Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:30:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082484.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_SRR3082484 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082484.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:30:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082484.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,027,507
Mapped reads	1,813,344 / 89.44%
Unmapped reads	214,163 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,634 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	61,046 / 3.01%
Duplication rate	2.5%
Clipped reads	693,181 / 34.19%

2.2. ACGT Content

Number/percentage of A's	36,059,643 / 28.95%
Number/percentage of C's	23,274,634 / 18.69%
Number/percentage of T's	38,177,501 / 30.65%
Number/percentage of G's	27,036,421 / 21.71%
Number/percentage of N's	2,569 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.3651

2.4. Mapping Quality

Mean Mapping Quality	46.83

2.5. Mismatches and indels

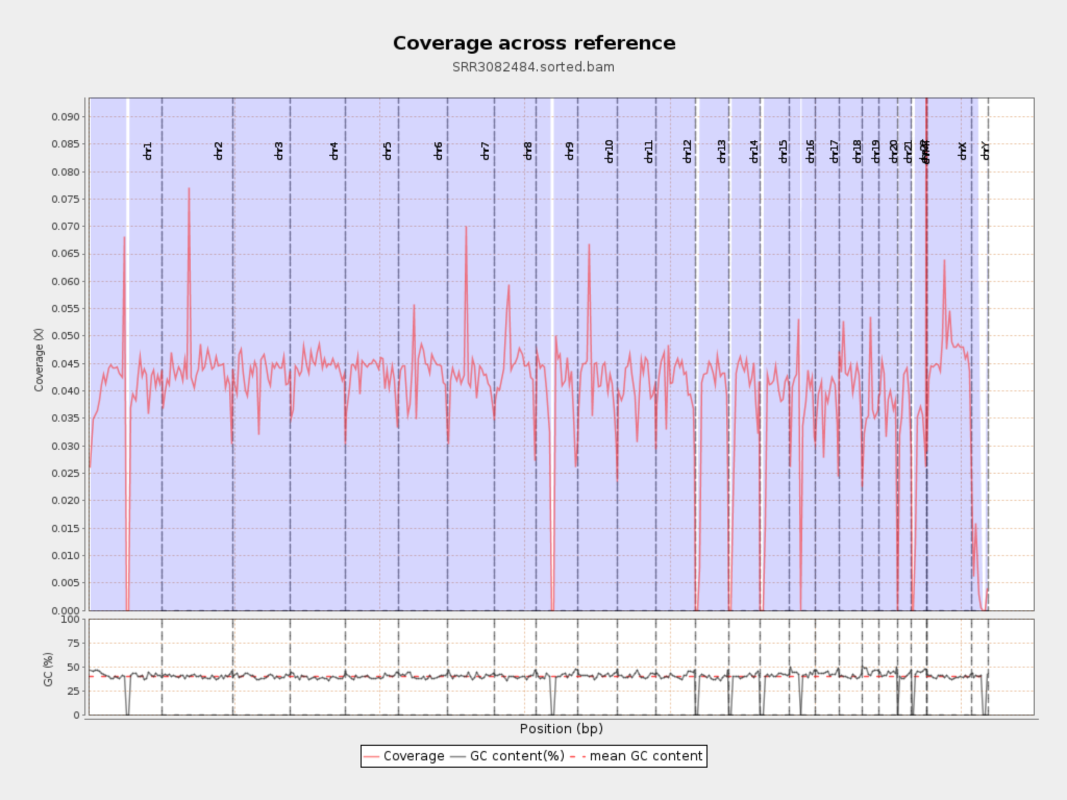
General error rate	0.85%
Mismatches	1,046,781
Insertions	10,142
Mapped reads with at least one insertion	0.56%
Deletions	27,578
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.28%

2.6. Chromosome stats

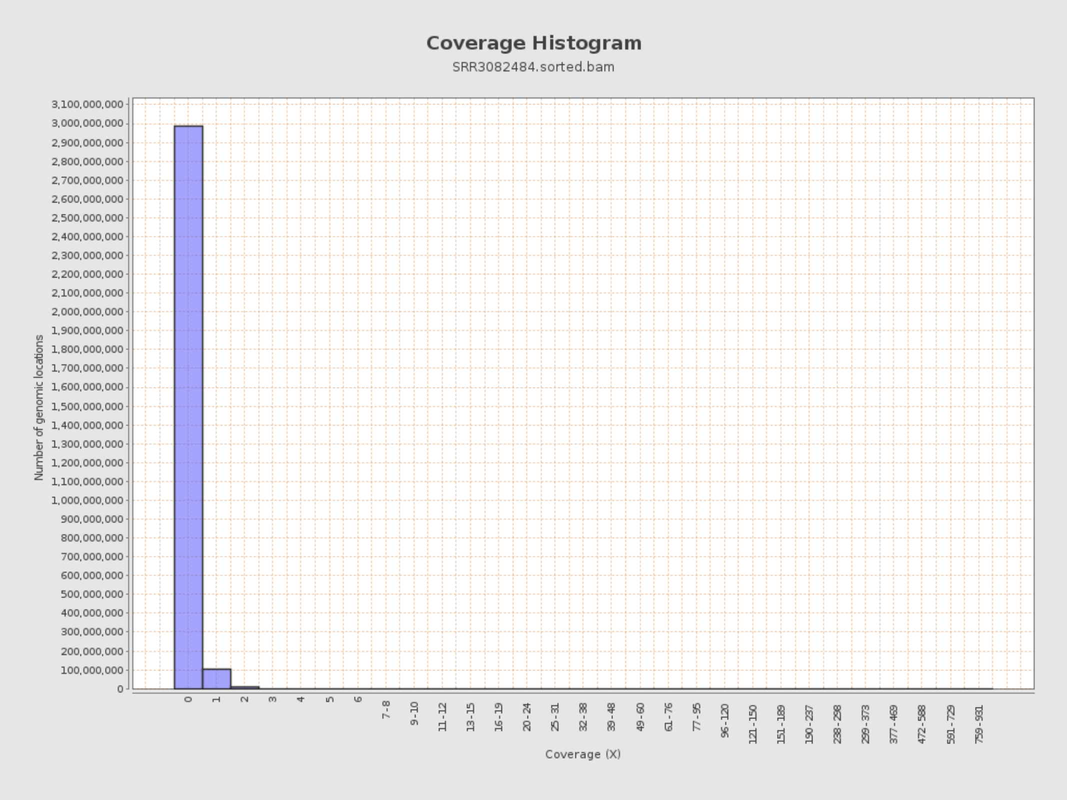
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9770844	0.0392	0.6525
chr2	243199373	10785983	0.0444	0.4169
chr3	198022430	8548092	0.0432	0.225
chr4	191154276	8454122	0.0442	0.2369
chr5	180915260	7799114	0.0431	0.2253
chr6	171115067	7480834	0.0437	0.2707
chr7	159138663	6889074	0.0433	0.4617

chr8	146364022	6486177	0.0443	0.6079
chr9	141213431	5265545	0.0373	0.3289
chr10	135534747	5845184	0.0431	0.3423
chr11	135006516	5536486	0.041	0.2987
chr12	133851895	5624704	0.042	0.226
chr13	115169878	4109300	0.0357	0.2035
chr14	107349540	3801530	0.0354	0.2255
chr15	102531392	3431802	0.0335	0.1991
chr16	90354753	3308780	0.0366	0.2324
chr17	81195210	3021104	0.0372	0.2266
chr18	78077248	3404523	0.0436	0.5866
chr19	59128983	2191379	0.0371	0.5104
chr20	63025520	2410052	0.0382	0.2162
chr21	48129895	1644955	0.0342	0.2127
chr22	51304566	1216192	0.0237	0.1655
chrMT	16571	3880	0.2341	0.5406
chrX	155270560	7263843	0.0468	0.2597
chrY	59373566	302718	0.0051	0.1256

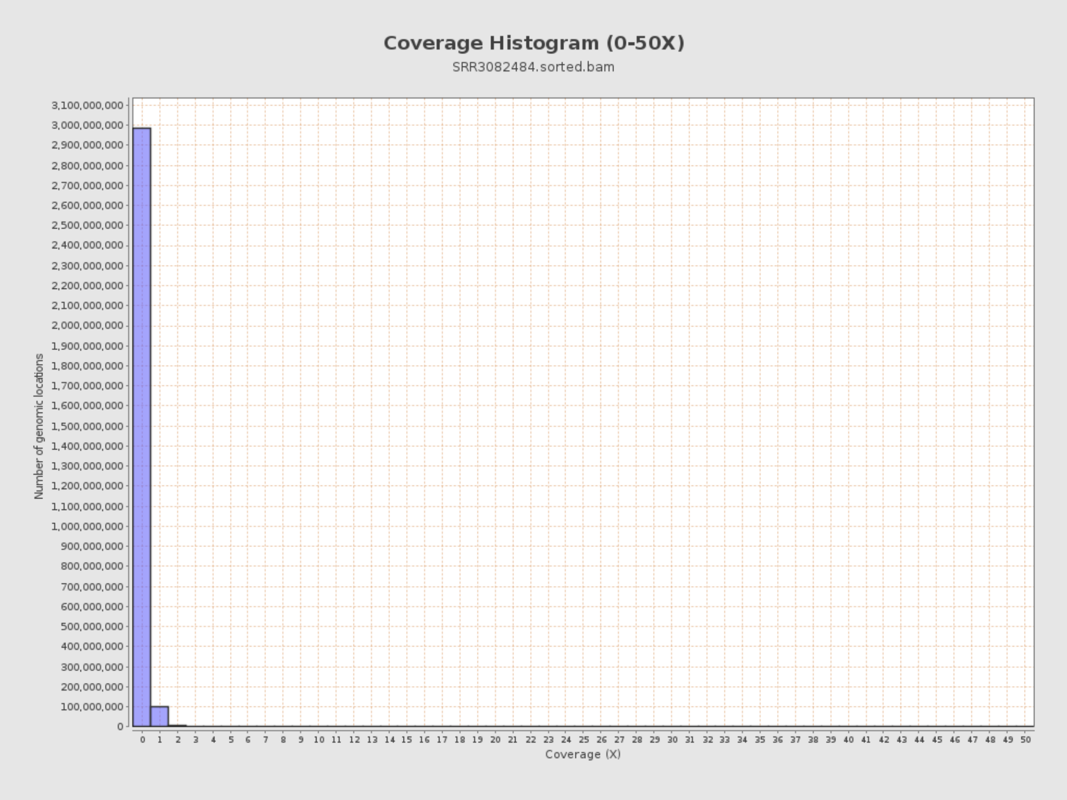
3. Results : Coverage across reference



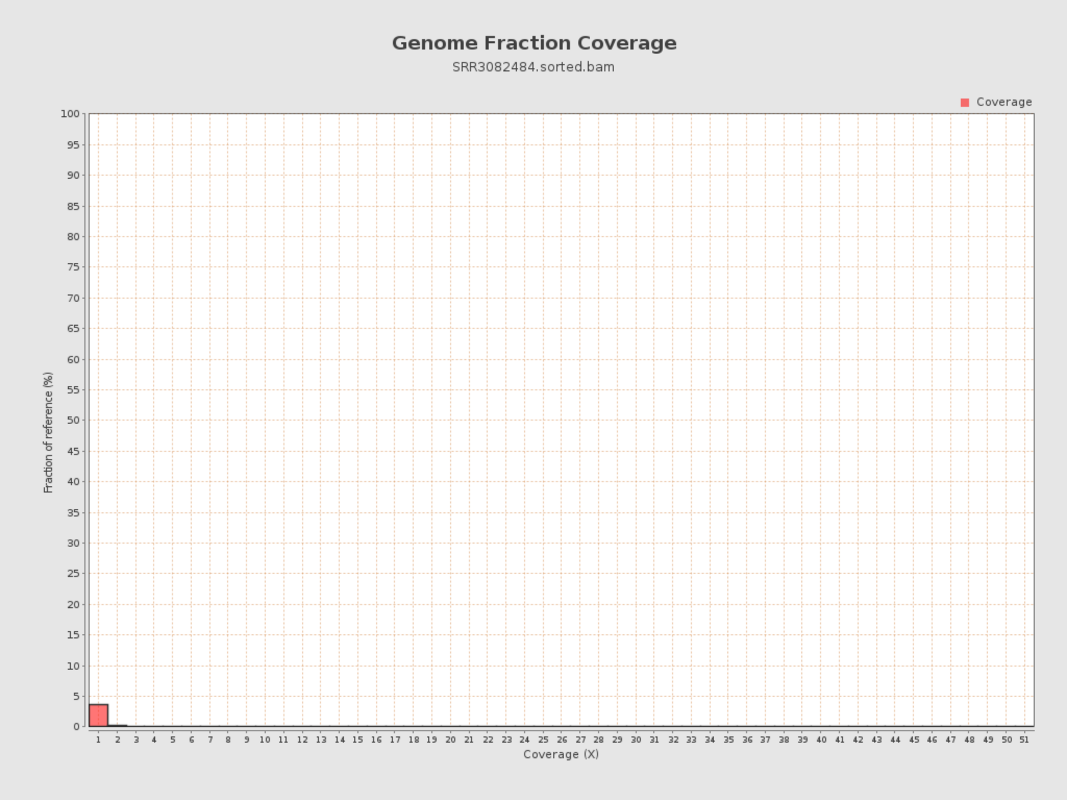
4. Results : Coverage Histogram



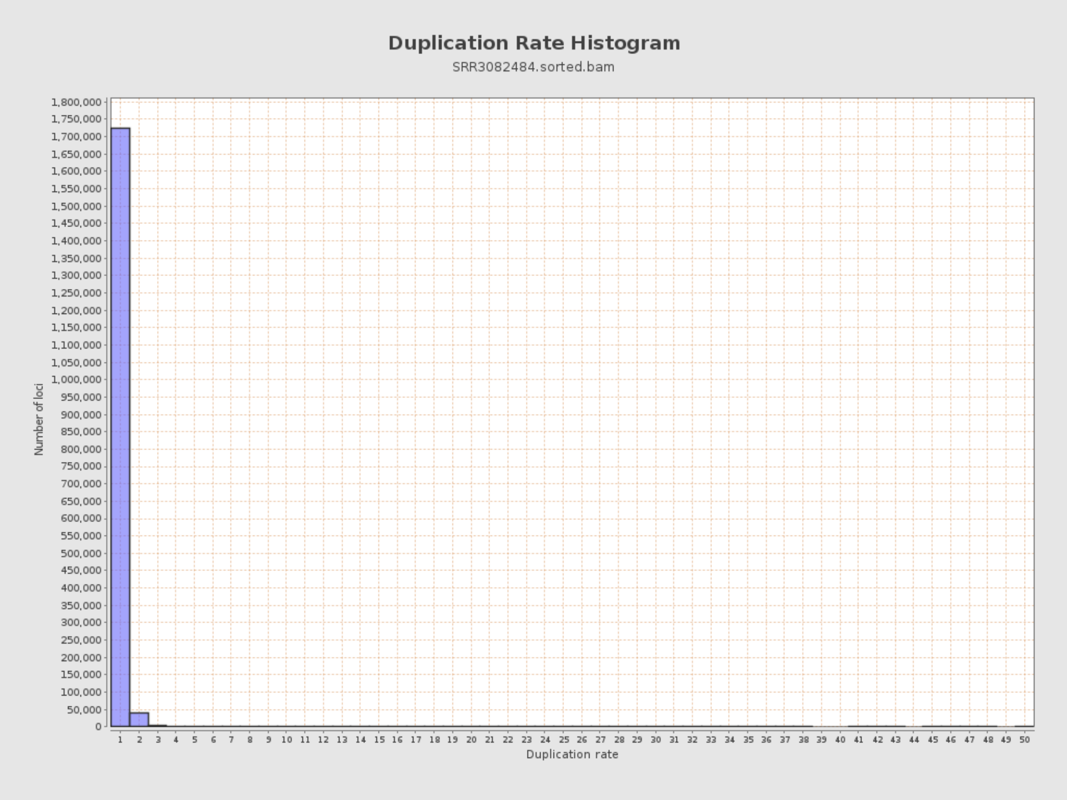
5. Results : Coverage Histogram (0-50X)



6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



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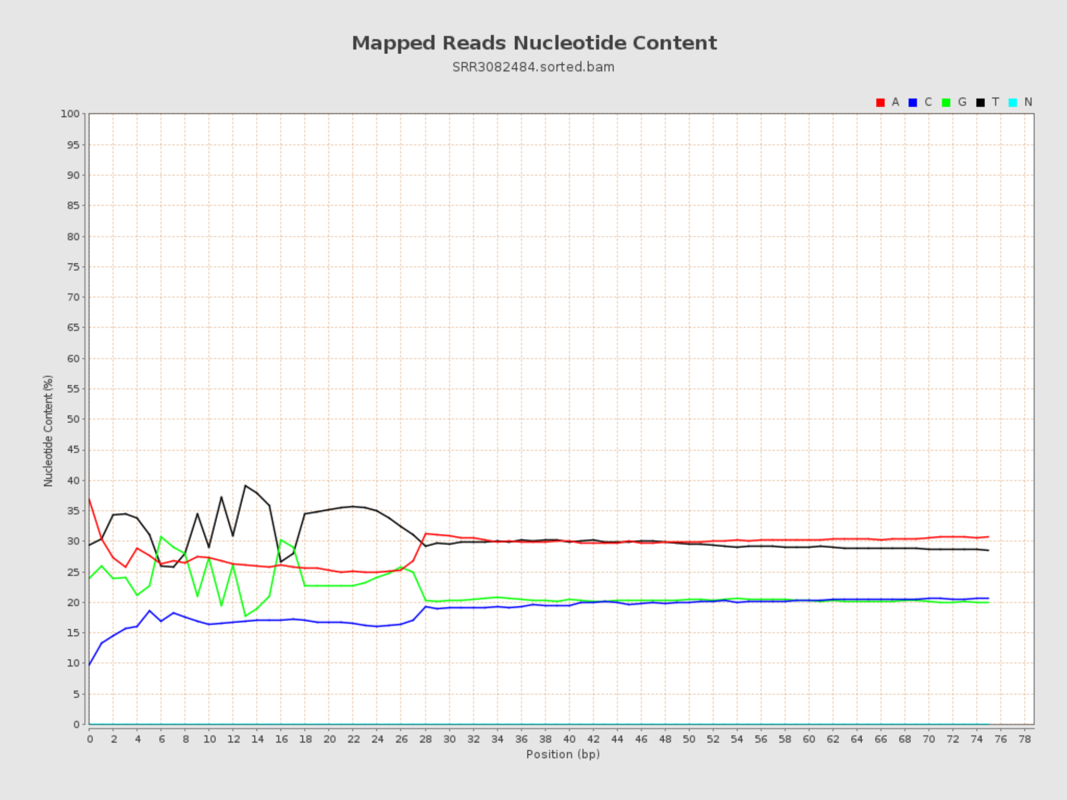
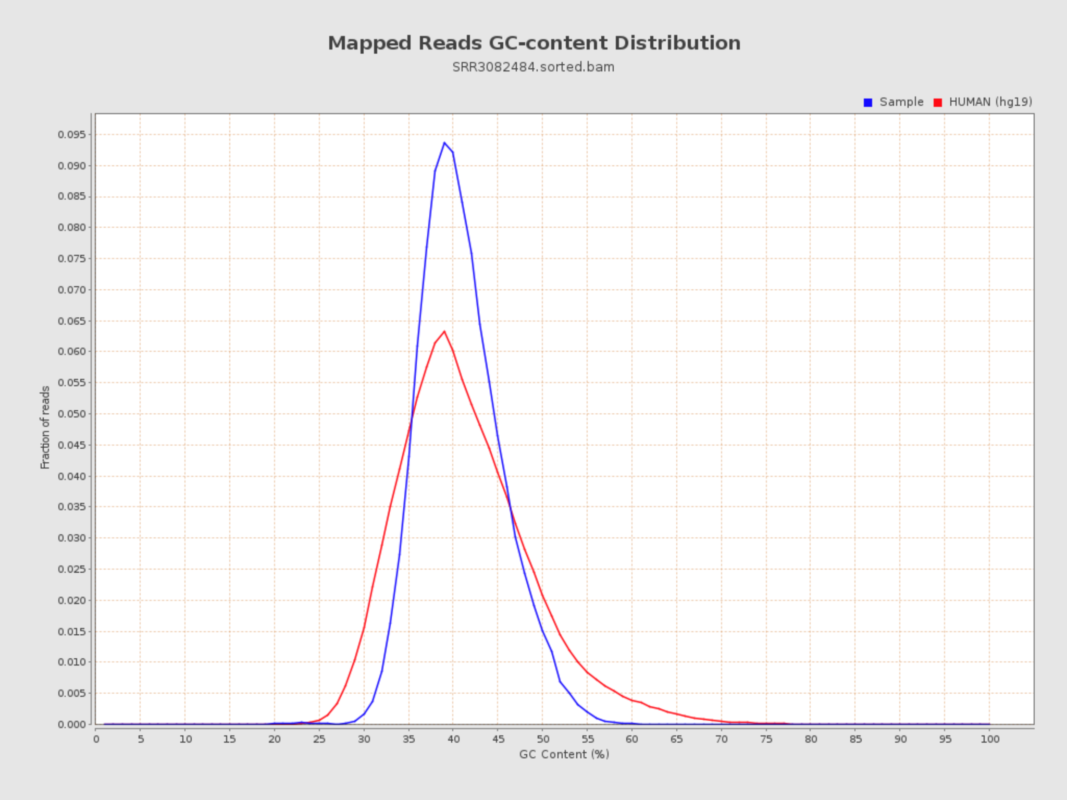
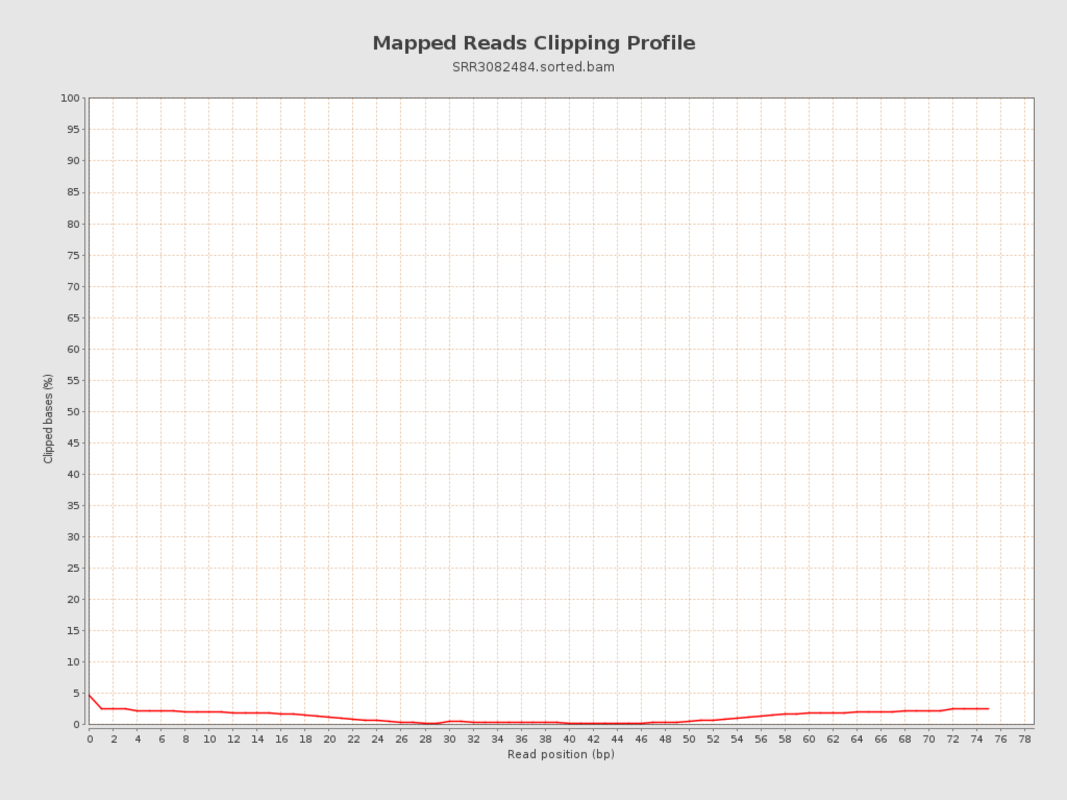
8. Results : Mapped Reads Nucleotide Content



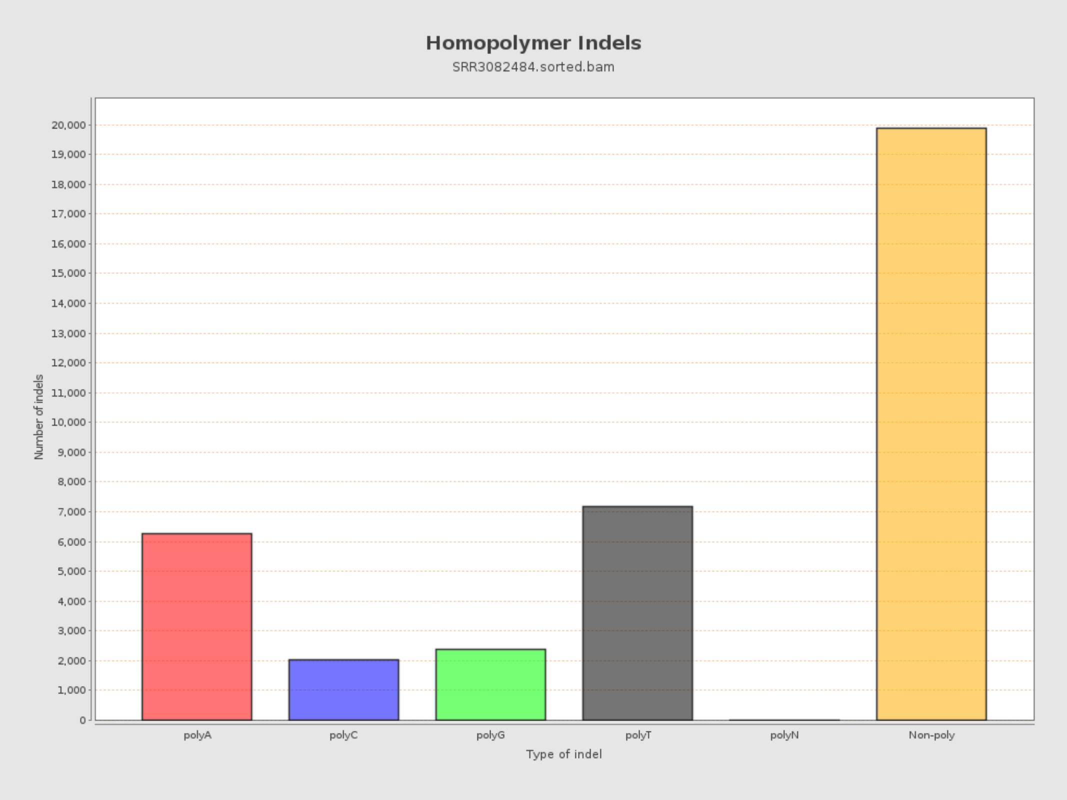
9. Results : Mapped Reads GC-content Distribution



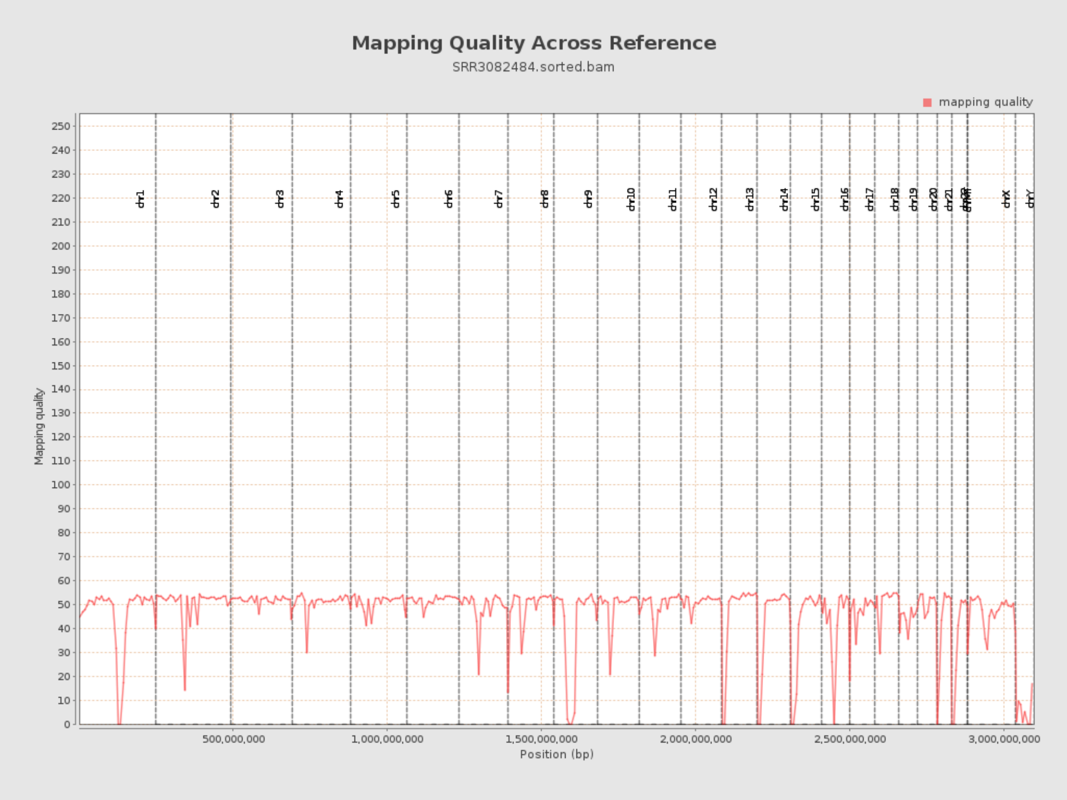
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram