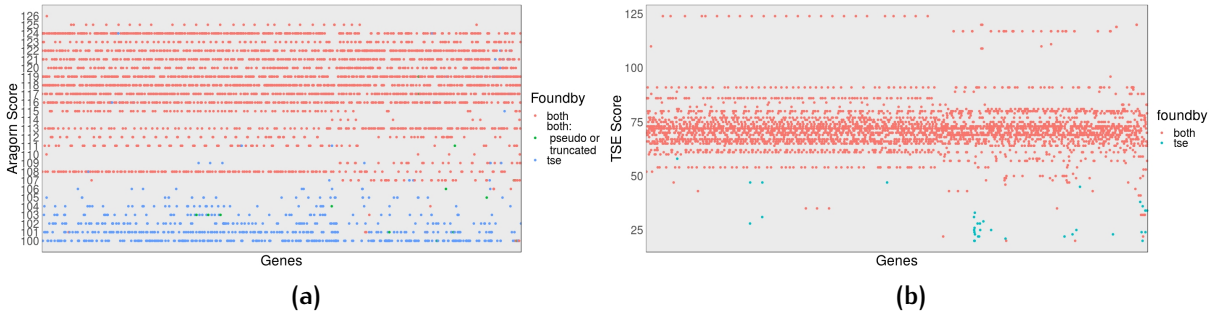
Using two gene finders Aragorn (ARA) and tRNAScan-SE (TSE), 4381 genes were predicted. Genes with tse score of less than 50 and aragorn score of less than 107 were dismissed. The cutoff score is set based on the ARA and TSE score distribution shown in figure 1a,b.



(a) (b)

Figure 1: a) ARA score of genes found by both genefinders TSE and ARA, and genes found by only ARA. b) TSE score of genes found by both genefinders and genes found by only TSE

3588 genes were left from which two genes marked as truncated by TSE were also removed. 22 genes in the remained gene set had different identity between TSE and ARA shown in table 1 and were partially removed.

Table 1: 22 genes with different anticodon assignment by two gene finders TSE and ARA

tse identity | ara identity	(g | w)	(m | l)	(y | n)
frequency	3	9	10

Each of these three ambiguties have been analysed and compared to the other genes of the same identity. Genes (y | n) were manually compare to the other identified genes with identity n and y found by both gene finders. In all cases these 10 genes were considerably more similar to the genes marked with identity Y than genes identified as N. Also, by looking at genes as clusters (a group of two or more genes found within a genome located within a thousand base pairs of each other) they were observed in clusters "LSMEM(y | n)V","V(y | n)MEMSL","LSMEMSM(y | n)V", and (y | n)V. Further we observed that there was no occurrence of genes NY or YN within any cluster, however there were 6 occurrences of YV or VY (one of them in cluster EMYV). Genes with ambiguty (m | l) were disregarded as they all appear as singleton genes, and not in any of the clusters. Genes with ambiguity (g | w) have also been removed since we were not able to resolve the ambiguity.

The final gene set has 3574 genes from which 36 genes are found only by aragorn and the rest are predicted by both gene finders.

Table 2: nucleotide composition of 46 TriTryp genomes

organism	A%	T%	C%	G%	AT%	GC%	Seq#	Gene#
TbruceigambienseDAL972	26	26	24	24	53	47	11	63
TevansiSTIB805	27	27	23	23	53	47	13	66
CfasciculataCfCl	21	22	29	28	43	57	31	105
TbruceiLister427	26	26	22	23	51	45	32	66
LpanamensisMHOMPA94PSC1	21	21	28	28	41	56	35	74
LdonovaniBHU1220	19	20	29	29	39	57	36	84
LdonovaniBPK282A1	19	20	29	29	39	57	36	85
LinfantumJPCM5	20	20	30	30	40	60	36	84
LmajorFriedlin	20	20	30	30	40	60	36	84
LmajorSD75.1	20	20	30	30	40	59	36	82
TcruziCLBrenerEsmeraldo-like	20	20	20	20	39	40	41	57
TcruziCLBrenerNon-Esmeraldo-like	21	21	22	22	42	43	41	57
TcruziSylvioX10-1	24	23	25	25	47	50	47	66
LpyrrhocorisH10	21	22	28	28	43	56	60	104
TbruceiTREU927	27	27	23	23	54	45	131	72
LbraziliensisMHOMBR75M2904	21	21	29	29	42	58	139	83
LgerbilliLEM452	20	20	30	29	40	59	142	81
LaethiopicaL147	19	20	30	29	39	59	160	83
LtropicaL590	19	19	29	28	38	57	160	87
LarabicaLEM1108	20	20	29	29	40	58	168	85
LturanicaLEM423	19	20	30	29	39	59	219	86
LspMARLEM2494	20	20	30	29	40	59	251	80
TtheileriEdinburgh	26	26	17	17	52	35	253	155
LenriettiiLEM3045	20	20	29	29	40	59	495	82
BayalaiB08-376	22	22	27	27	45	55	546	69
LmexicanaMHOMGT2001U1103	20	20	30	30	40	60	588	84
LbraziliensisMHOMBR75M2903	19	20	27	27	39	53	745	86
LmajorLV39c5	20	20	29	29	40	59	809	84
LpanamensisMHOMCOL81L13	21	21	29	28	42	57	856	88
TcruzicruziDm28c	24	24	26	26	48	52	1029	95
TcruziDm28c	25	25	26	25	49	50	1210	50
LseymouriATCC30220	22	22	28	28	44	55	1222	94
LtarentolaeParrotTarII	21	21	27	27	42	55	1351	78
EmonterogeiiLV88	23	23	26	26	46	52	1961	103
PconfusumCUL13	18	18	28	28	35	57	2188	61
LamazonensisMHOMBR71973M2269	20	20	30	30	41	59	2627	65
TcongolenseIL3000	21	21	20	20	43	40	2839	67
TgrayiANR4	23	23	27	27	46	54	2871	94
TrangeliSC58	24	23	27	26	47	53	7433	6
TvivaxY486	21	21	23	23	42	46	8290	79
TcruziJRcl4	24	23	26	24	47	50	15312	69
TcruziEsmeraldo	23	22	24	23	45	47	15803	74
TcruzimarinkelleiB7	22	22	23	23	43	45	16783	56
TcruziSylvioX10-1-2012	24	24	26	26	49	51	27019	68
TcruziCLBrener	23	23	27	27	47	53	29407	14
TcruziTulacl2	22	21	23	23	43	46	45711	119

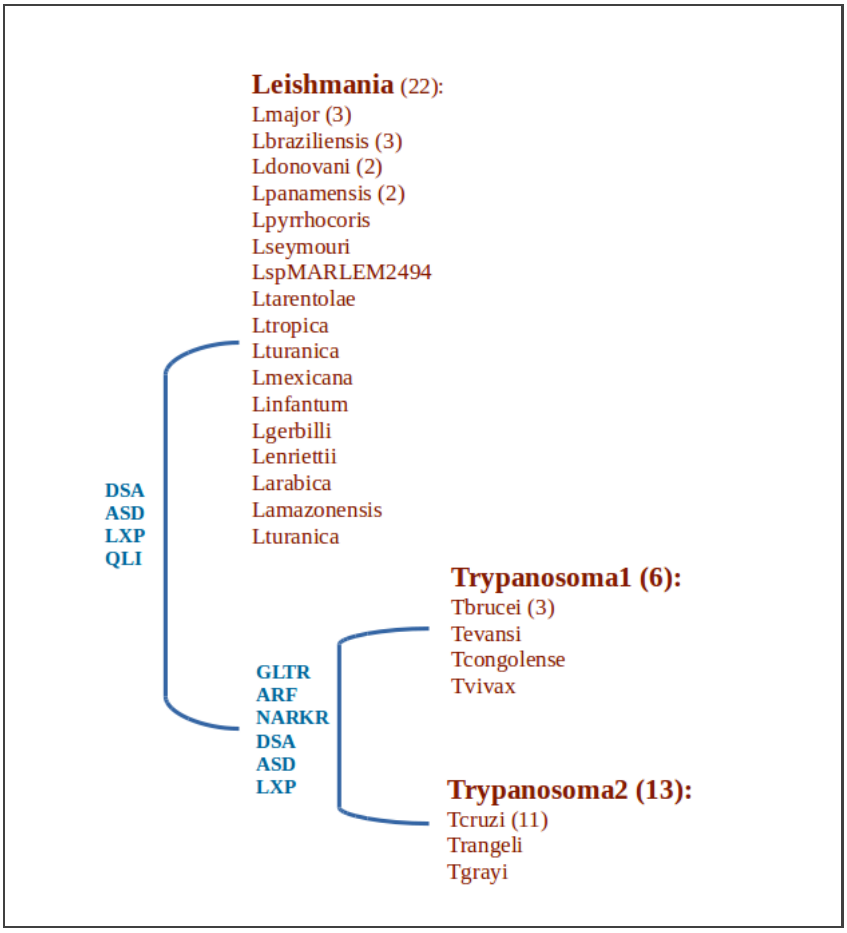


Figure 2: TriTryp genomes clustered into three classes of Leishmania(L), Trypanosoma1(T1), and Trypanosoma2(T2)

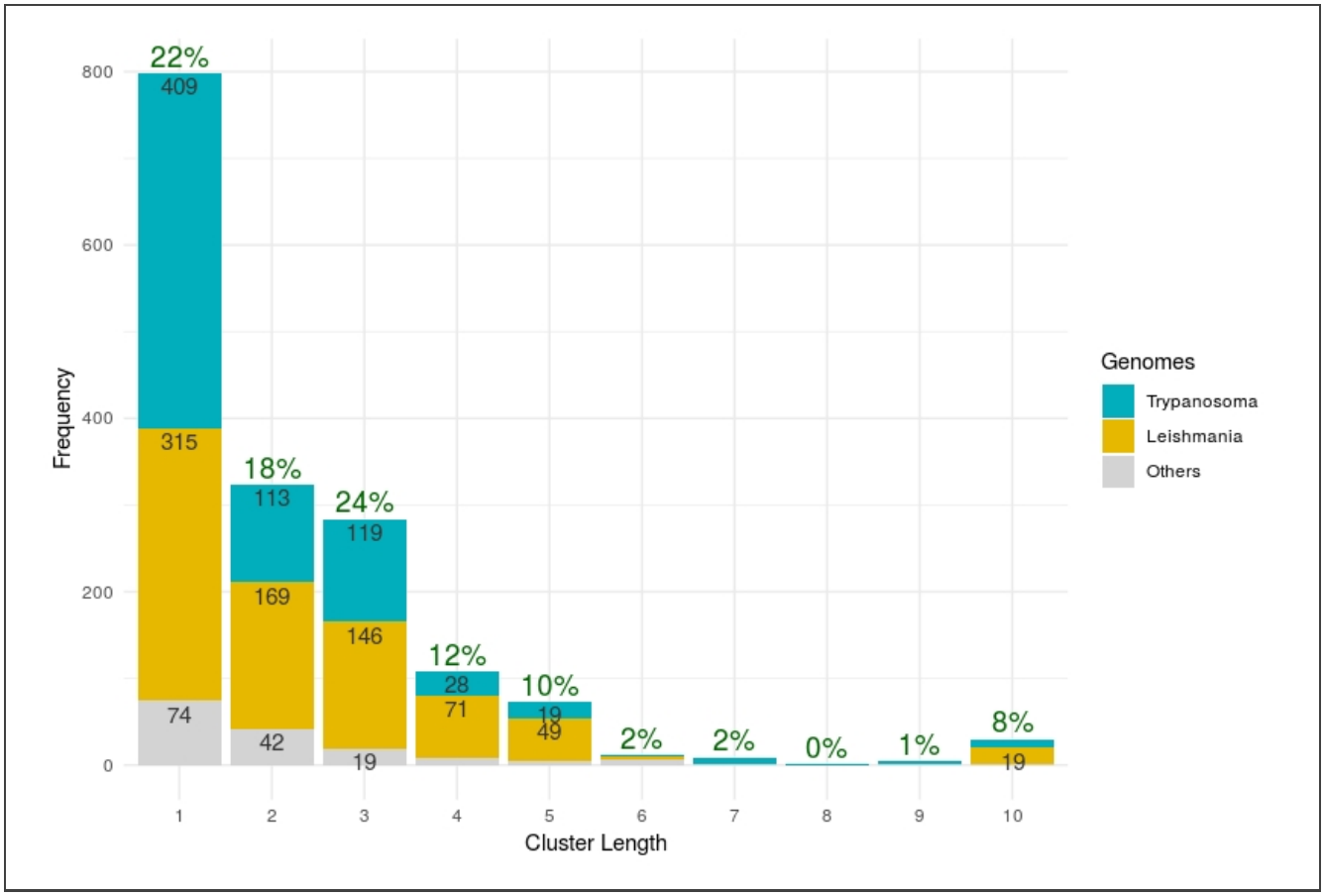


Figure 3: Cluster size distribution for three categories of TryTryp genomes. Labels in green on top of each bar show the percentage of total number of genes as cluster of a specific length. Each color refers to one category of TriTryp genomes. Numbers within each color section of the bar shows the counts of clusters with a specific length.

Table 3: frequecty of gene clusters of length > 3 with frequency of atleast 2. T% and L% refer to the percentage of Trypanosoma and Leishmania genomes, in order, that contain the cluster

Trypanosoma				Leishmania			
Cluster	dir	T%	L%	Cluster	dir	L%	T%
EVRH	−++	91	0	NARKR	+-+++	55	0
IVQRLTRKGW	+——++-+	82	0	IQVKGLTRKR	-++++−++-	35	0
VIMLS	-++-+	82	0	GLTR	++-+	30	0
CLXP	+−+	73	0	EMSV	-+-+	20	0
NYTPN	—++	64	0	IQVK	-+++	20	0
GTGP	+−+	55	0	ILQQI	+−++	15	0
NPTYN	−+++	36	0	LSMEMYV	-+-++-+	15	0
YTTY	−++	36	0	RKRTLGKVQI	+−++—-+	15	0
PGTTG	-++−	18	0	LSMEMYV	-+−+-+	10	0
SLMIV	-+−+	14	0				
EARR	−++	9	0				
YTTT	—+	9	0				

Table 4: frequecty of gene clusters of length > 2. T% and L% refer to the percentage of Trypanosoma and Leishmania genomes, in order, that contain the cluster

Trypanosoma (20 genomes)			
Cluster	dir	T%	L%
DSA	-++	95	55
EVRH	−++	91	0
PVK	+++	91	0
QLI	+-+	86	0
RRA	−+	86	0
IVQRLTRKGW	+——++-+	82	0
VIMLS	-++-+	82	0
CLXP	+−+	73	0
VHF	++-	68	0
NYTPN	—++	64	0
KGN	+−	59	0
GTGP	+−+	55	0
LAG	-++	45	0
NPTYN	−+++	36	0
YTTY	−++	36	0
GAL	−+	27	0
LXP	−+	23	30
PGTTG	-++−	18	0
SLMIV	-+−+	14	0
EARR	−++	9	0
KVP	—	9	0
MRR	-++	9	0
TGP	−+	9	0
YTTT	—+	9	0
ARR	-++	5	0
ASD	−+	5	30
DEDE	+-+-	5	0
DRTY	++++	5	0
EFHV	-+−	5	0
FHVRH	+−++	5	0
GEE	+−	5	0
GKWRTL	-+−++	5	0
GTGP	++-+	5	0
GTGPVK	+−+++	5	0
GTP	+-+	5	0
HRE	−+	5	0
ILIQ	-++-	5	0
IVQRLTKGW	+——+-+	5	0
IVQRLTRWKG	+——++-+	5	0
LAA	-++	5	0
NGK	++-	5	0
PTG	—	5	0
PXLC	-++-	5	0
QILI	+−+	5	0
QLQ	-+-	5	0
QVI	++-	5	0
RQVI	+++-	5	0
VHFE	++-+	5	0
VYIML	-+++-	5	0
VYIMLS	-+++-+	5	0
WGKRTL	-+−++	5	0
YTRD	—-	5	0
YTY	−+	5	0

Leishmania (22 genomes)			
Cluster	dir	L%	T%
DSA	-++	55	95
NARKR	+-+++	55	0
ARF	−+	50	0
IQL	-++	35	0
IQVKGLTRKR	-++++−++-	35	0
PTN	-++	35	0
ASD	−+	30	5
GLTR	++-+	30	0
LQI	−+	30	0
LXP	−+	30	23
PXL	-++	30	0
VEF	-++	30	0
FRA	-++	25	0
HEF	+++	25	0
LXP	+-+	25	0
VLM	—	25	0
EMSV	-+-+	20	0
IQVK	-+++	20	0
SLS	+−	20	0
FEV	−+	15	0
ILQQI	+−++	15	0
LSMEMYV	-+-++-+	15	0
RKRTLGKVQI	+−++—+	15	0
LSMEMYV	-+−+-+	10	0
NTP	−+	10	0
ARFARF	−+−+	5	0
ARKR	-+++	5	0
ASDD	−++	5	0
DSV	-++	5	0
EML	-++	5	0
EMYV	++-+	5	0
FIQ	—	5	0
FIQFIQ	——	5	0
ILQ	+−	5	0
IQI	+++	5	0
IQQL	−++	5	0
IQQLI	−++-	5	0
IQV	-++	5	0
IQVKGLTR	-++++−+	5	0
KGL	+++	5	0
KVQI	—+	5	0
LSM	-+-	5	0
LSMEMSMYV	-+-++-+-+	5	0
LTP	−+	5	0
MEM	−+	5	0
MEMSL	−+-+	5	0
MEMSL	-++-+	5	0
MMAP	—-	5	0
NARK	+-++	5	0
NWW	+++	5	0
PKP	+−	5	0
PTYN	-+-+	5	0
QFIQ	—-	5	0
QLI	-+-	5	0
QVK	+++	5	0
RHLP	++++	5	0
RKKK	+−+	5	0
RKR	—	5	0
RKRAN	—+-	5	0
RKRRA	—-+	5	0
RKRTLGKVQ	+−++—-	5	0
SLS	++-	5	0
VHEF	-+++	5	0
VYMEMSL	-+−+-+	5	0
VYMEMSL	-+-++-+	5	0
WWNN	—-	5	0

Table 5: frequecty of gene clusters of length > 2. T1% and T2% refer to the percentage of Trypanosoma1 and Trypanosoma2 genomes, in order, that contain the cluster

Trypanosoma1 (6 genomes)				Trypanosoma2 (13 genomes)			
Cluster	dir	T1%	T2%	Cluster	dir	T1%	T2%
ARF	–+	83	38	IQL	-++	54	0
DSA	-++	83	46	IQVKGLTRKR	-++++–++-	54	0
GLTR	++-+	83	8	PTN	-++	54	0
HEF	+++	83	0	DSA	-++	46	83
LXP	+-+	83	0	LQI	–+	46	0
NARKR	+-+++	83	46	NARKR	+-+++	46	83
VLM	—	83	0	VEF	-++	46	0
ASD	–+	67	15	ARF	–+	38	83
EMSV	-+-+	67	0	LXP	–+	38	17
IQVK	-+++	67	0	PXL	-++	38	0
SLS	+–	67	0	FRA	-++	31	0
ILQQI	+–++	50	0	FEV	–+	23	0
EML	-++	17	0	LSMEMYV	-+-++-+	23	0
FIQ	—	17	0	RKRTLGKVQI	+–++—-+	23	0
FIQFIQ	——	17	0	ASD	–+	15	67
ILQ	+–	17	0	LSMEMYV	-+–+-+	15	0
IQI	+++	17	0	NTP	–+	15	0
IQV	-++	17	0	ARFARF	–+–+	8	0
KGL	+++	17	0	ASDD	–++	8	0
LXP	–+	17	38	DSV	-++	8	0
QFIQ	—-	17	0	EMYV	++-+	8	0
QLI	-+-	17	0	GLTR	++-+	8	83
QVK	+++	17	0	IQQLI	–++-	8	0
RHLP	++++	17	0	IQVKGLTR	-++++–+	8	0
SLS	++-	17	0	LSM	-+-	8	0
				LSMEMSMYV	-+-++-+-+	8	0
				MEM	–+	8	0
				MEMSL	–+-+	8	0
				MMAP	—-	8	0
				NARK	+-++	8	0
				PTYN	-+-+	8	0
				RKKK	+–+	8	0
				RKR	—	8	0
				RKRAN	—+-	8	0
				RKRRA	—-+	8	0
				RKRTLGKVQ	+–++—-	8	0
				VYMEMSL	-+–+-+	8	0
				VYMEMSL	-+-++-+	8	0
				WWNN	—-	8	0

Table 6: Sets of clusters with potential variations (duplication,deletion,inversion). There are three genome classes T, L and O which refer to Trypanosoma, Leishmania and Other genomes in order.

clusters	set	Genomeclass	Tdirs	Ldirs	Odirs
GEE	0	L		-++	
LAA	0	L		+-+-	
MEM	0	L		++++	
PKP	0	L		−++	
RKKK	0	L		-+−	
YTY	0	L		+−++	
III	0	LT	−+	−+	
LSSS	0	O			+++
QLQ	0	O			−+-+
WWNN	0	O			−++-+
KKN	0	OL		+−+	+−+
YTTT	0	OL		−++	−++
MRR	0	OLT	-++	-++	-++
ARR	0	T	−+		
DEDE	0	T	−+−+		
GAA	0	T	-+++		
IQI	0	T	−++		
NWW	0	T	-++		
RKR	0	T	-++		
RRA	0	T	-+-+		
SLS	0	T	++-+		
YTTY	0	T	−+		
ARF	1	T	—		
ARFARF	1	T	——		
FRA	1	T	-++		
ENKRRA	2	L		−+	
NARK	2	L		+−	
NARKR	2	L		-+−++	
RKRAN	2	L		+−+|++-+	
RKRRA	2	L		+−+++	
RRAE	2	L		+-+	
ARKR	2	O			+−
EARR	2	O			—
RKAREN	2	T	++-+		
ASDD	3	L		−+	
DSA	3	O			−+
ASD	3	T	+++		
CLXP	4	L		-++-	
LXC	4	T	+−		
LXP	4	T	+−++		
LXPXP	4	T	+++		
PXL	4	T	-++		
PXLC	4	T	−++		
DNE	5	T	−++-		
DRTY	6	T	-++		
YTRD	6	T	-+++		
DSV	7	T	-++++−+		
HEF	9	L		+——+-+	
VEF	9	L		+——++-+	
EFHV	9	O			−++++-+-
FEV	9	O			+−
VHEF	9	OL		+——++-+	+—+-+-++
VHFE	9	OL		+−	+−
EFFVH	9	T	-++++−++-		
VHF	9	T	+++		
EMYV	10	L		—	
LSMEMSMYV	10	L		-++	
LSMEMYV	10	L		-++	
EML	10	O			++-
EMSV	10	O			−++
VIMLS	10	O			-+—+
VLM	10	O			——
VYIMLS	10	O			−++-+
VYMEMSL	10	O			—
LSM	10	T	—+		
LSMIVY	10	T	−+		
MEMSL	10	T	-+-		
MEYSL	10	T	-+-++-+-+		
SLMIV	10	T	-+-++-+|-+−+-+		
VYIML	10	T	−+		

clusters	set	Genomeclass	Tdirs	Ldirs	Odirs
EVRH	13	LT	+-+|−+	−+	
HRE	13	O			−+-+
RVHE	13	T	−+		
FHVRH	14	T	−+-+|-++-+		
QFIQ	15	L		-++	
FIQ	15	O			——+
FIQFIQ	15	T	——		
FSI	16	T	+-++		
KLAG	17	L		++-	
LAG	17	L		−+++	
GAL	17	T	+-+++		
ILQ	18	L		-++−	
IQL	18	L		—	
IQVKGLTR	18	L		-++-	
IVQRLTKGW	18	L		-+-	
IVQRLTRWKG	18	L		++-	
RKRTLGKVQI	18	L		+++-	
IVQRLTRKGW	18	O			+++
LQI	18	O			—++-
VGWRTQI	18	O			−++
WGKRTL	18	O			-++-
ILIQ	18	OL		—++	—++
IQV	18	OL		+++	+++
ITRLQVGWR	18	OL		+−+	+−+
RQVI	18	OL		−+	−+
IVQ	18	OLT	-+-	+-+	+-+
GKWRTL	18	T	−+		
GLTR	18	T	+++		
ILQQI	18	T	+−		
IQQL	18	T	-++		
IQQLI	18	T	-+-+		
IQVK	18	T	-++		
IQVKGLTRKR	18	T	——		
KGL	18	T	+++		
KVQI	18	T	++++		
LTRKGW	18	T	+−+		
QILI	18	T	—		
QLI	18	T	—+-		
QVI	18	T	—-+		
QVK	18	T	+−++—-		
RKRTLGKVQ	18	T	+−++—-+		
GTGP	19	L		-+−+	
TGP	19	L		++-+	
PGTTG	19	O			+-+-+−
GTP	19	OL		−+	−+
PVK	19	OL		++-	+++
GTGPVK	19	T	+−|++-		
KVP	19	T	-++		
PTG	19	T	-+++		
KGN	22	L		-++-+	
NGK	22	T	—		
LTP	24	L		-+++-	
MMAP	25	OL		-+++-+	-+++-+
NTP	26	L		-+−++	
YTN	26	L		—+	
PTN	26	O			—
PTYN	26	OL		—-	—-
NPTYN	26	T	-+-++-+|-+−+-+		
NYTPN	26	T	—-		
QPL	27	L		−++	
RHLP	28	L		−+	