Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:43:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085091.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_SRR3085091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:43:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,878,368
Mapped reads	1,533,027 / 81.61%
Unmapped reads	345,341 / 18.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,012 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	39,183 / 2.09%
Duplication rate	1.97%
Clipped reads	1,067,010 / 56.81%

2.2. ACGT Content

Number/percentage of A's	26,853,470 / 29.04%
Number/percentage of C's	18,462,360 / 19.97%
Number/percentage of T's	26,145,935 / 28.28%
Number/percentage of G's	20,995,288 / 22.71%
Number/percentage of N's	2,003 / 0%
GC Percentage	42.68%

2.3. Coverage

Mean	0.0299

Standard Deviation	0.2548

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

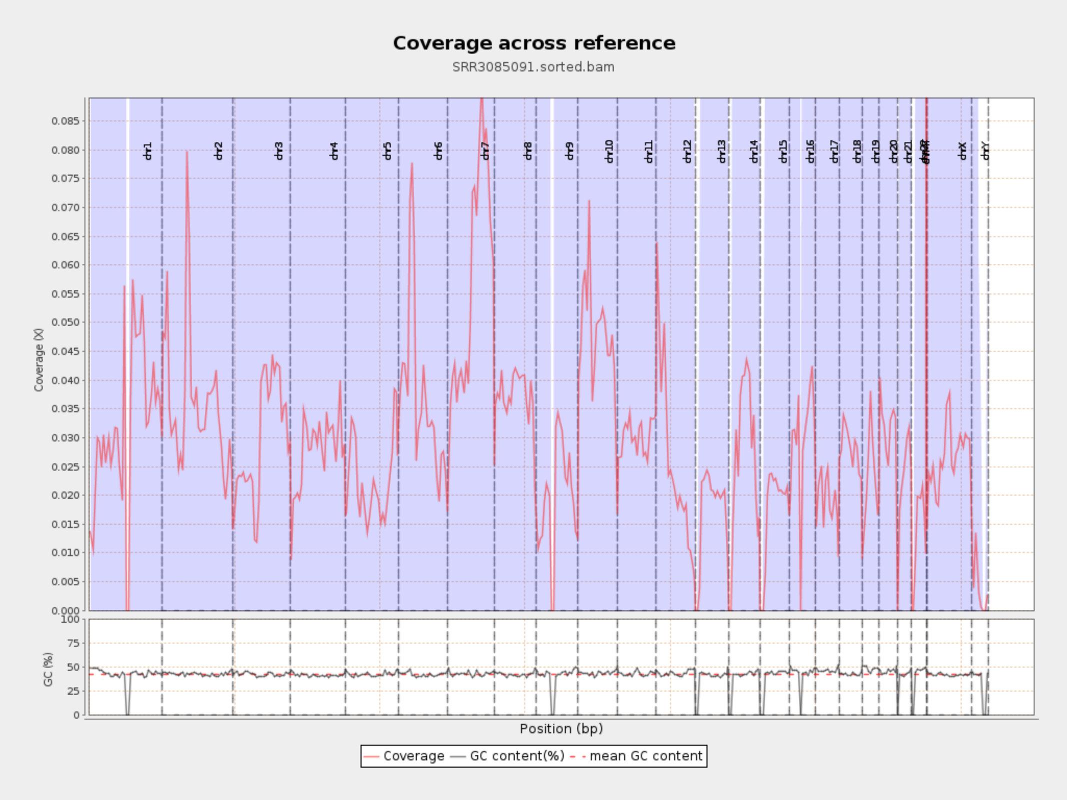
General error rate	0.91%
Mismatches	825,667
Insertions	7,375
Mapped reads with at least one insertion	0.48%
Deletions	18,682
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.65%

2.6. Chromosome stats

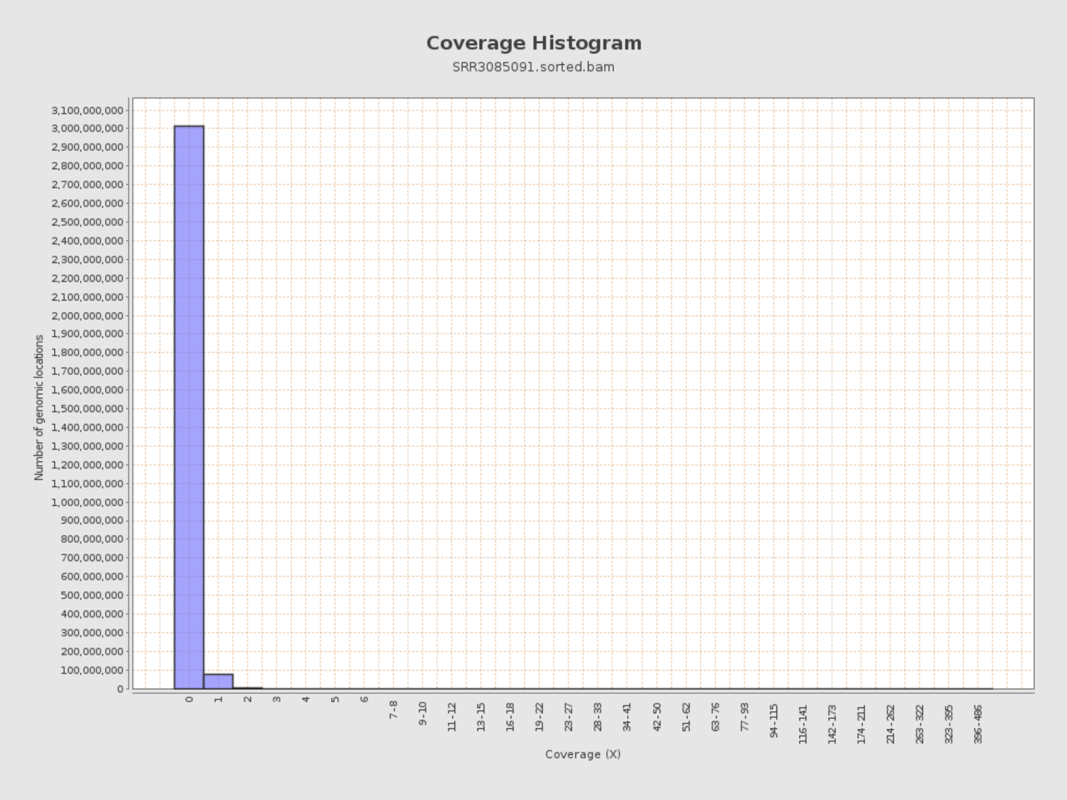
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8014093	0.0322	0.3913
chr2	243199373	8816578	0.0363	0.2958
chr3	198022430	5858558	0.0296	0.1868
chr4	191154276	5302654	0.0277	0.1874
chr5	180915260	4083902	0.0226	0.1611
chr6	171115067	6388672	0.0373	0.2477
chr7	159138663	9143181	0.0575	0.3024

chr8	146364022	5457508	0.0373	0.3554
chr9	141213431	2764932	0.0196	0.2224
chr10	135534747	6557942	0.0484	0.3683
chr11	135006516	4049638	0.03	0.255
chr12	133851895	3471939	0.0259	0.1755
chr13	115169878	1974737	0.0171	0.1382
chr14	107349540	2869528	0.0267	0.1836
chr15	102531392	1777410	0.0173	0.1403
chr16	90354753	2726249	0.0302	0.2013
chr17	81195210	1532226	0.0189	0.1657
chr18	78077248	2219533	0.0284	0.3779
chr19	59128983	1371273	0.0232	0.2987
chr20	63025520	1994750	0.0316	0.1936
chr21	48129895	1085568	0.0226	0.1726
chr22	51304566	678017	0.0132	0.1224
chrMT	16571	6925	0.4179	0.6795
chrX	155270560	4118341	0.0265	0.1948
chrY	59373566	224929	0.0038	0.0946

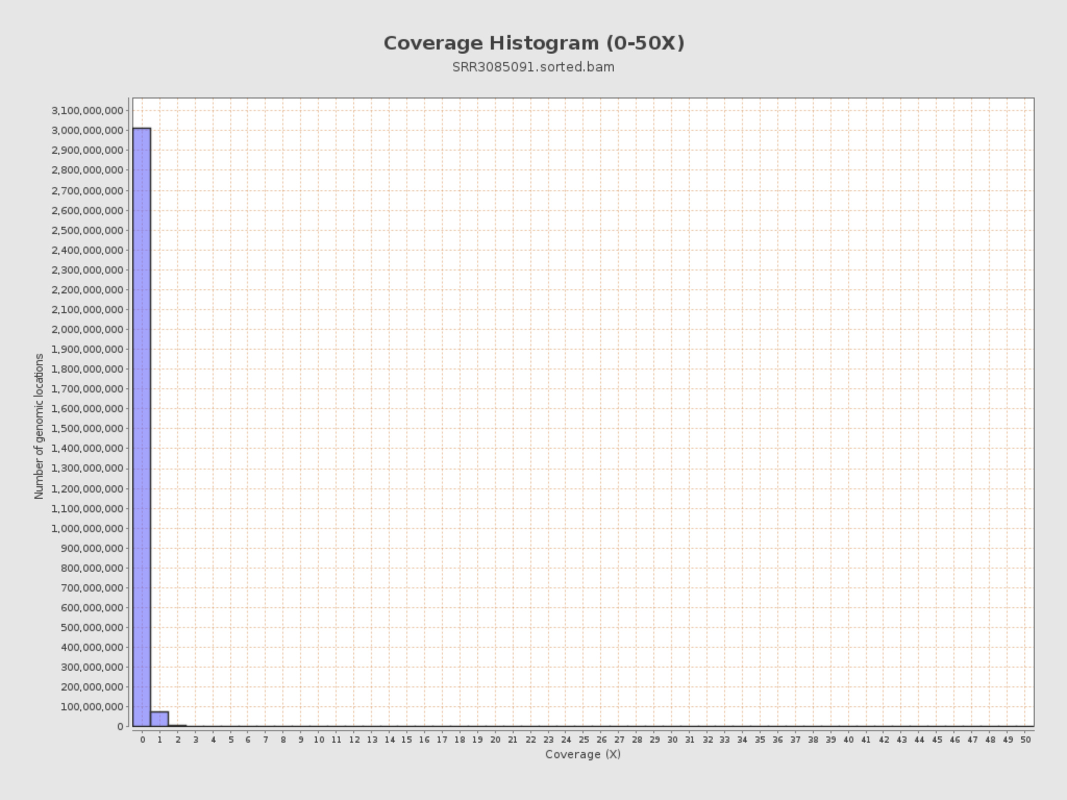
3. Results : Coverage across reference



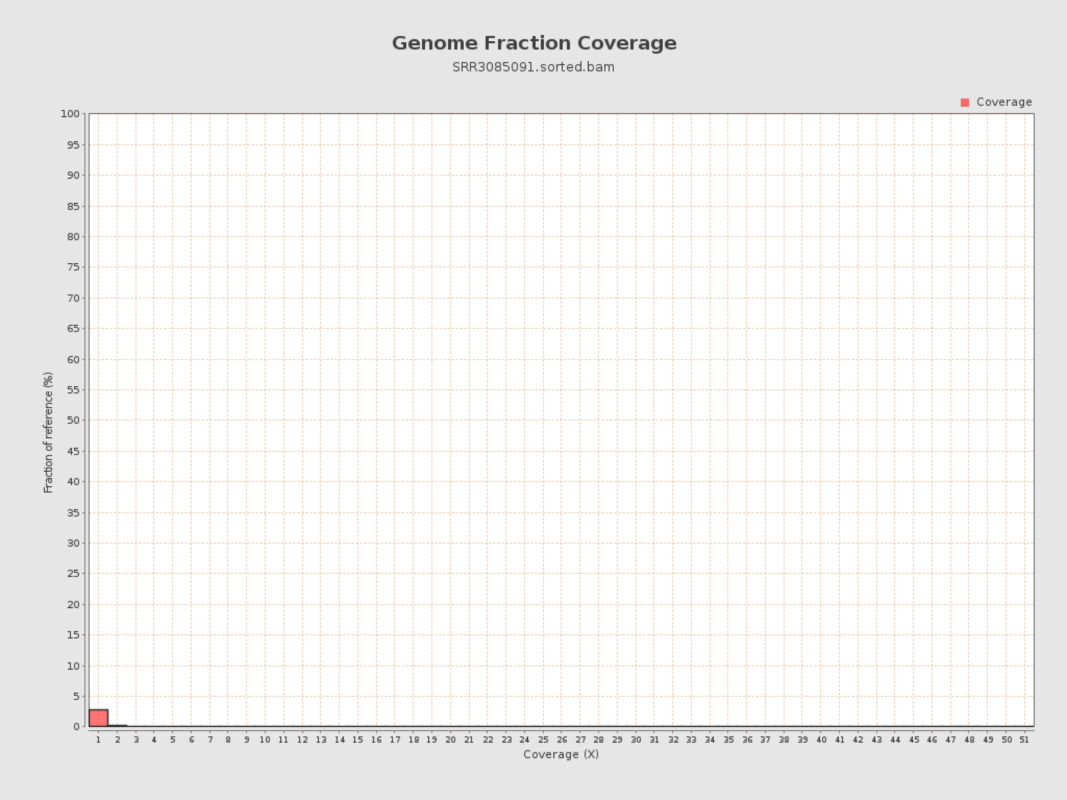
4. Results : Coverage Histogram



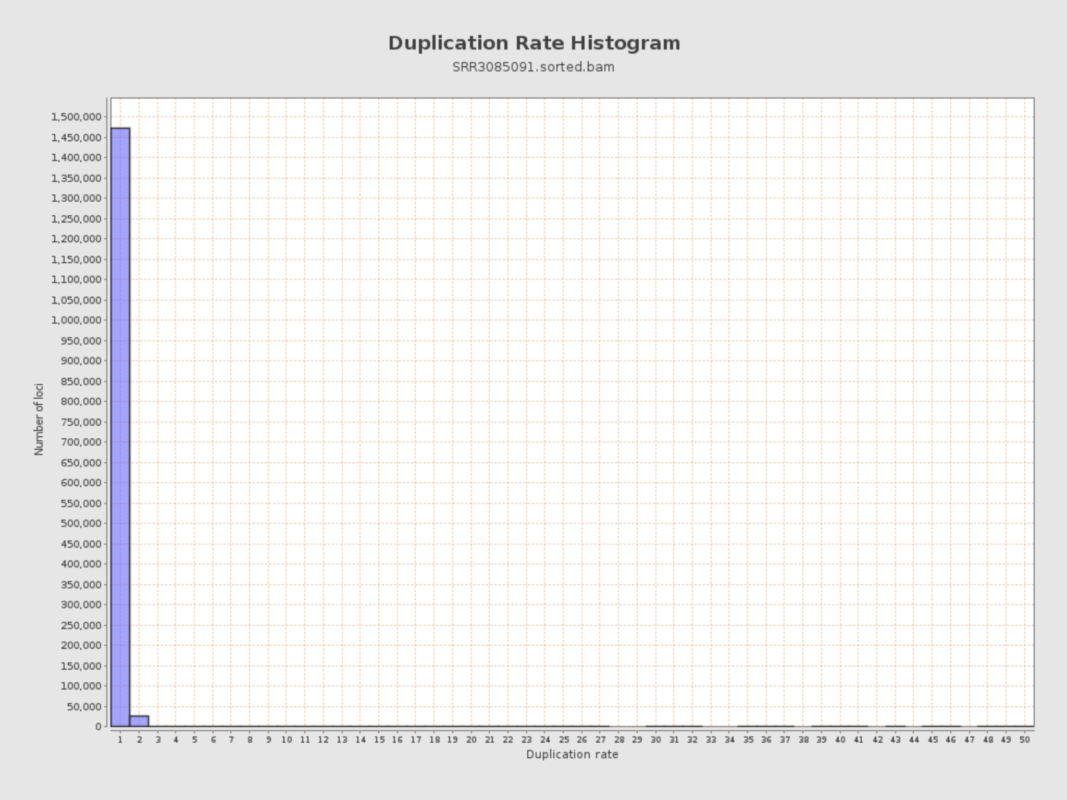
5. Results : Coverage Histogram (0-50X)



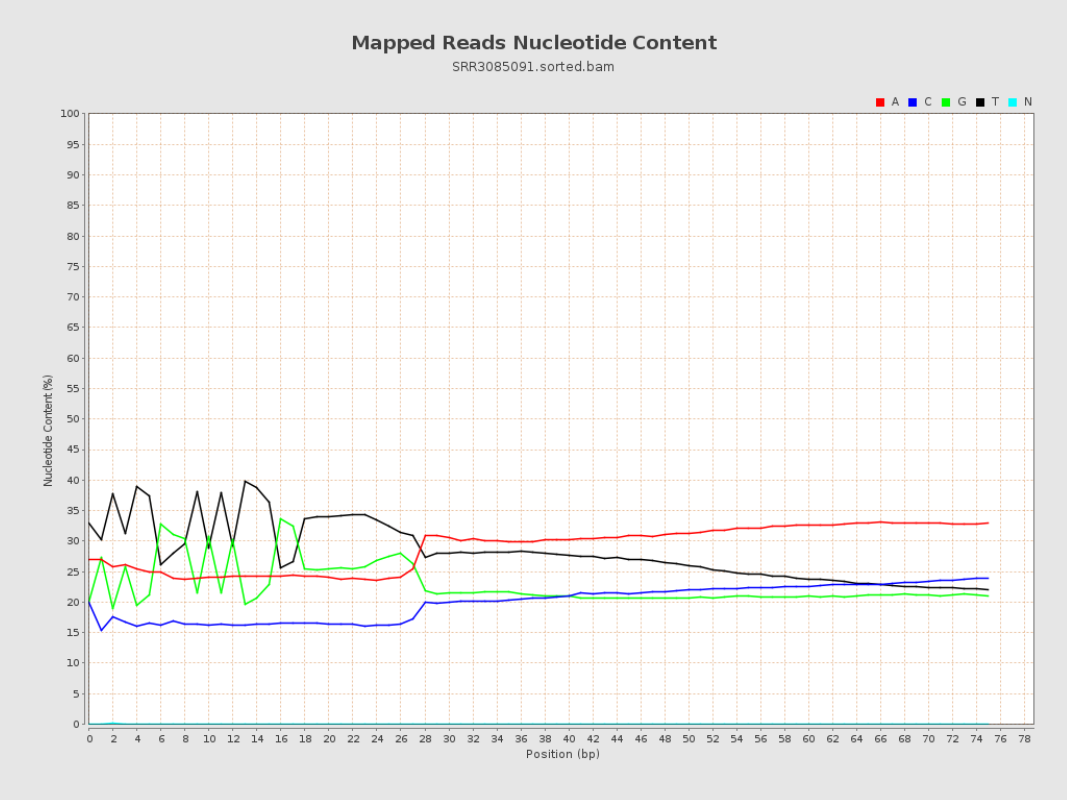
6. Results : Genome Fraction Coverage



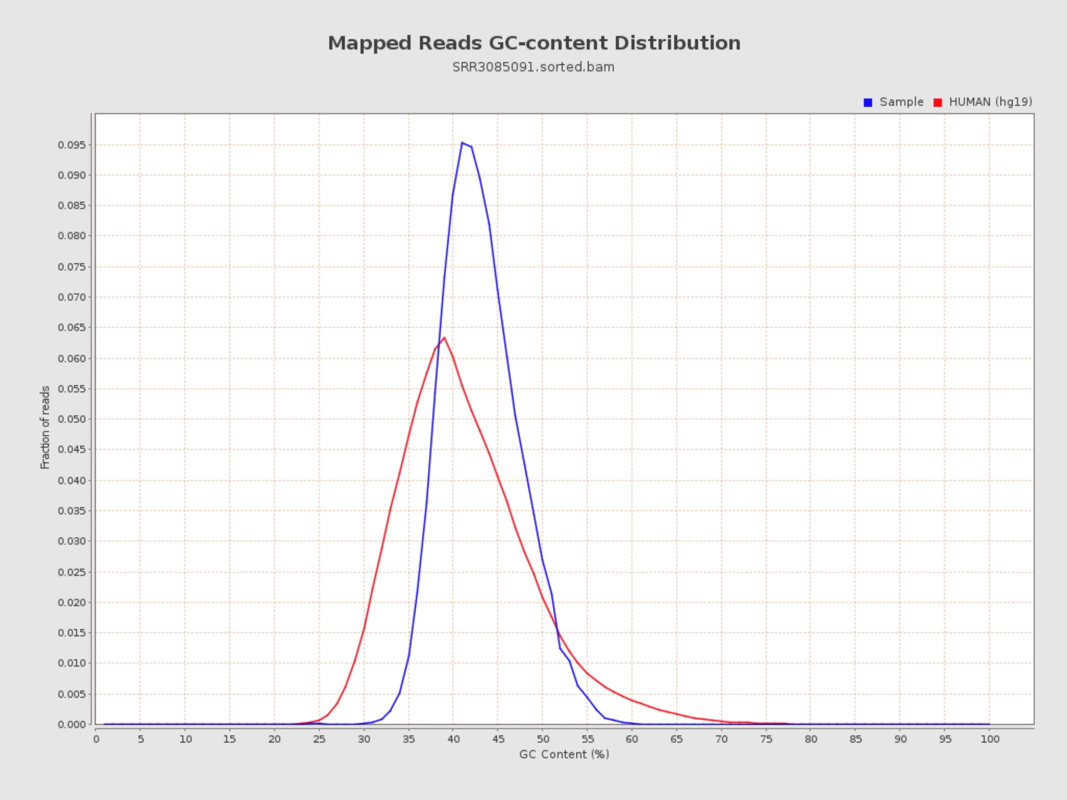
7. Results : Duplication Rate Histogram



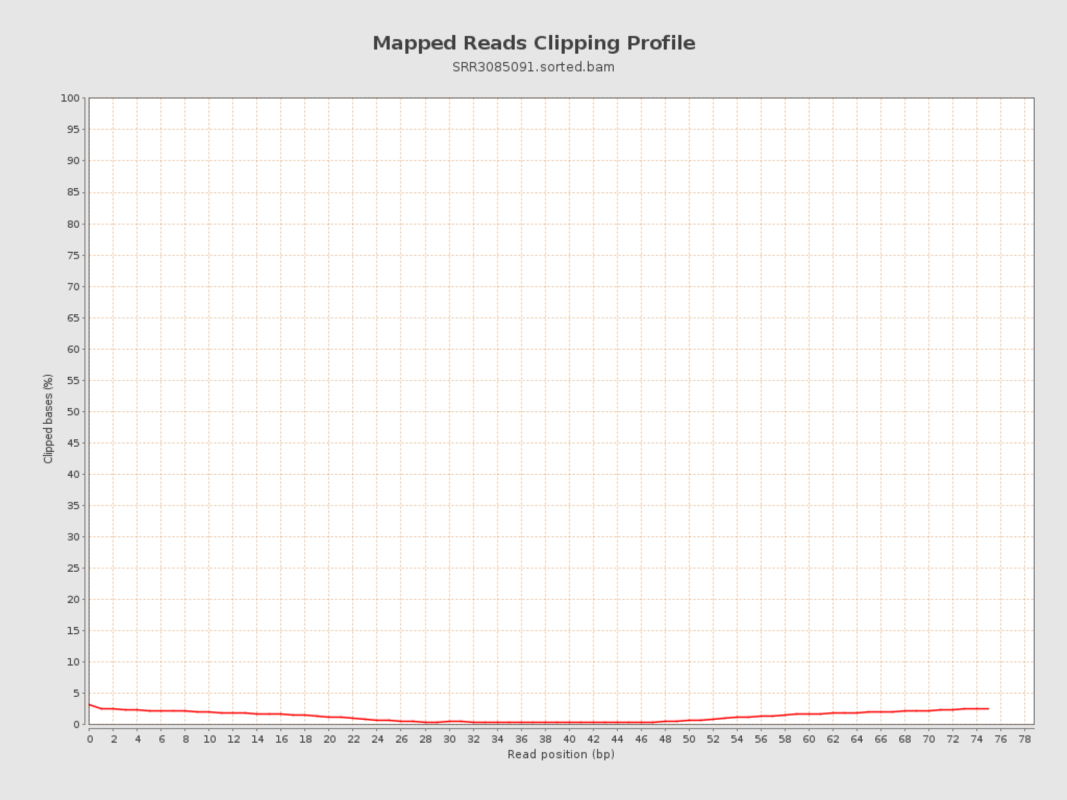
8. Results : Mapped Reads Nucleotide Content



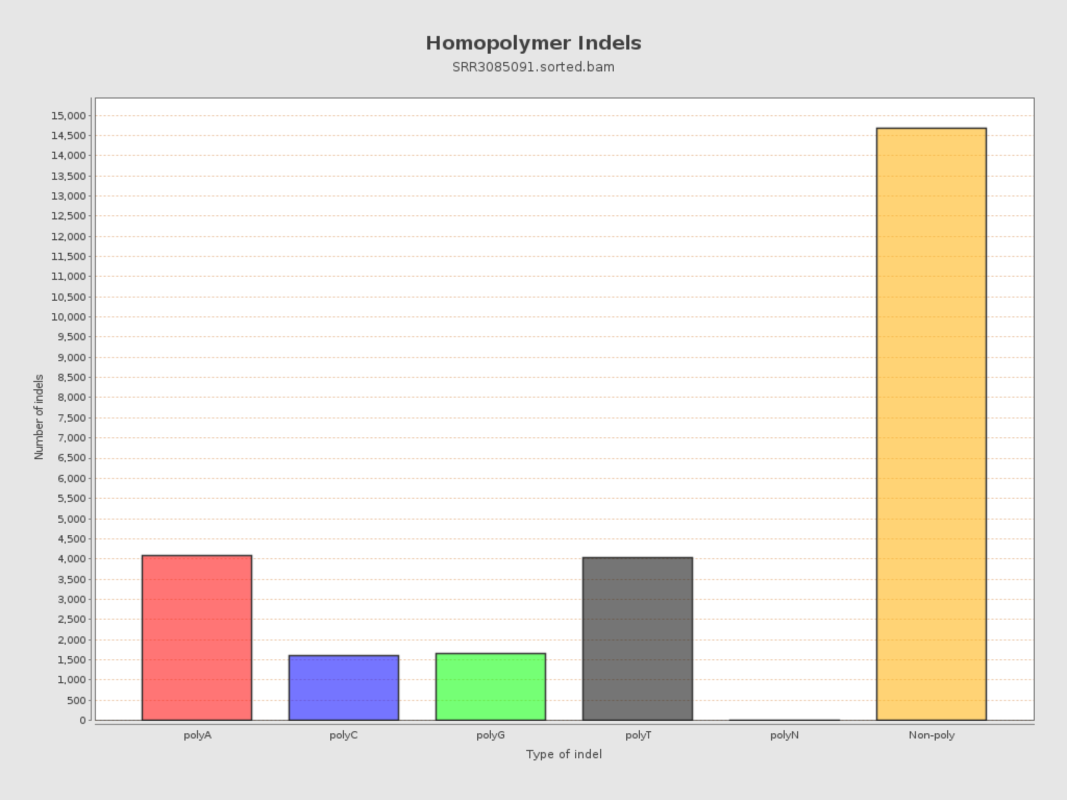
9. Results : Mapped Reads GC-content Distribution



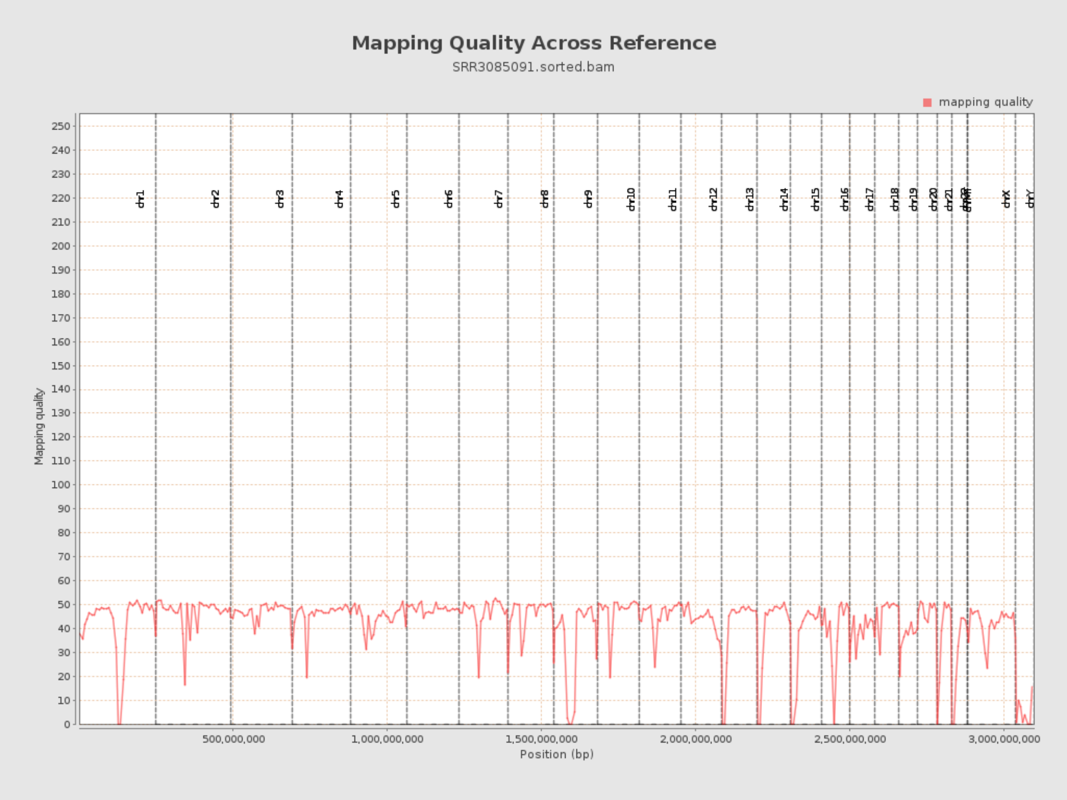
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram