

# Analisi di dati trascrittomici di RNA-seq da frazioni polisomiale e totale da una linea cellulare epiteliale tumorale

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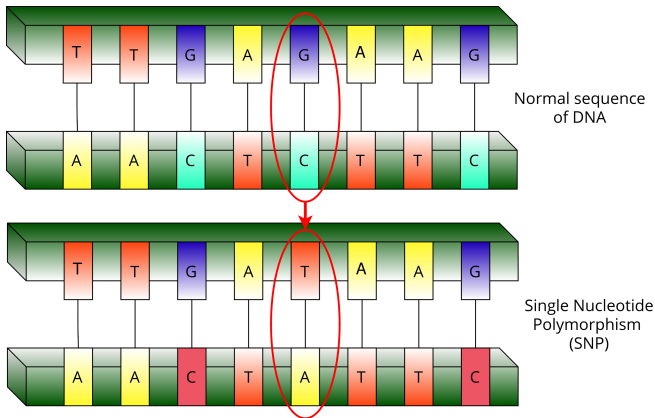
Laureando  
Giacomo Fantoni



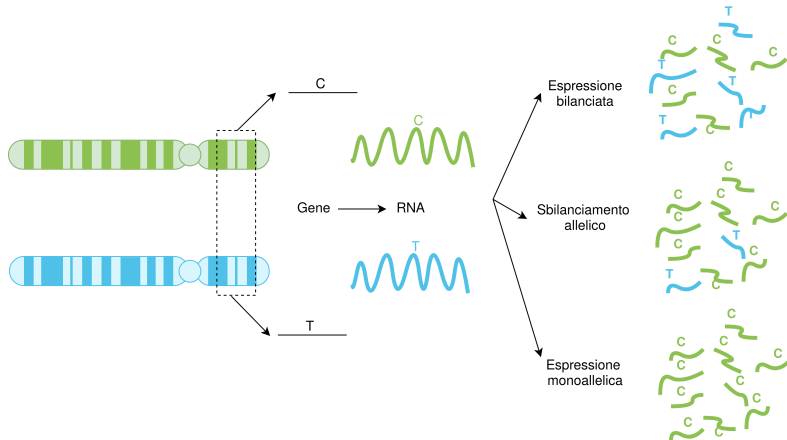
**UNIVERSITÀ  
DI TRENTO**

Dipartimento di Ingegneria e Scienza dell'informazione  
Corso di Laurea in  
Informatica

# TransSNP



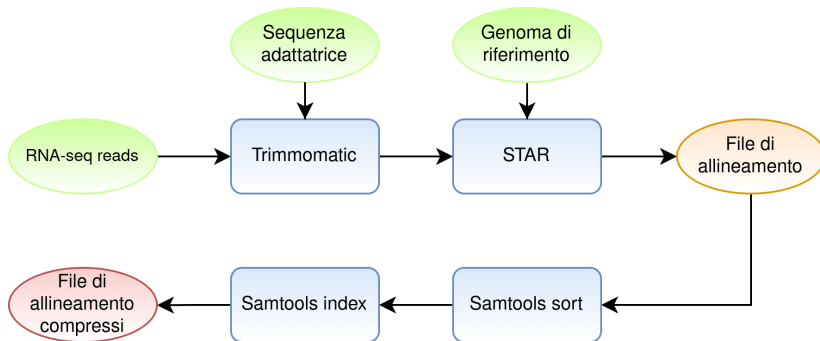
# Individuare transSNP



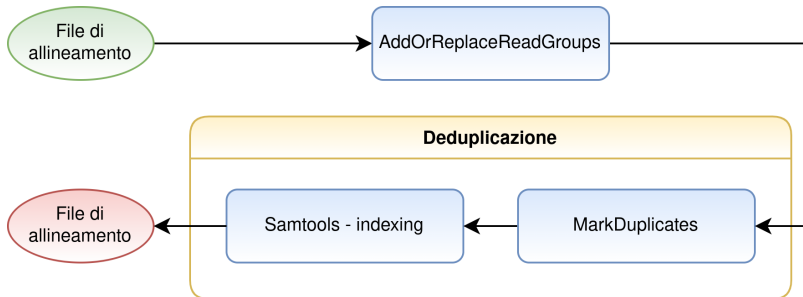
# Campioni

Nome	Trattamento	Linea cellulare
scr_DMSO	DMSO	HCT116
scr_NUTLIN	NUTLIN	HCT116
shDHX30_DMSO	DMSO	HCT116 con knockdown di DHX30
shDHX30_NUTLIN	NUTLIN	HCT116 con knockdown di DHX30
shPCBP2_DMSO	DMSO	HCT116 con knockdown di PCBP2
shPCBP2_NUTLIN	NUTLIN	HCT116 con knockdown di PCBP2

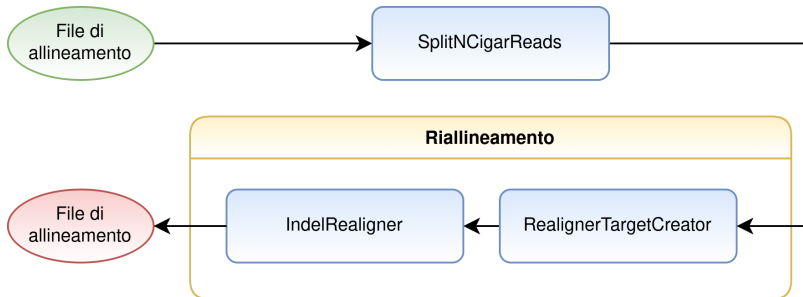
# Allineamento



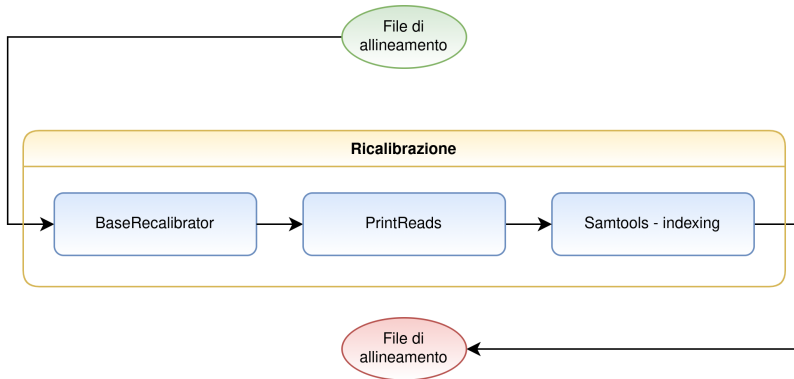
# Deduplicazione



# Riallineamento

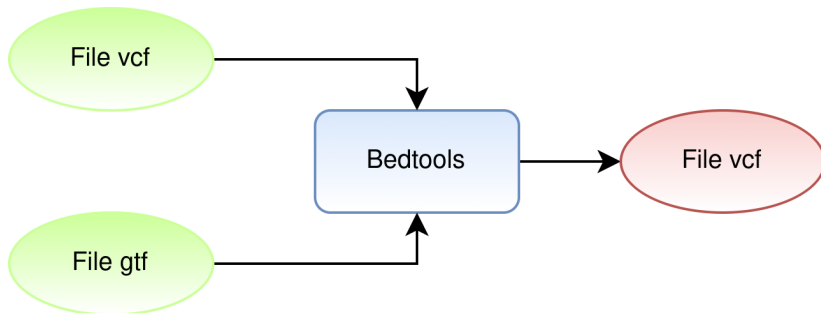


# Recalibrazione

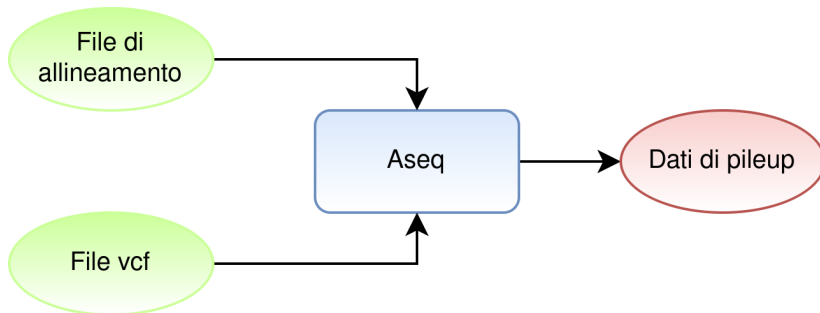




# Analisi dati WES



# ASEQ



# Analisi dei risultati

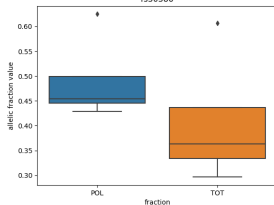
Condizione	Totali	3'-UTR	5'-UTR
scr_DMSO	27	8	2
scr_NUTLIN	33	11	2
shDHX30_DMSO	22	9	1
shDHX30_NUTLIN	25	11	0
shPCBP2_DMSO	24	10	1
shPCBP2_NUTLIN	30	11	2

Table: SNP individuati con p-value nominale inferiore a 0.05

# Geni individuati

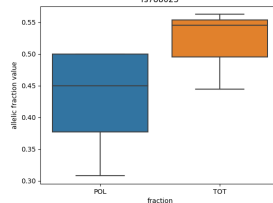
(a) TBC1D9B - scr\_NUTLIN

rs30386



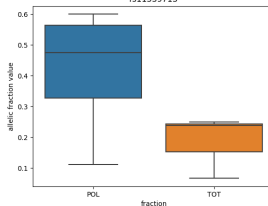
(b) SF3B1 - scr\_NUTLIN

rs788023



(c) KIF5B - shDHX30\_DMSO

rs11539713



# Grazie per l'attenzione.