Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/19 00:29:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536761.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_SRR536761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 19 00:29:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,326,306
Mapped reads	20,834,384 / 97.69%
Unmapped reads	491,922 / 2.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	542 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	221,277 / 1.04%
Duplication rate	1.05%
Clipped reads	285,045 / 1.34%

2.2. ACGT Content

Number/percentage of A's	320,356,004 / 30.83%
Number/percentage of C's	197,081,572 / 18.97%
Number/percentage of T's	320,639,173 / 30.86%
Number/percentage of G's	200,938,934 / 19.34%
Number/percentage of N's	36,673 / 0%
GC Percentage	38.31%

2.3. Coverage

Mean	0.3357

Standard Deviation	0.6677

2.4. Mapping Quality

Mean Mapping Quality	46.66

2.5. Mismatches and indels

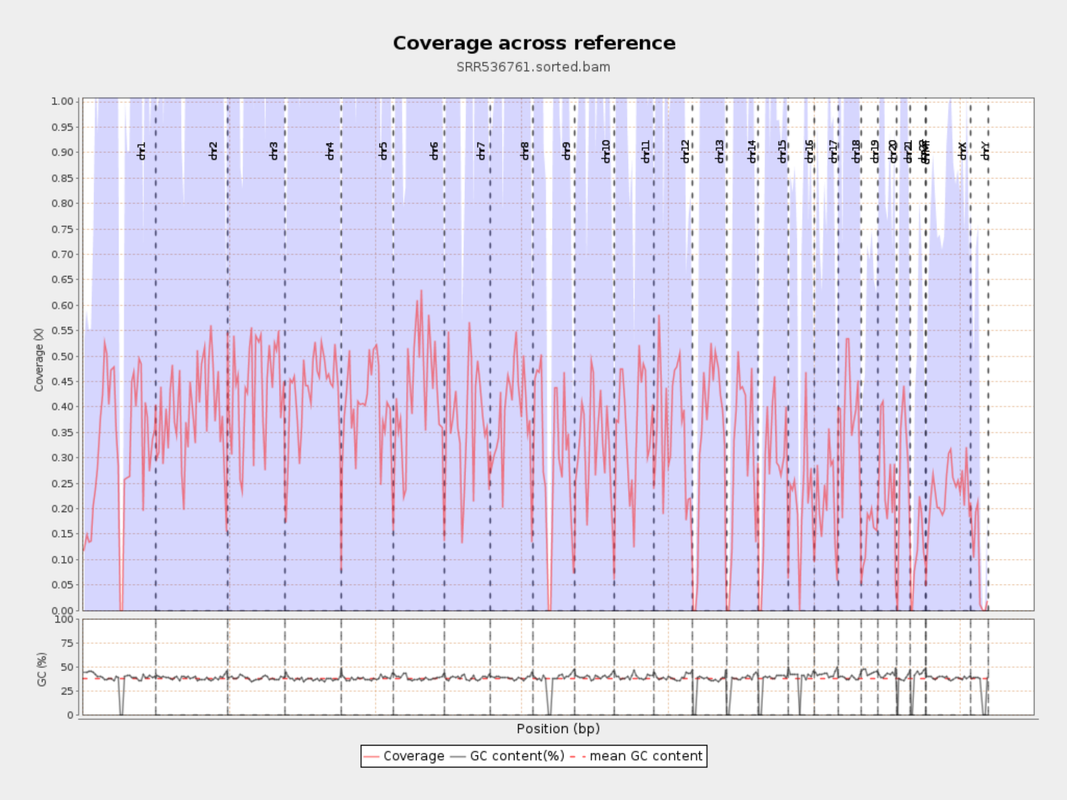
General error rate	0.2%
Mismatches	2,033,084
Insertions	61,038
Mapped reads with at least one insertion	0.29%
Deletions	55,181
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.34%

2.6. Chromosome stats

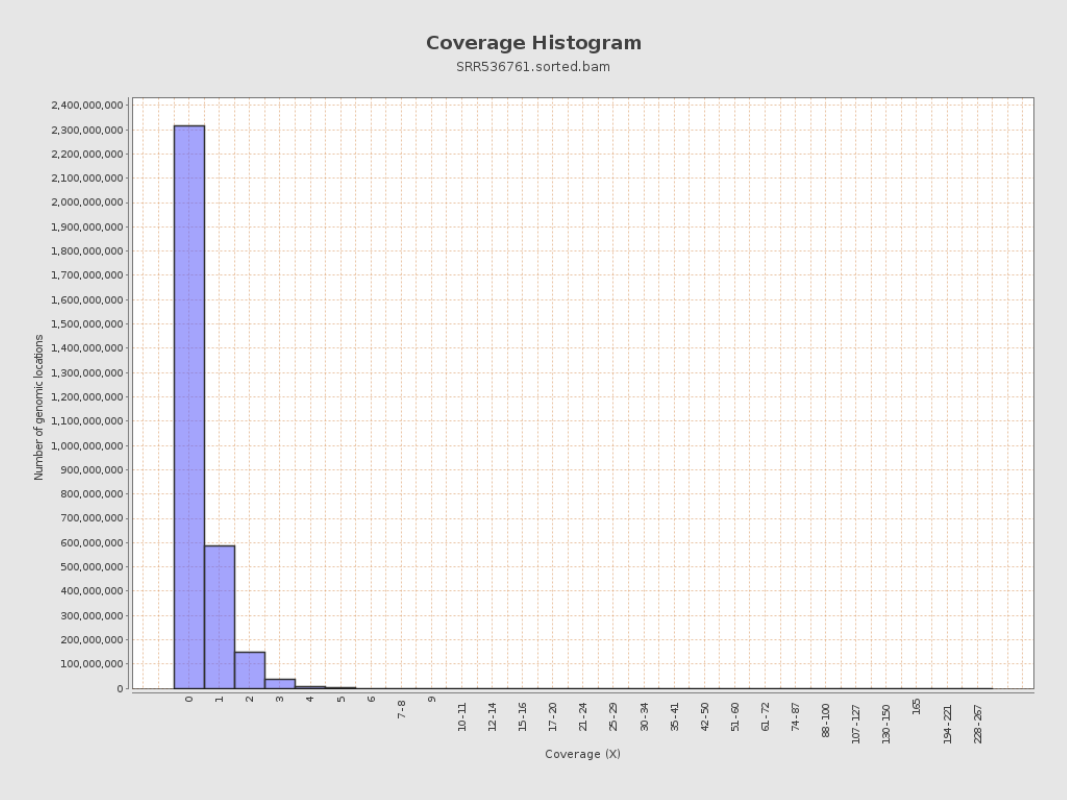
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	78984474	0.3169	0.6617
chr2	243199373	94019069	0.3866	0.7048
chr3	198022430	86718745	0.4379	0.7544
chr4	191154276	82172571	0.4299	0.7388
chr5	180915260	71497291	0.3952	0.7103
chr6	171115067	73947521	0.4322	0.7518
chr7	159138663	58177858	0.3656	0.693

chr8	146364022	56119736	0.3834	0.6982
chr9	141213431	42806945	0.3031	0.6429
chr10	135534747	44605175	0.3291	0.6476
chr11	135006516	48712654	0.3608	0.6964
chr12	133851895	47788595	0.357	0.6862
chr13	115169878	39609865	0.3439	0.6756
chr14	107349540	32412134	0.3019	0.6371
chr15	102531392	27810320	0.2712	0.6089
chr16	90354753	19553654	0.2164	0.5327
chr17	81195210	17786354	0.2191	0.5346
chr18	78077248	30384695	0.3892	0.7063
chr19	59128983	8939676	0.1512	0.4371
chr20	63025520	16921740	0.2685	0.5963
chr21	48129895	12937201	0.2688	0.6147
chr22	51304566	5798073	0.113	0.3835
chrMT	16571	797	0.0481	0.229
chrX	155270560	36371641	0.2342	0.5362
chrY	59373566	5066503	0.0853	0.3396

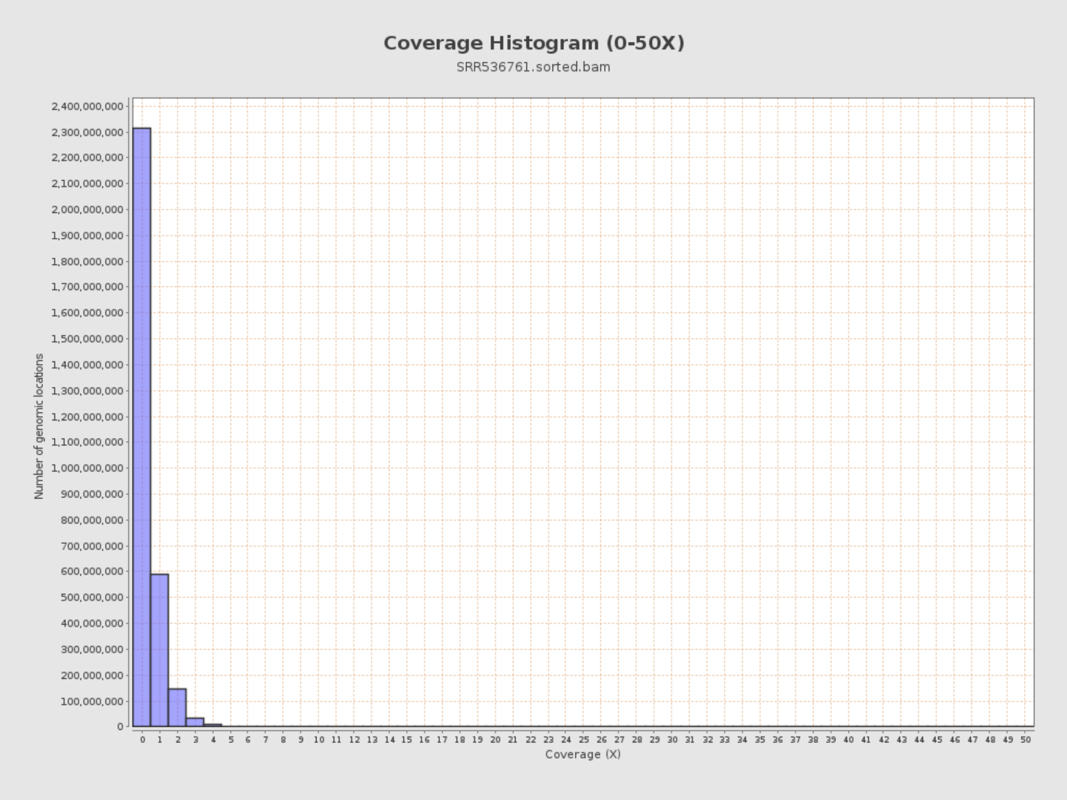
3. Results : Coverage across reference



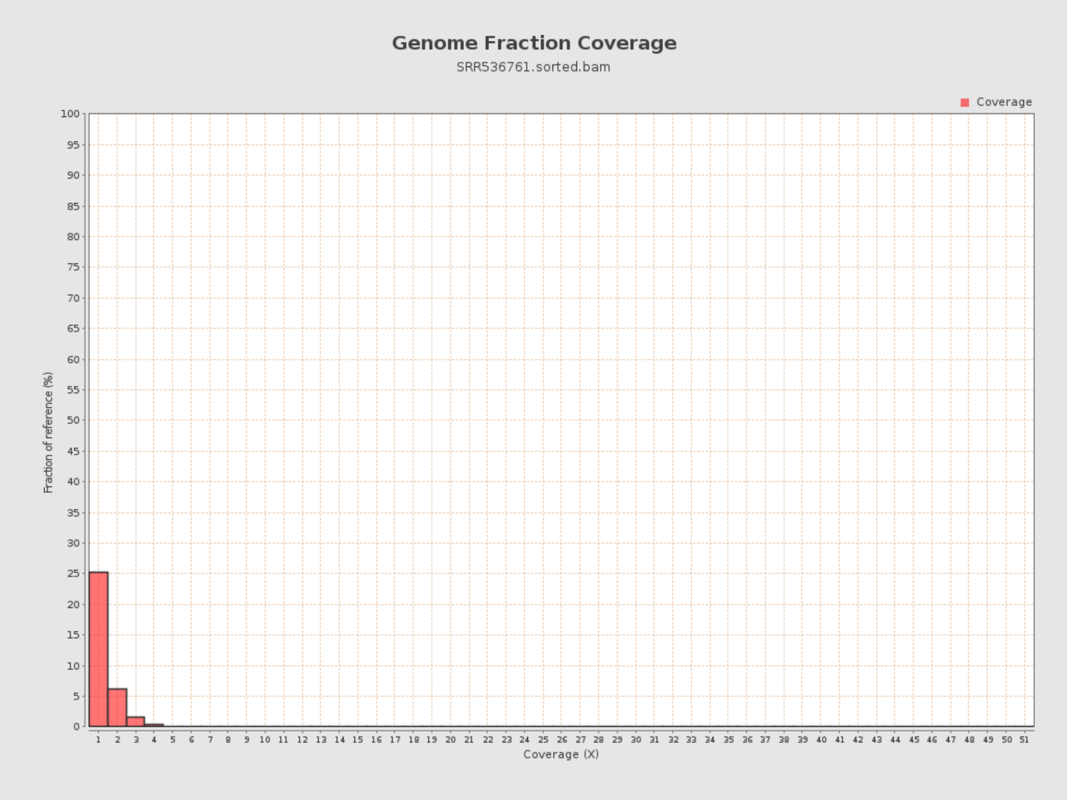
4. Results : Coverage Histogram



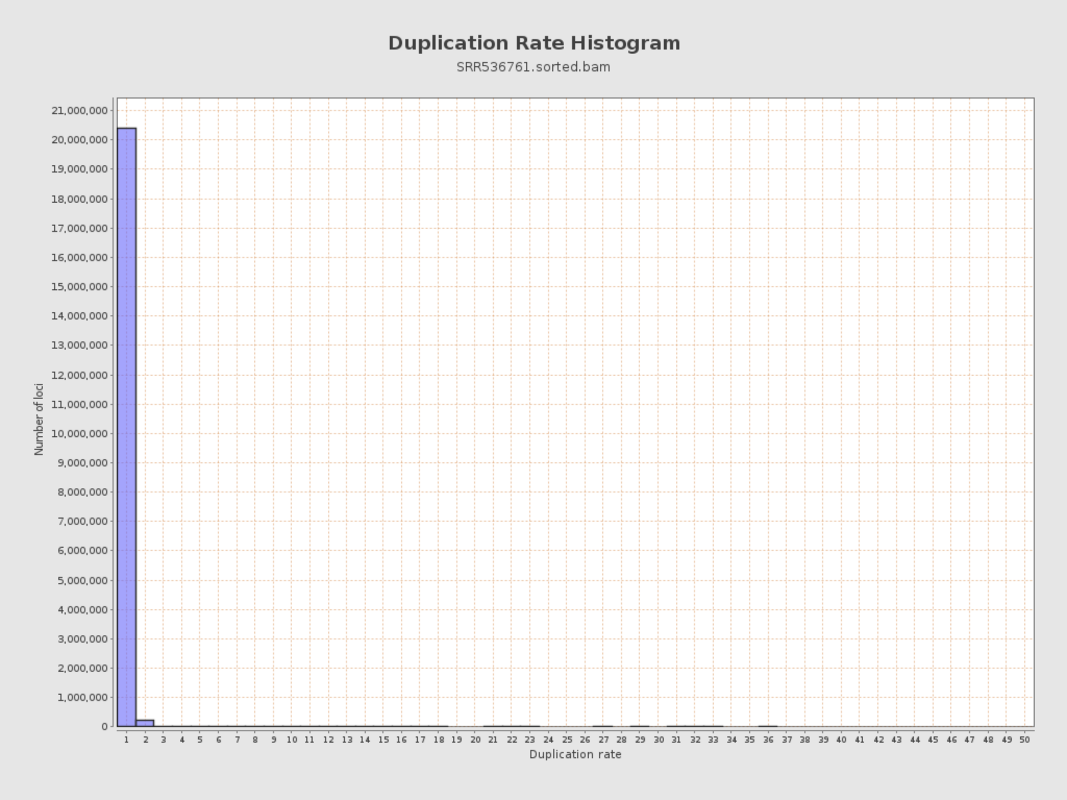
5. Results : Coverage Histogram (0-50X)



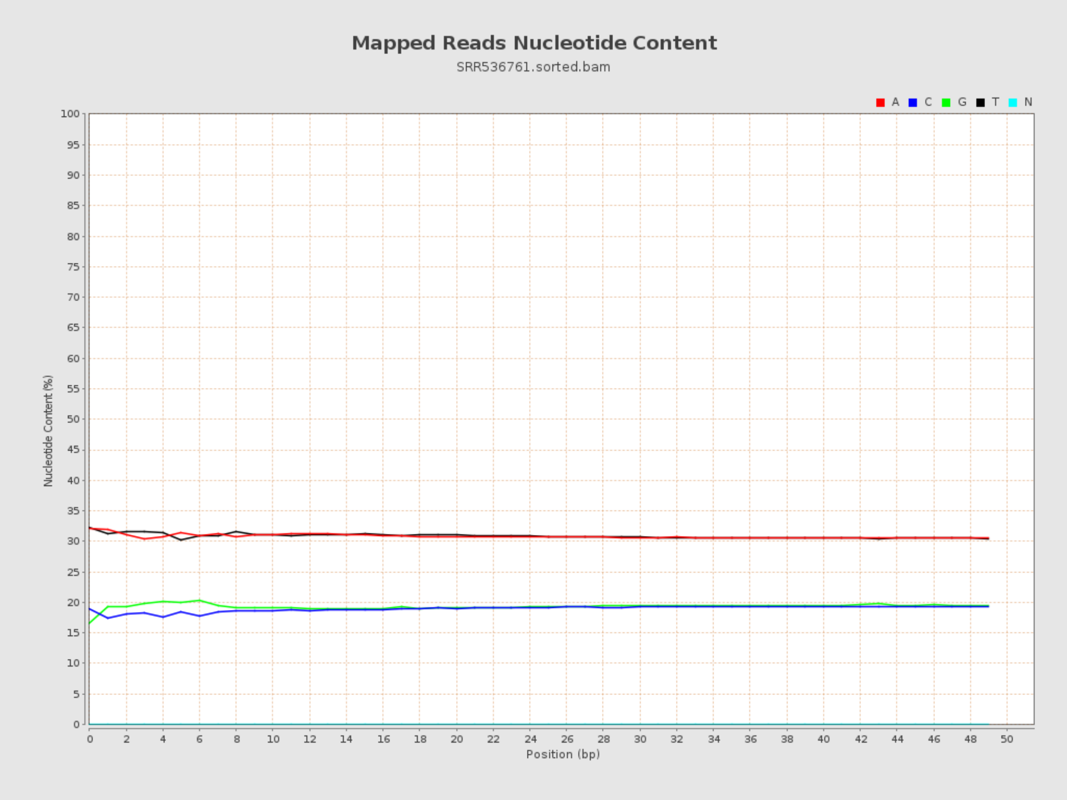
6. Results : Genome Fraction Coverage



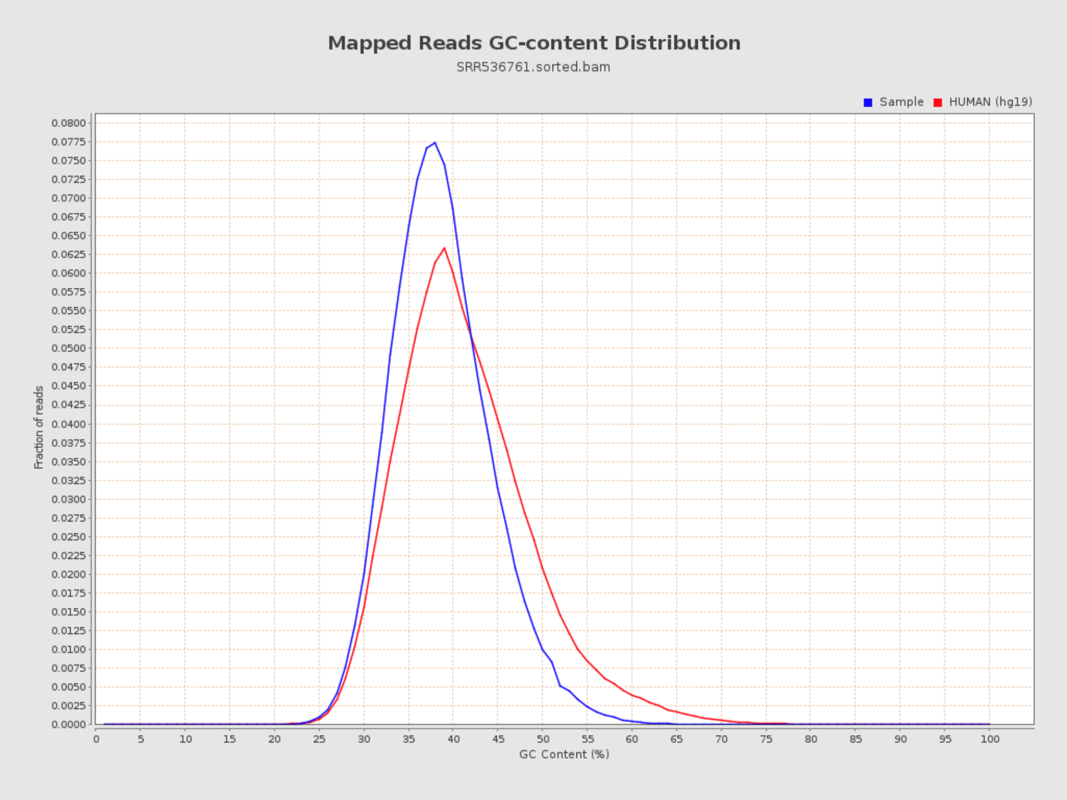
7. Results : Duplication Rate Histogram



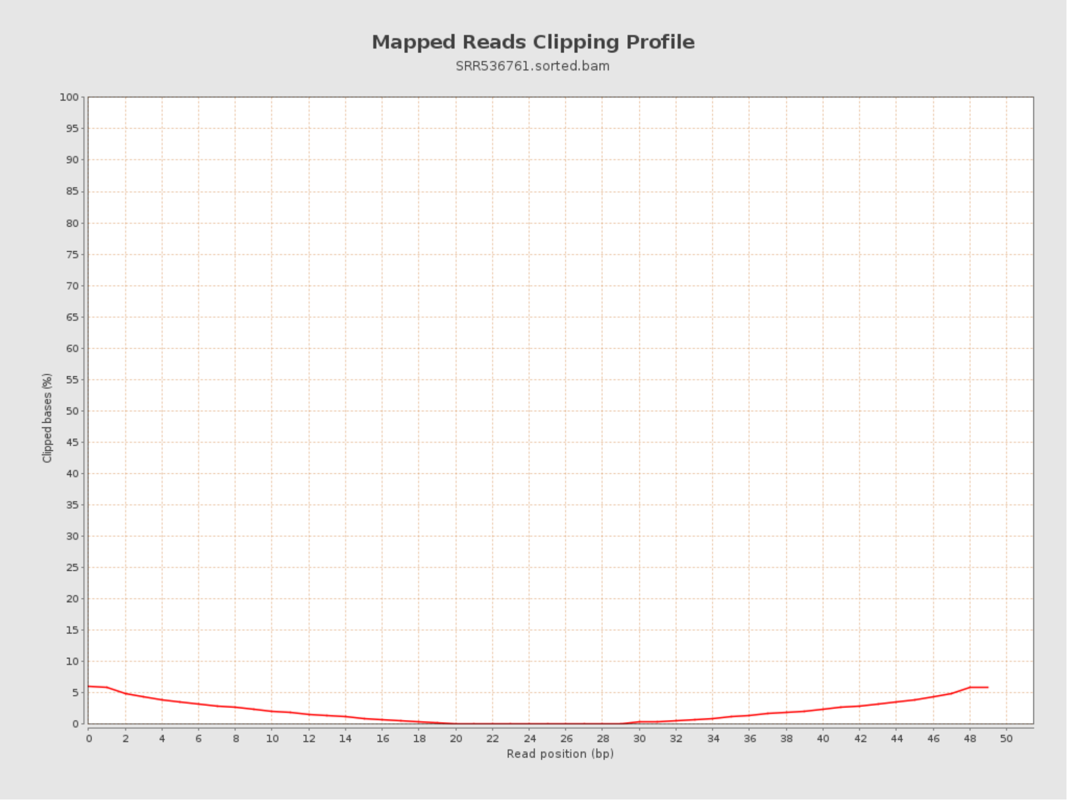
8. Results : Mapped Reads Nucleotide Content



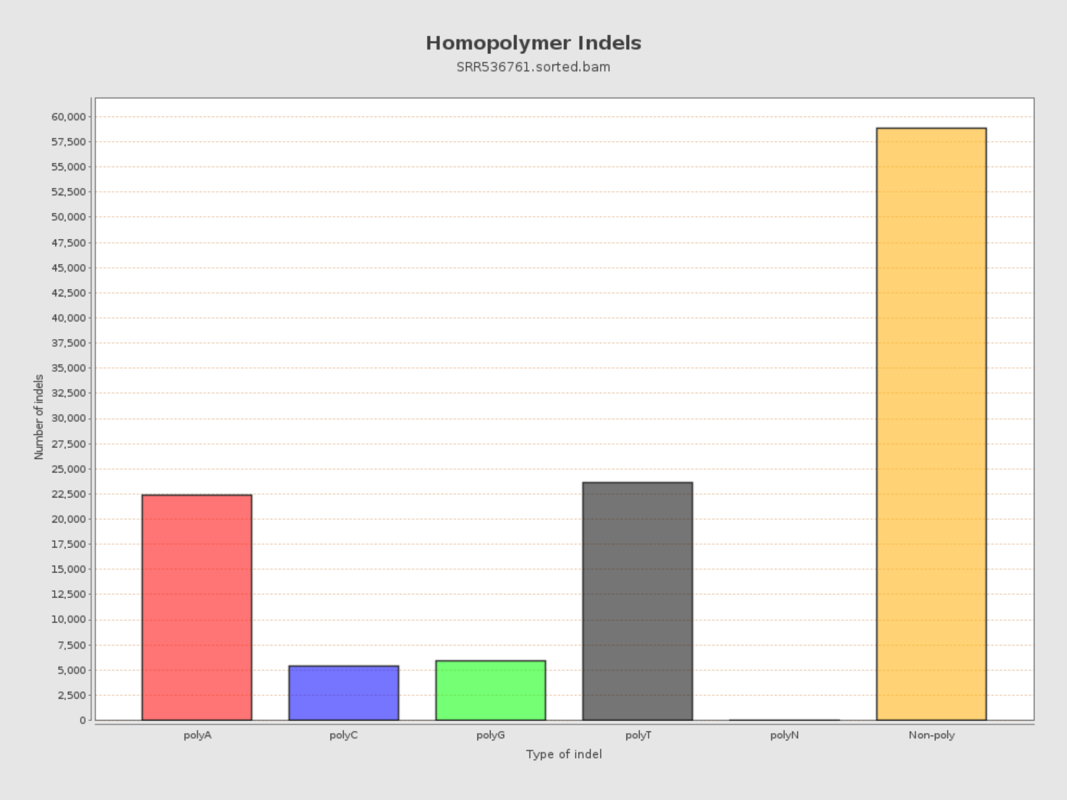
9. Results : Mapped Reads GC-content Distribution



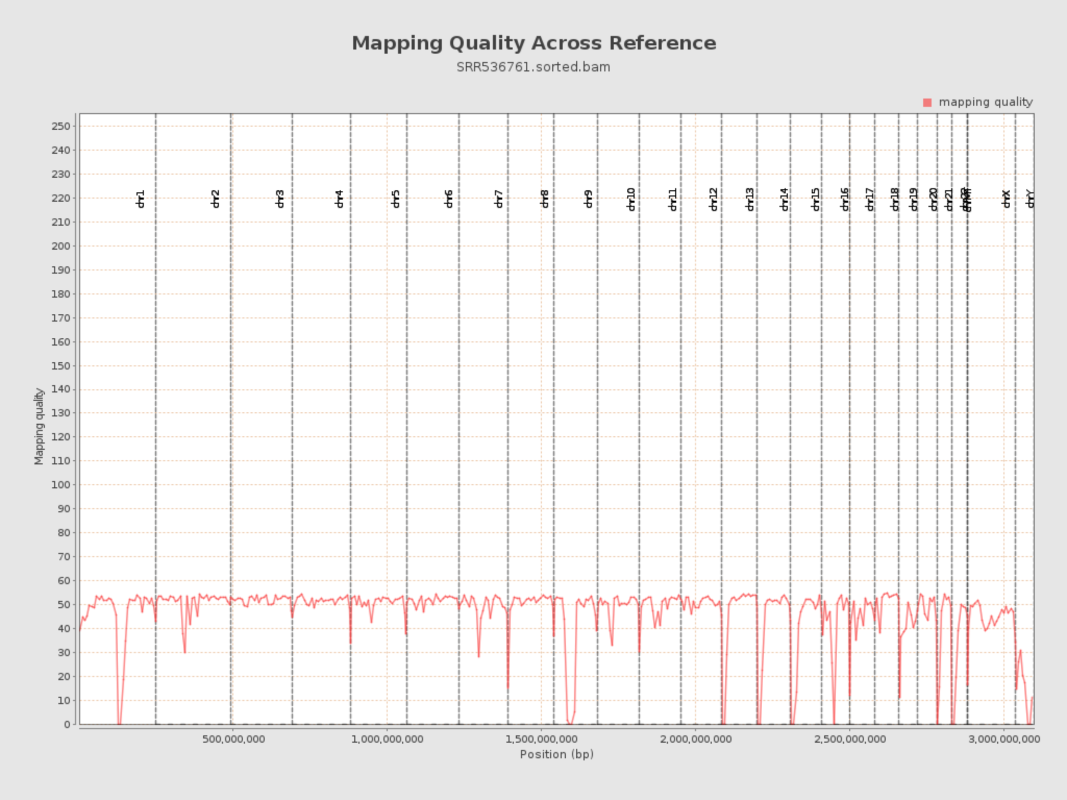
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram