# Nanobiosensing Using Plasmonic Nanoprobes

Supporting Online Material

Predicted secondary structures of the BRCA1 MS probe

Predicted secondary structures of the BRCA1 MS nanoprobes were evaluated with the help of Zucker DNA folding program (http://www.bioinfo.rpi.edu/applications/mfold/ old/dna/form1.cgi) which utilizes the free energy of formation of the stem to predict the melting temperature (Tm).
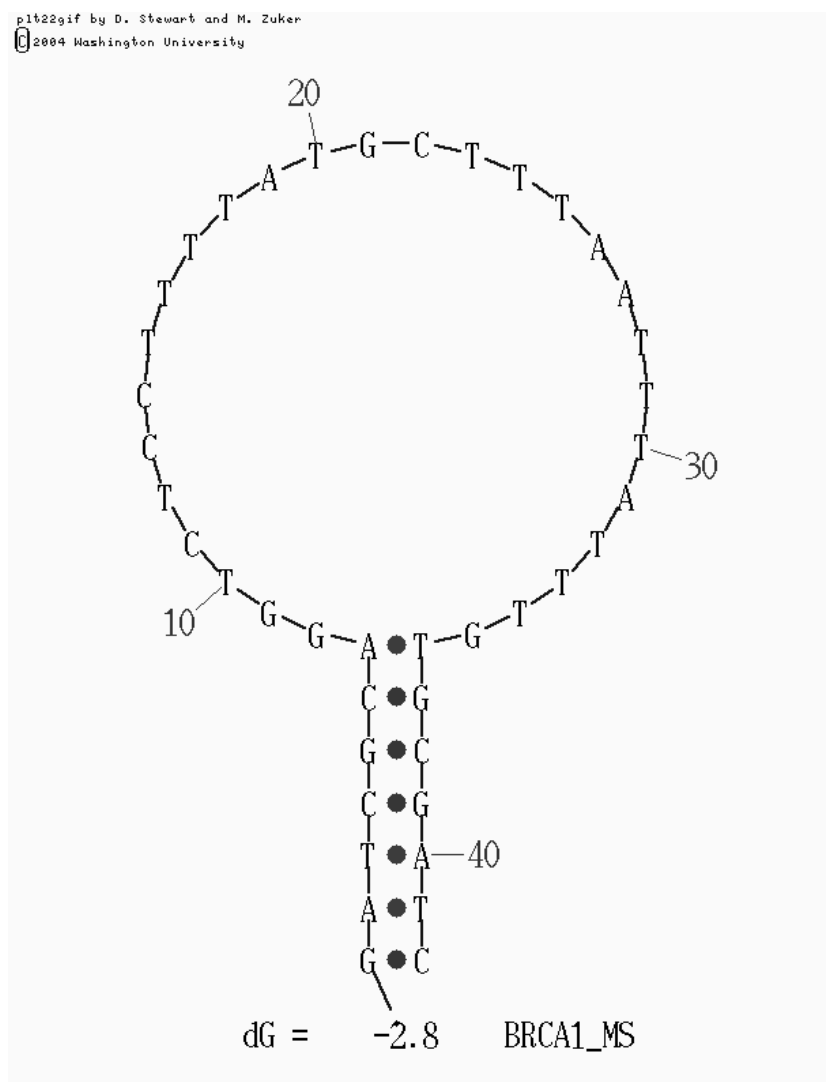
Figure S1. Computed generated structure from a 42-bp BRAC1 MS probe consisting of a complementary stem sequence (6-bp) and a loop sequence (30-bp) is shown in the figure below.

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DNA Target sequence

BRCA1: Homo sapiens breast and ovarian cancer susceptibility protein 1 gene (AY706911, 272 bp), exon 11 and partial cds. Detailed information is available from the National Center for Biotechnology Information (NCBI) data base.

Table S1. Partial DNA sequence for the breast cancer gene, BRAC1 used in this study.

DNA Probe	Sequence(5' to 3')
BRCA1 WT$^{GC\underline{A}}$ DNA (N1-100th)	GAGCCACAGA TAATACAAGA GCGTCCCCTC **ACAAATAAAT TAAAGCA*TAA AAGGAGACCT** ACATCAGGCC TTCATCCTGA GGATTTTATC AAGAAAGCAG
BRCA1 MT$^{GC\underline{G}}$ DNA(N1-100th)	GAGCCACAGA TAATACAAGA GCGTCCCCTC **ACAAATAAAT TAAAGCG*TAA AAGGAGACCT** ACATCAGGCC TTCATCCTGA GGATTTTATC AAGAAAGCAG
BRAC1 MS (N31-60th)	<u>GATCGC</u> AGG TCT CCT TTT ATG CTT TAA TTT ATT TGT <u>GCGATC</u>
Non-complementry DNA	TAATCAGGTA GAGACGCGAT CGTGTAACAC GACTC ACAAT AGAATCTGTG AATGCTCTCC CGGATATTAT TGTCTTCTTA AAGGATCATC CGGATGCAAG

The bold letters indicate the gene probe sequence; Underlined bases represent the stem sequence of the DNA hairpin. * A variation at site N47 on the BRCA1 gene that leads to Arginine 504/ Histidine missense mutation where A is replaced with G.