Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:11:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084275.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_SRR3084275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084275.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:11:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,815,066
Mapped reads	2,553,144 / 90.7%
Unmapped reads	261,922 / 9.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,111 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	87,666 / 3.11%
Duplication rate	2.75%
Clipped reads	1,278,885 / 45.43%

2.2. ACGT Content

Number/percentage of A's	45,683,586 / 27.16%
Number/percentage of C's	32,521,956 / 19.33%
Number/percentage of T's	51,277,094 / 30.48%
Number/percentage of G's	38,500,041 / 22.89%
Number/percentage of N's	226,350 / 0.13%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.3711

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

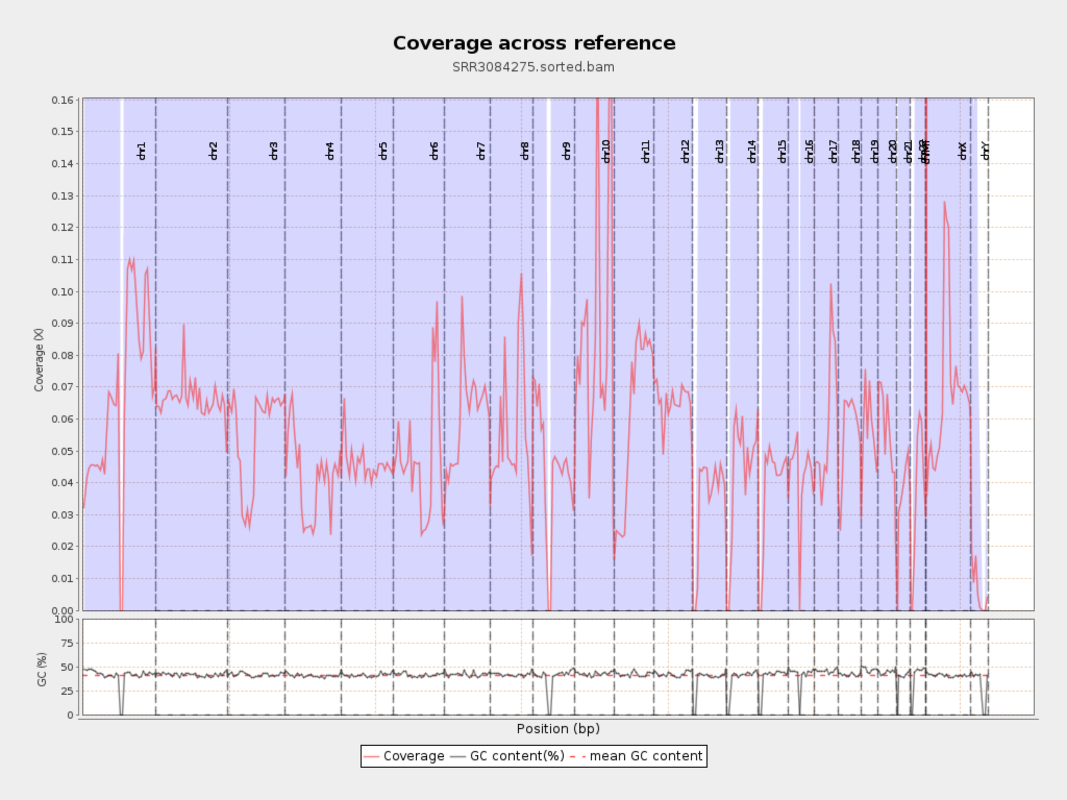
General error rate	1.02%
Mismatches	1,698,915
Insertions	12,617
Mapped reads with at least one insertion	0.49%
Deletions	35,189
Mapped reads with at least one deletion	1.37%
Homopolymer indels	45.52%

2.6. Chromosome stats

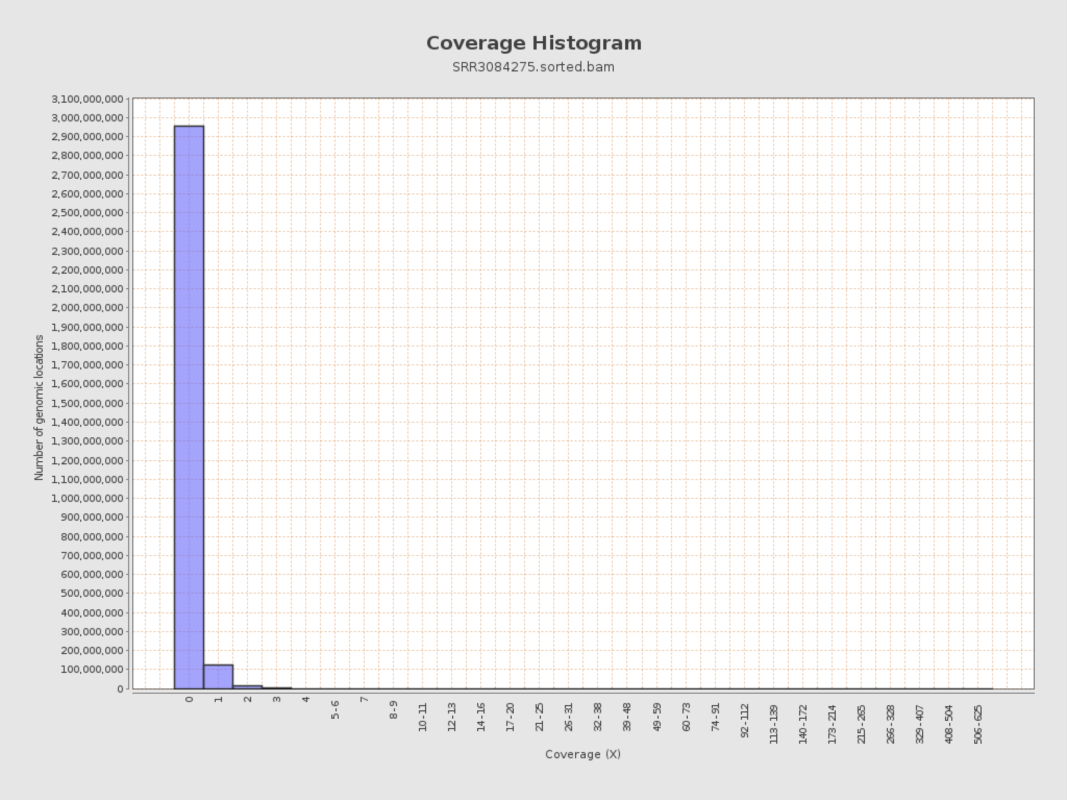
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16512207	0.0662	0.5612
chr2	243199373	16129876	0.0663	0.4501
chr3	198022430	10964045	0.0554	0.2736
chr4	191154276	7928526	0.0415	0.2431
chr5	180915260	8366631	0.0462	0.2449
chr6	171115067	8190321	0.0479	0.2902
chr7	159138663	9711373	0.061	0.5983

chr8	146364022	8051289	0.055	0.3307
chr9	141213431	6248174	0.0442	0.3043
chr10	135534747	12106887	0.0893	0.5611
chr11	135006516	8183985	0.0606	0.353
chr12	133851895	8760005	0.0654	0.2947
chr13	115169878	3979017	0.0345	0.214
chr14	107349540	4640098	0.0432	0.246
chr15	102531392	3824337	0.0373	0.231
chr16	90354753	3714527	0.0411	0.2585
chr17	81195210	4874156	0.06	0.3004
chr18	78077248	4348348	0.0557	0.4913
chr19	59128983	3392914	0.0574	0.444
chr20	63025520	3526565	0.056	0.2758
chr21	48129895	1736049	0.0361	0.2262
chr22	51304566	1887036	0.0368	0.2181
chrMT	16571	47853	2.8878	2.2434
chrX	155270560	10767012	0.0693	0.3349
chrY	59373566	374641	0.0063	0.1225

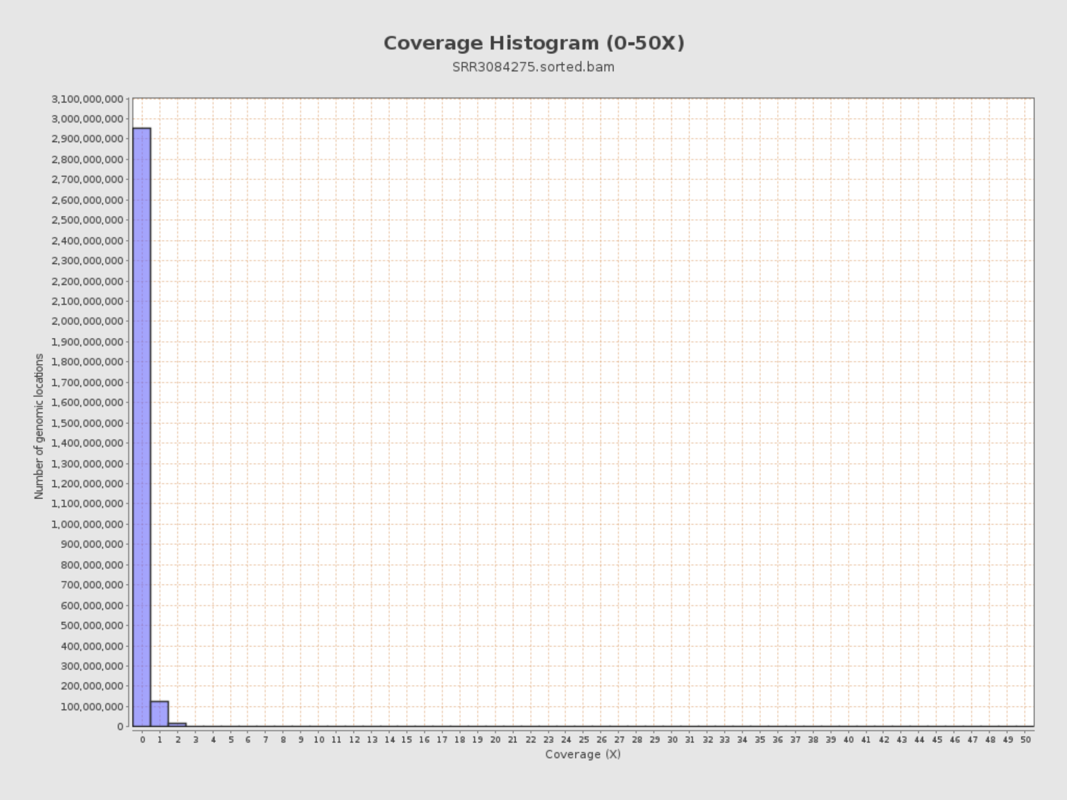
3. Results : Coverage across reference



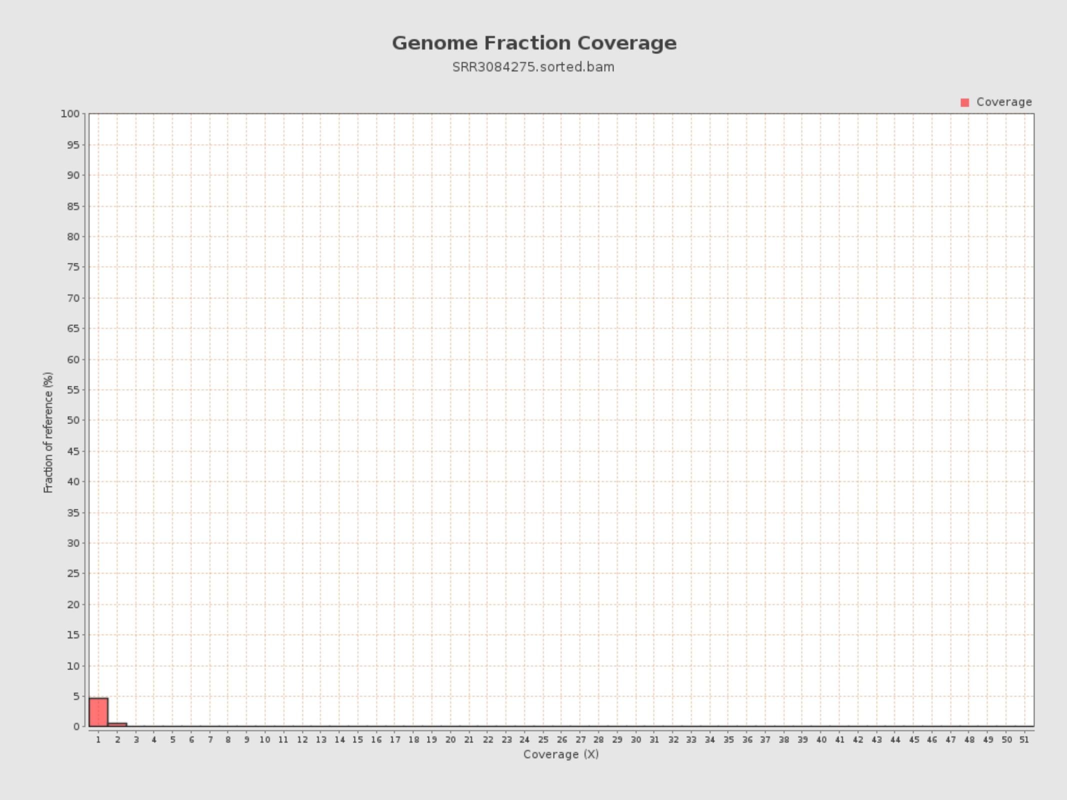
4. Results : Coverage Histogram



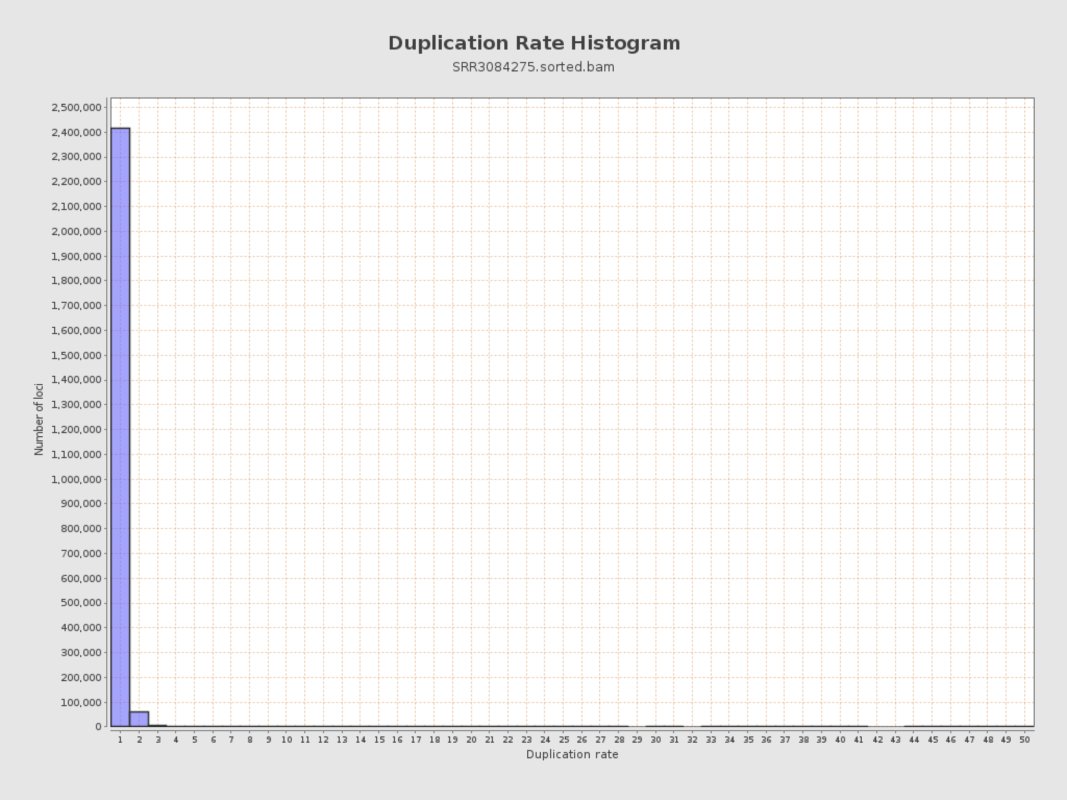
5. Results : Coverage Histogram (0-50X)



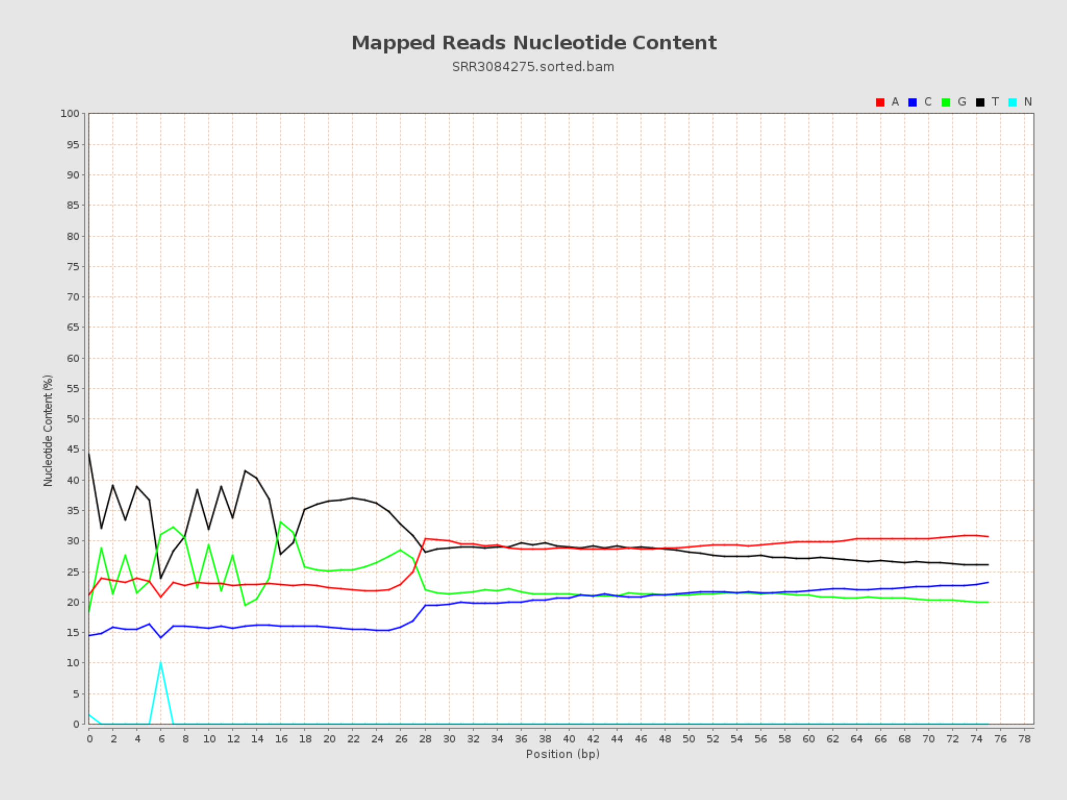
6. Results : Genome Fraction Coverage



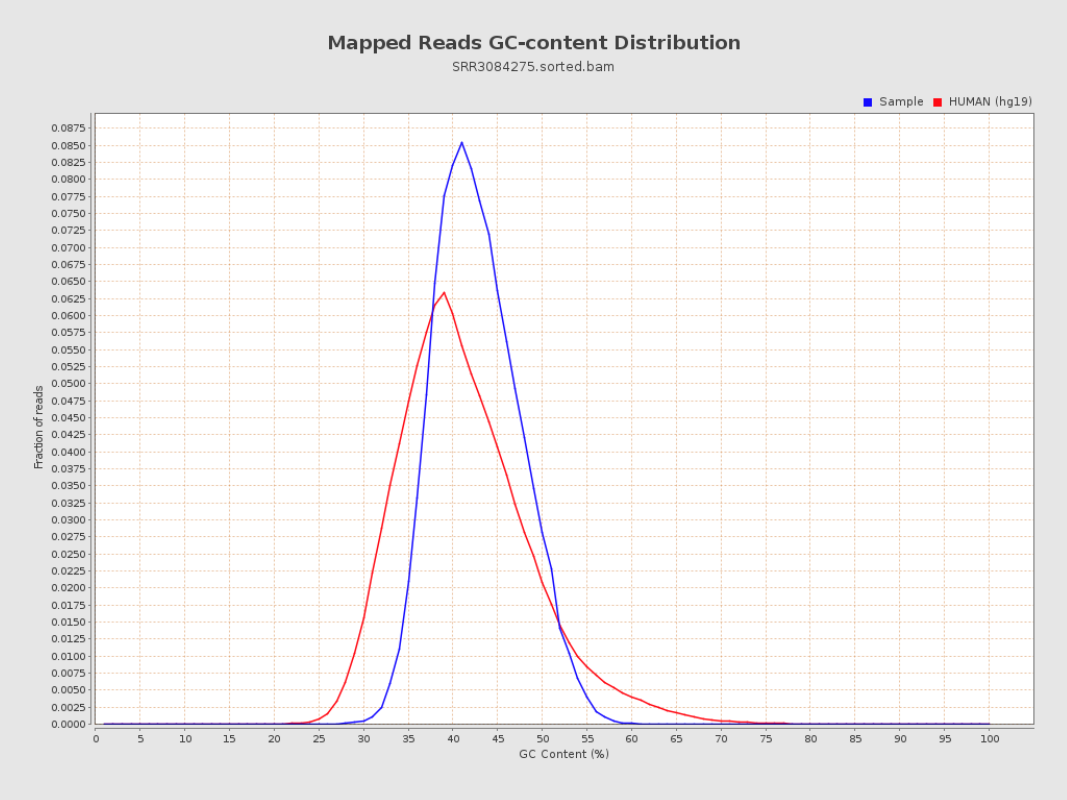
7. Results : Duplication Rate Histogram



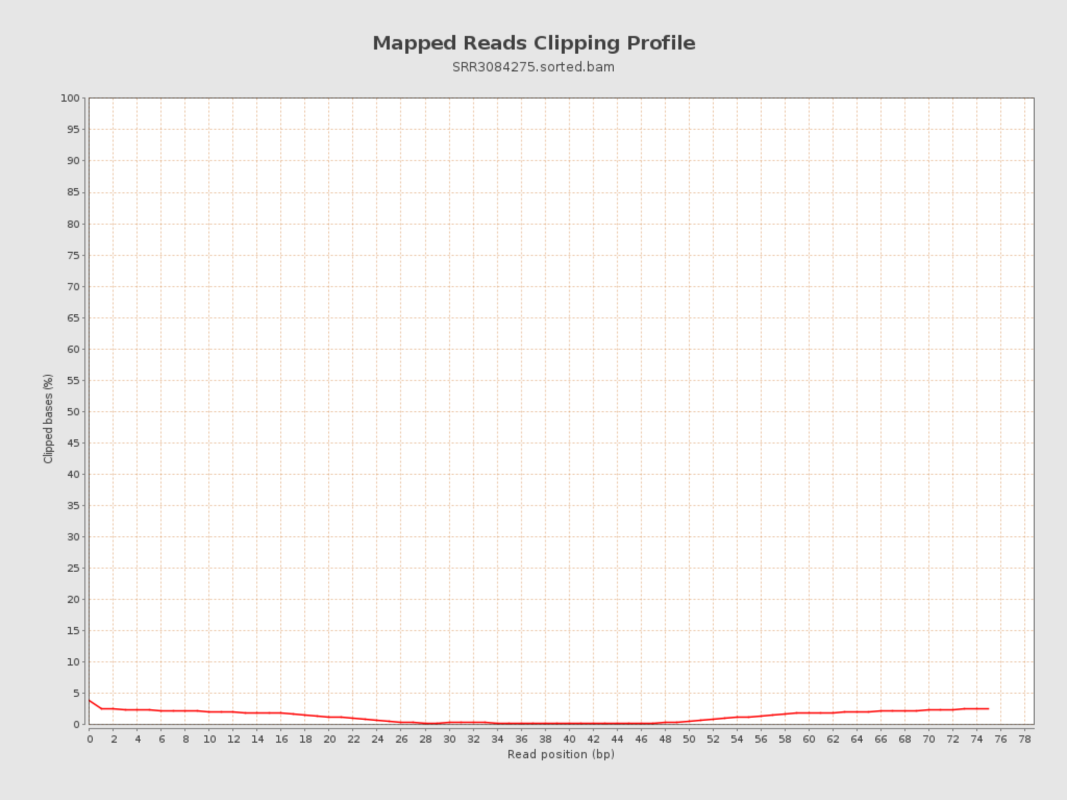
8. Results : Mapped Reads Nucleotide Content



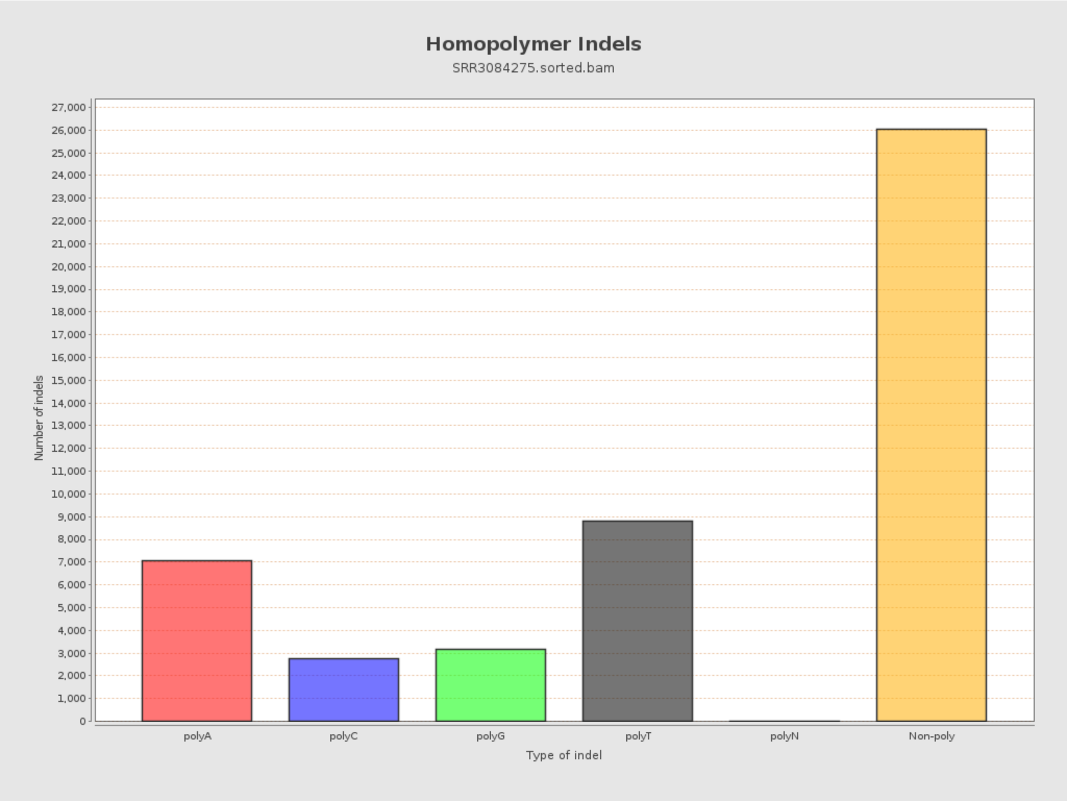
9. Results : Mapped Reads GC-content Distribution



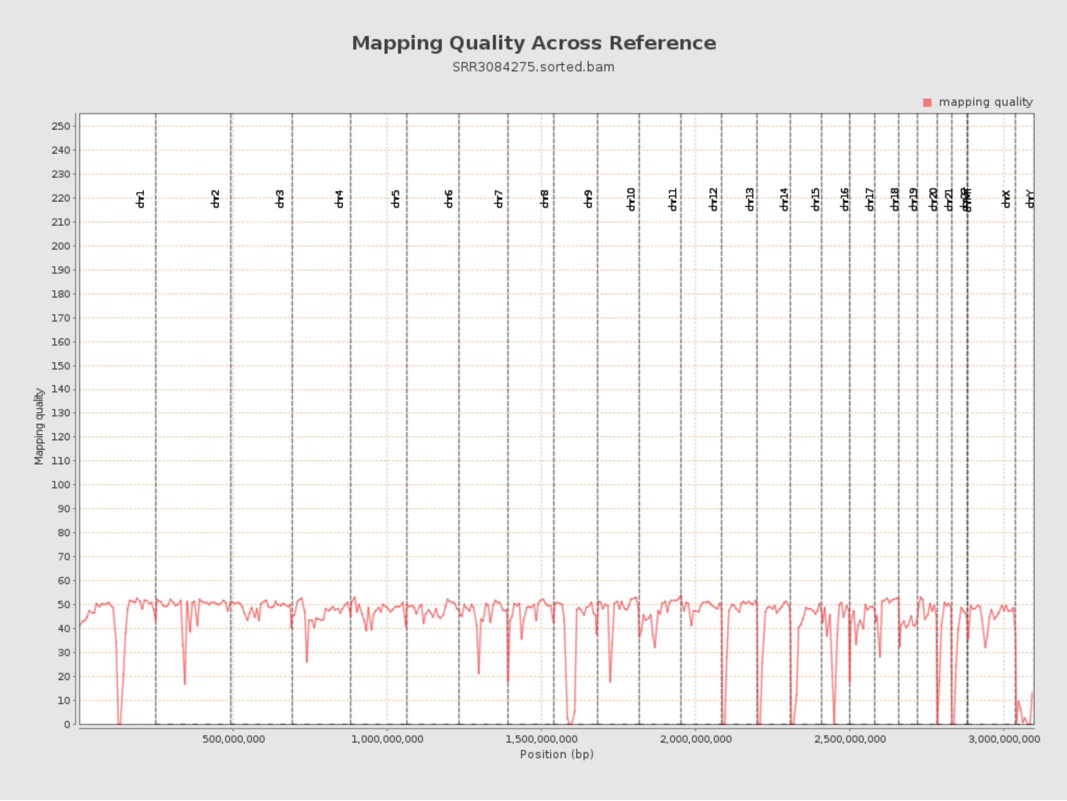
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram