

CONTENTS

1	Preparing Data	2
1.1	tRNA gene annotation	2
1.1.1	tRNA gene prediction	2
1.1.2	Initiator tRNA prediction	2
1.2	Summary of predicted TryTryp tRNA genes	3
2	TryTryp Classification	5

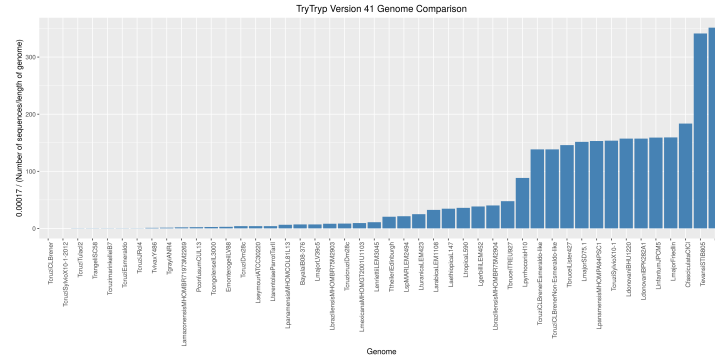


Figure 1: Comparing genomes based on formula $\left(\frac{f(x)}{\max(f(x))}\right)^{-1}$. $f(x)$ = Number of sequences in genome divided by the length of genome. The length of the bars shows how good the genomes are sequenced.

PREPARING DATA

TryTryp genome data. From tritrypdb website, we downloaded the version 41 of 46 TryTryp genomes released on 2018-12-05. Genomes are compared based on number of sequence fragments relative to their length as shown in figure 1. All the results, scripts for TryTryp version 41 can be found [here](#).

tRNA gene annotation

tRNA gene prediction

In order to annotate tRNA genes for the sequenced TryTryp genomes, we used two computational methods for tRNA prediction, tRNAscan-SE and Aragorn. We integrated the result of both genefinders by keeping the union of tRNA gene predictions generated by tRNAscan-SE v2.0 using default options (Lowe and Eddy 1997) and Aragorn v1.2.38 using options -i116 -t -br -seq -w -e -l -d (Laslett and Canback 2004). Genes with overlapped coordinate were considered as one gene. However, the identity and exact coordinate of both genefinders we saved separately to be analysed later.

Initiator tRNA prediction

We predicted the initiator tRNAs for the genes with anticodon 'CAT' from intersection of both tRNAscan (TSE) and Aragorn (ARA) Based on Conserved positions of initiators in Eukarya from the study by CHRISTIAN MARCK and HENRI GROSJEAN. Based on this study we have the following criteria for initiators:

1. In all eukaryotic tDNA-iMet, positions 11–24 are occupied by C-G, However, eukaryotic elongators also prefer C-G at these positions.
2. Initiator tDNAs from Eukarya use A54 and A60. Some eukaryotic elongators also use either A54 or A60 but none (with only one exception) uses both
3. Initiator tDNA-iMet (CAT) from all domains display the GGG sequence (Mandal et al+, 1996) or, very seldom, the AGG sequence at positions 29 to 31, pairing with the complementary CCC or CCT sequences at positions 39 to 41

4. Another domain-specific feature in all eukaryotic initiators is the systematic nonoccupancy of all optional positions of the D-loop (17, 17a, 20a, and 20b) whereas in elongators, only position 17a is always unoccupied.
5. At position 20, A is strictly conserved in all eukaryotic initiators

To investigate all these features we clustered CAT tRNA genes using Levenshtein (edit) distance between gene sequences and Ward.D2 method to measure the dissimilarity between each two clusters. We ended up with three clusters. Table 1 investigates each of these features in each column. from this table we see that only tRNA genes in cluster 1 have almost all the conserved features for eukaryotic initiators. So, we marked these genes as initiators represented with letter X in our gene file.

Table 1: Table of CAT clusters to show how many tRNA genes in each cluster satisfy each feature

Clusters	# tRNAs	11-24(C-G)	54-60(A-A)(T-T)	1-72(A-T)	29-31(GGG)	39-41(CCC/CCT)	# posisInDloop	20A	distanceRange
Cluster1	76	76	76	76	76	76	7	75	0-6
Cluster2	95	95	2	0	95	95	8	0	0-8
Cluster3	2	2	2	0	0	0	8/9	0	0-22

Summary of predicted TryTryp tRNA genes

To investigate and compare tRNA genes predicted by two gene finders TSE and ARA, we made four sets of genes. Set one, TSE and ARA intersection, Set two, TSE and ARA union, Set three, genes found by ARA and Set four, genes found by TSE . for intersection set, we dismissed genes which had different identity by ARA and TSE. for union set, we picked TSE identity over ARA. Table 2 shows a summary of these four sets. Further, to compare the coordinates of genes annotated by ARA and TSE we made a heatmap shown in figure 2. We see from this figure that the coordinates of same genes annotated by ARA and TSE do not always match. We Analysed the reason for each set of displacement in this figure as follow:

1. Genes with 0 displacement in both ends: These genes have same identity for both TSE and ARA except for 33 genes with Anticodon loop of more than 8bp. Also, both ARA and TSE reported genes up to base 73.
2. Genes with 0 displacement at 5 prime end and 1 displacement at 3 prime end: Identity of these genes matches between ARA and TSE. They all have anticodon loop of length 7. The reason for the displacement in 3 prime end is that ARA reports up to position 74, however, TSE reports only up to position 73.
3. Genes with one base displacement at both ends: In this case ARA reports one extra base at both ends which is because these two bases pair together and in most cases this makes the Amino Acid arm one base longer than what TSE reports. Although in a few cases, the AminoAcid arm will stay 7bp, but we see insertions in this arm.
4. Genes with two base displacement at 3 prime end and one at 5 prime end: In this case ARA is reporting 2 extra bases at one end and 1 for the other end which usually leads to a longer AminoAcid arm. Also, the extra 2 bases reported by ARA at 3 prime end are mostly 'ac'.
5. Genes with two base displacement at 3 prime end and 0 displacement at 5 prime end: In this case TSE reports up to position 73 as always,

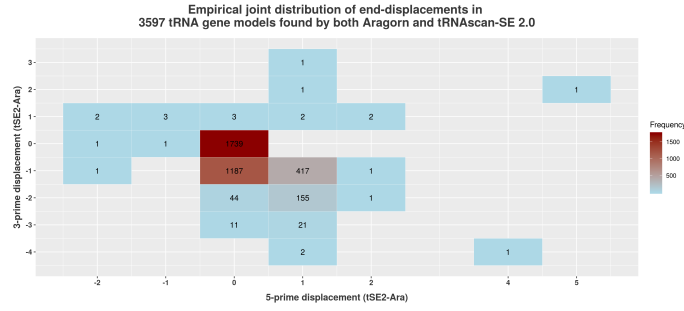


Figure 2: Empirical joint distribution of end-displacements in ? tRNA gene models found by both Aragorn and tRNAscan-SE 2.0.

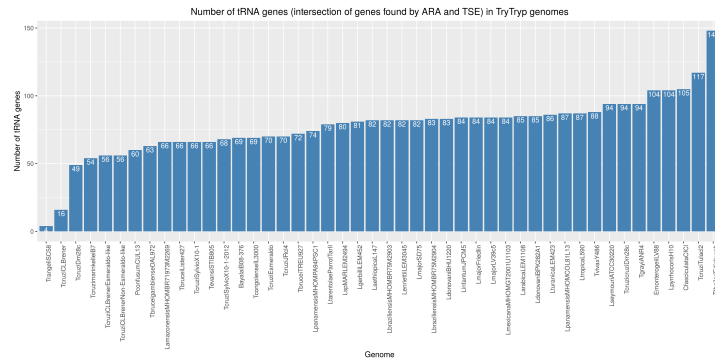


Figure 3: Number of genes annotated by both TSE and ARA for each TryTrypt genome.

but ARA is reporting genes up to position 75. the last three bases of ARA are mainly 'acc'

- Genes with three base displacement at 3 prime end and 0 displacement at 5 prime end. In this case ARA is reporting 3 extra bases at 3 prime end and these three bases are 'cc'.

We expect our genefinders to annotate tRNA genes of all 22 functional classes for each genome. To investigate this we visualized the number of genes annotated for each genome in Figure 3 and tRNA functional classes annotated by both TSE and ARA for each genome in Figure 4.

Table 2: summary of the predicted genes by TSE and ARA. We marked pseudo genes as \$, initiators as X, stop as #, sup as "?", sec as Z and pyl as O

Geneset	# RNA	# nucleotides	N/T	gene length	%A	%C	%G	%U	%Initiator	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	X	Z	#	O	
TSE	3914	270155	74.46	50-164	31.99	28.11	22.22	18.68	2.69	214	64	105	163	110	234	80	179	130	338	108	126	201	162	350	238	210	241	52	94	76	78	28	3	0
ARA	4347	379539	85.70	70-215	32.44	26.90	22.87	17.57	14.67	257	86	124	193	125	339	129	213	194	393	101	153	228	175	420	362	248	282	60	90	76	82	0	2	4
UNION	4381	377734	86.22	50-215	32.81	26.66	22.87	17.65	15.33	259	86	119	194	130	344	129	220	197	380	112	143	229	175	421	359	249	282	57	108	76	82	28	3	2
INTERSECTION	3986	285180	79.44	68-89	32.21	28.13	22.22	18.64	2.33	211	64	105	165	109	239	80	172	137	338	97	125	200	168	349	239	238	241	52	78	76	6	0	0	

from figure 3 we see that few of the 22 tRNA classes are not annotated for all the genomes. To improve the annotation we included 33 genes annotated by both gene finders, with mismatched identities. you can see a summary of these genes in table 3. To determind the identity of these genes we built a structural alignment of all the TryTrypt tRNA genes from our intersection set and 33 genes (We picked TSE reported sequences over ARA for alignment, because TSE reports genes up to position 73, however ARA can report a few bases after 73 as we see in figure 2. We used removed introns and other nucleotides in non-conserved positions, and variable arms prior to the alignment. We used covea v2.4.2 (Sean Eddy 1994) for the structural alignment and edited the alignment by removing sites with more than 99%

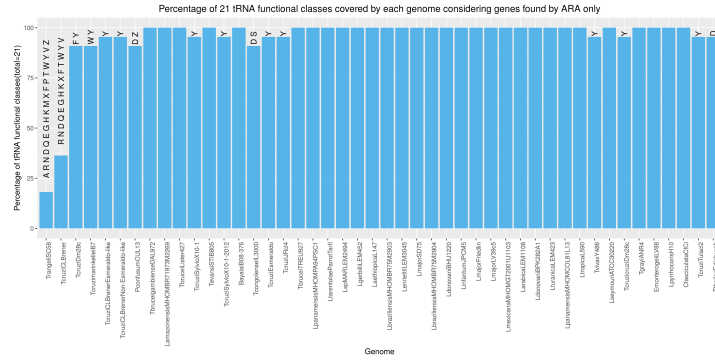


Figure 4: Percentage of 22 tRNA types annotated by both TSE and ARA for each TryTryp genomes. The label on top of each bar shows which tRNA classes are not annotated for the genome.

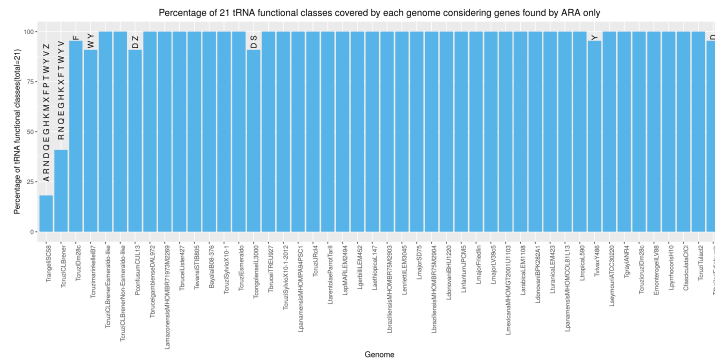


Figure 5: Percentage of 22 tRNA types annotated by both TSE and ARA for each TryTryp genomes after including 32 genes to intersection set. The label on top of each bar shows which tRNA classes are not annotated for the genome.

gap, genes with more than 8 gaps in their aligned sequence, and genes with letter N in their sequence.). Later, using only the intersection aligned genes we made a profile covariance model for 22 functional classes. We calculated the score of 33 genes for each of these 22 models. For each gene, we compared the score of two models made for the identities reported by TSE and ARA and picked the one with higher score. you can see the result in this [file](#). We were able to include 32 of these genes to our intersection set which improved the annotation of genomes as you can see in figure 5

Table 3: 33 genes annotated by both TSE and ARA with mismatched identity

ARA TSE	D I	L ?	L E	L M	N Y	O M	S R	W G
Number of genes	5	3	1	9	11	2	1	3

TRYTRYP CLASSIFICATION

We visualized differences in tRNA identity determinants between TryTryp and Human, and across TryTryp genomes, using four different Logos:

- 1 Function Logos to estimate the potential identity determinants for each genome
- 2 Information Difference logos (ID logos), to show the evolutionary gain or loss of functional information between Human and TryTryp genomes

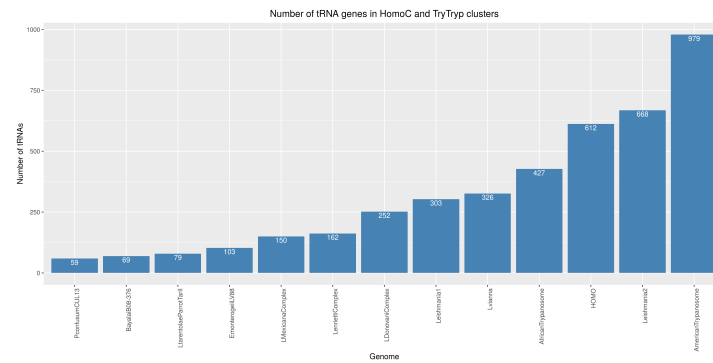


Figure 6: Number of genes annotated by both TSE and ARA for each TryTryp cluster.

- 3 KullbackLeibler divergence Difference logos (KLD logos) to show
changes in the functional associations of features between Human and
TryTryp genomes
4 Using Three Logos mentioned above, we made bubble plots to show
gains and shifts in functions of tRNAs in Trypanosoma contrasted
against human tRNAs.

Using phylogenetic trees of *Trypanosoma* in these works [11][12], we grouped TryTryp genomes as table 4. figure 6 shows a summary of the number of tRNA genes for each cluster and figure 7 shows the tRNA functional classes not annotated for clusters of genome. we excluded genome PconfusumCUL13 from the study, until we find a well sequenced version of this genome for which we can annotate all 22 functional classes of tRNAs. The Logo data for All TryTryp genomes and Human can be found here. In figure 8 you can see the bubble plots of each cluster in one page. in each page we have 22 models for each tRNA class.

Table 4: Classification of TryTryp genomes. genomes not mentioned here are clustered as one genome.

Leontide Complex	African Trypanosome	American Trypanosome	Leishmania 1	Leishmania 2	LDonovan Complex	LDemicus Complex	Lioma
		1. TrypanoINB4					
		2. TrypanoSC8					
		3. TrypanoCLBonne					
		4. TrypanoCLBonneFemeradillo					
	1. ThreosymbianL31472	5. TrypanoCLBonneFemeradillo			1. LeontideF1011		
	2. ThreosymbianL3147	6. TrypanoCLBonneFemeradillo			2. LeontideV395		
	3. ThreosymbianL3147	7. TrypanoCLBonneFemeradillo			3. LeontideV395		
	4. ThreosymbianL3147	8. TrypanoCLBonneFemeradillo			4. LeontideV395		
	5. ThreosymbianL3147	9. TrypanoCLBonneFemeradillo			5. LeontideV395		
	6. ThreosymbianL3147	10. TrypanoCLBonneFemeradillo			6. LeontideV395		
	7. ThreosymbianL3147	11. TrypanoCLBonneFemeradillo			7. LeontideV395		
	8. ThreosymbianL3147	12. TrypanoCLBonneFemeradillo			8. LeontideV395		
	9. ThreosymbianL3147	13. TrypanoCLBonneFemeradillo			9. LeontideV395		
	10. ThreosymbianL3147	14. TrypanoCLBonneFemeradillo			10. LeontideV395		
	11. ThreosymbianL3147	15. TrypanoCLBonneFemeradillo			11. LeontideV395		
	12. ThreosymbianL3147	16. TrypanoCLBonneFemeradillo			12. LeontideV395		
	13. ThreosymbianL3147	17. TrypanoCLBonneFemeradillo			13. LeontideV395		
	14. ThreosymbianL3147	18. TrypanoCLBonneFemeradillo			14. LeontideV395		
	15. ThreosymbianL3147	19. TrypanoCLBonneFemeradillo			15. LeontideV395		
	16. ThreosymbianL3147	20. TrypanoCLBonneFemeradillo			16. LeontideV395		
	17. ThreosymbianL3147	21. TrypanoCLBonneFemeradillo			17. LeontideV395		
	18. ThreosymbianL3147	22. TrypanoCLBonneFemeradillo			18. LeontideV395		
	19. ThreosymbianL3147	23. TrypanoCLBonneFemeradillo			19. LeontideV395		
	20. ThreosymbianL3147	24. TrypanoCLBonneFemeradillo			20. LeontideV395		
	21. ThreosymbianL3147	25. TrypanoCLBonneFemeradillo			21. LeontideV395		
	22. ThreosymbianL3147	26. TrypanoCLBonneFemeradillo			22. LeontideV395		
	23. ThreosymbianL3147	27. TrypanoCLBonneFemeradillo			23. LeontideV395		
	24. ThreosymbianL3147	28. TrypanoCLBonneFemeradillo			24. LeontideV395		
	25. ThreosymbianL3147	29. TrypanoCLBonneFemeradillo			25. LeontideV395		
	26. ThreosymbianL3147	30. TrypanoCLBonneFemeradillo			26. LeontideV395		
	27. ThreosymbianL3147	31. TrypanoCLBonneFemeradillo			27. LeontideV395		
	28. ThreosymbianL3147	32. TrypanoCLBonneFemeradillo			28. LeontideV395		
	29. ThreosymbianL3147	33. TrypanoCLBonneFemeradillo			29. LeontideV395		
	30. ThreosymbianL3147	34. TrypanoCLBonneFemeradillo			30. LeontideV395		
	31. ThreosymbianL3147	35. TrypanoCLBonneFemeradillo			31. LeontideV395		
	32. ThreosymbianL3147	36. TrypanoCLBonneFemeradillo			32. LeontideV395		
	33. ThreosymbianL3147	37. TrypanoCLBonneFemeradillo			33. LeontideV395		
	34. ThreosymbianL3147	38. TrypanoCLBonneFemeradillo			34. LeontideV395		
	35. ThreosymbianL3147	39. TrypanoCLBonneFemeradillo			35. LeontideV395		
	36. ThreosymbianL3147	40. TrypanoCLBonneFemeradillo			36. LeontideV395		
	37. ThreosymbianL3147	41. TrypanoCLBonneFemeradillo			37. LeontideV395		
	38. ThreosymbianL3147	42. TrypanoCLBonneFemeradillo			38. LeontideV395		
	39. ThreosymbianL3147	43. TrypanoCLBonneFemeradillo			39. LeontideV395		
	40. ThreosymbianL3147	44. TrypanoCLBonneFemeradillo			40. LeontideV395		
	41. ThreosymbianL3147	45. TrypanoCLBonneFemeradillo			41. LeontideV395		
	42. ThreosymbianL3147	46. TrypanoCLBonneFemeradillo			42. LeontideV395		
	43. ThreosymbianL3147	47. TrypanoCLBonneFemeradillo			43. LeontideV395		
	44. ThreosymbianL3147	48. TrypanoCLBonneFemeradillo			44. LeontideV395		
	45. ThreosymbianL3147	49. TrypanoCLBonneFemeradillo			45. LeontideV395		
	46. ThreosymbianL3147	50. TrypanoCLBonneFemeradillo			46. LeontideV395		
	47. ThreosymbianL3147	51. TrypanoCLBonneFemeradillo			47. LeontideV395		
	48. ThreosymbianL3147	52. TrypanoCLBonneFemeradillo			48. LeontideV395		
	49. ThreosymbianL3147	53. TrypanoCLBonneFemeradillo			49. LeontideV395		
	50. ThreosymbianL3147	54. TrypanoCLBonneFemeradillo			50. LeontideV395		
	51. ThreosymbianL3147	55. TrypanoCLBonneFemeradillo			51. LeontideV395		
	52. ThreosymbianL3147	56. TrypanoCLBonneFemeradillo			52. LeontideV395		
	53. ThreosymbianL3147	57. TrypanoCLBonneFemeradillo			53. LeontideV395		
	54. ThreosymbianL3147	58. TrypanoCLBonneFemeradillo			54. LeontideV395		
	55. ThreosymbianL3147	59. TrypanoCLBonneFemeradillo			55. LeontideV395		
	56. ThreosymbianL3147	60. TrypanoCLBonneFemeradillo			56. LeontideV395		
	57. ThreosymbianL3147	61. TrypanoCLBonneFemeradillo			57. LeontideV395		
	58. ThreosymbianL3147	62. TrypanoCLBonneFemeradillo			58. LeontideV395		
	59. ThreosymbianL3147	63. TrypanoCLBonneFemeradillo			59. LeontideV395		
	60. ThreosymbianL3147	64. TrypanoCLBonneFemeradillo			60. LeontideV395		
	61. ThreosymbianL3147	65. TrypanoCLBonneFemeradillo			61. LeontideV395		
	62. ThreosymbianL3147	66. TrypanoCLBonneFemeradillo			62. LeontideV395		
	63. ThreosymbianL3147	67. TrypanoCLBonneFemeradillo			63. LeontideV395		
	64. ThreosymbianL3147	68. TrypanoCLBonneFemeradillo			64. LeontideV395		
	65. ThreosymbianL3147	69. TrypanoCLBonneFemeradillo			65. LeontideV395		
	66. ThreosymbianL3147	70. TrypanoCLBonneFemeradillo			66. LeontideV395		
	67. ThreosymbianL3147	71. TrypanoCLBonneFemeradillo			67. LeontideV395		
	68. ThreosymbianL3147	72. TrypanoCLBonneFemeradillo			68. LeontideV395		
	69. ThreosymbianL3147	73. TrypanoCLBonneFemeradillo			69. LeontideV395		
	70. ThreosymbianL3147	74. TrypanoCLBonneFemeradillo			70. LeontideV395		
	71. ThreosymbianL3147	75. TrypanoCLBonneFemeradillo			71. LeontideV395		
	72. ThreosymbianL3147	76. TrypanoCLBonneFemeradillo			72. LeontideV395		
	73. ThreosymbianL3147	77. TrypanoCLBonneFemeradillo			73. LeontideV395		
	74. ThreosymbianL3147	78. TrypanoCLBonneFemeradillo			74. LeontideV395		
	75. ThreosymbianL3147	79. TrypanoCLBonneFemeradillo			75. LeontideV395		
	76. ThreosymbianL3147	80. TrypanoCLBonneFemeradillo			76. LeontideV395		
	77. ThreosymbianL3147	81. TrypanoCLBonneFemeradillo			77. LeontideV395		
	78. ThreosymbianL3147	82. TrypanoCLBonneFemeradillo			78. LeontideV395		
	79. ThreosymbianL3147	83. TrypanoCLBonneFemeradillo			79. LeontideV395		
	80. ThreosymbianL3147	84. TrypanoCLBonneFemeradillo			80. LeontideV395		
	81. ThreosymbianL3147	85. TrypanoCLBonneFemeradillo			81. LeontideV395		
	82. ThreosymbianL3147	86. TrypanoCLBonneFemeradillo			82. LeontideV395		
	83. ThreosymbianL3147	87. TrypanoCLBonneFemeradillo			83. LeontideV395		
	84. ThreosymbianL3147	88. TrypanoCLBonneFemeradillo			84. LeontideV395		
	85. ThreosymbianL3147	89. TrypanoCLBonneFemeradillo			85. LeontideV395		
	86. ThreosymbianL3147	90. TrypanoCLBonneFemeradillo			86. LeontideV395		
	87. ThreosymbianL3147	91. TrypanoCLBonneFemeradillo			87. LeontideV395		
	88. ThreosymbianL3147	92. TrypanoCLBonneFemeradillo			88. LeontideV395		
	89. ThreosymbianL3147	93. TrypanoCLBonneFemeradillo			89. LeontideV395		
	90. ThreosymbianL3147	94. TrypanoCLBonneFemeradillo			90. LeontideV395		
	91. ThreosymbianL3147	95. TrypanoCLBonneFemeradillo			91. LeontideV395		
	92. ThreosymbianL3147	96. TrypanoCLBonneFemeradillo			92. LeontideV395		
	93. ThreosymbianL3147	97. TrypanoCLBonneFemeradillo			93. LeontideV395		
	94. ThreosymbianL3147	98. TrypanoCLBonneFemeradillo			94. LeontideV395		
	95. ThreosymbianL3147	99. TrypanoCLBonneFemeradillo			95. LeontideV395		
	96. ThreosymbianL3147	100. TrypanoCLBonneFemeradillo			96. LeontideV395		
	97. ThreosymbianL3147	101. TrypanoCLBonneFemeradillo			97. LeontideV395		
	98. ThreosymbianL3147	102. TrypanoCLBonneFemeradillo			98. LeontideV395		
	99. ThreosymbianL3147	103. TrypanoCLBonneFemeradillo			99. LeontideV395		
	100. ThreosymbianL3147	104. TrypanoCLBonneFemeradillo			100. LeontideV395		
	101. ThreosymbianL3147	105. TrypanoCLBonneFemeradillo			101. LeontideV395		
	102. ThreosymbianL3147	106. TrypanoCLBonneFemeradillo			102. LeontideV395		
	103. ThreosymbianL3147	107. TrypanoCLBonneFemeradillo			103. LeontideV395		
	104. ThreosymbianL3147	108. TrypanoCLBonneFemeradillo			104. LeontideV395		
	105. ThreosymbianL3147	109. TrypanoCLBonneFemeradillo			105. LeontideV395		
	106. ThreosymbianL3147	110. TrypanoCLBonneFemeradillo			106. LeontideV395		
	107. ThreosymbianL3147	111. TrypanoCLBonneFemeradillo			107. LeontideV395		
	108. ThreosymbianL3147	112. TrypanoCLBonneFemeradillo			108. LeontideV395		
	109. ThreosymbianL3147	113. TrypanoCLBonneFemeradillo			109. LeontideV395		
	110. ThreosymbianL3147	114. TrypanoCLBonneFemeradillo			110. LeontideV395		
	111. ThreosymbianL3147	115. TrypanoCLBonneFemeradillo			111. LeontideV395		
	112. ThreosymbianL3147	116. TrypanoCLBonneFemeradillo			112. LeontideV395		
	113. ThreosymbianL3147	117. TrypanoCLBonneFemeradillo			113. LeontideV395		
	114. ThreosymbianL3147	118. TrypanoCLBonneFemeradillo			114. LeontideV395		
	115. ThreosymbianL3147	119. TrypanoCLBonneFemeradillo			115. LeontideV395		
	116. ThreosymbianL3147	120. TrypanoCLBonneFemeradillo			116. LeontideV395		
	117. ThreosymbianL3147	121. TrypanoCLBonneFemeradillo			117. LeontideV395		
	118. ThreosymbianL3147	122. TrypanoCLBonneFemeradillo			118. LeontideV395		
	119. ThreosymbianL3147	123. TrypanoCLBonneFemeradillo			119. LeontideV395		
	120. ThreosymbianL3147	124. TrypanoCLBonneFemeradillo			120. LeontideV395		
	121. ThreosymbianL3147	125. TrypanoCLBonneFemeradillo			121. LeontideV395		
	122. ThreosymbianL3147	126. TrypanoCLBonneFemeradillo			122. LeontideV395		
	123. ThreosymbianL3147	127. TrypanoCLBonneFemeradillo			123. LeontideV395		
	124. ThreosymbianL3147	128. TrypanoCLBonneFemeradillo			124. LeontideV395		
	125. ThreosymbianL3147	129. TrypanoCLBonneFemeradillo			125. LeontideV395		
	126. ThreosymbianL3147	130. TrypanoCLBonneFemeradillo			126. LeontideV395		
	127. ThreosymbianL3147	131. TrypanoCLBonneFemeradillo			127. LeontideV395		
	128. ThreosymbianL3147	132. TrypanoCLBonneFemeradillo			128. LeontideV395		
	129. ThreosymbianL3147	133. TrypanoCLBonneFemeradillo			129. LeontideV395		
	130. ThreosymbianL3147	134. TrypanoCLBonneFemeradillo			130. LeontideV395		
	131. ThreosymbianL3147	135. TrypanoCLBonneFemeradillo			131. LeontideV395		
	132. ThreosymbianL3147	136. TrypanoCLBonneFemeradillo			132. LeontideV395		
	133. ThreosymbianL3147	137. TrypanoCLBonneFemeradillo			133. LeontideV395		
	134. ThreosymbianL3147	138. TrypanoCLBonneFemeradillo			134. LeontideV395		
	135. ThreosymbianL3147	139. TrypanoCLBonneFemeradillo			135. LeontideV395		
	136. ThreosymbianL3147	140. TrypanoCLBonneFemeradillo			136. LeontideV395		
	137. ThreosymbianL3147	141. TrypanoCLBonneFemeradillo			137. LeontideV395		
	138. ThreosymbianL3147	142. TrypanoCLBonneFemeradillo			138. LeontideV395		
	139. ThreosymbianL3147	143. TrypanoCLBonneFemeradillo			139. LeontideV395		
	140. ThreosymbianL3147	144. TrypanoCLBonneFemeradillo			140. LeontideV395		
	141. ThreosymbianL3147	145. TrypanoCLBonneFemeradillo			141. LeontideV395		
	142. ThreosymbianL3147	146. TrypanoCLBonneFemeradillo			142. LeontideV395		
	143. ThreosymbianL3147	147. TrypanoCLBonneFemeradillo			143. LeontideV395		
	144. ThreosymbianL3147	148. TrypanoCLBonneFemeradillo			144. LeontideV395		
	145. ThreosymbianL3147	149. TrypanoCLBonneFemeradillo			145. LeontideV395		
	146. ThreosymbianL3147	150. TrypanoCLBonneFemeradillo			146. LeontideV395		
	147. ThreosymbianL3147	151. TrypanoCLBonneFemeradillo			147. LeontideV395		
	148. ThreosymbianL3147	152. TrypanoCLBonneFemeradillo			148. LeontideV395		
	149. ThreosymbianL3147	153. TrypanoCLBonneFemeradillo			149. LeontideV395		
	150. ThreosymbianL3147	154. TrypanoCLBonneFemeradillo			150. LeontideV395		
	151. ThreosymbianL3147	155. TrypanoCLBonneFemeradillo			151. LeontideV395		
	152. ThreosymbianL3147	156. TrypanoCLBonneFemeradillo			152. LeontideV395		
	153. ThreosymbianL3147	157. TrypanoCLBonneFemeradillo			153. LeontideV395		
	154. ThreosymbianL3147	158. TrypanoCLBonneFemeradillo			154. LeontideV395		
	155. ThreosymbianL3147	159. TrypanoCLBonneFemeradillo			155. LeontideV395		
	156. ThreosymbianL3147	160. TrypanoCLBonneFemeradillo			156. LeontideV395		
	157. ThreosymbianL3147	161. TrypanoCLBonneFemeradillo			157. LeontideV395		
	158. ThreosymbianL3147	162. TrypanoCLBonneFemeradillo			158. LeontideV395		
	159. ThreosymbianL3147	163. TrypanoCLBonneFemeradillo			159. LeontideV395		
	160. ThreosymbianL3147	164. TrypanoCL					

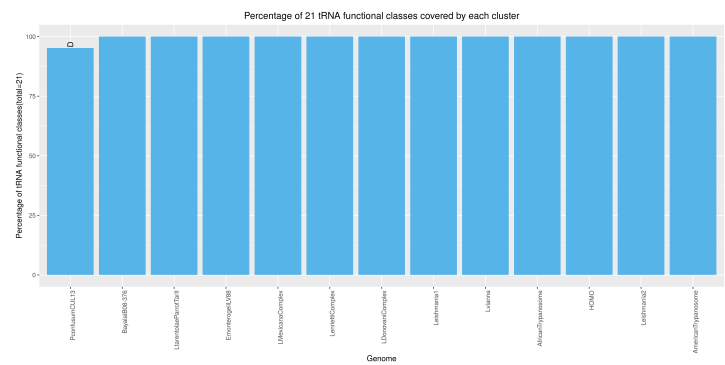


Figure 7: Percentage of 22 tRNA types annotated by both TSE and ARA for each TryTryp cluster. The label on top of each bar shows which tRNA classes are not annotated for the genome.

REFERENCES