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| Session/Day | Day1 (22th, Tue) | Day2 (23th, Wed) | Day3 (28th Mon) | Day4 (29th Tue) |
| Session1 | **Lecture 1** (KG)  Introduction of SVs and bulk genomics approaches | **Lecture 2** (KG)  Introduction of Strand-seq and single-cell genomics approaches | **Lecture and practice 3** (KG)  Interpretation of overview plot, identification of good quality libraries | **Bioinformatics practice 4**(HJ)  Software: Mosaicatcher  Data: Strand-seq  Mixture (VAF20% BM510)  WT 80 cells + BM510 20 cells  Goal: Find out subclonel SVs and cells in that subclones |
| Session2 | **Bioinformatics practice 1**(HJ)  Software: Delly  Data: WGS  RPE1 WT  BM510  Mixture (VAF 20% BM510)  Goal: Detect clonal and subclonal somatic SVs | **Bioinformatics practice 2**(HJ)  Software: Plotting pipeline  Data: Strand-seq  WT 25 cells  (20 good quality + 5 bad quality cells)  Goal: Make overview plot | **Bioinformatics practice 3**(HJ)  Software: BreakpointR  Data: Strand-seq  WT 20 good quality cells  Goal: Find breakpoint and explore it using UCSC genome browser | **Lecture 4** (WH)  Biological questions and new applications of Strand-seq  Evolution, inversion and TAD |

**Korbel Lab predoc course November 2019**

**Detecting genetic structural variation in the human genome in bulk experiments and single cells**