

PRIMER PICKING RESULTS FOR *Puccinia_recondita*_consensus_consensus_group_4

```

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 th</u>	<u>3' th</u>	<u>hairpin</u>	<u>seg</u>
LEFT PRIMER	101	20	58.71	55.00	1.88	0.00	0.00	gcagcattccgagtaactcc
RIGHT PRIMER	275	21	58.31	52.38	0.00	0.00	0.00	gagtttcttctcctggaacgg
INTERNAL OLIGO	155	20	59.96	55.00	16.21	0.00	41.33	gcggtagctgctgaatcttc

```
SEQUENCE SIZE: 400
INCLUDED REGION SIZE: 400
```

PRODUCT SIZE: 175, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 12.24

1 acagagactaaagcaagtgttgattcaaagctggNgttaaagagtataaattgacttat

[illegible]

121 tcaaccgagttcacctgaagaagcaggggtgcggtagctgctgaatcttactgg
 ^~^~^~^~^~^~^~^~^~^~

181 tacatggacaactgtgtggaccgatgggcttaccagccttgatcgttacaaaggacgatg

241 ctaccacatcgagcccgttccaggagaagaaactcaattttattgCGtatgtagcttaccc

301 cttagacctttttgaagaaggttcggttactaacatgtttacttcgattgtgggtaatgt

361 atttgggttcaaagccctggctgccctacgtctagaggat

KEYS (in order of precedence):

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

ADDITIONAL OLIGOS

	<u>start</u>	<u>len</u>	<u>tm</u>	<u>gc%</u>	<u>any th</u>	<u>3' th</u>	<u>hairpin</u>	<u>seq</u>
1 LEFT PRIMER	229	20	57.91	50.00	0.00	0.00	0.00	caaaggacgatgctaccaca
RIGHT PRIMER	397	19	58.97	63.16	1.26	1.26	0.00	ctctagacgtagggcagcc
INTERNAL OLIGO	283	20	59.15	50.00	0.00	0.00	35.57	tgcgtatgtagcttaccct

	PRODUCT SIZE:	169,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00	
2 LEFT PRIMER	1	23	58.87	43.48	0.00	0.00	0.00 acagagactaaagcaagtgttgg
RIGHT PRIMER	174	20	59.07	55.00	0.00	0.00	0.00 gaagattcagcagctaccgc
INTERNAL OLIGO	126	20	60.24	55.00	0.00	0.00	33.06 ccggagttccacctgaagaa
PRODUCT SIZE:	174,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
3 LEFT PRIMER	111	20	58.45	55.00	0.73	0.00	0.00 gagtaactcctcaacccgga
RIGHT PRIMER	309	21	57.23	47.62	0.00	0.00	0.00 aggtctaaggggtaagctaca
INTERNAL OLIGO	155	20	59.96	55.00	16.21	0.00	41.33 gcggtagctgctgaatcttc
PRODUCT SIZE:	199,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
4 LEFT PRIMER	89	22	59.26	50.00	3.98	0.00	0.00 ctgatatcttcggcagcattcc
RIGHT PRIMER	248	20	57.91	50.00	0.00	0.00	0.00 tgtggtagcatcgctccttg
INTERNAL OLIGO	155	20	59.96	55.00	16.21	0.00	41.33 gcggtagctgctgaatcttc
PRODUCT SIZE:	160,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
5 LEFT PRIMER	212	20	57.15	45.00	0.00	0.00	0.00 accagccttgatcgttacaa
RIGHT PRIMER	395	20	61.74	65.00	15.19	1.39	0.00 ctagacgtagggcagccagg
INTERNAL OLIGO	283	20	59.15	50.00	0.00	0.00	35.57 tgcgtatgtagcttaccct
PRODUCT SIZE:	184,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
6 LEFT PRIMER	108	20	58.45	55.00	1.88	0.00	0.00 tccgagtaactcctcaaccc
RIGHT PRIMER	307	23	57.88	47.83	0.00	0.00	0.00 gtctaaggggtaagctacatacg
INTERNAL OLIGO	155	20	59.96	55.00	16.21	0.00	41.33 gcggtagctgctgaatcttc
PRODUCT SIZE:	200,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
7 LEFT PRIMER	189	19	58.46	57.89	0.00	0.00	0.00 caactgtgtggaccgatgg
RIGHT PRIMER	355	23	58.61	39.13	0.00	0.00	0.00 acccacaatcgaagtaaacadgt
INTERNAL OLIGO	208	20	59.17	50.00	0.00	0.00	41.25 gcttaccagccttgatcggt
PRODUCT SIZE:	167,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
8 LEFT PRIMER	156	20	57.41	50.00	13.43	0.00	0.00 cggtagctgctgaatcttct
RIGHT PRIMER	338	23	57.52	39.13	10.51	0.00	0.00 acatgttagtaaccgaaccttct
INTERNAL OLIGO	187	20	59.75	55.00	0.00	0.00	39.15 gacaactgtgtggaccgatg
PRODUCT SIZE:	183,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
9 LEFT PRIMER	64	23	57.22	39.13	0.00	0.00	0.00 actcctgaatatgaaaccaagga
RIGHT PRIMER	231	20	57.15	45.00	0.00	0.00	0.00 ttgtaacgatcaaggctggt
INTERNAL OLIGO	155	20	59.96	55.00	16.21	0.00	41.33 gcggtagctgctgaatcttc
PRODUCT SIZE:	168,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
10 LEFT PRIMER	160	22	59.16	45.45	0.00	0.00	0.00 agctgctgaatcttctactggt
RIGHT PRIMER	335	23	57.47	39.13	10.51	0.00	0.00 tgtagtaaccgaaccttctca
INTERNAL OLIGO	187	20	59.75	55.00	0.00	0.00	39.15 gacaactgtgtggaccgatg
PRODUCT SIZE:	176,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		
11 LEFT PRIMER	6	23	57.31	39.13	0.00	0.00	0.00 gactaaagcaagtgttggattca
RIGHT PRIMER	196	21	57.87	47.62	0.00	0.00	0.00 cacagttgtccatgtaccagt
INTERNAL OLIGO	155	20	59.96	55.00	16.21	0.00	41.33 gcggtagctgctgaatcttc
PRODUCT SIZE:	191,	PAIR ANY_TH COMPL:	0.00,	PAIR 3'_TH COMPL:	0.00		

12 LEFT PRIMER 213 22 59.58 50.00 3.44 3.44 0.00 ccagccttgatcgttacaaagg
RIGHT PRIMER 372 23 57.01 39.13 0.00 0.00 0.00 ttgaacccaaatacattaccac
INTERNAL OLIGO 283 20 59.15 50.00 0.00 0.00 35.57 tgcgtatgtagcttaccct
PRODUCT SIZE: 160, 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	1346	23	0	0	0	149	0	500	267	0	0	164	0	0	243
Right	1367	0	0	0	0	79	0	638	291	0	0	97	19	0	243
Intl	3587	27	0	0	0	57	0	1186	1100	0	0	44	0	0	1173

Pair Stats:
considered 44536, unacceptable product size 44519, primer in pair overlaps a primer in a better pair 15161, ok 17
libprimer3 release 2.4.0

(primer3_results.cgi release 4.1.0)