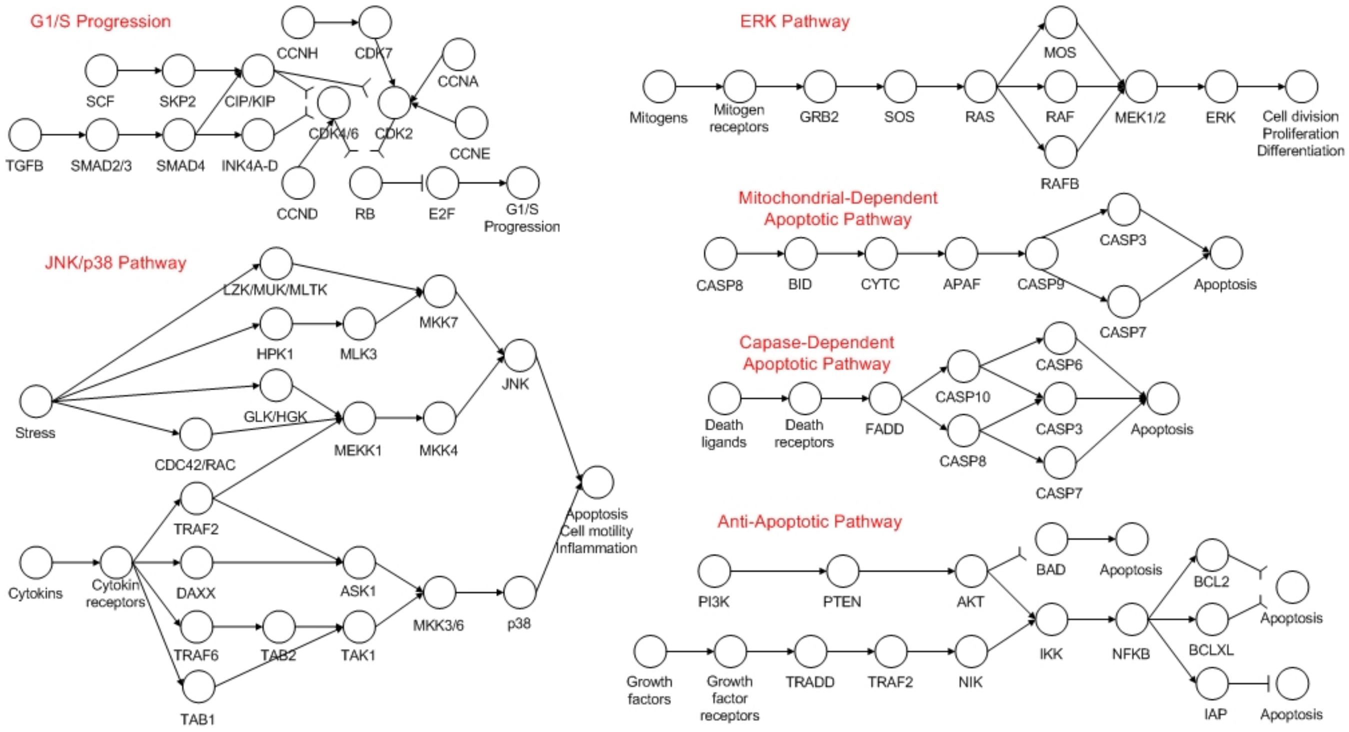

Fig. 1. Selected signaling pathways for the NPC study. For each pathway, the downstream events are represent as virtual nodes (contain no gene). "→" and "⊣" represent "stimulation" and "suppression" respectively.

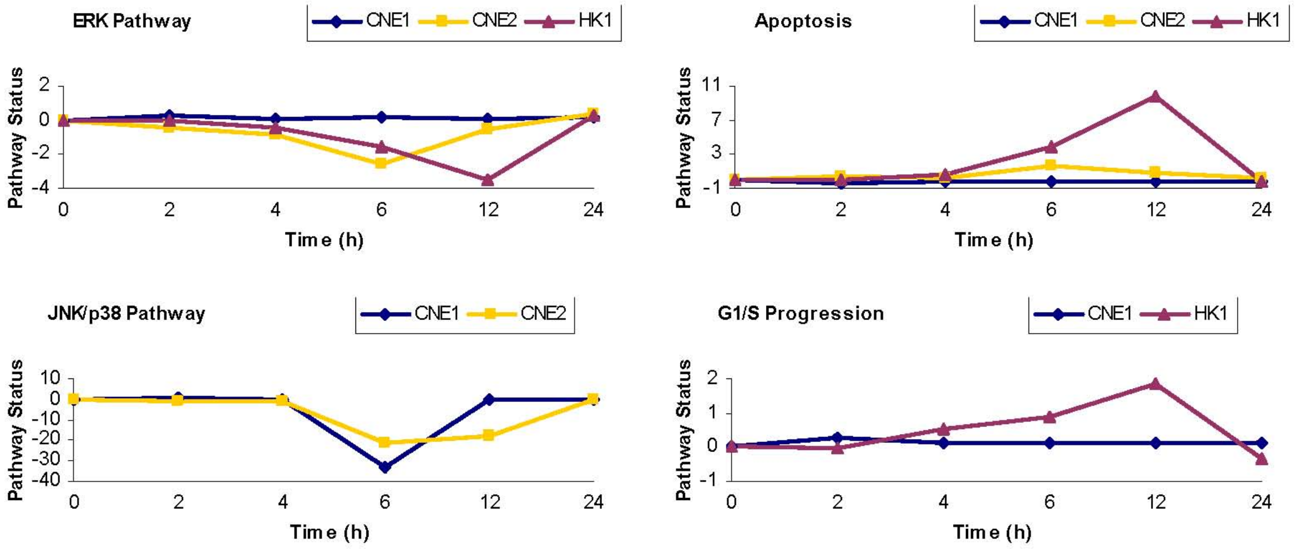

Fig. 2. Comparable status of the 4 signaling pathways of the 3 NPC cell lines along the treatment of CYC202.

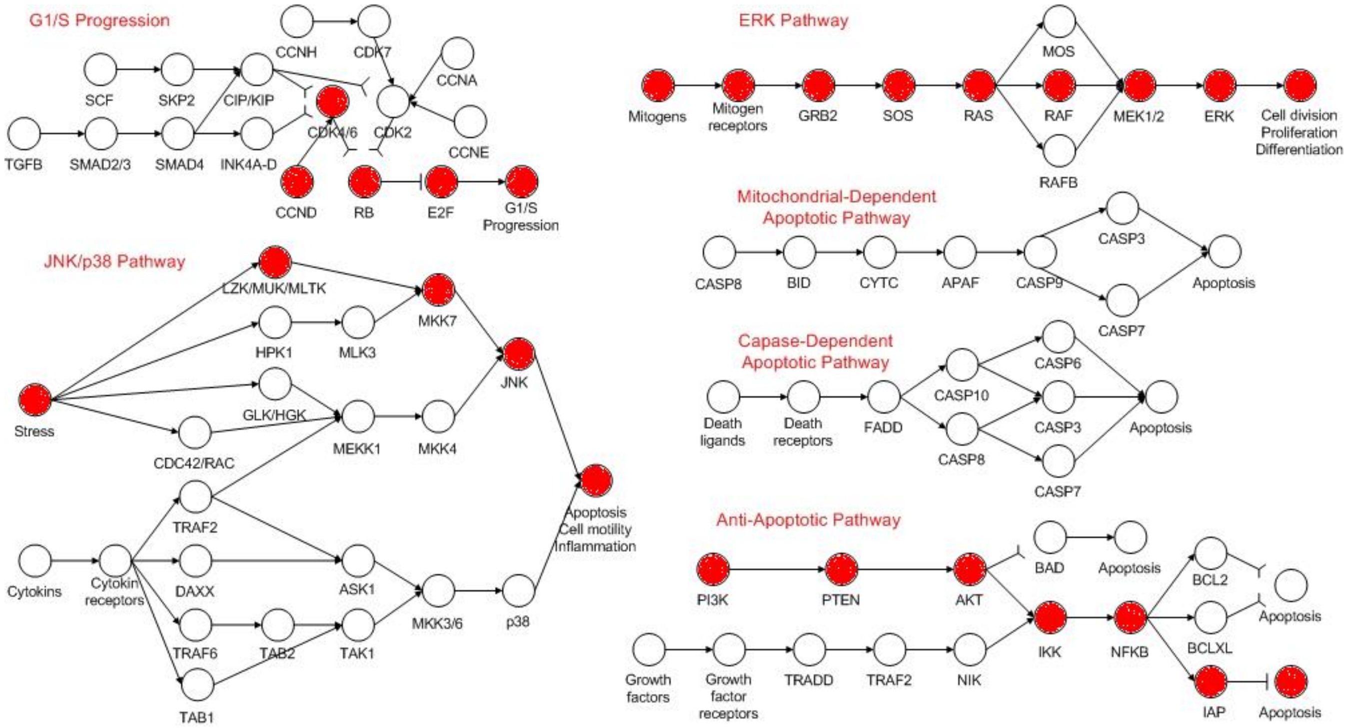

Fig. 3. The identified genetic pathways of CNE1: Genes on the identified pathways are highlighted. Statistical significance of the identifications is p-value$\leq$0.05.

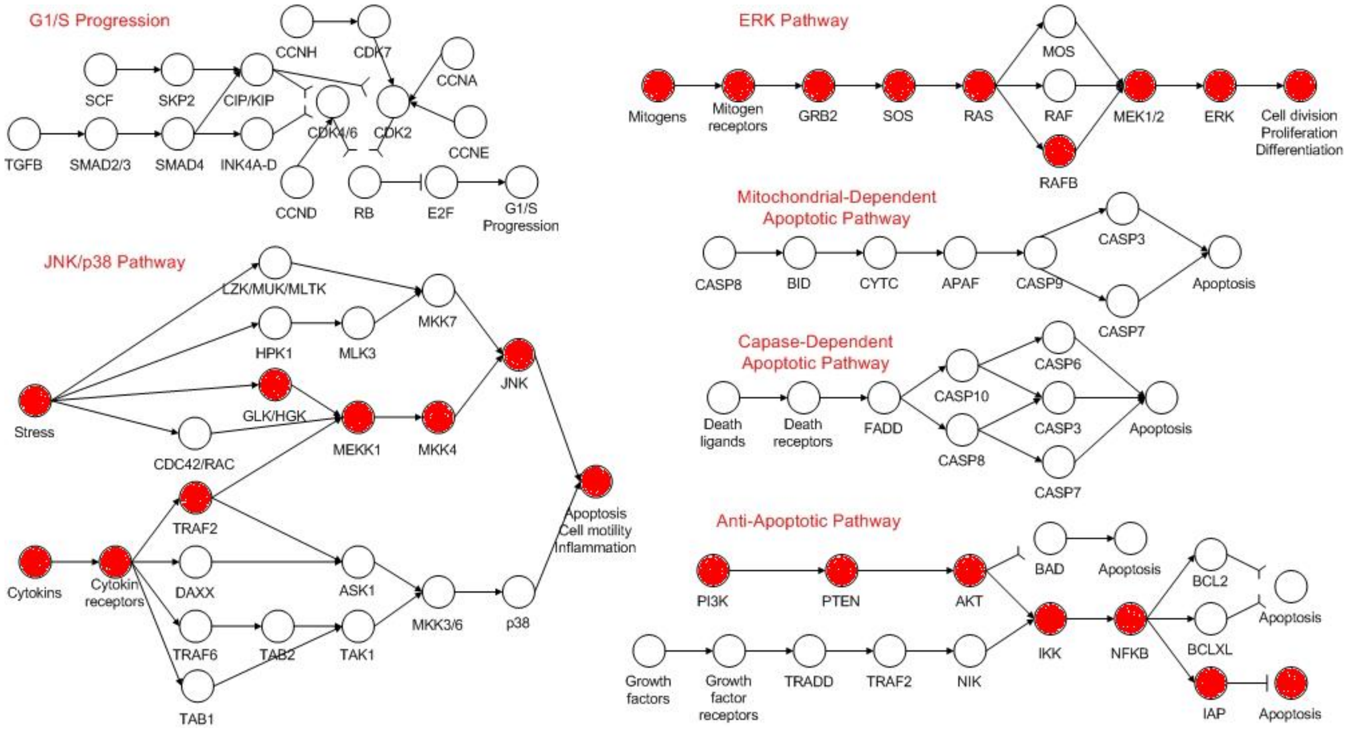

Fig. 4. The identified genetic pathways of CNE2.

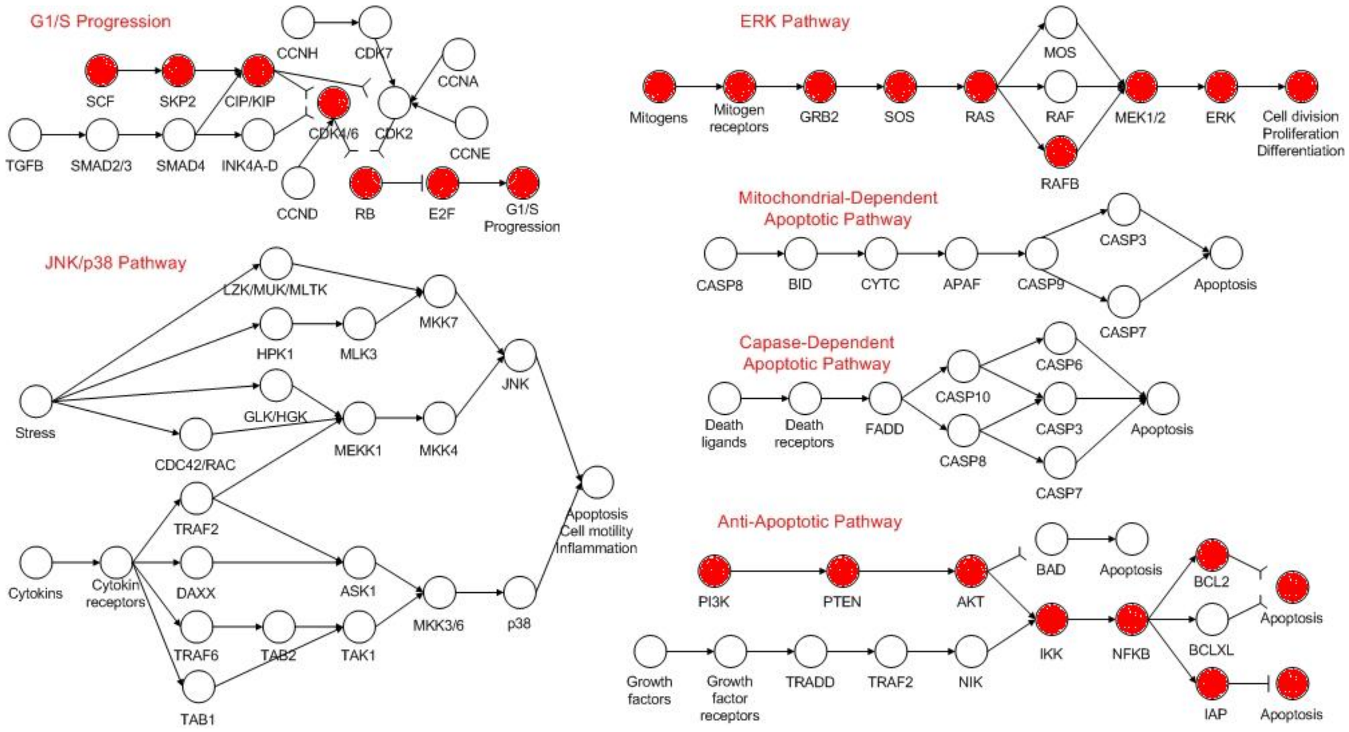

Fig. 5. The identified genetic pathways of HK1.

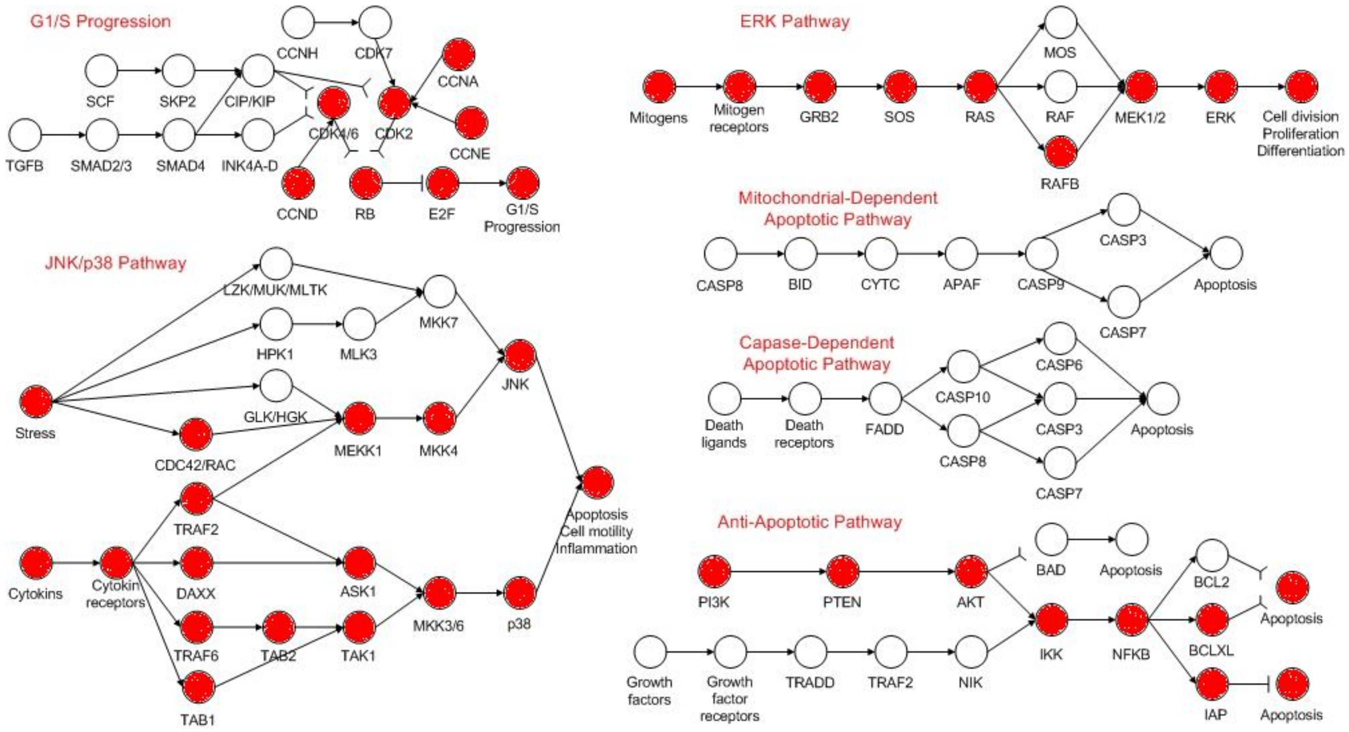

Fig. 6. The identified genetic pathways of Patient1.

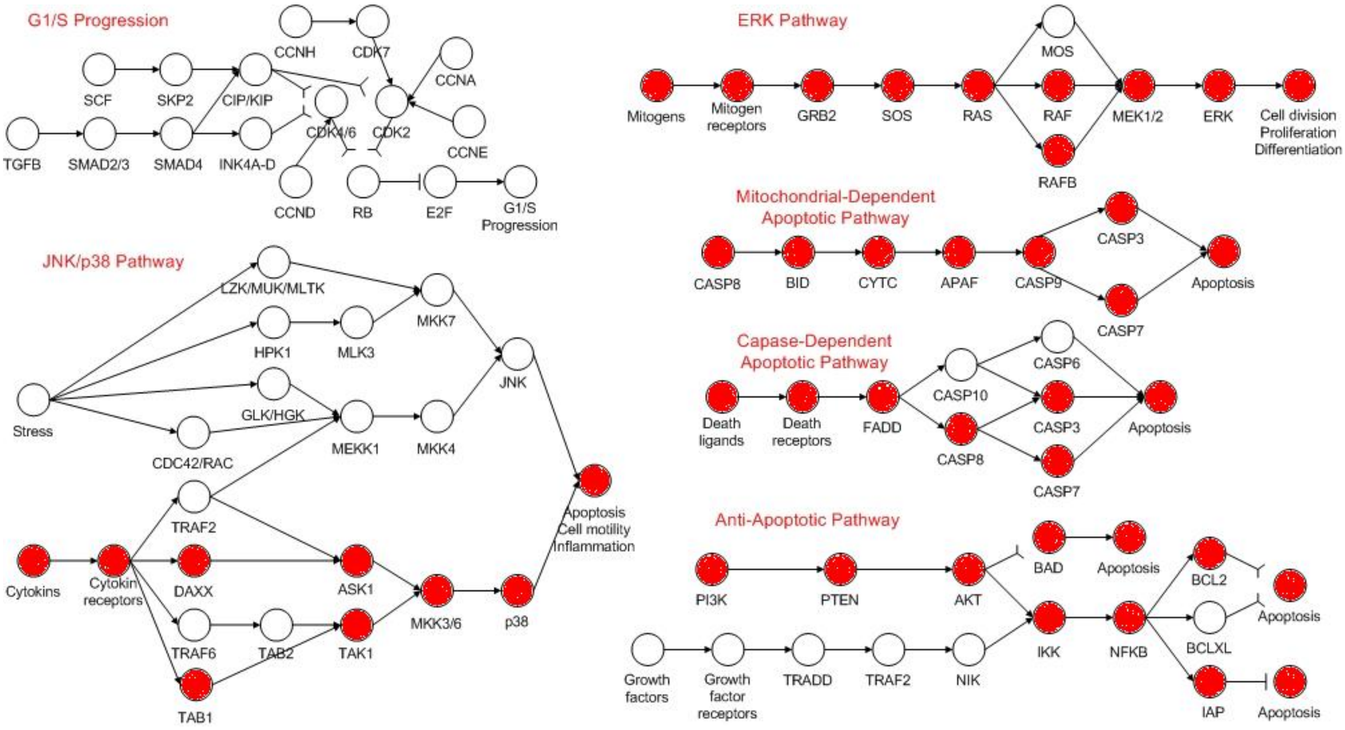

Fig. 7. The identified genetic pathways of Patient5.

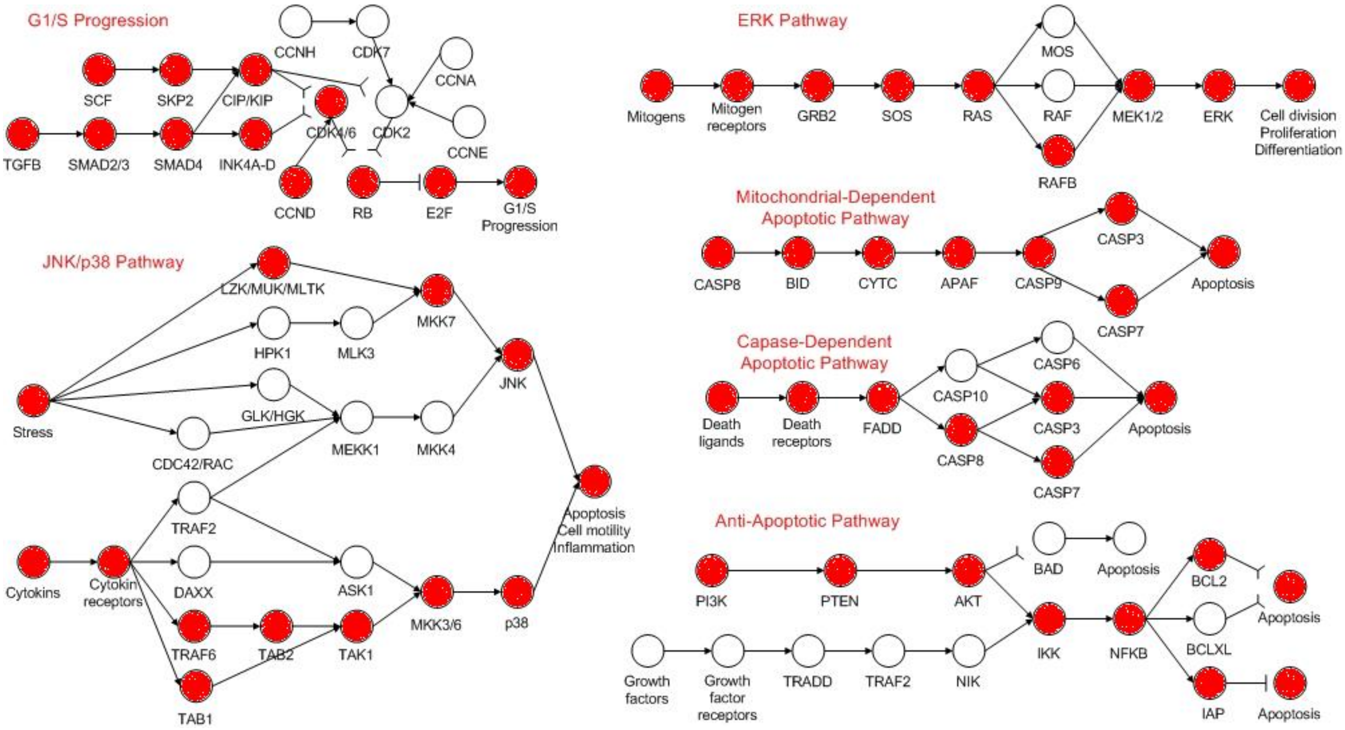

Fig. 8. The identified genetic pathways of Patient7.

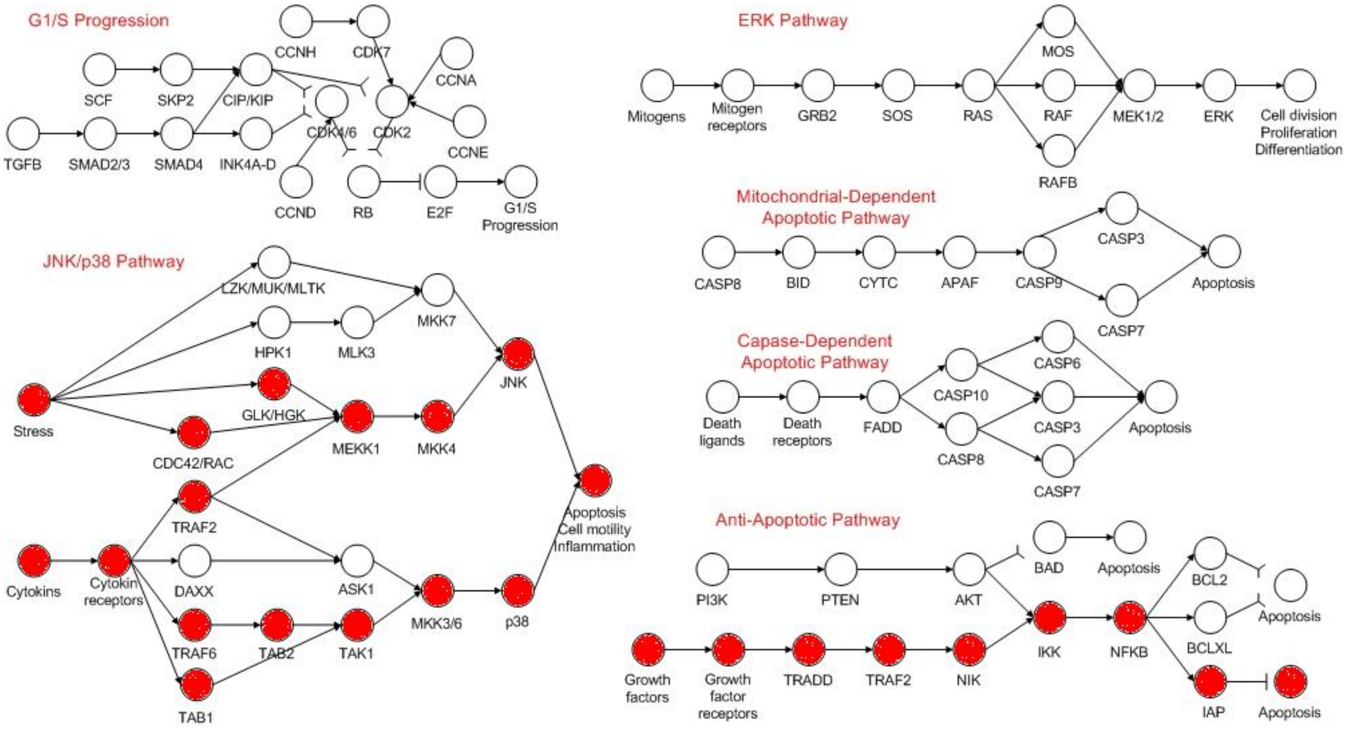

Fig. 9. The identified genetic pathways of Patient8.

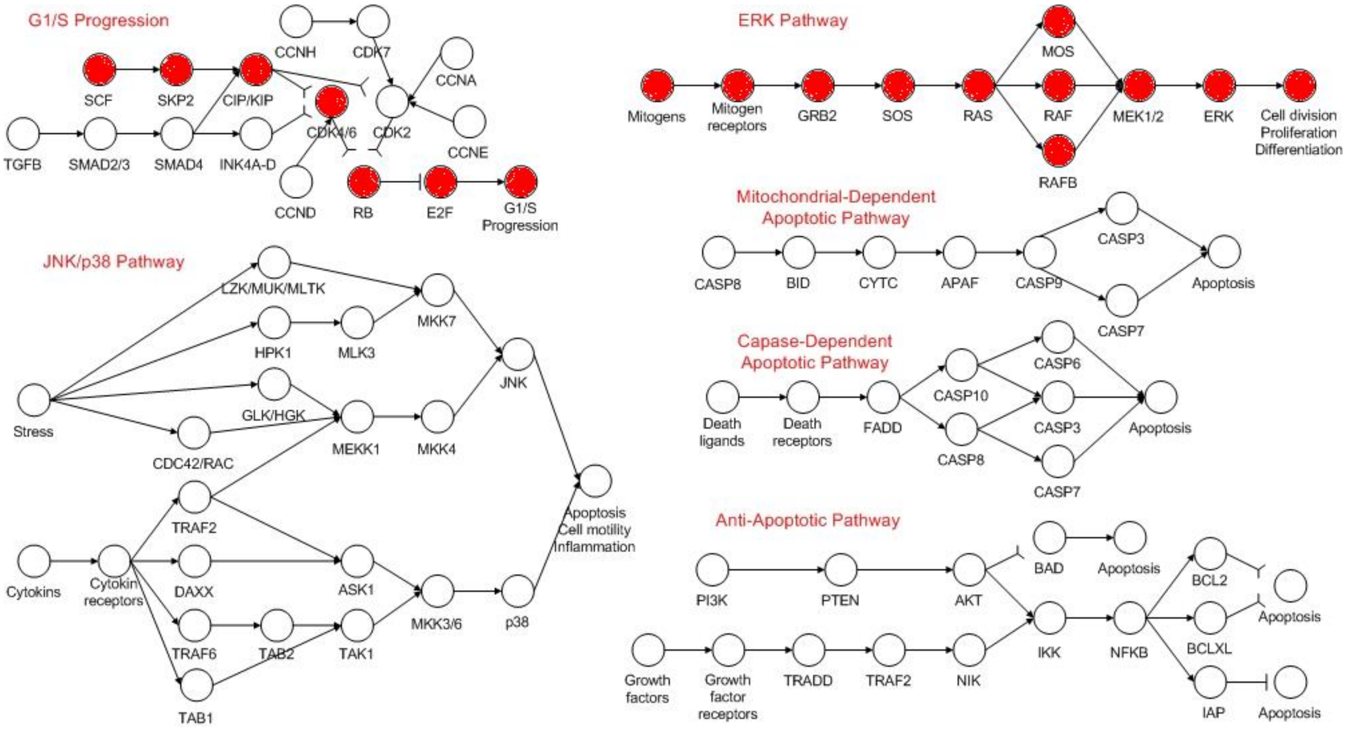

Fig. 10. The identified genetic pathways of Patient9.

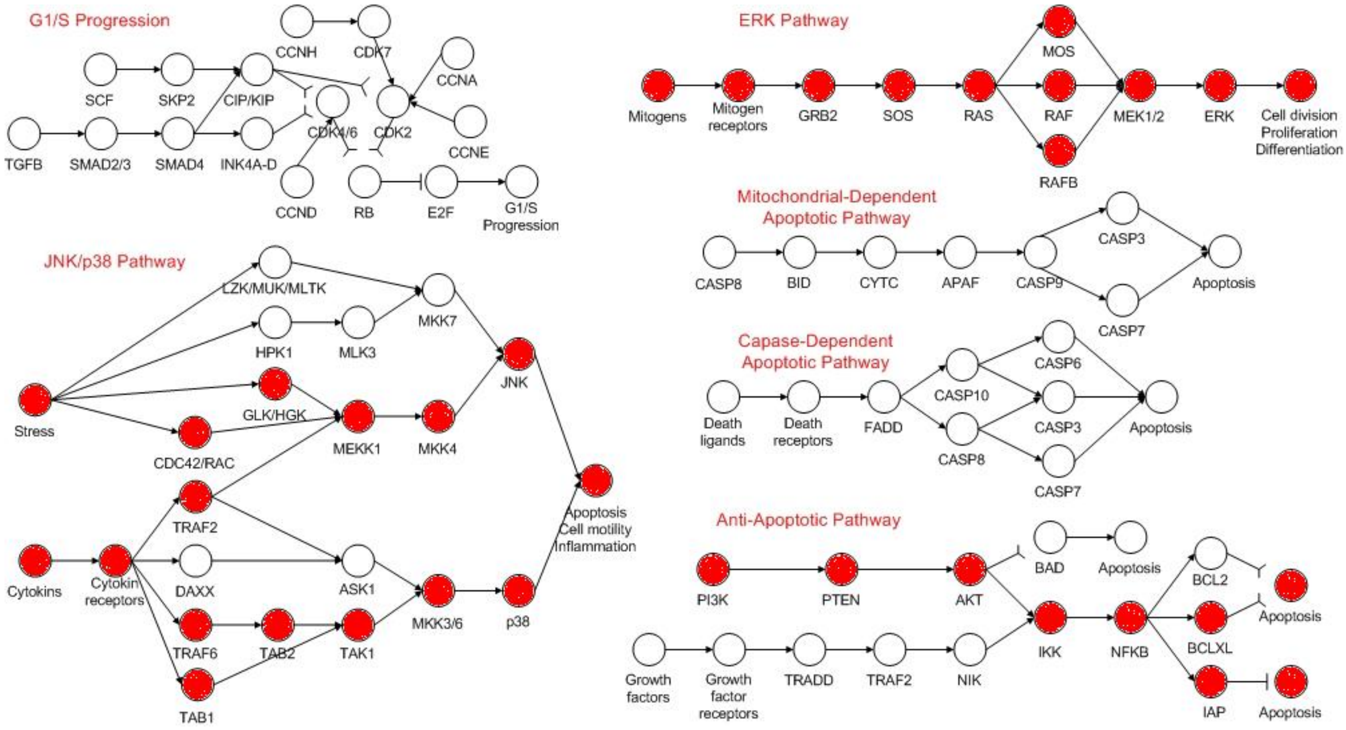

Fig. 11. The identified genetic pathways of Patient10.

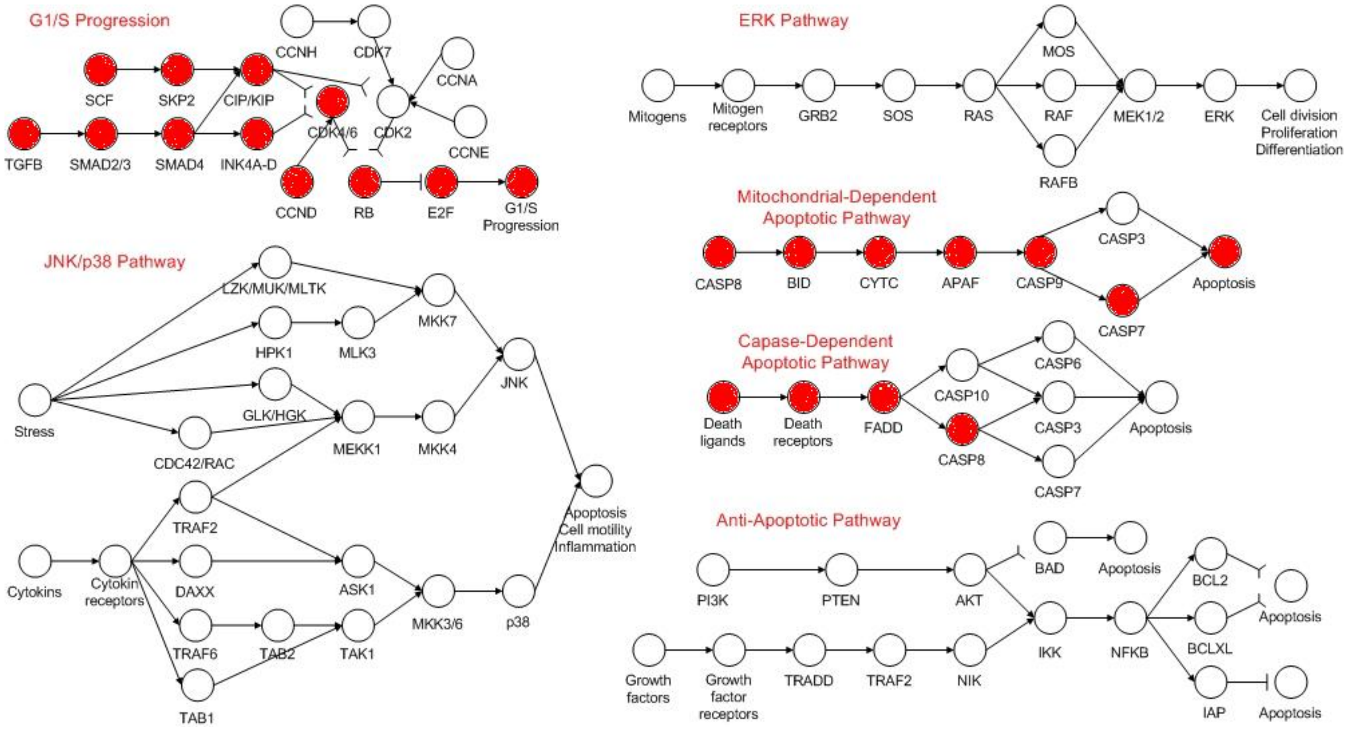

Fig. 12. The identified genetic pathways of Patient14.

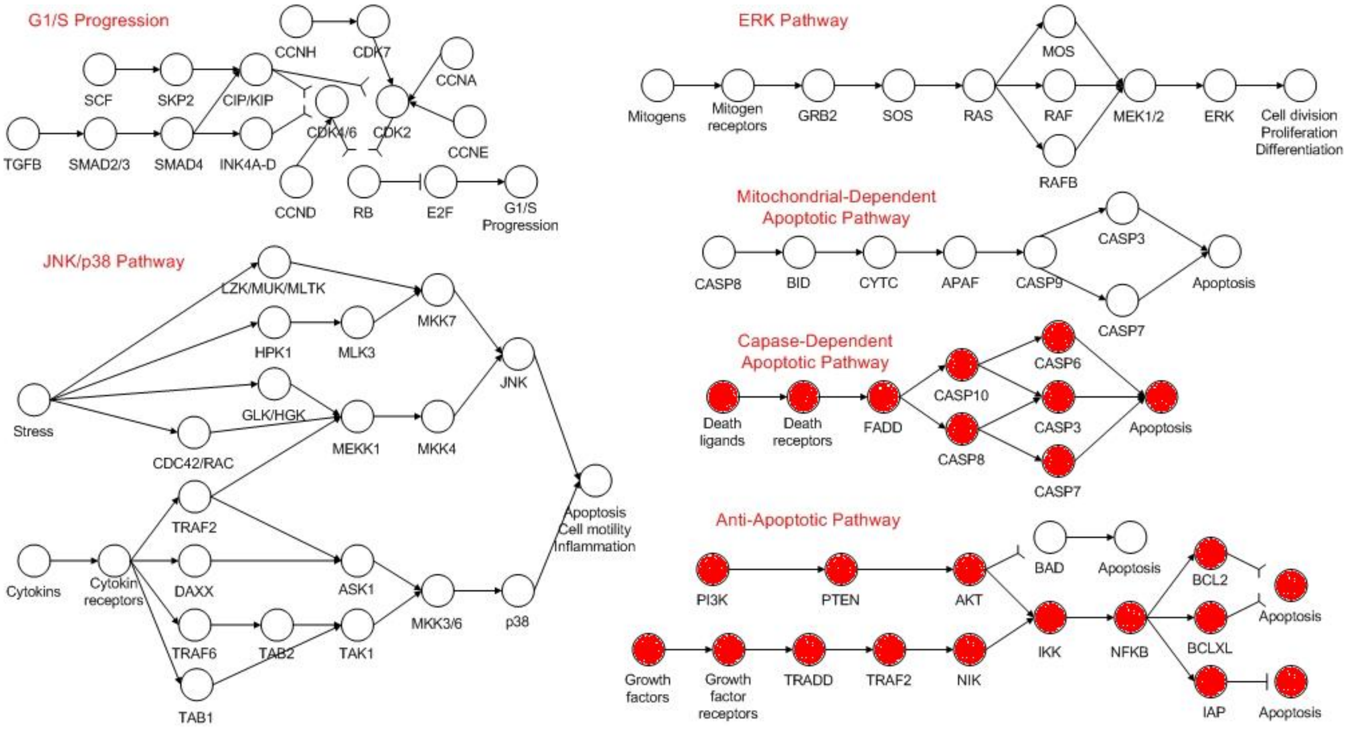

Fig. 13. The identified genetic pathways of Patient15.

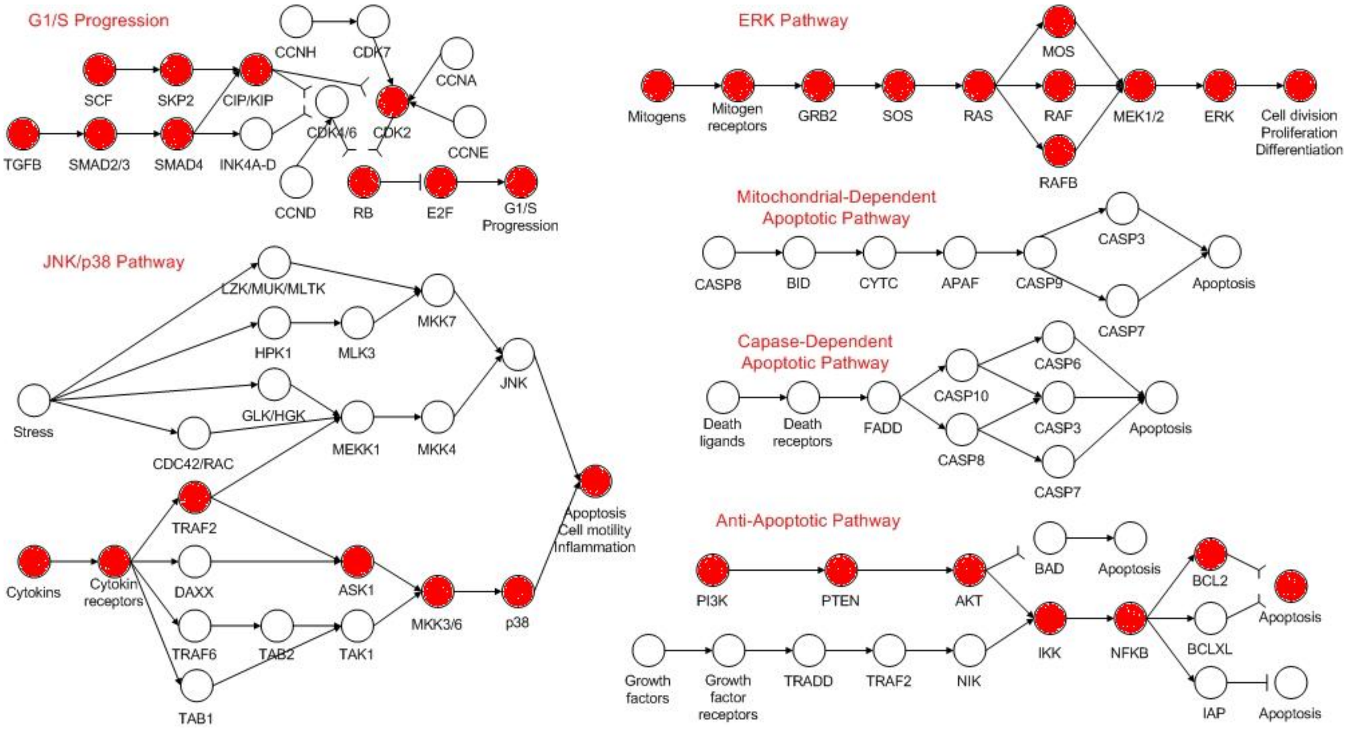

Fig. 14. The identified genetic pathways of Patient16.

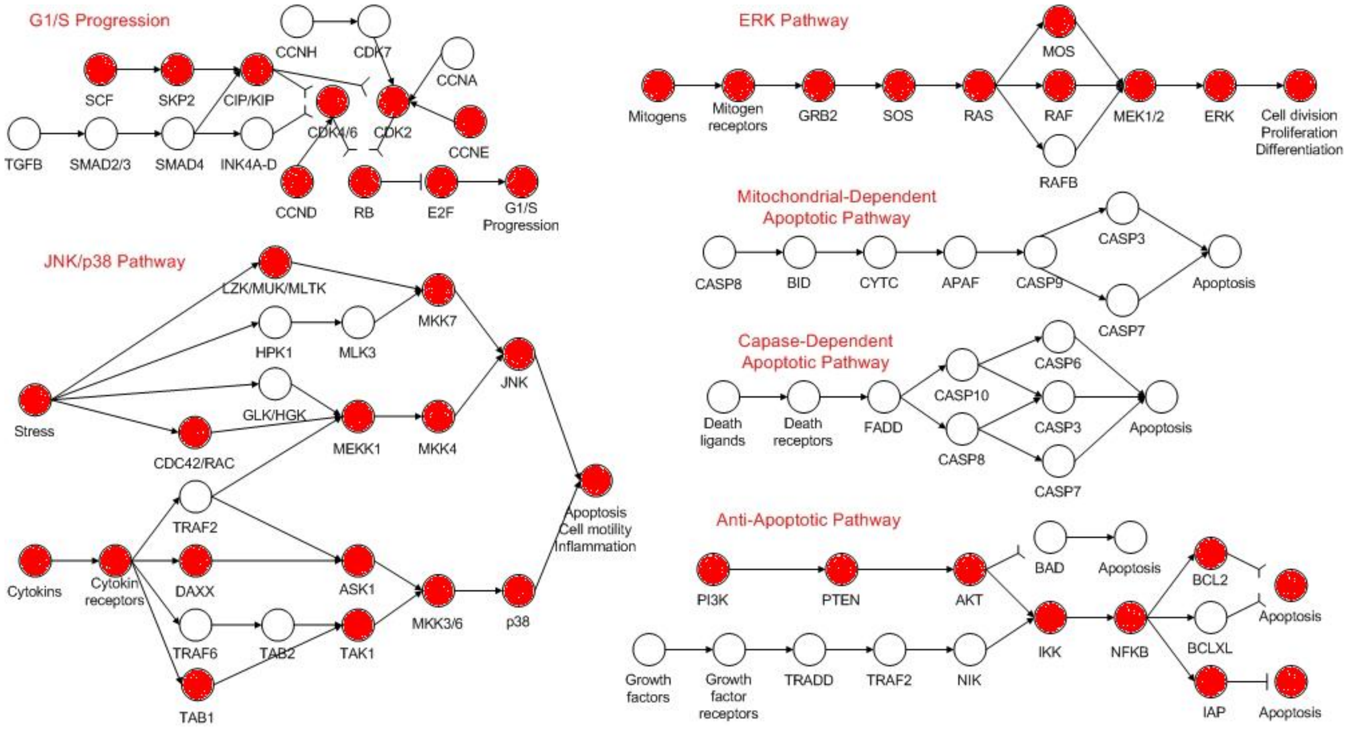

Fig. 15. The identified genetic pathways of Patient17.

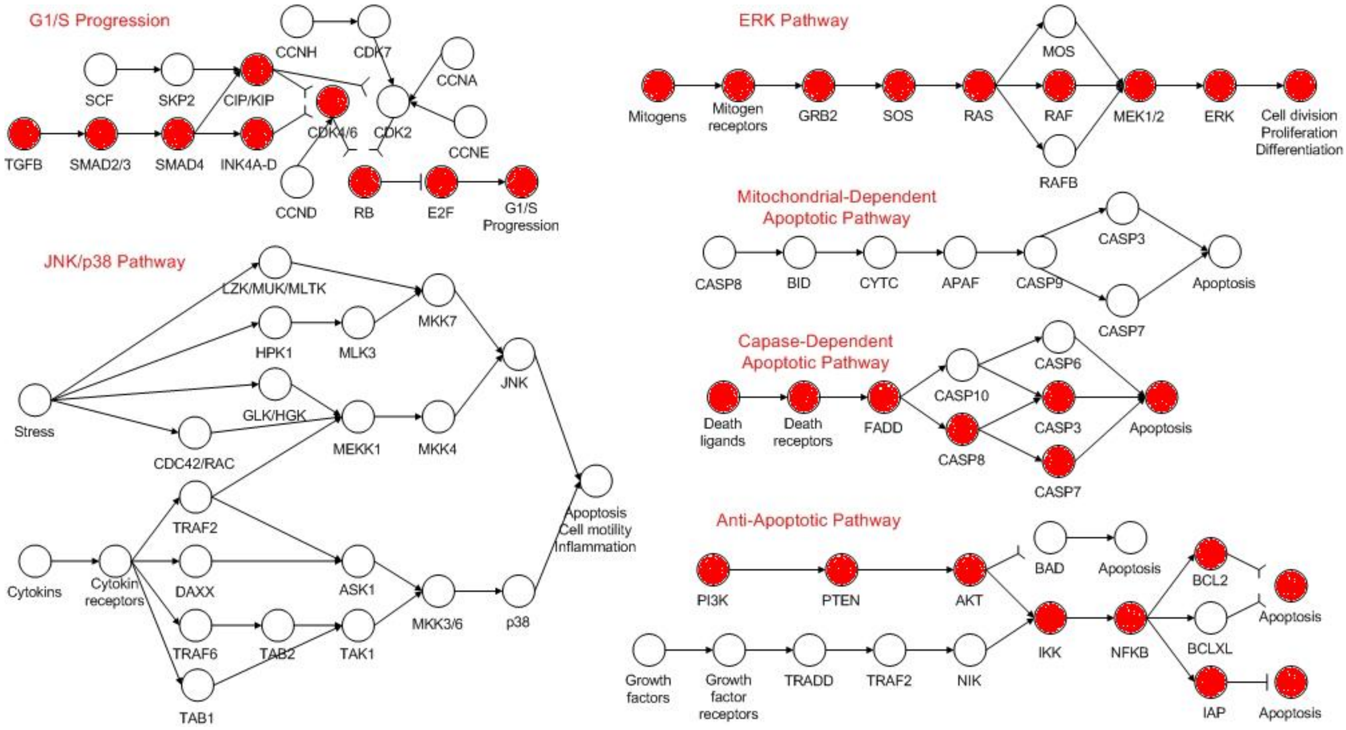

Fig. 16. The identified genetic pathways of Patient18.

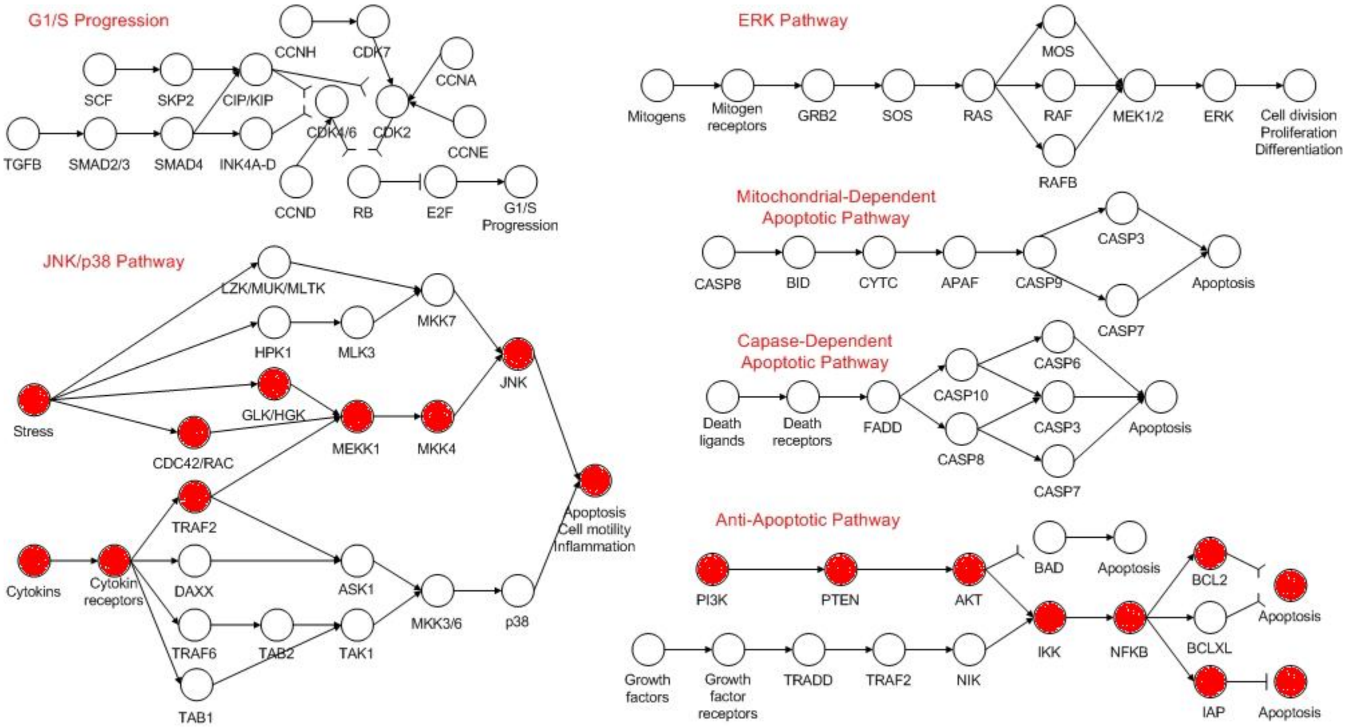

Fig. 17. The identified genetic pathways of Patient19.

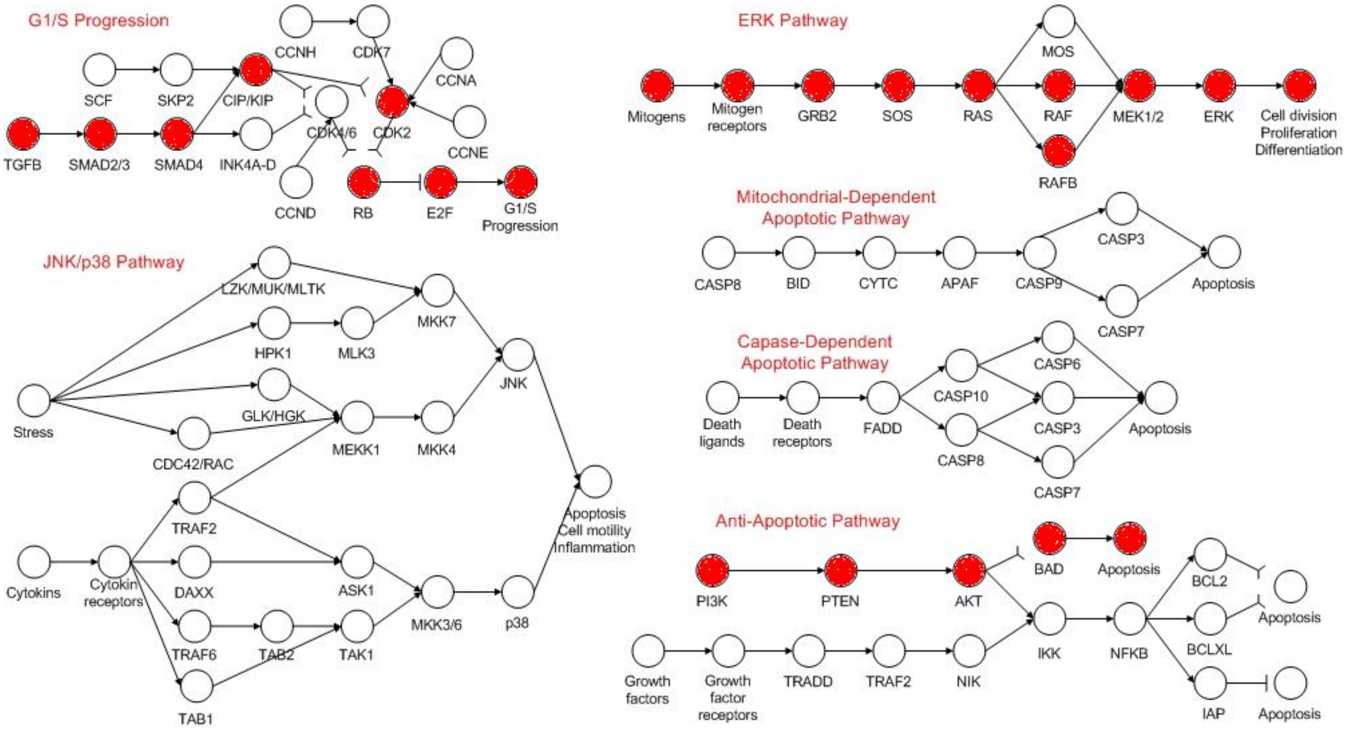

Fig. 18. The identified genetic pathways of Patient20.

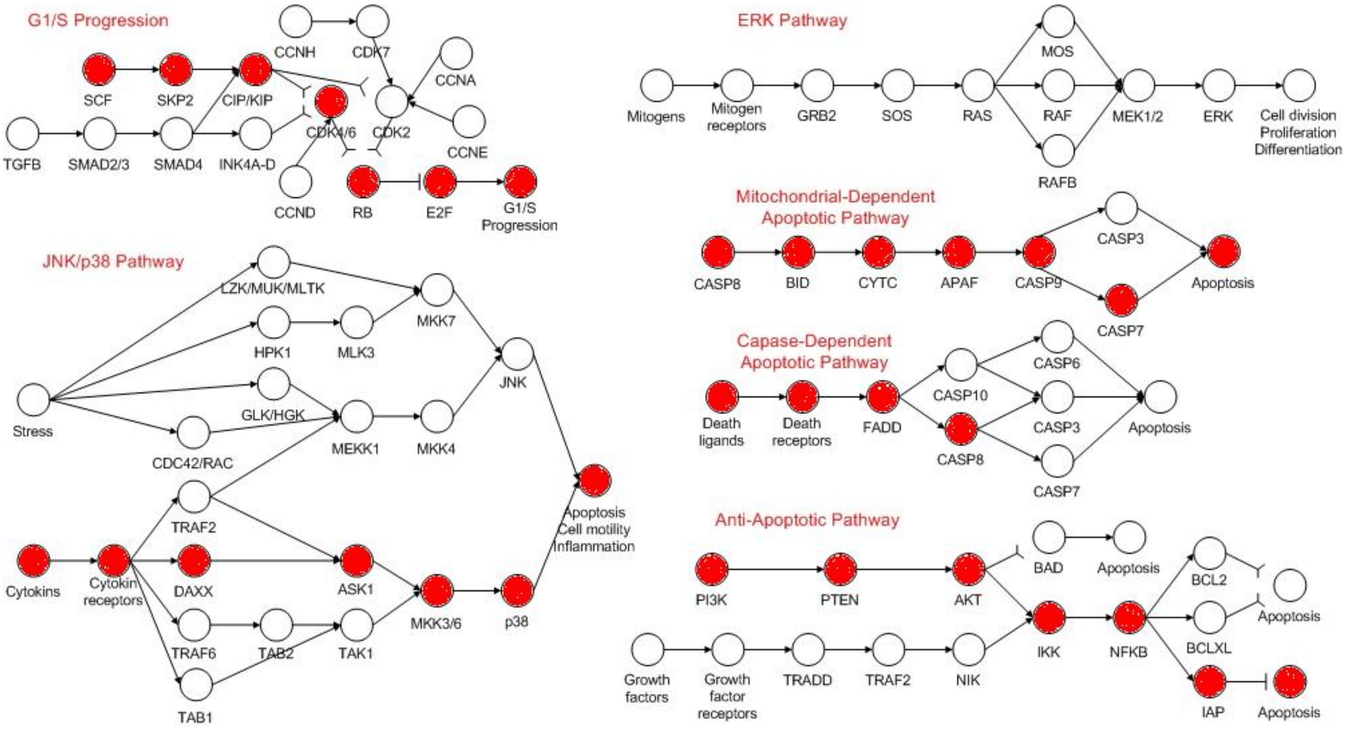

Fig. 19. The identified genetic pathways in the group of CYC202-responsive patients.

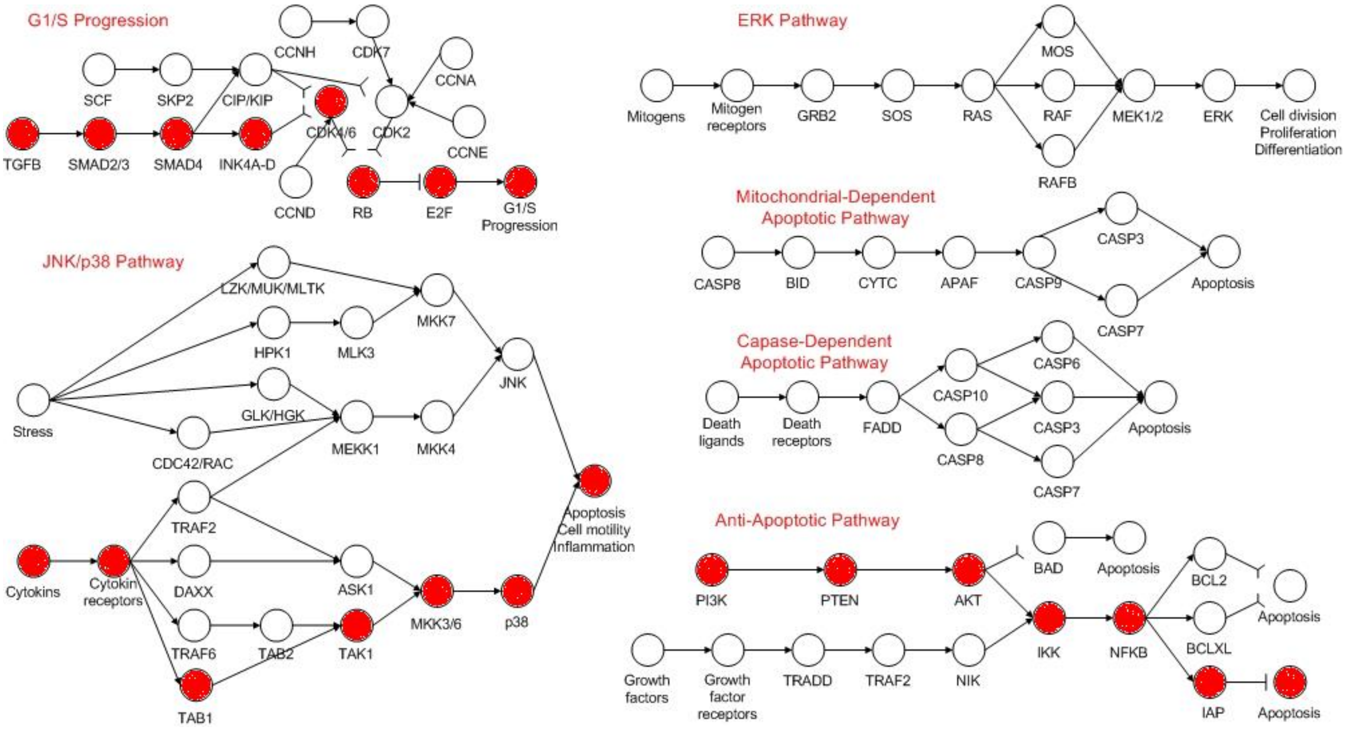

Fig. 20. The identified genetic pathways in the group of CYC202-resistant patients.