

## Supplementary material

**Table S1:** Mean relative abundance and standard deviation (SD) of phyla in fecal-microbiota composition of adult semi-captive white rhinoceroses at capture (4 males, 4 non-lactating females, 4 lactating females). Bacterial reads which could not be assigned to any phyla are listed as unclassified.

Phylum	Mean (%)	SD (%)
<i>Firmicutes</i>	50.60	8.64
<i>Bacteroidetes</i>	34.68	8.30
<i>Spirochaetes</i>	4.17	1.74
<i>Patescibacteria</i>	4.10	2.61
<i>Kiritimatiellaeota</i>	1.92	1.26
<i>Verrucomicrobia</i>	1.55	1.26
<i>Other</i>	1.23	0.54
<i>Fibrobacteres</i>	0.94	0.93
<i>Lentisphaerae</i>	0.34	0.25
<i>Actinobacteria</i>	0.34	0.65
<i>Proteobacteria</i>	0.31	0.37
<i>Armatimonadetes</i>	0.23	0.23
<i>Planctomycetes</i>	0.18	0.16
<i>Synergistetes</i>	0.17	0.19
<i>Tenericutes</i>	0.16	0.17
<i>Euryarchaeota</i>	0.08	0.13
<i>Chloroflexi</i>	0.07	0.18
<i>Elusimicrobia</i>	0.05	0.09
<i>Epsilonbacteraeota</i>	0.05	0.17
<i>Acidobacteria</i>	0.03	0.11
<i>Cyanobacteria</i>	0.01	0.02
Unclassified	< 0.01	0.02
<i>WPS 2</i>	< 0.01	0.01
<i>Gemmatimonadetes</i>	< 0.01	0.01
<i>Fusobacteria</i>	< 0.01	< 0.01

**Table S2:** Mean relative abundance and standard deviation (SD) of the 50 most abundant families in the fecal-microbiota composition of adult semi-captive white rhinoceroses at capture (4 males, 4 non-lactating females, 4 lactating females). Bacteria which could not be assigned up to family level are listed as unclassified.

Family	Mean (%)	SD (%)
<i>Lachnospiraceae</i>	18.26	6.37
<i>Ruminococcaceae</i>	17.53	3.97
<i>Prevotellaceae</i>	11.29	1.90
<i>Rikenellaceae</i>	8.88	2.46
unclassified <i>Bacteroidales</i>	7.17	5.82
<i>Christensenellaceae</i>	5.23	2.95
<i>Spirochaetaceae</i>	3.97	1.84
<i>Lactobacillaceae</i>	3.91	4.61
<i>Bacteroidales UCG-001</i>	3.58	0.99
<i>Other</i>	3.23	1.75
<i>Saccharimonadaceae</i>	2.58	1.79
unclassified <i>Kiritimatiellae</i>	1.91	1.36
unclassified <i>Verrucomicrobiae</i>	1.53	1.28
unclassified <i>Absconditabacteriales</i>	1.52	1.77
<i>Bacteroidales BS11 gut group</i>	1.37	1.25
<i>Defluviitaleaceae</i>	1.17	0.65
<i>Clostridiales Family XIII</i>	1.12	0.75
unclassified <i>Clostridiales</i>	1.07	0.88
<i>Fibrobacteraceae</i>	0.94	0.93
<i>Acidaminococcaceae</i>	0.84	0.35
<i>Porphyromonadaceae</i>	0.65	1.55
<i>Bacteroidetes BD2-2</i>	0.57	0.36
<i>Muribaculaceae</i>	0.46	0.32
<i>Streptococcaceae</i>	0.40	0.74
<i>Marinilabiliaceae</i>	0.33	0.30
<i>vadinBE97</i>	0.27	0.22
unclassified <i>Bacteroidia</i>	0.25	0.19
<i>Erysipelotrichaceae</i>	0.24	0.25
<i>Planococcaceae</i>	0.24	0.61
unclassified <i>Armatimonadetes</i>	0.23	0.37
unclassified <i>Spirochaetes</i>	0.20	0.40
<i>Veillonellaceae</i>	0.20	0.20
<i>Clostridiaceae 1</i>	0.18	0.40
<i>Synergistaceae</i>	0.17	0.19
<i>Pirellulaceae</i>	0.16	0.16
unclassified <i>Mollicutes</i>	0.11	0.15
<i>Eubacteriaceae</i>	0.11	0.10
unclassified <i>Bradymonadales</i>	0.08	0.13

<i>Oligosphaeraceae</i>	0.07	0.10
<i>Corynebacteriaceae</i>	0.06	0.14
<i>Eggerthellaceae</i>	0.06	0.11
<i>Methanocorpusculaceae</i>	0.05	0.12
<i>Campylobacteraceae</i>	0.05	0.17
<i>Bacteroidales_RF16_group1</i>	0.05	0.06
<i>Elusimicrobiaceae</i>	0.04	0.09
<i>Succinivibrionaceae</i>	0.04	0.07
<i>Methanobacteriaceae</i>	0.03	0.06
<i>Anaerolineaceae</i>	0.03	0.06
<i>Desulfovibrionaceae</i>	0.03	0.05
<i>Burkholderiaceae</i>	0.03	0.06

**Table S3:** The 50 most abundant amplicon sequence variants (ASVs) in the fecal-microbiota composition of adult semi-captive white rhinoceroses at capture (4 males, 4 non-lactating females, 4 lactating females). Mean relative abundance (Mean), standard deviation (SD) and taxonomy assignment up to the highest possible level are given. Abbreviations: n.a.: not cultured or not assigned at this level; P: Phylum; F: *Firmicutes*; B: *Bacteroidetes*; V: *Verrucomicrobia*; Pb: *Patescibacteria*; S: *Spirochaetes*; Fb: *Fibrobacteres*

ASV Number	Mean (%)	SD (%)	Taxonomy				
			P	Order	Family	Genus	Species
ASV 1	4.62	2.59	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Ruminococcus 1</i>	n.a.
ASV 4	2.66	2.19	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> <i>AC2044 group</i>	n.a.
ASV 3	2.52	3.23	F	<i>Lactobacillales</i>	<i>Lactobacillaceae</i>	<i>Ligilactobacillus</i>	<i>Ligilactobacillus equi</i> <i>DPC 6820</i>
ASV 5	1.65	1.38	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> <i>UCG-004</i>	n.a.
ASV 6	1.54	1.00	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Saccharofermentans</i>	n.a.
ASV 7	1.48	1.26	V	<i>LD1-PB3</i>	n.a.	n.a.	n.a.
ASV 14	1.22	1.37	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnoclostridium 10</i>	n.a.
ASV 11	1.21	1.05	Pb	<i>Saccharimonadales</i>	<i>Saccharimonadaceae</i>	<i>Candidatus</i> <i>Saccharimonas</i>	n.a.
ASV 9	1.13	1.22	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> <i>R-7 group</i>	n.a.
ASV 12	1.02	0.84	B	<i>Bacteroidales</i>	<i>Rikenellaceae</i>	<i>Rikenellaceae</i> <i>RC9 gut group</i>	n.a.
ASV 16	0.01	1.02	B	<i>Bacteroidales</i>	<i>Bacteroidales</i> <i>BS11 gut group</i>	n.a.	n.a.
ASV 13	0.94	0.45	B	<i>Bacteroidales</i>	<i>Rikenellaceae</i>	<i>Rikenellaceae</i> <i>RC9 gut group</i>	n.a.
ASV 18	0.89	1.02	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> <i>UCG-004</i>	n.a.
ASV 31	0.87	0.81	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 26	0.86	0.92	Pb	<i>Saccharimonadales</i>	<i>Saccharimonadaceae</i>	<i>Candidatus</i> <i>Saccharimonas</i>	n.a.
ASV 21	0.86	0.84	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 30	0.85	1.11	B	<i>Bacteroidales</i>	<i>Rikenellaceae</i>	<i>Rikenellaceae</i> <i>RC9 gut group</i>	n.a.
ASV 27	0.85	0.95	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> <i>UCG-004</i>	n.a.
ASV 20	0.78	0.82	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> <i>UCG-009</i>	n.a.
ASV 22	0.77	0.90	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> <i>R-7 group</i>	n.a.
ASV 23	0.75	1.17	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> <i>R-7 group</i>	n.a.
ASV 17	0.73	0.49	B	<i>Bacteroidales</i>	n.a.	n.a.	n.a.
ASV 33	0.71	0.38	B	<i>Bacteroidales</i>	<i>Bacteroidales</i> <i>UCG-001</i>	n.a.	n.a.

ASV 10	0.69	0.60	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> R-7 group	n.a.
ASV 24	0.66	0.29	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> XPB1014 group	n.a.
ASV 46	0.66	1.12	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> UCG-009	n.a.
ASV 47	0.66	0.72	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 45	0.65	0.42	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotella 1</i>	n.a.
ASV 15	0.66	0.67	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 39	0.62	0.37	S	<i>Spirochaetales</i>	<i>Spirochaetaceae</i>	<i>Treponema 2</i>	n.a.
ASV 29	0.61	0.45	F	<i>Clostridiales</i>	<i>Defluviitaleaceae</i>	<i>Defluviitaleaceae</i> UCG-011	n.a.
ASV 51	0.60	0.77	B	<i>Bacteroidales</i>	F082	n.a.	n.a.
ASV 61	0.59	0.65	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> AC2044 group	n.a.
ASV 41	0.59	1.03	F	<i>Lactobacillales</i>	<i>Lactobacillaceae</i>	<i>Ligilactobacillus</i>	<i>Ligilactobacillus equi</i> DPC 6820
ASV 32	0.57	0.67	B	<i>Bacteroidales</i>	p-251-o5	n.a.	n.a.
ASV 38	0.57	0.85	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	n.a.	n.a.
ASV 48	0.55	0.62	B	<i>Bacteroidales</i>	F082	n.a.	n.a.
ASV 56	0.54	0.90	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> R-7 group	n.a.
ASV 54	0.54	0.39	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> UCG-003	n.a.
ASV 50	0.53	0.92	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 53	0.52	0.64	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Papillibacter</i>	n.a.
ASV 58	0.51	0.53	B	<i>Bacteroidales</i>	<i>Rikenellaceae</i>	<i>Rikenellaceae</i> RC9 gut group	n.a.
ASV 49	0.51	0.74	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> UCG-009	n.a.
ASV 68	0.51	0.48	Fb	<i>Fibrobacterales</i>	<i>Fibrobacteraceae</i>	<i>Fibrobacter</i>	n.a.
ASV 40	0.50	0.57	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> UCG-004	n.a.
ASV 60	0.50	0.34	B	<i>Bacteroidales</i>	<i>Bacteroidales</i> UCG-001	n.a.	n.a.
ASV 63	0.49	0.48	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Ruminococcaceae</i> NK4A214 group	n.a.
ASV 44	0.49	0.65	F	<i>Clostridiales</i>	n.a.	n.a.	n.a.
ASV 36	0.48	0.46	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 55	0.47	0.57	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> UCG-001	n.a.

