Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 03:12:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085133.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_SRR3085133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 03:12:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,324,918
Mapped reads	2,051,334 / 88.23%
Unmapped reads	273,584 / 11.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,238 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	100,055 / 4.3%
Duplication rate	3.86%
Clipped reads	917,917 / 39.48%

2.2. ACGT Content

Number/percentage of A's	38,678,936 / 28.08%
Number/percentage of C's	25,810,067 / 18.73%
Number/percentage of T's	43,123,772 / 31.3%
Number/percentage of G's	30,125,860 / 21.87%
Number/percentage of N's	30,120 / 0.02%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0445

Standard Deviation	0.3963

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Mismatches and indels

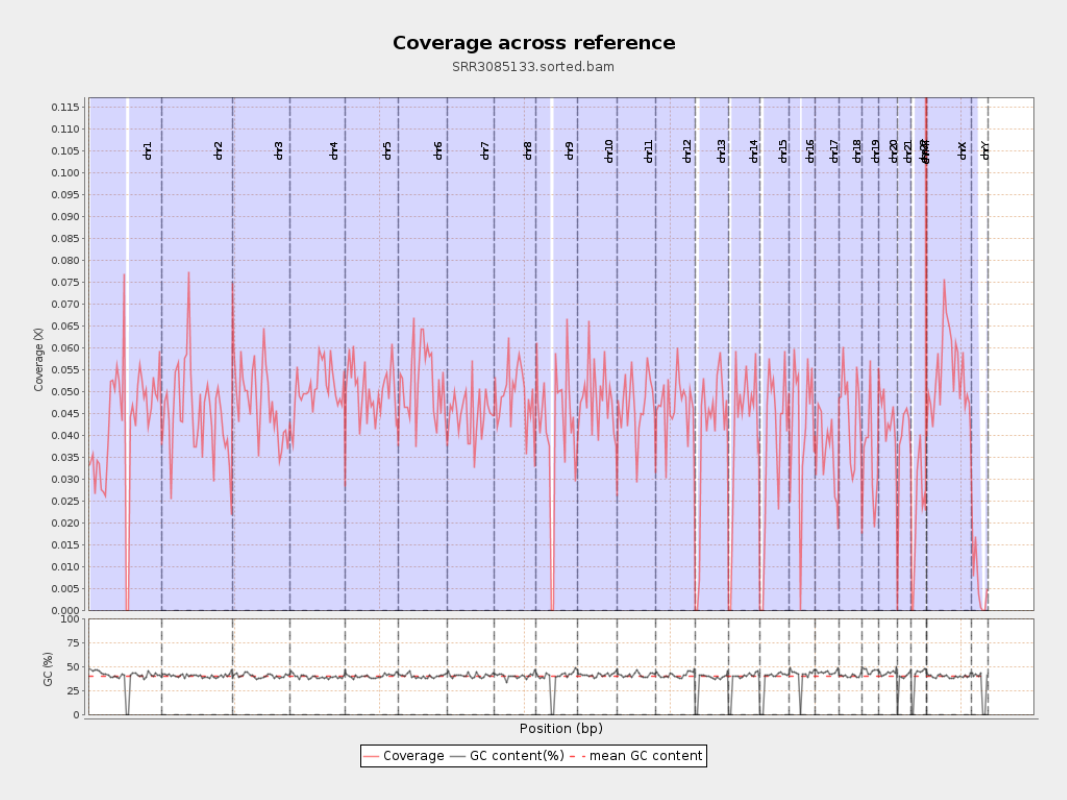
General error rate	0.91%
Mismatches	1,237,332
Insertions	10,860
Mapped reads with at least one insertion	0.53%
Deletions	32,917
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.15%

2.6. Chromosome stats

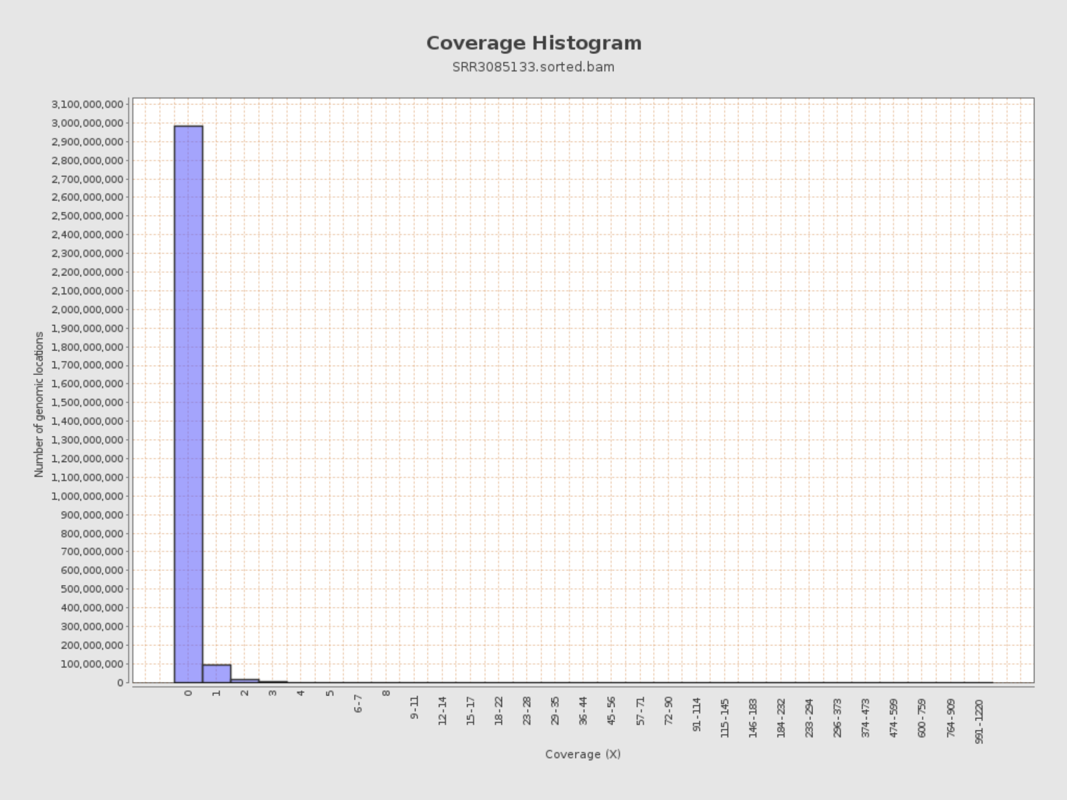
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10575129	0.0424	0.6097
chr2	243199373	10944703	0.045	0.4379
chr3	198022430	9516520	0.0481	0.2558
chr4	191154276	9669543	0.0506	0.2704
chr5	180915260	9071602	0.0501	0.2627
chr6	171115067	8857421	0.0518	0.3265
chr7	159138663	7138200	0.0449	0.3261

chr8	146364022	7151209	0.0489	0.7751
chr9	141213431	5808404	0.0411	0.3726
chr10	135534747	6562790	0.0484	0.3207
chr11	135006516	6276911	0.0465	0.4331
chr12	133851895	6257240	0.0467	0.2565
chr13	115169878	4562958	0.0396	0.2334
chr14	107349540	4375968	0.0408	0.2562
chr15	102531392	3901928	0.0381	0.2344
chr16	90354753	3836461	0.0425	0.2639
chr17	81195210	2880019	0.0355	0.2629
chr18	78077248	3546885	0.0454	0.7284
chr19	59128983	2112036	0.0357	0.4393
chr20	63025520	2743439	0.0435	0.2508
chr21	48129895	1816565	0.0377	0.2411
chr22	51304566	1095761	0.0214	0.1676
chrMT	16571	334686	20.1971	10.9719
chrX	155270560	8429691	0.0543	0.313
chrY	59373566	355225	0.006	0.1163

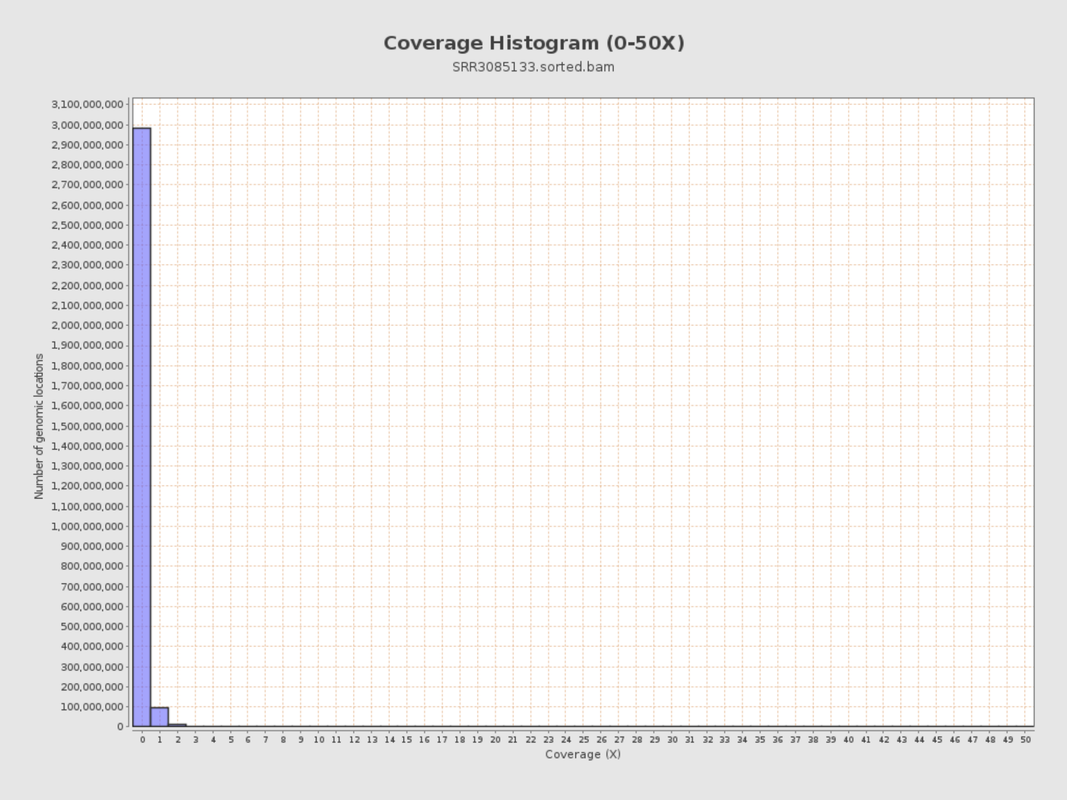
3. Results : Coverage across reference



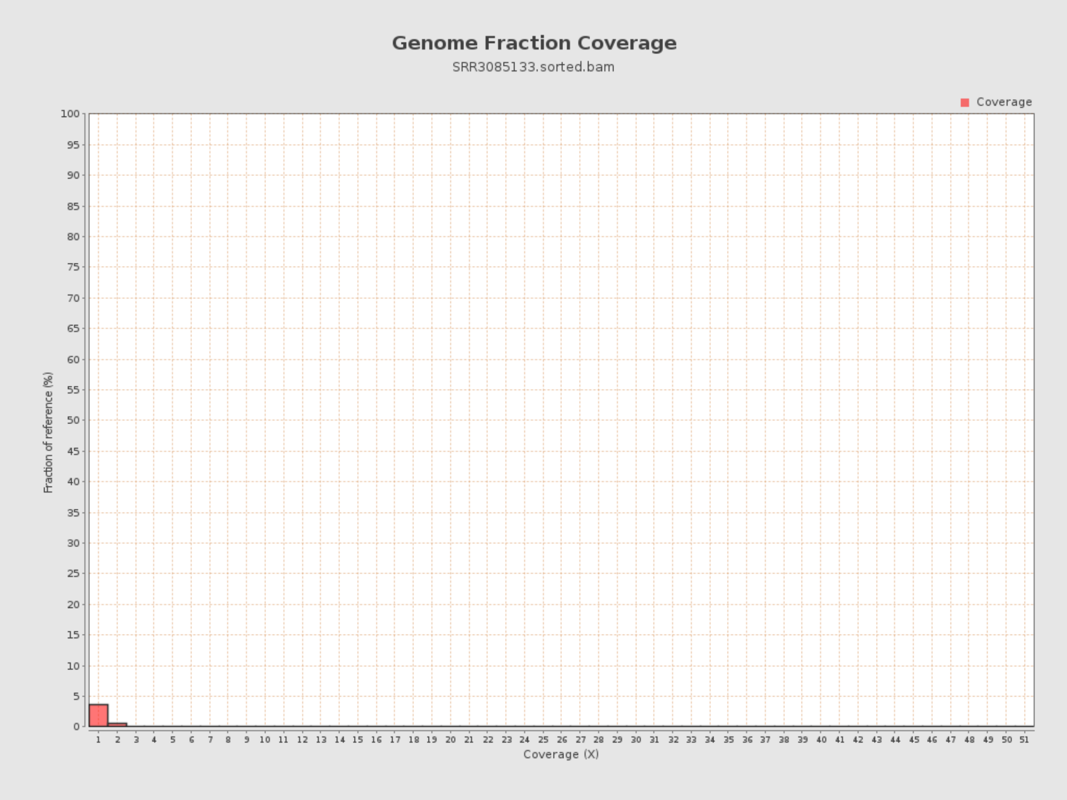
4. Results : Coverage Histogram



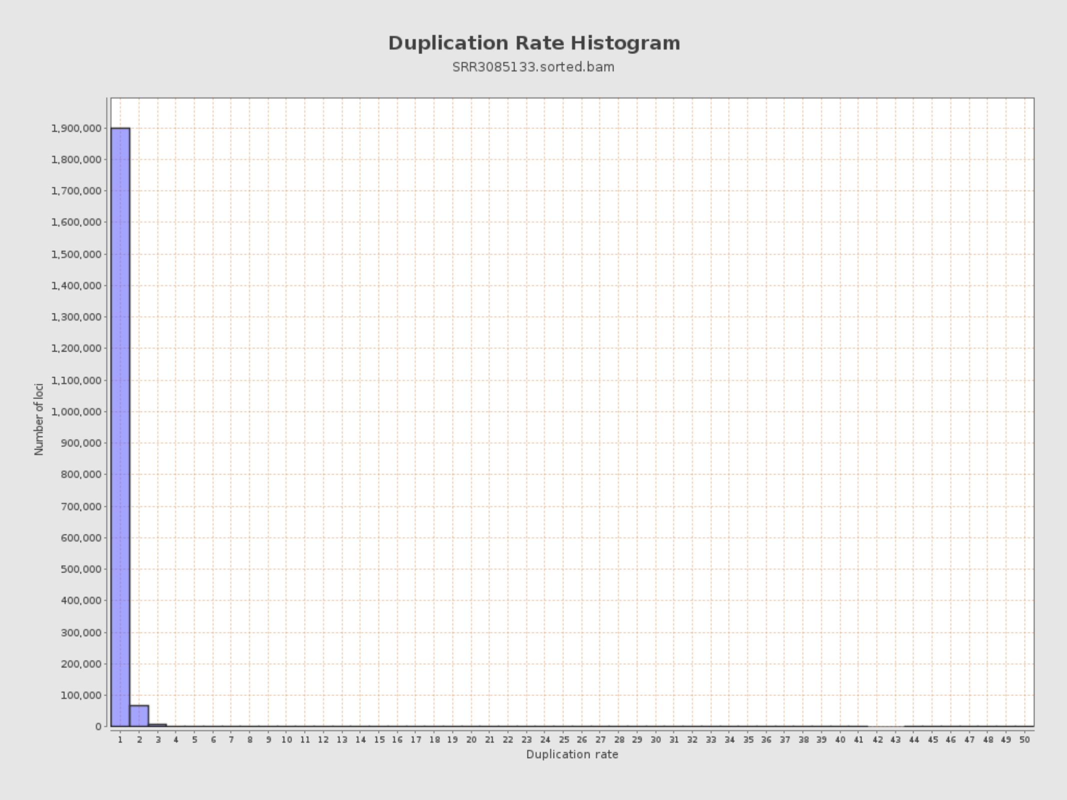
5. Results : Coverage Histogram (0-50X)



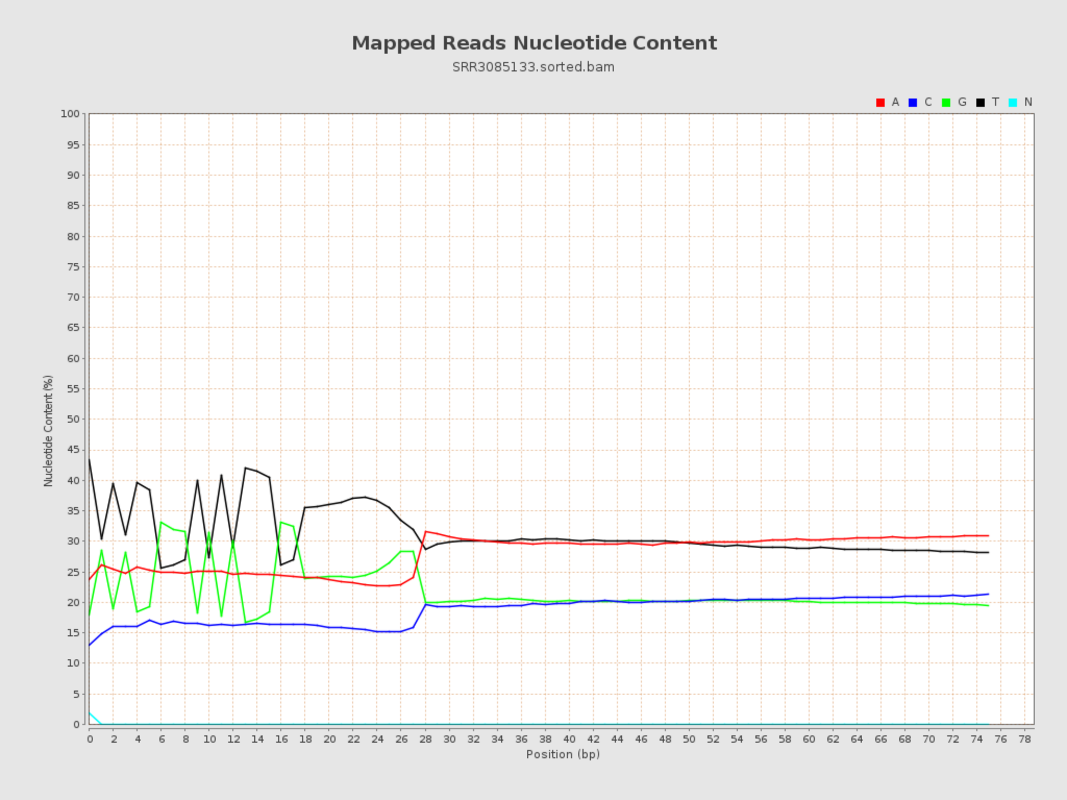
6. Results : Genome Fraction Coverage



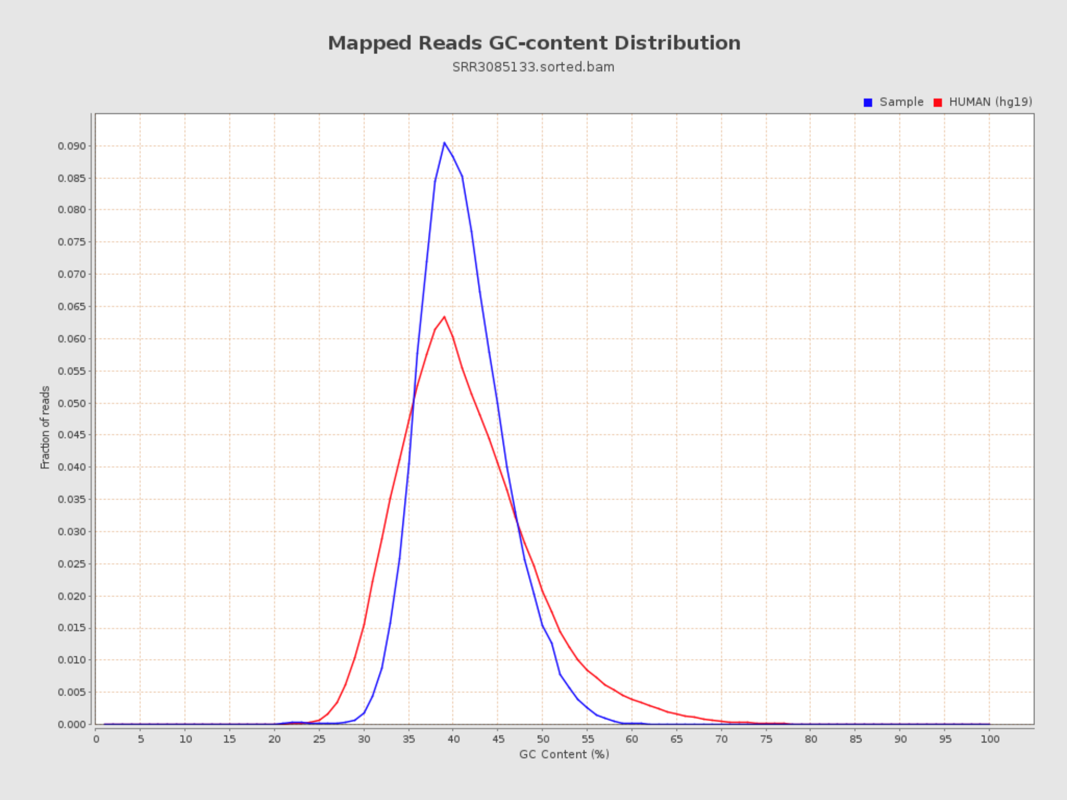
7. Results : Duplication Rate Histogram



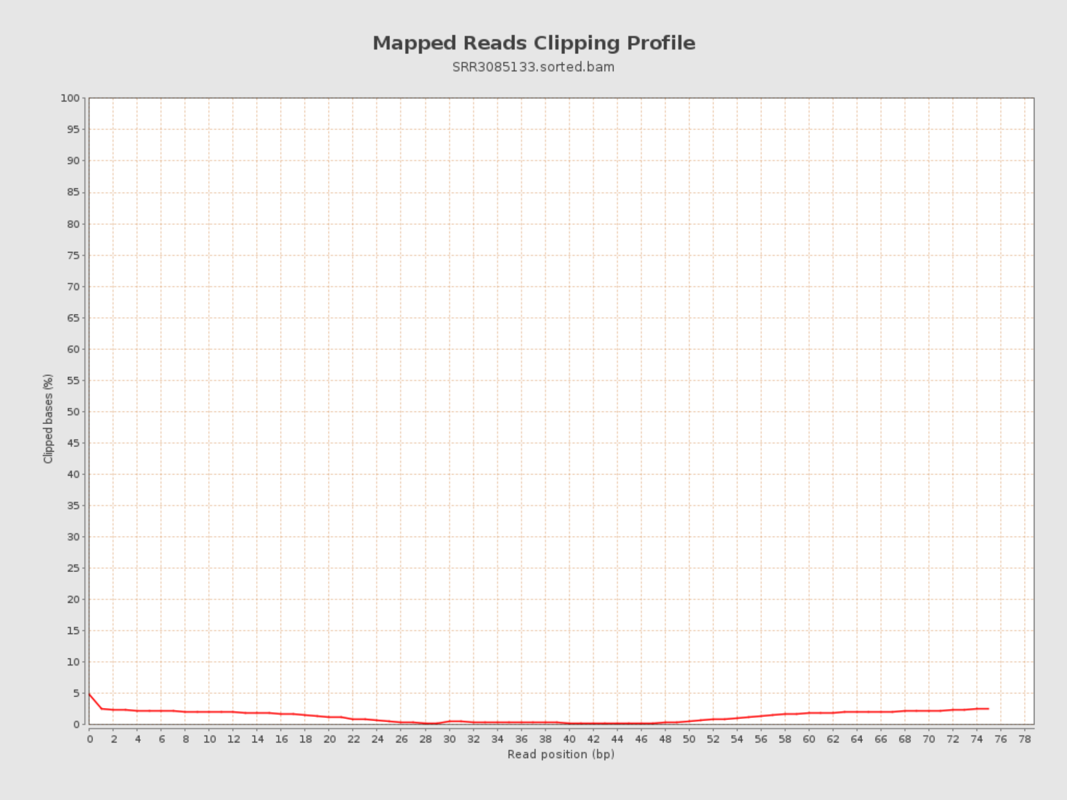
8. Results : Mapped Reads Nucleotide Content



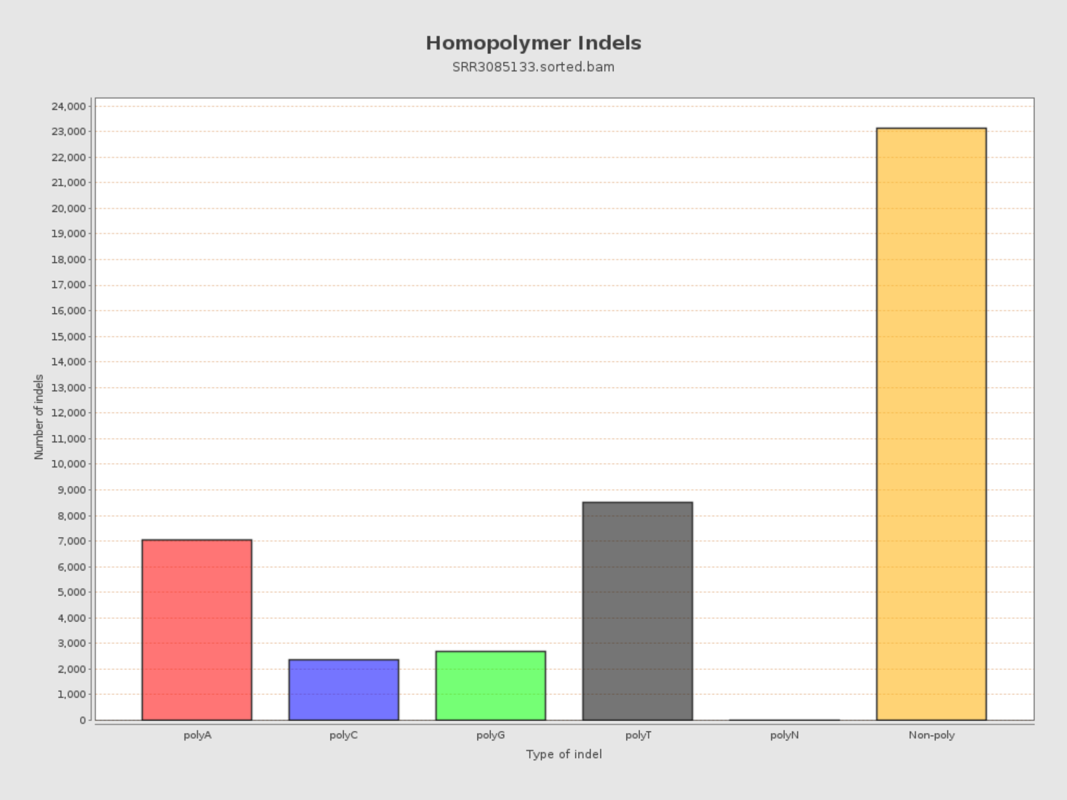
9. Results : Mapped Reads GC-content Distribution



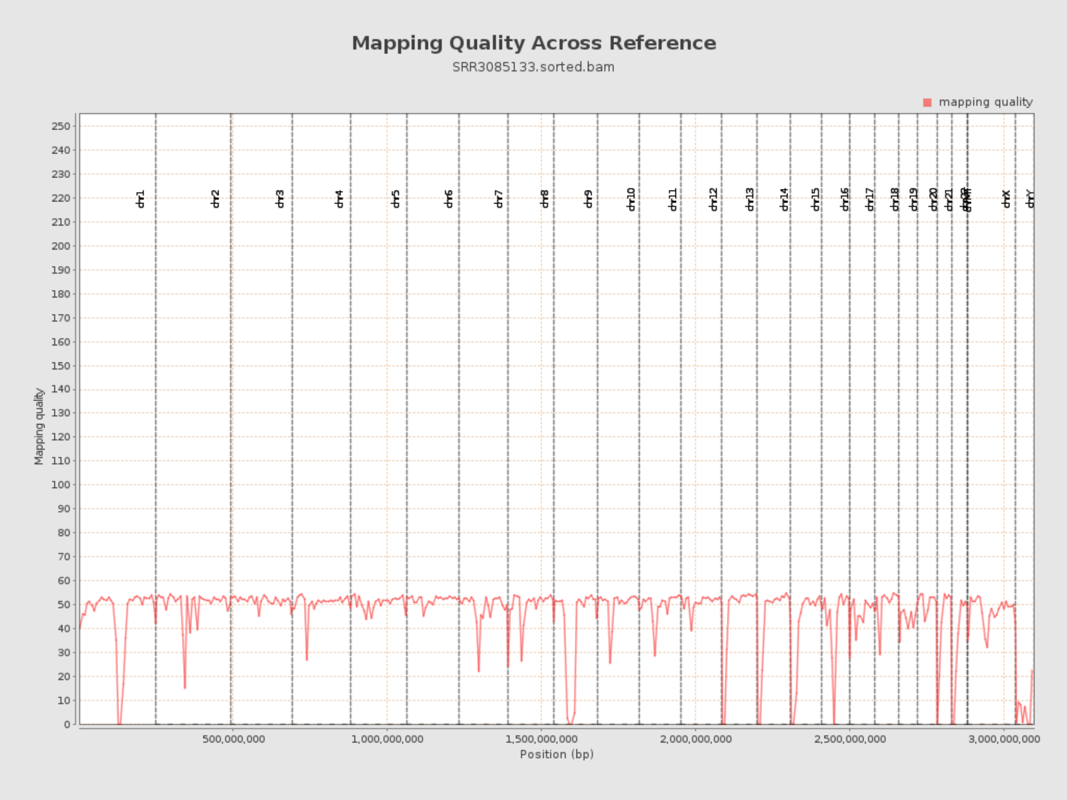
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram