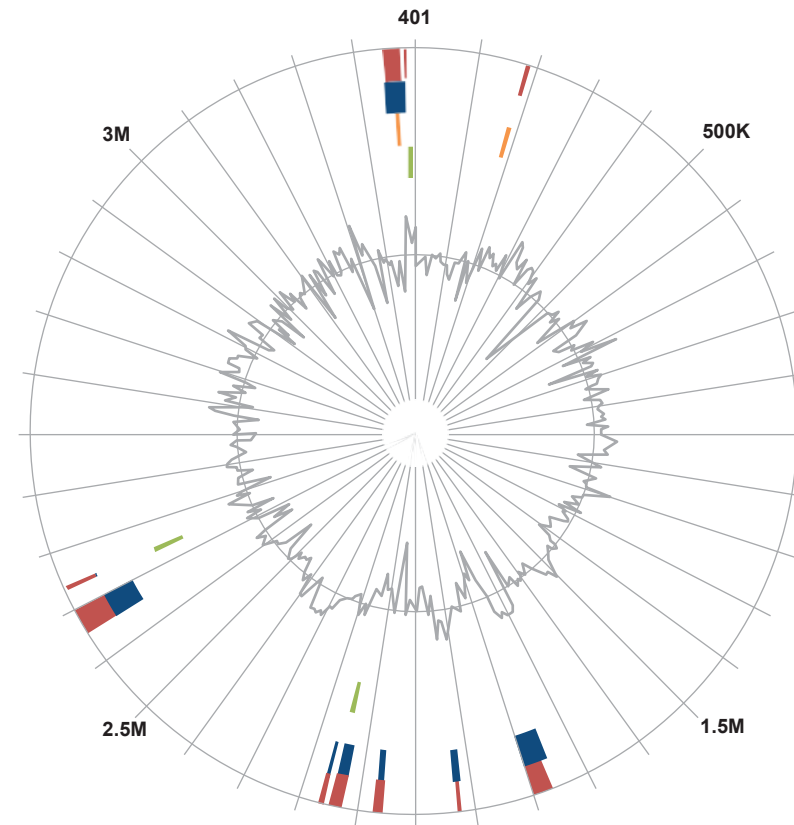**Supplementary Figure 1**
Region map of IslandViewer 4
analysis of ADS024 to assess potential
virulence factors and antimicrobial
**resistance genes.**

Legend

Prediction Methods
- Integrated
- IslandPath-DIMOB
- SIGH-HMM
- IslandPick
- Islander (Not available)

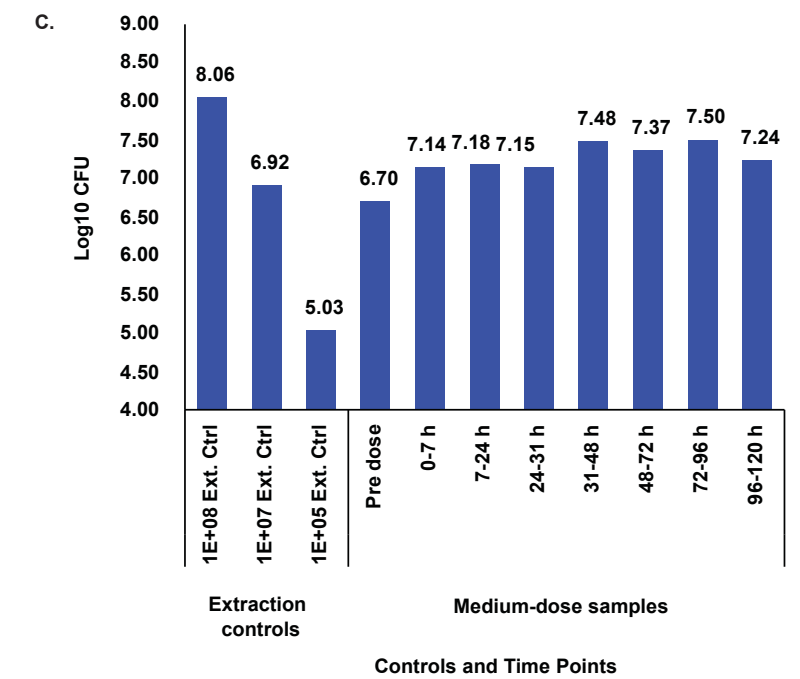**VF/AMR Annotations**
Curated virulence factors (no results found)
Homologs of virulence factors (no results found)
Curated resistance genes (no results found)
Homologs of resistance genes (no results found)
Pathogen-associated genes (no results found)

Supplementary Figure 2
Quantification of ADS024 (fresh culture) in mice intestine and colon (single-dose study).
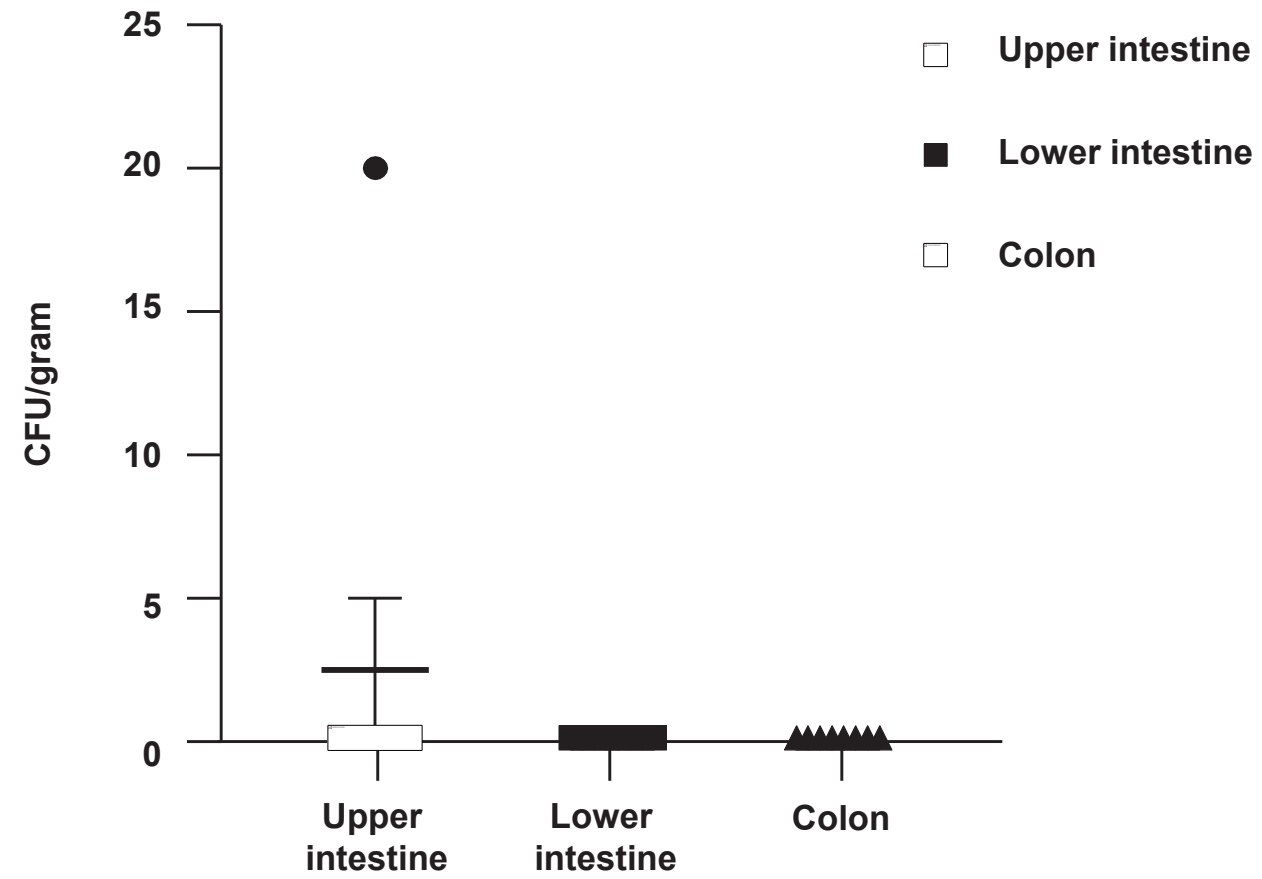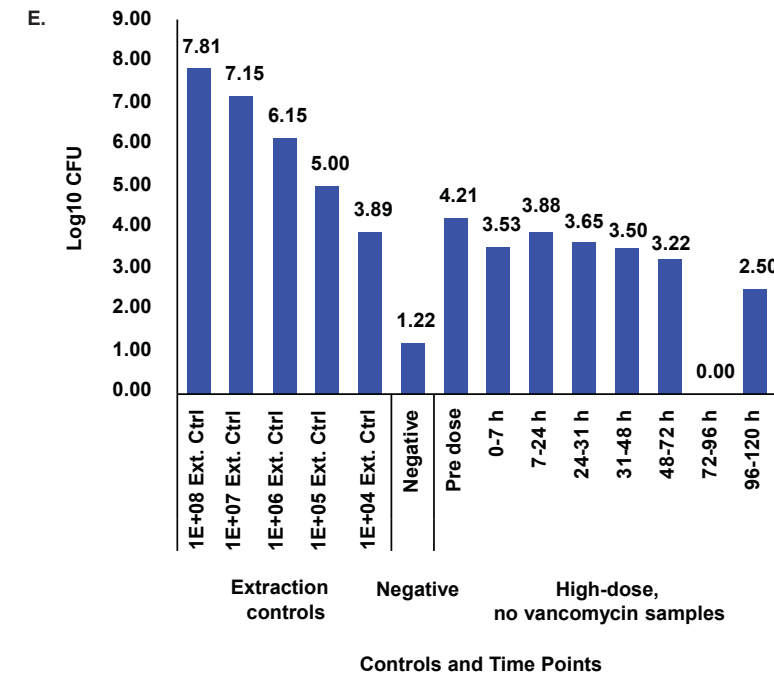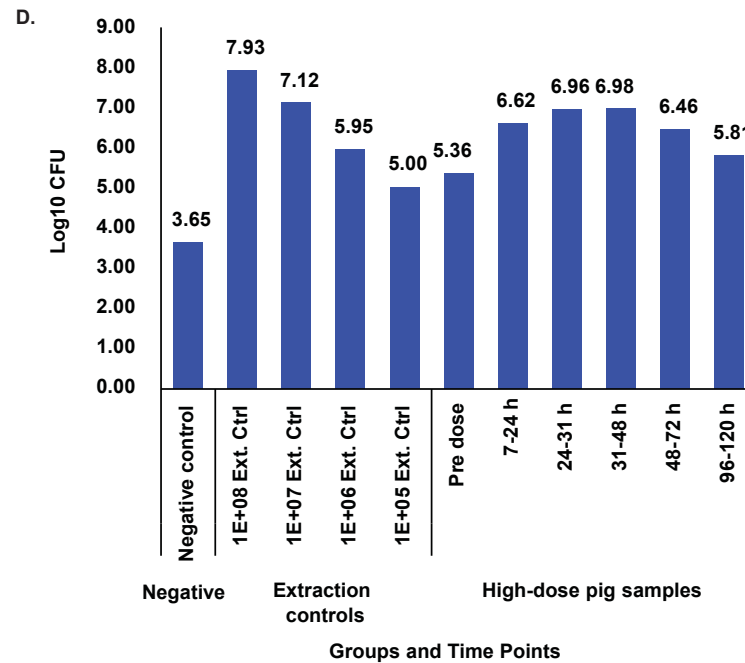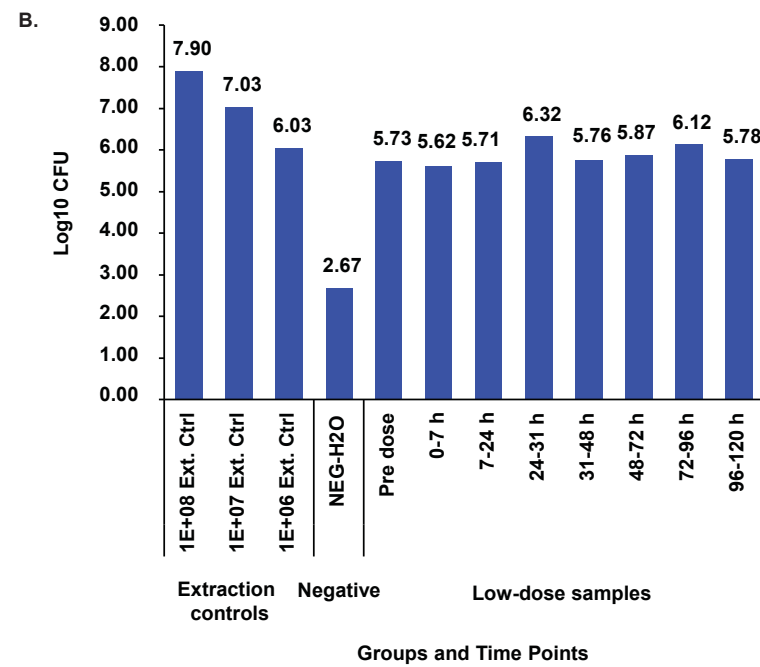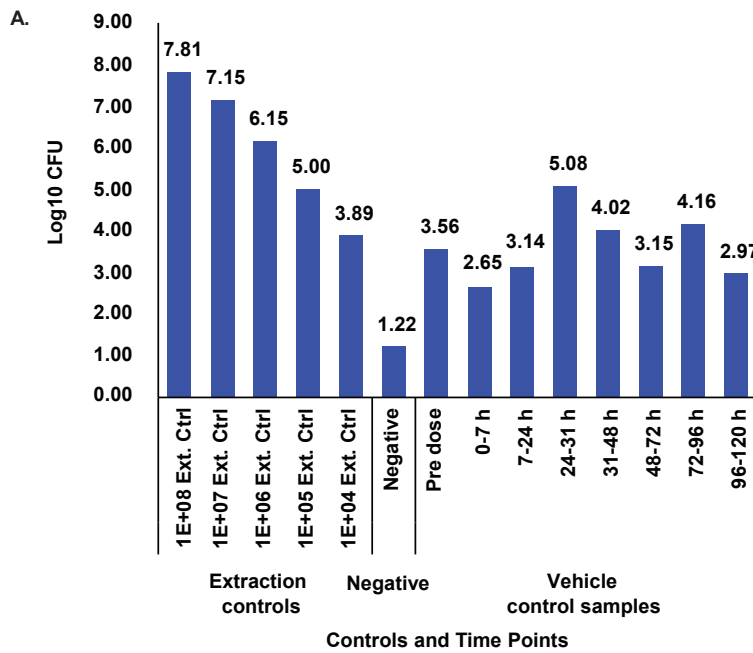
Supplementary Figure 3 Quantitative polymerase chain reaction estimation of ADS024 in miniature swine using the extraction controls factoring in mass balance.

Supplementary Figure 4
Quantitative polymerase chain reaction estimation of ADS024 in the control and ADS024-dosed miniature swine groups over time (pre dosing, day 15, day 29, recovery day 15) using the extraction controls.

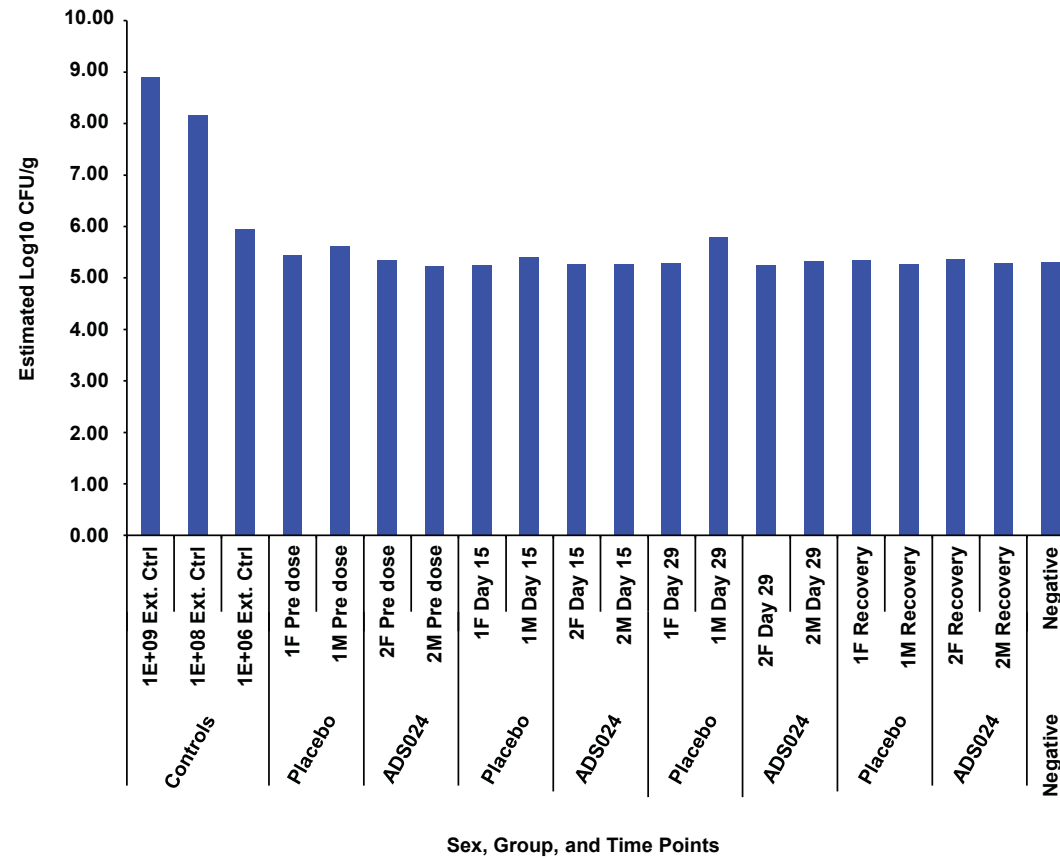**Supplementary Table 1 Individual scores of adverse health events.**

