SeqQual pipeline / program (prog) name	usage*	arguments (arg)	description (Process and parameters added to log.txt)	Works with program	Shell examples **
print_log-454ace_changename.pl	(perl ~/SeqQual/prog arg >> log.txt) = *(A)*		change ace name		
print_log-454ace_separate.pl	*(A)*		separate ace		
print_log-454phd_separate.pl	"		separate phd		
print_log-acedealing-haploid.pl	"		haploid_ace		
print_log-aceonly.pl	"		ace_only		
print_log-aln-diploid-ab1.pl	"	polyphred score, polyphred quality and 18 parameters for phrap	diploid_ab1; phrap parameters used in phrap, polyphred pamaters used in polyphred		1.1-diploid-ab1.sh
print_log-aln-haploid-ab1.pl	"	18 parameters from Phrap	haploid_ab1; phrap parameters used in phap		1.2-haploid-ab1.sh
print_log-arlequin-diploid.pl	"	up to 20 group names	write diploid arlequin input files; group numbers and group names		*fasta-*data.sh
print_log-arlequin-haploid.pl	"	up to 20 group names	write haploid arlequin input files; group numbers and group names		*fasta-*data.sh
print_log-fasta.pl	"		fasta_aln		*fasta-*data.sh
print_log-remove1.pl	"		remove bad positions with only "?" and "-"		1.1-diploid-ab1.sh, 1.2-haploid-ab1.pl
print_log-renamephd.pl	"		rename phd files		1.1-diploid-ab1.sh, 1.2-haploid-ab1.pl
print_log-replace.pl	"	max length of "isolated nucleotides"	replace isolated nucleotides which are surrouned by "?"; the max length of "isolated nuceotides" (which program is used)		1.1-diploid-ab1.sh
print_log-truncate.pl	"	number of nucleotides in the column from which truncate process is done	truncate; the number of nucleotides in the column from which the truncate process is done		1.1-diploid-ab1.sh
print_log-userphd-diploid-ab1.pl	"		inserting user phd/poly files		1.1-diploid-ab1.sh
print_log-userphd-haploid-ab1.pl	"		inserting user phd files		1.2-haploid-ab1.sh
print_log-write_aln-diploid.pl	"	phred score, genotype score	write fasta alignment from ace, phd, polyphred.out; phred score and genotype score		1.1-diploid-ab1.sh
print_log-write_aln-haploid.pl	"	phred score	write fasta alignment from polybayes.ace, phd		1.2-haploid-ab1.sh
print_log-write_haplotypealn.pl	"		write haploid phase unknown alignment files from diploid alignment files		*fasta-*data.sh
print_log-write_SNP-diploid.pl	"	phred score, genotype score	write SNP aligment; phred score, genotype score		*fasta-*data.sh
print_log-write_SNP-fasta_aln.pl	"		write SNP alignment		*fasta-*data.sh
print_log-write_unaln-diploid.pl	"	phred score, genotype score	write unaligned fasta files; phred score, genotype score		*fasta-*data.sh
print_log-write_unaln-haploid.pl	"	phred score	write unaligned fasta files; phred score		*fasta-*data.sh
print_log-write_unaln-fasta.pl	"		write unaligned fasta files		*fasta-*data.sh
take_log_to_output.pl	"		take log.txt to folder Output, check name to log_data&time.txt		1.1-diploid-ab1.sh, 1.2-haploid-ab1.sh, *fasta-*data.sh

* all scripts append log information to the log.txt file

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