Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 09:50:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090206.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_SRR090206 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090206.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 09:50:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090206.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,496,175
Mapped reads	22,726,894 / 92.78%
Unmapped reads	1,769,281 / 7.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	167,909 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	4,154,263 / 16.96%
Duplication rate	12.05%
Clipped reads	10,662,580 / 43.53%

2.2. ACGT Content

Number/percentage of A's	396,994,477 / 26.43%
Number/percentage of C's	278,666,814 / 18.55%
Number/percentage of T's	470,321,829 / 31.31%
Number/percentage of G's	355,705,000 / 23.68%
Number/percentage of N's	533,032 / 0.04%
GC Percentage	42.23%

2.3. Coverage

Mean	0.4854

Standard Deviation	3.5046

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

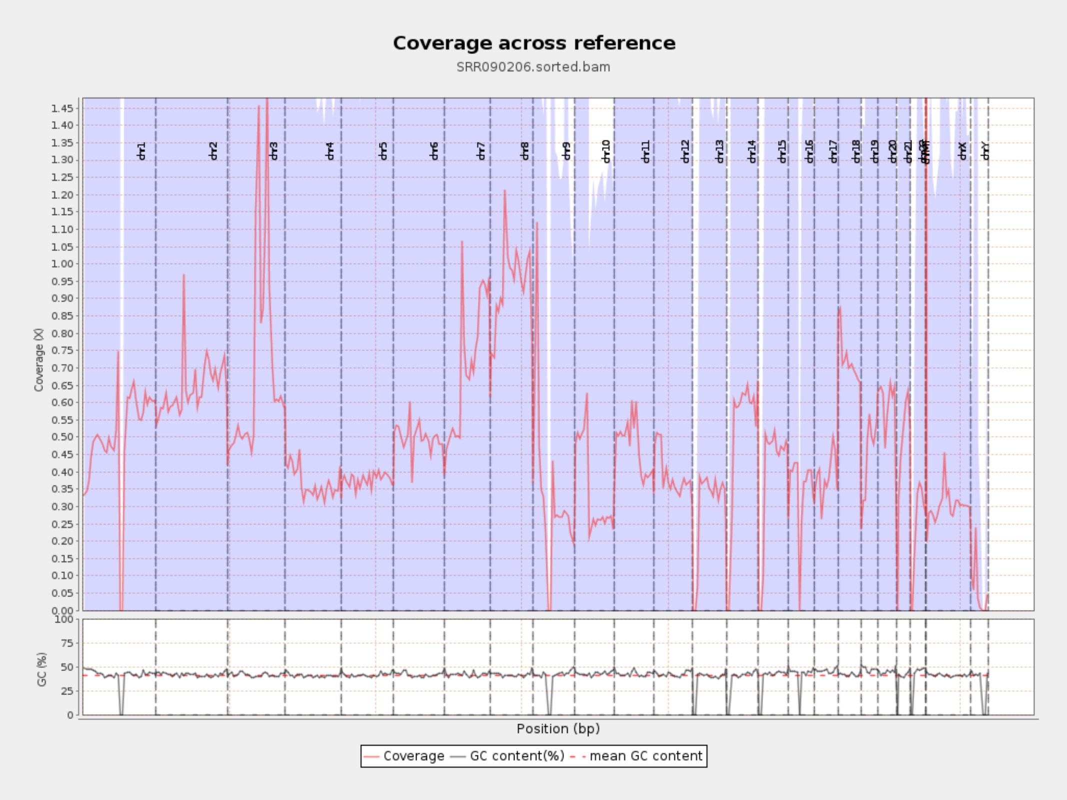
General error rate	0.59%
Mismatches	8,688,070
Insertions	96,452
Mapped reads with at least one insertion	0.42%
Deletions	312,566
Mapped reads with at least one deletion	1.36%
Homopolymer indels	47.55%

