

# Site Differences

## Luminal Dataset: Site\_General

Fixed effects: shannon ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	5.046404	0.1869831	230	26.988550	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.618353	0.2463746	43	-2.509807	0.0159
Sequencing_RunNovaSeq_Mar_Twenty	0.589189	0.5633134	43	1.045934	0.3014
SexMale	-0.055429	0.2238138	43	-0.247659	0.8056
Site_GeneralSI	-1.439385	0.1433985	230	-10.037660	0.0000

Fixed effects: observed\_otus ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	282.99532	11.35413	230	24.924444	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-32.79445	15.03846	43	-2.180706	0.0347
Sequencing_RunNovaSeq_Mar_Twenty	0.86154	34.34707	43	0.025083	0.9801
SexMale	9.65992	13.66145	43	0.707094	0.4833
Site_GeneralSI	-115.20840	8.43697	230	-13.655182	0.0000

Fixed effects: chao1 ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	333.1979	13.54867	230	24.592660	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-35.5298	18.12603	43	-1.960151	0.0565
Sequencing_RunNovaSeq_Mar_Twenty	16.6037	41.31333	43	0.401896	0.6898
SexMale	16.5133	16.46650	43	1.002841	0.3215
Site_GeneralSI	-117.2762	9.40234	230	-12.473088	0.0000

Fixed effects: pielou\_e ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.6175785	0.02089234	230	29.560051	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.0618424	0.02759381	43	-2.241170	0.0302
Sequencing_RunNovaSeq_Mar_Twenty	0.0800921	0.06305969	43	1.270101	0.2109
SexMale	-0.0135784	0.02506707	43	-0.541681	0.5908
Site_GeneralSI	-0.1272948	0.01579750	230	-8.057906	0.0000

## Mucosal Dataset: Site\_General

Fixed effects: shannon ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	5.053586	0.3221615	221	15.686497	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.404508	0.4574832	44	-0.884204	0.3814

Sequencing_RunNovaSeq_Mar_Twenty	1.731545	1.0465153	44	1.654582	0.1051
SexMale	-0.776099	0.4208949	44	-1.843925	0.0719
Site_GeneralSI	-1.616926	0.1154658	221	-14.003504	0.0000

Fixed effects: observed\_otus ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	302.08166	17.76538	221	17.003952	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-7.20383	25.03831	44	-0.287712	0.7749
Sequencing_RunNovaSeq_Mar_Twenty	73.83750	57.13044	44	1.292437	0.2030
SexMale	-43.77164	23.02019	44	-1.901445	0.0638
Site_GeneralSI	-112.96171	7.93804	221	-14.230430	0.0000

Fixed effects: chao1 ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	347.0675	20.63381	221	16.820329	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	10.1339	29.08151	44	0.348466	0.7292
Sequencing_RunNovaSeq_Mar_Twenty	88.4543	66.35625	44	1.333021	0.1894
SexMale	-44.0905	26.73754	44	-1.649012	0.1063
Site_GeneralSI	-116.5352	9.21628	221	-12.644491	0.0000

Fixed effects: pielou\_e ~ Sequencing\_Run + Sex + Site\_General

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.6082636	0.03878529	221	15.682845	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.0420446	0.05517480	44	-0.762025	0.4501
Sequencing_RunNovaSeq_Mar_Twenty	0.1999398	0.12629137	44	1.583163	0.1205
SexMale	-0.0837715	0.05077025	44	-1.650012	0.1061
Site_GeneralSI	-0.1616101	0.01294773	221	-12.481726	0.0000

## Luminal Dataset:Site

Fixed effects: shannon ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	4.733369	0.2319355	226	20.408128	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.625492	0.2458553	43	-2.544149	0.0146
Sequencing_RunNovaSeq_Mar_Twenty	0.629951	0.5618573	43	1.121194	0.2684
SexMale	-0.064143	0.2233475	43	-0.287190	0.7753
SiteProximal_Colon	0.312607	0.2400919	226	1.302029	0.1942
SiteCecum	0.641680	0.2400919	226	2.672642	0.0081
SiteIleum	-1.334510	0.2415425	226	-5.524948	0.0000
SiteJejunum	-1.324213	0.2400919	226	-5.515442	0.0000
SiteDuodenum	-0.678935	0.2446535	226	-2.775088	0.0060

Fixed effects: observed\_otus ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	266.12996	13.99030	226	19.022456	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-33.06082	15.01257	43	-2.202209	0.0331

Sequencing_RunNovaSeq_Mar_Twenty	2.85477	34.28117	43	0.083275	0.9340
SexMale	9.26819	13.63824	43	0.679574	0.5004
SiteProximal_Colon	22.17021	14.25864	226	1.554862	0.1214
SiteCecum	29.04255	14.25864	226	2.036839	0.0428
SiteIleum	-101.64604	14.34512	226	-7.085758	0.0000
SiteJejunum	-115.10638	14.25864	226	-8.072746	0.0000
SiteDuodenum	-76.20112	14.53045	226	-5.244235	0.0000

Fixed effects: chao1 ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	321.3243	16.33198	226	19.674553	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-35.9243	18.09548	43	-1.985264	0.0535
Sequencing_RunNovaSeq_Mar_Twenty	19.2442	41.23785	43	0.466664	0.6431
SexMale	15.9754	16.43906	43	0.971797	0.3366
SiteProximal_Colon	15.3605	15.90946	226	0.965492	0.3353
SiteCecum	21.1433	15.90946	226	1.328975	0.1852
SiteIleum	-112.7987	16.00689	226	-7.046888	0.0000
SiteJejunum	-124.2390	15.90946	226	-7.809125	0.0000
SiteDuodenum	-76.4352	16.21531	226	-4.713766	0.0000

Fixed effects: pielou\_e ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.5852670	0.02576003	226	22.719966	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.0627419	0.02753045	43	-2.279001	0.0277
Sequencing_RunNovaSeq_Mar_Twenty	0.0849603	0.06288218	43	1.351103	0.1837
SexMale	-0.0146369	0.02501013	43	-0.585237	0.5614
SiteProximal_Colon	0.0310319	0.02639238	226	1.175791	0.2409
SiteCecum	0.0677844	0.02639238	226	2.568333	0.0109
SiteIleum	-0.1238816	0.02655224	226	-4.665581	0.0000
SiteJejunum	-0.1141412	0.02639238	226	-4.324779	0.0000
SiteDuodenum	-0.0420237	0.02689494	226	-1.562514	0.1196

## Mucosal : Site

Fixed effects: shannon ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	4.686239	0.3421392	217	13.696880	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.426646	0.4572576	44	-0.933054	0.3559
Sequencing_RunNovaSeq_Mar_Twenty	1.734101	1.0462853	44	1.657388	0.1046
SexMale	-0.780793	0.4207378	44	-1.855772	0.0702
SiteProximal_Colon	0.877405	0.1913606	217	4.585085	0.0000
SiteCecum	0.195997	0.1913606	217	1.024227	0.3069
SiteIleum	-1.372335	0.1932855	217	-7.100043	0.0000
SiteJejunum	-1.258579	0.1958796	217	-6.425270	0.0000
SiteDuodenum	-1.076349	0.1986645	217	-5.417924	0.0000

Fixed effects: observed\_otus ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	305.76575	19.67708	217	15.539185	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-7.51911	25.09580	44	-0.299616	0.7659
Sequencing_RunNovaSeq_Mar_Twenty	73.89394	57.25353	44	1.290644	0.2036
SexMale	-44.68579	23.07402	44	-1.936628	0.0592
SiteProximal_Colon	4.80321	13.75329	217	0.349241	0.7272
SiteCecum	-13.67595	13.75329	217	-0.994377	0.3211
SiteIleum	-122.92857	13.89155	217	-8.849161	0.0000
SiteJejunum	-123.07679	14.07507	217	-8.744311	0.0000
SiteDuodenum	-100.96530	14.27429	217	-7.073228	0.0000

Fixed effects: chao1 ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	357.4016	22.84377	217	15.645479	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	9.9214	29.14616	44	0.340400	0.7352
Sequencing_RunNovaSeq_Mar_Twenty	88.5049	66.49577	44	1.330985	0.1900
SexMale	-45.4326	26.79825	44	-1.695356	0.0971
SiteProximal_Colon	-9.0706	15.94326	217	-0.568928	0.5700
SiteCecum	-18.2202	15.94326	217	-1.142818	0.2544
SiteIleum	-134.8745	16.10353	217	-8.375463	0.0000
SiteJejunum	-136.6876	16.31630	217	-8.377365	0.0000
SiteDuodenum	-105.0083	16.54725	217	-6.345967	0.0000

Fixed effects: pielou\_e ~ Sequencing\_Run + Sex + Site

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.5568829	0.04078847	217	13.652947	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.0448280	0.05509639	44	-0.813628	0.4202
Sequencing_RunNovaSeq_Mar_Twenty	0.2002557	0.12615140	44	1.587423	0.1196
SexMale	-0.0838919	0.05070435	44	-1.654531	0.1051
SiteProximal_Colon	0.1130778	0.02121323	217	5.330533	0.0000
SiteCecum	0.0359795	0.02121323	217	1.696088	0.0913
SiteIleum	-0.1235240	0.02142664	217	-5.764971	0.0000
SiteJejunum	-0.1076627	0.02171519	217	-4.957943	0.0000
SiteDuodenum	-0.0955890	0.02202422	217	-4.340175	0.0000

## Colon Data

Fixed effects: shannon ~ Sequencing\_Run + Sex + Site + Type

	Value	Std.Error	DF	t-value	p-value
(Intercept)	5.042106	0.2764287	227	18.240164	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.329861	0.3530214	45	-0.934395	0.3551
Sequencing_RunNovaSeq_Mar_Twenty	1.102511	0.8044915	45	1.370445	0.1773
SexMale	-0.821586	0.3118602	227	-2.634469	0.0090
SiteProximal_Colon	0.594711	0.1809752	227	3.286148	0.0012
SiteCecum	0.413226	0.1809752	227	2.283327	0.0233

```
TypeMucosal -0.311706 0.1474337 227 -2.114213 0.0356
```

Fixed effects: observed\_otus ~ Sequencing\_Run + Sex + Site + Type

	Value	Std.Error	DF	t-value	p-value
(Intercept)	289.48216	14.92943	227	19.390039	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	1.78874	18.70470	45	0.095631	0.9242
Sequencing_RunNovaSeq_Mar_Twenty	31.72996	42.57561	45	0.745261	0.4600
SexMale	-33.17094	16.62874	227	-1.994796	0.0473
SiteProximal_Colon	13.71421	10.38648	227	1.320391	0.1880
SiteCecum	7.77737	10.38648	227	0.748798	0.4548
TypeMucosal	-1.24341	8.45819	227	-0.147006	0.8833

Fixed effects: chao1 ~ Sequencing\_Run + Sex + Site + Type

	Value	Std.Error	DF	t-value	p-value
(Intercept)	342.1036	16.33081	227	20.948359	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	8.6147	20.28014	45	0.424784	0.6730
Sequencing_RunNovaSeq_Mar_Twenty	36.7953	46.13519	45	0.797553	0.4293
SexMale	-24.3647	18.07276	227	-1.348146	0.1790
SiteProximal_Colon	3.5008	11.65792	227	0.300296	0.7642
SiteCecum	1.7388	11.65792	227	0.149152	0.8816
TypeMucosal	-4.7411	9.49197	227	-0.499490	0.6179

Fixed effects: pielou\_e ~ Sequencing\_Run + Sex + Site + Type

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.6108578	0.03114950	227	19.610517	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.0373539	0.03960932	45	-0.943058	0.3507
Sequencing_RunNovaSeq_Mar_Twenty	0.1299892	0.09024155	45	1.440458	0.1567
SexMale	-0.0902669	0.03504625	227	-2.575650	0.0106
SiteProximal_Colon	0.0720662	0.02068747	227	3.483565	0.0006
SiteCecum	0.0512940	0.02068747	227	2.479473	0.0139
TypeMucosal	-0.0409308	0.01685178	227	-2.428873	0.0159

Pairwise comparisons using K-W test: **Shannon**

```
> kruskal.test(shannon ~ Type, DC)
```

Kruskal-Wallis rank sum test

data: shannon by Type

Kruskal-Wallis chi-squared = 0.013239, df = 1, p-value = 0.9084

```
> kruskal.test(shannon ~ Type, PC)
```

Kruskal-Wallis rank sum test

```
data: shannon by Type
Kruskal-Wallis chi-squared = 3.8034, df = 1, p-value = 0.05115

> kruskal.test(shannon ~ Type, cec)

Kruskal-Wallis rank sum test

data: shannon by Type
Kruskal-Wallis chi-squared = 10.245, df = 1, p-value = 0.001371
```

## OTUs

```
> kruskal.test(observed_otus ~ Type, DC)

Kruskal-Wallis rank sum test

data: observed_otus by Type
Kruskal-Wallis chi-squared = 2.6084, df = 1, p-value = 0.1063

> kruskal.test(observed_otus ~ Type, PC)

Kruskal-Wallis rank sum test

data: observed_otus by Type
Kruskal-Wallis chi-squared = 0.11983, df = 1, p-value = 0.7292

> kruskal.test(observed_otus ~ Type, cec)

Kruskal-Wallis rank sum test

data: observed_otus by Type
Kruskal-Wallis chi-squared = 4.2985, df = 1, p-value = 0.03814

>
```

## pielou

```
> kruskal.test(pielou_e ~ Type, DC)

Kruskal-Wallis rank sum test
```

```

data:  pielou_e by Type
Kruskal-Wallis chi-squared = 0.23512, df = 1, p-value = 0.6278

> kruskal.test(pielou_e ~ Type, PC)

      Kruskal-Wallis rank sum test

data:  pielou_e by Type
Kruskal-Wallis chi-squared = 4.8546, df = 1, p-value = 0.02757

> kruskal.test(pielou_e ~ Type, cec)

      Kruskal-Wallis rank sum test

data:  pielou_e by Type
Kruskal-Wallis chi-squared = 10.293, df = 1, p-value = 0.001336

```

## chao1

```

> kruskal.test(chao1 ~ Type, DC)

      Kruskal-Wallis rank sum test

data:  chao1 by Type
Kruskal-Wallis chi-squared = 1.3429, df = 1, p-value = 0.2465

> kruskal.test(chao1 ~ Type, PC)

      Kruskal-Wallis rank sum test

data:  chao1 by Type
Kruskal-Wallis chi-squared = 0.03463, df = 1, p-value = 0.8524

> kruskal.test(chao1 ~ Type, cec)

      Kruskal-Wallis rank sum test

data:  chao1 by Type
Kruskal-Wallis chi-squared = 1.7359, df = 1, p-value = 0.1877

```

## SI Data

```

Fixed effects: shannon ~ Sequencing_Run + Sex + Site + Type
              Value Std.Error   DF   t-value p-value

```

(Intercept)	3.348770	0.2245483	217	14.913364	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.726573	0.2649479	45	-2.742323	0.0087
Sequencing_RunNovaSeq_Mar_Twenty	1.220062	0.6068008	45	2.010646	0.0504
SexMale	0.165556	0.2387547	217	0.693417	0.4888
SiteJejunum	0.051798	0.1820898	217	0.284466	0.7763
SiteDuodenum	0.428941	0.1853970	217	2.313634	0.0216
TypeMucosal	-0.508098	0.1508265	217	-3.368761	0.0009

Fixed effects: observed\_otus ~ Sequencing\_Run + Sex + Site + Type

	Value	Std.Error	DF	t-value	p-value
(Intercept)	167.90205	13.35238	217	12.574691	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-42.31294	14.24583	45	-2.970198	0.0048
Sequencing_RunNovaSeq_Mar_Twenty	46.88988	32.61987	45	1.437463	0.1575
SexMale	4.38770	12.95067	217	0.338801	0.7351
SiteJejunum	-7.21730	12.76958	217	-0.565195	0.5725
SiteDuodenum	21.66622	12.98576	217	1.668459	0.0967
TypeMucosal	-1.06499	10.55395	217	-0.100910	0.9197

Fixed effects: chao1 ~ Sequencing\_Run + Sex + Site + Type

	Value	Std.Error	DF	t-value	p-value
(Intercept)	213.05369	16.31541	217	13.058434	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-33.40954	17.61331	45	-1.896835	0.0643
Sequencing_RunNovaSeq_Mar_Twenty	71.34927	40.32925	45	1.769169	0.0836
SexMale	5.45210	16.00210	217	0.340711	0.7337
SiteJejunum	-6.72800	15.36491	217	-0.437881	0.6619
SiteDuodenum	31.33129	15.62736	217	2.004901	0.0462
TypeMucosal	-6.48712	12.70203	217	-0.510715	0.6101

Fixed effects: pielou\_e ~ Sequencing\_Run + Sex + Site + Type

	Value	Std.Error	DF	t-value	p-value
(Intercept)	0.4529870	0.02767588	217	16.367575	0.0000
Sequencing_RunNovaSeq_Jan_Twenty	-0.0707686	0.03391422	45	-2.086693	0.0426
Sequencing_RunNovaSeq_Mar_Twenty	0.1456198	0.07769643	45	1.874215	0.0674
SexMale	0.0203883	0.03035307	217	0.671706	0.5025
SiteJejunum	0.0118491	0.02053381	217	0.577056	0.5645
SiteDuodenum	0.0498862	0.02091545	217	2.385135	0.0179
TypeMucosal	-0.0763934	0.01702405	217	-4.487383	0.0000

## Shannon

```
> kruskal.test(shannon ~ Type, duo)
```

Kruskal-Wallis rank sum test

data: shannon by Type

Kruskal-Wallis chi-squared = 5.5627, df = 1, p-value = 0.01835



```
> kruskal.test(shannon ~ Type, jej)
```

```
Kruskal-Wallis rank sum test
```

```
data: shannon by Type
```

```
Kruskal-Wallis chi-squared = 0.30906, df = 1, p-value = 0.5783
```

```
> kruskal.test(shannon ~ Type, ile)
```

```
Kruskal-Wallis rank sum test
```

```
data: shannon by Type
```

```
Kruskal-Wallis chi-squared = 0.71126, df = 1, p-value = 0.399
```

## OTUs

```
> kruskal.test(observed_otus ~ Type, duo)
```

```
Kruskal-Wallis rank sum test
```

```
data: observed_otus by Type
```

```
Kruskal-Wallis chi-squared = 0.046652, df = 1, p-value = 0.829
```

```
> kruskal.test(observed_otus ~ Type, jej)
```

```
Kruskal-Wallis rank sum test
```

```
data: observed_otus by Type
```

```
Kruskal-Wallis chi-squared = 0.7633, df = 1, p-value = 0.3823
```

```
> kruskal.test(observed_otus ~ Type, ile)
```

```
Kruskal-Wallis rank sum test
```

```
data: observed_otus by Type
```

```
Kruskal-Wallis chi-squared = 0.079041, df = 1, p-value = 0.7786
```

## Pielou

```
> kruskal.test(pielou_e ~ Type, duo)
```

```
Kruskal-Wallis rank sum test
```

```
data:  pielou_e by Type
Kruskal-Wallis chi-squared = 9.3533, df = 1, p-value = 0.002226
```

```
> kruskal.test(pielou_e ~ Type, jej)
```

```
Kruskal-Wallis rank sum test
```

```
data:  pielou_e by Type
Kruskal-Wallis chi-squared = 0.95423, df = 1, p-value = 0.3286
```

```
> kruskal.test(pielou_e ~ Type, ile)
```

```
Kruskal-Wallis rank sum test
```

```
data:  pielou_e by Type
Kruskal-Wallis chi-squared = 1.3177, df = 1, p-value = 0.251
```

## chao1

```
> kruskal.test(chao1 ~ Type, duo)
```

```
Kruskal-Wallis rank sum test
```

```
data:  chao1 by Type
Kruskal-Wallis chi-squared = 0.036125, df = 1, p-value = 0.8493
```

```
> kruskal.test(chao1 ~ Type, jej)
```

```
Kruskal-Wallis rank sum test
```

```
data:  chao1 by Type
Kruskal-Wallis chi-squared = 0.52231, df = 1, p-value = 0.4699
```

```
> kruskal.test(chao1 ~ Type, ile)
```

```
Kruskal-Wallis rank sum test
```

```
data:  chao1 by Type
Kruskal-Wallis chi-squared = 0.10757, df = 1, p-value = 0.7429
```