Second WZW Meeting on Next Generation Sequencing

Date: Thursday, 12.03.2015, 09:00 – 14:30

Place: Lecture Hall 17 (HS17), Liesel-Beckmann-Straße (Hochfeldweg) 1, 85354 Freising → get there

Food and drinks are provided during coffee break and lunch (free of charge)

Time	Speaker	Affiliation	Title
09:00 – 09:25	**Christine Wurmser**	Animal Breeding (TUM)	Next-Generation-Sequencing at the WZW and its application in Animal Breeding
09:25 – 09:50	**Klaus Neuhaus**	ZIEL, Microbial Ecology (TUM)	High-throughput phenotyping using NGS
09:50 – 10:15	**Thilo Klütsch**	Agilent Technologies	Agilent Oligo Library Synthesis: Arrays and Beyond
10:15 – 10:45			**Coffee Break**
10:45 – 11:10	**Bernhard Busch**	GATC Biotech AG	PacBio and Illumina - sequencing Amplicons, Transcriptomes and Genomes
11:10 – 11:35	**Mariana Mondragón**	Cell Biology and Plant Biochemistry (UR)	Measuring differential gene expression in established and emerging plant models: from piece of cake to hard cookie
11:35 – 12:00	**Karl Kramer**	Proteomics and Bioanalytics (TUM)	Comparative transcriptome and proteome analysis of cancer cell lines
12:00 – 12:45			**Lunch**
12:45 – 13:10	**Karl Kugler**	Plant Genome and Systems Biology (HMGU)	The genome and transcriptome of bread wheat - Bioinformatics approaches for deciphering an allohexaploid cereal
13:10 – 13:35	**Manuel Spannagl**	Plant Genome and Systems Biology (HMGU)	The transPLANT infrastructure to manage, query and analyse NGS and variation data in plants
13:35 – 14:00	**Christina Wolf**	Genetics (LMU/Tübingen University)	How to hack an Illumina Genome Analyzer to quantify protein-DNA binding affinities
14:00 – 14:25	**Stefan Altmann**	Plant Systems Biology (TUM)	Cost efficient identification of binary interaction pairs by barcode tagged NGS
14:25 – 14:30			**Closing remarks**