

Table S20: Statistical measures determining significance of the G+C content of the FCIRG 04558 xenologous gene pair (KIW 84299) 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
FCIRG 04558	53,2						
KIW 84299	55						
Xenologous genes mean	54,1	0,9	0,6364				
Contig 02138 coding genes	49,7	2,05	0,5479	0,011	2,9249	14	1,504
<i>F. circinatum</i> chromosome 3	47,92	0,299	0,13372	0,0001	15,2854	5	0,404
<i>F. circinatum</i> genome	47,3	0,449	0,13538	0,001	17,4525	11	0,39

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

H₁ = G+C content (%) of xenologous gene pair (FCIRG_04558) is higher than other genomic regions of *F. circinatum*