

THE MYTH OF JUNK DNA

JONATHAN WELLS

Description

According to a number of leading proponents of Darwin's theory, "junk DNA"—the non-protein coding portion of DNA—provides decisive evidence for Darwinian evolution and against intelligent design, since an intelligent designer would presumably not have filled our genome with so much garbage. But in this provocative book, biologist Jonathan Wells exposes the claim that most of the genome is little more than junk as an anti-scientific myth that ignores the evidence, impedes research, and is based more on theological speculation than good science.

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Publisher's Note

This book is part of a series published by the Center for Science & Culture at Discovery Institute in Seattle. Previous books include *The Deniable Darwin* by David Berlinski, *In the Beginning and Other Essays on Intelligent Design* by Granville Sewell, *God and Evolution: Protestants, Catholics, and Jews Explore Darwin's Challenge to Faith*, edited by Jay Richards, and *Darwin's Conservatives: The Misguided Quest* by John G. West.

Library Cataloging Data

The Myth of Junk DNA by Jonathan Wells (1942–)

Illustrations by Ray Braun

174 pages, 6 x 9 x 0.4 inches & 0.6 lb, 229 x 152 x 10 mm. & 0.26 kg

Library of Congress Control Number: 2011925471

BISAC: SCI029000 SCIENCE / Life Sciences / Genetics & Genomics

BISAC: SCI027000 SCIENCE / Life Sciences / Evolution

ISBN-13: 978-1-9365990-0-4 (paperback)

Publisher Information

Discovery Institute Press, 208 Columbia Street, Seattle, WA 98104

Internet: <http://www.discoveryinstitutepress.com/>

Published in the United States of America on acid-free paper.

First Edition, First Printing. May 2011.

Praise for *The Myth of Junk DNA*

"JONATHAN WELLS HAS CLEARLY DONE HIS HOMEWORK. IN *THE MYTH of Junk DNA*, he cites hundreds of research articles as he describes the expanding story of non-coding DNA—the supposed 'junk DNA.' It is quite possibly the most thorough review of the subject available. Dr. Wells makes it clear that our early understanding of DNA was incomplete, and genomics research is now revealing levels of control and complexity inside our cells that were undreamed of in the 1980s. Far from providing evidence for Darwinism, the story of non-coding DNA rather serves to increase our appreciation for the design of life."

Ralph Seelke, Ph.D.

*Professor of Microbial Genetics and Cell Biology
University of Wisconsin-Superior*

"CITING HUNDREDS OF PEER-REVIEWED ARTICLES WHICH SHOW THAT more and more of the genome is functional, Jonathan Wells delivers a powerful and carefully researched broadside against the 'junk DNA hypothesis.' Even biologists who firmly reject the notion of intelligent design must surely acknowledge on the evidence presented in this timely book that appealing to 'junk DNA' to defend the Darwinian framework no longer makes any sense."

Michael Denton, Ph.D.

Medical Geneticist and Author of Nature's Destiny

"THIS IS AN EXCELLENT AND IN-DEPTH DISCUSSION OF SEVERAL KEY points of the subject of 'junk-DNA.' The author shows for many prime examples still advanced by leading neo-Darwinians that the 'Darwin-of-the-gaps' approach doesn't function or is at least doubtful."

Wolf-Ekkehard Lönning, Ph.D.

*Senior Scientist, Department of Molecular Plant Genetics
Max Planck Institute for Plant Breeding Research (retired)*

"THERE IS A BOX IN THE BIOLOGICAL SCIENCES INTO WHICH ALL EVIDENCE must be placed. That box is called Darwinian evolution. In *The Myth of Junk DNA* Jonathan Wells tells the intriguing story of 'junk' DNA—the

idea that non-protein coding DNA, which accounts for the majority of the DNA in the genome, is non-functional and without purpose; the result of the unguided purposeless process of random mutation and natural selection that produced it. In recent years, however, numerous researchers—not necessarily opponents of Darwinian evolution or advocates of intelligent design—have discovered many functions for non-protein coding DNA, which are thoroughly reviewed by Wells in this book. Unfortunately, in their effort to keep the ‘junk’ label attached to non-protein coding DNA so that it remains in the box of Darwinian evolution, a number of prominent Darwinists continue to insist, in spite of the recent results to the contrary, that it is largely left-over waste from the evolutionary process. As Wells clearly demonstrates in his book, this dogmatic commitment inhibits the scientific process. Science needs to be guided by objective evaluation of the evidence, and scientists should not allow their thinking to be arbitrarily restricted by dogmatic ideas. We need scientists who think outside the Darwinian box. Wells’s book not only informs its readers of very recent research results, but also encourages them to think objectively and clearly about a key discovery in biology and to approach biological research with more creativity. It is a great read.”

*Russell W. Carlson, Ph.D.
Professor of Biochemistry and Molecular Biology
University of Georgia*

“FOR YEARS, DARWINISTS HAVE CLAIMED THAT MOST DNA IS LEFT-OVER detritus from failed evolutionary experiments. This ‘junk DNA’ has been offered as evidence for Darwinism and evidence against intelligent design. The only problem with the claim, as Jonathan Wells shows in this fascinating book, is that it’s not true. Careful scientists have known for some time that the non-coding regions of DNA have all manner of function, so it is surprising to see prominent Darwinian scientists and their spokesmen continue to push the party line. Now that the evidence against the junk DNA story is indisputable, its defenders will want to beat a hasty retreat. *The Myth of Junk DNA* will make it hard for them to cover their tracks.”

*Jay Richards, Ph.D.
Co-Author, *The Privileged Planet*, and Editor, *God and Evolution**

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NOTES

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1. Theodosius Dobzhansky, *Genetics and the Origin of Species*, Reprinted 1982. (New York: Columbia University Press, 1937), p. 12.
2. Keith Stewart Thomson, "Natural Selection and Evolution's Smoking Gun," *American Scientist* 85 (1997): 516–518.
3. Alan Linton, "Scant Search for the Maker," *The Times Higher Education Supplement* (April 20, 2001), Book Section, p. 29. Freely accessible (2011) at <http://www.timeshighereducation.co.uk/story.asp?storyCode=159282§ioncode=31>
4. Jonathan Wells, *The Politically Incorrect Guide to Darwinism and Intelligent Design* (Washington, DC: Regnery Publishing, 2006), Chapter 5. More information available online (2011) at <http://www.discovery.org/a/3699>
5. Jonathan Wells, *Icons of Evolution: Science or Myth?* (Washington, DC: Regnery Publishing, 2000). More information available online (2011) at <http://www.iconsofevolution.com/>
6. Charles Darwin, *The Origin of Species by Means of Natural Selection*, First Edition (London: John Murray, 1859), p. 130. Freely accessible (2011) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F373&pageseq=148>
7. Darwin, *The Origin of Species*, p. 282. Freely accessible (2010) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F373&pageseq=300>
8. James W. Valentine, Stanley M. Awramik, Philip W. Signor and Peter M. Sadler, "The Biological Explosion at the Precambrian-Cambrian Boundary," *Evolutionary Biology* 25 (1991): 279–356.
9. Jeffrey S. Levinton, "The Big Bang of Animal Evolution," *Scientific American* 267 (November, 1992): 84–91.
10. Jonathan Wells, "Deepening Darwin's Dilemma," *Discovery Institute* (September 16, 2009). Freely accessible (2011) at <http://www.discovery.org/a/12471>
11. W. Ford Doolittle, "The practice of classification and the theory of evolution, and what the demise of Charles Darwin's tree of life hypothesis means for both of them," *Philosophical Transactions of the Royal Society of London B* 364 (2009): 2221–2228.
12. Carl R. Woese & Nigel Goldenfeld, "How the Microbial World Saved Evolution from the Scylla of Molecular Biology and the Charybdis of the Modern Synthesis," *Microbiology and Molecular Biology Reviews* 73 (2009): 14–21. Freely accessible (2011) at <http://mmb.asm.org/cgi/rapidprint/73/1/14>
13. Wells, *The Politically Incorrect Guide to Darwinism and Intelligent Design*, Chapter 4.
14. Gavin de Beer, *Homology: An Unsolved Problem* (London: Oxford University Press, 1971), pp. 15–16.
15. Wells, *Icons of Evolution: Science or Myth?*, Chapter 4.
16. Charles Darwin, "Letter to Asa Gray, September 10, 1860," in Francis Darwin (editor), *The Life and Letters of Charles Darwin* (London: John Murray, 1887), Vol. II, p. 338. Freely accessible (2011) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F1452.2&pageseq=354>
17. Rudolf A. Raff, *The Shape of Life: Genes, Development, and the Evolution of Animal Form* (Chicago: The University of Chicago Press, 1996), pp. 195, 208–209.
18. Jonathan Wells, "Haeckel's Embryos & Evolution: Setting the Record Straight," *The American Biology Teacher* 61 (May, 1999): 345–349. Freely accessible (2011) at <http://www.discovery.org/a/3071>

19. Wells, *Icons of Evolution: Science or Myth?* Chapter 5.

2. JUNK DNA – THE LAST ICON OF EVOLUTION?

1. Horace Freeland Judson, *The Eighth Day of Creation* (New York: Simon and Schuster, 1979), p. 175.
2. Francis Darwin (editor), *The Life and Letters of Charles Darwin* (London: John Murray, 1887), Volume I, p. 309. Freely accessible (2011) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F1452.1&pageseq=327>
3. Francis Darwin & A.C. Seward (editors), *More Letters of Charles Darwin* (London: John Murray, 1903), Volume 1, p. 321. Freely accessible (2011) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F1548.1&pageeq=370>
4. Francis Darwin (editor), *The Life and Letters of Charles Darwin* (London: John Murray, 1887), Volume II, p. 312. Freely accessible (2011) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F1452.2&pageseq=328>
5. William Bateson, *Mendel's Principles of Heredity* (New York: G. P. Putnam's Sons, 1913), p. 329.
6. "Mendel, Mendelism," *The Catholic Encyclopedia*. Freely accessible (2011) at <http://www.newadvent.org/cathen/10180b.htm>
7. James D. Watson & Francis H. C. Crick, "Molecular Structure of Nucleic Acids: A Structure for Deoxyribose Nucleic Acid," *Nature* 171 (1953): 737–738. Freely accessible (2011) at <http://www.annals.org/cgi/reprint/138/7/581.pdf>
8. James D. Watson & Francis H. C. Crick, "Genetical Implications of the Structure of Deoxyribonucleic Acid," *Nature* 171 (1953): 964–967.
9. Francis H. C. Crick, "On Protein Synthesis," *The Biological Replication of Macromolecules*, Symposia of the Society for Experimental Biology, Number XII (Cambridge: Cambridge University Press, 1958), pp. 138–163.
10. Judson, *The Eighth Day of Creation*, p. 217.
11. Richard Dawkins, *The Selfish Gene* (New York: Oxford University Press, 1976), pp. 2, 24–25.
12. Susumu Ohno, "So much 'junk' DNA in our genome," *Brookhaven Symposia in Biology* 23 (1972): 366–70. Freely accessible (2011) at <http://www.junkdna.com/ohno.html>
13. David E. Comings, "The Structure and Function of Chromatin," *Advances in Human Genetics* 3 (1972): 237–431.
14. Dawkins, *The Selfish Gene*, p. 47.
15. W. Ford Doolittle & Carmen Sapienza, "Selfish genes, the phenotype paradigm and genome evolution," *Nature* 284 (1980): 601–603.
16. Leslie E. Orgel & Francis H. C. Crick, "Selfish DNA: the ultimate parasite," *Nature* 284 (1980): 604–607.
17. Thomas Cavalier-Smith, "How selfish is DNA?" *Nature* 285 (1980): 617–618.
18. Gabriel Dover, "Ignorant DNA?" *Nature* 285 (1980): 618–620.
19. Charles B. Thaxton, Walter L. Bradley & Roger L. Olsen, *The Mystery of Life's Origin* (Dallas, TX: Lewis and Stanley, 1984), pp. 210–211.
20. Michael Denton, *Evolution: A Theory in Crisis* (Bethesda, MD: Adler & Adler, 1985), p. 341.
21. Phillip E. Johnson, *Darwin On Trial*. (Washington, DC: Regnery Gateway, 1991), p. 144.
22. Kenneth R. Miller, "Life's Grand Design," *Technology Review* 97 (February–March 1994): 24–32. Freely accessible (2011) at <http://www.millerandlevine.com/km/evol/lgd/index.html>
23. Richard Dawkins, *A Devil's Chaplain: Reflections on Hope, Lies, Science, and Love* (New York: Mariner Books, 2004), p. 99.

24. Douglas J. Futuyma, *Evolution* (Sunderland, MA: Sinauer Associates, 2005), pp. 48–49, 456, 530.
25. Michael Shermer, *Why Darwin Matters: The Case Against Intelligent Design* (New York: Holt, 2006), pp. 74–75.
26. Francis S. Collins, *The Language of God: A Scientist Presents Evidence for Belief* (New York: Free Press, 2006), pp. 136–137.
27. Philip Kitcher, *Living With Darwin: Evolution, Design, and the Future of Faith* (New York: Oxford, 2007), pp. 57–58, 111.
28. Kenneth R. Miller, *Only a Theory: Evolution and the Battle for America's Soul* (New York: Viking, 2008), pp. 97–98.
29. Jerry A. Coyne, *Why Evolution Is True* (New York: Viking, 2009), pp. 66–67, 81.
30. Richard Dawkins, *The Greatest Show on Earth: The Evidence for Evolution* (New York: Free Press, 2009), pp. 332–333.
31. John C. Avise, *Inside the Human Genome: A Case for Non-Intelligent Design* (Oxford: Oxford University Press, 2010), pp. 82, 115.
32. John C. Avise, “Footprints of nonsentient design inside the human genome,” *Proceedings of the National Academy of Sciences USA* 107 Supplement 2 (2010): 8969–8976. Freely accessible (2011) at <http://www.pnas.org/content/107/suppl.2/8969.full.pdf+html>
3. Nobel Prize for Physiology or Medicine (1993) awarded to Richard J. Roberts and Phillip A. Sharp for their “discovery of split genes.” Press release available online (2011) at http://nobelprize.org/nobel_prizes/medicine/laureates/1993/press.html
4. David M. Glover & David S. Hogness, “A Novel Arrangement of the 18s and 28s Sequences in a Repeating Unit of *Drosophila melanogaster* rDNA,” *Cell* 10 (1977): 167–176.
5. Walter Gilbert, “Why genes in pieces?” *Nature* 271 (1978): 501.
6. P. M. B. Walker & Anne McLaren, “Fractionation of mouse deoxyribonucleic acid on hydroxyapatite,” *Nature* 208 (1965): 1175–1179.
7. Roy J. Britten & D. E. Kohne, “Repeated Sequences in DNA,” *Science* 161 (1968): 529–540.
8. Reviewed in W. G. Flamm, “Highly Repetitive Sequences of DNA in Chromosomes,” *International Review of Cytology* 32 (1972): 1–51.
9. Bruce Alberts, Alexander Johnson, Julian Lewis, Martin Raff, Keith Roberts & Peter Walter, *Molecular Biology of the Cell*, Fourth Edition (New York: Garland Science, 2002), p. 203.
10. Joshua Lederberg & Alexa T. McCray, “‘Ome Sweet ‘Omics—A Genealogical Treasury of Words,” *The Scientist* 15 (2001): 8. Freely accessible (2011) at <http://www.lhncbc.nlm.nih.gov/lhc/docs/published/2001/pub2001047.pdf>
11. Edmund Pillsbury, “A History of Genome Sequencing,” *Computational Biology and Bioinformatics*, Yale University (1997). Freely accessible (2011) at <http://bioinfo.mbb.yale.edu/course/projects/final-4/>
12. National Center for Biotechnology Information (GenBank). <http://www.ncbi.nlm.nih.gov/genbank/>

3. Most DNA Is

TRANSCRIBED INTO RNA

1. Francis H. C. Crick, “On Protein Synthesis,” *The Biological Replication of Macromolecules*, Symposia of the Society for Experimental Biology, Number XII (Cambridge: Cambridge University Press, 1958), pp. 138–163.
2. C. Mulder, J. R. Arrand, H. Delius, W. Keller, U. Pettersson, R. J. Roberts & P. A. Sharp, “Cleavage Maps of DNA from Adenovirus Types 2 and 5 by Restriction Endonucleases *EcoRI* and *HpaI*,” *Cold Spring Harbor Symposia on Quantitative Biology* 39 (1975): 397–400.

13. EMBL Nucleotide Sequence Database. <http://www.ebi.ac.uk/embl/>
14. DNA Data Bank of Japan. <http://www.ddbj.nig.ac.jp/>
15. "International Consortium Completes Human Genome Project," National Human Genome Research Institute, Bethesda, MD (April 14, 2003). Freely accessible (2011) at <http://www.genome.gov/11006929>
16. "The ENCODE Project," National Human Genome Research Institute, Bethesda, MD (December 28, 2009). Freely accessible (2011) at <http://www.genome.gov/10005107>
17. "History," RIKEN Omic Sciences Center, Yokohama, Japan (2009). Freely accessible (2011) at <http://www.osc.riken.jp/english/outline/history/>
18. FANTOM Consortium, Yokohama, Japan. <http://fantom.gsc.riken.jp/4/>
19. Fred A. Wright, William J. Lemon, Wei D. Zhao, Russell Sears, Degen Zhuo, Jian-Ping Wang, Hee-Yung Yang, Troy Baer, Don Stredney, Joe Spitzner, Al Stutz, Ralf Krahe & Bo Yuan, "A draft annotation and overview of the human genome," *Genome Biology* 2:7 (2001). Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2001-2-7-research0025.pdf>
20. Y. Okazaki, M. Furuno, T. Kasukawa, J. Adachi, H. Bono, S. Kondo, I. Nikaido, N. Osato, R. Saito, H. Suzuki, I. Yamanaka, H. Kiyosawa, K. Yagi, Y. Tomaru, Y. Hasegawa, A. Nogami, C. Schönbach, T. Gojobori, R. Baldarelli, D. P. Hill, C. Bult, D. A. Hume, J. Quackenbush, L. M. Schriml, A. Kanapin, H. Matsuda, S. Batalov, K. W. Beisel, J. A. Blake, D. Bradt, V. Brusica, C. Chothia, L. E. Corbani, S. Cousins, E. Dalla, T. A. Dragani, C. F. Fletcher, A. Forrest, K. S. Frazer, T. Gaasterland, M. Gariboldi, C. Gissi, A. Godzik, J. Gough, S. Grimmond, S. Gustincich, N. Hirokawa, I. J. Jackson, E. D. Jarvis, A. Kanai, H. Kawaji, Y. Kawasaki, R. M. Kedzierski, B. L. King, A. Konagaya, I. V. Kurochkin, Y. Lee, B. Lenhard, P. A. Lyons, D. R. Maglott, L. Maltais, L. Marchionni, L. McKenzie, H. Miki, T. Nagashima, K. Numata, T. Okido, W. J. Pavan, G. Pertea, G. Pesole, N. Petrovsky, R. Pillai, J. U. Pontius, D. Qi, S. Ramachandran, T. Ravasi, J. C. Reed, D. J. Reed, J. Reid, B. Z. Ring, M. Ringwald, A. Sandelin, C. Schneider, C. A. M. Semple, M. Setou, K. Shimada, R. Sultana, Y. Takenaka, M. S. Taylor, R. D. Teasdale, M. Tomita, R. Verardo, L. Wagner, C. Wahlestedt, Y. Wang, Y. Watanabe, C. Wells, L. G. Wilming, A. Wynshaw-Boris, M. Yanagisawa, I. Yang, L. Yang, Z. Yuan, M. Zavolan, Y. Zhu, A. Zimmer, P. Carninci, N. Hayatsu, T. Hirozane-Kishikawa, H. Konno, M. Nakamura, N. Sakazume, K. Sato, T. Shiraki, K. Waki, J. Kawai, K. Aizawa, T. Arakawa, S. Fukuda, A. Hara, W. Hashizume, K. Imotani, Y. Ishii, M. Itoh, I. Kagawa, A. Miyazaki, K. Sakai, D. Sasaki, K. Shibata, A. Shinagawa, A. Yasunishi, M. Yoshino, R. Waterston, E. S. Lander, J. Rogers, E. Birney & Y. Hayashizaki, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs," *Nature* 420 (2002): 563–573.
21. Philipp Kapranov, Simon E. Cawley, Jorg Drenkow, Stefan Bekiranov, Robert L. Strausberg, Stephen P. A. Fodor & Thomas R. Gingeras, "Large-Scale Transcriptional Activity in Chromosomes 21 and 22," *Science* 296 (2002): 916–919.
22. P. Carninci, T. Kasukawa, S. Katayama, J. Gough, M. C. Frith, N. Maeda, R. Oyama, T. Ravasi, B. Lenhard, C. Wells, R. Kodzius, K. Shimokawa, V. B. Bajic, S. E. Brenner, S. Batalov, A. R. R. Forrest, M. Zavolan, M. J. Davis, L. G. Wilming, V. Aidinis, J. E. Allen, A. Ambesi-Impiombato, R. Apweiler, R. N. Aturaliya, T. L. Bailey, M. Bansal, L. Baxter, K. W. Beisel, T. Bersano, H. Bono, A. M. Chalk, K. P. Chiu, V. Choudhary, A. Christofels, D. R. Clutterbuck, M. L. Crowe, E.

- Dalla, B. P. Dalrymple, B. de Bono, G. Della Gatta, D. di Bernardo, T. Down, P. Engstrom, M. Fagiolini, G. Faulkner, C. F. Fletcher, T. Fukushima, M. Furuno, S. Futaki, M. Gariboldi, P. Georgii-Hemming, T. R. Gingeras, T. Gojobori, R. E. Green, S. Gustincich, M. Harbers, Y. Hayashi, T. K. Hensch, N. Hirokawa, D. Hill, L. Huminiecki, M. Iacono, K. Ikeo, A. Iwama, T. Ishikawa, M. Jakt, A. Kanapin, M. Katoh, Y. Kawasaki, J. Kelso, H. Kitamura, H. Kitano, G. Kollias, S. P. T. Krishnan, A. Kruger, S. K. Kummerfeld, I. V. Kurochkin, L. F. Lareau, D. Lazarevic, L. Lipovich, J. Liu, S. Liuni, S. McWilliam, M. Madan Babu, M. Madera, L. Marchionni, H. Matsuda, S. Matsuzawa, H. Miki, F. Mignone, S. Miyake, K. Morris, S. Mottagui-Tabar, N. Mulder, N. Nakano, H. Nakauchi, P. Ng, R. Nilsson, S. Nishiguchi, S. Nishikawa, F. Nori, O. Ohara, Y. Okazaki, V. Orlando, K. C. Pang, W. J. Pavan, G. Pavesi, G. Pesole, N. Petrovsky, S. Piazza, J. Reed, J. F. Reid, B. Z. Ring, M. Ringwald, B. Rost, Y. Ruan, S. L. Salzberg, A. Sandelin, C. Schneider, C. Schönbach, K. Sekiguchi, C. A. M. Semple, S. Seno, L. Sessa, Y. Sheng, Y. Shibata, H. Shimada, K. Shimada, D. Silva, B. Sinclair, S. Sperling, E. Stupka, K. Sugitani, R. Sultana, Y. Takenaka, K. Taki, K. Tammoja, S. L. Tan, S. Tang, M. S. Taylor, J. Tegner, S. A. Teichmann, H. R. Ueda, E. van Nimwegen, R. Verardo, C. L. Wei, K. Yagi, H. Yamanishi, E. Zabarovsky, S. Zhu, A. Zimmer, W. Hide, C. Bult, S. M. Grimmond, R. D. Teasdale, E. T. Liu, V. Brusic, J. Quackenbush, C. Wahlestedt, J. S. Mattick, D. A. Hume, C. Kai, D. Sasaki, Y. Tomaru, S. Fukuda, M. Kanamori-Katayama, M. Suzuki, J. Aoki, T. Arakawa, J. Iida, K. Imamura, M. Itoh, T. Kato, H. Kawaji, N. Kawagashira, T. Kawashima, M. Kojima, S. Kondo, H. Konno, K. Nakano, N. Ninomiya, T. Nishio, M. Okada, C. Plessy, K. Shibata, T. Shiraki, S. Suzuki, M. Tagami, K. Waki, A. Watahiki, Y. Okamura-Oho, H. Suzuki, J. Kawai & Y. Hayashizaki, "The Transcriptional Landscape of the Mammalian Genome," *Science* 309 (2005): 1559–1563. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/309/5740/1559>
23. Michael Pheasant & John S. Mattick, "Raising the estimate of functional human sequences," *Genome Research* 17 (2007): 1245–1253. Freely accessible (2011) at <http://genome.cshlp.org/content/17/9/1245.full.pdf+html>
 24. Ewan Birney, John A. Stamatoyannopoulos, Anindya Dutta, Roderic Guigó, Thomas R. Gingeras, Elliott H. Margulies, Zhiping Weng, Michael Snyder, Emmanouil T. Dermitzakis, Robert E. Thurman, Michael S. Kuehn, Christopher M. Taylor, Shane Neph, Christoph M. Koch, Saurabh Asthana, Ankit Malhotra, Ivan Adzhubei, Jason A. Greenbaum, Robert M. Andrews, Paul Flicek, Patrick J. Boyle, Hua Cao, Nigel P. Carter, Gayle K. Clelland, Sean Davis, Nathan Day, Pawandeep Dhami, Shane C. Dillon, Michael O. Dorschner, Heike Fiegler, Paul G. Giresi, Jeff Goldy, Michael Hawrylycz, Andrew Haydock, Richard Humbert, Keith D. James, Brett E. Johnson, Ericka M. Johnson, Tristan T. Frum, Elizabeth R. Rosenzweig, Neerja Karnani, Kirsten Lee, Gregory C. Lefebvre, Patrick A. Navas, Fidencio Neri, Stephen C. J. Parker, Peter J. Sabo, Richard Sandstrom, Anthony Shafer, David Vetrie, Molly Weaver, Sarah Wilcox, Man Yu, Francis S. Collins, Job Dekker, Jason D. Lieb, Thomas D. Tullius, Gregory E. Crawford, Shamil Sunayev, William S. Noble, Ian Dunham, France Denoeud, Alexandre Reymond, Philipp Kapranov, Joel Rozowsky, Deyou Zheng, Robert Castelo, Adam Frankish, Jennifer Harrow, Srinka Ghosh, Albin Sandelin, Ivo L. Hofacker, Robert Baertsch, Damian Keefe, Sujit Dike, Jill Cheng, Heather A. Hirsch, Edward A. Sekinger, Julien Lagarde, Josep F. Abril, Atif Shahab, Christoph Flamm, Claudia Fried, Jörg Hack-

- ermüller, Jana Hertel, Manja Lindemeyer, Kristin Missal, Andrea Tanzer, Stefan Washietl, Jan Korbel, Olof Emanuelsson, Jakob S. Pedersen, Nancy Holroyd, Ruth Taylor, David Swarbreck, Nicholas Matthews, Mark C. Dickson, Daryl J. Thomas, Matthew T. Weirauch, James Gilbert, Jorg Drenkow, Ian Bell, XiaoDong Zhao, K. G. Srinivasan, Wing-Kin Sung, Hong Sain Ooi, Kuo Ping Chiu, Sylvain Foissac, Tyler Alioto, Michael Brent, Lior Pachter, Michael L. Tress, Alfonso Valencia, Siew Woh Choo, Chiou Yu Choo, Catherine Ucla, Caroline Manzano, Carine Wyss, Evelyn Cheung, Taane G. Clark, James B. Brown, Madhavan Ganesh, Sandeep Patel, Hari Tammana, Jacqueline Chrast, Charlotte N. Henriksen, Chikatoshi Kai, Jun Kawai, Ugrappa Nagalakshmi, Jiaqian Wu, Zheng Lian, Jin Lian, Peter Newburger, Xueqing Zhang, Peter Bickel, John S. Mattick, Piero Carninci, Yoshihide Hayashizaki, Sherman Weissman, Tim Hubbard, Richard M. Myers, Jane Rogers, Peter F. Stadler, Todd M. Lowe, Chia-Lin Wei, Yijun Ruan, Kevin Struhl, Mark Gerstein, Stylianos E. Antonarakis, Yutao Fu, Eric D. Green, Ulaf Karöz, William S. Noble, Alexandre Reymond, Adam Siepel, James Taylor, Thomas D. Tullius, Laura A. Liefer, Kris A. Wetterstrand, Peter J. Good, Elise A. Feingold, Mark S. Guyer, Gregory M. Cooper, George Asimenos, Daryl J. Thomas, Colin N. Dewey, Minmei Hou, Sergey Nikolaev, Juan I. Montoya-Burgos, Ari Löytynoja, Simon Whelan, Fabio Pardi, Tim Massingham, Haiyan Huang, Nancy R. Zhang, Ian Holmes, James C. Mullikin, Abel Ureta-Vidal, Benedict Paten, Michael Seringhaus, Deanna Church, Kate Rosenbloom, W. James Kent, Serafim Batzoglou, Nick Goldman, Ross C. Hardison, David Haussler, Webb Miller, Lior Pachter, Arend Sidow, Gerard G. Bouffard, Xiaobin Guan, Nancy F. Hansen, Jacquelyn R. Idol, Valerie V.B. Maduro, Baishali Maskeri, Jennifer C. McDowell, Morgan Park, Pamela J. Thomas, Alice C. Young, Robert W. Blakesley, Donna M. Muzny, Erica Sodergren, David A. Wheeler, Kim C. Worley, Huaiyang Jiang, George M. Weinstock, Richard A. Gibbs, Tina Graves, Robert Fulton, Elaine R. Mardis, Richard K. Wilson, Michele Clamp, James Cuff, Sante Gnerre, David B. Jaffe, Jean L. Chang, Kerstin Lindblad-Toh, Eric S. Lander, Maxim Koriabine, Mikhail Nefedov, Kazutoyo Osoegawa, Yuko Yoshinaga, Baoli Zhu, Pieter J. de Jong, Nathan D. Trinklein, Zhengdong D. Zhang, Leah Barrera, Rhona Stuart, David C. King, Adam Ameur, Stefan Enroth, Mark C. Bieda, Chia-Lin Wei, Jonghwan Kim, Akshay A. Bhinge, Paul G. Giresi, Nan Jiang, Jun Liu, Fei Yao, Wing-Kin Sung, Kuo Ping Chiu, Vinsensius B. Vega, Charlie W.H. Lee, Patrick Ng, Atif Shahab, Edward A. Sekinger, Annie Yang, Zarmik Moqtaderi, Zhou Zhu, Xiaoqin Xu, Sharon Squazzo, Matthew J. Oberley, David Inman, Michael A. Singer, Todd A. Richmond, Kyle J. Munn, Alvaro Rada-Iglesias, Ola Wallerman, Jan Komorowski, Gayle K. Clelland, Robert M. Andrews, Joanna C. Fowler, Phillippe Couttet, Keith D. James, Gregory C. Lefebvre, Alexander W. Bruce, Oliver M. Dovey, Peter D. Ellis, Pawandeep Dhami, Cordelia F. Langford, Nigel P. Carter, David Vetrie, David A. Nix, Ian Bell, Ghia Euskirchen, Stephen Hartman, Jiaqian Wu, Alexander E. Urban, Peter Kraus, Sara Van Calcar, Nate Heintzman, Tae Hoon Kim, Kun Wang, Chunxu Qu, Gary Hon, Rosa Luna, Christopher K. Glass, M. Geoff Rosenfeld, Shelley Force Aldred, Sara J. Cooper, Anason Halees, Jane M. Lin, Hennady P. Shulha, Xiaoling Zhang, Mousheng Xu, Jaafar N. S. Haidar, Yong Yu, Sherman Weissman, Yijun Ruan, Jason D. Lieb, Vishwanath R. Iyer, Roland D. Green, Claes Wadelius, Ian Dunham, Peggy J. Farnham, Bing Ren, Rachel A. Harte, Angie S. Hinrichs, Heather Trumbower, Hiram Clawson, Jennifer Hillman-Jack-

- son, Ann S. Zweig, Kayla Smith, Archana Thakkapallayil, Galt Barber, Robert M. Kuhn, Donna Karolchik, W. James Kent, Lluís Armengol, Christine P. Bird, Taane G. Clark, Paul I. W. de Bakker, Andrew D. Kern, Nuria Lopez-Bigas, Joel D. Martin, Barbara E. Stranger, Abigail Woodroffe, Serafim Batzoglou, Eugene Davydov, Antigone Dimas, Eduardo Eyras, Ingileif B. Hallgrímsson, Julian Huppert, Heather Trumbower, Michael C. Zody, James C. Mullikin, Gonçalo R. Abecasis & Xavier Estivill, "Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project," *Nature* 447 (2007): 799–816. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2212820/pdf/nihms27513.pdf>
25. Naoki Osato, Hitomi Yamada, Kouji Satoh, Hisako Ooka, Makoto Yamamoto, Kohji Suzuki, Jun Kawai, Piero Carninci, Yasuhiro Ohtomo, Kazuo Murakami, Kenichi Matsubara, Shoshi Kikuchi & Yoshihide Hayashizaki, "Antisense transcripts with rice full-length cDNAs," *Genome Biology* 5:1 (2003): R5. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2003-5-1-r5.pdf>
26. S. Katayama, Y. Tomaru, T. Kasukawa, K. Waki, M. Nakanishi, M. Nakamura, H. Nishida, C. C. Yap, M. Suzuki, J. Kawai, H. Suzuki, P. Carninci, Y. Hayashizaki, C. Wells, M. Frith, T. Ravasi, K. C. Pang, J. Hallinan, J. Mattick, D. A. Hume, L. Lipovich, S. Batalov, P. G. Engström, Y. Mizuno, M. A. Faghihi, A. Sandelin, A. M. Chalk, S. Mottagui-Tabar, Z. Liang, B. Lenhard & C. Wahlestedt, "Antisense Transcription in the Mammalian Transcriptome," *Science* 309 (2005): 1564–1566.
27. Pär G. Engström, Harukazu Suzuki, Noriko Ninomiya, Altuna Akalin, Luca Sessa, Giovanni Lavorgna, Alessandro Brozzi, Lucilla Luzi, Sin Lam Tan, Liang Yang, Galih Kurnarso, Edwin Lian-Chong Ng, Serge Batalov, Claes Wahlestedt, Chikatoshi Kai, Jun Kawai, Piero Carninci, Yoshihide Hayashizaki, Christine Wells, Vladimir B. Bajic, Valerio Orlando, James F. Reid, Boris Lenhard & Leonard Lipovich, "Complex Loci in Human and Mouse Genomes," *PLoS Genetics* 2:4 (2006): e47. Freely accessible (2011) at <http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.0020047>
28. Yiping He, Bert Vogelstein, Victor E. Velculescu, Nickolas Papadopoulos & Kenneth W. Kinzler, "The Antisense Transcriptomes of Human Cells," *Science* 322 (2008): 1855–1857.
29. Kevin V. Morris, Sharon Santoso, Anne-Marie Turner, Chiara Pastori, Peter G. Hawkins, "Bidirectional Transcription Directs Both Transcriptional Gene Activation and Suppression in Human Cells," *PLoS Genetics* 4:11 (2008): e1000258. Freely accessible (2011) at <http://www.plosgenetics.org/article/info:doi%2F10.1371%2Fjournal.pgen.1000258>
30. Stefano Gustincich, Albin Sandelin, Charles Plessy, Shintaro Katayama, Roberto Simone, Dejan Lazarevic, Yoshihide Hayashizaki & Piero Carninci, "The complexity of the mammalian transcriptome," *Journal of Physiology* 575:2 (2006): 321–332. Freely accessible (2011) at <http://jp.physoc.org/content/575/2/321.full.pdf+html>
31. Philipp Kapranov, Aaron T. Willingham & Thomas R. Gingeras, "Genome-wide transcription and the implications for genomic organization," *Nature Reviews Genetics* 8 (2007): 413–423.
32. Piero Carninci, "Constructing the landscape of the mammalian transcriptome," *Journal of Experimental Biology* 210 (2007): 1497–1506. Freely accessible (2011) at <http://jeb.biologists.org/cgi/reprint/210/9/1497>
33. Jia Qian Wu, Jiang Du, Joel Rozowsky, Zhengdong Zhang, Alexander E. Urban,

- Ghia Euskirchen, Sherman Weissman, Mark Gerstein & Michael Snyder, "Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome," *Genome Biology* 9:1 (2008): R3. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2008-9-1-r3.pdf>
34. Gill Bejerano, Michael Pheasant, Igor Makunin, Stuart Stephen, W. James Kent, John S. Mattick & David Haussler, "Ultraconserved Elements in the Human Genome," *Science* 304 (2004): 1321–1325.
35. Albin Sandelin, Peter Bailey, Sara Bruce, Pär G. Engström, Joanna M Klos, Wyeth W. Wasserman, Johan Ericson & Boris Lenhard, "Arrays of ultraconserved non-coding regions span the loci of key developmental genes in vertebrate genomes," *BMC Genomics* 5 (2004): 99. Freely accessible (2011) at <http://www.biomedcentral.com/1471-2164/5/99>
36. Adam Woolfe, Martin Goodson, Debbie K. Goode, Phil Snell, Gayle K. McEwen, Tanya Vavouri, Sarah F. Smith, Phil North, Heather Callaway, Krys Kelly, Klaudia Walter, Irina Abnizova, Walter Gilks, Yvonne J. K. Edwards, Julie E. Cooke & Greg Elgar, "Highly Conserved Non-coding Sequences Are Associated with Vertebrate Development," *PLoS Biology* 3:1 (2005): e7. Freely accessible (2011) at <http://www.plosbiology.org/article/info%3Adoi%2F10.1371%2Fjournal.pbio.0030007>
37. Adam Siepel, Gill Bejerano, Jakob S. Pedersen, Angie S. Hinrichs, Minmei Hou, Kate Rosenbloom, Hiram Clawson, John Spieth, LaDeana W. Hillier, Stephen Richards, George M. Weinstock, Richard K. Wilson, Richard A. Gibbs, W. James Kent, Webb Miller & David Haussler, "Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes," *Genome Research* 15 (2005): 1034–1050. Freely accessible (2011) at <http://genome.cshlp.org/content/15/8/1034.full.pdf+html>
38. Gil Bejerano, "Ultraconservation and the Human Genome Regulatory Landscape," Lecture at Stanford University (April 15, 2009). Freely accessible (2011) at <http://video.google.com/videoplay?docid=8213646681956800413#>
39. John A. Bernat, Gregory E. Crawford, Aleksey Y. Ogurtsov, Francis S. Collins, David Ginsburg & Alexey S. Kondrashov, "Distant conserved sequences flanking endothelial-specific promoters contain tissue-specific DNase-hypersensitive sites and over-represented motifs," *Human Molecular Genetics* 15 (2006): 2098–2105. Freely accessible (2011) at <http://hmg.oxfordjournals.org/cgi/reprint/15/13/2098>
40. Tanya Vavouri, Klaudia Walter, Walter R Gilks, Ben Lehner and Greg Elgar, "Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans," *Genome Biology* 8:2 (2007): R15. Freely accessible (2011) at <http://genome-biology.com/2007/8/2/R15>
41. Jasmina Ponjavic, Chris P. Ponting & Gerton Lunter, "Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs," *Genome Research* 17 (2007): 556–565. Freely accessible (2011) at <http://genome.cshlp.org/content/17/5/556.full.pdf+html>
42. Mitchell Guttman, Ido Amit, Manuel Garber, Courtney French, Michael F. Lin, David Feldser, Maite Huarte, Or Zuk, Bryce W. Carey, John P. Cassady, Moran N. Cabili, Rudolf Jaenisch, Tarjei S. Mikkelsen, Tyler Jacks, Nir Hacohen, Bradley E. Bernstein, Manolis Kellis, Aviv Regev, John L. Rinn & Eric S. Lander, "Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals," *Nature* 458 (2009): 223–227. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2754849/?tool=pubmed>

43. Maciej Szymanski, Mirosława Z. Barciszewska, Marek Zywicki & Jan Barciszewski, "Noncoding RNA transcripts," *Journal of Applied Genetics* 44 (2003): 1–19. Freely accessible (2011) at http://jag.igr.poznan.pl/2003-Volume-44/1/pdf/2003_Volume_44_1-1-19.pdf
44. John S. Mattick & Igor V. Makunin, "Non-coding RNA," *Human Molecular Genetics* 15 (2006): R17–R29. Freely accessible (2011) at http://hmg.oxfordjournals.org/cgi/reprint/15/suppl_1/R17
45. Luis M. Mendes Soares & Juan Valcárcel, "The expanding transcriptome: the genome as the 'Book of Sand,'" *EMBO Journal* 25 (2006): 923–931. Available online with registration (2011) at <http://www.nature.com/emboj/journal/v25/n5/full/7601023a.html>
46. John L. Rinn, Michael Kertesz, Jordon K. Wang, Sharon L. Squazzo, Xiao Xu, Samantha A. Bruggmann, Henry Goodnough, Jill A. Helms, Peggy J. Farnham, Eran Segal & Howard Y. Chang, "Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Non-Coding RNAs," *Cell* 129 (2007): 1311–1323. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2084369/?tool=pubmed>
47. Gennadi V. Glinsky, "Phenotype-defining functions of multiple non-coding RNA pathways," *Cell Cycle* 7 (2008): 1630–1639. Freely accessible (2011) at <http://www.landesbioscience.com/journals/cc/article/5976/>
48. Eugene V. Makeyev & Tom Maniatis, "Multilevel Regulation of Gene Expression by MicroRNAs," *Science* 319 (2008): 1789–1790
49. Paulo P. Amaral, Marcel E. Dinger, Tim R. Mercer & John S. Mattick, "The Eukaryotic Genome as an RNA Machine," *Science* 319 (2008): 1787–1789.
50. Tim R. Mercer, Marcel E. Dinger, Susan M. Sunkin, Mark F. Mehler & John S. Mattick, "Specific expression of long noncoding RNAs in the mouse brain," *Proceedings of the National Academy of Sciences USA* 105 (2008): 716–721. Freely accessible (2011) at <http://www.pnas.org/content/105/2/716.full.pdf+html>
51. Johannes H. Urban & Jörg Vogel, "Two Seemingly Homologous Noncoding RNAs Act Hierarchically to Activate glmS mRNA Translation," *PLoS Biology* 6:3 (2008): e64. Freely accessible (2011) at <http://www.plosbiology.org/article/info%3Adoi%2F10.1371%2Fjournal.pbio.0060064>
52. Piero Carninci, Jun Yasuda & Yoshihide Hayashizaki, "Multifaceted mammalian transcriptome," *Current Opinion in Cell Biology* 20 (2008): 274–280.
53. Archa H. Fox, Yun Wah Lam, Anthony K. L. Leung, Carol E. Lyon, Jens Andersen, Matthias Mann & Angus I. Lamond, "Paraspeckles: a novel nuclear domain," *Current Biology* 12 (2002): 13–25. Freely accessible (2011) at <http://www.cell.com/current-biology/retrieve/pii/S0960982201006327>
54. Charles S. Bond & Archa H. Fox, "Paraspeckles: nuclear bodies built on long noncoding RNA," *Journal of Cell Biology* 186 (2009): 637–644. Freely accessible (2011) at <http://jcb.rupress.org/content/186/5/637.full.pdf+html>
55. Archa H. Fox & Angus I. Lamond, "Paraspeckles," *Cold Spring Harbor Perspectives in Biology* 2 (2010): a000687. Freely accessible (2011) at <http://cshperspectives.cshlp.org/content/2/7/a000687.full.pdf+html>
56. Christine M. Clemson, John N. Hutchinson, Sergio A. Sara, Alexander W. Ensminger, Archa H. Fox, Andrew Chess & Jeanne B. Lawrence, "An architectural role for a nuclear noncoding RNA: NEAT1 RNA is essential for the structure of paraspeckles," *Molecular Cell* 33 (2009): 717–726. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/>

- pmc/articles/PMC2696186/pdf/nihms106615.pdf
57. Yasnory T. F. Sasaki, Takashi Ideue, Miho Sano, Toutai Mituyama & Tetsuro Hirose, "MEN ϵ / β noncoding RNAs are essential for structural integrity of nuclear paraspeckles," *Proceedings of the National Academy of Sciences USA* 106 (2009): 2525–2530. Freely accessible (2011) at <http://www.pnas.org/content/106/8/2525.full.pdf+html>
 58. Yasnory T. F. Sasaki & Tetsuro Hirose, "How to build a paraspeckle," *Genome Biology* 10 (2009): 227. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2009-10-7-227.pdf>
 59. Sylvie Souquere, Guillaume Beauclair, Francis Harper, Archa Fox & Gérard Pieron, "Highly-ordered spatial organization of the structural long noncoding NEAT1 RNAs within paraspeckle nuclear bodies," *Molecular Biology of the Cell* (September 2010). Freely accessible (2011) at <http://www.molbiolcell.org/cgi/reprint/E10-08-0690v1>
 60. Marcel E. Dinger, Paulo P. Amaral, Timothy R. Mercer & John S. Mattick, "Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications," *Briefings in Functional Genomics and Proteomics* 8 (2009): 407–423.
 61. Jeremy E. Wilusz, Hongjae Sunwoo & David L. Spector, "Long noncoding RNAs: functional surprises from the RNA world," *Genes & Development* 23 (2009): 1494–1504. Freely accessible (2011) at <http://genesdev.cshlp.org/content/23/13/1494.full.pdf+html>
 62. Jeannie T. Lee, "Lessons from X-chromosome inactivation: long ncRNA as guides and tethers to the epigenome," *Genes & Development* 23 (2009): 1831–1842. Freely accessible (2011) at <http://genesdev.cshlp.org/content/23/16/1831.full.pdf+html>
- #### 4. INTRONS AND THE SPLICING CODE
1. Stuart E. Leff, Michael G. Rosenfeld & Ronald M. Evans, "Complex transcriptional units: diversity in gene expression by alternative RNA processing," *Annual Review of Biochemistry* 55 (1986): 1091–1117.
 2. Richard A. Padgett, Paula J. Grabowski, Maria M. Konarska, Sharon Seiler & Philip A. Sharp, "Splicing of messenger RNA precursors," *Annual Review of Biochemistry* 55 (1986): 1119–1150.
 3. Tom Maniatis & Bosiljka Tasic, "Alternative pre-mRNA splicing and proteome expansion in metazoans," *Nature* 418 (2002): 236–243.
 4. Qun Pan, Ofer Shai, Leo J. Lee, Brendan J. Frey & Benjamin J. Blencowe, "Deep surveying of alternative splicing complexity in the human transcriptome by high-throughput sequencing," *Nature Genetics* 40 (2008): 1413–1415.
 5. Eric T. Wang, Rickard Sandberg, Shujun Luo, Irina Khrebukova, Lu Zhang, Christine Mayr, Stephen F. Kingsmore, Gary P. Schroth & Christopher B. Burge, "Alternative isoform regulation in human tissue transcriptomes," *Nature* 456 (2008): 470–476. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2593745/pdf/nihms-72491.pdf>
 6. Marc Sultan, Marcel H. Schulz, Hugues Richard, Alon Magen, Andreas Klingenhoff, Matthias Scherf, Martin Seifert, Tatjana Borodina, Aleksey Soldatov, Dmitri Parkhomchuk, Dominic Schmidt, Sean O'Keeffe, Stefan Haas, Martin Vingron, Hans Lehrach & Marie-Laure Yaspo, "A Global View of Gene Activity and Alternative Splicing by Deep Sequencing of the Human Transcriptome," *Science* 321 (2008): 956–960. Available online with registration (2011) at <http://www.sciencemag.org/content/321/5891/956.short>
 7. Timothy W. Nilsen & Brenton R. Graveley, "Expansion of the eukaryotic proteome

- by alternative splicing," *Nature* 463 (2010): 457–463.
8. Kevin P. Rosenblatt, Zhong-Ping Sun, Stefan Heller & A. J. Hudspeth, "Distribution of Ca^{2+} -activated K^+ channel isoforms along the tonotopic gradient of the chicken's cochlea," *Neuron* 19 (1997): 1061–1075.
 9. Dhasakumar S. Navaratnam, Thomas J. Bell, Tu Dinh Tu, Erik L. Cohen & J. Carl Oberholtzer, "Differential distribution of Ca^{2+} -activated K^+ channel splice variants among hair cells along the tonotopic axis of the chick cochlea," *Neuron* 19 (1997): 1077–1085.
 10. Dietmar Schmucker, James C. Clemens, Huidy Shu, Carolyn A. Worby, Jian Xiao, Marco Muda, Jack E. Dixon & S. Lawrence Zipursky, "*Drosophila* Dscam is an axon guidance receptor exhibiting extraordinary molecular diversity," *Cell* 101 (2000): 671–684.
 11. Kerry Kornfeld, Robert B. Saint, Philip A. Beachy, Peter J. Harte, Debra A. Peattie & David S. Hogness, "Structure and expression of a family of *Ultrabithorax* mRNAs generated by alternative splicing and polyadenylation in *Drosophila*," *Genes & Development* 3 (1989): 243–258. Freely accessible (2011) at <http://genesdev.cshlp.org/content/3/2/243.long>
 12. K. Moriarty, K. H. Kim and J. R. Bender, "Minireview: Estrogen Receptor-Mediated Rapid Signaling," *Endocrinology* 147 (2006): 5557–5563. Freely accessible (2011) at <http://endo.endojournals.org/cgi/reprint/147/12/5557>
 13. Benjamin J. Blencowe, "Alternative splicing: new insights from global analyses," *Cell* 126 (2006): 37–47.
 14. Alison Jane Tyson-Capper, "Alternative splicing: an important mechanism for myometrial gene regulation that can be manipulated to target specific genes associated with preterm labour," *BMC Pregnancy Childbirth* 7 Supplement 1 (2007): S13. Freely accessible (2011) at <http://www.biomedcentral.com/content/pdf/1471-2393-7-S1-S13.pdf>
 15. Stefan Hoppler & Claire Louise Kavanagh, "Wnt signalling: variety at the core," *Journal of Cell Science* 120 (2007): 385–93. Freely accessible (2011) at <http://jcs.biologists.org/cgi/reprint/120/3/385>
 16. Antonino Belfiore, Francesco Frasca, Giuseppe Pandini, Laura Sciacca & Riccardo Vigneri, "Insulin Receptor Isoforms and Insulin Receptor/Insulin-like Growth Factor Receptor Hybrids in Physiology and Disease," *Endocrine Reviews* 30 (2009): 586–623. Freely accessible (2011) at <http://edrv.endojournals.org/cgi-reprint/30/6/586>
 17. Ludmila Prokunina-Olsson, Cullan Welch, Ola Hansson, Neeta Adhikari, Laura J. Scott, Nicolle Usher, Maurine Tong, Andrew Sprau, Amy Swift, Lori L. Bonnycastle, Michael R. Erdos, Zhi He, Richa Saxena, Brennan Harmon, Olga Kotova, Eric P. Hoffman, David Altshuler, Leif Groop, Michael Boehnke, Francis S. Collins & Jennifer L. Hall, "Tissue-specific alternative splicing of *TCF7L2*," *Human Molecular Genetics* 18 (2009): 3795–3804. Freely accessible (2011) at <http://hmg.oxfordjournals.org/cgi-reprint/18/20/3795>
 18. Chiharu Sogawa, Chieko Mitsuhashi, Kei Kumagai-Morioka, Norio Sogawa, Kazumi Ohyama, Katsuya Morita, Katsuyuki Kozai, Toshihiro Dohi & Shigeo Kitayama, "Expression and Function of Variants of Human Catecholamine Transporters Lacking the Fifth Transmembrane Region Encoded by Exon 6," *PLoS One* 5:8 (2010): e11945. Freely accessible (2011) at <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0011945>
 19. Anna Kuta, Wenhan Deng, Ali Morsi El-Kadi, Gareth T. Banks, Majid Hafezparast, K. Kevin Pfister & Elizabeth M. C. Fisher, "Mouse Cytoplasmic Dynein Intermediate Chains: Identification of New

- Isoforms, Alternative Splicing and Tissue Distribution of Transcripts,” *PLoS One* 5:7 (2010): e11682. Freely accessible (2011) at <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0011682>
20. Ahmet Ucar, Vida Vafaizadeh, Hubertus Jarry, Jan Fiedler, Petra A. B. Klemmt, Thomas Thum, Bernd Groner & Kamal Chowdhury, “miR-212 and miR-132 are required for epithelial stromal interactions necessary for mouse mammary gland development,” *Nature Genetics* 42 (2010): 1101–1108.
 21. Tim R. Mercer, Marcel E. Dinger, Cameron P. Bracken, Gabriel Kolle, Jan M. Szubert, Darren J. Korbie, Marjan E. Askarian-Amiri, Brooke B. Gardiner, Gregory J. Goodall, Sean M. Grimmond & John S. Mattick, “Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome,” *Genome Research* 20 (2010): 1639–1650.
 22. Vidisha Tripathi, Jonathan D. Ellis, Zhen Shen, David Y. Song, Qun Pan, Andrew T. Watt, Susan M. Freier, C. Frank Bennett, Alok Sharma, Paula A. Bubulya, Benjamin J. Blencowe, Supriya G. Prasanth & Kannanganattu V. Prasanth, “The nuclear-retained noncoding RNA MALAT1 regulates alternative splicing by modulating SR splicing factor phosphorylation,” *Molecular Cell* 39 (2010): 925–938.
 23. Rotem Sorek & Gil Ast, “Intronic Sequences Flanking Alternatively Spliced Exons Are Conserved between Human and Mouse,” *Genome Research* 13 (2003): 1631–1637. Freely accessible (2011) at <http://genome.cshlp.org/content/13/7/1631.full.pdf+html>
 24. Simon Minovitsky, Sherry L. Gee, Shiruyeh Schokrpur, Inna Dubchak & John G. Conboy, “The splicing regulatory element, UGCAUG, is phylogenetically and spatially conserved in introns that flank tissue-specific alternative exons,” *Nucleic Acids Research* 33 (2005): 714–724. Freely accessible (2011) at <http://nar.oxfordjournals.org/content/33/2/714.full.pdf+html>
 25. Charles W. Sugnet, Karpagam Srinivasan, Tyson A. Clark, Georgeann O’Brien, Melissa S. Cline, Hui Wang, Alan Williams, David Kulp, John E. Blume, David Haussler & Manuel Ares Jr., “Unusual Intron Conservation near Tissue-regulated Exons Found by Splicing Microarrays,” *PLoS Computational Biology* 2:1 (2006): e4. Freely accessible (2011) at <http://www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.0020004>
 26. Andrea N. Ladd and Thomas A. Cooper, “Finding signals that regulate alternative splicing in the post-genomic era,” *Genome Biology* 3:11 (2002): reviews0008. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2002-3-11-reviews0008.pdf>
 27. Jingyi Hui, Lee-Hsueh Hung, Monika Heiner, Silke Schreiner, Norma Neumüller, Gregor Reither, Stefan A Haas & Albrecht Bindereif, “Intronic CA-repeat and CA-rich elements: a new class of regulators of mammalian alternative splicing,” *EMBO Journal* 24 (2005): 1988–1998. Freely accessible (2011) at <http://www.nature.com/emboj/journal/v24/n11/pdf/7600677a.pdf>
 28. Helder I. Nakaya, Paulo P. Amaral, Rodrigo Louro, André Lopes, Angela A. Fachel, Yuri B. Moreira, Tarik A. El-Jundi, Aline M. da Silva, Eduardo M. Reis & Sergio Verjovski-Almeida, “Genome mapping and expression analyses of human intronic noncoding RNAs reveal tissue-specific patterns and enrichment in genes related to regulation of transcription,” *Genome Biology* 8:3 (2007): R43. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1868932/pdf/gb-2007-8-3-r43.pdf>
 29. Michelle L. Hastings, Catherine M. Wilson & Stephen H. Munroe, “A purine-

- rich intronic element enhances alternative splicing of thyroid hormone receptor mRNA," *RNA* 7 (2001): 859–874. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1370135/pdf/11421362.pdf>
30. Shingo Nakahata & Sachiyo Kawamoto, "Tissue-dependent isoforms of mammalian Fox-1 homologs are associated with tissue-specific splicing activities," *Nucleic Acids Research* 33 (2005): 2078–2089. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1075922/pdf/gki338.pdf>
31. Eric J. Wagner, Andrew P. Baraniak, October M. Sessions, David Mauger, Eric Moskowitz & Mariano A. Garcia-Blanco, "Characterization of the Intronic Splicing Silencers Flanking FGFR2 Exon IIIb," *Journal of Biological Chemistry* 280 (2005): 14017–14027. Freely accessible (2011) at <http://www.jbc.org/content/280/14/14017.full.pdf+html>
32. Roberto Marcucci, Francisco E. Baralle & Maurizio Romano, "Complex splicing control of the human Thrombopoietin gene by intronic G runs," *Nucleic Acids Research* 35 (2007): 132–142. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1802585/pdf/gkl965.pdf>
33. Zefeng Wang & Christopher B. Burge, "Splicing regulation: from a parts list of regulatory elements to an integrated splicing code," *RNA* 14 (2008): 802–813. Freely accessible (2011) at <http://rnajournal.cshlp.org/content/14/5/802.full.pdf+html>
34. John W. S. Brown, David F. Marshall & Manuel Echeverria, "Intronic noncoding RNAs and splicing," *Trends in Plant Science* 13 (2008): 335–342.
35. Ji Wen, Akira Chiba & Xiaodong Cai, "Computational identification of tissue-specific alternative splicing elements in mouse genes from RNA-Seq," *Nucleic Acids Research* (August 4, 2010). Freely accessible (2011) at <http://nar.oxfordjournals.org/content/early/2010/08/04/nar.gkq679.full.pdf+html>
36. Shengdong Ke & Lawrence A. Chasin, "Intronic motif pairs cooperate across exons to promote pre-mRNA splicing," *Genome Biology* 11 (2010): R84. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2010-11-8-r84.pdf>
37. Yoseph Barash, John A. Calarco, Weijun Gao, Qun Pan, Xinchun Wang, Ofer Shai, Benjamin J. Blencowe & Brendan J. Frey "Deciphering the splicing code," *Nature* 465 (2010): 53–59.
38. Amir Ali Abbasi, Zissis Paparidis, Sajid Malik, Debbie K. Goode, Heather Callaway, Greg Elgar & Karl-Heinz Grzeschik, "Human GLI3 Intragenic Conserved Non-Coding Sequences Are Tissue-Specific Enhancers," *PLoS One* 2:4 (2007): e366. Freely accessible (2011) at <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0000366>
39. Rodrigo Louro, Tarik El-Jundi, Helder I. Nakaya, Eduardo M. Reis & Sergio Verjovski-Almeida, "Conserved tissue expression signatures of intronic noncoding RNAs transcribed from human and mouse loci," *Genomics* 92 (2008): 18–25.
40. Marc P. Hoepfner, Simon White, Daniel C. Jeffares & Anthony M. Poole, "Evolutionarily Stable Association of Intronic snoRNAs and microRNAs with Their Host Genes," *Genome Biology and Evolution* 2009 (2009): 420–428. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2817437/pdf/evp045.pdf>
41. Luis M. Mendes Soares & Juan Valcárcel, "The expanding transcriptome: the genome as the 'Book of Sand,'" *EMBO Journal* 25 (2006): 923–931. Available online with registration (2011) at <http://www.nature.com/emboj/journal/v25/n5/full/7601023a.html>

42. Antony Rodriguez, Sam Griffiths-Jones, Jennifer L. Ashurst & Allan Bradley, "Identification of Mammalian MicroRNA Host Genes and Transcription Units," *Genome Research* 14 (2004): 1902–1910. Freely accessible (2011) at <http://genome.cshlp.org/content/14/10a/1902.full.pdf+html>
43. Scott Baskerville & David P. Bartel, "Microarray profiling of microRNAs reveals frequent coexpression with neighboring miRNAs and host genes," *RNA* 11 (2005): 241–247. Freely accessible (2011) at <http://rnajournal.cshlp.org/content/11/3/241.full.pdf+html>
44. Young-Kook Kim & V. Narry Kim, "Processing of intronic microRNAs," *EMBO Journal* 26 (2007): 775–783. Freely accessible (2011) at <http://www.nature.com/emboj/journal/v26/n3/pdf/7601512a.pdf>
45. S. Hani Najafi-Shoushtari, Fjoralba Kristo, Yingxia Li, Toshi Shioda, David E. Cohen, Robert E. Gerszten & Anders M. Näär, "MicroRNA-33 and the SREBP Host Genes Cooperate to Control Cholesterol Homeostasis," *Science* 328 (2010): 1566–1569.
46. Alex Mas Monteys, Ryan M. Spengler, Ji Wan, Luis Tecedor, Kimberly A. Lennox, Yi Xing & Beverly L. Davidson, "Structure and activity of putative intronic miRNA promoters," *RNA* 16 (2010): 495–505. Freely accessible (2011) at <http://rnajournal.cshlp.org/content/16/3/495.long>
47. Michael Bulger & Mark Groudine, "Enhancers: The abundance and function of regulatory sequences beyond promoters," *Developmental Biology* 339 (2010): 250–257.
48. Shawn P. Grogan, Tsaiwei Olee, Koji Hiraoka & Martin K. Lotz, "Repression of Chondrogenesis through Binding of Notch Signaling Proteins HES-1 and HEY-1 to N-box Domains in the COL2A1 Enhancer Site," *Arthritis & Rheumatism* 58 (2008): 2754–2763. Freely accessible (2011) at <http://www.interscience.wiley.com/cgi-bin/fulltext/121391302/PDF-START>
49. Christopher J. Ott, Neil P. Blackledge, Jenny L. Kerschner, Shih-Hsing Leir, Gregory E. Crawford, Calvin U. Cotton & Ann Harris, "Intronic enhancers coordinate epithelial-specific looping of the active CFTR locus," *Proceedings of the National Academy of Sciences USA* 106 (2009): 19934–19939. Freely accessible (2011) at <http://www.pnas.org/content/106/47/19934.full.pdf+html>
50. Hani Alotaibi, Elif Yaman, Domenico Salvatore, Valeria Di Dato, Pelin Telkoparan, Roberto Di Lauro & Uygar H. Tazebay, "Intronic elements in the Na⁺/I symporter gene (NIS) interact with retinoic acid receptors and mediate initiation of transcription," *Nucleic Acids Research* 38 (2010): 3172–3185. Freely accessible (2011) at <http://nar.oxfordjournals.org/cgi/reprint/38/10/3172>
51. Eric I. Campos & Danny Reinberg, "Histones: annotating chromatin," *Annual Review of Genetics* 43 (2009): 559–599.
52. Natalia Soshnikova & Denis Duboule, "Epigenetic Temporal Control of Mouse Hox Genes in Vivo," *Science* 324 (2009): 1320–1323. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/324/5932/1320>
53. M. R. Hübner & D. L. Spector, "Chromatin dynamics," *Annual Review of Biophysics* 39 (2010): 471–489.
54. S. A. Lavrov & M. V. Kibanov, "Noncoding RNAs and Chromatin Structure," *Biochemistry (Moscow)* 72 (2007): 1422–1438. Freely accessible (2011) at http://protein.bio.msu.ru/biokhimiya/contents/v72/pdf/bcm_1422.pdf
55. Antonio Rodríguez-Campos & Fernando Azorín, "RNA Is an Integral Component of Chromatin that Contributes to Its Structural Organization," *PLoS One* 2:11 (2007): e1182. Freely accessible (2011) at <http://www.plosone.org/article/>

info%3Adoi%2F10.1371%2Fjournal.pone.0001182

56. Barbora Malecová & Kevin V Morris, "Transcriptional gene silencing through epigenetic changes mediated by non-coding RNAs," *Current Opinion in Molecular Therapeutics* 12 (2010): 214–222. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2861437/pdf/nihms195819.pdf>
 57. Daniel P. Caley, Ryan C. Pink, Daniel Trujillano & David R. F. Carter, "Long noncoding RNAs, chromatin, and development," *ScientificWorldJournal* 10 (2010): 90–102.
 58. Tanmoy Mondal, Markus Rasmussen, Gaurav Kumar Pandey, Anders Isaksson & Chandrasekhar Kanduri, "Characterization of the RNA content of chromatin," *Genome Research* 20 (2010): 899–907. Freely accessible (2011) at <http://genome.cshlp.org/content/20/7/899.full.pdf+html>
 59. W. F. Chen, K. H. Low, C. Lim & I. Edery, "Thermosensitive splicing of a clock gene and seasonal adaptation," *Cold Spring Harbor Symposia on Quantitative Biology* 72 (2007): 599–606.
 60. Dan Xia, Xinxin Huang & Hong Zhang, "The temporally regulated transcription factor sel-7 controls developmental timing in *C. elegans*," *Developmental Biology* 332 (2009): 246–257.
 61. David Gubb, "Intron-Delay and the Precision of Expression of Homeotic Gene Products in *Drosophila*," *Developmental Genetics* 7 (1986): 119–131.
 62. Carl S. Thummel, "Mechanisms of Transcriptional Timing in *Drosophila*," *Science* 255 (1992): 39–40.
 63. Ian A. Swinburne & Pamela A. Silver, "Intron Delays and Transcriptional Timing During Development," *Developmental Cell* 14 (2008): 324–330. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2825037/pdf/nihms176861.pdf>
- ## 5. PSEUDOGENES—NOT SO PSEUDO AFTER ALL
1. C. Jacq, J. R. Miller & G. G. Brownlee, "A pseudogene structure in 5S DNA of *Xenopus laevis*," *Cell* 12 (1977): 109–120.
 2. Nick Proudfoot, "Pseudogenes," *Nature* 286 (1980): 840–841.
 3. C. Deborah Wilde, "Pseudogenes," *Critical Reviews in Biochemistry* 19 (1986): 323–352.
 4. ZhaoLei Zhang & Mark Gerstein, "Large-scale analysis of pseudogenes in the human genome," *Current Opinion in Genetics & Development* 14 (2004): 328–335.
 5. Rajkumar Sasidharan & Mark Gerstein, "Protein fossils live on as RNA," *Nature* 453 (2008): 729–731.
 6. Kenneth R. Miller, *Only a Theory: Evolution and the Battle for America's Soul* (New York: Viking, 2008), pp. 97–98.
 7. Douglas J. Futuyma, *Evolution* (Sunderland, MA: Sinauer Associates, 2005), p. 530.
 8. Jerry A. Coyne, *Why Evolution Is True* (New York: Viking, 2009), pp. 66–67.
 9. Richard Dawkins, *The Greatest Show on Earth: The Evidence for Evolution* (New York: Free Press, 2009), pp. 332–333.
 10. John C. Avise, *Inside the Human Genome: A Case for Non-Intelligent Design* (Oxford: Oxford University Press, 2010), p. 115.
 11. Ilenia D'Errico, Gemma Gadaleta & Cecilia Saccone, "Pseudogenes in metazoa: Origin and features," *Briefings in Functional Genomics and Proteomics* 3 (2004): 157–167. Freely accessible (2011) at <http://bfgp.oxfordjournals.org/cgi/reprint/3/2/157?view=long&pmid=15355597>
 12. Thierry Tchénié, Evelyne Segal-Bendirdjian & Thierry Heidmann, "Generation of processed pseudogenes in murine cells," *EMBO Journal* 12 (1993): 1487–1497. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC413361/pdf/emboj00076-0228.pdf>

13. H.-H. M. Dahl, R. M. Brown, W. M. Hutchison, C. Maragos & G. K. Brown, "A testis-specific form of the human pyruvate dehydrogenase E1 alpha subunit is coded for by an intronless gene on chromosome 4," *Genomics* 8 (1990): 225–232.
14. J. Sorge, E. Gross, C. West & E. Beutler, "High level transcription of the glucocerebrosidase pseudogene in normal subjects and patients with Gaucher disease," *Journal of Clinical Investigation* 86 (1990): 1137–1141. Freely accessible (2011) at <http://www.jci.org/articles/view/114818>
15. I. Tountou, Q. Q. Cai & H. Rochefort, "17 beta Hydroxysteroid dehydrogenase 1 'pseudogene' is differentially transcribed: still a candidate for the breast-ovarian cancer susceptibility gene (BRCA1)," *Biochemical and Biophysical Research Communications* 201 (1994): 1327–1332.
16. Cornelia Schmutzler & Hans J. Gross, "Genes, variant genes, and pseudogenes of the human tRNA^{Val} gene family are differentially expressed in HeLa cells and in human placenta," *Nucleic Acids Research* 18 (1990): 5001–5008. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC332105/pdf/nar00201-0021.pdf>
17. Yasemin Kaçar, Hildburg Beier & Hans J. Gross, "The presence of tRNA pseudogenes in mammalia and plants and their absence in yeast may account for different specificities of pre-tRNA processing enzymes," *Gene* 156 (1995): 129–132.
18. Erich T. Boger, James R. Sellers & Thomas B. Friedman, "Human myosin XVBP is a transcribed pseudogene," *Journal of Muscle Research and Cell Motility* 22 (2001): 477–483.
19. Richard J. Cristiano, Sara J. Giordano & Alan W. Steggle, "The Isolation and Characterization of the Bovine Cytochrome b₅ Gene, and a Transcribed Pseudogene," *Genomics* 17 (1993): 348–354.
20. Rainer Fürbass & Jens Vanselow, "An aromatase pseudogene is transcribed in the bovine placenta," *Gene* 154 (1995): 287–291.
21. D. Aubert, C. Nisanz-Sever & M. Herzog, "Mitochondrial rps14 is a transcribed and edited pseudogene in *Arabidopsis thaliana*," *Plant Molecular Biology* 20 (1992): 1169–1174.
22. V. Quiñones, S. Zanlungo, A. Moenne, I. Gómez, L. Holuigue, S. Litvak & X. Jordana, "The rpl5-rps14-cob gene arrangement in *Solanum tuberosum*: rps14 is a transcribed and unedited pseudogene," *Plant Molecular Biology* 31 (1996) 937–943.
23. Deyou Zheng, Zhaolei Zhang, Paul M. Harrison, John Karro, Nick Carriero & Mark Gerstein, "Integrated pseudogene annotation for human chromosome 22: evidence for transcription," *Journal of Molecular Biology* 349 (2005): 27–45.
24. Paul M. Harrison, Deyou Zheng, Zhaolei Zhang, Nicholas Carriero & Mark Gerstein, "Transcribed processed pseudogenes in the human genome: an intermediate form of expressed retrosequence lacking protein-coding ability," *Nucleic Acids Research* 33 (2005): 2374–2383. Freely accessible (2011) at <http://nar.oxfordjournals.org/cgi/content/full/33/8/2374>
25. Deyou Zheng, Adam Frankish, Robert Baertsch, Philipp Kapranov, Alexandre Reymond, Siew Woh Choo, Yontao Lu, France Denoeud, Stylianos E. Antonarakis, Michael Snyder, Yijun Ruan, Chia-Lin Wei, Thomas R. Gingeras, Roderic Guigó, Jennifer Harrow & Mark B. Gerstein, "Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution," *Genome Research* 17 (2007): 839–851. Freely accessible (2011) at <http://genome.cshlp.org/content/17/6/839.long>
26. Michael J. Chorney, Ikuhisa Swada, Gerald A. Gillespie, Rakesh Srivastava, Julian Pan & Sherman M. Weissman, "Transcription Analysis, Physical Mapping, and

- Molecular Characterization of a Nonclassical Human Leukocyte Antigen Class I Gene," *Molecular and Cellular Biology* 10 (1990): 243–253. Freely accessible (2011) at <http://mcb.asm.org/cgi/reprint/10/1/243?view=long&pmid=2294403>
27. Tuan Nguyen, Roger Sunahara, Adriano Marchese, Hubert H. M. Van Tol, Philip Seeman & Brian F. O'Dowd, "Transcription of a human dopamine D5 pseudogene," *Biochemical and Biophysical Research Communications* 181 (1991): 16–21.
 28. Jonathan A. Bard, Stanley P. Nawoschik, Brian F. O'Dowd, Susan R. George, Theresa A. Branchek & Richard L. Weinshank, "The human serotonin 5-hydroxytryptamine1D receptor pseudogene is transcribed," *Gene* 153 (1995): 295–296.
 29. Christine Pourcel, Jean Jaubert, Michelle Hadchouel, Xue Wu & Johannes Schweizer, "A new family of genes and pseudogenes potentially expressing testis- and brain-specific leucine zipper proteins in man and mouse," *Gene* 249 (2000): 105–113.
 30. Mustapha Kandouz, Andrew Bier, George D. Carystinos, Moulay A. Alaoui-Jamali and Gerald Batist, "Connexin43 pseudogene is expressed in tumor cells and inhibits growth," *Oncogene* 23 (2004): 4763–4770.
 31. Markus Koller & Emanuel E. Strehler, "Characterization of an intronless human-calmodulin-like pseudogene," *FEBS Letters* 239 (1998): 121–128.
 32. Paul Yaswen, Amy Smoll, Junko Hosoda, Gordon Parry & Martha R. Stampfer, "Protein product of a human intronless calmodulin-like gene shows tissue-specific expression and reduced abundance in transformed cells," *Cell Growth & Differentiation* 3 (1992): 335–345. Freely accessible (2010) at <http://cgd.aacrjournals.org/cgi/reprint/3/6/335>
 33. Pete Jeffs & Michael Ashburner, "Processed pseudogenes in *Drosophila*," *Proceedings of the Royal Society (London)* B 244 (1991): 151–159.
 34. Manyuan Long & Charles H. Langley, "Natural Selection and the Origin of *jingwei*, a Chimeric Processed Functional Gene in *Drosophila*," *Science* 260 (1993): 91–95.
 35. Evgeniy S. Balakirev & Francisco J. Ayala, "Is Esterase-P Encoded by a Cryptic Pseudogene in *Drosophila melanogaster*?" *Genetics* 144 (1996): 1511–1518. Freely accessible (2011) at <http://www.genetics.org/cgi/reprint/144/4/1511>
 36. M. M. Dumancic, J. G. Oakeshott, R. J. Russell & M. J. Healy, "Characterization of the EstP protein in *Drosophila melanogaster* and its conservation in drosophilids," *Biochemical Genetics* 35 (1997): 251–271.
 37. Herman A. Dierick, Julian F. B. Mercer & Thomas W. Glover, "A phosphoglycerate mutase brain isoform (PGAM 1) pseudogene is localized within the human Menkes disease gene (ATP7 A)," *Gene* 198 (1997): 37–41.
 38. Esther Betrán, Wen Wang, Li Jin & Manyuan Long, "Evolution of the Phosphoglycerate Mutase Processed Gene in Human and Chimpanzee Revealing the Origin of a New Primate Gene," *Molecular Biology and Evolution* 19 (2002): 654–663. Freely accessible (2011) at <http://mbe.oxfordjournals.org/cgi/content/full/19/5/654>
 39. Agnès Moreau-Aubry, Soizic Le Guiner, Nathalie Labarrière, Marie-Claude Gesnel, Francine Jotereau & Richard Breathnach, "A Processed Pseudogene Codes for a New Antigen Recognized by a CD8⁺ T Cell Clone on Melanoma," *Journal of Experimental Medicine* 191 (2000): 1617–1624. Freely accessible (2011) at <http://jem.rupress.org/content/191/9/1617.full.pdf+html>
 40. Bing-Sen Zhou, David R. Beidler & Yung-Chi Cheng, "Identification of Antisense RNA Transcripts from a Human DNA Topoisomerase I Pseudogene," *Cancer Research* 52 (1992): 4280–4285. Freely

- accessible (2011) at <http://cancerres.aacr-journals.org/cgi/reprint/52/15/4280>
41. Dominique Weil, Mary-Anne Power, Graham C. Webb & Chung Leung Li, "Antisense transcription of a murine *FGFR-3* pseudogene during fetal development," *Gene* 187 (1997): 115–122.
 42. Andrew Fire, SiQun Xu, Mary K. Montgomery, Steven A. Kostas, Samuel E. Driver & Craig C. Mello, "Potent and specific genetic interference by double-stranded RNA in *Caenorhabditis elegans*," *Nature* 391 (1998): 806–811.
 43. Elisabetta Ullu, Appolinaire Djikeng, Huafang Shi & Christian Tschudi, "RNA interference: advances and questions," *Philosophical Transactions of the Royal Society of London B* 357 (2002): 65–70. Freely accessible (2011) at <http://rsta.royalsocietypublishing.org/content/357/1417/65.long>
 44. Gregory J. Hannon, "RNA interference," *Nature* 418 (2002): 244–251.
 45. Gunter Meister & Thomas Tuschl, "Mechanisms of gene silencing by double-stranded RNA," *Nature* 431 (2004): 343–349.
 46. Sergei A. Korneev, Ji-Ho Park & Michael O'Shea, "Neuronal Expression of Neural Nitric Oxide Synthase (nNOS) Protein Is Suppressed by an Antisense RNA Transcribed from an NOS Pseudogene," *Journal of Neuroscience* 19 (1999): 7711–7720. Freely accessible (2011) at <http://www.jneurosci.org/cgi/content/full/19/18/7711>
 47. Toshiaki Watanabe, Yasushi Totoki, Atsushi Toyoda, Masahiro Kaneda, Satomi Kuramochi-Miyagawa, Yayoi Obata, Hatsune Chiba, Yuji Kohara, Tomohiro Kono, Toru Nakano, M. Azim Surani, Yoshiyuki Sakaki & Hiroyuki Sasaki, "Endogenous siRNAs from naturally formed dsRNAs regulate transcripts in mouse oocytes," *Nature* 453 (2008): 539–543.
 48. Oliver H. Tam, Alexei A. Aravin, Paula Stein, Angélique Girard, Elizabeth P. Murchison, Sihem Cheloufi, Emily Hodges, Martin Anger, Ravi Sachidanandam, Richard M. Schultz & Gregory J. Hannon, "Pseudogene-derived small interfering RNAs regulate gene expression in mouse oocytes," *Nature* 453 (2008): 534–538.
 49. Xingyi Guo, Zhaolei Zhang, Mark B. Gerstein & Deyou Zheng, "Small RNAs Originated from Pseudogenes: cis- or trans-Acting?" *PLoS Computational Biology* 5:7 (2009): e1000449. Freely accessible (2011) at <http://www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1000449>
 50. Shinji Hirotsune, Noriyuki Yoshida, Amy Chen, Lisa Garrett, Fumihiro Sugiyama, Satoru Takahashi, Ken-ichi Yagami, Anthony Wynshaw-Boris & Atsushi Yoshiki, "An expressed pseudogene regulates the messenger-RNA stability of its homologous coding gene," *Nature* 423 (2003): 91–96.
 51. Yoshihisa Yano, Rintaro Saito, Noriyuki Yoshida, Atsushi Yoshiki, Anthony Wynshaw-Boris, Masaru Tomita & Shinji Hirotsune, "A new role for expressed pseudogenes as ncRNA: regulation of mRNA stability of its homologous coding gene," *Journal of Molecular Medicine* 82 (2004): 414–422.
 52. Ondrej Podlaha and Jianzhi Zhang, "Nonneutral Evolution of the Transcribed Pseudogene *Makorin1-p1* in Mice," *Molecular Biology and Evolution* 21 (2004): 2202–2209. Freely accessible (2011) at <http://mbe.oxfordjournals.org/cgi/content/full/21/12/2202>
 53. Jeannie T. Lee, "Molecular biology: Complicity of gene and pseudogene," *Nature* 423 (2003): 26–28.
 54. Todd A. Gray, Alison Wilson, Patrick J. Fortin & Robert D. Nicholls, "The putatively functional *Mkrn1-p1* pseudogene is neither expressed nor imprinted, nor does it regulate its source gene in trans," *Proceedings of the National Academy of Sciences*

- USA 103 (2006): 12039–12044. Freely accessible (2011) at <http://www.pnas.org/content/103/32/12039.full.pdf+html>
55. Saroko Kaneko, Ikuko Aki, Kaoru Tsuda, Kazuyuki Mekada, Kazuo Moriwaki, Naoyuki Takahata & Yoko Satta, "Origin and Evolution of Processed Pseudogenes That Stabilize Functional *Makorin1* mRNAs in Mice, Primates and Other Mammals," *Genetics* 172 (2006): 2421–2429. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1456392/pdf/GEN17242421.pdf>
56. José Manuel Franco-Zorrilla, Adrián Valli, Marco Todesco, Isabel Mateos, María Isabel Puga, Ignacio Rubio-Somoza, Antonio Leyva, Detlef Weigel, Juan Antonio García & Javier Paz-Ares, "Target mimicry provides a new mechanism for regulation of microRNA activity," *Nature Genetics* 39 (2007): 1033–1037.
57. Armin P. Pihler, Marit Hellum, Jürgen J. Wenzel, Ellen Kaminski, Kari Bente Foss Haug, Peter Kierulf & Wolfgang E. Kaminski, "The human ABC transporter pseudogene family: Evidence for transcription and gene-pseudogene interference," *BMC Genomics* 9 (2008): 165. Freely accessible (2011) at <http://www.biomedcentral.com/1471-2164/9/165>
58. Laura Poliseno, Leonardo Salmena, Jiangwen Zhang, Brett Carver, William J. Haveman & Pier Paolo Pandolfi, "A coding-independent function of gene and pseudogene mRNAs regulates tumour biology," *Nature* 465 (2010): 1033–1038.
59. Morimitsu Nishikimi & Kunio Yagi, "Molecular basis for the deficiency in humans of gulonolactone oxidase, a key enzyme for ascorbic acid biosynthesis," *American Journal of Clinical Nutrition* 54 (1991): 1203S–1208S. Freely accessible (2011) at <http://www.ajcn.org/cgi/reprint/54/6/1203S>
60. Morimitsu Nishikimi, Ryuichi Fukuyama, Sinsei Minoshima, Nobuyoshi Shimizu & Kunio Yagi, "Cloning and Chromosomal Mapping of the Human Nonfunctional Gene for L-Gulonolactone Oxidase, the Enzyme for L-Ascorbic Acid Biosynthesis Missing in Man," *Journal of Biological Chemistry* 269 (1994): 13685–13688. Freely accessible (2011) at <http://www.jbc.org/content/269/18/13685.long>
61. Örjan Svensson, Lars Arvestad & Jens Lagergren, "Genome-Wide Survey for Biologically Functional Pseudogenes," *PLoS Computational Biology* 2:5 (2006): e46. Freely accessible (2011) at <http://www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.0020046>
62. Evgeniy S. Balakirev & Francisco J. Ayala, "Pseudogenes: Are They 'Junk' or Functional DNA?" *Annual Review of Genetics* 37 (2003): 123–51.
63. Amit N. Khachane & Paul M. Harrison, "Assessing the genomic evidence for conserved transcribed pseudogenes under selection," *BMC Genomics* 10 (2009): 435. Freely accessible (2011) at <http://www.biomedcentral.com/1471-2164/10/435>

6. JUMPING GENES AND REPETITIVE DNA

1. Barbara McClintock, "The Origin and Behavior of Mutable Loci in Maize," *Proceedings of the National Academy of Sciences USA* 36 (1950): 344–355. Freely accessible (2011) at <http://www.pnas.org/content/36/6/344.full.pdf+html>
2. Georgii P. Georgiev, "Mobile genetic elements in animal cells and their biological significance," *European Journal of Biochemistry* 145 (1984): 203–220. Freely accessible (2011) at <http://www3.interscience.wiley.com/cgi-bin/fulltext/120761888/PDFSTART>
3. Nina Fedoroff, "How jumping genes were discovered," *Nature Structural Biology* 8 (2001): 300–301. Freely accessible (2011) at http://www.nature.com/nsmb/journal/v8/n4/full/nsb0401_300.html

4. David Baltimore, "Viral RNA-dependent DNA Polymerase: RNA-dependent DNA Polymerase in Virions of RNA Tumour Viruses," *Nature* 226 (1970): 1209–1211.
5. Howard M. Temin & Satoshi Mizutani, "Viral RNA-dependent DNA Polymerase: RNA-dependent DNA Polymerase in Virions of Rous Sarcoma Virus," *Nature* 226 (1970): 1211–1213.
6. P. M. B. Walker & Anne McLaren, "Fractionation of mouse deoxyribonucleic acid on hydroxyapatite," *Nature* 208 (1965): 1175–1179.
7. Roy J. Britten & D. E. Kohne, "Repeated Sequences in DNA," *Science* 161 (1968): 529–540.
8. W. G. Flamm, "Highly Repetitive Sequences of DNA in Chromosomes," *International Review of Cytology* 32 (1972): 1–51.
9. Maxine F. Singer, "SINEs and LINEs: Highly Repeated Short and Long Interspersed Sequences in Mammalian Genomes," *Cell* 28 (1982): 433–434.
10. Bruce Alberts, Alexander Johnson, Julian Lewis, Martin Raff, Keith Roberts & Peter Walter, *Molecular Biology of the Cell*, Fourth Edition (New York: Garland Science, 2002), p. 203
11. GenBank, "Homo sapiens RNA, 7SL, cytoplasmic 1 (RN7SL1), small cytoplasmic RNA," NCBI Reference Sequence: NR_002715.1 (28 February 2010). Freely accessible (2011) at http://www.ncbi.nlm.nih.gov/nuccore/NR_002715.1
12. Karen L. Bennett, Robert E. Hill, Dennis F. Pietras, Mary Woodworth-Gutai, Colleen Kane-Haas, Joanna M. Houston, John K. Heath & Nicholas D. Hastie, "Most Highly Repeated Dispersed DNA Families in the Mouse Genome," *Molecular and Cell Biology* 4 (1984): 1561–1571. Freely accessible (2011) at <http://mcb.asm.org/cgi/reprint/4/8/1561?view=long&pmid=6208477>
13. Geoffrey J. Faulkner, Yasumasa Kimura, Carsten O. Daub, Shivangi Wani, Charles Plessy, Katharine M. Irvine, Kate Schroder, Nicole Cloonan, Anita L. Steptoe, Timo Lassmann, Kazunori Waki, Nadine Hornig, Takahiro Arakawa, Hazuki Takahashi, Jun Kawai, Alistair R. R. Forrest, Harukazu Suzuki, Yoshihide Hayashizaki, David A. Hume, Valerio Orlando, Sean M. Grimmond & Piero Carninci, "The regulated retrotransposon transcriptome of mammalian cells," *Nature Genetics* 41 (2009): 563–571.
14. Amar Kumar & Jeffrey L. Bennetzen, "Retrotransposons: central players in the structure, evolution and function of plant genomes," *Trends in Plant Science* 5 (2000): 509–510.
15. Hidenori Nishihara, Arian F. A. Smit and Norihiro Okada "Functional noncoding sequences derived from SINEs in the mammalian genome," *Genome Research* 16 (2006): 864–874. Freely accessible (2011) at <http://genome.cshlp.org/content/16/7/864.full.pdf+html>
16. Craig B. Lowe, Gill Bejerano & David Haussler, "Thousands of human mobile element fragments undergo strong purifying selection near developmental genes," *Proceedings of the National Academy of Sciences USA* 104 (2007): 8005–8010. Freely accessible (2011) at <http://www.pnas.org/content/104/19/8005.full.pdf+html>
17. Aristotelis Tsirigos & Isidore Rigoutsos, "Alu and B1 Repeats Have Been Selectively Retained in the Upstream and Intronic Regions of Genes of Specific Functional Classes," *PLoS Computational Biology* 5:12 (2009): e1000610. Freely accessible (2011) at <http://www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1000610>
18. Susumu Ohno, W. D. Kaplan & R. Kinoshita, "Formation of the sex chromatin by a single X-chromosome in liver cells of *Rattus norvegicus*," *Experimental Cell Research* 18 (1959): 415–418.
19. Jeffrey A. Bailey, Laura Carrel, Aravinda Chakravarti & Evan E. Eichler, "Molecular evidence for a relationship between

- LINE-1 elements and X chromosome inactivation: the Lyon repeat hypothesis," *Proceedings of the National Academy of Sciences USA* 97 (2000): 6634–6639. Freely accessible (2011) at <http://www.pnas.org/content/97/12/6634.full.pdf+html>
20. Y. Amy Tang, Derek Huntley, Giovanni Montana, Andrea Cerase, Tatyana B. Nesterova & Neil Brockdorff, "Efficiency of Xist-mediated silencing on autosomes is linked to chromosomal domain organization," *Epigenetics & Chromatin* 3 (2010): 10. Freely accessible (2011) at <http://www.epigeneticsandchromatin.com/content/pdf/1756-8935-3-10.pdf>
21. Jennifer C. Chow, Constance Ciaudo, Melissa J. Fazzari, Nathan Mise, Nicolas Servant, Jacob L. Glass, Matthew Attreed, Philip Avner, Anton Wutz, Emmanuel Barillot, John M. Greally, Olivier Voinet & Edith Heard, "LINE-1 activity in facultative heterochromatin formation during X chromosome inactivation," *Cell* 141 (2010): 956–969.
22. Tammy A. Morrish, Nicolas Gilbert, Jeremy S. Myers, Bethaney J. Vincent, Thomas D. Stamato, Guillermo E. Tacicoli, Mark A. Batzer & John V. Moran, "DNA repair mediated by endonuclease-independent LINE-1 retrotransposition," *Nature Genetics* 31 (2002): 159–165.
23. José L. Garcia-Perez, Aurélien J. Doucet, Alain Bucheton, John V. Moran & Nicolas Gilbert, "Distinct mechanisms for trans-mediated mobilization of cellular RNAs by the LINE-1 reverse transcriptase," *Genome Research* 17 (2007): 602–611. Freely accessible (2011) at <http://genome.cshlp.org/content/17/5/602.full.pdf+html>
24. Elizabeth A. Shepard, Pritpal Chandan, Milena Stevanovic-Walker, Mina Edwards & Ian R. Phillips, "Alternative promoters and repetitive DNA elements define the species-dependent tissue-specific expression of the FMO1 genes of human and mouse," *Biochemical Journal* 406 (2007): 491–499. Freely accessible (2011) at <http://www.biochemj.org/bj/406/0491/4060491.pdf>
25. Corrado Spadafora, "A reverse transcriptase-dependent mechanism plays central roles in fundamental biological processes," *Systems Biology in Reproductive Medicine* 54 (2008): 11–21.
26. Anderly C. Chueh, Emma L. Northrop, Kate H. Brettingham-Moore, K. H. Andy Choo & Lee H. Wong, "LINE Retrotransposon RNA Is an Essential Structural and Functional Epigenetic Component of a Core Neocentromeric Chromatin," *PLoS Genetics* 5:1 (2009): e1000354. Freely accessible (2011) at <http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1000354>
27. Dylan R. Edwards, Craig L. J. Parfett & David T. Denhardt, "Transcriptional Regulation of Two Serum-induced RNAs in Mouse Fibroblasts: Equivalence of One Species to B2 Repetitive Elements," *Molecular and Cellular Biology* 5 (1985): 3280–3288. Freely accessible (2011) at <http://mcb.asm.org/cgi/reprint/5/11/3280?view=long&pmid=3837843>
28. Roy J. Britten, "Coding sequences of functioning human genes derived entirely from mobile element sequences," *Proceedings of the National Academy of Sciences USA* 101 (2004): 16825–16830. Freely accessible (2011) at <http://www.pnas.org/content/101/48/16825.full.pdf+html>
29. L. P. Yavachev, O. I. Georgiev, E. A. Braga, T. A. Avdonina, A. E. Bogomolova, V. B. Zhurkin, V. V. Nosikov & A. A. Hadjiolov, "Nucleotide sequence analysis of the spacer regions flanking the rat rRNA transcription unit and identification of repetitive elements," *Nucleic Acids Research* 14 (1986): 2799–2810. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC339699/pdf/nar00275-0387.pdf>
30. Richard H. Kimura, Prabhakara V. Choudary & Carl W. Schmid, "Silk worm

- Bm1 SINE RNA increases following cellular insults," *Nucleic Acids Research* 27 (1999): 3380–3387. Freely accessible (2011) at <http://nar.oxfordjournals.org/cgi/reprint/27/16/3380>
31. Richard H. Kimura, Prabhakara V. Choudary, Koni K. Stone & Carl W. Schmid, "Stress induction of Bm1 RNA in silkworm larvae: SINEs, an unusual class of stress genes," *Cell Stress & Chaperones* 6 (2001): 263–272. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC434408/pdf/i1466-1268-6-3-263.pdf>
 32. Phillip A. Yates, Robert W. Burman, Padmaja Mummaneni, Sandra Krussel & Mitchell S. Turker, "Tandem B1 Elements Located in a Mouse Methylation Center Provide a Target for de Novo DNA Methylation," *Journal of Biological Chemistry* 274 (1999): 36357–36361. Freely accessible (2011) at <http://www.jbc.org/content/274/51/36357.full.pdf+html>
 33. Celso A. Espinoza, Tiffany A. Allen, Aaron R. Hieb, Jennifer F. Kugel & James A. Goodrich, "B2 RNA binds directly to RNA polymerase II to repress transcript synthesis," *Nature Structural & Molecular Biology* 11 (2004): 822–829.
 34. Celso A. Espinoza, James A. Goodrich & Jennifer F. Kugel, "Characterization of the structure, function, and mechanism of B2 RNA, an ncRNA repressor of RNA polymerase II transcription," *RNA* 13 (2007): 583–596. Freely accessible (2011) at <http://rnajournal.cshlp.org/content/13/4/583.full.pdf+html>
 35. Gordon Vansant & Wanda F. Reynolds, "The consensus sequence of a major *Alu* subfamily contains a functional retinoic acid response element," *Proceedings of the National Academy of Sciences USA* 92 (1995): 8229–8233. Freely accessible (2011) at <http://www.pnas.org/content/92/18/8229.full.pdf+html>
 36. Peter D. Mariner, Ryan D. Walters, Celso A. Espinoza, Linda F. Drullinger, Stacy D. Wagner, Jennifer F. Kugel & James A. Goodrich, "Human *Alu* RNA is a modular transacting repressor of mRNA transcription during heat shock," *Molecular Cell* 29 (2008): 499–509.
 37. Julien Häslér & Katharina Strub, "*Alu* RNP and *Alu* RNA regulate translation initiation in vitro," *Nucleic Acids Research* 34 (2006): 2374–2385. Freely accessible (2011) at <http://nar.oxfordjournals.org/cgi/reprint/34/8/2374>
 38. Julien Häslér & Katharina Strub, "*Alu* elements as regulators of gene expression," *Nucleic Acids Research* 34 (2006): 5491–5497. Freely accessible (2011) at <http://nar.oxfordjournals.org/cgi/content/full/34/19/5491>
 39. Julien Häslér, T. Samuelsson & Katharina Strub, "Useful 'junk': *Alu* RNAs in the human transcriptome," *Cellular and Molecular Life Sciences* 64 (2007): 1793–1800.
 40. Tong J. Gu, Xiang Yi, Xi W. Zhao, Yi Zhao & James Q. Yin, "*Alu*-directed transcriptional regulation of some novel miRNAs," *BMC Genomics* 10 (2009): 563. Freely accessible (2011) at <http://www.biomedcentral.com/1471-2164/10/563>
 41. Michal Barak, Erez Y. Levanon, Eli Eisenberg, Nurit Paz, Gideon Rechavi, George M. Church & Ramit Mehr, "Evidence for large diversity in the human transcriptome created by *Alu* RNA editing," *Nucleic Acids Research* 37 (2009): 6905–6915. Freely accessible (2011) at <http://nar.oxfordjournals.org/cgi/reprint/37/20/6905>
 42. Ryan D. Walters, Jennifer F. Kugel & James A. Goodrich, "InvAluable junk: the cellular impact and function of *Alu* and B2 RNAs," *IUBMB Life* 61 (2009): 831–837.
 43. Ann L. Boyle, S. Gwyn Ballard & David C. Ward, "Differential distribution of long and short interspersed element sequences in the mouse genome: Chromosome karyotyping by fluorescence in situ hybridization," *Proceedings of the National Academy of Sciences USA* 87 (1990): 7757–

7761. Freely accessible (2011) at <http://www.pnas.org/content/87/19/7757.full.pdf+html>
44. J. M. Craig & W. A. Bickmore, "Chromosome bands—flavours to savour," *BioEssays* 15 (1993): 349–354.
 45. Yataro Daigo, Minoru Isomura, Tadashi Nishiwaki, Kazufumi Suzuki, Osamu Maruyama, Kumiko Takeuchi, Yuka Yamane, Rie Hayashi, Maiko Minami, Yoshiaki Hojo, Ikuo Uchiyama, Toshihisa Takagi & Yusuke Nakamura, "Significant Differences in the Frequency of Transcriptional Units, Types and Numbers of Repetitive Elements, GC content, and the Number of CpG Islands Between a 1010-kb G-band Genomic Segment on Chromosome 9q31.3 and a 1200-kb R-band Genomic Segment on Chromosome 3p21.3," *DNA Research* 6 (1999): 227–233. Freely accessible (2011) at <http://dnaresearch.oxfordjournals.org/cgi/reprint/6/4/227?view=long&cpmid=10492169>
 46. Sam Janssen, Olivier Cuvier, Martin Müller & Ulrich K Laemmli, "Specific gain- and loss-of-function phenotypes induced by satellite-specific DNA-binding drugs fed to *Drosophila melanogaster*," *Molecular Cell* 6 (2000): 1013–1024.
 47. Steven Henikoff & Danielle Vermaak, "Bugs on drugs go GAGAA," *Cell* 103 (2000): 695–698.
 48. Mary-Lou Pardue & P. Gregory Debaryshe, "*Drosophila* telomeres: two transposable elements with important roles in chromosomes," *Genetica* 107 (1999): 189–196.
 49. Mary-Lou Pardue & P. Gregory Debaryshe, "*Drosophila* telomere transposons: genetically active elements in heterochromatin," *Genetica* 109 (2000): 45–52.
 50. M.-L. Pardue, S. Rashkova, E. Casacuberta, P. G. Debaryshe, J. A. George & K. L. Traverse, "Two retrotransposons maintain telomeres in *Drosophila*," *Chromosome Research* 13 (2005): 443–453. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1255937/pdf/nihms3265.pdf>
 51. Zachary Lippman, Anne-Valérie Gendrel, Michael Black, Matthew W. Vaughn, Neilay Dedhia, W. Richard McCombie, Kimberly Lavine, Vivek Mittal, Bruce May, Kristin D. Kasschau, James C. Carrington, Rebecca W. Doerge, Vincent Colot & Rob Martienssen, "Role of transposable elements in heterochromatin and epigenetic control," *Nature* 430 (2004): 471–476.
 52. Zachary Lippman & Rob Martienssen, "The role of RNA interference in heterochromatic silencing," *Nature* 431 (2004): 364–370.
 53. Victoria V. Lunyak, Gratien G. Prefontaine, Esperanza Núñez, Thorsten Cramer, Bong-Gun Ju, Kenneth A. Ohgi, Kasey Hutt, Rosa Roy, Angel García-Díaz, Xiaoyan Zhu, Yun Yung, Lluís Montoliu, Christopher K. Glass & Michael G. Rosenfeld, "Developmentally regulated activation of a SINE B2 repeat as a domain boundary in organogenesis," *Science* 317 (2007): 248–251.
 54. Ram Parikshan Kumar, Ramamoorthy Senthilkumar, Vipin Singh & Rakesh K. Mishra, "Repeat performance: how do genome packaging and regulation depend on simple sequence repeats?" *BioEssays* 32 (2010): 165–174.
 55. Satoru Ide, Takaaki Miyazaki, Hisaji Maki & Takehiko Kobayashi, "Abundance of ribosomal RNA gene copies maintains genome integrity," *Science* 327 (2010): 693–696.
 56. Karen Bohmert, Isabelle Camus, Catherine Bellini, David Bouchez, Michel Caboche & Christoph Benning, "AGO1 defines a novel locus of *Arabidopsis* controlling leaf development," *EMBO Journal* 17 (1998): 170–180. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1170368/pdf/000170.pdf>
 57. Michelle A. Carmell, Zhenyu Xuan, Michael Q. Zhang & Gregory J. Hannon, "The Argonaute family: tentacles that

- reach into RNAi, developmental control, stem cell maintenance, and tumorigenesis," *Genes & Development* 16 (2002): 2733–2742. Freely accessible (2011) at <http://genesdev.cshlp.org/content/16/21/2733.full.pdf+html>
58. Andreas Lingel & Elisa Izaurralde, "RNAi: finding the elusive endonuclease," *RNA* 10 (2004): 1675–1679. Freely accessible (2011) at <http://rnajournal.cshlp.org/content/10/11/1675.full.pdf+html>
59. T. Hall, "Structure and function of argonaute proteins," *Structure* 13 (2005): 1403–1408.
60. George L. Sen & Helen M. Blau, "Argonaute 2/RISC resides in sites of mammalian mRNA decay known as cytoplasmic bodies," *Nature Cell Biology* 7 (2005): 633–636.
61. Tim A. Rand, Sean Petersen, Fenghe Du & Xiaodong Wang, "Argonaute2 cleaves the anti-guide strand of siRNA during RISC activation," *Cell* 123 (2005): 621–629.
62. Robert E. Collins & Xiaodong Cheng, "Structural and Biochemical Advances in Mammalian RNAi," *Journal of Cellular Biochemistry* 99 (2006): 1251–1266. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2688788/pdf/nihms-117419.pdf>
63. Emily Bernstein, Amy A. Caudy, Scott M. Hammond & Gregory J. Hannon, "Role for a bidentate ribonuclease in the initiation step of RNA interference," *Nature* 409 (2001): 363–366.
64. N. Baumberger & D. C. Baulcombe, "Arabidopsis ARGONAUTE1 is an RNA Slicer that selectively recruits microRNAs and short interfering RNAs," *Proceedings of the National Academy of Sciences USA* 102 (2005): 11928–11933. Freely accessible (2011) at <http://www.pnas.org/content/102/33/11928.full.pdf+html>
65. Haifan Lin & Allan C. Spradling, "A novel group of *pumilio* mutations affects the asymmetric division of germline stem cells in the *Drosophila* ovary," *Development* 124 (1997): 2463–2476. Freely accessible (2011) at <http://dev.biologists.org/content/124/12/2463.long>
66. Daniel N. Cox, Anna Chao & Haifan Lin, "*piwi* encodes a nucleoplasmic factor whose activity modulates the number and division rate of germline stem cells," *Development* 127 (2000): 503–514. Freely accessible (2011) at <http://dev.biologists.org/content/127/3/503.long>
67. Daniel N. Cox, Anna Chao, Jeff Baker, Lisa Chang, Dan Qiao & Haifan Lin, "A novel class of evolutionarily conserved genes defined by *piwi* are essential for stem cell self-renewal," *Genes & Development* 12 (1998): 3715–3727. Freely accessible (2011) at <http://genesdev.cshlp.org/content/12/23/3715.full.pdf+html>
68. Jin-Biao Ma, Yu-Ren Yuan, Gunter Meister, Yi Pei, Thomas Tuschl & Dinshaw J. Patel, "Structural basis for 5'-end-specific recognition of guide RNA by the *A. fulgidus* Piwi protein," *Nature* 434 (2005): 666–670.
69. Christopher R. Faehnle & Leemor Joshua-Tor, "Argonautes confront new small RNAs," *Current Opinion in Chemical Biology* 11 (2007): 569–577. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2077831/pdf/nihms-33482.pdf>
70. Julia Höck & Gunter Meister, "The Argonaute protein family," *Genome Biology* 9:2 (2008): 210. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2008-9-2-210.pdf>
71. Kuniaki Saito, Kazumichi M. Nishida, Tomoko Mori, Yoshinori Kawamura, Keita Miyoshi, Tomoko Nagami, Haruhiko Siomi & Mikiko C. Siomi, "Specific association of Piwi with rasiRNAs derived from retrotransposon and heterochromatic regions in the *Drosophila* genome," *Genes & Development* 20 (2006): 2214–2222. Freely accessible (2011) at <http://genesdev.cshlp.org/content/20/12/2214.full.pdf+html>

- cshlp.org/content/20/16/2214.full.pdf+html
72. Yoshinori Kawamura, Kuniaki Saito, Taishin Kin, Yukiteru Ono, Kiyoshi Asai, Takafumi Sunohara, Tomoko N. Okada, Mikiko C. Siomi & Haruhiko Siomi, "Drosophila endogenous small RNAs bind to Argonaute 2 in somatic cells," *Nature* 453 (2008): 793–797.
 73. Megha Ghildiyal, Hervé Seitz, Michael D. Horwich, Chengjian Li, Tingting Du, Soohyun Lee, Jia Xu, Ellen L.W. Kittler, Maria L. Zapp, Zhiping Weng & Philip D. Zamore, "Endogenous siRNAs Derived from Transposons and mRNAs in *Drosophila* Somatic Cells," *Science* 320 (2008): 1077–1081.
 74. Haifan Lin, "piRNAs in the germ line," *Science* 316 (2007): 397.
 75. Travis Thomson & Haifan Lin, "The Biogenesis and Function of PIWI Proteins and piRNAs: Progress and Prospect," *Annual Review of Cell and Developmental Biology* 25 (2009): 355–376. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2780330/pdf/nihms158620.pdf>
 76. Christel Rouget, Catherine Papin, Anthony Boureux, Anne-Cécile Meunier, Bénédicte Franco, Nicolas Robine, Eric C. Lai, Alain Pelisson & Martine Simonelig, "Maternal mRNA deadenylation and decay by the piRNA pathway in the early *Drosophila* embryo," *Nature* 467 (2010): 1128–1132.
 77. Howard M. Temin, "Homology Between RNA from Rous Sarcoma Virus and DNA from Rous Sarcoma Virus-Infected Cells," *Proceedings of the National Academy of Sciences USA* 52 (1964): 323–329. Freely accessible (2011) at <http://www.pnas.org/content/52/2/323.full.pdf+html>
 78. Heiner Westphal & Renato Dulbecco, "Viral DNA in Polyoma- and SV40-transformed Cell Lines," *Proceedings of the National Academy of Sciences USA* 59 (1968): 1158–1165. Freely accessible (2011) at <http://www.pnas.org/content/59/4/1158.full.pdf+html>
 79. Harold E. Varmus "Retroviruses," *Science* 240 (1988): 1427–1435.
 80. Peter N. Rosenthal, Harriet L. Robinson, William S. Robinson, Teruko Hanafusa & Hidesaburo Hanafusa, "DNA in Uninfected and Virus-Infected Cells Complementary to Avian Tumor Virus RNA," *Proceedings of the National Academy of Sciences USA* 68 (1971): 2336–2340. Freely accessible (2011) at <http://www.pnas.org/content/68/10/2336.full.pdf+html>
 81. Harold E. Varmus, Robin A. Weiss, Robert R. Friis, Warren Levinson & J. Michael Bishop, "Detection of Avian Tumor Virus-Specific Nucleotide Sequences in Avian Cell DNAs," *Proceedings of the National Academy of Sciences USA* 69 (1972): 20–24. Freely accessible (2011) at <http://www.pnas.org/content/69/1/20.full.pdf+html>
 82. Robin A Weiss, "The discovery of endogenous retroviruses," *Retrovirology* 3 (2006): 67. Freely accessible (2011) at <http://www.retrovirology.com/content/pdf/1742-4690-3-67.pdf>
 83. Motoharu Seiki, Seisuke Hattori & Mistuaki Yoshida, "Human adult T-cell leukemia virus: Molecular cloning of the provirus DNA and the unique terminal structure," *Proceedings of the National Academy of Sciences USA* 79 (1982): 6899–6902. Freely accessible (2011) at <http://www.pnas.org/content/79/22/6899.full.pdf+html>
 84. Joseph G. Sodroski, Craig A. Rosen & William A. Haseltine, "Trans-acting transcriptional activation of the long terminal repeat of human T lymphotropic viruses in infected cells," *Science* 225 (1984): 381–385.
 85. Robert G. Ramsay, Shunsuke Ishii & Thomas J. Gonda, "Interaction of the Myb Protein with Specific DNA Binding Sites," *Journal of Biological Chemistry* 267 (1992): 5656–5662. Freely accessible

- (2011) at <http://www.jbc.org/content/267/8/5656.full.pdf+html>
86. Nathalie de Parseval, Hanan Alkabani & Thierry Heidmann, "The long terminal repeats of the HERV-H human endogenous retrovirus contain binding sites for transcriptional regulation by the Myb protein," *Journal of General Virology* 80 (1999): 841–845. Freely accessible (2011) at <http://vir.sgmjournals.org/cgi/reprint/80/4/841>
 87. Patrik Medstrand, Josette-Renée Landry & Dixie L. Mager, "Long Terminal Repeats Are Used as Alternative Promoters for the Endothelin B Receptor and Apolipoprotein C-I Genes in Humans," *Journal of Biological Chemistry* 276 (2001): 1896–1903. Freely accessible (2011) at <http://www.jbc.org/content/276/3/1896.full.pdf+html>
 88. Josette-Renée Landry & Dixie L. Mager, "Functional Analysis of the Endogenous Retroviral Promoter of the Human Endothelin B Receptor Gene," *Journal of Virology* 77 (2003): 7459–7466. Freely accessible (2011) at <http://jvi.asm.org/cgi/reprint/77/13/7459>
 89. Anne E. Peaston, Alexei V. Evsikov, Joel H. Graber, Wilhelmine N. de Vries, Andrea E. Holbrook, Davor Solter & Barbara B. Knowles, "Retrotransposons regulate host genes in mouse oocytes and preimplantation embryos," *Developmental Cell* 7 (2004): 597–606.
 90. James A. Shapiro, "Retrotransposons and regulatory suites," *BioEssays* 27 (2005): 122–125.
 91. Jianhua Ling, Wenhui Pi, Roni Bollag, Shan Zeng, Meral Keskinetepe, Hatem Saliman, Sanford Krantz, Barry Whitney & Dorothy Tuan, "The Solitary Long Terminal Repeats of ERV-9 Endogenous Retrovirus Are Conserved during Primate Evolution and Possess Enhancer Activities in Embryonic and Hematopoietic Cells," *Journal of Virology* 76 (2002): 2410–2423. Freely accessible (2011) at <http://jvi.asm.org/cgi/reprint/76/5/2410>
 92. Elena Gogvadze, Elena Stukacheva, Anton Buzdin & Eugene Sverdlov, "Human-Specific Modulation of Transcriptional Activity Provided by Endogenous Retroviral Insertions," *Journal of Virology* 83 (2009): 6098–6105. Freely accessible (2011) at <http://jvi.asm.org/cgi/reprint/83/12/6098>
 93. Catherine A. Dunn, Patrik Medstrand & Dixie L. Mager, "An endogenous retroviral long terminal repeat is the dominant promoter for human β 1,3-galactosyltransferase 5 in the colon," *Proceedings of the National Academy of Sciences USA* 100 (2003): 12841–12846. Freely accessible (2011) at <http://www.pnas.org/content/100/22/12841.full.pdf+html>
 94. Catherine A. Dunn & Dixie L. Mager, "Transcription of the human and rodent SPAM1 / PH-20 genes initiates within an ancient endogenous retrovirus," *BMC Genomics* 6 (2005): 47. Freely accessible (2011) at <http://www.biomedcentral.com/content/pdf/1471-2164-6-47.pdf>
 95. Anton Buzdin, Elena Kovalskaya-Alexandrova, Elena Gogvadze & Eugene Sverdlov, "At Least 50% of Human-Specific HERV-K (HML-2) Long Terminal Repeats Serve in Vivo as Active Promoters for Host Nonrepetitive DNA Transcription," *Journal of Virology* 80 (2006): 10752–10762. Freely accessible (2011) at <http://jvi.asm.org/cgi/reprint/80/21/10752>
 96. Woo Jung Lee, Hyun Jin Kwun & Kyung Lib Jang, "Analysis of transcriptional regulatory sequences in the human endogenous retrovirus W long terminal repeat," *Journal of General Virology* 84 (2003): 2229–2235. Freely accessible (2011) at <http://vir.sgmjournals.org/cgi/reprint/84/8/2229>
 97. Andrew B. Conley, Jittima Piriyaopongsa & I. King Jordan, "Retroviral promoters in the human genome," *Bioinformatics* 24 (2008): 1563–1567. Freely accessible

- (2011) at <http://bioinformatics.oxford-journals.org/cgi/reprint/24/14/1563>
98. Ulrike Schön, Olivia Diem, Laura Leitner, Walter H. Günzburg, Dixie L. Mager, Brian Salmons & Christine Leib-Mösch, "Human Endogenous Retroviral Long Terminal Repeat Sequences as Cell Type-Specific Promoters in Retroviral Vectors," *Journal of Virology* 83 (2009): 12643–12650. Freely accessible (2011) at <http://jvi.asm.org/cgi/reprint/83/23/12643>
 99. Patrick J. W. Venables, Sharon M. Brookes, David Griffiths, Robin A. Weiss & Mark T. Boyd, "Abundance of an endogenous retroviral envelope protein in placental trophoblasts suggests a biological function." *Virology* 211 (1995): 589–592.
 100. Sha Mi, Xinhua Lee, Xiang-ping Li, Geertruida M. Veldman, Heather Finnerty, Lisa Racie, Edward LaValle, Xiang-Yang Tang, Philippe Edouard, Steve Howes, James C. Keith Jr. & John M. McCoy, "Syncytin is a captive retroviral envelope protein involved in human placental morphogenesis," *Nature* 403 (2000): 785–789.
 101. Jean-Luc Blond, Dimitri Lavillette, Valérie Cheynet, Olivier Bouton, Guy Oriol, Sylvie Chapel-Fernandes, Bernard Mandrand, François Mallet & François-Loïc Cosset, "An Envelope Glycoprotein of the Human Endogenous Retrovirus HERV-W Is Expressed in the Human Placenta and Fuses Cells Expressing the Type D Mammalian Retrovirus Receptor," *Journal of Virology* 74 (2000): 3321–3329. Freely accessible (2011) at <http://jvi.asm.org/cgi/reprint/74/7/3321>
 102. Jean-Louis Frendo, Delphine Olivier, Valérie Cheynet, Jean-Luc Blond, Olivier Bouton, Michel Vidaud, Michèle Rabreau, Danièle Evain-Brion & François Mallet, "Direct Involvement of HERV-W Env Glycoprotein in Human Trophoblast Cell Fusion and Differentiation," *Molecular and Cellular Biology* 23 (2003): 3566–3574.
 - Freely accessible (2011) at <http://mcb.asm.org/cgi/reprint/23/10/3566>
 103. I. Knerr, B. Huppertz, C. Weigel, J. Dötsch, C. Wich, R. L. Schild, M. W. Beckmann & W. Rascher, "Endogenous retroviral syncytin: compilation of experimental research on syncytin and its possible role in normal and disturbed human placentogenesis," *Molecular Human Reproduction* 10 (2004): 581–588. Freely accessible (2011) at <http://molehr.oxford-journals.org/cgi/reprint/10/8/581>
 104. Kathrin A. Dunlap, Massimo Palmarini, Mariana Varela, Robert C. Burghardt, Kanako Hayashi, Jennifer L. Farmer & Thomas E. Spencer, "Endogenous retroviruses regulate periimplantation placental growth and differentiation," *Proceedings of the National Academy of Sciences USA* 103 (2006): 14390–14395. Freely accessible (2011) at <http://www.pnas.org/content/103/39/14390.full.pdf+html>
 105. Ina Knerr, Ernst Beinder & Wolfgang Rascher, "Syncytin, a novel human endogenous retroviral gene in human placenta: Evidence for its dysregulation in pre-eclampsia and HELLP syndrome," *American Journal of Obstetrics and Gynecology* 186 (2002): 210–213.
 106. Joseph M. Antony, Kristofor K. Ellestad, Robert Hammond, Kazunori Imaizumi, François Mallet, Kenneth G. Warren & Christopher Power, "The Human Endogenous Retrovirus Envelope Glycoprotein, Syncytin-1, Regulates Neuroinflammation and its Receptor Expression in Multiple Sclerosis: A Role for Endoplasmic Reticulum Chaperones in Astrocytes," *Journal of Immunology* 179 (2007): 1210–1224. Freely accessible (2011) at <http://www.jimmunol.org/cgi/reprint/179/2/1210>
 107. Sandra Blaise, Nathalie de Parseval, Laurence Bénit & Thierry Heidmann, "Genomewide screening for fusogenic human endogenous retrovirus envelopes identifies syncytin 2, a gene conserved on primate evolution," *Proceedings of the*

- National Academy of Sciences USA 100 (2003): 13013–13018. Freely accessible (2011) at <http://www.pnas.org/content/100/22/13013.full.pdf+html>
108. Cécile Esnault, Stéphane Priet, David Ribet, Cécile Vernochet, Thomas Bruls, Christian Lavalie, Jean Weissenbach & Thierry Heidmann, "A placenta-specific receptor for the fusogenic, endogenous retrovirus-derived, human syncytin-2," *Proceedings of the National Academy of Sciences USA* 105 (2008): 17532–17537. Freely accessible (2011) at <http://www.pnas.org/content/105/45/17532.full.pdf+html>
109. Anne Dupressoir, Geoffroy Marceau, Cécile Vernochet, Laurence Bénit, Colette Kanellopoulos, Vincent Sapin & Thierry Heidmann, "Syncytin-A and syncytin-B, two fusogenic placenta-specific murine envelope genes of retroviral origin conserved in Muridae," *Proceedings of the National Academy of Sciences USA* 102 (2005): 725–730. Freely accessible (2011) at <http://www.pnas.org/content/102/3/725.full.pdf+html>
110. Anne Dupressoir, Cécile Vernochet, Olivia Bawa, Francis Harper, Gérard Pierron, Paule Opolon & Thierry Heidmann, "Syncytin-A knockout mice demonstrate the critical role in placenta of a fusogenic, endogenous retrovirus-derived, envelope gene," *Proceedings of the National Academy of Sciences USA* 106 (2009): 12127–12132. Freely accessible (2011) at <http://www.pnas.org/content/106/29/12127.full.pdf+html>
111. Odile Heidmann, Cécile Vernochet, Anne Dupressoir & Thierry Heidmann, "Identification of an endogenous retroviral envelope gene with fusogenic activity and placenta-specific expression in the rabbit: a new 'syncytin' in a third order of mammals," *Retrovirology* 6 (2009): 107. Freely accessible (2011) at <http://www.retrovirology.com/content/6/1/107>
112. Jonathan P. Stoye, "Proviral protein provides placental function," *Proceedings of the National Academy of Sciences USA* 106 (2009): 11827–11828. Freely accessible (2011) at <http://www.pnas.org/content/106/29/11827.full.pdf+html>
113. Sarah Prudhomme, Guy Oriol & François Mallet, "A Retroviral Promoter and a Cellular Enhancer Define a Bipartite Element which Controls *env* ERVWE1 Placental Expression," *Journal of Virology* 78 (2004): 12157–12168. Freely accessible (2011) at <http://jvi.asm.org/cgi/reprint/78/22/12157>
114. You-Hong Cheng, Brian D. Richardson, Michael A. Hubert & Stuart Handwerker, "Isolation and Characterization of the Human Syncytin Gene Promoter," *Biology of Reproduction* 70 (2004): 694–701. Freely accessible (2011) at <http://www.biolreprod.org/content/70/3/694.full.pdf+html>
115. François Mallet, Olivier Bouton, Sarah Prudhomme, Valérie Cheynet, Guy Oriol, Bertrand Bonnaud, Gérard Lucotte, Laurent Duret & Bernard Mandrand, "The endogenous retroviral locus *ERVWE1* is a bona fide gene involved in hominoid placental physiology," *Proceedings of the National Academy of Sciences USA* 101 (2004): 1731–1736. Freely accessible (2011) at <http://www.pnas.org/content/101/6/1731.full.pdf+html>
116. James A. Shapiro & Richard von Sternberg, "Why repetitive DNA is essential to genome function," *Biological Reviews* 80 (2005): 227–250. Freely accessible (2011) at <http://shapiro.bsd.uchicago.edu/Shapiro&Sternberg.2005.BiolRevs.pdf>
117. Francis S. Collins, *The Language of God: A Scientist Presents Evidence for Belief* (New York: Free Press, 2006), pp. 136–137.

7. FUNCTIONS INDEPENDENT OF EXACT SEQUENCE

1. David Gubb, "Intron-Delay and the Precision of Expression of Homeotic Gene

- Products in *Drosophila*," *Developmental Genetics* 7 (1986): 119–131.
2. Carl S. Thummel, "Mechanisms of Transcriptional Timing in *Drosophila*," *Science* 255 (1992): 39–40.
 3. Ian A. Swinburne & Pamela A. Silver, "Intron Delays and Transcriptional Timing during Development," *Developmental Cell* 14 (2008): 324–330. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2825037/pdf/nihms176861.pdf>
 4. Jennifer C. Chow, Constance Ciaudo, Melissa J. Fazzari, Nathan Mise, Nicolas Servant, Jacob L. Glass, Matthew Attreed, Philip Avner, Anton Wutz, Emmanuel Barillot, John M. Greally, Olivier Voinnet & Edith Heard, "LINE-1 activity in facultative heterochromatin formation during X chromosome inactivation," *Cell* 141 (2010): 956–969.
 5. Ann L. Boyle, S. Gwyn Ballard & David C. Ward, "Differential distribution of long and short interspersed element sequences in the mouse genome: chromosome karyotyping by fluorescence in situ hybridization," *Proceedings of the National Academy of Sciences USA* 87 (1990): 7757–7761. Freely accessible (2011) at <http://www.pnas.org/content/87/19/7757.full.pdf+html>
 6. J. M. Craig & W. A. Bickmore, "Chromosome bands—flavours to savour," *BioEssays* 15 (1993): 349–354.
 7. Yataro Daigo, Minoru Isomura, Tadashi Nishiwaki, Kazufumi Suzuki, Osamu Maruyama, Kumiko Takeuchi, Yuka Yamane, Rie Hayashi, Maiko Minami, Yoshiaki Hojo, Ikuro Uchiyama, Toshihisa Takagi & Yusuke Nakamura, "Significant Differences in the Frequency of Transcriptional Units, Types and Numbers of Repetitive Elements, GC Content, and the Number of CpG Islands Between a 1010-kb G-band Genomic Segment on Chromosome 9q31.3 and a 1200-kb R-band Genomic Segment on Chromosome 3p21.3," *DNA Research* 6 (1999): 227–233. Freely accessible (2011) at <http://dnaresearch.oxfordjournals.org/cgi/reprint/6/4/227?view=long&pmid=10492169>
 8. Roel van Driel, Paul F. Fransz & Pernette J. Verschure, "The eukaryotic genome: a system regulated at different hierarchical levels," *Journal of Cell Science* 116 (2003): 4067–4075. Freely accessible (2011) at <http://jcs.biologists.org/cgi/reprint/116/20/4067>
 9. Tom Misteli, "Beyond the sequence: cellular organization of genome function," *Cell* 128 (2007): 787–800.
 10. Emile Zuckerkandl, "Junk DNA and sectorial gene repression," *Gene* 205 (1997): 323–343.
 11. Emile Zuckerkandl, "Why so many non-coding nucleotides? The eukaryote genome as an epigenetic machine," *Genetica* 115 (2002): 105–129.
 12. Emile Zuckerkandl & Giacomo Cavalli, "Combinatorial epigenetics, 'junk DNA,' and the evolution of complex organisms," *Gene* 390 (2007): 232–242.
 13. Michael Bulger & Mark Groudine, "Looping versus linking: toward a model for long-distance gene activation," *Genes & Development* 13 (1999): 2465–2477. Freely accessible (2011) at <http://genesdev.cshlp.org/content/13/19/2465.full.pdf+html>
 14. Gong Hong Wei, De Pei Liu & Chih Chuan Liang, "Chromatin domain boundaries: insulators and beyond," *Cell Research* 15 (2005): 292–300. Freely accessible (2011) at <http://www.nature.com/cr/journal/v15/n4/pdf/7290298a.pdf>
 15. Susan E. Celniker & Robert A. Drewell, "Chromatin looping mediates boundary element promoter interactions," *BioEssays* 29 (2007): 7–10.
 16. Peter Fraser, "Transcriptional control thrown for a loop," *Current Opinion in Genetics & Development* 16 (2006): 490–495.
 17. Robert-Jan T. S. Palstra, "Close encounters of the 3C kind: long-range chromatin

- interactions and transcriptional regulation," *Briefings in Functional Genomics and Proteomics* 8 (2009): 297–309.
18. Anita Göndör & Rolf Ohlsson, "Chromosome crosstalk in three dimensions," *Nature* 461 (2009): 212–217.
 19. John L. Rinn, Michael Kertesz, Jordon K. Wang, Sharon L. Squazzo, Xiao Xu, Samantha A. Bruggmann, Henry Goodnough, Jill A. Helms, Peggy J. Farnham, Eran Segal & Howard Y. Chang, "Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Noncoding RNAs," *Cell* 129 (2007): 1311–1323. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2084369/pdf/nihms26949.pdf>
 20. Miao-Chih Tsai, Ohad Manor, Yue Wan, Nima Mosammaparast, Jordon K. Wang, Fei Lan, Yang Shi, Eran Segal & Howard Y. Chang, "Long Noncoding RNA as Modular Scaffold of Histone Modification Complexes," *Science* 329 (2010): 689–693. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2967777/pdf/nihms244741.pdf>
 21. Michaela Angermayr, Ulrich Oechsner, Kerstin Gregor, Gary P. Schroth & Wolfhard Bandlow, "Transcription initiation in vivo without classical transactivators: DNA kinks flanking the core promoter of the housekeeping yeast adenylate kinase gene, AKY2, position nucleosomes and constitutively activate transcription," *Nucleic Acids Research* 30 (2002): 4199–4207. Freely accessible (2011) at <http://nar.oxfordjournals.org/content/30/19/4199.full.pdf+html>
 22. Jason A. Greenbaum, Bo Pang & Thomas D. Tullius "Construction of a genome-scale structural map at single-nucleotide resolution," *Genome Research* 17 (2007): 947–953. Freely accessible (2011) at <http://genome.cshlp.org/content/17/6/947.full.pdf+html>
 23. Stephen C. J. Parker, Loren Hansen, Hatice Ozel Abaan, Thomas D. Tullius & Elliott H. Margulies, "Local DNA Topography Correlates with Functional Non-coding Regions of the Human Genome," *Science* 324 (2009): 389–392.
 24. Antonio Rodríguez-Campos & Fernando Azorín, "RNA Is an Integral Component of Chromatin that Contributes to Its Structural Organization," *PLoS One* 2:11 (2007): e1182. Freely accessible (2011) at <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0001182>
 25. Helder Maiato, Jennifer DeLuca, E. D. Salmon & William C. Earnshaw, "The dynamic kinetochore-microtubule interface," *Journal of Cell Science* 117 (2004): 5461–5477. Freely accessible (2011) at <http://jcs.biologists.org/cgi/reprint/117/23/5461>
 26. Xingkun Liu, Ian McLeod, Scott Anderson, John R. Yates III & Xiangwei He, "Molecular analysis of kinetochore architecture in fission yeast," *EMBO Journal* 24 (2005): 2919–2930. Freely accessible (2011) at <http://www.nature.com/emboj/journal/v24/n16/pdf/7600762a.pdf>
 27. Ajit P. Joglekar, David C. Bouck, Jeffrey N. Molk, Kerry S. Bloom & Edward D. Salmon, "Molecular architecture of a kinetochore-microtubule attachment site," *Nature Cell Biology* 8 (2006): 581–585. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2867088/pdf/nihms199890.pdf>
 28. Iain M. Cheeseman & Arshad Desai, "Molecular architecture of the kinetochore-microtubule interface," *Nature Reviews Molecular Cell Biology* 9 (2008): 33–46.
 29. Xiaohu Wan, Ryan P. O'Quinn, Heather L. Pierce, Ajit P. Joglekar, Walt E. Gall, Jennifer G. DeLuca, Christopher W. Carroll, Song-Tao Liu, Tim J. Yen, Bruce F. McEwen, P. Todd Stukenberg, Arshad Desai & Edward D. Salmon, "Protein Architecture of the Human Kinetochore Microtubule Attachment Site," *Cell*

- 137 (2009): 672–684. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2699050/pdf/nihms114285.pdf>
30. Ajit P. Joglekar, Kerry S. Bloom & Edward D. Salmon, “In vivo protein architecture of the eukaryotic kinetochore with nanometer scale accuracy,” *Current Biology* 19 (2009): 694–699. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2832475/pdf/nihms178290.pdf>
31. Katheleen Gardiner, “Clonability and gene distribution on human chromosome 21: reflections of junk DNA content?” *Gene* 205 (1997): 39–46.
32. James W. Gaubatz & Richard G. Cutler, “Mouse Satellite DNA Is Transcribed in Senescent Cardiac Muscle,” *Journal of Biological Chemistry* 265 (1990): 17753–17758. Freely accessible (2011) at <http://www.jbc.org/content/265/29/17753.long>
33. F. Rudert, S. Bronner, J. M. Garnier & P. Dollé, “Transcripts from opposite strands of gamma satellite DNA are differentially expressed during mouse development,” *Mammalian Genome* 6 (1995): 76–83.
34. Brenda J. Reinhart & David P. Bartel, “Small RNAs Correspond to Centromere Heterochromatic Repeats,” *Science* 297 (2002): 1831. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/297/5588/1831>
35. Bruce P. May, Zachary B. Lippman, Yuda Fang, David L. Spector & Robert A. Martienssen, “Differential Regulation of Strand-Specific Transcripts from *Arabidopsis* Centromeric Satellite Repeats,” *PLoS Genetics* 1:6 (2005): e79. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1317654/pdf/pgen.0010079.pdf>
36. Junjie Lu & David M. Gilbert, “Proliferation-dependent and cell cycle regulated transcription of mouse pericentric heterochromatin,” *Journal of Cell Biology* 179 (2007): 411–412. Freely accessible (2011) at <http://jcb.rupress.org/content/179/3/411.full.pdf+html>
37. Rachel J. O'Neill & Dawn M. Carone, “The role of ncRNA in centromeres: a lesson from marsupials,” *Progress in Molecular and Subcellular Biology* 48 (2009): 77–101.
38. Thomas A. Volpe, Catherine Kidner, Ira M. Hall, Grace Teng, Shiv I. S. Grewal & Robert A. Martienssen, “Regulation of Heterochromatic Silencing and Histone H3 Lysine-9 Methylation by RNAi,” *Science* 297 (2002): 1833–1837. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/297/5588/1833>
39. Christopher N. Topp, Cathy X. Zhong & R. Kelly Dawe, “Centromere-encoded RNAs are integral components of the maize kinetochore,” *Proceedings of the National Academy of Sciences USA* 101 (2004): 15986–15991. Freely accessible (2011) at <http://www.pnas.org/content/101/45/15986.full.pdf+html>
40. Haniaa Bouzinba-Segard, Adeline Guais & Claire Francastel, “Accumulation of small murine minor satellite transcripts leads to impaired centromeric architecture and function,” *Proceedings of the National Academy of Sciences USA* 103 (2006): 8709–8714. Freely accessible (2011) at <http://www.pnas.org/content/103/23/8709.full.pdf+html>
41. Federica Ferri, Haniaa Bouzinba-Segard, Guillaume Velasco, Florent Hubé & Claire Francastel, “Non-coding murine centromeric transcripts associate with and potentiate Aurora B kinase,” *Nucleic Acids Research* 37 (2009): 5071–5080. Freely accessible (2011) at <http://nar.oxfordjournals.org/cgi/reprint/37/15/5071>
42. Lee H. Wong, Kate H. Brettingham-Moore, Lyn Chan, Julie M. Quach, Melissa A. Anderson, Emma L. Northrop, Ross Hannan, Richard Saffery, Margaret L. Shaw, Evan Williams & K. H. Andy Choo, “Centromere RNA is a key component for the assembly of nucleoproteins at

- the nucleolus and centromere," *Genome Research* 17 (2007): 1146–1160. Freely accessible (2011) at <http://genome.cshlp.org/content/17/8/1146.full.pdf+html>
43. Shiv I. S. Grewal & Sarah C. R. Elgin, "Transcription and RNA interference in the formation of heterochromatin," *Nature* 447 (2007): 399–406.
 44. Tom Volpe, Vera Schramke, Georgina L. Hamilton, Sharon A. White, Grace Teng, Robert A. Martienssen & Robin C. Allshire, "RNA interference is required for normal centromere function in fission yeast," *Chromosome Research* 11 (2003): 137–146.
 45. André Verdel, Songtao Jia, Scott Gerber, Tomoyasu Sugiyama, Steven Gygi, Shiv I. S. Grewal & Danesh Moazed, "RNAi-Mediated Targeting of Heterochromatin by the RITS Complex," *Science* 303 (2004): 672–676. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/303/5658/672>
 46. Mohammad R. Motamedi, André Verdel, Serafin U. Colmenares, Scott A. Gerber, Steven P. Gygi & Danesh Moazed, "Two RNAi complexes, RITS and RDRC, physically interact and localize to noncoding centromeric RNAs," *Cell* 119 (2004): 789–802.
 47. Hiroaki Kato, Derek B. Goto, Robert A. Martienssen, Takeshi Urano, Koichi Furukawa & Yota Murakami, "RNA Polymerase II Is Required for RNAi-Dependent Heterochromatin Assembly," *Science* 309 (2005): 467–469. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/309/5733/467>
 48. Pavel Neumann, Huihuang Yan & Jiming Jiang, "The Centromeric Retrotransposons of Rice Are Transcribed and Differentially Processed by RNA Interference," *Genetics* 176 (2007): 749–761. Freely accessible (2011) at <http://www.genetics.org/cgi/reprint/176/2/749>
 49. Angeline Eymery, Mary Callanan & Claire Vourc'h, "The secret message of heterochromatin: new insights into the mechanisms and function of centromeric and pericentric repeat sequence transcription," *International Journal of Developmental Biology* 53 (2009): 259–268. Freely accessible (2011) at <http://www.ijdb.edu.es/web/paper.php?doi=10.1387/ijdb.082673ae>
 50. Jonathan C. Lamb & James A. Birchler, "The role of DNA sequence in centromere formation," *Genome Biology* 4:5 (2003): 214. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2003-4-5-214.pdf>
 51. Mary G. Schueler & Beth A. Sullivan, "Structural and functional dynamics of human centromeric chromatin," *Annual Review of Genomics and Human Genetics* 7 (2006): 301–313.
 52. Beth A. Sullivan, Michael D. Blower & Gary H. Karpen, "Determining centromere identity: cyclical stories and forking paths," *Nature Reviews Genetics* 2 (2001): 584–596.
 53. John J. Harrington, Gil Van Bokkelen, Robert W. Mays, Karen Gustashaw & Huntington F. Willard, "Formation of de novo centromeres and construction of first-generation human artificial microchromosomes," *Nature Genetics* 15 (1997): 345–355.
 54. Desirée du Sart, Michael R. Cancilla, Elizabeth Earle, Jen-i Mao, Richard Saffery, Kellie M. Tainton, Paul Kalitsis, John Martyn, Alyssa E. Barry & K. H. Andy Choo, "A functional neo-centromere formed through activation of a latent human centromere and consisting of non-alpha-satellite DNA," *Nature Genetics* 16 (1997): 144–153.
 55. Peter E. Warburton, "Chromosomal dynamics of human neocentromere formation," *Chromosome Research* 12 (2004): 617–626.
 56. W. C. Earnshaw & N. Rothfield, "Identification of a family of human centromere

- proteins using autoimmune sera from patients with scleroderma," *Chromosoma* 91 (1985): 313–321.
57. Douglas K. Palmer, Kathleen O'Day, Mark H. Wener, Brian S. Andrews & Robert L. Margolis, "A 17-kD Centromere Protein (CENP-A) Copurifies with Nucleosome Core Particles and with Histones," *Journal of Cell Biology* 104 (1987): 805–815. Freely accessible (2011) at <http://jcb.rupress.org/content/104/4/805.long>
 58. Peter E. Warburton, Carol A. Cooke, Sylvie Bourassa, Omid Vafa, Beth A. Sullivan, Gail Stetten, Giorgio Gimelli, Dorothy Warburton, Chris Tyler-Smith, Kevin F. Sullivan, Guy G. Poirier & William C. Earnshaw, "Immunolocalization of CENP-A suggests a distinct nucleosome structure at the inner kinetochore plate of active centromeres," *Current Biology* 7 (1997): 901–904.
 59. Aaron A. Van Hooser, Michael A. Mancini, C. David Allis, Kevin F. Sullivan & B. R. Brinkley, "The mammalian centromere: structural domains and the attenuation of chromatin modeling," *FASEB Journal* 13 Supplement (1999): S216–S220. Freely accessible (2011) at <http://www.fasebj.org/cgi/reprint/13/9002/S216>
 60. Kinya Yoda, Satoshi Ando, Setsuo Morishita, Kenichi Houmura, Keiji Hashimoto, Kunio Takeyasu & Tuneko Okazaki, "Human centromere protein A (CENP-A) can replace histone H3 in nucleosome reconstitution in vitro," *Proceedings of the National Academy of Sciences USA* 97 (2000): 7266–7271. Freely accessible (2011) at <http://www.pnas.org/content/97/13/7266.full.pdf+html>
 61. Ben E. Black, Melissa A. Brock, Sabrina Bédard, Virgil L. Woods, Jr. & Don W. Cleveland, "An epigenetic mark generated by the incorporation of CENP-A into centromeric nucleosomes," *Proceedings of the National Academy of Sciences USA* 104 (2007): 5008–5013. Freely accessible (2011) at <http://www.pnas.org/content/104/12/5008.full.pdf+html>
 62. Mònica Torras-Llort, Olga Moreno-Moreno & Fernando Azorín, "Focus on the centre: the role of chromatin on the regulation of centromere identity and function," *EMBO Journal* 28 (2009): 2337–2348. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2722248/pdf/emboj2009174a.pdf>
 63. Aaron A. Van Hooser, Ilia I. Ouspenski, Heather C. Gregson, Daniel A. Starr, Tim J. Yen, Michael L. Goldberg, Kyoko Yokomori, William C. Earnshaw, Kevin F. Sullivan & B. R. Brinkley, "Specification of kinetochore-forming chromatin by the histone H3 variant CENP-A," *Journal of Cell Science* 114 (2001): 3529–3542. Freely accessible (2011) at <http://jcs.biologists.org/cgi/reprint/114/19/3529>
 64. Larissa J. Vos, Jakub K. Famulski & Gordon K.T. Chan, "How to build a centromere: from centromeric and pericentromeric chromatin to kinetochore assembly," *Biochemistry and Cell Biology* 84 (2006): 619–639. Freely accessible (2011) at <http://article.pubs.nrc-cnrc.gc.ca/ppv/RPViewDoc?issn=0829-8211&volume=84&issue=4&startPage=619>
 65. Deborah L. Grady, Robert L. Ratliff, Donna L. Robinson, Erin C. McCanlies, Julianne Meyne & Robert K. Moyzis, "Highly conserved repetitive DNA sequences are present at human centromeres," *Proceedings of the National Academy of Sciences USA* 89 (1992): 1695–1699. Freely accessible (2011) at <http://www.pnas.org/content/89/5/1695.full.pdf+html>
 66. Jiming Jiang, Shuhei Nasuda, Fenggao Dong, Christopher W. Sherrer, Sung-Sick Woo, Rod A. Wing, Bikram S. Gill & David C. Ward, "A conserved repetitive DNA element located in the centromeres of cereal chromosomes," *Proceedings of the National Academy of Sciences USA* 93 (1996): 14210–14213. Freely accessible

- (2011) at <http://www.pnas.org/content/93/24/14210.full.pdf+html>
67. Huntington F. Willard, "Chromosome-Specific Organization of Human Alpha Satellite DNA," *American Journal of Human Genetics* 37 (1985): 524–532. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1684601/pdf/ajhg00158-0092.pdf>
 68. John S. Wayne & Huntington F. Willard, "Chromosome-specific alpha satellite DNA: nucleotide sequence analysis of the 2.0 kilobasepair repeat from the human X chromosome," *Nucleic Acids Research* 13 (1985): 2731–2743. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC341190/pdf/nar00302-0062.pdf>
 69. R. Heller, K. E. Brown, C. Burgtorf & W. R. A. Brown, "Mini-chromosomes derived from the human Y chromosome by telomere directed chromosome breakage," *Proceedings of the National Academy of Sciences USA* 93 (1996): 7125–7130. Freely accessible (2011) at <http://www.pnas.org/content/93/14/7125.full.pdf+html>
 70. Terence D. Murphy and Gary H. Karpen, "Centromeres Take Flight: Alpha Satellite and the Quest for the Human Centromere," *Cell* 93 (1998): 317–320.
 71. Brenda R. Grimes, Angela A. Rhoades & Huntington F. Willard, "Alpha-satellite DNA and vector composition influence rates of human artificial chromosome formation," *Molecular Therapy* 5 (2002): 798–805.
 72. M. Katharine Rudd, Robert W. Mays, Stuart Schwartz & Huntington F. Willard, "Human Artificial Chromosomes with Alpha Satellite-Based De Novo Centromeres Show Increased Frequency of Nondisjunction and Anaphase Lag," *Molecular and Cellular Biology* 23 (2003): 7689–7697. Freely accessible (2011) at <http://mcb.asm.org/cgi/rapid/23/21/7689>
 73. Gregory P. Copenhaver, Kathryn Nickel, Takashi Kuromori, Maria-Ines Benito, Samir Kaul, Xiaoying Lin, Michael Bevan, George Murphy, Barbara Harris, Laurence D. Parnell, W. Richard McCombie, Robert A. Martienssen, Marco Marra & Daphne Preuss, "Genetic Definition and Sequence Analysis of *Arabidopsis* Centromeres," *Science* 286 (1999): 2468–2474. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/286/5449/2468>
 74. Wolfgang Haupt, Thilo C. Fischer, Sabine Winderl, Paul Fransz & Ramón A. Torres-Ruiz, "The centromere1 (CEN1) region of *Arabidopsis thaliana*: architecture and functional impact of chromatin," *The Plant Journal* 27 (2001): 285–296.
 75. Sarah E. Hall, Gregory Kettler & Daphne Preuss, "Centromere Satellites from *Arabidopsis* Populations: Maintenance of Conserved and Variable Domains," *Genome Research* 13 (2003): 195–205. Freely accessible (2011) at <http://genome.cshlp.org/content/13/2/195.full.pdf+html>
 76. Anthony W. I. Lo, Jeffrey M. Craig, Richard Saffery, Paul Kalitsis, Danielle V. Irvine, Elizabeth Earle, Dianna J. Magliano & K. H. Andy Choo, "A 330 kb CENP-A binding domain and altered replication timing at a human neocentromere," *EMBO Journal* 20 (2001): 2087–2096. Freely accessible (2011) at <http://www.nature.com/emboj/journal/v20/n8/pdf/7593708a.pdf>
 77. Anderly C. Chueh, Lee H. Wong, Nicholas Wong & K.H. Andy Choo, "Variable and hierarchical size distribution of L1-retroelement-enriched CENP-A clusters within a functional human neocentromere," *Human Molecular Genetics* 14 (2005): 85–93. Freely accessible (2011) at <http://hmg.oxfordjournals.org/cgi/rapid/14/1/85>
 78. Anderly C. Chueh, Emma L. Northrop, Kate H. Brettingham-Moore, K. H. Andy Choo & Lee H. Wong, "LINE Retrotransposon RNA Is an Essential

- Structural and Functional Epigenetic Component of a Core Neocentromeric Chromatin," *PLoS Genetics* 5:1 (2009): e1000354. Freely accessible (2011) at <http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1000354>
79. Stephen M. Stack, David B. Brown & William C. Dewey, "Visualization of interphase chromosomes," *Journal of Cell Science* 26 (1977): 281–299. Limited access (2011) at <http://jcs.biologists.org/cgi/reprint/26/1/281>
 80. Jenny A. Croft, Joanna M. Bridger, Shelagh Boyle, Paul Perry, Peter Teague & Wendy A. Bickmore, "Differences in the Localization and Morphology of Chromosomes in the Human Nucleus," *Journal of Cell Biology* 145 (1999): 1119–1131. Freely accessible (2011) at <http://jcb.rupress.org/content/145/6/1119.full.pdf+html>
 81. Heiner Albiez, Marion Cremer, Cinzia Tiberi, Lorella Vecchio, Lothar Schermelleh, Sandra Dittrich, Katrin Küpper, Boris Joffe, Tobias Thormeyer, Johann von Hase, Siwei Yang, Karl Rohr, Heinrich Leonhardt, Irina Solovei, Christoph Cremer, Stanislav Fakan & Thomas Cremer, "Chromatin domains and the interchromatin compartment form structurally defined and functionally interacting nuclear networks," *Chromosome Research* 14 (2006): 707–733.
 82. Thomas Cremer & Marion Cremer, "Chromosome Territories," *Cold Spring Harbor Perspectives in Biology* 2 (2010): a003889. Freely accessible (2011) at <http://cshperspectives.cshlp.org/content/2/3/a003889.full.pdf+html>
 83. Emanuela V. Volpi, Edith Chevret, Tania Jones, Radost Vatcheva, Jill Williamson, Stephan Beck, R. Duncan Campbell, Michelle Goldsworthy, Stephen H. Powis, Jiannis Ragoussis, John Trowsdale & Denise Sheer, "Large-scale chromatin organization of the major histocompatibility complex and other regions of human chromosome 6 and its response to interferon in interphase nuclei," *Journal of Cell Science* 113 (2000): 1565–1576. Freely accessible (2011) at <http://jcs.biologists.org/cgi/reprint/113/9/1565>
 84. Li-Feng Zhang, Khanh D. Huynh & Jeannie T. Lee, "Perinucleolar targeting of the inactive X during S phase: evidence for a role in the maintenance of silencing," *Cell* 129 (2007): 693–706.
 85. Christian Lanctôt, Thierry Cheutin, Marion Cremer, Giacomo Cavalli & Thomas Cremer, "Dynamic genome architecture in the nuclear space: regulation of gene expression in three dimensions," *Nature Reviews Genetics* 8 (2007): 104–115.
 86. Boris Joffe, Heinrich Leonhardt & Irina Solovei, "Differentiation and large scale spatial organization of the genome," *Current Opinion in Genetics and Development* 20 (2010): 562–569.
 87. M. R. Hübner & D. L. Spector, "Chromatin dynamics," *Annual Review of Biophysics* 39 (2010): 471–489.
 88. Hideki Tanizawa, Osamu Iwasaki, Atsunari Tanaka, Joseph R. Capizzi, Priyankara Wickramasinghe, Mihee Lee, Zhiyan Fu & Ken-ichi Noma, "Mapping of long-range associations throughout the fission yeast genome reveals global genome organization linked to transcriptional regulation," *Nucleic Acids Research* 38 (2010): 8164–8177. Freely accessible (2011) at <http://nar.oxfordjournals.org/content/38/22/8164.long>
 89. Luis A. Parada, Philip G. McQueen & Tom Misteli, "Tissue-specific spatial organization of genomes," *Genome Biology* 5:7 (2004): R44. Freely accessible (2011) at <http://genomebiology.com/content/pdf/gb-2004-5-7-r44.pdf>
 90. Tom Sexton, Heiko Schöber, Peter Fraser & Susan M. Gasser, "Gene regulation through nuclear organization," *Nature Structural & Molecular Biology* 14 (2007): 1049–1055.

91. Takumi Takizawa, Karen J. Meaburn & Tom Misteli, "The meaning of gene positioning," *Cell* 135 (2008): 9–13.
92. Erik D. Andrulis, Aaron M. Neiman, David C. Zappulla & Rolf Sternglanz, "Perinuclear localization of chromatin facilitates transcriptional silencing," *Nature* 394 (1998): 592–595.
93. Shelagh Boyle, Susan Gilchrist, Joanna M. Bridger, Nicola L. Mahy, Juliet A. Ellis & Wendy A. Bickmore, "The spatial organization of human chromosomes within the nuclei of normal and emerin-mutant cells," *Human Molecular Genetics* 10 (2001): 211–219. Freely accessible (2011) at <http://hmg.oxfordjournals.org/content/10/3/211.full.pdf+html>
94. Lars Guelen, Ludo Pagie, Emilie Brasset, Wouter Meuleman, Marius B. Faza, Wendy Talhout, Bert H. Eussen, Annelies de Klein, Lodewyk Wessels, Wouter de Laat & Bas van Steensel, "Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions," *Nature* 453 (2008): 948–951.
95. Lee E. Finlan, Duncan Sproul, Inga Thomson, Shelagh Boyle, Elizabeth Kerr, Paul Perry, Bauke Ylstra, Jonathan R. Chubb & Wendy A. Bickmore, "Recruitment to the Nuclear Periphery Can Alter Expression of Genes in Human Cells," *PLoS Genetics* 4:3 (2008): e1000039. Freely accessible (2011) at <http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1000039>
96. K. L. Reddy, J. M. Zullo, E. Bertolino & H. Singh, "Transcriptional repression mediated by repositioning of genes to the nuclear lamina," *Nature* 452 (2008): 243–247.
97. Myriam Ruault, Marion Dubarry & Angela Taddei, "Re-positioning genes to the nuclear envelope in mammalian cells: impact on transcription," *Trends in Genetics* 24 (2008): 574–581.
98. Davide Marenduzzo, Cristian Micheletti & Peter R. Cook, "Entropy-Driven Genome Organization," *Biophysical Journal* 90 (2006): 3712–3721. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1440752/pdf/3712.pdf>
99. Peter R. Cook & Davide Marenduzzo, "Entropic organization of interphase chromosomes," *Journal of Cell Biology* 186 (2009): 825–834. Freely accessible (2011) at <http://jcb.rupress.org/content/186/6/825.full.pdf+html>
100. Jan Postberg, Olga Alexandrova, Thomas Cremer & Hans J. Lipps, "Exploiting nuclear duality of ciliates to analyse topological requirements for DNA replication and transcription," *Journal of Cell Science* 118 (2005): 3973–3983. Freely accessible (2011) at <http://jcs.biologists.org/cgi/reprint/118/17/3973>
101. L. D. Carter-Dawson & M. M. LaVail, "Rods and cones in the mouse retina. I. Structural analysis using light and electron microscopy," *Journal of Comparative Neurology* 188 (1979): 245–262.
102. Seth Blackshaw, Rebecca E. Fraioli, Takahisa Furukawa & Constance L. Cepko, "Comprehensive analysis of photoreceptor gene expression and the identification of candidate retinal disease genes," *Cell* 107 (2001): 579–589.
103. Dominique Helmlinger, Sara Hardy, Greta Abou-Sleymane, Adrien Eberlin, Aaron B. Bowman, Anne Gansmüller, Serge Picaud, Huda Y. Zoghbi, Yvon Trotter, László Tora & Didier Devys, "Glutamine-Expanded Ataxin-7 Alters TFC/STAGA Recruitment and Chromatin Structure Leading to Photoreceptor Dysfunction," *PLoS Biology* 4:3 (2006): e67. Freely accessible (2011) at <http://www.plosbiology.org/article/info%3Adoi%2F10.1371%2Fjournal.pbio.0040067>
104. Irina Solovei, Moritz Kreysing, Christian Lancrôt, Süleyman Kösem, Leo Peichl, Thomas Cremer, Jochen Guck &

- Boris Joffe, "Nuclear Architecture of Rod Photoreceptor Cells Adapts to Vision in Mammalian Evolution," *Cell* 137 (2009): 356–368.
105. Irina Solovei, Moritz Kreysing, Christian Lanctôt, Süleyman Kösem, Leo Peichl, Thomas Cremer, Jochen Guck & Boris Joffe, "Nuclear Architecture of Rod Photoreceptor Cells Adapts to Vision in Mammalian Evolution," *Cell* 137 (2009): Supplementary Data. Freely accessible (2011) at <http://download.cell.com/mmc/journals/0092-8674/PIIS0092867409001378.mmc1.pdf>
106. Caroline Kizilyaprak, Danièle Spehner, Didier Devys & Patrick Schultz, "In Vivo Chromatin Organization of Mouse Rod Photoreceptors Correlates with Histone Modifications," *PLoS One* 5:6 (2010): e11039. Freely accessible (2011) at <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0011039>
107. Moritz Kreysing, Lars Boyde, Jochen Guck & Kevin J. Chalut, "Physical insight into light scattering by photoreceptor cell nuclei," *Optics Letters* 35 (2010): 2639–2641.
3. Todd A. Gray, Alison Wilson, Patrick J. Fortin & Robert D. Nicholls, "The putatively functional *Mkrn1-p1* pseudogene is neither expressed nor imprinted, nor does it regulate its source gene in trans," *Proceedings of the National Academy of Sciences USA* 103 (2006): 12039–12044. Freely accessible (2011) at <http://www.pnas.org/content/103/32/12039.full.pdf+html>
4. José Manuel Franco-Zorrilla, Adrián Valli, Marco Todesco, Isabel Mateos, María Isabel Puga, Ignacio Rubio-Somoza, Antonio Leyva, Detlef Weigel, Juan Antonio García & Javier Paz-Ares, "Target mimicry provides a new mechanism for regulation of microRNA activity," *Nature Genetics* 39 (2007): 1033–1037.
5. Laura Poliseno, Leonardo Salmena, Jianguen Zhang, Brett Carver, William J. Haveman & Pier Paolo Pandolfi, "A coding-independent function of gene and pseudogene mRNAs regulates tumour biology," *Nature* 465 (2010): 1033–1038.
6. Kayoko Yamada, Jun Lim, Joseph M. Dale, Huaming Chen, Paul Shinn, Curtis J. Palm, Audrey M. Southwick, Hank C. Wu, Christopher Kim, Michelle Nguyen, Paul Pham, Rosa Cheuk, George Karlin-Newmann, Shirley X. Liu, Bao Lam, Hitomi Sakano, Troy Wu, Guixia Yu, Molly Miranda, Hong L. Quach, Matthew Tripp, Charlie H. Chang, Jeong M. Lee, Mitsue Toriumi, Marie M. H. Chan, Carolyn C. Tang, Courtney S. Onodera, Justine M. Deng, Kenji Akiyama, Yasser Ansari, Takahiro Arakawa, Jenny Banh, Fumika Banno, Leah Bowser, Shelise Brooks, Piero Carninci, Qimin Chao, Nathan Choy, Akiko Enju, Andrew D. Goldsmith, Mani Gurjal, Nancy F. Hansen, Yoshihide Hayashizaki, Chanda Johnson-Hopson, Vickie W. Hsuan, Kei Iida, Meagan Karnes, Shehnaz Khan, Eric Koesema, Junko Ishida, Paul X. Jiang, Ted Jones, Jun Kawai, Asako Kamiya, Cristina Meyers, Maiko Nakajima, Mari Narusaka, Motoaki Seki, Tetsuya Sakurai, Masakazu Satou, Racquel Tamse, Maria Vaysberg, Erika

8. SOME RECENT DEFENDERS OF JUNK DNA

1. Shinji Hirotsume, Noriyuki Yoshida, Amy Chen, Lisa Garrett, Fumihiro Sugiyama, Satoru Takahashi, Ken-ichi Yagami, Anthony Wynshaw-Boris & Atsushi Yoshiki, "An expressed pseudogene regulates the messenger-RNA stability of its homologous coding gene," *Nature* 423 (2003): 91–96.
2. William S. Harris & John H. Calvert, "Intelligent Design: The Scientific Alternative to Evolution," *The National Catholic Bioethics Quarterly* (August 2003): 531–561. Freely accessible (2011) at http://www.intelligentdesignnetwork.org/NCBQ3_3HarrisCalvert.pdf

- K. Wallender, Cecilia Wong, Yuki Yamamura, Shiaulou Yuan, Kazuo Shinozaki, Ronald W. Davis, Athanasios Theologis & Joseph R. Ecker, "Empirical Analysis of Transcriptional Activity in the *Arabidopsis* Genome," *Science* 302 (2003): 842–846. Available online with registration (2011) at <http://www.sciencemag.org/cgi/content/full/302/5646/842>
7. Jason M. Johnson, Stephen Edwards, Daniel Shoemaker & Eric E. Schadt, "Dark matter in the genome: evidence of widespread transcription detected by microarray tiling experiments," *Trends in Genetics* 21 (2005): 93–102.
 8. Guy Riddihough, "In the Forests of RNA Dark Matter," *Science* 309 (2005): 1507.
 9. Harm van Bakel & Timothy R. Hughes, "Establishing legitimacy and function in the new transcriptome," *Briefings in Functional Genomics & Proteomics* 8 (2009): 424–436.
 10. Harm van Bakel, Corey Nislow, Benjamin J. Blencowe & Timothy R. Hughes, "Most 'Dark Matter' Transcripts Are Associated With Known Genes," *PLoS Biology* 8:5 (2010): e1000371. Freely accessible (2011) at <http://www.plosbiology.org/article/info%3Adoi%2F10.1371%2Fjournal.pbio.1000371>
 11. The ENCODE Project Consortium, "Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project," *Nature* 447 (2007): 799–816. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2212820/pdf/nihms27513.pdf>
 12. Richard Robinson, "Dark Matter Transcripts: Sound and Fury, Signifying Nothing?" *PLoS Biology* 8:5 (2010): e1000370. Freely accessible (2011) at <http://www.plosbiology.org/article/info%3Adoi%2F10.1371%2Fjournal.pbio.1000370>
 13. Carl Zimmer, "How Many Sparks in the Genome?" *Discover Magazine: The Loom* (May 19, 2010). Freely accessible (2011) at <http://blogs.discovermagazine.com/loom/2010/05/19/how-many-sparks-in-the-genome/>
 14. RepeatMasker, *Institute for Systems Biology*. Freely accessible (2011) at <http://www.repeatmasker.org/>
 15. Jill Cheng, Philipp Kapranov, Jorg Drenkow, Sujit Dike, Shane Brubaker, Sandeep Patel, Jeffrey Long, David Stern, Hari Tammanna, Gregg Helt, Victor Sementchenko, Antonio Piccolboni, Stefan Bekiranov, Dione K. Bailey, Madhavan Ganesh, Srinka Ghosh, Ian Bell, Daniela S. Gerhard & Thomas R. Gingeras, "Transcriptional Maps of 10 Human Chromosomes at 5-Nucleotide Resolution," *Science* 308 (2005): 1149–1154.
 16. P. Z. Myers, "Junk DNA is still junk," *The Panda's Thumb* (May 19, 2010). Freely accessible (2011) at <http://pandasthumb.org/archives/2010/05/junk-dna-is-sti.html>
 17. Philipp Kapranov, Georges St. Laurent, Tal Raz, Fatih Ozsolak, C. Patrick Reynolds, Poul H. B. Sorensen, Gregory Reaman, Patrice Milos, Robert J. Arceci, John F. Thompson & Timothy J. Triche, "The majority of total nuclear-encoded non-ribosomal RNA in a human cell is 'dark matter' un-annotated RNA," *BMC Biology* 8:1 (2010): 149. Freely accessible (2011) at <http://www.biomedcentral.com/1741-7007/8/149>
 18. Mark Blaxter, "Revealing the Dark Matter of the Genome," *Science* 330 (2010): 1758–1759.
 19. Philipp Kapranov, Aaron T. Willingham & Thomas R. Gingeras, "Genome-wide transcription and the implications for genomic organization," *Nature Reviews Genetics* 8 (2007): 413–423.
 20. John L. Rinn, Michael Kertesz, Jordon K. Wang, Sharon L. Squazzo, Xiao Xu, Samantha A. Brugmann, Henry Goodnough, Jill A. Helms, Peggy J. Farnham, Eran Segal, and Howard Y. Chang, "Functional

- Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Non-Coding RNAs," *Cell* 129 (2007): 1311–1323. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2084369/?tool=pubmed>
21. Elizabeth Pennisi, "Shining a Light on the Genome's 'Dark Matter,'" *Science* 330 (2010): 1614.
22. T. Ryan Gregory, "Junk DNA: let me say it one more time," *Genomicron* (September 16, 2007). Freely accessible (2011) at <http://www.genomicron.evolverzone.com/2007/09/junk-dna-let-me-say-it-one-more-time/>
23. T. Ryan Gregory, "The onion test," *Genomicron* (April 25, 2007). Freely accessible (2011) at <http://www.genomicron.evolverzone.com/2007/04/onion-test/>
24. Roger Vendrely & Colette Vendrely, "La teneur du noyau cellulaire en acide désoxyribonucléique à travers les organes, les individus et les espèces animales: Techniques et premiers resultants," *Experientia* 4 (1948): 434–436.
25. A. E. Mirsky & Hans Ris, "The Desoxyribonucleic Acid Content of Animal Cells and Its Evolutionary Significance," *Journal of General Physiology* 34 (1951): 451–462. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2147229/pdf/451.pdf>
26. C. A. Thomas, Jr., "The Genetic Organization of Chromosomes," *Annual Review of Genetics* 5 (1971): 237–256.
27. Joseph G. Gall, "Chromosome Structure and the C-Value Paradox," *Journal of Cell Biology* 91 (1981): 3s–14s. Freely accessible (2011) at <http://jcb.rupress.org/content/91/3/3s.full.pdf>
28. Gordon P. Moore, "The C-Value Paradox," *BioScience* 34 (July/August 1984): 425–429.
29. Wen-Hsiung Li, *Molecular Evolution* (Sunderland, MA: Sinauer Associates, 1997), pp. 379–384.
30. Daniel L. Hartl, "Molecular melodies in high and low C," *Nature Reviews Genetics* 1 (2000): 145–149.
31. Thomas Cavalier-Smith, "Nuclear volume control by nucleoskeletal DNA, selection for cell volume and cell growth rate, and the solution of the DNA C-value paradox," *Journal of Cell Science* 34 (1978): 247–278. Freely accessible (2011) at <http://jcs.biologists.org/cgi/reprint/34/1/247>
32. Thomas Cavalier-Smith, "Cell Volume and the Evolution of Eukaryotic Genome Size," pp. 105–184 in Thomas Cavalier-Smith (editor), *The Evolution of Genome Size* (Chichester, UK: John Wiley & Sons, 1985).
33. Alexander E. Vinogradov, "Nucleotypic Effect in Homeotherms: Body-Mass-Corrected Basal Metabolic Rate of Mammals Is Related to Genome Size," *Evolution* 49 (1995): 1249–1259.
34. R. A. Van Den Bussche, J. L. Longmire & R. J. Baker, "How bats achieve a small C-value: frequency of repetitive DNA in *Macrotus*," *Mammalian Genome* 6 (1995): 521–525.
35. Austin L. Hughes & Marianne K. Hughes, "Small genomes for better flyers," *Nature* 377 (1995): 391.
36. Alexander E. Vinogradov, "Nucleotypic Effect in Homeotherms: Body-Mass Independent Resting Metabolic Rate of Passerine Birds Is Related to Genome Size," *Evolution* 51 (1997): 220–225.
37. T. Ryan Gregory, "A bird's-eye view of the C-value enigma: genome size, cell size, and metabolic rate in the class aves," *Evolution* 56 (2002): 121–130.
38. Stanley K. Sessions & Allan Larson, "Developmental Correlates of Genome Size in Plethodontid Salamanders and their Implications for Genome Evolution," *Evolution* 41 (1987): 1239–1251.
39. T. Ryan Gregory & Paul D. N. Hebert, "The Modulation of DNA Content: Proximate Causes and Ultimate Consequences," *Genome Research* 9 (1999): 317–324. Freely

- accessible (2011) at <http://genome.cshlp.org/content/9/4/317.full.pdf+html>
40. T. Ryan Gregory, "Genome size and developmental complexity," *Genetica* 115 (2002): 131–146.
 41. T. Ryan Gregory, "The C-value Enigma in Plants and Animals: A Review of Parallels and an Appeal for Partnership," *Annals of Botany* 95 (2005): 133–146. Freely accessible (2011) at <http://aob.oxfordjournals.org/content/95/1/133.full.pdf+html>
 42. T. Ryan Gregory & J. S. Johnston, "Genome size diversity in the family Drosophilidae," *Heredity* 101 (2008): 228–238.
 43. Emile Zuckerkandl, "Gene control in eukaryotes and the c-value paradox 'excess' DNA as an impediment to transcription of coding sequences," *Journal of Molecular Evolution* 9 (1976): 73–104.
 44. Sean Luke, "Evolutionary computation and the c-value paradox," *Proceedings of the 2005 conference on Genetic and Evolutionary Computation* (2005): 91–97.
 45. Thomas Cavalier-Smith, "Economy, speed and size matter: evolutionary forces driving nuclear genome miniaturization and expansion," *Annals of Botany* 95 (2005): 147–175.
 46. Ryan J. Taft, Michael Pheasant & John S. Mattick, "The relationship between non-protein-coding DNA and eukaryotic complexity," *BioEssays* 29 (2007): 288–299.
 47. L. I. Patrushev & I. G. Minkevich, "The Problem of the Eukaryotic Genome Size," *Biochemistry* (Moscow) 73 (2008): 1519–1552. Freely accessible (2011) at <http://protein.bio.msu.ru/biokhimiya/contents/v73/full/73131519.html>
 48. Eduard Kejnovsky, Ilia J. Leitch & Andrew R. Leitch, "Contrasting evolutionary dynamics between angiosperm and mammalian genomes," *Trends in Ecology and Evolution* 24 (2009): 572–582.
 49. T. Ryan Gregory, "Coincidence, coevolution, or causation? DNA content, cell size, and the C-value enigma," *Biological Reviews of the Cambridge Philosophical Society* 76 (2001): 65–101.
 50. T. Ryan Gregory, "Genome Size Evolution in Animals," pp. 3–87 in T. Ryan Gregory (editor), *The Evolution of the Genome* (Amsterdam: Elsevier, 2005), pp. 48–49.
 51. T. Ryan Gregory, "An opportunity for ID to be scientific," *Genomicron* (July 10, 2007). Freely accessible (2011) at <http://www.genomicron.evolverzone.com/2007/07/opportunity-for-id-to-be-scientific/>
 52. William A. Dembski, *Intelligent Design: The Bridge Between Science and Theology* (Downer's Grove, IL: InterVarsity Press, 2002), p. 150.
 53. William A. Dembski, *The Design Revolution* (Downer's Grove, IL: InterVarsity Press, 2004), p. 272.
 54. T. Ryan Gregory, "Function, non-function, some function: a brief history of junk DNA," *Genomicron* (June 14, 2007). Freely accessible (2011) at <http://www.genomicron.evolverzone.com/2007/06/function-non-function-some-function/>

9. A SUMMARY OF THE CASE FOR FUNCTIONALITY IN JUNK DNA

1. Luis M. Mendes Soares & Juan Valcárcel, "The expanding transcriptome: the genome as the 'Book of Sand,'" *EMBO Journal* 25 (2006): 923–931. Available online with registration (2011) at <http://www.nature.com/emboj/journal/v25/n5/full/7601023a.html>
2. Piero Carninci, Jun Yasuda & Yoshihide Hayashizaki, "Multifaceted mammalian transcriptome," *Current Opinion in Cell Biology* 20 (2008): 274–280.
3. Yoseph Barash, John A. Calarco, Weijun Gao, Qun Pan, Xinchun Wang, Ofer Shai, Benjamin J. Blencowe & Brendan J. Frey, "Deciphering the splicing code," *Nature* 465 (2010): 53–59.
4. Laura Poliseno, Leonardo Salmena, Jianguen Zhang, Brett Carver, William

- J. Haveman & Pier Paolo Pandolfi, "A coding-independent function of gene and pseudogene mRNAs regulates tumour biology," *Nature* 465 (2010): 1033–1038.
5. Ryan D. Walters, Jennifer F. Kugel & James A. Goodrich, "InvAluable junk: the cellular impact and function of *Alu* and B2 RNAs," *IUBMB Life* 61 (2009): 831–837.
 6. Victoria V. Lunyak, Gratien G. Prefontaine, Esperanza Núñez, Thorsten Cramer, Bong-Gun Ju, Kenneth A. Ohgi, Kasey Hutt, Rosa Roy, Angel García-Díaz, Xiaoyan Zhu, Yun Yung, Lluís Montoliu, Christopher K. Glass & Michael G. Rosenfeld, "Developmentally regulated activation of a SINE B2 repeat as a domain boundary in organogenesis," *Science* 317 (2007): 248–251.
 7. Jonathan P. Stoye, "Proviral protein provides placental function," *Proceedings of the National Academy of Sciences USA* 106 (2009): 11827–11828. Freely accessible (2011) at <http://www.pnas.org/content/106/29/11827.full.pdf+html>
 8. Emile Zuckerkandl, "Why so many non-coding nucleotides? The eukaryote genome as an epigenetic machine," *Genetica* 115 (2002): 105–129.
 9. Stephen C. J. Parker, Loren Hansen, Hatice Ozel Abaan, Thomas D. Tullius & Elliott H. Margulies, "Local DNA Topography Correlates with Functional Non-coding Regions of the Human Genome," *Science* 324 (2009): 389–392.
 10. T. Ryan Gregory, "Junk DNA: let me say it one more time," *Genomicron* (September 16, 2007). Freely accessible (2011) at <http://www.genomicron.evolverzone.com/2007/09/junk-dna-let-me-say-it-one-more-time/>
 11. T. Ryan Gregory, "The onion test," *Genomicron* (April 25, 2007). Freely accessible (2011) at <http://www.genomicron.evolverzone.com/2007/04/onion-test/>
 12. Harm van Bakel, Corey Nislow, Benjamin J. Blencowe & Timothy R. Hughes, "Most 'Dark Matter' Transcripts Are Associated With Known Genes," *PLoS Biology* 8 (2010): e1000371. Freely accessible (2011) at <http://www.plosbiology.org/article/info%3Adoi%2F10.1371%2Fjournal.pbio.1000371>
 13. P. Z. Myers, "Junk DNA is still junk," *The Panda's Thumb* (May 19, 2010). Freely accessible (2011) at <http://pandasthumb.org/archives/2010/05/junk-dna-is-sti.html>
 14. Philipp Kapranov, Georges St. Laurent, Tal Raz, Fatih Ozsolak, C. Patrick Reynolds, Poul H. B. Sorensen, Gregory Reaman, Patrice Milos, Robert J. Arceci, John F. Thompson & Timothy J. Triche, "The majority of total nuclear-encoded non-ribosomal RNA in a human cell is 'dark matter' un-annotated RNA," *BMC Biology* 8:1 (2010): 149. Freely accessible (2011) at <http://www.biomedcentral.com/1741-7007/8/149>

10. FROM JUNK DNA TO A NEW UNDERSTANDING OF THE GENOME

1. Francis S. Collins, *The Language of God: A Scientist Presents Evidence for Belief* (New York: Free Press, 2006), p. 136.
2. John C. Avise, *Inside the Human Genome: A Case for Non-Intelligent Design* (Oxford: Oxford University Press, 2010), p. 115.
3. Douglas J. Futuyma, *Evolution* (Sunderland, MA: Sinauer Associates, 2005), p. 456.
4. PubMed. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/sites/pubmed>
5. James A. Shapiro & Richard von Sternberg, "Why repetitive DNA is essential to genome function," *Biological Reviews* 80 (2005): 227–250. Freely accessible (2011) at <http://shapiro.bsd.uchicago.edu/Shapiro&Sternberg.2005.BiolRevs.pdf>
6. The ENCODE Project Consortium, "Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project," *Nature*

- 447 (2007): 799–816. Freely accessible (2011) at <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2212820/pdf/nihms27513.pdf>
7. Geoff Spencer & Anna-Lynn Wegener, "New Findings Challenge Established Views on Human Genome," *NIH News* (June 13, 2007). Freely accessible (2011) at <http://genome.gov/25521554>
8. Catherine Shaffer, "One Scientist's Junk Is a Creationist's Treasure," *Wired Magazine Blog* (June 13, 2007). Freely accessible (2011) at http://www.wired.com/science/discoveries/news/2007/06/junk_dna
9. Francis S. Collins, *The Language of Life: DNA and the Revolution in Personalized Medicine* (New York: HarperCollins, 2010), pp. 5–6, 9–10.
10. Collins, *The Language of Life*, p. 293.
11. Francis S. Collins, *The Language of God: A Scientist Presents Evidence for Belief* (New York: Free Press, 2006), pp. 199–203.
12. "About the BioLogos Foundation," BioLogos. Freely accessible (2011) at <http://biologos.org/about>
13. Darrel Falk, "A Rejoinder to Part II of Stephen C. Meyer's Response to Francisco Ayala," BioLogos Forum (March 11, 2010). Freely accessible (2011) at <http://biologos.org/blog/a-rejoinder-to-meyer-2>
14. Karl Giberson, "Does Intelligent Design Really Explain a Complex and Puzzling World?" BioLogos Forum (March 15, 2010). Freely accessible (2011) at <http://biologos.org/blog/does-intelligent-design-really-explain-a-complex-and-puzzling-world/>
15. Center for Science & Culture Staff, "Bibliography of Supplementary Resources for Science Instruction," *Discovery Institute* (March 11, 2002). Freely accessible (2011) at <http://www.discovery.org/a/1127>
16. NCSE Staff, "Analysis of the Discovery Institute's Bibliography," *National Center for Science Education* (June 1, 2002). Freely accessible (2011) at <http://ncse.com/creationism/general/analysis-discovery-institutes-bibliography>
17. NCSE Staff, "Analysis of the Discovery Institute's Bibliography: Appendix," *National Center for Science Education* (June 1, 2002). Freely accessible (2011) at <http://ncse.com/creationism/general/analysis-discovery-institutes-bibliography-appendix>
18. Center for Science & Culture Staff, "Questions and Answers About the Discovery Institute's Bibliography of Supplementary Resources for Ohio Science Instruction," *Discovery Institute* (April 15, 2002). Freely accessible (2011) at <http://www.arn.org/docs2/news/discoveryresponse-toncse041702.htm>
19. Charles Darwin, *The Origin of Species by Means of Natural Selection* (London: John Murray, 1859), p. 459. Freely accessible (2011) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F373&pageseq=477>
20. Darwin, *The Origin of Species*, p. 437. Freely accessible (2011) at <http://darwin-online.org.uk/content/frameset?viewtype=side&itemID=F373&pageseq=455>
21. Jonathan Wells, "Darwin's Straw God Argument," *Journal of Interdisciplinary Studies* 22 (2010): 67–88. An earlier version (December 31, 2008) is freely accessible (2011) at <http://www.discovery.org/a/8101>
22. Neal C. Gillespie, *Charles Darwin and the Problem of Creation* (Chicago: The University of Chicago Press, 1979), pp. 124–125, 146.
23. Cornelius G. Hunter, *Darwin's God* (Grand Rapids, MI: Brazos Press, 2001), pp. 48–49, 84, 158.
24. Paul A. Nelson, "The role of theology in current evolutionary reasoning," *Biology and Philosophy* 11 (1996): 493–517.
25. Gregory Radick, "Deviance, Darwinina-Style," *Metascience* (2005) 14:453–457. Freely accessible (2011) at <http://www.>

- personal.leeds.ac.uk/~phlgrm/Greg%20Articles/Deviance.pdf
26. Abigail J. Lustig, "Natural Atheology," pp. 69–83 in Abigail J. Lustig, Robert J. Richards & Michael Ruse (editors), *Darwinian Heresies* (Cambridge: Cambridge University Press: 2004).
 27. Elliott Sober, *Evidence and Evolution* (Cambridge: Cambridge University Press, 2008), pp. 126–128.
 28. Steven R. Scadding, "Vestigial organs do not provide scientific evidence for evolution," *Evolutionary Theory* 6 (1982): 171–173.
 29. Jonathan Wells, "Darwin of the Gaps: Francis Collins's Premature Surrender," pp. 117–128 in Jay W. Richards (editor), *God and Evolution* (Seattle, WA: Discovery Institute Press, 2010). An earlier version (March 26, 2008) is freely accessible (2011) at <http://www.discovery.org/a/4529>
 30. Miller, "Life's Grand Design" (1994). Freely accessible (2011) at <http://www.millerandlevine.com/km/evol/lgd/index.html>
 31. Bill Gates, *The Road Ahead* (New York: Penguin Books, 1995), p. 188.
 32. Stephen C. Meyer, "The origin of biological information and the higher taxonomic categories," *Proceedings of the Biological Society of Washington* 117 (2004): 213–239. Freely accessible (2011) at <http://www.discovery.org/a/2177>
 33. Stephen C. Meyer, *Signature in the Cell: DNA and the Evidence for Intelligent Design* (New York: HarperCollins, 2009). More information available online (2011) at <http://www.discovery.org/a/12311>
 34. William A. Dembski, *The Design Revolution: Answering the Toughest Questions about Intelligent Design* (Downer's Grove, IL: InterVarsity Press, 2004), pp. 317.
 35. Leon Brillouin, *Science and Information Theory*, Second Edition (New York: Academic Press, 1956).
 36. Hubert P. Yockey, *Information Theory and Molecular Biology* (Cambridge: Cambridge University Press, 1992).
 37. William A. Dembski, *The Design Inference* (Cambridge: Cambridge University Press, 1998).
 38. Wen-Yu Chung, Samir Wadhawan, Radek Szklarczyk, Sergei Kosakovsky Pond & Anton Nekrutenko, "A first look at ARFome: dual-coding genes in mammalian genomes," *PLoS Computational Biology* 3:5 (2007): e91. Freely Accessible (2011) at <http://www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.0030091>
 39. Shalev Itzkovitz & Uri Alon, "The genetic code is nearly optimal for allowing additional information within protein-coding sequences," *Genome Research* 17 (2007): 405–412. Freely accessible (2011) at <http://genome.cshlp.org/content/17/4/405.full.pdf+html>
 40. Tobias Bollenbach, Kalin Vetsigian & Roy Kishony, "Evolution and multilevel optimization of the genetic code," *Genome Research* 17 (2007): 401–404. Freely accessible (2011) at <http://genome.cshlp.org/content/17/4/401.full.pdf+html>
 41. Dembski, *The Design Revolution*, pp. 317.
 42. Danielle S. Bassett, Daniel L. Greenfield, Andreas Meyer-Lindenberg, Daniel R. Weinberger, Simon W. Moore & Edward T. Bullmore, "Efficient physical embedding of topologically complex information processing networks in brains and computer circuits," *PLoS Computational Biology* 6:4 (2010): e1000748. Freely accessible (2011) at <http://www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1000748>
 43. Richard v. Sternberg, "On the Roles of Repetitive DNA Elements in the Context of a Unified Genomic–Epigenetic System," *Annals of the New York Academy of Sciences* 981 (2002): 154–188.

44. Richard v. Sternberg, "DNA Codes and Information: Formal Structures and Relational Causes," *Acta Biotheoretica* 56 (2008): 205–232.
45. Richard v. Sternberg & James A. Shapiro, "How repeated retroelements format genome function," *Cytogenetic and Genome Research* 110 (2005): 108–116.
9. Régis Moreau & Konrad Dabrowski, "Gulonolactone oxidase presence in fishes: activity and significance," pp. 14–32 in Konrad Dabrowski (editor), *Ascorbic Acid in Aquatic Organisms* (Boca Raton, LA: CRC Press, 2001).

APPENDIX. THE VITAMIN C PSEUDOGENE

1. Juan M. Navia & Charles E. Hunt, "Nutrition, Nutritional Diseases, and Nutrition Research Applications," pp. 235–267 in Joseph E. Wagner & Patrick J. Manning (editors), *The Biology of the Guinea Pig* (New York: Academic Press, 1976).
2. Yasuo Nakajima, Torada R. Shantha & Geoffrey H. Bourne, "Histochemical detection of L-gulonolactone: phenazine methosulfate oxidoreductase activity in several mammals with special reference to synthesis of vitamin C in primates," *Histochemie* 18 (1969): 293–301.
3. R. N. Roy & B. C. Guha, "Species Differences in regard to the Biosynthesis of Ascorbic Acid," *Nature* 182 (1958): 319–320.
4. Elmer C. Birney, Robert Jenness & Kathleen M. Ayaz, "Inability of bats to synthesize L-ascorbic acid," *Nature* 260 (1976): 626–628.
5. Jie Cui, Yi-Hsuan Pan, Yijian Zhang, Gareth Jones & Shuyi Zhang, "Progressive Pseudogenization: Vitamin C synthesis and Its Loss in Bats," *Molecular Biology and Evolution* (October 29, 2010). doi:10.1093/molbev/msq286.
6. C. Ray Chaudhuri & I. B. Chatterjee, "L-Ascorbic Acid Synthesis in Birds: Phylogenetic Trend," *Science* 164 (1969): 435–436.
7. Carlos Martínez del Río, "Can Passerines Synthesize Vitamin C?" *The Auk* 114 (1997): 513–516.
8. J. E. Halver, R. R. Smith, B. M. Tolbert & E. M. Baker, "Utilization of Ascorbic Acid in Fish," *Annals of the New York Academy of Sciences* 258 (1975): 81–102.
10. Morimitsu Nishikimi & Kunio Yagi, "Molecular basis for the deficiency in humans of gulonolactone oxidase, a key enzyme for ascorbic acid biosynthesis," *American Journal of Clinical Nutrition* 54 (1991): 1203S–1208S. Freely accessible (2011) at <http://www.ajcn.org/cgi/reprint/54/6/1203S>
11. Morimitsu Nishikimi, Ryuichi Fukuyama, Sinsei Minoshima, Nobuyoshi Shimizu & Kunio Yagi, "Cloning and Chromosomal Mapping of the Human Nonfunctional Gene for L-Gulonolactone Oxidase, the Enzyme for L-Ascorbic Acid Biosynthesis Missing in Man," *Journal of Biological Chemistry* 269 (1994): 13685–13688. Freely accessible (2011) at <http://www.jbc.org/content/269/18/13685.long>
12. Kenneth R. Miller, *Only a Theory: Evolution and the Battle for America's Soul* (New York: Viking, 2008), p. 98.
13. Miller, *Only a Theory*, p. 99.
14. Jonathan Wells, "Should We Stop Criticizing the Doctrine of Universal Common Ancestry?" *Access Research Network* (November 3, 2001). Freely accessible (2011) at http://www.arn.org/docs/wells/jw_criticismcommonancestry1103.htm
15. William A. Dembski, *The Design Revolution: Answering the Toughest Questions About Intelligent Design* (Downer's Grove, IL: InterVarsity Press, 2004), p. 42.
16. Stephen C. Meyer, "Intelligent Design vs. Evolution," *Think Tank With Ben Wattenberg* (October 12, 2006). Freely accessible (2011) at <http://www.pbs.org/think-tank/transcript1244.html>

17. Paul A. Nelson, "Design and Common Ancestry," *Evolution News & Views* (May 7, 2007). Freely accessible (2011) at http://www.evolutionnews.org/2007/05/_most_people_including.html
18. Casey Luskin, "Wikipedia 'Intelligent Design' Entry Selectively Cites Poll Data to Present Misleading Picture of Support for Intelligent Design," *Evolution News & Views* (May 8, 2007). Freely accessible (2011) at http://www.evolutionnews.org/2007/05/wikipedia_intelligent_design_e003542.html
19. Michael J. Behe, *Darwin's Black Box: The Biochemical Challenge to Evolution* (New York: The Free Press, 1996), p. 231.
20. W. Ford Doolittle, "The practice of classification and the theory of evolution, and what the demise of Charles Darwin's tree of life hypothesis means for both of them," *Philosophical Transactions of the Royal Society of London B* 364 (2009): 2221–2228.
21. Carl R. Woese & Nigel Goldenfeld, "How the Microbial World Saved Evolution from the Scylla of Molecular Biology and the Charybdis of the Modern Synthesis," *Microbiology and Molecular Biology Reviews* 73 (2009): 14–21. Freely accessible (2011) at <http://mmb.asm.org/cgi/rapidprint/73/1/14>
22. David G. Popovich & Ellen S. Dierenfeld, "Gorilla Nutrition," in J. Ogden & D. Wharton (editors), *Management of Gorillas in Captivity* (Silver Spring, MD: American Association of Zoos and Aquariums, 1997). Freely accessible (2011) at <http://www.nagonline.net/HUSBANDRY/Diets%20pdf/Gorilla%20Nutrition.pdf>
23. Committee on Animal Nutrition, *Nutrient Requirements of Nonhuman Primates*, Second Revised Edition (Washington, DC: National Academies Press, 2003), pp. 137–149.
24. Gorilla (*Gorilla gorilla*). Ensembl (Cambridge). Freely accessible (2011) at http://uswest.ensembl.org/Gorilla_gorilla/Info/Index
25. Jerry A. Coyne, *Why Evolution Is True* (New York: Viking, 2009), p. 68.
26. Coyne, *Why Evolution Is True*, p. 69.
27. Jennifer F. Hughes, Helen Skaletsky, Tatyana Pyntikova, Tina A. Graves, Saskia K. M. van Daalen, Patrick J. Minx, Robert S. Fulton, Sean D. McGrath, Devin P. Locke, Cynthia Friedman, Barbara J. Trask, Elaine R. Mardis, Wesley C. Warren, Sjoerd Repping, Steve Rozen, Richard K. Wilson & David C. Page, "Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content," *Nature* 463 (2010): 536–539.
28. Don E. Wilson & DeeAnn M. Reeder (editors), *Mammal Species of the World: A Taxonomic and Geographic Reference*, Third Edition (Baltimore, MD: Johns Hopkins University Press, 2005). Freely accessible (2011) at <http://www.bucknell.edu/msw3/>
29. Yuriko Ohta & Morimitsu Nishikimi, "Random nucleotide substitutions in primate nonfunctional gene for L-gulonogamma-lactone oxidase, the missing enzyme in L-ascorbic acid biosynthesis," *Biochimica et Biophysica Acta* 1472 (1999): 408–411.
30. Yoko Inai, Yuriko Ohta & Morimitsu Nishikimi, "The whole structure of the human nonfunctional L-gulonogamma-lactone oxidase gene—the gene responsible for scurvy—and the evolution of repetitive sequences thereon," *Journal of Nutritional Science and Vitaminology* (Tokyo) 49 (2003): 315–319.
31. Evgeniy S. Balakirev & Francisco J. Ayala, "Pseudogenes: Are They 'Junk' or Functional DNA?" *Annual Review of Genetics* 37 (2003): 123–51.
32. Amit N. Khachane & Paul M. Harrison, "Assessing the genomic evidence for conserved transcribed pseudogenes under selection," *BMC Genomics* 10 (2009): 435. Freely accessible (2011) at <http://www.biomedcentral.com/1471-2164/10/435>