

CLAIMS

1. A companion diagnostic method, comprising:
 - a) assaying a biological sample obtained from a subject that is undergoing a cancer or tumor treatment with enzastaurin or is considered for a cancer or tumor treatment with enzastaurin, said cancer or tumor being diffuse large B-cell lymphoma (DLBCL) or glioma/glioblastoma (GBM) for one or more single nucleotide polymorphisms (SNPs) selected from the group consisting of rs309605, rs309604, a combination of rs309605 and rs309604, and a complementary SNP thereof; and
 - b) generating a score with a computer algorithm based on the assay results of said SNP or SNPs, in order to determine the likely responsiveness of said subject to said treatment,wherein the presence of thymidine in SNP rs309604 and/or rs309605 is indicative for improved survival when the patient is treated or to be treated with enzastaurin.
2. The method of claim 1, wherein step b) comprises assaying the biological sample for rs309605 and rs309604.
3. The method of claim 1, wherein step b) comprises assaying the biological sample for rs309605.
4. The method of claim 1, wherein step b) comprises assaying the biological sample for rs309604.
5. The method of any one of claims 1-4, wherein the SNP is or the SNPs are assayed by sequencing, polymerase chain reaction (PCR), capillary electrophoresis, mass spectrometry, single-strand conformation polymorphism (SSCP), electrochemical analysis, denaturing HPLC and gel electrophoresis, restriction fragment length polymorphism, hybridization analysis, single-base extension (SBE), allele specific primer extension (ASPE), restriction enzyme digestion, strand displacement amplification (SDA), transcription mediated amplification (TMA), ligase chain reaction (LCR), nucleic acid sequence based amplification (NASBA), primer extension, rolling circle amplification (RCA), self sustained sequence replication (3SR), loop-mediated isothermal amplification (LAMP), hybridization, nucleic acid sequencing, and/or microarray.

6. The method of claim 5, wherein the nucleic acid sequencing is selected from the group consisting of Maxam-Gilbert sequencing, shotgun sequencing, bridge PCR, single-molecule real-time sequencing, ion semiconductor (ion torrent sequencing), sequencing by synthesis, sequencing by ligation (SOLiD sequencing), chain termination (Sanger sequencing), massively parallel signature sequencing (MPSS), polony sequencing, 454 pyrosequencing, Illumina (Solexa) sequencing, DNA nano-ball sequencing, heliscope single molecule sequencing, single molecule real time (SMRT) sequencing, nanopore DNA sequencing, tunnelling currents DNA sequencing, sequencing by hybridization, sequencing with mass spectrometry, microfluidic Sanger sequencing, a microscopy-based technique, RNAP sequencing, and *in vitro* virus high-throughput sequencing.
7. The method of any one of claims 1-6, wherein the cancer or tumor is diffuse large B-cell lymphoma (DLBCL).
8. The method of any one of claims 1-6, wherein the cancer or tumor is glioma/glioblastoma (GBM).