

PRIMER PICKING RESULTS FOR *Puccinia\_recondita*\_consensus\_consensus\_group\_0

```
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	28	20	58.86	50.00	0.00	0.00	0.00	0.00	caactcgggttttggcattgc
RIGHT PRIMER	227	20	58.14	50.00	0.00	0.00	0.00	0.00	accttggttgggattcatg
INTERNAL OLIGO	132	20	60.10	50.00	15.55	0.00	41.87		gccaccgatcgtgtttcatt

```
SEQUENCE SIZE: 574
INCLUDED REGION SIZE: 574
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PRODUCT SIZE: 200, PAIR ANY\_TH COMPL: 0.00, PAIR 3'\_TH COMPL: 0.00

**1** atgtttccatacttgcagcctttgctccaactcggttttggaattgcgttggctaagtggN  
                        >>>>>>>>>>>>>>>>

61 attNtaagtttattattactgttaaccttcttgaacgtattgaagcagttacttttcaag

121 aatccaaatgagccaccgatcgtgtttcattggattcctatcattggaagtacaatttca

181 tatggaatgaatccctacaaattctttcatgaatccaagccaagggtcagttagcgctta  
<<<<<<<<<<<<<<<<<<<

241 cactctctgaggaatac gatattaattgaggtaaagtacggaaatatcttcactttcata

301 ttactgggtaagaagacgacggtatatctaggtcgacagggaaataattttattcttaat

361 ggaaaactcagagacgttaatgccgaagaaatttatacgggtcttgacgactcctgtcttc

421 gggactgatgtagtgtNtgactgtcctaattcaaaattaatggaacaaNagaaggtttta

481 aaatcatatggataactttcagaatcagactctgatatttgcacagttcatgaaagcagc

541 ccttacgactgaggccttccgctcttatgtacct

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	124	19	58.98	57.89	8.51	8.51	0.00	ccaaatgagccaccgatcg
RIGHT PRIMER	322	20	59.11	55.00	0.00	0.00	0.00	ccgtcgtcttcttaccagtt
INTERNAL OLIGO	231	20	59.95	50.00	0.00	0.00	0.00	ttgccgcttacactctctga
PRODUCT SIZE: 199, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
2 LEFT PRIMER	33	19	59.15	52.63	1.91	0.00	0.00	cggttttggcattgcgttg
RIGHT PRIMER	231	20	59.22	50.00	1.86	0.00	0.00	actgaccttggttgggatt
INTERNAL OLIGO	132	20	60.10	50.00	15.55	0.00	41.87	gccaccgatcgtgtttcatt
PRODUCT SIZE: 199, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
3 LEFT PRIMER	226	20	59.21	55.00	0.00	0.00	0.00	gtcagttgccgcttacactc
RIGHT PRIMER	386	21	59.18	47.62	4.32	0.00	0.00	tcggcattaacgtctctgagt
INTERNAL OLIGO	304	20	60.03	55.00	0.00	0.00	0.00	ctgggtaagaagacgacggt
PRODUCT SIZE: 161, PAIR ANY_TH COMPL: 2.17, PAIR 3'_TH COMPL: 6.67								
4 LEFT PRIMER	366	21	59.18	47.62	3.79	0.00	0.00	actcagagacgttaatgccga
RIGHT PRIMER	542	20	58.75	50.00	7.89	0.00	0.00	gggctgctttcatgaactgt
INTERNAL OLIGO	412	20	60.03	55.00	14.68	0.00	44.20	cctgtcttcgggactgatgt
PRODUCT SIZE: 177, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
5 LEFT PRIMER	229	20	59.03	50.00	0.00	0.00	0.00	agttgccgcttacactctct
RIGHT PRIMER	389	21	58.12	47.62	0.00	0.00	0.00	tcttcggcattaacgtctctg
INTERNAL OLIGO	304	20	60.03	55.00	0.00	0.00	0.00	ctgggtaagaagacgacggt
PRODUCT SIZE: 161, PAIR ANY_TH COMPL: 2.17, PAIR 3'_TH COMPL: 2.35								
6 LEFT PRIMER	369	21	58.12	47.62	0.00	0.00	0.00	cagagacgttaatgccgaaga
RIGHT PRIMER	547	20	58.26	50.00	0.00	0.00	0.00	cgttaagggtgctttcatga
INTERNAL OLIGO	412	20	60.03	55.00	14.68	0.00	44.20	cctgtcttcgggactgatgt
PRODUCT SIZE: 179, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
7 LEFT PRIMER	213	20	59.22	50.00	0.00	0.00	0.00	atcccaagccaagggtcagtt
RIGHT PRIMER	385	23	59.57	43.48	4.32	0.00	0.00	cggcattaacgtctctgagttt
INTERNAL OLIGO	304	20	60.03	55.00	0.00	0.00	0.00	ctgggtaagaagacgacggt
PRODUCT SIZE: 173, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
8 LEFT PRIMER	370	23	58.50	39.13	0.00	0.00	0.00	agagacgttaatgccgaagaaat
RIGHT PRIMER	561	19	59.11	57.89	5.23	0.00	0.00	cggaggcctcagtcgtaa
INTERNAL OLIGO	412	20	60.03	55.00	14.68	0.00	44.20	cctgtcttcgggactgatgt
PRODUCT SIZE: 192, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
9 LEFT PRIMER	135	20	57.53	45.00	15.09	0.00	0.00	accgatcgtgtttcattgga
RIGHT PRIMER	321	22	57.63	45.45	0.00	0.00	0.00	cgtcgtcttcttaccagtaat
INTERNAL OLIGO	231	20	59.95	50.00	0.00	0.00	0.00	ttgccgcttacactctctga
PRODUCT SIZE: 187, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
10 LEFT PRIMER	210	20	59.22	50.00	0.00	0.00	0.00	tgaatcccaagccaagggtca

RIGHT PRIMER	394	23	57.38	34.78	0.00	0.00	0.00	aaatttccttcggcattaacgtct
INTERNAL OLIGO	304	20	60.03	55.00	0.00	0.00	0.00	ctgggtaagaagacgacggt
PRODUCT SIZE: 185, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								
11 LEFT PRIMER	361	23	58.04	43.48	3.79	0.00	0.00	ggaaaactcagagacgttaatgc
RIGHT PRIMER	540	21	60.00	47.62	7.89	14.41	0.00	gctgctttcatgaactgtgca
INTERNAL OLIGO	412	20	60.03	55.00	14.68	0.00	44.20	cctgtcttcgggactgatgt
PRODUCT SIZE: 180, PAIR ANY_TH COMPL: 0.41, PAIR 3'_TH COMPL: 0.00								
12 LEFT PRIMER	137	22	58.06	45.45	7.03	0.00	0.00	cgatcgtgtttcattggattcc
RIGHT PRIMER	328	23	57.96	47.83	0.00	0.00	0.00	gatataccgtcgtcttcttacc
INTERNAL OLIGO	231	20	59.95	50.00	0.00	0.00	0.00	ttgccgcttacactctctga
PRODUCT SIZE: 192, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00								

# Statistics

	con sid ered	too many Ns	in tar get	in excl reg	not ok reg	bad GC% clamp	no GC 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	2370	28	0	0	0	425	0	1273	167	0	0	147	0	0	329
Right	2290	46	0	0	0	494	0	1227	148	0	0	75	0	0	300
Intl	4895	85	0	0	0	118	0	2334	836	0	0	51	0	0	1471

## Pair Stats:

considered 46007, unacceptable product size 45991, primer in pair overlaps a primer in a better pair 24048, ok 16  
libprimer3 release 2.4.0

(primer3\_results.cgi release 4.1.0)