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| Background research: |  |  |
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| Data processing: |  |  |
|  | Quality check of samples: purity, donor |  |
|  | Raw data and processed data format |  |
|  | QC, Normalization |  |
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| RNA-seq analysis: |  |  |
|  | Data pooling, multiple donor normalization |  |
|  | Differential gene expression analysis |  |
|  | Signature gene identification |  |
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| Differential DNA methylation analysis: | |  |
|  | Data pooling, multiple donor normalization |  |
|  | Active regulatory region definition/ analysis |  |
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| Histone modification analysis: | |  |
|  | Data pooling, multiple donor normalization |  |
|  | Active regulatory region definition/ analysis |  |
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| Transcription factor binding site enrichment: | |  |
|  | Active region pooling from DNA me and histone modification |  |
|  | TF binding site definition |  |
|  | Enrichment analysis |  |
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| TFBS vs expression data comparison: | |  |
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| Correlation between recognized TFs and gene expression signature: | |  |