Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:55:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068082.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_SRR6068082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:55:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,522,674
Mapped reads	2,157,889 / 85.54%
Unmapped reads	364,785 / 14.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,096 / 0.88%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	269,224 / 10.67%
Duplication rate	9.75%
Clipped reads	1,179,842 / 46.77%

2.2. ACGT Content

Number/percentage of A's	36,579,915 / 26.29%
Number/percentage of C's	25,789,286 / 18.54%
Number/percentage of T's	44,003,486 / 31.63%
Number/percentage of G's	32,759,688 / 23.55%
Number/percentage of N's	2,667 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.045

Standard Deviation	0.4525

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

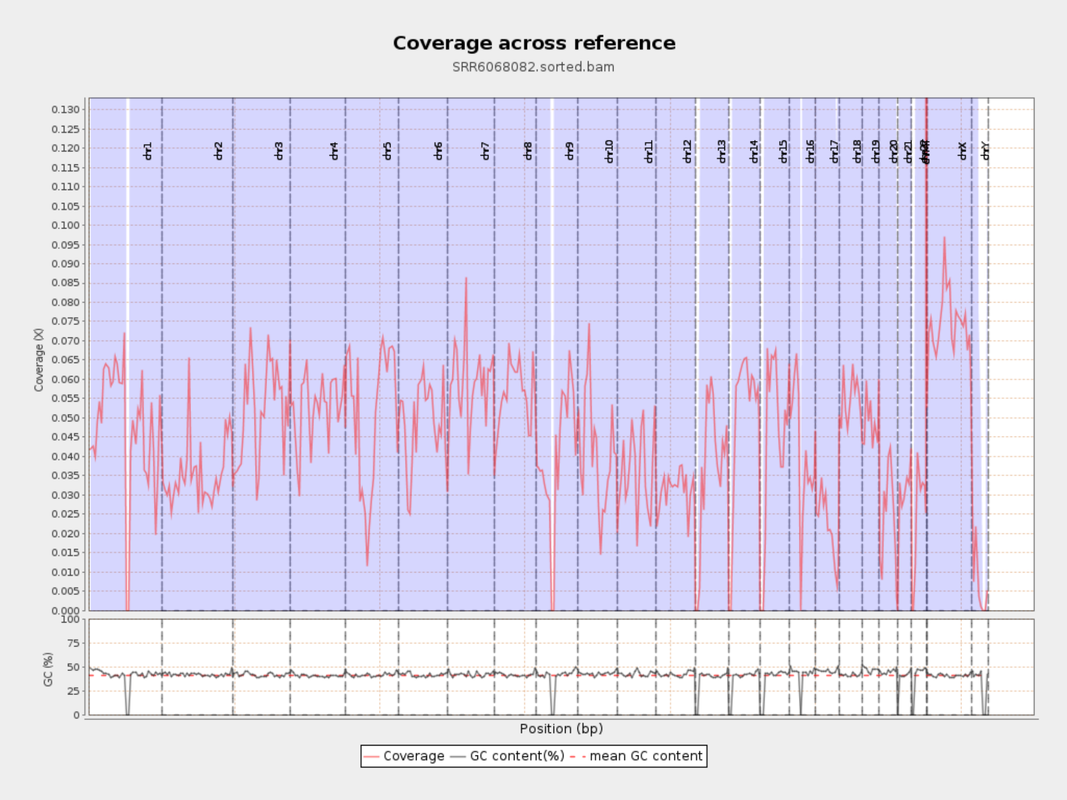
General error rate	0.83%
Mismatches	1,130,833
Insertions	10,336
Mapped reads with at least one insertion	0.48%
Deletions	35,951
Mapped reads with at least one deletion	1.65%
Homopolymer indels	46.25%

2.6. Chromosome stats

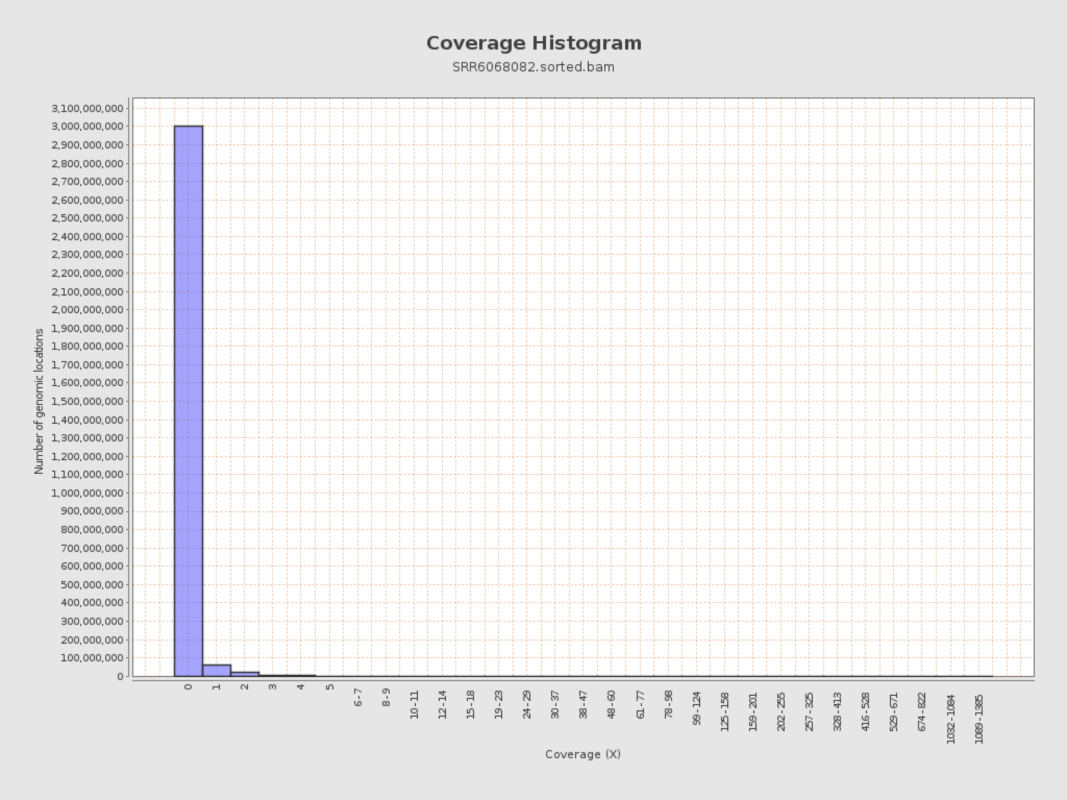
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11783492	0.0473	0.7086
chr2	243199373	8639378	0.0355	0.6838
chr3	198022430	10286684	0.0519	0.3196
chr4	191154276	10028352	0.0525	0.3499
chr5	180915260	9169748	0.0507	0.3178
chr6	171115067	8393607	0.0491	0.3454
chr7	159138663	9443745	0.0593	0.6759

chr8	146364022	8238995	0.0563	0.5251
chr9	141213431	5621916	0.0398	0.3743
chr10	135534747	5560502	0.041	0.3699
chr11	135006516	4876541	0.0361	0.3955
chr12	133851895	4165736	0.0311	0.2515
chr13	115169878	4292476	0.0373	0.2733
chr14	107349540	5366063	0.05	0.3204
chr15	102531392	4542742	0.0443	0.3045
chr16	90354753	3653926	0.0404	0.2939
chr17	81195210	1739354	0.0214	0.2414
chr18	78077248	4310775	0.0552	0.6411
chr19	59128983	2890285	0.0489	0.5416
chr20	63025520	1552154	0.0246	0.2301
chr21	48129895	1419543	0.0295	0.2562
chr22	51304566	1210809	0.0236	0.2122
chrMT	16571	26511	1.5998	2.1258
chrX	155270560	11549473	0.0744	0.4308
chrY	59373566	429339	0.0072	0.2019

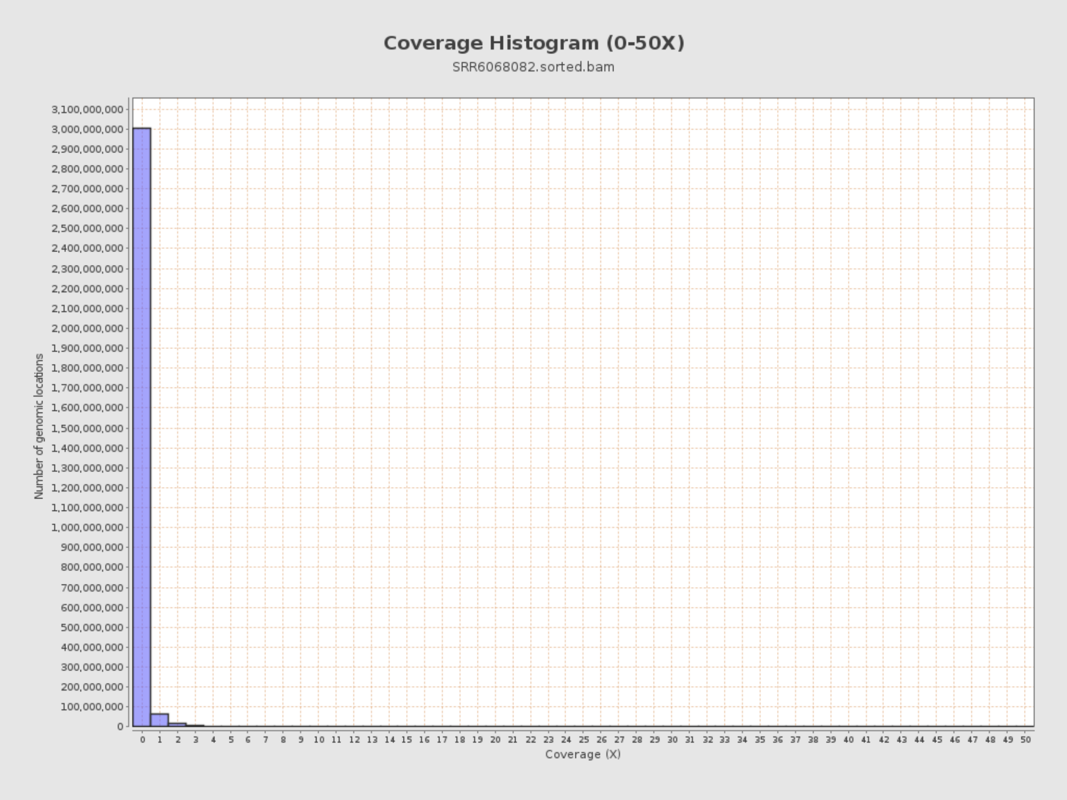
3. Results : Coverage across reference



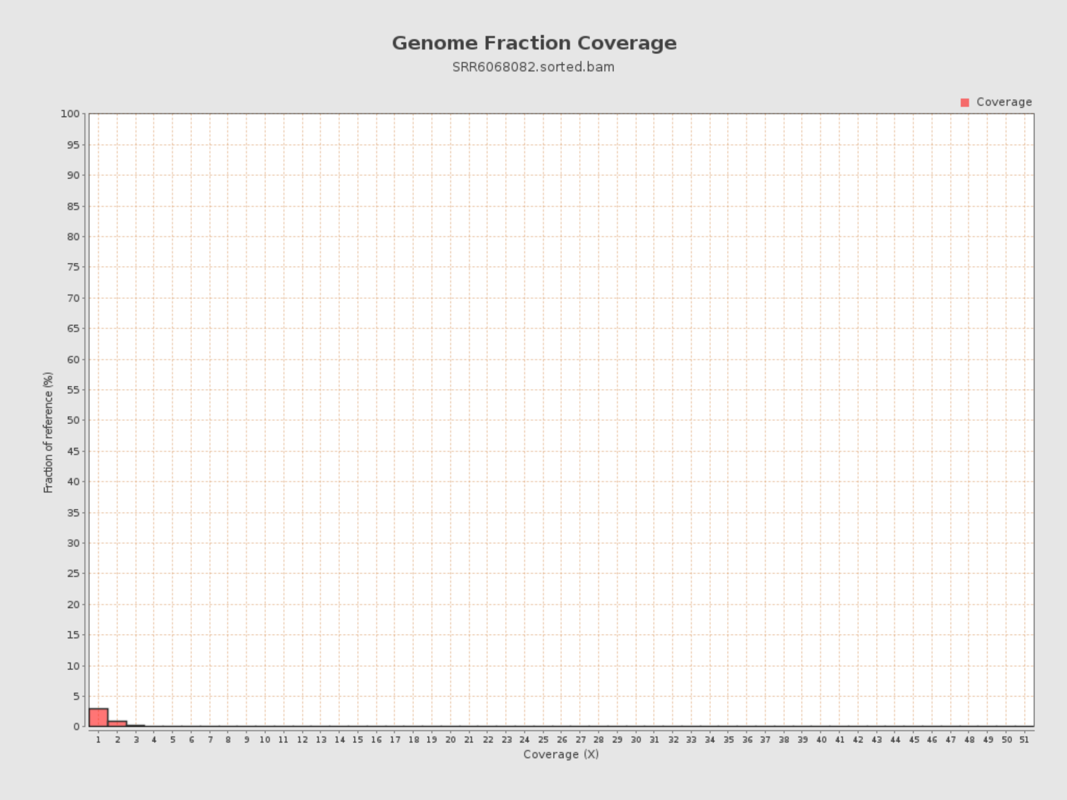
4. Results : Coverage Histogram



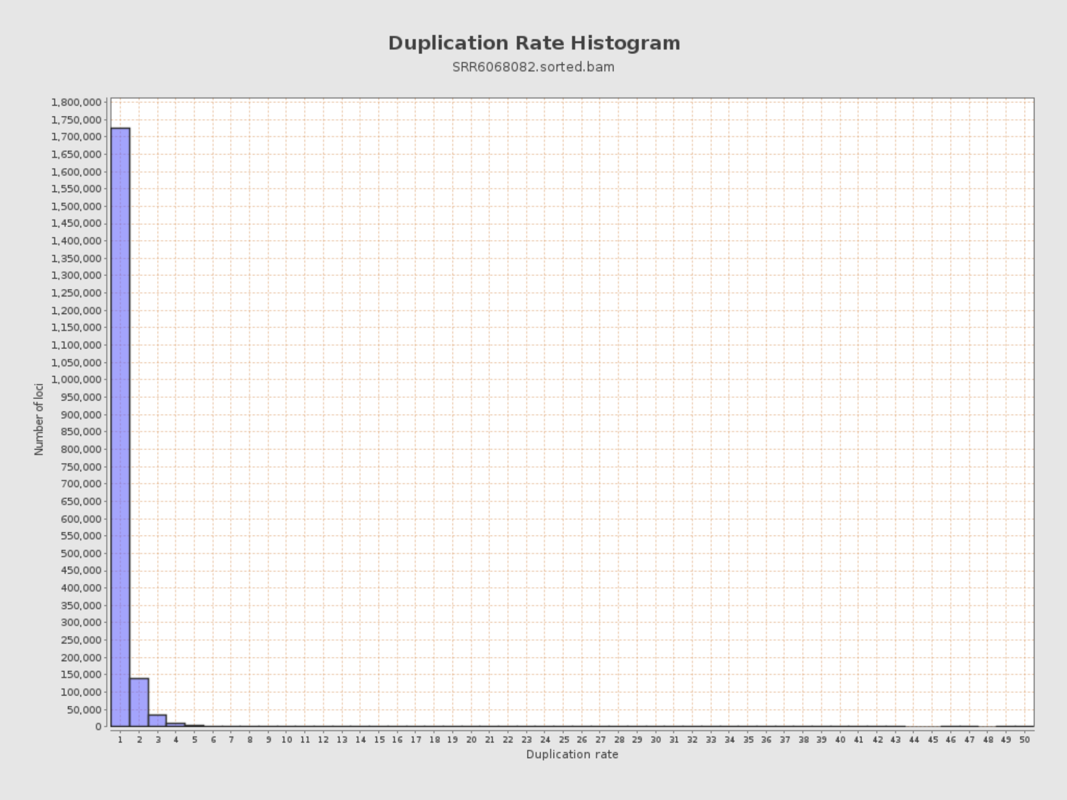
5. Results : Coverage Histogram (0-50X)



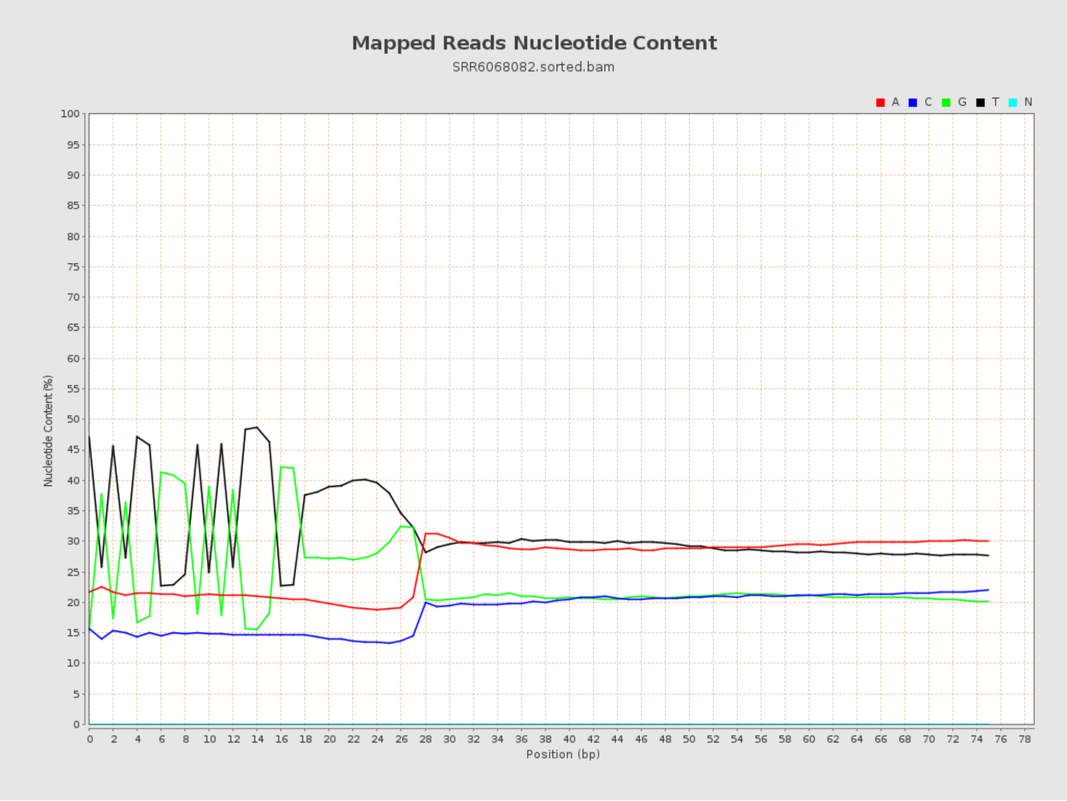
6. Results : Genome Fraction Coverage



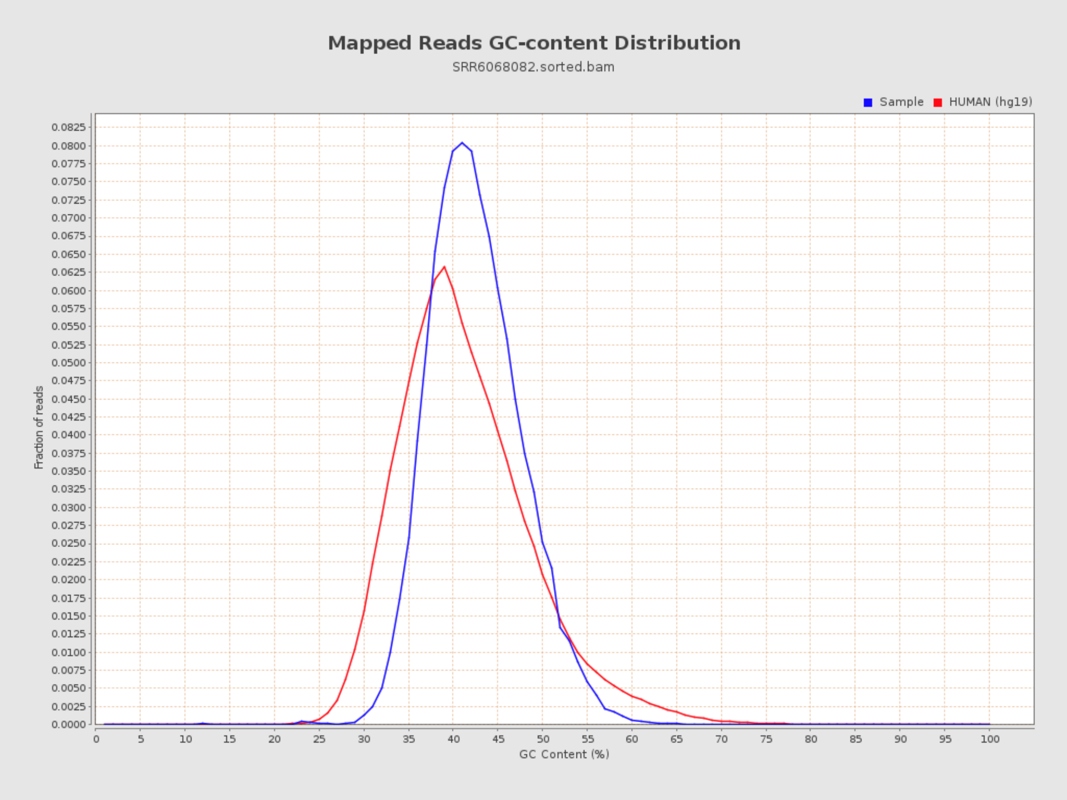
7. Results : Duplication Rate Histogram



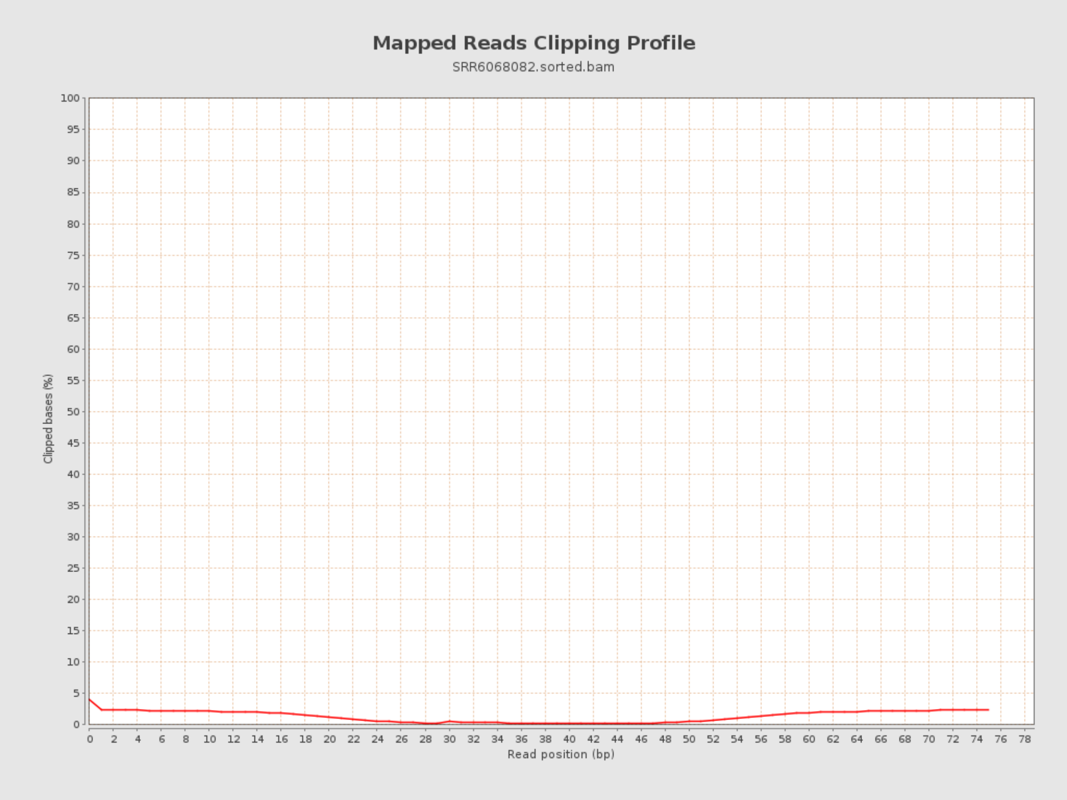
8. Results : Mapped Reads Nucleotide Content



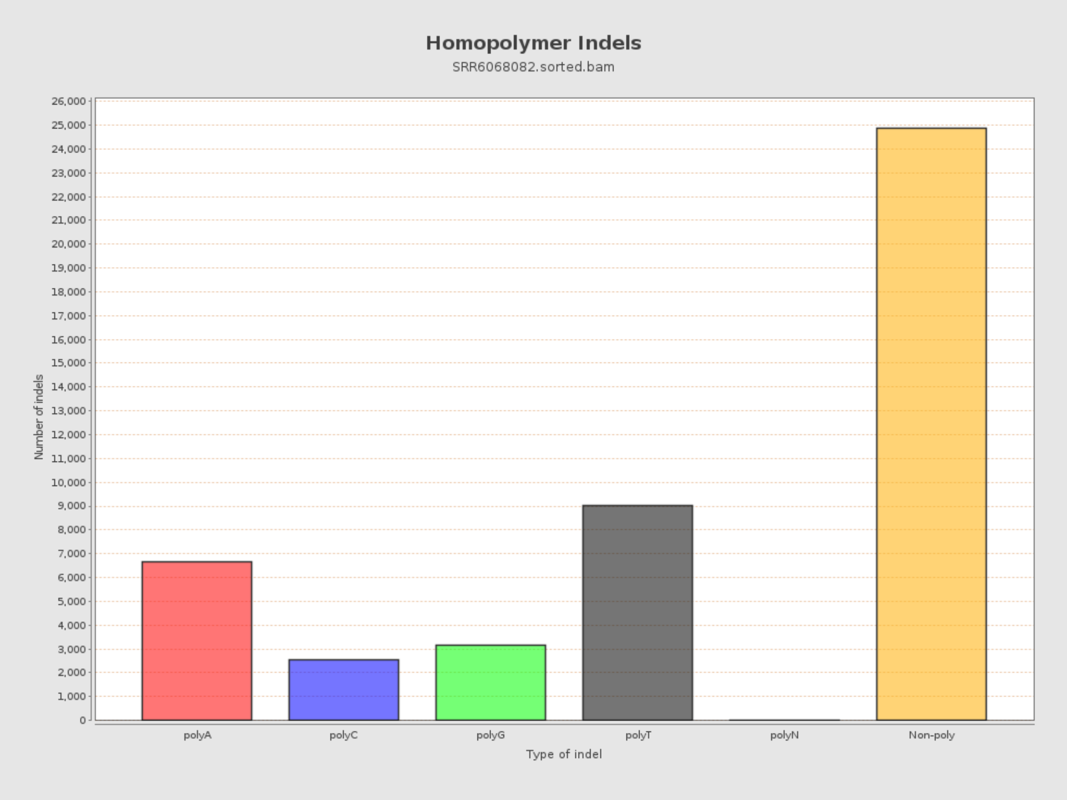
9. Results : Mapped Reads GC-content Distribution



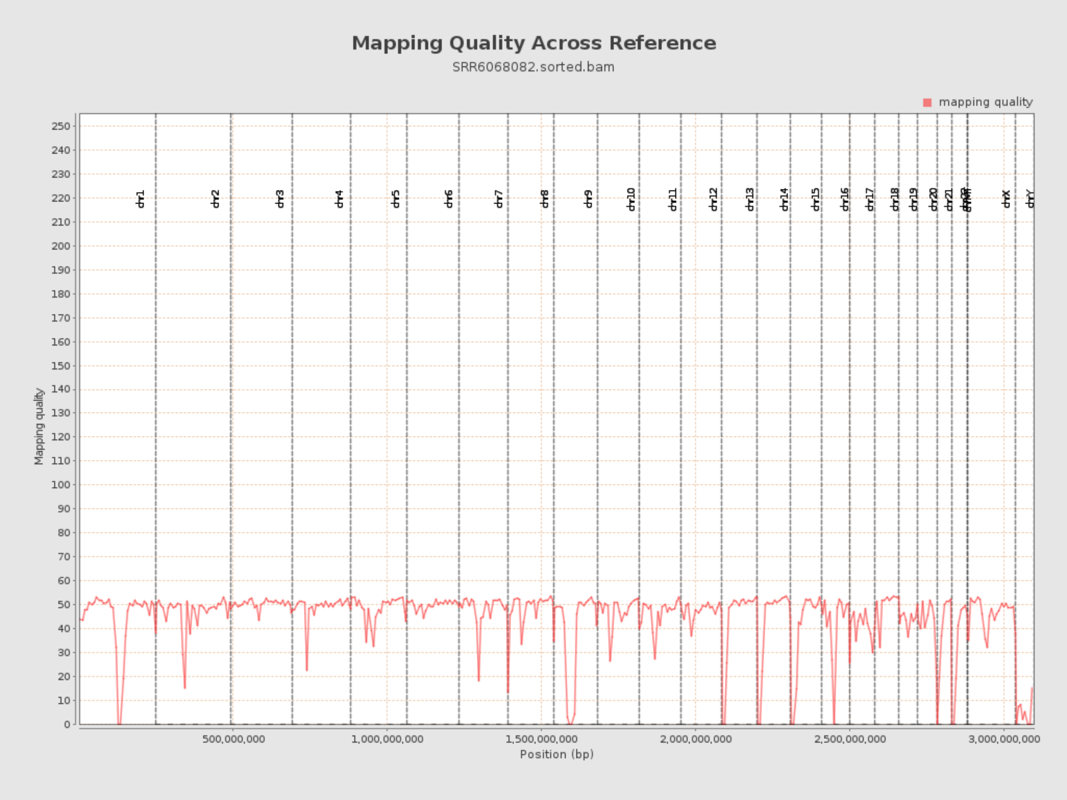
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram