Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:33:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068062.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_SRR6068062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:33:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,105,025
Mapped reads	1,590,097 / 75.54%
Unmapped reads	514,928 / 24.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,924 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	297,008 / 14.11%
Duplication rate	13.5%
Clipped reads	1,028,569 / 48.86%

2.2. ACGT Content

Number/percentage of A's	26,117,147 / 26.5%
Number/percentage of C's	18,408,661 / 18.68%
Number/percentage of T's	30,985,351 / 31.44%
Number/percentage of G's	23,051,526 / 23.39%
Number/percentage of N's	1,767 / 0%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.4028

2.4. Mapping Quality

Mean Mapping Quality	42.92

2.5. Mismatches and indels

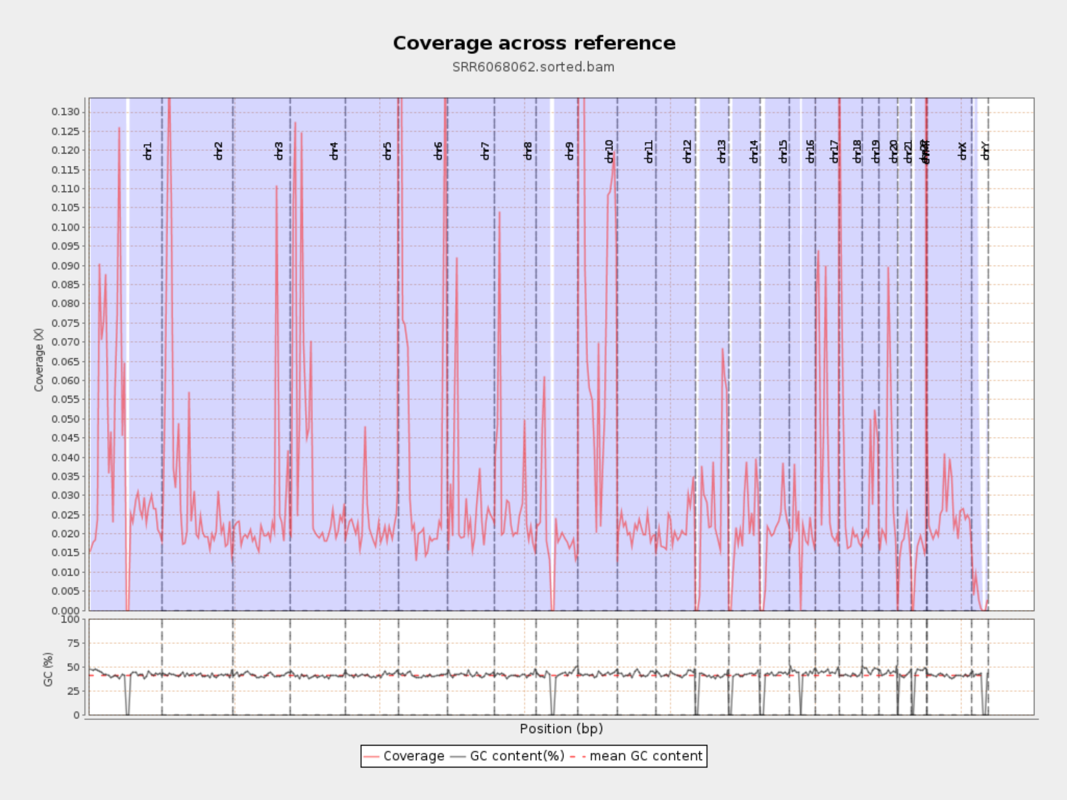
General error rate	0.81%
Mismatches	788,562
Insertions	7,091
Mapped reads with at least one insertion	0.44%
Deletions	23,872
Mapped reads with at least one deletion	1.49%
Homopolymer indels	44.84%

2.6. Chromosome stats

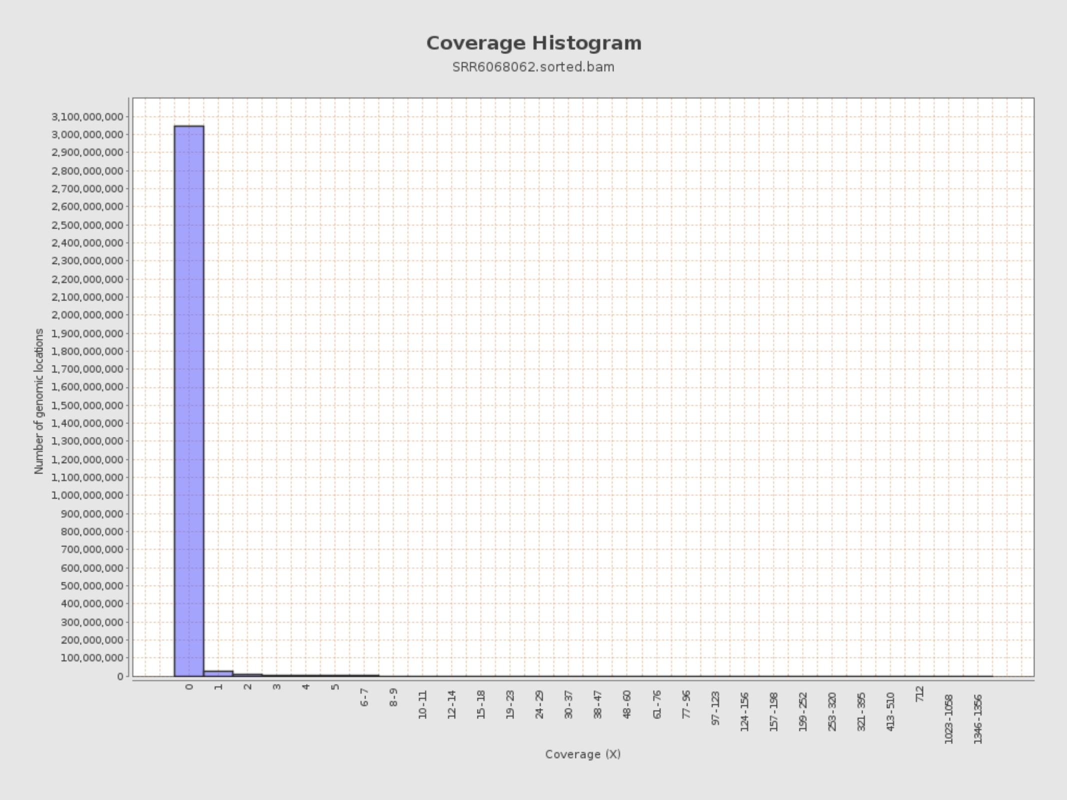
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9615193	0.0386	0.4737
chr2	243199373	8352379	0.0343	0.6981
chr3	198022430	4919559	0.0248	0.291
chr4	191154276	7710865	0.0403	0.3758
chr5	180915260	4007511	0.0222	0.2712
chr6	171115067	8646523	0.0505	0.4512
chr7	159138663	4500090	0.0283	0.3384

chr8	146364022	4408632	0.0301	0.4381
chr9	141213431	2893648	0.0205	0.2976
chr10	135534747	12280147	0.0906	0.5716
chr11	135006516	2829582	0.021	0.2818
chr12	133851895	2889767	0.0216	0.2716
chr13	115169878	3361913	0.0292	0.326
chr14	107349540	2278541	0.0212	0.3386
chr15	102531392	1969962	0.0192	0.3893
chr16	90354753	1803094	0.02	0.2623
chr17	81195210	3608983	0.0444	0.3907
chr18	78077248	2698707	0.0346	0.4033
chr19	59128983	1912452	0.0323	0.4192
chr20	63025520	2124925	0.0337	0.3441
chr21	48129895	783751	0.0163	0.2333
chr22	51304566	646652	0.0126	0.191
chrMT	16571	79501	4.7976	4.0508
chrX	155270560	4072452	0.0262	0.3258
chrY	59373566	206666	0.0035	0.1034

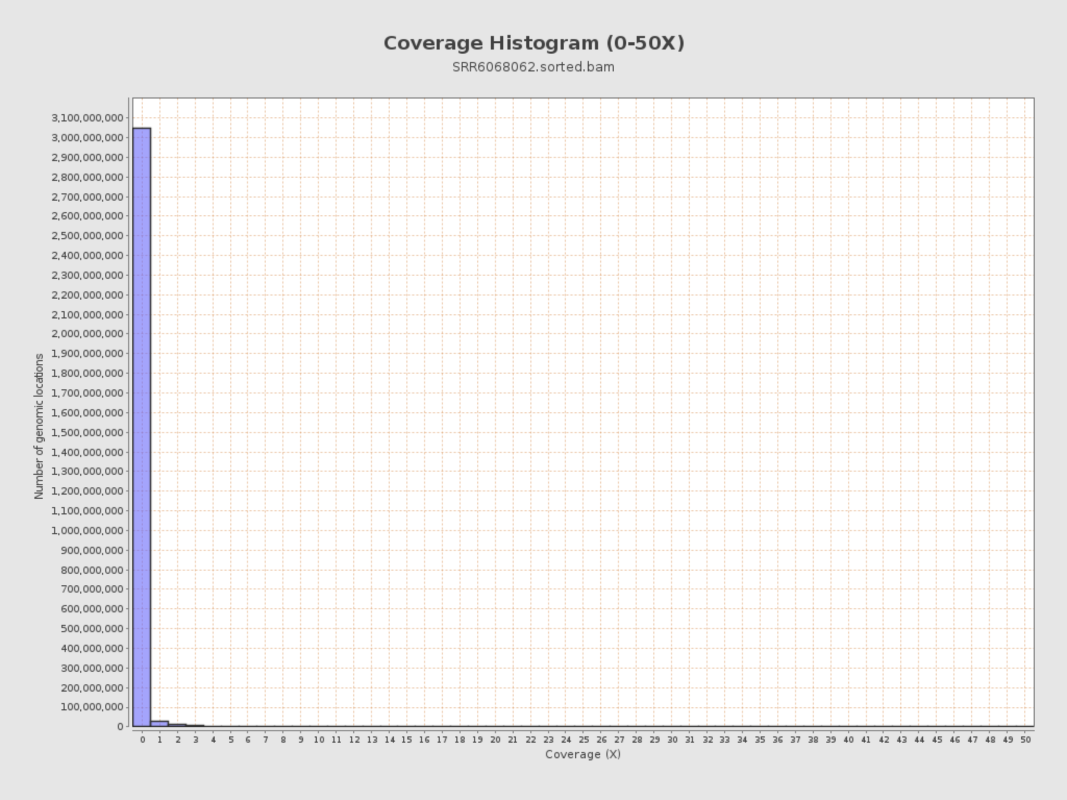
3. Results : Coverage across reference



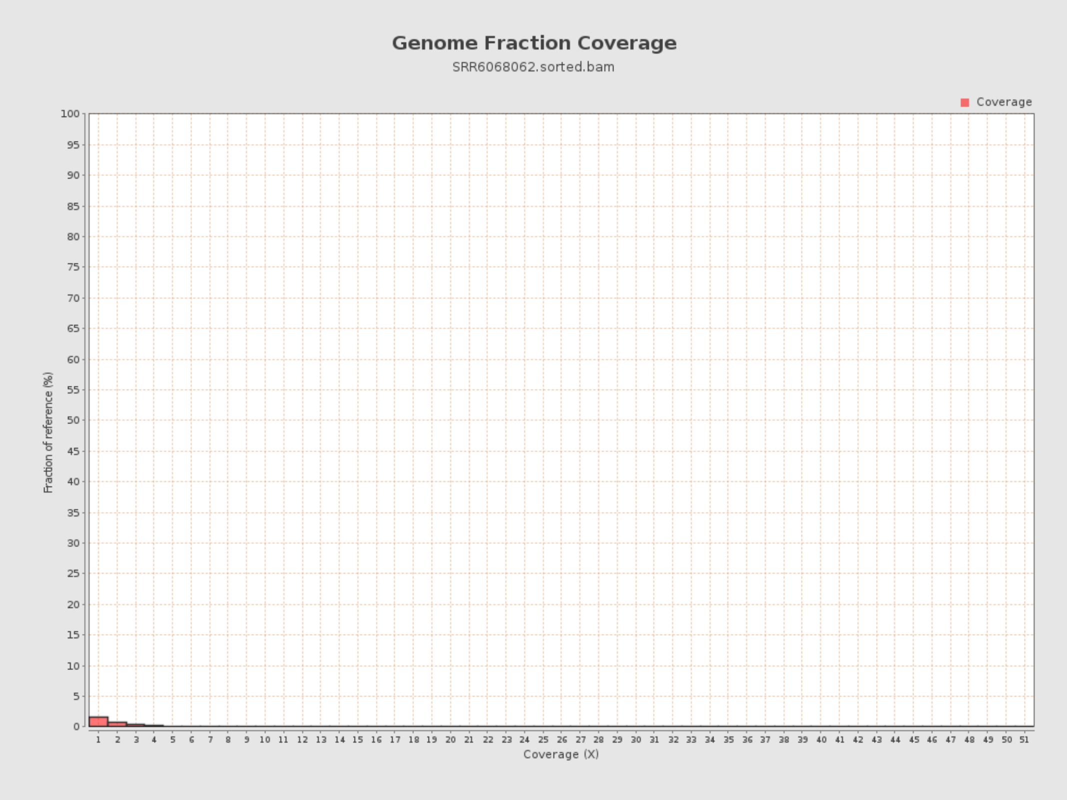
4. Results : Coverage Histogram



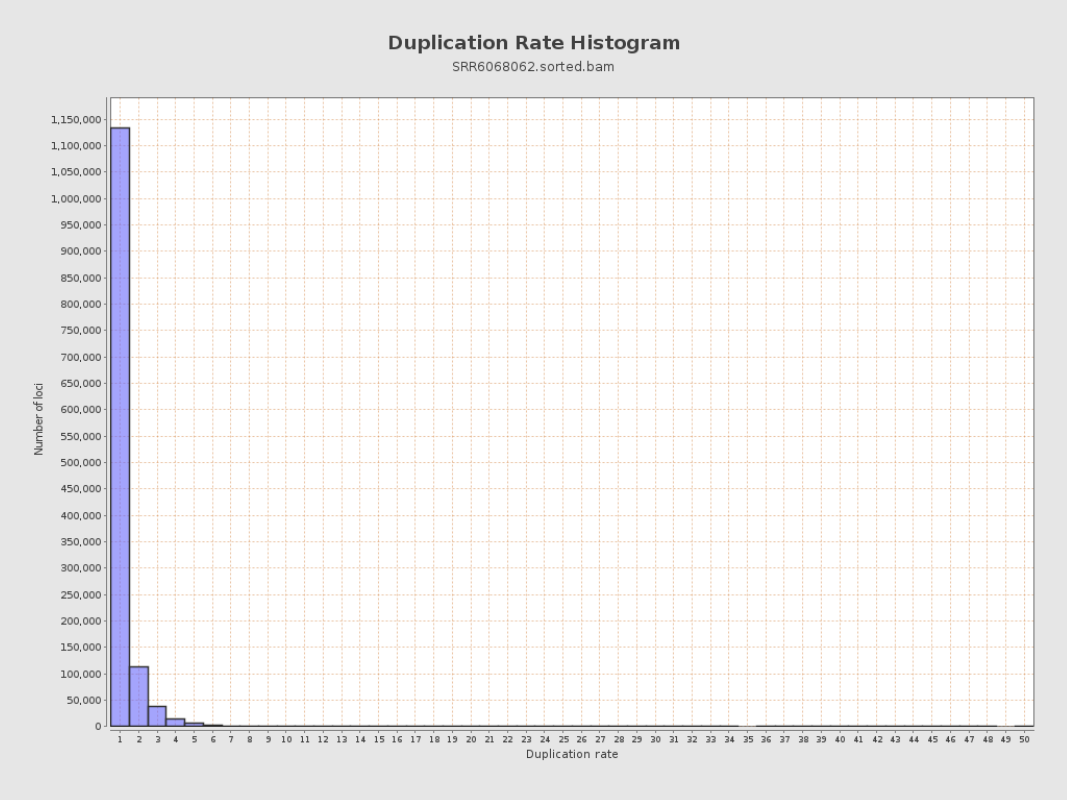
5. Results : Coverage Histogram (0-50X)



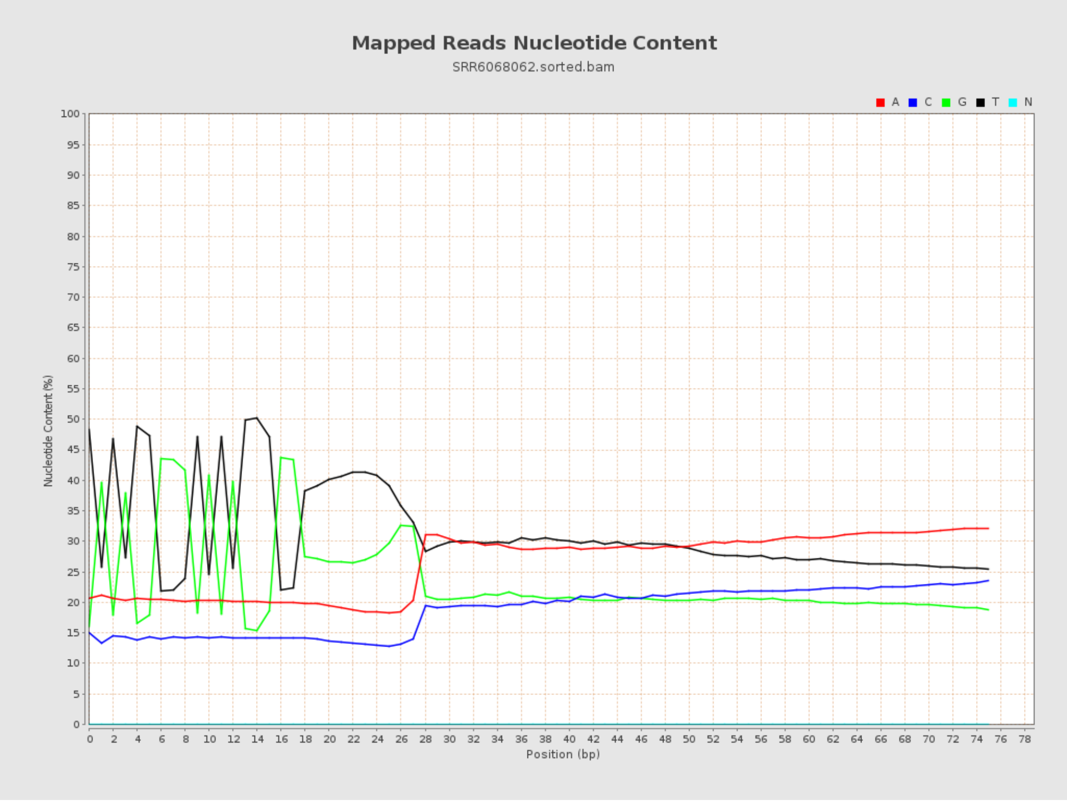
6. Results : Genome Fraction Coverage



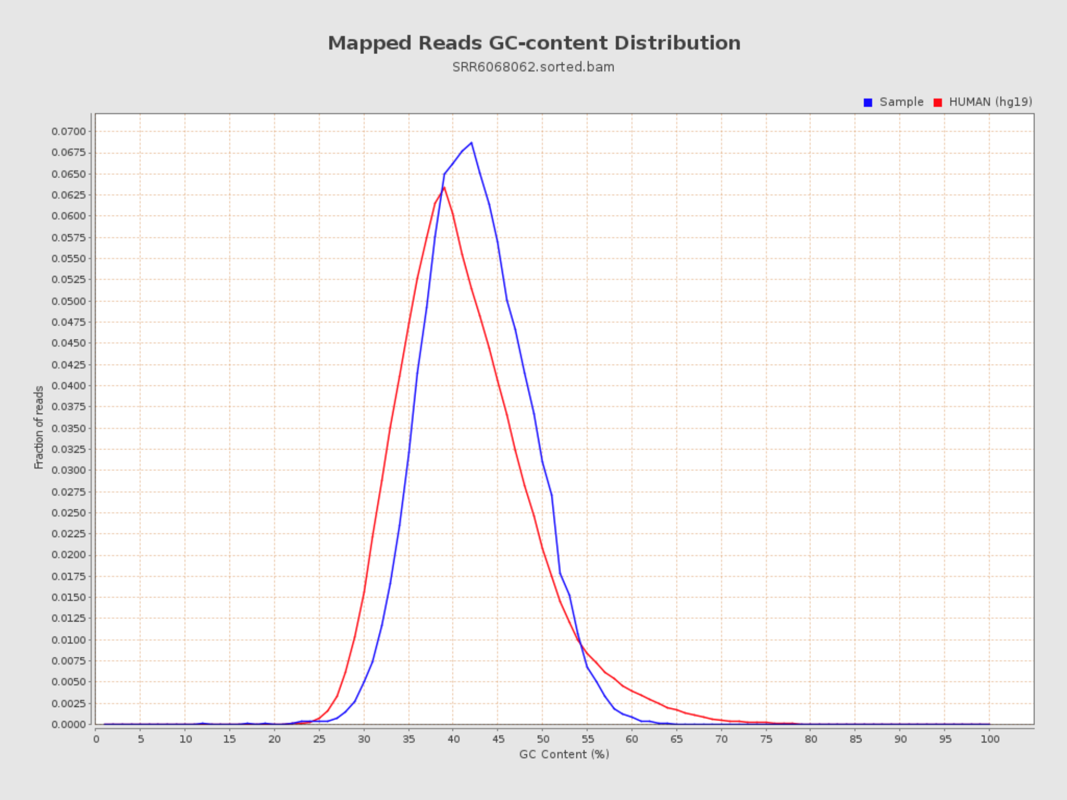
7. Results : Duplication Rate Histogram



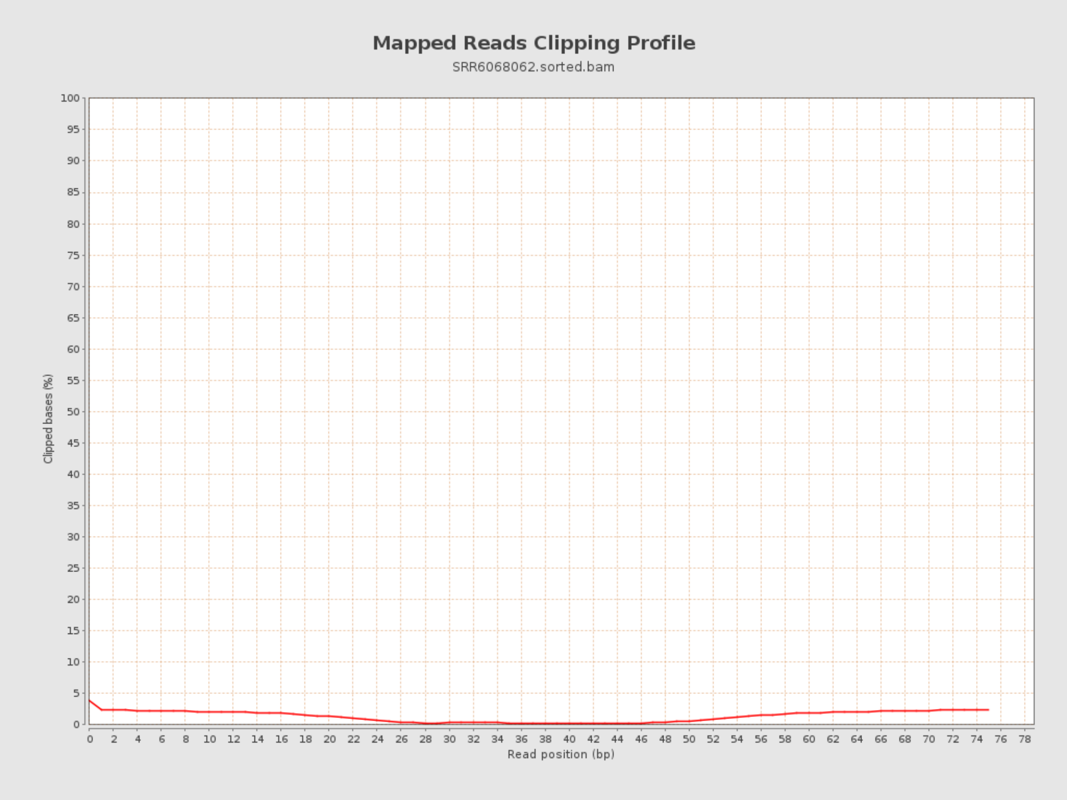
8. Results : Mapped Reads Nucleotide Content



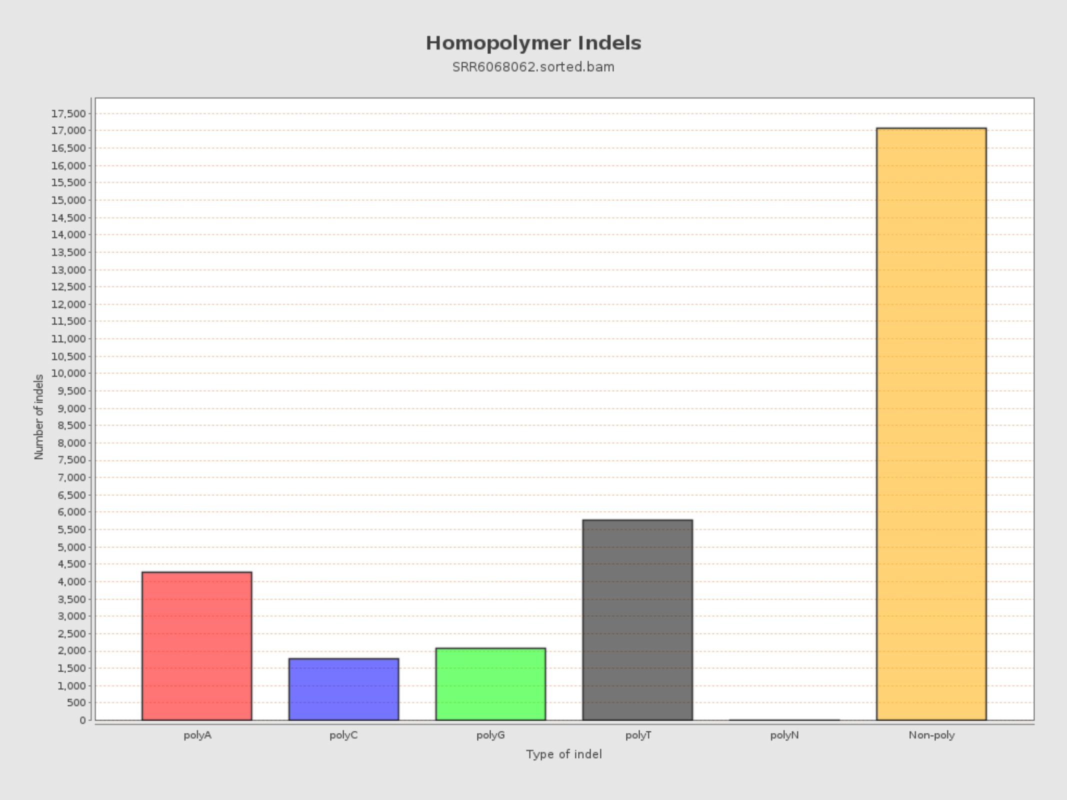
9. Results : Mapped Reads GC-content Distribution



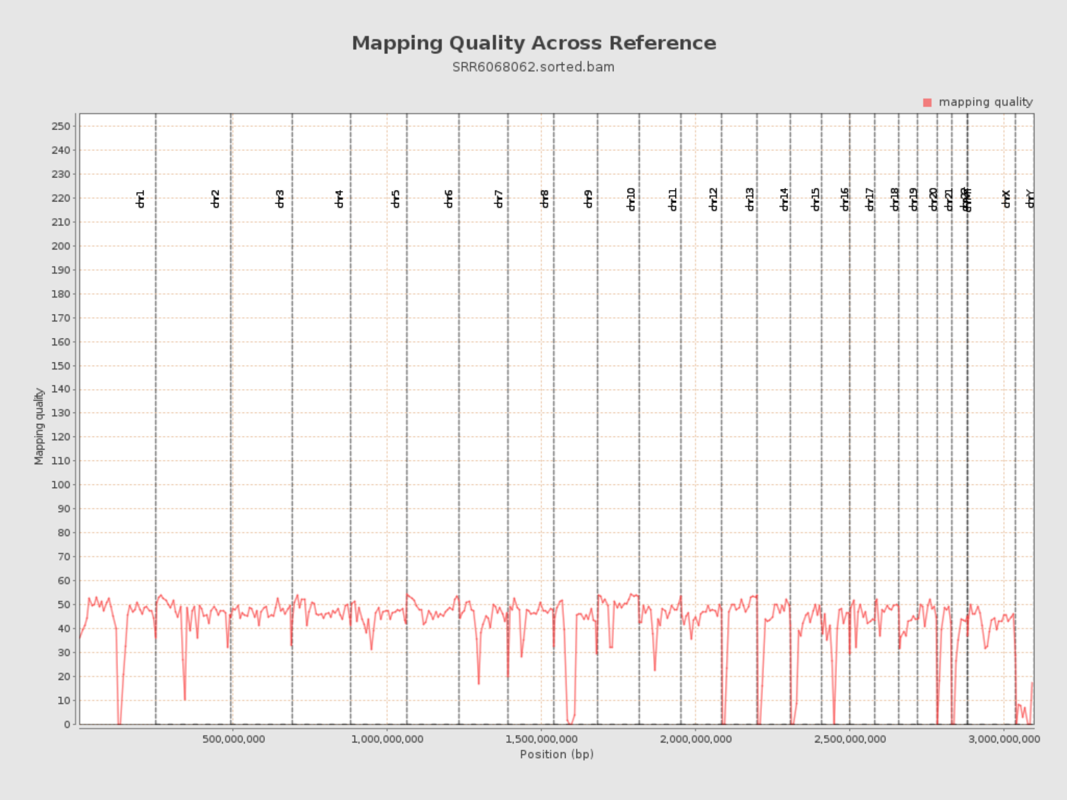
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram