Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:53:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085016.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_SRR3085016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:53:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,130,667
Mapped reads	2,822,391 / 90.15%
Unmapped reads	308,276 / 9.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,526 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	128,335 / 4.1%
Duplication rate	3.2%
Clipped reads	1,386,342 / 44.28%

2.2. ACGT Content

Number/percentage of A's	53,165,123 / 28.54%
Number/percentage of C's	34,403,197 / 18.47%
Number/percentage of T's	58,145,677 / 31.21%
Number/percentage of G's	40,573,723 / 21.78%
Number/percentage of N's	25,737 / 0.01%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0602

Standard Deviation	0.5969

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

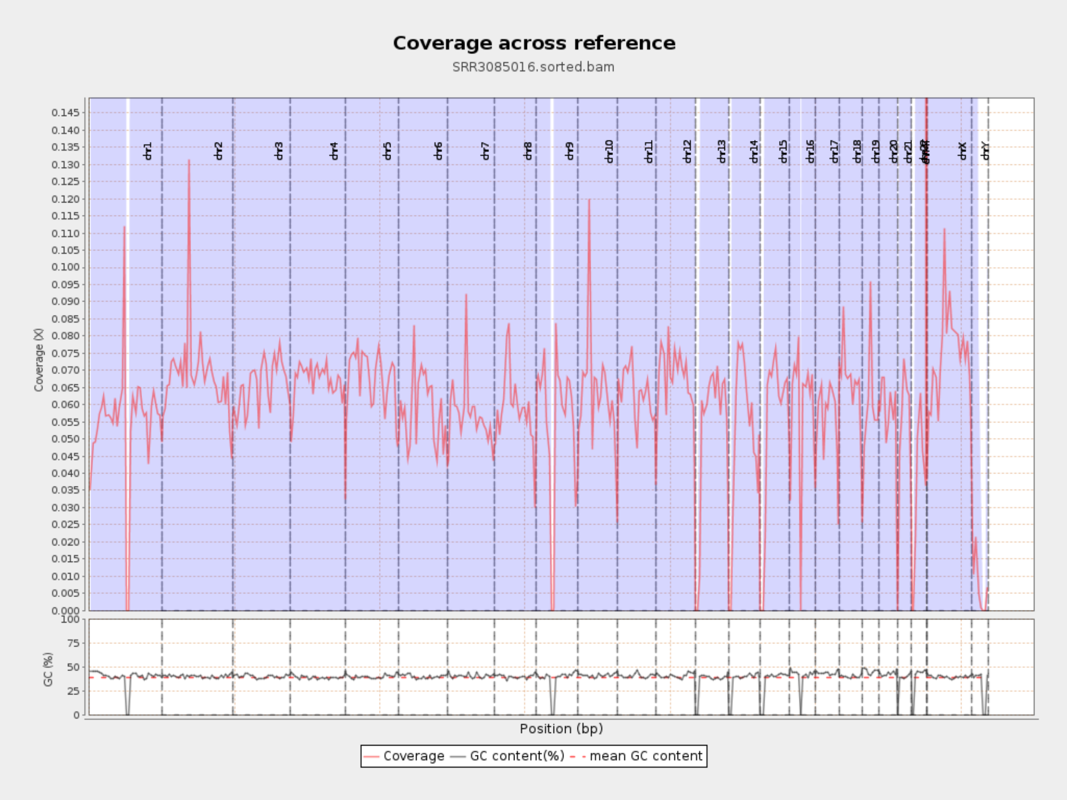
General error rate	0.87%
Mismatches	1,592,881
Insertions	14,761
Mapped reads with at least one insertion	0.52%
Deletions	42,919
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.46%

2.6. Chromosome stats

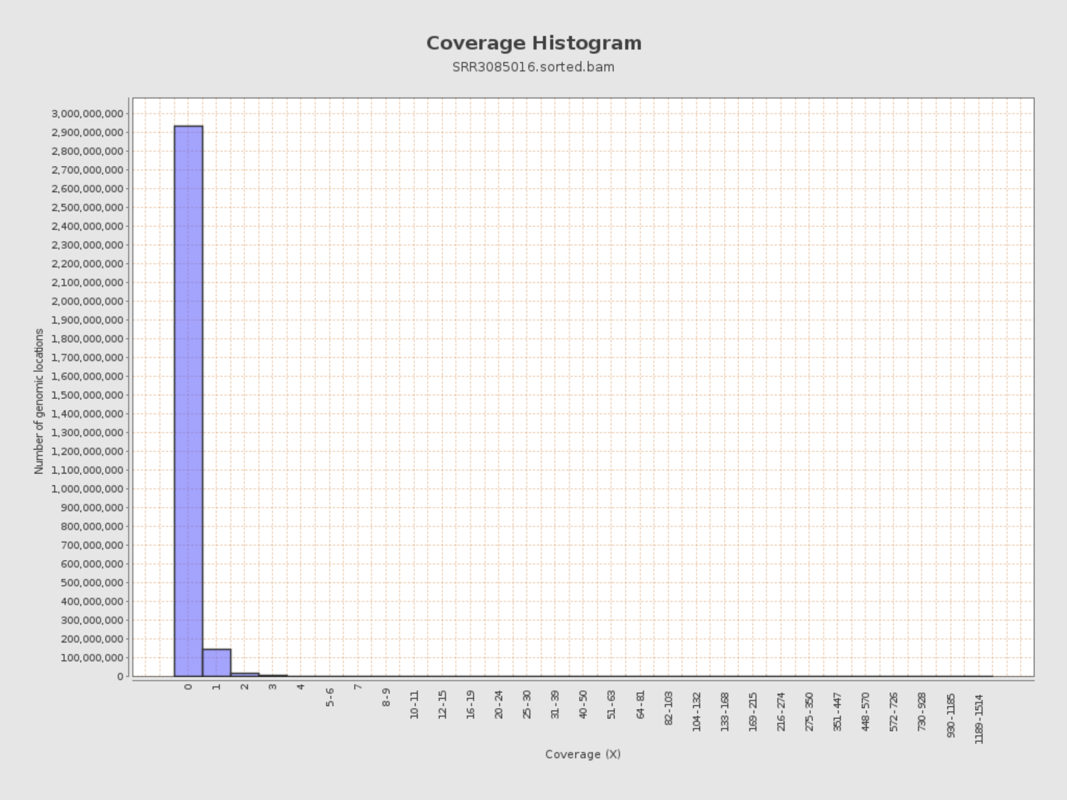
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13690052	0.0549	1.2242
chr2	243199373	16832132	0.0692	0.67
chr3	198022430	13033964	0.0658	0.2898
chr4	191154276	12849302	0.0672	0.2992
chr5	180915260	12304099	0.068	0.2985
chr6	171115067	10036238	0.0587	0.3823
chr7	159138663	9174766	0.0577	0.4884

chr8	146364022	8572443	0.0586	0.9586
chr9	141213431	7811697	0.0553	0.553
chr10	135534747	8747614	0.0645	0.6246
chr11	135006516	8475438	0.0628	0.5693
chr12	133851895	9132016	0.0682	0.3098
chr13	115169878	6043806	0.0525	0.2549
chr14	107349540	5483142	0.0511	0.3142
chr15	102531392	5529344	0.0539	0.2638
chr16	90354753	5304064	0.0587	0.3586
chr17	81195210	4540748	0.0559	0.3651
chr18	78077248	5285253	0.0677	1.0822
chr19	59128983	3540946	0.0599	0.8535
chr20	63025520	3677535	0.0583	0.2886
chr21	48129895	2508781	0.0521	0.2971
chr22	51304566	1778440	0.0347	0.2067
chrMT	16571	50334	3.0375	2.4818
chrX	155270560	11534103	0.0743	0.3999
chrY	59373566	445982	0.0075	0.1432

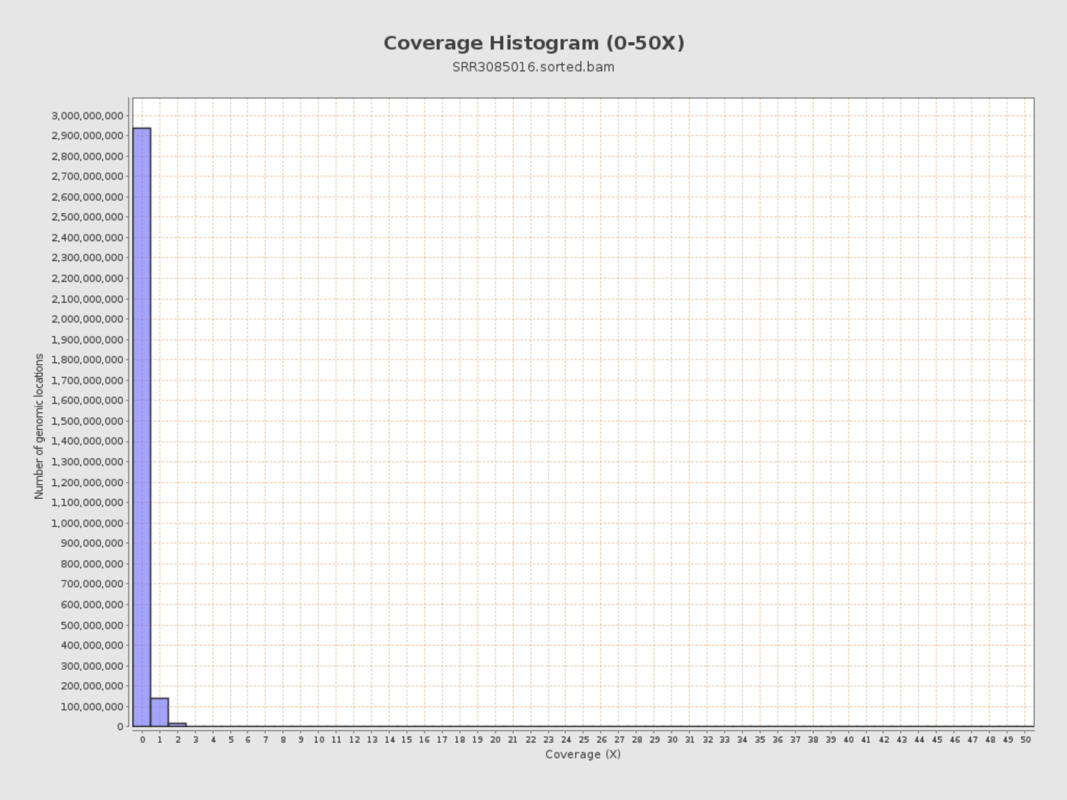
3. Results : Coverage across reference



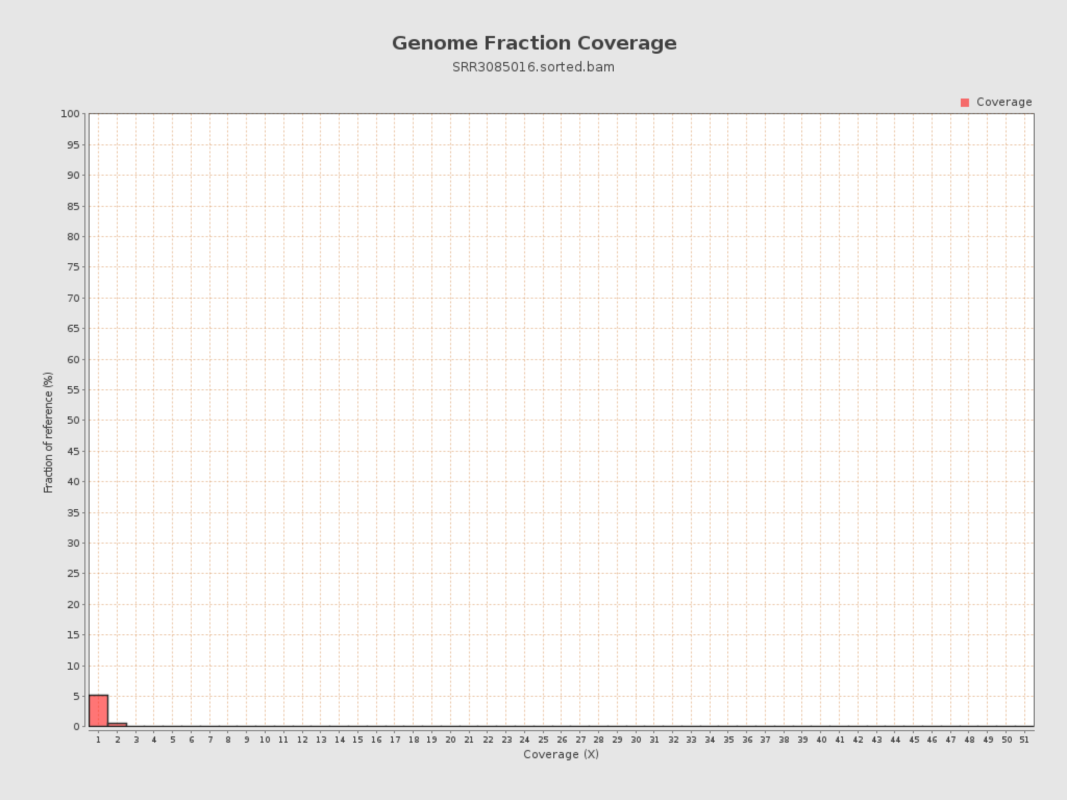
4. Results : Coverage Histogram



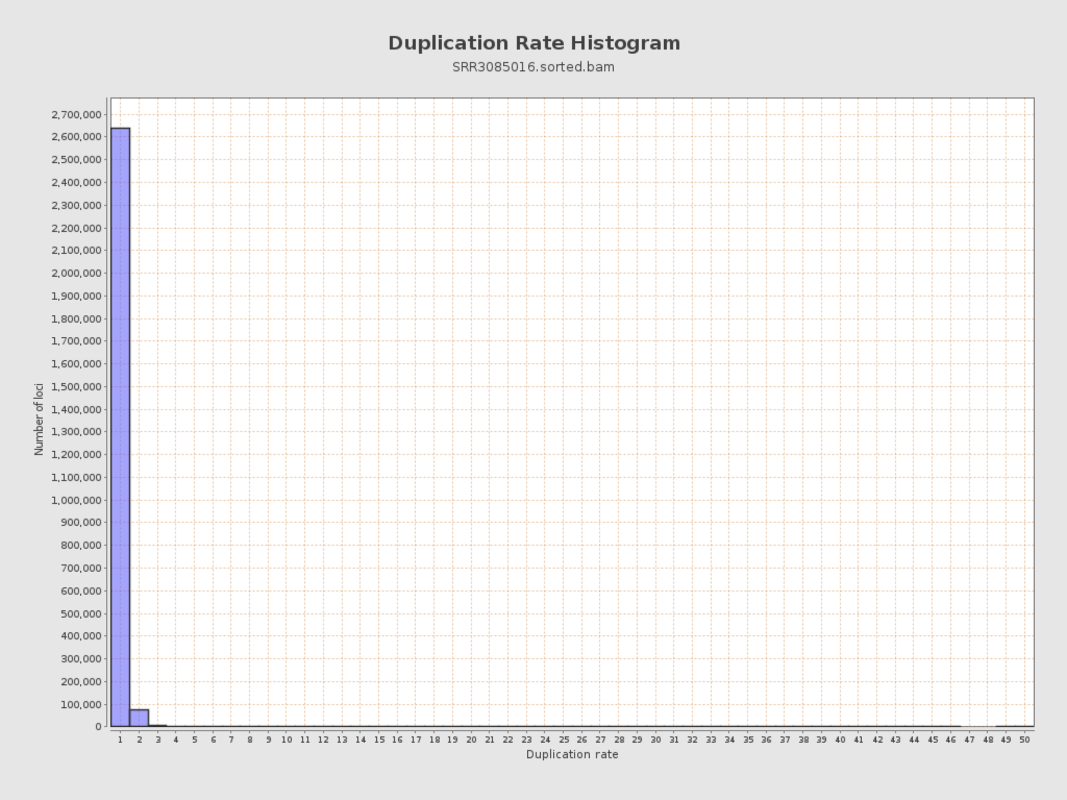
5. Results : Coverage Histogram (0-50X)



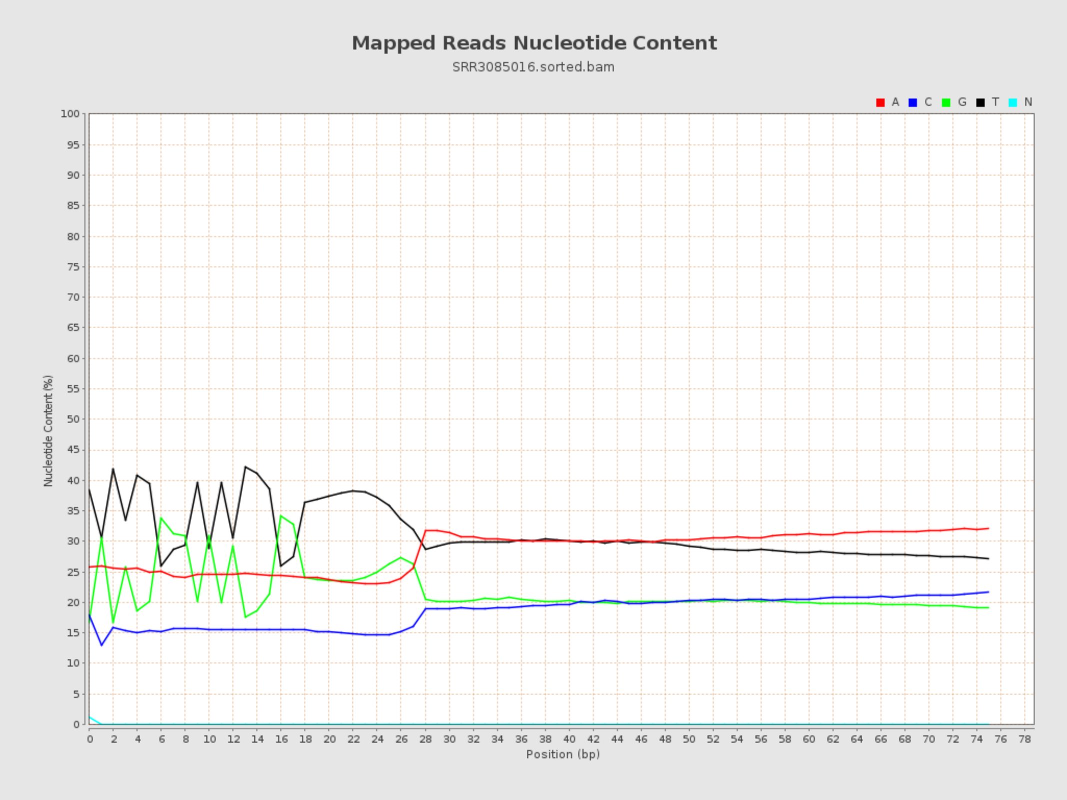
6. Results : Genome Fraction Coverage



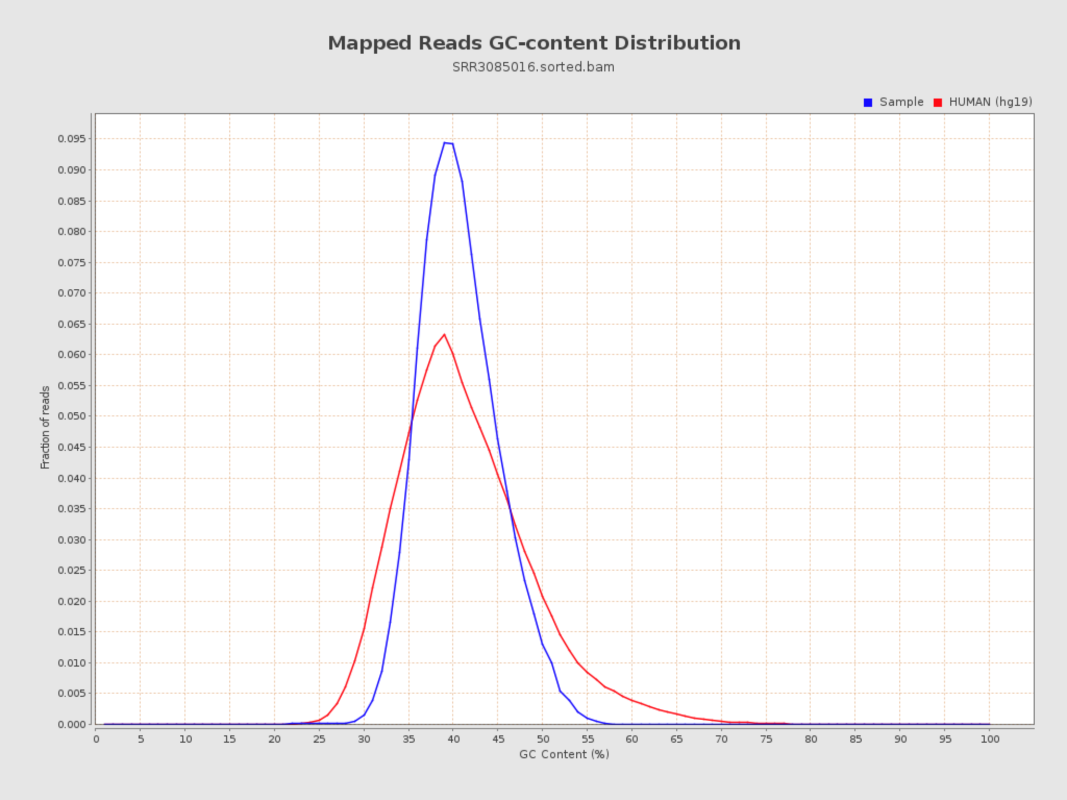
7. Results : Duplication Rate Histogram



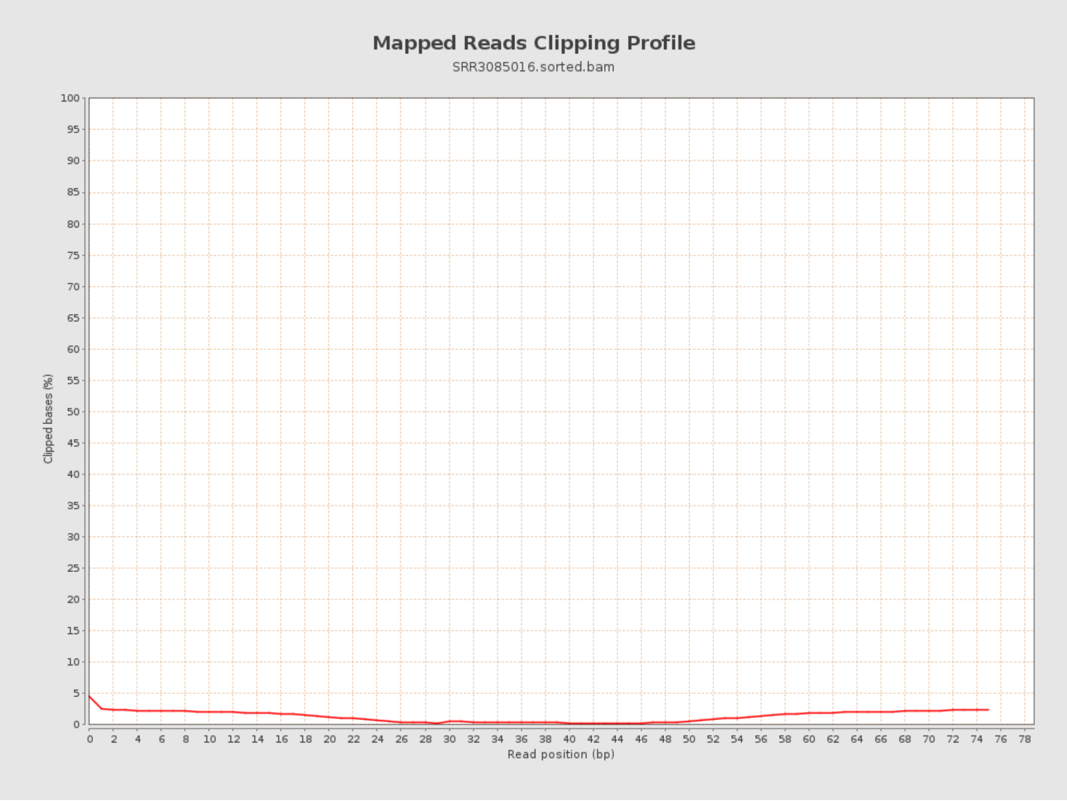
8. Results : Mapped Reads Nucleotide Content



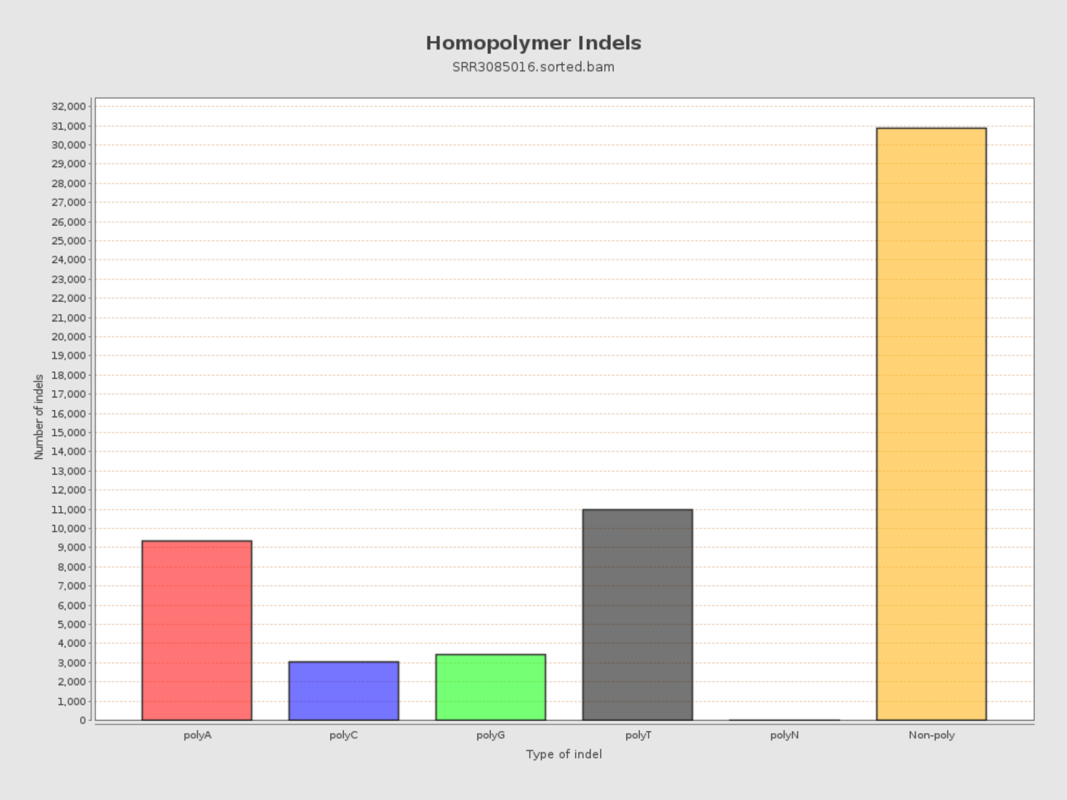
9. Results : Mapped Reads GC-content Distribution



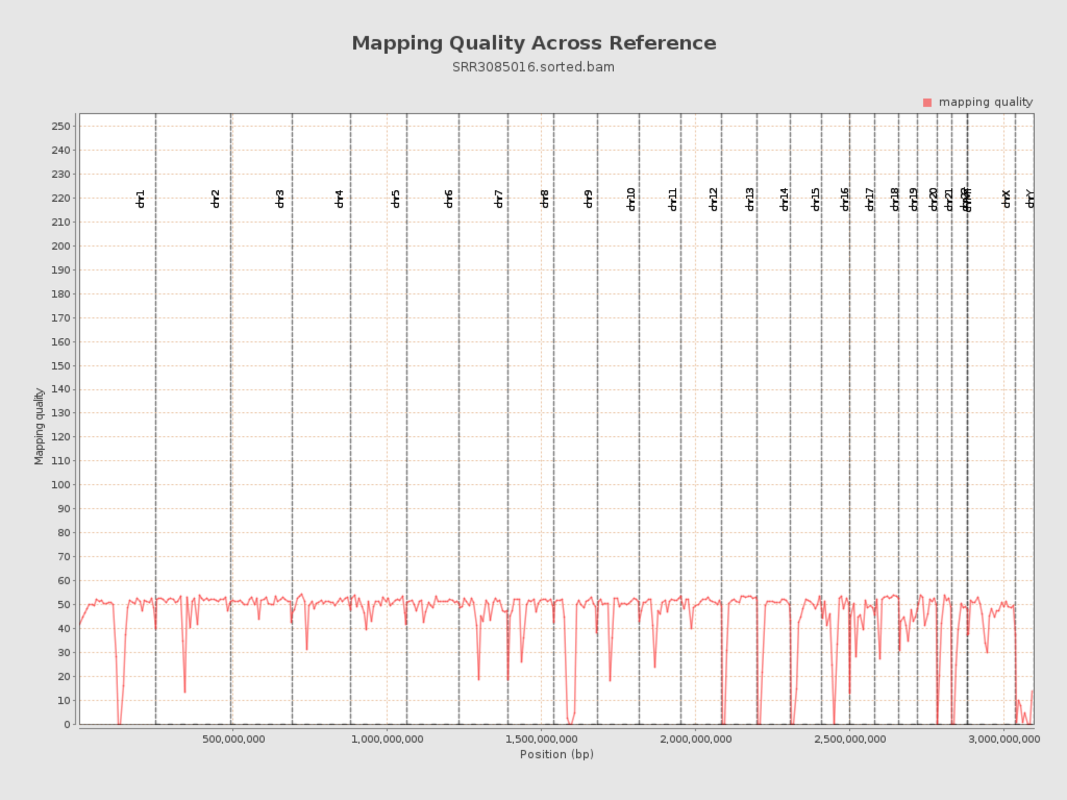
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram