A Manuscript Microscope 'Sentence Audit' of:

Heterochromatin renewal after release from growth arrest controls genome-wide transcription re-activation in S.cerevisiae

What is the Manuscript Microscope Sentence Audit?

The Manuscript Microscope Sentence Audit is a research paper introspection system that parses the text of your manuscript into minimal sentence components for faster, more accurate, enhanced proofreading.

Why use a Sentence Audit to proofread your manuscript?

- Accelerated Proofreading: Examine long technical texts in a fraction of the usual time.
- Superior Proofreading: Detect subtle errors that are invisible to traditional methods.
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Bonus 1: Improved Productivity: Rapidly refine rough drafts to polished papers.
Bonus 2: Improved Authorship: Cultivate a clear, concise, consistent, writing style.
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Manuscript Source: https://www.biorxiv.org/content/10.1101/603613v4

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Features of the Sentence Audit:

The Sentence Audit combines two complementary proofreading approaches:

1. Each sentence of your text is parsed and displayed in isolation for focused inspection.
2. Each individual sentence is further parsed into Minimal Sentence Components for a deeper review of the clarity, composition and consistency of the language you used.

The Minimal Sentence Components shown are the smallest coherent elements of each sentence of your text as derived from it's conjunctions, prepositions and selected punctuation symbols (i.e. commas, semicolons, round and square brackets).

The combined approaches ensure easier, faster, more effective proofreading.

Comments and Caveats:

• The sentence parsing is achieved using a prototype natural language processing pipeline written in Python and may include occasional errors in sentence segmentation.

• Depending on the source of the input text, the Sentence Audit may contain occasional html artefacts that are parsed as sentences (E.g. "Download figure. Open in new tab").

• Always consult the original research paper as the true reference source for the text.

Contact Information:

To get a Manuscript Microscope Sentence Audit of any other research paper, simply forward any copy of the text to John.James@OxfordResearchServices.com.

All queries, feedback or suggestions are also very welcome.

Research Paper Sections:

The sections of the research paper input text parsed in this audit.

Section No.	Headings	Sentences
Section: 1	Abstract	9
Section: 2	Introduction	18
N/A	--- --- --- --- --- --- ---	0
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The Sentence Audit Of The Research Paper

Title # Heterochromatin renewal after release from growth arrest controls genome-wide transcription re-activation in S.cerevisiae

S1 [001] Abstract

S1 [002] The budding yeast SIR complex (Silent Information Regulator) is the principal actor in heterochromatin formation, which causes epigenetically regulated gene silencing phenotypes.

The budding yeast SIR complex ...
... (Silent Information Regulator) ...
... is the principal actor ...
... in heterochromatin formation, ...
... which causes epigenetically regulated gene silencing phenotypes.

S1 [003] The dynamics of the SIR complex during the cell cycle are however not well understood.

The dynamics ...
... of the SIR complex ...
... during the cell cycle are however not well understood.

S1 [004] It is consequently still not known how the SIR complex is maintained and/or restored after genome replication and cell division, and how the underlying silenced state is transmitted form one cell generation to the next.

It is consequently still not known how the SIR complex is maintained ...
... and/or restored ...
... after genome replication ...
... and cell division, ...
... and how the underlying silenced state is transmitted form one cell generation ...
... to the next.

S1 [005] We used the tag switch RITE system to measure genome wide turnover rates of the SIR subunit Sir3p during and after exit from growth arrest caused by nutrient depletion.

We used the tag switch RITE system ...
... to measure genome wide turnover rates ...
... of the SIR subunit Sir3p ...
... during ...
... and after exit ...
... from growth arrest caused ...
... by nutrient depletion.

S1 [006] Our results show that Sir3p subunits have high rates of exchange immediately after release from growth arrest.

Our results show ...
... that Sir3p subunits have high rates ...

... of exchange immediately ...
... after release ...
... from growth arrest.

S1 [007] “Maternal” Sir3p is consequently almost completely replaced with newly synthesized Sir3p in subtelomeric regions by the end of the first cell cycle after release from growth arrest.

“Maternal” ...
... Sir3p is consequently almost completely replaced ...
... with newly synthesized Sir3p ...
... in subtelomeric regions ...
... by the end ...
... of the first cell cycle ...
... after release ...
... from growth arrest.

S1 [008] The sudden increase in the off rate of Sir3 upon release from growth arrest leads to SIR complex instability that is exacerbated in strains with sub optimal amounts of newly synthesized Sir3p.

The sudden increase ...
... in the off rate ...
... of Sir3 ...
... upon release ...
... from growth arrest leads ...
... to SIR complex instability ...
... that is exacerbated ...
... in strains ...
... with sub optimal amounts ...
... of newly synthesized Sir3p.

S1 [009] Unexpectedly, heightened SIR complex instability in these Sir3p “hypo-morphs” has global effects on gene expression with faster reactivation of hundreds of euchromatic genes upon exit from growth arrest.

Unexpectedly, ...
... heightened SIR complex instability ...
... in these Sir3p “hypo-morphs” ...
... has global effects ...
... on gene expression ...
... with faster reactivation ...
... of hundreds ...
... of euchromatic genes ...
... upon exit ...
... from growth arrest.

S2 [010] Introduction

S2 [011] Heterochromatin in budding yeast is a transcriptionally repressive structure located at the silent mating type loci (HMR and HML), telomeres and rDNA repeats.

Heterochromatin ...
... in budding yeast is a transcriptionally repressive structure located ...
... at the silent mating type loci ...
... (HMR ...
... and HML), ...
... telomeres ...
... and rDNA repeats.

S2 [012] The essential component of this structure is the non-histone protein complex SIR (Silent Information Regulator), which consists mainly of Sir2p, Sir3p and Sir4p.

The essential component ...
... of this structure is the non-histone protein complex SIR ...
... (Silent Information Regulator), ...
... which consists mainly ...
... of Sir2p, ...
... Sir3p ...
... and Sir4p.

S2 [013] Sir4p scaffolds the complex while Sir2p functions as an NAD-dependent H4K16 deacetylase, providing a high-affinity binding site for Sir3p which recruits Sir4p (for review see (1)).

Sir4p scaffolds the complex ...
... while Sir2p functions ...
... as an NAD-dependent H4K16 deacetylase, ...
... providing a high-affinity binding site ...
... for Sir3p ...
... which recruits Sir4p ...
... (for review see ...
... (1)).

S2 [014] In the classical polymerization model, SIR components are first recruited to silencer regions by a combination of silencer-binding factors (ORC –Origin Recognition Complex, Rap1p and Abf1p).

In the classical polymerization model, ...
... SIR components are first recruited ...
... to silencer regions ...
... by a combination ...
... of silencer-binding factors ...
... (ORC –Origin Recognition Complex, ...
... Rap1p ...
... and Abf1p).

S2 [015] The SIR complex then spreads from the nucleation site (silencer) through cycles of deacetylation and nucleosome binding, which continue until the SIR complex reaches boundary elements that prevent unwanted spreading to transcriptionally active regions (for review see (2)).

The SIR complex then spreads ...

... from the nucleation site ...

... (silencer) ...

... through cycles ...

... of deacetylation ...

... and nucleosome binding, ...

... which continue until the SIR complex reaches boundary elements ...

... that prevent unwanted spreading ...

... to transcriptionally active regions ...

... (for review see ...

... (2)).

S2 [016] It has been shown that over-expressed Sir3p can be incorporated into existing heterochromatin (3).

It has been shown ...

... that over-expressed Sir3p can be incorporated ...

... into existing heterochromatin ...

... (3).

S2 [017] However, beyond this bulk measurement, the locus-specific dynamics of the chromatin bound SIR complex within and from one cell generation to another have not yet been measured.

However, ...

... beyond this bulk measurement, ...

... the locus-specific dynamics ...

... of the chromatin bound SIR complex ...

... within ...

... and from one cell generation ...

... to another have not ...

... yet been measured.

S2 [018] How heterochromatic SIR complexes exchange their components during the cell cycle and how they are distributed to daughter chromatids after replication has important implications for how heterochromatic states are maintained and whether they may be inherited.

How heterochromatic SIR complexes exchange their components ...

... during the cell cycle ...

... and how they are distributed ...

... to daughter chromatids ...

... after replication has important implications ...

... for how heterochromatic states are maintained ...

... and ...

... whether they ...

... may be inherited.

S2 [019] The maternal SIR complex has to be disassembled during replication and if heterochromatin is to be restored on both daughter strands, the SIR complex has to be reformed on both strands to pre-replication levels.

The maternal SIR complex has ...

... to be disassembled ...

... during replication ...

... and ...

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

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