

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:17:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548951.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_SRR1548951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548951.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:16:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,664,634
Mapped reads	9,258,464 / 86.81%
Unmapped reads	1,406,170 / 13.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	685,879 / 6.43%
Duplication rate	6.14%
Clipped reads	575,915 / 5.4%

2.2. ACGT Content

Number/percentage of A's	105,177,013 / 28.66%
Number/percentage of C's	77,268,302 / 21.05%
Number/percentage of T's	106,578,458 / 29.04%
Number/percentage of G's	77,992,673 / 21.25%
Number/percentage of N's	505 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.1186
Standard Deviation	1.3157

2.4. Mapping Quality

Mean Mapping Quality	43.89
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2.5. Mismatches and indels

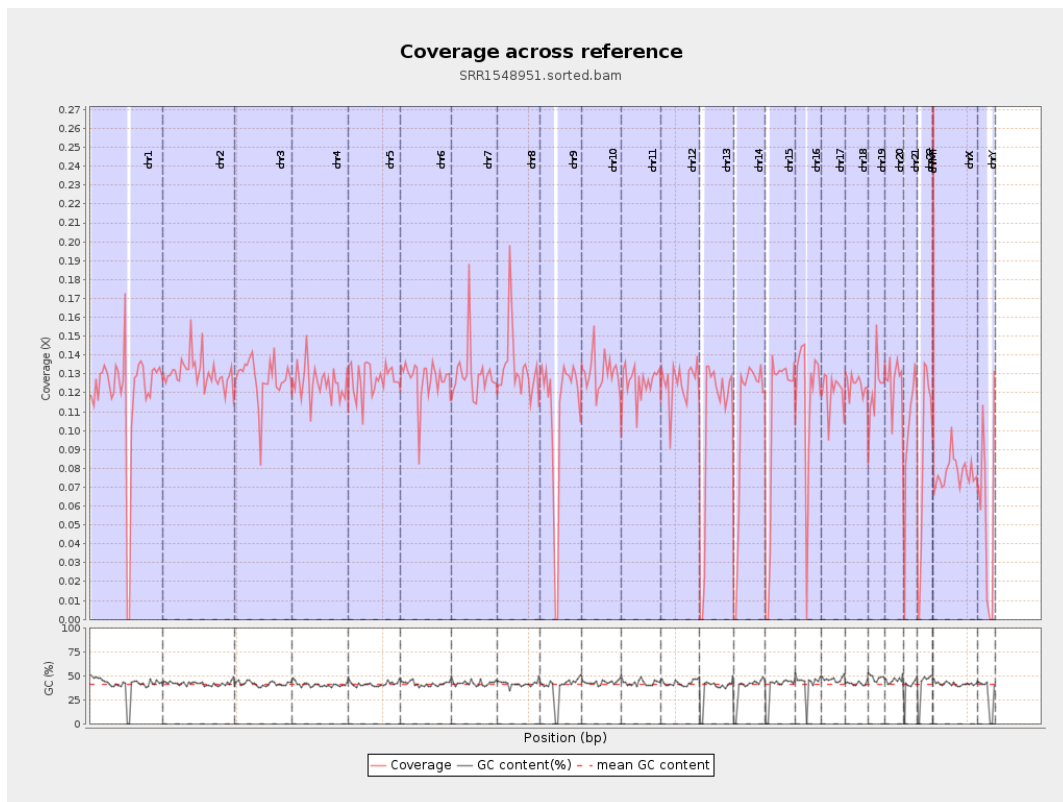
General error rate	0.23%
Mismatches	842,094
Insertions	10,073
Mapped reads with at least one insertion	0.11%
Deletions	27,697
Mapped reads with at least one deletion	0.3%
Homopolymer indels	43.62%

2.6. Chromosome stats

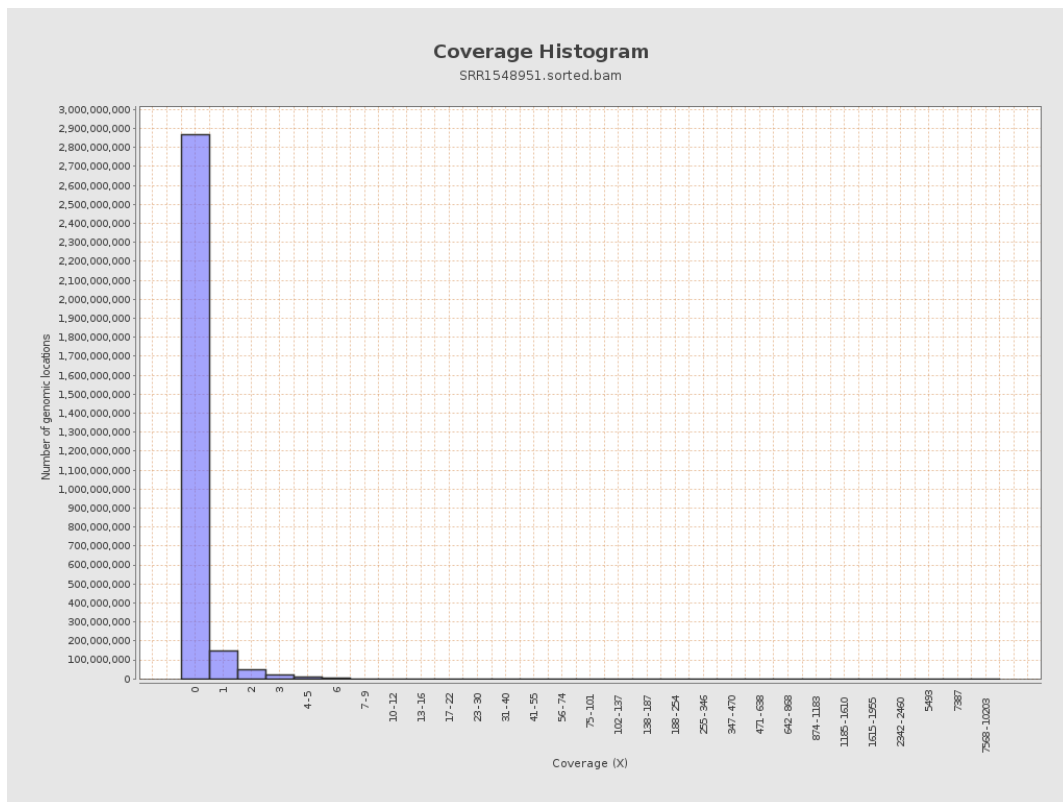
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29797498	0.1195	1.4692
chr2	243199373	31768636	0.1306	0.709
chr3	198022430	25208882	0.1273	0.532
chr4	191154276	24010286	0.1256	0.5613
chr5	180915260	23030271	0.1273	0.5362
chr6	171115067	21737286	0.127	0.5473
chr7	159138663	20638036	0.1297	1.1417
chr8	146364022	19501778	0.1332	4.9739

chr9	141213431	15570738	0.1103	0.6508
chr10	135534747	17668445	0.1304	0.6837
chr11	135006516	16960607	0.1256	0.7083
chr12	133851895	16846075	0.1259	0.5422
chr13	115169878	11973124	0.104	0.4765
chr14	107349540	11455365	0.1067	0.539
chr15	102531392	10790957	0.1052	0.4757
chr16	90354753	10599408	0.1173	0.5411
chr17	81195210	9819156	0.1209	0.5378
chr18	78077248	9698088	0.1242	1.0988
chr19	59128983	7268214	0.1229	1.1482
chr20	63025520	7921072	0.1257	0.5489
chr21	48129895	4827948	0.1003	0.5597
chr22	51304566	4445347	0.0866	0.6198
chrMT	16571	20901	1.2613	1.8668
chrX	155270560	12066472	0.0777	0.4939
chrY	59373566	3429422	0.0578	0.6448

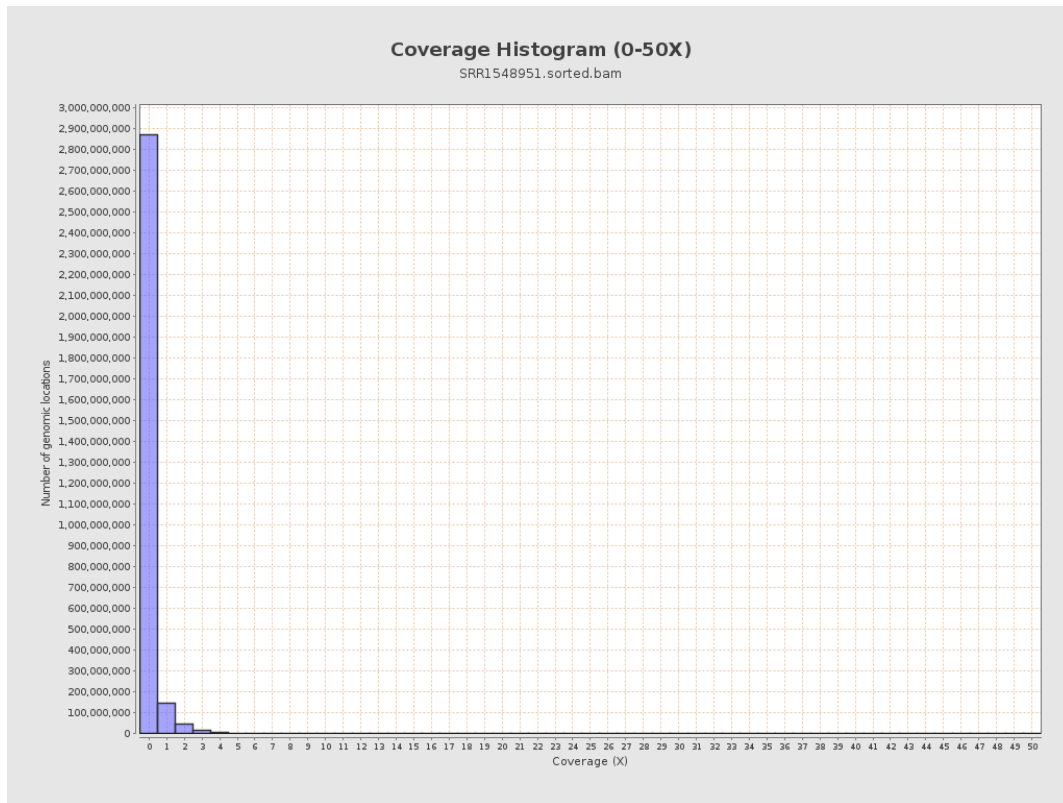
3. Results : Coverage across reference



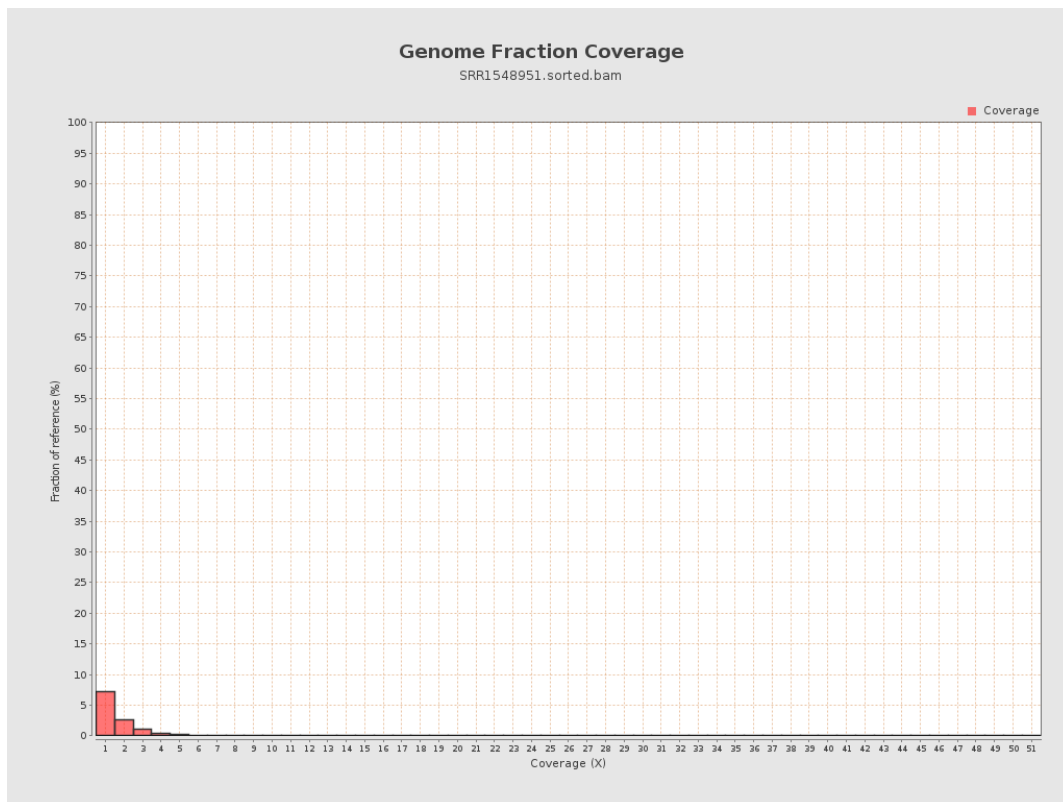
4. Results : Coverage Histogram



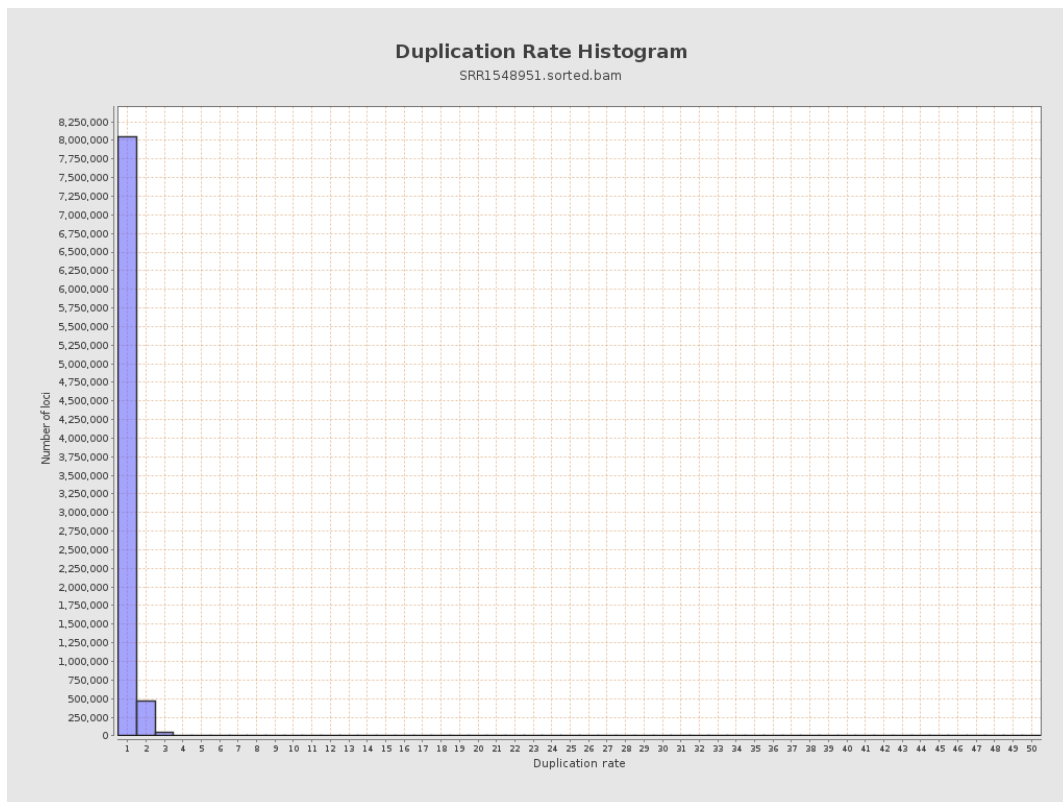
5. Results : Coverage Histogram (0-50X)



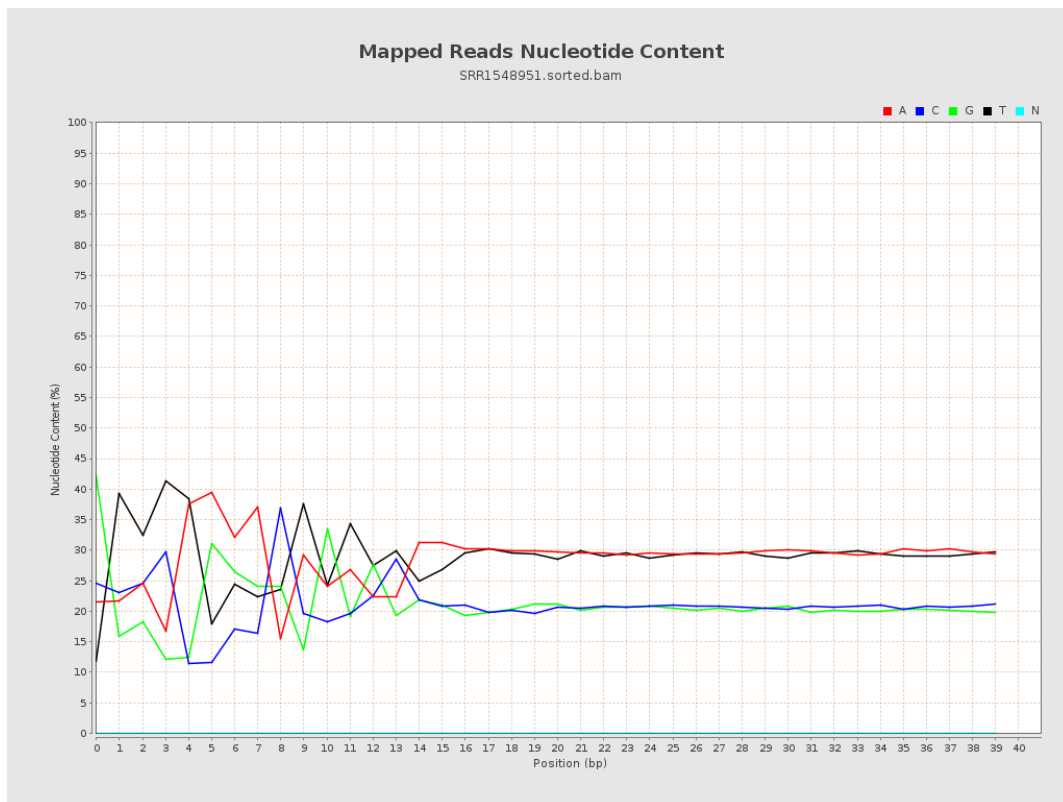
6. Results : Genome Fraction Coverage



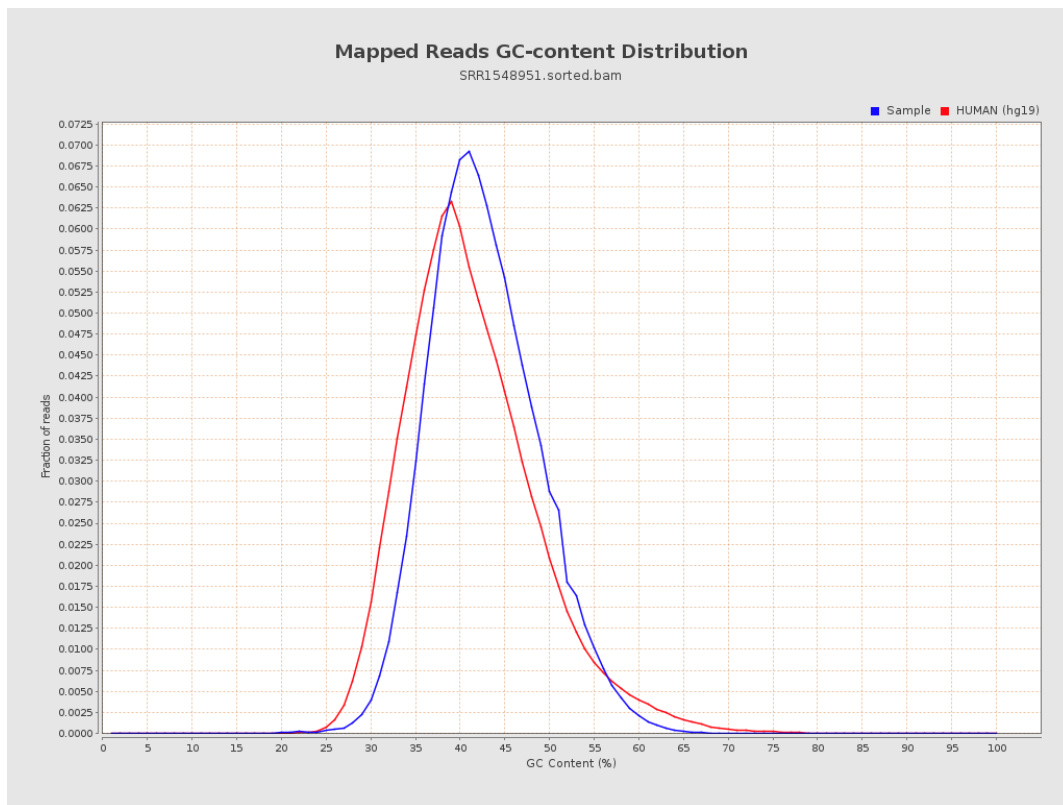
7. Results : Duplication Rate Histogram



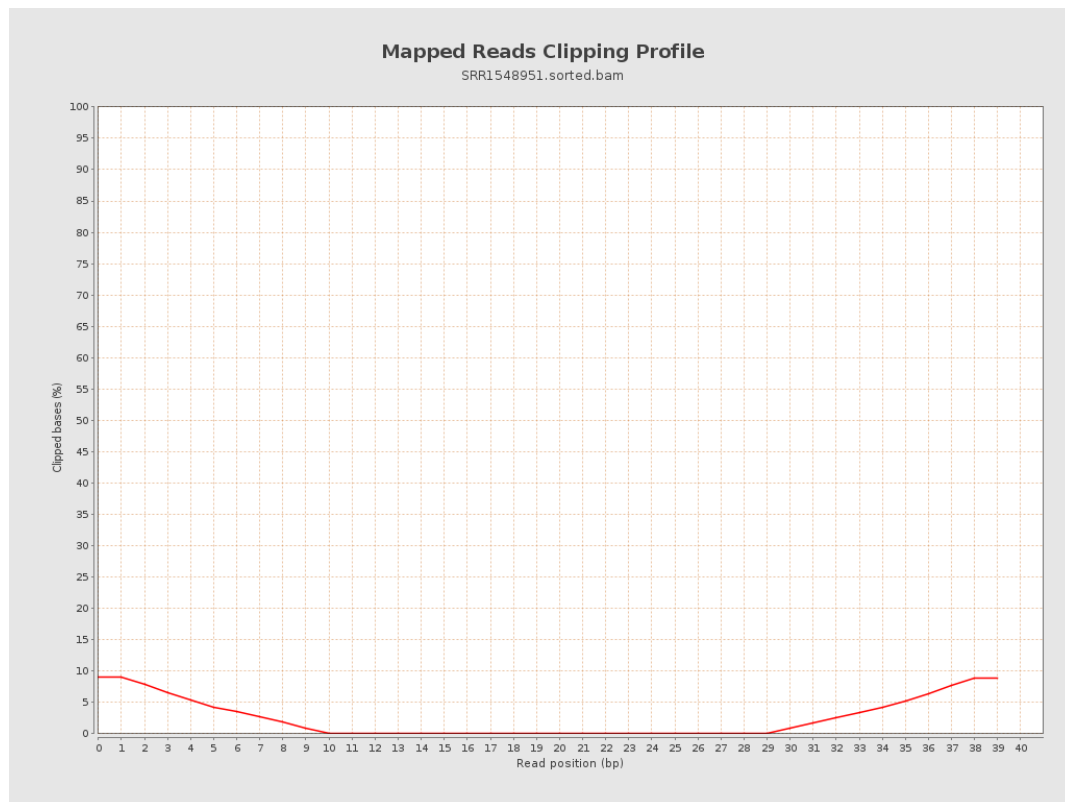
8. Results : Mapped Reads Nucleotide Content



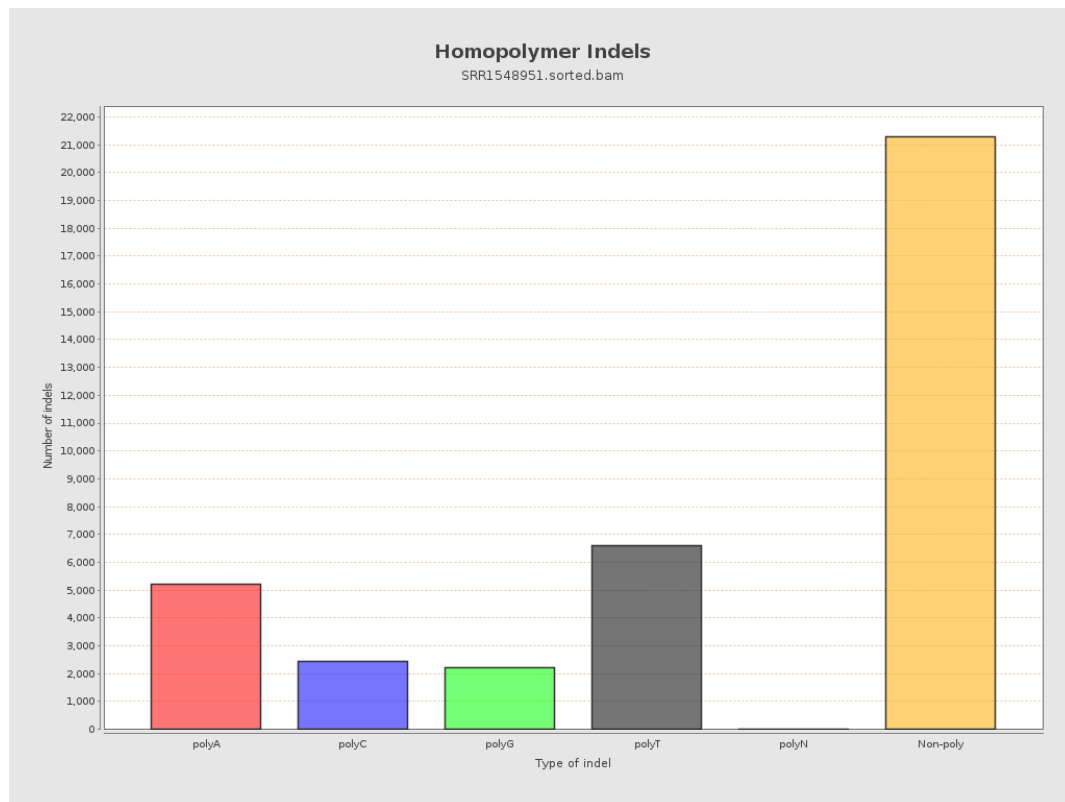
9. Results : Mapped Reads GC-content Distribution



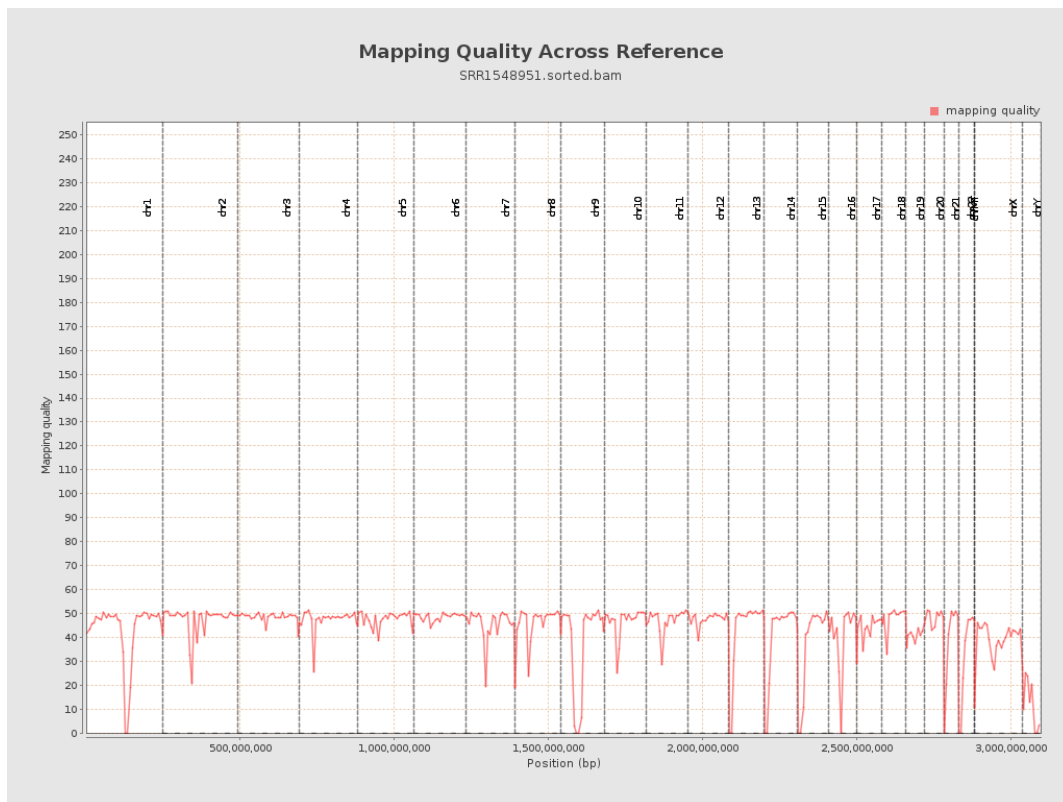
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

