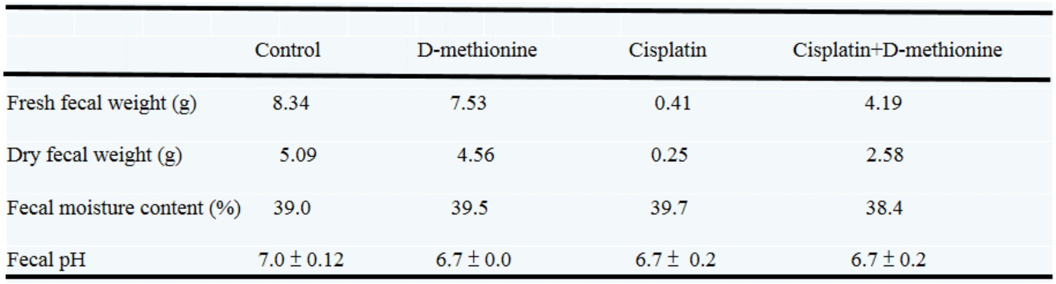
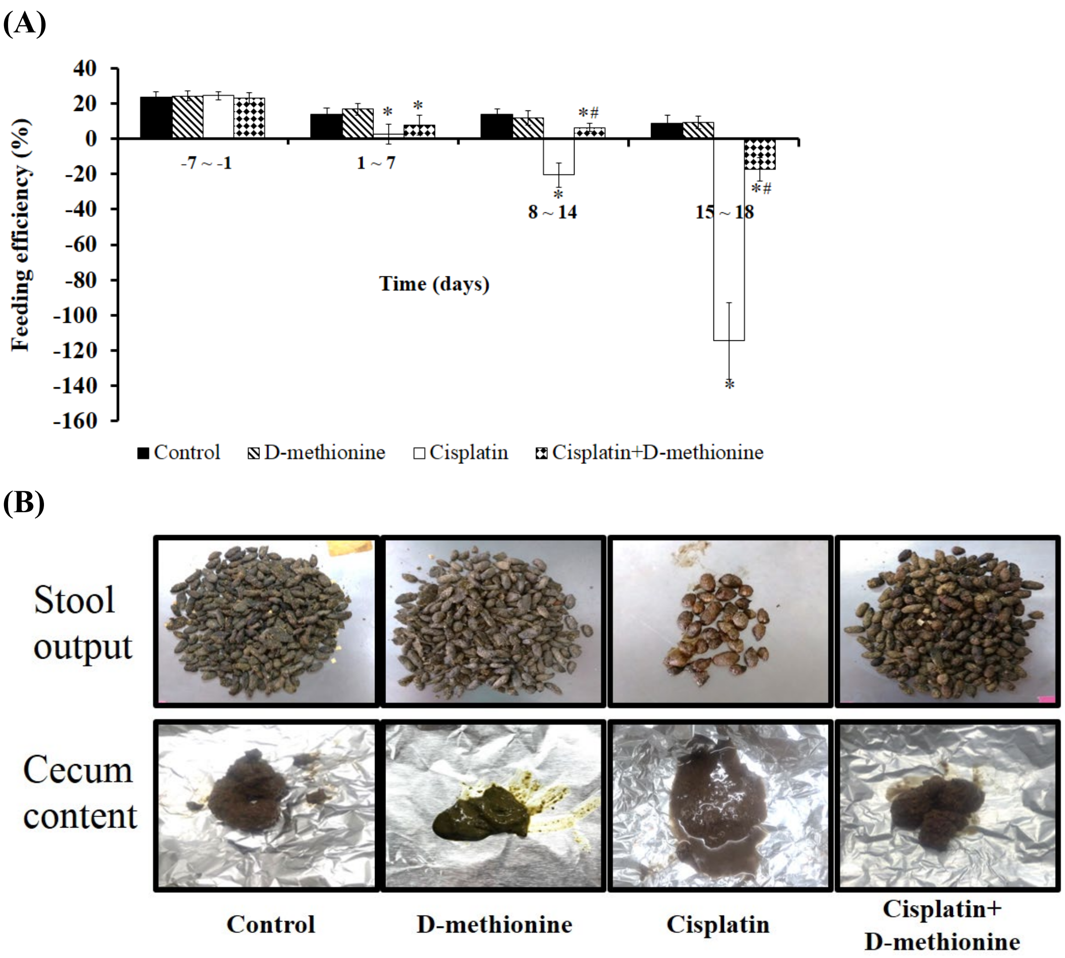
Supplementary results

Supplementary Table 1. Fecal moisture content, dry weight, fecal pH and stool appearance in experimental rats

