

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

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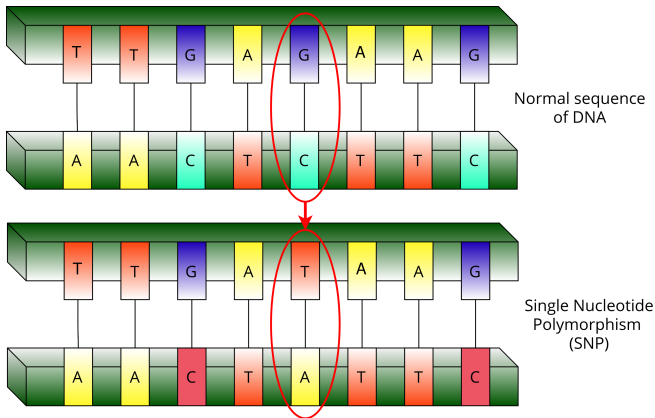
Laureando
Giacomo Fantoni



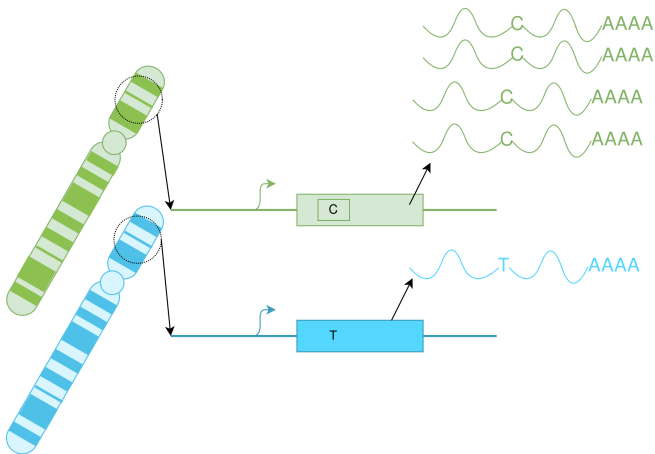
**UNIVERSITÀ
DI TRENTO**

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

TransSNP



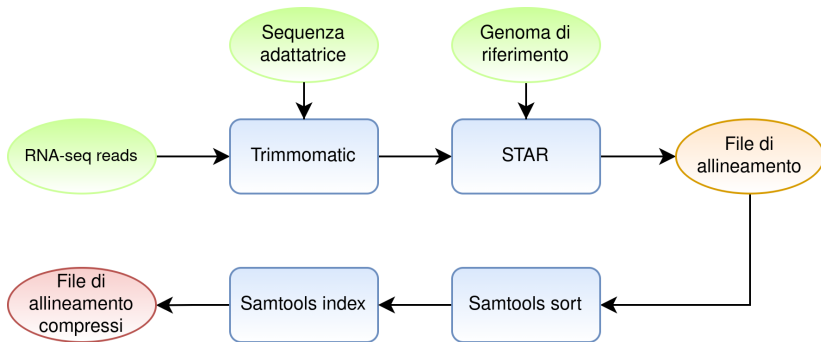
Individuare transSNP



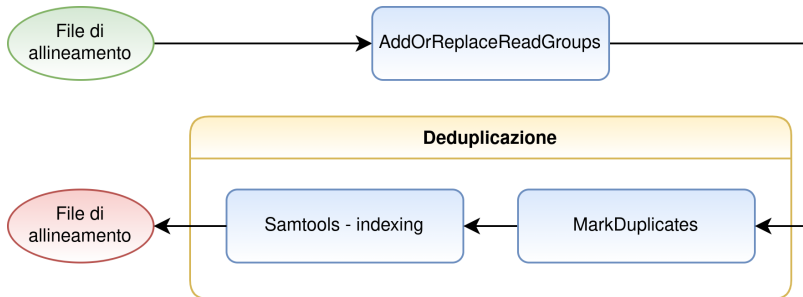
Campioni

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

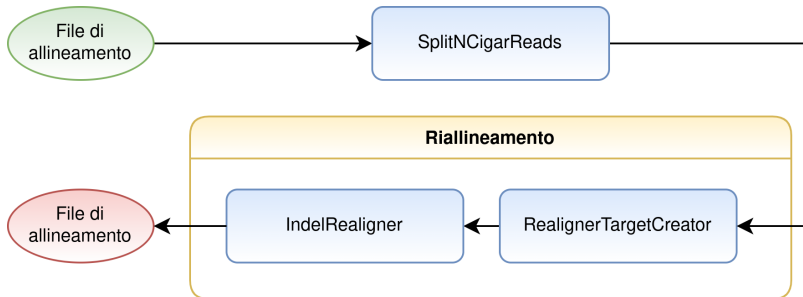
Allineamento



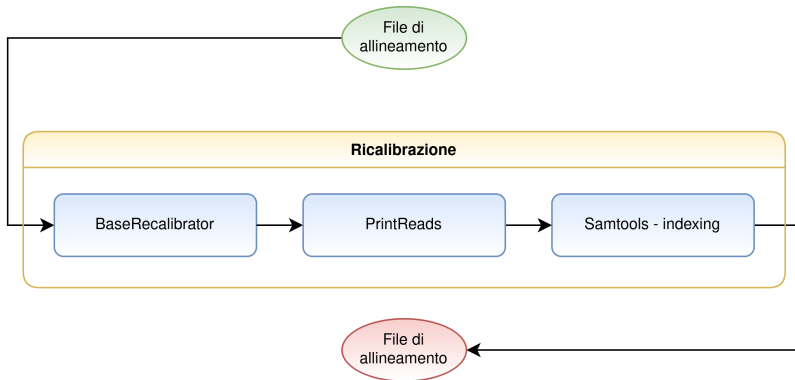
Deduplicazione



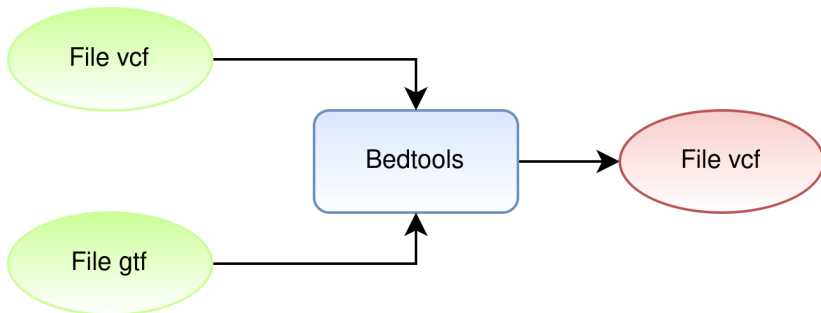
Riallineamento



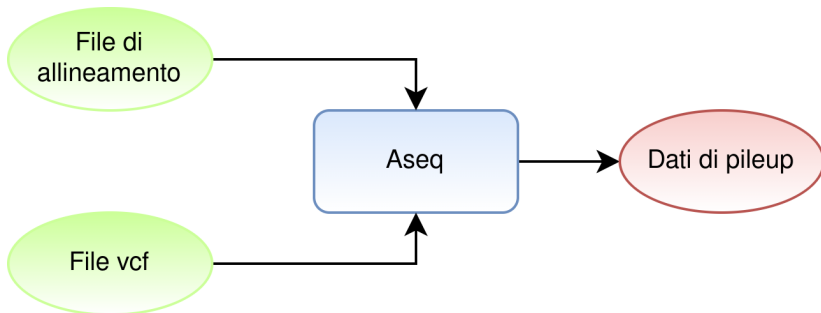
Recalibrazione



Analisi dati WES

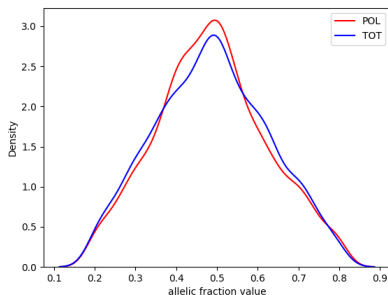


ASEQ



Analisi dati di pileup

dbsnp	ref	alt	A	C	G	T	af	cov
rs1423991279	G	A	6	0	5	0	0.545455	11
rs2272757	G	A	118	0	128	0	0.479675	246
rs975483396	G	A	6	0	6	0	0.500000	12



Filtri sugli SNP	SNP individuati
Input di ASEQ	40418219
$cov \geq 10$ e $0.2 \leq af \leq 0.8$	13681
Dati per 3 replicati	851

$$af = \frac{\#alt}{\#ref + \#alt}$$
$$cov = \#ref + \#alt$$

Analisi dei risultati

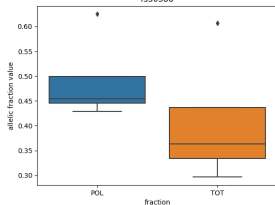
Condizione	Totali	3'-UTR	5'-UTR
scr_DMSO	27	8	2
scr_NUTLIN	33	11	2
shDHX30_DMSO	22	9	1
shDHX30_NUTLIN	25	11	0
shPCBP2_DMSO	24	10	1
shPCBP2_NUTLIN	30	11	2

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

Geni individuati

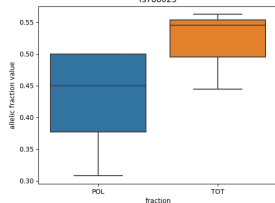
(a) TBC1D9B - scr_NUTLIN

rs30386



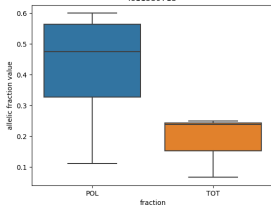
(b) SF3B1 - scr_NUTLIN

rs788023



(c) KIF5B - shDHX30_DMSO

rs11539713



Sviluppi futuri

- Validazione dei risultati trovati.
- Analisi di linkage.

Grazie per l'attenzione.