

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:09:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084883.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_SRR3084883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084883.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:09:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,636,436
Mapped reads	2,350,078 / 89.14%
Unmapped reads	286,358 / 10.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,995 / 0.64%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	107,076 / 4.06%
Duplication rate	3.68%
Clipped reads	788,488 / 29.91%

2.2. ACGT Content

Number/percentage of A's	47,458,263 / 29.13%
Number/percentage of C's	29,907,630 / 18.36%
Number/percentage of T's	52,172,702 / 32.02%
Number/percentage of G's	33,348,535 / 20.47%
Number/percentage of N's	25,887 / 0.02%
GC Percentage	38.83%

2.3. Coverage

Mean	0.0526

Standard Deviation	0.4759
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2.4. Mapping Quality

Mean Mapping Quality	47.61
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2.5. Mismatches and indels

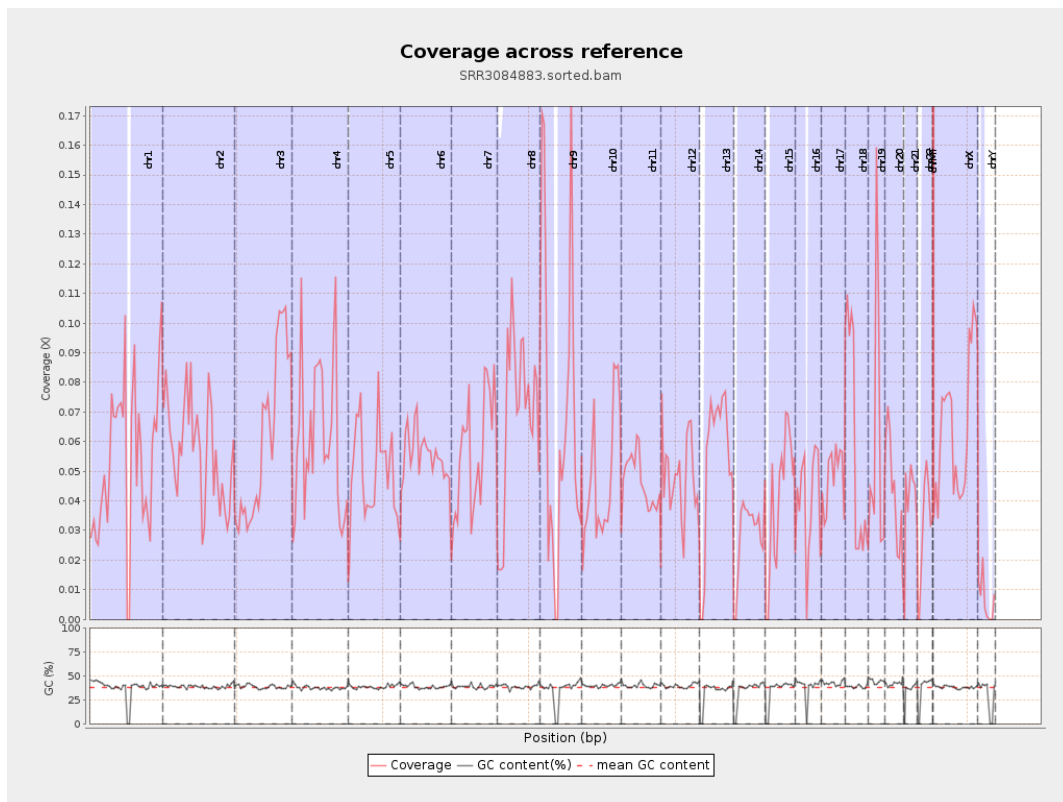
General error rate	0.84%
Mismatches	1,348,213
Insertions	13,280
Mapped reads with at least one insertion	0.56%
Deletions	35,118
Mapped reads with at least one deletion	1.48%
Homopolymer indels	48.23%

2.6. Chromosome stats

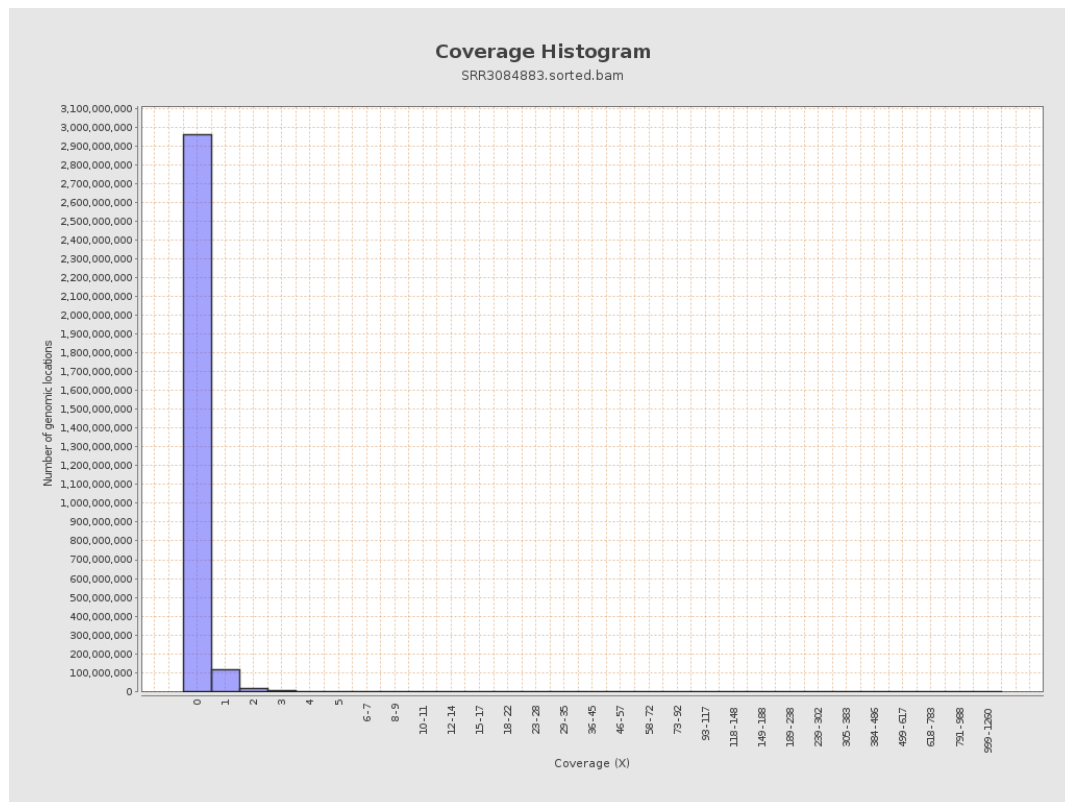
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13362580	0.0536	1.0398
chr2	243199373	13713776	0.0564	0.4217
chr3	198022430	12040748	0.0608	0.2848
chr4	191154276	11640347	0.0609	0.3028
chr5	180915260	8881733	0.0491	0.2759
chr6	171115067	9495270	0.0555	0.276
chr7	159138663	8943279	0.0562	0.4458

chr8	146364022	10173694	0.0695	0.8618
chr9	141213431	9688563	0.0686	0.4173
chr10	135534747	6396755	0.0472	0.3542
chr11	135006516	6282356	0.0465	0.343
chr12	133851895	6518993	0.0487	0.2575
chr13	115169878	6239486	0.0542	0.2668
chr14	107349540	3063874	0.0285	0.2082
chr15	102531392	4117339	0.0402	0.2294
chr16	90354753	3468917	0.0384	0.2497
chr17	81195210	3908013	0.0481	0.2687
chr18	78077248	4670978	0.0598	0.7415
chr19	59128983	3591448	0.0607	0.5881
chr20	63025520	2742900	0.0435	0.2572
chr21	48129895	1938388	0.0403	0.2555
chr22	51304566	1570242	0.0306	0.1982
chrMT	16571	119063	7.185	4.244
chrX	155270560	10013296	0.0645	0.3184
chrY	59373566	393345	0.0066	0.1596

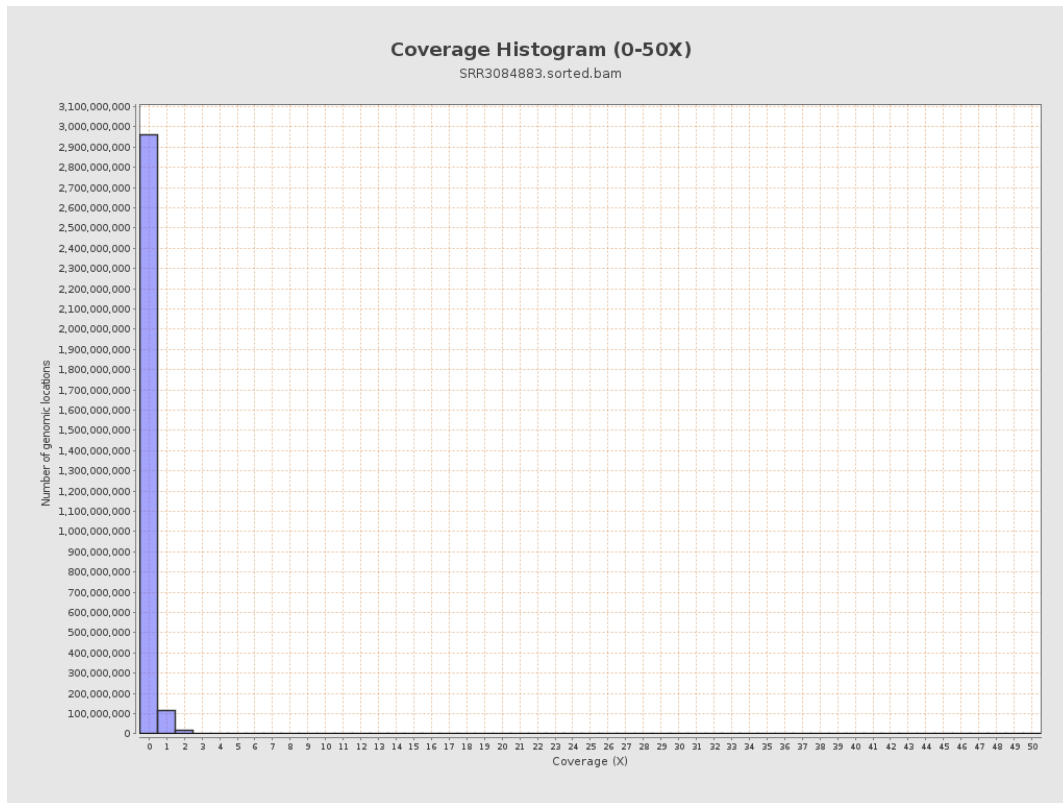
3. Results : Coverage across reference



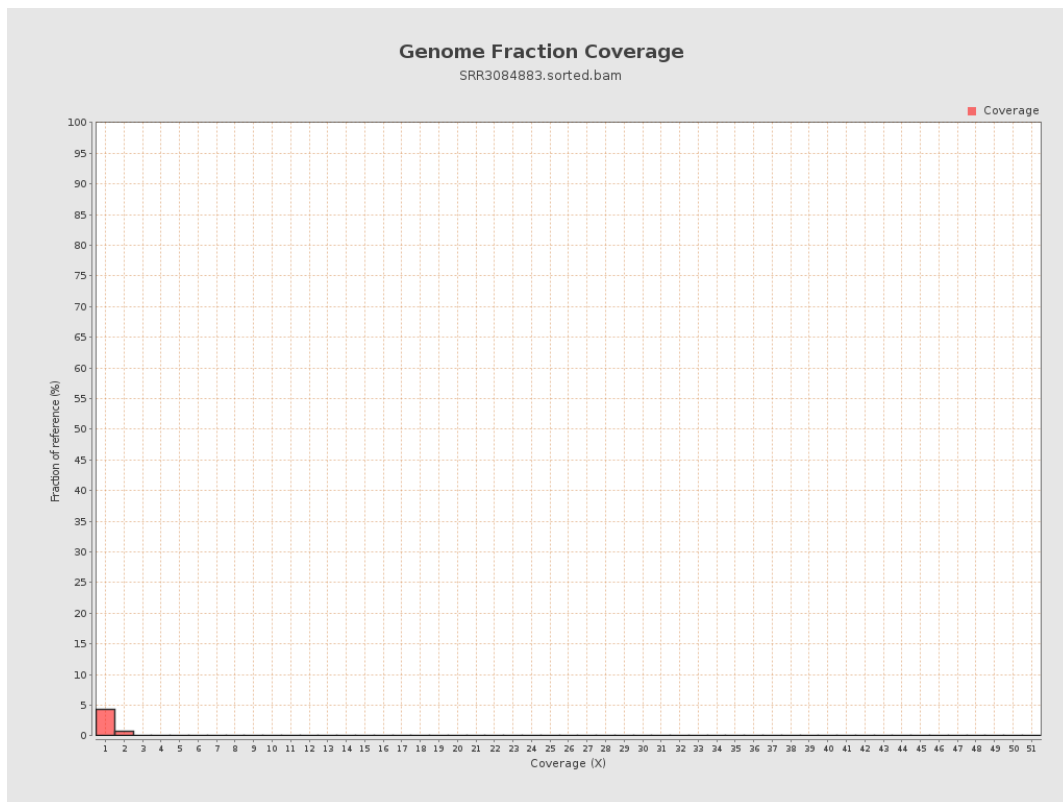
4. Results : Coverage Histogram



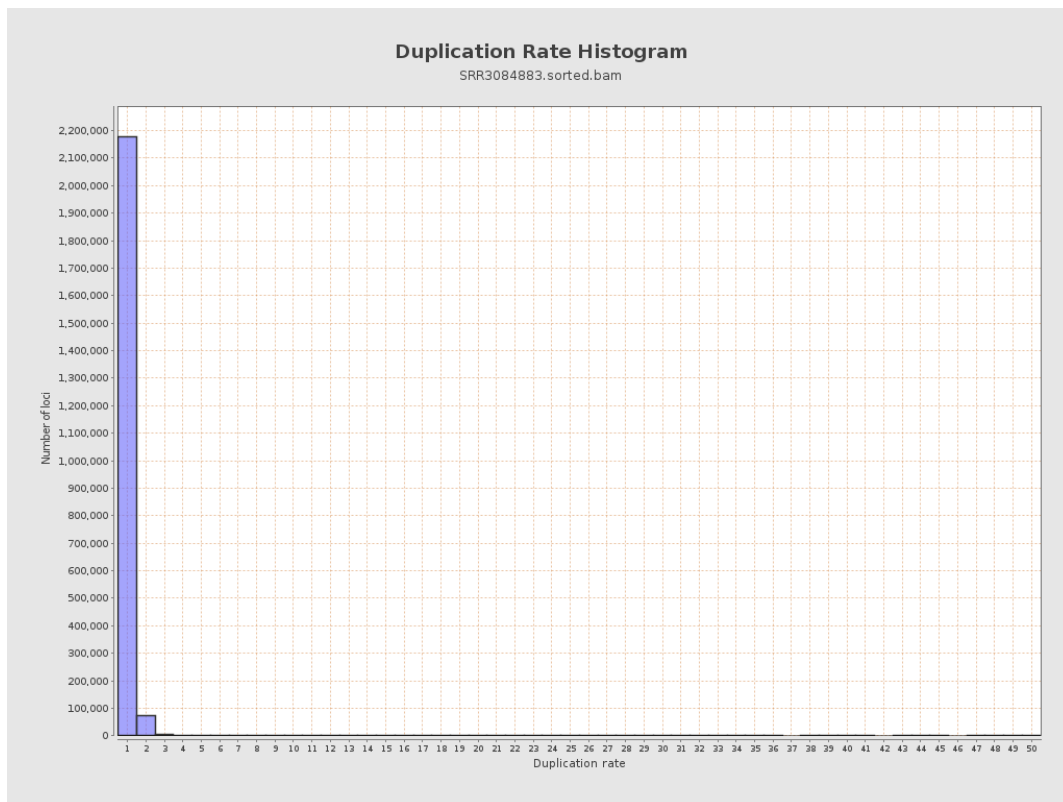
5. Results : Coverage Histogram (0-50X)



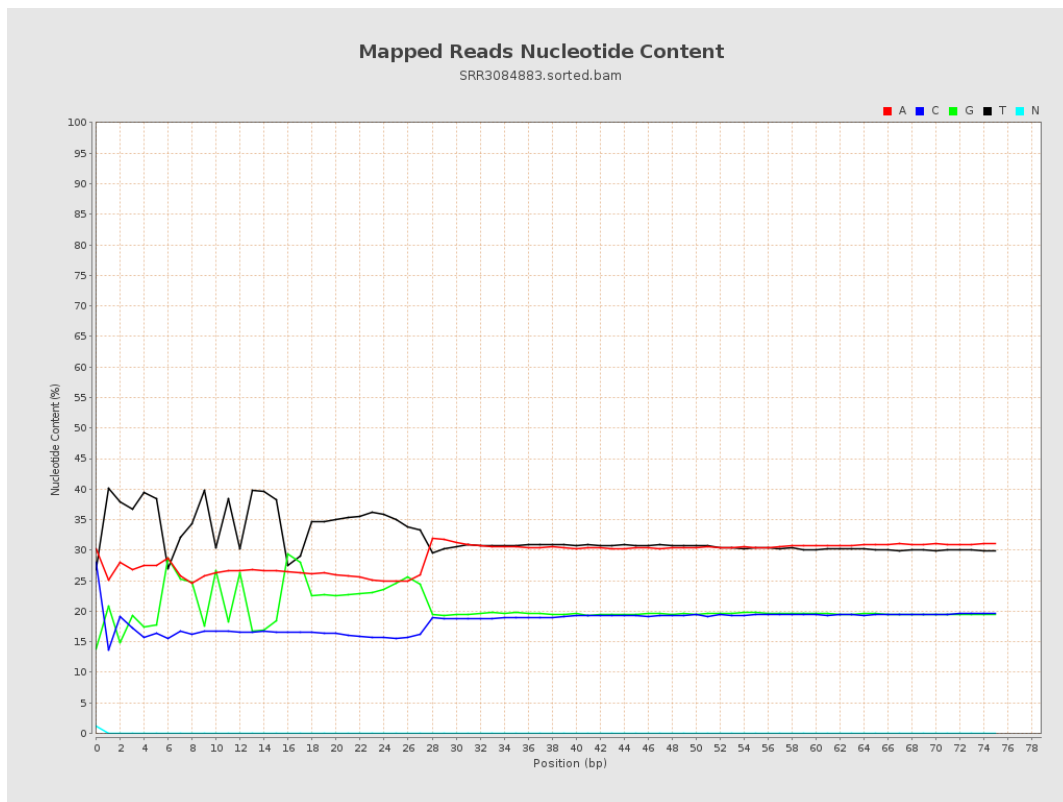
6. Results : Genome Fraction Coverage



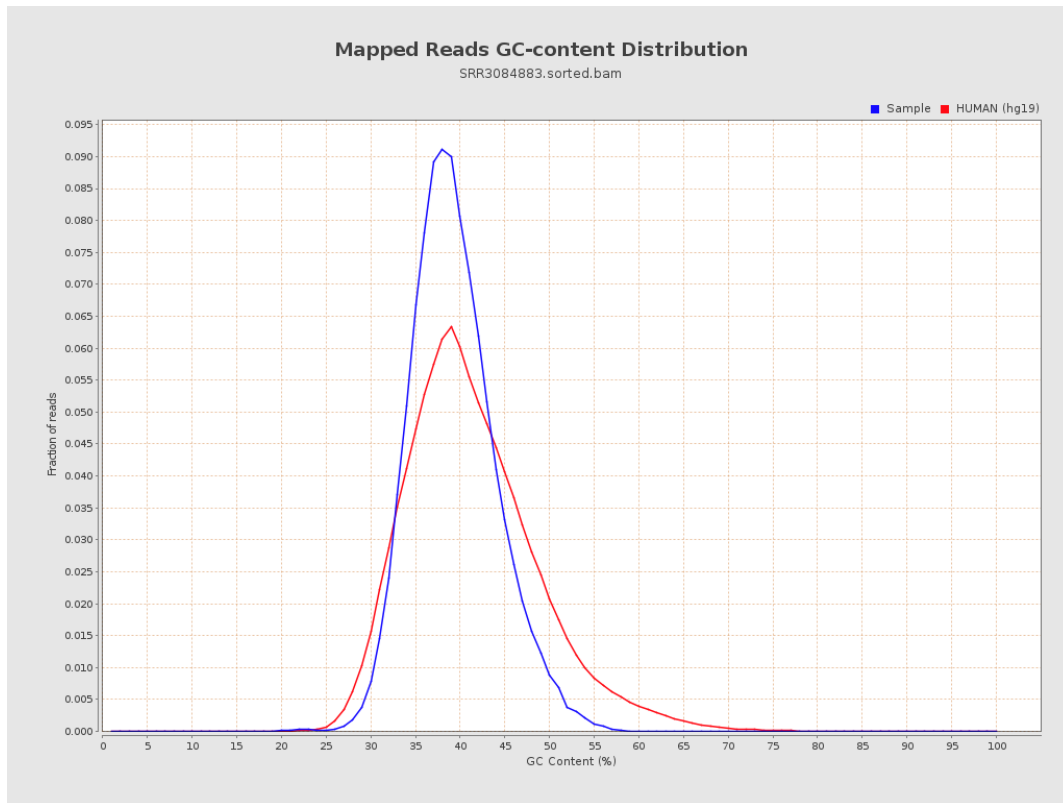
7. Results : Duplication Rate Histogram



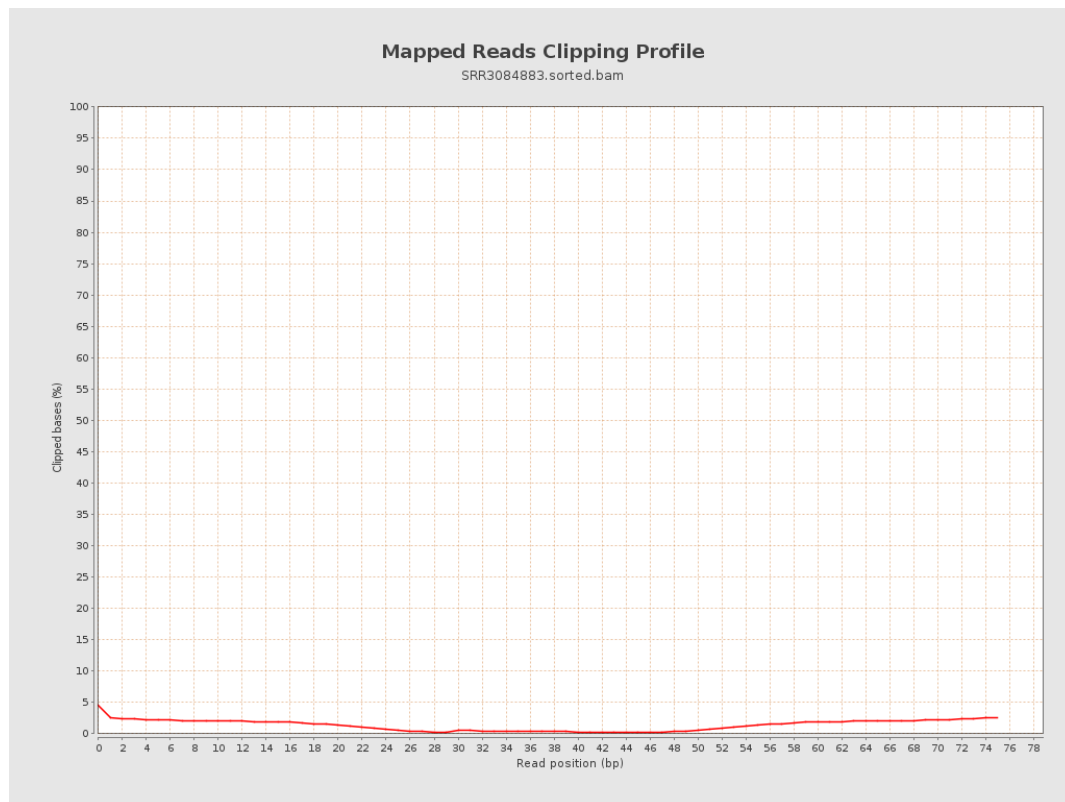
8. Results : Mapped Reads Nucleotide Content



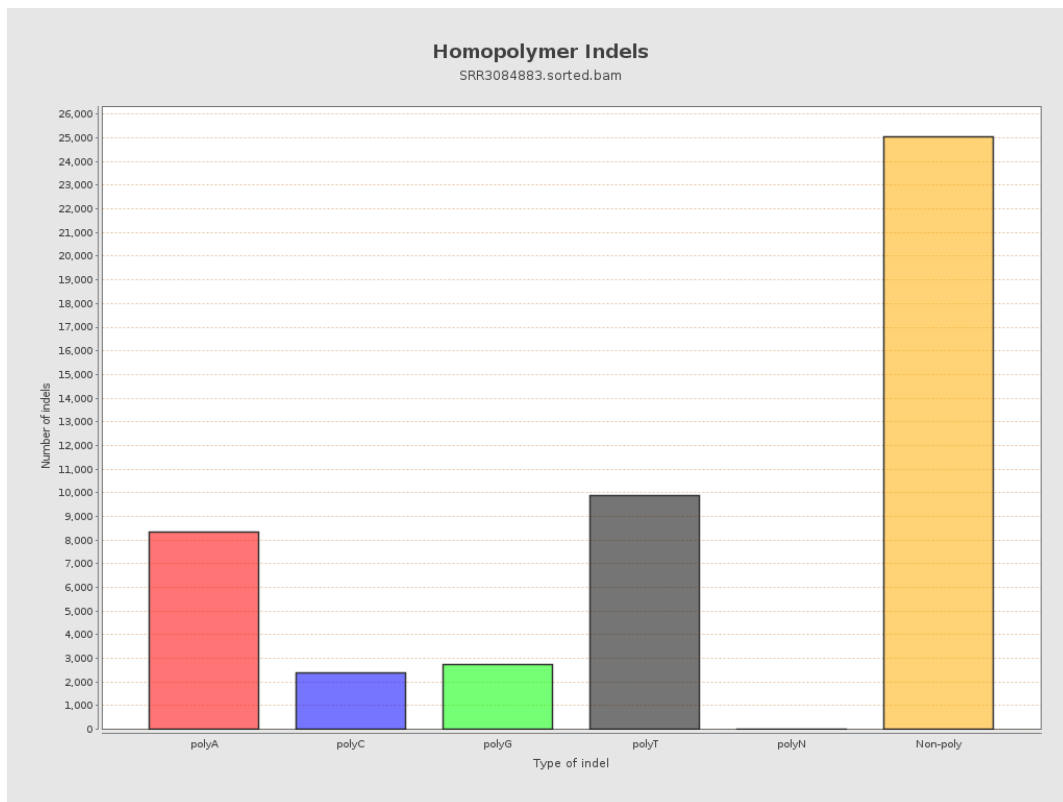
9. Results : Mapped Reads GC-content Distribution



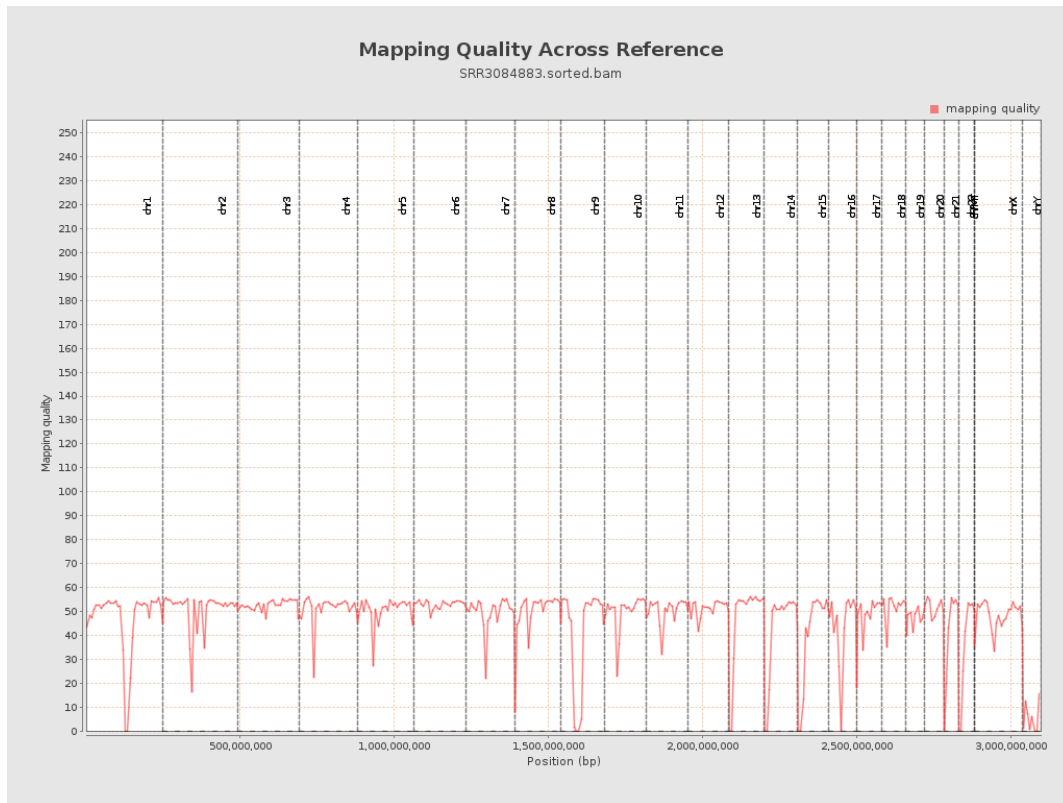
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

