

**Supplementary Table 2 — Similar and putatively homologous tRNA gene cluster variant groups of length at least three occurring in at least two *Trypanosoma* genomes.**

Group	Gene Cluster Variant / Strandedness	Frequency
1	<b>ARF</b> / --- +	10
1	<b>FRA</b> / - + +	5
2	<b>ASD</b> / --- +	7
2	<b>DSA</b> / - + +	14
3	<b>FEV</b> / --- +	5
3	<b>HEF</b> / + + +	6
3	<b>VEF</b> / - + +	7
4	<b>IQL</b> / - + +	7
4	<b>LQI</b> / --- +	6
4	<b>ILQQI</b> / + --- + +	3
5	<b>LXP</b> / --- +	6
5	<b>LXP</b> / + - +	5
5	<b>PXL</b> / - + +	6
6	<b>NTP</b> / --- +	2
6	<b>PTN</b> / - + +	8
7	<b>SLS</b> / + --	4
8	<b>VLM</b> / ---	5
8	<b>EMSV</b> / - + - +	4
8	<b>LSMEMYV</b> / - + --- + - +	2
8	<b>LSMEMYV</b> / - + - + + - +	3
8	<b>VYMEMSL</b> / - + --- + - +	2
9	<b>GLTR</b> / + + - +	6
9	<b>IQVKGLTRKR</b> / - + + + --- + + -	7
9	<b>RKRTLGKVQI</b> / + - - + + ----- +	3
10	<b>IQVK</b> / - + + +	4
11	<b>NARK</b> / + - + +	2
11	<b>NARKR</b> / + - + + +	11