

Table S16: Statistical measures determining significance of the G+C content of the *Fusarium circinatum*-specific genes against different genomic regions of the *Fusarium circinatum* host genome using Students t-test (unpaired)^A.

Description	Mean G + C content (%)	Standard Deviation	Standard Error of Mean	P-value	t	Degrees of Freedom	Standard error of difference
<i>Fusarium circinatum</i> -specific genes	51,2	1,32	0,5932959				
Contig02138	48	2,05	0,6482669	0,008	3,1273	13	1,017
Chromosome 3	47,29	0,299	0,1337169	0,002	6,429	8	0.608
<i>F. circinatum</i> genome	47	0,499	0,1504542	0,0001	9,4382	14	0,445

^A H₀ = G+C content (%) of *F. circinatum*-specific genes are similar to that of *F. circinatum* genomic region.

H₁ = G + C content (%) of *F. circinatum*-specific genes is significantly different than other genomic regions of *F. circinatum*.