

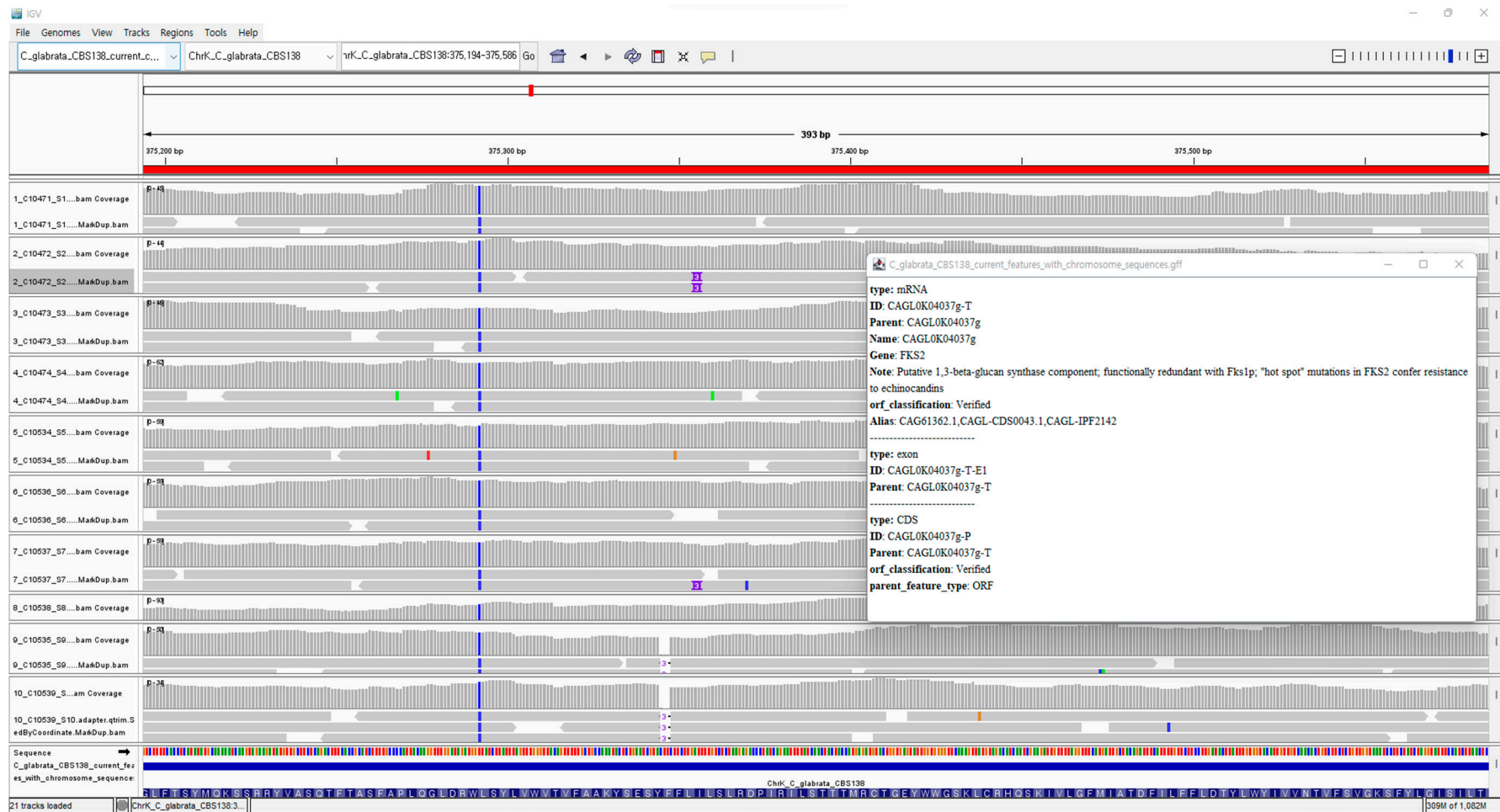
Supplementary Table S1. The list of possible genes associated with antifungal resistance in *C. glabrata*

Possible antifungal resistance genes										
ADA2	CAGL0B03355g	CAGL0G07689g	CAGL0K03377g	CAGL0L10318g	EPA3	FCY2	INO1	PDR13	SSD1	YOR1
ADH1	CAGL0B03421g	CAGL0G09273g	CAGL0K04301g	CAGL0L10604g	ERG1	FEN1	IPC1	PFK1	STB5	YPS5
ADK1	CAGL0C02981g	CAGL0G09603g	CAGL0K05995g	CAGL0L10736g	ERG2	FKS1	JJJ1	PGK1	STR3	
AHP1	CAGL0D00946g	CAGL0H02387g	CAGL0K08866g	CAGL0M01870g	ERG3	FKS2	MEC3	PUP1	SUR2	
AMT1	CAGL0D06512g	CAGL0H05181g	CAGL0K09460g	CAGL0M04631g	ERG4	FKS3	MET8	PYC1	SUR4	
AP1	CAGL0E00803g	CAGL0H06809g	CAGL0K09702g	CAGL0M05005g	ERG5	FLR1	MGE1	QDR2	SUT1	
AQR1	CAGL0E01353g	CAGL0H08866g	CAGL0K10934g	CAGL0M07766g	ERG6	FLR2	MSH2	ROX1	TDH3	
ATF2	CAGL0E04554g	CAGL0I01980g	CAGL0K11616g	CAGL0M08426g	ERG7	FPS1	MT-II	RPN4	TOG1	
BMT2	CAGL0E04576g	CAGL0I02464g	CAGL0K12100g	CAGL0M09713g	ERG8	FPS2	NCE103	RSB1	TPO1_1	
BRE5	CAGL0F04917g	CAGL0I04422g	CAGL0K12958g	CAGL0M10219g	ERG9	GAS1	NDT80	RTA1	TPO1_2	
CAGL0A01650g	CAGL0F05467g	CAGL0I07249g	CAGL0L01485g	CAGL0M12749g	ERG10	GLN3	NOP8	RTT106	TPO3	
CAGL0A02816g	CAGL0F06897g	CAGL0I07645g	CAGL0L02211g	CAGL0M12925g	ERG11	GPD2	NUD1	SDH2	TPO4	
CAGL0A04169g	CAGL0F07117g	CAGL0I10604g	CAGL0L03135g	CAGL0M14047g	ERG13	HAL9	OCH1	SEC53	UFD1	
CAGL0A04543g	CAGL0G01122g	CAGL0J00363g	CAGL0L03223g	CAGL0M14091g	ERG20	HFD1	PCK1	SET1	UGP1	
CAGL0A04829g	CAGL0G03861g	CAGL0J00451g	CAGL0L06864g	CDR1	ERG25	HSC82	PDC	SHM2	UPC2A	
CAGL0B01078g	CAGL0G05269g	CAGL0J00891g	CAGL0L07678g	CTA1	ERG26	HSP12	PDH1	SLG1	UPC2B	
CAGL0B01969g	CAGL0G06468g	CAGL0J07502g	CAGL0L08338g	ECM4	ERG27	HSP31	PDR1	SNQ2	VPH2	
CAGL0B02343g	CAGL0G07271g	CAGL0K02563g	CAGL0L10186g	ENO1	FCY1	IFA38	PDR12	SPE3	YBT1	

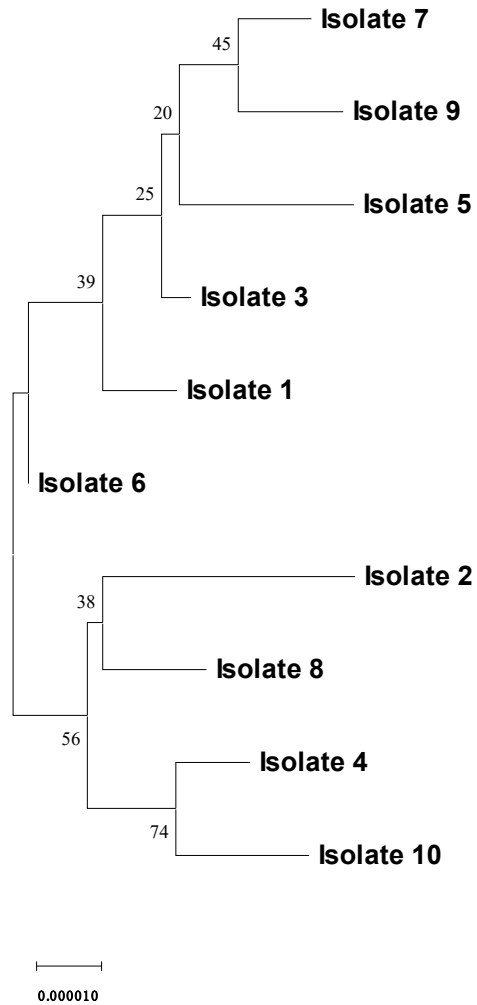
Supplementary Table S2. Sequencing and post-sequencing parameters of whole-genome sequencing in this study

Isolate no.	Sequencing parameter				Post-sequencing parameter				
	Total yield (Gb)	Cluster PF (%)	Cluster count PF (million)	≥Q30 (%)	Total reads	Trimming rate (%)	Mapping rate (%)	Duplicate rate (%)	Coverage
1	8.42	90.29 ± 0.73	26.81	93.57	5,172,324	0.07	98.2	0.05	60.6X
2					5,265,030	0.05	98.5	0.04	62.1X
3					5,979,756	0.06	98.7	0.04	70.8X
4					5,349,312	0.05	98.3	0.05	62.8X
5					4,772,064	0.06	98.6	0.03	56.4X
6					5,394,634	0.05	98.6	0.04	63.8X
7					4,684,438	0.05	98.6	0.04	55.4X
8					5,841,744	0.05	98.7	0.04	69.1X
9					4,739,146	0.04	98.7	0.04	56.1X
10					5,026,660	0.06	98.6	0.04	59.3X
Average	8.42	90.29 ± 0.73	26.81	93.57	5,222,511	0.05	98.6	0.04	61.6X

Abbreviations: PF, passing filter.



Supplementary Figure S1. An example of Integrative Genomics Viewer showing mutations on *FKS2* for 10 serial isolates of *C. glabrata*.



Supplementary Figure S2. Phylogenetic analysis of 10 serial *C. glabrata* isolates using SNP data for 182 resistance genes. Scale bar, number of nucleotide substitutions per site; numbers on nodes, bootstrap resampling values.