

Table S1 Ingredients of the purified rat chow diet

<u>Ingredients</u>	<u>g/kg</u>
casein	200.0
L-cystine	3.0
corn starch	300.5
maltodextrin	120.0
sucrose	100.0
soybean oil	70.0
cellulose	150.0
mineral mix	42.0
vitamin mix	12.0
choline bitartrate	2.5
TBHQ antioxidan	0.014

Table S2 The OTUs exhibiting a significant change in frequency from 0-6 days of exposure to 1.5% oxalate. Data are arranged in order of fold change as a range of values for the OTUs in that taxon. Fold change was \log_2 transformed so that a positive value reflects a significant increase in frequency and a negative value reflects a significant decrease. Taxons with OTUs that either increased or decreased are listed separately. Bolded taxa contain specific OTUs that exhibited a significant positive correlation with oxalate consumption in *N. albigula* (Miller in review)

A) Transplant group

Lowest Assigned Taxonomy	Taxonomic Level	# of OTUs	Fold Change	P
S24-7	family	54	0.38-7.78	<0.001-0.05
Oscillospira	genus	8	0.25-7.78	<0.001-0.02
Coproccoccus	genus	5	0.85-7.53	<0.001
Ruminococcus	genus	12	1.02-7.35	<0.001-0.02
Desulfovibrionaceae	family	1	6.15	<0.001
Clostridiales	order	47	0.33-5.71	<0.001-0.03
Lachnospiraceae	family	17	0.71-5.69	<0.001-0.03
Bacteroides	genus	27	0.33-5.24	<0.001-0.03
Allobaculum	genus	8	0.35-5.14	<0.001-0.02
Ruminococcaceae	family	10	0.72-3.26	<0.001-0.02
Parabacteroides	genus	7	0.22-3.15	<0.001-0.03
RF39	order	1	3.11	0.04
Coproccoccus	genus	1	3.05	0.001
YS2	order	2	1.58-3.02	<0.001
Rc4-4	genus	1	2.99	0.002
Proteus	genus	1	2.09	<0.001
Bacillus	genus	1	1.87	<0.001
Rikenellaceae	family	5	0.28-1.81	<0.001
Bacillaceae	family	1	1.79	<0.001
Bacteroidales	order	4	0.51-1.74	<0.001-0.04
Dorea	genus	1	1.38	<0.001
Bifidobacterium	genus	2	1.23-1.31	<0.001-0.01
Oxalobacter	genus	1	1.27	0.02
RF32	order	1	1.24	<0.001
Sutterella	genus	1	1.19	<0.001
CF231	genus	1	1.16	<0.001
Odoribacter	genus	4	0.69-1.09	<0.001-0.03
Bilophila	genus	1	1.04	<0.001
Lachnospira	genus	1	0.76	<0.001
Neisseriaceae	family	1	0.62	0.002
Akkermansia	genus	2	0.43-0.44	<0.001
Lactobacillus	genus	1	0.41	0.02
Turicibacter	genus	1	-4.29	<0.001
Rc4-4	genus	1	-3.77	<0.001
Proteus	genus	1	-3.18	0.01
Rothia	genus	1	-2.19	<0.001
Mogibacteriaceae	family	1	-2.12	<0.001
Pediococcus	genus	1	-1.95	0.01
Roseburia	genus	1	-0.67	<0.001
Parabacteroides	genus	1	-0.35	<0.001
Christensenellaceae	family	1	-0.77	0.003
Bacteroides	genus	1	-0.82	<0.001
Enterococcus	genus	1	-1.13	<0.001
Enterococcaceae	family	1	-1.52	<0.001
Blautia	genus	1	-1.88	<0.001
Adlecreutzia	genus	1	-1.91	<0.001
Streptococcus	genus	3	-(2.03-1.81)	<0.001
Actinomyces	genus	1	-2.09	<0.001
Enterobacteraceae	family	1	-2.16	<0.001
Clostridiaceae	family	2	-(2.68-1.99)	<0.001-0.002
Firmicutes	phylum	1	-2.83	<0.001
Oscillospira	genus	6	-(3.05-0.33)	<0.001-0.02
Lactobacillus	genus	4	-(3.18-1.69)	<0.001
S24-7	family	7	-(3.61-0.45)	<0.001
Allobaculum	genus	1	-3.63	<0.001
Coproccoccus	genus	2	-(3.81-0.91)	<0.001-0.001
Prevotella	genus	2	-(3.88-2.04)	<0.001-0.01
Lactococcus	genus	3	-(3.93-1.04)	<0.001
Ruminococcaceae	family	22	-(4.36-0.23)	<0.001-0.04
Desulfovibrio	genus	1	-5	<0.001
RF32	order	3	-(5.03-1.93)	<0.001
Ruminococcus	genus	19	-(5.64-0.35)	<0.001-0.02
Erysipelotrichaceae	family	7	-(7.54-2.02)	<0.001-0.02
Lachnospiraceae	family	17	-(8.42-0.65)	<0.001-0.02
Clostridiales	order	38	-(9.26-0.65)	<0.001-0.04
Coproccoccus	genus	1	-10.13	<0.001

B) No transplant group

Lowest Assigned Taxonomy	Taxonomic Level	# of OTUs	Fold Change	P
Coproccoccus	genus	3	0.54-7.28	<0.001-0.004
Proteus	genus	3	5.34-6.31	<0.001-0.005
Ruminococcus	genus	7	0.21-5.98	<0.001-0.03
Anaerostipes	genus	1	5.83	0.004
Lachnospiraceae	family	5	0.87-5.07	<0.001-0.03
RF39	order	1	4.26	<0.001
Clostridiales	order	25	0.43-3.79	<0.001-0.05
S24-7	family	8	0.78-3.49	<0.001-0.3
Parabacteroides	genus	7	0.21-3.02	<0.001-0.02
Bacteroides	genus	6	0.33-2.57	<0.001-0.002
Ruminococcaceae	family	4	0.53-2.48	<0.001-0.005
Peptococcaceae	family	3	0.74-1.19	<0.001
CH231	genus	1	0.57	<0.001
Desulfovibrio	genus	1	0.55	<0.001
Oscillospira	genus	1	0.15	0.004
Enterobacteriaceae	family	1	-0.24	<0.001
Akkermansia	genus	2	-0.56	<0.001
Desulfovibrionaceae	family	1	-0.81	<0.001
Butyricimonas	genus	2	-(1.11-.09)	0.002-0.003
Bacteroidales	order	1	-1.19	<0.001
Dores	genus	1	-1.44	0.007
Lactococcus	genus	2	-(1.47-1.45)	<0.001
Rothia	genus	1	-1.48	0.03
Streptococcus	genus	2	-(1.48-1.35)	<0.001
Rikenellaceae	family	5	-(1.61-0.39)	<0.001-0.05
Blautia	genus	1	-1.64	<0.001
Prevotella	genus	1	-2.22	<0.001
Coproccoccus	genus	3	-(3.42-1.43)	<0.001-0.01
Turicibacter	genus	1	-3.61	<0.001
Oscillospira	genus	15	-(4.04-0.39)	<0.001-0.03
Bifidobacterium	genus	2	-(4.57-4.02)	<0.001
Lachnospiraceae	family	12	-(4.85-0.66)	<0.001-0.02
Bacteroides	genus	5	-(4.92-0.28)	<0.001
Pediococcus	genus	1	-5.17	<0.001
RF39	order	3	-(5.37-1.86)	0.004-0.03
Clastridiaceae	family	3	-(5.72-1.44)	<0.001
Ruminococcaceae	family	30	-(6.26-0.19)	<0.001-0.05
Ruminococcus	genus	15	-(8.03-0.21)	<0.001-0.04
Lactobacillus	genus	10	-(8.44-1.81)	<0.001-0.04
Clostridiales	order	53	-(8.45-0.25)	<0.001-0.04
S24-7	family	32	-(9.46-0.41)	<0.001-0.05

Table S3 The OTUs that are present in both the Donor and the Transplant group, but not the No transplant group immediately after the transplant period

Lowest Assigned Taxonomy	Taxonomic Level	# of OTUs
Allobaculum	genus	14
Anaerostipes	genus	1
Bacteroidales	order	1
Bacteroides	genus	1
Bifidobacteriaceae	family	1
Bifidobacterium	genus	3
Caulobacteraceae	family	1
Christensenellaceae	family	2
Clostridiaceae	family	2
Clostridiales	order	85
Clostridium	genus	1
Coprococcus	genus	3
Desulfovermiculus	genus	1
Desulfovibrio	genus	7
Erysipelotrichaceae	family	2
Lachnospira	genus	1
Lacnospiraceae	family	16
Lactobacillus	genus	6
Lactobacillus reuter	species	1
Legionellaceae	family	1
Marinilabiaceae	family	1
Mycobacterium	genus	1
Odoribacter	genus	5
Oscillospira	genus	38
Oxalobacter	family	1
Oxalobacteraceae	family	1
Parabacteroides	genus	1
Peptococcaceae	family	1
Proteus	genus	1
RF16	family	7
RF32	order	2
RF39	order	2
Rikenellaceae	family	5
Ruminococcaceae	family	41
Ruminococcus	genus	8
Ruminococcus flavefaciens	species	23
Ruminococcus gnavus	species	3
S24-7	family	200
SBYG_4172	family	1
Sphingomonas	genus	1
Treponema	genus	1
Unassigned	NA	111
YS2	order	2

Figure S1 Rarefaction analysis for all samples. Curves are color-coded by microbial treatment

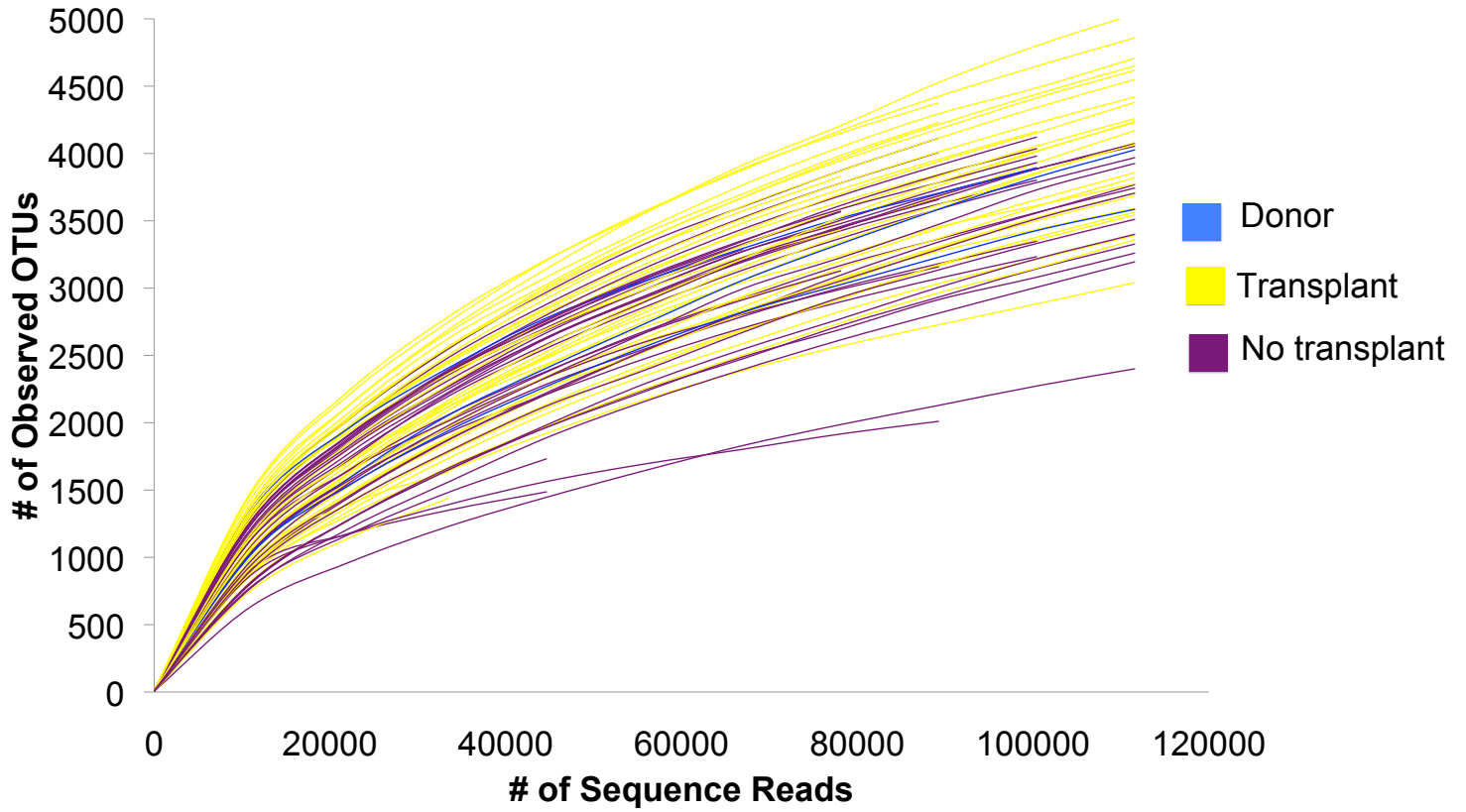


Figure S2 Venn diagram exhibiting the number of unique and shared OTUs among the donor, transplant, and no transplant groups immediately after the transfer period. Numbers in each section reflect OTUs in that section

