Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:55:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240025.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_SRR6240025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240025.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:55:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,858,299
Mapped reads	1,446,656 / 77.85%
Unmapped reads	411,643 / 22.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,598 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	217,492 / 11.7%
Duplication rate	12.13%
Clipped reads	997,251 / 53.66%

2.2. ACGT Content

Number/percentage of A's	23,623,559 / 26.94%
Number/percentage of C's	15,276,832 / 17.42%
Number/percentage of T's	28,707,963 / 32.74%
Number/percentage of G's	20,022,462 / 22.83%
Number/percentage of N's	54,422 / 0.06%
GC Percentage	40.26%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.346

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

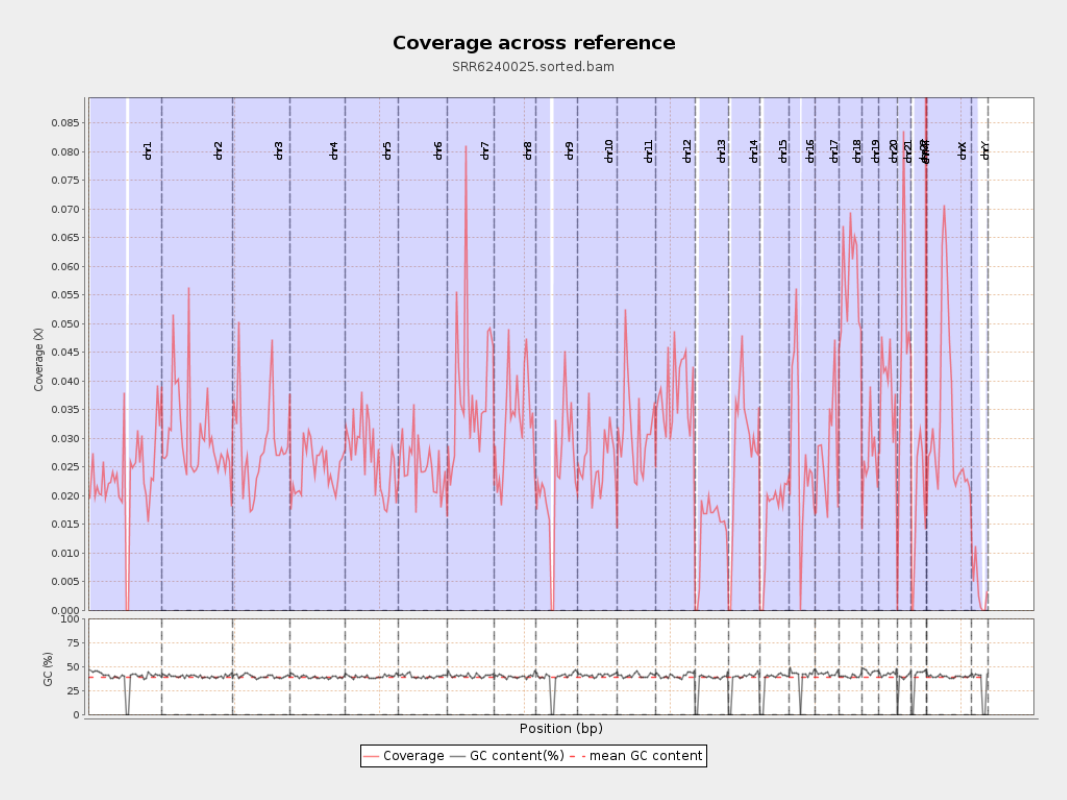
General error rate	1.03%
Mismatches	896,613
Insertions	6,300
Mapped reads with at least one insertion	0.43%
Deletions	30,416
Mapped reads with at least one deletion	2.08%
Homopolymer indels	48.68%

2.6. Chromosome stats

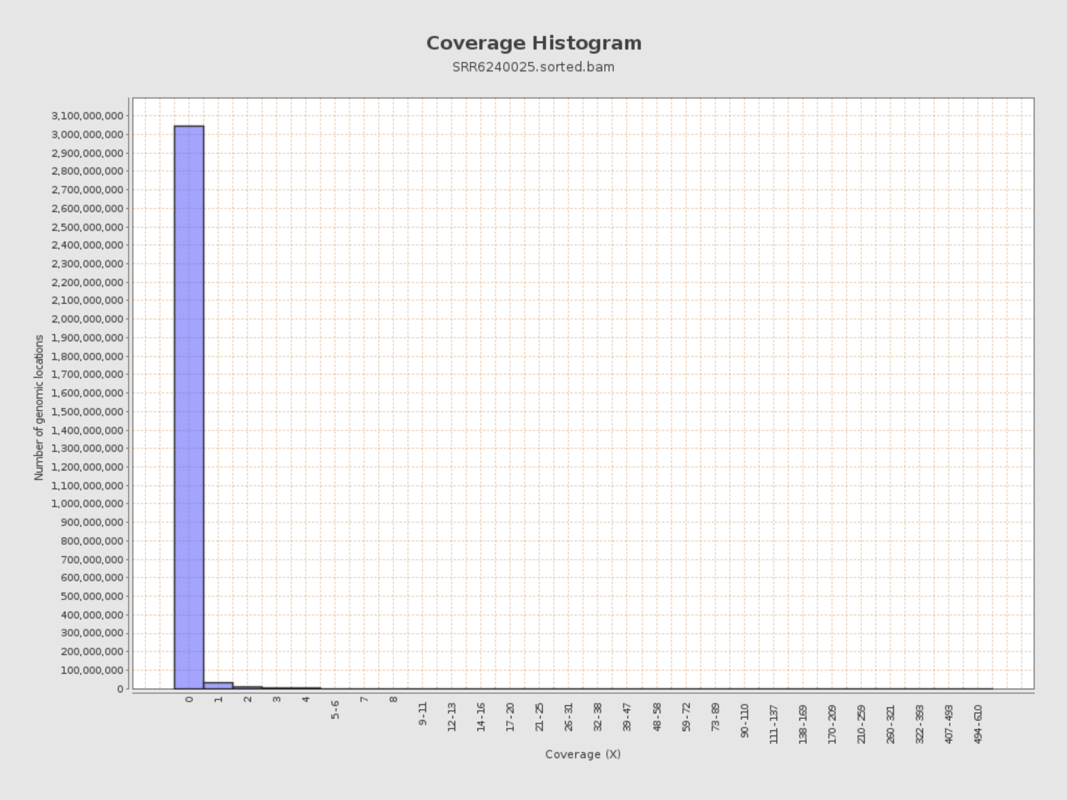
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5750459	0.0231	0.4269
chr2	243199373	7333203	0.0302	0.4006
chr3	198022430	5749658	0.029	0.2583
chr4	191154276	4721752	0.0247	0.2448
chr5	180915260	4833551	0.0267	0.2514
chr6	171115067	4269875	0.025	0.2594
chr7	159138663	6099933	0.0383	0.6741

chr8	146364022	4851212	0.0331	0.4164
chr9	141213431	3330737	0.0236	0.2883
chr10	135534747	3523870	0.026	0.3031
chr11	135006516	4233609	0.0314	0.2999
chr12	133851895	5043364	0.0377	0.2967
chr13	115169878	1612230	0.014	0.1812
chr14	107349540	3015470	0.0281	0.2644
chr15	102531392	1673299	0.0163	0.2012
chr16	90354753	2514368	0.0278	0.2581
chr17	81195210	2206780	0.0272	0.259
chr18	78077248	4520611	0.0579	0.5979
chr19	59128983	1583437	0.0268	0.3653
chr20	63025520	2430269	0.0386	0.3259
chr21	48129895	2174251	0.0452	0.3244
chr22	51304566	920672	0.0179	0.1943
chrMT	16571	80453	4.855	4.7515
chrX	155270560	5048138	0.0325	0.3106
chrY	59373566	215318	0.0036	0.0873

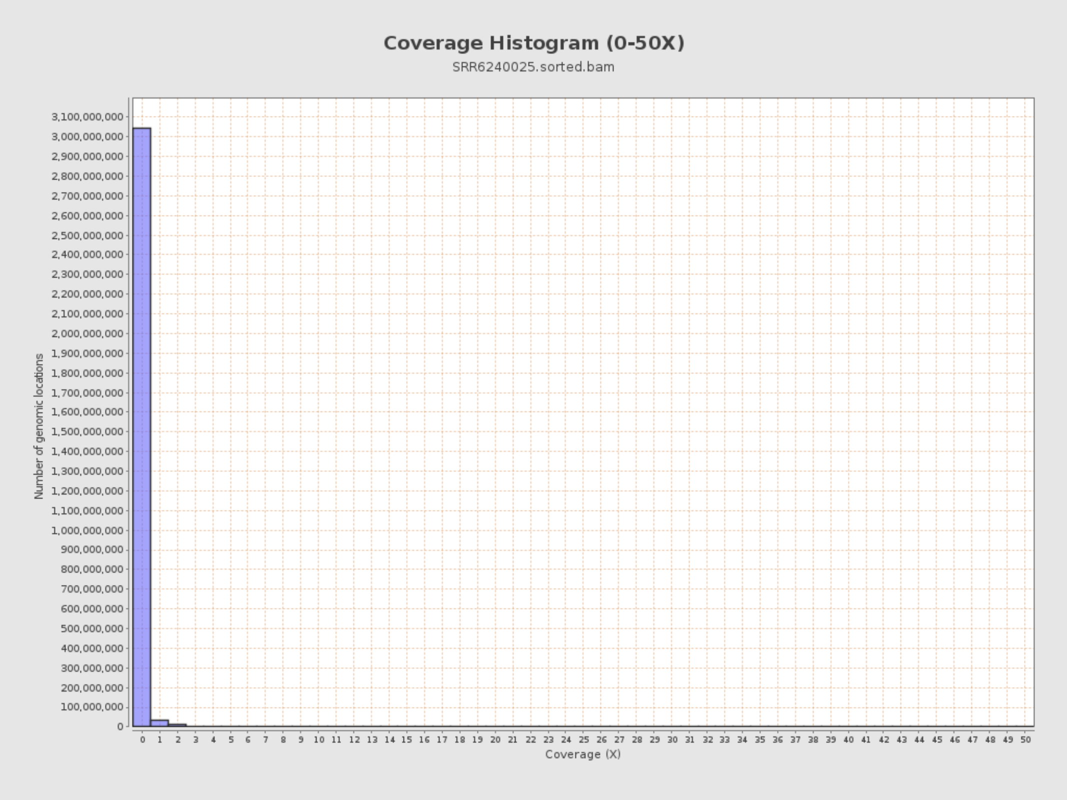
3. Results : Coverage across reference



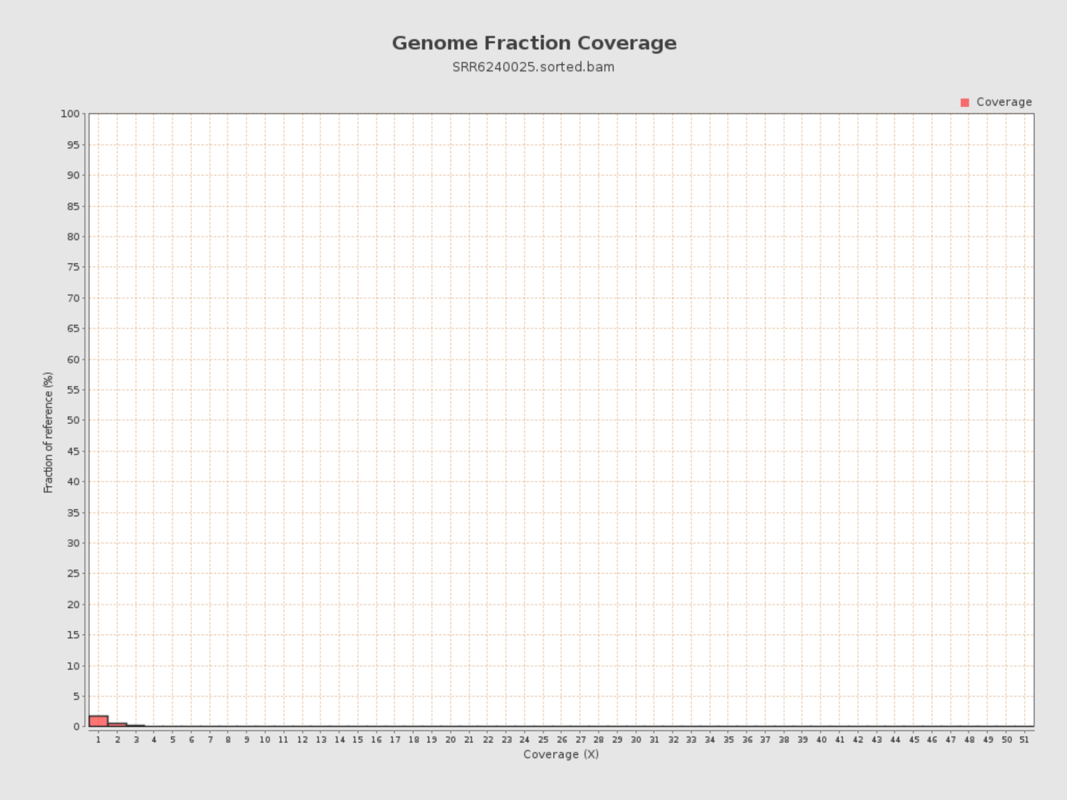
4. Results : Coverage Histogram



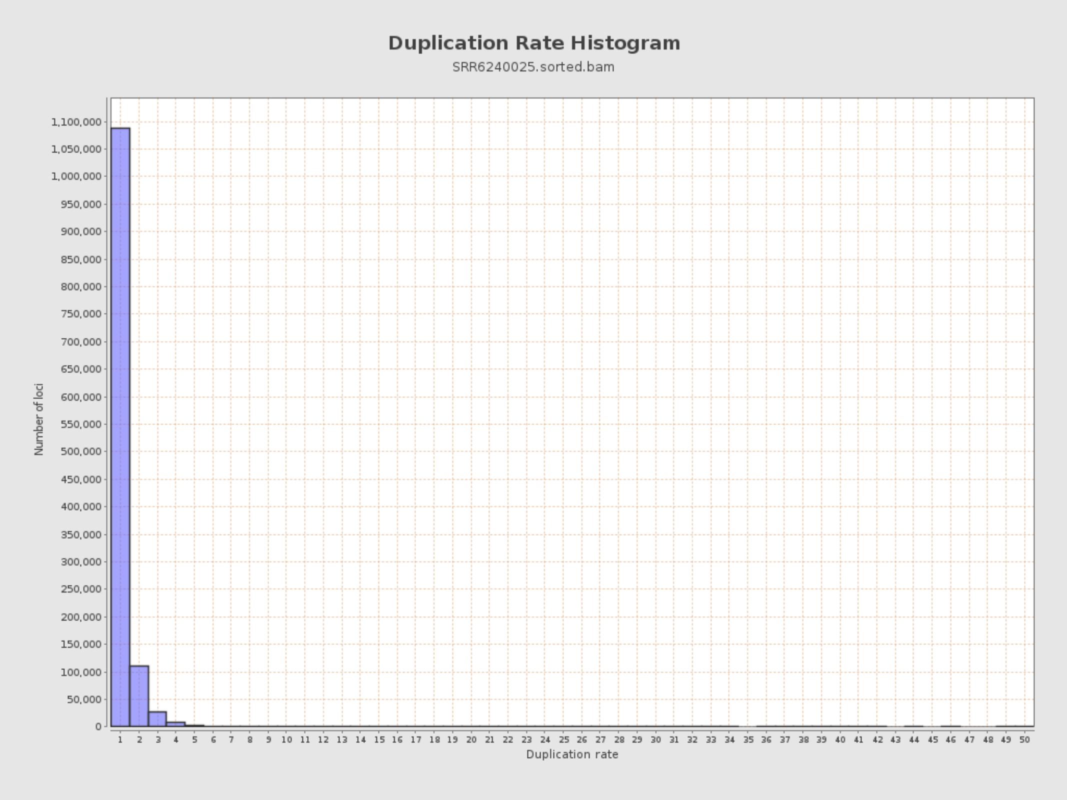
5. Results : Coverage Histogram (0-50X)



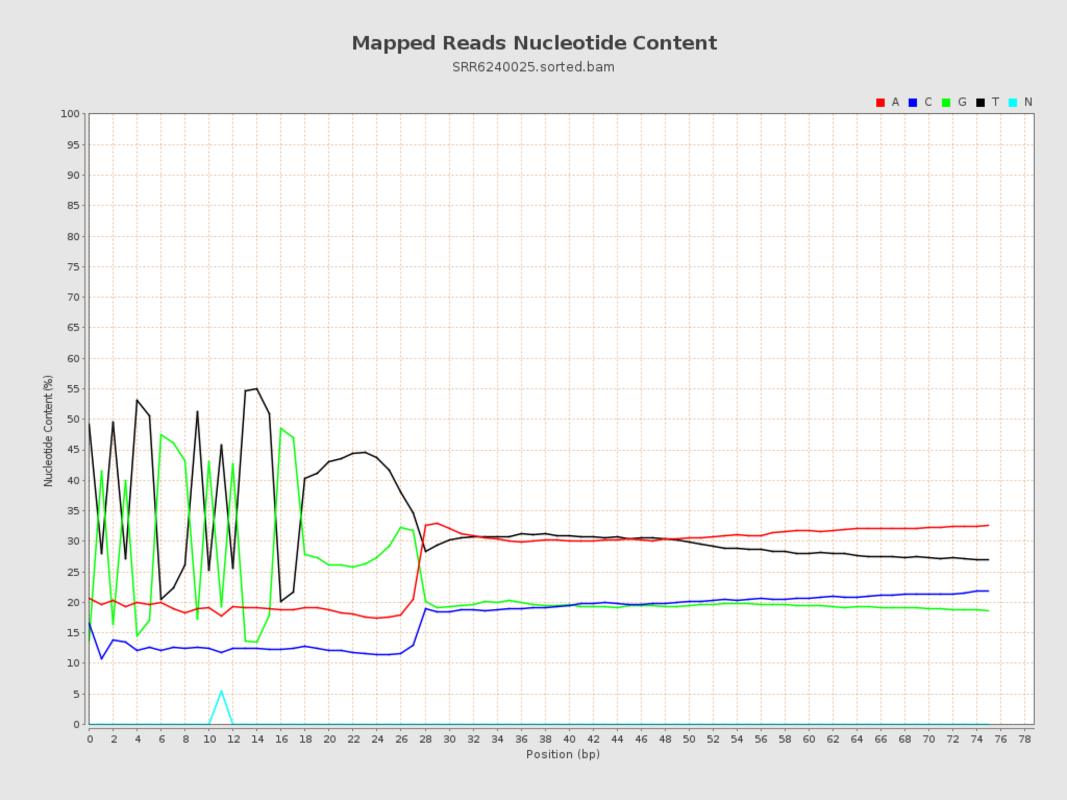
6. Results : Genome Fraction Coverage



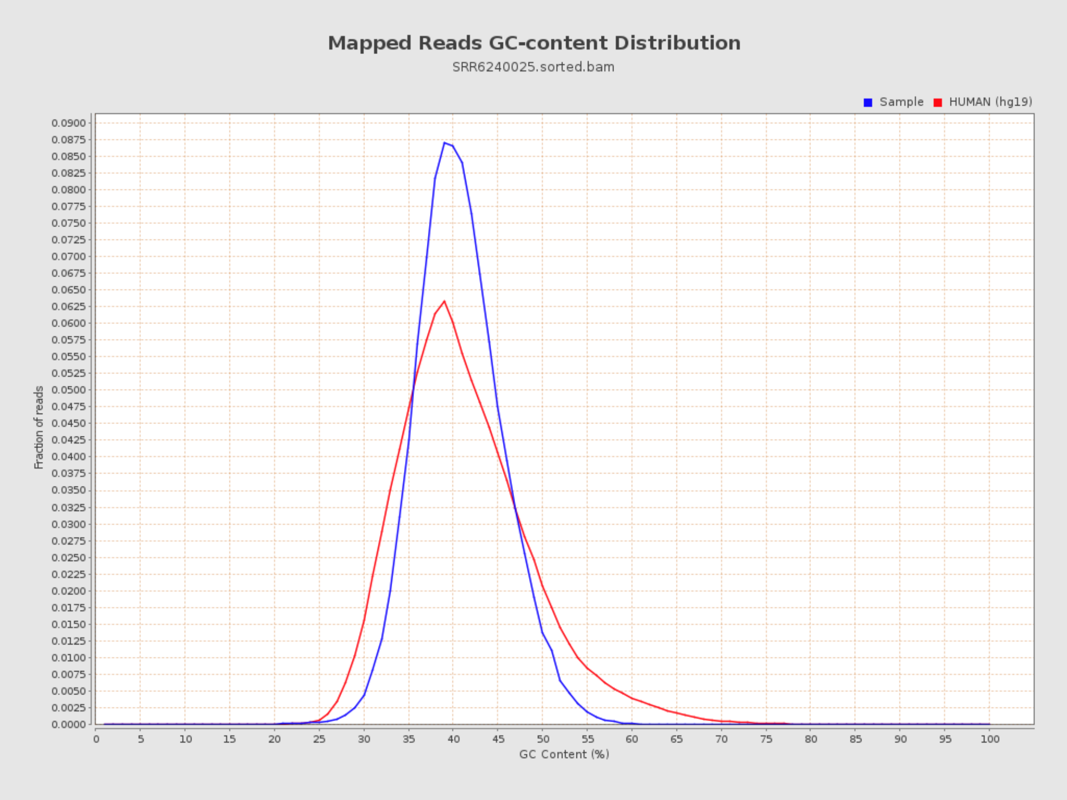
7. Results : Duplication Rate Histogram



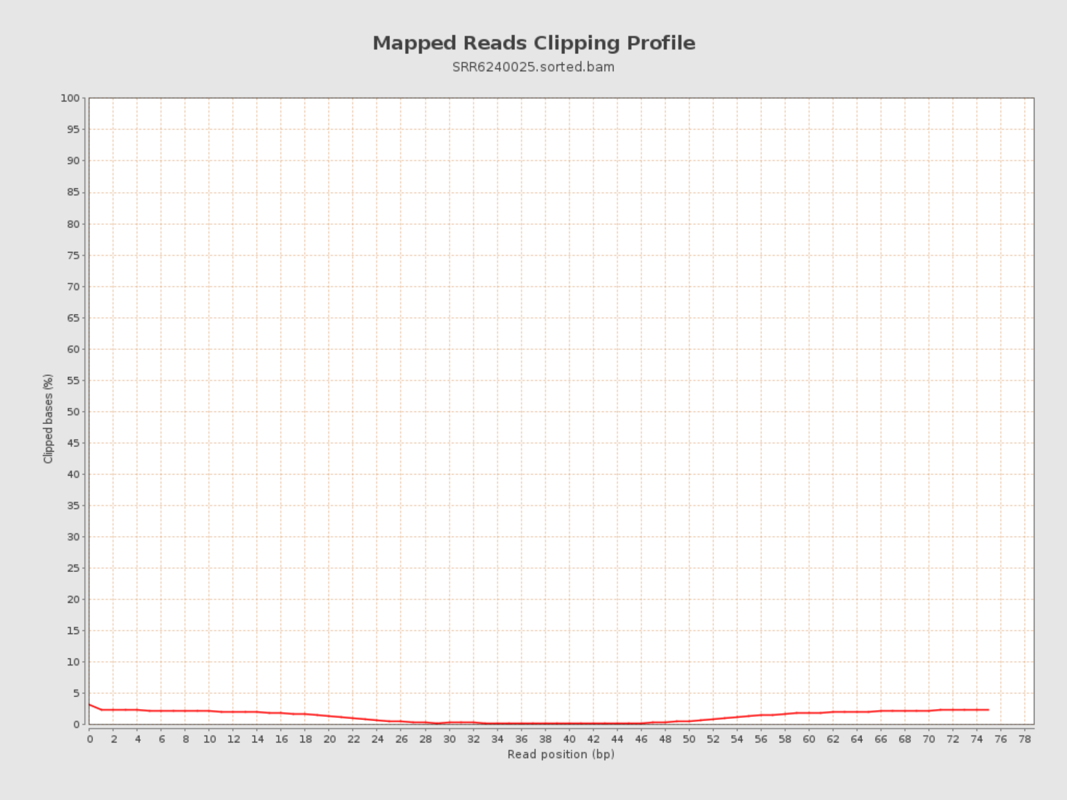
8. Results : Mapped Reads Nucleotide Content



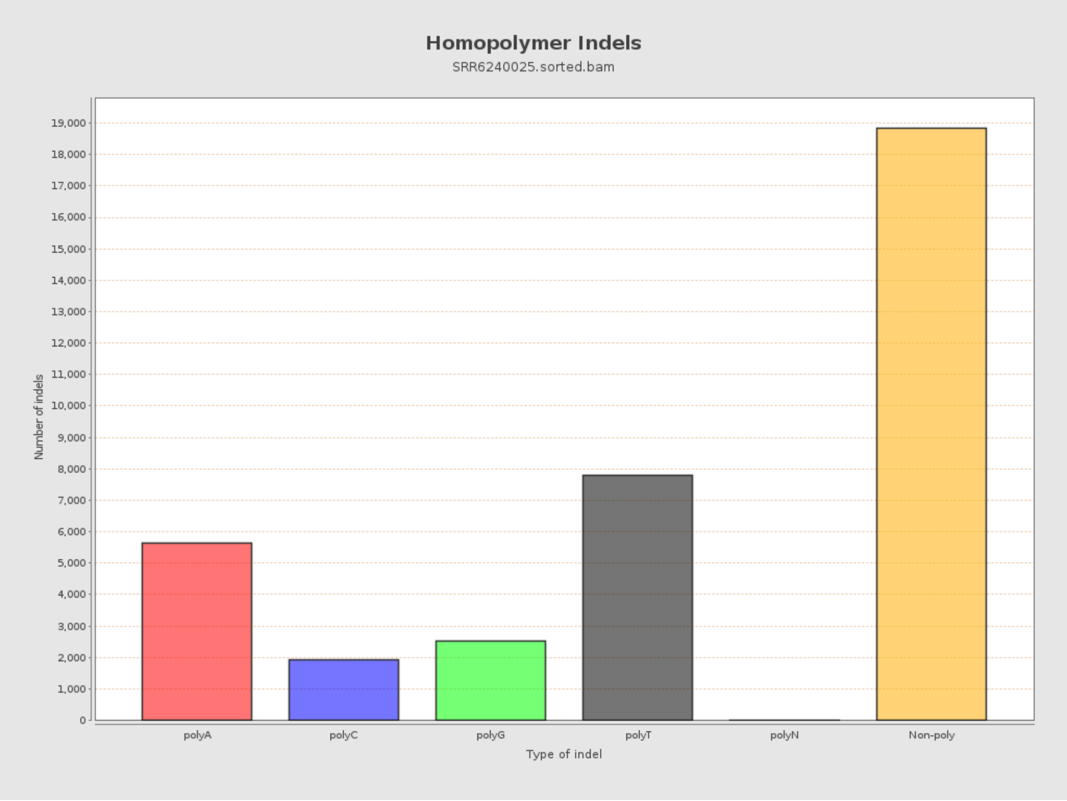
9. Results : Mapped Reads GC-content Distribution



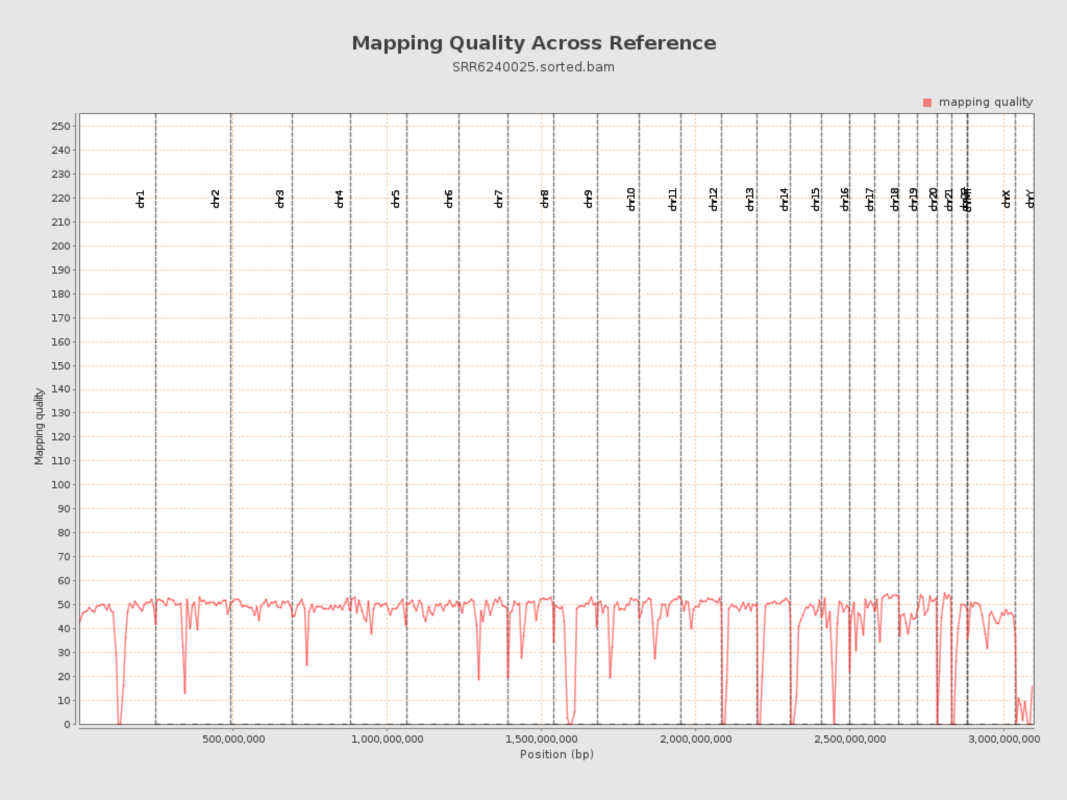
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram