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Modulo per la sottomissione abstract ricerca di LABORATORIO

Titolo (massimo **15 parole**)

Ultraconserved regions encoding ncRNAs are altered and have a prognostic role in human diffuse large b-cell lymphoma

Autori (cognome e iniziali, es: Grassi L.)

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Testo (massimo **250 parole**, preferibilmente in italiano (accettato anche in inglese), suddiviso in Introduzione, **Metodi, Risultati, Conclusioni e Finanziamento**)

A large portion of the human genome is actively transcribed into RNA molecules and, surprisingly, over than 90% of the RNA molecules made by a cell are not translated into proteins. A subgroup of them have nucleotide sequences longer than >200 bp and are named long ncRNA (lncRNA) which include ultra-conserved elements (ucRNAs) that are fully conserved across human and rodent genomes. The molecular function of transcribed ucRNAs is unknown. Although many lncRNAs lack primary sequence conservation across species, ucRNAs are highly conserved, suggesting an important evolutionarily conserved biological function for transcribed ucRNAs. We hypothesize that ucRNAs have unidentified roles in the pathogenesis of lymphoma, one of the most frequent cancer in human. In a pilot study, we examined ucRNA expression profiles in Diffuse Large B-cell Lymphoma (DLBCL) and normal counterpart. We developed CIANE a comprehensive t-UCRs detection pipeline that accurately quantifies t-UCRs from massive RNA-Seq data. T-UCRs quantified by CIANE clearly separate normal from pathological samples. Hierarchical clustering of DLBCL samples based on the expression level of t-UCRs show two transcriptional groups, termed group 1 (G1) and group 2 (G2). Importantly, the two groups were associated with different outcome under R-CHOP treatment (Log-rank test p-value = 0.048), with G2 showing worst prognosis compare to G1 (hazard ratio = 4.1). The t-UCRs driven groups did not appear dependent on the DLBCL cell of origin (COO) (chi-squared p-value = 0.56) and its prognostic value was indeed independent of the COO (multivariate Cox proportional hazards regression p-value = 0.035).

Visto superiore* (prego indicare **Nome e Cognome** del superiore) ***campo obbligatorio**

Francesco Bertoni

Criteria per sottomissione Abstract:
NO Case report
NO Abstract senza nessun risultato
VISTO da un superiore

Invio Abstract

