Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:37:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013220.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_SRR6013220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013220.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:37:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,753,352
Mapped reads	1,534,559 / 87.52%
Unmapped reads	218,793 / 12.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,743 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	72,189 / 4.12%
Duplication rate	3.65%
Clipped reads	654,584 / 37.33%

2.2. ACGT Content

Number/percentage of A's	28,551,425 / 27.84%
Number/percentage of C's	18,677,524 / 18.21%
Number/percentage of T's	32,856,553 / 32.03%
Number/percentage of G's	22,479,841 / 21.92%
Number/percentage of N's	1,352 / 0%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.3725

2.4. Mapping Quality

Mean Mapping Quality	47.03

2.5. Mismatches and indels

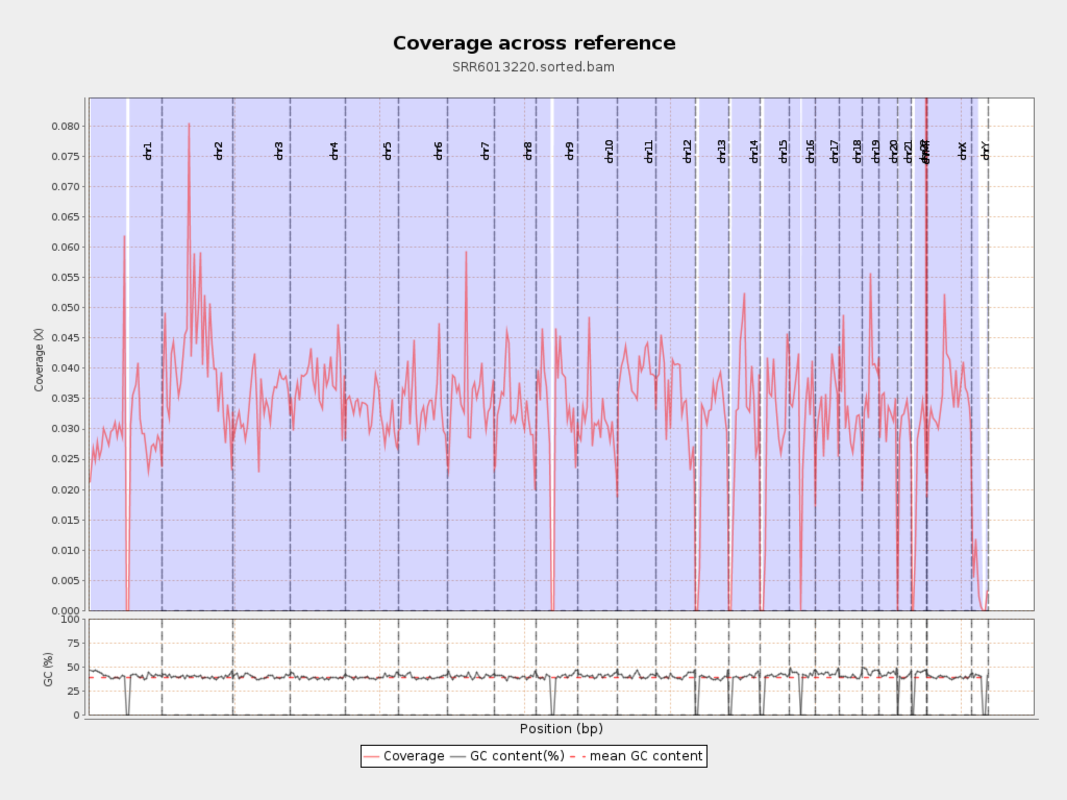
General error rate	0.71%
Mismatches	715,736
Insertions	7,165
Mapped reads with at least one insertion	0.46%
Deletions	24,844
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.18%

2.6. Chromosome stats

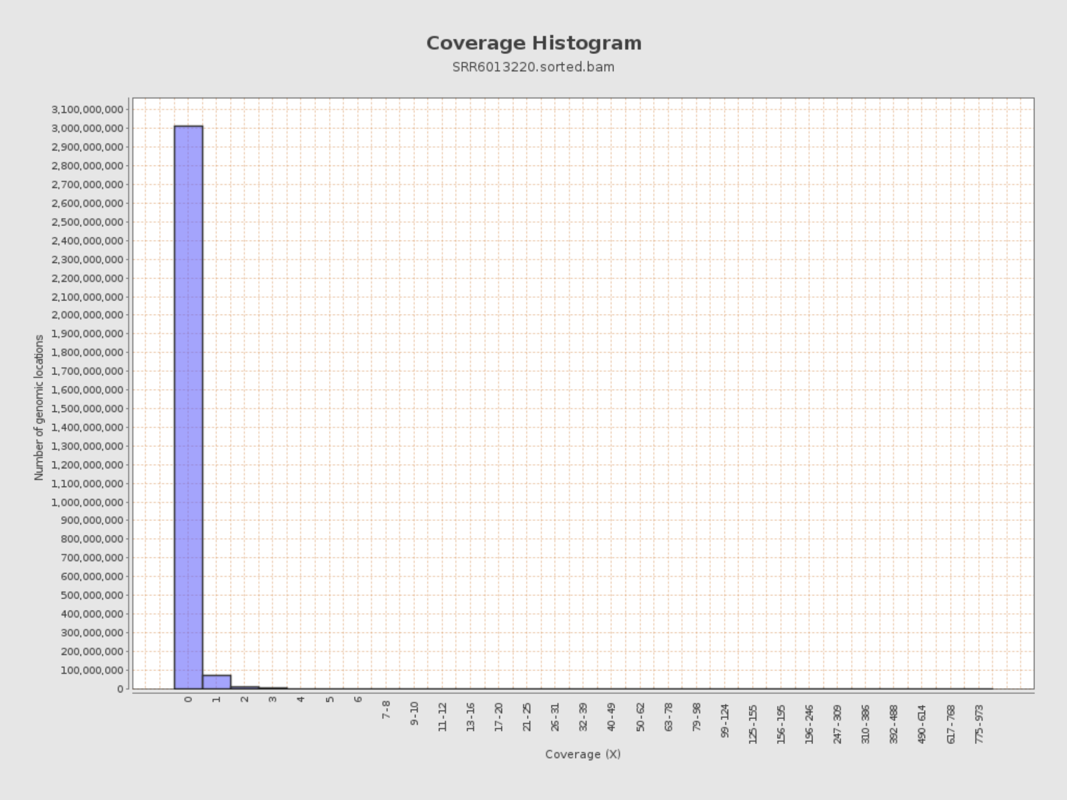
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7020625	0.0282	0.804
chr2	243199373	10304582	0.0424	0.3969
chr3	198022430	6802425	0.0344	0.216
chr4	191154276	7233768	0.0378	0.234
chr5	180915260	5904691	0.0326	0.2122
chr6	171115067	5849636	0.0342	0.2445
chr7	159138663	5683207	0.0357	0.4379

chr8	146364022	4806217	0.0328	0.5096
chr9	141213431	4591694	0.0325	0.3129
chr10	135534747	4232606	0.0312	0.2879
chr11	135006516	5299826	0.0393	0.2973
chr12	133851895	4713754	0.0352	0.2246
chr13	115169878	3281115	0.0285	0.1975
chr14	107349540	3296079	0.0307	0.2167
chr15	102531392	2888146	0.0282	0.1996
chr16	90354753	2895510	0.032	0.2223
chr17	81195210	2686967	0.0331	0.2328
chr18	78077248	2587872	0.0331	0.5593
chr19	59128983	2282545	0.0386	0.5177
chr20	63025520	2008524	0.0319	0.2216
chr21	48129895	1359811	0.0283	0.206
chr22	51304566	1089658	0.0212	0.1665
chrMT	16571	32172	1.9415	1.795
chrX	155270560	5521116	0.0356	0.2489
chrY	59373566	236752	0.004	0.0932

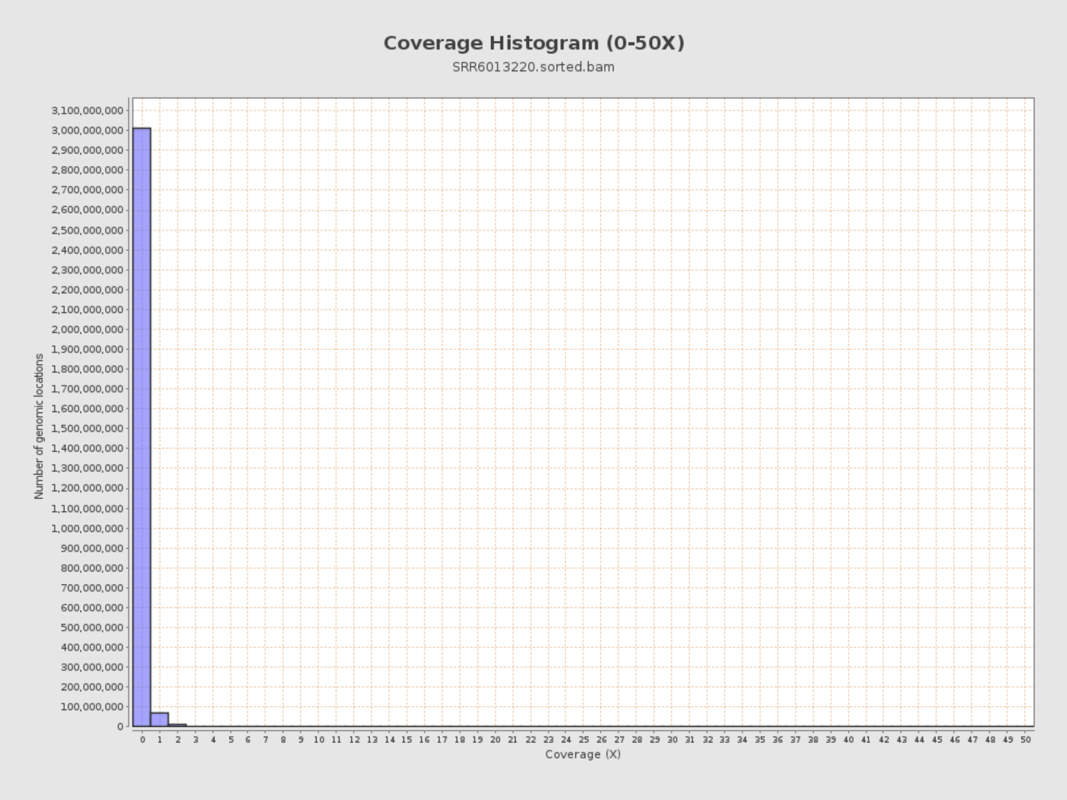
3. Results : Coverage across reference



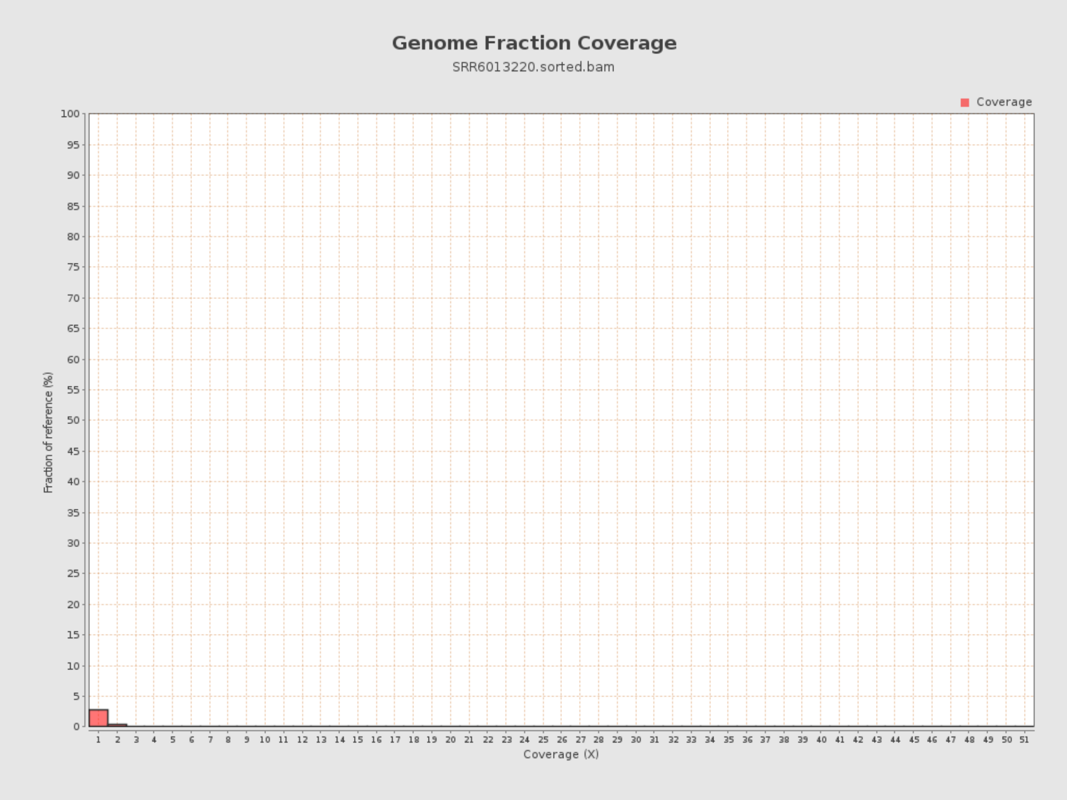
4. Results : Coverage Histogram



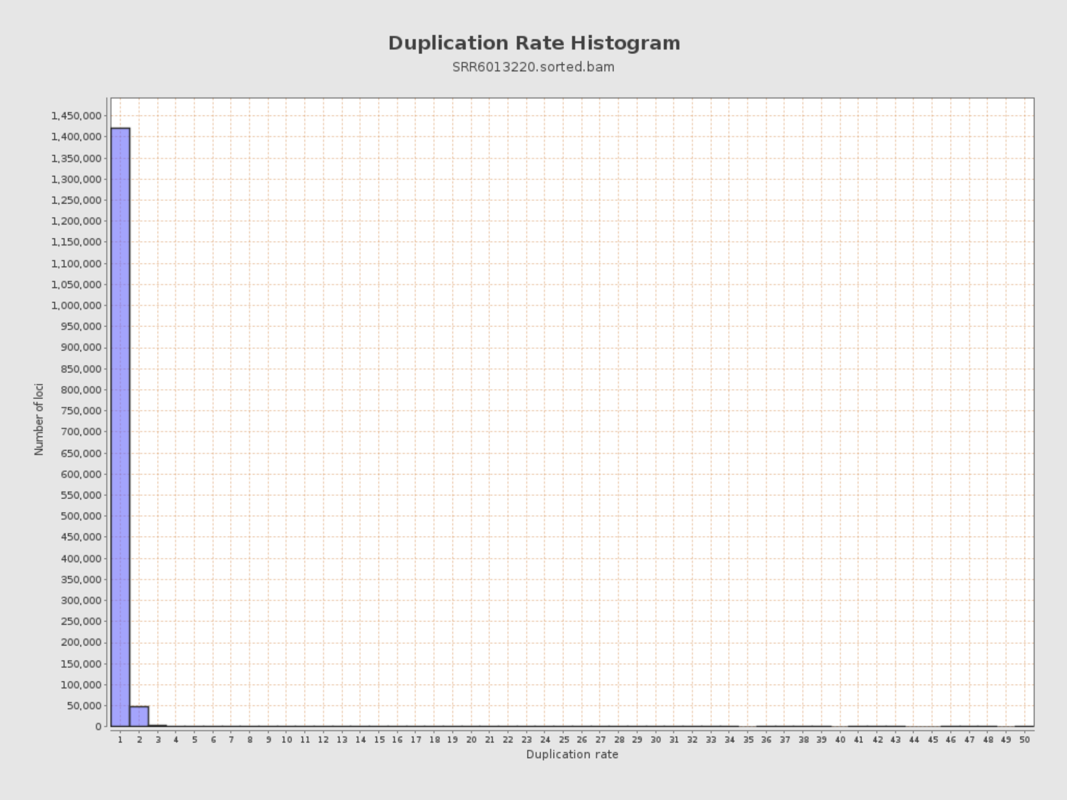
5. Results : Coverage Histogram (0-50X)



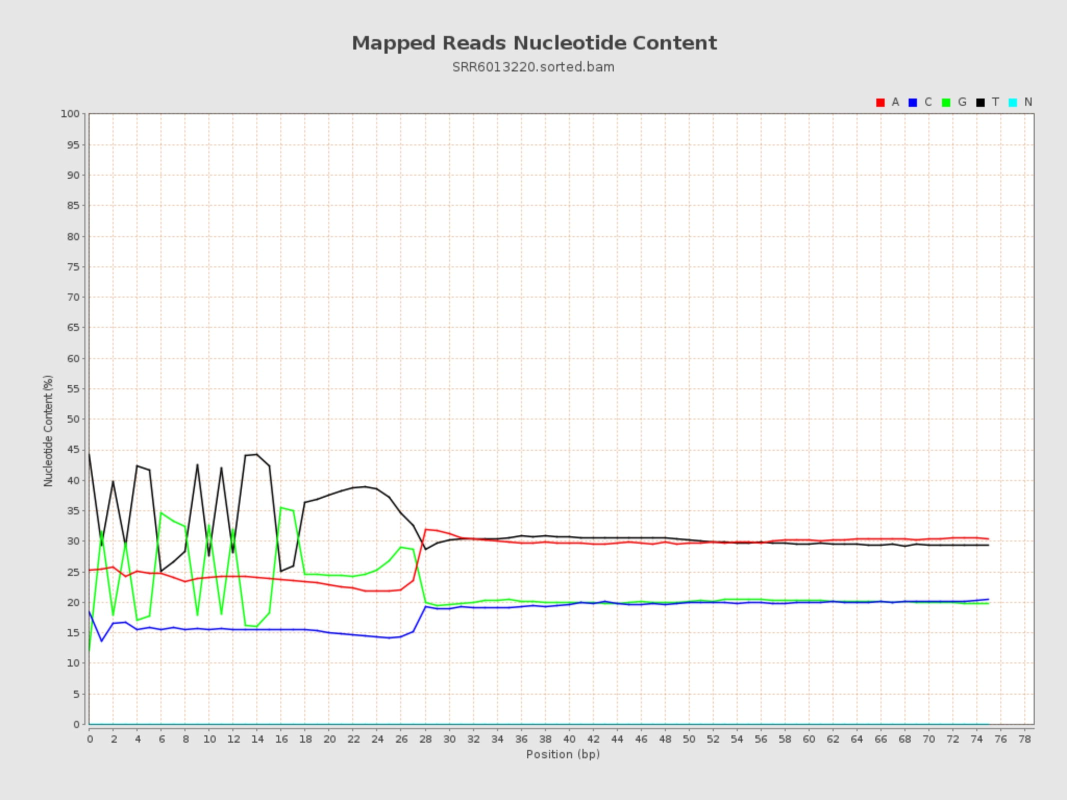
6. Results : Genome Fraction Coverage



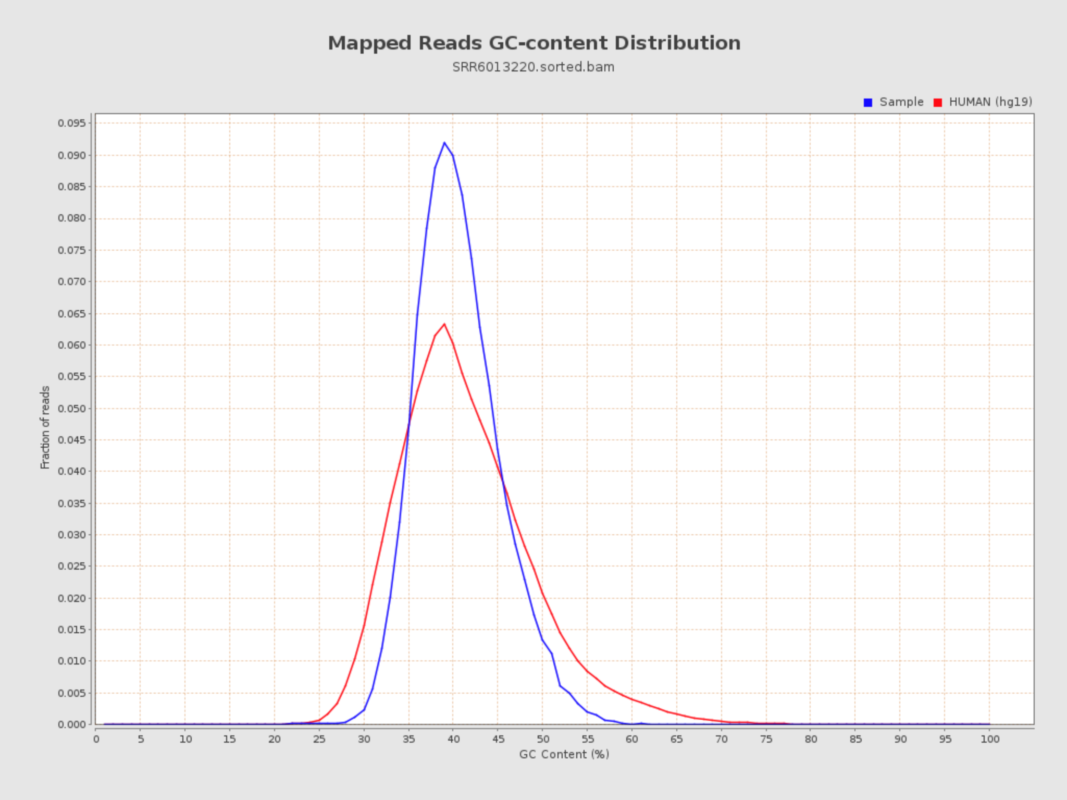
7. Results : Duplication Rate Histogram



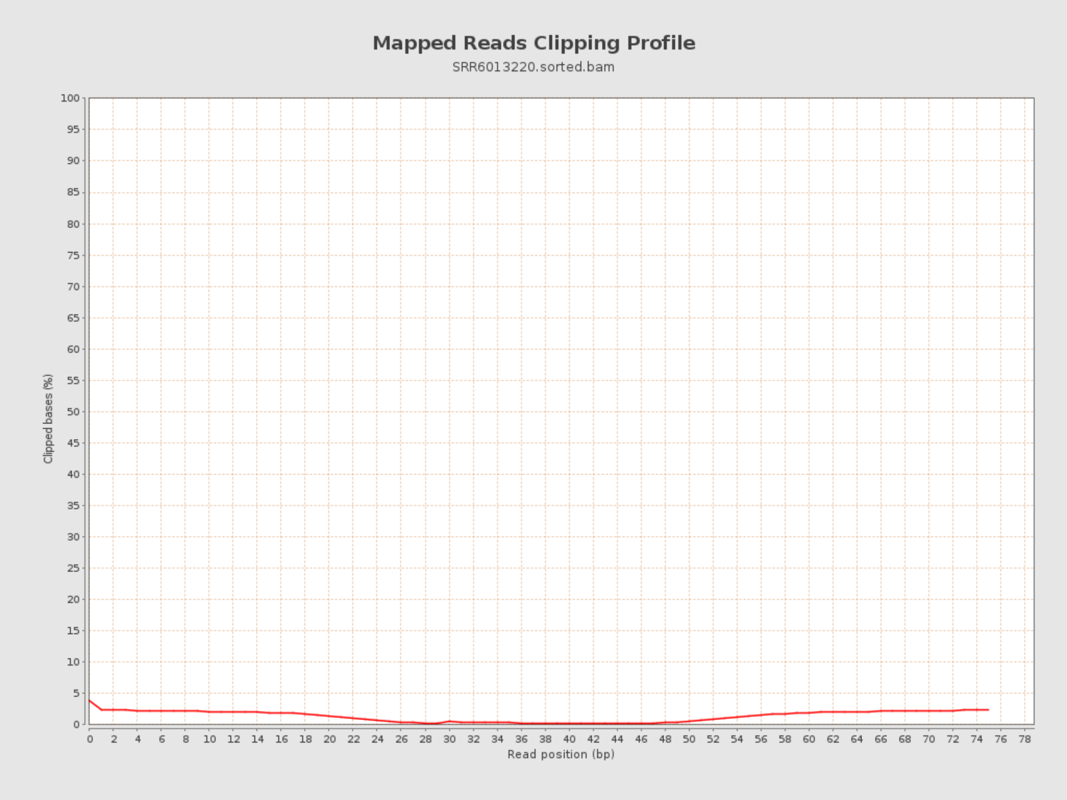
8. Results : Mapped Reads Nucleotide Content



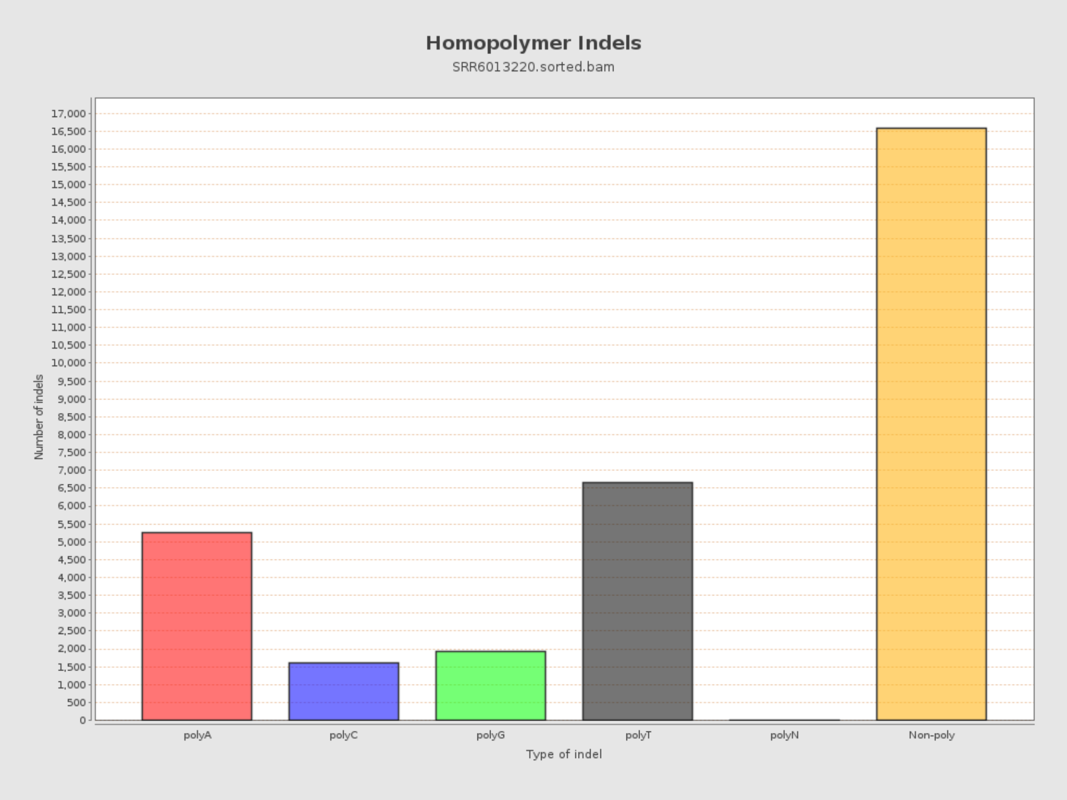
9. Results : Mapped Reads GC-content Distribution



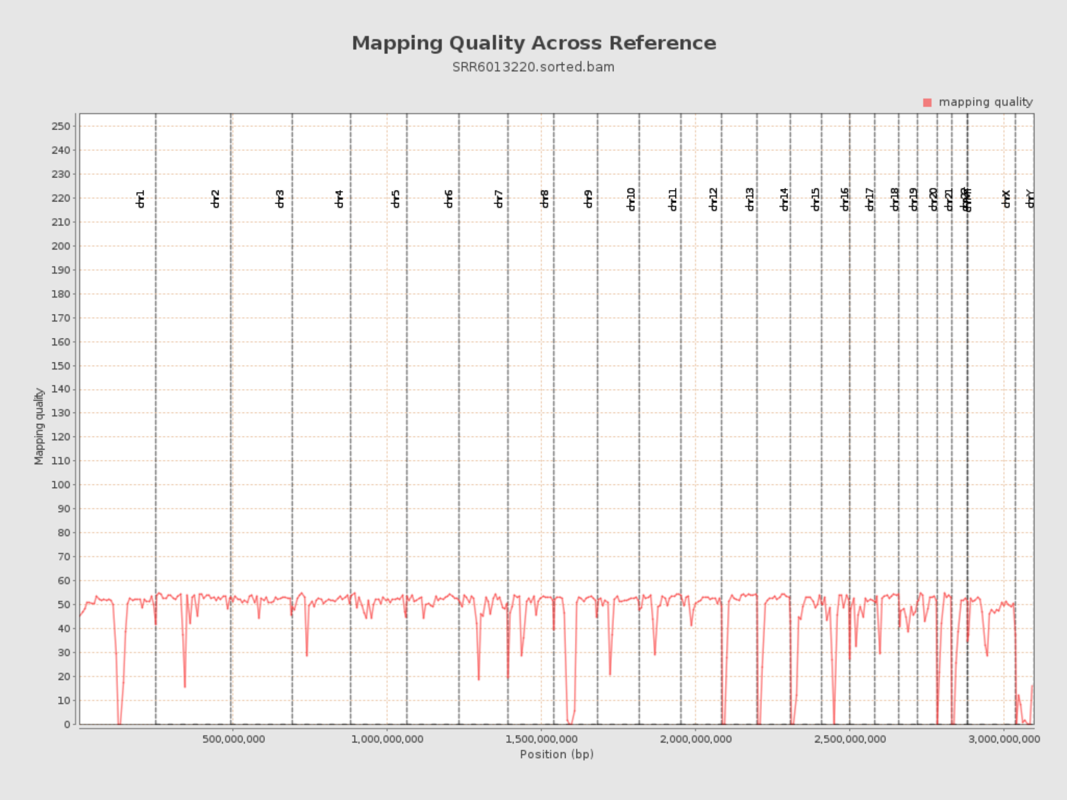
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram