SUPPLEMENTARY FIGURES AND TABLES.

Table S1. LimpiAL 2.5% topical cream formula.

Ingredients	Concentration (%)
water	64.05 %
hydrated HAc-40 (85-86% water, 14-15% hyaluronic acid, i.e. HA, conjugated with <1% of bacterial cell wall fragment, i.e. c-40)	17.85 %
caprylic/capric triglyceride	3 %
Chamomilla recutita flower oil extract	3 %
Helichrysum italicum glyceric extract	3 %
Sepilife™ nude	2.75 %
Fluidifeel™ easy	2 %
ammonium lactate	1 %
glycerin	1 %
glyceryl caprylate	0.80 %
butyrospermum parkii butter	0.50 %
decylene glycol	0.40 %
tocopheryl acetate	0.30 %
sodium hydroxide	0.25 %
zinc gluconate	0.10 %

Table S2. Statistical comparison between the sequencing outputs of NGS Illumina MiSeq. In the first column are reported the statistical significance values (p-values) obtained comparing the reads number of the indicated comparisons. In the second column are reported the statistical significance values (p-values) regarding the number of OTUs and calculated through the ANOVA test.

Comparison	**Reads** *Kolmogorov-Smirnov test (p-value)*	**OTUs** *ANOVA (p-value)*
T0 *vs* **CTRL**	0.36	0.32
T1 *vs* **CTRL**	0.74	0.34
T1 *vs* **T0**	0.40	0.90

Table S3. Statistical comparison of the alpha diversity indexes between the indicated comparisons and taxonomic levels. The blue values indicate the comparison was performed through the Kolmogorov-Smirnov test (p ≤0.05). The black ones were calculated using the Whelch's t-test (p ≤0.05).

	OTUs number			**Chao1**			**Shannon**		
Taxon	T0 *vs* CTRL	T1 *vs* CTRL	T1 *vs* T0	T0 *vs* CTRL	T1 *vs* CTRL	T1 *vs* T0	T0 *vs* CTRL	T1 *vs* CTRL	T1 *vs* T0
Phylum	0.097	0.147	0.345	0.945	0.100	0.099	0.452	0.426	0.603
Class	0.107	0.330	0.512	0.646	0.816	0.400	0.358	0.361	0.250
Order	0.086	0.368	0.726	0.591	0.982	0.811	0.358	0.127	0.537
Family	0.132	0.346	0.863	0.137	0.063	0.759	0.358	0.127	0.250
Genus	0.081	0.279	0.795	0.054	0.352	0.889	0.591	0.444	0.933
Species	0.089	0.324	0.785	0.093	0.314	0.715	0.078	0.244	0.533

Table S4. Taxa differentially modulated in the indicated compared microbiotas (DESeq2, p-value and FDR ≤ 0.05)

Comparison	Modulated taxon	OTUs ID	logFC	p-value	FDR	logFC.std
T0 *vs* CTR	Class	*Bacteroidetes;Cytophagia*	-3.0623	0.0002	0.0255	-3.4926
T1 *vs* CTR	Phylum	*Firmicutes*	2.6131	0.0013	0.0465	-1.2585
	Class	*Firmicutes;Bacilli*	2.6078	0.0004	0.0377	2.1609
	Order	*Firmicutes;Bacilli;Bacillales*	3.7885	4.34E-05	0.0054	2.6236
	Order	*Tenericutes;Mollicutes;Mycoplasmatales*	5.8157	9.03E-05	0.0075	4.8276
	Order	*Actinobacteria;Actinobacteria;Actinomycetales*	3.5652	0.0003	0.0208	3.2728

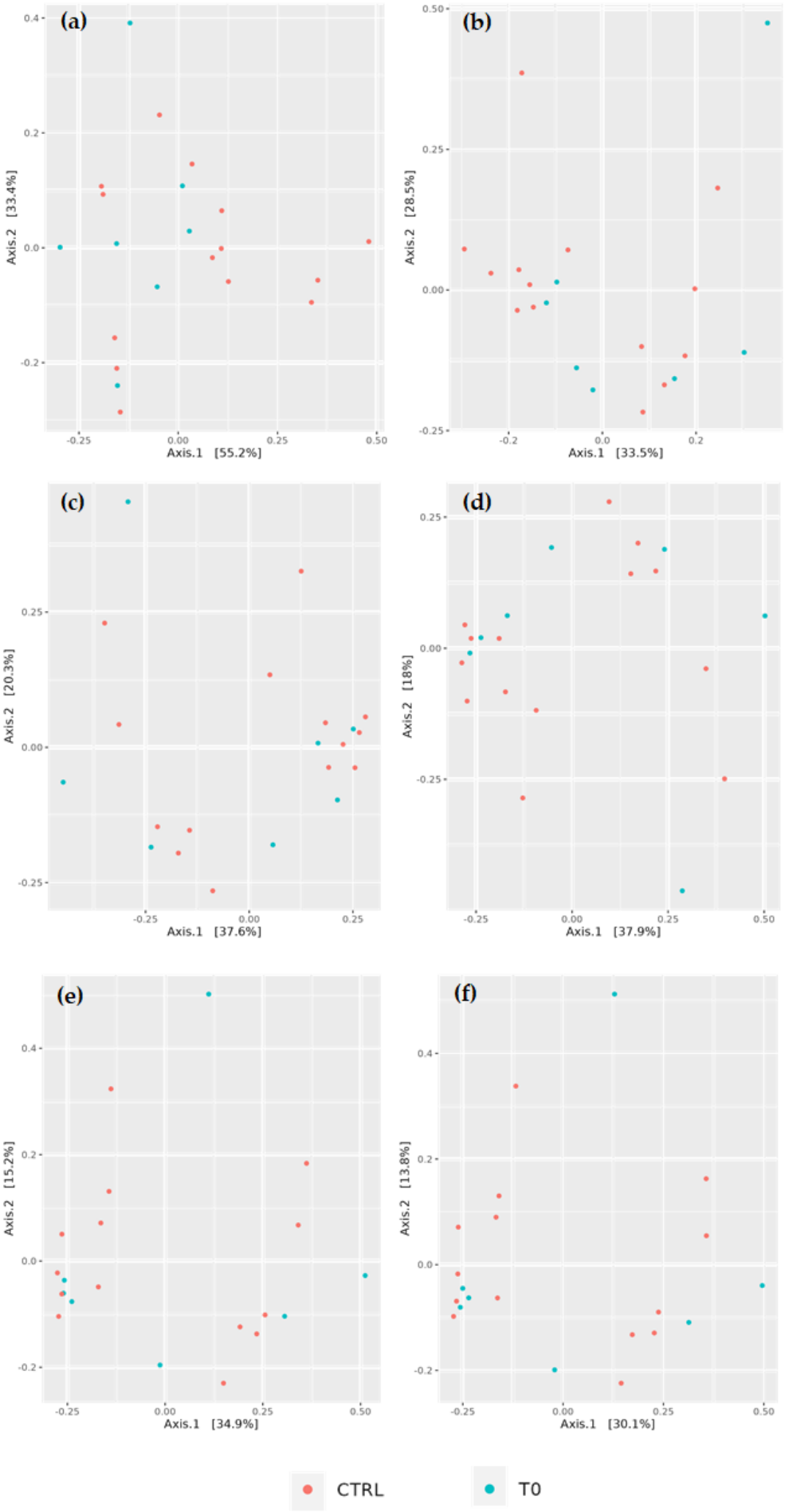

Figure S1. PCoA of Bray-Curtis distances between the T0 and CTRL samples at phylum (a), class (b), order (c), family (d), genus (e) and species (f) level.

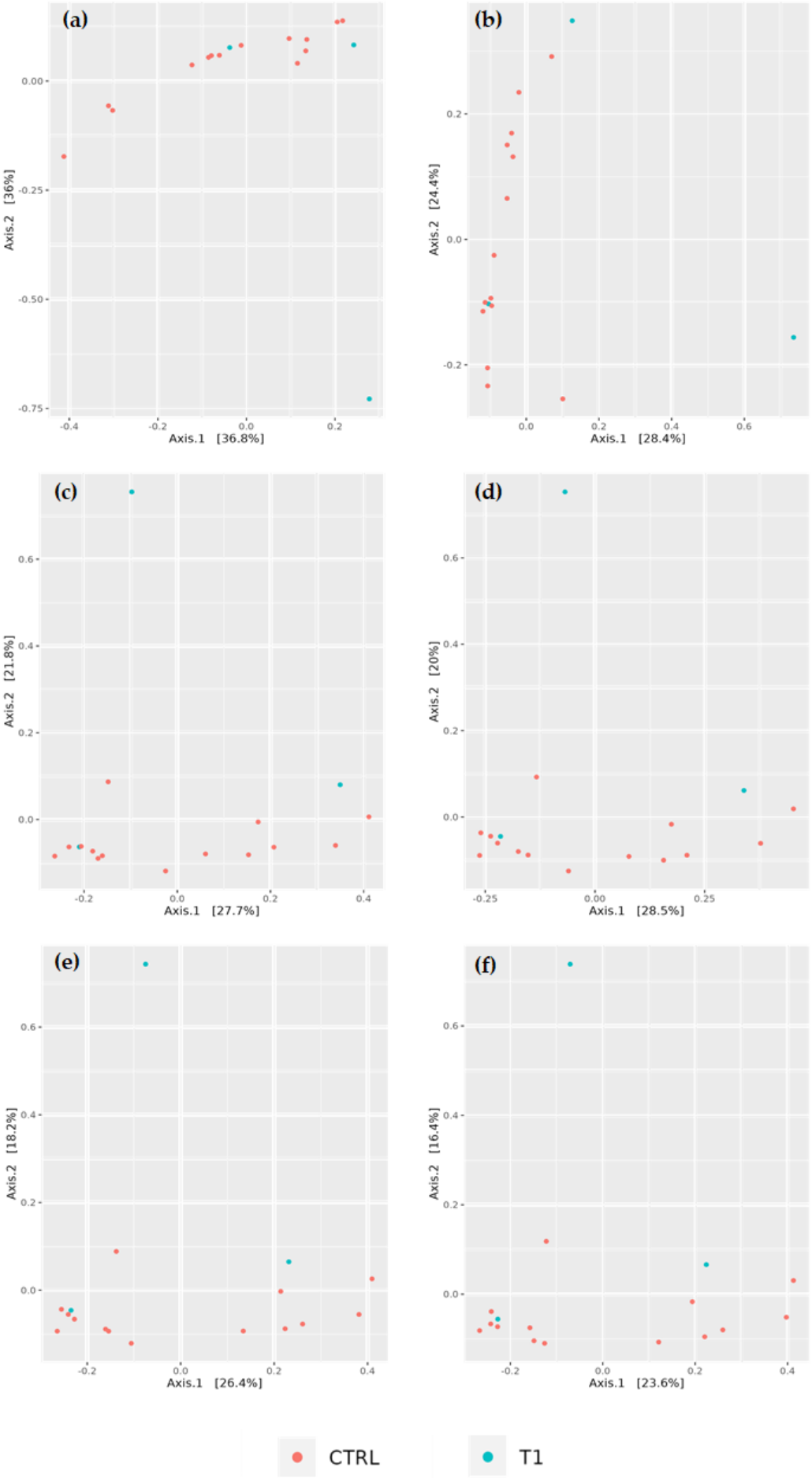

Figure S2. PCoA of Bray-Curtis distances between the T1 and CTRL samples at phylum (a), class (b), order (c), family (d), genus (e) and species (f) level.

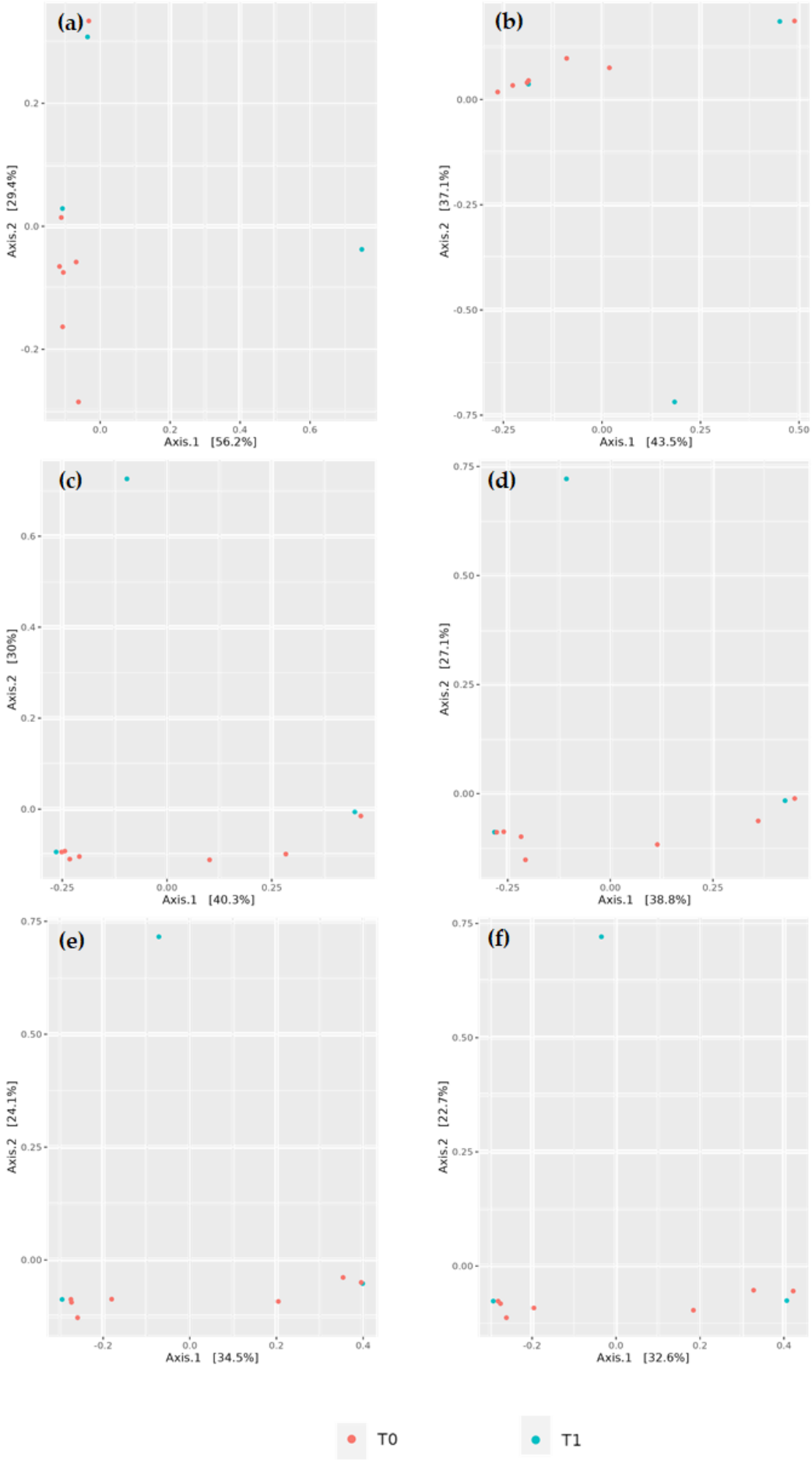

Figure S3. PCoA of Bray-Curtis distances between the T1 and T0 samples at phylum (a), class (b), order (c), family (d), genus (e) and species (f) level.

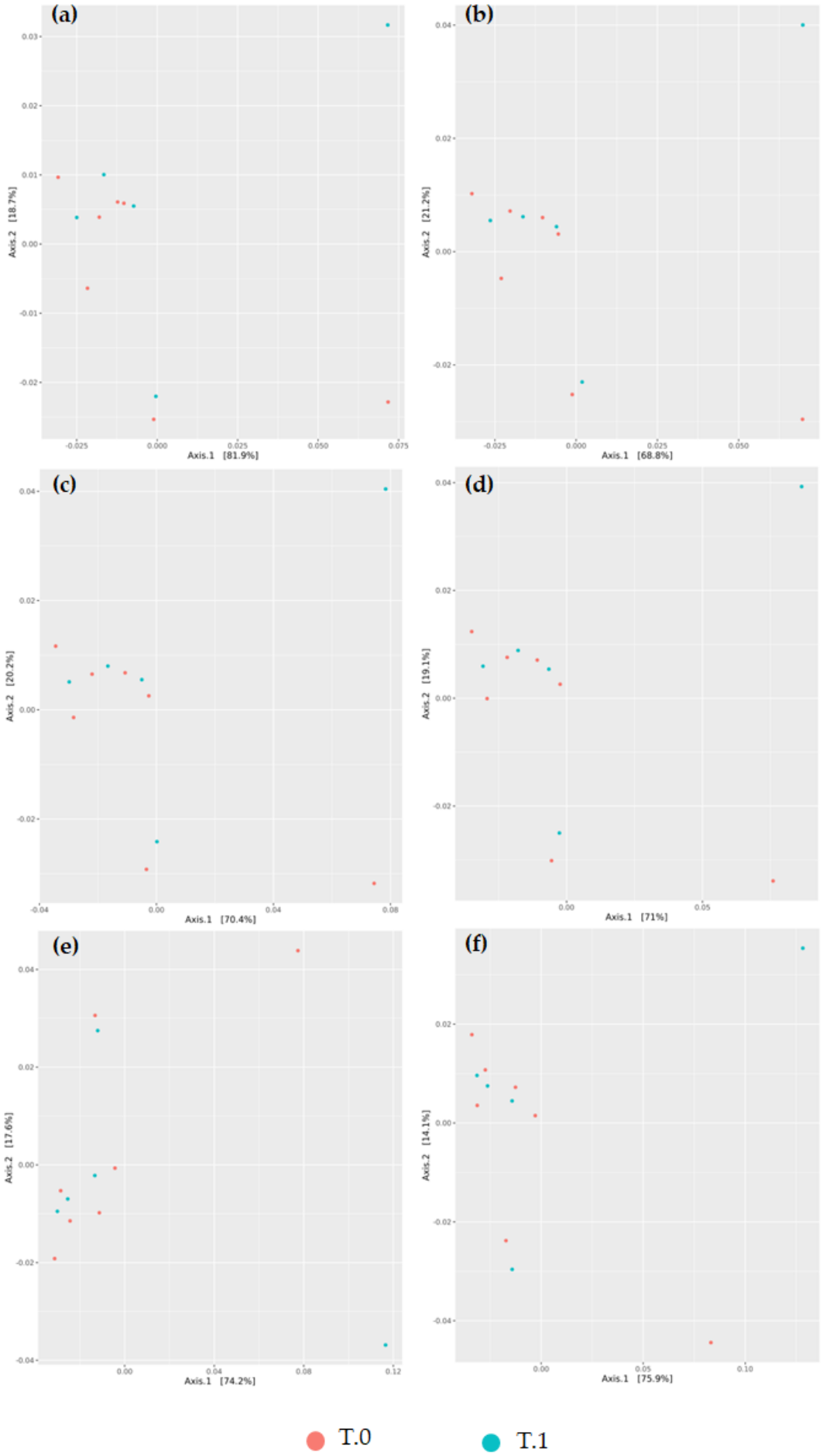

Figure S4. PCoA of Bray-Curtis distances between the T.1 and T.0 samples at phylum (a), class (b), order (c), family (d), genus (e) and species (f) level.