Diarrhea	Score	Fur	Score	Temp	Score	Hydration	Score	Posture	Score	Lethargy	Score	Dead	Score
Diarrhea	4												15
Wet Tail	3			Cold	3	Dehydrated	3	Hunched	3	Lethargy	3		
SI Wet Tail	2	Ruffled	2	Sl Cold	2	Sl Dehydrated	2	Sl Hunched	2				
Vs SI Wet Tail	1							Vs Hunched	1	Vs Lethargy	2		
Normal = 0													

Sl: Slightly; V: Very; Vs: Very slightly.

Supplementary Table 2 Distal colon model: phylum level.

Comparison of the median percentage relative abundance of human microbiota at the phylum level (ADS024 exposure vs untreated at 24 h post inoculation)	% relative abundance		*P* value	Significance value
	ADS024	Media only		
Actinomycetota	17.77%	5.17%	0.0000	e
Bacillota	70.68%	81.93%	0.0056	b
Fusobacteriota	0.0000%	0.0007%	0.0262	a
Verrucomicrobiota	0.06%	0.10%	0.0242	a

For statistical analyses, T24 samples of ADS024 inoculated fecal samples were compared with T24 uninoculated fecal samples (media only). There were no significant changes in Bacteroidota. a: *P* < 0.05, b: < 0.01, e: *P* < 0.001

Supplementary Table 3 Distal colon model: genus level.

Comparison of the median percentage relative abundance of human microbiota at the genus level (ADS024 exposure vs untreated at 24 h post inoculation)	ADS024	Media only	*P* value	Statistical value
Increase after ADS024 exposure				
Bifidobacterium	16.02%	4.28%	0.0000	e
Bacteroides	6.00%	4.00%	0.0414	a
Anaerococcus	1.00%	0.50%	0.0146	a
Lachnospiraceae.UCG.008	1.50%	1.00%	0.0149	a
Catenibacterium	1.00%	0.00%	0.0000	e
Erysipelotrichaceae.UCG.003	1.00%	0.00%	0.0107	a
Holdemanella	1.00%	0.00%	0.0001	e
Decrease after ADS024 exposure				
Leuconostoc	2.00%	4.50%	0.0019	b
Weissella	1.00%	2.50%	0.0027	b
Anaerostipes	0.00%	1.00%	0.0117	a
Phascolarctobacterium	1.00%	2.00%	0.0024	b
Veillonella	0.00%	1.00%	0.0334	a

For statistical analyses, T24 samples of ADS024 inoculated fecal samples were compared with T24 uninoculated fecal samples (media only). There were no significant changes in *Bacteroides*. a: *P* < 0.05, b: *P* < 0.01, e: *P* < 0.001