Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 07:37:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083785.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_SRR3083785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083785.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 07:37:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,973,435
Mapped reads	3,120,921 / 78.54%
Unmapped reads	852,514 / 21.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,096 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	134,977 / 3.4%
Duplication rate	3.48%
Clipped reads	1,813,644 / 45.64%

2.2. ACGT Content

Number/percentage of A's	55,877,181 / 28.41%
Number/percentage of C's	37,789,604 / 19.22%
Number/percentage of T's	59,366,783 / 30.19%
Number/percentage of G's	43,618,191 / 22.18%
Number/percentage of N's	2,205 / 0%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0635

Standard Deviation	0.4206

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

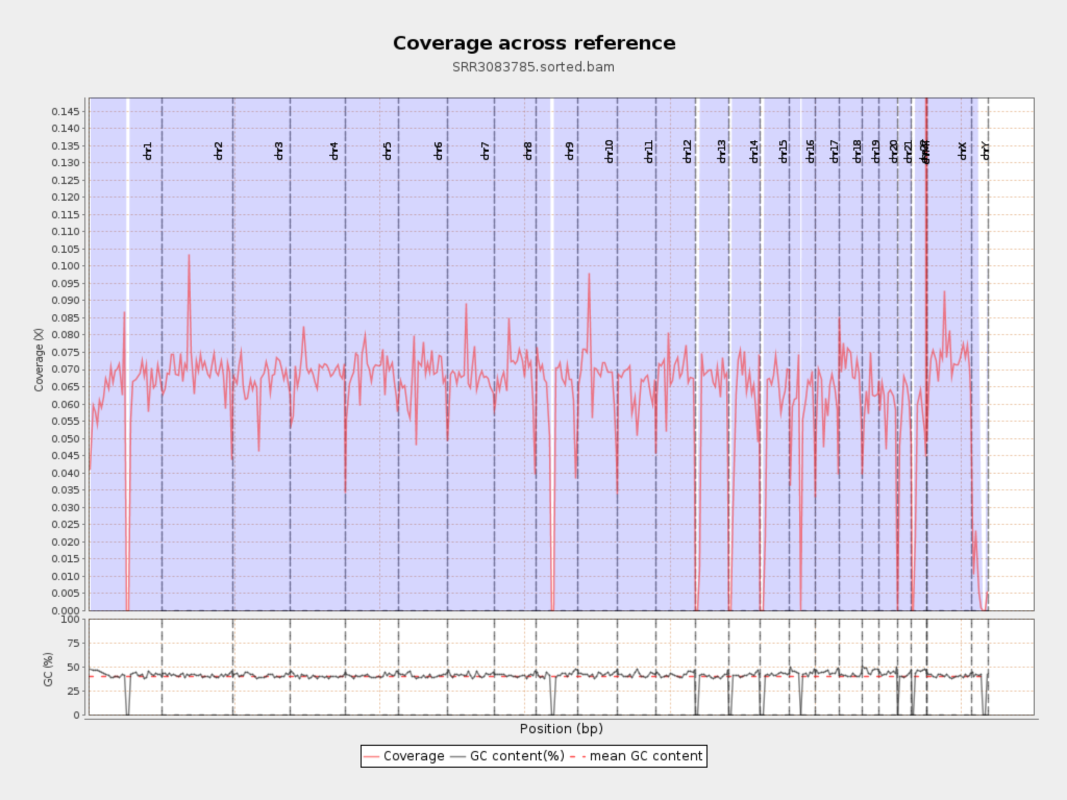
General error rate	0.85%
Mismatches	1,649,581
Insertions	14,704
Mapped reads with at least one insertion	0.47%
Deletions	40,476
Mapped reads with at least one deletion	1.29%
Homopolymer indels	45.53%

2.6. Chromosome stats

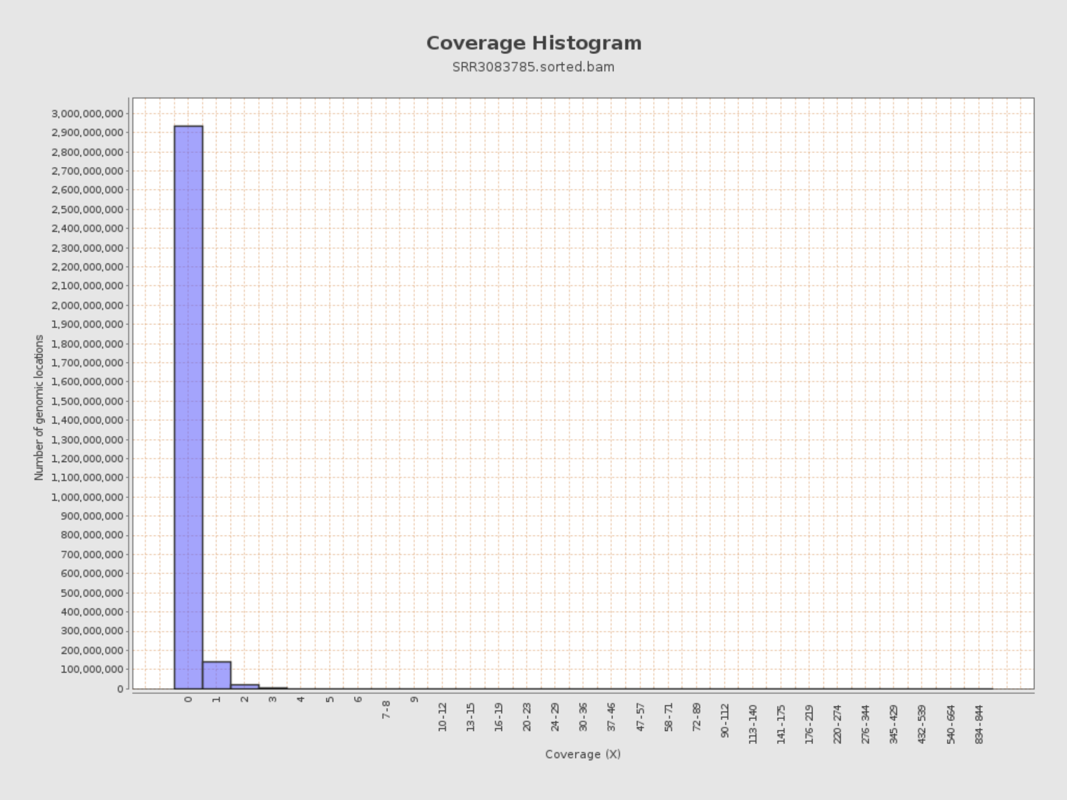
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15267284	0.0613	0.6169
chr2	243199373	17103515	0.0703	0.5681
chr3	198022430	13255891	0.0669	0.3006
chr4	191154276	13184608	0.069	0.3195
chr5	180915260	12511068	0.0692	0.3049
chr6	171115067	11574004	0.0676	0.3632
chr7	159138663	10907775	0.0685	0.5096

chr8	146364022	10047530	0.0686	0.4382
chr9	141213431	8248054	0.0584	0.4057
chr10	135534747	9490659	0.07	0.4465
chr11	135006516	8678498	0.0643	0.3673
chr12	133851895	9204940	0.0688	0.3086
chr13	115169878	6573259	0.0571	0.2806
chr14	107349540	5897654	0.0549	0.2978
chr15	102531392	5483499	0.0535	0.2807
chr16	90354753	5036132	0.0557	0.3167
chr17	81195210	4895324	0.0603	0.3207
chr18	78077248	5568527	0.0713	0.8284
chr19	59128983	3656409	0.0618	0.5074
chr20	63025520	3677753	0.0584	0.2958
chr21	48129895	2558318	0.0532	0.2833
chr22	51304566	2056120	0.0401	0.2322
chrMT	16571	67085	4.0483	3.0041
chrX	155270560	11299055	0.0728	0.3569
chrY	59373566	475154	0.008	0.1502

