

as the Model 373 from Applied Biosystems, Inc.). Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 95% identical, more typically at least about 96% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence may be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

[0164] In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of the polynucleotide in a nucleic acid molecule of the invention described above. By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides, and more preferably at least about 20 nucleotides, and still more preferably at least about 30 nucleotides, and even more preferably more than 30 nucleotides of the reference polynucleotide. These fragments that hybridize to the reference fragments are useful as diagnostic probes and primers. For the purpose of the invention, two sequences hybridize when they form a double-stranded complex in a hybridization solution of 6×SSC, 0.5% SDS, 5×Denhardt's solution and 100 μg of non-specific carrier DNA. See Ausubel et al., section 2.9, supplement 27 (1994). Sequences may hybridize at "moderate stringency," which is defined as a temperature of 60° C. in a hybridization solution of 6×SSC, 0.5% SDS, 5×Denhardt's solution and 100 μg of non-specific carrier DNA. For "high stringency" hybridization, the temperature is increased to 68° C. Following the moderate stringency hybridization reaction, the nucleotides are washed in a solution of 2×SSC plus 0.05% SDS for five times at room temperature, with subsequent washes with 0.1×SSC plus 0.1% SDS at 60° C. for 1 h. For high stringency, the wash temperature is increased to 68° C. For the purpose of the invention, hybridized nucleotides are those that are detected using 1 ng of a radiolabeled probe having a specific radioactivity of 10,000 cpm/ng, where the hybridized nucleotides are clearly visible following exposure to X-ray film at -70° C. for no more than 72 hours.

[0165] The present application is directed to such nucleic acid molecules which are at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to a nucleic acid sequence described in any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49-158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533-575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621-767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813-862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908-1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161-1571, 1572,

1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730-2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120-2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384-2460, 2461, 2466, 2471, 2476 and 2481. Preferred, however, are nucleic acid molecules which are at least 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequence shown in of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49-158, 159, 160, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275-472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533-575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621-767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813-862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908-1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161-1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730-2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120-2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384-2460, 2461, 2466, 2471, 2476 and 2481. Differences between two nucleic acid sequences may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

[0166] As a practical matter, whether any particular nucleic acid molecule is at least 95%, 96%, 97%, 98% or 99% identical to a reference nucleotide sequence refers to a comparison made between two molecules using standard algorithms well known in the art and can be determined conventionally using publicly available computer programs such as the BLASTN algorithm. See Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997).

[0167] In one embodiment of the invention, a nucleic acid comprises an antisense strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, wherein the antisense strand is complementary to a RNA sequence or a portion thereof encoding a protein that controls cell cycle or homologous recombination, and wherein said siNA further comprises a sense strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, and wherein said sense strand and said antisense strand are distinct nucleotide sequences where at least about 15 nucleotides in each strand are complementary to the other strand.

[0168] In one embodiment, the present invention provides double-stranded nucleic acid molecules of that mediate RNA interference gene silencing. In another embodiment, the siNA molecules of the invention consist of duplex nucleic acid molecules containing about 15 to about 30 base pairs between oligonucleotides comprising about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplex nucleic acid molecules with overhanging ends of about 1 to about 32 (e.g., about 1, 2, or 3)