Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:29:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013217.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_SRR6013217 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013217.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:29:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013217.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,211,196
Mapped reads	1,827,637 / 82.65%
Unmapped reads	383,559 / 17.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,003 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	108,794 / 4.92%
Duplication rate	4.91%
Clipped reads	956,406 / 43.25%

2.2. ACGT Content

Number/percentage of A's	31,822,231 / 27.03%
Number/percentage of C's	20,965,152 / 17.81%
Number/percentage of T's	38,282,125 / 32.51%
Number/percentage of G's	26,667,554 / 22.65%
Number/percentage of N's	1,502 / 0%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.3376

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

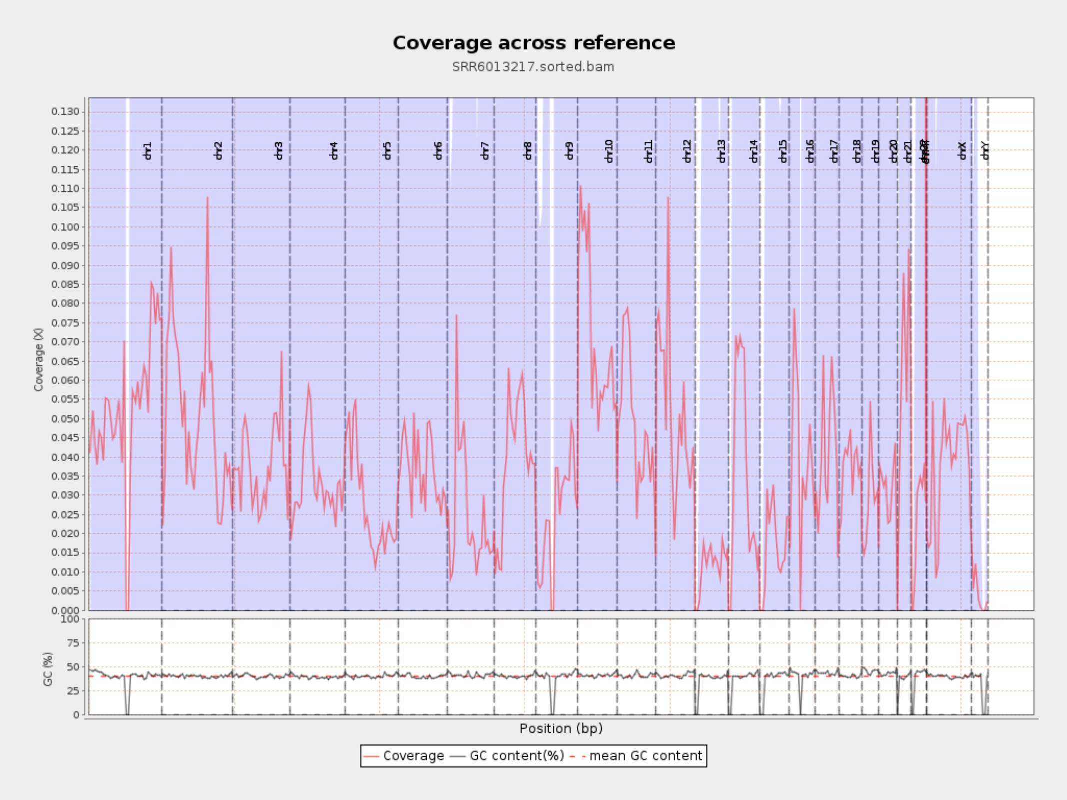
General error rate	0.77%
Mismatches	896,155
Insertions	7,941
Mapped reads with at least one insertion	0.43%
Deletions	31,077
Mapped reads with at least one deletion	1.68%
Homopolymer indels	46.41%

