

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:37:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818886.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1818886 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818886.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:37:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818886.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,383,355
Mapped reads	1,364,036 / 98.6%
Unmapped reads	19,319 / 1.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,586 / 1.49%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	214,842 / 15.53%
Duplication rate	13.02%
Clipped reads	1,379,176 / 99.7%

2.2. ACGT Content

Number/percentage of A's	36,657,721 / 29.06%
Number/percentage of C's	27,216,470 / 21.57%
Number/percentage of T's	35,704,048 / 28.3%
Number/percentage of G's	26,585,573 / 21.07%
Number/percentage of N's	1,798 / 0%
GC Percentage	42.64%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.5235
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2.4. Mapping Quality

Mean Mapping Quality	49.25
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2.5. Mismatches and indels

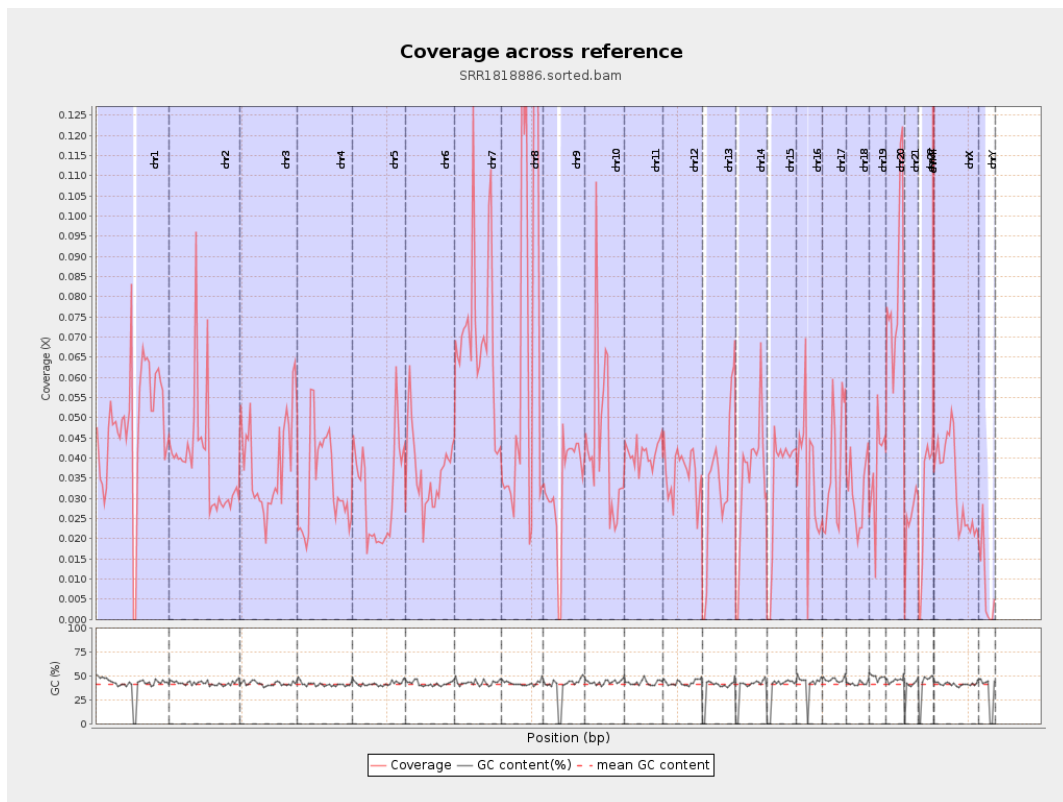
General error rate	0.64%
Mismatches	765,727
Insertions	17,519
Mapped reads with at least one insertion	1.24%
Deletions	40,871
Mapped reads with at least one deletion	2.93%
Homopolymer indels	41.75%

2.6. Chromosome stats

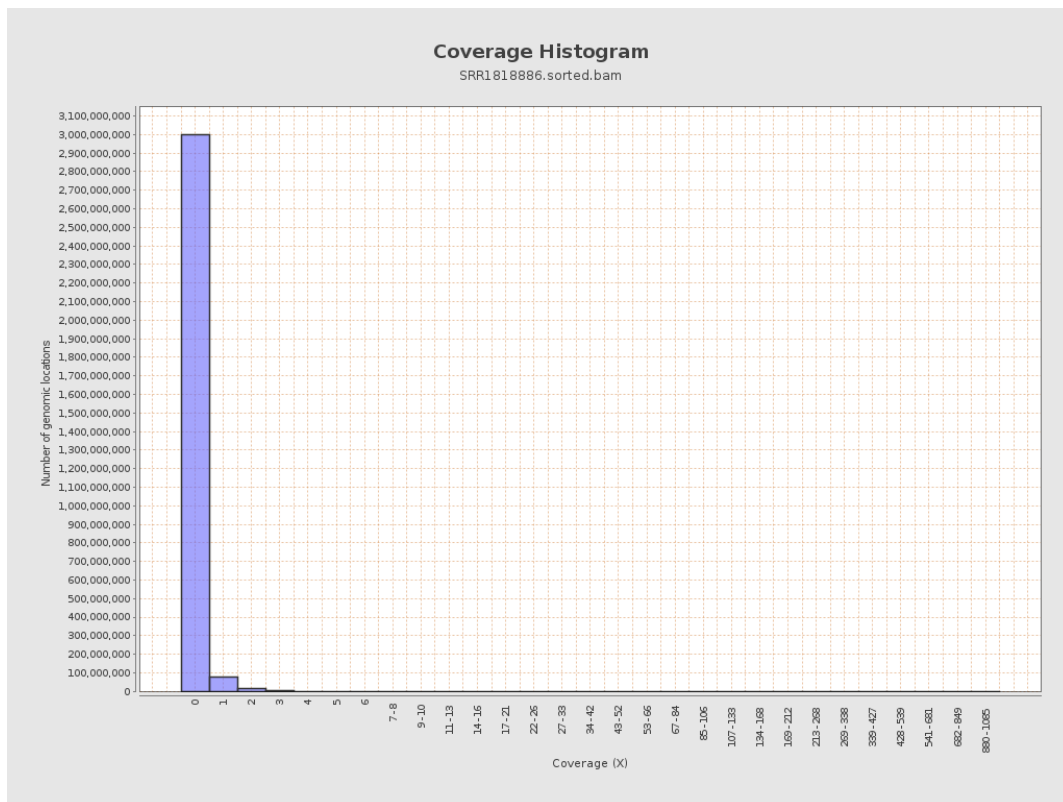
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11917275	0.0478	0.8333
chr2	243199373	9507060	0.0391	0.6976
chr3	198022430	7723839	0.039	0.243
chr4	191154276	6341651	0.0332	0.2944
chr5	180915260	5593310	0.0309	0.2308
chr6	171115067	6267383	0.0366	0.2653
chr7	159138663	11256974	0.0707	1.1791

chr8	146364022	11011615	0.0752	0.4263
chr9	141213431	4637672	0.0328	0.4319
chr10	135534747	5899477	0.0435	0.6861
chr11	135006516	5563476	0.0412	0.3187
chr12	133851895	4890593	0.0365	0.2394
chr13	115169878	3917157	0.034	0.2245
chr14	107349540	3763038	0.0351	0.2505
chr15	102531392	3484376	0.034	0.2245
chr16	90354753	3146678	0.0348	0.5168
chr17	81195210	3128005	0.0385	0.3196
chr18	78077248	2454243	0.0314	0.4981
chr19	59128983	2212066	0.0374	0.6936
chr20	63025520	5194608	0.0824	0.3801
chr21	48129895	1201930	0.025	0.2276
chr22	51304566	1460260	0.0285	0.2352
chrMT	16571	21340	1.2878	1.5319
chrX	155270560	5173302	0.0333	0.2887
chrY	59373566	477904	0.008	0.6048

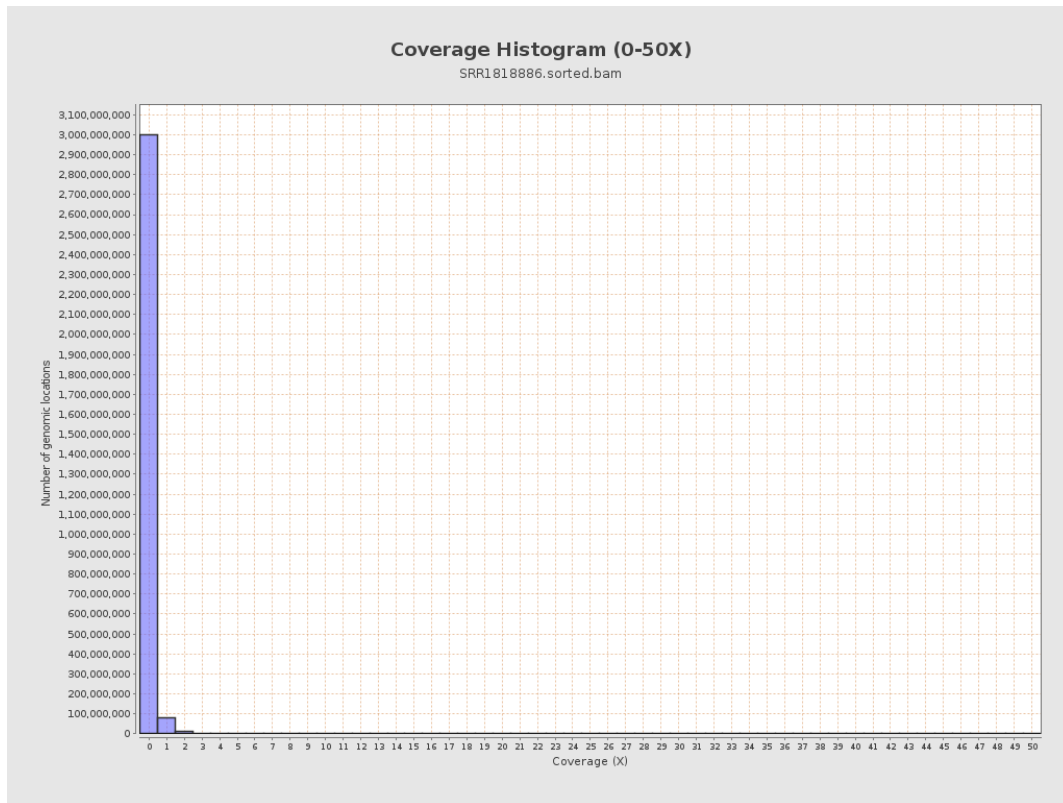
3. Results : Coverage across reference



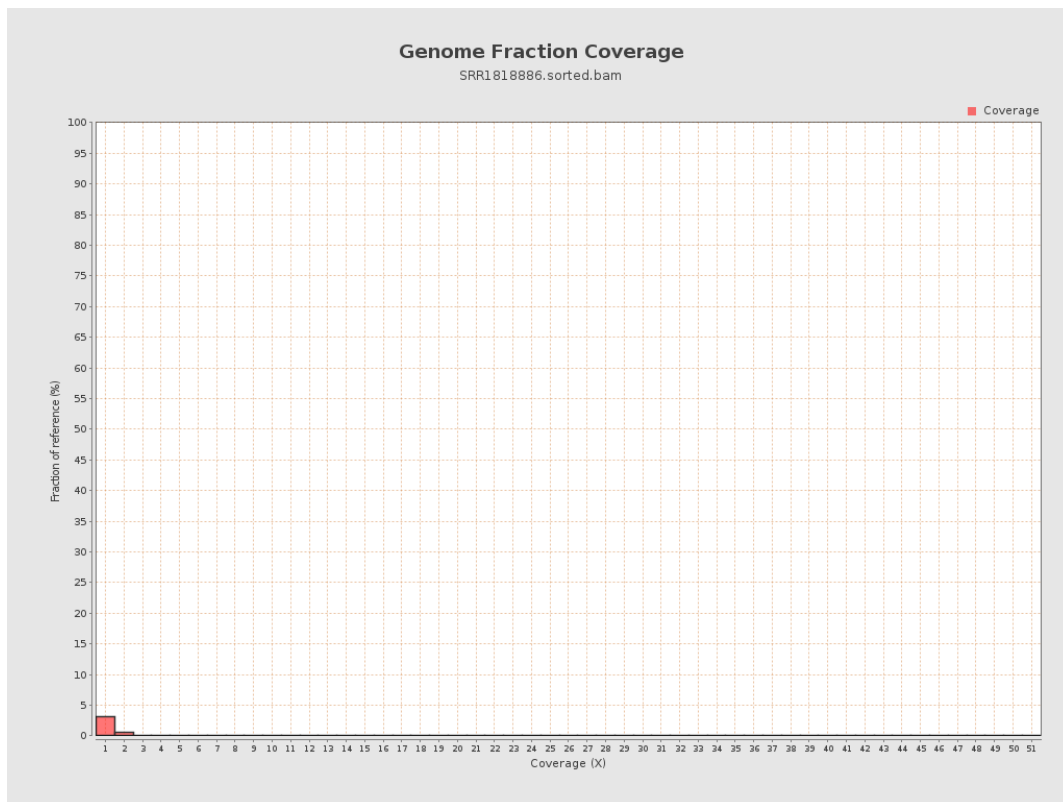
4. Results : Coverage Histogram



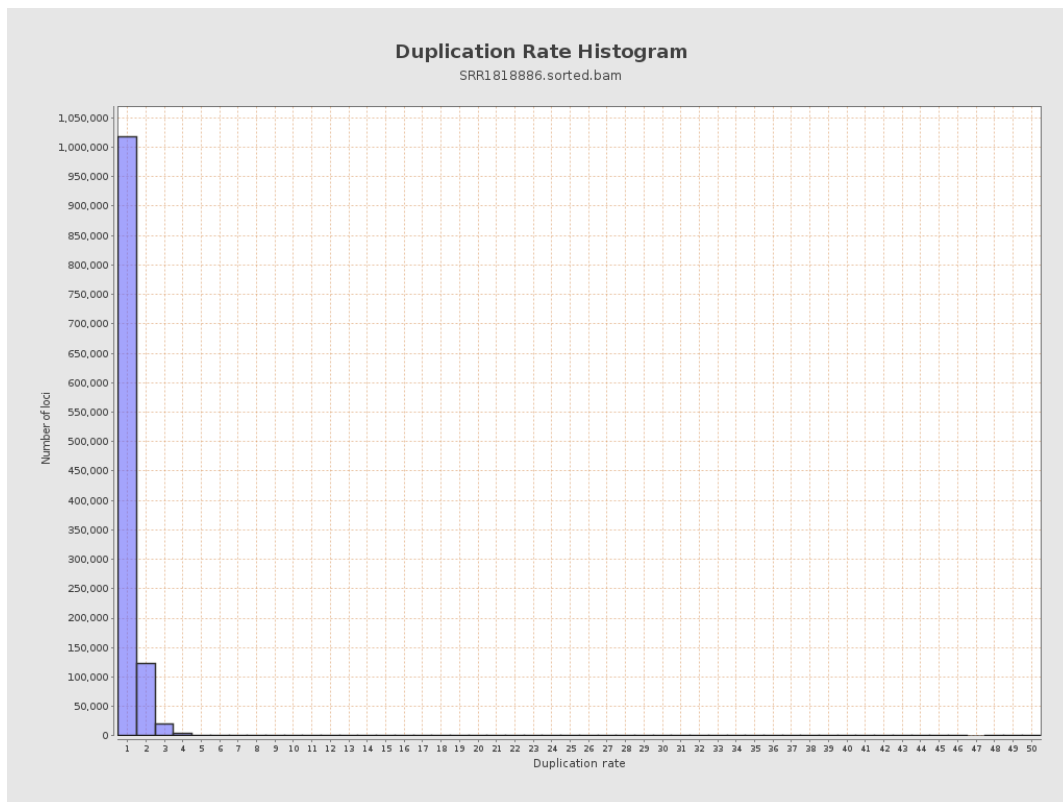
5. Results : Coverage Histogram (0-50X)



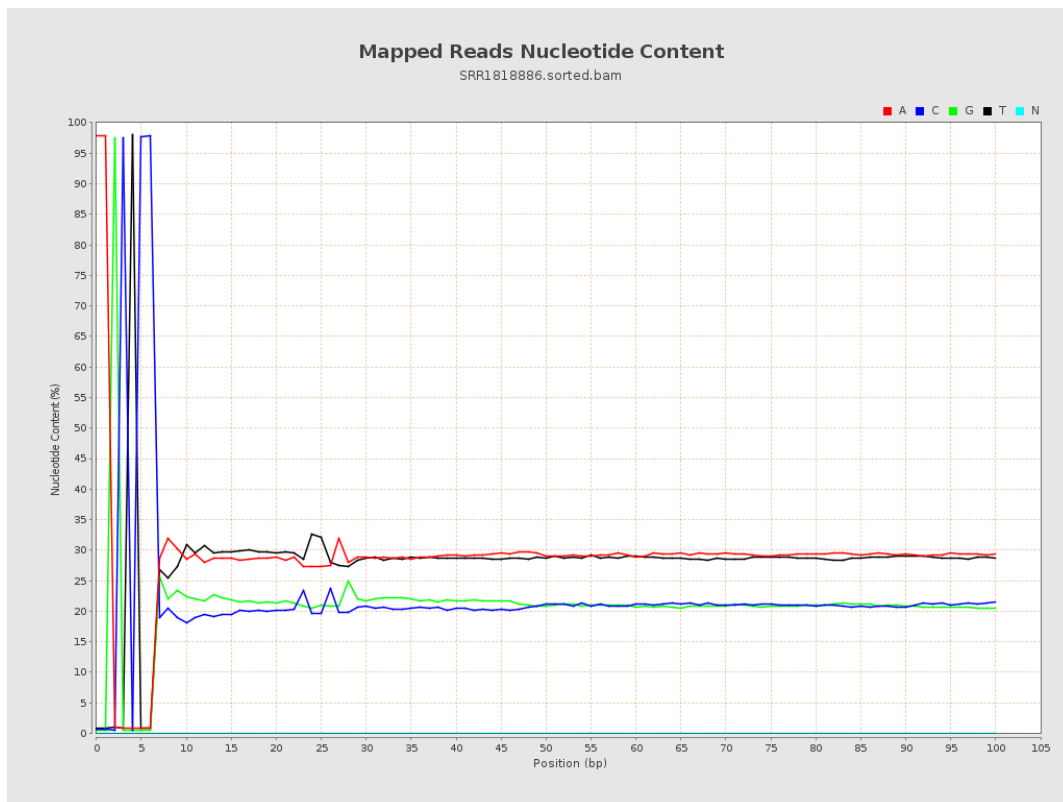
6. Results : Genome Fraction Coverage



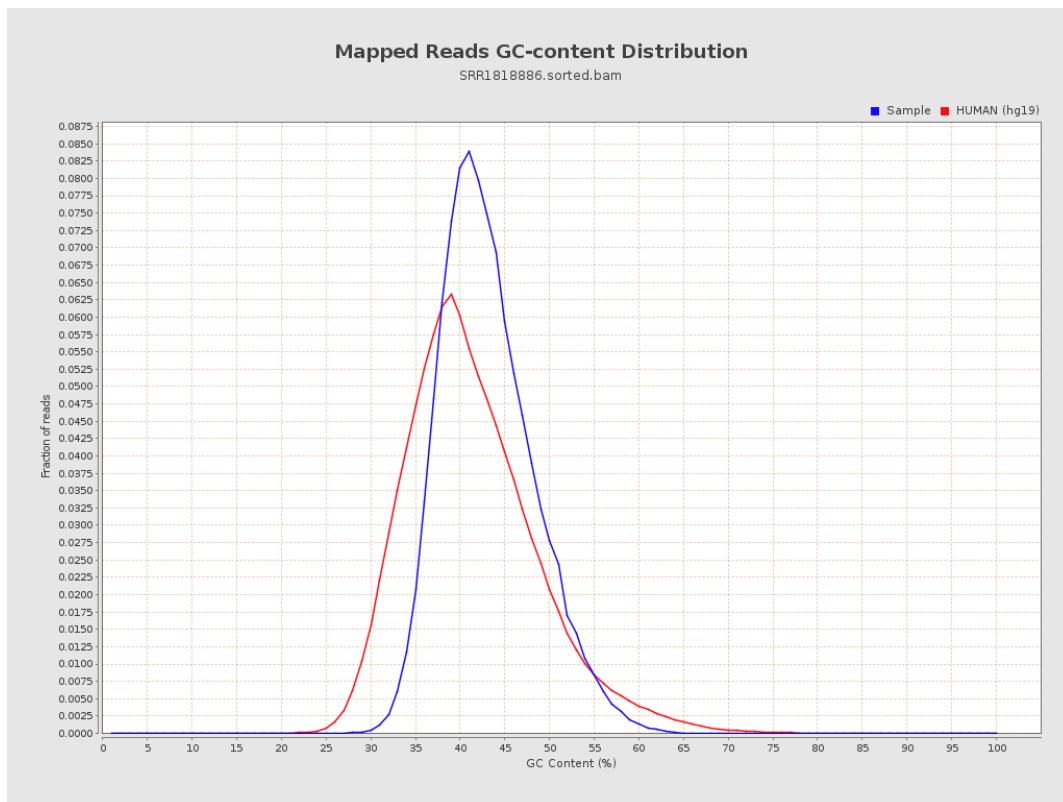
7. Results : Duplication Rate Histogram



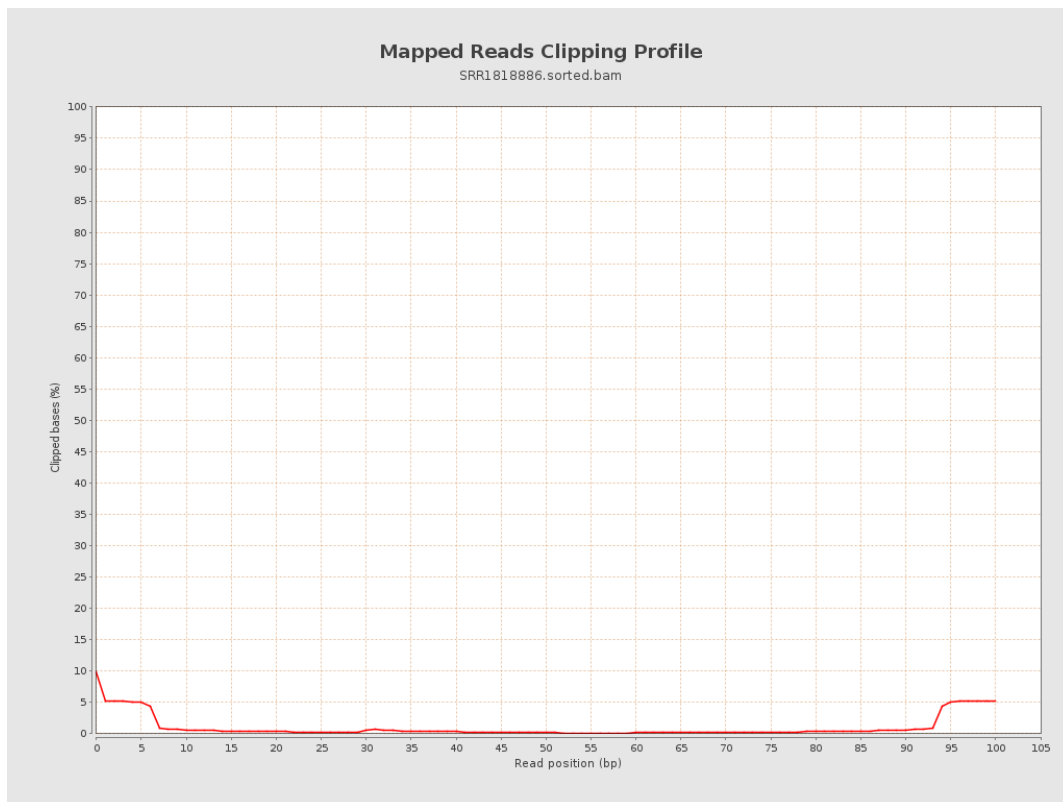
8. Results : Mapped Reads Nucleotide Content



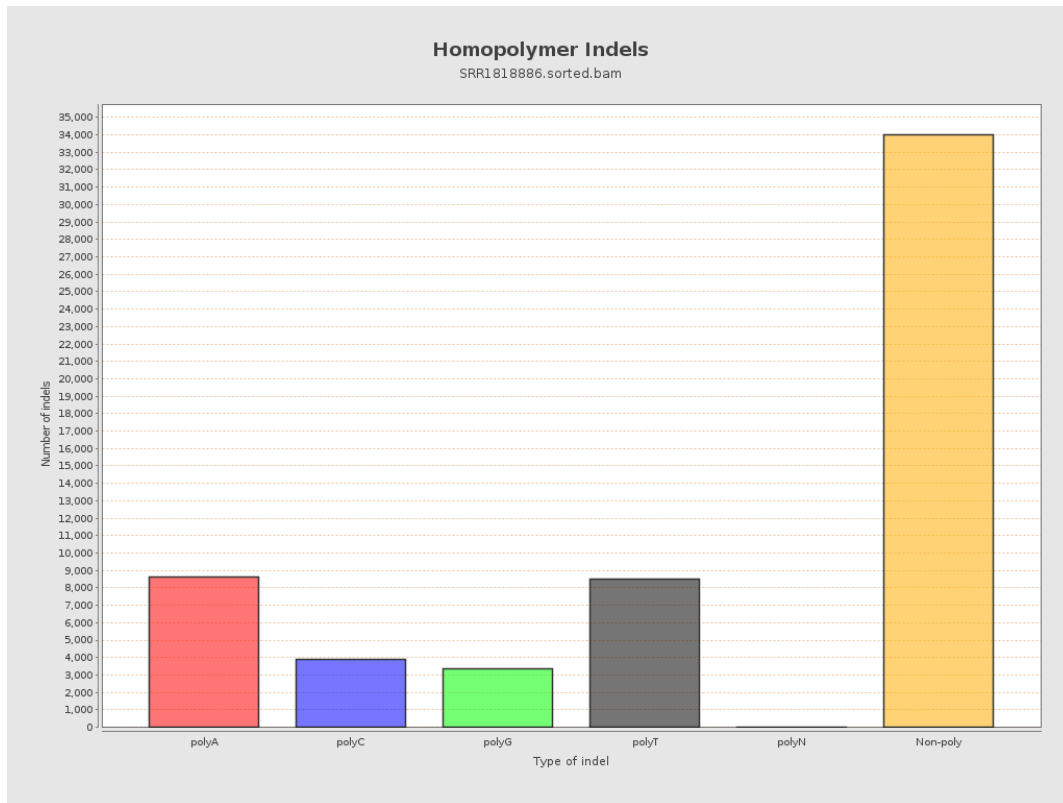
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

