

Table S3. Summary of metagenomic data sets.

	Chow (n = 3)	HFD (n = 4)	HFD+FTE (n = 4)
Raw reads	82.36 ± 2.86 M	76.97 ± 7.89 M	84.06 ± 14.57 M
High quality reads	81.89 ± 2.75 M	76.53 ± 7.85 M	83.62 ± 14.49 M
Host DNAs	13.53 ± 10.03%	16.37 ± 14.69%	11.15 ± 7.07%
Reads mapped back contigs	0.53 ± 0.17 M	0.53 ± 0.32 M	0.43 ± 0.08 M