

Primer3 Output

PRIMER PICKING RESULTS FOR Puccinia_recondita_subunit ribosomal RNA_internal transcribed spacer 2_18S ribosomal RNA_8S ribosomal RNA_28S ribosomal RNA_internal transcribed spacer 1_8S rRNA_26S rRNA_18S rRNA_28S rRNA

Template masking not selected
No mispriming library specified
No internal oligo mishyb library specified
Using 1-based sequence positions
NO PRIMERS FOUND - [Help](#)

WARNING: Unrecognized base in input sequence

SEQUENCE SIZE: 541
INCLUDED REGION SIZE: 541

```
1 ctgcgggaaNggNNcatttaccgaagNgaNgggcctccgagggtcggaNNcctNccaNcc
61 cttNtgtgaacacaNtcccNttNNNNNNggNggcgaccctgccgggcgcccccgaggac
121 caccaaaaaacactgcatcNtNatNtgcgtcggagtttacgagtaaaNcNaaacaNaac
181 tttcaacaacggatctcttggNNtctNgcatcgaNgagaacgcagcgaaNtgcgata
241 agttaaNtgtgaattgccagaNaattcNgtgaatcatcNaatctttgcaacgcacNttgc
301 gscclNNtggtattccNngNNgggcatgccNgttNgagNgtcattacaccNtccaagcc
361 tcgctgggtattggggcgctcttttcgcgggggaNcaNtccccgcgcgcctcaaagtct
421 cccggctgagcgggtctcgtctcccagcgttgtggcatcacgtctcgcgcggagttcacg
481 agccctcacggctcgttaaatcacaccatttctcaggttgacctcggatcNggtagggat
541 a
```

Statistics

	con sid ered	too many Ns	in tar get	in excl reg	not ok reg	bad GC%	no clamp	tm too low	tm too high	high any_th compl	high 3'_th compl	high- hair- pin	poly X	high end stab	ok
Left	581	337	0	0	0	95	0	32	50	0	0	13	24	0	30
Right	1059	249	0	0	0	103	0	135	377	0	0	53	16	0	126
Intl	1918	378	0	0	0	123	0	117	1012	0	0	0	11	0	277

Pair Stats:
considered 5043, unacceptable product size 5040, no internal oligo 3, ok 0
libprimer3 release 2.4.0

(primer3_results.cgi release 4.1.0)