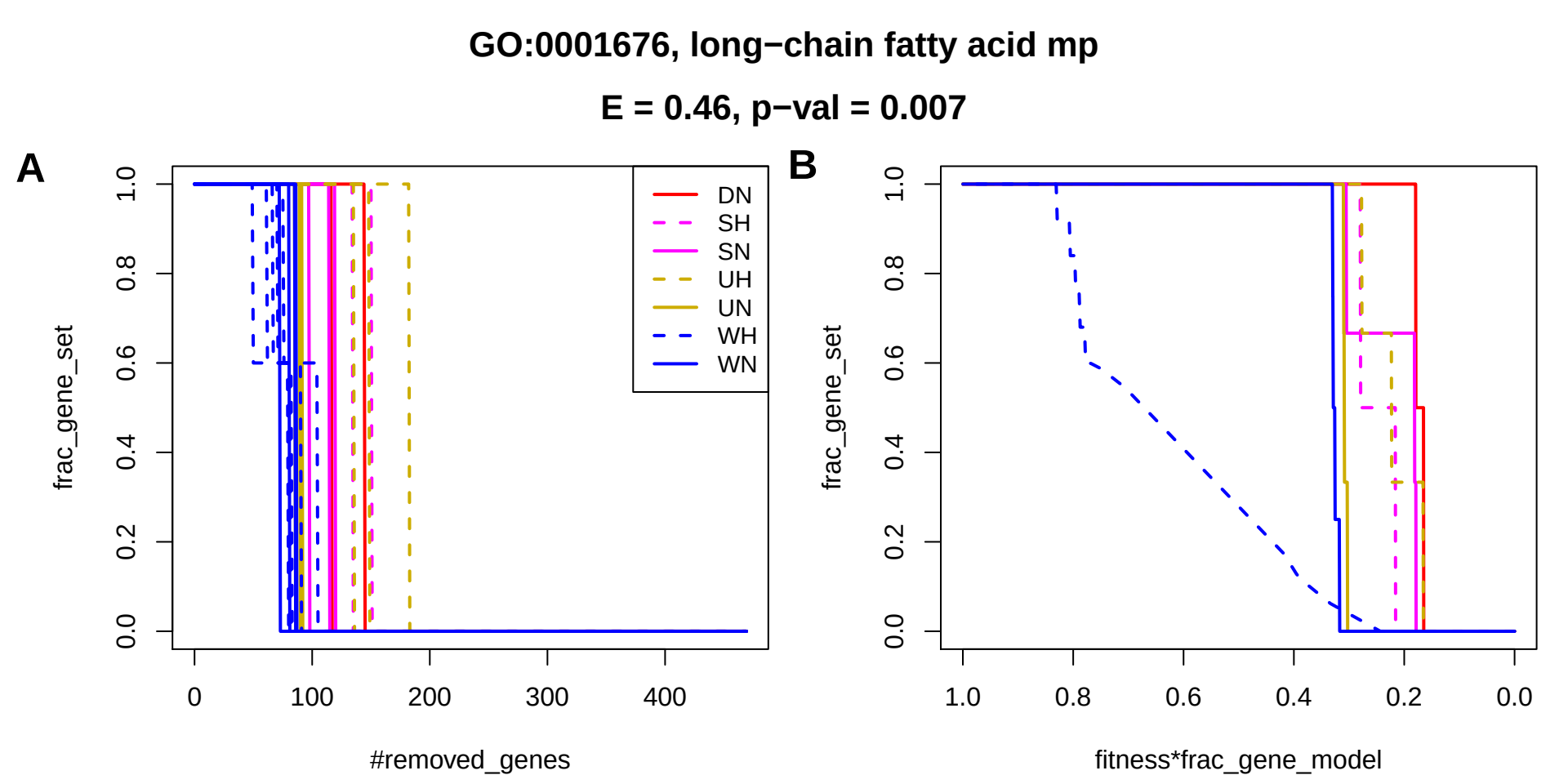
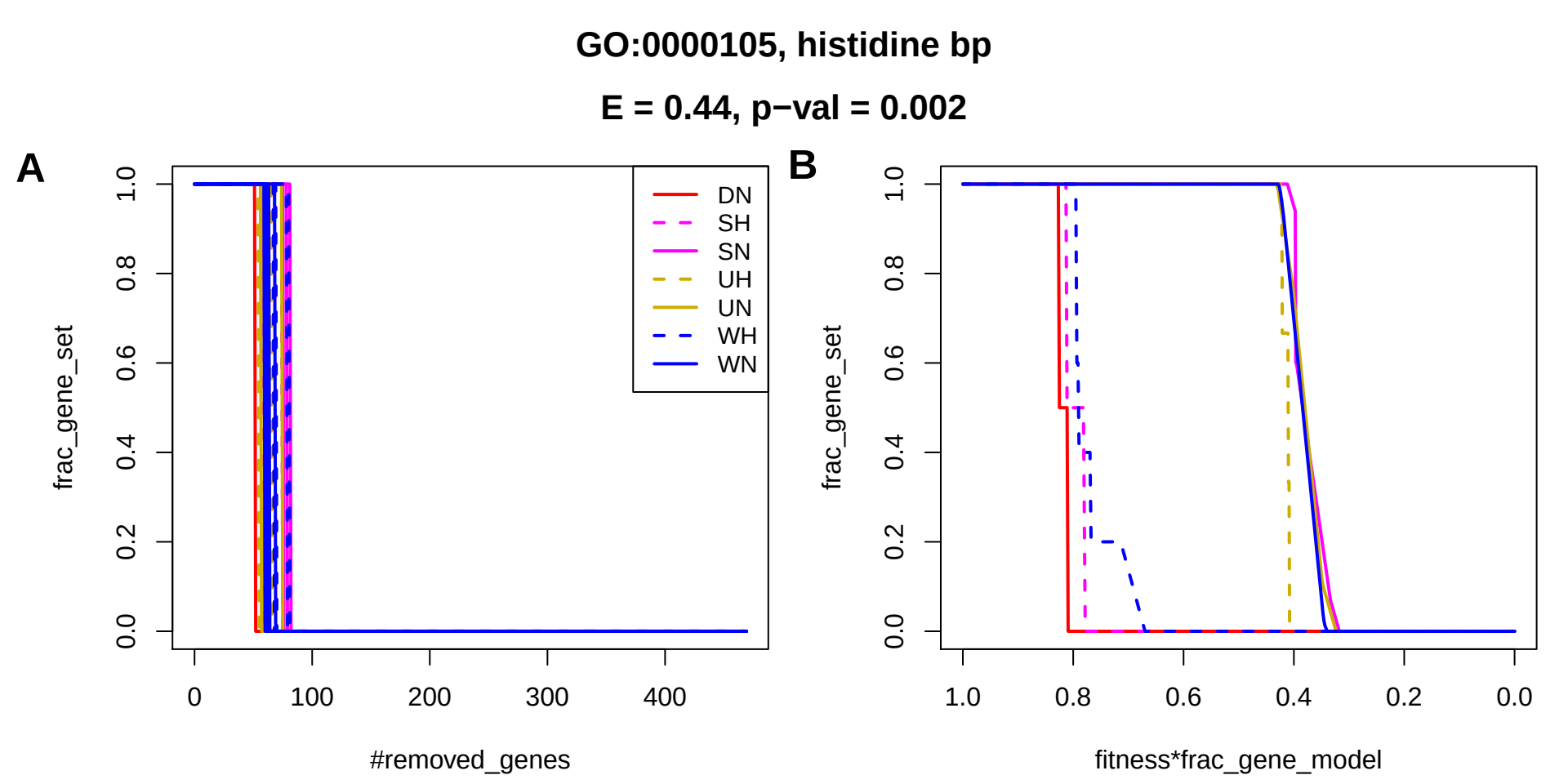
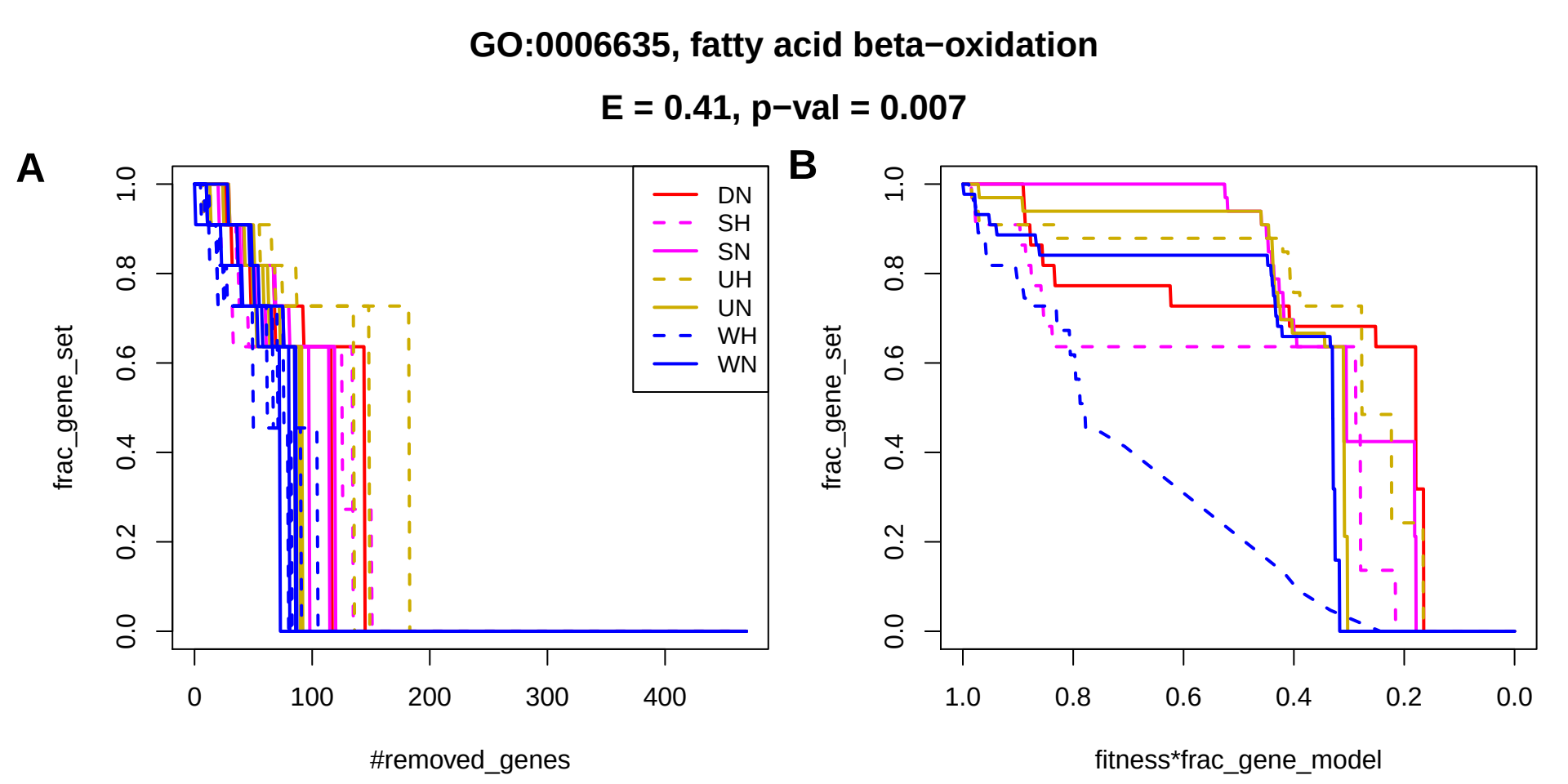
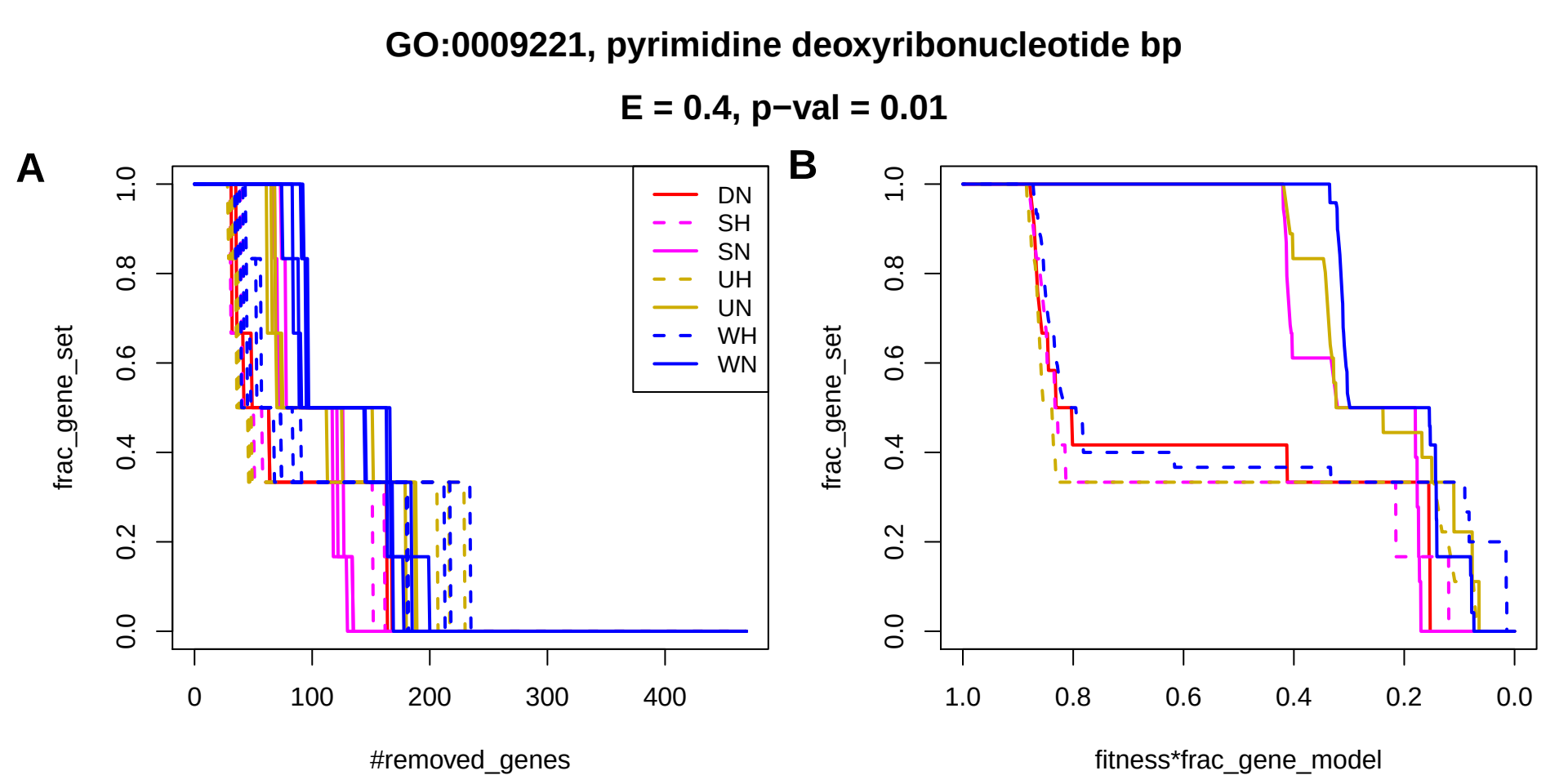

GO:0009082, branched−chain aa bp
E = 0.47, p−val = 0.002
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

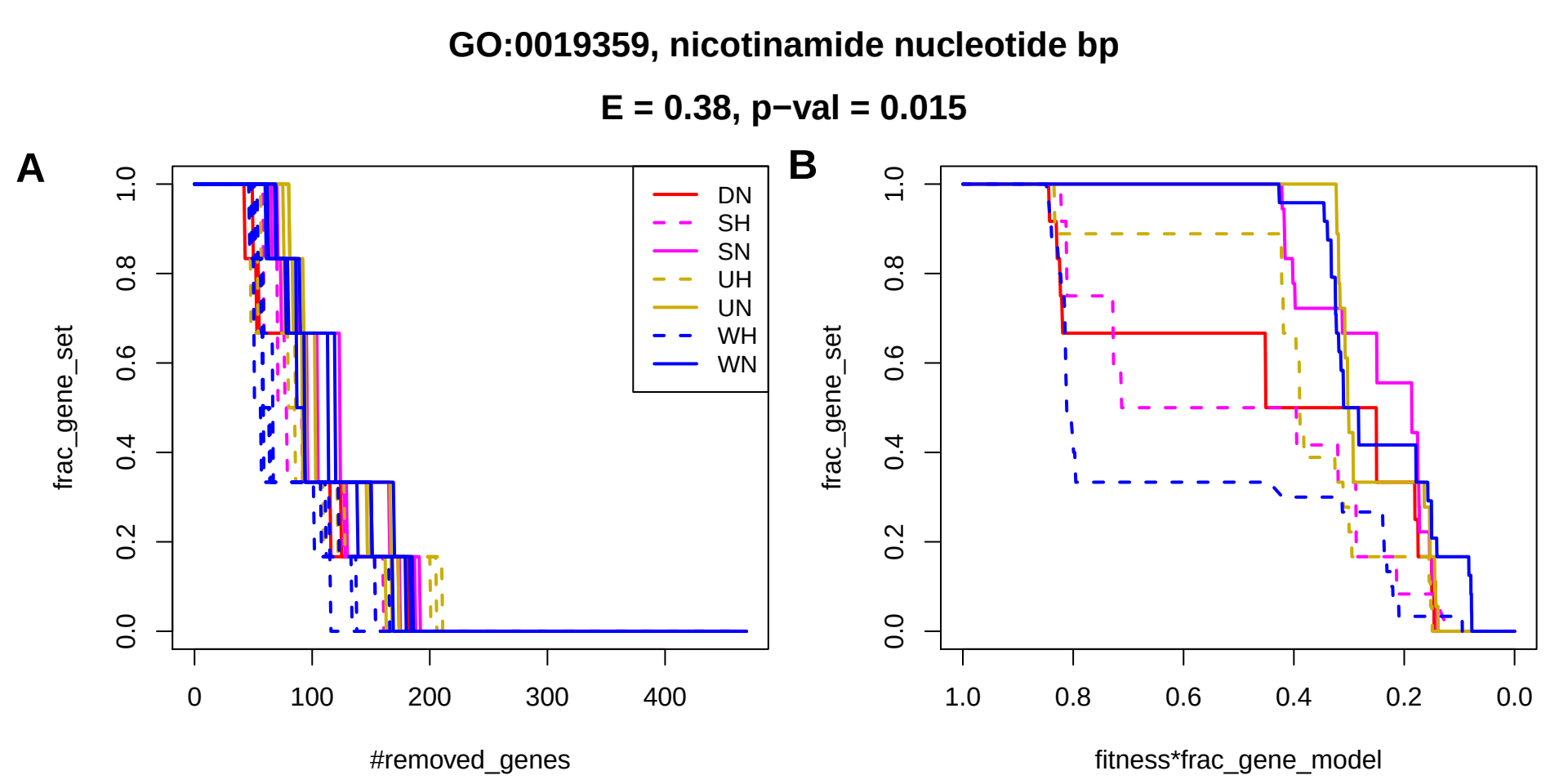

GO:0043649, dicarboxylic acid cp
E = 0.46, p−val = 0.004
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

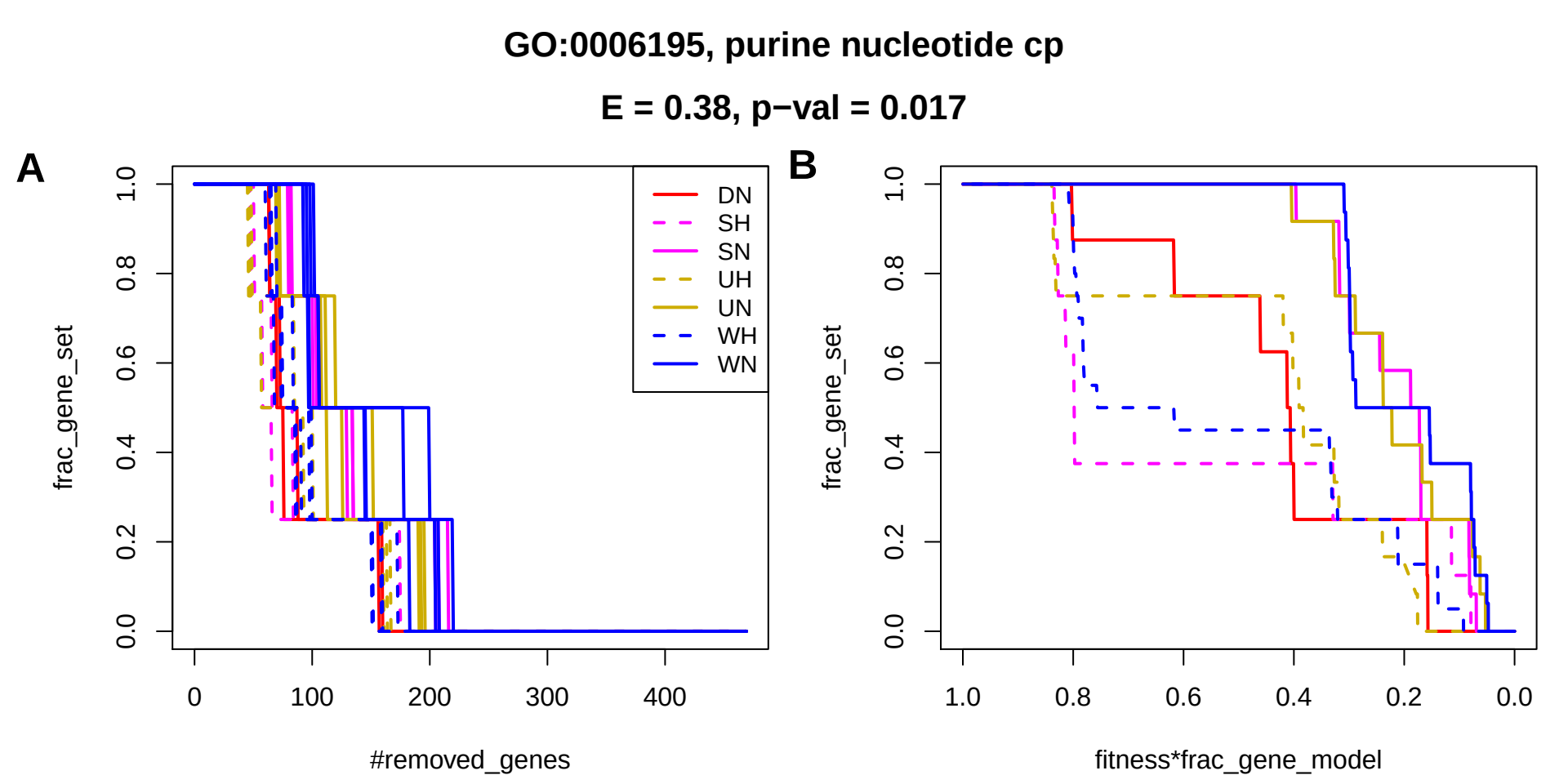

GO:0001676, long−chain fatty acid mp
E = 0.46, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

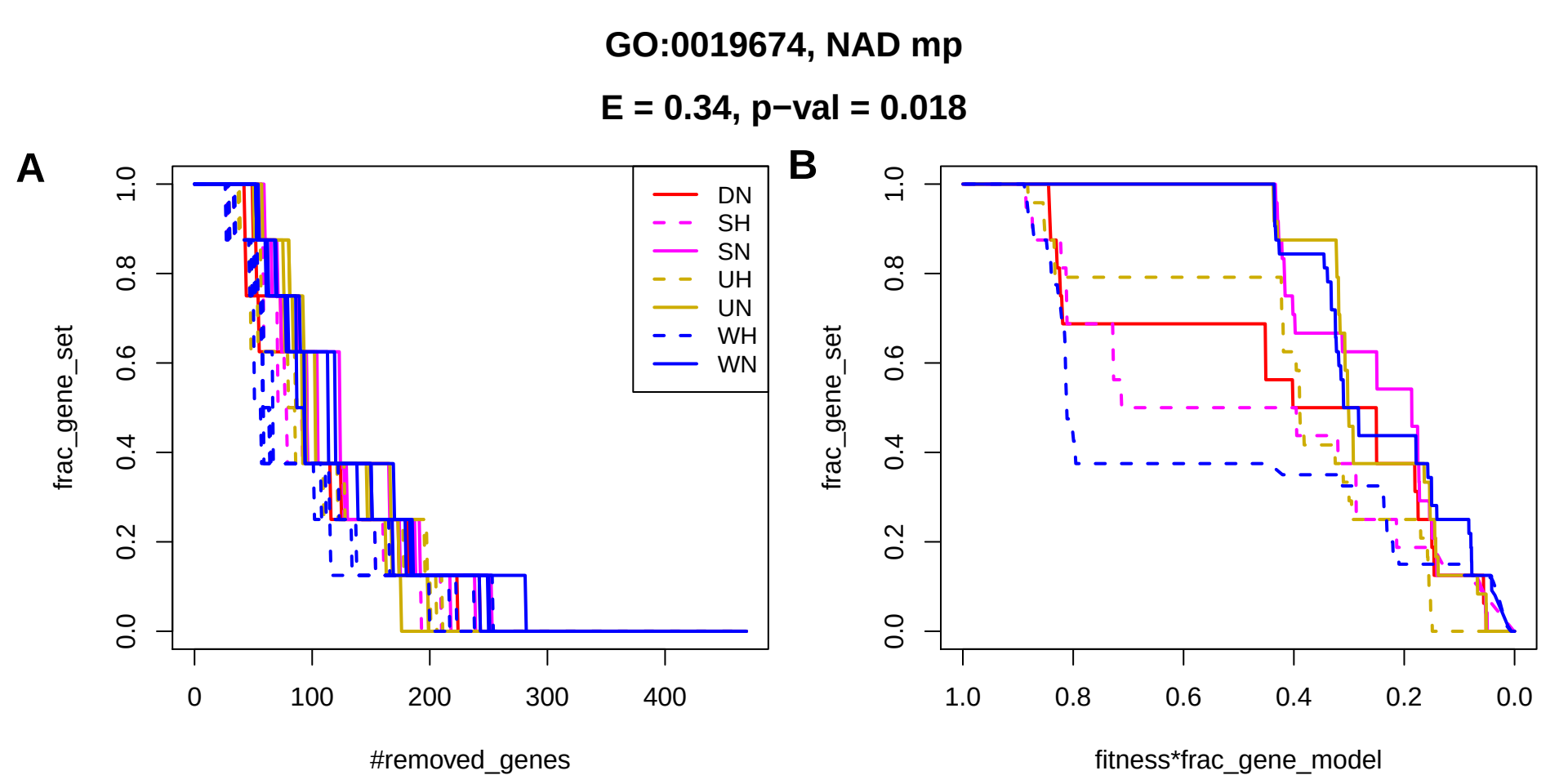

GO:0000105, histidine bp
E = 0.44, p−val = 0.002
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

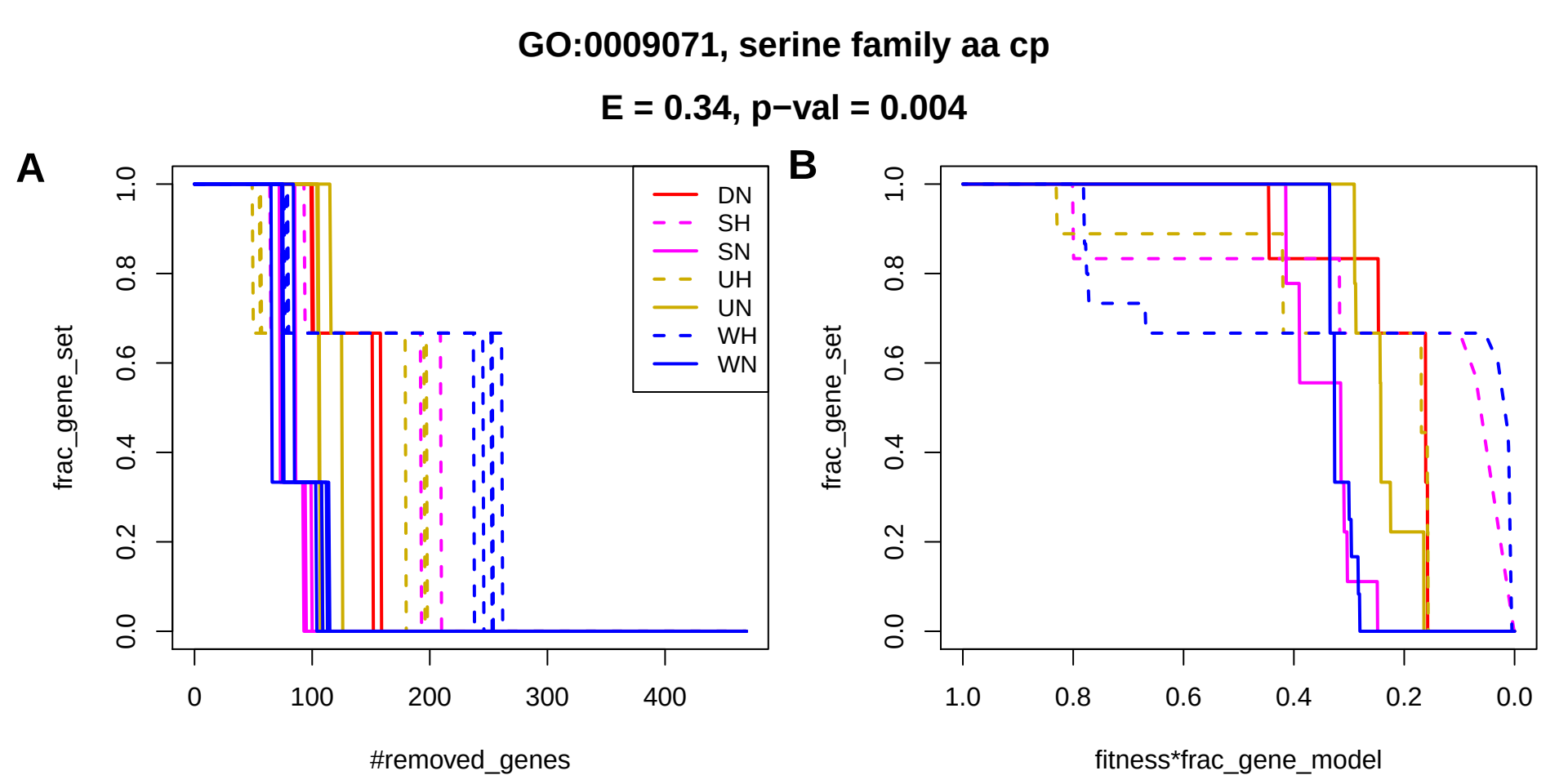

GO:0006635, fatty acid beta−oxidation
E = 0.41, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

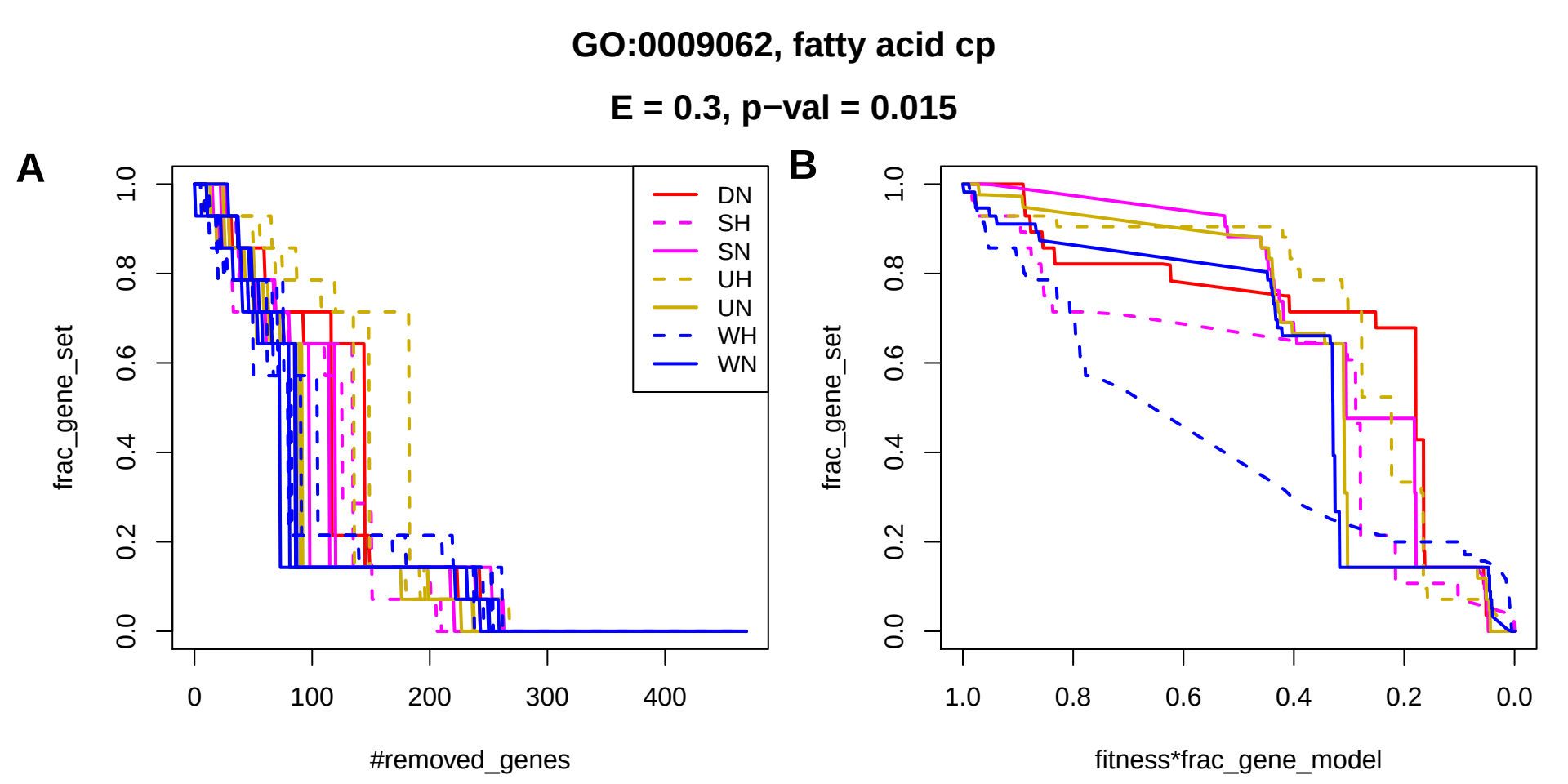

GO:0009221, pyrimidine deoxyribonucleotide bp
E = 0.4, p−val = 0.01
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

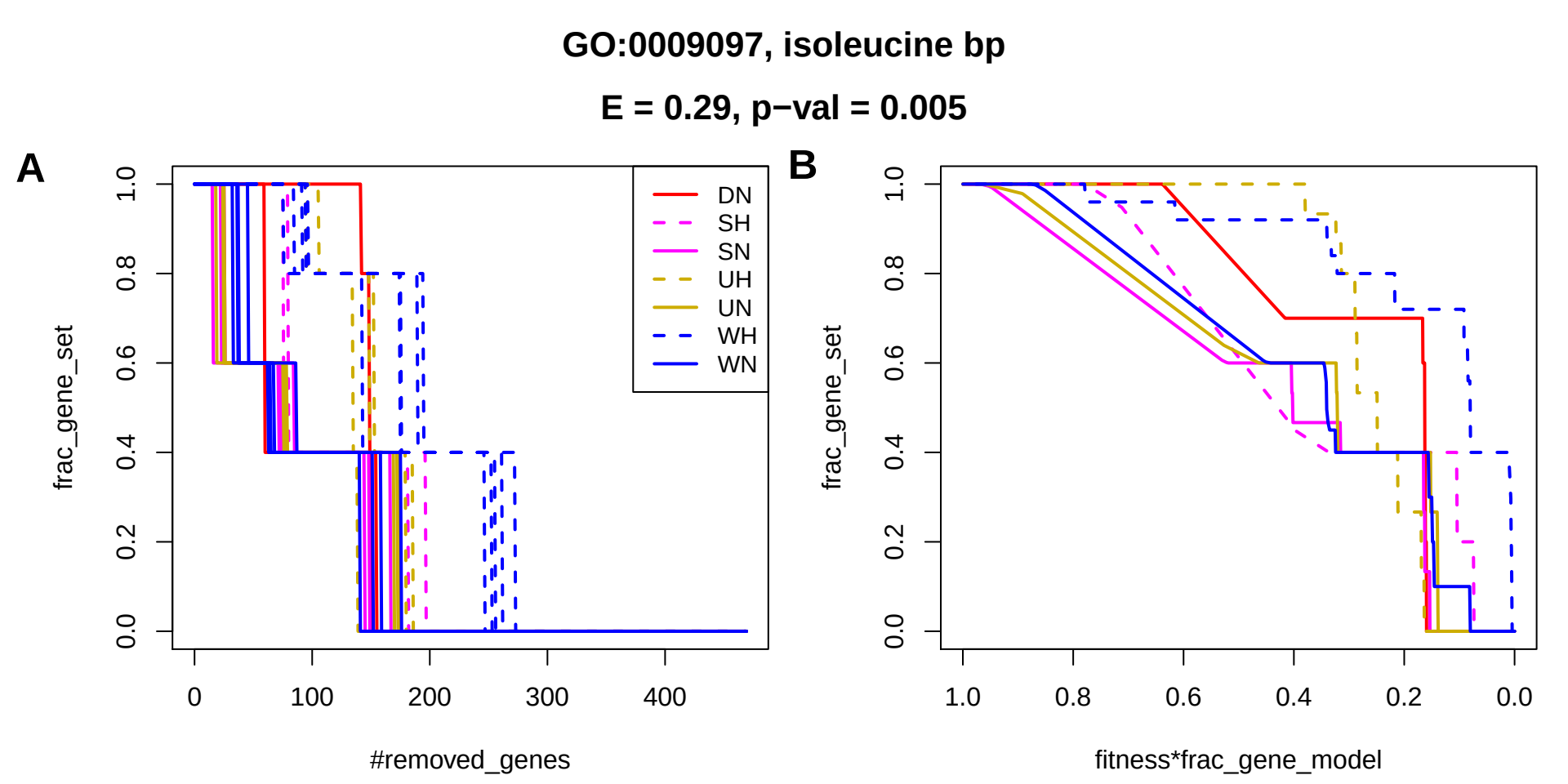

GO:0019359, nicotinamide nucleotide bp
E = 0.38, p−val = 0.015
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

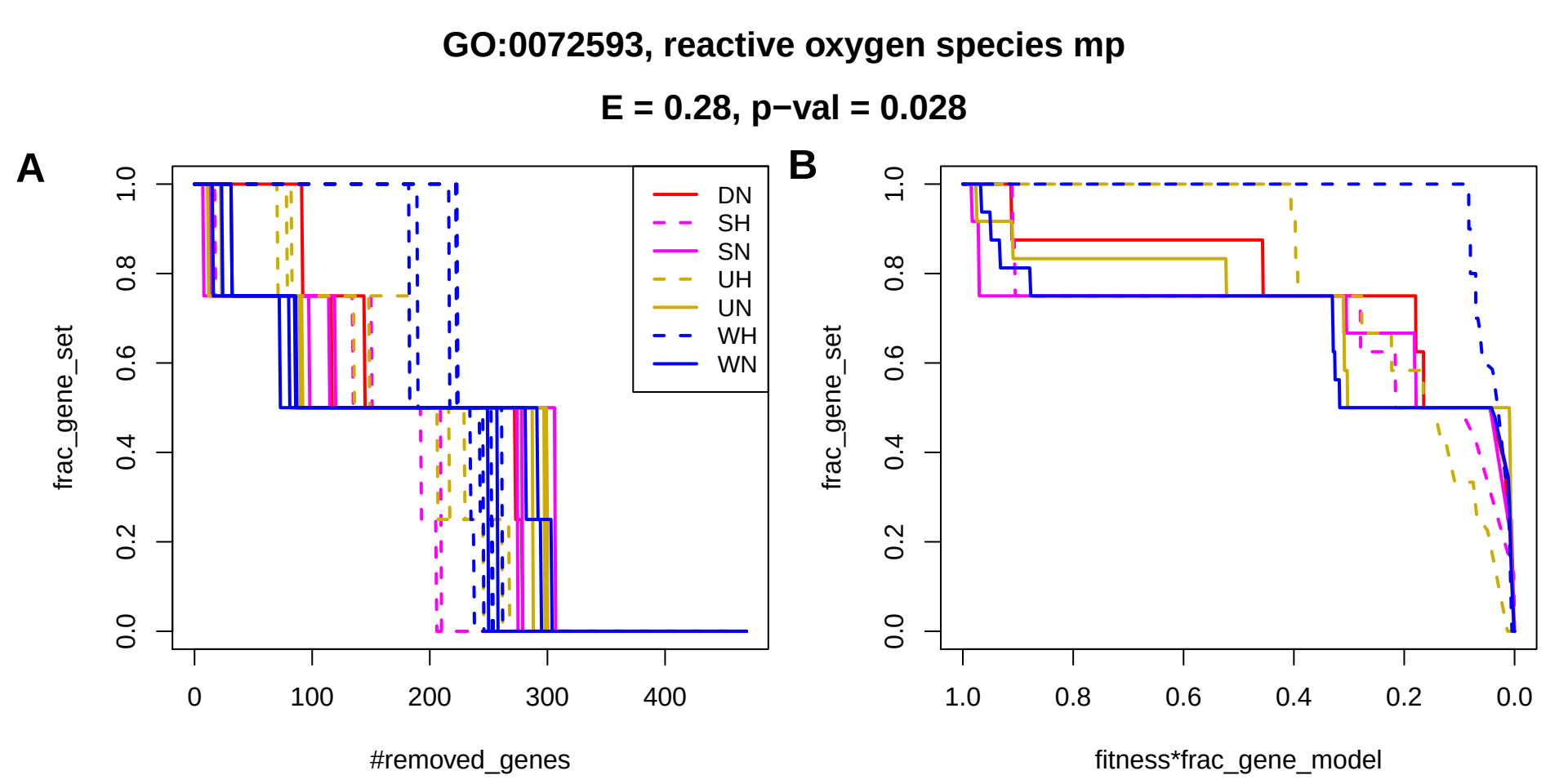

GO:0006195, purine nucleotide cp
E = 0.38, p−val = 0.017
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

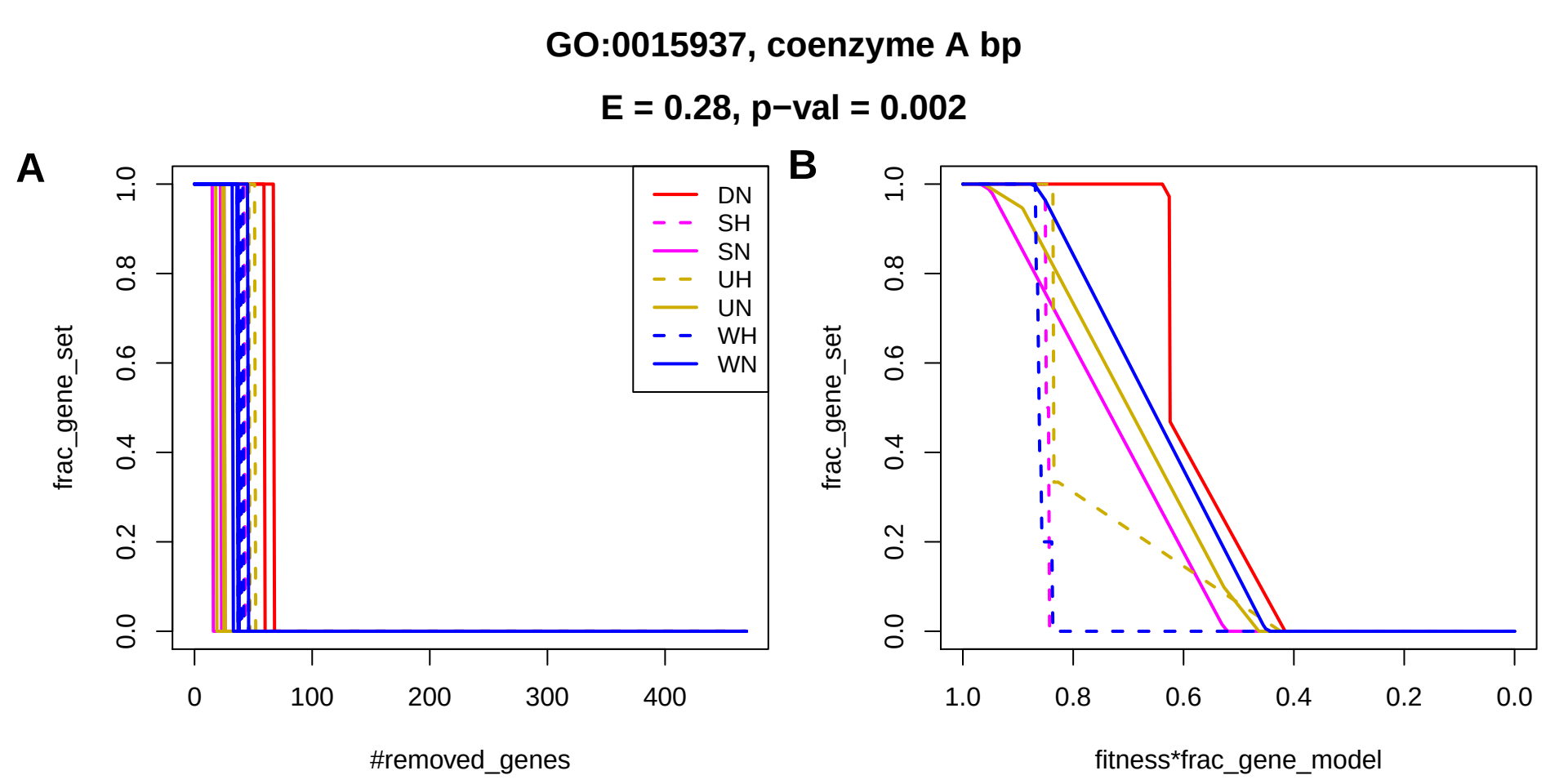

GO:0019674, NAD mp
E = 0.34, p−val = 0.018
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

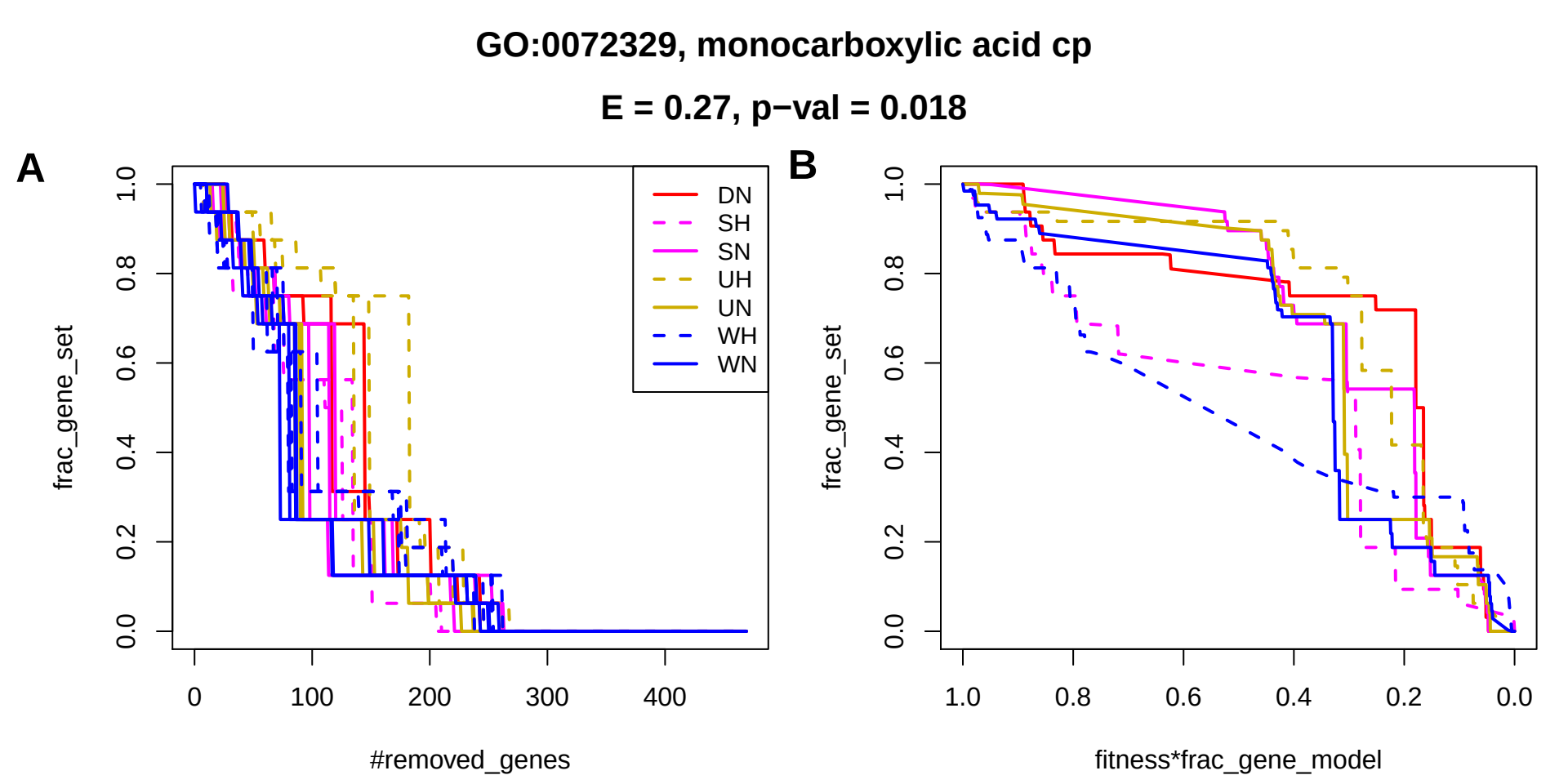

GO:0009071, serine family aa cp
E = 0.34, p−val = 0.004
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009062, fatty acid cp
E = 0.3, p−val = 0.015
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009097, isoleucine bp
E = 0.29, p−val = 0.005
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0072593, reactive oxygen species mp
E = 0.28, p−val = 0.028
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0015937, coenzyme A bp
E = 0.28, p−val = 0.002
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0072329, monocarboxylic acid cp
E = 0.27, p−val = 0.018
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
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0.4
0.6
0.8
1.0
0
100
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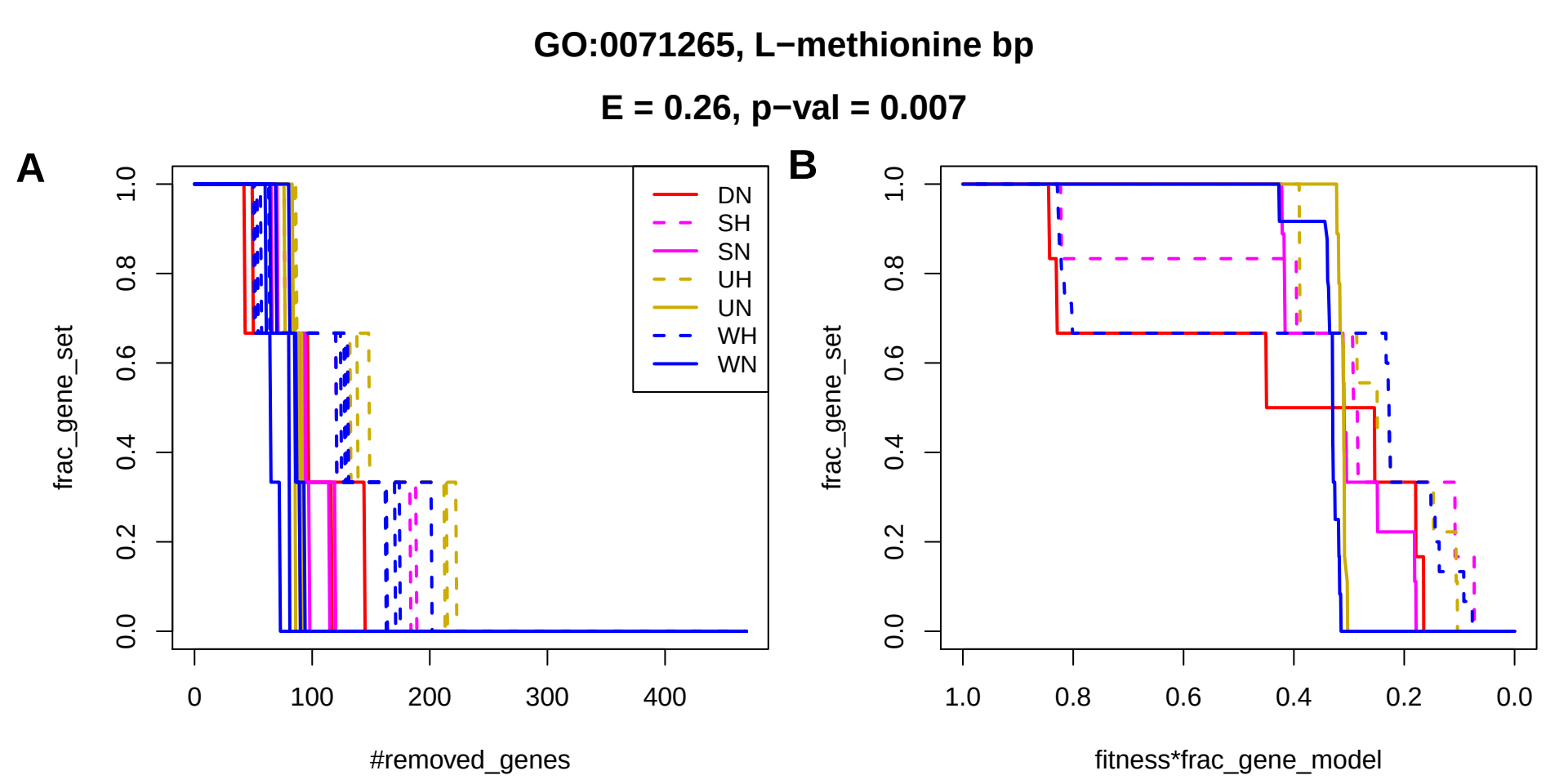
300
400


GO:0071265, L−methionine bp
E = 0.26, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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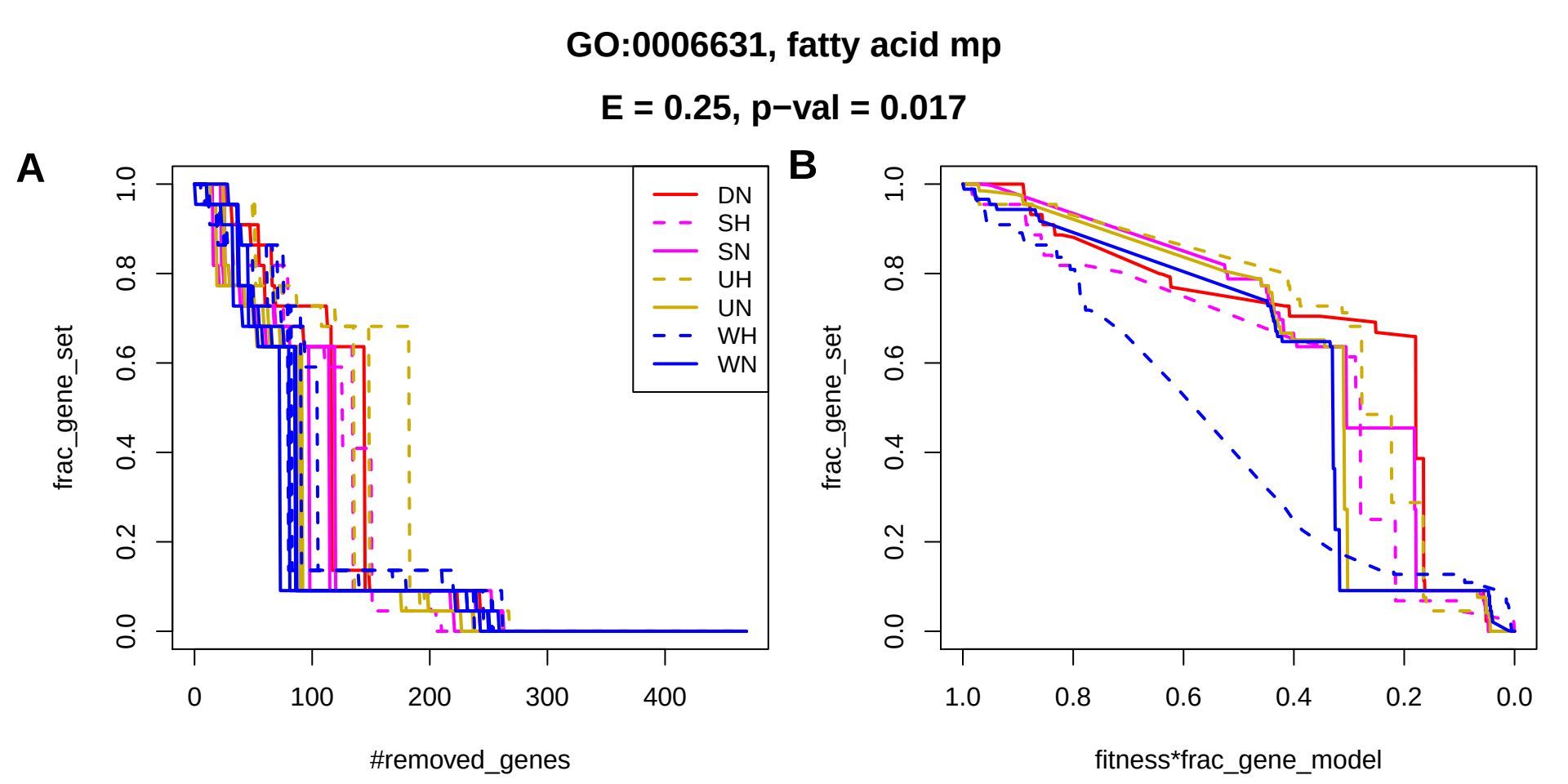
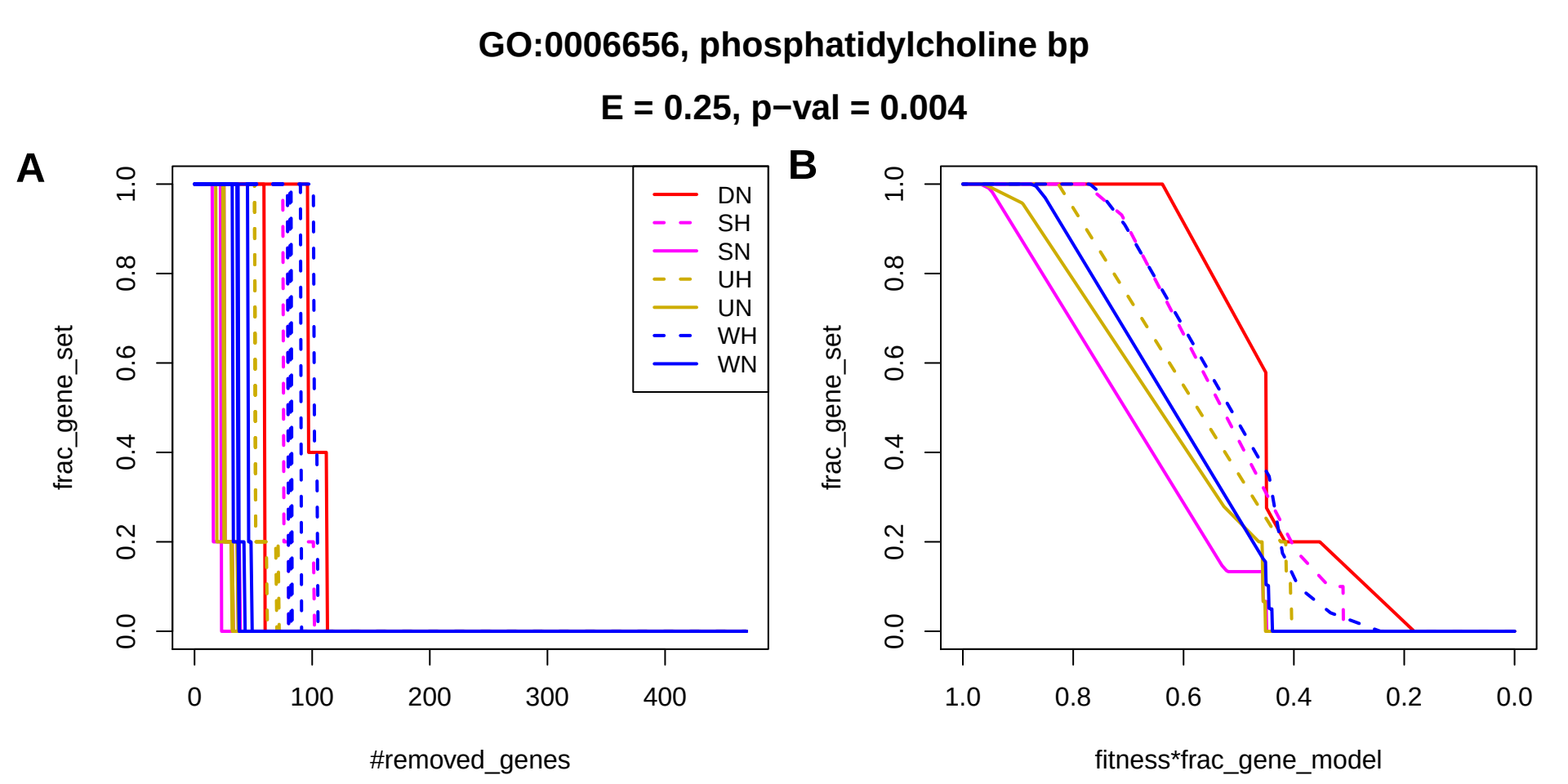
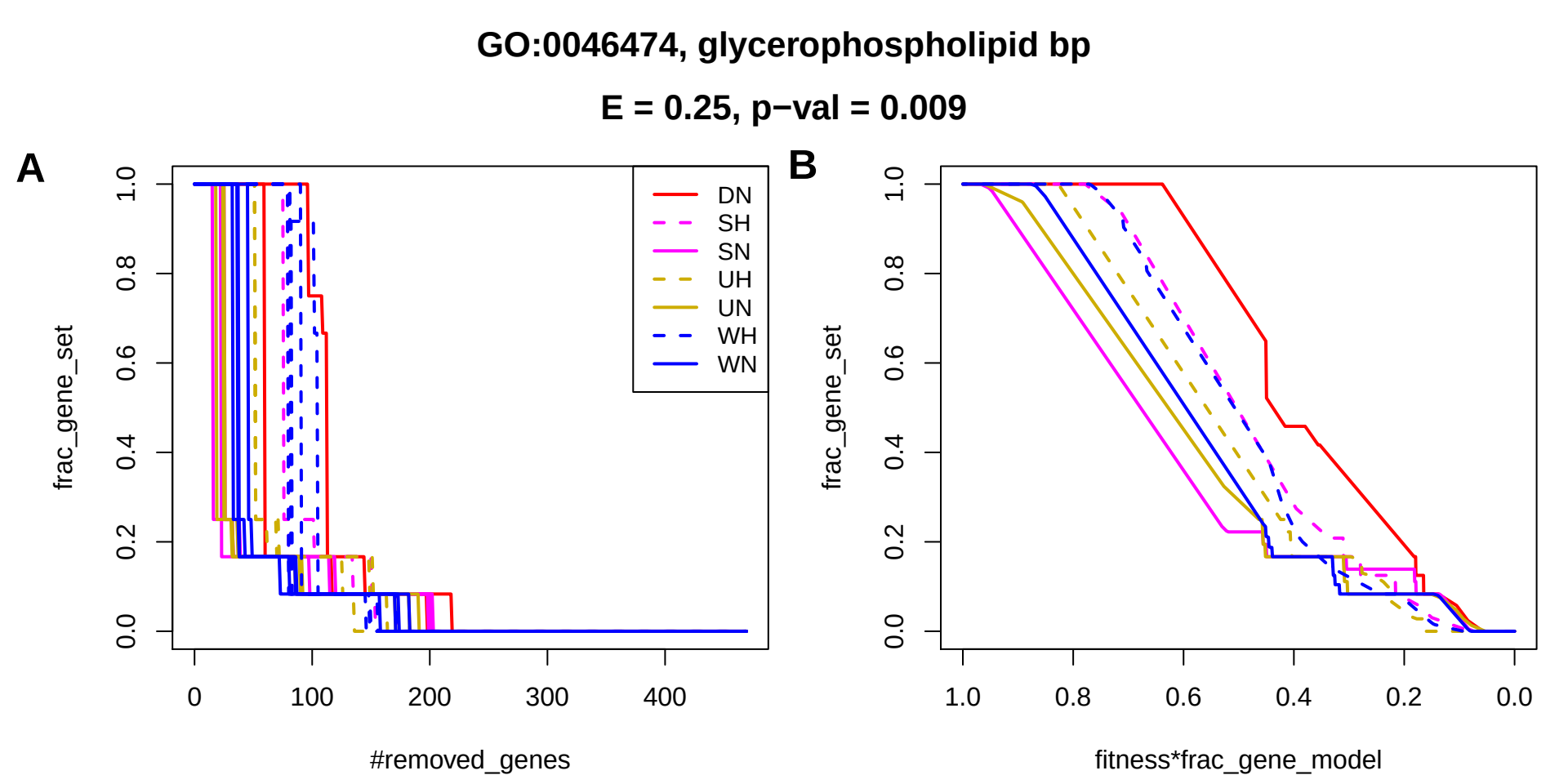
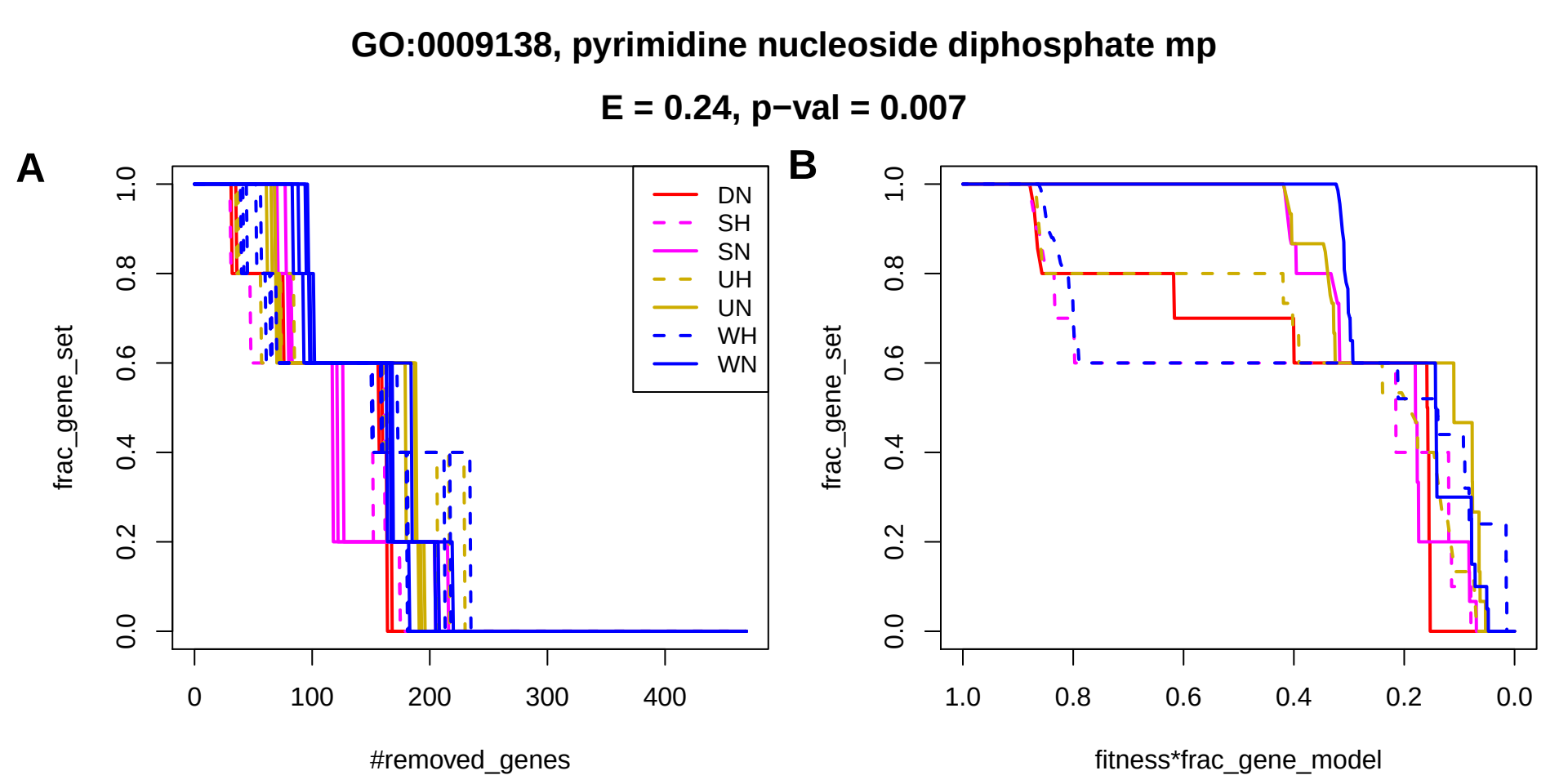
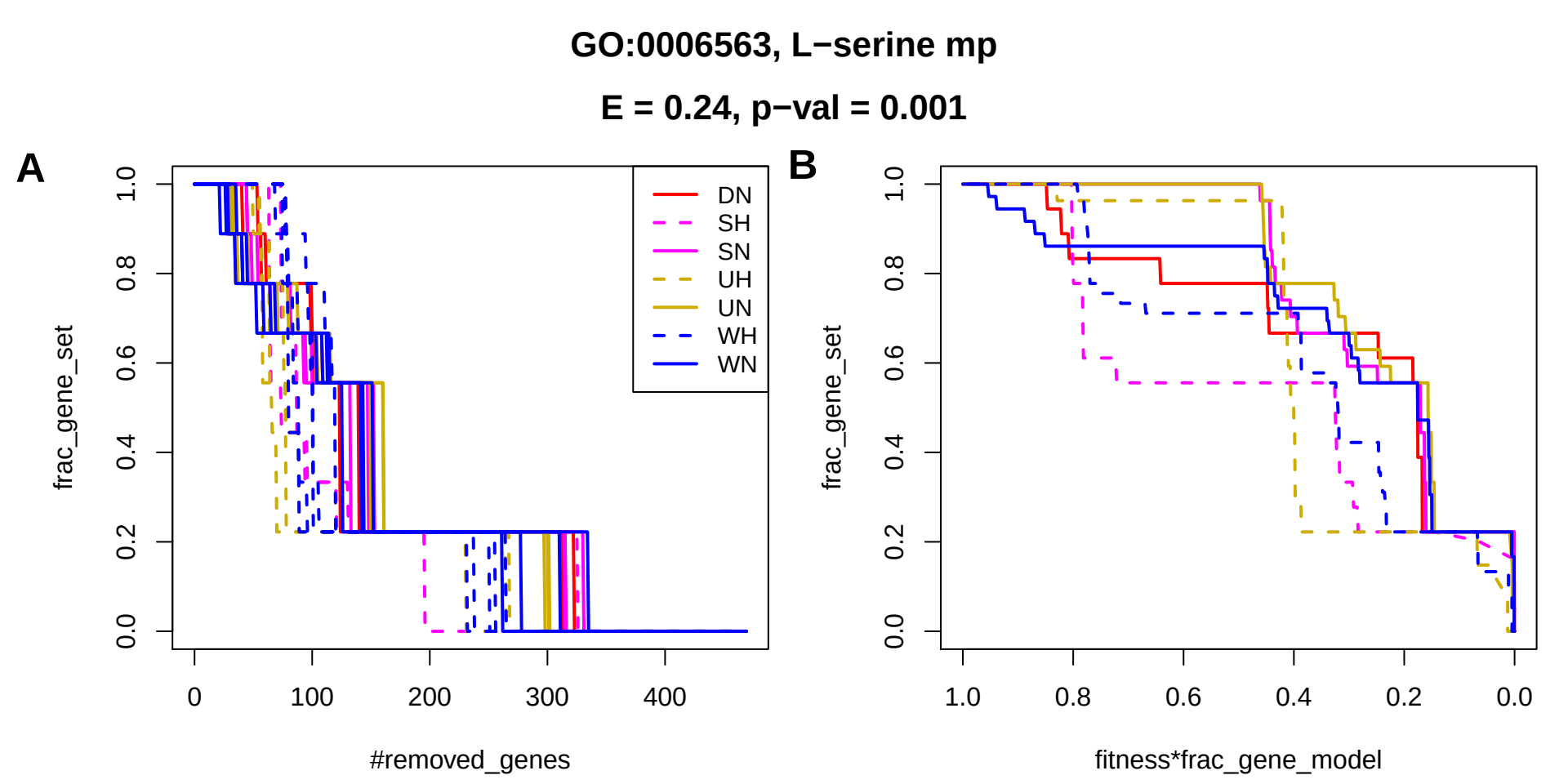
300
400

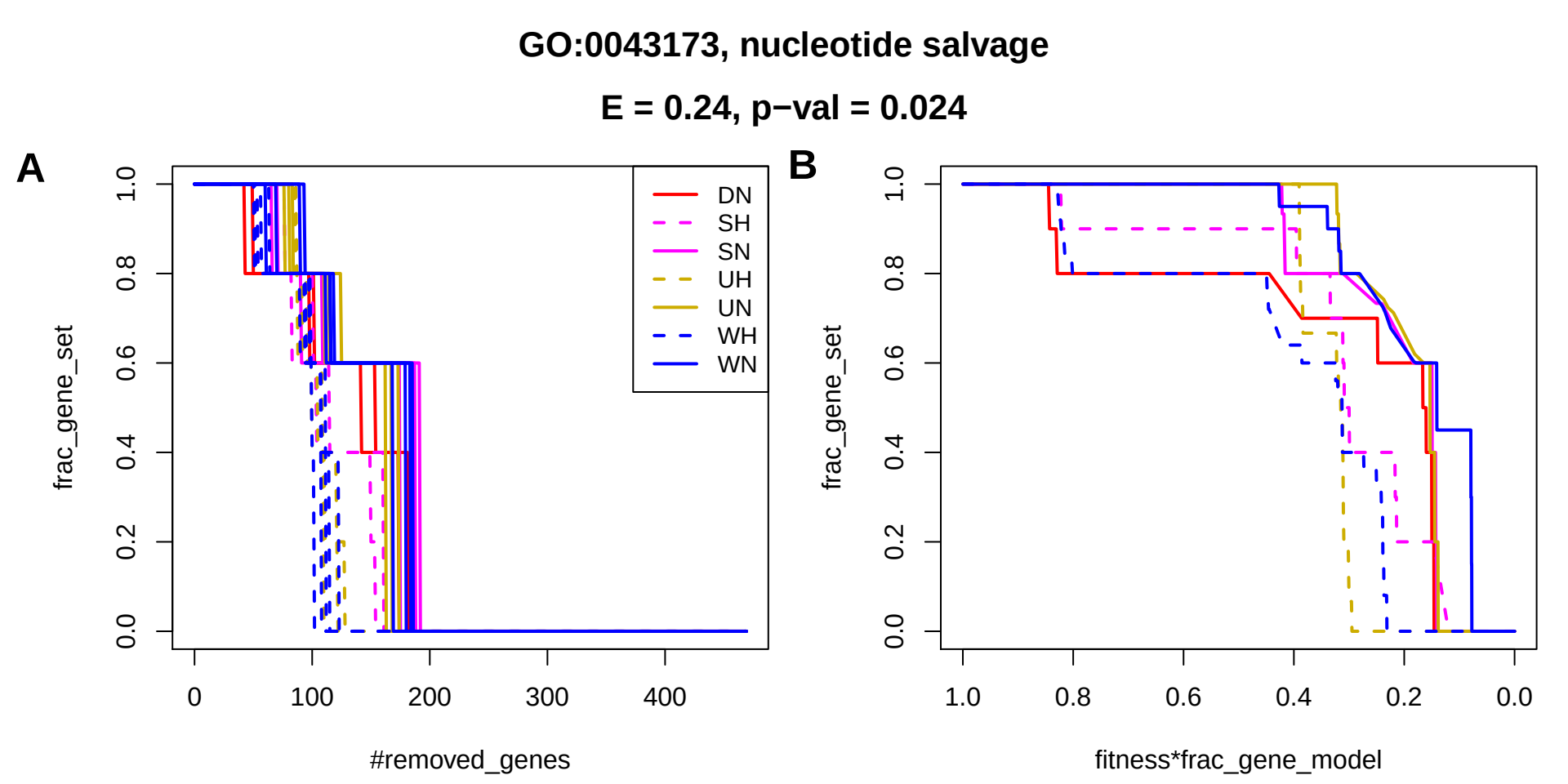

GO:0006631, fatty acid mp
E = 0.25, p−val = 0.017
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

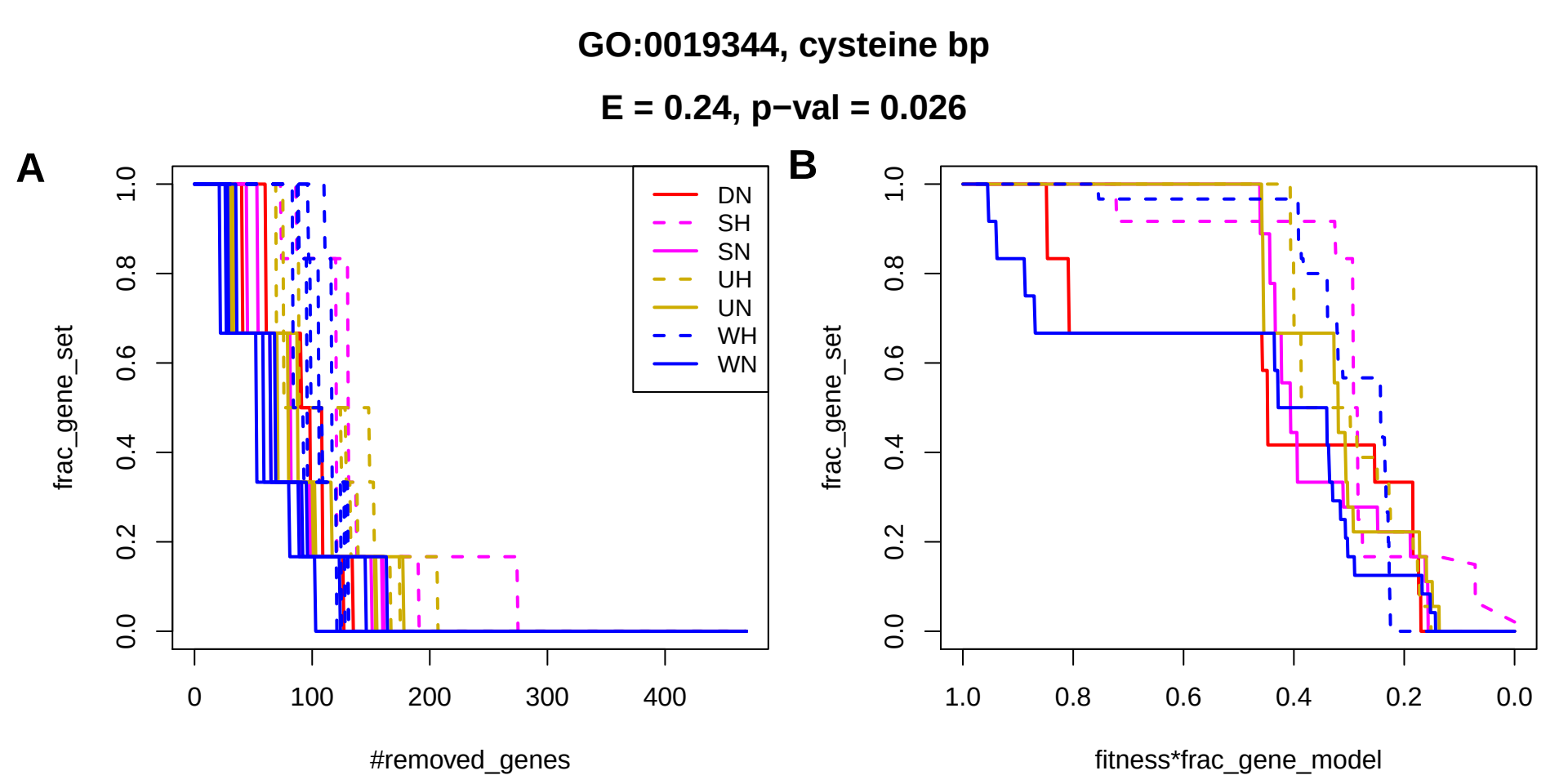

GO:0006656, phosphatidylcholine bp
E = 0.25, p−val = 0.004
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

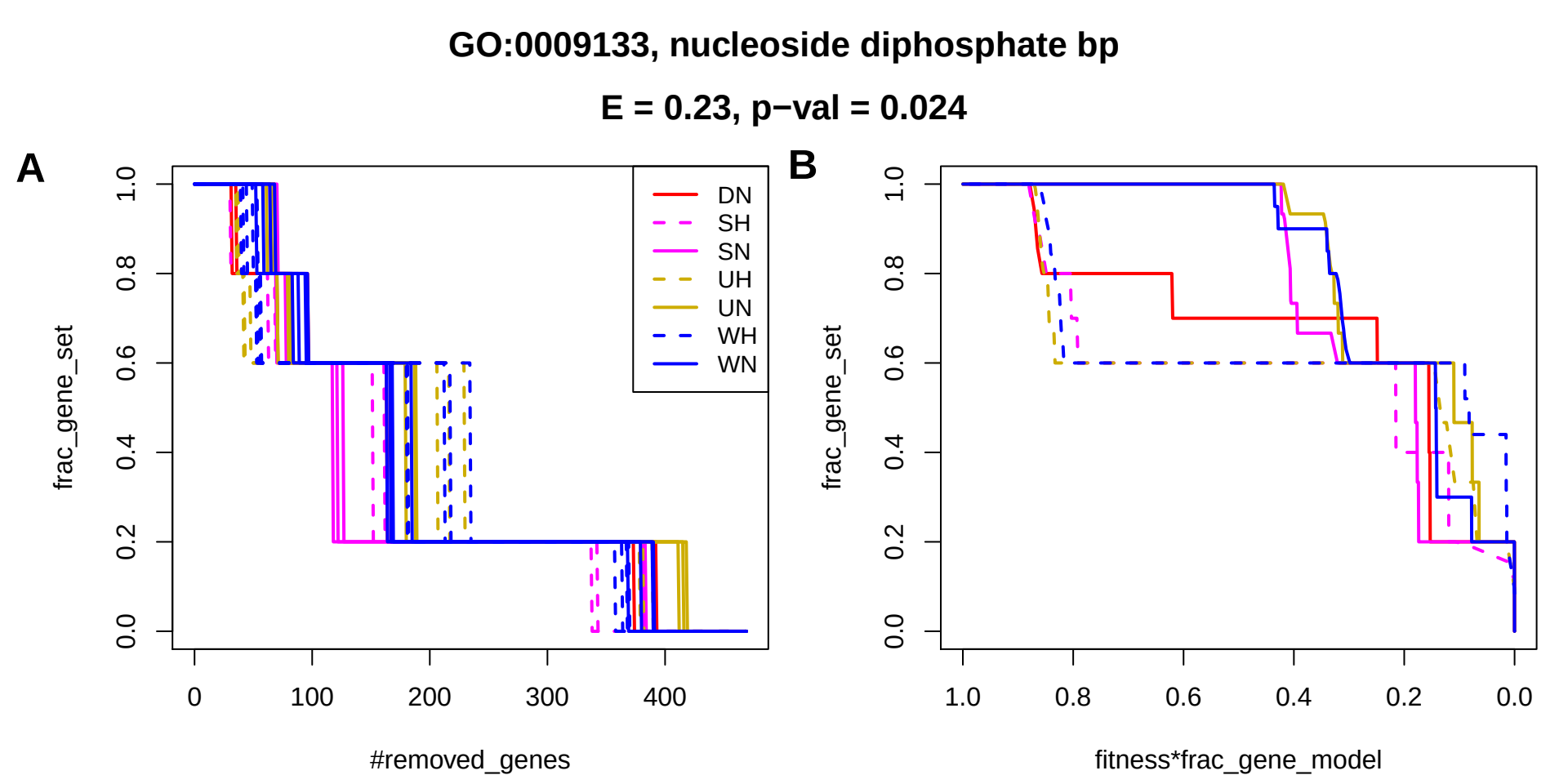

GO:0046474, glycerophospholipid bp
E = 0.25, p−val = 0.009
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

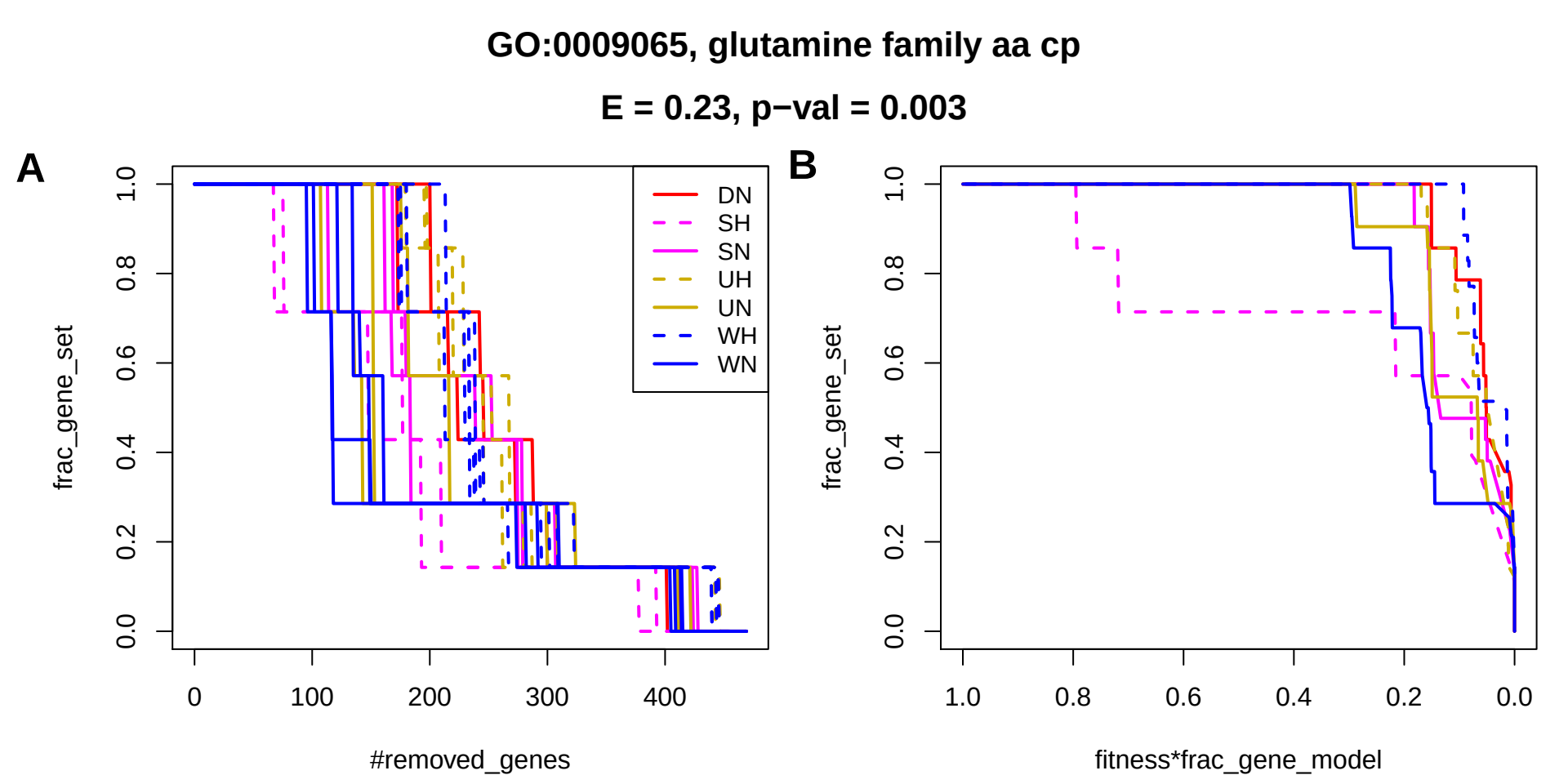

GO:0009138, pyrimidine nucleoside diphosphate mp
E = 0.24, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

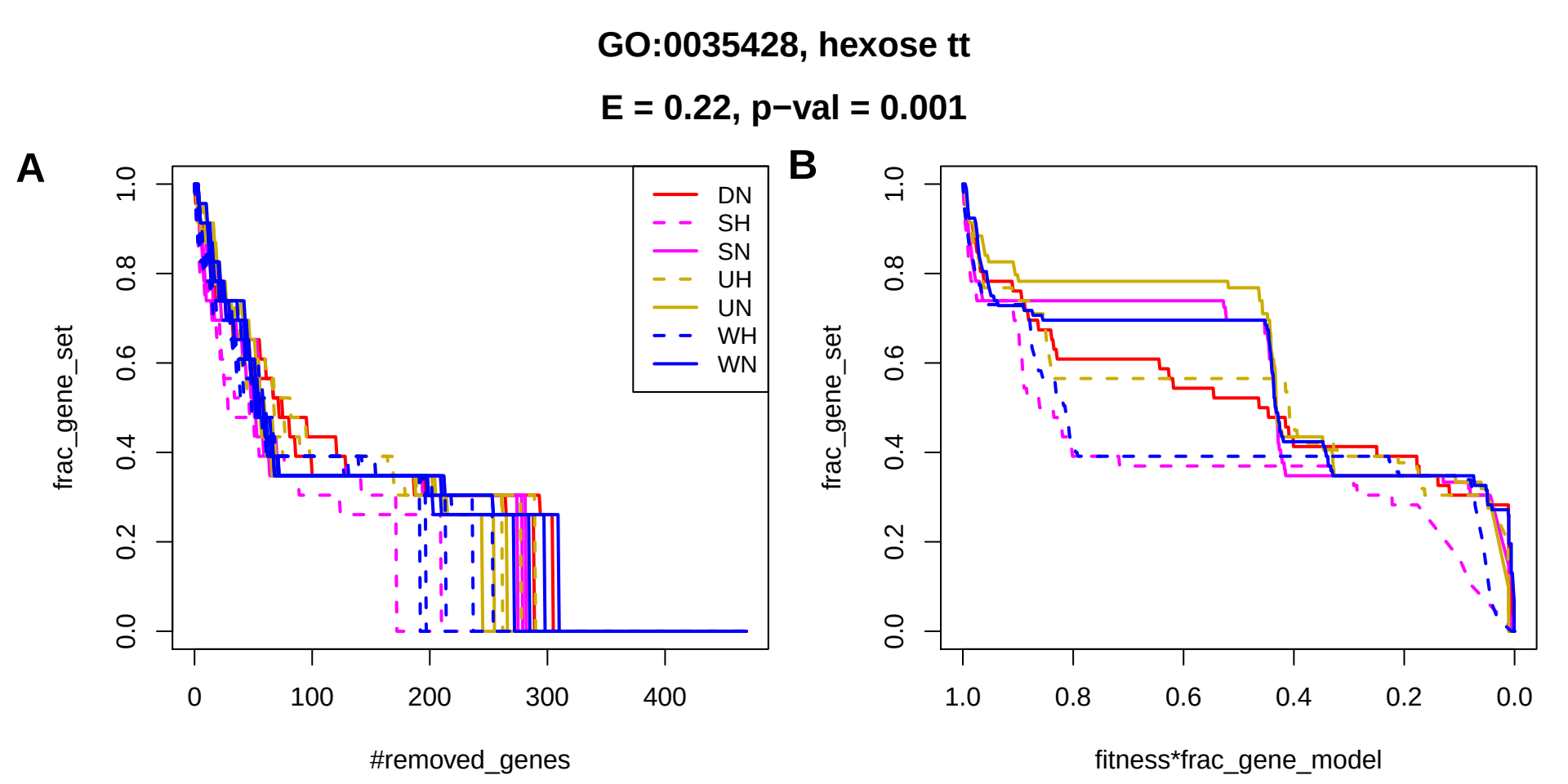

GO:0006563, L−serine mp
E = 0.24, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

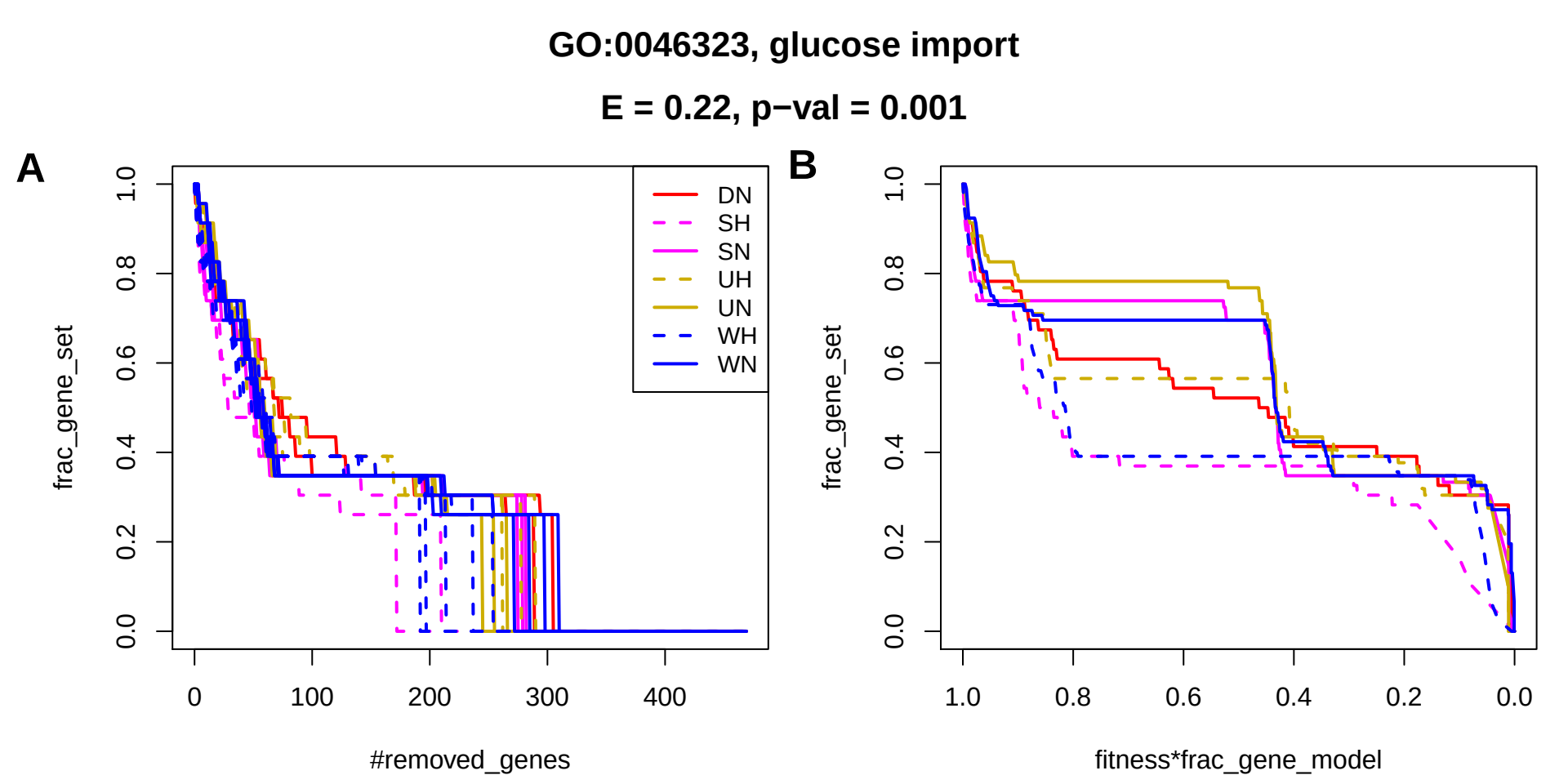

GO:0043173, nucleotide salvage
E = 0.24, p−val = 0.024
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

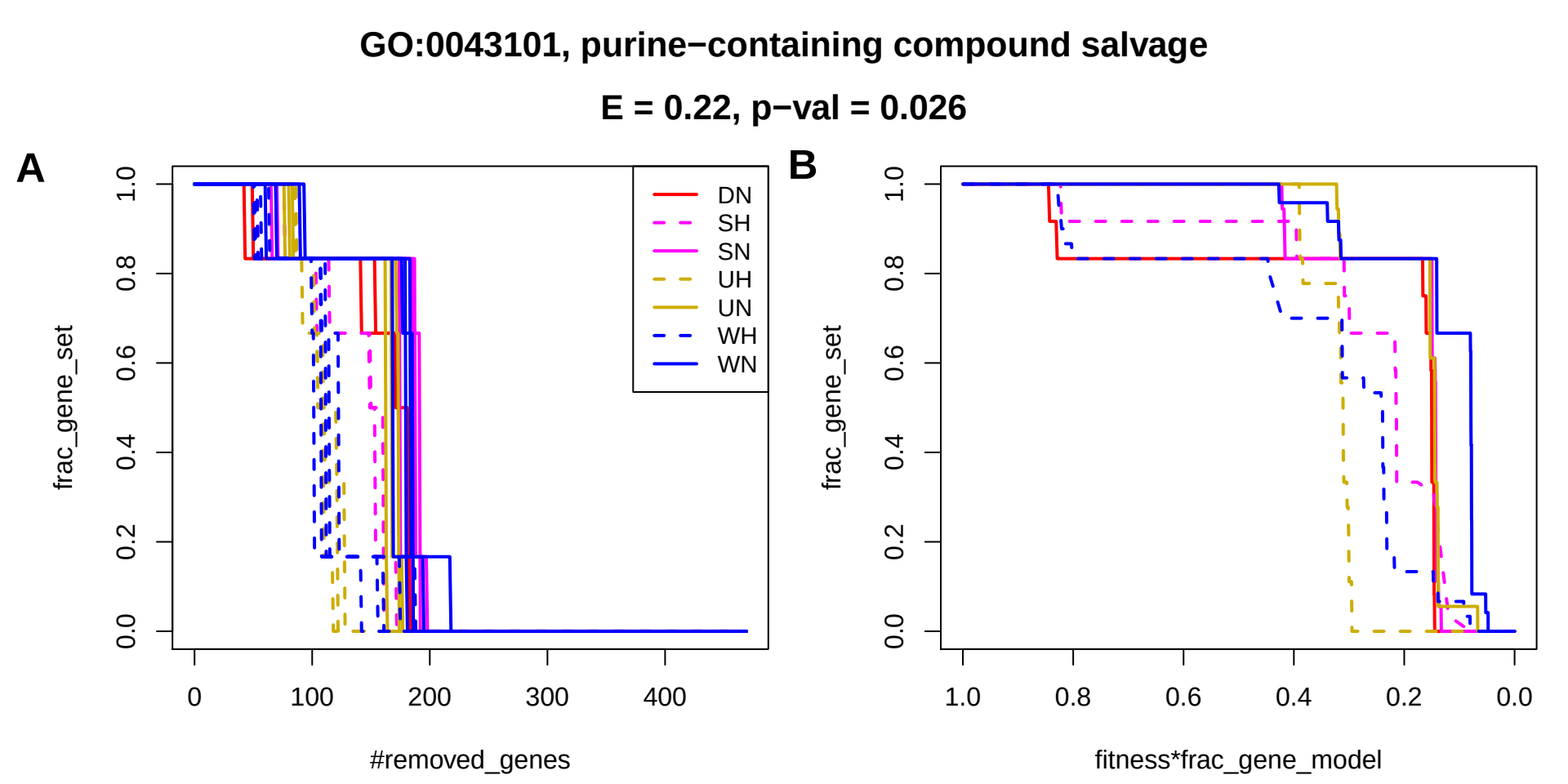

GO:0019344, cysteine bp
E = 0.24, p−val = 0.026
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

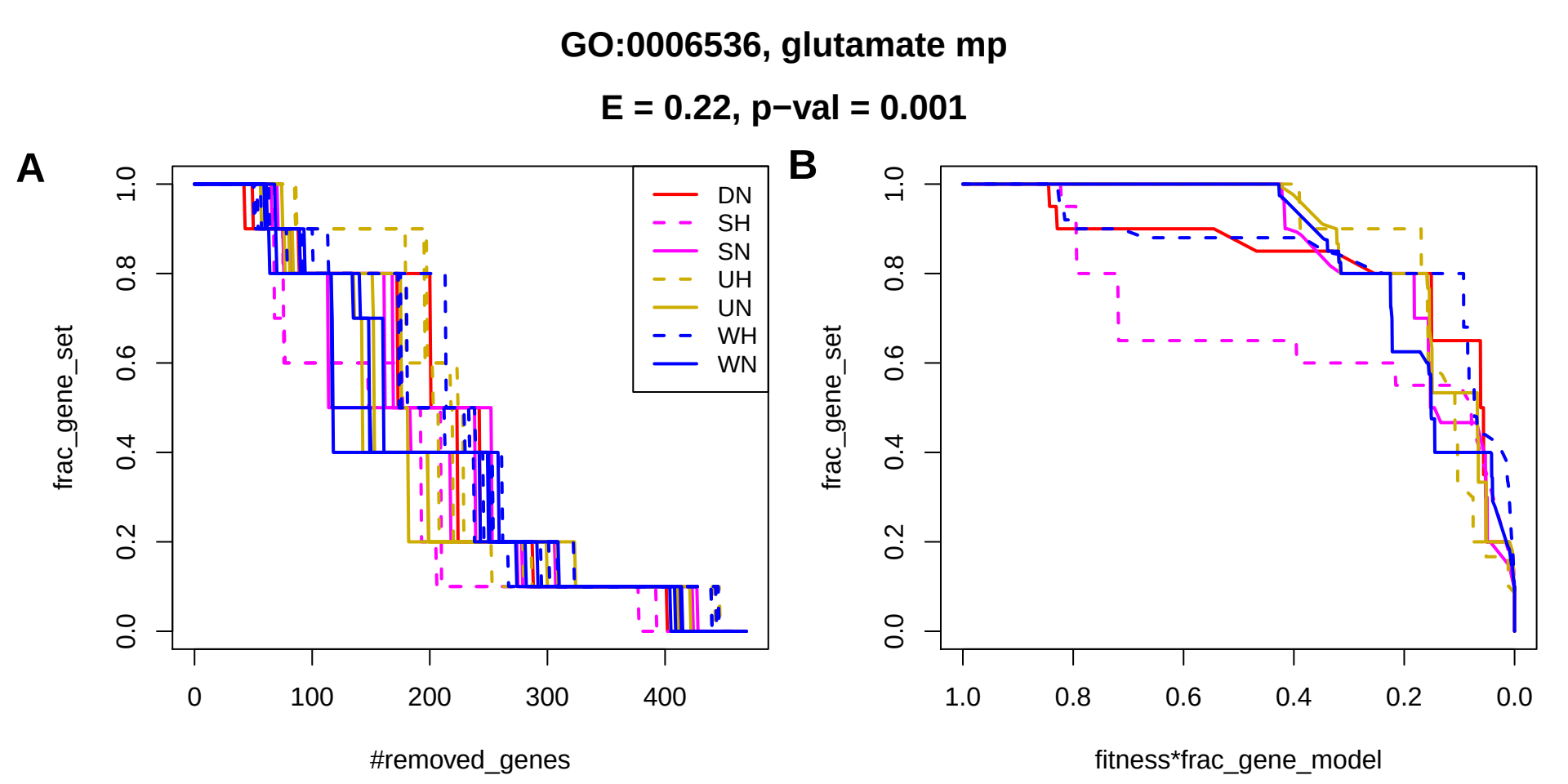

GO:0009133, nucleoside diphosphate bp
E = 0.23, p−val = 0.024
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009065, glutamine family aa cp
E = 0.23, p−val = 0.003
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0035428, hexose tt
E = 0.22, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0046323, glucose import
E = 0.22, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0043101, purine−containing compound salvage
E = 0.22, p−val = 0.026
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006536, glutamate mp
E = 0.22, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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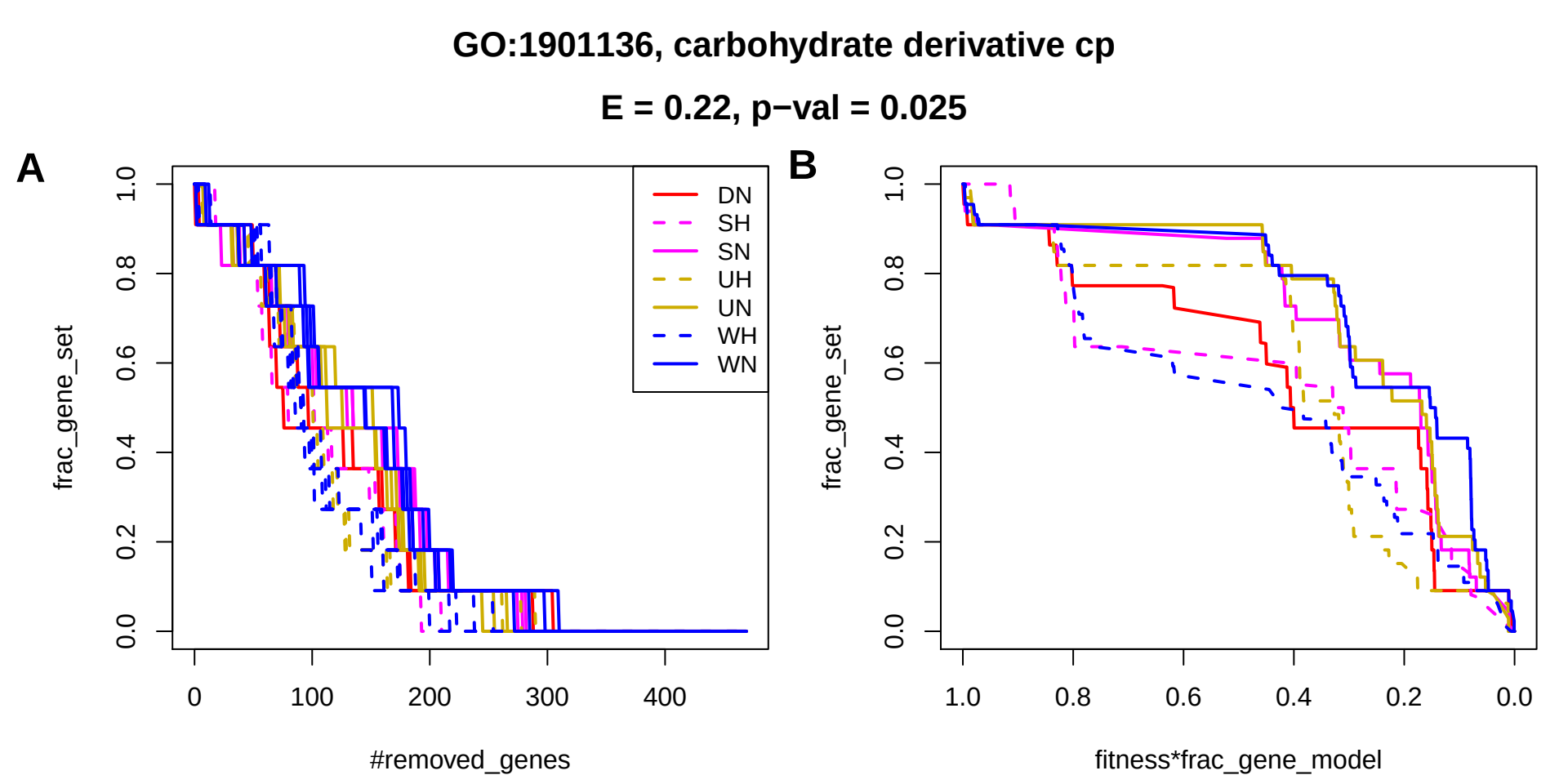
GO:1901136, carbohydrate derivative cp
E = 0.22, p−val = 0.025
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
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WH
WN
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0.2
0.4
0.6
0.8
1.0
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300
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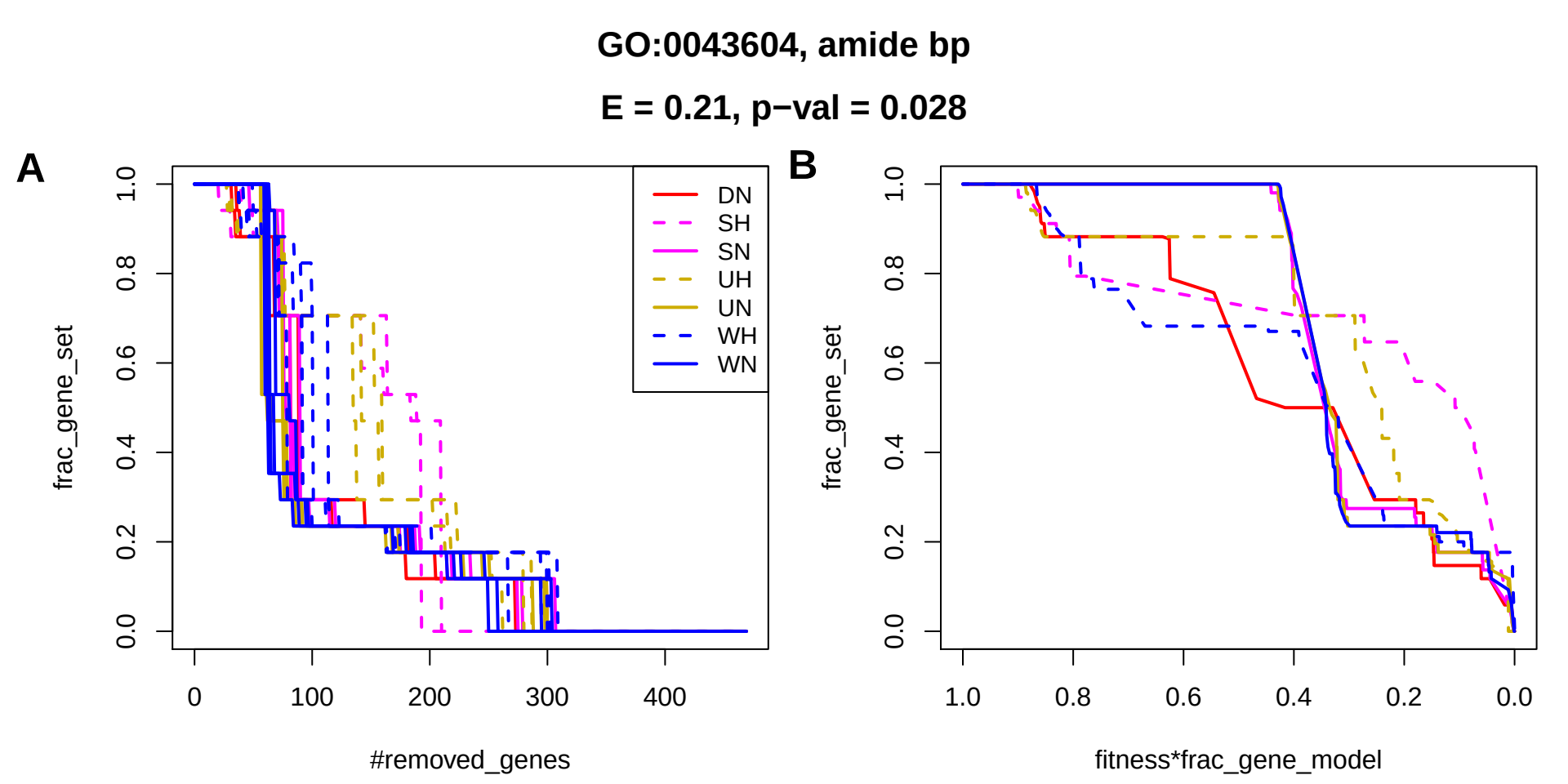
GO:0043604, amide bp
E = 0.21, p−val = 0.028
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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300
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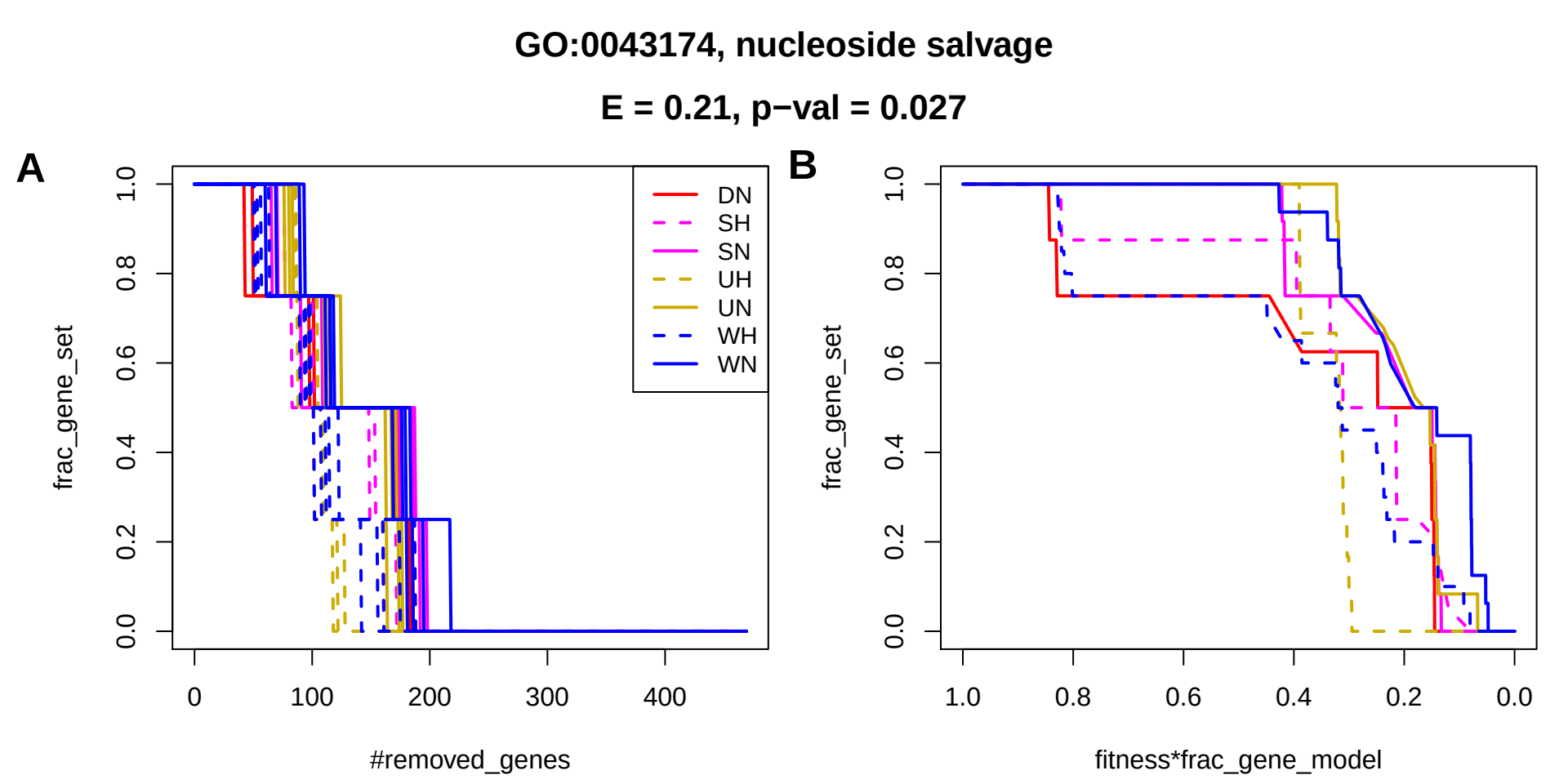
GO:0043174, nucleoside salvage
E = 0.21, p−val = 0.027
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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100
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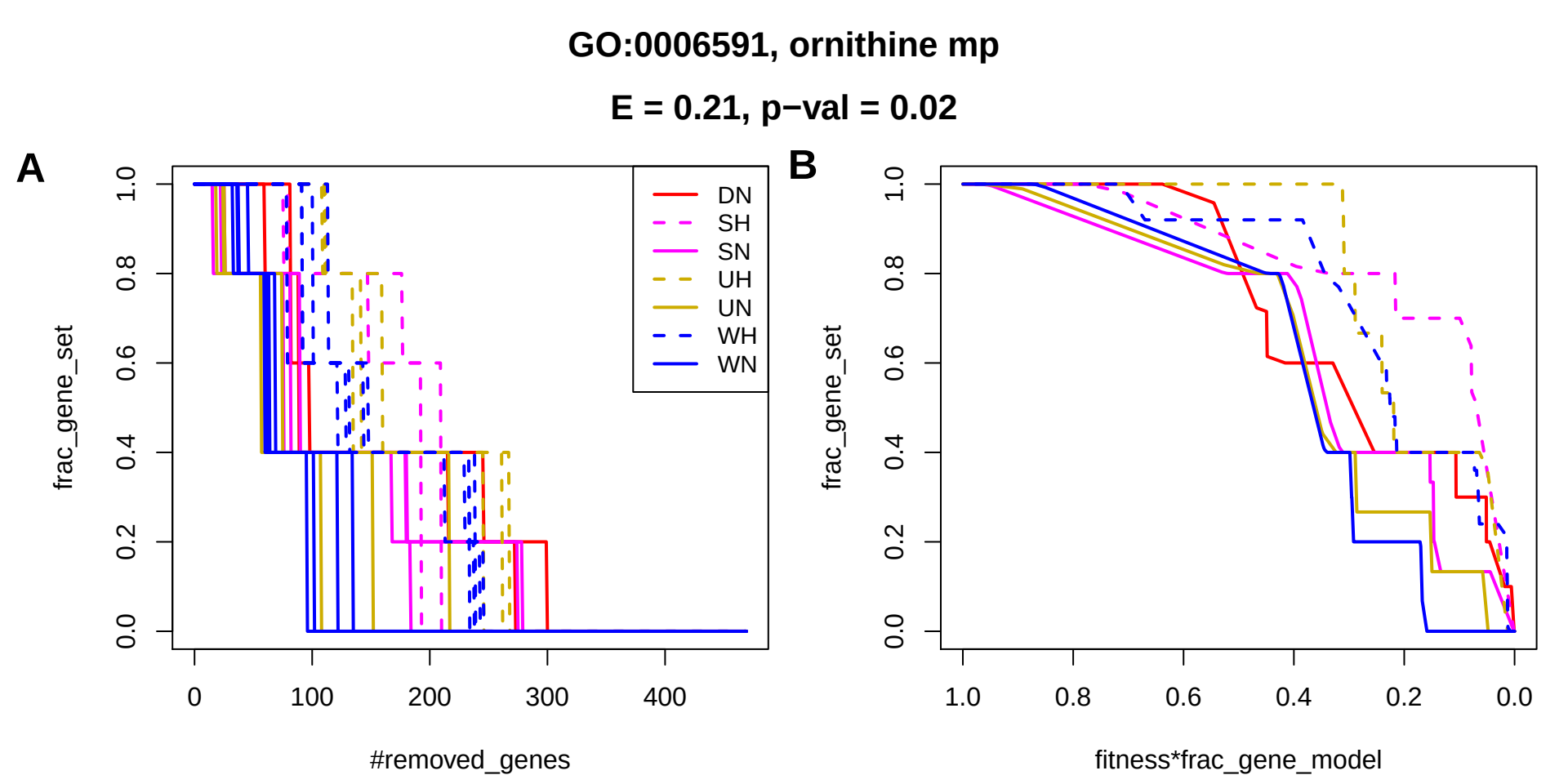
300
400


