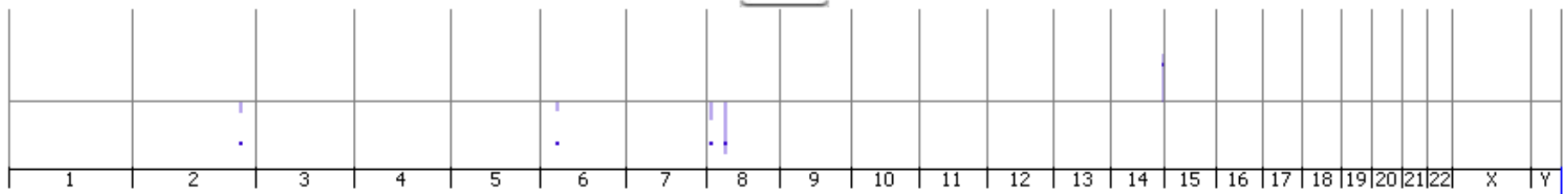
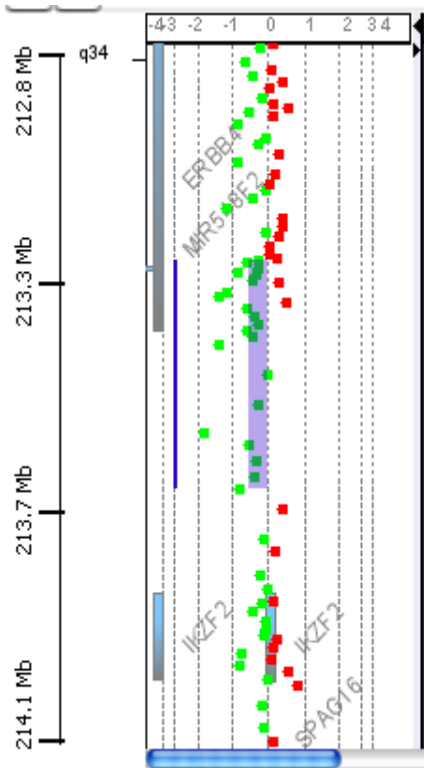


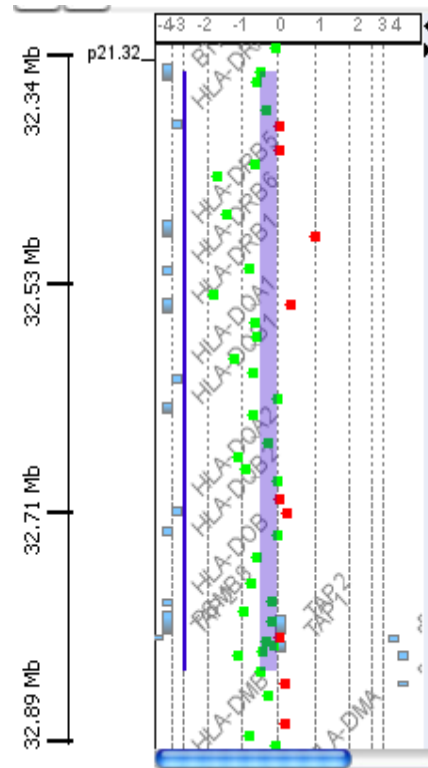
# IPSC-15nov23-05 (Simona: T20 iPSCs)



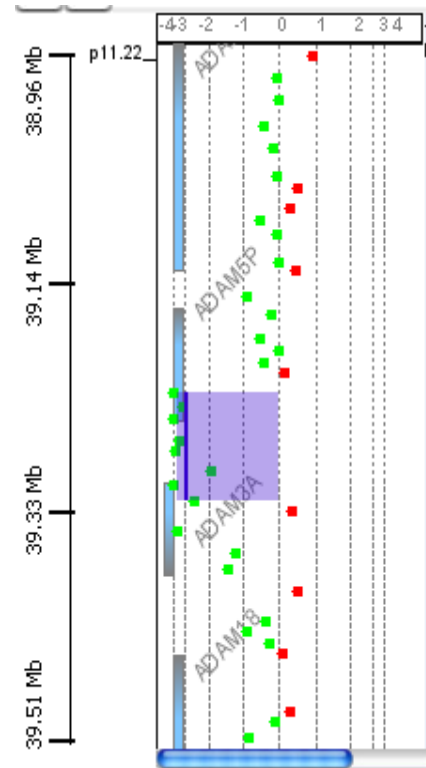
### Chr 2



### Chr 6



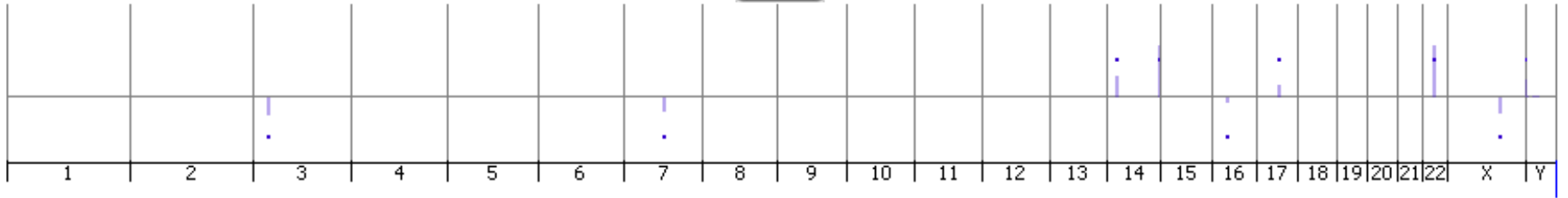
### Chr 8



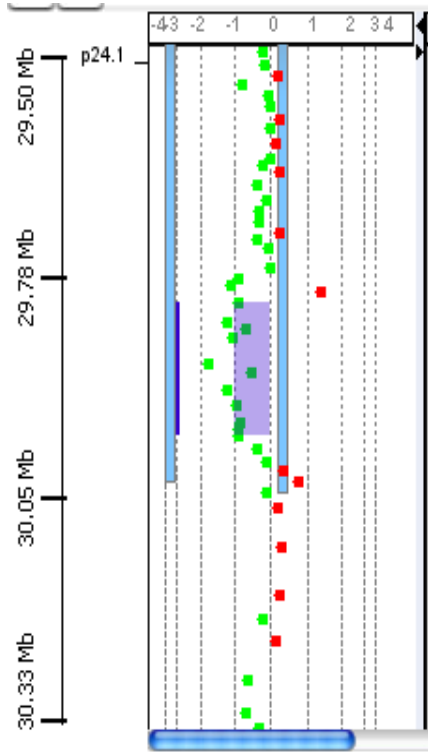
VARIANTI SIGNIFICATIVE: nessuna

(la loss su chr 8, che è la + netta, interessa uno pseudogene spesso deleta anche in altri DNA)

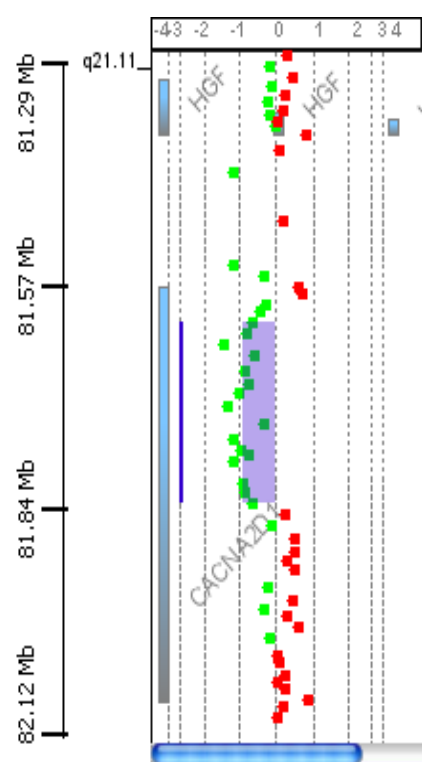
# IPSC-15nov23-06 (Simona: iPSCs Dock ? # 11 P19)



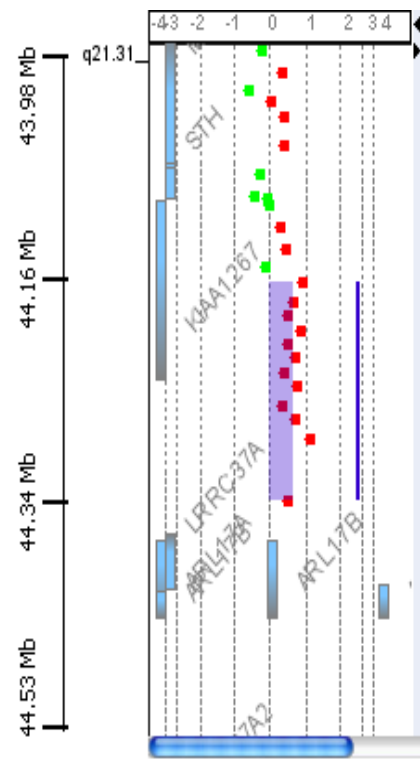
### Chr 3



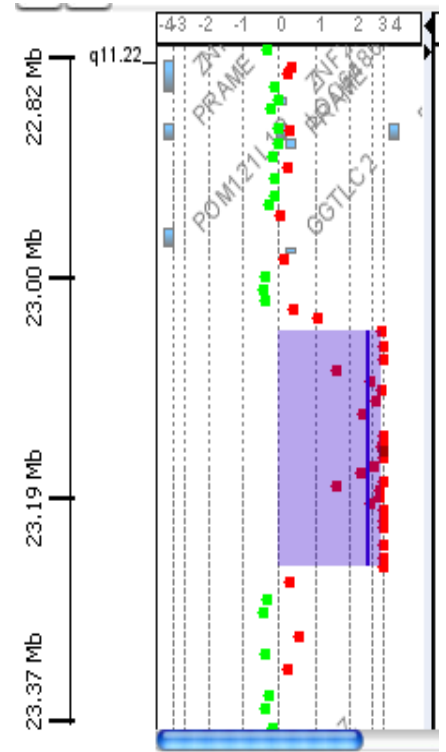
### Chr 7



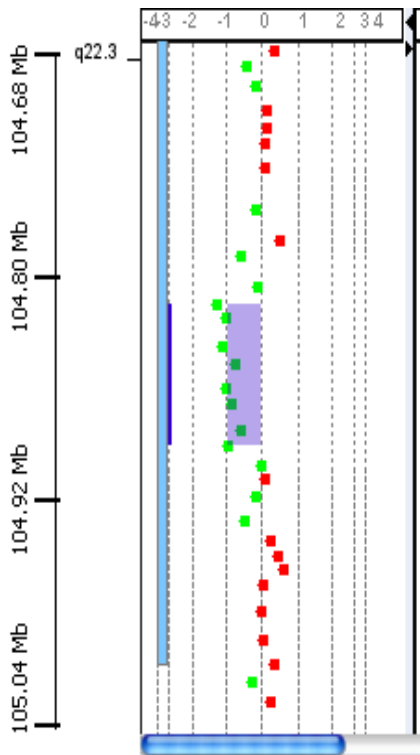
### Chr 17



### Chr 22



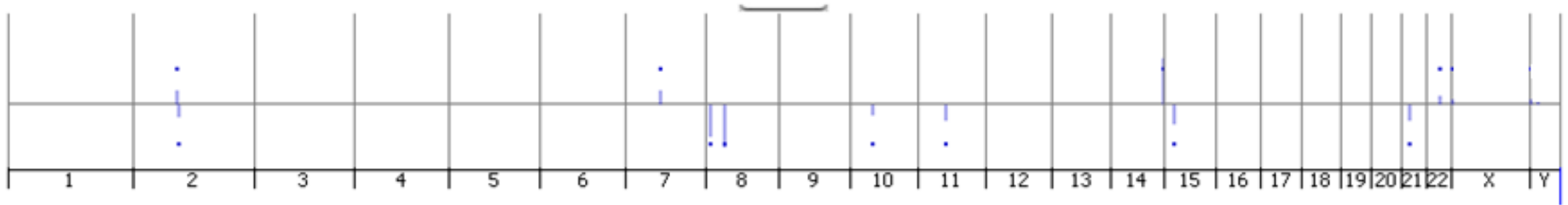
# Chr X



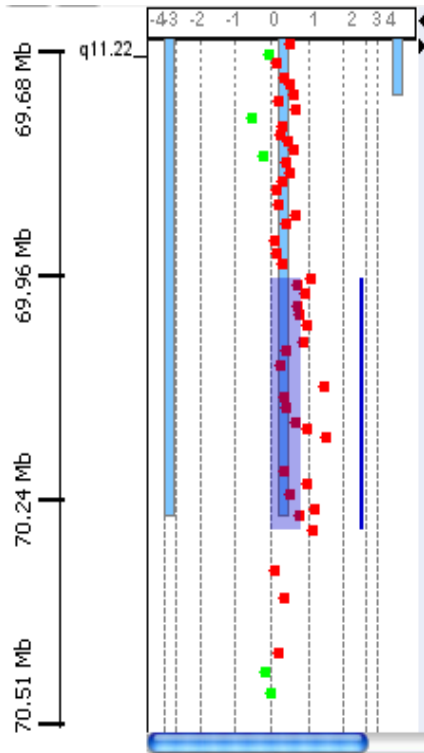
VARIANTI SIGNIFICATIVE: nessuna

(il gain sul chr 22, molto netto, non corrisponde a nessun gene, ed è spesso gain anche in altri DNA; la piccolissima loss sul chr X (Xq22.3) potrebbe essere reale, ma è davvero minima)

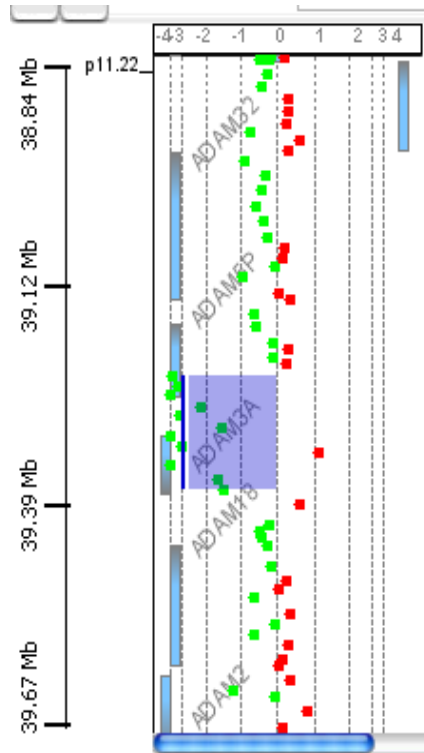
# IPSC-15nov23-07 (Simona: iPSCs Dock 2 # 5 P13)



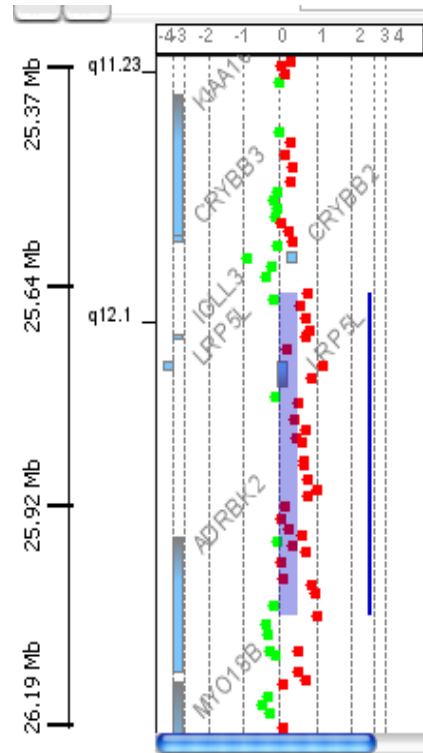
## Chr 7



## Chr 8



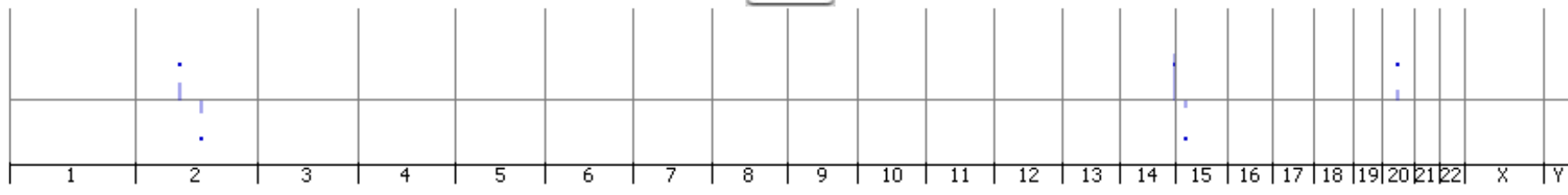
## Chr 22



VARIANTI SIGNIFICATIVE: nessuna

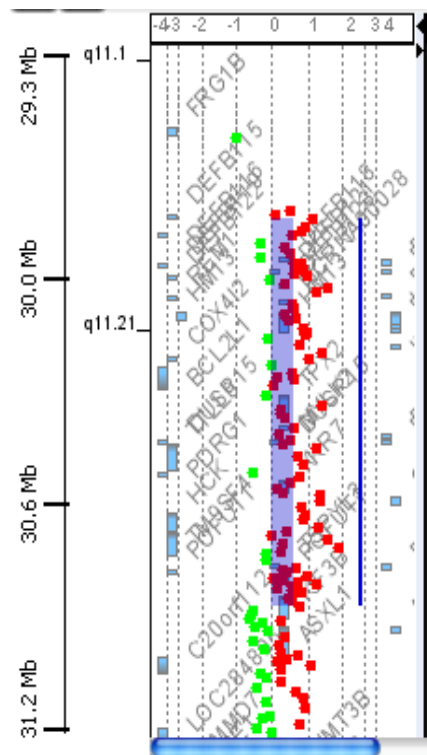
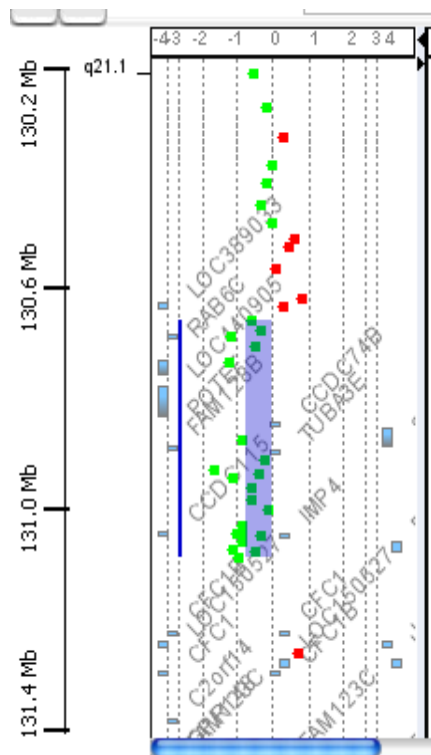
(la loss su chr 8, che è la + netta, interessa uno pseudogene spesso deleta anche in altri DNA)

# IPSC-15nov23-08 (Simona: iPSCs ASE P211)



## Chr 2

## Chr 20



VARIANTI SIGNIFICATIVE: nessuna

(il gain sul chr 20 comprende molte sonde ma è a inizio braccio q, dove può succedere di vedere uno sfasamento non reale, e poi le sonde non sono compatte)