Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:03:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008666.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_SRR6008666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008666.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:03:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,030,374
Mapped reads	1,796,574 / 88.48%
Unmapped reads	233,800 / 11.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,914 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	97,256 / 4.79%
Duplication rate	4.46%
Clipped reads	871,572 / 42.93%

2.2. ACGT Content

Number/percentage of A's	31,850,628 / 26.95%
Number/percentage of C's	21,923,568 / 18.55%
Number/percentage of T's	37,069,215 / 31.37%
Number/percentage of G's	27,279,013 / 23.08%
Number/percentage of N's	51,078 / 0.04%
GC Percentage	41.64%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.327

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

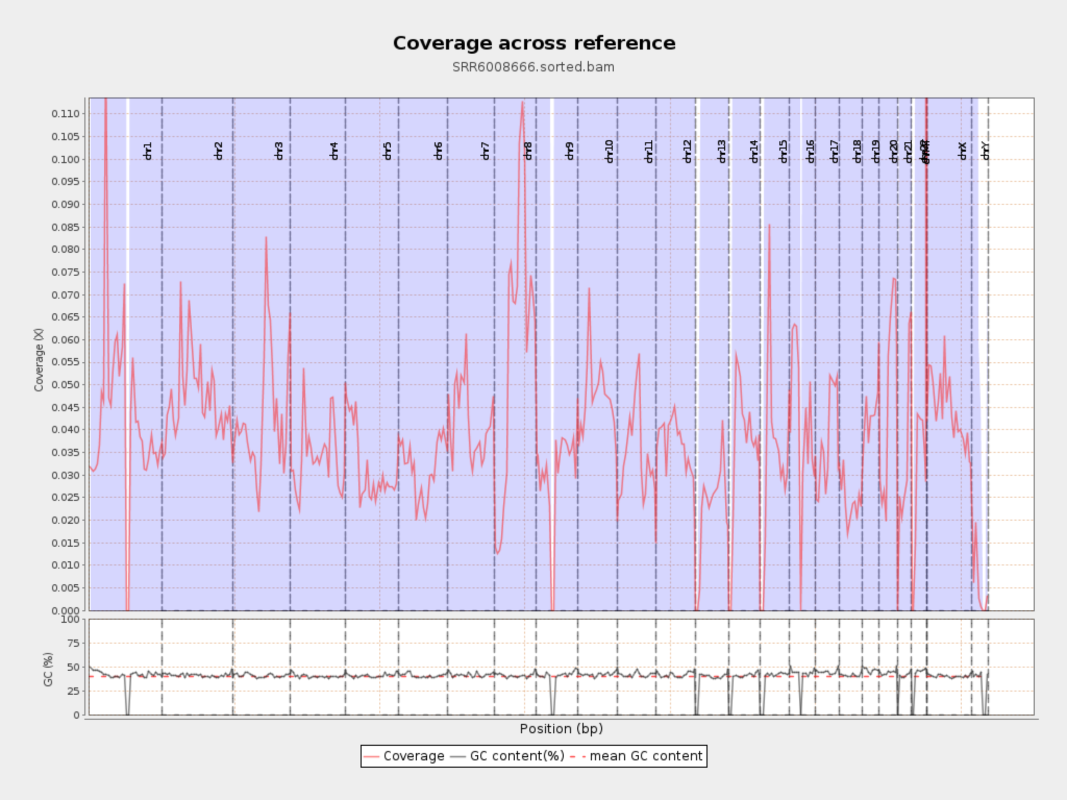
General error rate	0.84%
Mismatches	977,144
Insertions	9,161
Mapped reads with at least one insertion	0.51%
Deletions	33,738
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.87%

2.6. Chromosome stats

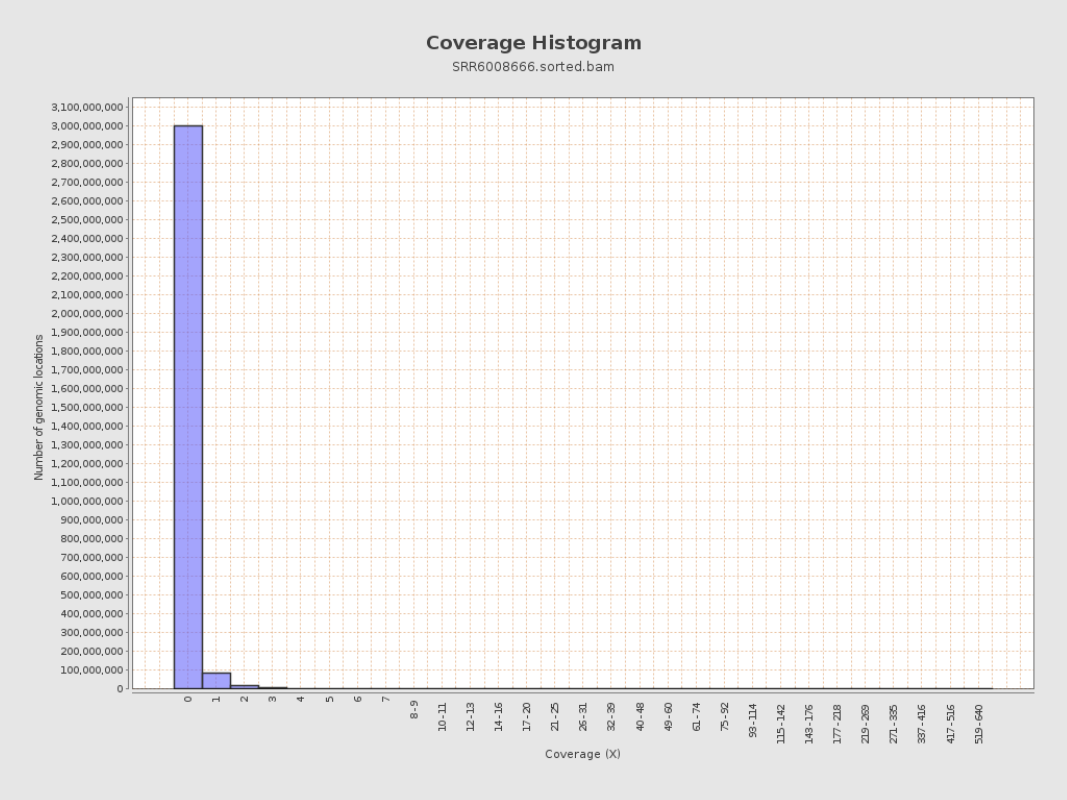
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10629377	0.0426	0.576
chr2	243199373	11517970	0.0474	0.4019
chr3	198022430	8487297	0.0429	0.2433
chr4	191154276	6422948	0.0336	0.245
chr5	180915260	5702356	0.0315	0.209
chr6	171115067	5413904	0.0316	0.2287
chr7	159138663	6640166	0.0417	0.4146

chr8	146364022	8602841	0.0588	0.3826
chr9	141213431	4170222	0.0295	0.2706
chr10	135534747	6450800	0.0476	0.3329
chr11	135006516	4701075	0.0348	0.3164
chr12	133851895	4969134	0.0371	0.2291
chr13	115169878	2593528	0.0225	0.1771
chr14	107349540	3864245	0.036	0.2264
chr15	102531392	3434092	0.0335	0.2171
chr16	90354753	3796652	0.042	0.2491
chr17	81195210	3094035	0.0381	0.2701
chr18	78077248	1892073	0.0242	0.4673
chr19	59128983	2550660	0.0431	0.405
chr20	63025520	2972298	0.0472	0.2591
chr21	48129895	1589165	0.033	0.2302
chr22	51304566	1428695	0.0278	0.1921
chrMT	16571	53471	3.2268	2.9471
chrX	155270560	6910375	0.0445	0.2707
chrY	59373566	341146	0.0057	0.1564

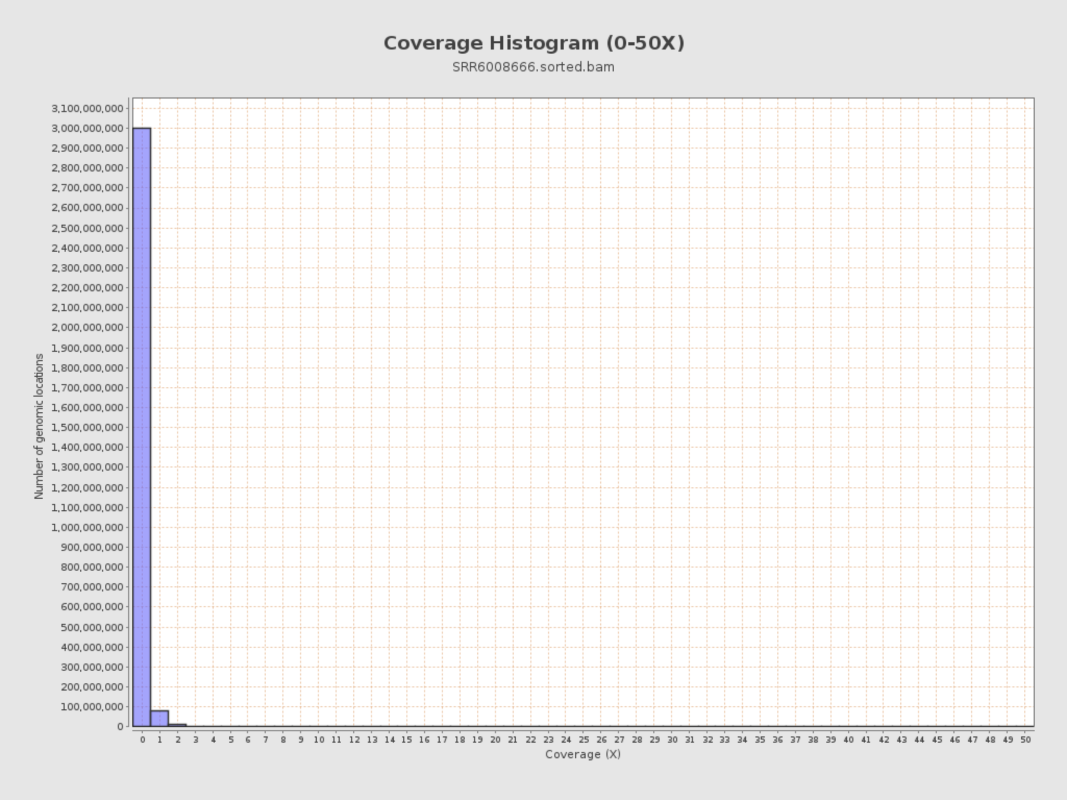
3. Results : Coverage across reference



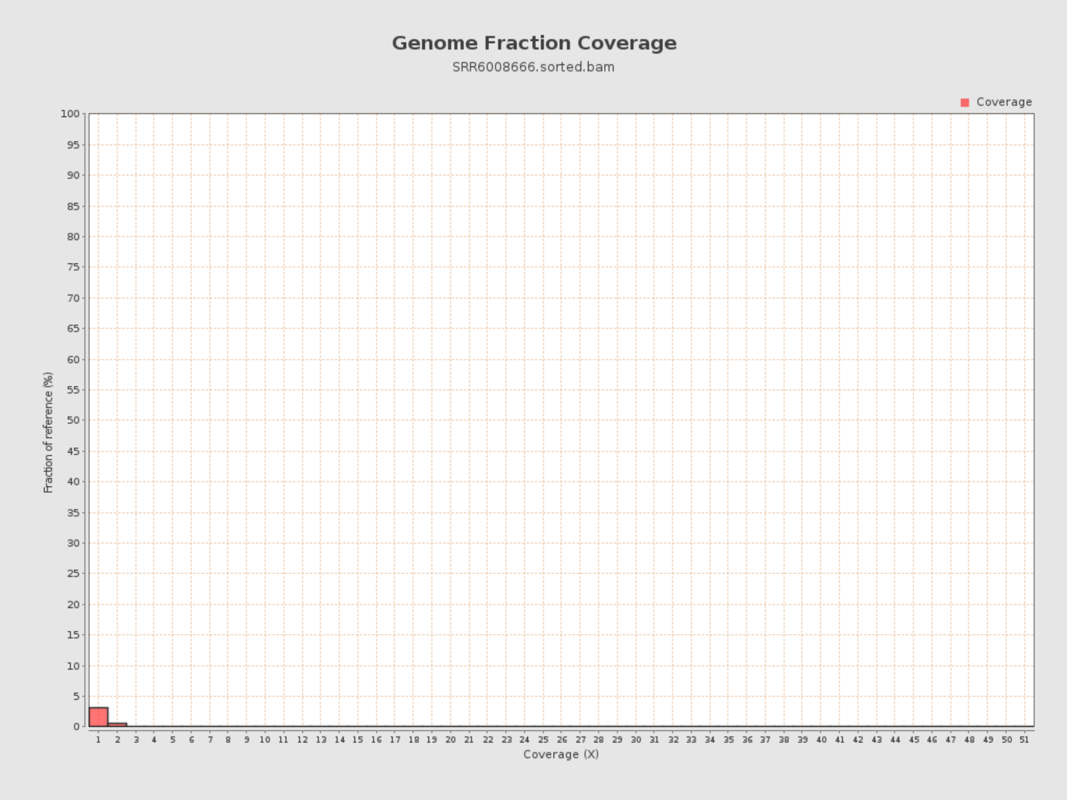
4. Results : Coverage Histogram



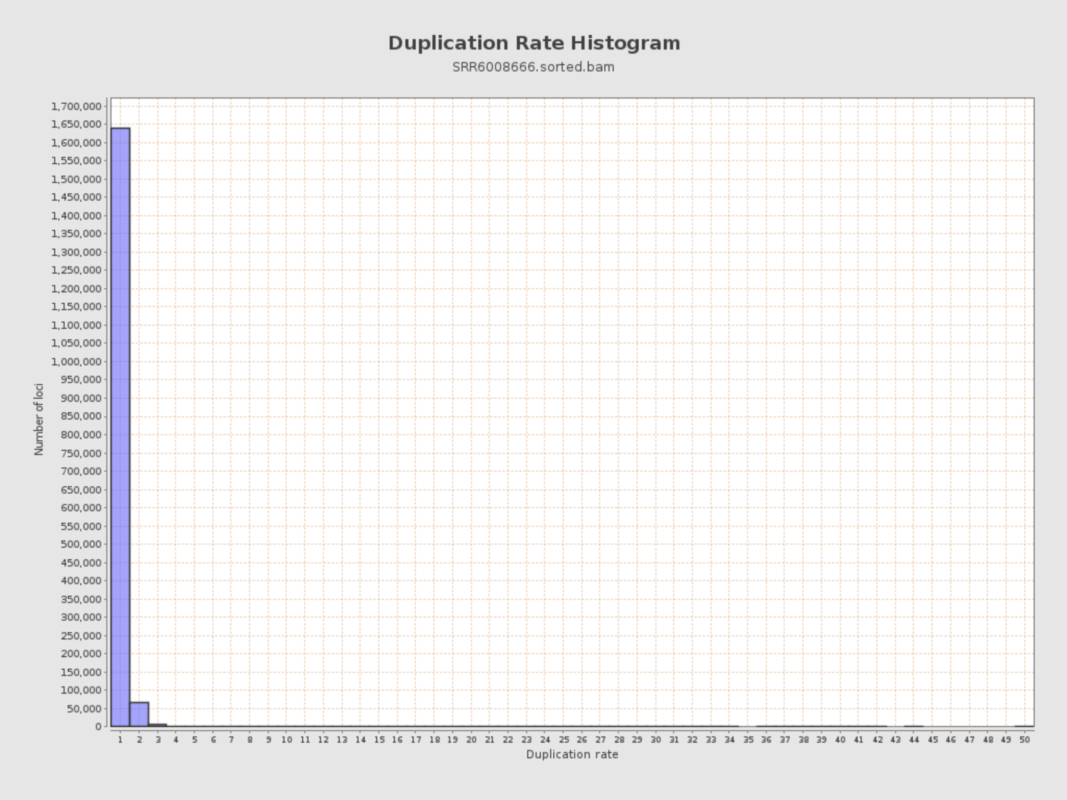
5. Results : Coverage Histogram (0-50X)



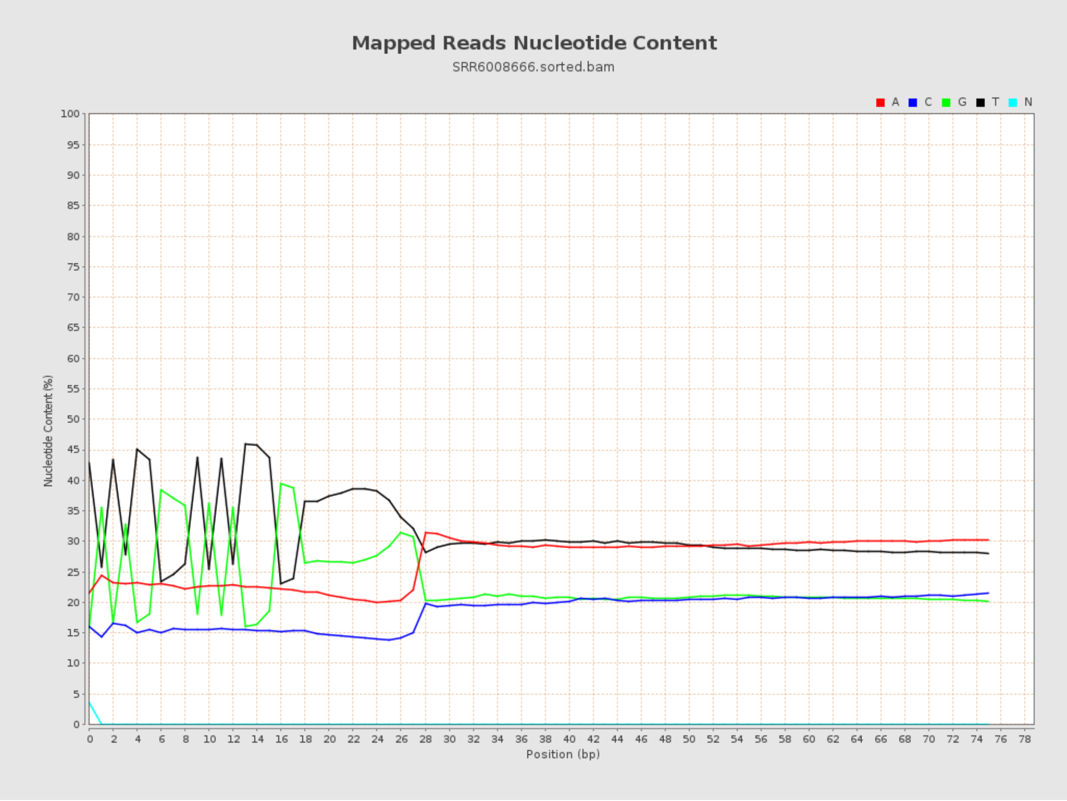
6. Results : Genome Fraction Coverage



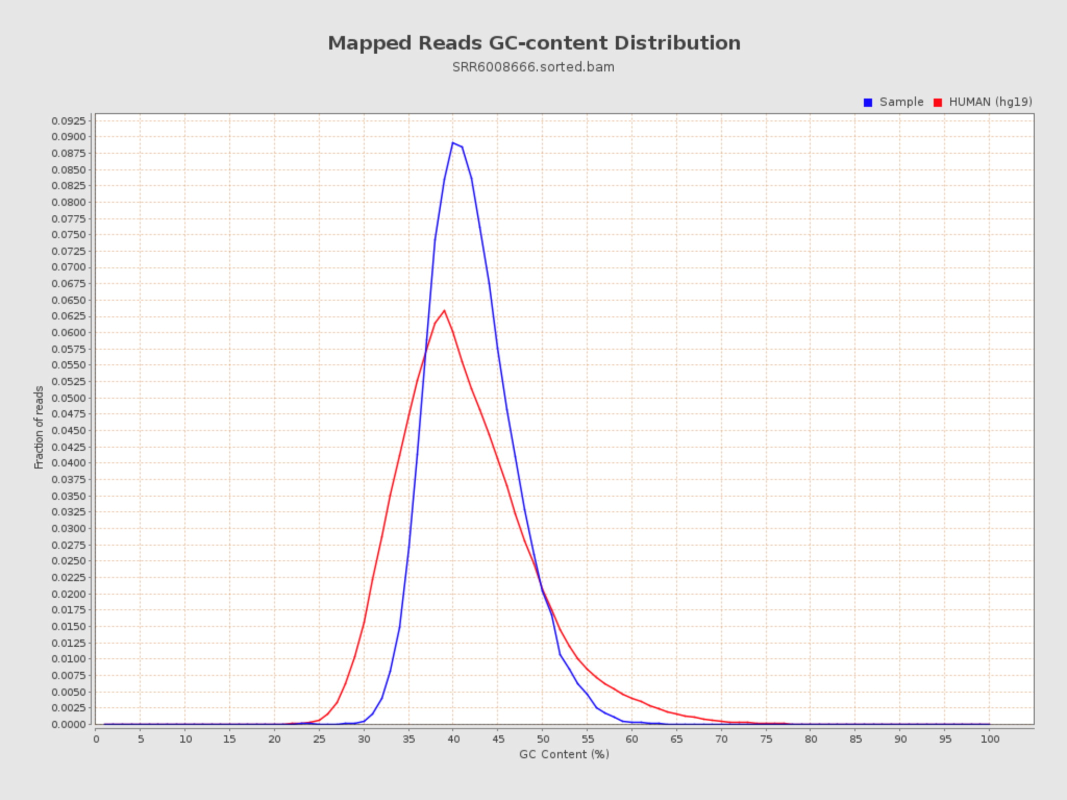
7. Results : Duplication Rate Histogram



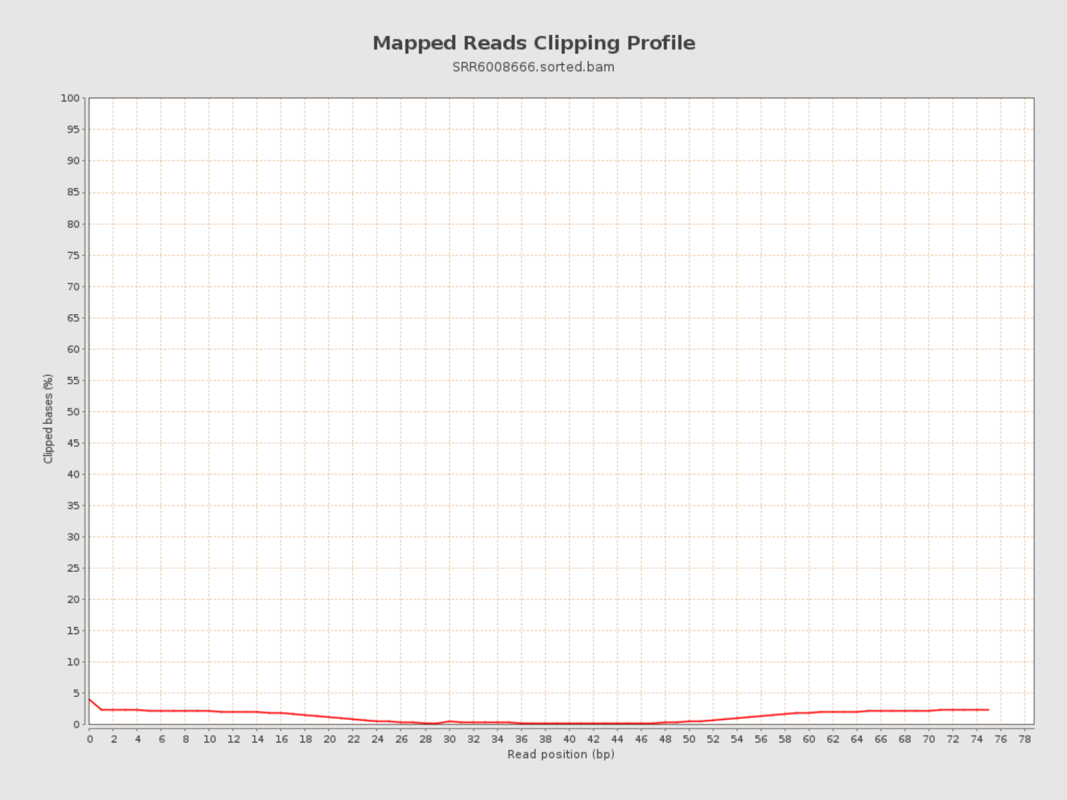
8. Results : Mapped Reads Nucleotide Content



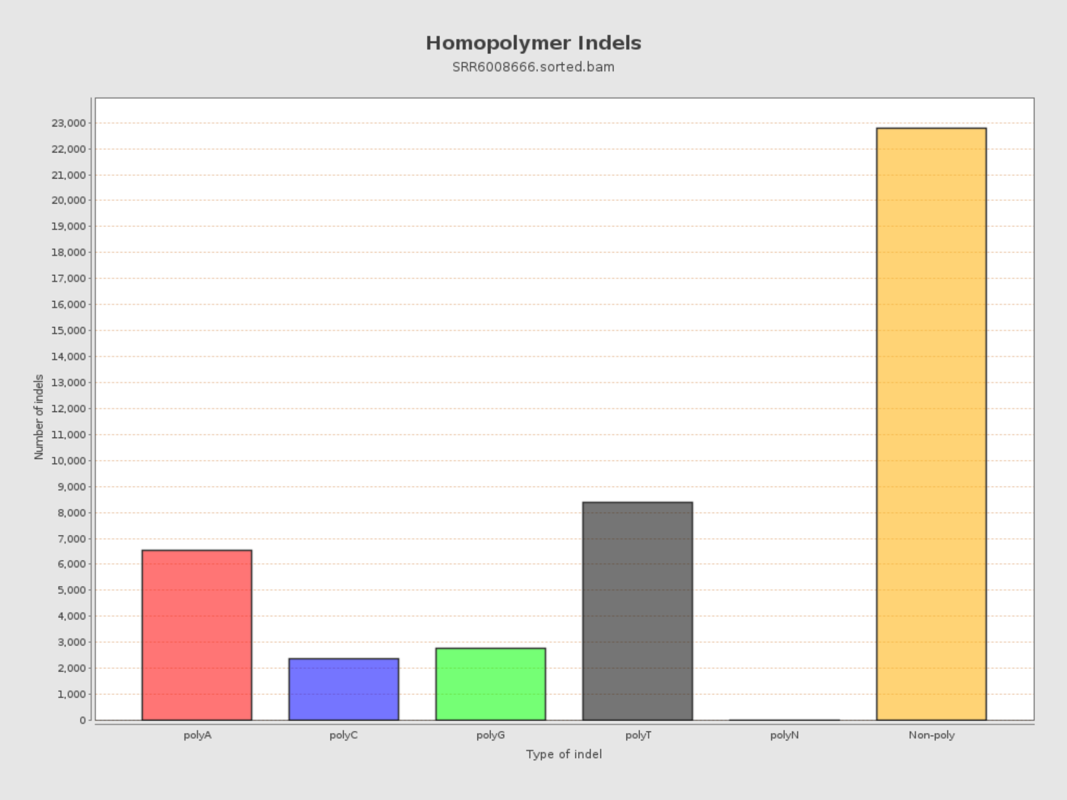
9. Results : Mapped Reads GC-content Distribution



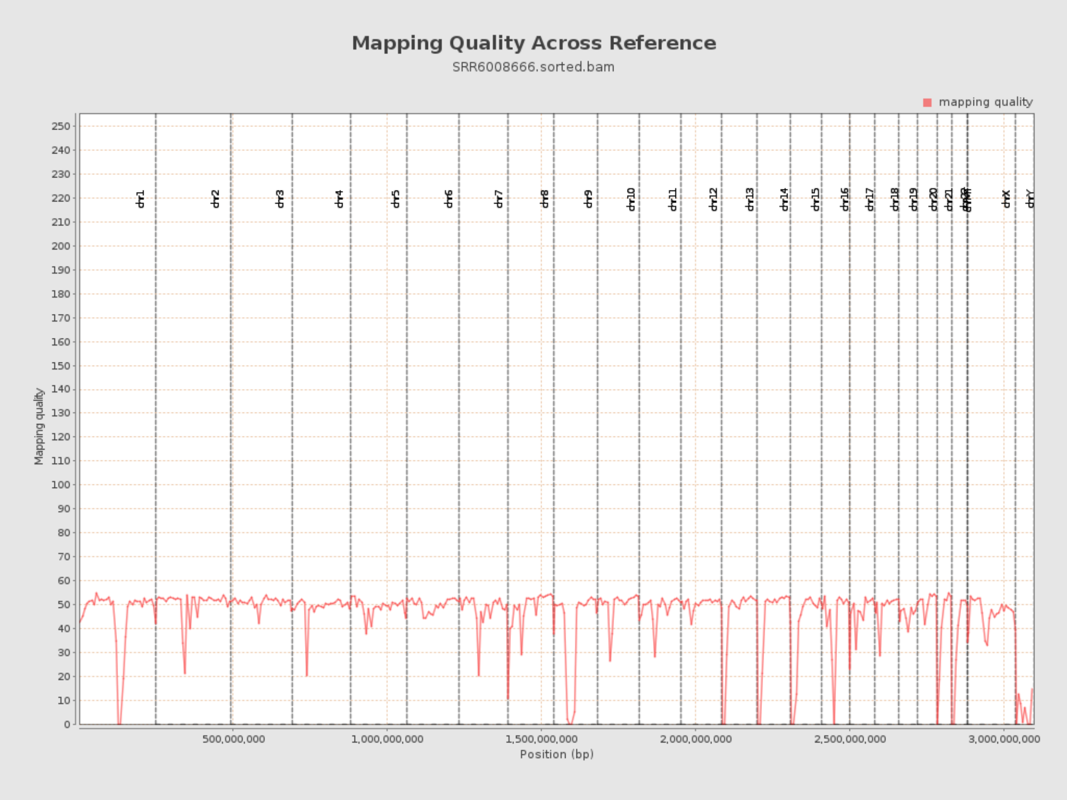
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram