Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:41:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549060.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_SRR1549060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:41:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,498,311
Mapped reads	10,807,740 / 86.47%
Unmapped reads	1,690,571 / 13.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	510,873 / 4.09%
Duplication rate	2.85%
Clipped reads	562,516 / 4.5%

2.2. ACGT Content

Number/percentage of A's	128,253,320 / 29.9%
Number/percentage of C's	86,183,698 / 20.09%
Number/percentage of T's	128,476,481 / 29.95%
Number/percentage of G's	86,001,632 / 20.05%
Number/percentage of N's	7,951 / 0%
GC Percentage	40.14%

2.3. Coverage

Mean	0.1386
Standard Deviation	1.6615

2.4. Mapping Quality

Mean Mapping Quality	43.1

2.5. Mismatches and indels

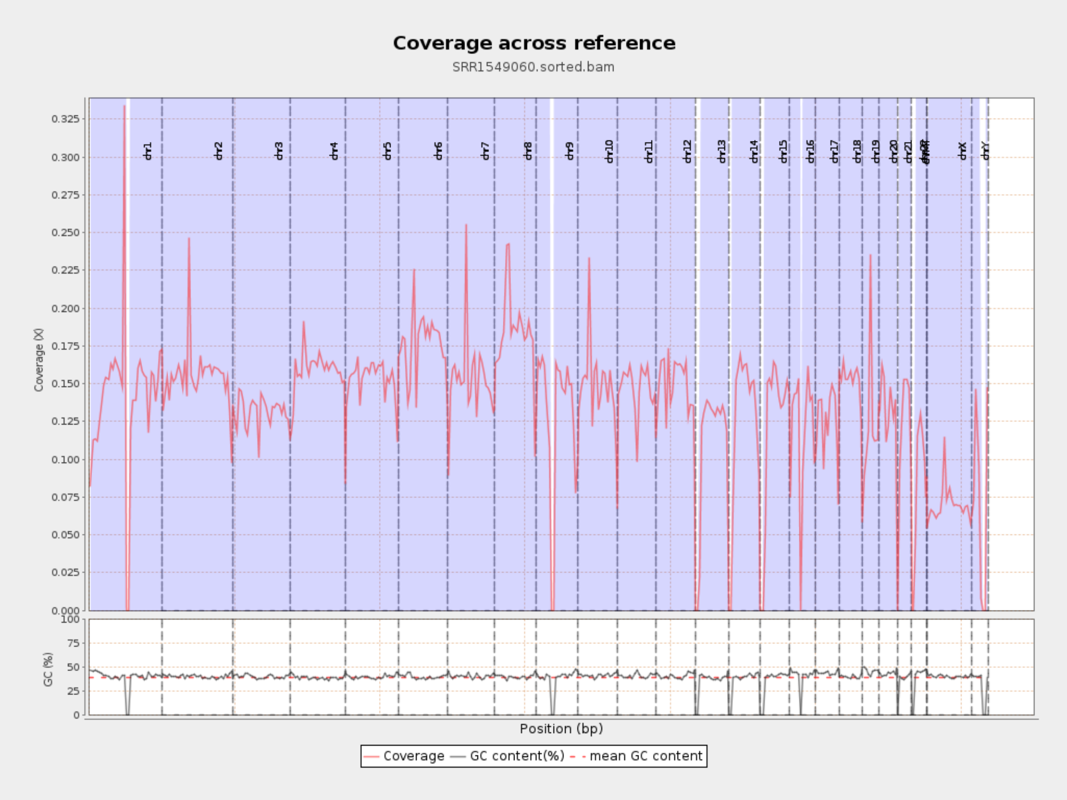
General error rate	0.33%
Mismatches	1,399,962
Insertions	11,591
Mapped reads with at least one insertion	0.11%
Deletions	36,825
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.9%

2.6. Chromosome stats

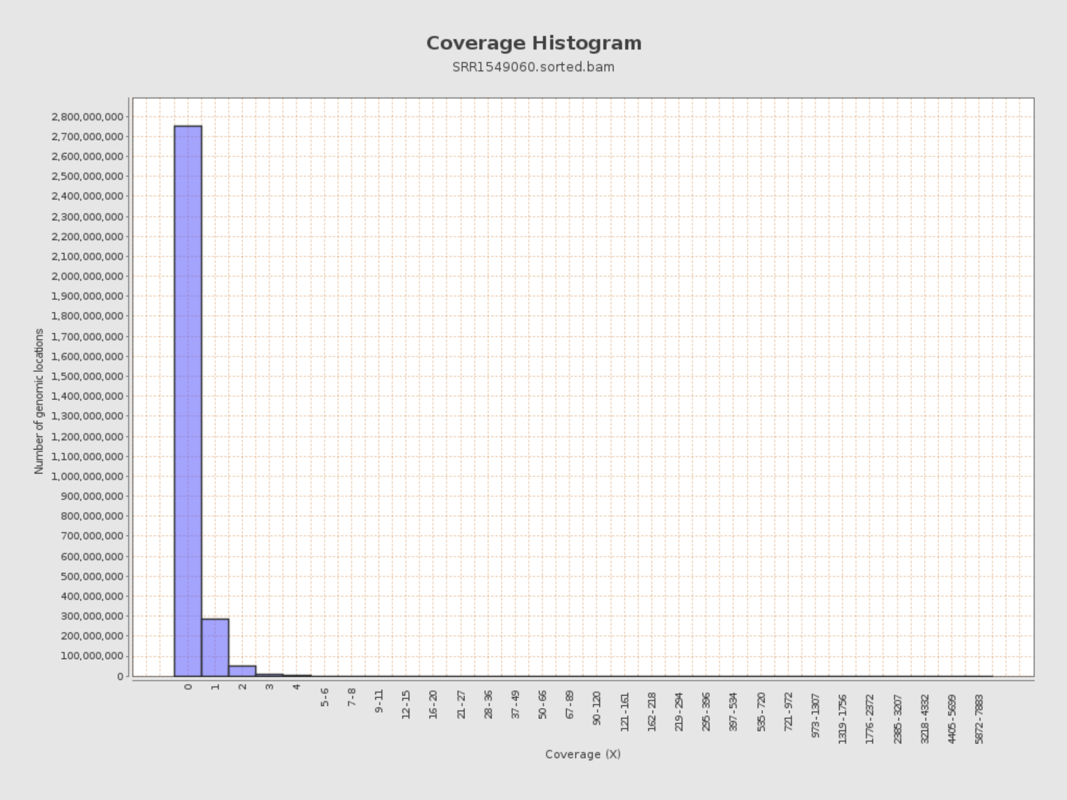
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	35238257	0.1414	4.0206
chr2	243199373	37766019	0.1553	1.0018
chr3	198022430	26085366	0.1317	0.4568
chr4	191154276	30406741	0.1591	0.542
chr5	180915260	27769705	0.1535	0.5037
chr6	171115067	30289045	0.177	0.7121
chr7	159138663	24665994	0.155	1.3634
chr8	146364022	26904240	0.1838	3.9079

chr9	141213431	18337340	0.1299	0.9133
chr10	135534747	20388058	0.1504	1.0132
chr11	135006516	19721721	0.1461	0.9185
chr12	133851895	19976736	0.1492	0.5316
chr13	115169878	12470135	0.1083	0.375
chr14	107349540	13406123	0.1249	0.541
chr15	102531392	12322582	0.1202	0.406
chr16	90354753	10812040	0.1197	0.5709
chr17	81195210	10064290	0.124	0.5037
chr18	78077248	12030370	0.1541	2.0833
chr19	59128983	7313296	0.1237	2.9791
chr20	63025520	8435172	0.1338	0.4848
chr21	48129895	5643234	0.1173	0.5603
chr22	51304566	4047240	0.0789	0.3876
chrMT	16571	1470	0.0887	0.3534
chrX	155270560	10879668	0.0701	0.5907
chrY	59373566	3994949	0.0673	0.7194

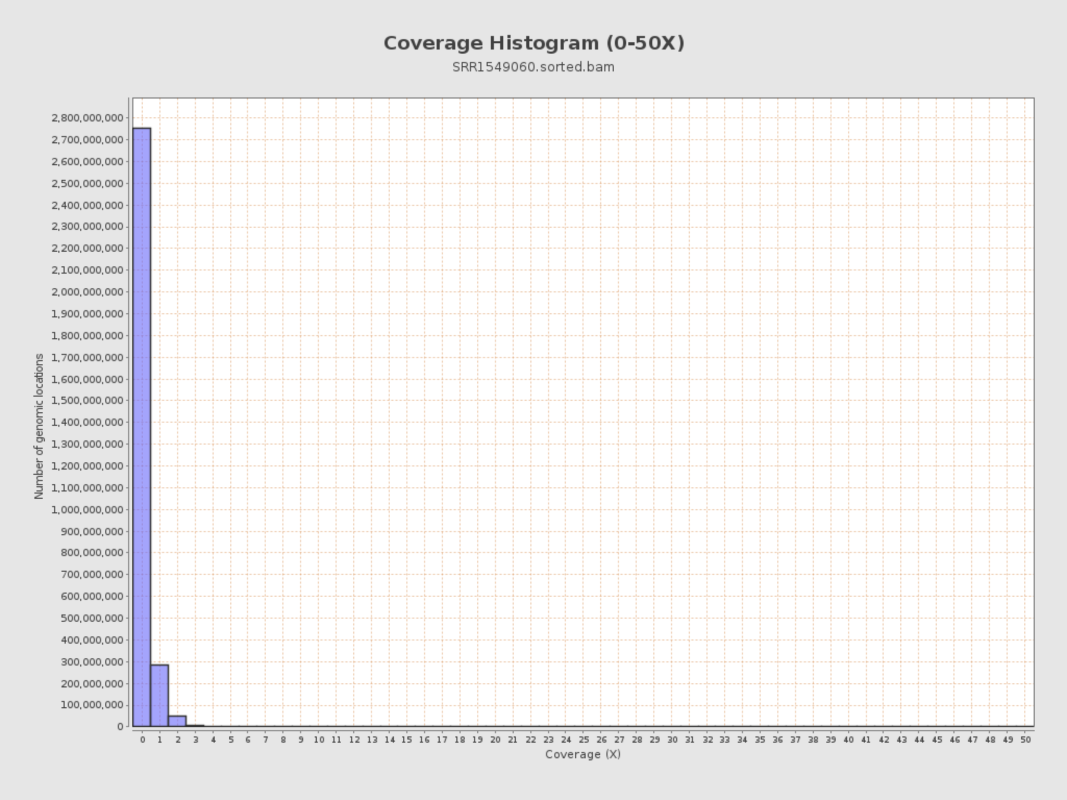
3. Results : Coverage across reference



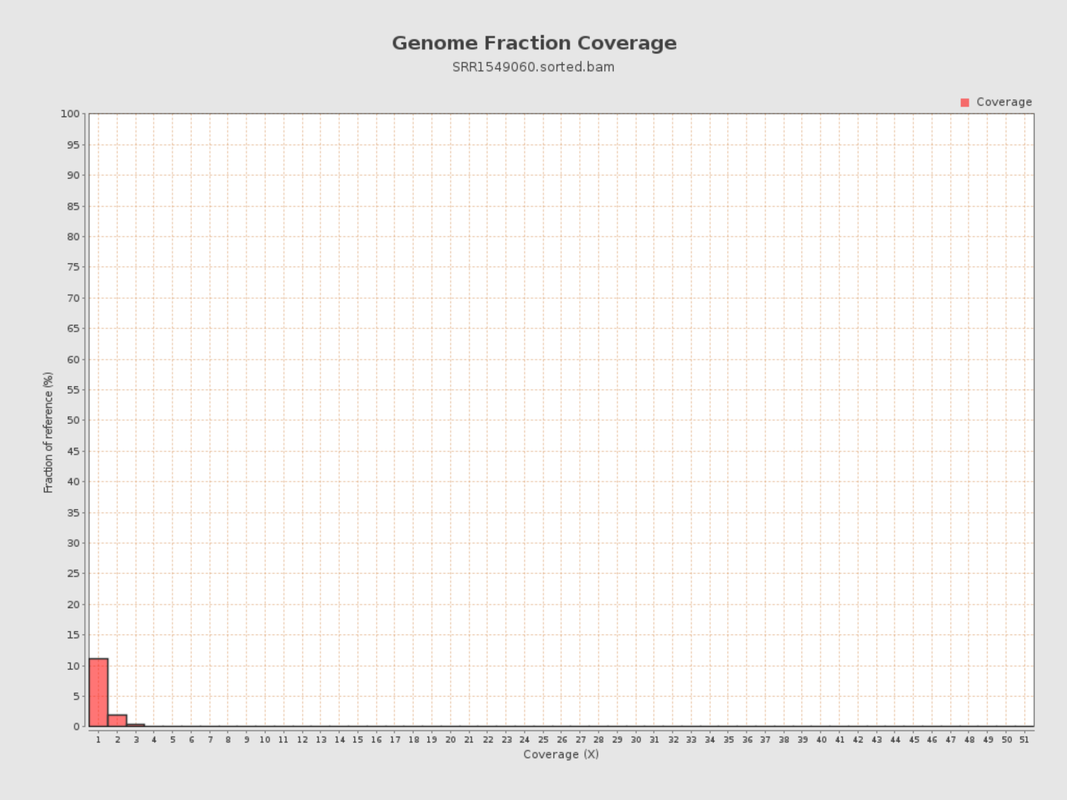
4. Results : Coverage Histogram



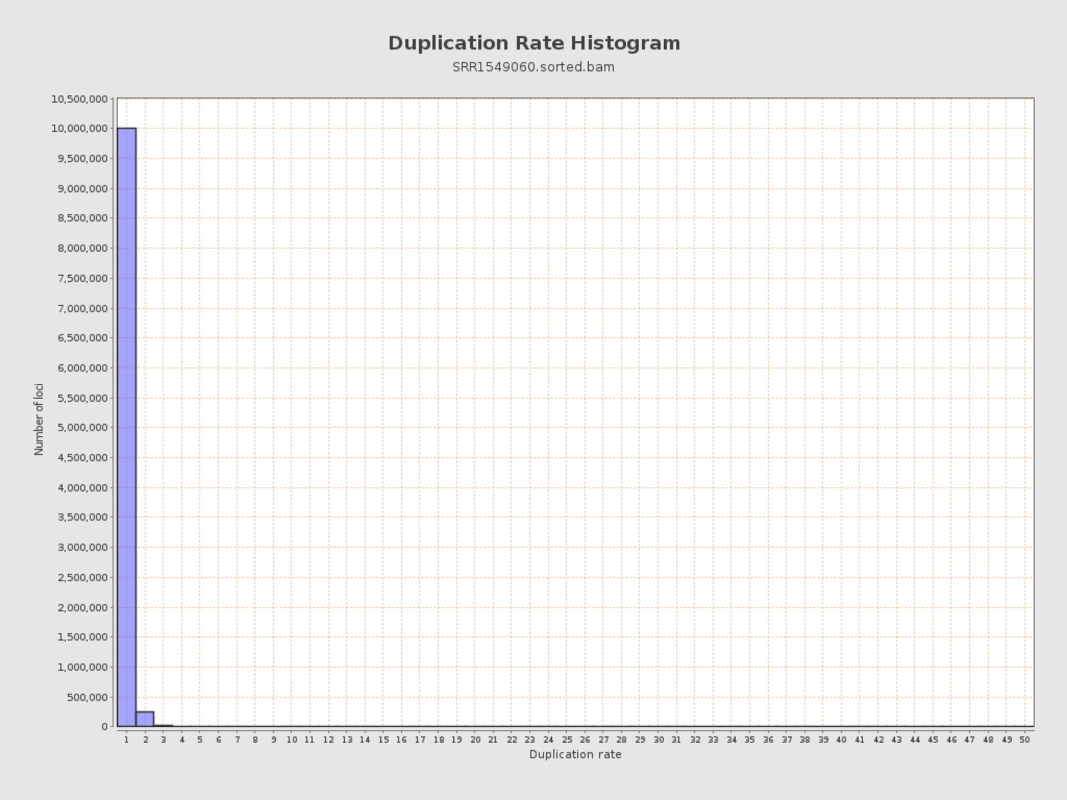
5. Results : Coverage Histogram (0-50X)



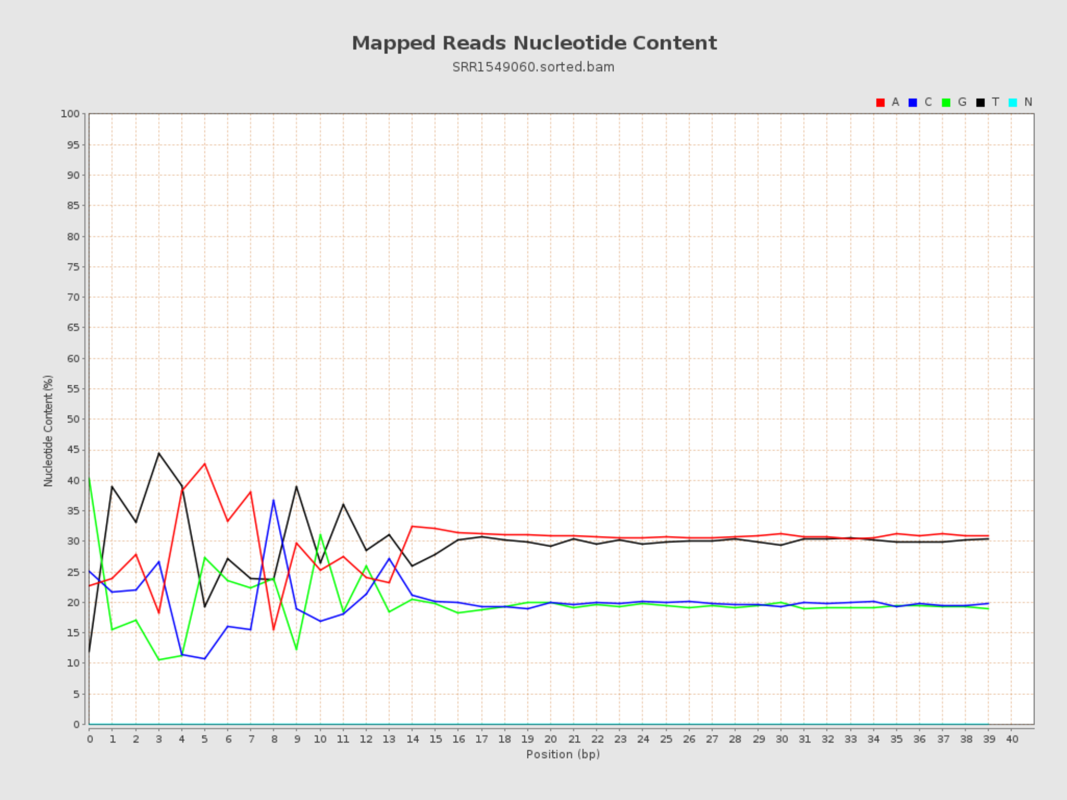
6. Results : Genome Fraction Coverage



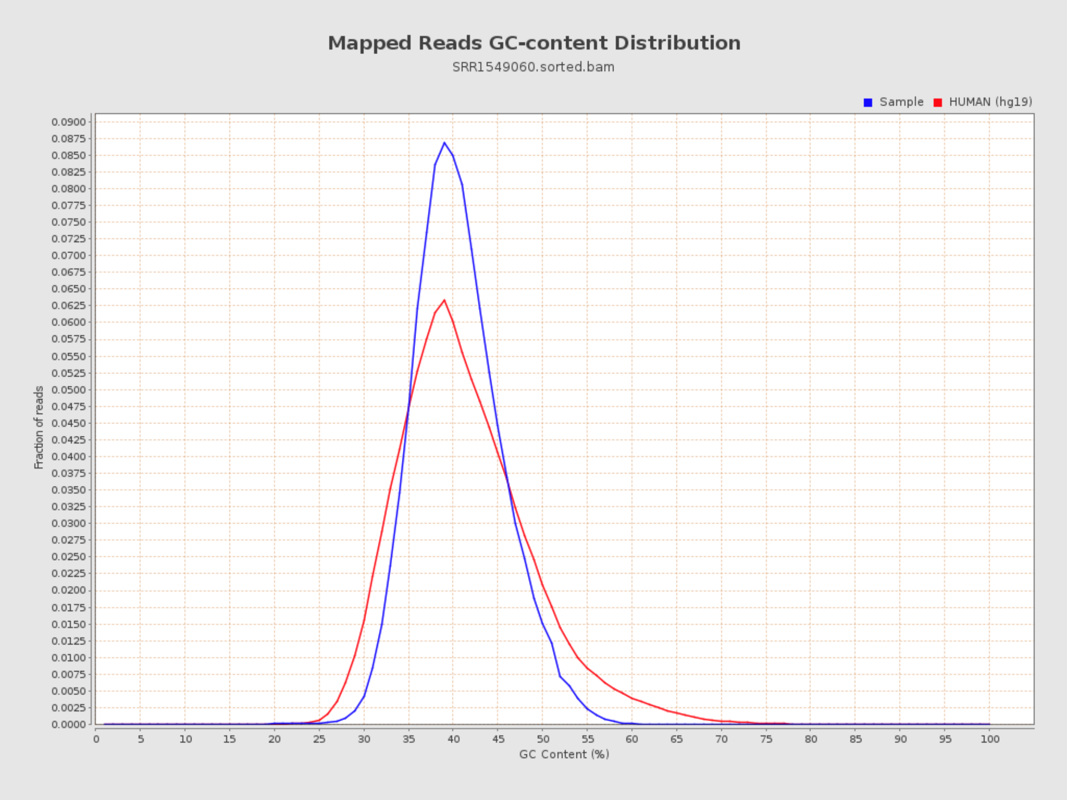
7. Results : Duplication Rate Histogram



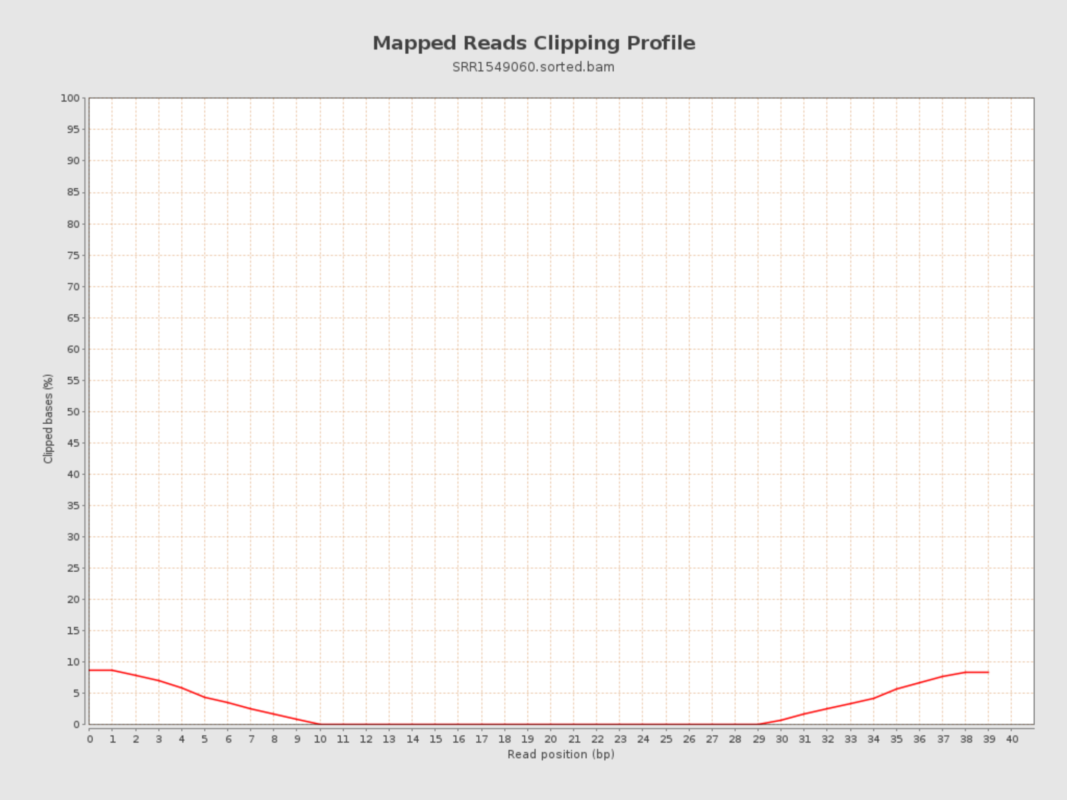
8. Results : Mapped Reads Nucleotide Content



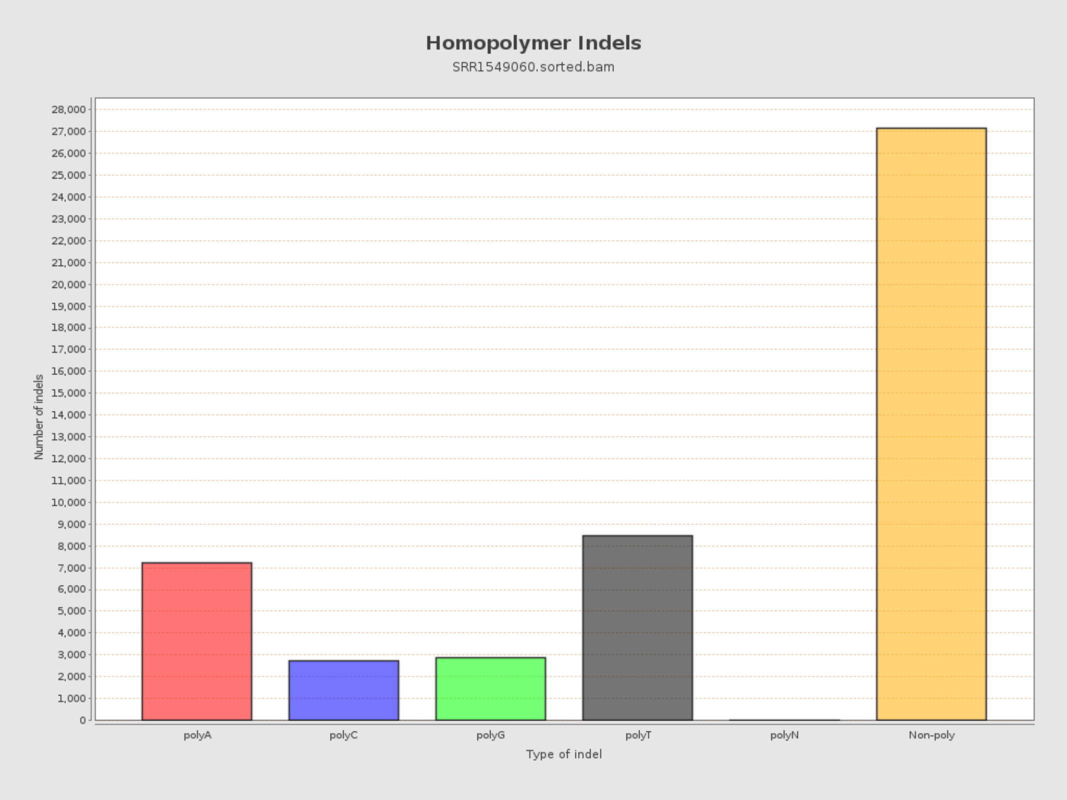
9. Results : Mapped Reads GC-content Distribution



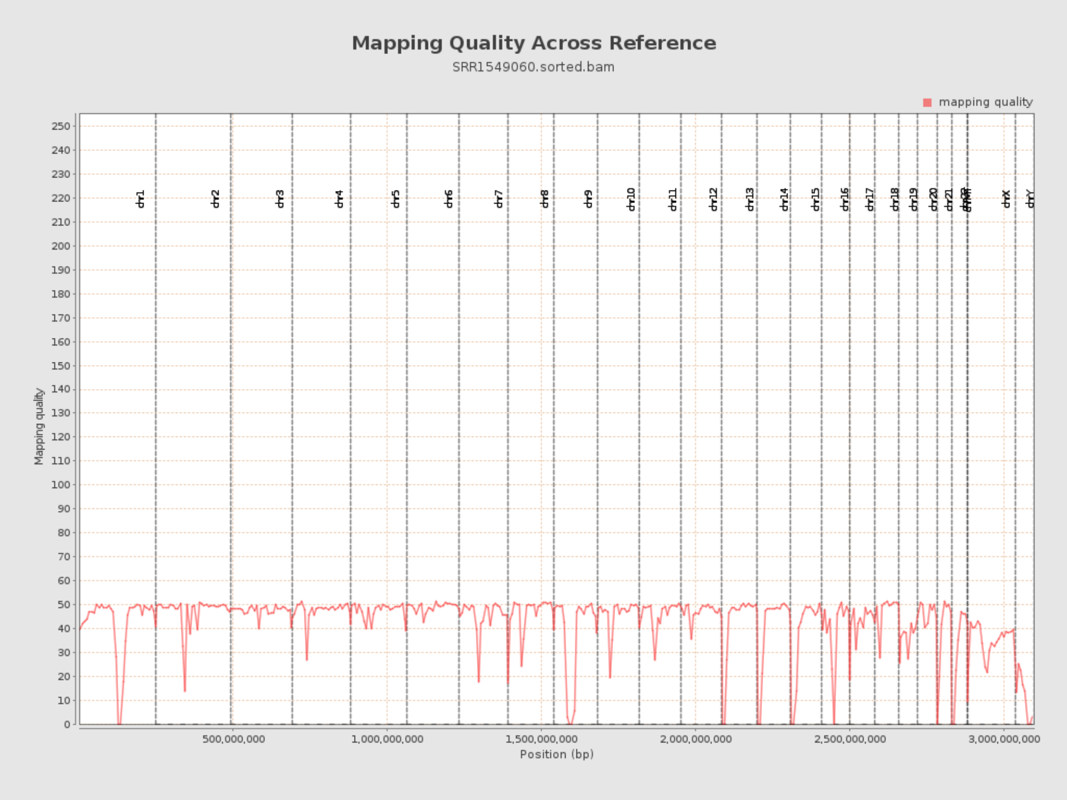
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram