Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/09/14 20:30:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013302.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_SRR6013302 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013302.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:30:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013302.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,853,089
Mapped reads	1,679,070 / 90.61%
Unmapped reads	174,019 / 9.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,297 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	108,705 / 5.87%
Duplication rate	5.31%
Clipped reads	812,759 / 43.86%

2.2. ACGT Content

Number/percentage of A's	30,598,934 / 27.7%
Number/percentage of C's	20,146,667 / 18.24%
Number/percentage of T's	35,394,242 / 32.04%
Number/percentage of G's	24,303,596 / 22%
Number/percentage of N's	12,091 / 0.01%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.3349

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

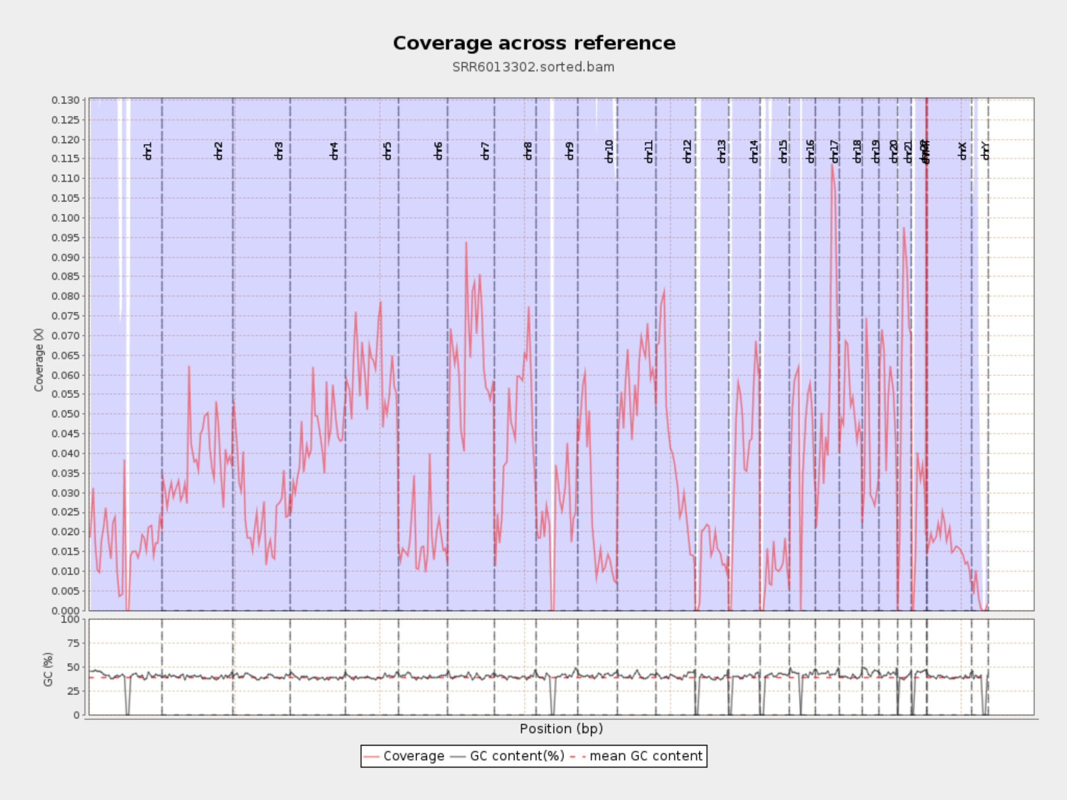
General error rate	0.8%
Mismatches	872,430
Insertions	8,151
Mapped reads with at least one insertion	0.48%
Deletions	39,607
Mapped reads with at least one deletion	2.33%
Homopolymer indels	45.18%

2.6. Chromosome stats

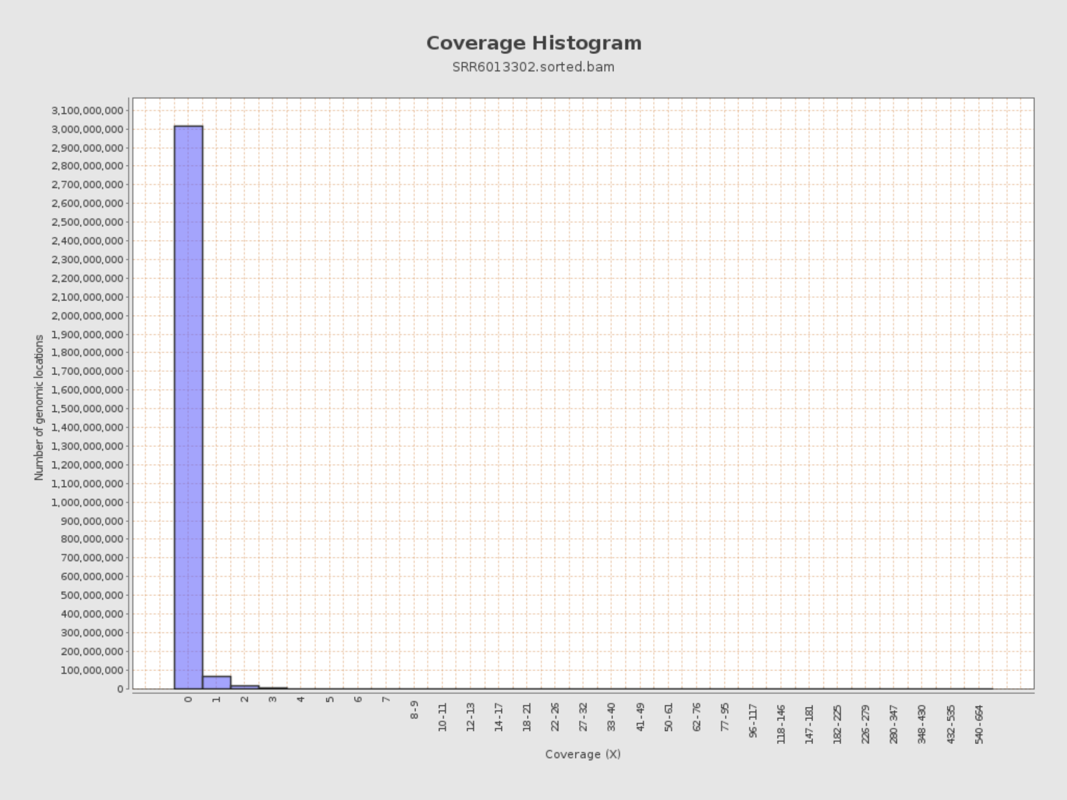
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4103216	0.0165	0.4187
chr2	243199373	9110441	0.0375	0.4457
chr3	198022430	5017135	0.0253	0.1994
chr4	191154276	8305840	0.0435	0.2703
chr5	180915260	10931007	0.0604	0.3147
chr6	171115067	3062456	0.0179	0.2252
chr7	159138663	10483501	0.0659	0.579

chr8	146364022	6691152	0.0457	0.4321
chr9	141213431	3349328	0.0237	0.2826
chr10	135534747	3416007	0.0252	0.2847
chr11	135006516	7795847	0.0577	0.3638
chr12	133851895	5372071	0.0401	0.2585
chr13	115169878	1569731	0.0136	0.1477
chr14	107349540	4541505	0.0423	0.2694
chr15	102531392	991169	0.0097	0.1225
chr16	90354753	4170252	0.0462	0.2787
chr17	81195210	4721468	0.0581	0.3271
chr18	78077248	4064454	0.0521	0.4743
chr19	59128983	2312067	0.0391	0.45
chr20	63025520	3480668	0.0552	0.3015
chr21	48129895	2983380	0.062	0.3263
chr22	51304566	1227352	0.0239	0.1918
chrMT	16571	6137	0.3703	0.7368
chrX	155270560	2629951	0.0169	0.1923
chrY	59373566	187711	0.0032	0.0962

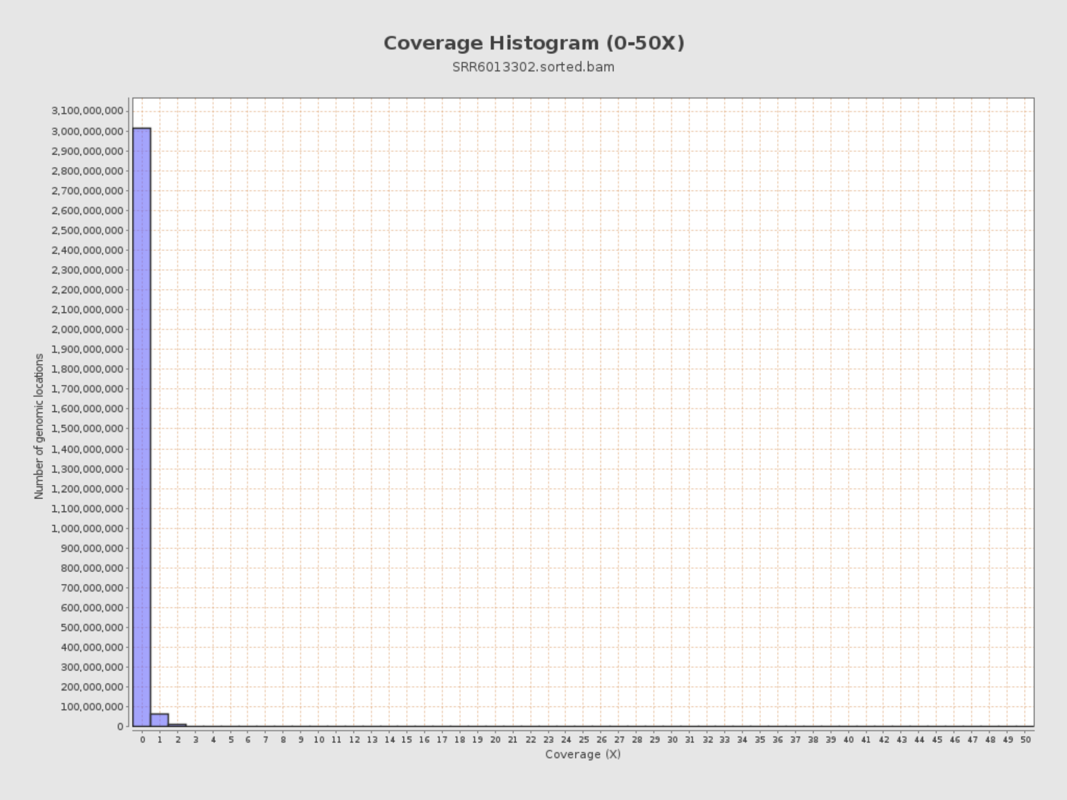
3. Results : Coverage across reference



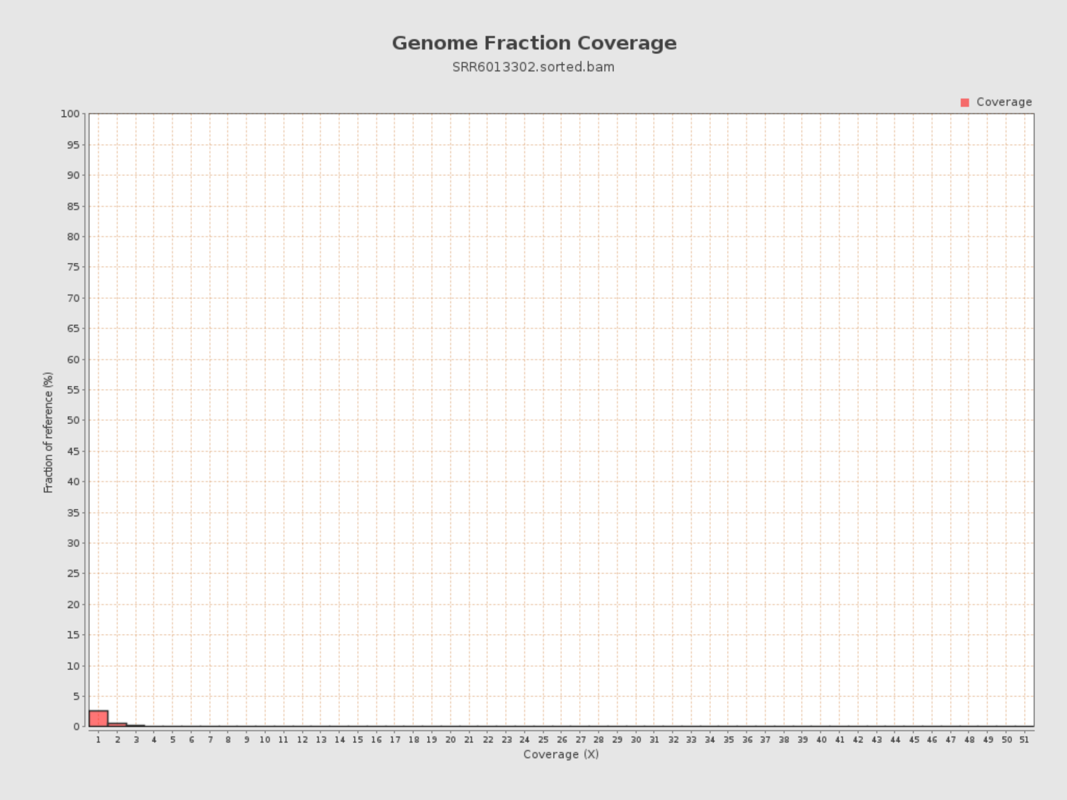
4. Results : Coverage Histogram



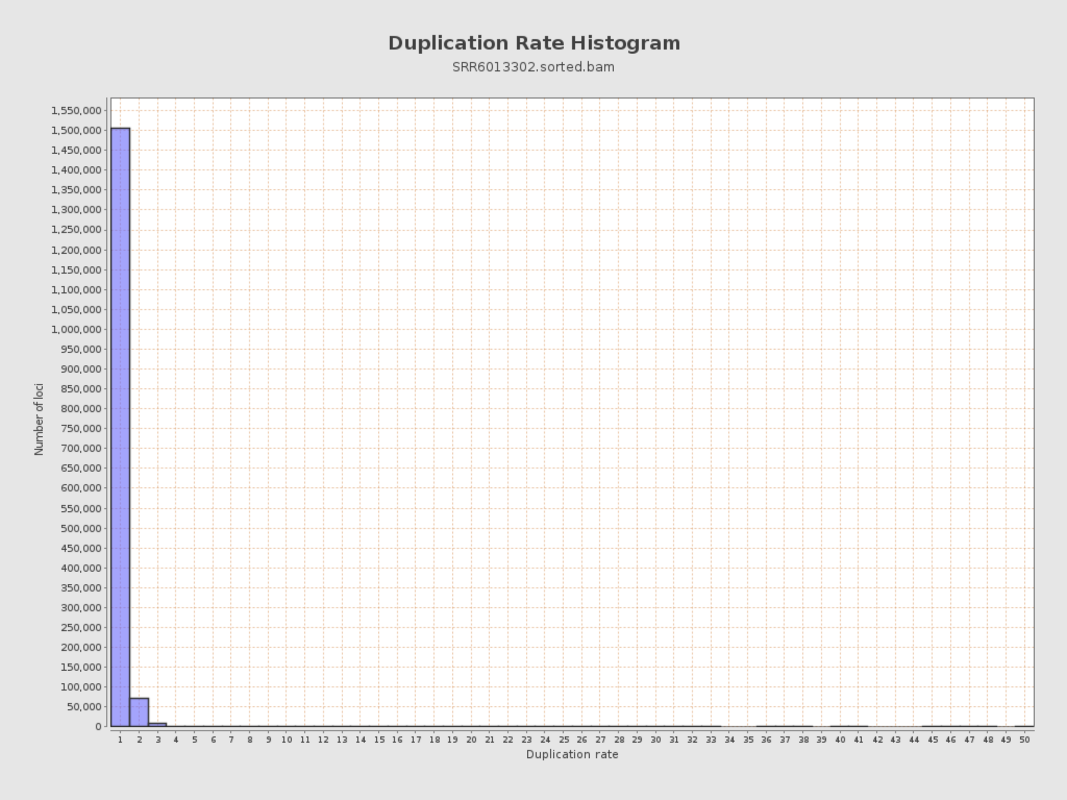
5. Results : Coverage Histogram (0-50X)



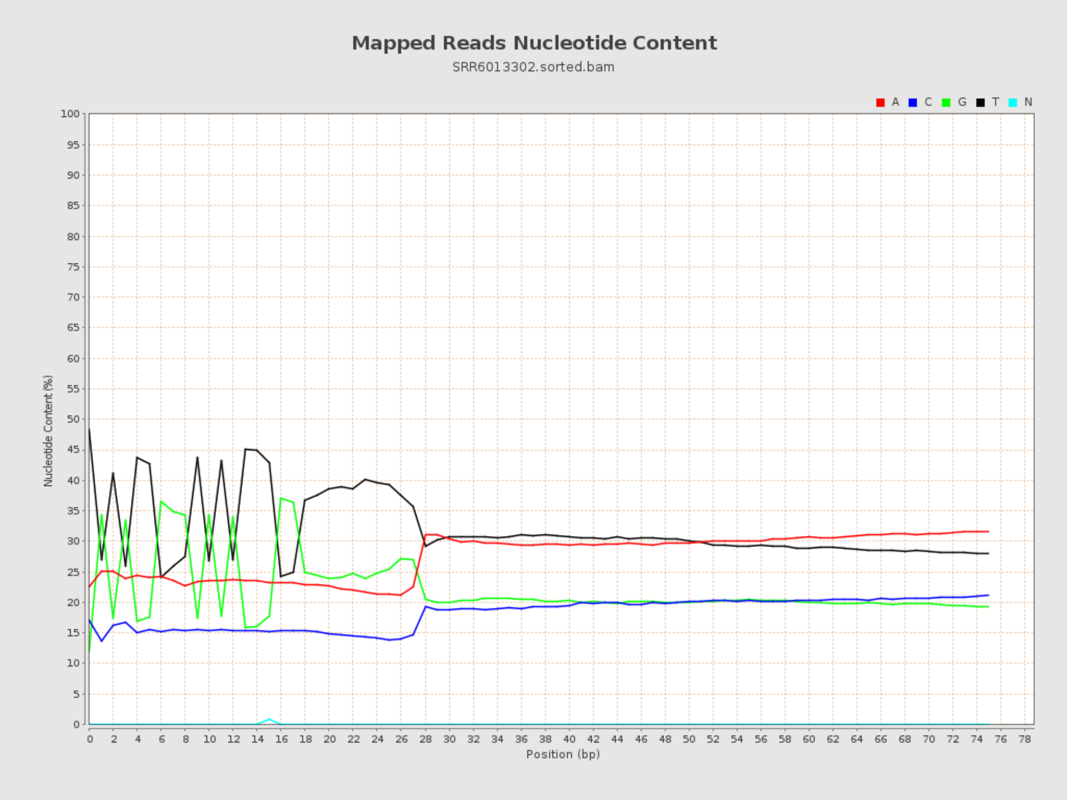
6. Results : Genome Fraction Coverage



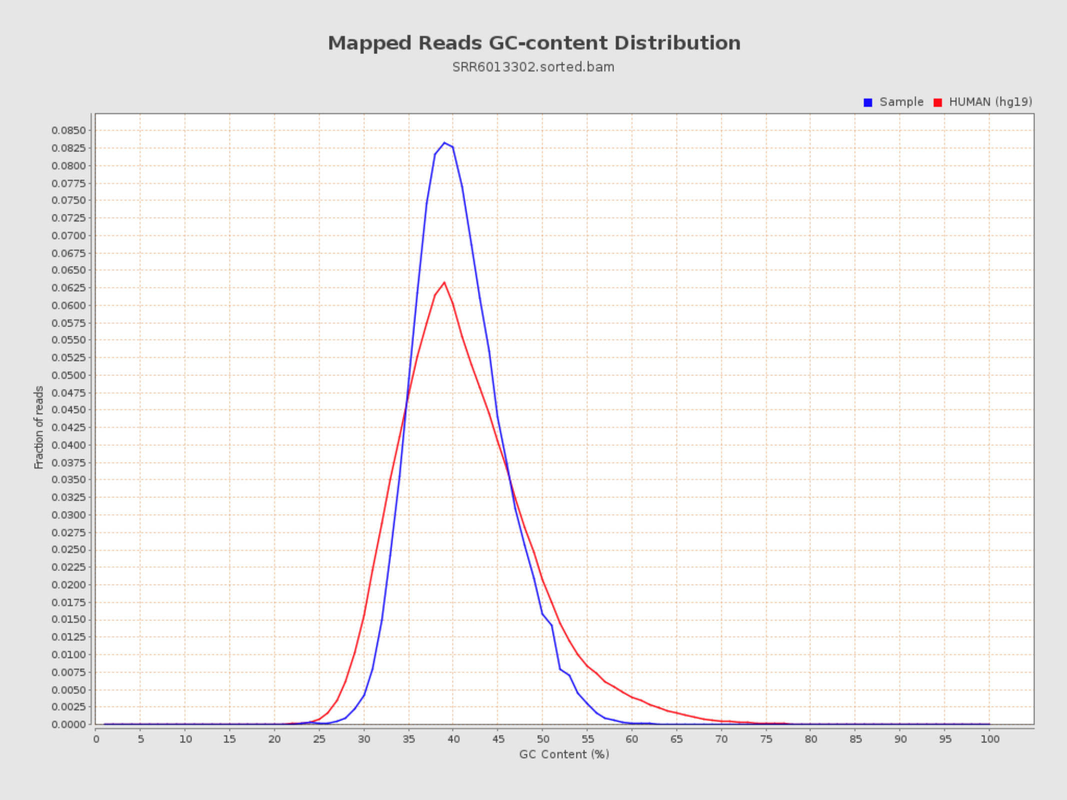
7. Results : Duplication Rate Histogram



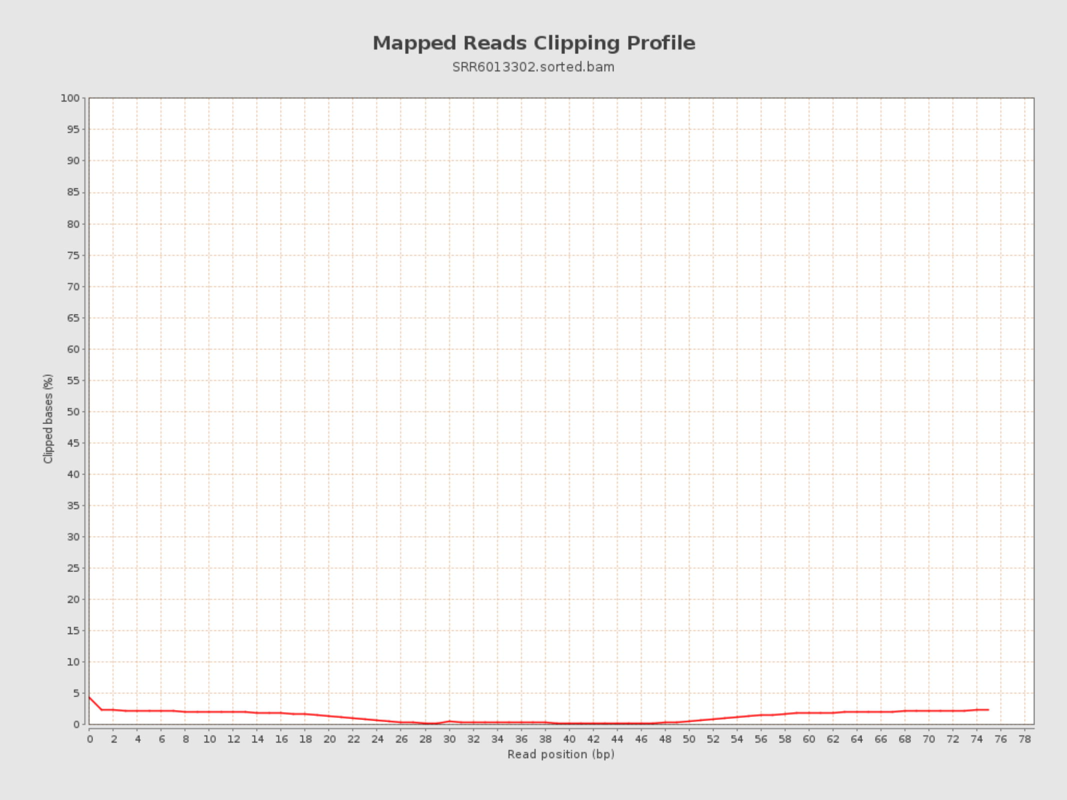
8. Results : Mapped Reads Nucleotide Content



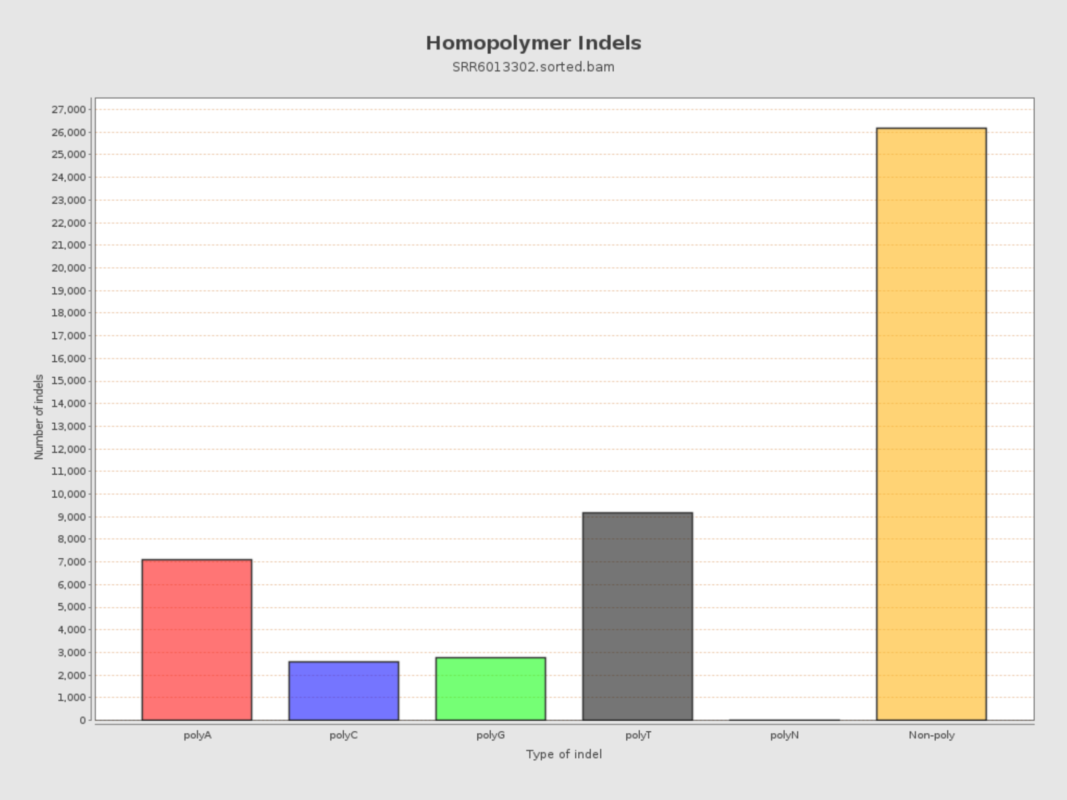
9. Results : Mapped Reads GC-content Distribution



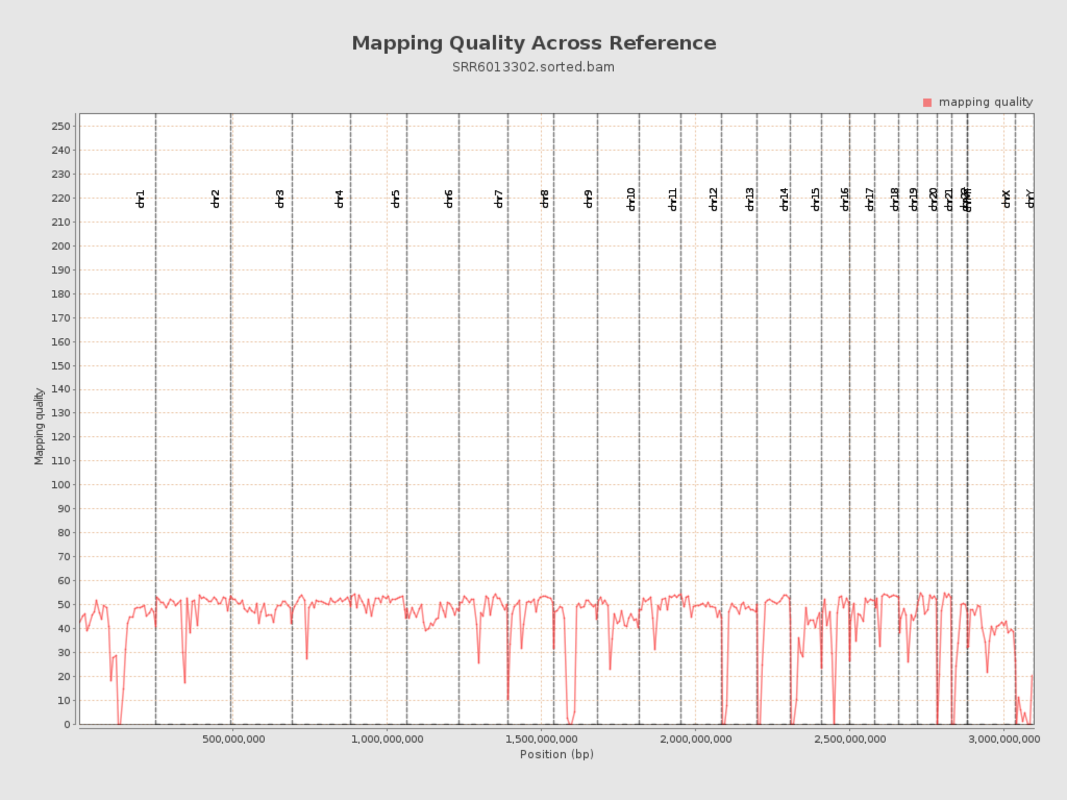
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram