Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:24:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008696.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_SRR6008696 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008696.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:24:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008696.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,831,615
Mapped reads	1,285,258 / 45.39%
Unmapped reads	1,546,357 / 54.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,656 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	130,966 / 4.63%
Duplication rate	8.31%
Clipped reads	1,019,848 / 36.02%

2.2. ACGT Content

Number/percentage of A's	20,184,580 / 27.48%
Number/percentage of C's	13,083,588 / 17.81%
Number/percentage of T's	23,171,661 / 31.55%
Number/percentage of G's	16,981,580 / 23.12%
Number/percentage of N's	24,245 / 0.03%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2351

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

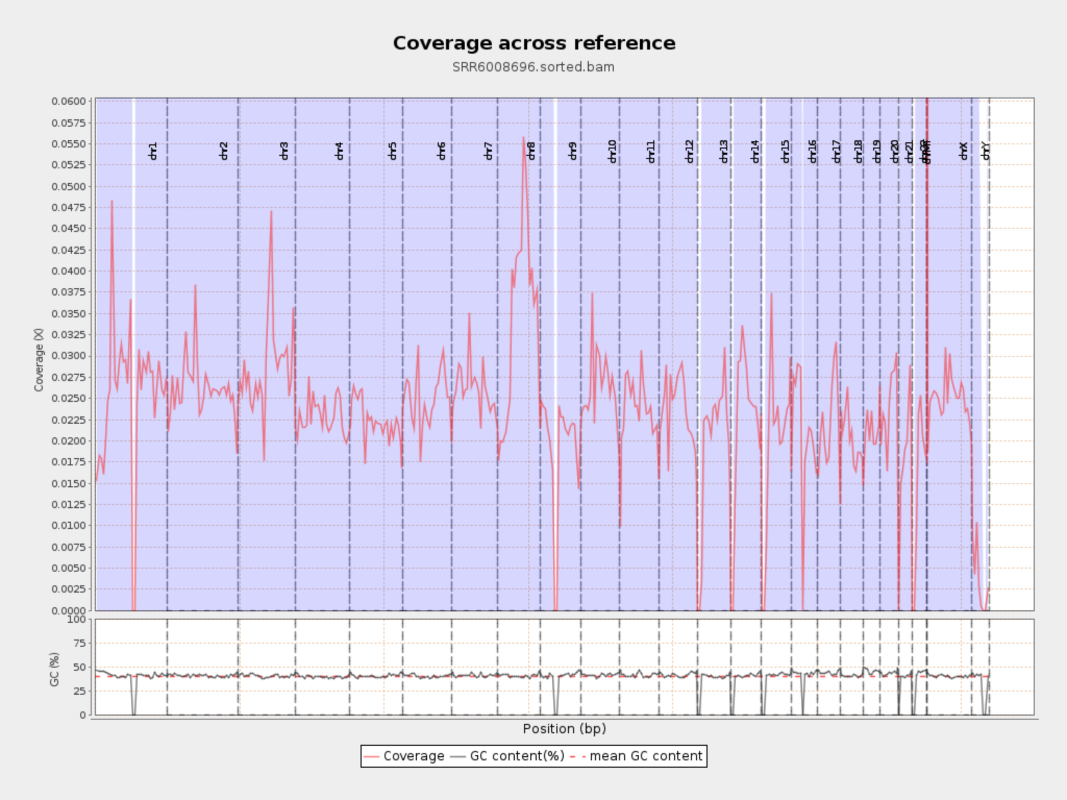
General error rate	1.08%
Mismatches	781,417
Insertions	5,812
Mapped reads with at least one insertion	0.45%
Deletions	28,516
Mapped reads with at least one deletion	2.19%
Homopolymer indels	47.71%

2.6. Chromosome stats

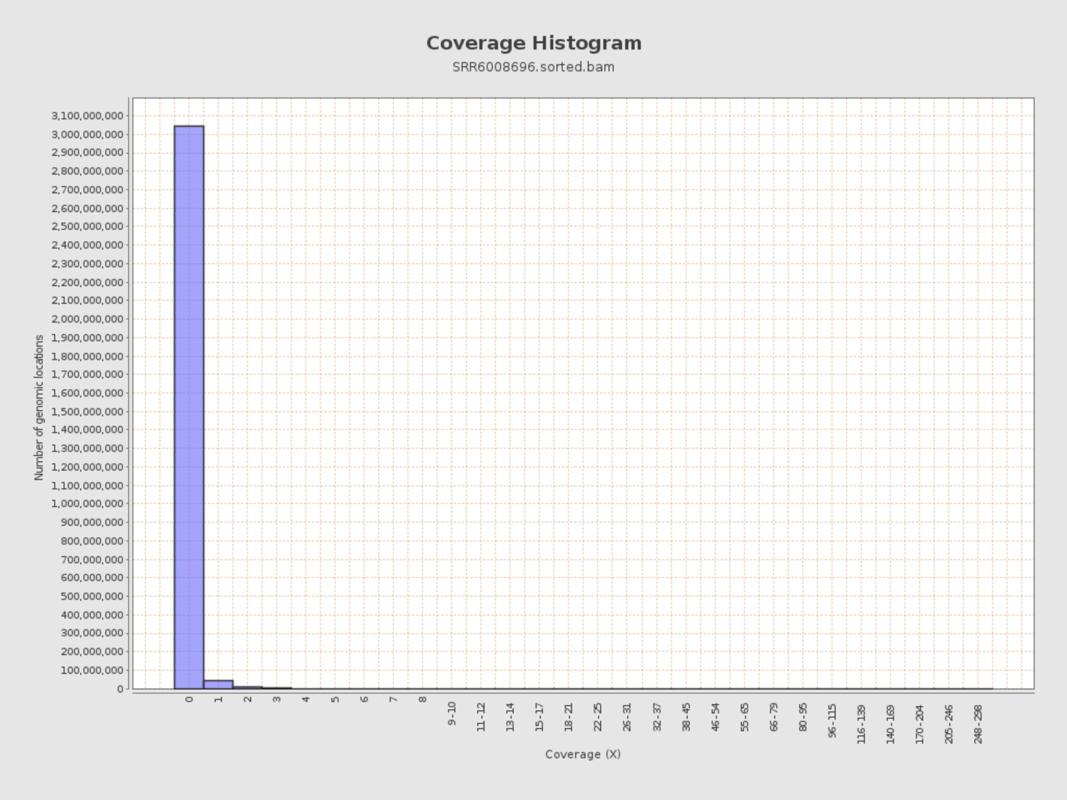
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6275540	0.0252	0.2988
chr2	243199373	6382284	0.0262	0.2722
chr3	198022430	5698885	0.0288	0.2301
chr4	191154276	4370921	0.0229	0.2062
chr5	180915260	4063927	0.0225	0.2009
chr6	171115067	4280349	0.025	0.2268
chr7	159138663	4166255	0.0262	0.2843

chr8	146364022	5131782	0.0351	0.3073
chr9	141213431	2678878	0.019	0.2046
chr10	135534747	3571507	0.0264	0.2439
chr11	135006516	3231336	0.0239	0.2312
chr12	133851895	3200777	0.0239	0.2105
chr13	115169878	2246018	0.0195	0.1895
chr14	107349540	2370376	0.0221	0.2088
chr15	102531392	2013355	0.0196	0.1888
chr16	90354753	1848331	0.0205	0.1978
chr17	81195210	1804514	0.0222	0.2049
chr18	78077248	1578787	0.0202	0.2723
chr19	59128983	1252396	0.0212	0.2283
chr20	63025520	1505648	0.0239	0.2095
chr21	48129895	876377	0.0182	0.1824
chr22	51304566	780212	0.0152	0.16
chrMT	16571	46043	2.7785	3.0545
chrX	155270560	3907583	0.0252	0.2216
chrY	59373566	206834	0.0035	0.0835

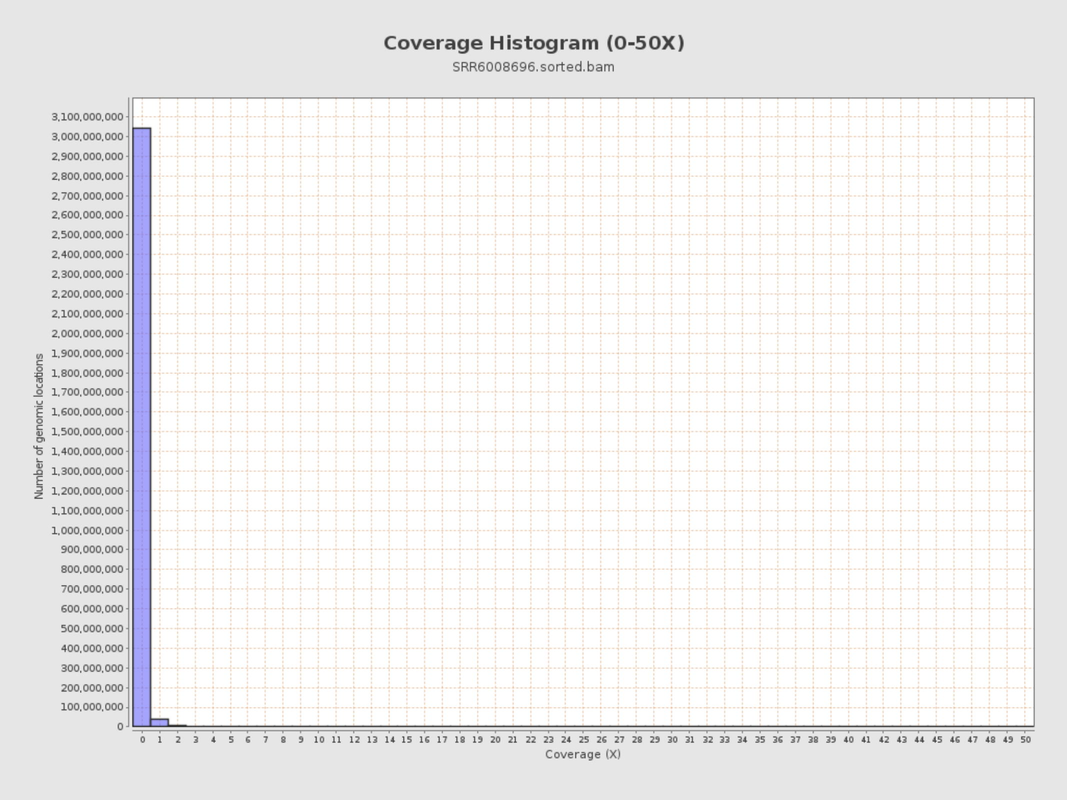
3. Results : Coverage across reference



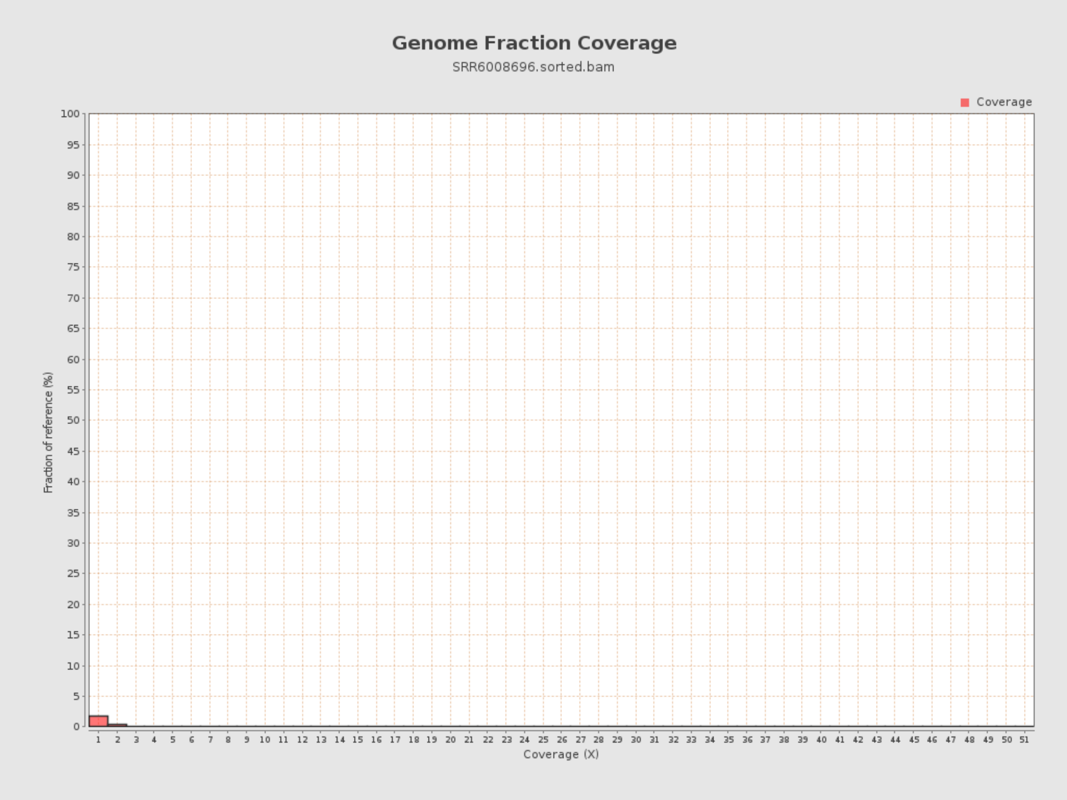
4. Results : Coverage Histogram



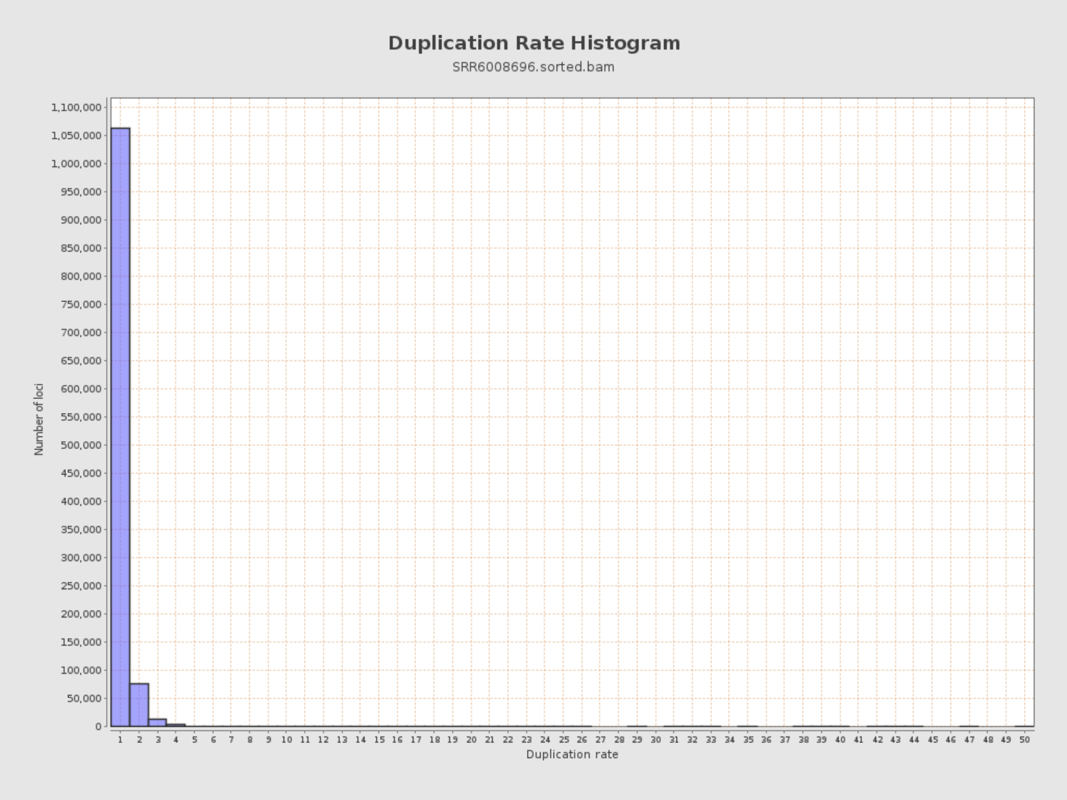
5. Results : Coverage Histogram (0-50X)



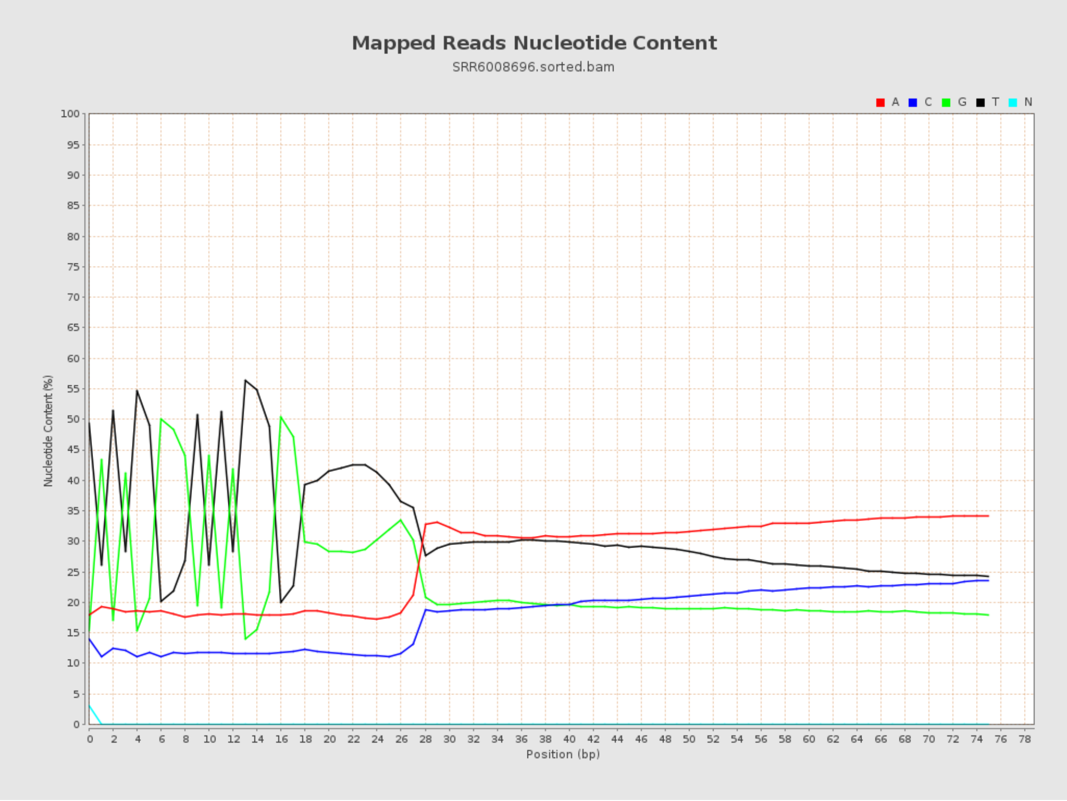
6. Results : Genome Fraction Coverage



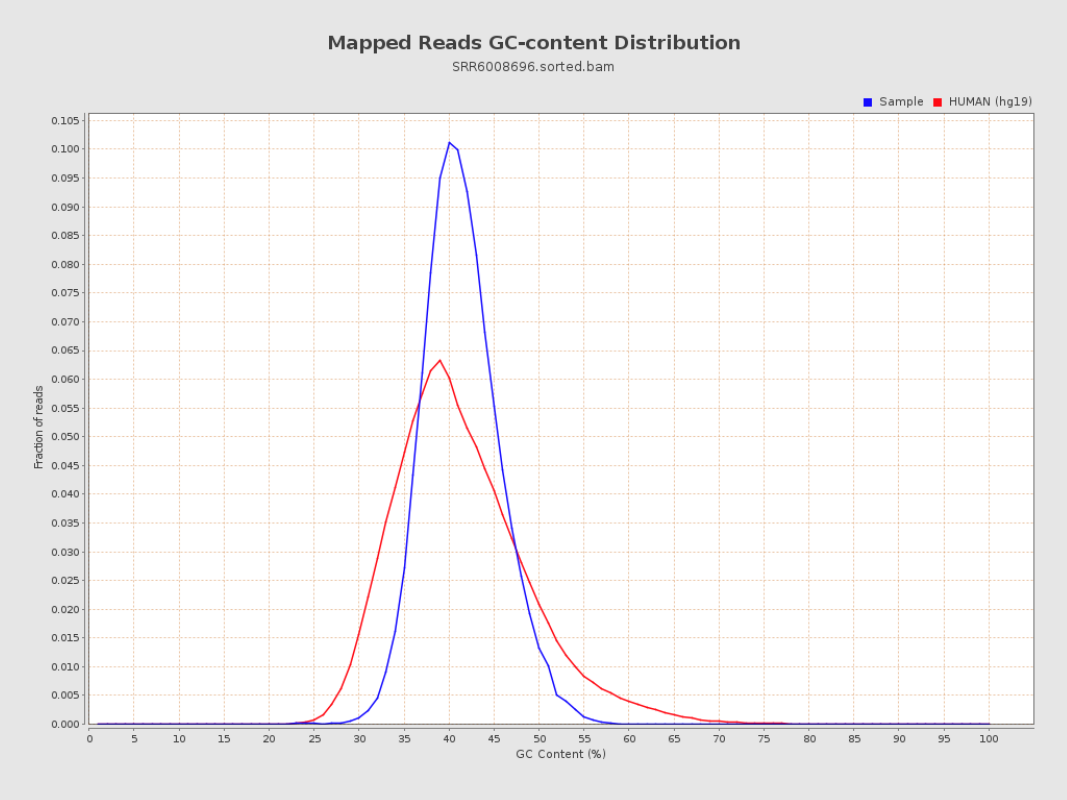
7. Results : Duplication Rate Histogram



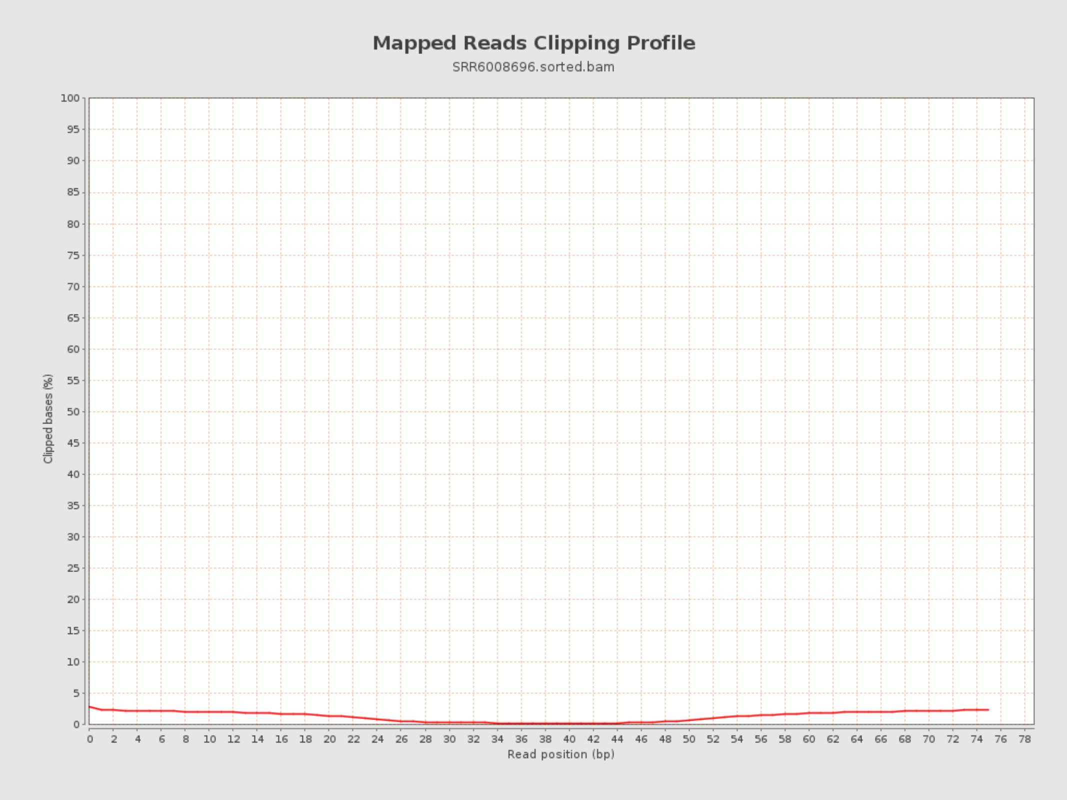
8. Results : Mapped Reads Nucleotide Content



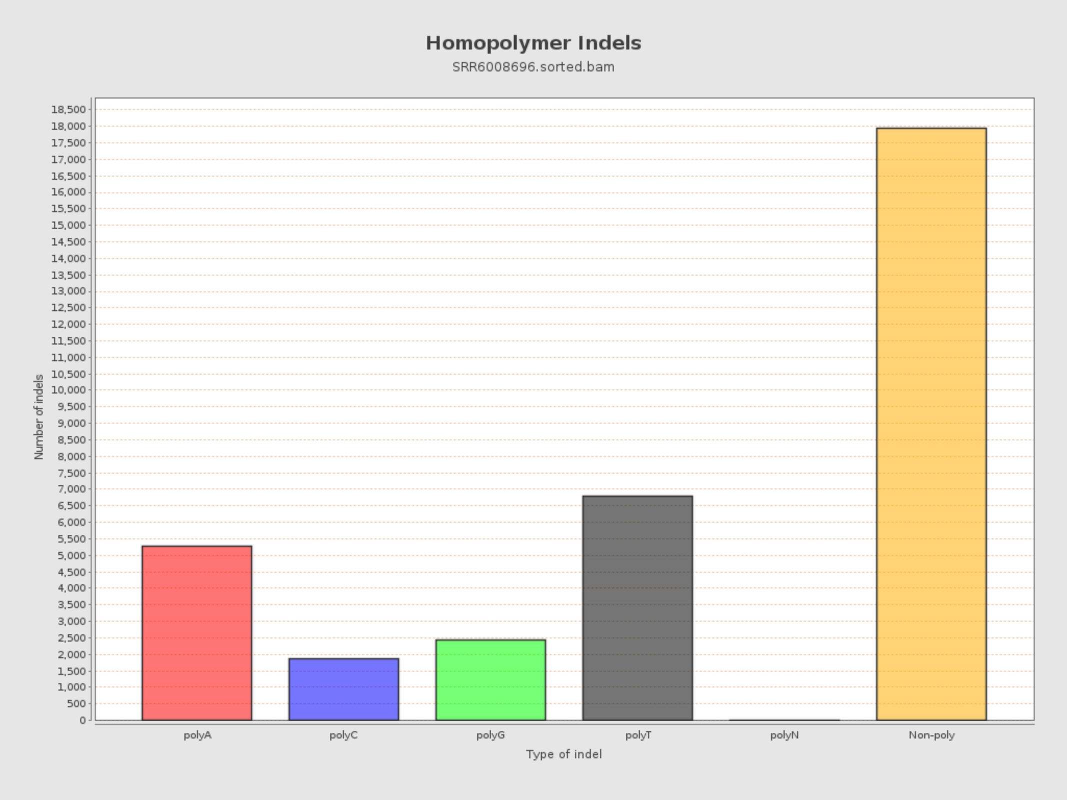
9. Results : Mapped Reads GC-content Distribution



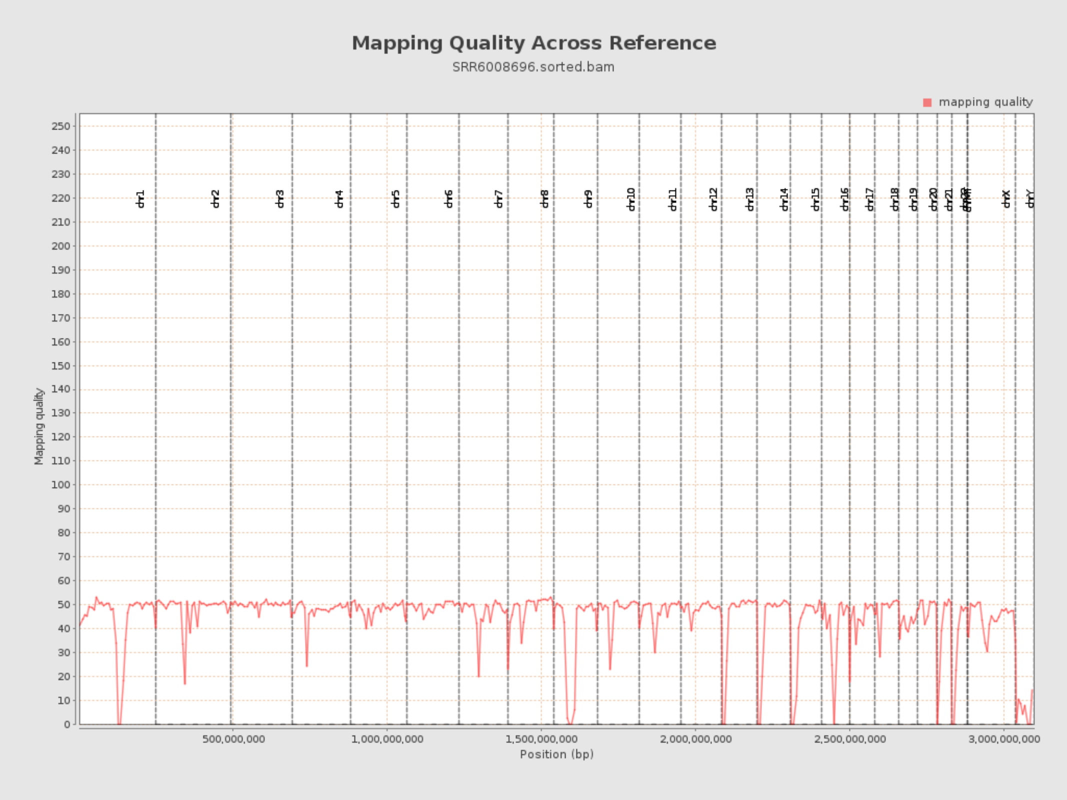
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram