Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:34:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240039.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_SRR6240039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240039.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:34:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,451,896
Mapped reads	1,871,568 / 76.33%
Unmapped reads	580,328 / 23.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,193 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	163,380 / 6.66%
Duplication rate	7.18%
Clipped reads	1,068,912 / 43.6%

2.2. ACGT Content

Number/percentage of A's	32,716,989 / 27.6%
Number/percentage of C's	21,167,871 / 17.86%
Number/percentage of T's	38,021,665 / 32.08%
Number/percentage of G's	26,536,265 / 22.39%
Number/percentage of N's	84,498 / 0.07%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3506

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

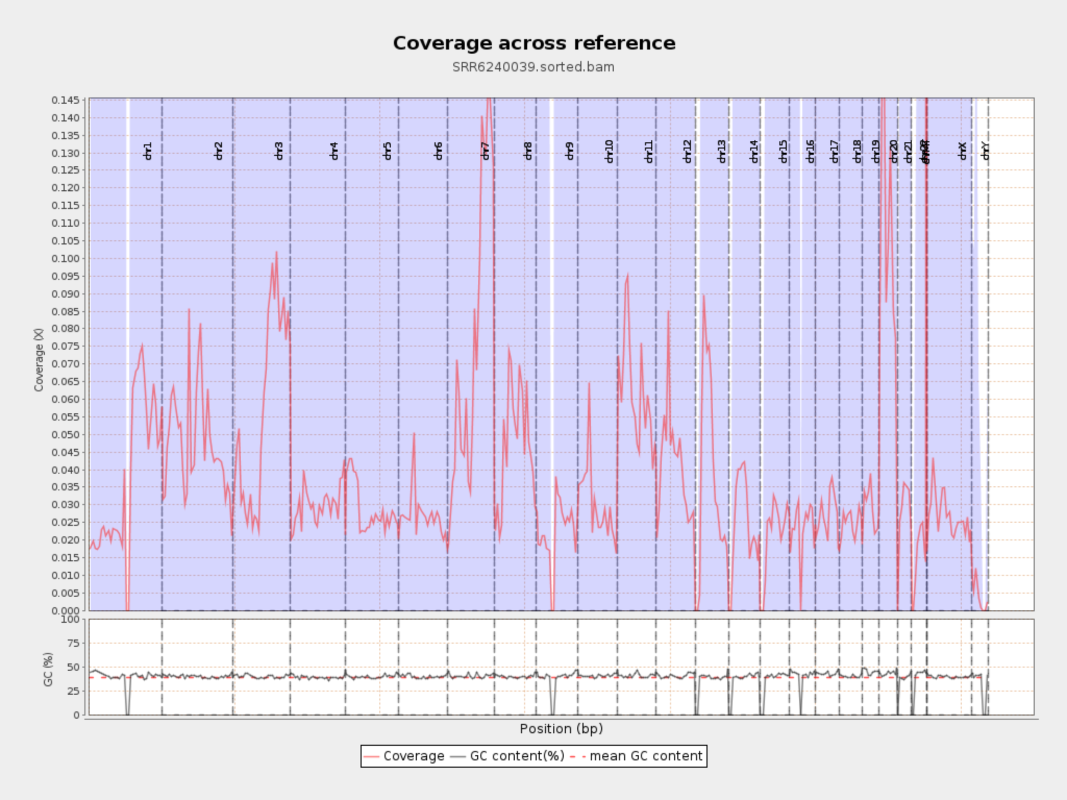
General error rate	0.9%
Mismatches	1,048,218
Insertions	7,730
Mapped reads with at least one insertion	0.41%
Deletions	32,362
Mapped reads with at least one deletion	1.71%
Homopolymer indels	48.07%