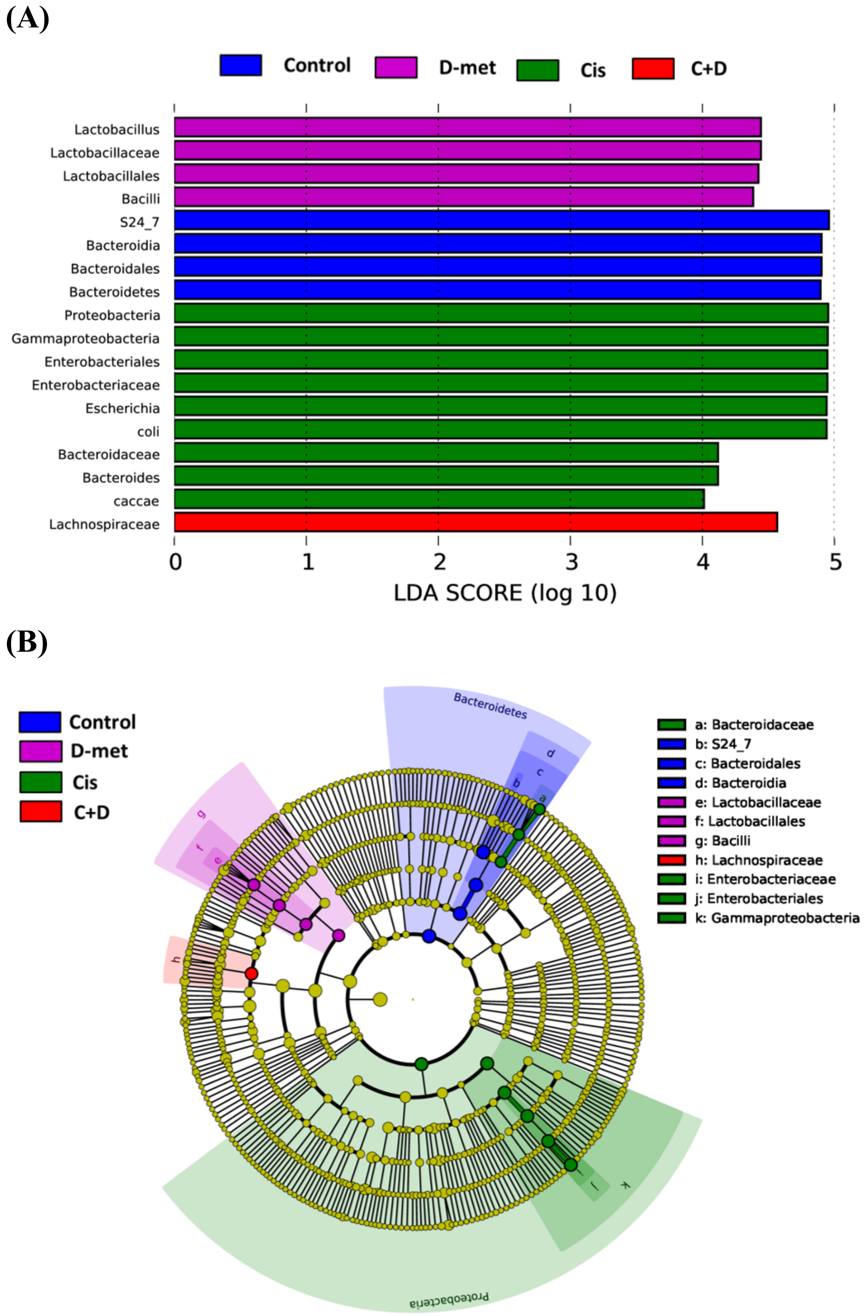


	Control	D-methionine	Cisplatin	Cisplatin+D-methionine
Fresh fecal weight (g)	8.34	7.53	0.41	4.19
Dry fecal weight (g)	5.09	4.56	0.25	2.58
Fecal moisture content (%)	39.0	39.5	39.7	38.4
Fecal pH	7.0 ± 0.12	6.7 ± 0.0	6.7 ± 0.2	6.7 ± 0.2



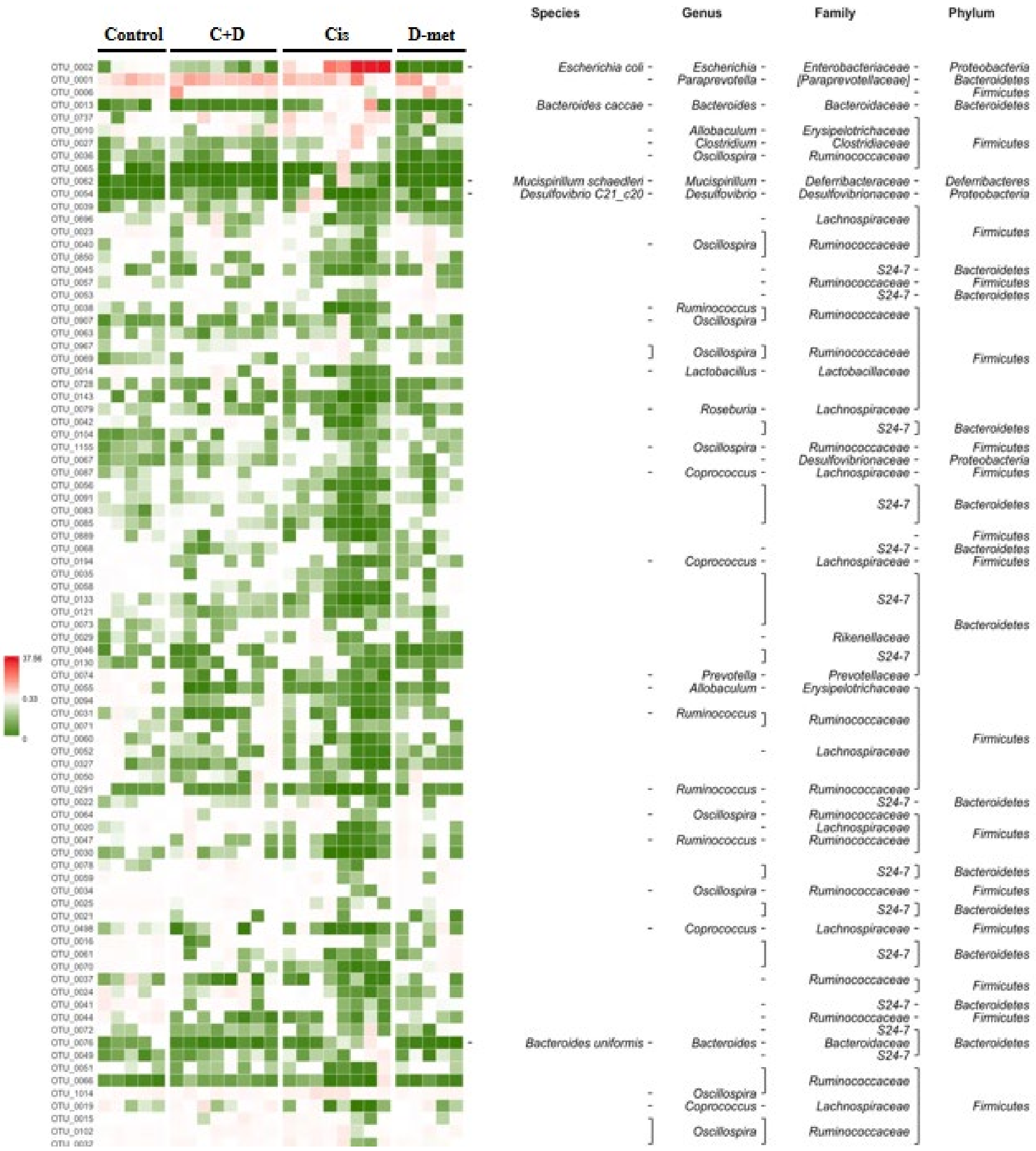
Supplementary Figure 1. (A) Feeding efficiencies during the experimental period. (B) Stool and cecum content appearance in experimental rats. Data are presented as mean ± SD, n=5-8. Differences were analyzed by one-way ANOVA.

The asterisks (*) represent significant difference when compared with the control group; whereas pound key (#) represent significant difference when compared with the cisplatin group ($p<0.05$).



Supplementary Figure 2. (A) Linear discriminant analysis (LDA). An LDA score higher than 4 indicated the biomarker in the corresponding group has significant different among four groups. An LDA length (LDA score) indicated affect degree of significant species. The 18 taxa with the largest effect sizes (LDA Score >4) are presented.

(B) Cladogram (circular hierarchical tree), radial pattern of from inner to outer circular represent from phylum to genus (species) and each dot represents a bacterial taxon at same level. The one innermost dot represent the highest level of taxonomy the kingdoms Bacteria, followed outwards by the lower levels, including phylum, class, order, family, genus and species. Each circle’s diameter is proportional to the taxon’s abundance. Each color represents different group. Blue indicates higher abundance in control animals, pink indicates higher abundance in D-methionine alone animals, green indicates higher abundance in cisplatin alone animals and yellow is higher abundance in cisplatin + D-methionine animals.



Supplementary Figure 3. Distribution heatmap of microbial genera arranged by hierarchical clustering of rats with different treatments. The abundance distributions of the 100 most dominant operational taxonomic units (OTUs) of the four groups are displayed on species abundance heat map and represented by color gradient. On the right side are bacterial taxa (species, genus, family and phylum) from 100 OTUs. Whether the abundance of each sample is higher or lower is reflected on color gradient and by locations of species and levels. The heat map was performed by discrepancies of species-relative abundance between groups, with colors gradually changed from deep red to deep green, in accordance with high relative abundance to low. The deeper red is represented richer of bacteria. In contrast, deeper green is represented fewer of bacteria.