Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:04:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013171.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_SRR6013171 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013171.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:04:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013171.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,260,917
Mapped reads	2,027,816 / 89.69%
Unmapped reads	233,101 / 10.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,075 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	92,826 / 4.11%
Duplication rate	3.68%
Clipped reads	866,013 / 38.3%

2.2. ACGT Content

Number/percentage of A's	38,144,033 / 28.09%
Number/percentage of C's	24,884,609 / 18.33%
Number/percentage of T's	43,354,187 / 31.93%
Number/percentage of G's	29,398,385 / 21.65%
Number/percentage of N's	1,784 / 0%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0439

Standard Deviation	0.3586

2.4. Mapping Quality

Mean Mapping Quality	43.23

2.5. Mismatches and indels

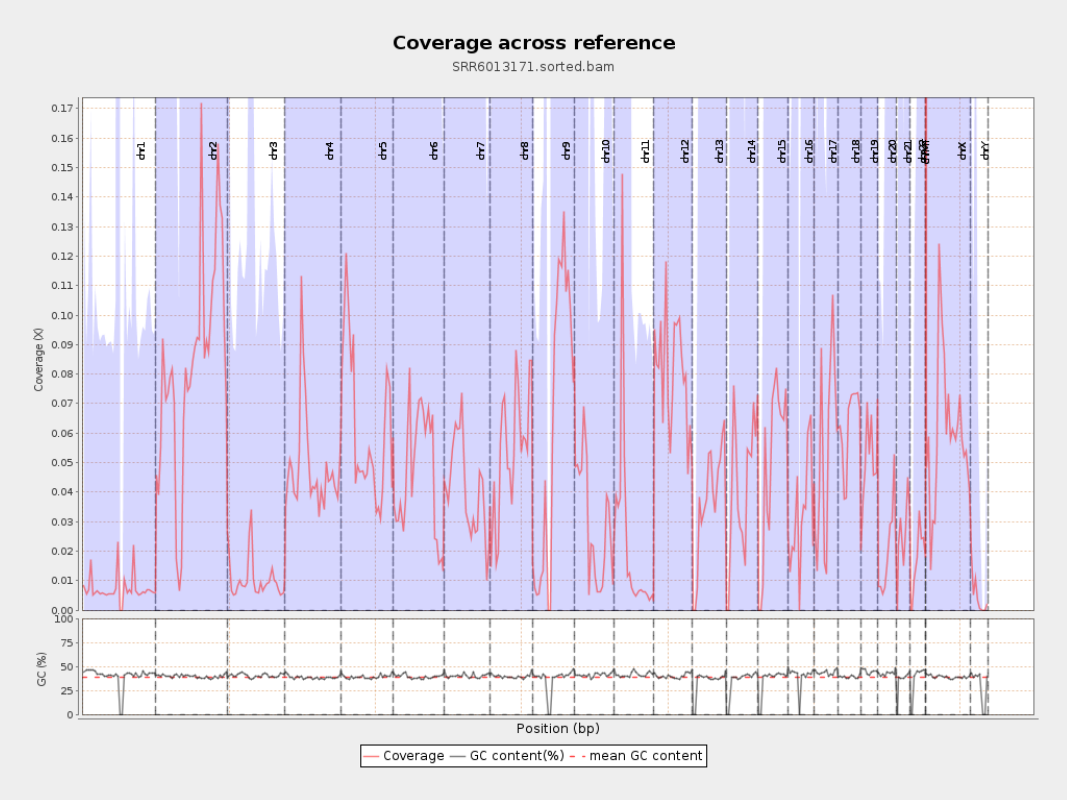
General error rate	0.72%
Mismatches	952,970
Insertions	9,927
Mapped reads with at least one insertion	0.49%
Deletions	33,826
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.3%

2.6. Chromosome stats

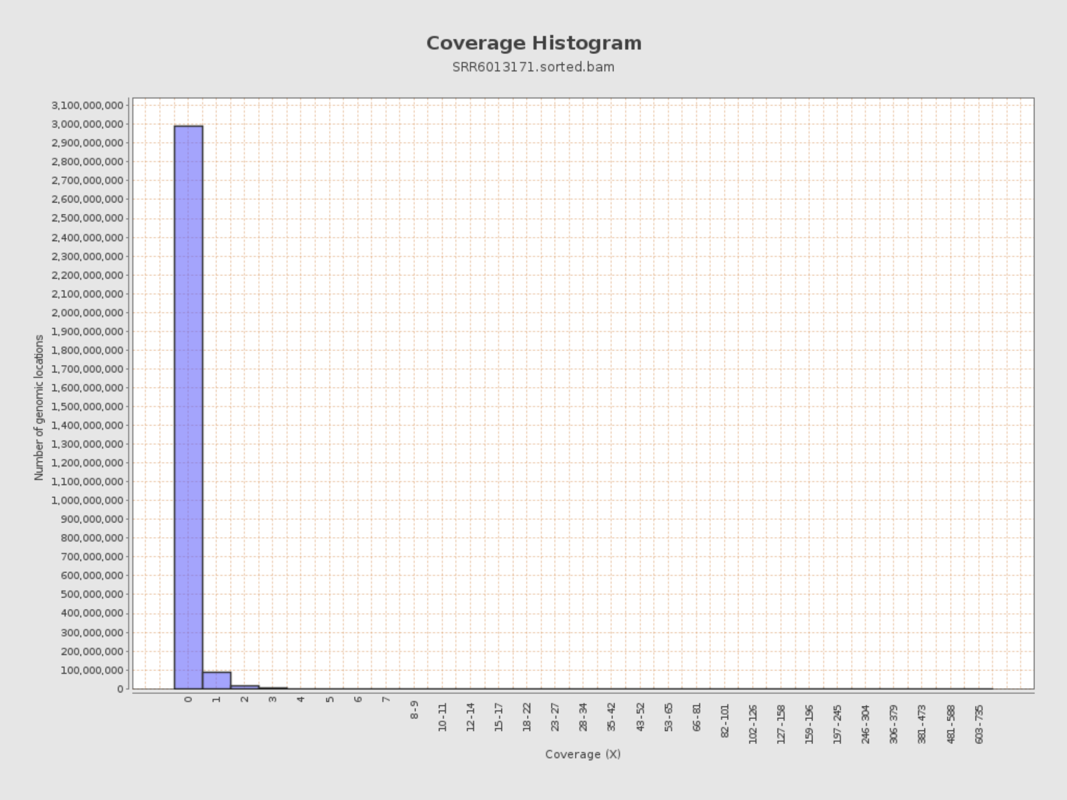
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1806715	0.0072	0.3347
chr2	243199373	20299884	0.0835	0.4755
chr3	198022430	2123310	0.0107	0.1233
chr4	191154276	9442666	0.0494	0.2775
chr5	180915260	11074233	0.0612	0.3044
chr6	171115067	8009555	0.0468	0.3902
chr7	159138663	6493898	0.0408	0.5213

chr8	146364022	7945823	0.0543	0.5114
chr9	141213431	8730101	0.0618	0.4082
chr10	135534747	3955140	0.0292	0.3323
chr11	135006516	3121134	0.0231	0.2551
chr12	133851895	10752463	0.0803	0.3491
chr13	115169878	4323175	0.0375	0.2337
chr14	107349540	4464653	0.0416	0.2809
chr15	102531392	5117570	0.0499	0.2721
chr16	90354753	2828538	0.0313	0.2479
chr17	81195210	4410433	0.0543	0.309
chr18	78077248	4857799	0.0622	0.7091
chr19	59128983	3046660	0.0515	0.3543
chr20	63025520	1288860	0.0204	0.1782
chr21	48129895	1249644	0.026	0.2163
chr22	51304566	893897	0.0174	0.1551
chrMT	16571	105686	6.3778	4.8568
chrX	155270560	9224438	0.0594	0.3449
chrY	59373566	274928	0.0046	0.1045

