Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:21:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080815.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_SRR3080815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080815.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:21:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,883,665
Mapped reads	2,684,624 / 93.1%
Unmapped reads	199,041 / 6.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,260 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	155,738 / 5.4%
Duplication rate	4.97%
Clipped reads	919,689 / 31.89%

2.2. ACGT Content

Number/percentage of A's	53,956,595 / 28.96%
Number/percentage of C's	35,164,218 / 18.87%
Number/percentage of T's	58,316,482 / 31.3%
Number/percentage of G's	38,845,200 / 20.85%
Number/percentage of N's	26,364 / 0.01%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0602

Standard Deviation	0.4031

2.4. Mapping Quality

Mean Mapping Quality	47.49

2.5. Mismatches and indels

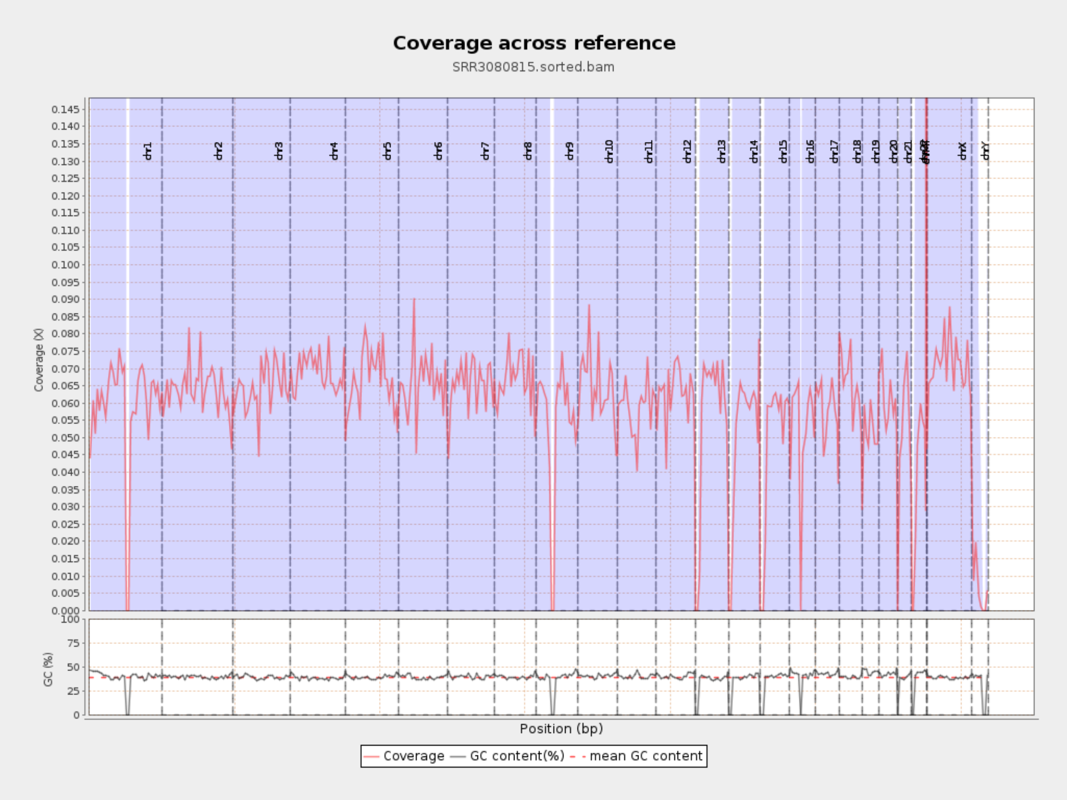
General error rate	0.8%
Mismatches	1,472,089
Insertions	13,481
Mapped reads with at least one insertion	0.5%
Deletions	38,530
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.6%

2.6. Chromosome stats

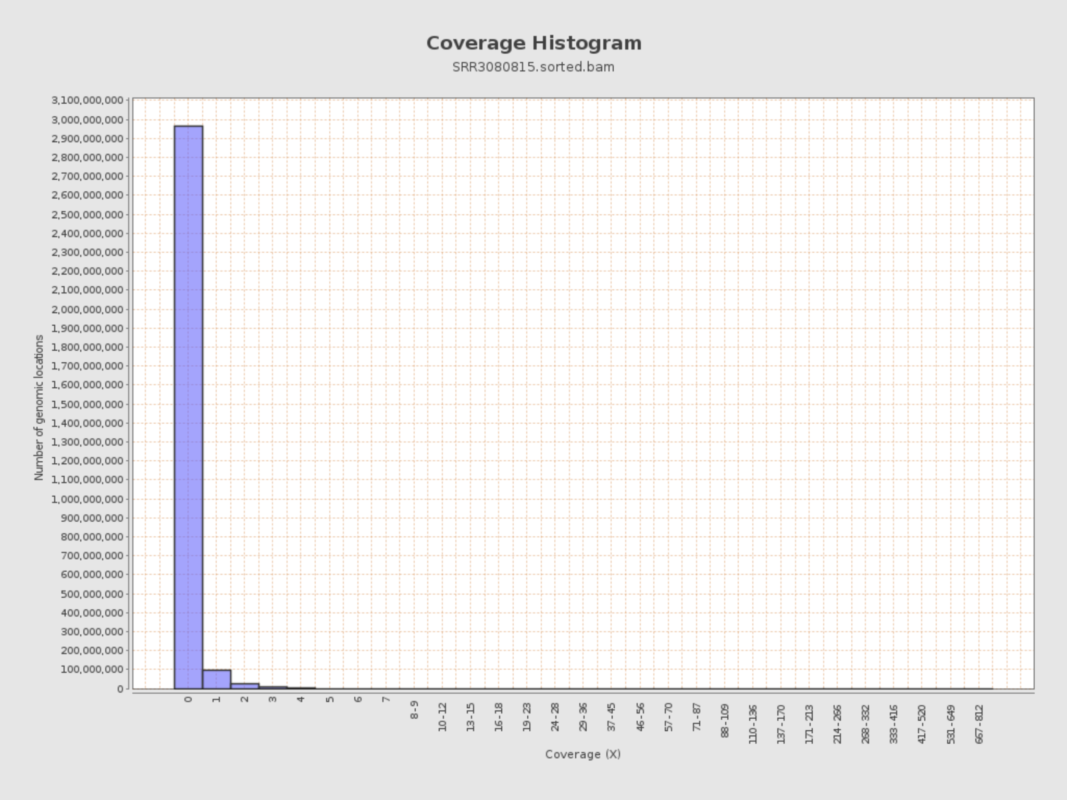
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14693697	0.059	0.5035
chr2	243199373	15599398	0.0641	0.458
chr3	198022430	12751660	0.0644	0.3368
chr4	191154276	13218385	0.0692	0.3556
chr5	180915260	12099115	0.0669	0.343
chr6	171115067	11293743	0.066	0.4166
chr7	159138663	10439284	0.0656	0.4363

chr8	146364022	9772595	0.0668	0.6132
chr9	141213431	7587964	0.0537	0.3703
chr10	135534747	8846350	0.0653	0.4592
chr11	135006516	7910994	0.0586	0.3653
chr12	133851895	8386170	0.0627	0.3339
chr13	115169878	6254443	0.0543	0.3094
chr14	107349540	5373796	0.0501	0.3113
chr15	102531392	4910783	0.0479	0.2891
chr16	90354753	4739181	0.0525	0.3203
chr17	81195210	4662868	0.0574	0.3298
chr18	78077248	5141612	0.0659	0.6079
chr19	59128983	3091196	0.0523	0.4206
chr20	63025520	3861739	0.0613	0.3338
chr21	48129895	2425263	0.0504	0.3125
chr22	51304566	1872989	0.0365	0.2512
chrMT	16571	18745	1.1312	1.4068
chrX	155270560	11013561	0.0709	0.3661
chrY	59373566	411467	0.0069	0.151

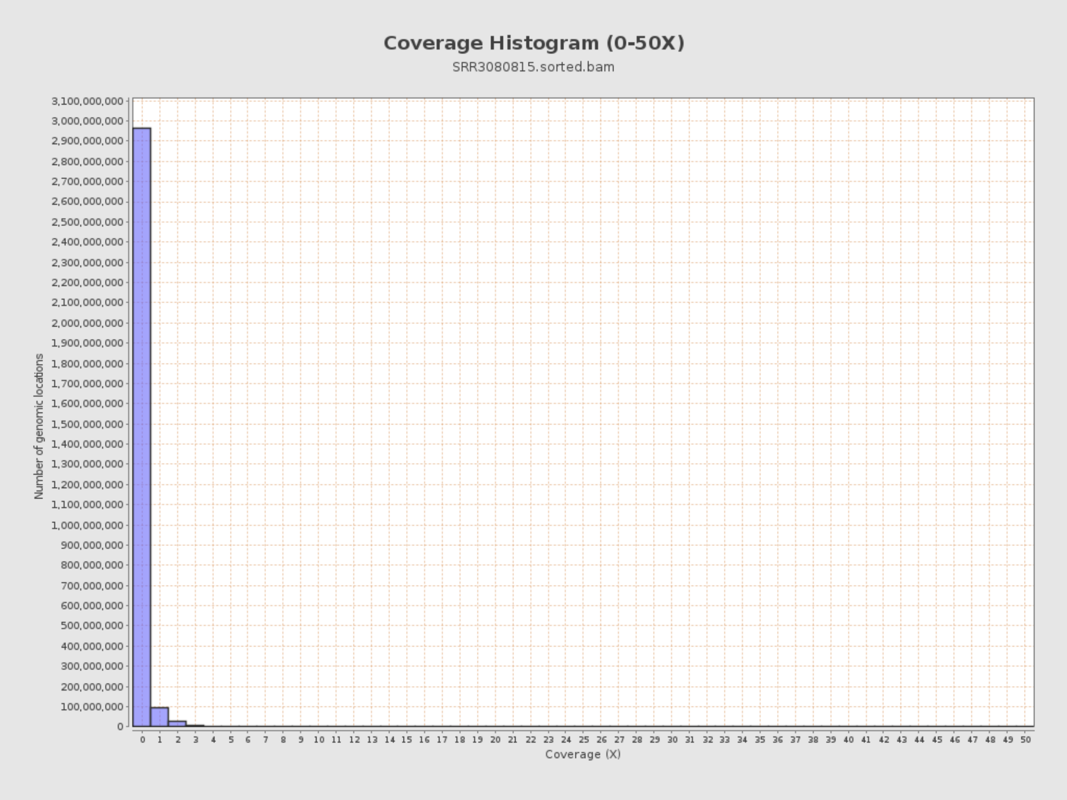
3. Results : Coverage across reference



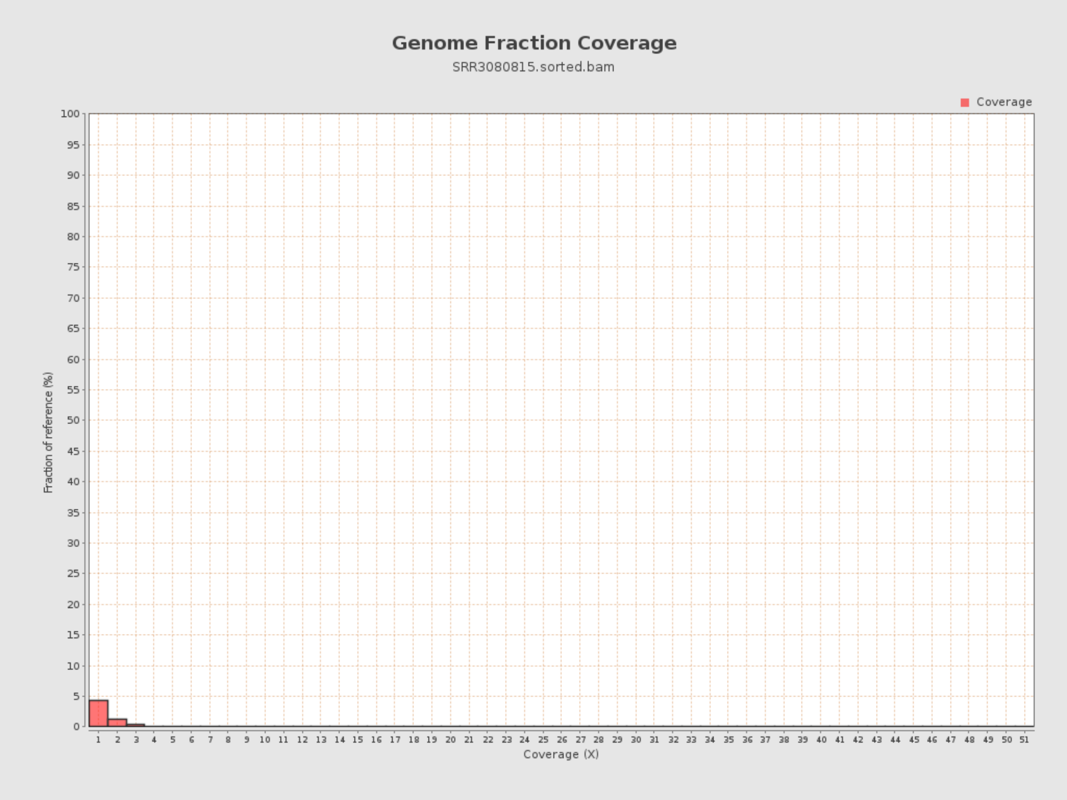
4. Results : Coverage Histogram



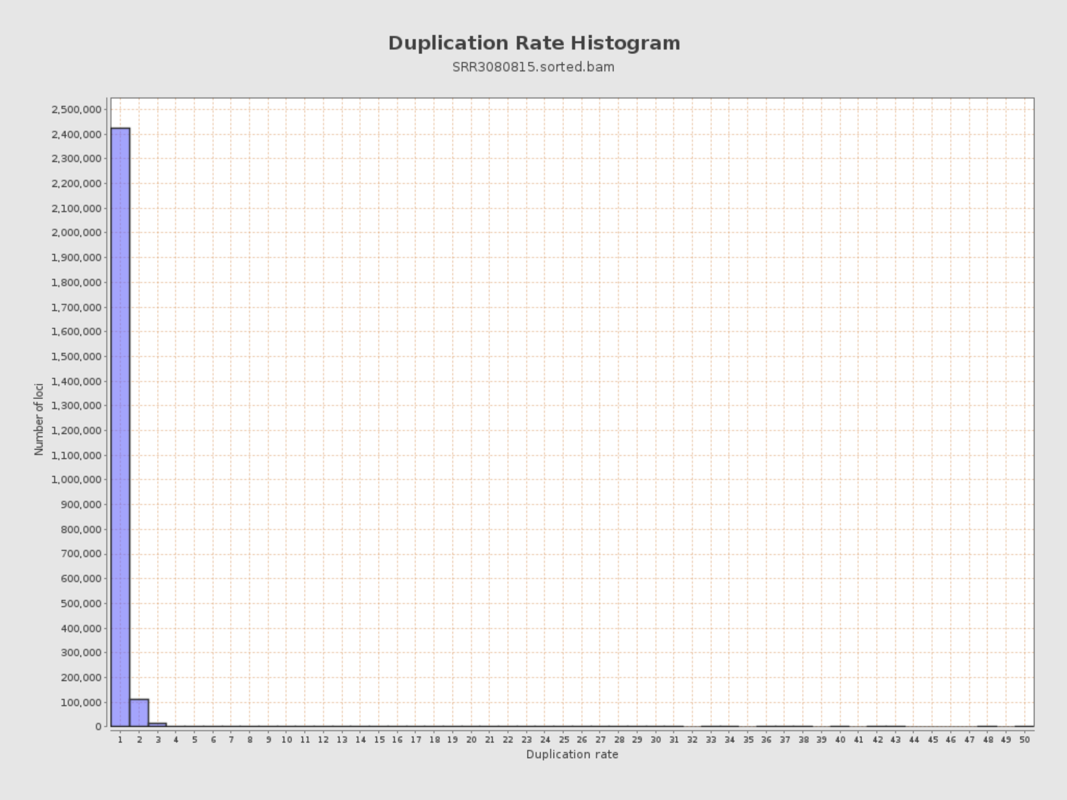
5. Results : Coverage Histogram (0-50X)



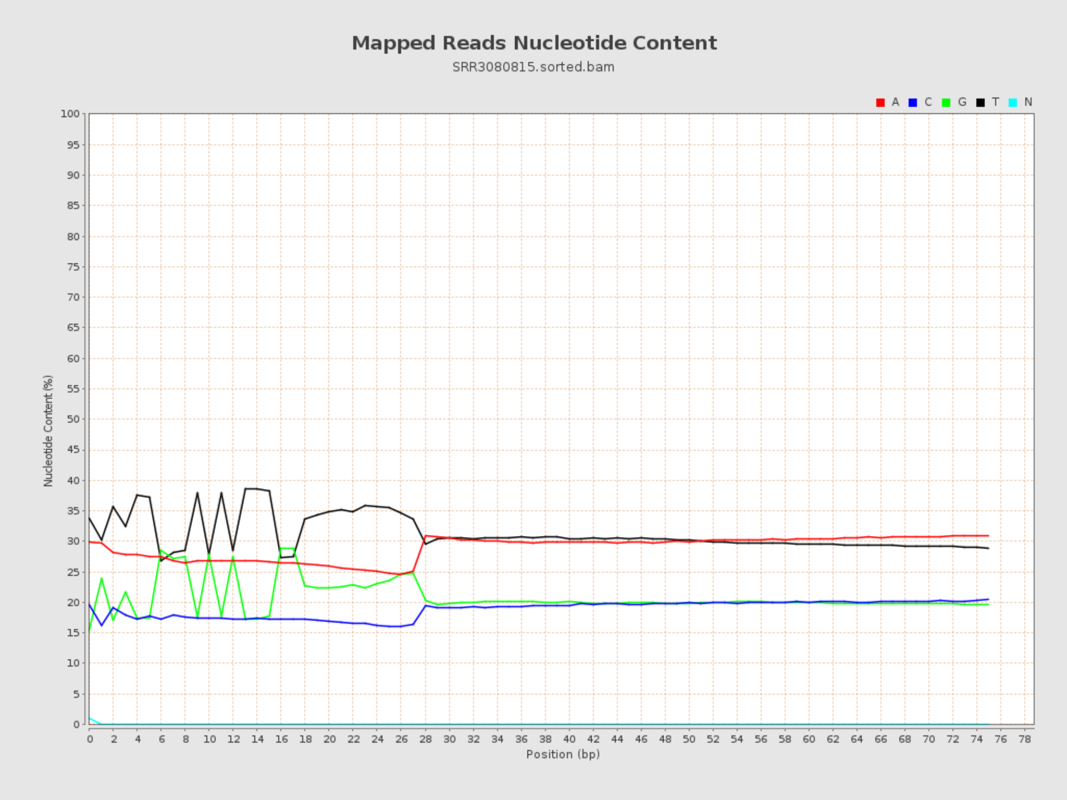
6. Results : Genome Fraction Coverage



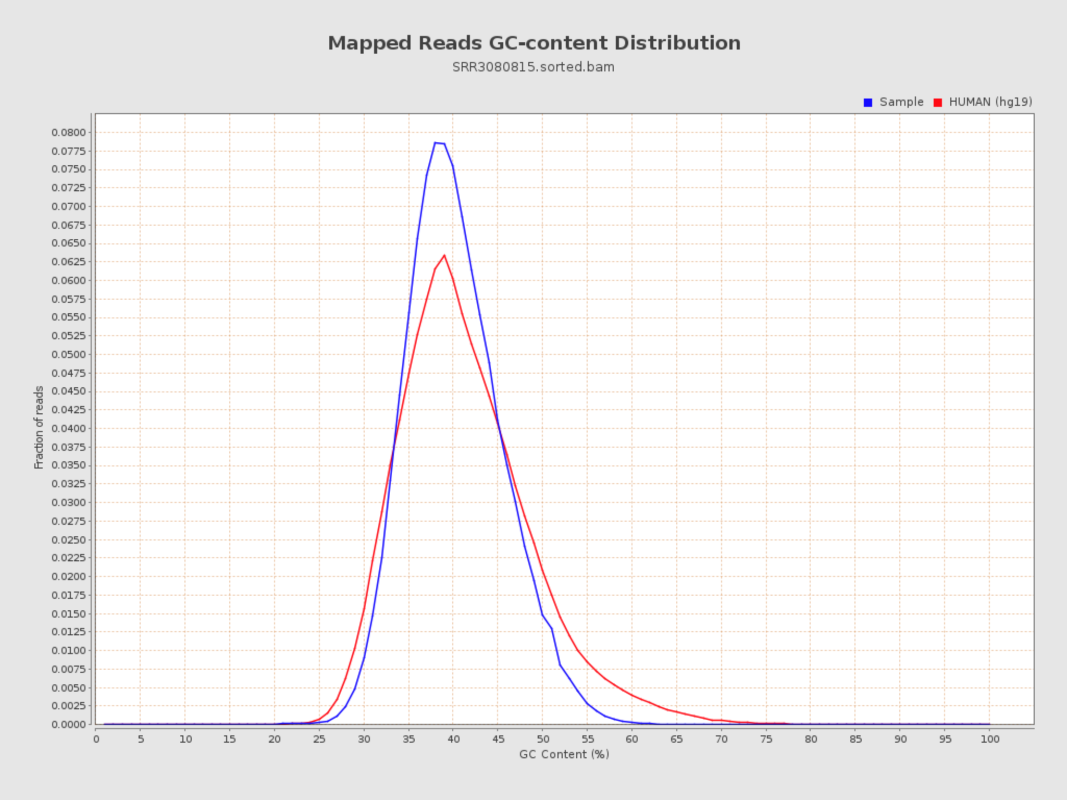
7. Results : Duplication Rate Histogram



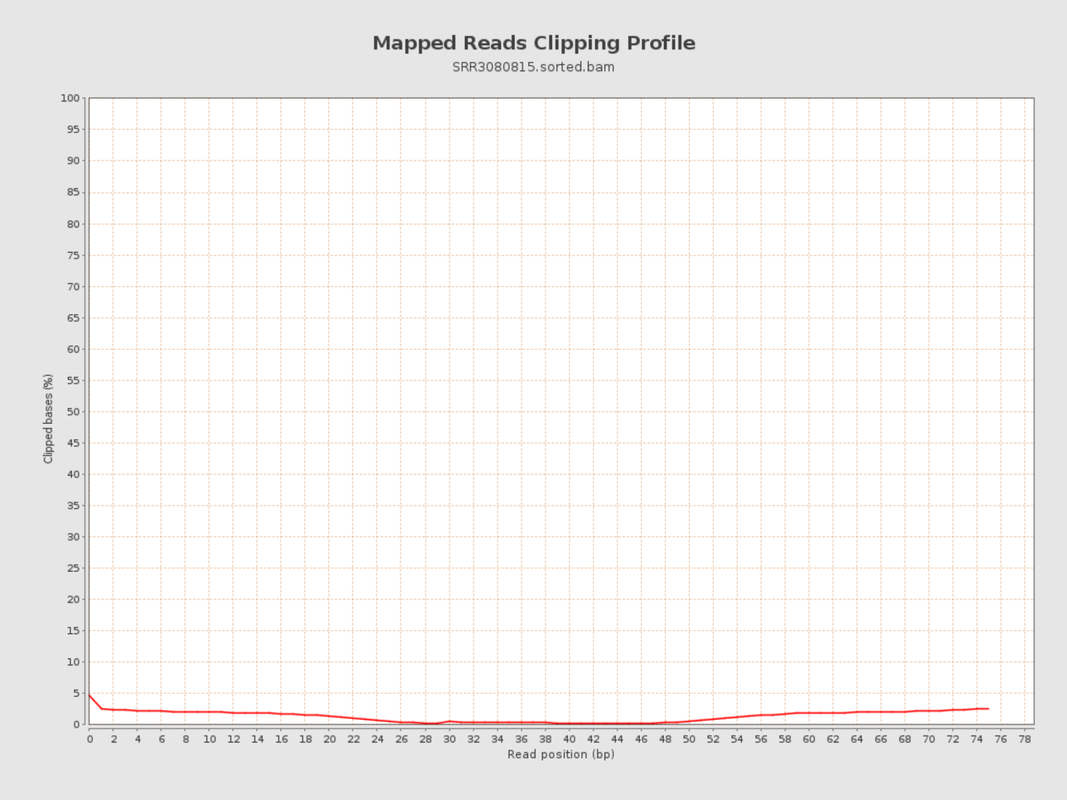
8. Results : Mapped Reads Nucleotide Content



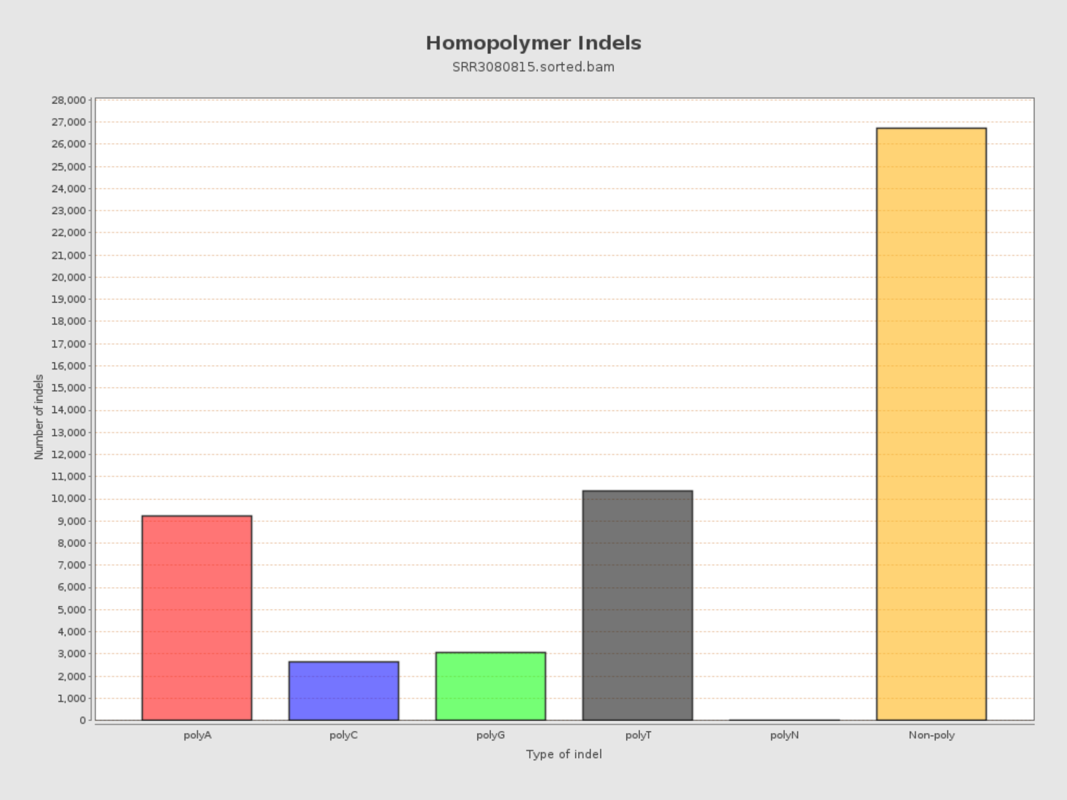
9. Results : Mapped Reads GC-content Distribution



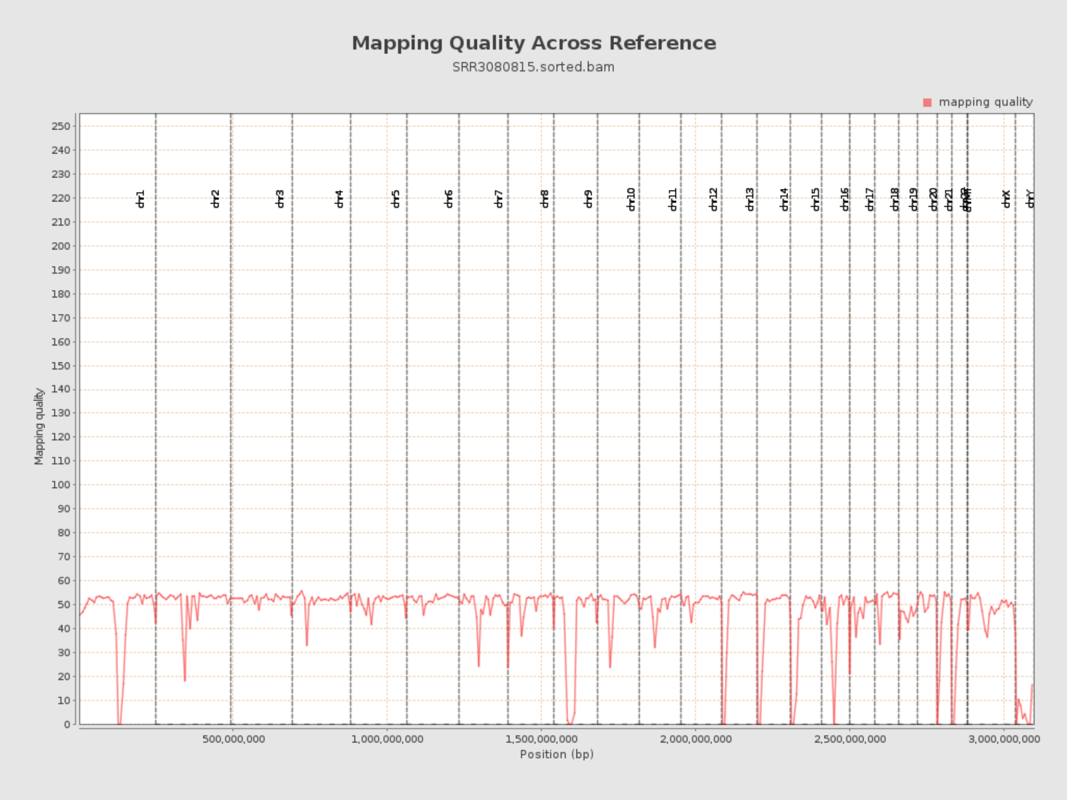
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram