Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:19:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013213.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_SRR6013213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:19:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,397,851
Mapped reads	53,719 / 3.84%
Unmapped reads	1,344,132 / 96.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	533 / 0.04%
Read min/max/mean length	30 / 76 / 76.01
Duplicated reads (estimated)	9,244 / 0.66%
Duplication rate	8.61%
Clipped reads	31,237 / 2.23%

2.2. ACGT Content

Number/percentage of A's	916,248 / 27.35%
Number/percentage of C's	603,361 / 18.01%
Number/percentage of T's	1,081,459 / 32.28%
Number/percentage of G's	748,534 / 22.34%
Number/percentage of N's	344 / 0.01%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0011

Standard Deviation	0.0868

2.4. Mapping Quality

Mean Mapping Quality	41

2.5. Mismatches and indels

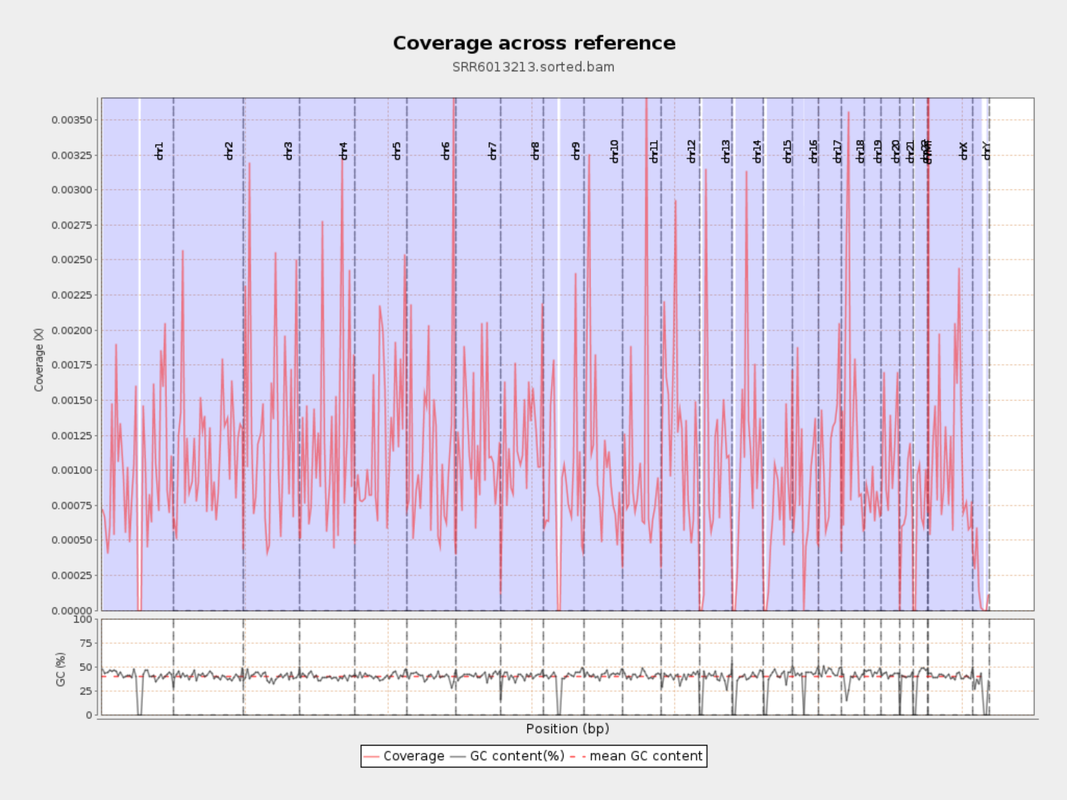
General error rate	1.19%
Mismatches	39,395
Insertions	274
Mapped reads with at least one insertion	0.51%
Deletions	763
Mapped reads with at least one deletion	1.41%
Homopolymer indels	44.55%

2.6. Chromosome stats

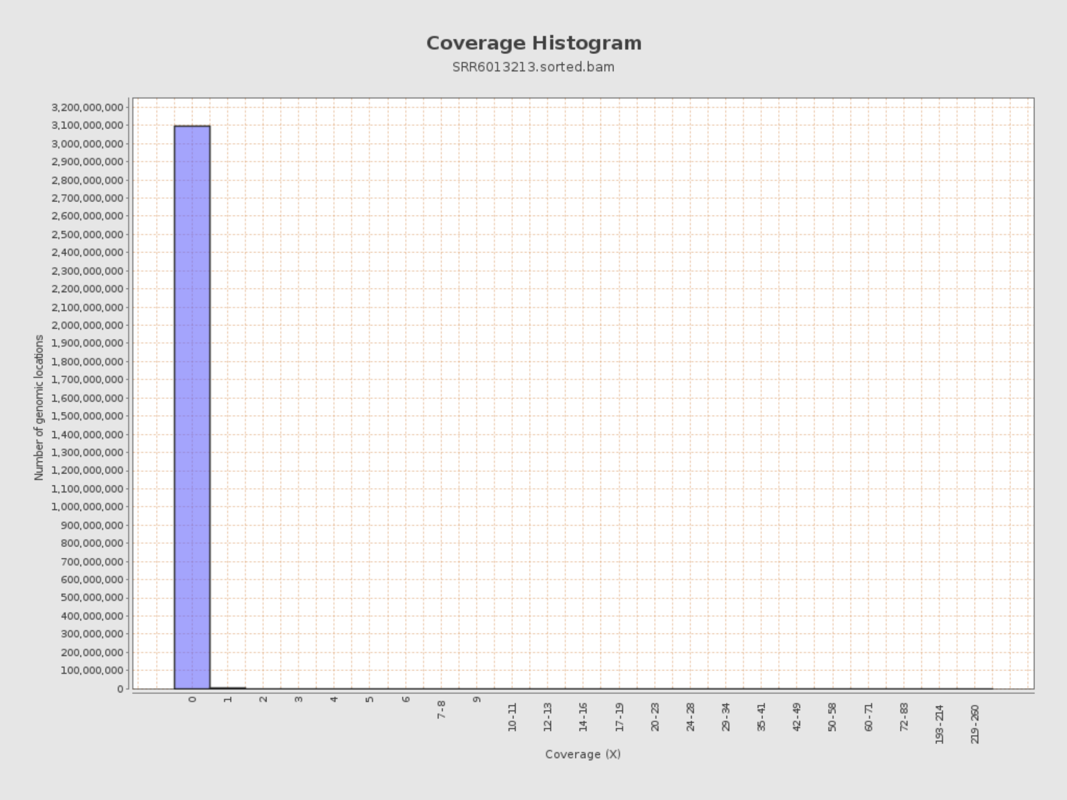
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	242052	0.001	0.0673
chr2	243199373	278933	0.0011	0.0705
chr3	198022430	255233	0.0013	0.0835
chr4	191154276	242230	0.0013	0.0733
chr5	180915260	225681	0.0012	0.0801
chr6	171115067	198395	0.0012	0.0952
chr7	159138663	186312	0.0012	0.0805

chr8	146364022	180938	0.0012	0.071
chr9	141213431	125198	0.0009	0.0561
chr10	135534747	147748	0.0011	0.0622
chr11	135006516	135275	0.001	0.0685
chr12	133851895	176959	0.0013	0.0882
chr13	115169878	108663	0.0009	0.0793
chr14	107349540	116006	0.0011	0.0782
chr15	102531392	69944	0.0007	0.0593
chr16	90354753	78852	0.0009	0.0556
chr17	81195210	93062	0.0011	0.0686
chr18	78077248	113810	0.0015	0.3136
chr19	59128983	46547	0.0008	0.0479
chr20	63025520	72983	0.0012	0.062
chr21	48129895	35799	0.0007	0.0431
chr22	51304566	34510	0.0007	0.0491
chrMT	16571	1616	0.0975	0.3365
chrX	155270560	173296	0.0011	0.0697
chrY	59373566	11197	0.0002	0.0255

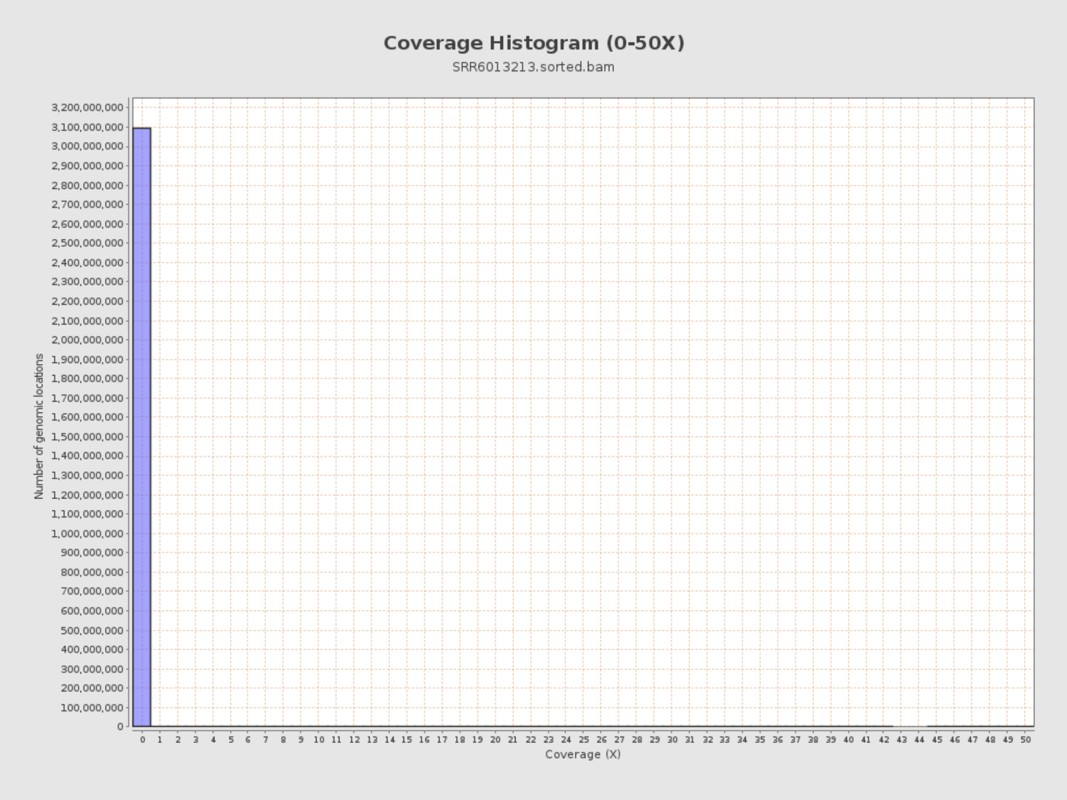
3. Results : Coverage across reference



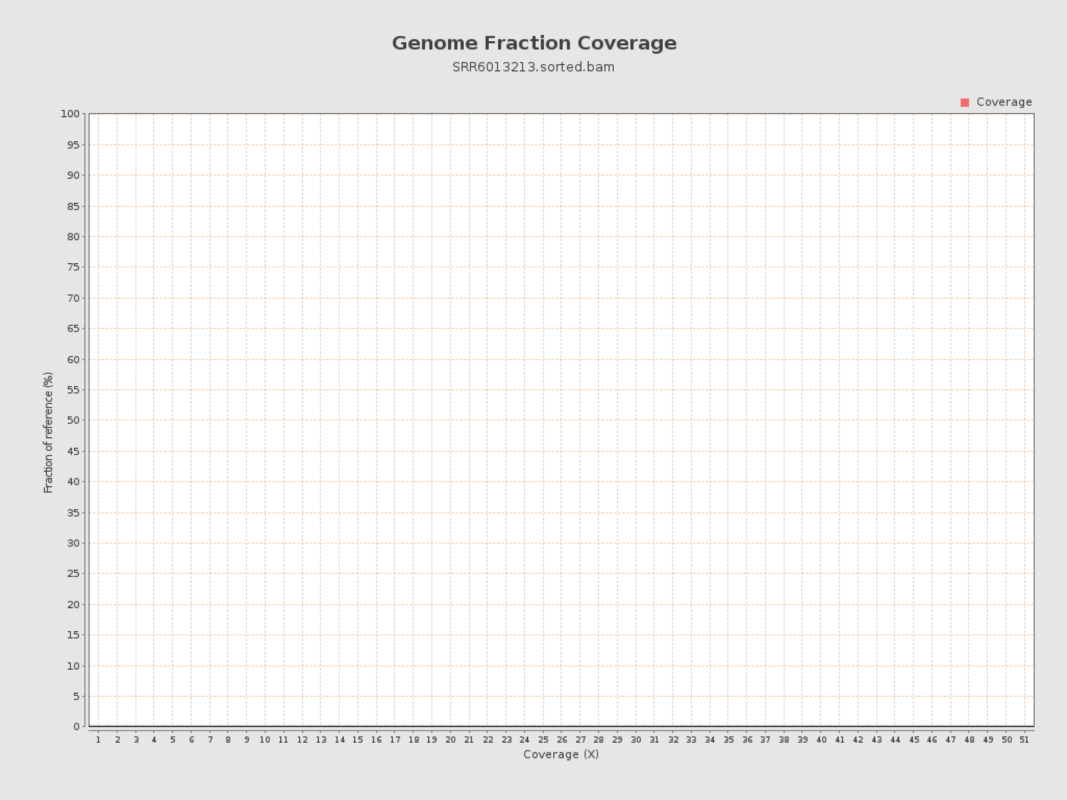
4. Results : Coverage Histogram



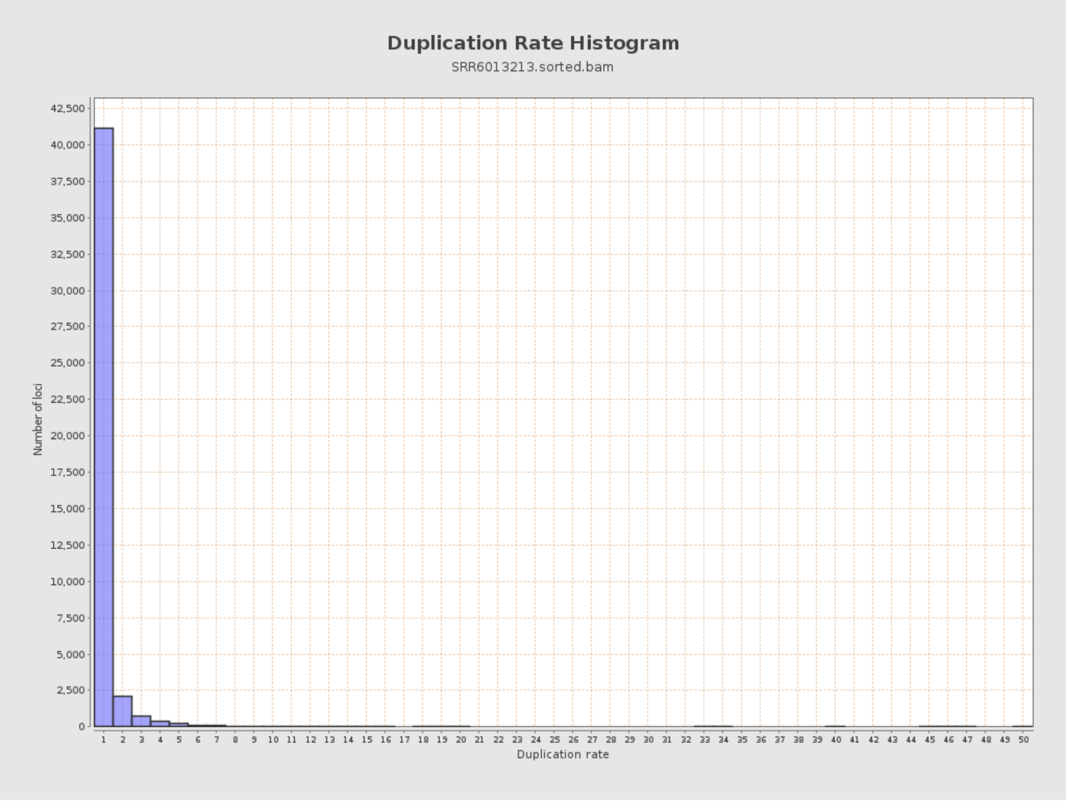
5. Results : Coverage Histogram (0-50X)



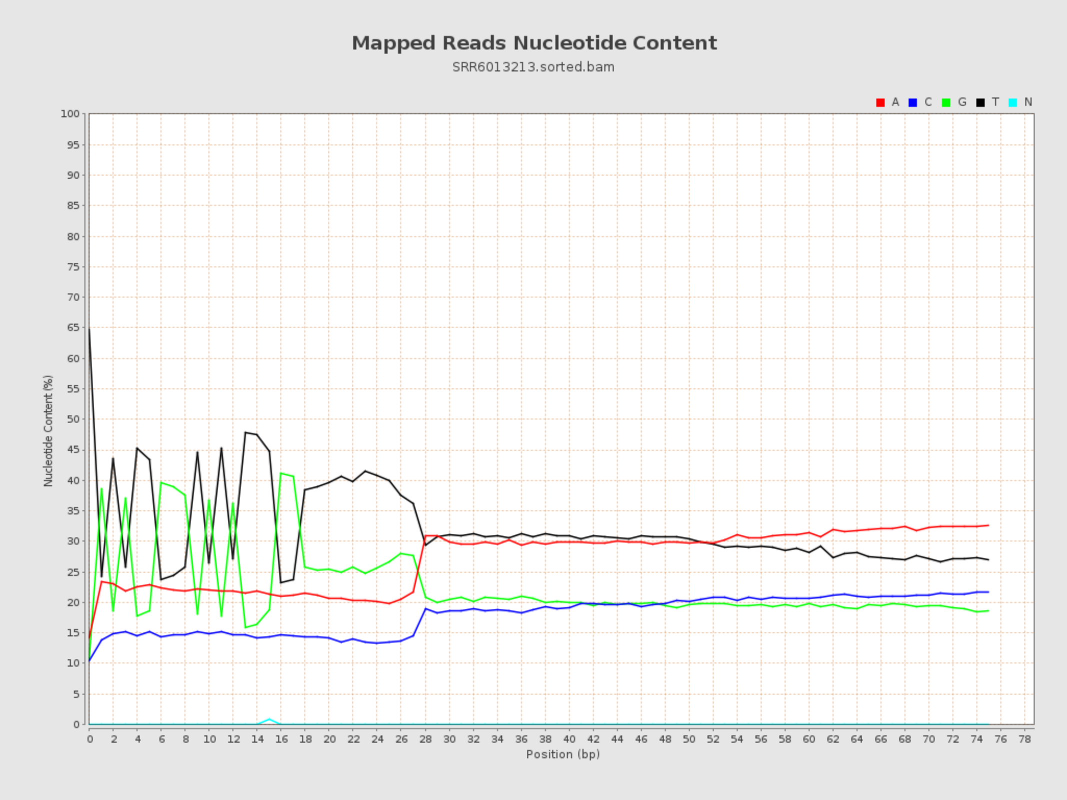
6. Results : Genome Fraction Coverage



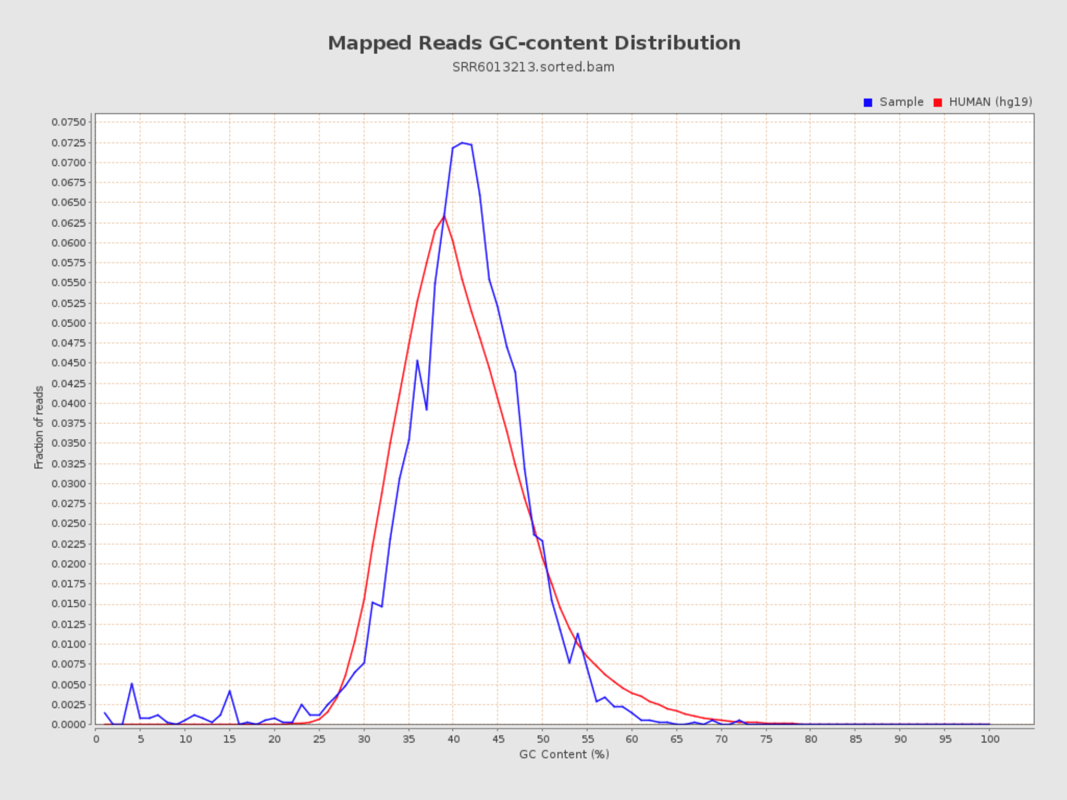
7. Results : Duplication Rate Histogram



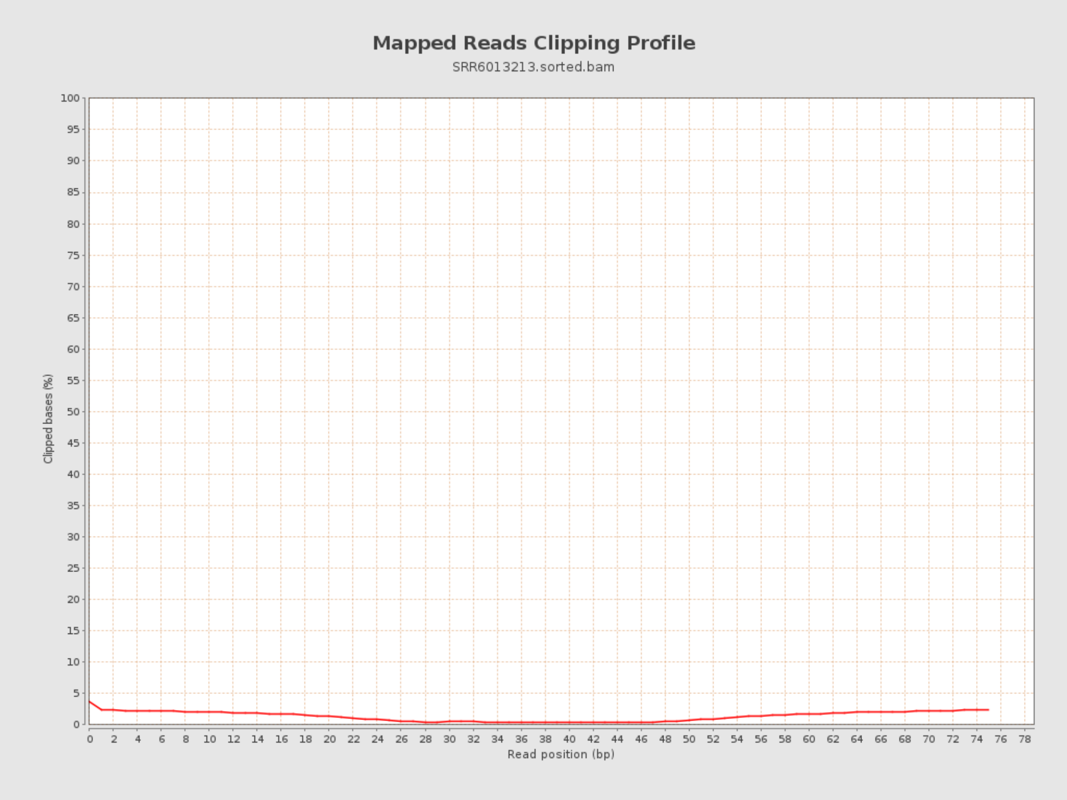
8. Results : Mapped Reads Nucleotide Content



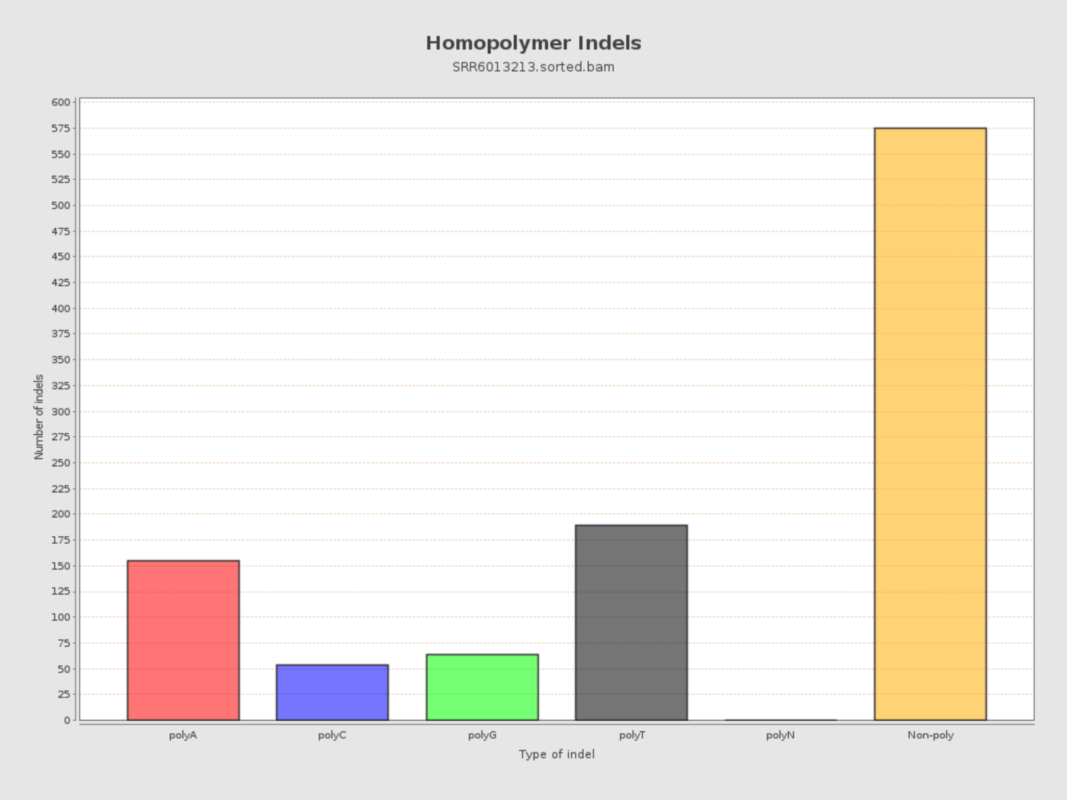
9. Results : Mapped Reads GC-content Distribution



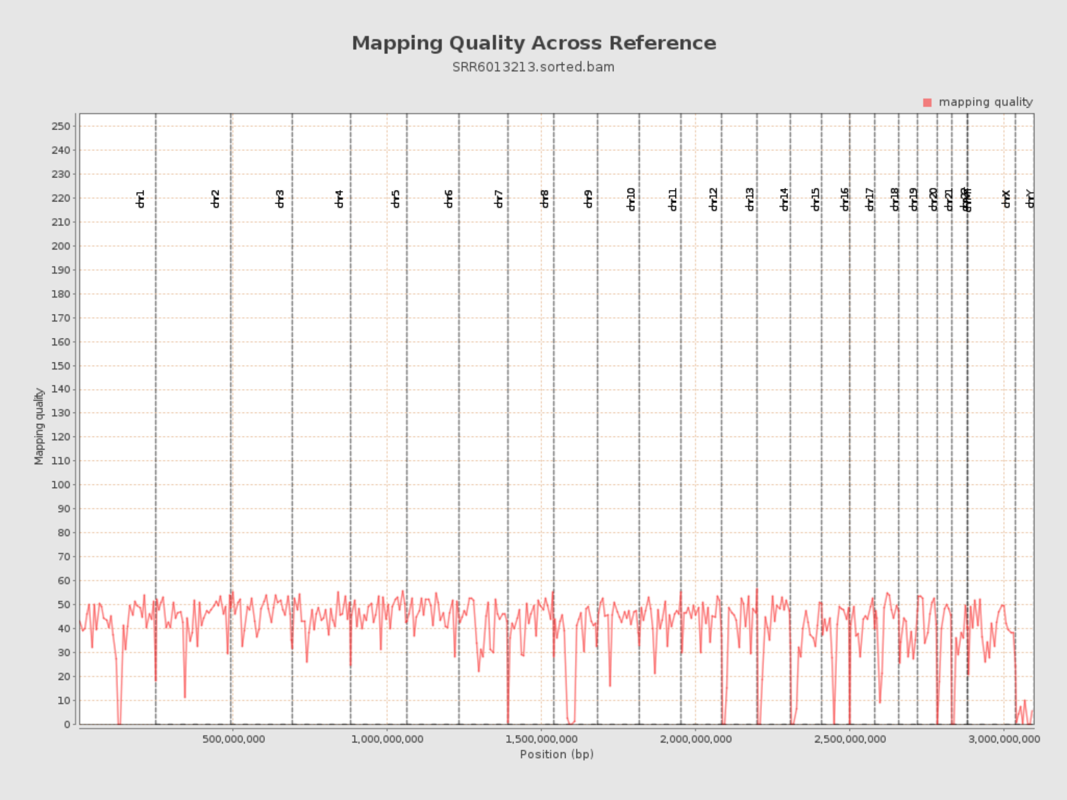
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram