

Supplementary Table 1. Wilcoxon and negative binomial mixed model (NBMM) analyses- mean baseline (B) (standard deviation) and absolute changes in abundance of specific taxa by chemotherapy treatment – neoadjuvant (neoADJ) versus adjuvant (ADJ) chemotherapy

Taxa abundance		Mean baseline and absolute changes in taxa abundance		Neoadjuvant vs Adjuvant		
		Neoadjuvant (neoADJ)	Adjuvant (ADJ)	Wilcoxon <sup>a</sup> Test	NBMM	
					No BMI adjustment	BMI Adjustment
		N=16	N=13	N=29	N=29	N=29
p_Actinobacteria	B	0.013 (0.005)	0.017 (.011)	0.23		
f_Micrococcaceae	change	-0.01 (0.003)	-0.006(.013)	0.034		
g_Rothia	P <sup>c</sup>	0.008	1.00		0.15	0.002
p_Actinobacteria	B	0.163 (.094)	0.081 (.044)	0.97		
f_Coriobacteriaceae	change	-0.043 (.102)	0.210 (.101)	0.35		
g_Eggerthella	P <sup>c</sup>	0.46	0.049		0.034	0.139
p_Actinobacteria	B	0.202 (0.11)	0.359 (.137)	0.55		
f_Coriobacteriaceae	change	-0.045 (0.13)	0.359(.214)	0.34		
g_Slackia	P <sup>c</sup>	0.84	0.21		0.022	0.614
P_Bacteroidetes	B	1.24 (0.31)	0.98 (0.36)	0.56		
F_Porphromonadaceae	change	-0.42 (0.27)	1.92 (1.57)	0.13		
g_Parabacteroides	P <sup>c</sup>	0.12	0.31		0.014	0.384
P_Bacteroidetes	B	8.19 (3.34)	7.78 (2.70)	0.74		
F_Prevotellaceae	change	-0.55 (4.34)	-4.82 (2.73)	0.21		
g_Prevotella	P <sup>c</sup>	0.93	0.033		0.043	0.900
P_Bacteroidetes	B	0.003(0.003)	0.026(0.011)	0.02		
f_Rikenellaceae	change	0.025(0.012)	-0.006(0.01)	0.13		
	P <sup>c</sup>	0.03	0.73		0.00019	0.719
p_Bacteroidetes	B	0.035 (0.015)	0.013(0.012)	0.13		
F_Rikenellaceae	Change	-0.032 (0.015)	0.014(0.008)	0.03		
g_Alistipes	P <sup>c</sup>	0.016	0.25		3.3 E10-7	0.82
P_Bacteroidetes	B	0.25 (0.17)	0.35 (0.16)	0.89		
F_S24-7	change	-0.11 (0.16)	-0.31(0.13)	0.33		
g_	P <sup>c</sup>	0.91	0.020		0.001	0.007
P_Bacteroidetes	B	0.337 (0.145)	0.159 (0.106)	0.89		
F_Barnesiellaceae	change	0.145 (0.148)	-0.017 (0.074)	0.15		
	P <sup>c</sup>	0.28	0.85		0.24	0.007
P_Bacteroidetes	B	0.272 (0.092)	0.311 (0.175)	0.89		
F_Odoribacteraceae	change	0.207 (0.158)	0.123 (0.269)	0.15		
g_Odoribacter	P <sup>c</sup>	0.22	0.59		0.151	0.004
p_Euryarchaeota	B	2.087 (1.78)	0.366 (0.258)	0.98		
f_Methanobacteriaceae]	change	-1.428 (1.17)	-0.202 (0.292)	0.29		
g_Methanobrevibacter	P <sup>c</sup>	0.16	0.74		0.0002	0.00005
P_Firmicutes	B	0.025 (0.015)	0.025 (0.016)	0.34		
	change	0.021(0.018)	-0.001(0.028)	0.034		
	P <sup>c</sup>	0.25	0.20		0.001	0.047
P_Firmicutes	B	0.005 (0.002)	0.009 (0.003)	0.58		
f_Gemellaceae	change	0.007 (0.006)	-0.003 (0.004)	0.51		
g_	P <sup>c</sup>	0.82	0.43		0.005	0.303
P_Firmicutes	B	0.021 (0.016)	0.026 (0.017)	0.40		
	change	-0.011 (0.017)	-0.019 (0.018)	0.83		
	P <sup>c</sup>	0.77	0.56		0.005	0.26

P_Firmicutes	B	0.14 (0.09)	0.16 (0.11)	0.60		
f_Enterococaceae,	Change	0.13(0.27)	-0.12(0.09)	0.28		
g_Enterococcus	P <sup>c</sup>	0.92	0.047		0.04	0.16
P_Firmicutes	B	0.112 (0.043)	2.108 (1.502)	0.20		
f_Lactobacillaceae	Change	0.199 (0.176)	-0.83 (1.802)	0.33		
g_Lactobacillus	P <sup>c</sup>	0.38	0.70		0.059	0.70
P_Firmicutes	B	0.051 (0.029)	0.031 (0.017)	0.42		
f_Streptococccaceae,	Change	0.021 (0.045)	-0.02 (0.02)	0.89		
g_Lactococcus	P <sup>c</sup>	1.00	0.46		0.087	0.001
P_Firmicutes	B	0.003(0.002)	0.05(0.031)	0.025		
f_Turicibacteraceae	change	0.014(0.009)	-0.023(0.04)	0.054		
g_Turicibacter	P <sup>c</sup>	0.15	0.69		0.13	0.26
P_Firmicutes	B	0.57 (0.134)	0.452 (0.115)	0.97		
	change	0.05 (0.138)	0.331 (0.245)	0.67		
	P <sup>c</sup>	0.74	0.22		0.486	0.014
P_Firmicutes	B	0.013 (0.01)	0.201 (0.18)	0.68		
f_Clostridiaceae	change	0.077 (0.05)	-0.191 (0.17)	0.30		
g_	P <sup>c</sup>	0.34	0.69		0.00023	0.025
P_Firmicutes	B	1.313 (0.352)	1.34 (0.288)	0.97		
f_Lachnospiraceae	change	0.026 (0.406)	-0.007 (0.372)	0.49		
	P <sup>c</sup>	0.21	1.00		0.775	0.045
P_Firmicutes	B	0.012 (0.006)	0.031 (0.015)	0.57		
f_Lachnospiraceae	change	0.029 (0.015)	0.058 (0.04)	0.97		
g_Anaerostipes	P <sup>c</sup>	0.07	0.11		0.692	0.011
P_Firmicutes	B	0.048(0.03)	0.032(0.03)	0.77		
f_Lachnospiraceae	change	-0.040(0.03)	0.198(0.12)	0.10		
g_Clostridium	P <sup>c</sup>	0.38	0.024		0.008	0.68
p_Firmicutes	B	1.55 (0.45)	1.45 (0.31)	0.75		
f_Ruminococaceae	change	0.51 (0.30)	-0.42(0.44)	0.078		
g_	P <sup>c</sup>	0.14	0.50		0.048	1.00
p_Firmicutes	B	0.004 (0.003)	0.001 (0.001)	0.85		
f_Ruminococaceae	change	-0.001 (0.003)	0.004 (0.003)	0.67		
g_Anaerotruncus	P <sup>c</sup>	0.81	0.31		0.075	2.3 E-08
p_Firmicutes	B	6.40 (1.02)	6.10 (1.14)	0.83		
f_Ruminococaceae	change	1.67 (0.81)	2.65(1.92)	0.80		
g_Faecalibacterium	P <sup>c</sup>	0.044	0.19		0.74	0.601
p_Firmicutes	B	0.872 (0.48)	0.033 (0.032)	0.57		
f_Veillonellaceae	change	-0.41 (0.552)	0.626 (0.459)	0.30		
g_Acidaminococcus	P <sup>c</sup>	0.84	0.13		0.008	0.009
p_Firmicutes	B	0.678 (0.255)	0.471 (0.251)	0.68		
f_Veillonellaceae	change	-0.079 (0.298)	-0.107 (0.392)	0.97		
g_Dialister	P <sup>c</sup>	0.90	0.59		0.82	0.00002
p_Firmicutes	B	0.05 (0.041)	0.034 (0.016)	0.75		
f_Mogibacteriaceae	change	0.018 (0.04)	-0.029 (0.016)	0.43		
g_Mogibacterium	P <sup>c</sup>	0.69	0.16		0.003	0.074
p_Firmicutes	B	0.094 (0.066)	0.247 (0.134)	0.83		
f_Erysipelotrichaceae	change	0.169 (0.106)	-0.241 (0.134)	0.12		
g_Catenibacterium	P <sup>c</sup>	0.16	0.13		0.000041	0.874
p_Firmicutes	B	0.09(0.03)	0.80 (0.24)	0.09		
f_Erysipelotrichaceae	change	0.16(0.07)	-0.57(0.23)	0.037		
g_[Eubacterium]	P <sup>c</sup>	0.042	0.020		0.000019	0.80

