Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:31:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068186.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_SRR6068186 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068186.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:31:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	787,021
Mapped reads	668,093 / 84.89%
Unmapped reads	118,928 / 15.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,999 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	19,123 / 2.43%
Duplication rate	2.22%
Clipped reads	249,086 / 31.65%

2.2. ACGT Content

Number/percentage of A's	13,174,435 / 28.86%
Number/percentage of C's	8,500,548 / 18.62%
Number/percentage of T's	14,130,437 / 30.96%
Number/percentage of G's	9,790,736 / 21.45%
Number/percentage of N's	48,549 / 0.11%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1942

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

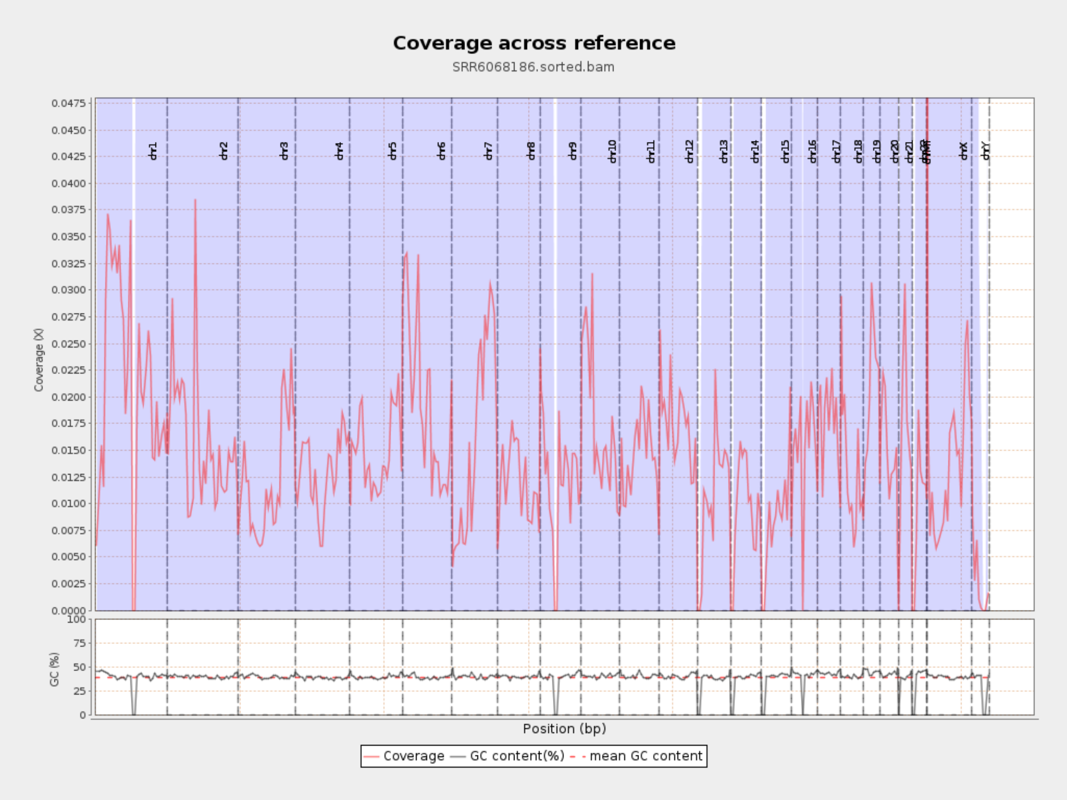
General error rate	0.93%
Mismatches	418,140
Insertions	3,507
Mapped reads with at least one insertion	0.52%
Deletions	13,191
Mapped reads with at least one deletion	1.95%
Homopolymer indels	47.38%

