

Recentrifuge S3 Appendix

Other microbial taxa found with possible sources of translocation into the blood in the SMS study of plasma for ME/CFS patients [1]

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S3App-1 Table. Other microbial taxa found with different possible sources of translocation into the blood.

Phylum/Group	Taxa	Samples	Most probable source of translocation into blood
Actinobacteria	<i>Rothia dentocariosa</i>	56/Lym 70/Hea 74/Hea	The buccal microbiota [2]
	<i>Gardnerella vaginalis</i>	51/Hea 90/Hea 101/Lup	Genitourinary microbiota [3]
Firmicutes	<i>Clostridium perfringens</i>	101/Lup (excl.)	Gut microbiota [4]
ssRNA virus	<i>Pegivirus C</i>	64/Hea 93/Hea	Refers to GBV-C/HGV in the genus <i>Pegivirus</i> of persistent GB viruses [5]
Basidiomycota	<i>Rhodosporidiobolus</i>	53/Lup (excl.)	The oral mycobiota [6]

In the samples column, those listed are the most representative in relative frequency. Besides, exclusiveness is indicated in parentheses, and the specimen group is after the slash: *Hea* for healthy individuals, *CFS* for ME/CFS patients, *Lym* for those suffering ADCLS, and *Lup* for those afflicted by SLE.

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References

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