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# Improving knowledge of Asian pteridophytes through DNA sampling of specimens in regional collections

📅 1 September 2021 - 28 February 2023    € 20,000

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*Brainea insignis*. Photo © 2021 Li-Yaung Kuo. All rights reserved.

*rbcl* A: 3558 B: 3146

*trnL-L-F* A: 7 B: 2559

### Variability

*trnL-L-F*  $\cong$

*matK*  $\gg$

*trnH-psbA*  $\cong$

*rbcl*

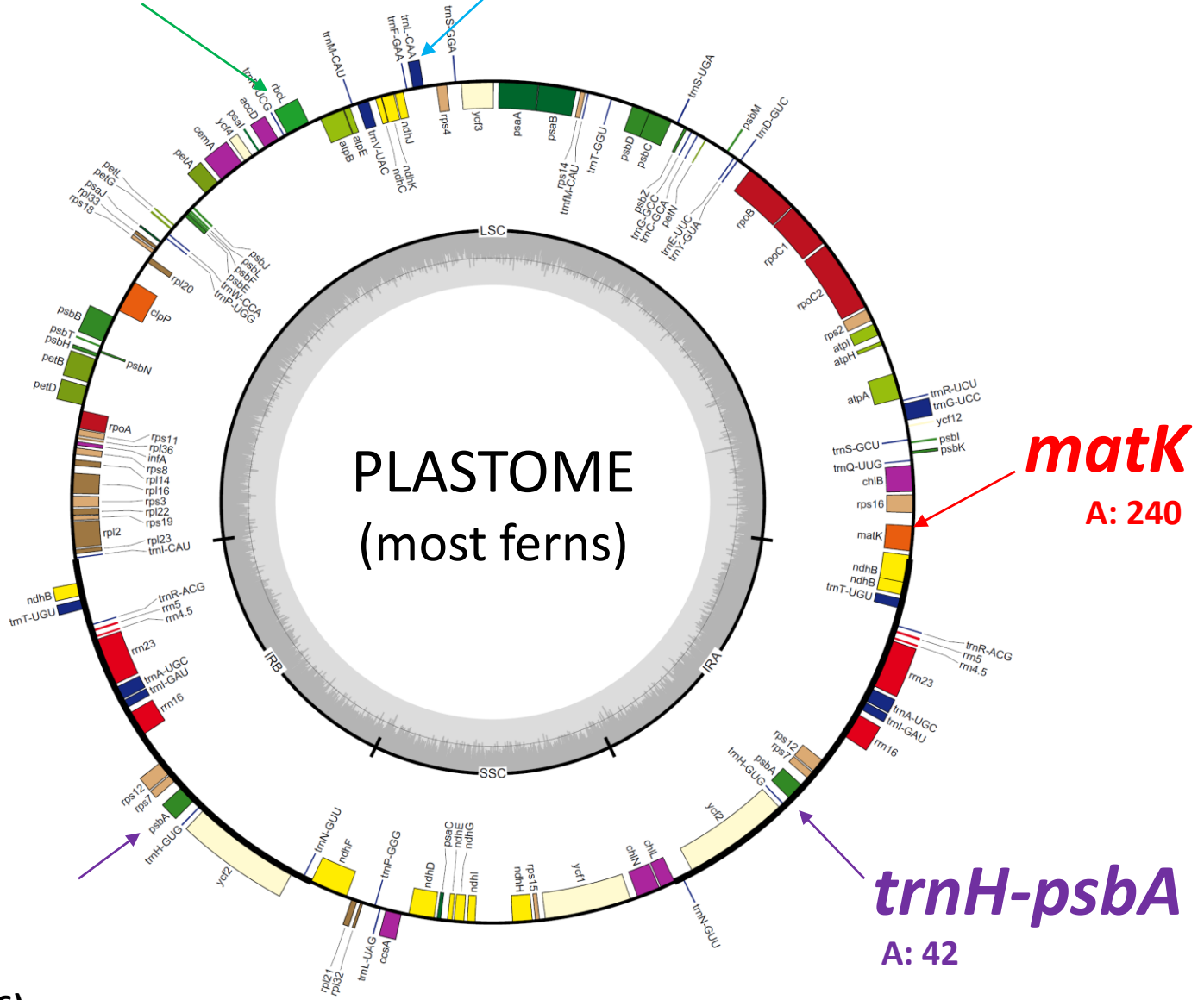
### Primer universality

*trnL-L-F*  $\cong$

*trnH-psbA*  $\cong$

*rbcl*  $\gg$

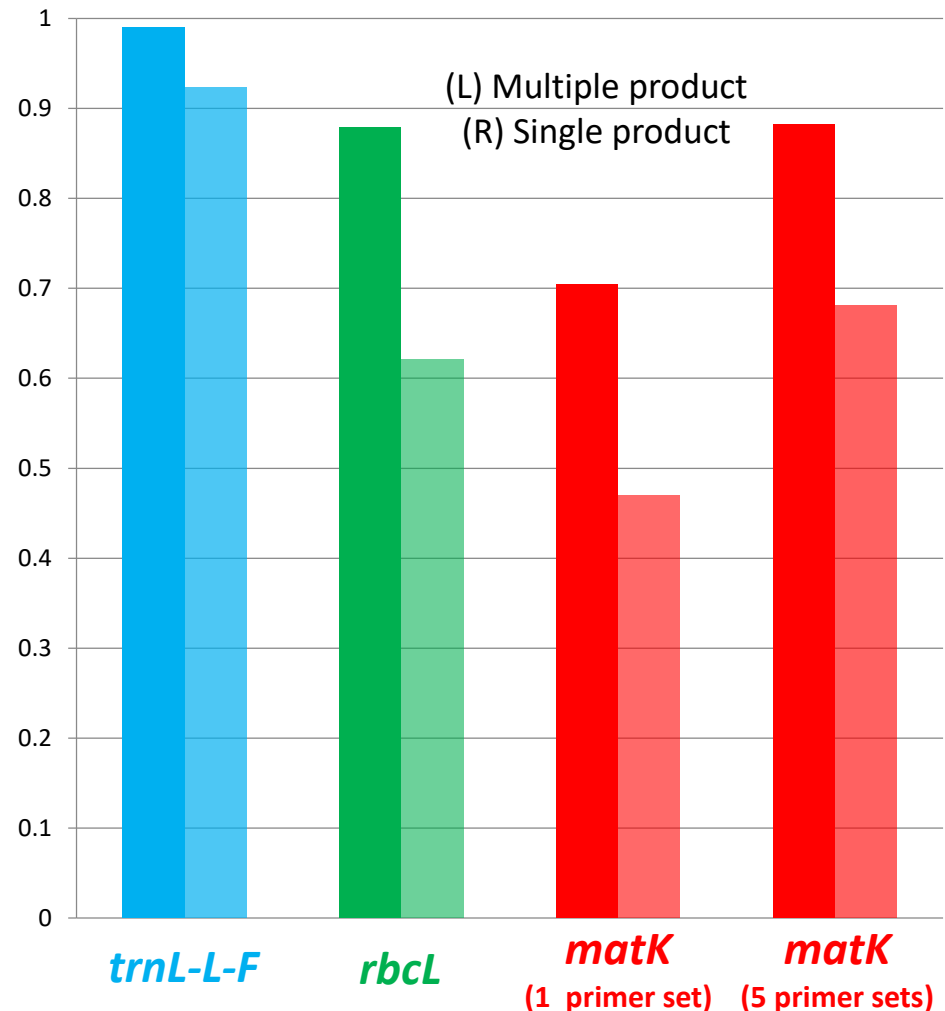
*matK*



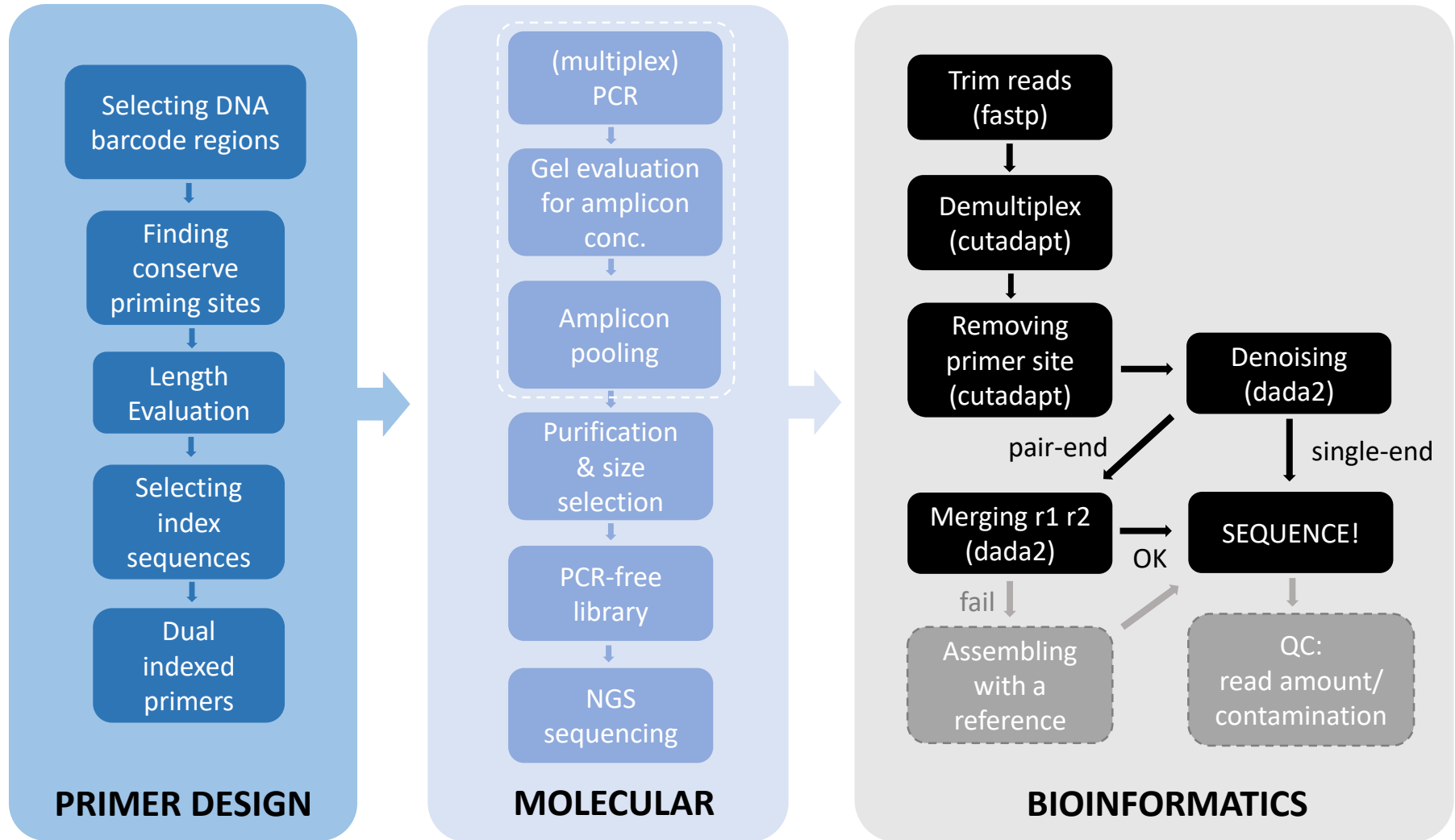
A: BOLD (2021)  
 B: Testo & Sundue (2016)

# High Universality of *trnL-L-F* Primer Set

Family	<i>trnL-L-F</i>	<i>rbcl</i>	<i>matK</i>
Hymenophyllaceae	100.00%	100.00%	54.55%
Gleicheniaceae	100.00%	100.00%	100.00%
Plagiogyriaceae	100.00%	100.00%	50.00%
Lindsaeaceae	100.00%	50.00%	0.00%
Dennstaedtiaceae	100.00%	100.00%	80.00%
Pteridaceae	80.00%	60.00%	80.00%
Dryopteridaceae	100.00%	91.67%	16.67%
Polypodiaceae	100.00%	76.92%	7.69%
Aspleniaceae	100.00%	85.71%	14.29%
Thelypteridaceae	100.00%	22.22%	44.44%
Arthyriaceae	100.00%	90.91%	100.00%



