The Mammalian NumtS Compilations Available Through the UCSC Genome Browser

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Motivation
The analysis of the NumtS (Nuclear MiTochondrial Sequences), variable in number within the mammalian clade and polymorphic both in their presence/absence and in SNPs content within each species, evidences evolutionary relationships among species specific NumtS and the way they spread during hominoids’ evolution. After the production in our group of the most exhaustive human NumtSome catalogue (1, 2), annotating 585 NumtS, implemented in the UCSC Genome Browser, NumtS evolutionary comparisons among Homo sapiens and other mammalian species are feasible at a glance. Starting from a pilot survey on genomes available in a complete assembly state (Pan troglodytes, Mus musculus), our aim is to produce NumtS annotations on various mammalian species and their implementation in the UCSC Genome Browser, in order to support a wide range of research applications.

Methods
Following the protocol described in Lascaro et Al. (2008) (1) and modified in Simone et Al. (2011) (2), NumtS annotations on P. troglodytes and M. musculus were produced by carrying out DB similarity searching approaches between the nuclear genome of each organism and the corresponding mitochondrial genome. The resulting data were implemented in the UCSC Genome Browser as custom tracks. The browsing of NumtS’ outfit in syntenic regions of different species was performed by simultaneously comparing the human NumtSeq tracks recently published at the UCSC Genome Browser (2) (in the Variation and Repeats section) and the Net tracks available in the Comparative Genomics section; resulting data were optimized and merged with the Galaxy toolset, obtaining the NumtS synteny tables.

Results
In P. troglodytes and in M. musculus 700 and 163 NumtS were detected, respectively, and the relative annotations were implemented as UCSC custom track in BED format. Our synteny analysis returned 114 H. sapiens NumtS not shared with P. troglodytes and 93 P. troglodytes NumtS not shared with H. sapiens. These results show the powerful support given to evolutionary analyses by the implementation of the NumtS tracks at the UCSC Genome Browser; therefore, chimp and murine tracks, so far produced and privately used, are now considered for a public release as the human NumtS tracks. Moreover, a NumtS annotation on Macaca mulatta, although the genome state assem-
bly is not already complete, could provide further insights into primates evolutionary story, as M. mulatta is an outgroup respect to the hominoids clade. Figure 1 reports an example of the NumtSseq UCSC tracks.

References

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