

QualTrace

The QualTrace™ DNA sequencing analysis software offers rapid detection of sample preparation problems that limit DNA sequencing read lengths. The QualTrace software offers –

- *Real-time analysis of traces files with the detection of eight problem types*
- *Compatibility with both the ABI KB and ABI 3XX base-callers on the ABI3730 and 3730xl DNA sequencing instruments*
- *Easy integration into existing trace data pipeline and bioinformatics infrastructure*

QualTrace DNA sequencing software

The QualTrace DNA sequencing software examines the raw data contained within the ABI files and identifies eight major problem types –

1. *Traces that contain no data due to failed reactions or capillaries*
2. *Mixed trace signal resulting from multiple DNA templates*
3. *Noisy trace signal*
4. *Very weak signal strength at the end of the DNA sequencing trace*
5. *Early mixed trace signal due to DNA template contamination by PCR products*
6. *Delayed starts of the sequencing trace signal*
7. *Problems with the DNA sequencer's spectral calibration settings*
8. *Significant leftover BigDye™ (dye blobs)*

The QualTrace DNA sequencing software can process either single DNA trace files or complete folders of trace files. The software generates a log file report containing the QualTrace category type and code for each trace. In addition, the signal to noise ratio for the early, mid, and late regions of each trace are recorded in the log file enabling any trace signal decay to be tracked.

Use of QualTrace in DNA sequencing

A set of 11,745 36cm array ABI 3730xl traces were analysed by QualTrace. The traces were sorted into their QualTrace predicted categories and the corresponding phred base-called sequences were aligned to the known consensus sequence. The average number of aligned Q20 bases for each of the nine QualTrace categories was calculated. This provided an accurate measurement of the predicative power of QualTrace in identifying traces with production problems that limit alignable read length.

Table 1. QualTrace analysis of ABI3730 traces

Category	Traces	Q20+	Align. Q20+
Excellent	7883	678	647
Good	773	627	606
Spectral	87	664	609
Mixed	1453	342	322
End weak	65	566	479
Early mixed	521	531	508
Noisy	147	220	175
Delayed	1	27	0
No signal	819	32	2
Total	11745	576	546

The QualTrace DNA sequencing software was able to identify a significant problem caused by mixed templates (~17%) resulting a major loss of sequence read length.

The QualTrace software is available for Windows 2000, XP and x86 Linux. For addition information on QualTrace please contact:

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