GO:0006591, ornithine mp
E = 0.21, p−val = 0.02
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
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0.4
0.6
0.8
1.0
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300
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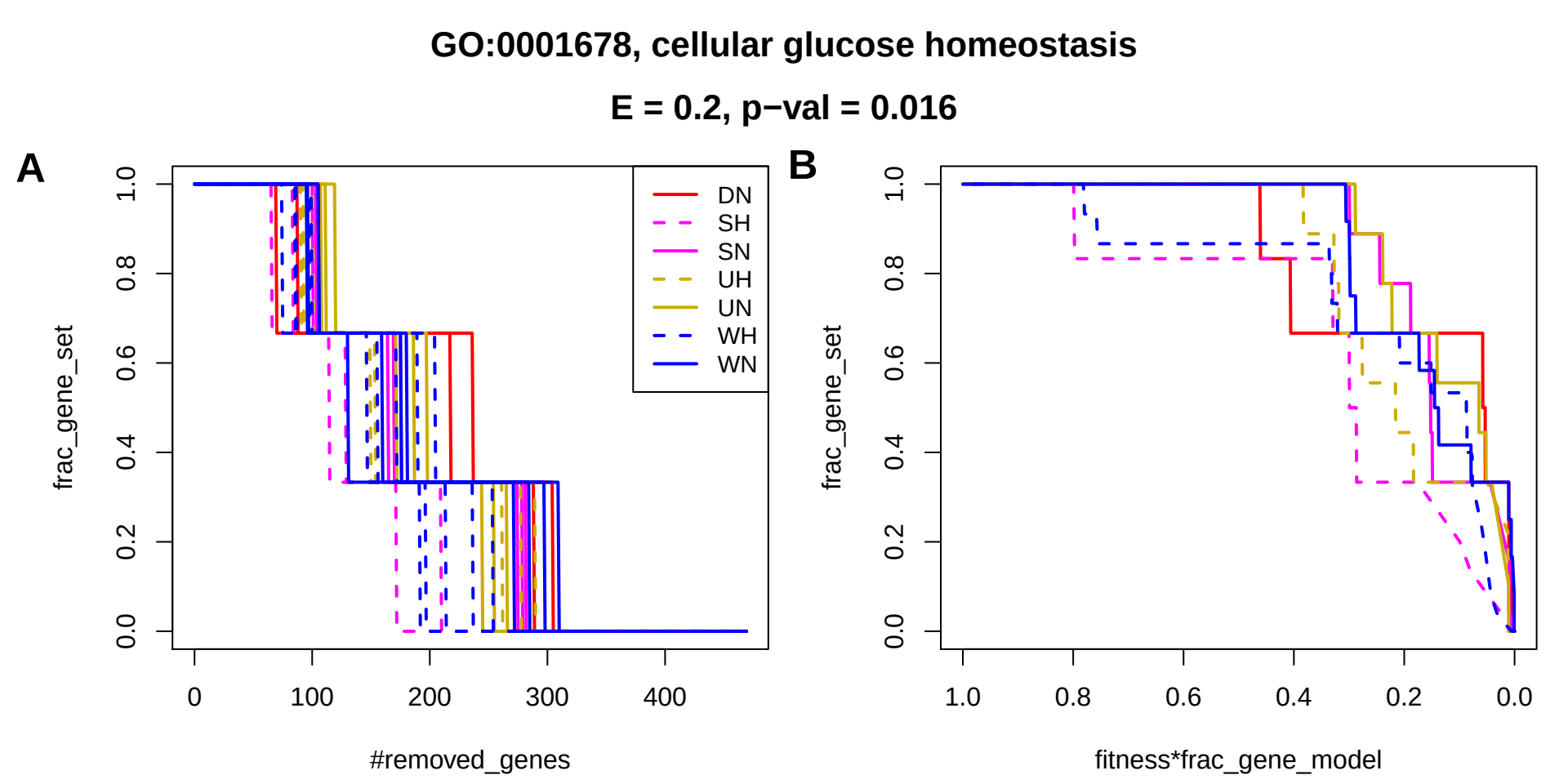
GO:0001678, cellular glucose homeostasis
E = 0.2, p−val = 0.016
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
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0.4
0.6
0.8
1.0
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300
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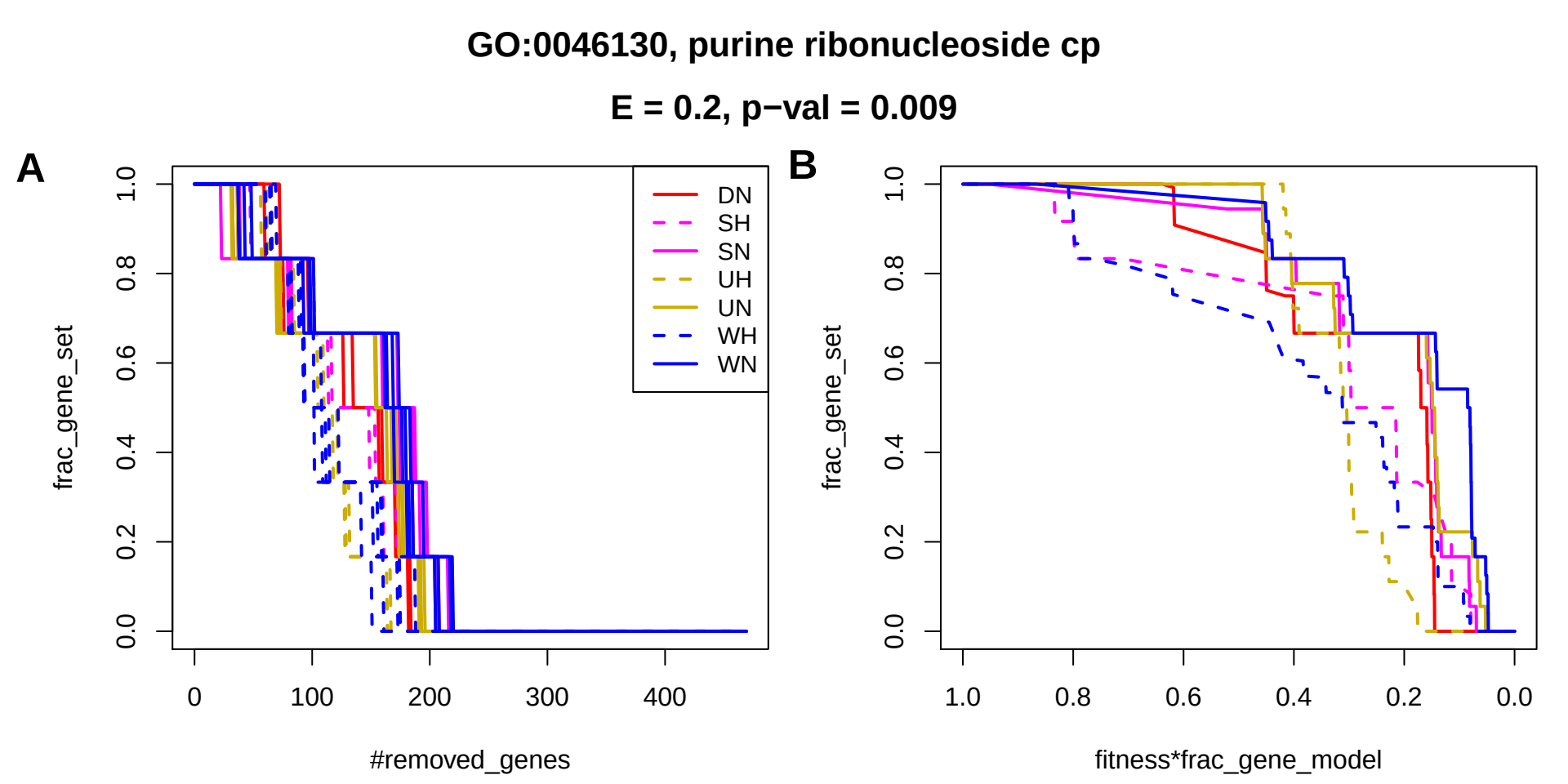
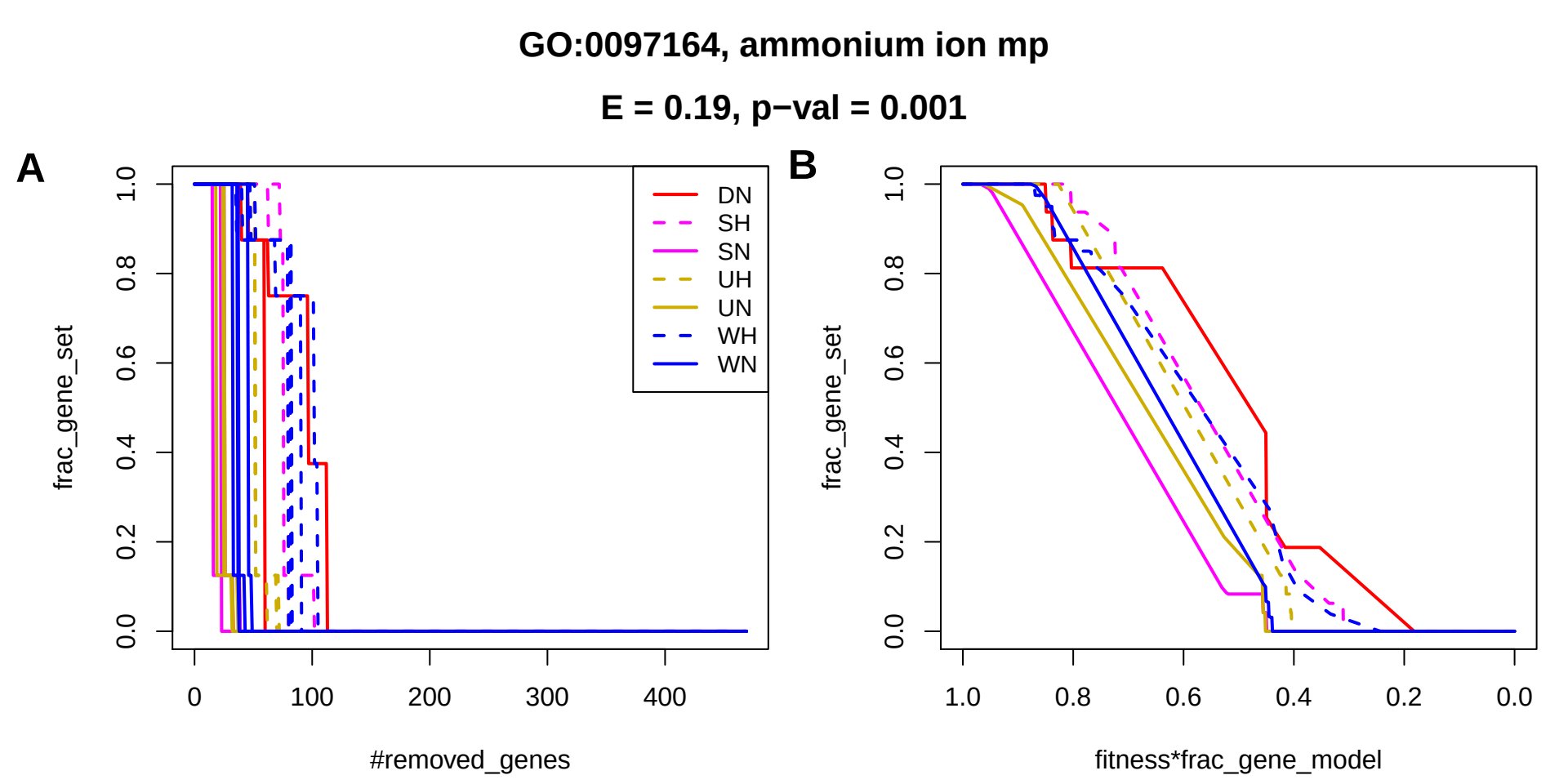
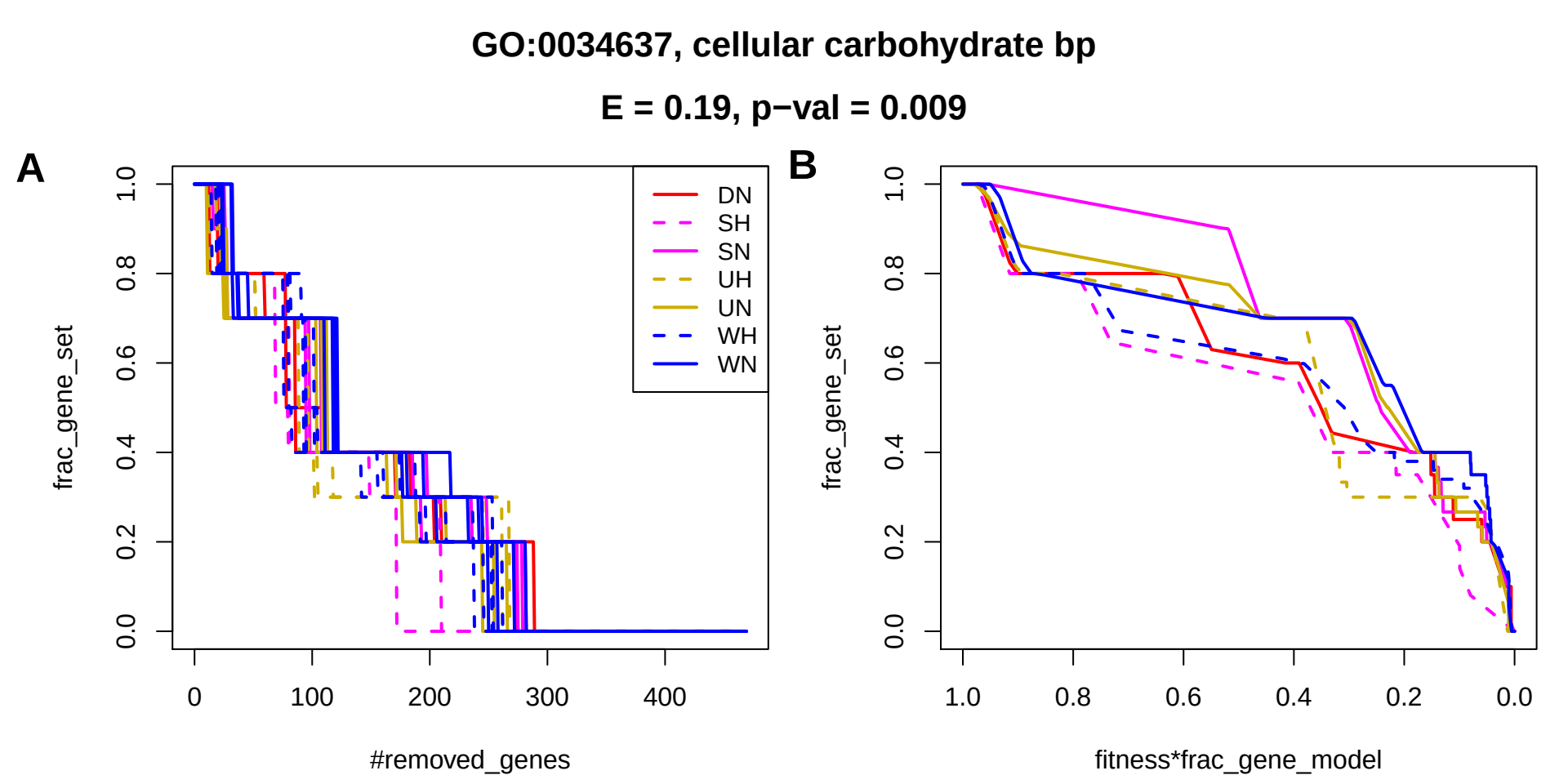
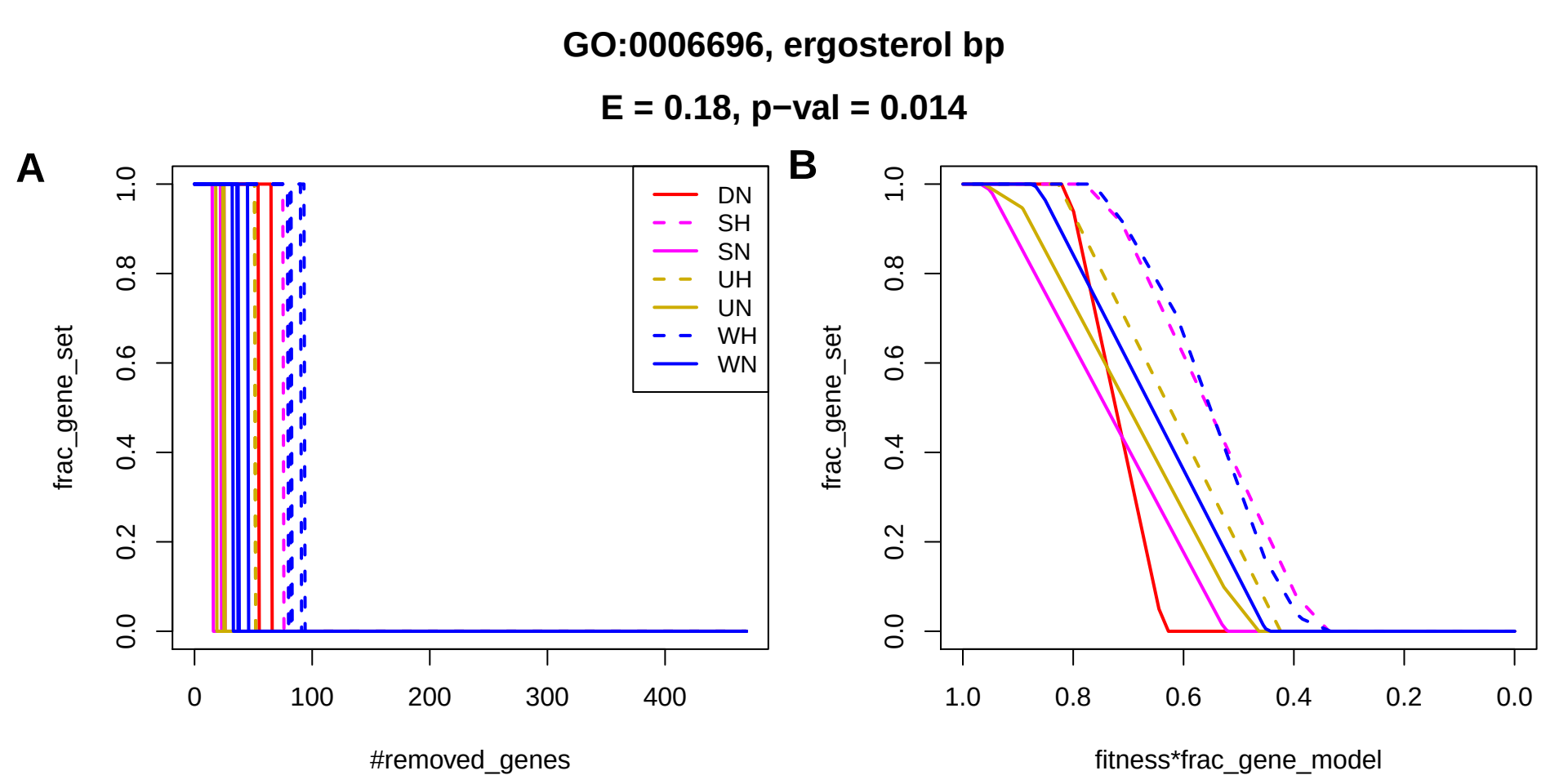
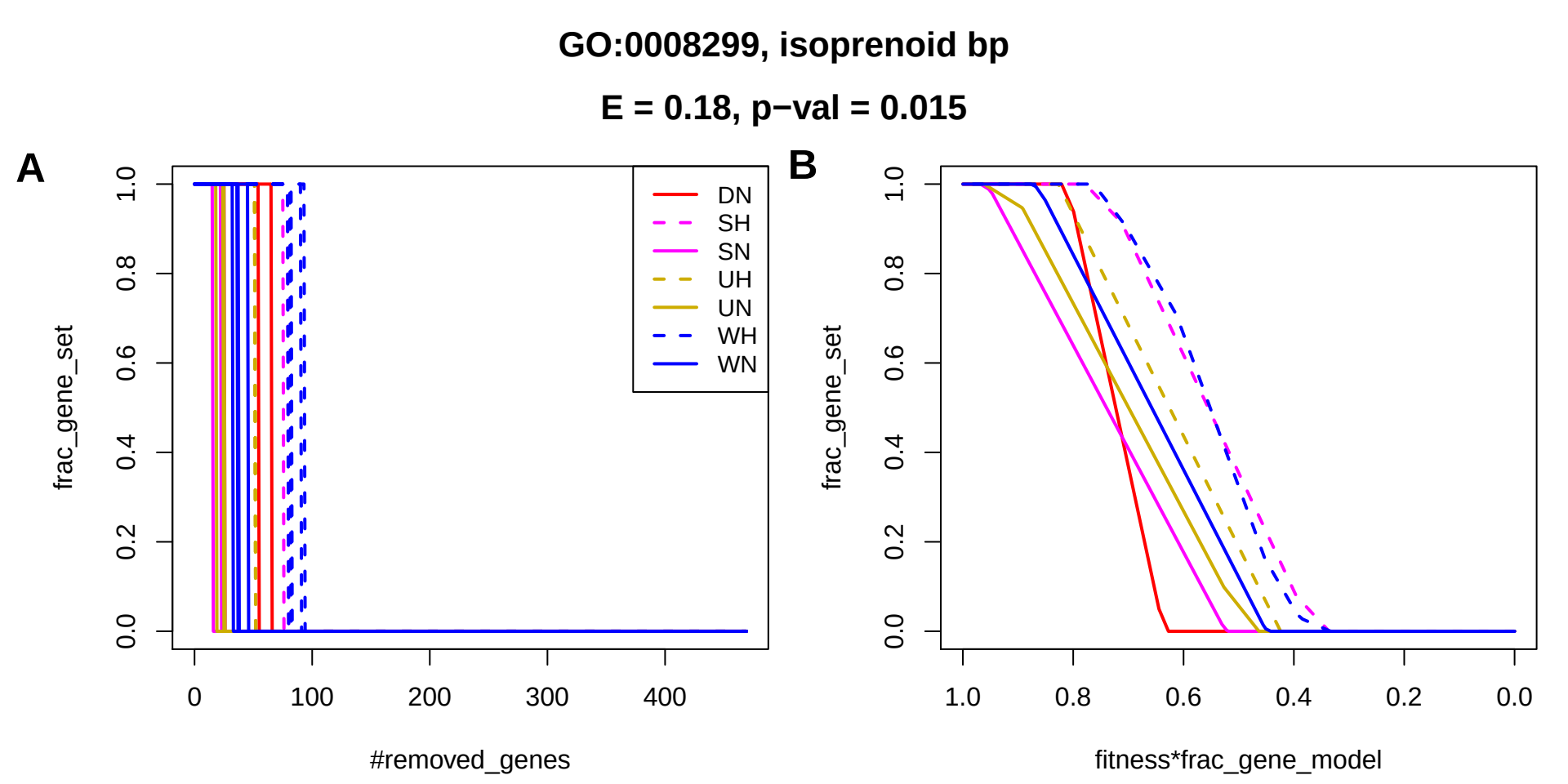
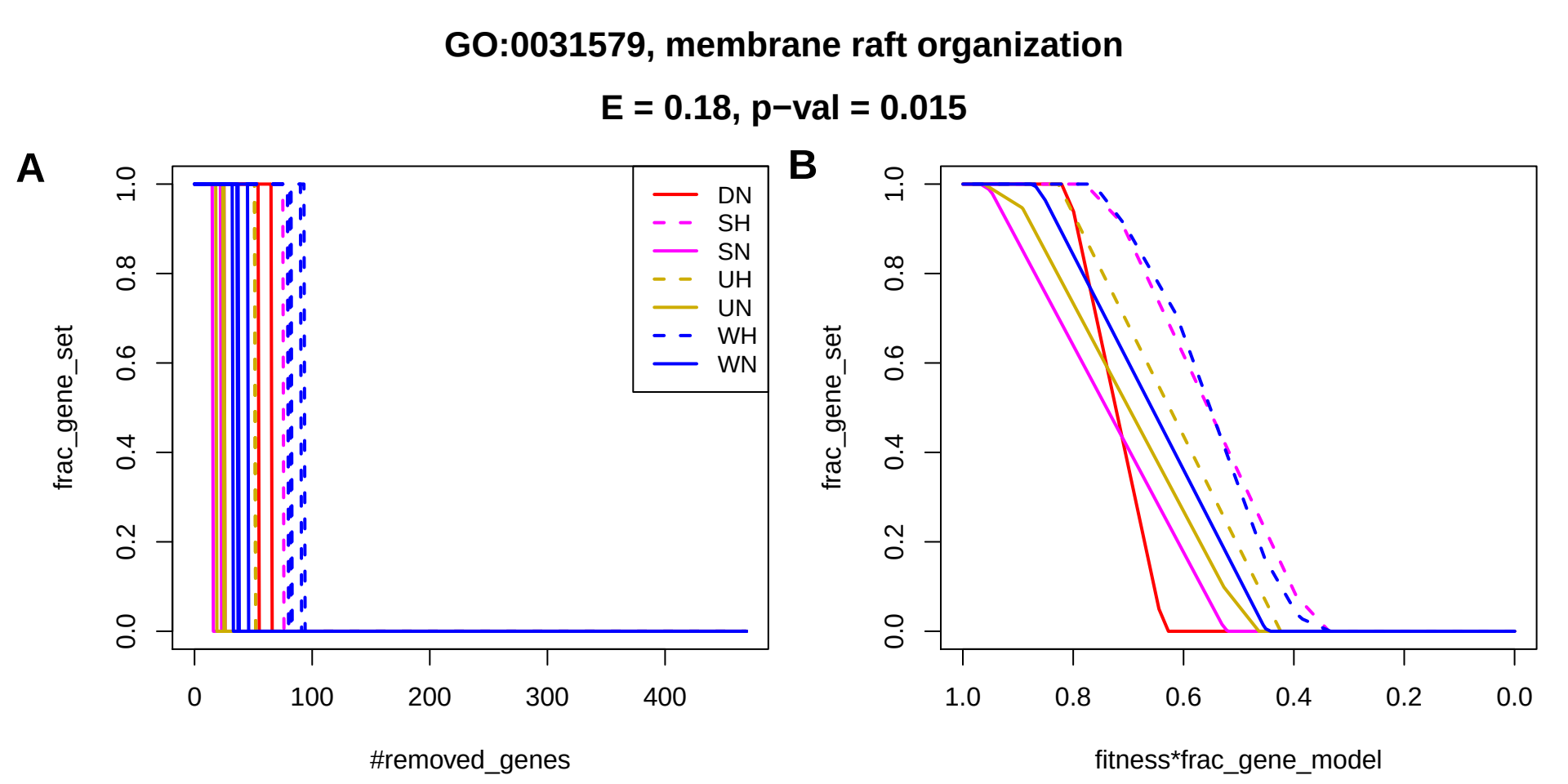

GO:0046130, purine ribonucleoside cp
E = 0.2, p−val = 0.009
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

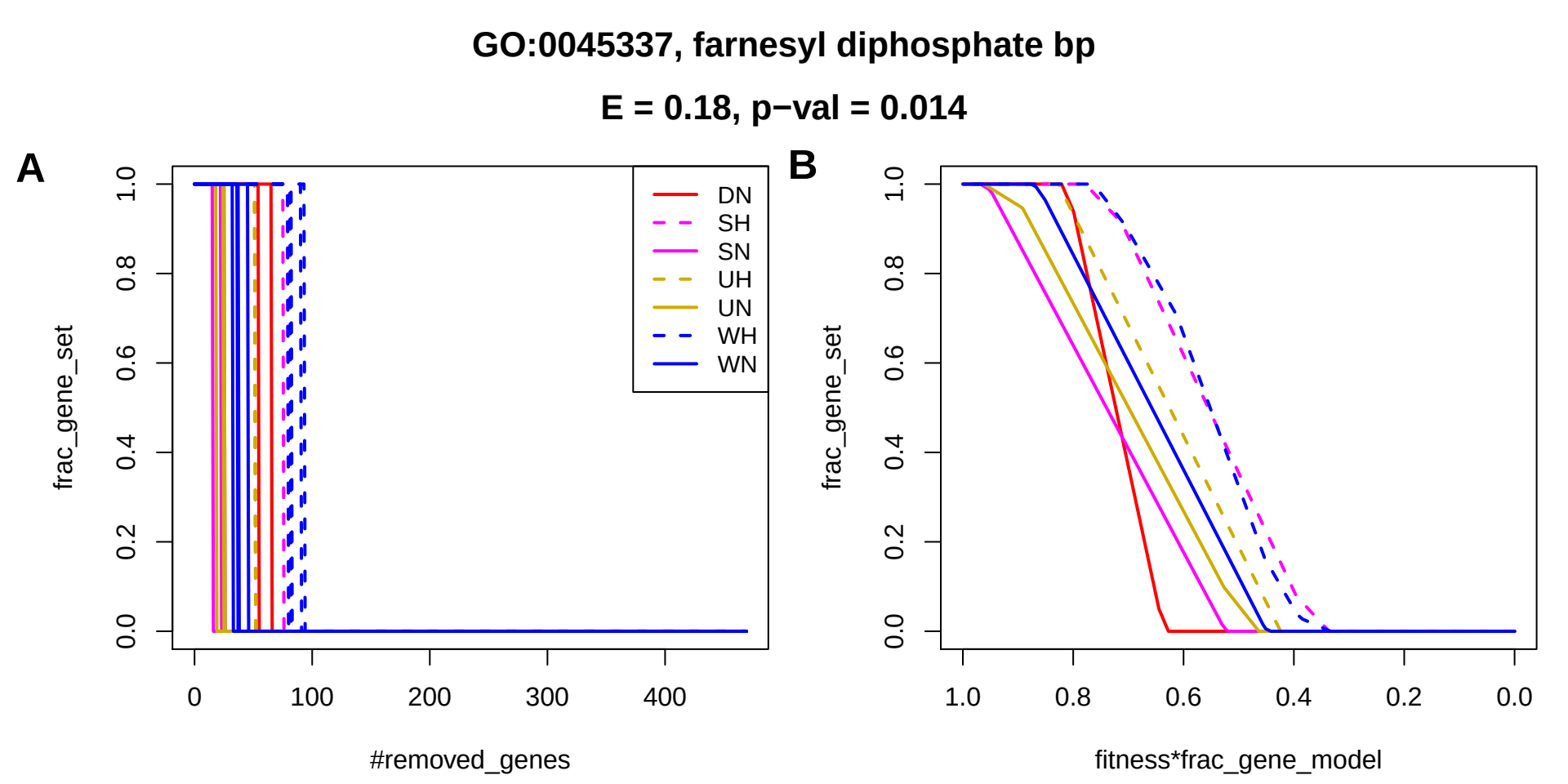

GO:0097164, ammonium ion mp
E = 0.19, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

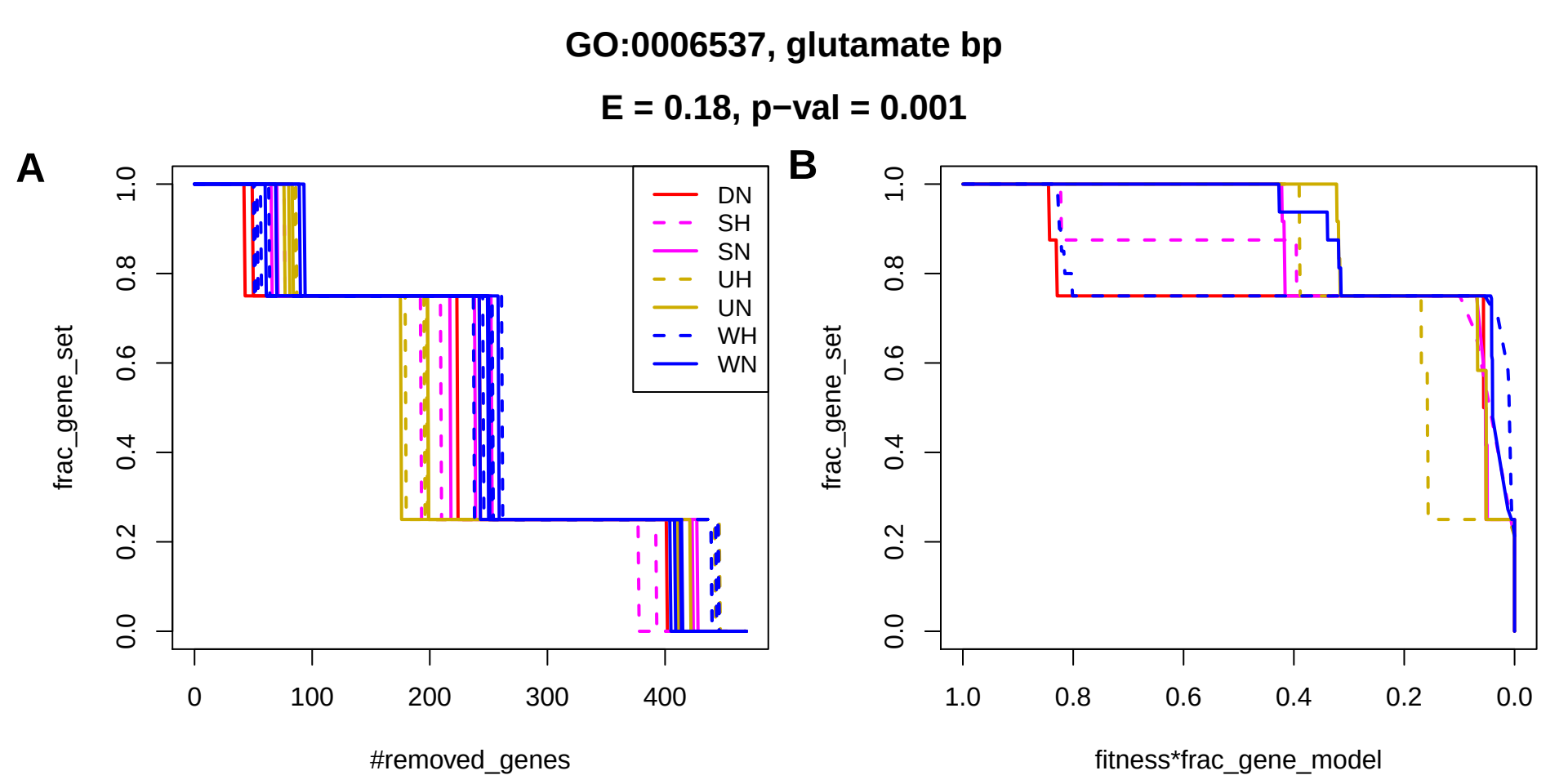

GO:0034637, cellular carbohydrate bp
E = 0.19, p−val = 0.009
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

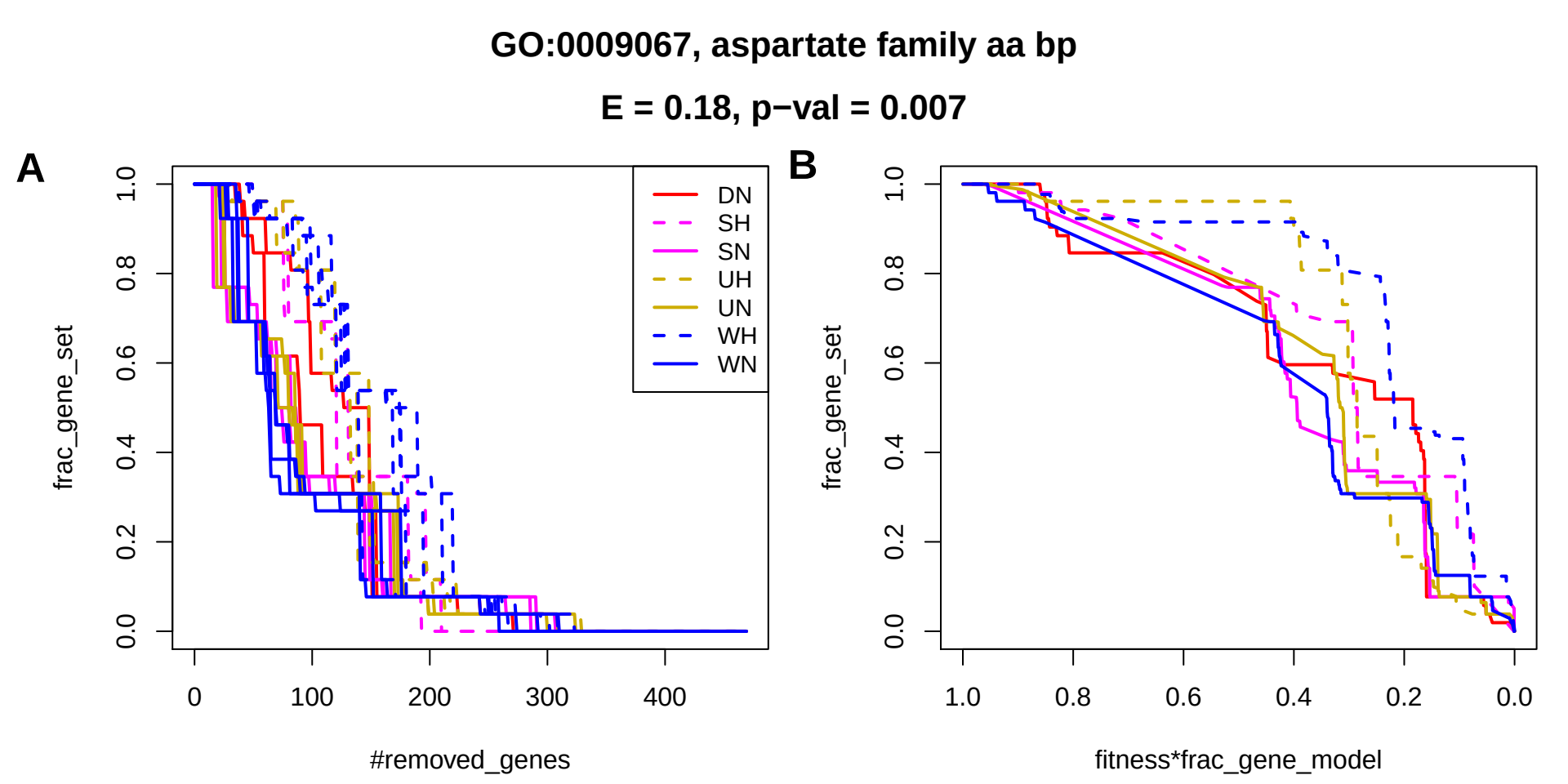

GO:0006696, ergosterol bp
E = 0.18, p−val = 0.014
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

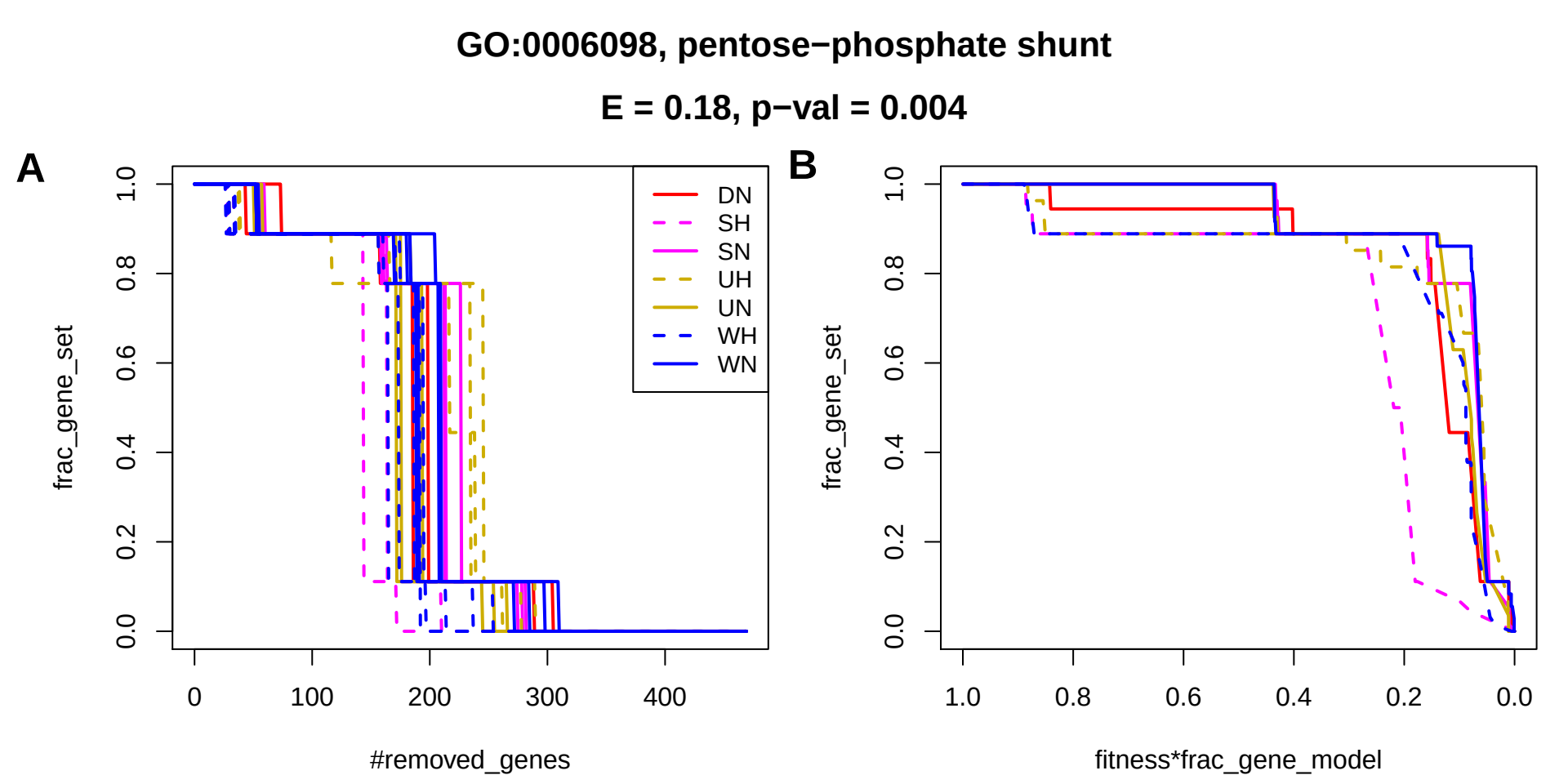

GO:0008299, isoprenoid bp
E = 0.18, p−val = 0.015
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

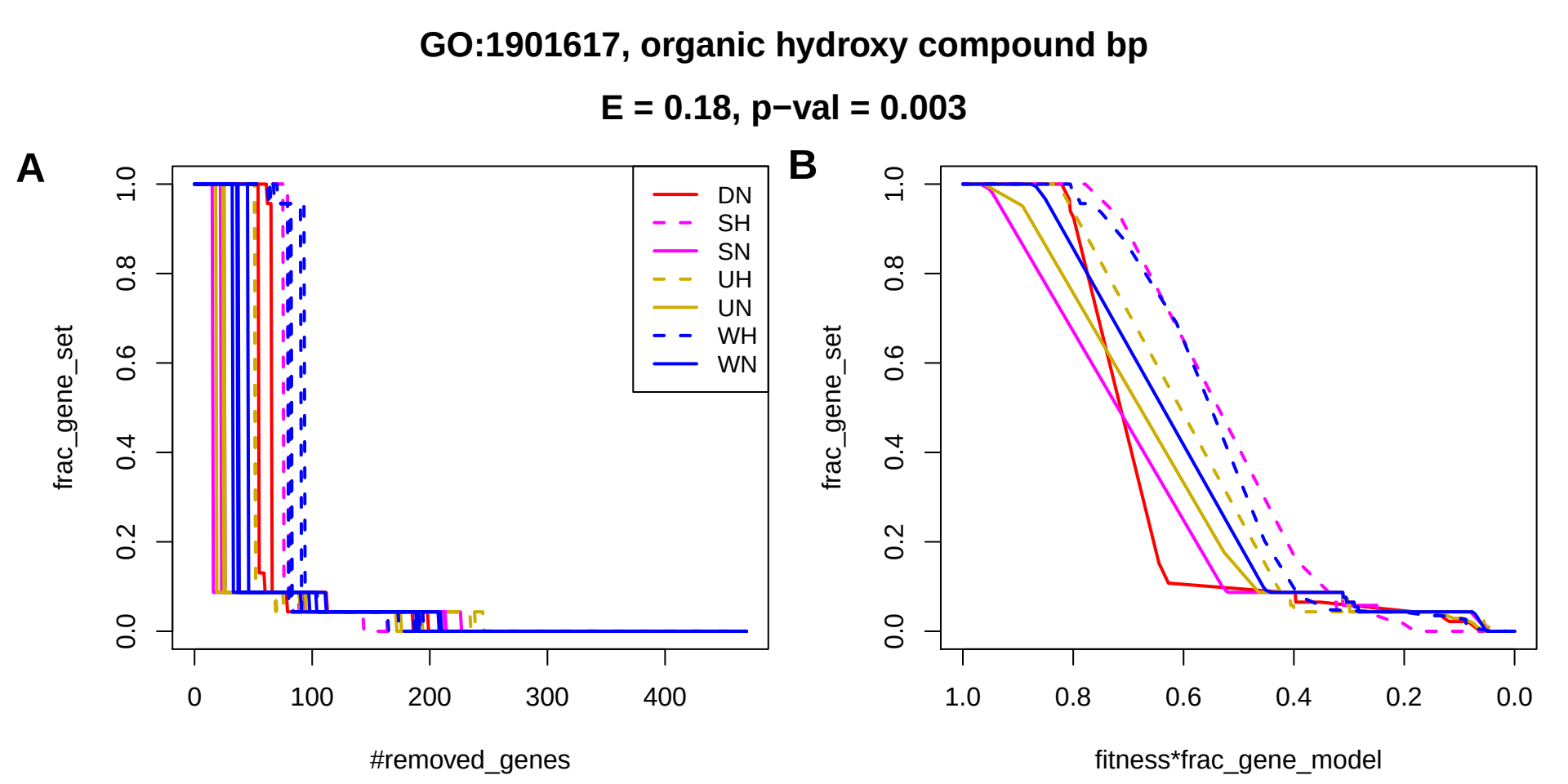

GO:0031579, membrane raft organization
E = 0.18, p−val = 0.015
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0045337, farnesyl diphosphate bp
E = 0.18, p−val = 0.014
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006537, glutamate bp
E = 0.18, p−val = 0.001
A
B
DN
SH
SN
UH
UN
WH
WN
frac_gene_set
#removed_genes
fitness*frac_gene_model
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009067, aspartate family aa bp
E = 0.18, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006098, pentose−phosphate shunt
E = 0.18, p−val = 0.004
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:1901617, organic hydroxy compound bp
E = 0.18, p−val = 0.003
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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300
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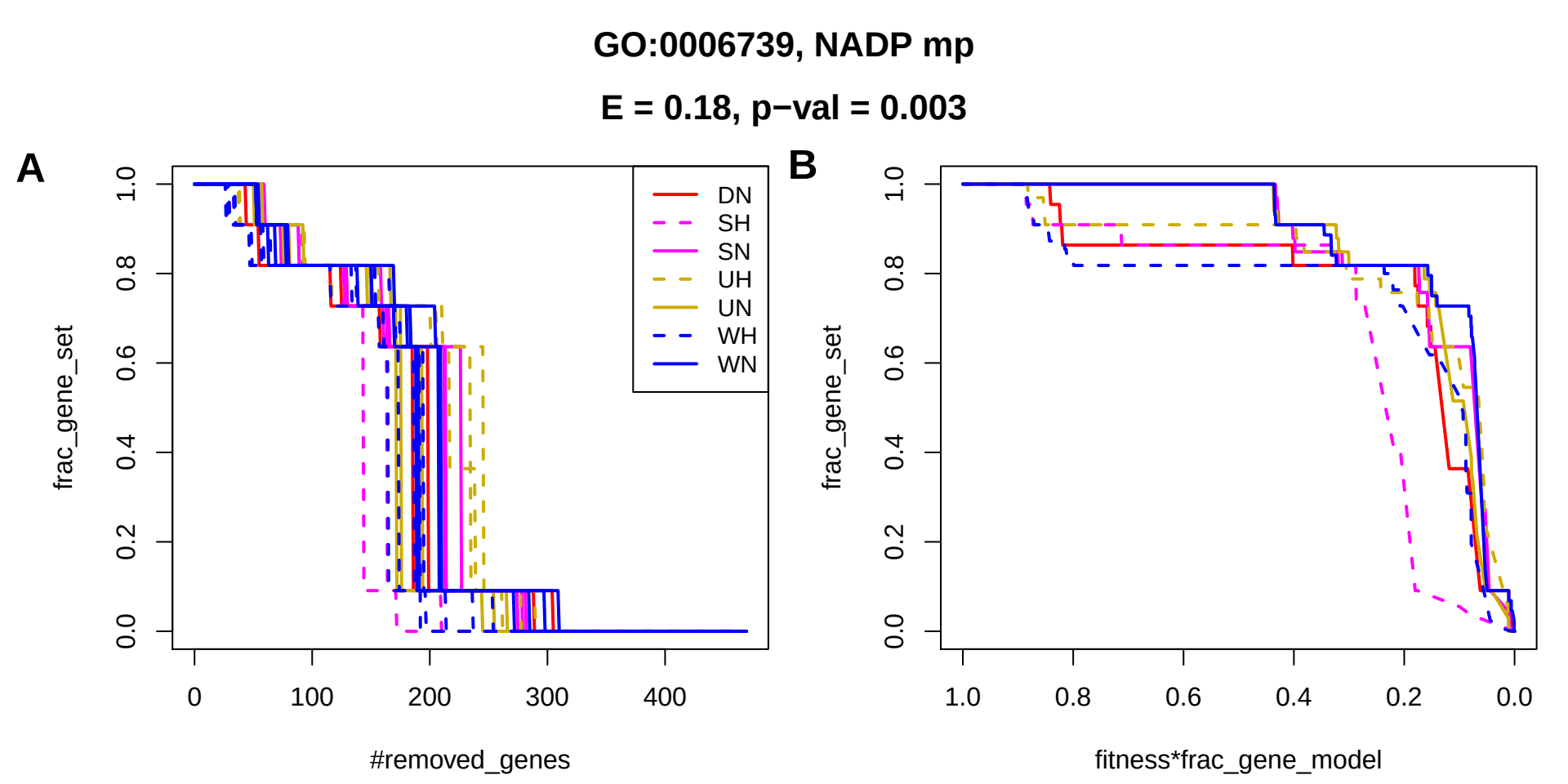
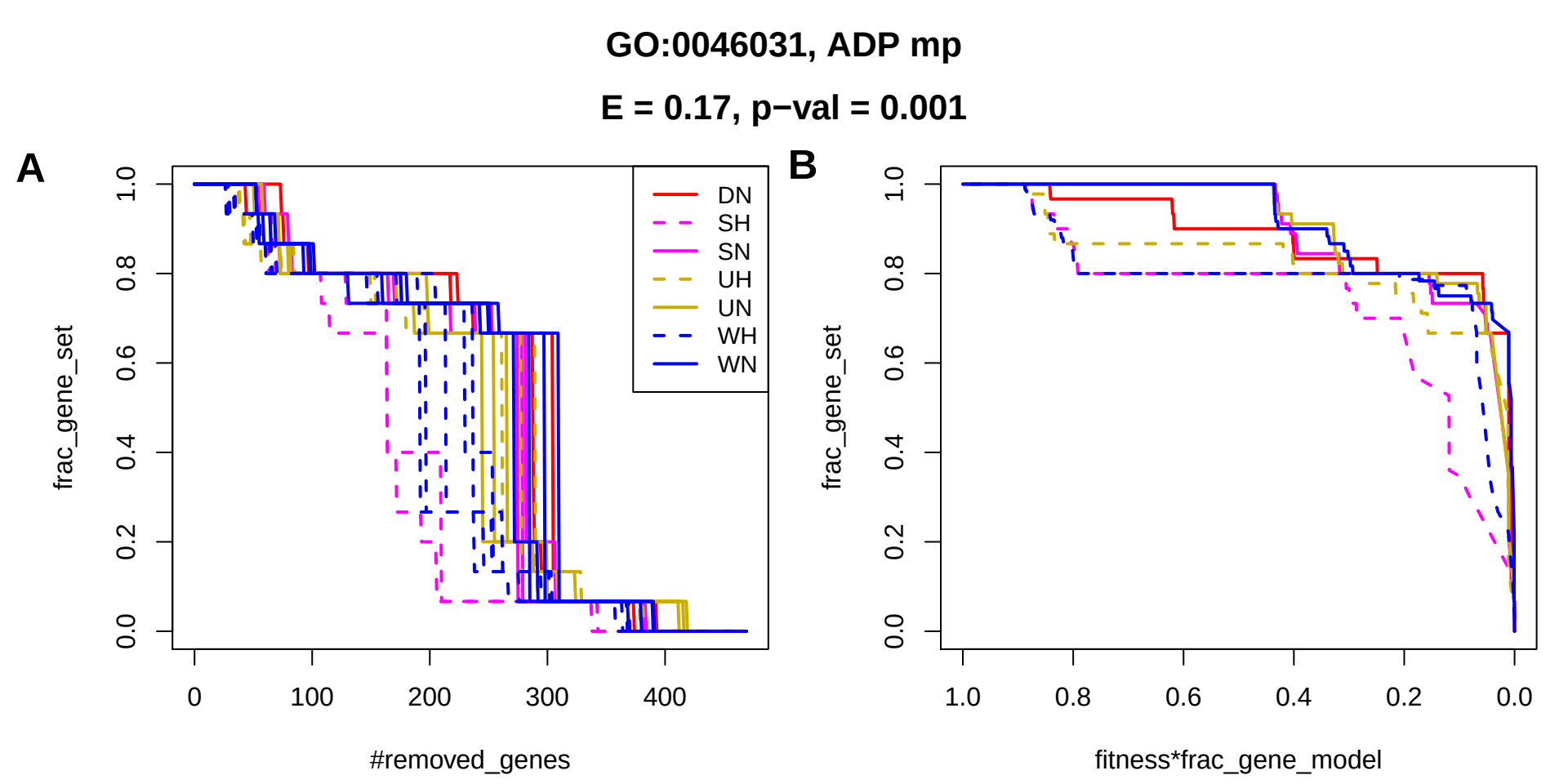
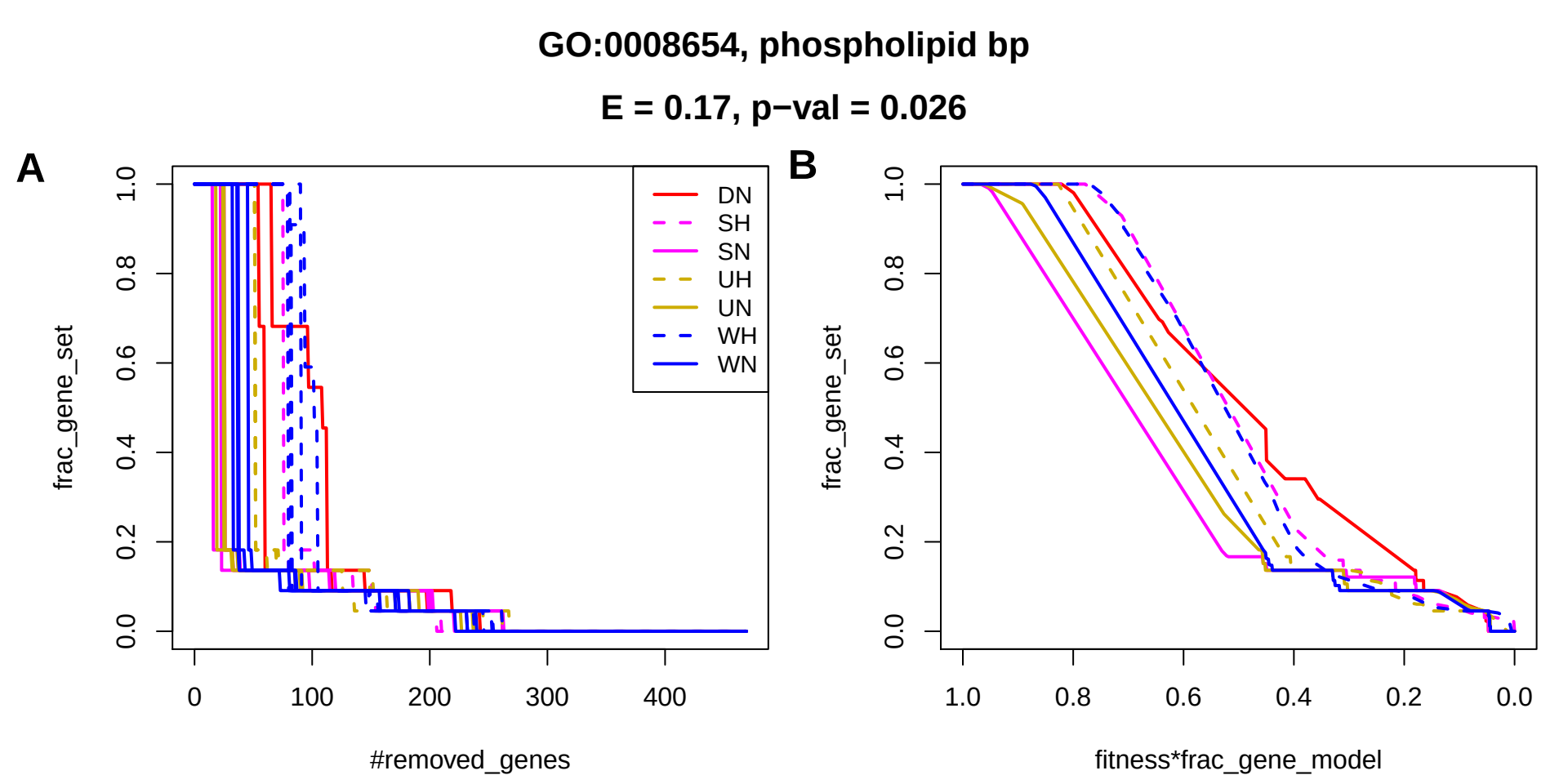
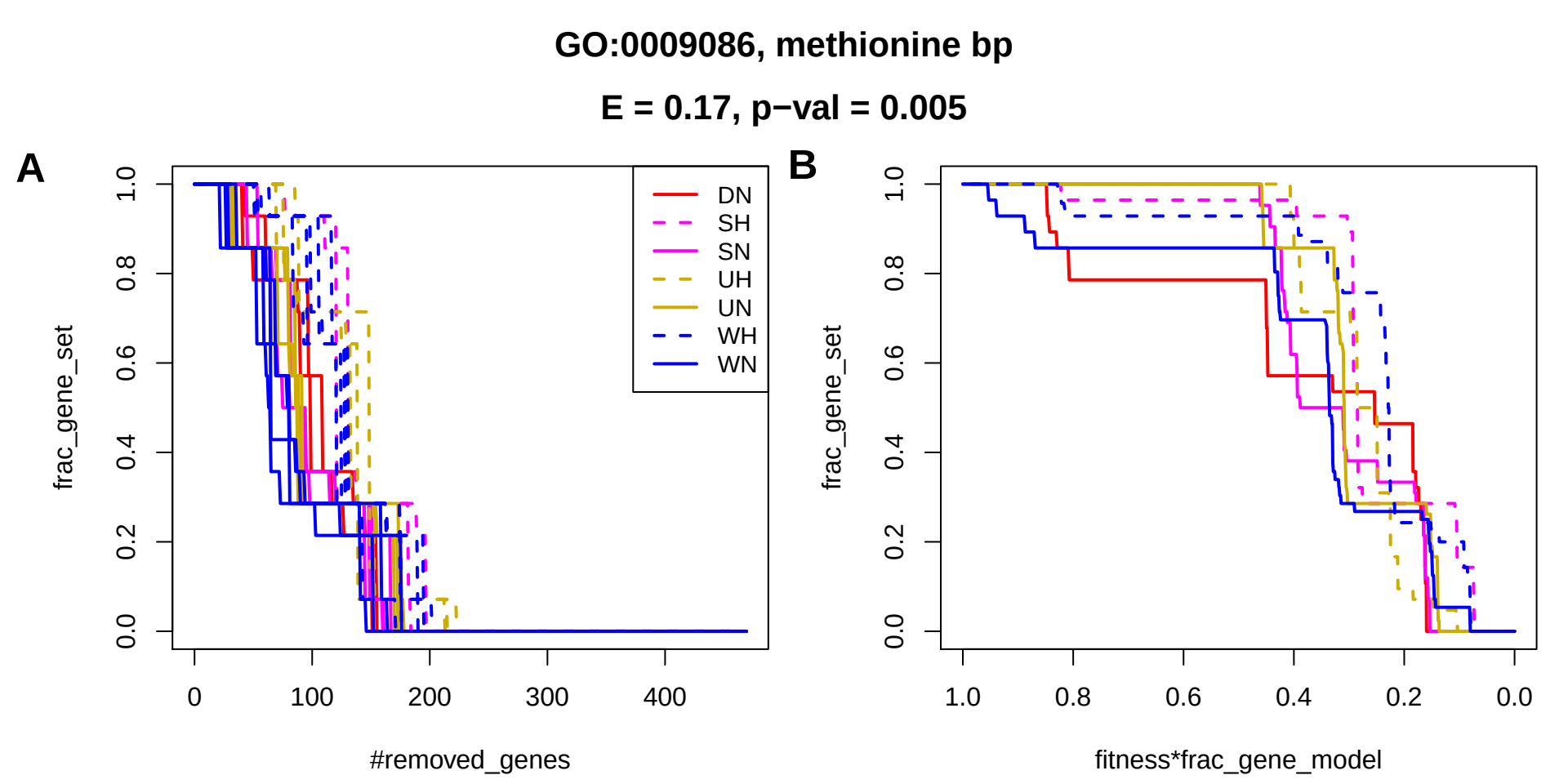

GO:0006739, NADP mp
E = 0.18, p−val = 0.003
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0046031, ADP mp
E = 0.17, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0008654, phospholipid bp
E = 0.17, p−val = 0.026
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009086, methionine bp
E = 0.17, p−val = 0.005
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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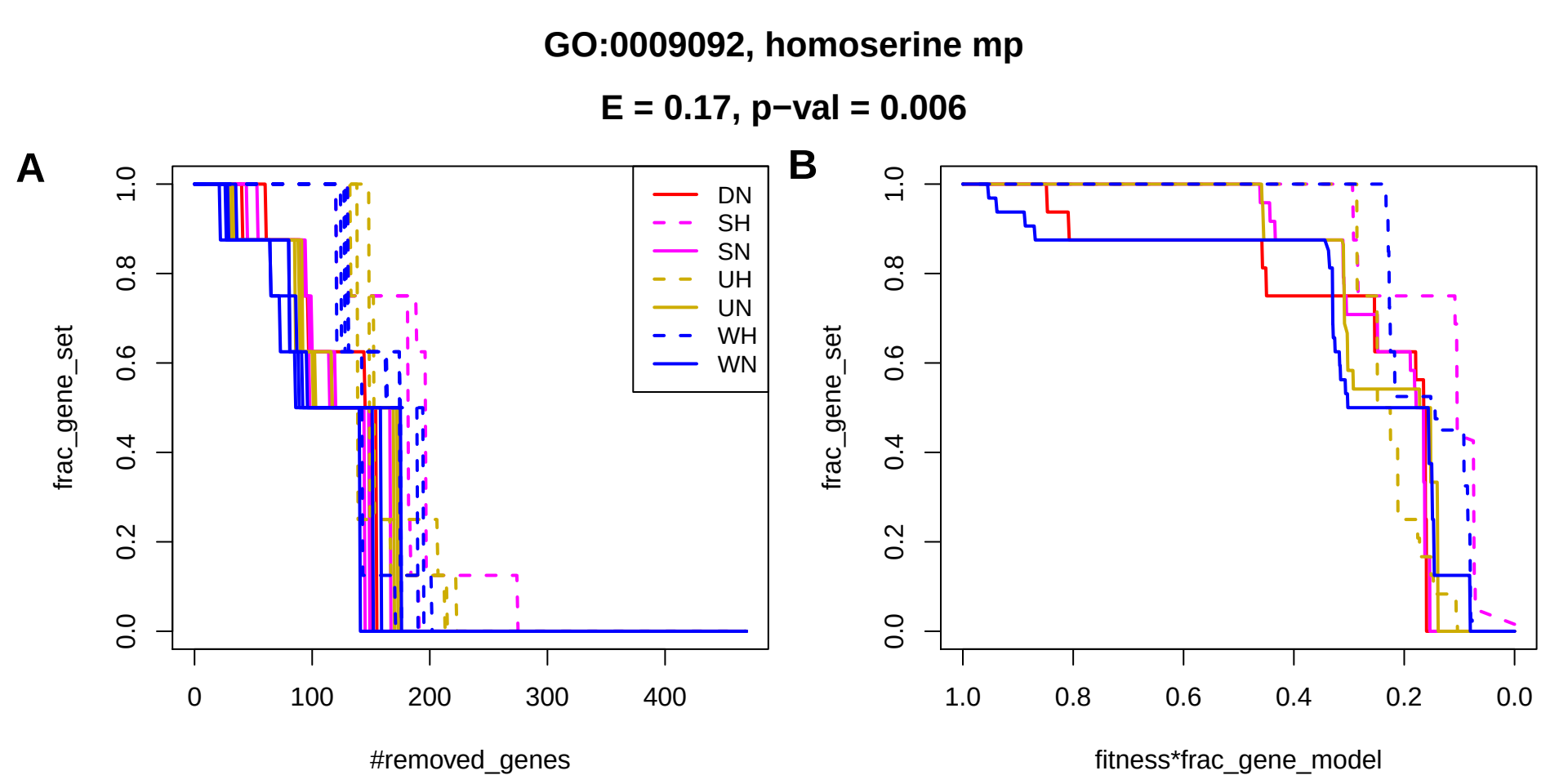
300
400


GO:0009092, homoserine mp
E = 0.17, p−val = 0.006
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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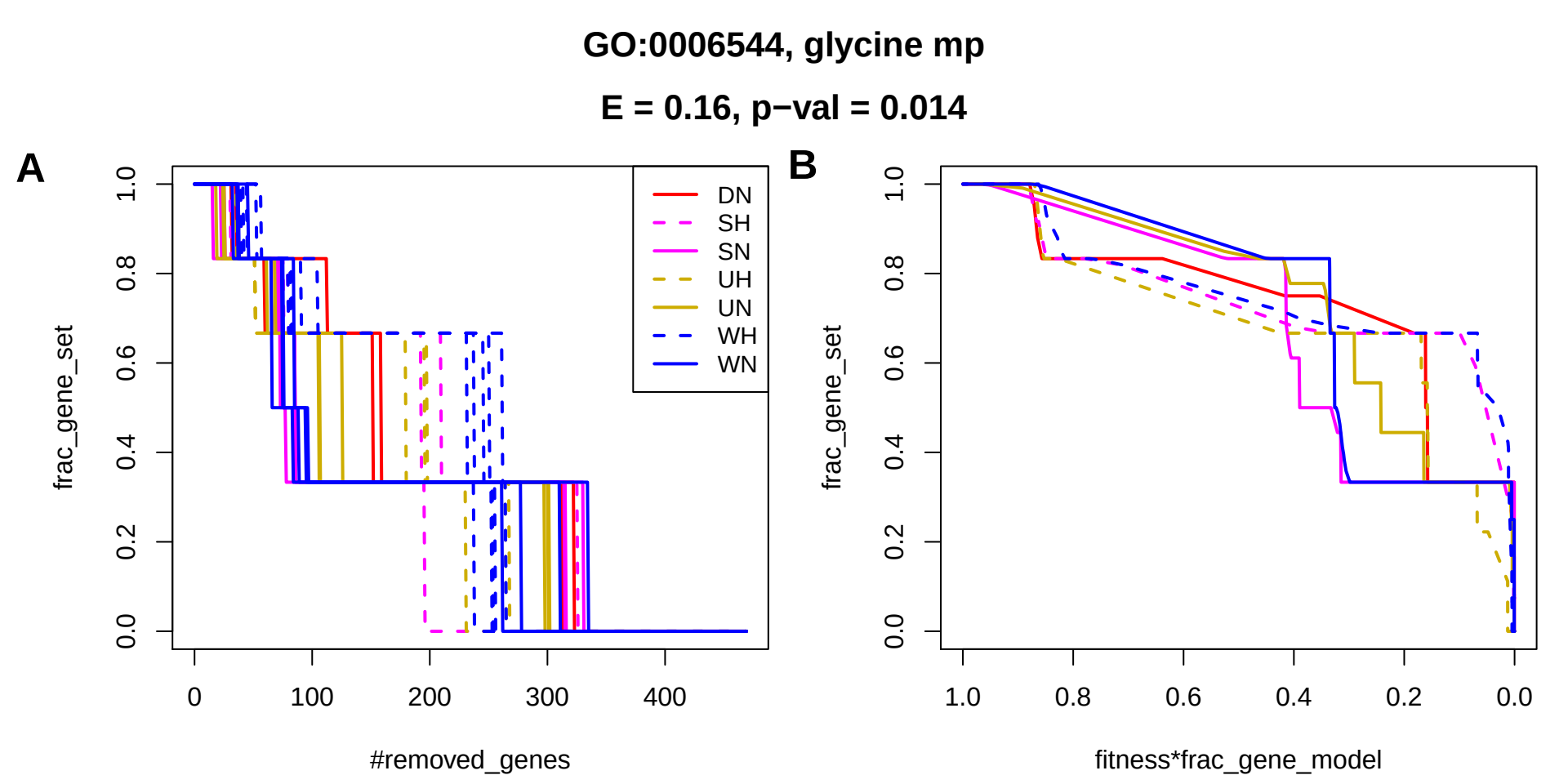
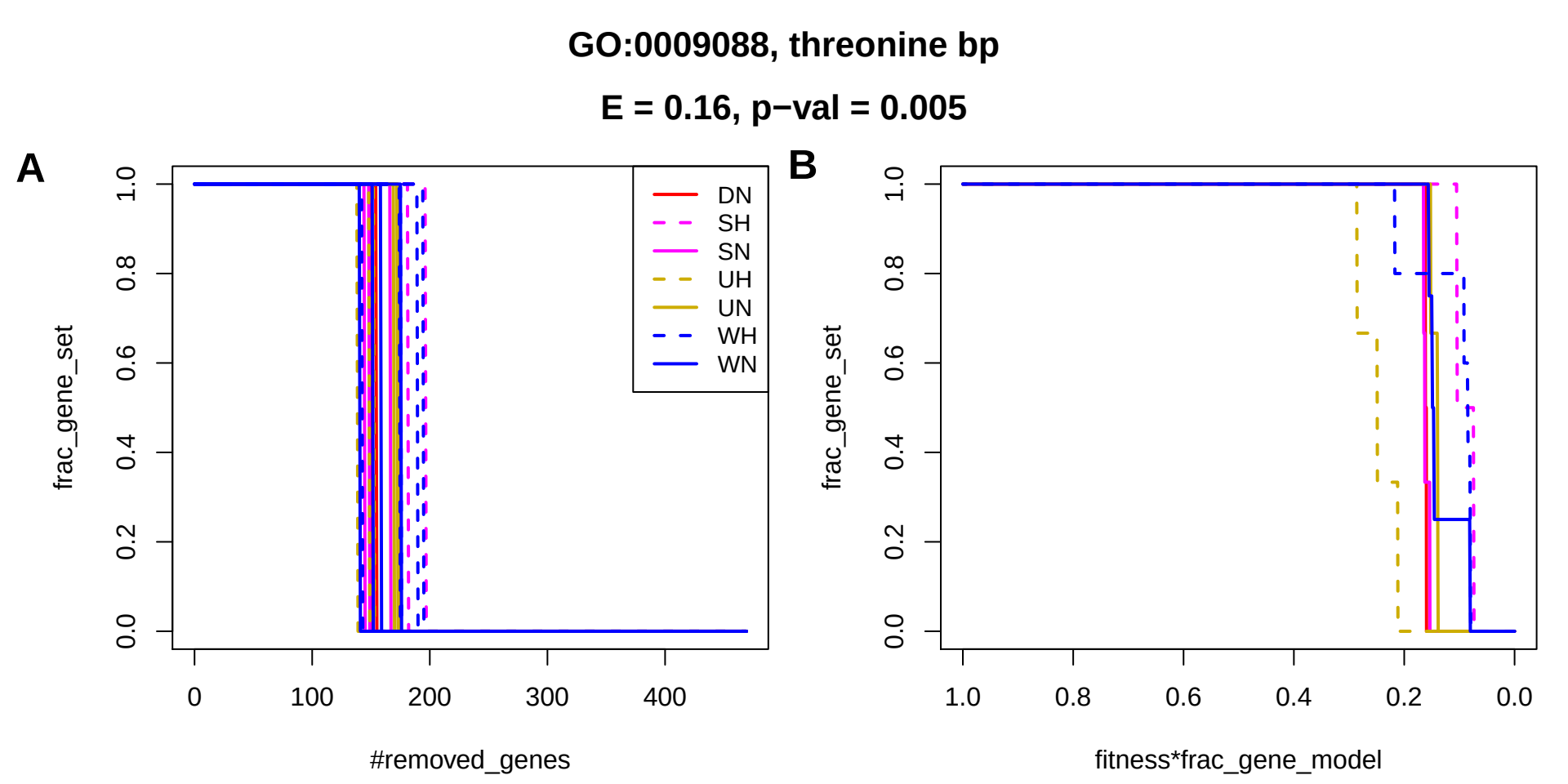
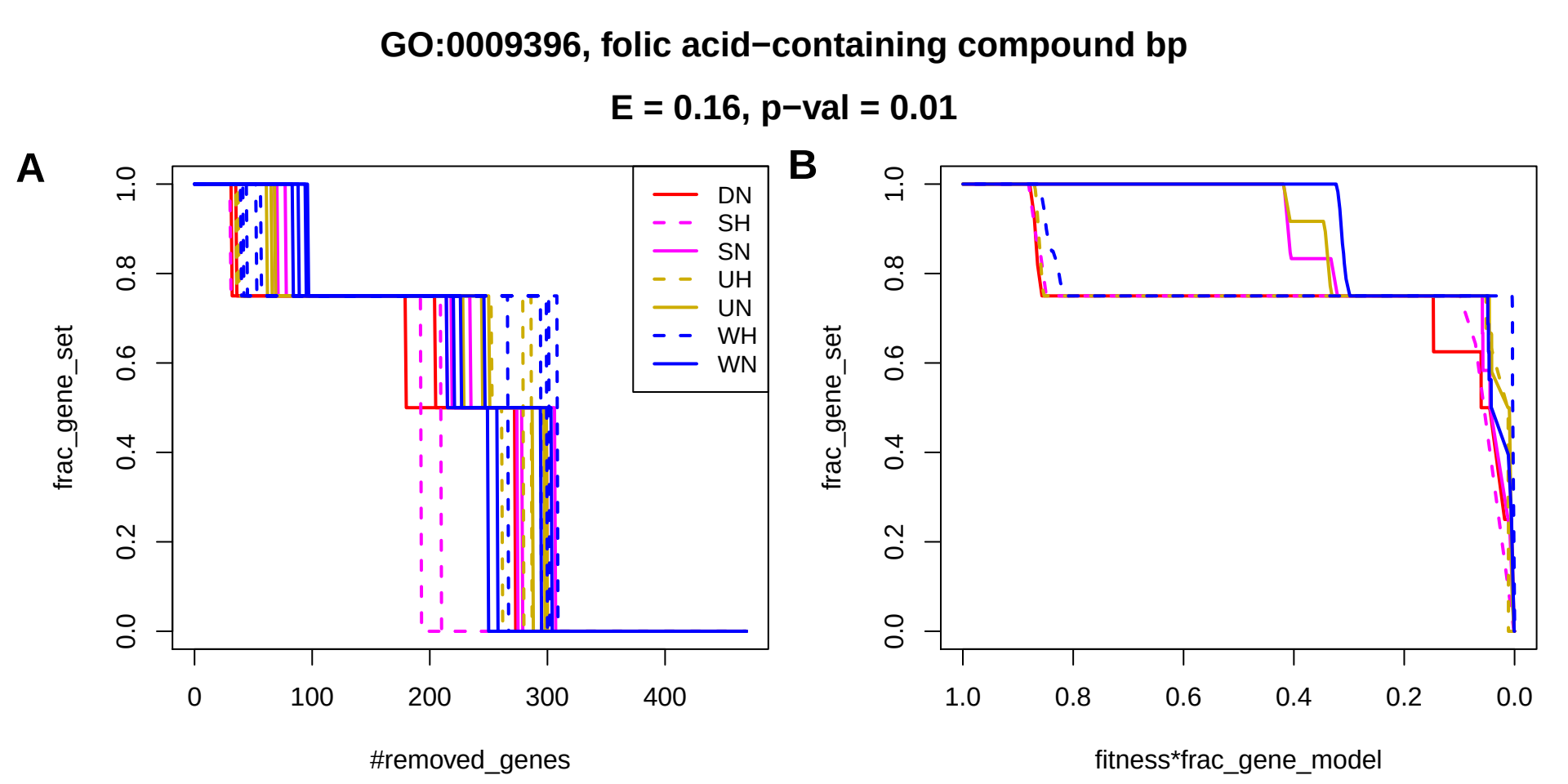
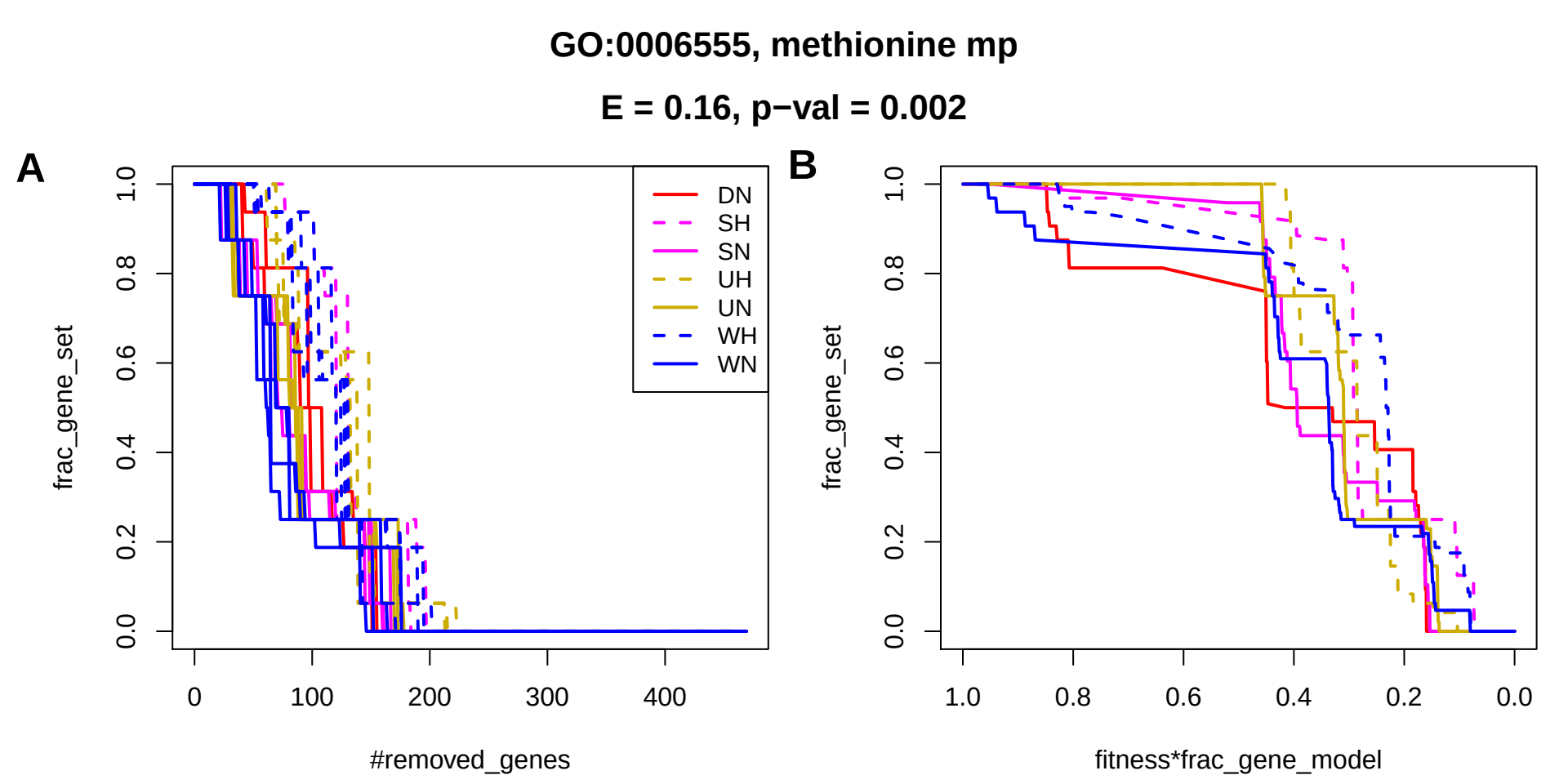
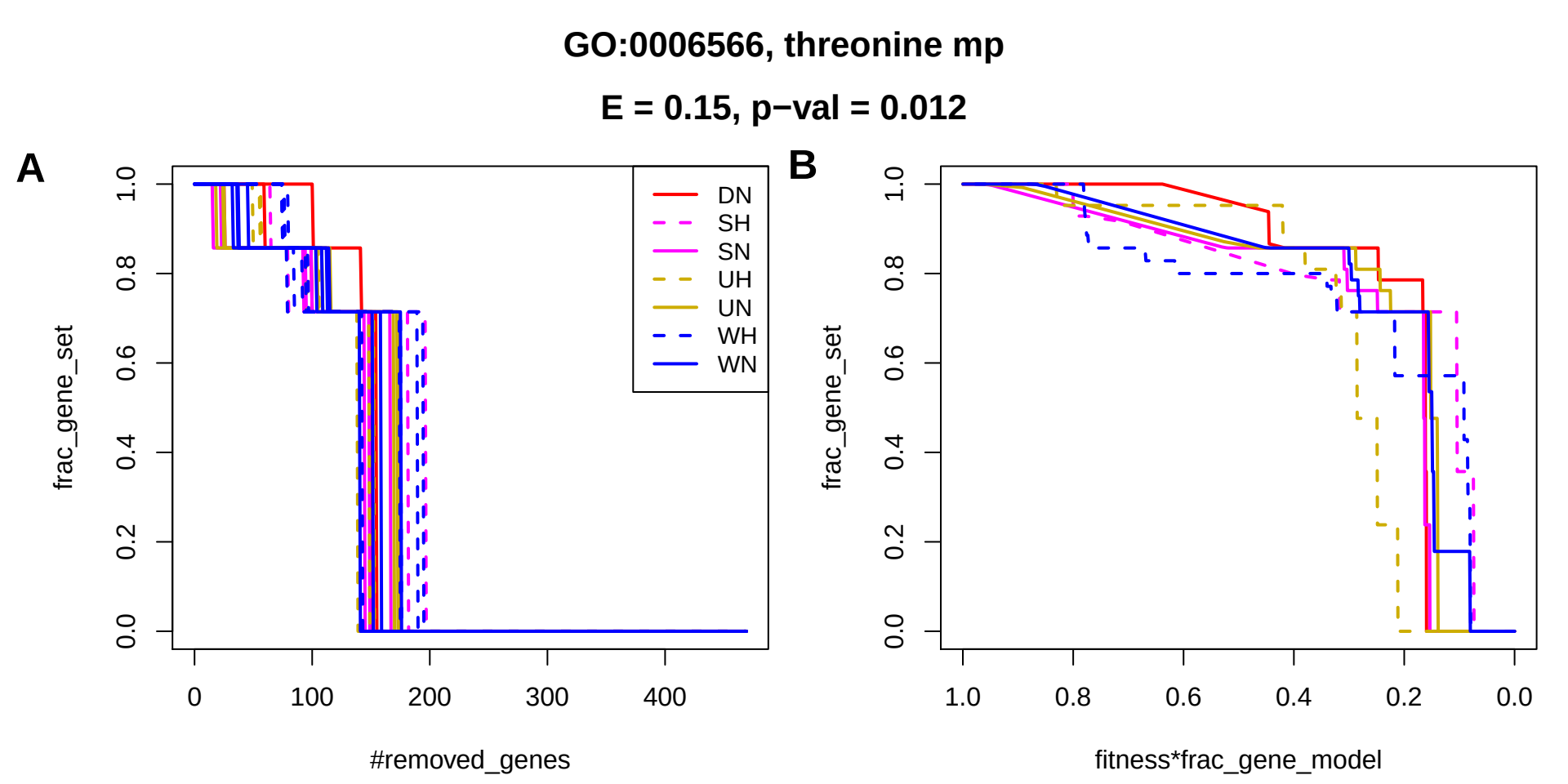
300
400

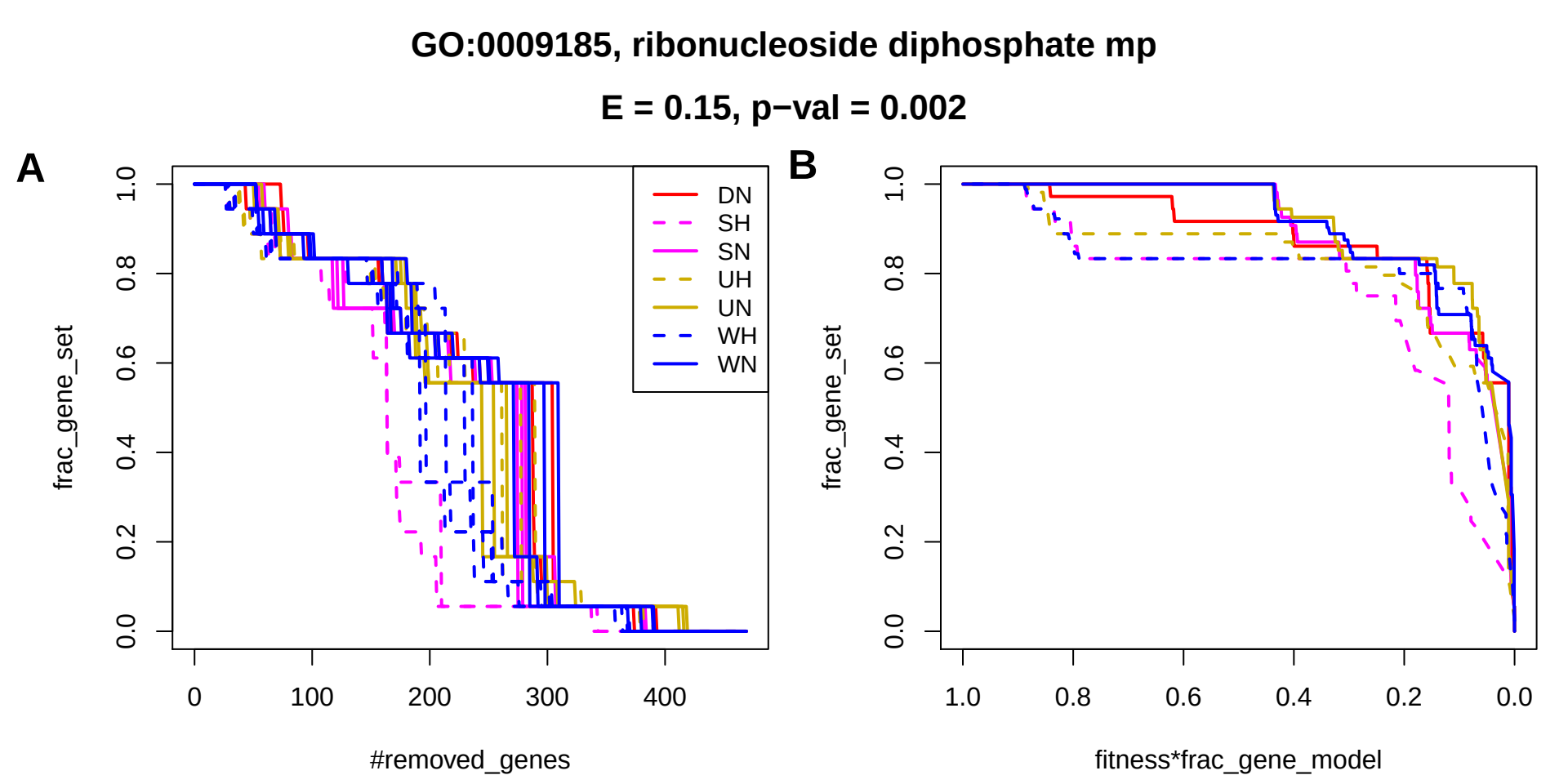

GO:0006544, glycine mp
E = 0.16, p−val = 0.014
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

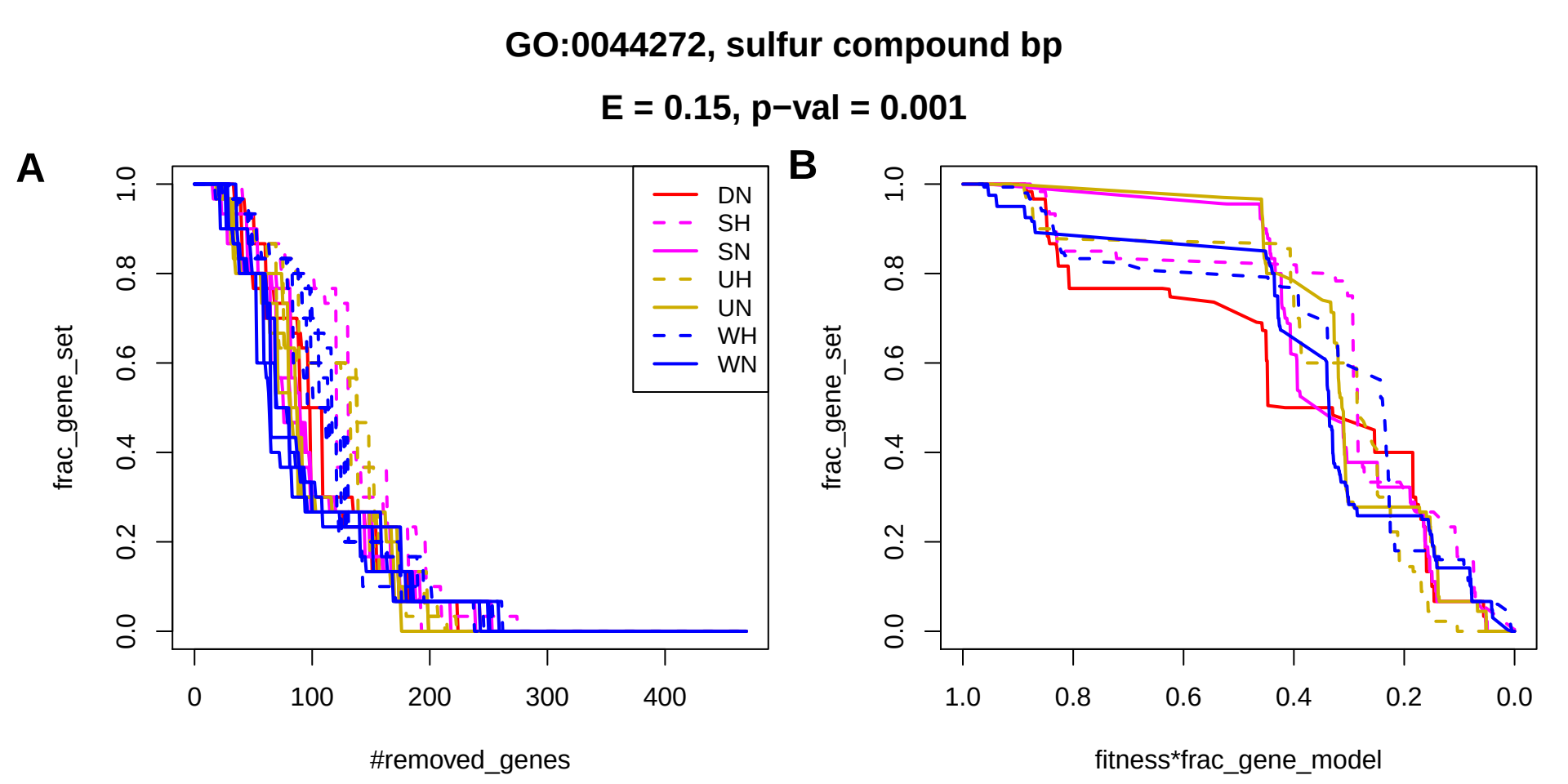

GO:0009088, threonine bp
E = 0.16, p−val = 0.005
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

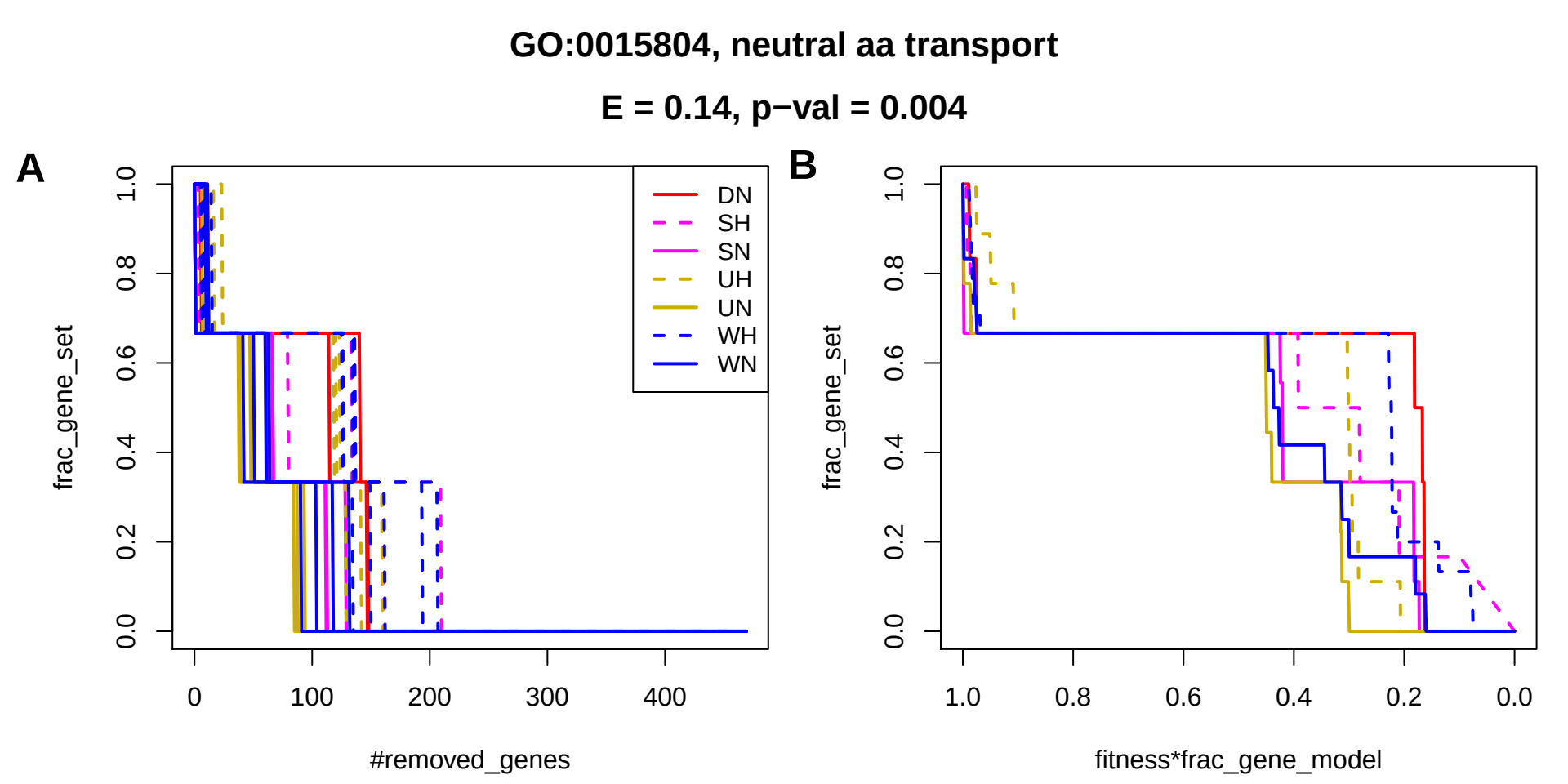

GO:0009396, folic acid−containing compound bp
E = 0.16, p−val = 0.01
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

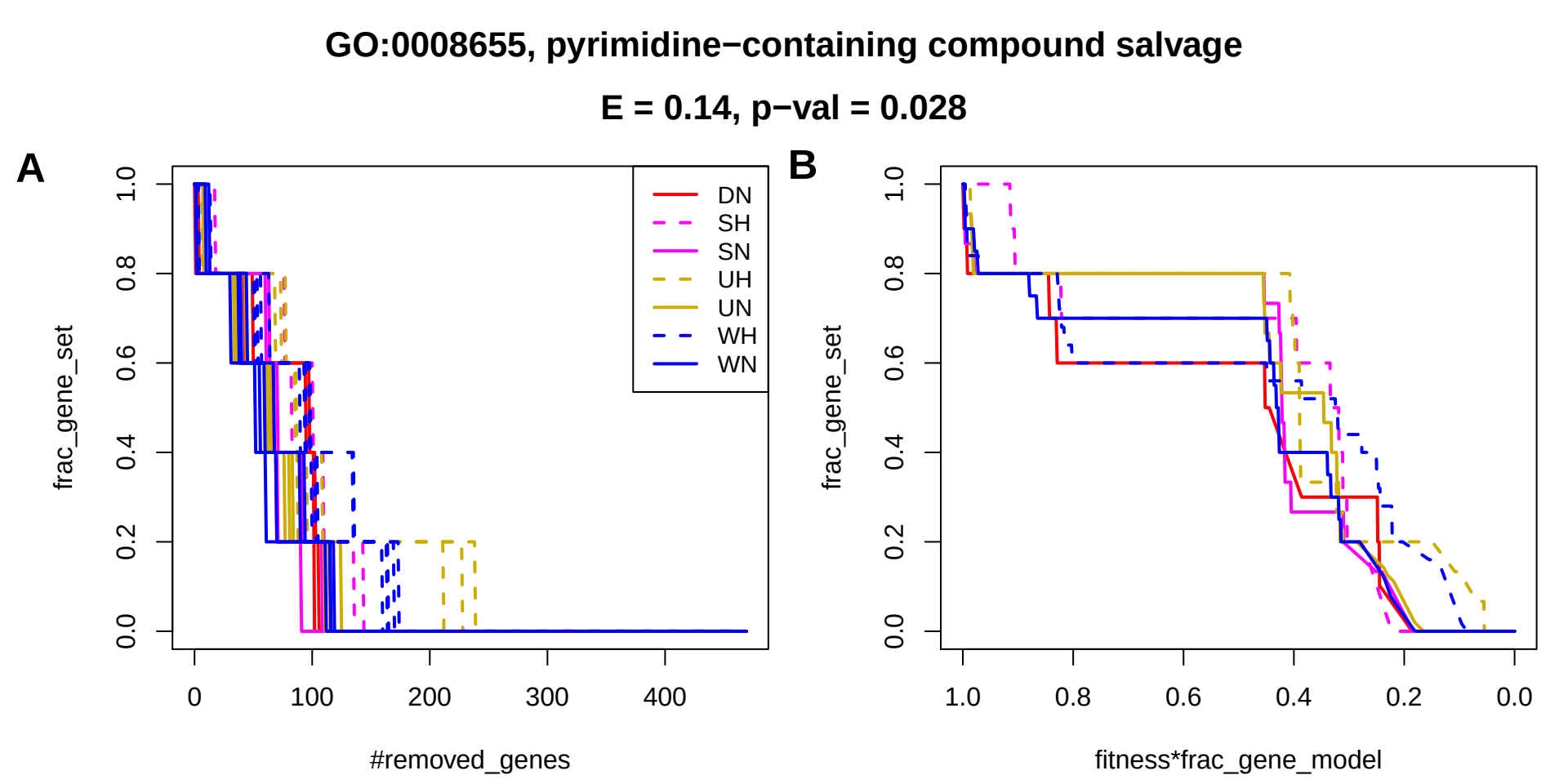

GO:0006555, methionine mp
E = 0.16, p−val = 0.002
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

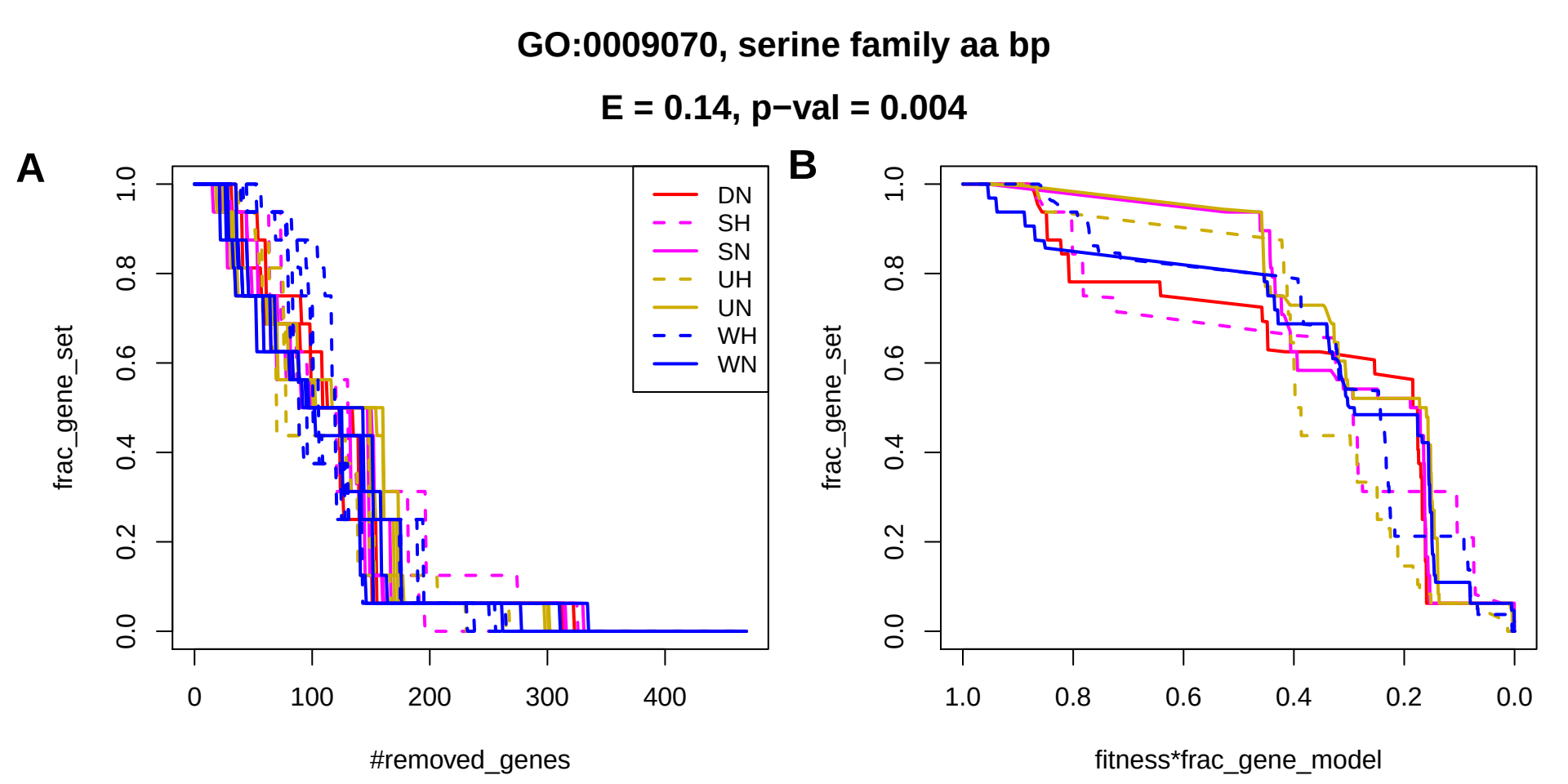

GO:0006566, threonine mp
E = 0.15, p−val = 0.012
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

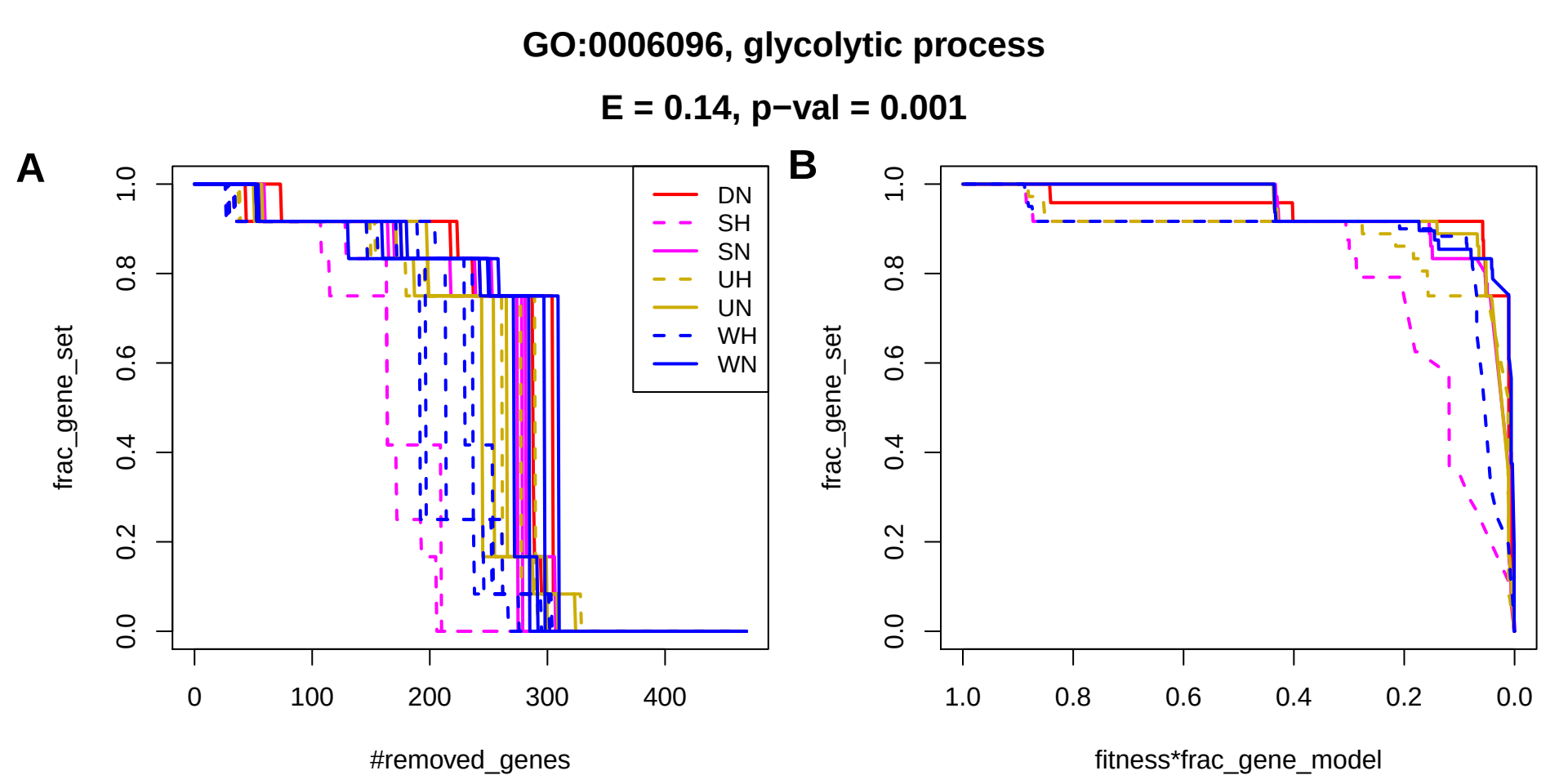

GO:0009185, ribonucleoside diphosphate mp
E = 0.15, p−val = 0.002
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

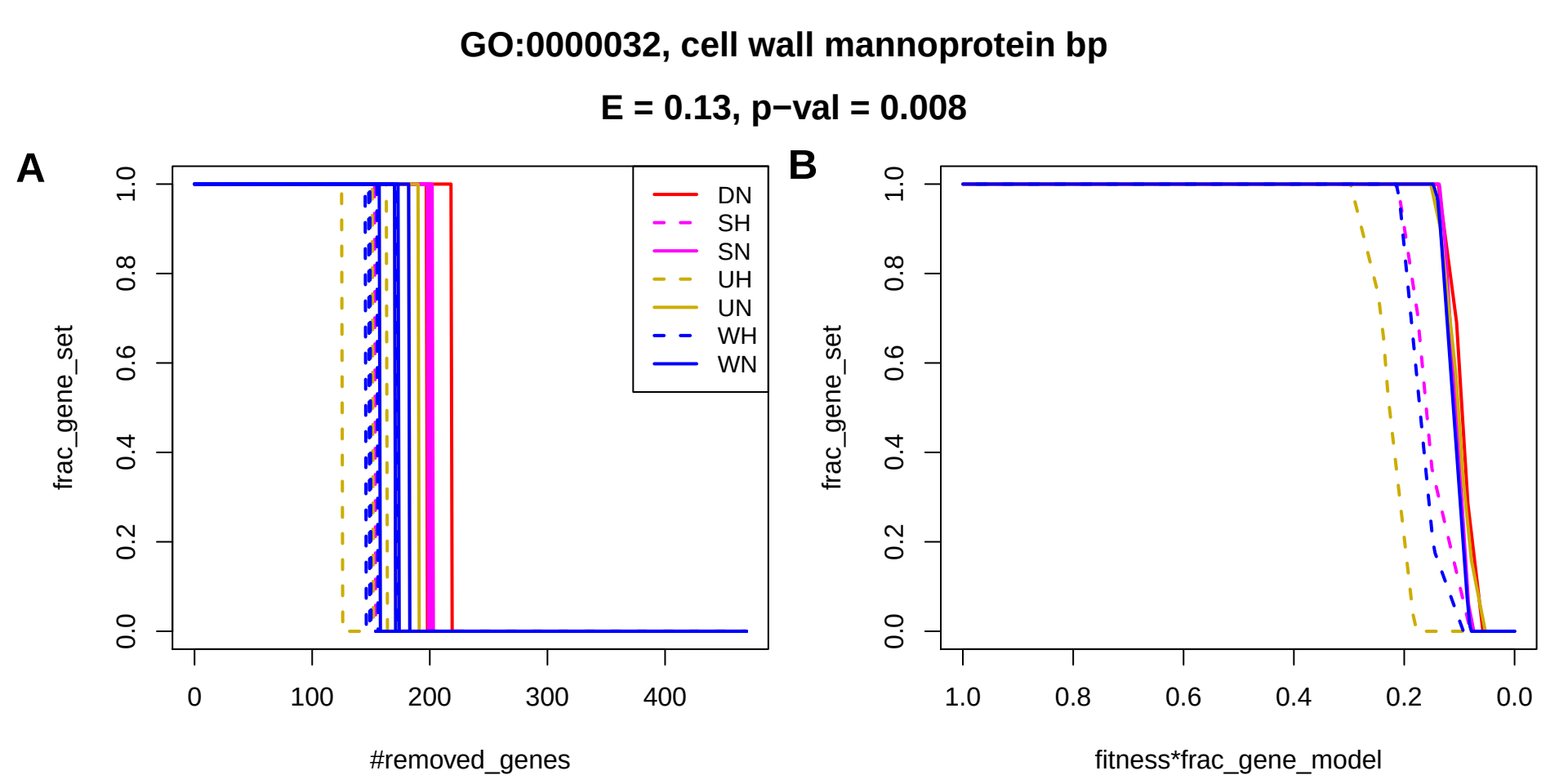

GO:0044272, sulfur compound bp
E = 0.15, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

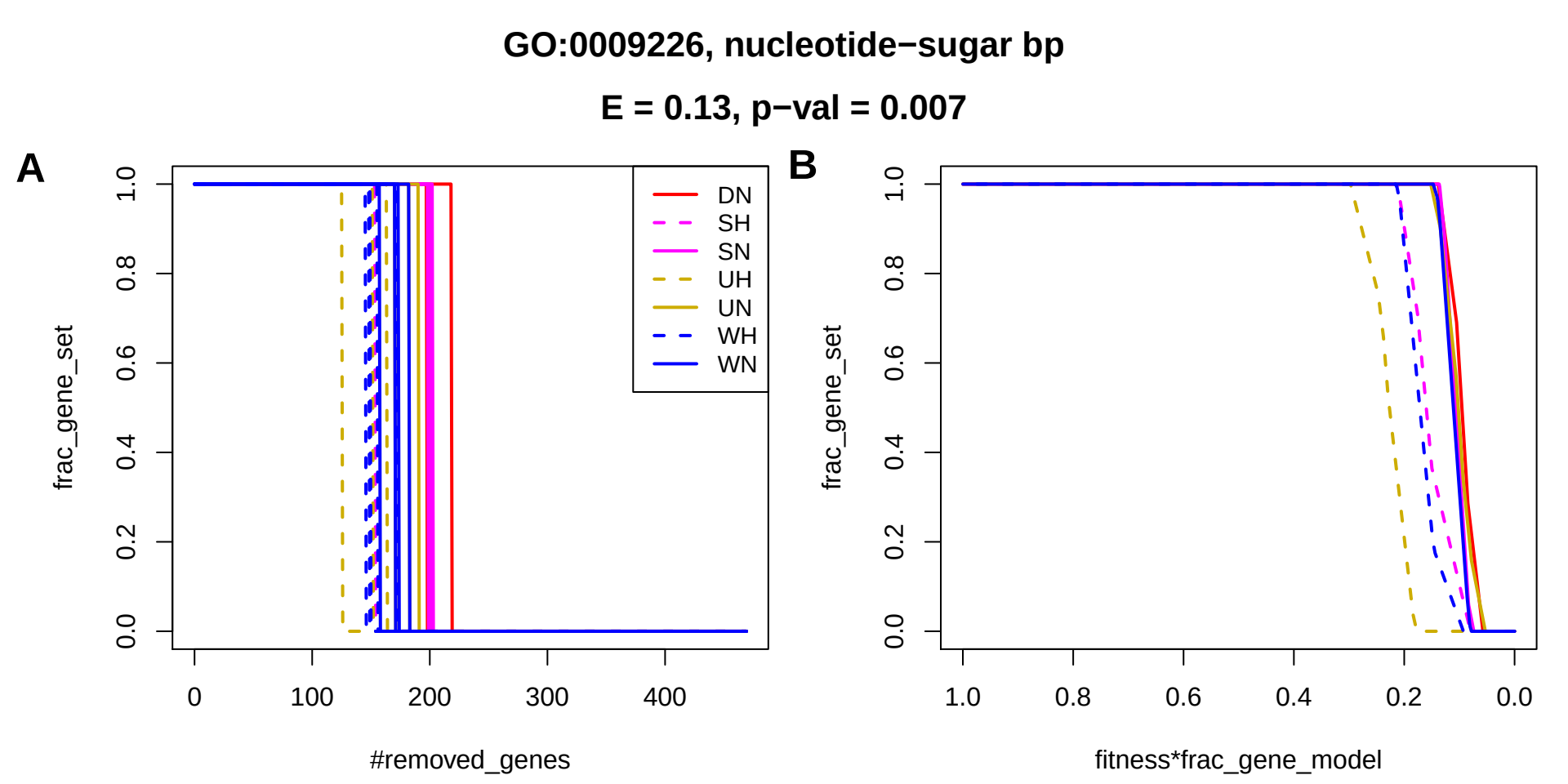

GO:0015804, neutral aa transport
E = 0.14, p−val = 0.004
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0008655, pyrimidine−containing compound salvage
E = 0.14, p−val = 0.028
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009070, serine family aa bp
E = 0.14, p−val = 0.004
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006096, glycolytic process
E = 0.14, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0000032, cell wall mannoprotein bp
E = 0.13, p−val = 0.008
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009226, nucleotide−sugar bp
E = 0.13, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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100
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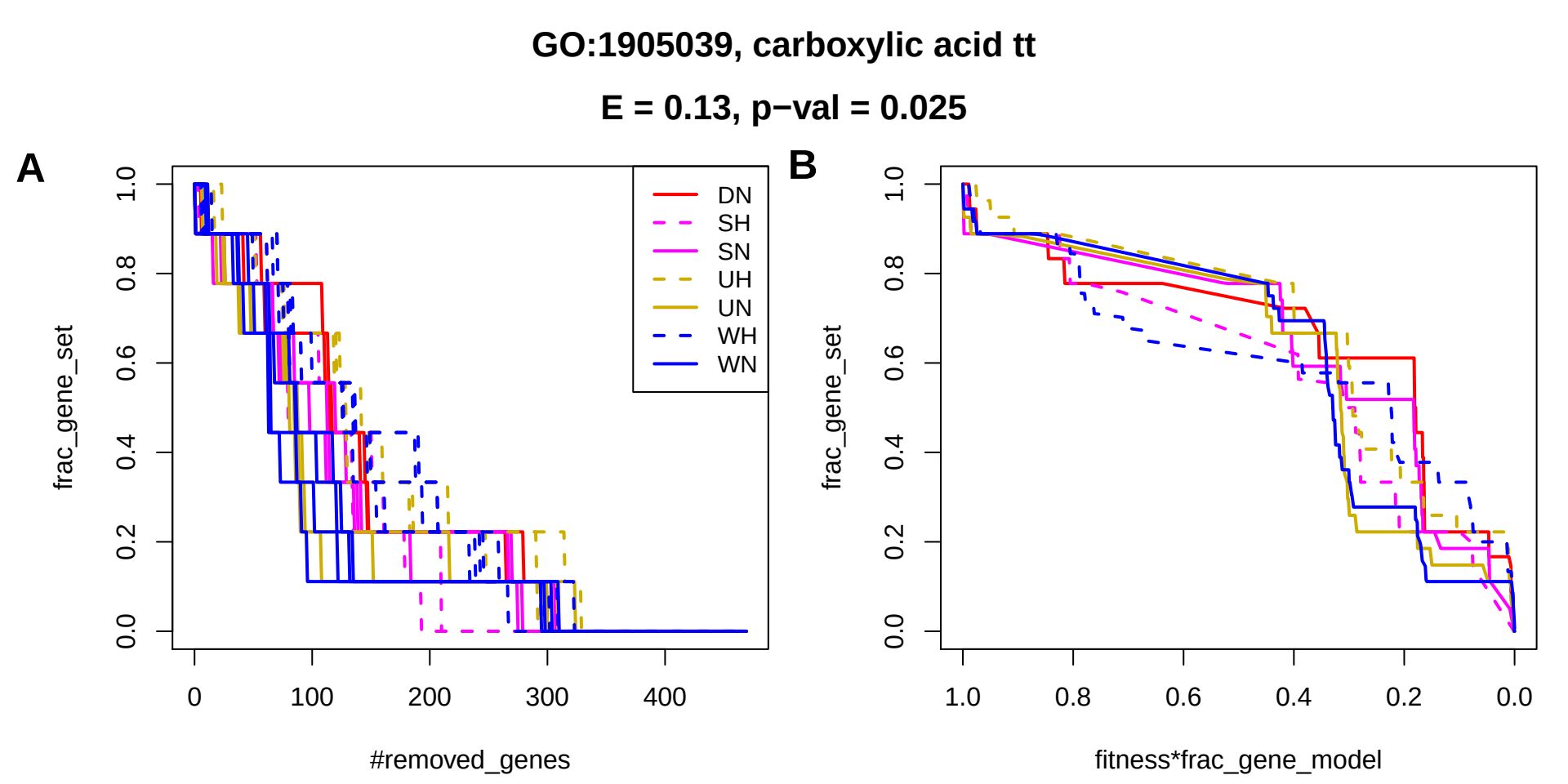
300
400


GO:1905039, carboxylic acid tt
E = 0.13, p−val = 0.025
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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100
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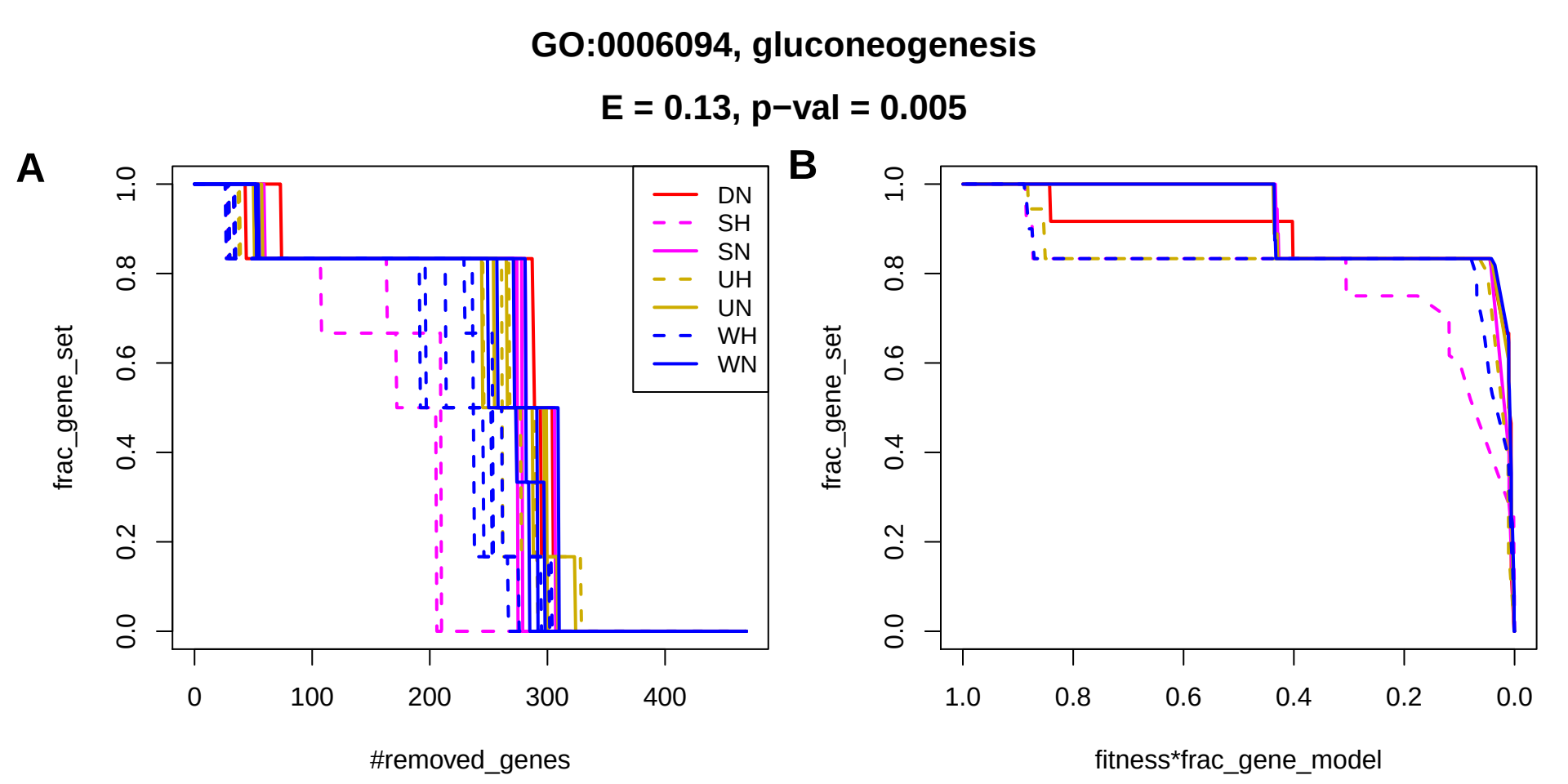
300
400


GO:0006094, gluconeogenesis
E = 0.13, p−val = 0.005
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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100
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300
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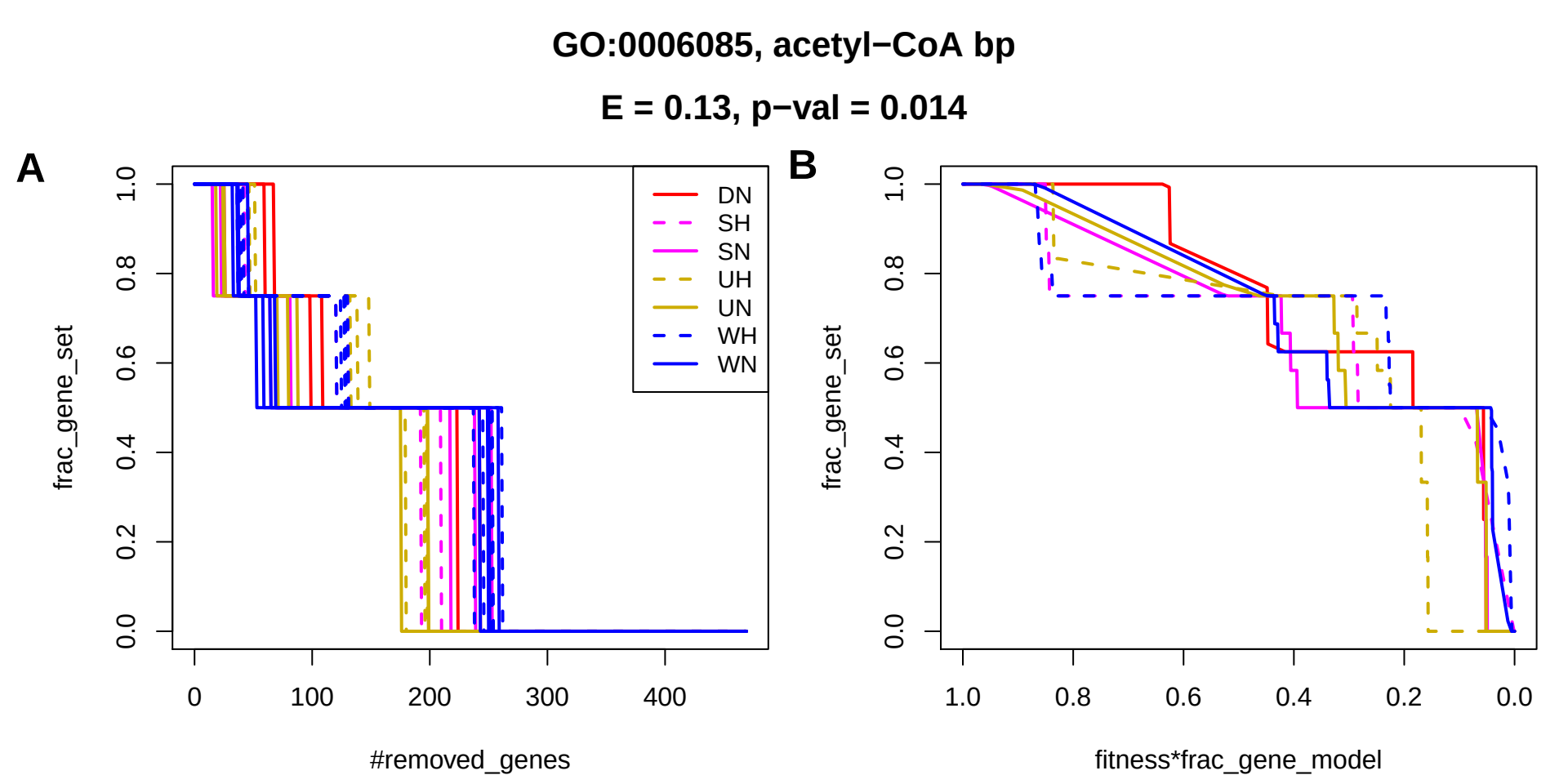
GO:0006085, acetyl−CoA bp
E = 0.13, p−val = 0.014
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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100
200
300
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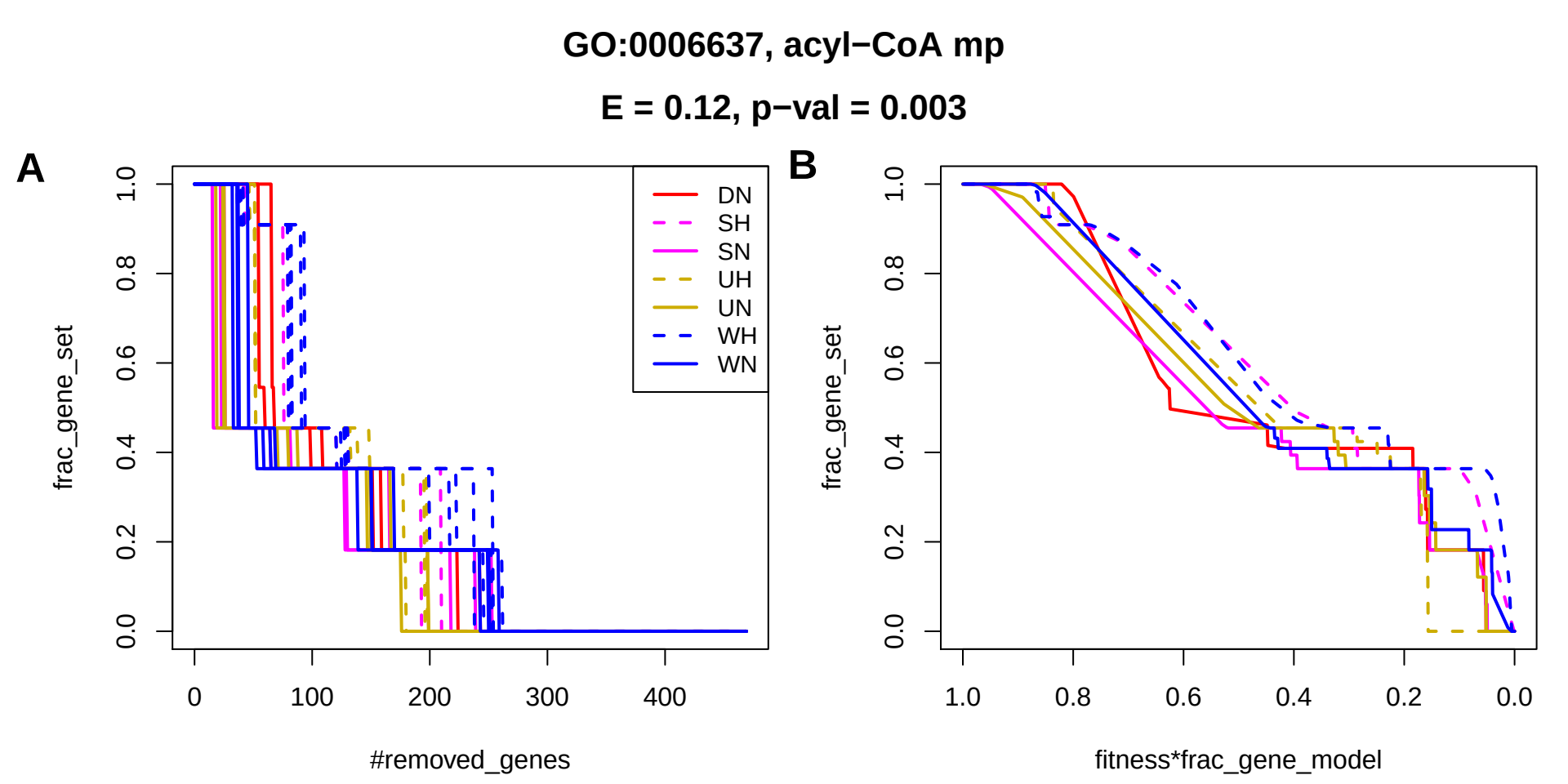
GO:0006637, acyl−CoA mp
E = 0.12, p−val = 0.003
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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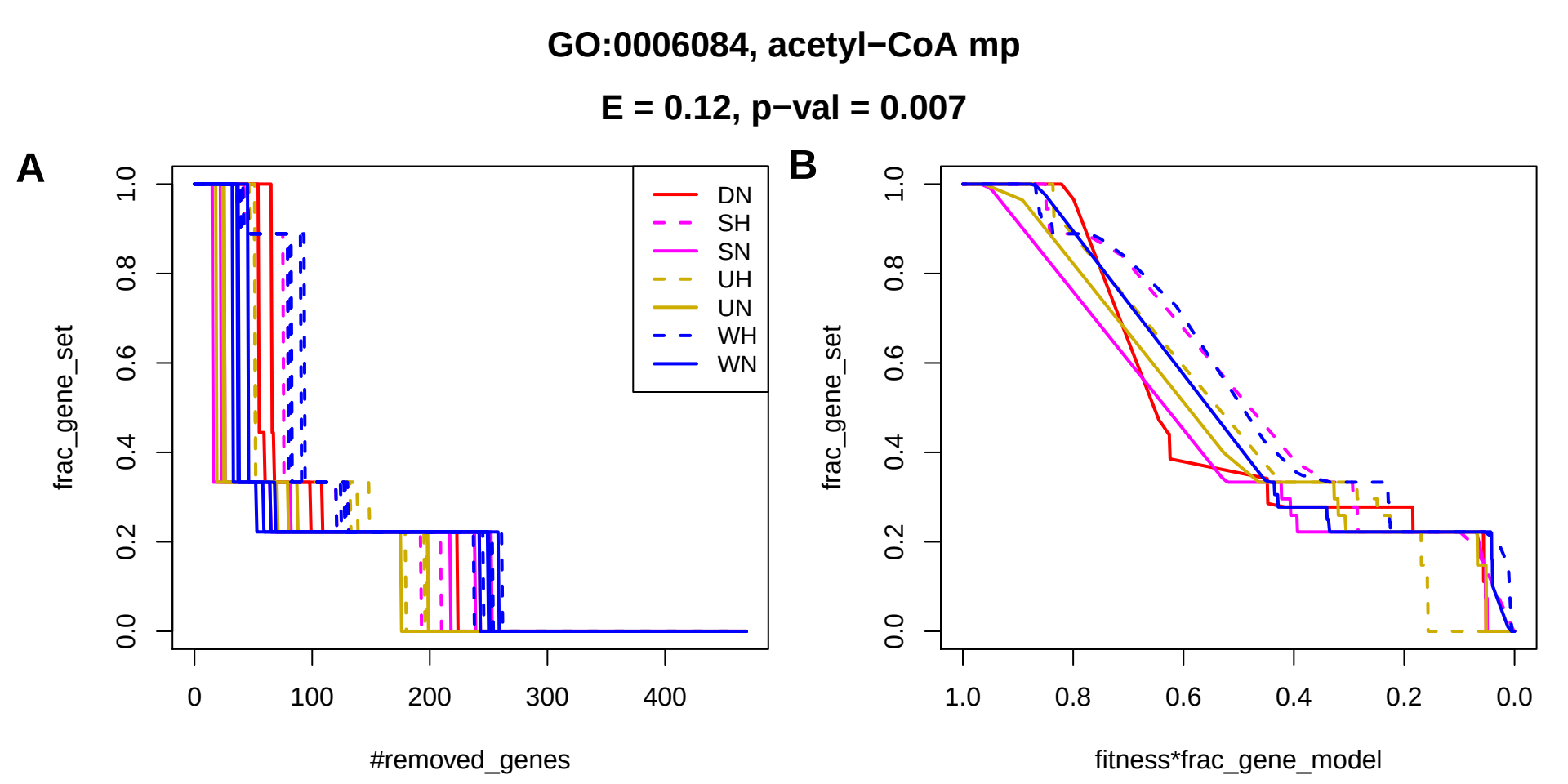
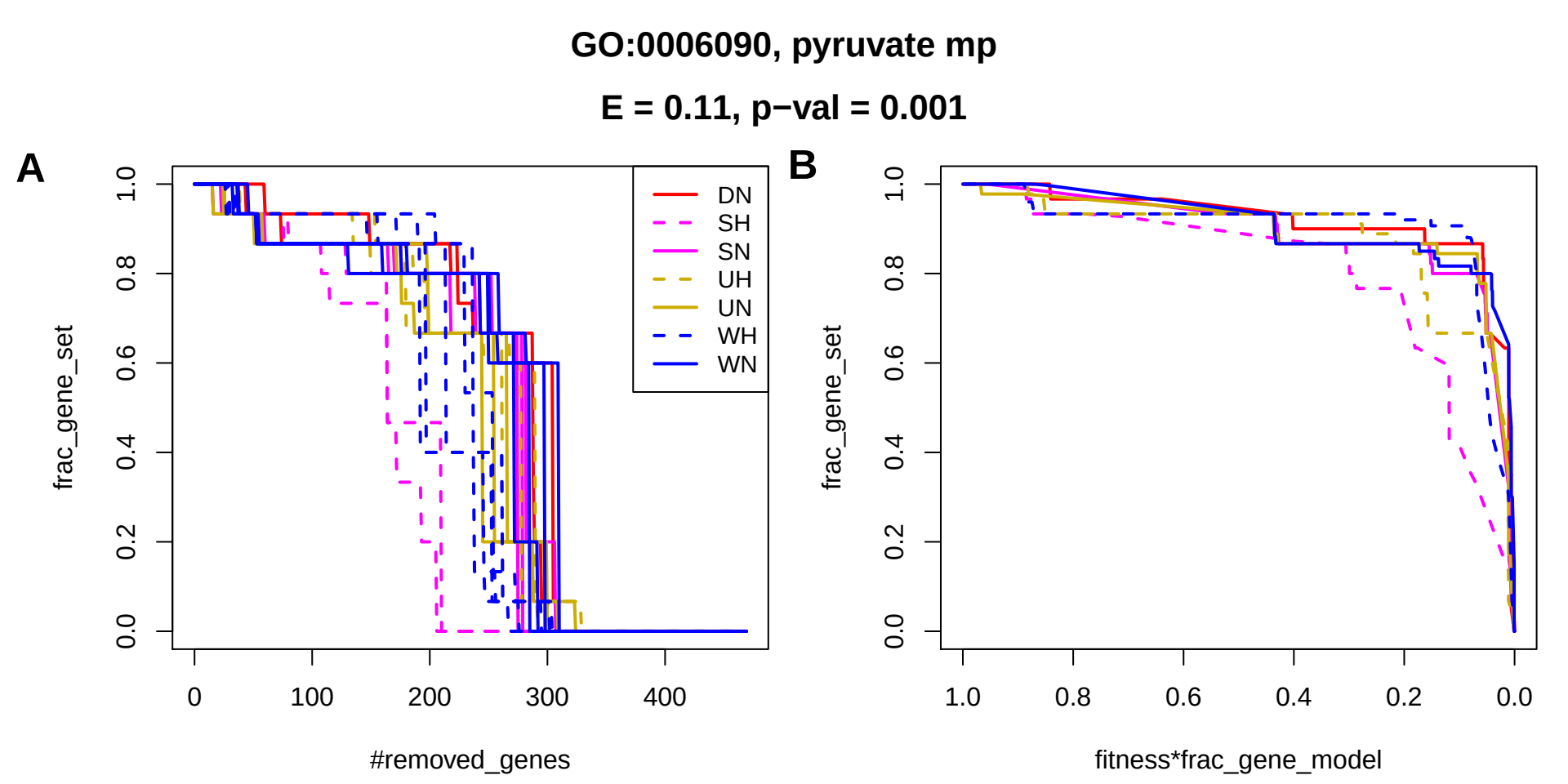
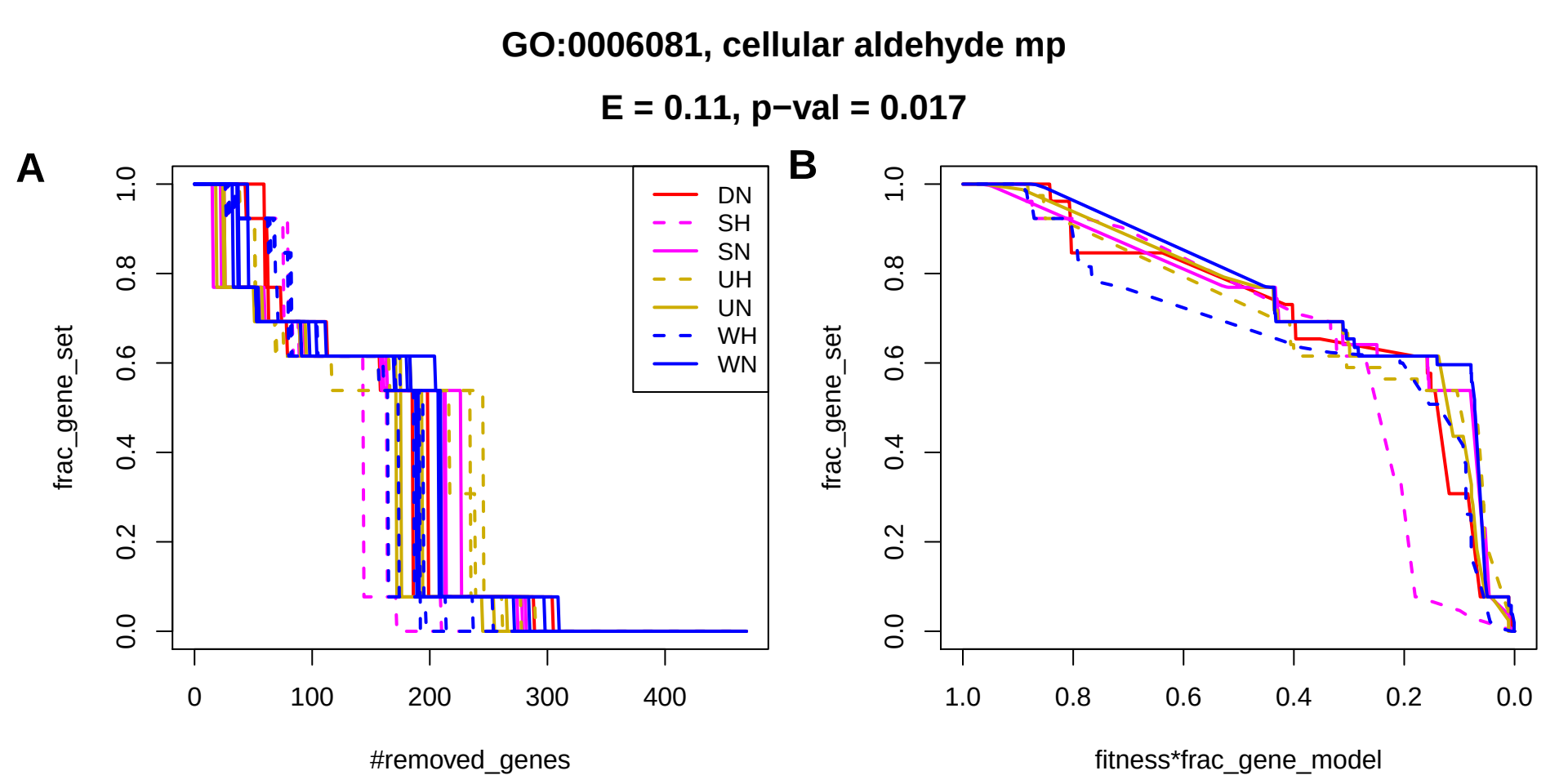
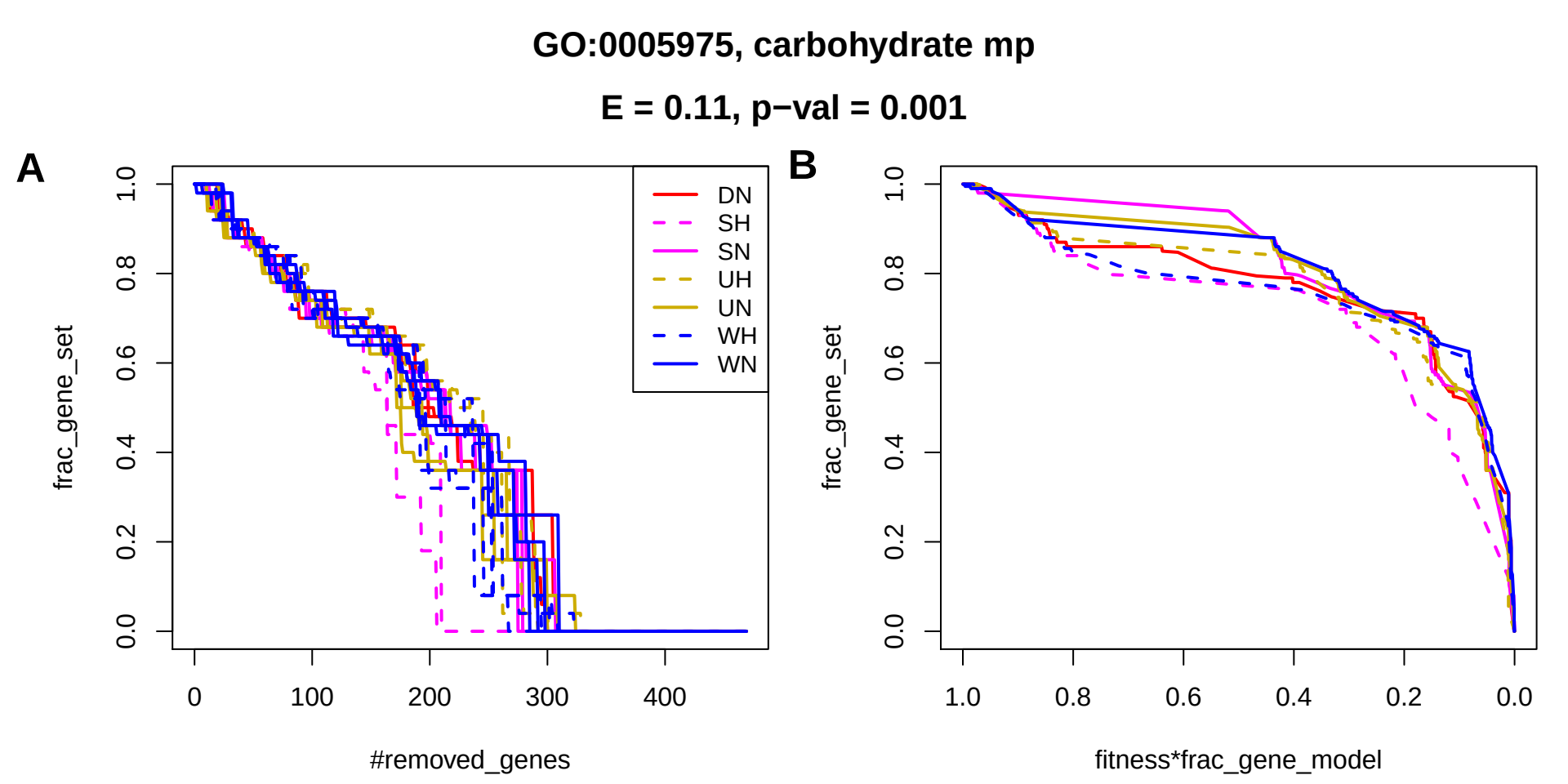
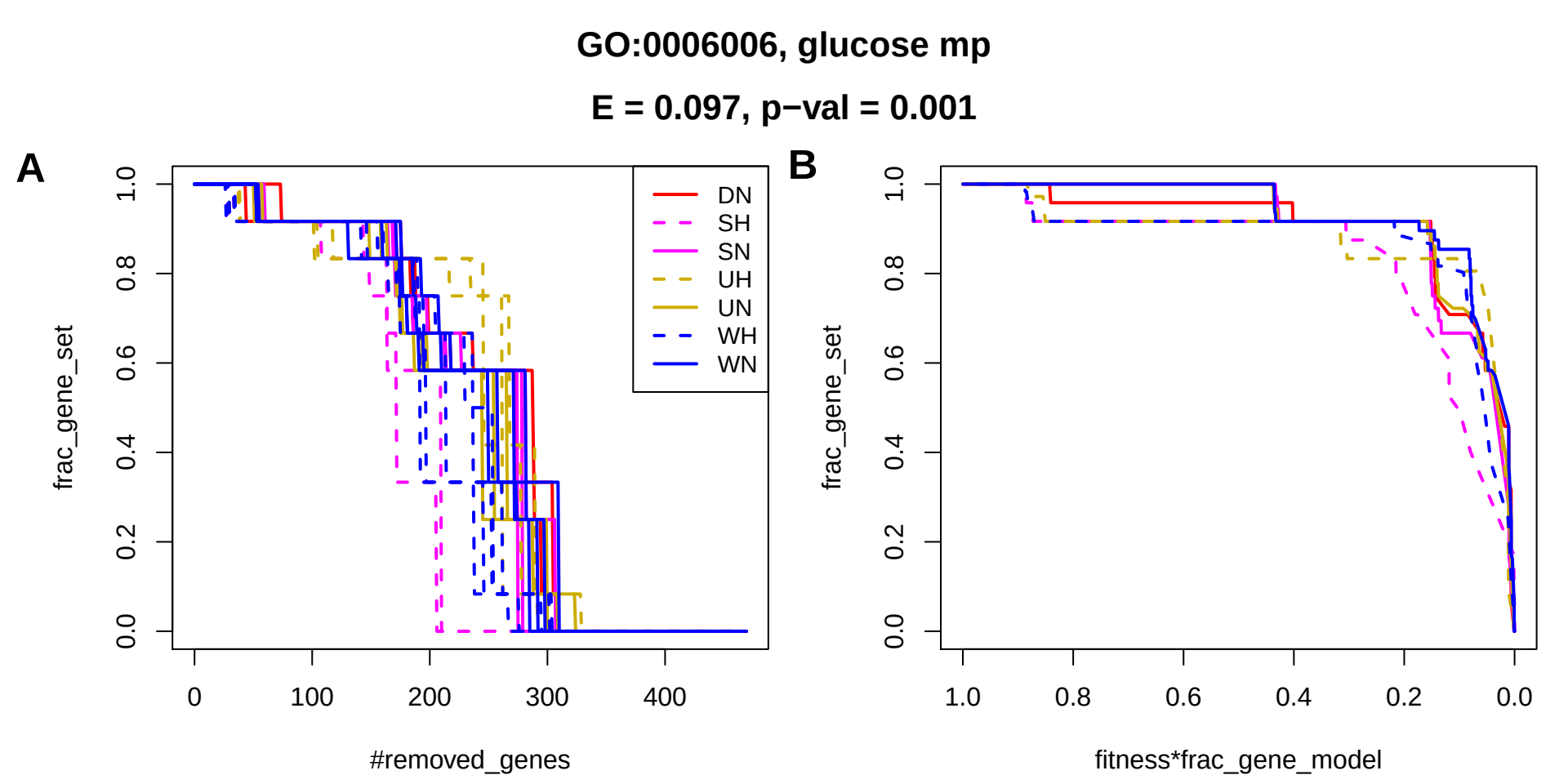
100
200
300
400

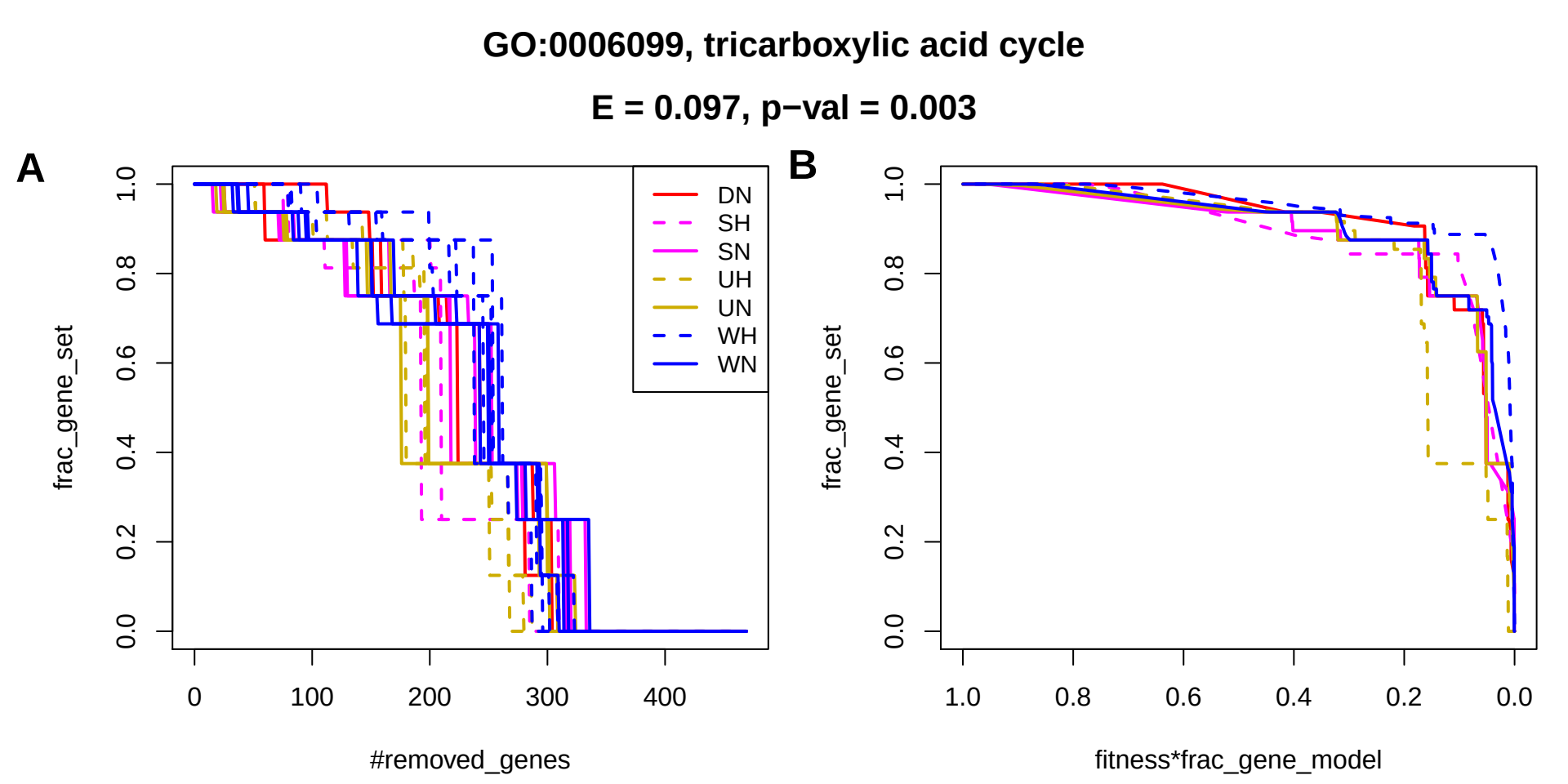

GO:0006084, acetyl−CoA mp
E = 0.12, p−val = 0.007
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

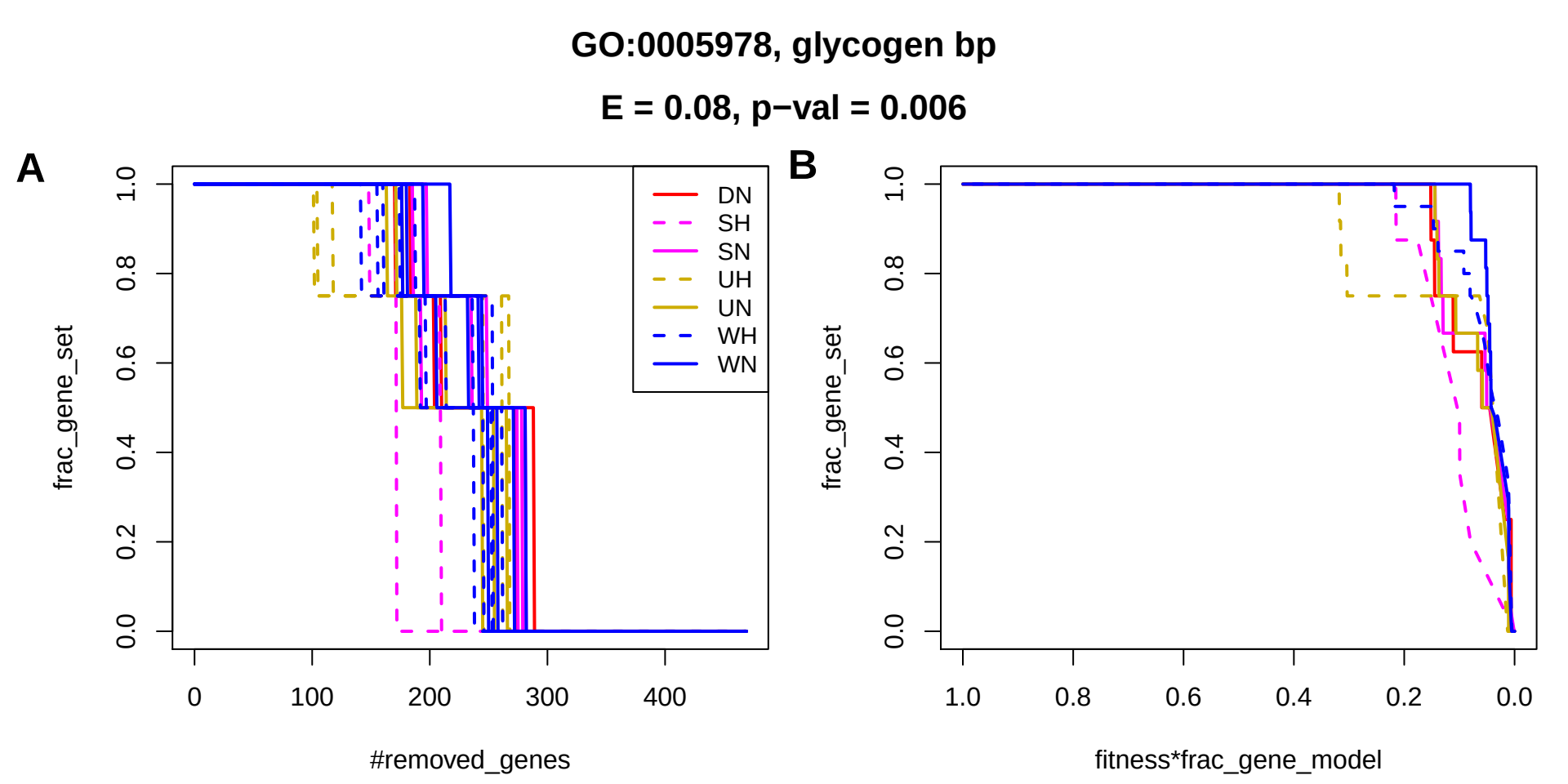

GO:0006090, pyruvate mp
E = 0.11, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

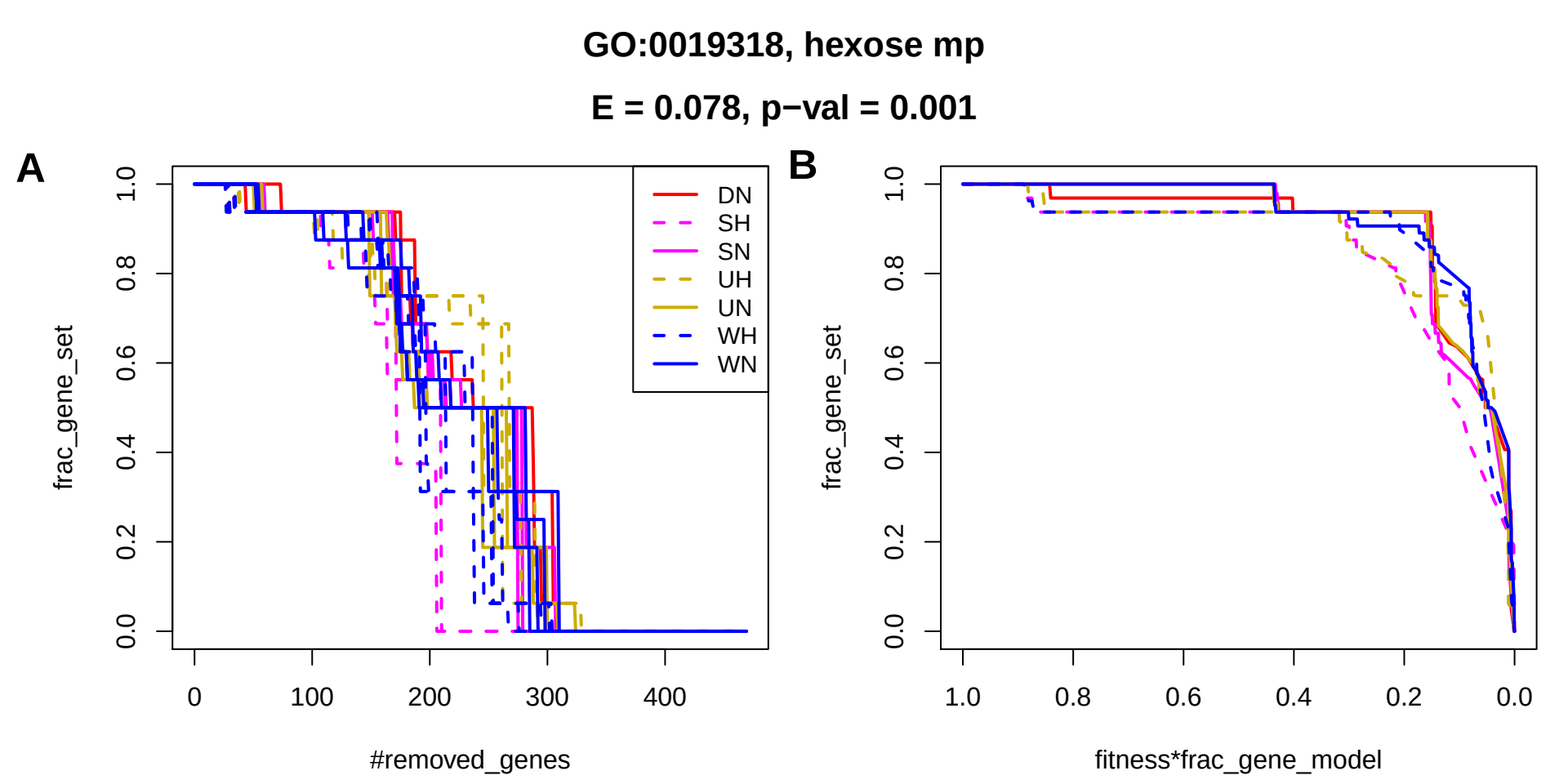

GO:0006081, cellular aldehyde mp
E = 0.11, p−val = 0.017
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

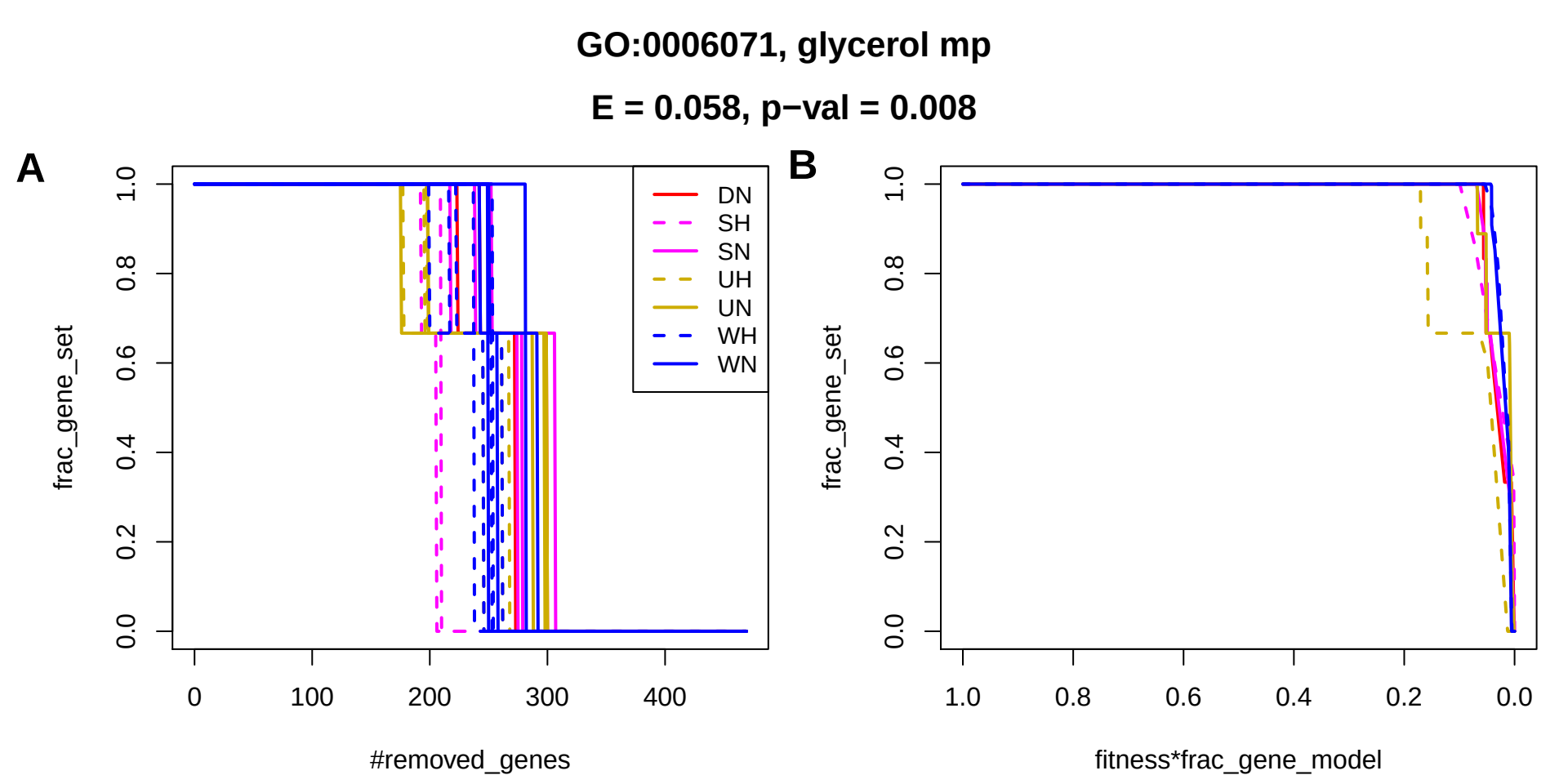

GO:0005975, carbohydrate mp
E = 0.11, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006006, glucose mp
E = 0.097, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006099, tricarboxylic acid cycle
E = 0.097, p−val = 0.003
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0005978, glycogen bp
E = 0.08, p−val = 0.006
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0019318, hexose mp
E = 0.078, p−val = 0.001
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006071, glycerol mp
E = 0.058, p−val = 0.008
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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300
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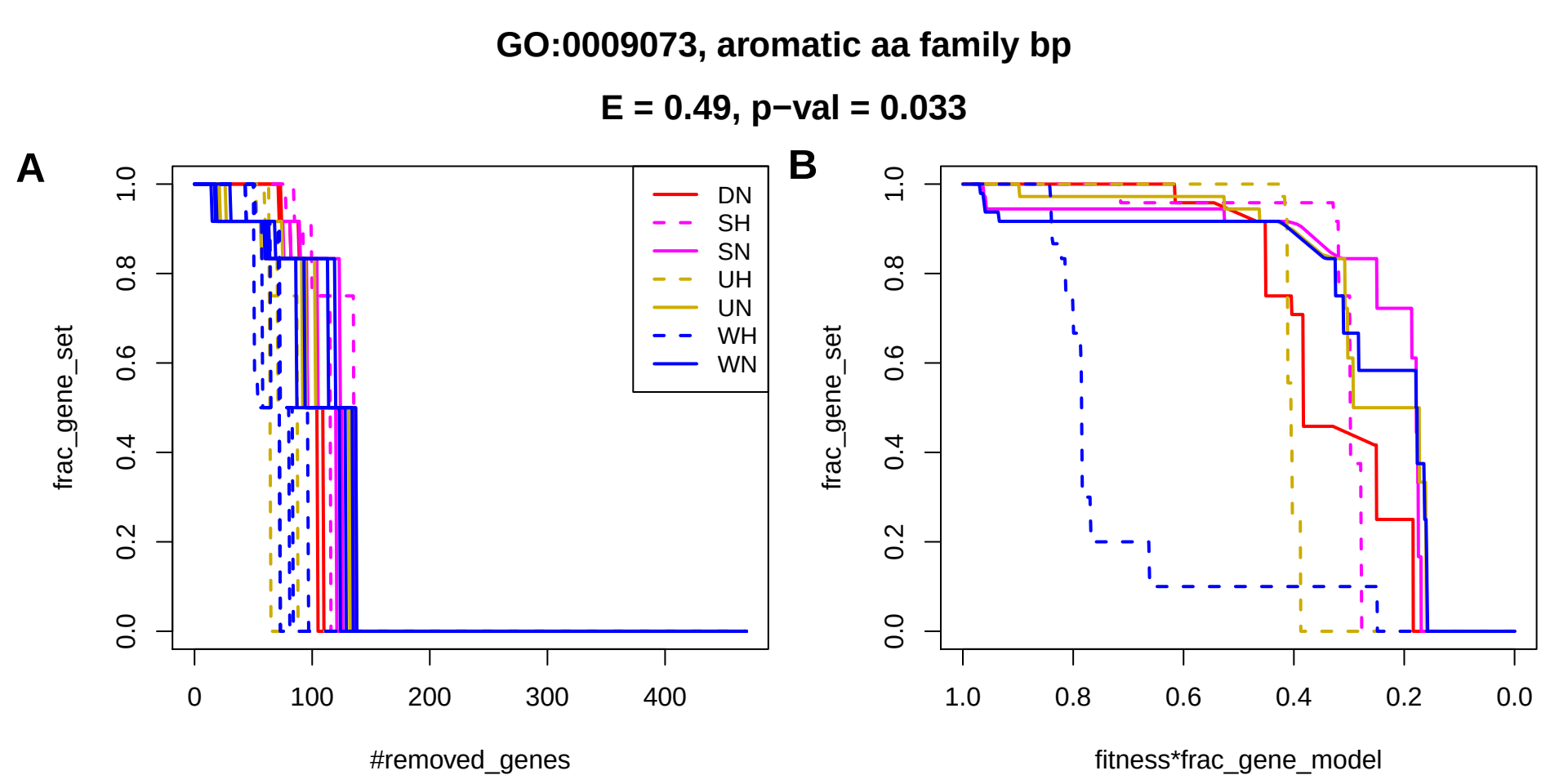
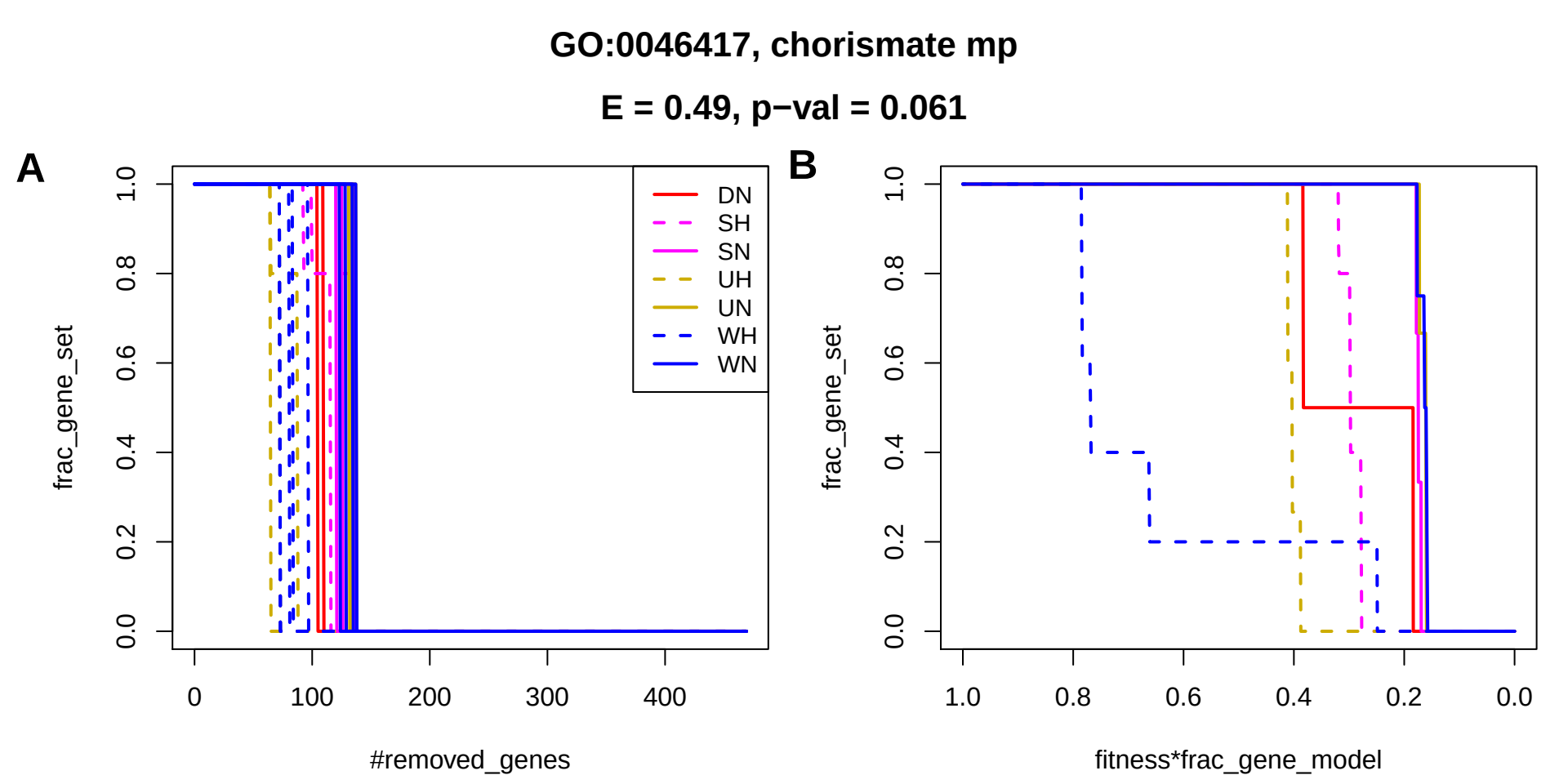
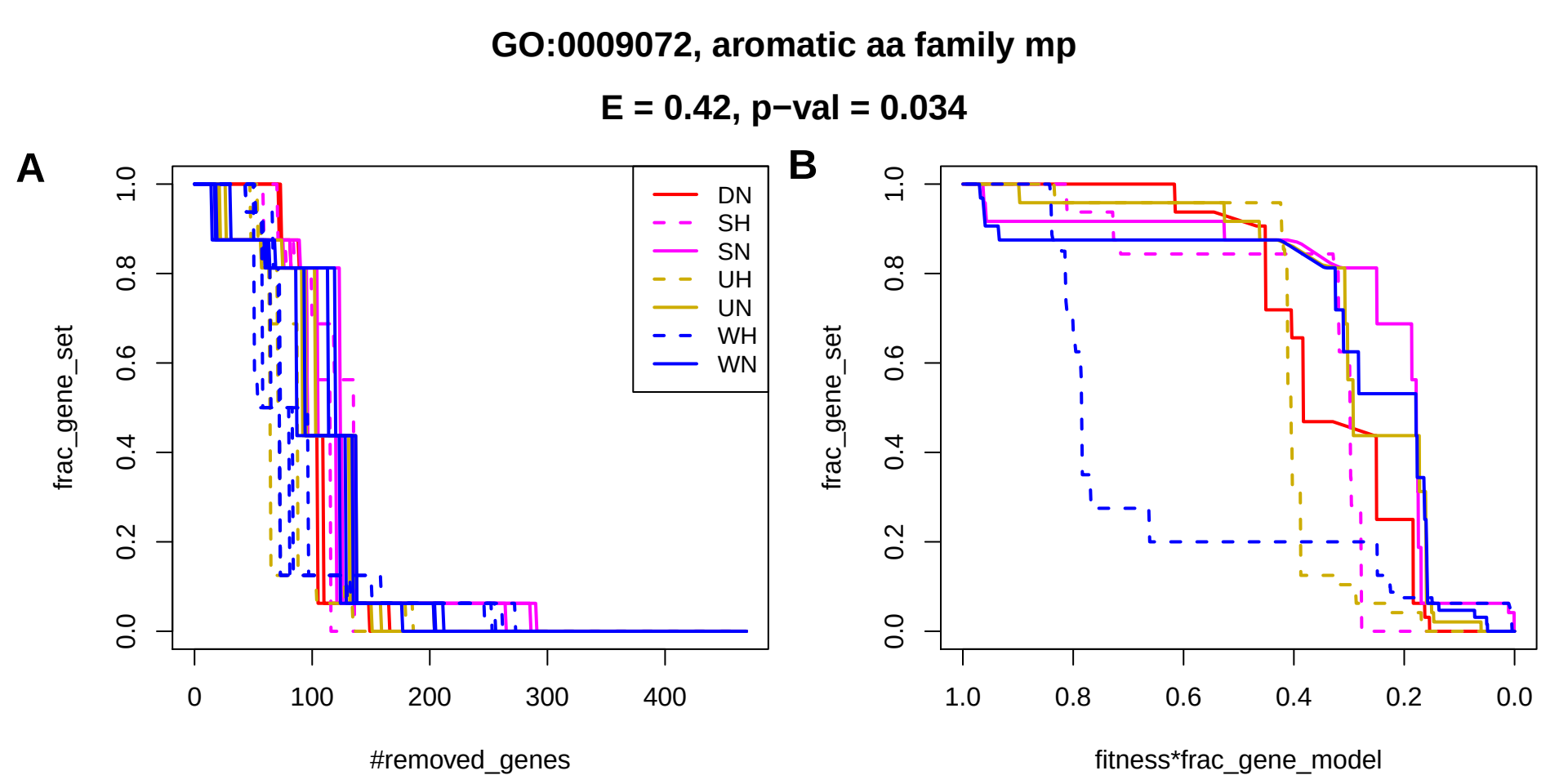
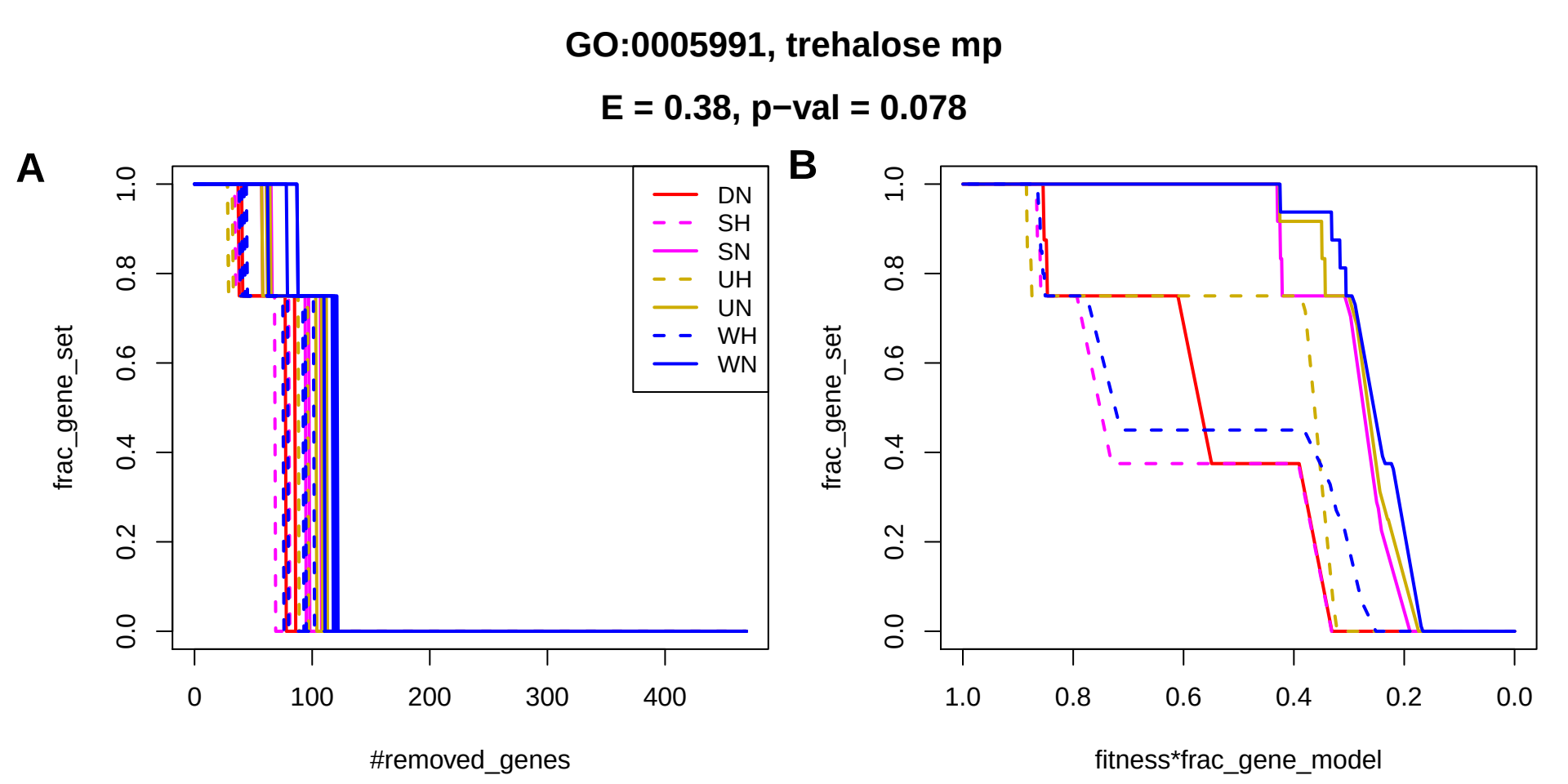
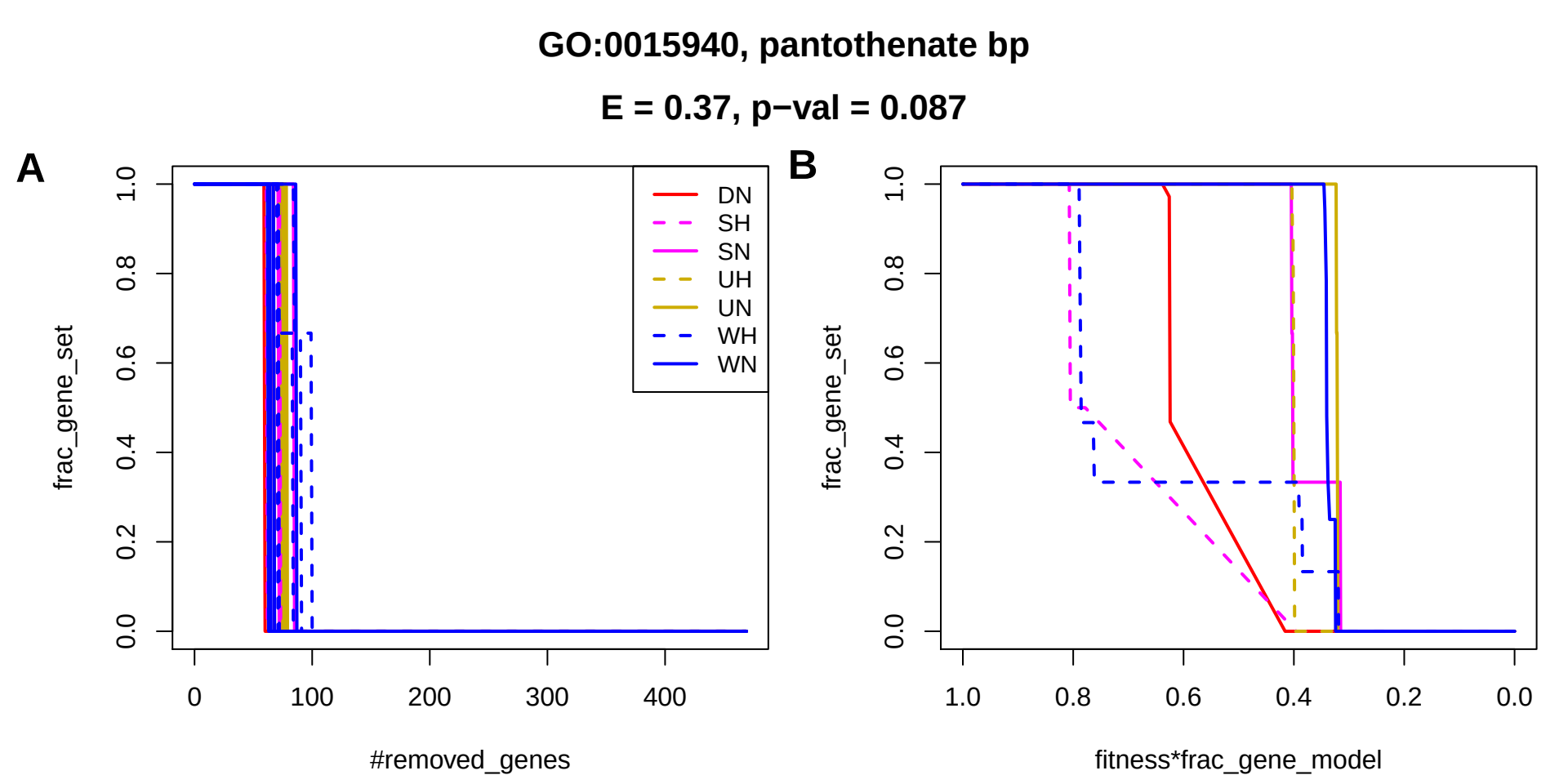
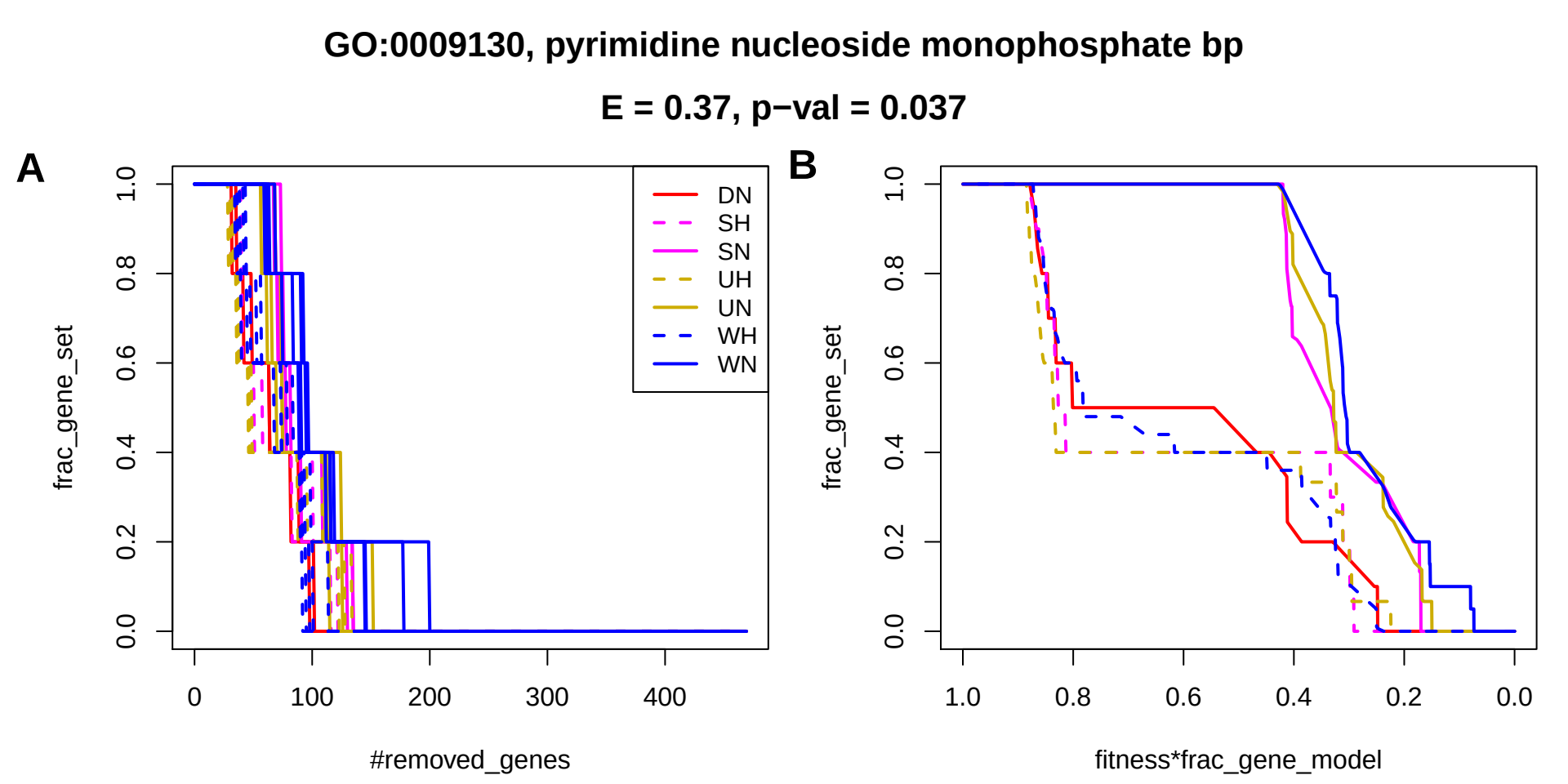