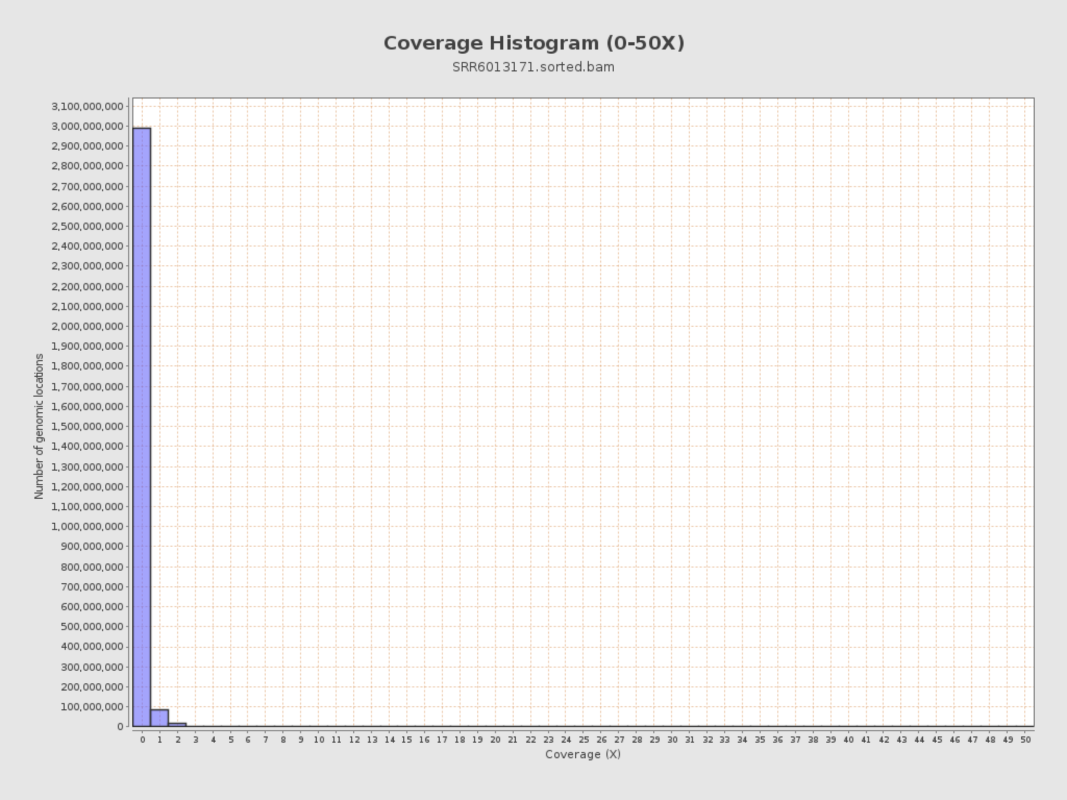
3. Results : Coverage across reference



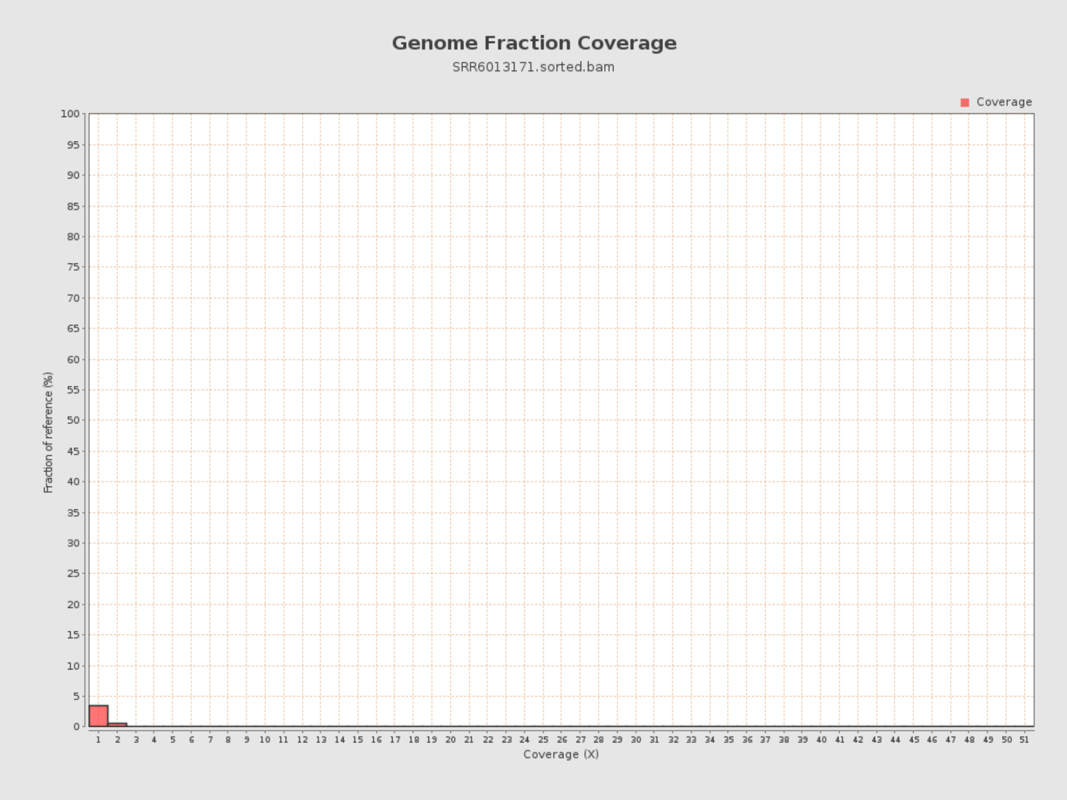
4. Results : Coverage Histogram



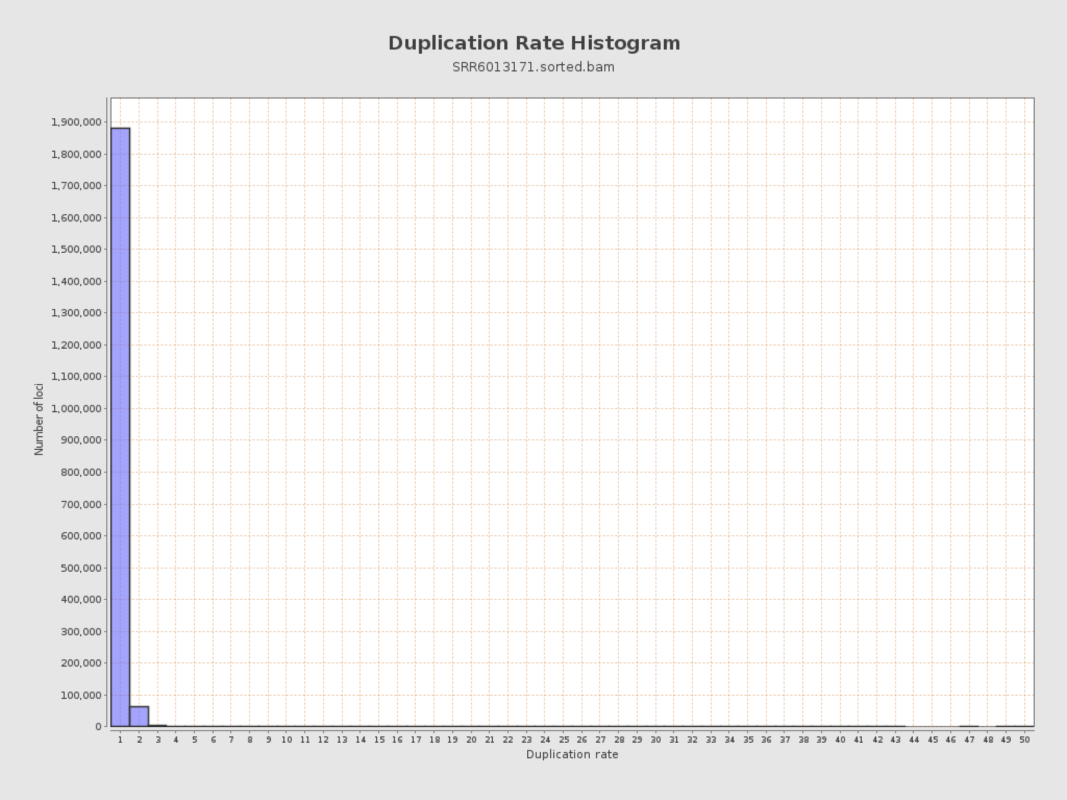
5. Results : Coverage Histogram (0-50X)



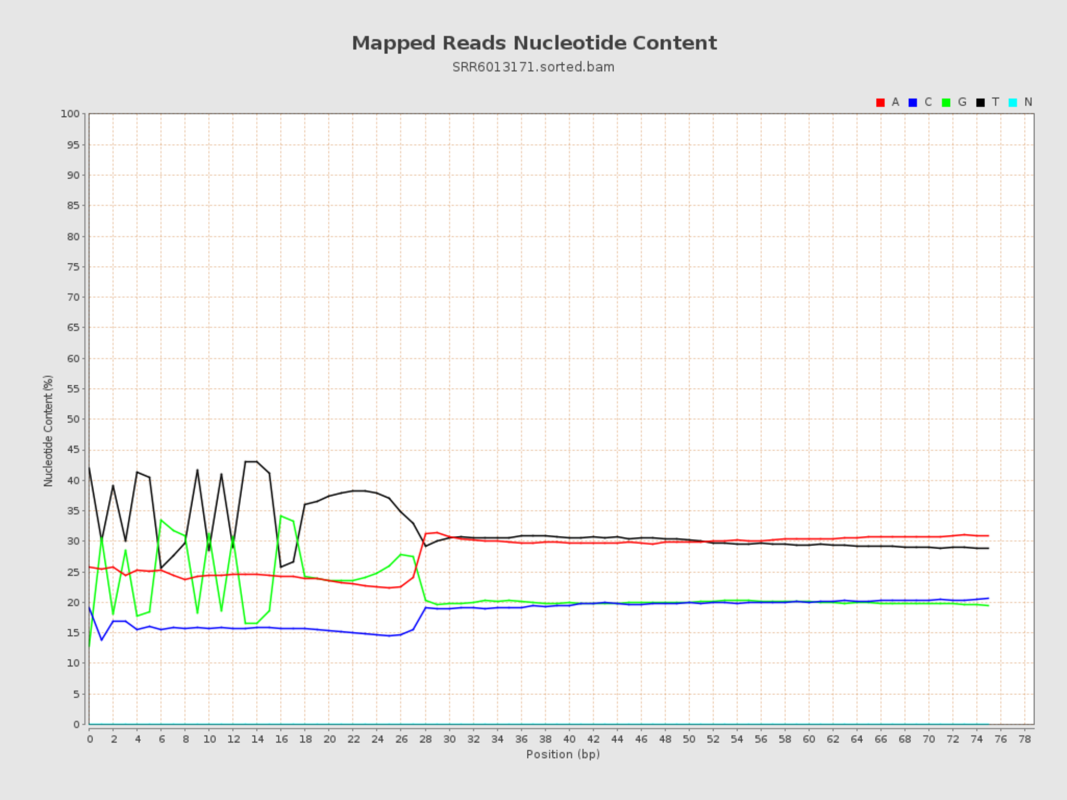
6. Results : Genome Fraction Coverage



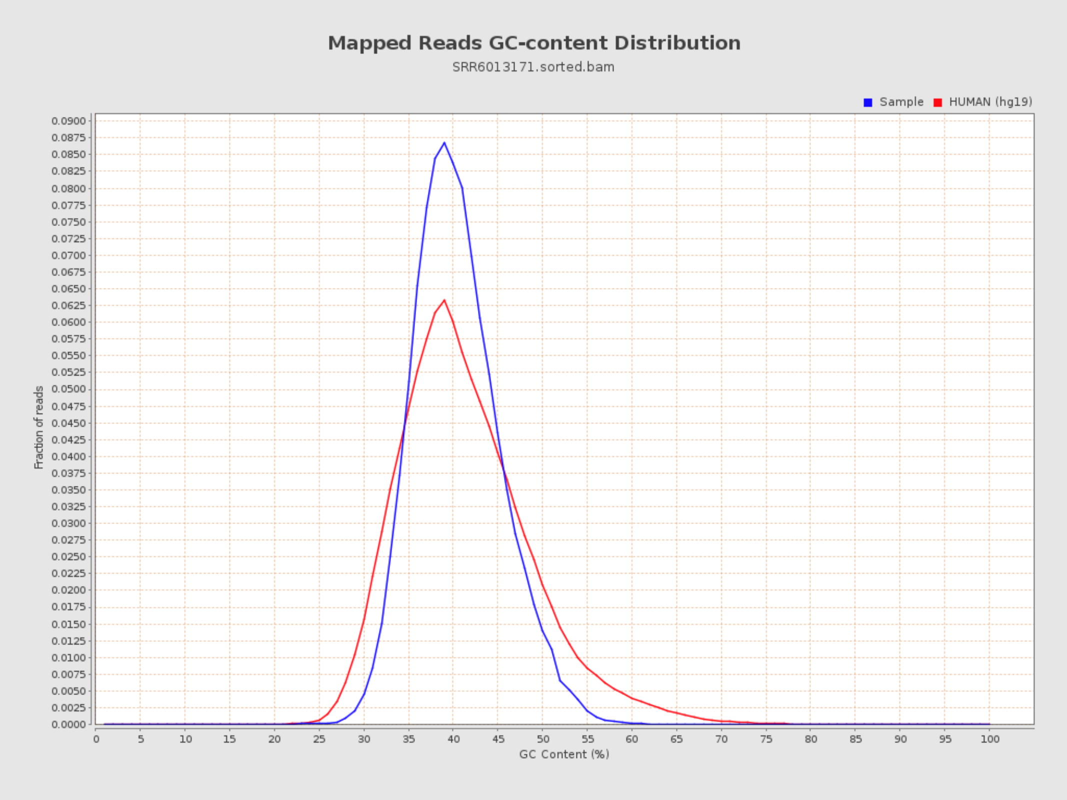
7. Results : Duplication Rate Histogram



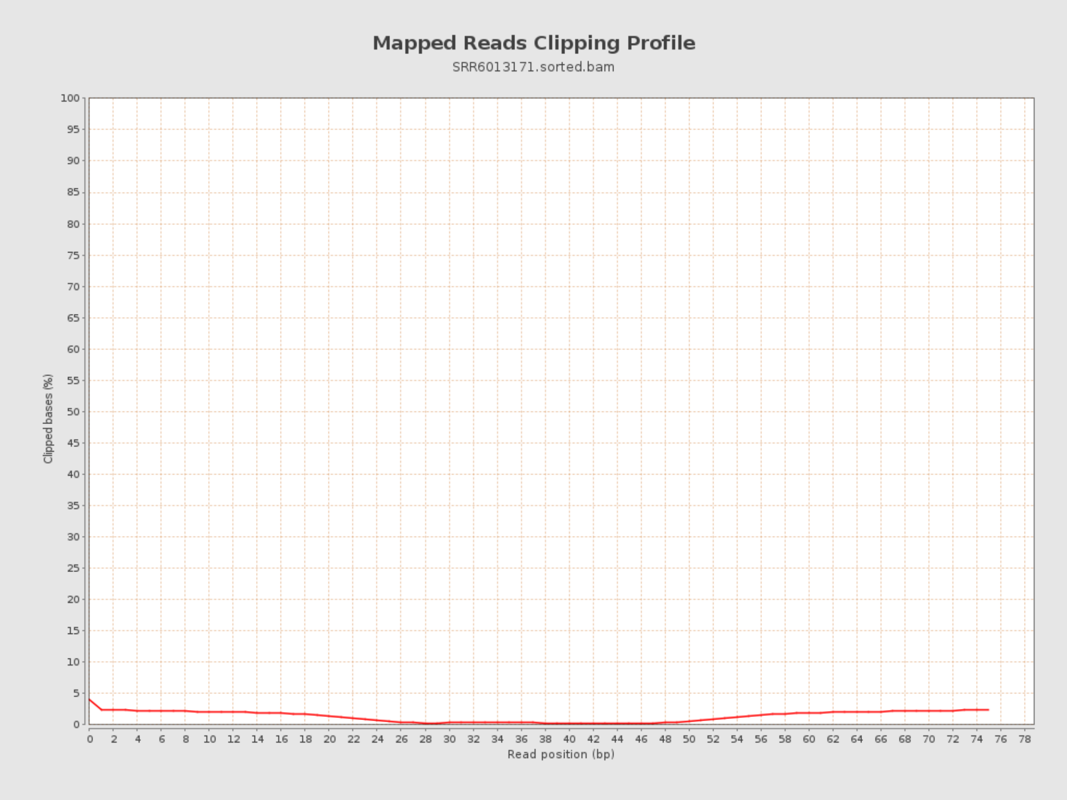
8. Results : Mapped Reads Nucleotide Content



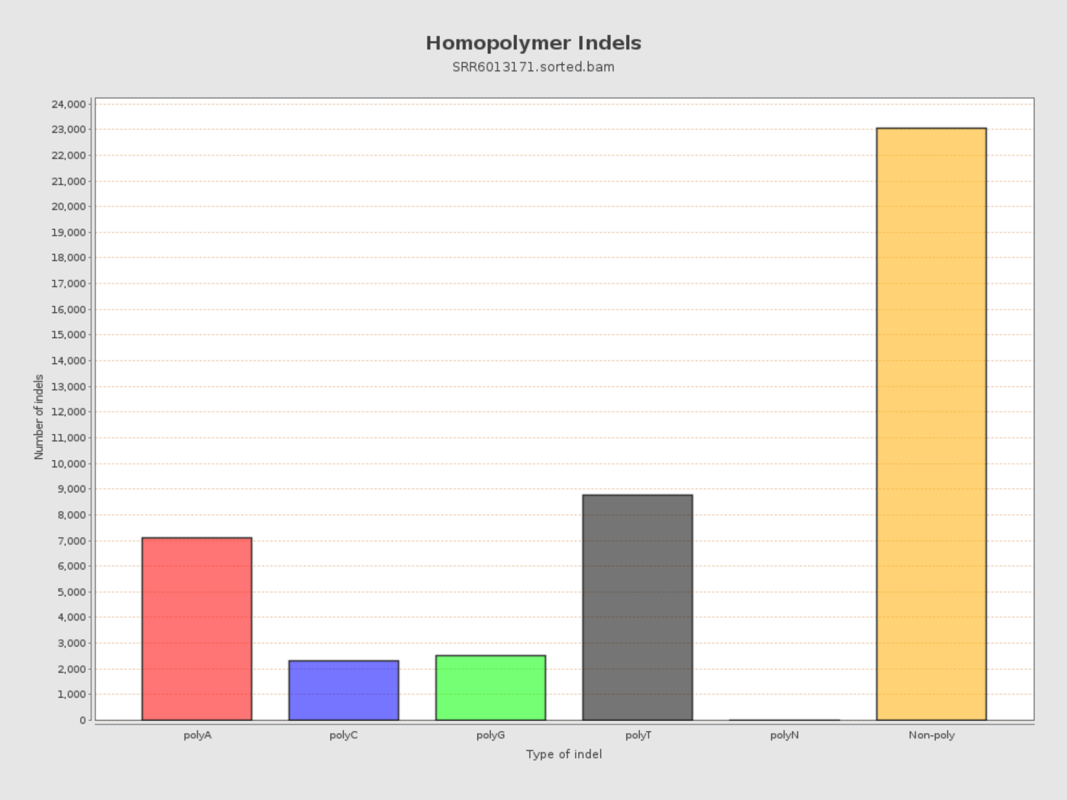
9. Results : Mapped Reads GC-content Distribution



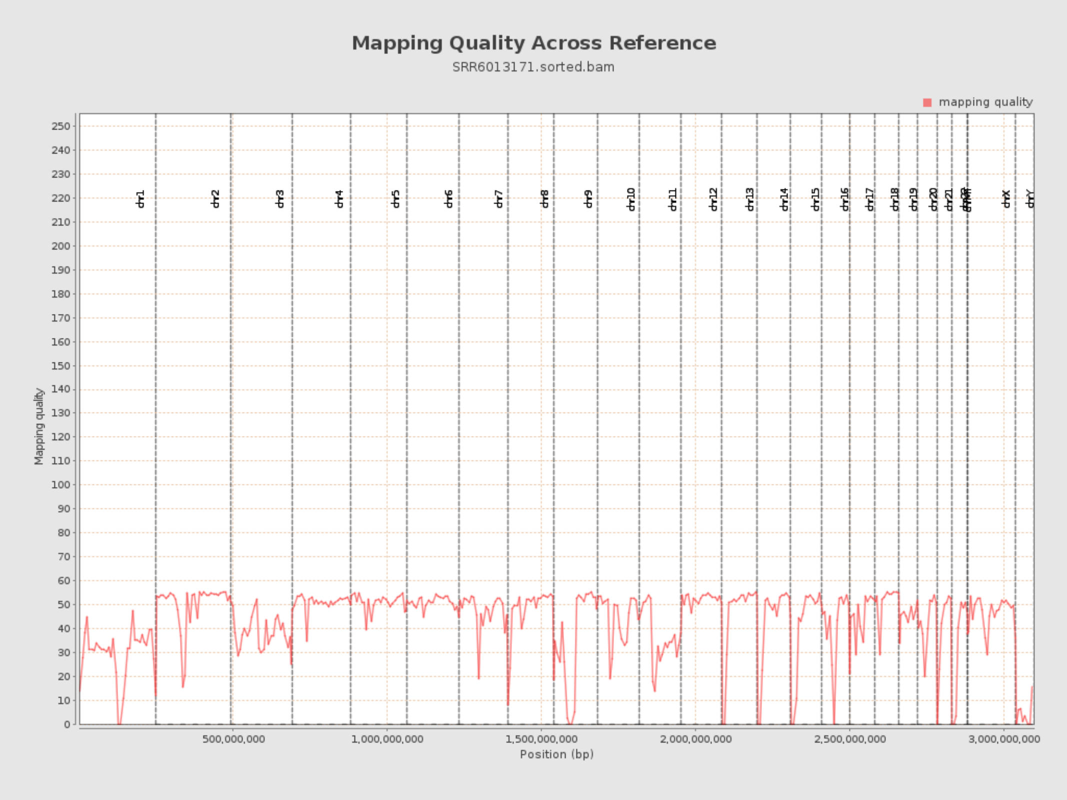
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram