A Manuscript Microscope 'Sentence Audit' of:

Chromatin accessibility and microRNA expression in nephron progenitor cells during kidney development

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.
- Focused Proofreading: Inspect each individual sentence component in isolation.
- Reliable Proofreading: Ensure every single word of your manuscript is correct.
- Easier Proofreading: Take the hardship out of crafting academic papers.

Bonus 1: Improved Productivity: Rapidly refine rough drafts to polished papers.
Bonus 2: Improved Authorship: Cultivate a clear, concise, consistent, writing style.
Bonus 3: Improved Reputation: Become known for rigorously precise publications.

Manuscript Source: https://www.biorxiv.org/content/10.1101/2021.03.05.434138v1

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Audit Date: 22/03/21 **Audit Identifier:** 0WER4UQ5D052BT9 **Code Version:** 3.6

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	8
Section: 2	Introduction	19
N/A	--- --- --- --- --- --- ---	0
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The Sentence Audit Of The Research Paper

Title **Chromatin accessibility and microRNA expression in nephron progenitor cells during kidney development**

S1 [001] Abstract

S1 [002] Mammalian nephrons originate from a population of nephron progenitor cells (NPCs), and it is known that NPCs' transcriptomes change throughout nephrogenesis during healthy kidney development.

Mammalian nephrons originate ...
... from a population ...
... of nephron progenitor cells ...
... (NPCs), ...
... and it is known ...
... that NPCs' transcriptomes change ...
... throughout nephrogenesis ...
... during healthy kidney development.

S1 [003] To characterize chromatin accessibility and microRNA (miRNA) expression throughout this process, we collected NPCs from mouse kidneys at embryonic day 14.5 (E14.5) and postnatal day zero (P0) and assayed cells for transposase-accessible chromatin and small RNA expression.

To characterize chromatin accessibility ...
... and microRNA ...
... (miRNA) ...
... expression ...
... throughout this process, ...
... we collected NPCs ...
... from mouse kidneys ...
... at embryonic day 14.5 ...
... (E14.5) ...
... and postnatal day zero ...
... (P0) ...
... and assayed cells ...
... for transposase-accessible chromatin ...
... and small RNA expression.

S1 [004] We observe 46,374 genomic regions of accessible chromatin, with 2,103 showing significant changes in accessibility between E14.5 and P0.

We observe 46,374 genomic regions ...
... of accessible chromatin, ...
... with 2,103 showing significant changes ...
... in accessibility ...
... between E14.5 ...
... and P0.

S1 [005] In addition, we detect 1,104 known microRNAs, with 114 showing significant changes in expression.

In addition, ...
... we detect 1,104 known microRNAs, ...
... with 114 showing significant changes ...
... in expression.

S1 [006] Genome-wide, changes in DNA accessibility and microRNA expression highlight biological processes like cellular differentiation, cell migration, extracellular matrix interactions, and developmental signaling pathways such as Notch.

Genome-wide, ...
... changes ...
... in DNA accessibility ...
... and microRNA expression highlight biological processes like cellular differentiation, ...
... cell migration, ...
... extracellular matrix interactions, ...
... and developmental signaling pathways ...
... such as Notch.

S1 [007] Furthermore, our data identify novel candidate cis-regulatory elements for Eya1 and Pax8, both genes with a role in NPC differentiation; we also associate expression-changing microRNAs, including let-7-5p, miR-125b-5p, miR-181a-2-3p, and miR-9-3p, with candidate cis-regulatory elements.

Furthermore, ...
... our data identify novel candidate cis-regulatory elements ...
... for Eya1 ...
... and Pax8, ...
... both genes ...
... with a role ...
... in NPC differentiation; ...
... we also associate expression-changing microRNAs, ...
... including let-7-5p, ...
... miR-125b-5p, ...
... miR-181a-2-3p, ...
... and miR-9-3p, ...
... with candidate cis-regulatory elements.

S1 [008] Overall, our data characterize NPCs during kidney development and point out new candidate regulatory elements for genes and microRNA with key roles in nephrogenesis.

Overall, ...
... our data characterize NPCs ...
... during kidney development ...
... and point out new candidate regulatory elements ...
... for genes ...
... and microRNA ...
... with key roles ...
... in nephrogenesis.

S2 [009] Introduction

S2 [010] The functional unit of the kidney is the nephron, which serves to filter waste and maintain normal homeostasis of water, acid-base, and electrolytes in the body.

The functional unit ...
... of the kidney is the nephron, ...
... which serves ...
... to filter waste ...
... and maintain normal homeostasis ...
... of water, ...
... acid-base, ...
... and electrolytes ...
... in the body.

S2 [011] Nephron number varies widely in humans (typically between two hundred thousand and greater than one million nephrons (Hughson et al., 2003)) and is established prior to birth (birth in humans, approximately post-natal day 2-3 in mice (Hartman et al., 2007; Hinchliffe et al., 1991)).

Nephron number varies widely ...
... in humans ...
... (typically ...
... between two hundred thousand ...
... and greater ...
... than one million nephrons ...
... (Hughson et al., 2003)) ...
... and is established ...
... prior to birth ...
... (birth ...
... in humans, ...
... approximately post-natal day 2-3 ...
... in mice ...
... (Hartman et al., 2007; ...
... Hinchliffe et al., 1991)).

S2 [012] Nephrons cannot regenerate after birth, and decreased nephron endowment is associated with an increased risk of chronic kidney disease and hypertension (Bertram et al., 2011).

Nephrons cannot regenerate ...
... after birth, ...
... and decreased nephron endowment is associated ...
... with an increased risk ...
... of chronic kidney disease ...
... and hypertension ...
... (Bertram et al., 2011).

S2 [013] Nephron number, in turn, is in large part determined by a population of cells called nephron progenitor cells (Cebrian et al., 2014a).

Nephron number, ...
... in turn, ...
... is ...

... in large part determined ...

... by a population ...

... of cells called nephron progenitor cells ...

... (Cebrian et al., 2014a).

S2 [014] During kidney development, one subset of nephron progenitor cells undergo mesenchymal-to-epithelial transitions (MET) to differentiate into cells of the early developing nephron (renal vesicle), while another continues to self-renew.

During kidney development, ...

... one subset ...

... of nephron progenitor cells undergo mesenchymal-to-epithelial transitions ...

... (MET) ...

... to differentiate ...

... into cells ...

... of the early developing nephron ...

... (renal vesicle), ...

... while another continues ...

... to self-renew.

S2 [015] In the latter stages of embryonic development, nephron progenitors increase their propensity to differentiate, which gradually depletes their population and marks the eventual cessation of nephrogenesis (Hartman et al., 2007; Rumballe et al., 2011; Volovelsky et al., 2018).

In the latter stages ...

... of embryonic development, ...

... nephron progenitors increase their propensity ...

... to differentiate, ...

... which gradually depletes their population ...

... and marks the eventual cessation ...

... of nephrogenesis ...

... (Hartman et al., 2007; ...

... Rumballe et al., 2011; ...

... Volovelsky et al., 2018).

S2 [016] Nephron progenitor differentiation is regulated by a series of coordinated events.

Nephron progenitor differentiation is regulated ...

... by a series ...

... of coordinated events.

S2 [017] Briefly, Bmp7-pSmad1/5/8 signaling induces the initial exit of self-renewing Cited1+/Six2+ nephron progenitors into a primed Cited1-/Six2+ state, followed by Wnt9b/β-catenin induction of differentiation (McMahon et al., 2016; Rumballe et al., 2011).

Briefly, ...

... Bmp7-pSmad1/5/8 signaling induces the initial exit ...

... of self-renewing Cited1+/Six2+ nephron progenitors ...

... into a primed Cited1-/Six2+ state, ...

... followed by Wnt9b/β-catenin induction ...

... of differentiation ...

... (McMahon et al., 2016; ...

... Rumballe et al., 2011).

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

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