p__Proteobacteria	B	0.133(0.033)	0.042(0.012)	0.09		
f_Desulfovibrionaceae	change	0.019(0.047)	0.214(0.132)	0.032		
g_Bilophila	P <sup>c</sup>	0.50	0.002		0.002	0.044
P__Proteobacteria	B	0.201 (0.096)	0.037 (0.026)	0.22		
F_Desulfovibrionaceae	change	0.114 (0.172)	0.033 (0.057)	0.46		
G_Desulfovibrio	P <sup>c</sup>	0.63	0.63		0.73	0.001
p__Proteobacteria	B	0.219 (0.126)	0.194 (0.129)	0.66		
f_Enterobacteriaceae	change	0.036(0.123)	1.40(1.001)	0.49		
g_Escherichia	P <sup>c</sup>	0.044	0.25		0.15	0.17
P_Verrucomicrobia	B	0.976 (0.758)	0.042 (0.036)	0.012		
f_Verrucomicrobiaceae	change	-0.738 (0.784)	0.370 (0.277)	0.096		
g_Akkermansia	P <sup>c</sup>	0.45	0.16		0.023	0.30

<sup>a</sup> Wilcoxon rank sum (1df) comparing neoadjuvant and adjuvant groups at baseline and last collections, and in the change between last and baseline samples

<sup>b</sup> Negative binomial mixed model test in R: `glm.nb (count at gena ~ period*wtchange2 + offset(log(totreads)), random = ~ 1|SubjectID)`, Period (final vs baseline), tchange2 (increase weight vs decrease weight). Age (continuous), race (Hispanics or not Hispanics), and total number of reads were included in the model.

<sup>c</sup> Wilcoxon signed rank (1df) to test changes between last and baseline samples

Supplementary Table 2. Wilcoxon and negative binomial mixed model (NBMM) analyses, mean baseline (standard deviation) and absolute changes in relative abundance of specific taxa between groups with loss in body mass index (BMI) and gain in BMI

Taxa abundance		Mean baseline and absolute changes in taxa abundance		BMI Loss vs BMI gain		
		BMI Loss	BMI gain	Wilcoxon <sup>a</sup> Test	NBMM	
		N=16	N=17		No chemo adjustment N=29	Chemo Adjustment N=29
p_Actinobacteria	B	0(0)	0.02(0.01)	0.30		
f_Micrococcaceae	change	0(0.01)	-0.02(0.01)	0.039		
g_Rothia	P <sup>c</sup>	0.70	0.054		0.25	0.26
p_Actinobacteria	B	2.75(1.05)	5.1(1.45)	0.11		
f_Bifidobacteriaceae	change	0.69(1.75)	2.71(2.19)	0.54		
g_Bifidobacterium	P <sup>c</sup>	1.00	0.35		0.07	0.44
p_Actinobacteria	B	6.87(1.29)	16.15(3.51)	0.04		
f_Coriobacteriaceae	change	0.11(1.44)	-3.59(4.55)	0.94		
g_Collinsella	P <sup>c</sup>	0.93	0.85		0.22	0.52
p_Actinobacteria	B	0.22(0.1)	0.03(0.01)	0.66		
f_Coriobacteriaceae	change	0.02(0.14)	0.17(0.07)	0.14		
g_Eggerthella	P <sup>c</sup>	1.00	0.01		0.98	0.74
p_Actinobacteria	B	0.28(0.14)	0.3(0.11)	0.85		
f_Coriobacteriaceae	change	0.03(0.08)	0.24(0.22)	0.21		
g_Slackia	P <sup>c</sup>	0.97	0.24		0.44	0.49
P Bacteroidetes	B	5.58(2.25)	8.42(3.19)	0.93		
f_Prevotellaceae	change	-0.41(2.59)	-3.7(3.89)	0.11		
g_Prevotella	P <sup>c</sup>	0.86	0.04		0.80	0.045
p_Bacteroidetes	B	0.01(0.01)	0.01(0.01)	0.81		
f_Rikenellaceae	change	0.01(0.01)	0.01(0.01)	0.85		
	P <sup>c</sup>	0.46	0.11		0.54	0.15
p_Bacteroidetes	B	0.03(0.01)	0.02(0.01)	0.48		
f_Rikenellaceae	change	-0.02(0.01)	-0.01(0.01)	0.20		
g_Alistipes	P <sup>c</sup>	0.22	0.69		0.66	0.56
P Bacteroidetes	B	0.38(0.17)	0.15(0.11)	0.10		
f_S24-7	change	-0.26(0.17)	-0.09(0.09)	0.85		
g_	P <sup>c</sup>	0.23	0.38		0.20	0.03
p_Bacteroidetes	B	0.10(0.06)	0.41(0.15)	0.30		
f_Barnesiellaceae	change	0.03(0.05)	0.07(0.15)	0.94		
g_	P <sup>c</sup>	0.70	0.84		0.78	0.99
p_Bacteroidetes	B	0.3(0.17)	0.08(0.04)	0.12		
f_Odoribacteraceae	change	-0.25(0.18)	0.01(0.07)	0.33		
g_Butyricimonas	P <sup>c</sup>	0.17	0.82		0.55	0.35
p_Euryarchaeota	B	2.5(1.77)	0.06(0.06)	0.006		
f_Methanobacteriaceae	change	-1.43(1.2)	0(0.08)	0.21		
g_Methanobrevibacter	P <sup>c</sup>	0.30	0.56		0.008	0.52
p_Firmicutes	B	0.04(0.02)	0.01(0)	0.11		
	change	0.02(0.03)	0(0)	0.34		
	P <sup>c</sup>	0.38	0.31		0.038	0.16
p_Firmicutes	B	0.01(0)	0.01(0)	0.66		
f_Gemellaceae	change	0.01(0.01)	0(0)	0.94		
g_	P <sup>c</sup>	0.97	0.64		0.19	0.18
P_Firmicutes	B	0.06(0.04)	0.21(0.11)	0.40		
f_Enterococcaceae	change	0(0.03)	0.03(0.26)	0.18		
g_Enterococcus	P <sup>c</sup>	0.85	0.19		0.43	0.93

p__Firmicutes	B	0.17(0.08)	1.56(1.16)	0.96		
f__Lactobacillaceae	change	0.53(0.34)	-0.92(1.32)	0.24		
g__Lactobacillus	P <sup>c</sup>	0.28	0.52		0.23	0.02
p__Firmicutes	B	0.05(0.03)	0.04(0.02)	0.47		
f__Streptococcaceae	change	0.04(0.04)	-0.04(0.02)	0.46		
g__Lactococcus	P <sup>c</sup>	0.97	0.11		0.002	0.64
P__Firmicutes	B	0.08(0.04)	0.01(0)	0.90		
f__Turicibacteraceae	change	-0.06(0.04)	0.03(0.02)	0.21		
g__Turicibacter	P <sup>c</sup>	0.20	0.23		0.21	0.19
p__Firmicutes	B	0.64(0.36)	0.04(0.03)	0.03		
f__Christensenellaceae	change	-0.39(0.3)	-0.02(0.03)	0.47		
g__	P <sup>c</sup>	1.00	0.84		0.65	0.21
p__Firmicutes	B	0.17(0.14)	0.02(0.02)	0.57		
f__Clostridiaceae	change	-0.07(0.15)	-0.01(0.02)	0.46		
g__	P <sup>c</sup>	0.57	0.91		0.42	0.57
p__Firmicutes	B	1.06(0.59)	0.55(0.32)	0.97		
f__Clostridiaceae	change	-0.55(0.57)	-0.15(0.36)	0.83		
g__Clostridium	P <sup>c</sup>	0.90	0.86		0.56	0.55
p__Firmicutes	B	0.01(0)	0.01(0.01)	0.98		
f__Dehalobacteriaceae	change	0(0)	-0.01(0)	0.04		
g__Dehalobacterium	P <sup>c</sup>	0.74	0.03		0.10	0.53
p__Firmicutes, f__Lachnospiraceae	B	1.4(0.28)	1.21(0.32)	0.37		
	change	0.28(0.3)	-0.33(0.39)	0.47		
	P <sup>c</sup>	0.38	1.00		0.22	0.31
p__Firmicutes	B	0.03(0.02)	0.03(0.01)	0.48		
f__Lachnospiraceae	change	0.01(0.02)	0.06(0.03)	0.20		
g__Anaerostipes	P <sup>c</sup>	0.56	0.04		0.18	0.45
p__Firmicutes	B	7.24(1.9)	3.52(0.82)	0.16		
f__Lachnospiraceae	change	-0.57(2.79)	-0.19(1.02)	0.28		
g__Blautia	P <sup>c</sup>	0.38	0.75		0.12	0.80
p__Firmicutes	B	0.02(0.01)	0.05(0.03)	0.813		
f__Lachnospiraceae	change	0.14(0.08)	-0.05(0.03)	0.007		
g__Lachnobacterium	P <sup>c</sup>	0.02	0.10		0.002	0.006
p__Firmicutes	B	0.51(0.14)	0.81(0.30)	0.66		
f__Lachnospiraceae	change	0.46(0.26)	0.26(0.26)	0.75		
g__lachnospira	P <sup>c</sup>	0.07	0.31		0.45	0.46
p__Firmicutes	B	2.13(0.51)	0.91(0.18)	0.04		
f__Ruminococcaceae	change	-0.02(0.62)	0.25(0.3)	0.19		
g__Oscillospira	P <sup>c</sup>	0.63	0.43		0.07	0.34
p__Firmicutes	B	0.08(0.04)	0.01(0)	0.13		
f__Erysipelotrichaceae	change	-0.06(0.04)	0.03(0.02)	0.03		
g__Clostridium	P <sup>c</sup>	0.16	0.41		0.49	0.62
p__Firmicutes	B	0.01(0.01)	0(0)	0.04		
f__Erysipelotrichaceae	change	-0.01(0.01)	0(0)	0.07		
g__Holdemania	P <sup>c</sup>	0.16	0.15		0.56	0.59

p__Firmicutes	B	0.24(0.11)	0.49(0.19)	0.912		
f__Erysipelotrichaceae	change	0.08(0.06)	-0.33(0.2)	0.009		
g__[Eubacterium]	P <sup>c</sup>	0.09	0.11		0.44	0.12
p__Proteobacteria	B	0.25(0.1)	0.02(0.02)	0.006		
f__Desulfovibrionaceae	change	0.15(0.17)	0.01(0.03)	0.80		
g__Desulfovibrio	P <sup>c</sup>	0.76	0.88		0.006	0.61
p__Proteobacteria	B	0.16(0.11)	0.54(0.3)	0.04		
f__Pasteurellaceae	change	0.1(0.13)	-0.45(0.3)	0.05		
g__Haemophilus	P <sup>c</sup>	0.11	0.25		0.09	0.38
p__Verrucomicrobia	B	0.96(0.76)	0.04(0.02)	0.51		
f__Verrucomicrobiaceae	change	-0.63(0.8)	0.32(0.21)	0.51		
g__Akkermansia	P <sup>c</sup>	0.85	0.27		0.86	0.19

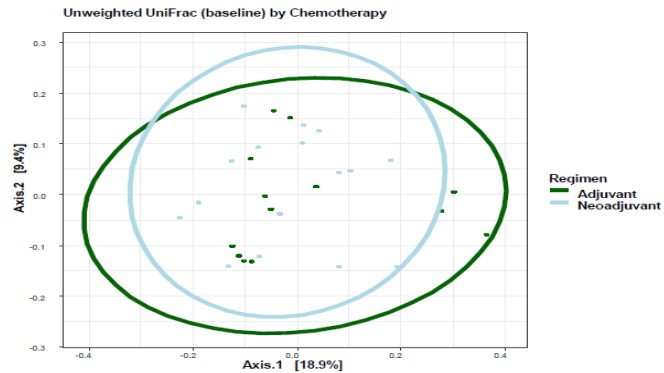
<sup>a</sup> Wilcoxon rank sum (1df) comparing BMI loss and BMI gain groups at baseline and last collections, and in the change between last and baseline samples

<sup>b</sup> Negative binomial mixed model test in R: `glm.nb(count at gena ~ period*wtchemo + offset(log(totreads)), random = ~ 1|SubjectID)`, Period (final vs baseline), tchange2 (adjuvant chemo vs neoadjuvant). Age (continuous), race (Hispanics or not Hispanics), and total number of reads were included in the model.

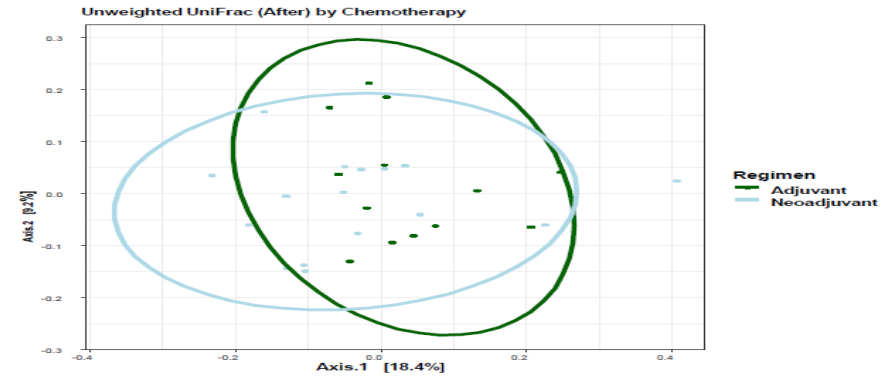
<sup>c</sup> Wilcoxon signed rank (1df) to test changes between last and baseline samples

# Supplementary Figure 1. Beta-diversity of 33 Breast Cancer Patients - Neoadjuvant vs Non-neoadjuvant groups (Panel A and B), Weight Loss vs Weight Gain groups (Panel C and D) between Baseline and Final Fecal Sample Collections

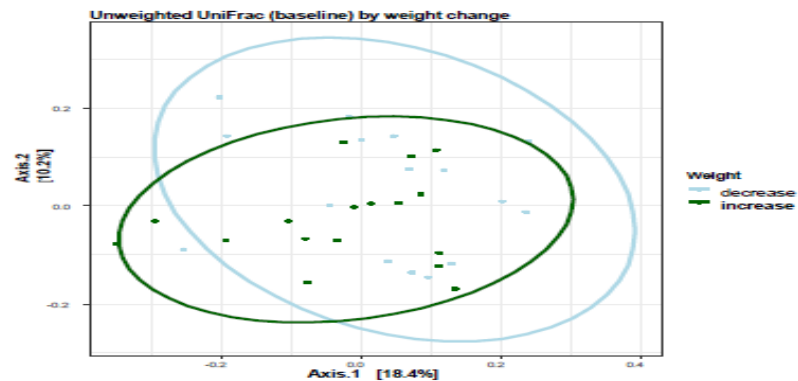
- Panel A, Baseline (p=0.61)



- Panel B, Final (p=0.94)



- Panel C, Baseline (p=0.62)



- Panel D, Final (p=0.17)

