GSC Groups

Analysis and Annotation Technology Development Informatics Assembly

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Outreach

Mapping

Production

Prefinishing

Finishing

GSC Group Designations

Added Value Activities

Analysis and Annotation

Technology Development

Informatics

Assembly

Outreach

Pipeline Activities

Mapping

Production

Prefinishing

Finishing

GSC Relationships











GSC Production Cost per Read

<u>2004</u>	<u>2005</u>	<u>Category</u>
45%	36%	Amortized Equipment
20%	21%	Indirect cost
10%	12%	Labor
2%	7%	Service Contracts
23%	24%	Supplies

GSC Production Cost per Read, Cost per Production Base Pair, and Amortized Equipment

Assume 1 sequencer and \$1,000 amortized equipment per machine:

13 runs/day @ 770 base pairs = 1,248 reads/day = 960,960 bases/day \$0.80 AE cost/read or \$1.04 AE cost/kb

18 runs/day @ 680 base pairs = 1,728 reads/day = 1,175,040 bases/day \$0.57 AE cost/read or \$0.85 AE cost/kb

24 runs/day @ 580 base pairs = 2,304 reads/day = 1,336,320 bases/day \$0.43 AE cost/read or \$0.74 AE cost/kb

Name of Center:	Washington U	niversity in	St. Louis			Progres	is Report for	Large-Scal	le Sequenci	ng Grants	Individual	Organism Re	port									\$		
Jee the upper tables to detail th	re sequencing st	rategies and	activities fo	inded for the t	hree month peri	od from Now	ember 1, 2004 ti	o January 31,	2005. Use th	a lower table	s to account fi	or the costs of th	ise activities. Th	ne shaded o	ās are pre-s	it to perfo								
Organism: Macaque	(please specify	ð																						
A. Sequence Production:	Currul	stive total as o	October 31, 2	2004		Mo (Novert	eth 1 ber 2004)			Pece	fanth 2 mber 2004)			Mont (January	2005)		Three month total	i for November	r 1, 2004 - Janua	ry 31, 2005	Cumu	lative total as i	f January 31, 2	005
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of reads attempted	7,756,565		6	215,424		0		32,44	32,256	6	6	5,164	3,184,032	0	1,364	130,176	3,216,288	6	1,344	167,808	10,972,880	- 0	1,36	•
f of successful reads2	6,865,800			99,125				19,747	28,000			2,095	2,853,546		645	96,283	2,801,104	6	40.00	110,125	9,776,990	- 0	43.00	
verage madlength4	609.5	0.0	0.0	532.2		40	0.0	544.7	617.5	0.0	0.0	427.0	621.4	0.0	555.2	567.3	621.4	0.0	555.2	561.2	655.3	0.0	555.2	1
fotal # of Q20 bases5	4,616,742,117	0.0	0.0	\$2,754,857	6	6	6	90,755,511	17,312,131	6	6	917,128	1,772,961,816	0	471,333	\$4,617,178	1790,273,947	6	471,222	66,289,817	6,407,016,064	- 0	471,22	5 118,0
Fof clones with two successful end	2,177,884			35,291				7,085	12,736	0		554	1,290,173		254	29,817	1,302,912	0	254	47,400	4,400,796		35	4
Total # of clones attempted?	4,020,880			107,701		0		16,224	16,120	0		2,593	1,594,800		672	65,054	1,010,920	0	672	84,480	5,631,808	0	675	2 :
Paired end rate13	825	0	05	725	95	02	25	725	91%	- 25	05	527	92%	05	825	125	925	05	125	80%	82%	075	822	d l
IB. Sequence Production: Shotgun Sequencing	Cumulative tot	a as of Octobe	r 31, 2004		(November 2004)	_		North 2 December 2004	0		(January 200	15)	The ADM Da	2005	4 10 Jan 31,	Cumulativ	e total as of Jan 31.	,2005						
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For reads attempted For successful reads2 Pass rate2			6	0		0		6		0	6		0	0	0	0		0						
verage read lengths	62	0.0	10	0.0	60	40	63	0.0	5 62	6.0	0.0		0.0	0.0	0.6	0.0	63	0.0						
iotal # of QUU bases	- ·								-				0	0		0								
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fotal # of clones attempted? Paired end rate13	01	01	01	0	0 0%	0	0	0	0 0	0 0%	0	01	0	0	0 0%	0 0%	0 0%	0 0%						
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Start #1 disk set sensession yeard exercises yeard exercises Design Sector Productions: Design Sector Producti	Cumulative tot an los plaanid 1 c c c c c c c c c c c c c c c c c c c	a as of Octobe g, ins. plasmit 1 C C C C C C C C C C C C C	C 01,2004 c11,2004 other C 0 C 0 C 0 C 0 C 0 C 0 C 0 C 0	0 0% 9% 9% 0% 0 0 0% 0% 0% 0% 0% 0% 0% 0% 0% 0% 0	0 Morth 1 North 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0her 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0% am ins plasmidt 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C C C C C	0 C C C C C C C C C C C C C C C C C C C	0 0% pharmid 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Cumulative stol	4 091	0 0% These numb tota jama an ina, plasmid 0 0 0 0 0 0 0 0 0 0 0 0 0	0 060000000000000000000000000000000000	6 0% 1,2004 lb 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0% Cumulative am. int. plasmid 0 0 0 0 0 0 0 0	0 0% 0% 004 as of January 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 0% 0% 0% 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0						
The first of constrained of the first of the f	Cumulative tot an. Ins. plaamid 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	a as of October g. ins. plasmid 1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	C 01, 2004 C 11, 2004 C 11, 2004 C 0 C 0 C 0 C 0 C 0 C 0 C 0 C 0	0 0% 0% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0% Morth 1 Vicenthar 2001 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0her 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0% 0% 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Control 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0% 0% plaamid? 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Cumulative Sol	() () () () () () () () () () () () () (0 0%	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 0% 1,2004 to 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0% Cumulative sm. inst. plasmid1 0 0 0 0 0 0 0 0 0 0 0	0 0% Utild an of January 3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0% 31,2005 00 00 00 00 00 00						

NHGRI Quarterly Progress Report for Production

NHGRI Quarterly Progress Report for Finishing

2. Products of Sequencing	Currulative total as of October 31, 2004	Month 1 (November 2004)	Meeth 1 Meeth 2 Meeth 2 Meeth 2 (January Joseph 2004) (January Joseph 2004)		Month 2 Month 3 (December 2004) (January 2005)		Three month total for November 1, 2004 - January 31, 2005	Cumulative total as of January 31, 2005			
a. Whole-Genome Activities5			PLEASE DE	PLEASE DESCRIBE THE PREFINISHING ACTIVITIES AT YOUR CENTER IN A SEPARATE DOCUMENT							
Total # of pre-finished grade A reads 9	0	0	0	0	0	0					
Total # of pre-finished grade A bp 10	0	0	0	0	0	0					
Total # of pre-finished grade B reads 9	0	0	0	0	0	0					
Total # of pre-finished grade B bp 10	0	0	0	0	0	0					
Total # of whole genome finished bp	0	0	0	0	0	٥					
b. BAC-based Activities 11											
Total # of pre-finished grade A reads 9	0	0	0	0	0	0					
Total # of pre-finished grade A bp 10	0	0	0	0	0	0					
Total # of pre-finished grade B reads 9	0	0	0	0	0	0					
Total # of pre-finished grade B bp 10	0	0	0	0	0	0					
Total # of BAC-based finished bp	0	0	0	0	0	0					
3. Data deposits:	Cumulative total as of October 31, 2004	Month 1 (November 2004)	Month 2 (December 2004)	Month 3 (January 2005)	Three month total for November 1, 2004 - January 31, 2005	Cumulative total as of January 31, 2005					
a. Traces											
Total # of depositions in the NCBI trace repository or made otherwise publicly available	6,945,983	۰	12,553	2,673,670	2686223	9632206					
b. Finished sequence											
Total phase_2 sequence bp deposited in Gentlank	٥	0	0	0	0	0					
Total finished bp deposited in Gentlank	٥	0	٥	0	0	0					
Non-redundant finishedbp deposited in Genblank	0	0	0	0	0	0					
4. Coverage:	Cumulative total as of October 31, 2004	Month 1 (November 2004)	Month 2 (December 2004)	Month 3 (January 2005)	Three month total for November 1, 2004 - January 31, 2005	Cumulative total as of January 31, 2005					
Clone coverage12	16.952109	1.316466667	0.181723667	10.70590557	12.208096	29.160205					
Sequence coverage	1.555551645	0.00358517	0.00507542	0.609350109	0.619011699	2.175563344					

Production Information Captured in the NHGRI Progress Report

1A. Sequence Production:	Cumulat	ive total as of	October 31, 2	004	Month 1 (November 2004)					
Whole Genome	sm. ins. plasmid1	lg. ins. plasmid1	fosmid	BAC end	sm. ins. plasmid1	lg. ins. plasmid1	fosmid	BAC end		
# of reads attempted	7,756,592	0	0	215,424	0	0	0	32,448		
# of successful reads2	6,895,806	0	0	99,126	0	0	0	19,747		
Pass rate3	88.9%			46.0%				60.9%		
Average read length4	669.5	0.0	0.0	532.2	0.0	0.0	0.0	544.7		
Total # of Q20 bases5	4,616,742,117	0.0	0.0	52,754,857	0	0	0	10,755,511		
# of clones with two successful end reads6	3,177,884	0	0	36,391	0	0	0	7,089		
Total # of clones attempted7	4,020,880	0	0	107,701	0	0	0	16,224		
Paired end rate13	92%	0%	0%	73%	0%	0%	0%	72%		

Finishing Information Captured in the NHGRI Progress Report

Cumulative total as of October 31, 2004	Month 1 (November 2004)			
6,945,983	0			
0	0			
0	0			
0	0			
	Cumulative total as of October 31, 2004 6,945,983 0 0 0 0	Cumulative total as of October 31, 2004 Month 1 (November 2004) 6,945,983 0 0 0 0 0 0 0 0 0 0 0		

Production and Finishing Statistics are used to calculate costs



The report also captures other activity costs. These costs are used to determine what percentage of the budget is used to support non-sequence related activities

All costs listed below are those not attributed to sequence production (shotgun and finishing) described on the previous worksheet.									
TECHNOLOGY DEVELOPMENT COSTS (incl new technologies developed elsewhere; impler etc.; excluded are costs spent on methods impl throughput, quality, and or de	udes all costs spent nentation/testing of r rovement aimed at in	on adaptation of new protocols, ncreasing	BIOINFORMATICS DEVELOPMENT COSTS (incli development of improved bioinformatics methods, e software and development of production software; e "routine" assembly	BIOINFORMATICS DEVELOPMENT COSTS (includes all costs related to the development of improved bioinformatics methods, e.g. assembly algorithms, annot software and development of production software; excluded are costs associated v 'routine' assembly					
Technology Development Cost Totals	\$ 640,894		Bioinformatics Development Cost Totals	s	1,649,481				
% of Total Costs	3	.70%	% of Total Costs	9.	53%				
MAPPING COSTS (includes all costs related to	the generation of fi	ingerprint maps)	OTHER COSTS (include all other costs for which N accounted for in the activities listed on this sheet or coordination costs and outreach costs); this does no Action	HGRI funds are use elsewhere (e.g. cor bt include funds for t	d which are not nmunity he Minority				
Mapping Cost Totals	s	803,739	Other Cost Totals	\$	775,583				
% of Total Costs	4	.65%	% of Total Costs	4.	48%				



NHGRI costs are used to figure the costs for other collaborators who access the GSC for sequencing work like Bio 4342

The GSC provides: Production Sequencing Prefinishing Finishing Analysis to collaborators at the university and outside the university

Production Company Cost by David Number in L disasting									
Total Number of 354 well trays									
Total Number of 95 well trays		_						_	
Total Number of Subclores		_			-			+	
One End Total Bouches of Davids		1		1	-	1		4	1
Total Number of Passion Reads					-			+	
Percent Success		015				90%	901	5	90%
Cost per read	\$ 0.	70	\$ 1	3.70	5	0.70	\$ 0.70	D.	\$ 0.70
Total Cost for Sequencing Reads	ş -		\$	-	\$		s -		\$.
Production Sequencing Cost by Read Number in 2 directions									
Total Number of 354 well trave									
Total Number of Subclores		Т			1			Т	
Two Ends		2		2		2		2	2
Total Number of Reads		_		-	_			4	
Total Number of Passing Reads				-	-	-		+	
Vercent Success	6 0	25		1 20	6	0.70	5 0.7		5 0.70
Total Cost for Sequencing Reads	\$.		\$		5	-	\$	1	\$ -
Production Sequencing Cost by Sequence Coverage									
Production - Development Costs									
Development - Fosmid libraries									
uevelopment - uost/Fosmid library Development - Total Cost for Fosmid Libraries	s 1,000.	20	s 1.00	2.00	5	1,000.00	5 1,000.00	4	5 1.000.00
Development - WGS libraries		_		-				-	
Development - Cost/WGS library	\$ 600.	00	\$ 60	00.0	\$	600.00	\$ 600.00	5	\$ 600.00
Development - Total Cost for WGS libraries	á .		5		5		4 .	Τ	ş .
Development - Clone-based libraries (BAC/fosmids)	_	_		_	_			-	
Development - Cost/Clone-based library	\$ 300.	00	\$ 30	0.00	\$	300.00	\$ 300.00		\$ 300.00
Development - Total Cost for Clone-based libraries	· · · ·	_	,	-	15			-	
Development - Cost/Read	\$ 2.	00	\$	2.00	5	2.00	\$ 2.00		\$ 2.00
Development - Total Cost/Read	ś .		\$		5		4 .		s .
Total Develoment Costs	s -		\$		5		s -		ş .
Library Construction Costs									
Production - rosmo spranes	4 1.020	00	e 100	1.00	1	1 000 00	6 1 000 00		4 1 000 00
Production - Calif/rolimid lanary Total Resolution Exempt Library Cost	5 1,050	00	s 1,00		3	1,000.00	5 1,000,00	4	5 1,000,00
Production - WGS libraries				-				-	
Production - Cost/WGS library	\$ 600.	20	\$ 60	2.00	5	600.00	\$ 600.00	2	\$ 600.00
Total Production WGS Library Cost	s -		\$	-	\$		s -		ş -
Production - Clone-based libraries		-						-	
Production - Cost/Clone-based library Total Production Close based Library	\$ 310.	20	\$ 30	2.00	5	300.00	\$ 300.0	2	\$ 300.00
Total Production Library Construction Cost	1		5		5		8 -	T	4 -
Shotgun coverage - up to 7 kb									
Genome Size or Size of Clone									
Insert Size									
Prog. read margari (00)									
Resulting physical coverage		Т			1		-	Т	
Number of reads in DS						1.00			
Number of reads attempt.								1	
Cost per read	<u>s</u> 0,	60	\$	2.60	5	0.60	\$ 0.60	2	\$ 0.60
Shotows coverage - 7 to 10 kh		_	\$	-	1.5		s -	-	· ·
Genome Size or Size of Clone									
Insert Size									
Avg. read length (bp)									
Desired Seq coverage (X)					-		_	-	
Resulting physical coverage		-		-	-			+	
number of reads attempt				-	-			1	
Cost per read	\$ 0	60	5	0.00	5	0,40	\$ 0.64	2	\$ 0.60
Project Production cost	5	-	\$		5	-	\$.		\$.
Fosmid shotgun coverage		-		-	-			-	
Genome Size or Size of Clone									
Insert Size									
Perger reason and gen (very) Desired Sen coverage (X)									
Resulting physical coverage		Т			T -		-	Т	-
Number of reads in DS						1.1			
Number of reads attempt.								T	
Cost per read	\$ 0.	60	\$	2.60	5	0.60	\$ 0.65	4	\$ 0.60
Project Production cost			3	-	\$		3 .	-	· ·
Each project total	s .	1	\$		5		5 .	Т	s .
and the second se									

At any one time the GSC has several ongoing projects for both NHGRI and outside collaborators

All of the projects are tracked weekly to ensure they move quickly through the pipeline

This is the current list of projects.





The schedule of reads are turned into a report with Q20 bases for NHGRI. Goals are evaluated quarterly.



GSC Production

<u>2004</u>	<u>2005</u>	
3.1M	7.0M	Reads Per Month
770 bp	680 bp	Read Length
92%	92%	Percent Success
4	4	Managers
10	9	Coordinators
40	50	Technicians

Production Goals

New Sequencing Technologies

Decrease labor and supply costs

Lower amortized equipment costs

Production Projects

Alignment with prefinishing Mutational Profiling Increase in special projects Refine database tools Loss Prevention/Monitoring

GSC Prefinishing

40 MB per month 400 clones per month Prefinished 12 genome projects 1 manager 1 coordinator 8 technicians



Prefinishing Goals

Increase Automation Complete Oracle Integration Increased role of freezer core Tools for whole genome projects Alignment of sorters with pathfinders

GSC Finishing

50 MB per month 270 clones per month Finished 6 whole genome projects 4 managers 1 assistant coordinators 40 finishers

Finishing Goals

Integration into Oracle db Implementation of automation Organization of finishing groups Improved draft sequence Map and sequence integration Decrease cost of a finished base