

(a) PE3

OsWaxy-P1 desired: -40 bp

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      1631      1641      1651      1661      1671      1681
GCAACGTACGCCAAGCCGAAACGGCAGGCAGCATCGCGCACGCACACACAGGCCACAGCACACGCG
.....*****..... 82
.....T.....*****..... 1
.....C.....*****..... 1
```

(b) PDel

OsGS3 desired: -25 bp

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      5101      5111      5121      5131      5141      5151
AATTTTTTTGTAGGGTTGACGAATTCATCGGAAGAACTCCTGATCCATTCATAACGATGTATGGATTTTC
.....*****..... 383
..*.....*****..... 1
.....*****.....A..... 1
.....*****.....T..... 1
.....T.....*****..... 1
```

(c) PDel/Syn

OsD18 desired: -18 bp

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      2691      2701      2711      2721      2731      2741
AGTCGAGGCGGAGAGGAGGATCGGCGAGAGGATGACGGCGACGGTGCACCTCAACTGGTACCCGAGGTGC
.....*****..C..T..G..... 170
.....*****..C..T..G.....T..... 1
.....*****..C..T..G..... 1
.....*****..C..T..G..... 1
.....G.....*****..C..T..G..... 1
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Supplementary Figure 1 Sequencing data of the precise deletions of PE3, PDel and PDel/Syn. "*" represents deletion, "." means the same nucleotide with wild type. Red letters in (c and d) represent positions of multiple synonymous base mutations. Reads fully covering the target region are extracted and counted, and numbers of every kind of reads are shown on the right of the sequence of reads.

