

**Supplementary Table 3 — Similar and putatively homologous tRNA gene cluster variant groups of length at least three spanning both *Leishmania* (L) and *Trypanosoma* (T) genera genomes. Only groups 1, 3 and 4 contain five gene cluster variants conserved in both genera, namely, ASD, DSA, LXP (two variants), and QLI, where “X” represents the initiator iMet tRNA gene.**

Group	Gene Cluster Variant / Strandedness	Frequency	Clade
1	<b>ARF</b> / -- +	10	T
1	<b>FRA</b> / - + +	5	T
1	<b>RRA</b> / -- +	19	L
1	<b>EARR</b> / -- + +	2	L
2	<b>ASD</b> / -- +	8	L, T
2	<b>DSA</b> / - + +	35	L, T
3	<b>FEV</b> / -- +	5	T
3	<b>HEF</b> / + + +	6	T
3	<b>VEF</b> / - + +	7	T
3	<b>VHF</b> / + + -	15	L
3	<b>EVRH</b> / -- + +	21	L
4	<b>IQL</b> / - + +	7	T
4	<b>LQI</b> / -- +	6	T
4	<b>QLI</b> / + - +	19	L, T
4	<b>ILQQI</b> / + - - + +	3	T
5	<b>LXP</b> / -- +	11	L, T
5	<b>LXP</b> / + - +	5	L, T
5	<b>PXL</b> / - + +	6	T
5	<b>CLXP</b> / + - - +	16	L
6	<b>NTP</b> / -- +	2	T
6	<b>PTN</b> / - + +	8	T
6	<b>NPTYN</b> / -- + + +	8	L
6	<b>NYTPN</b> / - - - + +	14	L
7	<b>VLM</b> / ---	5	T
7	<b>SLMIV</b> / - + - - +	3	L
7	<b>VIMLS</b> / - + + - +	18	L
8	<b>GLTR</b> / + + - +	6	T
8	<b>IQVKGLTRKR</b> / - + + + - - + + -	7	T
8	<b>IVQRLTRKGW</b> / + - - - + + - +	18	L
8	<b>RKRTLGKVQI</b> / + - - + + - - - +	3	T