

a)

```
s_ser_tRNA_modomics.fasta - Editor
Datei Bearbeiten Format Ansicht ?
>1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic
GGGCGTGTGGCGTAGTCGGTAGCGGCTCCCTTAGCATGGAGAGGTCCTCGGTTCCGACTCGTCCACCA
>2tRNA|Ala|TGC|Saccharomycescerevisiae|cytosolic
GGGCACATGGCGCAGTTGGTA...
```

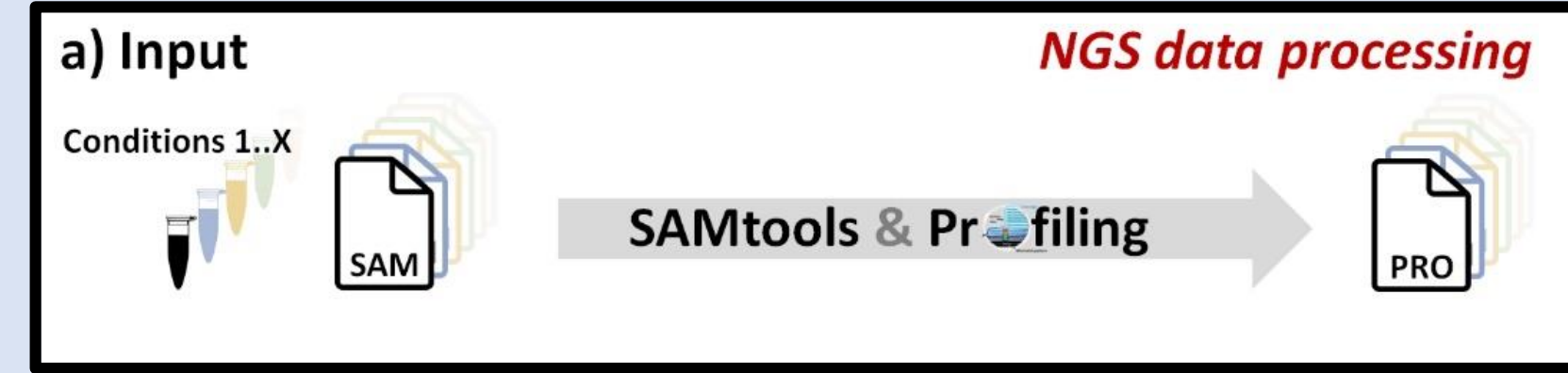
**.fasta & .sam files**

```
53 @SQ SN:52tRNA|Arg|ACG|LN:74
54 @SQ SN:53tRNA|Arg|NCT|Saccharomycescerevisiae|mitochondrial LN:76
55 @SQ SN:54tRNA|Ser|TGA|Saccharomycescerevisiae|mitochondrial LN:90
56 @SQ SN:55tRNA|Ser|TGA|Saccharomycescerevisiae|mitochondrial LN:90
57 @SQ SN:56tRNA|Thr|TAG|Saccharomycescerevisiae|mitochondrial LN:73
58 @SQ SN:57tRNA|Trp|!CA|Saccharomycescerevisiae|mitochondrial LN:74
59 @PG ID:bowtie2 PN:bowtie2 VN:2.2.5 CL:"/home/helm-bioinform/Desktop/programs/bowtie2-2.
60 @PG ID:bowtie2-4958F428 PN:bowtie2 VN:2.2.5 CL:"/home/helm-bioinform/Desktop/programs/bc
61 M01332:19:000000000-AG19L:1:1101:1382:1767 0
62 M01332:19:000000000-AG19L:1:1101:11957:1761 0
63 M01332:19:000000000-AG19L:1:1101:11084:1765 0
64 M01332:19:000000000-AG19L:1:1101:11090:1711 0
```

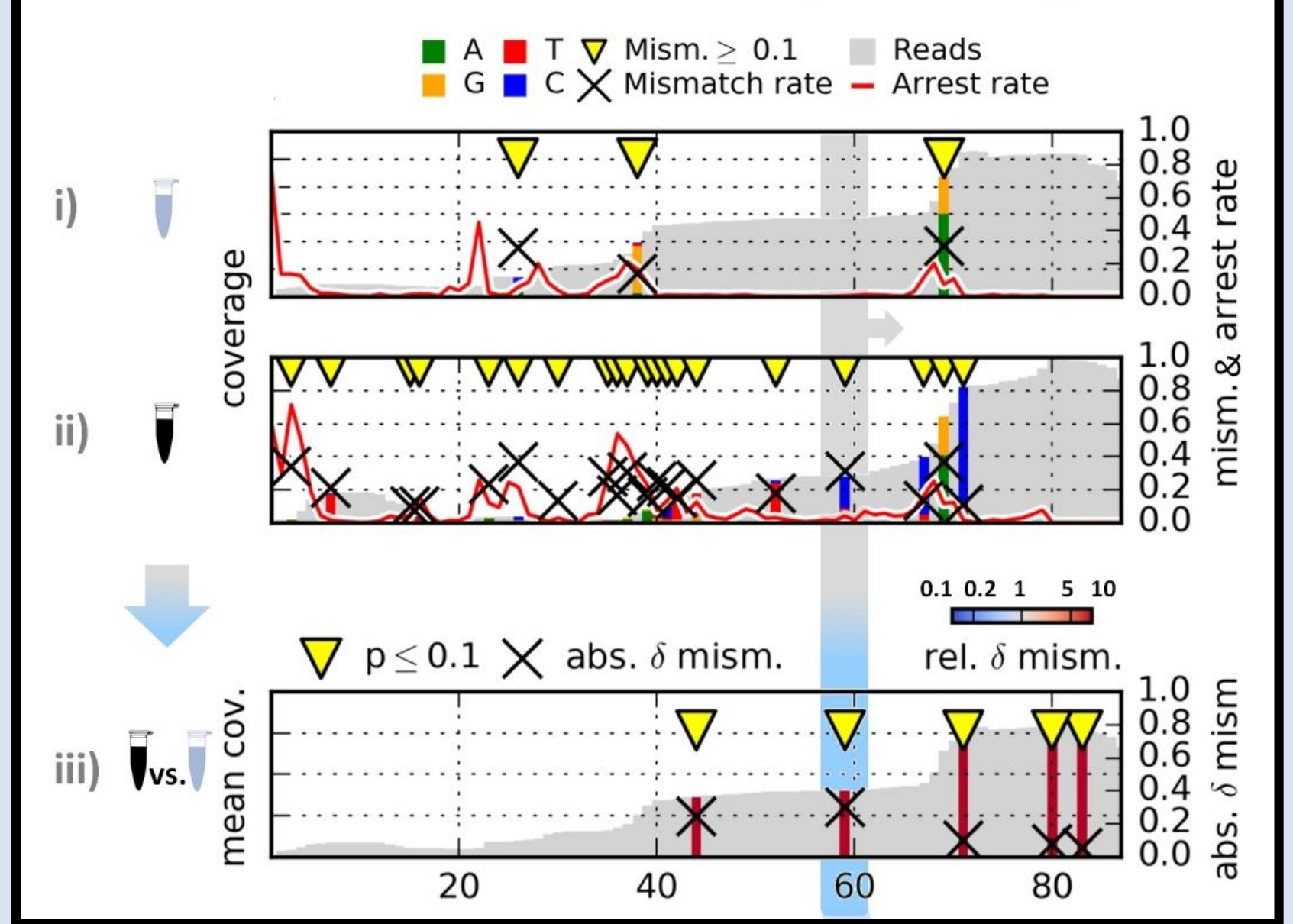
Normal text file length: 18994909 Ln: 57 Col: 66 Sel: UNIX UTF-8 w/o

```
C:\Users\Howie_MC\Documents\Promotion\V001\Windows64bit\16\seqanest\1\11.sam.sorted.bam.pileup.profile - Notepad++
11.sam.sorted.bam.pileup.profile
position refbase coverage mm_ratio a_mism g_mism t_mism c_mism arrest_rate
1 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 1 G 19 0.05263157894736842 0 18 0 0 0 0 0 1 0 0.486496
2 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 2 G 37 0.02702702702702703 0 36 0 0 0 0 0 1 0 0.026315
3 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 3 C 38 0.02631578947368421 0 37 0 0 0 0 0 1 0 0.073170
4 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 4 G 37 0.02702702702702703 0 36 0 0 0 0 0 1 0 0.026315
5 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 5 G 37 0.02702702702702703 0 36 0 0 0 0 0 1 0 0.026315
6 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 6 G 37 0.02702702702702703 0 36 0 0 0 0 0 1 0 0.026315
7 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 7 G 37 0.02702702702702703 0 36 0 0 0 0 0 1 0 0.026315
8 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 8 G 37 0.02702702702702703 0 36 0 0 0 0 0 1 0 0.026315
9 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 9 G 186 0.026881720430107527 0 181 4 1 0 0 0 0 0 0 0.26
10 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 10 G 252 0.01587301587301587 0 248 2 1 0 1 0 0 0 0.14
11 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 11 C 296 0.013513513513513514 0 0 2 292 0 1 1 0 0 0 0.06
12 1tRNA|Ala|AGC|Saccharomycescerevisiae|cytosolic 12 G 315 0.009523809523809525 1 312 0 1 0 0 0 1 0 0.00
```

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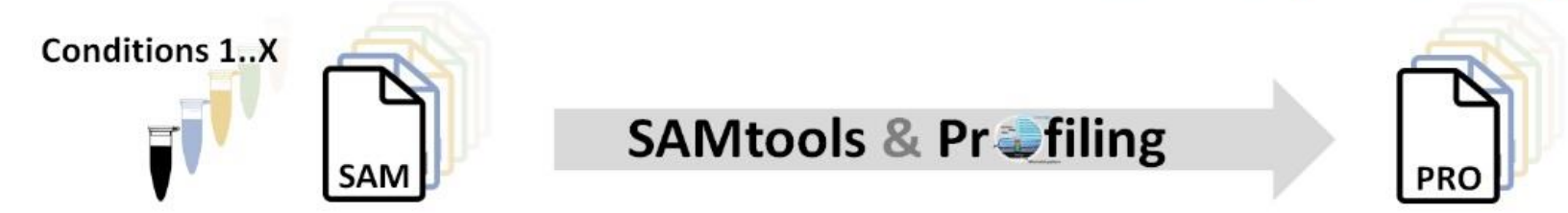


c) Visual inspection



### CoverageAnalyzer: workflow overview

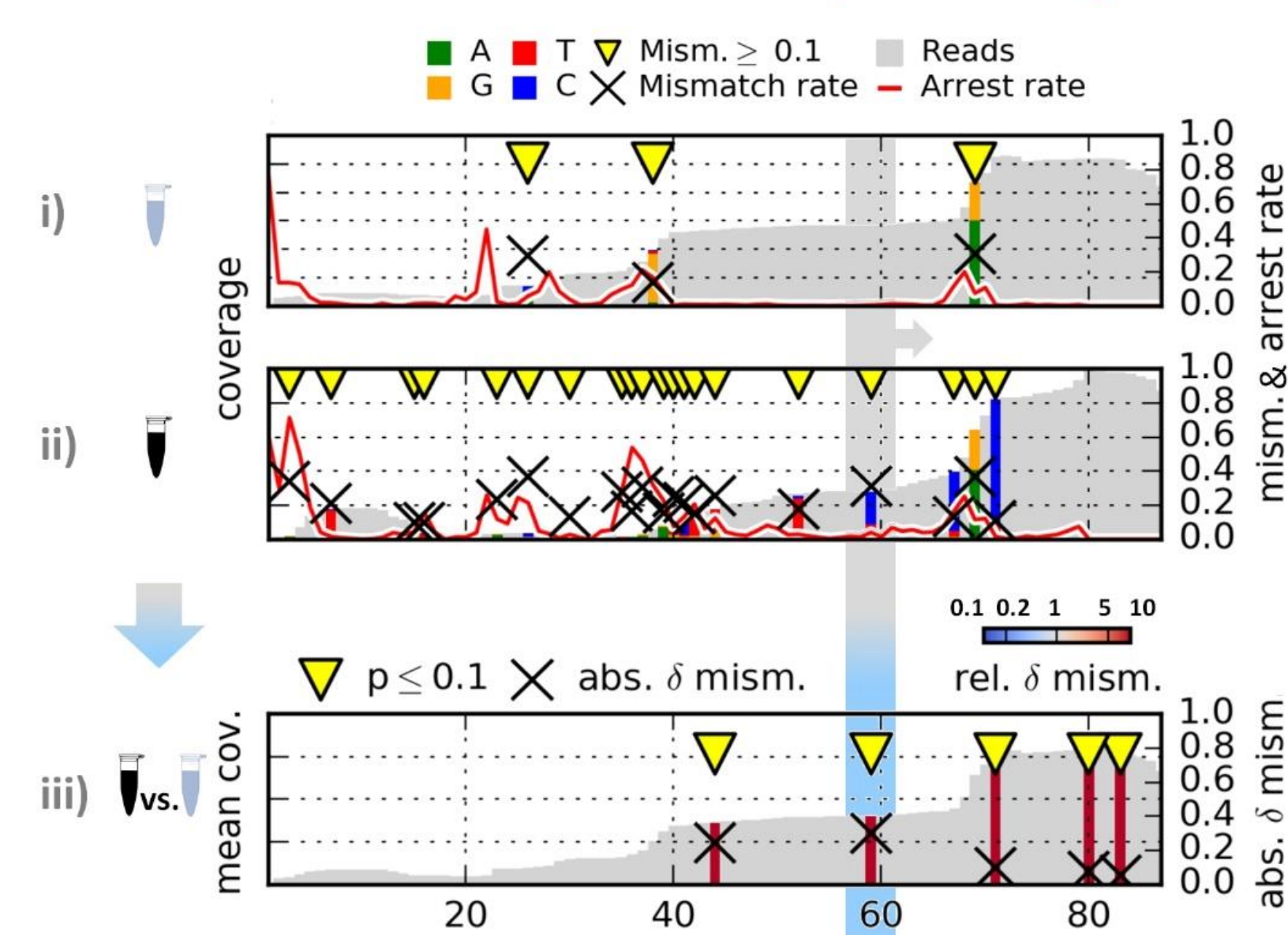
a) Input **NGS data processing**



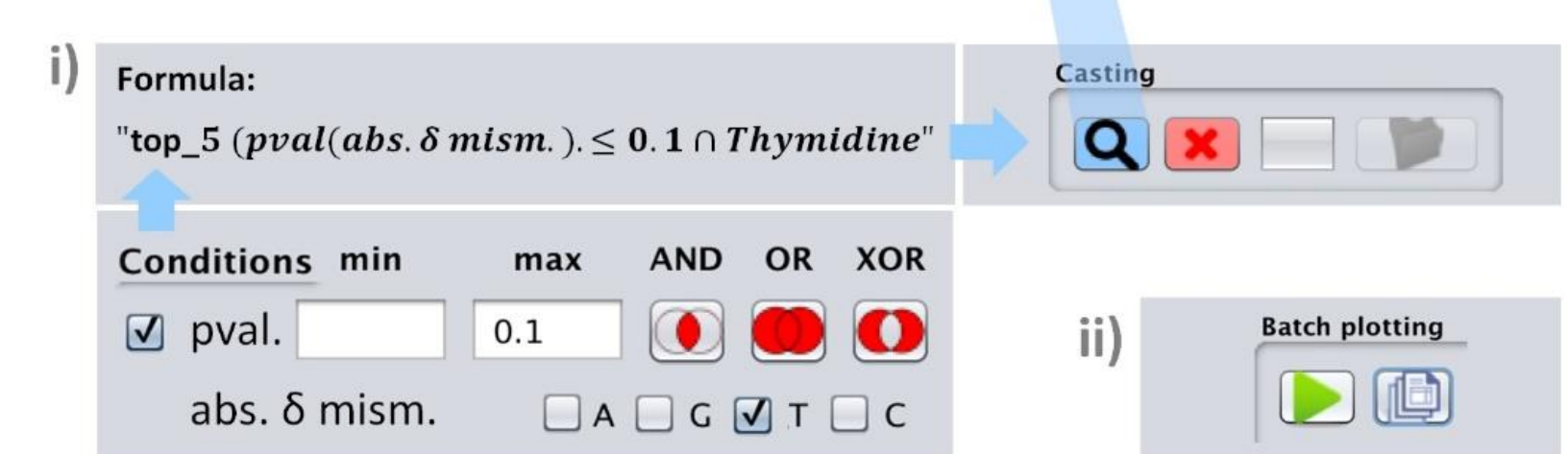
b) Selection **statistics & filtering**



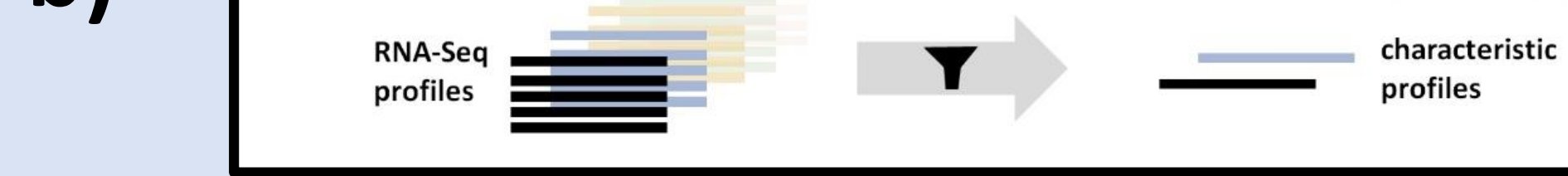
c) Visual inspection **independent & differential**



d) Candidate screening **formulas & batch plotting**

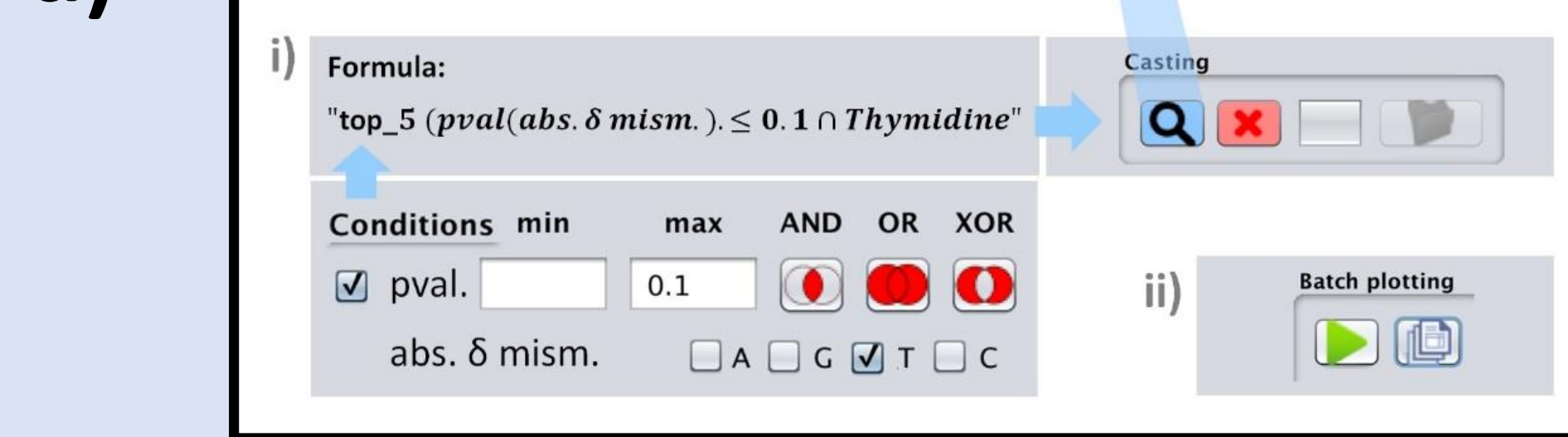


b) Selection **statistics & filtering**



Reference segment	Profile pa.	Ref.	Referenc.	Maximum	# Arrests	# Mismatch sit.	Hetero-mism.	# Mapped reads	Sample ID
19RNHajGTGSaccharomycescerevisiae cyt	CR-HBio	76	GGCCAT	6313	24	16	0	6605	1
19RNHajGTGSaccharomycescerevisiae cyt	CR-HBio	76	GGCCAT	9115	24	19	0	9482	2
19RNHajGTGSaccharomycescerevisiae cyt	CR-HBio	76	GGCCAT	9210	16	8	0	8827	1
19RNHajAATISaccharomycescerevisiae cyt	CR-HBio	77	GCTCTC	11207	30	23	3	11572	2
19RNHajAATISaccharomycescerevisiae cyt	CR-HBio	77	GCTCTC	14771	34	23	1	15244	2
19RNHajAATISaccharomycescerevisiae cyt	CR-HBio	77	GCTCTC	14912	20	17	1	14654	1
17RNHajIATISaccharomycescerevisiae cyt	CR-HBio	76	GCTCGT	2539	10	10	1	2709	3
17RNHajIATISaccharomycescerevisiae cyt	CR-HBio	76	GCTCGT	4268	10	11	2	4467	2
17RNHajIATISaccharomycescerevisiae cyt	CR-HBio	76	GCTCGT	4429	8	7	2	4365	1
18RNHajIuTAGISaccharomycescerevisiae cyt	CR-HBio	85	GGAGAT	1520	13	8	0	1785	3
18RNHajIuTAGISaccharomycescerevisiae cyt	CR-HBio	85	GGAGAT	3295	14	8	0	3587	2
18RNHajIuTAGISaccharomycescerevisiae cyt	CR-HBio	85	GGAGAT	5374	15	4	1	5679	1
19RNHajIuCAASaccharomycescerevisiae cyt	CR-HBio	86	GGTTGT	12958	34	28	1	13506	3
19RNHajIuCAASaccharomycescerevisiae cyt	CR-HBio	86	GGTTGT	20963	42	33	0	21267	3
19RNHajIuCAASaccharomycescerevisiae cyt	CR-HBio	86	GGTTGT	23248	18	11	1	25642	1
19RNHajIuCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGCGT	10392	28	24	1	10763	3
19RNHajIuCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGCGT	13358	30	22	1	13831	3
19RNHajIuCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGCGT	10957	17	11	1	10454	1
20RNHajIuTAASaccharomycescerevisiae cyt	CR-HBio	87	GGAGGG	2193	21	15	0	3205	3
20RNHajIuTAASaccharomycescerevisiae cyt	CR-HBio	87	GGAGGG	5531	19	22	0	6420	2
20RNHajIuTAASaccharomycescerevisiae cyt	CR-HBio	87	GGAGGG	10619	21	9	0	11604	3
21RNHajIuCTISaccharomycescerevisiae cyt	CR-HBio	76	GCCTTG	4620	27	12	1	5129	3
21RNHajIuCTISaccharomycescerevisiae cyt	CR-HBio	76	GCCTTG	8727	31	16	0	9301	2
21RNHajIuCTISaccharomycescerevisiae cyt	CR-HBio	76	GCCTTG	21153	15	5	1	21782	1
22RNHajIuSTISaccharomycescerevisiae cyt	CR-HBio	76	TCCTTG	4043	20	14	1	4307	3
22RNHajIuSTISaccharomycescerevisiae cyt	CR-HBio	76	TCCTTG	6959	25	16	1	8373	3
22RNHajIuSTISaccharomycescerevisiae cyt	CR-HBio	76	TCCTTG	7897	15	7	1	8018	1
22RNHajIuSTISaccharomycescerevisiae cyt	CR-HBio	76	TCCTTG	3168	15	11	0	3377	3
23RNHajIuCATISaccharomycescerevisiae cyt	CR-HBio	76	GCCTCA	5324	12	8	0	5562	2
23RNHajIuCATISaccharomycescerevisiae cyt	CR-HBio	76	GCCTCA	6227	10	7	0	6485	1
24RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	15587	19	9	1	19932	3
24RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	27100	19	9	1	27532	3
24RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	28446	14	8	1	28786	1
25RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	4455	13	9	1	4703	3
25RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	6983	9	9	1	7150	3
25RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	7036	10	6	1	7315	1
26RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	10468	17	27	1	11034	3
26RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	18506	17	31	1	19130	2
26RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	76	GGGAT	44691	13	22	1	42367	1
27RNHajIuPheCAASaccharomycescerevisiae cyt	CR-HBio	86	GGCCAT	1930	10	4	0	1917	1

d) Candidate screening **formulas & batch plotting**



**.candidates files**

ref	pos	cov_1	cov_3	tpcov_1	tpcov_3	arr_1	arr_3	d_abs_arr	d_rel_arr	pv_arr	mism_1
1	tRNA Ala AGC Saccharo							95.0		0.02777777777	
2	1tRNA Ala AGC Saccharo							110.0		0.0737913486	
3	1tRNA Ala AGC Saccharo							2996.0		0.0780368559	
4	1tRNA Ala AGC Saccharo							7825.0		0.01111111111	
5	1tRNA Ala AGC Saccharo							0.0307529162			
6	2tRNA Ala TGC Saccharomycescerevisiae cytosolic	21	914.0	76.0	943.0	99.0	0.0077232502				
7	2tRNA Ala TGC Saccharomycescerevisiae cytosolic	38	6169.0	815.0	6215.0	843.0	0.0026219956				
8	2tRNA Ala TGC Saccharomycescerevisiae cytosolic	58	6848.0	1481.0	6865.0	1542.0	0.0026219956				
9	3tRNA Arg TCT Saccharomycescerevisiae cytosolic	36	3828.0	250.0	5033.0	255.0	0.2400158950				
10	3tRNA Arg TCT Saccharomycescerevisiae cytosolic	43	6545.0	394.0	6739.0	387.0	0.0289360439				
11	3tRNA Arg TCT Saccharomycescerevisiae cytosolic	45	6851.0	432.0	6988.0	486.0	0.0201774470				
12	3tRNA Arg TCT Saccharomycescerevisiae cytosolic	48	7432.0	778.0	7555.0	816.0	0.0162860688				
13	3tRNA Arg TCT Saccharomycescerevisiae cytosolic	63	8459.0	1525.0	8428.0	1956.0	0.0043901281				

**.png pictures**

\$ Python CoverageAnalyzer2Modomics.py for .fasta annotation in Modomics format