http://www.vcru.wisc.edu/simonlab/sdata/MK000030.pdf

MK000030=IPI

Marker: IPI
Type:
Description: isopentenyl pyrophosphate isomerase
Reference: ① Brian Just Ph.D. Thesis, Table 2.1 ② Theor Appl Genet (2007) 114:693-704
Primers: IPI-F1.....5'-cctctagtgtggactaacacttgttg-3'
IPI-R1.....5'-acatacttgatctccgcgacttc-3'
PCR Reaction:
PCR Program: Annealing temperature 55°C
Screening Method: Not used
Product Sizes: 0.6kb
Example:
Comments: IPI could not be included on the map because no polymorphic sequences were identified
Genbank Reference:: DQ192183
Sequence Information: >IPI (277d) Consensus (cDNA sequence) Primers not in cDNA sequence, but gray shaded areas mark where the primers would be, based on the alignment with the VC000132 sequence below. Yellow shaded marks IPI-F2 and IPI-R2 primer locations.

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CATCACCATGTTGTTGGTAGCACCAGCAGCGGTAAAAGCACCGATACAAATAGCAGCATCCTTTACATCGAGATTCTCGCCTCTC
TCGTTTTCTAAATCTCGTTCGTGTTTAAACAACACTCTATATAACACCAGTAGCACTCATTTTACTGGTGCATCGCATCTCTCTG
TAACTACTACACCTCTTCGTCGTGAATCTCGCTGTTTCGCTGCCATGGCTACTACTGATGATACTACTATGGATGCTGTTCAGAG
ACGCCTTATGTTCGATGACGAGTGTATTTTGGTGGATGAGAATGATCGTGTTGTTGGTCATGAAAATAAATACAATTGTCACTTG
ATGGAGAATATTGAATCCAAAAATTTGCTTCACCGAGCTTTCAGTGTGTTCTTGTTCAACTCTAAATATGAGTTGCTTCTTCAGC
AACGTTCTGCCACCAAGGTAACATTCCCTTTGGTTTGGACAAACACCTGTTGCAGCCACCCTCTGTACAGGGAGTCCGAGCTTAT
CGAGGAAAAGGCATTAGGGGCAAGAAACGCTGCACAGAGGAAGCTTCTAGATGAGCTCGGTATTCCTGCTGAAGATGTTCCTGTT
GATCAGTTCTTGCCTGTGGGTCGTATTCTGTACAAAGCACCATCTGATGGCAAGTGGGGAGAACATGAATTGGATTACCTTCTTT
TTATTGTCCGTGATGTGAAAGTAAATCCCAACCCTGATGAAGTTGCTGACATCAAATATGTGAACCAAGATCAACTGAGAGAGTT
GCTGAGAAAAGCTGATGCGGGTGAGGAAGGCTTGAAACTATCCCCATGGTTCCGACTAATTGTTGACAATTTCTTGTTCAAATTT
TGGGACCATGTTCAGAAAGGAACCCTCAAGGAAGTTGCTGATATGGAAACGATACACAAATTGACTTGAAAACAACAGAATTGCT
CTCCTATGGAAATTCCTGATGAATAAAATAGTGCCTGGAATTGCATAGGGGTAGGTTAGGGTTTCAATCCGAACTAGTAGGCACA
TCTGTGACTTTTGTATTTGAGACTAAAACTGCTGTCCTCCACCGCATAGGAATAGTTCAGGATTTTCATTTGAACTCACTATGTG
AGTTTGCAACTTTTGTTAAAAACTCTGTATCATCAGTTTTGACCTATGGTAAATGTCTTGGATTGGAC
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Sequence Information: >AF227951 (Esther's sequence), no reverse primer in this sequence

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ttcctctagtgtggactaacacatgttgcagccacccctctgtacagggagtccgagcttatcgaggaa
aaggcattaggggcaagaaacgctgcacagaggaagcttctagatgagctcggtattcctgctgaaga
tgttcctgttgatcagttcttgcctgtgggtcgtattctgtacaaagcaccatctgatggcaagtggg
gagaacatgaattggattaccttcttttattgtccgtgatgtgaaagtaaatcccaaccctgatgaa
gt
```

Sequence Information: >VC000132 IPP cDNA clone Esther Ph.D. Figure 3.1, 290 b.p. in cDNA, both primers are in this sequence

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NGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATAGGGCGAATTGGGCCCGACGTCGCATGCTCCCGGCCGCCATG
GCGGCCGCGGGAATTCGATTTCCTCTAGTGTGGACTAACACTTGTTGCAGCCACCCTCTGTACAGGGAGTCCGAGCTTATCGAGG
AAAAGGCATTAGGGGCAAGAAACGCTGCACAGAGGAAGCTTCTAGATGAGCTCGGTATTCCTGCTGAAGATGTTCCTGTTGATCA
GTTCTTGCCTGTGGGTCGTATTCTGTACAAAGCACCATCTGATGGCAAGTGGGGAGAACATGAATTGGATTACCTTCTTTTTATT
GTCCGTGATGTGAAAGTAAATCCCAACCCTGATGAAGTCGCGGAGATCAAGTATGTAAACAGGAATCACTAGTGAATTCGCGGCC
GCCTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAG
```

Sequence Information: Comparison of Brian's and Esther's sequences.

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IPI        448  ATTCCCTTTGGTTTGGACAAACACCTGTTGCAGCCACCCTCTGTACAGGGAGTCCGAGCT  507
                ||| ||| | || ||||| ||||| ||||||||||||||||||||||||||||||||||||
VC000132   103  ATTTCCTCTAGTGTGGACTAACACTTGTTGCAGCCACCCTCTGTACAGGGAGTCCGAGCT  162

IPI        508  TATCGAGGAAAAGGCATTAGGGGCAAGAAACGCTGCACAGAGGAAGCTTCTAGATGAGCT  567
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
VC000132   163  TATCGAGGAAAAGGCATTAGGGGCAAGAAACGCTGCACAGAGGAAGCTTCTAGATGAGCT  222

IPI        568  CGGTATTCCTGCTGAAGATGTTCCTGTTGATCAGTTCTTGCCTGTGGGTCGTATTCTGTA  627
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
VC000132   223  CGGTATTCCTGCTGAAGATGTTCCTGTTGATCAGTTCTTGCCTGTGGGTCGTATTCTGTA  282

IPI        628  CAAAGCACCATCTGATGGCAAGTGGGGAGAACATGAATTGGATTACCTTCTTTTTATTGT  687
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
VC000132   283  CAAAGCACCATCTGATGGCAAGTGGGGAGAACATGAATTGGATTACCTTCTTTTTATTGT  342
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IPI        688  CCGTGATGTGAAAGTAAATCCCAACCCTGATGAAGTTGCTGACATCAAATATGTGAAC  745
                ||||||||||||||||||||||||||||||||| || || ||||| ||||| |||
VC000132   343  CCGTGATGTGAAAGTAAATCCCAACCCTGATGAAGTCGCGGAGATCAAGTATGTAAAC  400
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SPIDEY alignment of AC018363 (Arabidopsis) with DQ192183 (Brian's cDNA sequence) shows this:

EXON	Genomic coordinates	mRNA coordinates	length	identity	mis-matches	gaps	Donor site	Acc. site
Exon 1	81839-81868	238-267	30	93.3%	2	0		
Exon 2	81872-81881	289-298	10	80.0%	2	0	d	
Exon 3	82477-82496	299-318	20	90.0%	2	0		a
Exon 4	82680-82761	339-420	82	85.4%	12	0		
Exon 5	83067-83143	440-516	77	81.8%	14	0		
Exon 6	83264-83389	539-664	126	81.7%	23	0		
Exon 7	83527-83560	710-743	34	88.2%	4	0		
Exon 8	83590-83690	773-873	101	82.2%	18	0		

Primer coordinates were