Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:45:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240234.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_SRR6240234 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240234.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:45:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,409,637
Mapped reads	2,209,184 / 64.79%
Unmapped reads	1,200,453 / 35.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,855 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	350,886 / 10.29%
Duplication rate	11.4%
Clipped reads	998,331 / 29.28%

2.2. ACGT Content

Number/percentage of A's	41,970,897 / 28.47%
Number/percentage of C's	27,348,607 / 18.55%
Number/percentage of T's	46,880,632 / 31.8%
Number/percentage of G's	31,177,496 / 21.15%
Number/percentage of N's	57,283 / 0.04%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.5837

2.4. Mapping Quality

Mean Mapping Quality	47.12

2.5. Mismatches and indels

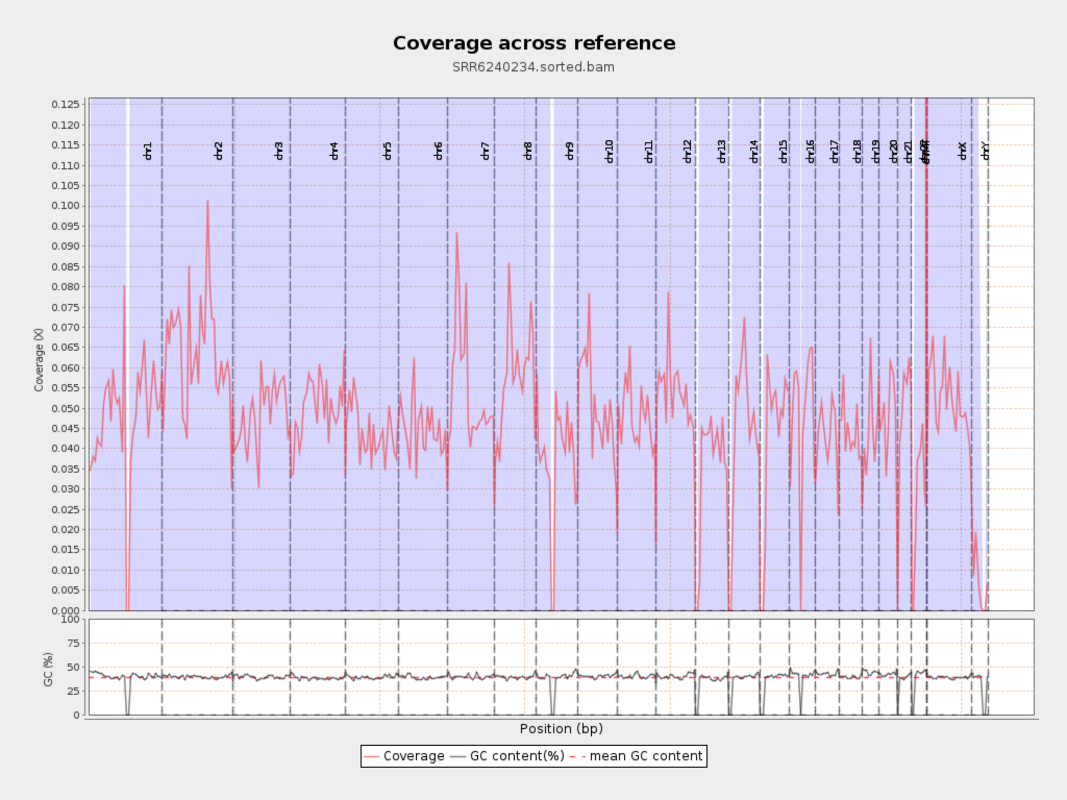
General error rate	0.87%
Mismatches	1,258,971
Insertions	10,783
Mapped reads with at least one insertion	0.48%
Deletions	39,931
Mapped reads with at least one deletion	1.79%
Homopolymer indels	48.5%

2.6. Chromosome stats

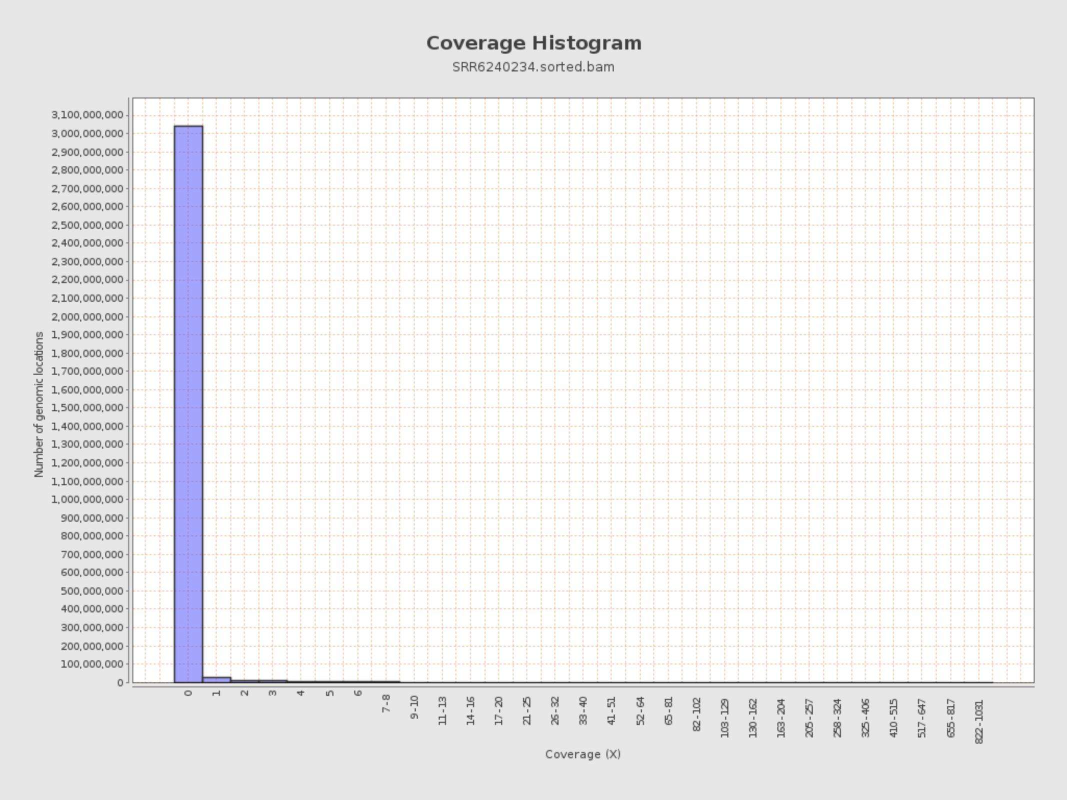
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11826113	0.0474	0.968
chr2	243199373	15582802	0.0641	0.6389
chr3	198022430	9623611	0.0486	0.4725
chr4	191154276	9532065	0.0499	0.4812
chr5	180915260	7964082	0.044	0.4511
chr6	171115067	7684175	0.0449	0.5006
chr7	159138663	8736217	0.0549	0.7156

chr8	146364022	8478612	0.0579	0.7718
chr9	141213431	5172885	0.0366	0.4663
chr10	135534747	6933398	0.0512	0.5536
chr11	135006516	6422607	0.0476	0.5439
chr12	133851895	7239385	0.0541	0.5108
chr13	115169878	3999370	0.0347	0.3958
chr14	107349540	4785979	0.0446	0.4591
chr15	102531392	4381626	0.0427	0.4433
chr16	90354753	4376680	0.0484	0.4643
chr17	81195210	3449034	0.0425	0.4557
chr18	78077248	3467244	0.0444	0.7417
chr19	59128983	2634694	0.0446	0.6432
chr20	63025520	3010129	0.0478	0.4658
chr21	48129895	2326914	0.0483	0.474
chr22	51304566	1351804	0.0263	0.3361
chrMT	16571	40620	2.4513	3.8096
chrX	155270560	8064474	0.0519	0.5138
chrY	59373566	420782	0.0071	0.1635

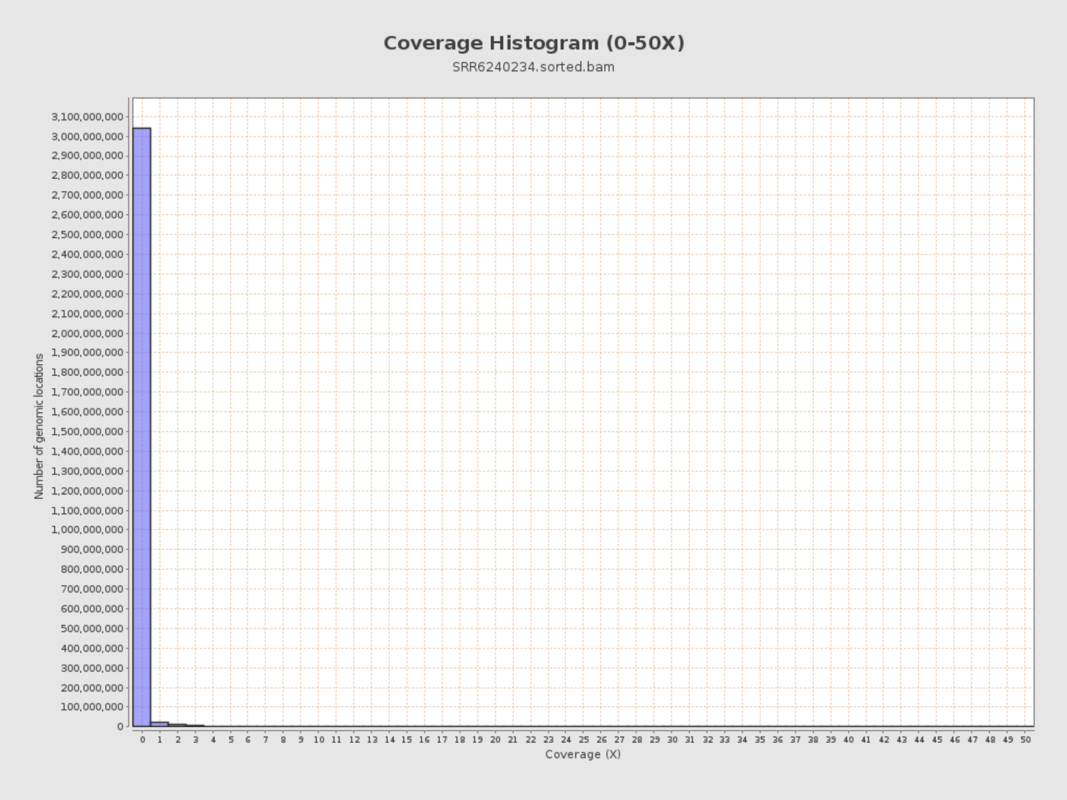
3. Results : Coverage across reference



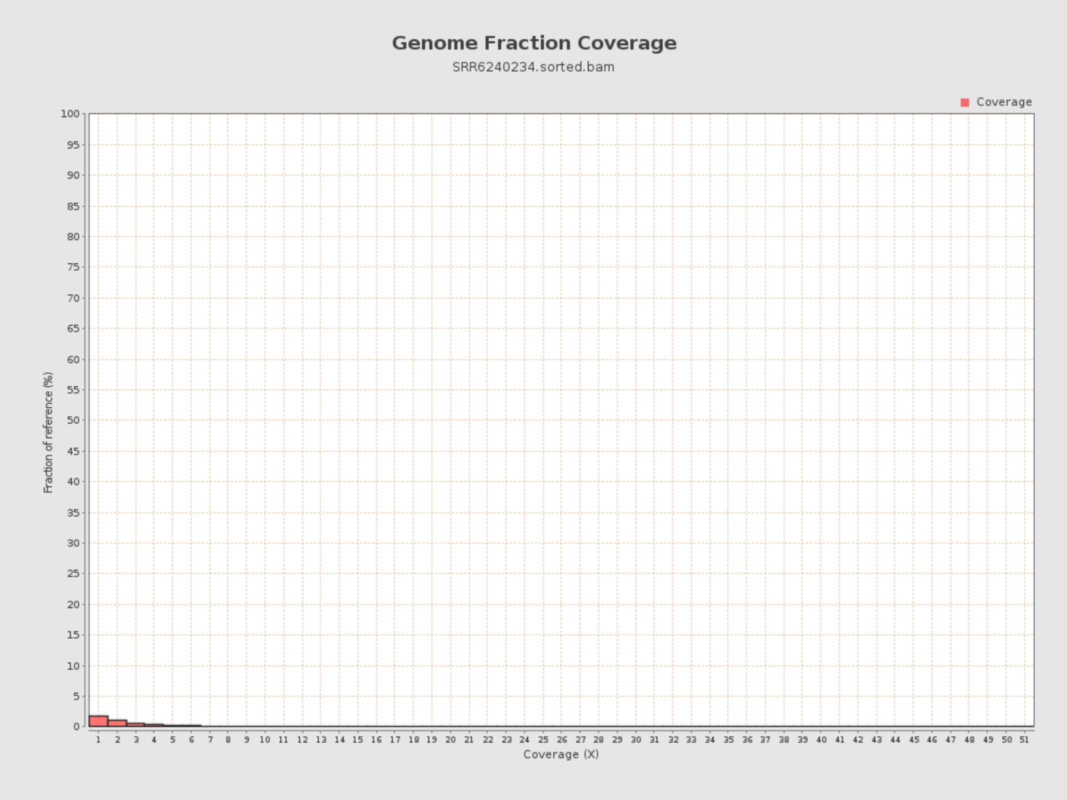
4. Results : Coverage Histogram



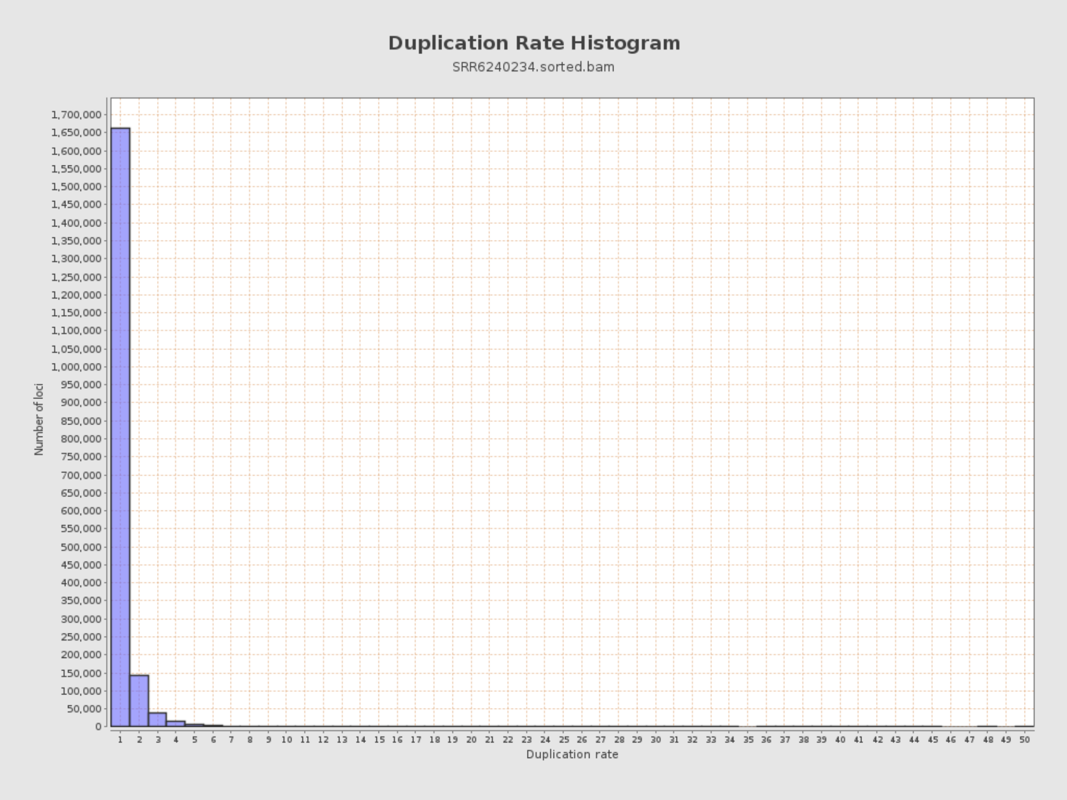
5. Results : Coverage Histogram (0-50X)



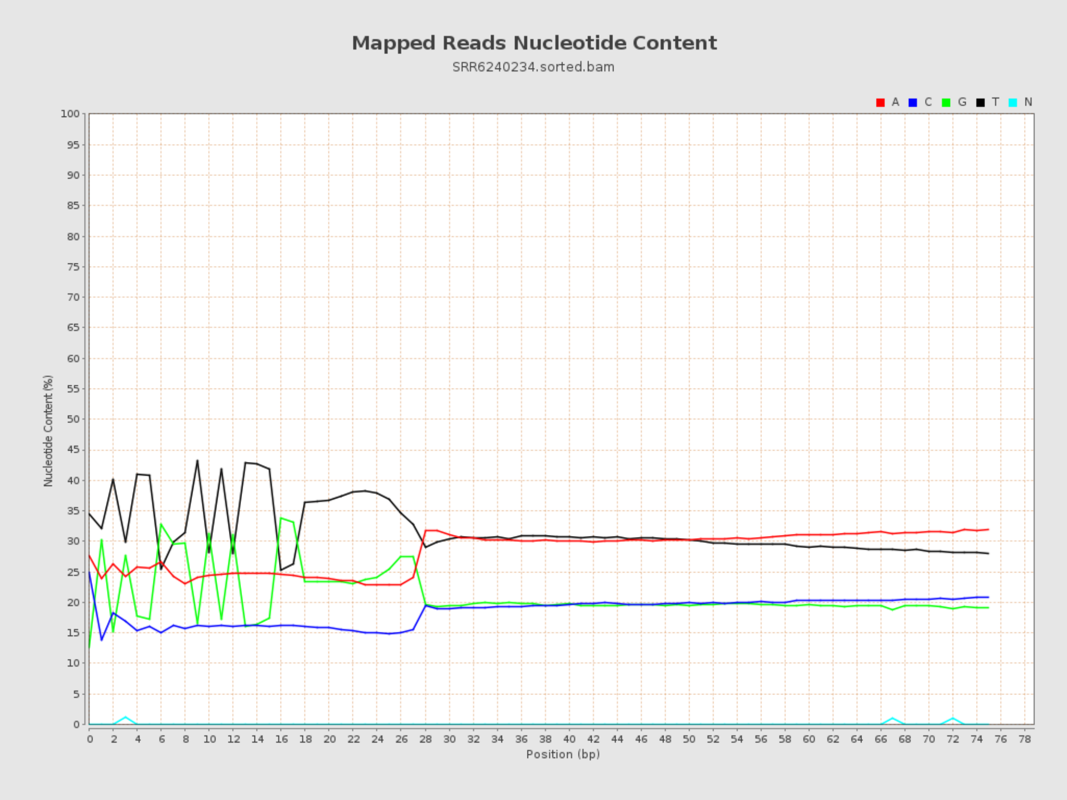
6. Results : Genome Fraction Coverage



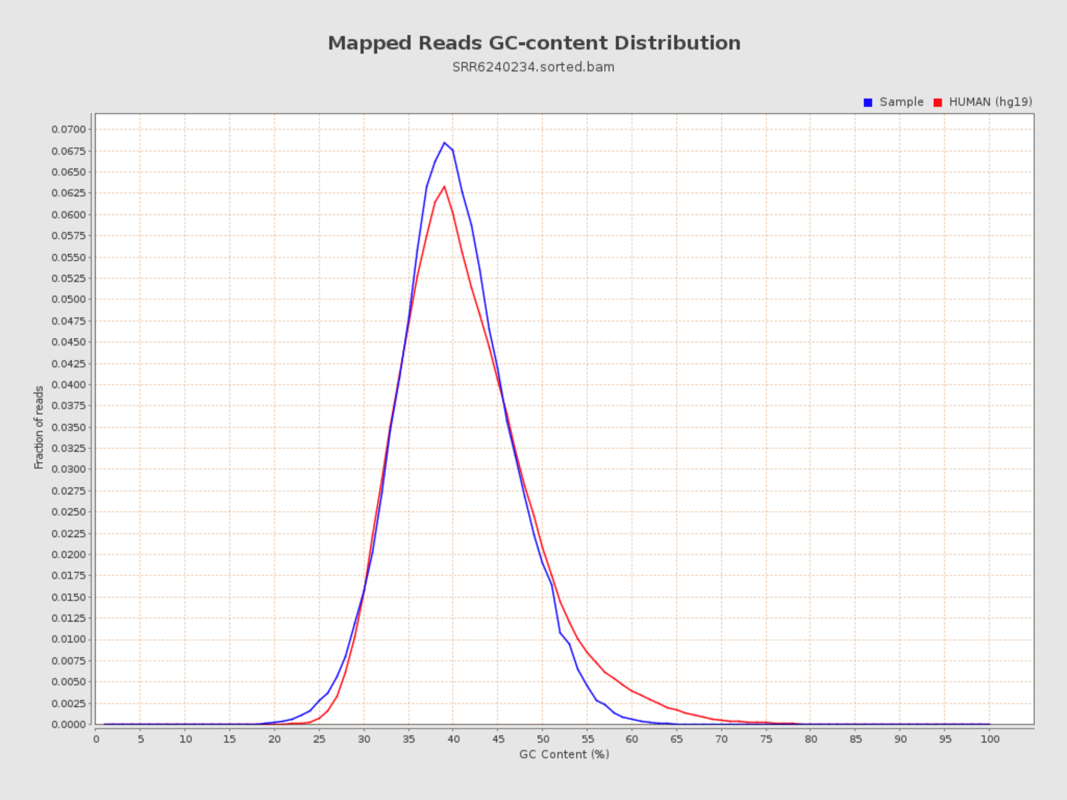
7. Results : Duplication Rate Histogram



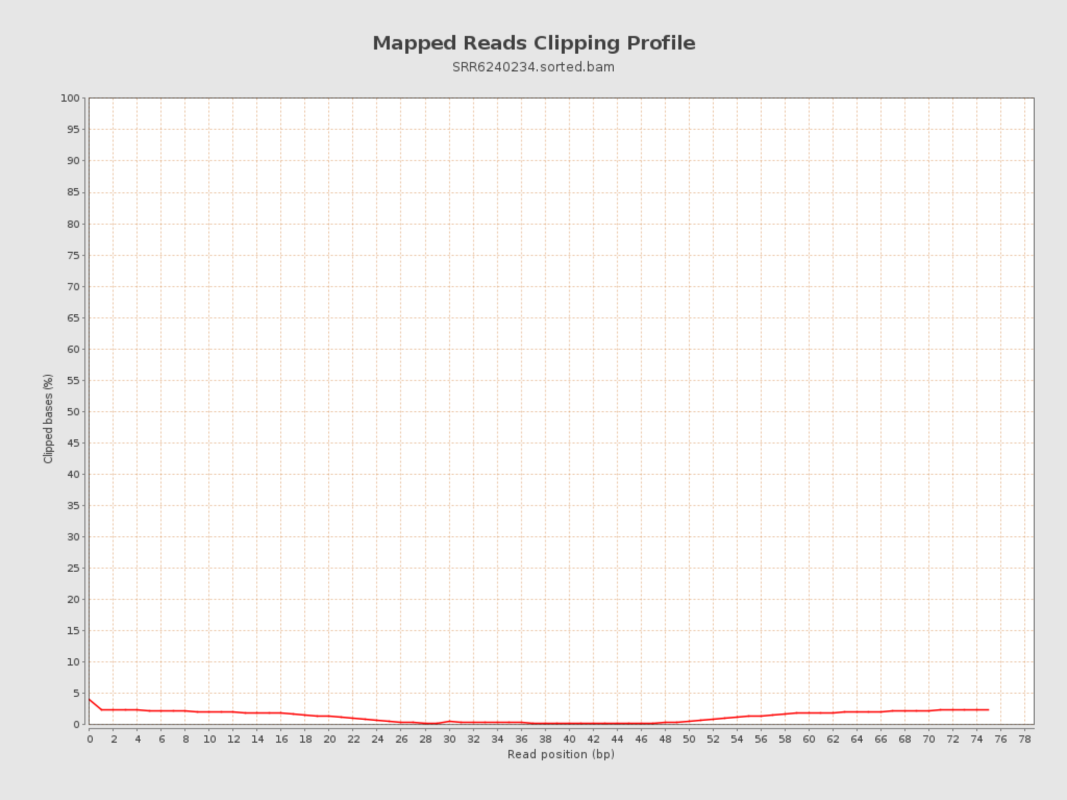
8. Results : Mapped Reads Nucleotide Content



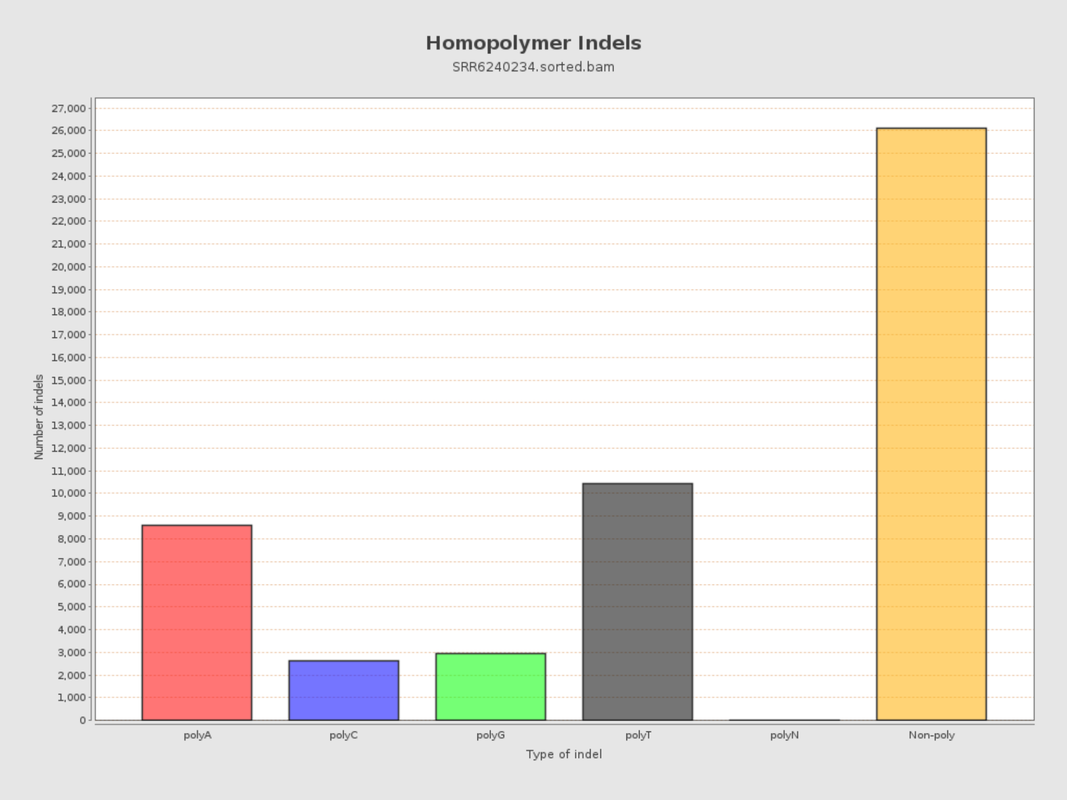
9. Results : Mapped Reads GC-content Distribution



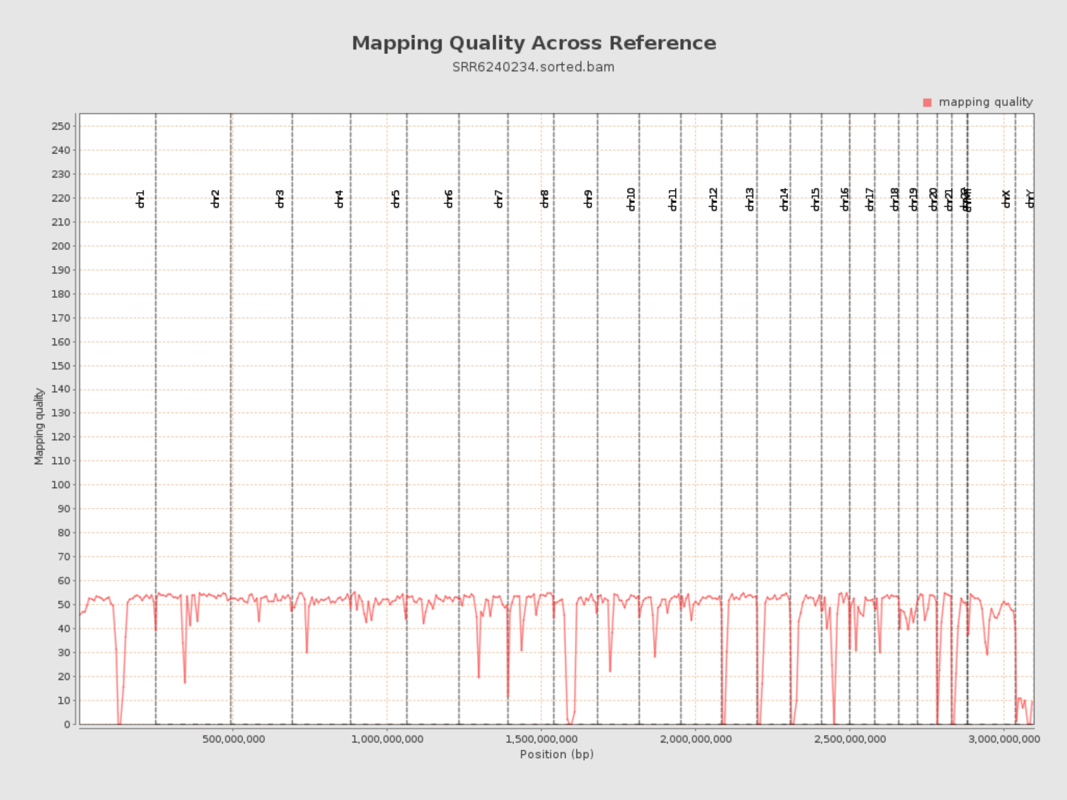
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram