Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:47:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083660.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_SRR3083660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083660.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:47:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,418,047
Mapped reads	1,974,323 / 81.65%
Unmapped reads	443,724 / 18.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,537 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	57,728 / 2.39%
Duplication rate	2.42%
Clipped reads	1,471,590 / 60.86%

2.2. ACGT Content

Number/percentage of A's	35,013,647 / 30.12%
Number/percentage of C's	23,255,879 / 20%
Number/percentage of T's	33,579,562 / 28.88%
Number/percentage of G's	24,400,289 / 20.99%
Number/percentage of N's	6,689 / 0.01%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.2969

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

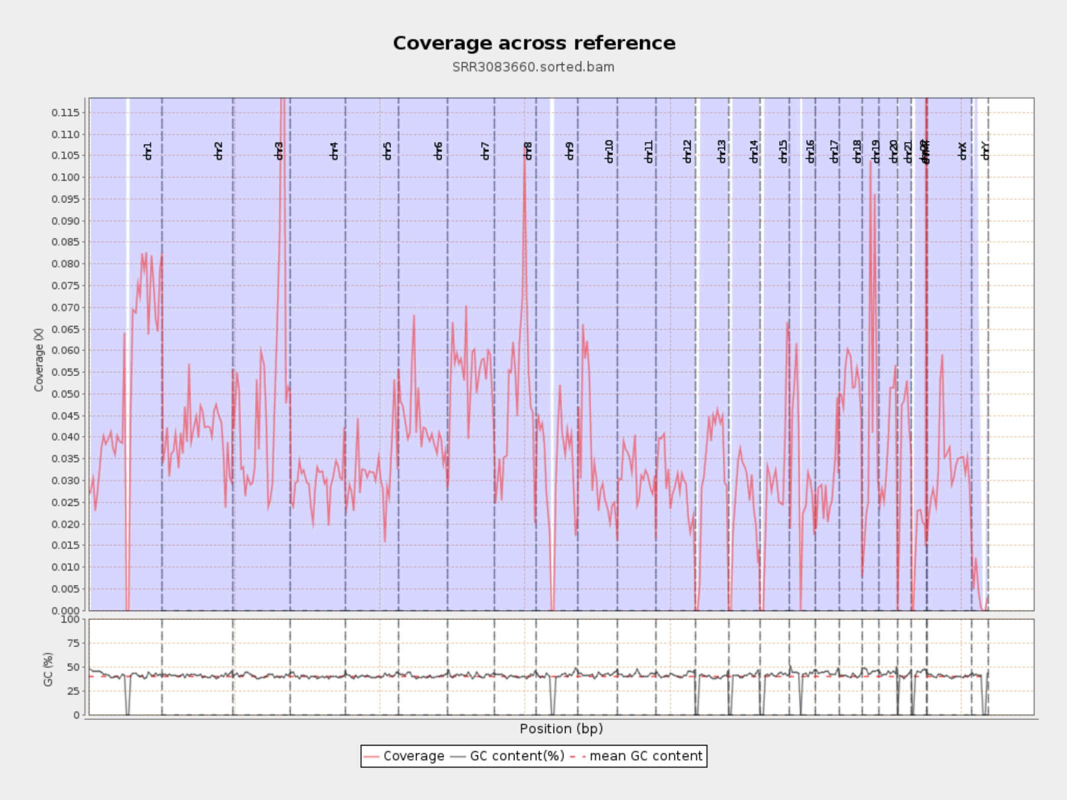
General error rate	0.81%
Mismatches	934,508
Insertions	7,945
Mapped reads with at least one insertion	0.4%
Deletions	21,801
Mapped reads with at least one deletion	1.1%
Homopolymer indels	45.11%

2.6. Chromosome stats

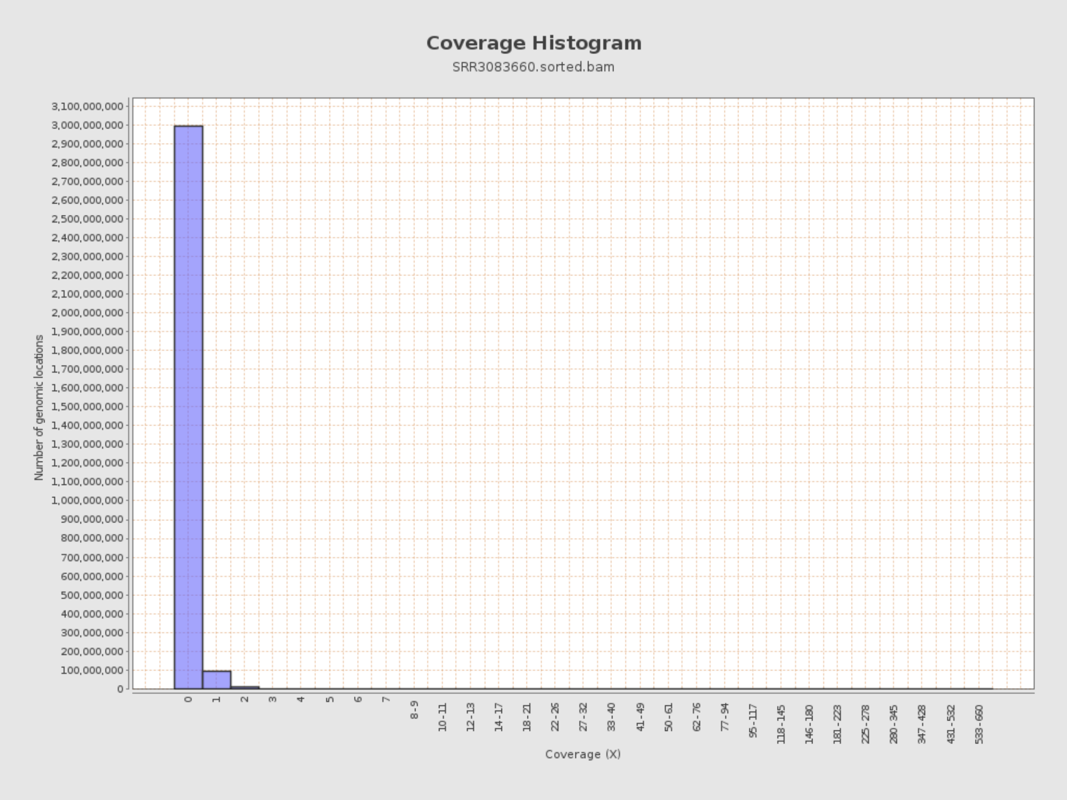
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12525076	0.0503	0.5736
chr2	243199373	9776851	0.0402	0.2865
chr3	198022430	9978498	0.0504	0.2483
chr4	191154276	5695440	0.0298	0.1903
chr5	180915260	5730737	0.0317	0.1952
chr6	171115067	7420205	0.0434	0.2592
chr7	159138663	8820602	0.0554	0.4628

chr8	146364022	7272678	0.0497	0.3767
chr9	141213431	4566899	0.0323	0.2373
chr10	135534747	4775115	0.0352	0.2459
chr11	135006516	4261636	0.0316	0.2102
chr12	133851895	3908857	0.0292	0.1886
chr13	115169878	3652749	0.0317	0.1943
chr14	107349540	2563430	0.0239	0.1711
chr15	102531392	2912149	0.0284	0.1851
chr16	90354753	2856092	0.0316	0.2021
chr17	81195210	2297334	0.0283	0.1898
chr18	78077248	4144117	0.0531	0.3708
chr19	59128983	2664802	0.0451	0.4025
chr20	63025520	2438554	0.0387	0.2195
chr21	48129895	1820861	0.0378	0.2155
chr22	51304566	794362	0.0155	0.1338
chrMT	16571	14237	0.8592	1.0496
chrX	155270560	5163827	0.0333	0.2088
chrY	59373566	235213	0.004	0.0812

3. Results : Coverage across reference



4. Results : Coverage Histogram



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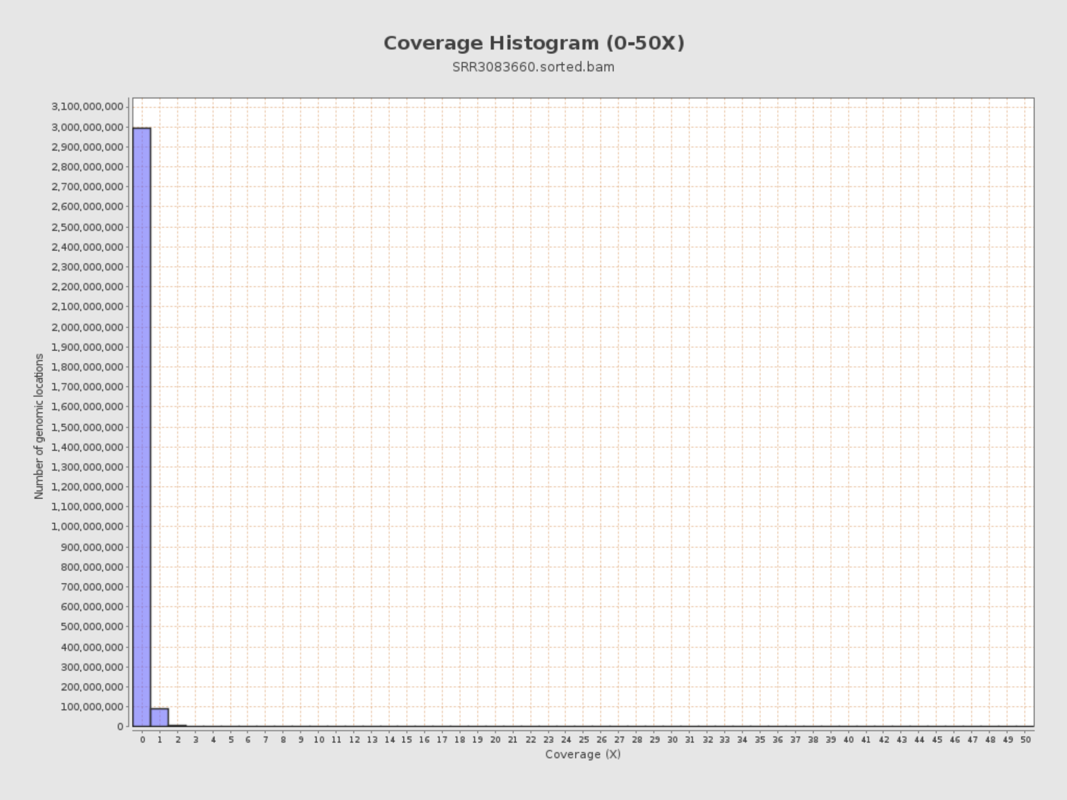
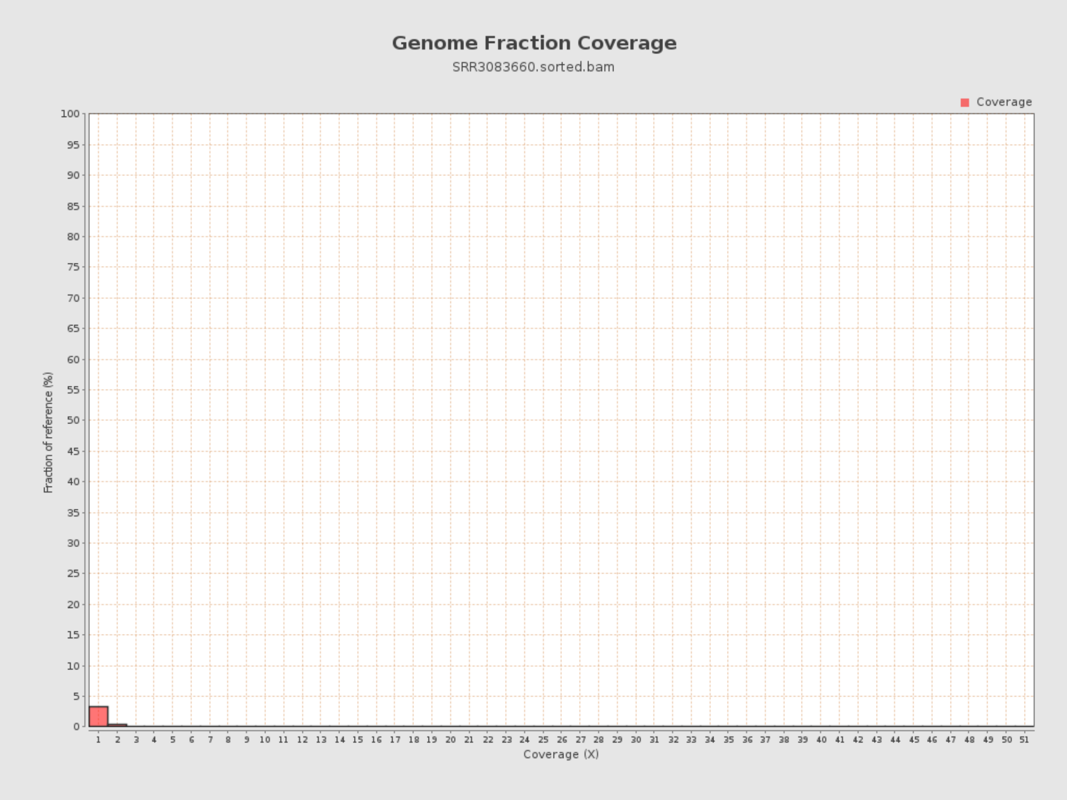
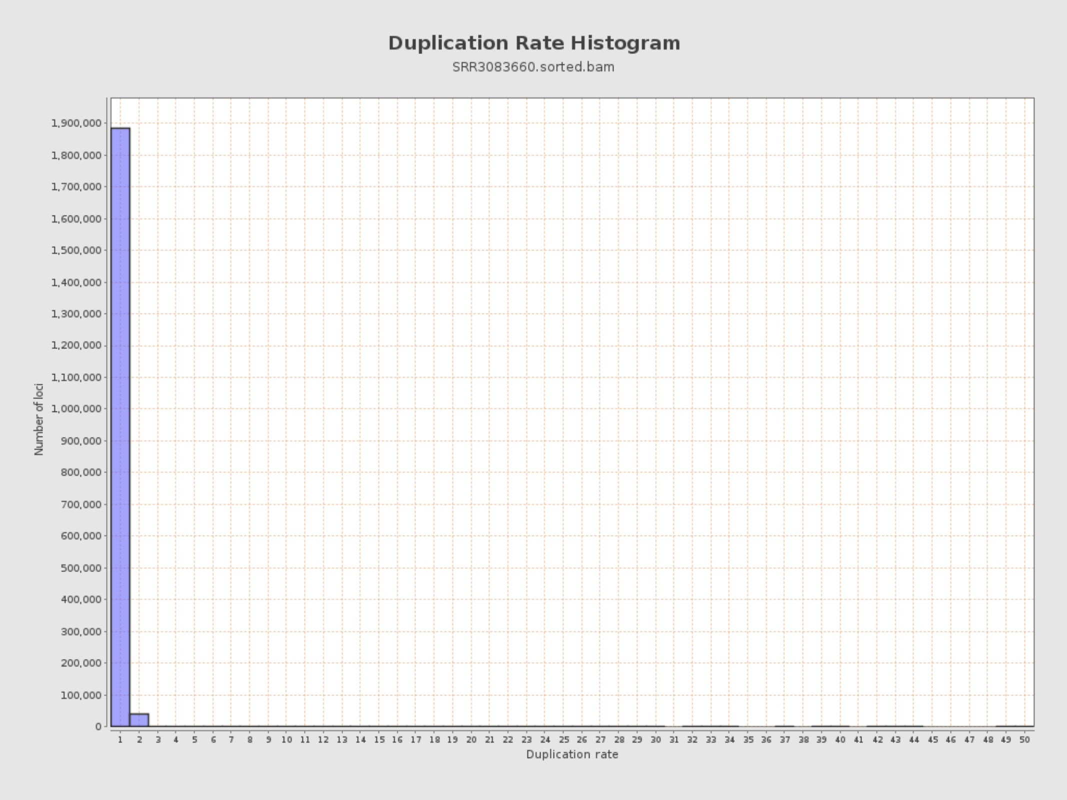
5. Results : Coverage Histogram (0-50X)



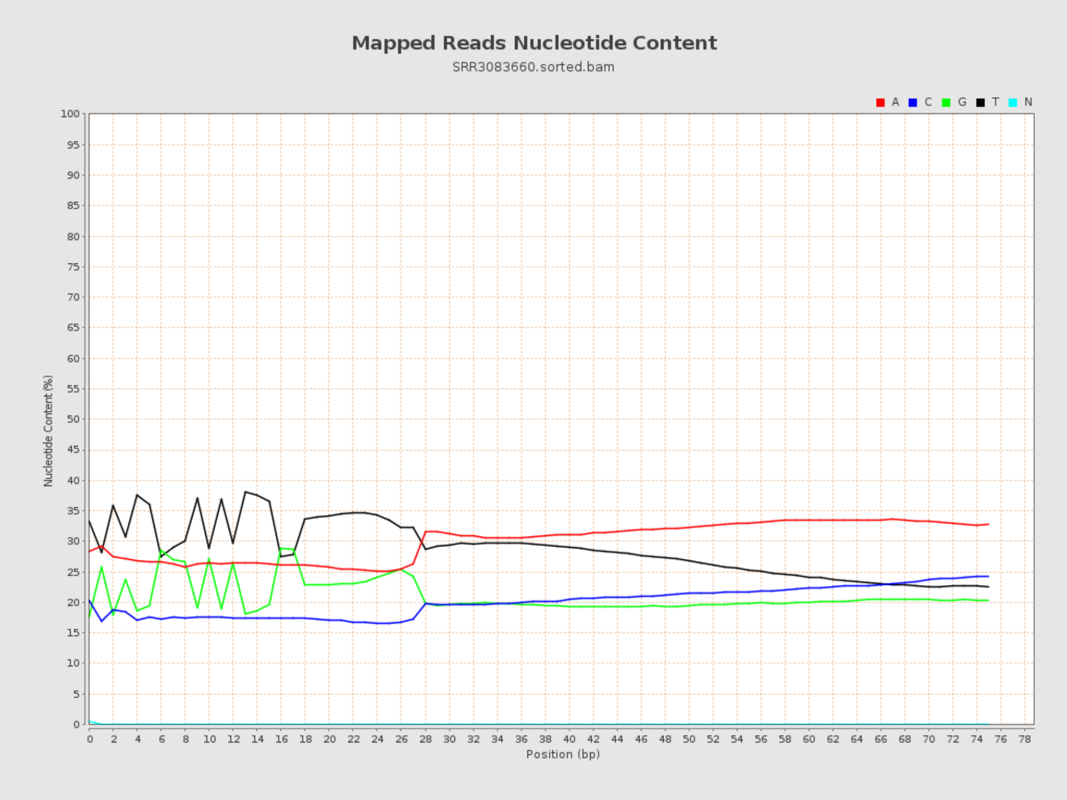
6. Results : Genome Fraction Coverage



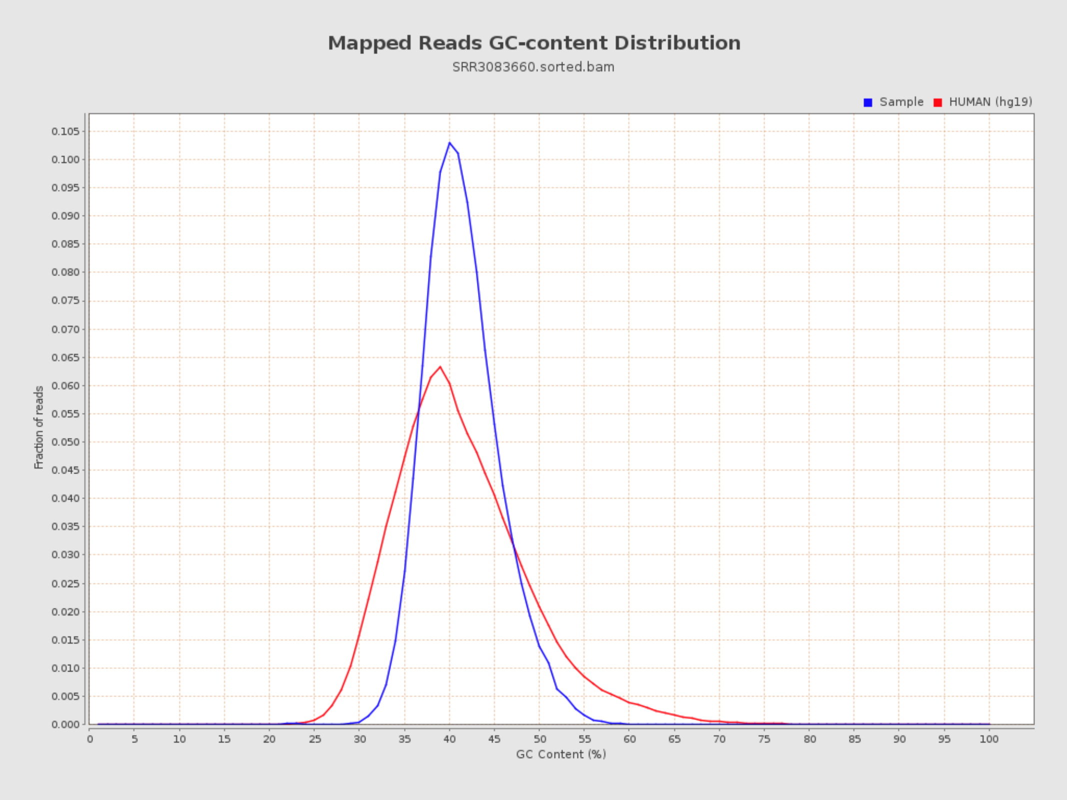
7. Results : Duplication Rate Histogram



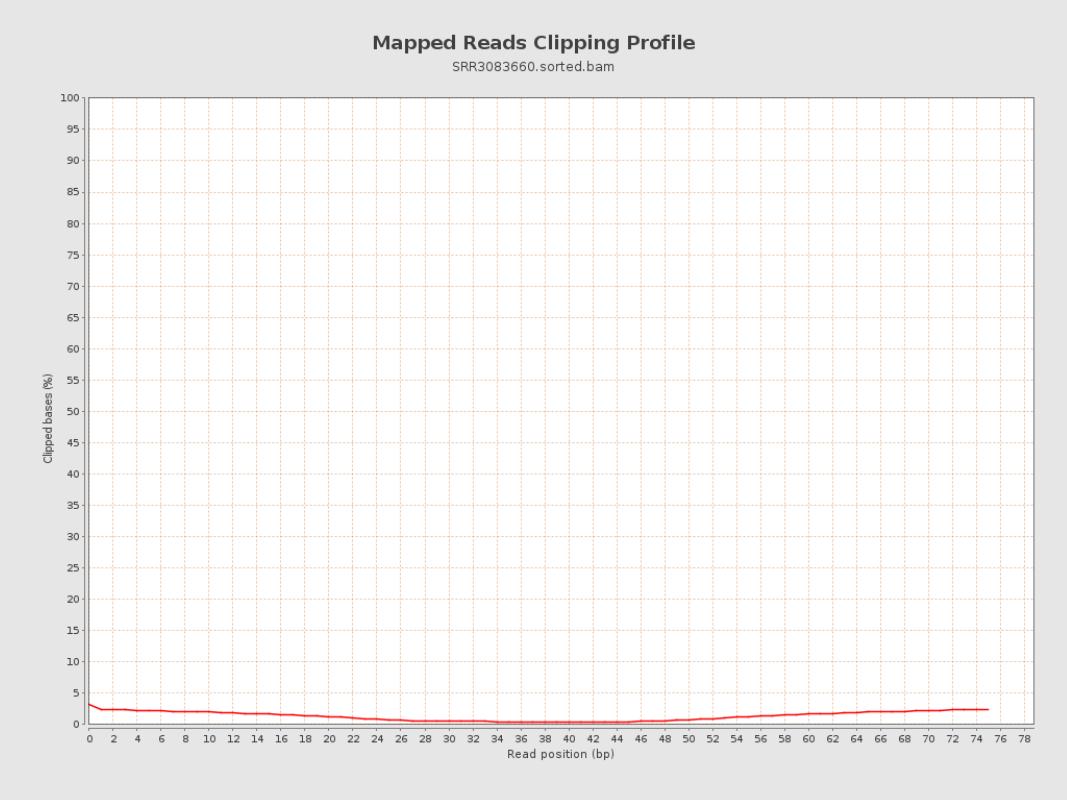
8. Results : Mapped Reads Nucleotide Content



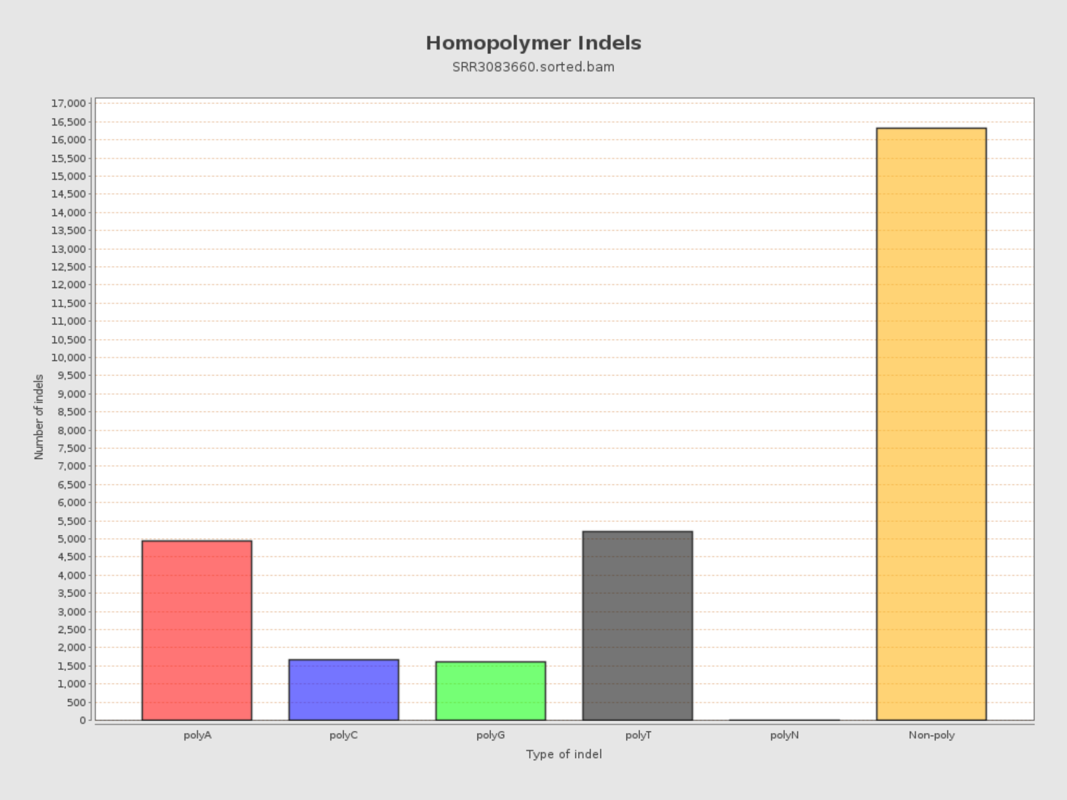
9. Results : Mapped Reads GC-content Distribution



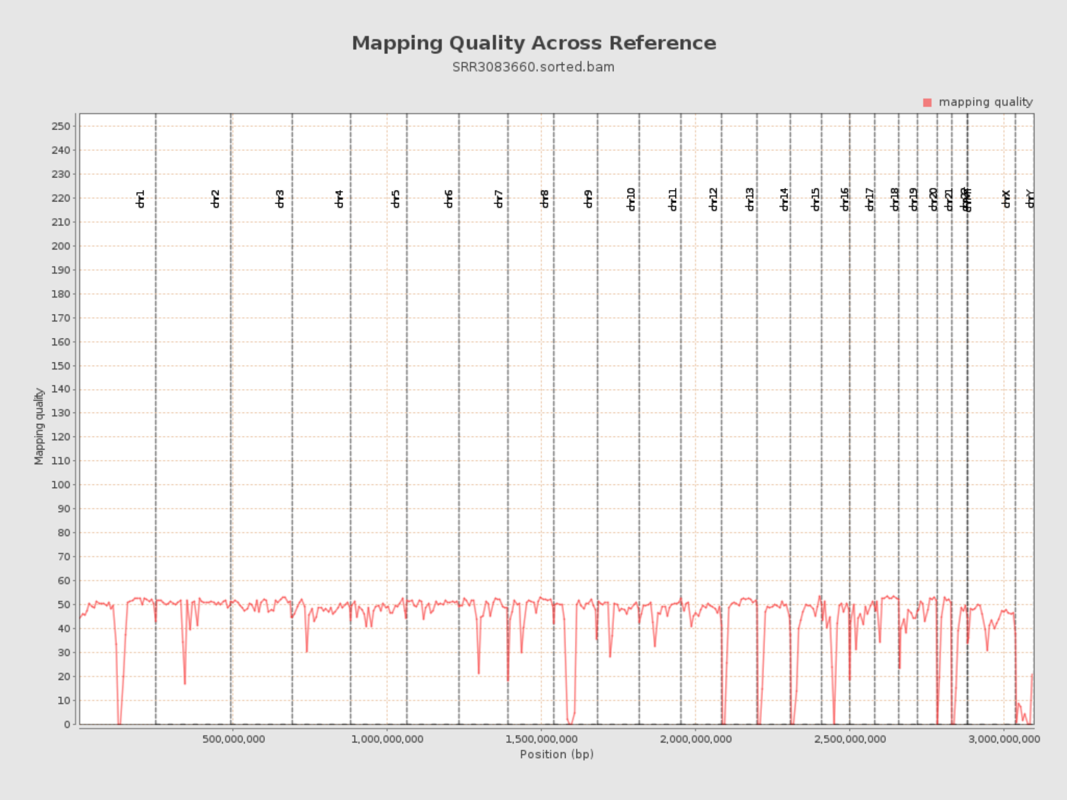
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram