Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:09:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230373.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_SRR6230373 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230373.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:09:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230373.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,908,656
Mapped reads	1,467,334 / 76.88%
Unmapped reads	441,322 / 23.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,055 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	297,607 / 15.59%
Duplication rate	13.04%
Clipped reads	710,909 / 37.25%

2.2. ACGT Content

Number/percentage of A's	27,210,868 / 28.22%
Number/percentage of C's	17,619,678 / 18.27%
Number/percentage of T's	30,836,151 / 31.98%
Number/percentage of G's	20,729,850 / 21.5%
Number/percentage of N's	40,654 / 0.04%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.4976

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

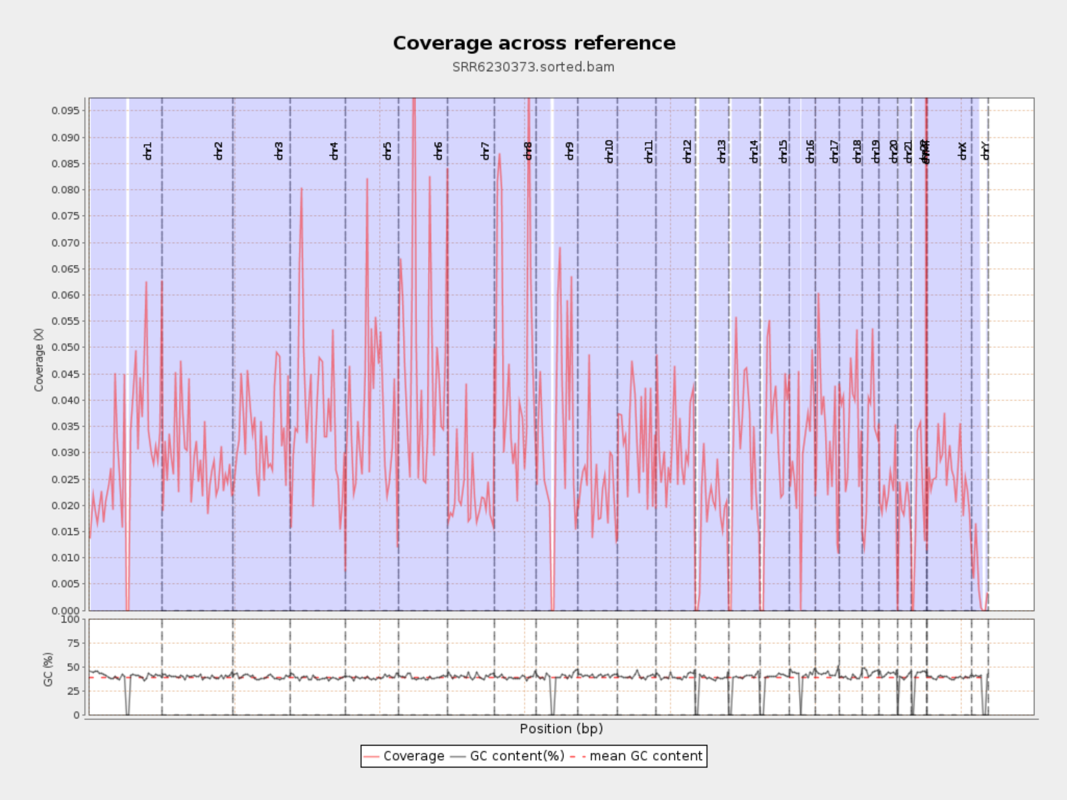
General error rate	0.87%
Mismatches	829,502
Insertions	7,718
Mapped reads with at least one insertion	0.52%
Deletions	25,848
Mapped reads with at least one deletion	1.74%
Homopolymer indels	46.8%

