Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:34:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085088.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_SRR3085088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:34:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,794,725
Mapped reads	1,461,871 / 81.45%
Unmapped reads	332,854 / 18.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,726 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	39,631 / 2.21%
Duplication rate	2.08%
Clipped reads	891,301 / 49.66%

2.2. ACGT Content

Number/percentage of A's	27,082,773 / 29.52%
Number/percentage of C's	17,582,685 / 19.16%
Number/percentage of T's	27,316,625 / 29.77%
Number/percentage of G's	19,767,367 / 21.54%
Number/percentage of N's	2,019 / 0%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2697

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

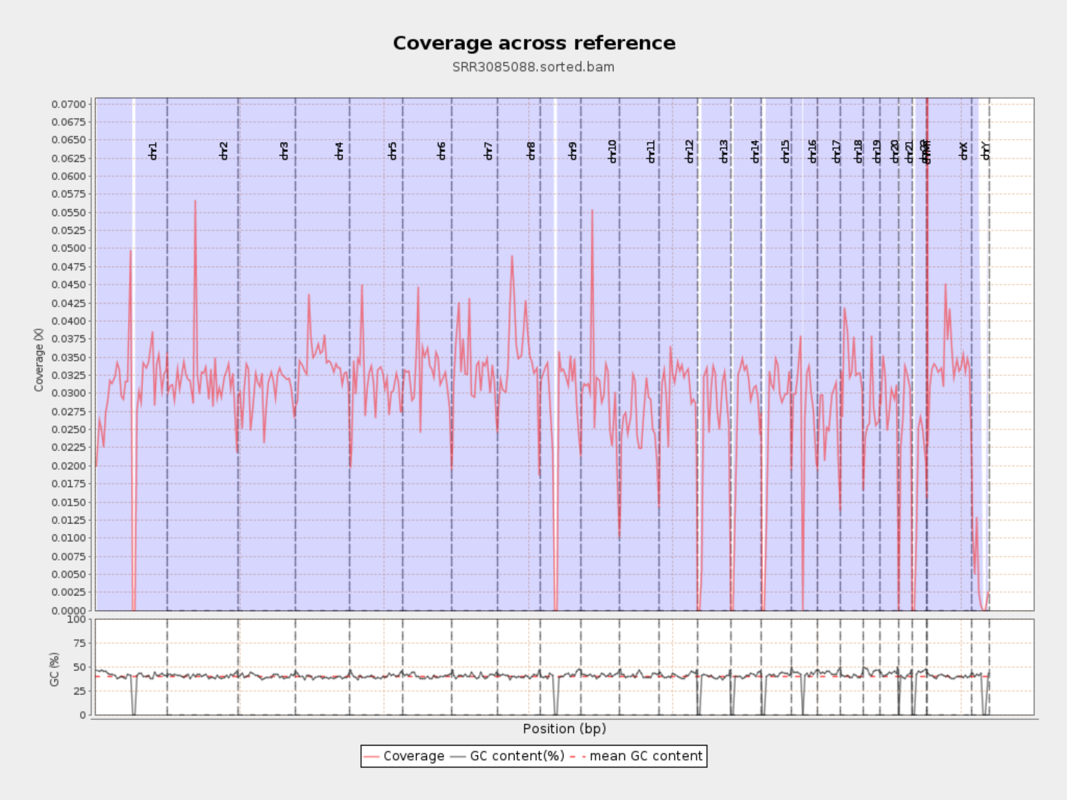
General error rate	0.91%
Mismatches	821,830
Insertions	7,428
Mapped reads with at least one insertion	0.5%
Deletions	20,500
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.79%

2.6. Chromosome stats

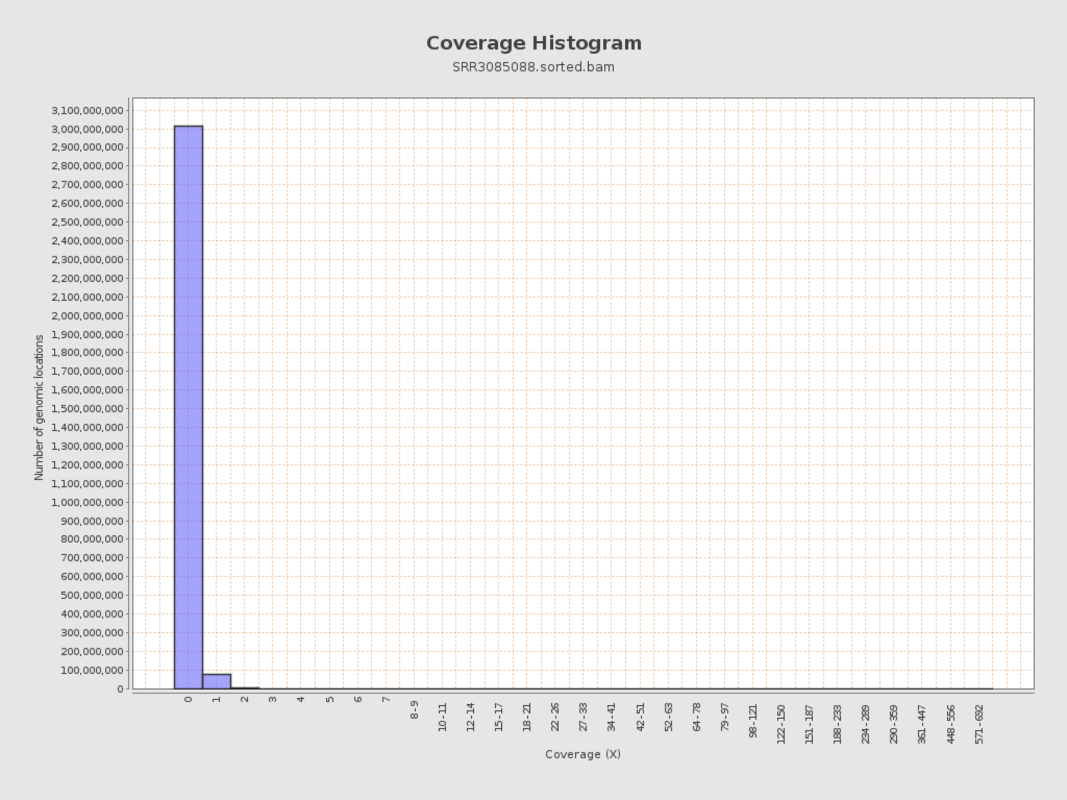
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7355309	0.0295	0.4482
chr2	243199373	7808353	0.0321	0.2782
chr3	198022430	6047162	0.0305	0.1885
chr4	191154276	6542559	0.0342	0.2069
chr5	180915260	5684171	0.0314	0.1905
chr6	171115067	5608061	0.0328	0.2319
chr7	159138663	5297892	0.0333	0.2572

chr8	146364022	5175789	0.0354	0.4526
chr9	141213431	3952900	0.028	0.2539
chr10	135534747	4045953	0.0299	0.2866
chr11	135006516	3538056	0.0262	0.2356
chr12	133851895	4136306	0.0309	0.1911
chr13	115169878	2849218	0.0247	0.1679
chr14	107349540	2797856	0.0261	0.1868
chr15	102531392	2616312	0.0255	0.1709
chr16	90354753	2438262	0.027	0.1949
chr17	81195210	2115791	0.0261	0.1878
chr18	78077248	2648468	0.0339	0.4651
chr19	59128983	1604163	0.0271	0.3198
chr20	63025520	1846612	0.0293	0.191
chr21	48129895	1236993	0.0257	0.1832
chr22	51304566	865788	0.0169	0.1386
chrMT	16571	37655	2.2723	2.0175
chrX	155270560	5294812	0.0341	0.2177
chrY	59373566	240131	0.004	0.0935

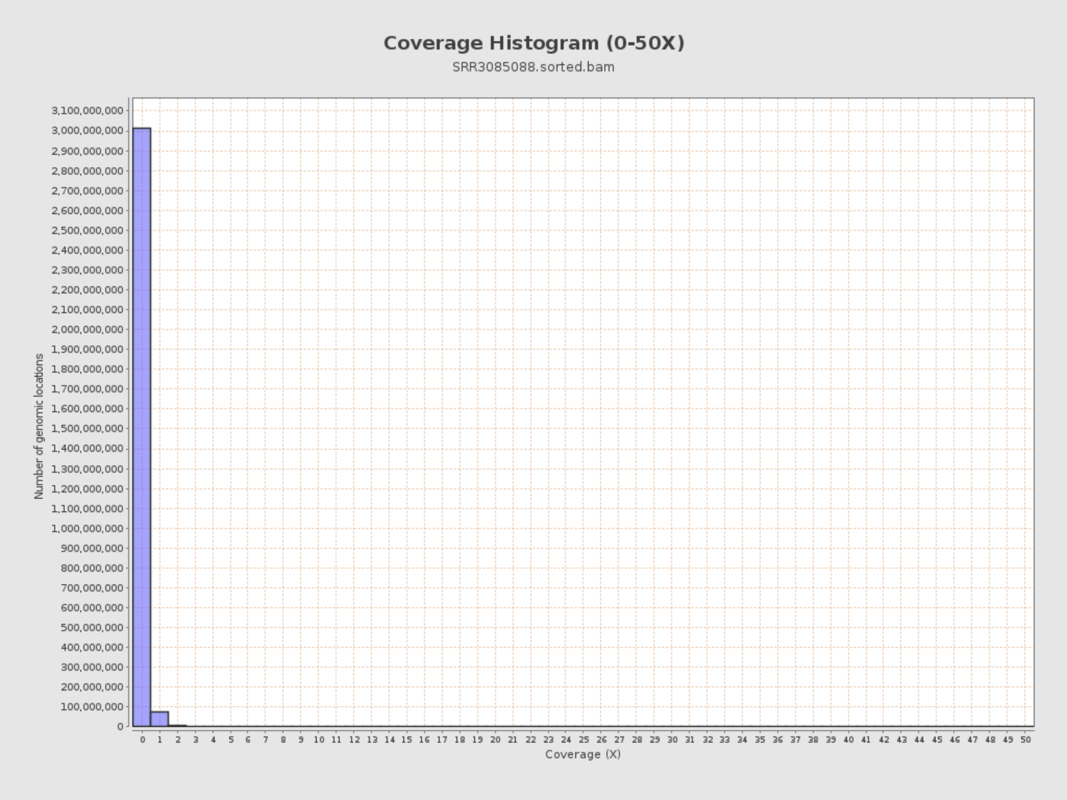
3. Results : Coverage across reference



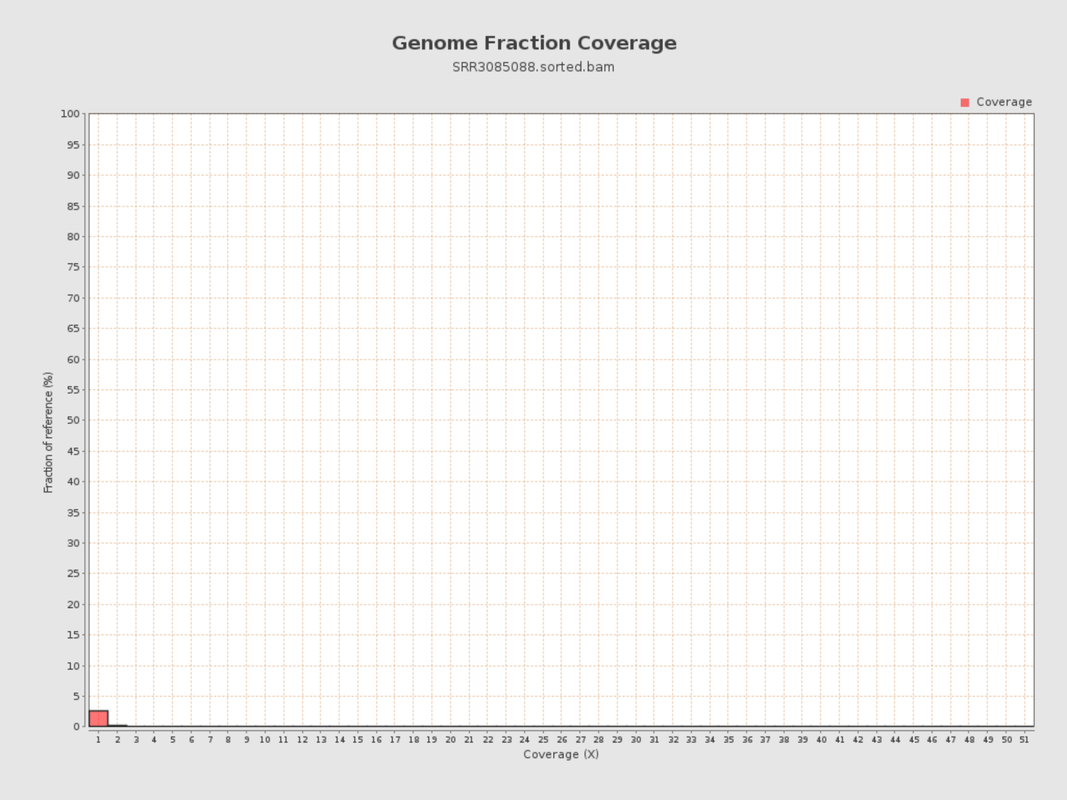
4. Results : Coverage Histogram



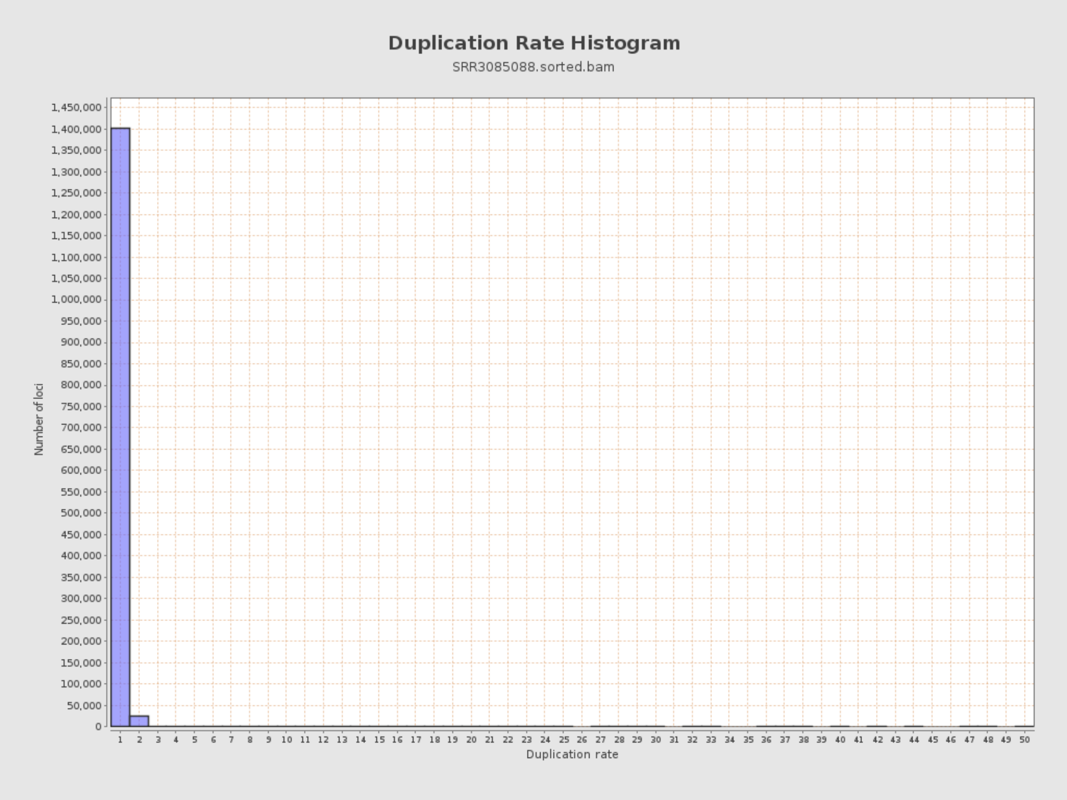
5. Results : Coverage Histogram (0-50X)



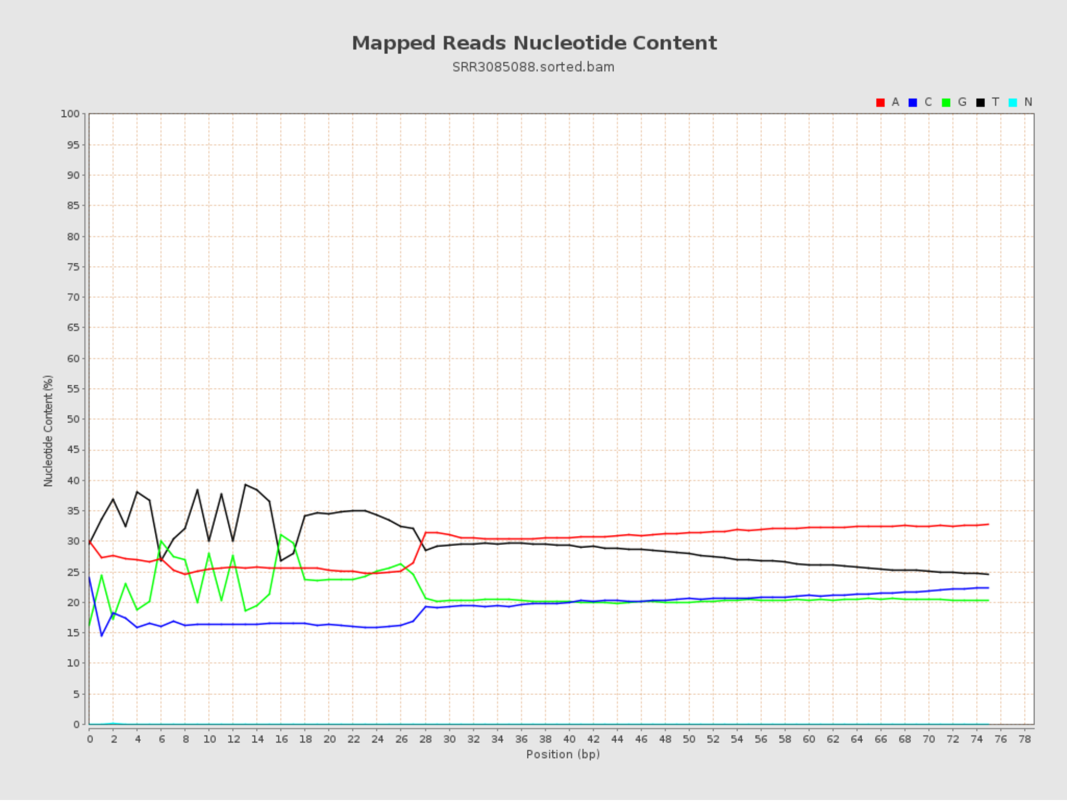
6. Results : Genome Fraction Coverage



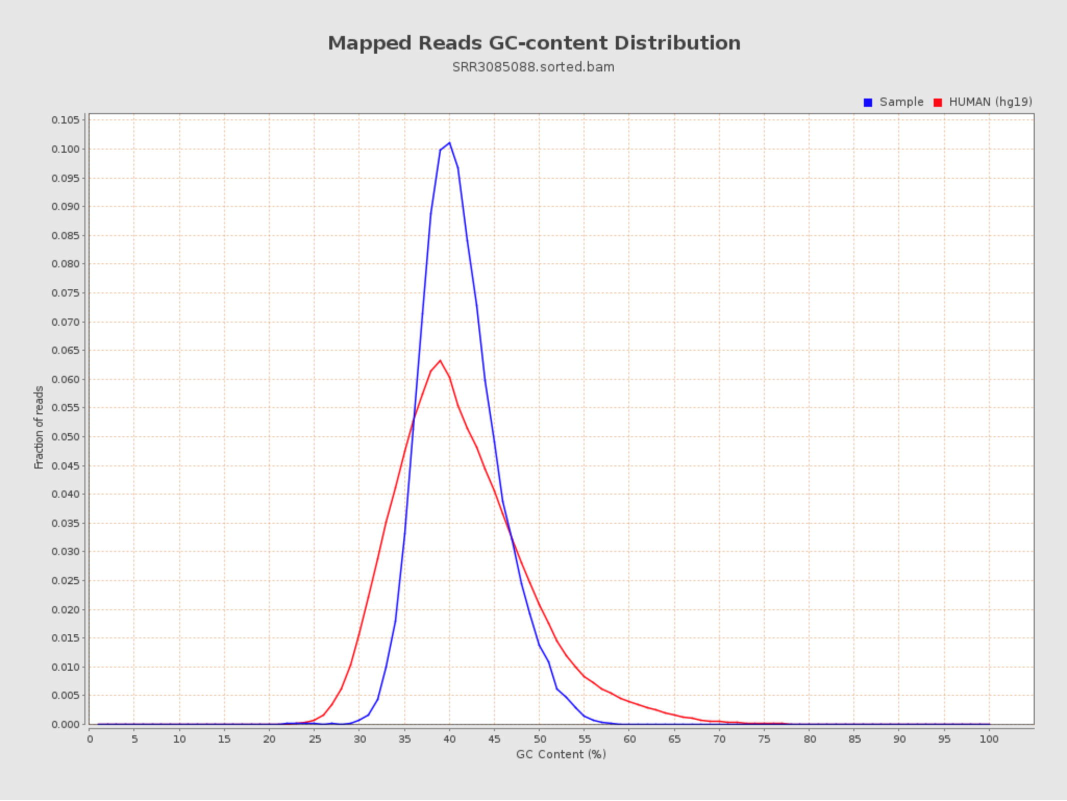
7. Results : Duplication Rate Histogram



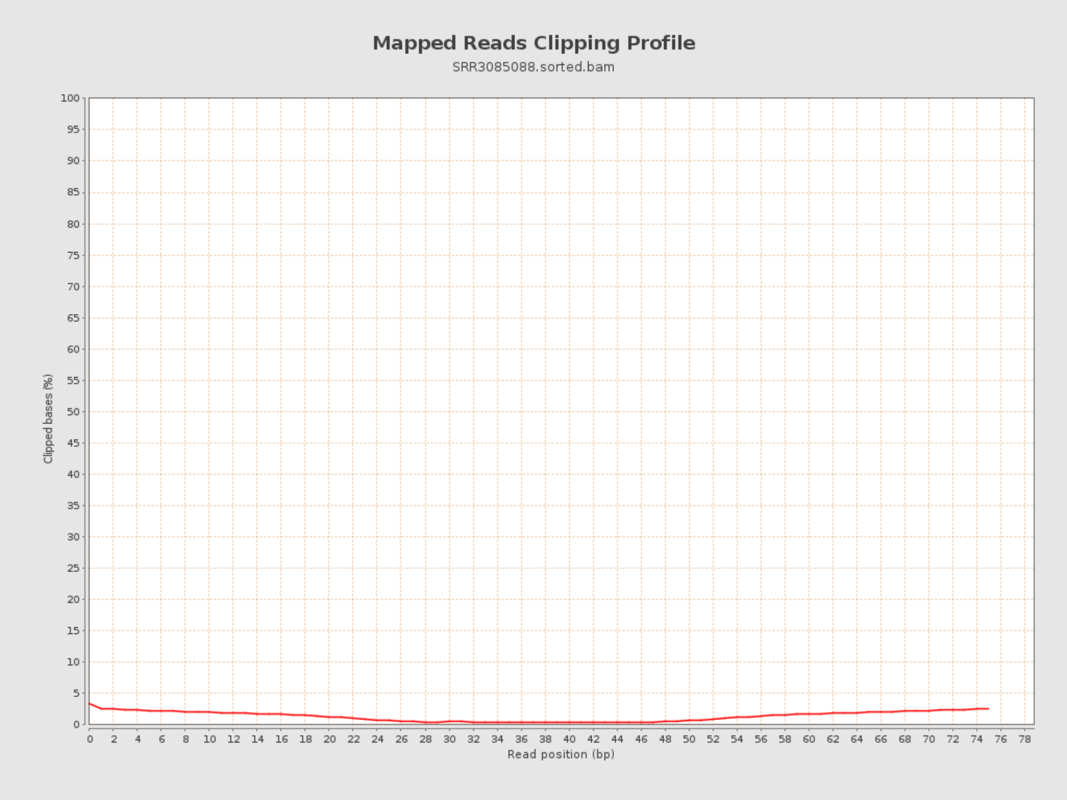
8. Results : Mapped Reads Nucleotide Content



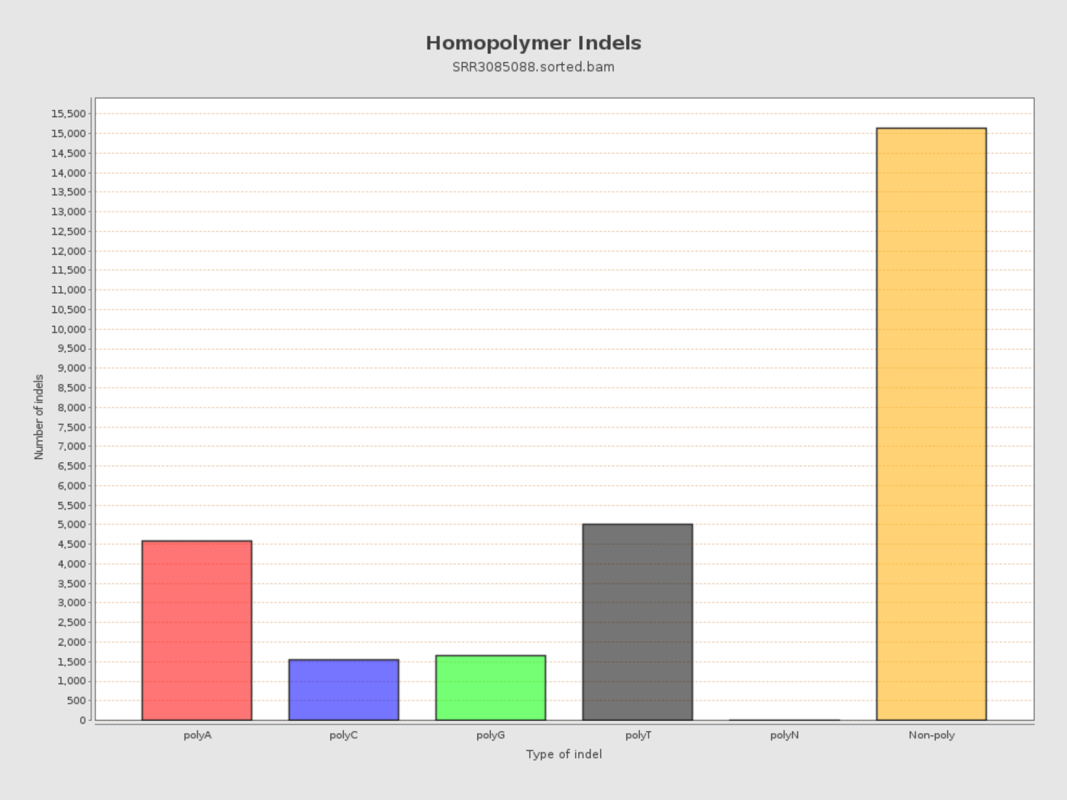
9. Results : Mapped Reads GC-content Distribution



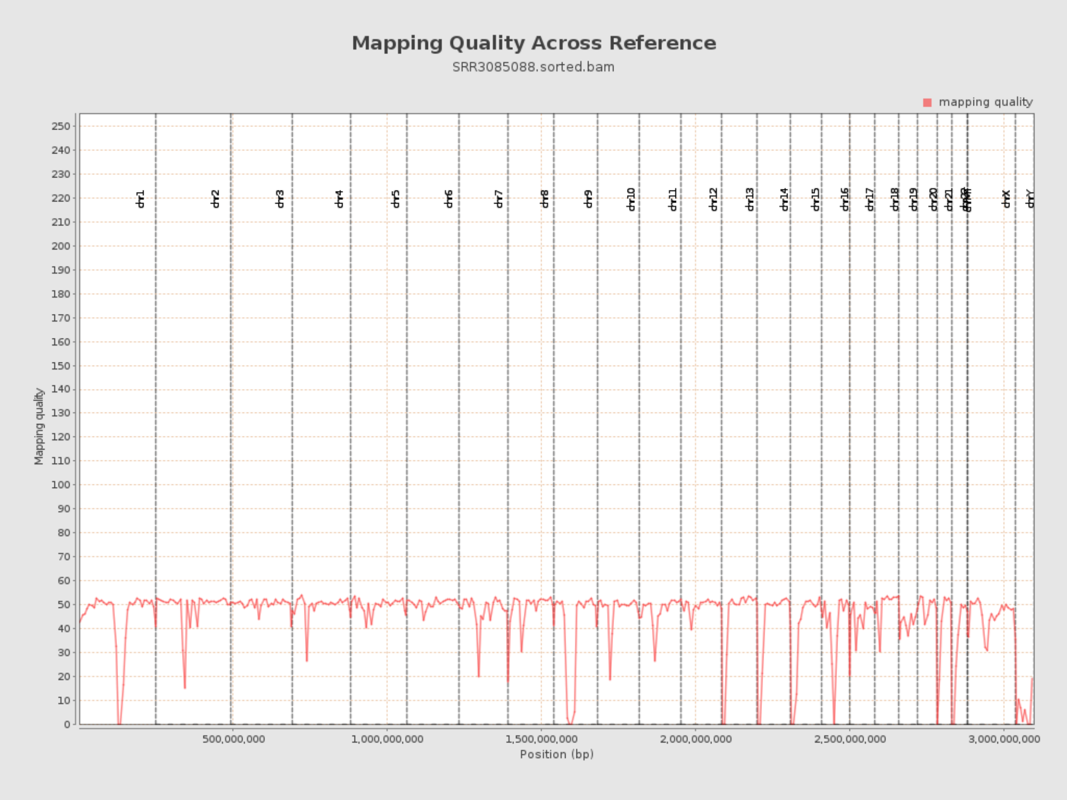
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram