

Program Name	Argument(s)	Process and parameters added to log.txt
print_log-454ace_changename.pl		change ace name
print_log-454ace_separate.pl		separate ace
print_log-454phd_separate.pl		separate phd
print_log-acedealing-diploid.pl		diploid_ace
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
print_log-aln-diploiddraw-ab1.pl	18 parameters from Phrap	diploiddraw_ab1; phrap parameters used in phrap
print_log-aln-haploid-ab1.pl	18 parameters from Phrap	haploid_ab1; phrap parameters used in phap
print-log-arlequin-diploid.pl	up to 10 group names	write diploid arlequin input files; group numbers and group names
print-log-arlequin-haploid.pl	up to 10 group names	write haploid arlequin input files; group numbers and group names
print-log-fasta.pl		fasta_aln
print-log-remove.pl		remove bad positions with only "?" and "-"
print-log-renamephd.pl		rename phd files
print-log-replace.pl	max length of "isolated nucleotides"	replace isolated nucleotides which are surrounded by "?"; the max length of "isolated nuceotides" (which program is used)
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
print-log-userphd-diploid-ab1.pl		inserting user phd/poly files
print-log-userphd-haploid-ab1.pl		inserting user phd files
print-log-write_aln-diploid.pl	phred score, genotype score	write fasta alignment from ace, phd, polyphred.out; phred score and genotype score
print-log-write_aln-diploiddraw.pl	phred score, heterzygote score	write fasta alignment from ace, phd, poly; phred score and heterzygote score
print-log-write_aln-haploid.pl	phred score	write fasta alignment from polybayes.ace, phd
print-log-write_haploptypealn.pl		write haploid phase unknown alignment files from diploid alignment files
print-log-write_SNP-diploid.pl	phred score, genotype score	write SNP aligment; phred score, genotype score
print-log-write_SNP-fasta_aln.pl		write SNP alignment
print-log-write_unaln-diploid.pl	phred score, genotype score	write unaligned fasta files; phred score, genotype score
print-log-write_unaln-diploiddraw.pl	phred score, heterzygote score	write unaligned fasta files; phred score, heterzygote score
print-log-write_unaln-haploid.pl	phred score	write unaligned fasta files; phred score
print-log-write_unaln-fasta.pl		write unaligned fasta files