Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 03:31:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085136.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_SRR3085136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 03:31:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,736,489
Mapped reads	1,533,055 / 88.28%
Unmapped reads	203,434 / 11.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,006 / 1.44%
Read min/max/mean length	30 / 76 / 76.5
Duplicated reads (estimated)	54,172 / 3.12%
Duplication rate	2.1%
Clipped reads	748,910 / 43.13%

2.2. ACGT Content

Number/percentage of A's	29,238,259 / 28.66%
Number/percentage of C's	19,431,959 / 19.05%
Number/percentage of T's	30,586,839 / 29.98%
Number/percentage of G's	22,745,090 / 22.29%
Number/percentage of N's	18,119 / 0.02%
GC Percentage	41.34%

2.3. Coverage

Mean	0.033

Standard Deviation	0.4473

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Mismatches and indels

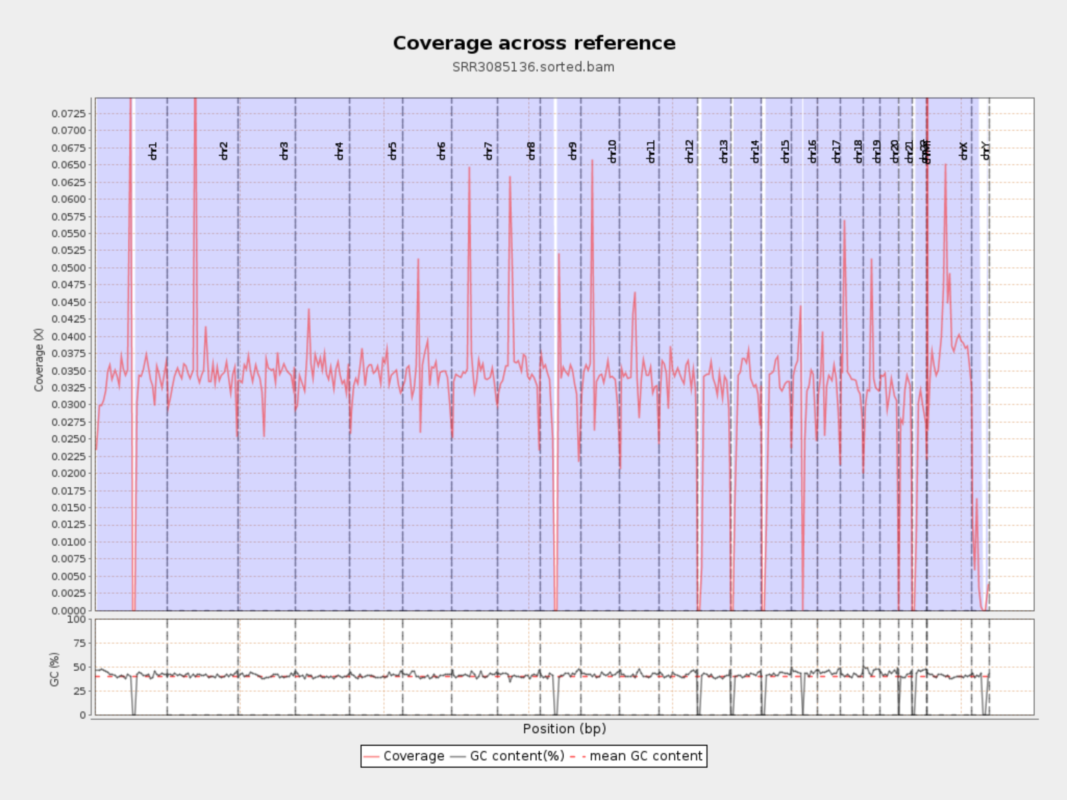
General error rate	0.92%
Mismatches	925,415
Insertions	9,260
Mapped reads with at least one insertion	0.6%
Deletions	21,552
Mapped reads with at least one deletion	1.39%
Homopolymer indels	43.56%

2.6. Chromosome stats

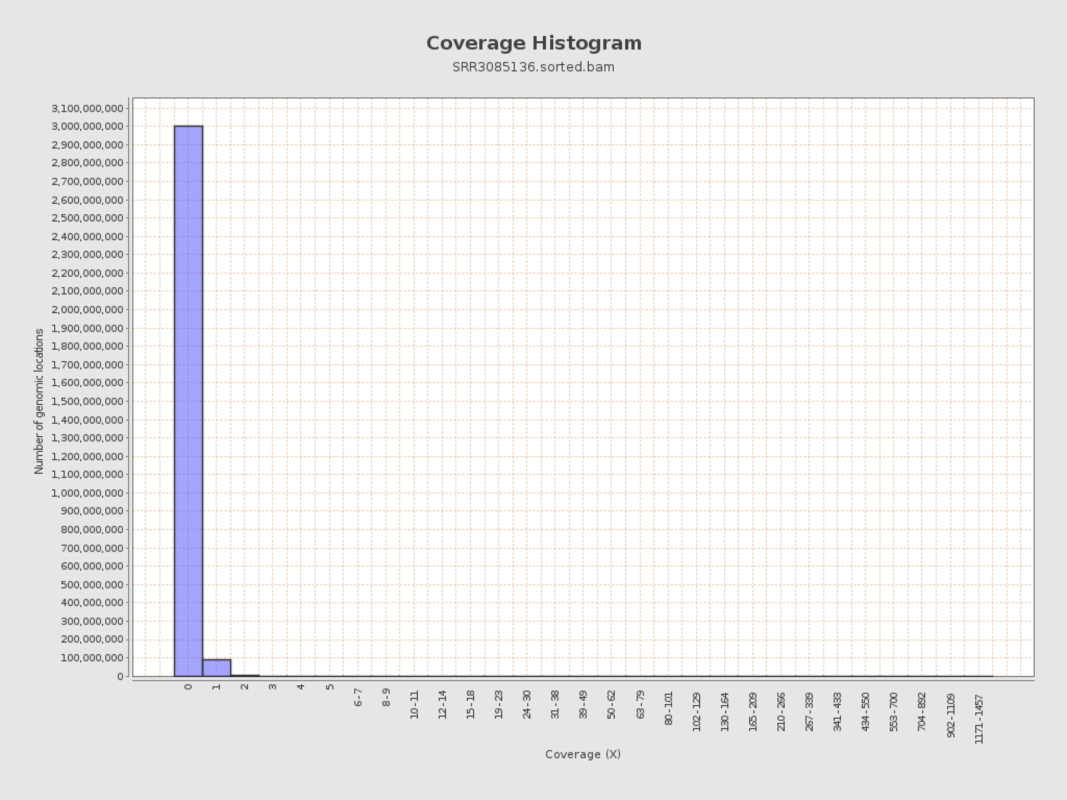
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8163134	0.0328	0.8914
chr2	243199373	8733422	0.0359	0.462
chr3	198022430	6811970	0.0344	0.1962
chr4	191154276	6645309	0.0348	0.2103
chr5	180915260	6227606	0.0344	0.1989
chr6	171115067	5956037	0.0348	0.2764
chr7	159138663	5652425	0.0355	0.4099

chr8	146364022	5365651	0.0367	0.8994
chr9	141213431	4319113	0.0306	0.4007
chr10	135534747	4769076	0.0352	0.369
chr11	135006516	4682650	0.0347	0.4594
chr12	133851895	4576661	0.0342	0.2046
chr13	115169878	3187438	0.0277	0.1738
chr14	107349540	3062890	0.0285	0.2209
chr15	102531392	2835603	0.0277	0.1796
chr16	90354753	2719178	0.0301	0.2325
chr17	81195210	2639509	0.0325	0.2617
chr18	78077248	2788994	0.0357	0.8235
chr19	59128983	2012549	0.034	0.5579
chr20	63025520	1995987	0.0317	0.2035
chr21	48129895	1323643	0.0275	0.2018
chr22	51304566	1060617	0.0207	0.1502
chrMT	16571	35134	2.1202	1.8078
chrX	155270560	6192655	0.0399	0.2756
chrY	59373566	298526	0.005	0.1341

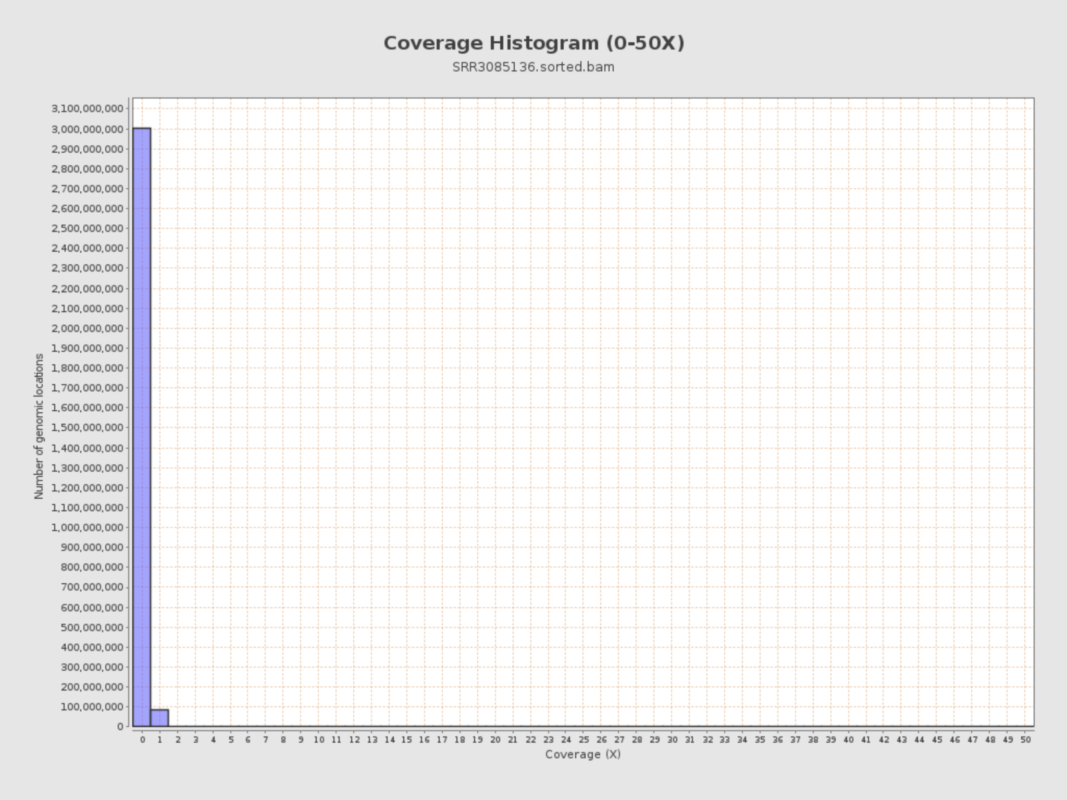
3. Results : Coverage across reference



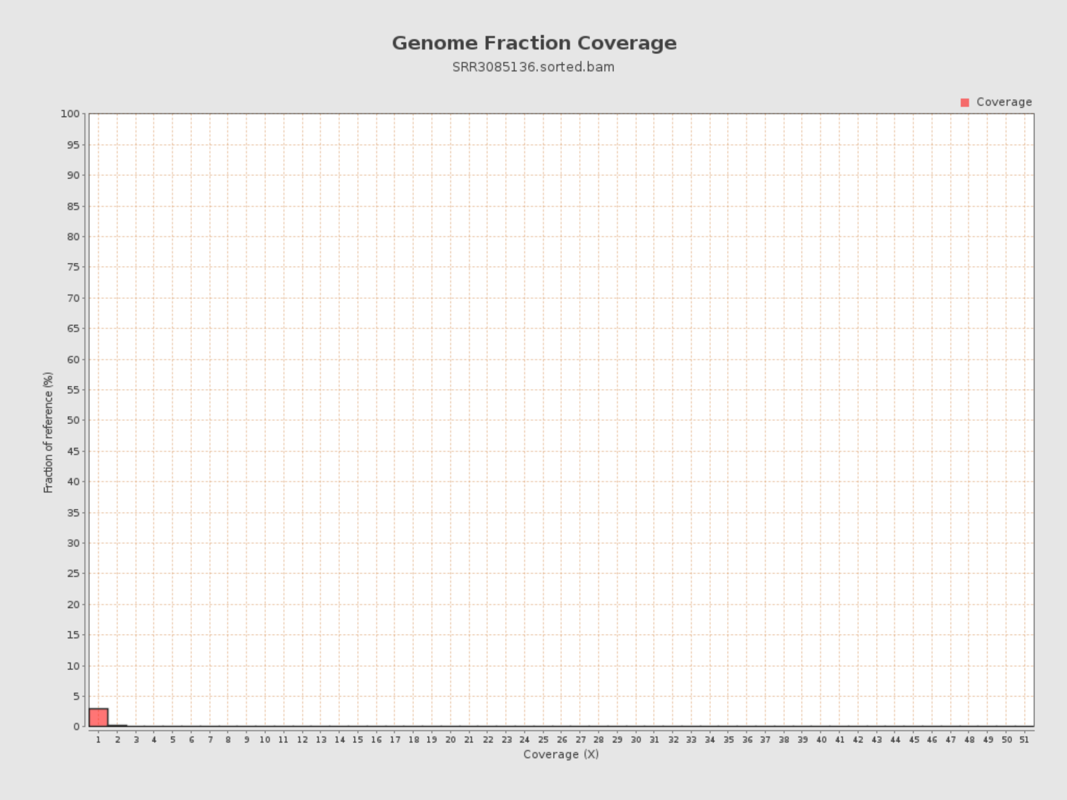
4. Results : Coverage Histogram



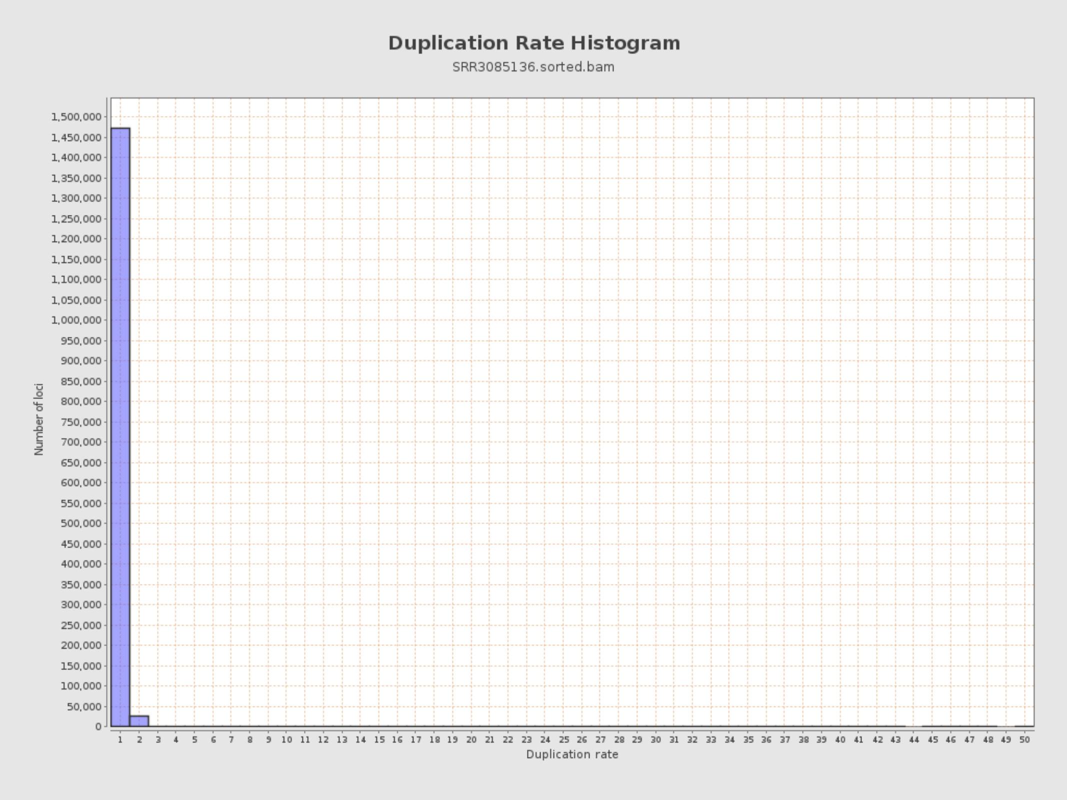
5. Results : Coverage Histogram (0-50X)



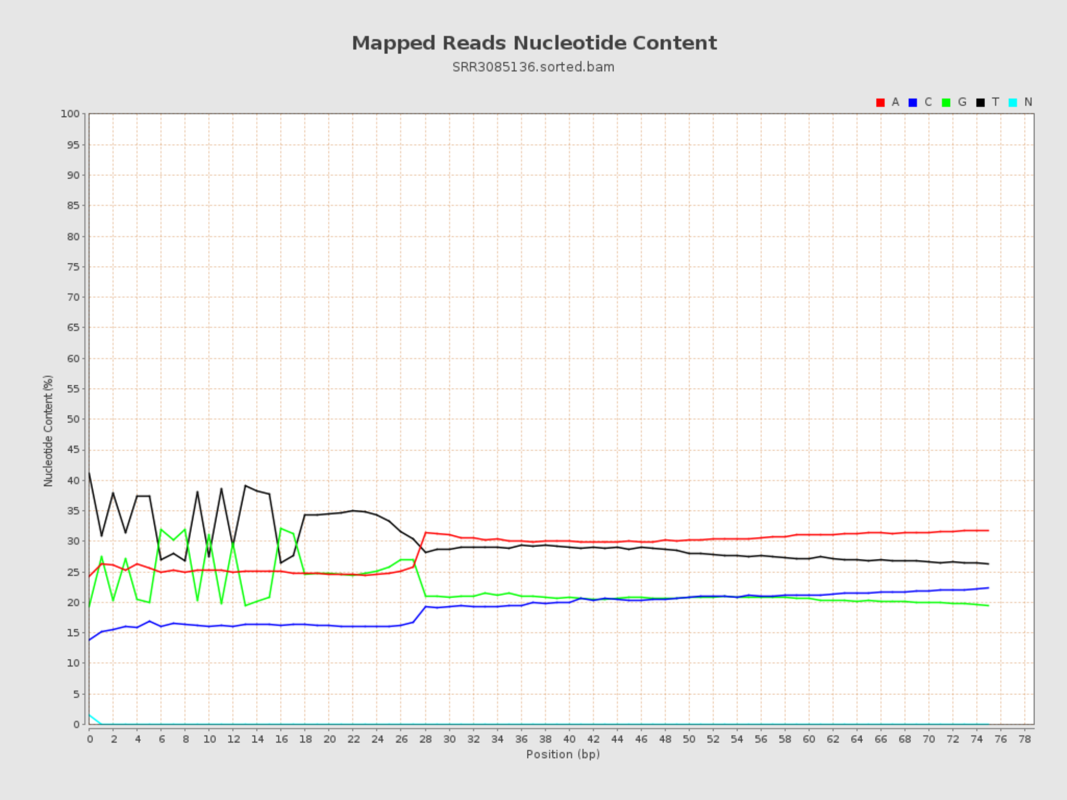
6. Results : Genome Fraction Coverage



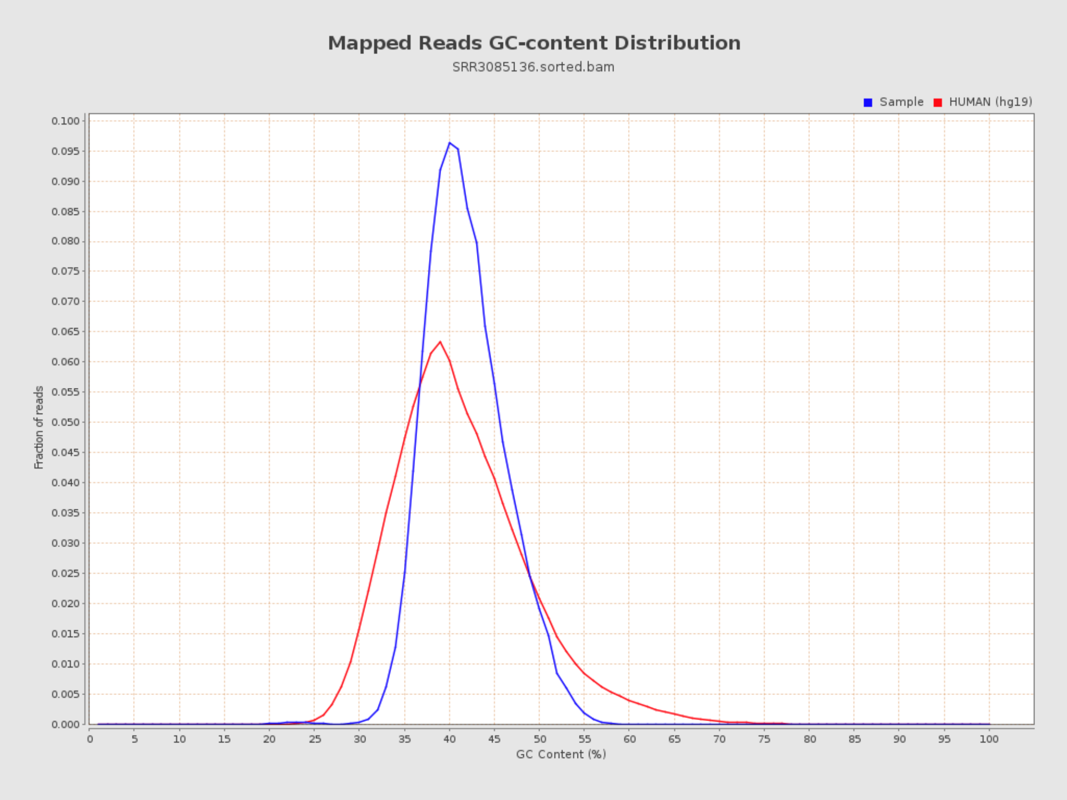
7. Results : Duplication Rate Histogram



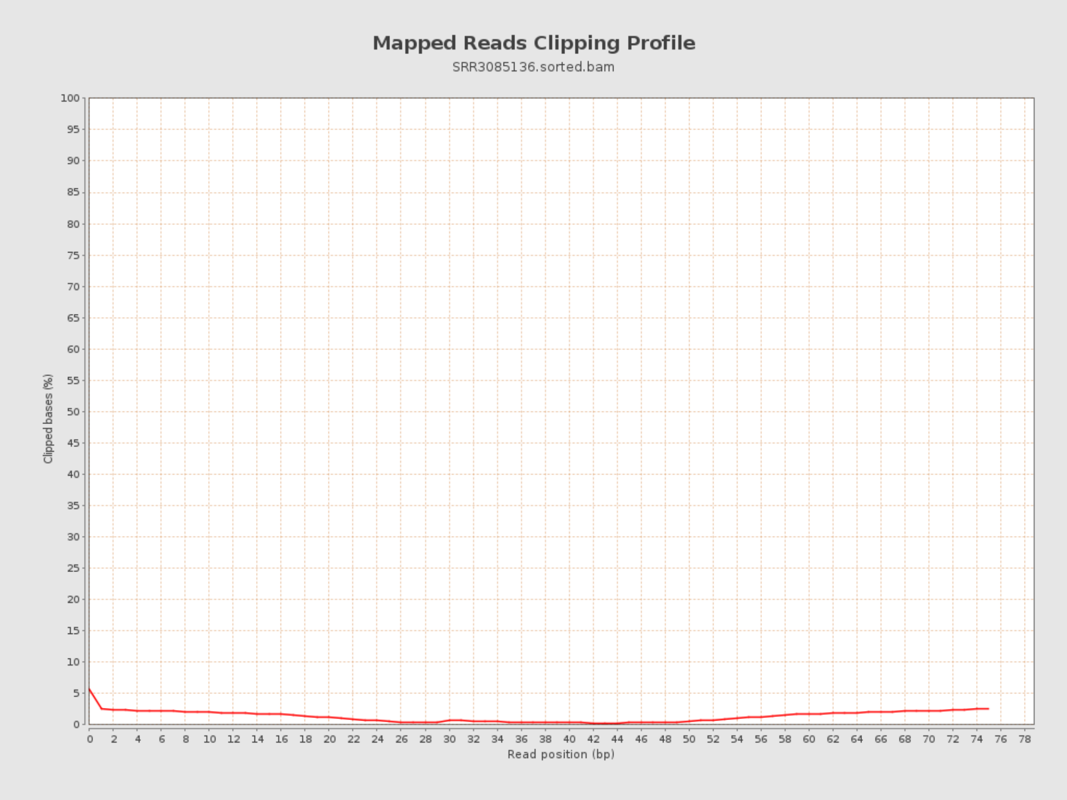
8. Results : Mapped Reads Nucleotide Content



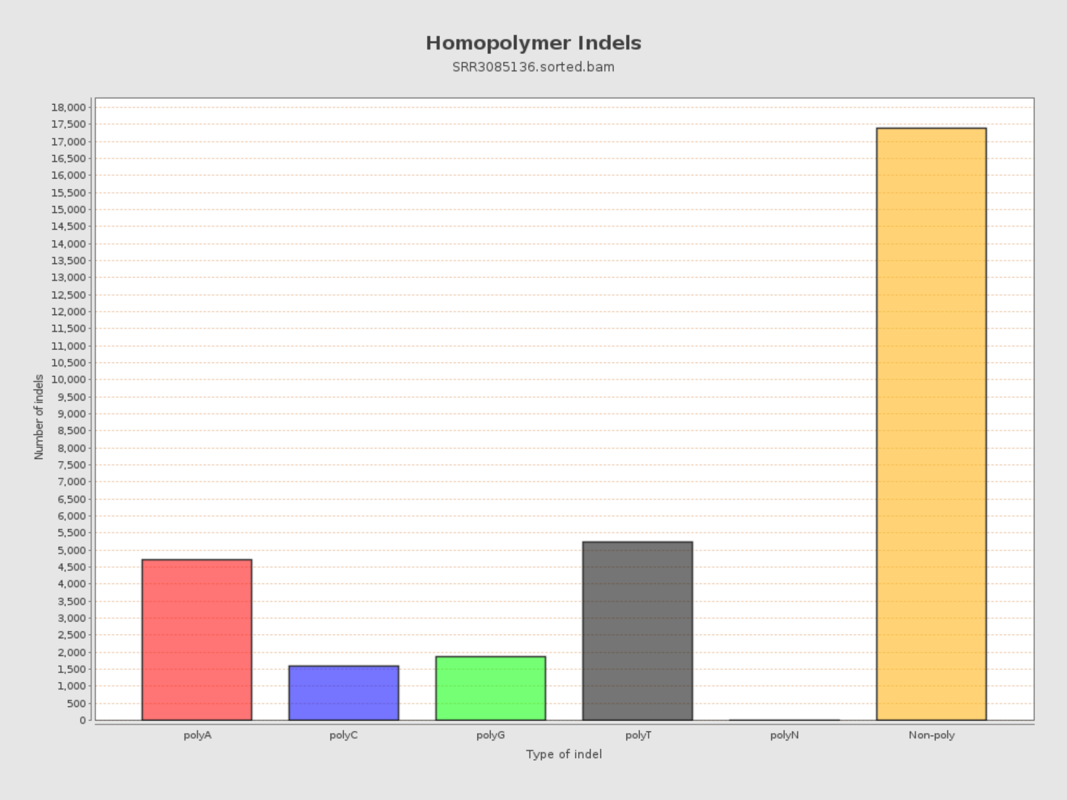
9. Results : Mapped Reads GC-content Distribution



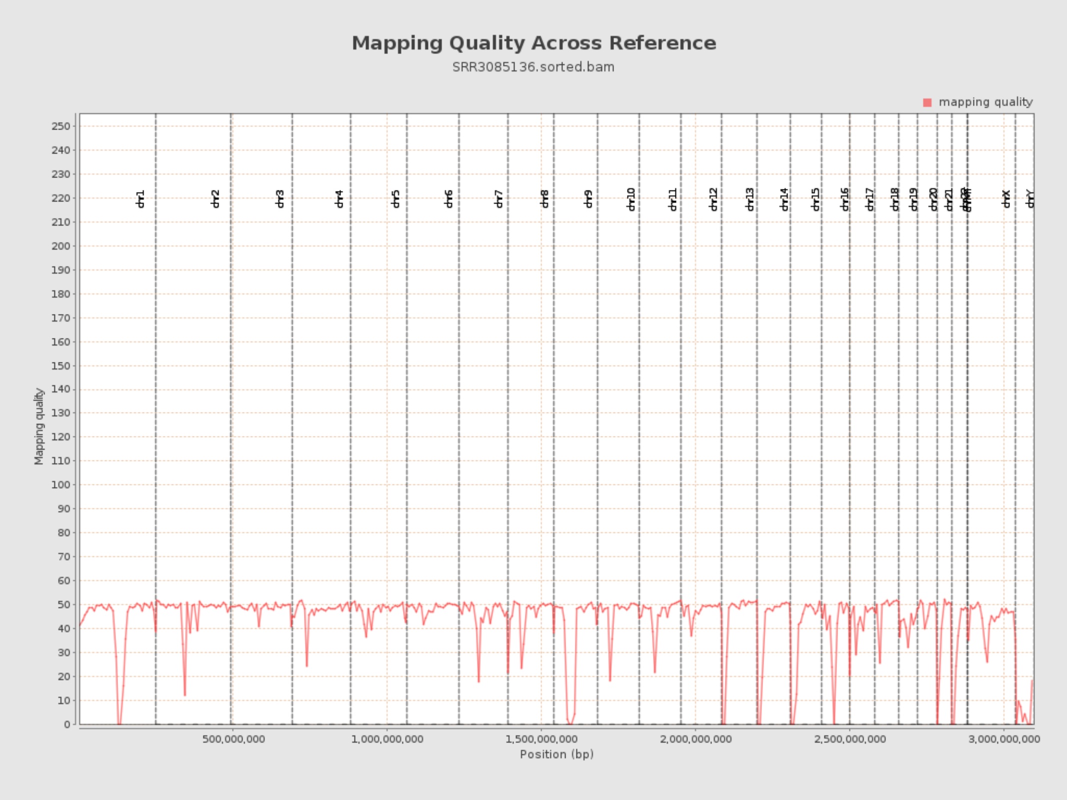
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram