Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:55:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068112.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_SRR6068112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:55:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,708,753
Mapped reads	1,442,779 / 84.43%
Unmapped reads	265,974 / 15.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,063 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	175,141 / 10.25%
Duplication rate	9.4%
Clipped reads	726,338 / 42.51%

2.2. ACGT Content

Number/percentage of A's	25,868,367 / 27.47%
Number/percentage of C's	16,319,407 / 17.33%
Number/percentage of T's	31,232,114 / 33.16%
Number/percentage of G's	20,664,614 / 21.94%
Number/percentage of N's	92,479 / 0.1%
GC Percentage	39.27%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.4524

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Mismatches and indels

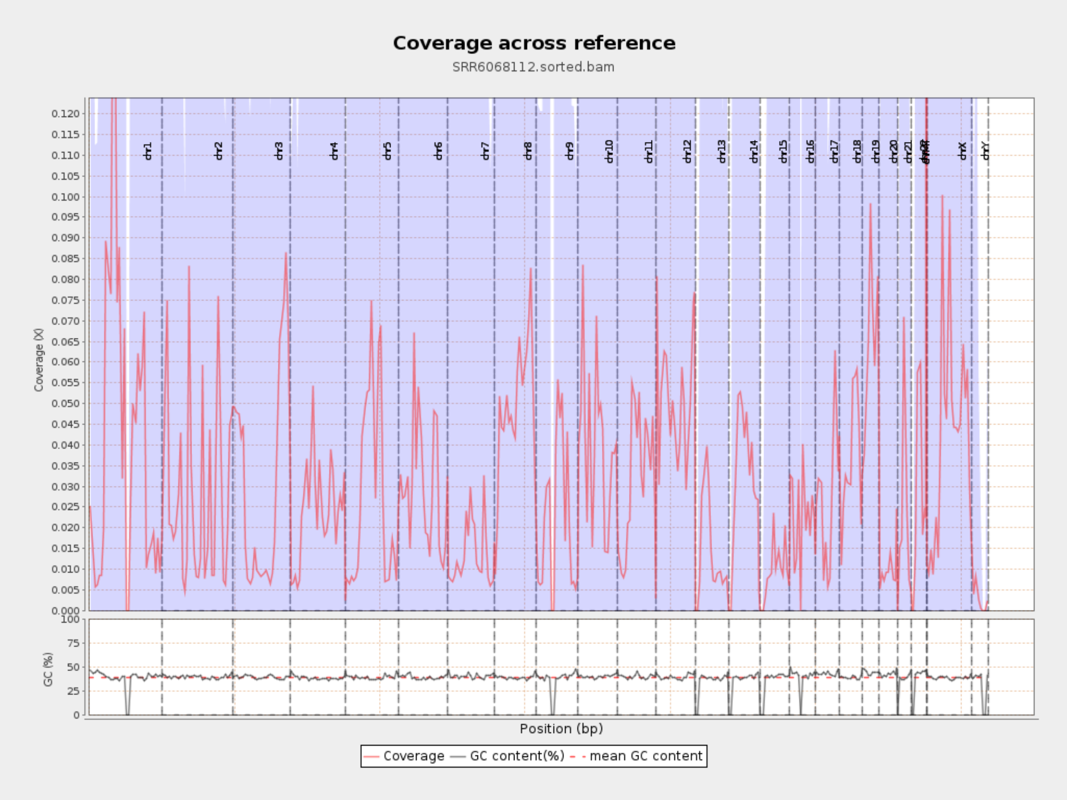
General error rate	0.98%
Mismatches	907,734
Insertions	7,193
Mapped reads with at least one insertion	0.5%
Deletions	34,056
Mapped reads with at least one deletion	2.33%
Homopolymer indels	44.84%

2.6. Chromosome stats

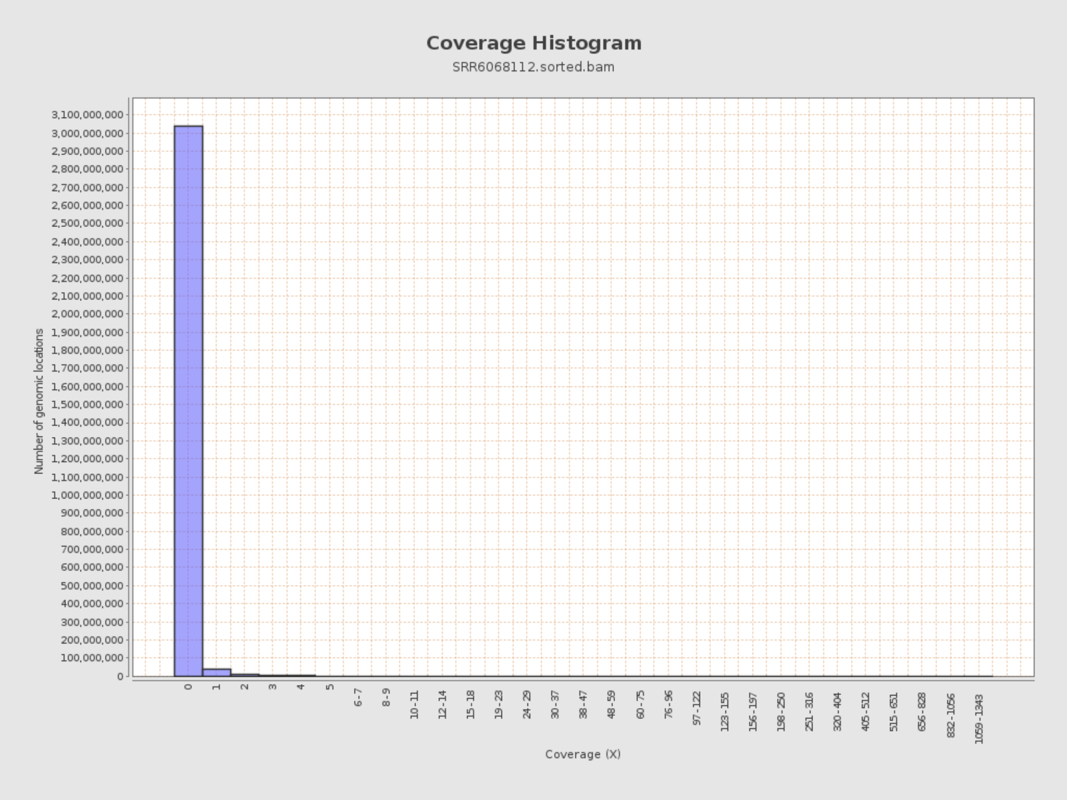
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10604805	0.0425	1.136
chr2	243199373	6874448	0.0283	0.3856
chr3	198022430	6190972	0.0313	0.2723
chr4	191154276	4653095	0.0243	0.2421
chr5	180915260	5009136	0.0277	0.2628
chr6	171115067	4987840	0.0291	0.3438
chr7	159138663	2218177	0.0139	0.2288

chr8	146364022	7248664	0.0495	0.5099
chr9	141213431	3095709	0.0219	0.2995
chr10	135534747	5499165	0.0406	0.4312
chr11	135006516	4249232	0.0315	0.3006
chr12	133851895	6794723	0.0508	0.3536
chr13	115169878	1596664	0.0139	0.1833
chr14	107349540	3492199	0.0325	0.2889
chr15	102531392	981212	0.0096	0.1483
chr16	90354753	2017253	0.0223	0.2433
chr17	81195210	2143510	0.0264	0.2421
chr18	78077248	2929957	0.0375	0.5178
chr19	59128983	3809555	0.0644	0.7356
chr20	63025520	597897	0.0095	0.1663
chr21	48129895	1060920	0.022	0.2329
chr22	51304566	1390264	0.0271	0.2465
chrMT	16571	11141	0.6723	1.1786
chrX	155270560	6590830	0.0424	0.3359
chrY	59373566	184774	0.0031	0.0845

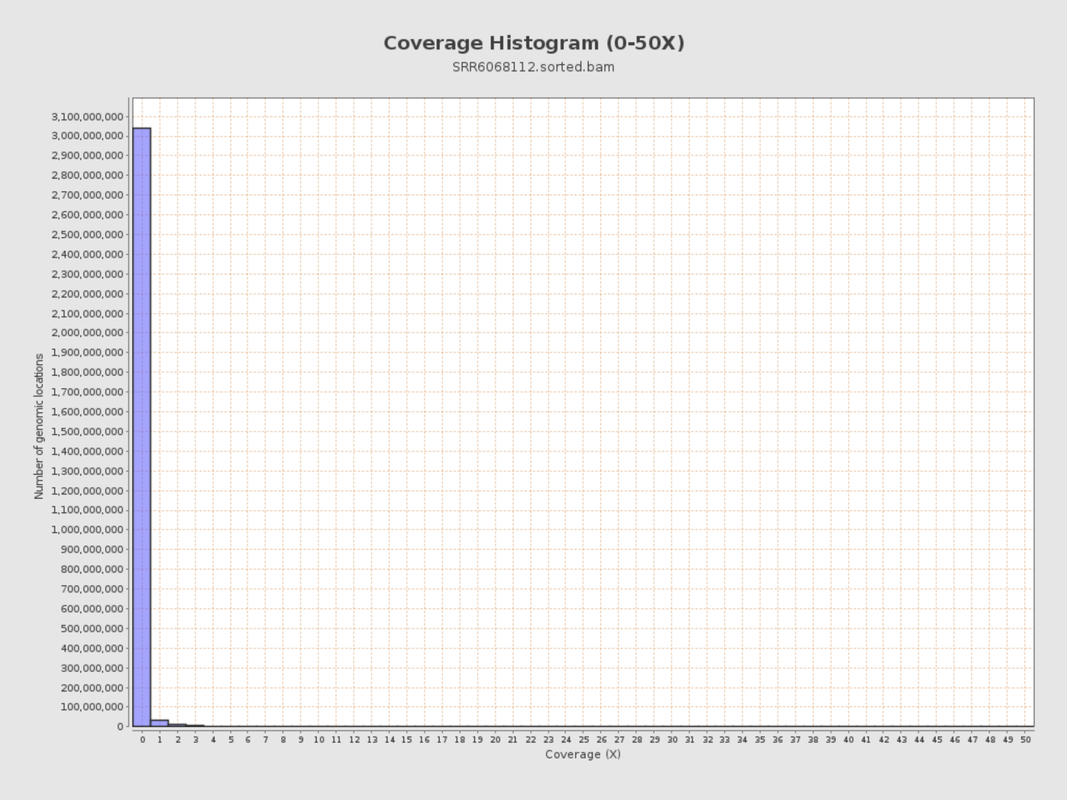
3. Results : Coverage across reference



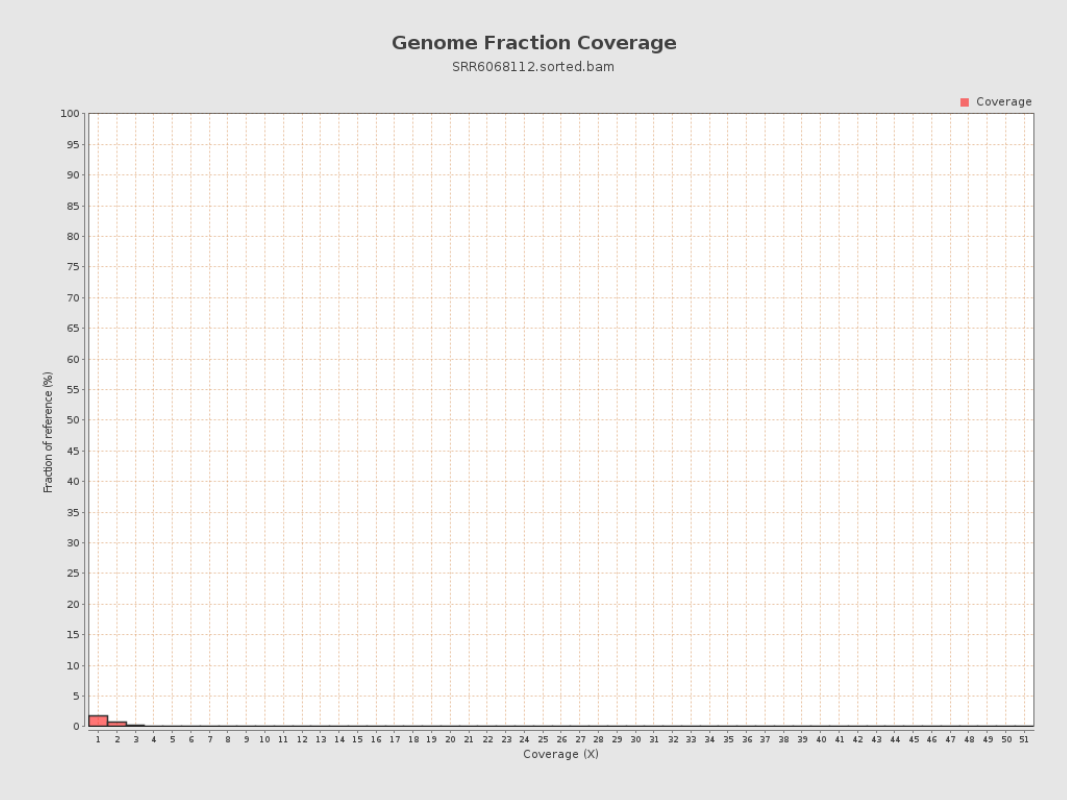
4. Results : Coverage Histogram



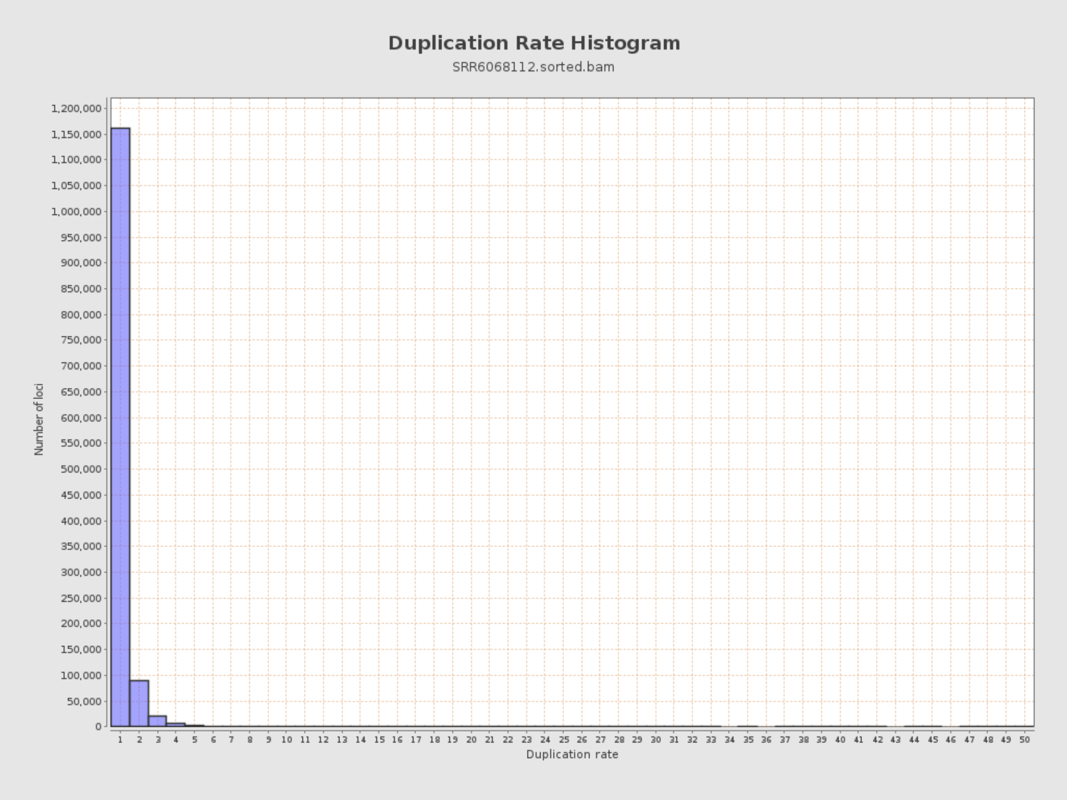
5. Results : Coverage Histogram (0-50X)



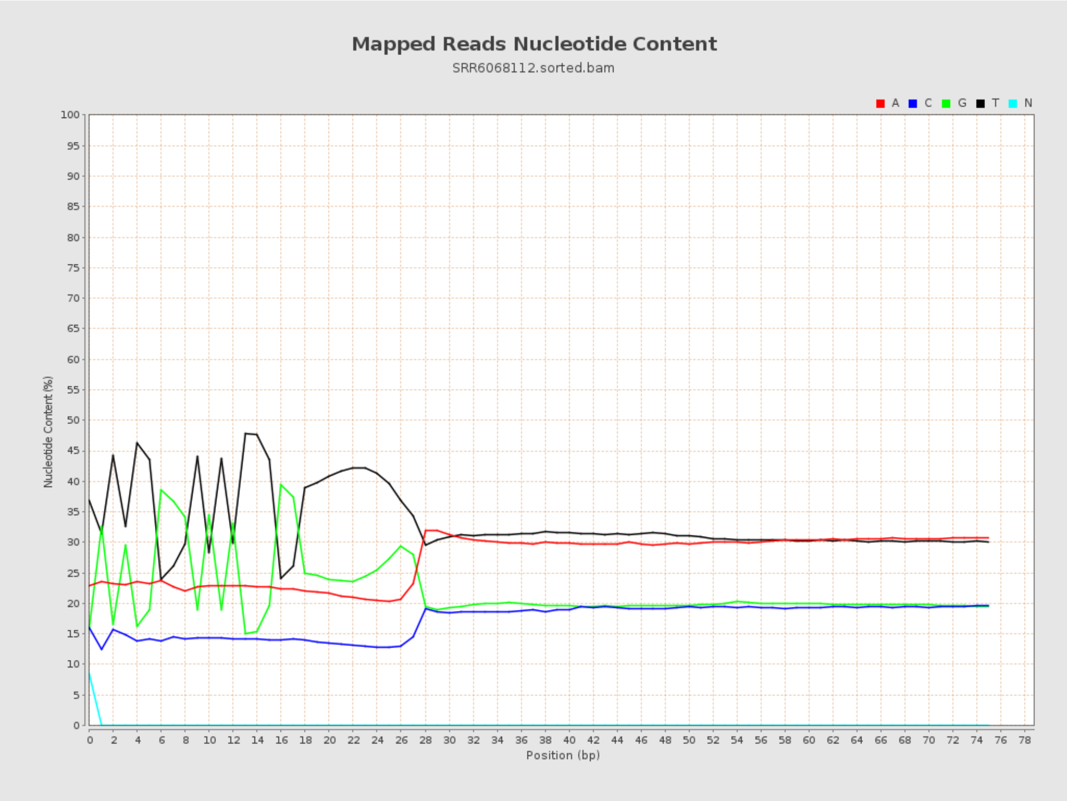
6. Results : Genome Fraction Coverage



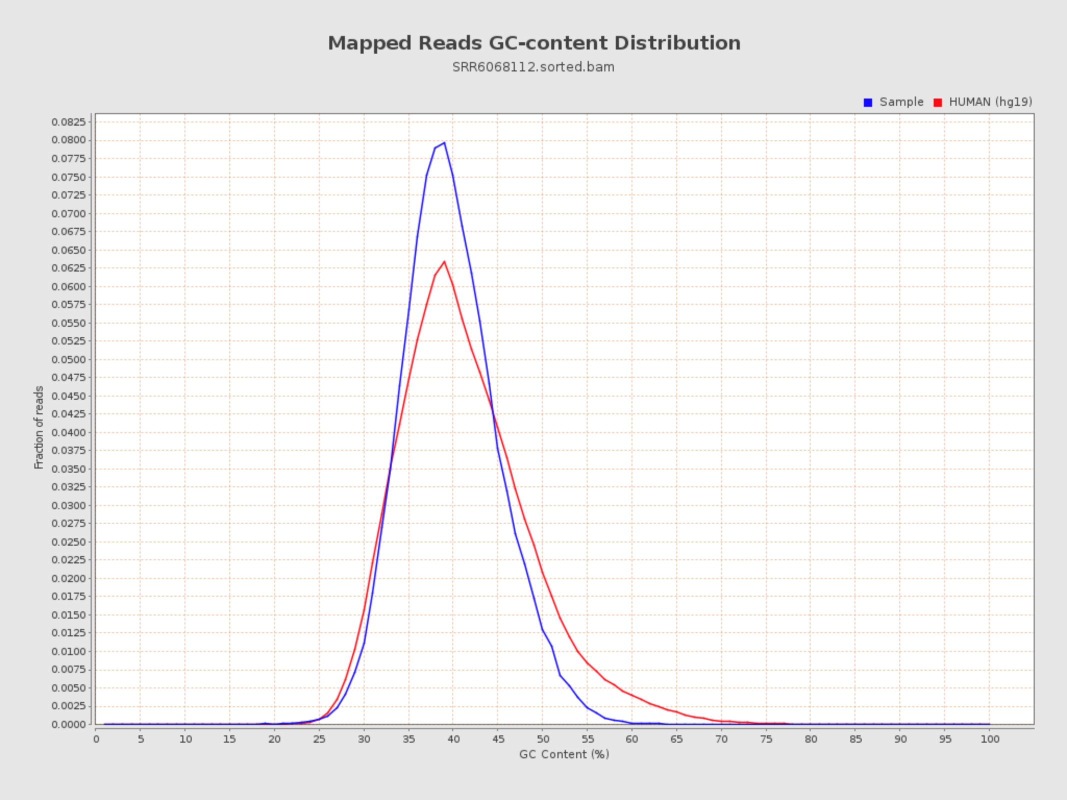
7. Results : Duplication Rate Histogram



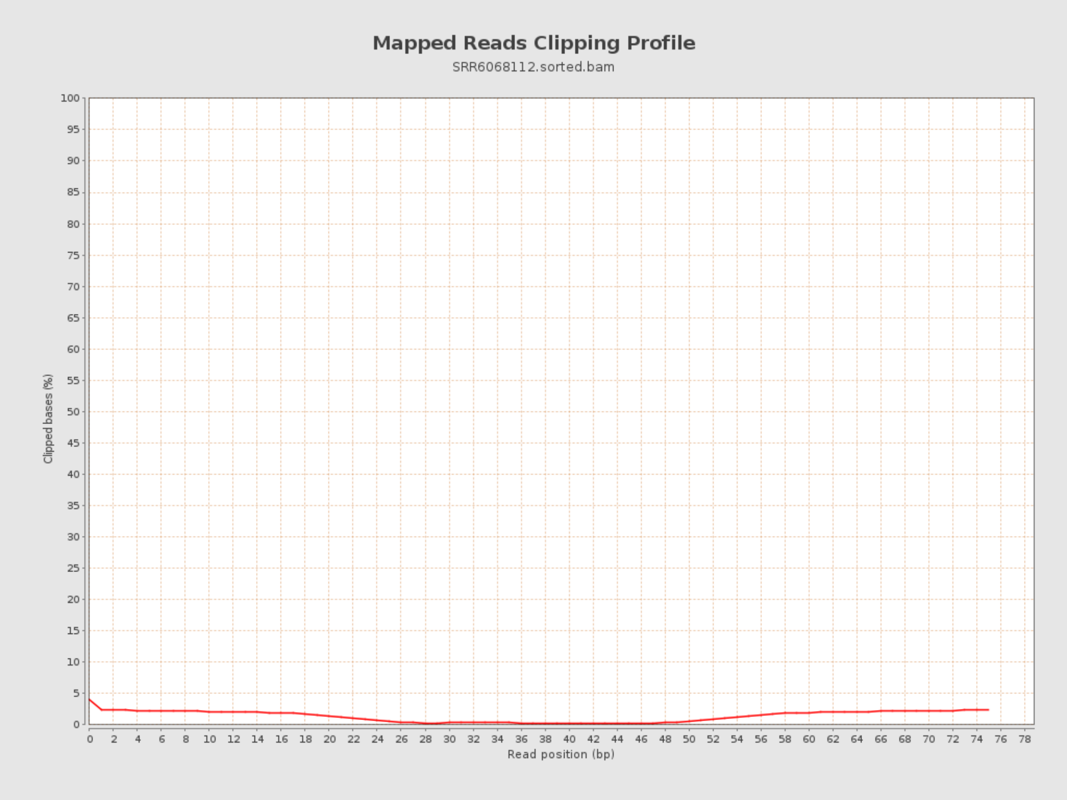
8. Results : Mapped Reads Nucleotide Content



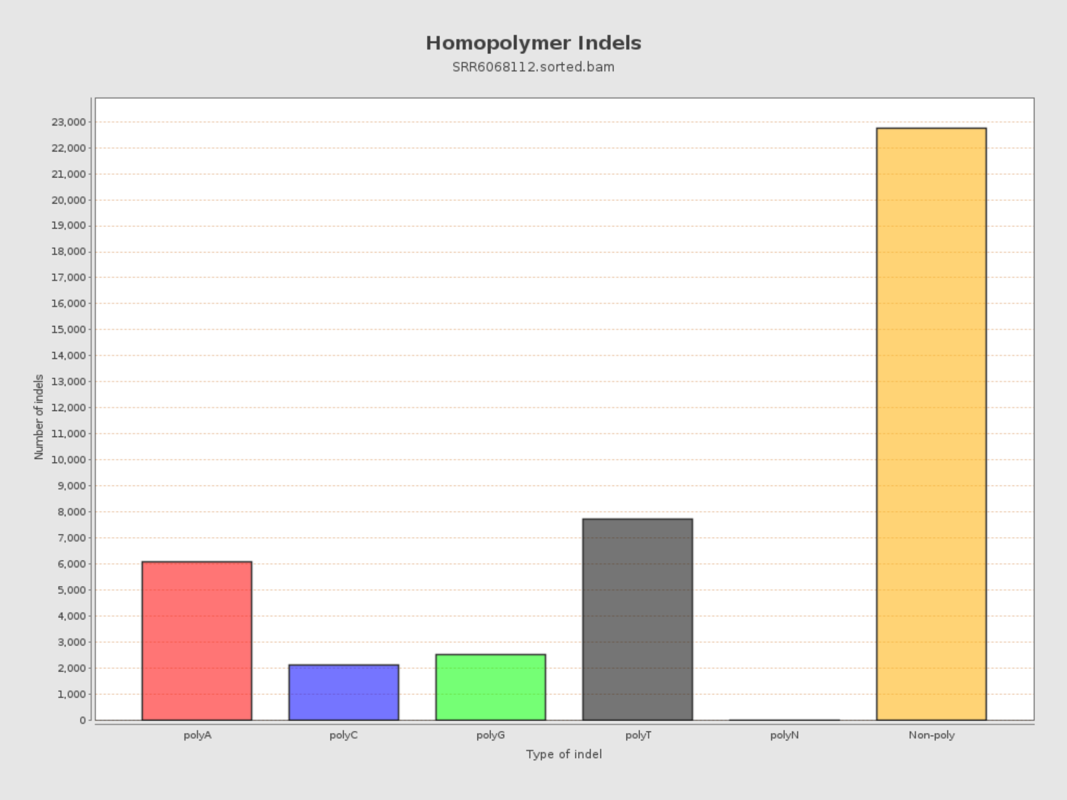
9. Results : Mapped Reads GC-content Distribution



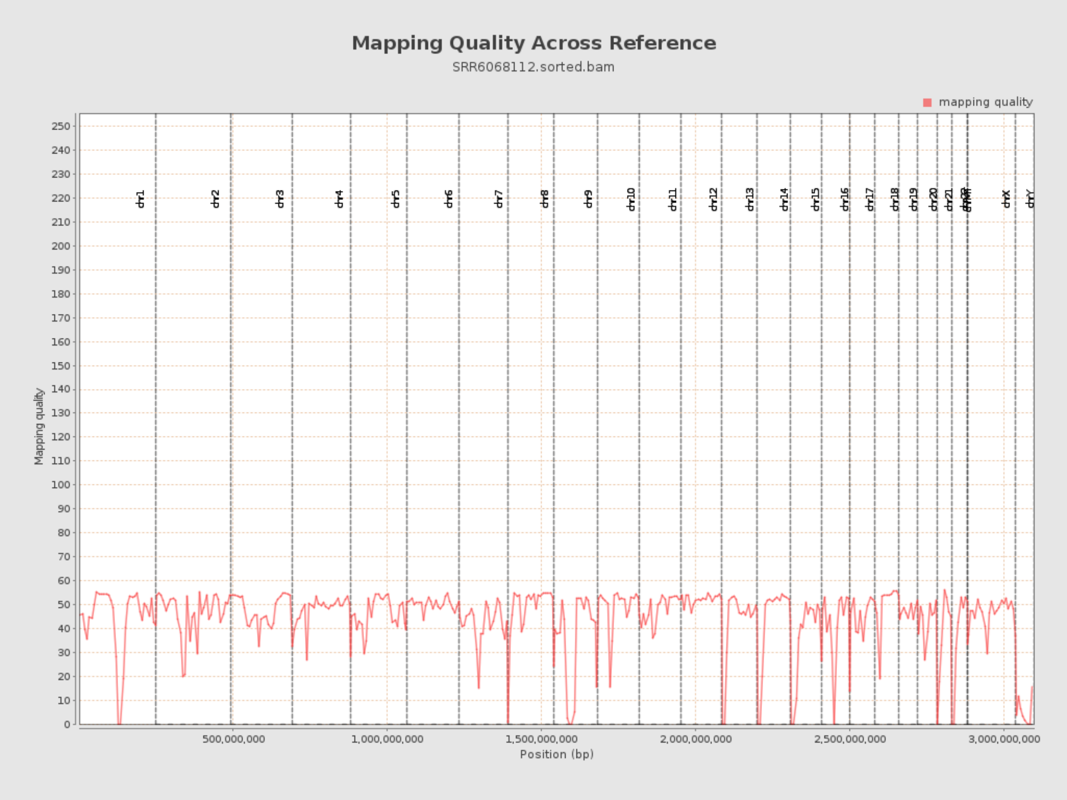
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram