



Next Generation and Sanger Sequencing Submission Form

Date of Submission: _____

Genomics Core Use Only-
 Project#: _____
 Sample Location: _____
 Received By: _____
 VMSR Sample ID: _____

Section 1: Contact Information

Principal Investigator:	Contact Person:
Department:	Phone #:
Institution:	Email:
Phone #:	
Email:	Human Subjects Approval: <input type="checkbox"/> Yes <input type="checkbox"/> No
Affiliation: If other, please specify:	IRB#:

Billing

Billing Contact:	Account #:
Phone #:	
Email:	
PI Signature (Indicates financial commitment for services provided):	

Section 2: Service Information

Service Type:	<u>For Target Region Sequencing, please specify:</u>
Next-Generation Sequencing Method:	
Multiplex <input type="checkbox"/> Yes <input type="checkbox"/> No	
If yes, # of samples per chip:	

Section 3: Sequencing and Fragment Sizing Sample Information

*For Sanger Sequencing, please only complete section 4.

#	Sample Name	Sample Type	Concentration (ng/μl)	Volume (μl)	Well # on Gel Image
1.					
2.					
3.					
4.					
5.					
6.					
7.					
8.					
9.					
10.					
11.					
12.					
13.					
14.					
15.					
16.					
17.					
18.					
19.					
20.					

*Please attach gel image

Section 4: Sanger Sequencing Sample Information

Section A- REQUIRED						Section B or C - REQUIRED						
Section A						Section B				OR	Section C	
	Variant Name	HUGO Gene	Nucleotide Reference	Nucleotide Variant	Zygoty (Het,Homo,Hemi)	Genome Build #	Chr #	Genomic Position - Start	Genomic Position - End		Transcript ID (NM#)	cDNA Position #
SNV example	MSH2_var1	MSH2	C	A	Heterozygous	36	6	572433	572433		NM_425	c.255
DEL example	JAG1_var1	JAG1	TG	--	Heterozygous	37	20	10633150	10633150		NM_000214.2	c.852_853
1												
2												
3												
4												
5												
6												
7												
8												
9												
10												

Section 4: Bioinformatics Service Types

Type	Description	Fee Applied
Initial Consultation (30 minutes)	➤ Brief discussion and overview of project scope.	NO; Initial 30 minutes
Tutorial	➤ Provide basic training with standard analysis tool training suitable to next generation sequencing data.	YES
A La Carte	<ul style="list-style-type: none"> ➤ Analyze the data for investigator. ➤ Option only available to researchers generating next generation sequencing data within MPG Core. 	YES
Collaborative	➤ Intended for large scale projects difficult to assess nature of analysis required.	NO; Requires percentage of effort within grant proposal

Data Deliverable Format

Alignment Genome, (i.e. hg19):

Variant Calling Analysis	<input type="checkbox"/> Standard Deliverables	<input type="checkbox"/> Extended Deliverables (Additional fees apply)	<input type="checkbox"/> Custom Deliverable (Additional fees apply)
	Includes: Ion Torrent .basecaller.bam .bam .bai .vcf Illumina .bcl .fastq .bam .bai .vcf	Includes: .fastq .sam .sai FastQC output BAM QC output Coverage report (Coverage may be standard output from Torrent Suite, CASAVA or our custom scripts) Genotyping QC report/filtered VCF Copy number analysis report	Any changes to the standard workflow are considered a custom analysis. Please contact us for additional information.
RNA Sequencing	<input type="checkbox"/> Standard Deliverables	<input type="checkbox"/> Extended Deliverables (Additional fees apply)	<input type="checkbox"/> Custom Deliverable (Additional fees apply)
	Includes: Ion Torrent .basecaller.bam .bam .bai Illumina .bcl .fastq .bam .bai	Includes: .fastq .sam .sai FastQC output BAM QC output Coverage report	Any changes to the standard workflow are considered a custom analysis. Please contact us for additional information.

Additional Notes:

Laboratory:

Bioinformatics

Sample Requirements and Shipping Instructions

Sample Requirements

	Genomic DNA Requirements	Total RNA Requirements	PCR Amplicon	Data Only
Sample Type	Purified DNA (PureGene Extraction Preferred); 260/280 ratio 1.75-2.00	Purified RNA; RNA Integrity Number(RIN) 8.0-10.0	"Load Only" reactions should be submitted dry and ready to reconstitute for loading. All other samples must be amplified with PCR primers including M13 universal primer sequences at 5' ends. M13 fwd primer sequence: 5'-TGTAACGACGGCCAGT-3' M13 rev primer sequence: 5'-CAGGAACAGCTATGACC-3'	Media/hard drive
Collection Type	Screw cap tube	Screw cap tube	Screw cap tube	Encrypted. Retain original data source; lab not responsible for damage during shipping.
Collection Volume and/or Concentration	4.0ug @ 75ng/ul suspended in nuclease free water.	2.0ug @ 100ng/ul suspended in nuclease free water.	Submit 25ul of your PCR product for sequencing or 10ul of your diluted PCR product for Fragment Analysis. For Fragment Analysis, amplicons must be between 35 and 500bp and labeled with FAM, VIC, NED, or PET; (the core suggests running a serial dilution for each locus if you are unfamiliar with the correct dilution of your amplicons).	N/A
Labeling of Collection Type	Ensure label on tube is legible and matches information on submission sheet. Sample names should be alphanumeric with no more than 6 characters. Each tube must have a unique sample name.			

Shipping Instructions

Packaging Instructions	If needed, sample packaging instructions are available as a pdf from FEDEX: Biological Substance: http://images.fedex.com/us/packaging/guides/UN3373_fxcom.pdf Media/Hard Drive: http://images.fedex.com/us/packaging/guides/Computer_fxcom.pdf			
Shipping Instructions	Ship at ambient temperature Ship via overnight courier(FedEx,UPS)	Ship on dry ice Ship via overnight courier(FedEx,UPS)	Ship on ice packs Ship via overnight courier(FedEx,UPS)	Send on encrypted media/hard drive. Provide encryption method and key via email. Ship via overnight courier(FedEx,UPS)
Shipping Address	Molecular Pathology Genomics Core Children's Hospital Los Angeles 4650 Sunset Boulevard, MS #103 Los Angeles, California 90027			