2.6. Chromosome stats

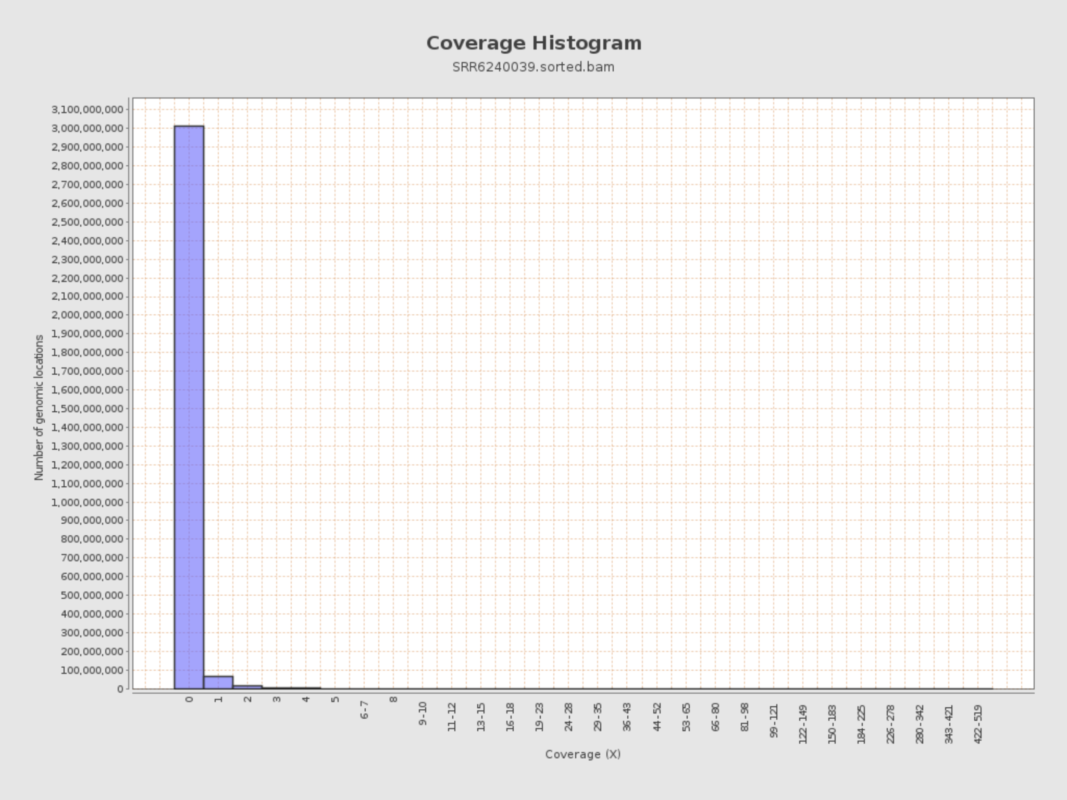
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9261005	0.0372	0.4489
chr2	243199373	11725857	0.0482	0.5395
chr3	198022430	11306241	0.0571	0.3195
chr4	191154276	5738461	0.03	0.2354
chr5	180915260	5241100	0.029	0.2271
chr6	171115067	4641834	0.0271	0.2723
chr7	159138663	12364679	0.0777	0.5632

chr8	146364022	6940798	0.0474	0.388
chr9	141213431	3087565	0.0219	0.3323
chr10	135534747	4138638	0.0305	0.3692
chr11	135006516	8371427	0.062	0.4001
chr12	133851895	5448279	0.0407	0.2741
chr13	115169878	4270502	0.0371	0.2546
chr14	107349540	2637390	0.0246	0.214
chr15	102531392	2186799	0.0213	0.203
chr16	90354753	2091394	0.0231	0.2083
chr17	81195210	2221264	0.0274	0.2552
chr18	78077248	1934350	0.0248	0.3685
chr19	59128983	1748408	0.0296	0.3166
chr20	63025520	6735186	0.1069	0.4407
chr21	48129895	1347939	0.028	0.2276
chr22	51304566	748637	0.0146	0.1546
chrMT	16571	17940	1.0826	1.512
chrX	155270560	4152872	0.0267	0.2366
chrY	59373566	223759	0.0038	0.0864

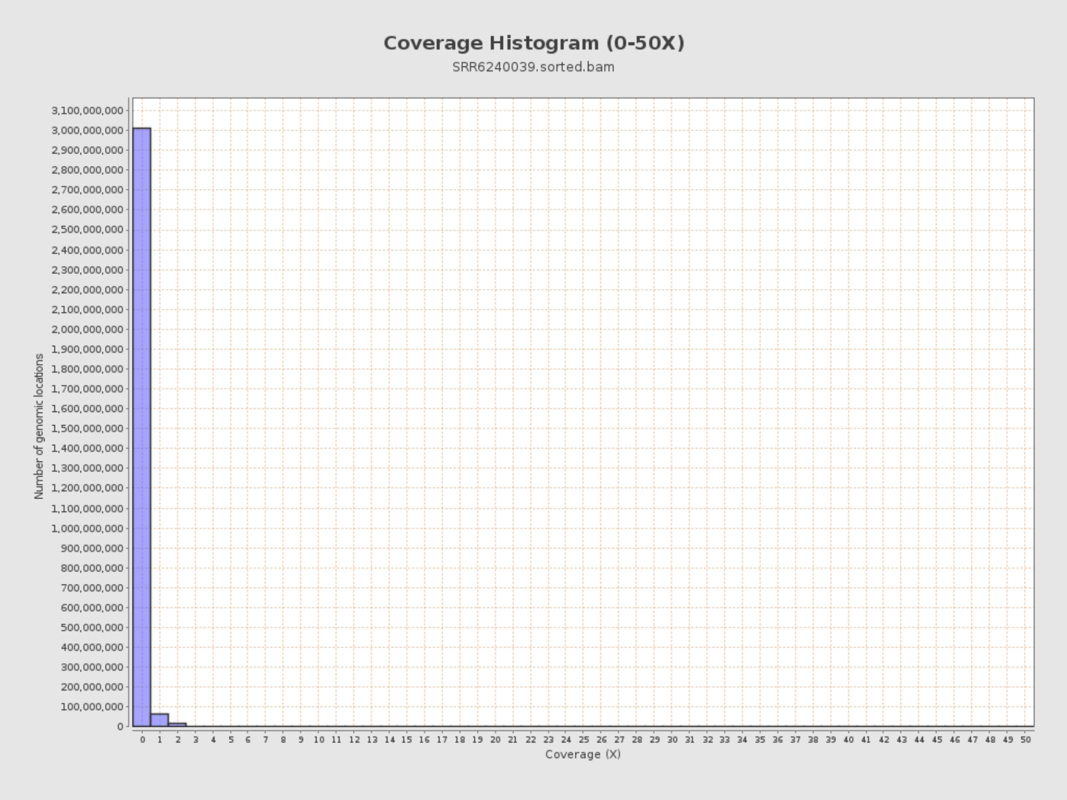
3. Results : Coverage across reference



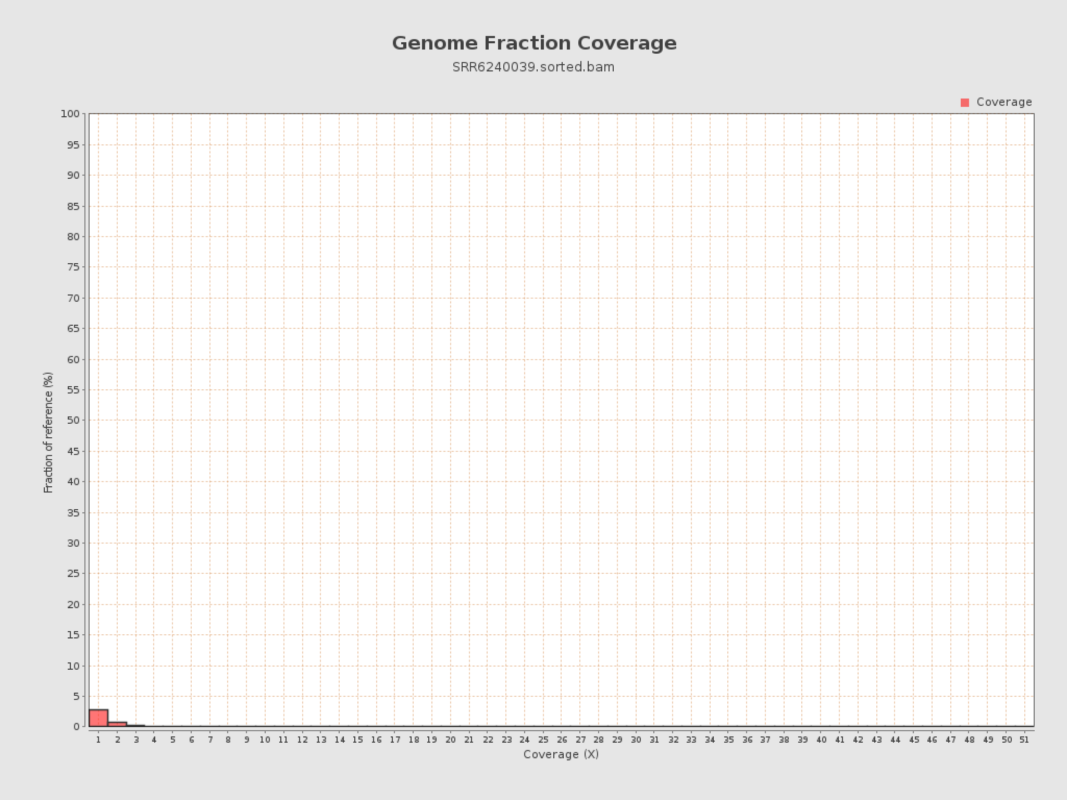
4. Results : Coverage Histogram



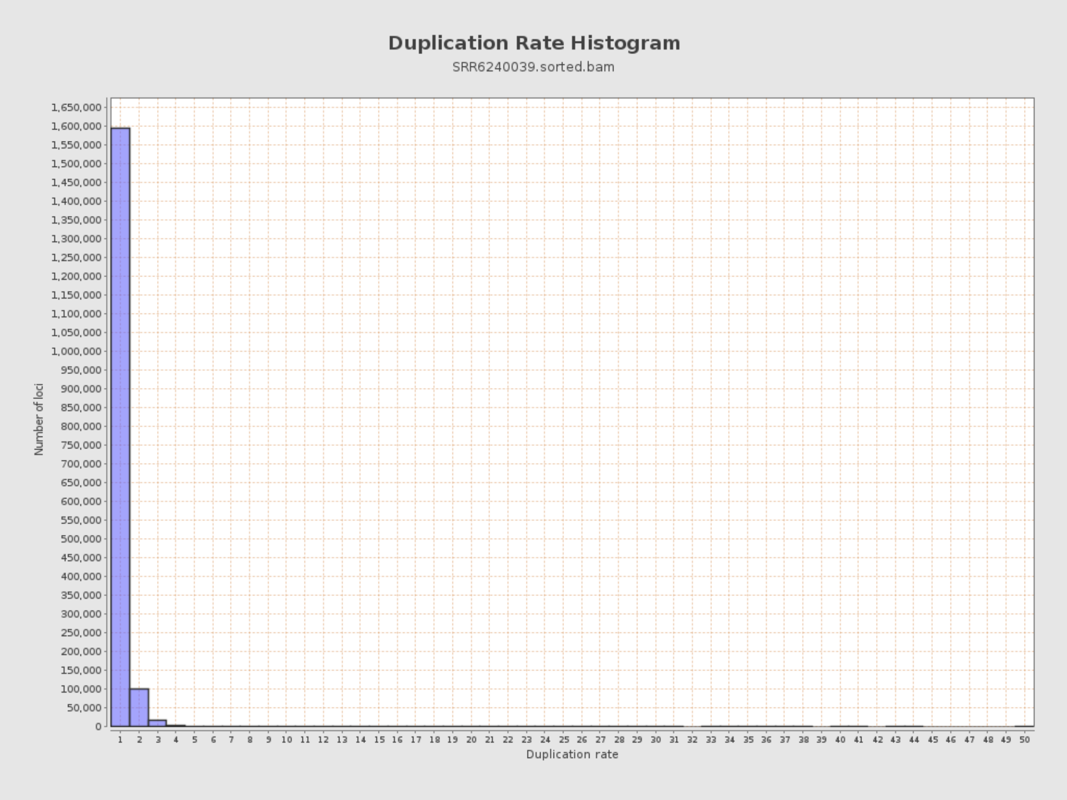
5. Results : Coverage Histogram (0-50X)



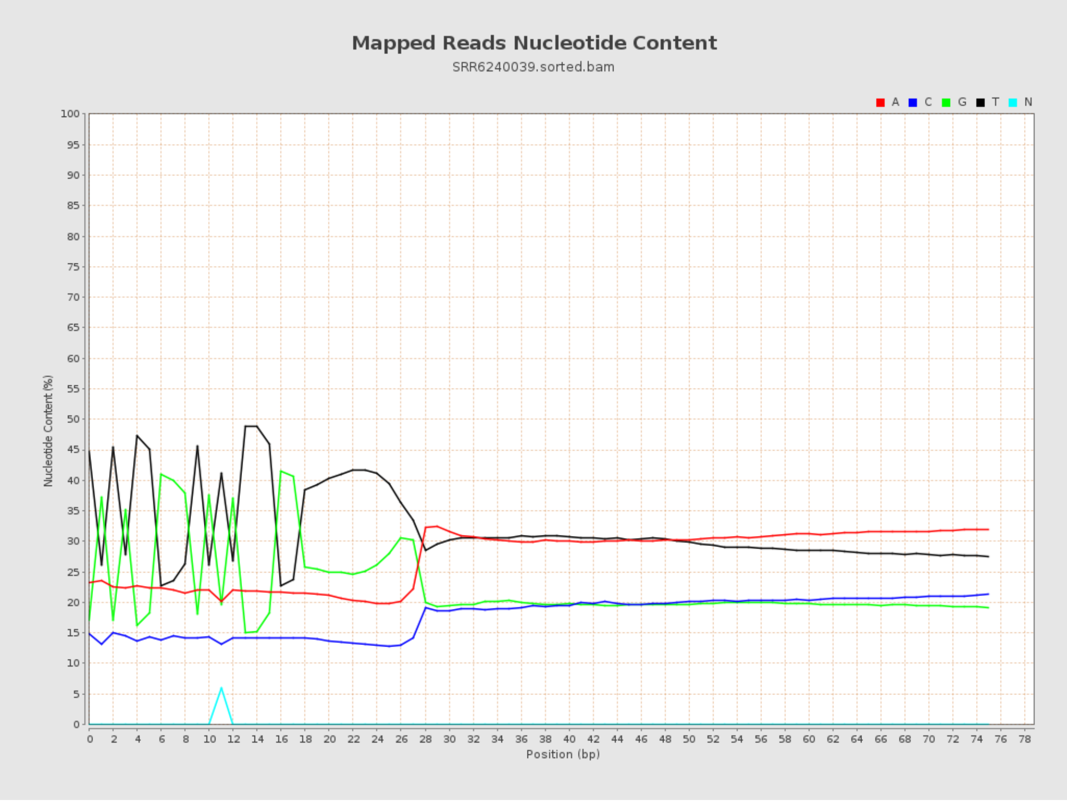
6. Results : Genome Fraction Coverage



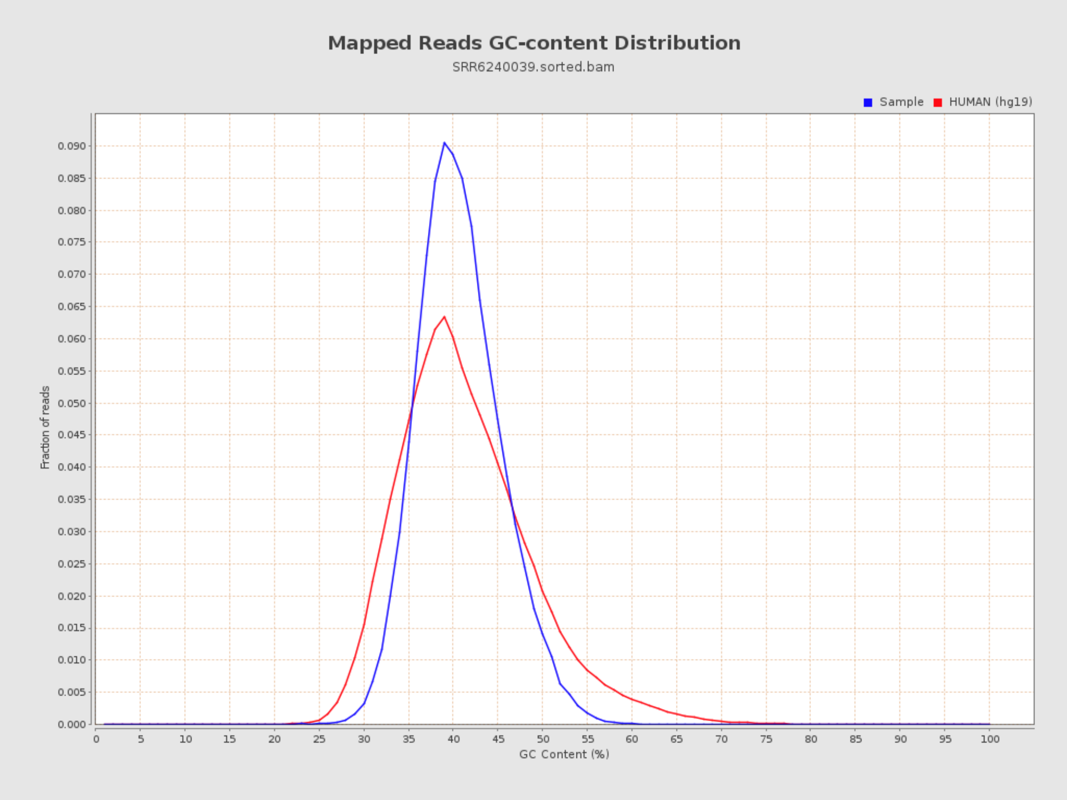
7. Results : Duplication Rate Histogram



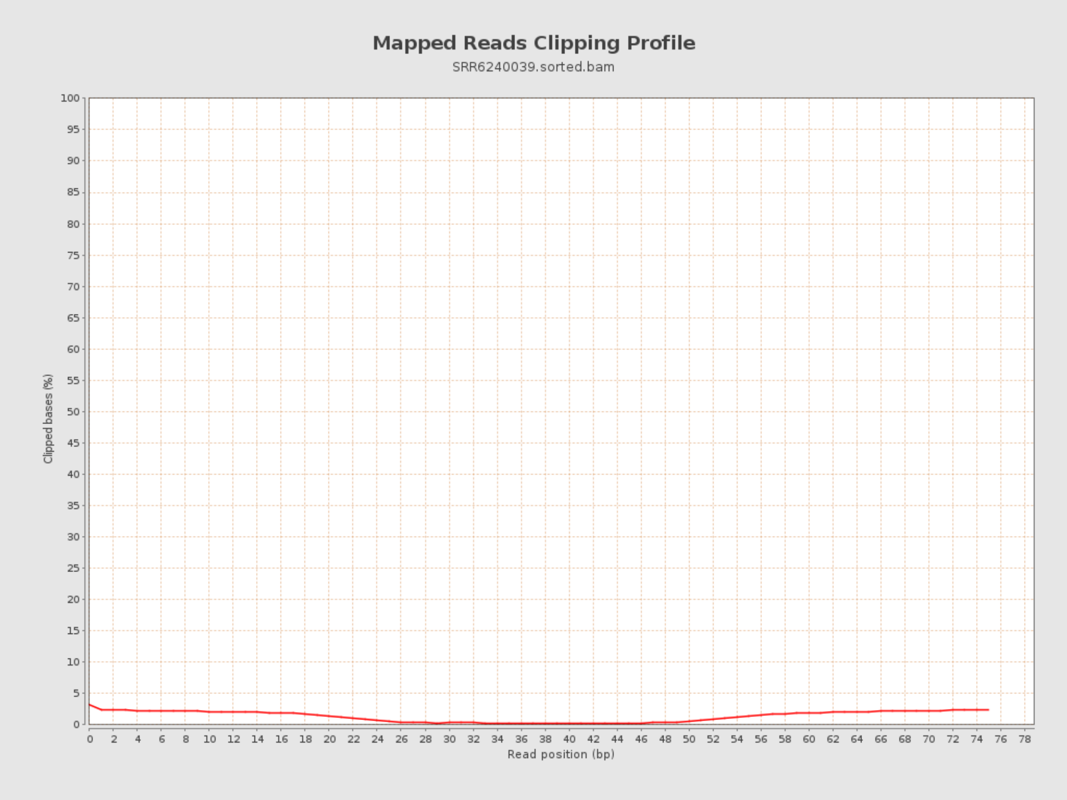
8. Results : Mapped Reads Nucleotide Content



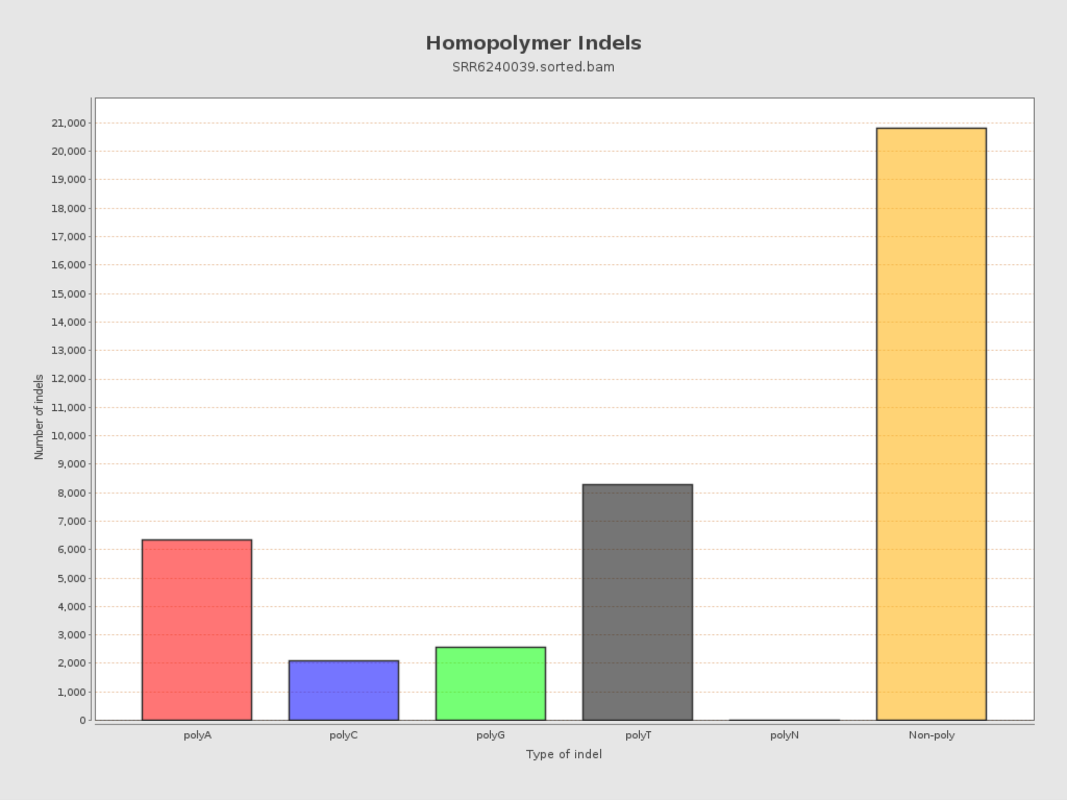
9. Results : Mapped Reads GC-content Distribution



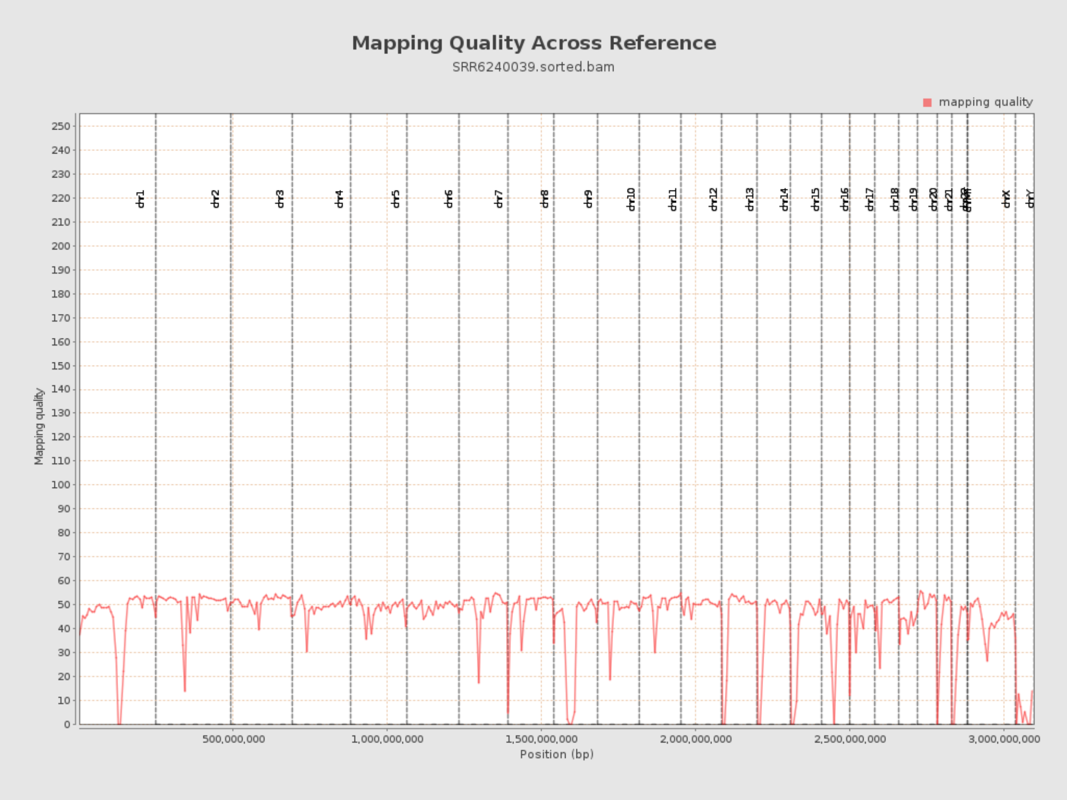
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram