

- Vogelstein B, Kinzler KW. Cancer genes and the pathways they control. *Nat Med* 2004;10:789–799.
- Kinzler KW, Vogelstein B. Lessons from hereditary colon cancer. *Cell* 1996; 87:159–170.
- International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature* 2004;431:931–945.
- Stehelin D, Varmus HE, Bishop JM, et al. DNA related to the transforming gene(s) of avian sarcoma viruses is present in normal avian DNA. *Nature* 1976;260:170–173.
- Rous P. Transmission of a malignant new growth by means of a cell-free filtrate. *J Am Med Assoc* 1911;56:198.
- International HapMap Consortium. The International HapMap Project. *Nature* 2003;426:89–96.
- International HapMap Consortium. A haplotype map of the human genome. *Nature* 2005;437:1299–1320.
- Sanger F, Nicklen S, Coulson AR. DNA sequencing with chain-terminating inhibitors. *Proc Natl Acad Sci U S A* 1977;74:5463–5467.
- Davies H, Bignell GR, Cox C, et al. Mutations of the BRAF gene in human cancer. *Nature* 2002;417:949–954.
- Rajagopalan H, Bardelli A, Lengauer C, et al. Tumorigenesis: RAF/RAS oncogenes and mismatch-repair status. *Nature* 2002;418:934.
- Moodie SA, Wolfman A. The 3Rs of life: Ras, Raf and growth regulation. *Trends Genet* 1994;10:44–48.
- Hafen E, Dickson B, Brunner D, et al. Genetic dissection of signal transduction mediated by the sevenless receptor tyrosine kinase in *Drosophila*. *Prog Neurobiol* 1994;42:287–292.
- Bardelli A, Parsons DW, Silliman N, et al. Mutational analysis of the tyrosine kinase in colorectal cancers. *Science* 2003;300:949.
- Greenman C, Stephens P, Smith R, et al. Patterns of somatic mutation in human cancer genomes. *Nature* 2007;446:153–158.
- Samuels Y, Wang Z, Bardelli A, et al. High frequency of mutations of the PIK3CA gene in human cancers. *Science* 2004;304:554.
- Wang Z, Shen D, Parsons DW, et al. Mutational analysis of the tyrosine phosphatome in colorectal cancers. *Science* 2004;304:1164–1166.
- Vivanco I, Sawyers CL. The phosphatidylinositol 3-Kinase AKT pathway in human cancer. *Nat Rev Cancer* 2002;2:489–501.
- Broderick DK, Di C, Parrett TJ, et al. Mutations of PIK3CA in anaplastic oligodendrogliomas, high-grade astrocytomas, and medulloblastomas. *Cancer Res* 2004;64:5048–5050.
- Lee JW, Soung YH, Kim SY, et al. PIK3CA gene is frequently mutated in breast carcinomas and hepatocellular carcinomas. *Oncogene* 2005;24:1477–1480.
- Bachman KE, Argani P, Samuels Y, et al. The PIK3CA gene is mutated with high frequency in human breast cancers. *Cancer Biol Ther* 2004;3:772–775.
- Oda K, Stokoe D, Taketani Y, et al. High frequency of coexistent mutations of PIK3CA and PTEN genes in endometrial carcinoma. *Cancer Res* 2005;65:10669–10673.
- Samuels Y, Waldman T. Oncogenic mutations of PIK3CA in human cancers. *Curr Top Microbiol Immunol* 2010;2:21–42.
- Parsons DW, Wang TL, Samuels Y, et al. Colorectal cancer: mutations in a signalling pathway. *Nature* 2005;436:792.
- Lopez-Otin C, Overall CM. Protease degradomics: a new challenge for proteomics. *Nat Rev Mol Cell Biol* 2002;3:509–519.
- Liotta LA, Tryggvason K, Garbisa S, et al. Metastatic potential correlates with enzymatic degradation of basement membrane collagen. *Nature* 1980;284:67–68.
- Lopez-Otin C, Hunter T. The regulatory crosstalk between kinases and proteases in cancer. *Nat Rev Cancer* 2010;10:278–292.
- Egeblad M, Werb Z. New functions for the matrix metalloproteinases in cancer progression. *Nat Rev Cancer* 2002;2:161–174.
- Lopez-Otin C, Matrisian LM. Emerging roles of proteases in tumour suppression. *Nat Rev Cancer* 2007;7:800–808.
- Wood LD, Parsons DW, Jones S, et al. The genomic landscapes of human breast and colorectal cancers. *Science* 2007;318:1108–1113.
- Palavalli LH, Prickett TD, Wunderlich JR, et al. Analysis of the matrix metalloproteinase family reveals that MMP8 is often mutated in melanoma. *Nat Genet* 2009;41:518–520.
- Lopez-Otin C, Palavalli LH, Samuels Y. Protective roles of matrix metalloproteinases: from mouse models to human cancer. *Cell Cycle* 2009;8:3657–3662.
- Hanahan D, Weinberg RA. The hallmarks of cancer. *Cell* 2000;100:57–70.
- Teitz T, Wei T, Valentine MB, et al. Caspase 8 is deleted or silenced preferentially in childhood neuroblastomas with amplification of MYCN. *Nat Med* 2000;6:529–535.
- Mandruzzato S, Brasseur F, Andry G, et al. A CASP-8 mutation recognized by cytolytic T lymphocytes on a human head and neck carcinoma. *J Exp Med* 1997;186:785–793.
- Soung YH, Lee JW, Kim SY, et al. CASPASE-8 gene is inactivated by somatic mutations in gastric carcinomas. *Cancer Res* 2005;65:815–821.
- Frailie JM, Quesada V, Rodríguez D, et al. Deubiquitinases in cancer: new functions and therapeutic options. *Oncogene* 2012;31:2373–2388.
- Bignell GR, Warren W, Seal S, et al. Identification of the familial cylindromatosis tumour-suppressor gene. *Nat Genet* 2000;25:160–165.
- Schmitz R, Hansmann ML, Bohle V, et al. TNFAIP3 (A20) is a tumor suppressor gene in Hodgkin lymphoma and primary mediastinal B cell lymphoma. *J Exp Med* 2009;206:981–989.
- Compagno M, Lim WK, Grunn A, et al. Mutations of multiple genes cause deregulation of NF-kappaB in diffuse large B-cell lymphoma. *Nature* 2009;459:717–721.
- Kato M, Sanada M, Kato I, et al. Frequent inactivation of A20 in B-cell lymphomas. *Nature* 2009;459:712–716.
- Novak U, Rinaldi A, Kwee I, et al. The NF-kappa B negative regulator TNFAIP3 (A20) is inactivated by somatic mutations and genomic deletions in marginal zone lymphomas. *Blood* 2009;113:4918–4921.
- Harbour JW, Onken MD, Roberson ED, et al. Frequent mutation of BAP1 in metastasizing uveal melanomas. *Science* 2010;330:1410–1413.
- Carbone M, Yang H, Pass HI, et al. BAP1 and cancer. *Nat Rev Cancer* 2013; 13:153–159.
- Sjöblom T, Jones S, Wood LD, et al. The consensus coding sequences of human breast and colorectal cancers. *Science* 2006;314:268–274.
- Jones S, Zhang X, Parsons DW, et al. Core signaling pathways in human pancreatic cancers revealed by global genomic analyses. *Science* 2008;321:1801–1806.
- Parsons DW, Jones S, Zhang X, et al. An integrated genomic analysis of human glioblastoma multiforme. *Science* 2008;321:1807–1812.
- Jones S, Wang TL, Shih leM, et al. Frequent mutations of chromatin remodeling gene ARID1A in ovarian clear cell carcinoma. *Science* 2010;330:228–231.
- Parsons DW, Li M, Zhang X, et al. The genetic landscape of the childhood cancer medulloblastoma. *Science* 2011;331:435–439.
- Yan H, Parsons DW, Jin G, et al. IDH1 and IDH2 mutations in gliomas. *N Engl J Med* 2009;360:765–773.
- Bleeker FE, Lamba S, Leenstra S, et al. IDH1 mutations at residue p.R132 (IDH1(R132)) occur frequently in high-grade gliomas but not in other solid tumors. *Hum Mutat* 2009;30:7–11.
- Hartmann C, Meyer J, Bals J, et al. Type and frequency of IDH1 and IDH2 mutations are related to astrocytic and oligodendroglial differentiation and age: a study of 1,010 diffuse gliomas. *Acta Neuropathol* 2009;118:469–474.
- Hayden JT, Frühwald MC, Hasselblatt M, et al. Frequent IDH1 mutations in supratentorial primitive neuroectodermal tumors (sPNET) of adults but not children. *Cell Cycle* 2009;8:1806–1807.
- Ichimura K, Pearson DM, Kocialkowski S, et al. IDH1 mutations are present in the majority of common adult gliomas but rare in primary glioblastomas. *Neuro Oncol* 2009;11:341–347.
- Kang MR, Kim MS, Oh JE, et al. Mutational analysis of IDH1 codon 132 in glioblastomas and other common cancers. *Int J Cancer* 2009;125:353–355.
- Watanabe T, Nobusawa S, Kleihues P, et al. IDH1 mutations are early events in the development of astrocytomas and oligodendrogliomas. *Am J Pathol* 2009;174:1149–1153.
- Mardis ER, Ding L, Dooling DJ, et al. Recurring mutations found by sequencing an acute myeloid leukemia genome. *N Engl J Med* 2009;361:1058–1066.
- Green A, Beer P. Somatic mutations of IDH1 and IDH2 in the leukemic transformation of myeloproliferative neoplasms. *N Engl J Med* 2010; 362:369–370.
- Gross S, Cairns RA, Minden MD, et al. Cancer-associated metabolite 2-hydroxyglutarate accumulates in acute myelogenous leukemia with isocitrate dehydrogenase 1 and 2 mutations. *J Exp Med* 2010;207:339–344.
- Mardis ER, Wilson RK. Cancer genome sequencing: a review. *Hum Mol Genet* 2009;18:R163–R168.
- Meyerson M, Gabriel S, Getz G. Advances in understanding cancer genomes through second-generation sequencing. *Nat Rev Genet* 2010;11:685–696.
- Metzker ML. Sequencing technologies - the next generation. *Nat Rev Genet* 2010;11:31–46.
- Bell DW. Our changing view of the genomic landscape of cancer. *J Pathol* 2010;220:231–243.
- Campbell PJ, Pleasance ED, Stephens PJ, et al. Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. *Proc Natl Acad Sci U S A* 2008;105:13081–13086.
- Kidd JM, Cooper GM, Donahue WF, et al. Mapping and sequencing of structural variation from eight human genomes. *Nature* 2008;453:56–64.
- Drmanac R, Sparks AB, Callow MJ, et al. Human genome sequencing using unchained base reads on self-assembling DNA nanoarrays. *Science* 2010; 327:78–81.
- Clarke J, Wu HC, Jayasinghe L, et al. Continuous base identification for single-molecule nanopore DNA sequencing. *Nat Nanotechnol* 2009;4: 265–270.
- Schadt EE, Turner S, Kasarskis A. A window into third-generation sequencing. *Hum Mol Genet* 2010;19:R227–R240.
- Dressman D, Yan H, Traverso G, et al. Transforming single DNA molecules into fluorescent magnetic particles for detection and enumeration of genetic variations. *Proc Natl Acad Sci U S A* 2003;100:8817–8822.
- Fedoruk M, Romieu A, Williams S, et al. BTA, a novel reagent for DNA attachment on glass and efficient generation of solid-phase amplified DNA colonies. *Nucleic Acids Res* 2006;34:e22.
- Harris TD, Buzby PR, Babcock H, et al. Single-molecule DNA sequencing of a viral genome. *Science* 2008;320:106–109.

71. Morozova O, Hirst M, Marra MA. Applications of new sequencing technologies for transcriptome analysis. *Annu Rev Genomics Hum Genet* 2009;10:135–151.
72. Pop M, Salzberg SL. Bioinformatics challenges of new sequencing technology. *Trends Genet* 2008;24:142–149.
73. Ley TJ, Mardis ER, Ding L, et al. DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. *Nature* 2008;456:66–72.
74. Garraway LA, Lander ES. Lessons from the cancer genome. *Cell* 2013;15:17–37.
75. Vogelstein B, Papadopoulos N, Velculescu VE, et al. Cancer genome landscapes. *Science* 2013;339:1546–1558.
76. Watson IR, Takahashi K, Futreal PA, et al. Emerging patterns of somatic mutations in cancer. *Nat Rev Genet* 2013;14:703–718.
77. Campbell PJ, Yachida S, Mudie LJ, et al. The patterns and dynamics of genomic instability in metastatic pancreatic cancer. *Nature* 2010;467:1109–1113.
78. Lee W, Jiang Z, Liu J, et al. The mutation spectrum revealed by paired genome sequences from a lung cancer patient. *Nature* 2010;465:473–477.
79. Marcucci G, Maharry K, Wu YZ, et al. IDH1 and IDH2 gene mutations identify novel molecular subsets within de novo cytogenetically normal acute myeloid leukemia: a Cancer and Leukemia Group B study. *J Clin Oncol* 2010;28:2348–2355.
80. Paschka P, Schlenk RF, Gaidzik VI, et al. IDH1 and IDH2 mutations are frequent genetic alterations in acute myeloid leukemia and confer adverse prognosis in cytogenetically normal acute myeloid leukemia with NPM1 mutation without FLT3 internal tandem duplication. *J Clin Oncol* 2010;28:3636–3643.
81. Shah SP, Morin RD, Khattra J, et al. Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature* 2009;461:809–813.
82. Yachida S, Jones S, Bozic I, et al. Distant metastasis occurs late during the genetic evolution of pancreatic cancer. *Nature* 2010;467:1114–1117.
83. Pleasance ED, Cheetham RK, Stephens PJ, et al. A comprehensive catalogue of somatic mutations from a human cancer genome. *Nature* 2010;463:191–196.
84. Pleasance ED, Stephens PJ, O'Meara S, et al. A small-cell lung cancer genome with complex signatures of tobacco exposure. *Nature* 2010;463:184–190.
85. Ding L, Ellis MJ, Li S, et al. Genome remodelling in a basal-like breast cancer metastasis and xenograft. *Nature* 2010;464:999–1005.
86. Ley TJ, Ding L, Walter MJ, et al. DNMT3A mutations in acute myeloid leukemia. *N Engl J Med* 2010;363:2424–2433.
87. Alexandrov LB, Nik-Zainal S, Wedge DC, et al. Signatures of mutational processes in human cancer. *Nature* 2013;500:415–421.
88. Ward PS, Patel J, Wise DR, et al. The common feature of leukemia-associated IDH1 and IDH2 mutations is a neomorphic enzyme activity converting alpha-ketoglutarate to 2-hydroxyglutarate. *Cancer Cell* 2010;17:225–234.
89. Jones SJ, Laskin J, Lu YY, et al. Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. *Genome Biol* 2010;11:R82.
90. Navin N, Kendall J, Troge J, et al. Tumour evolution inferred by single-cell sequencing. *Nature* 2011;472:90–94.
91. Vanharanta S, Massague J. Origins of metastatic traits. *Cancer Cell* 2013;24:410–421.
92. Huang FW, Hodis E, Xu MJ, et al. Highly recurrent TERT promoter mutations in human melanoma. *Science* 2013;339:957–959.
93. Horn S, Figl A, Rachakonda PS, et al. TERT promoter mutations in familial and sporadic melanoma. *Science* 2013;339:959–961.
94. Ying Z, Li Y, Wu J, et al. Loss of miR-204 expression enhances glioma migration and stem cell-like phenotype. *Cancer Res* 2013;73:990–999.
95. Liang YJ, Wang QY, Zhou CX, et al. MiR-124 targets Slug to regulate epithelial-mesenchymal transition and metastasis of breast cancer. *Carcinogenesis* 2013;34:713–722.
96. Cooper C, Guo J, Yan Y, et al. Increasing the relative expression of endogenous non-coding Steroid Receptor RNA Activator (SRA) in human breast cancer cells using modified oligonucleotides. *Nucleic Acids Res* 2009;37:4518–4531.
97. Stephens PJ, Greenman CD, Fu B, et al. Massive genomic rearrangement acquired in a single catastrophic event during cancer development. *Cell* 2011;144:27–40.
98. Korbel JO, Campbell PJ. Criteria for inference of chromothripsis in cancer genomes. *Cell* 2013;152:1226–1236.
99. Baca SC, Prandi D, Lawrence MS, et al. Punctuated evolution of prostate cancer genomes. *Cell* 2013;153:666–677.
100. Turner EH, Lee C, Ng SB, et al. Massively parallel exon capture and library-free resequencing across 16 genomes. *Nat Methods* 2009;6:315–316.
101. Gnirke A, Melnikov A, Magueire J, et al. Solution hybrid selection with ultralong oligonucleotides for massively parallel targeted sequencing. *Nat Biotechnol* 2009;27:182–189.
102. Levin JZ, Berger MF, Adiconis X, et al. Targeted next-generation sequencing of a cancer transcriptome enhances detection of sequence variants and novel fusion transcripts. *Genome Biol* 2009;10:R115.
103. Lawrence MS, Stojanov P, Polak P, et al. Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature* 2013;499:214–218.
104. Kandoth C, McLellan MD, Vandin F, et al. Mutational landscape and significance across 12 major cancer types. *Nature* 2013;502:333–339.
105. Gartner JJ, Parker SC, Prickett TD, et al. Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. *Proc Natl Acad Sci U S A* 2013;110:13481–13486.
106. Stegh AH, Brennan C, Mahoney JA, et al. Glioma oncoprotein Bcl2L12 inhibits the p53 tumor suppressor. *Genes Dev* 2010;24:2194–2204.
107. Mullaney JM, Mills RE, Pittard WS, et al. Small insertions and deletions (INDELs) in human genomes. *Hum Mol Genet* 2010;19:R131–R136.
108. Tomlins SA, Rhodes DR, Perner S, et al. Recurrent fusion of TMPRSS2 and ETS transcription factor genes in prostate cancer. *Science* 2005;310:644–648.
109. Soda M, Choi YL, Enomoto M, et al. Identification of the transforming EML4-ALK fusion gene in non-small-cell lung cancer. *Nature* 2007;448:561–566.
110. Palanisamy N, Ateeq B, Kalyana-Sundaram S, et al. Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. *Nat Med* 2010;16:793–798.
111. Leary RJ, Kinde I, Diehl F, et al. Development of personalized tumor biomarkers using massively parallel sequencing. *Sci Transl Med* 2010;2:20ra14.
112. Maher CA, Kumar-Sinha C, Cao X, et al. Transcriptome sequencing to detect gene fusions in cancer. *Nature* 2009;458:97–101.
113. Stephens PJ, McBride DJ, Lin ML, et al. Complex landscapes of somatic rearrangement in human breast cancer genomes. *Nature* 2009;462:1005–1010.
114. Feng H, Shuda M, Chang Y, et al. Clonal integration of a polyomavirus in human Merkel cell carcinoma. *Science* 2008;319:1096–1100.
115. Hermer A, Sauliunaite D, Michalski CW, et al. Glutamate increases pancreatic cancer cell invasion and migration via AMPA receptor activation and Kras-MAPK signaling. *Int J Cancer* 2011;129:2349–2359.
116. Wei X, Walia V, Lin JC, et al. Exome sequencing identifies GRIN2A as frequently mutated in melanoma. *Nat Genet* 2011;43:442–446.
117. Prickett TD, Wei X, Cardenas-Navia I, et al. Exon capture analysis of G protein-coupled receptors identifies activating mutations in GRM3 in melanoma. *Nat Genet* 2011;43:1119–1126.
118. Krauthammer M, Kong Y, Ha BH, et al. Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. *Nat Genet* 2012;44:1006–1014.
119. Davies H, Hunter C, Smith R, et al. Somatic mutations of the protein kinase gene family in human lung cancer. *Cancer Res* 2005;65:7591–7595.
120. Bozic I, Antal T, Ohtsuki H, et al. Accumulation of driver and passenger mutations during tumor progression. *Proc Natl Acad Sci U S A* 2010;107:18545–18550.
121. Parmigiani G, Boca S, Lin J, et al. Design and analysis issues in genome-wide somatic mutation studies of cancer. *Genomics* 2009;93:17–21.
122. Kaminker JS, Zhang Y, Waugh A, et al. Distinguishing cancer-associated missense mutations from common polymorphisms. *Cancer Res* 2007;67:465–473.
123. Futreal PA. Backseat drivers take the wheel. *Cancer Cell* 2007;12:493–494.
124. Greenman C, Wooster R, Futreal PA, et al. Statistical analysis of pathogenicity of somatic mutations in cancer. *Genetics* 2006;173:2187–2198.
125. Baudot A, Real FX, Izarzugaza JM, et al. From cancer genomes to cancer models: bridging the gaps. *EMBO Rep* 2009;10:359–366.
126. Carter H, Chen S, Isik L, et al. Cancer-specific high-throughput annotation of somatic mutations: computational prediction of driver missense mutations. *Cancer Res* 2009;69:6660–6667.
127. Ng PC, Henikoff S. SIFT: Predicting amino acid changes that affect protein function. *Nucleic Acids Res* 2003;31:3812–3814.
128. Kohli M, Rago C, Lengauer C, et al. Facile methods for generating human somatic cell gene knockouts using recombinant adeno-associated viruses. *Nucleic Acids Res* 2004;32:e3.
129. Downing JR, Wilson RK, Zhang J, et al. The Pediatric Cancer Genome Project. *Nat Genet* 2012;44:619–622.
130. Hudson TJ, Anderson W, Artez A, et al. International network of cancer genome projects. *Nature* 2010;464:993–998.
131. Bignell GR, Greenman CD, Davies H, et al. Signatures of mutation and selection in the cancer genome. *Nature* 2010;463:893–898.
132. Sieber OM, Tomlinson SR, Tomlinson IP. Tissue, cell and stage specificity of (epi)mutations in cancers. *Nat Rev Cancer* 2005;5:649–655.
133. Benvenuti S, Frattini M, Arena S, et al. PIK3CA cancer mutations display gender and tissue specificity patterns. *Hum Mutat* 2008;29:284–288.
134. Karakas B, Bachman KE, Park BH. Mutation of the PIK3CA oncogene in human cancers. *Br J Cancer* 2006;94:455–459.
135. Brennan CW, Verhaak RG, McKenna A, et al. The somatic genomic landscape of glioblastoma. *Cell* 2013;155:462–477.
136. Cancer Genome Atlas Network. Comprehensive molecular characterization of human colon and rectal cancer. *Nature* 2012;487:330–337.
137. Cancer Genome Atlas Network. Comprehensive molecular portraits of human breast tumours. *Nature* 2012;490:61–70.
138. Cancer Genome Atlas Research Network. Integrated genomic analyses of ovarian carcinoma. *Nature* 2011;474:609–615.
139. Cancer Genome Atlas Research Network. Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature* 2013;499:43–49.
140. Cancer Genome Atlas Research Network. Integrated genomic characterization of endometrial carcinoma. *Nature* 2013;497:67–73.
141. Weischenfeldt J, Simon R, Feuerbach L, et al. Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. *Cancer Cell* 2013;23:159–170.
142. Cancer Genome Atlas Research Network. Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *N Engl J Med* 2013;368:2059–2074.
143. Dawson SJ, Rueda OM, Aparicio S, et al. A new genome-driven integrated classification of breast cancer and its implications. *EMBO J* 2013;32:617–628.

144. Plass C, Pfister SM, Lindroth AM, et al. Mutations in regulators of the epigenome and their connections to global chromatin patterns in cancer. *Nat Rev Genet* 2013;14:765–780.
145. Shen H, Laird PW. Interplay between the cancer genome and epigenome. *Cell* 2013;153:38–55.
146. Yamamoto E, Suzuki H, Yamano HO, et al. Molecular dissection of premalignant colorectal lesions reveals early onset of the CpG island methylator phenotype. *Am J Pathol* 2012;181:1847–1861.
147. Gao J, Aksoy BA, Dogrusoz U, et al. Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. *Sci Signal* 2013;6:p11.
148. Bleeker FE, Bardelli A. Genomic landscapes of cancers: prospects for targeted therapies. *Pharmacogenomics* 2007;8:1629–1633.
149. Paez JG, Jänne PA, Lee JC, et al. EGFR mutations in lung cancer: correlation with clinical response to gefitinib therapy. *Science* 2004;304:1497–1500.
150. Ciardiello F, Tortora G. EGFR antagonists in cancer treatment. *N Engl J Med* 2008;358:1160–1174.
151. Janku F, Stewart DJ, Kurzrock R. Targeted therapy in non-small-cell lung cancer—is it becoming a reality? *Nat Rev Clin Oncol* 2010;7:401–414.
152. Pao W, Chmielecki J. Rational, biologically based treatment of EGFR-mutant non-small-cell lung cancer. *Nat Rev Cancer* 2010;10:760–774.
153. Gerber DE, Minna JD. ALK inhibition for non-small cell lung cancer: from discovery to therapy in record time. *Cancer Cell* 2010;18:548–551.
154. Andreyev HJ, Norman AR, Cunningham D, et al. Kirsten ras mutations in patients with colorectal cancer: the multicenter “RASCAL” study. *J Natl Cancer Inst* 1998;90:675–684.
155. Roth AD, Tejpar S, Delorenzi M, et al. Prognostic role of KRAS and BRAF in stage II and III resected colon cancer: results of the translational study on the PETACC-3, EORTC 40993, SAKK 60-00 trial. *J Clin Oncol* 2010;28:466–474.
156. Bardelli A, Siena S. Molecular mechanisms of resistance to cetuximab and panitumumab in colorectal cancer. *J Clin Oncol* 2010;28:1254–1261.
157. Siena S, Sartore-Bianchi A, Di Nicolantonio F, et al. Biomarkers predicting clinical outcome of epidermal growth factor receptor-targeted therapy in metastatic colorectal cancer. *J Natl Cancer Inst* 2009;101:1308–1324.
158. Tejpar S, Bertagnolli M, Bosman F, et al. Prognostic and predictive biomarkers in resected colon cancer: current status and future perspectives for integrating genomics into biomarker discovery. *Oncologist* 2010;15:390–404.
159. Gerlinger M, Rowan AJ, Horswell S, et al. Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. *N Engl J Med* 2012;366:883–892.
160. Mandel P, Metais P. [Not Available]. *C R Seances Soc Biol Fil* 1948;142:241–243.
161. Crowley E, Di Nicolantonio F, Loupakis F, et al. Liquid biopsy: monitoring cancer-genetics in the blood. *Nat Rev Clin Oncol* 2013;10:472–484.
162. Diehl F, Li M, Dressman D, et al. Detection and quantification of mutations in the plasma of patients with colorectal tumors. *Proc Natl Acad Sci U S A* 2005;102:16368–16373.
163. Diehl F, Schmidt K, Choti MA, et al. Circulating mutant DNA to assess tumor dynamics. *Nat Med* 2008;14:985–990.
164. Frattini M, Gallino G, Signoroni S, et al. Quantitative and qualitative characterization of plasma DNA identifies primary and recurrent colorectal cancer. *Cancer Lett* 2008;263:170–181.
165. Chan KC, Jiang P, Zheng YW, et al. Cancer genome scanning in plasma: detection of tumor-associated copy number aberrations, single-nucleotide variants, and tumoral heterogeneity by massively parallel sequencing. *Clin Chem* 2013;59:211–224.
166. Murtaza M, Dawson SJ, Tsui DW, et al. Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. *Nature* 2013;497:108–112.
167. Bardelli A, Corso S, Bertotti A, et al. Amplification of the MET receptor drives resistance to anti-EGFR therapies in colorectal cancer. *Cancer Discov* 2013;3:658–673.
168. Higgins MJ, Jelovac D, Barnathan E, et al. Detection of tumor PIK3CA status in metastatic breast cancer using peripheral blood. *Clin Cancer Res* 2012;18:3462–3469.
169. Leary RJ, Sausen M, Kinde I, et al. Detection of chromosomal alterations in the circulation of cancer patients with whole-genome sequencing. *Sci Transl Med* 2012;4:162ra154.
170. Misale S, Yaeger R, Hobor S, et al. Emergence of KRAS mutations and acquired resistance to anti-EGFR therapy in colorectal cancer. *Nature* 2012;486:532–536.
171. Diaz LA Jr, Williams RT, Wu J, et al. The molecular evolution of acquired resistance to targeted EGFR blockade in colorectal cancers. *Nature* 2012;486:537–540.
172. Robbins PF, Lu YC, El-Gamil M, et al. Mining exomic sequencing data to identify mutated antigens recognized by adoptively transferred tumor-reactive T cells. *Nat Med* 2013;19:747–752.
173. Hunter C, Smith R, Cahill DP, et al. A hypermutation phenotype and somatic MSH6 mutations in recurrent human malignant gliomas after alkylator chemotherapy. *Cancer Res* 2006;66:3987–3991.
174. Cahill DP, Levine KK, Betensky RA, et al. Loss of the mismatch repair protein MSH6 in human glioblastomas is associated with tumor progression during temozolomide treatment. *Clin Cancer Res* 2007;13:2038–2045.
175. Engelman JA, Zejnullahu K, Mitsudomi T, et al. MET amplification leads to gefitinib resistance in lung cancer by activating ERBB3 signaling. *Science* 2007;316:1039–1043.
176. Gorre ME, Mohammed M, Ellwood K, et al. Clinical resistance to STI-571 cancer therapy caused by BCR-ABL gene mutation or amplification. *Science* 2001;293:876–880.
177. Heinrich MC, Corless CL, Blanke CD, et al. Molecular correlates of imatinib resistance in gastrointestinal stromal tumors. *J Clin Oncol* 2006;24:4764–4774.
178. Shepherd FA, Rodrigues Pereira J, Ciuleanu T, et al. Erlotinib in previously treated non-small-cell lung cancer. *N Engl J Med* 2005;353:123–132.
179. Kobayashi S, Boggon TJ, Dayaram T, et al. EGFR mutation and resistance of non-small-cell lung cancer to gefitinib. *N Engl J Med* 2005;352:786–792.
180. Kwak EL, Sordella R, Bell DW, et al. Irreversible inhibitors of the EGF receptor may circumvent acquired resistance to gefitinib. *Proc Natl Acad Sci U S A* 2005;102:7665–7670.
181. Pao W, Miller VA, Politi KA, et al. Acquired resistance of lung adenocarcinomas to gefitinib or erlotinib is associated with a second mutation in the EGFR kinase domain. *PLoS Med* 2005;2:e73.
182. Shih JY, Gow CH, Yang PC. EGFR mutation conferring primary resistance to gefitinib in non-small-cell lung cancer. *N Engl J Med* 2005;353:207–208.
183. Bell DW, Gore I, Okimoto Ra, et al. Inherited susceptibility to lung cancer may be associated with the T790M drug resistance mutation in EGFR. *Nat Genet* 2005;37:1315–1316.
184. Inukai M, Toyooka S, Ito S, et al. Presence of epidermal growth factor receptor gene T790M mutation as a minor clone in non-small cell lung cancer. *Cancer Res* 2006;66:7854–7858.
185. Daub H, Specht K, Ullrich A. Strategies to overcome resistance to targeted protein kinase inhibitors. *Nat Rev Drug Discov* 2004;3:1001–1010.
186. Choi YL, Soda M, Yamashita Y, et al. EML4-ALK mutations in lung cancer that confer resistance to ALK inhibitors. *N Engl J Med* 2010;363:1734–1739.
187. Flaherty KT, Puzanov I, Kim KB, et al. Inhibition of mutated, activated BRAF in metastatic melanoma. *N Engl J Med* 2010;363:809–819.
188. Nazarian R, Shi H, Wang Q, et al. Melanomas acquire resistance to B-RAF(V600E) inhibition by RTK or N-RAS upregulation. *Nature* 2010;468:973–977.
189. Pompetti F, Spadano A, Sau A, et al. Long-term remission in BCR/ABL-positive AML-M6 patient treated with Imatinib Mesylate. *Leuk Res* 2007;31:563–567.
190. Druker BJ, Builhot F, O'Brien SC, et al. Five-year follow-up of patients receiving imatinib for chronic myeloid leukemia. *N Engl J Med* 2006;355:2408–2417.