

Omit two sequencing runs and luminal samples and perform combat seq

Then filter on sequencing depth of 10k or less, and prevalence filter to 10%

Genotype* Site_General interaction

Permutation: free
Number of permutations: 10000

Terms added sequentially (first to last)

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) | |
|-----------------------|-----|-----------|---------|---------|---------|-----------|-----|
| Sequencing_Run | 1 | 21.98 | 21.975 | 18.305 | 0.03730 | 9.999e-05 | *** |
| Sex | 1 | 2.78 | 2.782 | 2.317 | 0.00472 | 0.09689 | . |
| Genotype | 2 | 38.68 | 19.340 | 16.110 | 0.06566 | 9.999e-05 | *** |
| Site_General | 1 | 192.28 | 192.285 | 160.170 | 0.32640 | 9.999e-05 | *** |
| Genotype:Site_General | 2 | 2.06 | 1.028 | 0.856 | 0.00349 | 0.49525 | |
| Residuals | 276 | 331.34 | 1.201 | | 0.56243 | | |
| Total | 283 | 589.11 | | | 1.00000 | | |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Genotype* Site Interaction

Permutation: free
Number of permutations: 10000

Terms added sequentially (first to last)

| | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) | |
|----------------|-----|-----------|---------|---------|---------|-----------|-----|
| Sequencing_Run | 1 | 21.98 | 21.975 | 21.635 | 0.03730 | 9.999e-05 | *** |
| Sex | 1 | 2.78 | 2.782 | 2.739 | 0.00472 | 0.06259 | . |
| Genotype | 2 | 38.68 | 19.340 | 19.040 | 0.06566 | 9.999e-05 | *** |
| Site | 5 | 249.42 | 49.884 | 49.113 | 0.42339 | 9.999e-05 | *** |
| Genotype:Site | 10 | 8.11 | 0.811 | 0.798 | 0.01376 | 0.72883 | |
| Residuals | 264 | 268.15 | 1.016 | | 0.45517 | | |
| Total | 283 | 589.11 | | | 1.00000 | | |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