GO:0009073, aromatic aa family bp
E = 0.49, p−val = 0.033
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0046417, chorismate mp
E = 0.49, p−val = 0.061
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009072, aromatic aa family mp
E = 0.42, p−val = 0.034
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0005991, trehalose mp
E = 0.38, p−val = 0.078
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0015940, pantothenate bp
E = 0.37, p−val = 0.087
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009130, pyrimidine nucleoside monophosphate bp
E = 0.37, p−val = 0.037
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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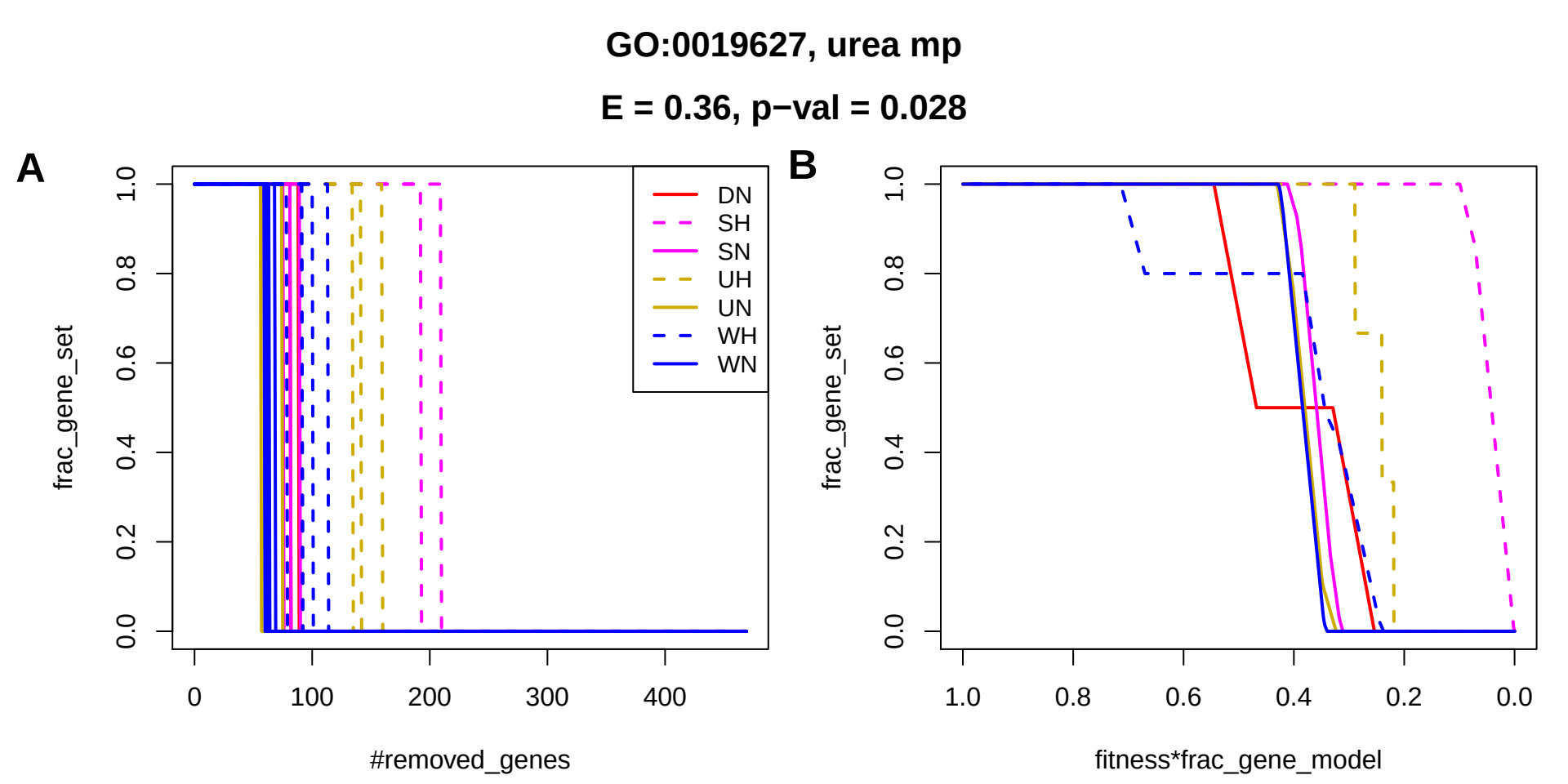
300
400


GO:0019627, urea mp
E = 0.36, p−val = 0.028
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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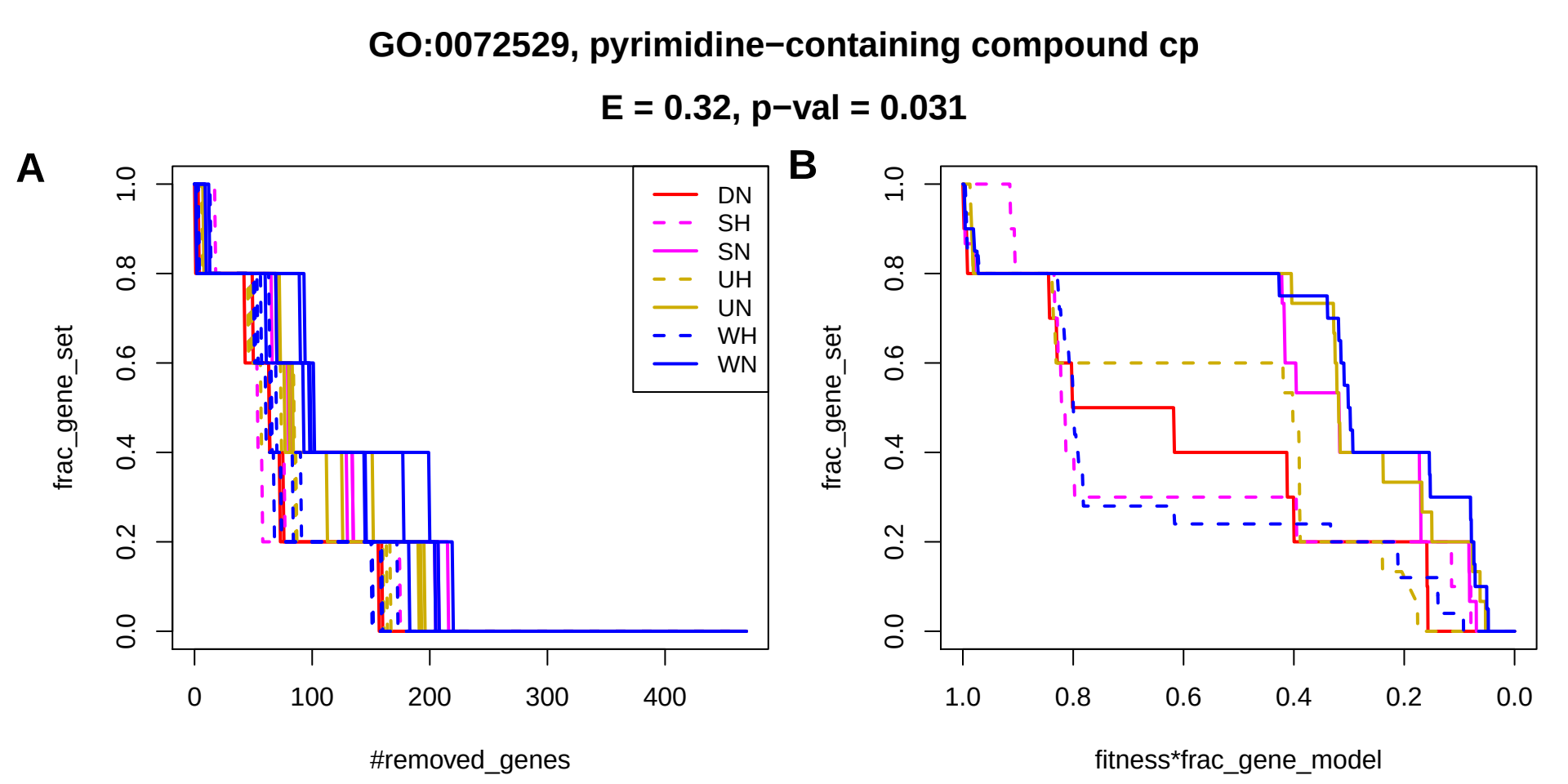
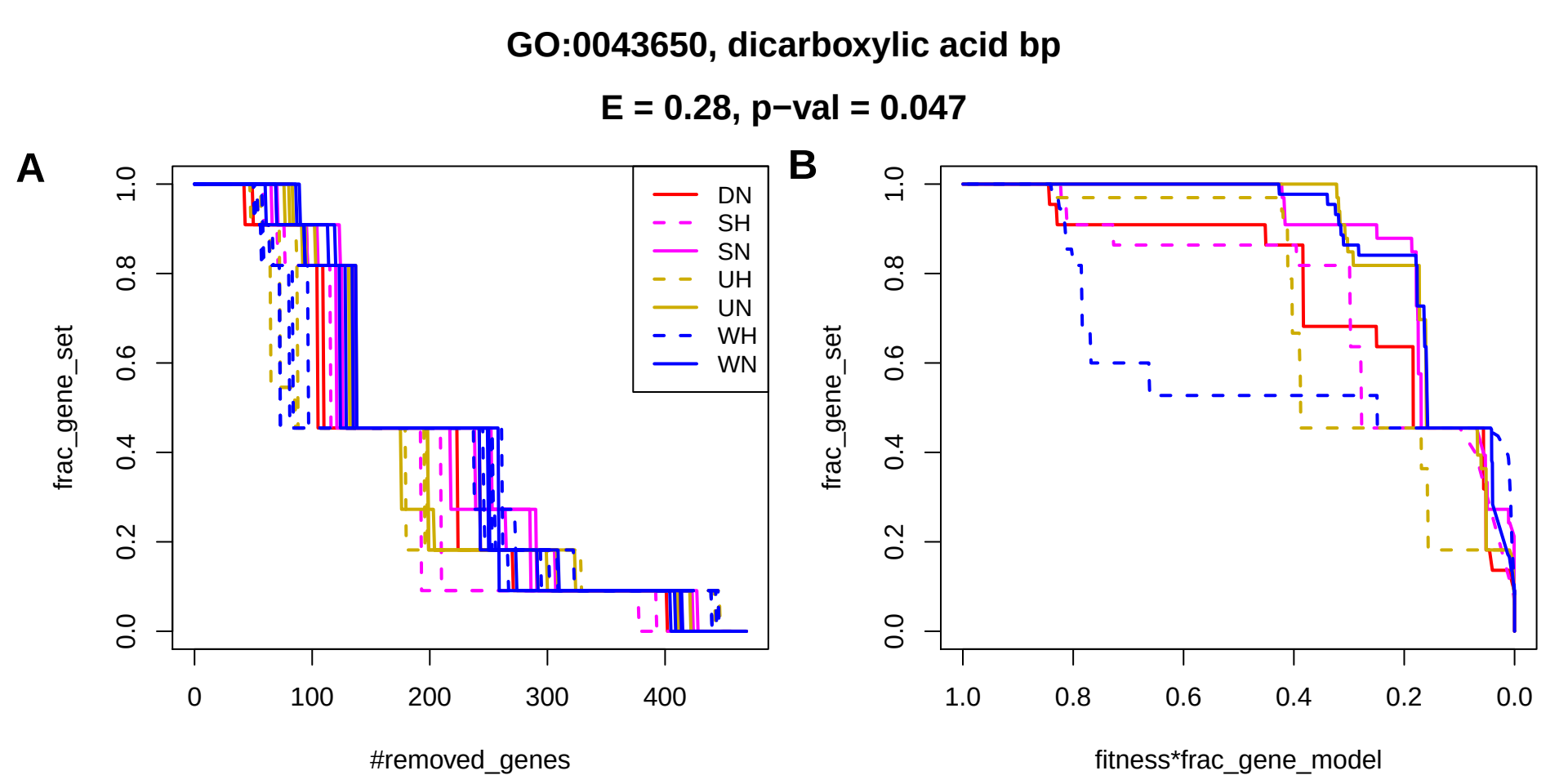
300
400


GO:0072529, pyrimidine−containing compound cp
E = 0.32, p−val = 0.031
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0043650, dicarboxylic acid bp
E = 0.28, p−val = 0.047
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
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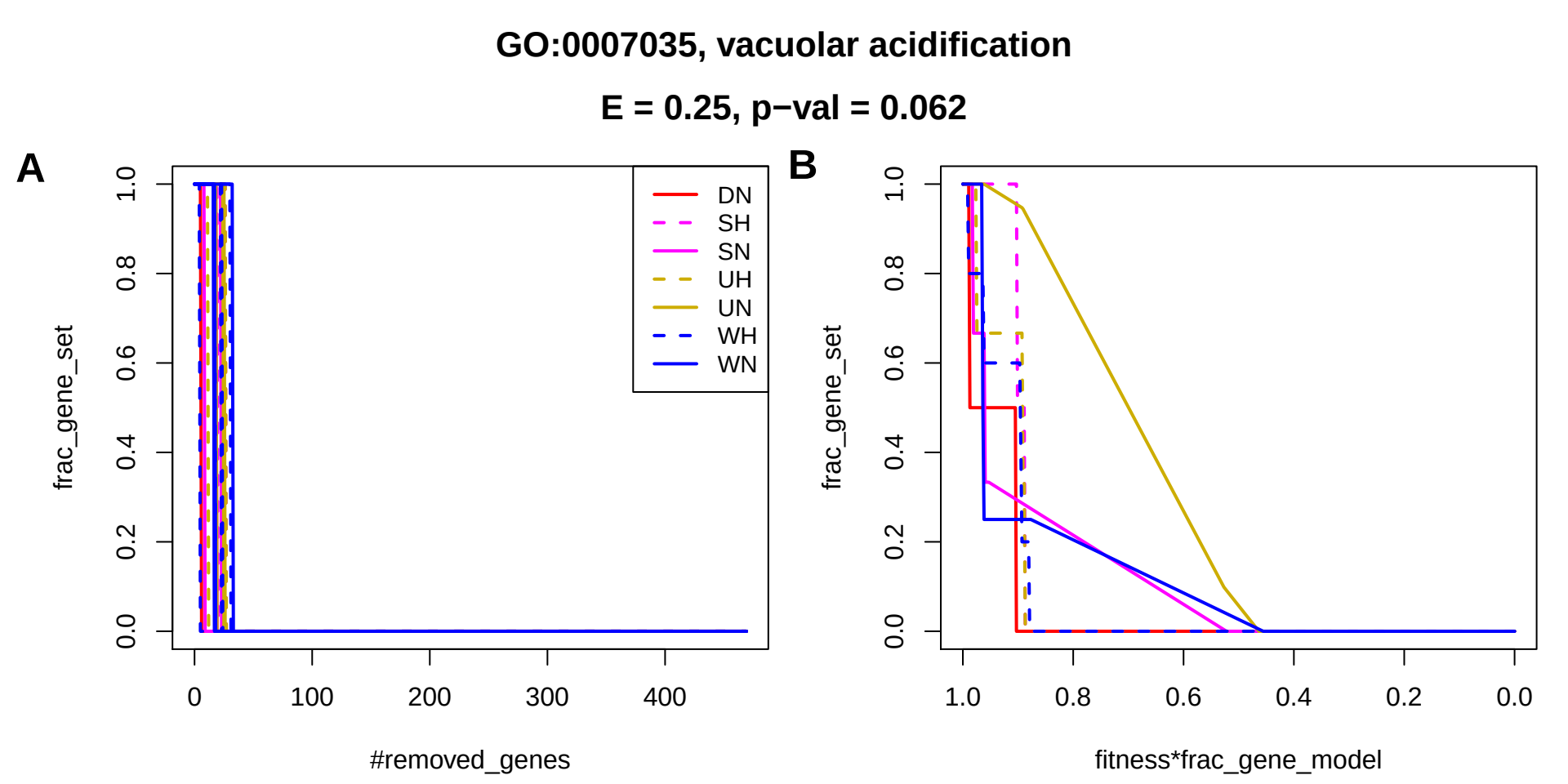
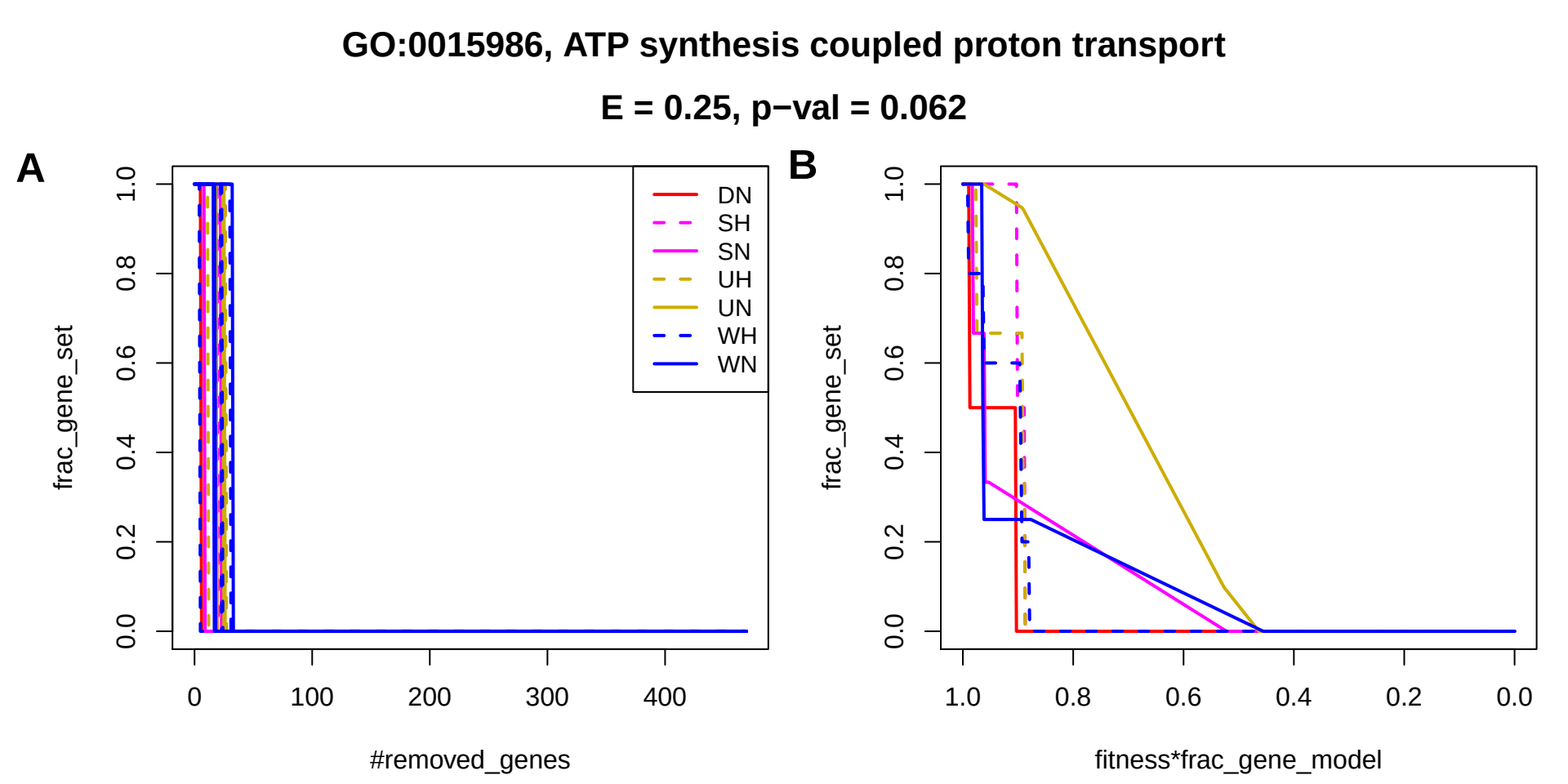
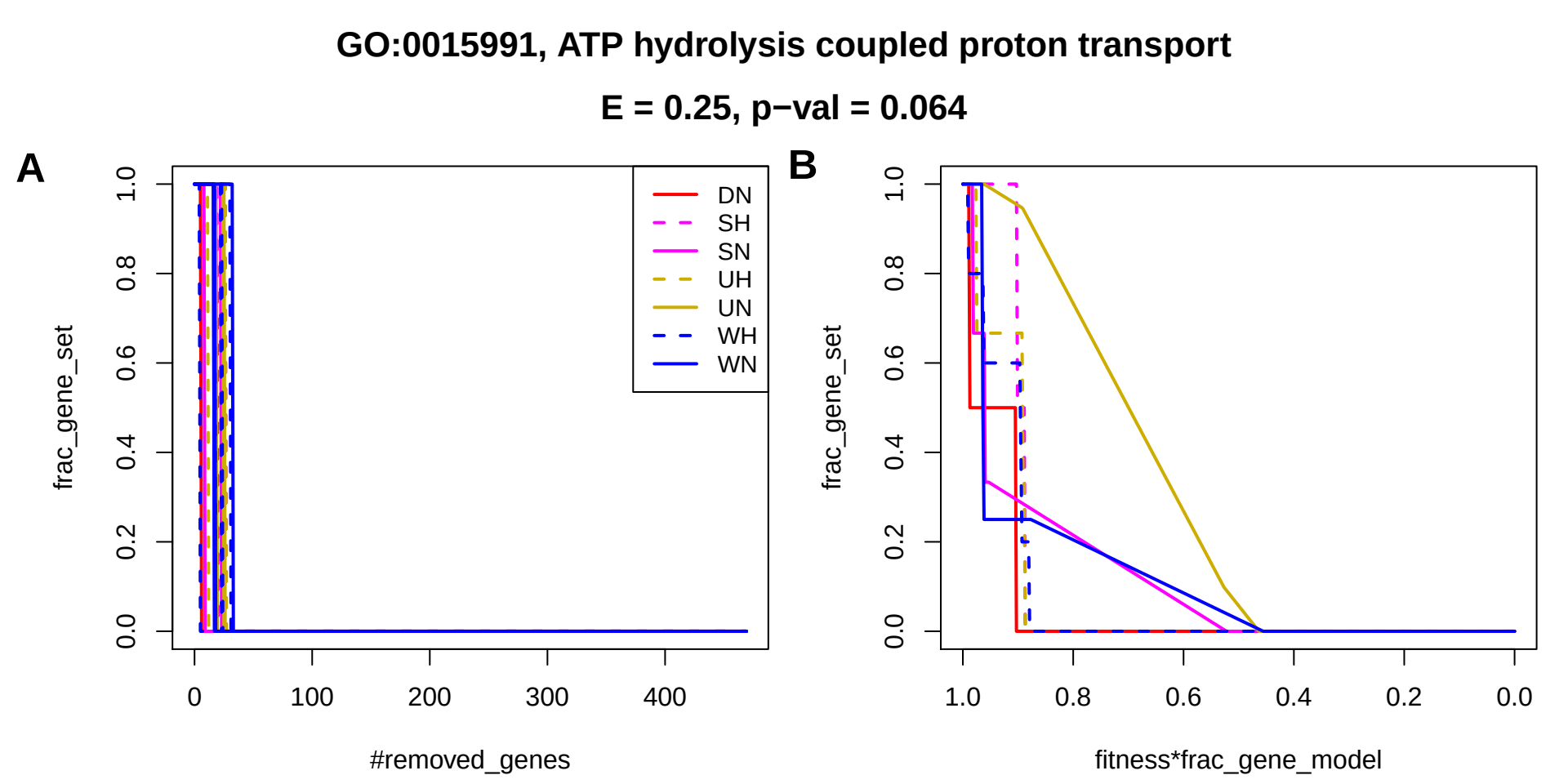
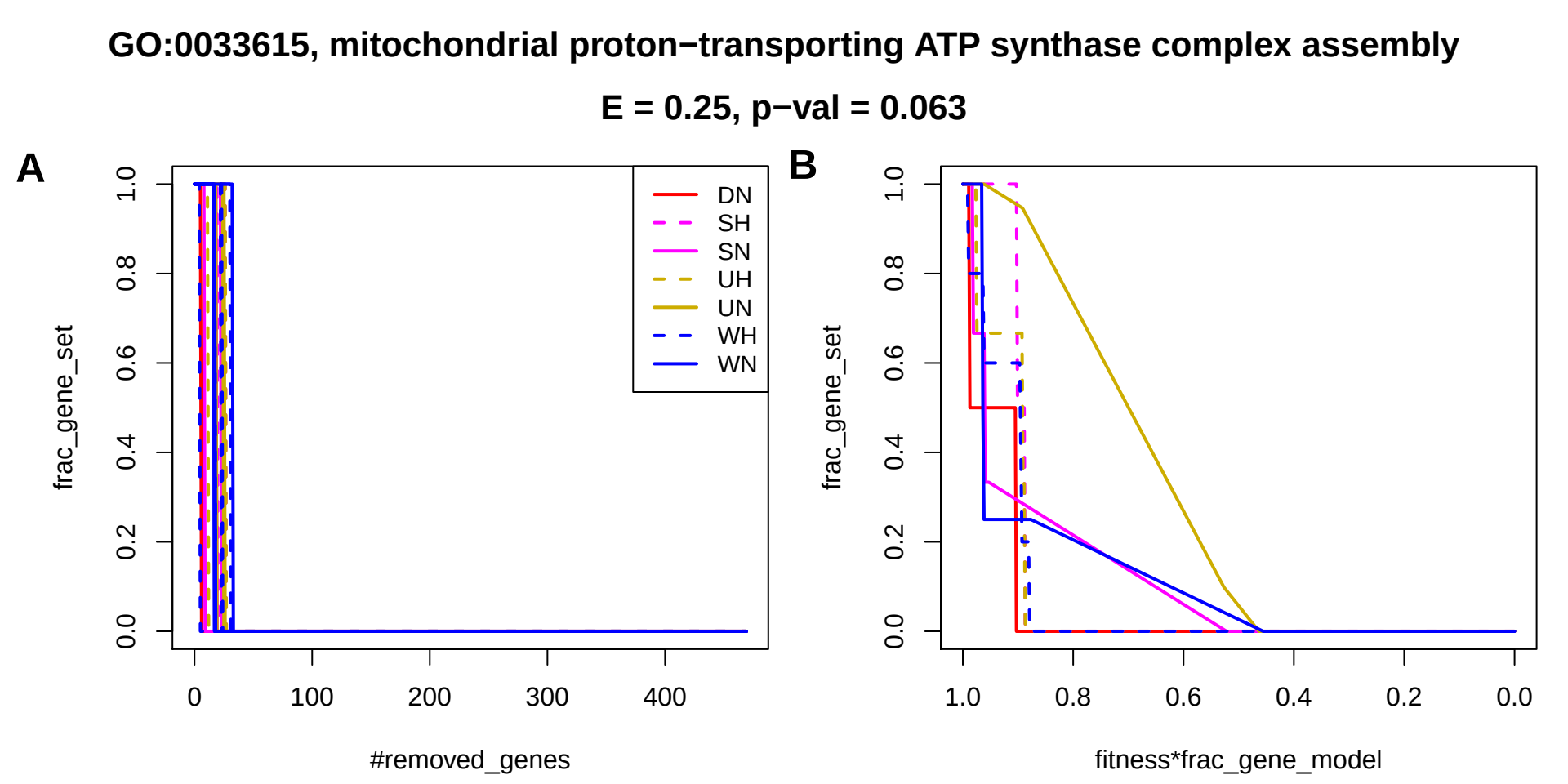
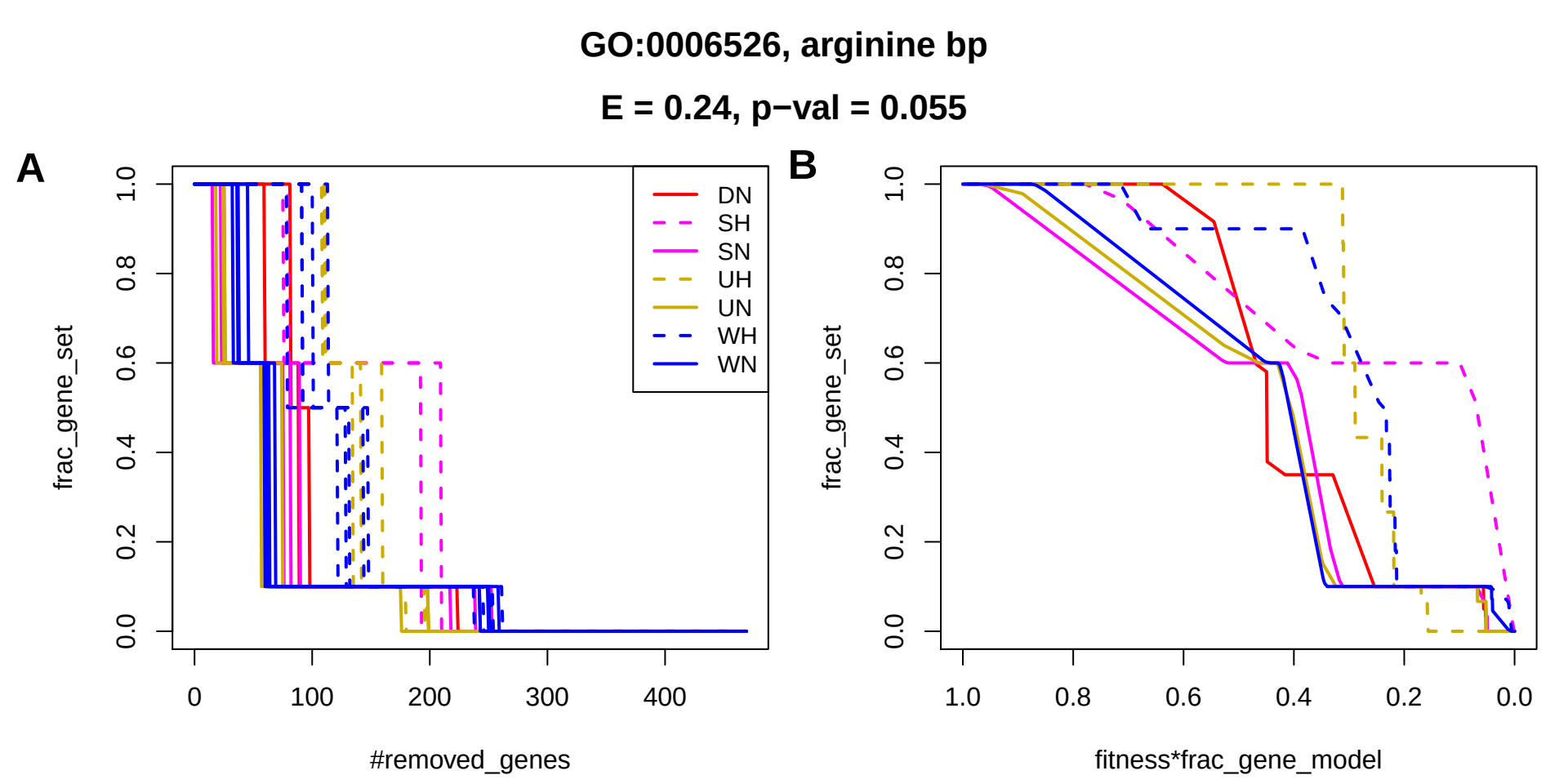
300
400

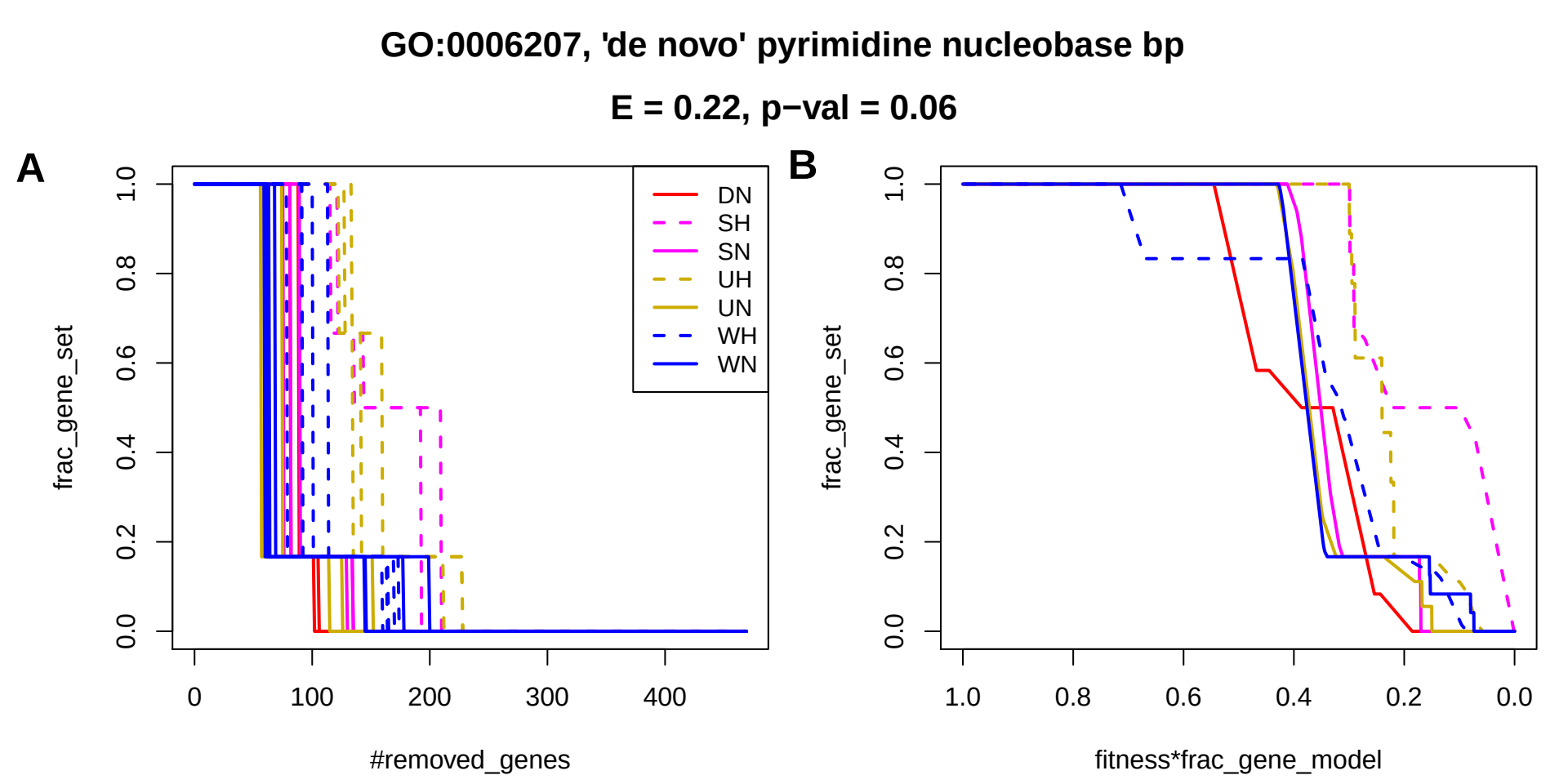

GO:0007035, vacuolar acidification
E = 0.25, p−val = 0.062
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

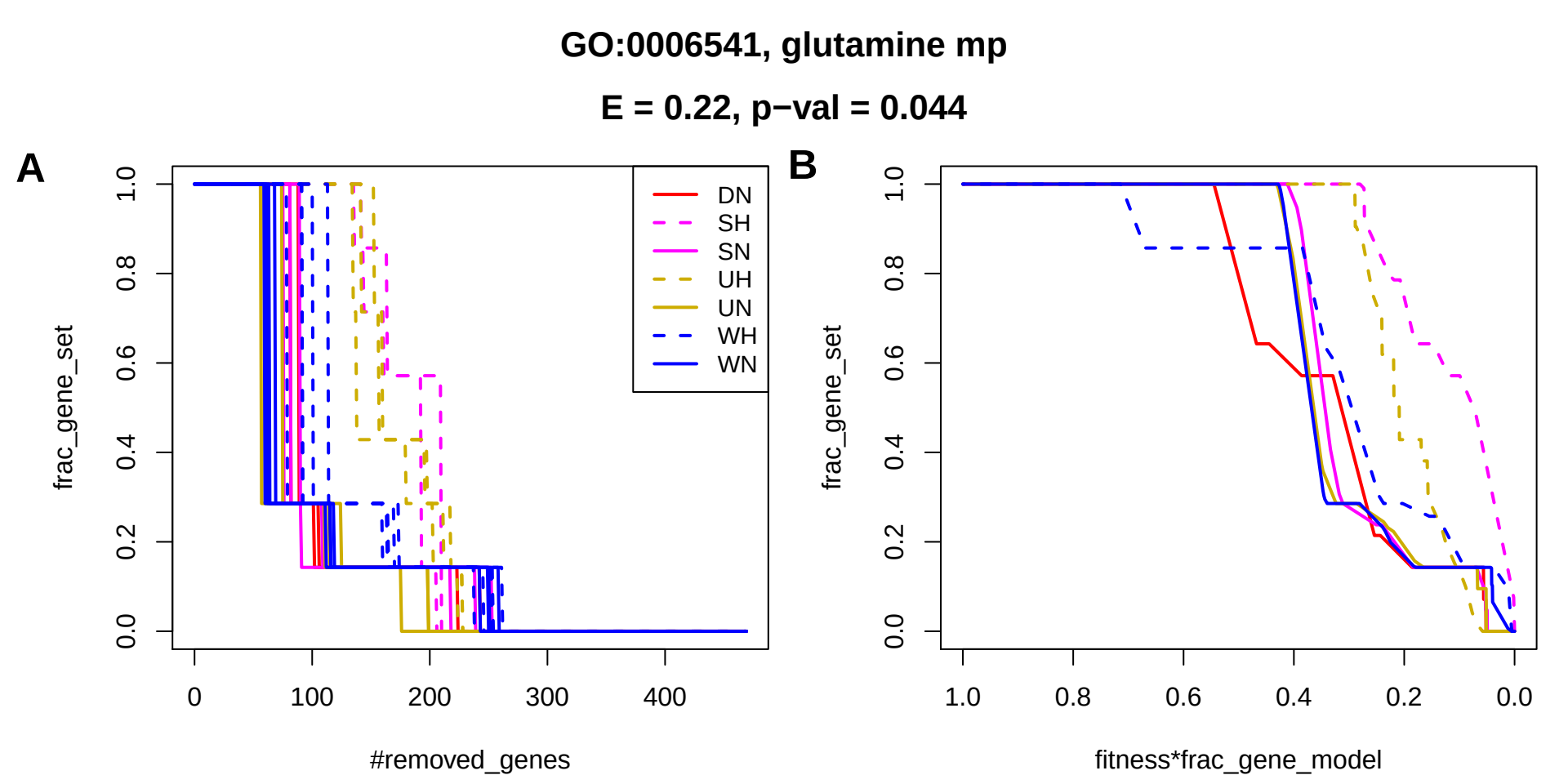

GO:0015986, ATP synthesis coupled proton transport
E = 0.25, p−val = 0.062
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

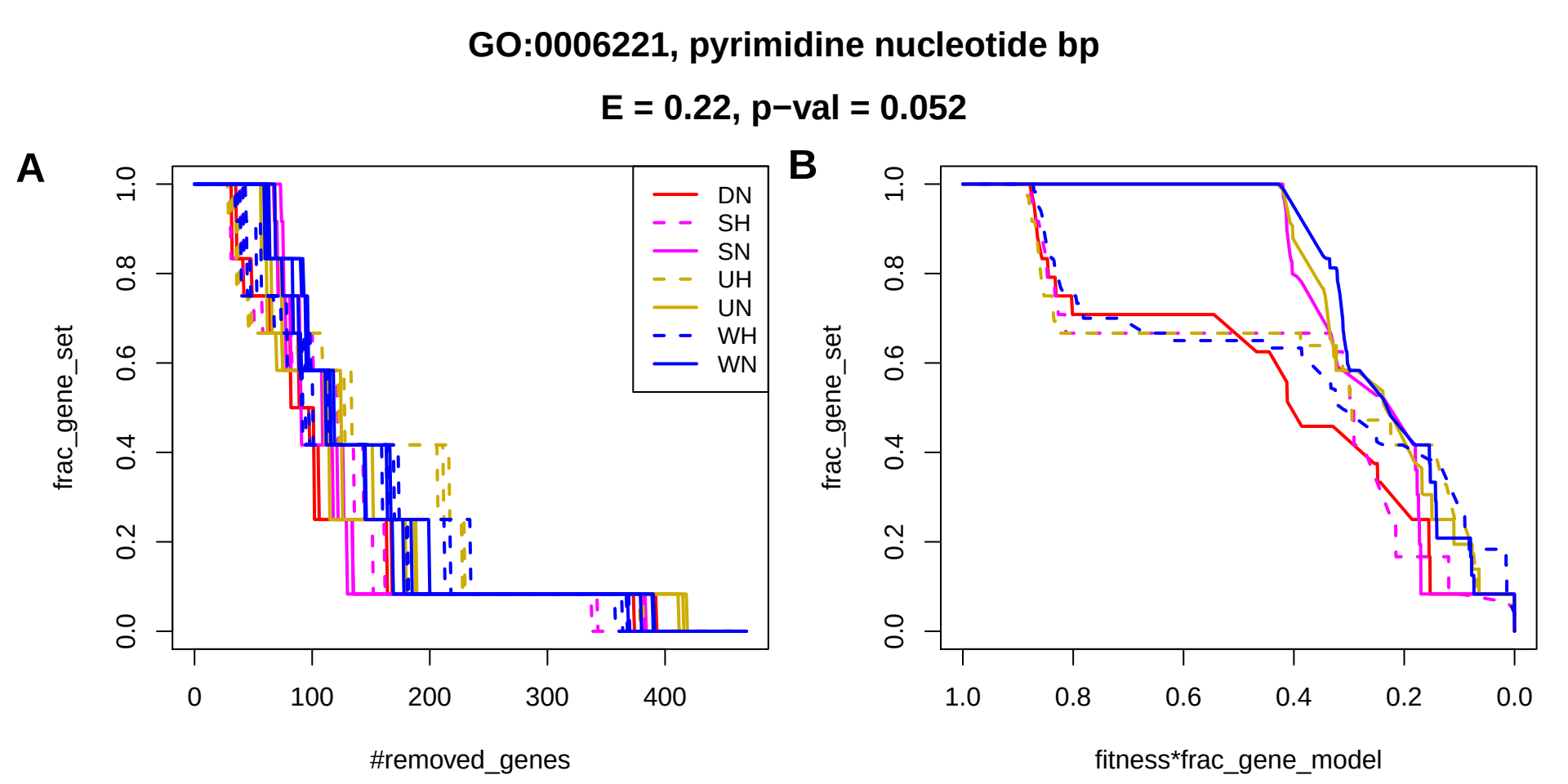

GO:0015991, ATP hydrolysis coupled proton transport
E = 0.25, p−val = 0.064
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

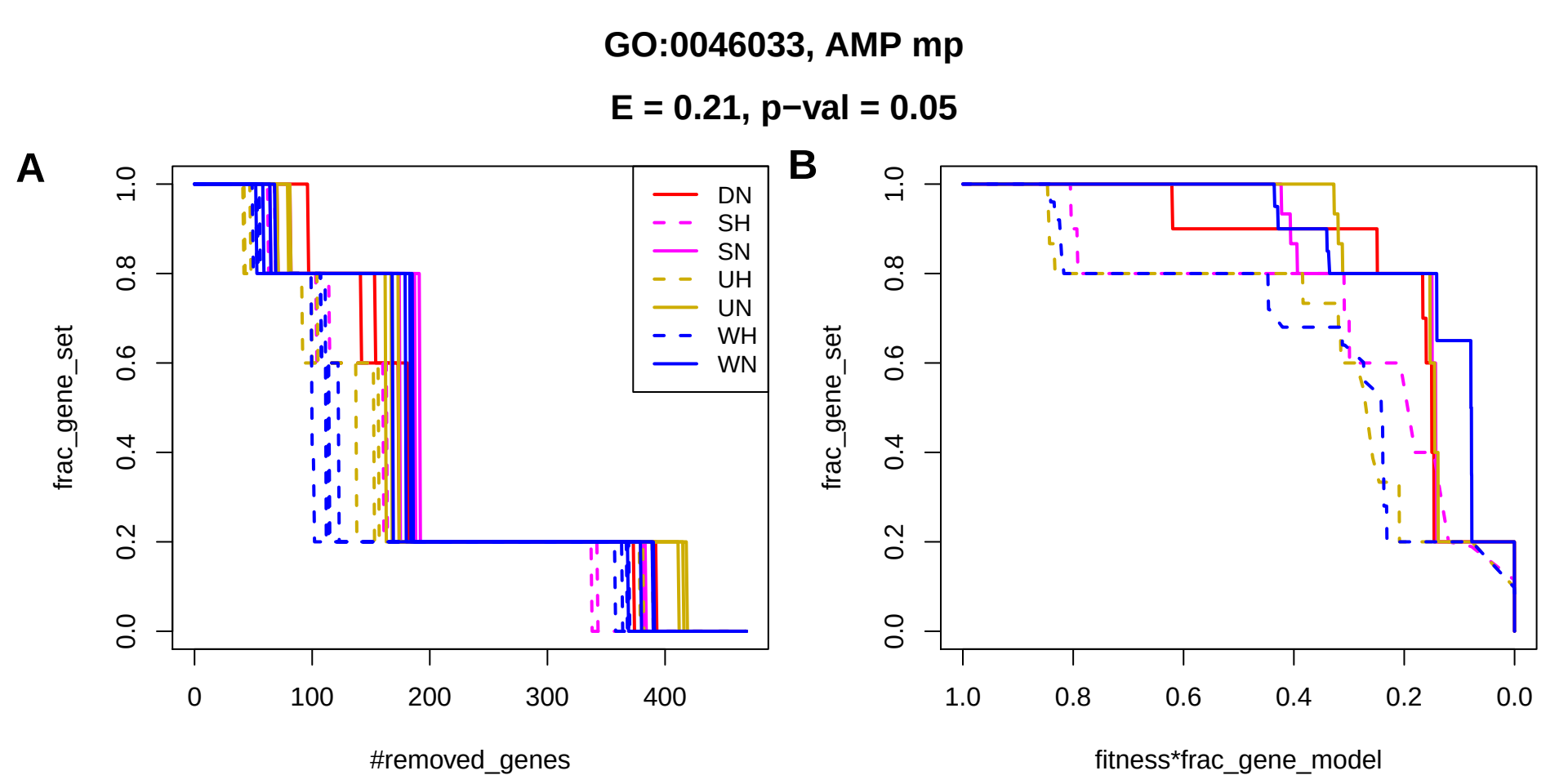

GO:0033615, mitochondrial proton−transporting ATP synthase complex assembly
E = 0.25, p−val = 0.063
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

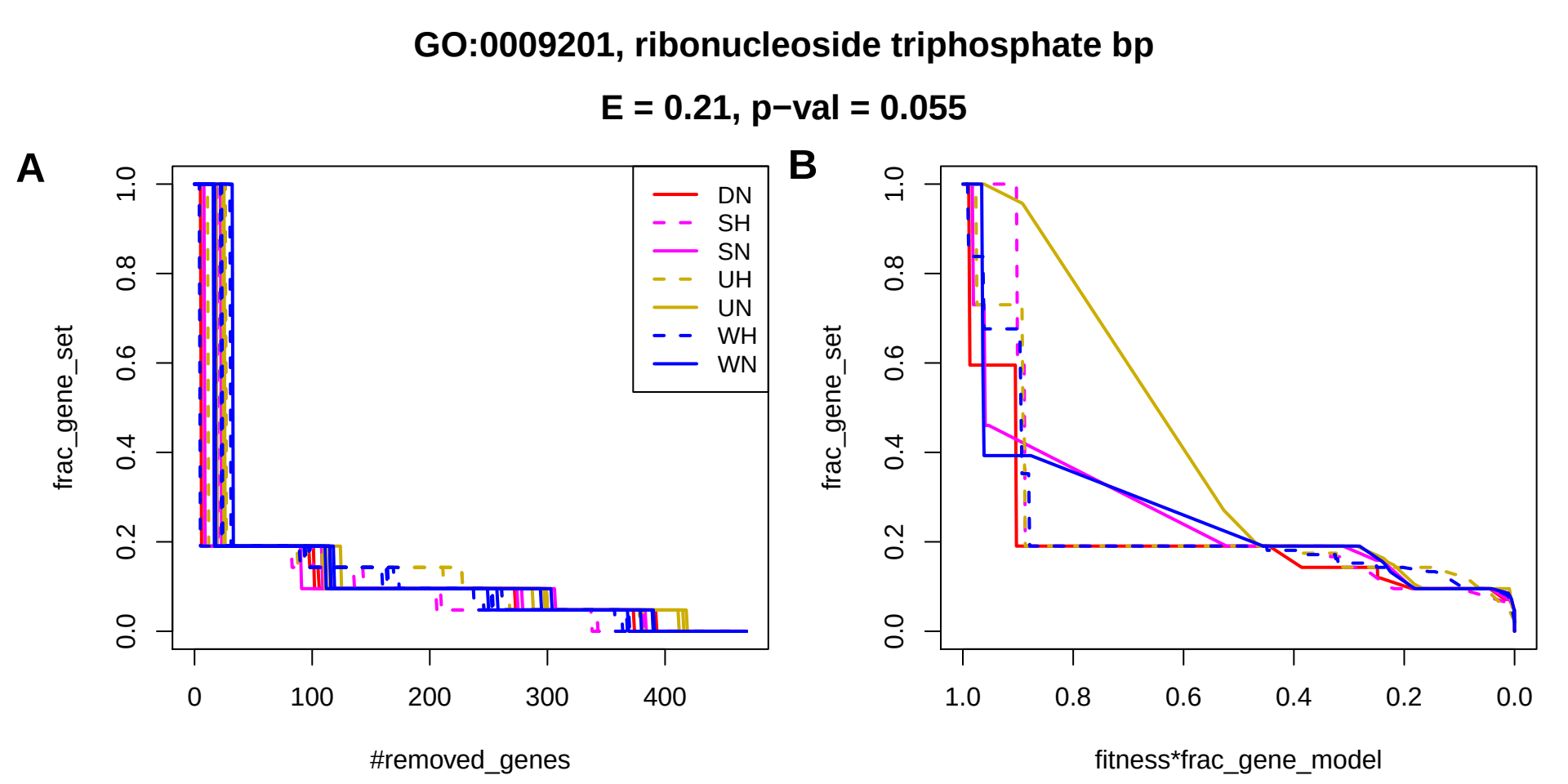

GO:0006526, arginine bp
E = 0.24, p−val = 0.055
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

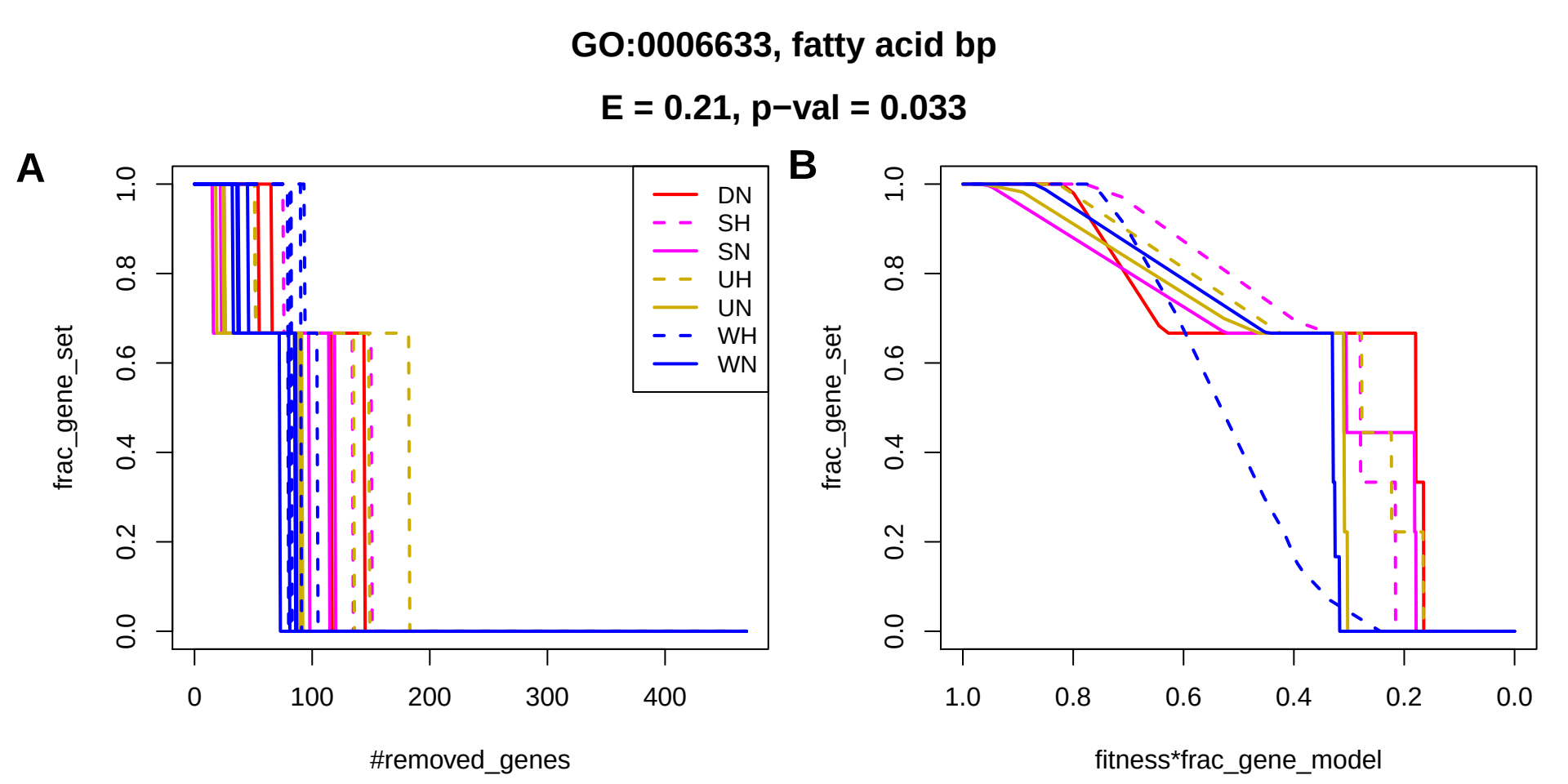

GO:0006207, 'de novo' pyrimidine nucleobase bp
E = 0.22, p−val = 0.06
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

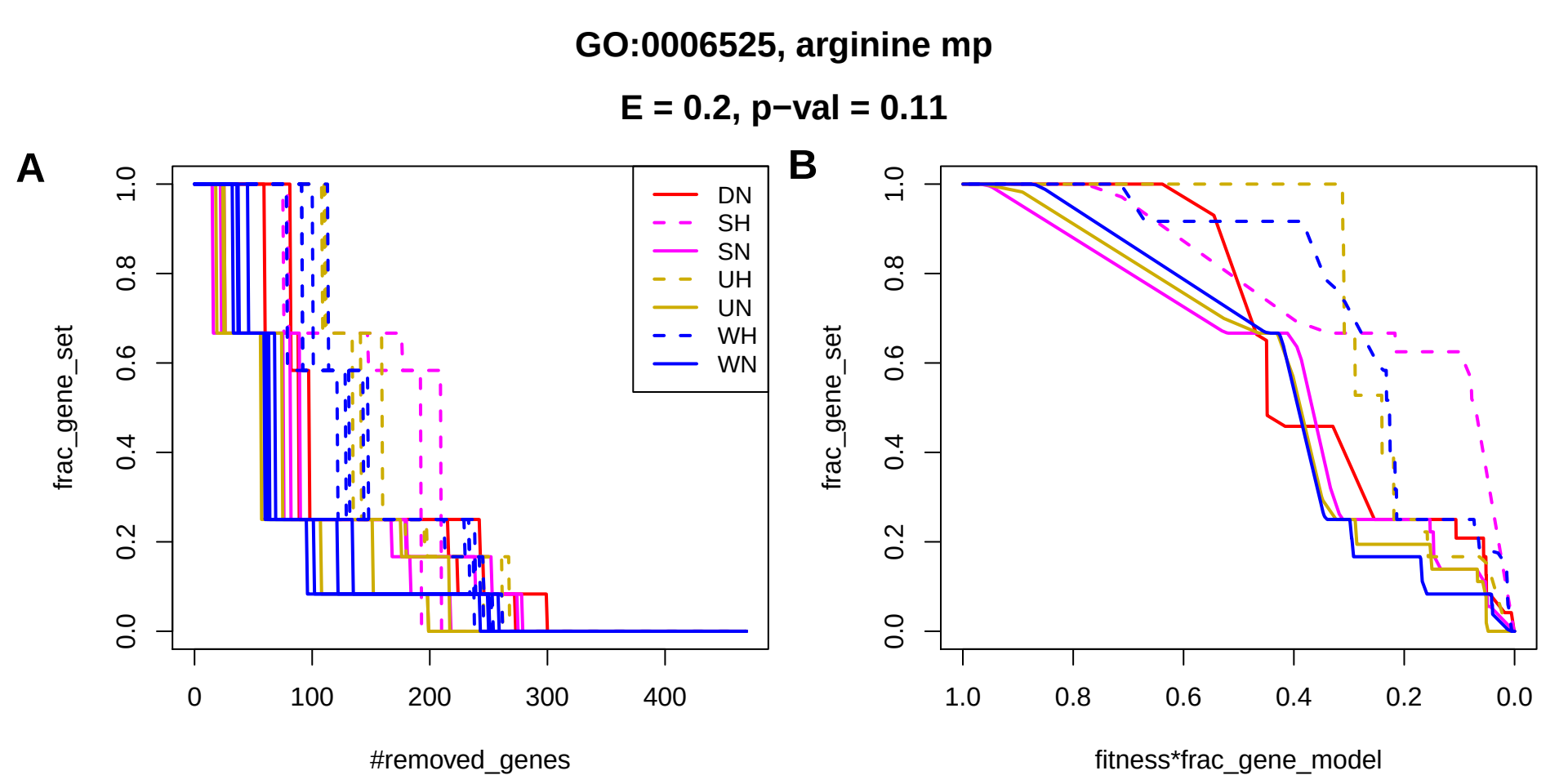

GO:0006541, glutamine mp
E = 0.22, p−val = 0.044
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

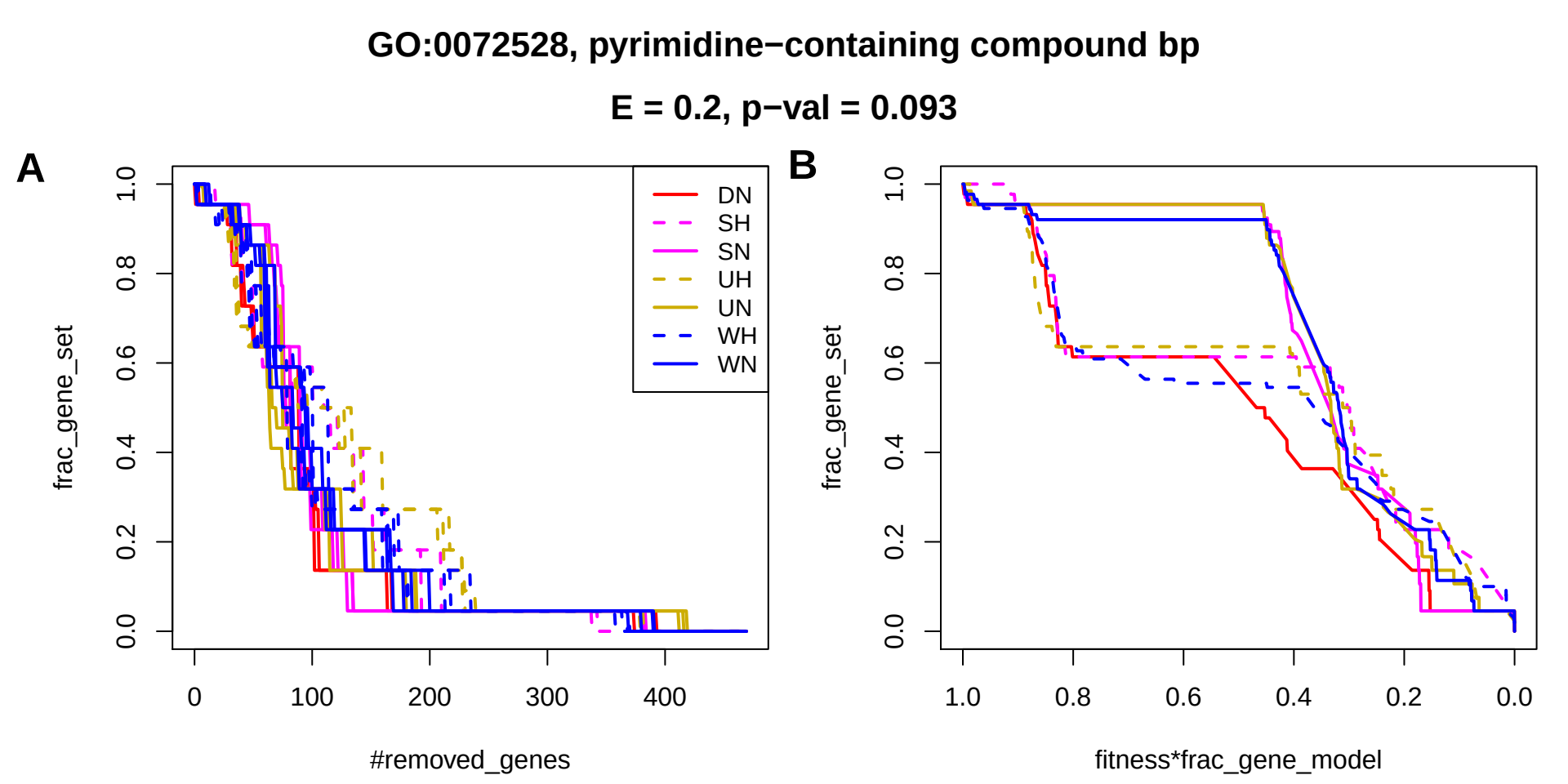

GO:0006221, pyrimidine nucleotide bp
E = 0.22, p−val = 0.052
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

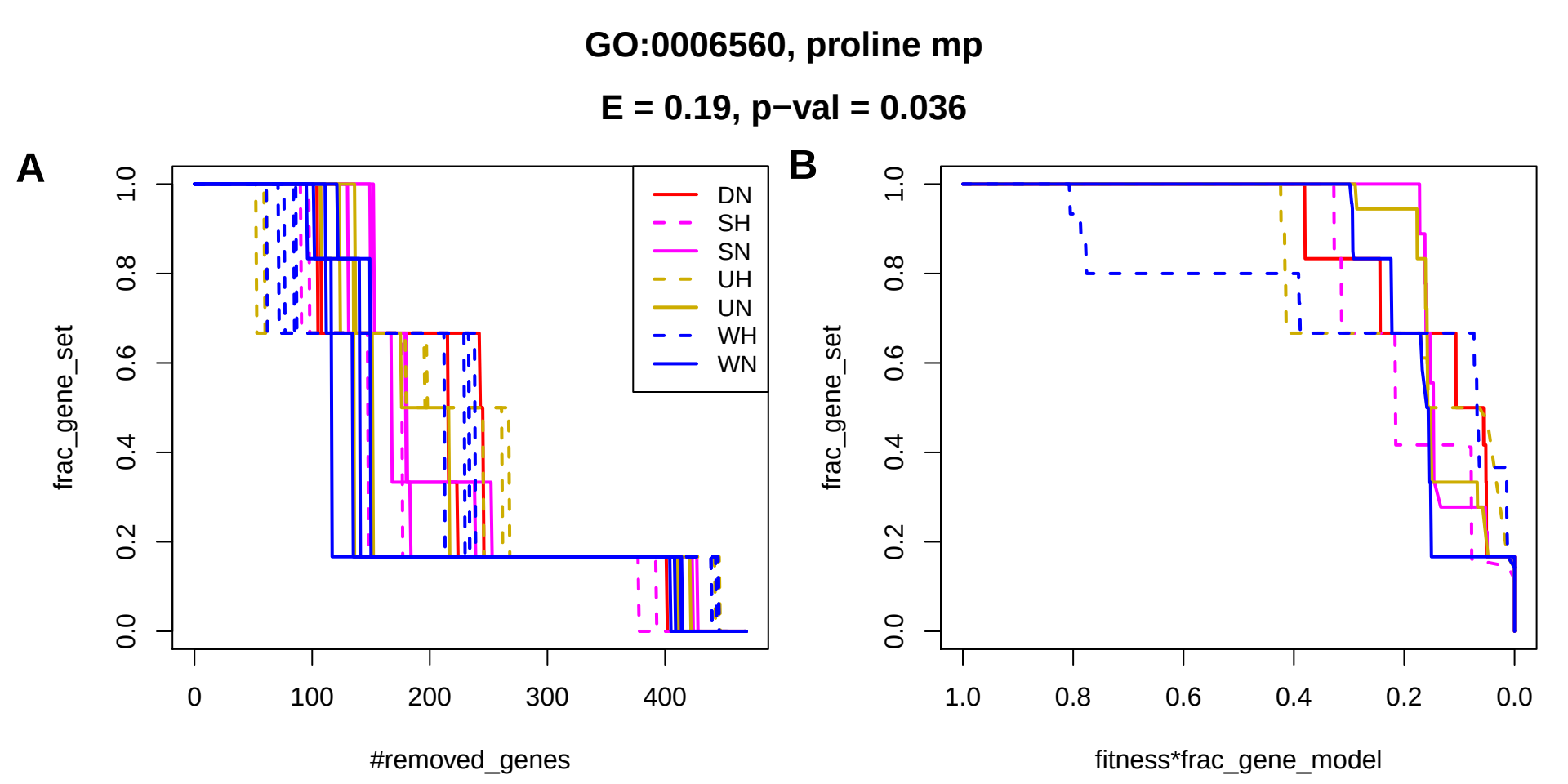

GO:0046033, AMP mp
E = 0.21, p−val = 0.05
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

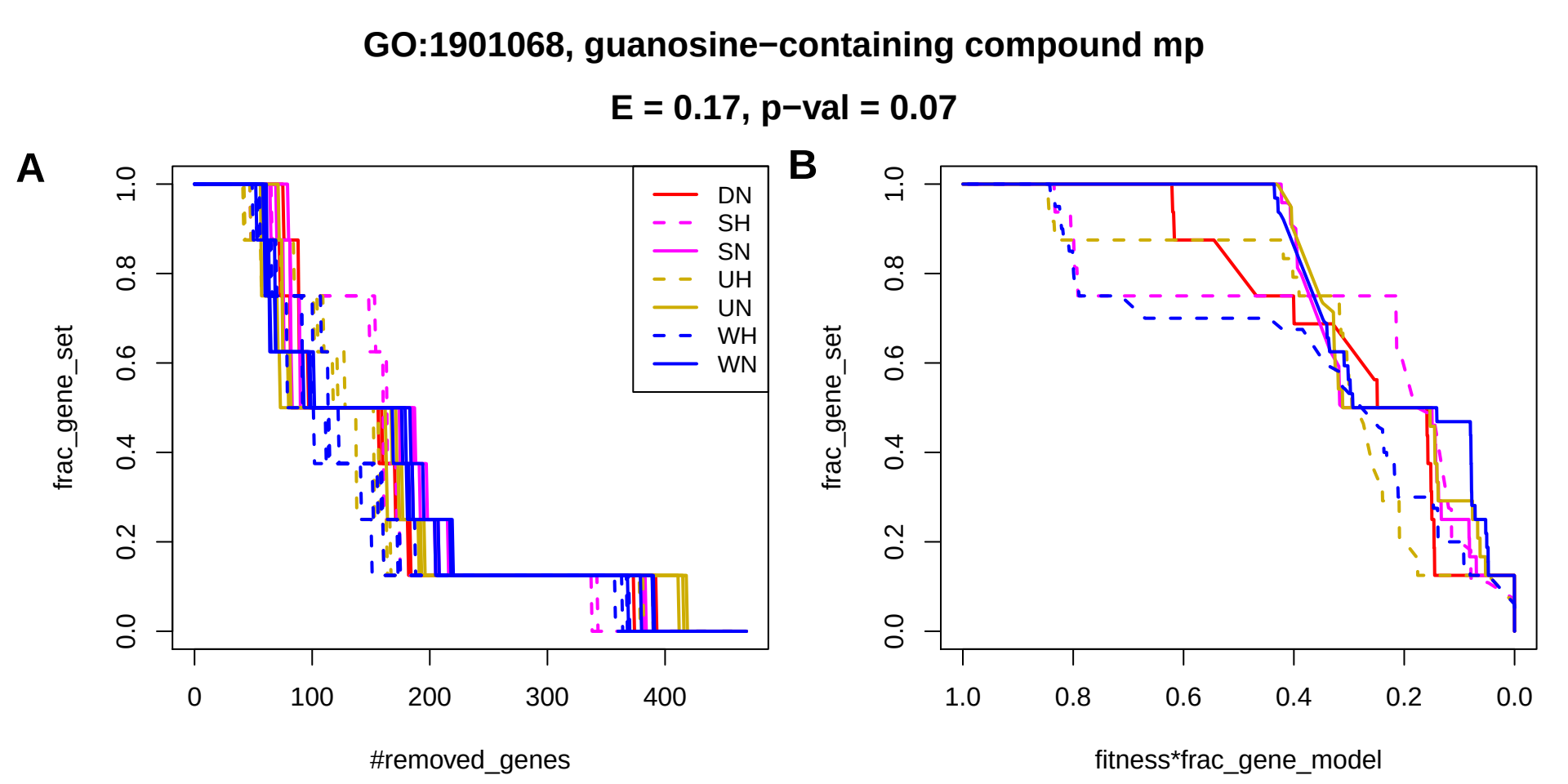

GO:0009201, ribonucleoside triphosphate bp
E = 0.21, p−val = 0.055
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

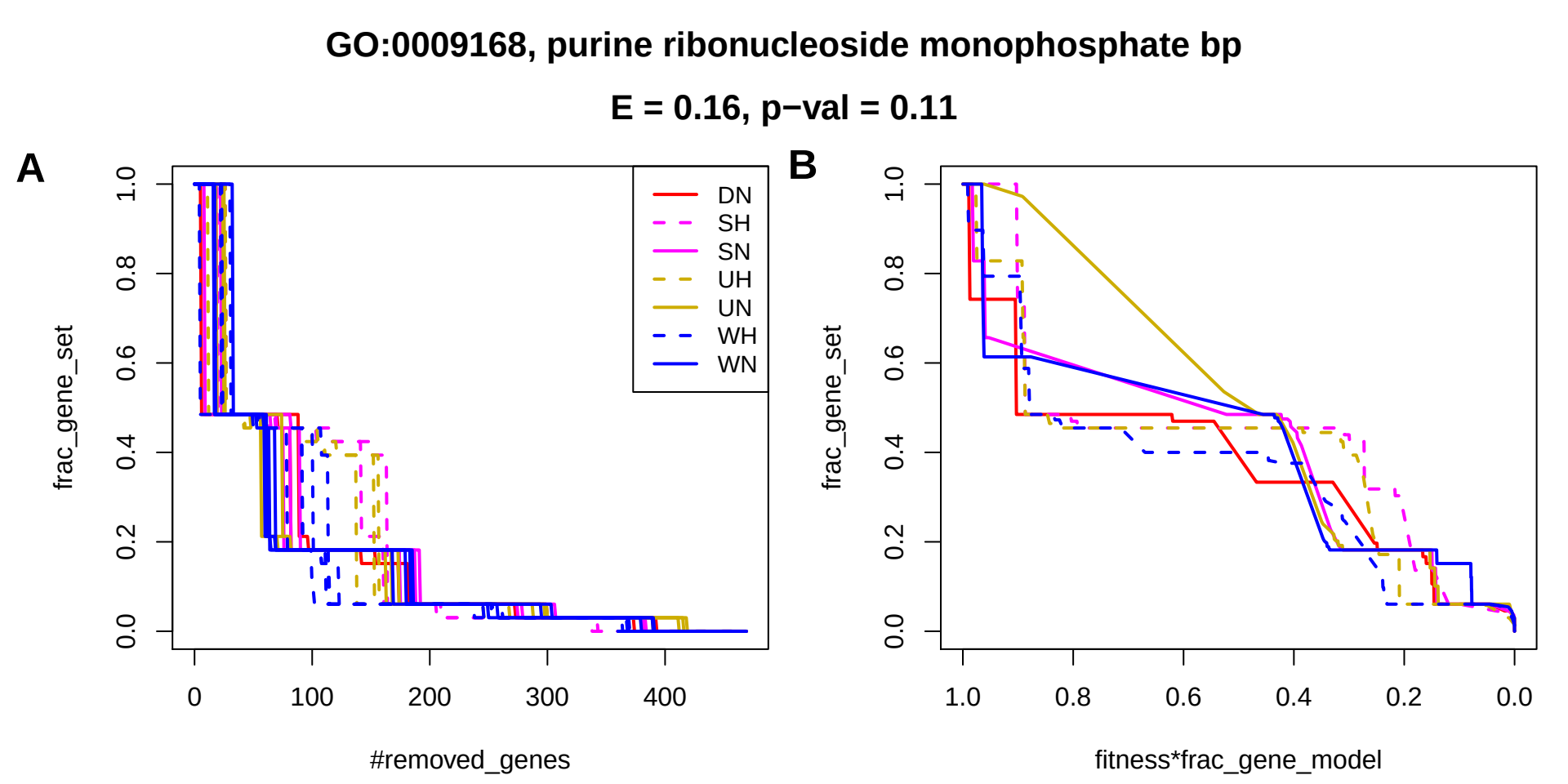

GO:0006633, fatty acid bp
E = 0.21, p−val = 0.033
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

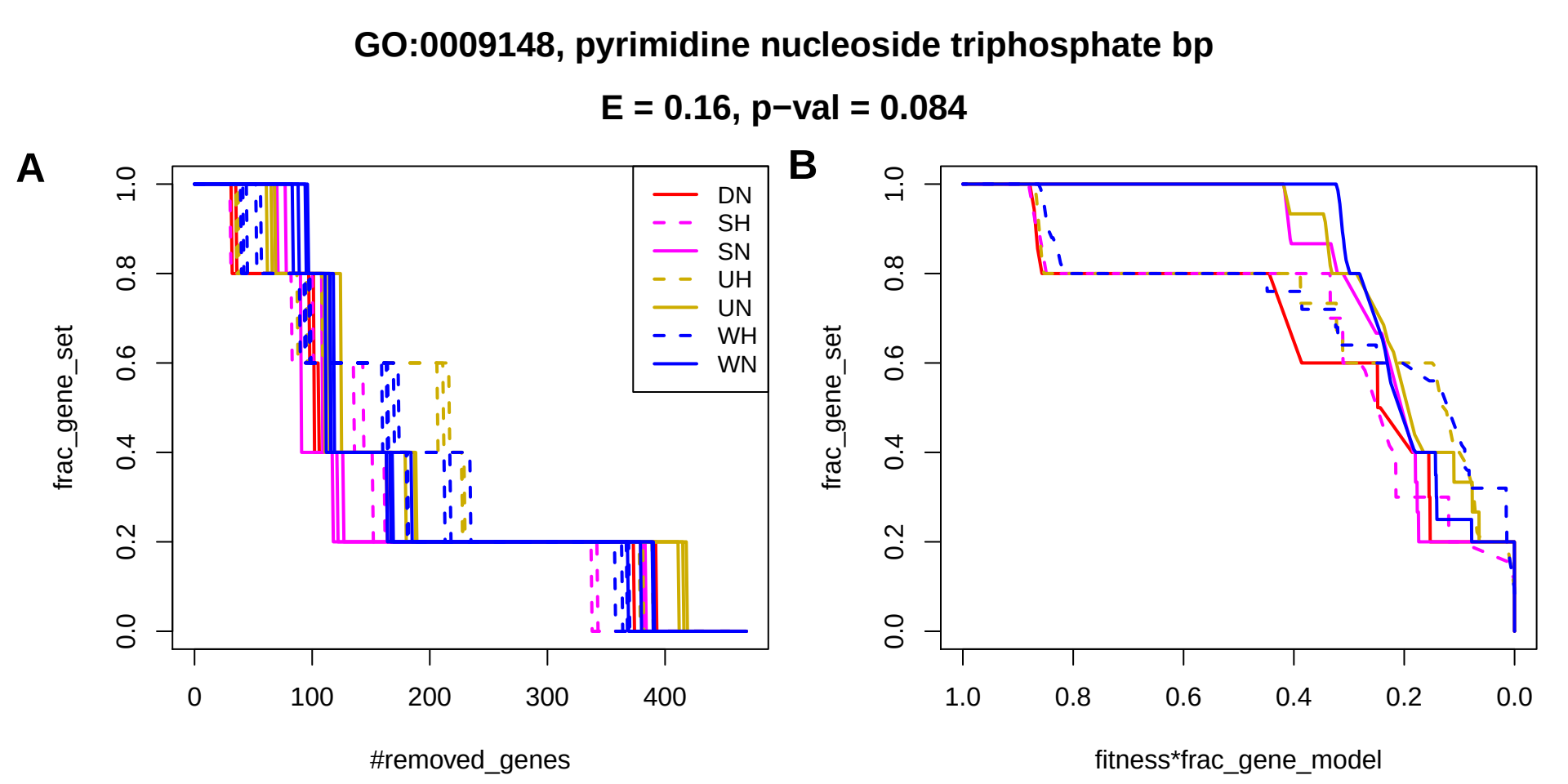

GO:0006525, arginine mp
E = 0.2, p−val = 0.11
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

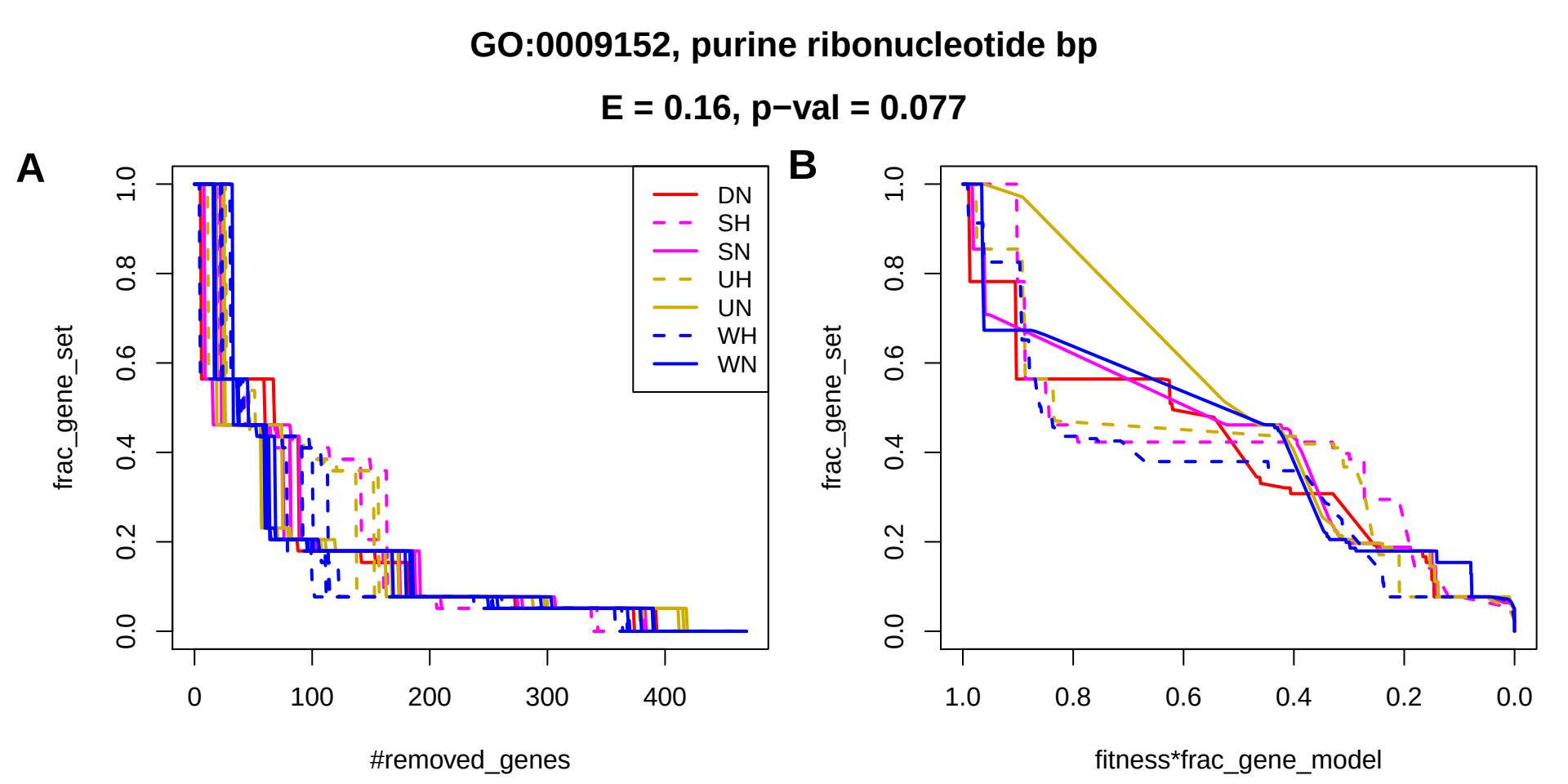

GO:0072528, pyrimidine−containing compound bp
E = 0.2, p−val = 0.093
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

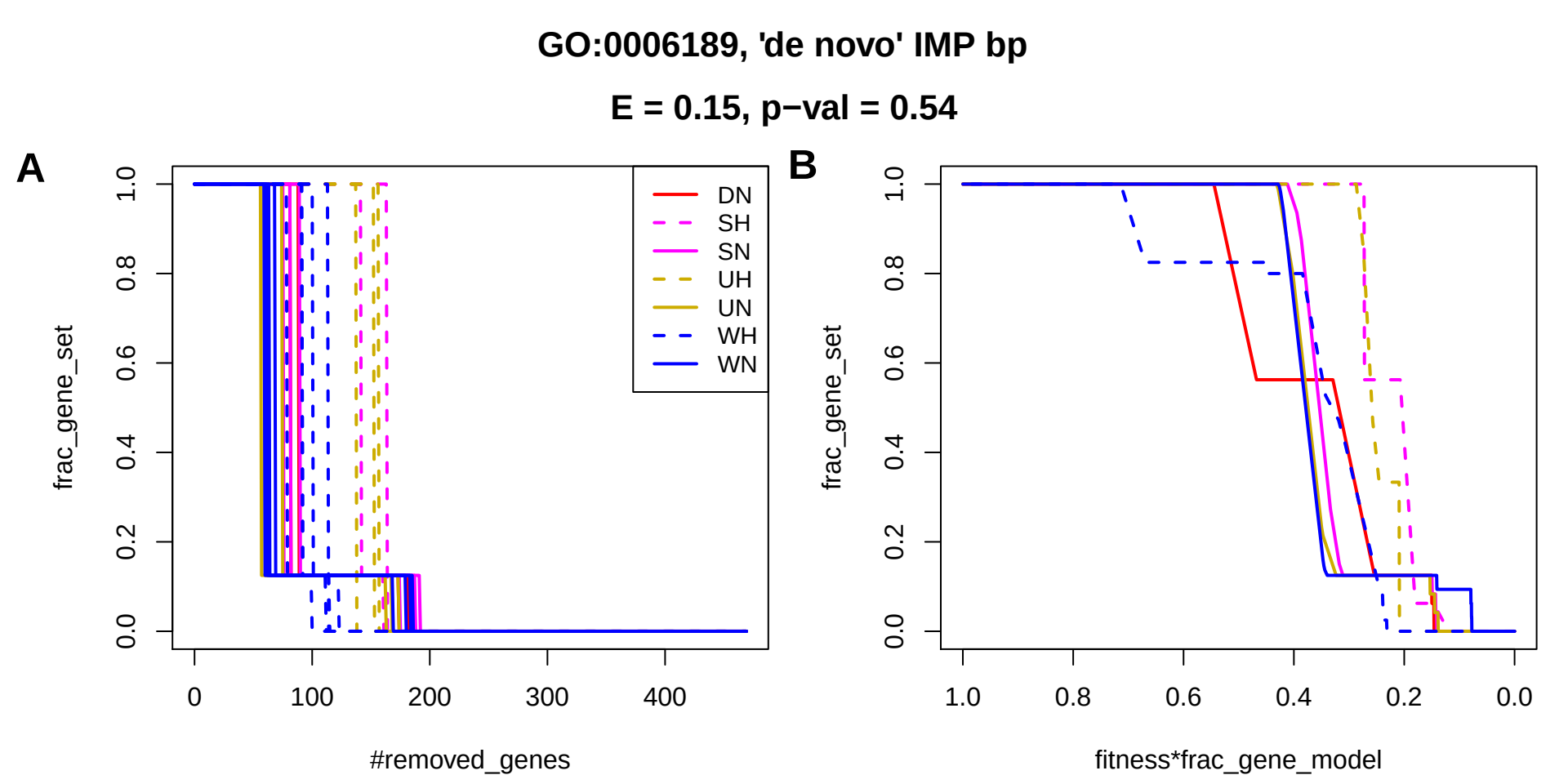

GO:0006560, proline mp
E = 0.19, p−val = 0.036
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

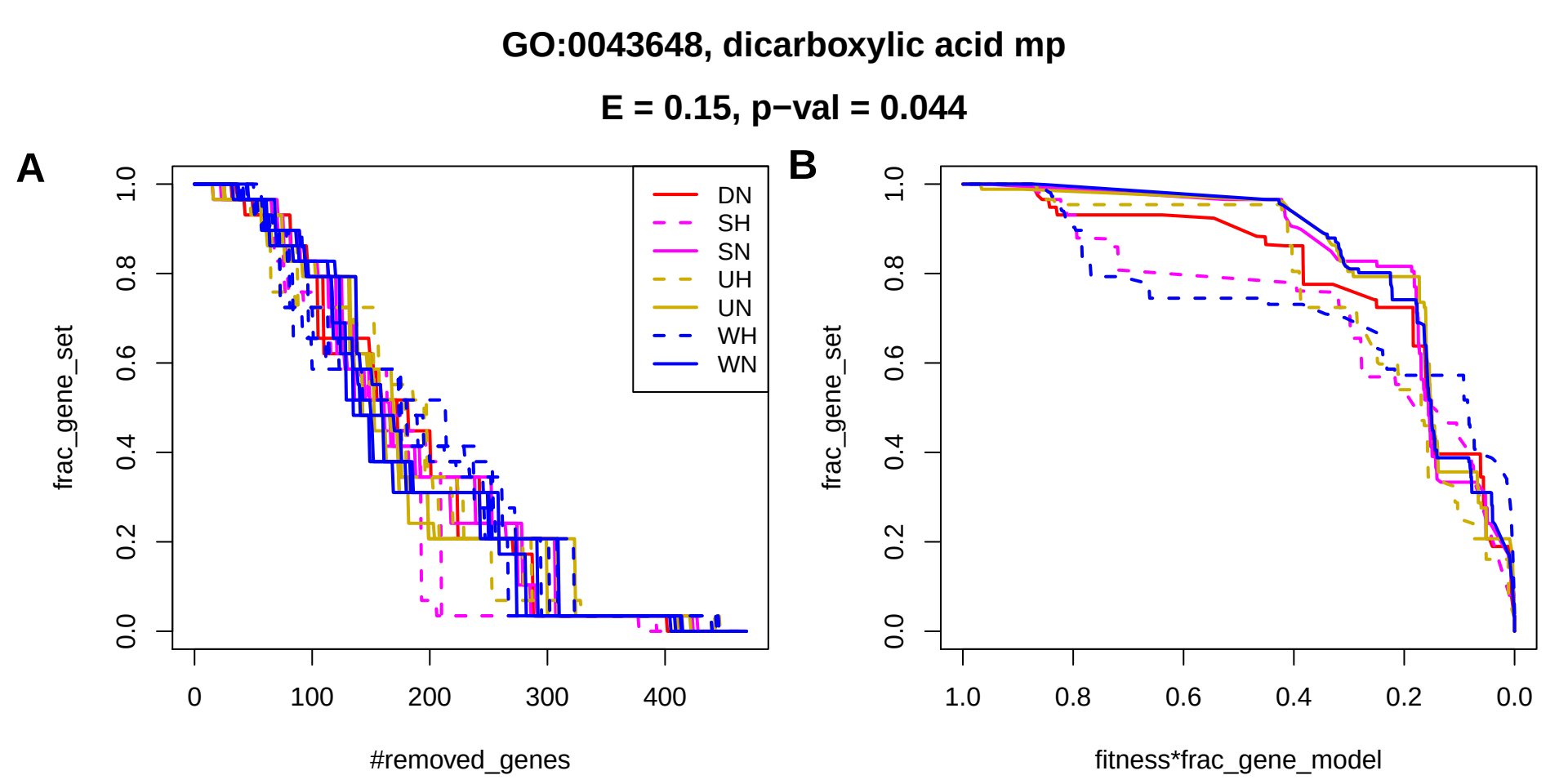

GO:1901068, guanosine−containing compound mp
E = 0.17, p−val = 0.07
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

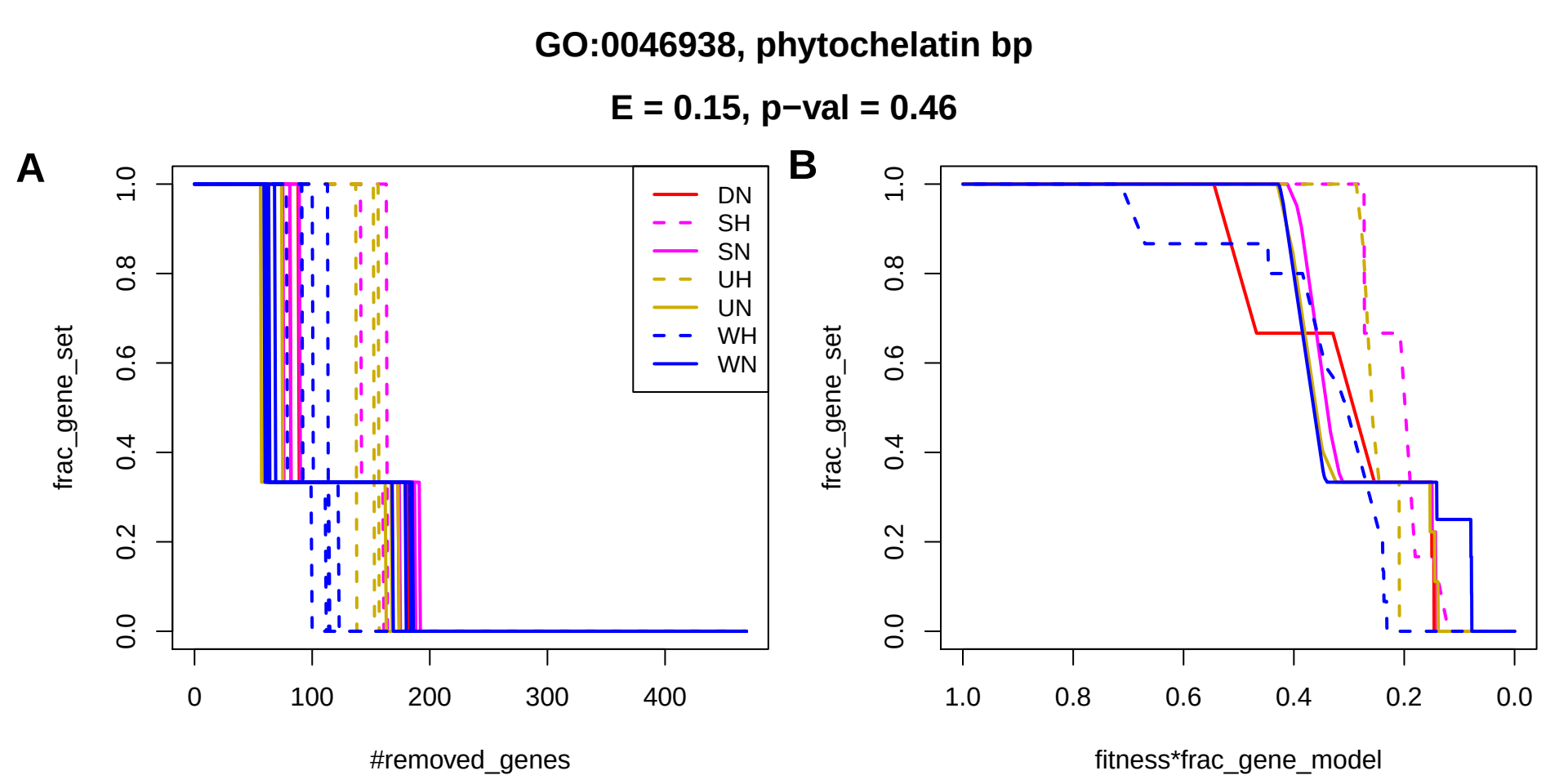

GO:0009168, purine ribonucleoside monophosphate bp
E = 0.16, p−val = 0.11
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

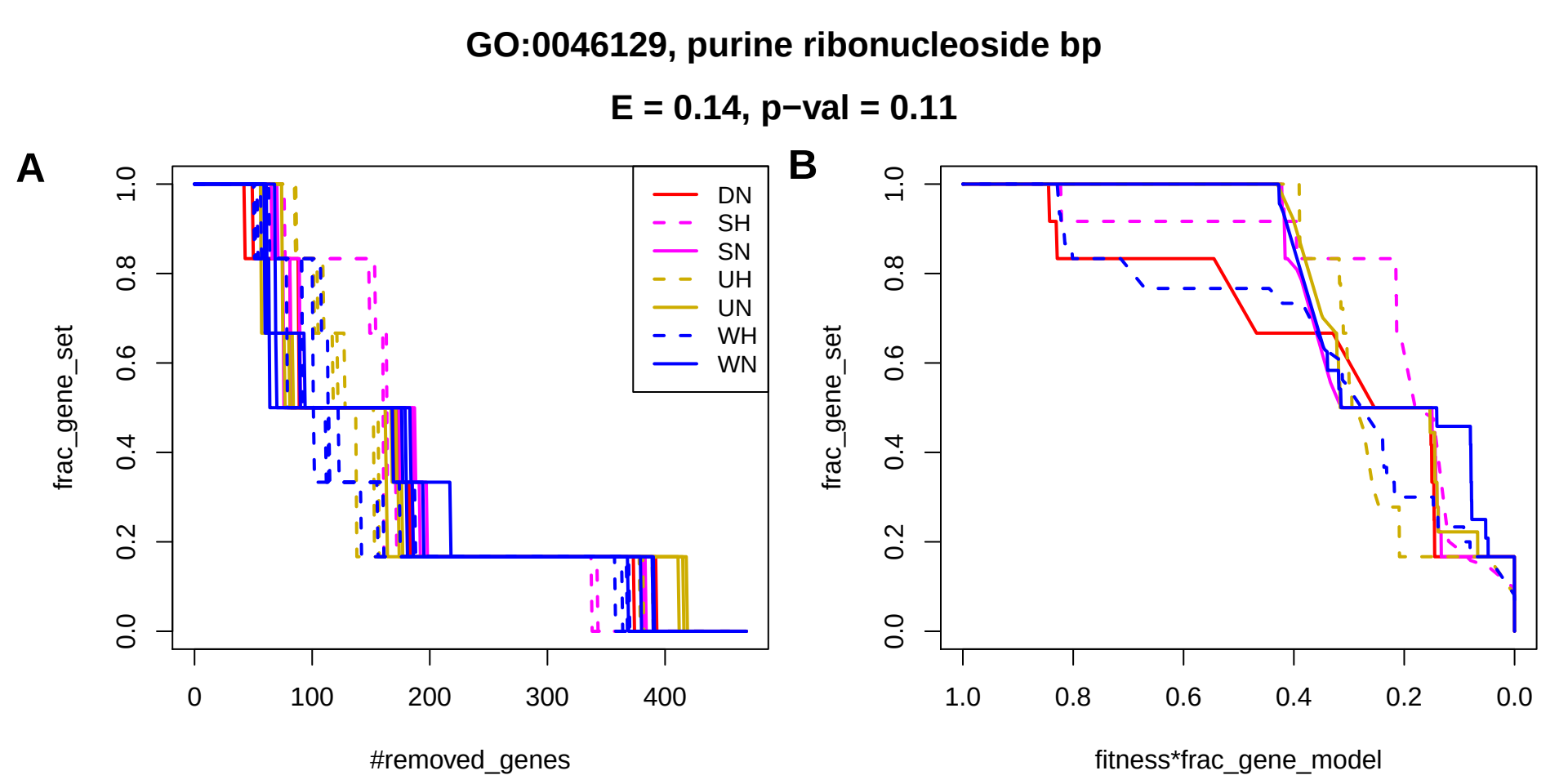

GO:0009148, pyrimidine nucleoside triphosphate bp
E = 0.16, p−val = 0.084
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

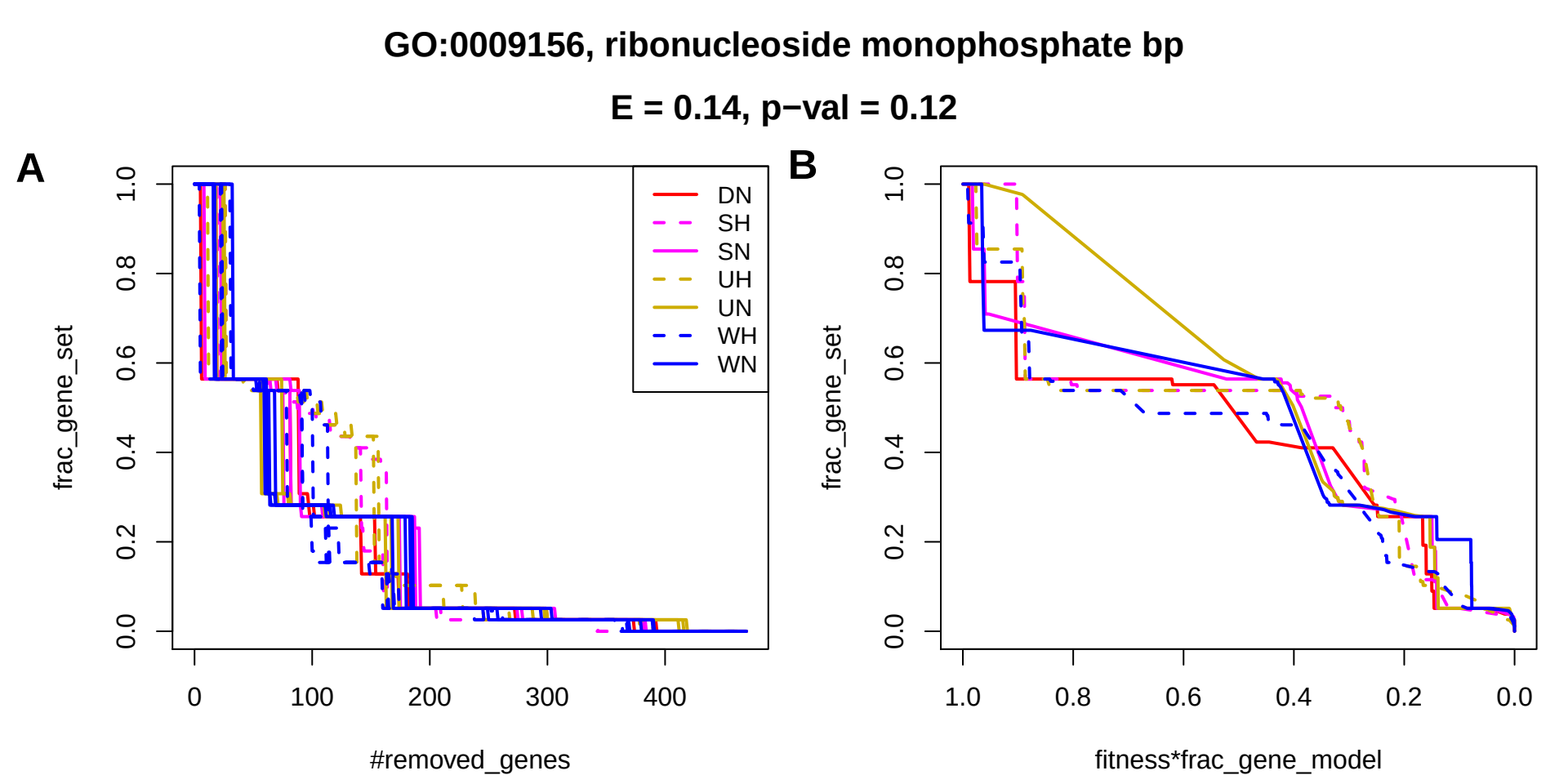

GO:0009152, purine ribonucleotide bp
E = 0.16, p−val = 0.077
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

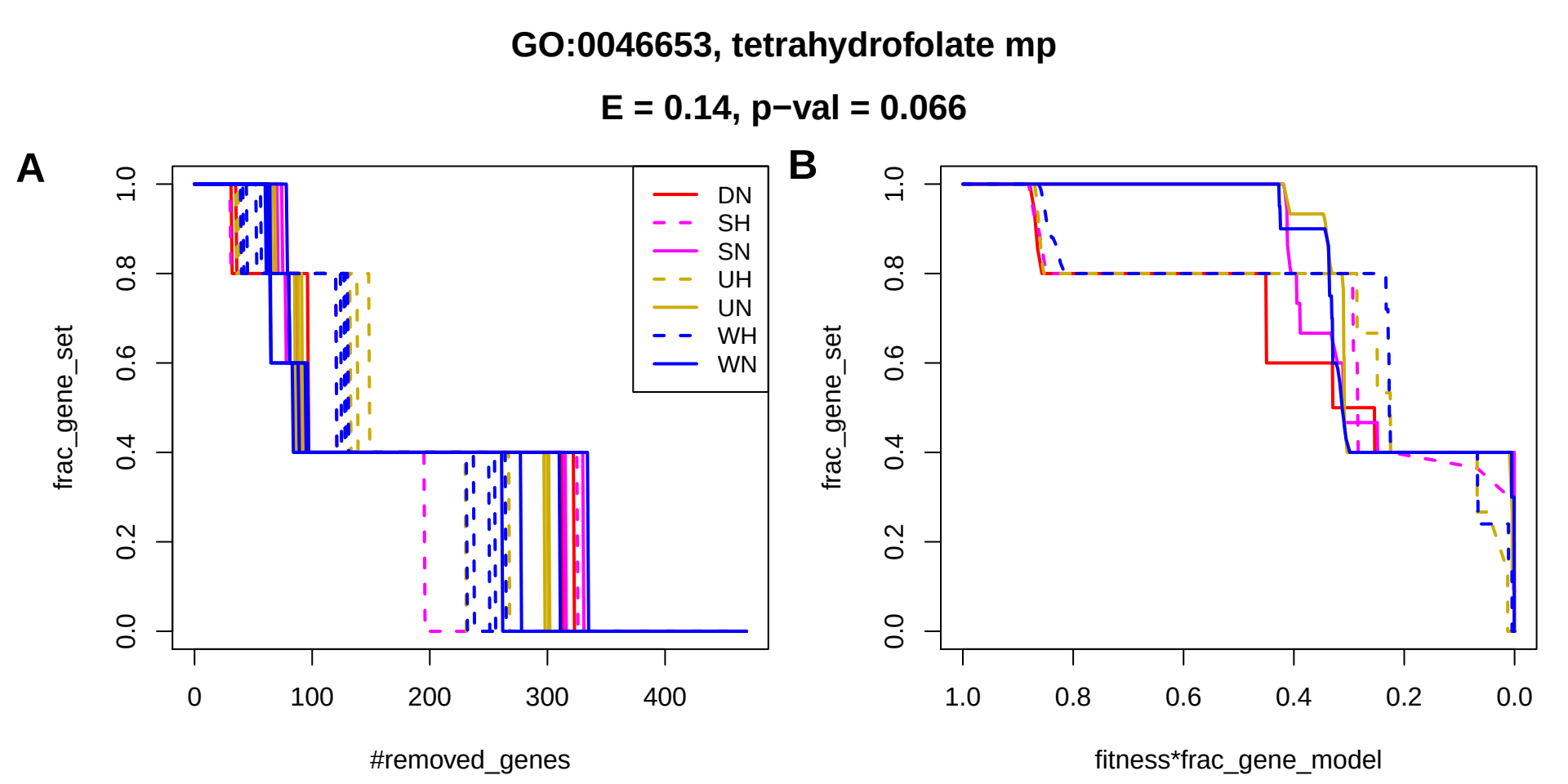

GO:0006189, 'de novo' IMP bp
E = 0.15, p−val = 0.54
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

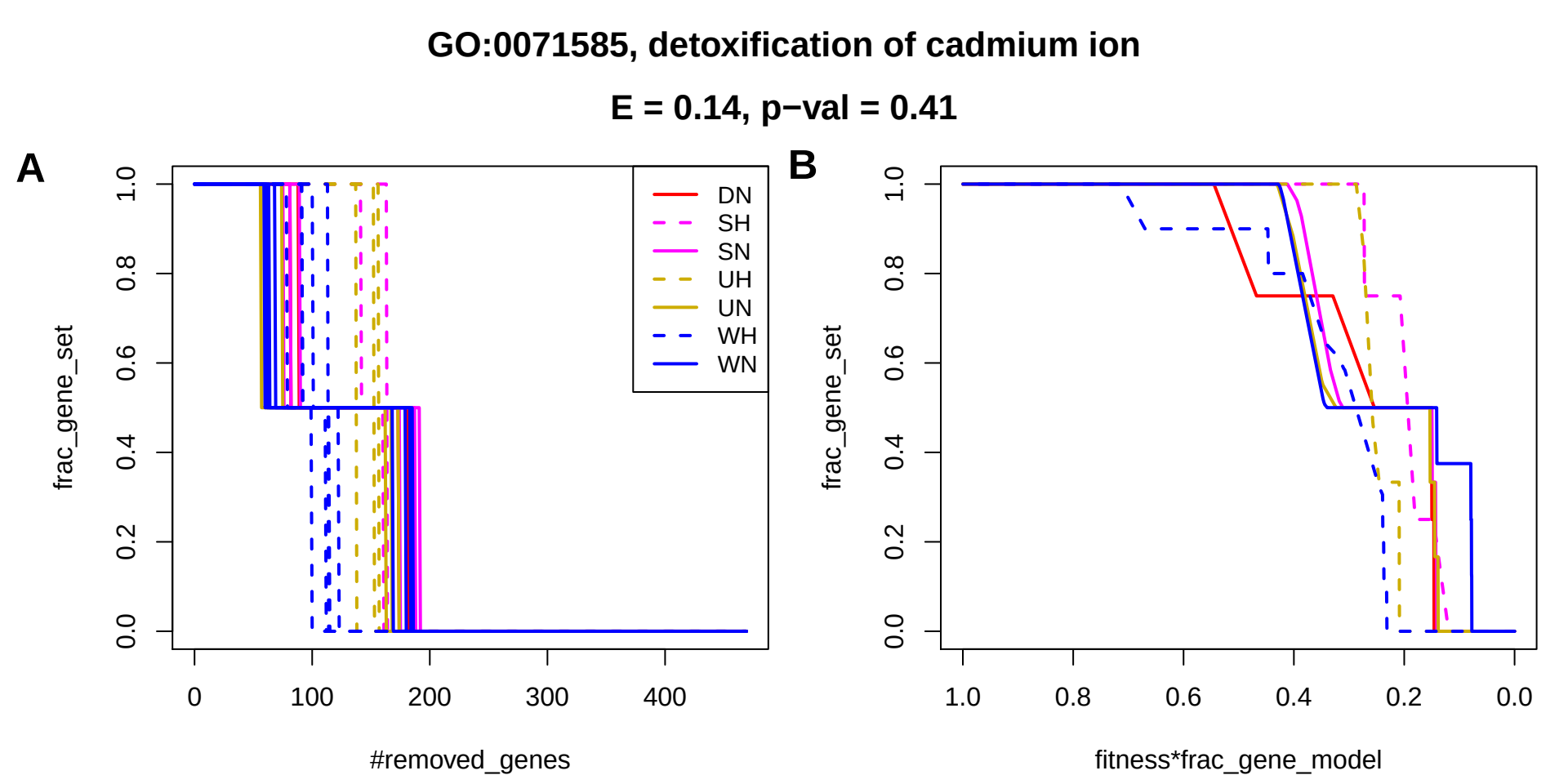

GO:0043648, dicarboxylic acid mp
E = 0.15, p−val = 0.044
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

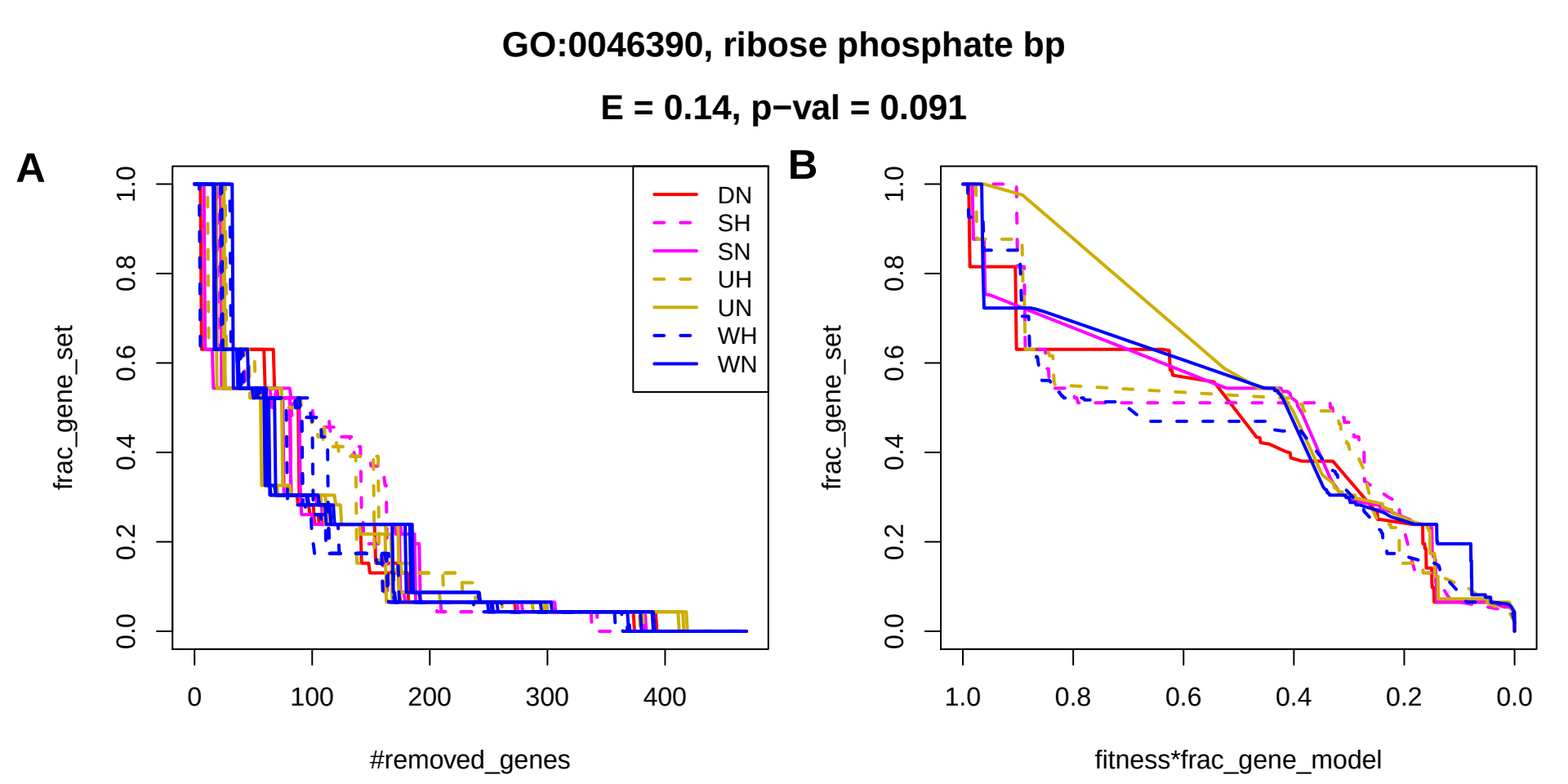

GO:0046938, phytochelatin bp
E = 0.15, p−val = 0.46
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

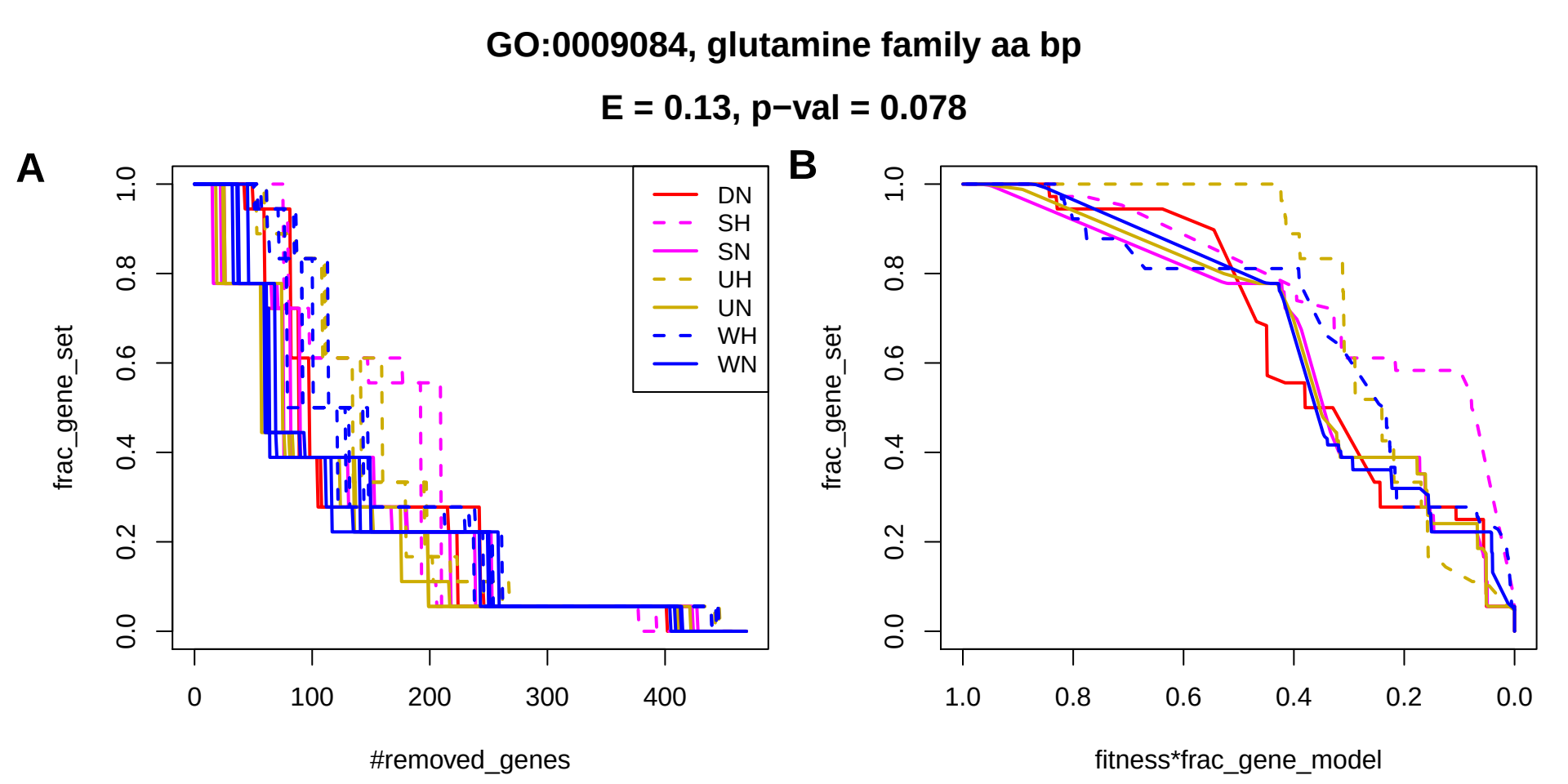

GO:0046129, purine ribonucleoside bp
E = 0.14, p−val = 0.11
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

