Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:49:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013224.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_SRR6013224 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013224.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:49:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,004,263
Mapped reads	1,703,319 / 84.98%
Unmapped reads	300,944 / 15.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,850 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	120,104 / 5.99%
Duplication rate	5.68%
Clipped reads	861,469 / 42.98%

2.2. ACGT Content

Number/percentage of A's	30,044,262 / 27.11%
Number/percentage of C's	20,079,970 / 18.12%
Number/percentage of T's	35,645,274 / 32.17%
Number/percentage of G's	25,036,199 / 22.59%
Number/percentage of N's	1,405 / 0%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.3752

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

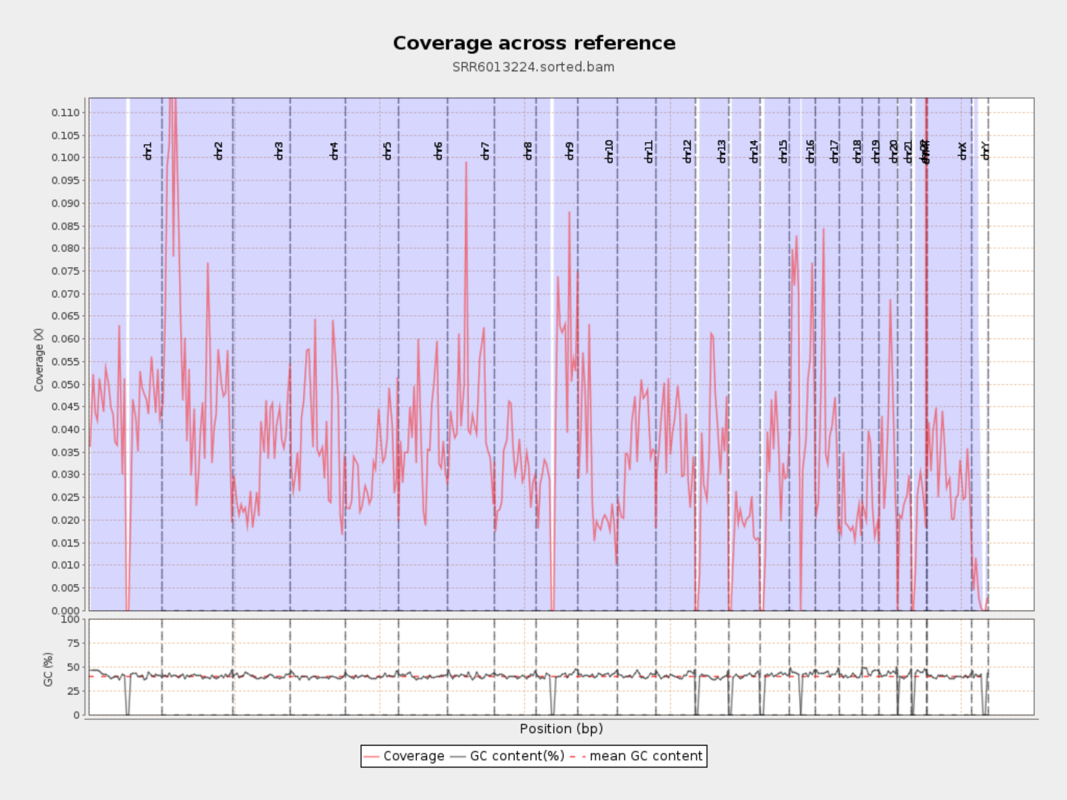
General error rate	0.75%
Mismatches	817,590
Insertions	7,743
Mapped reads with at least one insertion	0.45%
Deletions	28,658
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.47%

2.6. Chromosome stats

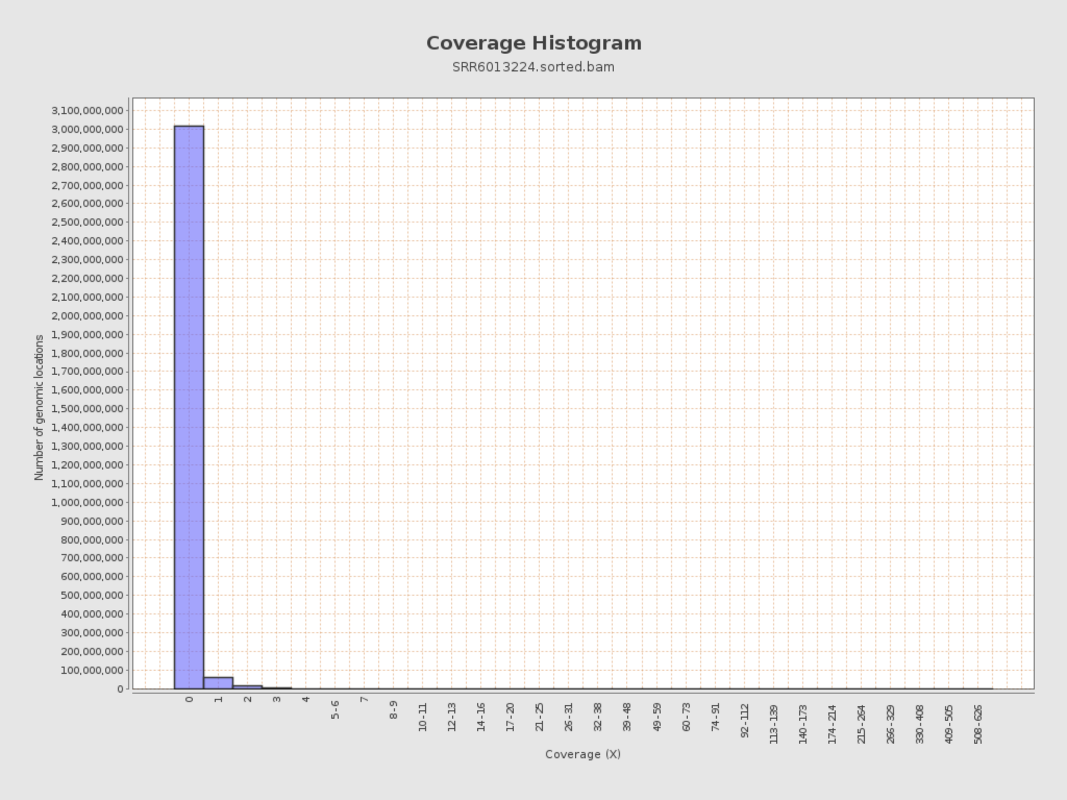
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10579166	0.0424	0.5723
chr2	243199373	13850374	0.057	0.4373
chr3	198022430	6378397	0.0322	0.2335
chr4	191154276	7383749	0.0386	0.2659
chr5	180915260	5644390	0.0312	0.231
chr6	171115067	6353899	0.0371	0.2971
chr7	159138663	7264246	0.0456	0.7622

chr8	146364022	4568382	0.0312	0.355
chr9	141213431	6004707	0.0425	0.3691
chr10	135534747	3770816	0.0278	0.3455
chr11	135006516	4929871	0.0365	0.3078
chr12	133851895	5013068	0.0375	0.2566
chr13	115169878	3909167	0.0339	0.2386
chr14	107349540	1805050	0.0168	0.2041
chr15	102531392	2891462	0.0282	0.2166
chr16	90354753	4885377	0.0541	0.3214
chr17	81195210	3245245	0.04	0.3439
chr18	78077248	1581336	0.0203	0.5688
chr19	59128983	1470824	0.0249	0.4577
chr20	63025520	2345069	0.0372	0.2612
chr21	48129895	1028226	0.0214	0.2114
chr22	51304566	914927	0.0178	0.1684
chrMT	16571	35659	2.1519	2.381
chrX	155270560	4789159	0.0308	0.2436
chrY	59373566	214281	0.0036	0.1022

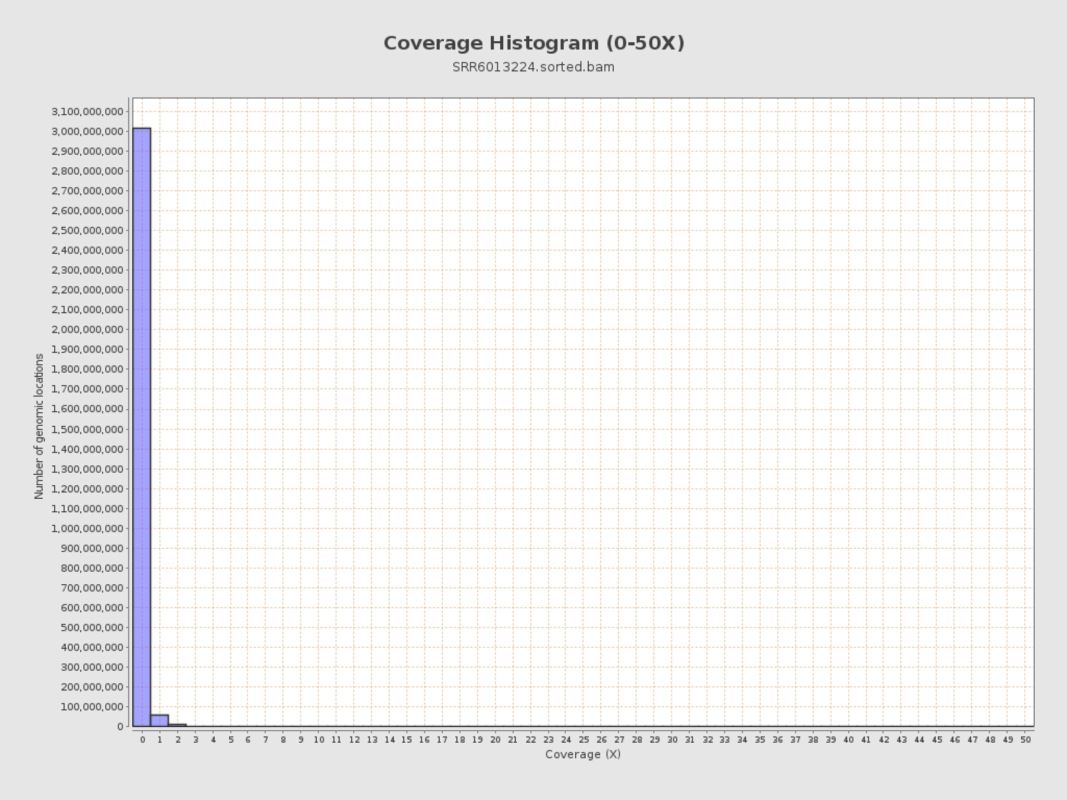
3. Results : Coverage across reference



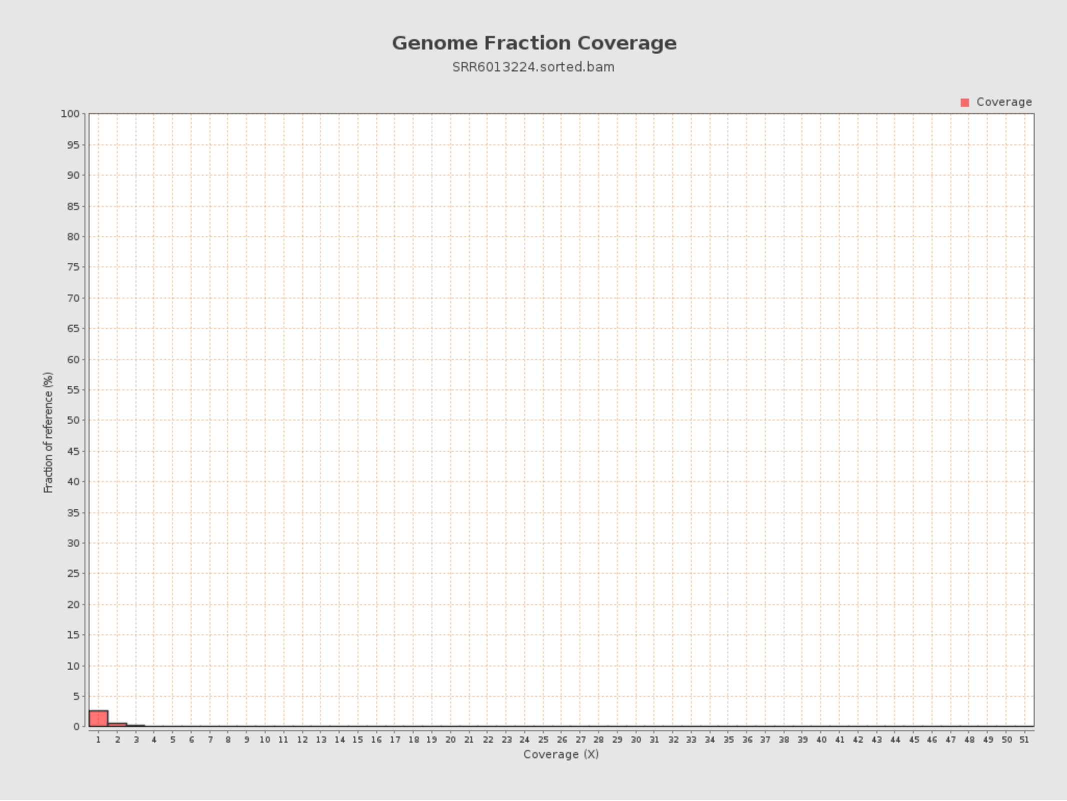
4. Results : Coverage Histogram



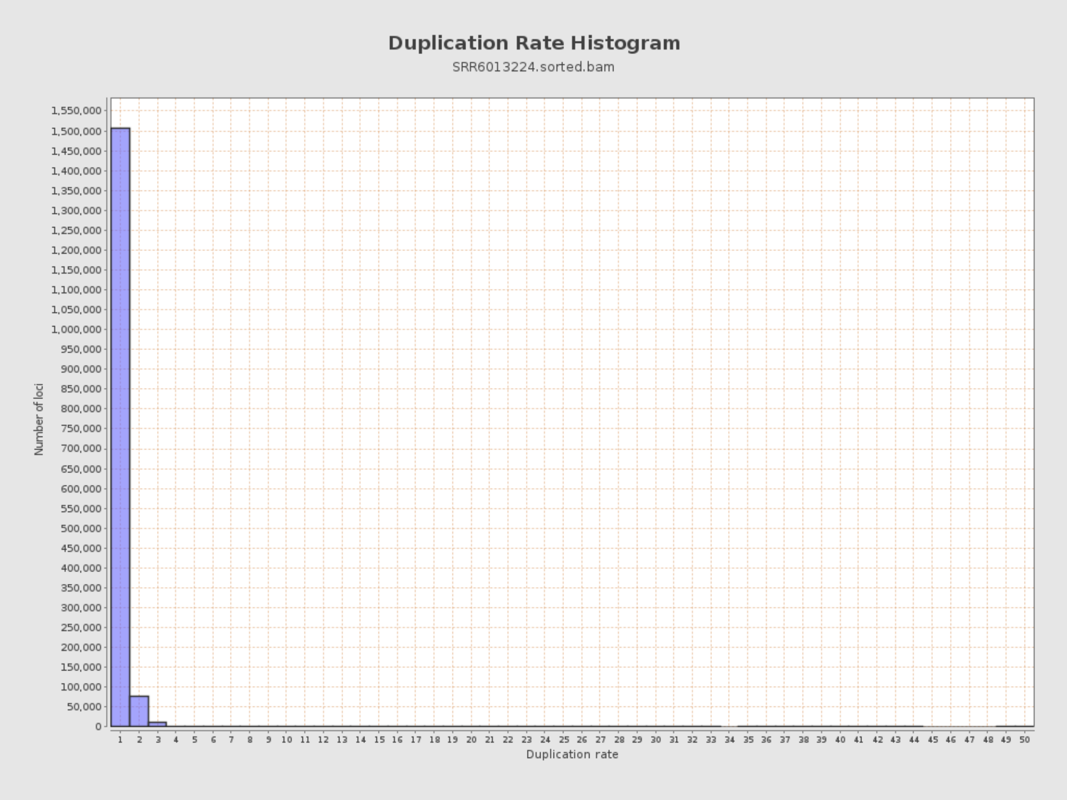
5. Results : Coverage Histogram (0-50X)



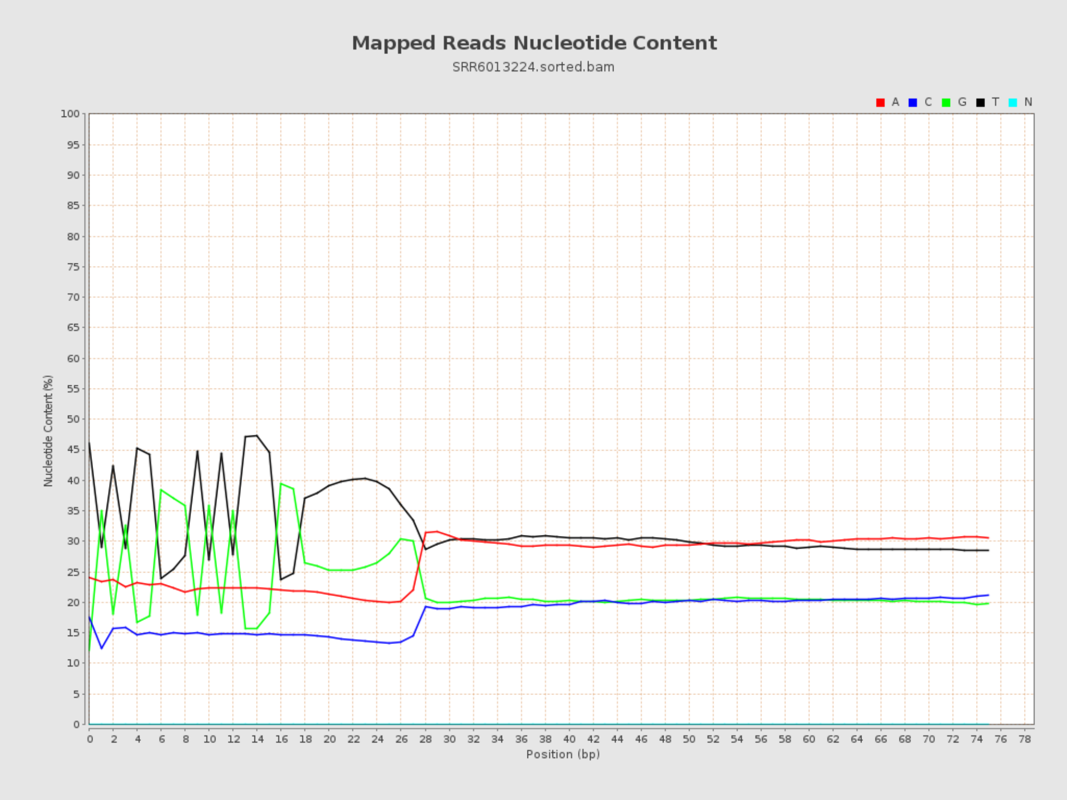
6. Results : Genome Fraction Coverage



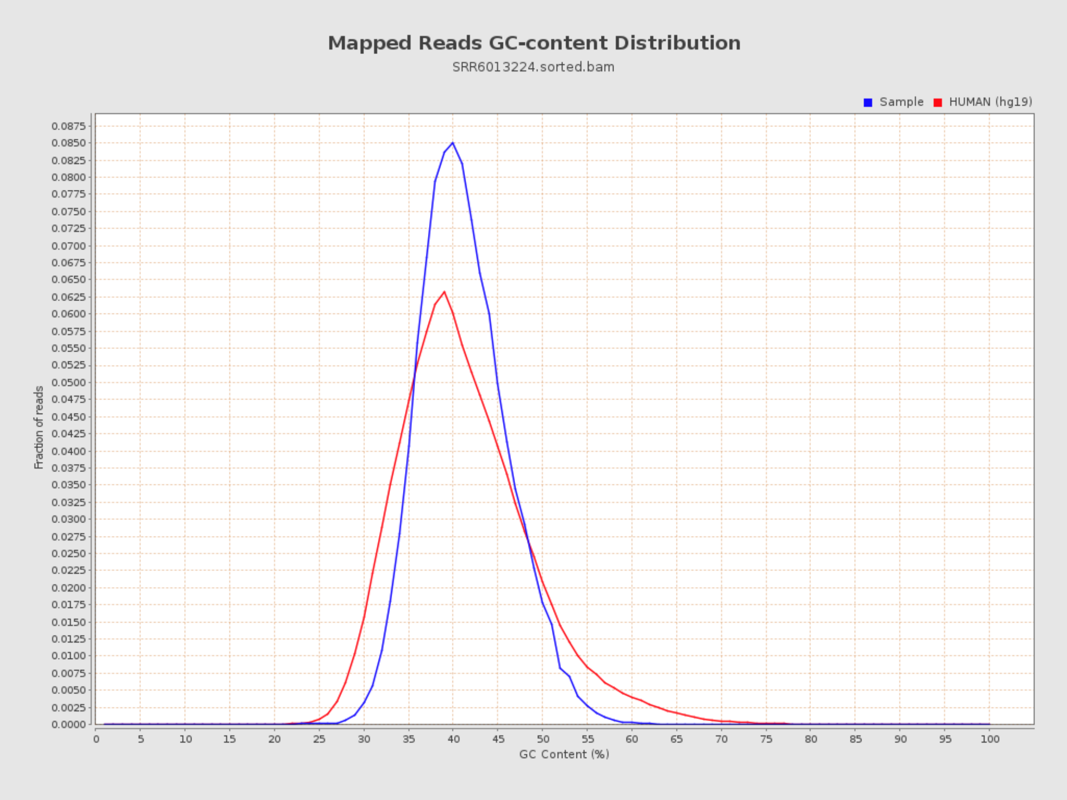
7. Results : Duplication Rate Histogram



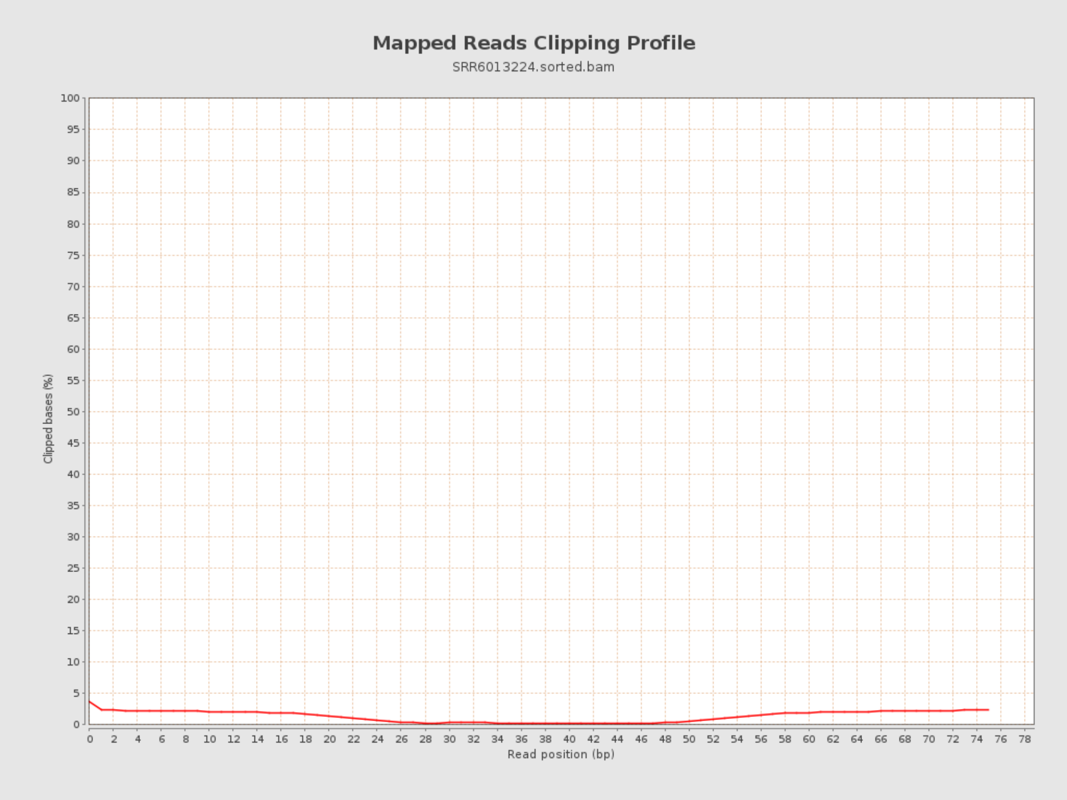
8. Results : Mapped Reads Nucleotide Content



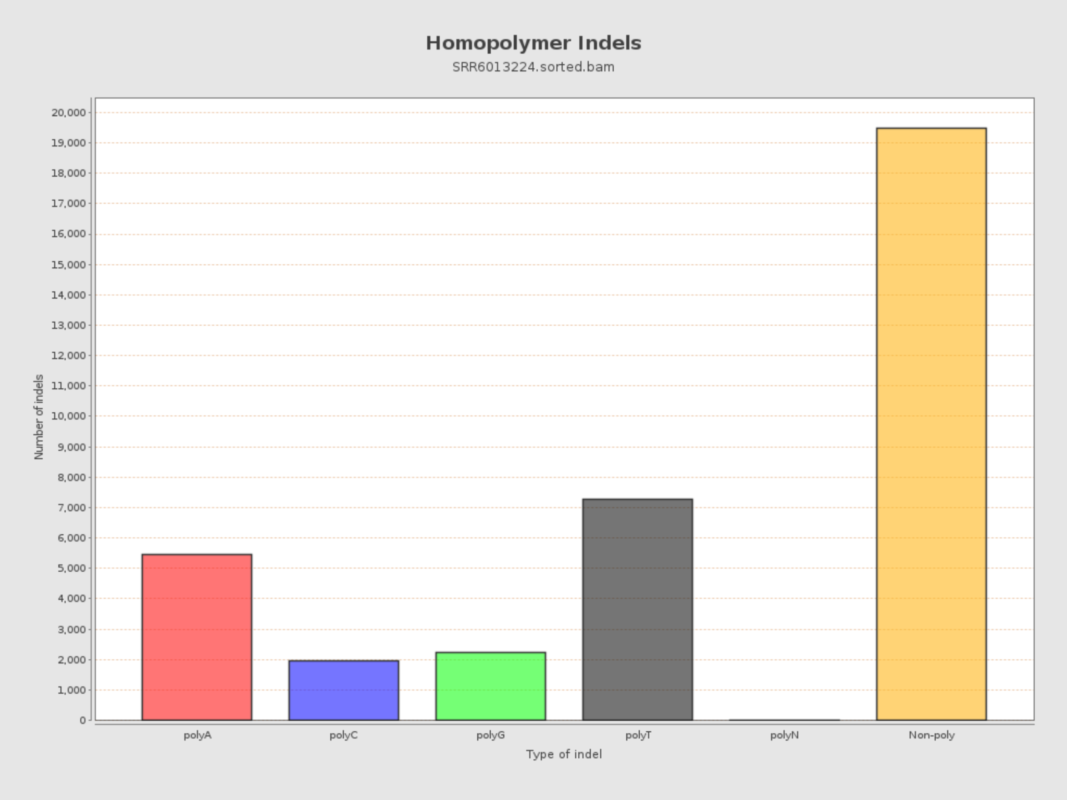
9. Results : Mapped Reads GC-content Distribution



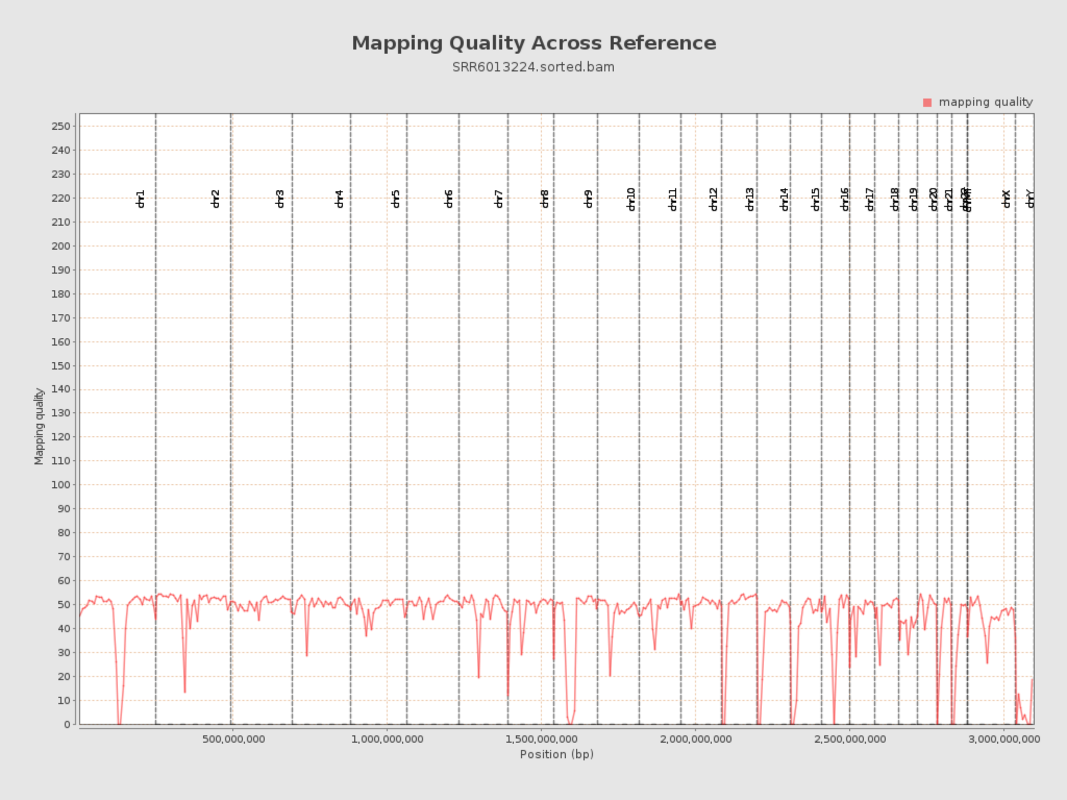
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram