

## REFERENCES

- [1] Vilenchik MM, Knudson AG. Endogenous DNA double-strand breaks: production, fidelity of repair, and induction of cancer. *Proc Natl Acad Sci U S A*. 2003 Oct 28;100(22):12871-6.
- [2] Van Gent DC, Hoeijmakers JH, Kanaar R. Chromosomal stability and the DNA double-stranded break connection. *Nat Rev Genet*. 2001 Mar;2(3):196-206.
- [3] Mills KD, Ferguson DO, Alt FW. The role of DNA breaks in genomic instability and tumorigenesis. *Immunol Rev*. 2003 Aug;194:77-95.
- [4] Zhou BB, Elledge SJ. The DNA damage response: putting checkpoints in perspective. *Nature*. 2000 Nov 23;408(6811):433-9.
- [5] Valerie K, Povirk LF. Regulation and mechanisms of mammalian double-strand break repair. *Oncogene*. 2003 Sep 1;22(37):5792-812.
- [6] Dasika GK, Lin SC, Zhao S, Sung P, Tomkinson A, Lee EY. DNA damage-induced cell cycle checkpoints and DNA strand break repair in development and tumorigenesis. *Oncogene*. 1999 Dec 20;18(55):7883-99.
- [7] Wang HC, Chou WC, Shieh SY, Shen CY. Ataxia telangiectasia mutated and checkpoint kinase 2 regulate BRCA1 to promote the fidelity of DNA end-joining. *Cancer Res*. 2006 Feb 1;66(3):1391-400.
- [8] Durant ST, Nickoloff JA. Good timing in the cell cycle for precise DNA repair by BRCA1. *Cell Cycle*. 2005 Sep;4(9):1216-22.
- [9] Lengauer C, Kinzler KW, Vogelstein B. Genetic instabilities in human cancers. *Nature*. 1998 Dec 17;396(6712):643-9.
- [10] Takata M, Sasaki MS, Sonoda E, Morrison C, Hashimoto M, Utsumi H, et al. Homologous recombination and non-homologous end-joining pathways of DNA double-strand break repair have overlapping roles in the maintenance of

chromosomal integrity in vertebrate cells. Embo J. 1998 Sep 15;17(18):5497-508.

[11] Pornthanakasem W, Kongruttanachok N, Phuangphairoj C, Suyarnsestakorn C, Sanghangthum T, Oonsiri S, et al. LINE-1 Methylation Status of Endogenous DNA Double Strand Breaks (in press). Nucleic Acids Research. 2008.

[12] Smith GC, Jackson SP. The DNA-dependent protein kinase. Genes Dev. 1999 Apr 15;13(8):916-34.

[13] Kim JS, Krasieva TB, Kurumizaka H, Chen DJ, Taylor AM, Yokomori K. Independent and sequential recruitment of NHEJ and HR factors to DNA damage sites in mammalian cells. J Cell Biol. 2005 Aug 1;170(3):341-7.

[14] Kanellis P, Gagliardi M, Banath JP, Szilard RK, Nakada S, Galicia S, et al. A screen for suppressors of gross chromosomal rearrangements identifies a conserved role for PLP in preventing DNA lesions. PLoS Genet. 2007 Aug;3(8):e134.

[15] Falck J, Coates J, Jackson SP. Conserved modes of recruitment of ATM, ATR and DNA-PKcs to sites of DNA damage. Nature. 2005 Mar 31;434(7033):605-11.

[16] Gottlieb TM, Jackson SP. The DNA-dependent protein kinase: requirement for DNA ends and association with Ku antigen. Cell. 1993 Jan 15;72(1):131-42.

[17] Hendrickson EA. Cell-cycle regulation of mammalian DNA double-strand-break repair. Am J Hum Genet. 1997 Oct;61(4):795-800.

[18] Modesti M, Budzowska M, Baldeyron C, Demmers JA, Ghirlando R, Kanaar R. RAD51AP1 is a structure-specific DNA binding protein that stimulates joint molecule formation during RAD51-mediated homologous recombination. Mol Cell. 2007 Nov 9;28(3):468-81.

- [19] Daboussi F, Dumay A, Delacote F, Lopez BS. DNA double-strand break repair signalling: the case of RAD51 post-translational regulation. *Cell Signal.* 2002 Dec;14(12):969-75.
- [20] Burma S, Chen BP, Murphy M, Kurimasa A, Chen DJ. ATM phosphorylates histone H2AX in response to DNA double-strand breaks. *J Biol Chem.* 2001 Nov 9;276(45):42462-7.
- [21] Paull TT, Lee JH. The Mre11/Rad50/Nbs1 complex and its role as a DNA double-strand break sensor for ATM. *Cell Cycle.* 2005 Jun;4(6):737-40.
- [22] Arthur LM, Gustausson K, Hopfner KP, Carson CT, Stracker TH, Karcher A, et al. Structural and functional analysis of Mre11-3. *Nucleic Acids Res.* 2004;32(6):1886-93.
- [23] Khanna KK, Jackson SP. DNA double-strand breaks: signaling, repair and the cancer connection. *Nat Genet.* 2001 Mar;27(3):247-54.
- [24] Paull TT, Cortez D, Bowers B, Elledge SJ, Gellert M. Direct DNA binding by Brca1. *Proc Natl Acad Sci U S A.* 2001 May 22;98(11):6086-91.
- [25] Zhang J, Willers H, Feng Z, Ghosh JC, Kim S, Weaver DT, et al. Chk2 phosphorylation of BRCA1 regulates DNA double-strand break repair. *Mol Cell Biol.* 2004 Jan;24(2):708-18.
- [26] Lengauer C, Kinzler KW, Vogelstein B. DNA methylation and genetic instability in colorectal cancer cells. *Proc Natl Acad Sci U S A.* 1997 Mar 18;94(6):2545-50.
- [27] Cahill DP, Kinzler KW, Vogelstein B, Lengauer C. Genetic instability and darwinian selection in tumours. *Trends Cell Biol.* 1999 Dec;9(12):M57-60.
- [28] Breivik J. Don't stop for repairs in a war zone: Darwinian evolution unites genes and environment in cancer development. *Proc Natl Acad Sci U S A.* 2001 May 8;98(10):5379-81.

- [29] Aaltonen LA, Peltomaki P, Leach FS, Sistonen P, Pylkkanen L, Mecklin JP, et al. Clues to the pathogenesis of familial colorectal cancer. Science. 1993 May 7;260(5109):812-6.
- [30] Lynch HT, Lynch JF. 25 years of HNPCC. Anticancer Res. 1994 Jul-Aug;14(4B):1617-24.
- [31] Lynch HT, Smyrk TC. Identifying hereditary nonpolyposis colorectal cancer. N Engl J Med. 1998 May 21;338(21):1537-8.
- [32] Lipkin SM, Wang V, Jacoby R, Banerjee-Basu S, Baxevanis AD, Lynch HT, et al. MLH3: a DNA mismatch repair gene associated with mammalian microsatellite instability. Nat Genet. 2000 Jan;24(1):27-35.
- [33] Peltomaki P, de la Chapelle A. Mutations predisposing to hereditary nonpolyposis colorectal cancer. Adv Cancer Res. 1997;71:93-119.
- [34] Jallepalli PV, Lengauer C. Chromosome segregation and cancer: cutting through the mystery. Nat Rev Cancer. 2001 Nov;1(2):109-17.
- [35] Jallepalli PV, Waizenegger IC, Bunz F, Langer S, Speicher MR, Peters JM, et al. Securin is required for chromosomal stability in human cells. Cell. 2001 May 18;105(4):445-57.
- [36] Michel LS, Liberal V, Chatterjee A, Kirchwegger R, Pasche B, Gerald W, et al. MAD2 haplo-insufficiency causes premature anaphase and chromosome instability in mammalian cells. Nature. 2001 Jan 18;409(6818):355-9.
- [37] Mohaghegh P, Hickson ID. Premature aging in RecQ helicase-deficient human syndromes. Int J Biochem Cell Biol. 2002 Nov;34(11):1496-501.
- [38] Khakhar RR, Cobb JA, Bjergbaek L, Hickson ID, Gasser SM. RecQ helicases: multiple roles in genome maintenance. Trends Cell Biol. 2003 Sep;13(9):493-501.

