Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:27:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240227.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_SRR6240227 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240227.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:27:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240227.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,500,628
Mapped reads	1,007,013 / 67.11%
Unmapped reads	493,615 / 32.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,169 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	270,406 / 18.02%
Duplication rate	16.95%
Clipped reads	657,618 / 43.82%

2.2. ACGT Content

Number/percentage of A's	16,772,307 / 27.11%
Number/percentage of C's	10,896,172 / 17.61%
Number/percentage of T's	20,173,084 / 32.61%
Number/percentage of G's	14,004,136 / 22.64%
Number/percentage of N's	14,689 / 0.02%
GC Percentage	40.25%

2.3. Coverage

Mean	0.02

Standard Deviation	0.345

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

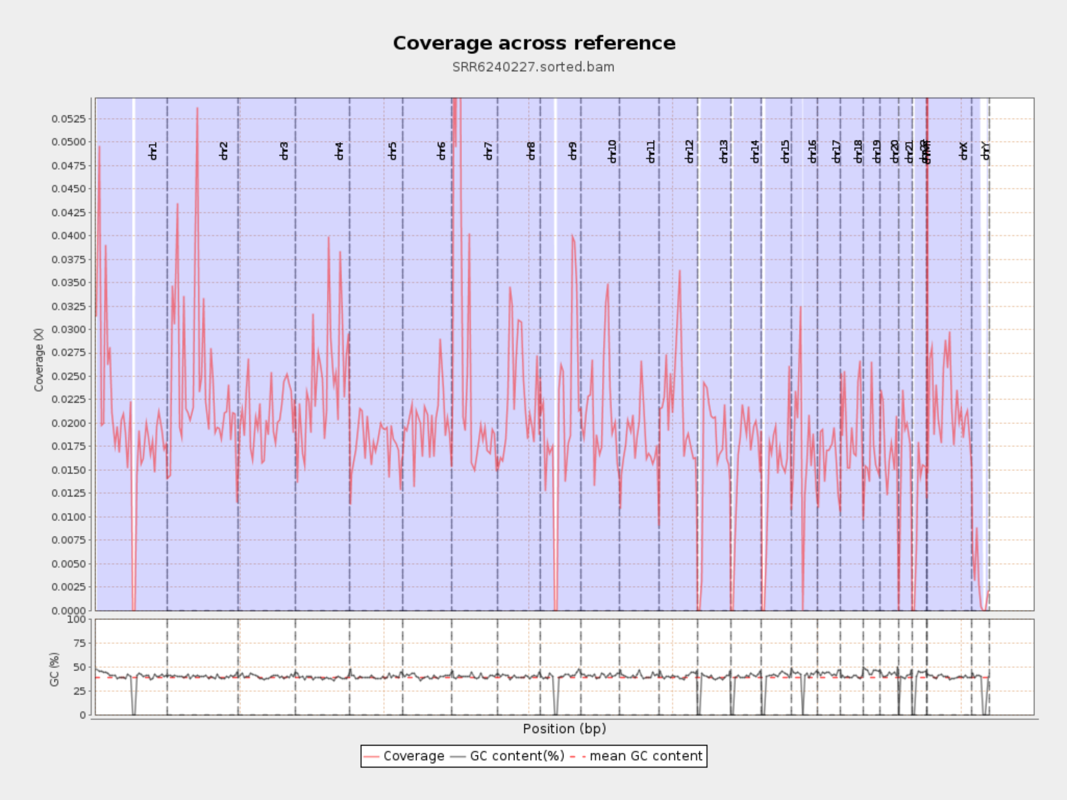
General error rate	0.89%
Mismatches	546,087
Insertions	4,264
Mapped reads with at least one insertion	0.42%
Deletions	17,341
Mapped reads with at least one deletion	1.7%
Homopolymer indels	49.57%

2.6. Chromosome stats

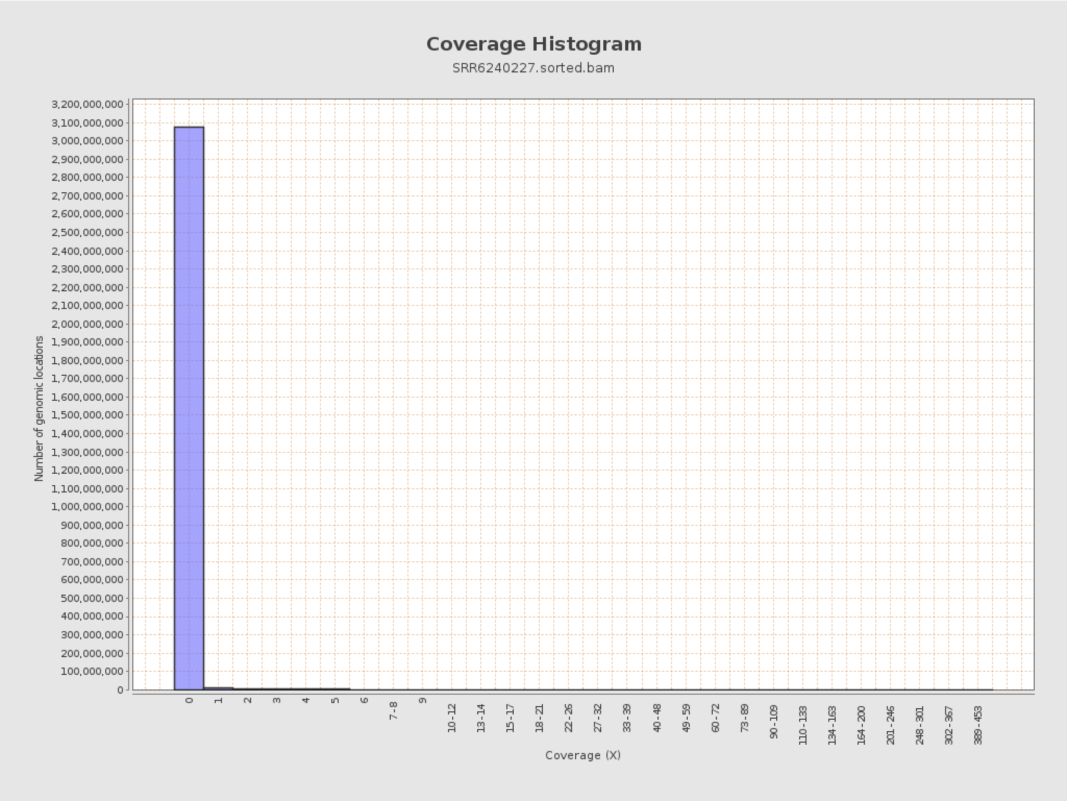
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4946194	0.0198	0.3958
chr2	243199373	5967152	0.0245	0.4051
chr3	198022430	4085091	0.0206	0.3308
chr4	191154276	4698217	0.0246	0.3681
chr5	180915260	3228565	0.0178	0.2962
chr6	171115067	3408177	0.0199	0.3304
chr7	159138663	4474202	0.0281	0.4456

chr8	146364022	3355316	0.0229	0.427
chr9	141213431	2905315	0.0206	0.336
chr10	135534747	2926648	0.0216	0.3408
chr11	135006516	2449940	0.0181	0.3228
chr12	133851895	2974976	0.0222	0.3286
chr13	115169878	1874276	0.0163	0.2876
chr14	107349540	1689901	0.0157	0.287
chr15	102531392	1477440	0.0144	0.2621
chr16	90354753	1508284	0.0167	0.278
chr17	81195210	1302782	0.016	0.2691
chr18	78077248	1553057	0.0199	0.4142
chr19	59128983	981053	0.0166	0.3097
chr20	63025520	1093090	0.0173	0.2938
chr21	48129895	782456	0.0163	0.282
chr22	51304566	563241	0.011	0.2276
chrMT	16571	27555	1.6628	2.8865
chrX	155270560	3450176	0.0222	0.3467
chrY	59373566	166951	0.0028	0.1048

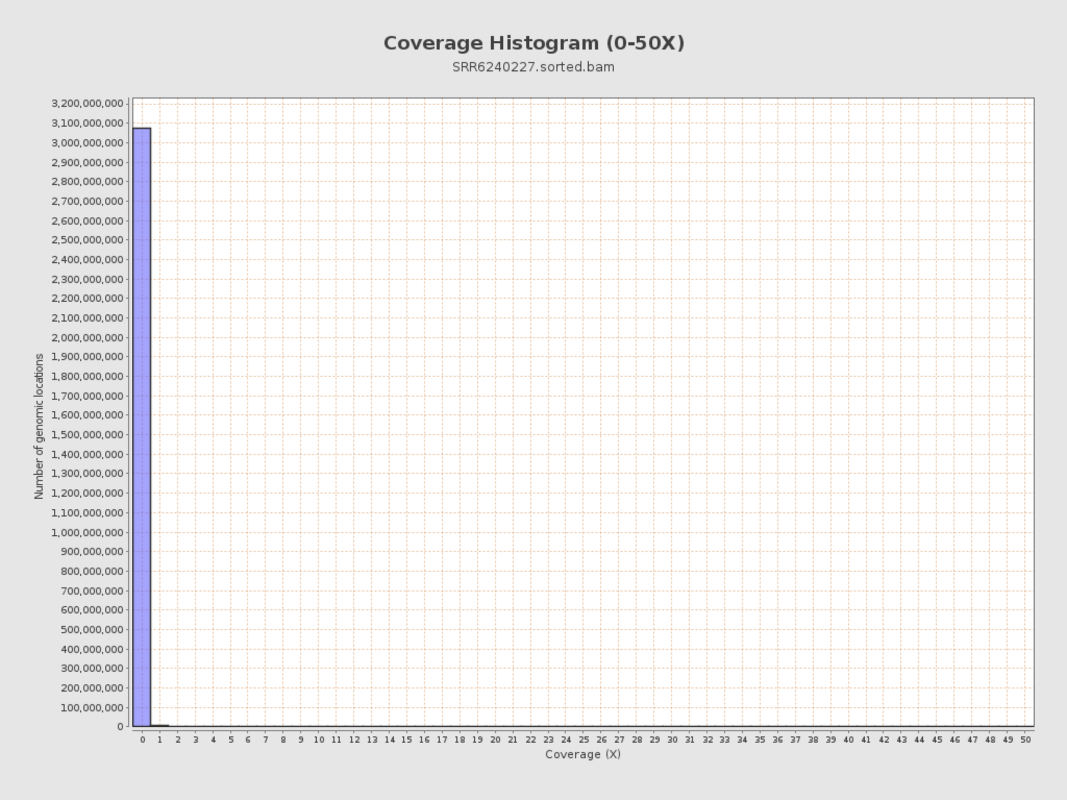
3. Results : Coverage across reference



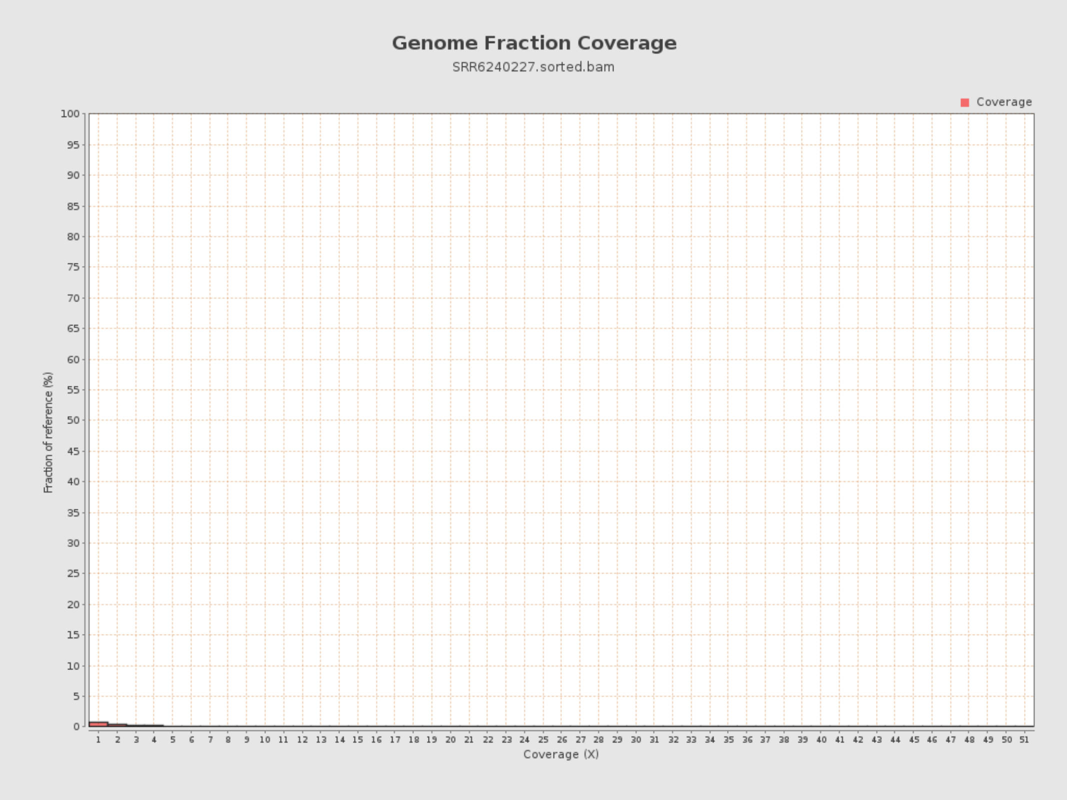
4. Results : Coverage Histogram



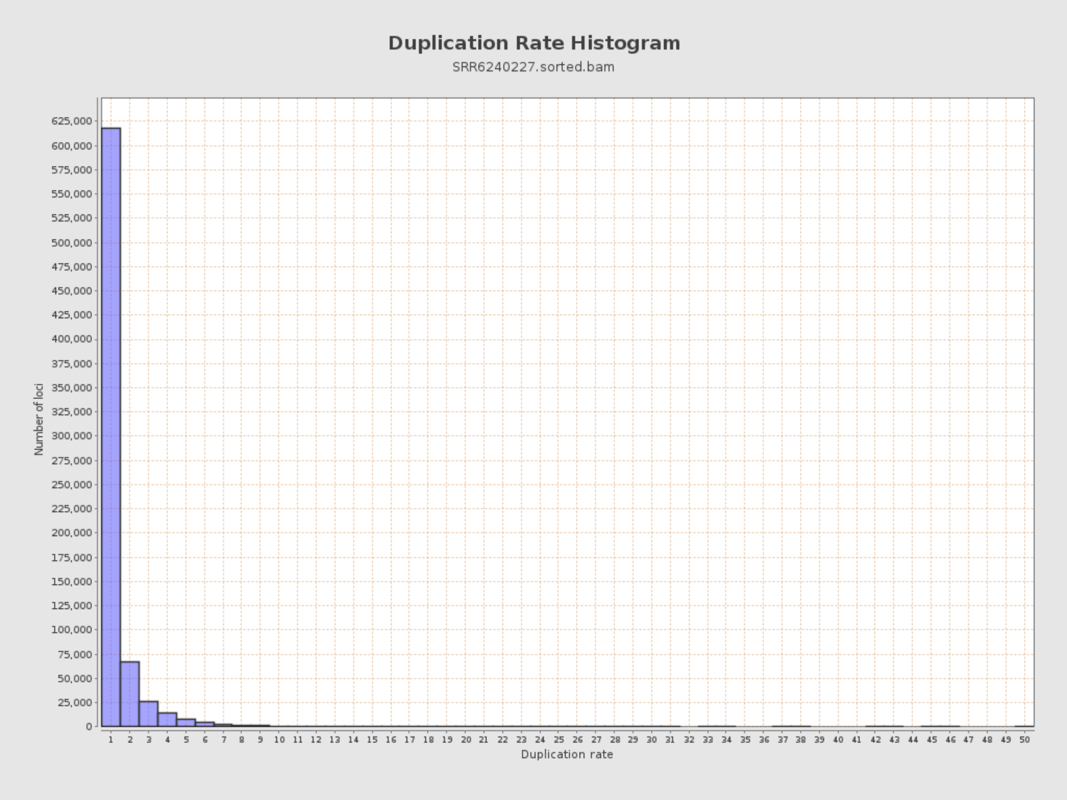
5. Results : Coverage Histogram (0-50X)



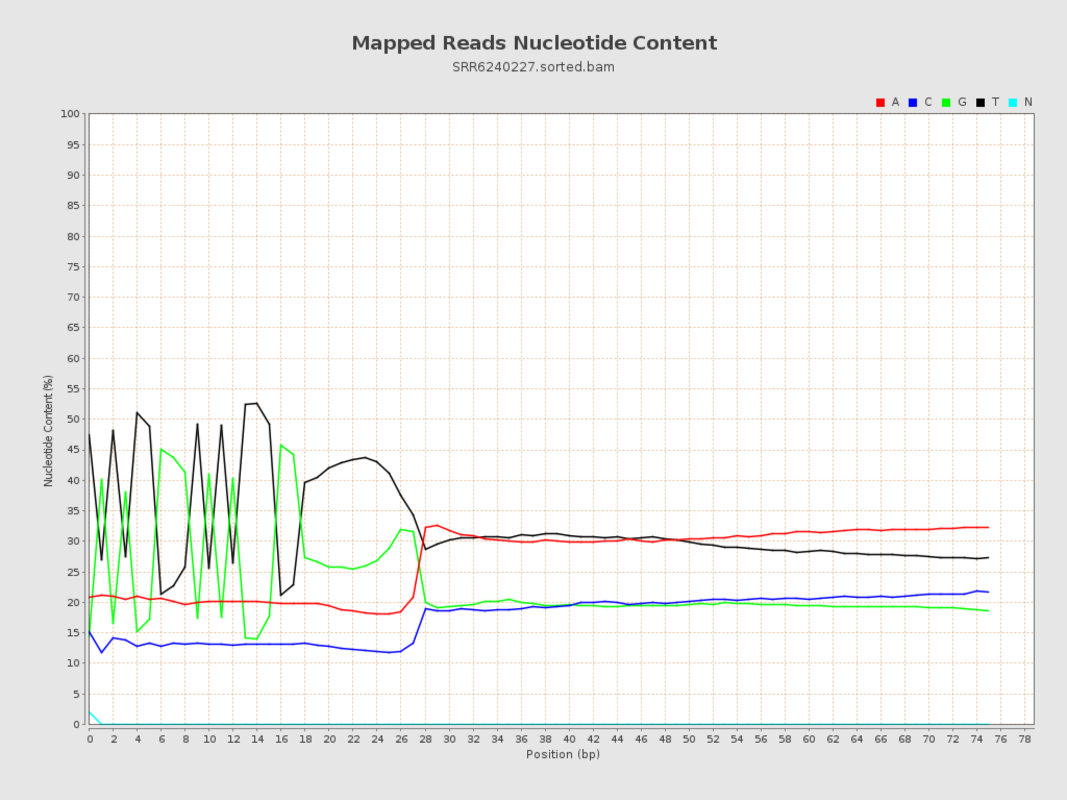
6. Results : Genome Fraction Coverage



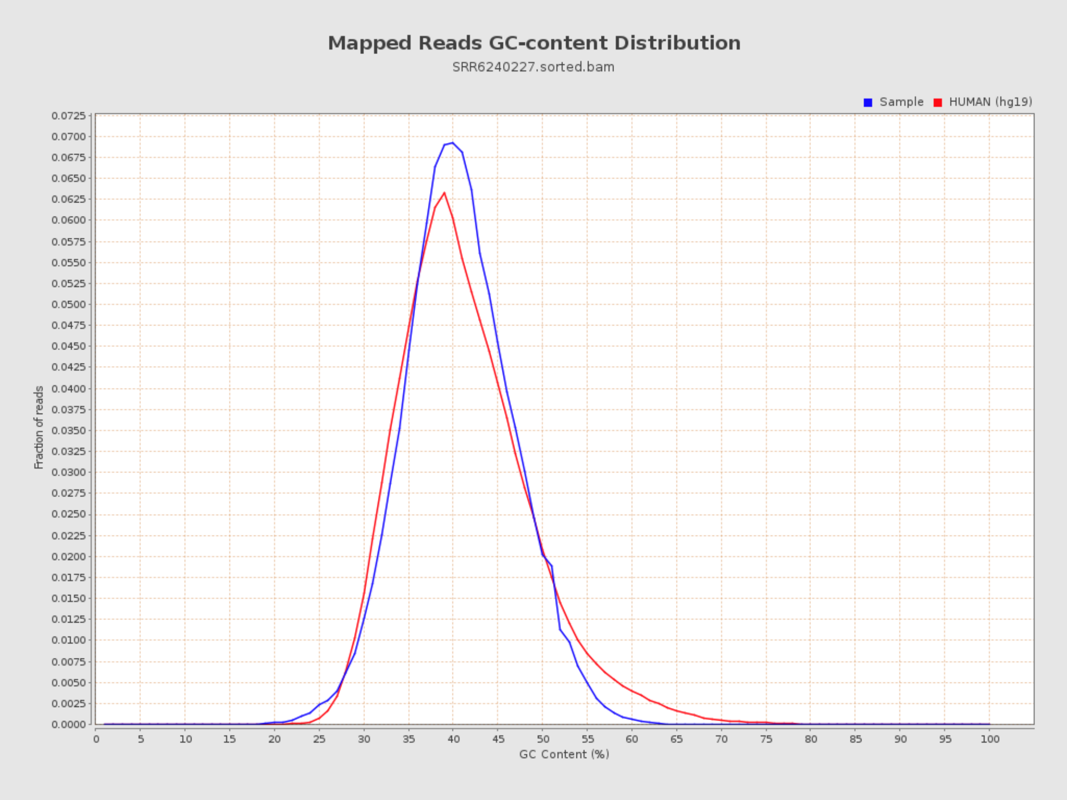
7. Results : Duplication Rate Histogram



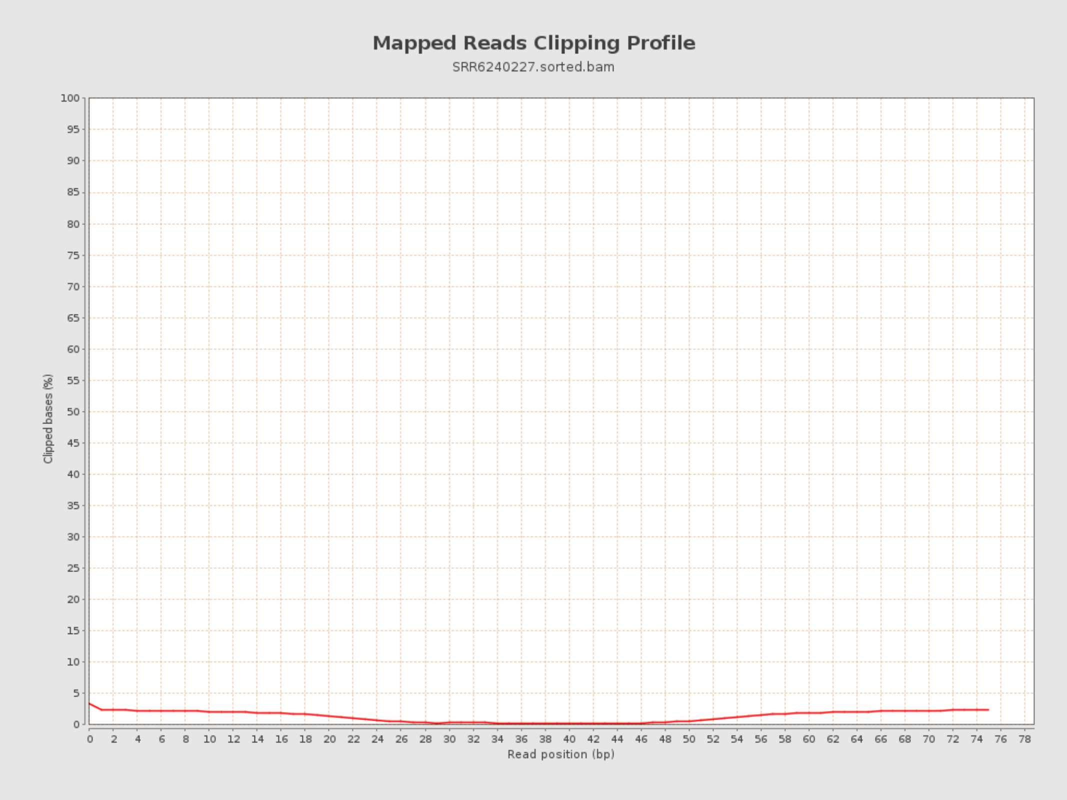
8. Results : Mapped Reads Nucleotide Content



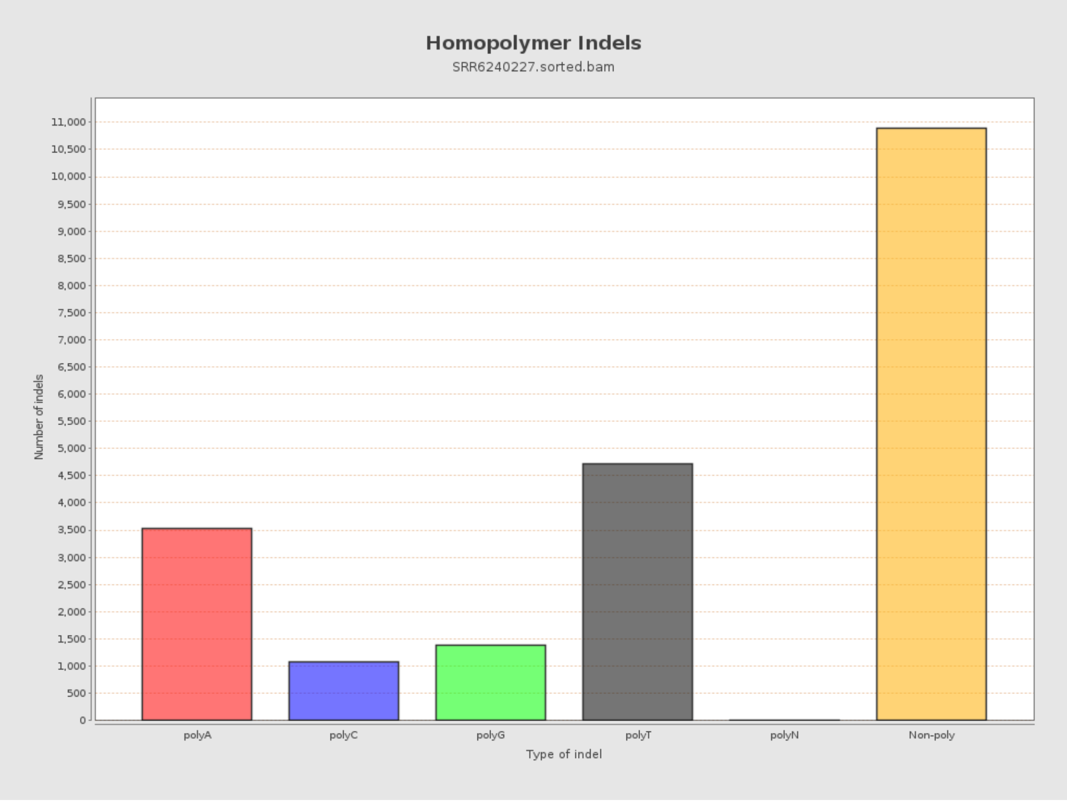
9. Results : Mapped Reads GC-content Distribution



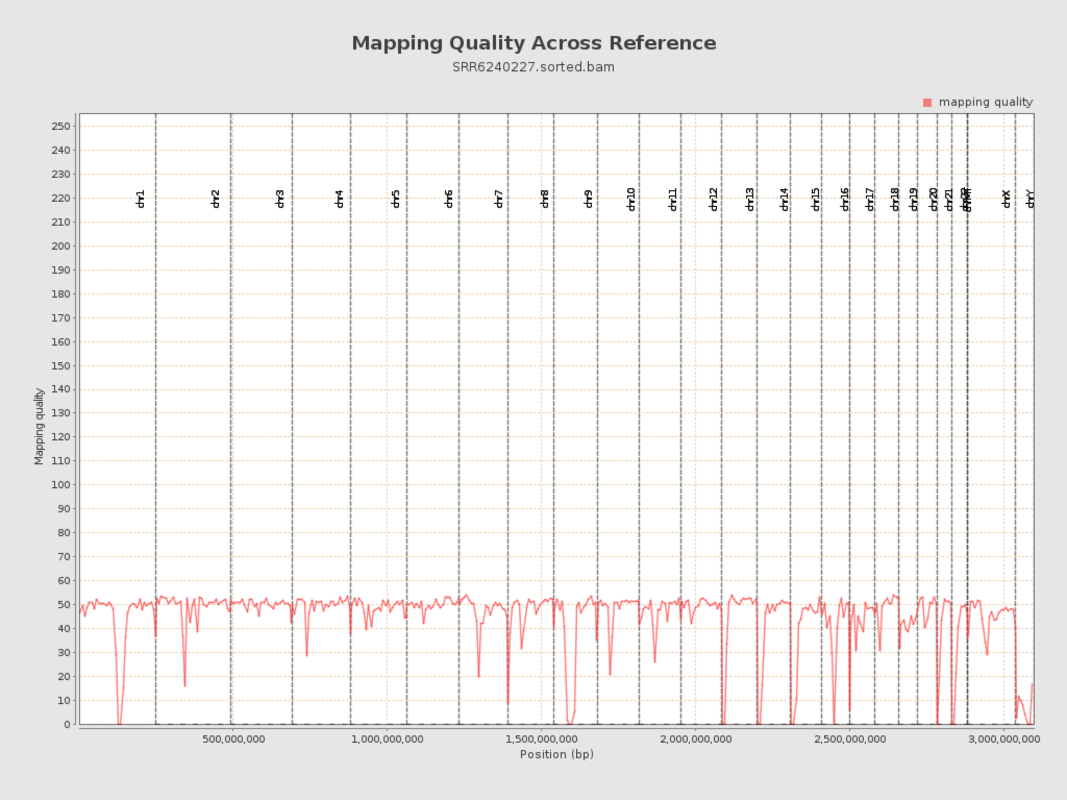
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram