Sex dependent effects of silver nanoparticles on the zebrafish gut microbiota

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Code	Trimed tags	Bases(bp)	Average Length (bp)
FC_1	39088	17043335	436.02
FC_2	21176	9234447	436.08
FC_3	22663	9916591	437.57
FC_4	23529	10221120	434.41
FC_5	35221	15423175	437.9
FH_1	23543	10423293	442.73
FH_2	21091	9294101	440.67
FH_3	27345	12032529	440.03
FH_4	36459	16047935	440.16
FH_5	32077	13963100	435.3
FL_1	29034	12675211	436.56
FL_2	22048	9556084	433.42
FL_3	23210	10039753	432.56
FL_4	33735	14658125	434.51
FL_5	33827	14697908	434.5
FM_1	24775	10867228	438.64
FM_2	30127	13182571	437.57
FM_3	32760	14249387	434.96
FM_4	23029	10051664	436.48
FM_5	37092	16195437	436.63
MC_1	29050	12665018	435.97
MC_2	29096	12833999	441.09
MC_3	29838	13157284	440.96
MC_4	31837	14149109	444.42
MC_5	21700	9531192	439.23
MH_1	31950	13916232	435.56
MH_2	31988	13915580	435.03
MH_3	28483	12458727	437.41
MH_4	31423	13603986	432.93
MH_5	23826	10431807	437.83
ML_1	29501	12969933	439.64
ML_2	28159	12339894	438.22
ML_3	27539	12110961	439.77
ML_4	35190	15437575	438.69
ML_5	38715	17060275	440.66
MM_1	36276	15966317	440.13
MM_2	33847	14882160	439.69
MM_3	27016	11764965	435.48
MM_4	26615	11577701	435.01
MM 5	27970	12198931	436.14

Table S1 MiSeq sequences quality information

Trimmed tags number: the numbers of reads remaining after the removal of primers and low-quality data

			0103	clusicis			
Sample ID	Reads	ΟΤυ	ace	chao	coverage	shannon	simpson
MC 1	27310	276	321	321	0.997876	3.04	0.096
MC ²	26038	266	274	276	0.999232	3.25	0.1368
MC_3	27584	219	224	227	0.999637	3.98	0.0432
MC ⁴	30439	189	195	200	0.999606	2.31	0.3397
MC_5	20649	201	382	315	0.996319	2.91	0.0955
Average	26404	230	279	268	0.998534	3.10	0.1422
SD	3597	39	75	53	0.001431	0.60	0.1153
ML_1	27991	242	271	280	0.998464	2.01	0.3054
ML_2	27132	143	201	194	0.998268	2.01	0.2548
ML_3	25927	167	214	200	0.998264	1.99	0.2563
ML_4	34157	194	235	233	0.998595	2.11	0.2377
ML_5	36516	216	278	273	0.998302	1.81	0.312
Average	30345	192	240	236	0.998379	1.99	0.2732
SD	4690	39	34	40	0.000146	0.11	0.0333
MM_1	34983	232	257	267	0.998942	2.73	0.1496
MM_2	32870	136	171	173	0.998844	1.78	0.2979
MM ₃	26037	231	275	273	0.997888	2.42	0.2405
MM_4	25717	137	285	220	0.997861	1.71	0.3693
MM_5	27173	185	231	226	0.998123	1.86	0.3517
Average	29356	184	244	232	0.998332	2.1	0.2818
SD	4273	48	46	41	0.000524	0.45	0.0894
MH 1	30765	122	164	154	0.998765	1.57	0.3898
MH_2	30541	170	269	230	0.998265	2.06	0.2643
MH_3	27428	136	184	176	0.998323	1.4	0.3807
MH_4	30379	108	239	167	0.998552	1.22	0.5137
MH_5	23178	95	228	141	0.998274	1.31	0.4079
Average	28458	126	217	174	0.998436	1.51	0.3912
SD	3252	29	42	34	0.000218	0.33	0.0887
FC_1	37494	133	180	167	0.998826	1.51	0.4046
FC_2	20662	137	187	168	0.997919	1.53	0.3974
FC_3	21581	134	255	211	0.997405	1.59	0.3501
FC_4	22541	109	158	159	0.998048	1.32	0.5052
FC_5	33092	238	270	273	0.99864	2.92	0.0965
Average	27074	150	210	196	0.998168	1.78	0.35076
SD	7691	50	49	48	0.000573	0.30	0.1530
FL_1	25512	328	338	341	0.999059	4.02	0.0632
FL_2	21031	72	138	136	0.998193	0.99	0.5836
FL_3	22229	67	98	94	0.998785	0.84	0.637
FL_4	32481	137	212	230	0.998153	1.12	0.5089
FL_5	31657	107	244	181	0.998547	1.31	0.4563

Table S2 Miseq sequences data statistics summary and bacterial diversity based on 97 % OTUs clusters

Average	26582	142	206	196	0.998547	1.7	0.4498
SD	5279	108	94	95	0.000387	1.37	0.2269
FM_1	22951	61	149	137	0.99878	1.23	0.3993
FM_2	28845	128	181	170	0.998267	1.4	0.3761
FM_3	31771	186	235	223	0.998332	1.57	0.4265
FM_4	22246	154	199	185	0.997977	1.51	0.3912
FM_5	35592	261	296	300	0.998651	2.13	0.3018
Average	28281	158	212	203	0.998401	1.57	0.3790
SD	5718	74	56	62	0.00032	0.34	0.0469
FH_1	22772	156	210	212	0.997804	2.29	0.1548
FH_2	19862	93	214	145	0.997986	1.53	0.2948
FH_3	26365	116	176	165	0.998179	1.5	0.3079
FH_4	34990	144	203	195	0.998457	1.34	0.3504
FH_5	30910	221	264	263	0.998285	2.16	0.2376
Average	26980	146	213	196	0.998142	1.76	0.2691
SD	6090	49	32	46	0.000255	0.43	0.0756



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Figure S2 Shannon rarefaction curve of sequences (97% similarity level).



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