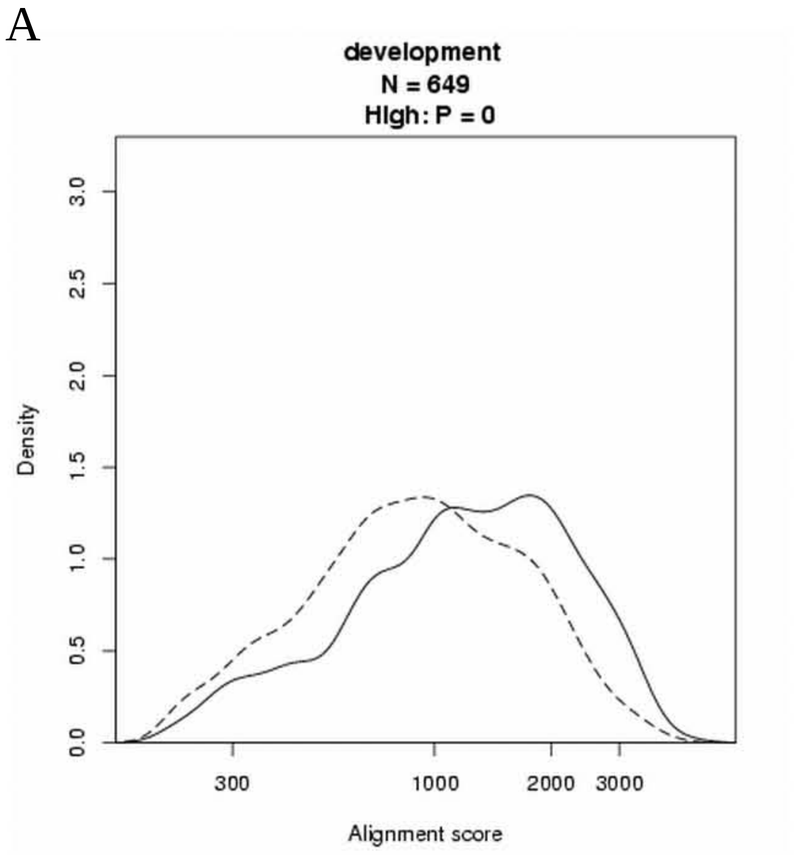
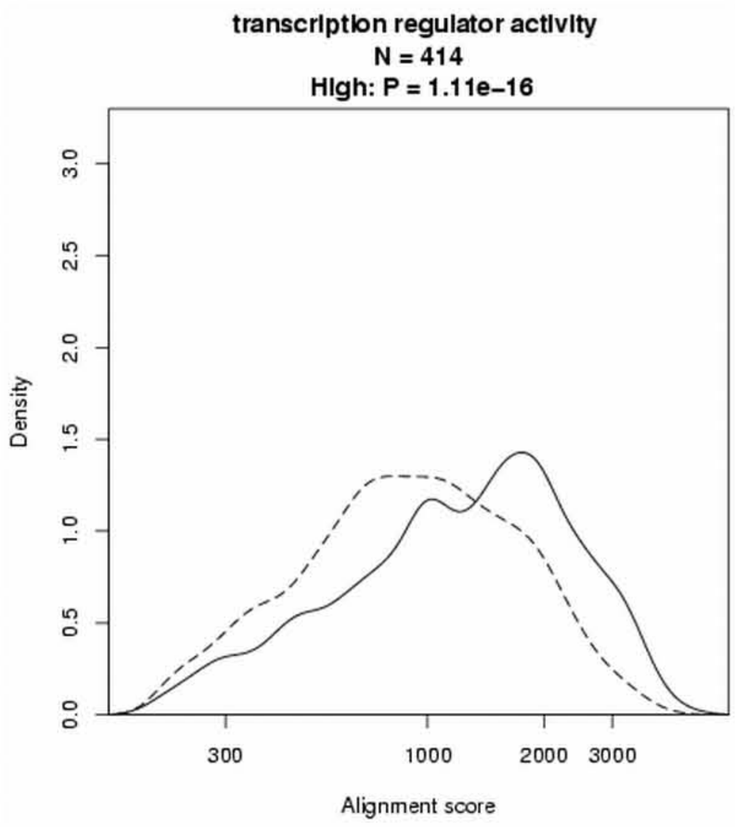
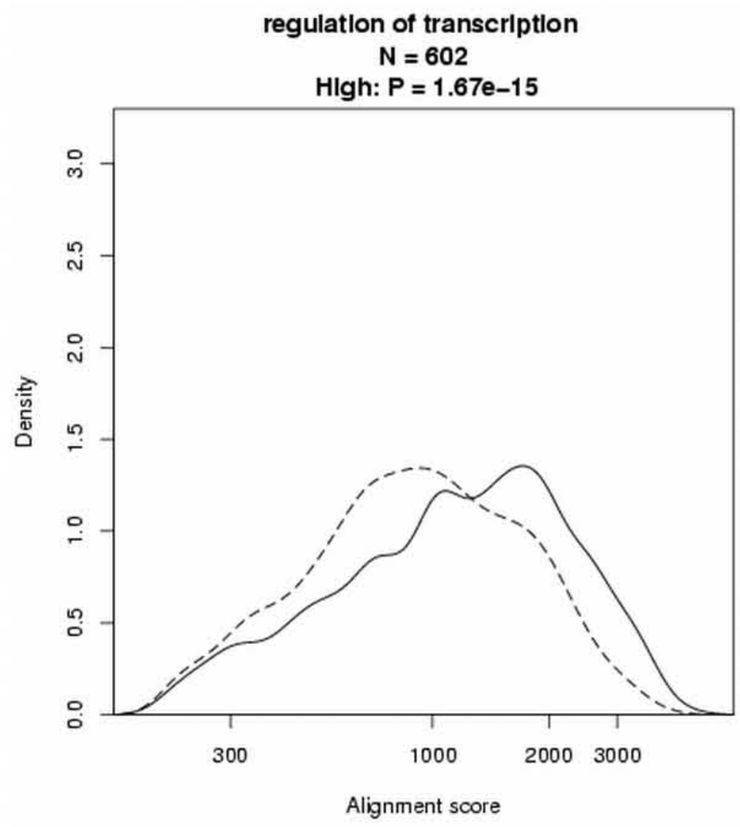
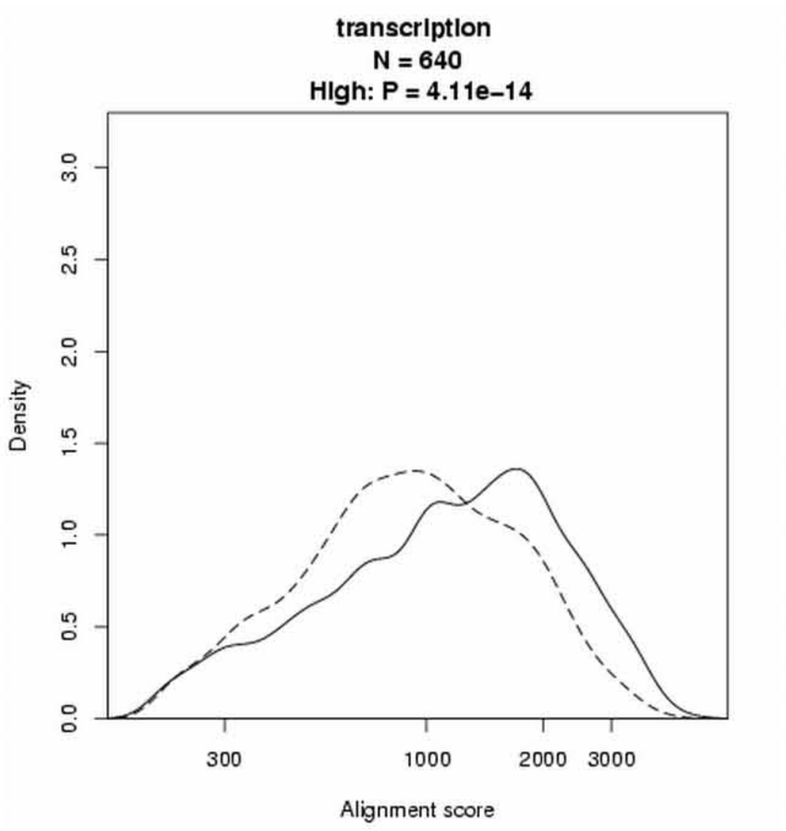
Additional file 4