# A new workflow adopting NGS platforms



**PRIMER DESIGN**

**MOLECULAR**

**BIOINFORMATICS**

\$\$ > Sanger's

\$\$ << Sanger's

\$\$ << Sanger's

# Sequencing Costs (incl. library)

	Miseq PE 300	PacBio sequel, SMART
Min. per run	22,000 NTD— 1.66 M reads— 1 GB (1/10lane)	92,000 NTD— 0.75 M reads <sup>b</sup> — 15 GB (one flow cell)
Max. sample per run	16667 (50X) <sup>a</sup> 8333 (100X) <sup>a</sup>	15000 (50X) <sup>b</sup>
Coverage 50X	1.32 NTD per sample	6.13 NTD per sample
Coverage 100X	2.65 NTD per sample	12.26 NTD per sample

<sup>a</sup>Separate into two amplicons within ~1kb region

<sup>b</sup>CCS reading 20 times per DNA molecular

# Fern Plastome List

Here is a list of fern plastomes published in [genbank](#). You can download the csv below. The list includes complete plastomes as well as fragments greater than 10 kb. This list is based on a search using a Biopython script written by Carol Rowe and Paul Wolf, then rewritten in R by Tanner Robison Sept 2018.

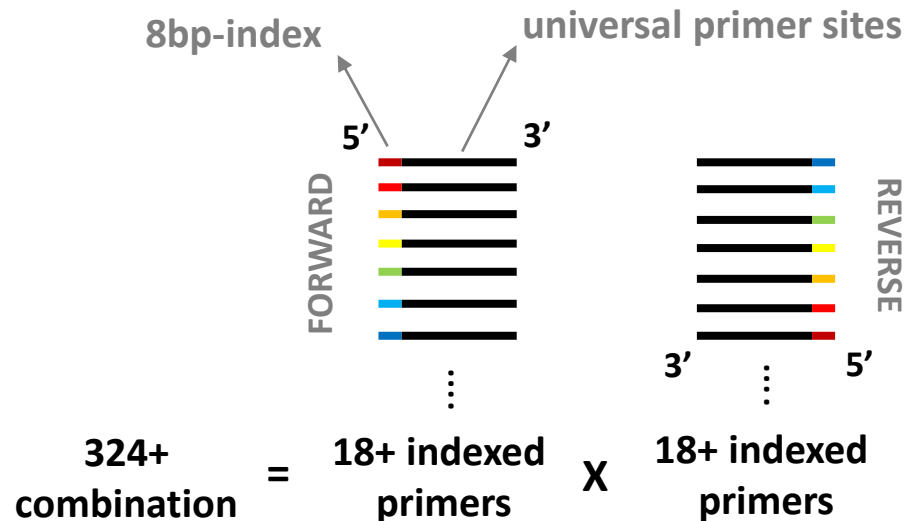
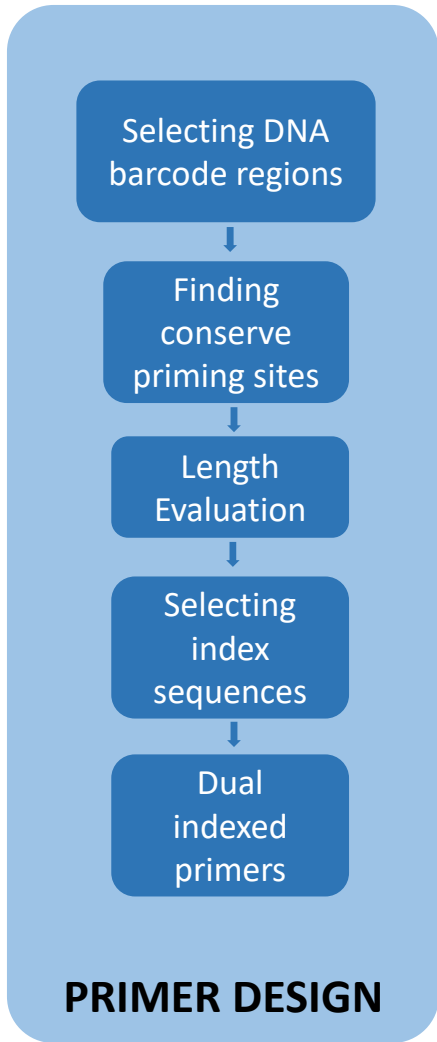
The list can be download here: [all\\_fern\\_plastomes.csv](#)

**250 plastomes (2020/9/24)**

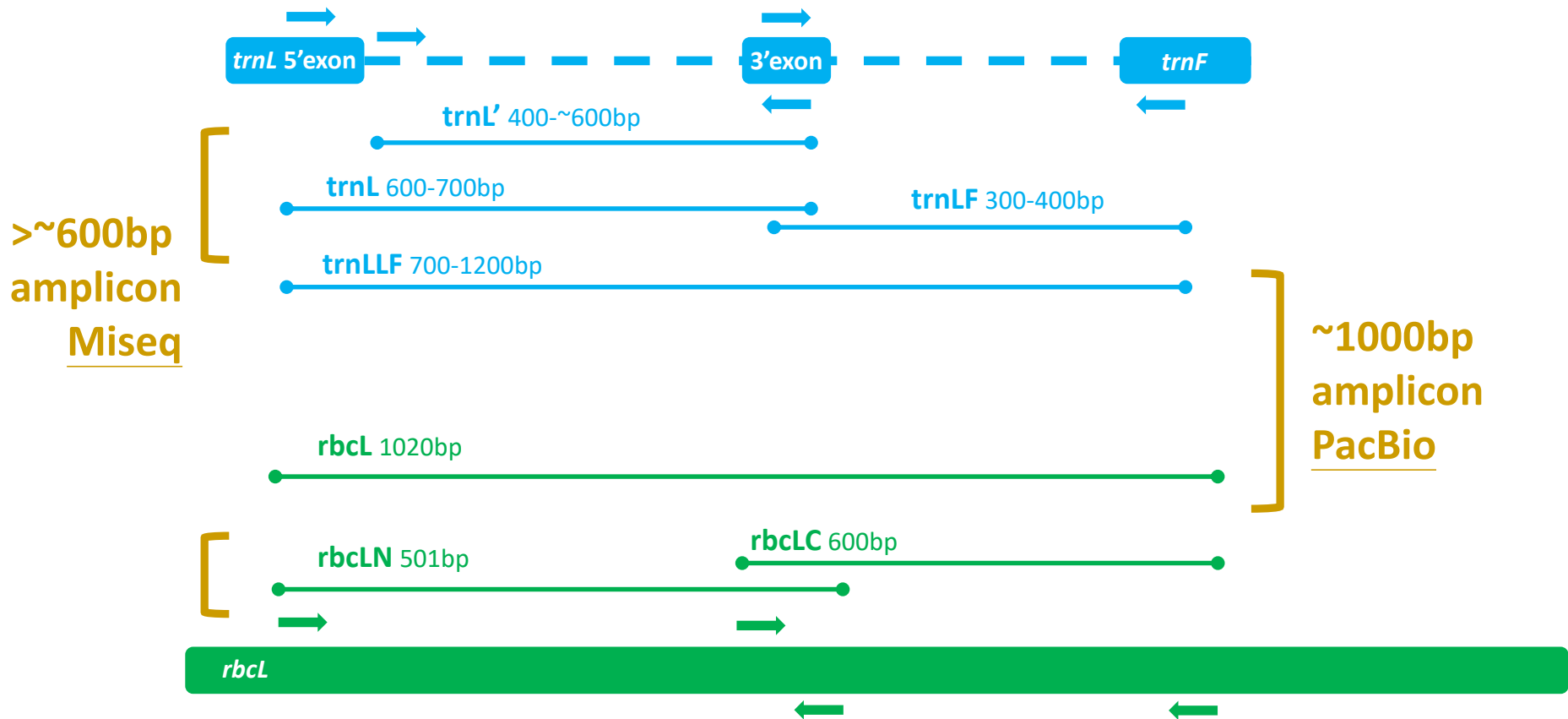
**A custom Python script finding 20-25bp conserved priming sites (Wu et al. 2022)**

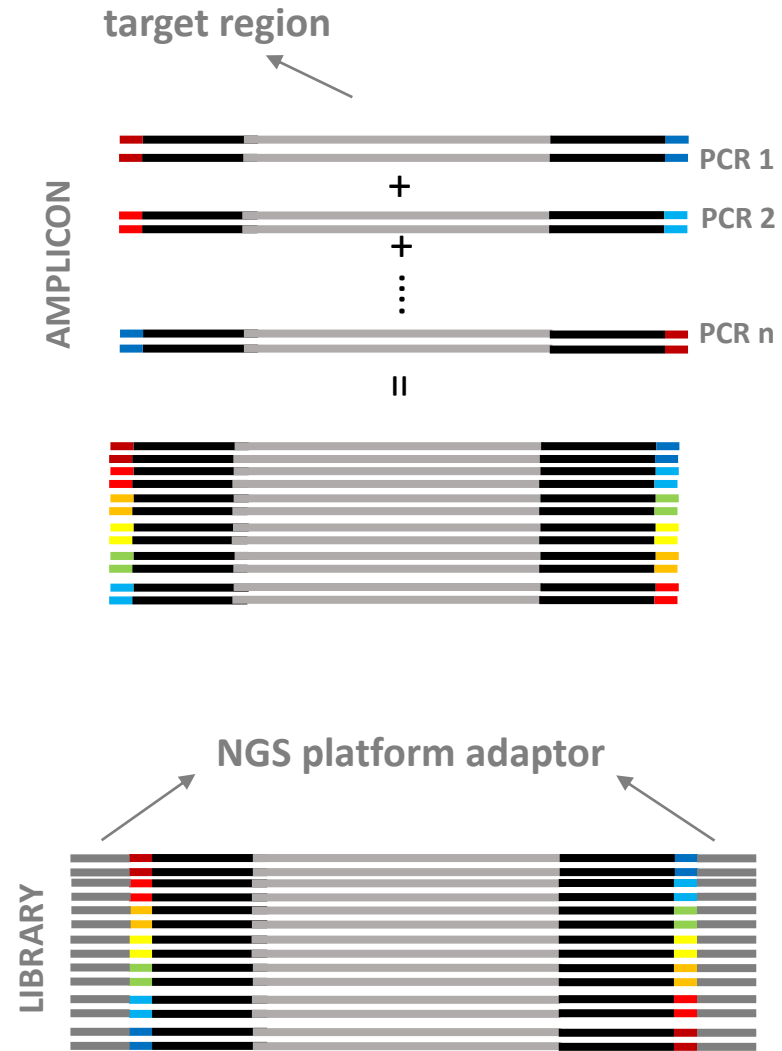
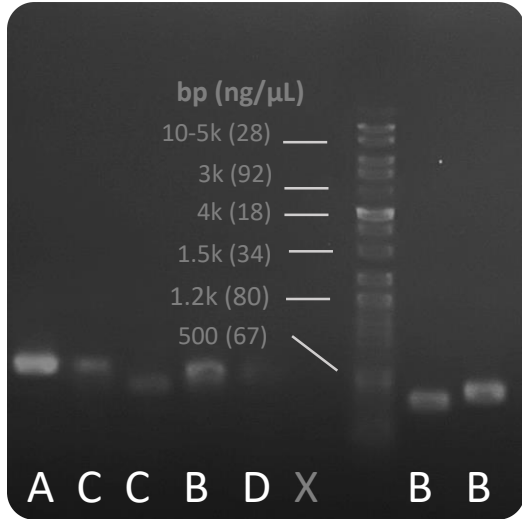
**Target region ~1,000bp or < 540bp**

**A custom Python script evaluate mismatches of 18+ 8bp-indexes at 5' of priming sites**

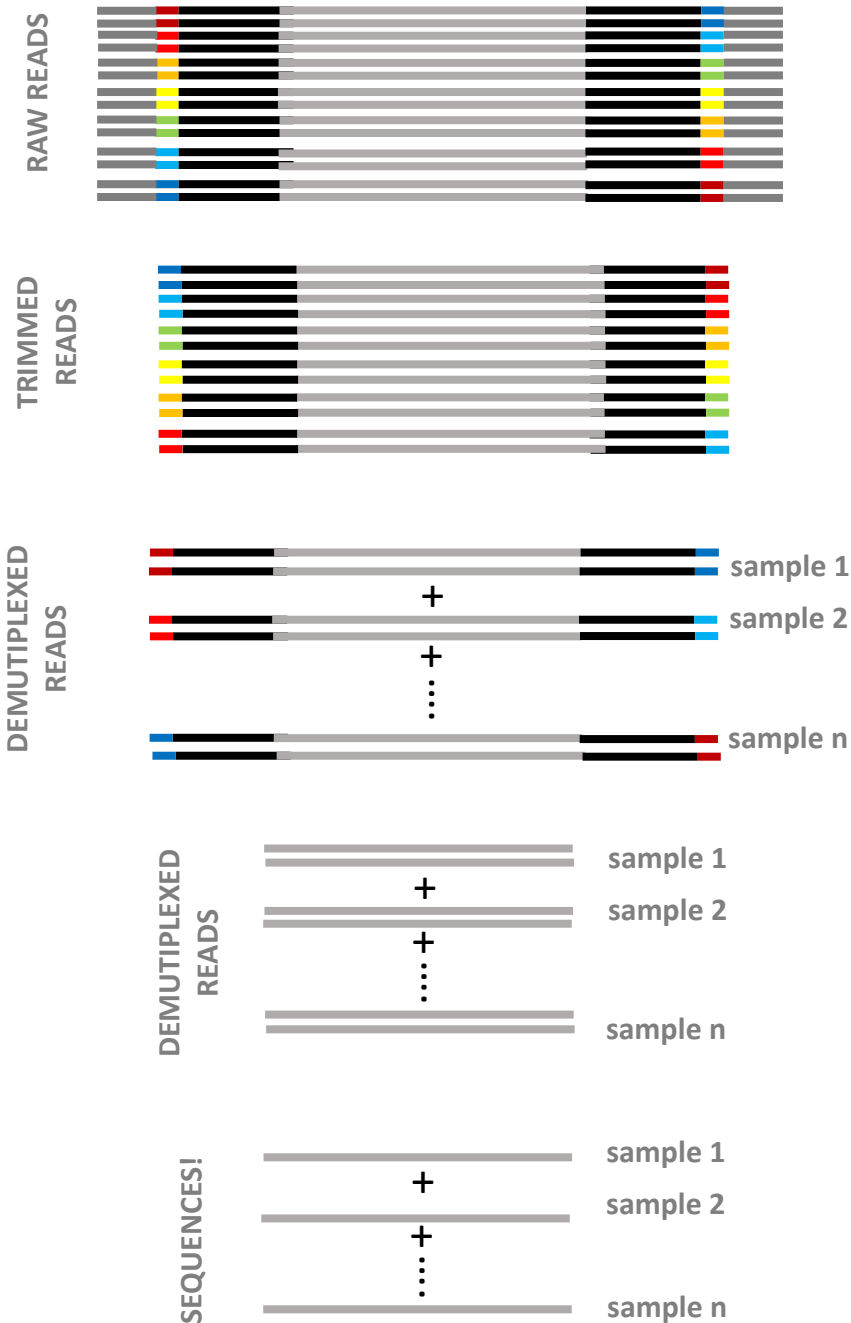


# Primer sets & Amplicon Design









A pipeline:  
<https://github.com/PowerBarcoder>

