Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:34:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240230.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_SRR6240230 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240230.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:34:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,459,360
Mapped reads	1,137,955 / 77.98%
Unmapped reads	321,405 / 22.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,458 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	119,533 / 8.19%
Duplication rate	8.38%
Clipped reads	552,318 / 37.85%

2.2. ACGT Content

Number/percentage of A's	21,322,520 / 28.34%
Number/percentage of C's	14,020,224 / 18.63%
Number/percentage of T's	23,753,296 / 31.57%
Number/percentage of G's	16,082,599 / 21.38%
Number/percentage of N's	58,134 / 0.08%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2973

2.4. Mapping Quality

Mean Mapping Quality	46.74

2.5. Mismatches and indels

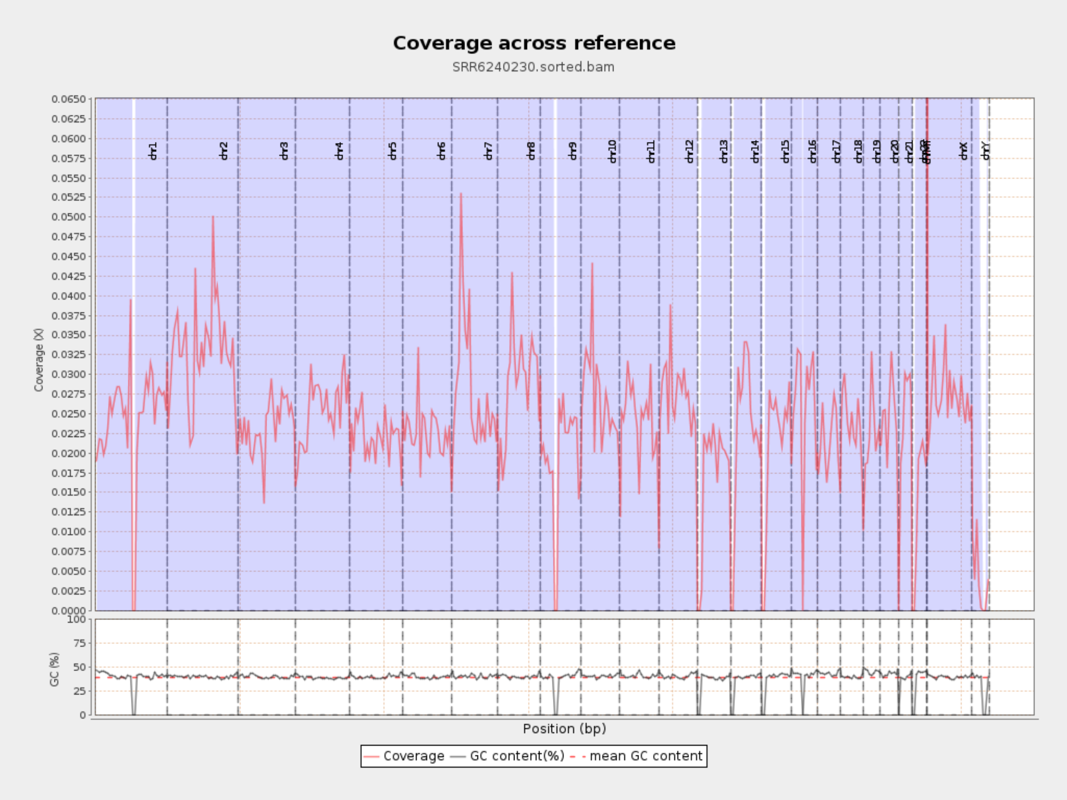
General error rate	0.91%
Mismatches	677,600
Insertions	5,337
Mapped reads with at least one insertion	0.47%
Deletions	20,087
Mapped reads with at least one deletion	1.74%
Homopolymer indels	47.9%

2.6. Chromosome stats

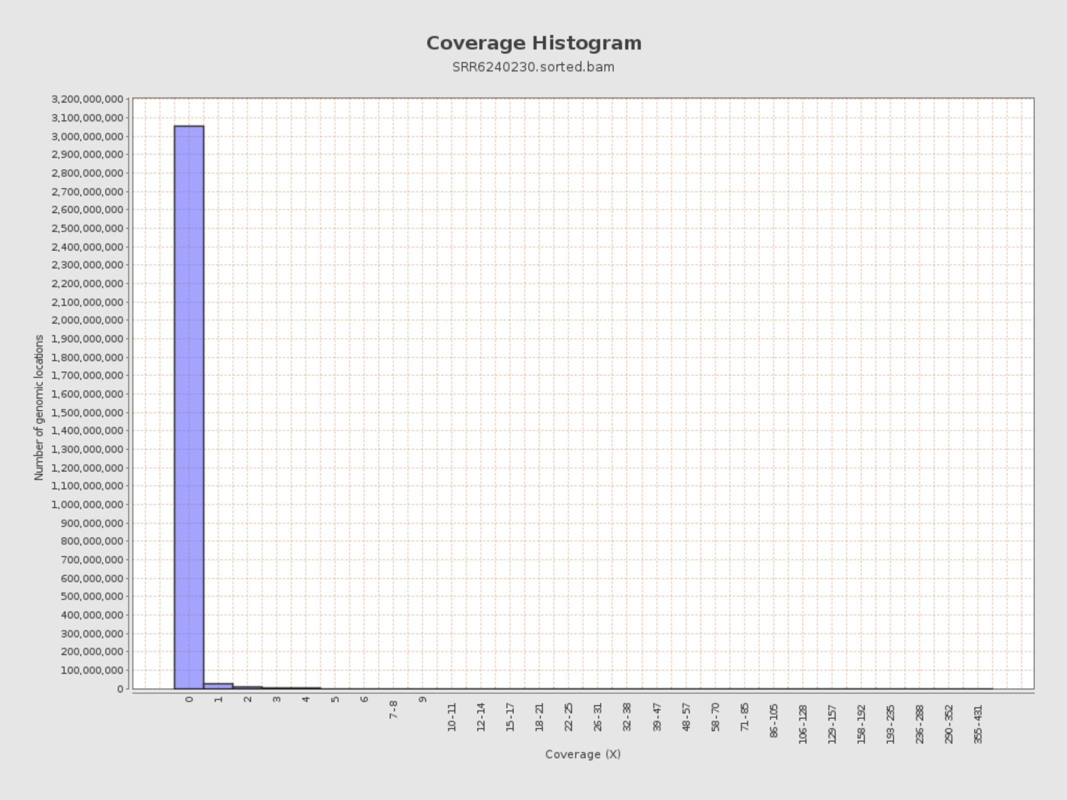
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6052223	0.0243	0.4419
chr2	243199373	8038508	0.0331	0.335
chr3	198022430	4658243	0.0235	0.2469
chr4	191154276	4863790	0.0254	0.258
chr5	180915260	4021265	0.0222	0.2382
chr6	171115067	3895881	0.0228	0.2607
chr7	159138663	4479699	0.0281	0.3612

chr8	146364022	4217681	0.0288	0.3611
chr9	141213431	2748421	0.0195	0.2611
chr10	135534747	3677180	0.0271	0.3071
chr11	135006516	3305673	0.0245	0.3011
chr12	133851895	3682589	0.0275	0.2674
chr13	115169878	1976343	0.0172	0.2128
chr14	107349540	2427659	0.0226	0.2502
chr15	102531392	2112010	0.0206	0.24
chr16	90354753	2293710	0.0254	0.2558
chr17	81195210	1737474	0.0214	0.2465
chr18	78077248	1886972	0.0242	0.378
chr19	59128983	1324296	0.0224	0.3144
chr20	63025520	1541882	0.0245	0.2524
chr21	48129895	1139360	0.0237	0.2483
chr22	51304566	718889	0.014	0.1828
chrMT	16571	16564	0.9996	1.4739
chrX	155270560	4229073	0.0272	0.2759
chrY	59373566	226048	0.0038	0.1046

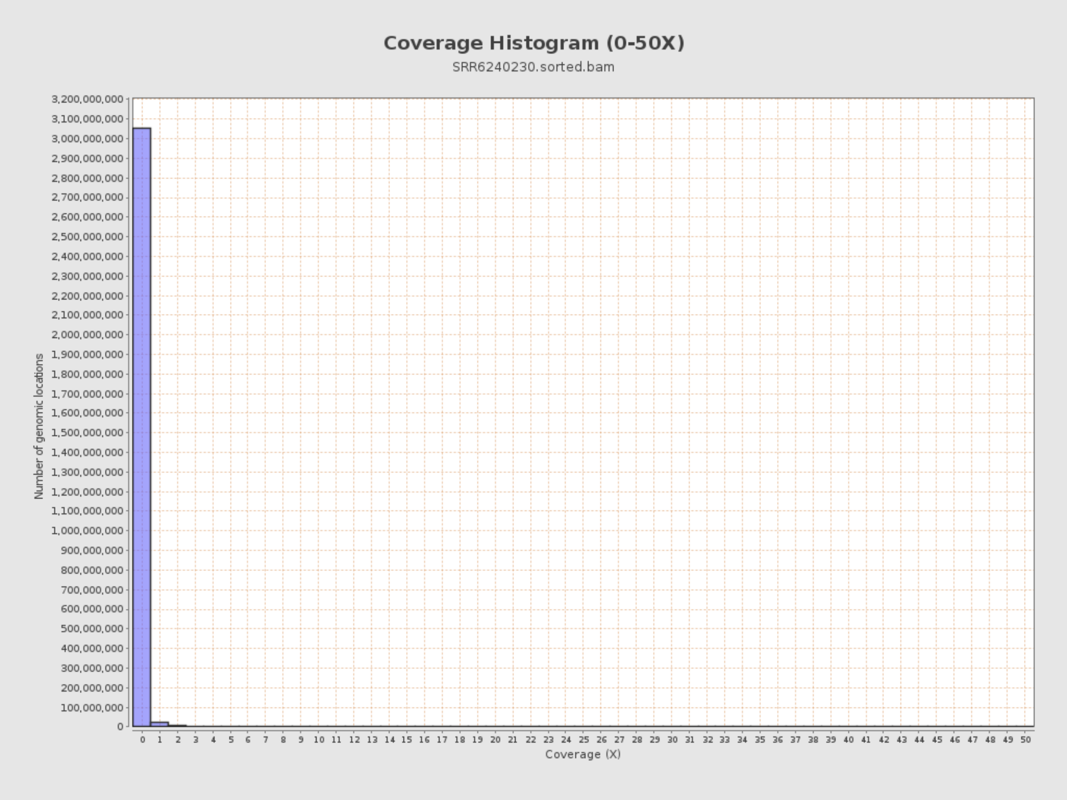
3. Results : Coverage across reference



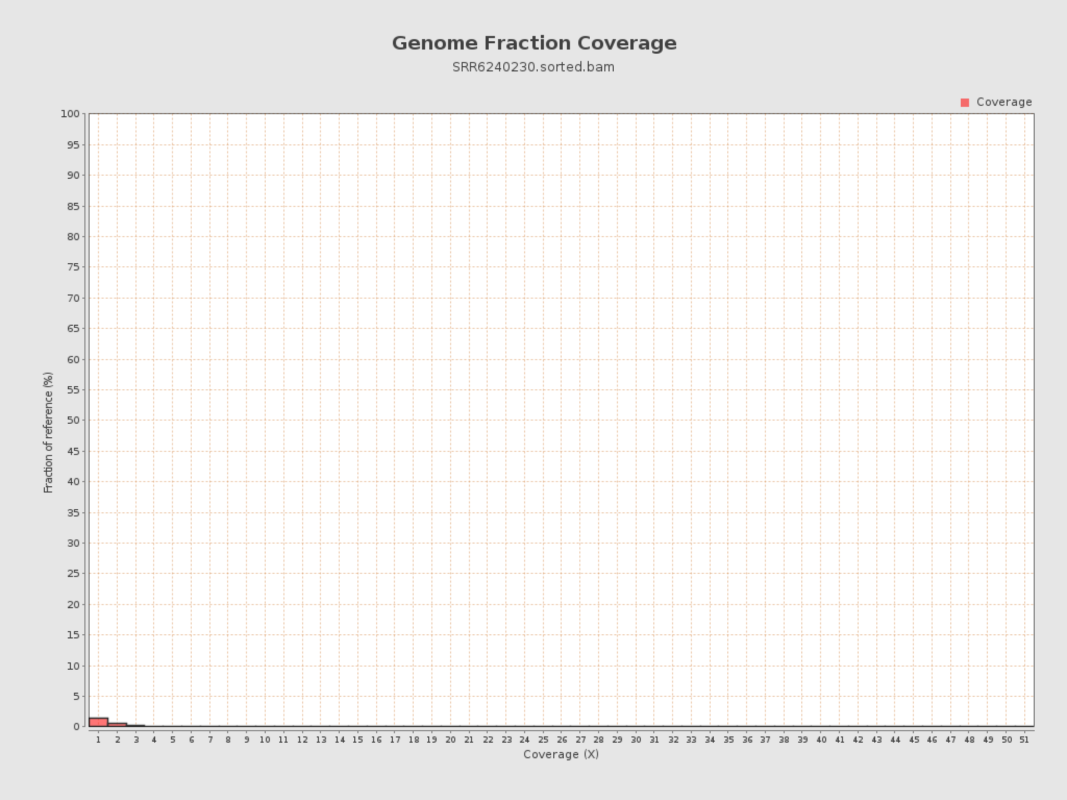
