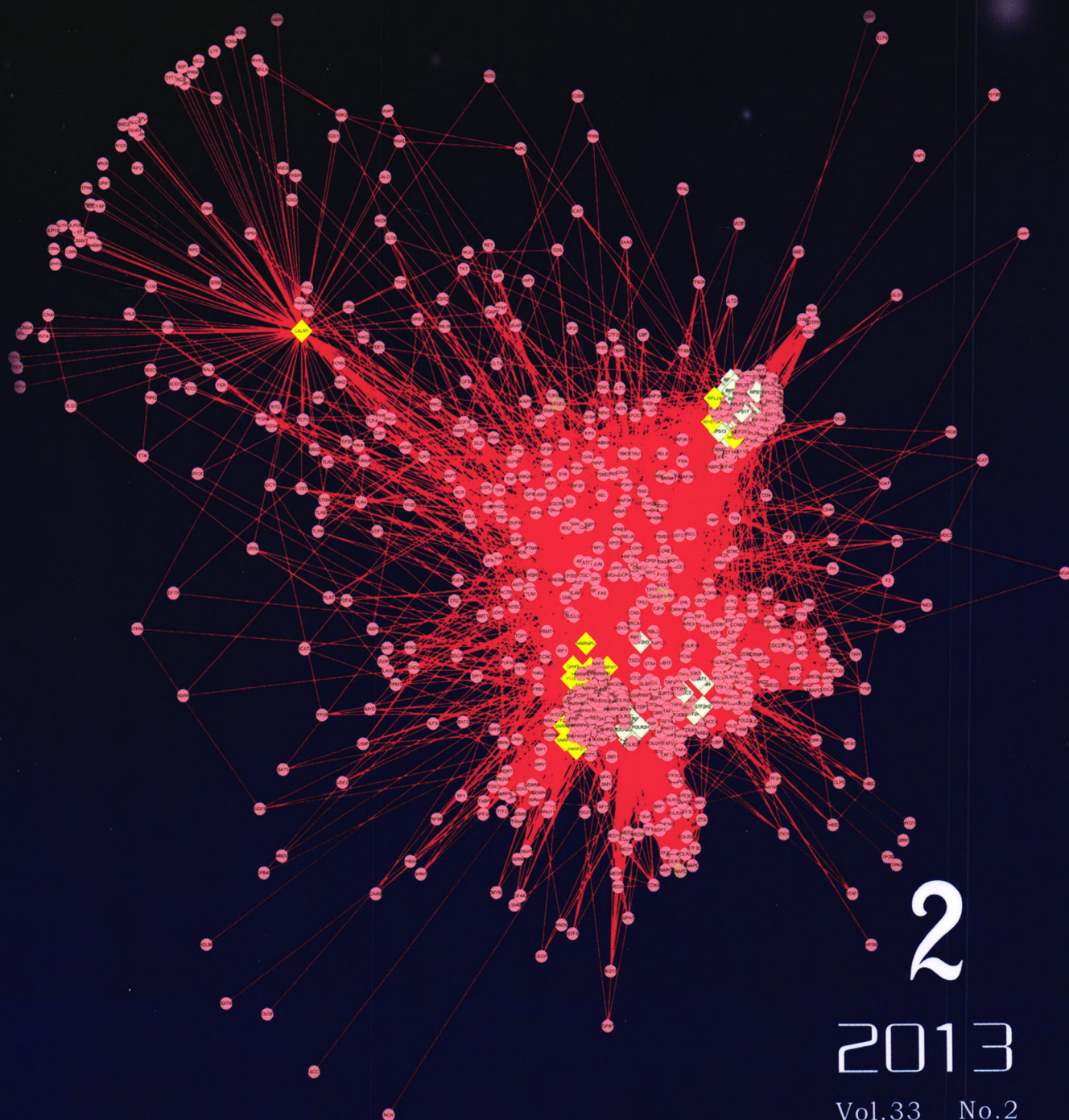


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封面图片:基因集富集分析(GSEA)与生物网络分析两种筛选关键基因方法的比较:将使用两种方法获得的肝移植相关基因进行蛋白质-蛋白质相互作用网络分析,以cytoscape软件进行可视化处理(◆代表使用GSEA筛选的基因,◊代表生物网络分析筛选出的基因,●为邻近作用基因)。获得的生物网络图像显示两种方法筛选出的基因在网络中的分布位置基本一致,说明两种分析结果具有相似性,也表明联合应用两种方法具有更强的可靠性(徐洪来,华中科技大学同济医学院附属同济医院器官移植研究所,全文见本期166页)。

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Cover image: Provided by XU Honglai (Institute of Organ Transplantation, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology). This image represents the result of visualization using Cytoscape software of the differentially expressed genes in liver and kidney transplantation recipients identified by combining gene set enrichment analysis (GSEA) and biological network analysis. See full-text article on page 166 in this issue.

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