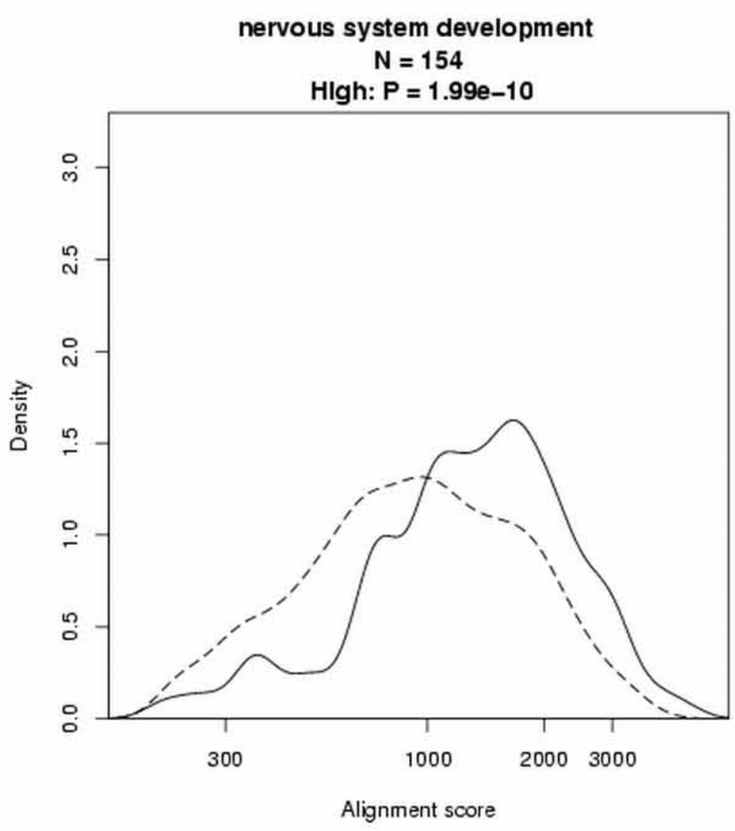
A

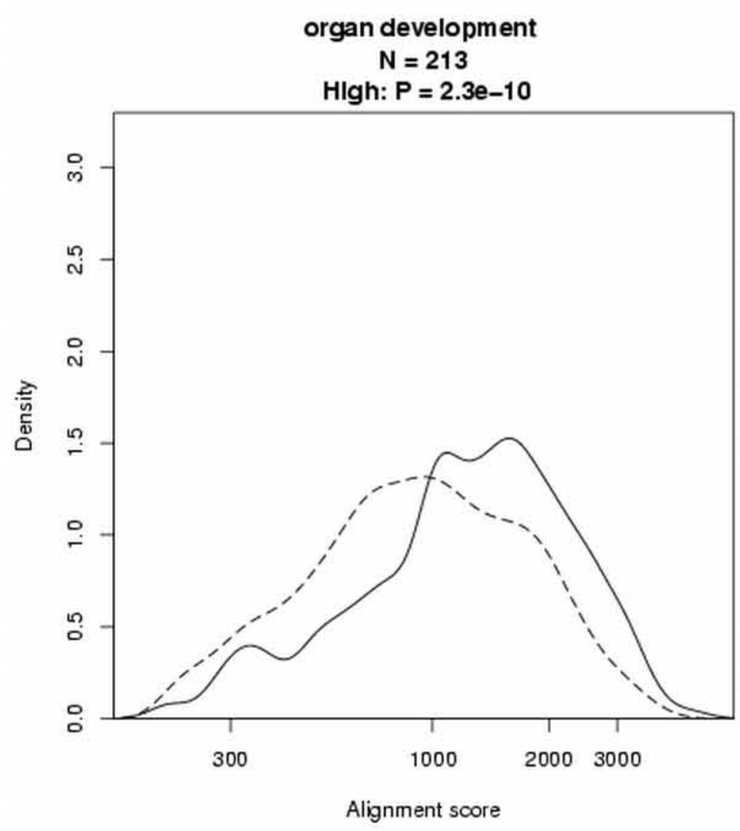


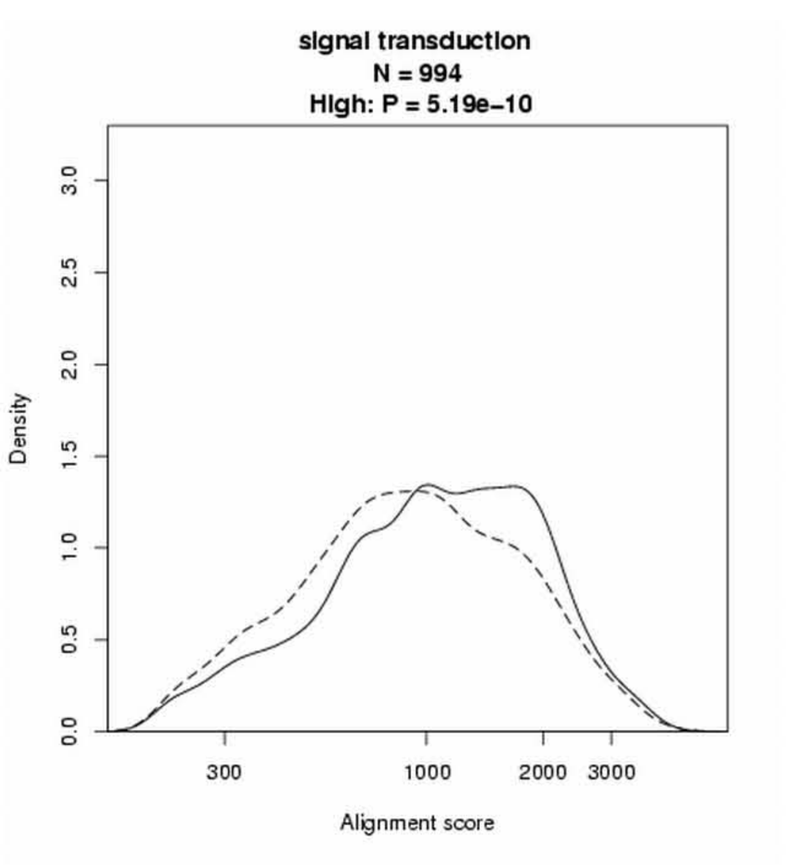


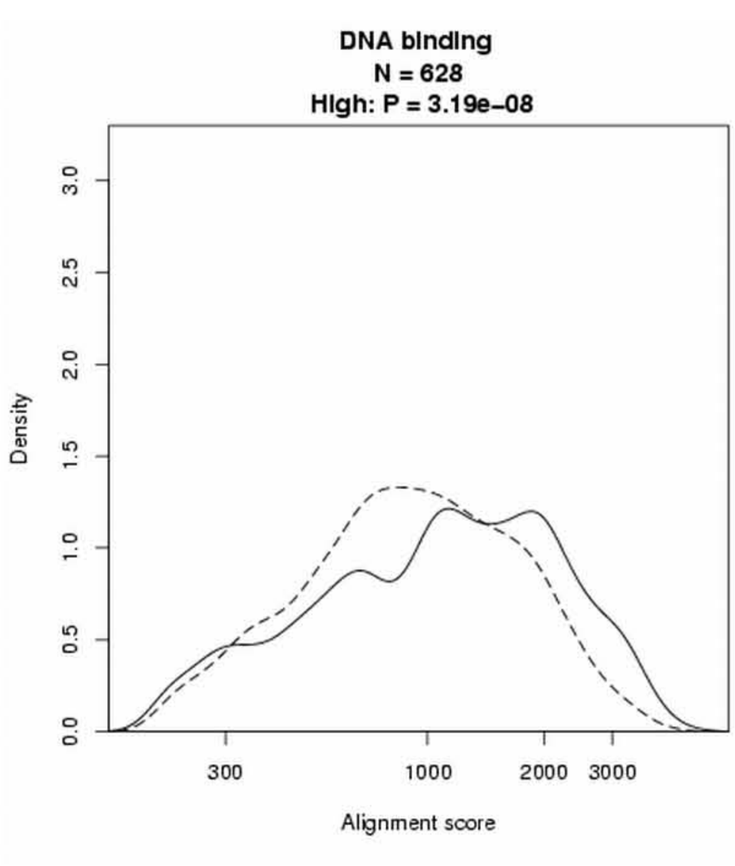


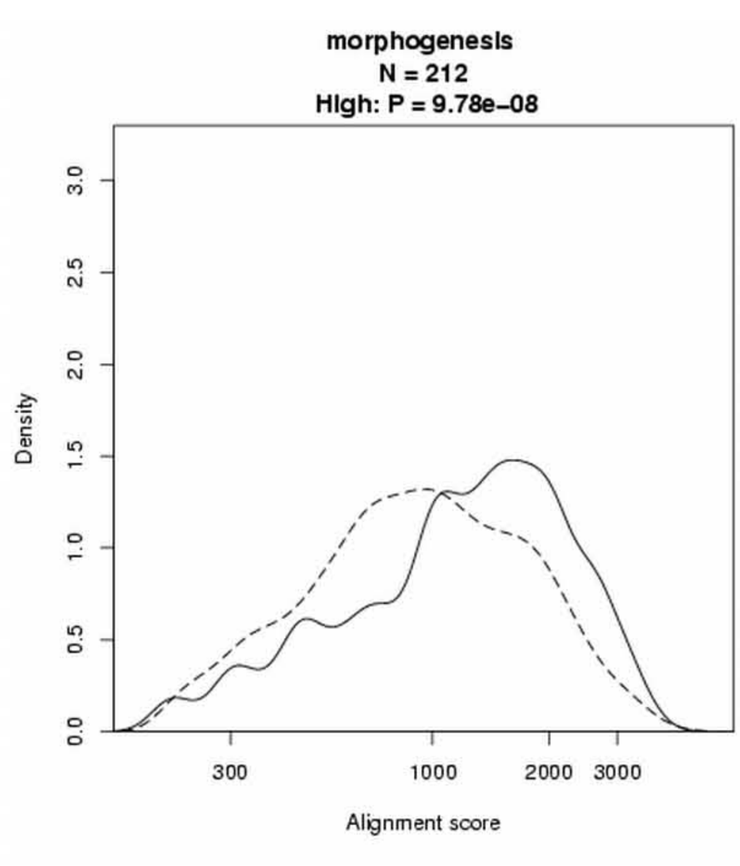


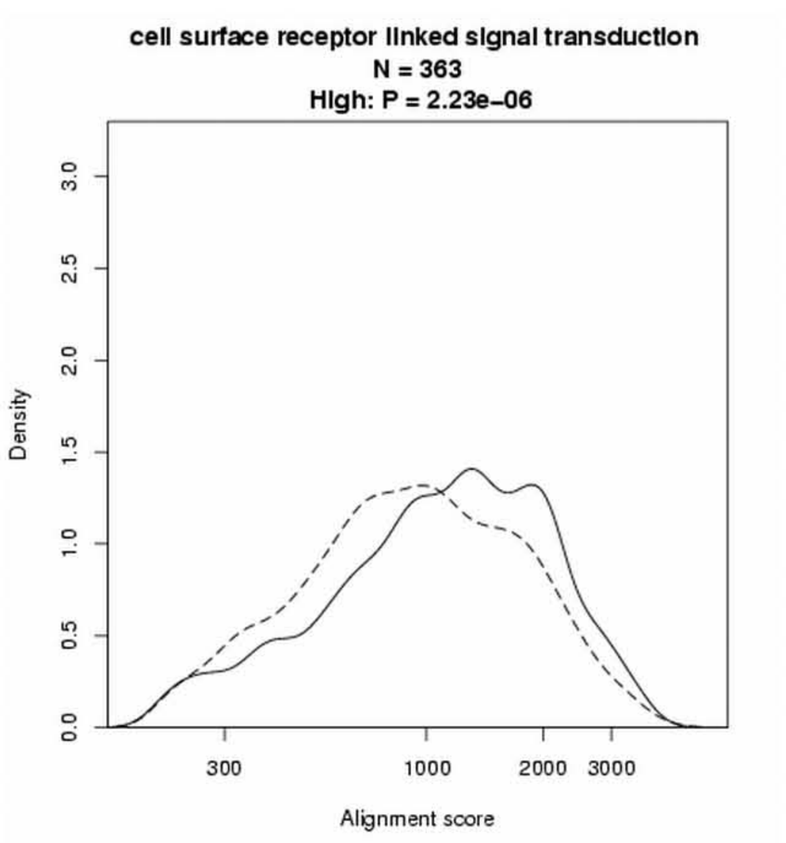


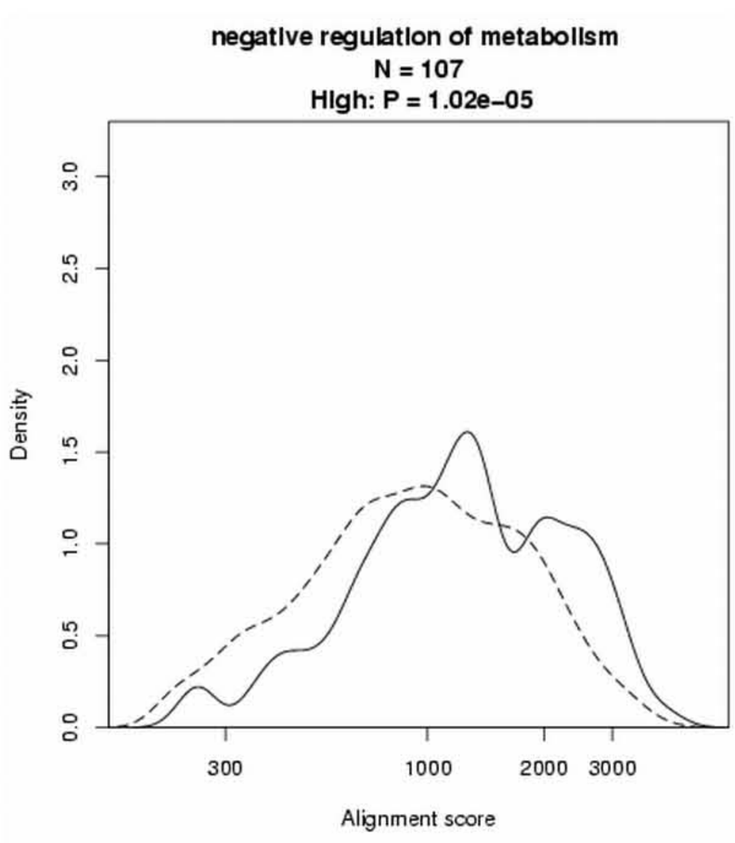


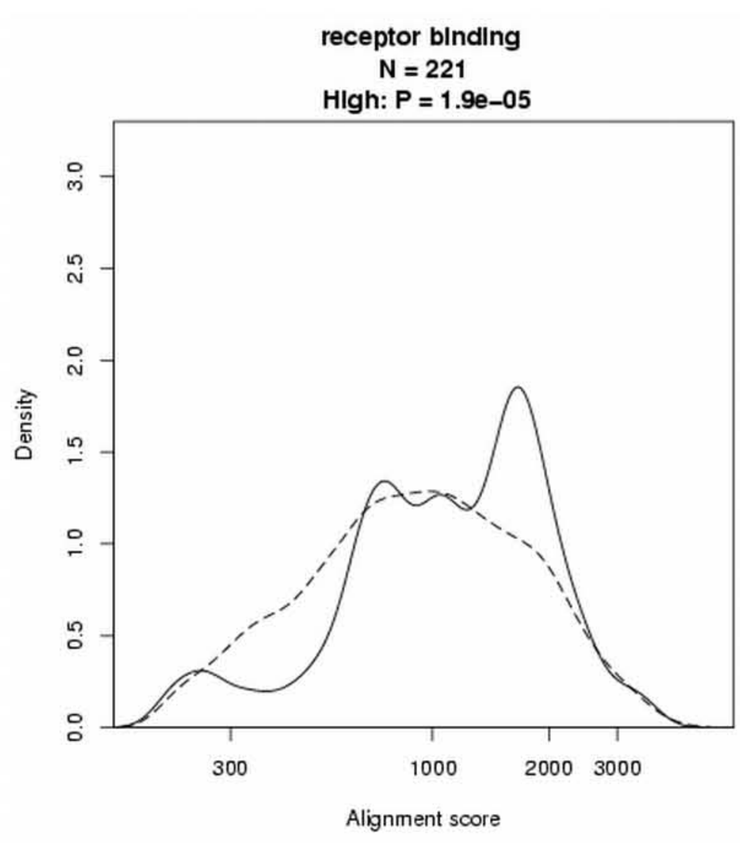


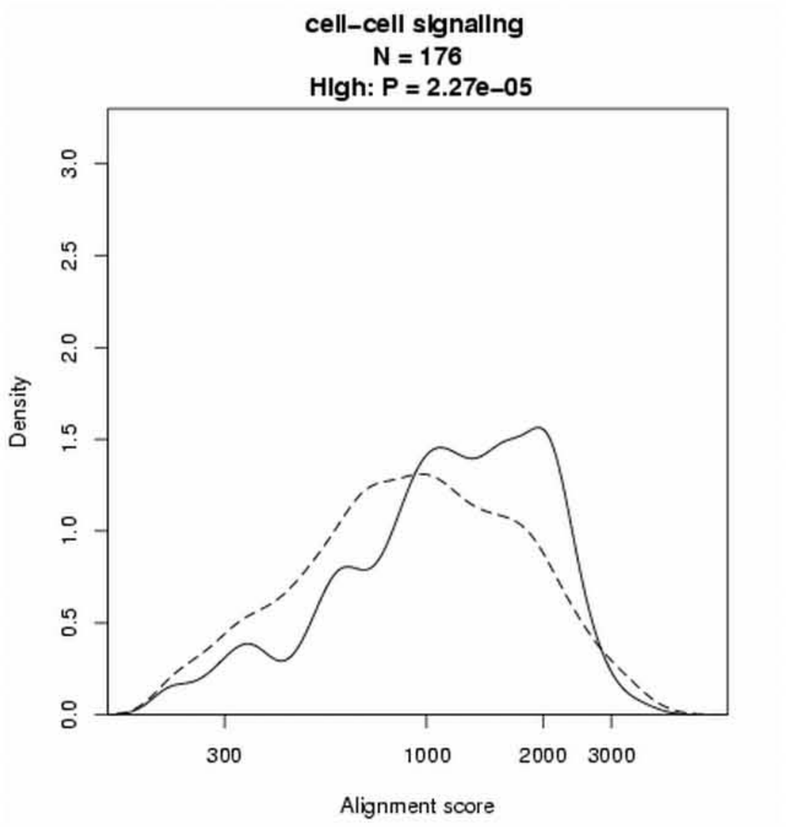


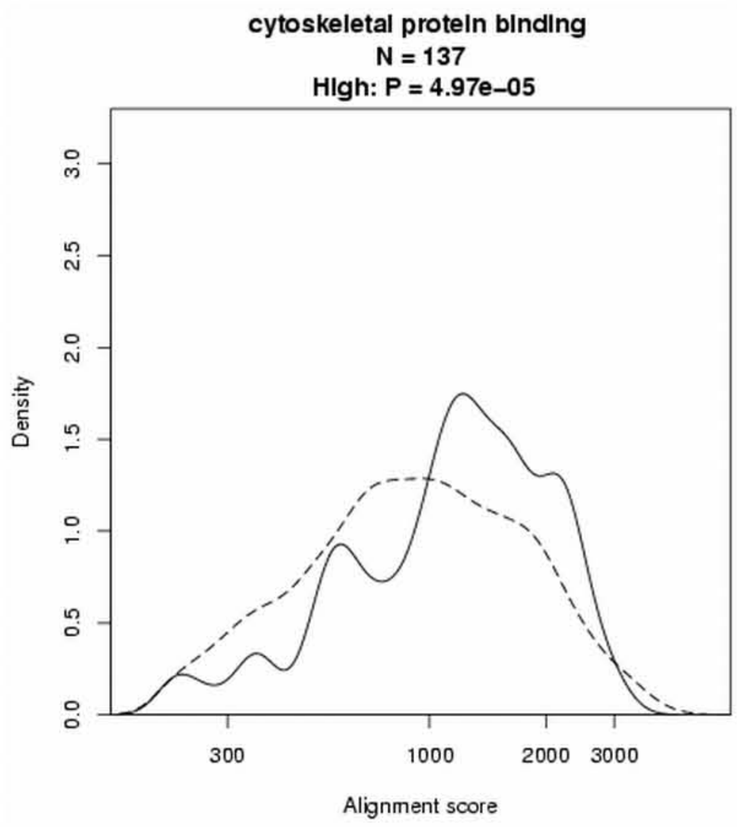


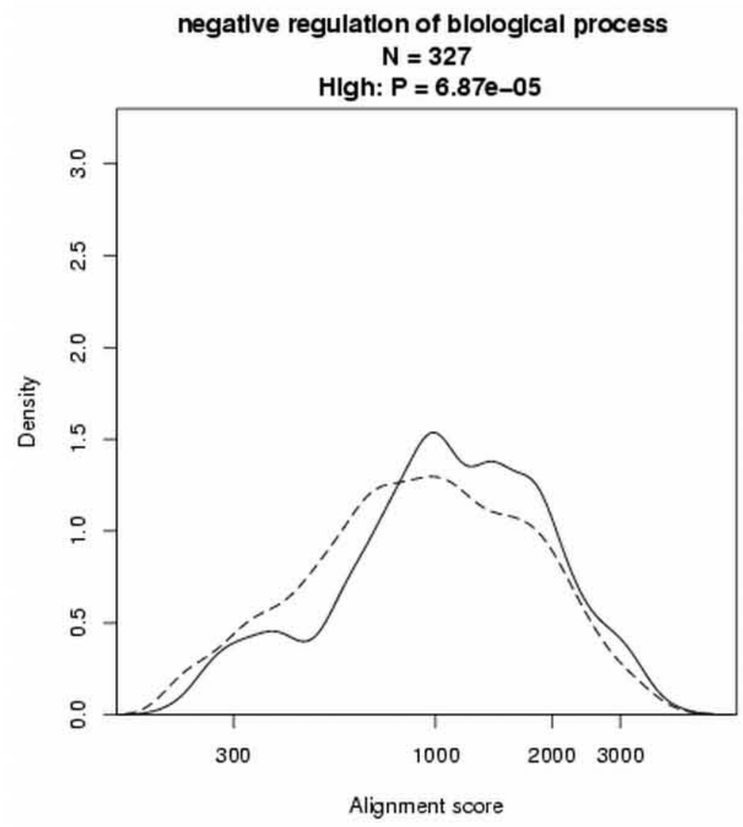


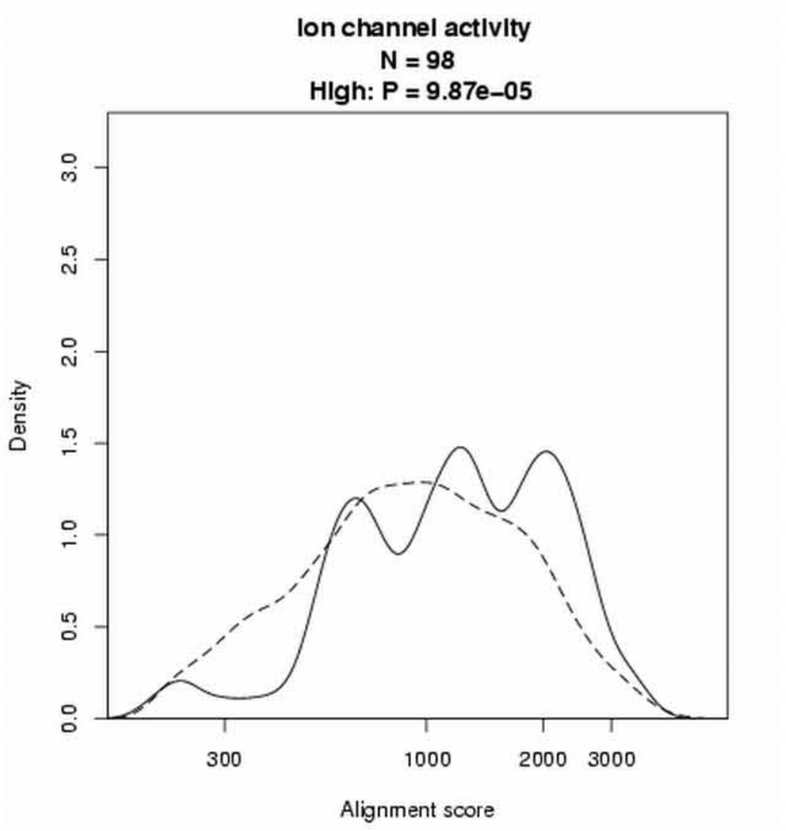


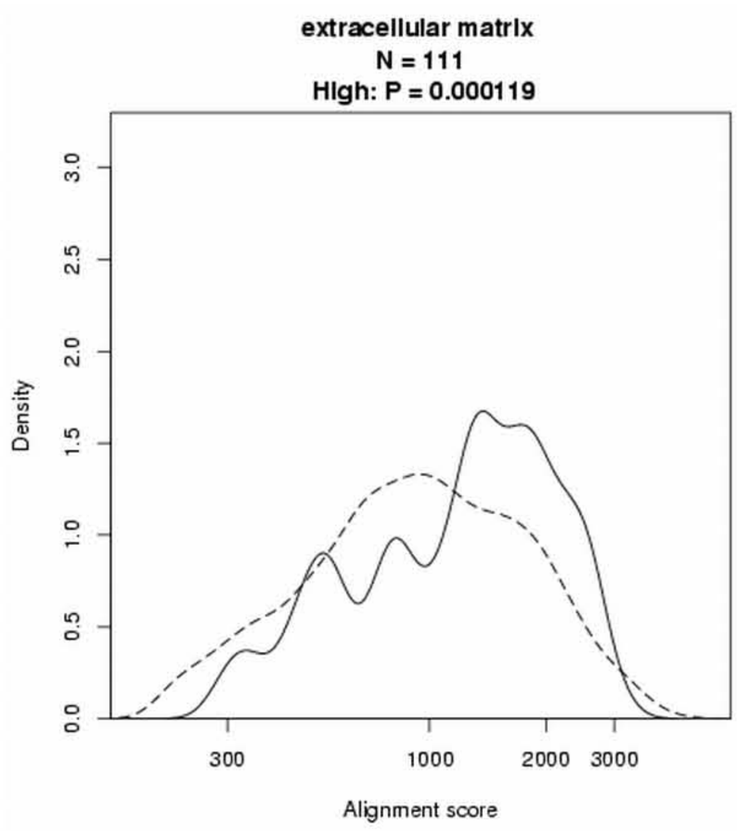


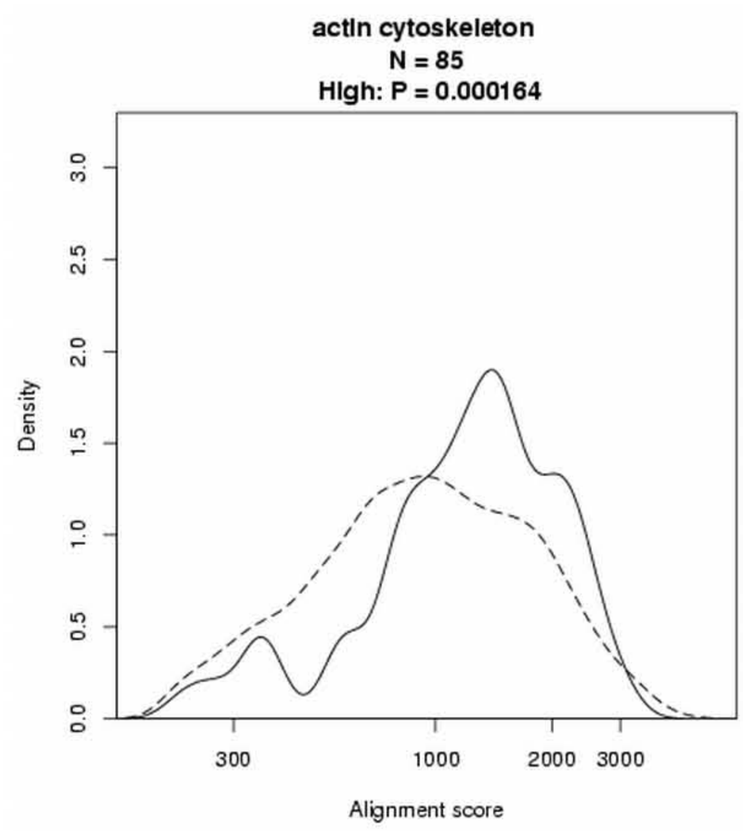

cell−cell signaling
N = 176
High: P = 2.27e−05
Density
Alignment score

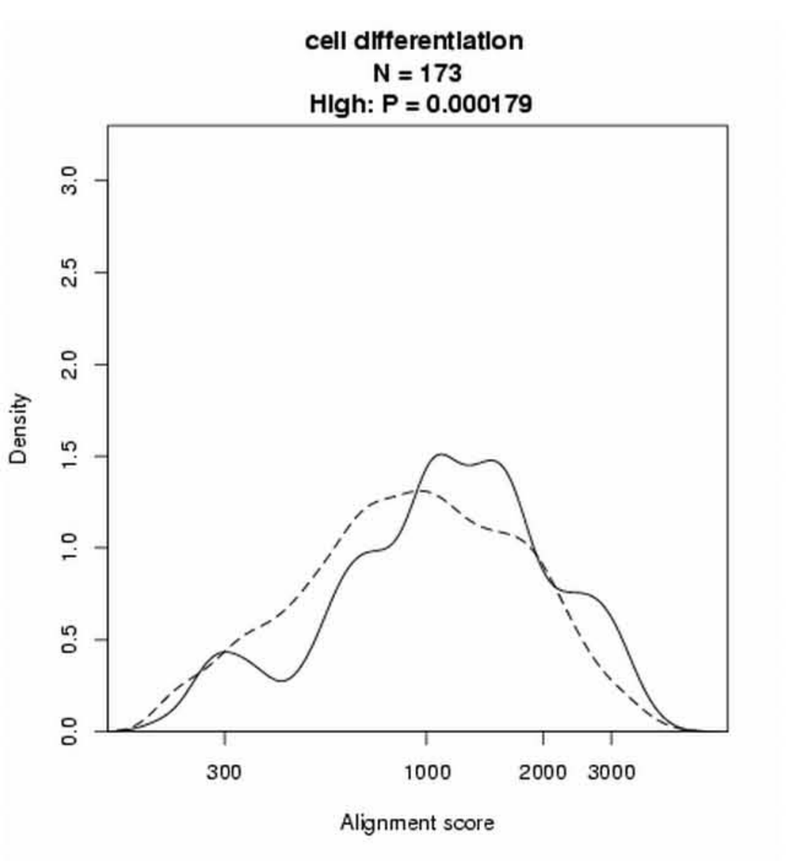

cytoskeletal protein binding
N = 137
High: P = 4.97e−05
Density
Alignment score

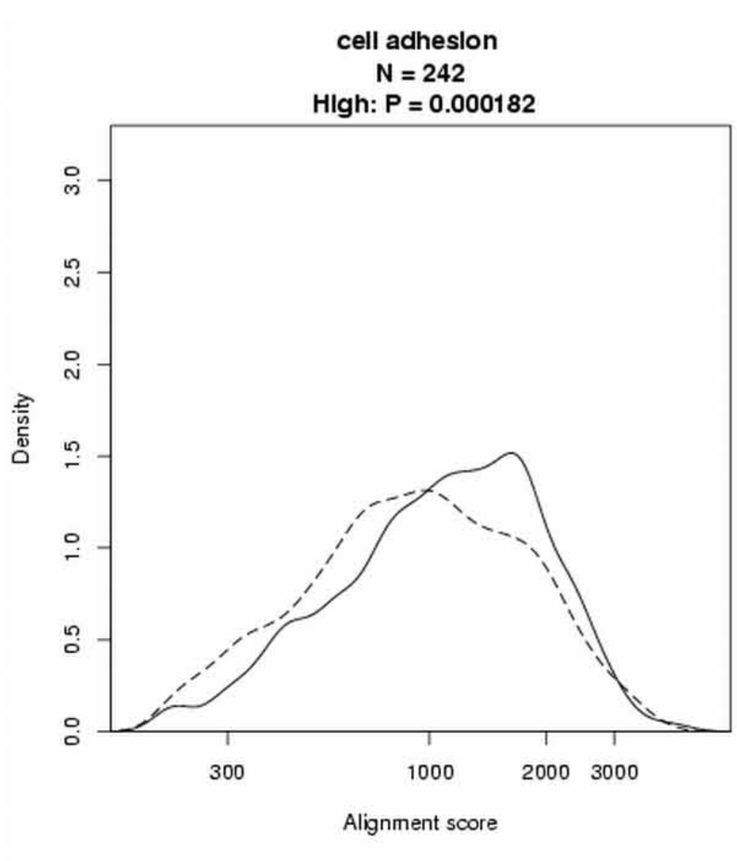

negative regulation of biological process
N = 327
High: P = 6.87e−05
Density
Alignment score

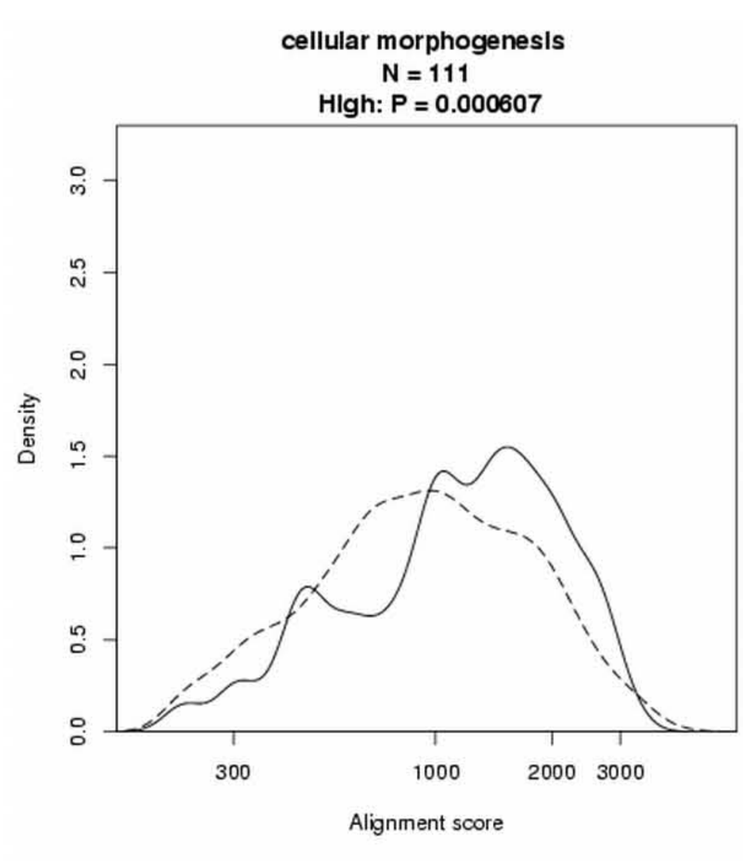

ion channel activity
N = 98
High: P = 9.87e−05
Density
Alignment score

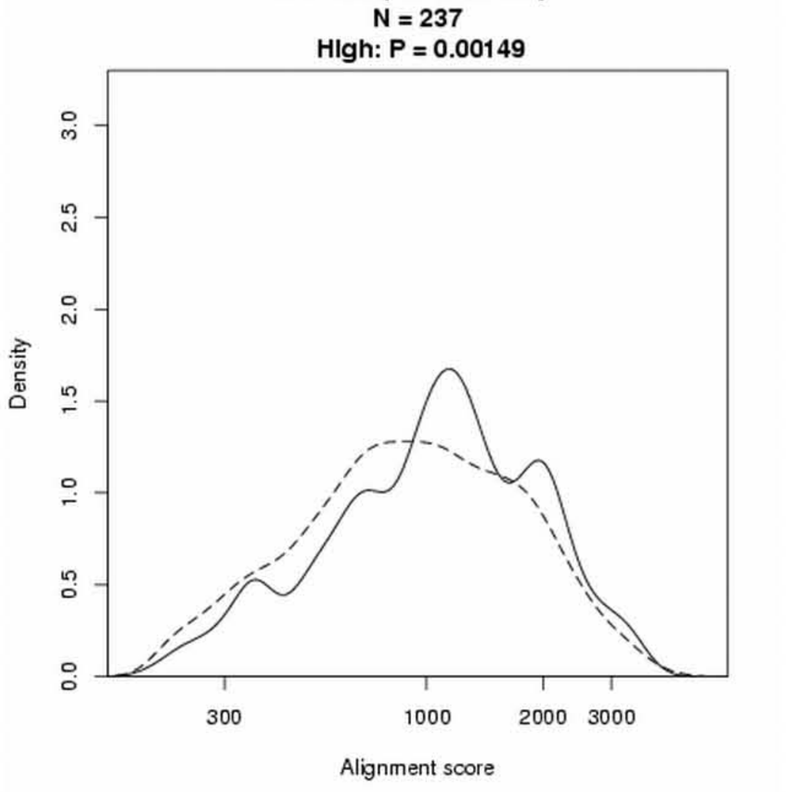

extracellular matrix
N = 111
High: P = 0.000119
Density
Alignment score

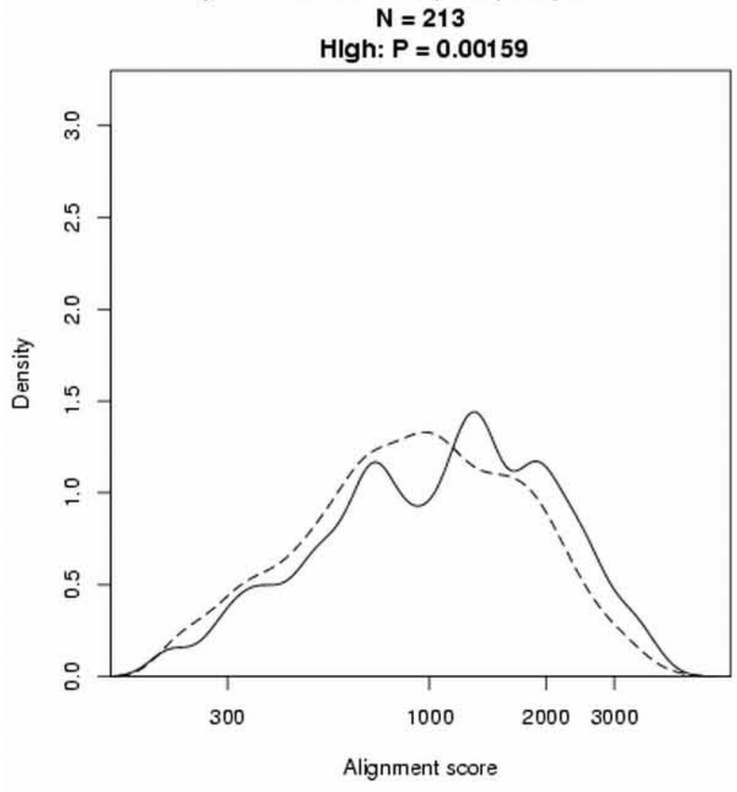

actin cytoskeleton
N = 85
High: P = 0.000164
Density
Alignment score

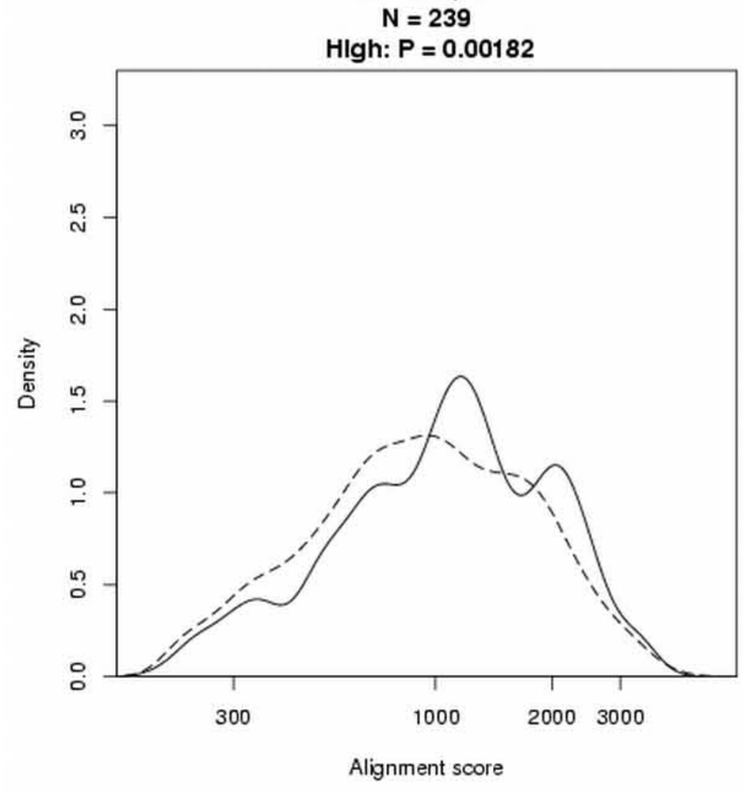

cell differentiation
N = 173
High: P = 0.000179
Density
Alignment score

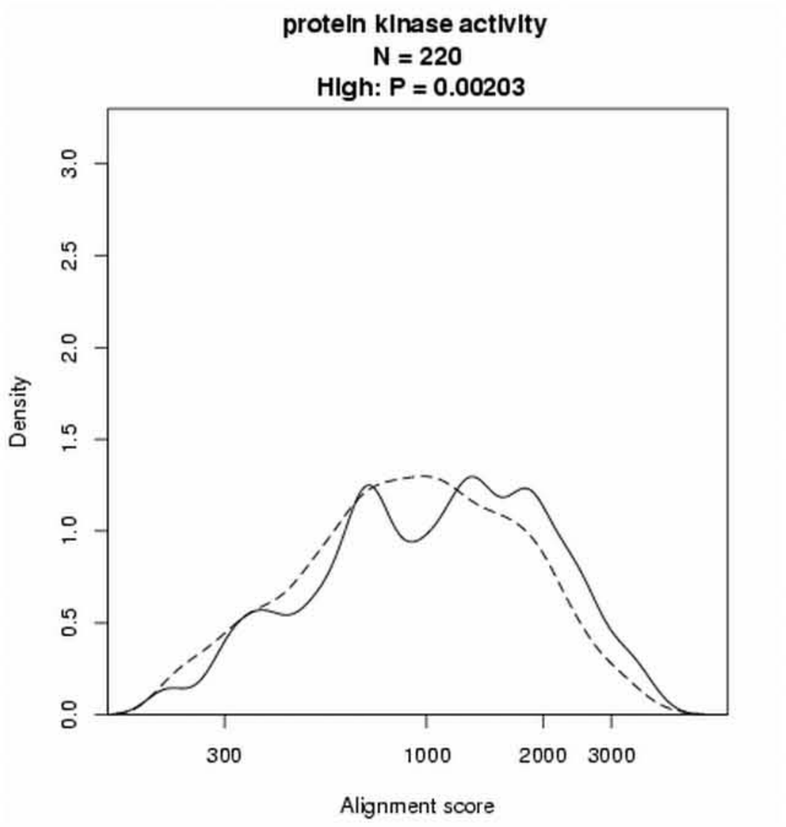

cell adhesion
N = 242
High: P = 0.000182
Density
Alignment score

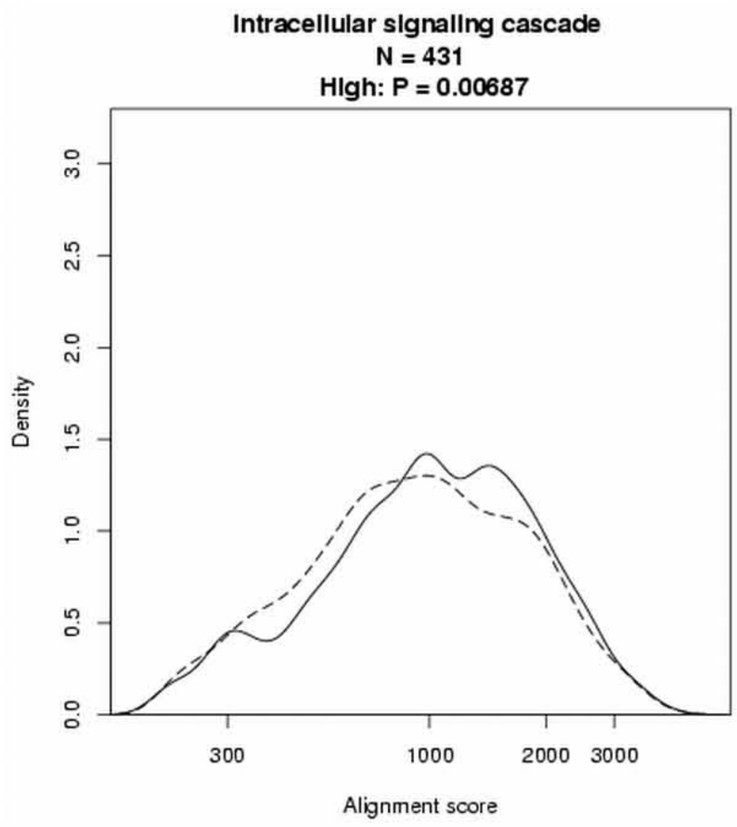

cellular morphogenesis
N = 111
High: P = 0.000607
Density
Alignment score

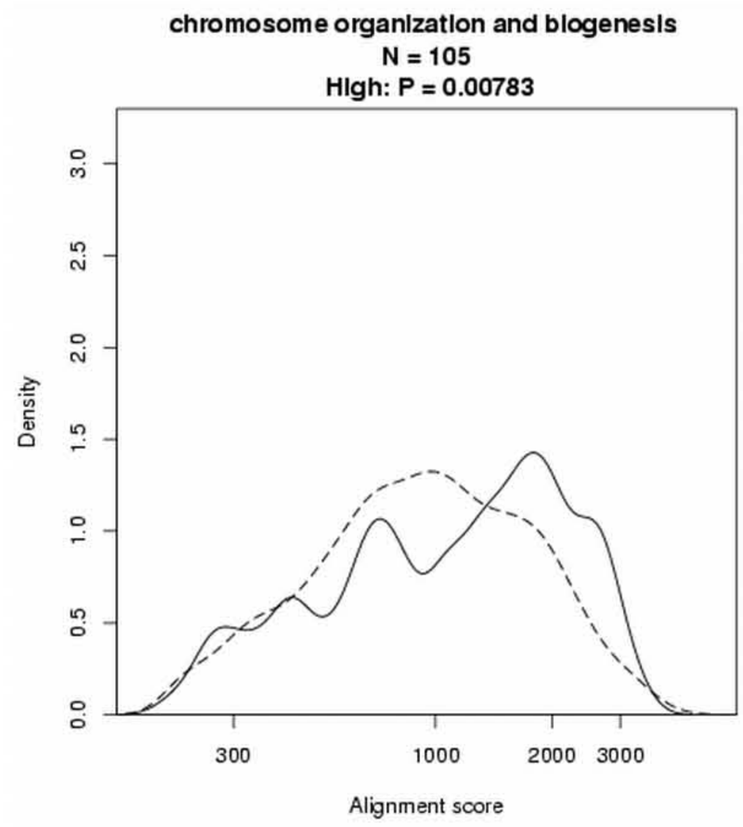

ion transporter activity
N = 237
High: P = 0.00149
Density
Alignment score

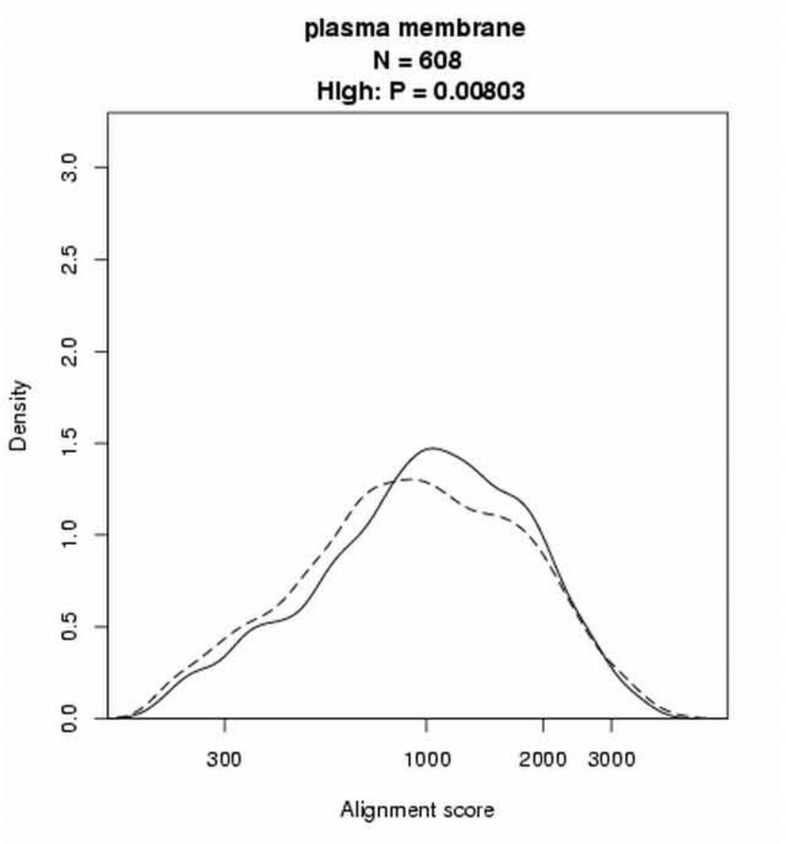

protein amino acid phosphorylation
N = 213
High: P = 0.00159
Density
Alignment score


ion transport
N = 239
High: P = 0.00182
Density
Alignment score

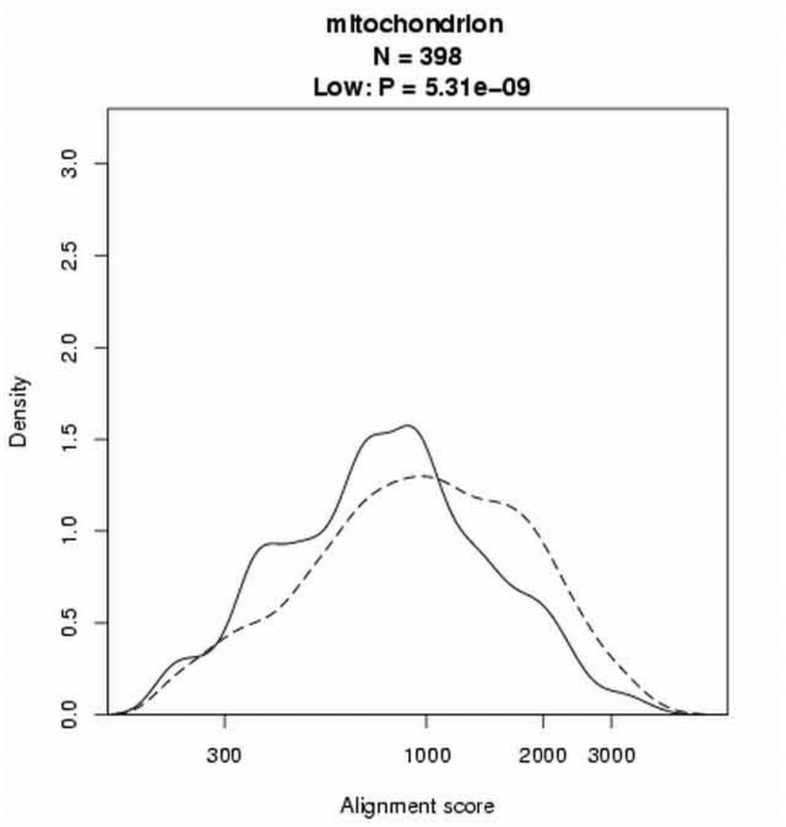

protein kinase activity
N = 220
High: P = 0.00203
Density
0.0
0.5
1.0
1.5
2.0
2.5
3.0
300
1000
2000
3000
Alignment score

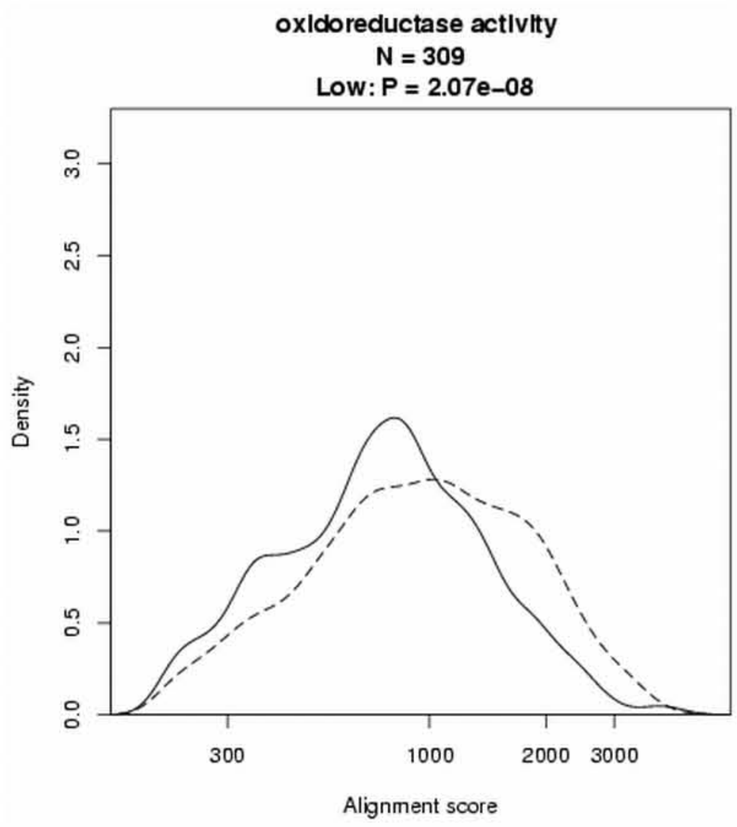

intracellular signaling cascade
N = 431
High: P = 0.00687
Density
0.0
0.5
1.0
1.5
2.0
2.5
3.0
300
1000
2000
3000
Alignment score

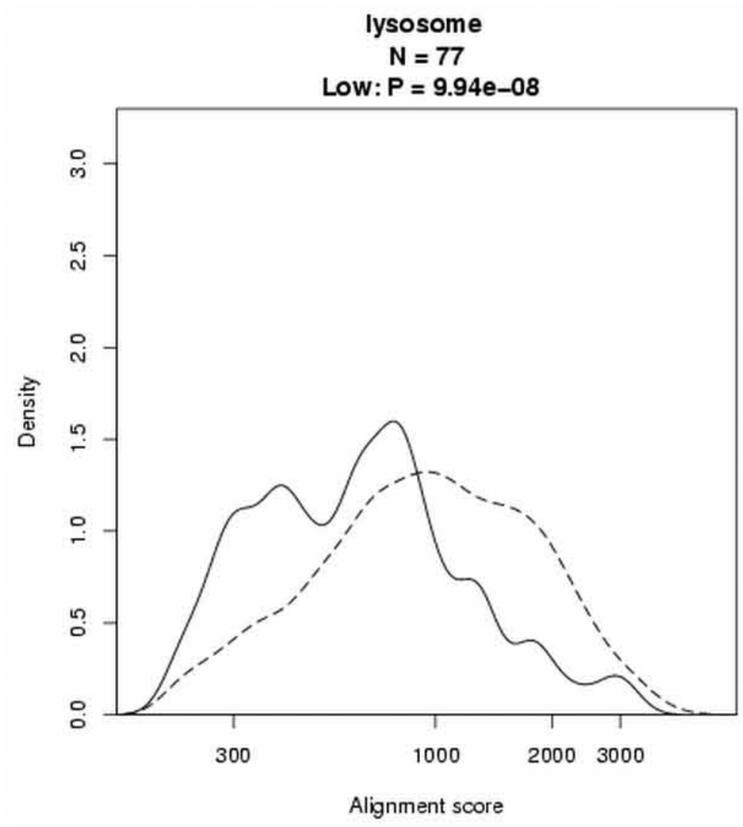

chromosome organization and biogenesis
N = 105
High: P = 0.00783
Density
0.0
0.5
1.0
1.5
2.0
2.5
3.0
300
1000
2000
3000
Alignment score

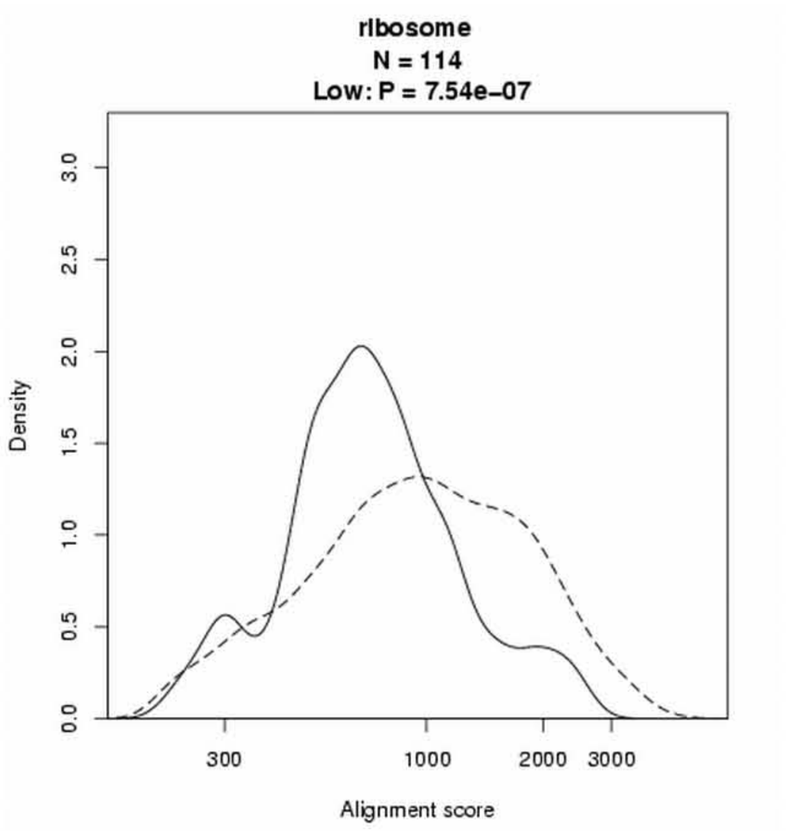

plasma membrane
N = 608
High: P = 0.00803
Density
0.0
0.5
1.0
1.5
2.0
2.5
3.0
300
1000
2000
3000
Alignment score

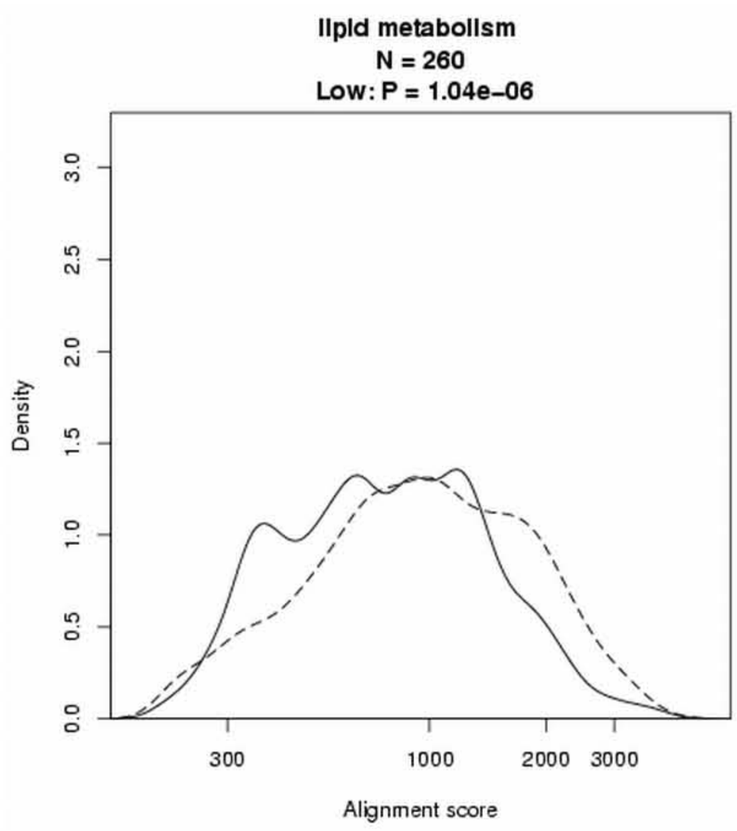
B

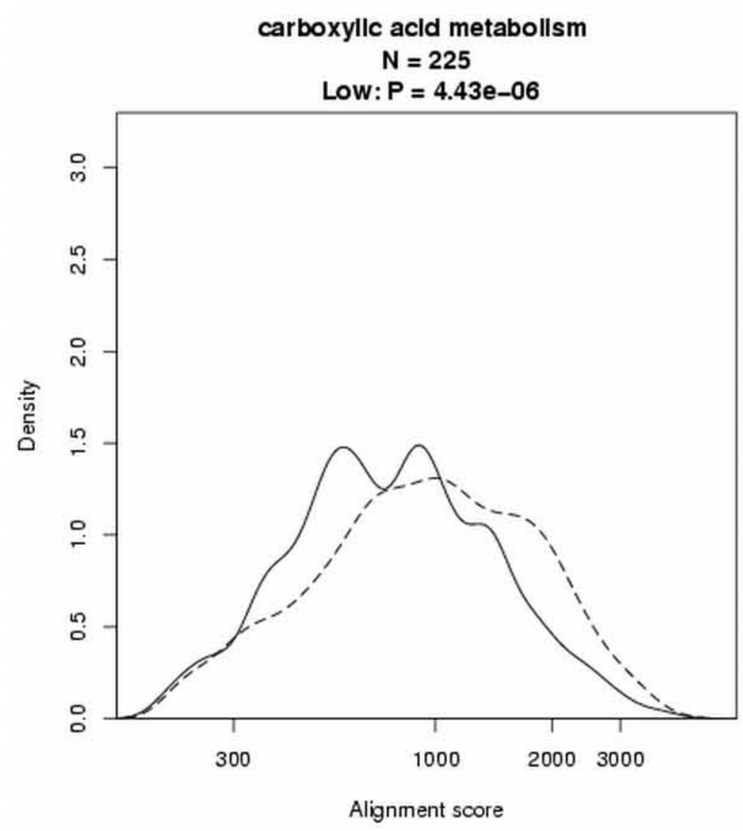

mitochondrion
N = 398
Low: P = 5.31e−09
Density
Alignment score

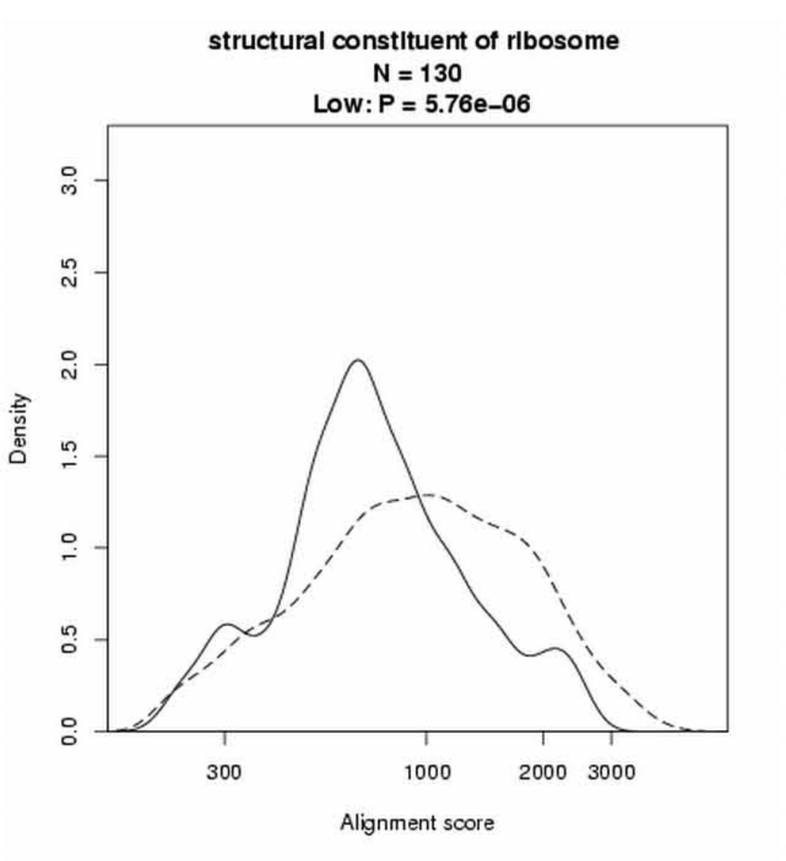

oxidoreductase activity
N = 309
Low: P = 2.07e−08
Density
Alignment score

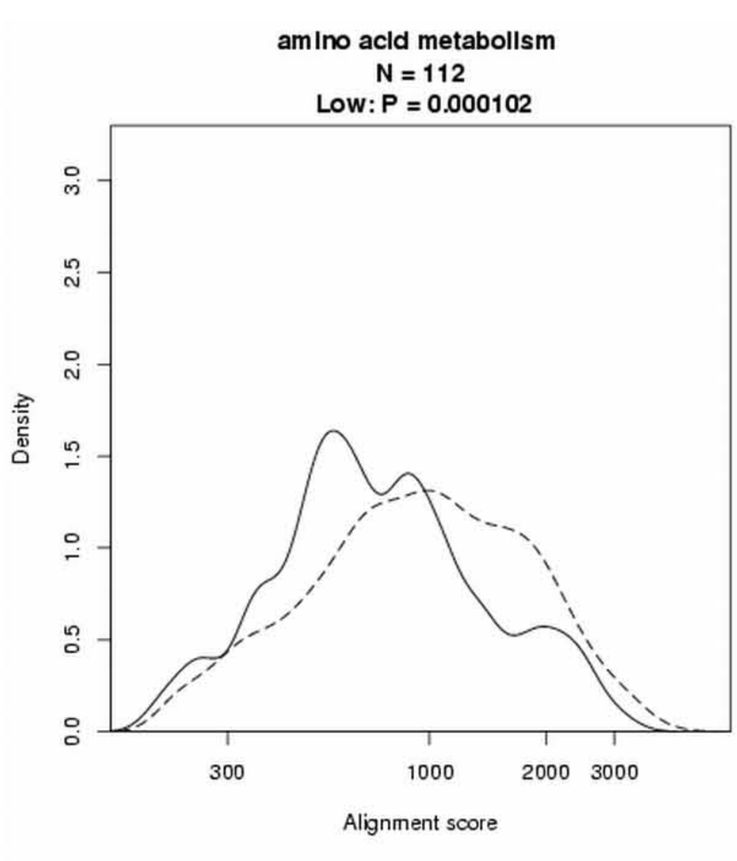

lysosome
N = 77
Low: P = 9.94e−08
Density
Alignment score

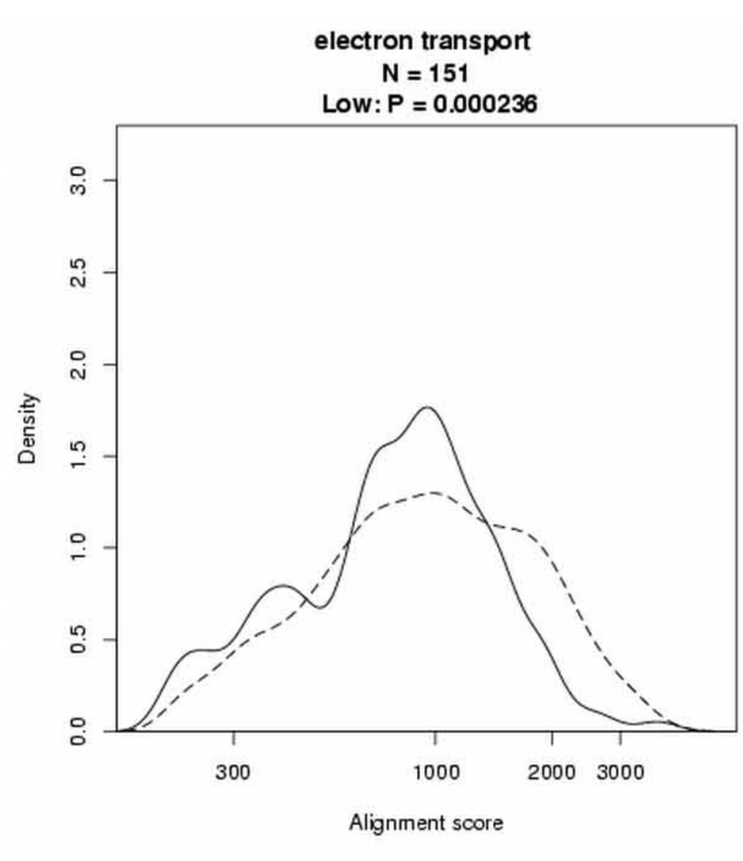

ribosome
N = 114
Low: P = 7.54e−07
Density
Alignment score

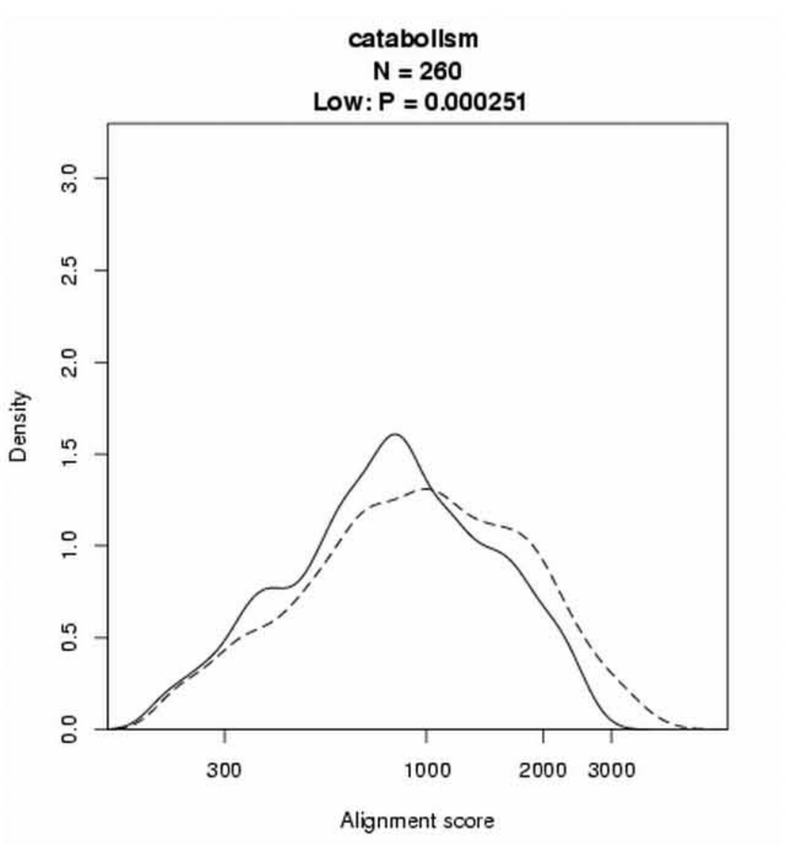

lipid metabolism
N = 260
Low: P = 1.04e−06
Density
Alignment score

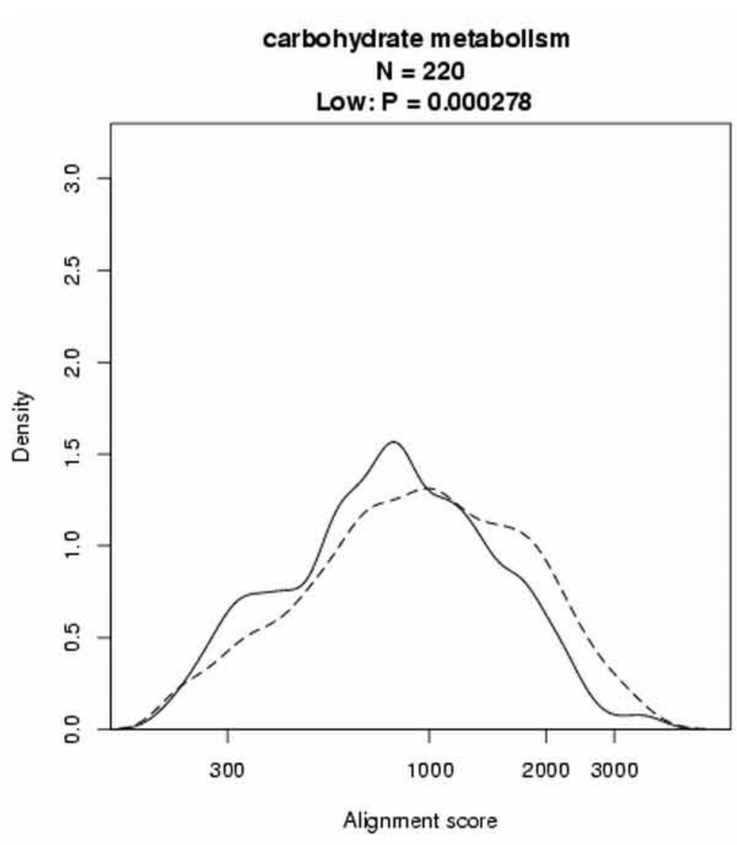

carboxylic acid metabolism
N = 225
Low: P = 4.43e−06
Density
Alignment score

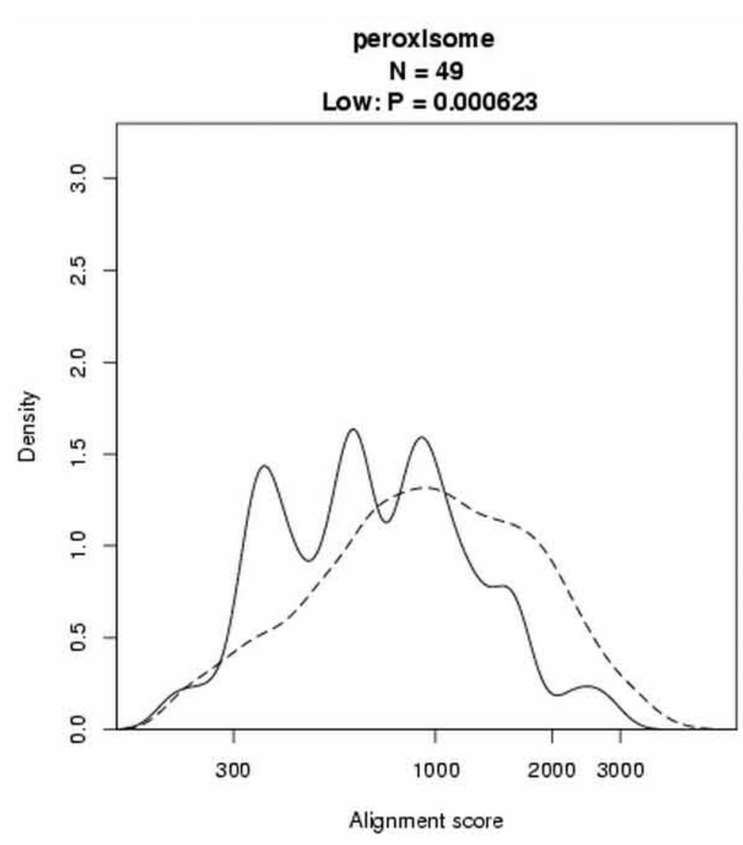

structural constituent of ribosome
N = 130
Low: P = 5.76e−06
Density
Alignment score

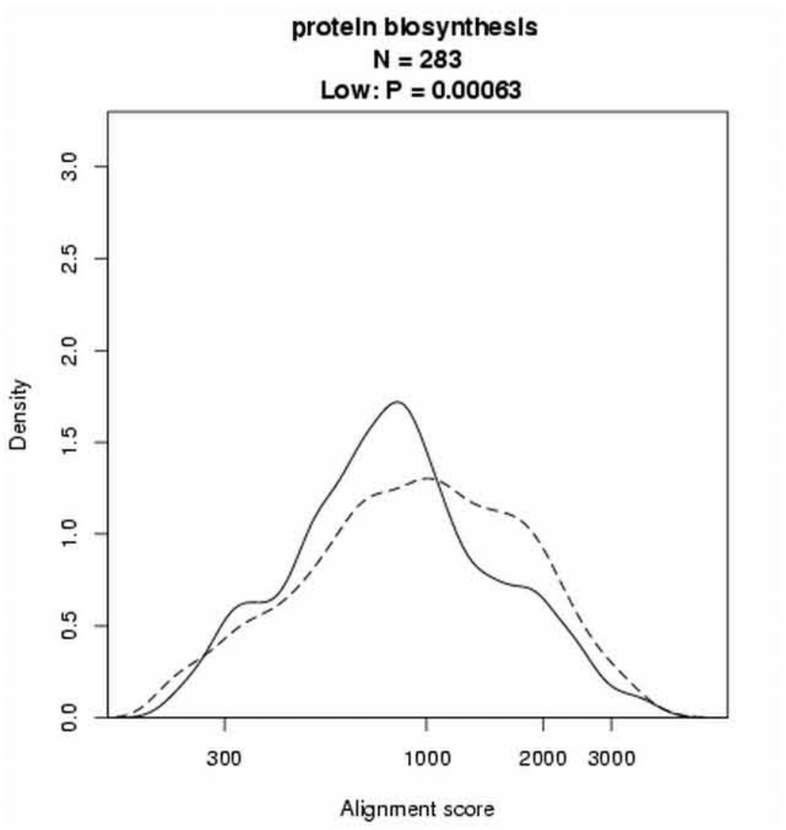

amino acid metabolism
N = 112
Low: P = 0.000102
Density
Alignment score

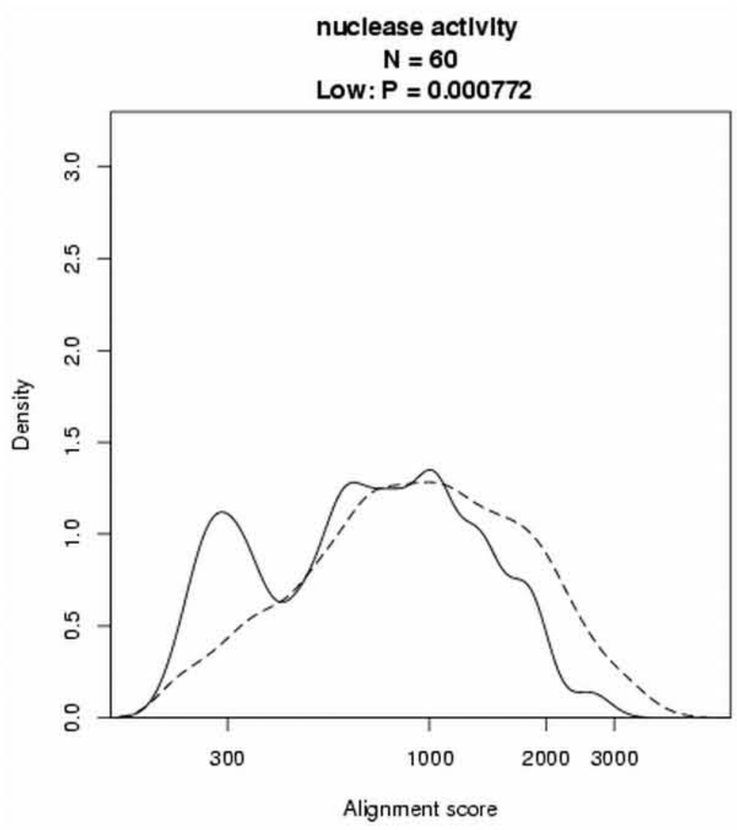

electron transport
N = 151
Low: P = 0.000236
Density
Alignment score

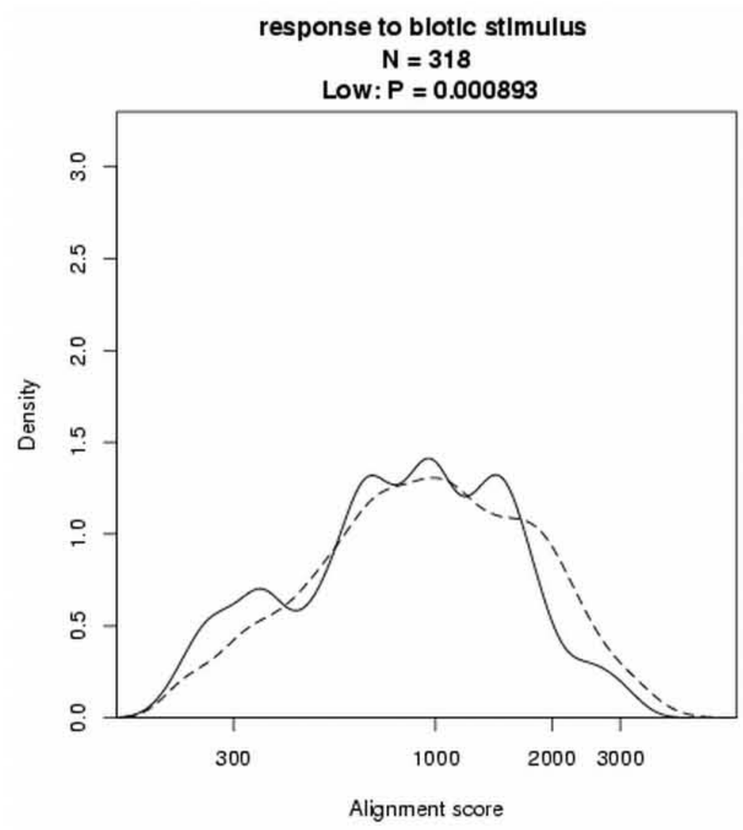

catabolism
N = 260
Low: P = 0.000251
Density
Alignment score

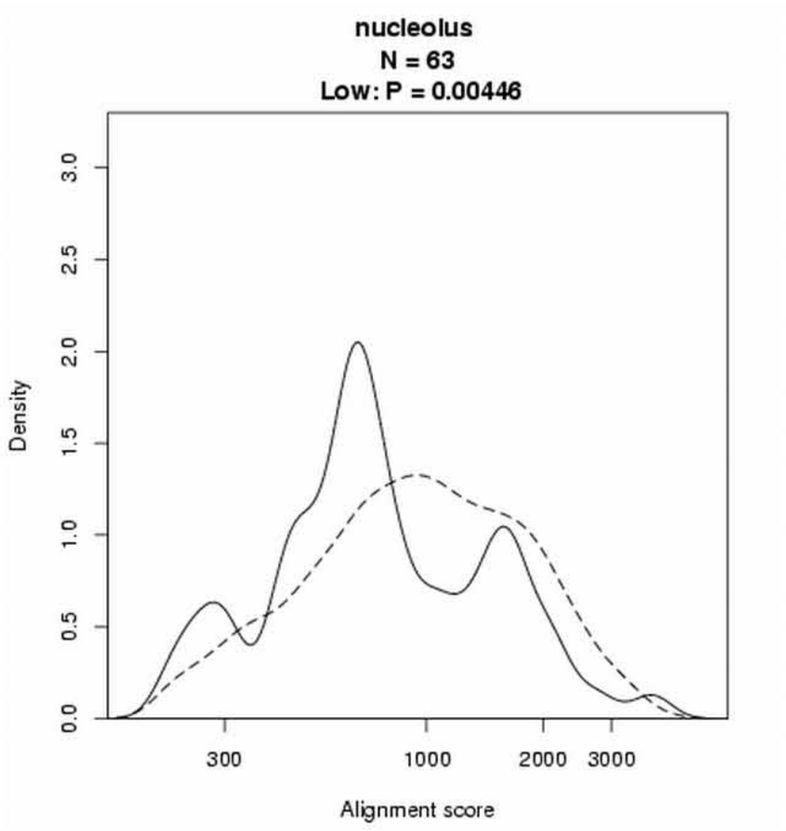

carbohydrate metabolism
N = 220
Low: P = 0.000278
Density
Alignment score

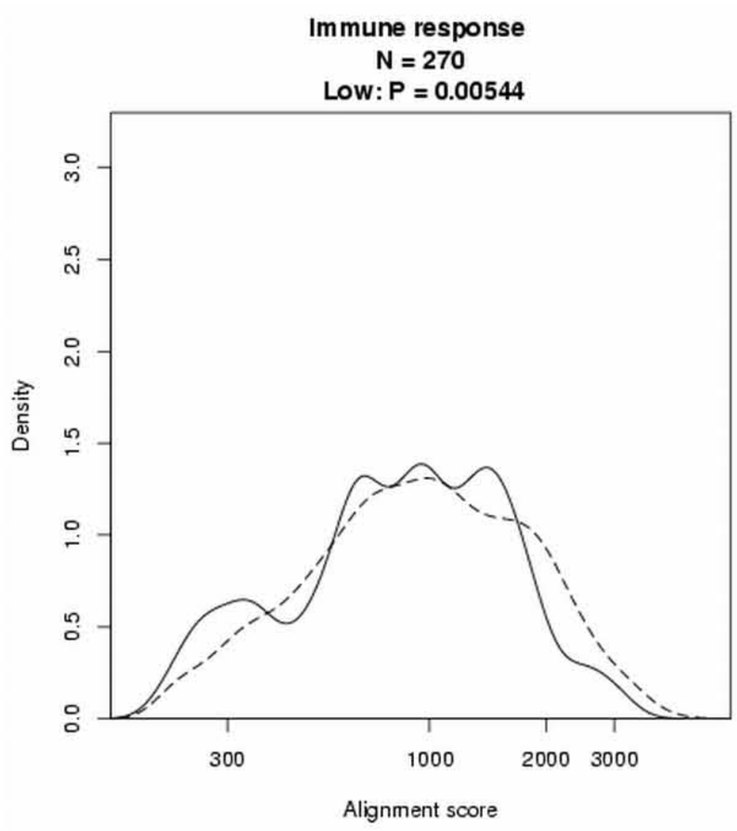

peroxisome
N = 49
Low: P = 0.000623
Density
Alignment score

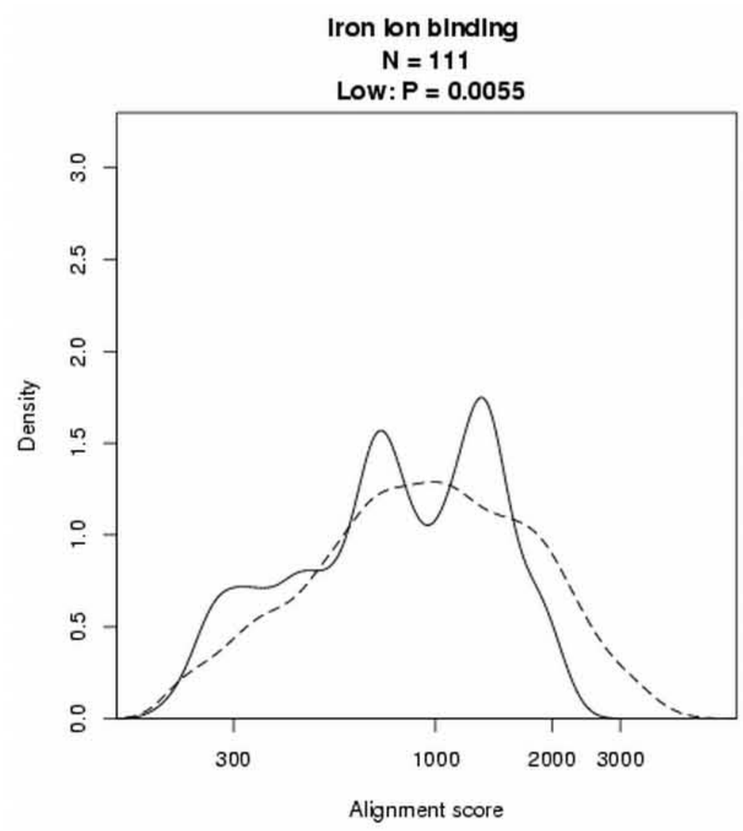

protein biosynthesis
N = 283
Low: P = 0.00063
Density
Alignment score

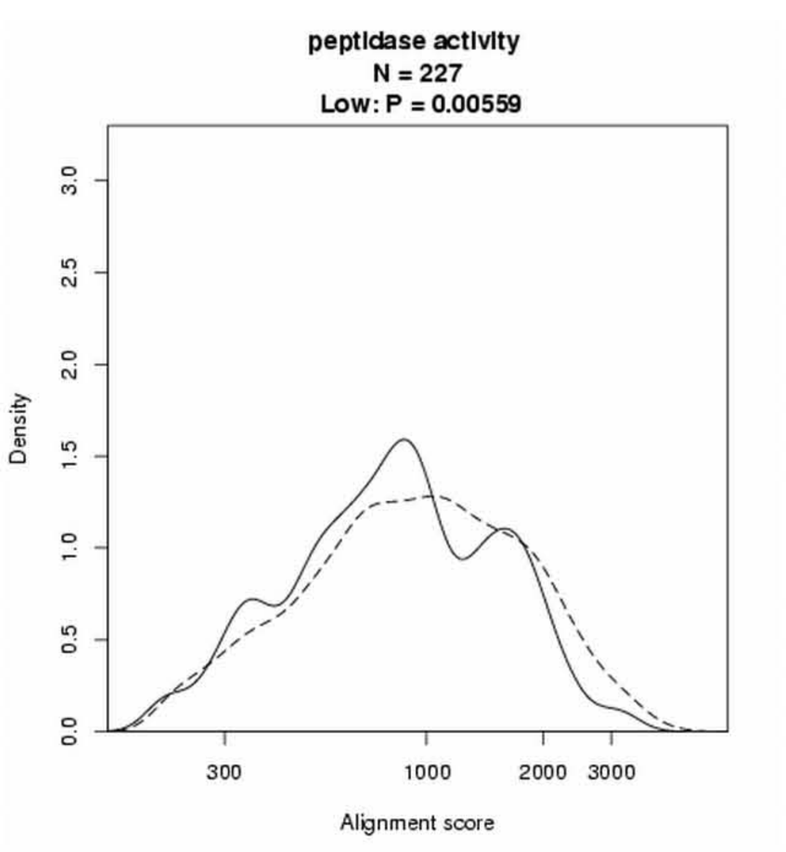

nuclease activity
N = 60
Low: P = 0.000772
Density
Alignment score

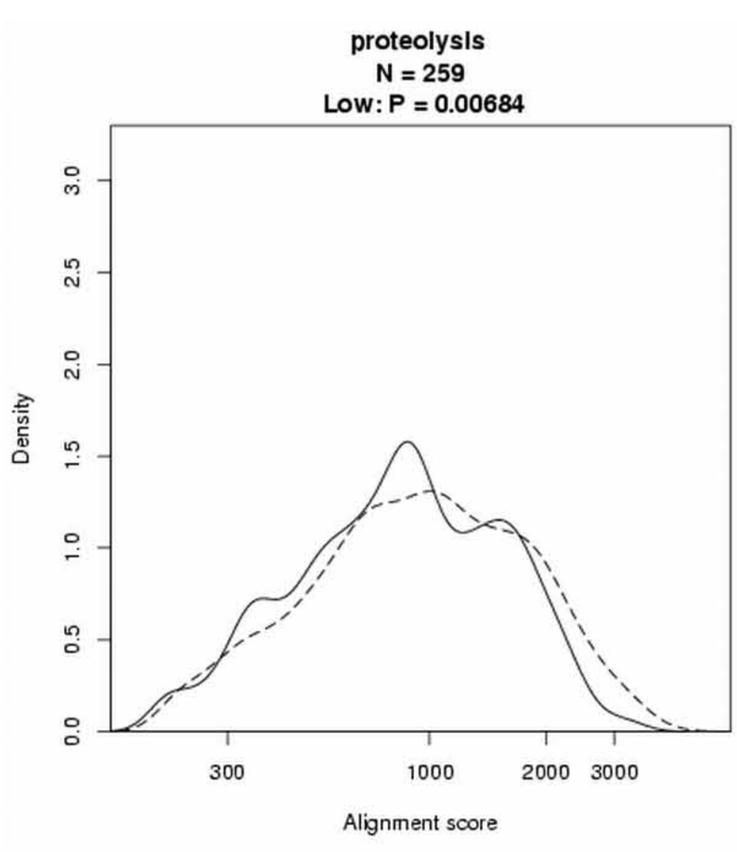

response to biotic stimulus
N = 318
Low: P = 0.000893
Density
Alignment score


nucleolus
N = 63
Low: P = 0.00446
Density
Alignment score


Immune response
N = 270
Low: P = 0.00544
Density
Alignment score


Iron ion binding
N = 111
Low: P = 0.0055
Density
Alignment score


peptidase activity
N = 227
Low: P = 0.00559
Density
Alignment score


proteolysis
N = 259
Low: P = 0.00684
Density
Alignment score