Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 07:25:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090135.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_SRR090135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 07:25:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,754,983
Mapped reads	10,148,856 / 86.34%
Unmapped reads	1,606,127 / 13.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	86,960 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,415,979 / 12.05%
Duplication rate	10.46%
Clipped reads	7,013,489 / 59.66%

2.2. ACGT Content

Number/percentage of A's	171,610,169 / 28.12%
Number/percentage of C's	114,024,669 / 18.69%
Number/percentage of T's	187,026,071 / 30.65%
Number/percentage of G's	137,127,391 / 22.47%
Number/percentage of N's	385,721 / 0.06%
GC Percentage	41.16%

2.3. Coverage

Mean	0.1972

Standard Deviation	1.5829

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

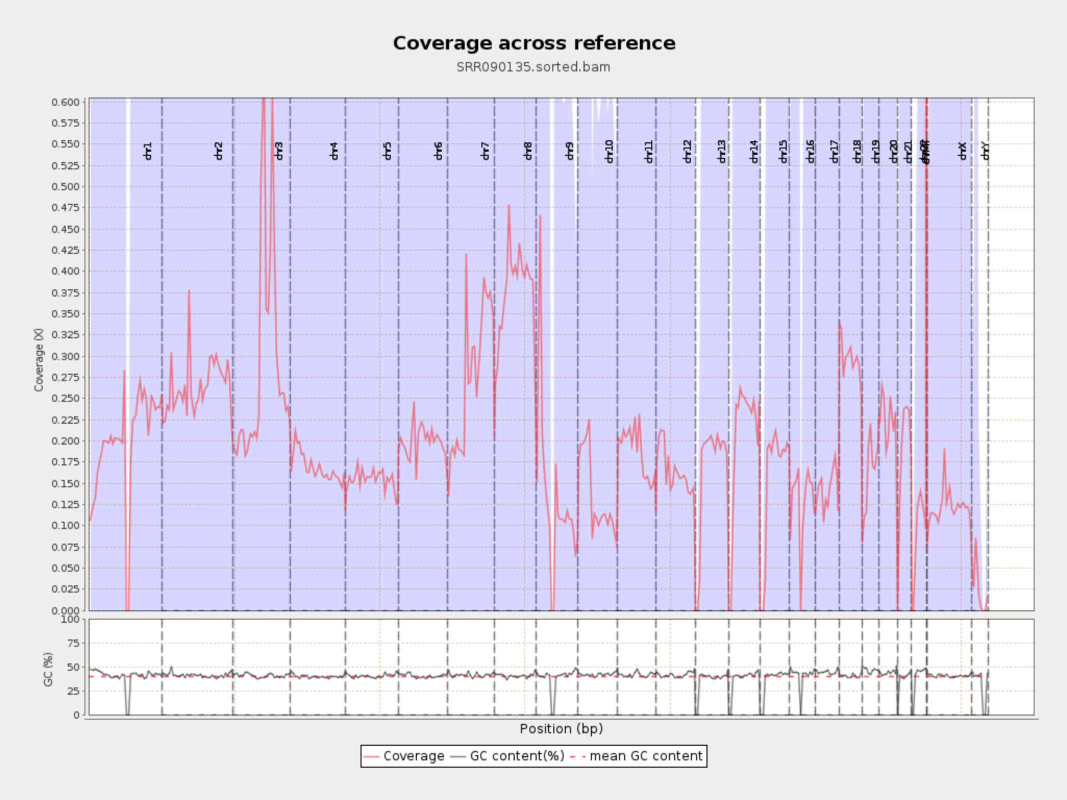
General error rate	0.67%
Mismatches	4,000,487
Insertions	42,422
Mapped reads with at least one insertion	0.41%
Deletions	126,012
Mapped reads with at least one deletion	1.23%
Homopolymer indels	47.33%

2.6. Chromosome stats

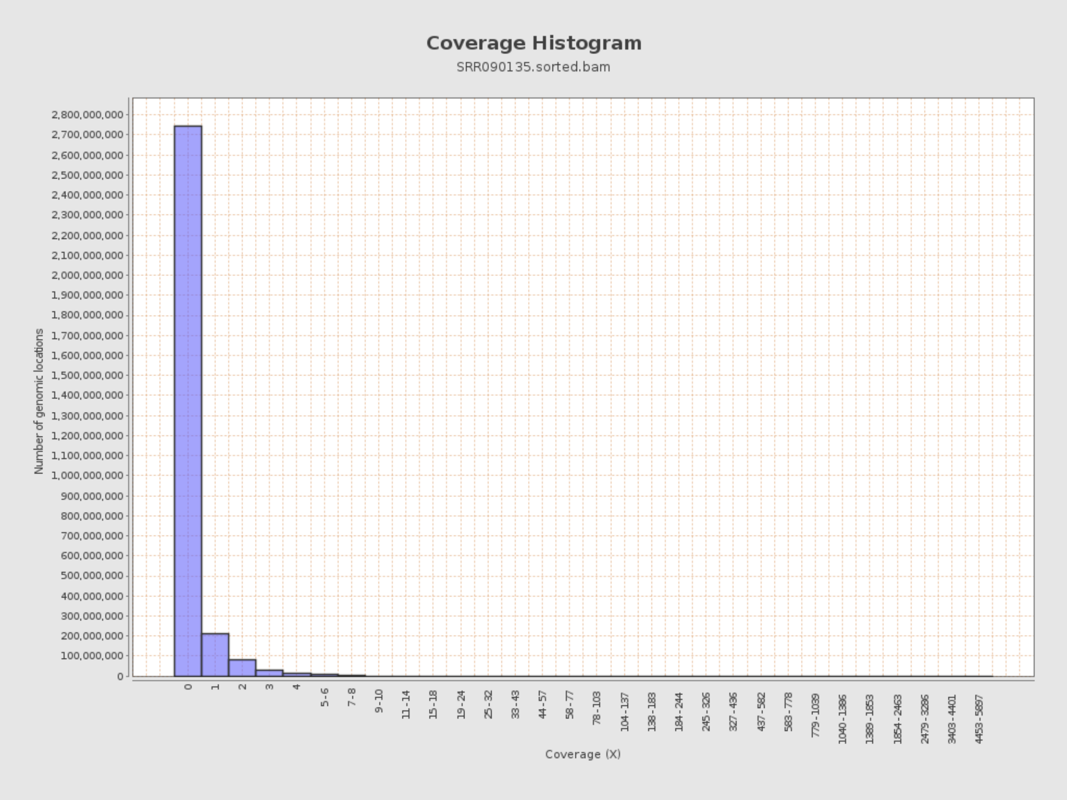
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	49278464	0.1977	2.3289
chr2	243199373	64505582	0.2652	2.3722
chr3	198022430	57497000	0.2904	0.8705
chr4	191154276	32283184	0.1689	0.7293
chr5	180915260	27977529	0.1546	0.6299
chr6	171115067	34180227	0.1997	1.0215
chr7	159138663	44433571	0.2792	2.6235

chr8	146364022	55044948	0.3761	3.6445
chr9	141213431	19238957	0.1362	1.1404
chr10	135534747	18566896	0.137	1.1245
chr11	135006516	25148570	0.1863	1.0652
chr12	133851895	21958175	0.164	0.7625
chr13	115169878	18810616	0.1633	0.6242
chr14	107349540	21537178	0.2006	0.7963
chr15	102531392	15787270	0.154	0.7496
chr16	90354753	11654939	0.129	0.6509
chr17	81195210	11522804	0.1419	0.7166
chr18	78077248	23256579	0.2979	1.9741
chr19	59128983	9783538	0.1655	1.5552
chr20	63025520	14118979	0.224	0.8051
chr21	48129895	8940398	0.1858	0.7225
chr22	51304566	4529607	0.0883	0.4408
chrMT	16571	121227	7.3156	5.3609
chrX	155270560	18845505	0.1214	0.7352
chrY	59373566	1361167	0.0229	0.7616

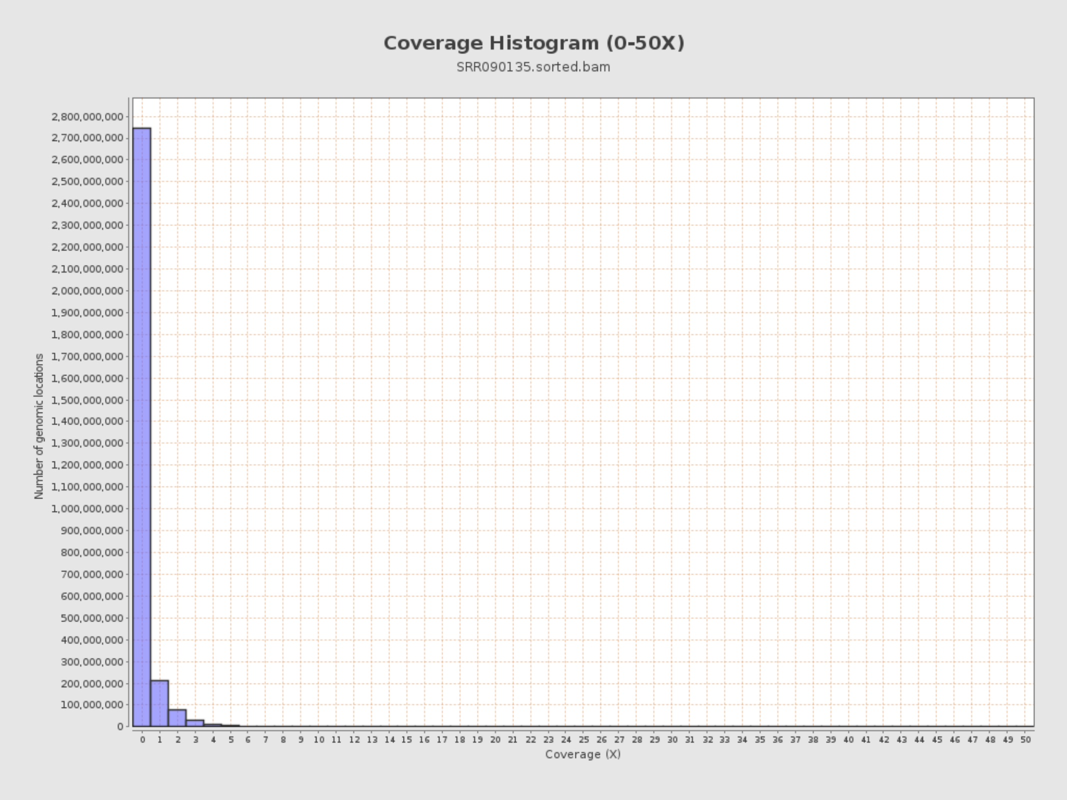
3. Results : Coverage across reference



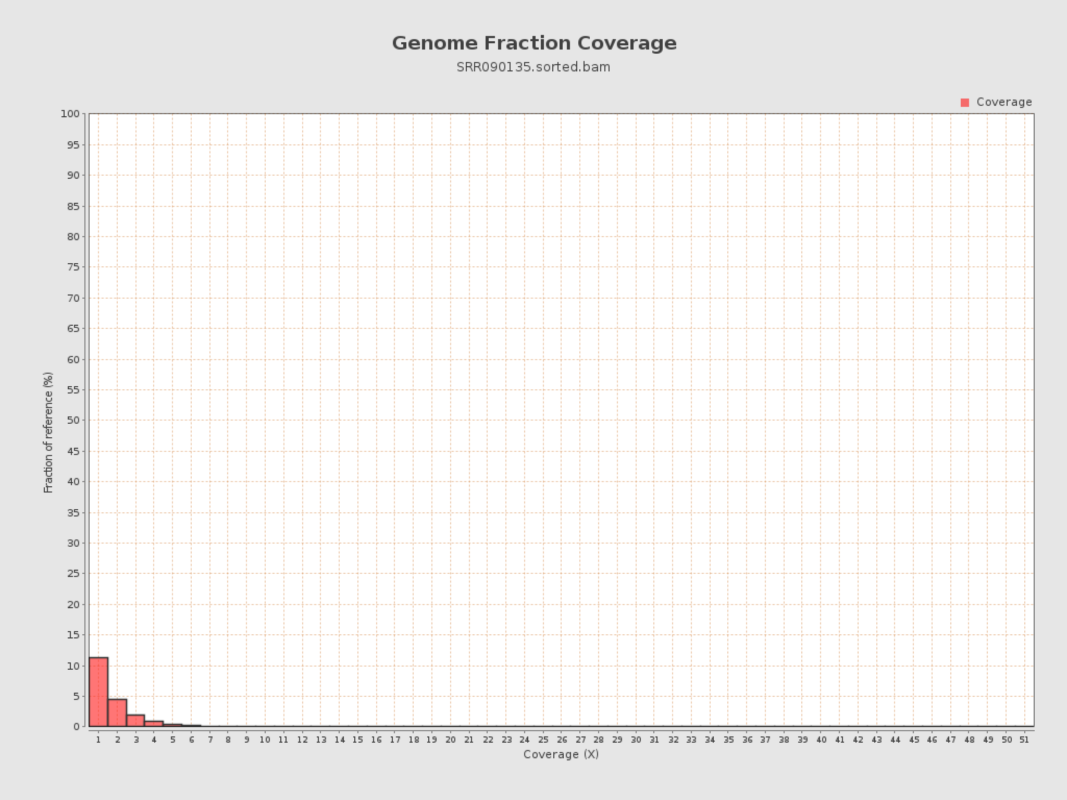
4. Results : Coverage Histogram



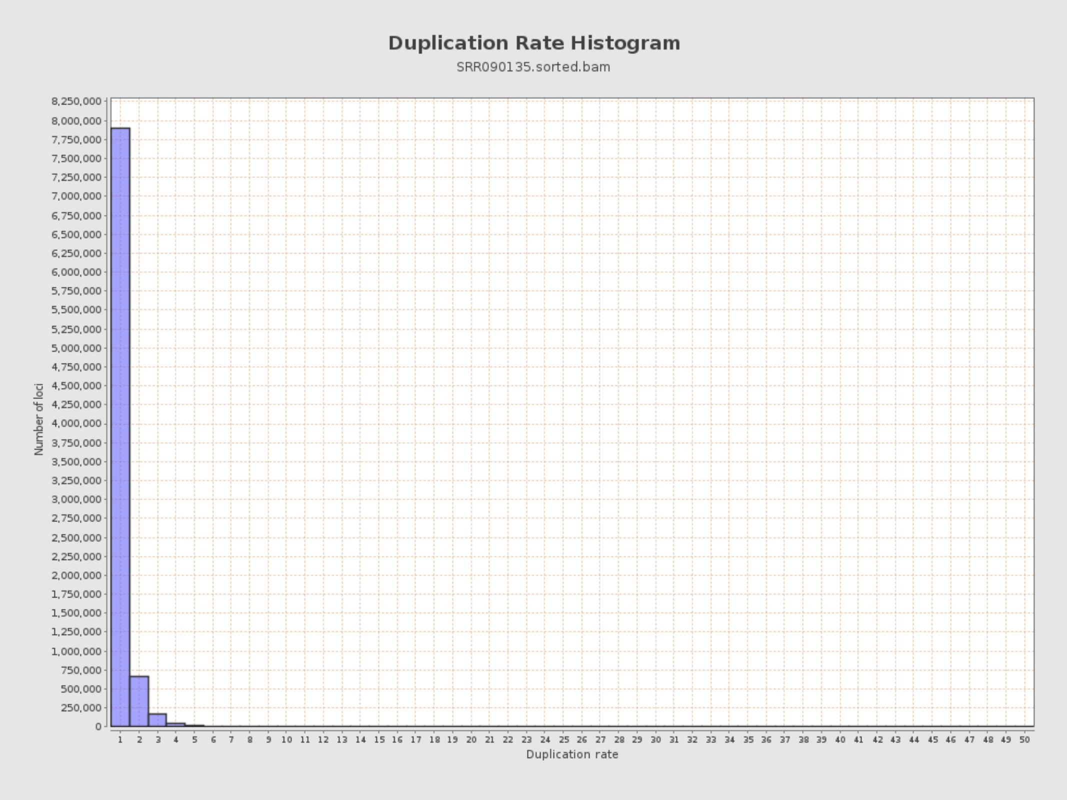
5. Results : Coverage Histogram (0-50X)



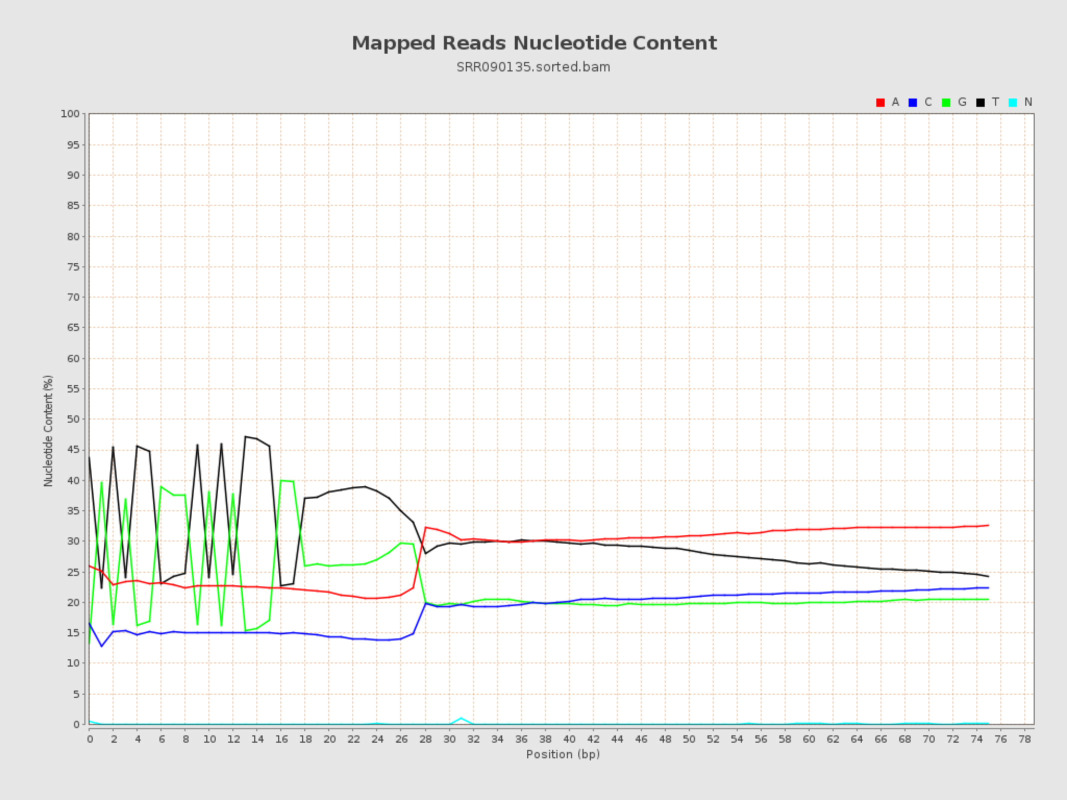
6. Results : Genome Fraction Coverage



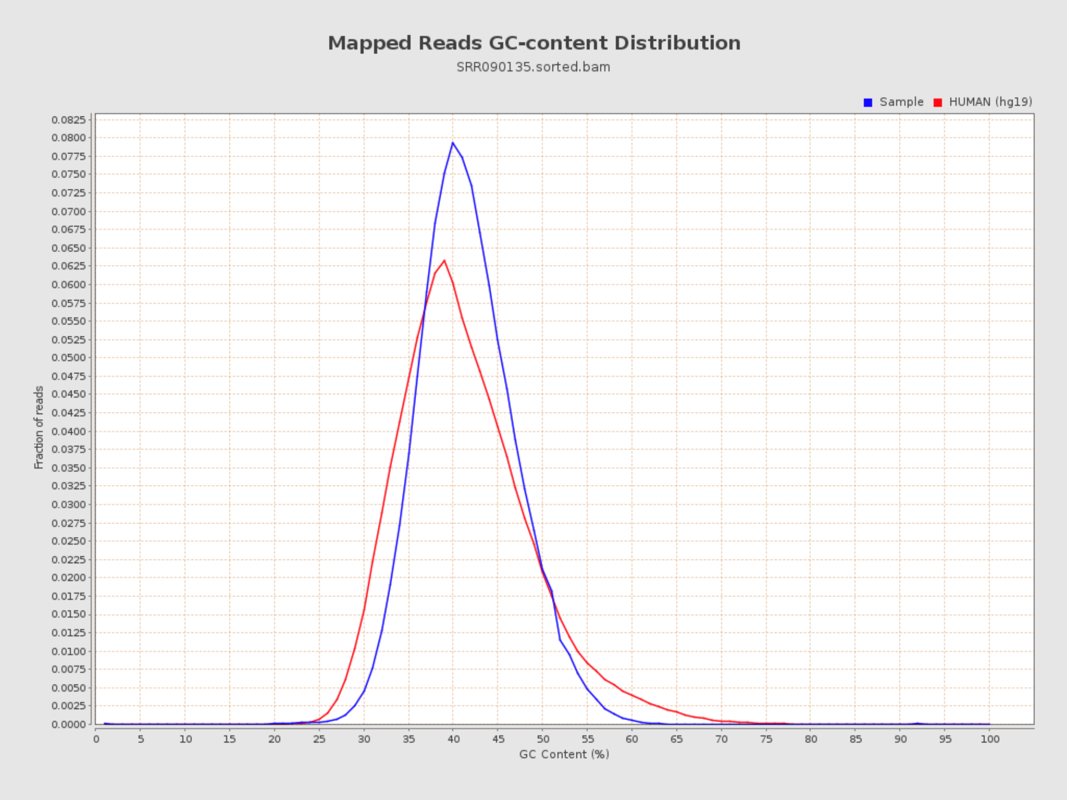
7. Results : Duplication Rate Histogram



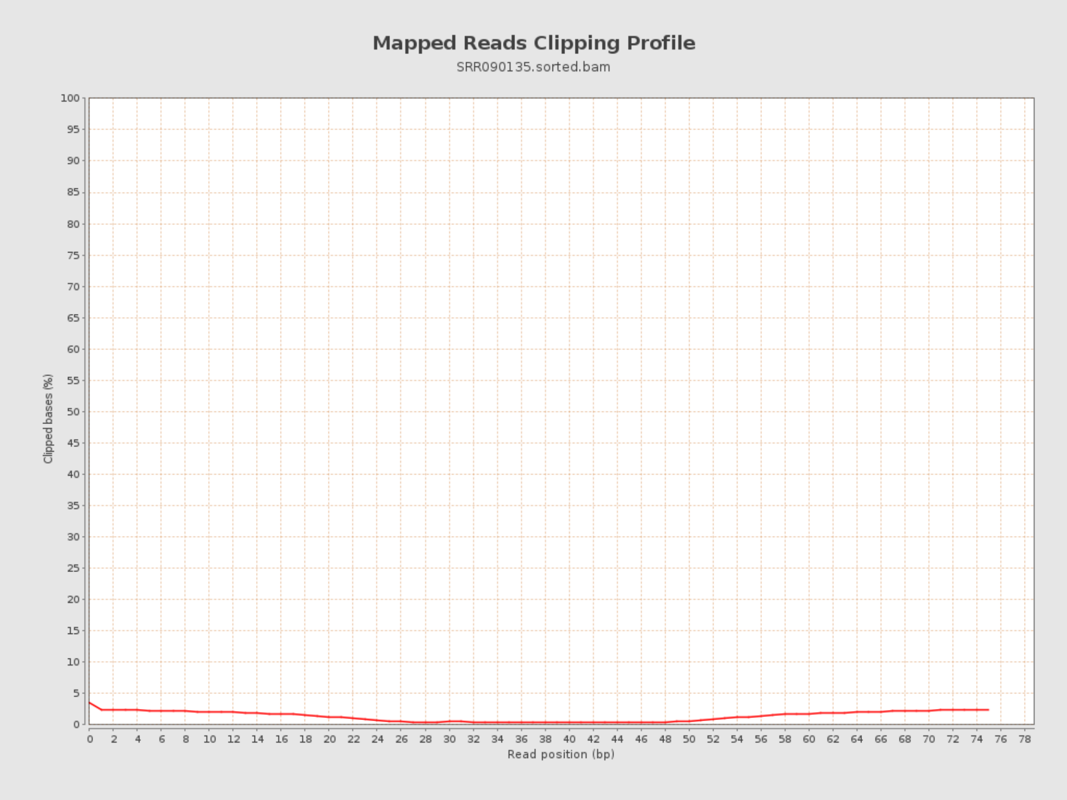
8. Results : Mapped Reads Nucleotide Content



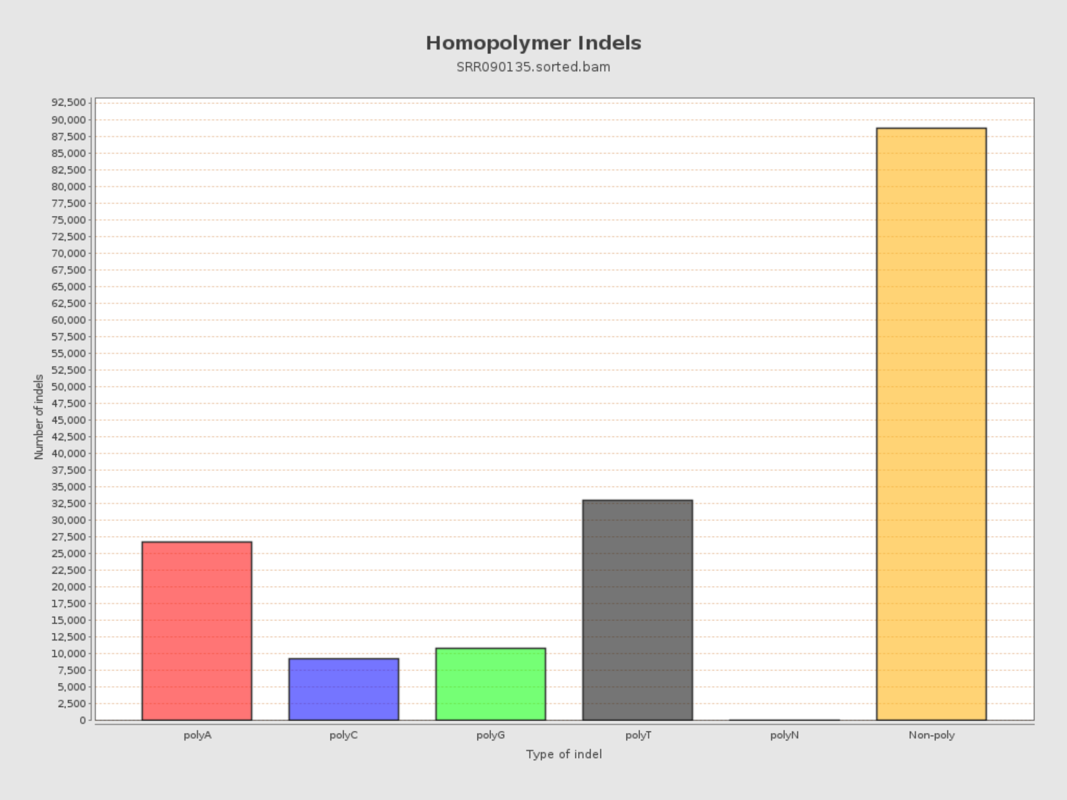
9. Results : Mapped Reads GC-content Distribution



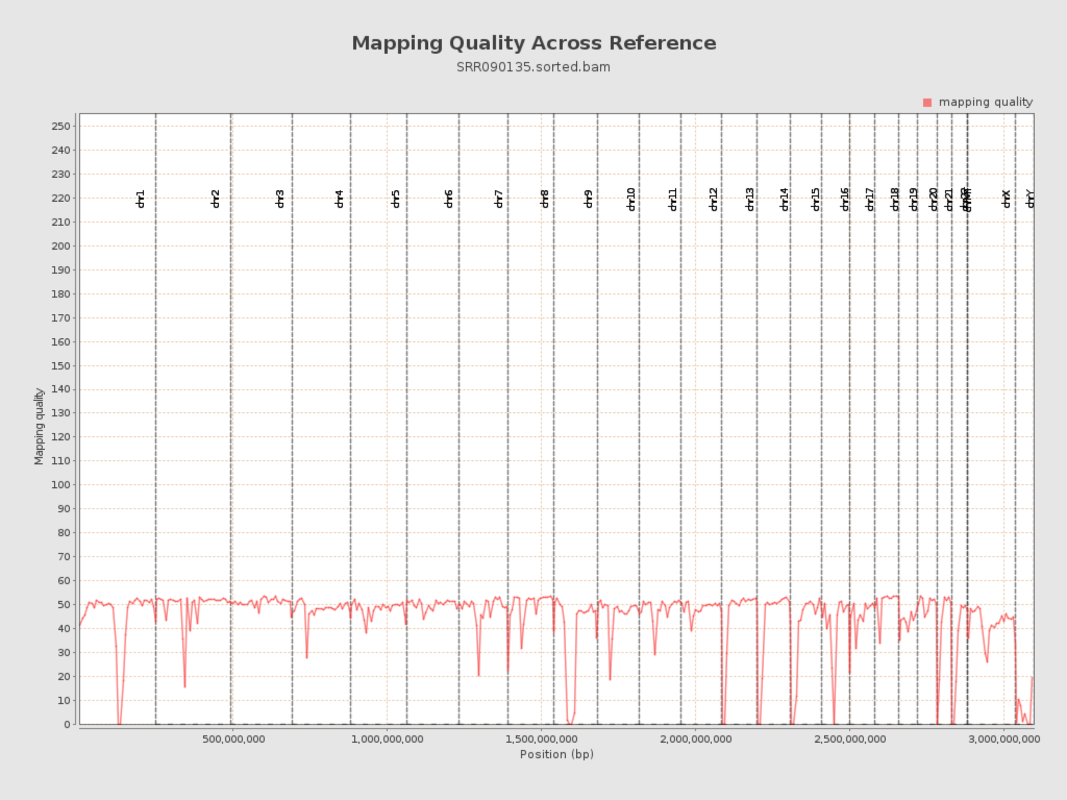
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram