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Osteosarcoma gene prioritization through combined bioinformatics analysis.

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Abstract: This is the abstract section in English (mandatory). One paragraph only (Maximum 300 words approx.).

Osteosarcoma (OS) is a rare genetic disease that represents 20% of all types of malignant and benign neoplasms of the bone, and 2% of pediatric cancers. Therefore, our aim in this study is to generate a consensus gene list associated with the pathogenicity of OS by using several theoretical approaches that let to propose new drivers associated to this sarcoma, and also possible biomarkers. Firstly, we evaluated the consensus between 9 prioritization strategies to early determine pathogenic genes related to OS. From these genes, we performed a communality analysis in the protein-protein interaction network further enrichment analysis. The consensus prioritized gene list consisted of 1295 genes. Our results revealed that consensus strategy proposes genes related to control in the cell cycle that describe the etiology of cancer in general, and prioritizes not only suppressors already described for OS such as RB1 and TP53, but also postulates new candidates that would help to describe its pathogenesis.

Keywords: Consensus analysis; Gene periodization; Osteosarcoma, Communality analysis; Pathogenesis; Early recognition.

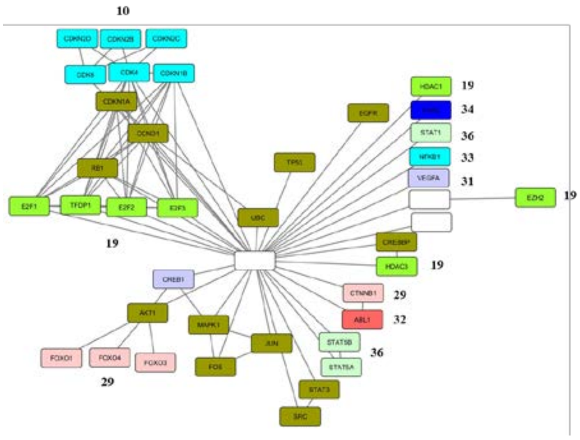

Figure 1. Network analysis from gene communities prioritized for OS.

Protein interaction of prioritized OS genes base on STRING database. Each community is represented by specific colors: light blue, comm. 10; green, 19; light green, 36; blue, 34; pink, 29; red, 32; purple. Genes present in two or more communities are olive-green colored.

References and Notes

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