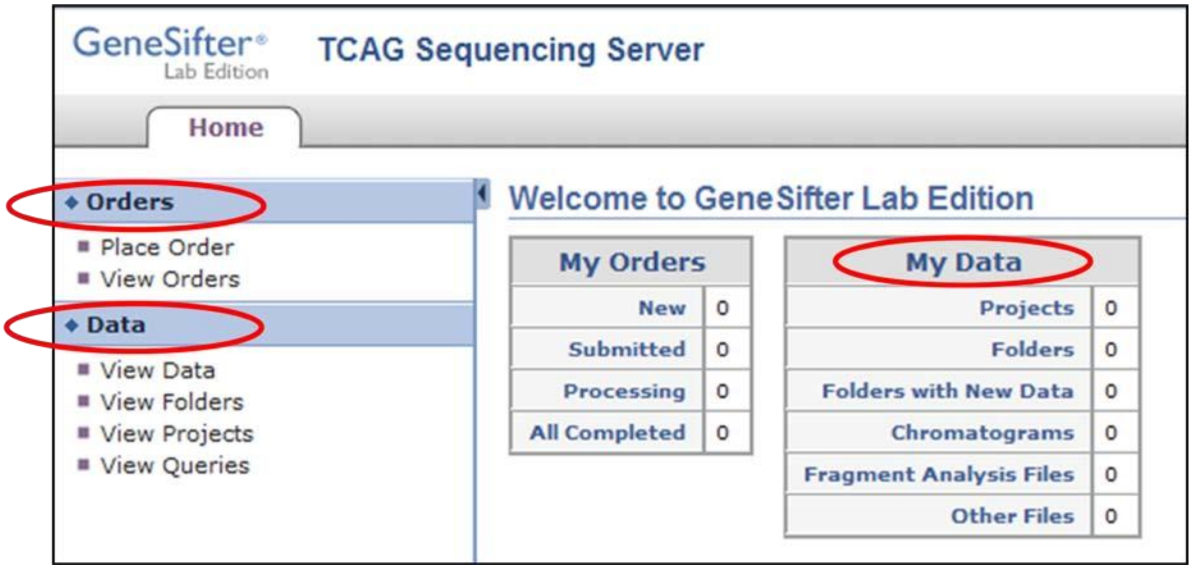
The Centre for Applied Genomics DNA
Sequencing Facility

Retrieving Results in GSLE

The account holder will receive an email from TCAG Sequencing when the order data is ready to be reviewed and downloaded. Please add this email (tcag_sequencing@sickkids.ca) to your contacts to be sure you receive our notifications (so that the message is not directed to your junk folder or deleted as spam). Also note that this email is meant for out-going notifications only and is not monitored.

Finding Results

- All orders, folders and individual data can be found by clicking on the appropriate link in the left-hand navigation panel or in the central panel on the homepage.



My Orders	
New	0
Submitted	0
Processing	0
All Completed	0

My Data	
Projects	0
Folders	0
Folders with New Data	0
Chromatograms	0
Fragment Analysis Files	0
Other Files	0

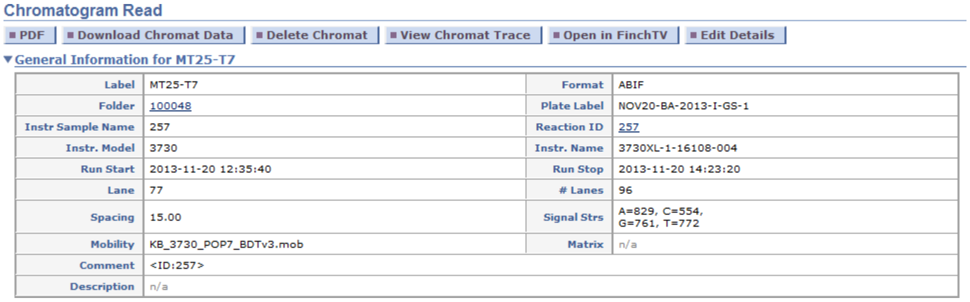
- In ‘View Data’ or ‘View Folders’, click on the desired order number.

Note: ‘View Data’ is a consolidated list of all orders and all samples – the list may continue onto to multiple pages.

Viewing results

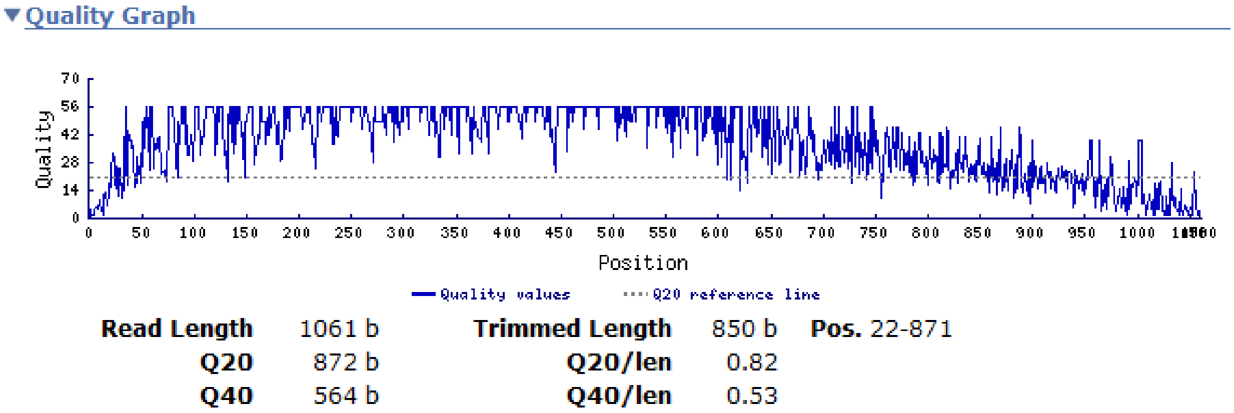
All data for a particular order can be viewed by clicking on the folder name, and individual samples can be examined by clicking on their name.

- ***Chromatogram Read*** summarizes the attributes of the sample (eg. name, run plate, signal strength)



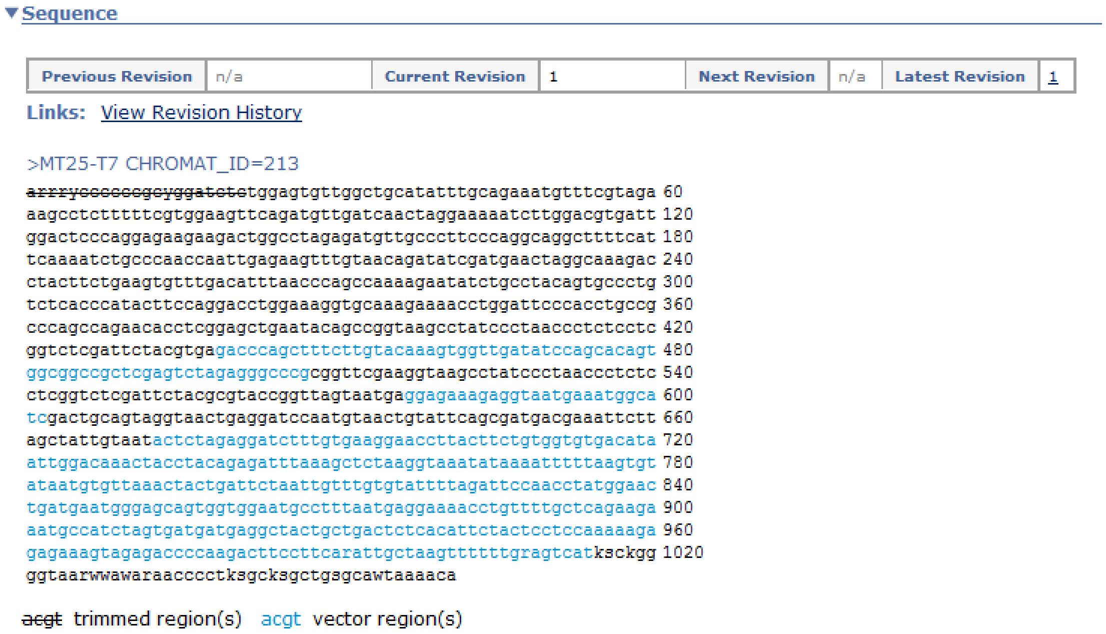
Label	MT25-T7	**Format**	ABIF
Folder	100048	**Plate Label**	NOV20-BA-2013-I-GS-1
Instr Sample Name	257	**Reaction ID**	257
Instr. Model	3730	**Instr. Name**	3730XL-1-16108-004
Run Start	2013-11-20 12:35:40	**Run Stop**	2013-11-20 14:23:20
Lane	77	**# Lanes**	96
Spacing	15.00	**Signal Strs**	A=829, C=554, G=761, T=772
Mobility	KB_3730_POP7_BDTv3.mob	**Matrix**	n/a
Comment	<ID:257>		
Description	n/a		

- ***Quality Graph*** shows the quality score (Q) versus the position of each base in the sequence read. At Q20, the probability of miscalling a base is 1%. Above Q20, the probability of miscalling a base is lower than 1%; below Q20, the probability of a miscall increases. The read length, trimmed length (after vector and poor sequence have been trimmed), and the number of bases with a Q value >20 are given below the graph.



Read Length	1061 b	**Trimmed Length**	850 b	**Pos.** 22-871
Q20	872 b	**Q20/len**	0.82	
Q40	564 b	**Q40/len**	0.53	

- The nucleotide ***Sequence*** can be viewed. Low-quality sequence is trimmed from the final text (strikethrough text). Vector sequences (if present in the sequence) are denoted in light blue text.

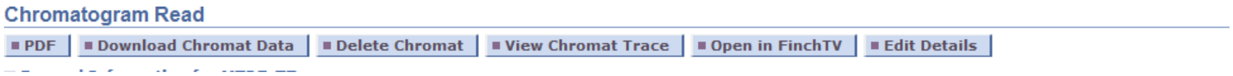


>MT25-T7 CHROMAT_ID=213

~~arrryccccccgcyggatctc~~tggagtgttggctgcatatttgcagaaatgtttcgtaga 60
aagcctctttttcgtggaagttcagatgttgatcaactaggaaaaatcttggacgtgatt 120
ggactcccaggagaagaagactggcctagagatgttgcccttcccaggcaggcttttcat 180
tcaaaatctgcccaaccaattgagaagtttgtaacagatatcgatgaactaggcaaagac 240
ctacttctgaagtgtttgacatttaacccagccaaaagaatatctgcctacagtgccctg 300
tctcacccatacttccaggacctggaaaggtgcaaagaaaacctggattcccacctgccg 360
cccagccagaacacctcggagctgaatacagccggtaagcctatccctaaccctctcctc 420
ggtctcgattctacgtgagacccagctttcttgtacaaagtggttgatatccagcacagt 480
ggcggccgctcgagtctagagggcccgcggttcgaaggtaagcctatccctaaccctctc 540
ctcggtctcgattctacgcgtaccggttagtaatgaggagaaagaggtaatgaaatggca 600
tcgactgcagtaggtaactgaggatccaatgtaactgtattcagcgatgacgaaattctt 660
agctattgtaatactctagaggatctttgtgaaggaaccttacttctgtggtgtgacata 720
attggacaaactacctacagagatttaaagctctaaggtaaatataaaatttttaagtgt 780
ataatgtgttaaactactgattctaattgtttgtgtattttagattccaacctatggaac 840
tgatgaatgggagcagtggtggaatgcctttaatgaggaaaacctgttttgctcagaaga 900
aatgccatctagtgatgatgaggctactgctgactctcacattctactcctccaaaaaga 960
gagaaagtagagaccccaagacttccttcarattgctaagtttttttgragtcatksckgg 1020
ggtaarwwawaraacccctksgcksgctgsgcawtaaaaca

~~acgt~~ trimmed region(s) acgt vector region(s)

Action buttons at the top of the page allow the user to delete, download, view or generate a PDF report for the sample.



Viewing chromatograms

Electropherogram viewers are freely available for Microsoft Windows, MacOS Classic, and MacOSX from these sites. Users may be required to register to access the freeware. TCAG does not endorse or support any of this software.

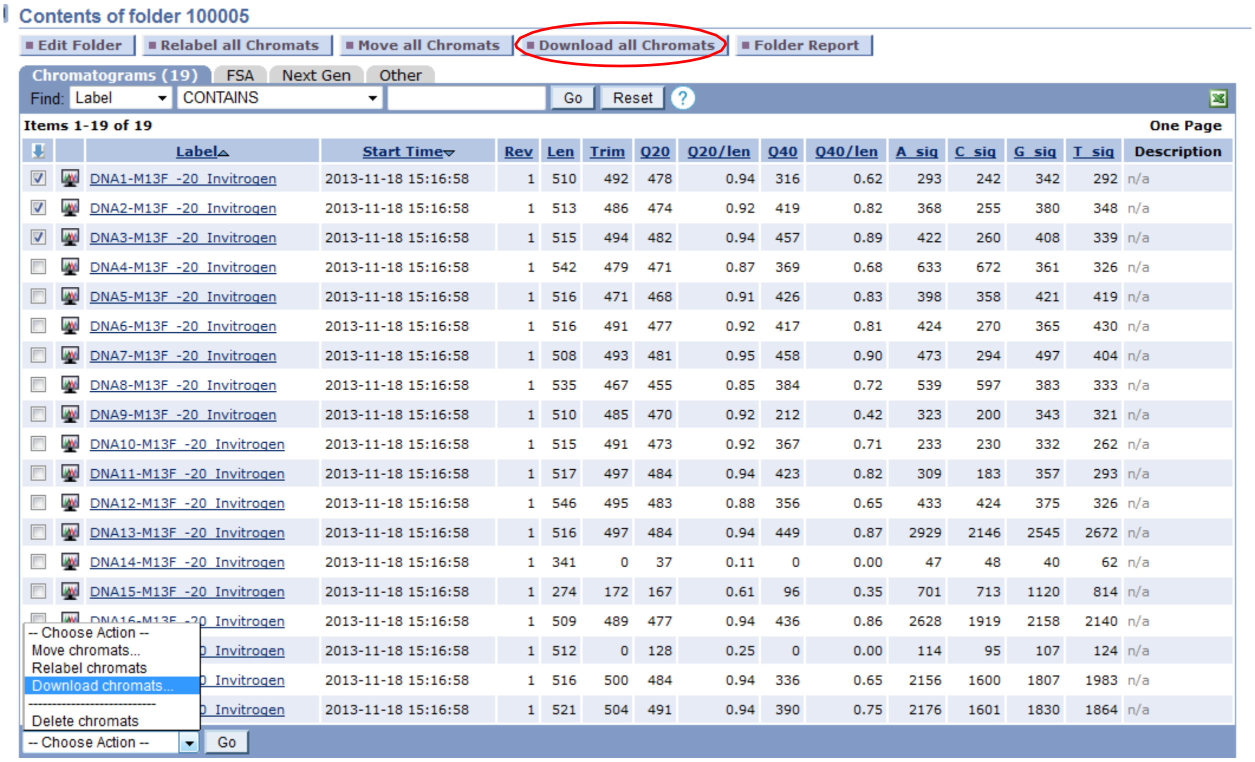
- Applied Biosystems Sanger Analysis Tools - cloud-based data analysis
- CHROMAS LITE CHROMATOGRAM VIEWER - Microsoft Windows
- 4Peaks - MacOS 10.7+
- Sequence Scanner (Applied Biosystems Genetic Analyzer)

Other useful tools. TCAG does not endorse or support these tools.

- UCSC In-Silico PCR
- Primer3 for design of PCR Primers
- BioEdit Sequence Alignment Editor for Windows

Downloading multiple files

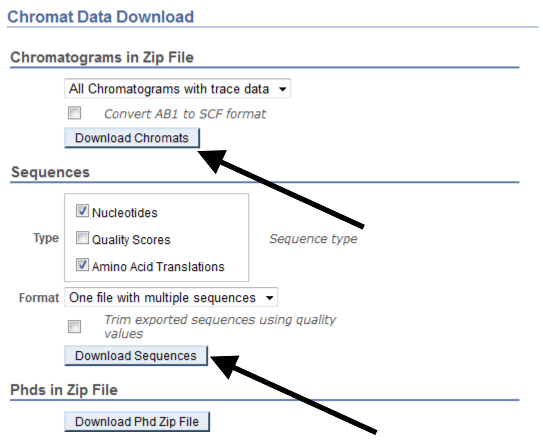
In the folder view, choose samples to be downloaded by checking the empty box to the left of the sample name ***or*** click on the ‘Download all Chromats’ button at the top of the page.



Items 1-19 of 19

One Page

		Label	Start Time	Rev	Len	Trim	Q20	Q20/len	Q40	Q40/len	A sig	C sig	G sig	T sig	Description
☑		DNA1-M13F -20 Invitrogen	2013-11-18 15:16:58	1	510	492	478	0.94	316	0.62	293	242	342	292	n/a
☑		DNA2-M13F -20 Invitrogen	2013-11-18 15:16:58	1	513	486	474	0.92	419	0.82	368	255	380	348	n/a
☑		DNA3-M13F -20 Invitrogen	2013-11-18 15:16:58	1	515	494	482	0.94	457	0.89	422	260	408	339	n/a
☐		DNA4-M13F -20 Invitrogen	2013-11-18 15:16:58	1	542	479	471	0.87	369	0.68	633	672	361	326	n/a
☐		DNA5-M13F -20 Invitrogen	2013-11-18 15:16:58	1	516	471	468	0.91	426	0.83	398	358	421	419	n/a
☐		DNA6-M13F -20 Invitrogen	2013-11-18 15:16:58	1	516	491	477	0.92	417	0.81	424	270	365	430	n/a
☐		DNA7-M13F -20 Invitrogen	2013-11-18 15:16:58	1	508	493	481	0.95	458	0.90	473	294	497	404	n/a
☐		DNA8-M13F -20 Invitrogen	2013-11-18 15:16:58	1	535	467	455	0.85	384	0.72	539	597	383	333	n/a
☐		DNA9-M13F -20 Invitrogen	2013-11-18 15:16:58	1	510	485	470	0.92	212	0.42	323	200	343	321	n/a
☐		DNA10-M13F -20 Invitrogen	2013-11-18 15:16:58	1	515	491	473	0.92	367	0.71	233	230	332	262	n/a
☐		DNA11-M13F -20 Invitrogen	2013-11-18 15:16:58	1	517	497	484	0.94	423	0.82	309	183	357	293	n/a
☐		DNA12-M13F -20 Invitrogen	2013-11-18 15:16:58	1	546	495	483	0.88	356	0.65	433	424	375	326	n/a
☐		DNA13-M13F -20 Invitrogen	2013-11-18 15:16:58	1	516	497	484	0.94	449	0.87	2929	2146	2545	2672	n/a
☐		DNA14-M13F -20 Invitrogen	2013-11-18 15:16:58	1	341	0	37	0.11	0	0.00	47	48	40	62	n/a
☐		DNA15-M13F -20 Invitrogen	2013-11-18 15:16:58	1	274	172	167	0.61	96	0.35	701	713	1120	814	n/a
☐		DNA16-M13F -20 Invitrogen	2013-11-18 15:16:58	1	509	489	477	0.94	436	0.86	2628	1919	2158	2140	n/a
		0 Invitrogen	2013-11-18 15:16:58	1	512	0	128	0.25	0	0.00	114	95	107	124	n/a
		0 Invitrogen	2013-11-18 15:16:58	1	516	500	484	0.94	336	0.65	2156	1600	1807	1983	n/a
		0 Invitrogen	2013-11-18 15:16:58	1	521	504	491	0.94	390	0.75	2176	1601	1830	1864	n/a



Chromat Data Download

Chromatograms in Zip File

All Chromatograms with trace data ▾

☐ *Convert AB1 to SCF format*

Sequences

Type: ☑ Nucleotides ☐ Quality Scores ☑ Amino Acid Translations — *Sequence type*

Format: One file with multiple sequences ▾

☐ *Trim exported sequences using quality values*

Phds in Zip File

Choose to download ***Sequence Text Files*** or ***Chromatograms*** from this window. If you are downloading an entire folder, the chromat files will be saved as a .tar file and will need to be extracted (unzipped) to view the individual files. There are several free programs (e.g. 7-Zip or JustZIPit) available to do this extraction step.