

GENOPLANTE™ SPADS parameters

Name	Description	Possible value	Default value ^a	Function
Reference database (-db)	BLAST database used for definition of divergent regions	Database containing genome or multigene sequences	Default	To avoid cross-hybridization (microarray, Northern blot)
GST identity (-I)	Maximum accepted identity (%) of amplicon with any other sequences	40 - 100%	70%	To select GSTs (40%) or primer pairs for PCR or RT-PCR
Amplicon length (-l, -O, -L)	Minimum, optimum and maximum of the amplicon	*	150/300/500	To select the range of amplicon lengths
Intron (-intron)	Ability to design amplicon containing intron(s)	Yes-no	No	To include or exclude intronic sequences in the amplicon
Intron forced (-intronF)	Selection of PCR primers always in two distinct exons	Yes-no	No	To select PCR products differing in size when amplified from gDNA or cDNA
Intronic sequence allowed (-i)	Maximum percentage of intronic sequence in the amplicon (only with "intron" or "intron forced" option selected)	0-100%	50%	To determine the maximum fraction of intronic sequences in the amplicon
Template database (-pdb)	BLAST database used for definition of template-specific primer pairs	Database containing PCR template DNA sequences	Default	To avoid spurious PCR amplification
Primer length (-pl, -pL)	Minimum and maximum primer length	*	18/25	To fine tune primer design
Primer Tm (-pt, -pT)	Minimum and maximum Tm of primers	*	50/65	To fine tune primer design
Primer GC% (-pg, -pG)	Minimum and maximum %GC of primers	*	40/80	To fine tune primer design
Primer max Tm ? (-pdiff)	Maximum Tm difference between primers in a PCR pair	*	4	To fine tune primer design
Phase (-phase)	Selection of all primers with 3' nucleotide corresponding to the 1st nucleotide of a codon	Yes-no	No	To PCR amplify fragments of one species with primers designed using sequences of another close species

^a Default values chosen for template-specific amplification of GSTs.

* Values linked to Primer3 software options.

All "general primer picking conditions" of Primer3 (Rozen and Skaletsky, 2000) can be modified by users excepted parameters involved in the amplicon position since they are managed by GENOPLANTE™ SPADS itself.