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# Natural selection against insufficiency in sarcomeric proteins reduces the risks of cardiomyopathy in humans versus chimpanzees as conventionally the nearest wild congeners, for whom it is the most common cause of spontaneous mortality

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*Motivation and Aim*: Cardiomyopathy is the most common cause of spontaneous death in chimpanzees, who is our nearest wild congeners [1].
*Methods and Algorithms*: Using our previously published Web service SNP_TATA_Comparator, we analyzed single-nucleotide polymorphisms (SNPs) within 70 bp proximal promoters of eight human sarcomeric protein genes, as shown in Figure.
*Results:* After analyzing 637 such SNPs, we identified 92 and 54 candidate SNP markers for worsened and relieved respectively, hypertrophic cardiomyopathy (HC), as susceptibility to heart failure. Among them, 84 and 62 candidate SNP markers overexpressing and underexpressing respectively, these genes as natural selection against the human sarcomeric protein deficit, being resistance to heart failure. This simultaneity of susceptibility and resistance to heart failure means disruptive natural selection of the considered human genes as if humans could exposed self-domestication that is debatable. We tested this using public 5591 differentially expressed gene (DEGs) of domestic versus wild animals. In the domestic animals, the overexpressed sarcomeric protein DEGs dominated the underexpressed ones (29 vs 15 respectively) just as natural selection against the human sarcomeric protein deficiency. Amounts of the domestic animal DEGs corresponding to relieved HC condition in humans surpassed those in wild animals (8 vs 1).
*Conclusion*: Thus, natural selection against the sarcomeric proteins deficit reduces the risks of cardiomyopathy in humans versus chimpanzees as the nearest wild congeners, for whom it is the most common cause of spontaneous death.
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*References*

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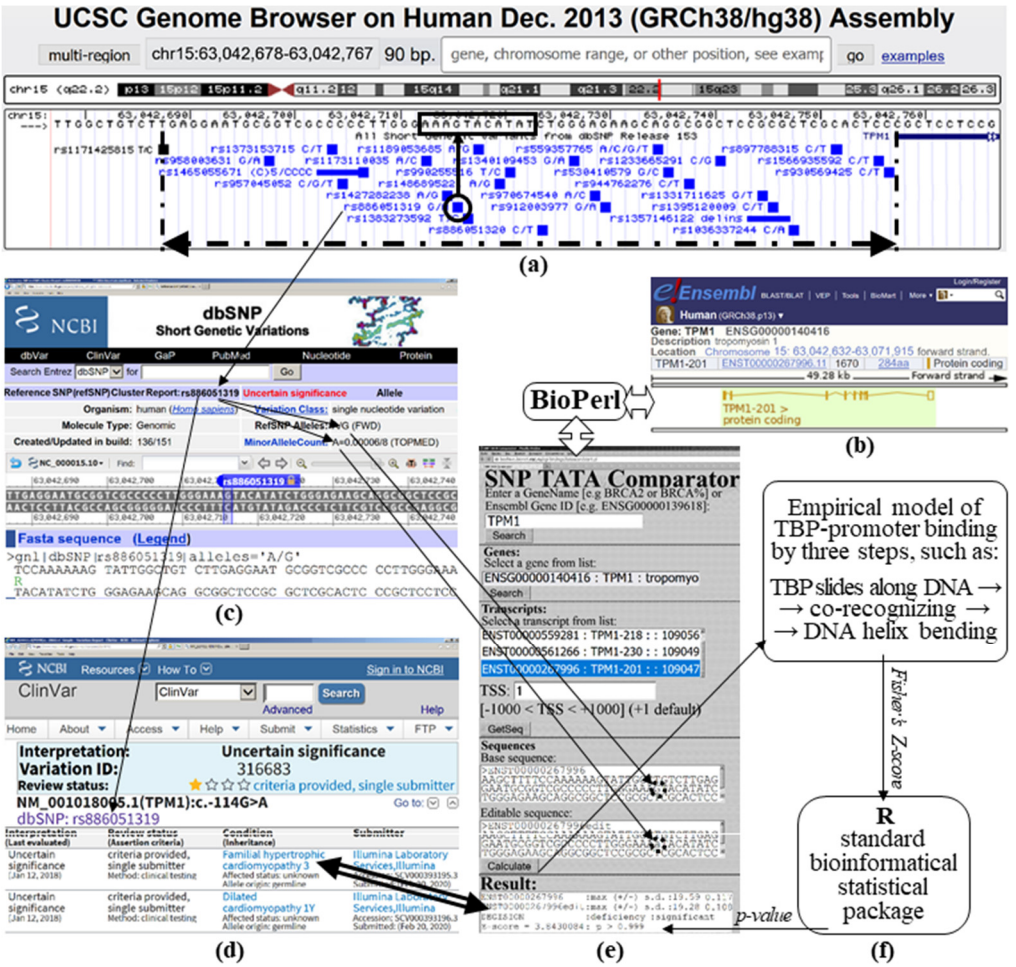


**Fig. 1.** An example of the results SNP_TATA_Comparator in the case of the clinically proven hypertrophic cardiomyopathy-related SNP marker (rs886051319) increasing risks of this disease via TPM1 downregulation: a) The UCSC Genome Browser visualizes a 70 bp promoter (double-headed dash-and-dot arrow) of the human TPM1 gene where there is only one TBP-binding site (framed) and SNP rs886051319 with an arrow pointing to it (circle); (b) the Ensembl database. (c) The dbSNP database. (d) The ClinVar database. (e) Our prediction of TPM1 deficiency (textbox "Result": row 3) caused by SNP rs886051319 (dotted circles) by means of its both alleles (i.e., ancestral and minor ones as input data within two textboxes "Basic sequence" and "Editable sequence," respectively). Double-headed open arrows depict how our Web service SNP_TATA_Comparatorretrieved the ancestral DNA sequence of the human TPM1 promoter from the Ensembl database using the Bioperl toolkit. (f) Our bioinformatics model of the TBP–promoter binding in three steps, Double-headed double arrow, a consistency between the clinical data on rs886051319 as a clinically proven SNP marker of both familial hypertrophic cardiomyopathy 3, dilated cardiomyopathy 1Y, which are within the ClinVar database on one hand and the service SNP_TATA_Comparator result that the minor allele of this SNP can cause TPM1 underexpression linked clinically with hypertrophic cardiomyopathy on another hand