Transcript Survey

We want to improve NCBI's products and services. We would like to learn more about how NCBI helps you with your work, and what we can do better. Please click "next" below to get started.

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Transcript Survey

Genes and transcripts are clearly key concepts in the interpretation of biological phenomena. This survey is intended to solicit information on how a 'primary' transcript should be chosen for a particular gene. Choosing a 'primary' transcript could be done from several perspectives: coding sequence content, expression levels, clinical variant reporting, historical usage, etc. Given the broad use of the transcripts, we would like your feedback for the impact on your work and to discover what different communities want in these transcript sets.

The two global sources of transcript annotation (RefSeq and Ensembl/GENCODE) will take your responses into account when formulating future strategies and resources.

This survey has four sections. It should take approximately 8 minutes to complete. The examples we use in the survey are all based on scenarios we frequently encounter during our curation.

Section 1 - Transcript choice (6 questions)
Section 2 - Variant interpretation and reporting (5 questions)
Section 3 - Reference sequence sources (2 questions)
Section 4 - About you

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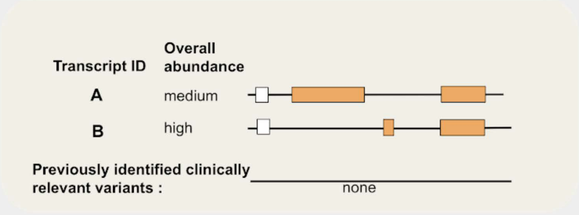
Section 1 - Transcript choice

1. Considering the transcripts of a gene, for your work how important is it to have:

	Critical	Nice to have	Not needed
Only ONE primary transcript	○	○	○
A minimal set of transcripts to cover ALL EXONS with evidence of CLINICAL SIGNIFICANCE	○	○	○
A minimal set of transcripts to cover ALL ABUNDANT PROTEIN-CODING EXONS	○	○	○
A minimal set of transcripts to cover ALL ABUNDANT EXONS	○	○	○
A larger set of ALL known transcripts	○	○	○
All of the above	○	○	○

Other (please specify)

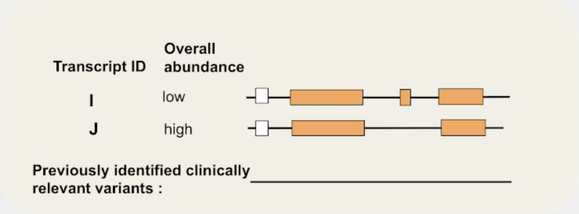
2. In the case of a gene WITHOUT any known clinically relevant variants, which transcript do you think should be the primary transcript?



- ○ The transcript that has the longest coding sequence (A)
- ○ The transcript that is the most abundant (B)

Additional comments

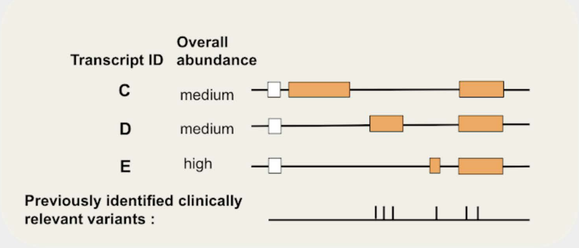
3. In the case of a gene WITHOUT any known clinically relevant variants, which transcript do you think should be the primary transcript?



- ○ The transcript that has the longest coding sequence (I)
- ○ The transcript that is the most abundant (J)

Additional comments

4. In the case of a gene WITH clinically relevant variants, which transcript should be the single primary transcript? Please answer based on which is best for your work.



- ○ Transcript that has the longest coding sequence (C)
- ○ Transcript that covers the most clinically relevant variants (D)
- ○ Transcript that is the most abundant (E)
- ○ Transcript that has been most used historically

Additional comments

5. Considering the sequence of a transcript, which is the most important to you?

- ○ That the sequence matches the reference assembly sequence (e.g. GRCh37/ hg19), even if it contains minor alleles
- ○ That the sequence does not contain any pathogenic alleles
- ○ That the sequence matches the global major allele
- ○ That the sequence does not change
- ○ It doesn't matter to me

6. For your work, when is it appropriate to make an update to the primary transcript? Please check all that apply.

- ☐ A change in coding sequence
- ☐ A change in UTR length
- ☐ A change to transcript splicing
- ☐ Never update
- ☐ Other (please specify)

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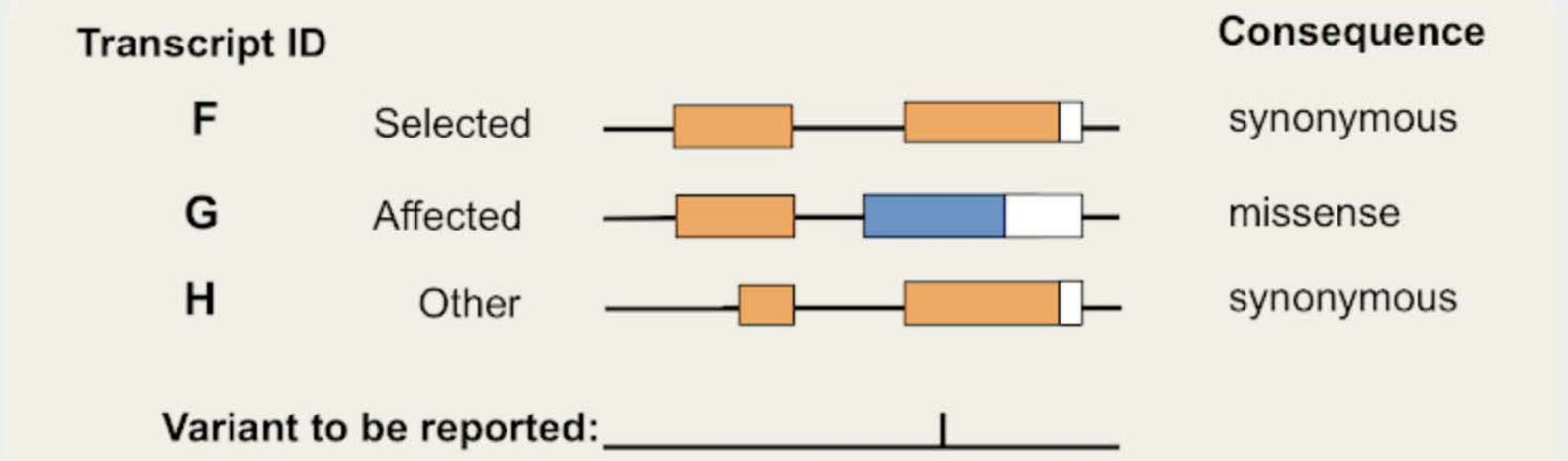
Section 2 - Variant interpretation and reporting

7. If there is one primary transcript per locus, what would you do?

- ( ) Use it, and only it, for INTERPRETING the consequence of variants?
- ( ) I wouldn't use just one transcript for INTERPRETATION unless it was the only one known
- ( ) Other (please specify)

8. If the most severe variant effect to be reported is not on the selected primary transcript (F), what would you do?



- ( ) Report the variant on the selected primary transcript (F) only
- ( ) Report the variant on the affected transcript (G) only
- ( ) Report the variant on both the selected primary transcript (F) and the affected transcript (G)
- ( ) Report the variant on all transcripts (F, G, H)
- ( ) I don't know
- ( ) Other (please specify)

9. Which reference sequences do you use for reporting variants? Please check all that apply.

- [ ] RefSeq transcripts or proteins
- [ ] Ensembl/GENCODE transcripts or proteins
- [ ] GRCh37/hg19 genome
- [ ] GRCh38/hg38 genome
- [ ] LRG transcripts or LRG proteins

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Section 3 - Reference sequence sources

10. Please check all that are true:

- [ ] I use RefSeq transcripts for my work
- [ ] I do not use RefSeq
- [ ] I use Ensembl/GENCODE transcripts for my work
- [ ] I do not use Ensembl/GENCODE
- [ ] Both RefSeq and Ensembl/GENCODE transcripts are useful for my work
- [ ] I do not know whether RefSeq or Ensembl/GENCODE produce the best transcripts for my work

11. What is most important to you?

- ( ) Having RefSeq and Ensembl/GENCODE agree on one primary transcript per gene
- ( ) Having different sets as each set has different strengths
- ( ) I have no preference
- ( ) Other (please specify)

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Transcript Survey

Section 4 - About you

12. Which professional categories best describe you? Please check all that apply.

- [ ] Healthcare professional
- [ ] Diagnostician
- [ ] Bioinformatics professional
- [ ] Life Science researcher
- [ ] Developer/engineer
- [ ] Educator
- [ ] Student
- [ ] Other (please specify)

13. Where do you work? Check all that apply.

- [ ] University/College/Academia/Non-profit/Research
- [ ] Clinical diagnostics
- [ ] Clinical research
- [ ] Commercial/Industry
- [ ] Government
- [ ] Other (please specify)

14. In what country do you work?

15. Question 1 revisited - a primary transcript

Do you want us to provide one primary transcript?

- ( ) Yes
- ( ) No
- ( ) I'm not sure

Please note, you may contact us at the help-desk to provide additional feedback about the resources in this survey or any other NCBI resource.

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