Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:12:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230374.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_SRR6230374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230374.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:12:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,118,901
Mapped reads	1,880,987 / 88.77%
Unmapped reads	237,914 / 11.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,626 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	62,050 / 2.93%
Duplication rate	2.24%
Clipped reads	657,461 / 31.03%

2.2. ACGT Content

Number/percentage of A's	39,851,941 / 30.26%
Number/percentage of C's	25,946,518 / 19.7%
Number/percentage of T's	38,084,591 / 28.92%
Number/percentage of G's	27,726,953 / 21.06%
Number/percentage of N's	72,033 / 0.05%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.4434

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

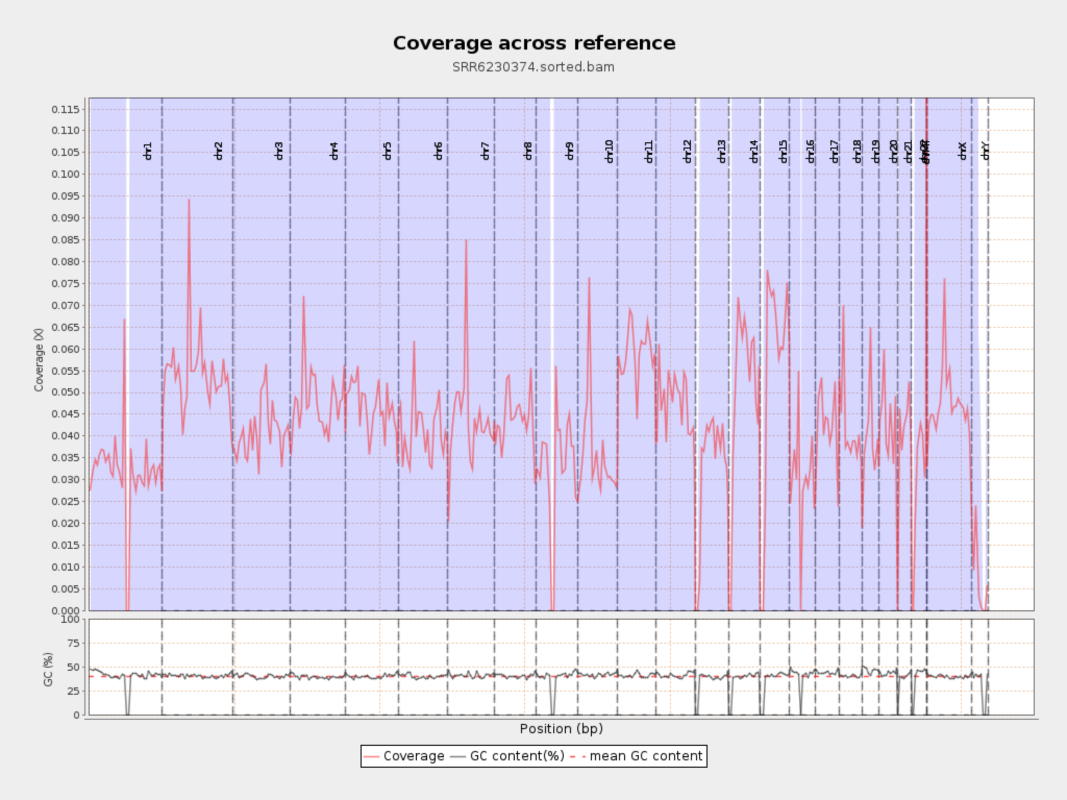
General error rate	1.1%
Mismatches	1,429,762
Insertions	12,645
Mapped reads with at least one insertion	0.67%
Deletions	52,357
Mapped reads with at least one deletion	2.74%
Homopolymer indels	45.61%

2.6. Chromosome stats

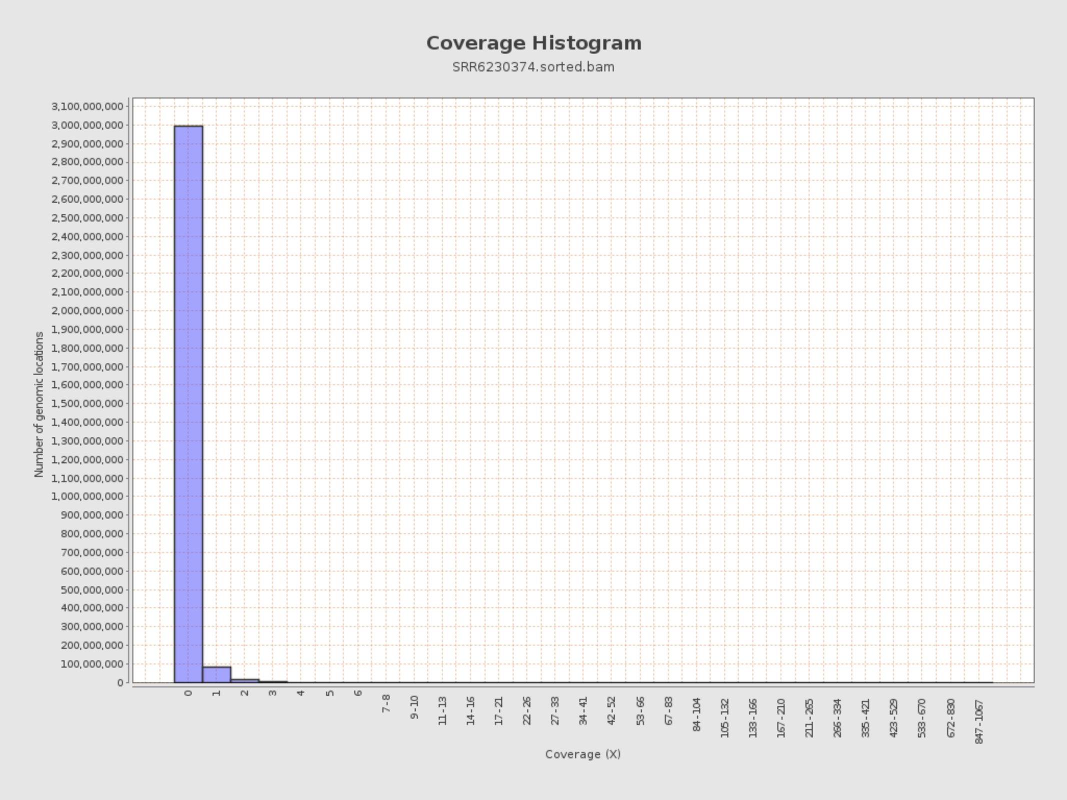
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7903275	0.0317	0.8138
chr2	243199373	13282744	0.0546	0.4752
chr3	198022430	8150135	0.0412	0.2495
chr4	191154276	9152346	0.0479	0.2995
chr5	180915260	8449665	0.0467	0.2694
chr6	171115067	7079354	0.0414	0.2908
chr7	159138663	7023050	0.0441	0.6073

chr8	146364022	6426109	0.0439	0.4387
chr9	141213431	4653214	0.033	0.3943
chr10	135534747	4854139	0.0358	0.3971
chr11	135006516	7919720	0.0587	0.5582
chr12	133851895	6399062	0.0478	0.2739
chr13	115169878	3738728	0.0325	0.2199
chr14	107349540	5400270	0.0503	0.2938
chr15	102531392	5669580	0.0553	0.291
chr16	90354753	2723039	0.0301	0.2865
chr17	81195210	3403242	0.0419	0.3155
chr18	78077248	3307331	0.0424	0.9337
chr19	59128983	2394905	0.0405	0.4946
chr20	63025520	2730077	0.0433	0.2677
chr21	48129895	1908720	0.0397	0.279
chr22	51304566	1410122	0.0275	0.2006
chrMT	16571	4297	0.2593	0.562
chrX	155270560	7375788	0.0475	0.3083
chrY	59373566	410848	0.0069	0.193

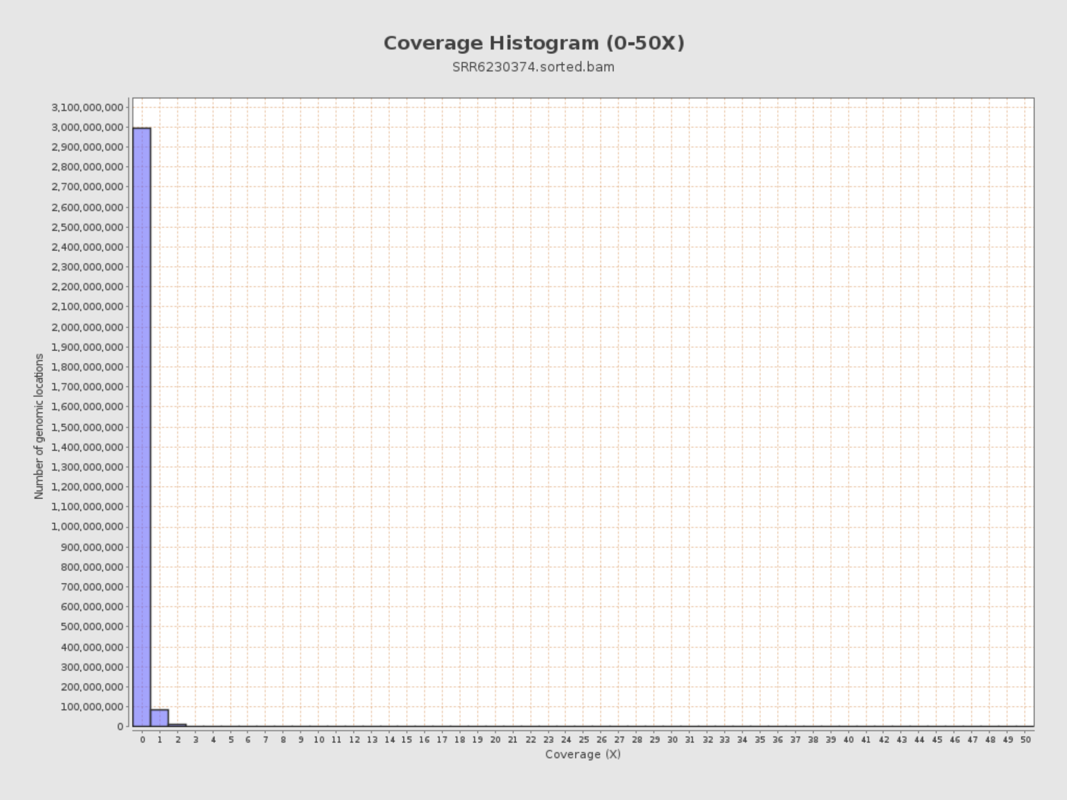
3. Results : Coverage across reference



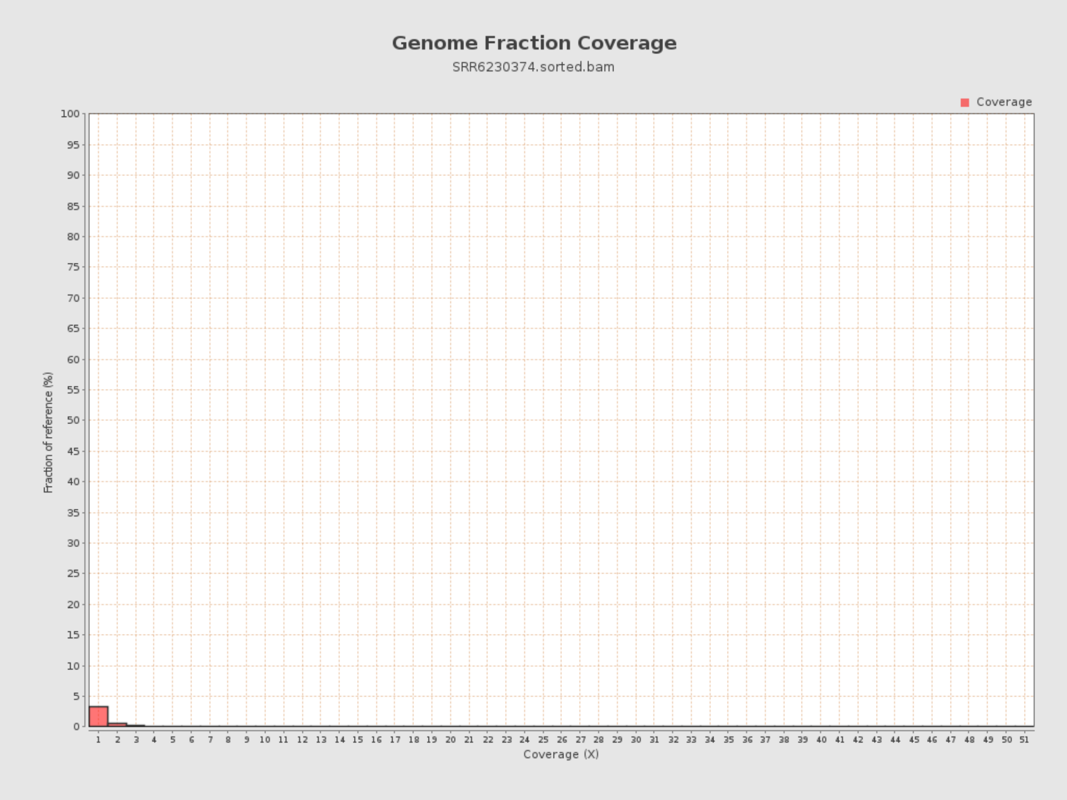
4. Results : Coverage Histogram



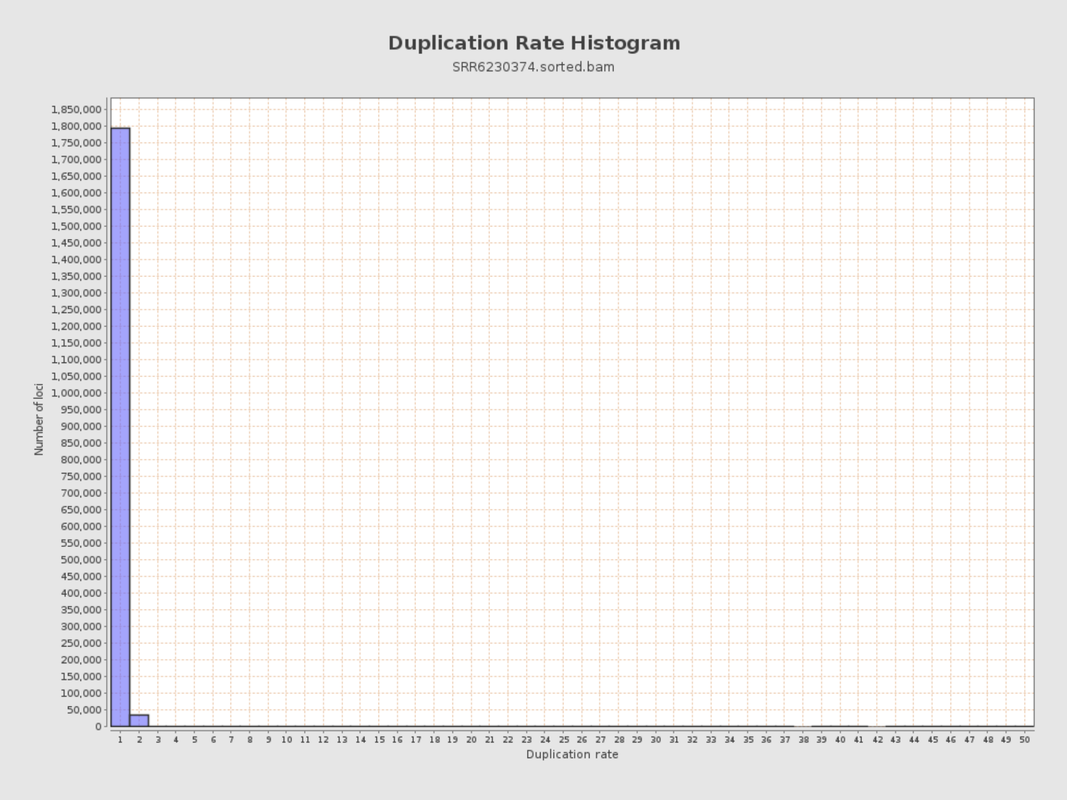
5. Results : Coverage Histogram (0-50X)



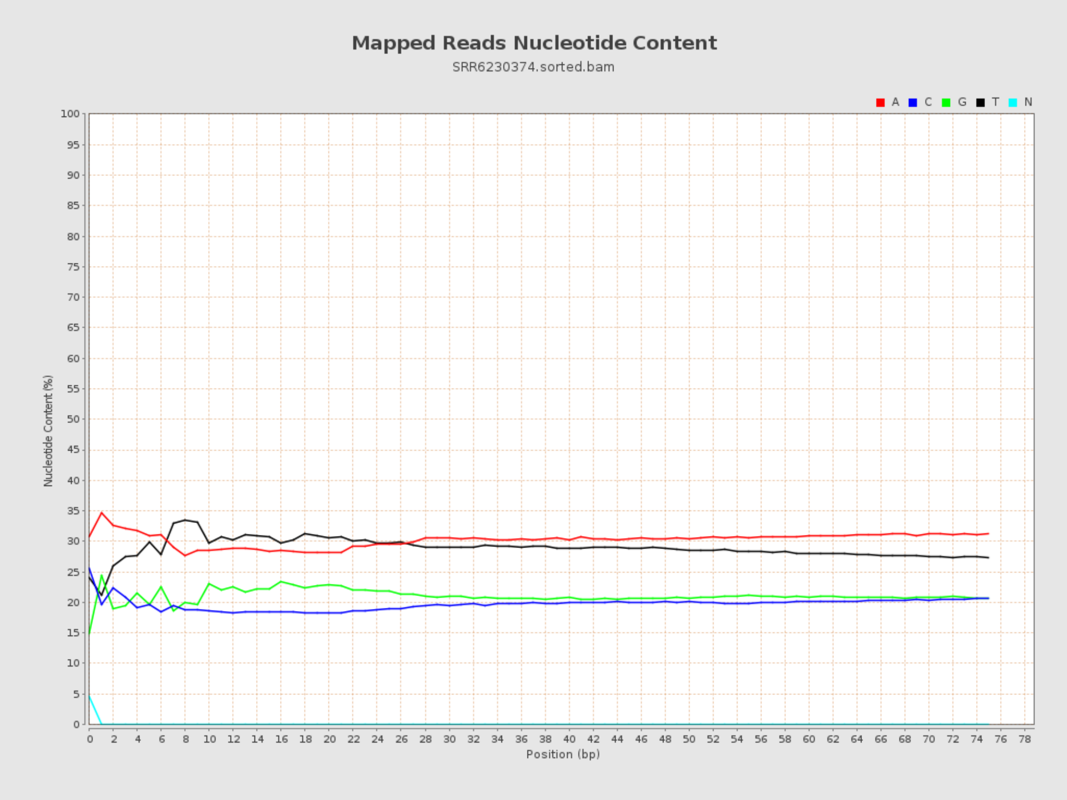
6. Results : Genome Fraction Coverage



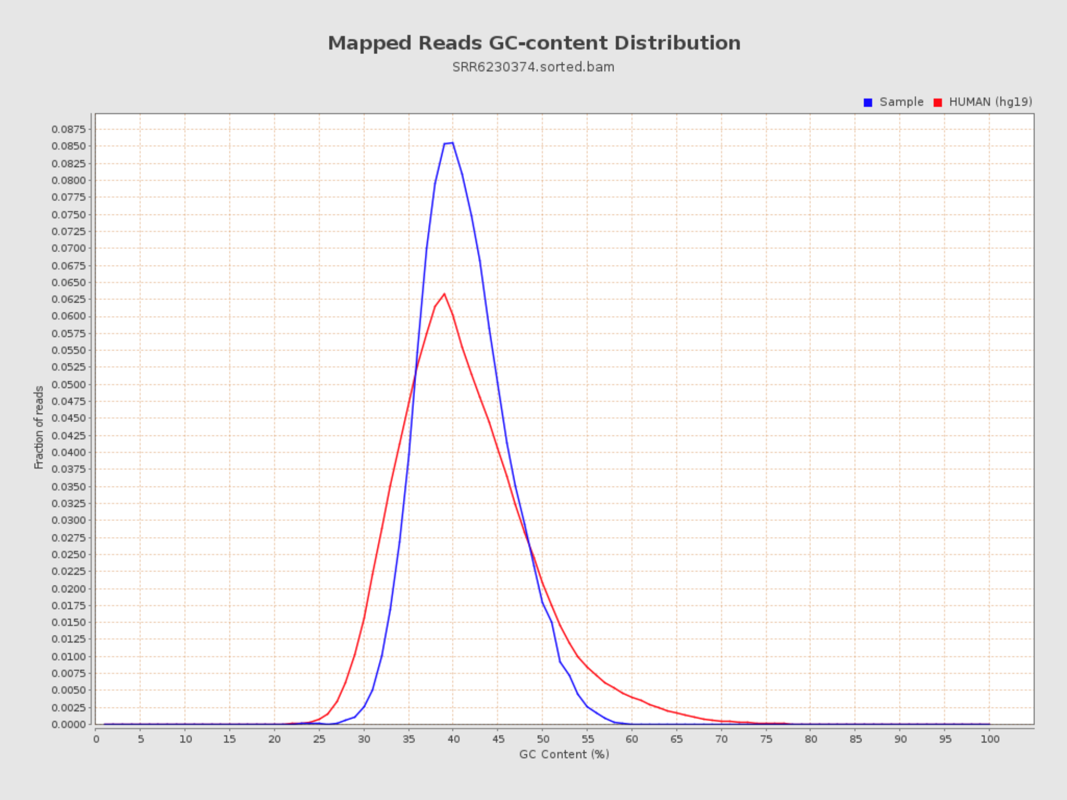
7. Results : Duplication Rate Histogram



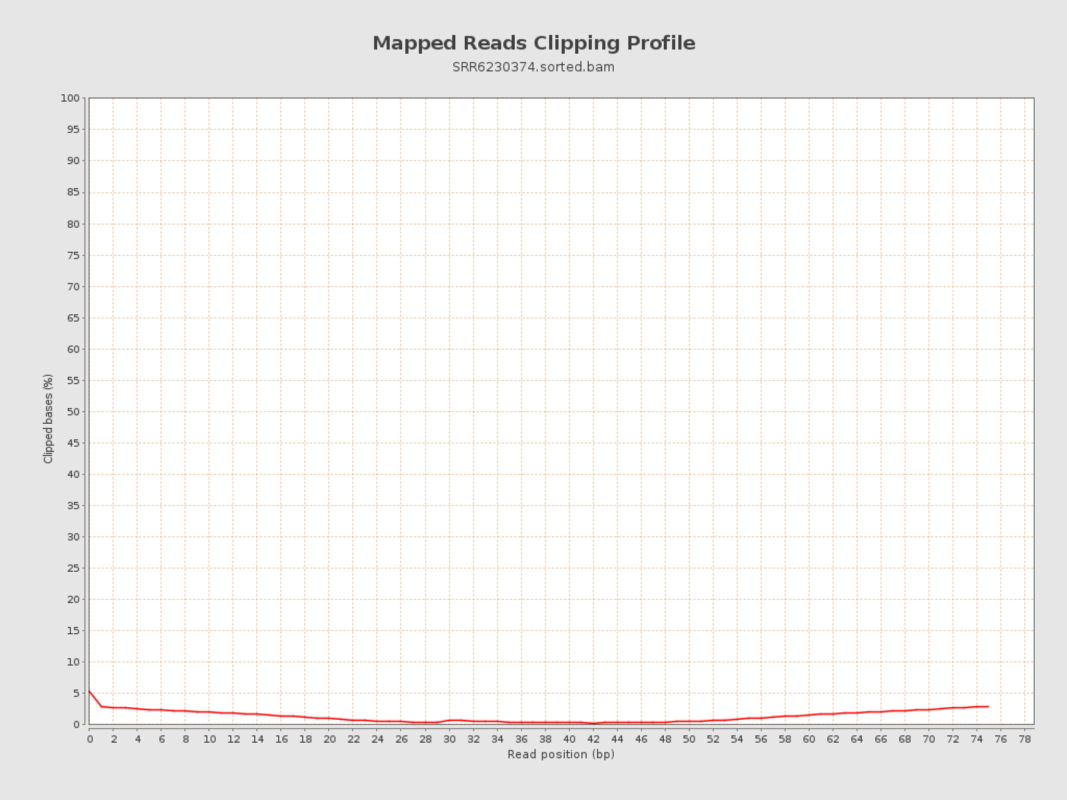
8. Results : Mapped Reads Nucleotide Content



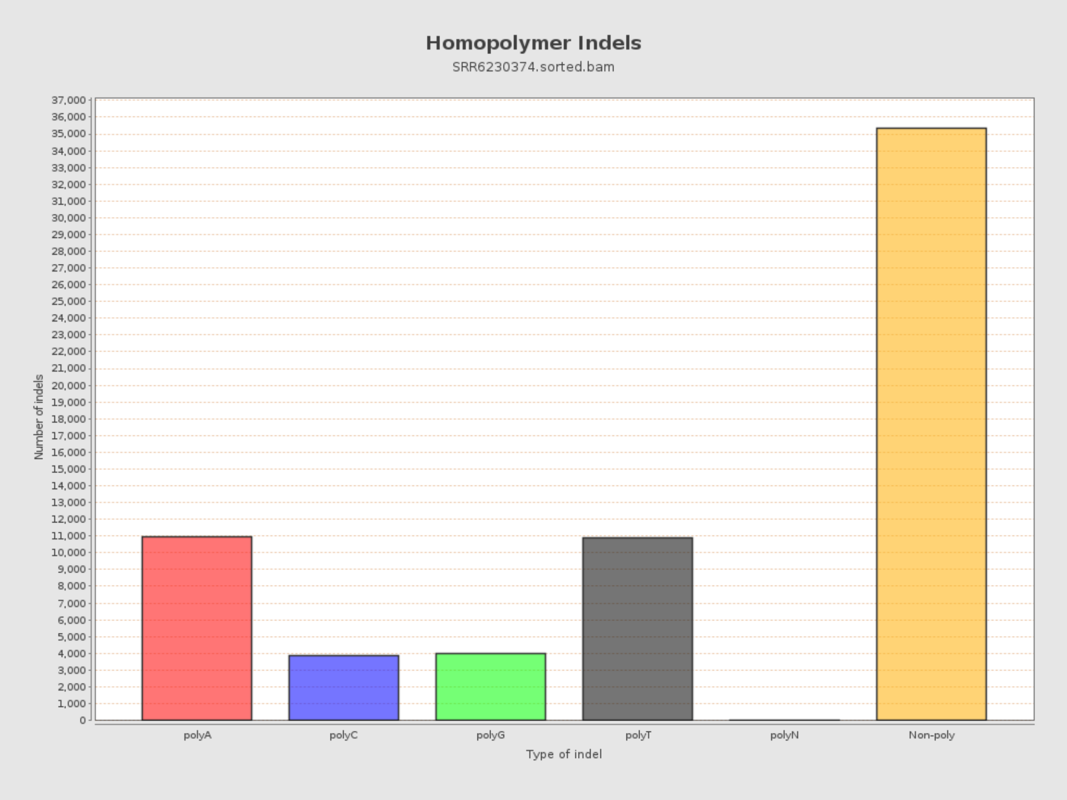
9. Results : Mapped Reads GC-content Distribution



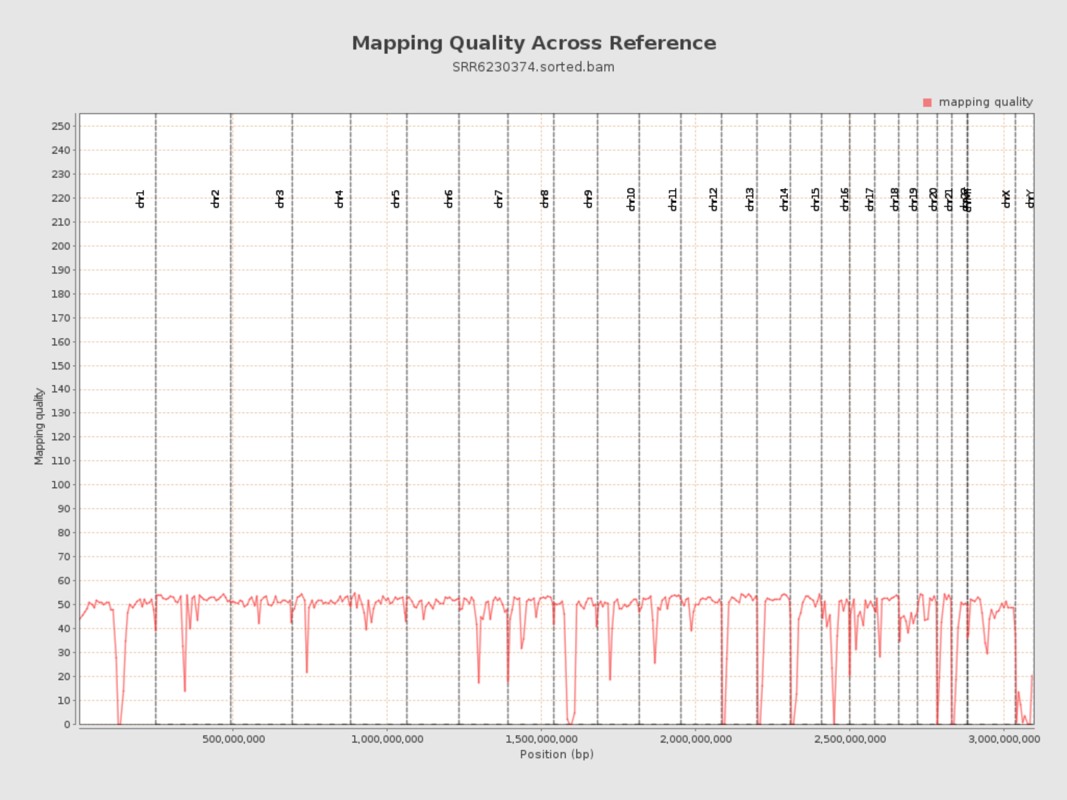
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram