Next Generation Sequencing:
Data analysis for genetic profiling

Raed Samara, Ph.D.
Global Product Manager
Raed.Samara@QIAGEN.com
Welcome to the NGS webinar series - 2015

- **Webinar 1**
  NGS: Introduction to technology, and applications
  January 5th, 1:00 am EDT, 10 am PDT, 6 pm GMT

- **Webinar 2**
  Targeted NGS for Cancer Research
  January 12th, 1:00 am EDT, 10 am PDT, 6 pm GMT

- **Webinar 3**
  NGS: Data analysis for genetic profiling
  January 19th, 1:00 am EDT, 10 am PDT, 6 pm GMT

- **Webinar 4**
  NGS: Advanced analysis with IVA & CLC bio Cancer Research Workbench
  January 26th, 1:00 am EDT, 10 am PDT, 6 pm GMT
Legal Disclaimer

- QIAGEN products shown here are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.

- For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.QIAGEN.com or can be requested from QIAGEN Technical Services or your local distributor.
Agenda

- NGS Data Analysis
  - Read Mapping
  - Variant Calling
  - Variant Annotation

- Targeted Enrichment
  - GeneRead Gene Panels

- GeneRead Data Analysis Portal
  - Workflow
  - Interface
  - Data Interpretation
Read Mapping

Millions of reads from a single run

- Alignment
- Mapping Quality

Programs for read-mapping
- Hash-based: MAQ, ELAND, SOAP, Novoalign
- Suffix array/Burrows Wheeler Transform based: BWA, BowTie, BowTie2, SOAP2
Variant Calling

Determine if there is enough statistical support to call a variant

Reference sequence
ACAGTTAAGCCTGAACCTAAGACTAGACTAGGATCGTCCTAGATAGTCTCGATAGCTCGATATC

Aligned reads
AACTAGACTAGGATCGTCCTAGATAGTCTCG
AACTAGACTAGGATCGTCCTAGATAGTCTCG
AACTAGACTAGGATCGTCCTAGATAGTCTCG
GATCGTCCTAGATAGTCTCGATAGCTCGAT
GATCGTCCTAGATAGTCTCGATAGCTCGAT
GATCGTCCTAGATAGTCTCGATAGCTCGAT

Multiple factors are considered in calling variants
- No. of reads with the variant
- Mapping qualities of the reads
- Base qualities at the variant position
- Strand bias (variant is seen in only one of the strands)

Variant Calling Software
- GATK Unified Genotyper, Torrent Variant Caller, SamTools, Mutect, …
**Variant Representation**

**VCF – Variant Call Format**

http://www.1000genomes.org/wiki/Analysis/Variant%20Call%20Format/vcf-variant-call-format-version-41

### Header lines

```plaintext
##fileformat=VCFv4.1
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Approximate read depth; some reads may have been filtered">
##INFO=<ID=FS,Number=1,Type=Float,Description="Phred-scaled p-value using Fisher's exact test to detect strand bias">
##INFO=<ID=MQ,Number=1,Type=Float,Description="RMS Mapping Quality">
##INFO=<ID=OND,Number=1,Type=Float,Description="Overall non-diploid ratio (alleles/(alleles+non-alleles))">
##INFO=<ID=QD,Number=1,Type=Float,Description="Variant Confidence/Quality by Depth">
##contig=<ID=chrM,length=16571,assembly=hg19>
##contig=<ID=chr1,length=249250621,assembly=hg19>
##contig=<ID=chr2,length=243199373,assembly=hg19>
##contig=<ID=chr3,length=198022430,assembly=hg19>
##contig=<ID=chr4,length=191154276,assembly=hg19>
```

### Variant calls

<table>
<thead>
<tr>
<th>CHROM</th>
<th>POS</th>
<th>ID</th>
<th>REF</th>
<th>ALT</th>
<th>QUAL</th>
<th>FILTER</th>
<th>INFO</th>
<th>FORMAT</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1</td>
<td>11181327</td>
<td>rs11121691</td>
<td>C</td>
<td>T</td>
<td>100.0</td>
<td>PASS</td>
<td>DP=1000;MQ=87.67 GT:AD:DP</td>
<td>0/1:146,45:191</td>
<td></td>
</tr>
<tr>
<td>chr1</td>
<td>11190646</td>
<td>rs2275527</td>
<td>G</td>
<td>A</td>
<td>100.0</td>
<td>PASS</td>
<td>DP=1000;MQ=67.38 GT:AD:DP</td>
<td>0/1:462,121:583</td>
<td></td>
</tr>
<tr>
<td>chr1</td>
<td>11205058</td>
<td>rs1057079</td>
<td>C</td>
<td>T</td>
<td>100.0</td>
<td>PASS</td>
<td>DP=1000;MQ=79.57 GT:AD:DP</td>
<td>0/1:49,143:192</td>
<td></td>
</tr>
</tbody>
</table>
## Variant Annotation

<table>
<thead>
<tr>
<th>Chromosome</th>
<th>Position</th>
<th>SNP ID</th>
<th>Ref</th>
<th>Alt</th>
<th>Gene Name</th>
<th>Mutation Type</th>
<th>Codon Change</th>
<th>AA Change</th>
<th>Filtered Coverage</th>
<th>Allele Frequency</th>
<th>Variant Frequency</th>
<th>snpEff Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1</td>
<td>11181327</td>
<td>rs11121691</td>
<td>C</td>
<td>T</td>
<td>MTOR</td>
<td>SNP</td>
<td>c.6909C&gt;T</td>
<td>p.L2303</td>
<td>1.924</td>
<td>C=0.761 T=0.239</td>
<td>0.239</td>
<td>SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr1</td>
<td>11190646</td>
<td>rs2275527</td>
<td>G</td>
<td>A</td>
<td>MTOR</td>
<td>SNP</td>
<td>c.5553G&gt;A</td>
<td>p.S1851</td>
<td>5.842</td>
<td>G=0.791 A=0.208</td>
<td>0.208</td>
<td>SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr1</td>
<td>11205058</td>
<td>rs1057079</td>
<td>C</td>
<td>T</td>
<td>MTOR</td>
<td>SNP</td>
<td>c.4731C&gt;T</td>
<td>p.A1577</td>
<td>1.928</td>
<td>C=0.254 T=0.746</td>
<td>0.746</td>
<td>SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr1</td>
<td>11288758</td>
<td>rs1064261</td>
<td>G</td>
<td>A</td>
<td>MTOR</td>
<td>SNP</td>
<td>c.2997G&gt;A</td>
<td>p.N999</td>
<td>5.186</td>
<td>G=0.212 A=0.788</td>
<td>0.788</td>
<td>SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr1</td>
<td>11300344</td>
<td>rs191073707</td>
<td>C</td>
<td>T</td>
<td>MTOR</td>
<td>SNP</td>
<td></td>
<td>210</td>
<td>C=0.92 T=0.076</td>
<td>A=0.759 G=0.241</td>
<td>0.241</td>
<td>INTRON</td>
</tr>
<tr>
<td>chr1</td>
<td>11301714</td>
<td>rs1135172</td>
<td>A</td>
<td>G</td>
<td>MTOR</td>
<td>SNP</td>
<td>c.1437A&gt;G</td>
<td>p.D479</td>
<td>3.965</td>
<td>A=0.248 G=0.752</td>
<td>0.752</td>
<td>SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr1</td>
<td>11322628</td>
<td>rs2295080</td>
<td>G</td>
<td>T</td>
<td>MTOR</td>
<td>SNP</td>
<td></td>
<td>339</td>
<td>G=0.239 T=0.755</td>
<td>0.755</td>
<td></td>
<td>UTR_3_PRIME</td>
</tr>
<tr>
<td>chr1</td>
<td>186641626</td>
<td>rs2853805</td>
<td>G</td>
<td>A</td>
<td>PTGS2</td>
<td>SNP</td>
<td></td>
<td>97</td>
<td>G=0.0 A=1.0</td>
<td>1</td>
<td></td>
<td>UTR_3_PRIME</td>
</tr>
<tr>
<td>chr1</td>
<td>186642429</td>
<td>rs2206593</td>
<td>A</td>
<td>G</td>
<td>PTGS2</td>
<td>SNP</td>
<td></td>
<td>3,552</td>
<td>A=0.167 G=0.833</td>
<td>0.83</td>
<td></td>
<td>UTR_3_PRIME</td>
</tr>
<tr>
<td>chr1</td>
<td>186643058</td>
<td>rs5275</td>
<td>A</td>
<td>G</td>
<td>PTGS2</td>
<td>SNP</td>
<td></td>
<td>237</td>
<td>A=0.759 G=0.241</td>
<td>0.241</td>
<td></td>
<td>UTR_3_PRIME</td>
</tr>
<tr>
<td>chr1</td>
<td>186645927</td>
<td>rs2066826</td>
<td>C</td>
<td>T</td>
<td>PTGS2</td>
<td>SNP</td>
<td></td>
<td>209</td>
<td>C=0.88 T=0.12</td>
<td>0.12</td>
<td></td>
<td>INTRON</td>
</tr>
<tr>
<td>chr2</td>
<td>29415792</td>
<td>rs1728828</td>
<td>G</td>
<td>A</td>
<td>ALK</td>
<td>SNP</td>
<td></td>
<td>2,520</td>
<td>G=0.0 A=1.0</td>
<td>1</td>
<td></td>
<td>UTR_3_PRIME</td>
</tr>
<tr>
<td>chr2</td>
<td>29416366</td>
<td>rs1881421</td>
<td>G</td>
<td>C</td>
<td>ALK</td>
<td>SNP</td>
<td>c.4587G&gt;C</td>
<td>p.D1529E</td>
<td>4,361</td>
<td>G=0.907 C=0.093</td>
<td>0.093</td>
<td>NON_SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr2</td>
<td>29416481</td>
<td>rs1881420</td>
<td>T</td>
<td>C</td>
<td>ALK</td>
<td>SNP</td>
<td>c.4472T&gt;C</td>
<td>p.K1491R</td>
<td>3,061</td>
<td>T=0.954 C=0.045</td>
<td>0.045</td>
<td>NON_SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr2</td>
<td>29416572</td>
<td>rs1670283</td>
<td>T</td>
<td>C</td>
<td>ALK</td>
<td>SNP</td>
<td>c.4381T&gt;C</td>
<td>p.L1461V</td>
<td>5,834</td>
<td>T=0.0 C=0.999</td>
<td>0.999</td>
<td>NON_SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr2</td>
<td>29419591</td>
<td>rs1670284</td>
<td>G</td>
<td>T</td>
<td>ALK</td>
<td>SNP</td>
<td></td>
<td>739</td>
<td>G=0.093 T=0.907</td>
<td>0.907</td>
<td></td>
<td>INTRON</td>
</tr>
<tr>
<td>chr2</td>
<td>29445458</td>
<td>rs3795850</td>
<td>G</td>
<td>T</td>
<td>ALK</td>
<td>SNP</td>
<td>c.3375G&gt;T</td>
<td>p.G1125</td>
<td>1,776</td>
<td>G=0.917 T=0.082</td>
<td>0.082</td>
<td>SYNONYMOUS_CODING</td>
</tr>
<tr>
<td>chr2</td>
<td>29446184</td>
<td>rs2276550</td>
<td>C</td>
<td>G</td>
<td>ALK</td>
<td>SNP</td>
<td></td>
<td>475</td>
<td>C=0.895 G=0.105</td>
<td>0.105</td>
<td></td>
<td>INTRON</td>
</tr>
</tbody>
</table>

### SIFT Score
- Predicts the deleterious effect of an amino acid change based on how conserved the sequence is among related species

### Polyphen Score
- Predicts the impact of the variant on protein structure
What is targeted sequencing?
- Sequencing a sub set of regions in the whole-genome

Why do we need targeted sequencing?
- Not all regions in the genome are of interest or relevant to a specific study
- Exome Sequencing: sequencing most of the exonic regions of the genome (exome). Protein-coding regions constitute less than 2% of the entire genome
- Focused panel/hot spot sequencing: focused on the genes or regions of interest

What are the advantages of focused panel sequencing?
- More coverage per sample, more sensitive mutation detection
- More samples per run, lower cost per sample
**Multiplex PCR**

- Small DNA input (40ng)
- Short processing time (several hrs)
- Relatively small throughput (KB - MB region)
Variants Identifiable through Multiplex PCR

- **SNPs** – single nucleotide polymorphisms
- **Indels**
  - Indels < 20 bp in length
- **Variants callable with the help of a reference**
  - Copy number variants (CNVs)
- **Variants not callable**
  - Structural variants
    - Large indels
    - Inversions

- CNV
- Large insertion
- Inversion
GeneRead DNAseq Gene Panel

- Multiplex PCR technology based targeted enrichment for DNA sequencing
- Cover all human exons (coding regions)
- Division of gene primers sets into 4 tubes; up to 2400 plex in each tube
## GeneRead DNASEq Gene Panels

<table>
<thead>
<tr>
<th>Type</th>
<th>Panel name</th>
<th># Genes</th>
<th># Amplicons</th>
<th>Target region (bases)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Solid tumors</strong></td>
<td><strong>Tumor Actionable Mutations</strong></td>
<td>8</td>
<td>118</td>
<td>7104</td>
</tr>
<tr>
<td></td>
<td><strong>Clinically Relevant Tumor</strong></td>
<td>24</td>
<td>602</td>
<td>39603</td>
</tr>
<tr>
<td><strong>Hematologic malignancy</strong></td>
<td><strong>Myeloid Neoplasms</strong></td>
<td>50</td>
<td>2536</td>
<td>236319</td>
</tr>
<tr>
<td><strong>Disease-specific</strong></td>
<td><strong>Breast Cancer</strong></td>
<td>44</td>
<td>2915</td>
<td>268621</td>
</tr>
<tr>
<td></td>
<td><strong>Colorectal Cancer</strong></td>
<td>38</td>
<td>1954</td>
<td>182851</td>
</tr>
<tr>
<td></td>
<td><strong>Liver Cancer</strong></td>
<td>33</td>
<td>2052</td>
<td>191170</td>
</tr>
<tr>
<td></td>
<td><strong>Lung Cancer</strong></td>
<td>45</td>
<td>3586</td>
<td>332999</td>
</tr>
<tr>
<td></td>
<td><strong>Ovarian Cancer</strong></td>
<td>32</td>
<td>2021</td>
<td>198058</td>
</tr>
<tr>
<td></td>
<td><strong>Prostate Cancer</strong></td>
<td>32</td>
<td>1837</td>
<td>167195</td>
</tr>
<tr>
<td></td>
<td><strong>Gastric Cancer</strong></td>
<td>29</td>
<td>2377</td>
<td>222333</td>
</tr>
<tr>
<td></td>
<td><strong>Cardiomyopathy</strong></td>
<td>58</td>
<td>2657</td>
<td>249727</td>
</tr>
<tr>
<td><strong>Comprehensive</strong></td>
<td><strong>Carrier Testing</strong></td>
<td>157</td>
<td>6943</td>
<td>664735</td>
</tr>
<tr>
<td></td>
<td><strong>Cancer Predisposition</strong></td>
<td>143</td>
<td>6582</td>
<td>620318</td>
</tr>
<tr>
<td></td>
<td><strong>Comprehensive Cancer</strong></td>
<td>160</td>
<td>7951</td>
<td>744835</td>
</tr>
</tbody>
</table>
GeneRead DNAseq Custom Panel

Species:  Human

Gene Symbol, Refseq ID or NCBI Gene ID

Notch1
Wnt3a
Wnt5a
KRAS
GeneRead data analysis work flow

- **Read mapping**
  - Identify the possible position of the read within the reference
  - Align the read sequence to reference sequences

- **Primer trimming**
  - Remove primer sequences from the reads

- **Variant calling**
  - Identify differences between the reference and reads

- **Variant filtering and annotation**
  - Functional information about the variant
Typical NGS raw read from targeted sequencing:

Adapter  Barcode  Primer  Insert sequence  Primer  Adapter
5'--3'    5'--3'    5'--3'    5'--3'    5'--3'

Removal of adapters and de-multiplexing:

Primer  Insert sequence  Primer
5'--3'    5'--3'    5'--3'

Read length can vary: only part of the insert or the 3' primer may be present:

5'--3'
5'--3'
5'--3'
5'--3'
Align reads to the reference genome

Reference sequence

Aligned reads
Primer Trimming

Primer sequences must be trimmed for accurate variant calling

Reference sequence

Frequency of `C` without primer trimming = 4/13 = 31%

Frequency of `C` after primer trimming = 4/7 = 57%

Aligned reads
GeneRead Variant Calling Overview

**Read mapping and post-processing**
- Raw reads from the sequencer (de-multiplexed)
- GeneRead panel ID
- Analysis mode

**Sequencing platform**
- IonTorrent
- TMAP

**Variant calling and filtering**
- MiSeq/HiSeq
- BowTie2/BWA
- GATK Indel Realigner
- GATK Base Quality Score Recalibrator
- Primer Trimming
- BAQ Computation
- BAQ Computation

**Annotation**
- snpEff (basic annotation)
- dbSNP
- Cosmic
- ClinVar
- dbNSFP

**Additional filtering**
- Torrent Variant Caller (TVC)
- GATK Variant Annotator
- GATK Variant Filtration

**Variants in Excel format**

**Variants in Ingenuity® Variant Analysis™**

*Separate interface, free preview available*

- Eliminates some false-positive variant calls around indels
- Read aligners can not eliminate these alignment errors since they align reads independently
- Multiple sequence alignment can identify these errors and correct them

- Eliminates sequencer-specific biases
  - Lane-specific/sample-specific biases
  - Instrument-specific under-reporting/over-reporting of quality scores
  - Systematic errors based on read position
  - Di-nucleotide-specific sequencing errors
- Recalibration leads to improved variant calls
Variant Filtration

- **Variant Frequency**
  - Somatic mode
    - SNPs with frequency < 4% and indels with frequency < 20%
  - Germline mode
    - SNPs with frequency < 20% and indels with frequency < 25%

- **Strand Bias**
  - SNPs with FS ≤ 60
  - Indels with FS ≤ 200

- **Mapping Quality**
  - SNPs with MQ ≤ 40.0

- **Haplotype Score**
  - SNPs with HaplotypeScore ≤ 13.0
  - Not applicable for pooled samples

Strand Bias: variants that are present in reads from only one of the two strands
- CNV calls made by comparison to normalized read depths in a reference sample
- High specificity and sensitivity possible due pooling evidence from multiple amplicons
Specificity Analysis

- **Specificity**: the percentage of sequences that map to the intended targets region of interest
  
  \[
  \text{specificity} = \frac{\text{number of on-target reads}}{\text{total number of reads}}
  \]

- **Coverage depth (or depth of coverage)**: how many times each base has been sequenced

- **Coverage uniformity**: evenness of the coverage depth along the target region

![Diagram showing Reference sequence, NGS reads, On-target reads, Off-target reads, and ROI 1 and ROI 2.]
GeneRead Data Analysis Web Portal

FREE Complete & Easy to use Data Analysis with Web-based Software

- .bam file (Ion Torrent)
- .fastq or .fastq.gz (MiSeq/HiSeq)

- Submit runs for analysis
- View output files
- Delete/manage files
Features of Variant Report

- SNP detection
- Indel detection
- dbSNP and COSMIC ID (hyperlink)
- Predicted amino acid change
- Effect of SNP
- Impact of SNP
- Link to qPCR somatic mutation assay

<table>
<thead>
<tr>
<th>Chrom</th>
<th>Pos</th>
<th>ID</th>
<th>Ref</th>
<th>Alt</th>
<th>Gene Name</th>
<th>Mutation type</th>
<th>Codon Change</th>
<th>AA Change</th>
<th>Filtered Coverage</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr7</td>
<td>116436097</td>
<td>rs41737 COSM150G</td>
<td>A</td>
<td>G</td>
<td>MET</td>
<td>SNP</td>
<td>c.4146G&gt;A</td>
<td>p.P1382</td>
<td>1.283</td>
</tr>
<tr>
<td>chr7</td>
<td>116437606</td>
<td>rs1621</td>
<td>G</td>
<td>A</td>
<td>MET</td>
<td>SNP</td>
<td></td>
<td></td>
<td>125</td>
</tr>
<tr>
<td>chr9</td>
<td>21968199</td>
<td>rs11515 COSM142C</td>
<td>G</td>
<td>C</td>
<td>CDKN2A</td>
<td>SNP</td>
<td></td>
<td></td>
<td>121</td>
</tr>
<tr>
<td>chr12</td>
<td>25362217</td>
<td>rs9266</td>
<td>A</td>
<td>G</td>
<td>KRAS</td>
<td>SNP</td>
<td></td>
<td></td>
<td>31</td>
</tr>
<tr>
<td>chr12</td>
<td>25362652</td>
<td>rs712</td>
<td>C</td>
<td>T</td>
<td>KRAS</td>
<td>SNP</td>
<td></td>
<td></td>
<td>80</td>
</tr>
<tr>
<td>chr12</td>
<td>25368462</td>
<td>rs4362222</td>
<td>C</td>
<td>T</td>
<td>KRAS</td>
<td>SNP</td>
<td></td>
<td></td>
<td>48</td>
</tr>
<tr>
<td>chr14</td>
<td>105236287</td>
<td>rs35416681</td>
<td>A</td>
<td>C</td>
<td>AKT1</td>
<td>SNP</td>
<td></td>
<td></td>
<td>403</td>
</tr>
<tr>
<td>chr14</td>
<td>105242966</td>
<td>rs2494735</td>
<td>T</td>
<td>C</td>
<td>AKT1</td>
<td>SNP</td>
<td></td>
<td></td>
<td>318</td>
</tr>
<tr>
<td>chr17</td>
<td>7577121</td>
<td>rs121913343 COSM</td>
<td>G</td>
<td>T</td>
<td>TP53</td>
<td>SNP</td>
<td></td>
<td></td>
<td>158</td>
</tr>
<tr>
<td>chr17</td>
<td>7579445</td>
<td>rs2001430</td>
<td>G</td>
<td>T</td>
<td>TP53</td>
<td>SNP</td>
<td></td>
<td></td>
<td>70</td>
</tr>
<tr>
<td>chr17</td>
<td>7579645</td>
<td>rs2001430</td>
<td>G</td>
<td>T</td>
<td>TP53</td>
<td>SNP</td>
<td></td>
<td></td>
<td>48</td>
</tr>
</tbody>
</table>

Sample & Assay Technologies
Biological Interpretation Using IVA

VCF to Ingenuity Variant Analysis

- Built-in optimized support for uploading called variant files in VCF format
- Create analysis by answering a few questions about study

![Focus the Analysis](image)

**Study Type**

- Name: Tumor
- Description: Enter description

**What does the analysis concern?**

- Genetic disease - I'm studying a hereditary disease or syndrome and am seeking its causal variant(s)
- Cancer - I'm seeking to identify cancer driver variants
- Stratification study - I have two groups of samples (responders and non-responders) and am looking for variants that distinguish the two
- Personal genome - I have a single sample and am looking for those variants with known disease or phenotypic associations
- Other
- Use settings from analysis

Next
Features of Ingenuity Variant Analysis

- Annotate samples with Ingenuity Knowledge Base
- Compare what’s genetically distinctive
- Identify and share the most promising variants
FOCUS ON YOUR RELEVANT GENES

- Focused:
  - Biologically relevant content selection enables deep sequencing on relevant genes and identification of rare mutations

- Flexible:
  - Mix and match any gene of interest

- NGS platform independent:
  - Functionally validated for PGM, MiSeq/HiSeq

- Free analysis:
  - Free, complete and easy to use data analysis tool
Welcome to the NGS webinar series - 2015

- **Webinar 1**
  NGS: Introduction to technology, and applications
  January 5th, 1:00 pm EDT, 10 am PDT, 6 pm GMT

- **Webinar 2**
  Targeted NGS for Cancer Research
  January 12th, 1:00 pm EDT, 10 am PDT, 6 pm GMT

- **Webinar 3**
  NGS: Data analysis for genetic profiling
  January 19th, 1:00 pm EDT, 10 am PDT, 6 pm GMT

- **Webinar 4**
  NGS: Advanced analysis with IVA & CLC bio Cancer Research Workbench
  January 26th, 1:00 pm EDT, 10 am PDT, 6 pm GMT
Contact Technical Support

Phone: 1-800-362-7737

BRCsupport@qiagen.com

Webinar related questions: Qiawebinars@qiagen.com