

Table S1. Operative taxonomic units (OTUs) assigned to *Haemophilus*, *Pseudomonas*, *Staphylococcus*, *Streptococcus* and *Aspergillus* identified to the species level. Data presented in total read count and relative abundance among the genus.

	Reads count	(%)
<i>Haemophilus</i>	482,366	100
<i>H. influenzae</i>	416,443	86.3
<i>Haemophilus</i> sp.	65,923	13.6
<i>Pseudomonas</i>	185,542	100
<i>P. aeruginosa</i>	106,977	57.7
<i>P. mosselii</i>	43,574	23.4
<i>P. migulae</i>	29,039	15.6
<i>P. synxantha</i>	3,206	1.7
<i>Pseudomonas</i> sp.	2,746	1.7
<i>Staphylococcus</i>	202,784	100
<i>S. aureus</i>	186,534	91.9
<i>S. lugdunensis</i>	6,994	3.4
<i>S. carnosus</i>	4,860	2.4
<i>S. epidermidis</i>	4,229	2.1
<i>S. caprae</i>	175	0.08
<i>S. saprophyticus</i>	27	<0,01
<i>Staphylococcus</i> sp.	15	<0,01
<i>Streptococcus</i>	69,020	100
<i>S. intermedius</i>	36,994	53.6
<i>S. pneumoniae</i>	17,766	25.7
<i>S. constellatus</i>	14,144	20.5
<i>S. sanguinis</i>	60	0.1
<i>S. dysgalactiae</i>	46	0.1
<i>Streptococcus</i> sp.	10	<0.01
<i>Aspergillus</i>	1,075,193	100
<i>Aspergillus</i> section <i>Fumigati</i>	868,848	80.8
<i>Aspergillus</i> section <i>Flavi</i>	165,693	15.4
<i>Aspergillus</i> section <i>Nidulantes</i>	40,365	3.7
<i>Aspergillus</i> sp.	287	0.03

Figure S1. Fungal richness and diversity calculated based on ITS1 and ITS2. Alpha, inverse Simpson, Shannon and Simpson are displayed.

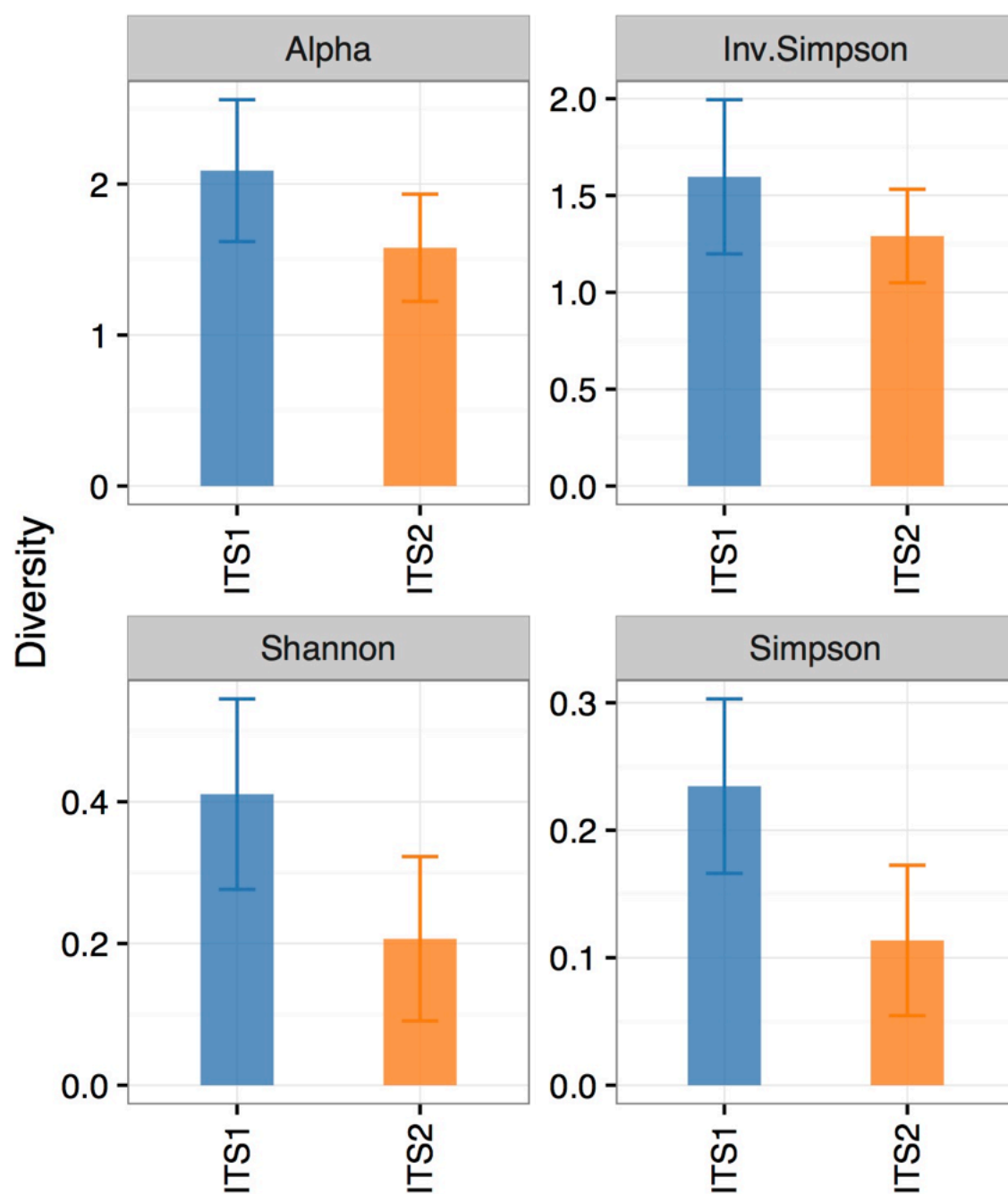
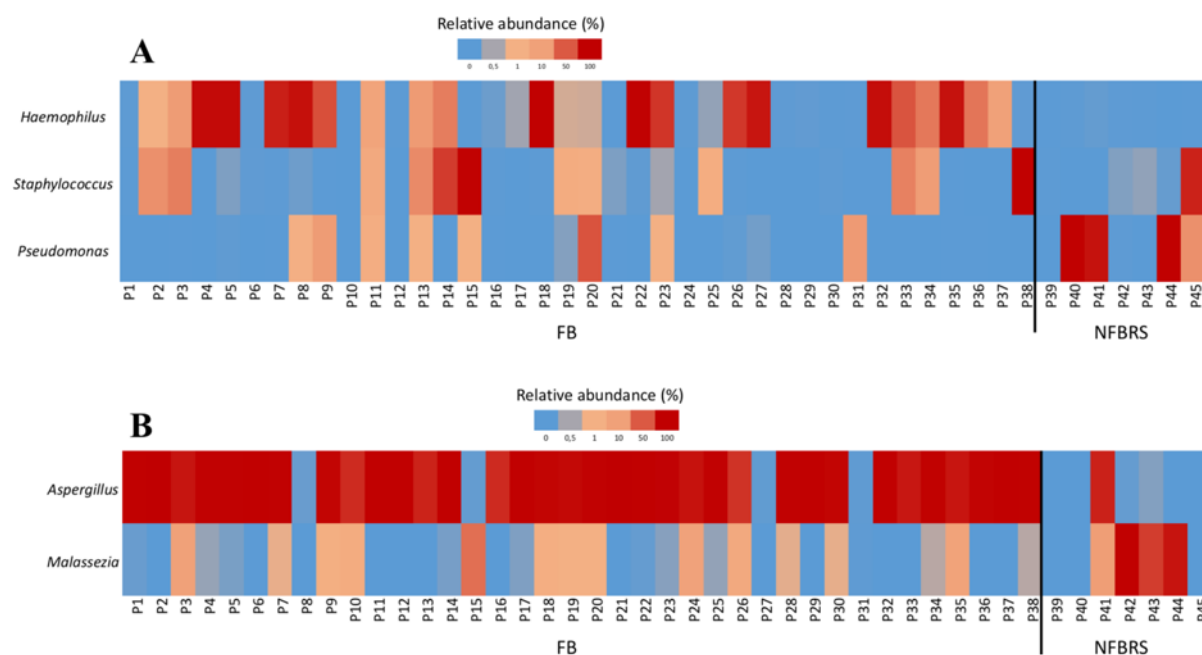


Figure S2: Heatmap of the relative abundance of major* (A) bacterial and (B) fungal taxa among the 45 samples analysed through 16S and ITS2 targeted metagenomic analysis respectively.



*major bacterial and fungal taxa were considered if taxa was >1% relative abundance in >25% samples. FB: fungal balls; NFBRs: Non-fungal ball rhinosinusitis

Figure S3. Bacterial diversity represented in number of reads and relative abundance for all taxa found

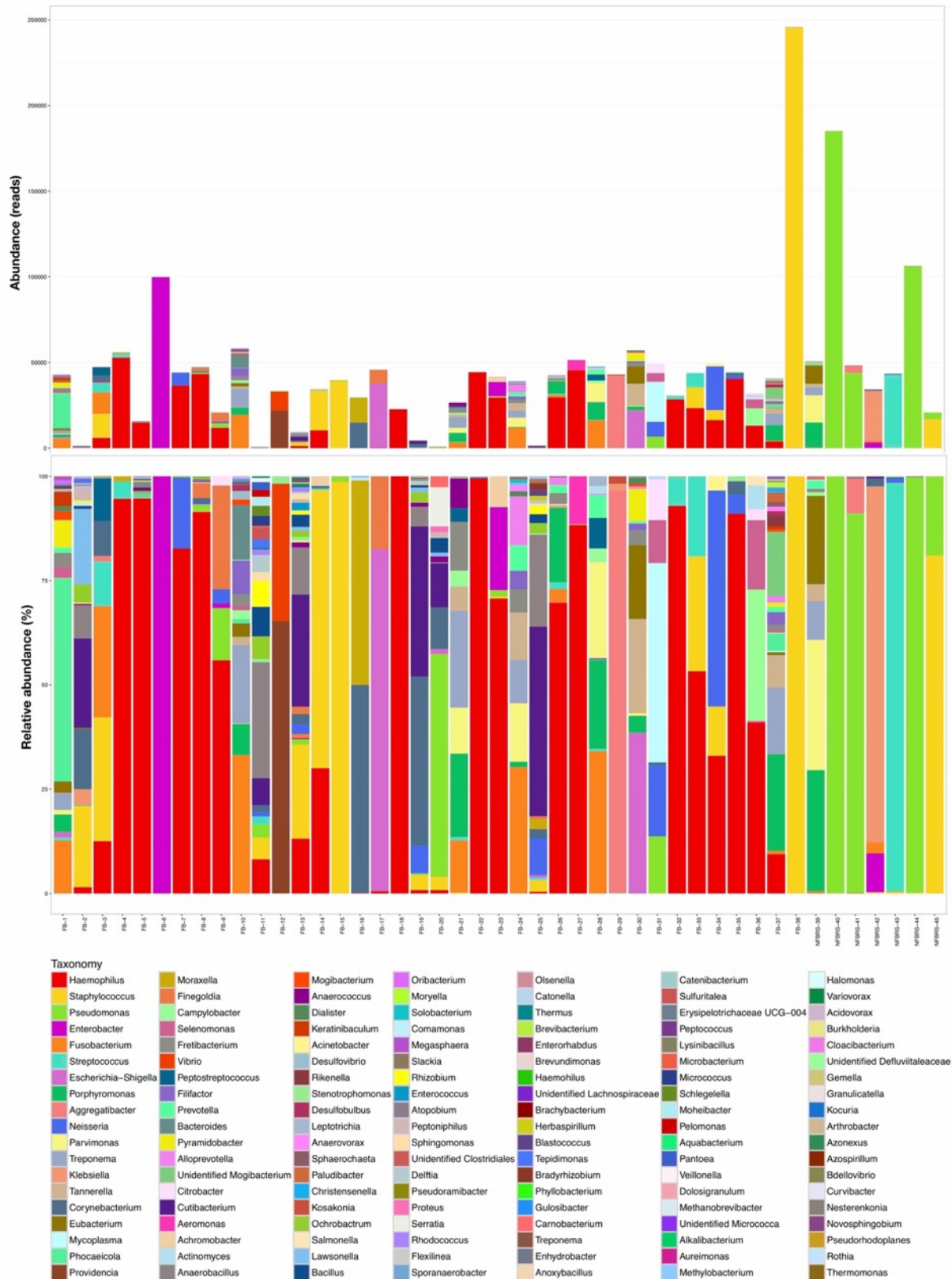


Figure S4. Fungal diversity represented in number of reads and relative abundance for all taxa found

