



SDI Review Form 1.6

Journal Name:	Annual Research & Review in Biology
Manuscript Number:	Ms_ARRB_51032
Title of the Manuscript:	POWER-LAW BEHAVIOR OF ALTERNATIVE SPLICING OF EXONS IN HUMAN TRANSCRIPTOME
Type of the Article	Original Research Article

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound. To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

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PART 1: Review Comments

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
Compulsory REVISION comments	<p>The manuscript "POWER-LAW BEHAVIOR OF ALTERNATIVE SPLICING OF EXONS IN HUMAN TRANSCRIPTOME" is very informative, well presented. This manuscript needs major revision and might be accepted for publication.</p> <p>Comments as follows:</p> <ol style="list-style-type: none"> 1. Gene name should be <i>italic</i> and please follow gene nomenclature guidelines for human and mouse. 2. How many genes were taken into consideration? Explain in abstract and method section of the manuscript. 3. Do non-coding transcripts like circular RNA, small nuclear RNA, long/small non-coding RNA genes were also part of analysis or excluded from analysis? 4. Dataset 1 and formed Dataset 2 should be provided as supplementary table. <p>There are many typing errors and grammar mistakes</p>	<p>In revision manuscript, the gene names are given in <i>italic</i> and according to HUGO Gene Nomenclature Committee (last update 2019-08-16).</p> <p>The relevant information was added to ABSTRACT and MATERIAL AND METHODS.</p> <p>We excluded all one-exon transcripts from our datasets and used only multi-exons transcripts for downstream analysis. So, any spliced non-coding RNAs were also included in analysis. This explanation has been added to the MATERIAL AND METHODS.</p> <p>Dataset 1 (and Dataset 2 as well) is based on a collection of the human mRNA and ESTs sequences deposited in GenBank. Current version of our Dataset 1 is a local SQLite database of 283.177 MB. It seems impractical to attach this database as a supplementary table. On the contrary, we offer everyone to use our original R code to generate their own database similar to Dataset 1 or Dataset 2. This code is available upon request and respective information was included into MATERIAL AND METHODS.</p> <p>The text has been corrected as much as possible. English has been corrected by our colleagues at Memorial Sloan Kettering Cancer Center (New York, USA).</p>
Minor REVISION comments		
Optional/General comments		

PART 2:

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
Are there ethical issues in this manuscript?	<i>(If yes, Kindly please write down the ethical issues here in details)</i>	