

Supporting Information

Rapid Separation of Bacteria from Primary Nasal Samples using inertial microfluidics

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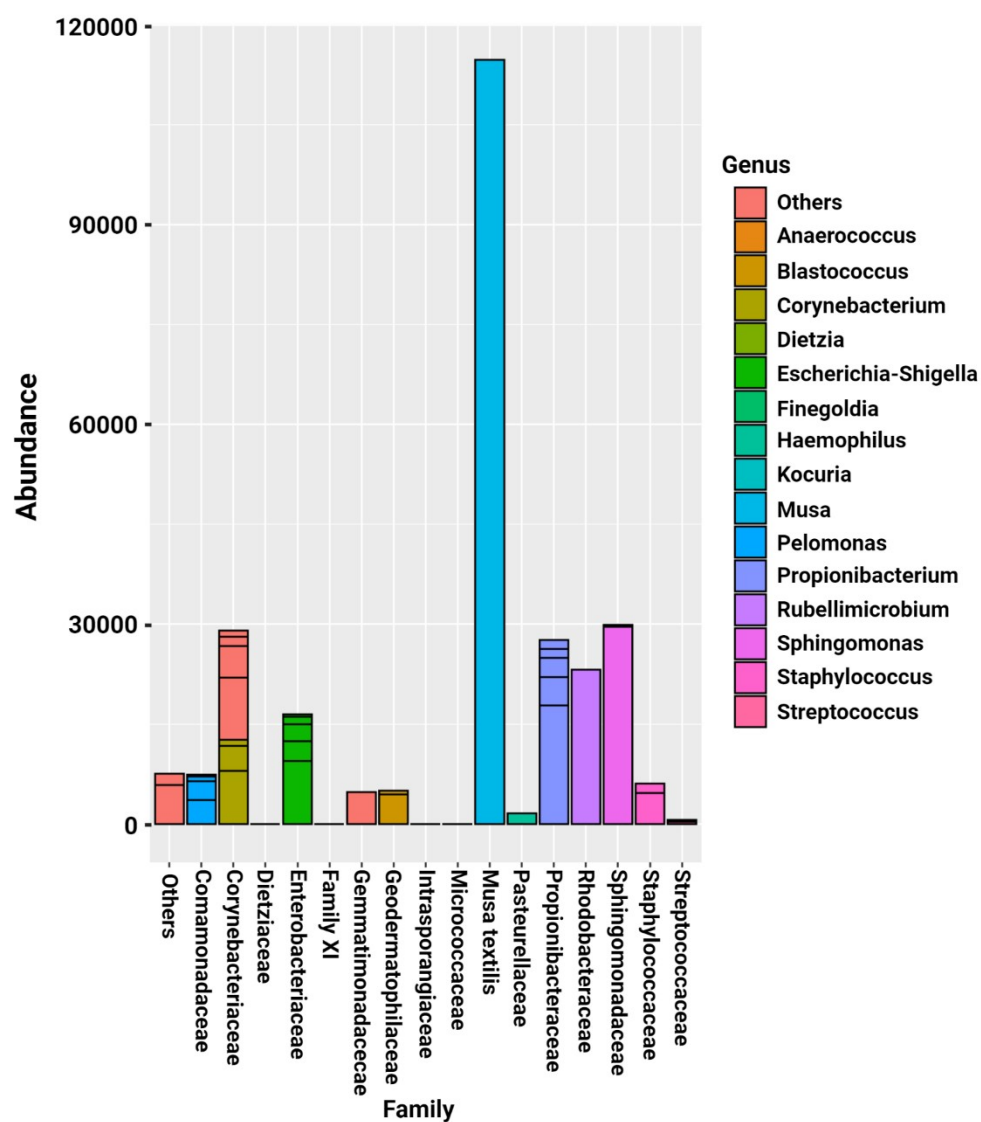


Fig. S1: Barplot of top bacterial families and genera identified in samples collected using the microfluidic zig-zag channel.

Table S1: Differential abundance of bacteria species in the samples collected using microfluidic zig-zag channels.

	Base Mean	log2Fold Change	lfcSE	Stat	P Value	P adjusted
k_Bacteria; p_Firmicutes; c_Bacilli; o_Bacillales; f_Staphylococcaceae; g_Staphylococcus; s_aureus	3119.203217	-30	3.454407	-8.6845587	3.80E-18	1.33E-16
k_Bacteria; p_Firmicutes; c_Bacilli; o_Bacillales; f_Staphylococcaceae; g_Staphylococcus; s_epidermidis	872.1555106	-28.90342201	3.4544541	-8.3670013	5.91E-17	1.03E-15
k_Bacteria; p_Firmicutes; c_Bacilli; o_Bacillales; f_Staphylococcaceae; g_Staphylococcus; s_capitis-caprae-epidermidis	2132.005435	-14.82569364	3.0884942	-4.8002983	1.58E-06	1.39E-05
k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Corynebacteriales; f_Corynebacteriaceae; g_Corynebacterium; s_accolens-macginleyi	2126.178462	-14.82219769	3.07293	-4.8234739	1.41E-06	1.39E-05
k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Family XI; g_Anaerococcus; s_octavius	466.7432513	-12.62603181	3.4404494	-3.6698786	0.0002427	0.00169866
k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Corynebacteriales; f_Corynebacteriaceae; g_Corynebacterium; s_mucifaciens-ureicelerivorans	281.9496935	-11.898965	3.4405299	-3.4584687	0.0005433	0.00316899
k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Streptococcaceae; g_Streptococcus; s_infantis-sanguinis	164.7195316	-11.12320495	3.4406745	-3.2328559	0.0012256	0.00546752
k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Bradyrhizobiaceae; g_Bradyrhizobium; s_sp43375	162.4852768	-11.10404423	3.4406792	-3.2272827	0.0012497	0.00546752
k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Micrococcales; f_Micrococcaceae; g_Rothia; s_dentocariosa	146.9777554	-10.95896401	3.4407164	-3.185082	0.0014471	0.00562773
k_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhodobacterales; f_Rhodobacteraceae; g_Paracoccus-Paracoccus; s_huijuniae-sp44862	95.4970958	-10.33697666	3.4409264	-3.0041261	0.0026634	0.00932207

Table S2: Relative abundance of bacterial species in the samples collected using microfluidic zig-zag channels.

	Microfluidic Zig-zag				
	1	2	3	4	5
k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Propionibacteriales; f_Propionibacteriaceae; g_Propionibacterium; s_acnes	0.100692	0.480077	0.368008	0.352739	0.224201
k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Pasteurellales; f_Pasteurellaceae; g_Haemophilus; s_parainfluenzae	0	0.183382	0	0	0
k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Corynebacteriales; f_Corynebacteriaceae; g_Corynebacterium; s_pseudogenitalium-tuberculostrictum	0.256385	0	0	0.252183	0
k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae; g_Escherichia-Shigella; s_coli	0.091615	0.335182	0.197534	0.078063	0.19309
k_Bacteria; p_Proteobacteria; c_Betaproteobacteria; o_Burkholderiales; f_Comamonadaceae; g_Pelomonas; s_saccharophila	0.051231	0	0.074308	0.088383	0.218545
k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Corynebacteriales; f_Corynebacteriaceae; g_Corynebacterium; s_accolens	0.031615	0.001358	0.166231	0	0
k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Corynebacteriales; f_Corynebacteriaceae; g_ ; s_sp5276	0.110846	0	0.193919	0.228632	0.364165
k_Bacteria; p_Firmicutes; c_Bacilli; o_Bacillales; f_Staphylococcaceae; g_Staphylococcus; s_caprae-epidermidis	0.357615	0	0	0	0

Supplementary Video 1: Distribution of epithelial cells and cellular debris present in the human nasopharyngeal swab samples at 150 $\mu\text{l}/\text{min}$ flow rate in the zig-zag channel.