- [39] Narod SA, Foulkes WD. BRCA1 and BRCA2: 1994 and beyond. Nat Rev Cancer. 2004 Sep;4(9):665-76.
- [40] Venkitaraman AR. Cancer susceptibility and the functions of BRCA1 and BRCA2. Cell. 2002 Jan 25;108(2):171-82.
- [41] Marx J. Debate surges over the origins of genomic defects in cancer. Science. 2002 Jul 26;297(5581):544-6.
- [42] Adams JM, Harris AW, Pinkert CA, Corcoran LM, Alexander WS, Cory S, et al. The c-myc oncogene driven by immunoglobulin enhancers induces lymphoid malignancy in transgenic mice. Nature. 1985 Dec 12-18;318(6046):533-8.
- [43] Adams JM, Harris AW, Langdon WY, Pinkert CA, Brinster RL, Palmiter RD, et al. c-myc-induced lymphomagenesis in transgenic mice and the role of the Pvt-1 locus in lymphoid neoplasia. Curr Top Microbiol Immunol. 1986;132:1-8.
- [44] Faderl S, Talpaz M, Estrov Z, O'Brien S, Kurzrock R, Kantarjian HM. The biology of chronic myeloid leukemia. N Engl J Med. 1999 Jul 15;341(3):164-72.
- [45] Wong S, Witte ON. Modeling Philadelphia chromosome positive leukemias. Oncogene. 2001 Sep 10;20(40):5644-59.
- [46] Hayashi Y. The molecular genetics of recurring chromosome abnormalities in acute myeloid leukemia. Semin Hematol. 2000 Oct;37(4):368-80.
- [47] Bartram CR. Molecular genetic aspects of myelodysplastic syndromes. Hematol Oncol Clin North Am. 1992 Jun;6(3):557-70.
- [48] Doerfler W. DNA methylation and gene activity. Annu Rev Biochem. 1983;52:93-124.
- [49] Luczak MW, Jagodzinski PP. The role of DNA methylation in cancer development. Folia Histochem Cytobiol. 2006;44(3):143-54.

- [50] Okano M, Xie S, Li E. Cloning and characterization of a family of novel mammalian DNA (cytosine-5) methyltransferases. *Nat Genet.* 1998 Jul;19(3):219-20.
- [51] Okano M, Bell DW, Haber DA, Li E. DNA methyltransferases Dnmt3a and Dnmt3b are essential for de novo methylation and mammalian development. *Cell.* 1999 Oct 29;99(3):247-57.
- [52] Feinberg AP, Vogelstein B. Hypomethylation distinguishes genes of some human cancers from their normal counterparts. *Nature.* 1983 Jan 6;301(5895):89-92.
- [53] Feinberg AP, Tycko B. The history of cancer epigenetics. *Nat Rev Cancer.* 2004 Feb;4(2):143-53.
- [54] Eden A, Gaudet F, Waghmare A, Jaenisch R. Chromosomal instability and tumors promoted by DNA hypomethylation. *Science.* 2003 Apr 18;300(5618):455.
- [55] Goelz SE, Vogelstein B, Hamilton SR, Feinberg AP. Hypomethylation of DNA from benign and malignant human colon neoplasms. *Science.* 1985 Apr 12;238(4696):187-90.
- [56] Dunn BK. Hypomethylation: one side of a larger picture. *Ann N Y Acad Sci.* 2003 Mar;983:28-42.
- [57] Kaneda A, Tsukamoto T, Takamura-Enya T, Watanabe N, Kaminishi M, Sugimura T, et al. Frequent hypomethylation in multiple promoter CpG islands is associated with global hypomethylation, but not with frequent promoter hypermethylation. *Cancer Sci.* 2004 Jan;95(1):58-64.
- [58] Sugimura T. Cancer prevention: past, present, future. *Mutat Res.* 1998 Jun 18;402(1-2):7-14.
- [59] Jurgens B, Schmitz-Drager BJ, Schulz WA. Hypomethylation of L1 LINE sequences prevailing in human urothelial carcinoma. *Cancer Res.* 1996 Dec 15;56(24):5698-703.

- [60] Kazazian HH, Jr., Moran JV. The impact of L1 retrotransposons on the human genome. Nat Genet. 1998 May;19(1):19-24.
- [61] Florl AR, Lower R, Schmitz-Drager BJ, Schulz WA. DNA methylation and expression of LINE-1 and HERV-K provirus sequences in urothelial and renal cell carcinomas. Br J Cancer. 1999 Jul;80(9):1312-21.
- [62] Takai D, Yagi Y, Habib N, Sugimura T, Ushijima T. Hypomethylation of LINE1 retrotransposon in human hepatocellular carcinomas, but not in surrounding liver cirrhosis. Jpn J Clin Oncol. 2000 Jul;30(7):306-9.
- [63] Suter CM, Martin DI, Ward RL. Hypomethylation of L1 retrotransposons in colorectal cancer and adjacent normal tissue. Int J Colorectal Dis. 2004 Mar;19(2):95-101.
- [64] Santourlidis S, Florl A, Ackermann R, Wirtz HC, Schulz WA. High frequency of alterations in DNA methylation in adenocarcinoma of the prostate. Prostate. 1999 May 15;39(3):166-74.
- [65] Xiong Z, Laird PW. COBRA: a sensitive and quantitative DNA methylation assay. Nucleic Acids Res. 1997 Jun 15;25(12):2532-4.
- [66] Chalitchagorn K, Shuangshoti S, Hourpai N, Kongruttanachok N, Tangkijvanich P, Thong-ngam D, et al. Distinctive pattern of LINE-1 methylation level in normal tissues and the association with carcinogenesis. Oncogene. 2004 Nov 18;23(54):8841-6.
- [67] Costello JF, Plass C. Methylation matters. J Med Genet. 2001 May;38(5):285-303.
- [68] Del Senno L, Maestri I, Piva R, Hanau S, Reggiani A, Romano A, et al. Differential hypomethylation of the c-myc protooncogene in bladder cancers at different stages and grades. J Urol. 1989 Jul;142(1):146-9.

- [69] Vachtenheim J, Horakova I, Novotna H. Hypomethylation of CCGG sites in the 3' region of H-ras protooncogene is frequent and is associated with H-ras allele loss in non-small cell lung cancer. *Cancer Res.* 1994 Mar 1;54(5):1145-8.
- [70] Guo Y, Pakneshan P, Gladu J, Slack A, Szyf M, Rabbani SA. Regulation of DNA methylation in human breast cancer. Effect on the urokinase-type plasminogen activator gene production and tumor invasion. *J Biol Chem.* 2002 Nov 1;277(44):41571-9.
- [71] Ostertag EM, Kazazian HH, Jr. Biology of mammalian L1 retrotransposons. *Annu Rev Genet.* 2001;35:501-38.
- [72] Martin SL, Branciforte D. Synchronous expression of LINE-1 RNA and protein in mouse embryonal carcinoma cells. *Mol Cell Biol.* 1993 Sep;13(9):5383-92.
- [73] Brathauer GL, Fanning TG. Active LINE-1 retrotransposons in human testicular cancer. *Oncogene.* 1992 Mar;7(3):507-10.
- [74] Staley K, Blaschke AJ, Chun J. Apoptotic DNA fragmentation is detected by a semi-quantitative ligation-mediated PCR of blunt DNA ends. *Cell Death Differ.* 1997 Jan;4(1):66-75.
- [75] Xu GL, Bestor TH, Bourc'his D, Hsieh CL, Tommerup N, Bugge M, et al. Chromosome instability and immunodeficiency syndrome caused by mutations in a DNA methyltransferase gene. *Nature.* 1999 Nov 11;402(6758):187-91.
- [76] Hernandez R, Frady A, Zhang XY, Varela M, Ehrlich M. Preferential induction of chromosome 1 multibranched figures and whole-arm deletions in a human pro-B cell line treated with 5-azacytidine or 5-azadeoxycytidine. *Cytogenet Cell Genet.* 1997;76(3-4):196-201.
- [77] Strathdee G, Brown R. Aberrant DNA methylation in cancer: potential clinical interventions. *Expert Rev Mol Med.* 2002 Mar 4;2002:1-17.

- [78] Chen RZ, Pettersson U, Beard C, Jackson-Grusby L, Jaenisch R. DNA hypomethylation leads to elevated mutation rates. *Nature*. 1998 Sep 3;395(6697):89-93.
- [79] Bostock CJ, Prescott DM, Kirkpatrick JB. An evaluation of the double thymidine block for synchronizing mammalian cells at the G1-S border. *Exp Cell Res*. 1971 Sep;68(1):163-8.
- [80] Sherwood SW, Schimke RT. Cell cycle analysis of apoptosis using flow cytometry. *Methods Cell Biol*. 1995;46:77-97.
- [81] Zhang X, Succi J, Feng Z, Prithivirajsingh S, Story MD, Legerski RJ. Artemis is a phosphorylation target of ATM and ATR and is involved in the G2/M DNA damage checkpoint response. *Mol Cell Biol*. 2004 Oct;24(20):9207-20.
- [82] Cameron EE, Bachman KE, Myohanen S, Herman JG, Baylin SB. Synergy of demethylation and histone deacetylase inhibition in the re-expression of genes silenced in cancer. *Nat Genet*. 1999 Jan;21(1):103-7.
- [83] Rivera-Calzada A, Spagnolo L, Pearl LH, Llorca O. Structural model of full-length human Ku70-Ku80 heterodimer and its recognition of DNA and DNA-PKcs. *EMBO Rep*. 2007 Jan;8(1):56-62.
- [84] Wang H, Perrault AR, Takeda Y, Qin W, Wang H, Iliakis G. Biochemical evidence for Ku-independent backup pathways of NHEJ. *Nucleic Acids Res*. 2003 Sep 15;31(18):5377-88.
- [85] Sun Y, Jiang X, Chen S, Fernandes N, Price BD. A role for the Tip60 histone acetyltransferase in the acetylation and activation of ATM. *Proc Natl Acad Sci U S A*. 2005 Sep 13;102(37):13182-7.
- [86] Peng Y, Woods RG, Beamish H, Ye R, Lees-Miller SP, Lavin MF, et al. Deficiency in the catalytic subunit of DNA-dependent protein kinase causes down-regulation of ATM. *Cancer Res*. 2005 Mar 1;65(5):1670-7.

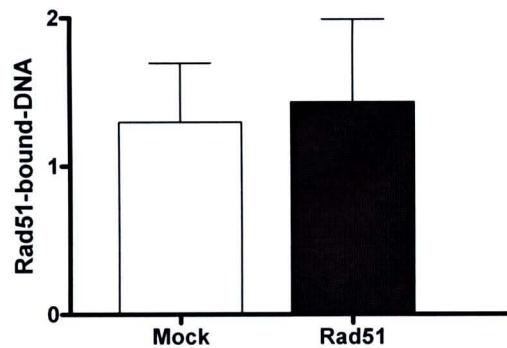
- [87] Wang H, Rosidi B, Perrault R, Wang M, Zhang L, Windhofer F, et al. DNA ligase III as a candidate component of backup pathways of nonhomologous end joining. Cancer Res. 2005 May 15;65(10):4020-30.
- [88] Perrault R, Wang H, Wang M, Rosidi B, Iliakis G. Backup pathways of NHEJ are suppressed by DNA-PK. J Cell Biochem. 2004 Jul 1;92(4):781-94.
- [89] Pastwa E, Blasiak J. Non-homologous DNA end joining. Acta Biochim Pol. 2003;50(4):891-908.
- [90] Sancar A, Lindsey-Boltz LA, Unsal-Kacmaz K, Linn S. Molecular mechanisms of mammalian DNA repair and the DNA damage checkpoints. Annu Rev Biochem. 2004;73:39-85.
- [91] Esashi F, Christ N, Gannon J, Liu Y, Hunt T, Jasin M, et al. CDK-dependent phosphorylation of BRCA2 as a regulatory mechanism for recombinational repair. Nature. 2005 Mar 31;434(7033):598-604.

## **APPENDICES**

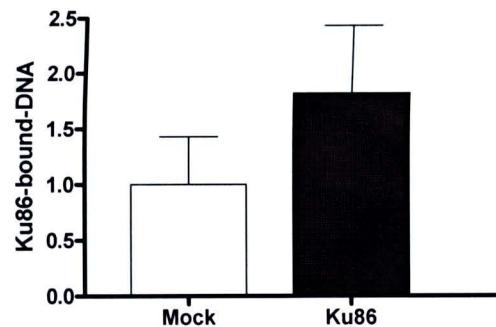
## APPENDIX A

### Detect Ku86 and Rad51 bound DNA by ChIP assay

Homologous recombination (HR) and Non-homologous end joining (NHEJ) are the main DSB repair pathway in cell. Rad51 and Ku86 are the key protein in HR and NHEJ, respectively. To mature DSB repair in each pathway, we detected the quantity of Rad51-bound and Ku86-bound DNA by Chromatin immunoprecipitation (ChIP) assay. Subsequently, precipitated Rad51 and Ku86-bound DNA was detected the quantity by realtime PCR with 5'L1 primers, termed realtime 5'L1PCR. From this data show that DNA precipitated by Rad51 or Ku86 was not 2 fold greater than DNA precipitated by normal mouse IgG antibody like  $\gamma$ -H2AX-bound DNA in previous study. Suggesting that Rad51 and Ku86-bound DNA shorter than  $\gamma$ -H2AX-bound DNA. Therefore the possibility to precipitate Rad51 and Ku86-bound may lower too.



Level of Rad51-bound DNA in HeLa cells.



Level of Ku86-bound DNA in HeLa cells.

### Chromatin immunoprecipitation (ChIP)

The ChIP assay was performed essentially as previously described with some modifications. Histone cross-linking to DNA was induced by adding formaldehyde directly to culture medium at a final concentration of 1%, with incubation at 37 °C for 10 min. After stopping the reaction with glycine (0.125 M final concentration) and incubation for 5 min at room temperature, adherent cells were washed twice with ice-cold PBS, and then scraped into ice-cold PBS containing protease Inhibitor. Non-adherent cells were collected by centrifugation for 4 min at 510 g at 4 °C and washed as above. Nuclei were isolated by resuspending the cell pellet in cell lysis buffer (5 mM PIPES pH 8.0, 85 mM KCl, 0.5% Nonidet P-40, containing protease Inhibitor) and incubated on ice for 20 min. Intact nuclei were collected by centrifugation at 3,210 g for 5 min at 4 °C, resuspended in nuclear lysis buffer (1% SDS, 50 mM Tris-HCl pH 8.1, 10 mM EDTA, containing protease Inhibitor), and incubated on ice for 10 min. Chromatin was sheared with an Ultrasonics sonicator at 30% power output for four 30 s intervals on ice to an average size of 500–1000 bp. After centrifugation at 21,720 g for 10 min at 4 °C, the chromatin solution was diluted 10-fold with dilution buffer (0.01% SDS, 1.1% Triton X-100, 1.2 mM EDTA, 16.7 mM Tris-HCl pH 8.1, 167 mM NaCl, containing protease Inhibitor) and then precleared for 30 min at 4 °C with protein G Plus-Agarose with rotation. The agarose beads were pelleted for 1 min at 180 g and the chromatin fragments were immunoprecipitated overnight at 4 °C with Rad51 monoclonal antibody, Ku86 monoclonal antibody or normal mouse IgG antibody as a negative control on a rotator. Protein-DNA-antibody complexes were isolated by the addition of protein G Plus-Agarose. After 2 h, agarose beads were collected by centrifugation at 120 g for 1 min, washed once each in 500 mM, 550 mM and 600 mM high-salt wash buffers (0.1% SDS, 1% Triton X-100, 20 mM Tris-HCl pH 8, 2 mM EDTA, 500–600 mM NaCl), and twice in wash buffer (100 mM Tris-HCl pH 8, 500 mM LiCl, 1% Nonidet P-40, 1% deoxycholic acid). Complexes were eluted with elution buffer (50 mM NaHCO<sub>3</sub>, 1% SDS) for 15 min at room temperature. Cross-links were reversed by adding NaCl (200 mM final concentration) and RNA was removed by adding 10 mg/ml of RNase A, followed by incubation for 4 h at 65 °C, and then precipitated overnight with ethanol. Samples were deproteinized with proteinase K. After phenol/chloroform extraction, the DNA was

precipitated with ethanol. The precipitated DNA was subjected to realtime 5'L1PCR and COBRA-L1.

### Realtime 5' L1 PCR

Quantification of the amount of immunoprecipitated DNA was carried out by realtime PCR using SYBR Green according to the manufacturer's instructions. Briefly, 1x QuantiTect SYBR Green PCR Master Mix, 0.2  $\mu$ M forward primer (L1.2HpaIIIRFLPF: 5'-CTCCCAGCGTGAGCGAC-3'), and 0.2  $\mu$ M reverse primer (5'LIDSIP1st: 5'-ACTCCCTAGTGAGATGAACCCG-3') were used for each PCR assay. The PCR program was initiated at 95  $^{\circ}$ C for 15 min to activate the HotStarTaq DNA polymerase, followed by 50 thermal cycles of 15 s at 95  $^{\circ}$ C, 20 s at 57  $^{\circ}$ C and 20 s at 72  $^{\circ}$ C. A melting curve test (68  $^{\circ}$ C) was always carried out after the final reaction step to confirm that appropriate amplification products were obtained. Each sample was analyzed in triplicate PCR reactions. One sample with less than double the amount of the mock control was excluded.

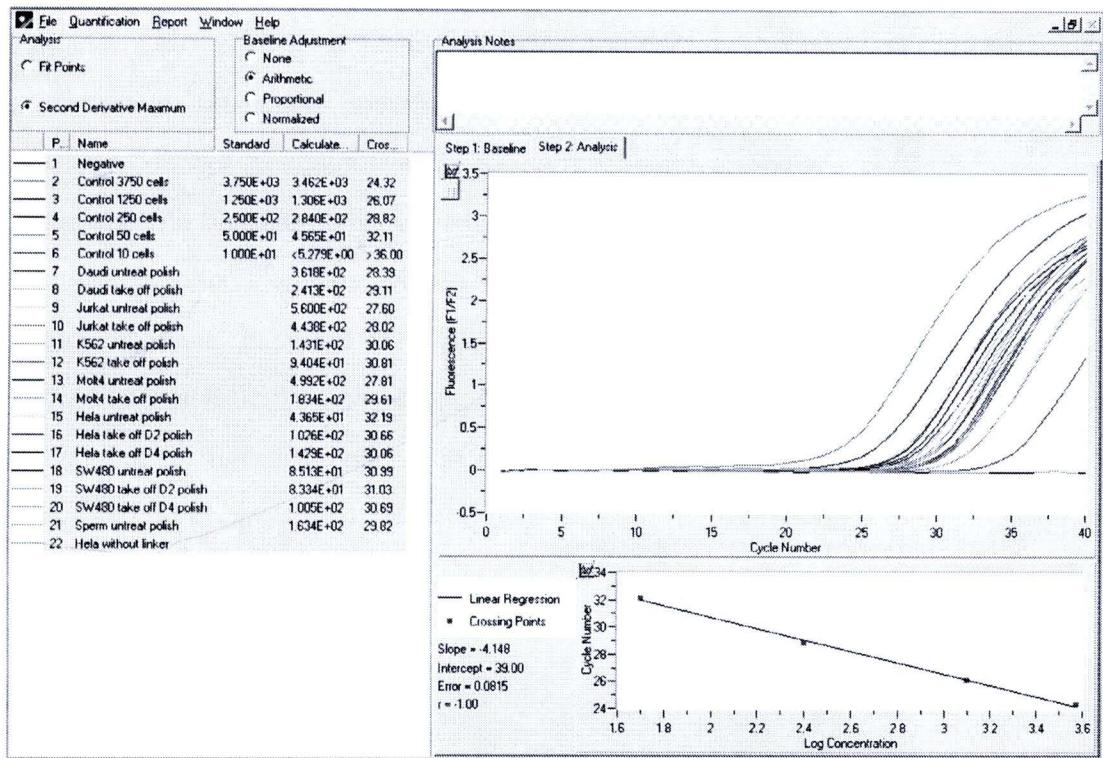
## APPENDIX B

### LM-PCR and COBRA-L1 EDSB method

In order to determine quantity of EDSB, we performed a technique for the detection of EDSBs, called L1-EDSB-LMPCR. Locus-specific EDSBs can be detected using ligation-mediated polymerase chain reaction (LMPCR) (20), a commonly used PCR technique designed for the analysis of EDSBs during lymphoid development, such as V(D)J recombination and somatic hypermutation (21). Since general EDSBs are believed to occur rarely and randomly throughout the genome, repetitive sequences that widely intersperse in the human genome can be applied in a similar assay for the detection of EDSBs in their proximity, which would represent genome-wide EDSBs. Therefore, we combined LMPCR with interspersed repetitive sequence PCR (IRSPCR) (22) using LINE-1 (L1) human retrotransposons (54) (L1-EDSB-LMPCR). In this assay, linker oligonucleotides are ligated to EDSBs in high molecular weight DNA preparation and quantitatively analyzed by realtime PCR using an L1 primer and a Taqman probe complementary to the linker. The figure 3 showed an example of results of L1-EDSB-LMPCR by using realtime PCR. It indicated that EDSBs could be quantitated by this technique.

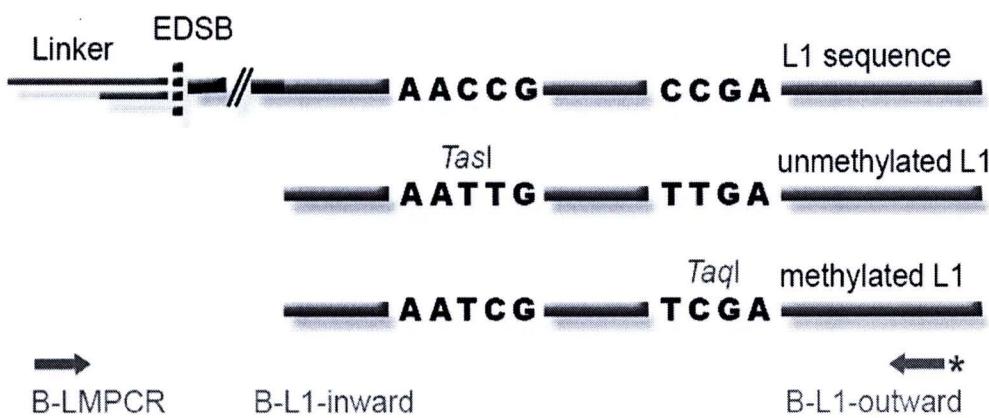


Schematic Illustration of L1-EDSB-LMLPCR. L1 sequence ligated by linker at EDSB. The white rectangle is Taqman probe complementary to LMPCR linker. Arrows are PCR primers.

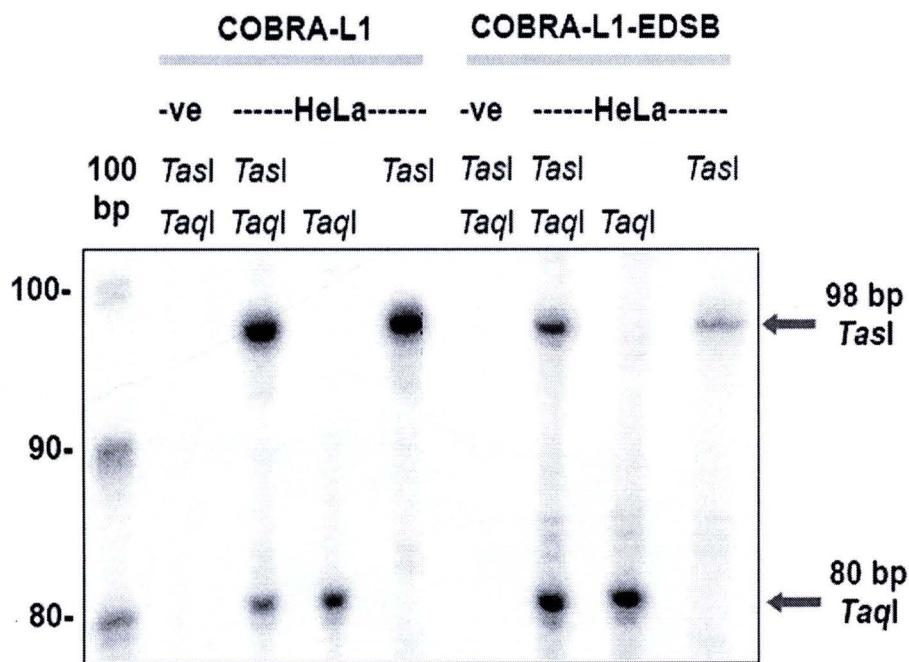


An example of results of L1 PCR by using realtime PCR

We assessed the amount of EDSBs and their methylation status in G0. We performed PCR combined with bisulfite restriction analysis (COBRA) of L1s (COBRA-L1) (3). To compare percentage of methylation level between genomic DNA and EDSBs, matched pair degree of methylation between L1 and L1-EDSB sequences was examined by COBRA-L1 and COBRA-L1-EDSB, respectively. COBRA-L1 was performed as previously described to quantify genome-wide methylation status. For COBRA-L1-EDSB, all ligated HMW DNA samples were chemically modified by bisulfite. Treatment with bisulfite converts unmethylated cytosines, but not methylated cytosines, to uracils and then thymines after PCR. Subsequently, the PCR products of bisulfite 5'L1 sequences were digested with *TaqI* and *TasI* as restriction enzymes. While *TaqI* detected methylated L1 sequences, *TasI* detected nonmethylated L1 sequences. The percentage of *TaqI* digestible amplicon was measured as COBRA-L1 methylation level by  $\alpha$ -<sup>32</sup>P-labeled-bisulfite-L1-outward, B-L1-outward, radiation intensity. For COBRA-L1-EDSB, the same protocol was adopted but the B-L1-inward primer was replaced by a linker primer, B-LMPCR.



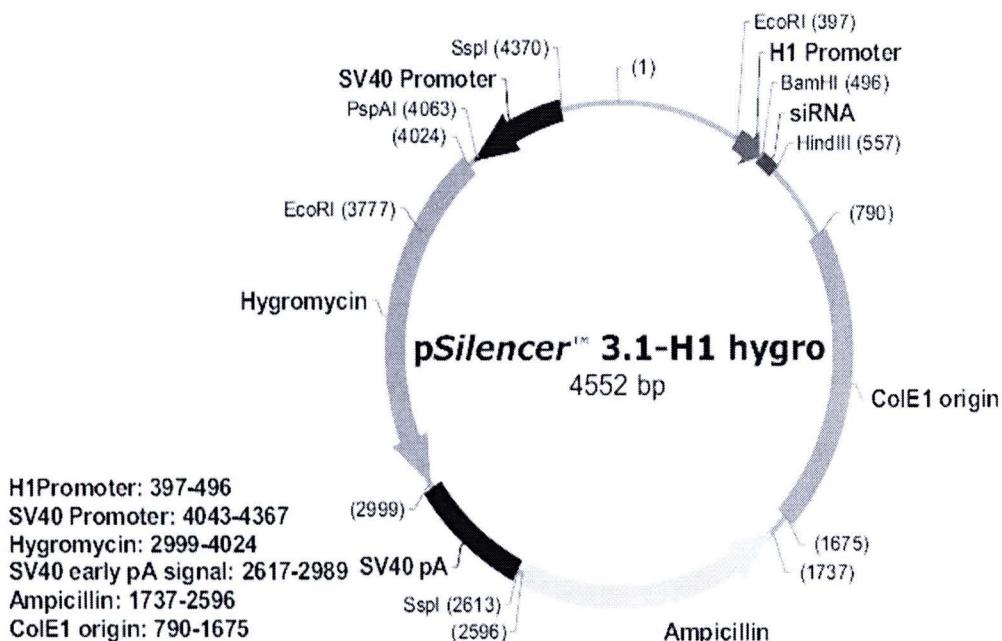
Schematic Illustration of COBRA-L1 and COBRA-L1-EDSB. L1 sequence ligated by linker at EDSB. Arrows are PCR primers, with star indicating 5' labeled primer with <sup>32</sup>P for COBRA. AACCG and CCGA are L1 sequences; when treated with bisulfite and PCR, unmethylated AACCG will be converted to AATTG (*TasI* site) and methylated CCGA to TCGA (*TaqI* site).



A Typical Example of Results form COBRA-L1 and COBRA-L1-EDSB Experiments. The arrow at 98 bp indicates *TasI* digested unmethylated L1 sequences and the arrow at 80 bp indicates *TaqI* digested methylated L1 sequences –ve is dH<sub>2</sub>O for COBRA-L1 and nonligated HMW DNA for COBRA-L1-EDSB. *TasI* and *TaqI* are enzymes added in each experiment.

APPENDIX C  
PLASMID AND siRNA SEQUENCES

1. *pSilencer™ 3.1-H1* hygro



2. siRNA sequences

Negative siRNA from *pSilencer™* kit (Ambion, Cat # 5760) was used as control

Ku86 siRNA	5'-GACGGTGTGCTCATGCGGC-3'
ATM siRNA	5'-GGGCGCUAAUCGUACUGAA-3'
DNA-PKcs siRNA	5'- GCACCAGUCCAGUAUUGGC-3'
Rad51 siRNA	5'-GAGCUUGACAAACUACUUC-3'

**APPENDIX D**  
**BUFFER AND REAGENT**

**1. Lysis I buffer**

Sucrose	109.54	g
1 M Tris-HCl (pH 7.5)	10	ml
1M MgCl <sub>2</sub>	5	ml
Triton X-100	10	ml
Distilled water to volume	1,000	ml

Sterilize the solution by autoclaving and store at 4°C.

**2. Lysis II buffer**

5 M NaCl	15	ml
0.5 M EDTA (pH 8.0)	48	ml
Distilled water to volume	1,000	ml

Sterilize the solution by autoclaving and store at room temperature.

**3. 10% SDS solution**

Sodium dodecyl sulfate	10	g
Distilled water to volume	100	ml

Mix the solution and store at room temperature.

**4. Proteinase K**

Proteinase K	20	mg
Distilled water to volume	1	ml

Mix the solution and store at -20°C.

**5. 1 M Tris-HCl (pH 7.5)**

Tris base	12.11	g
Distilled water to volume	100	ml

Dissolve in distilled water and adjusted pH to 7.5 with HCl (conc)

Distilled water to volume	100	ml
Sterilize the solution by autoclaving and store at room temperature.		

### 6. 0.5 M EDTA (pH 8.0)

Disodium ethyleneidamine tetraacetate	18.66	g
Dissolve in distilled water and adjusted pH to 8.0 with NaOH		

Distilled water to volume	100	ml
---------------------------	-----	----

Sterilize the solution by autoclaving and store at room temperature.

### 7. 1 M MgCl<sub>2</sub>

MgCl <sub>2</sub> .6H <sub>2</sub> O	20.33	g
Distilled water to volume	100	ml

Sterilize the solution by autoclaving and store at room temperature.

### 8. 5 M NaCl

NaCl	29.25	g
Distilled water to volume	100	ml

Sterilize the solution by autoclaving and store at room temperature.

### 9. 10X TBE buffer

Tris-base	108	g
Boric acid	55	g
0.5 M EDTA (pH 8.0)	40	ml
Distilled water to volume	1,000	ml

Mix the solution and store at room temperature.

### 10. 6X loading dye

Ficoll 400	15	g
Bromphenol blue	0.25	g
Xylene cyanol	0.25	g
1 M Tris (pH 8.0)	1	ml
Distilled water to volume	100	ml

Mix well and store at room temperature.

**11. 10 M NH<sub>4</sub>OAc**

NH <sub>4</sub> OAc	77.08	g
Distilled water to volume	100	ml

Sterilize the solution by autoclaving and store at room temperature.

**12. 25:24:1 (v/v) phenol : chloroform : isoamyl alcohol**

Saturated phenol	50	ml
Chloroform	48	ml
Isoamyl alcohol	2	ml

Mix the reagent vigorously, cover with TE buffer and store at 4°C.

**13. TE buffer (pH 8.0)**

1 M Tris-HCl (pH 8.0)	10	ml
0.5 M EDTA (pH 8.0)	2	ml
Distilled water to volume	1,000	ml

Sterilize the solution by autoclaving and store at room temperature.

**14. HMW digestion buffer**

1 M Tris-HCl (pH 8.0)	50	µl
20 mg/ml proteinase K	50	µl
10 % Sodium lauryl sarcosine	100	µl
0.2 M EDTA (pH 8.0)	100	µl
Distilled water	500	µl

Mix the solution and use 400 µl per agarose plug.

**15. 10% Sodium lauryl sarcosine**

Sodium lauryl sarcosine	10	g
Distilled water to volume	100	ml

Mix the solution and store at room temperature.

**16. 20mg/ml glycogen**

Glycogen	200	mg
Distilled water to volume	10	ml

Sterilize the solution by filter through 0.2  $\mu$ m membrane, aliquot and store at -20°C.

**17. 200 mM Thymidine**

Thymidine	48.44	mg
Distilled water to volume	1	ml

Sterilize the solution by filter through 0.2  $\mu$ m membrane and store at 4°C.

**18. 10X PBS**

NaCl	80	g
Na <sub>2</sub> HPO <sub>4</sub>	2	g
KCl	14.4	g
KH <sub>2</sub> PO <sub>4</sub>	2.4	g
Distilled water to volume	1,000	ml

Mix to dissolve and adjust pH to 7.4

Sterilize the solution by autoclaving and store at room temperature.

**19. 10X TBS**

Tris base	61	g
NaCl	90	g
Distilled water to volume	1,000	ml

Mix to dissolve and adjust pH to 7.6

Sterilize the solution by autoclaving and store at room temperature.

**20. 1X SDS Buffer (Lysis Buffer)**

1 M Tris-HCl pH 8.8	6.25	ml
10% SDS	20	ml
Glycerol (87%)	11.5	ml
Distilled water to volume	100	ml

### 21. 6X Sample loading buffer

1 M Tris-HCl pH 6.8	3	ml
SDS	1.2	g
Glycerol (100%)	6	ml
Bromphenol blue	30	mg
Distilled water to volume	10	ml

Add 24%  $\beta$ -mercaptoethanol before using (stock 14.2 M and working 864 nM)

### 22. 8% SDS polyacrylamide gel electrophoresis (SDS-PAGE)

#### Resolving gel (10 ml)

40% Acrylamide:Bis (37.5:1)	2	ml
1 M Tris-HCl (pH 8.8)	2.5	ml
10% SDS	100	$\mu$ l
10% $(\text{NH}_4)_2\text{S}_2\text{O}_8$	50	$\mu$ l
TEMED	5	$\mu$ l
Distilled water	5.5	ml

#### Stacking gel (4 ml)

40% Acrylamide:Bis (37.5:1)	0.4	ml
0.5 M Tris-HCl (pH 6.8)	1	ml
10% SDS	40	$\mu$ l
10% $(\text{NH}_4)_2\text{S}_2\text{O}_8$	20	$\mu$ l
TEMED	4	$\mu$ l
Distilled water	2.6	ml

### 23. 1 M Tris-HCl (pH 8.8)

Tris base	12.11	g
-----------	-------	---

Dissolve in distilled water and adjusted pH to 8.8 with HCl (conc)

Distilled water to volume	100	ml
---------------------------	-----	----

Sterilize the solution by autoclaving and store at room temperature.

**24. 0.5 M Tris-HCl (pH 6.8)**

Tris base	6.055	g
Dissolve in distilled water and adjusted pH to 6.8 with HCl (conc)		
Distilled water to volume	100	ml
Sterilize the solution by autoclaving and store at room temperature.		

**25. 10X Tris-glycine (pH 8.3)**

Tris base	6.055	g
Glycine	147.1372	g
Dissolve in distilled water and adjusted pH to 8.3		
Distilled water to volume	1,000	ml
Sterilize the solution by autoclaving and store at room temperature.		

**26. Running Buffer**

10X Tris-glycine (pH 8.3)	100	ml
10% SDS	10	ml
Distilled water	890	ml

Mix the solution and store at room temperature.

**27. Transfer buffer**

10X Tris-glycine (pH 8.3)	100	ml
Methanol	200	ml
Distilled water	800	ml

Mix the solution and store at room temperature.

**28. Cell Lysis buffer (Lysed Buffer)**

1M PIPES (pH 8.3)	500	µl
KCl	0.634	g
100% NP40	500	µl
Distilled water to volume	100	ml

Sterilize the solution by autoclaving and store at room temperature.

### 29. Nuclei Lysis buffer (Lysis Buffer)

1 M Tris-HCl (pH 8.1)	5	ml
0.5 M EDTA (pH 8.0)	2	ml
10% SDS	10	ml
Distilled water to volume	100	ml

Sterilize the solution by autoclaving and store at room temperature.

### 30. 2.5 M Glycine

Glycine	9.384	g
---------	-------	---

Dissolve in distilled water and adjusted pH to 8.0 with NaOH to get to dissolve

Distilled water to volume	100	ml
---------------------------	-----	----

Sterilize the solution by autoclaving and store at room temperature.

### 31. IP Dilution buffer (ChIP Buffer)

10% SDS	100	µl
100% Triton X 100	1.1	ml
0.5 M EDTA (pH 8.0)	240	µl
1 M Tris-HCl (pH 8.1)	1.67	ml
5 M NaCl	3.34	ml
Distilled water to volume	100	ml

Sterilize the solution by autoclaving and store at room temperature.

### 32. High Salt 500 mM

10% SDS	2	ml
100% Triton X 100	2	ml
0.5 M EDTA (pH8.0)	800	µl
1 M Tris-HCl	4	ml
5 M NaCl	20	ml
Distilled water to volume	500	ml

Sterilize the solution by autoclaving and store at room temperature.

**33. High Salt 550 mM**

10% SDS	2	ml
100% Triton X 100	2	ml
0.5 M EDTA (pH8.0)	800	µl
1 M Tris-HCl	4	ml
5 M NaCl	22	ml
Distiled water to volume	500	ml

Sterilize the solution by autoclaving and store at room temperature.

**34. High Salt 600 mM**

10% SDS	2	ml
100% Triton X 100	2	ml
0.5 M EDTA (pH8.0)	800	µl
1 M Tris-HCl	4	ml
5 M NaCl	24	ml
Distiled water to volume	500	ml

Sterilize the solution by autoclaving and store at room temperature.

**35. IP Wash buffer**

1 M Tris-HCl (pH8.0)	50	ml
LiCl	10.6	g
100% NP40	5	ml
Deoxycholic acid	5	g
Distiled water to volume	500	ml

Sterilize the solution by autoclaving and store at room temperature.

**36. RNaseA**

RNaseA	100	mg
Distiled water to volume	10	ml

Heat at 100°C for 20 minutes and store at -20°C.

**37. Elution buffer**

NaHCO <sub>3</sub>	0.21	g
10% SDS	5	ml
Distilled water to volume	50	ml

Sterilize the solution by autoclaving and store at room temperature.

**38. 5X PK buffer**

1 M Tris-HCl (pH 7.5)	0.5	ml
0.5 M EDTA (pH 8.0)	0.5	ml
10% SDS	1.25	ml
Distilled water to volume	10	ml

Mix the solution and store at -20°C

**APPENDIX E**  
**SEQUENCE OF LINE-1**

>gi|339773|gb|M80343.1|HUMTNL22 Human transposon L1.2

GGGGGGAGGAGCCAAGATGGCGAATAGGAACAGCTCCGGTCTACAGCTCCCAGCGTGAGCGACGCAGAA  
 GACGGTGATTCTGCATTCATCTGAGGTACCGGGTTCATCTCACTAGGGAGTGCCAGACAGTGGCGC  
 AGGCCAGTGTGTGCGCACCGTGCAGGCCAGACAGCAGGGCAGGCATTGCCTCACCTGGAAAGCGAA  
 GGGTCAGGGAGTTCCCTTCTGAGTCAAAGAAAGGGGTGACGGTCGACCTGGAAAATGGGTCACTCC  
 CACCCGAATATTGCGCTTTCAGACCGCTTAAGAAACGGCGACCACGAGACTATATCCCACACTGGC  
 TCGGAGGGTCTCACGCCACCGAATCTCGTGTAGCTAGCACAGCAGTCTGAGATCAAATGCAAGCG  
 GCAACGAGGCCTGGGGAGGGCGCCATTGCCAGGCTGCTTAGGTAACAAAGCAGCGGGAAAGC  
 TCGAACTGGGTGGAGGCCACACAGCTCAAGGAGGGCTGCCTGCCTCTGTAGGCTCCACCTGGGGCA  
 GGGCACAGACAACAAAAAGACAGCTAACCTCTGCAGACTTAAGTGTCCCTGTGACAGCTTGAAG  
 AGAGCAGTGGTCTCCCAGCACCGAGCTGGAGACTGAGAACGGCAGACAGACTGCCTCCTCAAGTGG  
 TCCCTGACTCTGACCCCCGAGCAGCCTAAGTGGAGGCACCCCCCAGCAGGGCAGACTGACACCTCAC  
 ACGGCAGGGTATTCAAACAGACCTGCAGCTGAGGTCTGTAGGAGAAAATAACACCAGAAA  
 GGACATCTACACCGAAAACCCATCTGTACATCACCACATCAAAGACCAAAAGTAGATAAAACCACAAAG  
 ATGGGGAAAAAACAGAACAGAAAAACTGGAACACTCTAAACCGCAGAGCGCCTCTCTCAAAGGAAC  
 GCAGTTCCTCACCAGCAACAGAACAGCTGGATGGAGAATGATTTGACGAGCTGAGAGAAGAGCTT  
 CAGACGATCAAATTACTCTGAGCTACGGGAGGACATTCAAACCAAGGCAAAGAAGTGTGAAACTTGA  
 AAAAATTTAGAAGAATGTATAACTAGAATAACCAATACAGAGAAGTGTCTAAAGGAGCTGATGGAGCTGA  
 AAACCAAGGCTCGAGAACACTACGTGAAGAACATGCAGAACGCTCAGGAGGCCATGCGATCAACTGGAAGAAC  
 GGTATCAGCAATGGAAGATGAAATGAATGAAATGAAGCGAGAAGGGAAAGTTAGAGAAAAAGAATAAAA  
 AGAAATGAGCAAAGCCTCAAGAAATATGGGACTATGTGAAAGACCAATCTACGCTGATGGTGTAC  
 CTGAAAGTGTGGAGAATGGAACCAAGTGGAAAACACTCTGCAGGATATTATCAGGAGAACCTCC  
 CAATCTAGCAAGGCAGGCCAACGTTAGATTAGGAAATACAGAGAACGCCACAAAGATACTCCTCGAGA  
 AGAGCAACTCCAAGACACATAATTGTCAGATTCAACAAAGTGAATGAAGGAAAAATGTTAAGGGCAG  
 CCAGAGAGAAAGGTGGGTTACCTCAAGGAAAGCCATCAGACTAACAGTGGATCTCTCGCAGAAC  
 CCTACAAGCCAGAAGAGAGTGGGGCAATATTCAACATTCTAAAGAAAAGAATTTCACCCAGAATT  
 TCATATCCAGCCAAACTAACGTTACAAGTGAAGGAGAATAACTTATAGACAAGCAAATGTTGA  
 GAGATTTGTCACCACCAAGGCCTGCCCTAAAAGAGCTCTGAGGAAGCAACTAACATGGAAGGAA  
 CCGTACCGCCGCTGCAAATCATGCCAAATGTAAGACATCGAGACTAGGAAGAAACTGCATCAAC  
 TAATGAGCAAATCACCAGCTAACATCATAATGACAGGATCAATTACACATAACAAATTAAACTTAA  
 ATATAAATGGACTAAATTCTGCAATTAAAAGACACAGACTGGCAAGTTGGATAAGAGTCAGACCCATC  
 AGTGTGCTGTATTAGGAAACCCATCTCACGTGAGAGACACATAGGCTCAAATAAAAGGATGGAGG  
 AAGATCTACCAAGCCAATGGAAAACAAAAAAGGCAGGGTTGCAATCTAGTCTGTGATAAAACAGACT  
 TTAAACCAACAAAGATCAAAGAGACAAAGAAGGCCATTACATAATGGTAAAGGATCAATTCAACAAGA  
 GGAGCTAACTATCCTAAATATTTATGCACCAATACAGGAGCACCCAGATTCAAAAGCAAGTCTCAGT  
 GACCTACAAAGAGACTTAGACTCCCACACATTAATAATGGGAGACTTTAACACCCACTGTCACATTAG  
 ACAGATCAACGAGACAGAAAGTCACAAAGGATACCCAGGAATTGAACCTAGCTCTGCACCAAGCAGACCT  
 AATAGACATCTACAGAACACTCTCCACCCAAATCAACAGAAATATACTTTTCTGACACCACACCAC  
 TATTCCAAAATTGACCACATAGTTGGAGTAAAGCTCTCCTCAGCAAATGTAAGAAAGAGAAATTATAA  
 CAAACTATCTCTCAGACCCACAGTGCATCAAACAGTCAAACAGTCAAACAGTCAAAGCCGCTC  
 AACTACATGAAACTGAACAACTGCTCTGAAATGACTACTGGGTACATAACGAAATGAAGGAGAAATA  
 AAGATGTTCTTGAAACCAACGAGAACAAAGACACCACATACCGAAATCTCTGGGACGCATTCAAAGCAG  
 TGTGTAGAGGGAAATTATAGCACTAAATGCCTACAAAGAGAACAGAGAAAGATCCAAAATTGACACCC  
 AACATCACAAATTAAAAGAACTAGAAAAGCAAGAGAACACATTCAAAGCTAGCAGAGGCAAGAAATA  
 ACTAAAATCAGAGCAGAACTGAAGGAATAGAGACACAAAAACCTCTAAAAATCAATGAATCCGGGA  
 GCTGGTTTTGAAAGGATCAACAAATTGATAGACCGCTAGCAAGACTATAAAAGAAAAAGAGAGAA  
 GAATCAAATAGACACAAATAAAAGATAAAGGGATATCACCACGATCCACAGAAATCAAACACTACC  
 ATCAGAGAAACTACAAACACCTCTACGCAAATAAAACTAGAAAATCTAGAAGAAATGGATCATTCCTCG  
 ACACATACACTCTCCCAAGACTAAACCCAGGAAGAAGTGAATCTGAAATAGCCAATAACAGGCTCTGA  
 ATTGTGGCAATAATCAATAGTTACCAACAAAAAGACTCCAGGACAGTGGATTACAGCCGAATT  
 TACCAAGAGGTACATGGAGGAACCTGTTACATTCTCTGAAACTATTCAAATCAATAGAAAAGAGGGAA  
 TCCTCCCTAACTCATTTATGAGGCCAGCATCATTCTGATACCAAGGCCGGCAGAGACACACCAAA  
 AGAGAATTTCAGACCAATATCCTGATGAACATTGATGCAAACCTCAATAAAATACTGGCAACCGA  
 ATCCAGCAGCACATCAAAGCTTATCCACCATGATCAAGTGGCTCATCCCTGGGATGCAAGGCTGGT  
 TCAATATACGCAAATCAATAAAATGTAATCCAGCATATAACAGAGCAGAACAAAACCACATGATT  
 CTCAATAGATGCAGAAAAAGCCTTGACAAAATTCAACACCCCTCATGCTAAAAACTCTCAATAAAATT  
 GGTATTGATGGGACGTATTCAAAATAAAGAGCTATCTATGACAAACCCACAGCCAATATCATACTGA

ATGGGCAAAACTGGAAGCATTCCCTTGAAAACCGGCACAAGACAGGGATGCCCTCTCACCGCTCCT  
ATTCAACATAGTGTGGAAGTCTGCCAGGGCAATCAGGCAGGAGAAGGAATAAAGGGTATTGATTA  
GGAAAAGAGGAAGTCAAATTGTCCTGTTGAGACAGCATGATTGTATATCTAGAAAACCCCATCGTCT  
CAGCCCCAAATCTCCTTAAGCTGATAAGCAACTTCAGCAAAGTCTCAGGATACAAAATCAATGTACAAA  
ATCACAAGCATTCTTACACCAACACAGACAACAGAGGCCAATCATGGGTGAACTCCCATTGTA  
ATTGCTTCAAAGAGAATAAAACCTAGGAATCCAACTTACAAGGGATGTGAAGGACCTTCAAGGAGA  
ACTACAAACCACTGCTAAGGAATAAAAGAGGACACAAACAAATGGAAGAACATTCCATGCTCATGGGT  
AGGAAGAATCAATATCGTAAAATGCCACTGCCCAAGGTATTTACAGATTCAATGCCATCCCCATC  
AAGCTACCAATGACTTTCTCACAGAATTGGAAAAACTACTTAAAGTCAATGGAACCAAAAAGAG  
CCCGCATTGCCAAGTCAATCCTAACGCAAAGAACAAAGCTGGAGGCATCACACTACCTGACTTCAAAC  
ATACTACAAAGGCTACAGTAACAAAACAGCATGGTACTGGTACCAAAACAGAGATATAGATCAATGGAAC  
AGAACAGGCCCTCAGAAATAATGCCGATATCTACAACTATCTGATCTTGACAAACCTGAGAAAAACA  
AGCAATGGGAAAGGATTCCCTATTTAATAAATGGTGTGGAAAAGTGGCTAGCCATATGTAGAAAGCT  
GAACACTGGATCCCTCCTACACCTTACACAAACAAATCAATTCAAGATGGTAAAGATTAAACGTTAAA  
CCTAAAACCATAAAAACCCCTAGAAGAAAACCTAGGCATTACCATTCAAGGACATAGGCGTGGGCAAGGACT  
TCATGTCCAAAACACCAAAAGCAATGGCAACAAAAGACAAAATTGACAAATGGATCTAATTAAACTAAA  
GAGCTTCTGCACAGCAAAGAAACTACCATCAGAGTGAACAGGCAACCTACAACATGGGAGAAAATTTC  
GCAACCTACTCATCTGACAAAGGCTAATATCCAGAATCTACAATGAACCAAACAAATTACAAGAAAA  
AAACAAACAACCCCCTACAAAAGTGGCGAAGGACATGAACAGACACTCTCAAAAGAACATTTATGC  
AGCCAAAAAACACATGAAGAAATGCTCATCATCACTGGCCATCAGAGAAAATGCAAATCAAACCAACTATG  
AGATATCATCTCACACCAGTTAGAATGGCAATCATTAAAAGTCAGGAAACAACAGGTGCTGGAGAGGAT  
GCGGAGAAATAGGAACACTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTGGAAAGTCAGT  
GTGGCGATTCCCTCAGGGATCTAGAAACTAGAAATACCATTGACCCAGCCATCCCATTACTGGGTATATAC  
CCAAATGAGTATAATCATGCTGCTATAAGACACATGCACACGTATGTTATTGCGGCACTATTCAA  
TAGCAAAGACTTGGAACCAACCCAAATGTCCAACAATGATAGACTGGATTAAGAAAATGTGGCACATATA  
CACCATGGAATACTATGCAGCCATAAAAATGATGAGTTCATATCCTTGTAGGGACATGGATGAAATTG  
GAAACCATCATTCTCAGTAAACTATCGCAAGAACAAAAACCAACACCGCATATTCTCACTCATAGGTG  
GGAATTGAACAATGAGATCACATGGACACAGGAAGGGGAATATCACACTCTGGGACTGTGGTGGGTG  
GGGGAGGGGGAGGGATAGCATTGGGAGATATACCTAATGCTAGATGACACATTAGGGTGCAGCGCAC  
CAGCATGGCACATGTATACATATGTAACCTGCACAAATGTGCACATGTACCCCTAAACTAGAGTAT  
AATAAAAAAAAAAAAAAAAAAAAAAA

## BIOGRAPHY

Miss Wanpen Pongyeam was born in Bangkok in 1982. In 2004, she graduated from faculty of Science, Chulalongkorn University in Biochemistry program and then attended to participate in Medical Science program in Faculty of Medicine for her master degree.



