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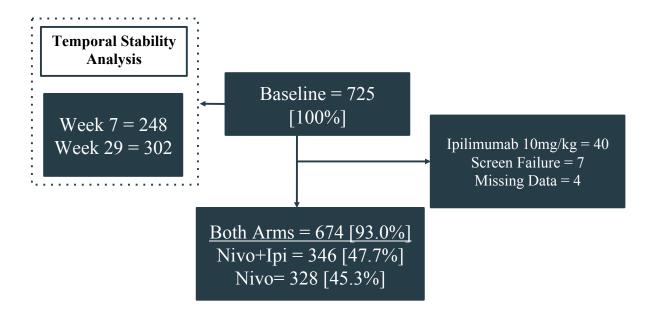
Region	Recurrence Associated Strain	OR	95% CI, low	95% CI, high	p-val	q-val
North America	Firmicutes bacterium CAG:137	0.17	0.25	0.11	1.64E-05	0.028
North America	Firmicutes bacterium CAG:884	0.40	0.49	0.33	8.43E-06	0.015
North America	Clostridium sp. CAG:780	0.21	0.30	0.15	9.26E-06	0.016
North America	Eubacterium sp. CAG:115	0.054	0.10	0.030	9.76E-07	0.0017
North America	Eubacterium sp. CAG:786	0.09	0.13	0.058	1.67E-10	2.89E-07
North America	Peptostreptococcus anaerobius	0.49	0.58	0.42	1.13E-05	0.020
North America	Eubacterium siraeum	0.088	0.15	0.052	3.39E-06	0.006
North America	Ruminococcus sp. CAG:177	0.059	0.11	0.033	9.74E-07	0.0017
North America	Aeromonas salmonicida	0.42	0.51	0.34	2.37E-05	0.041
Western Europe	Bariatricus massiliensis	1.49	1.64	1.36	1.50E-05	0.028
Western Europe	Blautia schinkii	1.45	1.58	1.33	1.13E-05	0.021
Eastern Europe	Lawsonia intracellularis	2.50	3.09	2.02	1.62E-05	0.030
Rest of World	Clostridiales bacterium 1_7_47FAA	0.22	0.31	0.15	1.60E-05	0.032

Supplemental Table 1. Region Stratified ANCOM-BC Results

ly ann. Ouus fallo: (ORS) are shown p-va adjusted values using the "holm" method.

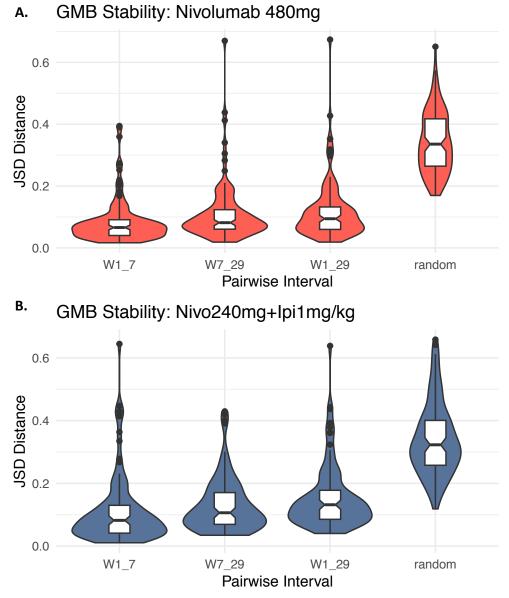
Supplemental Table 2: Patients with Longitudinal Sampling

Variable	Νο	Yes	OR	pval
Ν	424	301		
Recurrence				
No	228 (55.2%)	219 (72.8%)	0.46 (0.33 - 0.64)	1.68E-06
Yes	185 (44.8%)	82 (27.2%)	-	-
Missing (n = 11)				
Age Mean± SD	54.54± 14.32	55.4± 13.3	-	0.685
Gender				
Female	178 (42.4%)	120 (39.9%)	1.11 (0.81 - 1.52)	0.54
Male	242 (57.6%)	181 (60.1%)	-	-
Missing $(n = 4)$	· · ·			
Region				
Australia	77 (18.2%)	64 (21.3%)	-	0.13
Eastern Europe	24 (5.7%)	21 (7%)	-	0.125
ROW	29 (6.8%)	19 (6.3%)	-	0.284
North America	66 (15.6%)	39 (13%)	-	0.295
Western Europe	224 (52.8%)	158 (52.5%)	-	0.148
Stage at entry				
Not Reported	7 (1.7%)	0 (0%)	-	1
Stage IIIB	113 (26.7%)	102 (33.9%)	-	0.125
Stage IIIC	234 (55.2%)	152 (50.5%)	-	0.16
Stage IIID	10 (2.4%)	5 (1.7%)	-	0.53
Stage IV	56 (13.2%)	42 (14%)	-	0.141
B.Raf.Mut				
Invalid/Not Reported	104 (24.5%)	75 (24.9%)	-	0.145
Mutant	119 (28.1%)	79 (26.2%)	-	0.157
Wildtype	197 (46.5%)	147 (48.8%)	-	0.141
Melanoma Subtypes				
Acral	14 (3.3%)	9 (3%)	-	0.268
Cutaneous	357 (84.2%)	264 (87.7%)	-	0.142
Mucosal	4 (0.9%)	1 (0.3%)	_	1
Not Reported	8 (1.9%)	0 (0%)	-	1
Other	37 (8.7%)	27 (9%)	-	0.146
	218.92± 85.25			



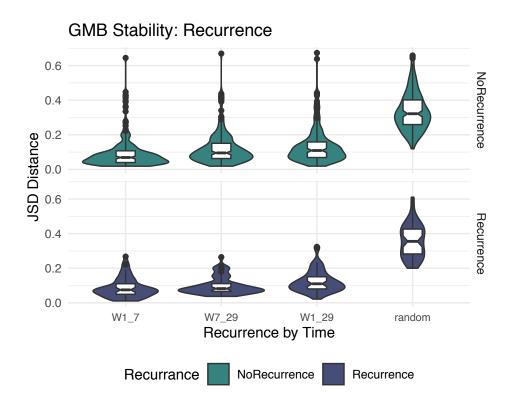
Supplemental Figure 1. Study Consort Chart

725 represented baseline. Of these , approximately half of the patients had follow-up sampling at weeks 7 and 29. From the baseline samples, 51 individuals were excluded due to coming from a supplementary arm of the original trial (n = 40), being screen failures (n = 7) or having missing randomization data (n = 4). Overall we utilized 674/725 (93.0%) of the available shotgun metagenomic samples for our core analysis.



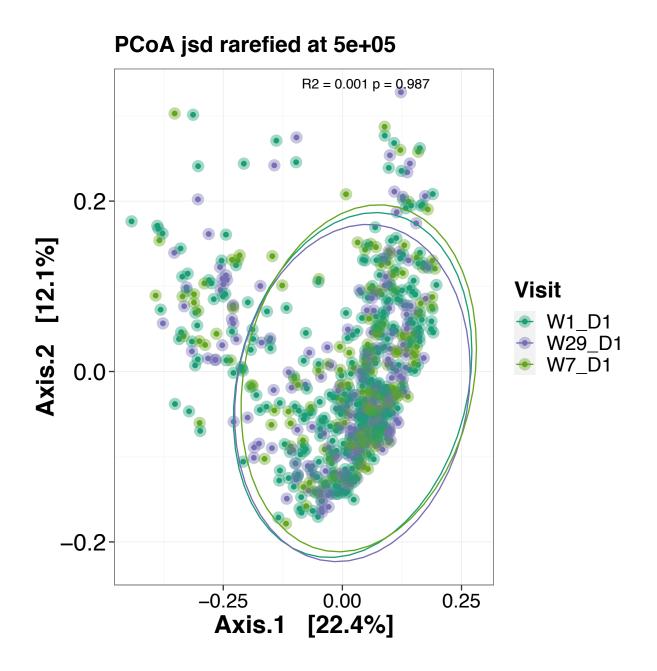
Supplemental Figure 2. JSD Distances Across Time, Stratified by Trial Arm

The figure shows the bacterial β -diversity measured using Jensen Shannon divergence between measured visits (intra-patient variation) as well as between all unpaired samples for reference (inter-patient variation), stratified by the treatment arm (red, panel A is mono treatment and blue panel B is combination treatment). Overall GMB was largely unchanged across baseline, week 7 and week 29 measurements in both arms.



Supplemental Figure 3. JSD Distances Across Time, Stratified by Recurrence Status

The figure shows the bacterial β -diversity measured using Jensen Shannon divergence between measured visits (intra-patient variation) as well as between all unpaired samples for reference (inter-patient variation), stratified by recurrence status (green, panel A: no recurrence group and navy, panel B, recurrence group). Overall GMB was largely unchanged across baseline, week 7 and week 29 measurements in both panels.



Supplemental Figure 3. PCOA plot by Time Points PCOA plat for three-time points as the outcome for the BMS patients using JSD distances.