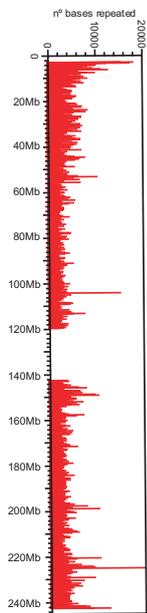
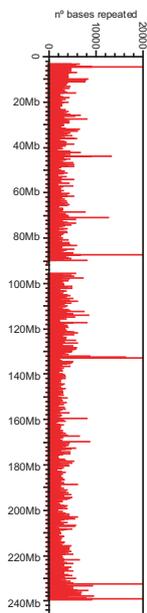


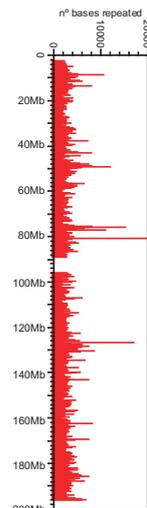
**Supplementary Figure 2:** Distribution of base pair implicated tandem repeats along all human chromosomes represented as windows of 250000bp each. The distribution of base pair implicated tandem repeats in the pericentromeric and subtelomeric areas has been omitted in order to clarify the presence of outlayers.



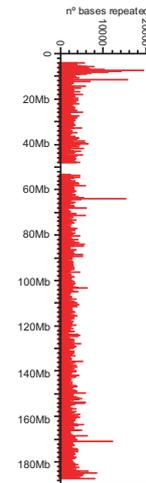
hsa1



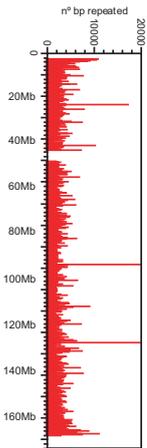
hsa2



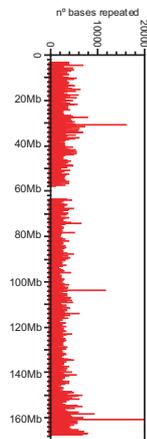
hsa3



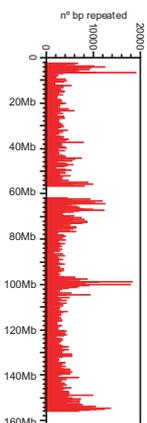
hsa4



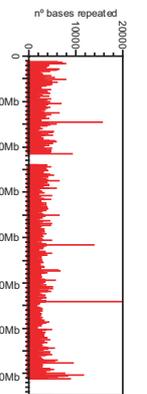
hsa5



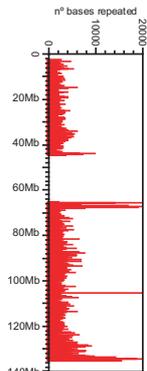
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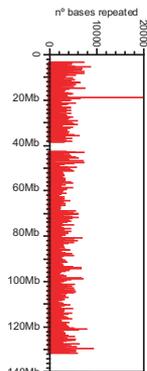
hsa7



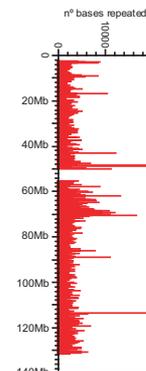
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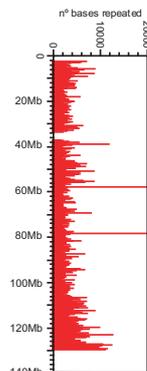
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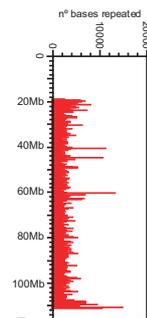
hsa10



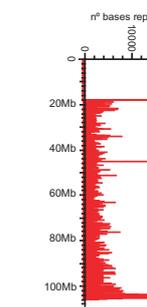
hsa11



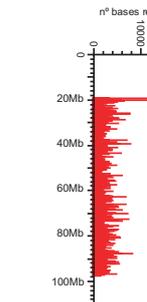
hsa12



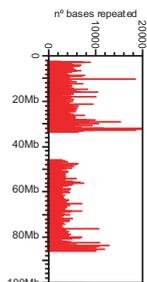
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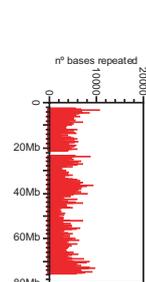
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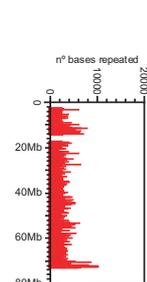
hsa15



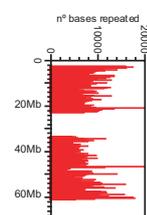
hsa16



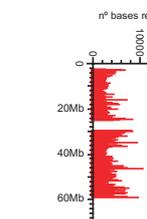
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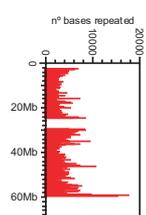
hsa18



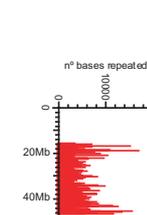
hsa19



hsa20



hsa21



hsa22