

High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations

Zhang, Yiqun; Chen, Fengju; Fonseca, Nuno A.; He, Yao; Fujita, Masashi; Nakagawa, Hidewaki; Zhang, Zemin; Brazma, Alvis; Amin, Samirkumar B.; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 736 <https://doi.org/10.1038/s41467-019-13885-w>
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