

ATTdb: A Tumor and Tissue Specific Natural Antisense Transcripts Database

Fang Rong Hsu^{1,*}, M.C. Lee¹, Nai Wan Hsiao², and Wei Chung Shia¹

¹Department of Information Engineering and Computer Science,

Feng Chia University,

Taichung, Taiwan 40724, ROC

frhsu@fcu.edu.tw, kazekawa.tw@yahoo.com.tw, jomessha@gmail.com

²Institute of Biotechnology,

National Chunghua University of Education,

Changhua 500, Taiwan ROC

nady@cc.ncue.edu.tw

Received 1 October 2010; Revised 10 November 2010; Accepted 10 December 2010

Abstract. The natural antisense transcripts (NATs) may cause RNA masking, RNA editing, RNA interference, alternative splicing and translational regulation amongst other effects. Over 2500 mammalian NATs have been found recently. In recent investigations indicate that there is a relationship between sense-antisense RNA expression and tissue-specific RNA expression. We also identified cis-NATs in mouse, rat, fruit fly, nematode and arabidopsis genomes by the same methodology. We identified cis-NATs in 6 organisms, and found 15253, 2572, 1159, 239, 391 and 272 NAT clusters in human, mouse, rat, fruit fly, nematode and arabidopsis genomes respectively. In tissue-specific human natural antisense transcripts, there are 3,394 NATs (LOD > 2). Tissue-specific NATs in the mouse genome were also found. In this article, we present our tissue-specific natural antisense transcripts database (ATTdb) and provide a user-friendly interface for visualization. ATTdb enables detailed and visual information of NATs in six organisms. Tissue-specific NATs are also available in ATTdb. ATTdb is freely available at <http://biolab.iecs.fcu.edu.tw/attdb>.

Keywords: Natural antisense transcripts, RNA editing, EST, RFID

References

- [1] M. E. Fahey, T. F. Moore, D. G. Higgins, "Overlapping Antisense Transcription in the Human Genome," *Comparative and Functional Genomics*, Vol. 3, No. 3, pp. 244-253, 2002.
- [2] B. Lehner, G. Williams, R. D. Campbell, C. M. Sanderson, "Antisense Transcripts in the Human Genome," *Trends Genet*, Vol. 18, No. 2 pp. 63-65. 2002.
- [3] J. Shendure and G. M. Church, "Computational Discovery of Sense-antisense Transcription in the Human and Mouse Genomes," *Genome Biol*, Vol. 3 No. 9, 2002.
- [4] H. Kiyosawa, I. Yamanaka, N. Osato, S. Kondo, RIKEN GER Group and GSL Members, Y. Hayashizaki "Antisense Transcripts with FANTOM2 Clone Set and Their Implications for Gene Regulation," *Genome Research*, Vol. 13, No. 6, pp. 1324-1334, 2003.
- [5] R. Yelin, D. Dahary, R. Sorek, E. Y. Levanon, O. Goldstein, A. Shoshan, A. Diber, S. Biton, Y. Tamir, R. Khosravi, S. Nemzer, E. Pinner, S. Walach, J. Bernstein, K. Savitsky, G. Rotman, "Widespread Occurrence of Antisense Transcription in the Human Genome," *Nat. Biotechnol*, Vol. 21, No. 4, pp. 379-386, 2003.

* Correspondence author

- [6] Y. Zhang, X.S. Liu, Q.R. Liu, L. Wei, "Genome-wide in Silico Identification and Analysis of Cis Natural Antisense Transcripts Cis-NATs in Ten Species," *Nucleic Acids Research*, Vol. 34, No. 12, pp.3465-3475, 2006.
- [7] G. Lavorgna, D. Dahary, B. Lehner, R. Sorek, C. M. Sanderson, G. Casari, "In Search of Antisense," *Trends Biochemical Sciences*, Vol. 29, No. 2, pp. 88-94, 2004.
- [8] C. V. Brossollet and C. Vaquero, "Do Natural Antisense Transcripts Make Sense in Eukaryotes?" *Gene*, Vol. 211, No. 1, pp. 1-9, 1998.
- [9] M. Kumar and G. G. Carmichael, "Antisense RNA: Function and Fate of Duplex RNA in Cells of Higher Eukaryotes," *Microbiology and Molecular Biology Reviews*, Vol. 62, No. 4, pp. 1415-1434, 1998.
- [10] G. Alfano, C. Vitiello, C. Caccioppoli, T. Caramico, A. Carola, M. J. Szego, R. R. McInnes, A. Auricchio, S. Banfi, "Natural Antisense Transcripts Associated with Genes Involved in Eye Development," *Human Molecular Genetics*, Vol. 14, No. 7, pp. 913-23, 2005.
- [11] A. Werner, G. Schmutzler, M. Carlile, C. G. Miles, H. Peters, "Expression Profiling of Antisense Transcripts on DNA Arrays," *Physiol Genomics*. Vol. 28. pp. 294-300, 2006.
- [12] J. Chen, M. Sun, W.J. Kent, X. Huang, H. Xie, W. Wang, G. Zhou, R.Z. Shi, J.D. Rowley, "Over 20% of Human Transcripts Might form Sense-antisense Pair," *Nucleic Acids Research*, Vol. 32 No. 16, pp. 4812-4820, 2004.
- [13] F.R. Hsu, H.Y. Chang, Y.L. Lin, Y.T. Tsai, H.L. Peng, Y.T. Chen, C.Y. Cheng, M.Y. Shih, C.H. Liu, C.F. Chen, "AVATAR: A Database for Genome-wide Alternative Splicing Event Detection Using Large Scale ESTs and mRNAs," *Bioinformatics*, Vol. 1, No. 1, pp. 16-18, 2005.
- [14] M. Buset, I. A. Seledtsov, V. V. Solovyev, "Analysis of Canonical and Non-canonical Splice Sites in Mammalian Genomes," *Nucleic Acids Research*, Vol. 28, No. 21, pp. 4364-4375, 2000.
- [15] E. S. Lander, L. M. Linton, B. Birren, C. Nusbaum, M. C. Zody, J. Baldwin, K. Devon, K. Dewar, M. Doyle, W. FitzHugh, R. Funke, D. Gage, K. Harris, A. Heaford, J. Howland, L. Kann, J. Lehoczy, R. LeVine, P. McEwan, K. McKernan, J. Meldrim, J. P. Mesirov, C. Miranda, W. Morris, J. Naylor, C. Raymond, M. Rosetti, R. Santos, A. Sheridan, C. Sougnez, N. Stange-Thomann, N. Stojanovic, A. Subramanian, D. Wyman, J. Rogers, J. Sulston, R. Ainscough, S. Beck, D. Bentley, J. Burton, C. Clee, N. Carter, A. Coulson, R. Deadman, P. Deloukas, A. Dunham, I. Dunham, R. Durbin, L. French, D. Grafham, S. Gregory, T. Hubbard, S. Humphray, A. Hunt, M. Jones, C. Lloyd, A. McMurray, L. Matthews, S. Mercer, S. Milne, J. C. Mullikin, A. Mungall, R. Plumb, M. Ross, R. Shownkeen, S. Sims, R. H. Waterston, R. K. Wilson, L. W. Hillier, J. D. McPherson, M. A. Marra, E. R. Mardis, L. A. Fulton, A. T. Chinwalla, K. H. Pepin, W. R. Gish, S. L. Chissoe, M. C. Wendl, K. D. Delehaunty, T. L. Miner, A. Delehaunty, J. B. Kramer, L. L. Cook, R. S. Fulton, D. L. Johnson, P. J. Minx, S. W. Clifton, T. Hawkins, E. Branscomb, P. Predki, P. Richardson, S. Wenning, T. Slezak, N. Doggett, J. F. Cheng, A. Olsen, S. Lucas, C. Elkin, E. Uberbacher, M. Frazier, R. A. Gibbs, D. M. Muzny, S. E. Scherer, J. B. Bouck, E. J. Sodergren, K. C. Worley, C. M. Rives, J. H. Gorrell, M. L. Metzker, S. L. Naylor, R. S. Kucherlapati, D. L. Nelson, G. M. Weinstock, Y. Sakaki, A. Fujiyama, M. Hattori, T. Yada, A. Toyoda, T. Itoh, C. Kawagoe, H. Watanabe, Y. Totoki, T. Taylor, J. Weissenbach, R. Heilig, W. Saurin, F. Artiguenave, P. Brottier, T. Bruls, E. Pelletier, C. Robert, P. Wincker, D. R. Smith, L. Doucette-Stamm, M. Rubenfield, K. Weinstock, H. M. Lee, J. Dubois, A. Rosenthal, M. Platzer, G. Nyakatura, S. Taudien, A. Rump, H. Yang, J. Yu, J. Wang, G. Huang, J. Gu, L. Hood, L. Rowen, A. Madan, S. Qin, R. W. Davis, N. A. Federspiel, A. P. Abola, M. J. Proctor, R. M. Myers, J. Schmutz, M. Dickson, J. Grimwood, D. R. Cox, M. V. Olson, R. Kaul, C. Raymond, N. Shimizu, K. Kawasaki, S. Minoshima, G. A. Evans, M. Athanasiou, R. Schultz, B. A. Roe, F. Chen, H. Pan, J. Ramser, H. Lehrach, R. Reinhardt, W. R. McCombie, I. a. de, N. Dedhia, H. Blöcker, K. Hornischer, G. Nordtsiek, R. Agarwala,

- L. Aravind, J. A. Bailey, A. Bateman, S. Batzoglou, E. Birney, P. Bork, D. G. Brown, C. B. Burge, L. Cerutti, H. C. Chen, D. Church, M. Clamp, R. R. Copley, T. Doerks, S. R. Eddy, E. E. Eichler, T. S. Furey, J. Galagan, J. G. Gilbert, C. Harmon, Y. Hayashizaki, D. Haussler, H. Hermjakob, K. Hokamp, W. Jang, L. S. Johnson, T. A. Jones, S. Kasif, A. Kasprzyk, S. Kennedy, W. J. Kent, P. Kitts, E. V. Koonin, I. Korf, D. Kulp, D. Lancet, T. M. Lowe, A. McLysaght, T. Mikkelsen, J. V. Moran, N. Mulder, V. J. Pollara, C. P. Ponting, G. Schuler, J. Schultz, G. Slater, A. F. Smit, E. Stupka, J. Szustakowski, D. Thierry-Mieg, J. Thierry-Mieg, L. Wagner, J. Wallis, R. Wheeler, A. Williams, Y. I. Wolf, K. H. Wolfe, S. P. Yang, R. F. Yeh, F. Collins, M. S. Guyer, J. Peterson, A. Felsenfeld, K. A. Wetterstrand, A. Patrinos, M. J. Morgan, P. de John, J. J. Catanese, K. Osoegawa, H. Shizuya, S. Choi, Y. J. Chen, International Human Genome Sequencing Consortium, "Initial Sequencing and Analysis of The Human Genome," *Nature*, Vol. 409, pp. 860-921, 2001.
- [16] H. Caron, B. V. Schaik, M. V. D. Mee, F. Baas, G. Riggins, P. V. Sluis, M. C. Hermus, R. V. Asperen, K. Boon, P. A. Voute, S. Heisterkamp, A. V. Kampen, R. Versteeg, "The Human Transcriptome Map: Clustering of Highly Expressed Genes in Chromosomal Domains," *Science*, Vol. 291, No. 5507 pp. 1289-1292, 2001.
- [17] W. J. Kent, C. W. Sugnet, T. S. Furey, K. M. Roskin, T. H. Pringle, A. M. Zahler, D. Haussler, "The Human Genome Browser at UCSC," *Genome Research*, Vol. 12, No. 6, pp. 996-1006, 2002.