**File S1**

**Strain construction**

*C. albicans* strain AF1006 producing C-terminally HA-tagged Sch9 was constructed by transformation of heterozygous strain CAS2 by a tagging cassette generated by oligonucleotides Sch9-HA for/rev, as described (SCHAEKEL *et al.* 2013). Correct chromosomal integration was verified by colony PCR using primers Sch9ver and 3′ test HA-tag. Both alleles of *SCH9* were deleted in *C. albicans* strain RM1000AH (SANYAL *et al.* 2004) and 8675 (JOGLEKAR *et al.* 2008) using the URA blaster method. The construction of the URA blaster deletion cassette for *SCH9* was described previously (STICHTERNOTH *et al.* 2011). After the deletion of the first copy, the heterozygous strains were grown on 5-FOA plate to make the cells auxotroph for *URA3* to obtain RMKS1A, RMKS1B and 8675t. Then the same cassette was again used to disrupt the second allele of the gene, to get strains RMKS2A, RMKS2B and 8675T, respectively. To obtain the re-integrant of Sch9 in heterozygous and homozygous mutant background, the entire ORF along with its promoter and terminator was cloned in *Kpn*I and *Sal*I sites in CIp10 integration vector (MURAD *et al.* 2000). Sch9 orf was re-integrated at *RPS10* locus in the *Candida* genome using *Stu*I to obtain RMKS1AR, RMKS1BR, RMKS2AR and RMKS2BR. The correct chromosomal integration of CIp10 was verified by PCR using primers UP-RPS10 and NV207. To check the binding pattern of CENP-A across the centromere in *sch9* mutant by ChIP, one copy of CENP-A was tagged with Prot A using plasmid construct pCaCse4TAPNAT (THAKUR and SANYAL 2013). pCaCse4-TAP-NAT was partially digested with *Xho*I and transformed into RMKS2A to get Prot A tagged CENP-A strain.

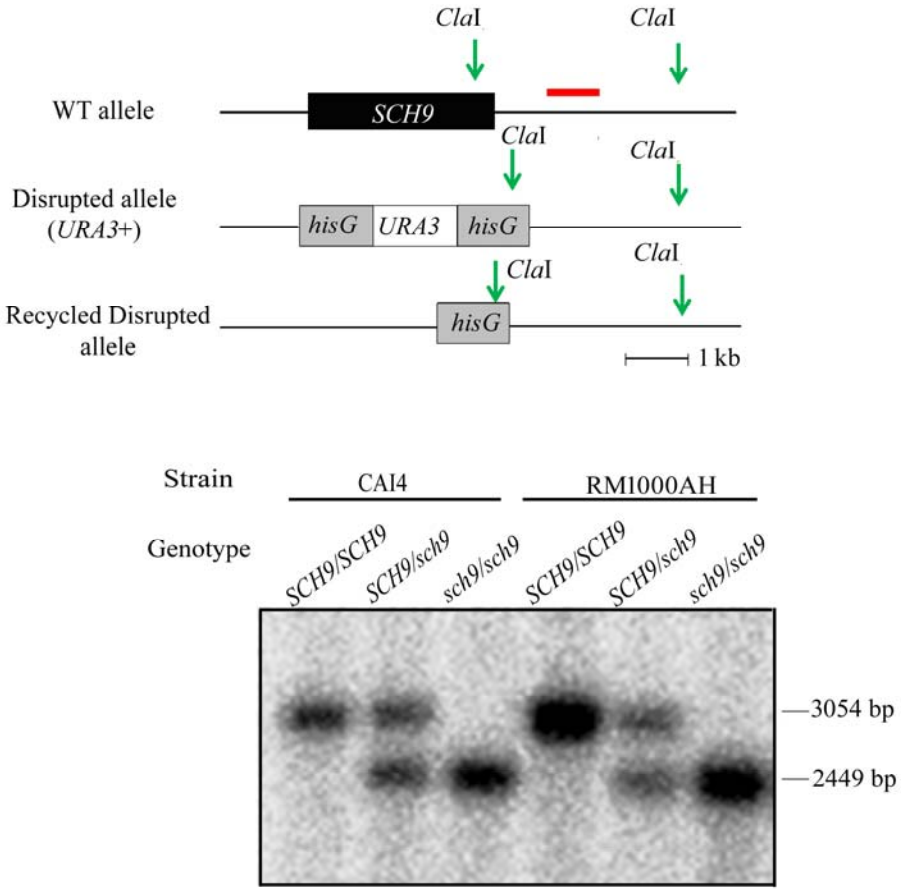


**Figure S1** Southern blot analysis. Line diagrams showing wild-type and disrupted alleles of *SCH9*. *Cla*I digested DNA from wild-type strains (CAI4, RM1000AH) and corresponding heterozygous and null mutant strains lacking one or both copies of *SCH9* gene was separated on a agarose gel, blotted and probed with a region marked by the red line. Green arrows indicate *Cla*I sites. Bar, 1 kb.

| | Percentage of cells with indicated morphology | | | | Total no. of cells counted |
|---|---|---|---|---|---|
| |  | | | | |
| CAI4 | 61.1 | 24.7 | 0.4 | 13.8 | 247 |
| CAS1 | 69.1 | 24.7 | 0.7 | 6 | 133 |
| CCS3 | 79.2 | 10.9 | 1.2 | 3.6 | 164 |

**Figure S2** *C. albicans* wild-type (*SCH9/SCH9*), heterozygous (*SCH9/sch9*) and homozygous null mutant (*sch9/sch9*) strains were grown till $OD_{600}$ ~ 1 at 30° in normoxic condition in YPDU and were stained with DAPI. A table showing percentages of cells with indicated morphologies of DAPI-stained nuclei.

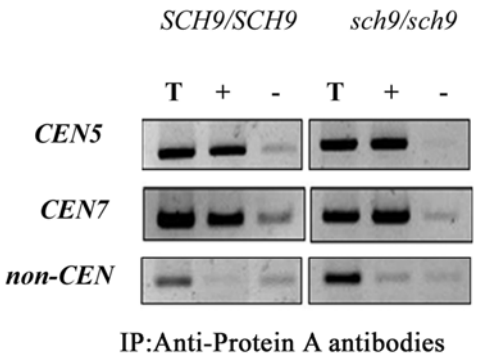


**Figure S3** Cse4 localisation at the centromere is not affected by absence of Sch9. Standard ChIP assays were performed on strains CAKS102 (*CSE4-TAP/CSE4;SCH9/SCH9*) and J200T (*CSE4-TAP/Cse4; sch9/sch9* ) (grown at 30°) using anti-Protein A (Cse4) antibodies. Enrichment at *CEN7*, *CEN5* and non-centromeric region was analysed using semi- quantitative PCR. PCR using total DNA (T) or ChIP DNA fractions with (+) or without (-) antibodies was performed.

**Table S1 Strains used in this study**

| Name | Parent | Genotype | Reference |
|---|---|---|---|
| CAI4 | SC5314 | *ura3*::*imm434*/*ura3*::*imm434* | Fonzi *et al* 1993 |
| CAS1 | CAI4 | as CAI4 but *SCH9/sch9::hisG-URA3-hisG* | Stichternoth *et al*, 2011 |
| CAS2 | CAS1 | as CAI4 but *SCH9/sch9*::*hisG* | Stichternoth *et al*, 2011 |
| CCS3 | CAS2 | as CAI4 but *sch9*::*hisG/sch9*::*hisG URA3/ura3*::*imm434* | Stichternoth *et al*, 2011 |
| AF1006 | CAS2 | as CAS2 but *SCH9*::(*3xHA-URA3*)*/sch9*::*hisG* | This study |
| RM1000AH | RM1000 | *Δura3*::*imm434/Δura3*::*imm434Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4* | Sanyal *et al*, 2004 |
| RMKS1A | RM1000AH | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/SCH9* | This study |
| RMKS1B | RM1000AH | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/SCH9* | This study |
| RMKS2A | RMKS1A | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/sch9*::*hisG-URA3-hisG* | This study |
| RMKS2B | RMKS1B | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/sch9*::*hisG-URA3-hisG* | This study |
| RMKS1AR | RMKS1A | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/SCH9/Cip10-SCH9* | This study |
| RMKS1BR | RMKS1B | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/SCH9/ Cip10-SCH9* | This study |
| RMKS2AR | RMKS2A | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/sch9*::*hisG-URA3-hisG/ Cip10-SCH9* | This study |
| RMKS2BR | RMKS2B | *Δura3*::*imm434/ Δura3*::*imm434 Δhis1*::*hisG/ Δhis1*::*hisG arg4*::*HIS1/ARG4 sch9*::*hisG/sch9*::*hisG-URA3-hisG/ Cip10-SCH9* | This study |
| 8675 | BWP17 | *Δ ura3*::*λimm434/ Δ ura3*::*imm434 Δhis1*::*hisG/Δhis1*::*hisGΔarg4*::*hisG/arg4*::*hisG CSE4/CSE4:GFP:CSE4* | Joglekar*et al*, 2008 |

| | | | |
|---|---|---|---|
| 8675t | 8675 | *Δ ura3::λimm434/Δura3::imm434 Δhis1::hisG/Δhis1::hisGΔarg4::hisG/Δarg4:: hisG CSE4/CSE4:GFP:CSE4 sch9::hisG/SCH9* | This study |
| 8675T | 8675t | *Δ ura3::λimm434/Δura3::imm434 Δhis1::hisG/Δhis1::hisGΔarg4::hisG/Δarg4:: hisG CSE4/CSE4:GFP:CSE4 sch9::hisG/sch9::hisG-URA3-hisG* | This study |
| CAKS102 | SN148 | *Δura3::imm434/Δura3::imm434, Δhis1::hisG/Δhis1::hisG, Δarg4::hisG/Δarg4::hisG, Δleu2::hisG/Δleu2::hisG CSE4/CSE4-TAP(URA3)* | Mitra *et al*, 2014 |
| J200 | RM1000AH | *Δura3::imm434/ Δura3::imm434 Δhis1::hisG/ Δhis1::hisG arg4::HIS1/ARG4 CSE4/CSE4TAP-NAT* | Thakur *et al*, 2013 |
| J200T | J200 | *ura3::imm434/ ura3::imm434 his1::hisG/his1::hisG arg4::HIS1/ARG4 sch9::hisG/sch9::hisG-URA3-hisG CSE4::CSE4-TAP-NAT* | This study |

**Table S2 Primers used in this study**

| Primer name | Sequence | Description |
|---|---|---|
| 2498-21 | CTG GTG CAA GAC CCT CAT AGA AGC | Semi-quantitative ChIP PCR primers for CEN7 |
| 2498-22 | CCT GAC ACT GTC GTT TCC CAT AGC | Semi-quantitative ChIP PCR primers for CEN7 |
| CEN5e | TGTTCTGACATACTGGGTAGACTTT | Semi-quantitative ChIP PCR primers for CEN5 |
| CEN5f | CGAAGCATTTTGTATAACAGCCC | Semi-quantitative ChIP PCR primers for CEN5 |
| CACH5R1 | TTCATGGAAGAGGGGTTTCA | qPCR primers for CEN5 |
| CACH5F1 | CCCGCAAATAAGCAAACACT | qPCR primers for CEN5 |
| NCEN7-3 | GCATACCTGACACTGTCGTT | qPCR primers for CEN7 |
| NCEN7-4 | AACGGTGCTACGTTTTTTTA | qPCR primers for CEN7 |
| Ctrl 7 a | ACTCGCCTTCCCCTCCTTTAAATAG | qPCR and semi-quantitative ChIP PCR primers for non centromeric region |
| Ctrl 7 b | CCACTACTACGACTGTGGATTCACT | qPCR and semi-quantitative ChIP PCR primers for non centromeric region |
| Sch9-HA for | GAAGAAGAAGATGAAATGGAAGTTGATGAAGAT CAACATATGGATGATGAATTTGTCAATGGAAGAT TTGATCTTGGTGGTGGTCGGATCCCCGGGTTAAT TAA | HA tagging |
| Sch9-HA rev | GCACAAAATGGAGAAGGAGAAAAAGTAGGAAC GGAATTCTATTGAATGGAACAGTTTAGTTCTAGA AGGACCACCTTTGATTG | HA tagging |
| Sch9ver | GTTGATTTCTGGTCATTAGG | Tagging verification primers |
| 3‘ test HA-tag | CATCGTATGGGTAAAAGATG | Tagging verification primers |
| NV195 | AGTGGTACCGGTCGATGTATAACTTCATTTCAT | CIp10 cloning forward |
| NV196 | ACGCGTCGAGCAC AGA CAT TGG GCA AGA AA | CIp10 cloning reverse |
| UP-RPS10 | TTCTGGTGTTCTCTCACTGTTAAGC | CIp10 integration confirmation forward |
| NV207 | GAGTTATTAGCCCTGCGATCTTTG | CIp10 integration confirmation reverse |

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