Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:18:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240224.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_SRR6240224 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240224.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:18:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,469,719
Mapped reads	1,947,379 / 78.85%
Unmapped reads	522,340 / 21.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,710 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	217,797 / 8.82%
Duplication rate	8.58%
Clipped reads	954,258 / 38.64%

2.2. ACGT Content

Number/percentage of A's	37,125,483 / 28.81%
Number/percentage of C's	24,158,872 / 18.75%
Number/percentage of T's	40,549,103 / 31.46%
Number/percentage of G's	27,029,858 / 20.97%
Number/percentage of N's	11,348 / 0.01%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0416

Standard Deviation	0.4675

2.4. Mapping Quality

Mean Mapping Quality	46.89

2.5. Mismatches and indels

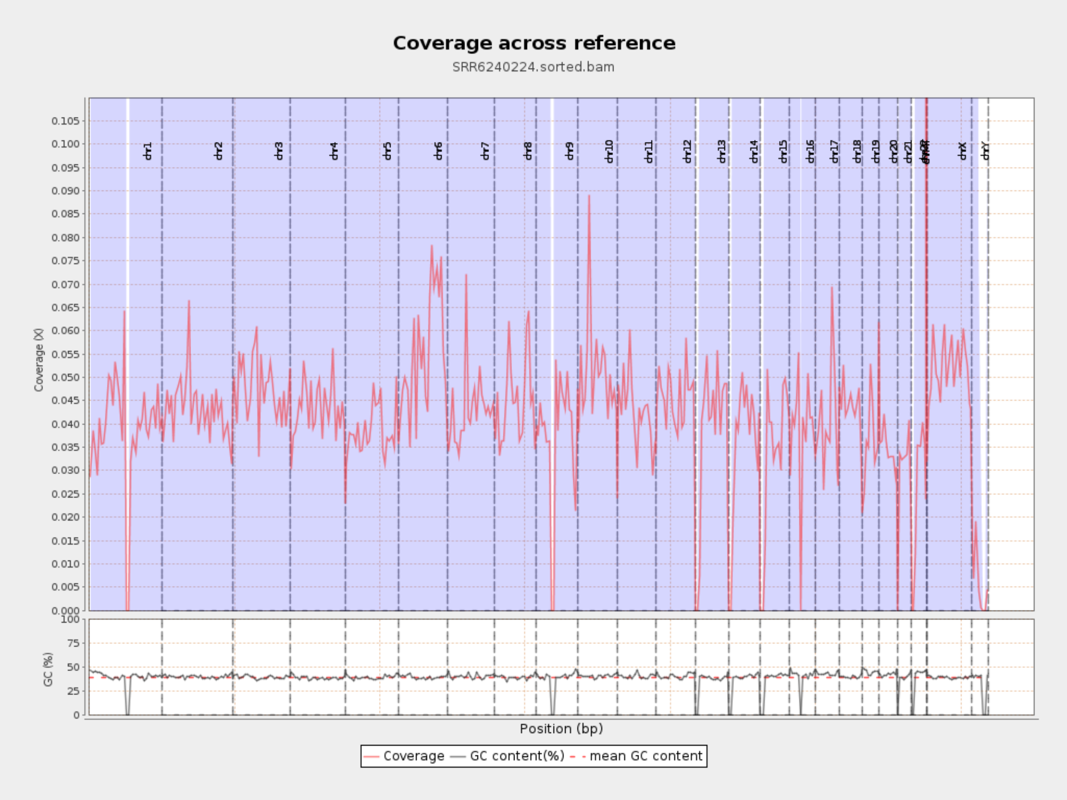
General error rate	0.8%
Mismatches	1,014,986
Insertions	9,378
Mapped reads with at least one insertion	0.48%
Deletions	30,227
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.41%

2.6. Chromosome stats

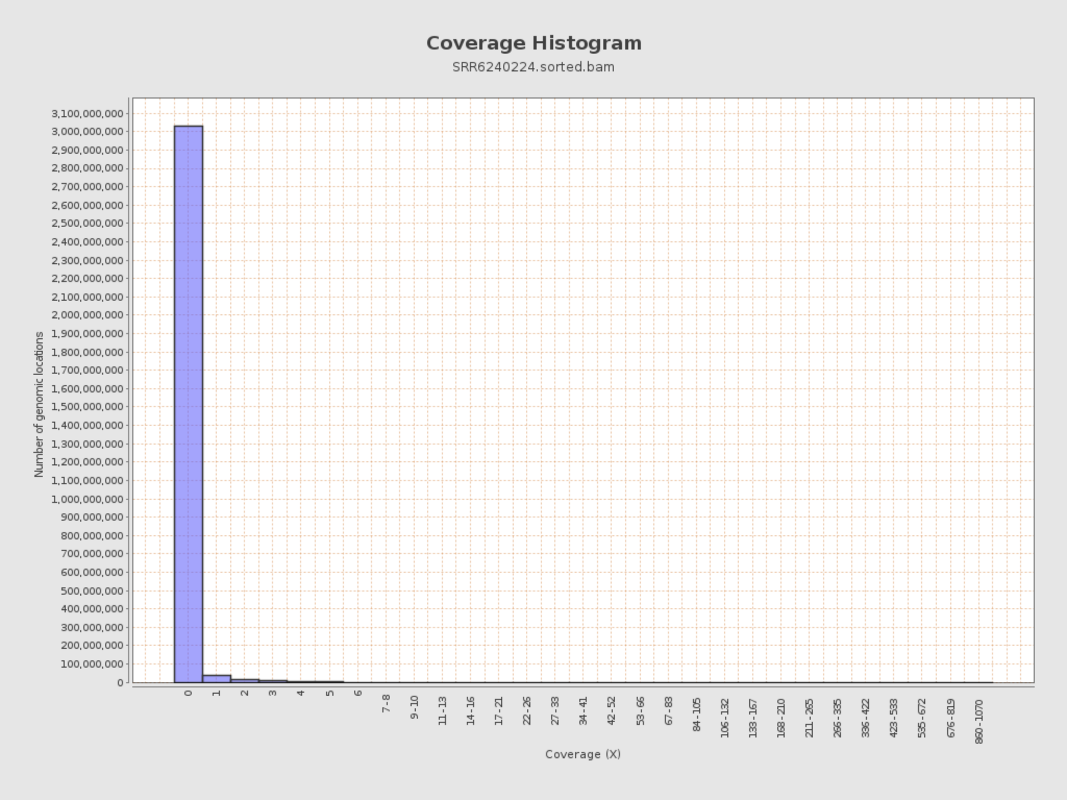
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9650064	0.0387	0.7219
chr2	243199373	10554450	0.0434	0.483
chr3	198022430	9457091	0.0478	0.3726
chr4	191154276	8257806	0.0432	0.3692
chr5	180915260	6996431	0.0387	0.3362
chr6	171115067	9381664	0.0548	0.4266
chr7	159138663	6889489	0.0433	0.5016

chr8	146364022	6650185	0.0454	0.7377
chr9	141213431	5158553	0.0365	0.4457
chr10	135534747	6953170	0.0513	0.4739
chr11	135006516	5721284	0.0424	0.4323
chr12	133851895	6131431	0.0458	0.3699
chr13	115169878	4319100	0.0375	0.3357
chr14	107349540	3754311	0.035	0.3324
chr15	102531392	3402648	0.0332	0.313
chr16	90354753	3473161	0.0384	0.3602
chr17	81195210	3234340	0.0398	0.3796
chr18	78077248	3462284	0.0443	0.7578
chr19	59128983	2209463	0.0374	0.5019
chr20	63025520	2179490	0.0346	0.3197
chr21	48129895	1430657	0.0297	0.3014
chr22	51304566	1277812	0.0249	0.2594
chrMT	16571	27002	1.6295	2.1427
chrX	155270560	8018099	0.0516	0.4342
chrY	59373566	337810	0.0057	0.1379

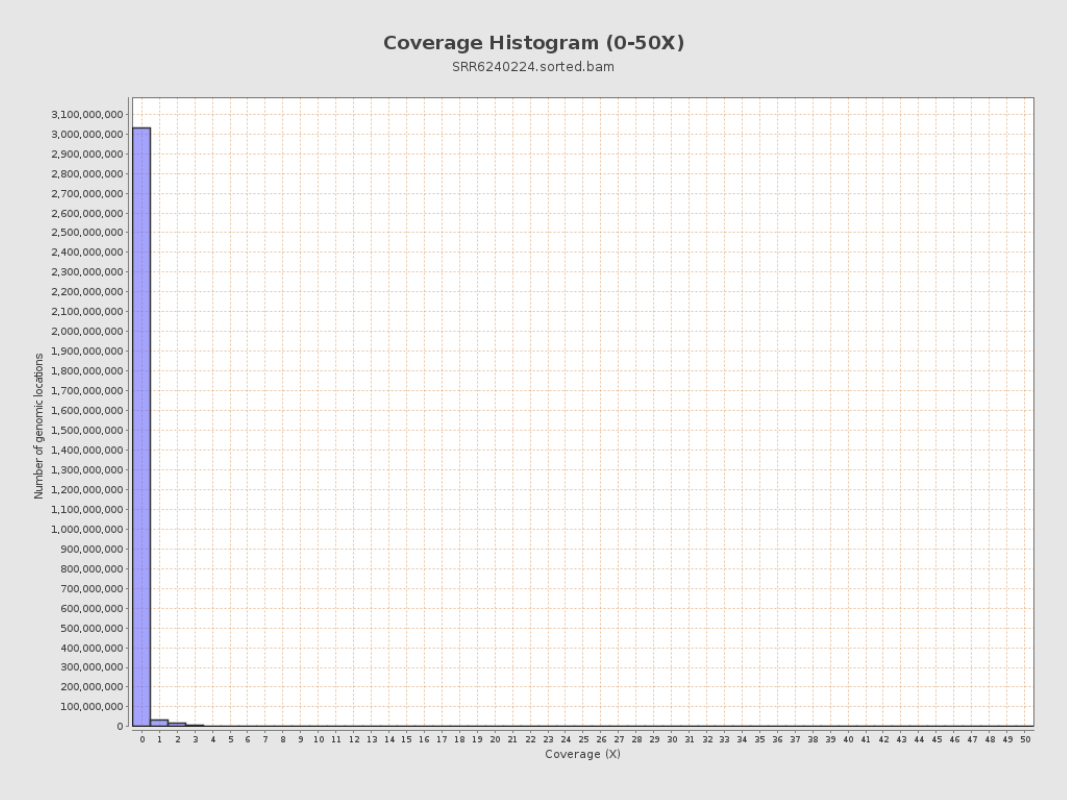
3. Results : Coverage across reference



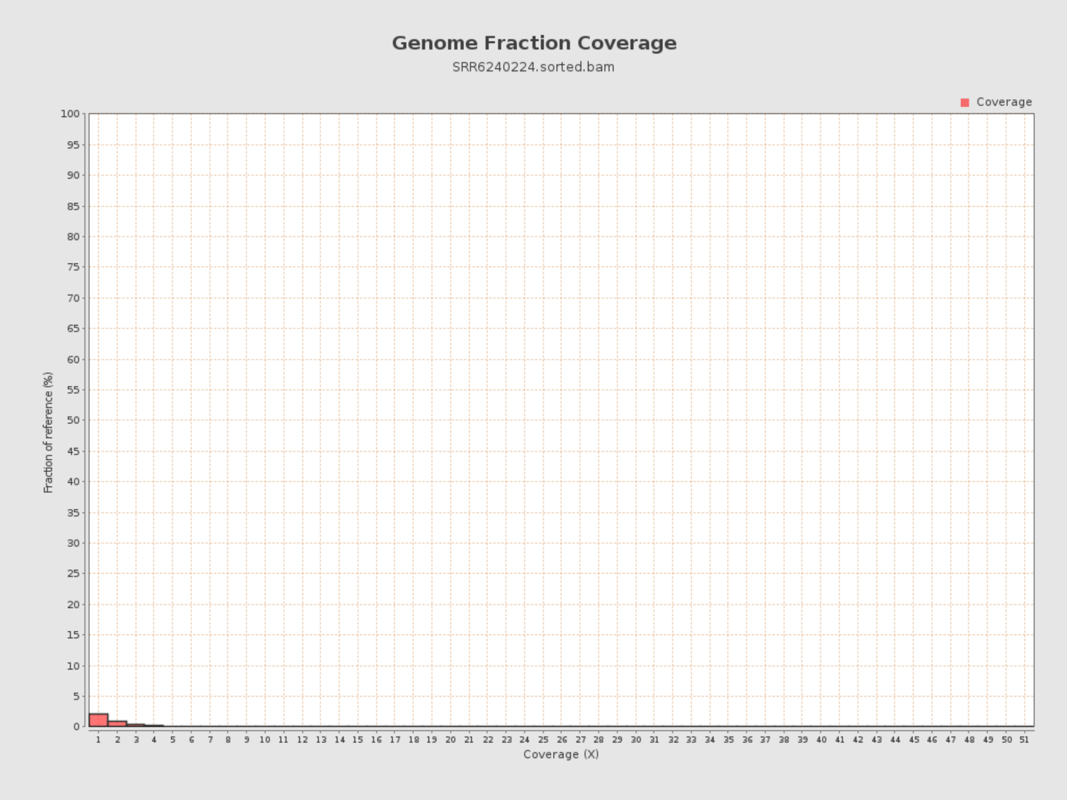
4. Results : Coverage Histogram



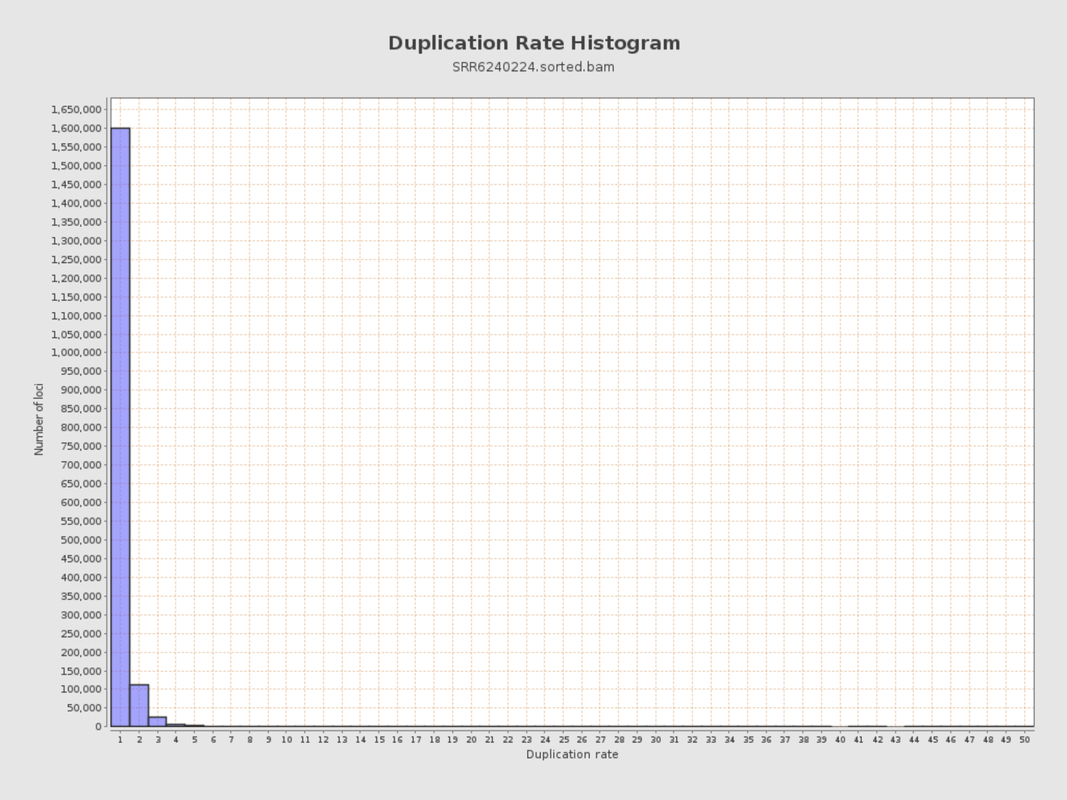
5. Results : Coverage Histogram (0-50X)



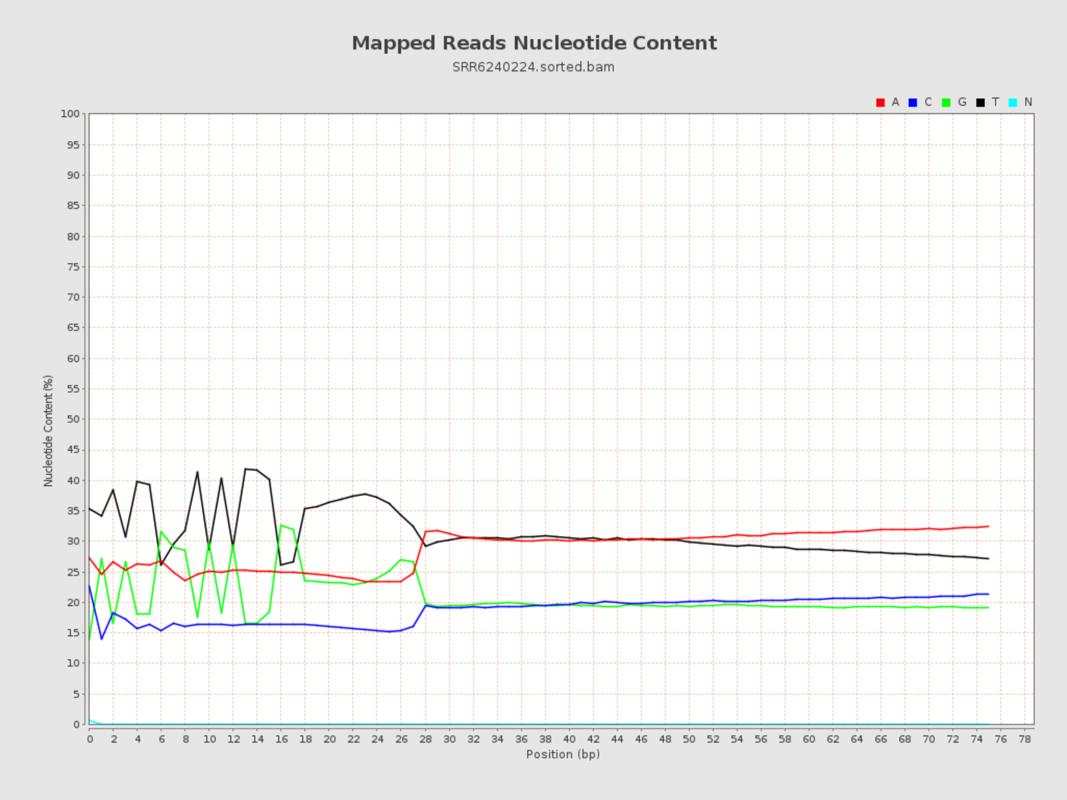
6. Results : Genome Fraction Coverage



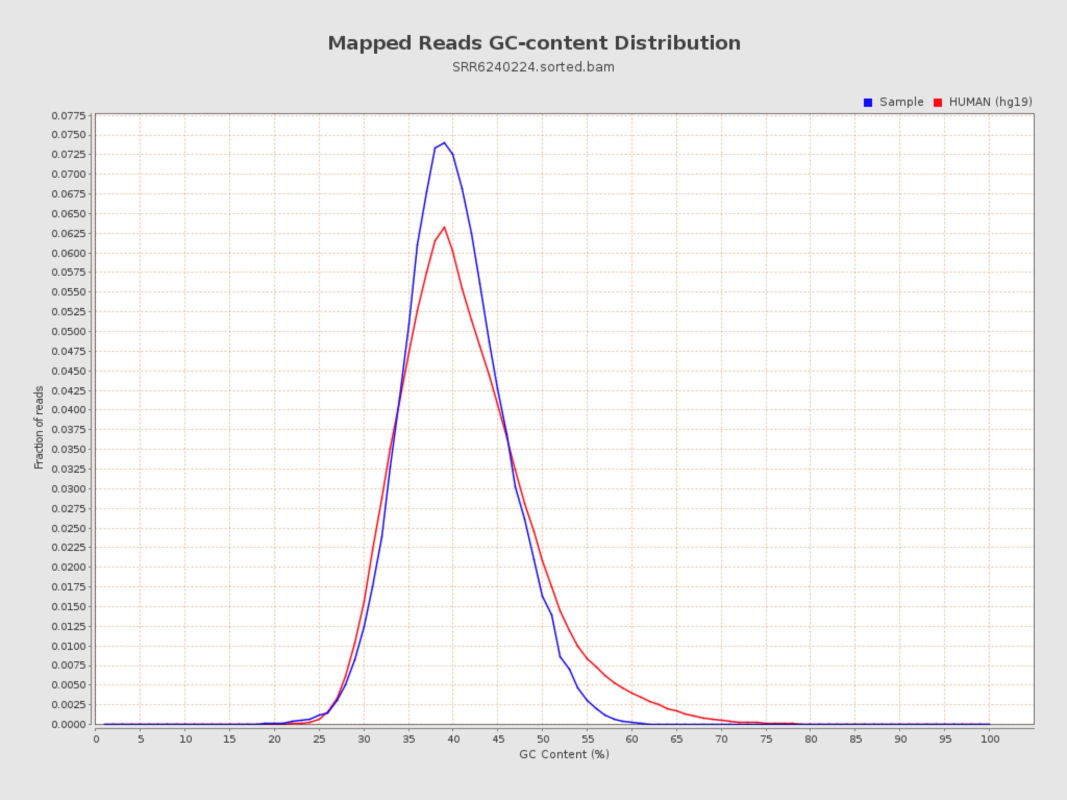
7. Results : Duplication Rate Histogram



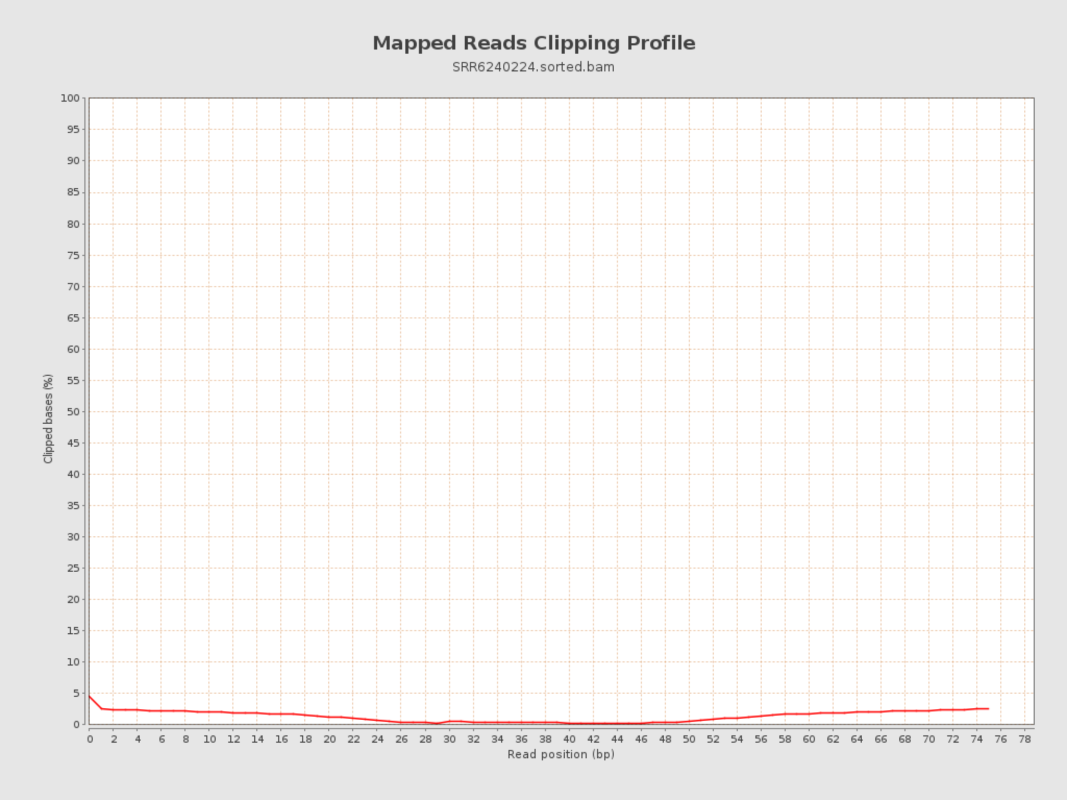
8. Results : Mapped Reads Nucleotide Content



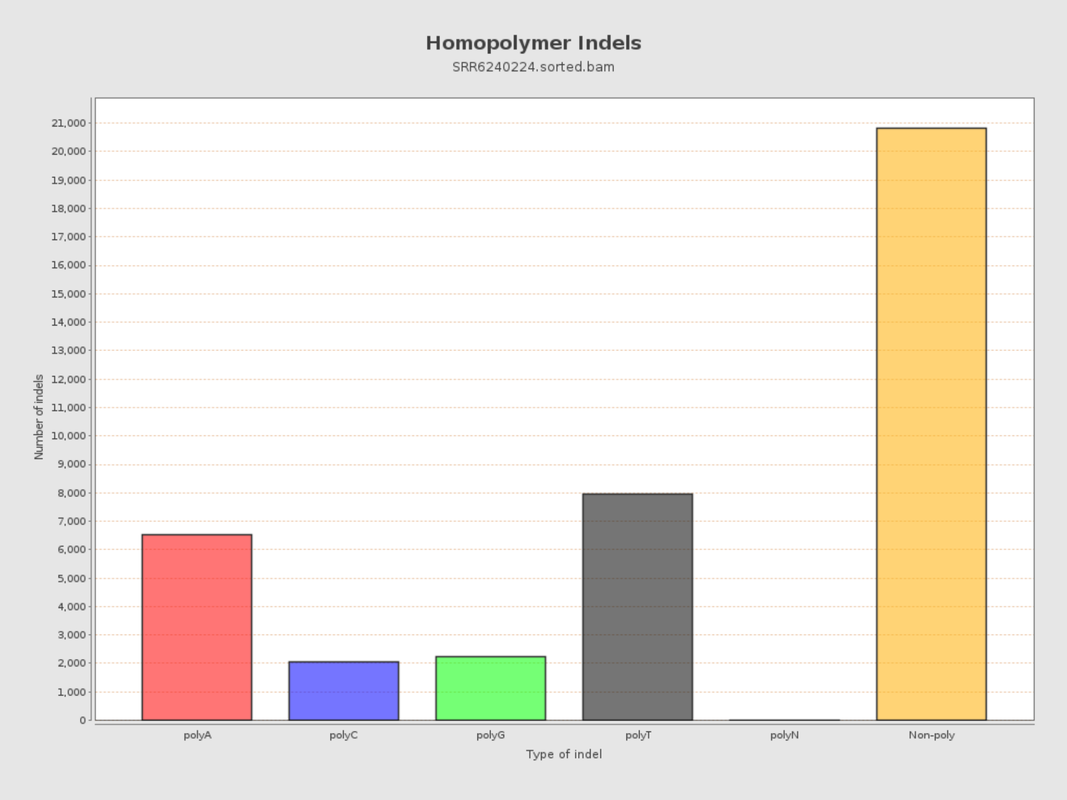
9. Results : Mapped Reads GC-content Distribution



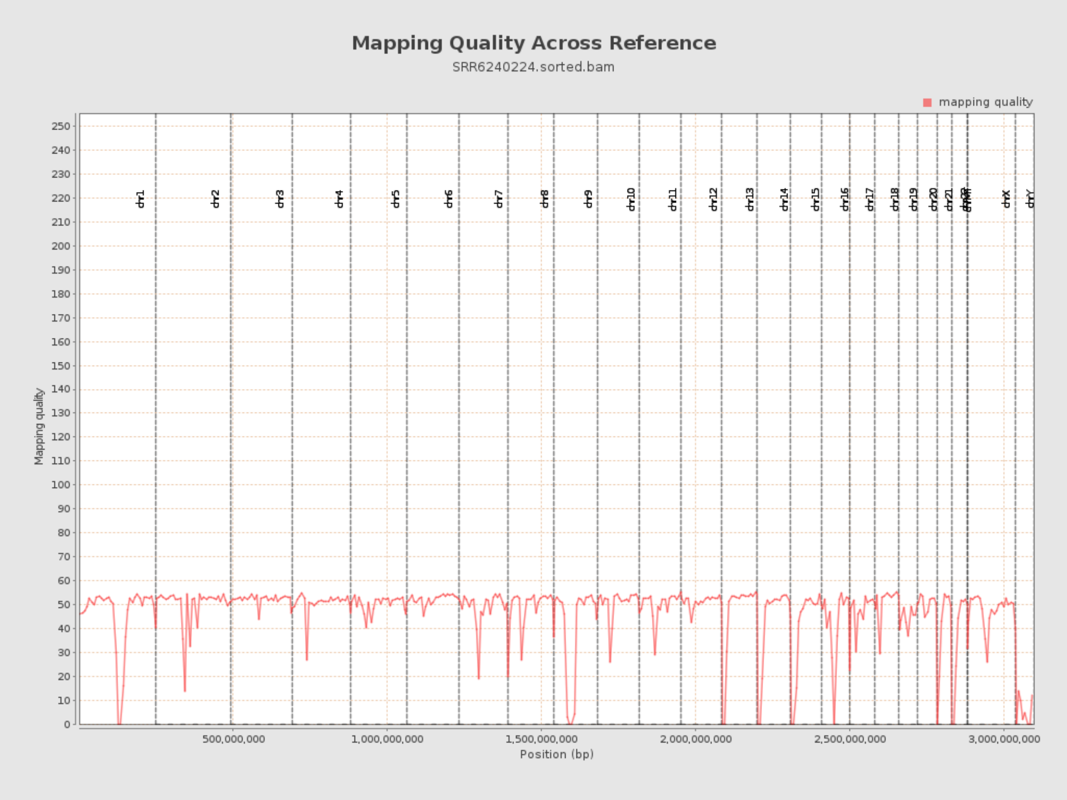
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram