

Publication List - Agilent SureSelect Platform

Mendelian Diseases

Rafiq MA, Kuss AW, Puettmann L, Noor A, Ramiah A, Ali G, Hu H, Kerio NA, Xiang Y, Garshasbi M, Khan MA, Ishak GE, Weksberg R, Ullmann R, Tzschach A, Kahrizi K, Mahmood K, Naeem F, Ayub M, Moremen KW, Vincent JB, Ropers HH, Ansar M, Najmabadi H. **Mutations in the Alpha 1,2-Mannosidase Gene, MAN1B1, Cause Autosomal-Recessive Intellectual Disability.** Am J Hum Genet. 2011 Jul 15;89(1):176-82.

Sergouniotis PI, Davidson AE, Mackay DS, Li Z, Yang X, Plagnol V, Moore AT, Webster AR. **Recessive Mutations in KCNJ13, Encoding an Inwardly Rectifying Potassium Channel Subunit, Cause Leber Congenital Amaurosis.** Am J Hum Genet. 2011 Jul 15;89(1):183-90.

Sanna-Cherchi S, Burgess KE, Nees SN, Caridi G, Weng PL, Dagnino M, Bodria M, Carrea A, Allegretta MA, Kim HR, Perry BJ, Gigante M, Clark LN, Kisselev S, Cusi D, Gesualdo L, Allegri L, Scolari F, D'Agati V, Shapiro LS, Pecoraro C, Palomero T, Ghiggeri GM, Gharavi AG. **Exome sequencing identified MYO1E and NEIL1 as candidate genes for human autosomal recessive steroid-resistant nephrotic syndrome.** Kidney Int. 2011 Jun 22.

Le Goff C, Mahaut C, Wang LW, Allali S, Abhyankar A, Jensen S, Zylberberg L, Collod-Beroud G, Bonnet D, Alanay Y, Brady AF, Cordier MP, Devriendt K, Genevieve D, Kiper PO, Kitoh H, Krakow D, Lynch SA, Le Merrer M, Mégarbane A, Mortier G, Odent S, Polak M, Rohrbach M, Sillence D, Stolte-Dijkstra I, Superti-Furga A, Rimoin DL, Topouchian V, Unger S, Zabel B, Bole-Feysot C, Nitschke P, Handford P, Casanova JL, Boileau C, Apte SS, Munnich A, Cormier-Daire V. **Mutations in the TGF β Binding-Protein-Like Domain 5 of FBN1 Are Responsible for Acromicric and Geleophysic Dysplasias.** Am J Hum Genet. 2011 Jun 15.

Yariz KO, Walsh T, Uzak A, Spiliopoulos M, Duman D, Onalan G, King MC, Tekin M. **Inherited mutation of the luteinizing hormone/choriogonadotropin receptor (LHCGR) in empty follicle syndrome.** Fertil Steril. 2011 Jun 16.

Comino-Méndez I, Gracia-Aznárez FJ, Schiavi F, Landa I, Leandro-García LJ, Letón R, Honrado E, Ramos-Medina R, Caronia D, Pita G, Gómez-Graña A, de Cubas AA, Inglada-Pérez L, Maliszewska A, Taschin E, Bobisse S, Pica G, Loli P, Hernández-Lavado R, Díaz JA, Gómez-Morales M, González-Neira A, Roncador G, Rodríguez-Antona C, Benítez J, Mannelli M, Opocher G, Robledo M, Cascón A. **Exome sequencing identifies MAX mutations as a cause of hereditary pheochromocytoma.** Nat Genet. 2011 Jun 19;43(7):663-7.

Rope AF, Wang K, Evjenth R, Xing J, Johnston JJ, Swensen JJ, Johnson WE, Moore B, Huff CD, Bird LM, Carey JC, Opitz JM, Stevens CA, Jiang T, Schank C, Fain HD, Robison R, Dalley B, Chin S, South ST, Pysher TJ, Jorde LB, Hakonarson H, Lillehaug JR, Biesecker LG, Yandell M, Arnesen T, Lyon GJ. **Using VAAST to identify an X-Linked Disorder Resulting in Lethality in Male Infants Due to N-Terminal Acetyltransferase Deficiency.** Am J Hum Genet. 2011 Jun 22.

Hoischen A, van Bon BW, Rodríguez-Santiago B, Gilissen C, Vissers LE, de Vries P, Janssen I, van Lier B, Hastings R, Smithson SF, Newbury-Ecob R, Kjaergaard S, Goodship J, McGowan R, Bartholdi D, Rauch A, Peippo M, Cobben JM, Wieczorek D, Gillessen-Kaesbach G, Veltman JA, Brunner HG, de Vries BB. **De novo nonsense mutations in ASXL1 cause Bohring-Opitz syndrome.** *Nat Genet.* 2011 Jun 26.

Liu L, Okada S, Kong XF, Kreins AY, Cypowyj S, Abhyankar A, Toubiana J, Itan Y, Audry M, Nitschke P, Masson C, Toth B, Flatot J, Migaud M, Chrabieh M, Kochetkov T, Bolze A, Borghesi A, Toulon A, Hiller J, Eyerich S, Eyerich K, Gulácsy V, Chernyshova L, Chernyshov V, Bondarenko A, María Cortés Grimaldo R, Blancas-Galicia L, Madrigal Beas IM, Roesler J, Magdorf K, Engelhard D, Thumerelle C, Burgel PR, Hoernes M, Drexel B, Seger R, Kusuma T, Jansson AF, Sawalle-Belohradsky J, Belohradsky B, Jouanguy E, Bustamante J, Bué M, Karin N, Wildbaum G, Bodemer C, Lortholary O, Fischer A, Blanche S, Al-Muhsen S, Reichenbach J, Kobayashi M, Rosales FE, Lozano CT, Kilic SS, Oleastro M, Etzioni A, Traidl-Hoffmann C, Renner ED, Abel L, Picard C, Maródi L, Boisson-Dupuis S, Puel A, Casanova JL. **Gain-of-function human STAT1 mutations impair IL-17 immunity and underlie chronic mucocutaneous candidiasis.** *J Exp Med.* 2011 Jul 4.

