Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:46:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085029.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_SRR3085029 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085029.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:46:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,824,564
Mapped reads	1,658,718 / 90.91%
Unmapped reads	165,846 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,548 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	47,800 / 2.62%
Duplication rate	2.23%
Clipped reads	739,272 / 40.52%

2.2. ACGT Content

Number/percentage of A's	31,035,301 / 27.95%
Number/percentage of C's	21,491,245 / 19.35%
Number/percentage of T's	33,928,336 / 30.55%
Number/percentage of G's	24,588,624 / 22.14%
Number/percentage of N's	5,486 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.2993

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

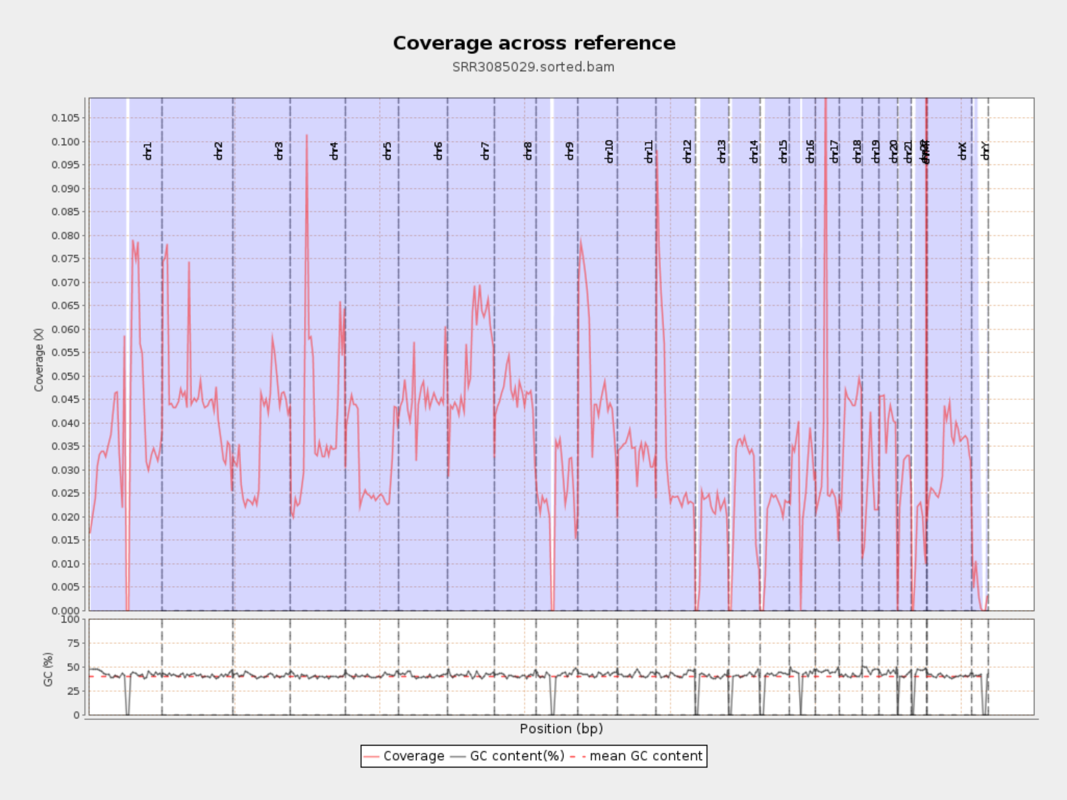
General error rate	0.86%
Mismatches	942,845
Insertions	7,866
Mapped reads with at least one insertion	0.47%
Deletions	21,900
Mapped reads with at least one deletion	1.31%
Homopolymer indels	46.69%

2.6. Chromosome stats

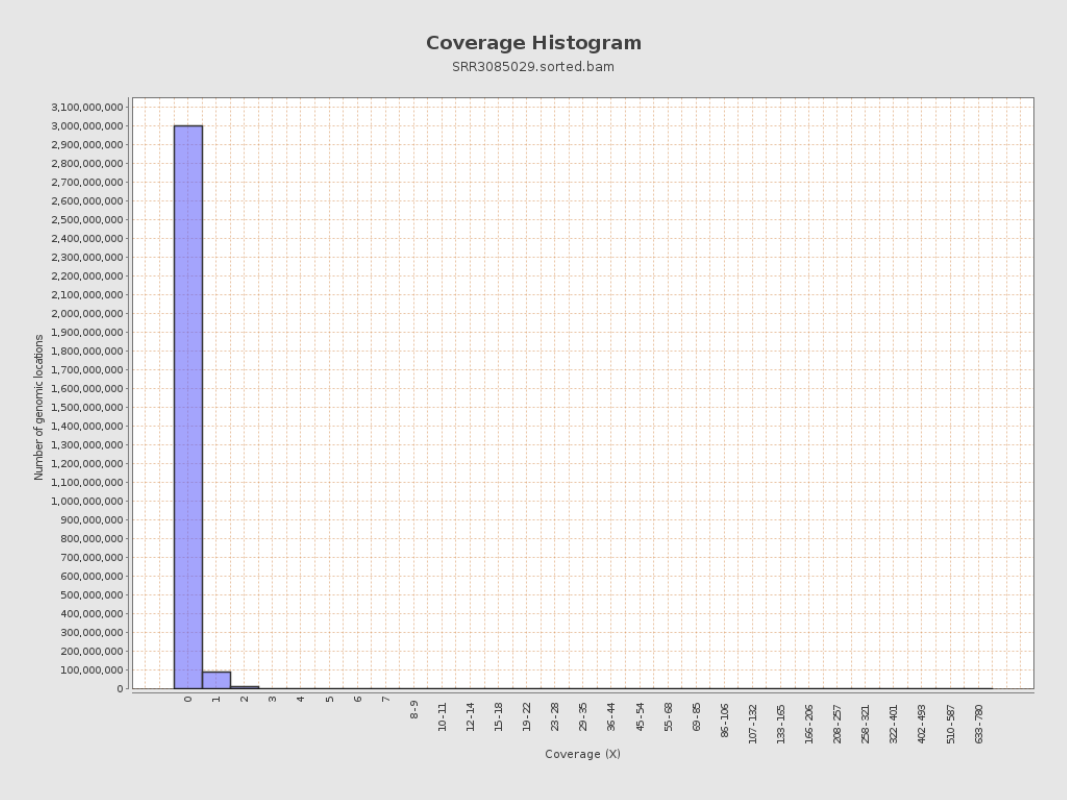
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9453583	0.0379	0.4435
chr2	243199373	11268389	0.0463	0.3936
chr3	198022430	7322002	0.037	0.2106
chr4	191154276	7731449	0.0404	0.226
chr5	180915260	5637864	0.0312	0.1938
chr6	171115067	7794072	0.0455	0.2822
chr7	159138663	8596299	0.054	0.3374

chr8	146364022	6679561	0.0456	0.5233
chr9	141213431	3365321	0.0238	0.2678
chr10	135534747	7031672	0.0519	0.3287
chr11	135006516	4544836	0.0337	0.2759
chr12	133851895	4779771	0.0357	0.2136
chr13	115169878	2191948	0.019	0.1512
chr14	107349540	2742629	0.0255	0.1893
chr15	102531392	1903273	0.0186	0.1523
chr16	90354753	2631630	0.0291	0.2003
chr17	81195210	2788217	0.0343	0.2304
chr18	78077248	3236011	0.0414	0.4414
chr19	59128983	1490042	0.0252	0.3273
chr20	63025520	2573459	0.0408	0.2248
chr21	48129895	1269674	0.0264	0.1863
chr22	51304566	688622	0.0134	0.1255
chrMT	16571	6838	0.4126	0.7019
chrX	155270560	5137376	0.0331	0.2205
chrY	59373566	222056	0.0037	0.0819

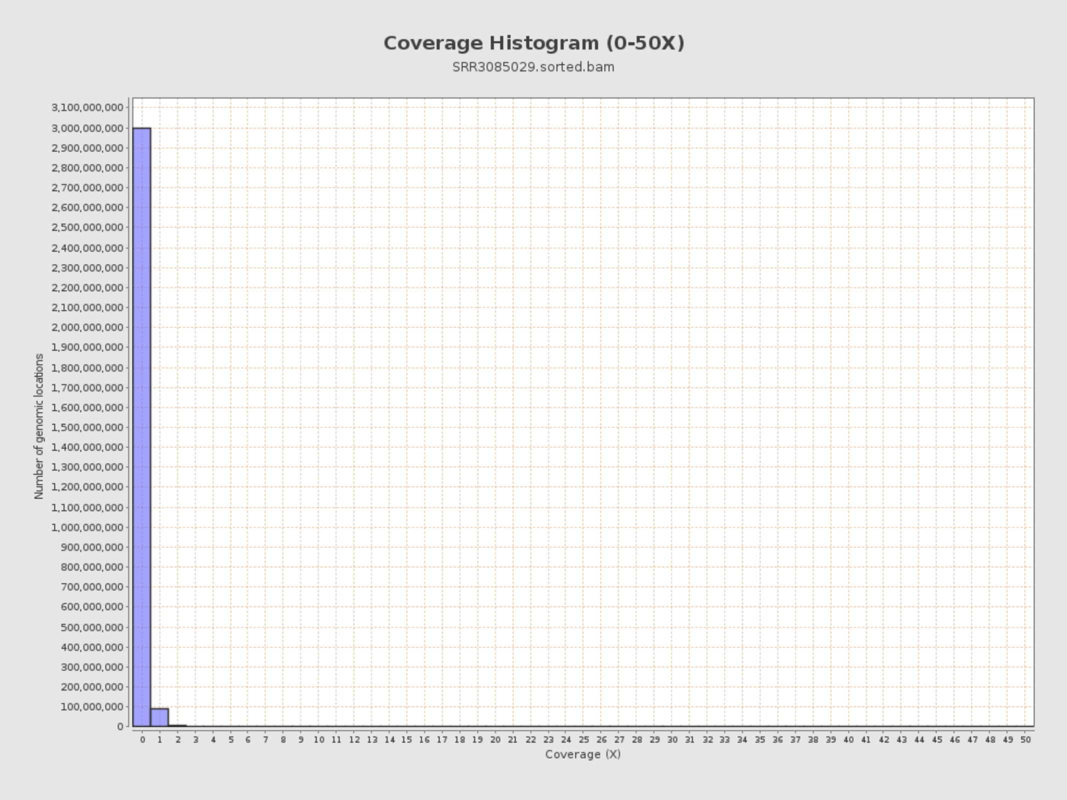
3. Results : Coverage across reference



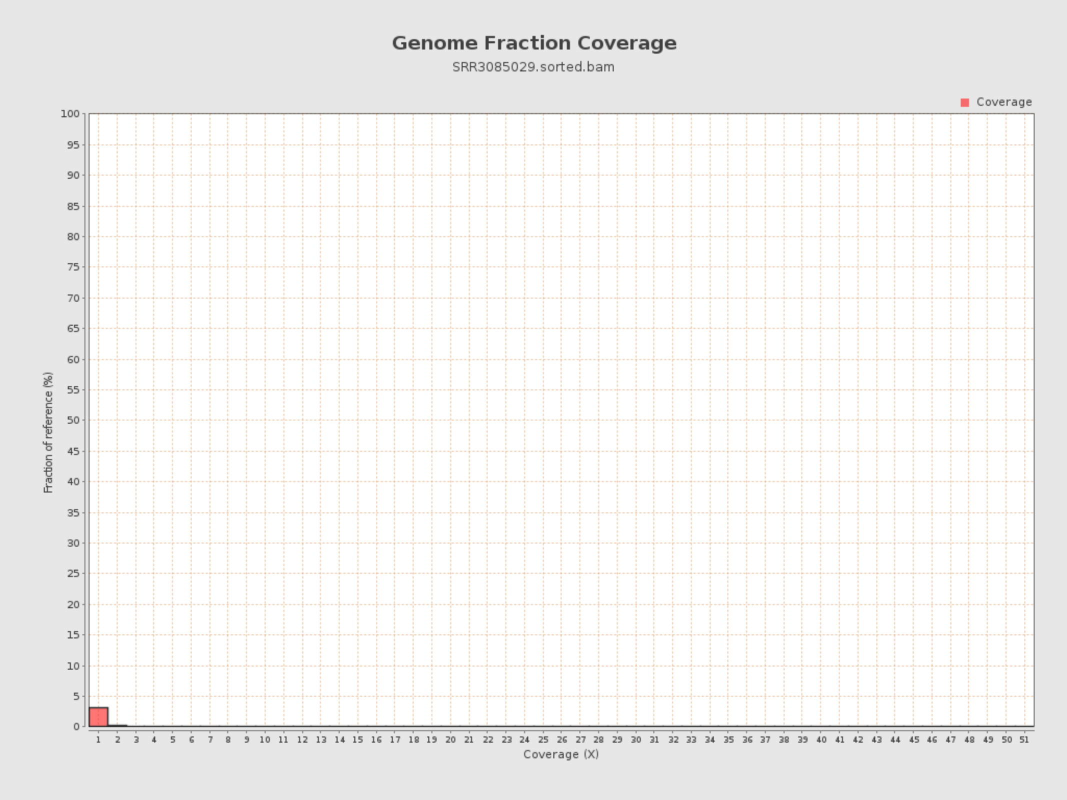
4. Results : Coverage Histogram



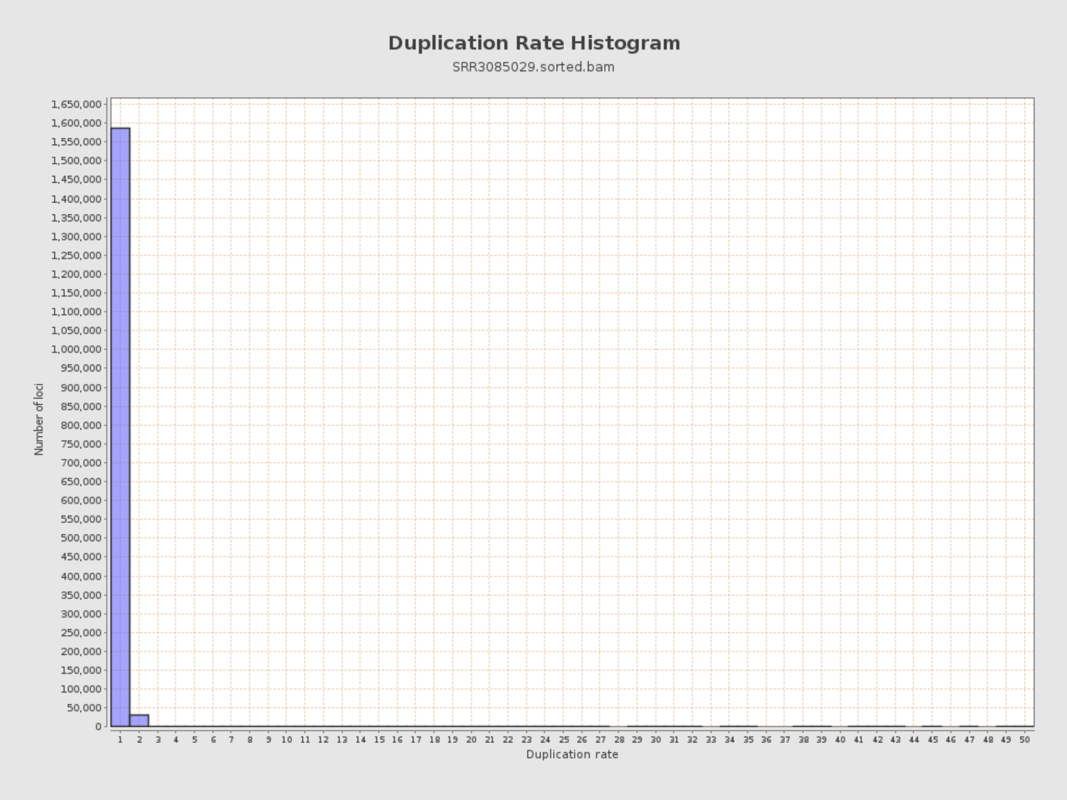
5. Results : Coverage Histogram (0-50X)



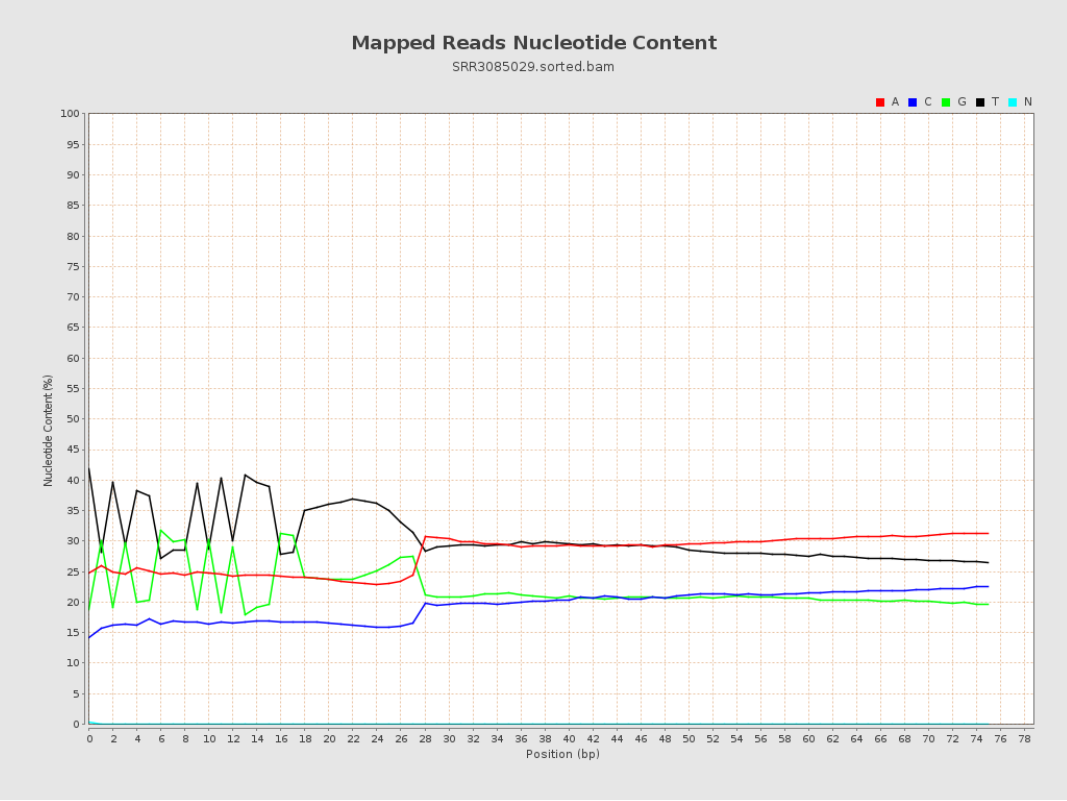
6. Results : Genome Fraction Coverage



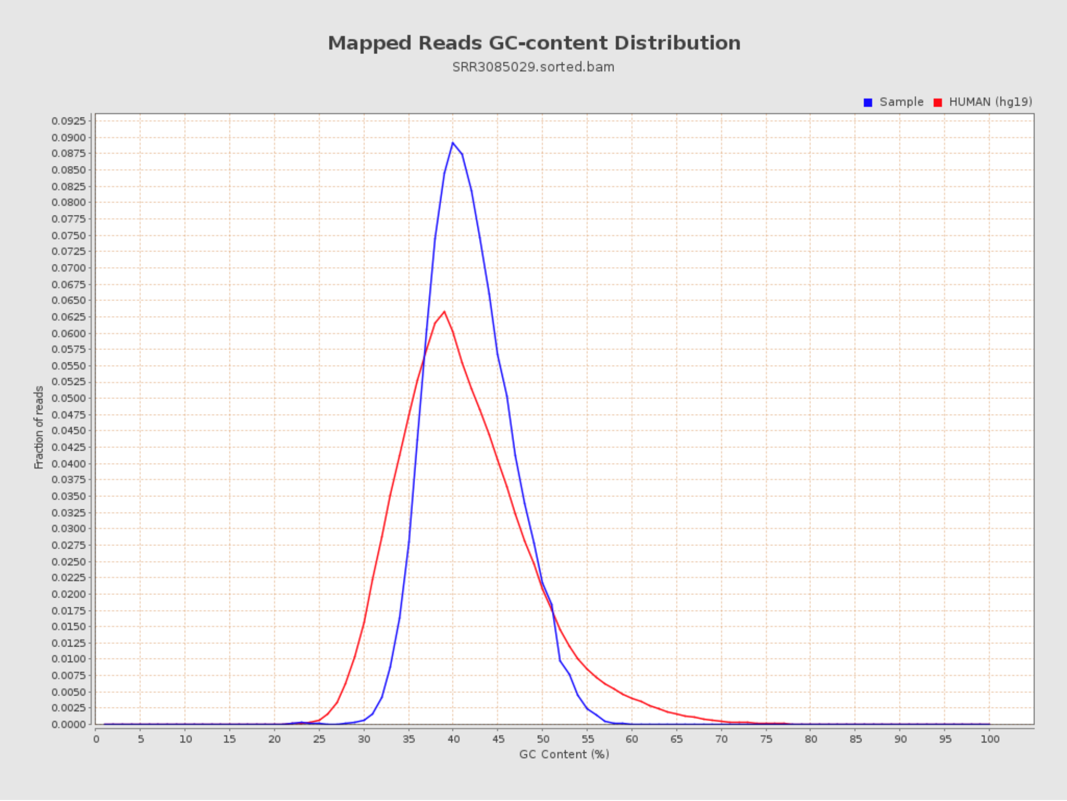
7. Results : Duplication Rate Histogram



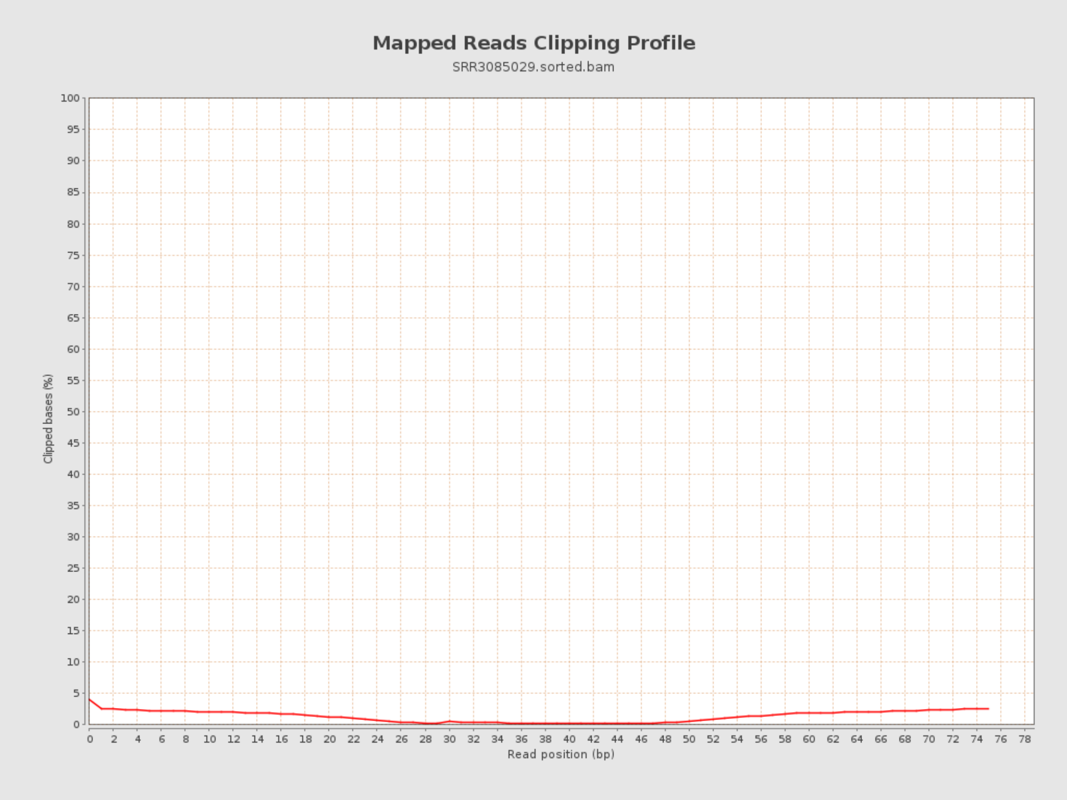
8. Results : Mapped Reads Nucleotide Content



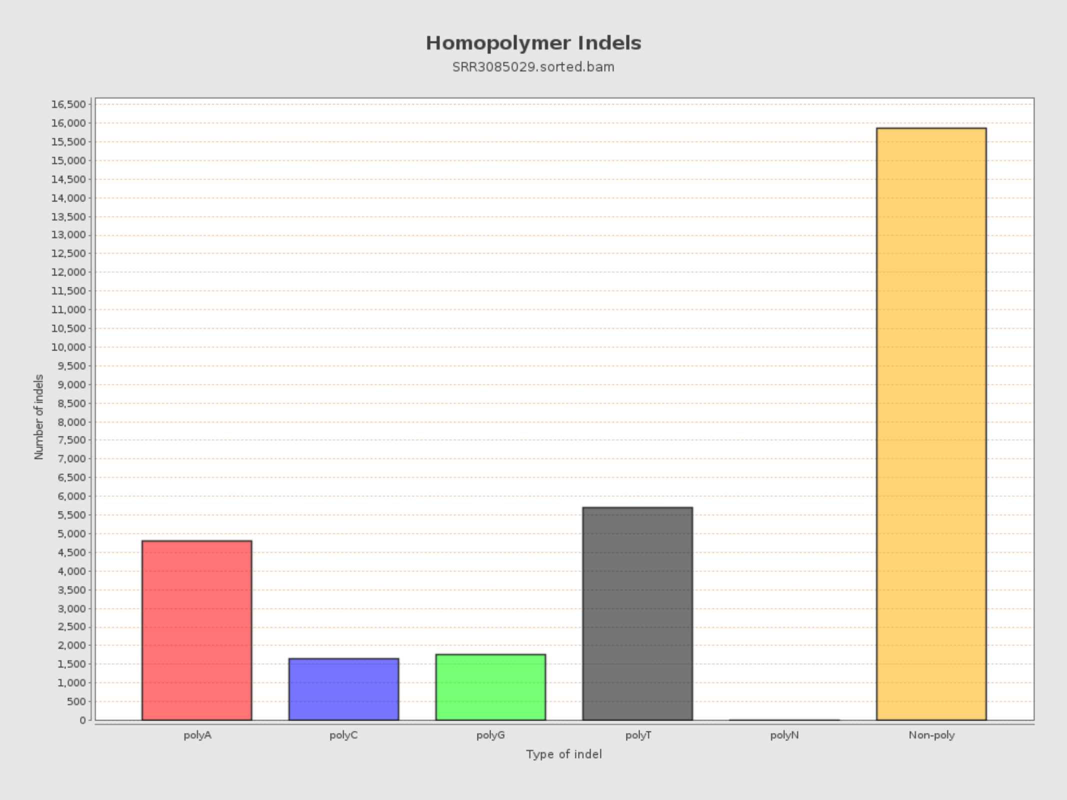
9. Results : Mapped Reads GC-content Distribution



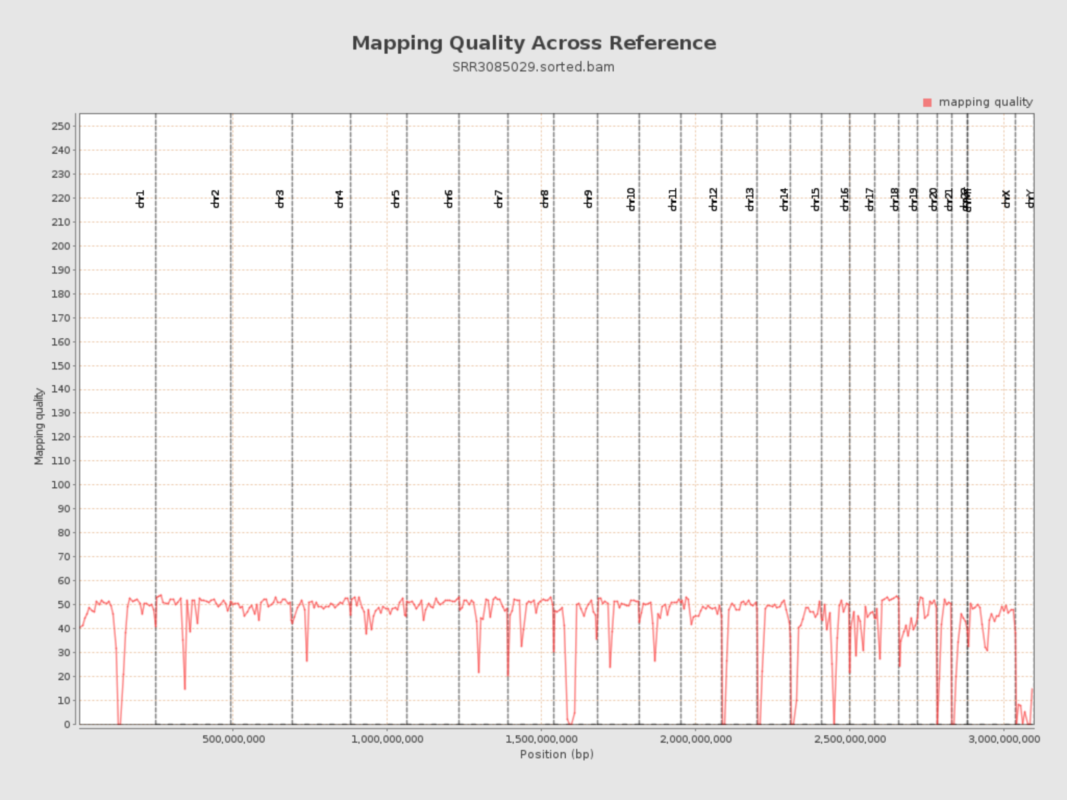
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram