Annaluru, N., Muller, H., Mitchell, L.A., Ramalingam, S., Stracquadanio, G., Richardson, S.M., Dymond, J.S., Kuang, Z., Scheifele, L.Z., Cooper, E.M., et al. (2014). Total synthesis of a functional designer eukaryotic chromosome. Science 344, 55–58.

Bang, D., and Church, G.M. (2008). Gene synthesis by circular assembly amplification. Nature methods 5, 37–39.

Barrangou, R., Fremaux, C., Deveau, H., Richards, M., Boyaval, P., Moineau, S., Romero, D.A., and Horvath, P. (2007). CRISPR provides acquired resistance against viruses in prokaryotes. Science 315, 1709–1712.

Bebenek, K., Abbotts, J., Wilson, S.H., and Kunkel, T.A. (1993). Error-prone polymerization by HIV-1 reverse transcriptase. Contribution of template-primer misalignment, miscoding, and termination probability to mutational hot spots. The Journal of biological chemistry 268, 10324–10334.

Bikard, D., Euler, C.W., Jiang, W., Nussenzweig, P.M., Goldberg, G.W., Duportet, X., Fischetti, V.A., and Marraffini, L.A. (2014). Exploiting CRISPR-Cas nucleases to produce sequence-specific antimicrobials. Nature biotechnology 32, 1146–1150.
Bikard, D., Jiang, W., Samai, P., Hochschild, A., Zhang, F., and Marraffini, L.A. (2013). Programmable repression and activation of bacterial gene expression using an engineered CRISPR-Cas system. Nucleic acids research 41, 7429–7437.

Binder, S., Siedler, S., Marienhagen, J., Bott, M., and Eggeling, L. (2013). Recombineering in Corynebacterium glutamicum combined with optical nanosensors: a general strategy for fast producer strain generation. Nucleic acids research 41, 6360–6369.

Bonde, M.T., Kosuri, S., Genee, H.J., Sarup-Lytzen, K., Church, G.M., Sommer, M.O., and Wang, H.H. (2014). Direct Mutagenesis of Thousands of Genomic Targets Using Microarray-Derived Oligonucleotides. ACS synthetic biology.

Carr, P.A., Wang, H.H., Sterling, B., Isaacs, F.J., Lajoie, M.J., Xu, G., Church, G.M., and Jacobson, J.M. (2012). Enhanced multiplex genome engineering through co-operative oligonucleotide co-selection. Nucleic acids research 40, e132.

Chan, L.Y., Kosuri, S., and Endy, D. (2005). Refactoring bacteriophage T7. Molecular systems biology 1, 2005 0018.

Chin, J.W. (2014). Expanding and reprogramming the genetic code of cells and animals. Annual review of biochemistry 83, 379–408.

Citorik, R.J., Mimee, M., and Lu, T.K. (2014). Sequence-specific antimicrobials using efficiently delivered RNA-guided nucleases. Nature biotechnology 32, 1141–1145.

Cleary, M.A., Kilian, K., Wang, Y., Bradshaw, J., Cavet, G., Ge, W., Kulkarni, A., Paddison, P.J.,

Chang, K., Sheth, N., et al. (2004). Production of complex nucleic acid libraries using highly parallel in situ oligonucleotide synthesis. Nature methods 1, 241–248.

Cong, L., Ran, F.A., Cox, D., Lin, S., Barretto, R., Habib, N., Hsu, P.D., Wu, X., Jiang, W., Marraffini, L.A., et al. (2013). Multiplex genome engineering using CRISPR/Cas systems. Science 339, 819–823.

Costantino, N., and Court, D.L. (2003). Enhanced levels of lambda Red-mediated recombinants in mismatch repair mutants. Proceedings of the National Academy of Sciences of the United States of America 100, 15748–15753.

Court, D.L., Sawitzke, J.A., and Thomason, L.C. (2002). Genetic engineering using homologous recombination. Annual review of genetics 36, 361–388.

Cudd, A. (2013). Contractarianism. In The Stanford Encyclopedia of Philosophy, E.N. Zalta, ed. (http://plato.stanford.edu/archives/win2013/entries/contractarianism/).

Daniel, R., Rubens, J.R., Sarpeshkar, R., and Lu, T.K. (2013). Synthetic analog computation in living cells. Nature 497, 619–623.

DiCarlo, J.E., Chavez, A., Dietz, S.L., Esvelt, K.M., and Church, G.M. (2015). Safeguarding CRISPR-Cas9 gene drives in yeast. Nature biotechnology 33, 1250–1255.

Dill, K.A., and MacCallum, J.L. (2012). The protein-folding problem, 50 years on. Science 338, 1042–1046.

Dymond, J.S., Richardson, S.M., Coombes, C.E., Babatz, T., Muller, H., Annaluru, N., Blake, W.J., Schwerzmann, J.W., Dai, J., Lindstrom, D.L., et al. (2011). Synthetic chromosome arms function in yeast and generate phenotypic diversity by design. Nature 477, 471–476.

Dymond, J.S., Scheifele, L.Z., Richardson, S., Lee, P., Chandrasegaran, S., Bader, J.S., and Boeke, J.D. (2009). Teaching synthetic biology, bioinformatics and engineering to undergraduates: the interdisciplinary Build-a-Genome course. Genetics 181, 13–21.

Enyeart, P.J., Chirieleison, S.M., Dao, M.N., Perutka, J., Quandt, E.M., Yao, J., Whitt, J.T., Keatinge-Clay, A.T., Lambowitz, A.M., and Ellington, A.D. (2013). Generalized bacterial genome editing using mobile group II introns and Cre-lox. Molecular systems biology 9, 685.

Farzadfard, F., and Lu, T.K. (2014). Genomically encoded analog memory with precise in vivo DNA writing in living cell populations. Science 346, 1256272.

Fu, Y., Foden, J.A., Khayter, C., Maeder, M.L., Reyon, D., Joung, J.K., and Sander, J.D. (2013). High-frequency off-target mutagenesis induced by CRISPR-Cas nucleases in human cells. Nature biotechnology 31, 822–826.

Gaj, T., Gersbach, C.A., and Barbas, C.F., 3rd (2013). ZFN, TALEN, and CRISPR/Cas-based methods for genome engineering. Trends in biotechnology 31, 397–405.

Gallagher, R.R., Li, Z., Lewis, A.O., and Isaacs, F.J. (2014). Rapid editing and evolution of bacterial genomes using libraries of synthetic DNA. Nature protocols 9, 2301–2316.

Gantz, V.M., and Bier, E. (2015). Genome editing. The mutagenic chain reaction: a method for converting heterozygous to homozygous mutations. Science 348, 442–444.

Gersbach, C.A. (2014). Genome engineering: the next genomic revolution. Nature methods 11, 1009–1011.

Gibson, D.G. (2009). Synthesis of DNA fragments in yeast by one-step assembly of overlapping oligonucleotides. Nucleic acids research 37, 6984–6990.

Gibson, D.G., Benders, G.A., Andrews-Pfannkoch, C., Denisova, E.A., Baden-Tillson, H., Zaveri, J., Stockwell, T.B., Brownley, A., Thomas, D.W., Algire, M.A., et al. (2008).

Complete chemical synthesis, assembly, and cloning of a Mycoplasma genitalium genome. Science 319, 1215–1220.

Gibson, D.G., Glass, J.I., Lartigue, C., Noskov, V.N., Chuang, R.Y., Algire, M.A., Benders, G.A., Montague, M.G., Ma, L., Moodie, M.M., et al. (2010). Creation of a bacterial cell controlled by a chemically synthesized genome. Science 329, 52–56.

Gibson, D.G., Young, L., Chuang, R.Y., Venter, J.C., Hutchison, C.A., 3rd, and Smith, H.O. (2009). Enzymatic assembly of DNA molecules up to several hundred kilobases. Nature methods 6, 343–345.

Gilbert, L.A., Larson, M.H., Morsut, L., Liu, Z., Brar, G.A., Torres, S.E., Stern–Ginossar, N., Brandman, O., Whitehead, E.H., Doudna, J.A., et al. (2013). CRISPR–mediated modular RNA–guided regulation of transcription in eukaryotes. Cell 154, 442–451.

Gregg, C.J., Lajoie, M.J., Napolitano, M.G., Mosberg, J.A., Goodman, D.B., Aach, J., Isaacs, F.J., and Church, G.M. (2014). Rational optimization of tolC as a powerful dual selectable marker for genome engineering. Nucleic acids research 42, 4779–4790.

Heinemann, I.U., Rovner, A.J., Aerni, H.R., Rogulina, S., Cheng, L., Olds, W., Fischer, J.T., Soll, D., Isaacs, F.J., and Rinehart, J. (2012). Enhanced phosphoserine insertion during Escherichia coli protein synthesis via partial UAG codon reassignment and release factor 1 deletion. FEBS letters 586, 3716–3722.

Heller, M.J. (2002). DNA microarray technology: devices, systems, and applications. Annual review of biomedical engineering 4, 129–153.

Hoess, R.H., Wierzbicki, A., and Abremski, K. (1986). The role of the loxP spacer region in P1 site–specific recombination. Nucleic acids research 14, 2287–2300.

Horwitz, Andrew A., Walter, Jessica M., Schubert, Max G., Kung, Stephanie H., Hawkins, K., Platt, Darren M., Hernday, Aaron D., Mahatdejkul–Meadows, T., Szeto, W., Chandran, Sunil S., et al. Efficient Multiplexed Integration of Synergistic Alleles and Metabolic Pathways in Yeasts via CRISPR–Cas. Cell Systems.

Huang, J., Koide, A., Makabe, K., and Koide, S. (2008). Design of protein function leaps by directed domain interface evolution. Proceedings of the National Academy of Sciences of the United States of America 105, 6578–6583.

Hutchison, C.A., 3rd, Chuang, R.Y., Noskov, V.N., Assad–Garcia, N., Deerinck, T.J., Ellisman, M.H., Gill, J., Kannan, K., Karas, B.J., Ma, L., et al. (2016). Design and synthesis of a minimal bacterial genome. Science 351, aad6253.

Hutchison, C.A., Peterson, S.N., Gill, S.R., Cline, R.T., White, O., Fraser, C.M., Smith, H.O., and Venter, J.C. (1999). Global transposon mutagenesis and a minimal Mycoplasma genome. Science 286, 2165–2169.

Isaacs, F.J., Carr, P.A., Wang, H.H., Lajoie, M.J., Sterling, B., Kraal, L., Tolonen, A.C., Gianoulis, T.A., Goodman, D.B., Reppas, N.B., et al. (2011). Precise manipulation of chromosomes in vivo enables genome-wide codon replacement. Science 333, 348–353.

Jiang, W., Bikard, D., Cox, D., Zhang, F., and Marraffini, L.A. (2013). RNA-guided editing of bacterial genomes using CRISPR-Cas systems. Nature biotechnology 31, 233–239.

Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J.A., and Charpentier, E. (2012). A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. Science 337, 816–821.

Jinek, M., East, A., Cheng, A., Lin, S., Ma, E., and Doudna, J. (2013). RNA-programmed genome editing in human cells. eLife 2, e00471.

Kabadi, A.M., Ousterout, D.G., Hilton, I.B., and Gersbach, C.A. (2014). Multiplex CRISPR/Cas9-based genome engineering from a single lentiviral vector. Nucleic acids research 42, e147.

Kim, H., and Kim, J.S. (2014). A guide to genome engineering with programmable nucleases. Nature reviews Genetics 15, 321–334.

Kodumal, S.J., Patel, K.G., Reid, R., Menzella, H.G., Welch, M., and Santi, D.V. (2004). Total synthesis of long DNA sequences: synthesis of a contiguous 32-kb polyketide synthase gene cluster. Proceedings of the National Academy of Sciences of the United States of America 101, 15573–15578.

Konermann, S., Brigham, M.D., Trevino, A.E., Joung, J., Abudayyeh, O.O., Barcena, C., Hsu, P.D., Habib, N., Gootenberg, J.S., Nishimasu, H., et al. (2014). Genome-scale transcriptional activation by an engineered CRISPR-Cas9 complex. Nature.

Kosuri, S., and Church, G.M. (2014). Large-scale de novo DNA synthesis: technologies and applications. Nature methods 11, 499–507.

Kosuri, S., Eroshenko, N., Leproust, E.M., Super, M., Way, J., Li, J.B., and Church, G.M. (2010). Scalable gene synthesis by selective amplification of DNA pools from high-fidelity microchips. Nature biotechnology 28, 1295–1299.

Lajoie, M.J., Rovner, A.J., Goodman, D.B., Aerni, H.R., Haimovich, A.D., Kuznetsov, G., Mercer, J.A., Wang, H.H., Carr, P.A., Mosberg, J.A., et al. (2013). Genomically recoded organisms expand biological functions. Science 342, 357–360.

Lajoie, M.J., Kosuri, S., Mosberg, J.A., Gregg, C.J., Zhang, D., and Church, G.M. (2013). Probing the limits of genetic recoding in essential genes. Science 342, 361–363.

Lartigue, C., Glass, J.I., Alperovich, N., Pieper, R., Parmar, P.P., Hutchison, C.A., 3rd, Smith, H.O., and Venter, J.C. (2007). Genome transplantation in bacteria: changing one species to another. Science 317, 632–638.

Loenen, W.A., Dryden, D.T., Raleigh, E.A., Wilson, G.G., and Murray, N.E. (2014). Highlights of the DNA cutters: a short history of the restriction enzymes. Nucleic acids research 42, 3–19.

Ma, N.J., Moonan, D.W., and Isaacs, F.J. (2014). Precise manipulation of bacterial chromosomes by conjugative assembly genome engineering. Nature protocols 9, 2285–2300.

Mali, P., Yang, L., Esvelt, K.M., Aach, J., Guell, M., DiCarlo, J.E., Norville, J.E., and Church, G.M. (2013). RNA-guided human genome engineering via Cas9. Science 339, 823–826.

Mandell, D.J., Lajoie, M.J., Mee, M.T., Takeuchi, R., Kuznetsov, G., Norville, J.E., Gregg, C.J., Stoddard, B.L., and Church, G.M. (2015). Biocontainment of genetically modified organisms by synthetic protein design. Nature 518, 55–60.

Mansell, T.J., Warner, J.R., and Gill, R.T. (2013). Trackable multiplex recombineering for gene-trait mapping in E. coli. Methods in molecular biology 985, 223–246.

Martin, C.H., Nielsen, D.R., Solomon, K.V., and Prather, K.L. (2009). Synthetic metabolism: engineering biology at the protein and pathway scales. Chemistry & biology 16, 277–286.

Mattanovich, D., and Borth, N. (2006). Applications of cell sorting in biotechnology. Microbial cell factories 5, 12.

Miller, J.C., Holmes, M.C., Wang, J., Guschin, D.Y., Lee, Y.L., Rupniewski, I., Beausejour, C.M., Waite, A.J., Wang, N.S., Kim, K.A., et al. (2007). An improved zinc-finger nuclease architecture for highly specific genome editing. Nature biotechnology 25, 778–785.

Mitchell, L.A., Chuang, J., Agmon, N., Khunsriraksakul, C., Phillips, N.A., Cai, Y., Truong, D.M., Veerakumar, A., Wang, Y., Mayorga, M., et al. (2015). Versatile genetic assembly system (VEGAS) to assemble pathways for expression in S. cerevisiae. Nucleic acids research.

Mojica, F.J., Diez-Villasenor, C., Garcia-Martinez, J., and Almendros, C. (2009). Short motif sequences determine the targets of the prokaryotic CRISPR defence system. Microbiology 155, 733-740.

Neylon, C. (2004). Chemical and biochemical strategies for the randomization of protein encoding DNA sequences: library construction methods for directed evolution. Nucleic acids research 32, 1448-1459.

Nielsen, A.A., Der, B.S., Shin, J., Vaidyanathan, P., Paralanov, V., Strychalski, E.A., Ross, D., Densmore, D., and Voigt, C.A. (2016). Genetic circuit design automation. Science 352, aac7341.

O'Donoghue, P., Ling, J., Wang, Y.S., and Soll, D. (2013). Upgrading protein synthesis for synthetic biology. Nature chemical biology 9, 594-598.

Pal, C., Papp, B., and Posfai, G. (2014). The dawn of evolutionary genome engineering. Nature reviews Genetics 15, 504-512.

Pines, G., Freed, E.F., Winkler, J.D., and Gill, R.T. (2015). Bacterial Recombineering: Genome Engineering via Phage-Based Homologous Recombination. ACS synthetic biology.

Posfai, G., Plunkett, G., 3rd, Feher, T., Frisch, D., Keil, G.M., Umenhoffer, K., Kolisnychenko, V., Stahl, B., Sharma, S.S., de Arruda, M., et al. (2006). Emergent properties of reduced-genome Escherichia coli. Science 312, 1044-1046.

Quan, J., Saaem, I., Tang, N., Ma, S., Negre, N., Gong, H., White, K.P., and Tian, J. (2011). Parallel on-chip gene synthesis and application to optimization of protein expression. Nature biotechnology 29, 449-452.

Raman, S., Rogers, J.K., Taylor, N.D., and Church, G.M. (2014). Evolution-guided optimization of biosynthetic pathways. Proceedings of the National Academy of Sciences of the United States of America 111, 17803-17808.

Ran, F.A., Hsu, P.D., Lin, C.Y., Gootenberg, J.S., Konermann, S., Trevino, A.E., Scott, D.A., Inoue, A., Matoba, S., Zhang, Y., et al. (2013). Double nicking by RNA-guided CRISPR Cas9 for enhanced genome editing specificity. Cell 154, 1380–1389.

Rovner, A.J., Haimovich, A.D., Katz, S.R., Li, Z., Grome, M.W., Gassaway, B.M., Amiram, M., Patel, J.R., Gallagher, R.R., Rinehart, J., et al. (2015). Recoded organisms engineered to depend on synthetic amino acids. Nature 518, 89–93.

Roy, S., and Caruthers, M. (2013). Synthesis of DNA/RNA and their analogs via phosphoramidite and H-phosphonate chemistries. Molecules 18, 14268–14284.
Ryan, O.W., Skerker, J.M., Maurer, M.J., Li, X., Tsai, J.C., Poddar, S., Lee, M.E., DeLoache, W., Dueber, J.E., Arkin, A.P., et al. (2014). Selection of chromosomal DNA libraries using a multiplex CRISPR system. eLife 3.

Sanger, F., Nicklen, S., and Coulson, A.R. (1977). DNA sequencing with chain-terminating inhibitors. Proceedings of the National Academy of Sciences of the United States of America 74, 5463–5467.

Sawitzke, J.A., Thomason, L.C., Costantino, N., Bubunenko, M., Datta, S., and Court, D.L. (2007). Recombineering: in vivo genetic engineering in E. coli, S. enterica, and beyond. Methods in enzymology 421, 171–199.

Smanski, M.J., Bhatia, S., Zhao, D., Park, Y., L, B.A.W., Giannoukos, G., Ciulla, D., Busby, M., Calderon, J., Nicol, R., et al. (2014). Functional optimization of gene clusters by combinatorial design and assembly. Nature biotechnology 32, 1241–1249.

Srinivasan, G., James, C.M., and Krzycki, J.A. (2002). Pyrrolysine encoded by UAG in Archaea: charging of a UAG-decoding specialized tRNA. Science 296, 1459–1462.
Stemmer, W.P. (1994). Rapid evolution of a protein in vitro by DNA shuffling. Nature 370, 389–391.

Stemmer, W.P., Crameri, A., Ha, K.D., Brennan, T.M., and Heyneker, H.L. (1995). Single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides. Gene 164, 49–53.

Temme, K., Zhao, D., and Voigt, C.A. (2012). Refactoring the nitrogen fixation gene cluster from Klebsiella oxytoca. Proceedings of the National Academy of Sciences of the United States of America 109, 7085–7090.

Tian, J., Gong, H., Sheng, N., Zhou, X., Gulari, E., Gao, X., and Church, G. (2004). Accurate multiplex gene synthesis from programmable DNA microchips. Nature 432, 1050–1054.

Tsai, S.Q., Wyvekens, N., Khayter, C., Foden, J.A., Thapar, V., Reyon, D., Goodwin, M.J., Aryee, M.J., and Joung, J.K. (2014). Dimeric CRISPR RNA–guided FokI nucleases for highly specific genome editing. Nature biotechnology 32, 569–576.

Wang, H.H., Isaacs, F.J., Carr, P.A., Sun, Z.Z., Xu, G., Forest, C.R., and Church, G.M. (2009). Programming cells by multiplex genome engineering and accelerated evolution. Nature 460, 894–898.

Wang, H.H., Kim, H., Cong, L., Jeong, J., Bang, D., and Church, G.M. (2012a). Genome–scale promoter engineering by coselection MAGE. Nature methods 9, 591–593.

Wang, H.H., Xu, G., Vonner, A.J., and Church, G. (2011). Modified bases enable high–efficiency oligonucleotide–mediated allelic replacement via mismatch repair evasion. Nucleic acids research 39, 7336–7347.

Wang, L., Brock, A., Herberich, B., and Schultz, P.G. (2001). Expanding the genetic code of Escherichia coli. Science 292, 498–500.

Wang, Y., Weng, J., Waseem, R., Yin, X., Zhang, R., and Shen, Q. (2012b). Bacillus subtilis genome editing using ssDNA with short homology regions. Nucleic acids research 40, e91.

Warner, J.R., Reeder, P.J., Karimpour–Fard, A., Woodruff, L.B., and Gill, R.T. (2010). Rapid profiling of a microbial genome using mixtures of barcoded oligonucleotides. Nature biotechnology 28, 856–862.