Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:15:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013211.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_SRR6013211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013211.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:15:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,866,404
Mapped reads	1,702,015 / 91.19%
Unmapped reads	164,389 / 8.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,921 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	72,909 / 3.91%
Duplication rate	3%
Clipped reads	718,657 / 38.5%

2.2. ACGT Content

Number/percentage of A's	32,460,822 / 28.34%
Number/percentage of C's	21,031,982 / 18.36%
Number/percentage of T's	36,264,307 / 31.66%
Number/percentage of G's	24,744,864 / 21.61%
Number/percentage of N's	24,116 / 0.02%
GC Percentage	39.97%

2.3. Coverage

Mean	0.037

Standard Deviation	0.4231

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

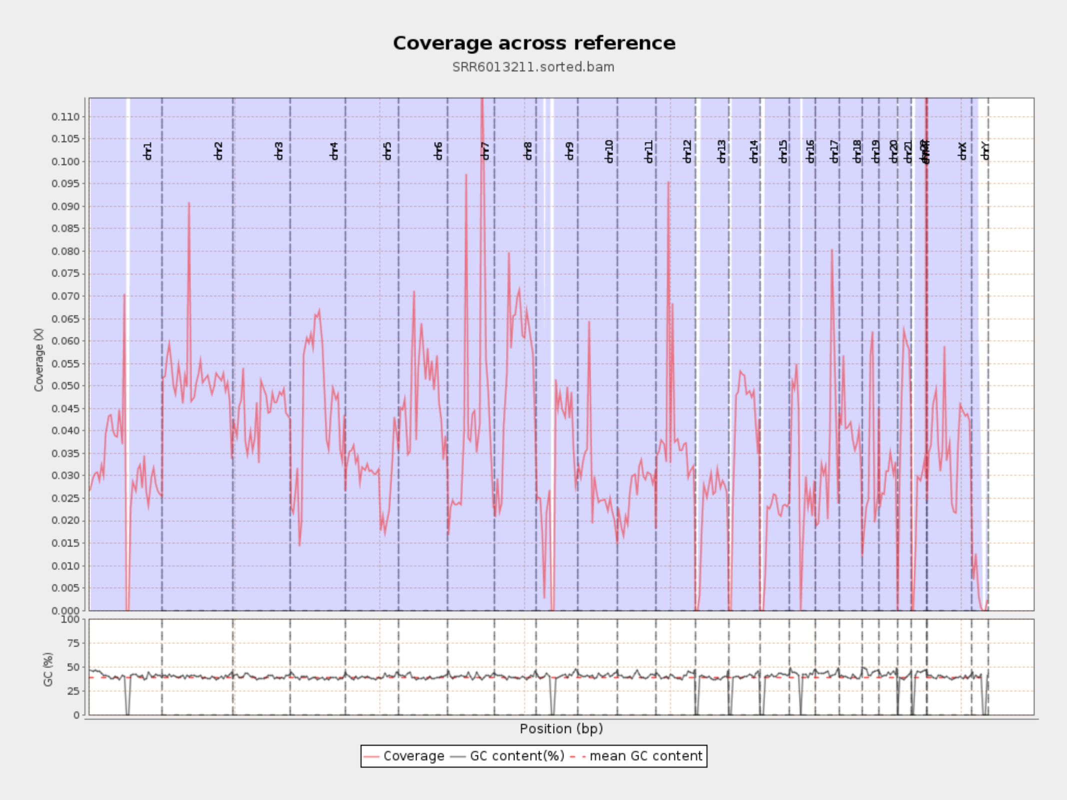
General error rate	0.81%
Mismatches	908,552
Insertions	8,761
Mapped reads with at least one insertion	0.51%
Deletions	27,274
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.26%

2.6. Chromosome stats

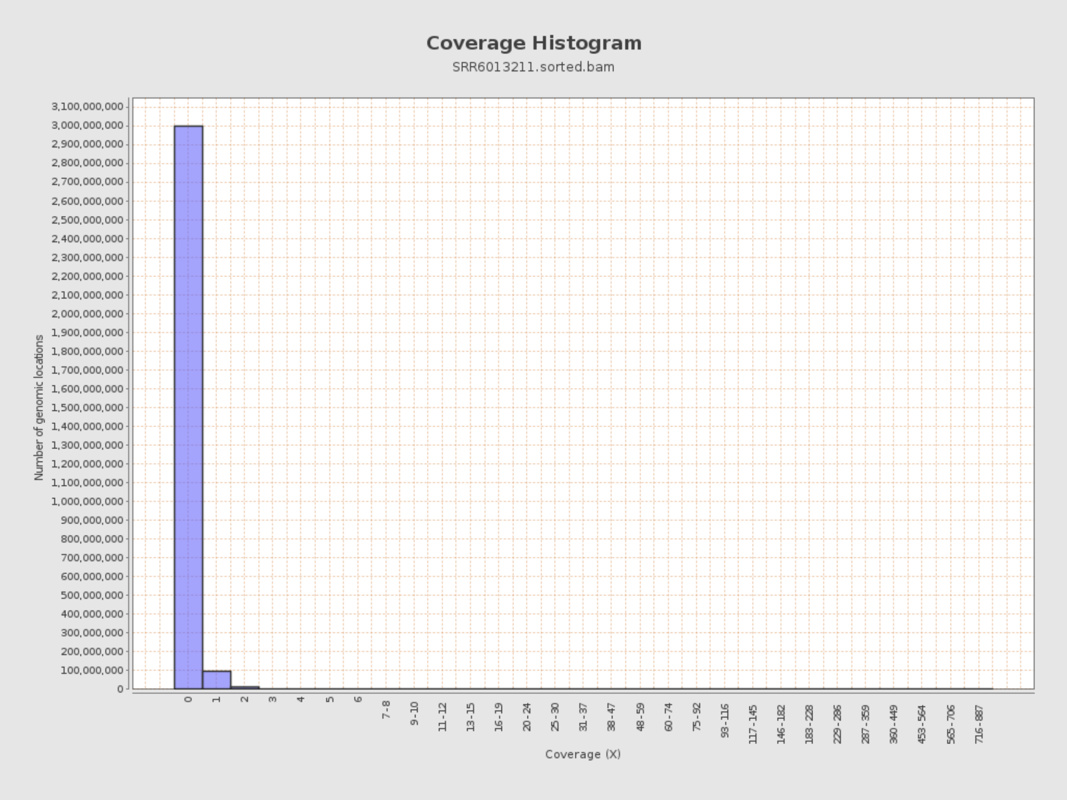
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7793943	0.0313	0.7433
chr2	243199373	12687213	0.0522	0.4829
chr3	198022430	8724028	0.0441	0.2301
chr4	191154276	8565462	0.0448	0.2557
chr5	180915260	5521213	0.0305	0.1943
chr6	171115067	8295326	0.0485	0.3124
chr7	159138663	7112702	0.0447	0.8282

chr8	146364022	7799816	0.0533	0.5568
chr9	141213431	4364440	0.0309	0.3632
chr10	135534747	3876300	0.0286	0.414
chr11	135006516	3571686	0.0265	0.2661
chr12	133851895	5380334	0.0402	0.2305
chr13	115169878	2569696	0.0223	0.1634
chr14	107349540	4296241	0.04	0.2429
chr15	102531392	1944643	0.019	0.1539
chr16	90354753	2827355	0.0313	0.2268
chr17	81195210	2860822	0.0352	0.2158
chr18	78077248	3188850	0.0408	0.7427
chr19	59128983	1912729	0.0323	0.5688
chr20	63025520	1834976	0.0291	0.1971
chr21	48129895	2210005	0.0459	0.2547
chr22	51304566	1110980	0.0217	0.1586
chrMT	16571	47767	2.8826	2.2645
chrX	155270560	5827931	0.0375	0.2442
chrY	59373566	248747	0.0042	0.1244

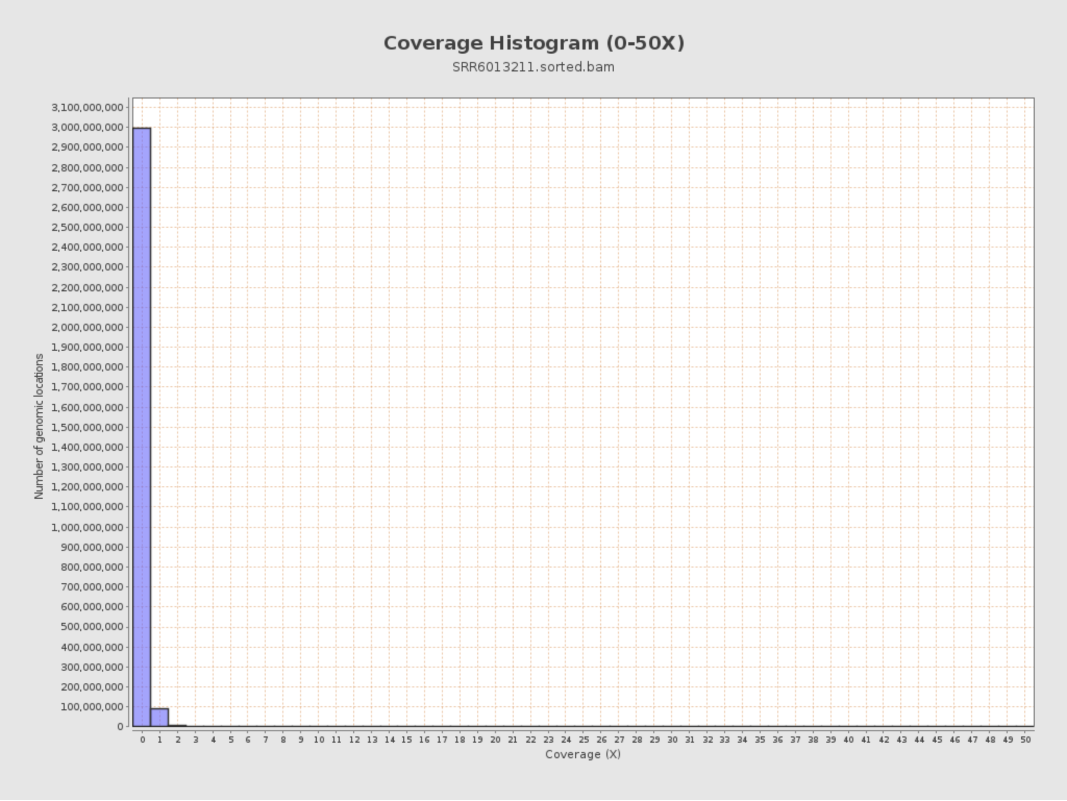
3. Results : Coverage across reference



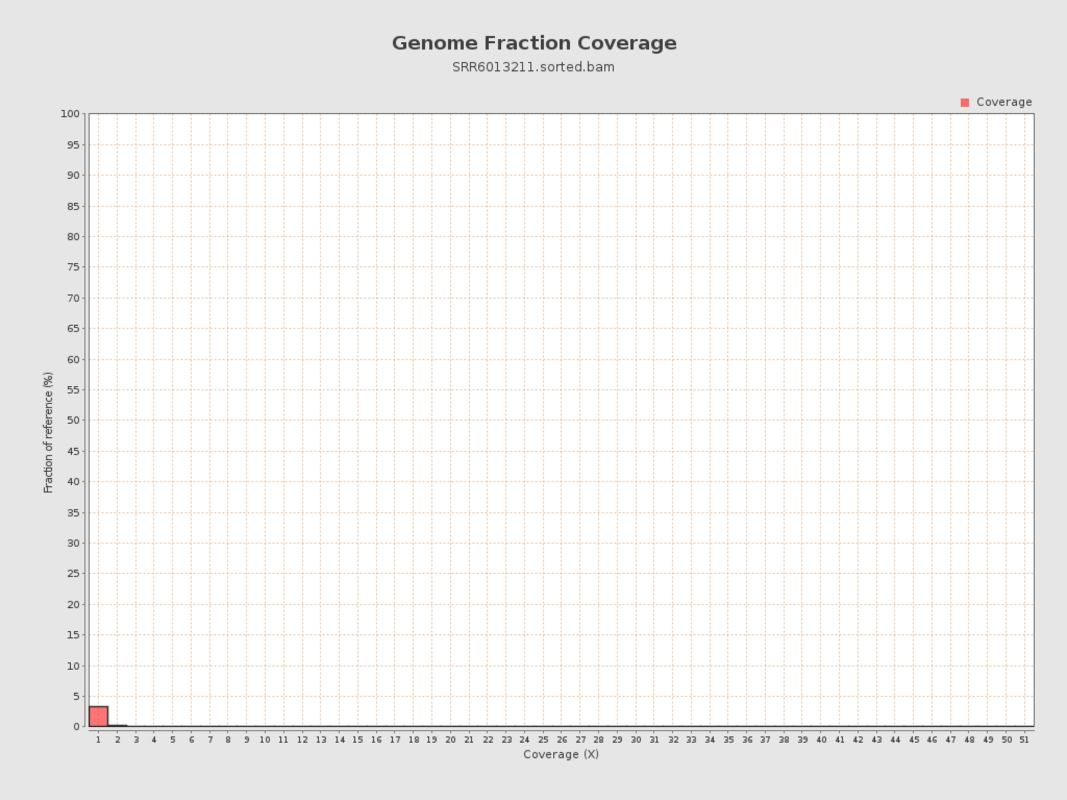
4. Results : Coverage Histogram



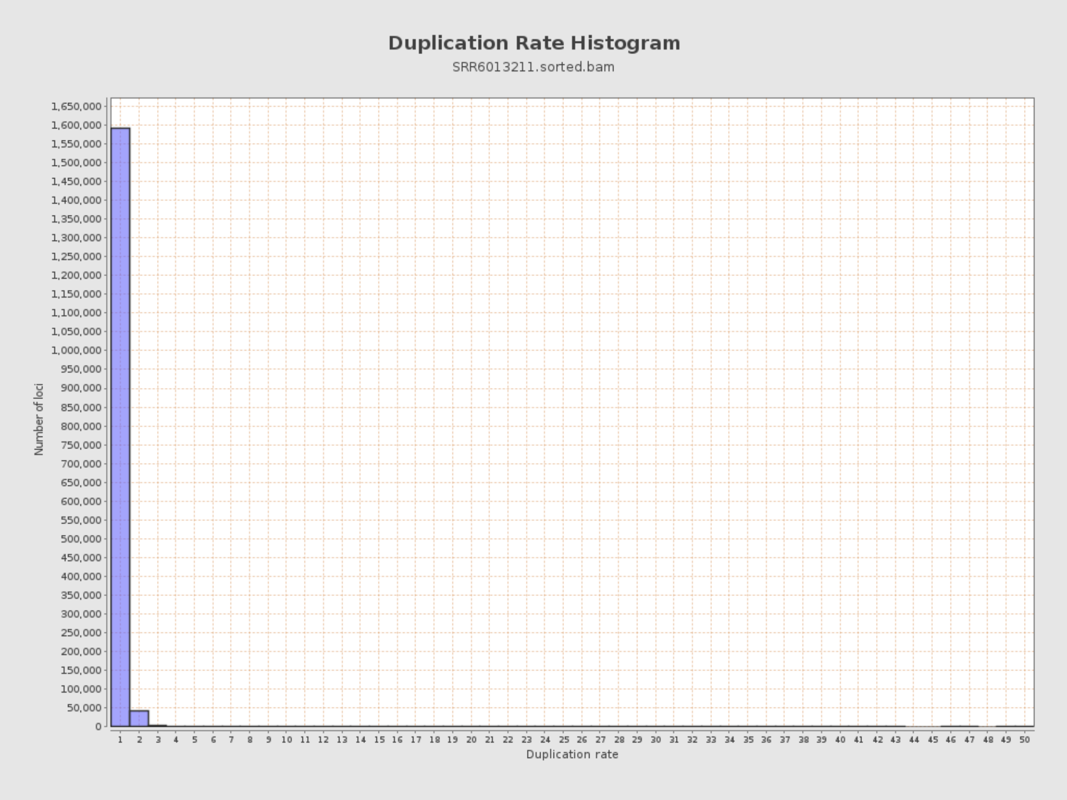
5. Results : Coverage Histogram (0-50X)



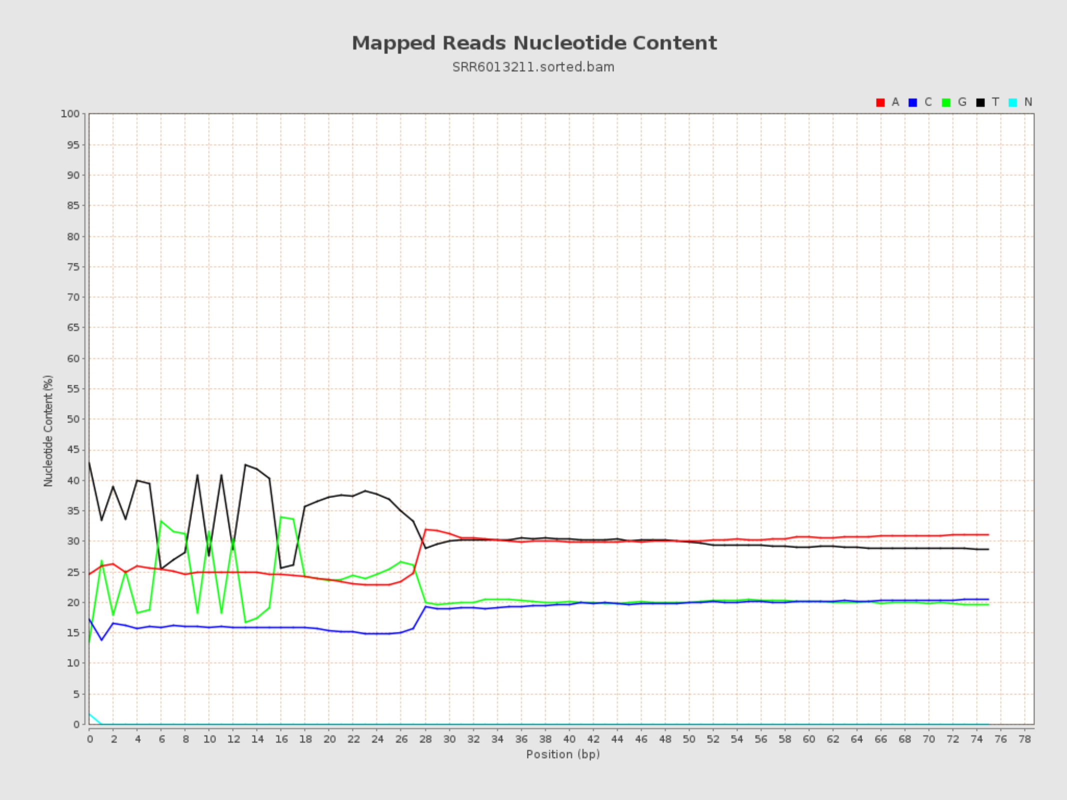
6. Results : Genome Fraction Coverage



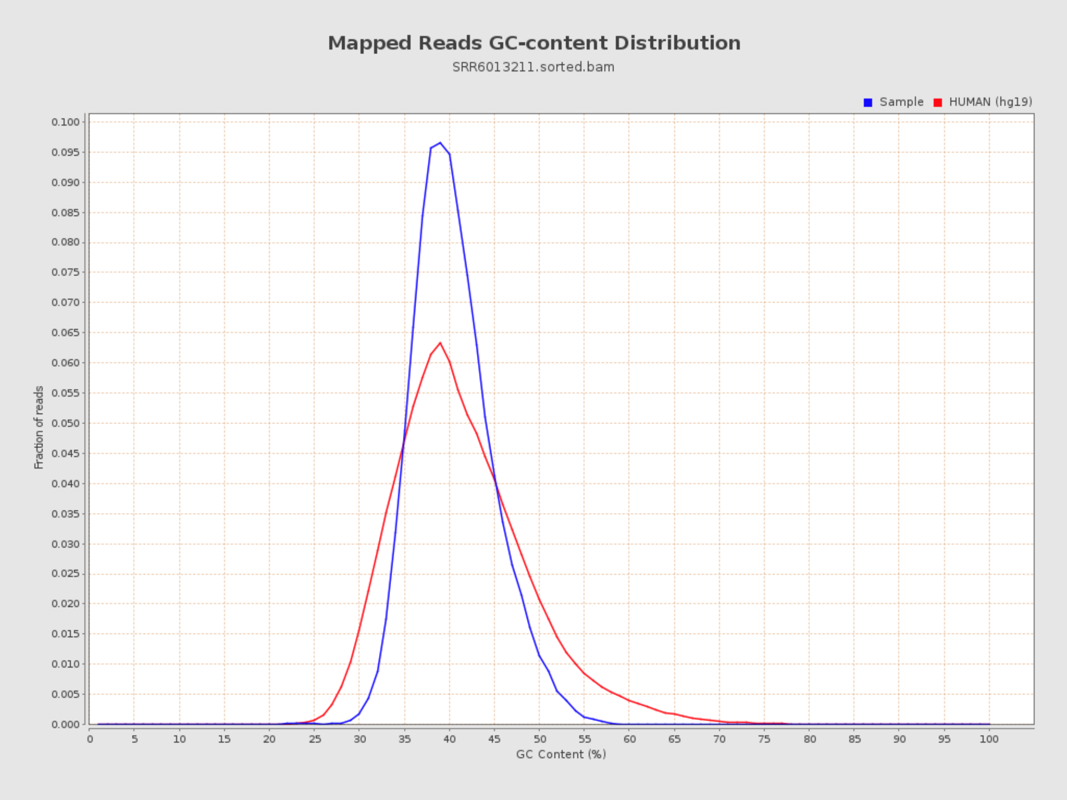
7. Results : Duplication Rate Histogram



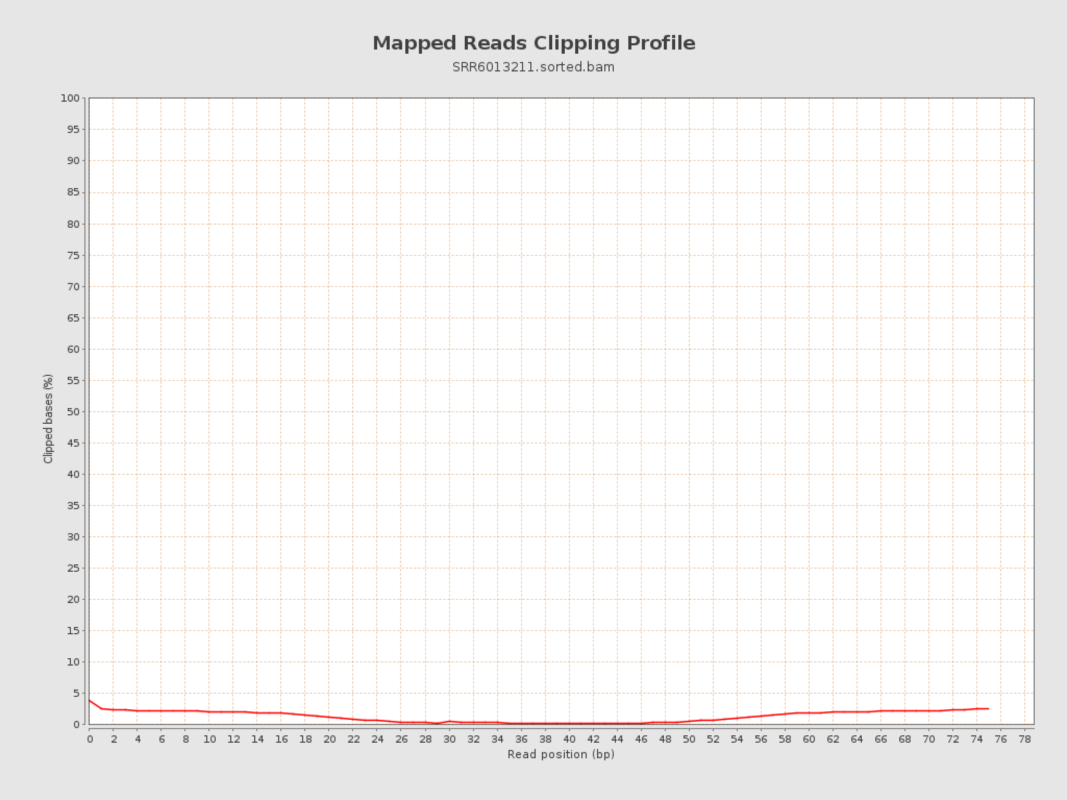
8. Results : Mapped Reads