2.6. Chromosome stats

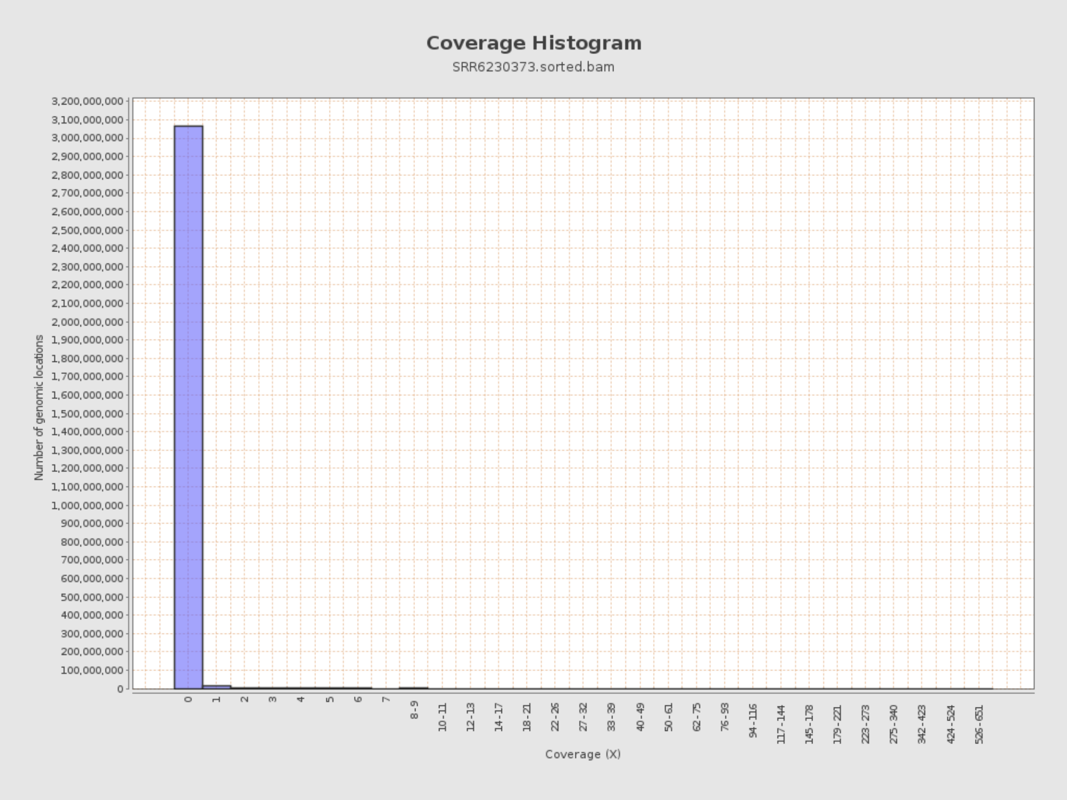
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7218184	0.029	0.6909
chr2	243199373	6974182	0.0287	0.5007
chr3	198022430	6689384	0.0338	0.4677
chr4	191154276	7108063	0.0372	0.4913
chr5	180915260	6737604	0.0372	0.4779
chr6	171115067	8274193	0.0484	0.5966
chr7	159138663	3507683	0.022	0.4169

chr8	146364022	6937029	0.0474	0.6416
chr9	141213431	4775584	0.0338	0.4925
chr10	135534747	3246915	0.024	0.42
chr11	135006516	4426822	0.0328	0.5085
chr12	133851895	4172233	0.0312	0.4355
chr13	115169878	2051940	0.0178	0.3456
chr14	107349540	3227297	0.0301	0.4625
chr15	102531392	3298895	0.0322	0.508
chr16	90354753	2770837	0.0307	0.4209
chr17	81195210	2598352	0.032	0.425
chr18	78077248	2907705	0.0372	0.6263
chr19	59128983	1907534	0.0323	0.4987
chr20	63025520	1456753	0.0231	0.3858
chr21	48129895	895317	0.0186	0.3363
chr22	51304566	982427	0.0191	0.3262
chrMT	16571	12329	0.744	1.6736
chrX	155270560	4027101	0.0259	0.4171
chrY	59373566	275359	0.0046	0.1646

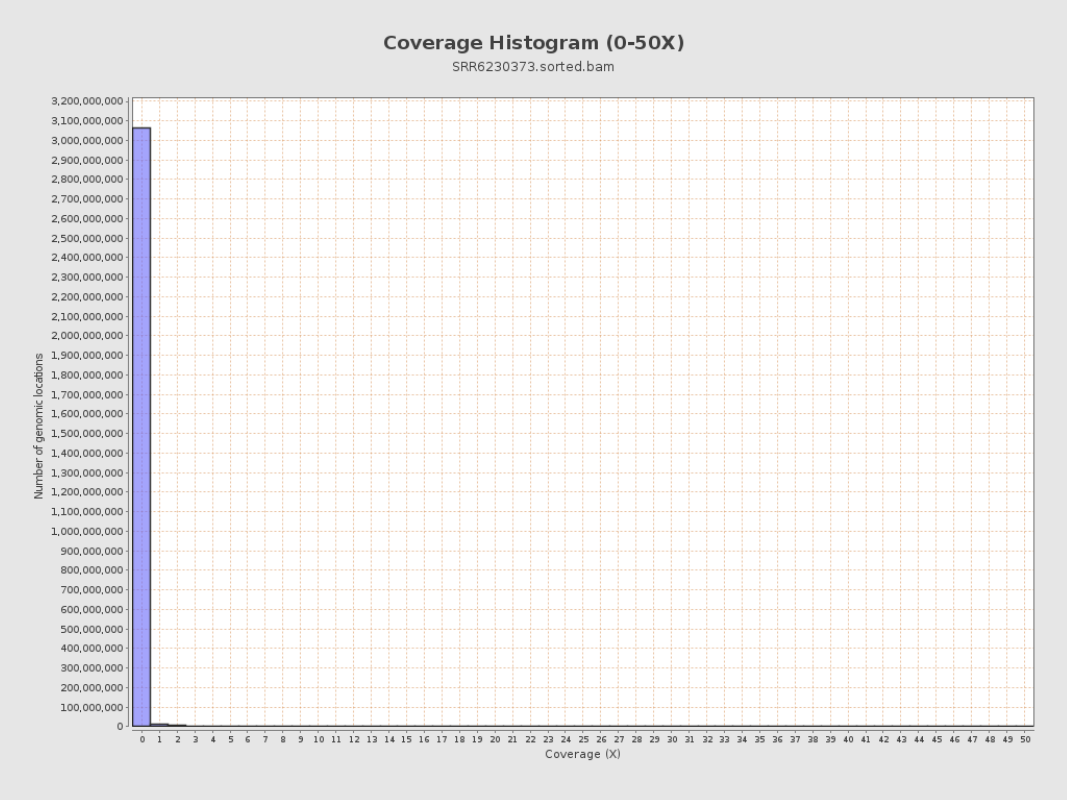
3. Results : Coverage across reference



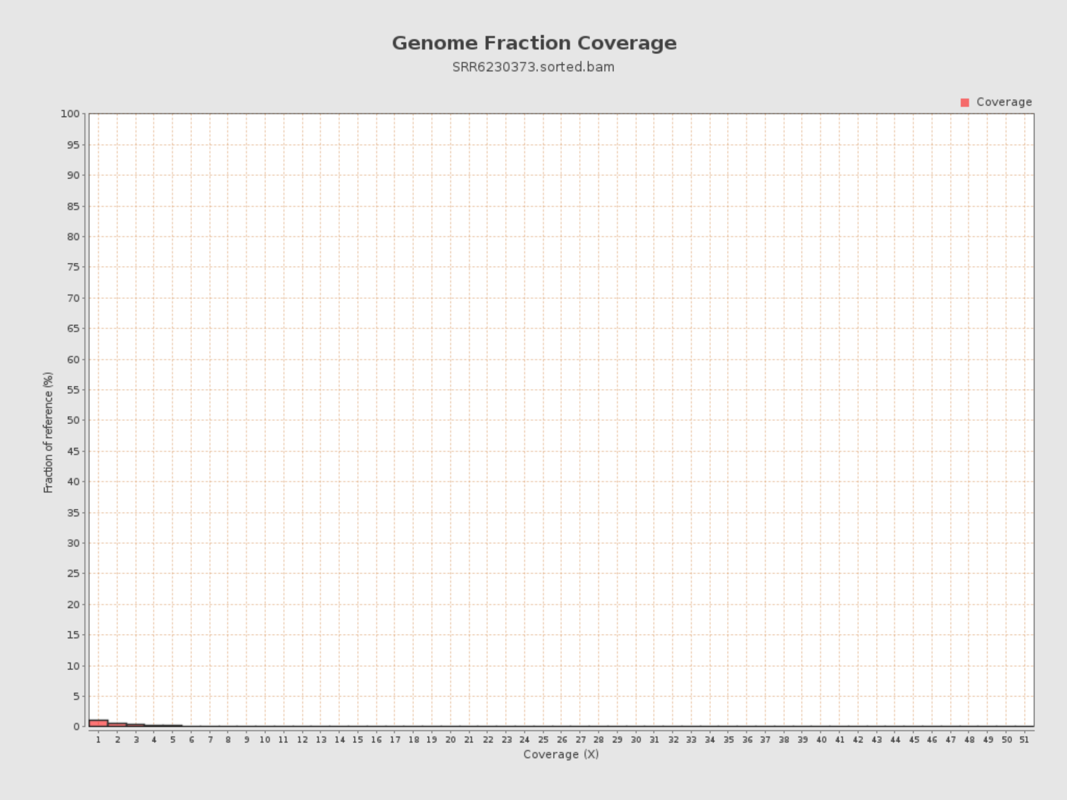
4. Results : Coverage Histogram



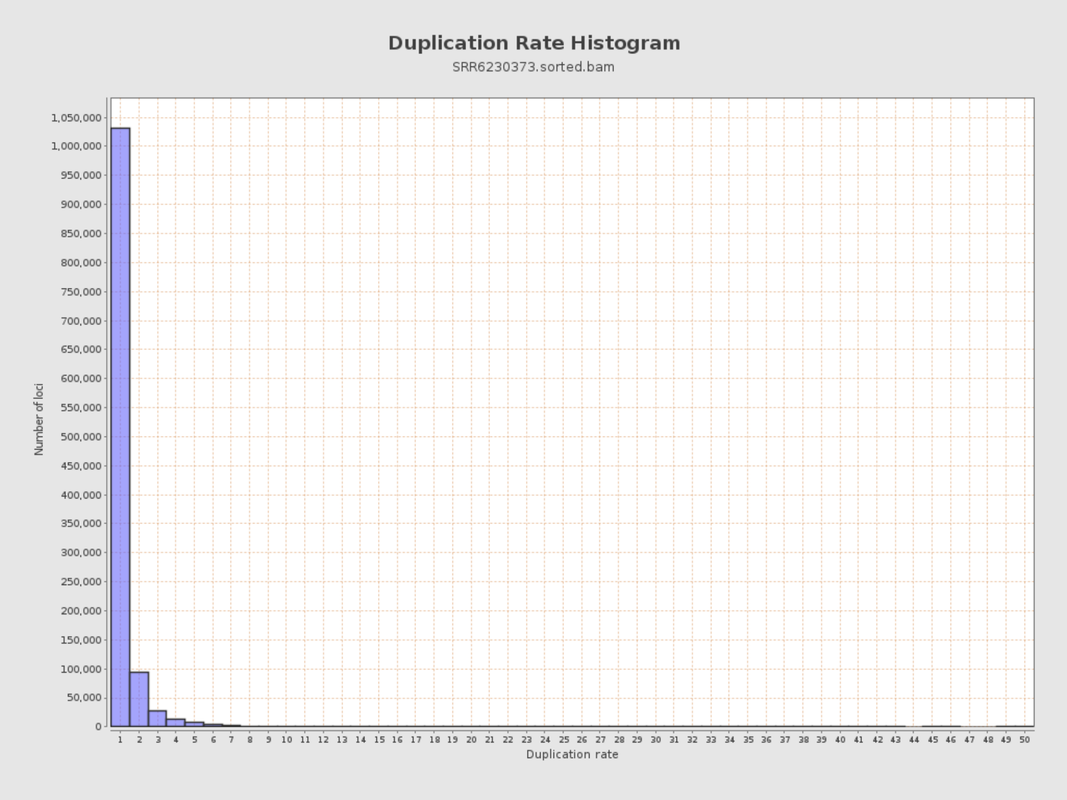
5. Results : Coverage Histogram (0-50X)



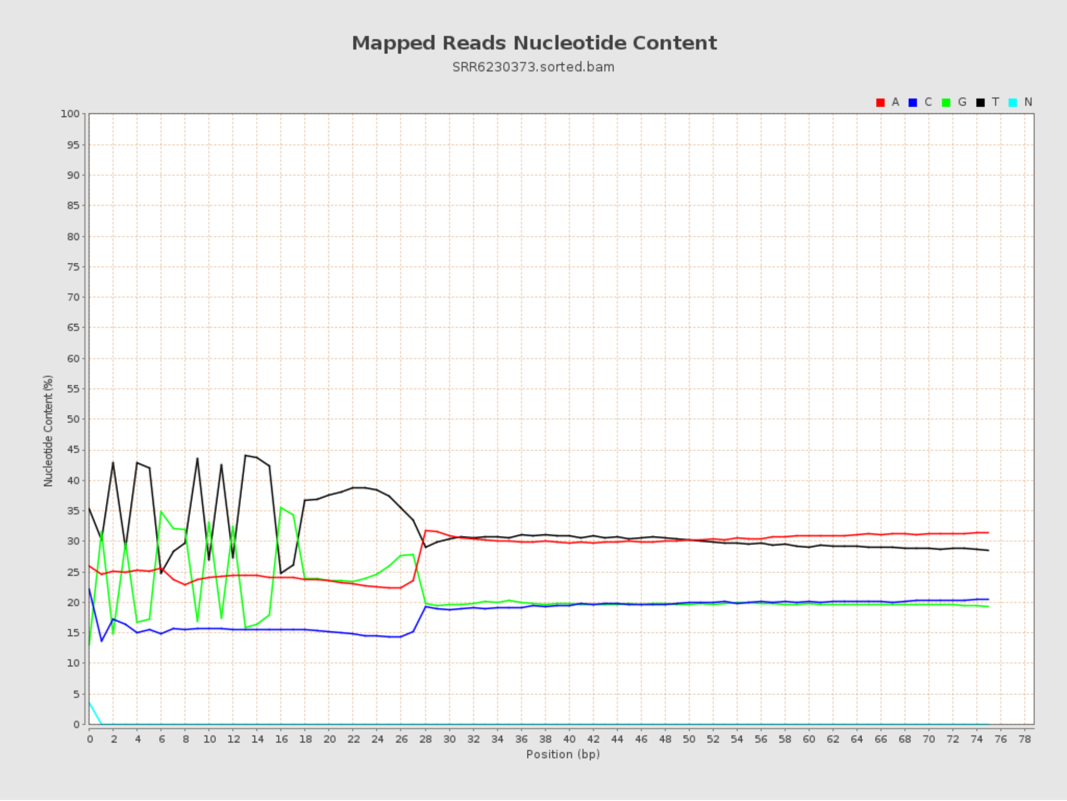
6. Results : Genome Fraction Coverage



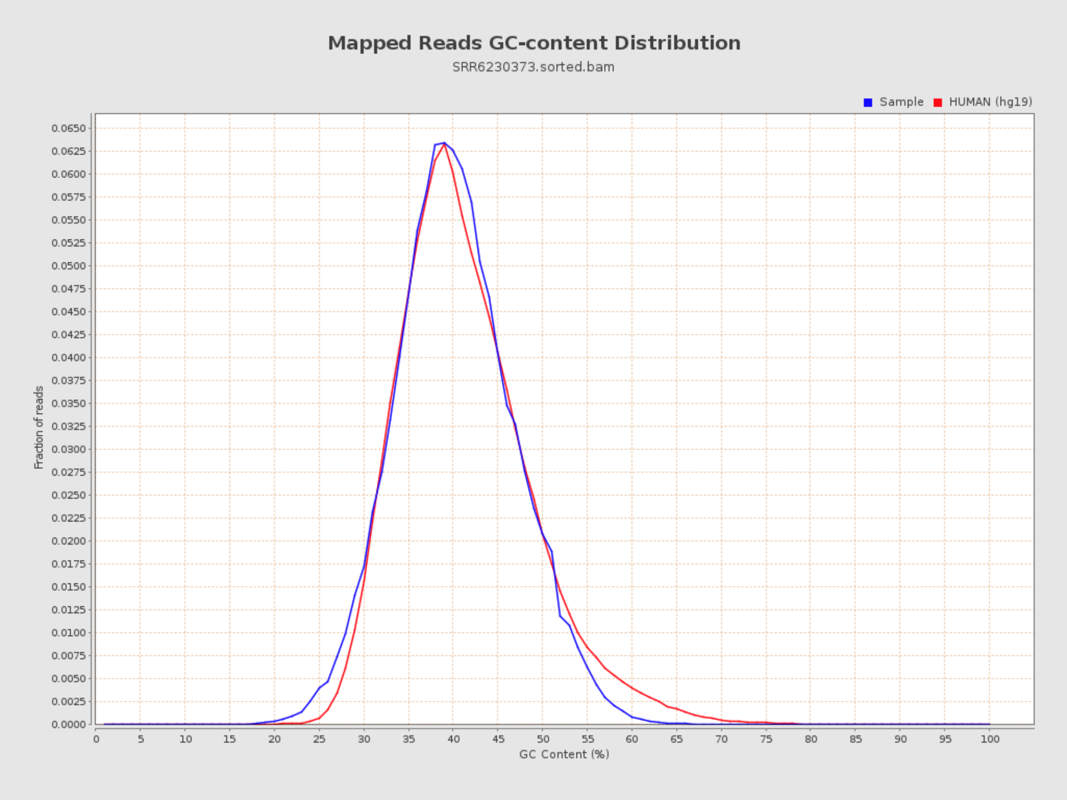
