

**Table 17:** Orthologous tRNA gene clusters conserved within Trypanosoma clade. This table only shows clusters of length at least 3 with frequency of at least 2. Clusters with same group id are considered similar. Similarity of clusters is calculated based on Jaccard distance, and gene clusters are clustered into similar groups using Ward.D2 method.

Group ID	Cluster	Frequency
1	ARF , - - +	10
1	FRA , - + +	5
2	ASD , - - +	7
2	DSA , - + +	14
3	FEV , - - +	5
3	HEF , + + +	6
3	VEF , - + +	7
4	IQL , - + +	7
4	LQI , - - +	6
4	IQVK , - + + +	4
4	ILQQI , + - - + +	3
5	LXP , - - +	6
5	LXP , + - +	5
5	PXL , - + +	6
6	NTP , - - +	2
6	PTN , - + +	8
7	SLS , + - -	4
8	VLM , - - -	5
8	EMSV , - + - +	4
8	LSMEMYV , - + - - + - +	2
8	LSMEMYV , - + - + + - +	3
8	VYMEMSL , - + - - + - +	2
9	GLTR , + + - +	6
9	IQVKGLTRKR , - + + + + - - + + -	7
9	RKRTLGVQI , + - - + + - - - - +	3
10	NARK , + - + +	2
10	NARKR , + - + + +	11

**Table 18:** Orthologous tRNA gene clusters conserved within Leishmania clade. This table shows only clusters of length at least 3 with frequency of at least 2. Clusters with same group id are considered similar. Similarity of clusters is calculated based on Jaccard distance, and gene clusters are clustered into similar groups using Ward.D2 method.

Group ID	Cluster	Frequency
1	DSA , - + +	21
2	GAL , - - +	7
2	LAG , - + +	10
3	KGN , + - -	13
4	KVP , - - -	2
4	PVK , + + +	20
5	LXP , - - +	5
5	CLXP , + - - +	16
6	MRR , - + +	2
7	QLI , + - +	19
7	IVQRLTRKGW , + - - - - + + - +	18
8	RRA , - - +	19
8	EARR , - - + +	2
9	TGP , - - +	2
9	GTGP , + - - +	12
9	PGTTG , - + + - -	4
10	VHF , + + -	15
10	EVRH , - - + +	21
11	YTTT , - - - +	2
11	YTTY , - - + +	8
12	NPTYN , - - + + +	8
12	NYTPN , - - - + +	14
13	SLMIV , - + - - +	3
13	VIMLS , - + + - +	18

**Table 19:** Orthologous tRNA gene clusters conserved within both Leishmania and Trypanosoma clade. Clusters DSA,LXP,QLI and LXP are the only clusters conserved within both clades. However, this table shows groups of similar clusters within both clades. Note that this tables only shows clusters of length at least 3, however does not apply the frequency limits applied in table 1 and 2.

Group ID	Cluster	Frequency	Clade
1	ASD , - - +	8	L,T
1	DSA , - + +	35	L,T
2	HEF , + + +	6	T
2	VHF , + + -	15	L
3	IQL , - + +	7	T
3	LQI , - - +	6	T
3	QLI , + - +	19	L,T
3	ILQQI , + - - + +	3	T
4	LXP , - - +	11	L,T
4	LXP , + - +	5	L,T
4	PXL , - + +	6	T
4	CLXP , + - - +	16	L
5	NTP , - - +	2	T
5	PTN , - + +	8	T
5	NPTYN , - - + + +	8	L
5	NYTPN , - - - + +	14	L
6	VLM , - - -	5	T
6	SLMIV , - + - - +	3	L
6	VIMLS , - + + - +	18	L
7	IQVKGLTRKR , - + + + + - - + + -	7	T
7	IVQRLTRKGW , + - - - - + + - +	18	L
7	RKRTLGVQI , + - - + + - - - +	3	T