

1. *A Novel Role for miR-1305 in Regulation of Pluripotency-Differentiation Balance, Cell Cycle, and Apoptosis in Human Pluripotent Stem Cells*. Jin S, Collin J, Zhu L, **Montaner D**, Armstrong L, Neganova I, Lako M. Stem cells (Dayton, Ohio). 2016;
2. *Integrated gene set analysis for microRNA studies*. Garcia-Garcia F, Panadero J, Dopazo J, **Montaner D**. Bioinformatics (Oxford, England). 2016;
3. *Brief Report: Inhibition of miR-145 Enhances Reprogramming of Human Dermal Fibroblasts to Induced Pluripotent Stem Cells*. Barta T, Peskova L, Collin J, **Montaner D**, Neganova I, Armstrong L, Lako M. Stem cells (Dayton, Ohio). 2016; 34(1):246-51.
4. *Family-based genome-wide association study in Patagonia confirms the association of the DMD locus and cleft lip and palate*. Fonseca RF, de Carvalho FM, Poletta FA, **Montaner D**, Dopazo J, Mereb JC, Moreira MA, Seunanez HN, Vieira AR, Castilla EE, Orioli IM. European journal of oral sciences. 2015;
5. *Therapeutic targets for olive pollen allergy defined by gene markers modulated by Ole e 1-derived peptides*. Calzada D, Aguerri M, Baos S, **Montaner D**, Mata M, Dopazo J, Quiralte J, Florido F, Lahoz C, Cárdbaba B. Molecular immunology. 2015; 64(2):252-61.
6. *Babelomics 5.0: functional interpretation for new generations of genomic data*. Alonso R, Salavert F, Garcia-Garcia F, Carbonell-Caballero J, Bleda M, Garcia-Alonso L, Sanchis-Juan A, Perez-Gil D, Marin-Garcia P, Sanchez R, Cubuk C, Hidalgo MR, Amadoz A, Hernansaiz-Ballesteros RD, Alemán A, Tarraga J, **Montaner D**, Medina I, Dopazo J. Nucleic acids research. 2015; 43(W1):W117-21.
7. *A new overgrowth syndrome is due to mutations in RNF125*. Tenorio J, Mansilla A, Valencia M, Martínez-Glez V, Romanelli V, Arias P, Castrejón N, Poletta F, Guillén-Navarro E, Gordo G, Mansilla E, García-Santiago F, González-Casado I, Vallespín E, Palomares M, Mori MA, Santos-Simarro F, García-Miñaur S, Fernández L, Mena R, Benito-Sanz S, del Pozo Á, Silla JC, Ibañez K, López-Granados E, Martín-Trujillo A, **Montaner D**, Heath KE, Campos-Barros Á, Dopazo J, Nevado J, Monk D, Ruiz-Pérez VL, Lapunzina P. Human mutation. 2014; 35(12):1436-41.
8. *Quantitative modeling of clinical, cellular, and extracellular matrix variables suggest prognostic indicators in cancer: a model in neuroblastoma*. Tadeo I, Piqueras M, **Montaner D**, Villamón E, Berbegall AP, Cañete A, Navarro S, Noguera R. Pediatric research. 2014; 75(2):302-14.
9. *Understanding disease mechanisms with models of signaling pathway activities*. Sebastian-Leon P, Vidal E, Minguez P, Conesa A, Tarazona S, Amadoz A, Armero C, Salavert F, Vidal-Puig A, **Montaner D**, Dopazo J. BMC systems biology. 2014; 8:121.
10. *Pathway network inference from gene expression data*. Ponzoni I, Nueda M, Tarazona S, Götz S, **Montaner D**, Dussaut J, Dopazo J, Conesa A. BMC systems biology. 2014; 8 Suppl 2:S7.
11. *A novel locus for a hereditary recurrent neuropathy on chromosome 21q21*.

- Calpena E, Martínez-Rubio D, Arpa J, García-Peñas JJ, **Montaner D**, Dopazo J, Palau F, Espinós C. Neuromuscular disorders : NMD. 2014; 24(8):660-5.
12. *Defining the genomic signature of totipotency and pluripotency during early human development.* Galan A, Diaz-Gimeno P, Poo ME, Valbuena D, Sanchez E, Ruiz V, Dopazo J, **Montaner D**, Conesa A, Simon C. PloS one. 2013; 8(4):e62135.
  13. *Differential gene-expression analysis defines a molecular pattern related to olive pollen allergy.* Aguerri M, Calzada D, **Montaner D**, Mata M, Florido F, Quiralte J, Dopazo J, Lahoz C, Cardaba B. Journal of biological regulators and homeostatic agents. 2013; 27(2):337-50.
  14. *Extensive translational remodeling during ER stress response in mammalian cells.* Ventoso I, Kochetov A, **Montaner D**, Dopazo J, Santoyo J. PloS one. 2012; 7(5):e35915.
  15. *The protease MT1-MMP drives a combinatorial proteolytic program in activated endothelial cells.* Koziol A, Gonzalo P, Mota A, Pollán Á, Lorenzo C, Colomé N, **Montaner D**, Dopazo J, Arribas J, Canals F, Arroyo AG. FASEB journal : official publication of the Federation of American Societies for Experimental Biology. 2012; 26(11):4481-94.
  16. *Four new loci associations discovered by pathway-based and network analyses of the genome-wide variability profile of Hirschsprung's disease.* Fernández RM, Bleda M, Núñez-Torres R, Medina I, Luzón-Toro B, García-Alonso L, Torroglosa A, Marbà M, Enguix-Riego MV, **Montaner D**, Antiñolo G, Dopazo J, Borrego S. Orphanet journal of rare diseases. 2012; 7:103.
  17. *Large-scale transcriptional profiling and functional assays reveal important roles for Rho-GTPase signalling and SCL during haematopoietic differentiation of human embryonic stem cells.* Yung S, Ledran M, Moreno-Gimeno I, Conesa A, **Montaner D**, Dopazo J, Dimmick I, Slater NJ, Marenah L, Real PJ, Paraskevopoulou I, Bisbal V, Burks D, Santibanez-Koref M, Moreno R, Mountford J, Menendez P, Armstrong L, Lako M. Human molecular genetics. 2011; 20(24):4932-46.
  18. *Differential lipid partitioning between adipocytes and tissue macrophages modulates macrophage lipotoxicity and M2/M1 polarization in obese mice.* Prieur X, Mok CY, Velagapudi VR, Núñez V, Fuentes L, **Montaner D**, Ishikawa K, Camacho A, Barbarroja N, O'Rahilly S, Sethi JK, Dopazo J, Orešić M, Ricote M, Vidal-Puig A. Diabetes. 2011; 60(3):797-809.
  19. *The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models.* Shi L, Campbell G, Jones WD, Campagne F, Wen Z, Walker SJ, Su Z, Chu TM, Goodsaid FM, Pusttai L, Shaughnessy JD Jr, Oberthuer A, Thomas RS, Paules RS, Fielden M, Barlogie B, Chen W, Du P, Fischer M, Furlanetto C, Gallas BD, Ge X, Megherbi DB, Symmans WF, Wang MD, Zhang J, Bitter H, Brors B, Bushel PR, Bylesjo M, Chen M, Cheng J, Cheng J, Chou J, Davison TS, Delorenzi M, Deng Y, Devanarayan V, Dix DJ, Dopazo J, Dorff KC, Elloumi F, Fan J, Fan S, Fan X, Fang H, Gonzaludo N, Hess KR, Hong H, Huan J, Irizarry RA, Judson R, Juraeva

- D, Lababidi S, Lambert CG, Li L, Li Y, Li Z, Lin SM, Liu G, Lobenhofer EK, Luo J, Luo W, McCall MN, Nikolsky Y, Pennello GA, Perkins RG, Philip R, Popovici V, Price ND, Qian F, Scherer A, Shi T, Shi W, Sung J, Thierry-Mieg D, Thierry-Mieg J, Thodima V, Trygg J, Vishnuvajjala L, Wang SJ, Wu J, Wu Y, Xie Q, Yousef WA, Zhang L, Zhang X, Zhong S, Zhou Y, Zhu S, Arasappan D, Bao W, Lucas AB, Berthold F, Brennan RJ, Bunes A, Catalano JG, Chang C, Chen R, Cheng Y, Cui J, Czika W, Demichelis F, Deng X, Dosymbekov D, Eils R, Feng Y, Fostel J, Fulmer-Smentek S, Fuscoe JC, Gatto L, Ge W, Goldstein DR, Guo L, Halbert DN, Han J, Harris SC, Hatzis C, Herman D, Huang J, Jensen RV, Jiang R, Johnson CD, Jurman G, Kahlert Y, Khuder SA, Kohl M, Li J, Li L, Li M, Li QZ, Li S, Li Z, Liu J, Liu Y, Liu Z, Meng L, Madera M, Martinez-Murillo F, Medina I, Meehan J, Miclaus K, Moffitt RA, **Montaner D**, Mukherjee P, Mulligan GJ, Neville P, Nikolskaya T, Ning B, Page GP, Parker J, Parry RM, Peng X, Peterson RL, Phan JH, Quanz B, Ren Y, Riccadonna S, Roter AH, Samuelson FW, Schumacher MM, Shambaugh JD, Shi Q, Shippy R, Si S, Smalter A, Sotiriou C, Soukup M, Staedtler F, Steiner G, Stokes TH, Sun Q, Tan PY, Tang R, Tezak Z, Thorn B, Tsyganova M, Turpaz Y, Vega SC, Visintainer R, von Frese J, Wang C, Wang E, Wang J, Wang W, Westermann F, Willey JC, Woods M, Wu S, Xiao N, Xu J, Xu L, Yang L, Zeng X, Zhang J, Zhang L, Zhang M, Zhao C, Puri RK, Scherf U, Tong W, Wolfinger RD. *Nature biotechnology*. 2010; 28(8):827-38. NIHMSID: NIHMS235927
20. *Hypoxia promotes efficient differentiation of human embryonic stem cells to functional endothelium*. Prado-Lopez S, Conesa A, Armiñán A, Martínez-Losa M, Escobedo-Lucea C, Gandia C, Tarazona S, Melguizo D, Blesa D, **Montaner D**, Sanz-González S, Sepúlveda P, Götz S, O'Connor JE, Moreno R, Dopazo J, Burks DJ, Stojkovic M. *Stem cells (Dayton, Ohio)*. 2010; 28(3):407-18.
  21. *Initial genomics of the human nucleolus*. Németh A, Conesa A, Santoyo-Lopez J, Medina I, **Montaner D**, Péterfia B, Solovei I, Cremer T, Dopazo J, Längst G. *PLoS genetics*. 2010; 6(3):e1000889.
  22. *FM19G11, a new hypoxia-inducible factor (HIF) modulator, affects stem cell differentiation status*. Moreno-Manzano V, Rodríguez-Jiménez FJ, Aceña-Bonilla JL, Fustero-Lardies S, Erceg S, Dopazo J, **Montaner D**, Stojkovic M, Sánchez-Puelles JM. *The Journal of biological chemistry*. 2010; 285(2):1333-42.
  23. *Multidimensional gene set analysis of genomic data*. **Montaner D**, Dopazo J. *PloS one*. 2010; 5(4):e10348.
  24. *Babelomics: an integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling*. Medina I, Carbonell J, Pulido L, Madeira SC, Goetz S, Conesa A, Tárrega J, Pascual-Montano A, Nogales-Cadenas R, Santoyo J, García F, Marbà M, **Montaner D**, Dopazo J. *Nucleic acids research*. 2010; 38(Web Server issue):W210-3.
  25. *Functional genomics of 5- to 8-cell stage human embryos by blastomere*

- single-cell cDNA analysis*. Galán A, **Montaner D**, Póo ME, Valbuena D, Ruiz V, Aguilar C, Dopazo J, Simón C. PloS one. 2010; 5(10):e13615.
26. *DNA methylation epigenotypes in breast cancer molecular subtypes*. Bediaga NG, Acha-Sagredo A, Guerra I, Viguri A, Albaina C, Ruiz Diaz I, Rezola R, Alberdi MJ, Dopazo J, **Montaner D**, Renobales M, Fernández AF, Field JK, Fraga MF, Liloglou T, de Pancorbo MM. Breast cancer research : BCR. 2010; 12(5):R77.
  27. *Parallel changes in gene expression in peripheral blood mononuclear cells and the brain after maternal separation in the mouse*. van Heerden JH, Conesa A, Stein DJ, **Montaner D**, Russell V, Illing N. BMC research notes. 2009; 2:195.
  28. *Gene set internal coherence in the context of functional profiling*. **Montaner D**, Minguez P, Al-Shahrour F, Dopazo J. BMC genomics. 2009; 10:197.
  29. *SNOW, a web-based tool for the statistical analysis of protein-protein interaction networks*. Minguez P, Götz S, **Montaner D**, Al-Shahrour F, Dopazo J. Nucleic acids research. 2009; 37(Web Server issue):W109-14.
  30. *Gene set-based analysis of polymorphisms: finding pathways or biological processes associated to traits in genome-wide association studies*. Medina I, **Montaner D**, Bonifaci N, Pujana MA, Carbonell J, Tarraga J, Al-Shahrour F, Dopazo J. Nucleic acids research. 2009; 37(Web Server issue):W340-4.
  31. *Cryptochrome-1 expression: a new prognostic marker in B-cell chronic lymphocytic leukemia*. Lewintre EJ, Martín CR, Ballesteros CG, **Montaner D**, Rivera RF, Mayans JR, García-Conde J. Haematologica. 2009; 94(2):280-4.
  32. *Analysis of chronic lymphocytic leukemia transcriptomic profile: differences between molecular subgroups*. Jantus Lewintre E, Reinoso Martín C, **Montaner D**, Marín M, José Terol M, Farrás R, Benet I, Calvete JJ, Dopazo J, García-Conde J. Leukemia & lymphoma. 2009; 50(1):68-79.
  33. *CLEAR-test: combining inference for differential expression and variability in microarray data analysis*. Valls J, Grau M, Solé X, Hernández P, **Montaner D**, Dopazo J, Peinado MA, Capellá G, Moreno V, Pujana MA. Journal of biomedical informatics. 2008; 41(1):33-45.
  34. *GEPAS, a web-based tool for microarray data analysis and interpretation*. Tarraga J, Medina I, Carbonell J, Huerta-Cepas J, Minguez P, Alloza E, Al-Shahrour F, Vegas-Azcárate S, Goetz S, Escobar P, Garcia-Garcia F, Conesa A, **Montaner D**, Dopazo J. Nucleic acids research. 2008; 36(Web Server issue):W308-14.
  35. *Molecular profiling related to poor prognosis in thyroid carcinoma. Combining gene expression data and biological information*. Montero-Conde C, Martín-Campos JM, Lerma E, Gimenez G, Martínez-Guitarte JL, Combalá N, **Montaner D**, Matías-Guiu X, Dopazo J, de Leiva A, Robledo M, Mauricio D. Oncogene. 2008; 27(11):1554-61.
  36. *Direct functional assessment of the composite phenotype through multivariate projection strategies*. Conesa A, Bro R, García-García F, Prats JM,

- Götz S, Kjeldahl K, **Montaner D**, Dopazo J. Genomics. 2008; 92(6):373-83.
37. *Babelomics: advanced functional profiling of transcriptomics, proteomics and genomics experiments*. Al-Shahrour F, Carbonell J, Minguez P, Goetz S, Conesa A, Tárraga J, Medina I, Alloza E, **Montaner D**, Dopazo J. Nucleic acids research. 2008; 36(Web Server issue):W341-6.
  38. *Functional profiling of microarray experiments using text-mining derived bioentities*. Minguez P, Al-Shahrour F, **Montaner D**, Dopazo J. Bioinformatics (Oxford, England). 2007; 23(22):3098-9.
  39. *Prophet, a web-based tool for class prediction using microarray data*. Medina I, **Montaner D**, Tárraga J, Dopazo J. Bioinformatics (Oxford, England). 2007; 23(3):390-1.
  40. *Evidence for systems-level molecular mechanisms of tumorigenesis*. Hernández P, Huerta-Cepas J, **Montaner D**, Al-Shahrour F, Valls J, Gómez L, Capellá G, Dopazo J, Pujana MA. BMC genomics. 2007; 8:185.
  41. *ISACGH: a web-based environment for the analysis of Array CGH and gene expression which includes functional profiling*. Conde L, **Montaner D**, Burguet-Castell J, Tárraga J, Medina I, Al-Shahrour F, Dopazo J. Nucleic acids research. 2007; 35(Web Server issue):W81-5.
  42. *Functional profiling and gene expression analysis of chromosomal copy number alterations*. Conde L, **Montaner D**, Burguet-Castell J, Tárraga J, Al-Shahrour F, Dopazo J. Bioinformatics. 2007; 1(10):432-5.
  43. *FatiGO +: a functional profiling tool for genomic data. Integration of functional annotation, regulatory motifs and interaction data with microarray experiments*. Al-Shahrour F, Minguez P, Tárraga J, Medina I, Alloza E, **Montaner D**, Dopazo J. Nucleic acids research. 2007; 35(Web Server issue):W91-6.
  44. *From genes to functional classes in the study of biological systems*. Al-Shahrour F, Arbiza L, Dopazo H, Huerta-Cepas J, Minguez P, **Montaner D**, Dopazo J. BMC bioinformatics. 2007; 8:114.
  45. *Self-reported smoking cessation interventions were not associated with quitting in older women*. Schroeder K, Lawlor DA, **Montaner D**, Ebrahim S. Journal of clinical epidemiology. 2006; 59(6):622-8.
  46. *The detection, treatment and control of high blood pressure in older British adults: cross-sectional findings from the British Women's Heart and Health Study and the British Regional Heart Study*. Patel R, Lawlor DA, Whincup P, **Montaner D**, Papacosta O, Brindle P, Ebrahim S. Journal of human hypertension. 2006; 20(10):733-41.
  47. *Next station in microarray data analysis: GEPAS*. **Montaner D**, Tárraga J, Huerta-Cepas J, Burguet J, Vaquerizas JM, Conde L, Minguez P, Vera J, Mukherjee S, Valls J, Pujana MA, Alloza E, Herrero J, Al-Shahrour F, Dopazo J. Nucleic acids research. 2006; 34(Web Server issue):W486-91.
  48. *Selective pressures at a codon-level predict deleterious mutations in human disease genes*. Arbiza L, Duchi S, **Montaner D**, Burguet J, Pantoja-Uceda D, Pineda-Lucena A, Dopazo J, Dopazo H. Journal of molecular biology. 2006; 358(5):1390-404.

49. *BABELOMICS: a systems biology perspective in the functional annotation of genome-scale experiments.* Al-Shahrour F, Minguez P, Tárraga J, **Montaner D**, Alloza E, Vaquerizas JM, Conde L, Blaschke C, Vera J, Dopazo J. *Nucleic acids research*. 2006; 34(Web Server issue):W472-6.
50. *Coronary heart disease prevention in clinical practice: are patients with diabetes special? Evidence from two studies of older men and women.* Emberson JR, Whincup PH, Lawlor DA, **Montaner D**, Ebrahim S. *Heart (British Cardiac Society)*. 2005; 91(4):451-5.
51. *How acceptable are innovative health-care technologies? A survey of public beliefs and attitudes in England and Wales.* Calnan M, **Montaner D**, Horne R. *Social science & medicine (1982)*. 2005; 60(9):1937-48.
52. *Clustering of risk factors and social class in childhood and adulthood in British women's heart and health study: cross sectional analysis.* Ebrahim S, **Montaner D**, Lawlor DA. *BMJ (Clinical research ed.)*. 2004; 328(7444):861.