```perl
#!/usr/bin/env perl -w
use Math::Complex;

#feed the large set of derived cutpoints into the condenser to assess the
distribution of derived cutpoints from the leave-5-out assessment.  Take the
frequency mean as the derived upper and lower cutpoints.

for $gene (qw/ CEBPG E2F1 CAT ERCC4 ERCC5 GPX1 GPX3 GSTM3 GSTP1 GSTT1 GSTZ1 MGST1
SOD1 XRCC1 /) {


my %upper = ();
my %lower = ();


open GENEDATAERROR, "<Validation-$gene.txt";
my @genedataset = ();
while (my $line = <GENEDATAERROR>) {  #push the genedataset into an array
   chomp ($line);
   my @linearray = split(",",$line);

   if (exists($upper{$linearray[0]})) {
      $upper{$linearray[0]}[1] = $upper{$linearray[0]}[1] + 1;
   } else {
      $upper{$linearray[0]} = [ "$linearray[0]","1" ];
   }

   if (exists($lower{$linearray[1]})) {
      $lower{$linearray[1]}[1] = $lower{$linearray[1]}[1] + 1;
   } else {
      $lower{$linearray[1]} = [ "$linearray[1]","1" ];
   }


#   $numKeys = keys(%upper);
   if (exists($upper{$linearray[0]})) {
      print "$upper{$linearray[0]}[1]\n";
   }
#   print "$numKeys\n";
}
close GENEDATAERROR;

print "\n -----------------------------\n";


open HISTOGRAMOUT, ">Validation-$gene-histogram.csv";

print HISTOGRAMOUT "Upper-Cutoffs\n";
for $logTA ( keys %upper) {
   print HISTOGRAMOUT "$upper{$logTA}[0],$upper{$logTA}[1]\n";
}

print HISTOGRAMOUT "Lower-Cutoffs\n";
for $logTA ( keys %lower) {
   print HISTOGRAMOUT "$lower{$logTA}[0],$lower{$logTA}[1]\n";
}


close HISTOGRAMOUT;


}
```

```
# The output will be readable in excel comma-delimited format.
```