Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:44:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008681.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_SRR6008681 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008681.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:44:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008681.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,742,651
Mapped reads	1,515,327 / 86.96%
Unmapped reads	227,324 / 13.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,412 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	56,535 / 3.24%
Duplication rate	3.1%
Clipped reads	827,991 / 47.51%

2.2. ACGT Content

Number/percentage of A's	26,474,990 / 27.36%
Number/percentage of C's	17,454,241 / 18.04%
Number/percentage of T's	30,706,618 / 31.73%
Number/percentage of G's	22,107,069 / 22.85%
Number/percentage of N's	18,372 / 0.02%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.2715

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

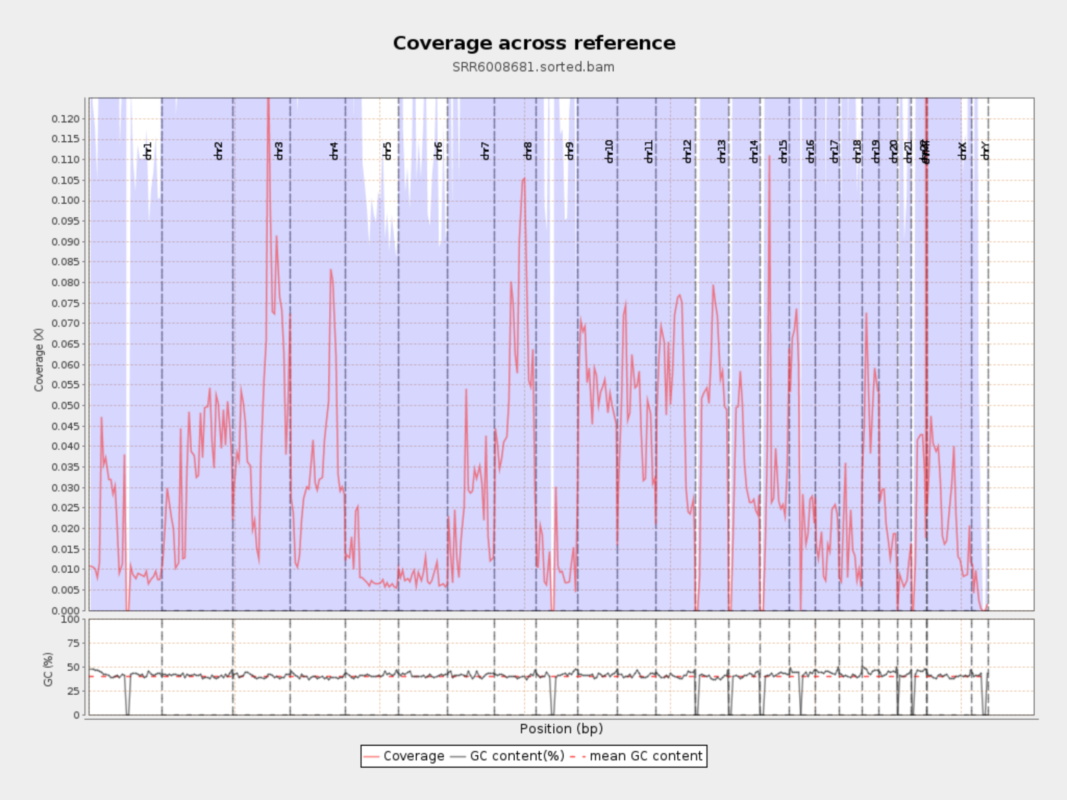
General error rate	0.71%
Mismatches	674,945
Insertions	7,411
Mapped reads with at least one insertion	0.49%
Deletions	26,292
Mapped reads with at least one deletion	1.71%
Homopolymer indels	48.02%

2.6. Chromosome stats

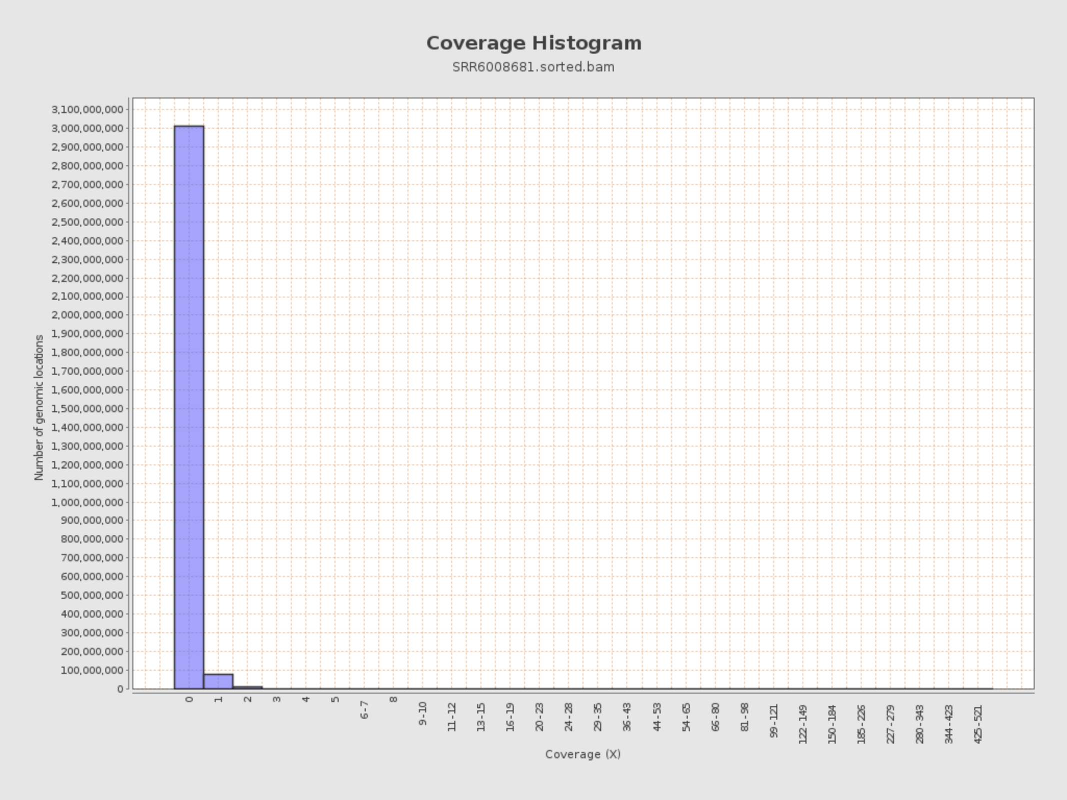
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3823535	0.0153	0.4614
chr2	243199373	8618446	0.0354	0.2583
chr3	198022430	10459899	0.0528	0.2551
chr4	191154276	6780120	0.0355	0.2106
chr5	180915260	1714592	0.0095	0.1106
chr6	171115067	1392212	0.0081	0.1181
chr7	159138663	3905476	0.0245	0.3705

chr8	146364022	8901373	0.0608	0.3239
chr9	141213431	1509042	0.0107	0.1676
chr10	135534747	7578659	0.0559	0.3189
chr11	135006516	6409780	0.0475	0.3581
chr12	133851895	7195212	0.0538	0.2579
chr13	115169878	5634187	0.0489	0.2435
chr14	107349540	3270808	0.0305	0.1997
chr15	102531392	3241217	0.0316	0.1979
chr16	90354753	3432508	0.038	0.2256
chr17	81195210	1378142	0.017	0.1655
chr18	78077248	1158751	0.0148	0.3411
chr19	59128983	3092483	0.0523	0.3624
chr20	63025520	1330438	0.0211	0.1656
chr21	48129895	402173	0.0084	0.1088
chr22	51304566	1370375	0.0267	0.1792
chrMT	16571	158949	9.592	5.2597
chrX	155270560	3844351	0.0248	0.1895
chrY	59373566	201086	0.0034	0.1038

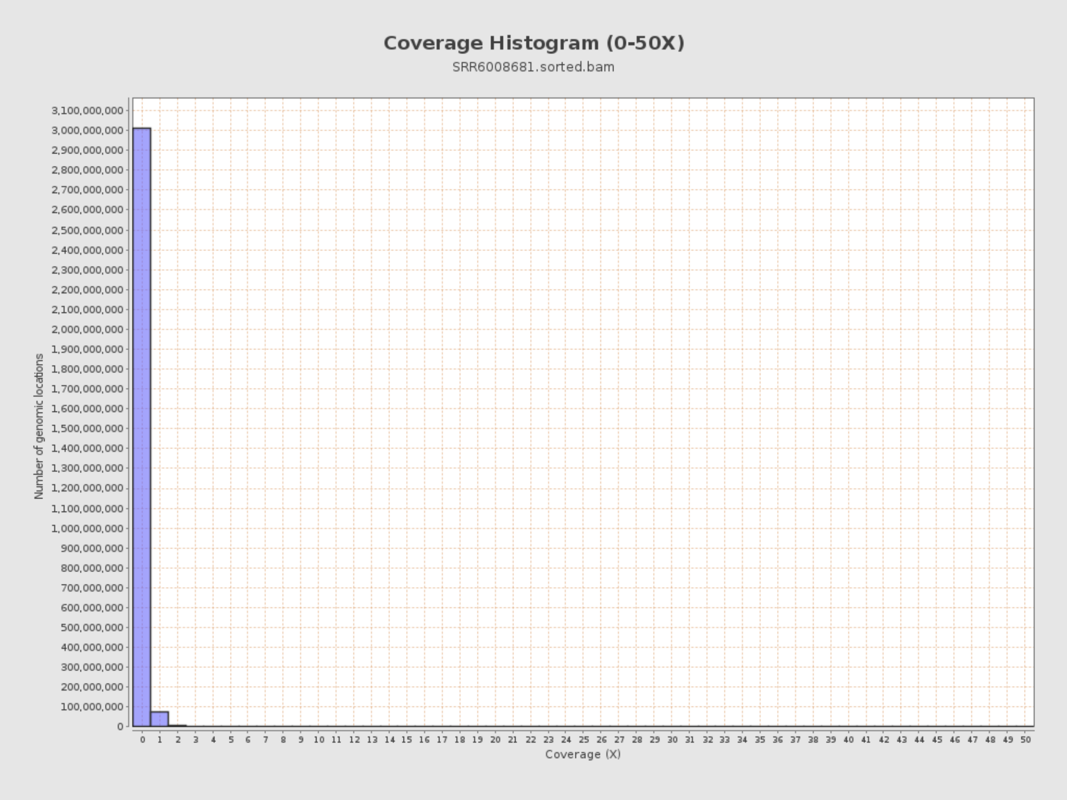
3. Results : Coverage across reference



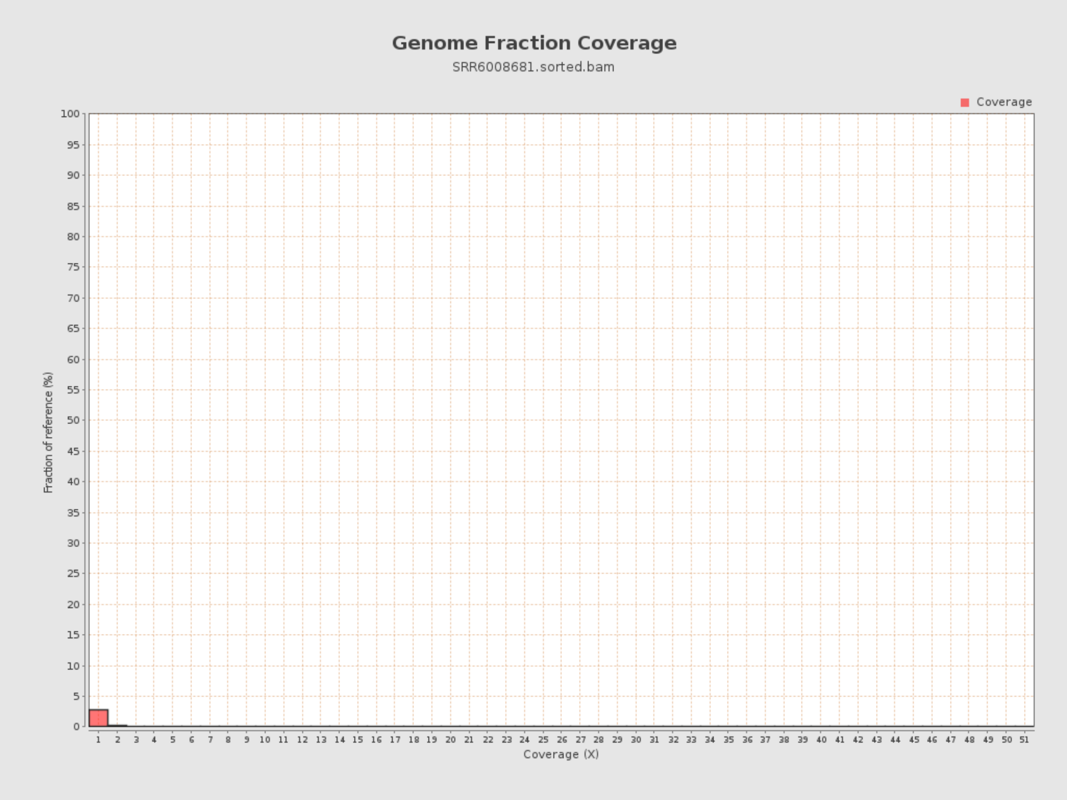
4. Results : Coverage Histogram



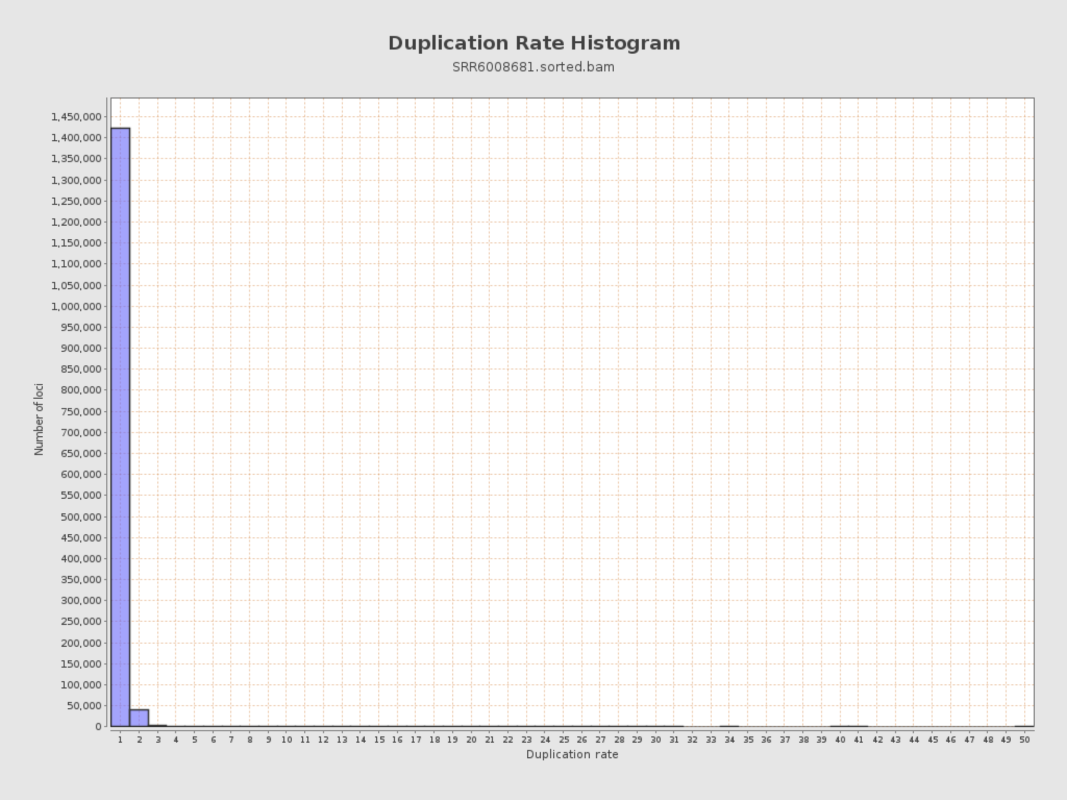
5. Results : Coverage Histogram (0-50X)



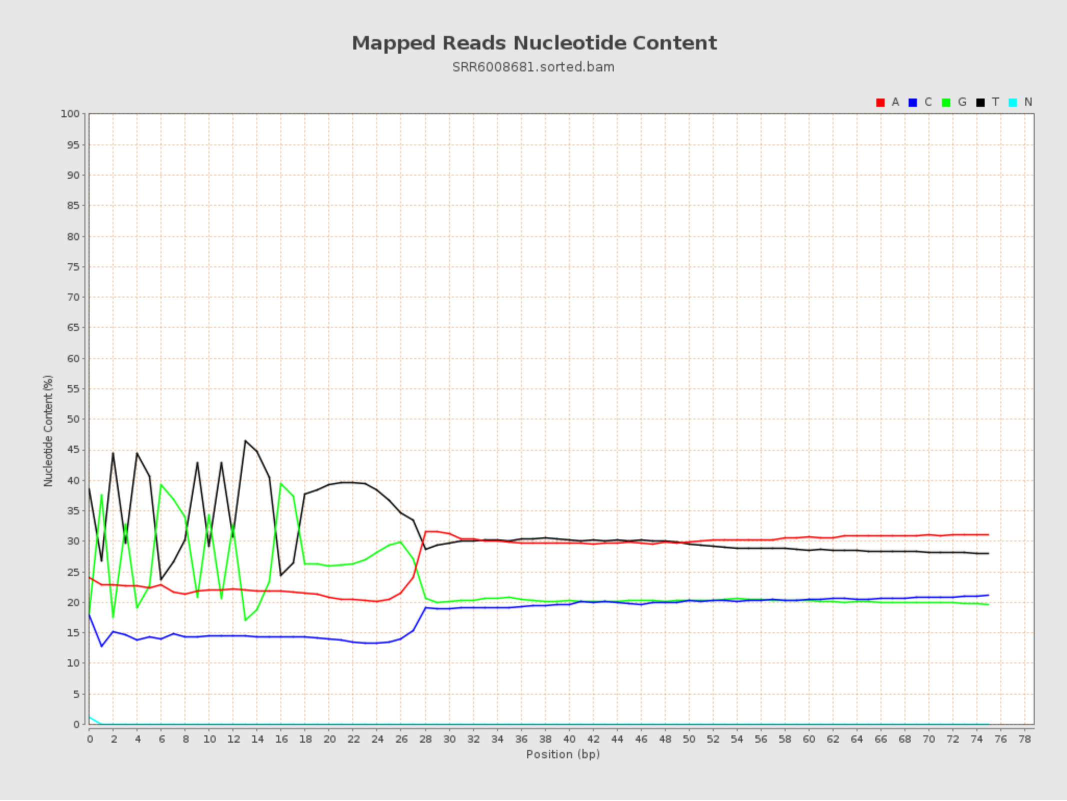
6. Results : Genome Fraction Coverage



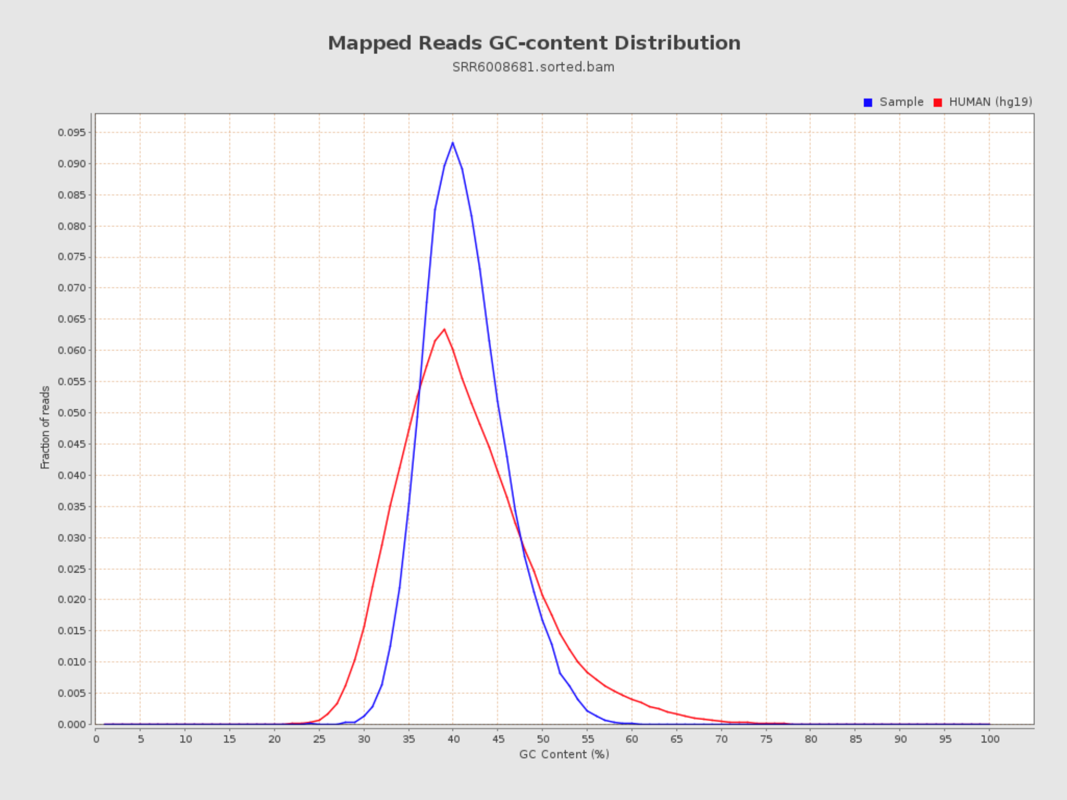
7. Results : Duplication Rate Histogram



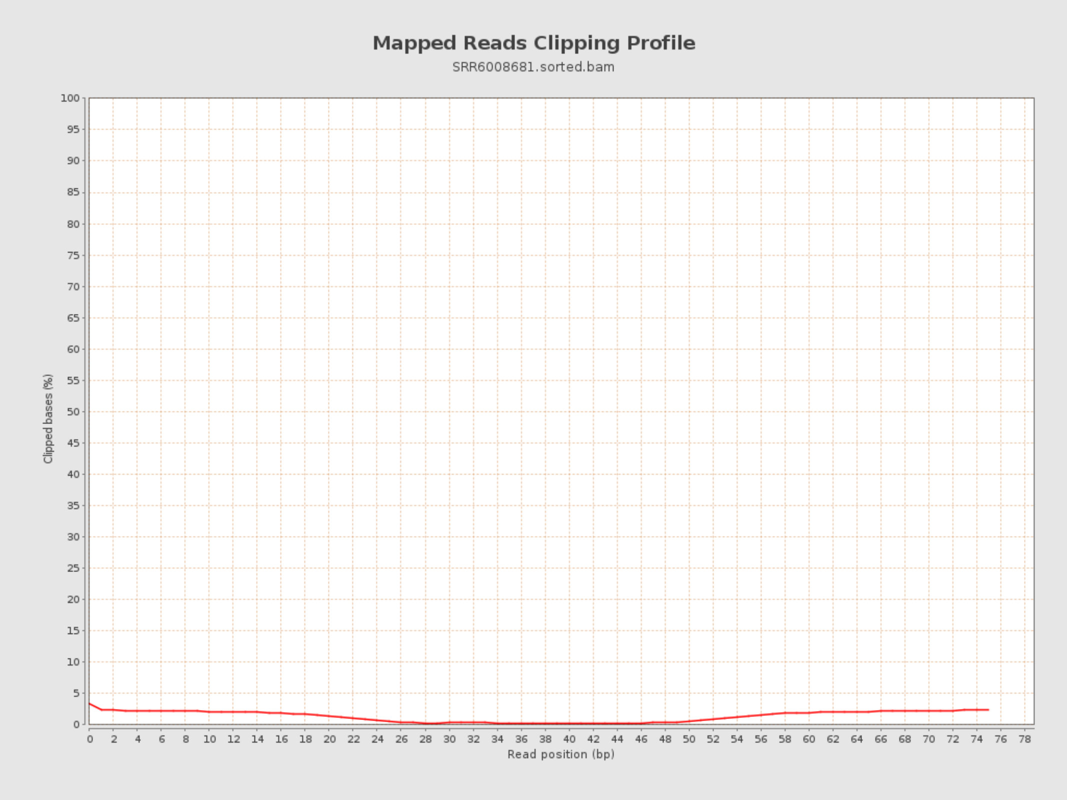
8. Results : Mapped Reads Nucleotide Content



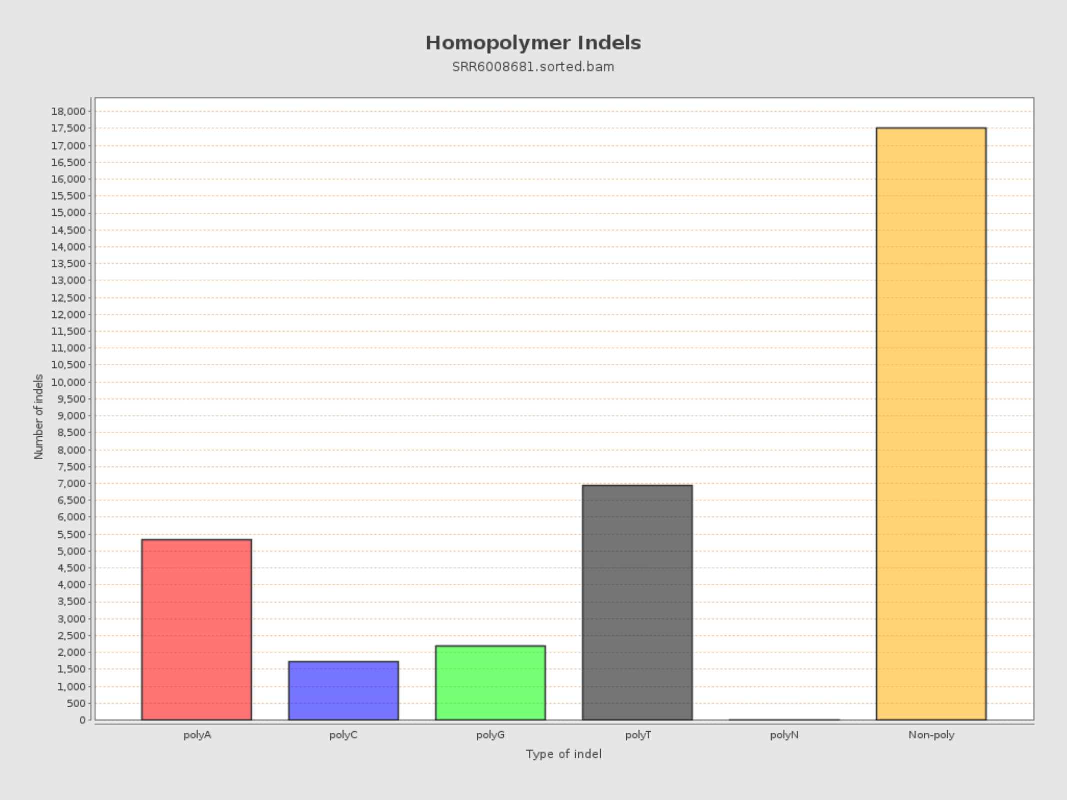
9. Results : Mapped Reads GC-content Distribution



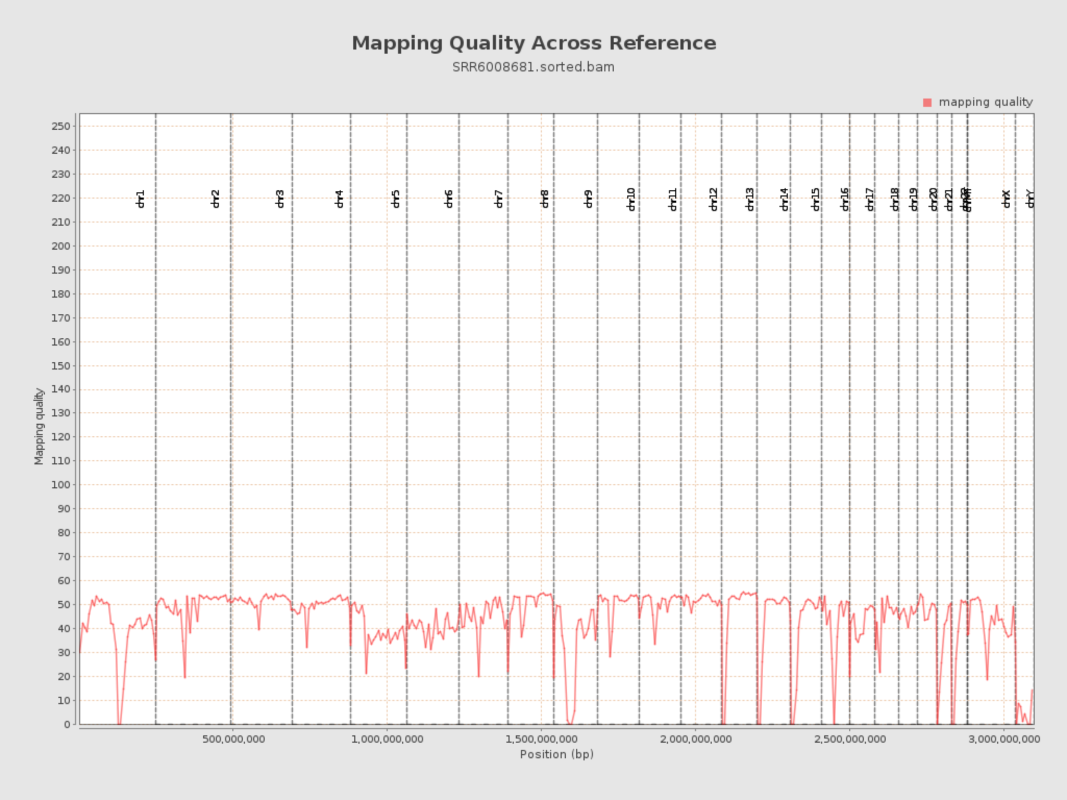
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram