Histone variant macroH2A1.1 Enhances nonhomologous end joining-dependent DNA double-strand-break repair and reprogramming efficiency of human iPSCs

Giallongo, Sebastiano; Řeháková, Daniela; Biagini, Tommaso; Lo Re, Oriana; Raina, Priyanka; Lochmanová, Gabriela; Zdráhal, Zbyněk; Resnick, Igor; **Pata, Pille**; **Pata, Illar**; Mistrík, Martin; De Magalhães, João Pedro; Mazza, Tommaso; Koutná, Irena; Vinciguerra, Manlio

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