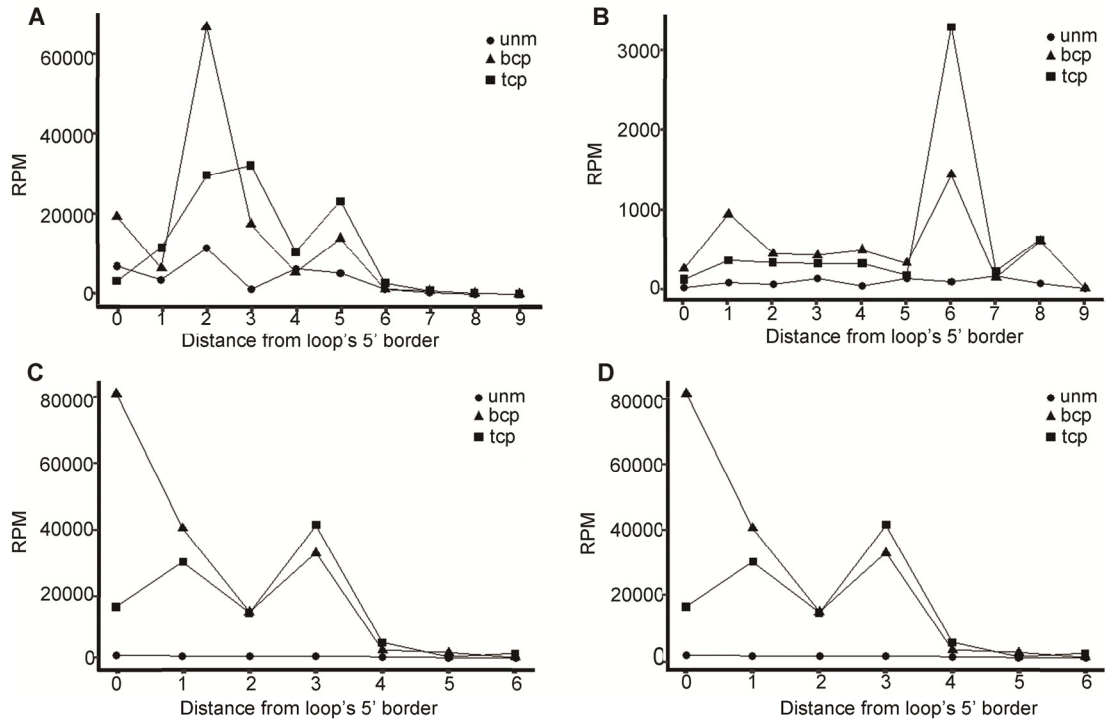
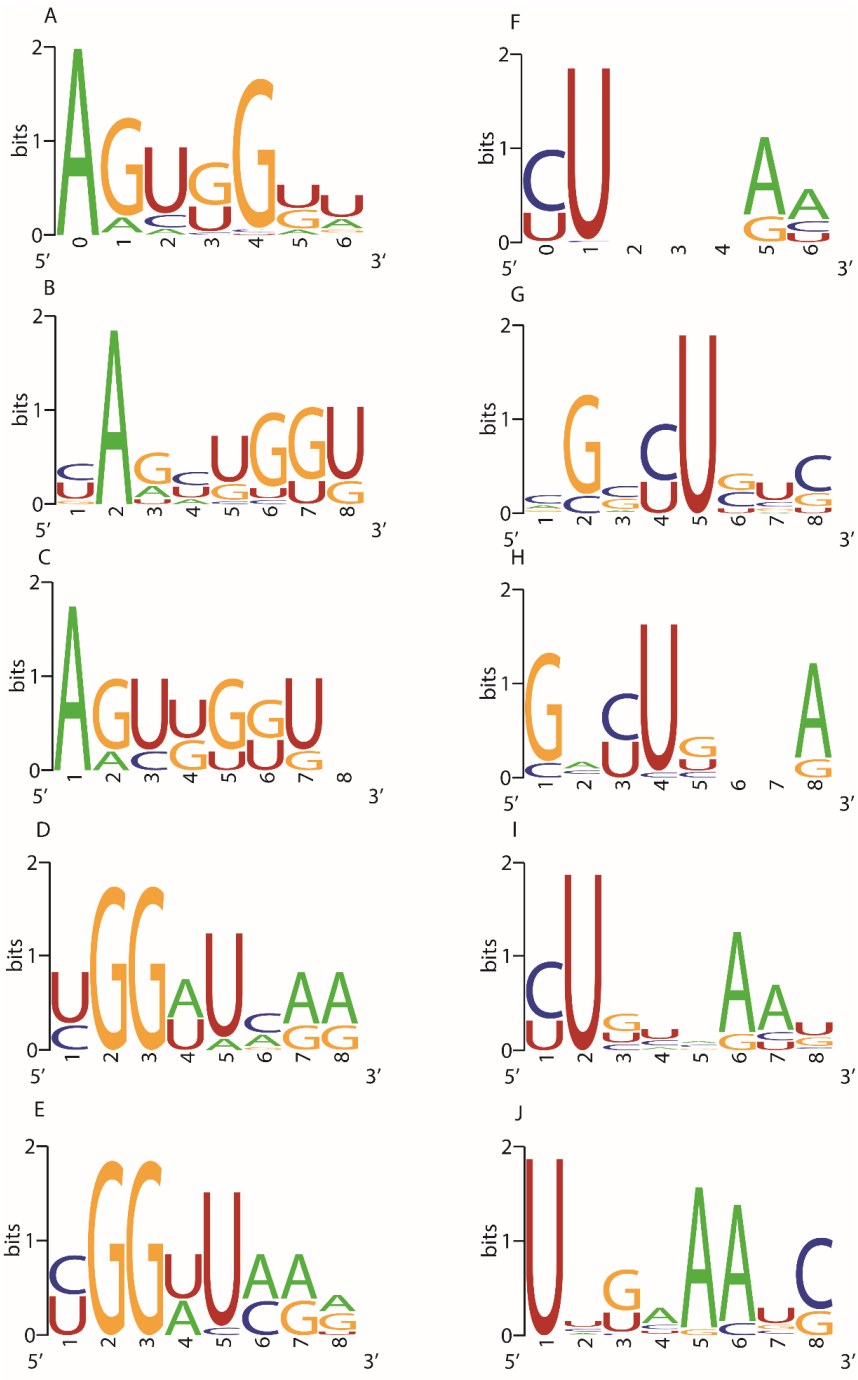


附图 1 水稻雄配子三类花粉的 tRF 在 D 环和反密码子环处终止或起始的位点

(A) D环上tRF 终点分布; **(B)** D环上tRF起点分布; **(C)** 反密码子环上tRF终点分布; **(D)** 反密码子环上tRF起点分布。unm、bcp 和 tcp 见图 1。RPM: 每百万条读段里的(目标)读段数。横轴为 0 表示刚好起始于环的第一个碱基。

Appendix figure 1 Distance between the tRFs' starting or ending base and D loop's or Anticodon loop's first base

(A) ending sites' distribution on D loop; **(B)** starting sites' distribution on D loop; **(C)** ending sites' distribution on Anticodon loop; **(D)** starting sites' distribution on Anticodon loop. unm, bcp and tcp see Figure 1. RPM: reads per million



附图 2 tRNA 剪切位置周围碱基分布情况(完整版)。A 和 F 为对照，其余图的横坐标 4 和 5 之间均为“剪切发生位置”

(A), (F) 所有 tRNA 的 D 环和反密码子环上前 7 个碱基分布 logo 图; **(B)** bcp 于 D 环第 3 个碱基终止的 tRF 对应 tRNA 序列 logo 图; **(C)** tcp 于 D 环第 4 个碱基终止的 tRF 对应 tRNA 序列 logo 图; **(D)** bcp 于 D 环第 7 碱基起始的 tRF 对应 tRNA 序列 logo 图; **(E)** tcp 于 D 环第 7 碱基起始的 tRF 对应 tRNA 序列 logo 图; **(G)** bcp 于反密码子环第 1 个碱基终止的 tRF 对应 tRNA 序列 logo 图; **(H)** bcp 于反密码子环第 2 个碱基终止的 tRF 对应 tRNA 序列 logo 图; **(I)** tcp 于反密码子环第 4 个碱基终止的 tRF 对应 tRNA 序列 logo 图; **(J)** tcp 于反密码子环第 6 个碱基起始的 tRF 对应 tRNA 序列 logo 图。

Appendix figure 2 Sequence motif logo for tRNA 8mer around cleavage sites. The position between 4 and 5 in x axis of B, C, D, E, G, H, I, J stand for cleavage site

(A), (F) sequence logo of all tRNA's first 7 bases of D loop, as control; **(A)** and Anticodon loop(**F**); **(B)** for bcp tRFs ended at the 3rd base of D loop; **(C)** for tcp tRFs ended at the 4th base of D loop; **(D)** for bcp tRFs started at the 7th base of D loop; **(E)** for tcp tRFs started at the 7th base of D loop; **(G)** for bcp tRFs ended at the 1st base of Anticodon loop; **(H)** for bcp tRFs ended at the 2nd base of Anticodon loop; **(I)** for tcp tRFs ended at the 4th base of Anticodon loop; **(J)** for tcp tRFs started at the 6th base of Anticodon loop

附表 1 一些基因的转录水平，里面的值是经过 log2 转化后的表达量

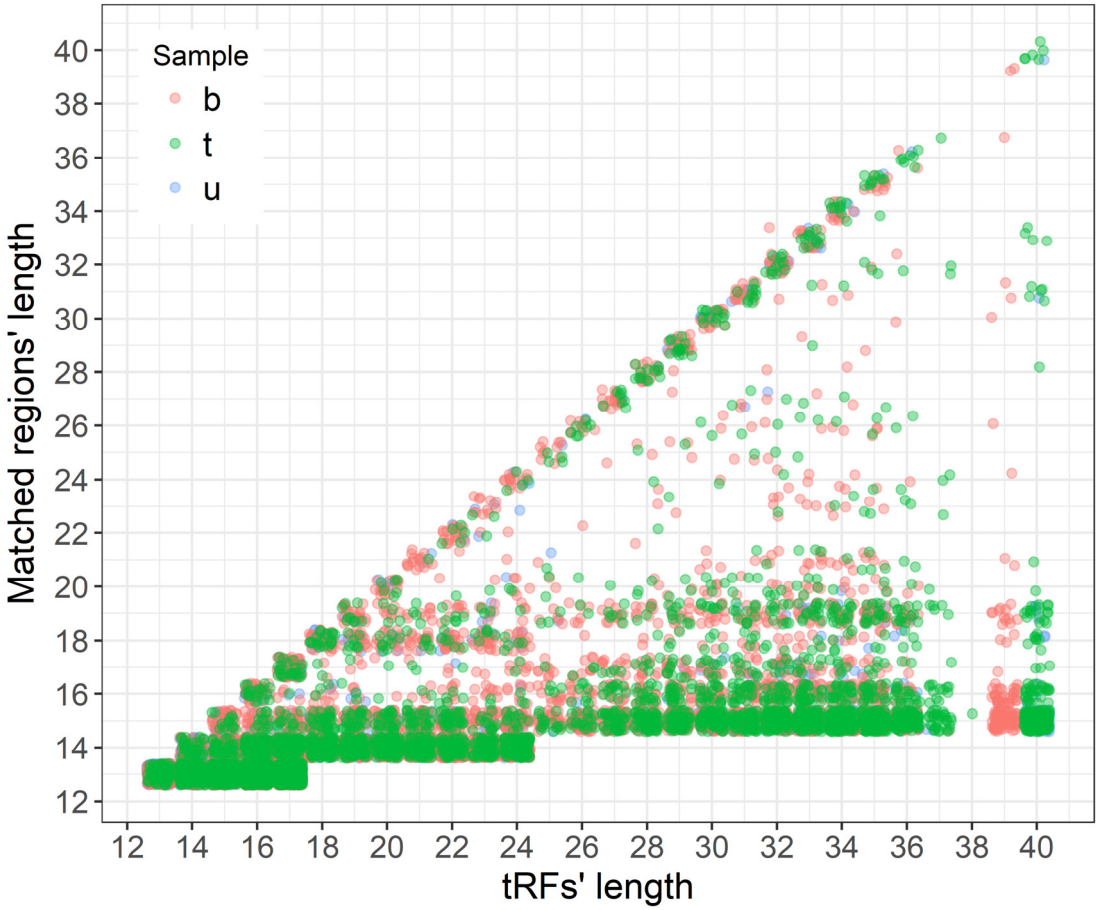
Appendix table 1 Some reference genes transcriptional level which was transferred to log2 scale

Gene_MSU_ID	Alias	Dommain	unm	bcp	tcp
LOC_Os06g49870.1	Dus	Dus	8.936	7.236	3.874
LOC_Os04g02730.1	Dus	zf-CCCH|Dus	9.385	8.597	4.727
LOC_Os04g20990.1	Dus	Dus	8.523	6.784	4.623
LOC_Os04g44890.1	Dus	Dus	6.949	3.982	3.311
LOC_Os08g37780.1	Nsun2	Nol1_Nop2_Fmu	6.021	5.586	3.732
LOC_Os01g42630.1	Dnmt2	DNA_methylase	6.286	5.645	4.044
LOC_Os07g43670.1	RNase T2	Ribonuclease_T2	6.283	5.159	4.931
LOC_Os01g67180.1	RNase T2	Ribonuclease_T2	9.822	7.878	6.049
LOC_Os08g33710.1	RNase T2	Ribonuclease_T2	3.57	3.381	4.935
LOC_Os09g36700.1	RNase T2	Ribonuclease_T2	5.214	4.625	5.423

数据来自 Peng 等(Peng, et al., 2012)。Data are according to *Peng et al., 2012*.

参考文献

Peng H, Chun J, Ai TB, Tong YA, Zhang R, Zhao MM, Chen F and Wang SH (2012). MicroRNA profiles and their control of male gametophyte development in rice. *Plant Mol Biol* **80**, 85-102.

