

Parameter Name	Value	Default Value	Description
MASTEROLIGONUMBEROFDIGITS	5	5	The default number of digits used to number an oligo; e.g. j5_00001_primer_description uses 5 digits
MASTERPLASMIDNUMBEROFDIGITS	5	5	The default number of digits used to number a plasmid; e.g. pj5_00001 uses 5 digits
GIBSONOVERLAPBPS	26	26	The minimum number of bps for SLIC/Gibson/CPEC overlaps (should be an even number); this is also the starting design length for the annealing portion of primers
GIBSONOVERLAPMINTM	60	60	The minimum desired Tm for SLIC/Gibson/CPEC overlaps
GIBSONOVERLAPMAXTM	70	70	The maximum desired Tm for SLIC/Gibson/CPEC overlaps
MAXIMUMOLIGOLENGTHBPS	110	110	The maximum oligo length to be ordered
MINIMUMFRAGMENTSIZEGIBSONBPS	250	250	The minimum fragment size for SLIC/Gibson assembly
GOLDENGATEOVERHANGBPS	4	4	The number of bps of the overhang resulting from the Golden-gate type IIs endonuclease digestion
GOLDENGATERECOGNITIONSEQ	GGTCTC	GGTCTC	The Golden-gate type IIs endonuclease recognition site sequence
GOLDENGATETERMINIEXTRASEQ	CACACCAGGTCTCA	CACACCAGGTCTCA	The extra 5' sequence required at each end of a Golden-gate assembly piece; e.g. NNNNNNNGGCTCTN for BsaI (Eco31I)
GOLDENGATETERMINIEXTRASEQDNASYNTHESISALT	CACACCAGGTCTCA	CACACCAGGTCTCA	The extra 5' sequence required at the 3' end of a DNA Synthesis Golden-gate assembly piece; e.g. NNNNNNNGGCTCTN for BsaI (Eco31I)
MAXIMUM_IDENTITIES_GOLDEN_GATE_OVERHANGS_COMPATIBLE	2	2	The maximum number of tolerable non-gapped aligned identities between compatible overhang sequences for Golden-gate assembly
OLIGOSYNTHESIS COST PER BP USD	0.08	0.08	The oligo synthesis cost per bp (\$US)
OLIGOPAGEPURIFICATIONCOSTPERPIECEUSD	40	40	The PAGE-purification cost per oligo (\$US)
OLIGOMAXLENGTHNOPAGEPURIFICATIONREQUIREDBPS	60	60	The maximum oligo length that does not require PAGE-purification
MINIMUMPCRPRODUCTBPS	100	100	The minimum PCR product size
DIRECTSYNTHESIS COST PER BP USD	0.09	0.09	The cost per bp to do direct synthesis (\$US)
DIRECTSYNTHESIS MINIMUM COST PER PIECE USD	27	27	The minimum cost of synthesis per piece (\$US)
PRIMER_GC_CLAMP	2	2	Primer3 parameter: length of the desired GC clamp (Primer3 default is 0)
PRIMER_MIN_SIZE	18	18	Primer3 parameter: the minimum length of a primer (Primer3 default is 18)
PRIMER_MAX_SIZE	36	36	Primer3 parameter: the maximum length of a primer (Primer3 default is 27; maximum is 36)
PRIMER_MIN_TM	60	60	Primer3 parameter: the minimum primer Tm (Primer3 default is 57)
PRIMER_MAX_TM	70	70	Primer3 parameter: the maximum primer Tm (Primer3 default is 63)
PRIMER_MAX_DIFF_TM	5	5	Primer3 parameter: the maximum primer pair difference in Tm (Primer3 default is 100)
PRIMER_MAX_SELF_ANY_TH	47	47	Primer3 parameter: the maximum primer self complementarity (Primer3 default is 47)
PRIMER_MAX_SELF_END_TH	47	47	Primer3 parameter: the maximum primer self end complementarity (Primer3 default is 47)
PRIMER_PAIR_MAX_COMPL_ANY_TH	47	47	Primer3 parameter: the maximum primer pair complementarity (Primer3 default is 47)
PRIMER_PAIR_MAX_COMPL_END_TH	47	47	Primer3 parameter: the maximum primer pair end complementarity (Primer3 default is 47)
PRIMER_TM_SANTALUCIA	1	1	Primer3 parameter: use the Santalucia formula for calculating Tms (1 = TRUE; 0 = FALSE) (Primer3 default is 0 (FALSE))
PRIMER_SALT_CORRECTIONS	1	1	Primer3 parameter: use the salt correction formula for calculating Tms (1 = TRUE; 0 = FALSE) (Primer3 default is 0 (FALSE))
PRIMER_DNA_CONC	250	250	Primer3 parameter: DNA concentration to use when calculating Tms in micromolar (IDT uses 250; Primer3 default is 50)
MISPRIMING_3PRIME_BOUNDARY_BP_TO_WARN_IF_HIT	4	4	Only warn of mispriming if the BLAST hit between the primer and the template contains the 3' end of the primer (within this number of bp)
MISPRIMING_MIN_TM	45	45	The minimum approximate Tm to consider a significant mispriming event
MISPRIMING_SALT_CONC	0.05	0.05	The salt concentration used when estimating the mispriming Tm in Molar
MISPRIMING_OLIGO_CONC	2.50E-07	2.50E-07	The oligo concentration used when estimating the mispriming Tm in Molar
OUTPUT_SEQUENCE_FORMAT	Genbank	Genbank	The output sequence file format. Options are: "Genbank", "FASTA", "jbei-seq", or "SBOLXML"
ASSEMBLY_PRODUCT_TYPE	circular	circular	Determines whether the assembled DNA product will be circular or linear. Options are: "circular" or "linear"
SUPPRESS_PURE_PRIMERS	TRUE	TRUE	Suppress the output of pure primers. Options are: "TRUE" or "FALSE"
SUPPRESS_PRIMER_ANNOTATIONS	FALSE	FALSE	Suppress primer annotations. Options are: "TRUE" or "FALSE"
HOMOLOGY_MIN_LENGTH_BPS	26	26	The minimum length in bps for a homologous sequence repeat to be considered significant
HOMOLOGY_MAX_FRACTION_MISMATCHES	0.05	0.05	The maximum fraction of mismatches for a homologous sequence repeat to be considered significant
APPEND_UUID_TO_PLASMID_OLIGO_AND_SYNTHESIS_NAME	FALSE	FALSE	Append UUIDs to all new plasmid, oligo, and DNA synthesis names. Options are: "TRUE" or "FALSE"
COMBINATORIAL_DESIGN_LAYOUT_TYPE	combinatorial	combinatorial	Determines whether a combinatorial design will be treated as full combinatorial or as a list (one combination per row). Options are: "combinatorial" or "list".
MINIMUMDNASYNTHESISLENGTHBPS	300	300	The minimum length in bps for a synthetic DNA fragment
INCLUDE_LINEAGE_FEATURES	FALSE	FALSE	Whether or not to include sequence lineage features. Options are: "TRUE" or "FALSE"