

PRIMER PICKING RESULTS FOR *Puccinia_recondita*_elongation factor 1 alpha_elongation factor 1_consensus_group_1

```

Template masking not selected
No mispriming library specified
No internal oligo mishyb library specified
Using 1-based sequence positions

```

OLIGO	<u>start</u>	<u>len</u>	<u>tm</u>	<u>gc%</u>	<u>any</u>	<u>th</u>	<u>3' th</u>	<u>hairpin</u>	<u>seq</u>
LEFT PRIMER	577	20	59.24	50.00	0.00	0.00	0.00	0.00	tctggcttcaacggagacaa
RIGHT PRIMER	736	20	58.95	60.00	0.00	0.00	0.00	0.00	ggaggggtttatcggtagg
INTERNAL OLIGO	667	20	59.59	50.00	9.84	0.00	0.00	0.00	accgaaaaactctctcga

```
SEQUENCE SIZE: 811
INCLUDED REGION SIZE: 811
```

PRODUCT SIZE: 160, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00

1 gtNaattacaataaaaNacctcNtaatNatccctcttttcgtctttNtttttcaatccgtt

61 NctctgaaNctNataaactgccacaggaagcagcagaactcggaaaaggatctttcaaat

121 acgcctgggtcctcNacaagctaaaNgccgaacgtgaacgtggtattacNattgacattg

181 ctctatggaaNtttgagactcctagatactacgtcaccgtcattggtaagaaatNNtNtc

241 aaattttNttactacaNtNctNacccgNtttcagacgctcctggacacagagatttNatc

301 aagaacatgattacNggaaacctctcaagctgactgtgccattctcatcatcgcggccggt

361 accggtgagttNgaggcaggtatttcaaaggatggtcaaaccagagaacatgcaNtgctt

421 gcgttcacattaggtgtcaaacaattgattgttgccattaaNaagatggacacggccaaa

481 tgggctgaagcNagataccttgaaatNatcaaggagacgaccaacttNataaagaaagtct

[illegible]

601 attgataattccgNNaactgcccctggtacaaaggctgggaaaaagaaaaNaagactgga

781 gttcctgttggacgtgtNgagaccggaatca

```
>>>>> left primer
<<<<< right primer
^^^^^ internal oligo
```

ADDITIONAL OLIGOS

```
start len tm gc% any th 3' th hairpin seq
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1 LEFT PRIMER	416	20	58.11	45.00	0.00	0.00	0.00	tgcttgcgttcacattaggt
RIGHT PRIMER	595	20	59.24	50.00	0.00	0.00	0.00	tgtctccggtgaagccagaa
INTERNAL OLIGO	463	20	59.74	50.00	2.58	0.00	42.78	aagatggacacggccaaatg
PRODUCT SIZE: 180, PAIR ANY TH COMPL: 0.00, PAIR 3' TH COMPL: 1.53								

2 LEFT PRIMER	574	20	57.14	45.00	0.00	0.00	0.00	atctctggccttcaacggaga
RIGHT PRIMER	752	20	58.53	55.00	0.00	0.00	0.00	tcttgtagtggtaggcggag
INTERNAL OLIGO	712	20	60.17	55.00	0.00	0.00	40.22	agtcgccctaccgataaacc
PRODUCT SIZE: 179, PAIR ANY TH COMPL: 0.00, PAIR 3' TH COMPL: 0.00								

3 LEFT PRIMER	579	22	58.73	45.45	0.00	0.00	0.00	tggtctcaacggagacaatatg
RIGHT PRIMER	743	20	59.60	60.00	0.00	0.00	0.00	ggtaggcggaggggtttatc
INTERNAL OLIGO	667	20	59.59	50.00	9.84	0.00	0.00	accggaaaaactctcctcga
PRODUCT SIZE: 165, PAIR ANY TH COMPL: 0.00, PAIR 3' TH COMPL: 0.00								

4 LEFT PRIMER	533	23	58.67	43.48	0.00	0.00	0.00	agaaagtcggtatttaaccccaag
RIGHT PRIMER	731	20	59.25	55.00	0.00	0.00	0.00	ggtttatcggtagggcgact
INTERNAL OLIGO	577	20	60.17	50.00	0.00	0.00	0.00	tctggcttcaacggagacaa
PRODUCT SIZE: 199, PAIR ANY TH COMPL: 0.00, PAIR 3' TH COMPL: 7.93								

5 LEFT PRIMER	322	20	59.31	50.00	0.00	0.00	0.00	tctcaagctgactgtgccat
RIGHT PRIMER	484	18	60.28	61.11	0.00	0.00	0.00	cccatattggccgtgtcca
INTERNAL OLIGO	416	20	59.02	45.00	0.00	0.00	0.00	tgcttgcgttcacattaggt
PRODUCT SIZE: 163, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								

6 LEFT PRIMER	375	22	58.63	45.45	0.00	0.00	0.00	ggcagggtattttcaaaggatggt
RIGHT PRIMER	556	20	57.20	50.00	0.00	0.00	0.00	ccttgggggttaaattccgact
INTERNAL OLIGO	463	20	59.74	50.00	2.58	0.00	42.78	aagatggacacggccaaatg
PRODUCT SIZE: 182, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								

7 LEFT PRIMER	558	23	58.62	39.13	0.00	0.00	0.00	tggttcatttgtgccatttctg
RIGHT PRIMER	738	19	58.87	57.89	0.00	0.00	0.00	gcggaggggtttatcggtg
INTERNAL OLIGO	667	20	59.59	50.00	9.84	0.00	0.00	accggaaaaactctcctcga
PRODUCT SIZE: 181, PAIR ANY TH COMPL: 0.00, PAIR 3' TH COMPL: 0.00								

8 LEFT PRIMER 196 23 58.04 47.83 0.00 0.00 0.00 agactcctagatactacgtcacc
RIGHT PRIMER 355 19 59.14 57.89 8.23 0.00 0.00 ccgcgatgatgagaatggc
INTERNAL OLIGO 269 20 60.88 55.00 0.00 0.00 35.47 tttcagacgctcctggacac
PRODUCT SIZE: 160, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00

9 LEFT PRIMER 581 23 57.26 39.13 0.00 0.00 0.00 gcttcaacggagacaatatgatt
RIGHT PRIMER 755 20 57.04 50.00 0.00 0.00 0.00 acatcttgtagtggtaggcg
INTERNAL OLIGO 712 20 60.17 55.00 0.00 0.00 40.22 agtcgccctaccgataaacc
PRODUCT SIZE: 175, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00

Statistics

	con	too	in	in	not		no	tm	tm	high	high	high		high	
	sid	many	tar	excl	ok	bad	GC	too	too	any_th	3'_th	hair-	poly	end	
	ered	Ns	get	reg	reg	GC%	clamp	low	high	compl	compl	pin	X	stab	ok
Left	1940	427	0	0	0	77	0	710	210	0	0	258	6	0	252
Right	2074	385	0	0	0	108	0	763	236	0	0	89	30	0	463
Intl	3693	533	0	0	0	1	0	916	948	0	0	114	0	0	1181

Pair Stats:
considered 81657, unacceptable product size 81641, primer in pair overlaps a primer in a better pair 30003, ok 16
libprimer3 release 2.4.0

(primer3_results.cgi release 4.1.0)