Nucleotide Content



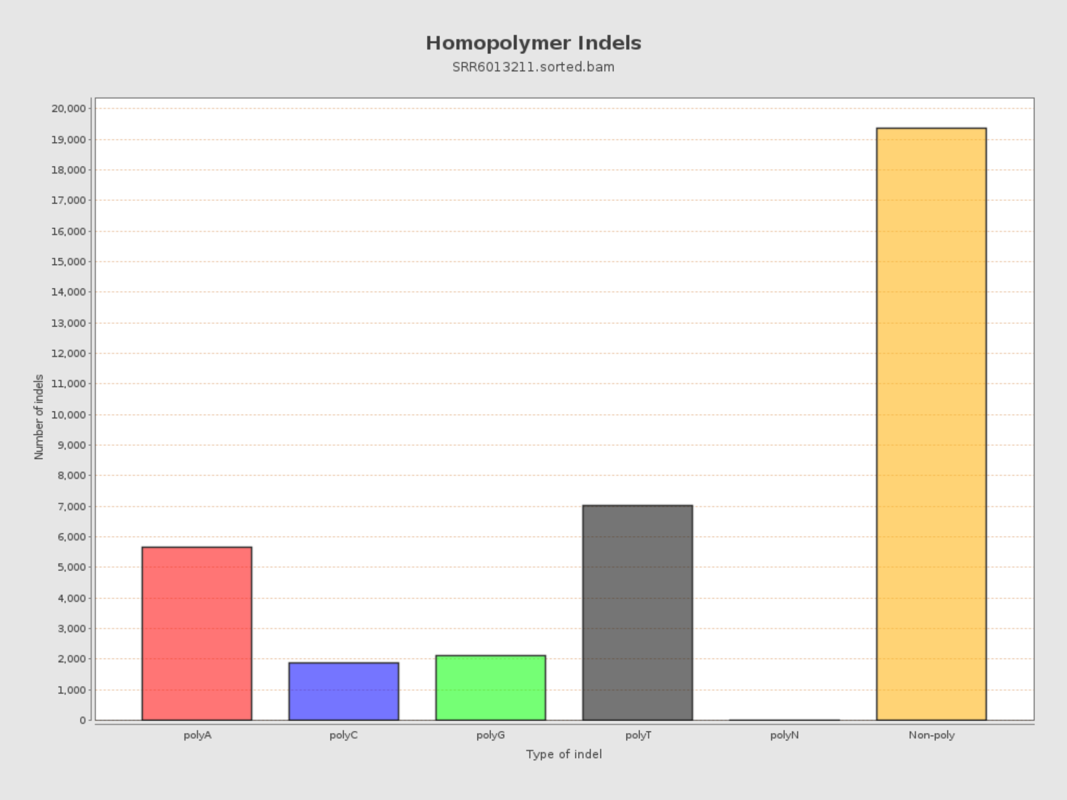
9. Results : Mapped Reads GC-content Distribution



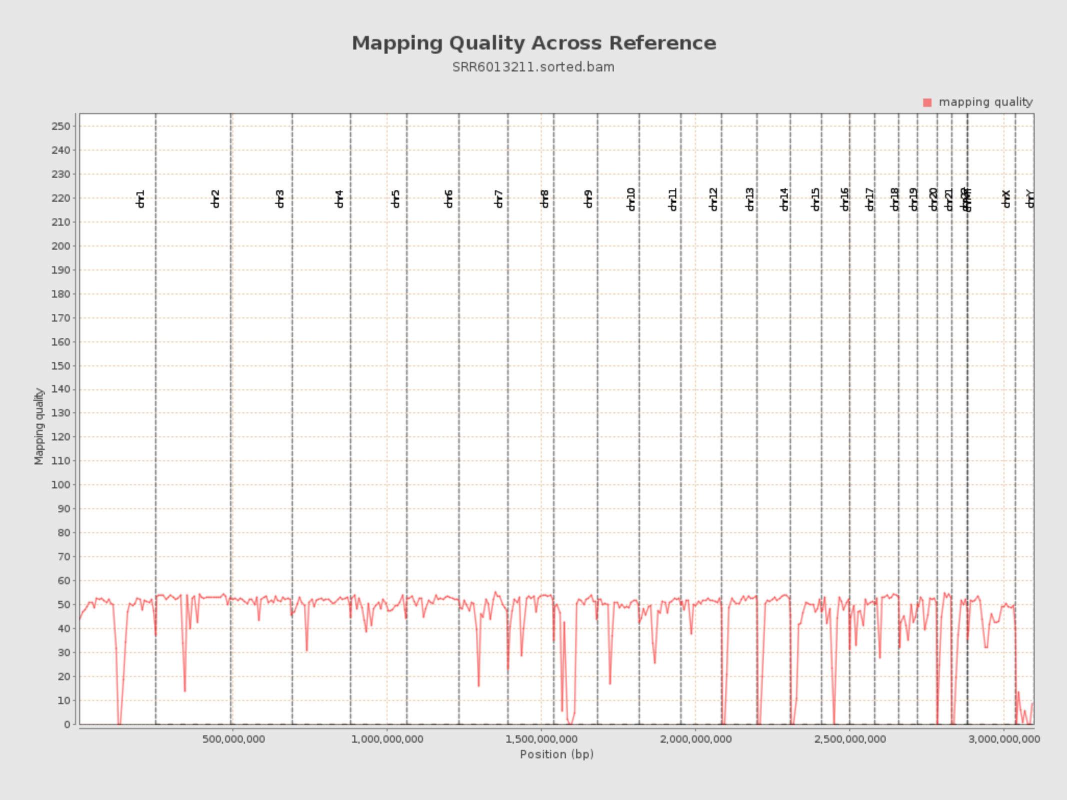
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram