

基于数据挖掘分析VHL, PBRM1, TTN, SETD2, BAP1在肾透明细胞癌中的表达及预后意义

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Title: Expression and prognostic significance of VHL,PBRM1,TTN,SETD2 and BAP1 in renal clear cell carcinoma based on data mining

作者: 王涛; 郭启振
中国医科大学附属盛京医院泌尿外科, 辽宁 沈阳 110004

Author(s): Wang Tao; Guo Qizhen
Department of Urology,Shengjing Hospital of China Medical University,Liaoning Shenyang 110004,China.

关键词: 肾透明细胞癌; TCGA数据库; 数据挖掘; TTN; PBRM1

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摘要: 目的: 研究相关基因在肾透明细胞癌中的表达变化, 评价相关基因与肾透明细胞癌的关系及其对预后的影响。方法: 在TCGA (The Cancer Genome Atlas) 数据库中配对肾透明细胞癌组织和正常肾细胞组织相关基因表达谱数据, 通过数据挖掘技术挖掘相关基因 (VHL, PBRM1, TTN, SETD2, BAP1) 与肾透明细胞癌表达及预后的关系。结果: 相对比正常肾透明细胞组织, VHL, PBRM1, SETD2, BAP1均呈低表达, TTN呈高表达, 通过建立相关生存曲线, 可知PBRM1低表达与TTN高表达能够减少肾透明细胞癌患者的生存时间, 而VHL、SETD2、BAP1基因低表达与肾透明细胞癌患者的生存时间无统计学差异。结论: PBRM1的低表达与TTN高表达是影响肾透明细胞癌预后的不良因素, 因此PRBM1、TTN基因的表达对判断肾透明细胞癌患者的生存预后具有参考价值。

Abstract: Objective:To study the genes mutation in renal clear cell carcinoma and evaluate the relationship and their effexts between the related genes in renal clear cell carcinoma.Methods:The gene expression profiles of renal clear cell carcinoma tissue and normal renal cell tissue were paired in the TCGA (The Cancer Genome Atlas) database.We chose VHL,PBRM1,TTN,SETD2,BAP1 in clear cell renal cell carcinoma to analysis their relationship with their survival.Results:Compared with normal renal clear cell tissue,VHL,PBRM1,SETD2,and BAP1 showed low expression and TTN was highly expressed.By establishing a survival curve,it can be seen that low expression of PBRM1 and high expression of TTN can reduce the survival of patients with renal clear cell carcinoma.while the low expression of VHL,SETD2,BAP1 gene and their survival time were not statistically different.Conclusion:Low expression of PBRM1 and high expression of TTN are adverse factors affecting the prognosis of renal clear cell carcinoma.Therefore,the expression of PRBM1 and TTN genes haveimportant role for the prognosis of patients with renal clear cell carcinoma.

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