Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:06:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472805.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_SRR3472805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:06:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,209,382
Mapped reads	2,246,424 / 70%
Unmapped reads	962,958 / 30%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,015 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	195,181 / 6.08%
Duplication rate	5.77%
Clipped reads	1,395,570 / 43.48%

2.2. ACGT Content

Number/percentage of A's	38,000,767 / 27.15%
Number/percentage of C's	27,364,584 / 19.55%
Number/percentage of T's	41,615,793 / 29.74%
Number/percentage of G's	32,956,425 / 23.55%
Number/percentage of N's	3,091 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.4154

2.4. Mapping Quality

Mean Mapping Quality	42.5

2.5. Mismatches and indels

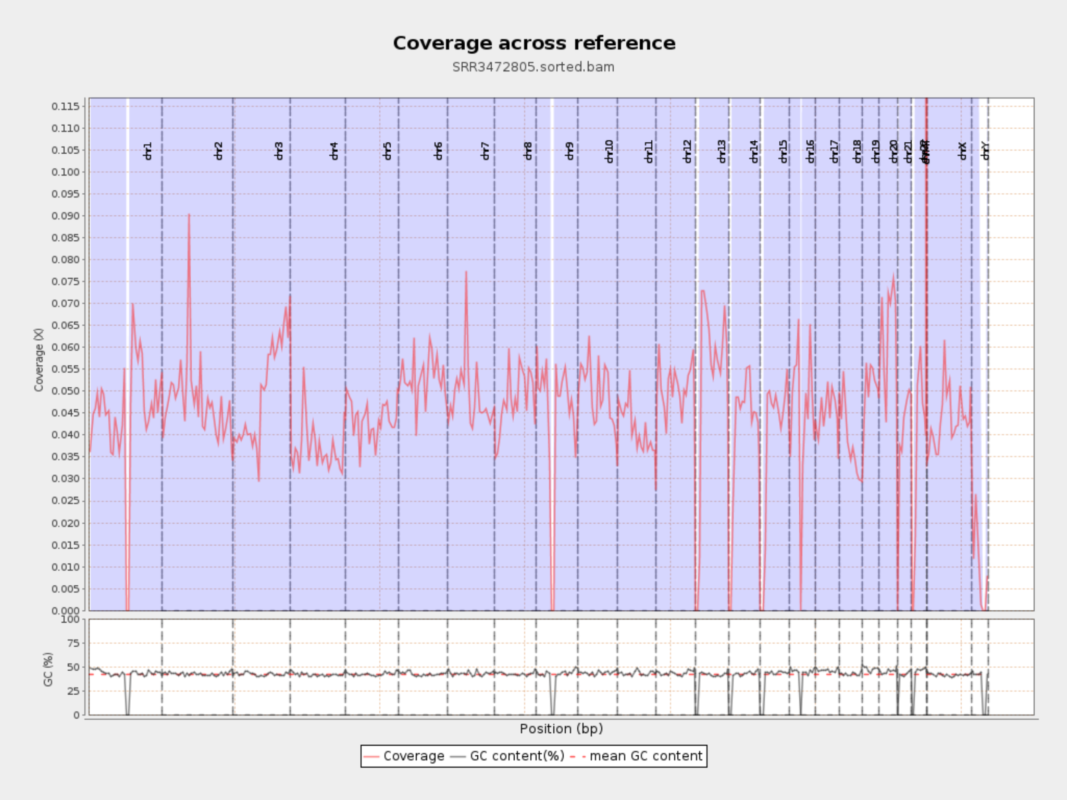
General error rate	0.94%
Mismatches	1,300,610
Insertions	11,224
Mapped reads with at least one insertion	0.49%
Deletions	38,812
Mapped reads with at least one deletion	1.71%
Homopolymer indels	46.14%

2.6. Chromosome stats

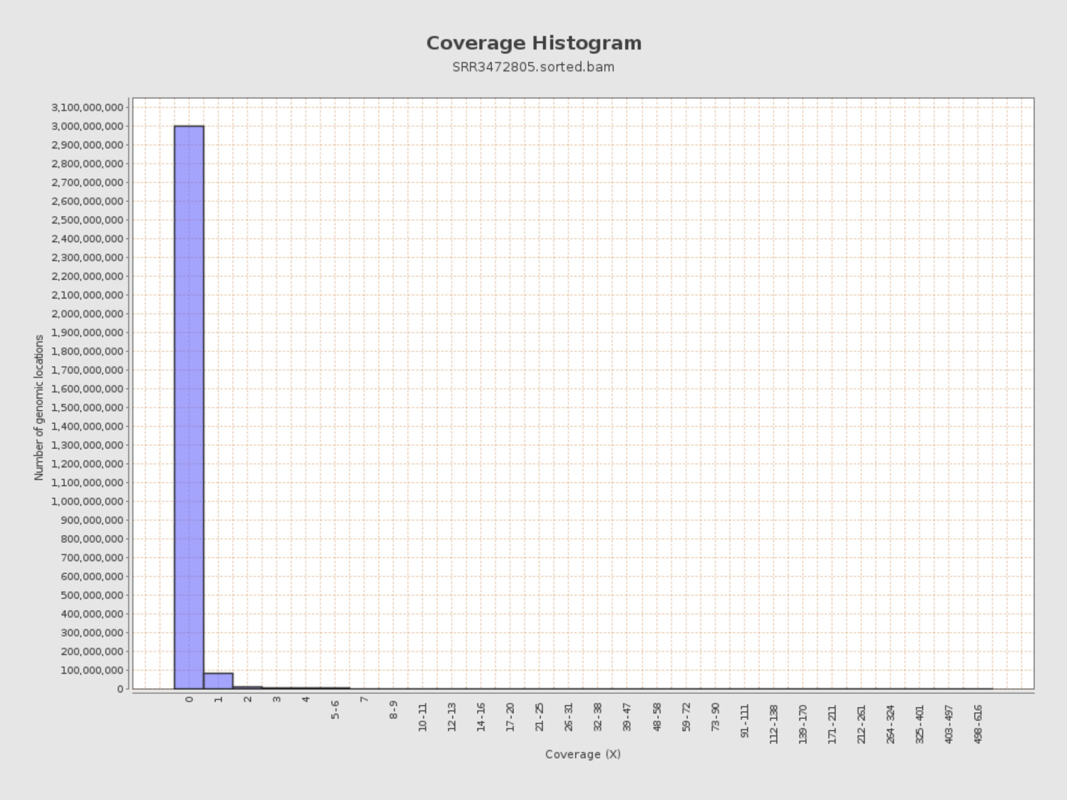
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11111801	0.0446	0.5011
chr2	243199373	11726559	0.0482	0.5238
chr3	198022430	9771630	0.0493	0.3263
chr4	191154276	7039627	0.0368	0.3196
chr5	180915260	7867574	0.0435	0.3151
chr6	171115067	9078716	0.0531	0.3709
chr7	159138663	7808982	0.0491	0.5738

chr8	146364022	7019863	0.048	0.4037
chr9	141213431	6158348	0.0436	0.4331
chr10	135534747	6770430	0.05	0.4054
chr11	135006516	5612996	0.0416	0.4312
chr12	133851895	6826766	0.051	0.362
chr13	115169878	5985927	0.052	0.3369
chr14	107349540	4289776	0.04	0.3621
chr15	102531392	3920909	0.0382	0.3509
chr16	90354753	4120647	0.0456	0.347
chr17	81195210	3661496	0.0451	0.3599
chr18	78077248	3036397	0.0389	0.7014
chr19	59128983	2999999	0.0507	0.4356
chr20	63025520	4019114	0.0638	0.4008
chr21	48129895	1920697	0.0399	0.3274
chr22	51304566	1781805	0.0347	0.2821
chrMT	16571	189839	11.4561	8.4902
chrX	155270560	6735541	0.0434	0.3573
chrY	59373566	555427	0.0094	0.1706

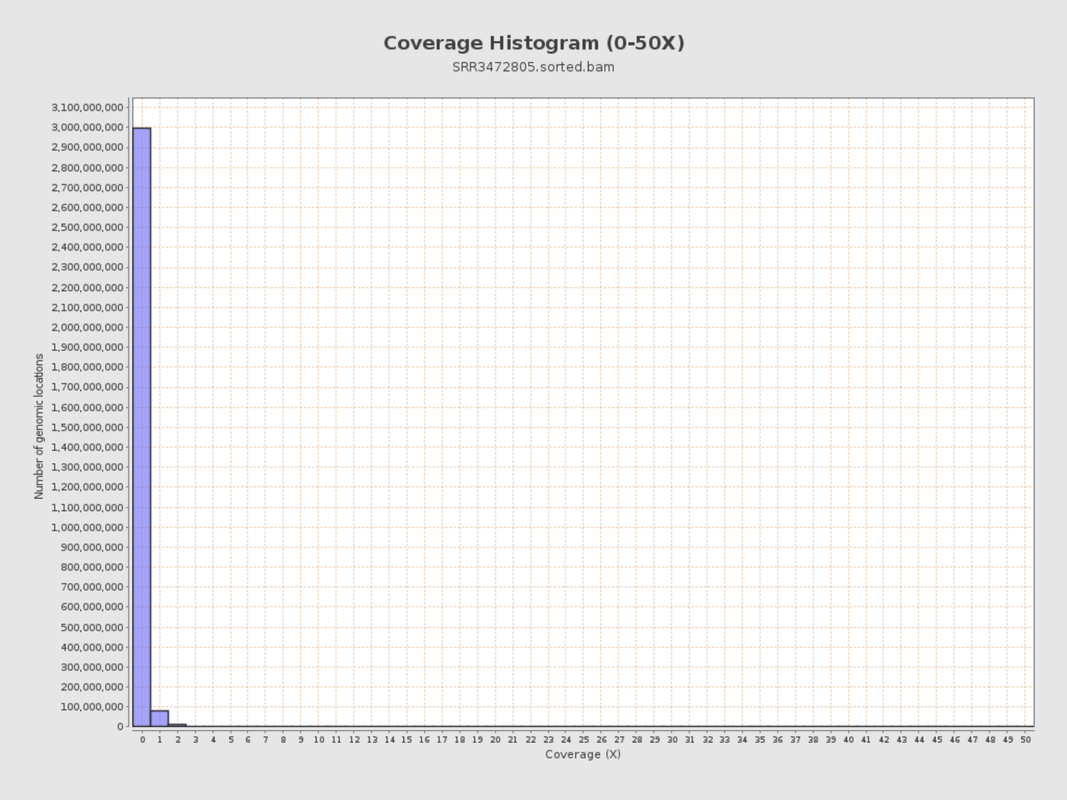
3. Results : Coverage across reference



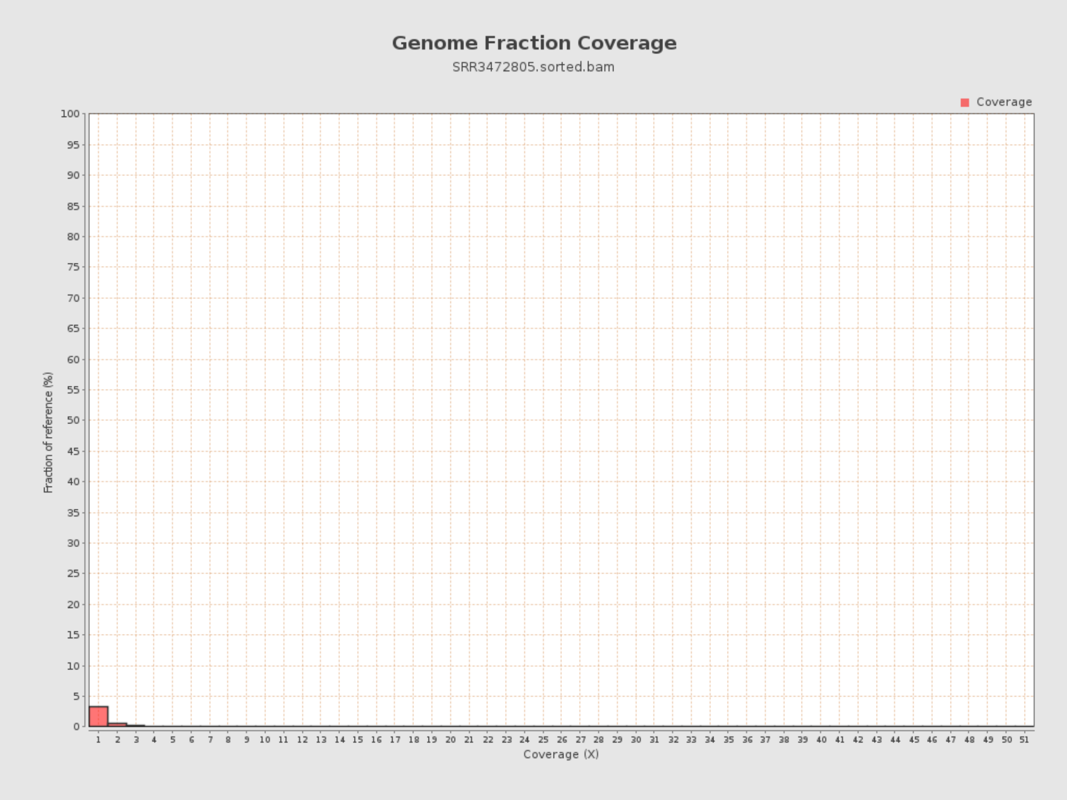
4. Results : Coverage Histogram



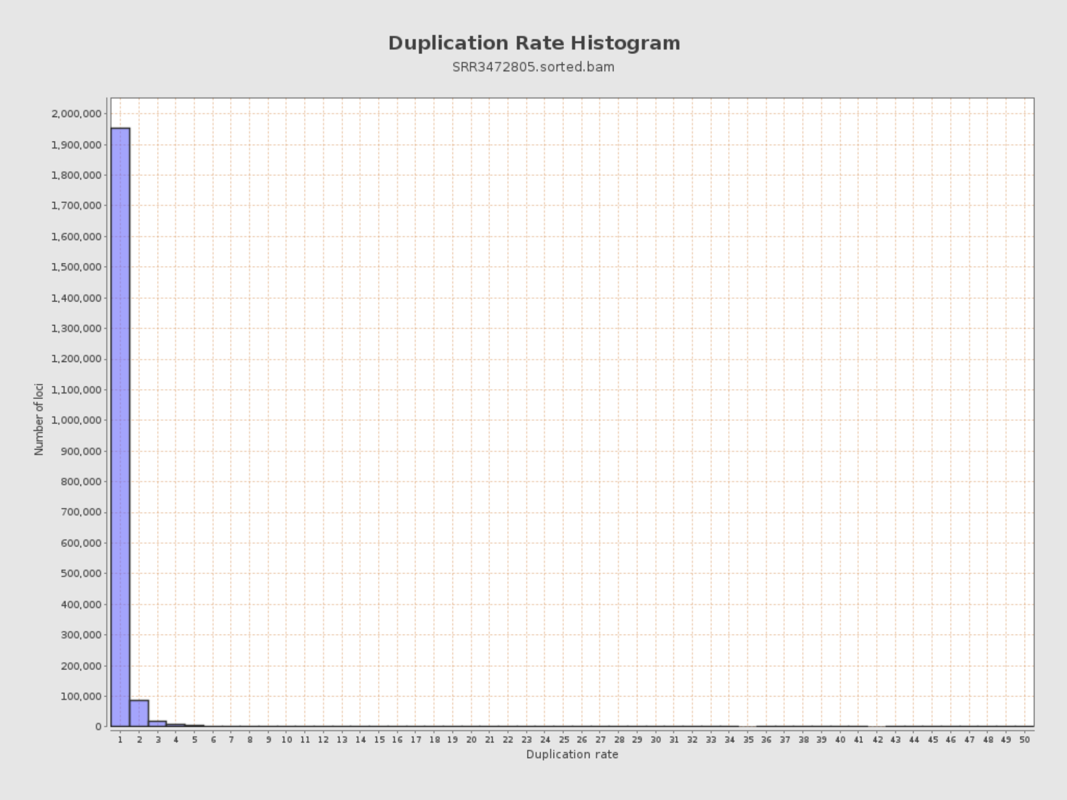
5. Results : Coverage Histogram (0-50X)



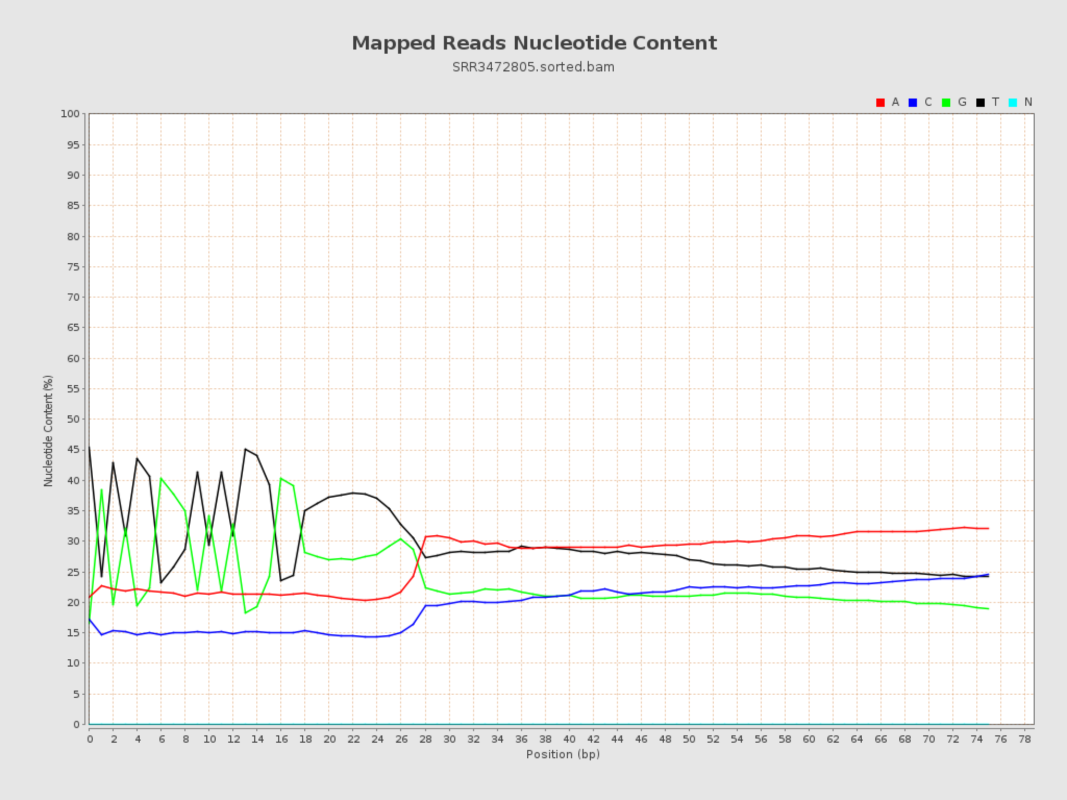
6. Results : Genome Fraction Coverage



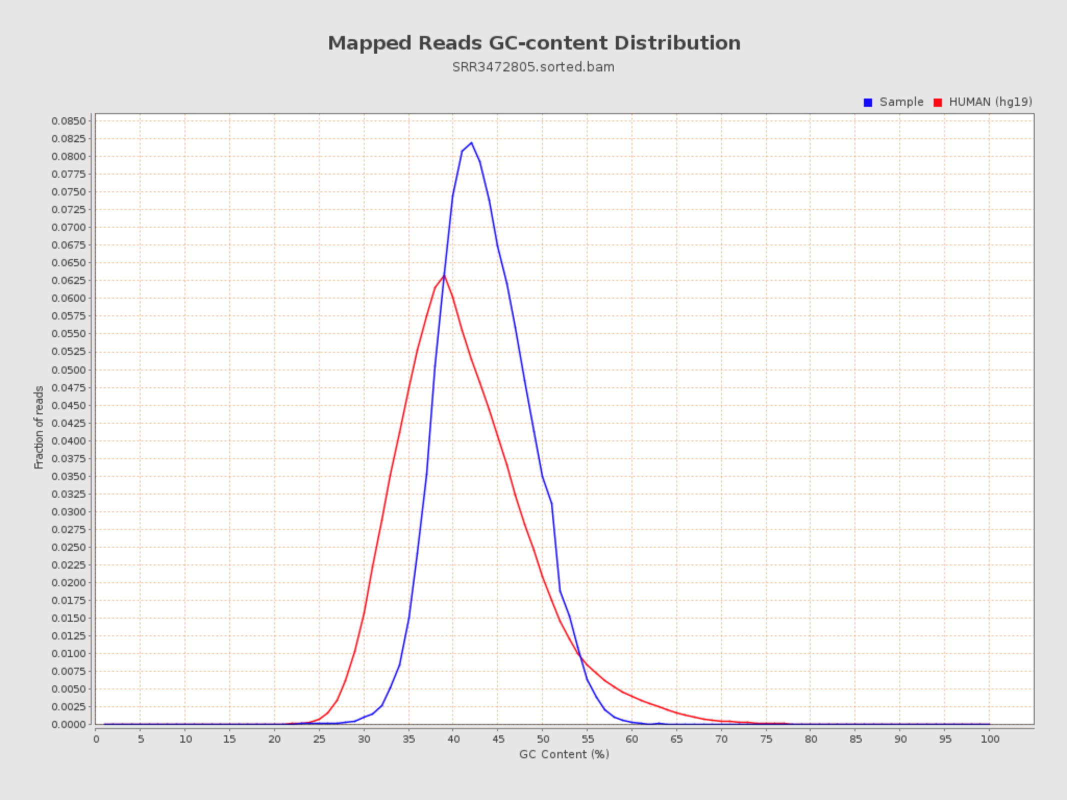
7. Results : Duplication Rate Histogram



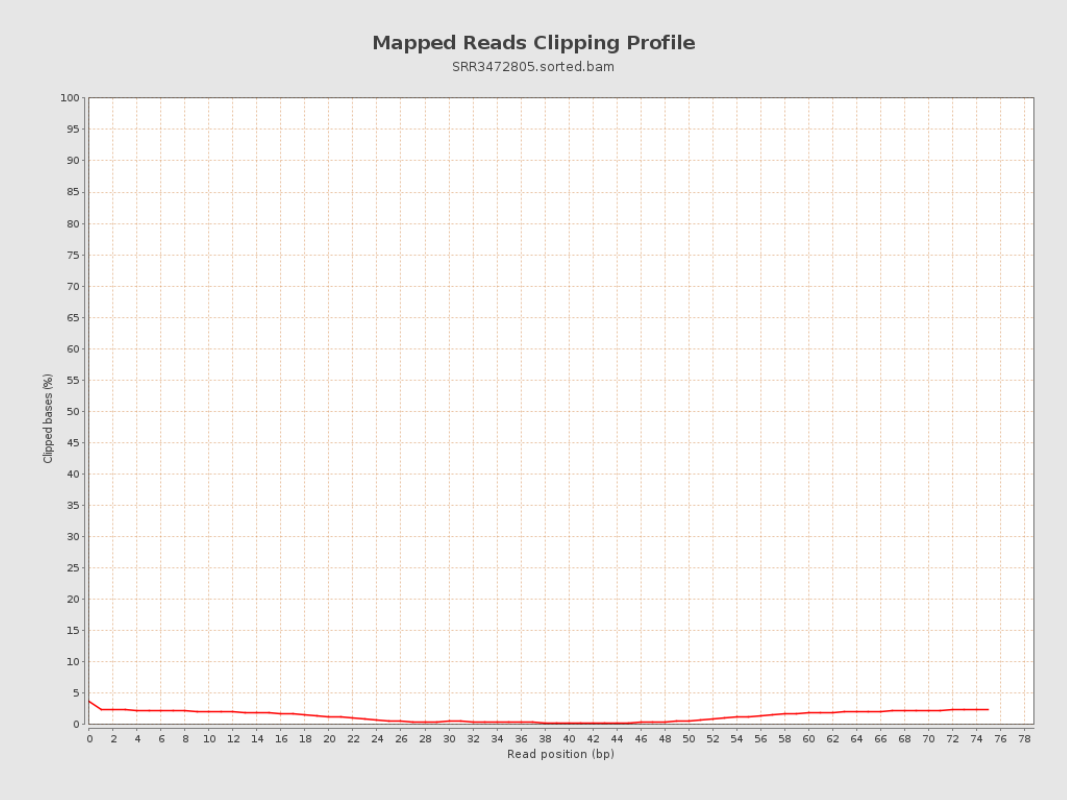
8. Results : Mapped Reads Nucleotide Content



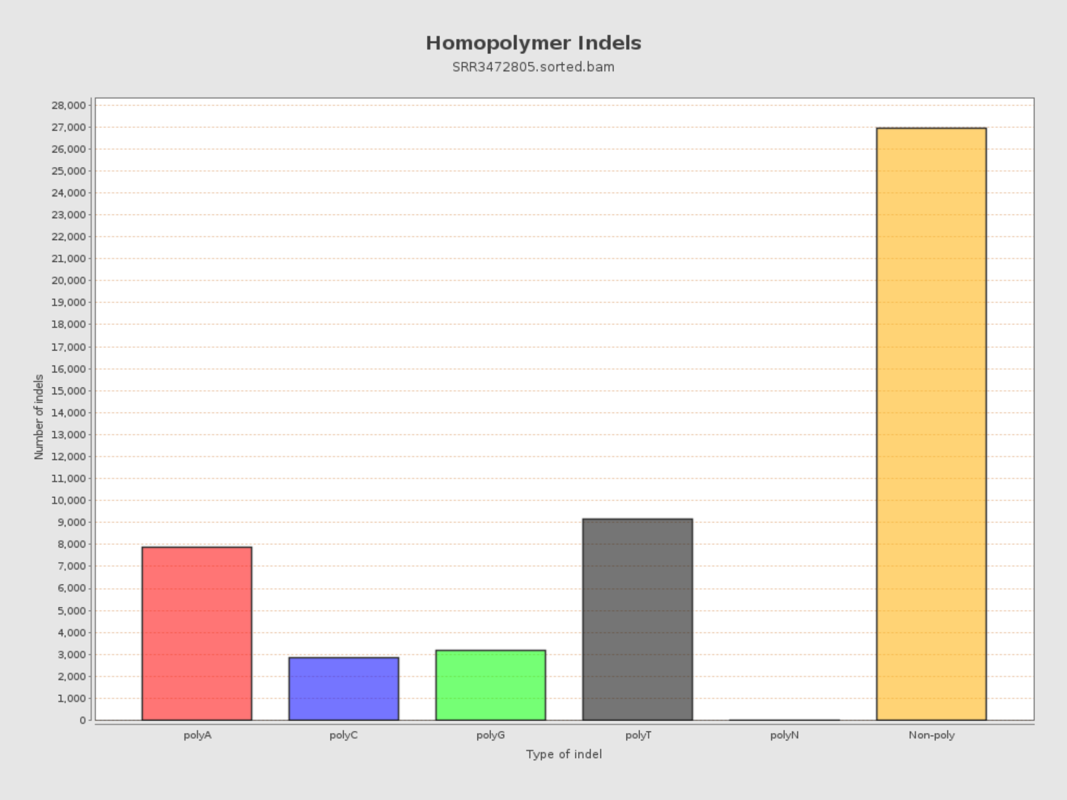
9. Results : Mapped Reads GC-content Distribution



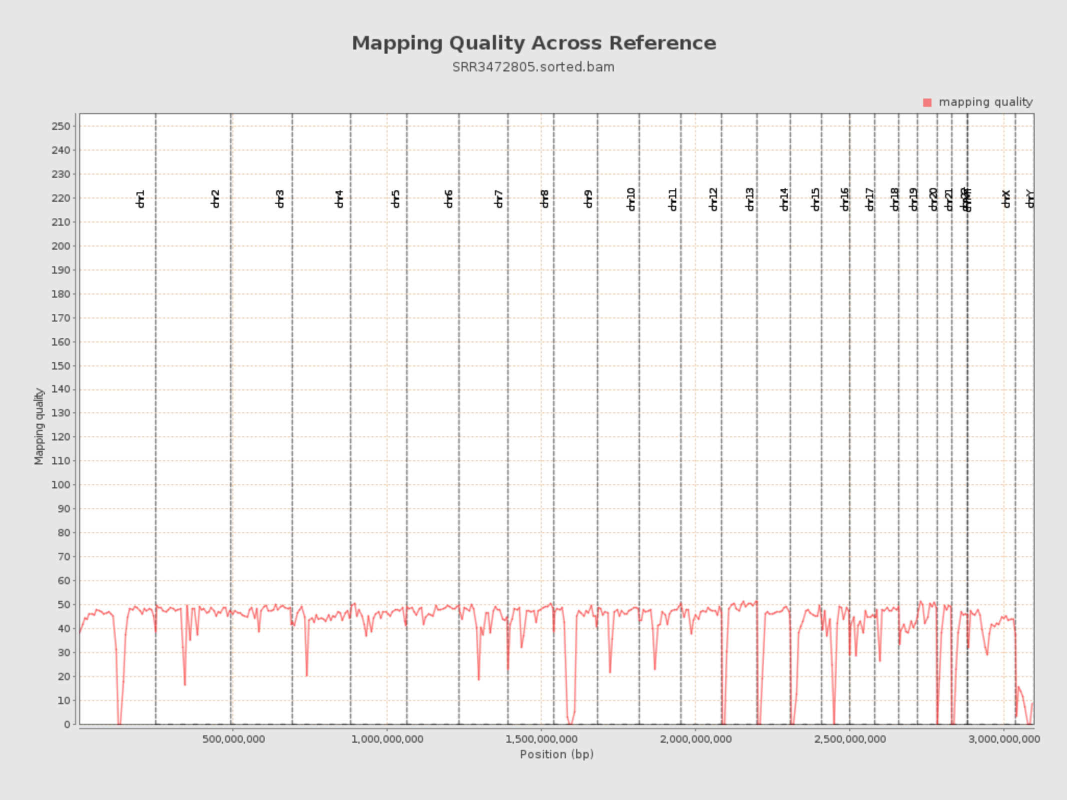
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram