facilities and biomolecular resources. ABRF Affiliates are special interest organizations that are autonomous from the ABRF, have common and complementary interests with the ABRF, and have the goal of developing a collaborative relationship with the ABRF. Please join us for the ABRF Affiliates and Chapters Open Mic Session from 6:00 pm to 6:45 pm on Sunday.

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The Midwest Association of Core Directors

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The Midwest Association of Core Directors (MWACD) was organized in 2010 by a group of scientists at 6 different institutions to foster closer interactions among directors and managers of core facilities throughout the Central Plains. The organization shares the same goals as ABRF, and it has applied to become a chapter of ABRF. The MWACD differs from ABRF only in that its focus is on regional matters rather than on issues of national concern. Towards this goal, the first annual meeting of the MWACD took place on October 21–23, 2010, at the Crowne Plaza Hotel in Chicago. The goal of the meeting was to provide an opportunity for networking among core directors and managers, to enable interactions with colleagues, sharing of technical advice, and discussions of continuing challenges associated with the operation of shared research resources and technologies. Keynote presentations were delivered by leaders of NIH-NCRR and FASEB, and there were panel discussions on networking, bioinformatics, and information management systems. There was a poster session, vendor exhibits, and breakout sessions on 8 different core-related topics. The meeting was attended by 120 researchers and supported by 17 corporate and not-for-profit organizations.

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Automated Isolation of Genomic DNA from Large Volumes of Whole Blood

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A key source for genomic DNA(gDNA) is blood drawn into a standard 10mL Vacutainer® tube. The Promega ReliaPrep™ Large Volume HT gDNA Isolation Syste integrated on the Hamilton MICROLAB® STARplus liquid handling workstation provides a unique and dependable system for isolating genomic DNA from large volumes (3 mL–10 mL) of blood. The novel chemistry and instrumentation resolve many challenges encountered when processing large-volume samples in a high-throughput format such as: loss of sample pellets during decanting of fluids, transport of full 50 mL tubes to various locations on a liquid handling robot, and manual re-suspension of final DNA pellets. Liquid handler resource constraints were removed by creation of a new accessory, the ReliaPrep HSM 32 LV instrument, which provides heating, shaking and magneti-

this device, the MICROLAB STARplus workstation and the ReliaPrep Large Volume HT gDNA Isolation System allows automated recovery of pure gDNA from up to 96 ten milliliter blood samples within 8 hours. We present verification studies demonstrating automated system performance. Comparisons between the ReliaPrep™ Large Volume HT gDNA Isolation System and a standard precipitation-based method were made for duplicate blood samples from multiple donors. Yield, purity, and integrity of extracted gDNAwere assessed using UV absorbance spectroscopy and gel electrophoresis. Genomic DNA yields from normal 10 mL whole blood samples were 200 400 μg (depending on white blood cell count) in an eluted volume of 1mL. Recovered DNA exhibited good purity with A260/A280 ratios greater than 1.7 and A260/A230 ratios between 1.8 and 2.2. Isolated DNA was suitable for storage and was used in many downstream analysis applications. Results of genomic DNA purification from frozen (hemolysed) blood samples and blood collected using common anticoagulants (EDTA, heparin, citrate)are also compared to demonstrate the efficacy of the new system.

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Overview of the Agilent Technologies SureSelect™ Target Enrichment System

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Next-generation DNA sequencing has revolutionized the discovery of rare polymorphisms, structural variants, and novel transcripts. To meet the demand for fast, cost-effective, and accurate genome analysis methods from small scale studies to large sample cohorts, Agilent Technologies has developed the SureSelect™ Target Enrichment System. Available for the Illumina, SOLiD, and 454 NGS sequencing platforms, SureSelect is a highly robust, customizable, and scalable system that focuses analyses on specific genomic loci by in-solution hybrid capture. In addition, Agilent has introduced SureSelect XT for Illumina and SOLiD, which combines gDNA prep, library prep, and SureSelect Target Enrichment reagents in one complete kit. Both SureSelect and SureSelect XT demonstrate high performance, as measured by capture efficiency, uniformity, reproducibility, and SNP detection. We highlight the utility of the SureSelect system across a wide range of target sizes and genome complexity using pre-designed catalog libraries targeting cancer gene sets, sequences encoding the kinome, and both human and mouse All Exon content. In addition, user-defined custom content can be easily developed using the Agilent eArray software with candidate variant coordinates as input. User-defined content can be manufactured on-demand as a custom SureSelect kit, or combined with pre-defined Agilent catalog content using the Plus option. We propose a novel approach for variant discovery - using SureSelect catalog designs to uncover candidate variants, followed by the design of smaller focused custom libraries for SNP validation and region profiling. By pooling many samples together per lane or slide,

validation across large sample cohorts with substantial cost savings. Accurate post target enrichment pooling is facilitated by the Agilent Bioanalyzer and QPCR NGS Library Quantification kits which ensure equal representation across samples. Further efficiencies are realized using the Bravo Automated Liquid Handling Platform to meet the need for parallel preparation of multiplexed libraries.

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Gene Synthesis: A Cost-Effective Alternative to Traditional Molecular Cloning

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Gene synthesis is the process of synthesizing a gene in vitro without the need for initial template. Contrary to what many researchers' beliefs, commercial gene synthesis service is quickly evolving to become a cost effective alternative to traditional cloning and other molecular biology procedures. The main reasons include: 1) Time savings: Traditional cloning involves a multi-step process that includes cloning strategy design, primer synthesis, PCR, gel extraction, bacteria transformation, and other complex steps. This process requires considerable amount of time and human resource that gene synthesis does not. 2) Cost savings: In most cases, it costs less to order a synthetic gene than it does to order oligos, cloning kits, and DNA sequencing services. 3) Enhanced DNA performance: Gene synthesis allows for codon optimization which has been proven to increase the efficiency of protein expression. 4) Convenience: Without the need for a physical template and without design restrictions associated with the traditional cloning process, a researcher can get a gene of his/her choice by simply supplying the nucleotide sequence or amino acid sequence. GENEWIZ is a global CRO that provides a wide range of DNA services, including gene synthesis. GENEWIZ's gene synthesis service features a 2-3 week turnaround and expert technical and project management support. This informational poster will present case studies of how GENEWIZ's gene synthesis service benefited researchers who had previously relied on traditional molecular cloning for plasmid construction.

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Nucleotide-Level Variant Analysis of Next-Generation Sequencing Data Using a Cloud-Based Data Analysis Pipeline

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To demonstrate the flexibility of a cloud-based solution for analyzing disparate sets of next-generation sequencing data, we looked at carefully chosen samples across different populations from the 1,000 Genomes Project (www.1000genomes.org) and conducted an extensive analysis on two Chinese populations, the "Chinese in Beijing" (CHB) and the "Chinese in metropolitan Denver" (CHD), each consisting of 28 exomes. Each dataset was uploaded into the system using raw data files acquired from the 1,000 Genomes Project. Using these data and a cloud-based data analysis pipeline, we performed a nucleotide-level variant analysis combined with [illegible] the two populations. To identify alleles that are significantly different across the two populations, a Pearson's chi-square test was applied, which resulted in a total of 1.5 Mio SNPs, of which 84 were non-synonymous with a p-value of less than 0.01. Interestingly, the genes associated with non-synonymous variants of the Chinese in metropolitan Denver population were enriched for biological annotations such as endocrine system disorder, metabolic disease, cardiac fibrosis, and inflammation (includes ZNF264, RPS6KA2, ROBO2, CRK, MUSK, CBL, CRK, and others). Furthermore, genes usually associated with liver injury were also identified for this population, suggesting the liver is exposed to toxic agents more so in this population compared to the CHB population. The observed genomic differences in these two different Chinese populations living in different parts of the world hint towards a potential link between nutrition and different diseases (e.g. heart disease or metabolic diseases). Using this analysis as a case study, we will demonstrate how a scalable computational infrastructure can provide researchers and sequencing service providers alike, a cost effective and secure cloud-based computing platform as a powerful and collaborative technology solution for large scale sequence data analysis and management.

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Genome Technology Center at the NYU Langone Medical Center: New Support for Clinical and Translational Science

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To significantly enhance support for clinical and translational research within the framework of its CTSI, the NYU Langone Medical Center consolidated the Microarray and DNA Sequencing Cores into a new Genome Technology Center, a shared resource overseen by the Office for Collaborative Science. The GTC's team of 4 technical personnel and one faculty level director assists >120 NYULMC laboratories in their basic, clinical and translational research. The Sequencing Unit operates 2 Illumina GAIIs, and a HiSeq sequencer will be added in Q1 2011. The GAII capacity is applied to research applications (ChIP-seq, small-RNA-seq and RIP-seq) and to identification of disease-related genome-level structure changes and correlates (e.g. RNA-seq of cancer transcriptomes). GTC also has a Roche GS FLX System (454) used for de novo sequencing of microbial species and for amplicon sequencing in clinical genetics, patient microbiome diversity, etc. The Microarray Unit operates Affymetrix GeneChip system and high-capacity QPCR (ABI 7900HT) with automated plate setup and loading for gene and microRNA profiling and for SNP genotyping in clinical genetics. The GTC cooperates closely with the newly established Center for Health Informatics and Bioinformatics (CHIBI) supported by the NIH/NCRR CTSA Award. CHIBI provides an HPC facility for sequencing and microarray data storage and offers a full range of informatics services. The GTC is committed to regional and nationwide collaborations with other Cores. GTC participates in the activities of the Genomic Analysis and Technology Excellence (GATE) Working Group of the Academy for [illegible]