iTP-Seq Report

tcx

2025-04-16

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iTP-Seq: A scalable profiling method to study context-dependent translation events in vitro.
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Motif: -2:A

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Motif: E:A

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Motif: E:P

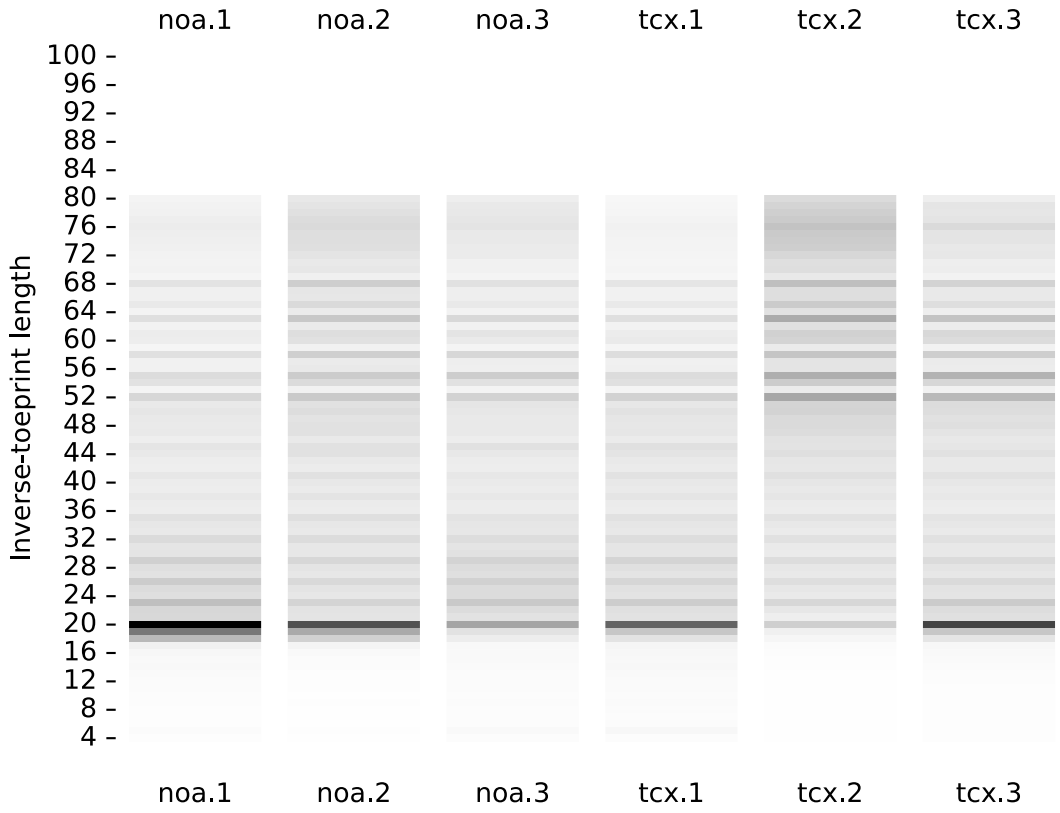
tcx vs noa 11

iTP-seq dataset

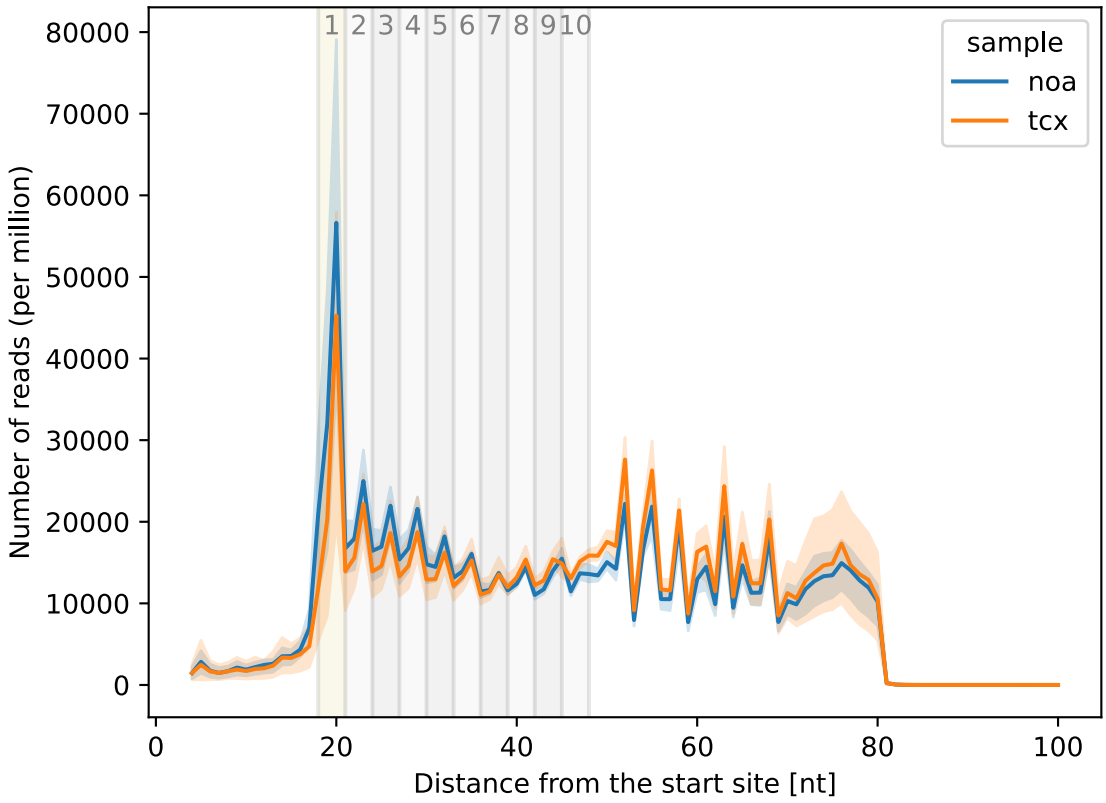
Statistics of the iTP reads

	total_sequences	noadaptor	contaminant	lowqual	tooshort	toolong	extra0	extra1	extra2	MAX_LEN
noa.1	9 036 255	799 955	1 219	700 374	299 502	3 376 581	2 434 092	2 709 762	3 092 446	44
noa.2	8 154 560	407 750	1 318	680 813	154 587	4 158 921	2 329 190	2 582 052	2 835 568	44
noa.3	7 725 561	623 037	1 065	353 401	279 104	3 505 909	2 216 460	2 402 957	2 483 107	44
tcx.1	8 384 889	714 414	1 192	685 017	385 537	3 341 987	2 308 291	2 528 638	2 833 546	44
tcx.2	9 120 203	498 202	1 659	513 308	104 071	5 664 107	2 673 062	2 972 850	2 976 089	44
tcx.3	8 490 958	1 043 590	1 328	409 697	187 746	4 004 073	2 243 720	2 555 783	2 647 865	44

Virtual inverse toeprint gel

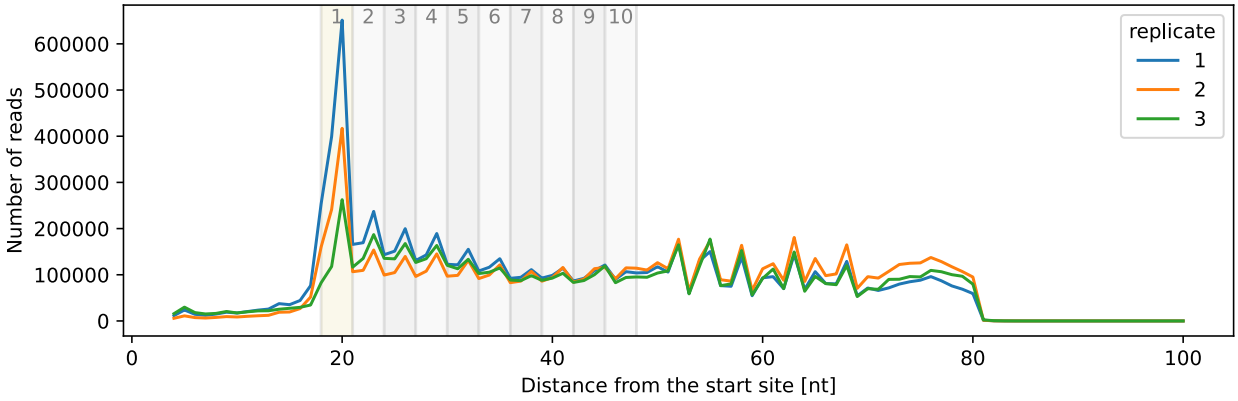


Distribution of iTP lengths

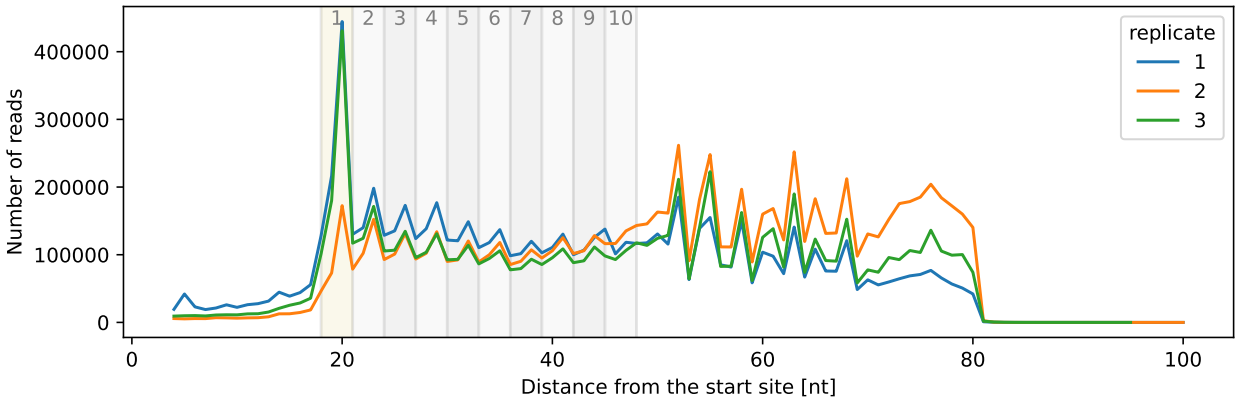


Distribution of iTP lengths per sample

noa

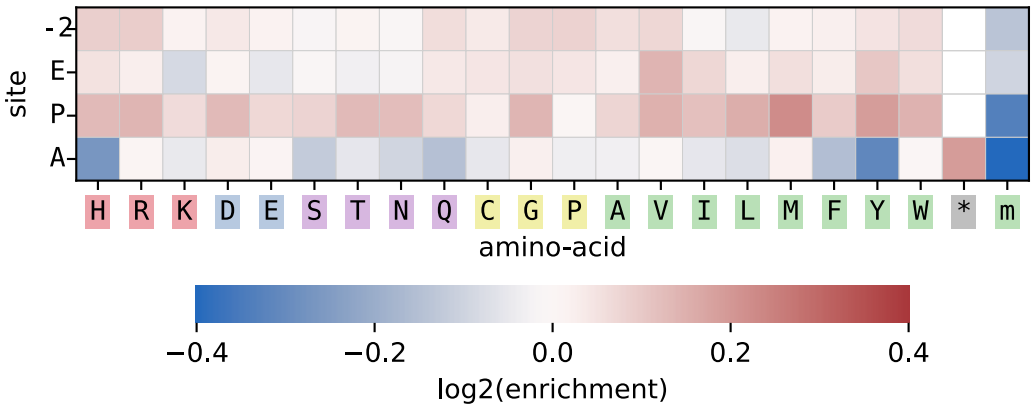


tcx


1 2 3 4 5 6 7 8 9 10
replicate
1
2
3
Number of reads
400000
300000
200000
100000
0
0
20
40
60
80
100
Distance from the start site [nt]

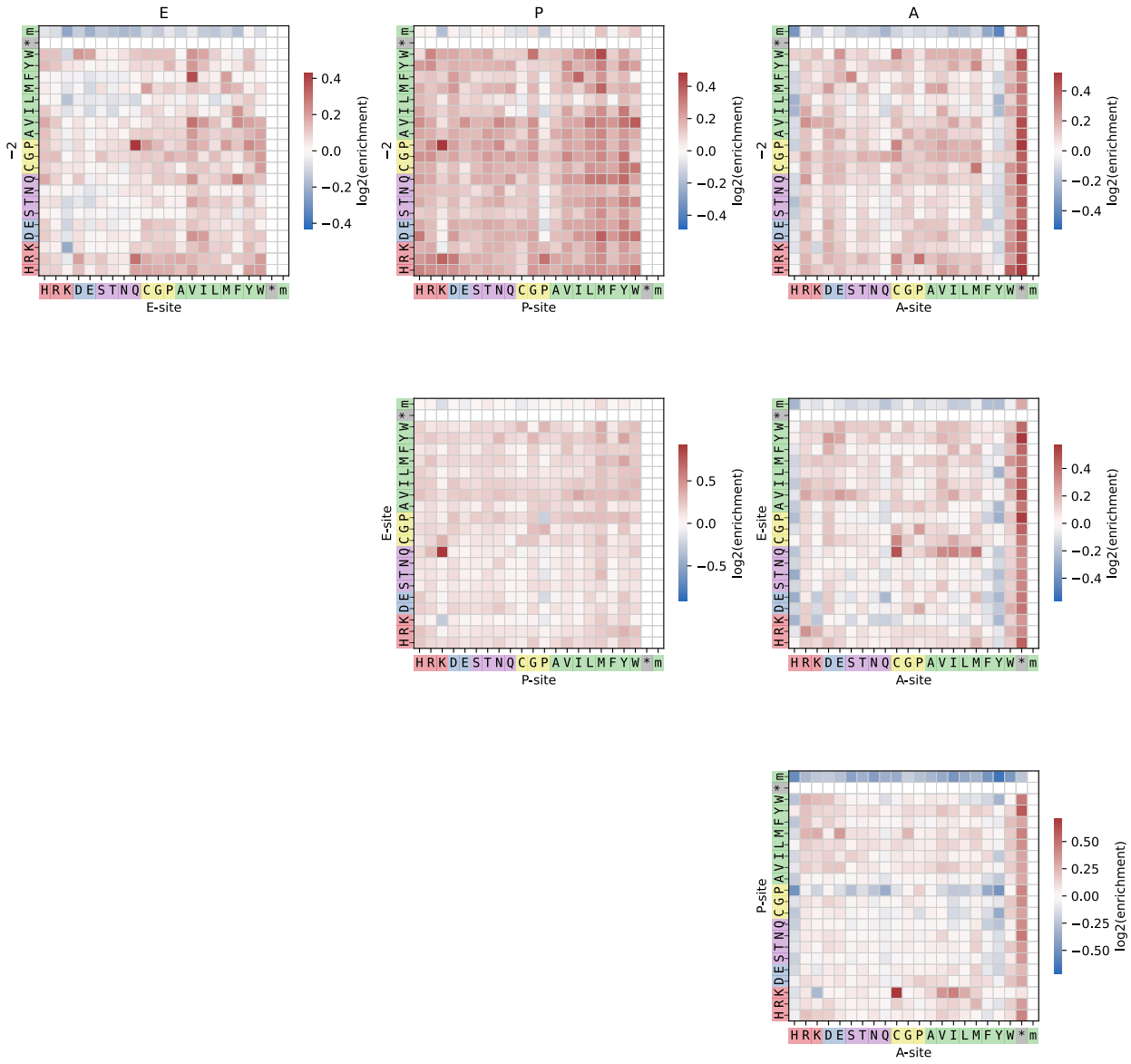
Amino-acid enrichment per position

tcx vs noa



Amino-acid enrichment per combination of positions

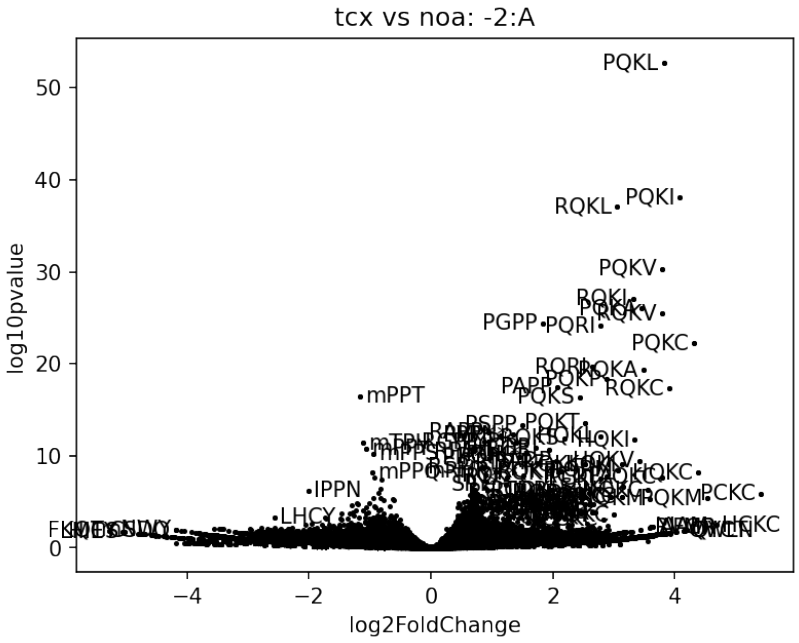
tcx vs noa



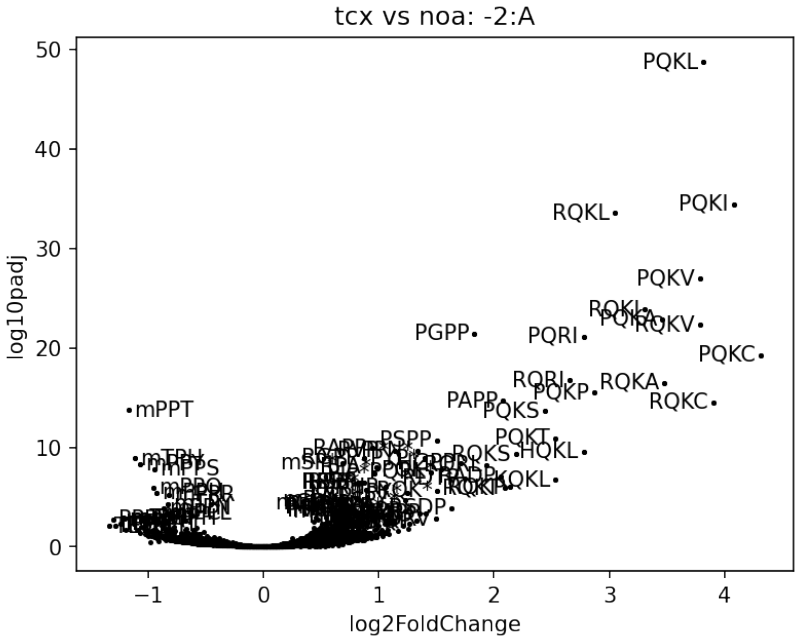
Motif: -2:A

tcx vs noa

p-value



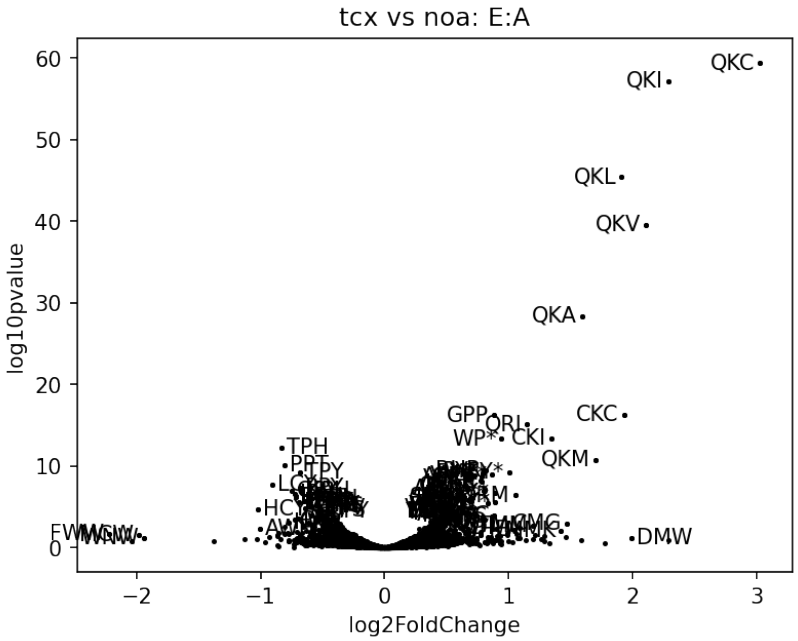
adjusted p-value



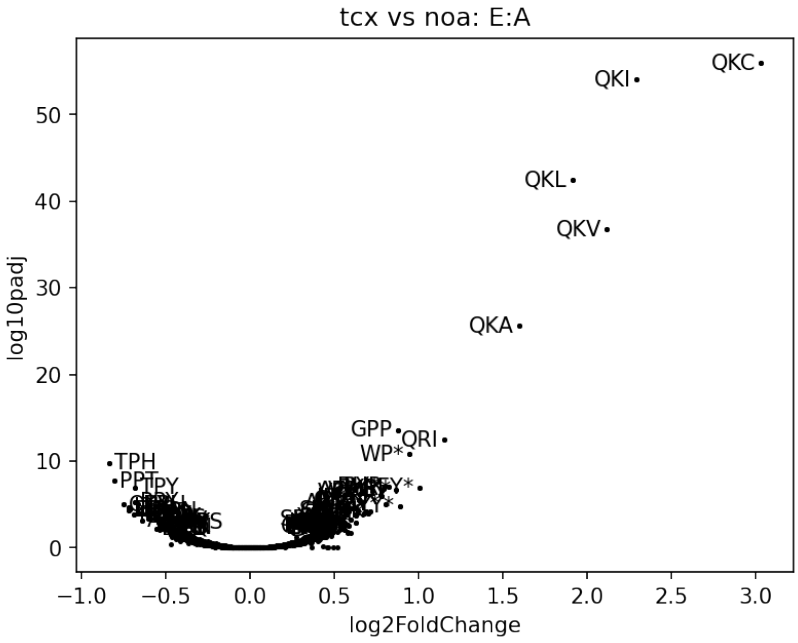
Motif: E:A

tcx vs noa

p-value



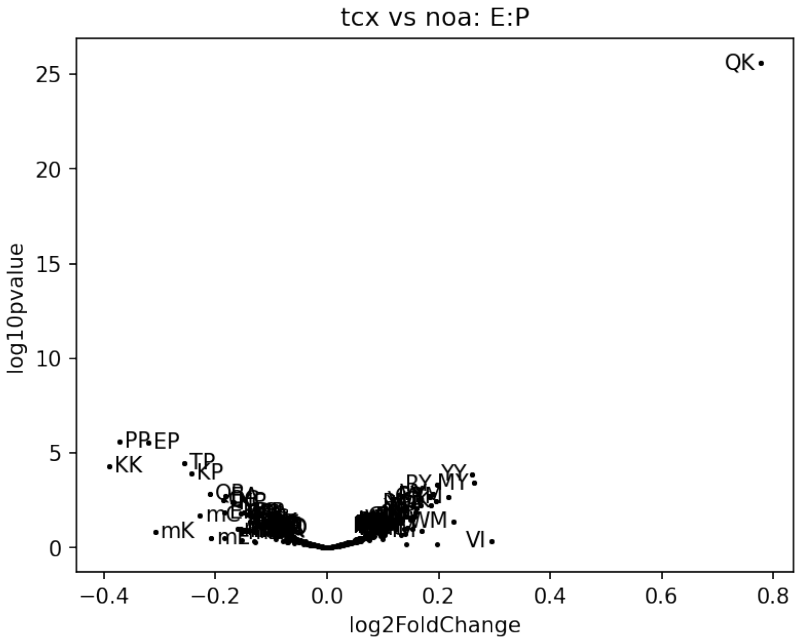
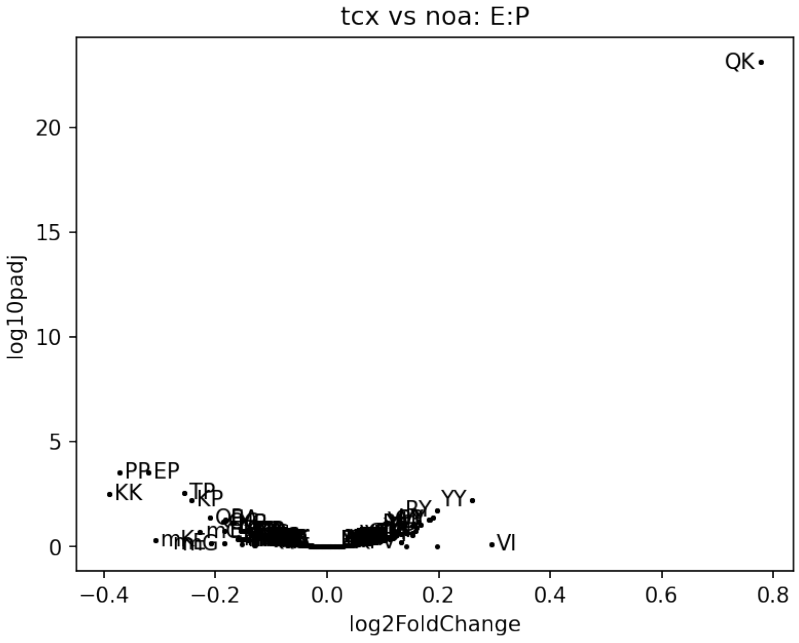
adjusted p-value



Motif: E:P

tcx vs noa

p-value



adjusted p-value