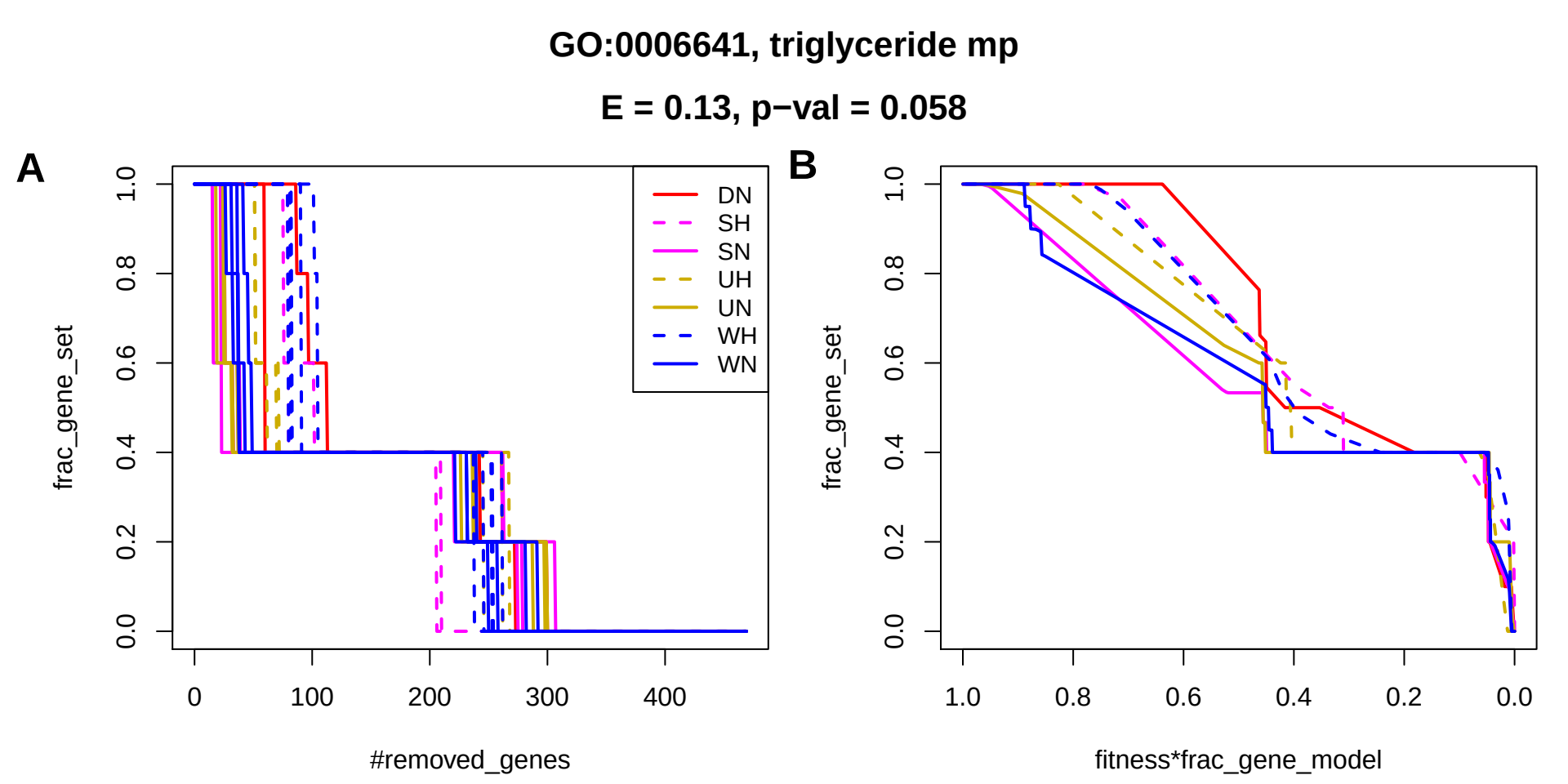

GO:0009156, ribonucleoside monophosphate bp
E = 0.14, p−val = 0.12
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0046653, tetrahydrofolate mp
E = 0.14, p−val = 0.066
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0071585, detoxification of cadmium ion
E = 0.14, p−val = 0.41
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0046390, ribose phosphate bp
E = 0.14, p−val = 0.091
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009084, glutamine family aa bp
E = 0.13, p−val = 0.078
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006641, triglyceride mp
E = 0.13, p−val = 0.058
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
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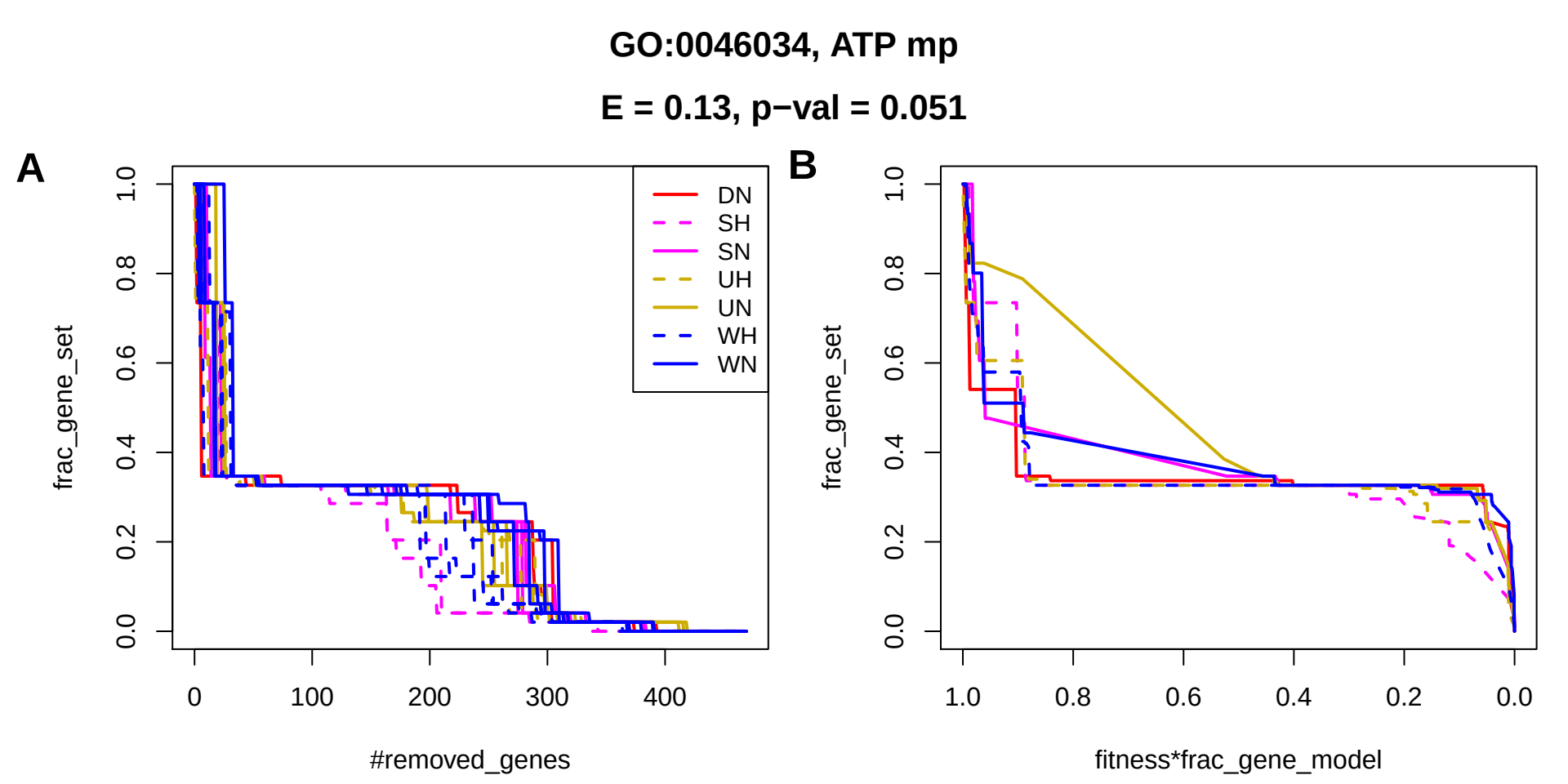
GO:0046034, ATP mp
E = 0.13, p−val = 0.051
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
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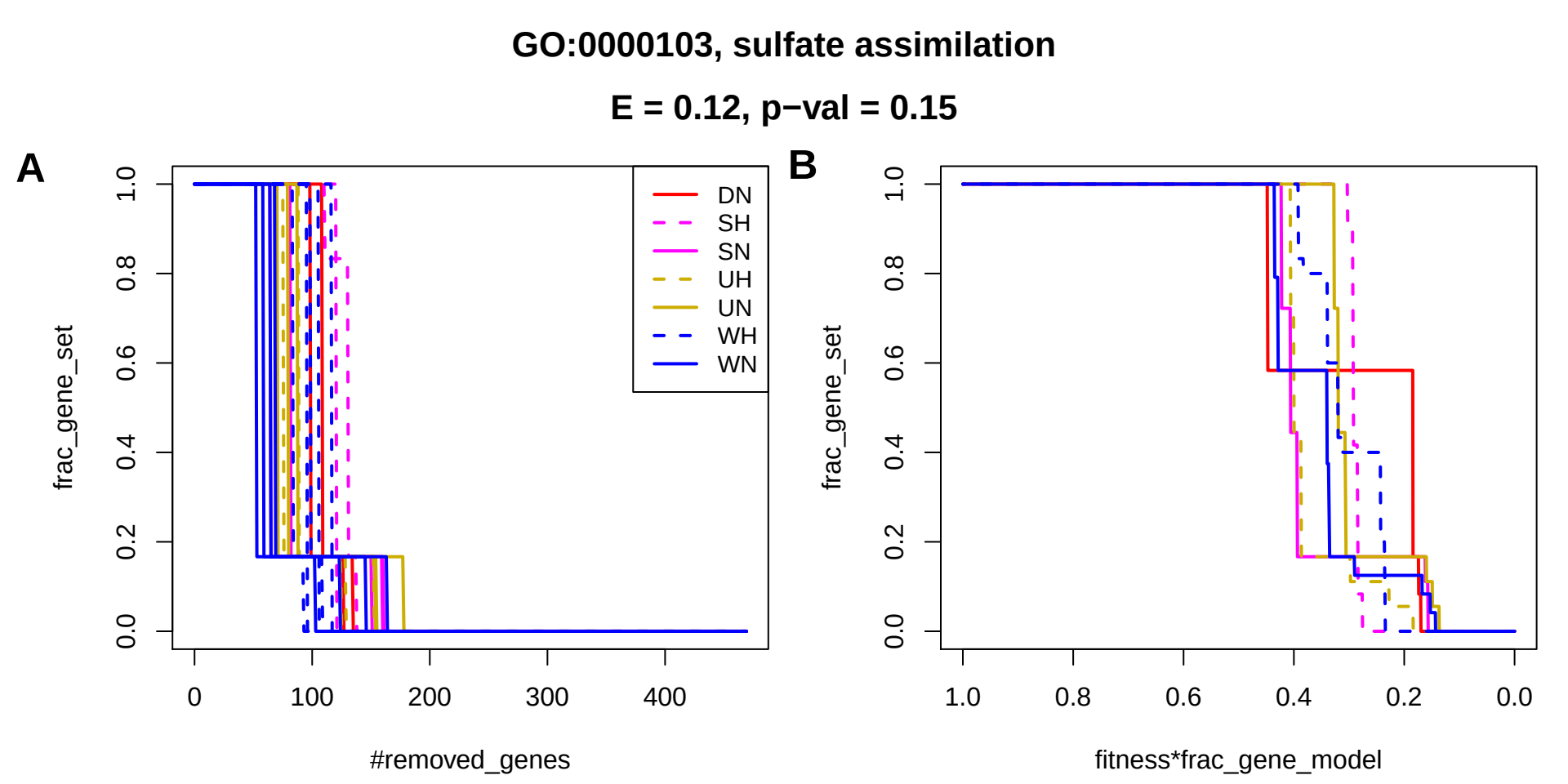
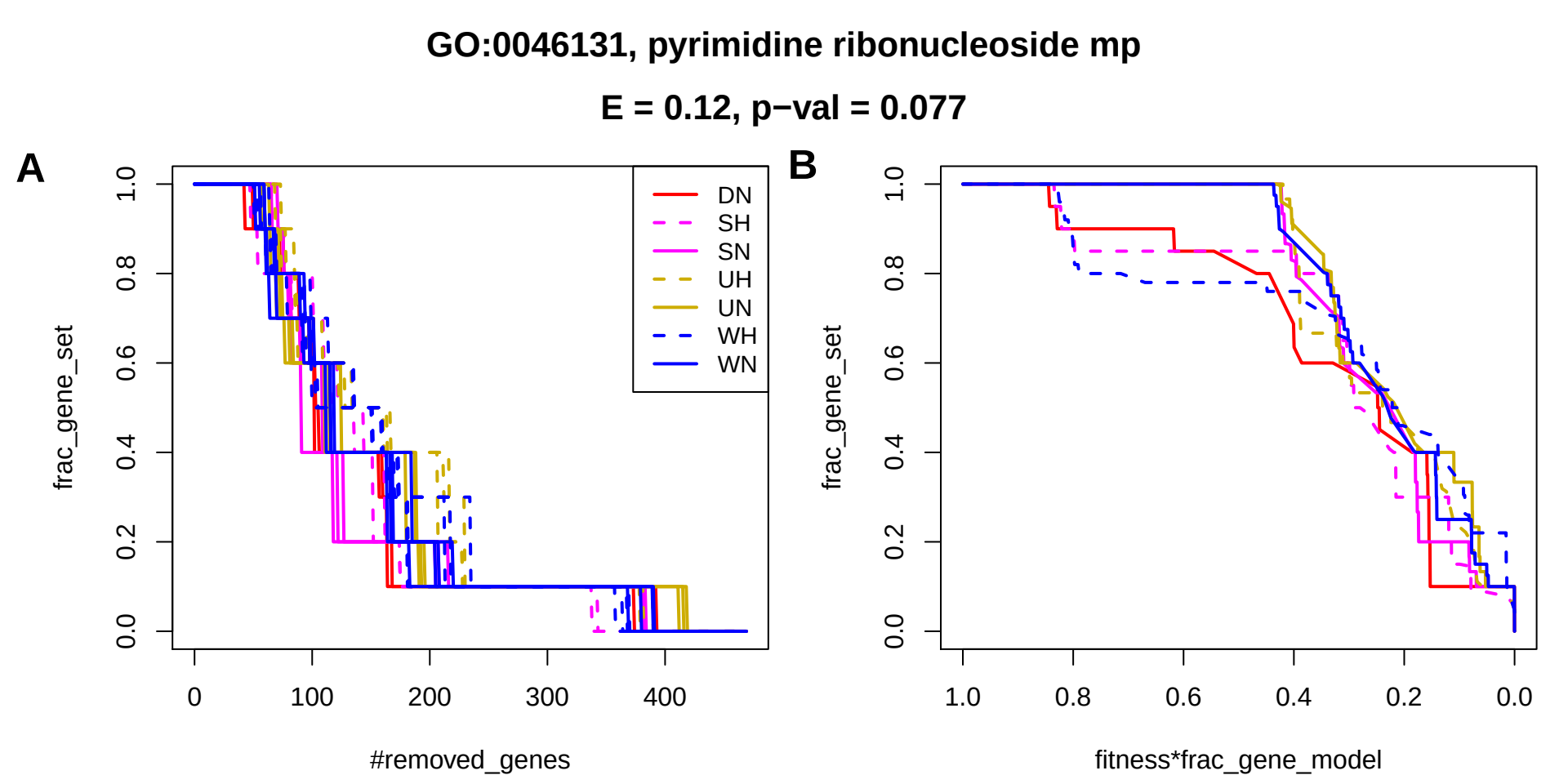
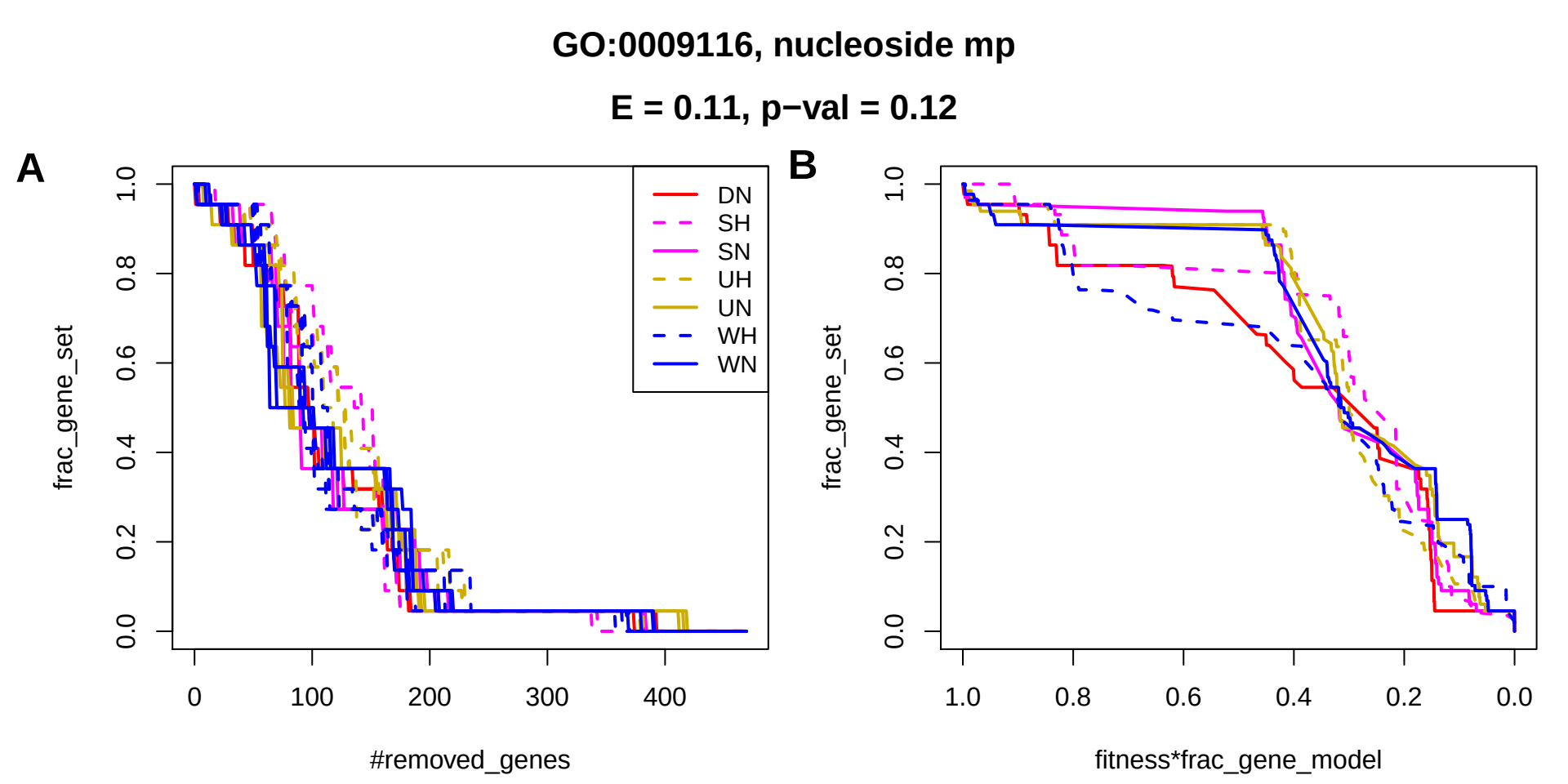
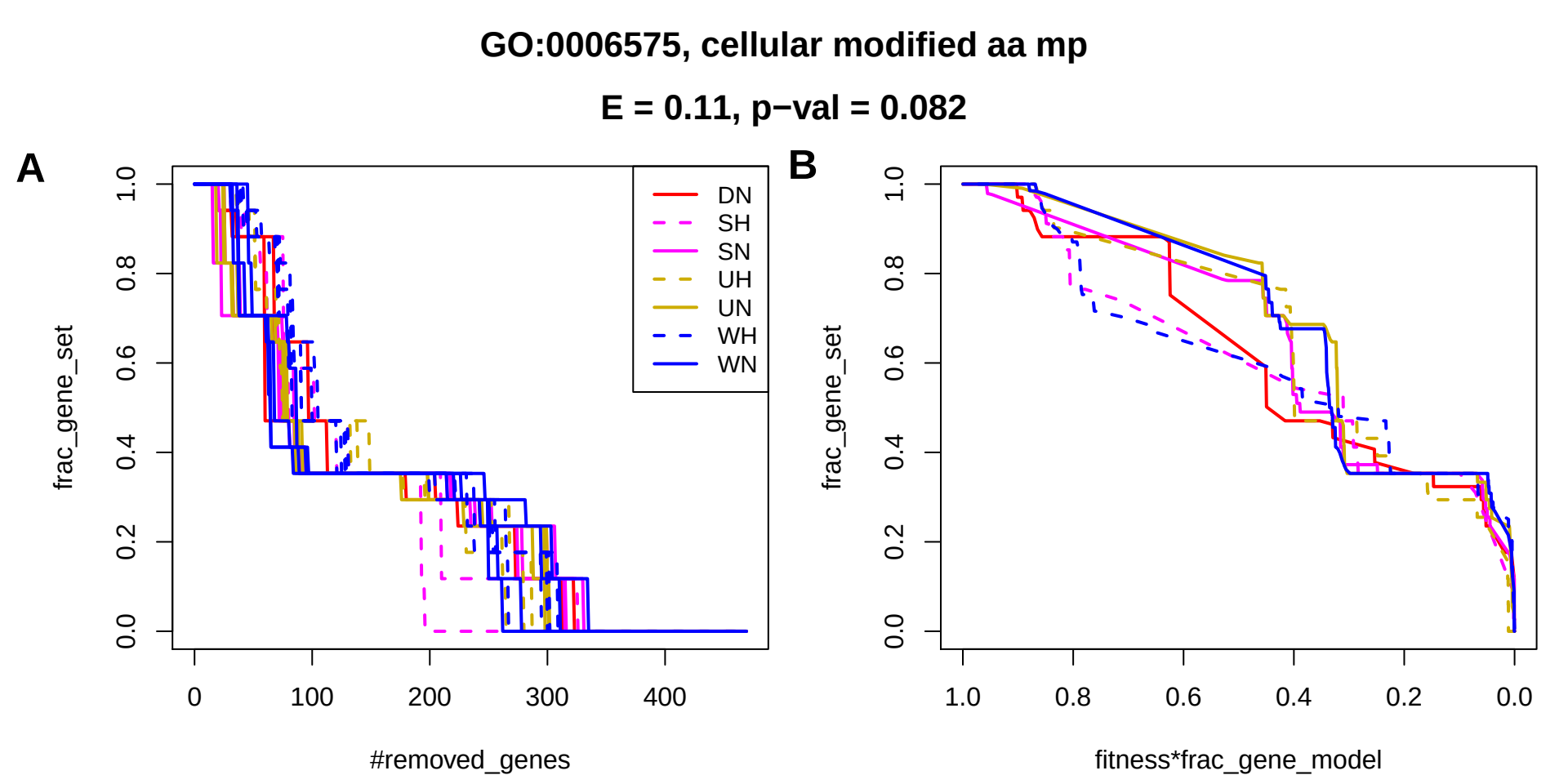
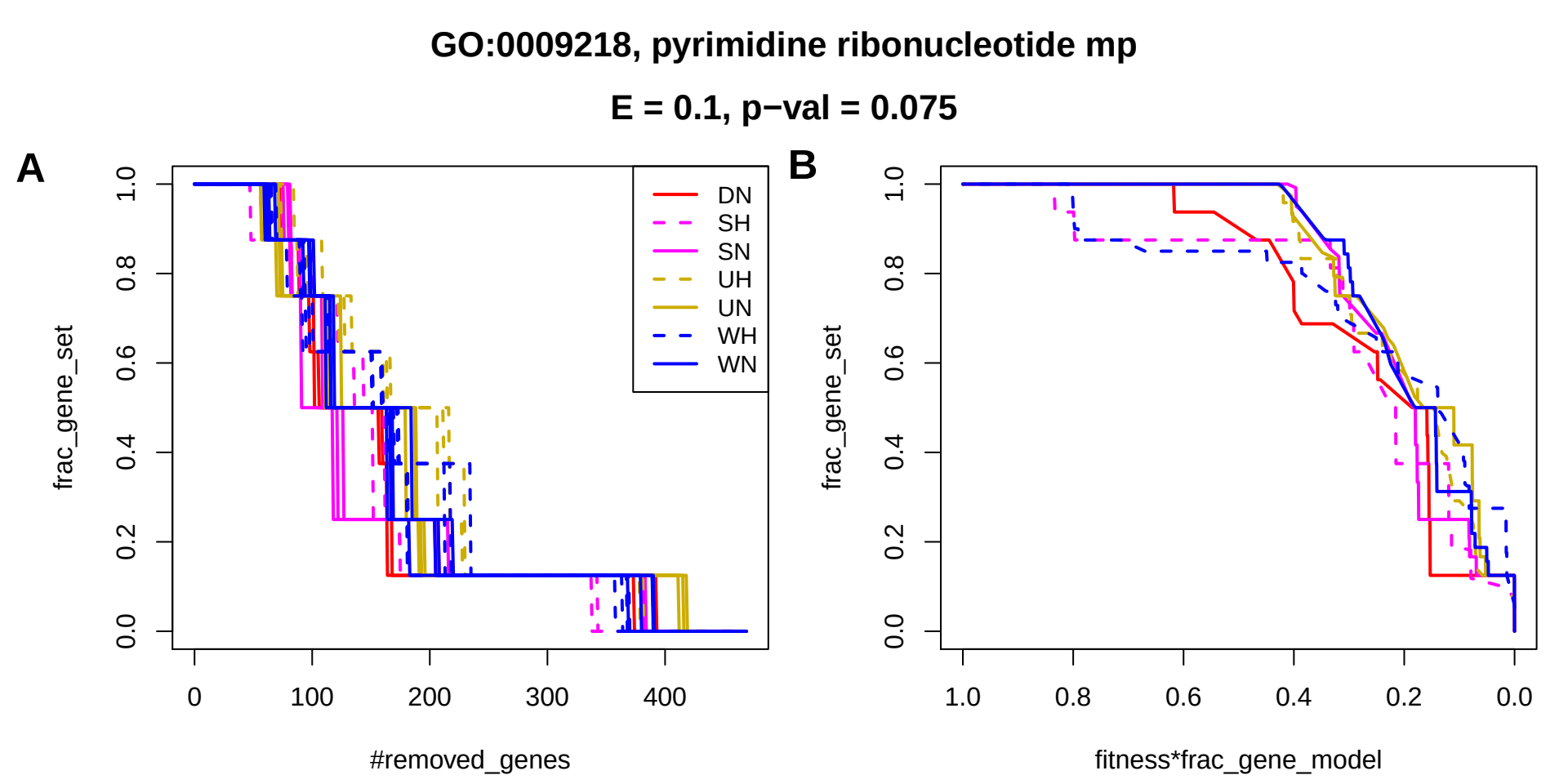
100
200
300
400

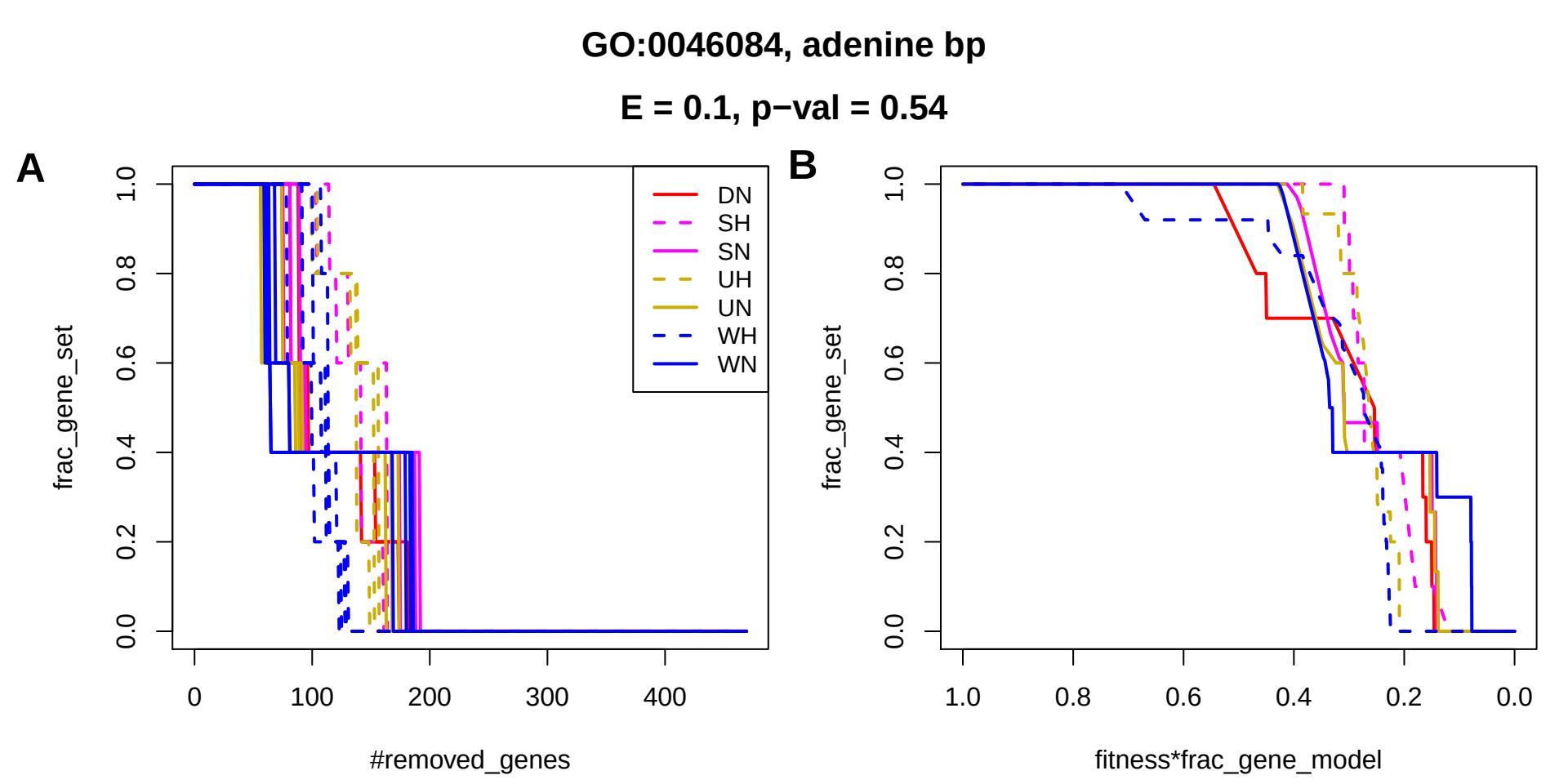

GO:0000103, sulfate assimilation
E = 0.12, p−val = 0.15
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

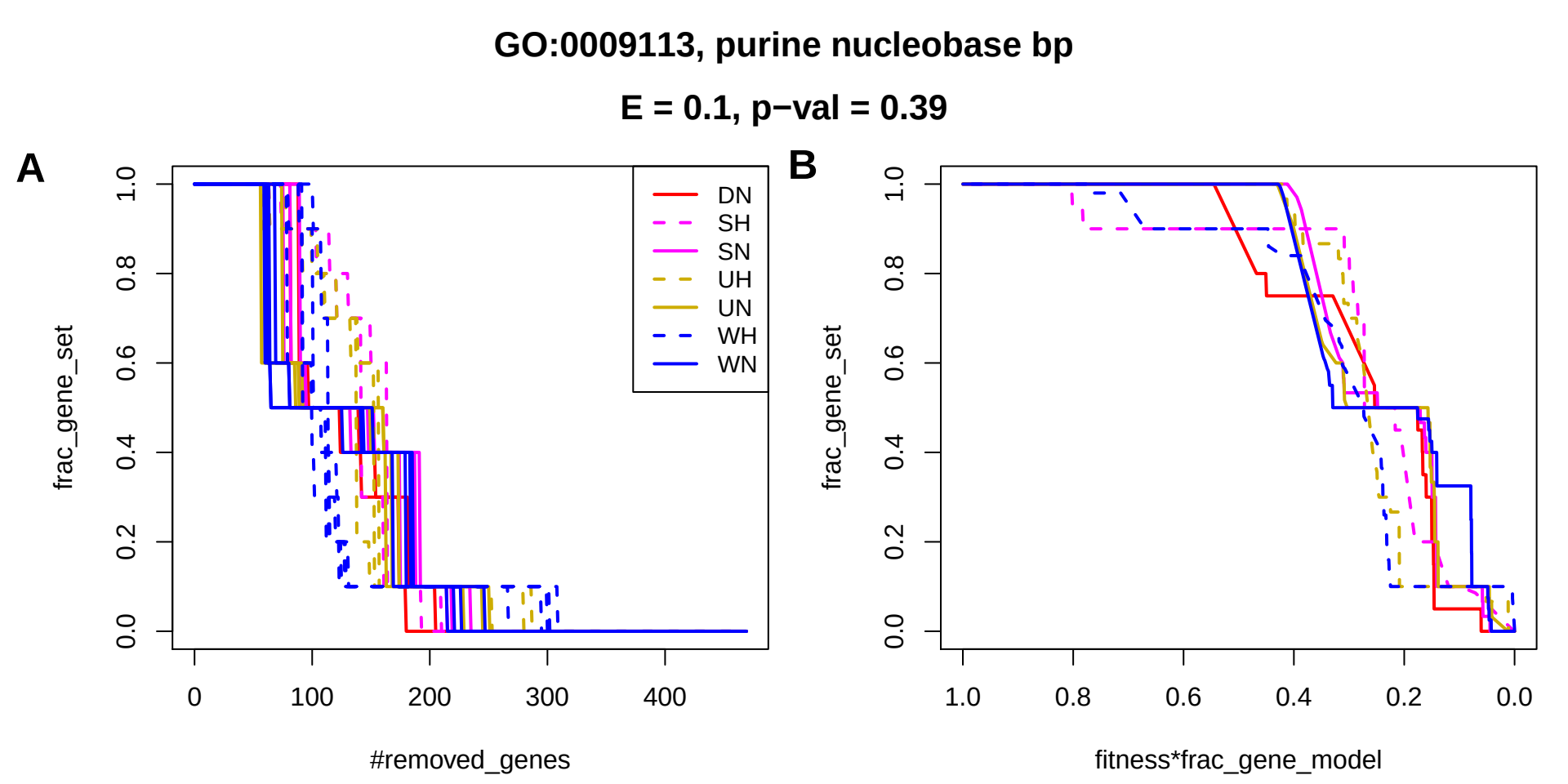

GO:0046131, pyrimidine ribonucleoside mp
E = 0.12, p−val = 0.077
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

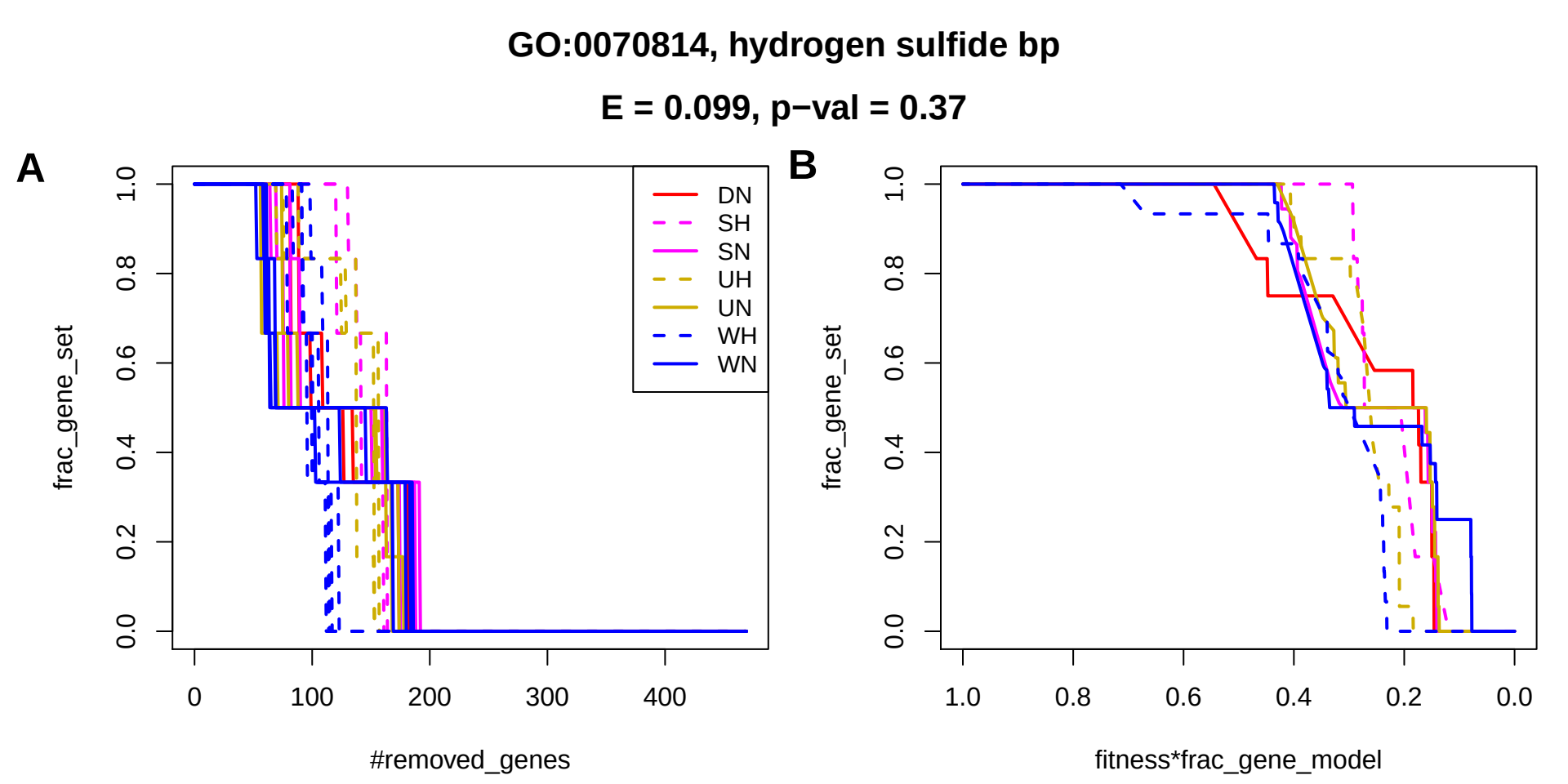

GO:0009116, nucleoside mp
E = 0.11, p−val = 0.12
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

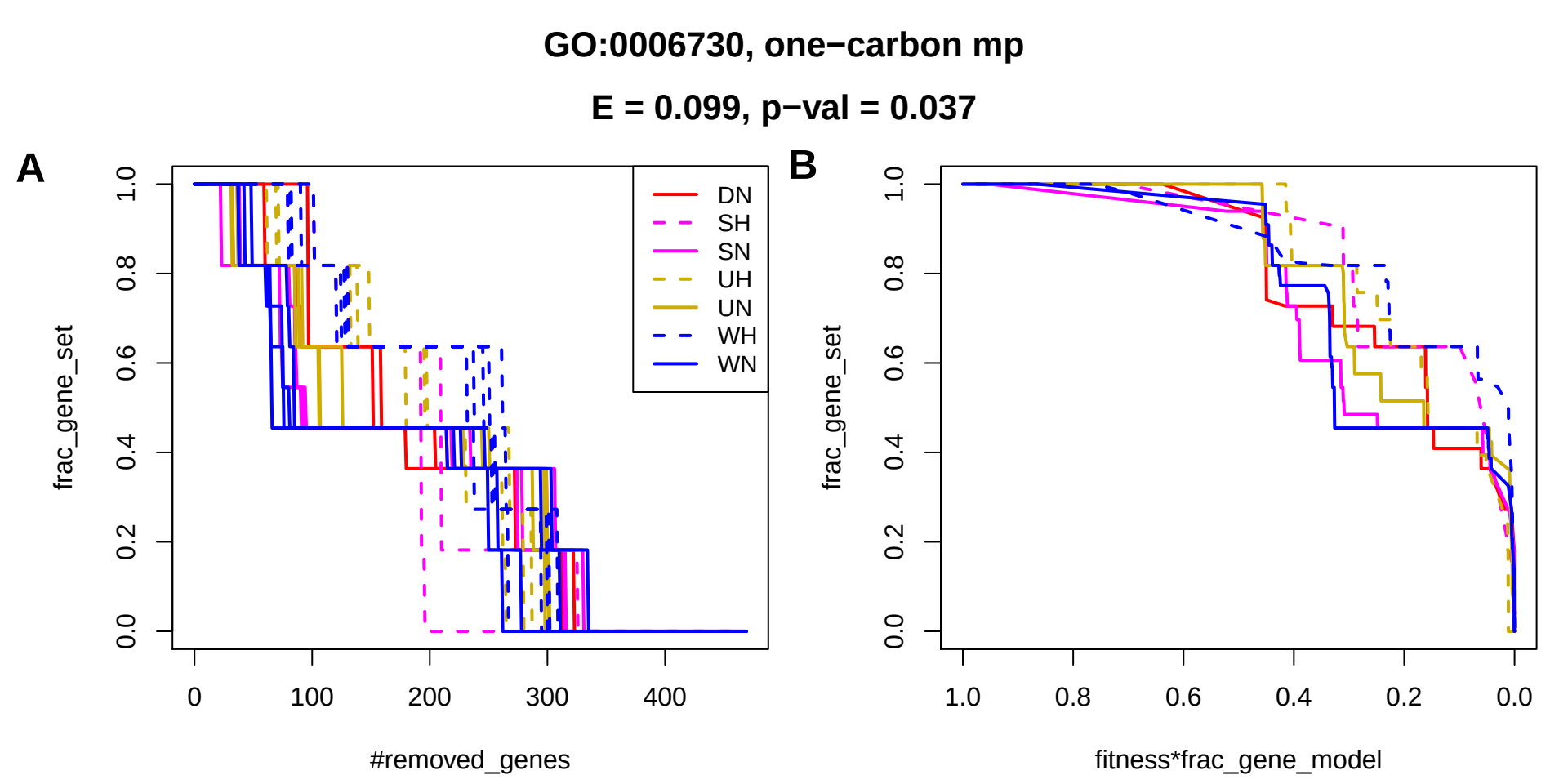

GO:0006575, cellular modified aa mp
E = 0.11, p−val = 0.082
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

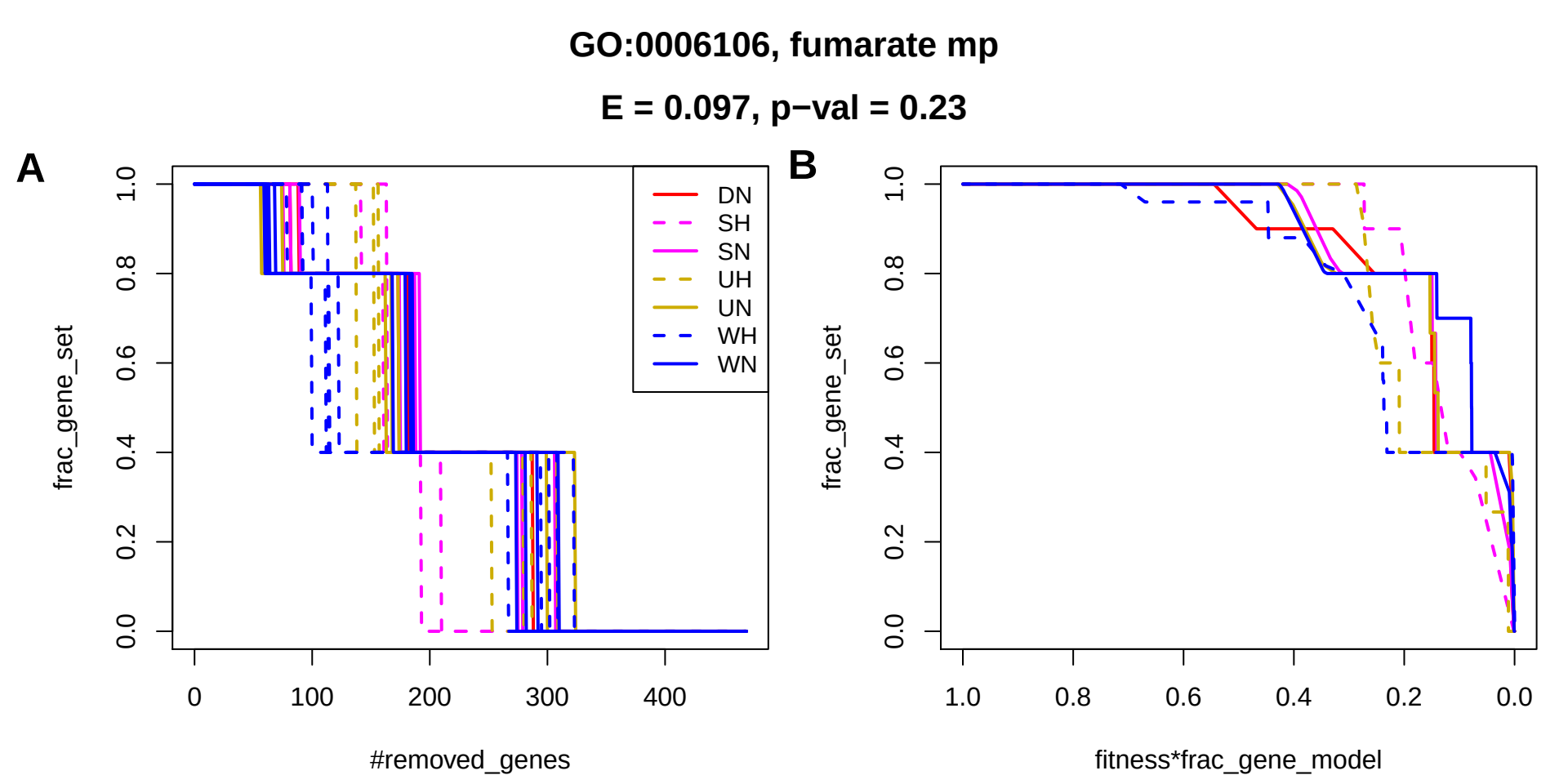

GO:0009218, pyrimidine ribonucleotide mp
E = 0.1, p−val = 0.075
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

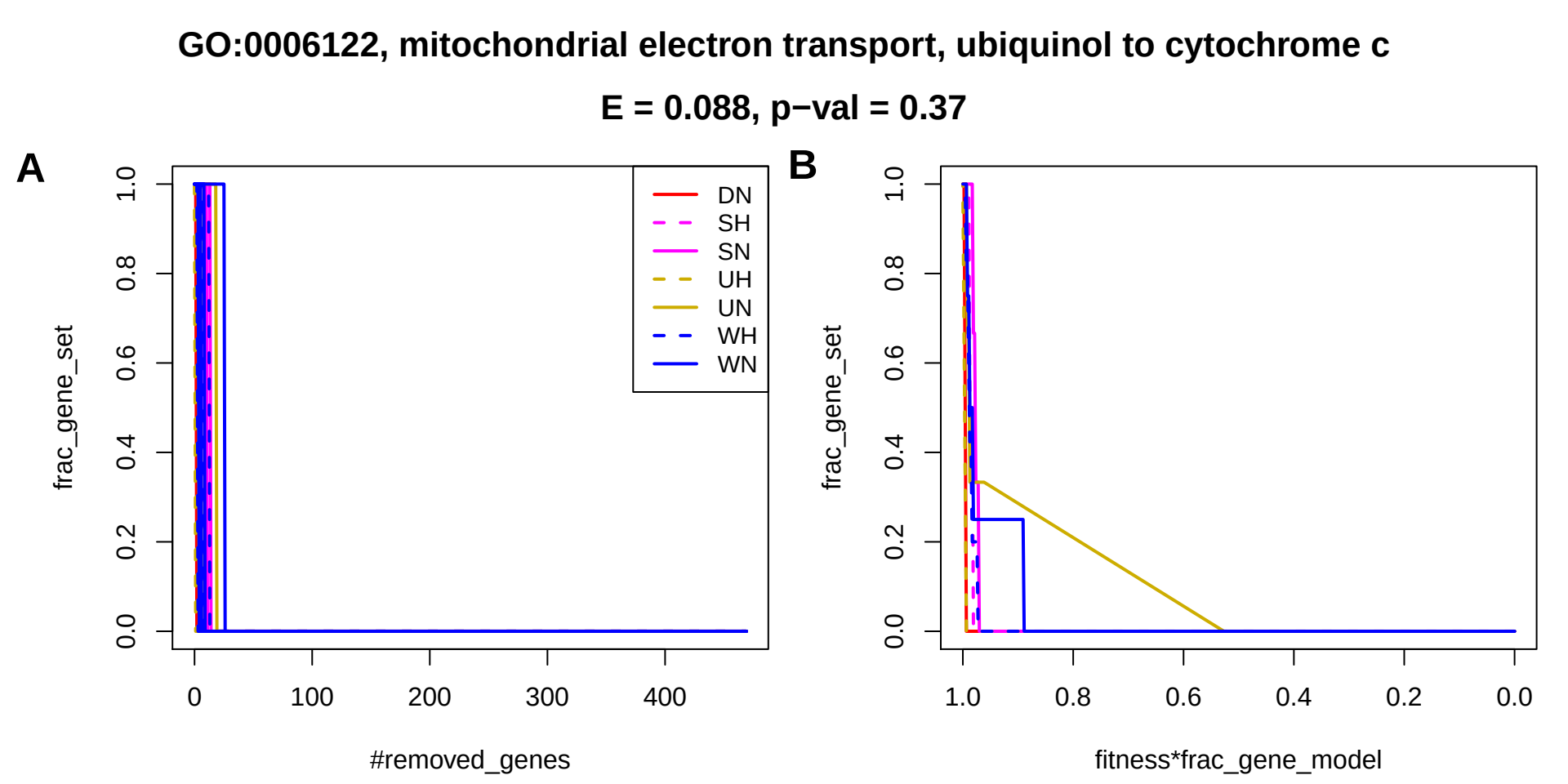

GO:0046084, adenine bp
E = 0.1, p−val = 0.54
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

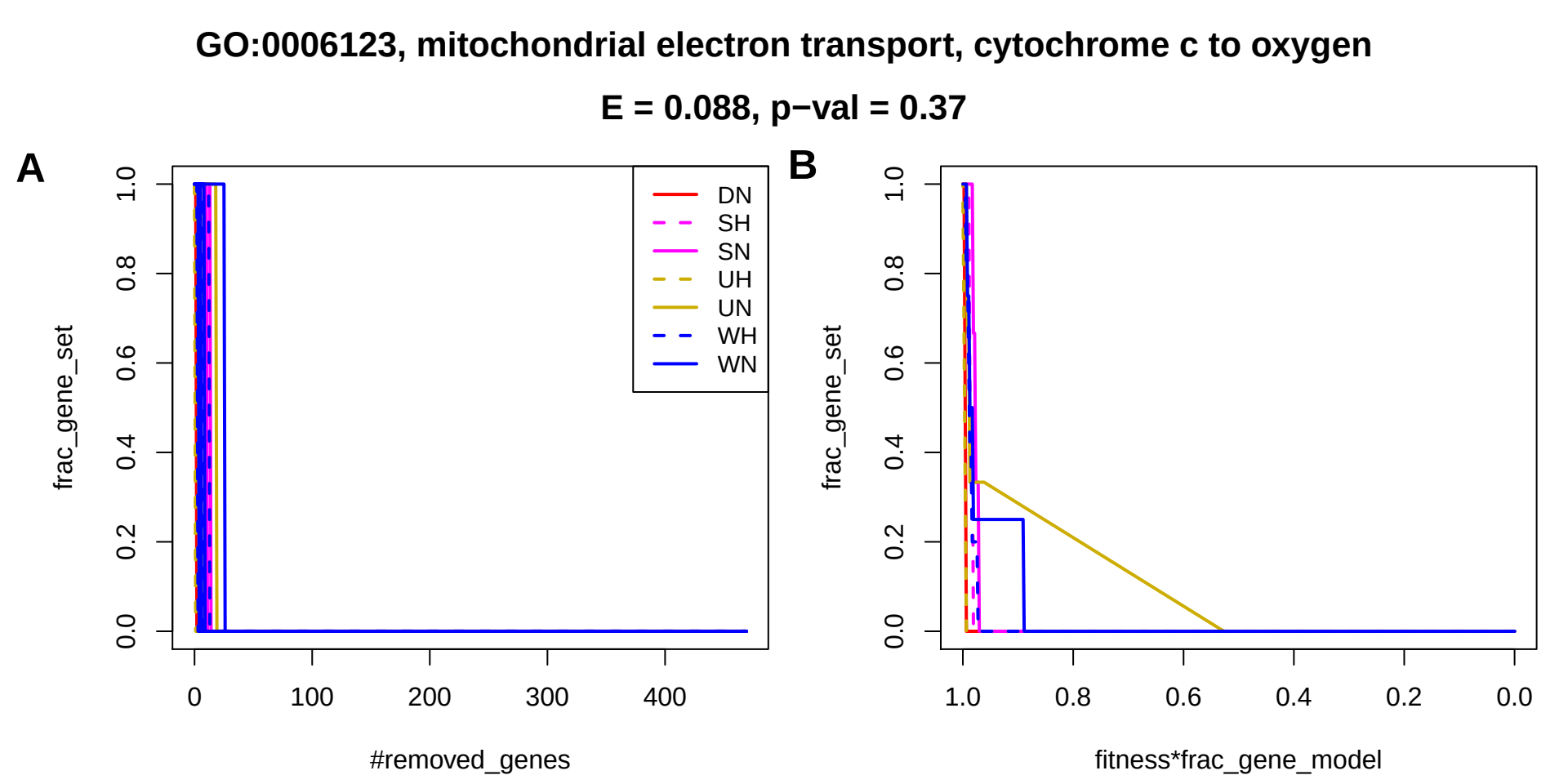

GO:0009113, purine nucleobase bp
E = 0.1, p−val = 0.39
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

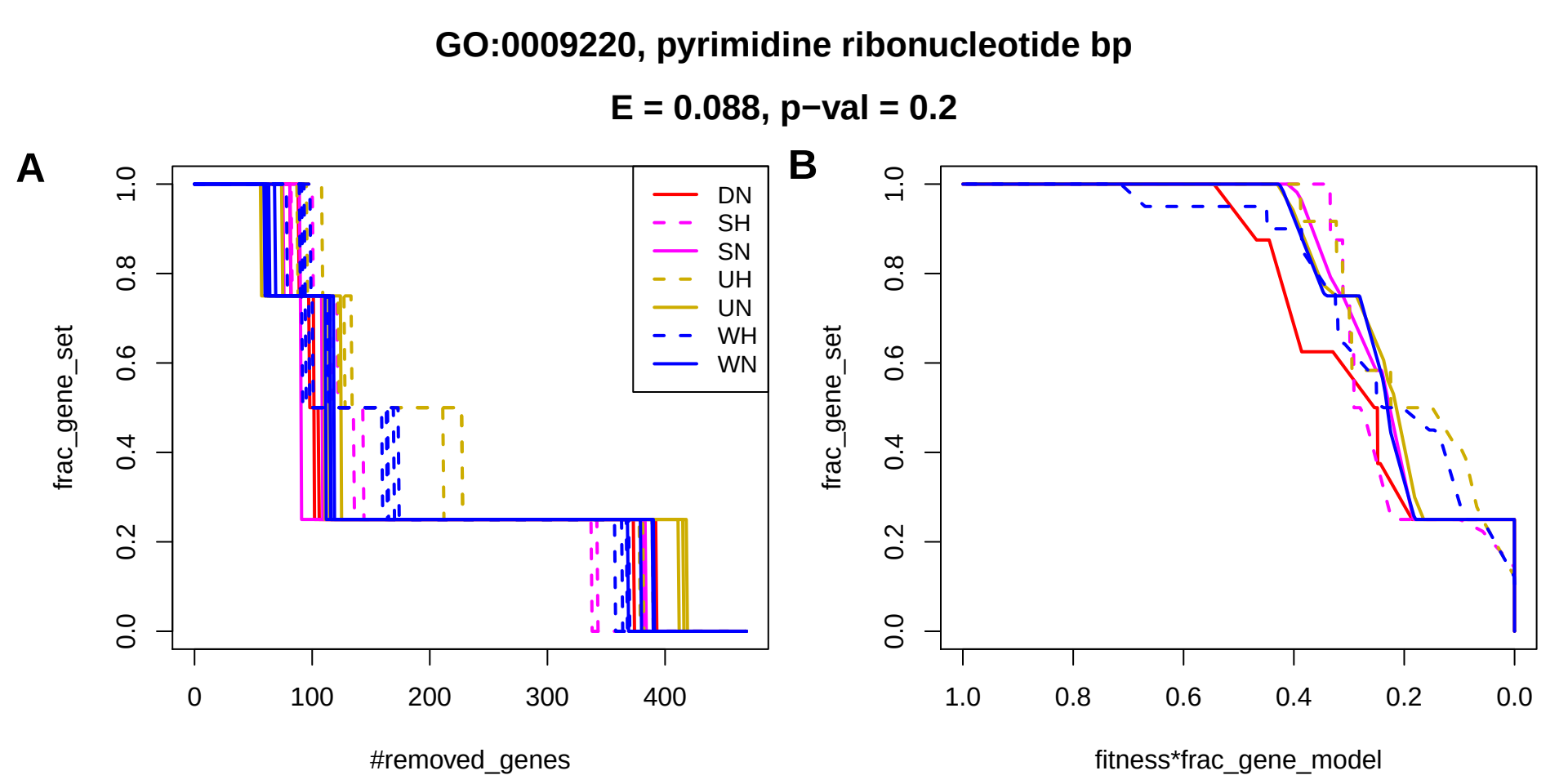

GO:0070814, hydrogen sulfide bp
E = 0.099, p−val = 0.37
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

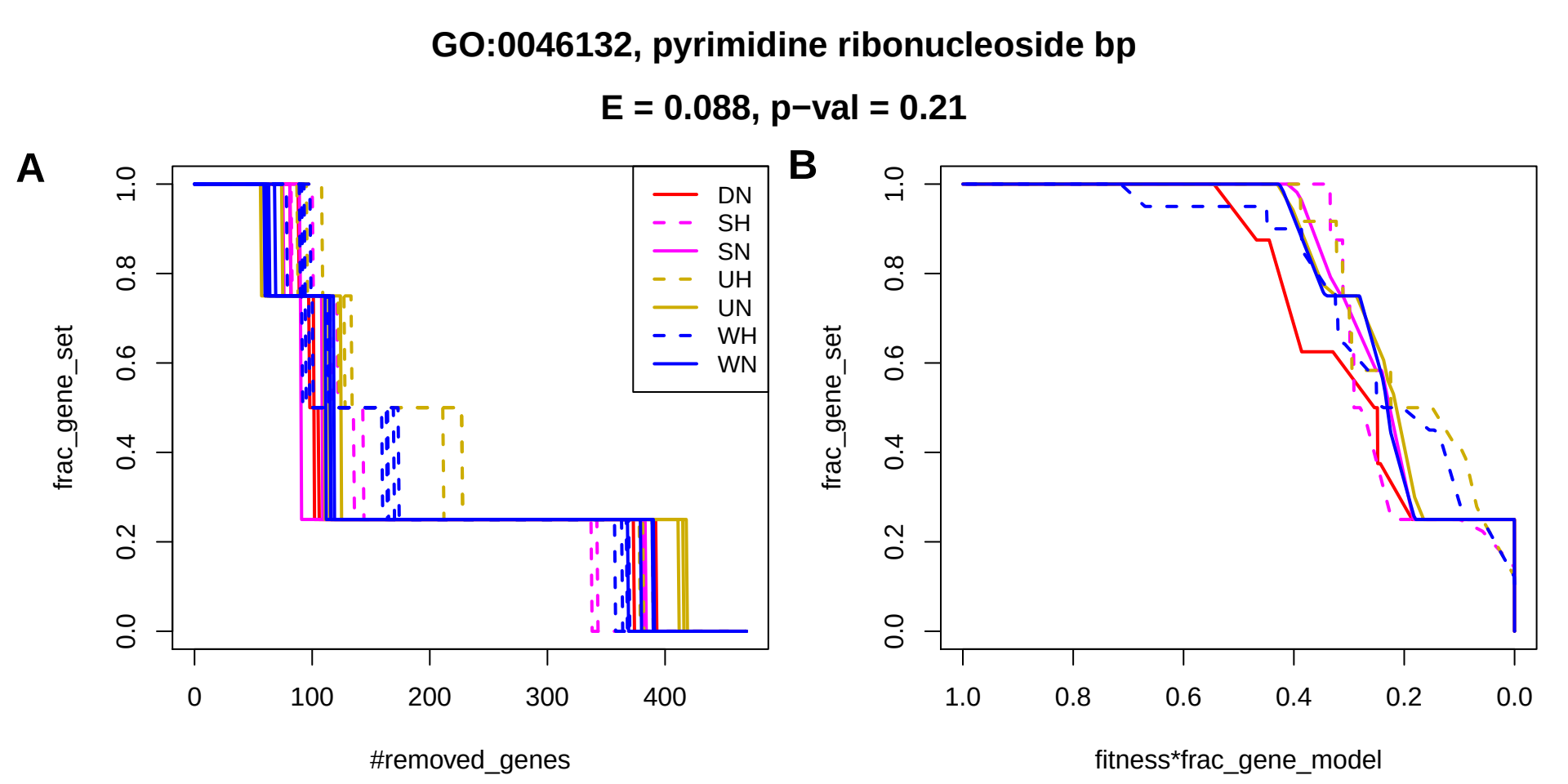

GO:0006730, one−carbon mp
E = 0.099, p−val = 0.037
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

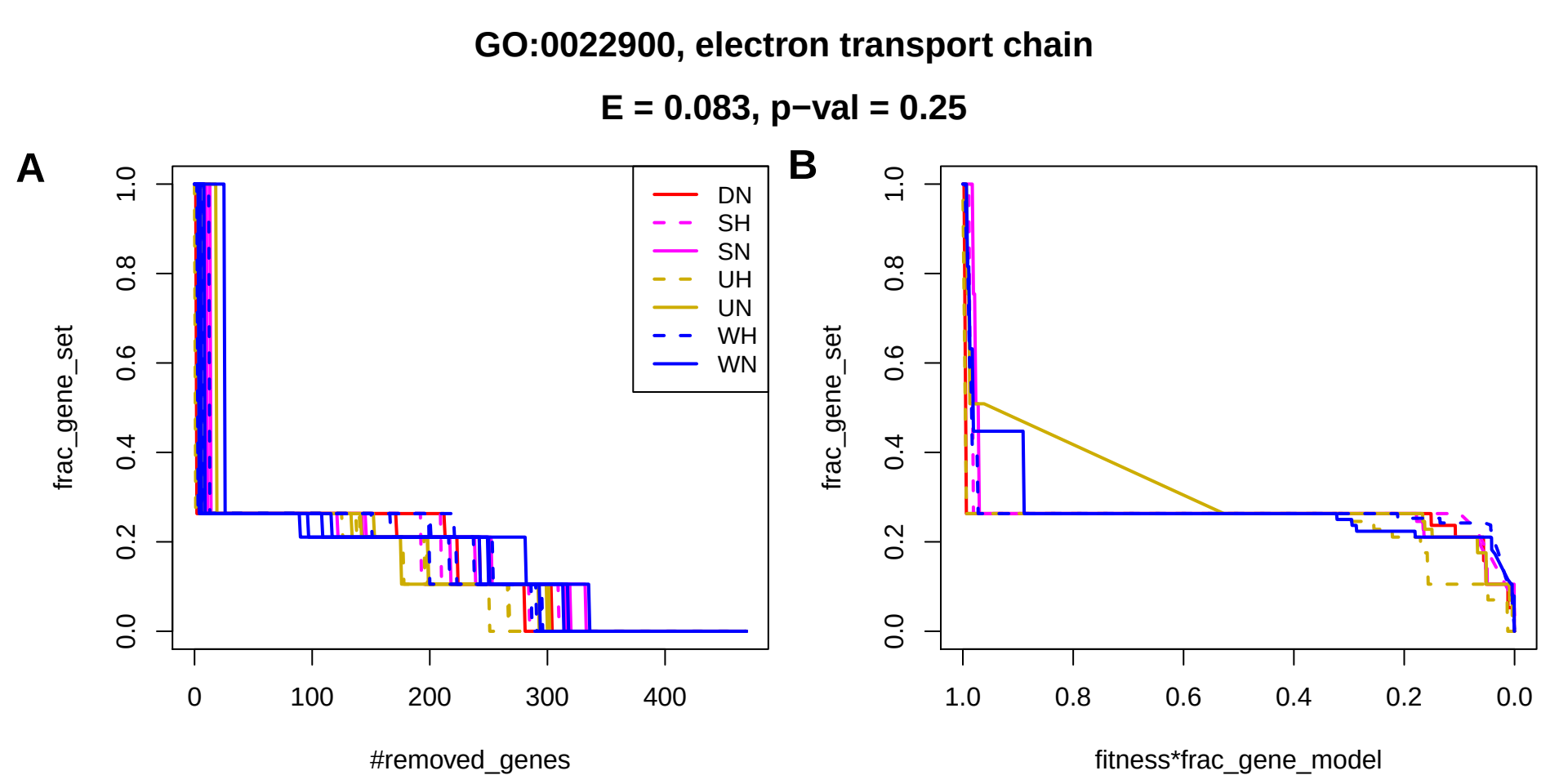

GO:0006106, fumarate mp
E = 0.097, p−val = 0.23
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400

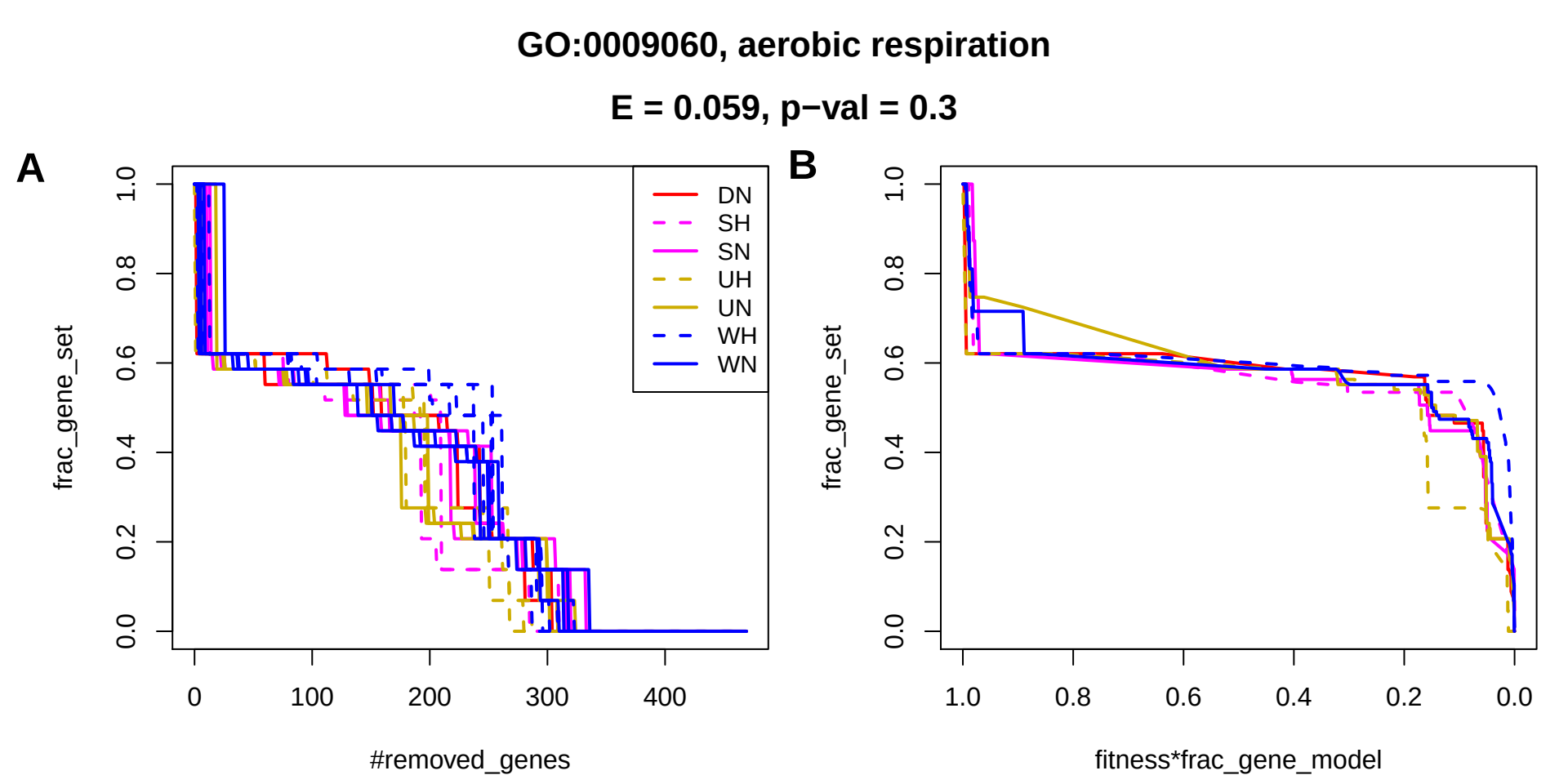

GO:0006122, mitochondrial electron transport, ubiquinol to cytochrome c
E = 0.088, p−val = 0.37
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0006123, mitochondrial electron transport, cytochrome c to oxygen
E = 0.088, p−val = 0.37
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009220, pyrimidine ribonucleotide bp
E = 0.088, p−val = 0.2
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0046132, pyrimidine ribonucleoside bp
E = 0.088, p−val = 0.21
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0022900, electron transport chain
E = 0.083, p−val = 0.25
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400


GO:0009060, aerobic respiration
E = 0.059, p−val = 0.3
A
B
frac_gene_set
#removed_genes
fitness*frac_gene_model
DN
SH
SN
UH
UN
WH
WN
0.0
0.2
0.4
0.6
0.8
1.0
0
100
200
300
400