Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:57:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013207.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_SRR6013207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013207.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:57:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,712,177
Mapped reads	1,221,686 / 71.35%
Unmapped reads	490,491 / 28.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,957 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	88,400 / 5.16%
Duplication rate	5.94%
Clipped reads	622,576 / 36.36%

2.2. ACGT Content

Number/percentage of A's	21,835,165 / 27.42%
Number/percentage of C's	14,250,469 / 17.89%
Number/percentage of T's	25,957,135 / 32.59%
Number/percentage of G's	17,579,136 / 22.07%
Number/percentage of N's	16,440 / 0.02%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2889

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

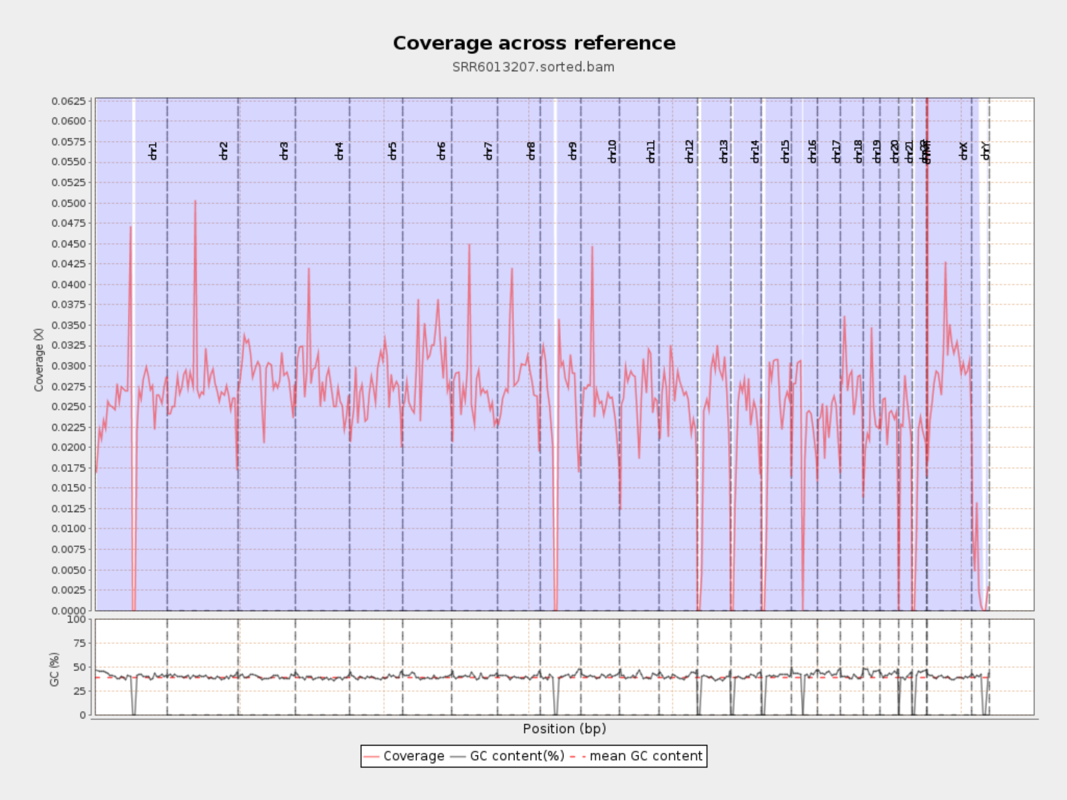
General error rate	0.85%
Mismatches	666,551
Insertions	5,864
Mapped reads with at least one insertion	0.48%
Deletions	17,722
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.45%

2.6. Chromosome stats

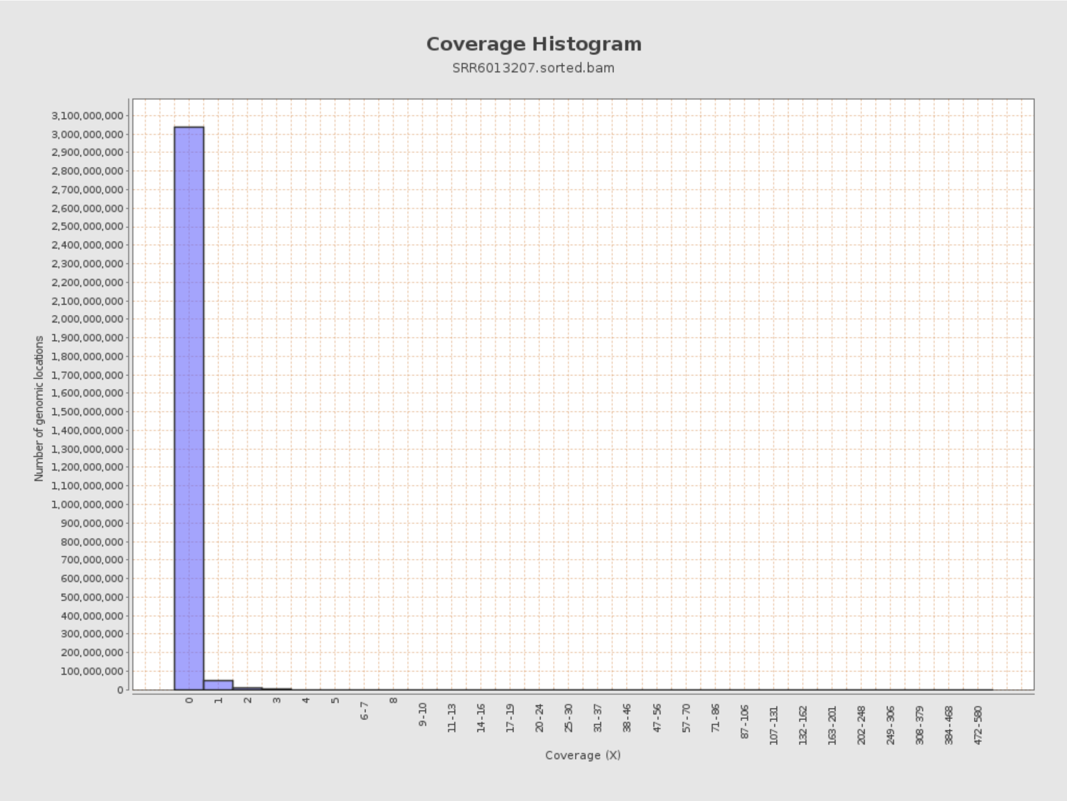
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6150496	0.0247	0.5022
chr2	243199373	6729531	0.0277	0.3412
chr3	198022430	5721045	0.0289	0.2165
chr4	191154276	5375278	0.0281	0.2226
chr5	180915260	4911247	0.0271	0.2106
chr6	171115067	5121119	0.0299	0.2457
chr7	159138663	4332731	0.0272	0.321

chr8	146364022	4171660	0.0285	0.3672
chr9	141213431	3511252	0.0249	0.2755
chr10	135534747	3561522	0.0263	0.2705
chr11	135006516	3626567	0.0269	0.2585
chr12	133851895	3491252	0.0261	0.2079
chr13	115169878	2668793	0.0232	0.1946
chr14	107349540	2245468	0.0209	0.1992
chr15	102531392	2301840	0.0225	0.1897
chr16	90354753	2013454	0.0223	0.2059
chr17	81195210	1881970	0.0232	0.207
chr18	78077248	2209080	0.0283	0.4628
chr19	59128983	1383454	0.0234	0.3443
chr20	63025520	1486160	0.0236	0.1989
chr21	48129895	1053706	0.0219	0.1985
chr22	51304566	786860	0.0153	0.1533
chrMT	16571	49772	3.0036	2.5438
chrX	155270560	4646926	0.0299	0.2333
chrY	59373566	237465	0.004	0.1124

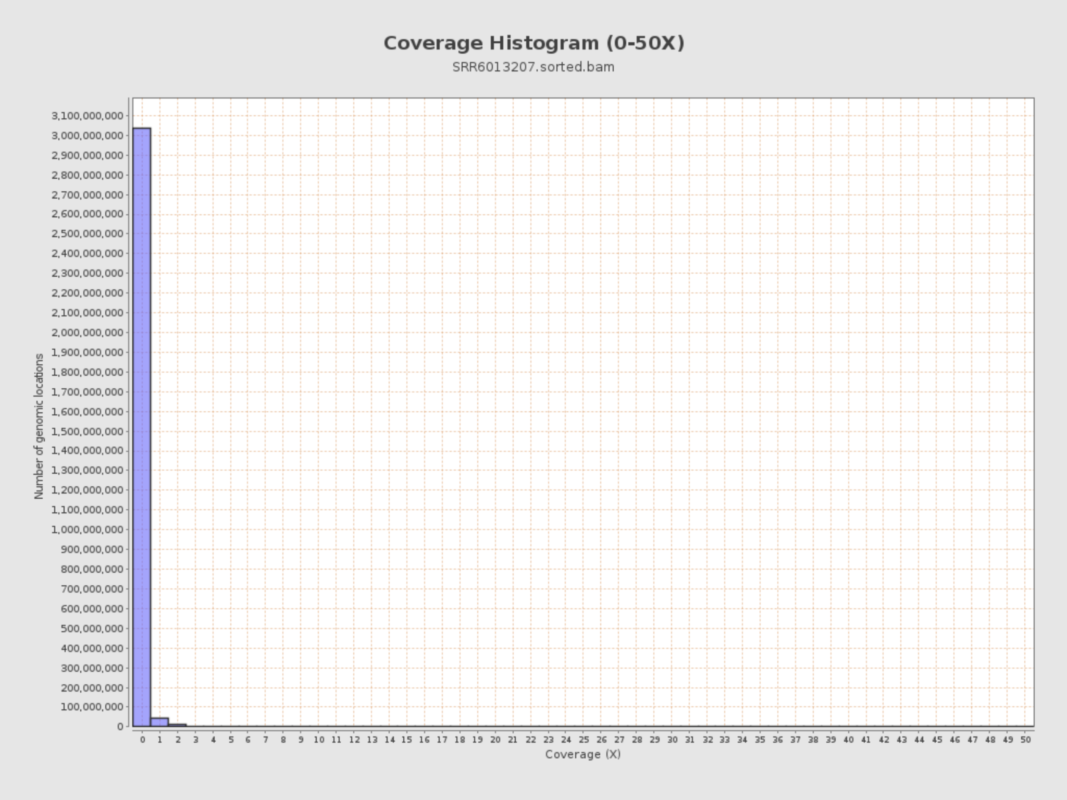
3. Results : Coverage across reference



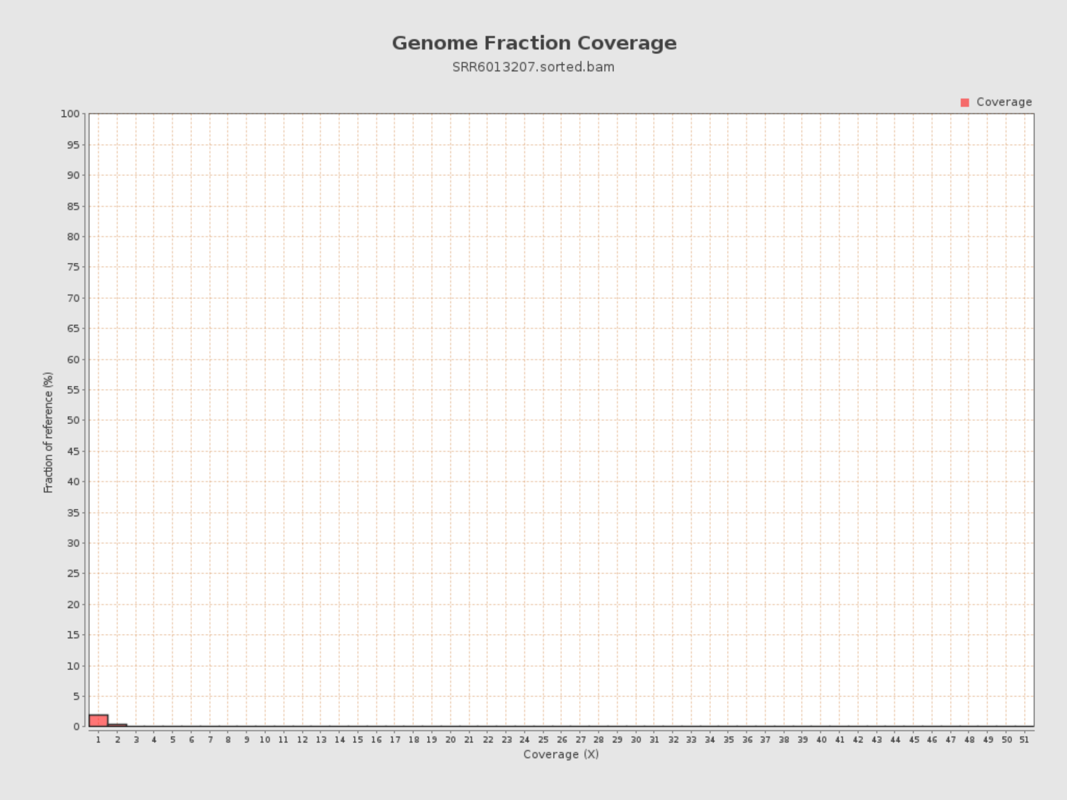
4. Results : Coverage Histogram



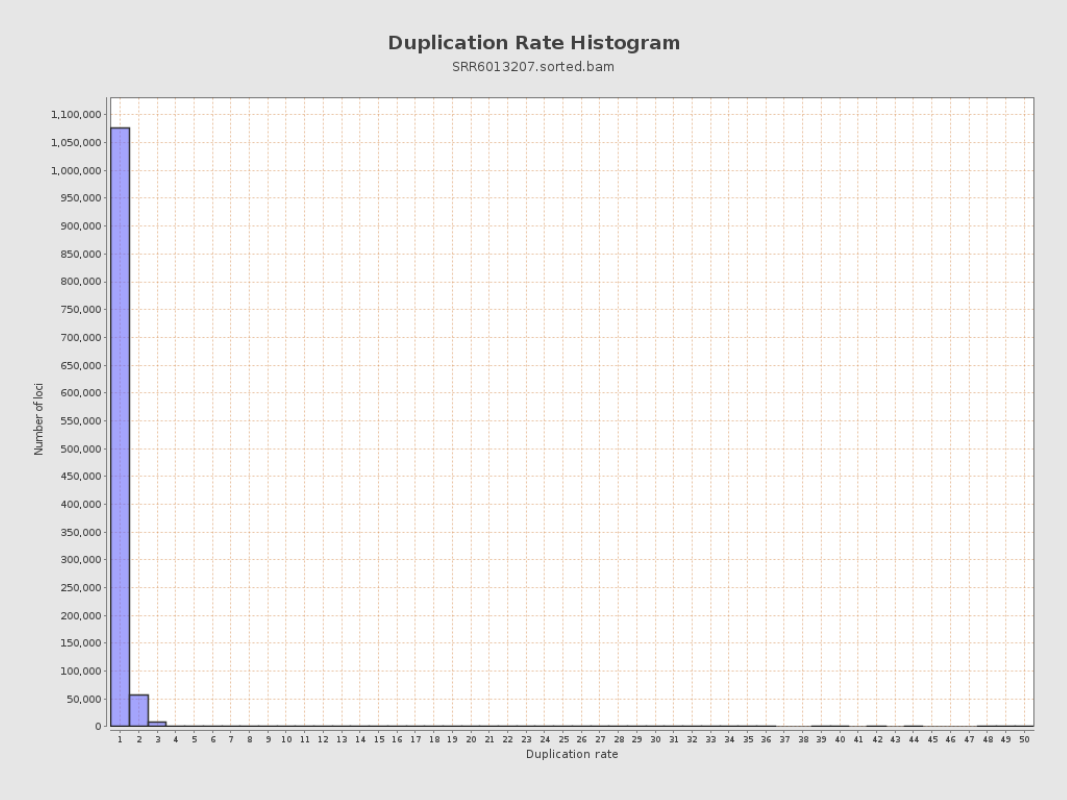
5. Results : Coverage Histogram (0-50X)



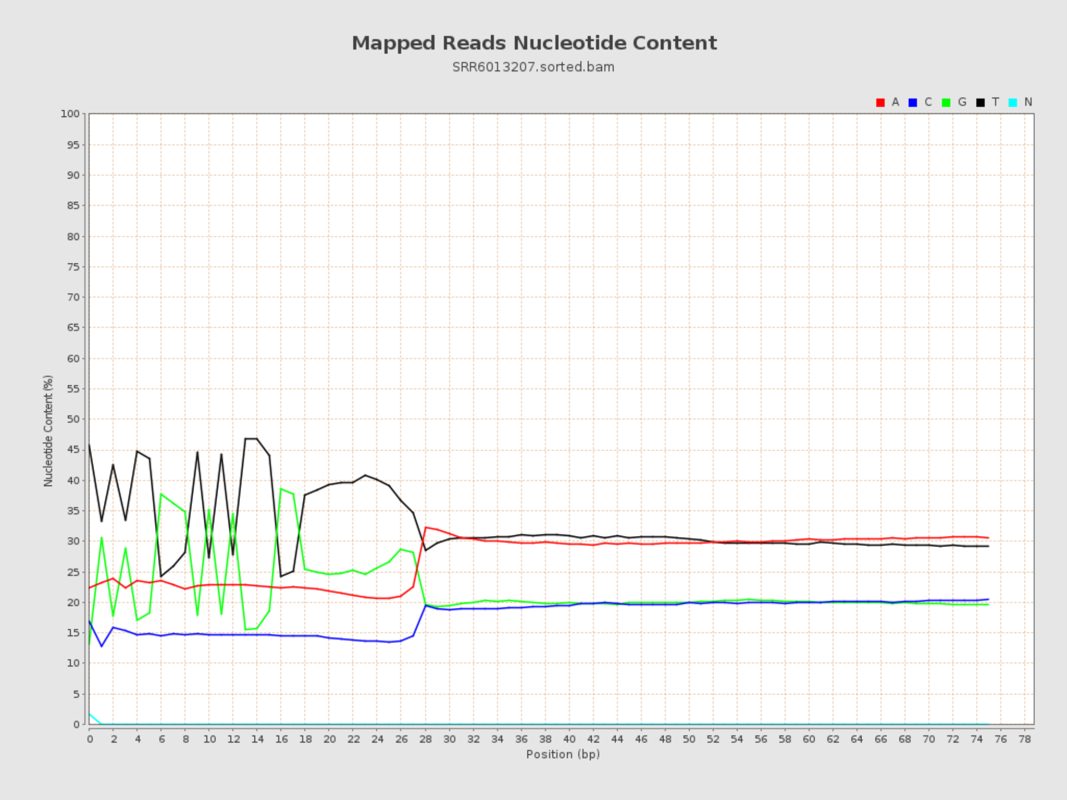
6. Results : Genome Fraction Coverage



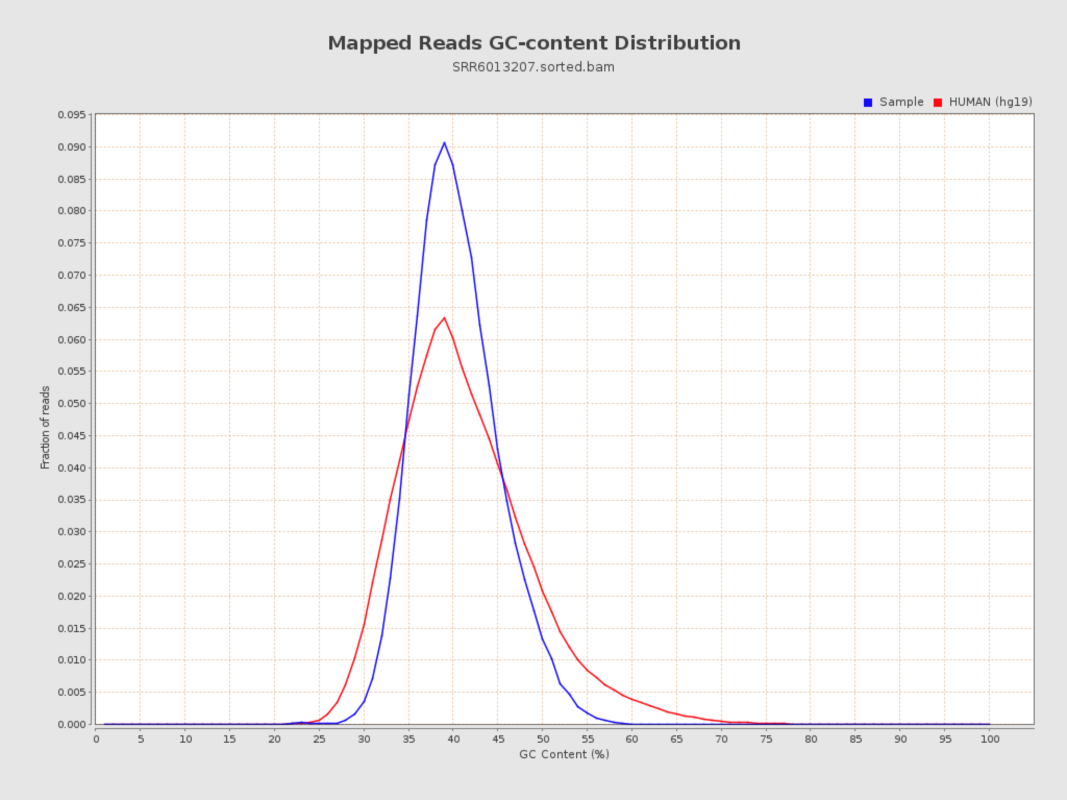
7. Results : Duplication Rate Histogram



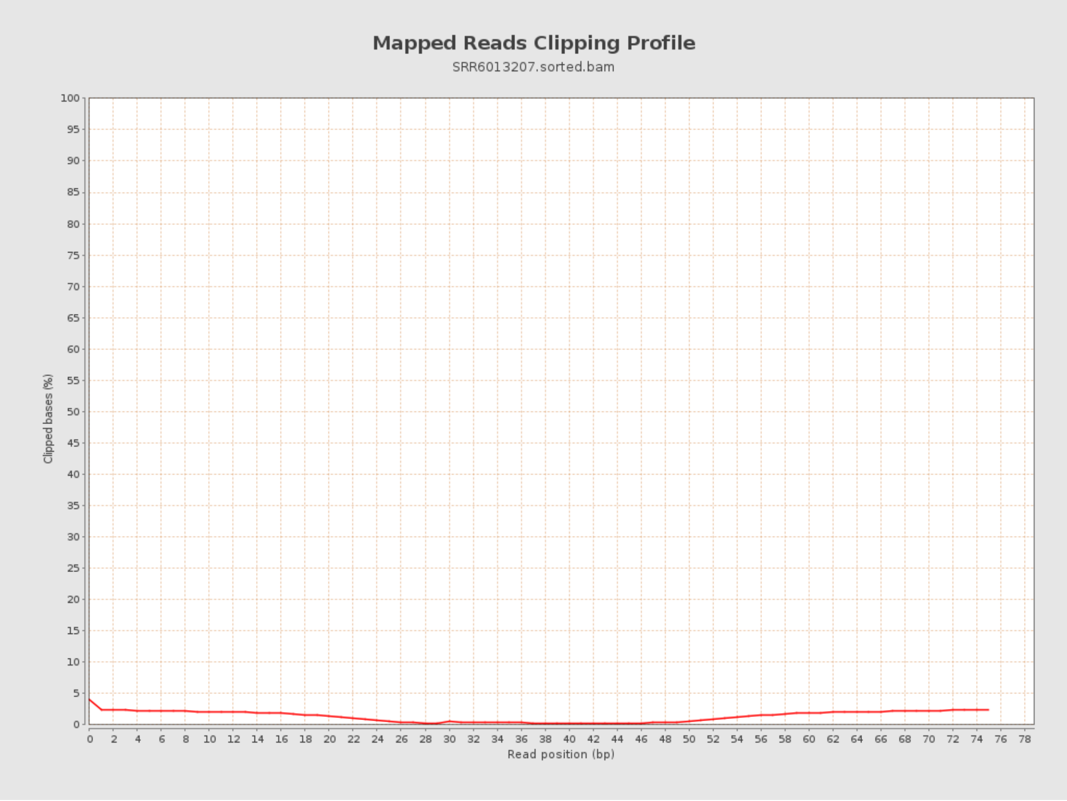
8. Results : Mapped Reads Nucleotide Content



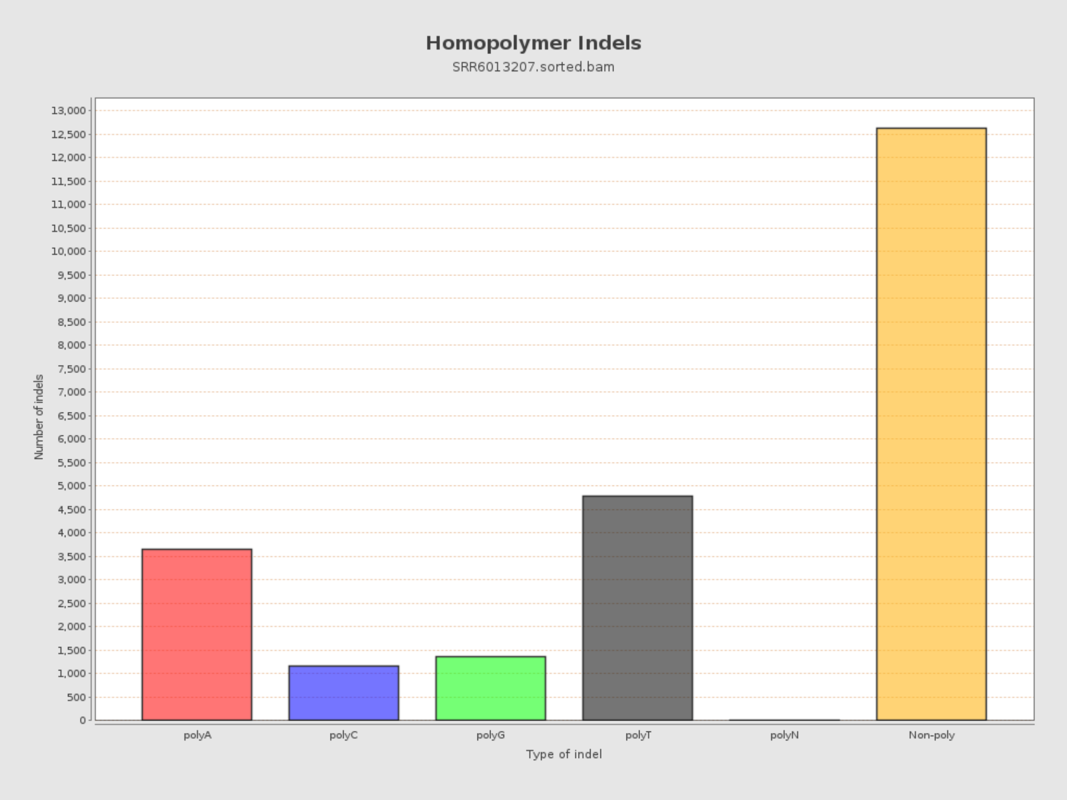
9. Results : Mapped Reads GC-content Distribution



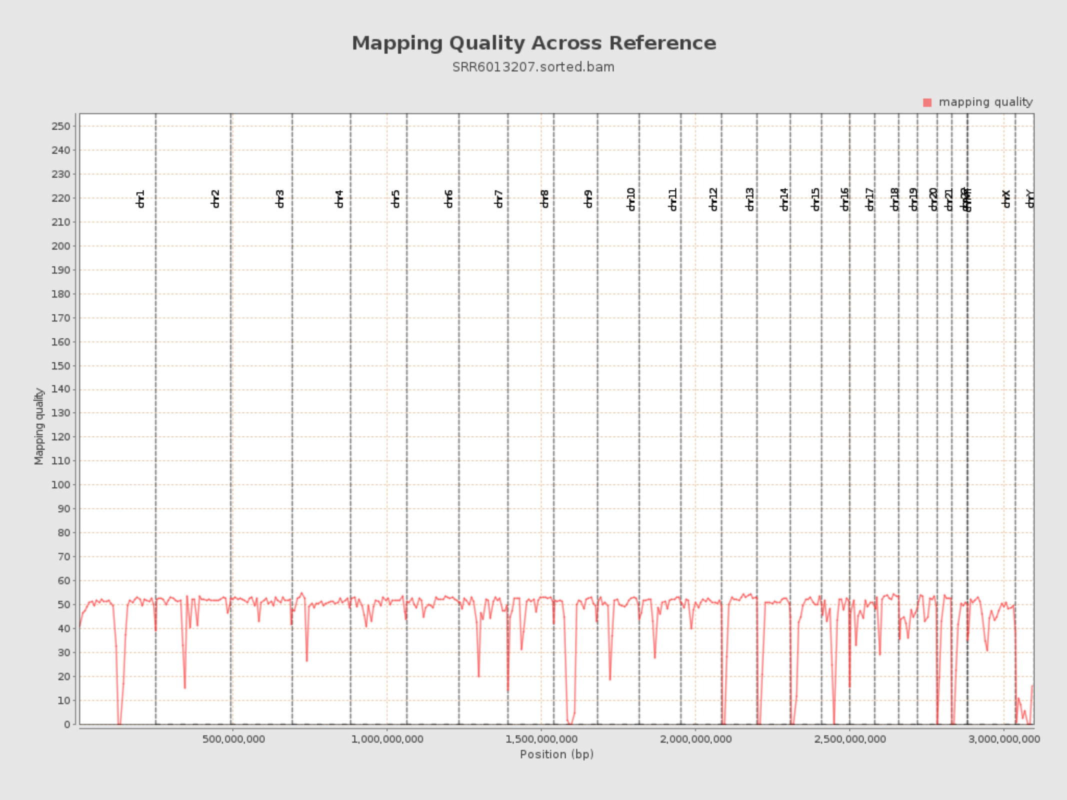
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram