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

Supervisore Alberto Inga Co-supervisori Alessandro Romanel Samuel Valentini Laureando

Giacomo Fantoni



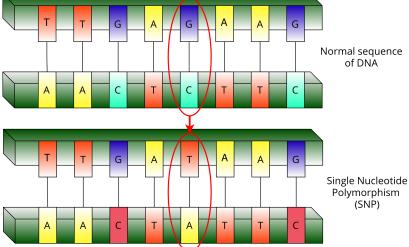
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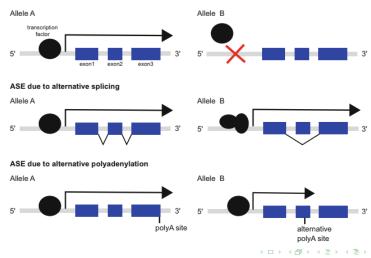
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Controllo traduzionale nel cancro



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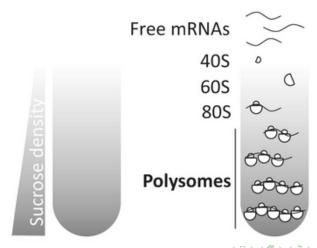
TransSNP



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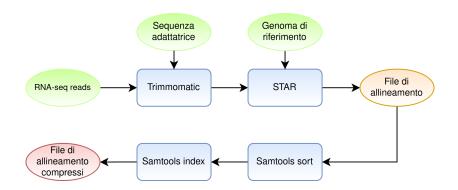
Individuare transSNP



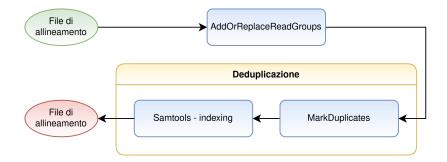
Campioni

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	

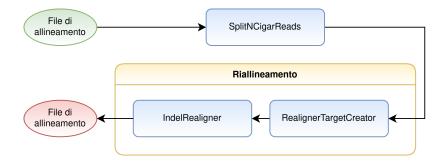
Allineamento



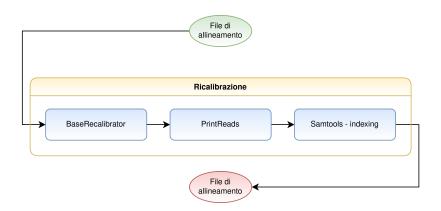
Deduplicazione



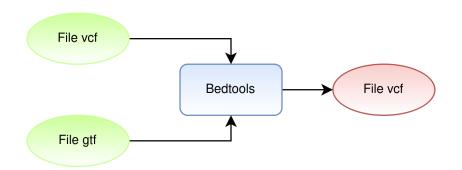
Riallineamento



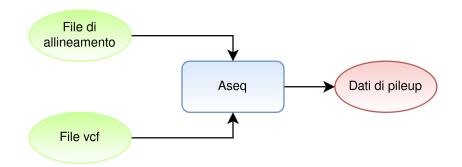
Recalibrazione



Analisi dati WES



ASEQ



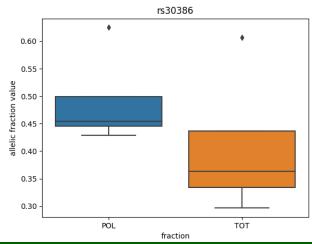
Analisi dei risultati

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

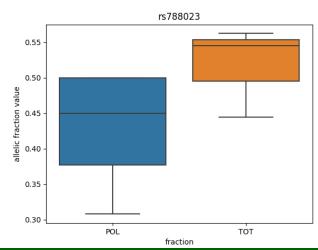
Table: SNP individuati con p-value nominale inferiore a 0.05



TBC1D9B - scr_NUTLIN

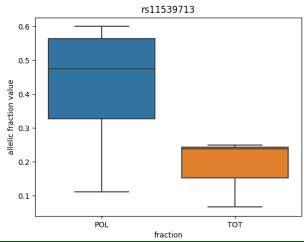


SF3B1 - scr_NUTLIN



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KIF5B - shDHX30_DMSO



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