

## CytoScan HD 2015 Publications

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1-

[2q31.1 microdeletion syndrome: case report and literature review](#)

Surasak Puvabanditsin\*, Melissa February, Tazeem Shaik, Arun Kashyap, Chantal Bruno and Rajeev Mehta

Department of Pediatrics, Rutgers Robert Wood Johnson Medical School, New Brunswick, New Jersey, USA  
Clinical Case Reports, June 2015, 3(6): 357–360.

We describe a preterm neonate with bilateral coloboma of the iris, upper and lower limb malformations including rocker bottom feet, camptodactyly, and clinodactyly together with microcephaly and small for gestational age whom cytogenetic diagnosis using SNP microarray detected an interstitial deletion of chromosome 2 between 2q31.1 and 33.1. ... SNP microarray analysis was performed using the Affymetrix **CytoScan HD** platform. There was a 23.16 megabase (MB) deletion between 2q31.1 and 2q33.1.

2-

[5p13.3p13.2 duplication associated with developmental delay, congenital malformations and chromosome instability manifested as low-level aneuploidy](#)

Ivan Y. Iourov<sup>123\*</sup>, Svetlana G. Vorsanova<sup>12</sup>, Irina A. Demidova<sup>12</sup>, Galina A. Aliamovskaia<sup>2</sup>, Elena S. Keshishian<sup>2</sup> and Yuri B. Yurov<sup>12</sup>

1 Mental Health Research Center, Russian Academy of Medical Sciences, Moscow 117152, Russia; 2 Russian National Research Medical University named after N.I. Pirogov, Separated Structural Unit "Clinical Research Institute of Pediatrics", Ministry of Health of Russian Federation, Moscow 125412, Russia ; 3 Dept of Medical Genetics, Russian Medical Academy of Postgraduate Education, Moscow 123995, Russia  
SpringerPlus, 15 October 2015, 4:616.

... High-resolution chromosomal SNP microarray analysis was performed on DNA isolated from peripheral blood lymphocytes using **CytoScan® HD Arrays** (Affymetrix ...

3-

[7q21.3 Deletion involving enhancer sequences within the gene DYNC111 presents with intellectual disability and split hand-split foot malformation with decreased penetrance](#)

Sara Delgado<sup>1</sup> and Milen Velinov<sup>123\*</sup>

1 Bronx-Lebanon Hospital Center, New York, Bronx ; 2 Albert Einstein College of Medicine, New York, Bronx ; 3 Dept of Human Genetics, New York State Institute for Basic Research in Developmental Disabilities, 1050 Forest Hill Rd, Staten Island 10314, New York

Molecular Cytogenetics, 13 June 2015, 8:37

... Oligo SNP array, Affimatrix **Cytoscan HD** (Quest Diagnostic, San Juan CA) identified an approximately 1 Mb deletion in chromosomal region 7q21.3.

4-

[7q21.11 Microdeletion in a Neonate With Goldenhar Syndrome: Case Report and a Literature Review](#)

Surasak Puvabanditsin, M.D., Melissa February, M.D., Lissa Francois, M.D., Eugene Garrow, M.D., Chantal Bruno, D.O., Rajeev Mehta, M.D.

The Cleft Palate-Craniofacial Journal, online 11 June 2015

... Chromosome microarray analysis was performed using both copy number and single-nucleotide polymorphism probes on a whole-genome array (Affymetrix **CytoScan HD** platform).

5-

[8p23.1 Interstitial Deletion in a Patient with Congenital Cardiopathy, Neurobehavioral Disorders, and Minor Signs Suggesting 22q11.2 Deletion Syndrome](#)

Molck, Miriam C.; Monteiro, Fabíola P.; Simioni, Milena; Gil-da-Silva-Lopes, Vera L.  
Journal of Developmental & Behavioral Pediatrics, September 2015, 36(7): 544–548.

... highlights the application of aGH to investigate 8p23.1 deletion in nonconfirmed 22q11.2 DS patients ... Array genomic hybridization analysis for the patient was performed using **CytoScan HD** chip (Affymetrix®) ...

6-

[A 12q24.31 interstitial deletion in an adult male with MODY3: Neuropsychiatric and neuropsychological characteristics](#)

Willem M.A. Verhoeven<sup>1,2,\*</sup>, Jos I.M. Egger<sup>1,3</sup>, Joop P.W. van den Bergh<sup>4,5</sup>, Ronald van Beek<sup>6</sup>, Tjitske Kleefstra<sup>6</sup> and Nicole de Leeuw<sup>6</sup>

<sup>1</sup>Vincent van Gogh Institute for Psychiatry, Centre of Excellence for Neuropsychiatry, Venray, The Netherlands; <sup>2</sup>Erasmus University Medical Centre, Department of Psychiatry, Rotterdam, The Netherlands; <sup>3</sup>Donders Institute for Brain, Cognition and Behaviour, Behavioural Science Institute, Radboud University Nijmegen, Nijmegen, The Netherlands; <sup>4</sup>VieCuri Medical Centre, Department of Internal Medicine, Venlo, The Netherlands; <sup>5</sup>Maastricht University Medical Centre, Dept of Internal Medicine, Maastricht, The Netherlands; <sup>6</sup>Dept of Human Genetics, Radboud University Medical Centre, Nijmegen, The Netherlands

American Journal of Medical Genetics Part A, January 2015, 167(1):169–173.

... This is the first patient with normal intelligence in whom the presence of subtle facial dysmorphisms were decisive for introducing genetic analysis that, in turn, disclosed a rare form of diabetes necessitating modifications in treatment regimen. ... Genomic array analysis with an average resolution of ~20 kb was performed using the Affymetrix **CytoScan HD array** platform ...

7-

[A Case Report: Jacobsen Syndrome Complicated by Paris-Trousseau Syndrome and Shone's Complex](#)

Malia, Laurie A; Wolkoff, Leslie I.; Mnayer, Laila; Tucker, Joseph W.; Parikh, Nehal S. Journal of Pediatric Hematology/Oncology, October 2015, 37(7): e429–e432.

... FIGURE 2. Microarray: SNP microarray was performed using the Affymetrix **CytoScan HD**. The array detected a 12.1 MB deletion (122,797,729-134,938,470) with 108 genes deleted. Microarray showing detailed view of deletion 11q.

8-

[A cryptic balanced translocation \(5;17\), a puzzle revealed through a critical evaluation of the pedigree and a FISH focused on candidate loci suggested by the phenotype](#)

A. Primerano<sup>1</sup>, E. Colao<sup>1</sup>, C. Vilella<sup>1</sup>, M. D. Nocera<sup>1</sup>, A. Ciambone<sup>1</sup>, E. Luciano<sup>1</sup>, L. D'Antona<sup>4</sup>, M. F. M. Vismara<sup>1</sup>, S. Loddo<sup>2</sup>, A. Novelli<sup>3</sup>, N. Perrotti<sup>1,4†</sup> and Paola Malatesta<sup>1\*†</sup>

<sup>1</sup> Unit of Medical Genetics, University Hospital Mater Domini, Catanzaro, Italy ; <sup>2</sup> Mendel Laboratory, Casa Sollievo della Sofferenza Hospital, IRCCS, San Giovanni Rotondo, Italy ; <sup>3</sup> Genetics Unit, Bambino Gesù Children's Hospital, IRCCS, Rome, Italy ; <sup>4</sup> Dept of "Scienze della Salute", Università UMG di Catanzaro, Catanzaro, Italy

Molecular Cytogenetics, 2 September 2015, 8:70

...The imbalances were confirmed by a new high resolution SNP array. ... Microarray analysis was performed using **CytoScan HD** (Affymetrix, ...

9-

[A germline chromothripsis event stably segregating in 11 individuals through three generations](#)

Birgitte Bertelsen PhD, Lusine Nazaryan-Petersen PhD, Wei Sun PhD, Mana M. Mehrjoui MSc, Gangcai Xie PhD, Wei Chen PhD, Lena E. Hjermland PhD, Peter E. M. Taschner PhD & Zeynep Tümer PhD, DMSc

Genetics in Medicine, online 27 August 2015

... Chromosomal microarray was performed for II:6 using Affymetrix **CytoScan HD array** (Affymetrix, Santa Clara, CA), and data were analyzed with ChAS software (Affymetrix) ...

10-

[A late onset sickle cell disease reveals a mosaic segmental uniparental isodisomy of chromosome 11p15](#)

Isabelle Vinatier a, Xavier Martin b, Jean-Marc Costa a, Anne Bazin a, Stéphane Giraudier c, Philippe Joly d

a Laboratoire CERBA, 95066 Cergy-Pontoise cedex 9, France; b Service de médecine polyvalente, Centre hospitalier Antoine Gayraud, 11890 Carcassonne cedex 9, France; c Service d'hématologie biologique, GH Henri-Mondor, 51 avenue du Maréchal de Lattre de Tassigny, 94010 Créteil Cedex, France; d Unité de Pathologie Moléculaire du Globule Rouge, Laboratoire de Biochimie et Biologie moléculaire, Hôpital Edouard Herriot, Hospices Civils de Lyon & Université Claude Bernard-Lyon 1, Lyon, France

Blood Cells, Molecules, and Diseases, January 2015, 54(1):53–55.

doi:10.1016/j.bcmd.2014.07.021

... A SNP array analysis (**CytoScan HD** SNP Affymetrix) confirmed this hypothesis as it revealed a 45.9 Mb LOH on almost the whole short arm of chromosome 11 ...

11-

[A maternally inherited 16p13.11-p12.3 duplication concomitant with a de novo SOX5 deletion in a male patient with global developmental delay, disruptive and obsessive behaviors and minor dysmorphic features](#)

Ines Quintela<sup>1</sup>, Francisco Barros<sup>2,\*</sup>, Ramon Lago-Leston<sup>3</sup>, Manuel Castro-Gago<sup>4</sup>, Angel Carracedo<sup>1,2,5</sup> and Jesus Eiris<sup>4</sup>

<sup>1</sup>Grupo de Medicina Xenomica - Universidad de Santiago de Compostela, Centro Nacional de Genotipado - Instituto Carlos III, Santiago de Compostela, Spain; <sup>2</sup>Grupo de Medicina Xenomica - USC, CIBERER, Fundacion Publica Galega de Medicina Xenomica - SERGAS, Santiago de Compostela, Spain; <sup>3</sup>Grupo de Medicina Xenomica - USC, Fundacion Publica Galega de Medicina Xenomica - SERGAS, Santiago de Compostela, Spain; <sup>4</sup>Departamento de Pediatria, Hospital Clinico Universitario de Santiago de Compostela - Unidad de Neurologia Pediatrica, Santiago de Compostela, Spain; <sup>5</sup>Center of Excellence in Genomic Medicine Research, King Abdulaziz University, Jeddah, Saudi Arabia

American Journal of Medical Genetics Part A, June 2015, 167(6): 1315–1322.

... DNA samples from both the patient and his parents were obtained from peripheral blood and genotyped using the **Cytogenetics Whole-Genome 2.7 M SNP array** and the **CytoScan High-Density SNP array** (Affymetrix, ...

12-

[A missense mutation in domain III in HSPG2 in Schwartz–Jampel syndrome compromises secretion of perlecan into the extracellular space](#)

Satoshi Iwata, Mikako Ito, Tomohiko Nakata, Yoichiro Noguchi, Tatsuya Okuno, Bisei Ohkawara, Akio Masuda, Tomohide Goto, Masanori Adachi, Hitoshi Osaka, Risa Nonaka, Eri Arikawa-Hirasawa, Kinji Ohno

Neuromuscular Disorders, August 2015, 25(8): 667–671.

... We also searched for copy number variations (CNVs) by the **CytoScan HD array** (Affymetrix).

13-

[A modified multiplex ligation-dependent probe amplification method for the detection of 22q11.2 copy number variations in patients with congenital heart disease](#)

Xiaoqing Zhang, Yuejuan Xu, Deyuan Liu, Juan Geng, Sun Chen, Zhengwen Jiang, Qihua Fu, Kun Sun

BMC Genomics, May 8, 2015, 16:364

... A genomic hybridization was performed on each sample with the **CytoScan HD array** (Affymetrix, ...

14-

[A mosaic small supernumerary marker chromosome 17 in a patient with Tourette syndrome, ADHD and intellectual disability: A case story and review of the literature](#)

Nanna Cornelius a, 1, Birgitte Bertelsen a, 1, Linea Melchior a, Lusine Nazaryan a, Zeynep Tümer a, Nanette Mol Debes b, Camilla Groth b, Liselotte Skov b

a Department of Clinical Genetics, Applied Human Molecular Genetics, Kennedy Center, Copenhagen University Hospital, Rigshospitalet, Glostrup, Denmark; b The Tourette Clinic, Department of Pediatrics, Herlev University Hospital, Herlev, Denmark

Psychiatry Research, 30 July 2015, 228(1): 179–181.

...The sSMC was present in mosaic form as 47,XY+mar/46,XY and microarray analysis using Affymetrix **CytoScan HD** ... a copy number gain corresponding to chromosome 17 spanning an approximately 6.3 Mb region at 17p11.2-q11.2 ...

15- **Meeting abstract**

[A new biomarker of response to 5-azacitidine therapy in MDS and AML patients: SIRPB1](#)

Viviana Guadagnuolo<sup>1</sup>, Cristina Papayannidis<sup>1</sup>, Ilaria Iacobucci<sup>1</sup>, Giorgia Simonetti<sup>1</sup>, Antonella Padella<sup>1</sup>, Stefania Paolini<sup>1</sup>, Mariachiara Abbenante<sup>1</sup>, Sarah Parisi<sup>1</sup>, Francesca Volpato<sup>1</sup>, Chiara Sartor<sup>1</sup>, Maria Chiara Fontana<sup>1</sup>, Massimo Delledonne<sup>2</sup>, Michele Malagola<sup>3</sup>, Carla Fili<sup>3</sup>, Domenico Russo<sup>3</sup>, Sandro Grilli<sup>4</sup>, Michele Cavo<sup>1</sup>, and Giovanni Martinelli<sup>1</sup>

<sup>1</sup>L. & A. Seragnoli, Bologna, Italy; <sup>2</sup>Dept of Biotechnology, Verona University, Verona, Italy; <sup>3</sup>Unit of Blood Diseases and Cell Therapies, University of Brescia - AO Spedali Civili Brescia, Brescia, Italy; <sup>4</sup>Dipartimento di Medicina Specialistica, Diagnostica e Sperimentale, Bologna, Italy.

Cancer Research, 2015, 75(15 Suppl):Abst #4835. [AACR 106<sup>th</sup> Annual Mtg, Apr 18-22, 2015, Philadelphia, PA]

... To identify the genes mostly predictive of treatment response, we use high-throughput genomic analysis (SNP arrays and/or NGS-RNA-seq and/or NGS-WES) in azacitidine-sensitive and resistant MDS/AML patients. Materials and Methods: NGS-WES or RNA seq HiSeq 2000 (Illumina) was positively done in 35/214 AML samples (16%). SNPs arrays (**CytoScan HD Array**, Affymetrix Inc.) was done in 125/214 AML samples (58%) and 18/32 MDS samples (56%) at diagnosis, then analyzed by Chromosome Analysis Suite (ChAS) v1.2 (Affymetrix Inc.), Nexus Copy Number™ v7.5 (BioDiscovery) and GeneGo MetaCore™ software. ...

16-

[A Novel 23.1 Mb Interstitial Deletion Involving 7q22.3q32.1 in a Girl with Short Stature, Motor Delay, and Craniofacial Dysmorphism.](#)

del Refugio Rivera-Vega M.a· Gómez-del Angel L.A.a· Valdes-Miranda J.M.a· Pérez-Cabrera A.a· Gonzalez-Huerta L.M.a· Toral-López J.b· Cuevas-Covarrubias S.a  
aDepartamento de Genética Médica, Hospital General de México/Facultad de Medicina, Universidad Nacional Autónoma de México (UNAM), México, DF, and bDepartamento de Genética Médica, Centro Médico Ecatepec, ISSEMYM, Toluca, México

Cytogenet Genome Research, 2015,145:1-5.

... Here, a Mexican girl with microcephaly, facial dysmorphism, short stature, hand anomalies, and intellectual disability was analyzed by **CytoScan HD array**. Her phenotype was associated with a de novo 7q22.3q32.1 deletion involving 109 loci ...

17-

[\*\*A novel large deletion of the ICR1 region including H19 and putative enhancer elements\*\*](#)

Helen Fryssira, Stella Amenta, Deniz Kanber, Christalena Sofocleous, Evangelia Lykopoulou, Christina Kanaka-Gantenbein, Flavia Cerrato, Hermann-Josef Lüdecke, Susanne Bens, Andrea Riccio and Karin Buiting

BMC Medical Genetics, May 6, 2015, 16:30

... Molecular karyotyping. Array analysis was carried out using the genome-wide high-resolution SNP array **CytoScan HD** (Affymetrix) ...

18-

[\*\*A Novel Whole Exon Deletion in WWOX Gene Causes Early Epilepsy, Intellectual Disability and Optic Atrophy\*\*](#)

Salma Ben-Salem<sup>1</sup>, Aisha M. Al-Shamsi<sup>2</sup>, Anne John<sup>1</sup>, Bassam R. Ali<sup>1</sup>, Lihadh Al-Gazali<sup>3</sup>

<sup>1</sup>. Dept of Pathology, College of Medicine and Health Sciences, United Arab Emirates University, Al-Ain, United Arab Emirates ; <sup>2</sup>. Dept of Paediatrics, Tawam Hospital, Al-Ain, United Arab Emirates ; <sup>3</sup>. Dept of Paediatrics, College of Medicine and Health Sciences, United Arab Emirates University, PO box 17666, Al-Ain, United Arab Emirates

Journal of Molecular Neuroscience, May 2015, 56(1):17-23.

... Chromosomal Microarray Genomic DNA from the index patient (Fig. 1, IV-3) was analyzed by chromosomal microarray (CMA) using whole- genome array by means of Affymetrix **cytoscan HD** platform ...

19-

[\*\*A pure familial 6q15q21 split duplication associated with obesity and transmitted with partial reduction\*\*](#)

Emilie Landais<sup>1,2</sup>, Camille Leroy<sup>1,3</sup>, Pascale Kleinfinger<sup>4</sup>, Stéphanie Brunet<sup>1</sup>, Valérie Koubi<sup>5</sup>, Christine Pietrement<sup>6</sup>, Marie-Laurence Poli-Mérol<sup>3,7</sup>, Caroline Fiquet<sup>7,8</sup>, Pierre-François Souchon<sup>6</sup>, Mylène Beri<sup>9</sup>, Philippe Jonveaux<sup>9</sup>, Roselyne Garnotel<sup>10</sup>, Dominique Gaillard<sup>1,3</sup> and Martine Doco-Fenzy<sup>1,8,\*</sup>

<sup>1</sup>CHU-Reims, HMB, Service de Génétique, France; <sup>2</sup>CHU-Reims, HMB, Plateforme Régionale de Biologie Innovante, France; <sup>3</sup>Université de Reims Champagne-Ardenne, UFR de médecine, France; <sup>4</sup>Laboratoire de Génétique, Pasteur Cerba, Cergy Pontoise, France; <sup>5</sup>Service de génétique Médicale, Laboratoire de génétique moléculaire, CHU Hopital Necker enfants malades, Paris, France; <sup>6</sup>CHU-Reims, American Memorial Hospital, Service de Pédiatrie A, France; <sup>7</sup>CHU-Reims, American Memorial Hospital, Service de Chirurgie pédiatrique, France; <sup>8</sup>SFR CAP Santé, Reims, France; <sup>9</sup>CHU-Nancy, Laboratoire de Génétique Médicale, Nancy Université, France; <sup>10</sup>CHU-Reims, Laboratoire de Biochimie Médicale et Biologie Moléculaire, CNRS UMR 6198, UFR, Médecine, France

American Journal of Medical Genetics Part A, June 2015, 167(6): 1275–1284.

... SNP analysis was then performed using Affymetrix high-density SNP arrays (**CytoScan® HD** Array Kit, Affymetrix, Santa Clara, CA), which analyze 750,000 genotypable SNPs, and CytoScan HD Array Chromosome Analysis Suite (ChAS) Software.

20-

[\*\*A rare but recurrent t\(8;13\)\(q24;q14\) translocation in B-cell chronic lymphocytic leukaemia causing MYC up-regulation and concomitant loss of PVT1, miR-15/16 and DLEU7 \[free access\]\*\*](#)

Gemma Macchia<sup>1</sup>, Angelo Lonoce<sup>1</sup>, Santina Venuto<sup>1</sup>, Ettore Macri<sup>2</sup>, Orazio Palumbo<sup>3</sup>, Massimo Carella<sup>3</sup>, Crocifissa Lo Cunsolo<sup>2</sup>, Paolo Iuzzolino<sup>2</sup>, María Hernández-Sánchez<sup>4</sup>, Jesus M. Hernandez-Rivas<sup>4</sup> and Clelia T. Storlazzi<sup>1</sup>

<sup>1</sup>Dept of Biology, University of Bari, Bari, Italy; <sup>2</sup>UO Anatomia Patologica, Ospedale S. Martino, Belluno, Italy; <sup>3</sup>Medical Genetics Unit, IRCCS Casa Sollievo della Sofferenza Hospital, San Giovanni Rotondo, Italy; <sup>4</sup>Servicio de Hematología, Hospital Universitario de Salamanca, IBSAL, IBMCC, Centro de Investigación del Cáncer, Universidad de Salamanca, CSIC, Salamanca, Spain

British Journal of Haematology, Article first published online: 26 May 2015

... Subsequently, single nucleotide polymorphism (SNP) array analysis of the patient's PB DNA, accomplished on a **CytoScan® HD Array** according to manufacturer protocols using the ChAS

Software (Affymetrix, Santa Clara, CA, USA), confirmed a deletion that included MIR15A/MIR16-1 and DLEU7 on the der(13) (chr13: 49.85–51.07 Mb).

21-

[A rare coincidence of different types of driver mutations among uterine leiomyomas \(UL\)](#)

Carsten Holzmann<sup>1</sup>, Dominique Nadine Markowski<sup>2</sup>, Sabine Bartnitzke<sup>2</sup>, Dirk Koczan<sup>3</sup>, Burkhard Maria Helmke<sup>4,5</sup> and Jörn Bullerdiek<sup>1,2\*</sup>

<sup>1</sup> Institute of Medical Genetics, University Rostock Medical Center, Ernst-Heydemann-Strasse 8, Rostock, D-18057, Germany; <sup>2</sup> Center of Human Genetics, University of Bremen, Leobener Strasse ZHG, Bremen, D-28359, Germany; <sup>3</sup> Institute of Immunology, University of Rostock, University Rostock Medical Center, Schillingallee 70, Rostock, D-18057, Germany; <sup>4</sup> Institute of Pathology, University of Heidelberg, Heidelberg, Germany

Molecular Cytogenetics, 14 October 2015, 8:76

... CNV (copy number variation) analysis was performed using premade **CytoScan HD Arrays** (Affymetrix ...

22-

[A recurrent deletion syndrome at chromosome bands 2p11.2-2p12 flanked by segmental duplications at the breakpoints and including REEP1](#)

Servi J C Stevens, Eveline W Blom, Ingrid T J Siegelaer and Eric E J G L Smeets

European Journal of Human Genetics, April 2015, 23(4):543-6.

... Genome-wide copy number profiling was done using high-resolution **CytoScan HD arrays** with 2.7 million markers, according to the manufacturer's protocol (Affymetrix ...

23- **Meeting abstract**

[A Specific Pattern of Somatic Mutations Associates with Poor Prognosis Aneuploid Acute Myeloid Leukemia: Results from the European NGS-PTL Consortium](#)

Giorgia Simonetti, PhD<sup>\*,1</sup>, Antonella Padella<sup>\*,1</sup>, Ítalo Faria do Valle<sup>\*,2</sup>, Marco Manfrini, PhD<sup>\*,3</sup>, Cristina Papayannidis, MD PhD<sup>3</sup>, Carmen Baldazzi, PhD<sup>\*,1</sup>, Maria Chiara Fontana<sup>\*,4</sup>, Viviana Guadagnuolo, PhD<sup>\*,1</sup>, Anna Ferrari, PhD<sup>\*,1</sup>, Elisa Zago, PhD<sup>\*,5</sup>, Marianna Garonzi<sup>\*,6</sup>, Simona Bernardi<sup>\*,7</sup>, Emanuela Ottaviani<sup>\*,1</sup>, Annalisa Astolfi, PhD<sup>\*,8</sup>, Maria Chiara Abbenante, MD<sup>\*,1</sup>, Giovanni Marconi, MD<sup>\*,1</sup>, Simona Soverini<sup>9</sup>, Michele Cavo, MD<sup>\*,10</sup>, Nicoletta Testoni<sup>\*,1</sup>, Alberto Ferrarini, PhD<sup>\*,6</sup>, Massimo Delledonne, PhD<sup>\*,5</sup>, Torsten Haferlach<sup>11</sup>, Daniel Remondini, PhD<sup>\*,2</sup>, Ilaria Iacobucci, PhD<sup>\*,10</sup>, and Giovanni Martinelli<sup>10</sup>

<sup>1</sup>University of Bologna, Bologna, Italy ; <sup>2</sup>Dept of Physics and Astronomy, University of Bologna, Bologna, Italy ; <sup>3</sup>Bologna University School of Medicine, Bologna, Italy ; <sup>4</sup>"Seràgnoli" Institute of Hematology, Bologna University School of Medicine, Bologna, Italy ; <sup>5</sup>Personal Genomics, Verona, Italy ; <sup>6</sup>Dept of Biotechnology, University of Verona, Verona, Italy ; <sup>7</sup>Unit of Blood Diseases and Stem Cells Transplantation, University of Brescia, Brescia, Italy ; <sup>8</sup>Centro Interdipartimentale per la Ricerca sul Cancro "G. Prodi", University of Bologna, Bologna, Italy ; <sup>9</sup>Institute of Hematology, S.Orsola-Malpighi University Hospital, Bologna, Italy ; <sup>10</sup>"Seràgnoli" Institute of Hematology, University of Bologna, Bologna, Italy ; <sup>11</sup>MLL Munich Leukemia Laboratory, Munich, Germany

Blood, 3 December 2015, 126(23): 3840.

... AML samples were genotyped by **CytoScan HD Array (Affymetrix)**. Gene expression profiling (GEP) was also conducted on bone marrow cells from 24 A-AML, 33 E-AML (≥80% blasts) and 7 healthy controls (**HTA 2.0, Affymetrix**). ...

24-

[A t\(3;9\)\(q25.1;q34.3\) translocation leading to OLFM1 fusion transcripts in Gilles de la Tourette syndrome, OCD and ADHD](#)

Birgitte Bertelsen, Linea Melchior, Lars Riff Jensen, Camilla Groth, Lusine Nazaryan, Nanette Mol Debes, Liselotte Skov, Gangcai Xie, Wei Sun, Karen Brøndum-Nielsen, Andreas Walter Kuss, Wei Chen, Zeynep Tümer

Psychiatry Research, 28 February 2015, 225(3):268–275.

... Chromosome microarray was carried out using Affymetrix Genome-Wide Human **SNP Array 6.0** (translocation patient) or Affymetrix **CytoScan HD** (GTS-cohort), and data were analyzed using Genotyping Console Software or Chromosome Analysis Suite software (Affymetrix ...

25- **Open access**

[A Three-Generation Family with Idiopathic Facial Palsy Suggesting an Autosomal Dominant Inheritance with High Penetrance](#)

Christian Grønhøj Larsen,<sup>1</sup> Mette Gyldenløve,<sup>2</sup> Aia Elise Jønch,<sup>3</sup> Birgitte Charabi,<sup>1</sup> and Zeynep Tümer<sup>4</sup>

<sup>1</sup>Department of Otorhinolaryngology, Head and Neck Surgery, Copenhagen University Hospital of Rigshospitalet, 2100 Copenhagen, Denmark; <sup>2</sup>Department of Dermato-Allergology, Gentofte Hospital, University of Copenhagen, 2900 Hellerup, Denmark; <sup>3</sup>Clinical Genetic Clinic, Kennedy Center, Copenhagen University Hospital,

Rigshospitalet, 2600 Glostrup, Denmark; 4Applied Human Molecular Genetics, Kennedy Center, Copenhagen University Hospital, Rigshospitalet, 2600 Glostrup, Denmark

Case Reports in Otolaryngology, 2015, Volume 2015:Article# 683938.

... After two weeks, the patient had almost fully recovered with only minor muscle weakness remaining, which was still present two months later. Chromosome microarray analysis was carried out using **CytoScan HD** microarray platform (Affymetrix, USA) but did not reveal a microdeletion or duplication segregating with the disease in the family.

26-

[A Transition Zone Showing Highly Discontinuous or Alternating Levels of Stem Cell and Proliferation Markers Characterizes the Development of PTEN-Haploinsufficient Colorectal Cancer](#)

Kevin J. Arvai, Ya-Hsuan Hsu, Lobin A. Lee, Dan Jones

PLoS ONE, 22 June 2015, 10(6): e0131108.

... After macrodissection of FFPE tumor sections, genomic DNA was extracted using the QiaAmp DNA FFPE Tissue Kit (Qiagen, Valencia, CA) and assessed using the **CytoScan HD** 2.6 million-probe microarray platform (Affymetrix, Santa Clara, CA) according to the manufacturer's instructions.

27-

[Absence of Heterozygosity due to Template Switching during Replicative Rearrangements](#)

Claudia M.B. Carvalho, Rolph Pfundt, Daniel A. King, Sarah J. Lindsay, Luciana W. Zuccherato, Merryn V.E. Macville, Pengfei Liu, Diana Johnson, Pawel Stankiewicz, Chester W. Brown, DDD Study, Chad A. Shaw, Matthew E. Hurles, Grzegorz Ira, P.J. Hastings, Han G. Brunner, James R. Lupski

American Journal of Human Genetics, 2 April 2015, 96( 4): 555–564.

... DNA from subjects BAB3922, BAB3923, and BAB3924 plus parental DNA samples were hybridized on an Affymetrix **GeneChip 250k (Nspl) SNP array** platform or **CytoScan array**. ... To confirm triplication and AOH independently, samples were run on two different array platforms. For instance, BAB4539 plus parental samples were run on an Affymetrix **CytoScan SNP array** and samples BAB3922, BAB3923, and BAB3924 plus parental samples were analyzed with an Illumina array HumanOmniExpress-24 Beadchip at the Human Genome Sequencing Center of Baylor College of Medicine.

28-

[Acro-spondylo-pubic dysostosis associated with cataracts, microcephaly, and normal intelligence](#)

Oscar F. Chacon-Camacho<sup>1</sup>, Vanessa Villegas-Ruiz<sup>1</sup>, Beatriz Buentello-Volante<sup>1</sup>, Raul E. Piña-Aguilar<sup>2</sup>, Hugo Peláez-González<sup>3</sup>, Magdalena Ramírez<sup>3</sup>, Johanna González-Rodríguez<sup>1</sup>, Juan Carlos Zenteno<sup>1,4,\*</sup>

<sup>1</sup>Genetics Dept-Research Unit, Institute of Ophthalmology "Conde de Valenciana", Mexico City, Mexico; <sup>2</sup>Dept of Genetics, Centro Médico Nacional "20 de Noviembre", ISSSTE., Mexico City, Mexico; <sup>3</sup>Radiology Dept, Hospital General de Mexico, Mexico City, Mexico; <sup>4</sup>Biochemistry Dept, Faculty of Medicine, National Autonomous University of Mexico (UNAM), Mexico City, Mexico

American Journal of Medical Genetics Part A, Feb 2015, 167(2):282–286.

... Molecular karyotyping was performed on the patient's DNA using the genome-wide high-resolution SNP array **CytoScan HD** (Affymetrix, Santa Clara, CA, USA) chip.

29-

[Acrofacial Dysostosis, Cincinnati Type, a Mandibulofacial Dysostosis Syndrome with Limb Anomalies, Is Caused by POLR1A Dysfunction](#)

K. Nicole Weaver<sup>1, 9</sup>, Kristin E. Noack Watt<sup>2, 3, 9</sup>, Robert B. Hufnagel<sup>1</sup>, Joaquin Navajas Acedo<sup>2</sup>, Luke L. Linscott<sup>4</sup>, Kristen L. Sund<sup>1</sup>, Patricia L. Bender<sup>1</sup>, Rainer König<sup>5</sup>, Charles M. Lourenco<sup>6</sup>, Ute Hehr<sup>7</sup>, Robert J. Hopkin<sup>1</sup>, Dietmar R. Lohmann<sup>8</sup>, Paul A. Trainor<sup>2, 3, 10</sup>, Dagmar Wieczorek<sup>8, 10</sup>, Howard M. Saal<sup>1, 10</sup>

<sup>1</sup> Div of Human Genetics, Dept of Pediatrics, Cincinnati Children's Hospital Medical Center and University of Cincinnati College of Medicine, MLC 4006, 3333 Burnet Ave, Cincinnati, OH 45229, USA; <sup>2</sup> Stowers Institute for Medical Research, 1000 East 50th Street, Kansas City, MI 64110, USA; <sup>3</sup> University of Kansas Medical Center, Kansas City, MI 66160, USA; <sup>4</sup> Dept of Radiology, Cincinnati Children's Hospital Medical Center, Cincinnati, OH 45229, USA; <sup>5</sup> Institut für Humangenetik, Universitätsklinikum Frankfurt, Theodor-Stern-Kai 7, 60596 Frankfurt, Germany; <sup>6</sup> Neurogenetics Unit, Clinics Hospital of Ribeirao Preto, University of Sao Paulo, Avenue Bandeirantes 3900, Sao Paulo 14049-900, Brazil; <sup>7</sup> Zentrum für Humangenetik, Universitätsklinikum Regensburg, Franz-Josef-Strauß-Allee 11, 93053 Regensburg, Germany; <sup>8</sup> Institut für Humangenetik, Universitätsklinikum Essen, Universität Duisburg-Essen, Hufelandstr 55, 45122 Essen, Germany

American Journal of Human Genetics, 7 May 2015, 96(5):765–774.

... Individual 1A2 had a normal karyotype and Affymetrix **Cytoscan HD Array**.

30-

[Additional patients with 4q deletion: Severe growth delay and polycystic kidney disease associated with 4q21q22 loss](#)

Satoru Sakazume<sup>1,\*</sup>, Yasuhiro Kido<sup>1</sup>, Nobuyuki Murakami<sup>1</sup>, Tomoyo Matsubara<sup>1</sup>, Hironao Numabe<sup>2</sup>

<sup>1</sup>Dept of Pediatrics, Koshigaya Hospital, Dokkyo Medical University, Koshigaya, Japan; <sup>2</sup>Dept of Genetic Counseling, Graduate School of Human Genetics and Science, Ochanomizu University, Tokyo, Japan

*Pediatrics International*, October 2015, 57(5): 880–883.

... this is the third report concerning the 4q21q22 deletions. ... we used the same array platform to analyze genetic anomaly of both patients. ... performed at a commercial laboratory (LSI Medience Corporation Japan) using the **CytoScan HD array** (Affymetrix) ...

31-

[Adult Low-Hypodiploid Acute B-Lymphoblastic Leukemia With IKZF3 Deletion and TP53 Mutation Comparison With Pediatric Patients](#)

Min Fang, MD, PhD<sup>1,2,3</sup>, Pamela S. Becker, MD, PhD<sup>1,2</sup>, Michael Linenberger, MD<sup>1,2</sup>, Keith D. Eaton, MD, PhD<sup>1,2,3</sup>, Frederick R. Appelbaum, MD<sup>1,2,3</sup>, ZoAnn Dreyer, MD<sup>4</sup>, Gladstone Airewele, MD<sup>4</sup>, Michele Redell, MD, PhD<sup>4</sup>, Dolores Lopez-Terrada, MD, PhD<sup>4</sup>, Ankita Patel, PhD<sup>5</sup>, Karen R. Rabin<sup>4</sup>, Xinyan Lu, MD<sup>6</sup>

<sup>1</sup>From the Fred Hutchinson Cancer Research Center, Seattle, WA; <sup>2</sup>University of Washington, Seattle; <sup>3</sup>Seattle Cancer Care Alliance, Seattle, WA; <sup>4</sup>Texas Children's Cancer and Hematology Centers and Dept of Pediatrics, Baylor College of Medicine, Houston; <sup>5</sup>Dept of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX; <sup>6</sup>Dept of Hematopathology, University of Texas MD Anderson Cancer Center, Houston, TX.

*American Journal of Clinical Pathology*, 2015, 144:263-270.

...[chromosome genomic array testing] was critical in the genotype clarification of these cases ...and should be considered performing for B-ALL ... Adult DNA was processed using the **CytoScanHD** kit from Affymetrix ...Pediatric DNA was assayed using Infinium Cyto12 from Illumina ...

32-

[Alternating hypoglycemia and hyperglycemia in a toddler with a homozygous p.R1419H ABCC8 mutation: an unusual clinical picture](#)

Shira Harel<sup>1</sup> / Ana S.A. Cohen<sup>2, 3</sup> / Khalid Hussain<sup>4, 5</sup> / Sarah E. Flanagan<sup>4</sup> / Kamilla Schlade-Bartusiak<sup>3, 6</sup> / Millan Patel<sup>2, 3</sup> / Jaques Courtade<sup>3</sup> / Jenny B.W. Li<sup>7</sup> / Clara Van Karnebeek<sup>8</sup> / Harley Kurata<sup>7</sup> / Sian Ellard<sup>4</sup> / Jean-Pierre Chanoine<sup>1</sup> / William T. Gibson<sup>2, 3</sup>

<sup>1</sup>Endocrinology and Diabetes Unit, Dept of Pediatrics, British Columbia Children's Hospital, Univ of British Columbia, Vancouver, Canada; <sup>2</sup>Dept of Medical Genetics, University of British Columbia, Vancouver, Canada; <sup>3</sup>Child and Family Research Institute, Vancouver, Canada; <sup>4</sup>Institute of Biomedical and Clinical Science, Univ of Exeter Medical School, Exeter, UK; <sup>5</sup>Developmental Endocrinology Research Group, Clinical and Molecular Genetics, Institute of Child Health, Univ College London, London, UK; <sup>6</sup>Dept of Pathology and Laboratory Medicine, Univ of British Columbia, Vancouver, Canada; <sup>7</sup>Dept of Anesthesiology, Pharmacology and Therapeutics, Univ of British Columbia, Vancouver, Canada; <sup>8</sup>Div of Biochemical Diseases, Dept of Pediatrics, British Columbia Children's Hospital, Univ of British Columbia, Vancouver, Canada

*Journal of Pediatric Endocrinology and Metabolism*, March 2015 Mar, 28(3-4):345-351.

... This is the first description of a homozygous p.R1419H mutation. Our findings highlight that homozygous loss-of-function mutations of ABCC8 do not necessarily translate into early-onset severe hyperinsulinemia.

... **CytoScanHD** (Affymetrix, Inc., Santa Clara, CA, USA) single nucleotide polymorphism (SNP) array analysis was done ...

33-

[An apoptosis-enhancing drug overcomes platinum resistance in a tumour-initiating subpopulation of ovarian cancer](#)

D. M. Janzen, E. Tiourin, J. A. Salehi, D. Y. Paik, J. Lu, M. Pellegrini & S. Memarzadeh  
*Nature Communications*, 3 August 2015, 6:Article #7956

... DNA was isolated from S#-GODL cells and their respective parent tumours ... then hybridized to the Affymetrix **CytoScan HD** array ...

34-

[An infant with large fontanelles, aplasia cutis congenita, tессier facial cleft, polydactyly inversus, and toe syndactyly: A previously undescribed syndrome?](#)

Jessica Jackson<sup>1,\*</sup>, Paula Delk<sup>1</sup>, Emily Farrow<sup>2</sup>, Christopher Griffith<sup>1</sup>, Melissa Lah<sup>1</sup> and David D. Weaver<sup>1</sup>

<sup>1</sup>Dept of Medical and Molecular Genetics, Indiana University School of Medicine, Indianapolis, Indiana; <sup>2</sup>Center for Pediatric Genomic Medicine, Children's Mercy Hospital, Kansas City, Missouri

*American Journal of Medical Genetics Part A*, April 2015, 167(4):683–687.

... Results of a constitutional chromosomal microarray analysis (CMA) using the **Cytoscan HD** platform (Affymetrix, Santa Clara, CA) was also normal (Indiana University CytoGenetics Laboratory, Indianapolis, IN).

35-

[Anirdia-like phenotype caused by 6p25 dosage aberrations](#)

Karthikeyan Arcot Sadagopan<sup>1,2</sup>, Grace T. Liu<sup>1,3,4,\*</sup>, Jenina E. Capasso<sup>1</sup>, Wadakarn Wuthisiri<sup>1,5</sup>, Rosanne B. Keep<sup>1,5</sup>, Alex V. Levin<sup>1,6,7</sup>

<sup>1</sup>Ocular Genetics, Wills Eye Institute, Philadelphia, PA; <sup>2</sup>Dept of Pediatric Ophthalmology, Strabismus and Ocular Genetics, Ocular Genetics Service, Aravind Eye Hospital, Madurai, India; <sup>3</sup>Pediatric Ophthalmic Consultants, New York City, NY; <sup>4</sup>Dept of Ophthalmology, New York University, New York City, NY; <sup>5</sup>Dept of Ophthalmology, Faculty of Medicine, Ramathibodi Hospital Mahidol University, Bangkok, Thailand; <sup>6</sup>Quest Diagnostics, Madison, NJ; <sup>7</sup>Thomas Jefferson University, Philadelphia, PA

American Journal of Medical Genetics Part A, March 2015, 167(3):524–528

... In Patient 2, cytogenetic analysis with a 550 band resolution revealed a male karyotype with a 6p25.1 interstitial duplication, 46XY, dup(6)(25.1p25.3). SNP microarray analysis (Affymetrix **Cytoscan HD** platform) using 743,000 SNP probes ...

36-

[Aortopathy in the 7q11.23 microduplication syndrome](#)

Ashley Parrott<sup>1</sup>, Jeanne James<sup>1</sup>, Paula Goldenberg<sup>1</sup>, Robert B. Hinton<sup>1</sup>, Erin Miller<sup>1,\*</sup>, Amy Shikany<sup>1</sup>, Arthur S. Aylsworth<sup>2,3</sup>, Kathleen Kaiser-Rogers<sup>2,3,4</sup>, Sunita J. Ferns<sup>2</sup>, Seema R. Lalani<sup>5</sup>, Stephanie M. Ware<sup>6</sup>

<sup>1</sup>Dept of Pediatrics, Cincinnati Children's Hospital Medical Center, Heart Institute, Cincinnati, OH; <sup>2</sup>Dept of Pediatrics, University of North Carolina, Chapel Hill, NC; <sup>3</sup>Dept of Genetics, University of North Carolina, Chapel Hill, NC; <sup>4</sup>Dept of Pathology and Laboratory Medicine, University of North Carolina, Chapel Hill, NC; <sup>5</sup>Dept of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX; <sup>6</sup>Dept of Pediatrics and Medical and Molecular Genetics, Indiana University School of Medicine, Indianapolis, Indiana

American Journal of Medical Genetics Part A, Feb 2015, 167(2): 363–370.

... The 7q11.23 microduplication in patient 9 was also identified using a SNP microarray platform (**Affymetrix CytoScan HD**, Santa Clara, CA) and confirmed by both metaphase and interphase FISH using RP11–19F19 probe (Empire Genomics Buffalo, NY).

37- *Article in Chinese*

[\[Application of chromosome microarray analysis for fetuses with increased nuchal translucency and a normal karyotype\]](#)

Yang X, Fu F, Li R, Zhang Y, Wan J, Yang X, Han J, Pan M, Zhen L, Liao C.

Zhonghua Yi Xue Yi Chuan Xue Za Zhi. (Chinese Journal of Medical Genetics), June 10, 2015, 32(3):370-4.

... Genomic DNA was extracted, and microarray testing was performed using Affymetrix **CytoScan™ HD arrays**.

38- *Article in Chinese*

[\[Application of whole-genome and high-resolution chromosome microarray analysis for the investigation of fetuses with ultrasound abnormalities\].](#)

Zhang Y, Fu F, Li R, Xie G, Han J, Pan M, Zhen L, Yang X, Li D, Liao C.

Zhonghua Yi Xue Yi Chuan Xue Za Zhi. (Chinese Journal of Medical Genetics), 2015 Apr;32(2):169-74.

... Whole genome high-resolution **CytoScanHD** array from Affymetrix was employed to investigate 651 fetuses with structural abnormalities detected by ultrasound, for whom standard G-banded chromosome analysis has revealed a normal karyotype. ...

39-

[Assessing the utility of confirmatory studies following identification of large-scale genomic imbalances by microarray.](#)

Sanmann JN, Pickering DL, Golden DM, Stevens JM, Hempel TE, Althof PA, Wiggins ML, Starr LJ, Davé BJ, Sanger WG.

Genetics in Medicine, November 2015, 17(11):875-879.

... Table 1 Microarray platforms and resolutions ... 1.9 million copy-number markers and 750,000 genotypable SNPs: Affymetrix **Cytoscan HD** (Santa Clara, CA) ...

40-

[Association of an  \$\alpha\$ -Globin Gene Cluster Duplication and Heterozygous  \$\beta\$ -Thalassemia in a Patient with a Severe Thalassemia Syndrome](#)

Hua Jiang, Sha Liu, Yong-Ling Zhang, Jun-Hui Wan, Ru Li, and Dong-Zhi Li



1Department of Hematology/Oncology, Guangzhou Women & Children Medical Center affiliated to Guangzhou Medical University, Guangzhou, Guangdong, People's Republic of China; 2Prenatal Diagnostic Center, Guangzhou Women & Children Medical Center affiliated to Guangzhou Medical University, Guangzhou, Guangdong, People's Republic of China

Hemoglobin, online 18 February 2015, 39(2): 102-106.

... Array comparative genomic hybridization (CGH) (Affymetrix **CytoScan® High-Density Array**; Affymetrix Inc., Santa Clara, CA, USA) was also used to confirm the  $\alpha$ -globin gene rearrangement.

41-

[BCL6 – regulated by AhR/ARNT and wild-type MEF2B – drives expression of germinal center markers MYBL1 and LMO2](#)

Jie Ding,<sup>1</sup> Wilhelm G Dirks,<sup>1</sup> Stefan Ehrentraut,<sup>1</sup> Robert Geffers,<sup>2</sup> Roderick AF MacLeod,<sup>1</sup> Stefan Nagel,<sup>1</sup> Claudia Pommerenke,<sup>1</sup> Julia Romani,<sup>1</sup> Michaela Scherr,<sup>3</sup> Lea Al Vaas,<sup>1</sup> Margarete Zaborski,<sup>1</sup> Hans G Drexler,<sup>1</sup> and Hilmar Quentmeier<sup>1</sup>

<sup>1</sup>Leibniz-Institute DSMZ-German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany; <sup>2</sup>Helmholtz Centre for Infection Research, Genome Analysis Research Group, Braunschweig, Germany; <sup>3</sup>Medical School Hannover, Department of Hematology, Hemostasis, Oncology and Stem Cell Transplantation, Hannover, Germany

Haematologica, June 2015, 100(6): 801-809.

... **CytoScan HD** Array (Affymetrix; Santa Clara, CA, USA) hybridization analysis was performed to identify numerical aberrations.

42-

[Bone marrows from neuroblastoma patients: An excellent source for tumor genome analyses](#)

M. Reza Abbasi a, Fikret Rifatbegovic a, Clemens Brunner a, Ruth Ladenstein b, c, Inge M. Ambros a, Peter F. Ambros a, c

a Tumor Biology, Children's Cancer Research Institute, St. Anna Kinderkrebsforschung, Vienna, Austria; b SiRP, Children's Cancer Research Institute, St. Anna Kinderkrebsforschung, Vienna, Austria; c Dept of Pediatrics, Medical University of Vienna, Vienna, Austria

Molecular Oncology, March 2015, 9(3): 545–554.

... Genomic profile of tumor cells was examined by **CytoScan™ HD Array** (Affymetrix Inc., UK Ltd), a genome-wide UHD-SNP array technique with more than 2.6 million copy number and SNP markers.

43-

[Catel–Manzke syndrome: Further delineation of the phenotype associated with pathogenic variants in TGDS](#)

Rachel Pferdehirt a, Mahim Jain a, Maria A. Blazo b, Brendan Lee a, Lindsay C. Burrage a  
a Dept of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX 77030; b Dept of Genetics, Baylor Scott & White Health, Texas A&M Health Science Center College of Medicine, Temple, TX 76508, USA  
Molecular Genetics and Metabolism Reports, September 2015, 4: 89–91

... Routine chromosome analysis, comparative genomic hybridization microarray (Affymetrix **Cytoscan HD** Microarray System, Scott and White Healthcare Molecular Genetics Laboratories), ... only the second publication describing molecularly confirmed Catel–Manzke syndrome, ...

44-

[CD19-negative B-lymphoblastic leukemia associated with hypercalcemia, lytic bone lesions and aleukemic presentation](#)

Shafinaz Husseina, Kerice Pinkneyb, Vaidehi Jobanputraa, Govind Bhagata & Bachir Alobeida\*

Leukemia & Lymphoma, 2015, 56(5): 1533-1537.

... SNP-array analysis, using the Affymetrix **CytoScan HD** Array (Affymetrix, Santa Clara, CA) performed on DNA extracted from the BM biopsy sample targeting the lytic lesion, revealed no abnormalities.

45-

[Cerebral visual impairment, autism, and pancreatitis associated with a 9 Mbp deletion on 10p12.](#)

Bosch, Daniëlle G.M.a,b,c,d; Boonstra, Frouke N.a,c; Pfundt, Rolphb; Cremers, Frans P.M.b,d; de Vries, Bert B.A.b,c

Clinical Dysmorphology, January 2015, 24(1):34-37.

... Genome- wide array analysis was carried out on DNA from peripheral blood using the Affymetrix **CytoScan HD** array platform (Affymetrix ...

46-

[Characterization of a Complex Chromosomal Rearrangement Involving a de novo Duplication of 9p and 9q and a Deletion of 9q](#)

Martín-De Saro M.D.a · Valdés-Miranda J.M.b · Plaza-Benhumea L.c · Pérez-Cabrera A.b · Gonzalez-Huerta L.M.b · Guevara-Yañez R.d · Cuevas-Covarrubias S.A.b  
aDept of Medical Genetics, Hospital Materno Infantil ISSEMyM, Toluca, bDept of Medical Genetics, School of Medicine, General Hospital of Mexico, National Autonomous University of Mexico, cGenetics Dept, Children's Hospital IMIEM, and dLaboratorio BIOGEN, Mexico City, Mexico

Cytogenet Genome Res, 2015, 147:124-129

... we present a CCR in a patient with multiple congenital anomalies who represents the first case with partial 9p trisomy, partial 9q trisomy and partial 9q monosomy. ... analysis was carried out using **CytoScan HD** array ...

47-

[Chromosomal microarrays testing in children with developmental disabilities and congenital anomalies](#)

Lay-Son G1, Espinoza K2, Vial C2, Rivera JC2, Guzmán ML3, Repetto GM3.

1Center for Human Genetics, Facultad de Medicina, Clínica Alemana Universidad del Desarrollo, Santiago, Chile; Hospital Padre Hurtado, Santiago, Chile. Electronic address: glayson@udd.cl.; 2Center for Human Genetics, Facultad de Medicina, Clínica Alemana Universidad del Desarrollo, Santiago, Chile.; 3Center for Human Genetics, Facultad de Medicina, Clínica Alemana Universidad del Desarrollo, Santiago, Chile; Hospital Padre Hurtado, Santiago, Chile.

J Pediatr (Rio J), March-April 2015, 91(2):189-95.

... Chilean patients with developmental disabilities and congenital anomalies were studied with a high-density microarray (**CytoScan™ HD Array**, Affymetrix, Inc., Santa Clara, CA, USA).

48-

[Chromothriptic Cure of WHIM Syndrome](#)

David H. McDermott, Ji-Liang Gao, Qian Liu, Marie Siwicki, Craig Martens, Paejonette Jacobs, Daniel Velez, Erin Yim, Christine R. Bryke, Nancy Hsu, Zunyan Dai, Martha M. Marquesen, Elina Stregovsky, Nana Kwatema, Narda Theobald, Debra A. Long Priel, Stefania Pittaluga, Mark A. Raffeld, Katherine R. Calvo, Irina Maric, Ronan Desmond, Kevin L. Holmes, Douglas B. Kuhns, Karl Balabanian, Françoise Bachelerie, Stephen F. Porcella, Harry L. Malech, Philip M. Murphy

Cell, 12 February 2015, 160(4): 686–699.

... **Affymetrix CytoScan HD array** ... was used to identify chromosomal breakpoints .... monoclonal Abs used were CD45.1- PECy7 and CD45.2-eFlour450 from **eBioscience** ... and biotinylated CD34-streptavidin-PE (clone RAM) from **eBioscience**.

49-

[Clinical and molecular characterization of an infant with a tandem duplication and deletion of 19p13](#)

Ratna N. G. B. Tan1, Ruben S. G. M. Witlox1, Yvonne Hilhorst-Hofstee2, Cacha M. P. C. D. Peeters-Scholte3, Nicolette S. den Hollander2, Claudia A. L. Ruivenkamp2, Mariëtte J.V. Hoffer2, Kerstin B. Hansson2, Mark J. van Roosmalen4, Wigard P. Kloosterman4 and Gijs W. E. Santen2,\*

1Dept of Pediatrics, Leiden University Medical Center, Leiden, the Netherlands; 2Dept of Clinical Genetics, Leiden University Medical Center, Leiden, the Netherlands; 3Dept of Neurology, Leiden University Medical Center, Leiden, the Netherlands; 4Center for Molecular Medicine, Dept of Medical Genetics, University Medical Center Utrecht, Utrecht, the Netherlands

American Journal of Medical Genetics Part A, August 2015, 167(8): 1884–1889.

... A **Cytoscan HD array** (Affymetrix, Santa Clara, CA, USA) was performed according to the manufacturer's instructions. Fluorescence in situ hybridization (FISH) analysis was carried out ...

50-

[Clinical and molecular cytogenetic studies of an unrecognised 22q11.2 deletion in three families](#)

LINHUAN HUANG,1,\* YINGJUN XIE,1,\* YI ZHOU,1 YANMIN LUO,1 XUAN HUANG,1 ZHE XU,2 DANLEI CAI,3 and QUN FANG1

1Fetal Medicine Centre, Dept of Obstetrics and Gynaecology, The First Affiliated Hospital of Sun Yat-Sen University, Guangzhou, Guangdong 510080, P.R. China; 2Div of Cardiac Surgery, First Affiliated Hospital of Sun Yat-Sen Univ, Guangzhou, Guangdong 510080, P.R. China; 3Dept of Ultrasonic Medicine, First Affiliated Hospital of Sun Yat-Sen Univ, Guangzhou, Guangdong 510080, P.R. China

Exp Ther Med. 2015 Mar; 9(3): 823–828.

... The DNA samples (250 ng) were hybridised to **CytoScan HD arrays** (Affymetrix®, Santa Clara, CA, USA) according to the manufacturer's instructions.

51- *First CytoScan publication from Mexico*

[Clinical and Molecular Characterization of a Patient with 15q21.2q22.2 Deletion Syndrome](#)

Velázquez-Wong A.C.a· Ruiz Esparza-Garrido R.a, b· Velázquez-Flores M.Á.a· Huicochea-Montiel J.C.c· Cárdenas-Conejo A.c· Miguez-Muñoz C.P.e· Araujo-Solís M.A.c· Salamanca-Gómez F.d· Arenas-Aranda D.J.a

aUnidad de Investigación Médica en Genética Humana, bCátedras CONACyT, Consejo Nacional de Ciencia y Tecnología, cServicio de Genética, Hospital de Pediatría, and dCoordinación de Investigación en Salud, Centro Médico Nacional Siglo XXI, Instituto Mexicano del Seguro Social (IMSS), Mexico City, Mexico; eAffymetrix, Latinoamérica, São Paulo, Brazil

Cytogenetic and Genome Research, 2014: 144:183-189. **Posted 6 Feb 2015.**

... The girl was clinically diagnosed with probable Prader-Willi syndrome. Chromosomal analysis showed a de novo deletion 46,XX,del(15)(q21q22). However, the use of the Affymetrix **CytoScan HD Array** defined the exact breakpoints of the deleted 15q21q22 region. ...

52-

[Clinical characterization of a male patient with the recently described 8q21.11 microdeletion syndrome](#)

Ines Quintela<sup>1</sup>, Francisco Barros<sup>2,\*</sup>, Manuel Castro-Gago<sup>3</sup>, Angel Carracedo<sup>1,2,4</sup>, Jesus Eiris<sup>3</sup>

<sup>1</sup>Grupo de Medicina Xenómica, Universidade de Santiago de Compostela, Centro Nacional de Genotipado, Plataforma de Recursos Biomoleculares y Bioinformáticos, Instituto de Salud Carlos III (CeGen-PRB2-ISCI), Santiago de Compostela, Spain; <sup>2</sup>Grupo de Medicina Xenómica-USC, CIBERER, Fundación Pública Galega de Medicina Xenómica-SERGAS, Santiago de Compostela, Spain; <sup>3</sup>Departamento de Pediatría, Hospital Clínico Universitario de Santiago de Compostela, Unidad de Neurología Pediátrica, Santiago de Compostela, Spain; <sup>4</sup>King Abdulaziz University, Center of Excellence in Genomic Medicine Research, Jeddah, Saudi Arabia

American Journal of Medical Genetics Part A, June 2015, 167(6): 1369–1373.

... DNA samples from both the patient and his mother were obtained from peripheral blood and genotyped using the **Cytogenetics Whole-Genome 2.7 M SNP array** and the **CytoScan High-Density SNP array** (Affymetrix, Santa Clara, CA), respectively.

53-

[Clinical Severity of PGK1 Deficiency Due To a Novel p.E120K Substitution Is Exacerbated by Co-inheritance of a Subclinical Translocation t\(3;14\)\(q26.33;q12\), Disrupting NUBPL Gene](#)

Dezső David<sup>(1)</sup>, Lígia S. Almeida<sup>(1)</sup>, Maristella Maggi<sup>(2)(3)</sup>, Carlos Araújo<sup>(1)</sup>, Stefan Imreh<sup>(4)</sup>, Giovanna Valentini<sup>(2)</sup>, György Fekete<sup>(5)</sup>, Irén Haltrich<sup>(5)</sup>

<sup>1</sup>. Dept of Human Genetics, National Institute of Health Dr Ricardo Jorge, Lisbon, Portugal ; <sup>2</sup>. Dept of Biology and Biotechnology "L. Spallanzani", University of Pavia, Pavia, Italy ; <sup>3</sup>. Dept of Molecular Medicine, Unit of Immunology and Pathology, University of Pavia, Pavia, Italy ; <sup>4</sup>. Microbiology and Tumour Biology Center, Karolinska Institute, Stockholm, Sweden ; <sup>5</sup>. II Dept of Pediatrics, Semmelweis University, Budapest, Hungary

JIMD Reports, 2015, 23: 55-65.

... Genomic amplicons of der(3) and der(14) chromosomes were analyzed by array painting using **CytoScan HD array** (Affymetrix, Santa Clara, CA, USA).

54-

[Clinically relevant copy number variations detected in cerebral palsy](#)

Maryam Oskoui, Matthew J. Gazzellone, Bhooma Thiruvahindrapuram, Mehdi Zarrei, John Andersen, John Wei, Zhuozhi Wang, Richard F. Wintle, Christian R. Marshall, Ronald D. Cohn, Rosanna Weksberg, Dimitri J. Stavropoulos, Darcy Fehlings, Michael I. Shevell & Stephen W. Scherer

Nature Communications, 3 August 2015, 6: Article #7949.

... We utilized additional population control samples ... (both cohorts were run on the **Affymetrix 6.0** microarray); ... Ontario Population Genetics Platform (from the **CytoScan HD**).

55-

[Clival Encephalocele and 5q15 Deletion: A Case Report](#)

Surasak Puvabanditsin, MD<sup>1</sup>, Imran Malik, MD<sup>1</sup>, Eugene Garrow, MD<sup>2</sup>, Lissa Francois, MD<sup>3</sup>, Rajeev Mehta, MD, FRCP<sup>1</sup>

<sup>1</sup>Dept of Pediatrics, Rutgers Robert Wood Johnson Medical School, New Brunswick, NJ, USA ; <sup>2</sup>Dept of Surgery, SUNY Downstate Medical Center, Brooklyn, New York, NY, USA ; <sup>3</sup>Dept of Obstetrics and Gynecology, Rutgers RWJ Medical School, New Brunswick, NJ, USA

Journal of Child Neurology, Mar 2015; 30:505-508.

... We report a rare variant of a basal encephalocele ... microarray analysis was performed ... on a whole-genome array (**Affymetrix CytoScan HD platform**) showed an interstitial deletion of 496 oligonucleotide probe at 5q15 ...

56-

[CNV-ROC: A cost effective, computer-aided analytical performance evaluator of chromosomal microarrays](#)

Corey W. Goodman a, c, Heather J. Majore, William D. Walla, c, Val C. Sheffield, e, Thomas L. Casavanta, b, c, d, Benjamin W. Darbro e  
a Dept of Electrical and Computer Engineering, University of Iowa; b Dept of Biomedical Engineering, University of Iowa; c Center for Bioinformatics and Computational Biology, Univ of Iowa; d Ph.D. Program in Genetics, Univ of Iowa; e Dept of Pediatrics, Univ of Iowa

Journal of Biomedical Informatics, April 2015, 54: 106–113.

Chromosomal microarrays (CMAs) are routinely used in both research and clinical laboratories; yet, little attention has been given to the estimation of genome-wide true and false negatives during the assessment of these assays and how such information could be used to calibrate various algorithmic metrics to improve performance. Low-throughput, locus-specific methods such as fluorescence in situ hybridization (FISH), quantitative PCR (qPCR), or multiplex ligation-dependent probe amplification (MLPA) preclude rigorous calibration of various metrics used by copy number variant (CNV) detection algorithms. To aid this task, we have established a comparative methodology, CNV-ROC, which is capable of performing a high throughput, low cost, analysis of CMAs that takes into consideration genome-wide true and false negatives. ... comparing one of the NimbleGen CGH microarrays to an array manufactured by Affymetrix (**CytoScan HD**) ... Forty samples were used for comparisons, ... 20 additional samples for the 720K vs. **CytoScan HD** microarray comparisons.

57-

[Comparative mapping of the 22q11.2 deletion region and the potential of simple model organisms](#)

Alina Guna<sup>1</sup>, Nancy J. Butcher<sup>12</sup> and Anne S. Bassett<sup>12345\*</sup>

<sup>1</sup> Clinical Genetics Research Program and Campbell Family Mental Health Research Institute, Centre for Addiction and Mental Health, Toronto, ON, Canada ; <sup>2</sup> Institute of Medical Science, University of Toronto, Toronto, ON, Canada ; <sup>3</sup> Dalglish Family Hearts and Minds Clinic for Adults with 22q11.2 Deletion Syndrome, Div of Cardiology, Dep of Medicine, Dept of Psychiatry, and Toronto General Research Institute, University Health Network, Toronto, ON, Canada ; <sup>4</sup> Dept of Psychiatry, University of Toronto, Toronto, ON, Canada ; <sup>5</sup> Centre for Addiction and Mental Health, 33 Russell Street, Room 1100, Toronto, M5S 2S1, ON, Canada

Journal of Neurodevelopmental Disorders, 1 July 2015, 7:18

... The human 22q11.2DS deletion region, genetic content, and order were mapped from NCBI Gene Homo sapiens Annotation Release 105 using Affymetrix **CytoScan HD** (Santa Clara, CA, USA) array mean breakpoints (chr22:18,820, 303–21, 489,474) ascertained from 16 patients with confirmed 22q11.2 deletions (Fig. 1).

58-

[Comprehensive gene panels provide advantages over clinical exome sequencing for Mendelian diseases](#)

Saudi Mendeliome Group

Saudi Human Genome Project, King Abdulaziz City for Science and Technology, Riyadh, Saudi Arabia  
Genome Biology, 26 June 2015, 16:134

... we used SNP genotyping arrays (Affymetrix **Axiom GT1 chip** ... coming from 21 patients as a second method of testing the analytical sensitivity. ... **CytoScan HD** (Affymetrix) arrays was used for the majority of our patients. ...

59-

[Comprehensive genetic analysis of a pediatric pleomorphic myxoid liposarcoma reveals near-haploidization and loss of the RB1 gene](#)

Jakob Hofvander<sup>3,\*</sup>, Vickie Y. Jo<sup>1</sup>, Iman Ghanei<sup>2</sup>, David Gisselsson<sup>3</sup>, Emma Mårtensson<sup>3</sup>, Fredrik Mertens<sup>3</sup>

<sup>1</sup>Dept of Pathology, Brigham and Women's Hospital, Harvard Medical School, Boston, MA; <sup>2</sup>Dept of Orthopedics, Skåne University Hospital, Lund University, Lund, Sweden; <sup>3</sup>Dept of Clinical Genetics, University and Regional Laboratories, Skåne University Hospital, Lund University, Lund, Sweden

Histopathology, Accepted manuscript online: 9 Dec 2015.

... Banding analysis revealed a hyperdiploid/hypotriploid karyotype that at SNP array analysis could be shown to derive from a near-haploid ancestral clone ... analyzed using the Affymetrix **CytoScan HD array** (Affymetrix, ...

60-

[Comprehensive Pipeline for Analyzing and Visualizing Agilent and Affymetrix Array-Based CGH Data](#)

Frederic Commo

Inserm U981, Bioinformatics Group, Gustave Roussy, France

White paper, July 9, 2015

... We present *rCGH*, a comprehensive array-based CGH analysis workflow, integrating functionalities specifically designed for precision medicine. *rCGH* ensures a full traceability by saving all the process parameters, and facilitates genomic profiles interpretation and decision-making through interactive visualizations. *rCGH* supports Agilent (from 44K to 400K arrays), as well as **Affymetrix**, **SNP6** and **cytoScanHD arrays**.

61-

[Concurrent triplication and uniparental isodisomy: evidence for microhomology-mediated break-induced replication model for genomic rearrangements](#)

Trilochan Sahoo, Jia-Chi Wang, Mohamed M Elnaggar, Pedro Sanchez-Lara, Leslie P Ross, Loretta W Mahon, Katayoun Hafezi, Abigail Deming, Lynne Hinman, Yovana Bruno, James A Bartley, Thomas Liehr, Arturo Anguiano and Marilyn Jones

European Journal of Human Genetics, 2015, 23:61–66.

... We report on the identification and characterization of two cases with interstitial triplication followed by uniparental isodisomy (isoUPD) for remainder of the chromosomal arm. ... The above two cases were identified from over 14500 cases analyzed utilizing the **Affymetrix version 6.0 genechip** (5700 cases; ... or the **Affymetrix CytoScan HD Array** (8800 cases; whole-genome 2.7M array) ...

62-

[Confirmation of a maternal cryptal balanced translocation through analysis of a fetus using microarray \[article in Chinese\]](#)

Wu J1, Xie Y, Lin S, Chen B, Chen J, Zhang Z, Ji Y.

1Fetal Medicine Center, Department of Gynaecology and Obstetrics, The First Affiliated Hospital, Sun Yatsen University, Guangzhou, Guangdong 510080, P. R. China. Email: wujianzhu3140@126.com.

Zhonghua Yi Xue Yi Chuan Xue Za Zhi. [Chinese Journal of Medical Genetics], 10 Feb 2015, 32(1):69-72.

doi: 10.3760/cma.j.issn.1003-9406.2015.01.015.

**OBJECTIVE** To analyze a fetus with heart defects and to assess the recurrence risk for her family. **METHODS** Single nucleotide polymorphism-based arrays (SNP-Array) analysis using Affymetrix Genome Wide Human SNP **CytoHD** was performed to analyze the fetus and her parents. Karyotype analysis was also carried out. **RESULTS** SNP-Array has detected a 14.5 Mb duplication at 9p and a 14.7 Mb deletion at 11q. Karyotype analysis indicated that the fetus' mother has a karyotype of 46,XX,t(9;11)(p23;q24). Therefore, the fetus has inherited a derivative chromosome 11 derived from the maternal translocation, and her karyotype was 46,XX,der(11)t(9;11)(p23;q24)mat. **CONCLUSION** SNP-Array combined with high resolution GTG banding has confirmed that the fetus has a derivative chromosome 11 derived from her mother's balanced translocation, resulting in partial 9p trisomy and partial 11q monosomy. This couple therefore have a high recurrence risk. SNP-Array is capable of detecting small chromosomal imbalance in abnormal fetuses and can pinpoint the breakpoints. It therefore has the advantage for the detection of unbalanced translocation which is difficult to detect with GTG banding, which is important for assessment the recurrence risk for cryptic balanced translocation carriers.

63-

[Copy number variants including RAS pathway genes—How much RASopathy is in the phenotype?](#)

Christina Lissewski<sup>1</sup>, Sarina G. Kant<sup>2</sup>, Zornitza Stark<sup>3</sup>, Ina Schanze<sup>1</sup>, Martin Zenker<sup>1,\*</sup>

<sup>1</sup>Institute of Human Genetics, University Hospital Magdeburg, Magdeburg, Germany; <sup>2</sup>Department of Clinical Genetics, Leiden University Medical Center, Leiden, The Netherlands; <sup>3</sup>Victorian Clinical Genetics Service, MCRI, Royal Children's Hospital, Melbourne, Australia

American Journal of Medical Genetics Part A, November 2015, 167(11): 2685–269.

... Molecular karyotyping was performed in the index patient using **CytoScan HD Array** Affymetrix and revealed a duplication 19p13.3 (chr19:3947246-5098336, hg19) of at least 1.2 Mb.

64-

[Copy number variations in cryptogenic cerebral palsy](#)

Reeval Segel, MD\*, Hilla Ben-Pazi, MD\*, Sharon Zeligson, Aviva Fatal-Valevski, MD, Adi Aran, MD, Varda Gross-Tsur, MD, Nira Schneebaum-Sender, MD, Dorit Shmueli, MD, Dorit Lev, MD, Shira Perlberg, Luba Blumkin, MD, Lisa Deutsch, PhD and Ephrat Levy-Lahad, MD

From the Medical Genetics Institute (R.S., S.Z., S.P., E.L.-L.) and Neuropediatric Unit (H.B.-P., A.A., V.G.-T.), Shaare Zedek Medical Center, Jerusalem; Pediatric Neurology Unit (A.F.-V., N.S.-S.), Dana Children's Hospital, Tel Aviv; Jerusalem Child Development Center (D.S.), Clalit, Jerusalem; Metabolic-Neurogenetic Clinic (D.L., L.B.), Wolfson Medical Center, Holon; and Biostatistical Consulting (L.D.), BioStats, Israel.

Neurology April 21, 2015 vol. 84 no. 16 1660-1668

...Participants underwent neurologic and clinical genetic examinations before the genomic testing. Chromosomal microarray analysis to detect CNVs was performed using the Affymetrix platform. ...

We recommend CNV testing in individuals with CP of unknown etiology. ... Affymetrix **Cytoscan HD** arrays were used ...

65-

[CRB2 Mutations Produce a Phenotype Resembling Congenital Nephrosis, Finnish Type, with Cerebral Ventriculomegaly and Raised Alpha-Fetoprotein](#)

Anne Slavotinek,1,2,\* Julie Kaylor,3 Heather Pierce,4 Michelle Cahr,5 Stephanie J. DeWard,4

Dina Schneidman-Duhovny,6,7 Adnan Alsadah,1 Fadi Salem,8 Gabriela Schmajuk,9 and Lakshmi Mehta5

American Journal of Human Genetics, 8 Jan 2015, 96:162–169.

We report five fetuses and a child from three families who shared a phenotype comprising cerebral ventriculomegaly and echogenic kidneys with histopathological findings of congenital nephrosis. ... His last renal US continued to show diffusely echogenic kidneys with ascites. A SNP microarray (**CytoScanHD**,Affymetrix) was normal. ...

66-

[Cytogenetic, fluorescence in situ hybridization and genomic array characterization of chronic myeloid leukemia with cryptic BCR/ABL1 fusions](#)

Lina Shao, Sue Miller, Jennifer Keller-Ramey#, Yang Zhang, Diane Roulston

Clinical Cytogenetics Laboratory, Department of Pathology, University of Michigan, Ann Arbor, Michigan Cancer Genetics, July-Aug 2015, 208(7–8): 396–403.

... This study demonstrates for the first time the acquisition of additional BCR/ABL1 fusion genes through mitotic recombination in CML with cryptic BCR/ABL1. ... Genome-wide SNP array analysis using the Affymetrix **CytoScan HD** platform ...

67-

[De novo 9q gain in an infant with tetralogy of Fallot with absent pulmonary valve: Patient report and review of congenital heart disease in 9q duplication syndrome](#)

Ina E. Amarillo1, Shawn O'Connor2, Caroline K. Lee2, Marcia Willing2 and Jennifer A. Wambach2,\*

1Dept of Pathology and Immunology, Cytogenomics Laboratory, Washington University in St. Louis School of Medicine, St. Louis, Missouri; 2Dept of Pediatrics, Washington University in St. Louis School of Medicine, St. Louis, Missouri

American Journal of Medical Genetics Part A, December 2015, 167(12): 2966–2974.

... first report implicating RXRA in CHD with 9q duplication ... highlights the significance of CMA in the clinical diagnosis ... Genomic DNA was isolated from cord blood lymphocytes of the infant (proband) for CMA and data output was analyzed using **CytoScan HD** (Affymetrix, ...

68-

[De novo microduplication of CHL1 in a patient with non-syndromic developmental phenotypes](#)

Orazio Palumbo1, Rita Fischetto2, Pietro Palumbo1, Francesco Nicastro2, Francesco Papadia2, Leopoldo Zelante1 and Massimo Carella1\*

1 Laboratorio di Genetica Medica, IRCCS Casa Sollievo della Sofferenza, San Giovanni Rotondo, (FG), Italy; 2 Unità Operativa Malattie Metaboliche Genetica Medica, P.O. Giovanni XXIII, A.O.U. Policlinico Consorziale, Bari, Italy

Molecular Cytogenetics, 16 August 2015, 8:66.

... We extracted DNA from the lymphocytes of patient and his parents using BioRobot EZ1 (Qiagen, Solna, Sweden). Genomic screening for copy number variations (CNVs) was carried out using the **CytoScan HD array** platform (Affymetrix, ...

69-

[Deleción en el gen RPS6KA3 en una mujer con un fenotipo clásico del síndrome de Coffin-Lowry incluyendo episodios de caída inducidos por estímulo](#)

Inés Quintela b, Francisco Barros-Angueira b, Laura Pérez-Gay d, Manuel Castro-Gago d, Ángel Carracedo a,b,c, Jesús Eirís-Puñal d

a King Abdulaziz University. Center of Excellence in Genomic Medicine Research. Jeddah, Arabia Saudí. b Grupo de Medicina Xenómica. Universidade de Santiago de Compostela. Centro Nacional de Genotipado, Plataforma de Recursos Biomoleculares y Bioinformáticos, Instituto de Salud Carlos III (CeGen-PRB2-ISCIII). c Grupo de Medicina Xenómica-USC, CIBERER, Fundación Pública Galega de Medicina Xenómica- SERGAS. d Departamento de Pediatría. Unidad de Neurología Pediátrica. Hospital Clínico Universitario de Santiago de Compostela. Santiago de Compostela, A Coruña, España.

Rev Neurol 2015; 61(2): 94-96

... Las muestras de ADN de la paciente y su madre se obtuvieron de sangre periférica y se genotiparon con el panel Affymetrix **CytoScan High-Density** (Affymetrix, Santa Clara, CA) ...

70-

[Deletion of 7q33-q35 in a Patient with Intellectual Disability and Dysmorphic Features: Further Characterization of 7q Interstitial Deletion Syndrome](#)

Kristen Dilzell,<sup>1</sup> Diana Darcy,<sup>2</sup> John Sum,<sup>3</sup> and Robert Wallerstein<sup>2</sup>

<sup>1</sup>Dept of Medical Genetics, University of Pennsylvania, Philadelphia, PA 19104, USA; <sup>2</sup>Silicon Valley Genetics Center, Santa Clara Valley Medical Center, San Jose, CA 95128, USA; <sup>3</sup>Pediatric Neurology, Santa Clara Valley Medical Center, San Jose, CA 95128, USA

Case Reports in Genetics Volume 2015 (2015), Article ID 131852.

This case report concerns a 16-year-old girl with a 9.92 Mb, heterozygous interstitial chromosome deletion at 7q33-q35, identified using array comparative genomic hybridization. ... SNP microarray was performed by Integrated Genetics using the Affymetrix **Cytoscan HD** platform ...

71-

[Deletion of 11q12.3–11q13.1 in a patient with intellectual disability and childhood facial features resembling Cornelia de Lange syndrome](#)

Martine Isabel Boyle, Cathrine Jespersgaard, Lusine Nazaryan, Kirstine Ravn, Karen Brøndum-Nielsen, Anne-Marie Bisgaard, Zeynep Tümer

Applied Human Molecular Genetics, Kennedy Center, Dept of Clinical Genetics, Univ of Copenhagen, Rigshospitalet, Glostrup, Denmark

Gene, Available online 8 July 2015, In Press, Corrected Proof

... Deletions within 11q12.3-11q13.1 are very rare ... a 1.6 Mb deletion at chromosome region 11q12.3-11q13.1 was detected by chromosome microarray. ... Chromosome microarray analysis was performed in the proband using the Affymetrix **CytoScan HD platform** ...

72-

[Deletion of 16q24.1 Supports a Role for the ATP2C2 Gene in Specific Language Impairment](#)

Amena W. Smith, MD, PhD<sup>1</sup>, Kenton R. Holden, MD<sup>1,2,3</sup>, Alka Dwivedi, PhD<sup>3</sup>, Barbara R. Dupont, PhD<sup>3</sup>, Michael J. Lyons, MD<sup>3†</sup>

<sup>1</sup>Dept of Neurosciences (Neurology), Medical University of South Carolina, Charleston, SC, USA ; <sup>2</sup>Dept of Pediatrics, Medical University of South Carolina, Charleston, SC, USA ; <sup>3</sup>Greenwood Genetic Center, Greenwood, SC, USA

J Child Neurol, March 2015, 30(4):517-521.

A 10-year-old boy presented with a history of significant delay in language acquisition ... Chromosomal microarray analysis and quantitative polymerase chain reaction determined that he had a de novo 159-kilobase deletion of chromosome 16q24.1 that included the ATP2C2 gene. .... Whole-genome chromosomal microarray analysis (Affymetrix **Cytoscan HD** Microarray system) revealed a 159-kilobase ...

73-

[Detailed analysis of therapy-driven clonal evolution of TP53 mutations in chronic lymphocytic leukemia](#)

J Malcikova, K Stano-Kozubik, B Tichy, B Kantorova, S Pavlova, N Tom, L Radova, J Smardova, F Pardy, M Doubek, Y Brychtova, M Mraz, K Plevova, E Diviskova, A Oltova, J Mayer, S Pospisilova and M Trbusek

Leukemia, 2015, 29: 877–885.

... Deep sequencing can shift TP53 mutation identification to a period before therapy administration, which might be of particular importance for clinical trials.... cn-LOH 17p—17p copy-neutral loss of heterozygosity involving TP53 gene detected by **Cytoscan** Affymetrix arrays.

74-

[Detailed Biochemical and Bioenergetic Characterization of FBXL4-Related Encephalomyopathic Mitochondrial DNA Depletion](#)

Ghadi Antoun (1), Skye McBride (2), Jason R. Vanstone (2), Turaya Naas (2) (4), Jean Michaud (3), Stephanie Redpath (2), Hugh J. McMillan (2), Jason Brophy (2), Hussein Daoud (2), Pranesh Chakraborty (2) (4), David Dymment (2), Martin Holcik (2), Mary-Ellen Harper (1), Matthew A. Lines [mlines@cheo.on.ca](mailto:mlines@cheo.on.ca) (2)

1. Dept of Biochemistry, Microbiology, and Immunology, Faculty of Medicine, University of Ottawa, Ottawa, ON, Canada; 2. Children's Hospital of Eastern Ontario Research Institute, Ottawa, ON, Canada; 3. Dept of Pathology and Laboratory Medicine, Children's Hospital of Eastern Ontario and Faculty of Medicine, University of Ottawa, Ottawa, ON, Canada; 4. Newborn Screening Ontario, Ottawa, ON, Canada

JIMD Reports, online 25 September 2015

... Microarray was performed clinically (Affymetrix **CytoScan HD**) according to standard protocols.

75-

[Detecting copy-number variations in whole-exome sequencing data using the eXome Hidden Markov Model: an 'exome-first' approach](#)

Satoko Miyatake<sup>1</sup>, Eriko Koshimizu<sup>1</sup>, Atsushi Fujita<sup>1</sup>, Ryoko Fukai<sup>1</sup>, Eri Imagawa<sup>1</sup>, Chihiro Ohba<sup>1</sup>, Ichiro Kuki<sup>2</sup>, Megumi Nukui<sup>2</sup>, Atsushi Araki<sup>3</sup>, Yoshio Makita<sup>4</sup>, Tsutomu Ogata<sup>5</sup>, Mitsuko Nakashima<sup>1</sup>, Yoshinori Tsurusaki<sup>1</sup>, Noriko Miyake<sup>1</sup>, Hiroto Saito<sup>1</sup> and Naomichi Matsumoto<sup>1</sup>

<sup>1</sup>Dept of Human Genetics, Yokohama City University Graduate School of Medicine, Yokohama, Japan; <sup>2</sup>Dept of Pediatric Neurology, Pediatric Medical Care Center, Osaka City General Hospital, Osaka, Japan; <sup>3</sup>Dept of Pediatrics, Kansai Medical University, Hirakata, Japan; <sup>4</sup>Education Center, Asahikawa Medical University, Asahikawa, Japan; <sup>5</sup>Dept of Pediatrics, Hamamatsu University School of Medicine, Hamamatsu, Japan

Journal of Human Genetics, 2015, 60: 175–182.

... we performed WES CNV analysis using the eXome Hidden Markov Model (XHMM). We validated its performance using 27 rare CNVs previously identified by microarray as positive controls, ... Either Affymetrix **CytoScan HD** or Human **Mapping 250 K Nsp Array** for Cytogenetics (Affymetrix, Santa Clara, CA, USA) were used for all the 21 samples.

76-

[DGCR6 at the proximal part of the DiGeorge critical region is involved in conotruncal heart defects](#)

Wenming Gao, Takashi Higaki, Minenori Eguchi-Ishimae, Hidehiko Iwabuki, Zhouying Wu, Eiichi Yamamoto, Hidemi Takata, Masaaki Ohta, Issei Imoto, Eiichi Ishii, Mariko Eguchi

Human Genome Variation, online 12 Feb 2015, 2, Article #15004

... when copy number alteration was analyzed by high-resolution array analysis, a small deletion or duplication in the proximal end of DiGeorge critical region was detected in two patients. ... Copy number analysis was performed using a genome-wide high-resolution Affymetrix **CytoScan HD** array ...

77-

[Diagnosis of 9q22.3 microdeletion syndrome in utero following identification of craniosynostosis, overgrowth, and skeletal anomalies](#)

Sara Chadwick Reichert<sup>1,\*</sup>, Kristin Zelle<sup>2</sup>, Kim E. Nichols<sup>3</sup>, Moriah Eberhard<sup>1</sup>, Elaine H. Zackai<sup>4</sup> and Juan Martinez-Poyer<sup>1</sup>

<sup>1</sup>Center for Fetal Diagnosis and Treatment, Children's Hospital of Philadelphia, Philadelphia, PA; <sup>2</sup>Div of Oncology, Children's Hospital of Philadelphia, Philadelphia, PA; <sup>3</sup>Div of Cancer Predisposition, St Jude Children's Research Hospital, Memphis, TN; <sup>4</sup>Div of Clinical Genetics, Children's Hospital of Philadelphia, Philadelphia, PA

American Journal of Medical Genetics Part A, April 2015, 167(4):862–865.

... We describe a patient with prenatally diagnosed 9q22.3 microdeletion syndrome following the ultrasonographic identification of trigonocephaly, macrosomia, organomegaly, ventriculomegaly, and anomalous vertebrae. ... Follow-up parental SNP microarray was performed on whole blood by Quest Diagnostics Nichols Institute using the Affymetrix **Cytoscan HD** platform.

78-

[Diagnosis of D-Bifunctional Protein Deficiency through Whole-Genome Sequencing: Implications for Cost-Effective Care](#)

Khromykh A.a· Solomon B.D.a,b,d· Bodian D.L.a· Leon E.L.f· Iyer R.K.a, e· Baker R.L.b, c· Ascher D.P.b, d· Baveja R.b, c· Vockley J.G.a, c· Niederhuber J.E.a

<sup>a</sup>Inova Translational Medicine Institute, <sup>b</sup>Inova Children's Hospital, Inova Health System, and <sup>c</sup>Fairfax Neonatal Associates, Falls Church, Va., <sup>d</sup>Depts of <sup>d</sup>Pediatrics and <sup>e</sup>Obstetrics and Gynecology, Virginia Commonwealth University School of Medicine, Richmond, VA, and <sup>f</sup>Div of Genetics and Metabolism, Children's National Medical Center, Washington, D.C., USA

Molecular Syndromology, 2015, 6:141-146.

... Commercially performed cytogenetic or molecular testing on peripheral blood included: initial FISH for Trisomy 21, karyotyping, high-density microarray (oligonucleotide-single nucleotide polymorphism microarray via Affymetrix **CytoScan HD**), spinal muscular atrophy via ...

79-

[Diagnosis of intrachromosomal amplification of chromosome 21 \(iAMP21\) by molecular cytogenetics in pediatric acute lymphoblastic leukemia](#)

Nicolas Duployez<sup>1,2,3,\*</sup>, Elise Boudry-Labis<sup>1,3</sup>, Gauthier Decool<sup>2</sup>, Guillaume Grzych<sup>2</sup>, Nathalie Gardel<sup>2</sup>, Wadih Abou Chahla<sup>4</sup>, Claude Preudhomme<sup>2,3</sup> and Catherine Roche-Lestienne<sup>1,3</sup>

<sup>1</sup>Medical Cytogenetics Institute, Jeanne de Flandre Hospital, Lille, France; <sup>2</sup>Laboratory of Hematology, Biology and Pathology Center, Lille, France; <sup>3</sup>INSERM UMR-S 1172, Cancer Research Institute, Lille, France; <sup>4</sup>Pediatric Hematology Department, Jeanne de Flandre Hospital, Lille, France

Clinical Case Reports, October 2015, 3(10): 814–816.



... Single-nucleotide polymorphism (SNP)-array was performed ... using Affymetrix® **Cytoscan High Density Array**. ... **SNP-array is a useful method** to confirm the accuracy of iAMP21 diagnosis ... its use is of increasing importance to refine risk stratification in pediatric BCP-ALL ...

80-

[Diagnostic value of multiple café-au-lait macules for neurofibromatosis 1 in Chinese children](#)

Ruen Yao<sup>1</sup>, Lili Wang<sup>2</sup>, Yongguo Yu<sup>2</sup>, Jian Wang<sup>1</sup> and Yiping Shen<sup>1,3,4,\*</sup>

<sup>1</sup>Shanghai Children's Medical Center, Shanghai Jiaotong University School of Medicine, Shanghai, China; <sup>2</sup>Xinhua Hospital, Institute for Pediatric Research, Shanghai, China; <sup>3</sup>Boston Children's Hospital, Boston, MA, USA; <sup>4</sup>Claritas Genomics, Cambridge, MA, USA.

The Journal of Dermatology, first published online: 13 October 2015

... Molecular testing is necessary ... as an adjunct and sometimes as the main tool for confirming and diagnosing children of NF1 at early age ... Chromosomal microarray analysis was applied to detect large structural variants using a **CytoScan HD® chip** (Affymetrix, ...

81-

[Differentiation of genetic abnormalities in early pregnancy loss](#)

S. T. Romero<sup>1,2,\*</sup>, K. B. Geiersbach<sup>3</sup>, C. N. Paxton<sup>4</sup>, N. C. Rose<sup>2</sup>, E. F. Schisterman<sup>5</sup>, D. W. Branch<sup>2</sup> and R. M. Silver<sup>1</sup>

<sup>1</sup>Dept of Obstetrics and Gynecology, University of Utah School of Medicine, Salt Lake City, UT, USA; <sup>2</sup>Div of Maternal Fetal Medicine, Intermountain Medical Center, Salt Lake City, UT, USA; <sup>3</sup>Dept of Pathology, University of Utah School of Medicine, Salt Lake City, UT, USA; <sup>4</sup>ARUP Institute for Clinical and Experimental Pathology®, University of Utah School of Medicine, Salt Lake City, UT, USA; <sup>5</sup>Epidemiology Branch, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, MD  
Ultrasound in Obstetrics & Gynecology [Special issue: Fetal cfDNA and microarray], January 2015, 45(1):89–94.

... Chromosomal microarray analysis (CMA) was performed on 74 samples (including two samples from a twin pregnancy); 15 were pre-embryonic (no visible embryo on ultrasound examination), 31 were embryonic (embryo; 6 + 0 to 9 + 6 weeks' gestation) and 28 were fetal (fetus; 10 + 0 to 19 + 6 weeks' gestation) losses. ... Labeled DNA fragments were denatured and hybridized to **CytoScan SNP arrays** (Affymetrix ...

82-

[Differing Microdeletion Sizes and Breakpoints in Chromosome 7q11.23 in Williams-Beuren Syndrome Detected by Chromosomal Microarray Analysis](#)

Li L., Huang L., Luo Y., Huang X., Lin S., Fang Q.

Dept of Gynecology and Obstetrics, Fetal Medicine Center, First Affiliated Hospital of Sun Yat-sen University, Guangzhou, PR China

Molecular Syndromology, 2015, 6: 268-275.

... We analyzed 10 patients diagnosed with 7q11.23 microdeletion syndrome by chromosomal microarray analysis. ... hybridized to the Affymetrix **CytoScan HD** array chip

...

83-

[Digital PCR Validates 8q Dosage as Prognostic Tool in Uveal Melanoma](#)

Mieke Versluis, Mark J. de Lange, Sake I. van Pelt, Claudia A. L. Ruivenkamp, Wilma G.

M. Kroes, Jinfeng Cao, Martine J. Jager, Gre P. M. Luyten, Pieter A. van der Velden

PLoS ONE, March 12, 2015, 10(3): e0116371.

... We used SNP microarray data that was acquired for clinical purposes on UM samples to determine chromosomal aberrations. Two types of SNP microarray chips were used. The **Affymetrix 250K\_NSP chip**, which contains roughly 250 000 probes across the genome and the Affymetrix **Cytoscan HD** chip, with approximately 750 000 probes across the genome. A first set of 28 samples was analyzed with the Affymetrix **250K\_NSP** chip. Since this chip was no longer available, the remaining 36 samples were measured with the Affymetrix **Cytoscan HD** chip.

84-

[Discordant noninvasive prenatal testing and cytogenetic results: a study of 109 consecutive cases](#)

Jia-Chi Wang MD, PhD, Trilochan Sahoo MD, Steven Schonberg PhD, Kimberly A. Kopita MS, Leslie Ross MS, Kyla Patek MS & Charles M. Strom MD, PhD

Genetics in Medicine, March 2015, 17(3):234-236.

... These findings raise concerns about the limitations of noninvasive prenatal testing and the need for analysis of a larger number of false-positive cases to provide true positive predictive values ... and/or oligo–single-nucleotide polymorphism microarrays (**CytoScanHD**; Affymetrix, Santa Clara, CA) after NIPT.

85-

[Discovery of a novel cystathionine-beta-synthase mutation and diagnosis of homocystinuria by whole exome sequencing in a family from rural Honduras](#)

Scott A. Turner<sup>1</sup>, Mary Beth P. Dinulos<sup>2, 3</sup>, Stephanie E. Vallee<sup>2, 3</sup>, Linda Kennedy<sup>4</sup>, Peter Mason<sup>5</sup>, Dean Seibert<sup>5</sup>, Marco Tulio Martinez<sup>4</sup>, Heather B. Steinmetz<sup>2</sup>, Gregory J. Tsongalis<sup>1, 2, 4</sup>, Joel A. Lefferts<sup>1, 2</sup>

<sup>1</sup>Dept of Pathology, Geisel School of Medicine at Dartmouth, Hanover, NH, USA. <sup>2</sup>Dept of Pathology, Dartmouth-Hitchcock Medical Center, Lebanon, NH, USA. <sup>3</sup>Dept of Pediatrics, Dartmouth-Hitchcock Medical Center, Lebanon, NH. <sup>4</sup>Norris Cotton Cancer Center, Geisel School of Medicine at Dartmouth, Hanover, NH, USA. <sup>5</sup>Dept of Medicine, Geisel School of Medicine at Dartmouth, Hanover, NH, USA.

Case Reports in Clinical Pathology, published online 17 April 2015, 2(3):59-65.

... Microarray analysis was done using **CytoScanHD Array** (Affymetrix, Santa Clara, CA) and Chromosomal Analysis Suite (ChAS) v1.2 (Affymetrix) software.

86-

[Distal 22q11.2 microduplication combined with typical 22q11.2 proximal deletion: A case report](#)

Miriam Coelho Molck<sup>1</sup>, Társis Paiva Vieira<sup>1</sup>, Milena Simioni<sup>1</sup>, Ilária Cristina Sgardioli<sup>1</sup>, Ana Paula dos Santos<sup>1</sup>, Ana Carolina Xavier<sup>2</sup> and Vera Lúcia Gil-da-Silva-Lopes<sup>1,3,\*</sup>

<sup>1</sup>Dept of Medical Genetics, Faculty of Medical Sciences, University of Campinas (UNICAMP), Sao Paulo, Brazil; <sup>2</sup>Center for Research and Rehabilitation of Lip and Palate Lesions (CRRLPL) Centrinho Prefeito Luiz Gomes, Joinville, Santa Catarina, Brazil; <sup>3</sup>Assistance Center for Cleft Lip and Palate (CAIF), Curitiba, Parana, Brazil  
American Journal of Medical Genetics Part A, January 2015,167(1): 215-220.

... Array genomic hybridization (aGH) analysis for the patient was performed using the Genome-Wide Human **SNP Array 6.0** (Affymetrix®) and analyzed by GeneChip® Operating Software (GCOS) (Affymetrix®). aGH analysis for patient's mother and father was performed using the **CytoScan HD** chip (Affymetrix®) ...

87-

[Duplication Xp11.22-p14 in females: Does X-inactivation help in assessing their significance?](#)

Christina Evers<sup>1</sup>, Diana Mitter<sup>2</sup>, Gertrud Strobl-Wildemann<sup>3</sup>, Ulrich Haug<sup>4</sup>, Karl Hackmann<sup>5</sup>, Bianca Maas<sup>1</sup>, Johannes W. G. Janssen<sup>1</sup>, Anna Jauch<sup>1</sup>, Katrin Hinderhofer<sup>1</sup>, Ute Moog<sup>1,\*</sup>

<sup>1</sup>Institute of Human Genetics, Heidelberg University, Heidelberg, Germany; <sup>2</sup>Institute of Human Genetics, University Hospital Leipzig, Leipzig, Germany; <sup>3</sup>Humangenetik Ulm MVZ, Ulm, Germany; <sup>4</sup>Center for Child Neurology and Social Pediatrics Maulbronn, Maulbronn, Germany; <sup>5</sup>Institut fuer Klinische Genetik, Medizinische Fakultät Carl Gustav Carus, Technische Universität Dresden, Dresden, Germany

American Journal of Medical Genetics Part A, March 2015, 167(3):553–562.

... Array analysis of Patient 1 and her parents was performed using the Affymetrix® **CytoScan HD Array**. Patients 2 and 3 and parental samples were analyzed with the Affymetrix® **Genome-Wide Human SNP Array 2.7** ...

88-

[Effects of Integrating and Non-Integrating Reprogramming Methods on Copy Number Variation and Genomic Stability of Human Induced Pluripotent Stem Cells](#)

Xiangjin Kang, Qian Yu, Yuling Huang, Bing Song, Yaoyong Chen, Xingcheng Gao, Wenyin He, Xiaofang Sun, Yong Fan

PLoS ONE, 1 July 2015, 10(7): e0131128.

... using the Affymetrix **Cytoscan HD** array, we investigated the genomic aberration profiles of 19 human cell lines ... from which the iPSCs were derived. ... importance of determining the molecular mechanisms ... in reprogramming somatic cells to be pluripotent ...

89-

[EMT-associated factors promote invasive properties of uveal melanoma cells](#)

Laura Asnaghi,<sup>1</sup> Gülçin Gezgin,<sup>2</sup> Arushi Tripathy,<sup>1</sup> James T. Handa,<sup>3</sup> Shannath L. Merbs,<sup>3,4</sup> Pieter A. van der Velden,<sup>2</sup> Martine J. Jager,<sup>2</sup> J. William Harbour,<sup>5</sup> Charles G. Eberhart<sup>1,3,4</sup>

<sup>1</sup>Dept of Pathology, Johns Hopkins University, School of Medicine, Baltimore, MD; <sup>2</sup>Dept of Ophthalmology, Leiden University Medical Center, Leiden, The Netherlands; <sup>3</sup>Dept of Ophthalmology, Johns Hopkins University, School of Medicine, Baltimore, MD; <sup>4</sup>Dept of Oncology, Johns Hopkins University, School of Medicine, Baltimore, MD; <sup>5</sup>Ocular Oncology, Bascom Palmer Eye Institute and Sylvester Comprehensive Cancer Center, University of Miami Miller School of Medicine, Miami, FL

Molecular Vision, 25 August 2015, 21:919-929.

... The **Affymetrix 250K\_NSP chip** was used to analyze 28 tumor specimens. The remaining 36 tumor specimens were analyzed with the Affymetrix **Cytoscan HD** chip ...

90- **Meeting abstract**

[Establishment, characterization, and clinical correlation of a platform of ovarian patient-derived xenograft \(PDX\) models](#)

Sangeetha S. Palakurthi<sup>1</sup>, Joyce F. Liu<sup>2</sup>, Qing Zeng<sup>1</sup>, Shan Zhou<sup>1</sup>, Wei Huang<sup>1</sup>, Elena Ivanova<sup>1</sup>, Cloud Paweletz<sup>1</sup>, John R. Murgu<sup>1</sup>, Justin Evangelista<sup>1</sup>, Melissa Buttimer<sup>1</sup>, Jennifer Curtis<sup>3</sup>, Huiying Piao<sup>2</sup>, Prafulla Gokhale<sup>1</sup>, Colin Pritchard<sup>4</sup>, Jessie M. English<sup>1</sup>, Paul Kirschmeier<sup>1</sup>, Kwok-Kin Wong<sup>1</sup>, Ursula A. Matulonis<sup>2</sup>, and Ronny Drapkin<sup>5</sup>

<sup>1</sup>Belfer Institute for Applied Cancer Science, DFCI, Boston, MA; <sup>2</sup>Dept of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA; <sup>3</sup>Dept of Cancer Biology, Dana-Farber Cancer Institute, Boston, MA; <sup>4</sup>Dept of Laboratory Medicine, University of Washington, Seattle, WA; <sup>5</sup>Dept of Medical Oncology, Dana-Farber Cancer Institute and Department of Pathology, Brigham and Women's Hospital, Boston, MA.

Cancer Research, 2015, 75(15 Suppl):Abst #1471. [AACR 106<sup>th</sup> Annual Mtg, Apr 18-22, 2015, Philadelphia, PA]

... Ovarian PDXs were established by implanting mice intraperitoneally with fresh human ovarian cancer cells purified from operative or paracentesis samples under an IRB-approved protocol. ... DNA from patient material and matched established PDX models was extracted and subjected to CNV on the Affymetrix **Cytoscan™ HD microarray** platform and BROCA cancer risk panel targeted sequencing. Data from these analyses indicated that the PDXs are molecularly diverse and faithfully maintain the genetic alterations and copy number variation profiles of the patient tumors. ...

91- **Meeting abstract**

[Evaluation of SNP Genomic Microarray Analysis as an Alternative to FISH Analysis of Pediatric Solid Tumors](#)

Anthony Arnoldo, James Stavropoulos, Paul Thorner, Cynthia Hawkins, Gino R. Somers, Mary Shago

Cancer Genetics, June 2015, 208(6): 361–362.

... We have validated the use of the genomic microarray platform Affymetrix **Cytoscan HD** and Chromosome Analysis Suite (ChAS) software as an alternative to FISH analysis for the assessment of copy number changes in these tumors.

92-

[Evidence for the multiple hits genetic theory for inherited language impairment: a case study](#)

Tracy M. Centanni, Jordan R. Green, Jenya Iuzzini-Seigel, Christopher W. Bartlett, Tiffany P. Hogan

Frontiers in Genetics, 24 August 2015, 6: 272.

... High-resolution genome-wide analysis was performed on genomic DNA using the **CytoScanHD™ array** (Affymetrix, Santa Clara, CA, USA) according to manufacturer's instruction.

89- **Open access**

[Exceptional Complex Chromosomal Rearrangements In Three Generations](#)

Hannie Kartapradja, Nanis Sacharina Marzuki, Mark Pertile, David Francis, Lita Putri Suciati, Helena Woro Anggaratri, Debby Dwi Ambarwati, Firman Prathama Idris, Harry Lesmana, Hidayat Trimarsanto, Chrysantine Paramayuda, and Alida Roswita Harahap  
Case Reports in Genetics, accepted 19 January 2015.

We report an exceptional Complex Chromosomal Rearrangement (CCR) found in three individuals in a family that involves 4 chromosomes with 5 breakpoints. The CCR was ascertained in a phenotypically abnormal newborn with additional chromosomal material on the short arm of chromosome 4. Maternal karyotyping indicated that the mother carried an apparently balanced CCR involving chromosomes 4, 6, 11 and 18. Maternal transmission of the derivative chromosome 4 resulted in partial trisomy for chromosomes 6q and 18q, and a partial monosomy of chromosome 4p in the proband. Further family studies found that the maternal grandmother carried the same apparently balanced CCR as the proband's mother, which was confirmed using whole chromosome painting (WCP) FISH. High resolution whole genome microarray analysis of DNA from the proband's mother found no evidence for copy number imbalance in the vicinity of the CCR translocation breakpoints, or elsewhere in the genome, providing evidence that the mother and grandmother's CCRs were balanced at a molecular level. This structural rearrangement can be categorized as an

exceptional CCR due to its complexity and is a rare example of an exceptional CCR being transmitted in balanced and/or unbalanced form across three generations.

Excerpt: To investigate whether the BCCR was balanced at a molecular level, we analysed DNA from the proband's mother using Affymetrix **CytoScan HD** microarray (Affymetrix, Santa Clara, CA, USA), with interpretation based on the NCBI36/hg18 (March 2006) human reference sequence. The microarray result showed no clinically significant genomic imbalance.

90-

[Exome sequencing identifies a novel heterozygous TGFB3 mutation in a disorder overlapping with Marfan and Loeys-Dietz syndrome](#)

Alma Kuechler, Janine Altmüller, Peter Nürnberg, Stefan Kotthoff, Christian Kubisch, Guntram Borck

Molecular and Cellular Probes, Available online 13 July 2015, Accepted Manuscript  
Marfan syndrome (MFS) and Loeys-Dietz syndrome (LDS) are clinically related autosomal dominant systemic connective tissue disorders. ...We performed whole exome sequencing in two of three affected individuals from a family with phenotypic features overlapping MFS and LDS. ... Molecular karyotyping (Affymetrix **CytoscanHD array**) was also normal.

91-

[Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency](#)

Michal Kovac, Claudia Blattmann, Sebastian Ribí, Jan Smida, Nikola S. Mueller, Florian Engert, Frances Castro-Giner, Joachim Weischenfeldt, Monika Kovacova, Andreas Krieg, Dimosthenis Andreou, Per-Ulf Tunn, Hans Roland Dürr, Hans Rechl, Klaus-Dieter Schaser, Ingo Melcher, Stefan Burdach, Andreas Kulozik, Katja Specht, Karl Heinemann, Simone Fulda, Stefan Bielack, Gernot Jundt, Ian Tomlinson, Jan O. Korbel, Michaela Nathrath & Daniel Baumhoer

Nature Communications, 3 December, 6: Article #8940.

... Affymetrix **CytoscanHD arrays** were processed with ChaS 2.1 and Nexus 7.5 software such that SCNA events larger than 50 kb with a minimum support of 21 probes were considered for subsequent analysis.

92-

[Expanding the Molecular and Clinical Phenotype of SSR4-CDG](#)

Bobby G. Ng<sup>1</sup>, Kimiyo Raymond<sup>2</sup>, Martin Kircher<sup>3</sup>, Kati J. Buckingham<sup>4</sup>, Tim Wood<sup>5</sup>, Jay Shendure<sup>3</sup>, Deborah A. Nickerson<sup>3</sup>, Michael J. Bamshad<sup>3,4</sup>, University of Washington Center for Mendelian Genomics<sup>1</sup>, Jonathan T.S. Wong<sup>1</sup>, Fabiola Paoli Monteiro<sup>6,7</sup>, Brett H. Graham<sup>8</sup>, Sheryl Jackson<sup>9</sup>, Rebecca Sparkes<sup>9</sup>, Angela E. Scheuerle<sup>10</sup>, Sara Cathey<sup>5</sup>, Fernando Kok<sup>7,11</sup>, James B. Gibson<sup>12</sup> and Hudson H. Freeze<sup>1,\*</sup>

<sup>1</sup>Human Genetics Program, Sanford – Burnham – Prebys Medical Discovery Institute, La Jolla, CA; <sup>2</sup>Biochemical Genetics Laboratory, Mayo Clinic College of Medicine, Rochester, MN; <sup>3</sup>Dept of Genome Sciences, University of Washington, Seattle, WA; <sup>4</sup>Dept of Pediatrics, University of Washington, Seattle, WA; <sup>5</sup>Dept of Clinical Genetics, Greenwood Genetic Center, Charleston Office, North Charleston, SC; <sup>6</sup>Dept of Medical Genetics, University of Campinas (UNICAMP), São Paulo, Brazil; <sup>7</sup>Mendelics Genomic Analysis, São Paulo, São Paulo, Brazil; <sup>8</sup>Dept of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX; <sup>9</sup>Dept of Medical Genetics, University of Calgary, Calgary, AB, Canada; <sup>10</sup>Dept of Pediatrics, University of Texas Southwestern Medical Center, Dallas, TX; <sup>11</sup>Dept of Neurology, University of São Paulo, São Paulo, Brazil; <sup>12</sup>Clinical and Metabolic Genetics, Specially for Children, Austin, TX

Human Mutation, November 2015, 36(11): 1048–1051.

... Family 405 is of European ancestry and are the only family in which exome sequencing was not performed. Instead, an Affymetrix **CytoScan HD** microarray was performed at Greenwood Genetics Center and showed that the affected male (P4) was ...

93-

[Familial transmission of 5p13.2 duplication due to maternal der\(X\)ins\(X;5\)](#)

Lauren C. Walters-Sen, Kathy Windemuth, Katie Angione, Jenisha Nandhlal, Jeff M. Milunsky,

Center for Human Genetics, Inc., Cambridge, MA, USA

European Journal of Medical Genetics, May 2015, 58(5):305–309.

... first report of an inherited duplication of 5p13.2 with multiple affected family members. ... Analysis by **SNP 6.0** Microarray (Affymetrix ... in the consultand discovered a 341 kb duplication at 5p13.2 ... the proband's array was performed using the **Cytoscan HD** ...

94-

[First contiguous gene deletion causing biotinidase deficiency: The enzyme deficiency in three Sri Lankan children \[open access\]](#)

Danika Nadeen Senanayake a, Eresha. A. Jasinge b, Kirit Pindolia c, d, Jithangi Wanigasinghe e, Kristin Monaghan f, 1, Sharon F. Suchy f, Sainan Wei g, Subashini Jaysena b, Barry Wolf c, d

a Dept of Chemical Pathology, North Columbo Teaching Hospital, Colombo, Sri Lanka; b Chemical Pathology, Lady Ridgeway Hospital for Children, Colombo, Sri Lanka; c Dept of Research Administration, Henry Ford Health System, Detroit, MI 48202; d Center for Molecular Medicine and Genetics, Wayne State Univ School of Medicine, Detroit, MI 48201; e Pediatric Neurology, University of Colombo, Colombo, Sri Lanka; f GeneDx, Gaithersburg, MD 20877; g Dept of Pediatrics and Human Development, Michigan State Univ, East Lansing, MI 48824

Molecular Genetics and Metabolism Reports, May 2015, 2: 81-84.

We report three symptomatic children with profound biotinidase deficiency from Sri Lanka. All three children presented with typical clinical features of the disorder. ... High density SNP microarray studies were performed using Affymetrix **Cytoscan HD SNP Array™**.

95-

[Five patients with a chromosome 1q21.1 triplication show macrocephaly, increased weight and facial similarities](#)

Anke Van Dijck a, b, Ilse M. van der Werf a, Edwin Reyniers a, b, Stefaan Scheers a, b, Meron Azage c, Kiana Siefkas d, Nathalie Van der Aa a, Amy Lacroix e, Jill Rosenfeld f, Bob Argiropoulos g, h, Kellie Davis g, A. Micheil Innes g, h, Heather C. Mefford d, e, Geert Mortier a, b, Marije Meuwissen b, R. Frank Kooy a

a Dept of Medical Genetics, University of Antwerp, Belgium; b Dept of Medical Genetics, University Hospital Antwerp, Belgium; c Dept of Medical Genetics, Children's Hospital of Pittsburgh, PA, USA; d Dept of Medical Genetics, Seattle Children's Hospital, Seattle, WA, USA; e Dept of Pediatrics, University of Washington, Seattle, WA, USA; f Signature Genomic Laboratories, Spokane, WA, USA; g Dept of Medical Genetics, Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada; h Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada

European Journal of Medical Genetics, October 2015, 58(10): 503–508

... For the first time, we describe five patients, including monozygotic twins, with a triplication of the 1q21.1 chromosomal segment. ... SNP array analysis of the patient C-II.1 was performed with an Affymetrix **Cytoscan HD**. ...

96-

[Genetic alterations in renal cell carcinoma with rhabdoid differentiation](#)

Carmen M. Perrino, MDa, 1, Vishwanathan Huchtagowder, PhDa, 1, Michael Evenson, BSa, Shashikant Kulkarni, PhDa, Peter A. Humphrey, MD, PhD\*

\*Dept of Pathology, Yale School of Medicine, 310 Cedar St, LB11, PO Box 208023, New Haven, CT, 06520-8023.

Human Pathology, January 2015, 46(1):9–16.

Also presented at U.S. and Canadian Academy of Pathology Annual Meeting (USCAP), Mar 1-7, 2014, San Diego, CA, Abstr #1042.

... After extraction, DNA was subjected to **CytoScan HD array** (Affymetrix, Santa Clara, CA) assay using manufacturer's recommended protocol at Washington University's microarray core facility ...

97- **Meeting abstract**

[Genetic Analysis Using a High Density SNP Array in Myelodysplastic Syndrome: Clinical Utility and Comparative Analysis Study Compared to Metaphase Chromosome Analysis](#)

Sally Jeffries\*, 1, Nicola Trim\*, 2, Emma Huxley\*, 2, Laura Ford\*, 2, Manoj Raghavan\*, 3, Jane Soden\*, 2, and Michael John Griffiths, BSc\*, 2

1Birmingham Women's NHS Foundation Trust, West Midlands Regional Genetics Laboratory, Birmingham, UK;

2West Midlands Regional Genetics Laboratory, Birmingham, UK; 3Centre for Clinical Haematology, University Hospitals Birmingham NHS Foundation Trust, Birmingham, UK

Blood, 3 December 2015, 126(23): 5259.

There is no single technology capable of detecting the various genetic and genomic aberrations observed in patients with neoplasia. Patients with myelodysplastic syndrome (MDS) may present with chromosomal copy number changes (duplication, deletion, and amplification), balanced chromosome rearrangements, copy neutral loss of heterozygosity (CN-LOH) and/or gene mutations. Currently only microscopic chromosomal changes, as dictated by the international prognostic scoring system (IPSS-R), are used to determine the genetic risk in MDS. ... The Affymetrix **CytoScan® HD Array** is a high definition array with over 2.6 million markers (both copy number and SNP) allowing resolution capabilities way beyond that of metaphase chromosome analysis. The incorporation of 750,000 SNPs also allows for detection of CN-LOH, regions known to harbour bi-allelic gene mutations. A real-time comparative study using the Affymetrix **CytoScan® HD Array** against traditional metaphase chromosome analysis is being performed on patients with confirmed or highly suspected MDS referred for genetic analysis at the West Midlands Regional Genetics Laboratory, UK. The study is expected to utilise 600 arrays over two years at presentation and on serial surveillance samples. The preliminary results available after the first 100 patients are presented with examples demonstrating the capabilities and clinical utility of SNP array genetic analysis. ... The study so far, in patients with MDS at presentation, has demonstrated: •An increased number of genetic aberrations (CN changes

and CN-LOH) detected by SNP array (38/105 (36%) by metaphase analysis and 62/105 (60%) by SNP array analysis). ... Patient benefits are expected to be the potential to improve patient outcomes through improved confidence in diagnosis, prognosis and monitoring. Disclosures Jeffries: **Affymetrix: Research Funding.**

98-

[Genetic variation analysis in a Chinese Maffucci syndrome patient](#)

Yang Xue, MDa, Jinwen Ni, MSa, Mi Zhou, MSa, Weiqi Wang, MSb, Yuan Liu, MDc, Yaowu Yang, MDb, , (Professor), Xiaohong Duan, PHDa, , (Professor)

a State Key Laboratory of Military Stomatology, Department of Oral Biology, Clinic of Oral Rare and Genetic Diseases, School of Stomatology, the Fourth Military Medical University, 145 West Changle Road, Xi'an 710032, P. R. China; b State Key Laboratory of Military Stomatology, Department of Oral and Maxillofacial Surgery, School of Stomatology, the Fourth Military Medical University, 145 West Changle Road, Xi'an 710032, P. R. China; c State Key Laboratory of Military Stomatology, Department of Oral Histology and Pathology, School of Stomatology, the Fourth Military Medical University, 145 West Changle Road, Xi'an 710032, P. R. China

Journal of Cranio-Maxillofacial Surgery, September 2015, 43(7): 1248–1255.

... Genomic DNA was extracted from blood and a hemangioma sample from the patient, and also from her mother's blood, for chromosome microarray analysis (CMA) by Affymetrix **CytoScan HD** array. ... This is the first molecular genetic analysis report on a Chinese patient with Maffucci syndrome ...

99-

[Genome-wide analysis of the role of copy number variation in schizophrenia risk in chinese](#)

Zhiqiang Li, Ph.Da, b, c, Jianhua Chen, Ph.Da, d, Yifeng Xu, MDd, Qizhong Yi, MDe, Weidong Ji, MDc, f, Peng Wang, MDg, Jiawei Shen, Ph.Da, Zhijian Song, Ph.Da, Meng Wang, Ping Yang, MDg, Qingzhong Wang, Ph.Da, Guoyin Fengd, Benxiu Liu, MDh, Wensheng Sun, MDh, Qi Xu, MDi, Baojie Li, Ph.Da, Lin He, Ph.Da, c, j, Guang He, Ph.Da, Wenjin Li, Ph.Da, Zujia Wen, Ph.Da, Ke Liu, Ph.Da, Fang Huang, Juan Zhoua, Jue Jia, Xingwang Li, Ph.Da, Yongyong Shi, Ph.Da, b, c, e, f, k

a Bio-X Institutes, Key Laboratory for the Genetics of Developmental and Neuropsychiatric Disorders (Ministry of Education) and the Collaborative Innovation Center for Brain Science, Shanghai Jiao Tong University, Shanghai 200030, P.R. China; b Institute of Social Cognitive and Behavioral Sciences, Shanghai Jiao Tong University, Shanghai 200240, P.R. China; c Institute of Neuropsychiatric Science and Systems Biological Medicine, Shanghai Jiao Tong University, Shanghai 200042, P.R. China; d Shanghai Key Laboratory of Psychotic Disorders, Shanghai Mental Health Center, Shanghai Jiao Tong University School of Medicine, Shanghai 200030, P.R. China; e Dept of Psychiatry, the First Teaching Hospital of Xinjiang Medical University, Urumqi 830054, P.R. China; f Changning Mental Health Center, Shanghai 200042, P.R. China; g Wuhu Fourth People's Hospital, Wuhu 241002, P.R. China; h Longquan Mountain Hospital of Guangxi Province, Liuzhou 545005, P.R. China; i Nat Laboratory of Medical Molecular Biology, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, 100730, P.R. China; j Institutes of Biomedical Sciences, Fudan University, Shanghai 200032, P.R. China; k The Affiliated Hospital of Qingdao University, Qingdao 266003, P.R. China

Biological Psychiatry, online 26 November 2015, In Press, Accepted Manuscript

... Our data confirm increased genome-wide CNVs (> 500 Kb and < 1%) burden in schizophrenia, and the increasing trend was more significant when only > 1 Mb CNVs were considered. ... CNV validation by Affymetrix **CytoScan HD** Arrays. ...

100- **Meeting abstract**

[Genome-Wide Molecular Portrait of Aggressive Systemic Mastocytosis and Mast Cell Leukemia Depicted By Whole Exome Sequencing and Copy Number Variation Analysis](#)

Simona Soverini, PhD<sup>1</sup>, Caterina De Benedittis, PhD<sup>\*1</sup>, Manuela Mancini, PhD<sup>\*1</sup>, Michela Rondoni, MD<sup>\*2</sup>, Cristina Papayannidis, MD PhD<sup>3</sup>, Antonella Padella<sup>\*4</sup>, Giorgina Specchia, Pr, MD<sup>5</sup>, Roberta Zanotti, MD<sup>\*6</sup>, Livio Pagano<sup>\*7</sup>, Viviana Guadagnuolo, PhD<sup>\*1</sup>, Maria Chiara Fontana<sup>\*1</sup>, Massimo Delledonne, PhD<sup>\*8</sup>, Alberto Ferrarini, PhD<sup>\*9</sup>, Italo Do Valle<sup>\*10</sup>, Daniel Remondini, PhD<sup>\*11</sup>, Gastone Castellani<sup>\*12</sup>, Raffaele Calogero<sup>\*13</sup>, Serena Merante, MD<sup>\*14</sup>, Chiara Elena, MD<sup>\*14</sup>, Peter Valent, MD<sup>15</sup>, Michele Cavo<sup>\*16</sup>, and Giovanni Martinelli, MD PhD<sup>3</sup>

<sup>1</sup>"Seràgnoli" Institute of Hematology, Bologna University School of Medicine, Bologna, Italy; <sup>2</sup>Area Vasta Romagna, Centro ServiziPievesestina, AUSL Romagna, Pievesestina di Cesena (FC), Italy; <sup>3</sup>Bologna University School of Medicine, Bologna, Italy; <sup>4</sup>University of Bologna, Bologna, Italy; <sup>5</sup>Department of Emergency and Organ Transplantation, Section of Hematology with Transplantation, Medical Sch, University of Bari, Bari, Italy; <sup>6</sup>Section of Haematology, Verona, Italy; <sup>7</sup>Institute of Hematology, Catholic University, Rome, Italy; <sup>8</sup>Personal Genomics, Verona, Italy; <sup>9</sup>Dep of Biotechnology, University of Verona, Verona, Italy; <sup>10</sup>CAPES Foundation, Ministry of Education of Brazil, Brasília, Brazil; <sup>11</sup>Dept of Physics and Astronomy, University of Bologna, Bologna, Italy; <sup>12</sup>Department of Physics and Astronomy, University of Bologna, Bologna, Italy; <sup>13</sup>University of Turin, Bioinformatics and Genomics Unit, Turin, Italy; <sup>14</sup>Policlinico S. Matteo IRCCS, Pavia, Italy; <sup>15</sup>Ludwig Boltzmann Cluster Oncology, Medical University of Vienna, Vienna, Austria; <sup>16</sup>Seràgnoli Institute of Hematology, Bologna University School of Medicine, Bologna, Italy.

Blood, 3 December 2015, 126 (23): 4085.

... A discovery panel including 6 patients with ASM and 6 patients with MCL was studied using whole exome sequencing (WES) and copy number variation (CNV) analysis. WES (80x) was performed on a HiSeq 2500 (Illumina). CNV was done using **Cytoscan HD Arrays** (Affymetrix). ...

101-

[Genome-wide profiling of HPV integration in cervical cancer identifies clustered genomic hot spots and a potential microhomology-mediated integration mechanism](#)

Zheng Hu, Da Zhu, Wang, Weiyang Li, Wenlong Jia, Xi Zeng, Wencheng Ding, Lan Yu, Xiaoli Wang, Liming Wang, Hui Shen, Changlin Zhang, Hongjie Liu, Xiao Liu, Yi Zhao, Xiaodong Fang, Shuaicheng Li, Wei Chen, Tang Tang, Aisi Fu, Zou Wang, Gang Chen, Qinglei Gao, Shuang Li, Ling Xi  
Nature Genetics, 2015, 47: 158–163.

... Ligated DNA was amplified, fragmented, end-labeled with biotin and then hybridized to an Affymetrix **CytoScan HD** Array.

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[Genomic Alterations in Ethanol-Exposed Trophoblast Cell Lines Induced by Chronic Ethanol Treatment](#)

Sergi Clave<sup>1,2,7</sup>, Xavier Joya<sup>1,2</sup>, Anna Puiggros<sup>3</sup>, Marta Bódalo<sup>4</sup>, Judith Salat-Batlle<sup>1,2</sup>, Marta Salido<sup>3</sup>, Blanca Espinet<sup>3</sup>, Óscar Garcia-Algar<sup>1,2,5,6,\*</sup> and Oriol Vall<sup>1,2,5,6</sup>  
1Grup de Recerca Infància i Entorn (GRIE), Institut Hospital del Mar d'Investigacions Mèdiques (IMIM), Barcelona, Spain; 2Red de Salud Materno-Infantil y del Desarrollo (SAMID), Programa RETIC, Fondos FEDER, Instituto Carlos III, Madrid, Spain; 3Laboratori de Citogenètica Molecular. Servei de Patologia, Hospital del Mar, Barcelona, Spain; 4Servei d'Anàlisi de Microarrays, Institut Hospital del Mar d'Investigacions Mèdiques (IMIM), Barcelona, Spain; 5Departament Pediatria, Obstetrícia i Ginecologia, i Medicina Preventiva, Universitat Autònoma Barcelona (UAB), Bellaterra, Spain; 6Servei de Pediatria, Parc de Salut Mar, Barcelona, Spain; 7Laboratori de Citogenètica Molecular. Servei de Patologia, Hospital del Mar, Barcelona, Spain  
Journal of Steroids & Hormonal Science, 2015, 6: 3.

... The aim of this study is to determine ethanol-caused genomic alterations in placental cell lines after a repeated ethanol treatment in order to describe new genomic targets of cell damage. ...

Genomewide high resolution Single Nucleotide Polymorphisms (SNPs) array **CytoScan HD** (Affymetrix, Santa Clara, CA, USA) was used ...

103-

[Genomic analysis of clonal origin of Langerhans cell histiocytosis following acute lymphoblastic leukaemia](#)

Motohiro Kato<sup>1,2,3,†</sup>, Masafumi Seki<sup>1,†</sup>, Kenichi Yoshida<sup>4</sup>, Yusuke Sato<sup>4</sup>, Ryo Oyama<sup>5</sup>, Yuki Arakawa<sup>5</sup>, Hiroshi Kishimoto<sup>6</sup>, Tomohiko Taki<sup>7</sup>, Masaharu Akiyama<sup>8</sup>, Yuichi Shiraishi<sup>9</sup>, Kenichi Chiba<sup>9</sup>, Hiroko Tanaka<sup>10</sup>, Noriko Mitsuiki<sup>11</sup>, Michiko Kajiwara<sup>11</sup>, Shuki Mizutani<sup>11</sup>, Masashi Sanada<sup>4,12</sup>, Satoru Miyano<sup>9,10</sup>, Seishi Ogawa<sup>4</sup>, Katsuyoshi Koh<sup>5</sup> and Junko Takita<sup>1</sup>

1Dept of Paediatrics, University of Tokyo, Tokyo, Japan; 2Div of Transplantation and Cell Therapy, Children's Cancer Centre, Tokyo, Japan; 3Dept of Paediatric Haematology and Oncology Research, Natl Centre for Child Health and Development, Tokyo, Japan; 4Dept of Pathology and Tumor Biology, Kyoto Univ, Kyoto, Japan; 5Dept of Haematology/Oncology, Saitama Children's Medical Centre, Saitama, Japan; 6Dept of Pathology, Saitama Children's Medical Centre, Saitama, Japan; 7Dept of Molecular Diagnostics and Therapeutics, Kyoto Prefectural Univ of Medicine Graduate School of Medical Science, Kyoto, Japan; 8Dept of Paediatrics, Jikei University School of Medicine, Tokyo, Japan; 9Laboratory of DNA Information Analysis, Human Genome Centre, Institute of Medical Science, University of Tokyo, Tokyo, Japan; 10Laboratory of Sequence Data Analysis, Human Genome Centre, Institute of Medical Science, University of Tokyo, Tokyo, Japan; 11Dept of Paediatrics, Tokyo Medical and Dental University, Tokyo, Japan; 12Dept of Advanced Diagnosis, Clinical Research Centre, National Hospital Organization, Nagoya Medical Centre, Nagoya, Japan.

British Journal of Haematology, first published online: 5 November 2015

... DNA extracted from the obtained samples was analysed using SNP-chip (GeneChip **Human Mapping 250K Nspl/Cytoscan HD**; Affymetrix, ... LCH is not a secondary malignancy ... but was instead derived from a founding clone with genomic alterations common to ALL.

104--

[Genomic copy number variation affecting genes involved in the cell cycle pathway: implications for somatic mosaicism](#)

Ivan Y. Iourov,<sup>1,2,3</sup> Svetlana G. Vorsanova,<sup>1,2</sup> Maria A. Zelenova,<sup>1,2</sup> Sergei A. Korostelev,<sup>4</sup> and Yuri B. Yurov<sup>1,2</sup>

1Mental Health Research Center, Moscow 117152, Russia; 2Separated Structural Unit "Clinical Research Institute of Pediatrics", Pirogov Russian National Research Medical University, Ministry of Health of Russian Federation, Moscow 125412, Russia; 3Dept of Medical Genetics, Russian Medical Academy of Postgraduate Education, Moscow 123995, Russia; 4I.M. Sechenov First Moscow Medical University, Moscow 119991, Russia  
International Journal of Genomics, 2015, 2015:Article ID 757680.

... Here, we have evaluated genomic copy number variation (CNV) in genes implicated in the cell cycle pathway (according to Kyoto Encyclopedia of Genes and Genomes/KEGG) within a cohort of patients with intellectual disability, autism, epilepsy and/or congenital malformations, in which the phenotype was not associated with genomic rearrangements altering this pathway. ... Genomic CNVs were analyzed using **CytoScan HD Arrays** (Affymetrix, Santa Clara, CA) consisting of approximately 2.7 million markers for CNV evaluation and approximately 750,000 SNPs.

105-

[Genomic Instability of Osteosarcoma Cell Lines in Culture: Impact on the Prediction of Metastasis Relevant Genes](#)

Roman Muff, Prisni Rath, Ram Mohan Ram Kumar, Knut Husmann, Walter Born, Michael Baudis, Bruno Fuchs

PLoS ONE, May 19, 2015, 10(5): e0125611.

... Microarray CGH was performed with the **CytoScan HD Array Kit** (Affymetrix, Santa Clara, CA) according to the instructions of the manufacturer at the Laboratory for Oncology Diagnostics (Kinderspital Zurich, Switzerland).

106-

[Genomic Landscape of Primary Mediastinal B-Cell Lymphoma Cell Lines](#)

Haiping Dai, Stefan Ehrentraut, Stefan Nagel, Sonja Eberth, Claudia Pommerenke, Wilhelm G. Dirks, Robert Geffers, Sri laxmi Kalavalapalli, Maren Kaufmann, Corrina Meyer, Silke Faehrich, Suning Chen, Hans G. Drexler, Roderick A. F. MacLeod

PLOS ONE, 23 November 2015, 10(11): e0139663.

... **CytoScan High Density Arrays** which combine oligonucleotide and SNP probes (Affymetrix, High Wycombe/UK) were used to detect genomic copy number alterations/gains/losses (CNA/G/L), losses of heterozygosity (LOH) and unbalanced chromosome translocation breakpoints at high resolution. ... Samples were hybridized to Affymetrix GeneChip **HG-U133 2.0 Plus** for 16 h at 45°C. ... For microRNA profiling the Affymetrix **GeneChip miRNA 2.0** system was used together with samples drawn from the DSMZ cell bank as comparison data sets.

107- **Meeting abstract**

[Genomic Landscape Predictive of Minimal Residual Disease \(MRD\) in Multiple Myeloma \(MM\)](#)

Mehmet K Samur, PhD\*,1,2, Stephane Minvielle\*,3, Florence Magrangeas\*,3, Giovanni Parmigiani, PhD\*,1, Kenneth C Anderson4, Philippe Moreau, MD\*,5, Michel Attal6, Hervé Avet-Loiseau, MD\*,7, and Nikhil C. Munshi, MD8,2

1Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston, MA ; 2LeBow Institute for Myeloma Therapeutics and Jerome Lipper Multiple Myeloma Center, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA ; 3Centre Hospitalier Universitaire de Nantes, Unité Mixte de Genomique du Cancer, Nantes, France ; 4The Jerome Lipper Multiple Myeloma Center, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA ; 5Nantes University Hospital, Hôtel Dieu, Nantes, France ; 6Institut Universitaire du Cancer de Toulouse-Oncopole, Toulouse, France ; 7Centre de Recherche en Cancérologie de Toulouse Institut National de la Santé, Toulouse, France ; 8VA Medical Hospital, Boston, MA

Blood, 3 December, 2015, 126(23): 4212.

... Here we are evaluating the genomic alterations that may predict attainment of MRD negative status in MM. MRD status was evaluated in 279 patients from IFM/DFCI 2009 trial. We obtained gene expression by RNA-seq, and copy number profile by **cytoScan HD array** to evaluate genomic differences between MRD negative and MRD positive groups. We generated copy number data for 175 / 279 patients (72 MRD- and 103 MRD+) with Affymetrix **Cytoscan HD array** and compared genome wide copy number alterations. ... In conclusion, we here report a first genomic landscape predictive of minimal residual disease (MRD) in Multiple Myeloma (MM). ...

108-

[Genomic microarray in fetuses with increased nuchal translucency and normal karyotype - a systematic review and meta-analysis](#)

Maribel Grande1, Fenna A.R. Jansen2, Yair J. Blumenfeld3, Allan Fisher4, Anthony O. Odibo5, Monique C. Haak2 and Antoni Borrell1,\*

1Dept of Maternal-Fetal Medicine, Institute Gynecology, Obstetrics and Neonatology, Hospital Clinic of Barcelona, Catalonia, Spain; 2Leiden University Medical Center, Department of Obstetrics and Fetal Medicine, Leiden, The Netherlands; 3Dept of Obstetrics & Gynecology, Stanford University School of Medicine, Stanford, California, USA; 4Elliot Health System, Manchester, New Hampshire, USA; 5Dept of Obstetrics & Gynecology, Division of Maternal Fetal Medicine, University of South Florida, Tampa, Florida, USA

Ultrasound in Obstetrics & Gynecology, Accepted manuscript online: 20 April 2015

...systematic review of the literature ...and estimate the incremental yield of genomic microarray over karyotyping in fetuses with increased nuchal translucency diagnosed by first trimester prenatal ultrasound. ...**Whole Genome 2.7M SNP array** or **Cytoscan HD SNP array** ...



109-

[Genomic profile of a Li-Fraumeni-like syndrome patient with a 45,X/46,XX karyotype, presenting neither mutations on TP53 nor clinical stigmata of Turner syndrome](#)

Tatiane R. Basso, Rolando A.R. Villacis, Luisa M. Canto, Vinicius M.F. Alves, Rainer M.L. Lapa, Amanda F. Nobrega, Maria I. Achatz, Silvia R. Rogatto

Cancer Genetics, June 2015, 208(6): 341–344.

... Genome-wide analysis of copy number variations (CNVs) was assessed in DNA from peripheral blood cells and saliva (Affymetrix **CytoScan HD**).

110- *One sentence comment only*

[Genomic Variants Revealed by Invariably Missing Genotypes in Nelore Cattle](#)

Joaquim Manoel da Silva, Poliana Fernanda Giachetto, Luiz Otávio Campos da Silva, Leandro Carrijo Cintra, Samuel Rezende Paiva, Alexandre Rodrigues Caetano, Michel Eduardo Beleza Yamagishi

PLOS ONE, 25 August 2015, 10(8): e0136035.

... Our study has shown that often-discarded missing genotypes can be effectively used to identify population-specific genomic variants which in turn can be used in a wide range of applications. ... Companies that manufacture genotyping chips could develop denser HD genotyping chips and minimize this weakness by designing probes to cover every non-repetitive loci in the genome under study. This prospect is a trend at least in humans as the **CytoScanHD Human array** from Affymetrix has 2.67 million probes, 1.9 of which are non-polymorphic and designed to empower the results of CNV studies, but which are also compatible with our approach.

111- *Meeting abstract*

[Genomic-Wide Analysis By High Resolution SNP Array Identifies Novel Genomic Alteration in Acute Myeloid Leukemia](#)

Maria Chiara Fontana\*,1, Viviana Guadagnuolo, PhD\*,2, Cristina Papayannidis, MD PhD3, Giorgia Simonetti, PhD\*,2, Antonella Padella\*,2, Anna Ferrari, PhD\*,2, Marco Manfrini, PhD\*,3, Italo Faria do Valle\*,4,5, Barbara Santacroce\*,6, Margherita Perricone\*,7, Giovanni Marconi, MD\*,2, Emanuela Ottaviani\*,2, Jelena D. Milosevic Feenstra, PhD\*,8, Doris Chen, PhD\*,8, Nicole C.C. Them\*,8, Simona Soverini9, Daniel Remondini, PhD\*,5, Gerardo Musuraca\*,10, Michele Cavo, MD\*,11, Robert Kralovics, PhD8, and Giovanni Martinelli11

1Seragnoli Institute, University of Bologna, Bologna, Italy; 2University of Bologna, Bologna, Italy; 3Bologna University School of Medicine; 4Ministry of Education of Brazil, CAPES Foundation, Brazilia, Brazil; 5Dept of Physics and Astronomy, University of Bologna, Bologna, Italy; 6DIMES - Department of Experimental, Diagnostic and Specialty Medicine, Institute of Hematology, University of Bologna, Bologna, Italy; 7Institute of Hematology "Seragnoli", University of Bologna, Bologna, Italy; 8CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria; 9Institute of Hematology, S.Orsola-Malpighi University Hospital, Bologna, Italy; 10Istituto Scientifico Romagnolo Per Lo Studio E La Cura Dei Tumori, Meldola (FC), Meldola, Italy; 11"Seràgnoli" Institute of Hematology, University of Bologna, Bologna, Italy

Blood, 3 December 2015, 126(23): 2600.

Introduction: Novel array-based technique-single-nucleotide polymorphism (SNP) microarray can detect cytogenetic lesions mostly involving structural alterations with losses or gains of chromosomal material. ... **SNP microarray** can also detect copy-neutral loss of heterozygosity (CN-LOH), ... We analyzed 279 AML patients (pts) at diagnosis by **SNP Array 6.0** or **Cytoscan HD Array** (Affymetrix). ... By SNP array we have identified CNAs involving novel potential leukemia-related genes. Our results suggest that the comparison between SNP and WES data could provide important findings on the prognosis of AML pts. ...

112-

[Giant breast tumors in a patient with Beckwith–Wiedemann syndrome](#)

Gerarda Cappuccio1,\* , Agostina De Crescenzo2, Giuseppe Ciancia3, Luigi Canta4, Marzia Moio4, Ilaria Mataro4, Valeria Varone3, Guido Pettinato3, Orazio Palumbo5, Massimo Carella5, Andrea Riccio2,6, Nicola Brunetti-Pierri1,7

1Dept of Translational Medicine, Section of Pediatrics, Federico II University, Naples, Italy; 2Dept of Environmental, Biological and Pharmaceutical Sciences and Technologies at the Second University of Naples, Naples, Italy; 3Dept of Pathology, Federico II University, Naples, Italy; 4Dept of Plastic Surgery, Federico II University, Naples, Italy; 5Medical Genetics Unit, IRCCS Casa Sollievo Della Sofferenza Hospital, San Giovanni Rotondo, Italy; 6Institute of Genetics and Biophysics A. Buzzati-Traverso at the Consiglio Nazionale delle Ricerche (CNR), Naples, Italy; 7Telethon Institute of Genetics and Medicine, Naples, Italy

American Journal of Medical Genetics Part A, January 2014, 164(1):182–185.

... Further investigations with a SNP array performed by **CytoScan HD array** (Affymetrix, Santa Clara, CA) ruled out the presence of smaller (<100 kb) deletion/duplications on chromosome 11p15.5 which are found very rarely in BWS [Begemann et al., 2012].

113-

[Global patterns of large copy number variations in the human genome reveal complexity in chromosome organization](#)

AVINASH M. VEERAPPA<sup>a1</sup>, RAVIRAJ V. SURESHA<sup>a1</sup> †, SANGEETHA VISHWESWARAIAH<sup>a1</sup> †, KUSUMA LINGAIAH<sup>a1</sup> †, MEGHA MURTHY<sup>a1</sup> †, DINESH S. MANJEGOWDA<sup>a2</sup>, PRAKASH PADAKANNAYAA<sup>a3</sup> and NALLUR B. RAMACHANDRA<sup>a1</sup> c1  
a1 Genetics and Genomics Lab, Dept of Studies in Genetics & Genomics, University of Mysore, Manasagangotri, Mysore-06, Karnataka, India; a2 Nitte University Centre for Science Education & Research, K. S. Hegde Medical Academy, Nitte, University, Deralakatte, Mangalore-18, Karnataka, India; a3 Dept of Studies in Psychology, University of Mysore, Manasagangotri, Mysore-06, Karnataka, India

Genetics Research (Cambridge), online 22 September 2015, 97: e18.

... analysis was performed using the Affymetrix Genome-Wide Human **SNP Array 6.0** chip and **CytoScan High-Density arrays**. ... established the first drafts of population-specific CNV maps providing a rationale for prioritizing chromosomal regions.

114-

[Global Spectrum of Copy Number Variations Reveals Genome Organizational Plasticity and Proposes New Migration Routes](#)

Avinash M. Veerappa, Sangeetha Vishweswaraiah, Kusuma Lingaiah, Megha Murthy, Raviraj V. Suresh, Dinesh S. Manjegowda, Nallur B. Ramachandra  
PLoS ONE, 24 April 2015, 10(4): e0121846.

... Genome-wide genotyping was performed using an Affymetrix Genome-wide Human **SNP Array 6.0** chip and Affymetrix **CytoScan High-Density (HD) Array** having 1.8 million and 2.6 million combined SNP and CNV markers with the median inter- marker distance of 500–600 bases ... These chips provide maximum panel power and the highest physical coverage of the genome [47–50].

115-

[Heterozygous deletion at the SOX10 gene locus in two patients from a Chinese family with Waardenburg syndrome type II](#)

He Wenzhi a, 1, Wen Ruijin b, 1, Li Jieliang a, 2, Ma Xiaoyan a, Liu Haibo a, Wang Xiaoman a, Xian Jiajia a,

Li Shaoying a, Li Shuanglin a, Li Qing a,

a Key Laboratory for Major Obstetric Diseases of Guangdong Province, Key Laboratory of Reproduction and Genetics of Guangdong Higher Education Institutes, Experimental Department of Institute of Gynecology and Obstetrics, The Third Affiliated Hospital of Guangzhou Medical University, Guangzhou 510150, Guangdong, China; b Dept of Otolaryngology, Guangzhou Women and Children's Medical Center, Guangzhou 510623, Guangdong, China

International Journal of Pediatric Otorhinolaryngology, October 2015, 79(10): 1718–1721

... This report is the first to describe SOX10 heterozygous deletions in Chinese WS2 patients. ... Array-CGH was performed using the Affymetrix **CytoScan HD** platform (Affymetrix, Santa Clara, USA).

116-

[High resolution single nucleotide polymorphism array reveals cryptic indicating information about myelodysplastic syndrome-related myeloid malignancies](#)

Kun Chiab, Yang Lib, Qiulan Dingc, Lan Xud, Yu Chend & Xuefeng Wangc\*

a Dept of Laboratory Medicine, Qingdao Women & Children's Hospital, Qingdao, China; b State Key Laboratory of Medical Genomics, Shanghai Institute of Hematology, Shanghai, China; c Dept of Laboratory Medicine, Shanghai, China; d Dept of Hematology, Ruijin Hospital, Shanghai Jiaotong University School of Medicine, Shanghai, China  
Leukemia & Lymphoma, 2015, 56(10): 2969-2972.

... Genomic hybridization of the extracted DNA was performed with a **CytoScan™ HD array** (Affymetrix ... UPDs were detected in 20 patients (60.6%) by **CytoScan™ HD array**.

117-

[Histo-genomic stratification reveals the frequent amplification/overexpression of CCNE1 and BRD4 genes in non-BRCAness high grade ovarian carcinoma](#)

Oumou Goundiam<sup>1,2,3,†,\*</sup>, Pierre Gestraud<sup>4,5,6,†</sup>, Tatiana Popova<sup>7,†</sup>, Thibault De la Motte Rouge<sup>8</sup>, Virginie Fourchette<sup>9</sup>, David Gentien<sup>3</sup>, Philippe Hupé<sup>4,5,6,10</sup>, Véronique Becette<sup>1</sup>, Claude Houdayer<sup>1,7,11</sup>, Sergio Roman-Roman<sup>3</sup>, Marc-Henri Stern<sup>1,7</sup>, Xavier Sastre-Garau<sup>1,2</sup>

<sup>1</sup>Dept of Biopathology, Institut Curie, Paris, France; <sup>2</sup>EA4340-BCOH, Versailles Saint-Quentin-en-Yvelines University, Guyancourt, France; <sup>3</sup>Department of Translational Research, Institut Curie, Paris, France;

<sup>4</sup>Bioinformatics and Computational Systems Biology of Cancer, Institut Curie, Paris, France; <sup>5</sup>Mines Paris Tech,

Paris, France; 6Inserm U900, Paris, France; 7Inserm U830 Institut Curie, Paris, France; 8Dept of Medical Oncology, Institut Curie, Paris, France; 9Dept of Surgery, and on behalf of the Gynecologic Study Group, Institut Curie, Paris, France; 10CNRS UMR 144; 11Université Paris Descartes, Sciences Pharmaceutiques et Biologiques, Sorbonne Paris Cité, Paris, France

International Journal of Cancer, 15 October 2015, 137(8): 1890–1900.

... Copy number and expression arrays DNA samples (105 tumors) were hybridized on **Cytoscan® HD** arrays (Affymetrix)

118-

[Homozygosity Mapping and Targeted Sanger Sequencing Reveal Genetic Defects Underlying Inherited Retinal Disease in Families from Pakistan](#)

Maleeha Maria , Muhammad Ajmal , Maleeha Azam , Nadia Khalida Waheed, Sorath Noorani Siddiqui,

Bilal Mustafa, Humaira Ayub, Liaqat Ali, Shakeel Ahmad, Shazia Micheal, Alamdar Hussain, Syed Tahir Abbas Shah, Syeda Hafiza Benish Ali, Waqas Ahmed, Yar Muhammad Khan, Anneke I. den Hollander, Lonneke Haer-Wigman, Rob W. J. Collin, Muhammad Imran Khan , Raheel Qamar , Frans P. M. Cremers

PLoS ONE 10(3): e0119806.

... Genetic linkage analysis was carried out for 53 of 81 families using microsatellite markers or whole genome SNP array platforms such as Illumina\_10K, **Affymetrix\_6K**, Human Omni express\_700k and **Cytoscan HD** (Fig. 1, Table 1).

119-

[Homozygosity mapping of autosomal recessive intellectual disability loci in 11 consanguineous Pakistani families](#)

Iltaf Ahmed 1,2, Muhammad Arshad Rafiq 1, John B. Vincent 1,3,4, Attya Bhatti 2, Muhammad Ayub 5, Peter John 2

1 Molecular Neuropsychiatry & Development (MiND) Lab, Centre for Addiction and Mental Health, Campbell Family Mental Health Research Institute, Toronto, Ontario, Canada ; 2 Atta-ur-Rehman School of Applied Biosciences (ASAB), Natl University of Sciences and Technology (NUST), Islamabad, Pakistan ; 3 Dept of Psychiatry, University of Toronto, Toronto, Ontario, Canada ; 4 Institute of Medical Science, University of Toronto, Toronto, Ontario, Canada; 5 Dept of Psychiatry, Div of Developmental Disabilities, Queen's University, Kingston, Ontario, Canada

Acta Neuropsychiatrica, February 2015, 27(1):38-47.

... Microarray genotyping (**Affymatrix 250K**) was performed to identify homozygosity-by-descent (HBD) in all affected families. ... In total, 15 healthy and 44 affected individuals were genotyped, using either Affymetrix **250K Nspl (Affymetrix, Santa Clara, CA, USA)** or Affymetrix® **CytoScan™ HD Array (Affymetrix)**, and for one family using Illumina CoreExome beadchip arrays ...

120-

[Identification of disrupted AUTS2 and EPHA6 genes by array painting in a patient carrying a de novo balanced translocation t\(3;7\) with intellectual disability and neurodevelopment disorder](#)

Anouck Schneider1,\* , Jacques Puechberty2, Bee Ling Ng3, Christine Coubes2, Vincent Gatinois1, Magali Tournaire1, Manon Girard1, Bruno Dumont1, Pauline Bouret1, Julia Magnetto4, Amaria Baghdadi4, Franck Pellestor1 and David Geneviève1,2

1Laboratoire de Génétique Chromosomique, Plateforme de puces à ADN, CHRU de Montpellier, France; 2Département de Génétique Médicale, CHRU de Montpellier, France; 3Cytometry Core Facility, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK; 4CRA, Département de Psychiatrie de l'Enfant et de l'Adolescent, Centre de Ressources Autisme, CHRU de Montpellier, France

American Journal of Medical Genetics Part A, December 2015, 167(12): 3031–3037.

... we used the high resolution GeneChip® Human Mapping **Cytoscan HD Array (Affymetrix)**.

121-

[Identifying the similarities and differences between single nucleotide polymorphism array \(SNPa\) analysis and karyotyping in acute myeloid leukemia and myelodysplastic syndromes](#)

Thiago Rodrigo de Noronha, Sandra Serson Rohr, Maria de Lourdes Lopes Ferrari Chauffaille

Revista Brasileira de Hematologia e Hemoterapia, Jan-Feb 2015, 37(1):48-54.

...Twenty-two patients diagnosed with acute myeloid leukemia and three with myelodysplastic syndromes were studied. The G-banding karyotyping and single nucleotide polymorphism array analysis (**CytoScan® HD**) were performed using cells from bone marrow, DNA extracted from mononuclear cells from bone marrow and buccal cells (BC).

122-

[Impaired PRC2 activity promotes transcriptional instability and favors breast tumorigenesis](#)

Michel Wassef<sup>1,2,3</sup>, Veronica Rodilla<sup>1,2,3</sup>, Aurélie Teissandier<sup>1,4,5</sup>, Bruno Zeitouni<sup>1,4,5</sup>, Nadege Gruel<sup>1</sup>, Benjamin Sadacca<sup>1</sup>, Marie Irondele<sup>1</sup>, Margaux Charruel<sup>1,2,3</sup>, Bertrand Ducos<sup>6,7,8</sup>, Audrey Michaud<sup>1,2,3</sup>, Matthieu Caron<sup>1,2,3</sup>, Elisabetta Marangoni<sup>1</sup>, Philippe Chavrier<sup>1</sup>, Christophe Le Tourneau<sup>9,10</sup>, Maud Kamal<sup>9</sup>, Eric Pasmant<sup>11,12,13</sup>, Michel Vidaud<sup>11,12,13</sup>, Nicolas Servant<sup>1,4,5</sup>, Fabien Reyat<sup>1</sup>, Dider Meseure<sup>1,14</sup>, Anne Vincent-Salomon<sup>1</sup>, Silvia Fre<sup>1,2,3</sup> and Raphaël Margueron<sup>1,2,3</sup>

<sup>1</sup>Institut Curie, Paris Sciences et Lettres Research University, 75005 Paris, France; <sup>2</sup>U934, Institut National de la Santé et de la Recherche Médicale, 75005 Paris, France; <sup>3</sup>UMR3215, Centre National de la Recherche Scientifique, 75005 Paris, France; <sup>4</sup>U900, Institut National de la Santé et de la Recherche Médicale, 75005 Paris, France; <sup>5</sup>Mines ParisTech, 77300 Fontainebleau, France; <sup>6</sup>Laboratoire de Physique Statistique-Ecole Normale Supérieure de Paris, Centre National de la Recherche Scientifique, 75005 Paris, France; <sup>7</sup>UMR 8550, Centre National de la Recherche Scientifique, 75005 Paris, France; <sup>8</sup>Plateforme de PCR Quantitative à Haut Débit Genomic Paris Centre, Institut de Biologie de l'École Normale Supérieure, 75005 Paris, France; <sup>9</sup>Dept of Medical Oncology, Institut Curie, 75005 Paris, France; <sup>10</sup>EA7285, Université de Versailles, Saint-Quentin-en-Yvelines, 78000 Versailles, France; <sup>11</sup>UMR\_S745, EA7331, Institut National de la Santé et de la Recherche Médicale, 75006 Paris, France; <sup>12</sup>Faculté des Sciences Pharmaceutiques et Biologiques, Université Paris Descartes, Sorbonne Paris Cité, 75006 Paris, France; <sup>13</sup>Service de Biochimie et Génétique Moléculaire, Assistance Publique-Hôpitaux de Paris, Hôpital Cochin, 75014 Paris, France; <sup>14</sup>Platform of Investigative Pathology, 75005 Paris, France

Genes & Development, 2015, 29: 2547-2562.

... provides an unexpected understanding of EZH2's contribution to solid tumors ... in breast cancer metastases previously analyzed by Affymetrix **CytoScan** arrays ... Transcriptome data analysis ... using Affymetrix **Mouse Gene 1.1 ST arrays** ...

123-

[Influence of total genomic alteration and chromosomal fragmentation on response to a combination of azacitidine and lenalidomide in a cohort of patients with very high risk MDS](#)

Christina Ganster a, Katayoon Shirneshan a, Gabriela Salinas-Riester b, Friederike Braulke a, Julie Schanz a, Uwe Platzbecker c, 1, Detlef Haase a, 1

a Dept of Hematology and Medical Oncology, University Hospital, University Göttingen, Göttingen, Germany; b DNA Microarray Facility, Georg August Univ, Göttingen, Germany; c Medical Clinic and Polyclinic I, Univ Hospital, Technical University Dresden, Dresden, Germany

Leukemia Research, October 2015, 39(10): 1079–1087.

... The **CytoScan HD array** (17 samples) and the Genome-Wide Human **SNP 6.0 array** (one sample) were used for MK (both Affymetrix, Santa Clara, CA, USA).

124-

[Inherited 15q24 microdeletion syndrome in twins and their father with phenotypic variability](#)

Lena Samuelsson, Theofanis Zagoras, Maria Hafström

European Journal of Medical Genetics, February 2015, 58(2):111–115.

regarding cases of intellectual deficiency in children.

... Samples were analysed by high-density SNP array using the Genome-Wide Human **SNP 6.0 Array**, and **CytoScan HD** from Affymetrix. ... high-resolution SNP array (**CytoScan HD** from Affymetrix) in the twin brother and father showed that deletion breakpoints are similar in the three cases, with no differences in genetic content ...

125-

[Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma](#)

Masafumi Seki, Riki Nishimura, Kenichi Yoshida, Teppei Shimamura, Yuichi Shiraishi, Yusuke Sato, Motohiro Kato, Kenichi Chiba, Hiroko Tanaka, Noriko Hoshino, Genta Nagae, Yusuke Shiozawa, Yusuke Okuno, Hajime Hosoi, Yukichi Tanaka, Hajime Okita, Mitsuru Miyachi, Ryota Souzaki, Tomoaki Taguchi, Katsuyoshi Koh, Ryoji Hanada, Keisuke Kato, Yuko Nomura, Masaharu Akiyama, Akira Oka, Takashi Igarashi, Satoru Miyano, Hiroyuki Aburatani, Yasuhide Hayashi, Seishi Ogawa, Junko Takita

Nature Communications, 3 July 2015, 6:Article #7557

... DNA extracted from RMS samples was subjected to SNP array analysis using Affymetrix **GeneChip 250K Nsp** or **CytoScan HD** (Affymetrix) according to the manufacturer's protocol.

126-

[Integrated genomics elucidates relative spatial homogeneity of embryonal brain tumors](#)

Marc Remke<sup>12\*</sup>, Florence Cavalli<sup>1</sup>, A Sorana Morrissy<sup>1</sup>, Vijay Ramaswamy<sup>1</sup>, David Jones<sup>3</sup>, Roger Packer<sup>4</sup>, Eric Bouffet<sup>1</sup>, Gary Bader<sup>5</sup>, Arndt Borkhardt<sup>2</sup>, Stefan Pfister<sup>3</sup>, Nada Jabado<sup>6</sup>, Marco Marra<sup>7</sup>, Michael D Taylor<sup>1</sup>

<sup>1</sup> Hospital for Sick Children, Toronto, Ontario, Canada; <sup>2</sup> University Hospital Düsseldorf (UKD) and German Cancer Consortium (DKTK), Düsseldorf, Germany; <sup>3</sup> German Cancer Research Center (DKFZ), Heidelberg, Germany; <sup>4</sup> Children's National Medical Center, Washington, D.C., USA; <sup>5</sup> University of Toronto, Toronto, Ontario,

Canada; 6 McGill University and the McGill University Health Center Research Institute, Montreal, Quebec, Canada; 7 Michael Smith Genome Sciences Centre, BC Cancer Agency, Vancouver, British Columbia, Canada  
Molecular and Cellular Pediatrics, 1 July 2015, 2(Suppl 1):A10 [This article is part of the supplement: Abstracts of the 51st Workshop for Pediatric Research Meeting abstract]  
... we conducted multiregion whole exome sequencing, high-resolution DNA copy number analysis (**Cytoscan HD**), and transcriptional profiling on 39 distinct pediatric and adult tumors with a median of six spatially distant biopsies per tumor (range 4-11). ...

127- **Meeting abstract**

[Integrated molecular characterization of mast cell leukemia reveals recurrent inactivation of the SETD2 tumor suppressor gene](#)

Simona Soverini<sup>1</sup>, Caterina De Benedittis<sup>1</sup>, Michela Rondoni<sup>2</sup>, Manuela Mancini<sup>1</sup>, Cristina Papayannidis<sup>1</sup>, Luca Zazzeroni<sup>1</sup>, Viviana Guadagnuolo<sup>1</sup>, Elisa Zago<sup>3</sup>, Francesca Griggio<sup>3</sup>, Alberto Ferrarini<sup>3</sup>, Marianna Garonzi<sup>3</sup>, Massimo Delledonne<sup>3</sup>, Giorgina Specchia<sup>4</sup>, Roberta Zanotti<sup>5</sup>, Omar Perbellini<sup>5</sup>, Livio Pagano<sup>6</sup>, Michele Cavo<sup>1</sup>, Peter Valent<sup>7</sup>, and Giovanni Martinelli<sup>1</sup>

<sup>1</sup>University of Bologna, Bologna, Italy; <sup>2</sup>Area Vasta Romagna, Centro Servizi Pievesestina, Cesena, Italy; <sup>3</sup>Univ of Verona, Verona, Italy; <sup>4</sup>Univ of Bari, Bari, Italy; <sup>5</sup>Univ of Verona, UO Hematology, Verona, Italy; <sup>6</sup>Hematology, Universita' Cattolica S. Cuore, Rome, Italy; <sup>7</sup>University of Wien, Wien, Austria.

Cancer Research, 2015;75(15 Suppl):Abst #3957. [AACR 106<sup>th</sup> Annual Mtg, Apr 18-22, 2015, Philadelphia, PA]

Systemic mastocytosis (SM) includes a heterogeneous group of disorders ranging from indolent SM to the rare and aggressive mast cell leukemia (MCL). Somatic mutations in the KIT receptor kinase (most frequently, D816V) can be detected in >90% of patients and are thought to play an important pathogenetic role. ... we undertook an integrated molecular genetic study of a KIT gene mutation-negative MCL case who came to our attention in 2012. ... High resolution karyotyping was also performed with **Cytoscan HD arrays** (Affymetrix, Santa Clara CA). ... In line with the role of SETD2-dependent H3K36Me3 in DNA repair and genome stability, **Cytoscan HD** arrays and WES showed that several losses at many chromosomal loci, together with more than 70 additional point mutations, undetectable at diagnosis, were acquired at the time of progression. ...

128-

[Integration of cytogenomic data for furthering the characterization of pediatric B-ALL: a multi-institution, multi-platform microarray study](#)

L.B. Baughn, J.A. Biegel, S.T. South, T. Smolarek, S. Volkert, A. Carroll, N.A. Heerema, K.R. Rabin, P.A. Zweidler-McKay, M. Loh, B. Hirsch

Cancer Genetics, Jan-Feb 2015, 208(1-2):1-18.

... The present investigation demonstrates the feasibility and usefulness of integrating array results from multiple laboratories (ARUP, Children's Hospital of Philadelphia, Cincinnati Children's Hospital Medical Center, and University of Minnesota Medical Center) that utilize different array platforms (**Affymetrix**, Agilent, or Illumina) in their respective clinical settings. ... At ARUP, DNA was extracted using a Gentra Puregene kit from Qiagen, and patient DNA was analyzed using the **CytoScan HD®** microarray assay (Affymetrix, Santa Clara, CA) which contains 743,304 SNP-based oligonucleotides

...

129-

[Intellectual disability secondary to a 16p13 duplication in a 1;16 translocation. Extended phenotype in a four-generation family](#)

Amal Mahmoud Mohamed<sup>1,\*</sup>, Alaa Kamel<sup>1</sup>, Wael Mahmoud<sup>1</sup>, Ehab Abdelraouf<sup>2</sup> and Nagwa Meguid<sup>2</sup>

<sup>1</sup>Human Cytogenetics Department, National Research Centre, Cairo, Egypt; <sup>2</sup>Research on Children with Special Needs Department, National Research Centre, Cairo, Egypt

American Journal of Medical Genetics Part A, January 2015, 167(1):128-136.

... Array CGH analysis by **Cytoscan HD** (Affymetrix) was used according to the manufacturer manual. Microarrays were scanned with GeneChip® Scanner 3000 7G.

130-

[Interstitial 1p32.1p32.3 deletion in a patient with multiple congenital anomalies](#)

Martin Kehrer<sup>1</sup>, Karin Schäferhoff<sup>1</sup>, Michael Bonin<sup>1,2</sup>, Anna Jauch<sup>3</sup>, Andrea Bevot<sup>4</sup>, Andreas Tzschach<sup>1,5,\*</sup>

<sup>1</sup>Institute of Medical Genetics and Applied Genomics, University of Tuebingen, Tuebingen, Germany; <sup>2</sup>IMGM Laboratories GmbH, Martinsried, Germany; <sup>3</sup>Institute of Human Genetics, University of Heidelberg, Heidelberg, Germany; <sup>4</sup>University Children's Hospital, University of Tuebingen, Tuebingen, Germany; <sup>5</sup>Institute of Clinical Genetics, Technische Universität Dresden, Dresden, Germany

American Journal of Medical Genetics Part A, October 2015, 167(10): 2406-2410.

... Figure 2. Graphical representation of chromosome 1 and the hybridization results of the patient and his parents (Affymetrix **CytoScan SNP Array**). The deletion in 1p32.1p32.3 is highlighted by an arrow.

131-

[Interstitial duplication of chromosome region 1q25.1q25.3: Report of a patient with mild cognitive deficits, tall stature and facial dysmorphisms](#)

Martin Kehrer<sup>1</sup>, Thomas Liehr<sup>2,\*</sup>, Tanja Benkert<sup>1</sup>, Sylke Singer<sup>1</sup>, Ute Grasshoff<sup>1</sup>, Karin Schaeferhoff<sup>1</sup>, Michael Bonin<sup>1</sup>, Annette Weichselbaum<sup>3</sup>, Andreas Tzschach<sup>1</sup>

<sup>1</sup>Institute of Medical Genetics and Applied Genomics, University of Tuebingen, Tuebingen, Germany; <sup>2</sup>Jena Univ Hospital, Friedrich Schiller University, Institute of Human Genetics, Jena, Germany; <sup>3</sup>University Children's Hospital, University of Tuebingen, Tuebingen, Germany

American Journal of Medical Genetics Part A, March 2015, 167(3):653–656.

... High-resolution chromosome analysis (SNP array analysis) was performed using the Affymetrix Human Mapping **CytoScan™ HD Array** ...

132-

[Intratumoral genome diversity parallels progression and predicts outcome in pediatric cancer](#)

Linda Holmquist Mengelbier, Jenny Karlsson, David Lindgren, Anders Valind, Henrik Lilljebjörn, Caroline Jansson, Daniel Bexell, Noémie Braekeveldt, Adam Ameer, Tord Jonson, Hanna Göransson Kultima, Anders Isaksson, Jurate Asmundsson, Rogier Versteeg, Marianne Rissler, Thoas Fioretos, Bengt Sandstedt, Anna Börjesson, Torbjörn Backman, Niklas Pal, Ingrid Øra, Markus Mayrhofer & David Gisselsson

Nature Communications, online 27 January 2015, 6: Article #6125.

... was hybridized to HumanCNV370-Duo/Quad Genotyping BeadChips, 1 M Genotyping BeadChip HumanOmni1-Quad (Illumina Inc., San Diego, CA), or Affymetrix **Cytoscan HD** ...

133- *Book chapter*

[Introduction: Rationale for Precision Medicine Clinical Trials](#)

Christophe Le Tourneau MD, PhD christophe.letourneau@curie.fr 3,4

3. Dept of Medical Oncology, Institut Curie, Saint-Cloud, Paris, France; 4. EA7285, Versailles-Saint-Quentin-en-Yvelines University, Versailles, France

In Pan-Cancer Integrative Molecular Portrait Towards a New Paradigm in Precision Medicine, pp 1-8

Springer : 2015.

... Molecular alterations were evaluated on a tumor sample from a metastatic site using NGS for mutations screening, **CytoScan HD** for gene copy number variations, and IHC for estrogen, progesterone, and androgen receptor expression analyses.

134-

[Is Chromosome 15q13.3 Duplication Involving CHRNA7 Associated With Oral Clefts?](#)

Yingjun Xie, PhD<sup>1,2</sup>

<sup>1</sup>Dept of Prenatal Diagnosis, The First Affiliated Hospital of Sun Yat-sen University, Guangzhou, China; <sup>2</sup>Key Laboratory for Major Obstetric Diseases of Guangdong Province, Key Laboratory of Reproduction and Genetics of Guangdong Higher Education Institutes, The Third Affiliated Hospital of Guangzhou Medical University, Guangzhou, China

Child Neurology Open, October-December 2015, 2(4): 2329048X15618918

... peripheral blood or umbilical cord blood was collected ... and hybridized to the **CytoScan HD array** platform (Affymetrix, ... our study is the first to establish the relationship between 15q13.3 microduplication involving CHRNA7 and oral clefts.

135-

[Jacobsen Syndrome: Surgical Complications due to Unsuspected Diagnosis, the Importance of Molecular Studies in Patients with Craniosynostosis](#)

Linares Chávez E.P.a · Toral López J.c · Valdés Miranda J.M.a · González Huerta L.M.a · Perez Cabrera A.a · del Refugio Rivera Vega M.a · Messina Baas O.M.b · Cuevas-Covarrubias S.A.a

Departamentos de aGenética Médica and bOftalmología, Hospital General de México, Facultad de Medicina, Universidad Nacional Autónoma de México (UNAM), Mexico City, and cDepartamento de Genética Médica, Centro Médico Ecatepec, ISSEMYM, Edomex México, México

Molecular Syndromology, 2015, 6: 229-235.

... Oligonucleotide-SNP array analysis using the GeneChip Human **Cytoscan HD** was carried out for the patient from genomic DNA. The SNP array showed a 14.2-Mb deletion in chromosome 11q23.3q25 ...

136-

[Keratoconus in an adult with 22q11.2 deletion syndrome](#)

Norman Saffra, Benjamin Reinherz

Department of Ophthalmology, St John's Episcopal Hospital, Far Rockaway, New York, USA

BMJ Case Reports, published 16 January 2015; doi:10.1136/bcr-2014-203737

22q11.2 Deletion syndrome is one of the most common microdeletional syndromes, with an incidence of 1:4000 live-births, and potentially affects every organ in the body. ... Keratoconus has been reported once before in association with 22q11.2 deletion syndrome in a young adult. We report the second case of keratoconus in association with 22q11.2 deletion syndrome. ... High-resolution chromosome analysis and oligo-SNP (oligonucleotide, single nucleotide polymorphism, Affymetrix **CytoScan HD**) assay were performed in a Clinical Laboratory Improvement Amendments (CLIA)-approved laboratory.

137-

[KIT Mutation and Loss of 14q May Be Sufficient for the Development of Clinically Symptomatic Very Low-Risk GIST](#)

Olaf Karl Klinke, Tuba Mizani, Gouri Baldwin, Brigitte Bancel, Mojgan Devouassoux-Shisheboran, Jean-Yves Scoazec, Pierre-Paul Bringuier, Regina Feederle, Anna Jauch, Katrin Hinderhofer, Philippe Taniere, Henri-Jacques Delecluse

PLoS ONE, 23 June 2015, 10(6): e0130149.

... Molecular karyotyping using 50 ng of tumour DNA was performed with the Affymetrix **CytoScan HD** Array ...

138-

[Langerhans Cell Histiocytosis: Diagnosis on Thyroid Aspirate and Review of the Literature](#)

Anjali Saqi<sup>1</sup>, Adriana P. Kuker<sup>2</sup>, Susana A. Ebner<sup>2</sup>, John Ausiello<sup>2</sup>, Vaidehi Jobanputra<sup>1</sup>, Govind Bhagat<sup>1</sup>,

Tamar A. Giorgadze<sup>3</sup>

1. Dept of Pathology and Cell Biology, Columbia University College of Physicians and Surgeons, New York, NY, USA ; 2. Div of; Endocrinology, Columbia University College of Physicians and Surgeons, New York, NY ; 3. Dept of Pathology and Laboratory Medicine, Weill Cornell Medical College, Cornell University, 525 East 68th St, Suite F-766, New York, NY, 10065

Head and Neck Pathology, December 2015, 9(4): 496-502.

... On performing SNP array analysis, using the **CytoScan HD array** (Affymetrix), no distinct somatic copy number alteration (chromosome gain or loss) or loss of heterozygosity was observed, supporting the G-band karyotype results.

139-

[Language impairment in a case of a complex chromosomal rearrangement with a breakpoint downstream of FOXP2 \[open access\]](#)

Daniela Moralli, Ron Nudel, May T. M. Chan, Catherine M. Green, Emanuela V. Volpi, Antonio Benítez-Burraco, Dianne F. Newbury, Paloma García-Bellido

Molecular Cytogenetics, 10 June 2015, 8:36.

... Figure S3. CNVs were mapped in the probands and parents using **Affymetrix Cytoscan** and copy number changes were called within Affymetrix Chromosome Analysis Suite (ChAS).

140-

[Limb-girdle weakness in a marfanoid man: distinguishing calpainopathy from Becker's muscular dystrophy](#)

Gasnat Shaboodien<sup>1,2</sup>, David A Watkins<sup>1,2</sup>, Komala Pillay<sup>3</sup>, Peter Beighton<sup>4</sup>, Jeannine M Heckmann<sup>5</sup>, Bongani M Mayosi<sup>1,2</sup>

1Cardiovascular Genetics Laboratory, Hatter Institute of Cardiovascular Research in Africa, Cape Town, South Africa ; 2Dept of Medicine, Groote Schuur Hospital and University of Cape Town, Cape Town, South Africa ; 3Div of Anatomical Pathology, Dept of Clinical Laboratory Sciences, Natl Health Lab Service and Univ of Cape Town, Cape Town, South Africa ; 4Div of Human Genetics, Univ of Cape Town, Cape Town, South Africa ; 5Div of Neurology, Dept of Medicine, Groote Schuur Hospital and University of Cape Town, Cape Town, South Africa  
Practical Neurology, Mar 2015, 15:152-154.

... We proceeded with a genome-wide high-resolution single nucleotide polymorphism (SNP) array, **CytoScan HD** (Affymetrix), with 99% sensitivity and specificity for copy number changes ...

141-

[Long contiguous stretches of homozygosity spanning shortly the imprinted loci are associated with intellectual disability, autism and/or epilepsy](#)

Ivan Y. Iourov<sup>123\*</sup>, Svetlana G. Vorsanova<sup>12</sup>, Sergei A. Korostelev<sup>4</sup>, Maria A. Zelenova<sup>12</sup> and Yuri B. Yurov<sup>12</sup>

1 Mental Health Research Center, Moscow, 117152, Russia ; 2 Separated Structural Unit "Clinical Research Institute of Pediatrics", Russian National Research Medical University named after N.I. Pirogov, Ministry of Health of Russian Federation, Moscow, 125412, Russia ; 3 Dept of Medical Genetics, Russian Medical Academy of

Postgraduate Education, Moscow, 123995, Russia ; 4 Research Centre for Medical Genetics, Moscow, 115478, Russia

Molecular Cytogenetics, 15 October 2015, 8:77

... SNP chromosomal microarrays may lead to a 5 % improvement in etiological yield by uncovering LCSH at imprinted loci. ... CNV and LCSH were analyzed by **CytoScan HD** Arrays (Affymetrix ...

142- **Only 1 sentence mentions CytoScan**

[Low Rates of Genetic Testing in Children With Developmental Delays, Intellectual Disability, and Autism Spectrum Disorders](#)

John Peabody, MD, PhD<sup>1,2</sup>, Lisa DeMaria, MA<sup>1</sup>, Diana Tamandong-LaChica, MD<sup>1</sup>, Jhiedon Florentino, MS<sup>1</sup>, Maria Czarina Acelajado, MD<sup>1</sup>, Trever Burgon, PhD<sup>1</sup>  
1QURE Healthcare, San Francisco, CA, USA ; 2University of California, San Francisco and Los Angeles, USA  
Global Pediatric Health January-December 2015, 2 : 2333794X15623717

... The physicians used standard platform CMAs (45.3%) rather than enhanced CMA testing (10.4%) with more probes (eg, tests that include **Cytoscan HD** and FirstStepDx PLUS; P < .0001).

143- **Invited review**

[Malignant hematopoietic cell lines: In vitro models for the study of primary mediastinal B-cell lymphomas](#)

Hans G. Drexler, Stefan Ehrentraut, Stefan Nagel, Sonja Eberth, Roderick A.F. MacLeod  
Leibniz-Institute DSMZ-German Collection of Microorganisms and Cell Cultures, Dept. Human and Animal Cell Lines, Braunschweig, Germany

Leukemia Research, January 2015, 39(1):18–29. doi:10.1016/j.leukres.2014.11.002

... **CytoScan high density** genomic/SNP arrays were obtained from Affymetrix (High Wycombe, UK) and analyzed using Chromosome Analysis Suite software (Affymetrix).

144--

[Mayer-Rokitansky-Küster-Hauser syndrome discordance in monozygotic twins:matrix metalloproteinase 14, low-density lipoprotein receptor–related protein 10, extracellular matrix, and neoangiogenesis genes identified as candidate genes in a tissue-specific mosaicism](#)

Katharina Rall, M.D.a, Simone Eisenbeis, Ph.D.a, Gianmaria Barresi, M.D.a, Daniel Rückner, M.D.a, Michael Walter, Ph.D.b, Sven Pothsb, Diethelm Wallwiener, M.D.a, Olaf Riess, M.D.b, Michael Bonin, Ph.D.b, Sara Brucker, M.D.a  
Fertility and Sterility, February 2015, 103(2):494–502.e3.

... For validation of the initial analysis, we reanalyzed the twin pairs' DNA with the Affymetrix **Cytoscan HD Array**. ... Validation of the initial analysis was possible by reanalyzing the twin pairs' DNA with the use of the Affymetrix **CytoScan HD Array**. ...

145- **Meeting abstract**

[MG-127 Diagnostic accuracy of chromosome microarray in children with epilepsy and neurological abnormalities of unknown aetiology](#)

Sarah E Buerki<sup>1</sup>, Erin Slade<sup>1</sup>, Kamilla Schlade-Bartusiak<sup>2</sup>, Lindsay Brown<sup>2</sup>, Evica Rajcan-Separovic<sup>2</sup>, Patrice Eydoux<sup>2</sup>, Mary B Connolly<sup>1</sup>, Michelle K Demos<sup>1</sup>

<sup>1</sup>Pediatric Neurology, University of BC, BC Children's Hospital, British Columbia, BC, Canada ; <sup>2</sup>Cytogenetics, Children's and Women's Health Center of BC, University of BC, Vancouver, BC, Canada

Journal of Medical Genetics, 2015, 52:A7.

... The purpose of this study is to describe the results of performed CMA on 706 children with unexplained epilepsy associated with developmental delay/intellectual disability, autism spectrum disorders and/or multiple congenital anomalies ('epilepsy plus'). Design/method Retrospective chart review on clinical and genetic aspects of CNVs identified in 706 patients with 'epilepsy plus', seen at the Vancouver BC Children's Hospital from 2009 to 2014. All patients had CMA performed using Affymetrix Genome-Wide Human **SNP Array 6.0** or **CytoScanHD®**. ... Conclusions CMA revealed pathogenic CNVs in epilepsy "hotspots", and known microdeletion syndromes like Phelan-McDermid syndrome in 11.3% of children with 'epilepsy plus'. ...

146-

[Microarray analysis unmasked two siblings with pure hereditary spastic paraplegia shared a run of homozygosity region on chromosome 3q28–q29](#)

Wenqian Yu a, 1, Xiangdong You b, 1, Dong Wang a, Kai Dong a, Jing Su c, Chuanfen Li c, Jinxiu Liu a, Qianqian Zhang a, Feng You a, Xiangrong Wang a, Jing Huang a, Bin Qiao a, 2, Wenyuan Duan a, 2



a Institute of Cardiovascular Disease, General Hospital of Jinan Military Region, 8 Lashan Road, Jinan 250022, China; b Div of Quality Management, Shandong Center for Disease Control and Prevention, 16992 Jingshi Road, Jinan 250014, China; c Dept of Neurology, General Hospital of Jinan Military Region, 25 Shifan Road, Jinan 250031, China

Journal of the Neurological Sciences, 15 December 2015, 359(1-2): 351–355.

... we describe a Chinese non-consanguineous family with two affected siblings manifesting early-onset autosomal recessive HSP... **CytoScan HD** array analysis was performed ... first clinical description of a pure form spastic paraplegia in a non-consanguineous family ...

147-

[Microduplication of chromosome Xq25 encompassing STAG2 gene in a boy with intellectual disability.](#)

Yingjun X1, Wen T2, Yujian L3, Lingling X3, Huimin H3, Qun F4, Junhong C4.

1Dept of Prenatal Diagnosis, The First Affiliated Hospital of Sun Yat-sen University, Guangzhou 510080, China; Key Laboratory for Major Obstetric Diseases of Guangdong Province, Key Laboratory of Reproduction and Genetics of Guangdong Higher Education Institutes, The Third Affiliated Hospital of Guangzhou Medical University, 510080, China.; 2Dept of Pediatric Intensive Care Unit, The First Affiliated Hospital, Sun Yat-sen University, Guangzhou 510080, China. Electronic address: [tangwenr@21cn.com](mailto:tangwenr@21cn.com).; 3Dept of Pediatric Intensive Care Unit, The First Affiliated Hospital, Sun Yat-sen University, Guangzhou 510080, China.; 4Dept of Prenatal Diagnosis, The First Affiliated Hospital of Sun Yat-sen University, Guangzhou 510080, China.

Eur J Med Genetics, February 2015, 58(2):116-21.

... We report a 4-year-old boy with a de novo 591 kb duplication at Xq25. The duplication was first detected by a **CytoScan HD array** platform (Affymetrix, USA) and was confirmed by real-time quantitative PCR (qPCR) of the STAG2 gene, and by fluorescence in situ hybridization (FISH). ...

148-

[MMP21 is mutated in human heterotaxy and is required for normal left-right asymmetry in vertebrates](#)

Anne Guimier, George C Gabriel, Fanny Bajolle, Michael Tsang, Hui Liu, Aaron Noll, Molly Schwartz, Rajae El Malti, Laurie D Smith, Nikolai T Klena, Gina Jimenez, Neil A Miller, Myriam Oufadem, Anne Moreau de Bellaing, Hisato Yagi, Carol J Saunders, Candice N Baker, Sylvie Di Filippo, Kevin A Peterson, Isabelle Thiffault, Christine Bole-Feysot, Linda D Cooley, Emily G Farrow, Cécile Masson, Patric Schoen, Jean-François Deleuze, Patrick Nitschké, Stanislas Lyonnet, Loic de Pontual, Stephen A Murray, Damien Bonnet, Stephen F Kingsmore, Jeanne Amiel, Patrice Bouvagnet, Cecilia W Lo & Christopher T Gordon

Nature Genetics, online 5 October 2015, 47:1260–1263.

... For validation of the deletion identified by whole-genome sequencing in family 2, genomic DNA was isolated using the Gentra PureGene kit for whole blood. Test sample DNA was hybridized to Affymetrix **CytoScan HD** CN+SNP microarray chips.

149-

[Modeling colorectal cancer using CRISPR-Cas9-mediated engineering of human intestinal organoids](#)

Mami Matano, Shoichi Date, Mariko Shimokawa, Ai Takano, Masayuki Fujii, Yuki Ohta, Toshiaki Watanabe, Takanori Kanai & Toshiro Sato

Nature Medicine, 2015, 21, 256–262.

... Microarray hybridization was performed on the GeneChip **Prime View** Human Gene Expression Array (Affymetrix) ... organoids was extracted using the QIAamp DNA Blood Mini Kit (Qiagen) and analyzed by **Cytoscan HD** (Affymetrix).

150-

[Molecularly targeted therapy based on tumour molecular profiling versus conventional therapy for advanced cancer \(SHIVA\): a multicentre, open-label, proof-of-concept, randomised, controlled phase 2 trial](#)

Dr Christophe Le Tourneau, MDa, u, Prof Jean-Pierre Delord, MDb, Prof Anthony Gonçalves, MDc, Céline Gavoille, MDd, Coraline Dubot, MDe, Nicolas Isambert, MDf, Prof Mario Campone, MDg, Olivier Trédan, MDi, Marie-Ange Massiani, MDk, Cécile Mauborgne, MScl, Sebastien Armanet, MScm, Nicolas Servant, PhDt, Ivan Bièche, PhDn, Virginie Bernard, PhDp, David Gentien, PhDo, Pascal Jezequel, MDh, Valéry Attignon, PhDj, Sandrine Boyault, PhDj, Anne Vincent-Salomon, MDr, Vincent Servois, MDs, Marie-Paule Sablin, MDq, Maud Kamal, PhDq, Xavier Paoletti, PhDl, t, for the SHIVA investigators  
a Dept of Medical Oncology, Institut Curie, Paris & Saint-Cloud, France; b Dept of Medical Oncology, Institut Claudius Régaud, Toulouse, France; c Dept of Medical Oncology, Institut Paoli-Calmettes, Marseille, France; d Dept of Medical Oncology, Centre Alexis Vautrin, Nancy, France; e Dept of Medical Oncology, Institut Curie, Saint-Cloud, France; f Dept of Medical Oncology, Centre Georges-François Leclerc, Dijon, France; g Dept of Medical

Oncology, Centre René Gauducheau, Nantes, France; h Genomic Unit, Centre René Gauducheau, Nantes, France; i Dept of Medical Oncology, Centre Léon Bérard, Lyon, France; j Genomic Unit, Centre Léon Bérard, Lyon, France; k Dept of Pneumology, Hopital Foch, Suresnes, France; l Dept of Biostatistics, Institut Curie, Paris, France; m Clinical Trial Management Unit, Institut Curie, Paris, France; n Pharmacogenomics Unit, Institut Curie, Paris, France; o Translational Research Department, Institut Curie, Paris, France; p NGS Platform, Institut Curie, Paris, France; q Dept of Medical Oncology, Institut Curie, Paris, France; r Dept of Biopathology, Institut Curie, Paris, France; s Dept of Radiology, Institut Curie, Paris, France; t Unité INSERM U900, Paris, France; u EA7285: Risques cliniques et sécurité en santé des femmes et en santé périnatale, Versailles Saint-Quentin-en Yvelines University, Montigny-le-Bretonneux, France

The Lancet Oncology, October 2015, 16(13):1324–1334

... Molecular analyses included assessment of mutations by targeted next generation sequencing (AmpliSeq cancer panel on an Ion Torrent/PGM system, ... gene copy number alterations by **Cytoscan HD** (Affymetrix, ...

151-

[Mosaic paternal genome-wide uniparental isodisomy with down syndrome](#)

Diana Darcy<sup>1</sup>, Paldeep Singh Atwal<sup>2</sup>, Cathy Angell<sup>3</sup>, Inder Gadi<sup>4</sup> and Robert Wallerstein<sup>1,\*</sup>

<sup>1</sup>Silicon Valley Genetics Center, Santa Clara Valley Medical Center, San Jose, CA; <sup>2</sup>Stanford University Medical Center, Palo Alto, CA; <sup>3</sup>Neonatology, O'Connor Hospital, San Jose, CA; <sup>4</sup>Laboratory Corporation of America, Research Triangle Park, NC

American Journal of Medical Genetics Part A, October 2015, 167(10): 2463–2469.

... microarray results suggest that the cell line with trisomy 21 is biparentally inherited ... this patient is the only reported case that also involves trisomy 21. ... The sample was run using an Affymetrix **Cytoscan HD** microarray ...

152-

[Mosaic tetrasomy 20p associated with osteoporosis and recurrent fractures](#)

Asmaa S. Abu Maziad<sup>1</sup> and Laurie H. Seaver<sup>1,2,\*</sup>

<sup>1</sup>Dept of Pediatrics, Univ of Hawaii John A. Burns School of Medicine, Honolulu, Hawaii; <sup>2</sup>Kapi'olani Medical Specialists, Honolulu, Hawaii

American Journal of Medical Genetics Part A, July 2015, 167(7): 1582–1586.

... The results showed a 31.62 MB mosaic terminal duplication of 20pter>q11.21 consistent with a supernumerary mosaic isodicentric chromosome 20 (arr 20p13q11.21 (61,568-31,620, 951) x2~4 (Affymetrix **Cytoscan HD** based on the GRCh37/HG19 assembly, Affymetrix, Santa ...

153-

[Mosaic trisomy 15 in a liveborn infant](#)

Jacob McPadden<sup>1</sup>, Benjamin M. Helm<sup>1,2</sup>, Brooke B. Spangler<sup>1,2</sup>, Leslie P. Ross<sup>3</sup>, Debra B. Boles<sup>4</sup> and Samantha A. Schrier Vergano<sup>1,2,\*</sup>

<sup>1</sup>Dept of Pediatrics, Eastern Virginia Medical School, Norfolk, Virginia; <sup>2</sup>Division of Medical Genetics and Metabolism, Children's Hospital of The King's Daughters, Norfolk, Virginia; <sup>3</sup>Quest Diagnostics, Denver, Colorado; <sup>4</sup>Quest Diagnostics, Nichols Institute, Chantilly, Virginia

American Journal of Medical Genetics Part A, April 2015, 167(4): 821–825.

... A sample of the proband's blood was analyzed using an oligo-SNP (oligonucleotide, single nucleotide polymorphism, Affymetrix **CytoScan HD**) assay through Quest Diagnostics (Chantilly, VA).

154- **Meeting abstract**

[MSS HNPCC frequently contain CNVs in chromatin regulators](#)

WeiXiang Chen<sup>1</sup>, Xia sheng<sup>2</sup>, and Jun Ding<sup>1</sup>

<sup>1</sup>Shanghai Gongli Hospital, Shanghai, China; <sup>2</sup>Shanghai Putuo Hospital, Shanghai, China.

Cancer Research, 2015;75(15 Suppl):Abst #3902. [AACR 106<sup>th</sup> Annual Mtg, Apr 18-22, 2015, Philadelphia, PA]

**Note: This abstract was not presented at the meeting.**

... We examined genomic DNA samples from 95 primary HNPCCs and adjacent normal appearing mucosae from patients undergoing surgery. We performed the copy number variation (CNV) of the entire genome using the **Cytoscan HD** Array in 20 MSS and 4 MSI HNPCC tumors and their adjacent normal tissues. Extensive comparison with somatic alterations in MSI HNPCCs allowed segregation of MSS HNPCC-exclusive alterations. ...

155- **Meeting abstract**

[Multicenter Total Therapy Gimema LAL 1509 Protocol for De Novo Adult Ph+ Acute Lymphoblastic Leukemia \(ALL\) Patients. Updated Results and Refined Genetic-Based Prognostic Stratification](#)

Sabina Chiaretti\*,1, Antonella Vitale\*,1, Loredana Elia\*,1, Anna Lucia Fedullo\*,1, Silvana Albino\*,1, Alfonso Piciocchi\*,2, Paola Fazi\*,2, Francesco Di Raimondo<sup>3</sup>, Antonella Fornaro\*,4, Francesco Fabbiano<sup>5</sup>, Alfonso Maria D'Arco\*,6, Giovanni Martinelli, MD PhD<sup>7</sup>, Francesca Ronco\*,8, Lidia Edwige Santoro\*,9, Nicola Cascavilla, MD\*,10, Piero Galieni\*,11, Alessandra Tedeschi, MD\*,12, Simona Sica\*,13, Nicola Di Renzo<sup>14</sup>, Angela Melpignano\*,15, Angelo Michele Carella<sup>16</sup>, Felicetto Ferrara<sup>17</sup>, Marco Vignetti\*,2, and Robin Foà\*,1

1Hematology, Dept of Cellular Biotechnologies and Hematology, "Sapienza" University, Rome, Italy; 2GIMEMA Data Center, Rome, Italy; 3Dept of Biomedical Sciences, Division of Hematology, Ospedale Ferrarotto, University of Catania, Italy, Catania, Italy; 4Dept of Hematology, Ospedale Civile dello Spirito Santo - Pescara, Pescara, Italy; 5Ospedali Riuniti Villa Sofia-Cervello, Palermo, Italy, Palermo, Italy; 6Division of Onco-hematology - Ospedale Umberto I - Nocera Inferiore (SA), Nocera Inferiore, Italy; 7Bologna University School of Medicine, Bologna, Italy; 8hematology, azienda ospedaliera bianchi-melacrino-morelli, reggio calabria, Italy; 9Div of Hematology -Azienda Ospedaliera S.G.Moscato, Avellino, Italy, Avellino, Italy; 10Hematology and BMT Unit, Casa Sollievo della Sofferenza, San Giovanni Rotondo, Italy; 11Hematology and Cellular Therapy, Ospedale Mazzoni, Ascoli Piceno, Italy; 12Div of Hematology, Niguarda Ca' Granda Hospital, Milan, Italy; 13Institute of Hematology, Catholic University, Rome, Italy; 14Hematology, Vito Fazzi Hospital, Lecce, Italy; 15Ospedale A. Perrino, Brindisi, Brindisi, Italy; 16Div of Hematology 1, IRCCS A.O.U. San Martino IST, Genova, Genova, Italy; 17Div of Hematology, Cardarelli Hospital, Napoli, Italy;

Blood, 3 December 2015, 126(23): Abstract #81.

... Mutational screening was performed in relapsed cases, based on material availability. SNP array analysis was carried out using the **Cytoscan HD arrays** (Affymetrix, Santa Clara, CA) to identify genomic aberrations. ... **SNP array** analysis, performed in 39 cases with available DNA, showed that the most frequent aberrations were deletions of IKZF1 (85%), PAX5 (38%), CDKN2A/B (33%), MLLT3 (33%), RB1 (28%) and JAK2 (28%). ...

156-

#### [Mutational landscape and clonal architecture in grade II and III gliomas](#)

Hirokichi Suzuki, Kosuke Aoki, Kenichi Chiba, Yusuke Sato, Yusuke Shiozawa, Yuichi Shiraishi, Teppei Shimamura, Atsushi Niida, Kazuya Motomura, Fumiharu Ohka, Takashi Yamamoto, Kuniaki Tanahashi, Melissa Ranjit, Toshihiko Wakabayashi, Tetsuichi Yoshizato, Keisuke Kataoka, Kenichi Yoshida, Yasunobu Nagata, Aiko Sato-Otsubo, Hiroko Tanaka, Masashi Sanada, Yutaka Kondo, Hideo Nakamura, Masahiro Mizoguchi, Tatsuya Abe, Yoshihiro Muragaki, Reiko Watanabe, Ichiro Ito, Satoru Miyano, Atsushi Natsume & Seishi Ogawa

Nature Genetics, online 13 April 2015, 47: 458–468.

... We assessed the genome-wide copy number alterations for 291 tumors using GeneChip **Human Mapping 250K Nspl** or **CytoScan HD** arrays (Affymetrix) ... For GISTIC analysis, the different probe sets for the different array platforms (**250K Nspl**, **CytoScan HD** and **SNP Array 6.0**) were adjusted by uniformly using the 250K Nspl SNPs as surrogates for SNPs that were marginally located within the abnormal copy number segments on the **CytoScan HD** and SNP Array 6.0.

157-

#### [MYC amplification in multiple marker chromosomes and EZH2 microdeletion in a man with acute myeloid leukemia](#)

Zhifu Xiang, Al-Ola Abdallah, Rangaswamy Govindarajan, Paulette Mehta, Peter D. Emanuel, Peter Papenhausen, Steven A. Schichman

Cancer Genetics, March 2015, 208(3): 96–100.  
... Whole genome SNP was performed using Affymetrix Genome-wide **Cytoscan SNP Array** (~2.7 million probes with ~700,000 SNPs) following standard protocol per the manufacturer's instructions.  
...

158-

#### [Neuroblastoma patient-derived orthotopic xenografts retain metastatic patterns and genotypes of patient tumours](#)

Noémie Braekeveldt<sup>1</sup>, Caroline Wigerup<sup>1</sup>, David Gisselsson<sup>2,3</sup>, Sofie Mohlin<sup>1</sup>, My Merselius<sup>1</sup>, Siv Beckman<sup>1</sup>, Tord Jonson<sup>2</sup>, Anna Börjesson<sup>4</sup>, Torbjörn Backman<sup>4</sup>, Irene Tadeo<sup>5</sup>, Ana P. Berbegall<sup>5,6</sup>, Ingrid Öra<sup>7</sup>, Samuel Navarro<sup>6</sup>, Rosa Noguera<sup>6</sup>, Sven Pählman<sup>1</sup>, Daniel Bexell<sup>1,\*</sup>

1Translational Cancer Research, Lund University, Lund, Sweden; 2Dept of Clinical Genetics, Lund University, Lund, Sweden; 3Dept of Pathology, University and Regional Laboratories, Lund, Sweden; 4Dept of Paediatric Surgery, Skåne University Hospital, Lund, Sweden; 5Medical Research Foundation INCLIVA, Hospital Clínico, Valencia, Spain; 6Dept of Pathology, Medical School, University of Valencia, Spain; 7Dept of Paediatrics, Clinical Sciences, Lund University, Lund, Sweden

International Journal of Cancer, 1 March 2015, 136(5): E252–E261.

... DNA was extracted from the cells and tissues using DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany) according to the instructions. We used the Affymetrix **CytoScan HD platform** for SNP array analysis of cultured SK-N-BE(2)c cells, SK-N-BE(2)c tumours, PDXs and patient tumour #3.

159- **Meeting abstract**

[NEW DELETION OF JAK2 DETECTED BY SNP ARRAY: A ROLE IN OVERALL SURVIVAL IN ACUTE MYELOID LEUKEMIA PATIENTS](#)

M.C. Fontana,1,\* V. Guadagnuolo,1,\* C. Papayannidis,1 I. Iacobucci,1 M. Manfrini,1 A. Padella,1 G. Simonetti,1 A. Ferrari,1 G. Marconi,1 S. Paolini,1 M.C. Abbenante,1 S. Parisi,1 C. Sartor,1 E. Ottaviani,1 M. Cavo,1 R. Kralovics,2 J. Milosevic,2 N. Them,2 D. Chen,2 G. Martinelli1

1Dept of Hematology and Medical Sciences "L. and A. Seràgnoli", Bologna University, Bologna, Italy; 2Research Center for Molecular Medicine of the Austrian Academy of Sciences, Wien, Austria; \*These authors contribute equally to this work

Haematologica, 2015, 100(Sup3) : Abstr #C080, p.18. [45° Congress of the Italian Society of Hematology

Florence, Italy, October 4-7, 2015

... Our objective is to evaluate the prognostic impact of these genetic alterations on clinical outcome. Materials and Methods: We analyzed 272 AML patients (pts): 229 performed by **SNP Array 6.0** (Affymetrix), 6 by **CytoScan HD Array** (Affymetrix) and 37 performed by **Cytoscan HD Array** ... Conclusions: By SNP arrays we have identified CNAs involving important cancer genes in AML and we showed that a new deletion in JAK2 may play a role in the overall survival. ...

160-

[Next Generation Diagnostics: Gene Panel, Exome or Whole Genome?](#)

Yu Sun1,3, Claudia A.L. Ruivenkamp1, Mariëtte J.V. Hoffer1, Terry Vrijenhoek2, Marjolein Kriek1, Christi J. van Asperen1, Johan T. den Dunnen1 and Gijs W.E. Santen1,\*

1Dept of Clinical Genetics, Leiden University Medical Center, Leiden, The Netherlands; 2Centre for Genome Diagnostics, Department of Medical Genetics, Universitair Medisch Centrum Utrecht, Utrecht, The Netherlands; 3Shanghai Institute for Pediatric Research, Xin Hua Hospital affiliated to Shanghai Jiaotong University School of Medicine, Shanghai, China

Human Mutation, June 2015, 36(6): 648–655.

... Twelve of these 13 samples were also analyzed using Affymetrix **Cytoscan HD arrays** ... An additional 5/21 (24%) variants would probably have been identified by the Affymetrix **Cytoscan HD** array, FISH studies or by CNV-calling on exome data ...

161-

[NFkB is activated by multiple mechanisms in hairy cell leukemia](#)

Stefan Nagel\*, Stefan Ehrentraut, Corinna Meyer, Maren Kaufmann, Hans G. Drexler, Roderick A.F. MacLeod

Dept of Human and Animal Cell Lines, Leibniz-Institute DSMZ – German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany

Genes, Chromosomes and Cancer, July 2015, 54(7): 418–432.

... Labeling, hybridization, and washing were performed using the recommended kits and **CytoScan HD** arrays according to the manufacturers protocols (Affymetrix, High Wycombe, UK).

162- **Meeting abstract**

[Novel germline copy number variations in patients with hereditary colorectal carcinoma with no mutation in the mismatch repair genes](#)

Rolando André Rios Villacis1, Erika Maria Monteiro Santos2, Dirce Maria Carraro1, Benedito Mauro Rossi3, and Silvia Regina Rogatto4

1CIPE - Research Center, AC Camargo Cancer Center, São Paulo, Brazil; 2Oncology Center, Sirio-Libanês Hospital, São Paulo, Brazil; 3Dept of Oncogenetics, Barretos Cancer Hospital, São Paulo, Brazil; 4CIPE - Research Center, AC Camargo Cancer Center/Dept of Urology, Faculty of Medicine, UNESP, São Paulo/Botucatu, Brazil.

Cancer Research, 2015;75(15 Suppl):Abst #2754. [AACR 106<sup>th</sup> Annual Mtg, Apr 18-22, 2015, Philadelphia, PA]

...100 healthy Brazilian individuals (evaluated with 180K Agilent platform) and 1038 phenotypically healthy individuals (**Affymetrix database**). It was identified 263 CNVs: 86 were classified as rare ( $\leq 1\%$  of reference databases) and 10 (in different chromosomes and cases) were completely new. Eleven out of 58 cases were re-evaluated using a higher-density microarray platform (Affymetrix **CytoScan HD**, 2.6 million probes), being the data analyzed with the Chromosome Analysis Suite v2.1 (Affymetrix) software. We identified more CNVs per case with the Affymetrix platform compared to the **Agilent platform** (179 to 68). ... By using Affymetrix **CytoScan HD** platform, two unrelated cases presented a rare duplication of 82kb on chromosome 2p22.3 encompassing two genes and one microRNA, that were previously associated with CRC. ...

163-

[Novel homozygous deletion of segmental KAL1 and entire STS cause Kallmann syndrome and X-linked ichthyosis in a Chinese family](#)

H. Xu<sup>1</sup>, Z. Li<sup>2</sup>, T. Wang<sup>1</sup>, S. Wang<sup>1</sup>, J. Liu<sup>1\*</sup> and D. W. Wang<sup>2\*</sup>

<sup>1</sup>Dept of Urology, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China; <sup>2</sup>Dept of Internal Medicine and Gene Therapy Center, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Andrologia, December 2015, 47(10) : 1160–1165.

... A genomic hybridisation was performed with the **CytoScan™ HD array** (Affymetrix, Santa Clara, CA, USA) in accordance with the manufacturer's instruction in patient III-2. The array is characterised by more than 2 600 000 copy number variation markers including 750 000 SNP ...

164-

[NUP98/11p15 translocations affect CD34+ cells in myeloid and T lymphoid leukemias](#)

Barbara Crescenzi a, Valeria Nofrini a, Gianluca Barba a, Caterina Matteucci a, Danika Di Giacomo a, Paolo Gorello a, Berna Beverloo b, Antonella Vitale c, Iwona Wlodarska d, Peter Vandenberghe d, Roberta La Starza a, Cristina Mecucci a

a Laboratory of Molecular Medicine, CREO, University of Perugia and A.O. Perugia, 06132 Perugia, Italy; b Dept of Clinical Genetics, Erasmus MC, 3000 CB Rotterdam, The Netherlands; c Hematology, Dept of Cellular Biotechnologies and Hematology, La Sapienza University, Via Benevento 6, 06161 Rome, Italy; d Center for Human Genetics, K.U. Leuven, Gasthuisberg, Herestraat 49, Box 602, B-3000 Leuven, Belgium

Leukemia Research, July 2015, 39(7): 769–772.

... Single Nucleotide Polymorphism-Array (SNPa) was performed with **CytoScan HD** Affymetrix platform, ... high quality genomic DNA obtained from unsorted bone marrow cells of patients ...

165-

[Panventriculomegaly with a wide foramen of Magendie and large cisterna magna](#)

Hiroshi Kageyama, MD<sup>1,2,3</sup>, Masakazu Miyajima, MD, PhD<sup>1</sup>, Ikuko Ogino, BPHARM<sup>1</sup>, Madoka Nakajima, MD, PhD<sup>1</sup>, Kazuaki Shimoji, MD, PhD<sup>1</sup>, Ryoko Fukai, MD, PhD<sup>2</sup>, Noriko Miyake, MD, PhD<sup>2</sup>, Kenichi Nishiyama, MD, PhD<sup>4</sup>, Naomichi Matsumoto, MD, PhD<sup>2</sup>, and Hajime Arai, MD, PhD<sup>1</sup>

<sup>1</sup>Dept of Neurosurgery, Graduate School of Medicine, Juntendo University, Tokyo; <sup>2</sup>Dept of Human Genetics, Yokohama City University Graduate School of Medicine, Yokohama; <sup>3</sup>Dept of Neurosurgery, Kuki General Hospital, Kuki, Saitama; and <sup>4</sup>Brain Research Institute, University of Niigata, Japan

Journal of Neurosurgery, published online December 4, 2015. DOI:

10.3171/2015.6.JNS15162.

... the first clinical, radiological, and genetic studies of panventriculomegaly defined by a wide foramen of Magendie and large cisterna magna. ... copy number analysis was performed using a **Cytoscan HD Array** (Affymetrix) ...

166-

[PAPSS2 deficiency causes androgen excess via impaired DHEA sulfation--in vitro and in vivo studies in a family harboring two novel PAPSS2 mutations.](#)

Oostdijk W, Idkowiak J, Mueller JW, House PJ, Taylor AE, O'Reilly MW, Hughes BA, de Vries MC, Kant SG, Santen GW, Verkerk AJ, Uitterlinden AG, Wit JM, Losekoot M, Arlt W. J Clin Endocrinol Metab. 2015 Apr;100(4):E672-80.

... Cytogenetic microarray analysis was performed using the **CytoScan HD Array** (Affymetrix) according to the manufacturer's protocol. Copy number was assessed using Chromosome Analysis Suite software (Affymetrix).

167-

[Parkinson's Disease in Saudi Patients: A Genetic Study](#)

Bashayer R. Al-Mubarak, Saeed A. Bohlega, Thamer S. Alkhairallah, Amna I. Magrashi, Maha I. AlTurki, Dania S. Khalil, Basma S. AlAbdulaziz, Hussam Abou Al-Shaar, Abeer E. Mustafa, Eman A. Alyemni, Bashayer A. Alsaffar, Asma I. Tahir, Nada A. Al Tassan PlosONE, 14 August 2015, 10(8): e0135950.

... Out of the 98 samples, 25 representative samples were screened for dosage alterations of both common and associated-PD genes using the **Cyto Scan HD array** (Affymetrix, Santa Clara, CA,USA) which contains 2.6 million markers for genome coverage. The data was analyzed using the Chromosome Analysis Suite version Cyto 3.0 using GRC 38/hg19 of the UCSC Genome Browser.

168-

[Partial USH2A deletions contribute to Usher syndrome in Denmark](#)

Shzeena D1, Rendtorff ND2, Kann E1, Albrechtsen A3, Mehrjouy MM4, Bak M4, Tommerup N4, Tranebjærg L2, Rosenberg T5, Jensen H5, Møller LB1.

<sup>1</sup>Clinical Genetics Clinic, The Kennedy Center, Rigshospitalet, University of Copenhagen, Glostrup, Denmark.; <sup>2</sup>Dept of Cellular and Molecular Medicine, Univ of Copenhagen, Copenhagen, Denmark [<sup>2</sup>] Dept of

Otorhinolaryngology, Head and Neck Surgery and Audiology, Bispebjerg Hospital/Rigshospitalet, Copenhagen, Denmark.; 3Dept of Biology, Computational and RNA Biology, University of Copenhagen, Copenhagen, Denmark.; 4Dept of Cellular and Molecular Medicine, Univ of Copenhagen, Copenhagen, Denmark.; 5Dept of Ophthalmology, The National Eye Clinic, Copenhagen University Hospital, The Kennedy Center, Glostrup, Denmark.  
European Journal of Human Genetics, December 2015, 23(12):1646-1651.  
... The Affymetrix **CytoScan HD** array (AROS Applied Biotechnology AS, Aarhus, Denmark) was used to confirm ...

169-

[PAX5-KIAA1549L: a novel fusion gene in a case of pediatric B-cell precursor acute lymphoblastic leukemia](#)

Stefanie Anderl<sup>1</sup>, Margit König<sup>1</sup>, Andishe Attarbaschi<sup>2, 3</sup>, Sabine Strehl<sup>1\*</sup>

<sup>1</sup> CCRI, Children's Cancer Research Institute, St. Anna Kinderkrebsforschung e.V., Vienna, Austria ; <sup>2</sup> Dept of Pediatrics, St. Anna Children's Hospital, Vienna, Austria ; <sup>3</sup> Medical University of Vienna, Vienna, Austria

Molecular Cytogenetics, 8 July 2015, 8:48

... Our report underlines the high diversity of PAX5 fusion partners in BCP-ALL and we describe the second involvement of KIAA1549L in a genetic rearrangement in acute leukemia. ... Genome-wide CNAs were determined using the **CytoScan HD** array platform (Affymetrix, USA).

170-

[Persistence of müllerian duct structures in a genetic male with distal monosomy 10q](#)

Mustafa Tosur<sup>1,\*</sup>, Cara A. Geary<sup>1</sup>, Reuben Matalon<sup>1</sup>, Ravi S. Radhakrishnan<sup>1,2</sup>, Leonard E. Swischuk<sup>3</sup>, William F. Tarry<sup>2</sup>, Jianli Dong<sup>4</sup> and Phillip D. K. Lee<sup>1</sup>

<sup>1</sup>Dept of Pediatrics, University of Texas Medical Branch, Galveston, TX; <sup>2</sup>Dept of Surgery, Univ of Texas Medical Branch, Galveston, TX; <sup>3</sup>Dept of Radiology, University of Texas Medical Branch, Galveston, TX; <sup>4</sup>Dept of Pathology, Univ of Texas Medical Branch, Galveston, TX

American Journal of Medical Genetics Part A, April 2015, 167(4):791–796.

... Chromosome karyotyping analysis showed 46,XY,add(10)(q25.2). Cytogenomic SNP microarray (**Cytoscan HD Array**, Affymetrix, Santa Clara, CA) revealed an 8.2 MB interstitial deletion of 10q25.3q26.13 (117,012,878-125,217,066) x1, indicating monosomy of this region.

171-

[Positional mapping of PRKD1, NRP1 and PRDM1 as novel candidate disease genes in truncus arteriosus](#)

Ranad Shaheen<sup>1</sup>, Amal Al Hashem<sup>2,3</sup>, Mohammed H Alghamdi<sup>4</sup>, Mohammed Zain Seidahmad<sup>5</sup>, Salma M Wakil<sup>1</sup>, Khalid Dagriri<sup>6</sup>, Bernard Keavney<sup>7</sup>, Judith Goodship<sup>8</sup>, Saad Alyousif<sup>5</sup>, Fahad M Al-Habshan<sup>9</sup>, Khalid Alhusein<sup>5</sup>, Agaadir Almoisheer<sup>1</sup>, Niema Ibrahim<sup>1</sup>, Fowzan S Alkuraya<sup>1,3</sup>

<sup>1</sup>Dept of Genetics, King Faisal Specialist Hospital and Research Center, Riyadh, Saudi Arabia ; <sup>2</sup>Dept of Pediatrics, Prince Sultan Military Medical City, Riyadh, Saudi Arabia ; <sup>3</sup>Dept of Anatomy and Cell Biology, College of Medicine, Alfaisal University, Riyadh, Saudi Arabia ; <sup>4</sup>Dept of Cardiac Sciences, College of Medicine, King Saud University, Riyadh, Saudi Arabia ; <sup>5</sup>Dept of Pediatrics, Security Forces Hospital, Riyadh, Saudi Arabia ; <sup>6</sup>Dept of Pediatric Cardiology, Prince Sultan Cardiac Center, Riyadh, Saudi Arabia ; <sup>7</sup>Institute of Cardiovascular Sciences, University of Manchester, Manchester, UK ; <sup>8</sup>Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne, UK ; <sup>9</sup>Dept of Cardiology, King Saud bin Abdulaziz University for Health Sciences, Riyadh, Saudi Arabia  
Journal of Medical Genetics, 2015, 52:322-329.

... Molecular karyotyping Detection of CNVs at the DNA level (molecular karyotyping) was performed using the **CytoScan HD** Array platform according to the manufacturer's instructions.

172-

[Prader–Willi syndrome and Tay–Sachs disease in association with mixed maternal uniparental isodisomy and heterodisomy 15 in a girl who also had isochromosome Xq](#)

Susan Zeesman<sup>1</sup>, Elizabeth McCready<sup>2,3</sup>, Bekim Sadikovic<sup>2,3</sup> and Małgorzata JM Nowaczyk<sup>1,2,3,\*</sup>

<sup>1</sup>Dept of Pediatrics, McMaster University, Hamilton, Ontario, Canada; <sup>2</sup>Dept of Pathology and Molecular Medicine, McMaster University, Hamilton, Ontario, Canada; <sup>3</sup>Hamilton Regional Laboratory Medicine Program, Hamilton Health Sciences and St. Joseph's Healthcare, Hamilton, Ontario, Canada

American Journal of Medical Genetics Part A, January 2015, 167(1):180–184.

... To further investigate this finding, SNP oligonucleotide microarray (**Cytoscan HD** microarray, Affymetrix, Santa Carla, USA) was performed. ... Figure 1. Characterization of chromosome 15 isodisomy segment by SNP oligonucleotide array. DNA extracted from peripheral blood was analyzed using the **Cytoscan HD** genomic microarray (Affymetrix ...

173-

[Prader-Willi Syndrome With a Long-Contiguous Stretch of Homozygosity Not Covering the Critical Region](#)

Xie Yingjun, MD1, Zhou Yi, MD1, Wu Jianzhu, BD1, Sun Yunxia, MD2, Chen Yongzhen, BD1, Zhong Liangying, MD3, Jing Xiangyi, PhD4, Fang Qun, MD1

1Fetal Medicine Center, the First Affiliated Hospital of Sun Yat-sen University, Guangzhou, China ; 2Dept of Neonatology, Guangdong General Hospital, Guangdong Academy of Medical Sciences, Guangzhou, China ; 3Dept of Laboratory Medicine, the First Affiliated Hospital of Sun Yat-sen University, Guangzhou, China; 4Dept of Medical Genetics, Zhongshan School of Medicine and Center for Genome Research, Sun Yat-Sen University, Guangzhou, China

J Child Neurol, Mar 2015, 30:371-377.

... DNA was amplified, labeled, and hybridized to the **CytoScan HD array** (Affymetrix) platform according to the manufacturer's... CEL files obtained by scanning **CytoScan arrays** were analyzed with Chromosome Analysis Suite Software...

174-

[Prenatal diagnosis of chromothripsis, with nine breaks characterized by karyotyping, FISH, microarray and whole-genome sequencing†](#)

M. J. Macera1, A. Sobrino1, B. Levy2, V. Jobanputra2, V. Aggarwal2, A. Mills1, C. Esteves1, C. Hanscom4, S. Pereira5, V. Pillalamarri4, Z. Ordulu, C. Morton5,6, M. Talkowski4 and D. Warburton3,\*

1New York-Presbyterian Hospital, Columbia Univ Medical Center, New York, NY; 2Dept of Pathology, Columbia Univ, New York, NY; 3Depts of Genetics and Development and Pediatrics, Columbia Univ, New York, NY; 4Center for Human Genetic Research and Dept of Neurology, Massachusetts General Hospital and Harvard Medical School, Boston, MA; 5Depts of Obstetrics, Gynecology and Reproductive Biology, Harvard Medical School, Boston, MA; 6Pathology, Brigham and Women's Hospital, Harvard Medical School, Boston, MA

Prenatal Diagnosis, March 2015, 35(3):299–301.

... SNP oligonucleotide microarray analysis (**Affymetrix Cytoscan HD**) on fetal DNA showed no loss or gain of chromosomal material at any of the breakpoints.

175-

[Prognostic significance of acquired copy-neutral loss of heterozygosity in acute myeloid leukemia](#)

Christine M. Gronseth1, Scott E. McElhone1, Barry E. Storer PhD2, Kathleen A. Kroeger1, Vicky Sandhu MD3, Matthew L. Fero MD3,4,6, Frederick R. Appelbaum MD3,4,6, Elihu H. Estey MD3,4,6, Min Fang MD, PhD3,5,6,\*

1Cytogenetics Dept, Seattle Cancer Care Alliance, Seattle, WA; 2Clinical Statistics Dept, Fred Hutchinson Cancer Research Center, Seattle, WA; 3Clinical Research Div, Fred Hutchinson Cancer Research Center, Seattle, WA; 4Dept of Medicine, University of Washington, Seattle, WA; 5Dept of Pathology, University of Washington, Seattle, WA; 6Seattle Cancer Care Alliance, Seattle, WA

Cancer, September 1, 2015, 121(17): 2900–2908.

... At the time of diagnosis or disease recurrence, CGAT was performed on DNA from bone marrow or blood specimens using **CytoScanHD** (Affymetrix ...

176-

[Quantitative analysis of genomic DNA degradation in whole blood under various storage conditions for molecular diagnostic testing](#)

Jessalyn Permenter a, Arjun Ishwar a, Angie Rounsavall a, Maddie Smith a, Jennifer Faske a, Charles J. Sailey a, b, 1, Maria P. Alfaro a, b

a Dept of Molecular Genetic Pathology, Arkansas Children's Hospital, 1 Children's Way, Little Rock, AR 72212, USA; b University of Arkansas for Medical Sciences, Little Rock, AR 72212, USA

Molecular and Cellular Probes, December 2015, 29(6): 449–453.

... Affymetrix Cytogenomic SNP Array as a high complexity test--Approximately 250 ng of gDNA was hybridized onto the **CytoScan® HD array** ... quality of SNP array data (**Cytoscan HD**, ... stored at room temperature was considered inadequate after 30 days.

177-

[RAG1 Deficiency May Present Clinically as Selective IgA Deficiency](#)

Tamaki Kato(1), Elena Crestani(2), Chikako Kamae(1), Kenichi Honma(1), Tomoko Yokosuka(3)

Takeshi Ikegawa(4), Naonori Nishida(5), Hirokazu Kanegane(5)(6), Taizo Wada(7), Akihiro Yachie(7), Osamu Ohara(8)(9), Tomohiro Morio(6), Luigi D. Notarangelo(2), Kohsuke Imai(1)(6), Shigeaki Nonoyama(1)

1. Dept of Pediatrics, National Defense Medical College, Tokorozawa, Saitama, Japan; 2. Div of Immunology, Children's Hospital Boston, Harvard Medical School, Boston, MA, USA; 3. Dept of Hemato-oncology/Regeneration Medicine, Kanagawa Children's Medical Center, Yokohama, Kanagawa, Japan; 4. Dept of Pediatrics, Yokohama Rosai Hospital, Yokohama, Kanagawa, Japan; 5. Dept of Pediatrics, University of Toyama, Toyama, Japan; 6. Dept of Pediatrics, Tokyo Medical and Dental University (TMDU), 1-5-45, Yushima, Bunkyo-ku, Tokyo, 113-8519, Japan; 7. Dept of Pediatrics, Kanazawa University, Kanazawa, Ishikawa, Japan; 8. Laboratory for Integrative

Genomics, RIKEN Center for Integrative Medical Sciences, Yokohama, Kanagawa, Japan; 9. Dept of Technology Development, Kazusa DNA Research Institute, Kisarazu, Chiba, Japan  
Journal of Clinical Immunology, April 2015, 35(3):280-288.  
... A copy number and loss of heterozygosity (LOH) analysis in the patient was performed using a **CytoScan HD** Array (Affymetrix, Santa Clara, California, USA), according to the manufacturer's protocol.

178-

[Rare genomic rearrangement in a boy with Williams–Beuren syndrome associated to XYY syndrome and intriguing behavior](#)

Roberta L. Dutra<sup>1,2,\*</sup>, Flavia B. Piazzon<sup>2</sup>, Évelin A. Zanardo<sup>2</sup>, Thais Virginia Moura Machado Costa<sup>2</sup>, Marília M. Montenegro<sup>1,2</sup>, Gil M. Novo-Filho<sup>1,2</sup>, Alexandre T. Dias<sup>2</sup>, Amom M. Nascimento<sup>1,2</sup>, Chong Ae Kim<sup>1</sup> and Leslie D. Kulikowski<sup>2,3</sup>  
<sup>1</sup>Genetics Unit, Instituto da Criança, Faculdade de Medicina da Universidade de São Paulo (USP), São Paulo, Brazil; <sup>2</sup>Dept of Pathology, Cytogenomics Lab - LIM03, Faculdade de Medicina da Universidade de São Paulo (USP), São Paulo, Brazil; <sup>3</sup>Dept of Collective Health - Human Reproduction and Genetics Center, Faculdade de Medicina do ABC, Santo André, São Paulo, Brazil

American Journal of Medical Genetics Part A, December 2015, 167(12): 3197–3203.  
... (SNP-array) confirmed the alterations found by MLPA and revealed ... pathogenic CNVs, in the chromosomes 7 and X. ... demonstrates an association not yet described ... between Williams–Beuren syndrome and 47,XYY. ... performed with the **CytoScan™ HD Array** (Affymetrix ...

179-

[rCGH: a comprehensive array-based genomic profile platform for precision medicine](#)

Frederic Commo<sup>1,2,\*</sup>, Justin Guinney<sup>2</sup>, Charles Ferté<sup>1,2</sup>, Brian Bot<sup>2</sup>, Celine Lefebvre<sup>1</sup>, Jean-Charles Soria<sup>1,3</sup> and Fabrice André<sup>1,3</sup>  
<sup>1</sup>INSERM U981, Gustave Roussy, University Paris-Sud, Villejuif 94805, France, <sup>2</sup>Sage Bionetworks, Seattle, WA 98109; <sup>3</sup>Dept of Medical Oncology, Gustave Roussy, Villejuif 94805, France  
Bioinformatics, online 26 Dec 2015; 10.1093/bioinformatics/btv718.  
... As input rCGH supports Agilent Human CGH data, from 44K to 400K, and **Affymetrix, SNP6 and cytoScanHD**. All are provided in text format by platform-specific softwares: ... Affymetrix cychp.txt, cnchp.txt or probeset.txt files are obtained by processing Affymetrix CEL files through ChAS or Affymetrix Power Tools (APT) softwares ...

180-

[RCSD1-ABL1 Translocation Associated with IKZF1 Gene Deletion in B-Cell Acute Lymphoblastic Leukemia](#)

Shawana Kamran, 1, \* Gordana Raca, 2 and Kamran Nazir 3  
<sup>1</sup>Shifa International Hospital, Islamabad 44000, Pakistan; <sup>2</sup>University of Chicago, Chicago, IL 60637; <sup>3</sup>Combined Military Hospital, Kharian 50090, Pakistan  
Case Reports in Hematology, online 27 October 2015; 2015: 353247.  
... SNP array testing was performed using the Affymetrix **CytoScan HD** arrays ...

181-

[RCSD1-ABL2 fusion resulting from a complex chromosomal rearrangement in high-risk B-cell acute lymphoblastic leukemia](#)

Gordana Raca, Sandeep Gurbuxani, Zhiyu Zhang, Zejuan Li, Madina Sukhanova, Jennifer McNeer, Wendy Stock  
<sup>1</sup>Dept of Medicine, University of Chicago, Chicago, IL; <sup>2</sup>Dept of Pathology, Univ of Chicago, Chicago, IL; <sup>3</sup>Dept of Pediatrics, University of Chicago, Chicago, IL  
Leukemia & Lymphoma, 2015 Apr;56(4):1145-7.

... (CMA) was performed using the **CytoScan® HD arrays** (Affymetrix Inc., Santa Clara CA), to look for submicroscopic copy number alterations and/or extended regions of loss of heterozygosity. ...

182-

[Recessive ITPA mutations cause an early-infantile encephalopathy](#)

Sietske H. Kevelam<sup>1,2</sup>, Jörgen Bierau<sup>3</sup>, Ramona Salvarinova<sup>4</sup>, FRCPC, FCCMG<sup>4</sup>, Shakti Agrawal<sup>5</sup>, MRCPC, MRCPC<sup>5</sup>, Tomas Honzik<sup>6</sup>, PhD<sup>6</sup>, Dennis Visser<sup>3</sup>, Marjan M. Weiss<sup>7</sup>, PhD<sup>7</sup>, Gajja S. Salomons<sup>2,8</sup>, Truus E. M. Abbink<sup>1,2</sup>, Quinten Waisfisz<sup>7</sup> and Marjo S. van der Knaap<sup>1,2,9,\*</sup>  
<sup>1</sup>Dept of Child Neurology, VU University Medical Center, Amsterdam, the Netherlands; <sup>2</sup>Neuroscience Campus Amsterdam, VU University, Amsterdam, the Netherlands; <sup>3</sup>Dept of Clinical Genetics, Maastricht University Medical Center, Maastricht, the Netherlands; <sup>4</sup>Div of Biochemical Diseases, Dept of Pediatrics, University of British Columbia, British Columbia Children's Hospital, Vancouver, British Columbia, Canada; <sup>5</sup>Dept of Pediatric Neurology, Birmingham Children's Hospital, Birmingham, UK; <sup>6</sup>Dept of Pediatrics, First Faculty of Medicine, Charles University in Prague and General University Hospital in Prague, Prague, Czech Republic; <sup>7</sup>Dept of Clinical Genetics, VU University Medical Center, Amsterdam, the Netherlands; <sup>8</sup>Dept of Clinical Chemistry, Metabolic Unit,



VU University Medical Center, Amsterdam, the Netherlands; 9Dept of Functional Genomics, Center for Neurogenomics and Cognitive Research, VU University, Amsterdam, the Netherlands

Annals of Neurology, October 2015, 78(4): 649–658.

... SNP array revealed one overlapping homozygous region on chromosome 20 in the consanguineous families. ... the second consanguineous family were subjected to SNP-array analysis (Affymetrix **CytoScan HD array**) ...

183-

[Recessive Mutations in the  \$\alpha 3\$  \(VI\) Collagen Gene COL6A3 Cause Early-Onset Isolated Dystonia](#)

Michael Zech<sup>1, 2, 3, 10</sup>, Daniel D. Lam<sup>2, 10</sup>, Ludmila Francescato<sup>4, 10</sup>, Barbara Schormair<sup>1, 3, 5</sup>, Aaro V. Salminen<sup>3</sup>, Angela Jochim<sup>1</sup>, Thomas Wieland<sup>3</sup>, Peter Lichtner<sup>3, 5</sup>, Annette Peters<sup>6</sup>, Christian Gieger<sup>7</sup>, Hanns Lochmüller<sup>8</sup>, Tim M. Strom<sup>3, 5</sup>, Bernhard Haslinger<sup>1, 11</sup>, Nicholas Katsanis<sup>4, 11</sup>, Juliane Winkelmann<sup>1, 2, 3, 9</sup>

<sup>1</sup> Neurologische Klinik und Poliklinik, Klinikum rechts der Isar, Technische Universität München, 81675 Munich, Germany; <sup>2</sup> Dept of Neurology and Neurological Sciences and Center for Sleep Sciences and Medicine, Stanford University School of Medicine, Palo Alto, CA 94304, USA; <sup>3</sup> Institut für Humangenetik, Helmholtz Zentrum München, 85764 Munich, Germany; <sup>4</sup> Center for Human Disease Modeling, Dept of Cell Biology, Duke University, Durham, NC 27710, USA; <sup>5</sup> Institut für Humangenetik, Technische Universität München, 81675 Munich, Germany; <sup>6</sup> Institute of Epidemiology II, Helmholtz Zentrum München, 85764 Munich, Germany; <sup>7</sup> Institute of Genetic Epidemiology, Helmholtz Zentrum München, 85764 Munich, Germany; <sup>8</sup> John Walton Centre for Muscular Dystrophy Research, MRC Centre for Neuromuscular Diseases, Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne NE1 3BZ, UK; <sup>9</sup> Munich Cluster for Systems Neurology, SyNergy, 81377 Munich, Germany

American Journal of Human Genetics, Volume 96, Issue 6, 4 June 2015, Pages 883–893

... screening for larger CNVs was done with the **CytoScan HD Array** from Affymetrix ...

184-

[Recurrent CDKN1B \(p27\) mutations in hairy cell leukemia](#)

Sascha Dietrich<sup>1</sup>, Jennifer Hüllein<sup>2</sup>, Stanley Chun-Wei Lee<sup>3</sup>, Barbara Hutter<sup>4</sup>, David Gonzalez<sup>5</sup>, Sandrine Jayne<sup>6</sup>, Martin J.S. Dyer<sup>6</sup>, Małgorzata Oleś<sup>7</sup>, Monica Else<sup>8</sup>, Xiyang Liu<sup>2</sup>, Mikołaj Ślabicki<sup>2</sup>, Bian Wu<sup>2</sup>, Xavier Troussard<sup>9</sup>, Jan Dürig<sup>10</sup>, Mindaugas Andrulis<sup>11</sup>, Claire Dearden<sup>12</sup>, Christof von Kalle<sup>13</sup>, Martin Granzow<sup>14</sup>, Anna Jauch<sup>14</sup>, Stefan Fröhling<sup>2</sup>, Wolfgang Huber<sup>7</sup>, Manja Meggendorfer<sup>15</sup>, Torsten Haferlach<sup>15</sup>, Anthony D. Ho<sup>1</sup>, Daniela Richter<sup>2</sup>, Benedikt Brors<sup>4</sup>, Hanno Glimm<sup>2</sup>, Estella Matutes<sup>12</sup>, Omar Abdel Wahab<sup>3</sup>, Thorsten Zenz<sup>1,\*</sup>

<sup>1</sup> Dept of Medicine V, University Hospital Heidelberg, Heidelberg, Germany; <sup>2</sup> Dept of Translational Oncology, National Center for Tumor Diseases (NCT) and German Cancer Research Center (dkfz), Heidelberg, Germany; <sup>3</sup> Human Oncology and Pathogenesis Program, Leukemia Service, Dept. of Medicine, Memorial Sloan Kettering Cancer Center, New York, NY, United States; <sup>4</sup> Div. Applied Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany; <sup>5</sup> Centre for Molecular Pathology, Royal Marsden NHS FTI, London, United Kingdom; <sup>6</sup> Ernest and Helen Scott Hematological Research Institute, University of Leicester, Leicester, United Kingdom; <sup>7</sup> Genome Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany; <sup>8</sup> Div of Molecular Pathology, The Institute of Cancer Research, London, United Kingdom; <sup>9</sup> Laboratoire d'Hématologie, CHU Cote de Nacre, Caen, France; <sup>10</sup> Dept of Hematology, University Hospital, Essen, Germany; <sup>11</sup> Dept of General Pathology, Institute of Pathology, University of Heidelberg, Heidelberg, Germany; <sup>12</sup> Royal Marsden Hospital, London, United Kingdom; <sup>13</sup> Heidelberg Center for Personalized Oncology, DKFZ-HIPO, DKFZ, Heidelberg, Germany; <sup>14</sup> Institute of Human Genetics, University Hospital Heidelberg, Germany; <sup>15</sup> MLL Munich Leukemia Laboratory, Munich, Germany

Blood, Aug 2015; 126: 1005 - 1008.

... This revealed loss of chromosome 21 in all three patients (supplemental material). Although these findings were validated by Affymetrix **Cytoscan HD Arrays**, CNV analysis of 7 additional patients failed to reveal chromosome 21 abnormalities ...

185-

[Recurrent chromosomal gains and heterogeneous driver mutations characterise papillary renal cancer evolution](#)

Michal Kovac, Carolina Navas, Stuart Horswell, Max Salm, Chiara Bardella, Andrew Rowan, Mark Stares, Francesc Castro-Giner, Rosalie Fisher, Elza C. de Bruin, Monika Kovacova, Maggie Gorman, Seiko Makino, Jennet Williams, Emma Jaeger, Angela Jones, Kimberley Howarth, James Larkin, Lisa Pickering, Martin Gore, David L. Nicol, Steven Hazell, Gordon Stamp, Tim O'Brien, Ben Challacombe, Nik Matthews, Benjamin Phillimore, Sharmin Begum, Adam Rabinowitz, Ignacio Varela, Ashish Chandra, Catherine Horsfield, Alexander Polson, Maxine Tran, Rupesh Bhatt, Luigi Terracciano, Serenella Eppenberger-Castori, Andrew Protheroe, Eamonn Maher, Mona El Bahrawy, Stewart Fleming, Peter Ratcliffe, Karl Heinemann, Charles Swanton & Ian Tomlinson

Nature Communications, 19 March 2015, 6:6336.

... Twenty-three tumours were genotyped using the Affymetrix **2.7 M Cytogenetics array** or the **CytoScan HD array**.

186-

[Recurrent deletions and duplications of chromosome 2q11.2 and 2q13 are associated with variable outcomes](#)

Kacie N. Riley<sup>1,2</sup>, Lisa M. Catalano<sup>1</sup>, John A. Bernat<sup>3</sup>, Stacie D. Adams<sup>3</sup>, Donna M. Martin<sup>3,4</sup>, Seema R. Lalani<sup>5</sup>, Ankita Patel<sup>5</sup>, Rachel D. Burnside<sup>2</sup>, Jeffrey W. Innis<sup>3,4</sup> and M. Katharine Rudd<sup>1,\*</sup>

American Journal of Medical Genetics Part A, November 2015, 167(11): 2664–2673.

... Subjects 4–7 were tested using the Affymetrix **CytoScan HD** array and Subjects 11 and 14 were tested using the Illumina CytoSNP-850K BeadChip, both based on the GRCh37/hg19 genome assembly.

187-

[Recurrent inactivating RASA2 mutations in melanoma](#)

Rand Arafeh, Nouar Qutob, Rafi Emmanuel, Alona Keren-Paz, Jason Madore, Abdel Elkahlon, James S Wilmott, Jared J Gartner, Antonella Di Pizio, Sabina Winograd-Katz, Sivasish Sindiri, Ron Rotkopf, Ken Dutton-Regester, Peter Johansson, Antonia L Pritchard, Nicola Waddell, Victoria K Hill, Jimmy C Lin, Yael Hevroni, Steven A Rosenberg, Javed Khan, Shifra Ben-Dor, Masha Y Niv, Igor Ulitsky, Graham J Mann, Richard Scolyer, Nicholas K Hayward & Yardena Samuels

Nature Genetics, online 26 October 2015, 47:1408–1410.

... We profiled the copy number landscape of 22 samples using the **CytoScan High-Definition array** (Affymetrix) and found three focal deletions (13.6%). ...

188-

[Relapse after Allogeneic Hematopoietic Cell Transplantation for Myelodysplastic Syndromes: Analysis of Late Relapse Using Comparative Karyotype and Chromosome Genome Array Testing](#)

Cecilia Yeung<sup>1, 2, 3</sup>, Aaron T. Gerds<sup>4</sup>, Min Fang<sup>1, 2, 3</sup>, Bart L. Scott<sup>1, 2, 3</sup>, Mary E.D. Flowers<sup>1, 2, 3</sup>, Ted Gooley<sup>1, 2</sup>, H. Joachim Deeg<sup>1, 2, 3</sup>

<sup>1</sup> Fred Hutchinson Cancer Research Center, Seattle, WA; <sup>2</sup> University of Washington, Seattle, WA; <sup>3</sup> Seattle Cancer Care Alliance, Seattle, WA; <sup>4</sup> Cleveland Clinic, Cleveland, OH

Biology of Blood and Bone Marrow Transplantation, September 2015, 21(9):1565–1575.

... CGAT, a combination of comparative genome hybridization (CGH) and single nucleotide polymorphism (SNP)-array, was used for the detection of DNA copy number aberration (CNA) or SNP using **CytoScan HD** (Affymetrix, ...

189-

[Repressed BMP signaling reactivates NKL homeobox gene MSX1 in a T-ALL subset](#)

Stefan Nagel, Stefan Ehrentraut, Corinna Meyer, Maren Kaufmann, Hans G. Drexler, and Roderick A. F. MacLeod

Department of Human and Animal Cell Lines, Leibniz-Institute DSMZ – German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany

Leukemia & Lymphoma, February 2015, 56(2): 480-491.

... Labeling, hybridization and washing were performed using the recommended kits and **CytoScan HD arrays** according to the manufacturer's protocols (Affymetrix). The data were subsequently analyzed using Chromosome Analysis Suite software version 2.0.1.2 (Affymetrix). ...

190-

[Reversing chromatin accessibility differences that distinguish homologous mitotic metaphase chromosomes](#)

Wahab A. Khan<sup>1</sup>, Peter K. Rogan<sup>2,3\*</sup> and Joan H. M. Knoll<sup>1,3\*</sup>

<sup>1</sup> Dept of Pathology and Laboratory Medicine, Univ of Western Ontario, London N6A 5C1, ON, Canada; <sup>2</sup> Depts of Biochemistry, Computer Science, and Oncology, University of Western Ontario, London N6A 5C1, ON, Canada; <sup>3</sup> Cytognomix, Inc., London N6G 4X8, ON, Canada

Molecular Cytogenetics, 13 August 2015, 8:65

... Genomic locations of single copy probes were evaluated relative to locations of common CNVs ... samples have been tested with high resolution Affymetrix **Cytoscan HD** ... CNVs in cell line GM06326, initially characterized using Affymetrix Genome-Wide Human **SNP Array 6.0** ...

191-

[ROBO1 deletion as a novel germline alteration in breast and colorectal cancer patients](#)

Rolando A. R. Villacis<sup>1</sup>, Francine B. Abreu<sup>1</sup>, Priscila M. Miranda<sup>1</sup>, Maria A. C. Domingues<sup>2</sup>, Dirce M. Carraro<sup>1</sup>, Erika M. M. Santos<sup>3</sup>, Victor P. Andrade<sup>4</sup>, Benedito M. Rossi<sup>3</sup>, Maria I. Achatz<sup>5</sup>, Silvia R. Rogatto<sup>1,6</sup>

1. Intl Research Center (CIPE), A.C. Camargo Cancer Center, Rua Taguá 440, São Paulo, CEP: 01508-010, SP, Brazil; 2. Dept of Pathology, Faculty of Medicine, University of São Paulo State (UNESP), Botucatu, SP, Brazil; 3. Oncology Center, Sírio-Libanês Hospital, São Paulo, SP, Brazil; 4. Dept of Pathology, A.C. Camargo Cancer Center, São Paulo, SP, Brazil; 5. Dept of Oncogenetics, A.C. Camargo Cancer Center, São Paulo, SP, Brazil; 6. Dept of Urology, Faculty of Medicine, University of São Paulo State (UNESP), CEP: 18618-970, Botucatu, SP, Brazil

Tumor Biology, first online 1 October 2015.

... identical germline deep intronic deletion of ROBO1 was identified in three index patients using ... (Agilent 4x180K and Affymetrix **CytoScan HD**). ... Transcriptomic analysis (**HTA 2.0**, Affymetrix) in two breast carcinomas from a single patient revealed ROBO1 down-expression ...

192-

[Role of additional chromosomal changes in the prognostic value of t\(4;14\) and del\(17p\) in multiple myeloma: the IFM experience.](#)

Hebraud B1, Magrangeas F2, Cleynen A1, Lauwers-Cances V3, Chretien ML4, Hulin C5, Leleu X6, Yon E3, Marit G7, Karlin L8, Roussel M9, Stoppa AM10, Belhadji K11, Voillat L12, Garderet L13, Macro M14, Caillot D4, Mohty M13, Facon T6, Moreau P15, Attal M9, Munshi N16, Corre J1, Minvielle S2, Avet-Loiseau H17.

1Laboratory for Genomics in Myeloma, Institut Universitaire du Cancer and University Hospital; and CRCT INSERM U1037, Toulouse, France; 2Unite Mixte de Genomique du Cancer, University Hospital; and INSERM U892, Nantes, France; 3Service d'Epidemiologie, University Hospital, Toulouse, France; 4Hematology Dept, Univ Hospital, Dijon, France; 5Hematology Department, Univ Hospital, Nancy, France; 6Hematology Dept, University Hospital, Lille, France; 7Hematology Dept, University Hospital, Bordeaux, France; 8Hematology Dept, University Hospital, Lyon, France; 9Hematology Dept, Univ Hospital, Toulouse, France; 10Hematology Dept, Institut Paoli-Calmettes, Marseille, France; 11Hematology Dept, Henri Mondor University Hospital, Creteil, France; 12Hematology Dept, General Hospital, Chalon sur Saone, France; 13Hematology Dept, Saint-Antoine University Hospital, Paris, France; 14Hematology Dept, University Hospital, Caen, France; 15Hematology Dept, Univ Hospital, Nantes, France; 16Lebow Inst of Myeloma Therapeutics and Jerome Lipper Multiple Myeloma Center, Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA; 17Laboratory for Genomics in Myeloma, Institut Universitaire du Cancer and University Hospital; and CRCT INSERM U1037, Toulouse, France; avet-loiseau.h@chu-toulouse.fr.

Blood, 2015; 125(13):2095-2100.

... DNA was extracted, labeled and hybridized on Affymetrix chips ... We used either the **SNP 6.0** or the **CytoScan** chips, depending on the date of hybridization.

193-

[Simultaneous Detection of Both Single Nucleotide Variations and Copy Number Alterations by Next-Generation Sequencing in Gorlin Syndrome](#)

Kei-ichi Morita, Takuya Naruto, Kousuke Tanimoto, Chisato Yasukawa, Yu Oikawa, Kiyoshi Masuda, Issei Imoto, Johji Inazawa, Ken Omura, Hiroyuki Harada  
PLoS ONE, 6 November 2015, 10(11): e0140480.

... CNA validation and detailed mapping of altered regions were performed using an Affymetrix **CytoScan HD** chromosome microarray platform ...

194- *Meeting abstract*

[Single Cell Genotyping of Inv\(16\) AML in CBL Mutated Clonal Hematopoiesis Characterizes Clonal Architecture and Evolution of Exome Sequencing-Identified Mutations in the Protein Tyrosine Phosphatase Ptpn22 and Other Genes](#)

Christoph Niemöller, Sabine Bleul, Nadja Blagitko-Dorfs, Christine Greil, Kenichi Yoshida, Rainer Claus, Dietmar Pfeifer, Seishi Ogawa, Michael Lübbert, and Heiko Becker  
Blood, 3 Dec 2015; 126(23): Abstr #3834.

...WGA can lead to allele dropout (ADO), we also sequenced single nucleotide polymorphisms (SNPs), that were identified by **CytoScan HD array** (Affymetrix) to be heterozygous in the sample and that were located nearby the respective mutation loci.

195-

[SIPA1L3 identified by linkage analysis and whole-exome sequencing as a novel gene for autosomal recessive congenital cataract.](#)

Evers C1, Paramasivam N2, Hinderhofer K1, Fischer C1, Granzow M1, Schmidt-Bacher A3, Eils R4, Steinbeisser H1, Schlesner M2, Moog U1.

1Institute of Human Genetics, Heidelberg University, Heidelberg, Germany.; 2Div of Theoretical Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany; 3Dept of Ophthalmology, St Vincentius-Kliniken gAG Karlsruhe, Karlsruhe, Germany; 41] Division of Theoretical Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany [2] Dept for Bioinformatics and Functional Genomics, Institute for Pharmacy and Molecular Biotechnology (IPMB) and BioQuant, Heidelberg University, Heidelberg, Germany.

European Journal of Human Genetics, December 2015, 23(12):1627-1633.

... Array analysis/SNP genotyping Affymetrix **CytoScan HD** Oligo/SNP-Array was performed ...

196- **Meeting abstract**

[SIRPB1: BIOMARKER OF RESPONSE TO 5-AZACITIDINE TREATMENT IN MDS AND AML PATIENTS](#)

V. Guadagnuolo,1 M.C. Fontana,1 C. Papayannidis,1 I. Iacobucci,1 A. Padella,1 G. Simonetti,1 E. Imbrogno,1 S. Paolini,1 M. Abbenante,1 S. Parisi,1 C. Sartor,1 E. Ottaviani,1 A. Ferrari,1 M. Delledonne,2 M. Malagola,3 C. Fili ,3 D. Russo,3 M. Cavo,1 G. Martinelli1  
1L. and A. Seragnoli, Bologna University, Bologna; 2Dept of Biotechnology, Verona University, Verona;  
3University of Brescia, AO Spedali Civili, Brescia, Italy  
Haematologica, 2015, 100(Sup3) : Abstr #C106, p.18. [45° Congress of the Italian Society of Hematology

Florence, Italy, October 4-7, 2015

... To identify the genes mostly predictive of treatment response we use SNP arrays. Materials and Methods: SNPs array was performed by **CytoScan HD Array** (Affymetrix, Inc) ...

197-

[Small bowel malrotation in distal 15q duplication: evidence for a rare association.](#)

McLaughlin, Brooke M.; Hufnagel, Robert B.; Saal, Howard M.

Clinical Dysmorphology, April 2015, 24(2): 65–67.

... SNP microarray analysis was performed using the hybridized Affymetrix **Cytoscan HD GeneChip**

...

198- **Meeting abstract**

[SNP array reveals a new deletion of JAK2 in AML patients](#)

Viviana Guadagnuolo1, Maria Chiara Fontana1, Antonella Padella1, Ilaria Iacobucci1, Cristina Papayannidis1, Giorgia Simonetti1, Anna Ferrari1, Giovanni Marconi1, Stefania Paolini1, Maria Chiara Abbenante1, Sarah Parisi1, Francesca Volpato1, Chiara Sartor1, Emanuela Ottaviani1, Massimo Delledonne2, Michele Cavo1, Guido Biasco3, and Giovanni Martinelli1

1L. & A. Seragnoli, Bologna, Italy; 2Dept of Biotechnology, Verona, Italy; 3Dept of Specialized, Experimental & Diagnostic Medicine, Bologna, Italy.

Cancer Research, 2015;75(15 Suppl):Abst #4848. [AACR 106<sup>th</sup> Annual Mtg, Apr 18-22, 2015, Philadelphia, PA]

Introduction: In Acute Myeloid Leukemia (AML) there is a strong need to develop new diagnostic and therapeutic options: to identify the genes mostly predictive of treatment response, we use Single Nucleotide Polymorphism (SNP) Arrays and Whole Exome Sequencing (WES) in AML patients with heterogeneous karyotypes and different subgroups. Materials and Methods: SNP arrays (**CytoScan HD Array**, Affymetrix Inc.) was positively done in 58 AML samples ... Conclusion: By **SNP arrays** we have identified Copy Number Alterations involving important cancer genes AML and we showed that a new deletion in JAK2 may have a role in overall survival rate. ...

199-

[Somatic copy number losses on chromosome 9q21.33q22.33 encompassing the PTCH1 loci associated with cardiac fibroma](#)

Qianqian Zhang a, 1, Tongjian Wang a, 1, Dong Wang a, Jinxiu Liu a, Wenqian Yu a, Xiangju Liu b, Xiaoli Xiang c, Kai Dong a, Feng You a, Guichun Zhang a, Jifeng Ju a, Meng Zhu a, Wenyuan Duan a, , 2, Bin Qiao a, 2

a Institute of Cardiovascular Disease, General Hospital of Ji'nan Military Region, Ji'nan, China; b Genetics Diagnostic Lab, Tai'an Health Center for Women and Children, Tai'an, China; c Medical Information Institute of Sichuan Province, Chengdu, China

Cancer Genetics, December 2015, 208(12): 615–620.

... peripheral blood and tumor tissues of the patient were both investigated by Affymetrix **CytoScan HD** Chip for copy number analysis. It demonstrated copy number losses on chromosome 9q21.33q22.33 in cardiac fibroma tissue that didn't exist in peripheral blood ...

200-

[Somatic loss of polycystic disease genes contributes to the formation of isolated and polycystic liver cysts](#)

Manoe J Janssen1, Jody Salomon1, Wybrich R Cnossen1, Carsten Bergmann2,3, Rolf Pfundt4, Joost P H

1Dept of Gastroenterology & Hepatology, Radboudumc, Institute for Genetic and Metabolic Diseases, Nijmegen, The Netherlands; 2Dept of Bioscientia, Center for Human Genetics, Ingelheim, Germany; 3Renal Div, Dept of

Medicine, University Freiburg Medical Center, Freiburg, Germany; 4Dept of Human Genetics, Radboudumc, Institute for Genetic and Metabolic Diseases, Nijmegen, The Netherlands

Gut, 2015, 64:688-690.

...copy-number variations and loss of heterozygosity (LOH) regions through genome-wide high resolution cytogenetic array analysis (**CytoScan HD**, Affymetrix) and searched for intragenic mutations by sequencing.6 In the patients with autosomal dominant polycystic...

201-

[Split Hand/Foot Malformation Associated with 7q21.3 Microdeletion: A Case Report](#)

Sivasankaran A.a · Srikanth A.c · Kulshreshtha P.S.c · Anuradha D.b · Kadandale J.S.c · Samuel C.R.a

aDepartment of Genetics, Dr. ALM PG Institute of Basic Medical Sciences, University of Madras, and bDepartment of Medical Genetics, Institute of Obstetrics and Gynecology, Government Hospital for Women and Children, Madras Medical College, Chennai, and cCenter for Human Genetics, Biotech Park, Electronic City Phase I, Bangalore, India

Molecular Syndromology, 2015, 6:287-296.

... Whole-genome array-CGH analysis was performed using Affymetrix **CytoScan® 750K** microarray (Affymetrix Inc., Santa Clara, Calif., USA) consisting of 750,000 oligonucleotide probes across the genome (including 550K unique non-polymorphic probes and 200K SNP probes ...

202-

[Streamlining the OncoScan® Array Procedure for Use in a Clinical Laboratory.](#)

Paxton CN1, Rowe LR1, South ST1.

1ARUP Institute for Clinical and Experimental Pathology®, Salt Lake City, UT.

J Assoc Genet Technol. 2015;41(2):61-5.

... The objective of this study was to identify steps in the **OncoScan** procedure that could be modified to make the process more efficient and technician-friendly in the clinical laboratory setting. ... an adjustment to the overnight hybridization temperature to allow for simultaneous hybridization of **OncoScan** and **CytoScan® arrays**. ...

Related abstract by the same authors, [Validation of a Modified OncoScan Protocol for Use in a Clinical Laboratory](#), Cancer Genetics, June 2015, 208(6): 361.

203-

[Susceptibility allele-specific loss of miR-1324-mediated silencing of the INO80B chromatin-assembly complex gene in pre-eclampsia](#)

Cees B.M. Oudejans1,4,\* , Omar J. Michel1, Rob Janssen2,4, Rob Habets1, Ankie Poutsma1, Erik A. Siermans3, Marjan M. Weiss3, Danny Incarnato5,6, Salvatore Oliviero5,6, Gunilla Kleiverda7, Marie Van Dijk1,4 and Reynir Arngrímsson8

1Dept of Clinical Chemistry, 2Dept of Physiology, 3Dept of Clinical Genetics and 4Institute for Cardiovascular Research, VU University Medical Center, De Boelelaan 1117, 1081 HV Amsterdam, The Netherlands, 5Human Genetics Foundation (HuGeF), Via Nizza 52, 10126 Torino, Italy, 6Dipartimento di Biotecnologie, Chimica e Farmacia, Università degli Studi di Siena, Via Fiorentina 1, 53100 Siena, Italy, 7Depa of Gynecology, Flevo Hospital, Hospitaalweg 1, 1315 RA Almere, The Netherlands and 8Biomedical Center, University of Iceland, Vatnsmýrarvegi 16, 101 Reykjavík, Iceland

Human Molecular Genetics, 2015, 24(1): 118-127.

... The array used, **CytoScan HD**, has greater than 99% sensitivity and can reliably detect ...

204-

[Syndromic craniosynostosis associated with microdeletion of chromosome 19p13.12–19p13.2](#)

Sarah M. Lyon a, Darrel Waggoner b, Sara Halbach b, Erik C. Thorland c, Leila Khorasani d, Russell R. Reid d

a Pritzker School of Medicine, University of Chicago, IL; b Dept of Human Genetics and Pediatrics, University of Chicago, 5841 S. Maryland Ave, M/C 0077, Chicago, IL 60637; c Lab Medicine & Pathology, 200 First St SW, Hilton 970, Rochester, MN 55905-0001; d Dept of Surgery, University of Chicago, 5841 S. Maryland Ave, M/C 0077, Chicago, IL 60637

Genes & Diseases, December 2015, 2(4): 347–352.

... Cytogenomic array analysis was performed using either a custom Agilent oligonucleotide microarray ... analyzed on human genome build hg18 or the Affymetrix **CytoScan HD array** including 750,000 SNP probes and 1.9 million non-polymorphic probes analyzed on hg19.

205-

[Syndromic X-linked intellectual disability segregating with a missense variant in RLIM](#)

Elin Tønne<sup>1</sup>, Rita Holdhus<sup>2</sup>, Christine Stansberg<sup>2</sup>, Asbjørg Stray-Pedersen<sup>1</sup>, Kjell Petersen<sup>3</sup>, Han G Brunner<sup>4</sup>, Christian Gilissen<sup>2,4</sup>, Alexander Hoischen<sup>2,4</sup>, Trine Prescott<sup>1</sup>, Vidar M Steen<sup>2,5</sup> and Torunn Fiskerstrand<sup>2,5</sup>

<sup>1</sup>Dept of Medical Genetics, Oslo University Hospital, Oslo, Norway; <sup>2</sup>Dept of Clinical Science, University of Bergen, Bergen, Norway; <sup>3</sup>Computational Biology Unit, University of Bergen, Bergen, Norway; <sup>4</sup>Dept of Human Genetics, Radboud University Medical Center and Radboud Institute for Molecular Life Sciences (RIMLS), Nijmegen, The Netherlands; <sup>5</sup>Center for Medical Genetics and Molecular Medicine, Haukeland University Hospital, Bergen, Norway

European Journal of Human Genetics, 2015, 23: 1652–1656.

... Affymetrix **Cytoscan HD** containing 2.7 million oligonucleotides was performed ...

206- **Meeting abstract**

[Targeted Detection of Copy Number Variants Using a Myeloid Malignancy Next Generation Sequencing Mutation Panel Allows Comprehensive Genetic Analysis Using a Single Testing Method](#)

Wei Shen, PhD<sup>\*</sup>,<sup>1</sup>, Philippe Szankasi, PhD<sup>2</sup>, Maria Sederberg, MS<sup>\*</sup>,<sup>2</sup>, Jonathan Schumacher, MS<sup>\*</sup>,<sup>2</sup>, Kimberly Frizzell, PhD<sup>\*</sup>,<sup>1</sup>, Elaine P Gee, PhD<sup>\*</sup>,<sup>3</sup>, Jay L Patel, MD<sup>\*</sup>,<sup>4,2</sup>, Sarah T. South, PhD<sup>\*</sup>,<sup>4,5</sup>, Xinjie Xu, PhD<sup>\*</sup>,<sup>4,2</sup>, and Todd W Kelley, MD<sup>4,2</sup>

<sup>1</sup>Genomics, ARUP Laboratories, Salt Lake City, UT; <sup>2</sup>ARUP Institute for Clinical and Experimental Pathology®, Salt Lake City, UT; <sup>3</sup>Clinical Laboratory Informatics and Integration, ARUP Laboratories, Salt Lake City, UT; <sup>4</sup>Dept of Pathology, University of Utah, Salt Lake City, UT; <sup>5</sup>ARUP Institute for Clinical and Experimental Pathology, Salt Lake City, UT

Blood, 3 December 2015; 126: 2887.

... comprehensive genetic profiling of myeloid malignancies requires multiple testing strategies at high cost. In an effort to provide more efficient genetic profiling of these disorders, we designed and tested an algorithm to evaluate for CNVs using sequence coverage data derived from a NGS-based 53-gene myeloid mutation panel ... CNVs were detected using a circular binary segmentation algorithm. In a subset of cases (n=43) CNVs detected using NGS data were validated by comparing to the results obtained by SNP microarray (**CytoScan HD Array**, Affymetrix) testing, the current gold standard, and analyzed by CHAS 2.0 (Affymetrix) and Nexus 7.5 (Biodiscovery). ...

207-

[Thalassemia Intermedia Caused by 16p13.3 Sectional Duplication in a  \$\beta\$ -Thalassemia Heterozygous Child](#)

Sha Liu, Hua Jiang, Man-Yu Wu, Yong-Ling Zhang, and Dong-Zhi Li

Dept of Hematology/Oncology, Guangzhou Women & Children Medical Center affiliated to Guangzhou Medical University, Guangzhou, Guangdong, China; Prenatal Diagnostic Center, Guangzhou Women & Children Medical Center affiliated to Guangzhou Medical University, Guangzhou, Guangdong, China

Pediatric Hematology-Oncology, 2015, 32(5): 349-353.

... Sample preparation, array hybridization, and analysis of the results were performed according to the manufacturer's instructions (Affymetrix **CytoScan High-Density Array**; ...

208- **Meeting abstract**

[THE CODING GENOME OF NODAL MARGINAL ZONE LYMPHOMA REVEALS RECURRENT MOLECULAR ALTERATIONS OF PTPRD AND OTHER JAK/STAT SIGNALING GENES](#)

V. Spina,<sup>1</sup> A. Brusca, <sup>1</sup> H. Khiabani, <sup>2</sup> L. Martuscelli, <sup>1</sup> E. Spaccarotella, <sup>1</sup> M. Messina, <sup>3</sup> S. Monti, <sup>1</sup> A.B. Holmes, <sup>4</sup> S. Chiaretti, <sup>3</sup> L. Arcaini, <sup>5</sup> M. Lucioni, <sup>6</sup> F. Tabbò, <sup>7</sup> S. Rasi, <sup>1</sup> S. Zairis, <sup>2</sup> A. Ramponi, <sup>8</sup> R. Marasca, <sup>9</sup> M. Ponzoni, <sup>10</sup> E. Tiacci, <sup>11</sup> B. Falini, <sup>11</sup> F. Bertoni, <sup>12</sup> L. Pasqualucci, <sup>4</sup> R. Foà, <sup>3</sup> G. Inghirami, <sup>7</sup> R. Rabadan, <sup>2</sup> G. Gaidano, <sup>1</sup> D. Rossi<sup>1</sup>

<sup>1</sup>Div of Hematology, Dept of Translational Medicine, Amedeo Avogadro University of Eastern Piedmont, Novara, Italy; <sup>2</sup>Dept of Biomedical Informatics and Center for Computational Biology and Bioinformatics Columbia University, New York, USA; <sup>3</sup>Div of Hematology, Dept of Cellular Biotechnologies and Hematology, Sapienza University, Roma, Italy; <sup>4</sup>Institute for Cancer Genetics and the Herbert Irving Comprehensive Cancer Center, Columbia University, New York; <sup>5</sup>Dept of Hematology-Oncology, Fondazione IRCCS Policlinico San Matteo and Dept of Molecular Medicine, University of Pavia, Pavia, Italy; <sup>6</sup>Division of Pathology, Fondazione IRCCS Policlinico San Matteo, University of Pavia, Pavia, Italy; <sup>7</sup>Dept of Pathology and Laboratory Medicine, Weill Cornell Medical College, New York; <sup>8</sup>Div of Pathology, Dept of Health Science, Amedeo Avogadro University of Eastern Piedmont, Novara, Italy; <sup>9</sup>Div of Hematology, Dept of Oncology and Hematology, University of Modena and Reggio Emilia, Modena, Italy; <sup>10</sup>Unit of Lymphoid Malignancies, San Raffaele H. Scientific Institute, Milan, Italy; <sup>11</sup>Institute of Hematology, Ospedale S. Maria della Misericordia, Univ of Perugia, Perugia, Italy; <sup>12</sup>Lymphoma and Genomics Research Program, IOR Institute of Oncology Research and Oncology Institute of Southern Switzerland, Bellinzona, Switzerland

Haematologica, 2015, 100(Sup3) : Abstr #C028, p.18. [45° Congress of the Italian Society of Hematology

Florence, Italy, October 4-7, 2015

Nodal marginal zone lymphoma (NMZL) is one of the few B-cell tumors still remaining orphan of cancer gene lesions. Here we aim at disclosing the pathways that are molecularly deregulated in this lymphoma. The study was based on 35 NMZL with a diagnosis confirmed by pathological revision and

lack of clinico-radiological evidence of extranodal or splenic disease. WES (HiSeq 2500, Illumina) and high density SNP array (**Cytoscan HD**, Affymetrix) of tumor/normal DNA pairs from 18 discovery NMZL ...

209- *Meeting abstract*

[THE CLINICAL UTILITY OF SNP ARRAY ANALYSIS IN MYELODYSPLASTIC SYNDROME PATIENTS: RESULTS FROM A UK DIAGNOSTIC GENETIC LABORATORY USING THE AFFYMETRIX CYTOSCAN HD 2.6M SNP ARRAY](#)

N. Trim, E. Huxley, M. Griffiths, S. Jeffries

1West Midlands Regional Genetic Laboratory, Birmingham Women's Hospital, Birmingham, United Kingdom  
Leukemia Research, April 2015, 39(Sup 1):S80-S81, Abst #157. [13th Intl Symp Myelodysplastic Syndromes]

... The aim of the study is: to establish the benefits of using SNP arrays in a haematology setting; to determine the utility of SNP array as the primary test for MDS patients to replace metaphase chromosomes; to determine whether blood may be used instead of marrow; and to collate the additional genomic/genetic abnormalities that are detected. Analysis is being performed using the Affymetrix **Cytoscan HD** SNP array containing 2.6 million markers for copy number analysis including approximately 750,000 SNPs. We present some of the preliminary findings from the first 100 samples including abnormality rates, failure rates and types of abnormalities detected with focus on individual cases to demonstrate the clinical utility of SNP arrays above that of metaphase chromosome analysis.

210-

[The future of laboratory medicine — A 2014 perspective](#)

Larry J. Kricka a, Tracey G. Polsky a, b, Jason Y. Park c, Paolo Fortina d, e

aDept of Pathology and Laboratory Medicine, University of Pennsylvania School of Medicine, 7.103 Founders Pavilion, 3400 Spruce Street, Philadelphia, PA 19104; bDept of Pathology and Laboratory Medicine, Children's Hospital of Philadelphia, Philadelphia, PA 19104; cDept of Pathology and the Eugene McDermott Center for Human Growth and Development, Univ of Texas Southwestern Medical Center, Children's Medical Center, 1935 Medical District Dr, Dallas, TX 75235; dCancer Genomics Laboratory, Kimmel Cancer Center, Dept of Cancer Biology, Sidney Kimmel Medical College, Thomas Jefferson Univ, Philadelphia, PA; eDept of Molecular Med, Universita' La Sapienza, Rome, Italy

Clinica Chimica Acta, 1 January 2015, 438: 284–303. doi:10.1016/j.cca.2014.09.005

... This review surveys the many predictions, beginning in 1887, about the future of laboratory medicine and its sub-specialties such as clinical chemistry and molecular pathology. It provides a commentary on the accuracy of the predictions and offers opinions on emerging technologies, economic factors and social developments that may play a role in shaping the future of laboratory medicine. ... In 2014, the FDA cleared the **Cytoscan HD** high density SNP array (Affymetrix) for use in the diagnosis of developmental delay, intellectual disability and congenital anomalies [141].

211-

[The genomic landscape of pheochromocytoma](#)

Aidan Flynn, Diana Benn, Roderick Clifton-Bligh, Bruce Robinson, Alison H Trainer, Paul James, Annette Hogg, Kelly Waldeck, Joshy George, Jason Li, Stephen B Fox, Anthony J Gill, Grant McArthur, Rodney J Hicks, Richard W Tothill

The Journal of Pathology, May 2015, 236(1): 78–89.

Pheochromocytomas (PCC) and paragangliomas (PGL) are rare neural crest derived tumours originating from adrenal chromaffin cells or extra-adrenal sympathetic and parasympathetic tissues. ... To explore the genomic landscape of PCC/PGL we applied exome-sequencing, high-density SNP-array analysis and RNA-sequencing to 36 PCC and four functional PGL tumours. ... Affymetrix **Cytoscan HD** array data is made available through NCBI GEO (<http://www.ncbi.nlm.nih.gov/geo/>, GEO Accession ID: GSE61594 ...

212-

[The Human Glioblastoma Cell Culture Resource: Validated Cell Models Representing All Molecular Subtypes](#)

Yuan Xie a, 1, Tobias Bergström a, 1, Yiwen Jiang a, 1, Patrik Johansson a, 1, Voichita Dana Marinescu a, Nanna Lindberg b, Anna Segerman a, Grzegorz Wicher a, Mia Niklasson a, Sathishkumar Baskaran a, Smitha Sreedharan a, Isabelle Everlien a, Marianne Kastemar a, Annika Hermansson a, Lioudmila Elfineh a, Sylwia Libard a, Eric Charles Holland b, Göran Hesselager c, Irina Alafuzoff a, Bengt Westermark a, 2, Sven Nelander a, 2, Karin Forsberg-Nilsson a, 2, Lene Uhrbom a, 2

a Dept of Immunology, Genetics and Pathology, Science for Life Laboratory, Rudbeck Laboratory, Uppsala University, 751 85 Uppsala, Sweden; b Fred Hutchinson Cancer Research Center, 1100 Fairview Ave N., PO Box

19024, Seattle, WA 98109; c Dept of Neuroscience, Uppsala University, Uppsala University Hospital, SE-751 85 Uppsala, Sweden

EbioMedicine, October 2015, 2(10): 1351–1363.

... Total RNA extracted from 48 GC lines ... labeled and hybridized on Affymetrix GeneChip **Human Exon 1.0 ST** arrays. ... copy number aberration in all of our 48 GC lines employing Affymetrix **Cytoscan HD** arrays ... RNA was prepared from cells and tumor tissue and analyzed on the **Affymetrix HTA 2.0** platform.

213-

[The phenotype spectrum of X-linked ichthyosis identified by chromosomal microarray](#)

Jennifer L. Hand, MDa, b, c, Cassandra K. Runke, CGCd, Jennelle C. Hodge, PhDb, d, e  
a Dept of Dermatology, Mayo Clinic, Rochester, MN; b Dept of Medical Genetics, Mayo Clinic, Rochester, MN; c Dept of Pediatric and Adolescent Medicine, Mayo Clinic, Rochester, MN; d Dept of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, MN; e Dept of Pathology and Laboratory Medicine, Cedars-Sinai Medical Center, Los Angeles, CA

Dermatology, April 2015, 72(4): 617–627.

... submitted to the Mayo Clinic Cytogenetics Laboratory from March 4, 2008 to September 3, 2013 for CMA analysis using either a 4x44K or 4x180K oligonucleotide–based whole-genome cytogenomic microarray (**Agilent** Technologies, ... or **Cytoscan HD array** ...

214-

[The Protein Tyrosine Phosphatase Rptpζ Suppresses Osteosarcoma Development in Trp53-Heterozygous Mice](#)

Christina Baldauf, Anke Jeschke, Vincent Kanbach, Philip Catala-Lehnen, Daniel Baumhoer, Helwe Gerull, Sophia Buhs, Michael Amling, Peter Nollau, Sheila Harroch, Thorsten Schinke

PLoS ONE, 11 Sept 2015, 10(9): e0137745.

... We additionally isolated RNA from CD11b-negative osteoblast cultures at day 5 and day 12 of differentiation to perform genome-wide expression analysis using Affymetrix Gene Chips (**Affymetrix MG 430 2.0**). ... To address the question, if Rptpζ would also act as a tumor suppressor in human OS, we first analyzed copy number data sets (**CytoScan** Arrays) from 160 human OS samples for chromosomal alterations around the PTPRZ1 locus on chromosome 7q31.3, yet we did not detect any specific changes supporting a contribution of PTPRZ1 loss to OS development or severity.

215-

[The role of candidate-gene CNTNAP2 in childhood apraxia of speech and specific language impairment](#)

TM Centanni<sup>1,2</sup>, JN Sanmann<sup>3</sup>, JR Green<sup>1</sup>, J Iuzzini-Seigel<sup>1,4</sup>, C Bartlett<sup>5</sup>, WG Sanger<sup>3,†</sup>, TP Hogan<sup>1,\*</sup>

<sup>1</sup>MGH Institute of Health Professions, Boston, MA; <sup>2</sup>Massachusetts Institute of Technology, Cambridge, MA; <sup>3</sup>University of Nebraska Medical Center, Nebraska Medical Center, Omaha, NE; <sup>4</sup>Marquette University, Milwaukee, MI; <sup>5</sup>The Ohio State University, Columbus, OH

American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, October 2015, 168(7): 536–543.

... High-resolution genome-wide analysis was performed on genomic DNA using the **CytoScanHD™** array (Affymetrix, Santa Clara, CA) according to manufacturer's instruction. ...

216-

[The senescent microenvironment promotes the emergence of heterogeneous cancer stem-like cells](#)

Luis Jaime Castro-Vega<sup>1,2,\*</sup>, Karina Jouravleva<sup>1,2,\*</sup>, Paola Ortiz-Montero<sup>3</sup>, Win-Yan Liu<sup>1,2</sup>, Jorge Luis Galeano<sup>3</sup>, Martha Romero<sup>4</sup>, Tatiana Popova<sup>5</sup>, Silvia Bacchetti<sup>6</sup>, Jean Paul Vernot<sup>3</sup>, Arturo Londoño-Vallejo<sup>1,2</sup>

<sup>1</sup>UMR3244, Telomeres and Cancer Laboratory, "Labellisé Ligue", Institut Curie, Paris 75248, France; <sup>2</sup>UPMC University - Paris 06, Paris 75005, France; <sup>3</sup>Cellular and Molecular Physiology Group, Instituto de Investigaciones Biomédicas, Faculty of Medicine, Universidad Nacional de Colombia, Bogotá D.C, Colombia; <sup>4</sup>Dept of Pathology, Hospital Universitario-Fundación Santa Fe de Bogotá, Bogotá, Colombia; <sup>5</sup>U830 Genetics and Cancer Biology, Institut Curie, Paris 75248, France; <sup>6</sup>Dept of Experimental Oncology, Istituto Regina Elena, Rome 00158, Italy

Carcinogenesis, 2015, 36(10): 1180-1192.

... Here we show that post-crisis cells are not able to form tumors unless a senescent microenvironment is provided. ... Affymetrix **Cytoscan HD** arrays were hybridized with labeled DNA from PC1, PC2 and the four explanted cell lines.



217-

[TP53 mutation analysis in chronic lymphocytic leukemia: comparison of different detection methods.](#)

Kantorova B, Malcikova J, Smardova J, Pavlova S, Trbusek M, Tom N, Plevova K, Tichy B, Truong S, Diviskova E, Kotaskova J, Oltova A, Patten N, Brychtova Y, Doubek M, Mayer J, Pospisilova S.

Tumour Biol. 2015 May;36(5):3371-80.

... In 15 of the TP53-mutated patients, TP53 gene abnormalities or copy-neutral loss of heterozygosity (cn-LOH) were analyzed using **Cytogenetics Whole-Genome 2.7 M Array** (n=9; Affymetrix) and **CytoScan® High Density Array** (n=6; Affymetrix).

218-

[Typical and Atypical Associated Findings in a Group of 346 Patients with Mayer-Rokitansky-Kuester-Hauser Syndrome](#)

Katharina Rall, MD1, Simone Eisenbeis, PhD1, Verena Henninger, MD1, Melanie Henes, MD1, Diethelm Wallwiener, MD1, Michael Bonin, PhD2, Sara Brucker, MD1

1 University Hospital Tuebingen, Dept of Obstetrics and Gynecology, Tuebingen, Germany; 2 University Hospital Tuebingen, Dept of Medical Genetics, Microarray Facility, Tuebingen, Germany

Journal of Pediatric and Adolescent Gynecology, October 2015, 28(5): 362–368.

... The Mayer-Rokitansky-Kuester-Hauser (MRKH) syndrome is characterized by vaginal and uterine aplasia in a 46,XX individual. ... analysis using Human Mapping **CytoScan HD Array** (Affymetrix, Santa Clara, CA) detected 4 times euchromatin from the region 22q11.1-22q11.21.

219-

[Understanding the role of hyperdiploidy in myeloma prognosis: which trisomies really matter?](#)

Marie-Lorraine Chretien1,\* , Jill Corre2,\* , Valerie Lauwers-Cances3, Florence Magrangeas4, Alice Cleynen2, Edwige Yon3, Cyrille Hulin5, Xavier Leleu6, Frederique Orsini-Piocelle7, Jean-Sebastien Blade8, Claudine Sohn9, Lionel Karlin10, Xavier Delbrel11, Benjamin Hebraud12, Murielle Roussel12, Gerald Marit13, Laurent Garderet14, Mohamad Mohty14, Philippe Rodon15, Laurent Voillat16, Bruno Royer17, Arnaud Jaccard18, Karim Belhadj19, Jean Fontan20, Denis Caillot1, Anne-Marie Stoppa21, Michel Attal12, Thierry Facon6, Philippe Moreau22, Stephane Minvielle4, and Hervé Avet-Loiseau2

1Dept of Hematology, Centre Hospitalier Universitaire, Dijon, France; 2Unit for Genomics in Myeloma, Institut Universitaire du Cancer-Oncopole, and Centre de Recherches sur le Cancer de Toulouse INSERM 1037, Toulouse, France; 3Service d'Epidemiologie, Centre Hospitalier Universitaire, Toulouse, France; 4Unité Mixte de Génomique du Cancer, Centre Hospitalier Universitaire, and INSERM U892, Nantes, France; 5Dept of Hematology, Centre Hospitalier Universitaire, Nancy, France; 6Dept of Hematology, Centre Hospitalier Universitaire, Lille, France; 7Dept of Hematology, Centre Hospitalier, Annecy, France; 8Dept of Hematology, Centre Hospitalier Universitaire, Nancy, France; 9Dept of Hematology, Hopital Inter-Armées, Toulon, France; 10Dept of Hematology, Centre Hospitalier, Toulon, France; 11Dept of Hematology, Centre Hospitalier, Pau, France; 12Dept of Hematology, Institut Universitaire du Cancer, Toulouse, France; 13Dept of Hematology, Centre Hospitalier Universitaire, Bordeaux, France; 14Dept of Hematology, Centre Hospitalier Universitaire St-Antoine, Paris, France; 15Dept of Hematology, Centre Hospitalier, Perigueux, France; 16Dept of Hematology, Centre Hospitalier, Chalon sur Saone, France; 17Dept of Hematology, Centre Hospitalier Universitaire, Amiens, France; 18Dept of Hematology, Centre Hospitalier Universitaire, Limoges, France; 19Dept of Hematology, Centre Hospitalier Universitaire, Créteil, France; 20Dept of Hematology, Centre Hospitalier Universitaire, Besançon, France; 21Dept of Hematology, Institut Paoli Calmettes, Marseille, France; 22Dept of Hematology, Centre Hospitalier Universitaire, Nantes, France

Blood, 17 December 2015, 126(25): 2713 – 2719.

... For the first time ... we show that not all trisomies display the same prognostic impact. ... We analyzed by SNP array (Affymetrix, ... using either the **SNP6.0 array** or the **Cytoscan array** ...

220-

[Uniparental Trisomy of a Mutated HRAS Proto-Oncogene in Embryonal Rhabdomyosarcoma of a Patient With Costello Syndrome](#)

Jan Menke, Silke Pauli, Matthias Sigler, Ingrid Kühnle, Moneef Shoukier, Barbara Zoll, Christina Ganster, Gabriela Salinas-Riester and Inga-Marie Schaefer

University Medical Center Goettingen, Goettingen, Germany

Journal of Clinical Oncology, May 1, 2015, 33(13):e62-e65.

... In the tumor, fluorescent in situ hybridization and single nucleotide polymorphism (SNP) microarray analysis (**CytoScan HD**; Affymetrix, Santa Clara, CA) indicated trisomy of chromosome 11.

221- **Meeting abstract**

### [Unique pattern of copy number changes including chromothripsis in pulmonary adenocarcinoma with EML4-ALK fusion](#)

Hironori Ninomiya<sup>1</sup>, Motohiro Kato<sup>2</sup>, Seishi Ogawa<sup>2</sup>, Noriko Motoi<sup>1</sup>, Kengo Takeuchi<sup>1</sup>, Tatsushi Kodama<sup>3</sup>, Hiroshi Sakamoto<sup>3</sup>, Nobuya Ishii<sup>3</sup>, Mutsunori Fujiwara<sup>4</sup>, and  
<sup>1</sup>Japanese Foundation for Cancer Research, Tokyo, Japan; <sup>2</sup>Cancer Genomics Project, The University of Tokyo, Tokyo, Japan; <sup>3</sup>Chugai Pharmaceutical Co., Ltd., Kamakura, Japan; <sup>4</sup>Japanese Red Cross Medical Center, Tokyo, Japan.

Cancer Research, 2015;75(15 Suppl):Abst #3853. [AACR 106<sup>th</sup> Annual Mtg, Apr 18-22, 2015, Philadelphia, PA]

... To elucidate the underlying mechanisms resulting in gene fusion, two cancer cell lines positive for EML4-ALK fusion and surgically resected frozen specimens (33 ALK fusion-positive and 95 ALK fusion-negative adenocarcinomas) were analyzed using Affymetrix **CytoScan HD** Array with Chromosome Analysis Suite (ChAS) software for cell lines (JFCR-LC649 and JFCR-LC654) and Affymetrix **GeneChip Mapping 250K arrays** for surgical specimens. ...

222-

### [Unusual Genetic Aberrations Including a Deletion of KLF6 Tumor Suppressor Gene Revealed by Integrated Cytogenetic Approaches in a Pediatric Ewing Sarcoma](#)

White, Jason C. DO<sup>1\*</sup>; Halligan, Gregory E. MD<sup>\*</sup>; de Chadarévian, Jean-Pierre MD<sup>†</sup>; Pascasio, Judy M. MD<sup>†</sup>; Punnet, Hope H. PhD<sup>†</sup>; Liu, Jinglan PhD<sup>†</sup>

<sup>1\*</sup>Dept of Pediatrics, Section of Oncology <sup>†</sup>Dept of Pathology and Laboratory Medicine, Drexel University College of Medicine and St. Christopher's Hospital for Children, Philadelphia, PA.

Journal of Pediatric Hematology/Oncology, Jan 2015, 37(1):e51–e54.

... SNP microarray assay using Affymetrix **CytoScan HD SNP array** on the frozen tumor specimen showed an interstitial hemizygous deletion from nucleotide 3,032,920 to 6,609,423 (NCBI build 37.1/hg19) on the short arm of chromosome 10 at 10p15.2p14, spanning ...

223-

### [Unusual Presentation of Pelizaeus-Merzbacher Disease: Female Patient with Deletion of the Proteolipid Protein 1 Gene](#)

Teva Breder, Donna Wallerstein, John Sum, and Robert Wallerstein  
Silicon Valley Genetics Center, Santa Clara Valley Medical Center, San Jose, CA 95128, USA

Case Reports in Genetics, accepted 10 Feb 2015, 2015:Article #453105.

... Genetic testing performed by chromosome microarray using the Affymetrix **Cytoscan HD** platform with 743,000 SNP probes showed a 712KB interstitial deletion on the X chromosome at position Xq22.2.

224-

### [Use of Affymetrix arrays in the diagnosis of gene copy-number variation](#)

Farah R. Zahir and Marco A. Marra

<sup>1</sup>Canada's Michael Smith Genome Sciences Centre, BC Cancer Agency, Vancouver, British Columbia, Canada; <sup>2</sup>Univ of British Columbia, Dept of Medical Genetics, Vancouver, British Columbia, Canada

Current Protocols in Human Genetics, Unit 8.13, online 1 April 2015.

... Here we discuss the application of the **CytoScan high-density (HD) platform** for the detection of genomic imbalance. We provide an overview of the sequence of computational analyses involved in identifying pathogenic CNVs and highlight important parameters for consideration in assessing the pathogenicity of a detected CNV.

225-

### [Using extended pedigrees to identify novel autism spectrum disorder \(ASD\) candidate genes](#)

Marc Woodbury-Smith<sup>1,2</sup>, Andrew D. Paterson<sup>2,6</sup>, Bhooma Thiruvahindrapduram<sup>2</sup>, Anath C. Lionel<sup>2</sup>, Christian R. Marshall<sup>2</sup>, Daniele Merico<sup>2</sup>, Bridget A. Fernandez<sup>3</sup>, Eric Duku<sup>1</sup>, James S. Sutcliffe<sup>8</sup>, Irene O'Conner<sup>1</sup>, Christina Chrysler<sup>1</sup>, Ann Thompson<sup>1</sup>, Barbara Kellam<sup>2</sup>, Kristiina Tammimies<sup>2</sup>, Susan Walker<sup>2</sup>, Ryan K. C. Yuen<sup>2</sup>, Mohammed Uddin<sup>2</sup>, Jennifer L. Howe<sup>2</sup>, Morgan Parlier<sup>5</sup>, Kathy Whitten<sup>3</sup>, Peter Szatmari<sup>7</sup>, Veronica J. Vieland<sup>4</sup>, Joseph Piven<sup>5</sup>, Stephen W. Scherer<sup>2</sup>

<sup>1</sup>. Dept of Psychiatry and Behavioural Neurosciences, McMaster University, Chedoke Campus (Evel Building, Rm 457), Hamilton, ON, Canada; <sup>2</sup>. Program in Genetics and Genome Biology, The Centre for Applied Genomics, The Hospital for Sick Children, Toronto, ON, Canada; <sup>3</sup>. Provincial Medical Genetics Program, Memorial Hospital, St John's, Newfoundland, Canada; <sup>4</sup>. Battelle Center for Mathematical Medicine, Nationwide Children's Hospital, Columbus, OH, USA; <sup>5</sup>. Carolina Institute for Developmental Disabilities, University of North Carolina, Wilmington, NC; <sup>6</sup>. Dalla Lana School of Public Health, University of Toronto, Toronto, ON, Canada; <sup>7</sup>. Centre for Addiction and Mental Health, The Hospital for Sick Children and University of Toronto, Toronto, ON, Canada; <sup>8</sup>. Vanderbilt University Medical Center, Vanderbilt University, Nashville, TN

Human Genetics, February 2015, 134(2):191-201

... additional controls included 4,768 individuals from the SAGE and HABC datasets typed on Illumina1 M, 2,357 OHI and POPGEN controls typed on the Affymetrix **SNP 6.0** platform, and 863 OPGP controls typed on **Affymetrix CytoscanHD**.

226- **Meeting abstract**

[Very poor outcome and chemoresistance of acute myeloid leukemia patients with TP53 mutations: Correlation with complex karyotype and clinical outcome.](#)

Cristina Papayannidis, Anna Ferrari, Stefania Paolini, Carmen Baldazzi, Chiara Sartor, Maria Chiara Abbenante, Sarah Parisi, Francesca Volpato, Ilaria Iacobucci, Antonella Padella, Viviana Guadagnuolo, Margherita Perricone, Valentina Robustelli, Claudia Venturi, Giorgia Simonetti, Elisa Zuffa, Eugenia Franchini, Emanuela Ottaviani, Nicoletta Testoni, and Giovanni Martinelli

"Seràgnoli" Institute of Hematology, Bologna University School of Medicine, Bologna, Italy.

Clinical Cancer Research, Sep 2015; 21: Abstract #B03. [AACR Special Conference on Hematologic Malignancies: Translating Discoveries to Novel Therapies; September 20-23, 2014; Philadelphia, PA]

... we focused on a subgroup of 172/886 AML pts treated at the Seràgnoli Institute of Bologna between 2002 and 2013. ... 40 samples were genotyped with Genome-Wide Human **SNP 6.0 arrays** or with **CytoScan HD Array** (Affymetrix) and analysed by Nexus Copy Number™ v7.5 (BioDiscovery). ... Copy Number Alterations (CNAs) analysis performed on 40 cases by **Affymetrix SNP arrays** showed the presence of several CNAs in all cases ... We recommend TP53 mutation screening at least in AML pts carrying either complex karyotype or chr. 8 gain.

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[When Cri du chat syndrome meets Edwards syndrome](#)

Yingjun Xie, Yi Zhou, Jianzhu Wu, Yunxia Sun, Yongzhen Chen, Baojiang Chen

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Molecular Medicine Reports, 15 March 2015, 11(3): 1933-1938.

doi:10.3892/mmr.2014.2920

... CEL files obtained by scanning **CytoScan arrays** were analyzed with the Chromosome Analysis Suite software (Affymetrix), employing genome annotation data (version GRCH37, hg19).

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[Whole-exome sequencing of breast cancer, malignant peripheral nerve sheath tumor and neurofibroma from a patient with neurofibromatosis type 1](#)

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Cancer Medicine, December, 4(12): 1871–1878,.

... For higher resolution, the blood, dermal neurofibroma and primary breast tumor samples were assayed using the Affymetrix **CytoScan HD** platform ...

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[Whole-genome sequencing of quartet families with autism spectrum disorder](#)

Ryan K C Yuen, Bhooma Thiruvahindrapuram, Daniele Merico, Susan Walker, Kristiina Tammimies, Ny Hoang, Christina Chrysler, Thomas Nalpathamkalam, Giovanna Pellicchia, Yi Liu, Matthew J Gazzellone, Lia D'Abate, Eric Deneault, Jennifer L Howe, Richard S C Liu, Ann Thompson, Mehdi Zarrei, Mohammed Uddin, Christian R Marshall, Robert H Ring, Lonnie

Zwaigenbaum, Peter N Ray, Rosanna Weksberg, Melissa T Carter, Bridget A Fernandez, Wendy Roberts, Peter Szatmari, Stephen W Scherer  
Nature Medicine, 2015, 21: 185–191.

... 40 of the 85 quartet families were run in parallel using the **CytoScan HD Array** (Affymetrix, Santa Clara, CA).

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[Wiskott-Aldrich Syndrome in a Girl Caused by Heterozygous WASP Mutation and Extremely Skewed X-Chromosome Inactivation: A Novel Association with Maternal Uniparental Isodisomy 6](#)

Takimoto T.a· Takada H.b· Ishimura M.a· Kirino M.a· Hata K.d· Ohara O.c· Morio T.e· Hara T.a

aDepts of Pediatrics and bPerinatal and Pediatric Medicine, Graduate School of Medical Sciences, Kyushu University, Fukuoka, cDept of Human Genome Technology, Kazusa DNA Research Institute, Kisarazu, dDept of Maternal-Fetal Biology, National Research Institute for Child Health and Development, eDept of Pediatrics and Developmental Biology, Graduate School of Medicine, Tokyo Medical and Dental University, Tokyo, Japan  
Neonatology, 2015, 107: 185-190.

... SNP microarray analysis was performed using the Affymetrix **Cytoscan HD** platform [17] which uses over 743,000 SNP probes and 1,953,000 NPCN probes with a median spacing of 0.88 kb.

231- **Meeting abstract**

[Y Chromosome Microdeletion Detection by Cytoscan HD Microarray Platform](#)

Maria C. Sederberg, Leslie R. Rowe, Allen N. Lamb

ARUP Laboratories, Department of Pathology, University of Utah, Salt Lake City, UT, USA

Cancer Genetics, June 2015, 208(6): 359. Available online 22 July 2015

... Many laboratories do not report Y microdeletions in studies of patients with DD/ID, autism, or dysmorphism. It is important to understand how well the Affymetrix **Cytoscan HD** detects AZF deletions, to recognize when mosaicism exist, and when a rearranged Y is present. ...