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		
II.	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	
II	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	
11	checkinput.pl	perl prog arg	(B)	check if the folders listed in inputfile exist, give a warning if not			see arg	screen	
п	print_source-delete_files.pl¤	(perl prog arg > out source out) = (A)	<i>(B)</i>	(run <b>other prog</b> 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		
п	delete_empty_files.pl <mark>¤¤</mark>	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	
п	print_source-take_aln.p <mark>l¤</mark>	(A)	<i>(B)</i>	(C)	take_aln_to_output.pl	1.2-haploid- ab1.sh, 1.1- diploid-ab1.sh	see arg		x
11	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 p	hd*/poly* files	_						
ıı	<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{\finte}{\fint}}}}}}}{\frac{\frac{\fint}{\fint}}}}}}}}}}}}}}}}}}}}}}}}}}}}}}}}}}}}	1.1-diploid- ab1.sh	see arg, ab1/scf/abd files		X
п	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	
II	<pre>print_source-userphd-diploid- ab1.pl</pre>	(A)	(B)	copy user poly files and phd files into working direcotry		1 1-dinidid-	see arg, phd/poly files in same folder than ab1 files		X
n	<pre>print_source-renamephd.pl</pre>	(A)	<i>(B)</i>	(C)	rename_phd-ab1.pl, rename_phd-abd.pl, rename_phd-scf.pl	-חוחוחות-	see arg, phd/poly files in same folder than ab1 files		x
11 11	rename_phd-ab1.pl rename_phd-abd.pl rename_phd-scf.pl	perl prog perl prog perl prog		rename filename.phd.1 as filename.ab1.phd.1 rename filename.phd.1 as filename.abd.phd.1 rename filename.phd.1 as filename.scf.phd.1				rename-ab1.txt rename-abd.txt rename-scf.txt	
II	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		Tename sentite	X

11	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	
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 \$\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	1.2-haploid- ab1.sh	see arg, ab1/scf/abd files		x
11	<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
п	<pre>print_source-write_aln- haploid.pl</pre>	(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
11	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 <b>only if</b> 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	

<sup>\*</sup> 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

<sup>\*\*</sup> 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

<sup>\$</sup> 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)

<sup>\*\*\*</sup> these programs are needed if the print\_source programs are used