

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:47:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063566.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_SRR6063566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063566.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:47:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,672,073
Mapped reads	2,391,541 / 89.5%
Unmapped reads	280,532 / 10.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,442 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	89,774 / 3.36%
Duplication rate	2.66%
Clipped reads	1,124,060 / 42.07%

2.2. ACGT Content

Number/percentage of A's	44,136,959 / 27.86%
Number/percentage of C's	29,454,966 / 18.59%
Number/percentage of T's	49,110,676 / 31%
Number/percentage of G's	35,705,557 / 22.54%
Number/percentage of N's	3,175 / 0%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0512

Standard Deviation	0.4799
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2.4. Mapping Quality

Mean Mapping Quality	42.69
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2.5. Mismatches and indels

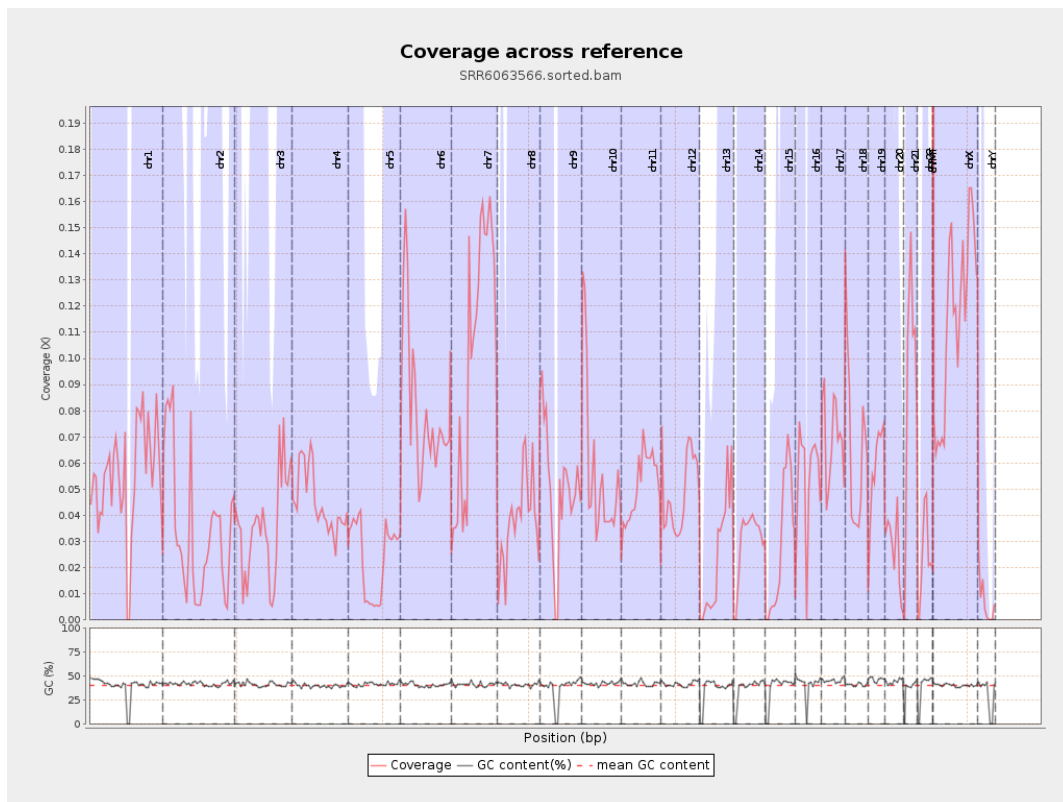
General error rate	0.82%
Mismatches	1,271,786
Insertions	12,118
Mapped reads with at least one insertion	0.5%
Deletions	43,232
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.16%

2.6. Chromosome stats

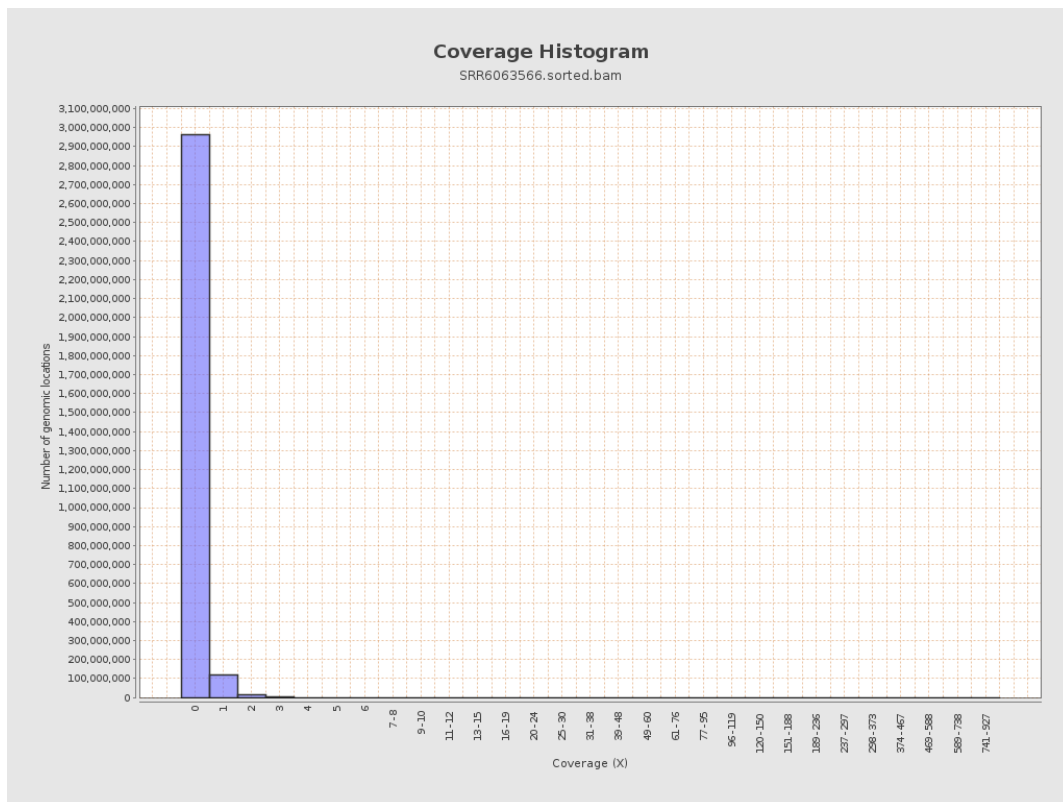
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13594328	0.0545	0.7493
chr2	243199373	8340406	0.0343	0.5904
chr3	198022430	6919546	0.0349	0.2121
chr4	191154276	8590767	0.0449	0.2437
chr5	180915260	4302222	0.0238	0.1767
chr6	171115067	13867687	0.081	0.4055
chr7	159138663	16038228	0.1008	1.0822

chr8	146364022	5550864	0.0379	0.4869
chr9	141213431	7008658	0.0496	0.4193
chr10	135534747	7696553	0.0568	0.3921
chr11	135006516	6923822	0.0513	0.3722
chr12	133851895	6545284	0.0489	0.262
chr13	115169878	2827385	0.0245	0.1765
chr14	107349540	3219119	0.03	0.2664
chr15	102531392	2843611	0.0277	0.1957
chr16	90354753	4731944	0.0524	0.2842
chr17	81195210	5694514	0.0701	0.3167
chr18	78077248	5040933	0.0646	0.7133
chr19	59128983	3413047	0.0577	0.5807
chr20	63025520	1647234	0.0261	0.2126
chr21	48129895	4266166	0.0886	0.3495
chr22	51304566	1208882	0.0236	0.1691
chrMT	16571	23570	1.4224	1.4432
chrX	155270560	17789696	0.1146	0.4828
chrY	59373566	396990	0.0067	0.1279

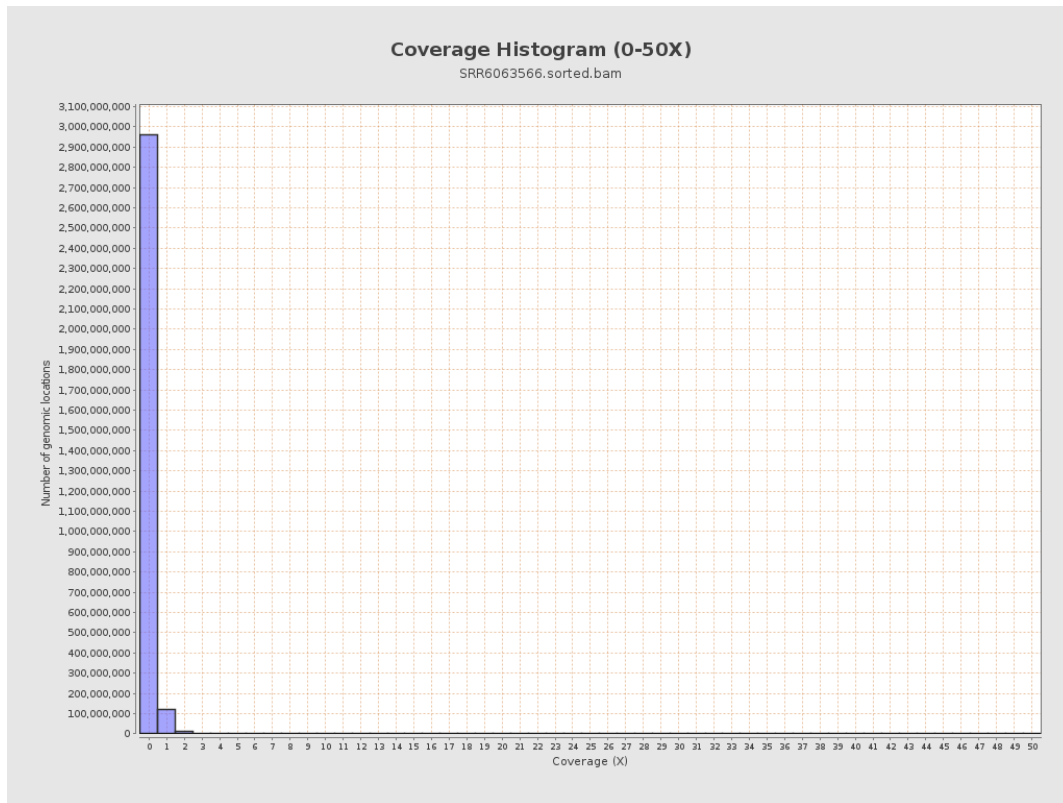
3. Results : Coverage across reference



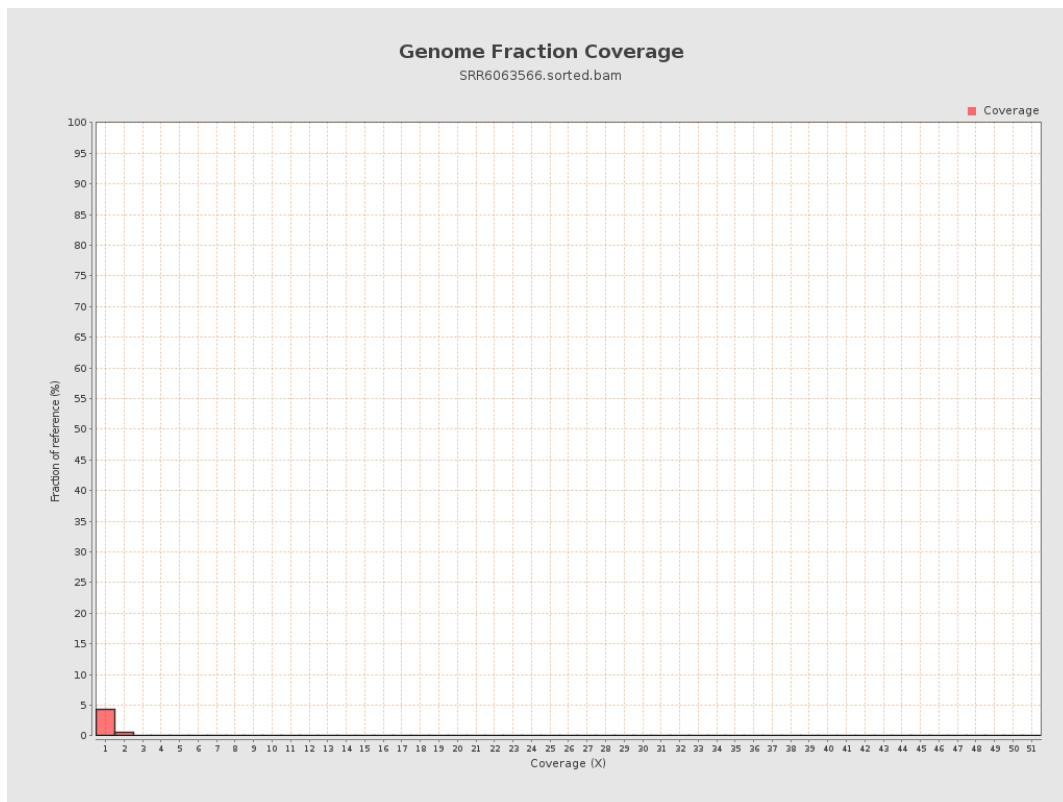
4. Results : Coverage Histogram



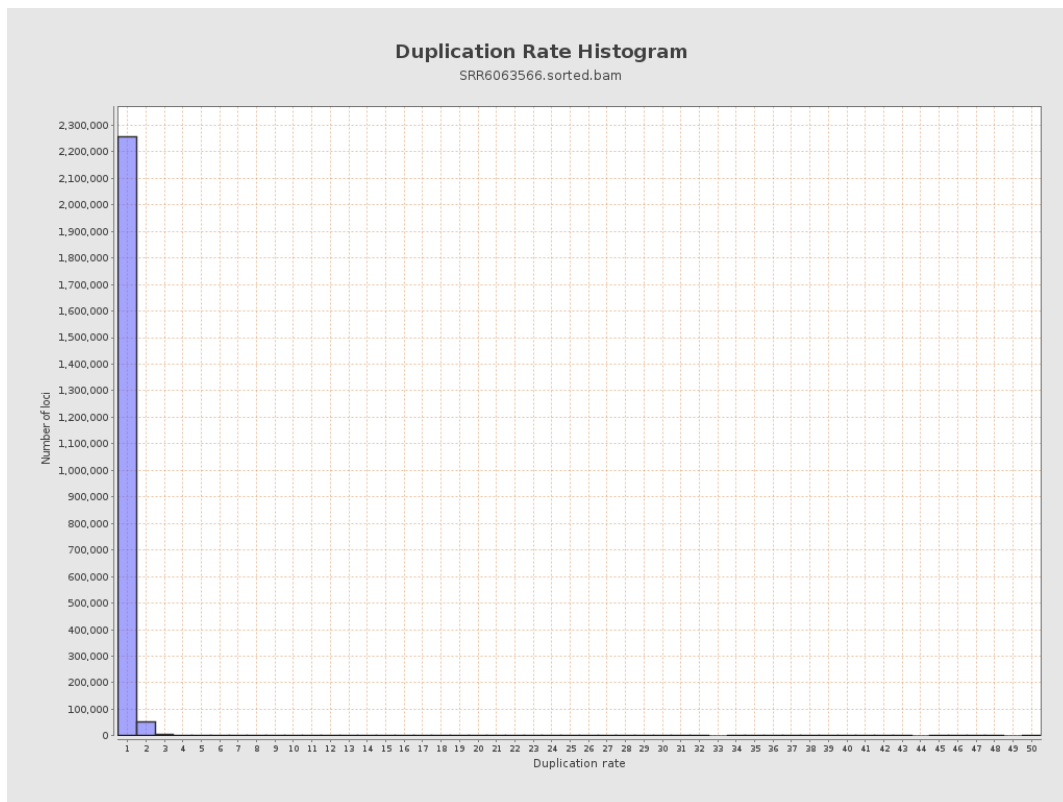
5. Results : Coverage Histogram (0-50X)



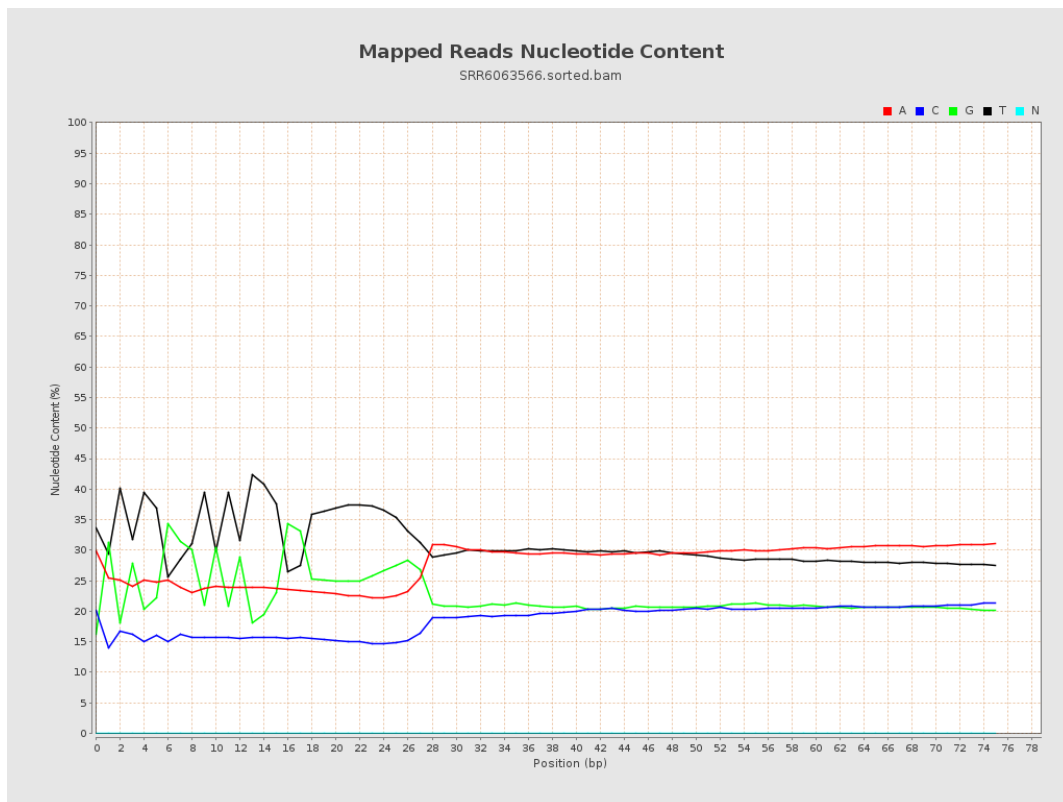
6. Results : Genome Fraction Coverage



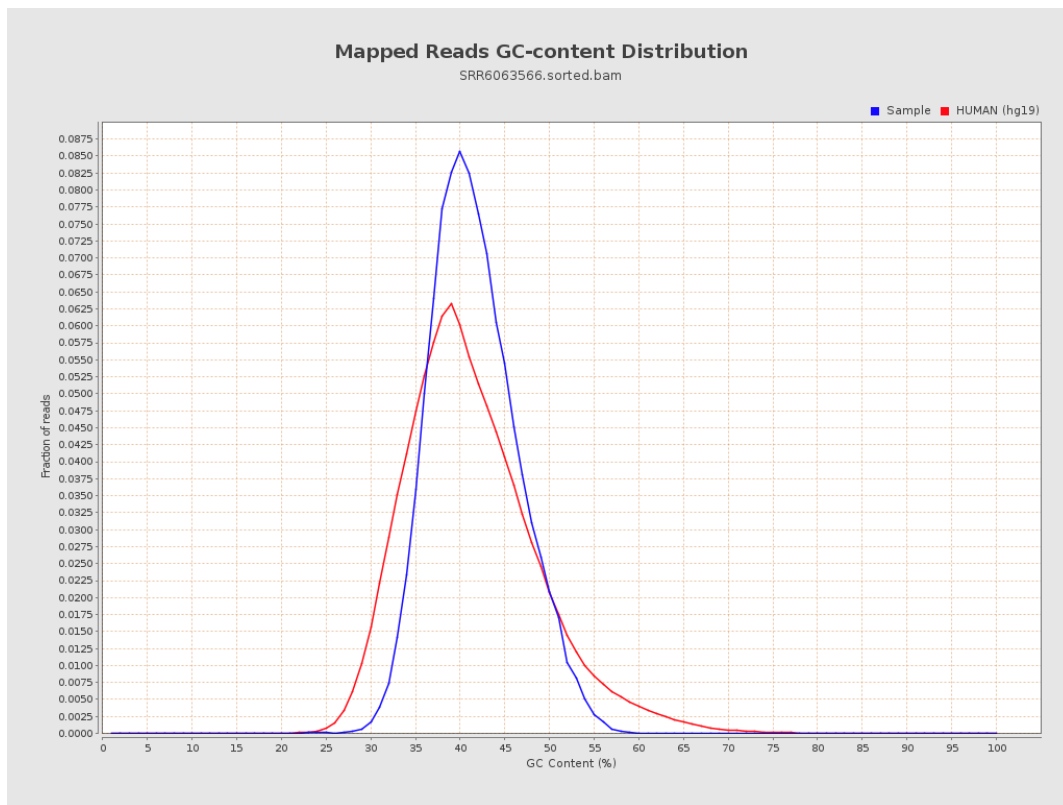
7. Results : Duplication Rate Histogram



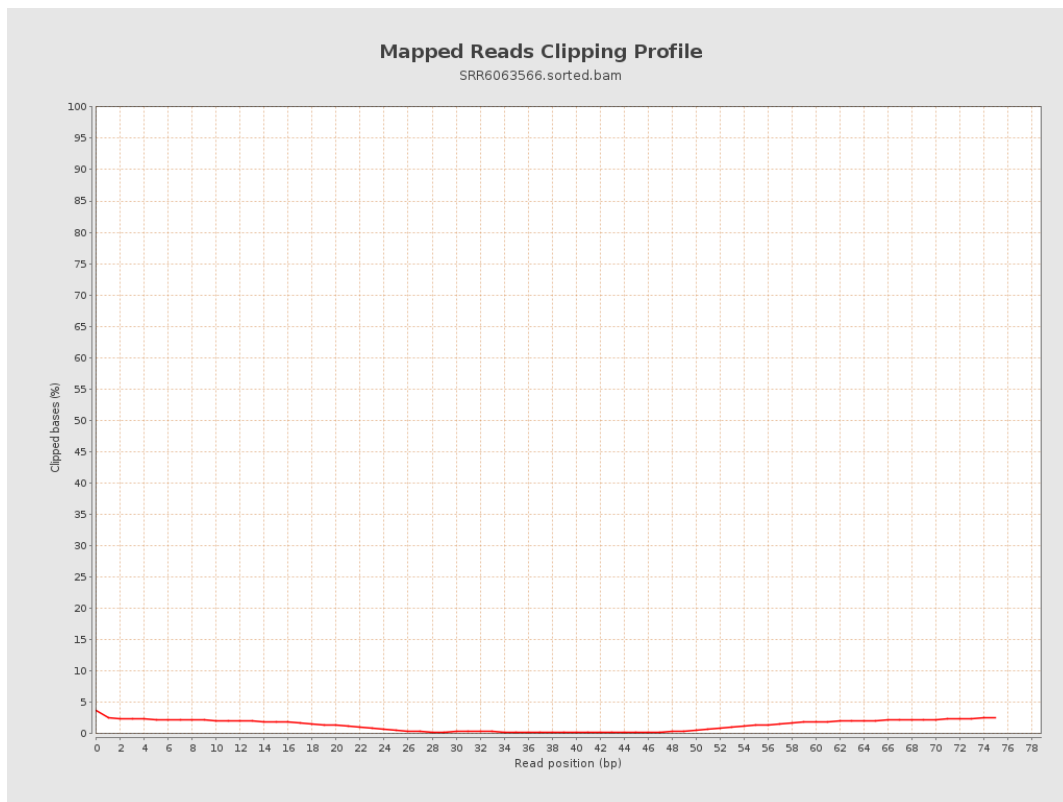
8. Results : Mapped Reads Nucleotide Content



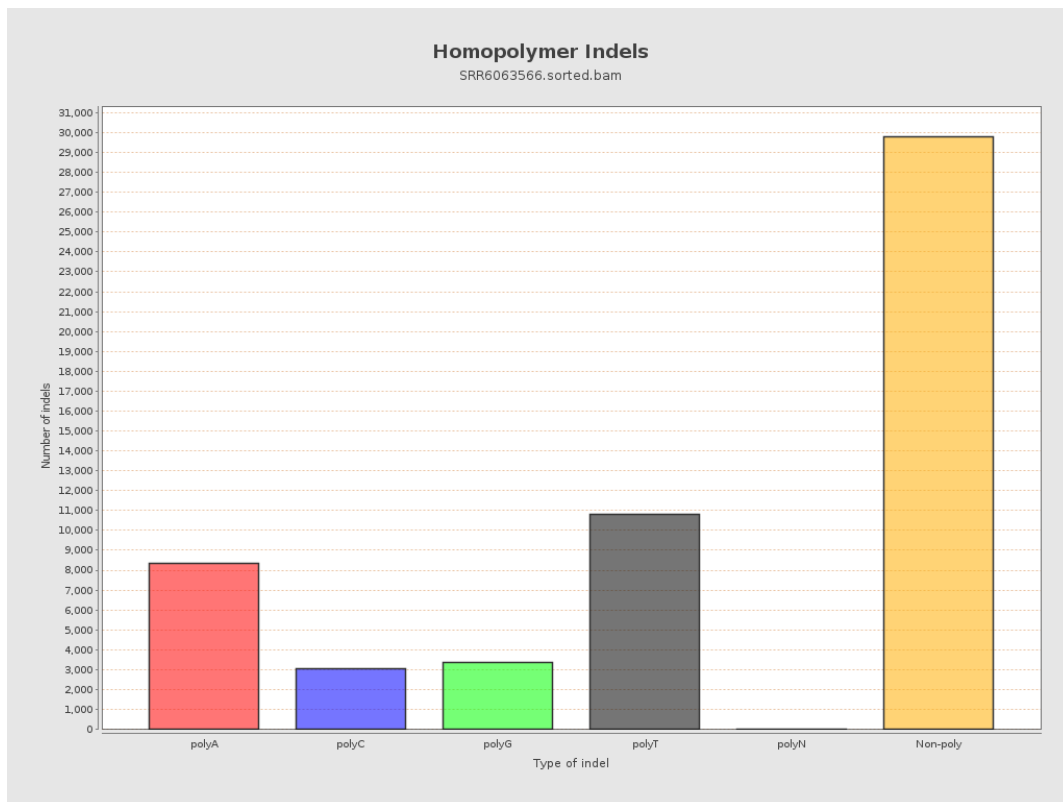
9. Results : Mapped Reads GC-content Distribution



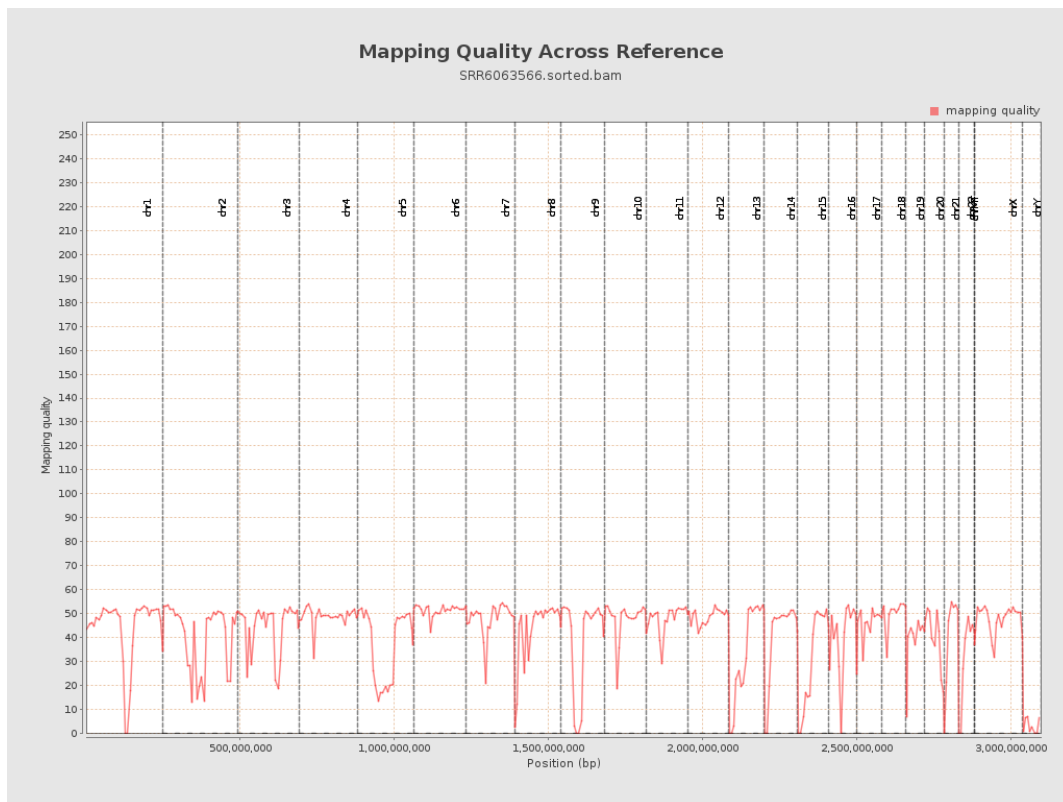
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

