

**Supplemental Table 3. Comparison of transcript levels**

Transcript ratio in <i>sch9</i> mutant versus wild-type or reconstituted mutant strains							
<u>gene</u>	<u>proposed function</u>	<u>normoxia</u>		<u>hypoxia</u>		<u>hypoxia + CO<sub>2</sub></u>	
		array <sup>1</sup>	qPCR <sup>2</sup>	array <sup>1</sup>	qPCR <sup>2</sup>	array <sup>1</sup>	qPCR <sup>2</sup>
<i>RNR22</i>	ribonucleoside diphosphate reductase	0.05	0.3	-	0.8	-	0.8
<i>ERG11</i>	lanosterol demethylase	-	2.4	3.6	1.9	3.6	5.9
<i>ECE1</i>	cell elongation associated	-	0.9	11	54	17	128
<i>ORF19.5831</i>	unknown	-	2.1	-	1.4	7.5	0.2
<i>CZF1</i>	transcription factor	-	2.1	2.8	1	-	2.5
<i>SCH9</i>	kinase	-	<0.002	-	<0.002	-	<0.002

<sup>1</sup>comparison of *sch9* mutant CCS3 to wild-type CAF2-1 by microarray analysis (Supplemental Table 2)

<sup>2</sup>comparison of *sch9* mutant CCS3 to reconstituted mutant CCS4 by qPCR