11656–11657 *Nucleic Acids Research, 2018, Vol. 46, No. 21*
doi: 10.1093/nar/gky979

Corrigendum

Novel diagnostic tool for prediction of variant spliceogenicity derived from a set of 395 combined in silico/in vitro studies: an international collaborative effort

Raphaël Leman[1,2,3,‡,§], Pascaline Gaildrat[2,‡,§], Gérald L. Gac[4], Chandran Ka[4], Yann Fichou[4], Marie-Pierre Audrezet[4], Virginie Caux-Moncoutier[5,6,7,§], Sandrine M. Caputo[7,‡,§], Nadia Boutry-Kryza[8,§], Mélanie Léone[8,§], Sylvie Mazoyer[9,‡,§], Françoise Bonnet-Dorion[10,§], Nicolas Sevenet[10,§], Marine Guillaud-Bataille[11,§], Etienne Rouleau[11,§], Brigitte Bressac-de Paillerets[11,§], Barbara Wappenschmidt[12,‡], Maria Rossing[13,‡], Danielle Muller[14,§], Violaine Bourdon[15,§], Françoise Revillon[16,§], Michael T. Parsons[17,‡], Antoine Rousselin[1,2,§], Grégoire Davy[1,2,§], Gaia Castelain[2,§], Laurent Castéra[1,2,§], Joanna Sokolowska[18,§], Florence Coulet[19,§], Capucine Delnatte[20,§], Claude Férec[4], Amanda B. Spurdle[17,‡], Alexandra Martins[2,‡,§], Sophie Krieger[1,2,3,*,†,‡,§] and Claude Houdayer[5,6,7,*,†,‡,§]

[1]Laboratoire de Biologie Clinique et Oncologique, Centre François Baclesse, 14000 Caen, France, [2]Inserm U1245 Genomics and Personalized Medecine in Cancer and Neurological Disorders, Normandie Univ, UNIROUEN, Normandy Centre for Genomic and Personalized Medicine, 76031 Rouen, France, [3]Normandie Univ, UNICAEN, 14000 Caen, France, [4]Inserm UMR1078, Genetics, Functional Genomics and Biotechnology, Université de Bretagne Occidentale, 29200 Brest, France, [5]Inserm U830, Institut Curie Centre de Recherches, 75005 Paris, France, [6]Université Paris Descartes, Sorbonne Paris Cité, 75005 Paris, France, [7]Service de Génétique, Institut Curie, 75005 Paris, France, [8]Unité Mixte de Génétique Constitutionnelle des Cancers Fréquents, Hospices Civils de Lyon, 69000 Lyon, France, [9]Lyon Neuroscience Research Center–CRNL, Inserm U1028, CNRS UMR 5292, University of Lyon, 69008 Lyon, France, [10]Inserm U916, Département de Pathologie, Laboratoire de Génétique Constitutionnelle, Institut Bergonié, 33000 Bordeaux, France, [11]Gustave Roussy, Université Paris-Saclay, Département de Biopathologie, 94805 Villejuif, France, [12]Division of Molecular Gynaeco-Oncology, Department of Gynaecology and Obstetrics, University Hospital of Cologne, 50937 Cologne, Germany, [13]Centre for Genomic Medicine, Rigshospitalet, University of Copenhagen, 1017 Copenhagen, Denmark, [14]Laboratoire d'Oncogénétique, Centre Paul Strauss, 67000 Strasbourg, France, [15]Laboratoire d'Oncogénétique Moléculaire, Institut Paoli-Calmettes, 13009 Marseille, France, [16]Laboratoire d'Oncogénétique Moléculaire Humaine, Centre Oscar Lambret, 59000 Lille, France, [17]Department of Genetics and Computational Biology, QIMR Berghofer Medical Research Institute, 4006 Herston, Queensland, Australia, [18]Service de Génétique, CHU Nancy, 54035 Nancy, France, [19]Service de génétique, Hôpital Pitié Salpétrière, AP-HP, 75013 Paris, France and [20]Laboratoire de génétique moléculaire, CHU Nantes, 44000 Nantes, France

---

[*] To whom correspondence should be addressed. Sophie Krieger. Tel: +332455054; Fax: +332455053; Email: s.krieger@baclesse.fr
Correspondence may also be addressed to Claude Houdayer. Tel: +33156245837; Fax: +33153102648; Email: claude.houdayer@curie.fr

[†] The authors wish it to be known that, in their opinion, the last two authors should be regarded as Joint Last Authors.

[‡] ENIGMA.

[§] Unicancer Genetic Group (UGG) Splice Network.

Present addresses:
Sophie Krieger, Laboratoire de biologie et génétique des cancers, Centre François Baclesse, Caen, France.
Claude Houdayer, Service de Génétique, Institut Curie, Paris, France.

Nucleic Acids Research, gky372, https://doi.org/10.1093/nar/gky372

In their article, the authors use HSF version 2.4 instead of HSF version 3.1 which is not imbedded in the Alamut software. To check whether HSF3.1 performed better than SPiCE, the authors have run HSF3.1 on the same training and validation datasets, using the methodology previously described in the published article.

The authors acknowledge that HSF3.1 does indeed perform better than HSF 2.4. However the new analyses confirm that SPiCE remains the best predictor of consensus elements.

The comparison between HSF 2.4, HSF3.1 and SPiCE and the underlying data are available as supplementary material.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.