List of parameters (Set in the *set_qdd_default.ini* **file or on the command line)**

*These parameter values are unlikely to be changed between runs.

You should set them in the set_qdd_default.ini file

Parameter name	Parameter value	Explanations	default	pipe1	pipe2	pipe3	pipe4
-input_file	Fasta file with full path	Fasta file sequences to be analyzed for 1-3; Primer table for pipe4	NA	yes	yes	yes	yes
General parameters							
-galaxy	0 or 1	1 for running QDD form Galaxy, 0 for running it from a terminal	0	yes	yes	yes	yes
-syst	win or linux	Operating system	* linux	yes	yes	yes	yes
-blast_path	Full path to BLAST+ executables		*	yes	yes	no	yes
-clust_path	Full path to clustalw executables		*	no	yes	no	no
-primer3_path	Full path to Primer3 executables		*	no	no	yes	no
-primer3_version	1 or 2	Version of Primer3	*2	no	no	yes	no
-qdd_folder	Full path to QDD scripts		*	yes	yes	yes	yes
-out_folder	Folder for output files	Folder (with full path) for output files. Must be created before running qdd	*	yes	yes	yes	yes
-del_files	0 or 1	1 for deleting temporary files after the run1	* 1	yes	yes	yes	yes
-outfile_string	alpha-numerical	String to specify the beginning of the names of the output files. If not specified, the input file name is used for naming output files		yes	yes	yes	yes
-debug	0 or 1	1 for printing out more details in log file for debugging	* 0	yes	yes	yes	yes
-num_threads	integer	number of threads (CPU) for BLAST and RepeatMasker	* 1	yes	yes	no	yes
Input sequence type							
-fastq	0 or 1	1 if input file is in fasq format, 0 if it is in fasta format	0	yes	no	no	yes

-contig	0 or 1	1 if sequences has been assembled (contigs, scaffolds, chromosomes); 0 if they are short (100-1000) sequencing reads; If -contig=1 -adapter must be 0	0	yes	no	yes	no
-flank_length	integer	Length of the flanking region on both sides if the microsatellite, when extracting microsatellites from contigs (-contig=1)	* 200	yes	no	no	no
Adapter clipping							
-adapter	0 or 1	1 for running adaptor/vector clipping step If -adapter = 1 => -adapter_file must be set.	0	yes	no	no	no
-adapter_file	fasta file (including full path)	File that contains the adapters to be removed from the sequences. For adapter clipping -adapter must be set to 1, it is not enough to set only the -adapter_file	NA	yes	no	no	no
Sequence length selection							
-length_limit	integer	Sequences shorter then length_limit (after adapter clipping) are eliminated	80	yes	no	no	no
Consensus							
-make_cons	0 or 1	Make consensus sequences	1	no	yes	no	no
-ident_limit	[80-100]	Minimum % of pairwise identity between sequences of a contig (only if -make_cons=1)	95	no	yes	no	no
-prop_maj	[0.5-1]	Proportion of sequences that must have the same base at a site to accept it as a consensus (only if -make_cons=1)	0.66	no	yes	no	no
RepeatMasker (checking similarity to transposable elements)							
-rm	0 or 1	1 for running RepeatMasker on the sequences with primers (not available for windows)	0	no	no	no	yes
-rm_path	Full path to RepeatMasker executables		*	no	no	no	yes
-rm_lib	Taxonomic group	A taxonomic group for which TE library is selected RepeatMasker e.g. metazoa, vertebrata, insecta...	eukaryota	no	no	no	yes
Compare sequences to NCBI							

-check_contamination	0 or 1	1 for checking contamination by blasting sequences against the nt database (blast can be remote or local)	0	no	no	no	yes
-local_blast	0 or 1	1 for running local blast for contamination check => blastdb needs to be defined; 0 for running remote blast for contamination check	* 0	no	no	no	yes
-blastdb	name (including full path) of a local ncbi database	Only needed if local BLAST is used for contamination check (-local_blast=1)	*	no	no	no	yes
Primer design							
-pcr_min	[40,10000]	Minimum PCR Product size	90	no	no	yes	no
-pcr_max	[40,10000]	Maximum PCR Product size	300	no	no	yes	no
-pcr_step	[20,10000]	PCR product size interval for iterative primer design	50	no	no	yes	no
-PRIMER_GC_CLAMP	[0,20]	Require the specified number of consecutive Gs and Cs at the 3' end of both the left and right primer	0	no	no	yes	no
-PRIMER_OPT_SIZE	[1,50]	Optimum length of a primer	20	no	no	yes	no
-PRIMER_MIN_SIZE	[1,50]	Minimum length of a primer	18	no	no	yes	no
-PRIMER_MAX_SIZE	[1,50]	Maximum length of a primer	27	no	no	yes	no
-PRIMER_OPT_TM	[1,100]	Optimum melting temperature	60	no	no	yes	no
-PRIMER_MIN_TM	[1,100]	Minimum melting temperature	57	no	no	yes	no
-PRIMER_MAX_TM	[1,100]	Maximum melting temperature	63	no	no	yes	no
-PRIMER_MAX_DIFF_TM	[1,100]	Maximum acceptable difference between the melting temperatures of primers	10	no	no	yes	no
-PRIMER_MIN_GC	[1,100]	Minimum percentage of Gs and Cs in any primer	20	no	no	yes	no
-PRIMER_OPT_GC_PERCENT	[1,100]	Optimum percentage of Gs and Cs in any primer	50	no	no	yes	no
-PRIMER_MAX_GC	[1,100]	Maximum percentage of Gs and Cs in any primer	80	no	no	yes	no
-PRIMER_SELF_ANY	[1,100]	The maximum allowable local alignment score for self- or pairwise-complementarity	8	no	no	yes	no

-PRIMER_SELF_END	[1,100]	The maximum allowable 3'-anchored global alignment score for self- or pairwise-complementarity	3	no	no	yes	no
-PRIMER_MAX_POLY_X	[1,10]	The maximum allowable length of a mononucleotide repeat in primer	3	no	no	yes	no
-PRIMER_NUM_RETURN	[1,10]	The maximum number of primer pairs to return for each Primer3 run (each PCR product length interval each stringency step on target region)	3	no	no	yes	no
QDD.pl							
-input_folder	Folder name including path	Folder that contains all input files for batch submission; must not contain other files	NA	QDD.pl	QDD.pl	QDD.pl	QDD.pl
-tag	0 or 1	1 for sorting input sequences according to tags	0	QDD.pl	QDD.pl	QDD.pl	QDD.pl
-tag_file	Fasta file including full path	fasta file with tag sequences	NA	QDD.pl	QDD.pl	QDD.pl	QDD.pl
-run_all	0 or 1	1 for running pipe1, pipe2, pipe3 and pipe4 in one go	1	QDD.pl	QDD.pl	QDD.pl	QDD.pl