**NGS Technical Training Workshop Agenda**

**2018**

**Professor Büttner**

|  |  |  |
| --- | --- | --- |
| **Timing** | **Session** | **Presenter** |
| **08:00 – 08:20** | **Arrival and refreshments** |  |
| **08:20 – 08:30** | **Welcome**   * Welcome and introductions * Aims of the workshop, review agenda * Housekeeping rules | S. Merkelbach-Bruse |
| **08:30 – 09:15** | **Molecular targets in NSCLC**   * Summarize the NSCLC treatment landscape and the shift towards personalized therapy * Describe the EGFR, ALK and ROS1 pathway and their roles as oncogenic drivers in NSCLC, highlighting TKI inhibition as a valuable treatment strategy | R. Büttner |
| **09:15 – 10:00** | **Perspectives on molecular testing in NSCLC**   * Discuss who, when and what to test for e.g. reflex testing for *EGFR* mutations, *ALK* and ROS1 rearrangements in all patients – which algorithm to follow? * Discuss optimal use of available tissue and option of cytology * Present an overview of the available testing methods | S. Merkelbach-Bruse |
| **10:00 – 10:45** | **NGS basics**   * Methdology of next generation sequencing * Introduction to enrichment technologies | C. Heydt |
| **10:45 – 11:00** | **Coffee break** |  |
| **11:00 – 11:30** | **Data evaluation and interpretation**   * Bioinformatic solutions for evaluation * Databases, variant annotation and reporting | S. Merkelbach-Bruse |
| **11:30 – 12:30** | Attendees split into two groups  **Group A: Labtour and hands-on part**  **Group B: Data evaluation of Challenging Cases** | R. Pappesch  M. Ihle |
| **12:30 – 13:15** | **Lunch** |  |
| **13:15 – 14:15** | Attendees split into two groups  **Group A: Data evaluation of Challenging Cases**  **Group B: Labtour and hands-on part** | M. Ihle  R. Pappesch |
| **14:15 – 15:00** | **NGS strategies for fusion and exon-skipping detection**   * Detection of rearrangements by hybrid-capture * Fusion probes and imbalance score * Detection of rearrangements by RNA sequencing | C. Heydt |
| **15:00 – 15:45** | **Determination of Tumor Mutational Burden**   * Tumor Mutational Burden as Biomarker for Checkpoint Inhibition * Exome Sequencing vs. Gene Cancer Panel | S. Merkelbach-Bruse |
| **15:45 – 16:15** | **Summary and Q&A session** | all |