2.6. Chromosome stats

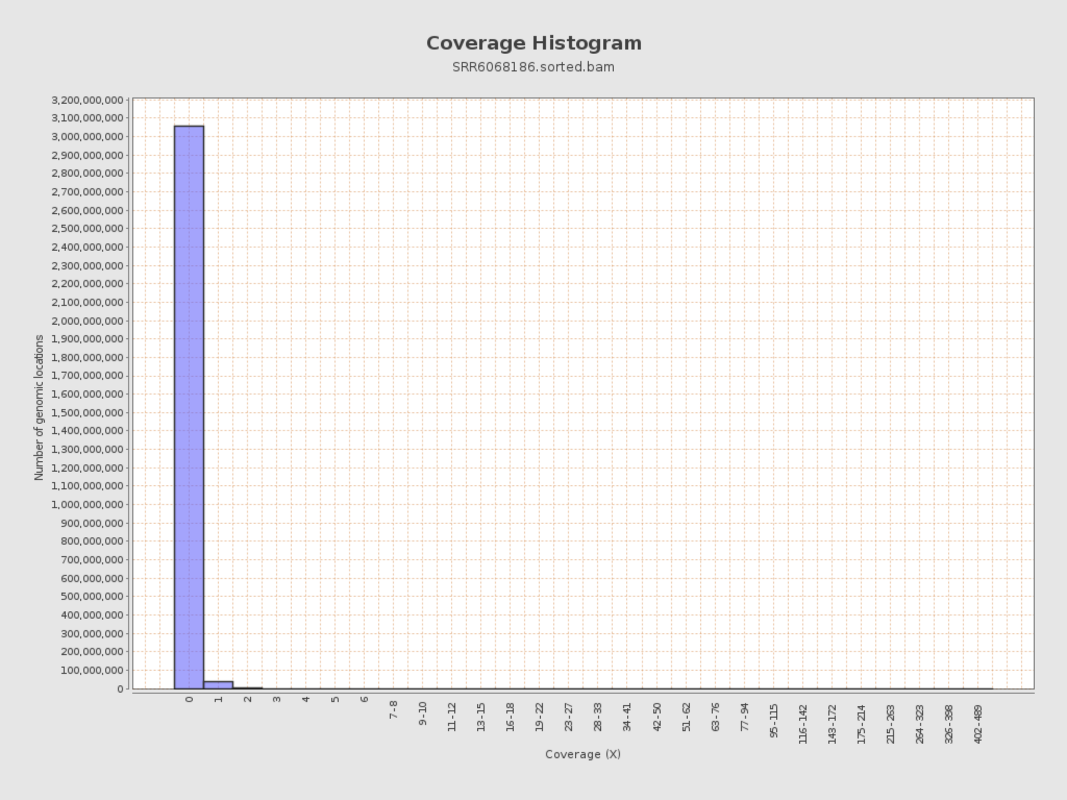
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5306813	0.0213	0.4196
chr2	243199373	3901961	0.016	0.1896
chr3	198022430	2391382	0.0121	0.1193
chr4	191154276	2491842	0.013	0.1252
chr5	180915260	2711178	0.015	0.1321
chr6	171115067	3342277	0.0195	0.1766
chr7	159138663	2581531	0.0162	0.1638

chr8	146364022	1760418	0.012	0.2033
chr9	141213431	1708868	0.0121	0.1746
chr10	135534747	2394637	0.0177	0.1932
chr11	135006516	2008957	0.0149	0.1563
chr12	133851895	2363390	0.0177	0.1436
chr13	115169878	1236152	0.0107	0.1103
chr14	107349540	1030783	0.0096	0.1141
chr15	102531392	859285	0.0084	0.0973
chr16	90354753	1357073	0.015	0.1415
chr17	81195210	1437564	0.0177	0.1478
chr18	78077248	995580	0.0128	0.2933
chr19	59128983	1230633	0.0208	0.2694
chr20	63025520	961839	0.0153	0.135
chr21	48129895	823385	0.0171	0.1459
chr22	51304566	502697	0.0098	0.1051
chrMT	16571	7089	0.4278	0.7342
chrX	155270560	2121808	0.0137	0.1301
chrY	59373566	140675	0.0024	0.0709

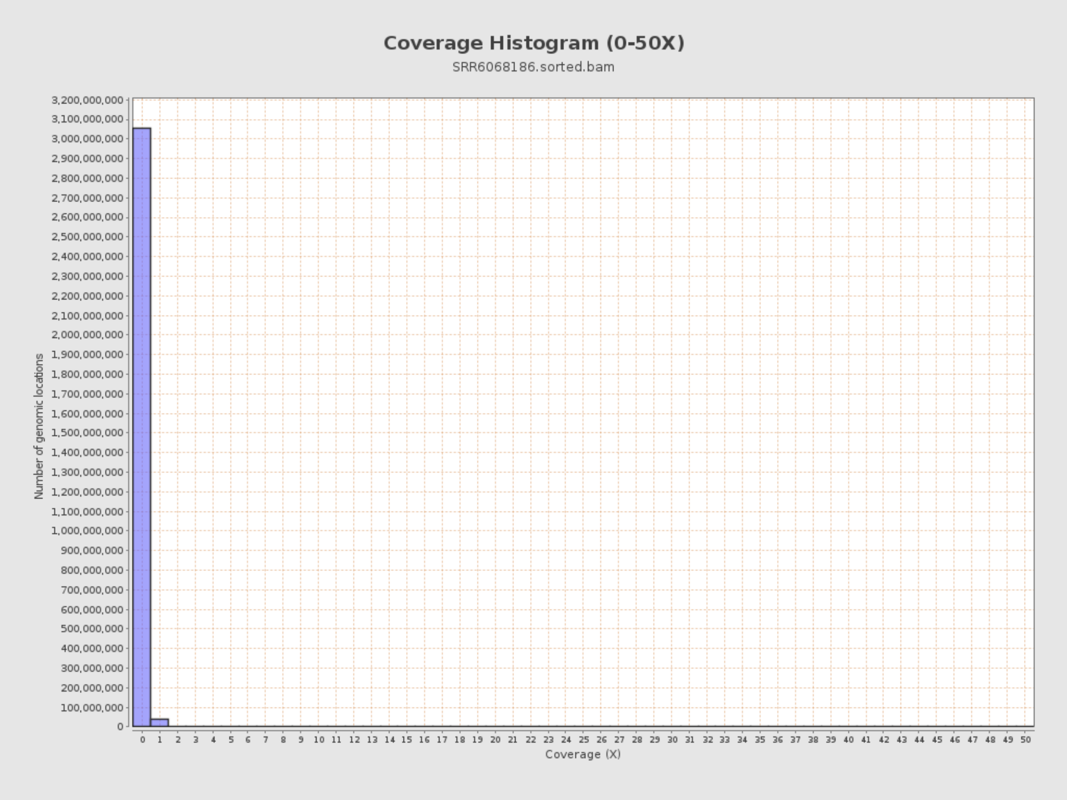
3. Results : Coverage across reference



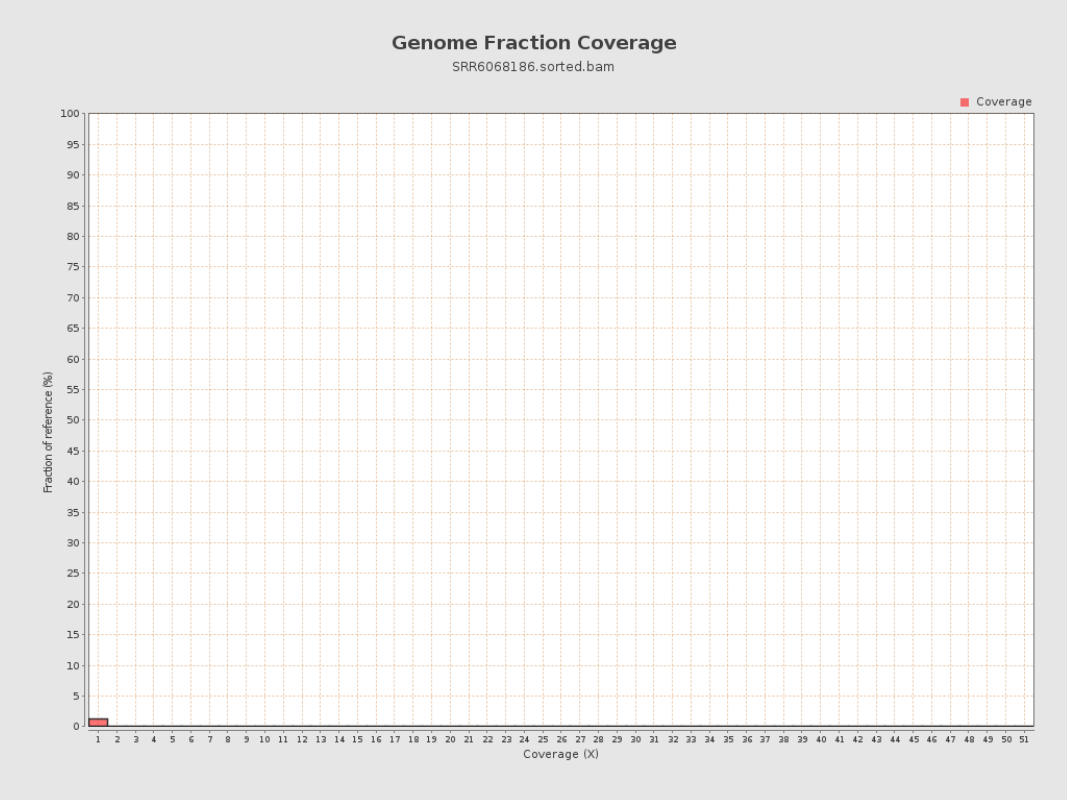
4. Results : Coverage Histogram



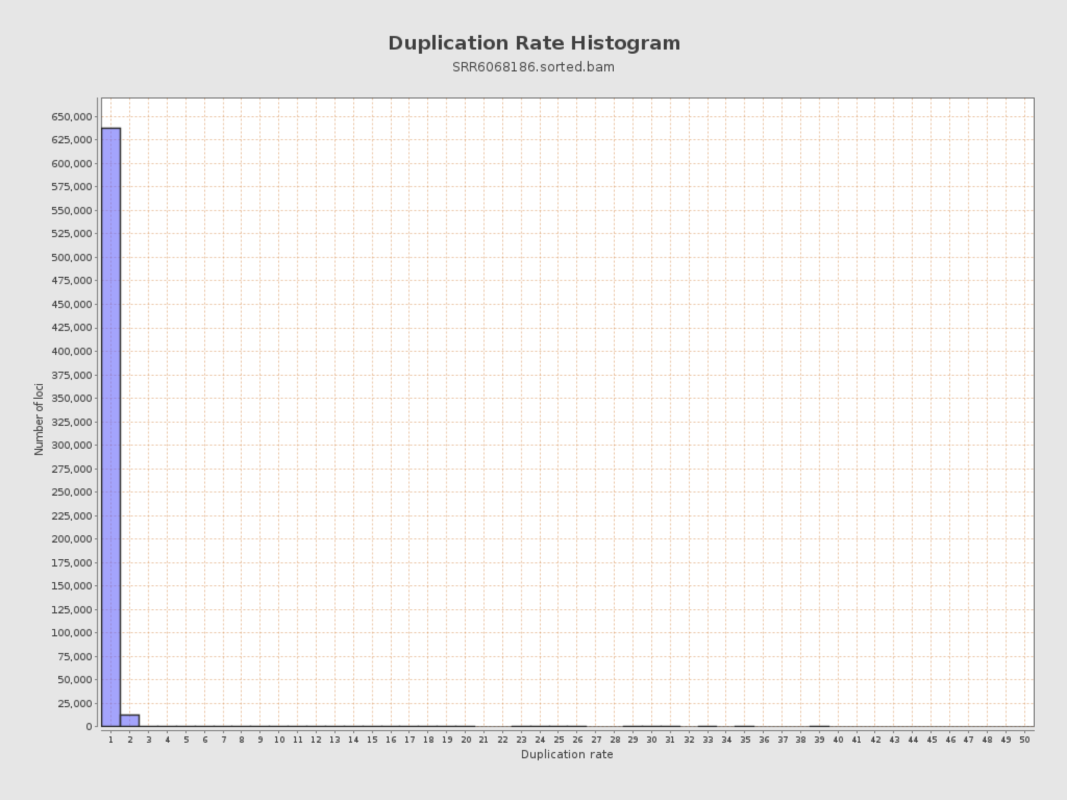
5. Results : Coverage Histogram (0-50X)



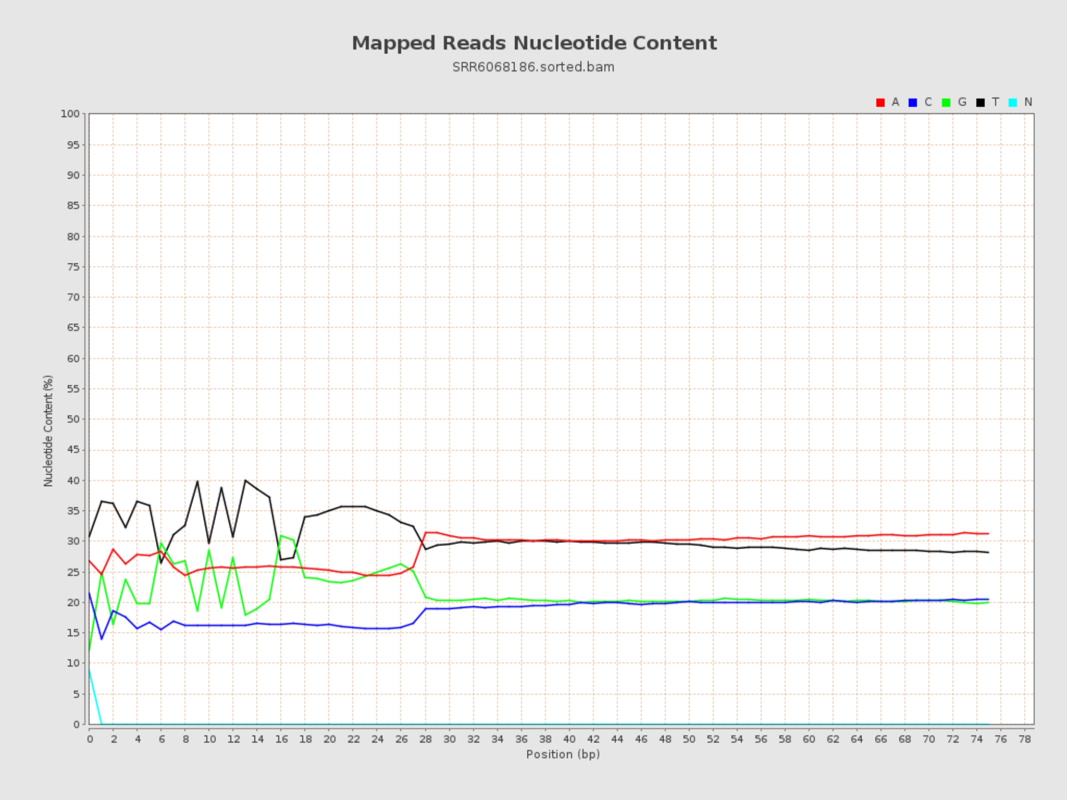
6. Results : Genome Fraction Coverage



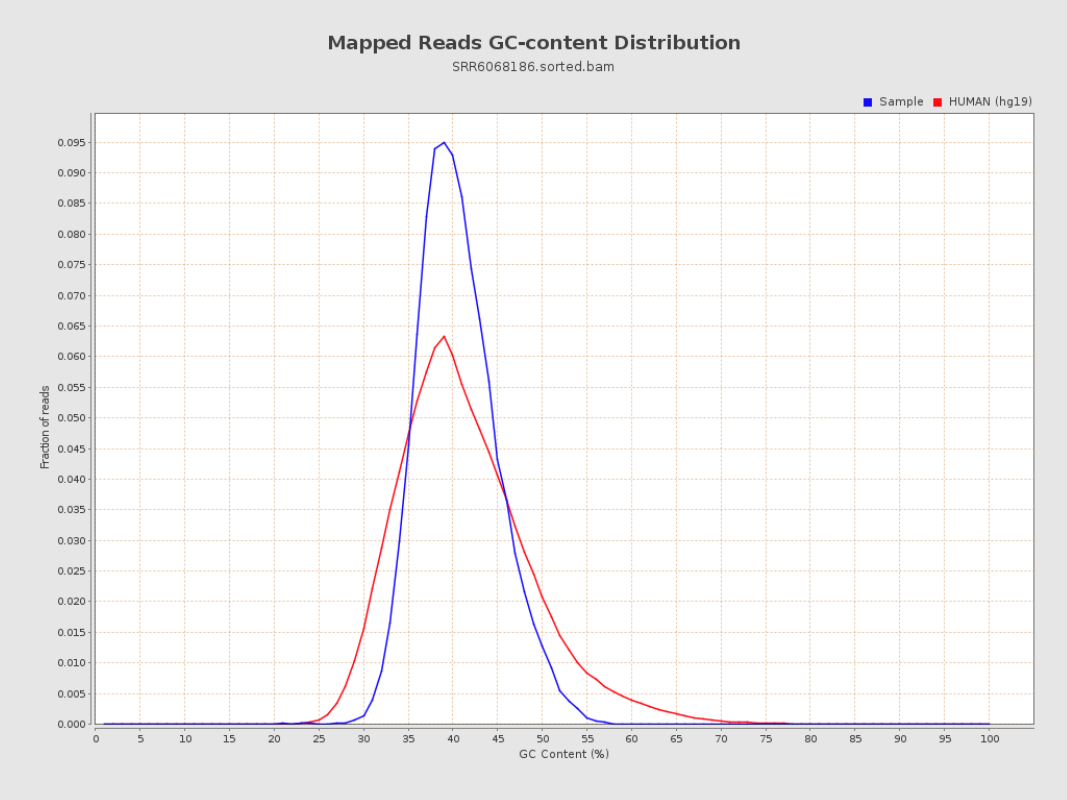
7. Results : Duplication Rate Histogram



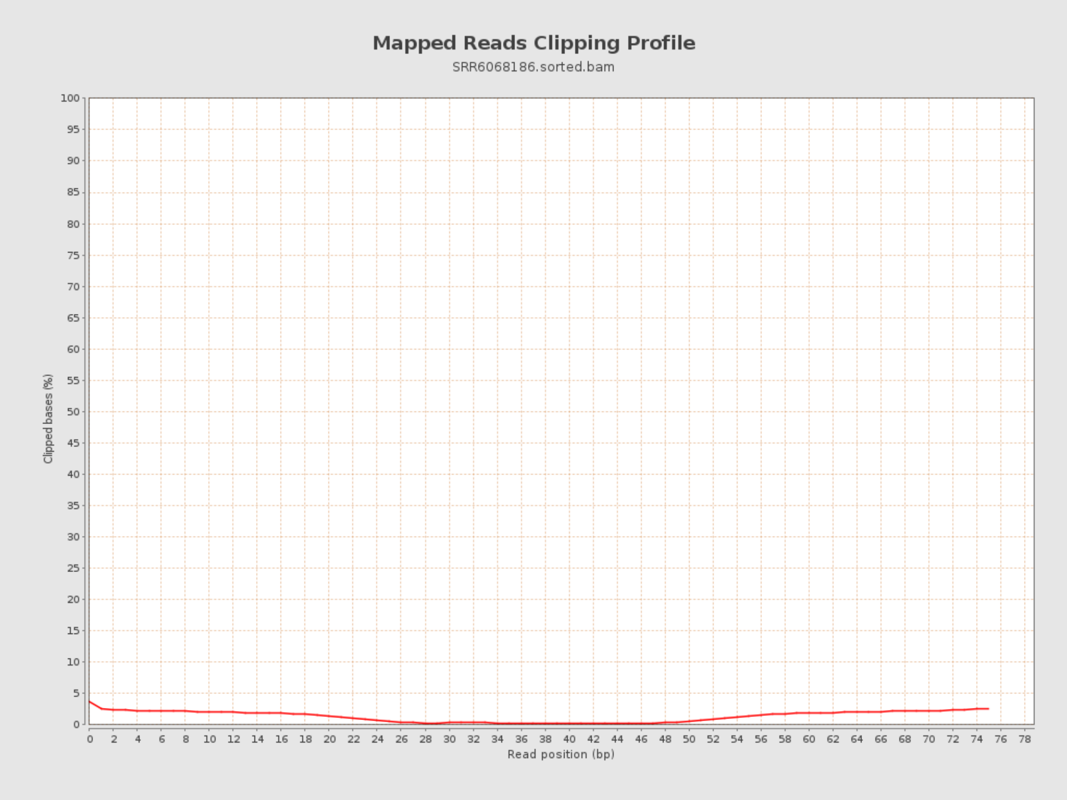
8. Results : Mapped Reads Nucleotide Content



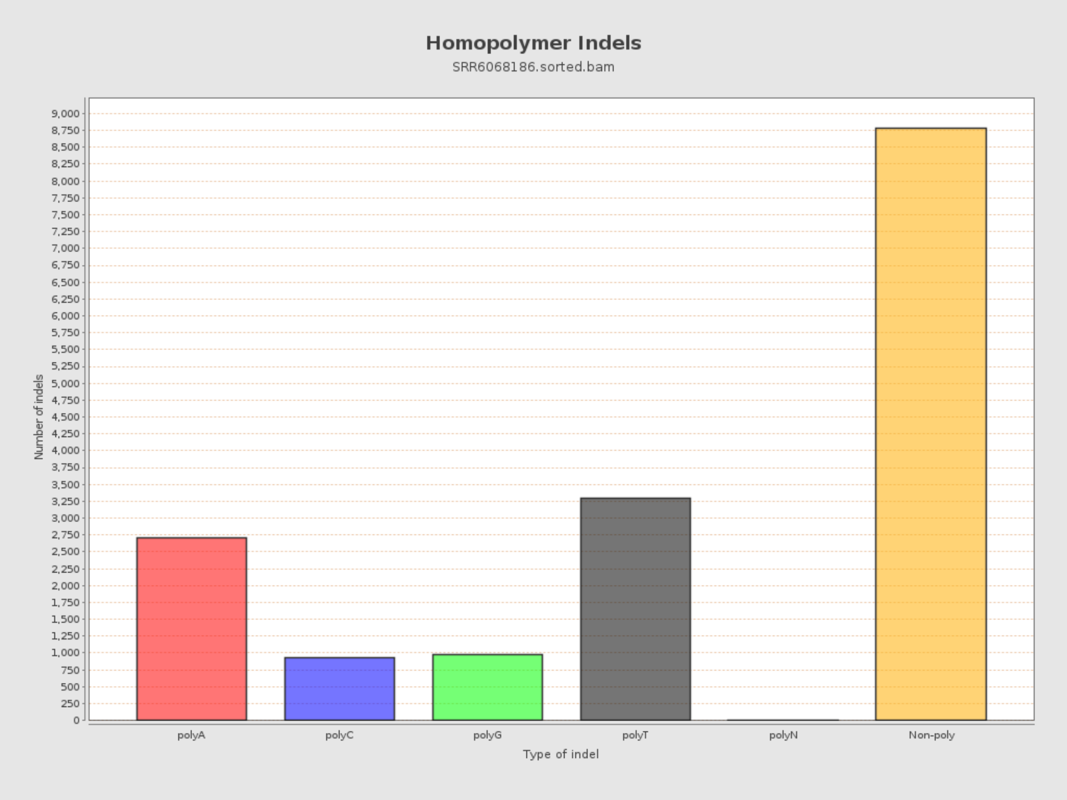
9. Results : Mapped Reads GC-content Distribution



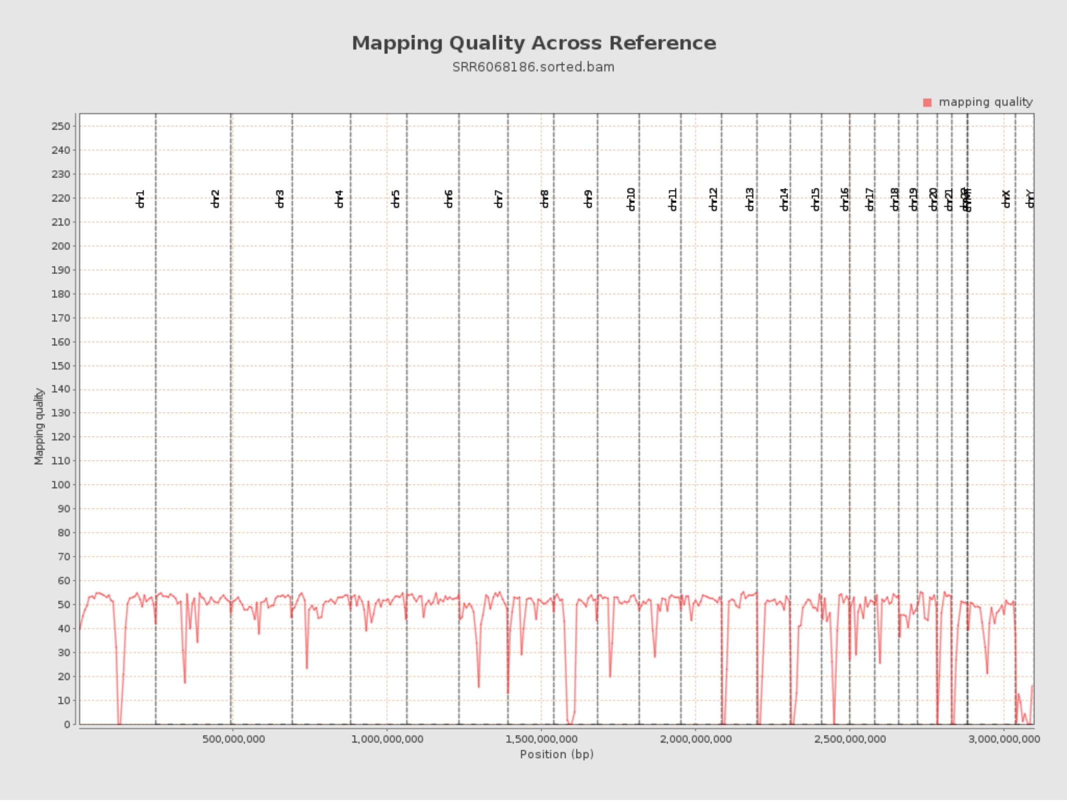
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram