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Abstract

Motivation: Text Text Text Text Text Text.

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1 Introduction

Clustered regularly interspaced short palindromic repeats (CRISPR) / CRIPSR-associated protein 9 (Cas9) systems is preferred over other biological research and human medicine technologies now, beacuse of it's efficiency, robustness and programmability. Cas9 nucleases can be directed by short guide RNAs (sgRNAs) to introduce site-specific DNA double-stranded breaks in target, so to enable editing site-specific within the mammalian genome (Jinek et al., 2012; Cong et al., 2013; Mali et al., 2013). CRISPR / Cas9, to a large extent, has developed genetic therapies at the cellular level, while there are still severe medical disadvantage even now which has greatly hindered the further clinical application of the CRISPR/Cas9 systems. One of these disadvantage is due to point mutations caused by off-target effects (Rubeis and Steger, 2018; Kang et al., 2016; Ishii, 2017; Liang et al., 2015). To overcome this disadvantage, a solution is to engineer CRISPR/Cas9 with higher specificities. That's why more and more higher specificities Cas9 variants, such as enhanced SpCas9 (eSpCas9(1.1)), Cas9-High Fidelity (SpCas9-HF1) (Ishii, 2017; Slaymaker et al., 2016), hyper-accurate Cas9 (HypaCas9) (Kleinstiver et al., 2016), been developed and bring a significant volume of experimental data, that is to say researchers have to face the difficulty of analyzing such huge and heterogeneous data.

2 Approach

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$$\sum x + y = Z \tag{1}$$

3 Methods

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2 Sample et al.

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Table 1. This is table caption

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row3	row3	row3	row3
row4	row4	row4	row4

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4 Sample et al.

FPO

Fig. 1. Caption, caption.

3.2 Test1

4 Discussion

5 Conclusion

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- 2. this is item, use enumerate
- 3. this is item, use enumerate

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