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A re-assigned American mink (*Neovison vison*) map optimal for genome-wide studies

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ABSTRACT

Our previously published second generation genetic map for the American mink (*Neovison vison*) has been used and redesigned in its best for genome-wide studies with maximum of efficiency. A number of 114 selected markers, including 33 newly developed microsatellite markers from the CHORI-231 mink Bacterial Artificial Chromosome (BAC) library, have been genotyped in a two generation population composed of 1200 individuals. The outcome reassigns the position of some markers on the chromosomes and it produces a more reliable map with a convenient distance between markers. A total of 104 markers mapped to 14 linkage groups corresponding to the mink autosomes. Six markers are unlinked and four markers are allocated to the X chromosome by homology but no linkage was detected. The sex-average linkage map spans 1192 centiMorgans (cM) with an average intermarker distance of 11.4 cM and 1648 cM when the ends of the linkage groups and the autosomal unlinked markers are added. Sex-specific genetic linkage maps were also generated. The male sex-specific map had a total length of 1014.6 cM between the linked markers and an average inter-marker interval of 9.7 cM. The female map has a corresponding length of 1378.6 cM and an average inter-marker interval of 13.3 cM. The study is complemented with additional anchorage for most of the chromosomes of the map by BAC *in situ* hybridization with clones containing microsatellites strategically selected from the various parts of the genome. This map provides an improved tool for genetic mapping and comparative genomics in mink, also useful for the future assembly of the mink genome sequence when this will be taken forward.

1. Introduction

Comprehensive genetic linkage maps are now available for most of the important animal species. They vary in length according to species (*e.g.* 1361 cM in mouse (Dietrich et al., 1996) and 4370 cM in cat (Menotti-Raymond et al., 2009). Recently, there have been substantial advances in investigating mink molecular genetics. A precise and reliable map of the mink genome is of crucial importance for genetic investigations and improvements. The latest genetic linkage and virtual maps (Anistoroaei et al., 2007, 2009) were enabled by the development of >200 markers and by the virtual localization of >350 markers. In addition, comparison of mink, human, and dog chromosomes by fluorescence *in situ* hybridization (Zoo-FISH) has provided information on chromosome segments that are evolutionarily conserved between these 3 species (Breen et al., 1999; Graphodatsky et al., 2000; Hameister et al., 1997). A comprehensive mink BAC library (http://bacpac.chori.org/library.php?id=487) has been produced and utilized as an important resource for genome sequencing and gene fishing (Anistoroaei et al., 2011), as well as marker development aimed at resolving gaps in the previous linkage maps (Anistoroaei et al., 2007, 2009). Within the last years, a large *Quantitative Trait Locus* (*QTL*) project (Thirstrup et al., in press) aimed at mapping traits of interest for the mink industry. The report hereby utilized the genotyped data derived from two of three generations included in this QTL project (158 F1 individuals and 1042 F2 individuals). The mink genome is organized in 14 autosome pairs and X/Y chromosomes (Christensen et al., 1996). In this report, we have illustrated the newest linkage map complemented with comparative data and *in situ* hybridization onto mink metaphases for some of the markers developed from BAC clones. This study has the advantage of using a very large mapping reference pedigree and adding markers efficiently, thus ensuring an optimal and wide distribution across the genome (Supplementary Table S1 and Fig. 1). The size of the resource families utilized in this study

Abbreviations: BAC, Bacterial Artificial Chromosome; cM, centiMorgan; FISH, Fluorescence *in situ* hybridization; NVI, *Neovison vison*; QTL, Quantitative Traits Loci.

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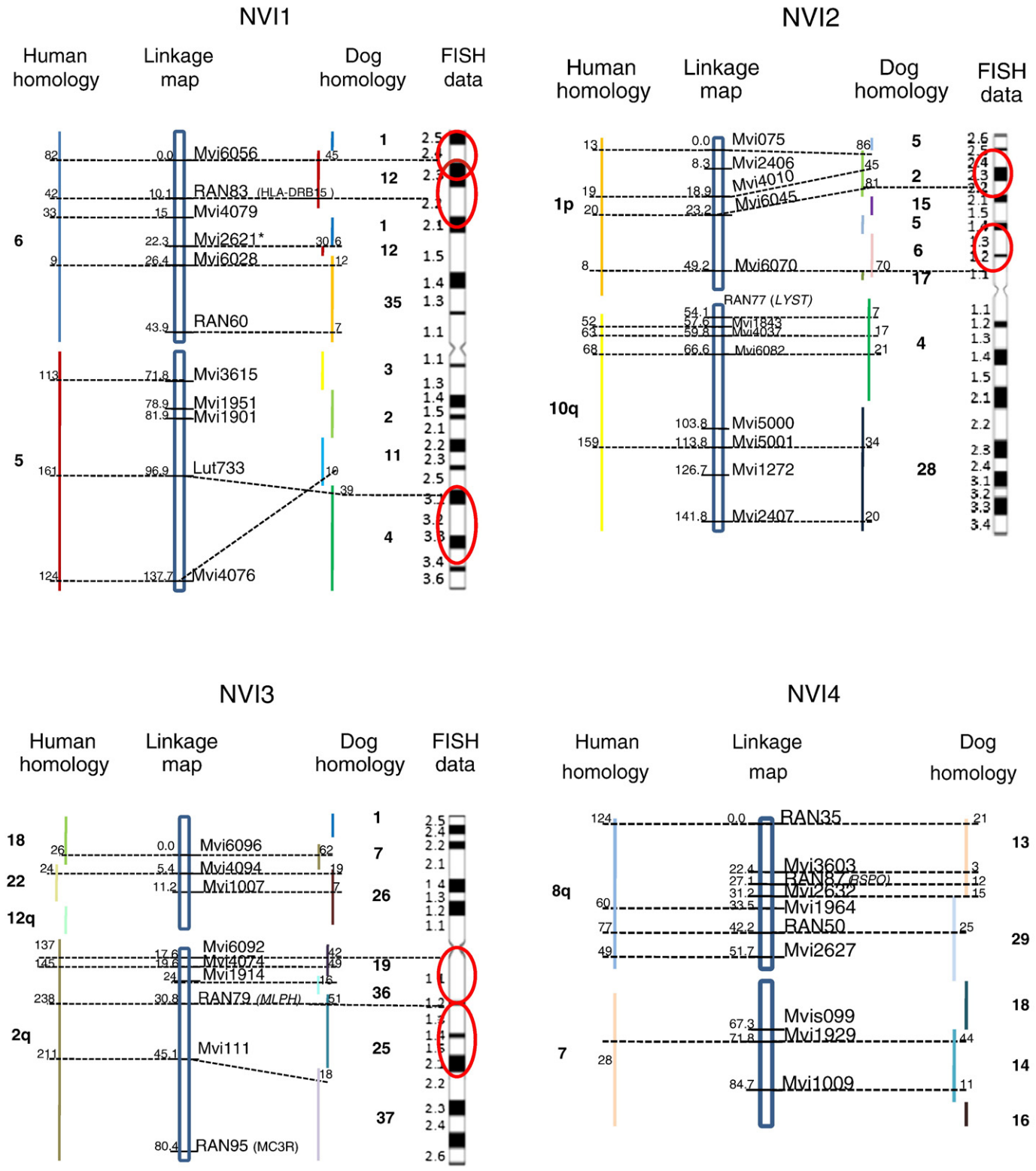

Fig. 1. Sex-averaged genetic linkage map for *Neovison vison* autosomes are shown in the middle, divided in the 2 chromosomal arms for each of them, except the acrocentric chromosome 14. The markers are shown on the right (genes are indicated on the corresponding markers where the case). Marker positions along the mink chromosome are stated in centiMorgans (cM) to the left. Colored bars to the left indicate proposed segments of conserved synteny between the mink linkage map and the human genome sequence (BUILD 37.2) according to Hameister et al. (1997). To the right are the proposed segments of conserved synteny between the mink linkage map and the dog genome sequence (BUILD 2.1) according to Graphodatsky et al. (2000) and Breen et al. (1999). The positions of matches with the human and dog chromosomes respectively are indicated in megabases provided by the human and dog genomes assemblies. *In situ* assignment for some markers (derived from the BAC library) is indicated on the diagrams of the chromosomes on the far right.
* Mvi2621 on chromosome 1 shares 2 different dog chromosome homologies, indicating a clear breakpoint.