2.6. Chromosome stats

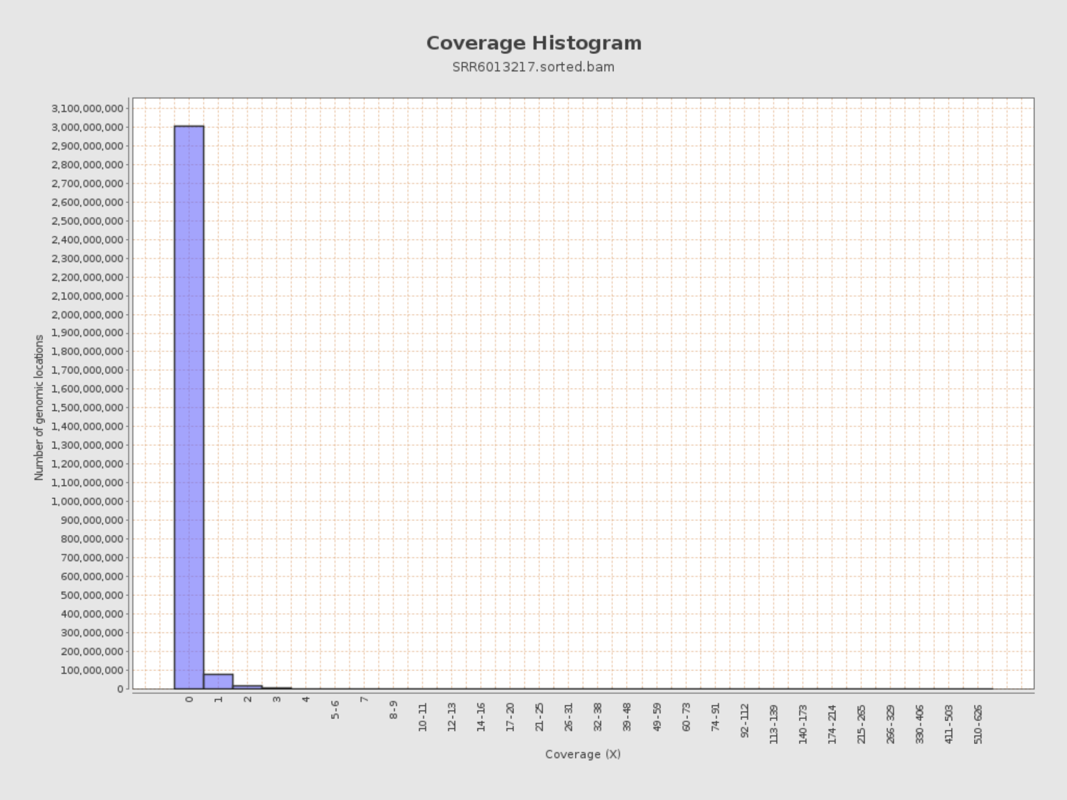
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13044519	0.0523	0.5921
chr2	243199373	12405070	0.051	0.4189
chr3	198022430	7470407	0.0377	0.2415
chr4	191154276	6329447	0.0331	0.2371
chr5	180915260	4948840	0.0274	0.2036
chr6	171115067	6273519	0.0367	0.2888
chr7	159138663	3926815	0.0247	0.3013

chr8	146364022	5756386	0.0393	0.3809
chr9	141213431	3467483	0.0246	0.2597
chr10	135534747	9848056	0.0727	0.4997
chr11	135006516	6587646	0.0488	0.3269
chr12	133851895	7008768	0.0524	0.2852
chr13	115169878	1328828	0.0115	0.1305
chr14	107349540	3796773	0.0354	0.2375
chr15	102531392	1723639	0.0168	0.1603
chr16	90354753	3673069	0.0407	0.2663
chr17	81195210	3313169	0.0408	0.2862
chr18	78077248	2891604	0.037	0.4601
chr19	59128983	1707829	0.0289	0.4541
chr20	63025520	2055090	0.0326	0.2271
chr21	48129895	2898013	0.0602	0.3135
chr22	51304566	1184417	0.0231	0.1837
chrMT	16571	45989	2.7753	2.2792
chrX	155270560	5859619	0.0377	0.263
chrY	59373566	246946	0.0042	0.1048

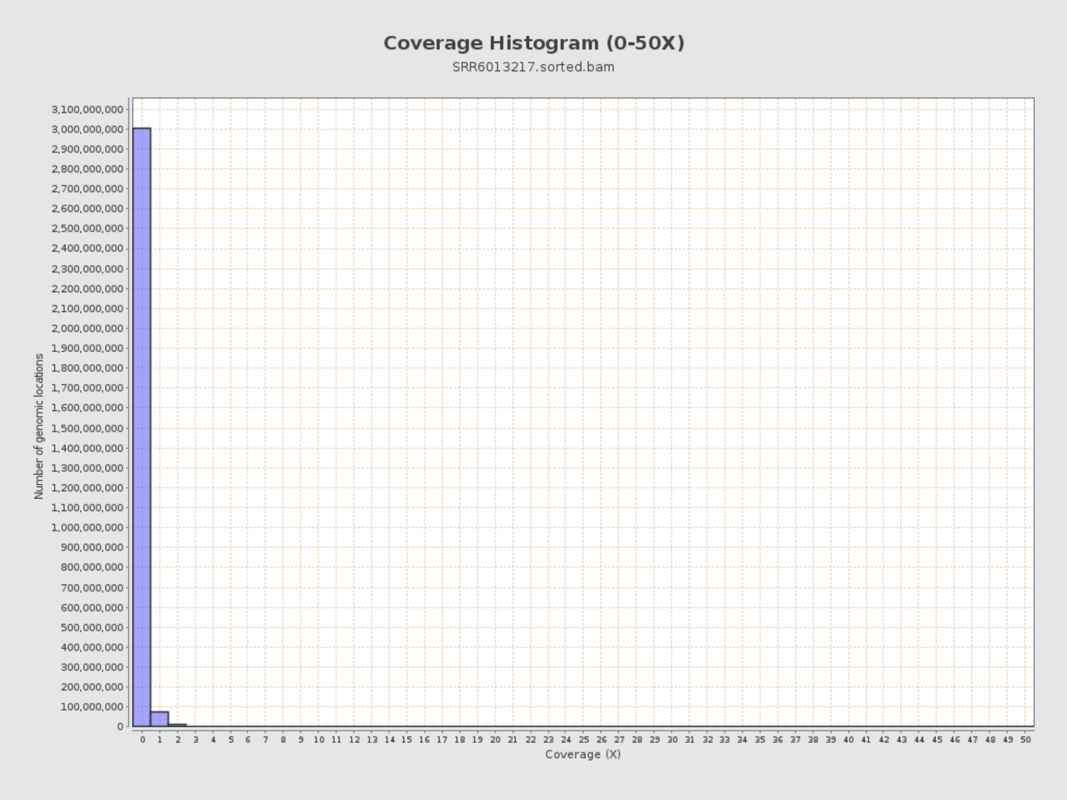
3. Results : Coverage across reference



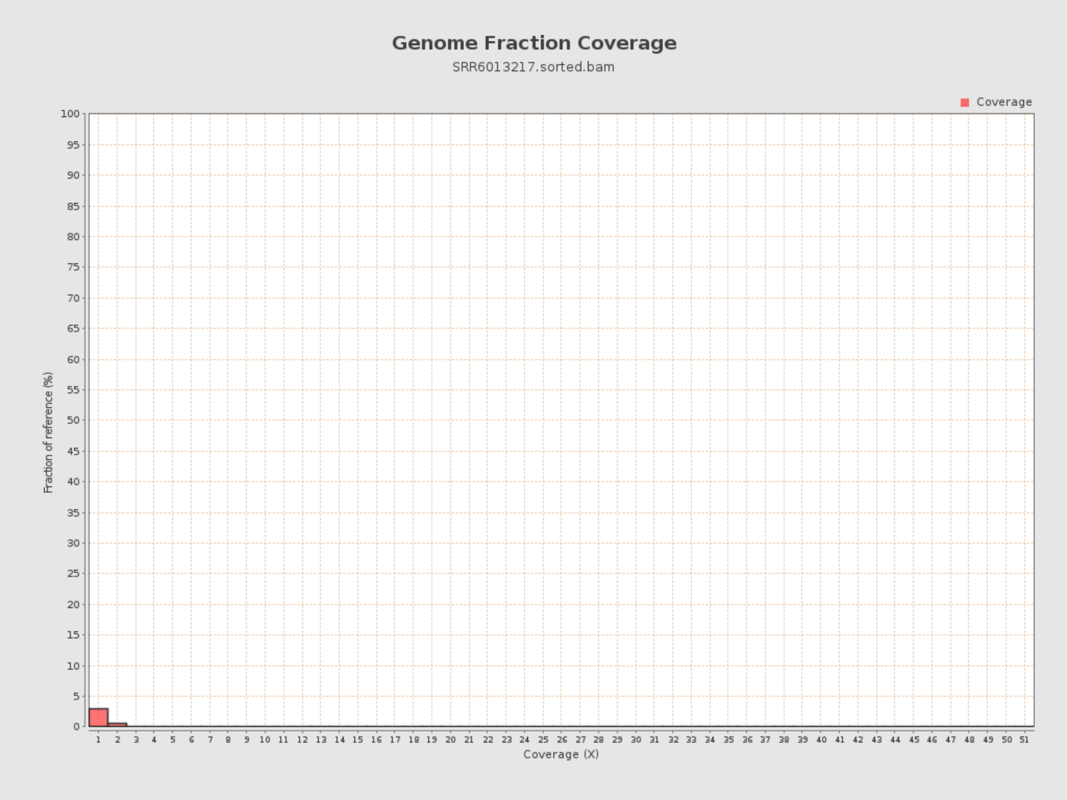
4. Results : Coverage Histogram



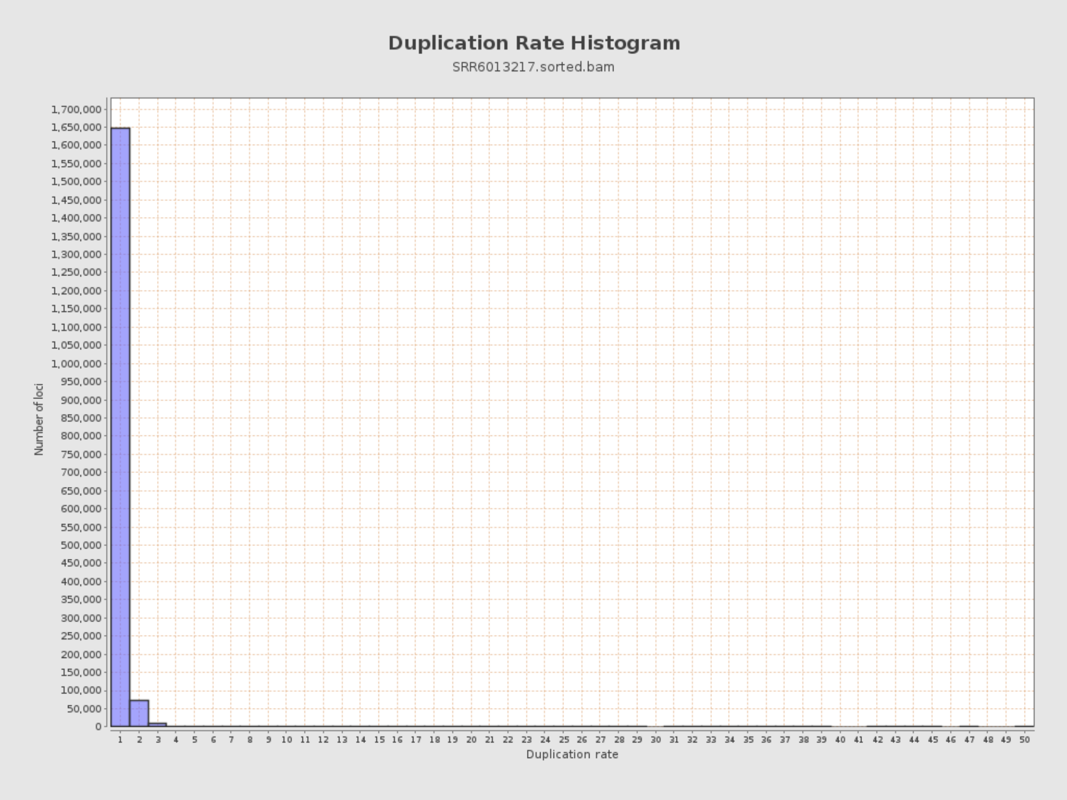
5. Results : Coverage Histogram (0-50X)



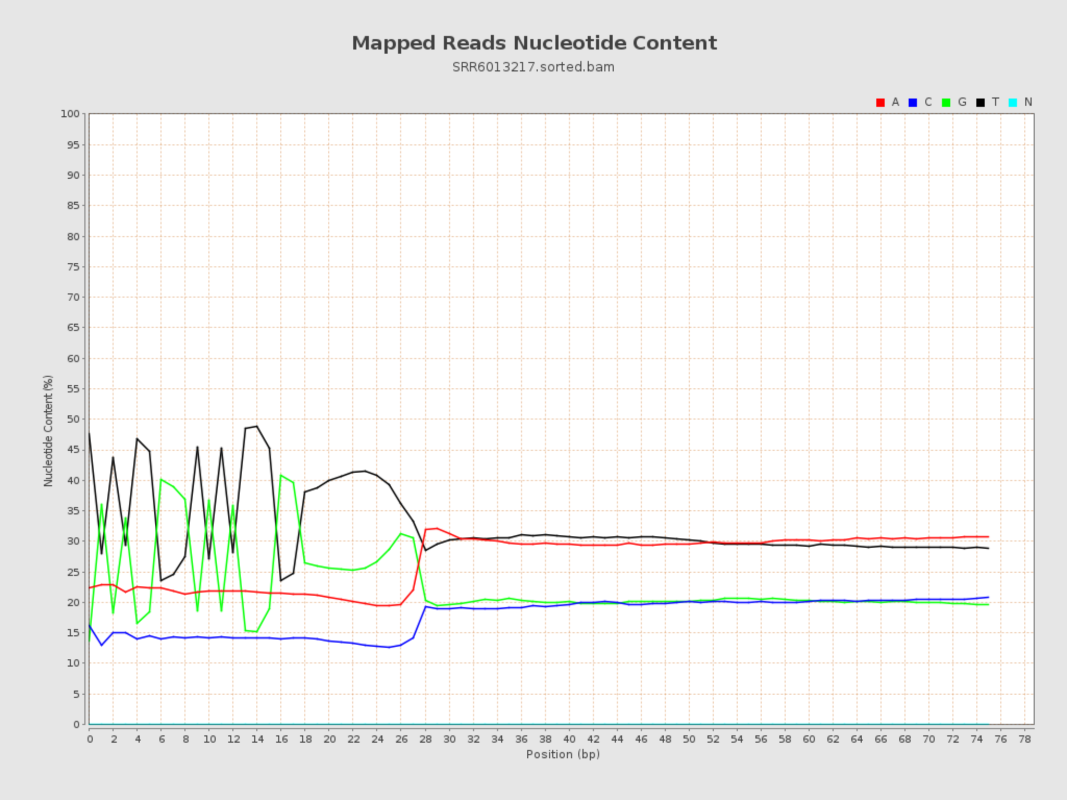
6. Results : Genome Fraction Coverage



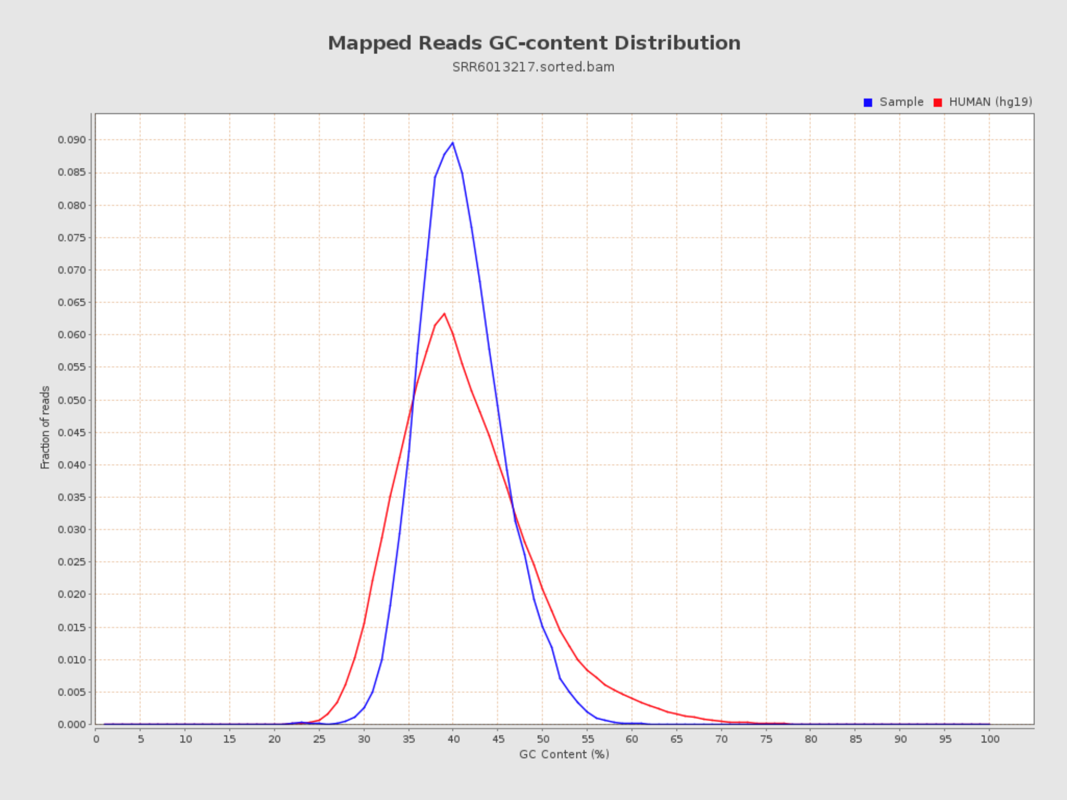
7. Results : Duplication Rate Histogram



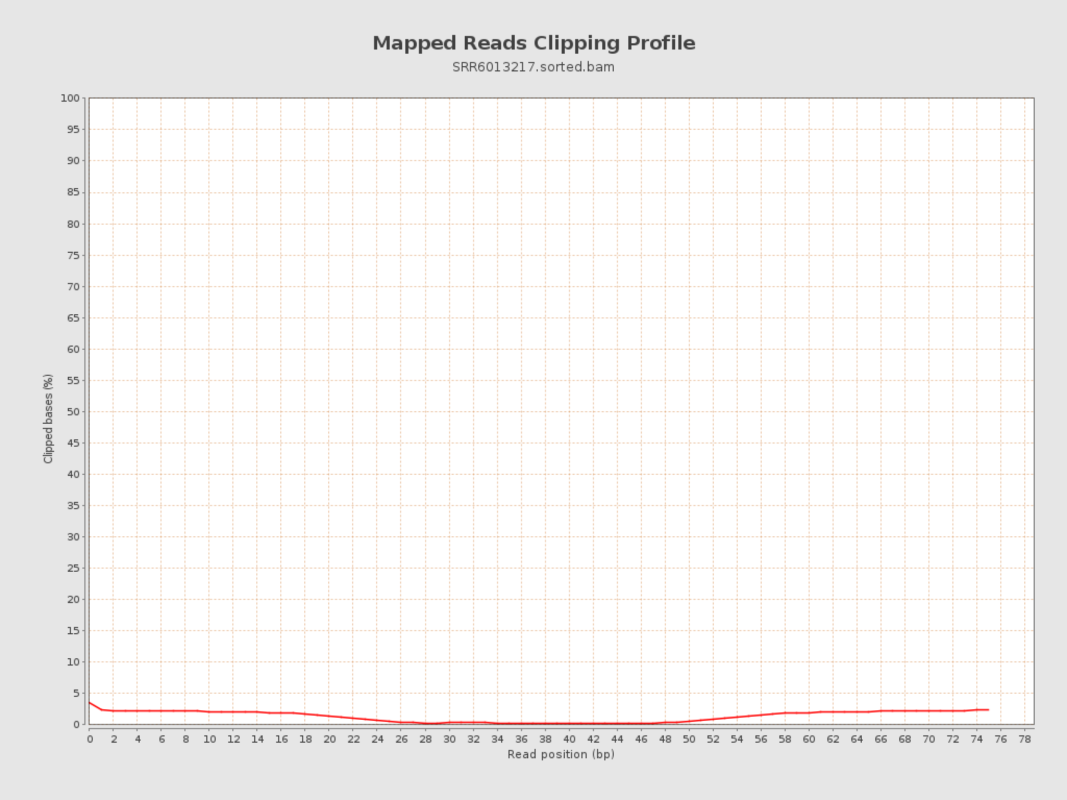
8. Results : Mapped Reads Nucleotide Content



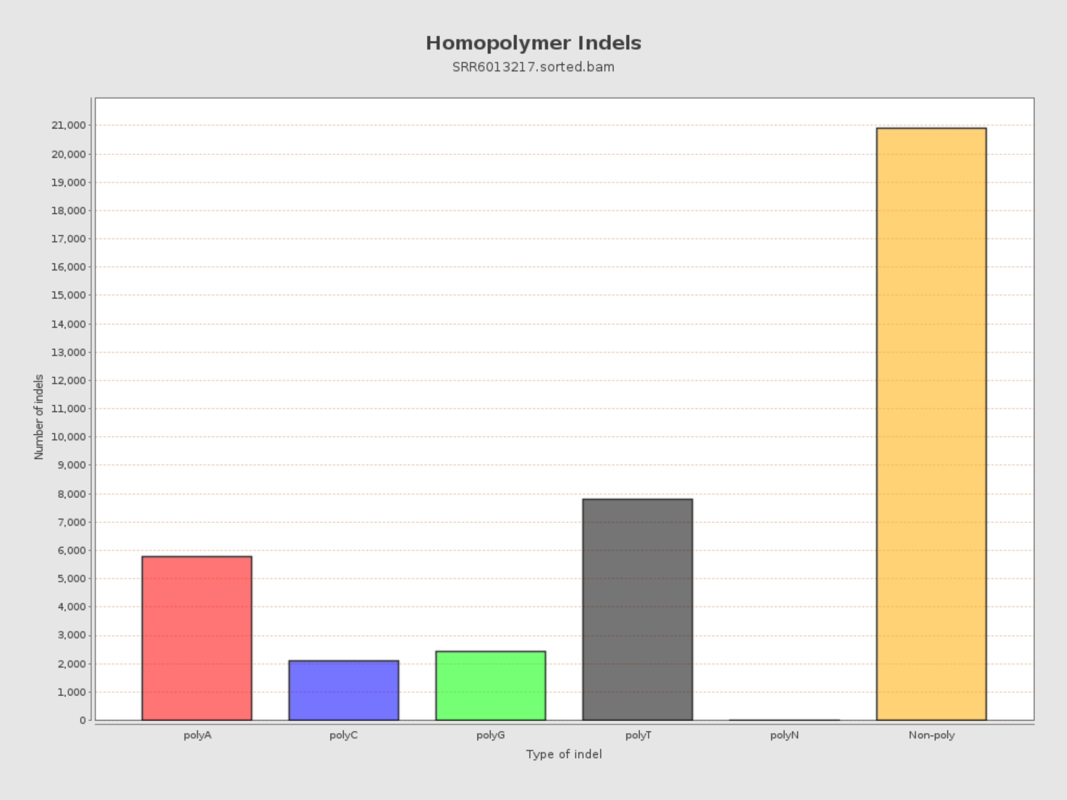
9. Results : Mapped Reads GC-content Distribution



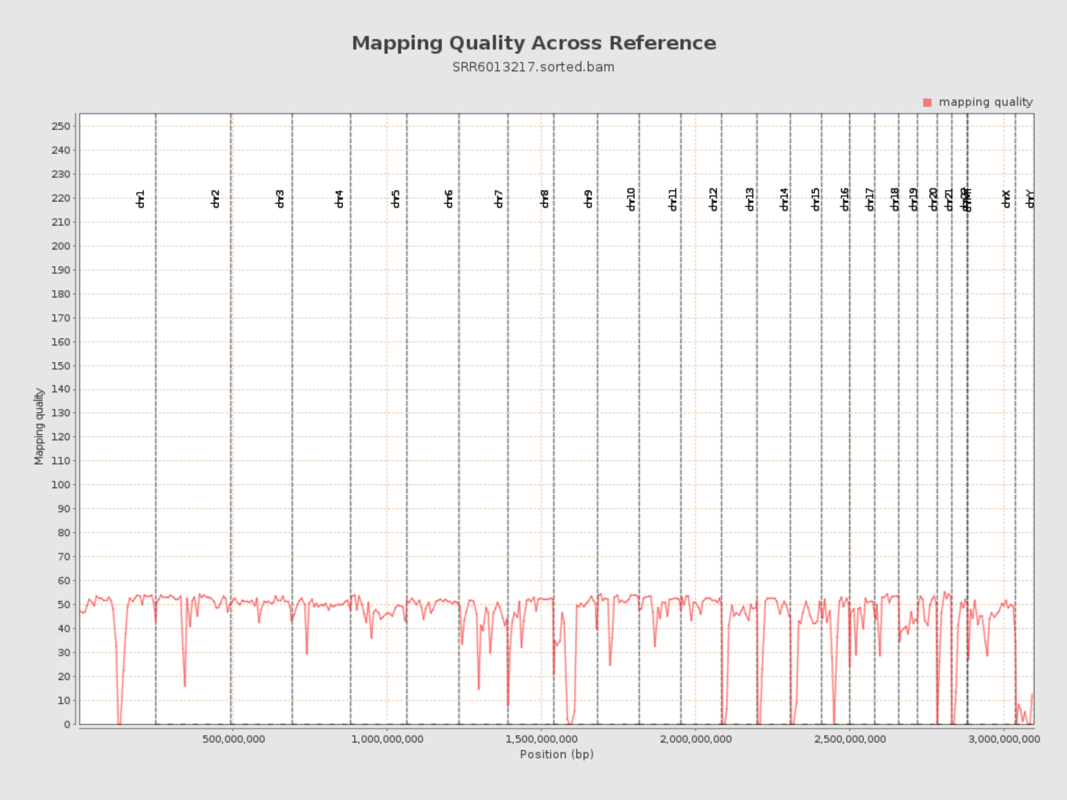
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram