Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:59:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008686.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_SRR6008686 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008686.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:59:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008686.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,045,106
Mapped reads	1,760,750 / 86.1%
Unmapped reads	284,356 / 13.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,795 / 0.33%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	64,208 / 3.14%
Duplication rate	2.54%
Clipped reads	1,016,085 / 49.68%

2.2. ACGT Content

Number/percentage of A's	28,779,397 / 25.93%
Number/percentage of C's	20,751,369 / 18.7%
Number/percentage of T's	34,238,831 / 30.85%
Number/percentage of G's	27,153,551 / 24.47%
Number/percentage of N's	46,304 / 0.04%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.3723

2.4. Mapping Quality

Mean Mapping Quality	43.31

2.5. Mismatches and indels

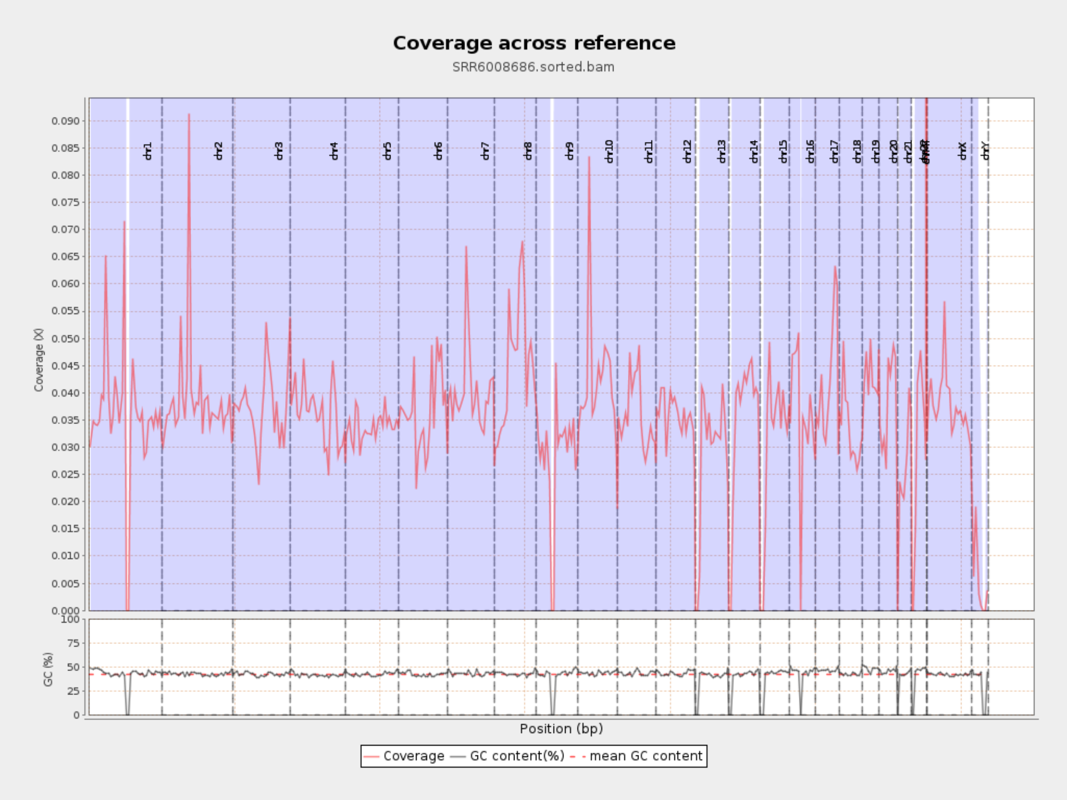
General error rate	0.87%
Mismatches	955,612
Insertions	7,741
Mapped reads with at least one insertion	0.44%
Deletions	41,422
Mapped reads with at least one deletion	2.32%
Homopolymer indels	42.96%

2.6. Chromosome stats

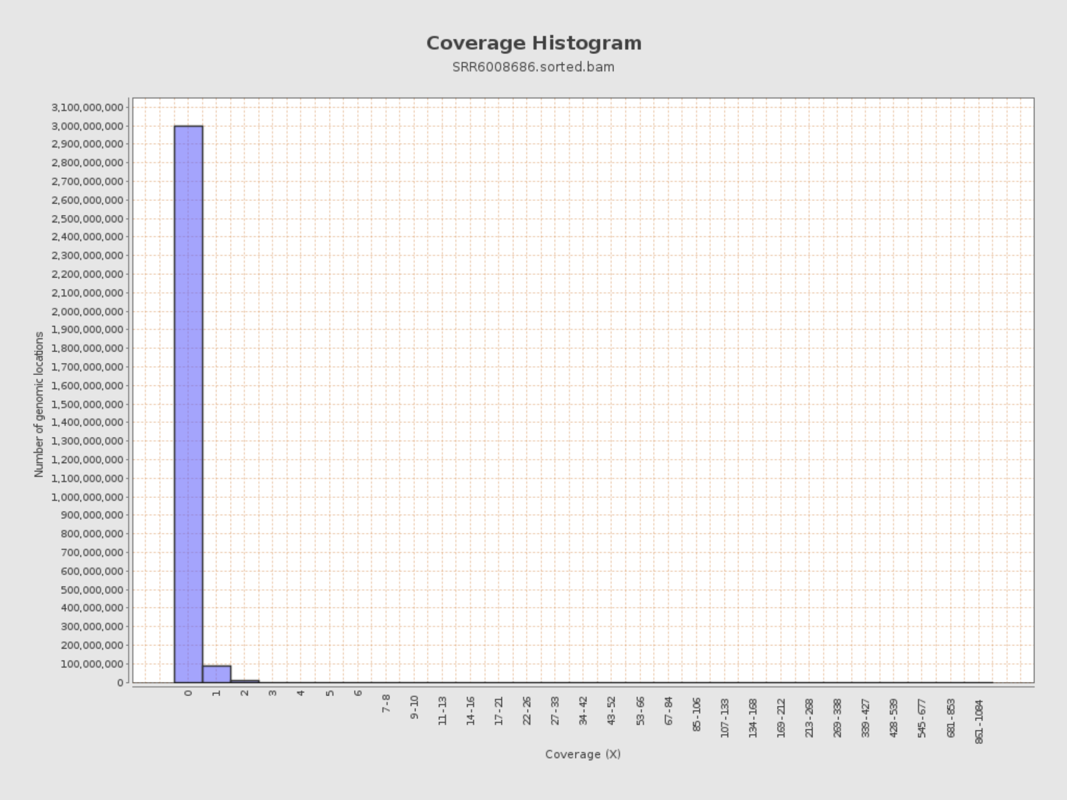
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8884612	0.0356	0.7646
chr2	243199373	9491092	0.039	0.4717
chr3	198022430	7378463	0.0373	0.2138
chr4	191154276	6910456	0.0362	0.2181
chr5	180915260	6109942	0.0338	0.2029
chr6	171115067	6275610	0.0367	0.247
chr7	159138663	6462740	0.0406	0.3958

chr8	146364022	6621556	0.0452	0.31
chr9	141213431	3947478	0.028	0.3434
chr10	135534747	5774109	0.0426	0.4075
chr11	135006516	4812785	0.0356	0.3224
chr12	133851895	4802325	0.0359	0.214
chr13	115169878	3296658	0.0286	0.1833
chr14	107349540	3731784	0.0348	0.2299
chr15	102531392	3153621	0.0308	0.1923
chr16	90354753	3249713	0.036	0.2558
chr17	81195210	3406987	0.042	0.266
chr18	78077248	2600350	0.0333	0.5885
chr19	59128983	2519271	0.0426	0.5176
chr20	63025520	2395173	0.038	0.2217
chr21	48129895	1228042	0.0255	0.19
chr22	51304566	1444470	0.0282	0.1826
chrMT	16571	332189	20.0464	10.5858
chrX	155270560	5874284	0.0378	0.2588
chrY	59373566	338156	0.0057	0.1595

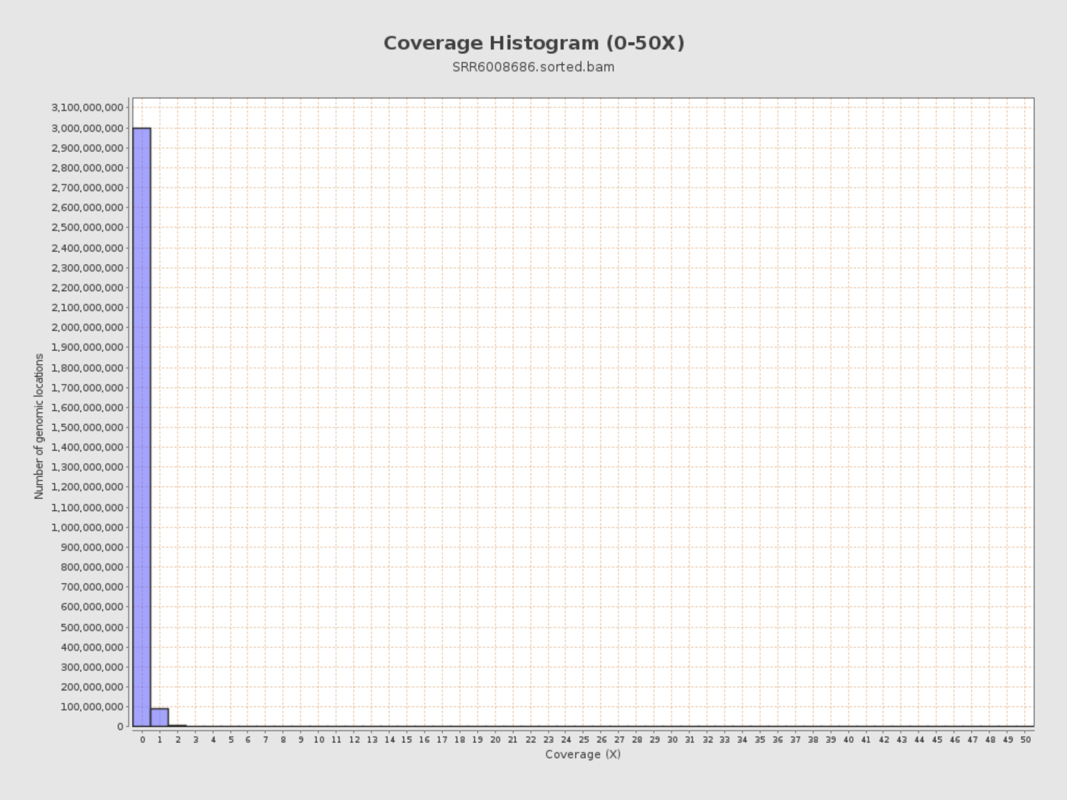
3. Results : Coverage across reference



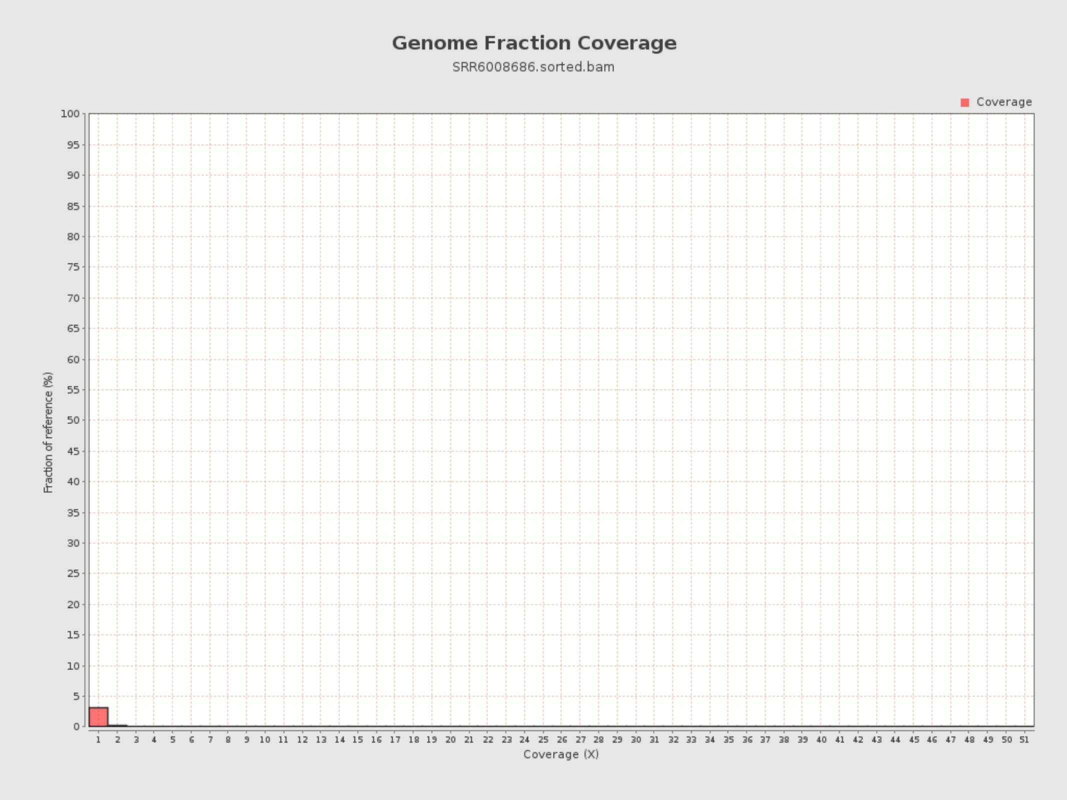
4. Results : Coverage Histogram



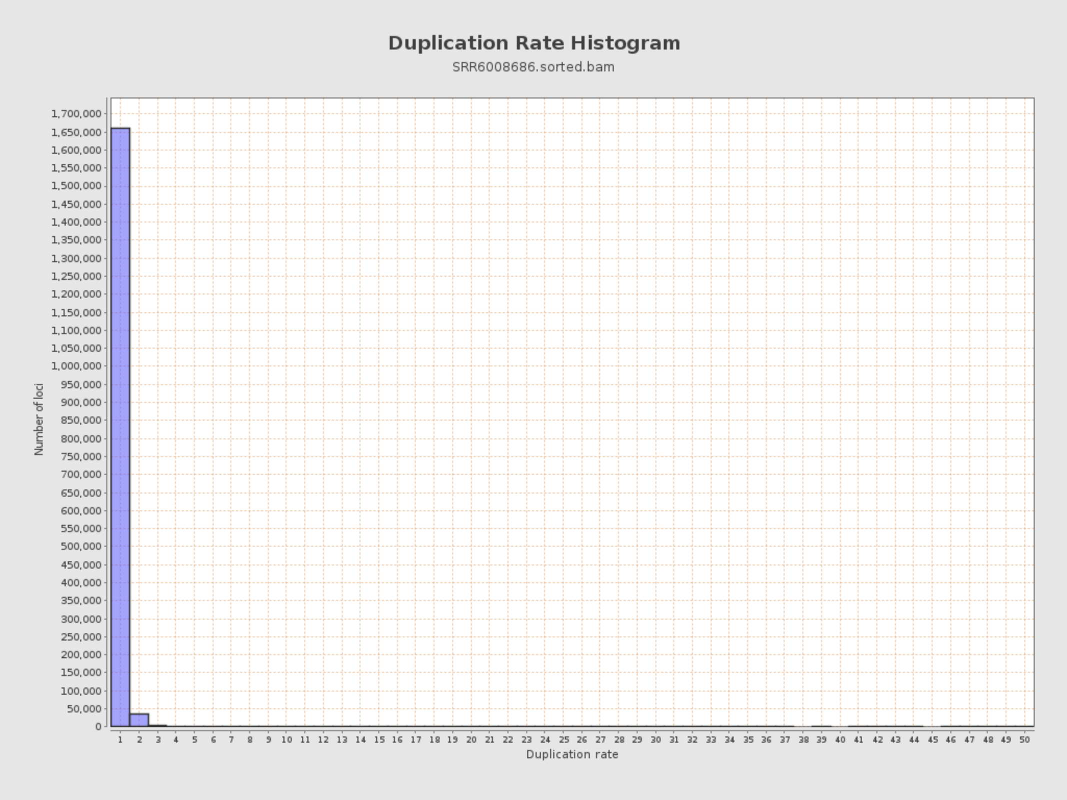
5. Results : Coverage Histogram (0-50X)



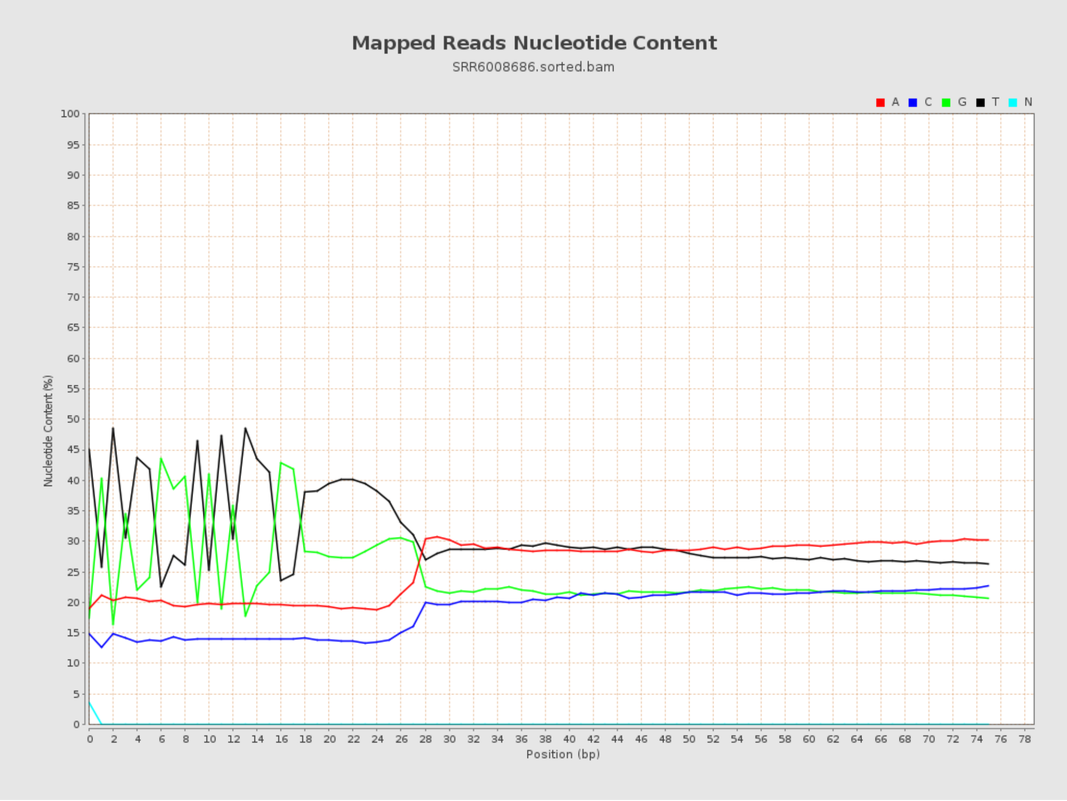
6. Results : Genome Fraction Coverage



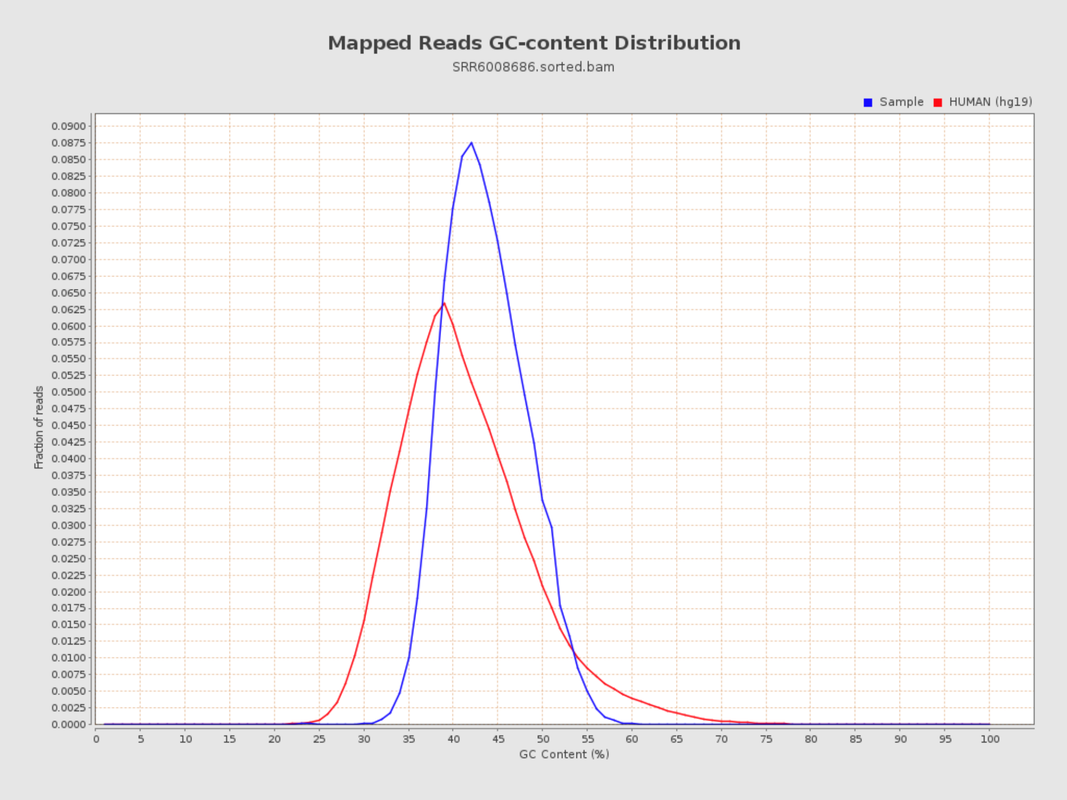
7. Results : Duplication Rate Histogram



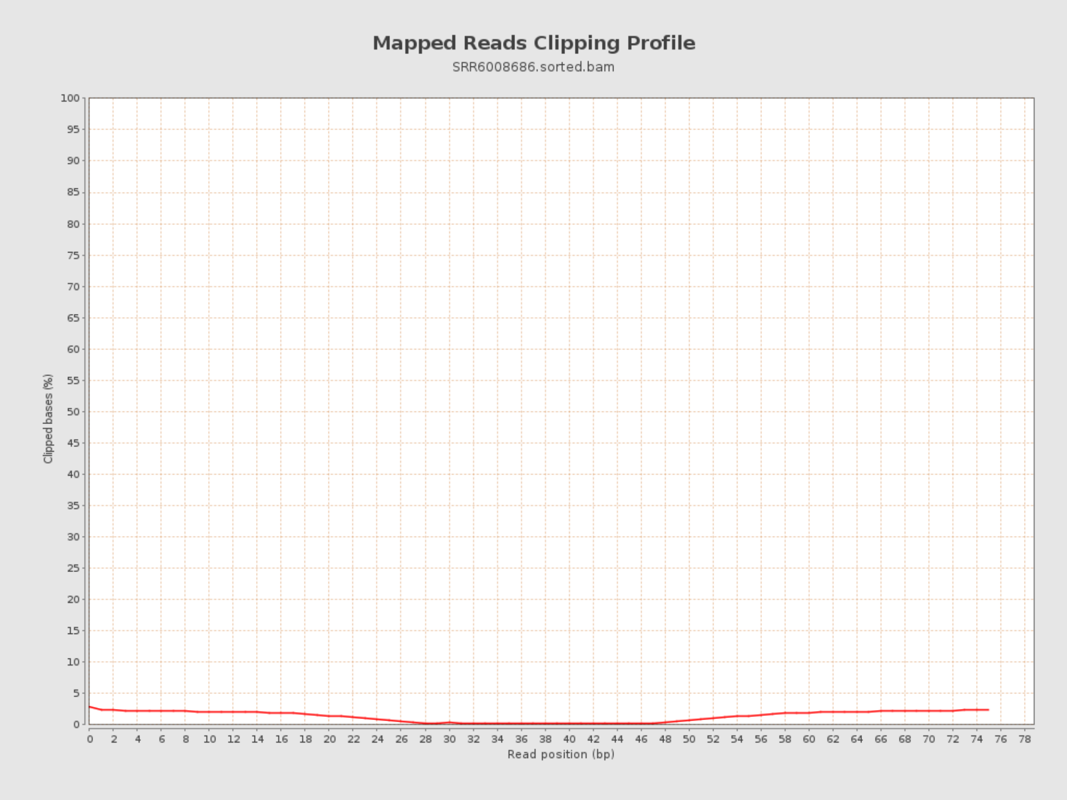
8. Results : Mapped Reads Nucleotide Content



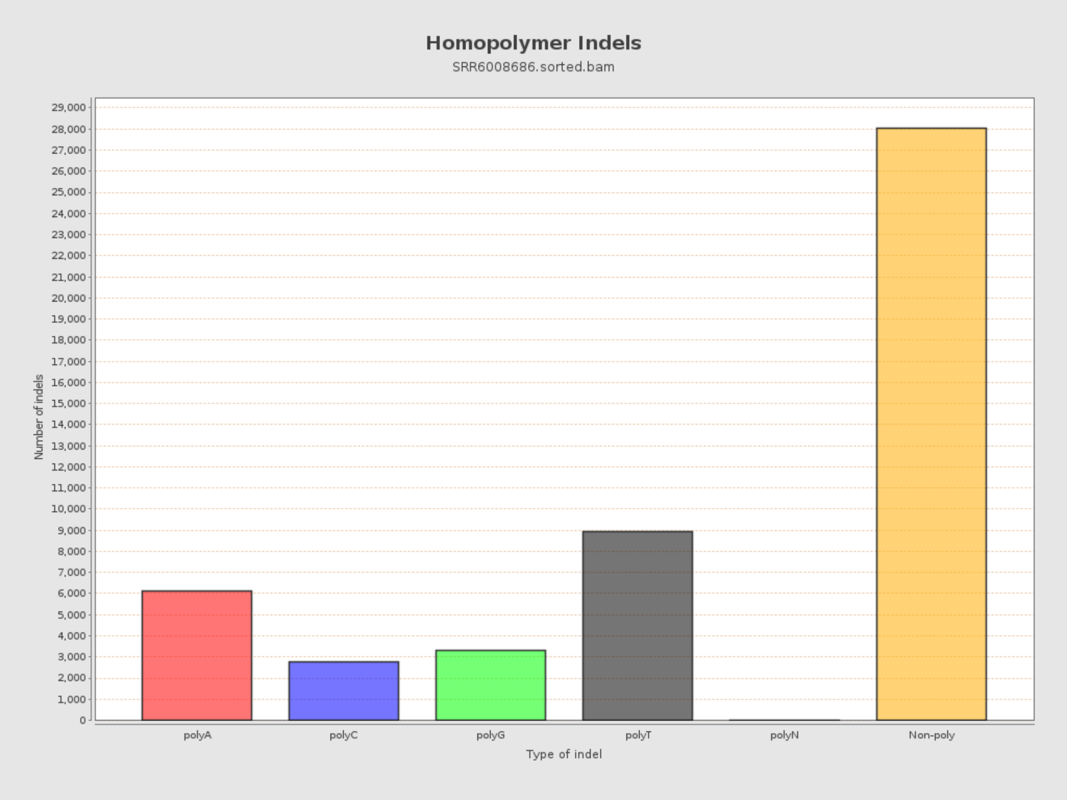
9. Results : Mapped Reads GC-content Distribution



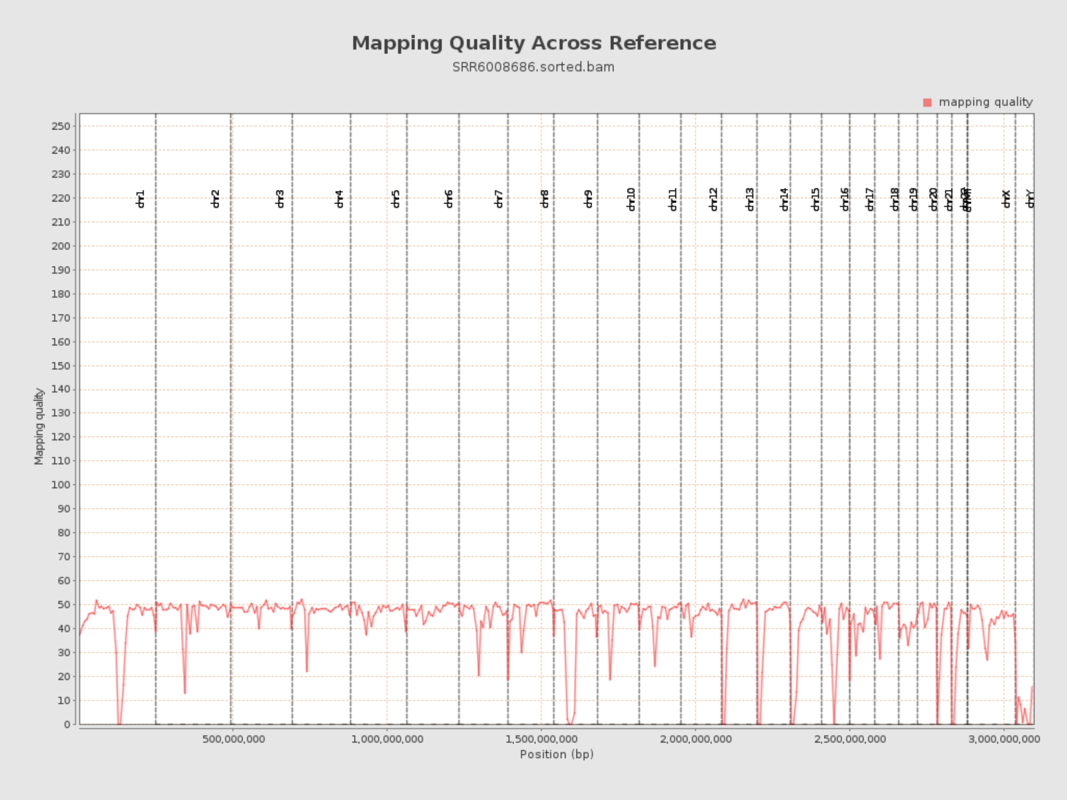
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram