Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:18:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013175.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_SRR6013175 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013175.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:18:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,877,687
Mapped reads	2,606,016 / 90.56%
Unmapped reads	271,671 / 9.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,895 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	78,088 / 2.71%
Duplication rate	2.08%
Clipped reads	1,305,936 / 45.38%

2.2. ACGT Content

Number/percentage of A's	46,993,041 / 27.73%
Number/percentage of C's	32,617,236 / 19.24%
Number/percentage of T's	51,281,596 / 30.26%
Number/percentage of G's	38,558,155 / 22.75%
Number/percentage of N's	39,919 / 0.02%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0548

Standard Deviation	0.4372

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

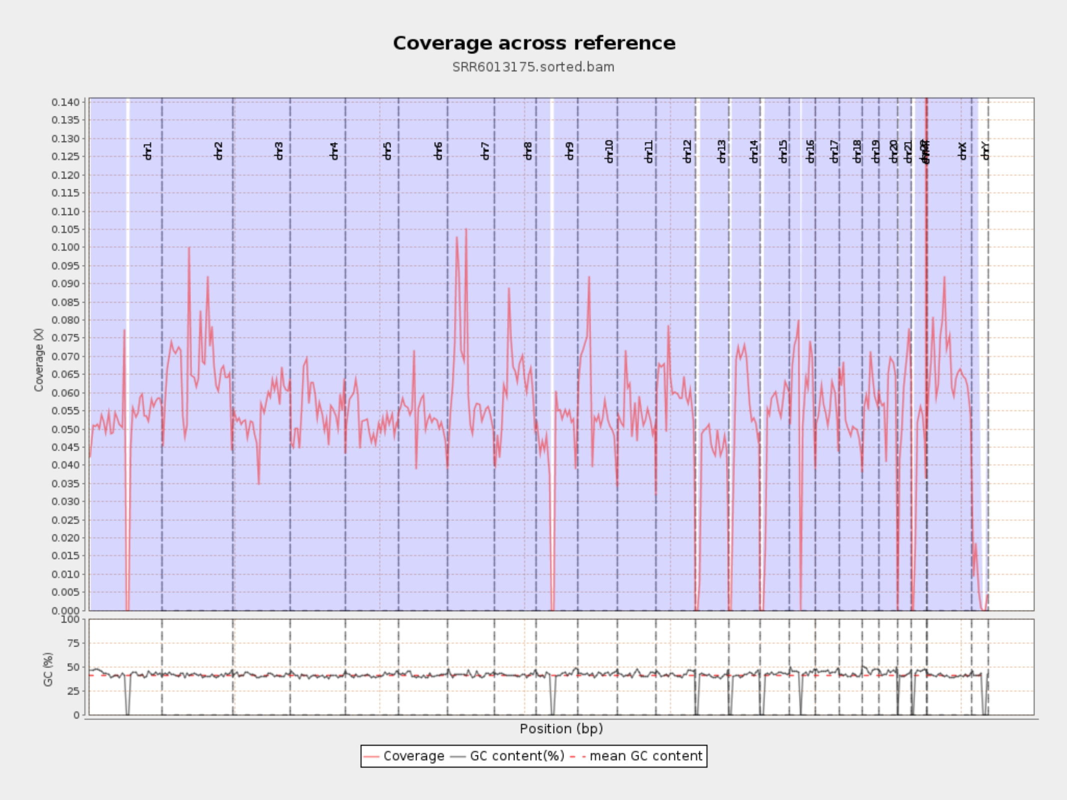
General error rate	0.8%
Mismatches	1,337,799
Insertions	11,613
Mapped reads with at least one insertion	0.44%
Deletions	41,492
Mapped reads with at least one deletion	1.58%
Homopolymer indels	44.53%

2.6. Chromosome stats

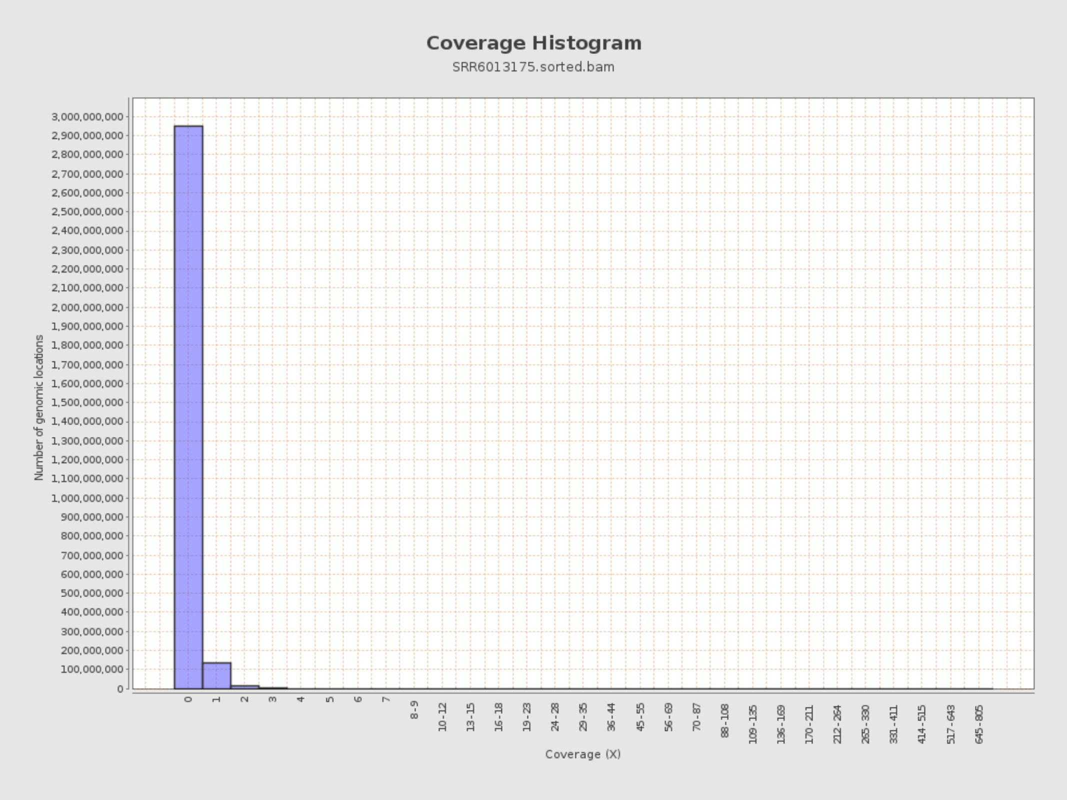
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12584746	0.0505	0.7191
chr2	243199373	16298776	0.067	0.5377
chr3	198022430	10936967	0.0552	0.2602
chr4	191154276	10542647	0.0552	0.274
chr5	180915260	9476278	0.0524	0.255
chr6	171115067	9178720	0.0536	0.3277
chr7	159138663	10117467	0.0636	0.7899

chr8	146364022	8972836	0.0613	0.3661
chr9	141213431	6290993	0.0445	0.3794
chr10	135534747	7929278	0.0585	0.4569
chr11	135006516	7299236	0.0541	0.3482
chr12	133851895	8164016	0.061	0.2763
chr13	115169878	4468762	0.0388	0.2192
chr14	107349540	5578606	0.052	0.291
chr15	102531392	4785802	0.0467	0.243
chr16	90354753	5412480	0.0599	0.314
chr17	81195210	4496706	0.0554	0.3029
chr18	78077248	4163016	0.0533	0.7452
chr19	59128983	3501781	0.0592	0.6023
chr20	63025520	3721883	0.0591	0.2763
chr21	48129895	2647673	0.055	0.2778
chr22	51304566	1828070	0.0356	0.2072
chrMT	16571	341494	20.6079	13.5923
chrX	155270560	10406007	0.067	0.3256
chrY	59373566	418092	0.007	0.1447

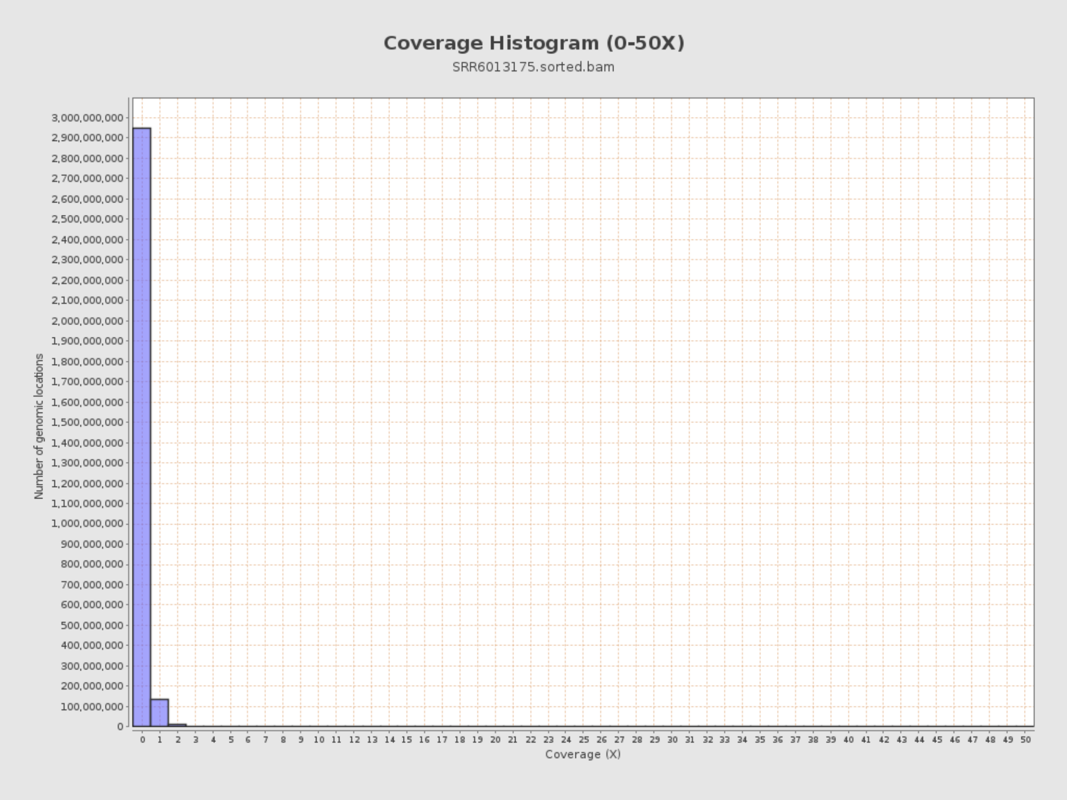
3. Results : Coverage across reference



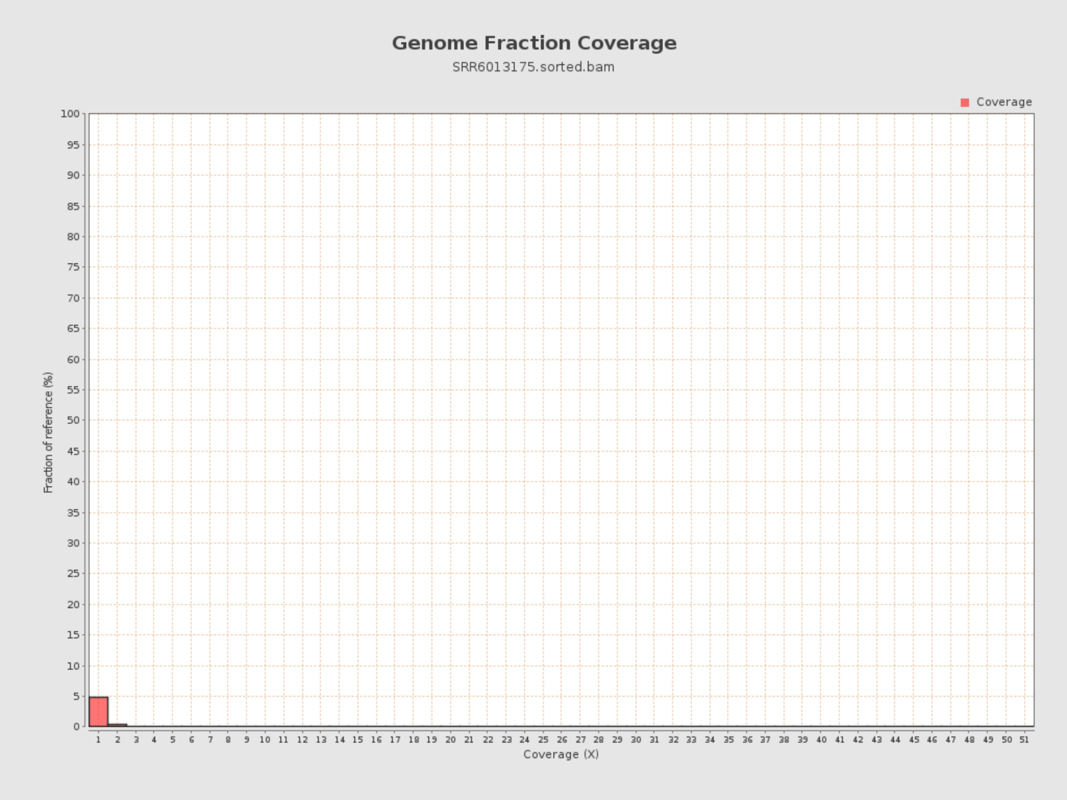
4. Results : Coverage Histogram



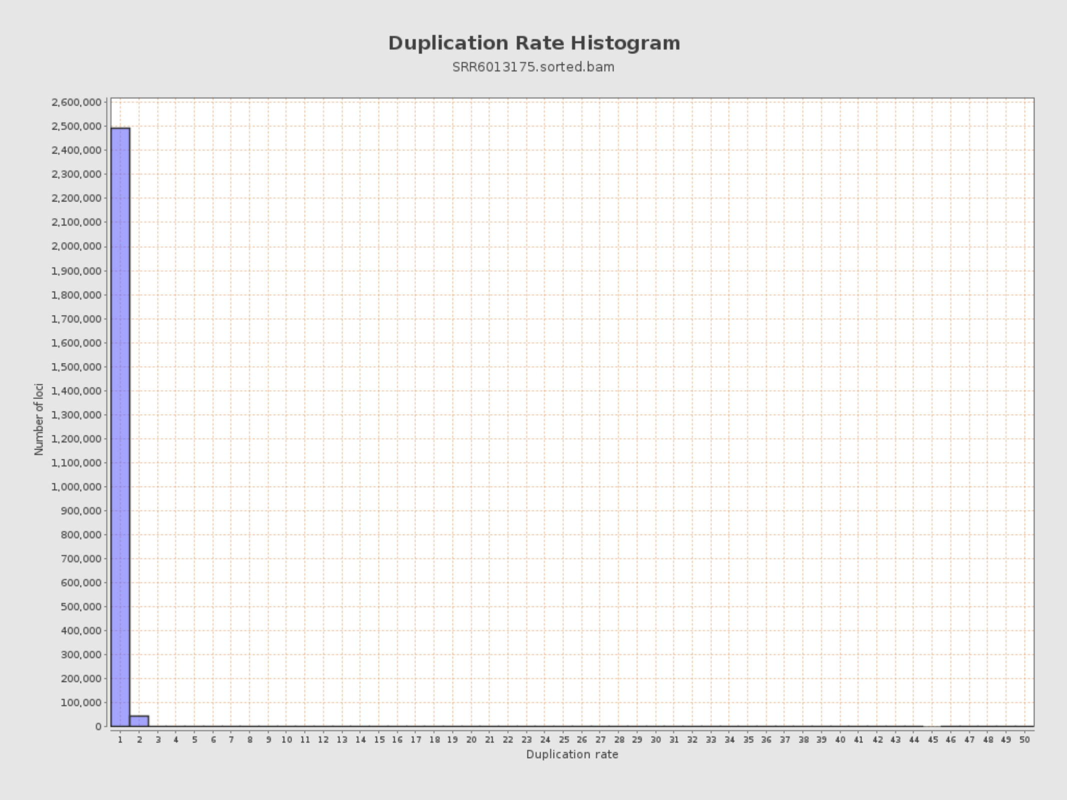
5. Results : Coverage Histogram (0-50X)



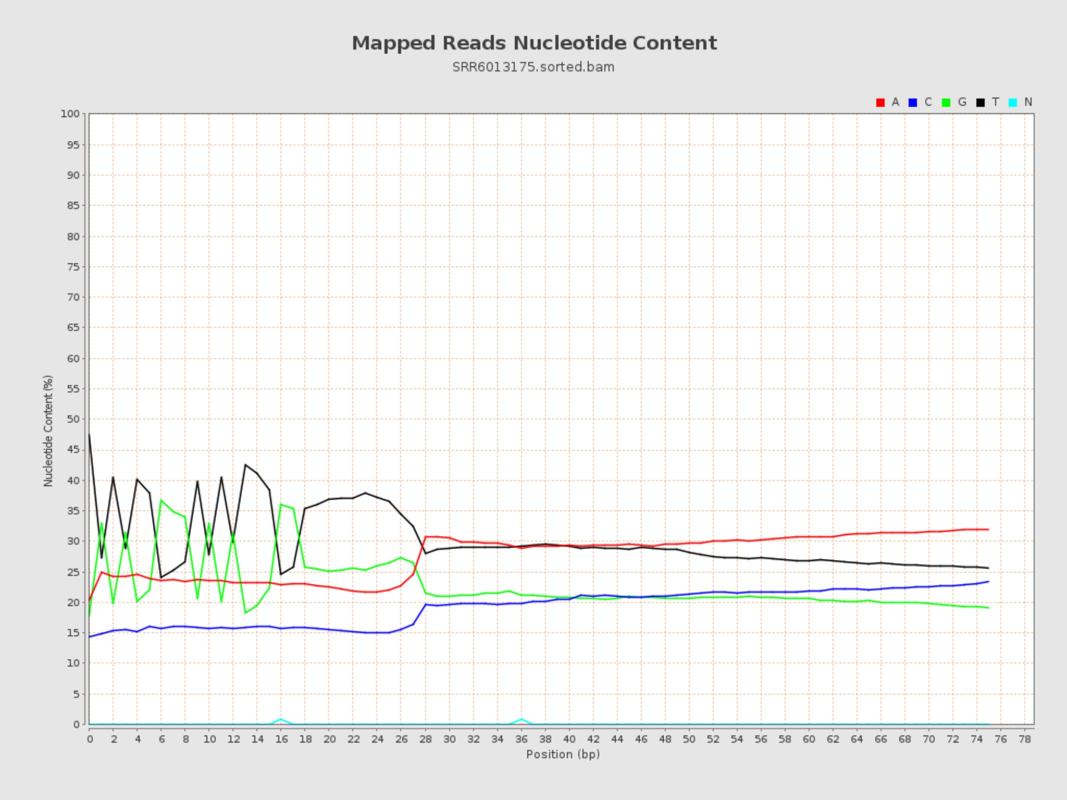
6. Results : Genome Fraction Coverage



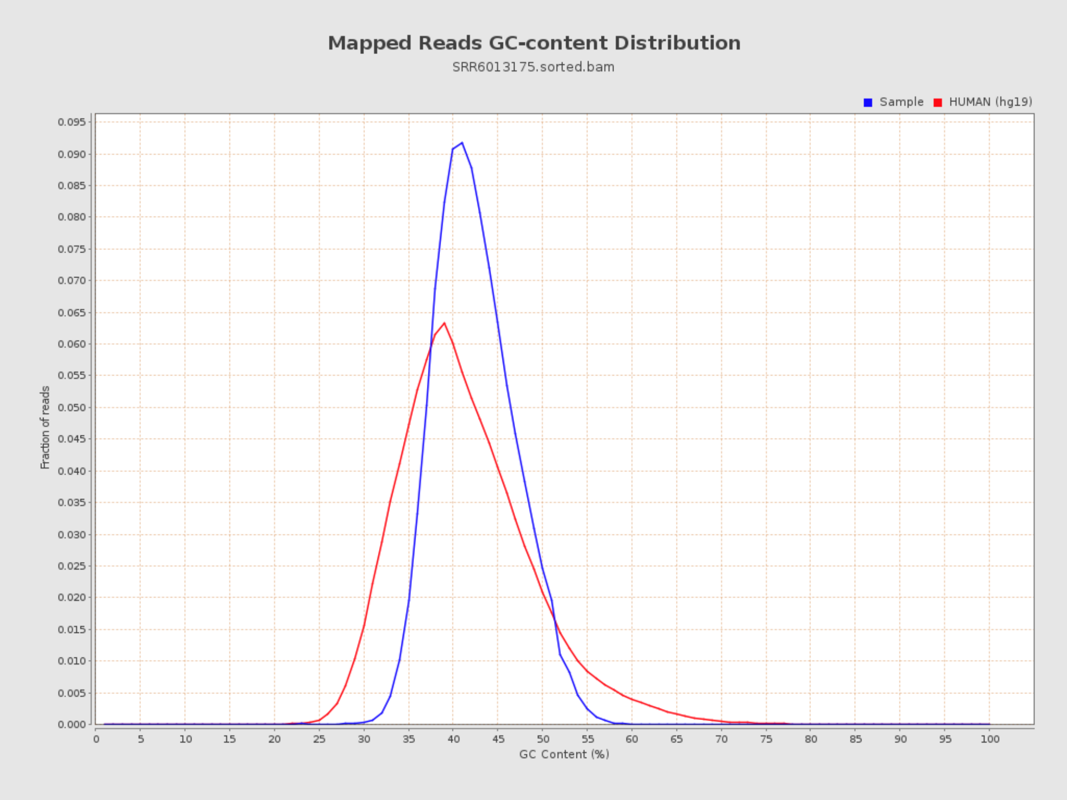
7. Results : Duplication Rate Histogram



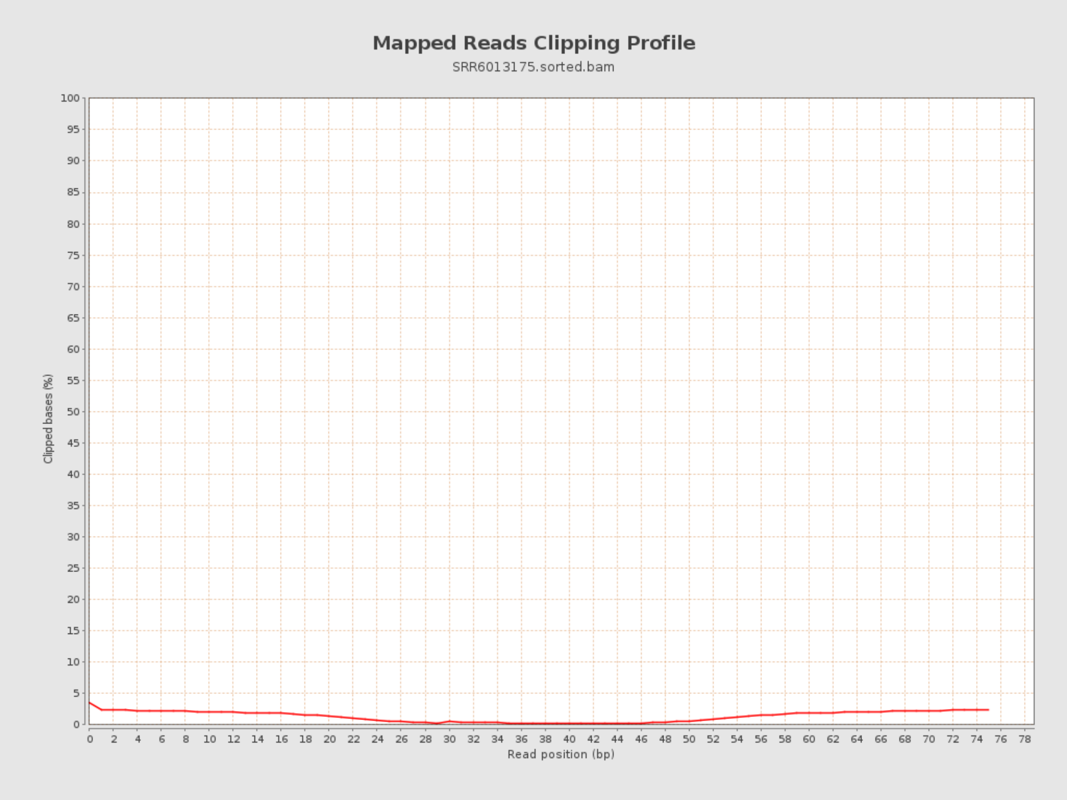
8. Results : Mapped Reads Nucleotide Content



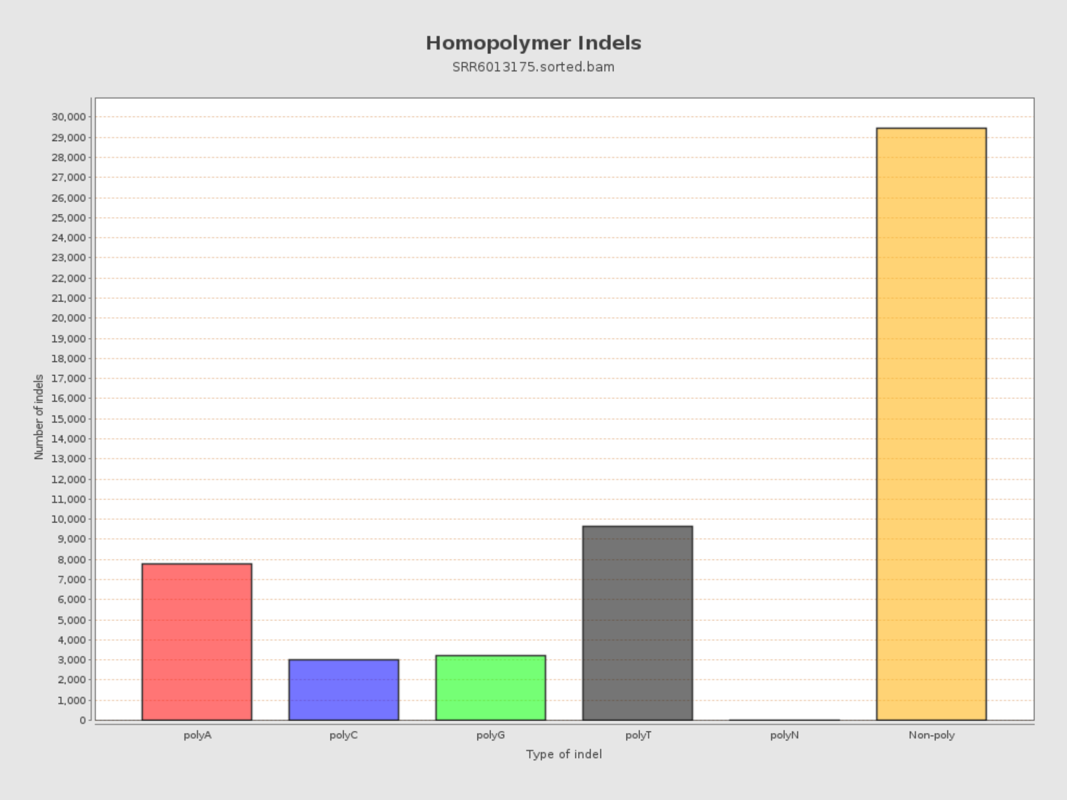
9. Results : Mapped Reads GC-content Distribution



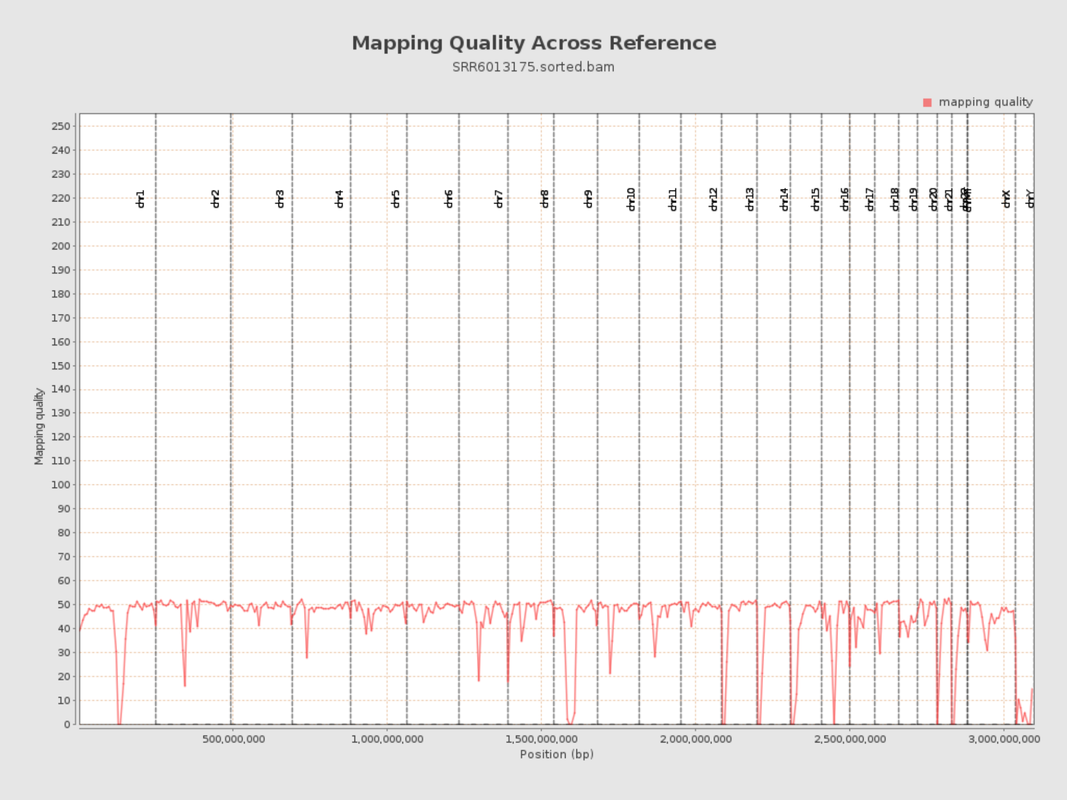
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram