**Table I. Genes, each corresponding to a distinct complementation group/subtype.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Complementation group** | **Gene** | **Locus** | **Other gene names/activities** |
| A | *FANCA* | 16q24.3 |  |
| B | *FANCB* | Xp22.2 |  |
| C | *FANCC* | 9q22.3 |  |
| D1 | *FANCD1* | 13q12.3 | BRCA2, breast cancer susceptibility 2 |
| D2 | *FANCD2* | 3p26 |  |
| E | *FANCE* | 6p22-p21 |  |
| F | *FANCF* | 11p15 |  |
| G | *FANCG* | 9p13 |  |
| I | *FANCI* | 15q26.1 |  |
| J | *FANCJ* | 17q22.2 | BACH1/BRIP1,DNA helicase |
| L | *FANCL* | 2p16.1 | E3 ubiquitin ligase |
| M | *FANCM* | 14q21.2 | Hef orthologue, DNA translocation |
| N | *FANCN* | 16p12 | PALB2, interacts with BRCA2 |
| O | *FANCO* | 17q25.1 | RAD51C |
| P | *FANCP* | 16p13.3 | SLX4, endonuclease |

(Adapted from Online Mendelian Inhertance in Man, NCBI (National Center for Biotechnology Information. 2012)