7. Results : Duplication Rate Histogram



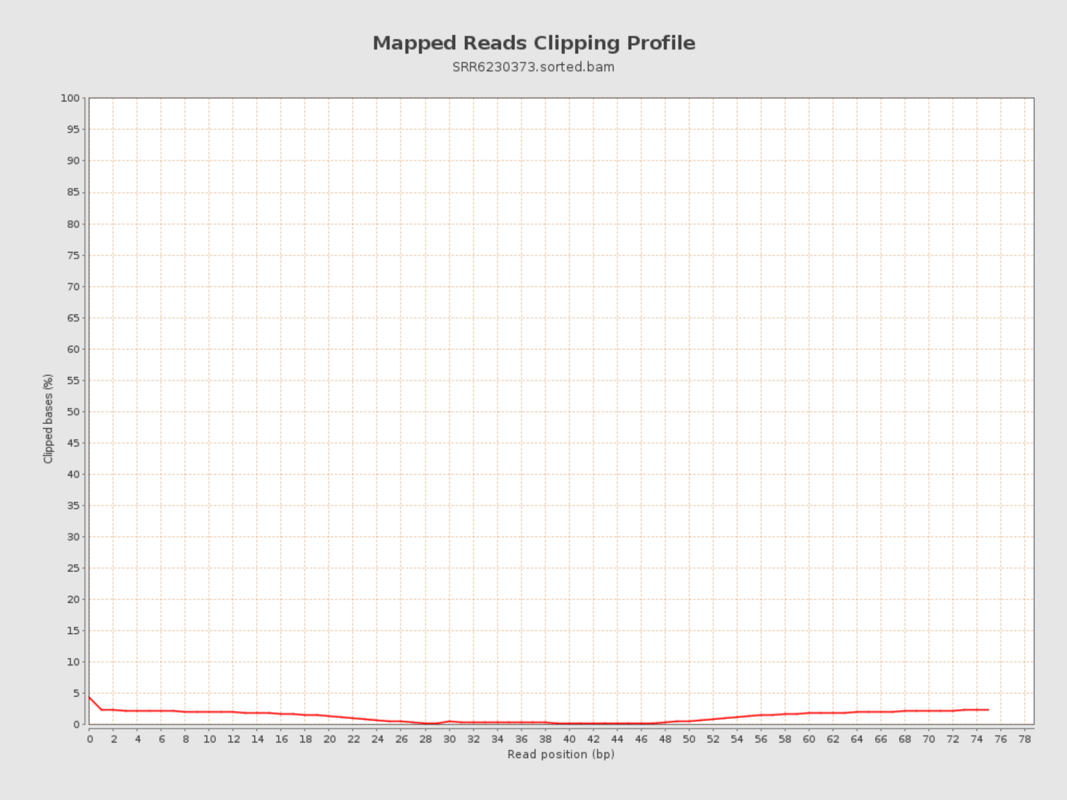
8. Results : Mapped Reads Nucleotide Content



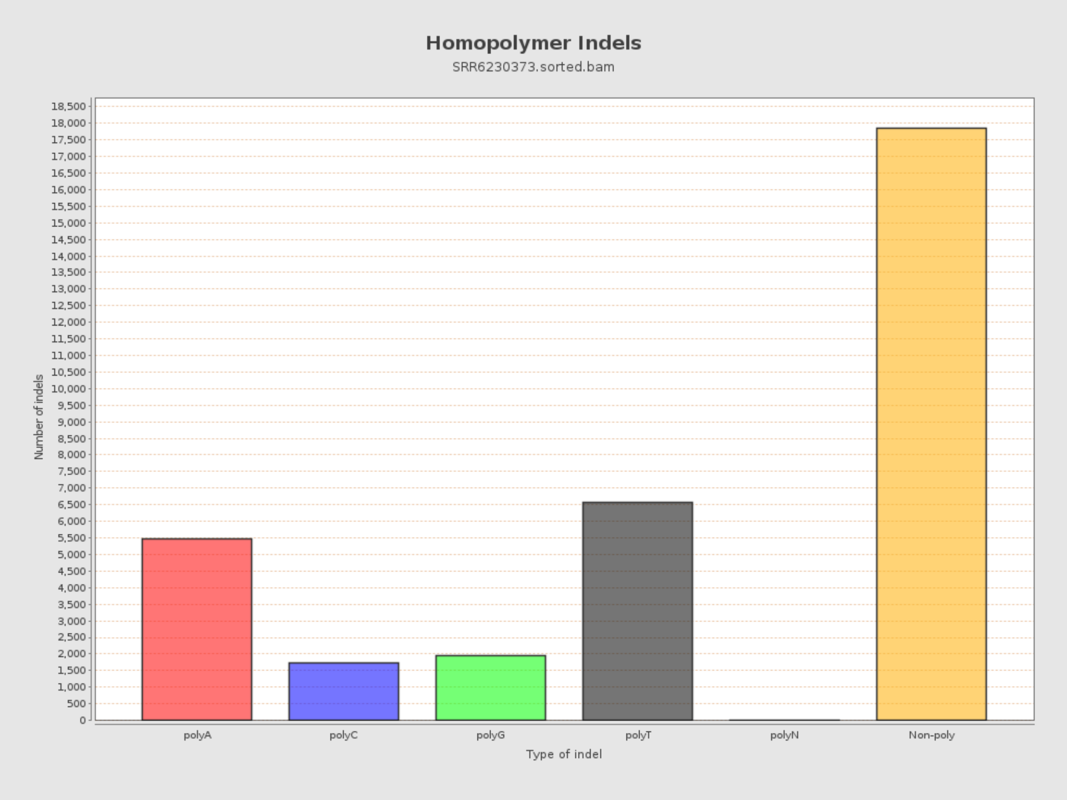
9. Results : Mapped Reads GC-content Distribution



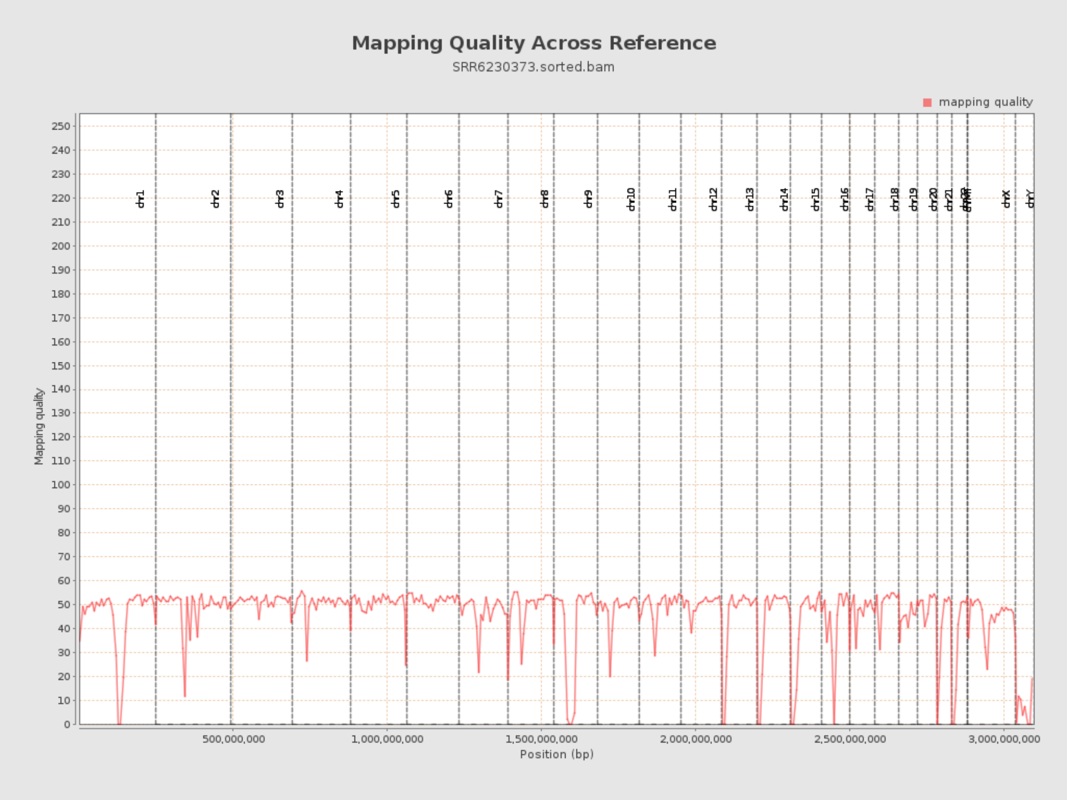
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram