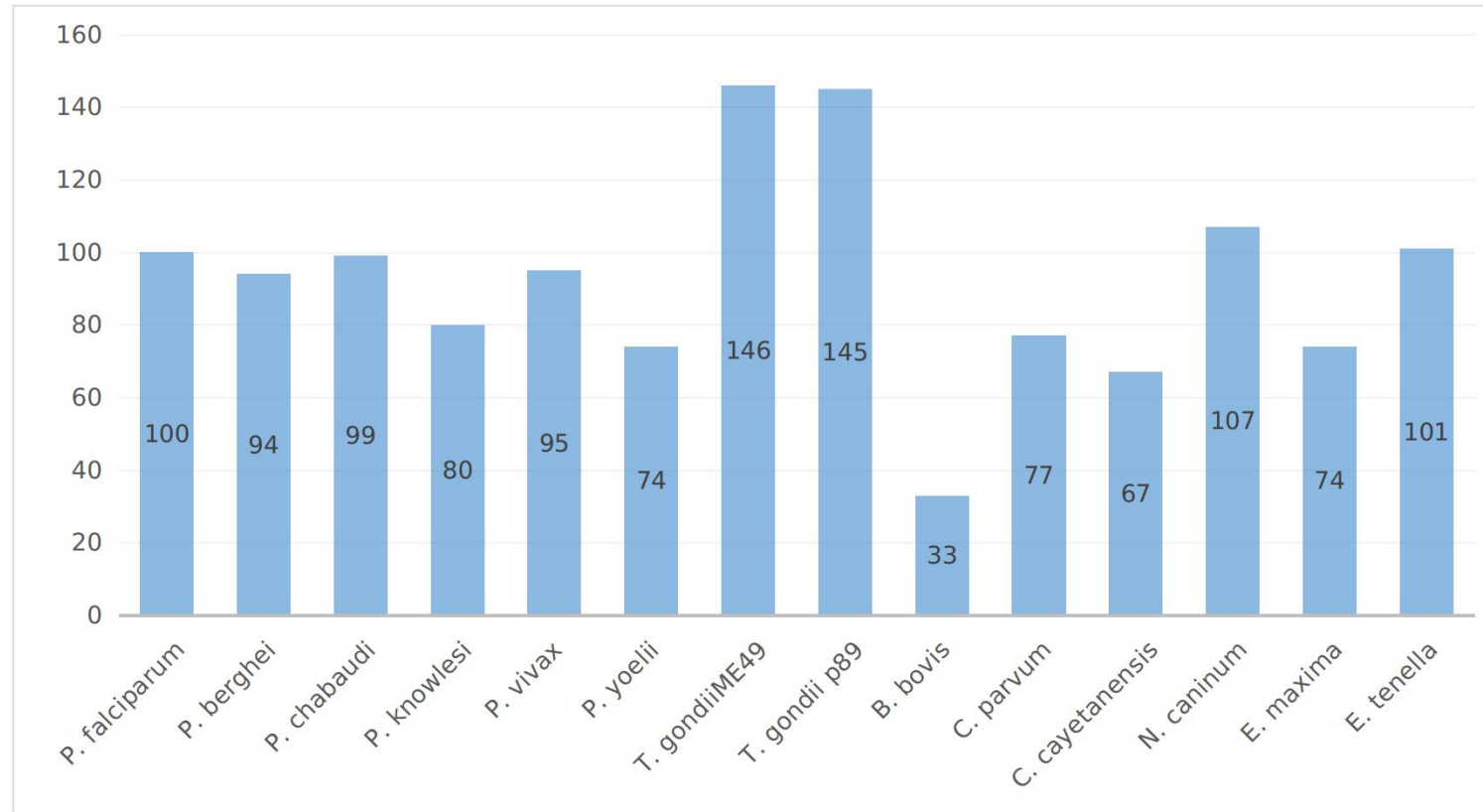
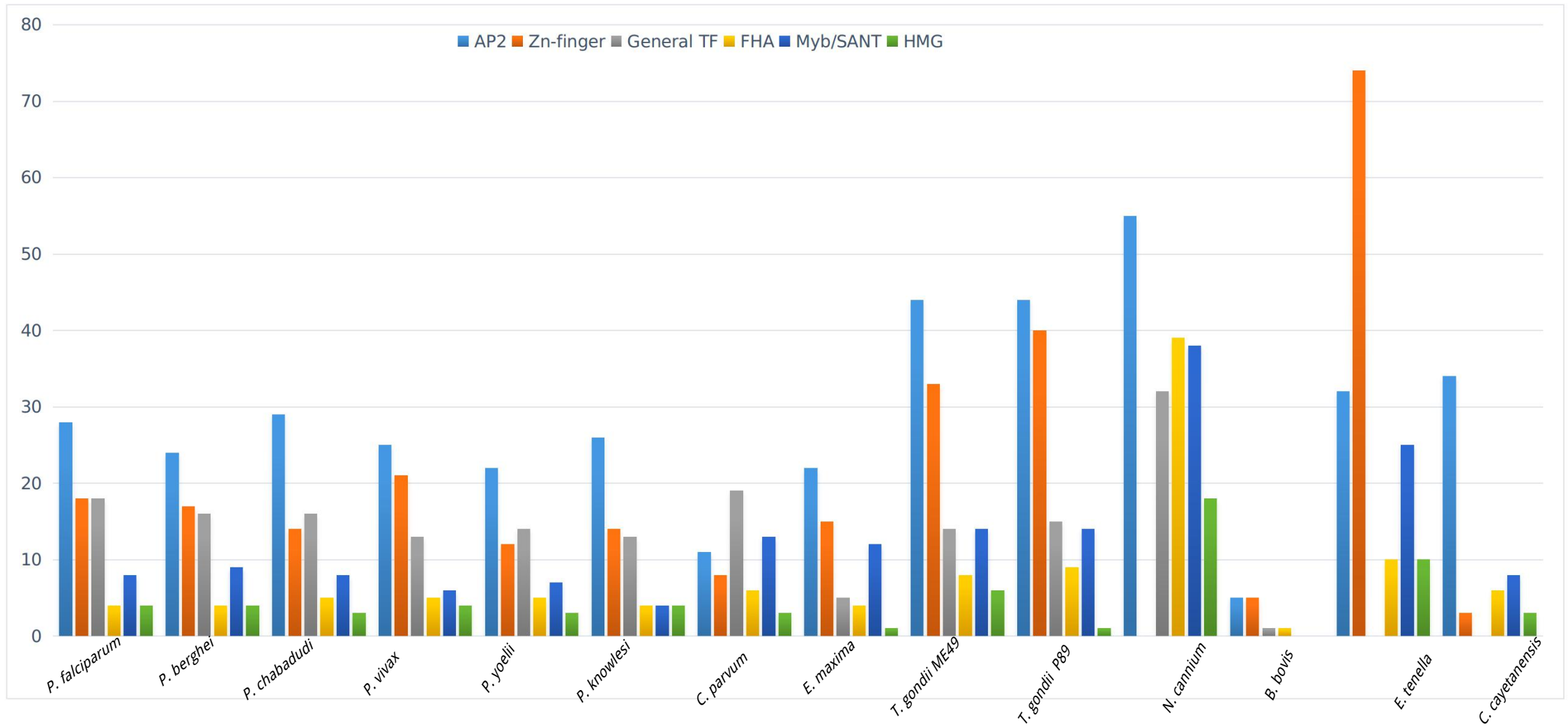


# TF proteins count across apicomplexans



# TF family distribution across Apicomplexans



# TF proteins distribution in apicomplexans

**Table1: TF proteins distribution in apicomplexans in ApicoTFdb including newly predicted TFs**

Species	Number of species	Total number of TF(ApicoTFdb)	Experimetaly verified
<i>P. falciparum, P. vivax, P. berghei, P. chabaudi, P. yoelii &amp; P. knowlesii</i>	6	542	89
<i>C. parvum</i>	1	77	1
<i>B. bovis</i>	1	33	0
<i>E. maxima, T. gondiiME49, T. gondiip89, E. tenella, N. caninum, C. cayetanensis</i>	6	650	3

# Updated transcription factors annotation in ApicoTFdb

Species	Genome Size (in Mb)	Total number of proteins (PlasmoDB ver.38)	PlasmoDB Text Search	Number of validated and predicted TFs in published databases				ApicoTFdb			
				DBD*		CisBP*		TF count	TF family	Experimentally verified	Unannotated proteins
				TF count	TF family	TF count	TF family				
<i>P. falciparum</i>	23.3	5635	548	18	7	44	10	100	17	27	7
<i>P. berghei</i>	18.5	5089	418	19	12	46	11	94	19	13	9
<i>P. chabaudi</i>	18.8	5282	372	19	7	46	11	99	18	13	12
<i>P. knowlesi</i>	24.3	5261	386	14	8	46	10	80	17	12	5
<i>P. vivax</i>	28.8	5390	372	15	7	49	8	95	17	12	30
<i>P. yoelii</i>	22.4	7774	360	15	6	46	9	74	14	10	36
<i>T. gondii</i> ME49	64.5	8920	443	N.A*	N.A*	81	14	146	17	1	12
<i>T. gondii</i> p89	64.1	9874	486	N.A*	N.A*	N.A*	N.A*	145	17	0	4
<i>B. bovis</i>	8.1	3721	126	N.A*	N.A*	N.A*	N.A*	33	6	0	11
<i>C. parvum</i>	9.1	4020	248	30	11	35	8	75	14	1	4
<i>C. cayetanensis</i>	44	7592	332	N.A*	N.A*	N.A*	N.A*	77	15	0	28
<i>N. caninum</i>	57.4	7266	361	N.A*	N.A*	84	11	114	16	2	65
<i>E. maxima</i>	49.9	6249	241	N.A*	N.A*	N.A*	N.A*	74	17	0	46
<i>E. tenella</i>	51.8	8634	307	N.A*	N.A*	N.A*	N.A*	101	12	0	53

total=1307

\*DBD- Transcription factor prediction database (Release 2.0)

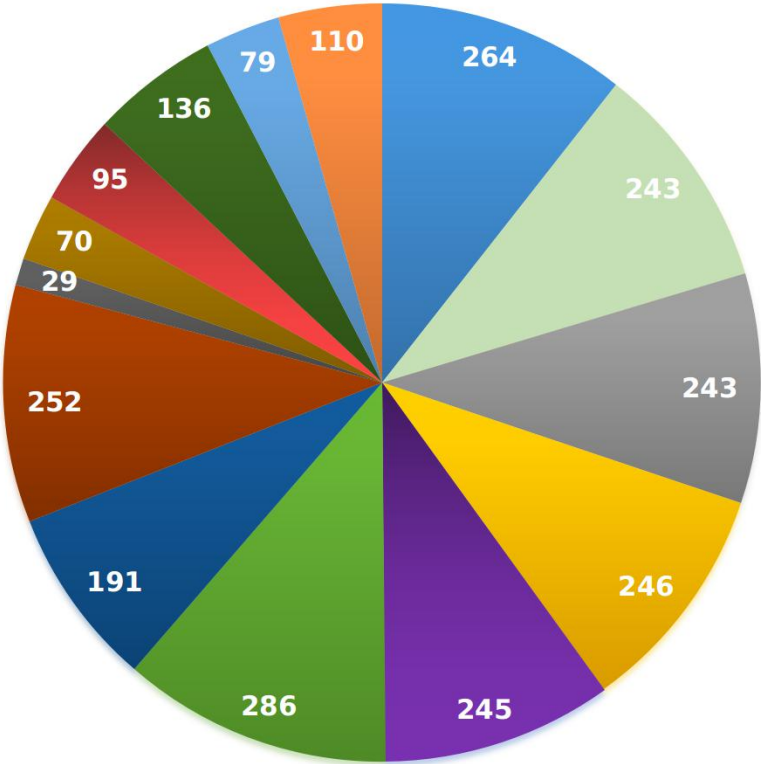
\*CisBP- Catalog of Inferred Sequence Binding Preferences (Last updated: Apr 5th, 2015 Database Build 1.02)

\*N.A - No information available

# TAFs classification (Total: 2490)

Table 2: Manually curated TAFs classification into TRs, RNARs and CRRs.					
<b>TAFs</b>	<b>Initial prediction</b>	<b>Manual curation</b>	<b>Ortholog Groups</b>	<b>Computed GO</b>	<b>Curated GO</b>
TF-regulators	678	666	134	124	36
RNA-regulators	2751	1410	301	257	87
Chromatin Regulators	761	415	113	139	53

# TAF distribution across apicomplexan



- P. falciparum
- P. berghei
- P. chabaudi
- P. knowlesi
- P. vivax
- P. yoelii
- T. gondii ME49
- T. gondii p89
- B. bovis
- C. parvum
- C. cayetanensis
- N. caninum
- E. maxima
- E. tenella

Species	Unannotated class	Gene Count	Classified TF-Families	New families
<i>P. falciparum</i>	Conserved protein, Unknown function	7	TUB, Myb/SANT, HTH, CCAAT, CBF, BSD, General-TF, ARID/BRIGHT	HTH, BSD, TUB
<i>P. berghei</i>	Conserved protein, Unknown function	9	TUB, Myb/SANT, HTH, GO-Based, General-TF, BSD, ARID/BRIGHT, CBF, CCAAT,	TUB, GO-Based, BSD
<i>P. chabaudi</i>	Conserved protein, Unknown function	12	TUB, Myb/SANT, HTH, General-TF, GO-Based, BSD, CCAAT, AP2, ARID/BRIGHT, CBF	TUB, HTH, GO-Based
<i>P. knowlesi</i>	Conserved protein, Unknown function	5	TUB, MYb/SANT, HTH, ARID/BRIGHT, General-TF, BSD	HTH, BSD, TUB
<i>P. vivax</i>	Hypothetical protein	30	Zn-Finger, TUB, SART, Myb/SANT, mTERF, HTH, GO-Based, FHA, Jmc, BSD	TUB, HTH, GO-Based, FHA, Jmc, BSDs
<i>P. yoelii</i>	Hypothetical protein	36	Zn-Finger, Myb/SANT, mTERF, General-TF, CBF, BSD, Jmc, CCAAT, BBOX, AP2	BBOX, JmC
<i>T. gondii ME49</i>	Hypothetical protein	12	Zn-Finger, Myb/SANT, mTERF, HTH, General-TF, FHA, Jmc	HTH, Jmc
<i>T. gondii p89</i>	Hypothetical protein	4	Zn-Finger, Myb/SANT, BSD	all
<i>B. bovis</i>	Conserved protein, Unknown function	11	AP2	AP2
<i>C. parvum</i>	Uncharacterized protein	4	Zn-Finger, HTH, AP2	HTH
<i>C. cayetanensis</i>	Hypothetical protein, Unspecified product	28	BSD, AP2, TUB, SART, MYB/SANT, FHA, MTERF, HMG, General-TF	TUB, FHA, BSD
<i>N. caninum</i>	Uncharacterized protein, Unspecified product, Conserved protein, Unknown function	65	mTERF, bZIP, AP2, NAC, General-TF, NAC, HTH, Myb/SANT, BSD, FHA	HTH, NAC, BSD, FHA
<i>E. maxima</i>	Hypothetical protein	46	Zn-Finger, SART, SANT, mTERF, HMG, GO-Based, General-TF, FHA, CBF, Jmc, BBOX, AP2	GO-Based, FHA, Jmc
<i>E. tenella</i>	Hypothetical protein	53	AP2, Zn-Finger, SART, NAC, Myb/SANT, General-TF	NAC

Total unannotated proteins: 322