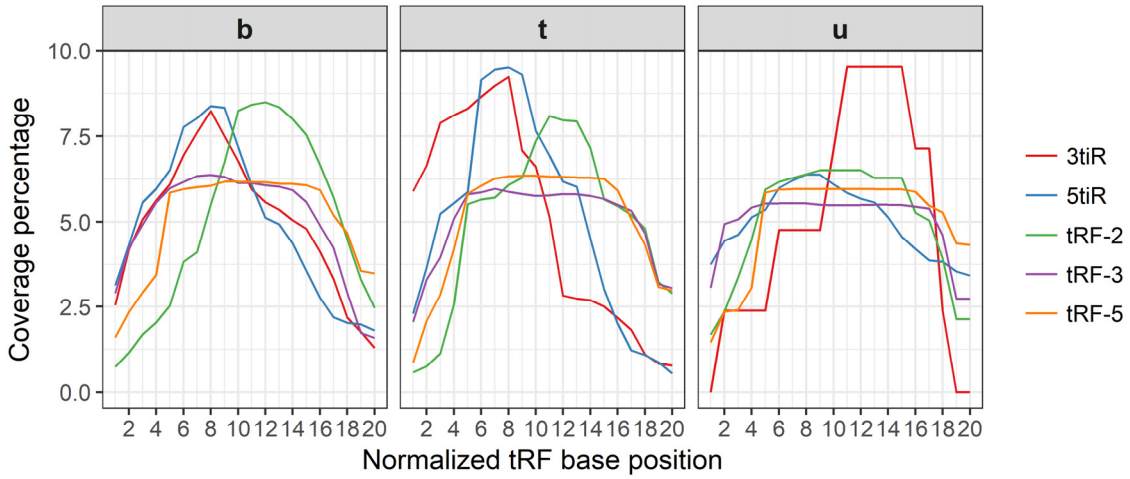


附图 3 tRF 匹配靶基因的长度分布

tRF 和靶基因配对的长度(y 轴)和 tRF 本身的长度(x 轴)的关系如图所示, u 表示样本 unm (蓝色), b 表示 bcp (红色), t 表示 tcp (绿色)。

Appendix figure 3 Distribution of matched regions' length over tRFs length

The axis Y stands for matched regions' length and the axis X stands for tRFs' length. 3 different samples are shown in blue (u, unm), red (b, bcp) and green (t, tcp).

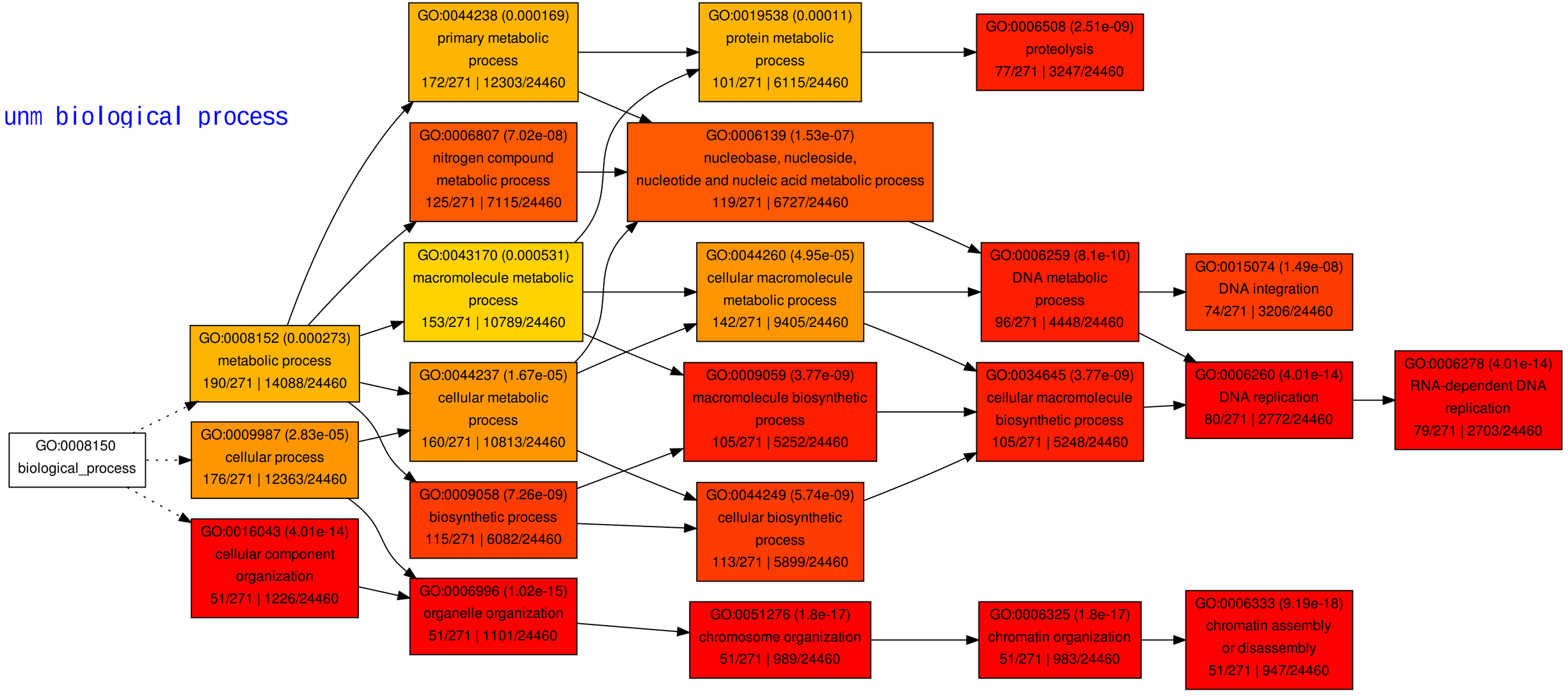


附图 4 tRF 和靶基因匹配碱基在 tRF 内分布的位置

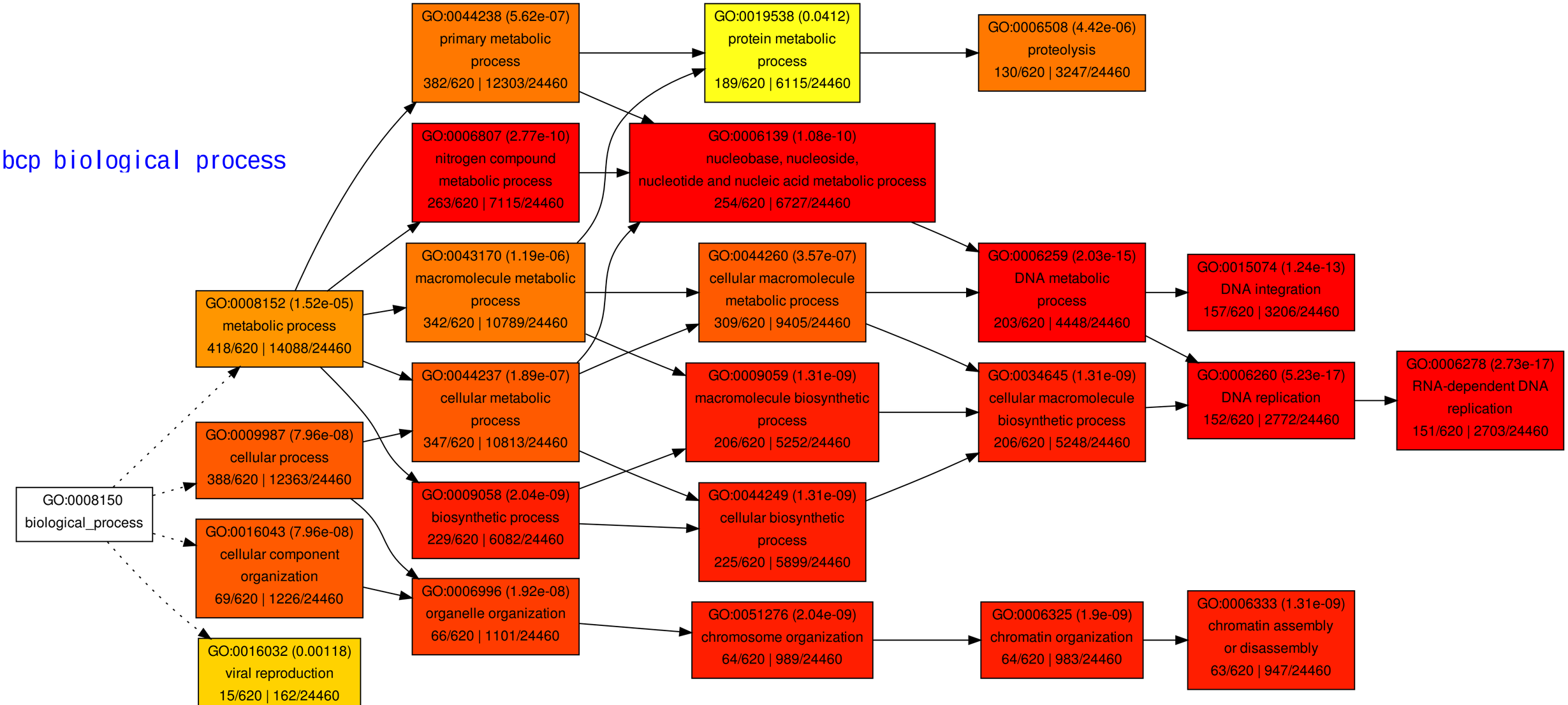
横轴是标准化的碱基位置，纵轴表示某位置匹配了靶基因的数量占该类 tRF 总量的比例。各颜色代表不同类的 tRF；顶部的 b 代表 bcp, t 代表 tcp, u 代表 unm。

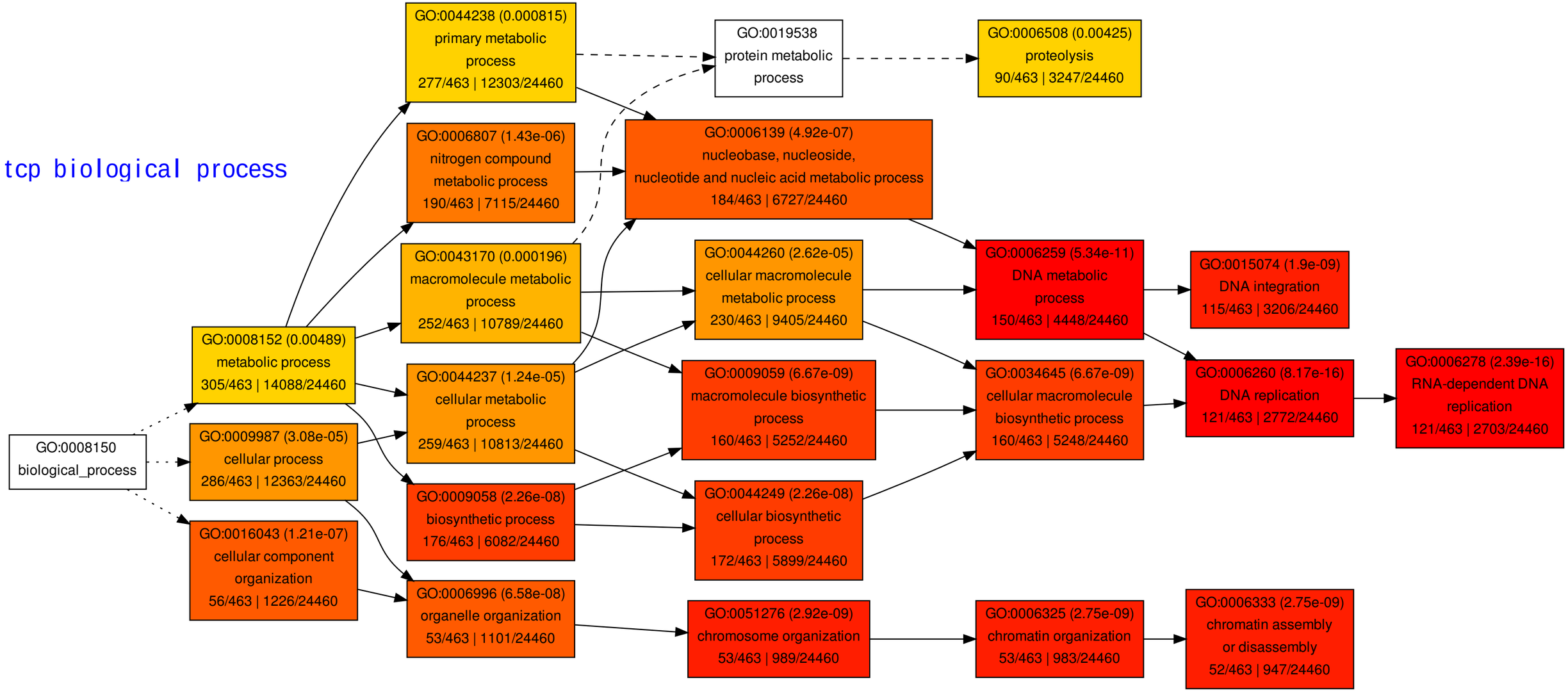
Appendix figure 4 Distribution of target matched tRF base positions over all tRF parts

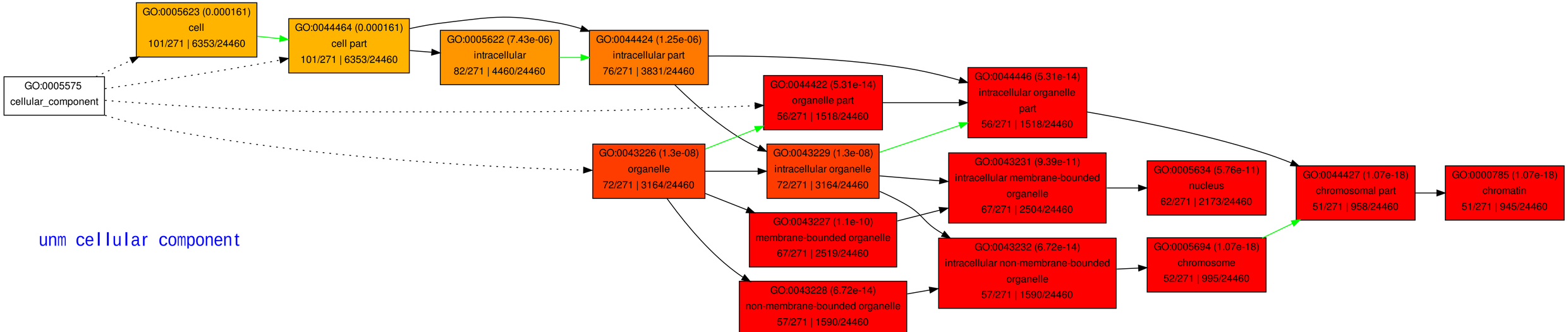
The x axis stands for normalized tRF base positions, the y axis stands for the percentage of target matched base positions. b: bcp; t: tcp; u: unm.


unm biological process
GO:0008150
biological_process
GO:0008152 (0.000273)
metabolic process
190/271 | 14088/24460
GO:0009987 (2.83e-05)
cellular process
176/271 | 12363/24460
GO:0016043 (4.01e-14)
cellular component
organization
51/271 | 1226/24460
GO:0044238 (0.000169)
primary metabolic
process
172/271 | 12303/24460
GO:0006807 (7.02e-08)
nitrogen compound
metabolic process
125/271 | 7115/24460
GO:0043170 (0.000531)
macromolecule metabolic
process
153/271 | 10789/24460
GO:0044237 (1.67e-05)
cellular metabolic
process
160/271 | 10813/24460
GO:0009058 (7.26e-09)
biosynthetic process
115/271 | 6082/24460
GO:0006996 (1.02e-15)
organelle organization
51/271 | 1101/24460
GO:0019538 (0.00011)
protein metabolic
process
101/271 | 6115/24460
GO:0006139 (1.53e-07)
nucleobase, nucleoside,
nucleotide and nucleic acid metabolic process
119/271 | 6727/24460
GO:0044260 (4.95e-05)
cellular macromolecule
metabolic process
142/271 | 9405/24460
GO:0009059 (3.77e-09)
macromolecule biosynthetic
process
105/271 | 5252/24460
GO:0044249 (5.74e-09)
cellular biosynthetic
process
113/271 | 5899/24460
GO:0051276 (1.8e-17)
chromosome organization
51/271 | 989/24460
GO:0006508 (2.51e-09)
proteolysis
77/271 | 3247/24460
GO:0006259 (8.1e-10)
DNA metabolic
process
96/271 | 4448/24460
GO:0034645 (3.77e-09)
cellular macromolecule
biosynthetic process
105/271 | 5248/24460
GO:0006325 (1.8e-17)
chromatin organization
51/271 | 983/24460
GO:0015074 (1.49e-08)
DNA integration
74/271 | 3206/24460
GO:0006260 (4.01e-14)
DNA replication
80/271 | 2772/24460
GO:0006278 (4.01e-14)
RNA-dependent DNA
replication
79/271 | 2703/24460
GO:0006333 (9.19e-18)
chromatin assembly
or disassembly
51/271 | 947/24460

bcp biological process




tcp biological process
GO:0008150
biological_process
GO:0008152 (0.00489)
metabolic process
305/463 | 14088/24460
GO:0009987 (3.08e-05)
cellular process
286/463 | 12363/24460
GO:0016043 (1.21e-07)
cellular component
organization
56/463 | 1226/24460
GO:0044238 (0.000815)
primary metabolic
process
277/463 | 12303/24460
GO:0006807 (1.43e-06)
nitrogen compound
metabolic process
190/463 | 7115/24460
GO:0043170 (0.000196)
macromolecule metabolic
process
252/463 | 10789/24460
GO:0044237 (1.24e-05)
cellular metabolic
process
259/463 | 10813/24460
GO:0009058 (2.26e-08)
biosynthetic process
176/463 | 6082/24460
GO:0006996 (6.58e-08)
organelle organization
53/463 | 1101/24460
GO:0019538
protein metabolic
process
GO:0006139 (4.92e-07)
nucleobase, nucleoside,
nucleotide and nucleic acid metabolic process
184/463 | 6727/24460
GO:0044260 (2.62e-05)
cellular macromolecule
metabolic process
230/463 | 9405/24460
GO:0009059 (6.67e-09)
macromolecule biosynthetic
process
160/463 | 5252/24460
GO:0044249 (2.26e-08)
cellular biosynthetic
process
172/463 | 5899/24460
GO:0051276 (2.92e-09)
chromosome organization
53/463 | 989/24460
GO:0006508 (0.00425)
proteolysis
90/463 | 3247/24460
GO:0006259 (5.34e-11)
DNA metabolic
process
150/463 | 4448/24460
GO:0034645 (6.67e-09)
cellular macromolecule
biosynthetic process
160/463 | 5248/24460
GO:0006325 (2.75e-09)
chromatin organization
53/463 | 983/24460
GO:0015074 (1.9e-09)
DNA integration
115/463 | 3206/24460
GO:0006260 (8.17e-16)
DNA replication
121/463 | 2772/24460
GO:0006333 (2.75e-09)
chromatin assembly
or disassembly
52/463 | 947/24460
GO:0006278 (2.39e-16)
RNA-dependent DNA
replication
121/463 | 2703/24460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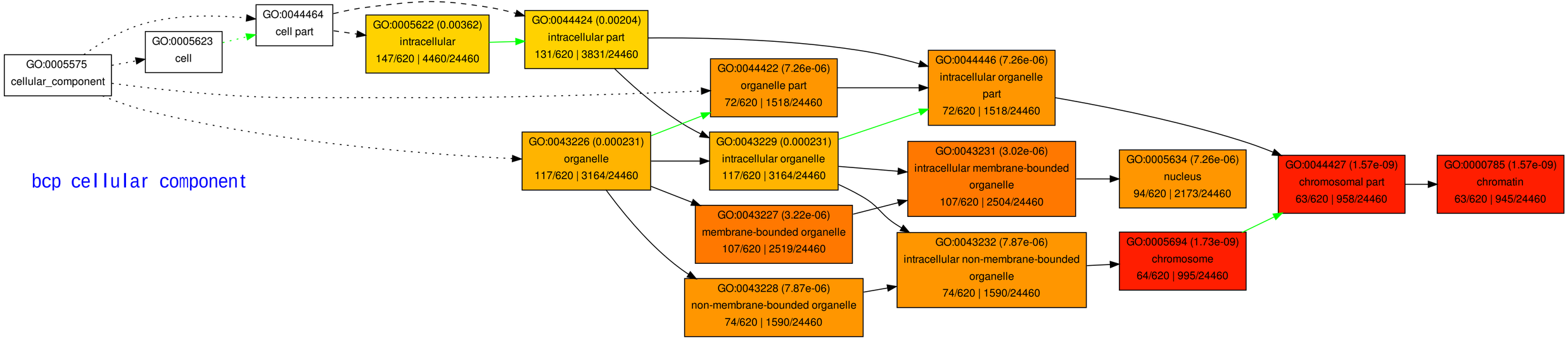
cellular_component
GO:0005623 (0.000161)
cell
101/271 | 6353/24460
GO:0044464 (0.000161)
cell part
101/271 | 6353/24460
GO:0005622 (7.43e-06)
intracellular
82/271 | 4460/24460
GO:0044424 (1.25e-06)
intracellular part
76/271 | 3831/24460
GO:0044422 (5.31e-14)
organelle part
56/271 | 1518/24460
GO:0044446 (5.31e-14)
intracellular organelle
part
56/271 | 1518/24460
GO:0043226 (1.3e-08)
organelle
72/271 | 3164/24460
GO:0043229 (1.3e-08)
intracellular organelle
72/271 | 3164/24460
GO:0043231 (9.39e-11)
intracellular membrane-bounded
organelle
67/271 | 2504/24460
GO:0005634 (5.76e-11)
nucleus
62/271 | 2173/24460
GO:0044427 (1.07e-18)
chromosomal part
51/271 | 958/24460
GO:0000785 (1.07e-18)
chromatin
51/271 | 945/24460
GO:0043227 (1.1e-10)
membrane-bounded organelle
67/271 | 2519/24460
GO:0043232 (6.72e-14)
intracellular non-membrane-bounded
organelle
57/271 | 1590/24460
GO:0005694 (1.07e-18)
chromosome
52/271 | 995/24460
GO:0043228 (6.72e-14)
non-membrane-bounded organelle
57/271 | 1590/24460
unm cellular component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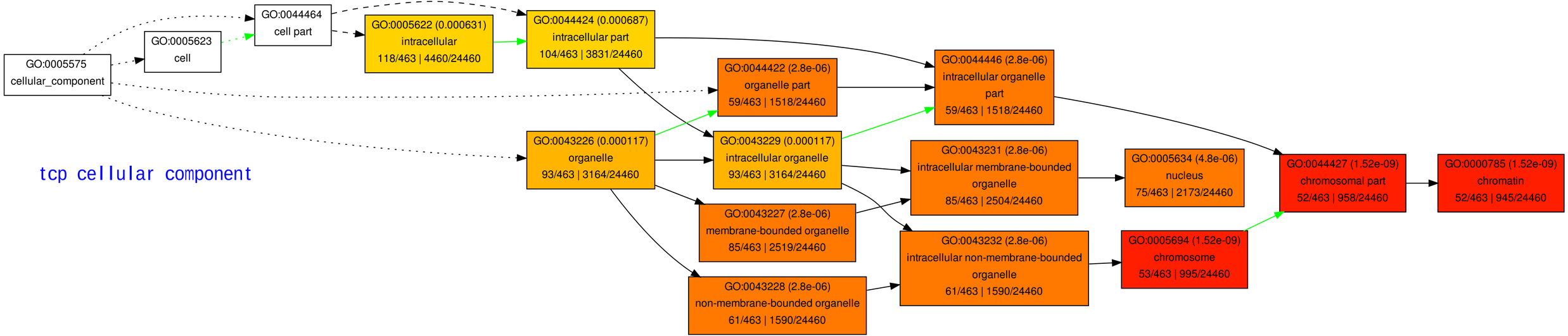
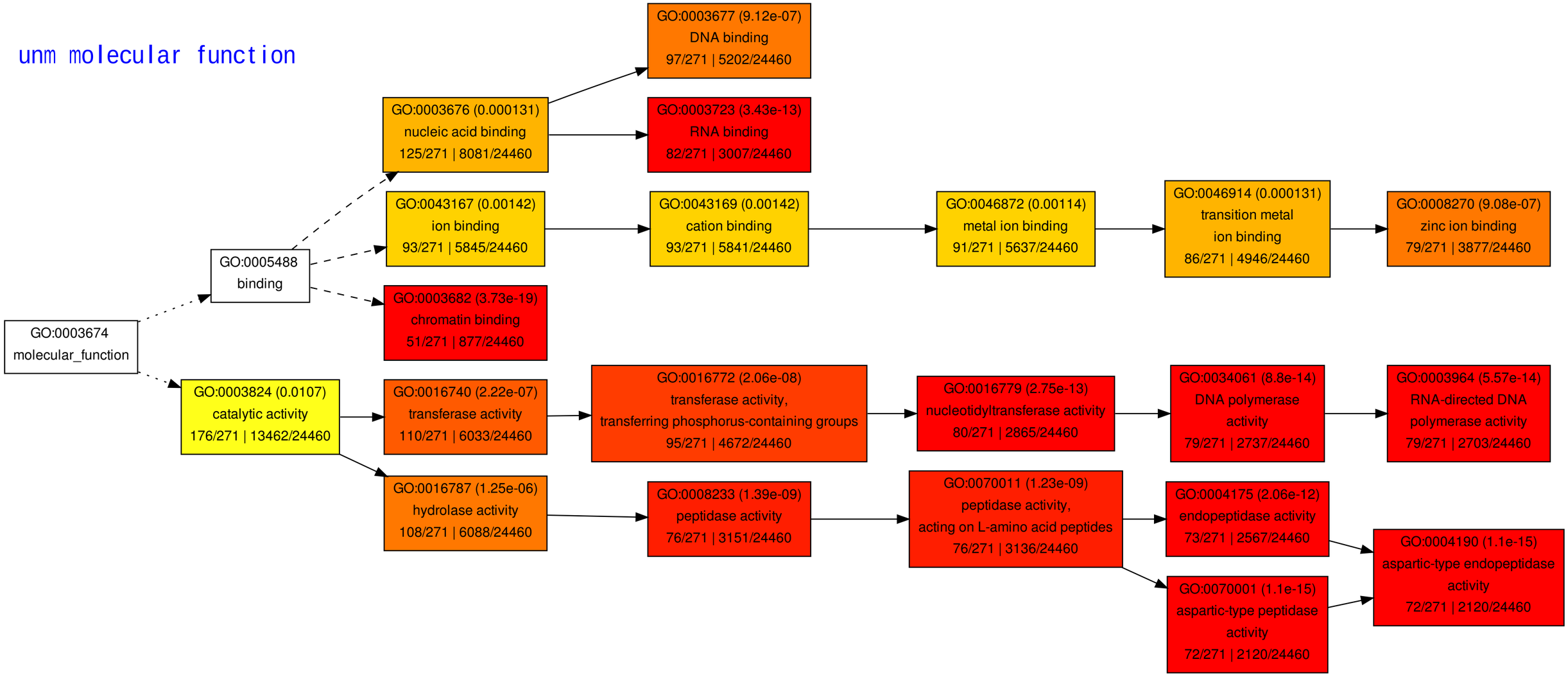
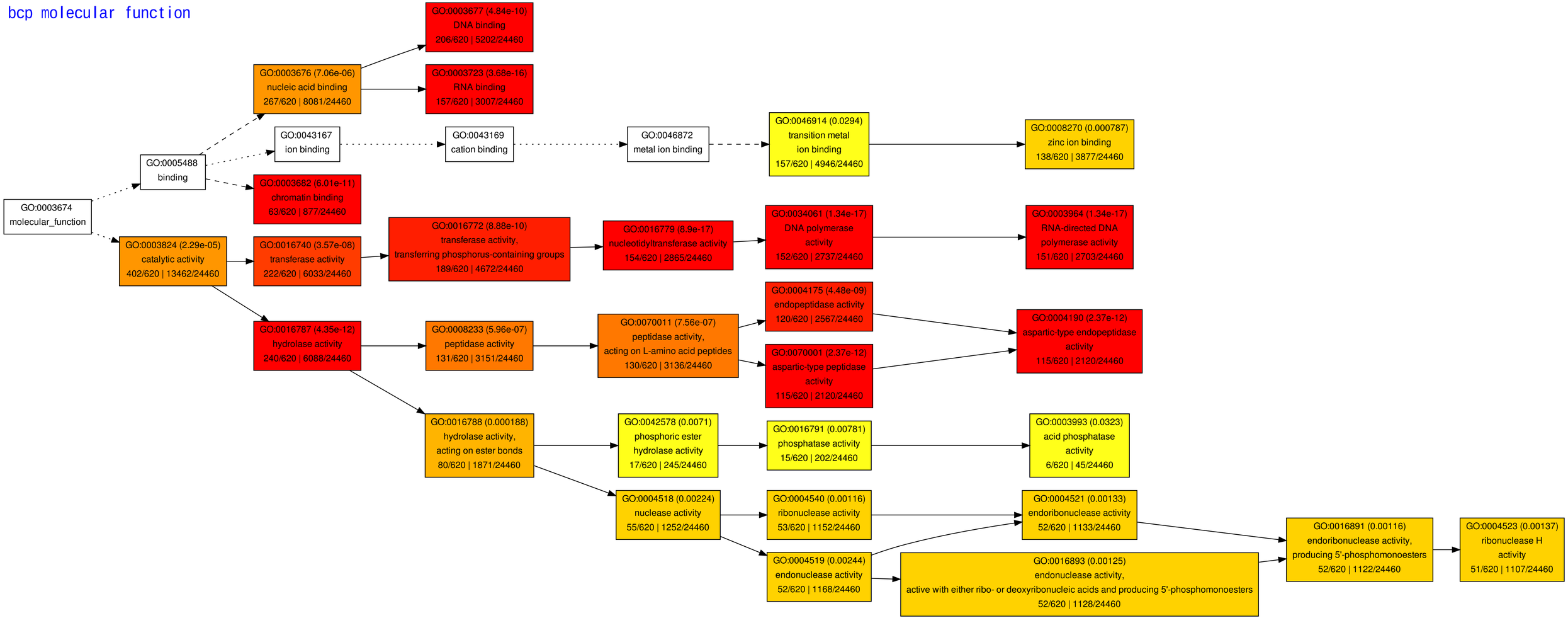
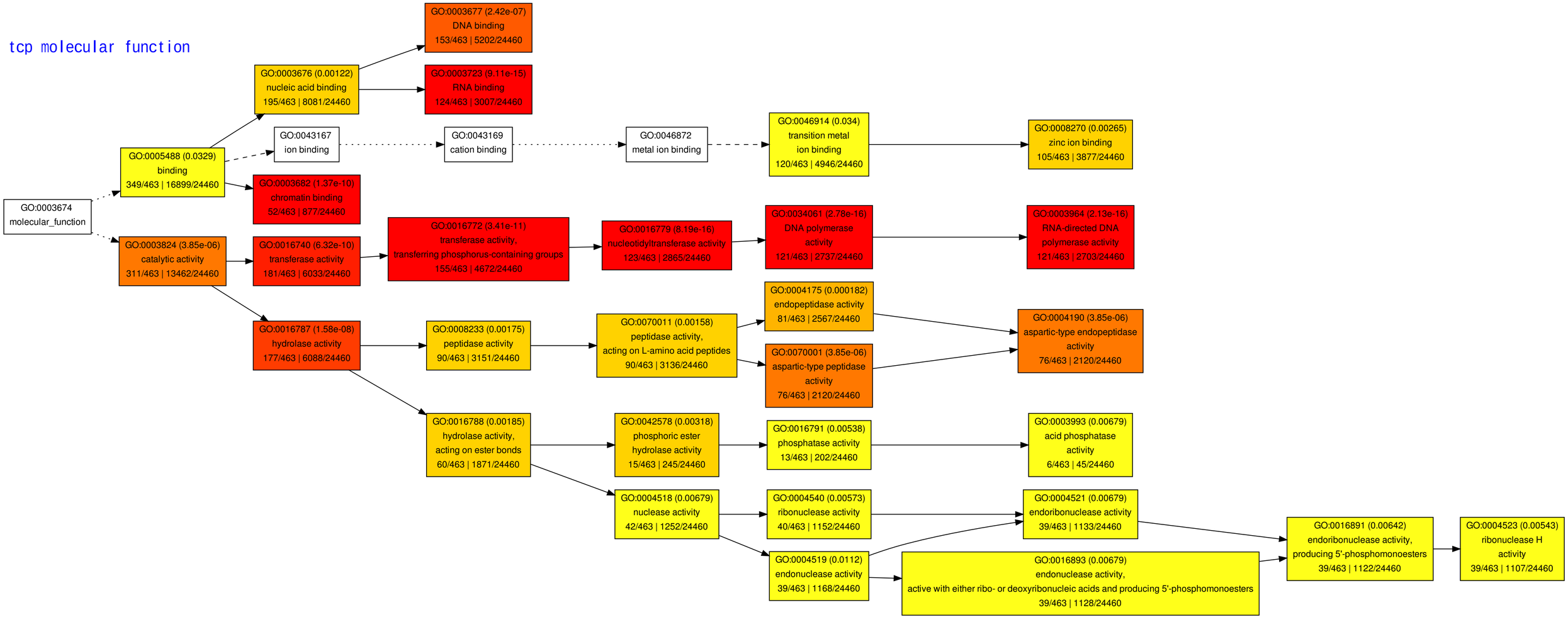
cellular_component
GO:0005623
cell
GO:0044464
cell part
GO:0005622 (0.00362)
intracellular
147/620 | 4460/24460
GO:0044424 (0.00204)
intracellular part
131/620 | 3831/24460
GO:0044422 (7.26e-06)
organelle part
72/620 | 1518/24460
GO:0044446 (7.26e-06)
intracellular organelle
part
72/620 | 1518/24460
GO:0043226 (0.000231)
organelle
117/620 | 3164/24460
GO:0043229 (0.000231)
intracellular organelle
117/620 | 3164/24460
GO:0043231 (3.02e-06)
intracellular membrane-bounded
organelle
107/620 | 2504/24460
GO:0005634 (7.26e-06)
nucleus
94/620 | 2173/24460
GO:0044427 (1.57e-09)
chromosomal part
63/620 | 958/24460
GO:0000785 (1.57e-09)
chromatin
63/620 | 945/24460
GO:0043227 (3.22e-06)
membrane-bounded organelle
107/620 | 2519/24460
GO:0043232 (7.87e-06)
intracellular non-membrane-bounded
organelle
74/620 | 1590/24460
GO:0005694 (1.73e-09)
chromosome
64/620 | 995/24460
GO:0043228 (7.87e-06)
non-membrane-bounded organelle
74/620 | 1590/24460
bcp cellular component


GO:0005575
cellular_component
GO:0005623
cell
GO:0044464
cell part
GO:0005622 (0.000631)
intracellular
118/463 | 4460/24460
GO:0044424 (0.000687)
intracellular part
104/463 | 3831/24460
GO:0044422 (2.8e-06)
organelle part
59/463 | 1518/24460
GO:0044446 (2.8e-06)
intracellular organelle
part
59/463 | 1518/24460
GO:0043226 (0.000117)
organelle
93/463 | 3164/24460
GO:0043229 (0.000117)
intracellular organelle
93/463 | 3164/24460
GO:0043231 (2.8e-06)
intracellular membrane-bounded
organelle
85/463 | 2504/24460
GO:0005634 (4.8e-06)
nucleus
75/463 | 2173/24460
GO:0044427 (1.52e-09)
chromosomal part
52/463 | 958/24460
GO:0000785 (1.52e-09)
chromatin
52/463 | 945/24460
GO:0043227 (2.8e-06)
membrane-bounded organelle
85/463 | 2519/24460
GO:0043232 (2.8e-06)
intracellular non-membrane-bounded
organelle
61/463 | 1590/24460
GO:0005694 (1.52e-09)
chromosome
53/463 | 995/24460
GO:0043228 (2.8e-06)
non-membrane-bounded organelle
61/463 | 1590/24460
tcp cellular component


unm molecular function
GO:0003674
molecular_function
GO:0005488
binding
GO:0003824 (0.0107)
catalytic activity
176/271 | 13462/24460
GO:0003676 (0.000131)
nucleic acid binding
125/271 | 8081/24460
GO:0043167 (0.00142)
ion binding
93/271 | 5845/24460
GO:0003682 (3.73e-19)
chromatin binding
51/271 | 877/24460
GO:0016740 (2.22e-07)
transferase activity
110/271 | 6033/24460
GO:0016787 (1.25e-06)
hydrolase activity
108/271 | 6088/24460
GO:0003677 (9.12e-07)
DNA binding
97/271 | 5202/24460
GO:0003723 (3.43e-13)
RNA binding
82/271 | 3007/24460
GO:0043169 (0.00142)
cation binding
93/271 | 5841/24460
GO:0016772 (2.06e-08)
transferase activity,
transferring phosphorus-containing groups
95/271 | 4672/24460
GO:0008233 (1.39e-09)
peptidase activity
76/271 | 3151/24460
GO:0046872 (0.00114)
metal ion binding
91/271 | 5637/24460
GO:0016779 (2.75e-13)
nucleotidyltransferase activity
80/271 | 2865/24460
GO:0070011 (1.23e-09)
peptidase activity,
acting on L-amino acid peptides
76/271 | 3136/24460
GO:0046914 (0.000131)
transition metal
ion binding
86/271 | 4946/24460
GO:0034061 (8.8e-14)
DNA polymerase
activity
79/271 | 2737/24460
GO:0004175 (2.06e-12)
endopeptidase activity
73/271 | 2567/24460
GO:0070001 (1.1e-15)
aspartic-type peptidase
activity
72/271 | 2120/24460
GO:0008270 (9.08e-07)
zinc ion binding
79/271 | 3877/24460
GO:0003964 (5.57e-14)
RNA-directed DNA
polymerase activity
79/271 | 2703/24460
GO:0004190 (1.1e-15)
aspartic-type endopeptidase
activity
72/271 | 2120/24460

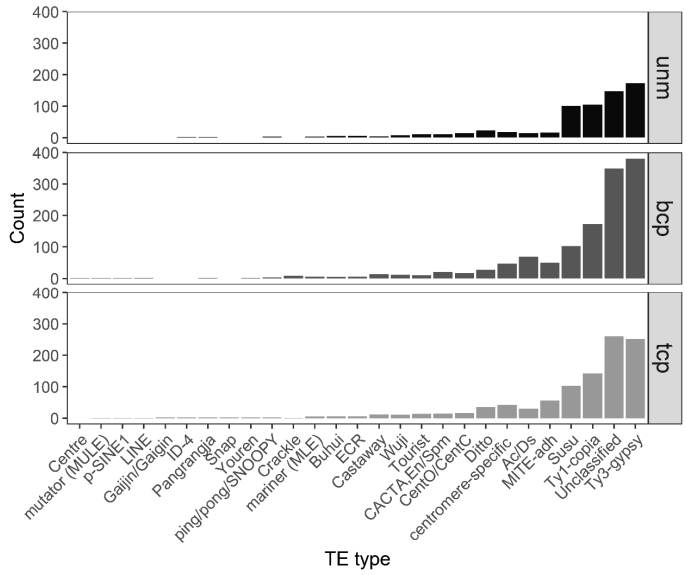
bcp molecular function




tcp molecular function
GO:0003674
molecular_function
GO:0005488 (0.0329)
binding
349/463 | 16899/24460
GO:0003824 (3.85e-06)
catalytic activity
311/463 | 13462/24460
GO:0003676 (0.00122)
nucleic acid binding
195/463 | 8081/24460
GO:0043167
ion binding
GO:0003682 (1.37e-10)
chromatin binding
52/463 | 877/24460
GO:0016740 (6.32e-10)
transferase activity
181/463 | 6033/24460
GO:0016787 (1.58e-08)
hydrolase activity
177/463 | 6088/24460
GO:0003677 (2.42e-07)
DNA binding
153/463 | 5202/24460
GO:0003723 (9.11e-15)
RNA binding
124/463 | 3007/24460
GO:0043169
cation binding
GO:0016772 (3.41e-11)
transferase activity,
transferring phosphorus-containing groups
155/463 | 4672/24460
GO:0008233 (0.00175)
peptidase activity
90/463 | 3151/24460
GO:0016788 (0.00185)
hydrolase activity,
acting on ester bonds
60/463 | 1871/24460
GO:0046872
metal ion binding
GO:0016779 (8.19e-16)
nucleotidyltransferase activity
123/463 | 2865/24460
GO:0070011 (0.00158)
peptidase activity,
acting on L-amino acid peptides
90/463 | 3136/24460
GO:0042578 (0.00318)
phosphoric ester
hydrolase activity
15/463 | 245/24460
GO:0004518 (0.00679)
nuclease activity
42/463 | 1252/24460
GO:0046914 (0.034)
transition metal
ion binding
120/463 | 4946/24460
GO:0034061 (2.78e-16)
DNA polymerase
activity
121/463 | 2737/24460
GO:0004175 (0.000182)
endopeptidase activity
81/463 | 2567/24460
GO:0070001 (3.85e-06)
aspartic-type peptidase
activity
76/463 | 2120/24460
GO:0016791 (0.00538)
phosphatase activity
13/463 | 202/24460
GO:0004540 (0.00573)
ribonuclease activity
40/463 | 1152/24460
GO:0004519 (0.0112)
endonuclease activity
39/463 | 1168/24460
GO:0008270 (0.00265)
zinc ion binding
105/463 | 3877/24460
GO:0003964 (2.13e-16)
RNA-directed DNA
polymerase activity
121/463 | 2703/24460
GO:0004190 (3.85e-06)
aspartic-type endopeptidase
activity
76/463 | 2120/24460
GO:0003993 (0.00679)
acid phosphatase
activity
6/463 | 45/24460
GO:0004521 (0.00679)
endoribonuclease activity
39/463 | 1133/24460
GO:0016893 (0.00679)
endonuclease activity,
active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters
39/463 | 1128/24460
GO:0016891 (0.00642)
endoribonuclease activity,
producing 5'-phosphomonoesters
39/463 | 1122/24460
GO:0004523 (0.00543)
ribonuclease H
activity
39/463 | 1107/24460

附图 5　tRF GO 分析

Appendix figure 5　tRF_target_GO analysis



附图 6 水稻雄配子三类花粉的 tRF 靶向的 TE 类型

横轴是各种 TE 的类型(家族), 包括了转座子和反转录转座子。unm、bcp 和 tcp 见图 1。

Appendix figure 6 tRFs targeted TE types

The X axis sticks shows different TE types (families) involved. unm, bcp and tcp see Figure 1.