Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:54:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013310.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_SRR6013310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013310.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:54:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,532,807
Mapped reads	1,147,838 / 74.88%
Unmapped reads	384,969 / 25.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,327 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	97,366 / 6.35%
Duplication rate	6.95%
Clipped reads	675,277 / 44.05%

2.2. ACGT Content

Number/percentage of A's	20,142,822 / 27.66%
Number/percentage of C's	13,263,340 / 18.21%
Number/percentage of T's	23,309,132 / 32%
Number/percentage of G's	16,098,665 / 22.1%
Number/percentage of N's	16,054 / 0.02%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0235

Standard Deviation	0.2777

2.4. Mapping Quality

Mean Mapping Quality	43.72

2.5. Mismatches and indels

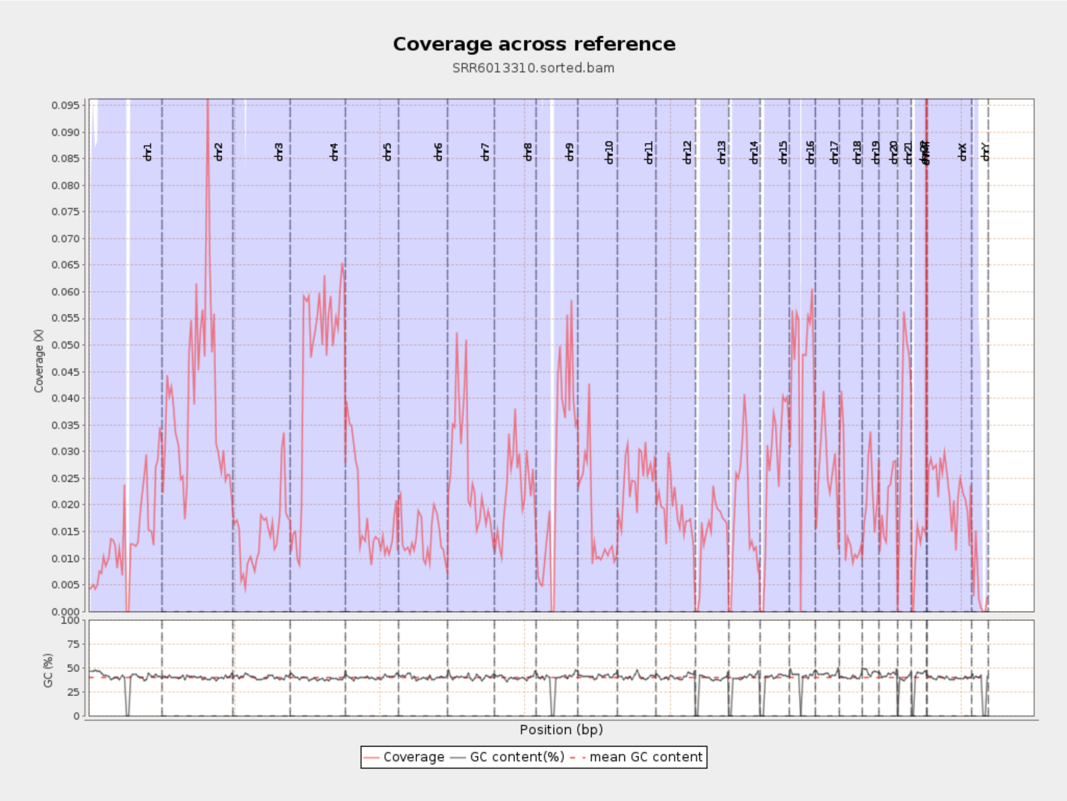
General error rate	1.04%
Mismatches	744,251
Insertions	5,627
Mapped reads with at least one insertion	0.49%
Deletions	39,420
Mapped reads with at least one deletion	3.36%
Homopolymer indels	41.59%

2.6. Chromosome stats

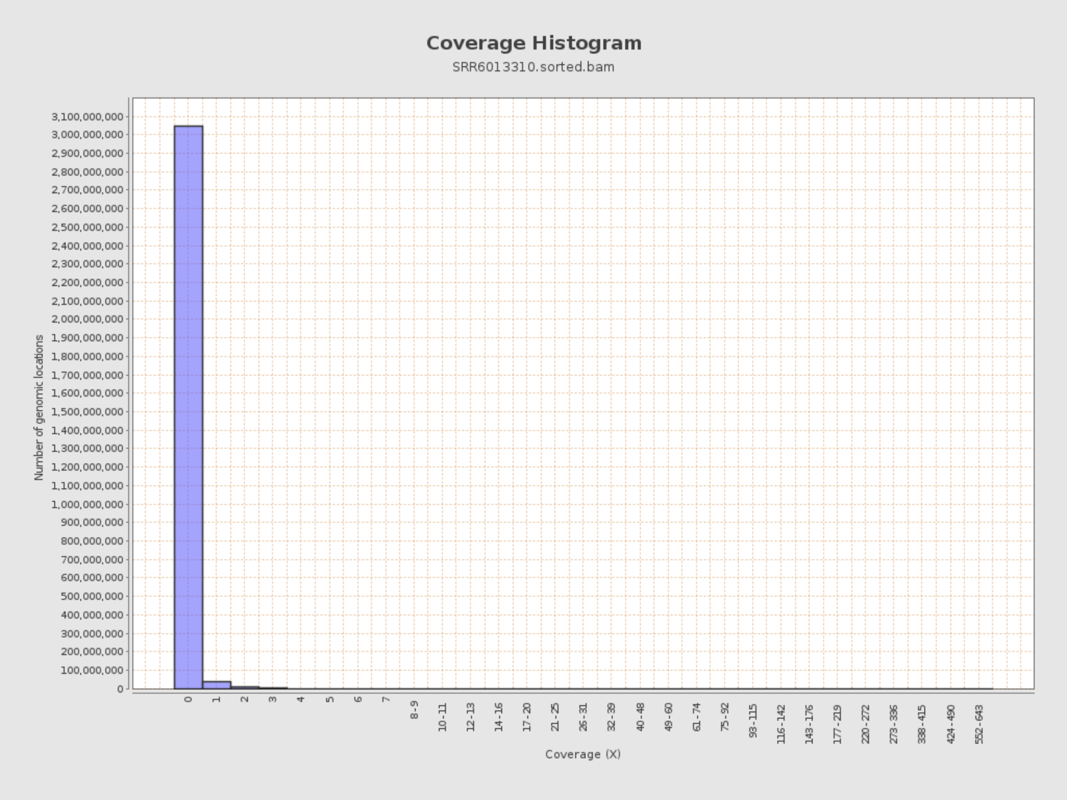
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3387140	0.0136	0.3502
chr2	243199373	9686774	0.0398	0.3728
chr3	198022430	2905253	0.0147	0.161
chr4	191154276	8804620	0.0461	0.3205
chr5	180915260	3343828	0.0185	0.1831
chr6	171115067	2356007	0.0138	0.1649
chr7	159138663	4251095	0.0267	0.42

chr8	146364022	3373347	0.023	0.406
chr9	141213431	3768269	0.0267	0.2542
chr10	135534747	2296873	0.0169	0.2781
chr11	135006516	3383598	0.0251	0.2296
chr12	133851895	2518160	0.0188	0.1866
chr13	115169878	1670398	0.0145	0.1644
chr14	107349540	1977358	0.0184	0.191
chr15	102531392	2789647	0.0272	0.2243
chr16	90354753	4190457	0.0464	0.3065
chr17	81195210	2142643	0.0264	0.2381
chr18	78077248	1348593	0.0173	0.3058
chr19	59128983	1320856	0.0223	0.3475
chr20	63025520	1263344	0.02	0.1973
chr21	48129895	1817066	0.0378	0.2797
chr22	51304566	566997	0.0111	0.1407
chrMT	16571	11585	0.6991	1.0453
chrX	155270560	3496154	0.0225	0.2074
chrY	59373566	229209	0.0039	0.145

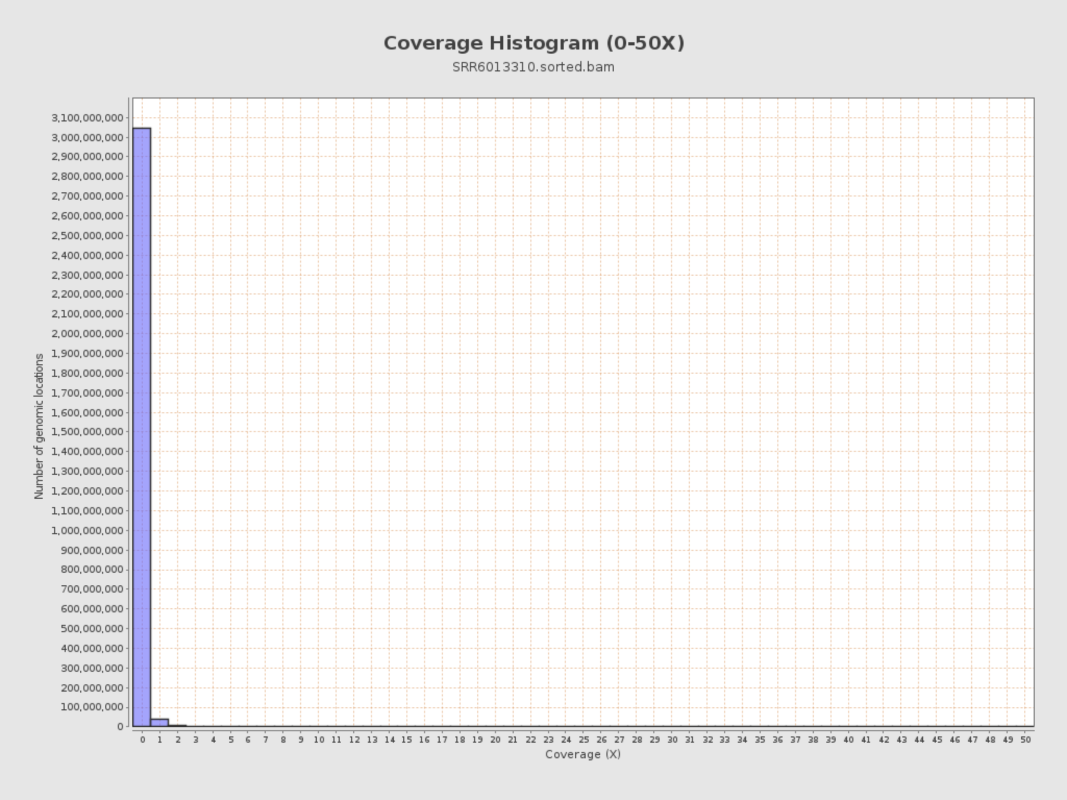
3. Results : Coverage across reference



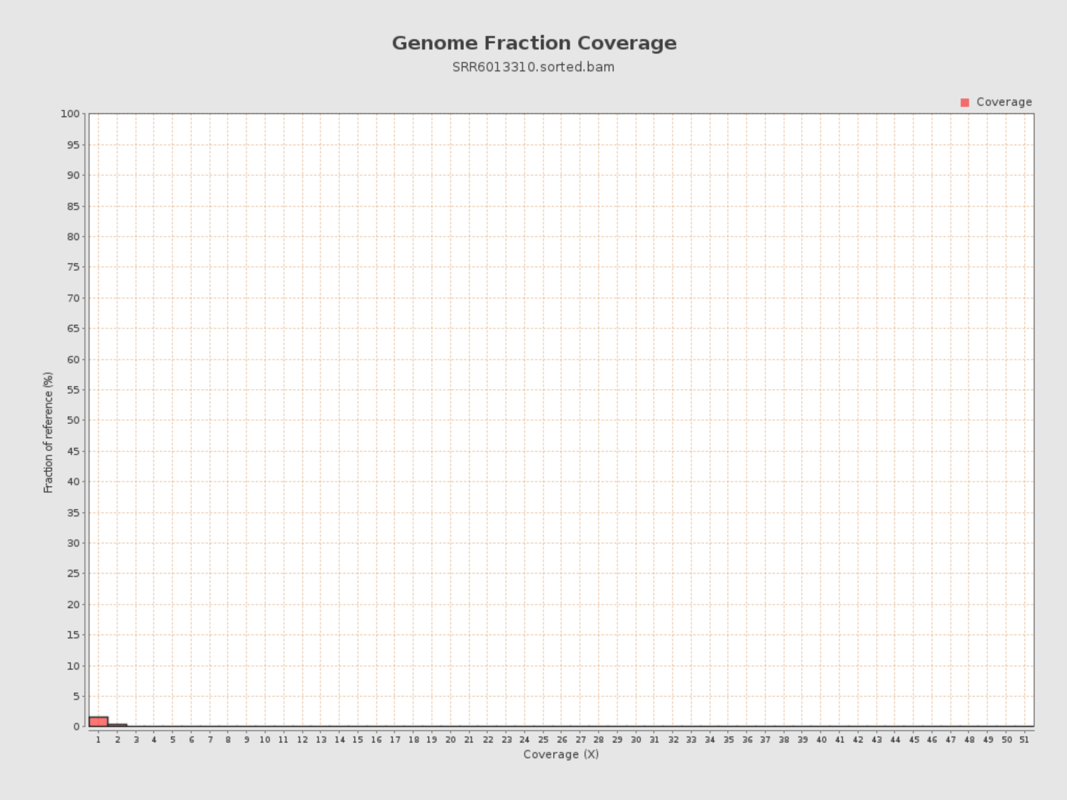
4. Results : Coverage Histogram



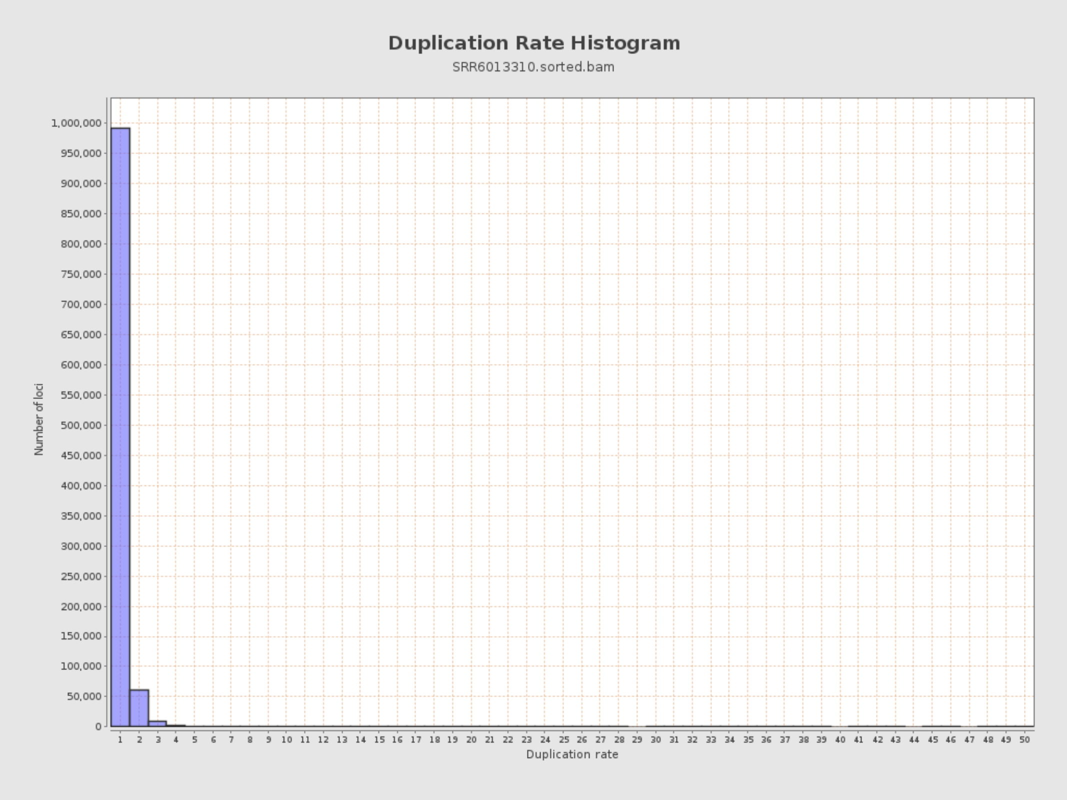
5. Results : Coverage Histogram (0-50X)



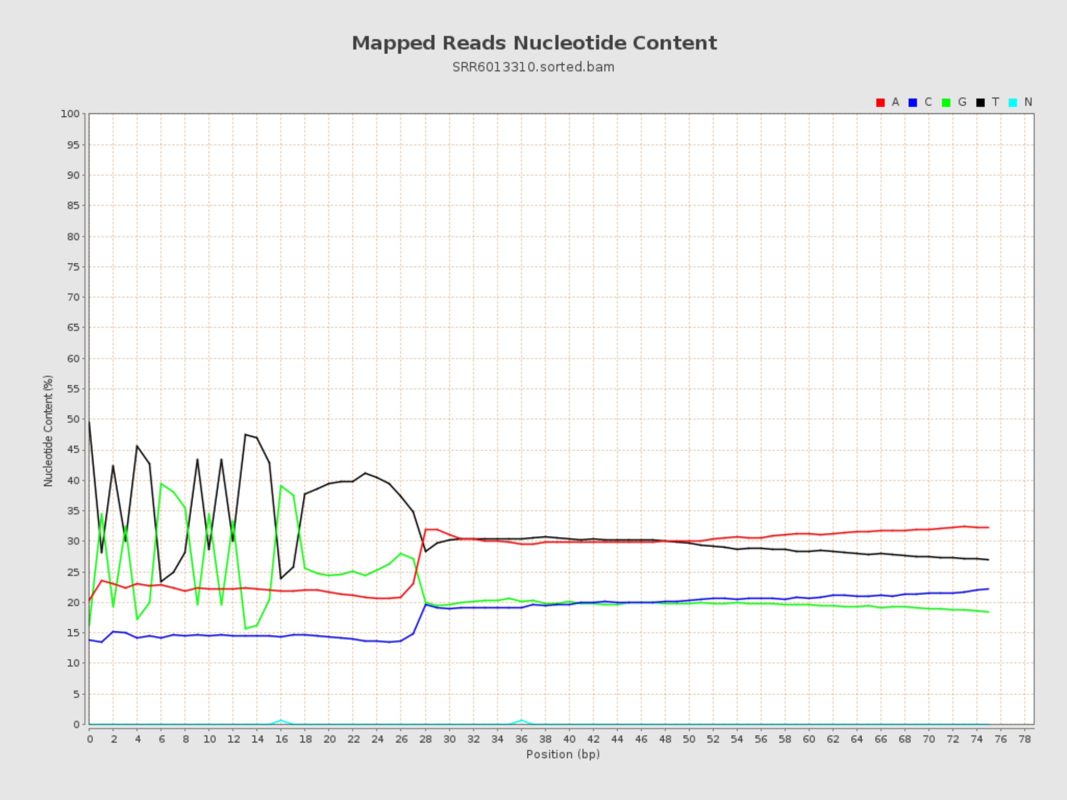
6. Results : Genome Fraction Coverage



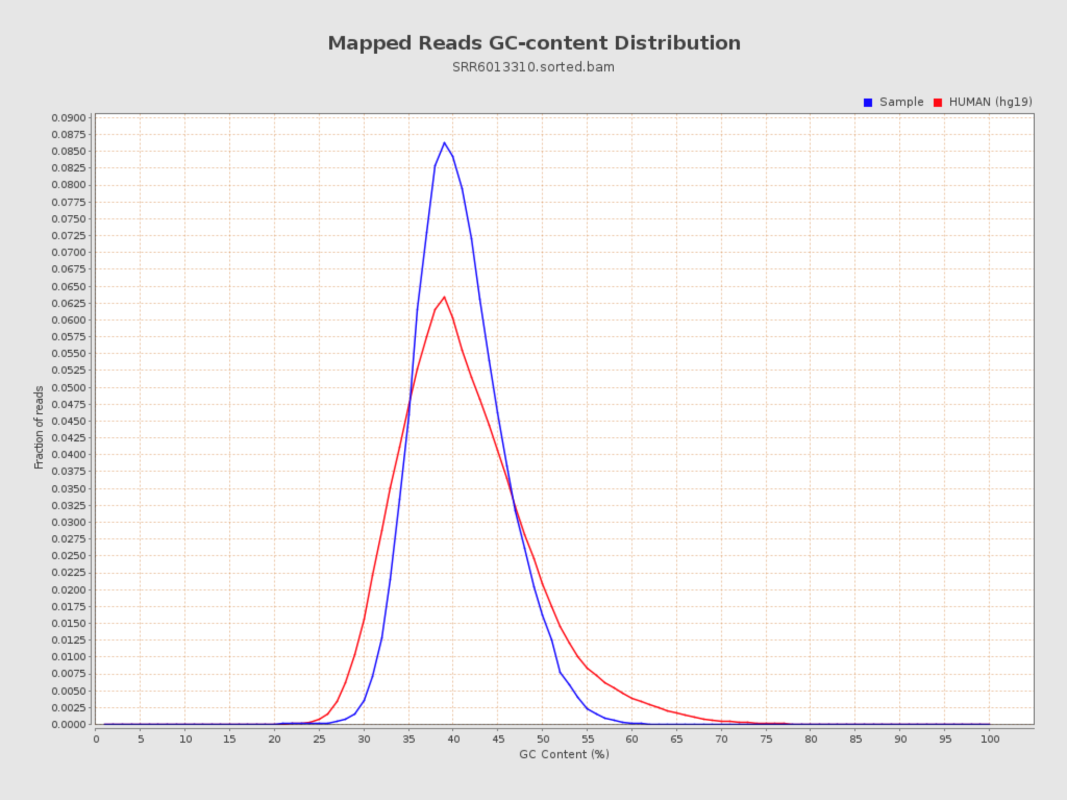
7. Results : Duplication Rate Histogram



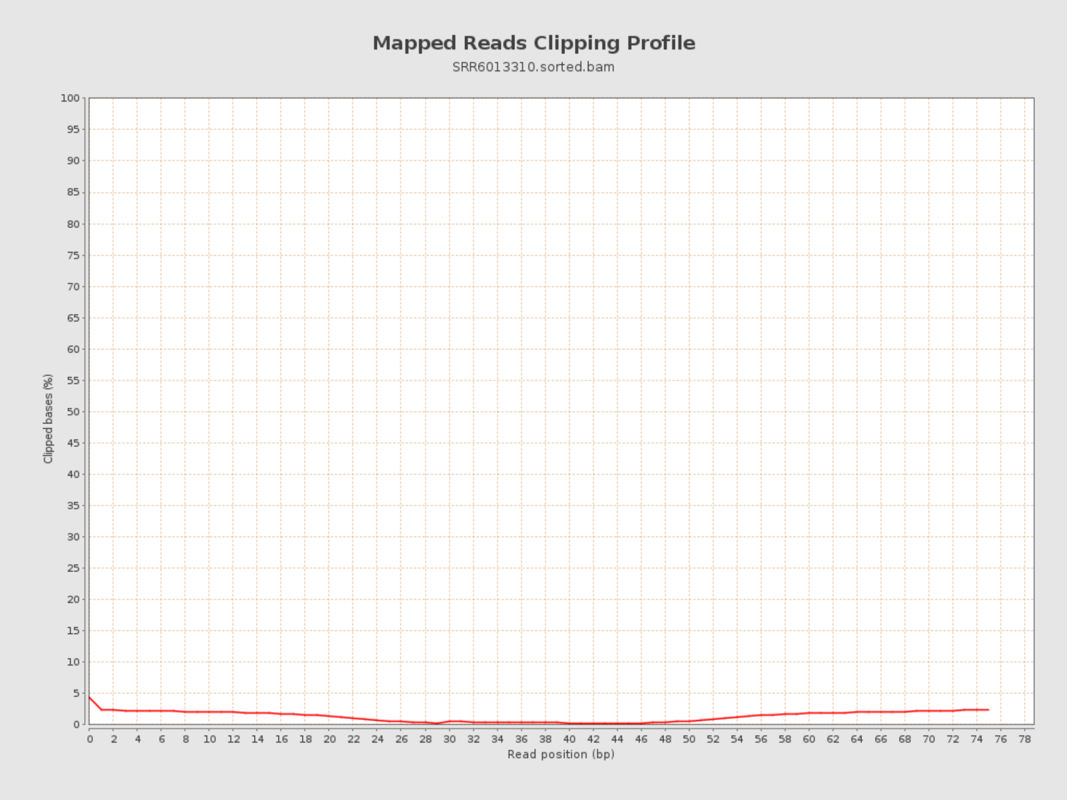
8. Results : Mapped Reads Nucleotide Content



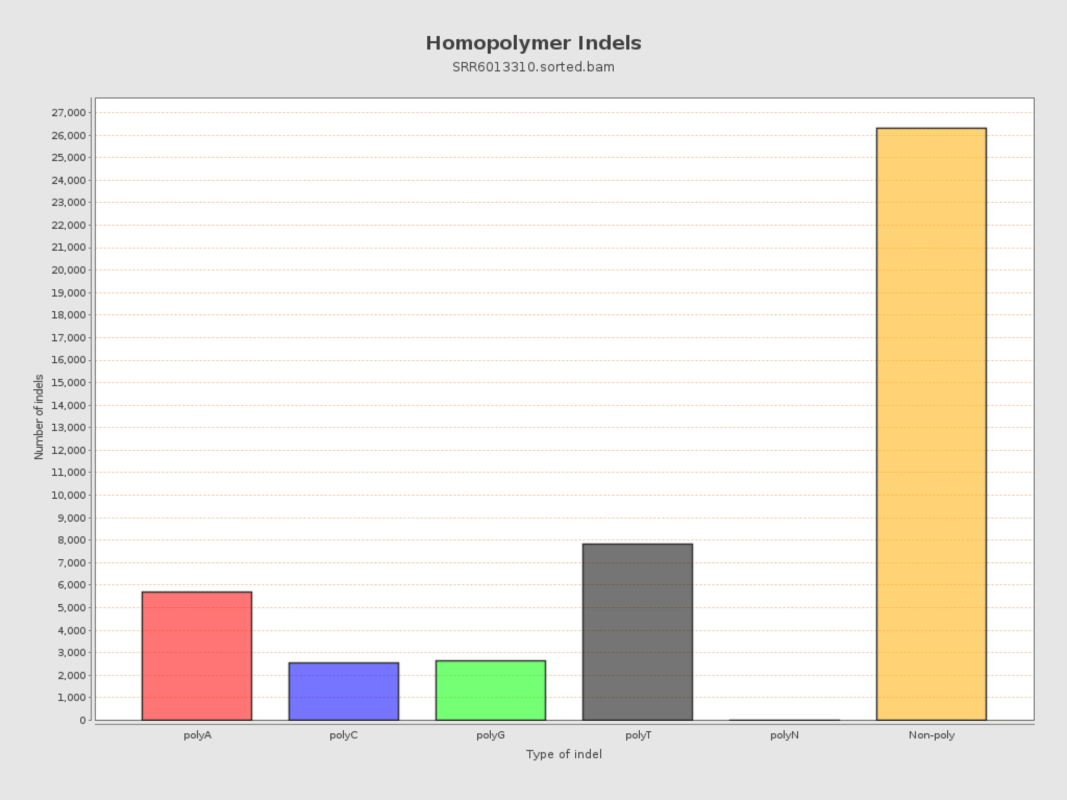
9. Results : Mapped Reads GC-content Distribution



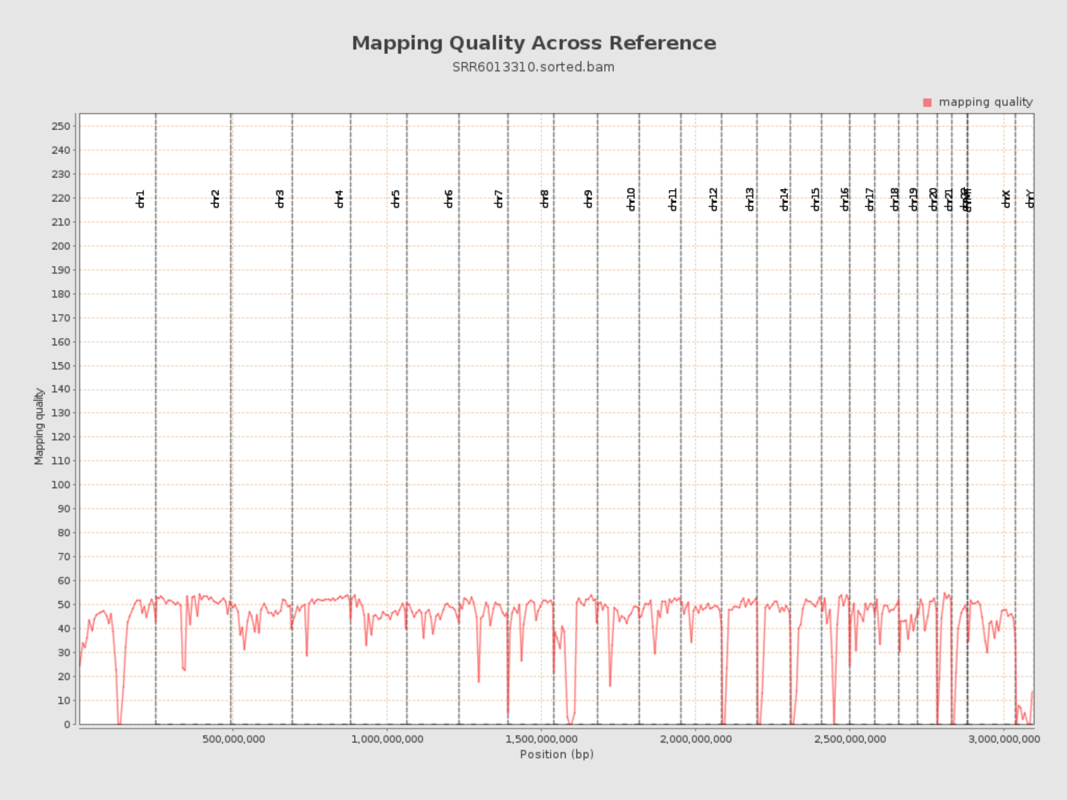
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram