

Favour primer pairs

- ☒ not amplifying genomic DNA (default)
☐ with high single primer specificity (when genomic contamination is not a problem)

Select best

Select all

Clear selection

	Fw sequence	Rev sequence	Amplicon size	Spans exon border	Rank score	Test results
AT5G49580.1						
☒	AGCTAGATGGTGCCAGGATTGC	TGCTGGGAAGCTTGTTCAACCC	78	Yes	0.9919	
☐	TGAACAAGCTTCCCAGCACGTC	TTGCAGGACATCTCATTCCCTGAC	134	Yes+	3.0362	
☐	CCGCGTGCTTATGTTTGTGCAG	TTGCAGGACATCTCATTCCCTGAC	82	Yes+	3.2064	
☐	AGCTTCCCAGCACGTCTTGTTT	TTGCAGGACATCTCATTCCCTGAC	128	Yes+	3.282	
☐	ATGCCGCGTGCTTATGTTTGTG	TTGCAGGACATCTCATTCCCTGAC	85	Yes+	3.7257	
☐	TGGTTGGGTTGAACAAGCTTCCC	TTGCAGGACATCTCATTCCCTGAC	143	Yes+	3.9696	
☐	AAGCTTCCCAGCACGTCTTGTTT	TTGCAGGACATCTCATTCCCTGAC	129	Yes+	4.0136	
☐	GGTTGAACAAGCTTCCCAGCAC	TTGCAGGACATCTCATTCCCTGAC	137	Yes+	4.1275	
☐	TTGAACAAGCTTCCCAGCACGTC	TTGCAGGACATCTCATTCCCTGAC	135	Yes+	4.2479	
☐	GGTTGGGTTGAACAAGCTTCCC	TTGCAGGACATCTCATTCCCTGAC	142	Yes+	4.4216	
AT5G53480.1						
☒	CGCCGCCGAGATTCTAGATAAACC	CGACAACAAGAAAACCCGCAAGG	148	Yes	3.1342	
☐	CGCCGCCGAGATTCTAGATAAAC	CGACAACAAGAAAACCCGCAAGG	149	Yes	3.1342	
☐	CGCCGCCGAGATTCTAGATAAACC	AGACTTTCTTCCGCGTGCTTACG	105	Yes	3.3733	

Export primer pairs

Data:

- ☒ Complete
☐ Brief

Format:

- ☒ European
☒ Windows
☐ US
☐ Unix
☐ Mac OS