

# CURRICULUM VITAE

## MARIEKE L. KUIJER, PhD



**Date of birth** February 5, 1982  
**Place of birth** Zaanstad, the Netherlands  
**Nationality** Dutch

### PROFESSIONAL EXPERIENCE

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<b>PERIOD</b>	<b>October 1, 2018 – present</b>	
<b>EMPLOYER</b>	<b>Centre for Molecular Medicine Norway</b>	Oslo, Norway
<b>UNIVERSITY</b>	<b>University of Oslo</b>	
<b>JOB TITLE</b>	<b>Group leader</b>	

<b>PERIOD</b>	<b>July 1, 2013 – August 31, 2018</b>	
<b>EMPLOYER</b>	<b>Dana-Farber Cancer Institute</b>	Boston, MA, USA
<b>UNIVERSITY</b>	<b>Harvard T.H. Chan School of Public Health</b>	
<b>DEPARTMENT</b>	<b>Biostatistics and Computational Biology</b>	
<b>JOB TITLE</b>	<b>Research Fellow</b>	

<b>PERIOD</b>	<b>May 6, 2013 – June 30, 2013</b>	
<b>EMPLOYER</b>	<b>Dana-Farber Cancer Institute</b>	Boston, MA, USA
<b>UNIVERSITY</b>	<b>Harvard T.H. Chan School of Public Health</b>	
<b>DEPARTMENT</b>	<b>Biostatistics and Computational Biology</b>	
<b>JOB TITLE</b>	<b>Visiting scientist</b>	

<b>PERIOD</b>	<b>December 1, 2008 – November 30, 2012</b>	
<b>EMPLOYER</b>	<b>Leiden University Medical Center</b>	Leiden, The Netherlands
<b>UNIVERSITY</b>	<b>Leiden University</b>	
<b>DEPARTMENT</b>	<b>Pathology</b>	
<b>JOB TITLE</b>	<b>PhD student</b>	

### EDUCATION

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<b>PERIOD</b>	<b>December 1, 2008 – June 26, 2013</b>	
<b>DEGREE</b>	<b>Doctor of Philosophy in Cancer Genomics</b>	
<b>UNIVERSITY</b>	<b>Leiden University</b>	Leiden, The Netherlands

Title of dissertation: “A systems biology approach to study high-grade osteosarcoma.” Advisors: Pancras Hogendoorn, MD PhD and Anne-Marie Cleton-Jansen, PhD.

<b>PERIOD</b>	<b>September 2006 – December 2008</b>	
<b>DEGREE</b>	<b>Master of Science in Biomedical Sciences</b>	
<b>UNIVERSITY</b>	<b>Leiden University</b>	Leiden, the Netherlands

Master’s thesis (Molecular Cell Biology): “Targeting sclerostin to control bone formation.” Advisors: Peter ten Dijke, PhD and David de Gorter, PhD. Master’s trainee (Human Genetics): “Integrated analysis of copy number and expression microarray data.” Mentor: Judith Boer, PhD.

PERIOD	<b>January – June 2005, September – December 2006, October 2007 – January 2008</b>
STUDIES	<b>Biomedical Sciences</b>
UNIVERSITY	<b>Karolinska Institutet</b> <span style="float: right;">Stockholm, Sweden</span>

Full undergraduate semester and Master’s degree specialization courses.

PERIOD	<b>September 2003 – July 2007</b>
DEGREE	<b>Bachelor of Science in Biomedical Sciences</b>
RANK	<b>Propaedeutics with distinction</b>
UNIVERSITY	<b>Leiden University</b> <span style="float: right;">Leiden, the Netherlands</span>

Bachelor’s thesis (Molecular Cell Biology): “Generating fluorescent pumilio proteins to measure pumilio mobility in living cells.” Advisor: Carolina Jost, PhD.

## AWARDS AND HONORS

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- Charles A. King Postdoctoral Fellowship, Sara Elizabeth O’Brien and Bank of America, co-Trustees. Project title: “Modeling the effects of gene regulation on cancer survival.” September 2016–August 2018 (\$94,350)
- National Cancer Institute Brain Cancer Specialized Program of Research Excellence Career Enhancement Program Award. Project title: “Modeling the effects of gene regulation on glioblastoma development and progression.” August 2016–July 2017 (\$50,000)
- Harvard T.H. Chan School of Public Health Program in Quantitative Genomics travel award for the AACR conference Computational and Systems Biology of Cancer. January 2015
- Hope Funds for Cancer Research postdoctoral fellowship finalist in 2014 (top 8/184 applications) and 2015 (top 20/240 applications)
- Leiden University PhD award for successfully completing the doctorate without extension of the contract. June 2013
- Dutch Cancer Society (KWF) sponsorship to cover printing costs of the PhD thesis. June 2013
- Leiden University Fund travel grant for the EMBO conference “From systems biology to functional genomics.” November 17–20, 2012, Heidelberg, Germany
- Best presentation award. Dutch Cancer Society (KWF) Tumor cell biology meeting. November 6, 2012, Lunteren, the Netherlands
- Two Outbound Study Grant scholarships for following Master’s courses at the Karolinska Institute, Stockholm Sweden in the academic years of 2006–2007 and 2007–2008
- Erasmus scholarship to study a semester at the Karolinska Institute, Stockholm Sweden. January–June 2005

## PROFESSIONAL SOCIETIES

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- Cancer Epigenetics Society, November 2016–present
- American Association for Cancer Research, December 2014–present

## EDITORIAL DUTIES

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- Editorial Board member of *Cancer Research*, February 2016 – present
- Reviewer for *Cancer Research*, *BMC Research Notes*, *BMC Medical Genomics*, *G3*, *Experimental and Molecular Pathology*, *ESUN*, *Journal of Carcinogenesis & Mutagenesis*, *Sarcoma*. Publons account: <http://tinyurl.com/publons-mkuijjer>
- Tool evaluation board member for the conference “Computational Methods in Systems Biology.” CMSB 2017, Darmstadt, Germany.

## TEACHING

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- Master’s thesis committee member, Computational Biology and Quantitative Genetics (HSPH). May 6, 2016
- Teaching assistant at Harvard Catalyst course Applications in Network Medicine. November 2, 2015
- Thesis mentor of students in Computational Biology and Quantitative Genetics (MSc, HSPH) and Bioinformatics (BSc, University of Applied Sciences Leiden)
- Graduate student mentor of students in Medicine (PhD), Biomedical Sciences (MSc), and Biology (MSc, all from Leiden University)
- Summer project mentor of graduate students in Biostatistics (PhD, HSPH) and Molecular Biology and Bioinformatics (MSc, University of Pavia, Italy), of undergraduate students in Statistics (Harvard University) and Biology (University of Massachusetts, California Institute of Technology), and of three high school students
- Lecturer at Studium Generale, a science symposium for the general public, 2012
- Lecturer, working group, and journal club leader at the Pathology course of the undergraduate program of Biomedical Sciences, Leiden University, 2009–2010

## ORGANIZATIONAL SKILLS

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- I co-organized the 2014–2015 Big Data Seminar series of the Department of Biostatistics, Harvard T.H. Chan School of Public Health
- I organized the Quackenbush weekly lab meeting from 2013–2014

## CERTIFICATIONS

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- Radiation Hygiene level 5B, Dutch Society for Radiation Hygiene, September 2003

## LANGUAGES

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<b>Dutch</b>	Native proficiency	<b>German</b>	Elementary proficiency
<b>English</b>	Full professional proficiency	<b>French</b>	Elementary proficiency
<b>Italian</b>	Full professional proficiency	<b>Swedish</b>	Elementary proficiency

## SKILLS

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<b>Programming</b>	R, MATLAB, Bash Shell Scripting, Git, C++, Perl, Python, AWK, SQL
<b>Bioinformatics skills</b>	High Performance Computing, RNA-Seq, DNase-Seq, microarray (SNP, mRNA/miRNA expression, methylation) pre-processing, QC, and analysis, motif mapping, gene set enrichment analysis, network reconstruction, network statistics, data integration, linear models, survival analysis, multivariate statistics
<b>Laboratory skills</b>	Cell culture, transfection, reporter and proliferation assays, western blotting, co-immunoprecipitation, qPCR, DNA/RNA prep, protein purification, tissue microarrays, fluorescent and confocal microscopy, kinome arrays, radiation safety
<b>Scientific writing</b>	Experienced with writing and reviewing scientific manuscripts and grant proposals, L <sup>A</sup> T <sub>E</sub> X

## PUBLICATIONS

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- Wong K, van der Weyden L, Schott CR, Foote A, Constantino-Casas F, Smith S, Dobson JM, Murchison EP, Wu H, Yeh I, Fullen DR, Joseph N, Bastian BC, Patel RM, Martincorena I, Robles-Espinoza CD, Iyer V, Kuijjer ML, Arends MJ, Brenn T, Harms PW, Wood GA, Adams DJ. Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma. *Nature Communications*. 2019 Jan 21;10(1):353
- Kang T, Zarringhalam K, Kuijjer ML, Quackenbush J, Ding W. Clustering on sparse data in non-overlapping feature space with applications to cancer subtyping. *IEEE International Conference on Data Mining (ICDM'18)*
- Lopes-Ramos CM, Kuijjer ML, Ogino S, Fuchs C, DeMeo DL, Glass K, Quackenbush J. Gene regulatory network analysis identifies sex-linked differences in colon cancer drug metabolism processes. *Cancer Research*, 2018 Oct 1;78(19):5538-5547
- Kuijjer ML\*, Paulson JN, Salzman P, Ding W, Quackenbush J. Cancer subtype identification using somatic mutation data. *Br J Cancer*. 2018 May 16
- Sonawane AR, Platig J, Fagny M, Chen CY, Paulson JN, Lopes-Ramos CM, Quackenbush J, Glass K†\*, Kuijjer ML†\*. Understanding Tissue-Specific Gene Regulation. *Cell Reports*. 2017 Oct 24;21(4):1077-1088
- Paulson JN, Chen CY, Lopes-Ramos CM, Kuijjer ML, Platig J, Sonawane AR, Fagny M, Glass K, Quackenbush J. Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. *BMC Bioinformatics*. 2017 Oct 3;18(1):437
- Lopes-Ramos CM†, Paulson JN†, Chen CY, Kuijjer ML, Fagny M, Platig J, Sonawane AR, DeMeo DL, Quackenbush J, Glass K. Regulatory network changes between cell lines and their tissues of origin. *BMC Genomics*. 2017 Sep 12;18(1):723
- Fagny M, Paulson JN, Kuijjer ML, Sonawane AR, Chen CY, Lopes-Ramos CM, Glass K, Quackenbush J, Platig J. Exploring regulation in tissues with eQTL networks. *Proc Natl Acad Sci U S A*. 2017 Sep 12;114(37):E7841-E7850
- Hill K, Kelly A, Kuijjer ML, Barry W, Rattani A, Kissick H, Janeway K, Perez-Atayde A, Goldsmith J, Gebhardt MC, Arredouani M, Cote G, Hornicek F, Choy E, Duan Z, Quackenbush J, Haibe-Kains B, Spentzos D. An imprinted non-coding genomic region at 14q32 defines clinically relevant molecular subtypes in osteosarcoma across multiple independent datasets. *J Hematol Oncol*. 2017 May 15;10(1):107
- van IJzendoorn DGP, Quackenbush J, Glass K, Kuijjer ML\*. PyPanda: A Python package for gene regulatory network reconstruction. *Bioinformatics*. 2016 Nov 1;32(21):3363-3365
- Baranski Z, Booij TH, Kuijjer ML, de Jong Y, Cleton-Jansen AM, Price LS, van de Water B, Bovée JVGM, Hogendoorn PCW, Danen EH. MEK inhibition induces apoptosis in osteosarcoma cells with constitutive ERK1/2 phosphorylation. *Genes Cancer*. 2015;6(11-12):503-512

- Buddingh EP, Ruslan SEN, Reijnders CMA, Szuhai K, Kuijjer ML, Roelofs H, Hogendoorn PCW, Egeler RM, Cleton-Jansen AM, Lankester AC. Mesenchymal stromal cells of osteosarcoma patients do not show evidence of neoplastic changes during long-term culture. *Clin Sarcoma Res.* 2015 Jun 23;5:16
- Wouters MC†, Dijkgraaf EM†, Kuijjer ML, Jordanova ES, Welters MJP, Nortier JWR, van der Hoeven JJM, Kroep JR, Deamen T, Nijman HW, van der Burg SH. IL-6, IL-6 receptor, pSTAT3 and myeloid cell populations in ovarian cancer. *OncoImmunology.* 2015 Jan 7;3(12):e962397
- Pahl JHW, Santos SJ, Kuijjer ML, Boerman H, Sand L, Szuhai K, Cleton-Jansen AM, Egeler RM, Bovée JV, Schilham MW, Lankester AC. Expression of the immune regulation antigen CD70 in osteosarcoma. *Cancer Cell Int.* 2015 Mar 18;15:31
- Pahl JHW, Kwappenberg KMC, Varypataki EM, Santos SJ, Kuijjer ML, Mohamed S, Wijnen JT, van Tol MJD, Cleton-Jansen AM, Egeler RM, Jiskoot W, Lankester AC, Schilham MW. Macrophages inhibit human osteosarcoma cell growth after activation with the bacterial cell wall derivative liposomal muramyl tripeptide in combination with interferon-gamma. *JECCR.* 2014 Mar 10;33(1):27
- Kuijjer ML, van den Akker BEWM, Hilhorst R, Mommersteeg M, Buddingh EP, Serra M, Bürger H, Hogendoorn PCW, Cleton-Jansen AM. Kinome and mRNA expression profiling of high-grade osteosarcoma identifies genomic instability, and reveals Akt as potential target for treatment. *BMC Med Genomics.* 2014 Jan 21;7:4 *Highly accessed*
- Kansara E, Leong HS, Lin DM, Popkiss S, Pang P, Garsed DW, Walkley CR, Cullinane C, Elul J, Haynes NM, Hicks R, Kuijjer ML, Cleton-Jansen AM, Hinds PW, Smyth MJ, Thomas DM. Senescence-related immunologic functions of the RB1 tumor suppressor in radiation-induced osteosarcoma. *J Clin Invest.* 2013 Dec 2;123(12):5351-60
- de Vos van Steenwijk PJ, Ramwadhoebe TH, Goedemans R, Doorduijn E, van den Ham JJ, Gorter A, van Hall T, Kuijjer ML, van Poelgeest MIE, van der Burg SH, Jordanova ES. Tumor infiltrating CD14 positive myeloid cells work side by side with T cells to prolong the survival in patients with cervical carcinoma. *Int J Cancer.* 2013;133(12):2884-94
- Kuijjer ML, Peterse EFP, van den Akker BEWM, Briaire-de Bruijn IH, Serra M, Meza-Zepeda LA, Myklebost O, Hassan AB, Hogendoorn PCW, Cleton-Jansen AM. IR/IGF1R signaling as potential target for treatment of high-grade osteosarcoma. *BMC Cancer.* 2013;20(13):245
- Kuijjer ML, Hogendoorn PCW, Cleton-Jansen AM. Genome-wide analyses on high-grade osteosarcoma; making sense of a most genomically instable tumor *Review.* *Int J Cancer.* 2013;133(11):2512-21
- Namløs HM, Meza-Zepeda LA, Barøy T, Østensen IHG, Kresse SH, Kuijjer ML, Serra M, Bürger H, Cleton-Jansen AM, Myklebost O. Modulation of the Osteosarcoma Expression Phenotype by MicroRNAs. *PlosONE.* 2012;7(10):e48086
- Mohseny AB, Cai Y, Kuijjer ML, Xiao W, van den Akker B, de Andrea CE, Jacobs R, ten Dijke P, Hogendoorn PC, Cleton-Jansen AM. The activities of Smad and Gli mediated signalling pathways in high-grade conventional osteosarcoma. *Eur J Cancer.* 2012 Dec;48(18):3429-38
- Lenos K, Grawenda AM, Lodder K, Kuijjer ML, Teunisse AF, Repapi E, Grochola LF, Bartel F, Hogendoorn PC, Wuerl P, Taubert H, Cleton-Jansen AM, Bond GL, Jochemsen AG. Alternate splicing of the p53 inhibitor HDMX offers a superior prognostic biomarker than p53 mutation in human cancer. *Cancer Res.* 2012 Aug 15;72(16):4074-84
- Kuijjer ML, Rydbeck H, Kresse SH, Buddingh EP, Lid AB, Roelofs H, Bürger H, Myklebost O, Hogendoorn PC, Meza-Zepeda LA, Cleton-Jansen AM. Identification of osteosarcoma driver genes by integrative analysis of copy number and gene expression data. *Genes Chromosomes Cancer.* 2012 Jul;51(7):696-706
- Pansuriya TC, van Eijk R, d'Adamo P, van Ruler MA, Kuijjer ML, Oosting J, Cleton-Jansen AM, van Oosterwijk JG, Verbeke SL, Meijer D, van Wezel T, Nord KH, Sangiorgi L, Toker B, Liegl-Atzwanger B, San-Julian M, Sciot R, Limaye N, Kindblom LG, Daugaard S, Godfraind C, Boon LM, Vikkula M, Kurek KC, Szuhai K, French PJ, Bovée JV. Somatic mosaic IDH1 and IDH2 mutations are associated with enchondroma and spindle cell hemangioma in Ollier disease and Maffucci syndrome. *Nat Genet.* 2011 Nov 6;43(12):1256-61
- Kuijjer ML, Namløs HM, Hauben EI, Machado I, Kresse SH, Serra M, Llombart-Bosch A, Hogendoorn PC, Meza-Zepeda LA, Myklebost O, Cleton-Jansen AM. mRNA expression profiles of primary high-grade central osteosarcoma are preserved in cell lines and xenografts. *BMC Med Genomics.* 2011 Sep 20;4:66

- **Kuijjer ML**†, Buddingh EP†, Duim RA, Bürger H, Agelopoulos K, Myklebost O, Serra M, Mertens F, Hogendoorn PC, Lankester AC, Cleton-Jansen AM. Tumor-infiltrating macrophages are associated with metastasis suppression in high-grade osteosarcoma: a rationale for treatment with macrophage activating agents. *Clin Cancer Res.* 2011 Apr 15;17(8):2110-9

†Shared first/last authorship; \*Corresponding author

## MANUSCRIPTS UNDER CONSIDERATION

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- **Kuijjer ML**†, Tung M†, Quackenbush J, Yuan GC, Glass K. Estimating sample-specific regulatory networks. *In revision*, pre-published on the arXiv <http://arxiv.org/abs/1505.06440>
- Chen CY†, Lopes-Ramos CM†, **Kuijjer ML**, Paulson JN, Sonawane AR, Fagny M, Platig J, Quackenbush J, Glass K, DeMeo DL. Sexual dimorphism in gene expression landscapes across human tissues. *In revision*, pre-published on the bioRxiv <https://doi.org/10.1101/082289>
- van IJzendoorn DGP, Szuhai K, Bovée JVGM†, **Kuijjer ML**†. Machine learning analysis of gene expression data reveals novel differential diagnostic and prognostic markers for soft tissue sarcomas. *In revision*
- Barnett I, Malik N, **Kuijjer ML**, Mucha P, Onnela JP. Data driven classification of social and biological networks. *In revision*, pre-published on the arXiv <http://arxiv.org/abs/1610.05868>
- **Kuijjer ML**, Paulson JN, Quackenbush J. Expression analysis. Book chapter in *Bioinformatics: A practical guide to the analysis of genes and proteins*, 4<sup>th</sup> edition. *Submitted*

†Shared first/last authorship

## SEMINARS

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- Estimating single-sample networks to model disruption of gene regulation in cancer. *Invited talk* at the Systems Biology of Immunity and Cancer symposium, Norwegian Society for Immunology (NSI). Jan 28, 2019, Oslo, Norway
- Using network models and computational tools to understand cancer. *Invited talk* at the Clinical Effectiveness Research Group, University of Oslo. Oct 25, 2018, Oslo, Norway
- Understanding cancer using integrative network models. *Selected for presentation* at the Turing Centre for Living Systems (CENTURI), Aix-Marseille University. May 29, 2018, Marseille, France
- Understanding tissue-specific gene regulation. *Invited talk* at the Program in Quantitative Genomics working group of the Harvard Chan School of Public Health, Boston, MA. March 20, 2018, Boston, MA
- Understanding cancer using integrative network models. *Selected for presentation* at the Ludwig Institute for Cancer Research and the Big Data Institute. March 12, 2018, Oxford, United Kingdom
- Using network models to understand gene regulation in healthy and diseased tissues. *Invited talk* at the Bioinformatics seminar of the Division of Immunology, Harvard Medical School. December 15, 2016, Boston, MA
- Understanding complex disease using integrative network models. *Selected for presentation* at the Independent Junior Group Leader in Models of Human Diseases Symposium, Berlin Institute for Medical Systems Biology. September 26–27, 2016, Berlin, Germany
- Identification of key regulatory pathways in ovarian cancer. *Invited talk* at the Network Science Seminar of the Channing Division of Network Medicine, Brigham and Women’s Hospital. December 11, 2015, Boston, MA
- Estimating regulatory networks for individual samples. Cancer Biology Seminar. Dana-Farber Cancer Institute. March 13, 2015, Boston, MA
- Metastasis suppression by tumor infiltrating macrophages in high-grade osteosarcoma. *Selected for presentation* at the Medical Genetics Centre (MGC) Symposium. September 19, 2010, Leiden, the Netherlands

- Big data integration—Inferring and using individual patient network models. *Invited talk* at the LabRoots Genetics and Genomics virtual conference. May 11–12, 2016. Presentation can be watched at: <http://tinyurl.com/bigdataintegration>
- Estimating sample-specific regulatory networks. *Selected for presentation* at the Statistical Modeling of Epigenomics and Gene Regulation conference. Harvard University. August 27, 2015, Cambridge, MA
- Estimating sample-specific regulatory networks. *Invited talk* at the Banff/BIRS conference: Statistical and Computational Challenges in Bridging Functional Genomics, Epigenomics, Molecular QTLs, and Disease Genetics (BIRS/Banff 15w5142). August 3–7, 2015, Banff, Canada. Presentation can be watched at: <http://tinyurl.com/birsbanff-lioness>
- Gene regulation by transcription factors and microRNAs in ovarian cancer. *Selected for presentation* at the Second Annual Celebration of Junior Investigators in Cancer Research of the Dana Farber/Harvard Cancer Center. September 24, 2014, Boston, MA
- Kinome profiling of osteosarcoma reveals Akt as target for treatment. Tumor cell biology meeting of the Dutch Cancer Society (KWF). November 5–6, 2012, Lunteren, the Netherlands (*best presentation award*)
- Identification of osteosarcoma driver genes by integrative analysis of copy number and gene expression data. Tumor cell biology meeting of the Dutch Cancer Society (KWF). November 9–10, 2011, Lunteren, the Netherlands
- Metastasis suppression by tumor-infiltrating macrophages in high-grade osteosarcoma. *Selected for presentation* at the United States and Canadian Academy of Pathology (USCAP) annual meeting. February 26 – March 4, 2011, San Antonio (TX), USA
- Integrative analysis of osteosarcoma copy number and gene expression data. *Selected for presentation* at the Annual EuroBoNeT meeting. January 10–12, 2011, Paris, France
- Osteosarcoma cell lines and xenografts are representative for the primary tumor from which they are derived. Tumor cell biology meeting of the Dutch Cancer Society (KWF). November 10–11, 2010, Lunteren, the Netherlands
- High expression of macrophage-associated genes in high-grade osteosarcoma is associated with a lower risk of developing metastases. *Selected for presentation* at the Annual EuroBoNeT meeting. January 18–20, 2010, Münster, Germany
- Expression profiling of high-grade osteosarcoma. EuroBoNeT bioinformatics meeting. October 1, 2009, Antwerp, Belgium