2.6. Chromosome stats

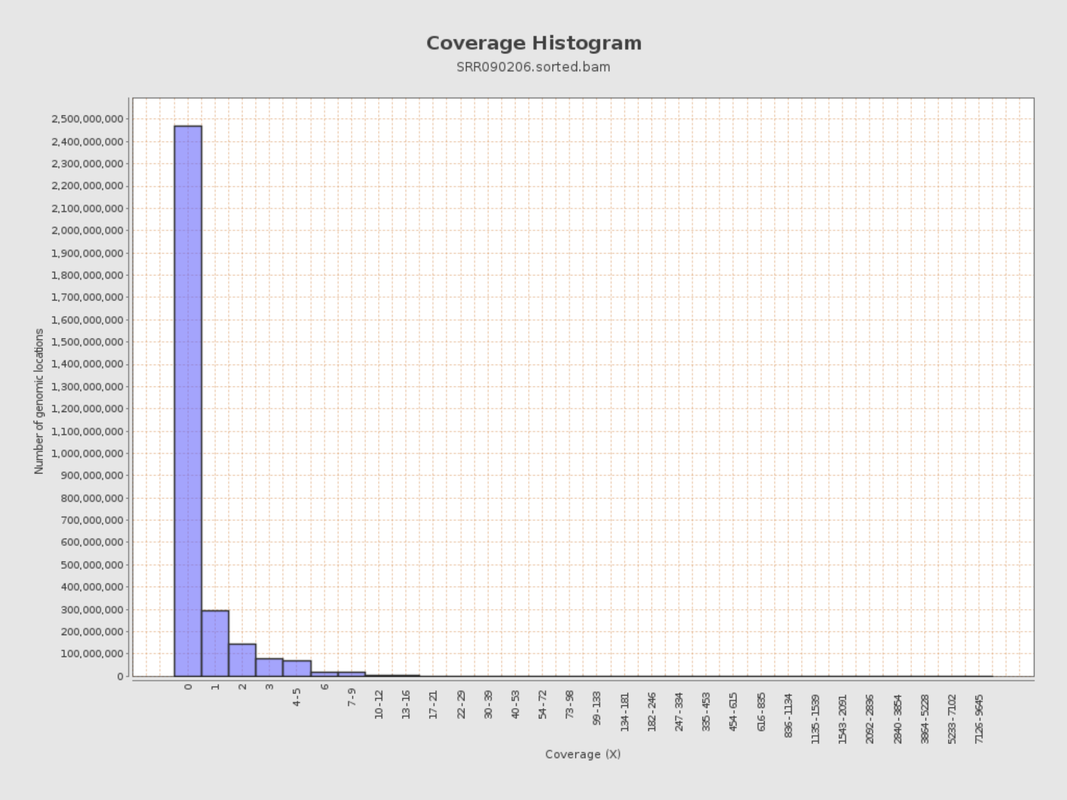
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	124051405	0.4977	6.4776
chr2	243199373	156833390	0.6449	3.7951
chr3	198022430	138108935	0.6974	1.7245
chr4	191154276	70422879	0.3684	1.451
chr5	180915260	68380227	0.378	1.2353
chr6	171115067	85379687	0.499	1.8651
chr7	159138663	112385093	0.7062	6.6784

chr8	146364022	137805825	0.9415	6.1863
chr9	141213431	47047018	0.3332	3.0619
chr10	135534747	46906113	0.3461	2.9174
chr11	135006516	63610354	0.4712	3.0442
chr12	133851895	52770342	0.3942	1.3498
chr13	115169878	34375178	0.2985	1.0273
chr14	107349540	54049948	0.5035	1.466
chr15	102531392	39412034	0.3844	1.2425
chr16	90354753	30856058	0.3415	1.3276
chr17	81195210	31841183	0.3922	1.6812
chr18	78077248	56544296	0.7242	5.3452
chr19	59128983	26973482	0.4562	3.5724
chr20	63025520	37638867	0.5972	1.7987
chr21	48129895	22305237	0.4634	1.6865
chr22	51304566	12304099	0.2398	0.9214
chrMT	16571	2366984	142.8389	66.5083
chrX	155270560	46857112	0.3018	1.4709
chrY	59373566	3546667	0.0597	2.6466

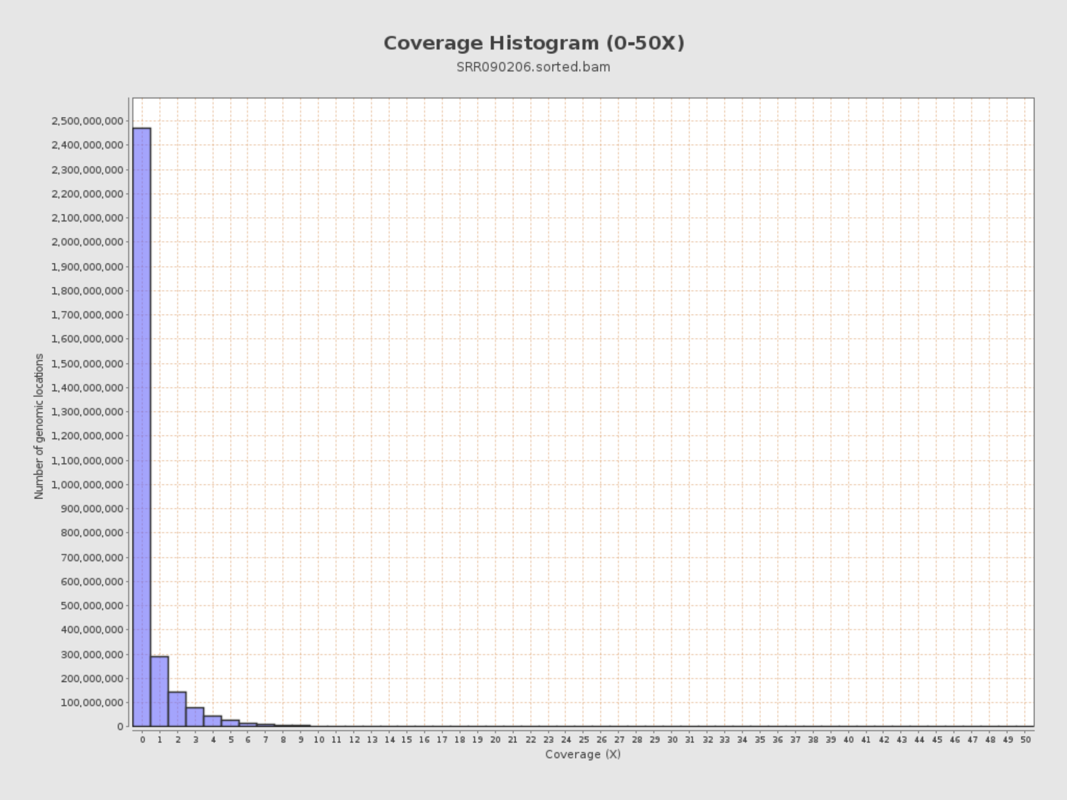
3. Results : Coverage across reference



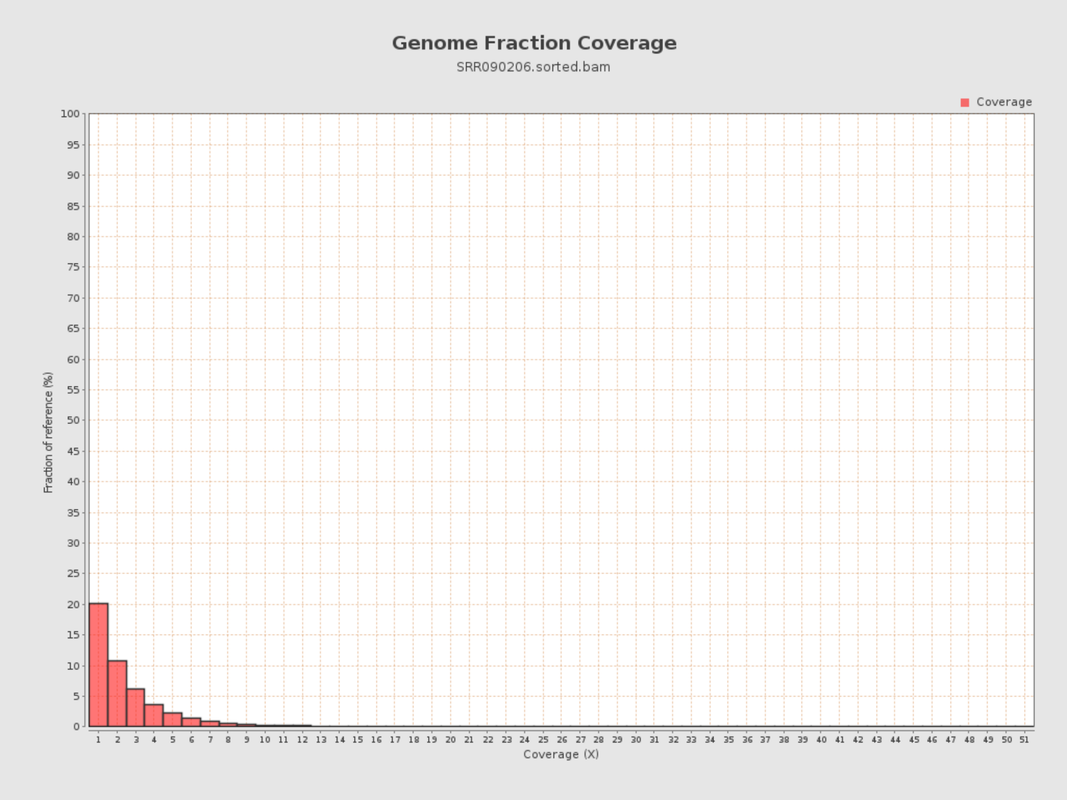
4. Results : Coverage Histogram



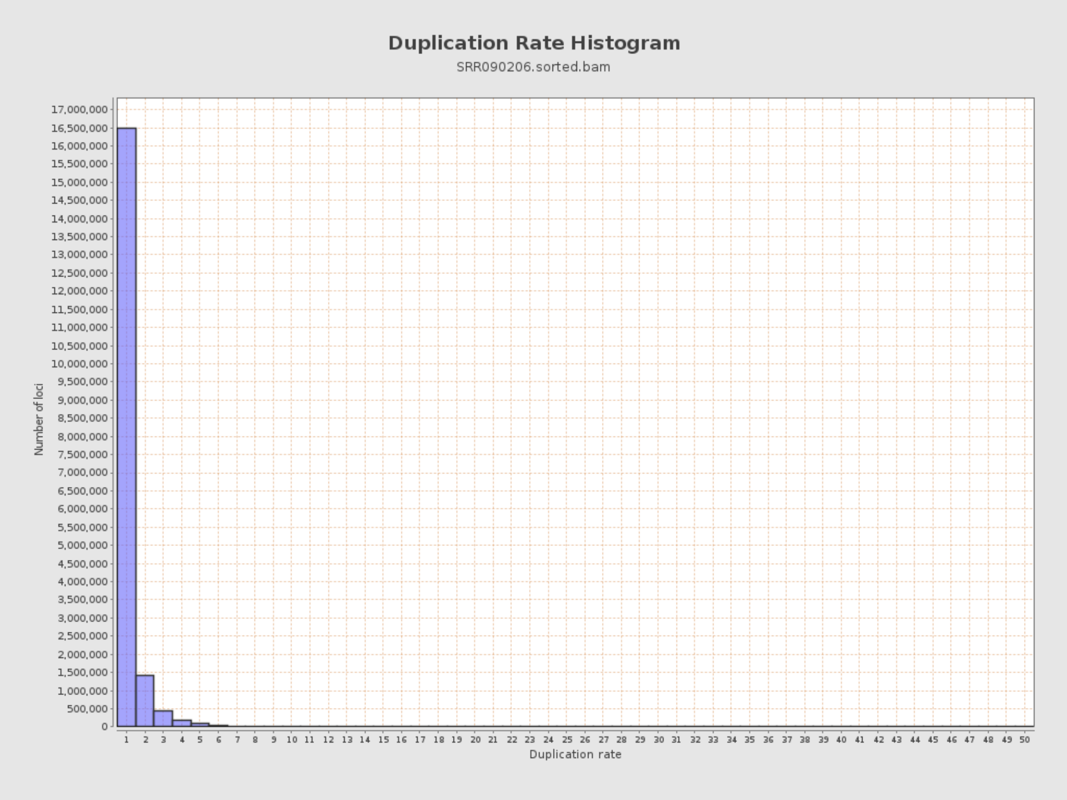
5. Results : Coverage Histogram (0-50X)



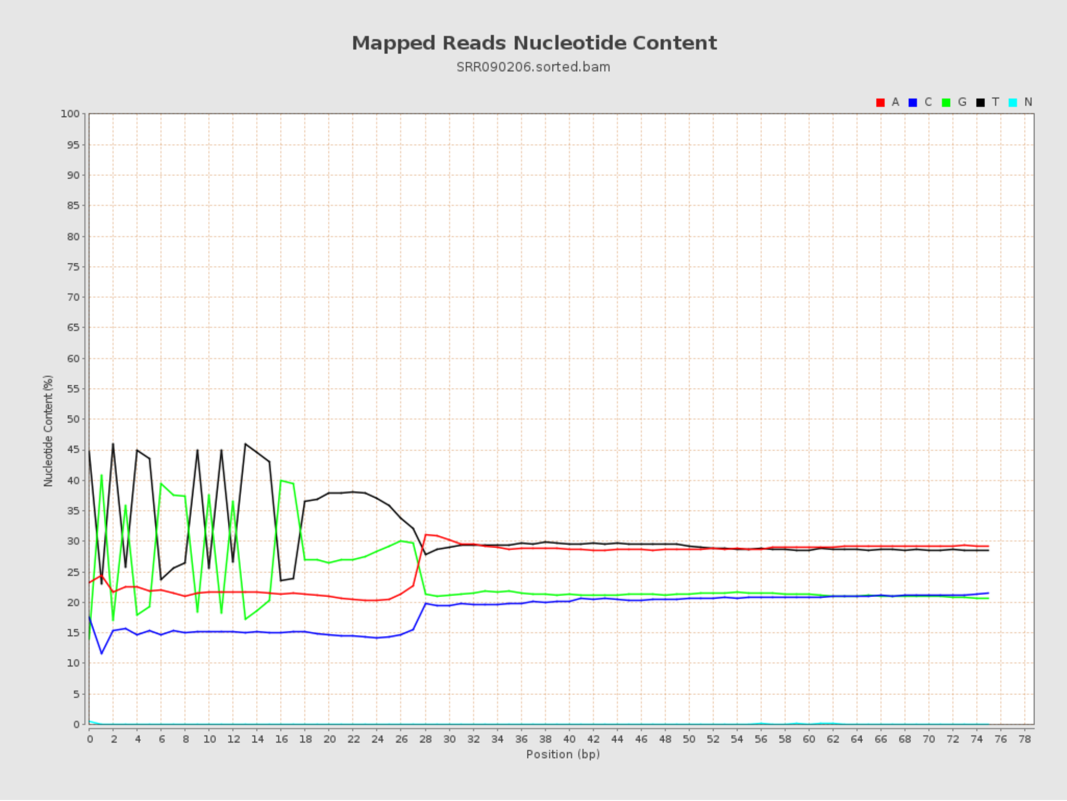
6. Results : Genome Fraction Coverage



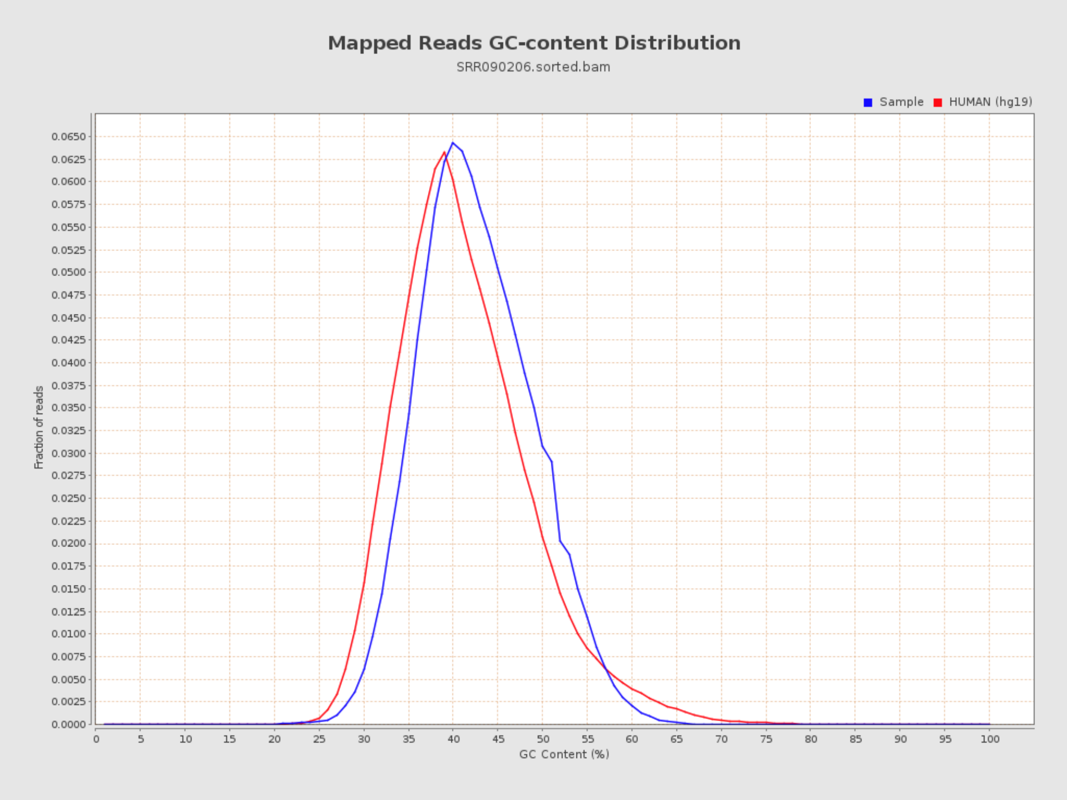
7. Results : Duplication Rate Histogram



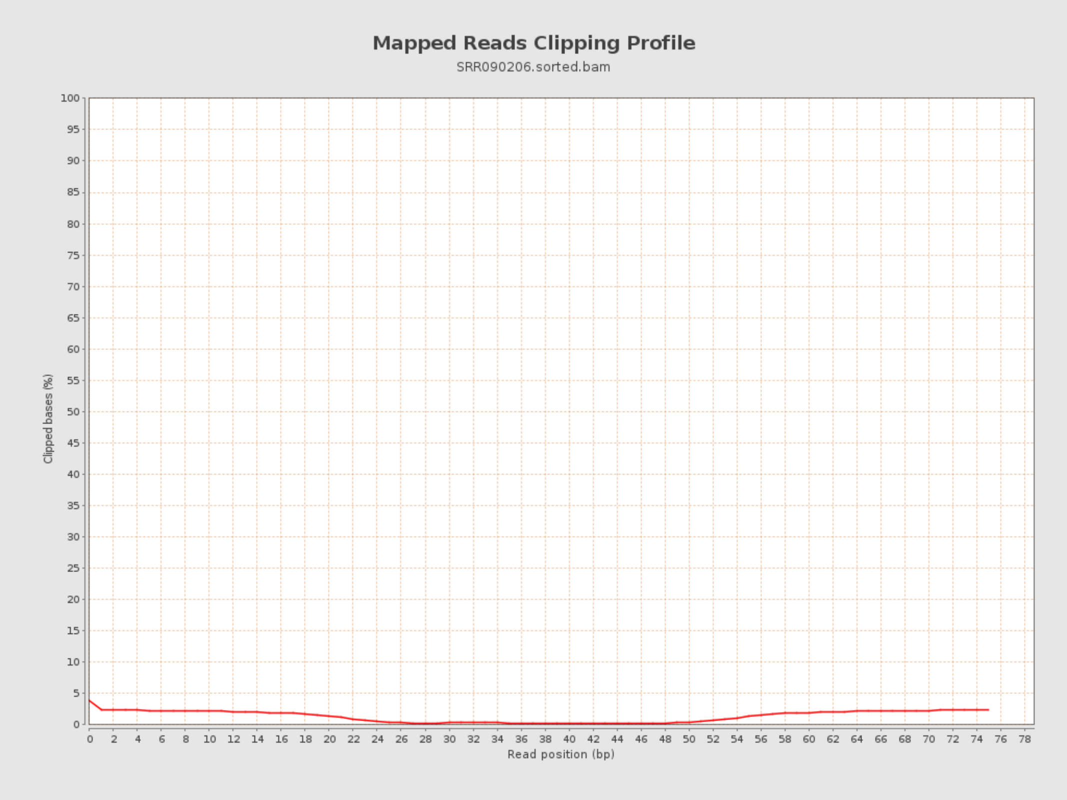
8. Results : Mapped Reads Nucleotide Content



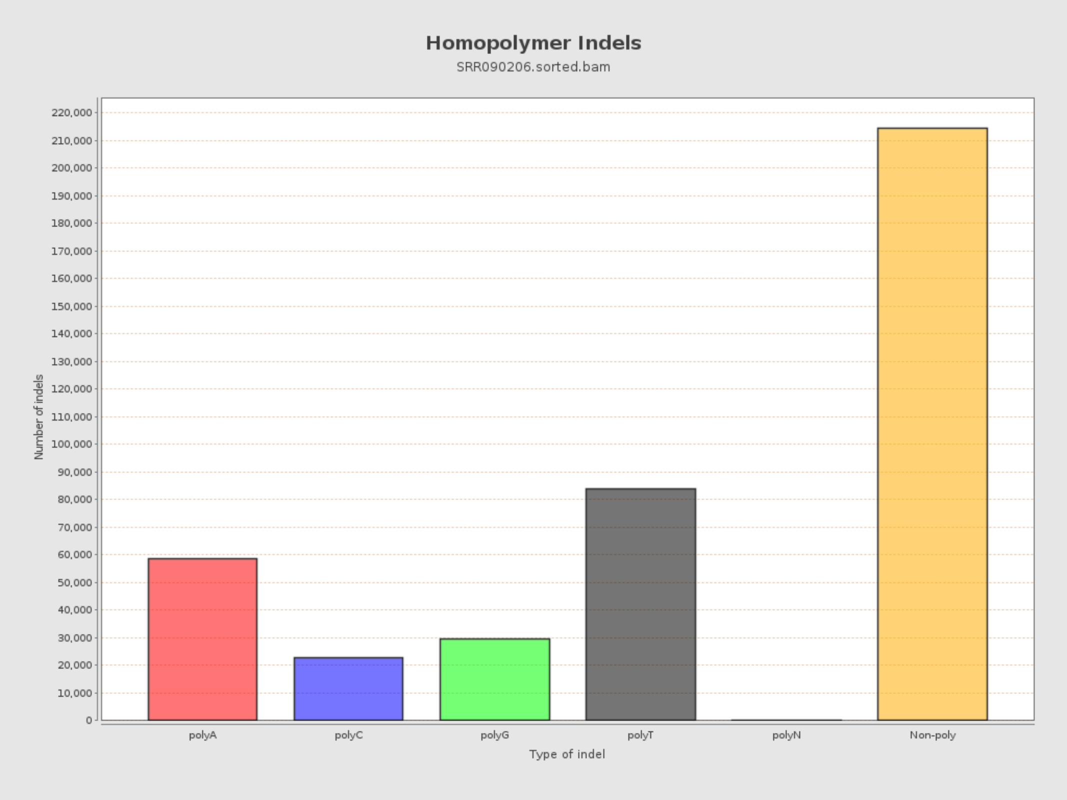
9. Results : Mapped Reads GC-content Distribution



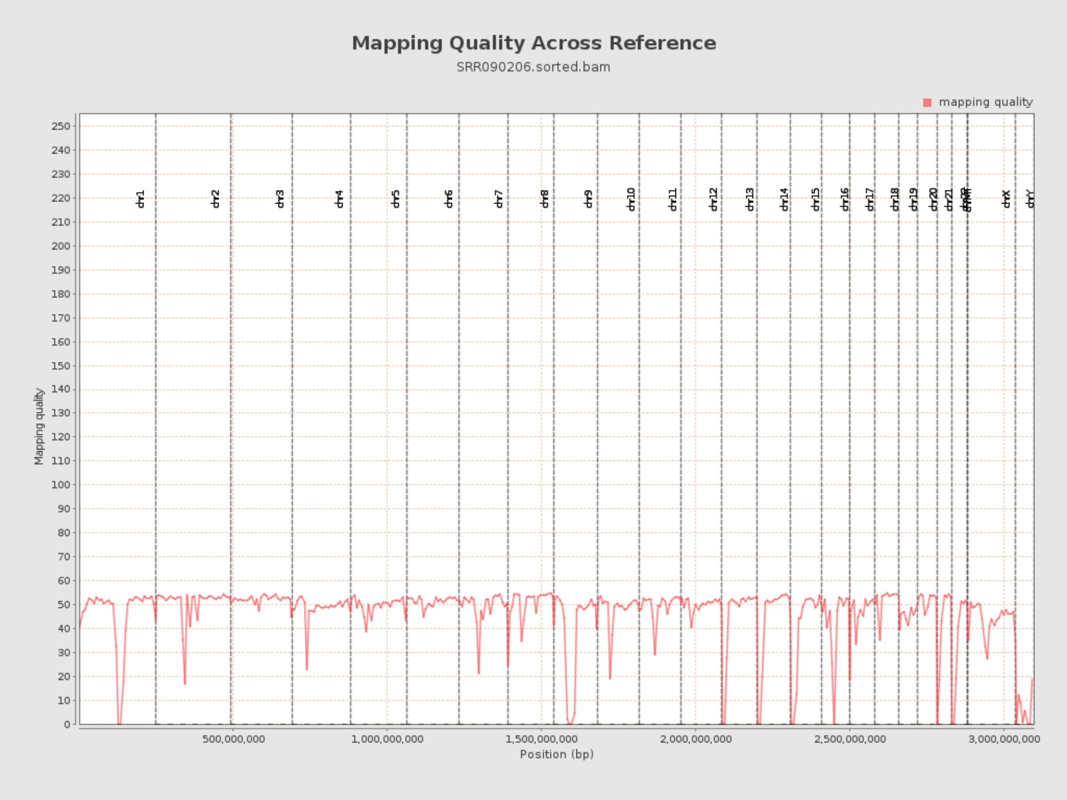
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram