

Finally, it is time that you apply all what you have learned on this practical to take a closer look at the BRCA2 gene region on your own. Upload a file here with your answers to the following questions (you can include screenshots if necessary):

Q1: Does this gene have orthologues to all 23 primates available in Ensembl? How identical is to its orthologue in the chimpanzee? Does this gene exist in birds and reptiles? And in fish? (Hint: Click the Gene tab and then Orthologues)

Yes. The human sequence to the ortholog is 99.27 % identical. Yes, it does exist in birds and reptiles (27 species) and also in fish (65 species)

Q2: Does this gene have paralogues in the human genome? If so, how many genes conform this gene family? (Hint: Click the Gene tab and then Paralogues; if the link is not accessible, there are no paralogues)

No.

Q3: Is there any species with more than one copy of the gene? How many copies of this gene do pigs have? (Hint: Click the Gene tab and then Gene gain/loss tree)

Golden-line barbel (2), Common carp (2), Three-toed box turtle (2). Pig has 1 copy.

Q4: Let's take a look at the syntenic blocks between human chromosome 13 (where BRCA2 gene is located) and the chromosomes of other species. (Hint: Click the Location tab and then Synteny). How long (qualitatively) are syntenic blocks between human chromosome 13 and any other primate chromosomes, as compared with other non-primate mammalian chromosomes, with bird chromosomes, or with fish chromosomes? You can select any species of the mentioned group (primates, birds, fishs) for the comparison. Does the size of the syntenic blocks correlate with phylogenetic distance between the species? Do you expect this? How do you explain this finding? Discuss your findings.

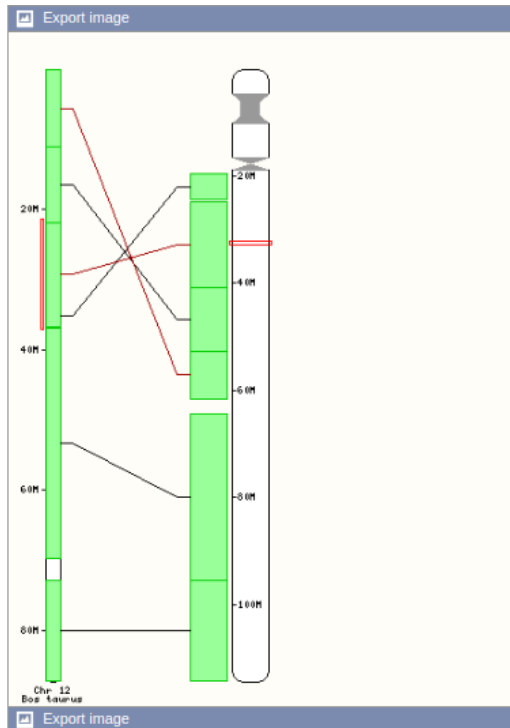
-Other primate chromosomes(Chimpanzee): Chr 13, Chr 26

-Other non-primate mammalian chromosomes(Cow): Chr 12

-Bird chromosomes(Duck): Chr 1

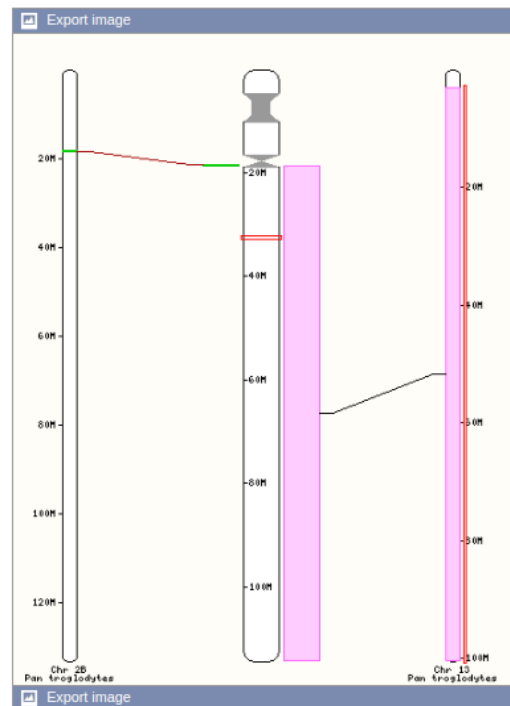
-Fish chromosomes(Reedfish): Chr 4

As we observed in the synteny of the species compared to the human, we see that the size of the blocks correlate with the conservation of the gene across the species. This can be confirmed when we observe the blocks. In the provided images we can see that the further we go into the closure of the species the less conserved is the gene. The chimpanzee shows a high similarity, then with the cow we still observe similarity but with some changes like translocations and when we compare it with a bird or a fish the difference is significant. So with this we can conclude that there exists a correlation between the size of the synthetic block and the phylogenetic distance between the species.



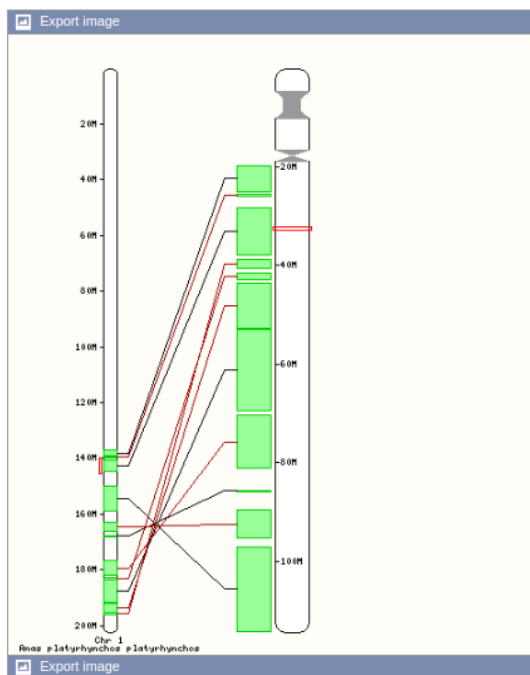
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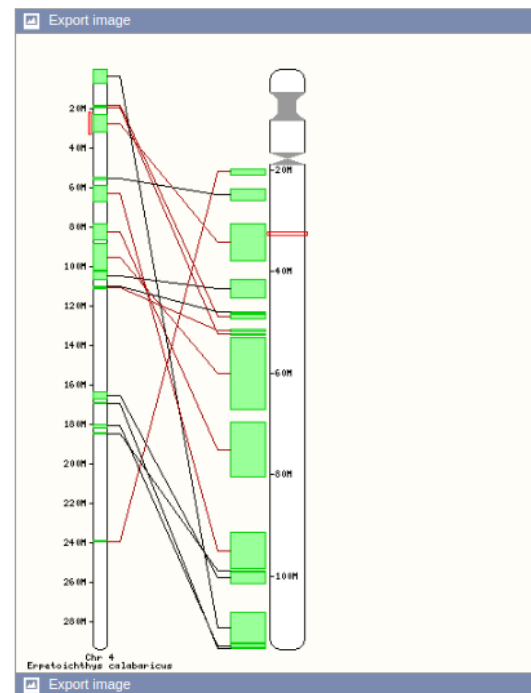
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