4. Results : Coverage Histogram



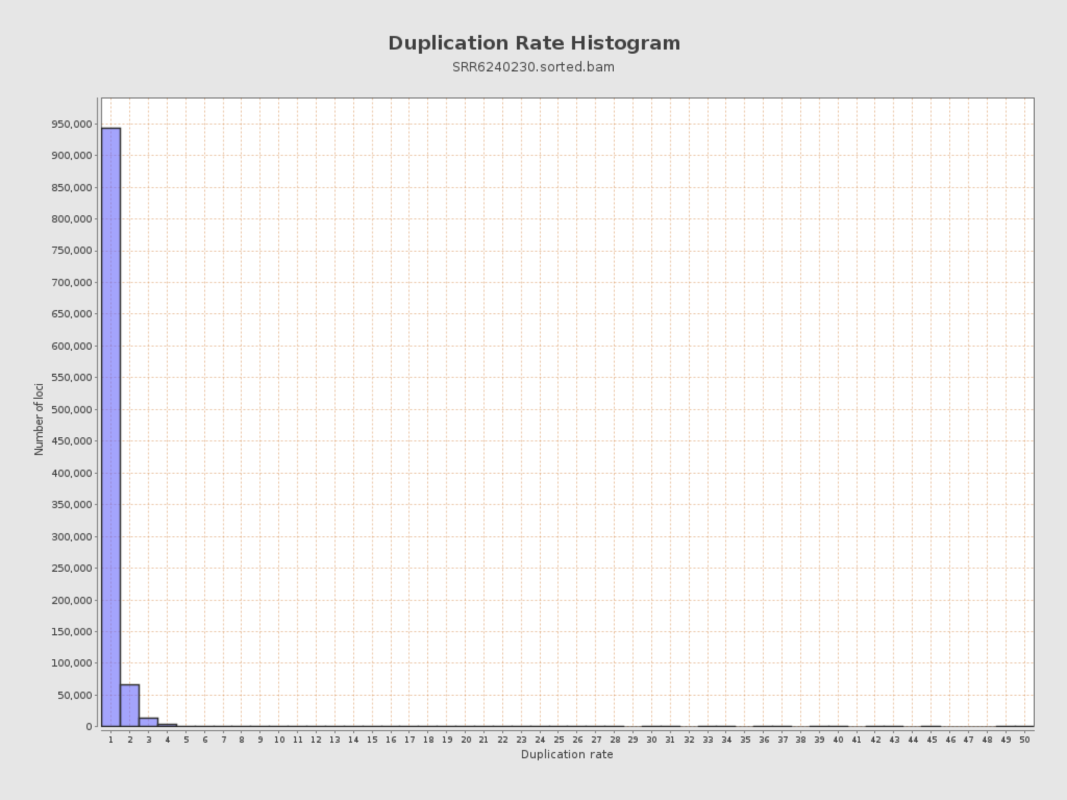
5. Results : Coverage Histogram (0-50X)



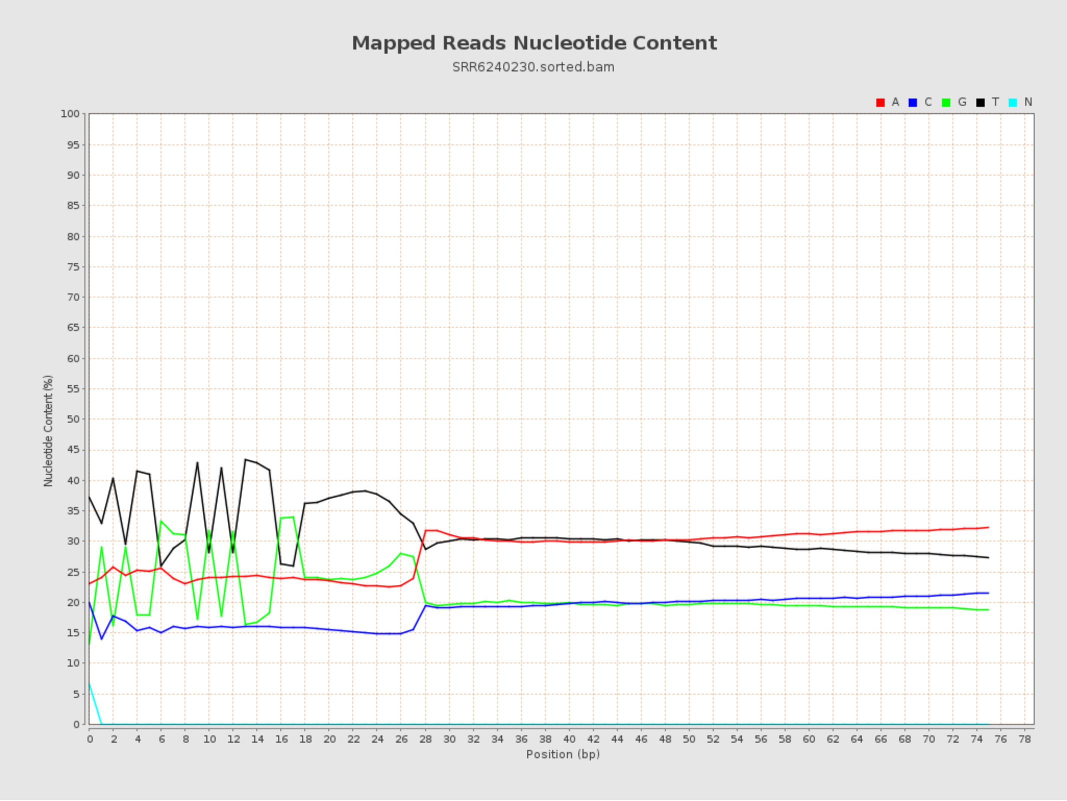
6. Results : Genome Fraction Coverage



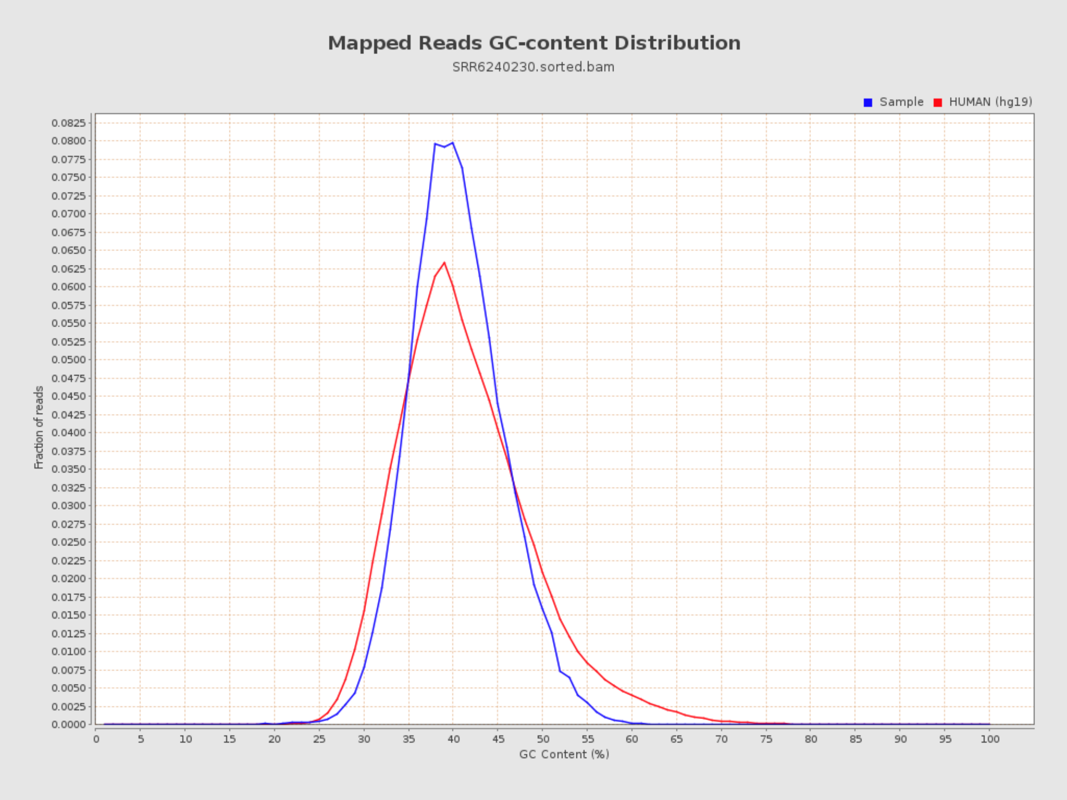
7. Results : Duplication Rate Histogram



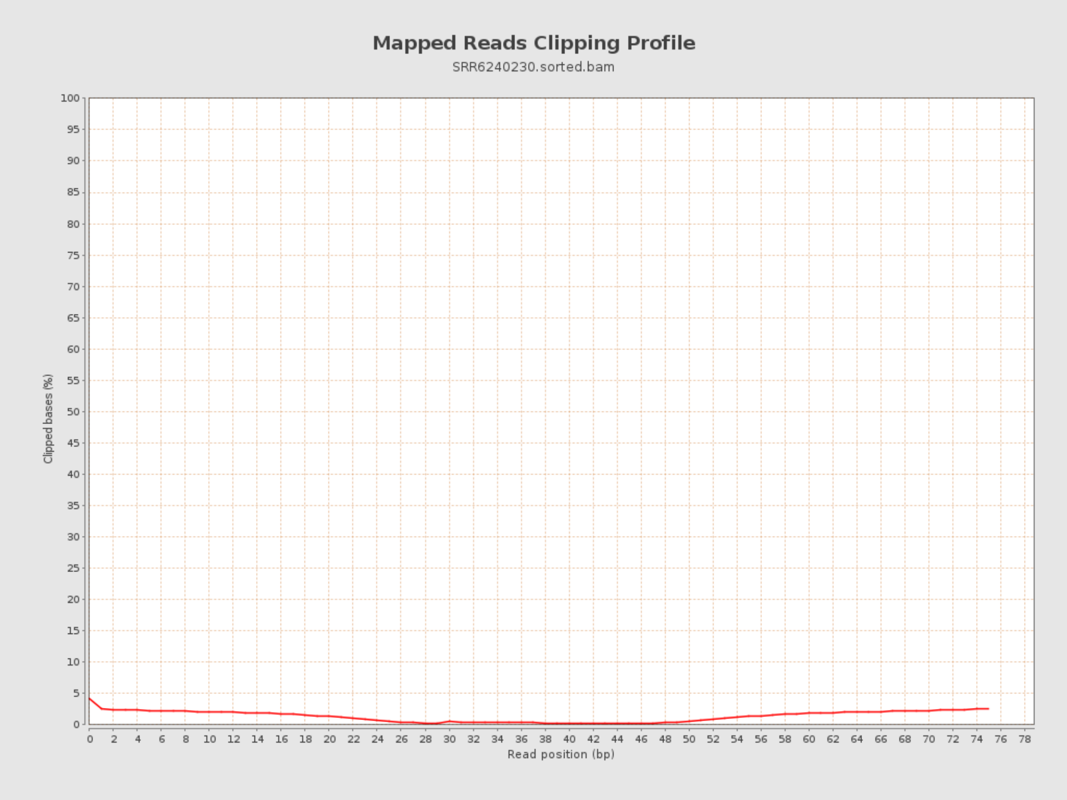
8. Results : Mapped Reads Nucleotide Content



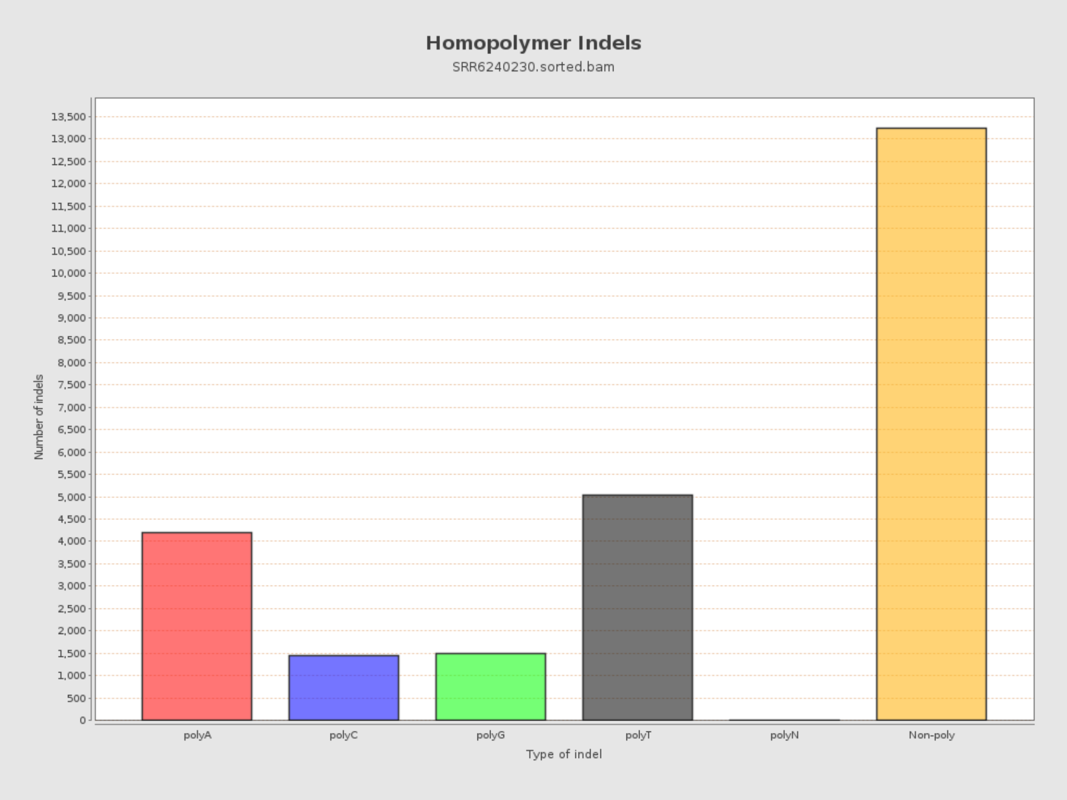
9. Results : Mapped Reads GC-content Distribution



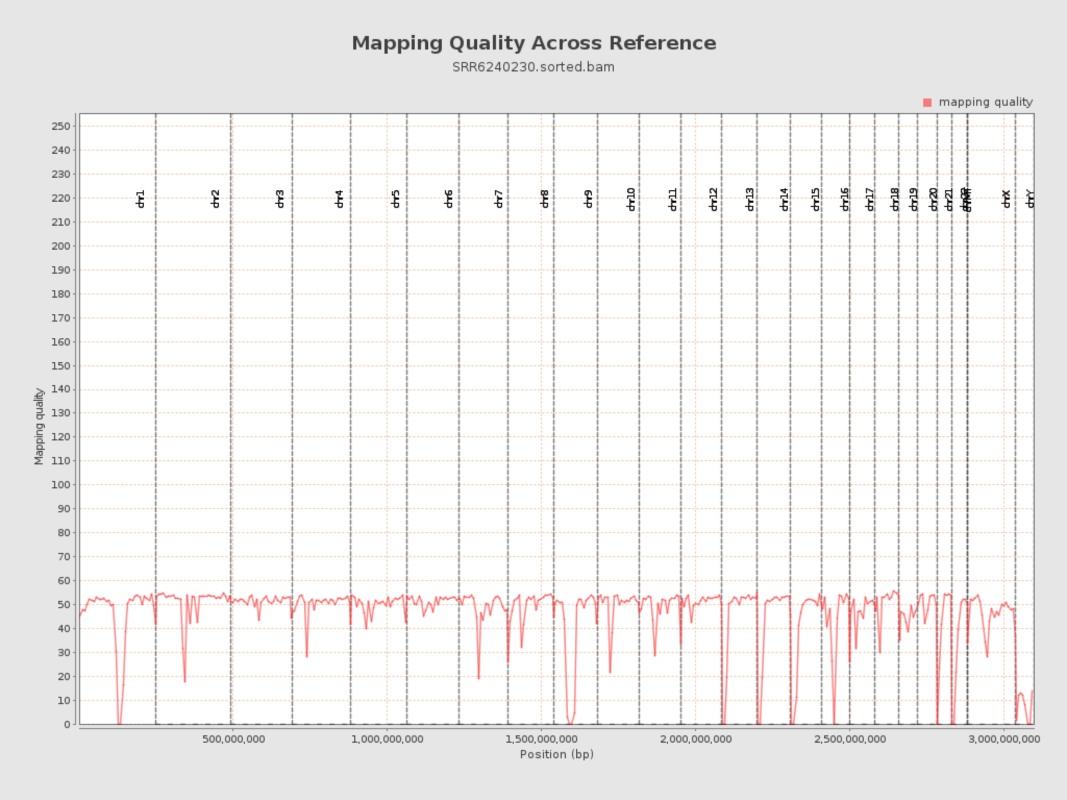
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram