

GSEQ 4.1 Release Notes

The following are known issues that exist in GSEQ 4.1:

1. If GSEQ 4.0 is already installed, you must uninstall GSEQ 4.0 before installing GSEQ 4.1 on the system.
2. For customers using CustomSeq arrays, please call Applications Support at 1-888-DNA-CHIP for a GSEQ 4.1 updated analysis configuration file for your custom arrays.
3. In GSEQ 4.1, the “default” settings are used to specify the location of input files (CEL) and location where the CHP and report files are saved.
4. The Resequencing Tool does not have the ability to generate the SNP report. A user can obtain similar information by exporting the data from the SNP table in the viewer. However, the SNP table does not report the SNP frequency.
5. When performing resequencing analysis, the default report name is set as “report.txt”. The user should modify the report name before starting the analysis. If a user does not change the name of the report before starting the analysis, any other report file with the same name will be over written without warning.
6. The “Find” option sometimes does not work in the SNP Viewer view. If this happens, the user can click on a CEL in the table and then the Find works properly.
7. In the Sequence viewer when using the find option to search for a fragment, the fragment is displayed in the Map and Base panes, however, the fragment position pane does not get updated and the user must scroll through the fragments in order to find the selected one.
8. The Start and End Genomic positions differ by 1 position between the Sequence and Table Views.
9. When exporting sequence in FASTA format, if SNP Flanking Sequence option is chosen. “No SNPs found” message may be displayed when fragment does contain SNPs. Please ignore the message. Correct sequences are exported in the txt file.
10. FASTA export does not export chromosome positions when the GPE file is used. The text file displays the Start-End positions instead of the chromosome Start-End positions.
11. The Start and Stop positions differ by 11 between the PCR file and the Sequence View.
12. In the Sequence View, the end position is displayed as the Start-End position instead of only the End position.
13. Invalid fragment error displayed when opening a CHP file with incorrect GPE file. The error message is “The fragment specified in the file xxx is not on the array xxx. The problem was found in the following record: xxx”

In order to resolve the issue, the user will have click on “Resequence Analysis Options” and ensure that correct GPE file is chosen. If they do not have a GPE or PCR file, uncheck the box and the error will go away.
14. Invalid fragment error displayed when opening a CHP file with incorrect PCR file. The error message is “Not able to process PCR fragments – No genomic position file

specified for PCR positions. The PCR file refers to genomic positions specified in the genomic file.”

In order to resolve the issue, the user will have click on “Resequencing Analysis Options” and ensure that correct PCR file is chosen. If they do not have a PCR file, uncheck the box and the error will go away.

15. When importing CEL/CHP data from GCOS (using DTT) or AGCC (using DEC), the CEL/CHP data must be reanalyzed with GSEQ 4.1 in order to see the full list of parameters in Algorithm 2.
16. If installing on Windows Vista operating system, an error message regarding unable to register the TList7 component will appear. This will cause the data tree refresh to be slow compared to running the application on Windows XP.
17. GSEQ 4.1 hangs when corrupt CEL or CHP files are trying to be opened. The application is set to the default location setting which contains the corrupted files. Please contact Applications Support for a resolution (1-888-DNA-CHIP).