

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:12:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971310.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_SRR2971310 /home/luna/Desktop/database/homo_hsa.fa SRR2971310.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:12:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,262,207
Mapped reads	9,526,887 / 92.83%
Unmapped reads	735,320 / 7.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,431 / 0.01%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	826,664 / 8.06%
Duplication rate	6.93%
Clipped reads	1,938,474 / 18.89%

2.2. ACGT Content

Number/percentage of A's	130,370,457 / 28.47%
Number/percentage of C's	96,412,236 / 21.05%
Number/percentage of T's	131,027,028 / 28.61%
Number/percentage of G's	100,125,575 / 21.86%
Number/percentage of N's	22,183 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.148

Standard Deviation	1.2633
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2.4. Mapping Quality

Mean Mapping Quality	36.21
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2.5. Mismatches and indels

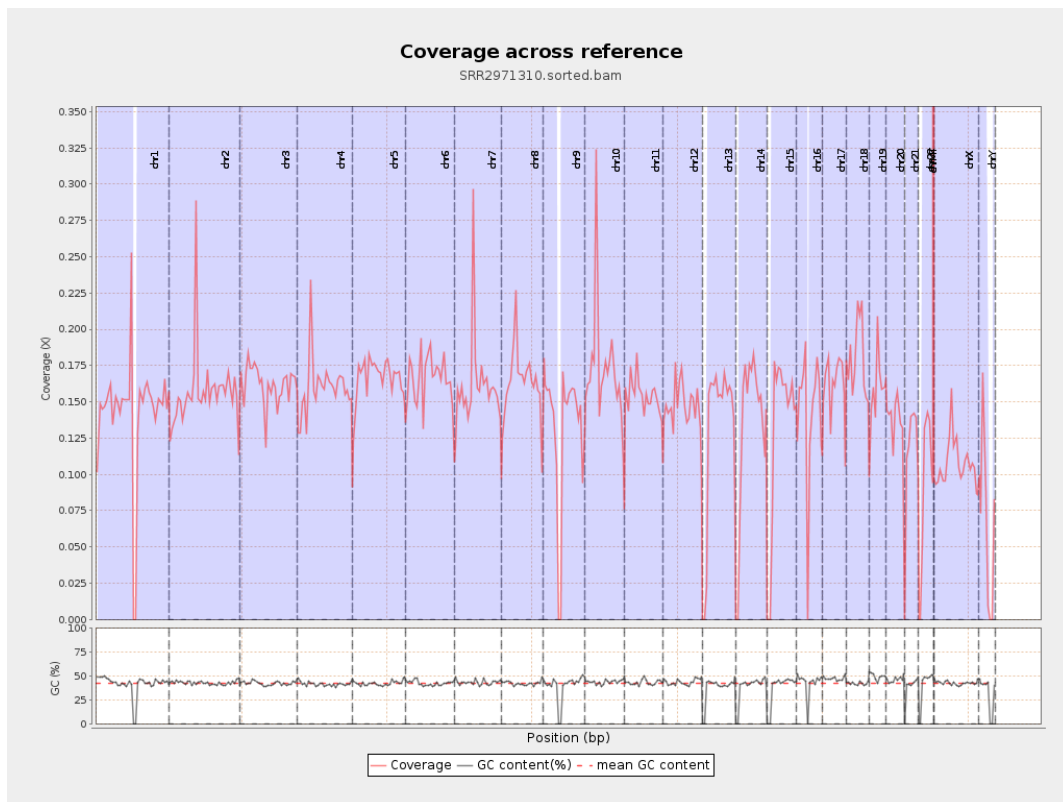
General error rate	0.52%
Mismatches	2,341,657
Insertions	29,972
Mapped reads with at least one insertion	0.31%
Deletions	67,629
Mapped reads with at least one deletion	0.71%
Homopolymer indels	41.03%

2.6. Chromosome stats

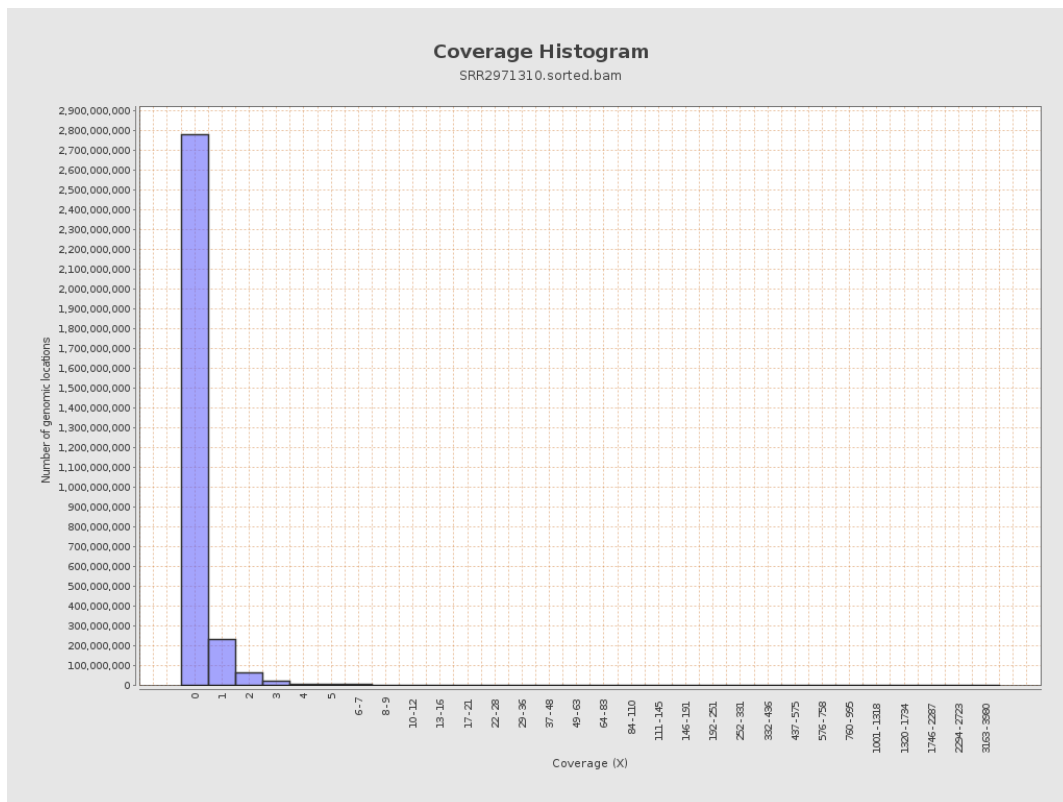
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	35566916	0.1427	2.3697
chr2	243199373	38165920	0.1569	1.1577
chr3	198022430	32016171	0.1617	0.5544
chr4	191154276	30464740	0.1594	0.7316
chr5	180915260	30204539	0.167	0.5668
chr6	171115067	28298321	0.1654	0.6096
chr7	159138663	25870358	0.1626	1.9335

chr8	146364022	23874411	0.1631	2.1364
chr9	141213431	18493531	0.131	1.2089
chr10	135534747	23420634	0.1728	1.3654
chr11	135006516	20632645	0.1528	1.0466
chr12	133851895	19709725	0.1473	0.5699
chr13	115169878	14994773	0.1302	0.4833
chr14	107349540	14129843	0.1316	0.7335
chr15	102531392	13522618	0.1319	0.5043
chr16	90354753	12855459	0.1423	0.6655
chr17	81195210	13097443	0.1613	0.7523
chr18	78077248	14071293	0.1802	2.3303
chr19	59128983	9468652	0.1601	2.0611
chr20	63025520	8547284	0.1356	0.5538
chr21	48129895	5517384	0.1146	0.7058
chr22	51304566	4575631	0.0892	0.4725
chrMT	16571	69581	4.199	3.8392
chrX	155270560	16685437	0.1075	0.6293
chrY	59373566	3802416	0.064	0.6641

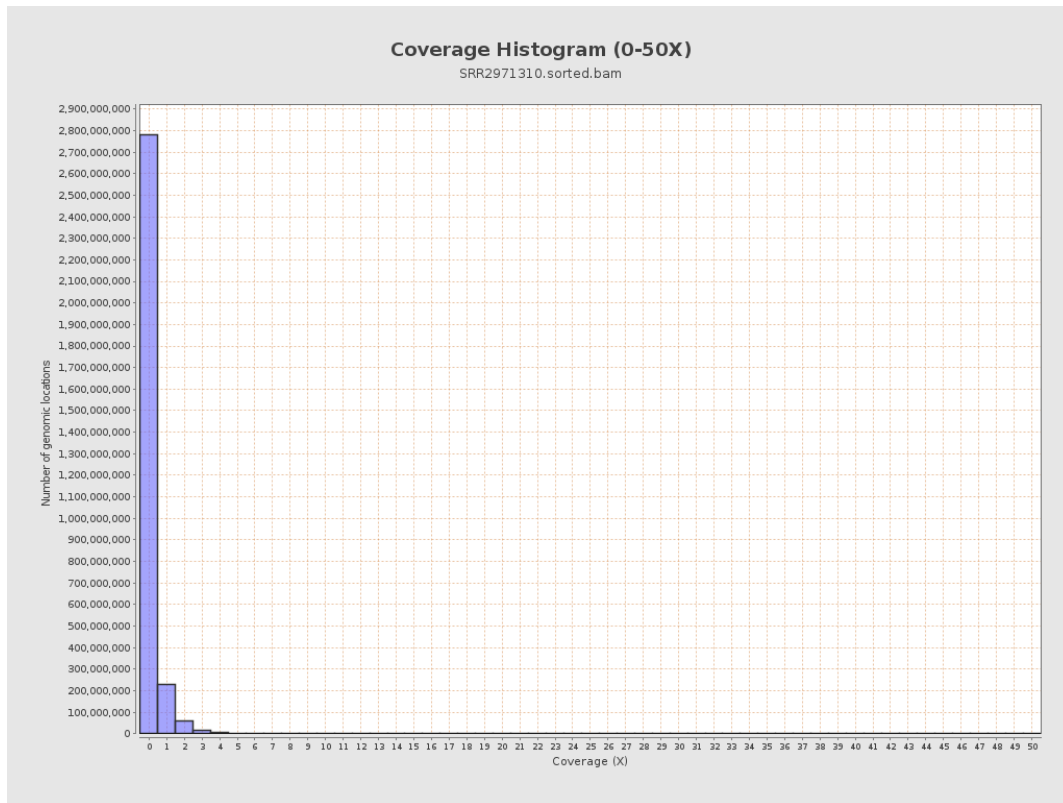
3. Results : Coverage across reference



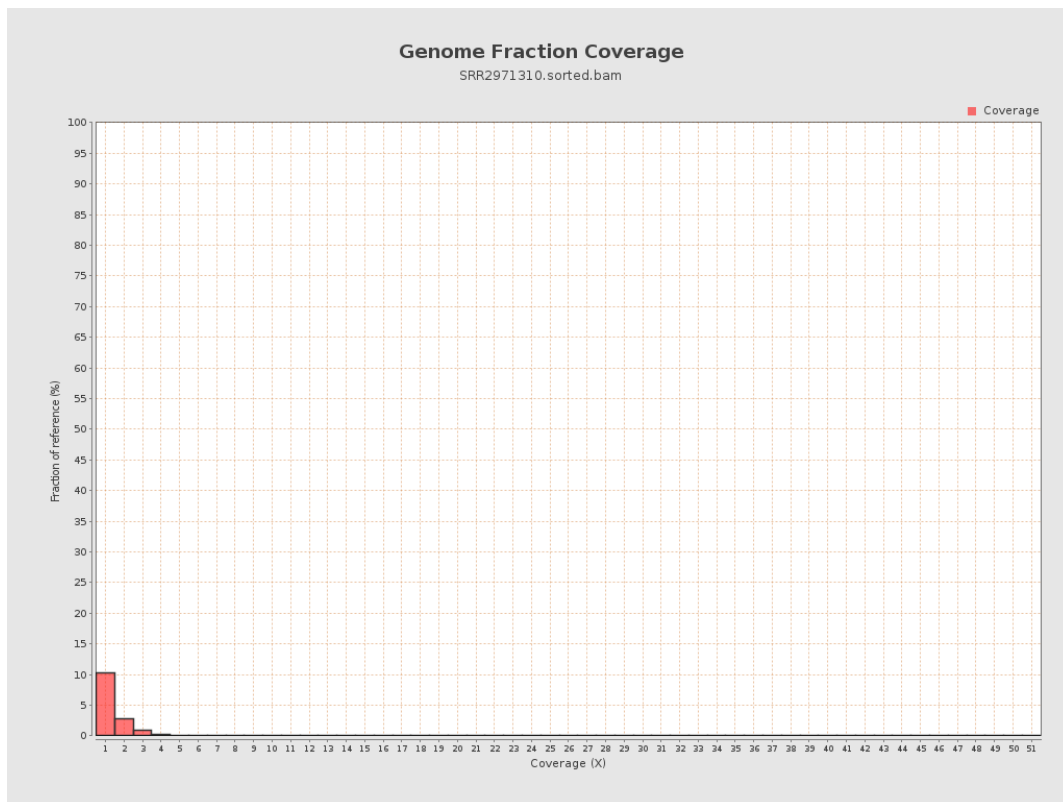
4. Results : Coverage Histogram



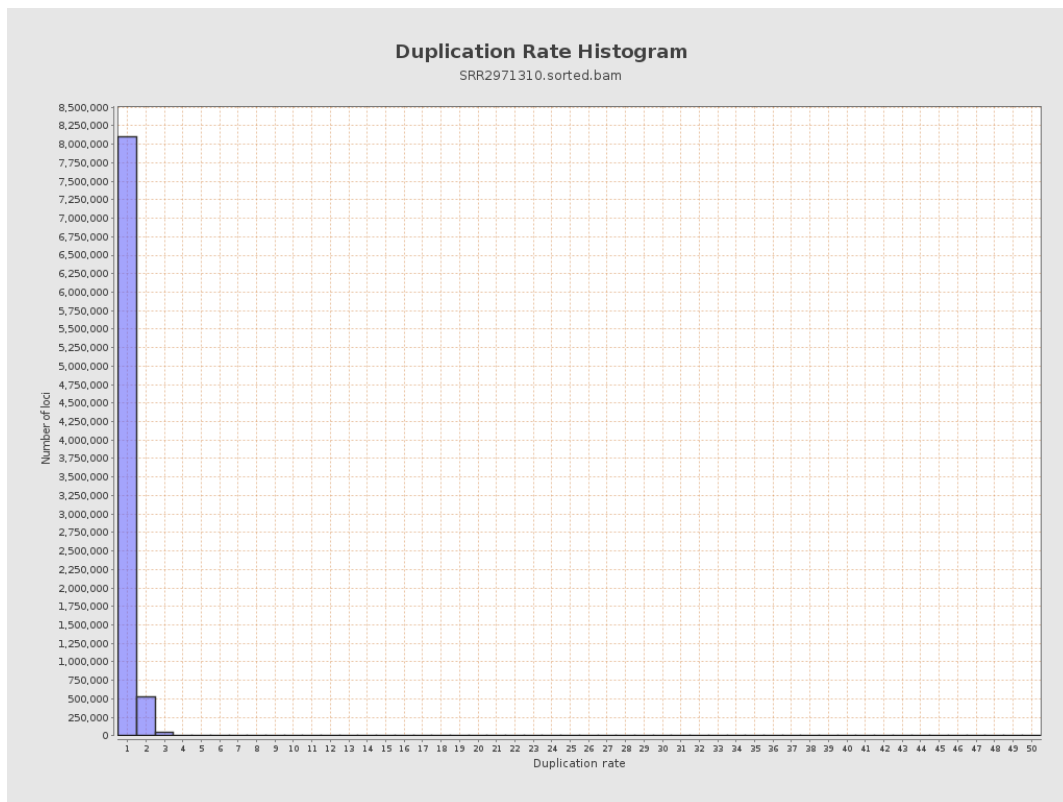
5. Results : Coverage Histogram (0-50X)



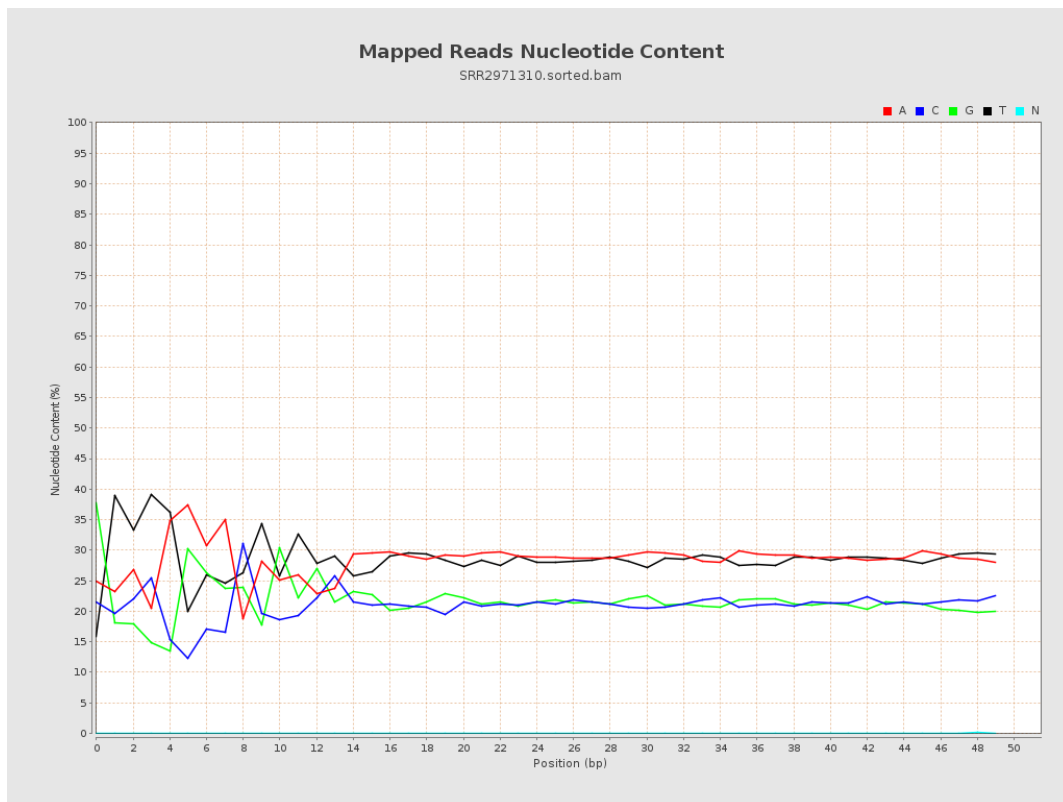
6. Results : Genome Fraction Coverage



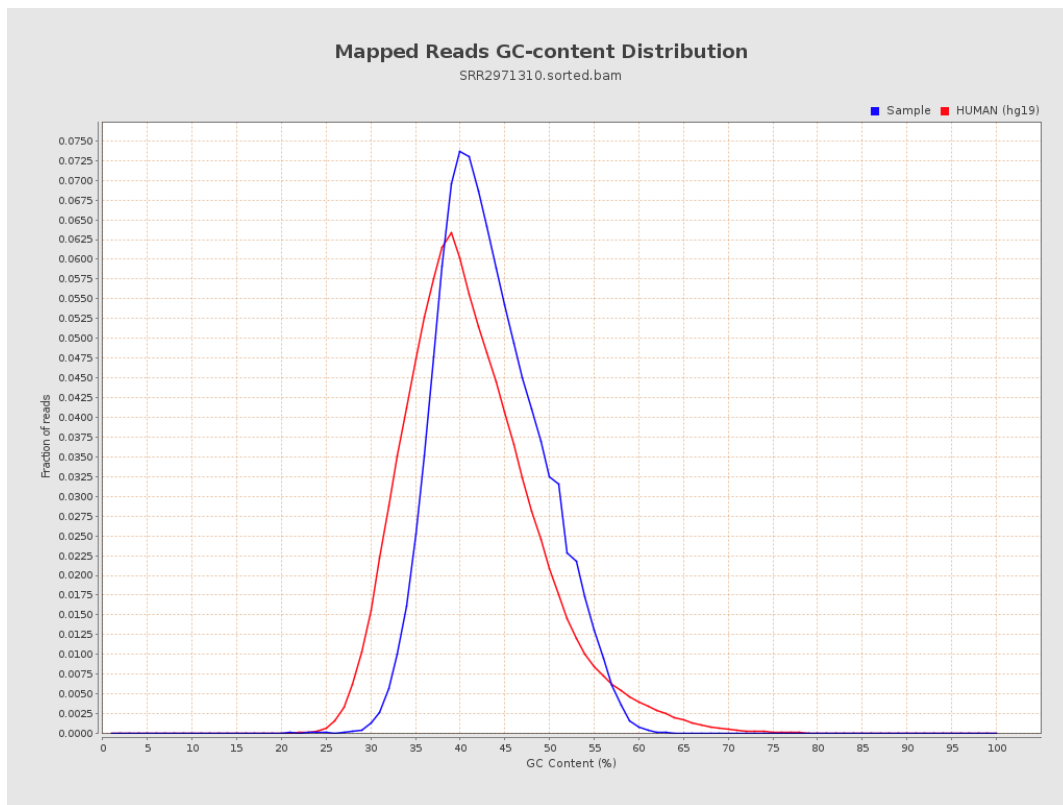
7. Results : Duplication Rate Histogram



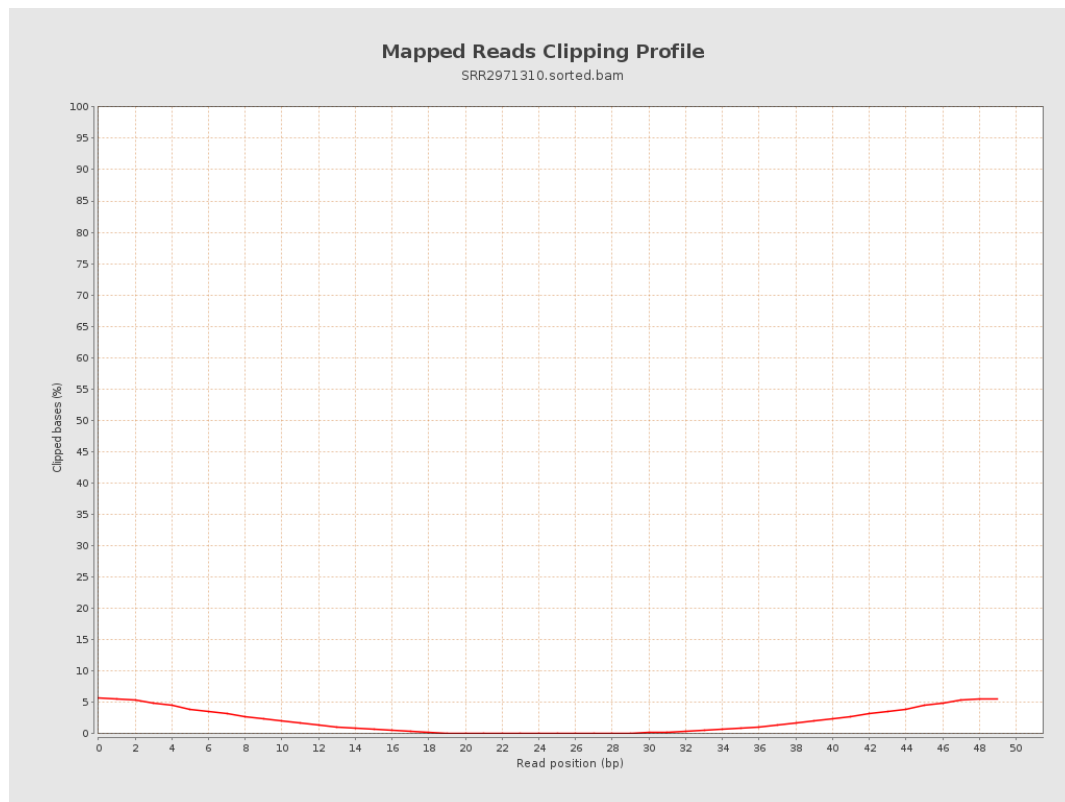
8. Results : Mapped Reads Nucleotide Content



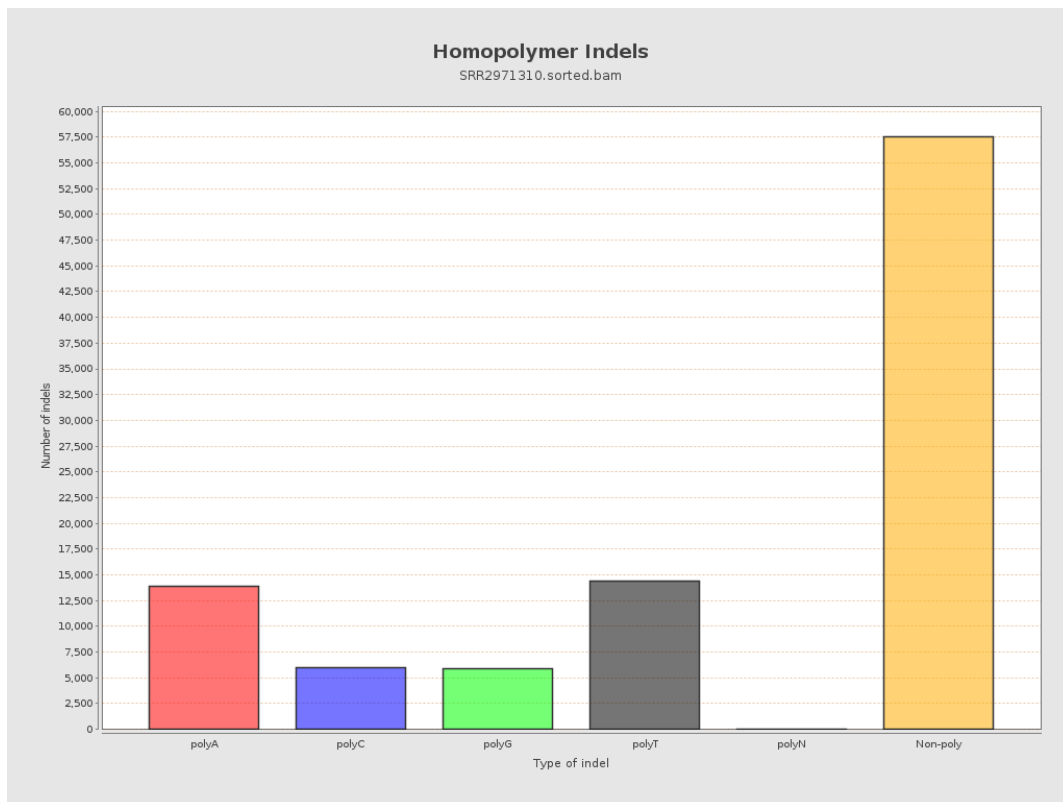
9. Results : Mapped Reads GC-content Distribution



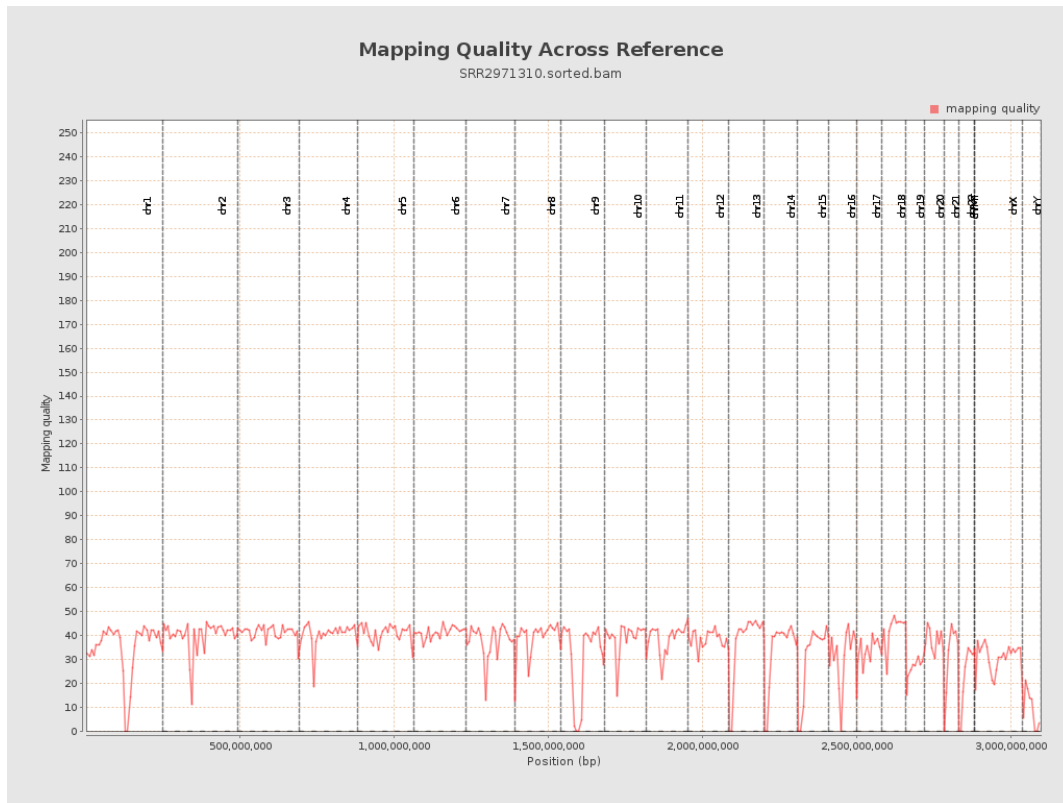
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

