Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:42:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085013.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_SRR3085013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:42:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,312,233
Mapped reads	2,093,982 / 90.56%
Unmapped reads	218,251 / 9.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,335 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	63,474 / 2.75%
Duplication rate	2.53%
Clipped reads	902,575 / 39.03%

2.2. ACGT Content

Number/percentage of A's	38,633,323 / 27.46%
Number/percentage of C's	27,827,827 / 19.78%
Number/percentage of T's	42,615,532 / 30.29%
Number/percentage of G's	31,579,660 / 22.45%
Number/percentage of N's	15,830 / 0.01%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0455

Standard Deviation	0.301

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

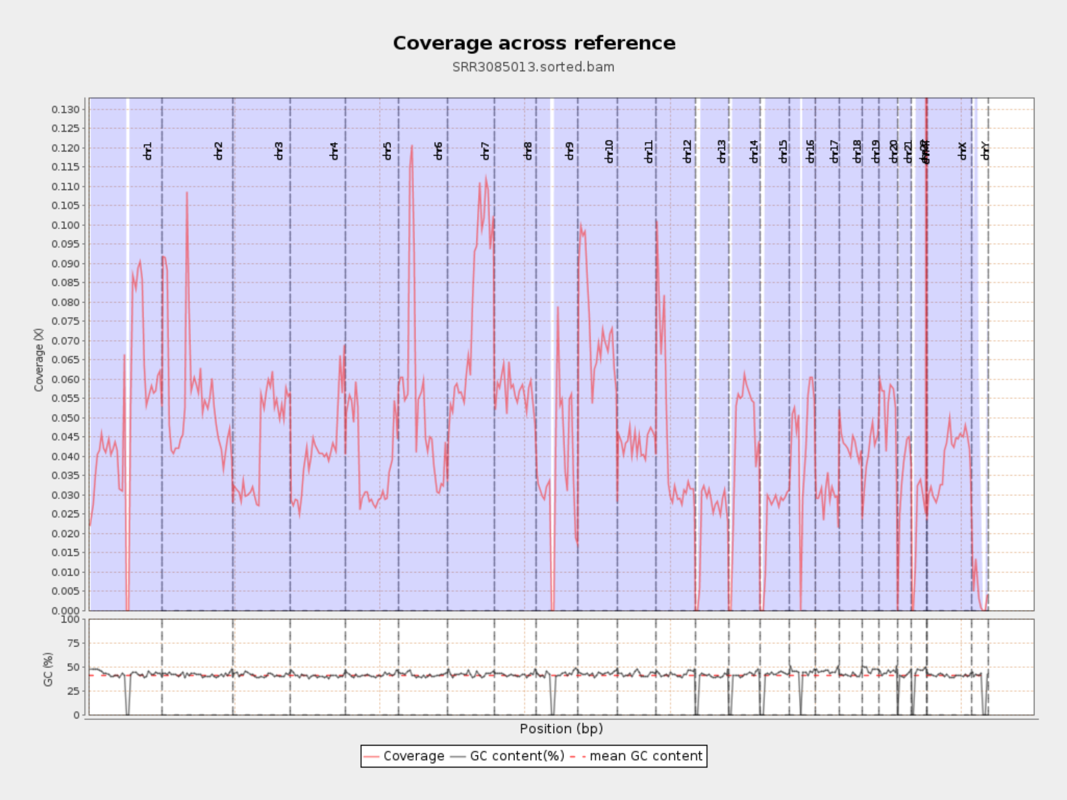
General error rate	0.9%
Mismatches	1,254,287
Insertions	9,120
Mapped reads with at least one insertion	0.43%
Deletions	29,577
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.7%

2.6. Chromosome stats

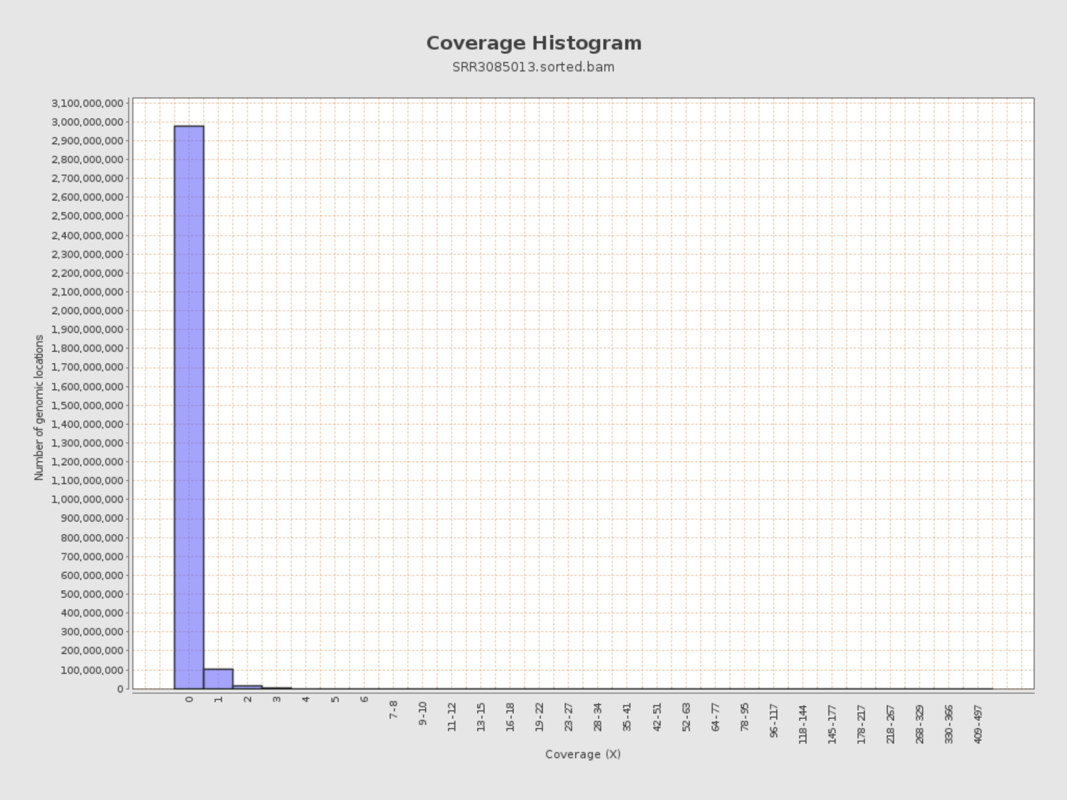
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12412315	0.0498	0.3963
chr2	243199373	13525460	0.0556	0.3685
chr3	198022430	8546463	0.0432	0.2338
chr4	191154276	7837110	0.041	0.2334
chr5	180915260	6915631	0.0382	0.2195
chr6	171115067	9368743	0.0548	0.3308
chr7	159138663	12357995	0.0777	0.373

chr8	146364022	8313933	0.0568	0.4019
chr9	141213431	5087408	0.036	0.2896
chr10	135534747	10116585	0.0746	0.372
chr11	135006516	5850784	0.0433	0.3384
chr12	133851895	5820662	0.0435	0.24
chr13	115169878	2760202	0.024	0.1717
chr14	107349540	4713782	0.0439	0.2469
chr15	102531392	2404419	0.0235	0.1777
chr16	90354753	4089134	0.0453	0.2461
chr17	81195210	2403673	0.0296	0.2121
chr18	78077248	3352434	0.0429	0.4282
chr19	59128983	2435135	0.0412	0.2952
chr20	63025520	3369101	0.0535	0.2629
chr21	48129895	1628045	0.0338	0.2198
chr22	51304566	1090416	0.0213	0.1616
chrMT	16571	15736	0.9496	1.1128
chrX	155270560	6040425	0.0389	0.2409
chrY	59373566	269419	0.0045	0.0953

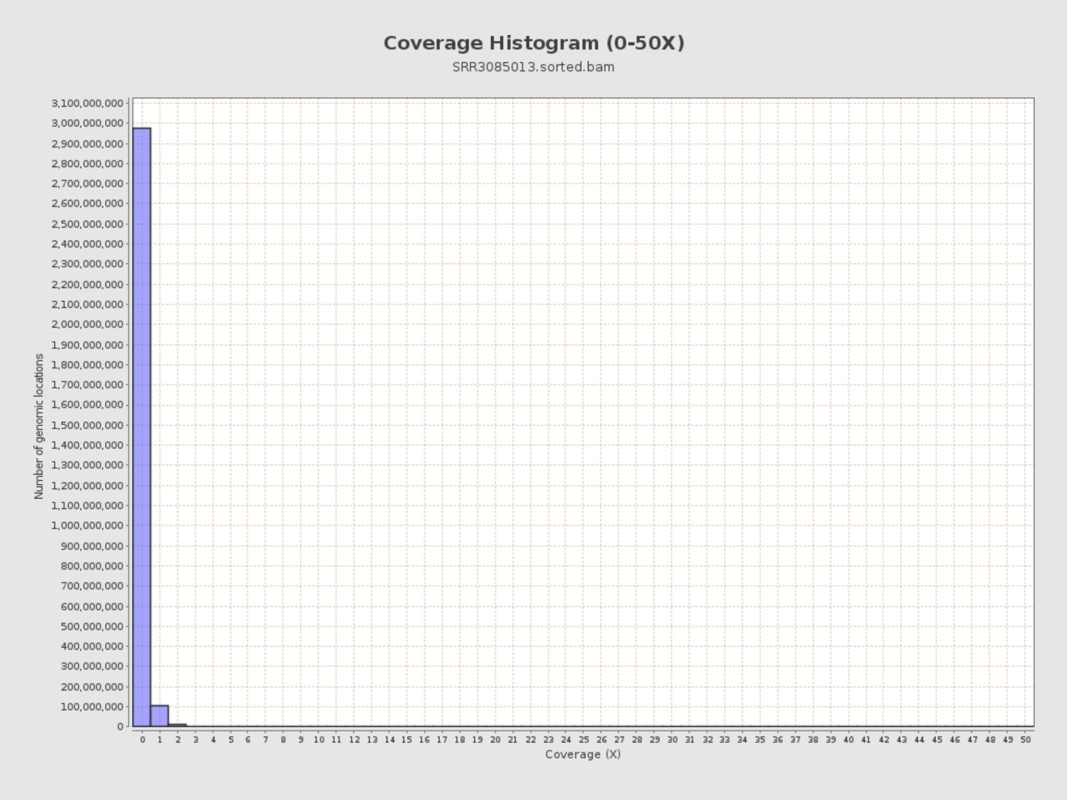
3. Results : Coverage across reference



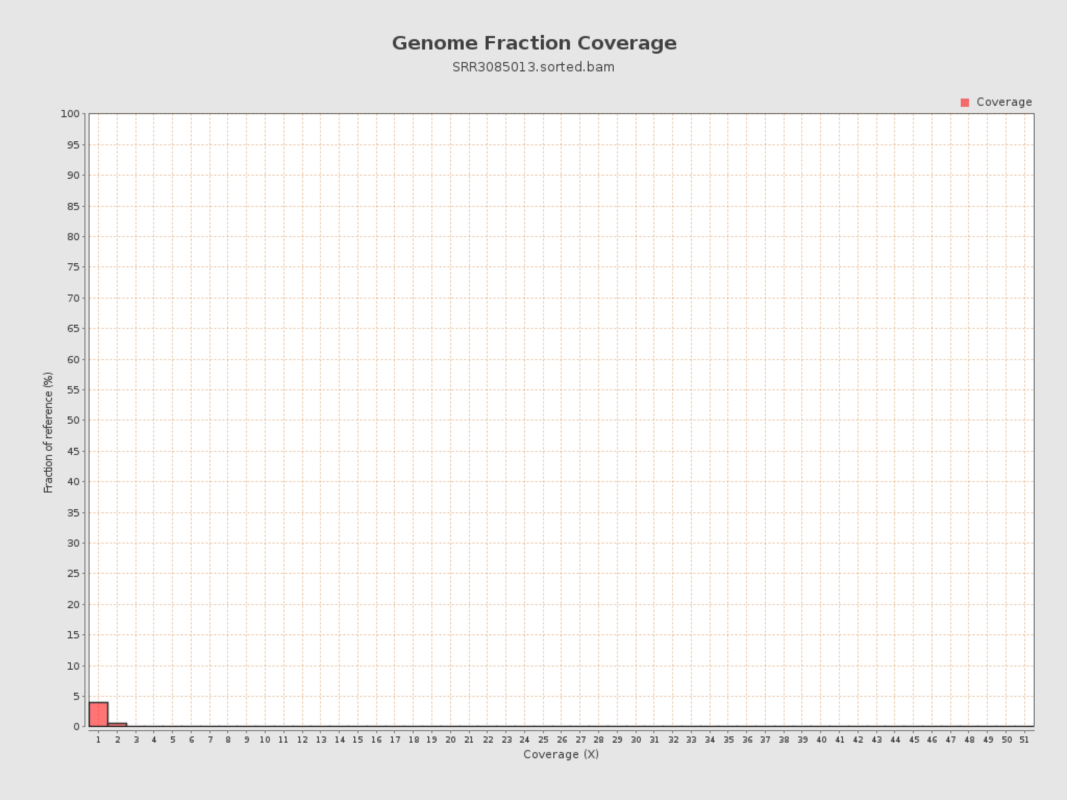
4. Results : Coverage Histogram



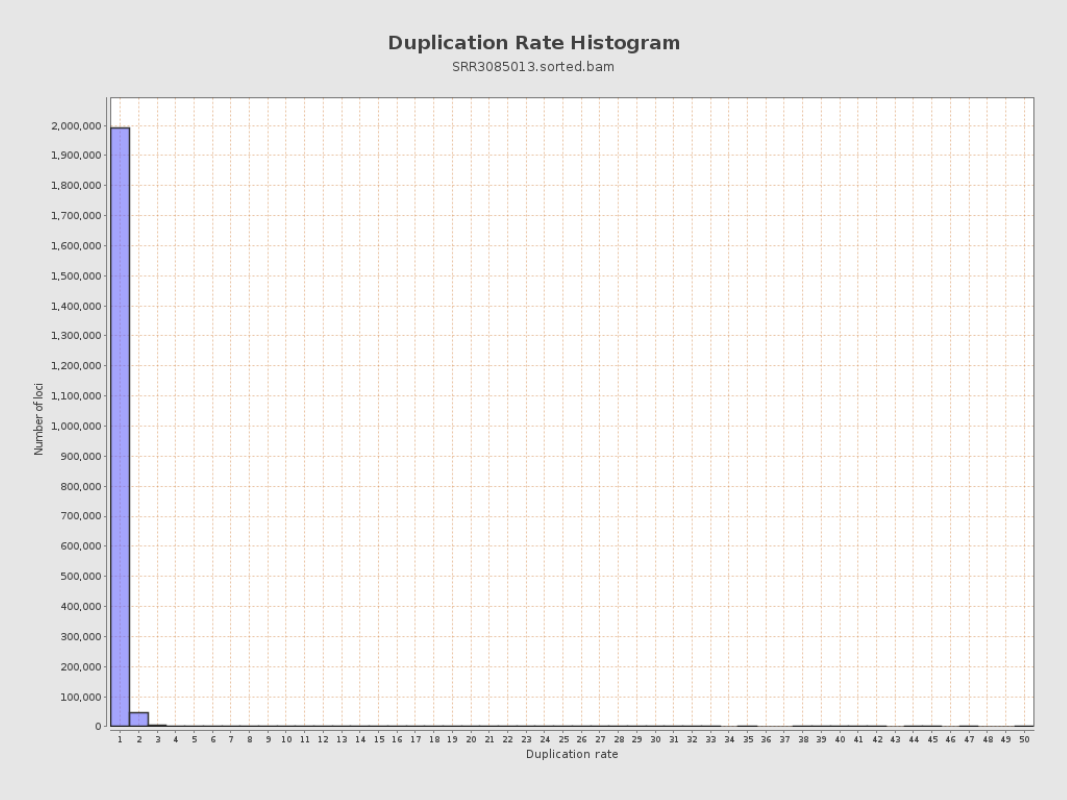
5. Results : Coverage Histogram (0-50X)



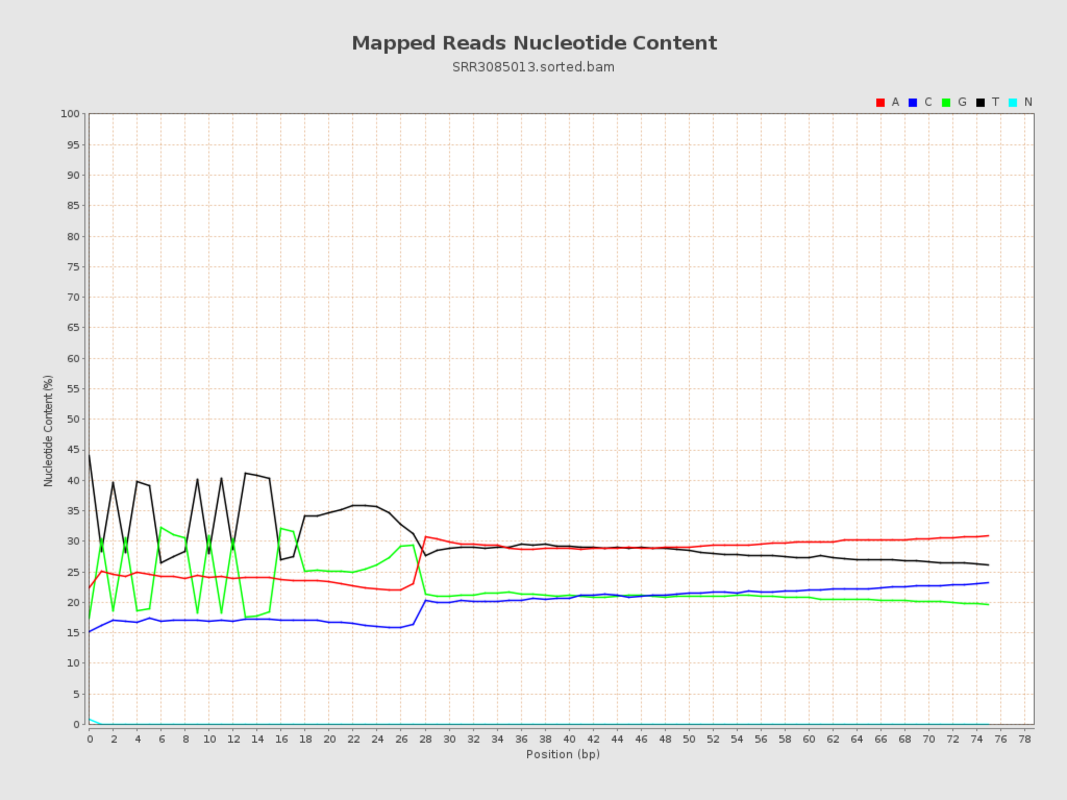
6. Results : Genome Fraction Coverage



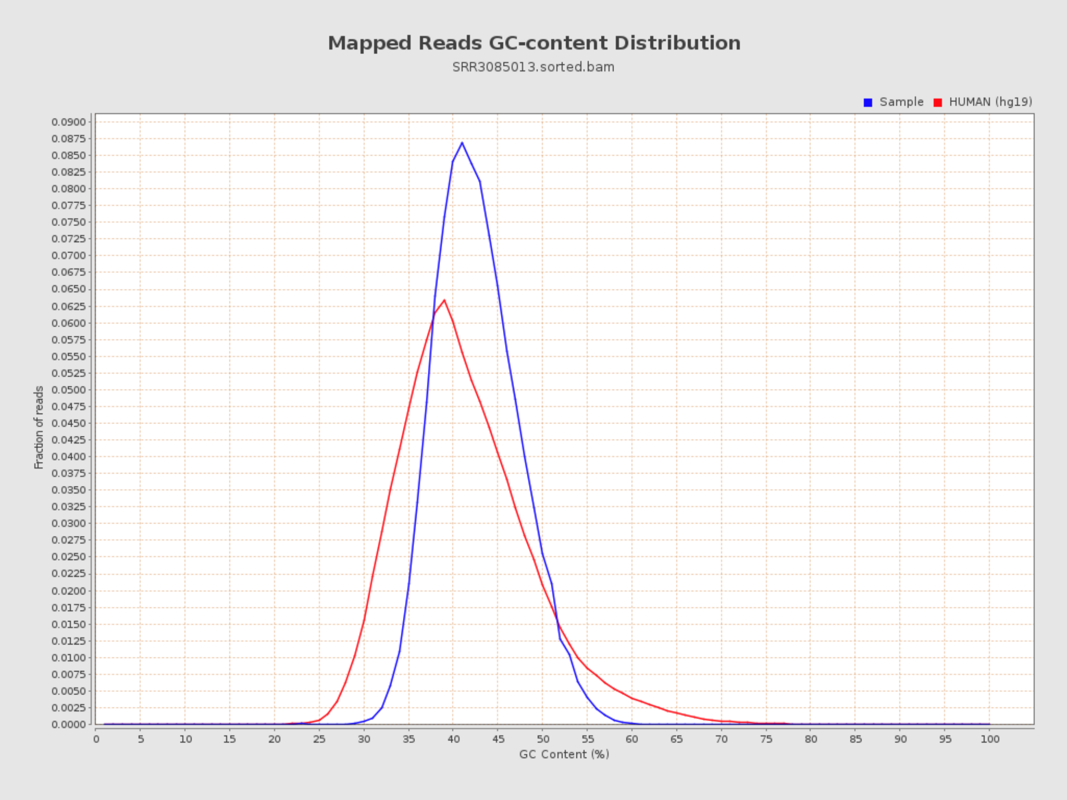
7. Results : Duplication Rate Histogram



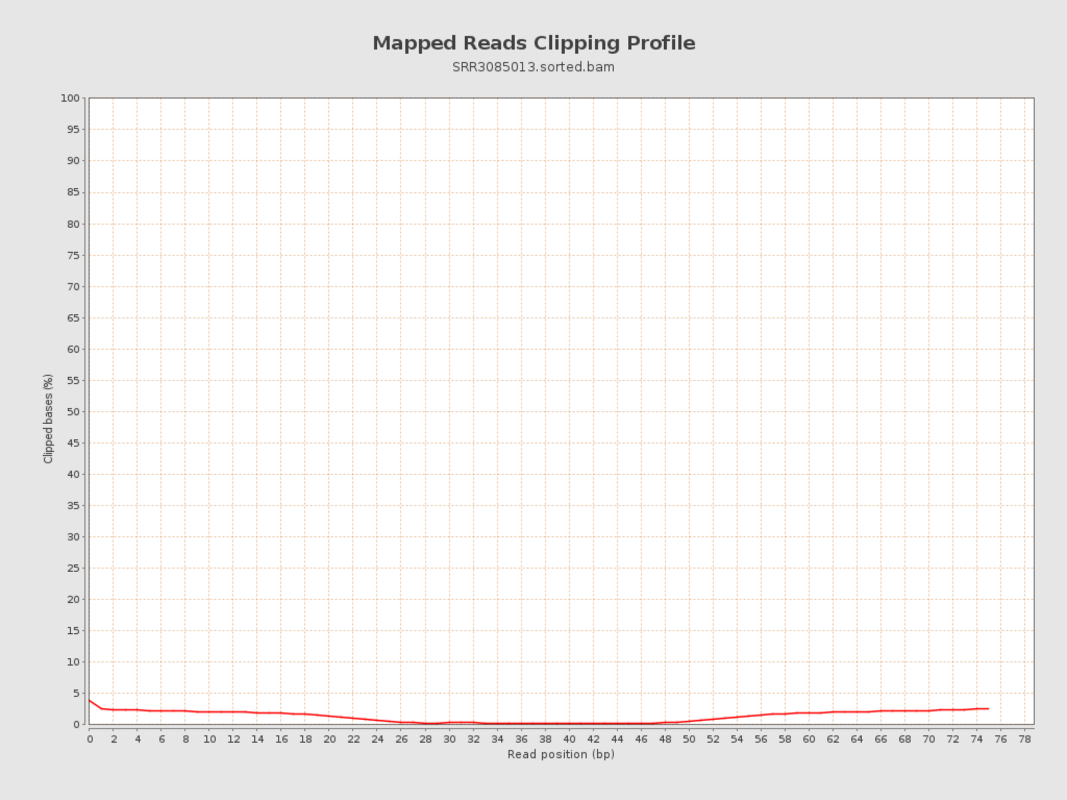
8. Results : Mapped Reads Nucleotide Content



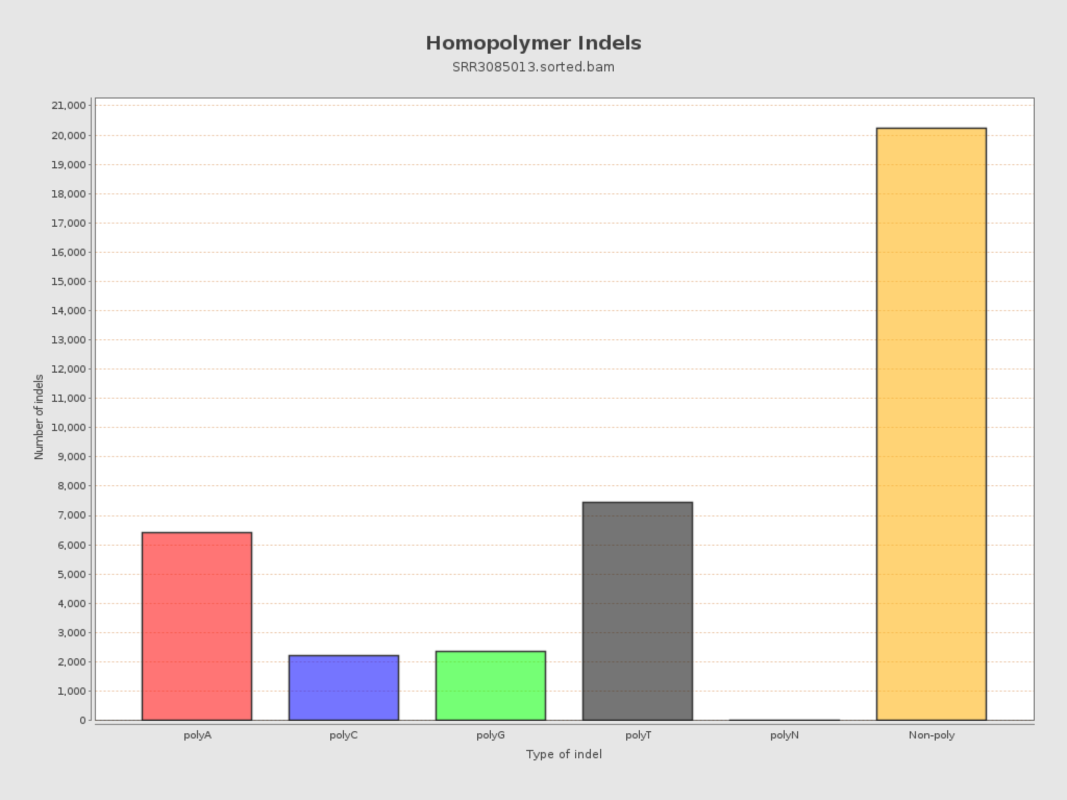
9. Results : Mapped Reads GC-content Distribution



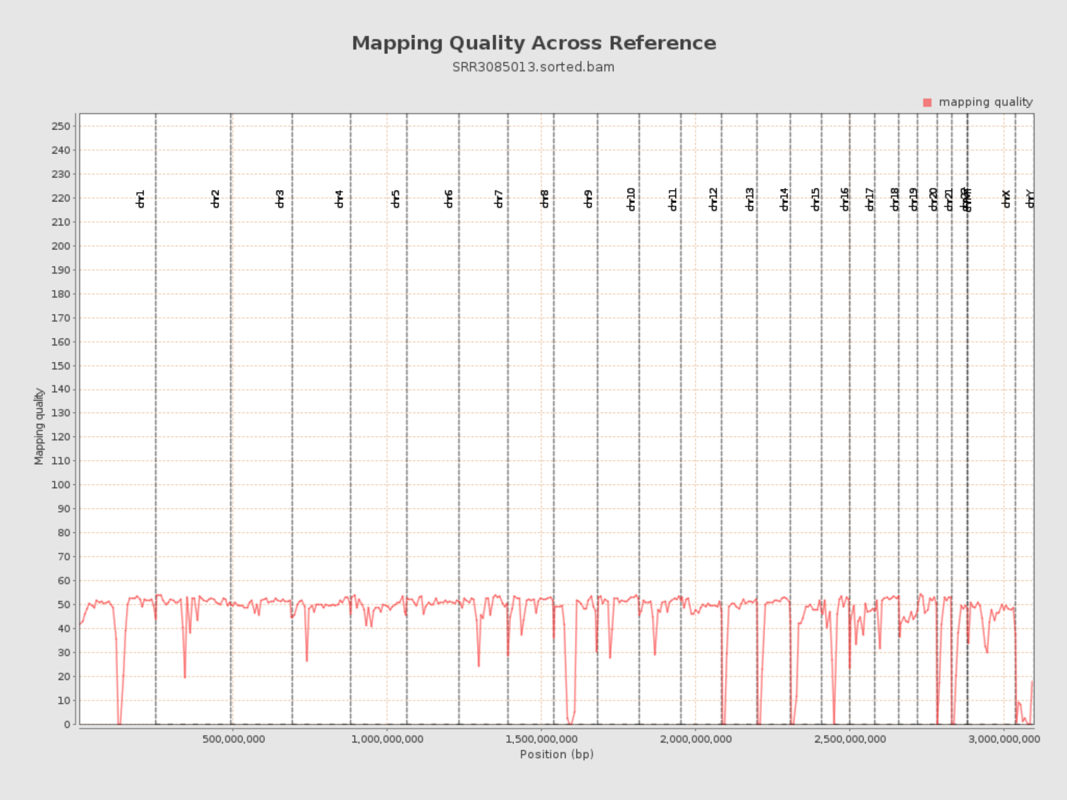
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram