

ERRATUM

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Erratum to: Diagnosis implications of the whole genome sequencing in a large Lebanese family with hyaline fibromatosis syndrome

Zahraa Haidar¹, Ramzi Temanni², Eliane Chouery¹, Puthen Jithesh², Wei Liu³, Rashid Al-Ali², Ena Wang³, Francesco M Marincola⁴, Nadine Jalkh¹, Soha Haddad⁵, Wassim Haidar⁶, Lotfi Chouchane⁷ and André Mégarbane^{8*}

Erratum

Shortly after the publication of this article [1], one of the authors noticed that his name had been misspelled. The article has been updated. ‘Puthen Jitesh’ has been changed to ‘Puthen Jithesh’.

Author details

¹Unité de Génétique Médicale, Faculté de Médecine, Université Saint-Joseph, Beirut, Lebanon. ²Bioinformatics Division, Sidra Medical & Research Center, Doha, Qatar. ³Genomics Core Laboratory, Translational Medicine Division, Sidra Medical & Research Center, Doha, Qatar. ⁴Research office, Sidra Medical & Research Center, Doha, Qatar. ⁵Department of Radiology, Hotel Dieu de France University hospital–Beirut, Beirut, Lebanon. ⁶Department of General surgery, Dar Al Amal University Hospital-Baalbeck, Baalbeck, Lebanon. ⁷Laboratory of Genetic Medicine and Immunology, Weill Cornell Medicine-Qatar, Doha, Qatar. ⁸Institut Jérôme Lejeune, 37, rue des Volontaires, Paris 75015, France.

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References

1. Zahraa H, Ramzi T, Eliane C, Puthen J, Wei L, Rashid A-A, Ena W, Marincola FM, Nadine J, Soha H, Wassim H, Lotfi C, André M. Diagnosis implications of the whole genome sequencing in a large Lebanese family with hyaline fibromatosis syndrome. BMC Genet. 2017;18:3. doi:10.1186/s12863-017-0471-0.

* Correspondence: andre.megarbane@yahoo.fr

⁸Institut Jérôme Lejeune, 37, rue des Volontaires, Paris 75015, France