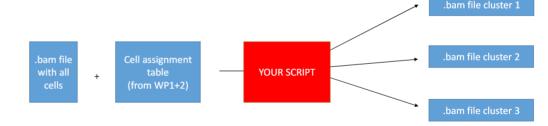
WP3

## Approach

- Obtain ATAC data per cluster
  - → .bam file with all cells + cell assignment table from WP 1+2
  - → bam files for each cluster
- Run TOBIAS footprinting for each cluster
- Comparison between clusters + normalization

## Splitting the .bam file into clusters

- Reads have barcodes
- Script to divide the file based on these bar codes and the assignment table
- Input:
  - ATAC of all cells (.bam)
  - barcodes and clusters (.tsv)
- Output: one .bam file per cluster



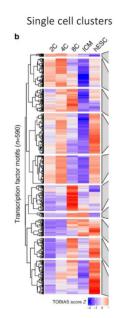
## Test data

158	A00519:269:H7FM2DRXX:1:2173:13060:9831 1187 s37d5 29406174 0 49M = 29406294 170 CTACTGTAGTAAAGGGAAATAACTTCATCTAAAAACCGAAACGGAAGCATT	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	BC:Z:GGTTGATG QT:Z:FF,FF:FF GP:i:983899088 MP:i:983899258 MQ:i:0 RG:Z:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:1	
159	A00519:269:H7FM2DRXX:1:2173:13060:9831 1107 s37d5 29406294 0 50M = 29406174 -170 AAACACACTTTCTGCAGAATCTGCAAGTGGATATTTGGACTTCTCTGAGG	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	CB:Z:AAACGAAAGCACGGT-1 BC:Z:GGTTGATG QT:Z:FF,FF:FF GP:i:983899258 MP:i:983899088 MQ:i:0 RG:Z:atac pbmc 10k v1:MissingLibrary:1:H7FM2DRXX:1	
160	A00519:269:H7FM2DRXX:2:2245:24117:20932 1123 s37d5 30061645 40 50M = 30061861 265 AGATATGTAAACGGCAGGAGATAGTAGGGAAACTGGACCCGTCTCCTCAT	
	:FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	CY:Z::F:FFFFFFF CB:Z:AAACGAAAGACACGGT-1 BC:Z:GGTTGATG QT:Z:FFFFFFFF GP:i:984554559 MP:i:984554824 MQ:i:45 RG:Z:atac pbmc 10k v1:MissingLibrary:1:H7FM2DRXX:2	
161	A00519:269:H7FM2DRXX:2:2245:24117:20932 1171 s37d5 30061861 45 49M = 30061645 -265 GGGACACTAAGAGCCCCAAAGGCCCCAAAGGACCCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCCAAAGGACCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCCCAAAGGACCACC	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	XA:Z:chr1,-147860177,49M,1;chr1,-143672664,49M,1;chr1,-147834056,43M6S,0;chr1,-143646568,43M6S,0; CR:Z:AAACGAAAGACACGGT CY:Z::F:FFFFFF CB:Z:AAACGAAAGACACGGT-1	
BC:Z:GGTTGATG OT:Z:FFFFFFF GP:i:984554824 MP:i:984554559 MO:i:40 RG:Z:atac pbmc 10k v1:MissingLibrary:1:H7FM2DRXX:2		
162	A00519:269:H7FM2DRXX:1:1228:22643:33191 147	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	CB:Z:AAACGAAAGACACGGT-1 BC:Z:GGTTGATG QT:Z:FFFFFFFF GP:i:985284650 MP:i:985284597 MQ:i:7 RG:Z:atac pbmc 10k v1:MissingLibrary:1:H7FM2DRXX:1	
163	A00519:269:H7FM2DRXX:1:1228:22643:33191 99	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	BC:Z:GGTTGATG QT:Z:FFFFFFF GP:i:985284597 MP:i:985284650 MQ:i:7 RG:Z:atac pbmc 10k v1:MissingLibrary:1:H7FM2DRXX:1	
164	A00519:269:H7FM2DRXX:1:1133:9064:13463 99 s37d5 31182129 0 50M = 31182130 50 GGGATGGAATGGGAAGGTGATCTTCCCCGGGAGCTTTGCCATCCAGAGGC	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	BC:Z:AAGCATAA QT:Z:FFFFFFF GP:i:985675043 MP:i:985675093 MQ:i:0 RG:Z:atac pbmc 10k v1:MissingLibrary:1:H7FM2DRXX:1	
165	A00519:269:H7FM2DRXX:1:1133:9064:13463 147 s37d5 31182130 0 49M = 31182129 -50 GGATGGAATGGGAAGATGATCTTCCCCGGGAGCTTTGCCATCCAGAGGC	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	BC:Z:AAGCATAA QT:Z:FFFFFFFF GP:i:985675093 MP:i:985675043 MQ:i:0 RG:Z:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:1	
166	A00519:269:H7FM2DRXX:1:1118:8205:32080 99 s37d5 34975365 60 50M = 34975558 242 CAGGAGCCCCGGGAATCTGGAGGGGCCGTGGGGCCGGGGCCTGC	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	BC:Z:CCCATCGC QT:Z:FFFFFFFF GP:i:989468279 MP:i:989468521 MQ:i:60 RG:Z:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:1	
167	A00519:269:H7FM2DRXX:1:1118:8205:32080 147 s37d5 34975558 60 49M = 34975365 -242 AAGTGGGGCCCGGGGAAGTCGCAGATGACTCGAGGTGACCGCGGCAGGG	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	BC:Z:CCCATCGC QT:Z:FFFFFFFF GP:::989468521 MP:::989468279 MQ:::60 RG:Z:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:1	
168	A00519:269:H7FM2DRXX:2:2161:31358:4163 77 * 0 0 * * 0 0 GTCCACGCACGCACGCCTGACACACACTTCCCTATTCGTAGACAACCCACATACA	
	FFF::FFFFFF,FFFF;FFFF,:FFF,:FFF,:FFF,:F	
	GP:i:-1 MP:i:-1 MQ:i:0 RG:Z:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:2	
169	A00519:269:H7FM2DRXX:2:2161:31358:4163 141 * 0 0 * * 0 0 CAAGACGCGATGTTACTGAGTTGTCTCGCGACATCGTAATAGTCCTCC	
	F:,F,FF,:,,,,,FF,:,CB:Z:AAAGAAAGACACGGT-1 BC:Z:CCCATCGC QT:Z:FFF,F:FF	
	GP:i:-1 MP:i:-1 MQ:i:0 RG:Z:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:2	
170	A00519:269:H7FM2DRXX:2:2170:32217:11600 77 * 0 0 * * 0 0 GTGATCCACGGAGGAGACACTCAGGCTGACTTTGTGTGTG	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	GP:i:-1 MP:i:-1 MQ:i:0 RG:Z:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:2	
171	A00519:269:H7FM2DRXX:2:2170:32217:11600 141 * 0 0 * * 0 GAGGTAAGGCCACAAAATATCCAGAGCCTTAATGACAACCATAATCACA	
	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	
	GP:i:-1 MP:i:-1 MQ:i:0 RG:2:atac_pbmc_10k_v1:MissingLibrary:1:H7FM2DRXX:2	

Bai code ctustei	
AAACGAAAGACACGGT-1	2
AAACGAAAGAGGTGGG-1	10
AAACGAAAGCACGTAG-1	14
AAACGAAAGCGCCTAC-1	3
AAACGAAAGCTTTCCC-1	2
AAACGAAAGGCGTCCT-1	1
AAACGAAAGGCTTTAC-1	4
AAACGAAAGTGATATG-1	14
AAACGAAAGTTTGGAA-1	2
AAACGAACAAACGACG-1	2
AAACGAACAATTGCCA-1	4
AAACGAACACCTCGTT-1	12
AAACGAACACGGTGTC-1	14
AAACGAACATCAGAAA-1	12
AAACGAAGTCAACTGT-1	6
AAACGAAGTGATTCCA-1	10
AAACGAAGTTTGACCA-1	11
AAACGAATCCAACGCG-1	2
AAACGAATCCATCTAT-1	2
	3
	11
AAACGAATCGCATAAC-1	11
AAACGAATCGGGACAA-1	9
AAACGAATCTGAACGT-1	2
AAACGAATCTGTCGTC-1	7
AAACTCGAGAAAGCAG-1	2
AAACTCGAGAGCTCCC-1	13
AAACTCGAGAGTGGTC-1	7
AAACTCGAGCGAATAT-1	4
AAACTCGAGCGTGTTT-1	9
AAACTCGAGGTACATA-1	2
AAACTCGAGTCGCGTC-1	4
AAACTCGAGTCTTAGC-1	4
AAACTCGAGTTCAAGA-1	12

## Running TOBIAS

- Requirements
  - bam files of each cluster
  - Depending on tool:
    - reference genome (.fasta)
    - peaks (.bed)
    - motifs (.pfm / .jaspar / .meme)
    - output of previous tools in the pipeline
- Main output: footprint score → heatmap to compare clusters



Transcription factors