06/05/2012 - Tuesday				
Time	Туре	Abstract #	Title	Speaker
7:30 - 8:30am	Breakfast	x	La Fonda Breakfast Buffet	Sponsored by NEB
8:30 - 8:45	Intro	x	Welcome Intro from Los Alamos National Laboratory	TBD
x	Session Chair	x	Session Chairs	Chair - Johar Ali Chair - Donna Muzny
8:45 - 9:30	Keynote	FF0032	Towards the Perfect Genome Sequence	Dr. George Weinstock
9:30 - 9:50	Speaker 1	FF0119	Building the DOE Systems Biology Knowledgebase	Tom Brettin
9:50 - 10:10	Speaker 2	FF0106	Genome Sequencing of a Mapping Population Reveals Loss of Heterozygosity as a Mechanism for Rapid Adaptation in the Vegetable Pathogen Phytophthora capsici	Joann Mudge
10:10 – 10:30	Break	x	Beverages and Snacks Provided	Sponsored by OpGen
10:30 – 10:50	Speaker 3	FF0159	Assembling with Longer Reads and Higher Depths	Jim Knight - Roche
10:50 – 11:10	Speaker 4	FF0122	Next Generation Sequencing Improvements	Haley Fiske - illumina
11:10 – 11:30	Speaker 5	FF0239	Using the Ion Torrent PGM for de novo Sequencing	Tim Harkins - LifeTech
11:30 – 11:50	Speaker 6	FF0038	Exploiting Single-Molecule Real-Time DNA Sequencing for Improved Genome Assembly and Methylome Analysis	Steve Turner - PacBio
11:50 - 12:40	Panel Discussion	x	Next Generation Sequencing Technology Panel Discussion	Chair - Bob Fulton Chair - Patrick Chain
12:40 – 2:00pm	Lunch	x	Coronado Lunch Buffet	Sponsored by illumina
x	Session Chair	x	Session Chairs	Chair - Alla Lapidus Chair - Bob Fulton
2:00 – 2:20	Speaker 7	FF0060	Ion Torrent Semiconductor Sequencing Allows Rapid, Low Cost Sequencing of the Human Exome	David Jenkins
2:20 - 2:40	Speaker 8	FF0209	En Route to the Clinic: Diagnostic Sequencing Applications Using the Ion Torrent	Donna Muzny
2:40 - 2:55	Speaker 9	FF0047	Next Generation Sequencing: Possible Application for Forensic DNA Analysis. What does the Person of Interest Look Like?	Tom Callaghan
2:55 – 3:10	Speaker 10	FF0136	Forensic DNA Standards for Next Generation Sequencing Platforms	Pete Vallone
3:10 – 3:30	Break	x	Beverages and Snacks Provided	Sponsored by OpGen
	Tech Time Talks (15 min each)	FF0149	Challenges in Genomic Cloud Computing	Daniel Bozinov
		FF0126	NGS for the Masses: Empowering Biologists to Improve Bioinformatic Productivity	Kashef Qaadri
		FF0070	The PerkinElmer Omics Laboratory	Todd Smith
		FF0120	The Best Finish First: Sequence Finishing with Whole Genome Mapping	Deacon Sweeney
3:30 - 5:50pm		FF0299	High Throughput Plasmid Sequencing with Illumina and CLC bio	Ajay Athavale
		FF0213a	Engineered Polymerases Provide Improved NGS Library Amplification and Enable Novel Sequencing Applications	Maryke Appel
		FF0144	Beyond Basic Target Enrichment: New Tools to Fuel Your NGS Research	Jennifer Carter
		FF0019	Better Computing for Better Bioinformatics	George Vacek
		FF0296	RAPID: Ultra High Throughput Sequencing Data Analysis for Quick Microbial Identification	Robert Yamamoto
6:00 – 7:30pm	Posters - even #s Meet & Greet Party	EVEN #s	Poster Session with Meet & Greet Party (Sponsored by Roche) Food & Drinks	Sponsored by Roche 6:00pm- 9:00pm
7:30 - 9:00pm	Posters - Odd #s Meet & Greet Party	ODD #s	Poster Session with Meet & Greet Party (Sponsored by Roche) Food & Drinks	Sponsored by Roche 6:00pm- 9:00pm
9:00 - bedtime	on your own	x	Night on Your Own - Enjoy!!!	x

06/06/2012 - Wednesday				
Time	Туре	Abstract #	Title	Speaker
7:30 - 8:30am	Breakfast	x	Santa Fe Breakfast Buffet	Sponsored by NEB
8:30 - 8:45	Intro	x	Welcome Back	TBD
x	Session Chair	x	Session Chairs	Chair - Mike Fitzgerald Chair - Tina Graves
8:45 - 9:30	Keynote	FF0043	Plague: A Highly Fit Clonal Pathogen Emerges and Shapes Human History	Dr. Paul Keim
9:30 - 9:50	Speaker 1	FF0101	Finishing and Special Motifs: Lessons Learned From CRISPR Analysis Using Next Generation Draft Sequences	Catherine Campbell
9:50 - 10:10	Speaker 2	FF0160	An Analysis of the Genomic Architecture at Risk Loci for SLE	Ward Wakeland
10:10 - 10:30	Speaker 3	FF0279	Resolve the Cancer Heterogeneity by Single Cell Sequencing	Xun Xu
10:30 - 11:00	Break	x	Beverages and Snacks Provided	x
11:00 - 11:20	Speaker 4	FF0075	Consed and BamView for Next-gen Sequencing	David Gordon
11:20 - 11:40	Speaker 5	FF0065	Integrating Data from Multiple Human Genome Sequencing Platforms and Bioinformatic Methods to Analyze their Error Profiles and Form Consensus Variant Calls	Justin Zook
11:40 - 12:00	Speaker 6	FF0088	One Chromosome, One Contig: Hybrid Error Correction and <i>de novo</i> Assembly of Single-Molecule Sequencing Reads	Sergey Koren
12:00 - 1:20pm	Lunch	x	New Mexican Lunch Buffet	Sponsored by Beckman Coulter
x	Session Chair	x	Session Chairs	Chair - Donna Muzny Chair - Johar Ali
1:20 - 1:40	Speaker 7	FF0108	Recent Advances in High-Throughput, Low-Latency Interfacing for Fast Scanning and Metrology in Genomics Applications	Scott Jordan
1:40- 2:00	Speaker 8	FF0186	Pilon Assembly Improvement Software	Bruce Walker
2:00 - 2:20	Speaker 9	FF0188	Putting the Pieces Together: From Assembly to Analysis	Sean Sykes
2:20 - 2:40	Speaker 10	FF0045a	Finding the Perfect Recipe for <i>de novo</i> Plant Genome Assembly: A Platform Bake-off	Dan Ader
2:40 - 3:00	Speaker 11	FF0170	Finished Prokaryotic Genome Assemblies From a Low-Cost Combination of Short and Long Reads	Shuangye Yin
3:00 - 3:20	Speaker 12	FF0211	Mercury: A Next Generation Sequencing Data Analysis and Annotation Pipeline	David Sexton
3:20 - 3:35	Speaker 13	FF0004	NCGR Informatics	John Chow
3:35 - 3:50	Speaker 14	FF0174	DTRA Algorithm Prize	Christian Whitchurch
3:50 - 5:15pm	Break & Round Table Discussion (Topics TBD)		Beverages and Snacks Provided for the Round Table  Topics TBD: attendees to select from a few choices the week before the meeting	x
5:45 - 8:00pm	Happy Hour	x	Happy Hour at Cowgirls Cafe - Sponsored by LifeTech - Map Will be Provided	Sponsored by LifeTech
8:00 - bedtime	on your own	x	Dinner and Night on Your Own - Enjoy!!!	x

06/07/2011 - Thursday				
Time	Туре	Abstract #	Title	Speaker
7:30 - 8:30am	Breakfast	x	Breakfast Buffet	Sponsored by NEB
8:30 - 8:45	Intro	x	Welcome Back	Chris Detter
x	Session Chair	x	Session Chairs	Chair - Patrick Chain Chair - Nadia Fedorova
8:45 - 9:30	Keynote	FF0042	Environmental Reservoirs of Human Pathogens: The Vibrio cholerae Paradigm	Dr. Rita Colwell
9:30 - 9:50	Speaker 1	FF0185	A Rapid Whole Genome Sequencing and Analysis System Supporting Genomic Epidemiology	Mike FitzGerald
9:50 – 10:10	Speaker 2	FF0173	Endosymbiont Hunting in the Metagenome of Asian Citrus Psyllid ( <i>Diaphorina citri</i> )	Surya Saha
10:10 - 10:30	Speaker 3	FF0221	SPAdes: A New Genome Assembly Algorithm and its Applications to Single-Cell Sequencing	Glenn Tesler
10:30 – 10:50	Break	x	Beverages and Snacks Provided	x
10:50 – 11:10	Speaker 4	FF0263	Assembly of Large Metagenome Data Sets Using a Convey HC-1 Hybrid-Core Computer	Alex Copeland
11:10 – 11:30	Speaker 5	FF0034	Metagenomic Assembly: Challenges, Successes, and Validation	Matt Scholz
11:30 – 11:50	Speaker 6	FF0208	Metagenomics for Etiological Agent Discovery	Matthew Ross
11:50 – 12:10	Speaker 7	FF0207	Nearly Finished Genomes Produced Using Gel Microdroplet Culturing Reveals Substantial Intraspecies Diversity within the Human Microbiome	Michael Fitzsimons
12:10 - 1:30pm	Lunch	x	La Fiesta Plaza Lunch	Sponsored by Agilent
x	Session Chair	x	Session Chairs	Chair - Mike Fitzgerald Chair - Alla Lapidus
1:30 - 1:50	Speaker 8	FF0006	Rapid Phylogenetic and Functional Classification of Short Genomic Fragments with Signature Peptides	Ben McMahon
1:50 - 2:10	Speaker 9	FF0229	PanFunPro: Pan-Genome Analysis Based on the Functional Profiles	Oksana Lukjancenko
2:10 - 2:30	Speaker 10	FF0114	Preparation of Nucleic Acid Libraries for Personalized Sequencing Systems Using an Integrated Microfluidic Hub Technology	Kamlesh Patel
2:30 - 2:50	Speaker 11	FF0142	Capturing Native Long-Range Contiguity by in situ Library Construction and Optical Sequencing	Jerrod Schwartz
2:50 - 3:10	Speaker 12	FF0256	Fosmid Cre-LoxP Inverse PCR Paired-End (Fosmid CLIP-PE), A Novel Method for Generating Fosmid Pair-End Library	Ze Peng
3:10 - 3:30	Speaker 13	FF0282	Automated Sequencing Library Preparation and Suppression for Rapid Pathogen Characterization	Todd Lane
3:30 - 3:50	Speaker 14	FF0109	Evaluation of Multiplexed 16S rRNA Microbial Population Surveys Using Ilumina MiSeq Platform	Julien Tremblay
3:50 - 4:00pm	Closing Discussions	x	Closing Discussions for General Meeting - Discuss Next Year's Meeting	Chair - Chris Detter
		x	Reminder for those interested there is a special Forensic's Session Friday from 8:00am - 12:30pm	x

06/08/2011 - Friday			Forensic Friday	
Time	Туре	Abstract #	Title	Speaker
7:30 - 8:30am	x	x	Breakfast on your own	x
8:30 - 8:35	Intro	x	Welcome Intro - Session Chair (LANL)	Cathy Clealand
8:35 - 8:45	Intro	x	Welcome Intro - Session Chair (US Army)	Ken Kroupa Jeff Salyards
8:45 – 9:05	Speaker 1	FF0047	Next Generation Sequencing; Possible Application for Forensic DNA Analysis. What does the Person of Interest Look Like?	Tom Callaghan
9:05 - 9:25	Speaker 2	FF0136	Forensic DNA Standards for Next Generation Sequencing Platforms	Pete Vallone
9:25 – 9:45	Speaker 3	FF0216	Short Tandem Repeat (STR) Analysis from Short Read Sequencing Data	Daniel Bornman
9:45 – 10:05	Speaker 4	FF0191	High Sensitivity Detection and Typing of Mixed Contributor DNA Samples Using Massively-Parallel Deep Amplicon Pyrosequencing	Jared Latiolais
10:05 – 10:20	Break	x	Break	x
10:20 - 10:40	Speaker 5	FF0114	Preparation of Nucleic Acid Libraries for Personalized Sequencing Systems Using an Integrated Microfluidic Hub Technology	Ken Patel
10:40 – 11:00	Speaker 6	FF0223	Forensic Genomics using Next Generation Sequencing by Synthesis (SBS)	Cydne Holt
11:00 – 11:20	Speaker 7	FF0153	A Highly Configurable SNP Caller for the Ion Torrent Personal Genome Machine	Christian Buhay
11:20 - 11:40	Speaker 8	FF0248	Short Tandem Repeat Sequencing on the 454 Platform	Melissa Scheible
11:40 - 12:00	Speaker 9	FF0280	STR Profiling From Personal Genomes: Happy Surprises	Yaniv Erlich
12:00 - 12:20	Closing Panel Discussions	x	Panel Discussion on Forensic Applications of Next Generation Sequencing (US Army and LANL)	Jeff Salyards Chris Detter
12:20 - 12:30	х	x	Thank you	Cathy Clealand