Reference	SeqQual pipeline / program (prog) name*,¤	usage**	arguments (arg)	description	using programs (other prog)	Shell examples **	Input file(s)	Output folder/file(s)	log file available $
file/folder management*									
lang et al.	clean_all.pl	perl prog arg	(text file with list of folder names, e.g. inputile) = ***(B)***	remove all "mydata" sub-folders in each folder of the inputfile list		clean_all.sh	see arg		
"	clean.pl	perl prog arg	***(B)***	remove older mydata sub-folders in each folder in the input list, keep the last one		clean.sh	see arg		
"	checkdir_mydata.pl	perl prog		create new folder mydata, if one already exists--> change it to mydata_current_date&time first				empty folder mydata	
"	checkdir_Output.pl	perl prog		create new folder Output, if it already exists, change it to Output_current_date&time first		1.2-haploid-ab1.sh, 1.1-diploid-ab1.sh		empty folder Output	
"	checkinput.pl	perl prog arg	***(B)***	check if the folders listed in inputfile exist, give a warning if not			see arg	screen	
"	**print_source**-delete_files.pl¤	**(perl prog arg > out source out) =** ***(A)***	***(B)***	(run **other prog** in batch on a set of folder given in arg , when sourcing the "out" text file) = ***(C)***	delete_empty_files.pl	1.2-haploid-ab1.sh, 1.1-diploid-ab1.sh	see arg		
"	delete_empty_files.pl¤¤	perl prog		delete empty fasta alignments (including ones with only consensus (names started with "Contig", can be changed in code) in the current directory				delete.txt	
"	**print_source**-take_aln.pl¤	***(A)***	***(B)***	***(C)***	take_aln_to_output.pl	1.2-haploid-ab1.sh, 1.1-diploid-ab1.sh	see arg		**X**
"	take_aln_to_output.pl	perl prog arg	***(B)***	look for files with extension ".aln"; rename as filenamenumber.aln, take file to Output/aln folder					
Processing ab1/scf/abd files with phd*/poly* files									
"	**print_source**-aln-diploid-ab1.pl	***(A)***	***(B)*** , polyphred score, polyphred quality, 18 parameters from phrap (see User doc & example *.sh)	***(C)*** , create working directories and files; run phredPhrap to create poly and phd files, run phrap, run polyphred	checkdir_mydata.pl, phred§§, phd2fasta§§, phrap_all_lang.pl, polyphred§§	1.1-diploid-ab1.sh	see arg, ab1/scf/abd files		**X**
"	phrap_all_lang.pl	perl prog	file with list of file names, and 18 parameters for Phrap	runs phrap in batch and get ace files	phrap§§		see arg	ace files from Phrap	
"	**print_source**-userphd-diploid-ab1.pl	***(A)***	***(B)***	copy user poly files and phd files into working directory, user phd/poly files should be initially located in the same directories than the corresponding original data		1.1-diploid-ab1.sh	see arg, phd/poly files in same folder than ab1 files		**X**
"	**print_source**-renamephd.pl	***(A)***	***(B)***	***(C)***	rename_phd-ab1.pl, rename_phd-abd.pl, rename_phd-scf.pl	1.1-diploid-ab1.sh	see arg, phd/poly files in same folder than ab1 files		**X**
"	rename_phd-ab1.pl	perl prog		rename filename.phd.1 as filename.ab1.phd.1				rename-ab1.txt	
"	rename_phd-abd.pl	perl prog		rename filename.phd.1 as filename.abd.phd.1				rename-abd.txt	
"	rename_phd-scf.pl	perl prog		rename filename.phd.1 as filename.scf.phd.1				rename-scf.txt	
"	**print_source**-write_aln-diploid.pl	***(A)***	***(B)*** , phred score, genotype score	***(C)*** , moves edited fasta alignments into output folder	write_acealn-heter_multinput.pl	1.1-diploid-ab1.sh			**X**

"	write_acealn-heter_multinput.pl	perl prog arg	phred score, genotype score	look for file(s) with extension ".ace"; write diploid alignment(s) with heterozygote IUPAC codes from polyphred.out files (in phd_dir folder), integrates quality by accepting nucleotides as valid only if their phd score is >= to the arg value given (non-valid ones considered as missing data and coded by "?")			*.ace files	folder aln with fasta files	
"	**print_source**-aln-haploid-ab1.pl	***(A)***	***(B)*** , 18 parameters from phrap	***(C)*** , create working directories and files	checkdir_mydata.pl, phred§§, phd2fasta§§, phrap_all_lang.pl	1.2-haploid-ab1.sh	see arg, ab1/scf/abd files		**X**
"	**print_source**-userphd-haploid-ab1.pl	***(A)***	***(B)***	copy user phd files into working directory, user phd files should initially be located in the same directories than the corresponding original data		1.2-haploid-ab1.sh	see arg, phd/poly files in same folder than ab1 files		**X**
"	**print_source**-write_aln-haploid.pl	***(A)***	***(B),*** phred score	***(C)*** , moves edited fasta alignments into output folder	write_acealn-onlyqual_multinput.pl	1.2-haploid-ab1.sh, 2.3-ace-qual.sh	see arg, phd/poly files in same folder than ab1 files	aln_final/*.aln fasta files	**X**
"	write_acealn-onlyqual_multinput.pl	perl prog arg	phred score	look for file(s) with extension ".ace"; write alignment(s) with quality from phd files in folder phd_dir, thuz accepting nucleotide as valid **only if** its phred score is >= to the arg value given, whether or not it is the same than the consensus sequence.			*.ace files	aln/*.aln fasta files	

* all shell scripts can be run by typing "source *.sh"

¤ All print_source scripts work by printing a txt file that needs to be sourced to launch other programs for batch treatment of files located in one or more folders. They also require a particular folder structure for printing results files (see start of example *.sh files for details)

¤¤ example of one other program, which can be used also independently to the print_source script

** To run print_source*.pl scripts, most other scripts are assumed to be located under "home/SeqQual" but this can easily be changed in the code

$ see the description and list of log related scripts in **SeqQual-log-related-scripts.pdf**

§§ from the phredphrap suite or polyphred programs that need to be installed (see User documentation)

*** these programs are needed if the print_source programs are used