

Table S1 Yeast strains used in this study

Strains ^a :	Genotypes ^b :					
FA/Cu resistance gene amplification assay						
Haploids:						
JAY357:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>			
JAY247:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>SFA1</i> :: <i>CUP1-HphMX4</i>			
JAY381:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>SFA1</i> :: <i>CUP1-HphMX4</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>		
JAY372:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>		
JAY378:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-KanMX4</i>		
HSZy1 and HSZy2 ^c :	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-KanMX4</i>	<i>msh2</i> Δ :: <i>hisG</i>	
Diploids:						
JAY275:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>CORE</i>			
	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>CORE</i>			
JAY386:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>		
	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>CORE</i>	<i>DDI1</i>		
JAY384:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>SFA1</i> :: <i>CUP1-HphMX4</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>	<i>CAN1</i>	
	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>	<i>can1</i> Δ :: <i>NatMX4</i>	
JAY385:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>SFA1</i> :: <i>CUP1-HphMX4</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>		
	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>SFA1</i> :: <i>CUP1-HphMX4</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>		
JAY350:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-KanMX4</i>	<i>CAN1</i>	
	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>	<i>can1</i> Δ :: <i>NatMX4</i>	
HSZy8 and HSZy9 ^c :	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-KanMX4</i>	<i>msh2</i> Δ :: <i>hisG</i>	<i>CAN1</i>
	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>	<i>msh2</i> Δ :: <i>hisG</i>	<i>can1</i> Δ :: <i>NatMX4</i>
JAY510:	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>	<i>ymrcty1-5</i> Δ :: <i>CORE</i>	
	<i>MAT</i> α	<i>cup1</i> Δ <i>RSC30</i>	<i>sfa1</i> Δ :: <i>hisG</i>	<i>DDI1</i> :: <i>SFA1-CUP1-HphMX4</i>	<i>ymrcty1-5</i> Δ :: <i>CORE</i>	

- Only the strains ultimately used in the experiments described in the article are shown. The genotypes of the intermediate strains used in the construction of these strains are available upon request.
- With the exception of YJM799, all strains are isogenic with MS71 and have in common the following genotype: *ade5-1*, *his7-2*, *leu2-3,112*, *LEU2*, *ura3-52*, and *trp1-289*. Only the relevant genotype modifications introduced in this study are shown in the table above.
- HSZy1 and HSZy2, as well as HSZy8 and HSZy9, are independent strain isolates of the same genotypes, and were all used in the selection of CNV clones.

Table S1 Yeast strains used in this study (continued)

Strains ^a :	Genotypes ^b :			
Chr13 candidate fragile site mapping				
Diverged haploids:				
YJM799 ^d :	<i>MATα</i>	<i>ho::hisG</i>	<i>ura3</i>	<i>gal2</i>
JAY405:	<i>MATα</i>	<i>cup1Δ RSC30</i>	<i>sfa1Δ::hisG</i>	<i>ADH6::CORE</i>
JAY794 and JAY795:	<i>MATα</i>	<i>cup1Δ RSC30</i>	<i>sfa1Δ::hisG</i>	<i>ura3Δ ADH6::CORE2</i>
Hybrid diploids:				
JAY408:	$\frac{MAT\alpha}{MAT\alpha}$	cross between YJM799 and JAY405		
JAY800 and JAY801:	$\frac{MAT\alpha}{MAT\alpha}$	cross between YJM799 and JAY794 or JAY795, respectively		

d. YJM799 is isogenic to YJM789, and was a generous gift from John McCusker.