Hanson D, Murray PG, O'Sullivan J, Urquhart J, Daly S, Bhaskar SS, Biesecker LG, Skae M, Smith C, Cole T, Kirk J, Chandler K, Kingston H, Donnai D, Clayton PE, Black GC. **Exome Sequencing Identifies CCDC8 Mutations in 3-M Syndrome, Suggesting that CCDC8 Contributes in a Pathway with CUL7 and OBSL1 to Control Human Growth.** *Am J Hum Genet.* 2011 Jul 5.

Klein CJ, Botuyan MV, Wu Y, Ward CJ, Nicholson GA, Hammans S, Hojo K, Yamanishi H, Karpf AR, Wallace DC, Simon M, Lander C, Boardman LA, Cunningham JM, Smith GE, Litchy WJ, Boes B, Atkinson EJ, Middha S, B Dyck PJ, Parisi JE, Mer G, Smith DI, Dyck PJ. **Mutations in DNMT1 cause hereditary sensory neuropathy with dementia and hearing loss.** *Nat Genet.* 2011 Jun;43(6):595-600.

Snape K, Hanks S, Ruark E, Barros-Núñez P, Elliott A, Murray A, Lane AH, Shannon N, Callier P, Chitayat D, Clayton-Smith J, Fitzpatrick DR, Gisselsson D, Jacquemont S, Asakura-Hay K, Micale MA, Tolmie J, Turnpenny PD, Wright M, Douglas J, Rahman N. **Mutations in CEP57 cause mosaic variegated aneuploidy syndrome.** *Nat Genet.* 2011 Jun;43(6):527-9.

Yamaguchi T, Hosomichi K, Narita A, Shirota T, Tomoyasu Y, Maki K, Inoue I. **Exome resequencing combined with linkage analysis identifies novel PTH1R variants in primary failure of tooth eruption in Japanese.** *J Bone Miner Res.* 2011 Jul;26(7):1655-61.

Cullinane AR, Vilboux T, O'Brien K, Curry JA, Maynard DM, Carlson-Donohoe H, Ciccone C; NISC Comparative Sequencing Program, Markello TC, Gunay-Aygun M, Huizing M, Gahl WA. **Homozygosity Mapping and Whole-Exome Sequencing to Detect SLC45A2 and G6PC3 Mutations in a Single Patient with Oculocutaneous Albinism and Neutropenia.** *J Invest Dermatol.* 2011 Jun 16.

Akoury E, El Zir E, Mansour A, Mégarbané A, Majewski J, Slim R. **A Novel 5-bp Deletion in Clarin 1 in a Family with Usher Syndrome.** *Ophthalmic Genet.* 2011 Jun 15.

Abou Jamra R, Philippe O, Raas-Rothschild A, Eck SH, Graf E, Buchert R, Borck G, Ekici A, Brockschmidt FF, Nöthen MM, Munnich A, Strom TM, Reis A, Colleaux L. **Adaptor protein complex 4 deficiency causes severe autosomal-recessive intellectual disability, progressive spastic paraplegia, shy character, and short stature.** Am J Hum Genet. 2011 Jun 10;88(6):788-95.

Bowne SJ, Humphries MM, Sullivan LS, Kenna PF, Tam LC, Kiang AS, Campbell M, Weinstock GM, Koboldt DC, Ding L, Fulton RS, Sodergren EJ, Allman D, Millington-Ward S, Palfi A, McKee A, Blanton SH, Slifer S, Konidari I, Farrar GJ, Daiger SP, Humphries P. **A dominant mutation in RPE65 identified by whole-exome sequencing causes retinitis pigmentosa with choroidal involvement.** Eur J Hum Genet. 2011 Jun 8.

Tsurusaki Y, Okamoto N, Suzuki Y, Doi H, Saito H, Miyake N, Matsumoto N. **Exome sequencing of two patients in a family with atypical X-linked leukodystrophy.** Clin Genet. 2011 Jun 3.

Southgate L, Machado RD, Snape KM, Primeau M, Dafou D, Ruddy DM, Branney PA, Fisher M, Lee GJ, Simpson MA, He Y, Bradshaw TY, Blaumeiser B, Winship WS, Reardon W, Maher ER, FitzPatrick DR, Wuyts W, Zenker M, Lamarche-Vane N, Trembath RC. **Gain-of-function mutations of ARHGAP31, a Cdc42/Rac1 GTPase regulator, cause syndromic cutis aplasia and limb anomalies.** Am J Hum Genet. 2011 May 13;88(5):574-85.

Alvarado DM, Buchan JG, Gurnett CA, Dobbs MB. **Exome Sequencing Identifies an MYH3 Mutation in a Family with Distal Arthrogryposis Type 1.** J Bone Joint Surg Am. 2011 Apr 29.

Bolze A, Byun M, McDonald D, Morgan NV, Abhyankar A, Premkumar L, Puel A, Bacon CM, Rieux-Lauzier F, Pang K, Britland A, Abel L, Cant A, Maher ER, Riedl SJ, Hambleton S, Casanova JL. **Whole-exome-sequencing-based discovery of human FADD deficiency.** Am J Hum Genet. 2010 Dec 10;87(6):873-81.

Kalay E, Yigit G, Aslan Y, Brown KE, Pohl E, Bicknell LS, Kayserili H, Li Y, Tüysüz B, Nürnberg G, Kiess W, Koegl M, Baessmann I, Buruk K, Toraman B, Kayipmaz S, Kul S, Ikbal M, Turner DJ, Taylor MS, Aerts J, Scott C, Milstein K, Dollfus H, Wieczorek D, Brunner HG, Hurles M, Jackson AP, Rauch A, Nürnberg P, Karagüzel A, Wollnik B. **CEP152 is a genome maintenance protein disrupted in Seckel syndrome.** Nat Genet. 2011 Jan;43(1):23-6.

Rajadhyaksha AM, Elemento O, Puffenberger EG, Schierberl KC, Xiang JZ, Putorti ML, Berciano J, Poulin C, Brais B, Michaelides M, Weleber RG, Higgins JJ. **Mutations in FLVCR1 cause posterior column ataxia and retinitis pigmentosa.** Am J Hum Genet. 2010 Nov 12;87(5):643-54.

Sirmaci A, Walsh T, Akay H, Spiliopoulos M, Sakalar YB, Hasaneffendioğlu-Bayrak A, Duman D, Farooq A, King MC, Tekin M. **MASP1 mutations in patients with facial, umbilical, coccygeal, and auditory findings of Carnevale, Malpuech, OSA, and Michels syndromes.** Am J Hum Genet. 2010 Nov 12;87(5):679-86.

Schraders M, Haas SA, Weegerink NJ, Oostrik J, Hu H, Hoefsloot LH, Kannan S, Huygen PL, Pennings RJ, Admiraal RJ, Kalscheuer VM, Kunst HP, Kremer H. **Next-Generation Sequencing Identifies Mutations of SMPX, which Encodes the Small Muscle Protein, X-Linked, as a Cause of Progressive Hearing Impairment.** Am J Hum Genet. 2011 May 4.

Puente XS, Quesada V, Osorio FG, Cabanillas R, Cadiñanos J, Fraile JM, Ordóñez GR, Puente DA, Gutiérrez-Fernández A, Fanjul-Fernández M, Lévy N, Freije JM, López-Otín C. **Exome Sequencing and Functional Analysis Identifies BANF1 Mutation as the Cause of a Hereditary Progeroid Syndrome.** Am J Hum Genet. 2011 May 4.

Erlich Y, Edvardson S, Hodges E, Zenvirt S, Thekkat P, Shaag A, Dor T, Hannon GJ, Elpeleg O. **Exome sequencing and disease-network analysis of a single family implicate a mutation in KIF1A in hereditary spastic paraparesis.** Genome Res. 2011 May;21(5):658-64.

Vissers LE, Lausch E, Unger S, Campos-Xavier AB, Gilissen C, Rossi A, Del Rosario M, Venselaar H, Knoll U, Nampoothiri S, Nair M, Spranger J, Brunner HG, Bonafé L, Veltman JA, Zabel B, Superti-Furga A. **Chondrodysplasia and Abnormal Joint Development Associated with Mutations in IMPAD1, Encoding the Golgi-Resident Nucleotide Phosphatase, gPAPP.** Am J Hum Genet. 2011 May 4.

Bowen ME, Boyden ED, Holm IA, Campos-Xavier B, Bonafé L, Superti-Furga A, Ikegawa S, Cormier-Daire V, Bovée JV, Pansuriya TC, de Sousa SB, Savarirayan R, Andreucci E, Vakkula M, Garavelli L, Pottinger C, Ogino T, Sakai A, Regazzoni BM, Wuyts W, Sangiorgi L, Pedrini E, Zhu M, Kozakewich HP, Kasser JR, Seidman JG, Kurek KC, Warman ML. **Loss-of-Function Mutations in PTPN11 Cause Metachondromatosis, but Not Ollier Disease or Maffucci Syndrome.** PLoS Genet. 2011 Apr;7(4):e1002050.

Götz A, Tyynismaa H, Euro L, Ellonen P, Hyötyläinen T, Ojala T, Hämäläinen RH, Tommiska J, Raivio T, Oresic M, Karikoski R, Tammela O, Simola KO, Paetau A, TyniT, Suomalainen A. **Exome Sequencing Identifies Mitochondrial Alanyl-tRNA Synthetase Mutations in Infantile Mitochondrial Cardiomyopathy.** Am J Hum Genet. 2011 May 4.

O'Sullivan J, Bitu CC, Daly SB, Urquhart JE, Barron MJ, Bhaskar SS, Martelli-Júnior H, Dos Santos Neto PE, Mansilla MA, Murray JC, Coletta RD, Black GC, Dixon MJ. **Whole-Exome Sequencing Identifies FAM20A Mutations as a Cause of Amelogenesis Imperfecta and Gingival Hyperplasia Syndrome.** Am J Hum Genet. 2011 May 4.

Al Badr W, Al Bader S, Otto E, Hildebrandt F, Ackley T, Peng W, Xu J, Li J, Owens KM, Bloom D, Innis JW. **Exome capture and massively parallel sequencing identifies a novel HPSE2 mutation in a Saudi Arabian child with Ochoa (urofacial) syndrome.** J Pediatr Urol. 2011 Mar 28.

Edery P, Marcaillou C, Sahbatou M, Labalme A, Chastang J, Touraine R, Tubacher E, Senni F, Bober MB, Nampoothiri S, Jouk PS, Steichen E, Berland S, Toutain A, Wise CA, Sanlaville D, Rousseau F, Clerget-Darpoux F, Leutenegger AL. **Association of TALS developmental disorder with defect in minor splicing component U4atac snRNA.** Science. 2011 Apr 8;332(6026):240-3.

Tsurusaki Y, Osaka H, Hamanoue H, Shimbo H, Tsuji M, Doi H, Saitsu H, Matsumoto N, Miyake N. **Rapid detection of a mutation causing X-linked leucoencephalopathy by exome sequencing.** J Med Genet. 2011 Mar 17.

Isidor B, Lindenbaum P, Pichon O, Bézieau S, Dina C, Jacquemont S, Martin-Coignard D, Thauvin-Robinet C, Le Merrer M, Mandel JL, David A, Faivre L, Cormier-Daire V, Redon R, Le Caignec C. **Truncating mutations in the last exon of NOTCH2 cause a rare skeletal disorder with osteoporosis.** *Nat Genet.* 2011 Mar 6;43(4):306-8.

Liu Y, Gao M, Lv YM, Yang X, Ren YQ, Jiang T, Zhang X, Guo BR, Li M, Zhang Q, Zhang P, Zhou FS, Chen G, Yin XY, Zuo XB, Sun LD, Zheng XD, Zhang SM, Liu JJ, Zhou Y, Li YR, Wang J, Wang J, Yang HM, Yang S, Li RQ, Zhang XJ. **Confirmation by Exome Sequencing of the Pathogenic Role of NCSTN Mutations in Acne Inversa (Hidradenitis Suppurativa).** *J Invest Dermatol.* 2011 Mar 24.

Simpson MA, Irving MD, Asilmaz E, Gray MJ, Dafou D, Elmslie FV, Mansour S, Holder SE, Brain CE, Burton BK, Kim KH, Pauli RM, Aftimos S, Stewart H, Kim CA, Holder-Espinasse M, Robertson SP, Drake WM, Trembath RC. **Mutations in NOTCH2 cause Hajdu-Cheney syndrome, a disorder of severe and progressive bone loss.** *Nat Genet.* 2011 Mar 6;43(4):303-5.

Ku CS, Naidoo N, Pawitan Y. **Revisiting Mendelian disorders through exome sequencing.** *Hum Genet.* 2011 Apr;129(4):351-70.

Zheng J, Miller KK, Yang T, Hildebrand MS, Shearer AE, Deluca AP, Scheetz TE, Drummond J, Scherer SE, Legan PK, Goodyear RJ, Richardson GP, Cheatham MA, Smith RJ, Dallos P. **Carcinoembryonic antigen-related cell adhesion molecule 16 interacts with {alpha}-tectorin and is mutated in autosomal dominant hearing loss (DFNA4).** *Proc Natl Acad Sci U S A.* 2011 Mar 8;108(10):4218-23.

Becker J, Semler O, Gilissen C, Li Y, Bolz HJ, Giunta C, Bergmann C, Rohrbach M, Koerber F, Zimmermann K, de Vries P, Wirth B, Schoenau E, Wollnik B, Veltman JA, Hoischen A, Netzer C. **Exome Sequencing Identifies Truncating Mutations in Human SERPINF1 in Autosomal-Recessive Osteogenesis Imperfecta.** *Am J Hum Genet.* 2011 Mar 11;88(3):362-71.

Ostergaard P, Simpson MA, Brice G, Mansour S, Connell FC, Onoufriadiis A, Child AH, Hwang J, Kalidas K, Mortimer PS, Trembath R, Jeffery S. **Rapid identification of mutations in GJC2 in primary lymphoedema using whole exome sequencing combined with linkage analysis with delineation of the phenotype.** *J Med Genet.* 2011 Apr;48(4):251-5.

Montenegro G, Powell E, Huang J, Speziani F, Edwards YJ, Beecham G, Hulme W, Siskind C, Vance J, Shy M, Züchner S. **Exome sequencing allows for rapid gene identification in a Charcot-Marie-Tooth family.** *Ann Neurol.* 2011 Mar;69(3):464-70.

Caliskan M, Chong JX, Uricchio L, Anderson R, Chen P, Sougnez C, Garimella K, Gabriel SB, Depristo MA, Shakir K, Matern D, Das S, Waggoner D, Nicolae DL, Ober C. **Exome sequencing reveals a novel mutation for autosomal recessive non-syndromic mental retardation in the TECR gene on chromosome 19p13.** *Hum Mol Genet.* 2011 Jan 13.

Bolze A, Byun M, McDonald D, Morgan NV, Abhyankar A, Premkumar L, Puel A, Bacon CM, Rieux-Lauca F, Pang K, Britland A, Abel L, Cant A, Maher ER, Riedl SJ, Hambleton S, Casanova JL. **Whole-exome sequencing-based discovery of human FADD deficiency.** *Am J Hum Genet.* 2010 Dec;10:873-81.

Johnson JO, Mandrioli J, Benatar M, Abramzon Y, Van Deerlin VM, Trojanowski JQ, Gibbs JR, Brunetti M, Gronka S, Wu J, Ding J, McCluskey L, Martinez-Lage M, Falcone D, Hernandez DG, Arepalli S, Chong S, Schymick JC, Rothstein J, Landi F, Wang YD, Calvo A, Mora G, Sabatelli M, Monsurro MR, Battistini S, Salvi F, Spataro R, Sola P, Borghero G; ITALSGEN Consortium, Galassi G, Scholz SW, Taylor JP, Restagno G, Chiò A, Traynor BJ. **Exome sequencing reveals VCP mutations as a cause of familial ALS.** *Neuron.* 2010 Dec 9;68(5):857-64.

Haack TB, Danhauser K, Haberberger B, Hoser J, Strecker V, Boehm D, Uziel G, Lamantea E, Invernizzi F, Poulton J, Rolinski B, Iuso A, Biskup S, Schmidt T, Mewes HW, Wittig I, Meitinger T, Zeviani M, Prokisch H. **Exome sequencing identifies ACAD9 mutations as a cause of complex I deficiency.** *Nat Genet.* 2010 Dec;42(12):1131-4.

Vissers LE, de Ligt J, Gilissen C, Janssen I, Steehouwer M, de Vries P, van Lier B, Arts P, Wieskamp N, Del Rosario M, van Bon BW, Hoischen A, de Vries BB, Brunner HG, Veltman JA. **A de novo paradigm for mental retardation.** *Nat Genet.* 2010 Dec;42(12):1109-12.

Krawitz PM, Schweiger MR, Rödelsperger C, Marcelis C, Kölsch U, Meisel C, Stephani F, Kinoshita T, Murakami Y, Bauer S, Isau M, Fischer A, Dahl A, Kerick M, Hecht J, Köhler S, Jäger M, Grünhagen J, de Condor BJ, Doelken S, Brunner HG, Meinecke P, Passarge E, Thompson MD, Cole DE, Horn D, Roscioli T, Mundlos S, Robinson PN. **Identity-by-descent filtering of exome sequence data identifies PIGV mutations in hyperphosphatasia mental retardation syndrome.** *Nat Genet.* 2010 Oct;42(10):827-9.

Anastasio N, Ben-Omran T, Teebi A, Ha KC, Lalonde E, Ali R, Almureikhi M, Der Kaloustian VM, Liu J, Rosenblatt DS, Majewski J, Jerome-Majewska LA. **Mutations in SCARF2 are responsible for Van Den Ende-Gupta syndrome.** *Am J Hum Genet.* 2010 Oct 8:87(4):553-9.

Bowden DW, An SS, Palmer ND, Brown WM, Norris JM, Haffner SM, Hawkins GA, Guo X, Rotter JI, Chen YD, Wagenknecht LE, Langefeld CD. **Molecular basis of a linkage peak: exome sequencing and family-based analysis identify a rare genetic variant in the ADIPOQ gene in the IRAS Family Study.** *Hum Mol Genet.* 2010 Oct 15;19(20):4112-20.

Byun M, Abhyankar A, Lelarge V, Plancoulaine S, Palanduz A, Telhan L, Boisson B, Picard C, Dewell S, Zhao C, Jouanguy E, Feske S, Abel L, Casanova JL. **Whole-exome sequencing-based discovery of STIM1 deficiency in a child with fatal classic Kaposi sarcoma.** *J Exp Med.* 2010 Oct 25;207(11):2307-12.

Gilissen C, Arts HH, Hoischen A, Spruijt L, Mans DA, Arts P, van Lier B, Steehouwer M, van Reeuwijk J, Kant SG, Roepman R, Knoers NV, Veltman JA, Brunner HG. **Exome sequencing identifies WDR35 variants involved in Sensenbrenner syndrome.** *Am J Hum Genet.* 2010 Sep 10:87(3):418-23.

Ng SB, Bigham AW, Buckingham KJ, Hannibal MC, McMillin MJ, Gildersleeve HI, Beck AE, Tabor HK, Cooper GM, Mefford HC, Lee C, Turner EH, Smith JD, Rieder MJ, Yoshiura K, Matsumoto N, Ohta T, Niikawa N, Nickerson DA, Bamshad MJ, Shendure J. **Exome sequencing identifies MLL2 mutations as a cause of Kabuki syndrome.** *Nat Genet.* 2010 Sep;42(9):790-3.

Lalonde E, Albrecht S, Ha KC, Jacob K, Bolduc N, Polychronakos C, Dechelotte P, Majewski J, Jabado N. **Unexpected allelic heterogeneity and spectrum of mutations in Fowler syndrome revealed by next-generation exome sequencing.** *Hum Mutat.* 2010 Aug;31(8):918-23.

Pierce SB, Walsh T, Chisholm KM, Lee MK, Thornton AM, Fiumara A, Opitz JM, Levy-Lahad E, Klevit RE, King MC. **Mutations in the DBP-deficiency protein HSD17B4 cause ovarian dysgenesis, hearing loss, and ataxia of Perrault Syndrome.** *Am J Hum Genet.* 2010 Aug 13;87(2):282-8.

Sun Y, Almomani R, Aten E, Celli J, van der Heijden J, Venselaar H, Robertson SP, Baroncini A, Franco B, Basel-Vanagaite L, Horii E, Drut R, Ariyurek Y, den Dunnen JT, Breuning MH. **Terminal osseous dysplasia is caused by a single recurrent mutation in the FLNA gene.** *Am J Hum Genet.* 2010 Jul 9;87(1):146-53.

Walsh T, Shahin H, Elkan-Miller T, Lee MK, Thornton AM, Roeb W, Abu Rayyan A, Loulus S, Avraham KB, King MC, Kanaan M. **Whole exome sequencing and homozygosity mapping identify mutation in the cell polarity protein GPSM2 as the cause of nonsyndromic hearing loss DFNB82.** *Am J Hum Genet.* 2010 Jul 9;87(1):90-4.

Hoischen A, van Bon BW, Gilissen C, Arts P, van Lier B, Steehouwer M, de Vries P, de Reuver R, Wieskamp N, Mortier G, Devriendt K, Amorim MZ, Revencu N, Kidd A, Barbosa M, Turner A, Smith J, Oley C, Henderson A, Hayes IM, Thompson EM, Brunner HG, de Vries BB, Veltman JA. **De novo mutations of SETBP1 cause Schinzel-Giedion syndrome.** *Nat Genet.* 2010 Jun;42(6):483-5.

Johnston JJ, Teer JK, Cherukuri PF, Hansen NF, Loftus SK; NIH Intramural Sequencing Center, Chong K, Mullikin JC, Biesecker LG. **Massively parallel sequencing of exons on the X chromosome identifies RBM10 as the gene that causes a syndromic form of cleft palate.** *Am J Hum Genet.* 2010 May 14;86(5):743-8.

Ng SB, Buckingham KJ, Lee C, Bigham AW, Tabor HK, Dent KM, Huff CD, Shannon PT, Jabs EW, Nickerson DA, Shendure J, Bamshad MJ. **Exome sequencing identifies the cause of a mendelian disorder.** *Nat Genet.* 2010 Jan;42(1):30-5.

Complex Diseases

Zimprich A, Benet-Pagès A, Struhal W, Graf E, Eck SH, Offman MN, Haubenberger D, Spielberger S, Schulte EC, Lichtner P, Rossle SC, Klopp N, Wolf E, Seppi K, Pirker W, Presslauer S, Mollenhauer B, Katzenbachler R, Foki T, Hotzy C, Reinthaler E, Harutyunyan A, Kralovics R, Peters A, Zimprich F, Brücke T, Poewe W, Auff E, Trenkwalder C, Rost B, Ransmayr G, Winkelmann J, Meitinger T, Strom TM. **A Mutation in VPS35, Encoding a Subunit of the Retromer Complex, Causes Late-Onset Parkinson Disease.** *Am J Hum Genet.* 2011 Jul 15;89(1):168-75.

Girard SL, Gauthier J, Noreau A, Xiong L, Zhou S, Jouan L, Dionne-Laporte A, Spiegelman D, Henrion E, Diallo O, Thibodeau P, Bachand I, Bao JY, Tong AH, Lin CH, Millet B, Jaafari N, Joober R, Dion PA, Lok S, Krebs MO, Rouleau GA. **Increased exonic de novo mutation rate in individuals with schizophrenia.** *Nat Genet.* 2011 Jul 10.

Barber LJ, Rosa Rosa JM, Kozarewa I, Fenwick K, Assiotis I, Mitsopoulos C, Sims D, Hakas J, Zvelebil M, Lord CJ, Ashworth A. **Comprehensive Genomic Analysis of a BRCA2 Deficient Human Pancreatic Cancer.** *PLoS One.* 2011;6(7):e21639.

Durinck S, Ho C, Wang N, Liao W, Jakkula Lakshmi, Collisson Eric, Pons J, Chan S, Lam E, Chu C, Park K, Hong S, Hur J, Huh N, Neuhaus I, Yu S, Grekin R, Mauro T, Cleaver J, Kwok P, LeBoit P, Getz G, Cibulskis K, Aster J, Huang H, Purdom E, Li J, 10, Bolund L, Arron S, Gray J, Spellman P, Cho R. **Temporal Dissection of Tumorigenesis in Primary cancers.** *Cancer Discovery.* 2011 Jun 29

Quivoron C, Couronné L, Della Valle V, Lopez CK, Plo I, Wagner-Ballon O, Do Cruzeiro M, Delhommeau F, Arnulf B, Stern MH, Godley L, Opolon P, Tilly H, Solary E, Duffourd Y, Dessen P, Merle-Beral H, Nguyen-Khac F, Fontenay M, Vainchenker W, Bastard C, Mercher T, Bernard OA. **TET2 Inactivation Results in PleiotropicHematopoietic Abnormalities in Mouse and Is a Recurrent Event during Human Lymphomagenesis.** *Cancer Cell.* 2011 Jun 29.

Tacci E, Trifonov V, Schiavoni G, Holmes A, Kern W, Martelli MP, Pucciarini A, Bigerna B, Pacini R, Wells VA, Sportoletti P, Pettrossi V, Mannucci R, Elliott O, Liso A, Ambrosetti A, Pulsoni A, Forconi F, Trentin L, Semenzato G, Inghirami G, Capponi M, Di Raimondo F, Patti C, Arcaini L, Musto P, Pileri S, Haferlach C, Schnittger S, Pizzolo G, Foà R, Farinelli L, Haferlach T, Pasqualucci L, Rabidan R, Falini B. **BRAF mutations in hairy-cell leukemia.** *N Engl J Med.* 2011 Jun 16;364(24):2305-15.

Greif PA, Yaghmaie M, Konstandin NP, Ksienzyk B, Alimoghaddam K, Ghavamzadeh A, Hauser A, Graf A, Krebs S, Blum H, Bohlander SK. **Somatic mutations in acute promyelocytic leukemia (APL) identified by exome sequencing.** *Leukemia.* 2011 May 24.

Saarinen S, Aavikko M, Aittomäki K, Launonen V, Lehtonen R, Franssila K, Lehtonen HJ, Kaasinen E, Broderick P, Tarkkanen J, Bain BJ, Bauduer F, Unal A, Swerdlow AJ, Cooke R, Mäkinen MJ, Houlston R, Vahtero P, Aaltonen LA. **Exome sequencing reveals germline NPAT mutation as a candidate risk factor for Hodgkin lymphoma.** *Blood.* 2011 May 11.

Qi XP, Ma JM, Du ZF, Ying RB, Fei J, Jin HY, Han JS, Wang JQ, Chen XL, Chen CY, Liu WT, Lu JJ, Zhang JG, Zhang XN. **RET Germline Mutations Identified by Exome Sequencing in a Chinese Multiple Endocrine Neoplasia Type 2A/Familial Medullary Thyroid Carcinoma Family.** *PLoS One.* 2011;6(5):e20353.

Rosa-Rosa JM, Gracia-Aznárez FJ, Hodges E, Pita G, Rooks M, Xuan Z, Bhattacharjee A, Brizuela L, Silva JM, Hannon GJ, Benitez J. **Deep sequencing of target linkage assay-identified regions in familial breast cancer: methods, analysis pipeline and troubleshooting.** *PLoS One.* 2010 Apr 2;5(4):e9976.

Totoki Y, Tatsuno K, Yamamoto S, Arai Y, Hosoda F, Ishikawa S, Tsutsumi S, Sonoda K, Totsuka H, hirakihara T, Sakamoto H, Wang L, Ojima H, Shimada K, Kosuge T, Okusaka T, Kato K, Kusuda J, Yoshida T, Aburatani H, Shibata T. **High-resolution characterization of a hepatocellular carcinoma genome.** *Nat Genet.* 2011 May;43(5):464-9.

Wei X, Walia V, Lin JC, Teer JK, Prickett TD, Gartner J, Davis S; NISC Comparative Sequencing Program, Stemke-Hale K, Davies MA, Gershenwald JE, Robinson W, Robinson S, Rosenberg SA, Samuels Y. **Exome sequencing identifies GRIN2A as frequently mutated in melanoma.** *Nat Genet.* 2011 May;43(5):442-6.

Jiao Y, Shi C, Edil BH, de Wilde RF, Klimstra DS, Maitra A, Schulick RD, Tang LH, Wolfgang CL, Choti MA, Velculescu VE, Diaz LA Jr, Vogelstein B, Kinzler KW, Hruban RH, Papadopoulos N. **DAXX/ATRX, MEN1, and mTOR pathway genes are frequently altered in pancreatic neuroendocrine tumors.** *Science.* 2011 Mar 4;331(6021):1199-203.

Varela I, Tarpey P, Raine K, Huang D, Ong CK, Stephens P, Davies H, Jones D, Lin ML, Teague J, Bignell G, Butler A, Cho J, Dalgleish GL, Galappaththige D, Greenman C, Hardy C, Jia M, Latimer C, Lau KW, Marshall J, McLaren S, Menzies A, Mudie L, Stebbings L, Largaespada DA, A Wessels LF, Richard S, Kahnkoski RJ, Anema J, A Tuveson D, Perez-Mancera PA, Mustonen V, Fischer A, Adams DJ, Rust A, Chan-On W, Subimber C, Dykema K, Furge K, Campbell PJ, Teh BT, Stratton MR, Futreal PA. **Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma.** *Nature.* 2011 Jan 19.

Timmermann B, Kerick M, Roehr C, Fischer A, Isau M, Boerno ST, Wunderlich A, Barmeyer C, Seemann P, Koenig J, Lappe M, Kuss AW, Garshasbi M, Bertram L, Trappe K, Werber M, Herrmann BG, Zatloukal K, Lehrach H, Schweiger MR. **Somatic mutation profiles of MSI and MSS colorectal cancer identified by whole exome next generation sequencing and bioinformatics analysis.** *PLoS One.* 2010 Dec 22;5(12):e15661.

Musunuru K, Pirruccello JP, Do R, Peloso GM, Guiducci C, Sougnez C, Garimella KV, Fisher S, Abreu J, Barry AJ, Fennell T, Banks E, Ambrogio L, Cibulskis K, Kernytsky A, Gonzalez E, Rudzicz N, Engert JC, DePristo MA, Daly MJ, Cohen JC, Hobbs HH, Altshuler D, Schonfeld G, Gabriel SB, Yue P, Kathiresan S. **Exome sequencing, ANGPTL3 mutations, and familial combined hypolipidemia.** *N Engl J Med.* 2010 Dec 2;363(23):2220-7.

Nazarian R, Shi H, Wang Q, Kong X, Koya RC, Lee H, Chen Z, Lee MK, Attar N, Sazegar H, Chodon T, Nelson SF, McArthur G, Sosman JA, Ribas A, Lo RS. **Melanomas acquire resistance to B-RAF(V600E) inhibition by RTK or N-RAS upregulation.** *Nature.* 2010 Nov 24

Jones S, Wang TL, Shih IeM, Mao TL, Nakayama K, Roden R, Glas R, Slamon D, Diaz LA Jr, Vogelstein B, Kinzler KW, Velculescu VE, Papadopoulos N. **Frequent mutations of chromatin remodeling gene ARID1A in ovarian clear cell carcinoma.** *Science.* 2010 Oct 8;330(6001):228-31.

Makishima H, Jankowska AM, Tiu RV, Szpurka H, Sugimoto Y, Hu Z, Saunthararajah Y, Quinta K, Keddache MA, -Putnam P, Sekeres MA, Moliterno AR, List AF, McDevitt MA, Maciejewski JP. **Novel homo- and hemizygous mutations in EZH2 in myeloid malignancies.** *Leukemia.* 2010 Oct;24(10):1799-804.

Van Vlierberghe P, Palomero T, Khiabanian H, Van der Meulen J, Castillo M, Van Roy N, De Moerloose B, Philippé J, González-García S, Toribio ML, Taghon T, Zuurbier L, Cauwelier B, Harrison CJ, Schwab C, Pisecker M, Strehl S, Langerak AW, Gecz J, Sonneveld E, Pieters R, Paietta E, Rowe JM, Wiernik PH, Benoit Y, Soulier J, Poppe B, Yao X, Cordon-Cardo C, Meijerink J, Rabadan R, Speleman F, Ferrando A. **PHF6 mutations in T-cell acute lymphoblastic leukemia.** *Nat Genet.* 2010 Apr;42(4):338-42.

Clinical Research

Liao GJ, Lun FM, Zheng YW, Chan KC, Leung TY, Lau TK, Chiu RW, Lo YM. **Targeted massively parallel sequencing of maternal plasma DNA permits efficient and unbiased detection of fetal alleles.** *Clin Chem.* 2011 Jan;57(1):92-101. Epub 2010 Nov 15.

Bell CJ, Dinwiddie DL, Miller NA, Hateley SL, Ganusova EE, Mudge J, Langley RJ, Zhang L, Lee CC, Schilkey FD, Sheth V, Woodward JE, Peckham HE, Schroth GP, Kim RW, Kingsmore SF. **Carrier testing for severe childhood recessive diseases by next-generation sequencing.** *Sci Transl Med.* 2011 Jan 12;3(65):65ra4.

Shearer AE, Deluca AP, Hildebrand MS, Taylor KR, Gurrola J 2nd, Scherer S, Scheetz TE, Smith RJ. **Comprehensive genetic testing for hereditary hearing loss using massively parallel sequencing.** *Proc Natl Acad Sci U S A.* 2010 Dec 7;107(49):21104-9.

Wesolowska A, Dalgaard MD, Borst L, Gautier L, Bak M, Weinhold N, Nielsen BF, Helt LR, Audouze K, Nersting J, Tommerup N, Brunak S, Sicheritz-Ponten T, Leffers H, Schmiegelow K, Gupta R. **Cost-effective multiplexing before capture allows screening of 25 000 clinically relevant SNPs in childhood acute lymphoblastic leukemia.** *Leukemia.* 2011 Mar 18.

Chmielecki J, Peifer M, Jia P, Soccia ND, Hutchinson K, Viale A, Zhao Z, Thomas RK, Pao W. **Targeted next-generation sequencing of DNA regions proximal to a conserved GXGXXG signaling motif enables systematic discovery of tyrosine kinase fusions in cancer.** *Nucleic Acids Res.* 2010 Nov 1;38(20):6985-96.

Bonnefond A, Durand E, Sand O, De Graeve F, Gallina S, Busiah K, Lobbens S, Simon A, Bellanné-Chantelot C, Létourneau L, Scharfmann R, Delplanque J, Sladek R, Polak M, Vaxillaire M, Froguel P. **Molecular diagnosis of neonatal diabetes mellitus using next-generation sequencing of the whole exome.** *PLoS One.* 2010 Oct 26;5(10):e13630.

Walsh T, Lee MK, Casadei S, Thornton AM, Stray SM, Pennil C, Nord AS, Mandell JB, Swisher EM, King MC. **Detection of inherited mutations for breast and ovarian cancer using genomic capture and massively parallel sequencing.** *Proc Natl Acad Sci U S A.* 2010 Jul 13;107(28):12629-33.

RNA Enrichment

Ozsolak F, Milos PM. **RNA sequencing: advances, challenges and opportunities.** *Nat Rev Genet.* 2011 Feb;12(2):87-98.

Automation

Fisher S, Barry A, Abreu J, Minie B, Delorey TM, Fennell TJ, Allen A, Ambrogio L, Berlin AM, Blumenstiel B, Cibulskis K, Friedrich D, Johnson R, Juhn F, Nolan J, Reilly B, Shammas R, Stalker J, Sykes SM, Thompson J, Walsh J, Young G, Zimmer A, Zwirko Z, Gabriel S, Nicol R, Nusbaum C. **A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries.** *Genome Biol.* 2011 Jan 4;12(1):R1.

Other

Cosart T, Beja-Pereira A, Chen S, Ng SB, Shendure J, Luikart G. **Exome-wide DNA Capture and Next Generation Sequencing in Domestic and Wild Species.** *BMC Genomics.* 2011 Jul 5;12(1):347.

Deng X. **SeqGene: a comprehensive software solution for mining exome- and transcriptome- sequencing data.** *BMC Bioinformatics.* 2011 Jun 29;12(1):267.

Kiialainen A, Karlberg O, Ahlford A, Sigurdsson S, Lindblad-Toh K, Syvänen AC. **Performance of microarray and liquid based capture methods for target enrichment for massively parallel sequencing and SNP discovery.** *PLoS One.* 2011 Feb 9;6(2):e16486.

Nijman IJ, Mokry M, van Boxtel R, Toonen P, de Brujin E, Cuppen E. **Mutation discovery by targeted genomic enrichment of multiplexed barcoded samples.** *Nat Methods.* 2010 Nov;7(11):913-5.

Chen D, Zhang W, Zhu ZD, Huang Y, Wang P, Zhou BB, Yang XN, Xiao HS, Zhang QH. **[Establishment of target genomic DNA capturing system for next generation sequencing].** *Yi Chuan.* 2010 Dec;32(12):1296-303. Chinese.

Hedges DJ, Guettouche T, Yang S, Bademci G, Diaz A, Andersen A, Hulme WF, Linker S, Mehta A, Edwards YJ, Beecham GW, Martin ER, Pericak-Vance MA, Zuchner S, Vance JM, Gilbert JR. **Comparison of Three Targeted Enrichment Strategies on the SOLiD Sequencing Platform.** *PLoS One.* 2011 Apr 29;6(4):e18595.

Talkowski ME, Ernst C, Heilbut A, Chiang C, Hanscom C, Lindgren A, Kirby A, Liu S, Muddukrishna B, Ohsumi TK, Shen Y, Borowsky M, Daly MJ, Morton CC, Gusella JF. **Next-generation sequencing strategies enable routine detection of balanced chromosome rearrangements for clinical diagnostics and genetic research.** *Am J Hum Genet.* 2011 Apr 8;88(4):469-81.

Bansal V, Tewhey R, Leproust EM, Schork NJ. **Efficient and cost effective population resequencing by pooling and in-solution hybridization.** *PLoS One.* 2011 Mar 30;6(3):e18353.

Rödelsperger C, Krawitz P, Bauer S, Hecht J, Bigham AW, Bamshad M, de Condor BJ, Schweiger MR, Robinson PN. **Identity-by-descent filtering of exome sequence data for disease-gene identification in autosomal recessive disorders.** *Bioinformatics.* 2011 Mar 15;27(6):829-36.

Coffey AJ, Kokocinski F, Calafato MS, Scott CE, Palta P, Drury E, Joyce CJ, Leproust EM, Harrow J, Hunt S, Lehesjoki AE, Turner DJ, Hubbard TJ, Palotie A. **The GENCODE exome: sequencing the complete human exome.** *Eur J Hum Genet.* 2011 Mar 2.

Perry GH, Marioni JC, Melsted P, Gilad Y. **Genomic-scale capture and sequencing of endogenous DNA from feces.** *Mol Ecol.* 2010 Dec;19(24):5332-44.

Kenny EM, Cormican P, Gilks WP, Gates AS, O'Dushlaine CT, Pinto C, Corvin AP, Gill M, Morris DW. **Multiplex Target Enrichment Using DNA Indexing for Ultra-High Throughput SNP Detection.** *DNA Res.* 2010 Dec 16.

Cummings N, King R, Rickers A, Kaspi A, Lunke S, Haviv I, Jowett JB. **Combining target enrichment with barcode multiplexing for high throughput SNP discovery.** *BMC Genomics.* 2010 Nov 18;11(1):641.

Buehler B, Hogrefe HH, Scott G, Ravi H, Pabón-Peña C, O'Brien S, Formosa R, Happe S. **Rapid quantification of DNA libraries for next-generation sequencing.** *Methods.* 2010 Apr;50(4):S15-8.

Ng SB, Turner EH, Robertson PD, Flygare SD, Bigham AW, Lee C, Shaffer T, Wong M, Bhattacharjee A, Eichler EE, Bamshad M, Nickerson DA, Shendure J. **Targeted capture and massively parallel sequencing of 12 human exomes.** *Nature.* 2009 Sep 10;461(7261):272-6.

Tewhey R, Nakano M, Wang X, Pabón-Peña C, Novak B, Giuffre A, Lin E, Happe S, Roberts DN, LeProust EM, Topol EJ, Harismendy O, Frazer KA. **Enrichment of sequencing targets from the human genome by solution hybridization.** *Genome Biol.* 2009;10(10):R116.

Gnirke A, Melnikov A, Maguire J, Rogov P, LeProust EM, Brockman W, Fennell T, Giannoukos G, Fisher S, Russ C, Gabriel S, Jaffe DB, Lander ES, Nusbaum C. **Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing.** *Nat Biotechnol.* 2009 Feb;27(2):182-9.