**Table S4:** Mean relative abundance and standard deviation (SD) of phyla in fecal-microbiota composition of semi-captive white rhinoceros calves at capture (1 male 5 months, 1 female 5 months, 2 female 16 months). Bacterial reads which could not be assigned to any phyla are listed as unclassified.

Phylum	Mean (%)	SD (%)
<i>Firmicutes</i>	53.51	12.94
<i>Bacteroidetes</i>	33.68	10.54
<i>Spirochaetes</i>	3.02	2.25
<i>Patescibacteria</i>	2.72	1.45
<i>Kiritimatiellaeota</i>	2.24	1.13
<i>Other</i>	1.62	0.42
<i>Verrucomicrobia</i>	1.06	0.24
<i>Actinobacteria</i>	0.89	0.36
<i>Proteobacteria</i>	0.49	0.26
<i>Euryarchaeota</i>	0.43	0.24
<i>Fibrobacteres</i>	0.42	0.55
<i>Synergistetes</i>	0.36	0.12
<i>Tenericutes</i>	0.23	0.08
<i>Lentisphaerae</i>	0.22	0.08
<i>Armatimonadetes</i>	0.21	0.26
<i>Chloroflexi</i>	0.19	0.08
<i>Acidobacteria</i>	0.10	0.13
<i>Planctomycetes</i>	0.09	0.07
<i>Elusimicrobia</i>	0.06	0.06
<i>Cyanobacteria</i>	0.04	0.04
Unclassified	0.02	0.02
<i>Chlamydiae</i>	0.01	0.02
<i>WPS 2</i>	< 0.01	0.02
<i>Epsilonbacteraeota</i>	< 0.01	0.01
<i>Gemmatimonadetes</i>	< 0.01	< 0.01
<i>BRC1</i>	< 0.01	< 0.01
<i>Fusobacteria</i>	< 0.01	< 0.01

**Table S5:** Mean relative abundance and standard deviation (SD) of the 50 most abundant families in the fecal-microbiota composition of semi-captive white rhinoceros calves at capture (1 male 5 months, 1 female 5 months, 2 female 16 months). Bacteria which could not be assigned up to family level are listed as unclassified.

Family	Mean (%)	SD (%)
<i>Lachnospiraceae</i>	18.67	6.18
<i>Ruminococcaceae</i>	17.56	2.14
<i>Prevotellaceae</i>	13.35	6.00
<i>Rikenellaceae</i>	7.18	3.37
unclassified <i>Bacteroidales</i>	6.74	3.38
<i>Christensenellaceae</i>	5.84	4.90
<i>Other</i>	3.82	0.43
unclassified <i>Clostridiales</i>	3.16	1.82
<i>Spirochaetaceae</i>	2.99	2.24
<i>Lactobacillaceae</i>	2.77	3.13
<i>Bacteroidales UCG-001</i>	2.60	1.55
<i>Clostridiales Family XIII</i>	2.43	1.04
unclassified <i>Kiritimatiellae</i>	2.24	1.23
<i>Muribaculaceae</i>	2.18	2.09
<i>Saccharimonadaceae</i>	2.04	0.91
<i>Bacteroidales BS11 gut group</i>	1.09	0.41
unclassified <i>Verrucomicrobiae</i>	1.04	0.23
<i>Defluviitaleaceae</i>	0.75	0.73
unclassified <i>Absoconditabacteriales</i>	0.68	0.68
<i>Erysipelotrichaceae</i>	0.58	0.16
<i>Veillonellaceae</i>	0.48	0.27
<i>Fibrobacteraceae</i>	0.42	0.55
<i>Acidaminococcaceae</i>	0.39	0.12
<i>Synergistaceae</i>	0.36	0.12
<i>Methanobacteriaceae</i>	0.35	0.28
<i>Planococcaceae</i>	0.29	0.47
<i>Eggerthellaceae</i>	0.25	0.06
<i>Eubacteriaceae</i>	0.22	0.03
unclassified <i>Armatimonadetes</i>	0.21	0.26
unclassified <i>Bacteroidia</i>	0.19	0.16
<i>Oligosphaeraceae</i>	0.18	0.08
<i>Streptococcaceae</i>	0.13	0.13
<i>Marinilabiliaceae</i>	0.12	0.06
<i>Bacteroidetes BD2.2</i>	0.12	0.13
unclassified <i>Mollicutes</i>	0.12	0.02
<i>Anaerolineaceae</i>	0.11	0.09
<i>Solibacteraceae_Subgroup_3</i>	0.08	0.11
<i>Sphingomonadaceae</i>	0.07	0.09

<i>Enterobacteriaceae</i>	0.07	0.09
<i>unclassified Coriobacteriales</i>	0.07	0.05
<i>Micrococcaceae</i>	0.07	0.08
<i>Methanocorpusculaceae</i>	0.07	0.07
<i>Actinomycetaceae</i>	0.07	0.07
<i>Atopobiaceae</i>	0.06	0.06
<i>uncultured bacterium</i>	0.06	0.06
<i>Acidothermaceae</i>	0.06	0.07
<i>Peptococcaceae</i>	0.06	0.04
<i>Desulfovibrionaceae</i>	0.06	0.04
<i>Clostridiaceae_1</i>	0.05	0.03
<i>Mycobacteriaceae</i>	0.05	0.06



**Table S6:** The 50 most abundant amplicon sequence variants (ASVs) in the fecal-microbiota composition of semi-captive white rhinoceros calves at capture (1 male 5 months, 1 female 5 months, 2 female 16 months). Mean relative abundance (Mean), standard deviation (SD) and taxonomy assignment up to the highest possible level are given. Abbreviations: n.a.: not cultured or not assigned at this level; P: Phylum; F: *Firmicutes*; B: *Bacteroidetes*; V: *Verrucomicrobia*; Pb: *Patescibacteria*; S: *Spirochaetes*; Fb: *Fibrobacteres*

ASV Number	Mean (%)	SD (%)	Taxonomy				
			P	Order	Family	Genus	Species
ASV15	2.34	3.09	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 3	2.14	2.51	F	<i>Lactobacillales</i>	<i>Lactobacillaceae</i>	<i>Ligilactobacillus</i>	<i>Ligilactobacillus equi</i> DPC 6820
ASV 10	1.85	3.02	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> R-7 group	n.a.
ASV 1	1.67	1.15	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Ruminococcus 1</i>	n.a.
ASV 19	1.63	2.51	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Saccharofermentans</i>	<i>rumen bacterium</i> NK4A65
ASV 5	1.56	1.11	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> UCG-004	n.a.
ASV 79	1.47	2.22	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Alloprevotella</i>	n.a.
ASV 72	1.32	1.85	F	<i>Firmicutes</i>	<i>Lachnospiraceae</i>	<i>Oribacterium</i>	n.a.
ASV 4	1.17	1.12	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> AC2044 group	n.a.
ASV 66	1.17	1.49	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Alloprevotella</i>	n.a.
ASV 21	0.96	0.63	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 13	0.95	0.66	B	<i>Bacteroidales</i>	<i>Rikenellaceae</i>	<i>Rikenellaceae</i> RC9 gut group	n.a.
ASV 7	0.93	0.25	V	LD1-PB3	n.a.	n.a.	n.a.
ASV 16	0.89	0.45	B	<i>Bacteroidales</i>	<i>Bacteroidales</i> BS11 gut group	n.a.	n.a.
ASV 20	0.87	0.79	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> UCG-009	n.a.
ASV 12	0.81	0.77	B	<i>Bacteroidales</i>	<i>Rikenellaceae</i>	<i>Rikenellaceae</i> RC9 gut group	n.a.
ASV 40	0.78	0.45	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> UCG-004	n.a.
ASV 24	0.74	0.81	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	<i>Lachnospiraceae</i> XPB1014 group	n.a.
ASV 11	0.74	0.59	Pb	<i>Saccharimonadales</i>	<i>Saccharimonadaceae</i>	<i>Candidatus</i> <i>Saccharimonas</i>	n.a.
ASV 32	0.73	0.70	B	<i>Bacteroidales</i>	p-251-o5	n.a.	n.a.
ASV 6	0.73	0.84	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Saccharofermentans</i>	n.a.
ASV 94	0.73	0.95	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> UCG-001	n.a.
ASV 18	0.70	0.75	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> UCG-004	n.a.
ASV 17	0.69	0.52	B	<i>Bacteroidales</i>	n.a.	n.a.	n.a.
ASV 57	0.69	0.35	F	<i>Firmicutes</i>	n.a.	n.a.	n.a.
ASV 112	0.68	1.08	F	<i>Firmicutes</i>	n.a.	n.a.	n.a.

ASV 167	0.67	1.16	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Alloprevotella</i>	n.a.
ASV 36	0.64	0.46	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 53	0.63	0.35	F	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	<i>Papillibacter</i>	n.a.
ASV 34	0.61	0.78	B	<i>Bacteroidetes</i>	<i>Muribaculaceae</i>	n.a.	n.a.
ASV 9	0.59	0.67	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> <i>R-7 group</i>	n.a.
ASV 80	0.58	0.73	F	<i>Firmicutes</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 23	0.56	0.65	F	<i>Clostridiales</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> <i>R-7 group</i>	n.a.
ASV 50	0.53	0.41	F	<i>Clostridiales</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 84	0.49	0.15	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> <i>UCG-001</i>	n.a.
ASV 62	0.46	0.50	F	<i>Firmicutes</i>	<i>Ruminococcaceae</i>	<i>Ruminococcaceae</i> <i>NK4A214 group</i>	n.a.
ASV 67	0.44	0.34	B	<i>Bacteroidetes</i>	<i>F082</i>	n.a.	n.a.
ASV 29	0.44	0.43	F	<i>Clostridiales</i>	<i>Defluviitaleaceae</i>	<i>Defluviitaleaceae</i> <i>UCG-011</i>	n.a.
ASV 54	0.44	0.40	B	<i>Bacteroidales</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> <i>UCG-003</i>	n.a.
ASV 64	0.44	0.38	B	<i>Bacteroidetes</i>	<i>F082</i>	n.a.	n.a.
ASV 76	0.43	0.67	F	<i>Firmicutes</i>	<i>Ruminococcaceae</i>	<i>Saccharofermentans</i>	<i>uncultured rumen</i> <i>bacterium 5C0d-4</i>
ASV 44	0.41	0.24	F	<i>Clostridiales</i>	n.a.	n.a.	n.a.
ASV 39	0.41	0.18	S	<i>Spirochaetales</i>	<i>Spirochaetaceae</i>	<i>Treponema 2</i>	n.a.
ASV 75	0.41	0.37	F	<i>Firmicutes</i>	<i>Ruminococcaceae</i>	<i>Ruminococcaceae</i> <i>UCG-010</i>	n.a.
ASV 187	0.40	0.54	Pb	<i>Patescibacteria</i>	<i>Saccharimonadaceae</i>	<i>Candidatus</i> <i>Saccharimonas</i>	n.a.
ASV 155	0.40	0.61	F	<i>Firmicutes</i>	<i>Christensenellaceae</i>	<i>Christensenellaceae</i> <i>R-7 group</i>	n.a.
ASV 97	0.40	0.21	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> <i>UCG-001</i>	n.a.
ASV 81	0.39	0.33	F	<i>Firmicutes</i>	<i>Lachnospiraceae</i>	n.a.	n.a.
ASV 48	0.39	0.28	B	<i>Bacteroidales</i>	<i>F082</i>	n.a.	n.a.
ASV 174	0.38	0.30	B	<i>Bacteroidetes</i>	<i>Prevotellaceae</i>	<i>Prevotellaceae</i> <i>UCG-</i> <i>001</i>	n.a.

**Table S7:** Mean relative abundance and standard deviation (SD) of phyla in fecal-microbiota composition of adult semi-captive white rhinoceroses after transport (1 male, 2 non-lactating females, 4 lactating females). Bacterial reads which could not be assigned to any phyla are listed as unclassified.

Phylum	Mean (%)	SD (%)
<i>Firmicutes</i>	50.47	20.28
<i>Bacteroidetes</i>	25.25	16.28
<i>Proteobacteria</i>	11.09	15.35
<i>Actinobacteria</i>	5.75	10.06
<i>Kiritimatiellaeota</i>	1.80	2.03
<i>Patescibacteria</i>	1.73	1.65
<i>Spirochaetes</i>	1.04	1.28
<i>Verrucomicrobia</i>	0.59	0.48
<i>Synergistetes</i>	0.51	0.62
<i>Chloroflexi</i>	0.43	0.34
<i>Armatimonadetes</i>	0.24	0.36
<i>Euryarchaeota</i>	0.23	0.26
<i>Acidobacteria</i>	0.21	0.28
<i>Tenericutes</i>	0.16	0.20
<i>Planctomycetes</i>	0.15	0.12
<i>Lentisphaerae</i>	0.14	0.18
<i>Cyanobacteria</i>	0.07	0.16
<i>Elusimicrobia</i>	0.06	0.10
<i>Fibrobacteres</i>	0.03	0.05
unclassified	0.01	0.02
<i>Gemmatimonadetes</i>	0.01	0.01
<i>WPS 2</i>	< 0.01	0.01
<i>Deinococcus Thermus</i>	< 0.01	< 0.01
<i>Nitrospirae</i>	< 0.01	< 0.01

**Table S8:** Mean relative abundance and standard deviation (SD) of the 50 most abundant families in the fecal-microbiota composition of adult semi-captive white rhinoceroses after transport (1 male, 2 non-lactating females, 4 lactating females). Bacteria which could not be assigned up to family level are listed as unclassified.

<b>Family</b>	<b>Mean (%)</b>	<b>SD (%)</b>
<i>Planococcaceae</i>	11.63	12.24
<i>Ruminococcaceae</i>	8.80	6.90
<i>Other</i>	6.71	4.03
<i>Lachnospiraceae</i>	5.91	4.97
<i>Aerococcaceae</i>	5.27	12.70
<i>Rikenellaceae</i>	4.73	3.49
<i>Prevotellaceae</i>	4.56	4.79
<i>Flavobacteriaceae</i>	4.10	9.60
<i>Christensenellaceae</i>	3.88	3.17
<i>Moraxellaceae</i>	3.28	5.41
<i>Muribaculaceae</i>	3.18	4.30
<i>Unclassified Bacteroidales</i>	3.09	3.41
<i>Lactobacillaceae</i>	2.72	3.25
<i>Micrococcaceae</i>	2.61	6.30
<i>Enterobacteriaceae</i>	2.24	3.28
<i>Staphylococcaceae</i>	2.16	5.41
<i>Carnobacteriaceae</i>	1.99	3.23
<i>Pseudomonadaceae</i>	1.88	4.73
<i>Unclassified Clostridiales</i>	1.83	1.63
<i>Unclassified Kiritimatiellae</i>	1.80	2.04
<i>Weeksellaceae</i>	1.55	4.04
<i>Saccharimonadaceae</i>	1.55	1.48
<i>Burkholderiaceae</i>	1.47	3.65
<i>Corynebacteriaceae</i>	1.42	2.40
<i>Sphingobacteriaceae</i>	1.83	2.79
<i>Clostridiaceae_1</i>	1.33	1.86
<i>Bacteroidales_UCG.001</i>	1.25	1.16
<i>Clostridiales_Family_XIII</i>	1.07	1.12
<i>Spirochaetaceae</i>	1.02	1.24
<i>Streptococcaceae</i>	0.91	0.95
<i>Xanthomonadaceae</i>	0.86	1.79
<i>Defluviitaleaceae</i>	0.67	1.23
<i>Veillonellaceae</i>	0.63	1.08
<i>Synergistaceae</i>	0.51	0.62
<i>Unclassified Verrucomicrobiae</i>	0.50	0.55
<i>Acidaminococcaceae</i>	0.48	0.77
<i>Erysipelotrichaceae</i>	0.46	0.55

<i>Eggerthellaceae</i>	0.37	0.29
<i>Anaerolineaceae</i>	0.32	0.33
<i>Clostridiales_Family_XI</i>	0.30	0.78
<i>Crocinitomicaceae</i>	0.29	0.75
<i>Bacteroidales_BS11_gut_group</i>	0.28	0.33
<i>Devosiaceae</i>	0.28	0.56
<i>unclassified_Armatimonadetes</i>	0.24	0.36
<i>Sphingomonadaceae</i>	0.23	0.38
<i>Chitinophagaceae</i>	0.23	0.41
<i>Methanobacteriaceae</i>	0.22	0.25
<i>Atopobiaceae</i>	0.21	0.23
<i>Rhizobiaceae</i>	0.18	0.31
<i>unclassified_Absconditabacteriale</i>	0.18	0.20

**Table S9:** The 50 most abundant amplicon sequence variants (ASVs) in the fecal-microbiota composition of adult semi-captive white rhinoceroses after transport (1 male, 2 non-lactating females, 4 lactating females). Mean relative abundance (Mean), standard deviation (SD) and taxonomy assignment up to the highest possible level are given. Abbreviations: n.a.: not cultured or not assigned at this level; P: Phylum; A: *Actinobacteria*; B: *Bacteroidetes*; F: *Firmicutes*; Fb: *Fibrobacteres*; P: *Proteobacteria*; Pb: *Patescibacteria*; S: *Spirochaetes*; V: *Verrucomicrobia*

ASV Number	Mean (%)	SD (%)	Taxonomy				
			P	Order	Family	Genus	Species
ASV 2	7.72	8.71	F	Bacillales	Planococcaceae	Rummeliibacillus	n.a.
ASV 8	3.16	7.23	F	Lactobacillales	Aerococcaceae	Facklamia	n.a.
ASV 25	1.88	2.76	P	Enterobacteriales	Enterobacteriaceae	Escherichia-Shigella	n.a.
ASV 28	1.80	4.74	B	Flavobacteriales	Flavobacteriaceae	Flavobacterium	n.a.
ASV3	1.78	2.05	F	Lactobacillales	Lactobacillaceae	Ligilactobacillus	Ligilactobacillus equi DPC 6820
ASV 35	1.50	3.86	F	Lactobacillales	Aerococcaceae	Aerococcus	n.a.
ASV 37	1.43	3.71	B	Flavobacteriales	Flavobacteriaceae	Flavobacterium	n.a.
ASV 43	1.35	3.57	A	Micrococcales	Micrococcaceae	Rothia	n.a.
ASV 52	1.26	3.31	B	Flavobacteriales	Weeksellaceae	n.a.	Chishuiella sp. YIM 102668
ASV 59	1.13	2.19	P	Pseudomonadales	Moraxellaceae	Acinetobacter	n.a.
ASV 74	0.96	1.74	F	Clostridiales	Clostridiaceae 1	Fonticella	n.a.
ASV 34	0.95	1.40	B	Bacteroidales	Muribaculaceae	n.a.	n.a.
ASV 9	0.79	0.73	F	Clostridiales	Christensenellaceae	Christensenellaceae R-7 group	n.a.
ASV 17	0.71	1.32	B	Bacteroidales	n.a.	n.a.	n.a.
ASV 107	0.66	1.09	P	Pseudomonadales	Moraxellaceae	Acinetobacter	n.a.
ASV 10	0.66	0.65	F	Clostridiales	Christensenellaceae	Christensenellaceae R-7 group	n.a.
ASV 108	0.65	1.64	P	Pseudomonadales	Moraxellaceae	Acinetobacter	n.a.
ASV 109	0.65	1.73	P	Pseudomonadales	Pseudomonadaceae	Pseudomonas	n.a.
ASV 111	0.65	1.67	B	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	n.a.
ASV 113	0.65	1.69	P	Betaproteobacteriales	Burkholderiaceae	Comamonas	n.a.
ASV 116	0.63	1.29	F	Lactobacillales	Carnobacteriaceae	Desemzia	n.a.
ASV 42	0.61	0.78	F	Lactobacillales	Streptococcaceae	Streptococcus	n.a.
ASV 6	0.60	0.64	F	Clostridiales	Ruminococcaceae	Saccharofermentans	n.a.
ASV 126	0.56	1.28	F	Bacillales	Planococcaceae	Lysinibacillus	n.a.

ASV 127	0.56	1.47	P	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	n.a.
ASV 131	0.55	0.90	F	Bacillales	Planococcaceae	Solibacillus	n.a.
ASV 22	0.51	0.61	F	Clostridiales	Christensenellaceae	Christensenellaceae R-7 group	n.a.
ASV 62	0.51	0.48	F	Clostridiales	Ruminococcaceae	Ruminococcaceae NK4A214 group	n.a.
ASV 73	0.51	0.62	B	Synergistiales	Synergistaceae	n.a.	n.a.
ASV 7	0.50	0.54	V	LD1-PB3	n.a.	n.a.	n.a.
ASV 85	0.49	0.58	B	Bacteroidales	Rikenellaceae	Rikenellaceae RC9 gut group	n.a.
ASV 92	0.49	0.74	F	Clostridiales	n.a.	n.a.	n.a.
ASV 142	0.49	1.29	P	Pseudomonadales	Pseudomonadaceae	Pseudomonas	n.a.
ASV 29	0.49	1.02	F	Clostridiales	Defluviitaleaceae	Defluviitaleaceae UCG-011	n.a.
ASV 146	0.47	0.88	B	Flavobacteriales	Flavobacteriaceae	Flavobacterium	n.a.
ASV 57	0.46	0.41	F	Clostridiales	n.a.	n.a.	n.a.
ASV 12	0.45	0.76	B	Bacteroidales	Rikenellaceae	Rikenellaceae RC9 gut group	n.a.
ASV 124	0.43	0.80	B	Bacteroidales	Muribaculaceae	n.a.	n.a.
ASV 164	0.42	0.98	F	Bacillales	Staphylococcaceae	Jeotgalicoccus	n.a.
ASV 26	0.42	0.45	Pb	Saccharimonadales	Saccharimonadaceae	Candidatus Saccharimonas	n.a.
ASV 19	0.41	0.42	F	Clostridiales	Ruminococcaceae	Saccharofermentans	Rumen bacterium NK4A65
ASV 170	0.41	1.08	F	Lactobacillales	Aerococcaceae	Facklamia	n.a.
ASV 13	0.39	0.41	B	Bacteroidales	Rikenellaceae	Rikenellaceae RC9 gut group	n.a.
ASV 181	0.39	1.02	F	Lactobacillales	Carnobacteriaceae	Atopostipes	n.a.
ASV 18	0.37	0.41	B	Bacteroidales	Prevotellaceae	Prevotellaceae UCG-004	n.a.
ASV 24	0.37	0.38	F	Clostridiales	Lachnospiraceae	Lachnospiraceae XPB1014 group	n.a.
ASV 23	0.37	0.45	F	Clostridiales	Christensenellaceae	Christensenellaceae R-7 group	n.a.
ASV 192	0.36	0.96	A	Micrococcales	Micrococcaceae	Micrococcus	n.a.
ASV 195	0.36	0.96	F	Bacillales	Staphylococcaceae	Staphylococcus	n.a.
ASV 1	0.35	0.35	F	Clostridiales	Ruminococcaceae	Ruminococcus 1	n.a.

**Table S10:** Mean (SD) relative abundances of significantly shifted amplicon sequence variants (ASVs) in the fecal-microbiota composition of calves compared to adult semi-captive white rhinoceroses at capture and the corresponding P-values for the Wilcoxon rank sum test with continuity correction. Adjusted P-values ( $P_{adj} \leq 0.100$ ) were considered significant. Phylum: A: *Actinobacteria*; Ar: *Armatimonadetes*; B: *Bacteroidetes*; EU: *Euryarchaeota*; F: *Firmicutes*; K: *Kiritimatiellaeota*; M: *Mycoplasmata*; Pb: *Patascibacteria*;

ASV	Phylum	Family	Genus	P <sub>adj.</sub>	Adults		Calves	
					Mean (%)	SD (%)	Mean (%)	SD (%)
807	F	Lachnospiraceae	UCG-009	0.075	0.00	0.00	0.07	0.07
1732	F	Ruminococcaceae	n.a.	0.075	0.00	0.00	0.01	<0.01
1786	F	Ruminococcaceae	n.a.	0.075	0.00	0.00	0.01	0.01
445	F	Lachnospiraceae	n.a.	0.075	<0.01	<0.01	0.19	0.18
803	F	Lachnospiraceae	n.a.	0.075	<0.01	<0.01	0.06	0.05
1458	F	Lachnospiraceae	UCG-006	0.075	<0.01	<0.01	0.02	0.01
1554	F	Erysipelotrichaceae	n.a.	0.075	<0.01	<0.01	0.02	<0.01
537	F	Ruminococcaceae	NK4A214 group	0.075	<0.01	0.01	0.09	0.09
763	F	Christensenellaceae	R-7 group	0.075	<0.01	<0.01	0.04	0.03
1764	F	Lachnospiraceae	Oribacterium	0.075	<0.01	<0.01	0.01	0.01
691	F	Family XIII	Anaerovorax	0.075	<0.01	<0.01	0.09	0.13
836	F	Family XIII	n.a.	0.075	<0.01	<0.01	0.09	0.04
1098	F	Erysipelotrichaceae	Anaerorhabdus furcosa group	0.075	<0.01	<0.01	0.03	0.02
1401	F	Christensenellaceae	n.a.	0.075	<0.01	<0.01	0.02	0.01
167	B	Prevotellaceae	Alloprevotella	0.075	<0.01	0.02	0.67	1.16
419	F	Family XIII	Anaerovorax	0.075	<0.01	0.01	0.17	0.18
670	F	Family XIII	Anaerovorax	0.075	<0.01	0.01	0.08	0.06
1017	F	Lachnospiraceae	n.a.	0.075	<0.01	<0.01	0.02	0.02
1029	F	Family XIII	Anaerovorax	0.075	<0.01	<0.01	0.04	0.02
230	B	Muribaculaceae	n.a.	0.075	0.00	0.00	0.17	0.11
826	B	Prevotellaceae	UCG-001	0.075	0.00	0.00	0.07	0.09
1242	F	Ruminococcaceae	UCG-01	0.075	0.00	0.00	0.02	0.01
1290	F	Lachnospiraceae	Eubacterium hallii group	0.075	0.00	0.00	0.01	<0.01
1297	F	n.a.	n.a.	0.075	0.00	0.00	0.02	0.03
1341	B	Bacteroidales RF16 group	n.a.	0.075	0.00	0.00	0.01	0.01
1491	A	Eggerthellaceae	n.a.	0.075	0.00	0.00	0.01	0.01
1589	Ar	n.a.	n.a.	0.075	0.00	0.00	0.02	0.02
1627	A	Eggerthellaceae	n.a.	0.075	0.00	0.00	0.02	0.01
1646	Pb	Saccharimonadaceae	n.a.	0.075	0.00	0.00	0.02	0.01



1763	F	Erysipelotrichaceae	n.a.	0.075	0.00	0.00	0.01	0.01
1858	F	Ruminococcaceae	n.a.	0.075	0.00	0.00	0.01	0.01
2602	A	Eggerthellaceae	Enterorhabdus	0.075	0.00	0.00	<0.01	<0.01
2702	K	n.a.	n.a.	0.075	0.00	0.00	0.01	0.01
434	F	Christensenellaceae	R-7 group	0.087	0.01	0.02	0.09	0.07
1540	M	n.a.	n.a.	0.087	<0.01	0.01	0.02	0.01
79	B	Prevotellaceae	Alloprevotella	0.087	0.02	0.04	1.47	2.22
222	EU	Methanobacteriaceae	Methanobrevibacter	0.087	0.02	0.04	0.31	0.24
263	F	n.a.	n.a.	0.087	0.02	0.04	0.33	0.33
708	F	Lachnospiraceae	n.a.	0.087	<0.01	0.01	0.08	0.10
860	F	Veillonellaceae	n.a.	0.087	<0.01	<0.01	0.05	0.03
1124	F	Lachnospiraceae	n.a.	0.087	<0.01	<0.01	0.02	0.01
1324	F	Ruminococcaceae	Eubacterium coprostanoligenes group	0.087	<0.01	<0.01	0.01	<0.01

**Table S11:** Mean (SD) relative abundances of the 50 most shifted families in the fecal-microbiota composition of adult semi-captive white rhinoceroses at capture compared to after transport and the corresponding P-values for the Wilcoxon rank sum test with continuity correction. Adjusted P-values ( $P_{adj} \leq 0.100$ ) were considered significant. Phylum: A: *Actinobacteria*; Ad: *Acidobacteria*; B: *Bacteroidetes*; Ch: *Chloroflexi*; EU: *Euryarchaeota*; F: *Firmicutes*; Fb: *Fibrobacteres*; L: *Lentisphaerae*; P: *Proteobacteria*; Pb: *Patescibacteria*; Pm: *Planctomycetes*; S: *Spirochaetes*; V: *Verrucomicrobia*.

Phylum	Family	P <sub>adj.</sub>	At capture		After transport	
			Mean (%)	SD (%)	Mean (%)	SD (%)
B	Flavobacteriaceae	0.016	< 0.01	< 0.01	4.10	9.60
P	Enterobacteriaceae	0.018	<0.01	<0.01	2.24	3.28
P	Moraxellaceae	0.021	0.00	0.00	3.28	5.41
F	Lachnospiraceae	0.021	18.26	6.37	5.91	4.97
B	Bacteroidales UCG-001	0.021	3.58	0.99	1.25	1.16
A	Micrococcaceae	0.021	< 0.01	0.02	0.08	0.17
B	Chitinophagaceae	0.021	0.01	0.04	0.23	0.41
F	Aerococcaceae	0.022	0.00	0.00	0.46	0.32
P	Pseudomonadaceae	0.022	0.00	0.00	1.88	4.73
F	Enterococcaceae	0.022	0.00	0.00	0.17	0.32
S	Spirochaetaceae	0.027	3.96	1.84	1.02	1.24
F	Planococcaceae	0.029	0.24	0.61	11.63	12.24
P	Sphingomonadaceae	0.032	0.02	0.06	0.23	0.38
Fb	Fibrobacteraceae	0.036	0.94	0.93	0.03	0.05
B	Prevotellaceae	0.042	11.29	1.90	4.56	4.79
A	Acidothermaceae	0.042	0.02	0.06	0.05	0.04
B	Weeksellaceae	0.042	0.00	0.00	1.55	4.04
P	Xanthomonadaceae	0.042	0.00	0.00	0.86	1.79
P	Rhodobacteraceae	0.042	0.00	0.00	0.16	0.37
A	Bifidobacteriaceae	0.042	0.00	0.00	0.01	0.02
Ad	Solibacteraceae Subgroup_3	0.042	0.02	0.08	0.14	0.18
A	Solirubrobacteraceae	0.042	0.01	0.05	0.08	0.13
F	Ruminococcaceae	0.051	17.53	3.97	8.80	6.89
F	Carnobacteriaceae	0.051	<0.01	<0.01	1.99	3.23
B	Sphingobacteriaceae	0.058	<0.01	<0.01	1.38	2.79
Ch	Anaerolineaceae	0.058	0.03	0.06	0.32	0.33
A	Atopobiaceae	0.058	0.03	0.05	0.21	0.23
P	Xanthobacteraceae	0.058	0.01	0.04	0.06	0.09
P	Beijerinckiaceae	0.058	0.01	0.04	0.06	0.12
A	Intrasporangiaceae	0.058	0.01	0.04	0.05	0.07

P	unclassified_Elsterales	0.058	0.01	0.03	0.03	0.05
Pm	Isosphaeraceae	0.058	<0.01	0.02	0.03	0.04
Ch	Ktedonobacteraceae	0.058	<0.01	0.02	0.03	0.05
V	Chthoniobacteraceae	0.058	<0.01	0.02	0.02	0.03
Pb	Unclassified Absconditabacteriales	0.058	1.21	1.22	0.16	0.17
L	VadinBE97	0.058	0.27	0.22	0.05	0.05
B	Rikenellaceae	0.059	8.88	2.46	4.73	3.49
B	Bacteroidetes BD2.2	0.069	0.57	0.36	0.16	0.26
A	Mycobacteriaceae	0.069	0.02	0.06	0.07	0.07
F	Staphylococcaceae	0.069	<0.01	<0.01	2.16	5.42
P	Burkholderiaceae	0.069	0.03	0.06	1.47	3.65
F	Clostridiaceae_1	0.069	0.18	0.40	1.32	1.86
EU	Methanobacteriaceae	0.069	0.03	0.06	0.22	0.25
F	Peptococcaceae	0.069	0.01	0.02	0.06	0.07
A	Eggerthellaceae	0.069	0.06	0.11	0.37	0.29
B	Crocinitomicaceae	0.069	0.00	0.00	0.29	0.75
P	Rhizobiaceae	0.069	0.00	0.00	0.18	0.31
A	Unclassified Solirubrobacterales	0.069	0.00	0.00	0.01	0.01
A	Rubrobacteriaceae	0.069	0.00	0.00	<0.01	0.01
Ad	Acidobacteriaceae Subgroup_1	0.069	<0.01	0.01	0.03	0.05