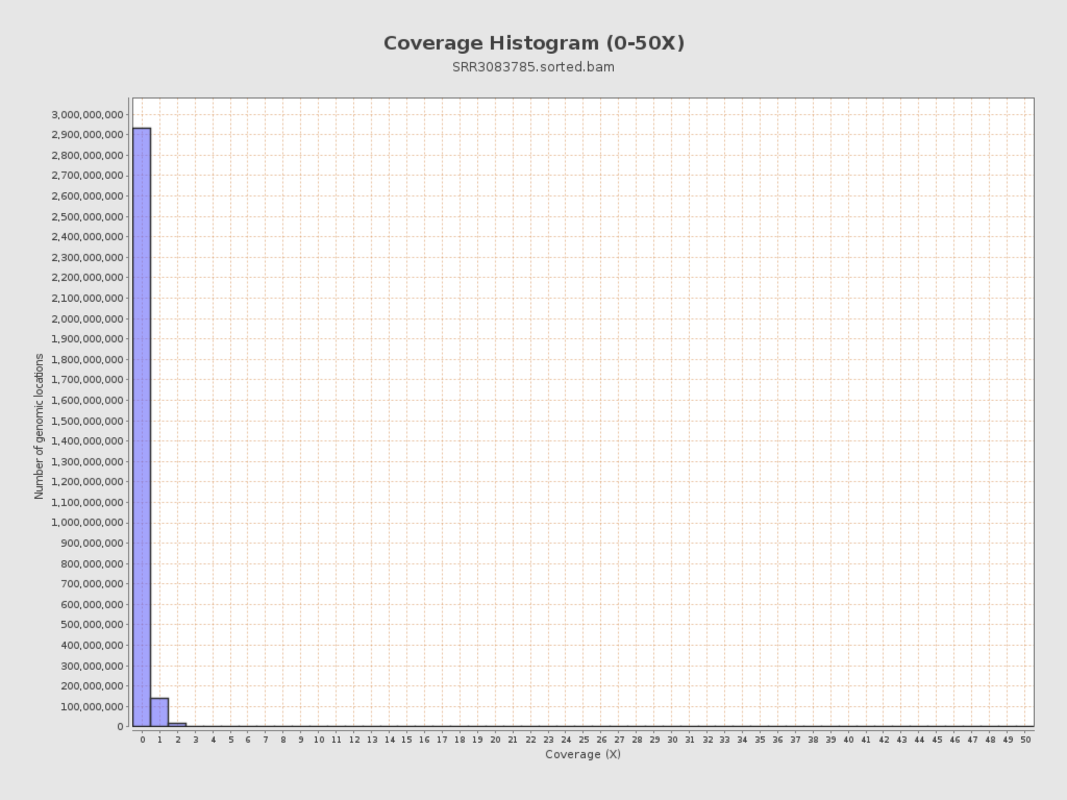
3. Results : Coverage across reference



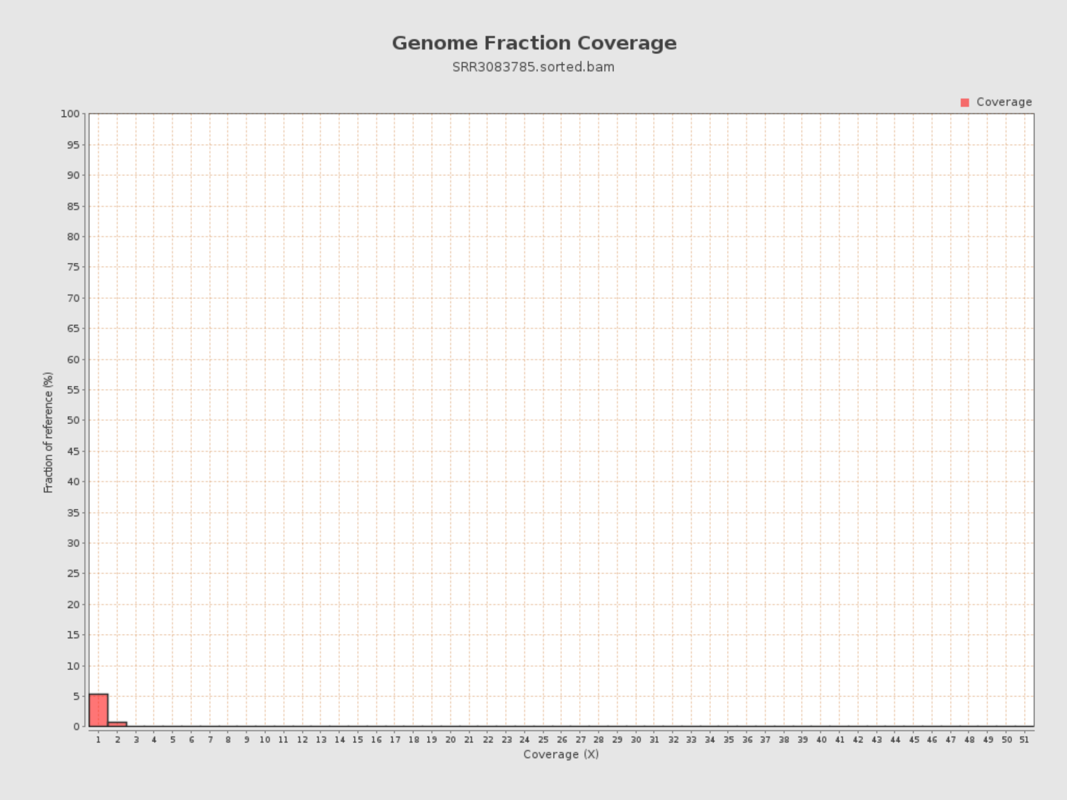
4. Results : Coverage Histogram



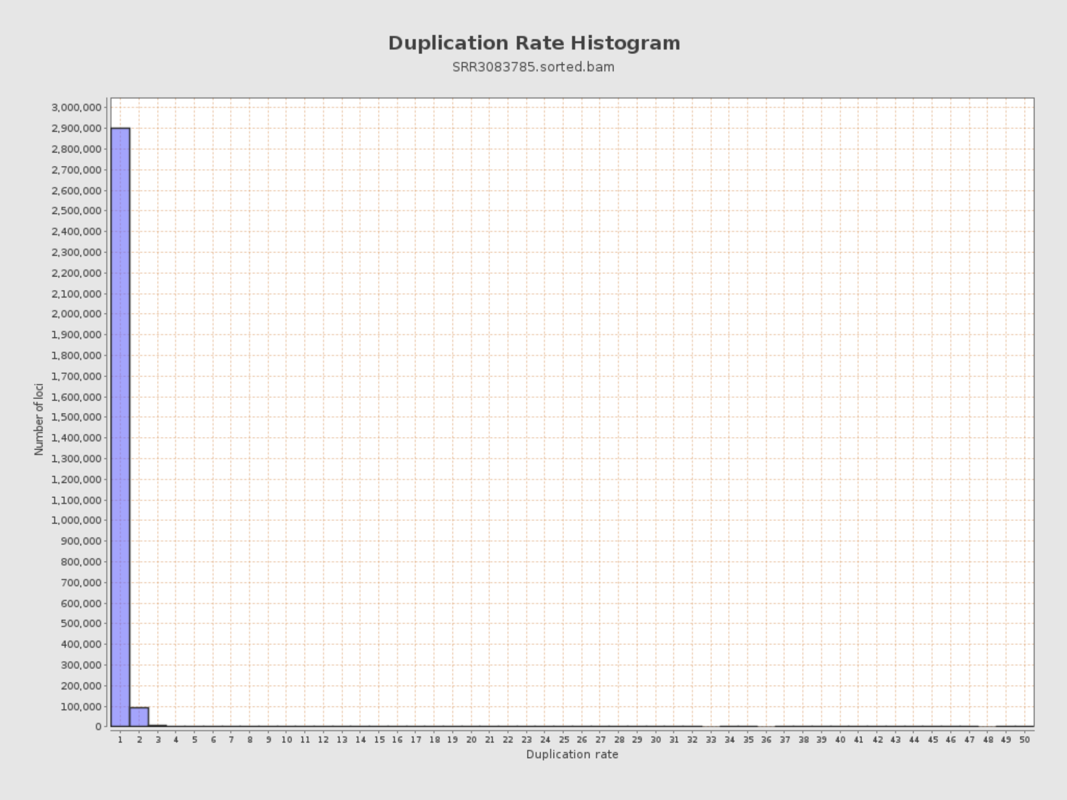
5. Results : Coverage Histogram (0-50X)



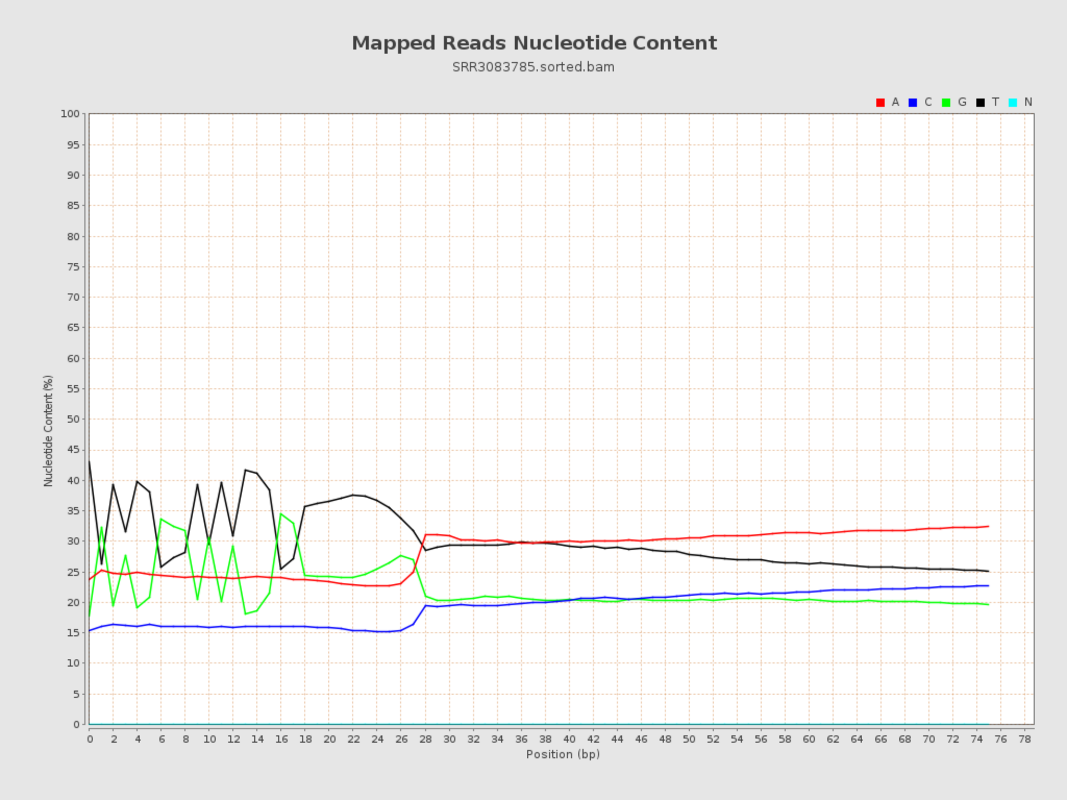
6. Results : Genome Fraction Coverage



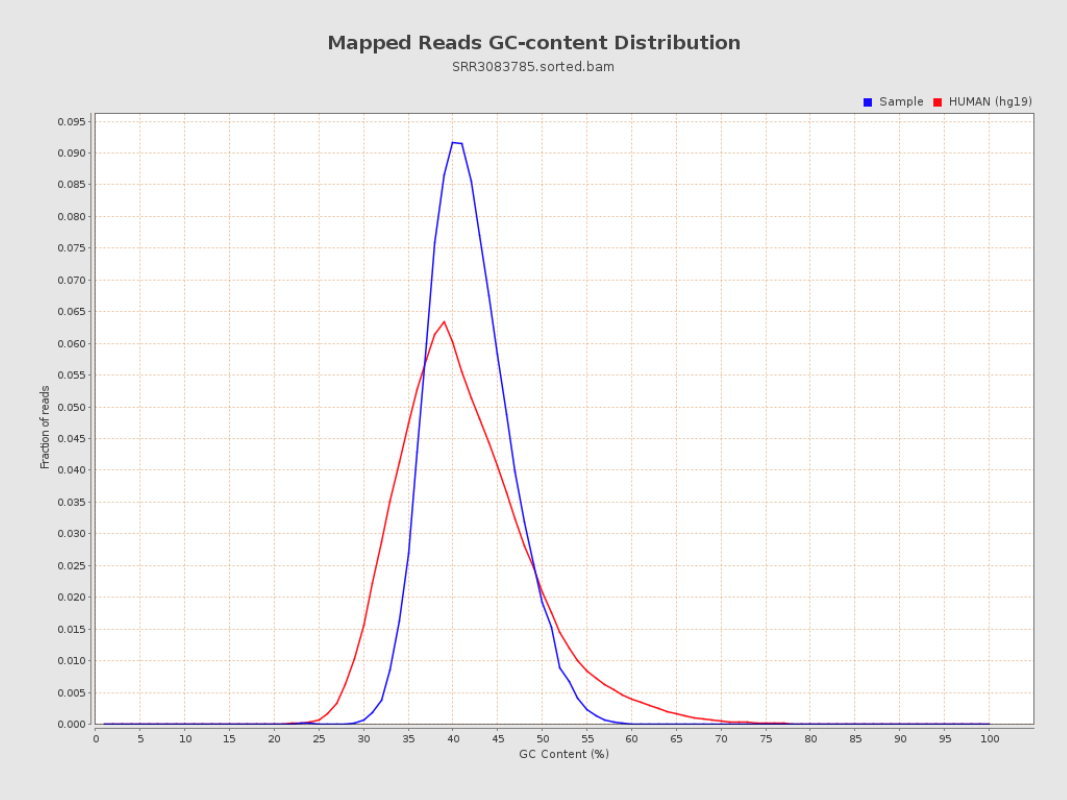
7. Results : Duplication Rate Histogram



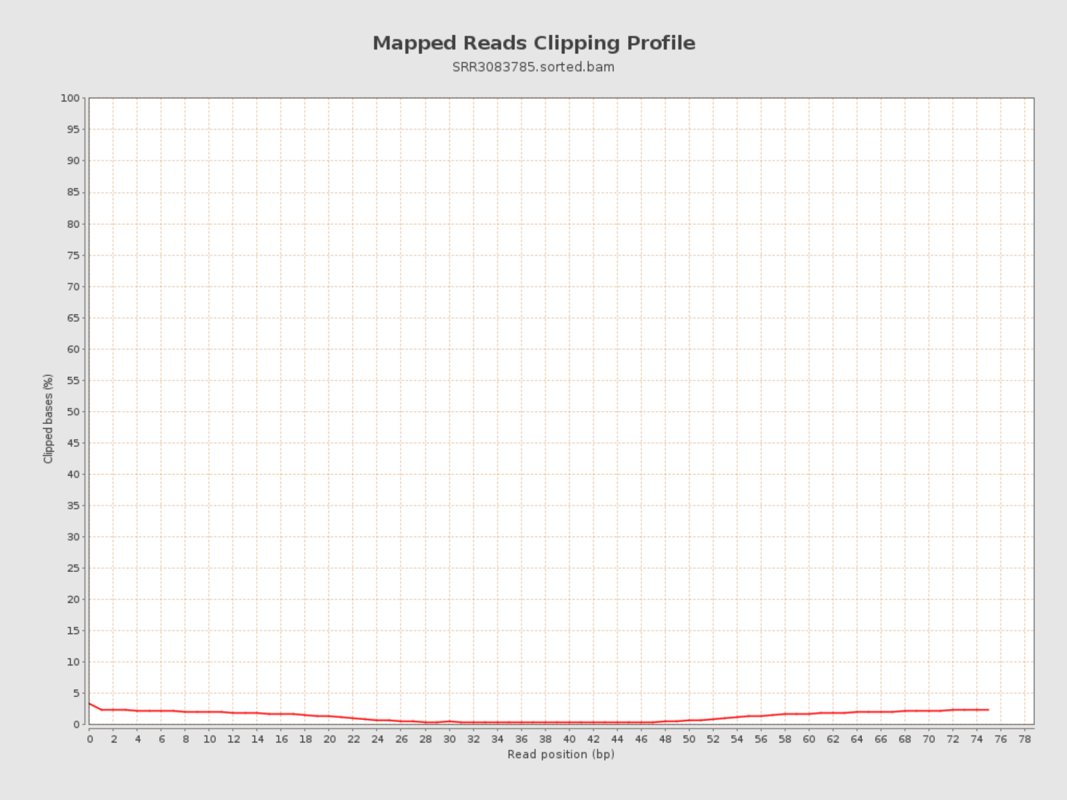
8. Results : Mapped Reads Nucleotide Content



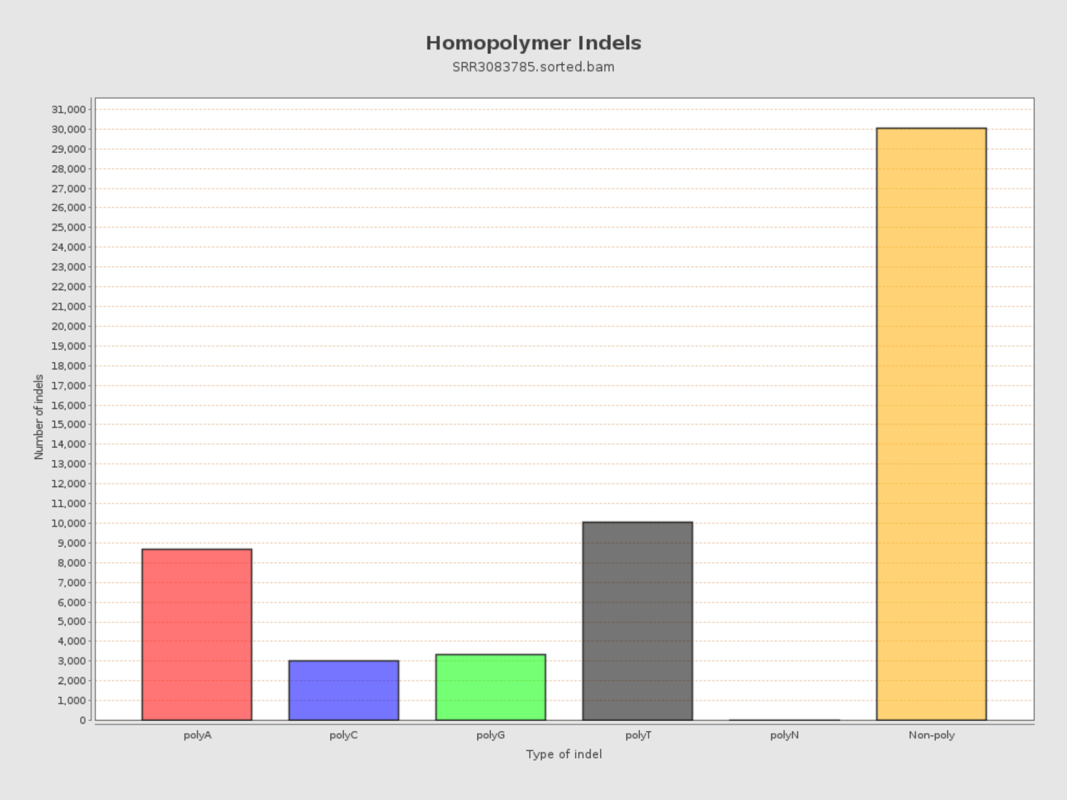
9. Results : Mapped Reads GC-content Distribution



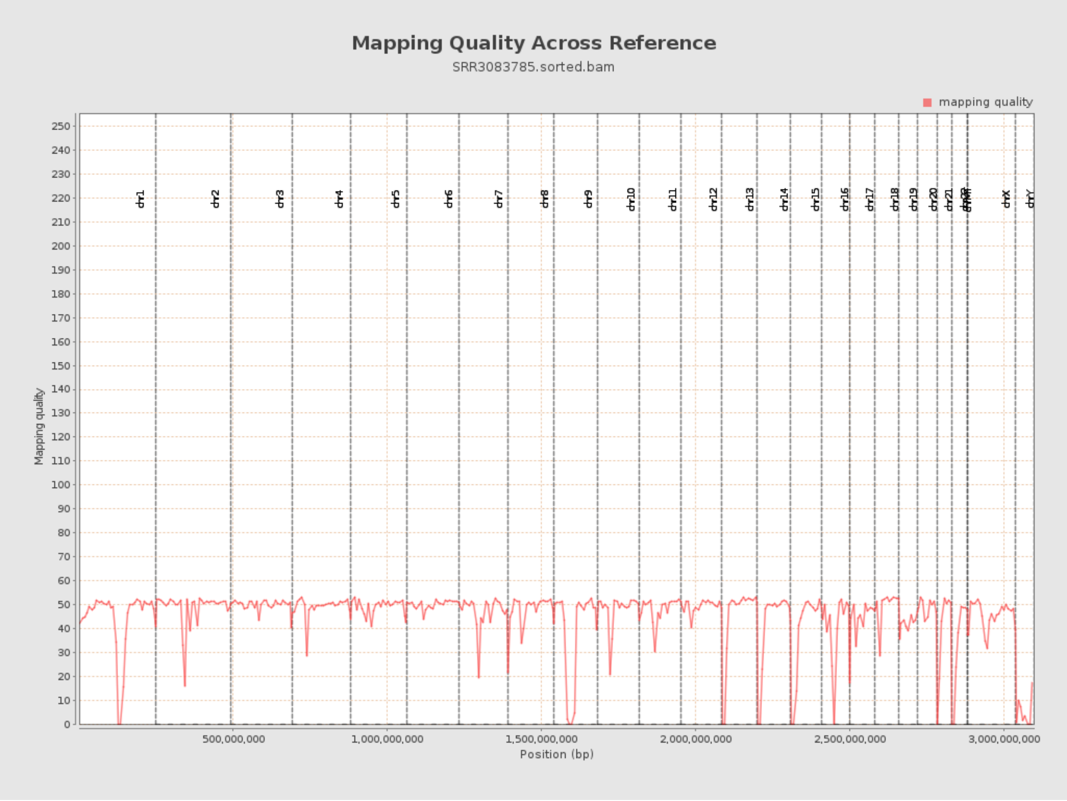
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram