Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:45:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013244.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_SRR6013244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013244.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:45:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,929,378
Mapped reads	1,662,593 / 86.17%
Unmapped reads	266,785 / 13.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,223 / 1.15%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	138,584 / 7.18%
Duplication rate	6.8%
Clipped reads	898,734 / 46.58%

2.2. ACGT Content

Number/percentage of A's	30,480,655 / 28.39%
Number/percentage of C's	18,756,684 / 17.47%
Number/percentage of T's	35,287,060 / 32.87%
Number/percentage of G's	22,806,368 / 21.24%
Number/percentage of N's	24,434 / 0.02%
GC Percentage	38.72%

2.3. Coverage

Mean	0.0347

Standard Deviation	0.408

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

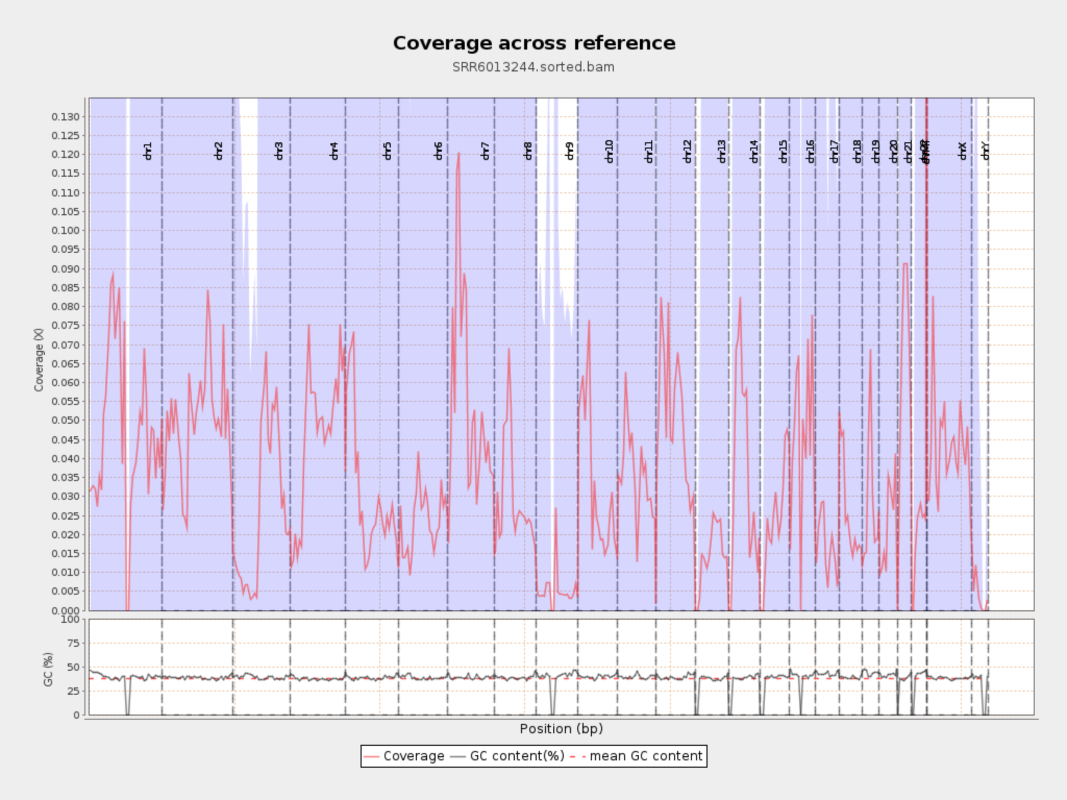
General error rate	0.95%
Mismatches	1,007,135
Insertions	7,542
Mapped reads with at least one insertion	0.45%
Deletions	50,078
Mapped reads with at least one deletion	2.96%
Homopolymer indels	42.75%

2.6. Chromosome stats

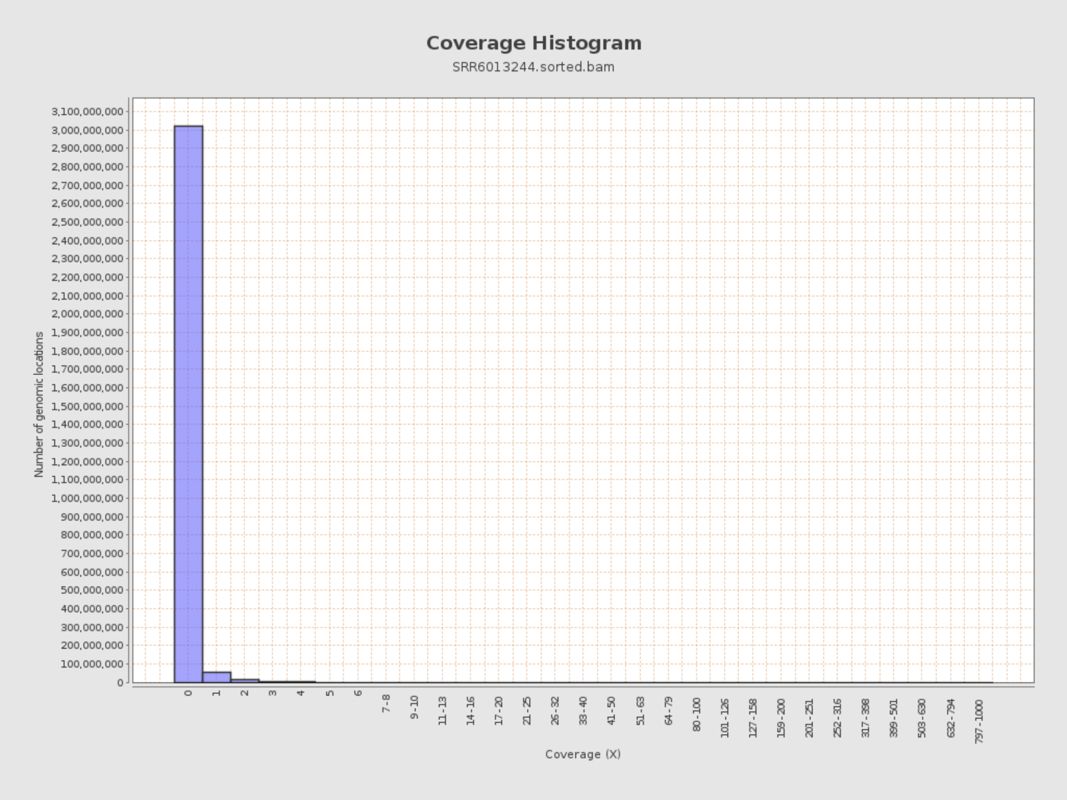
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11794815	0.0473	0.8801
chr2	243199373	12115397	0.0498	0.4149
chr3	198022430	5232761	0.0264	0.2187
chr4	191154276	8835945	0.0462	0.2925
chr5	180915260	5568544	0.0308	0.2408
chr6	171115067	4010459	0.0234	0.2427
chr7	159138663	8932116	0.0561	0.6218

chr8	146364022	4341682	0.0297	0.5137
chr9	141213431	760413	0.0054	0.1786
chr10	135534747	4715486	0.0348	0.3605
chr11	135006516	4792066	0.0355	0.2973
chr12	133851895	6777669	0.0506	0.3063
chr13	115169878	1679572	0.0146	0.1611
chr14	107349540	3892547	0.0363	0.2624
chr15	102531392	2436505	0.0238	0.2047
chr16	90354753	4184018	0.0463	0.3105
chr17	81195210	1298844	0.016	0.1929
chr18	78077248	2003855	0.0257	0.4268
chr19	59128983	1731351	0.0293	0.6042
chr20	63025520	1442522	0.0229	0.2083
chr21	48129895	3046772	0.0633	0.3455
chr22	51304566	964742	0.0188	0.1783
chrMT	16571	10199	0.6155	1.0709
chrX	155270560	6624951	0.0427	0.2966
chrY	59373566	249505	0.0042	0.09

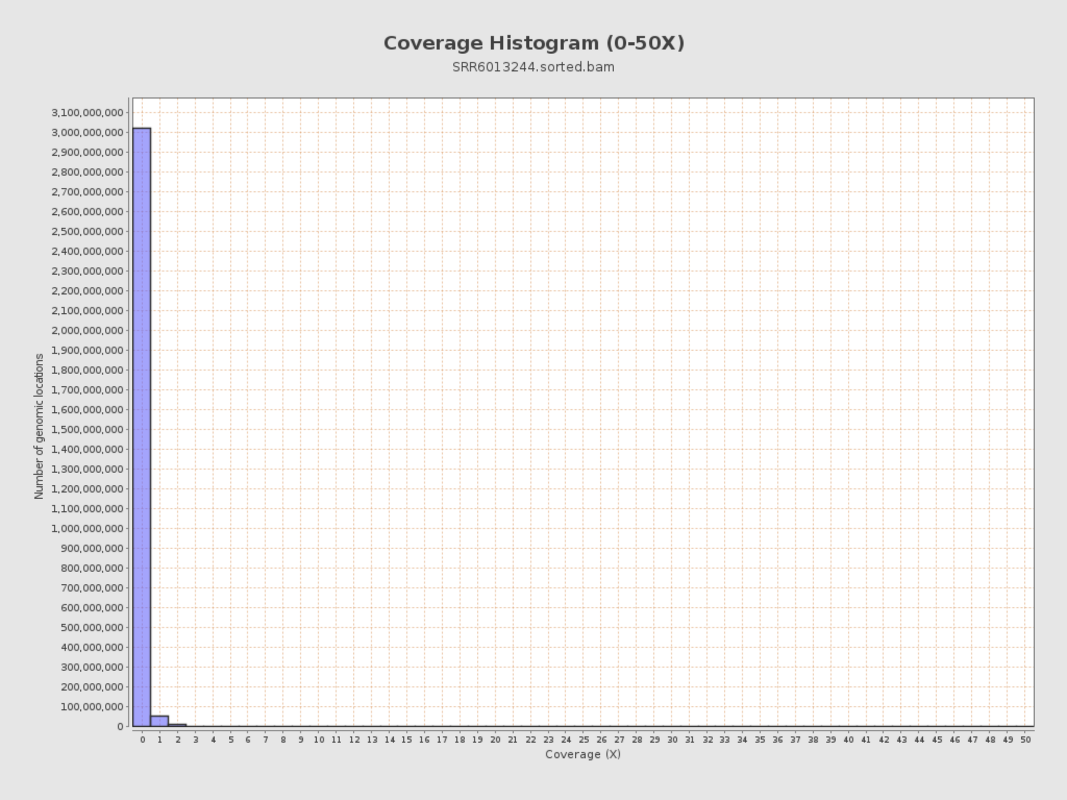
3. Results : Coverage across reference



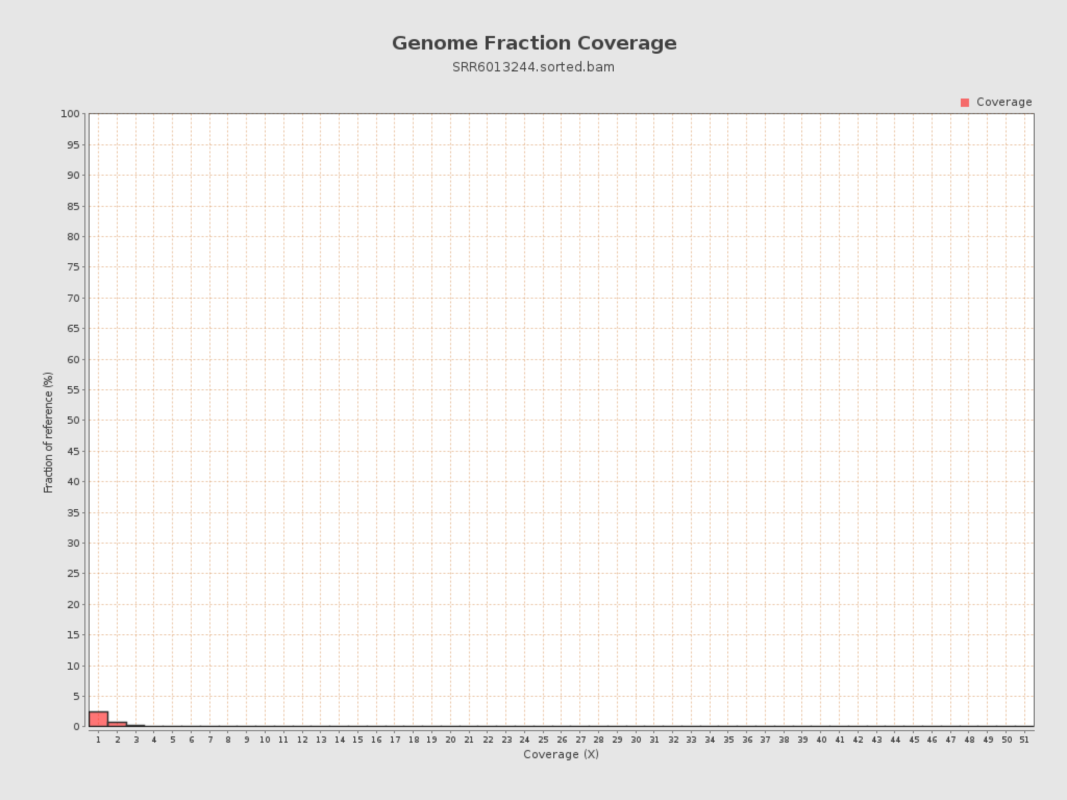
4. Results : Coverage Histogram



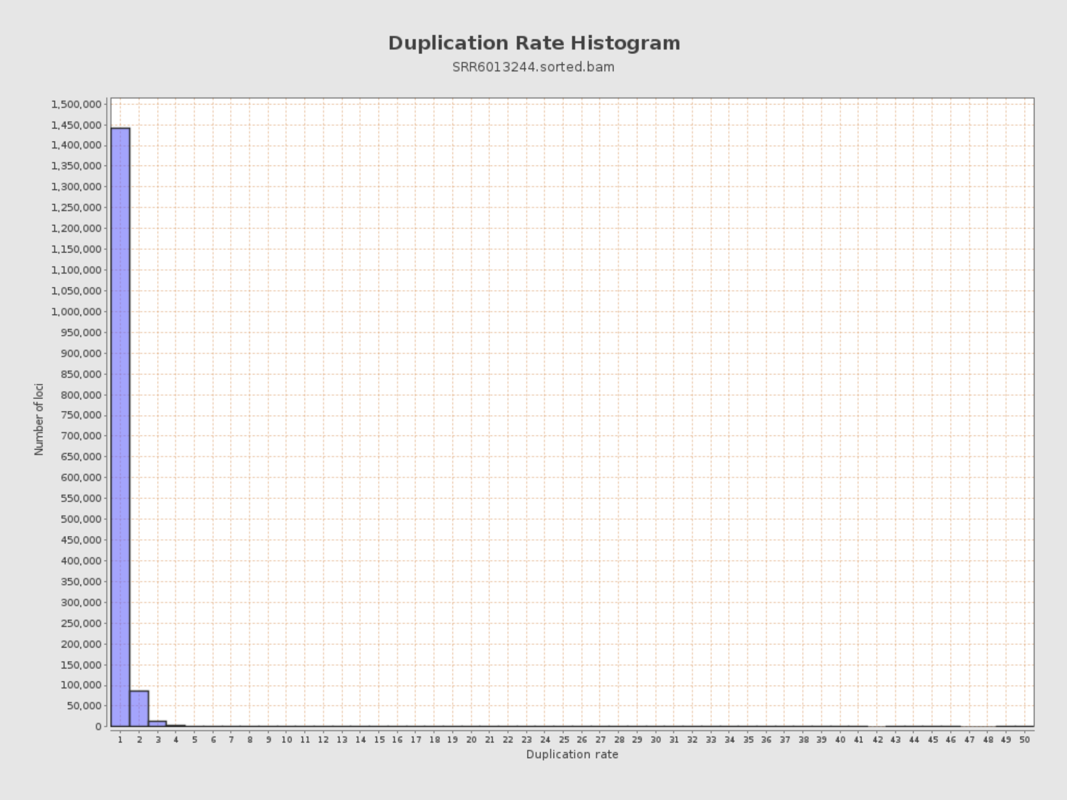
5. Results : Coverage Histogram (0-50X)



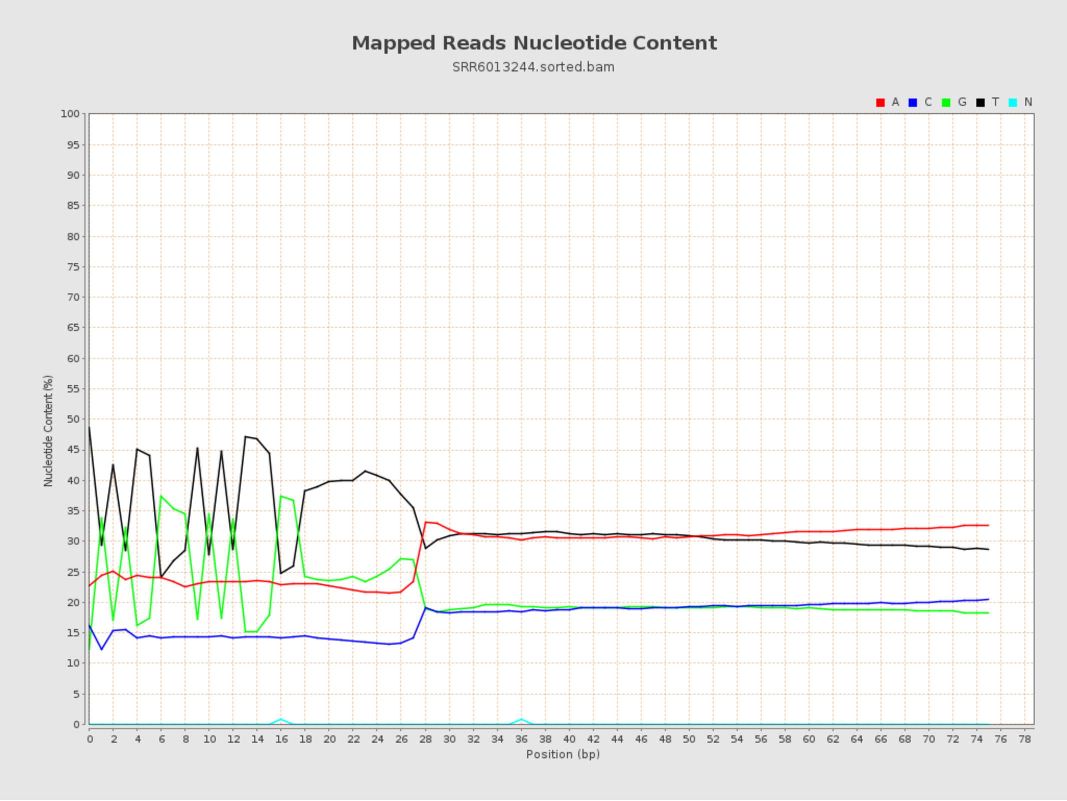
6. Results : Genome Fraction Coverage



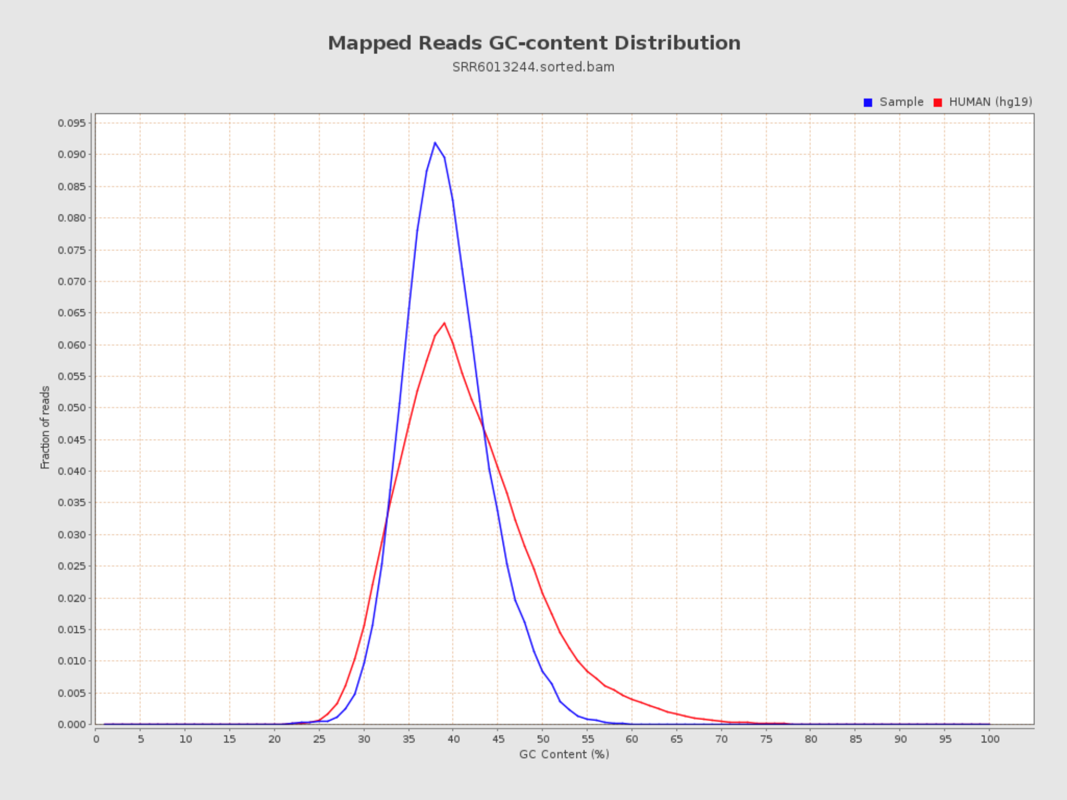
7. Results : Duplication Rate Histogram



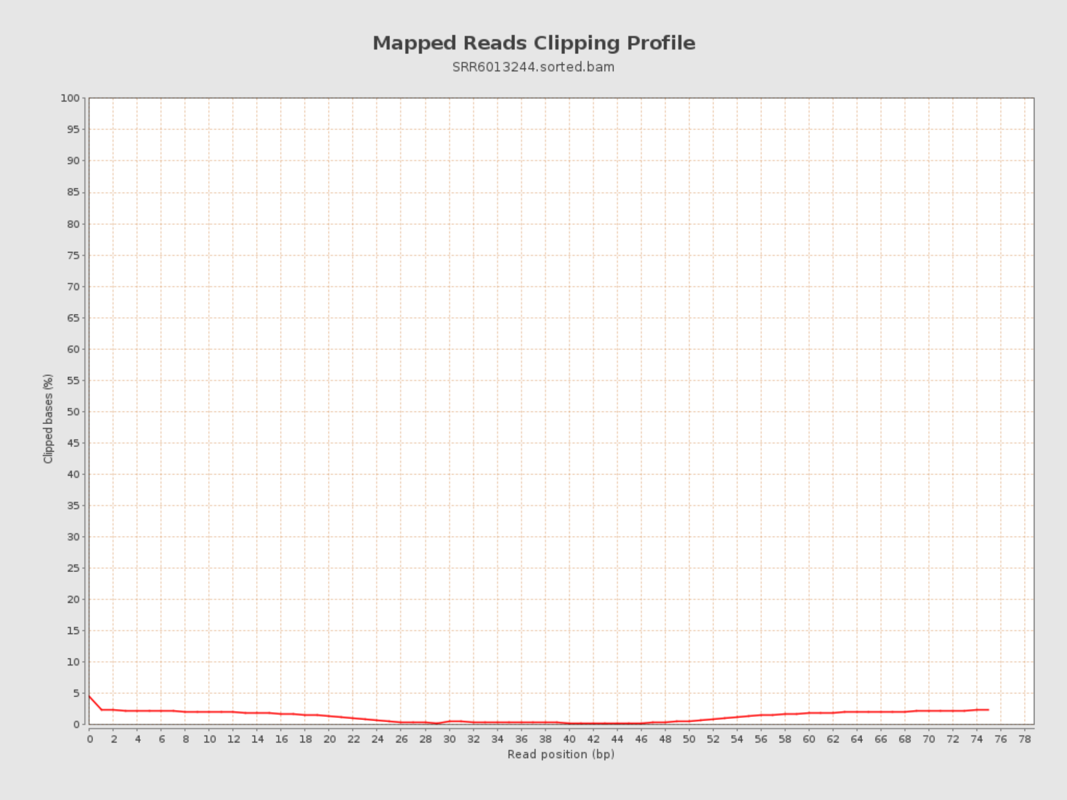
8. Results : Mapped Reads Nucleotide Content



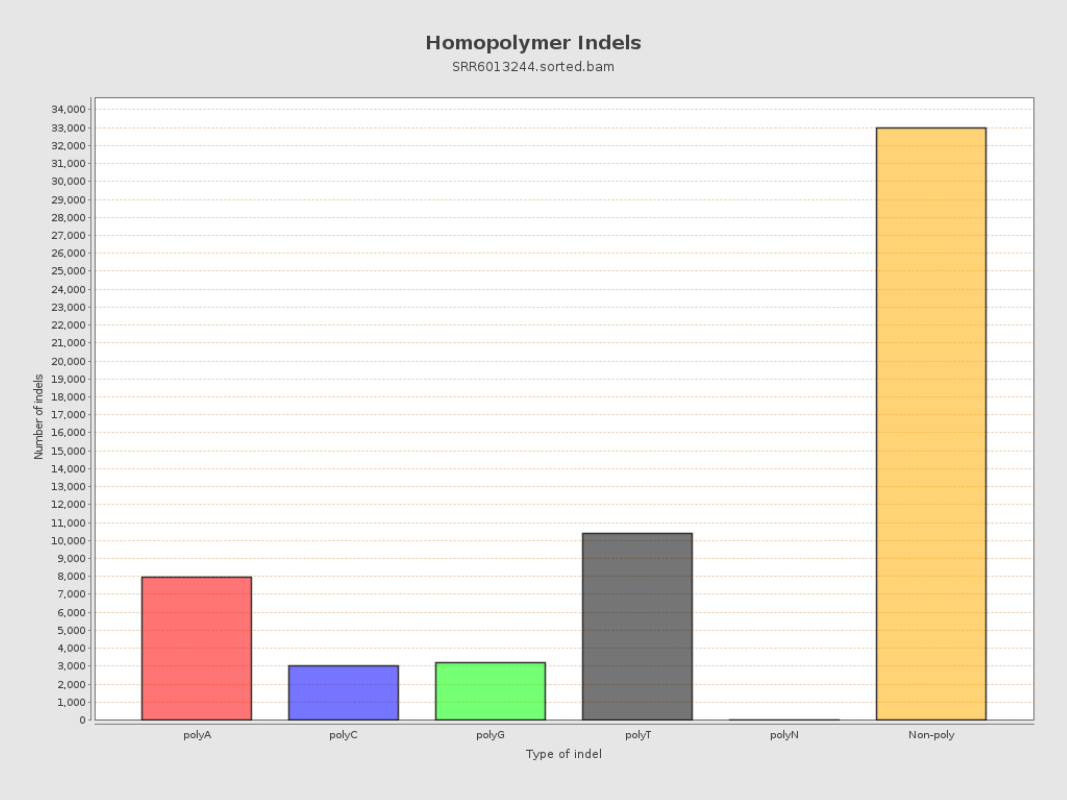
9. Results : Mapped Reads GC-content Distribution



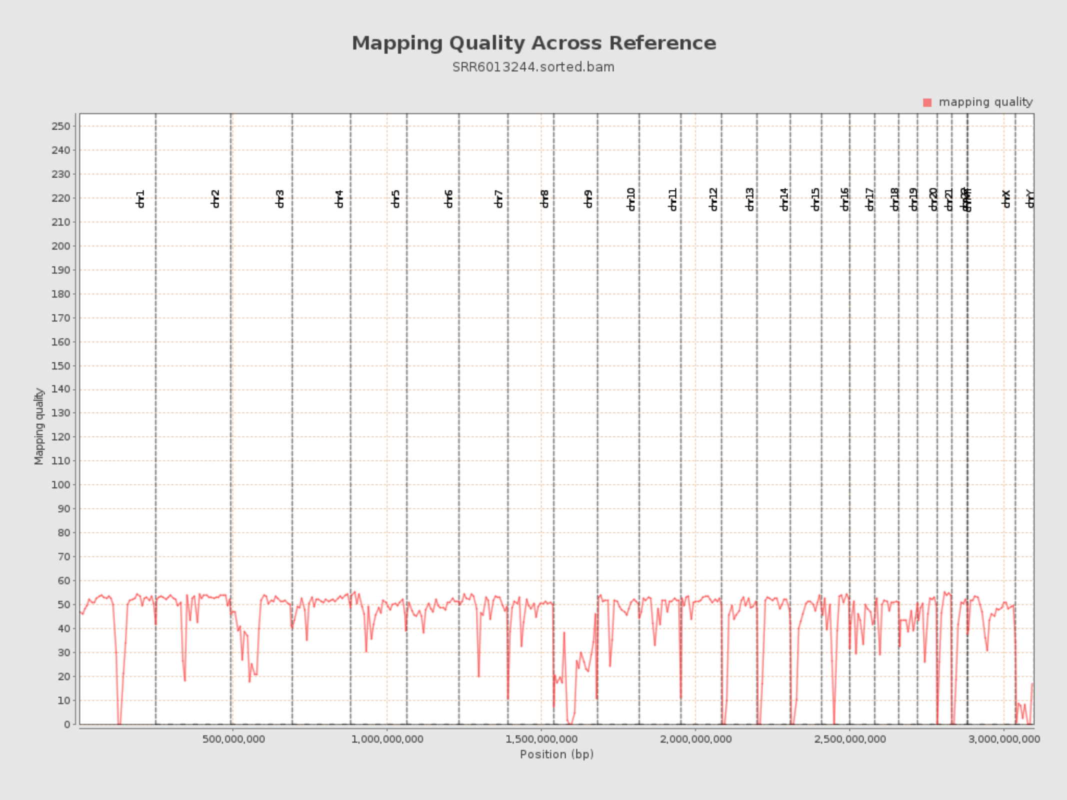
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram