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 in the input list		clean_all.sh	see arg		
n .	clean.pl	perl prog arg	(B)	remove older (not the last one) mydata sub-folders in each folder in the input list, keep the lastest one		clean.sh	see arg		
п	checkdir_mydata.pl	perl prog		create new folder mydata, if one already exists> change it to mydata_current_date&time first				empty folder mydata	
11	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	
п	checkinput.pl	perl prog arg	(B)	check if the folders listed in inputfile exist, give a warning if not			see arg	screen	
n.	print_source-delete_files.pl¤	(perl prog arg > out source out) = (A)	(B)	(run other prog in batch on a set of folder given as arg, when sourcing the "out" text file) = (C)	delete_empty_files.pl	1.2-haploid-ab1.sh, 1.1-diploid-ab1.sh	see arg		
п	delete_empty_files.pl <b>ងង</b>	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	
11	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
п	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 with phd*/p	ooly* files							
11	<pre>print_source-aln-diploid-ab1.pl</pre>	(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 \$\frac{\fir}{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\fir}{\fir}}}}}}{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\fir}\f{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac{\frac	1.1-diploid-ab1.sh	see arg, ab1/scf/abd files		X
11	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	
п	<pre>print_source-userphd-diploid- ab1.pl</pre>	(A)	(B)	copy user poly files and phd files into working direcotry		1.1-diploid-ab1.sh	see arg, phd/poly files in same folder than ab1 files		X
п	<pre>print_source-renamephd.pl</pre>	(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	
п	rename_phd-abd.pl rename_phd-scf.pl	perl prog perl prog		rename filename.phd.1 as filename.abd.phd.1 rename filename.phd.1 as filename.scf.phd.1				rename-abd.txt rename-scf.txt	
11	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
n	write_acealn-heter_multinput.pl	perl prog arg	phred score, genotype score	look for file with extension ".ace"; write alignment with quality and heterozygote IUPAC codes from folder phd_dir which has phd and polyphred.out files thus accepting nucleotides as valid only if their score is >= to the arg value given (the rest being considered as missing data and coded by "?")			*.ace files	folder aln with fasta files	

11	<pre>print_source-aln-haploid-ab1.pl</pre>	(A)	(B), 18 parameters from phrap	(C) , create working directories and files	checkdir_mydata.pl, phred ss phred phrap_all_lang.pl	1.2-haploid-ab1.sh	see arg, ab1/scf/abd files		X
"	<pre>print_source-userphd-haploid- ab1.pl</pre>	(A)	(B)	copy user phd files into working direcotry		1.2-haploid-ab1.sh	see arg, phd/poly files in same folder than ab1 files		X
II	<pre>print_source-write_aln- haploid.pl</pre>	(A)	(B), phred score	(C) , moves edited fasta alignments into output folder	write_acealn- qual_multinput.pl	1.2-haploid-ab1.sh	see arg, phd/poly files in same folder than ab1 files		X
11	write_acealn-qual_multinput.pl	perl prog arg	phred score	look for file with extension ".ace"; write alignment with quality from phd files in folder phd_dir, thus accepting nucleotide as valid only if its phred score is >= to the arg value given			*.ace files	folder aln with fasta files	

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

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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 different folders. They also require a particular folder structure for printing results files (see start of example \*.sh files for details)

But all other programs can be used also independently

To run print\_source\*.pl prog, most other programs are assumed to be located under home/SeqQual but this can easily be changed in the code see log related scripts in **SeqQual\_log.pdf** 

these programs have been modified/or bug corrected compared to original publications

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