

Supplementary Table 1 —Similar and putatively homologous tRNA gene cluster variant groups of length at least three occurring in at least two *Leishmania* genomes.

Group	Gene Cluster Variant / Strandedness	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