

What is claimed is

1. Use of a Checkpoint kinase 1 (Chk1) inhibitor in the manufacture of a medicament for treating cancer in a subject, wherein a therapeutically effective amount of the Chk1 inhibitor is to be administered to the subject identified as having cancer cells with a genetic abnormality in one or more genes selected from cell cycle regulation genes, replication stress genes, DNA damage response and repair network genes, and oncogenic driver genes.
2. The use of claim 1, wherein the genetic abnormality is an alteration, amplification, overexpression, or underexpression of the one or more genes.
3. The use of claim 1 or 2, wherein the one or more genes is selected from cell cycle regulation genes associated with the G1/S checkpoint and/or the p53 pathway.
4. The use of claim 1, wherein the one or more genes is selected from MDM2, TP53, RB1, CDKN1A/B and CDKN2A/B/C.
5. The use of claim 1 or 2, wherein the one or more genes is selected from replication stress genes implicated in Chk1 pathway sensitivity.
6. The use of claim 5, wherein the one or more genes is selected from *Chk1* and *ATR*.
7. The use of claim 1 or 2, wherein the one or more genes is selected from DNA damage response and repair genes associated with homologous recombination (HR), nonhomologous end joining (NHEJ), Fanconi anemia (FA), or mismatch repair, and a gene encoding chromatin or DNA polymerase.
8. The use of claim 7, wherein the one or more genes is selected from *PALB2*, *ATM*, *BRCA1/A2*, *RAD51B*, *RAD51C*, *PRKDC*, *CDK12*, *FANCA*, *FANCD2*, *FANCE*, *FANCG*, *FANCI*, *FANCM*, *RAD52*, *RAD50*, *RAD51C*, *RAD54L*, *MLL2*, *ARID1A*, *ARID1B*, *MLH1*, *MSH2*, *MSH6*, *PMS2*, *POLD1*, and *POLE*.
9. The use of claim 1 or 2, wherein the one or more genes are oncogenic driver genes of the following subclasses: CCNE, MYC and PI3K/AKT.
10. The use of claim 9, wherein the one or more genes are of the CCNE subclass and selected from *CCNE1*, *FBXW7*, and *PARK2*.

11. The use of claim 9, wherein the one or more genes are of the MYC subclass and selected from *MYC*, *MYCN*, and *MYCL1*.
12. The use of claim 9, wherein the one or more genes are of the PI3K/AKT subclass and selected from *PIK3CA*, *PTEN*, *AKT1*, *AKT2*, and *AKT3*.
13. The use of claim 7, wherein the one or more genes is selected from DNA damage response and repair genes of the FA/BRCA replication fork subclass.
14. The use of claim 13, wherein the one or more genes of the FA/BRCA replication fork subclass is selected from *BRCA1/2*, *RAD51B*, *RAD51C*, *PRKDC*, *CDK12*, *FANCA*, *FANCD2*, *FANCE*, *FANCG*, *FANCI*, *FANCM*, *RAD52*, *RAD50*, *RAD51C*, and *RAD54L*.