

Table 01: 16S amplicon reads per sample after every processing step.

Sample_ID	Demultiplexing	Merging	EE-filtering	Chimeras-Artifacts	Abundance filter
BDA Live 1	64376	46687	46634	30716	30443
BDA Live 2	63579	46281	46218	30113	29844
BDA Live 3	57014	42030	41975	27392	27150
NDALive 1	72804	56017	55944	36934	36649
NDALive 2	68344	52509	52451	34763	34517
NDALive 3	63472	49072	49021	32174	31906
BDA hi 1	55485	40808	40738	29456	29290
BDA hi 2	52441	38148	38084	27140	26990
BDA hi 3	56359	39652	39591	28021	27887
NDA hi 1	96259	74127	74057	48938	48529
NDA hi 2	61878	48036	47978	31537	31277
NDA hi 3	74659	55777	55707	35424	35074
BDA hi DNA 1	58365	43084	43016	33607	33431
BDA hi DNA 2	56786	41644	41567	30612	30446
BDA hi DNA 3	64375	46433	46349	33894	33686
NDAhi DNA 1	48276	37684	37643	25205	25024
NDAhi DNA 2	80056	60811	60744	39656	39337
NDAhi DNA 3	73894	55466	55397	36179	35902

Table 02: Metagenomics reads per sample after every processing step.

Sample_ID	DNA ng/μl	Raw Reads	Adapter removal	Quality filtering	human reads	non-human reads
BDA 1	0.61	8445993	8147200	7282731	3607	7279124
BDA 2	1.98	2168592	2144669	2032292	316	2031976
BDA3	2.5	480960	474169	444292	2635	441639
BDA control	0	810	666	536	145	391
NDA 1	5.4	3257170	3164944	2837747	741	2837006
NDA 2	6.9	1864545	1796326	1590207	1393	1588814
NDA 3	6.8	719178	693425	670545	725	669793
NDA control	0	11374	5749	4345	1903	2442
BDA PBMC 1	2.54	5908301	5838956	5470908	23015	5447893
BDA PBMC 2	2.56	9703454	9519374	8787552	22296	8765256
BDA PBMC 3	2.72	24951792	24489770	22659487	100043	22559444
BDA control	0	810	666	536	145	391
NDA PBMC 1	22.2	4423878	4338383	4251904	3419946	831958
NDA PBMC 2	27.2	9494653	9237603	8150548	6571662	156886
NDA PBMC 3	29.2	3266623	3170090	2726353	2224846	501507
NDA control	0	11374	5749	4345	1903	2442

Table 03: Metagenomics based taxa relative abundances

	BDA1	BDA2	BDA3	NDA1	NDA2	NDA3
<i>C. pseudodiphtheriticum</i>	1.11	0.92	0.66	0.20	0.19	0.09
<i>C. striatum</i>	6.27	6.63	7.50	1.17	1.04	2.10
<i>M. luteus</i>	1.33	1.44	1.45	0.66	0.28	0.82
<i>B. horneckiae</i>	2.46	2.55	2.61	3.86	3.93	5.08
<i>B. simplex</i>	0.02	0.00	0.00	0.57	0.48	0.19
<i>S. aureus</i>	19.96	25.40	29.91	11.63	14.72	17.85
<i>S. epidermidis</i>	8.12	10.78	13.60	6.00	7.87	9.98
<i>S. hominis</i>	1.46	1.84	2.14	0.87	0.78	1.00
<i>E. coli</i>	47.09	49.88	37.64	14.19	14.71	17.48
<i>P. mirabilis</i>	11.87	0.43	4.50	54.15	51.57	38.85
<i>P. aeruginosa</i>	0.01	0.00	0.00	7.22	4.97	7.14

Table 04: Metagenomics based taxa relative abundances in sampled containing PBMCs

	BDA1- PBMCs	BDA2- PBMCs	BDA3- PBMCs	NDA1- PBMCs	NDA2- PBMCs	NDA3- PBMCs
<i>C. pseudodiphtheriticum</i>	1.04	1.21	1.18	0.30	0.50	0.24
<i>C. striatum</i>	6.31	5.54	6.49	2.37	2.56	2.55
<i>M. luteus</i>	2.80	2.91	2.56	0.75	0.81	0.73
<i>B. horneckiae</i>	1.75	2.07	2.10	5.72	5.76	5.14
<i>B. simplex</i>	0.00	0.00	0.00	0.69	0.73	0.76
<i>S. aureus</i>	25.01	25.72	25.87	13.84	13.26	13.39
<i>S. epidermidis</i>	9.24	10.08	10.15	6.70	7.46	9.56
<i>S. hominis</i>	1.48	1.71	1.86	0.73	0.62	1.22
<i>E. coli</i>	48.86	50.38	45.69	21.72	21.30	20.79
<i>P. mirabilis</i>	2.61	0.05	3.50	38.56	38.46	37.97
<i>P. aeruginosa</i>	0.70	0.24	0.41	8.41	8.57	7.43