Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:50:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240215.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_SRR6240215 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240215.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:50:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240215.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,716,126
Mapped reads	2,129,303 / 78.39%
Unmapped reads	586,823 / 21.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,903 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	337,251 / 12.42%
Duplication rate	11.53%
Clipped reads	1,066,416 / 39.26%

2.2. ACGT Content

Number/percentage of A's	39,408,661 / 28.16%
Number/percentage of C's	26,026,006 / 18.59%
Number/percentage of T's	44,301,957 / 31.65%
Number/percentage of G's	30,219,723 / 21.59%
Number/percentage of N's	12,926 / 0.01%
GC Percentage	40.18%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.5338

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

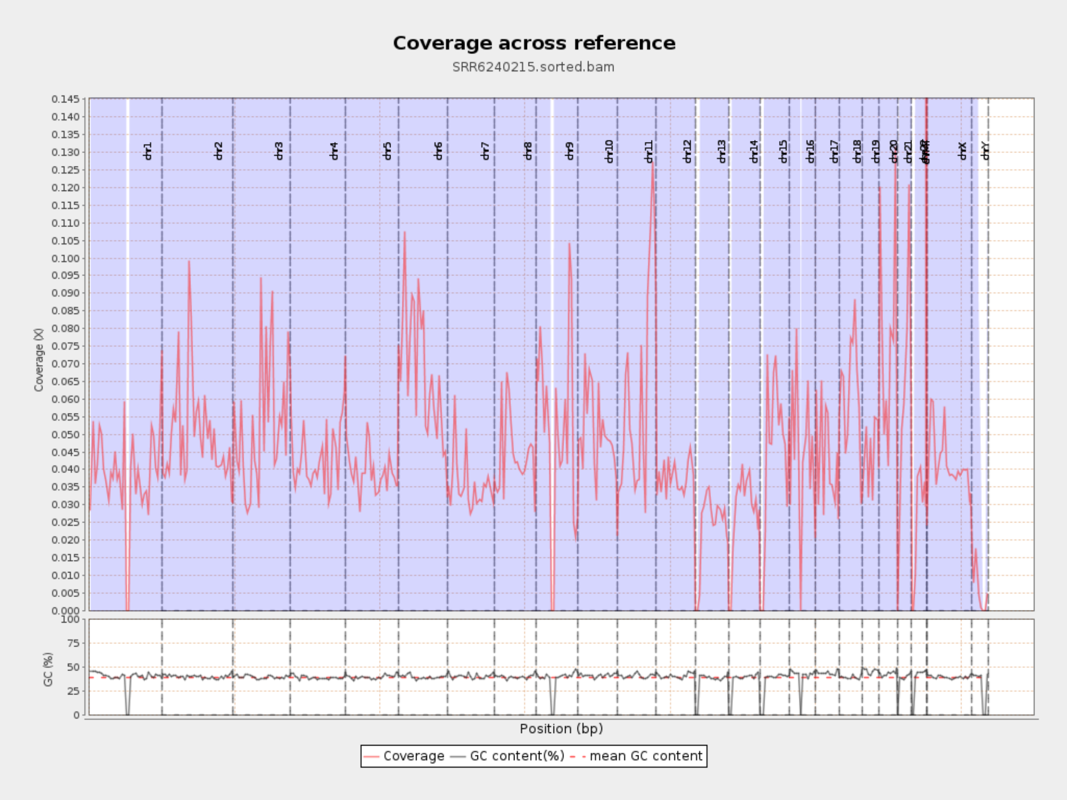
General error rate	0.82%
Mismatches	1,133,026
Insertions	10,302
Mapped reads with at least one insertion	0.48%
Deletions	34,998
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.42%

2.6. Chromosome stats

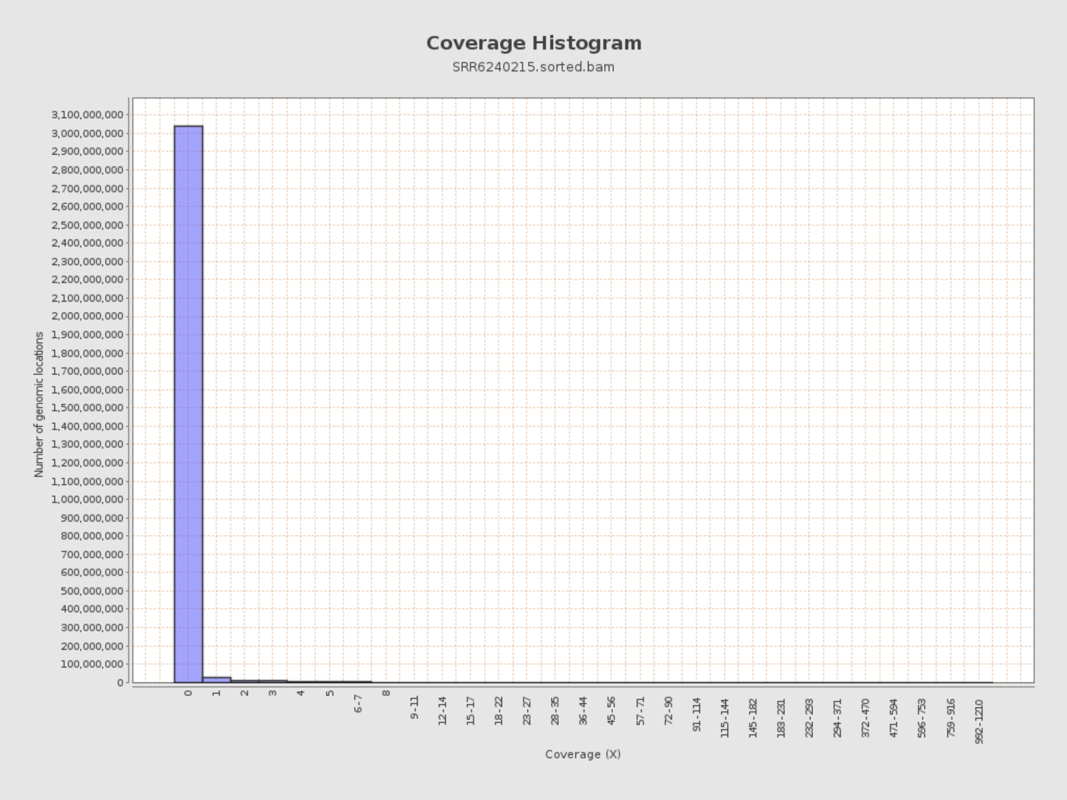
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9502465	0.0381	0.6982
chr2	243199373	12123519	0.0499	0.5769
chr3	198022430	10402577	0.0525	0.4758
chr4	191154276	8205114	0.0429	0.4316
chr5	180915260	7147555	0.0395	0.3967
chr6	171115067	11613576	0.0679	0.5844
chr7	159138663	5699277	0.0358	0.4511

chr8	146364022	6495205	0.0444	0.8358
chr9	141213431	7212686	0.0511	0.5478
chr10	135534747	6909543	0.051	0.501
chr11	135006516	8213690	0.0608	0.5945
chr12	133851895	5016949	0.0375	0.3964
chr13	115169878	2688559	0.0233	0.3111
chr14	107349540	2998528	0.0279	0.3751
chr15	102531392	4552846	0.0444	0.4235
chr16	90354753	4095314	0.0453	0.4499
chr17	81195210	3540488	0.0436	0.4238
chr18	78077248	4963313	0.0636	0.9188
chr19	59128983	2626788	0.0444	0.5343
chr20	63025520	4908563	0.0779	0.584
chr21	48129895	2898160	0.0602	0.5076
chr22	51304566	1266655	0.0247	0.3202
chrMT	16571	119561	7.2151	7.0101
chrX	155270560	6492430	0.0418	0.4361
chrY	59373566	336010	0.0057	0.1575

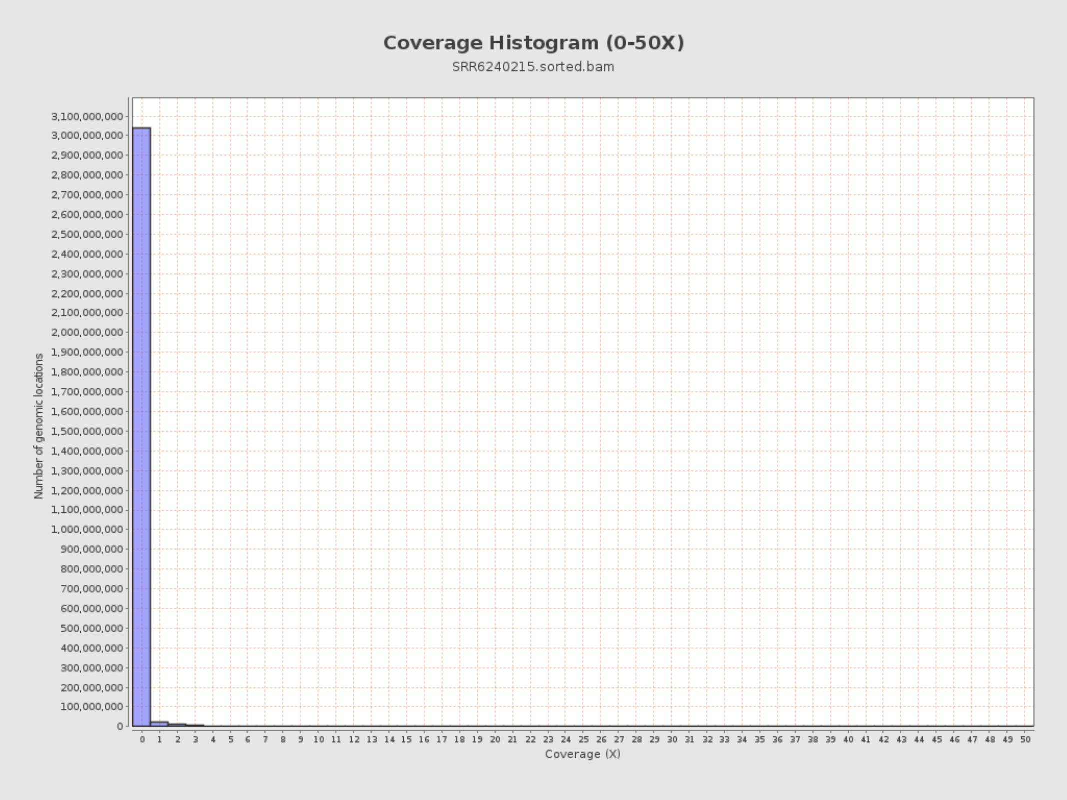
3. Results : Coverage across reference



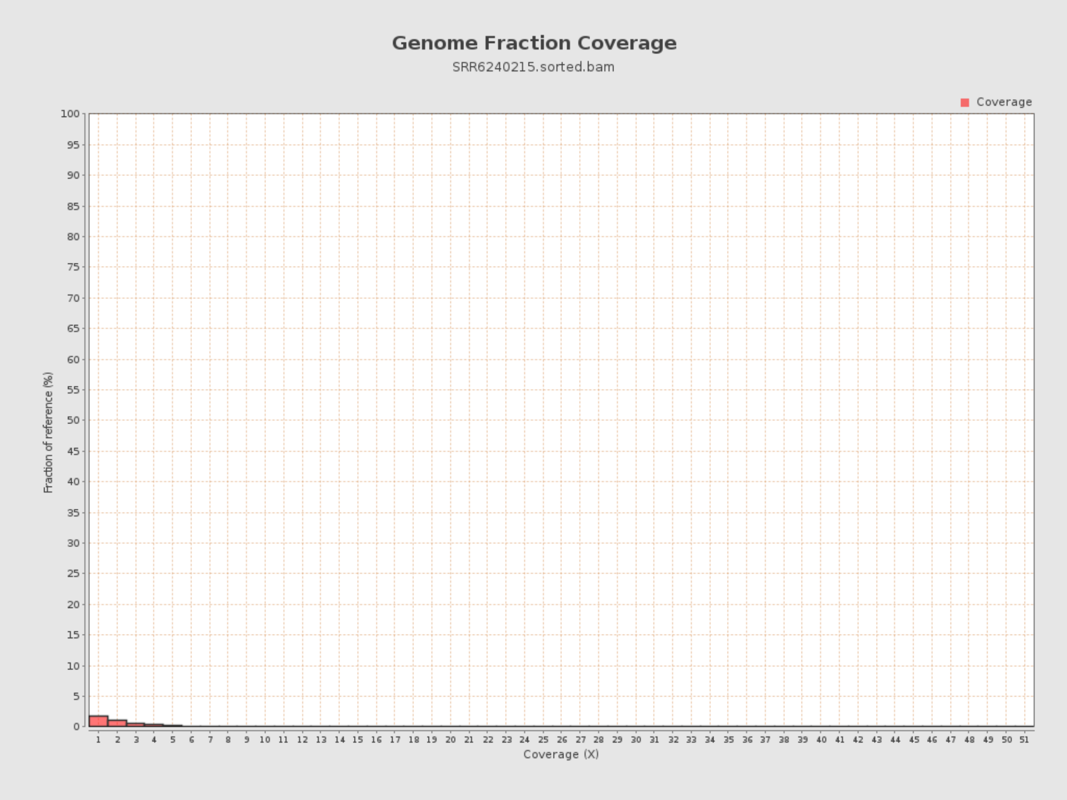
4. Results : Coverage Histogram



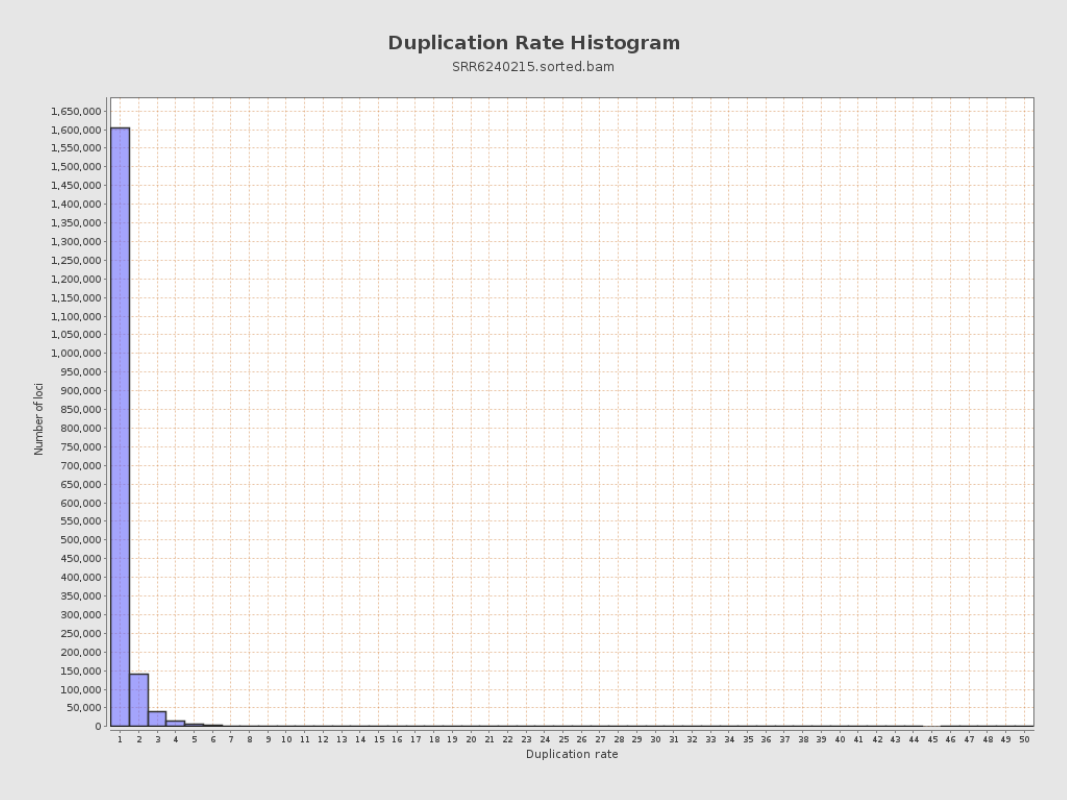
5. Results : Coverage Histogram (0-50X)



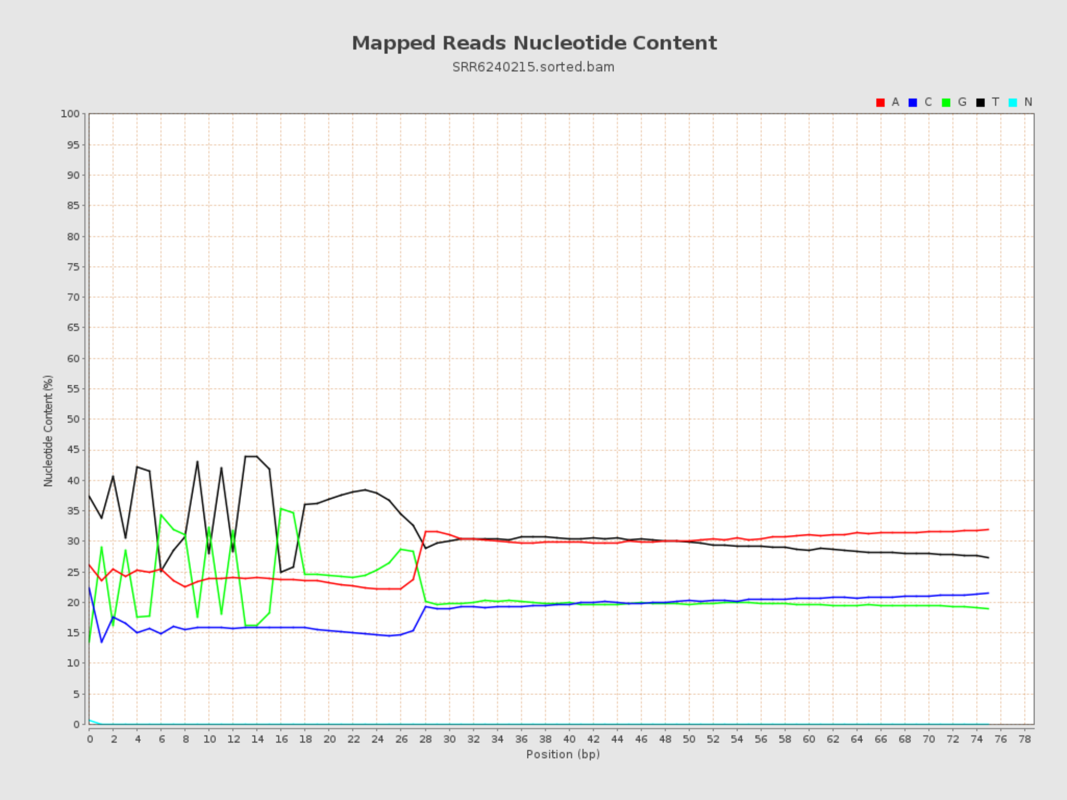
6. Results : Genome Fraction Coverage



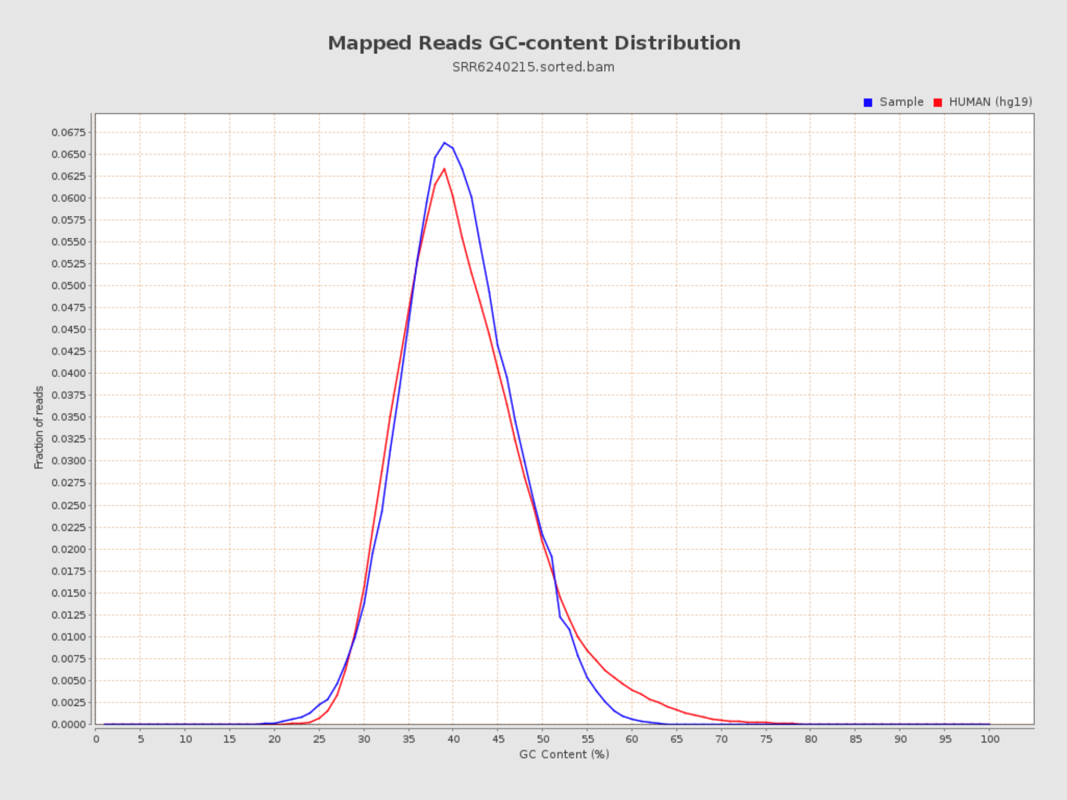
7. Results : Duplication Rate Histogram



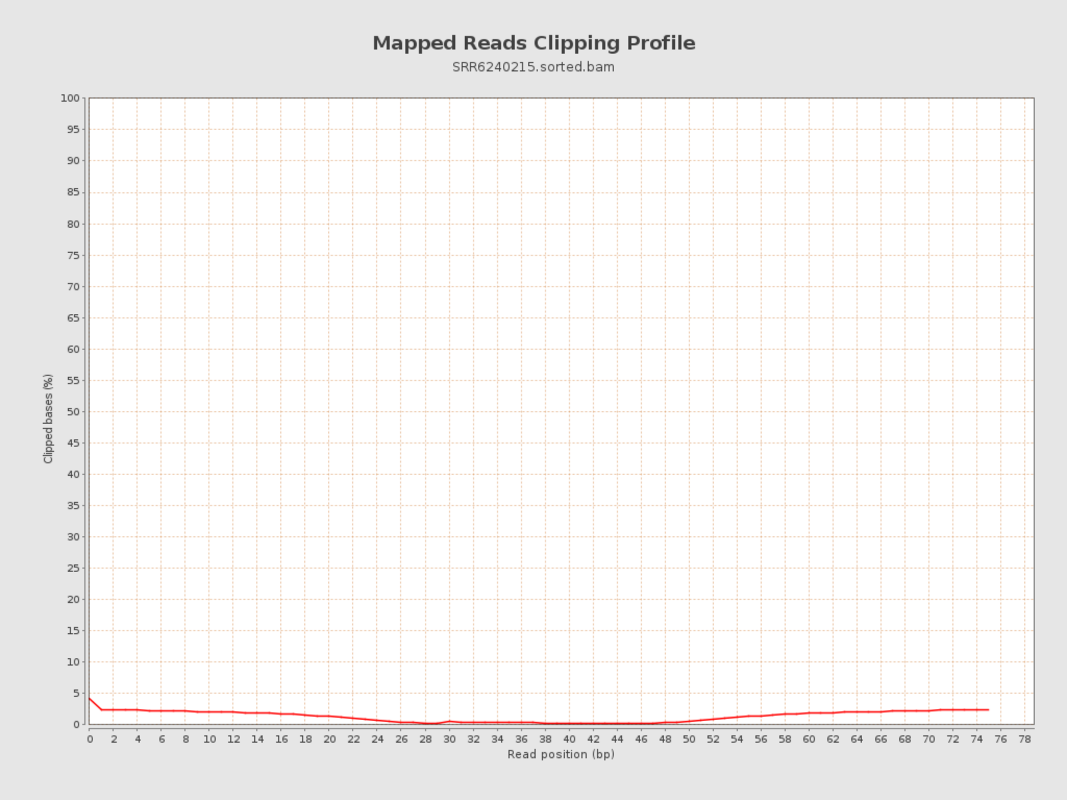
8. Results : Mapped Reads Nucleotide Content



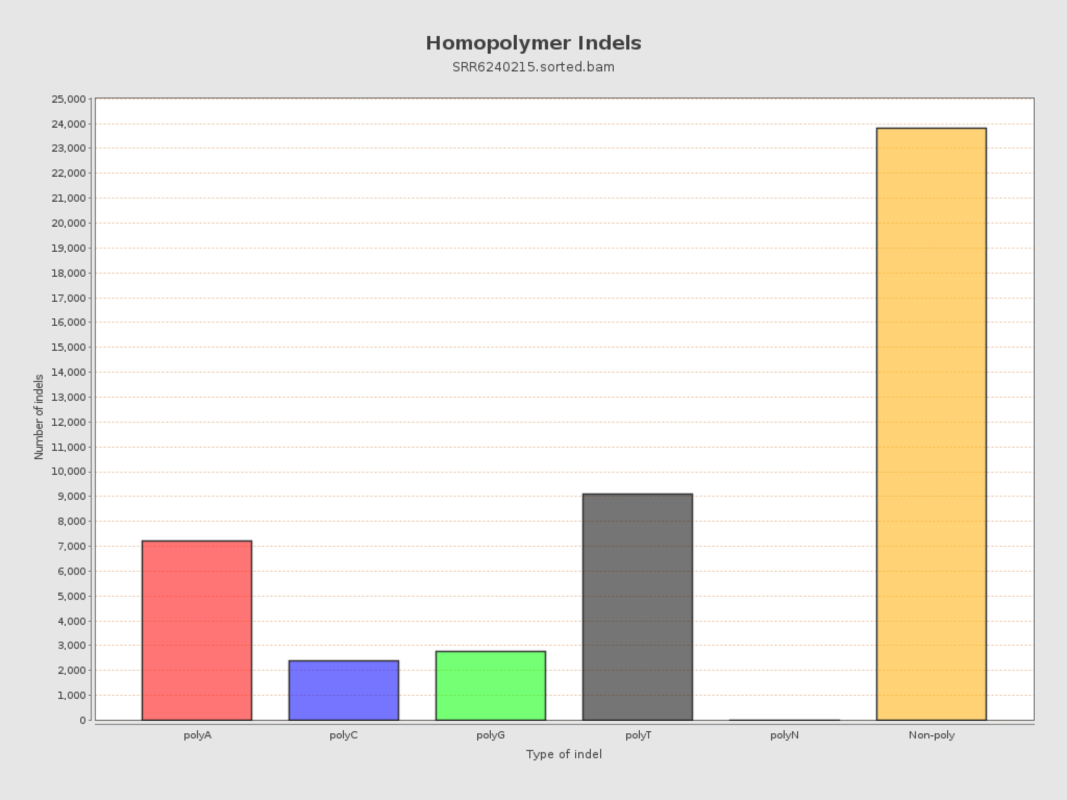
9. Results : Mapped Reads GC-content Distribution



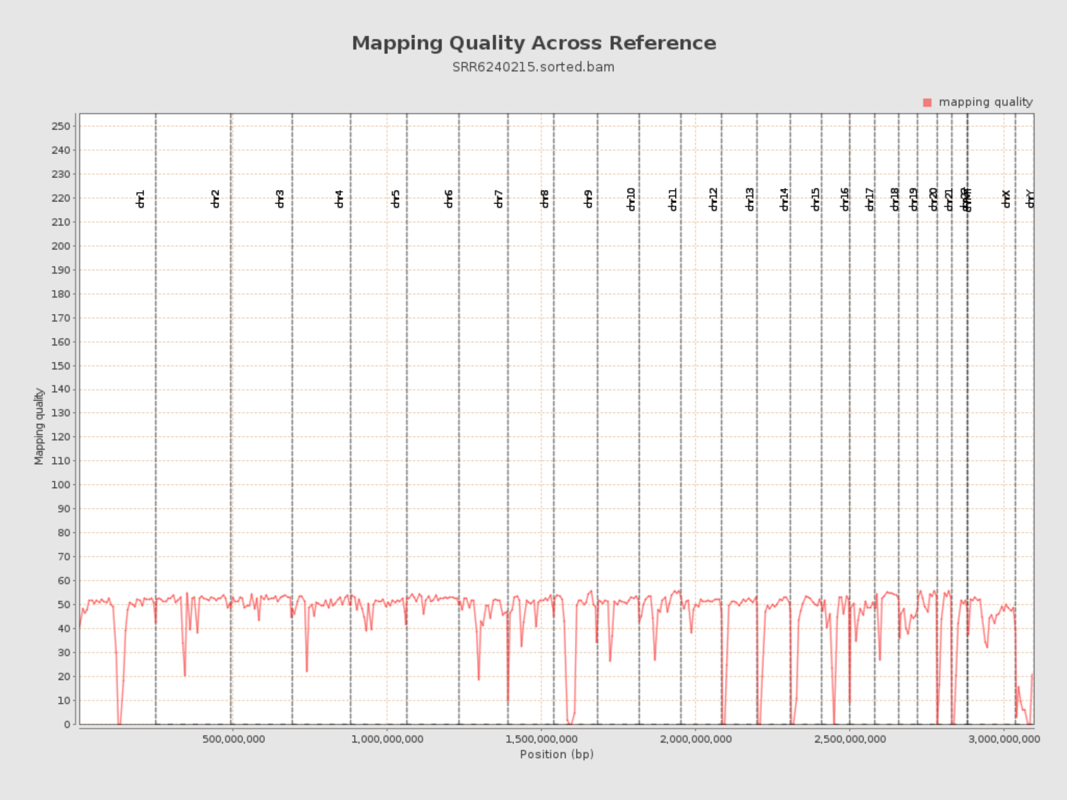
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram