Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 08:03:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090144.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_SRR090144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 08:03:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,593,939
Mapped reads	24,640,873 / 89.3%
Unmapped reads	2,953,066 / 10.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	176,720 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	2,731,849 / 9.9%
Duplication rate	7.4%
Clipped reads	11,662,749 / 42.27%

2.2. ACGT Content

Number/percentage of A's	454,367,785 / 27.83%
Number/percentage of C's	306,057,278 / 18.74%
Number/percentage of T's	503,402,471 / 30.83%
Number/percentage of G's	368,049,141 / 22.54%
Number/percentage of N's	967,359 / 0.06%
GC Percentage	41.28%

2.3. Coverage

Mean	0.5277

Standard Deviation	4.5239

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

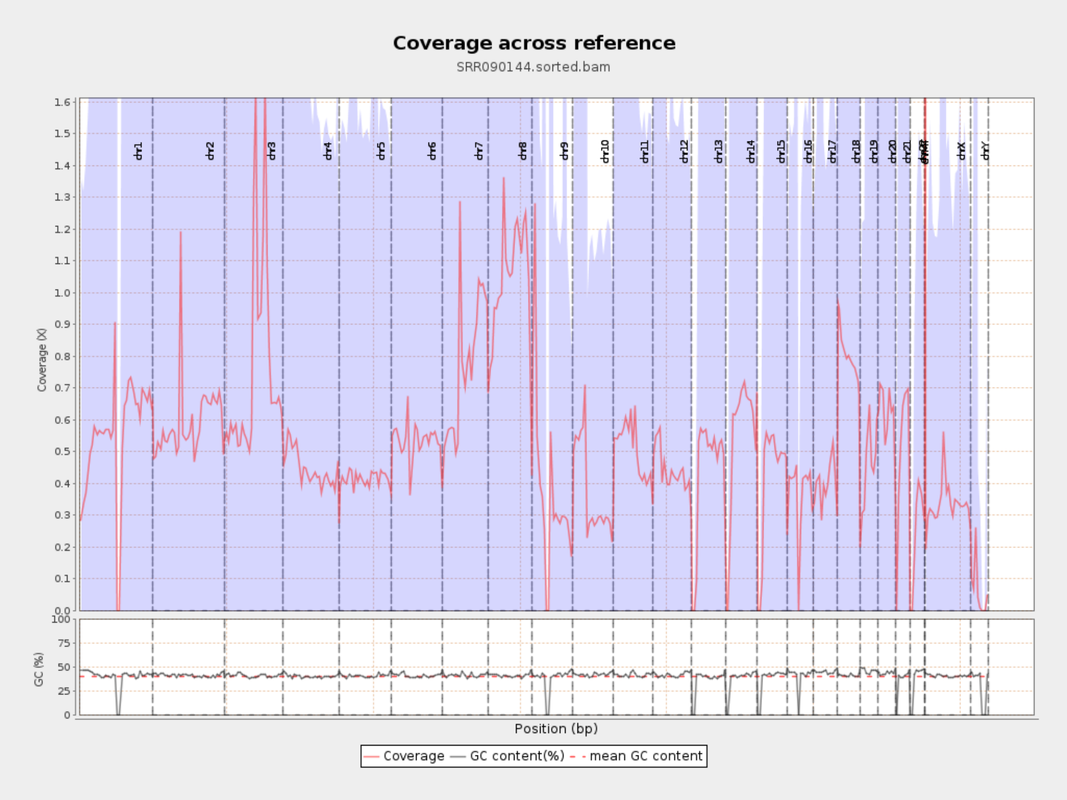
General error rate	0.82%
Mismatches	13,196,510
Insertions	115,299
Mapped reads with at least one insertion	0.46%
Deletions	373,899
Mapped reads with at least one deletion	1.5%
Homopolymer indels	45.99%

2.6. Chromosome stats

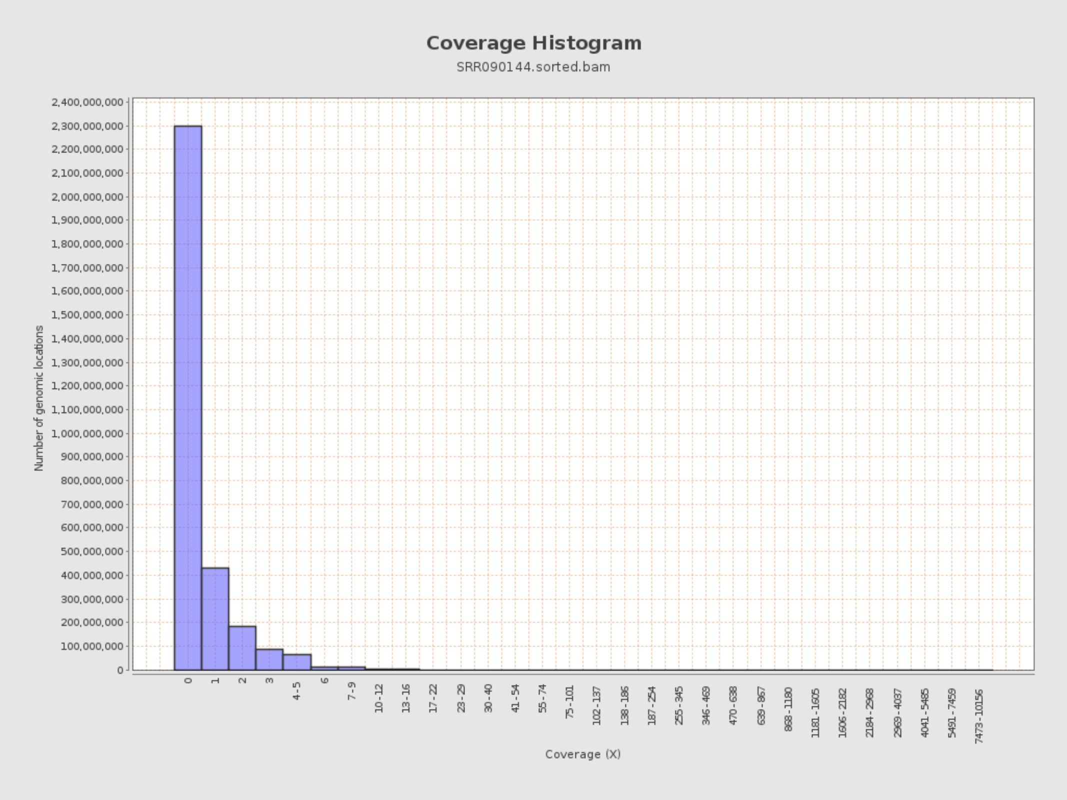
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	137664693	0.5523	8.2788
chr2	243199373	145004456	0.5962	6.4347
chr3	198022430	152978653	0.7725	1.6593
chr4	191154276	85569900	0.4476	1.5324
chr5	180915260	74775547	0.4133	1.1959
chr6	171115067	91690645	0.5358	2.0217
chr7	159138663	122978030	0.7728	9.3093

chr8	146364022	154226324	1.0537	7.0157
chr9	141213431	52061499	0.3687	4.3604
chr10	135534747	50891805	0.3755	3.2507
chr11	135006516	68471985	0.5072	3.6356
chr12	133851895	59352847	0.4434	1.3488
chr13	115169878	50589969	0.4393	1.1108
chr14	107349540	57796022	0.5384	1.6238
chr15	102531392	42031657	0.4099	1.1883
chr16	90354753	32224396	0.3566	1.391
chr17	81195210	32313641	0.398	1.752
chr18	78077248	62906928	0.8057	6.3548
chr19	59128983	26281879	0.4445	4.9618
chr20	63025520	39199076	0.622	1.6622
chr21	48129895	24940954	0.5182	1.6112
chr22	51304566	12752691	0.2486	0.8162
chrMT	16571	967377	58.3777	31.6512
chrX	155270560	51973931	0.3347	1.9267
chrY	59373566	3829063	0.0645	2.6478

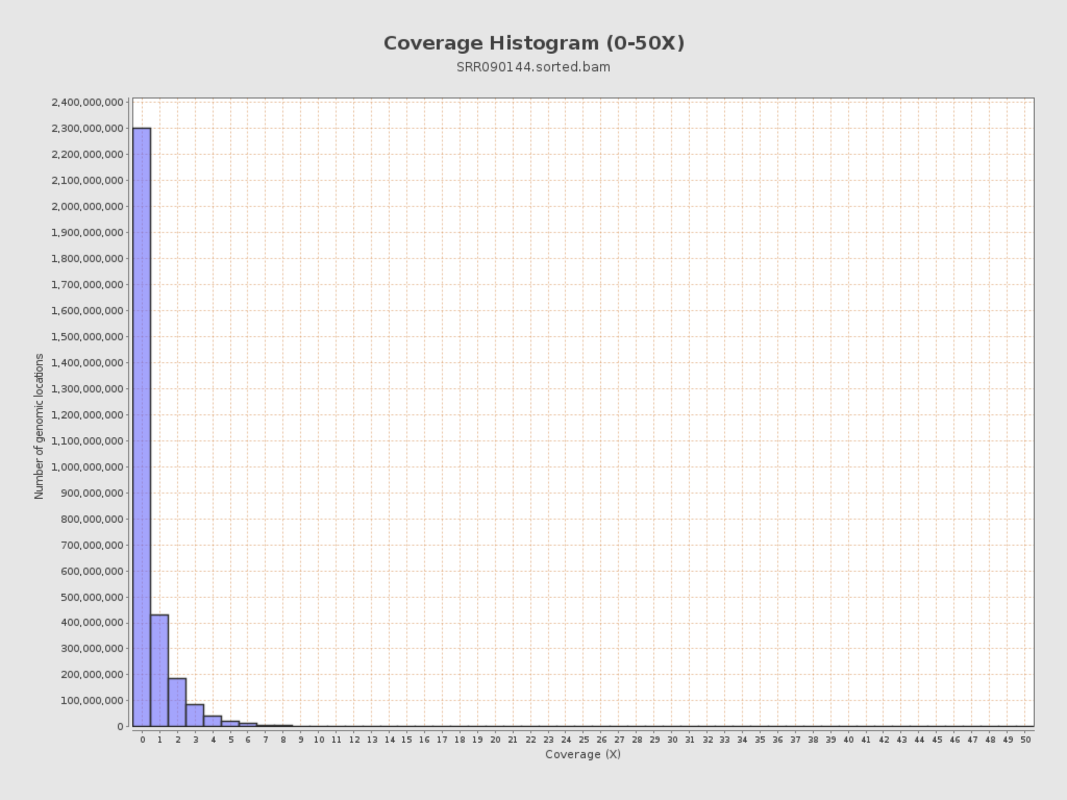
3. Results : Coverage across reference



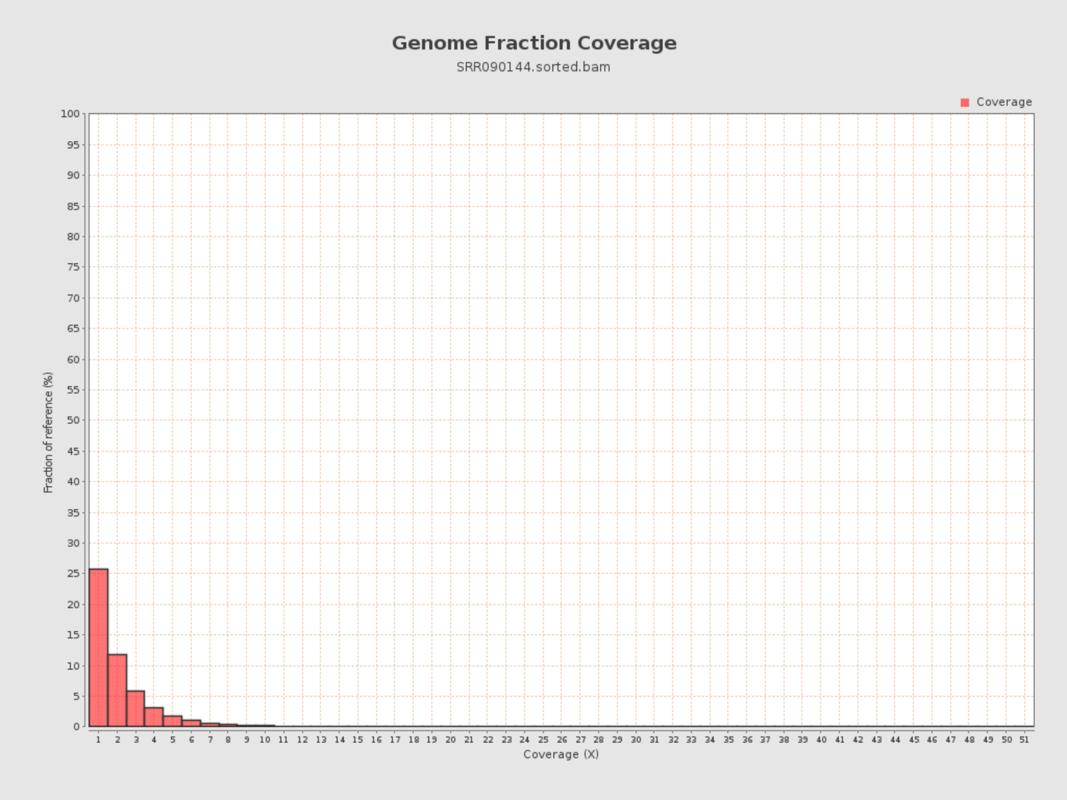
4. Results : Coverage Histogram



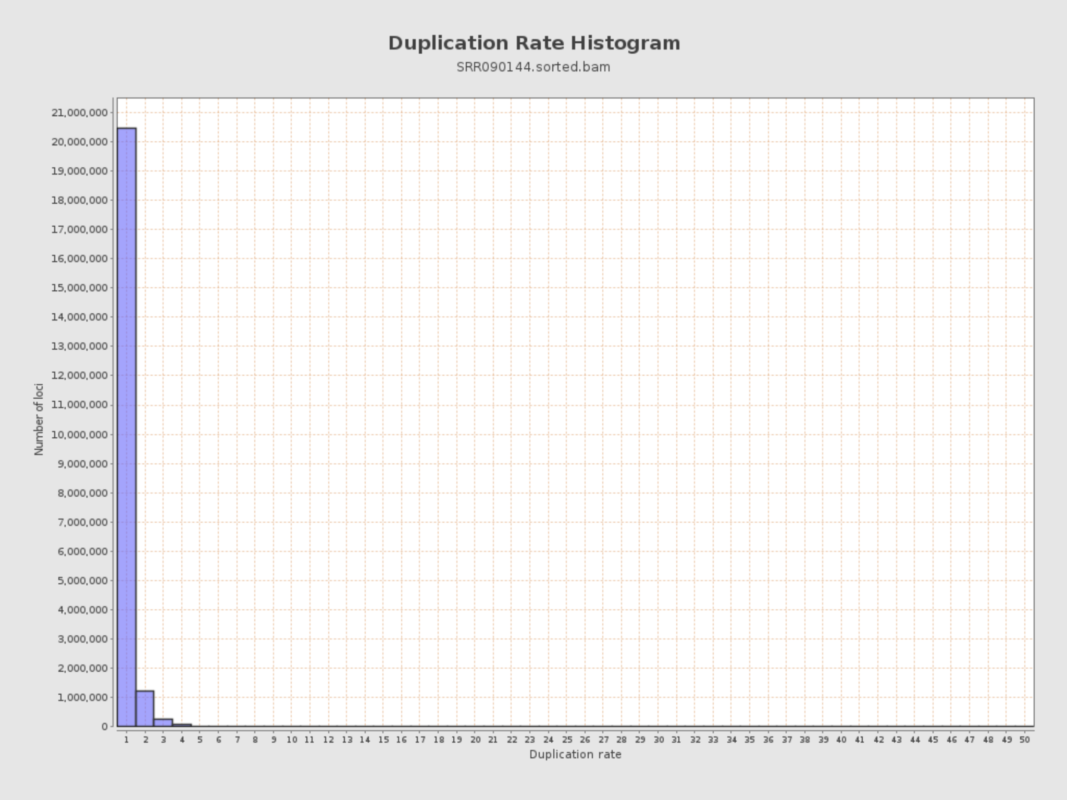
5. Results : Coverage Histogram (0-50X)



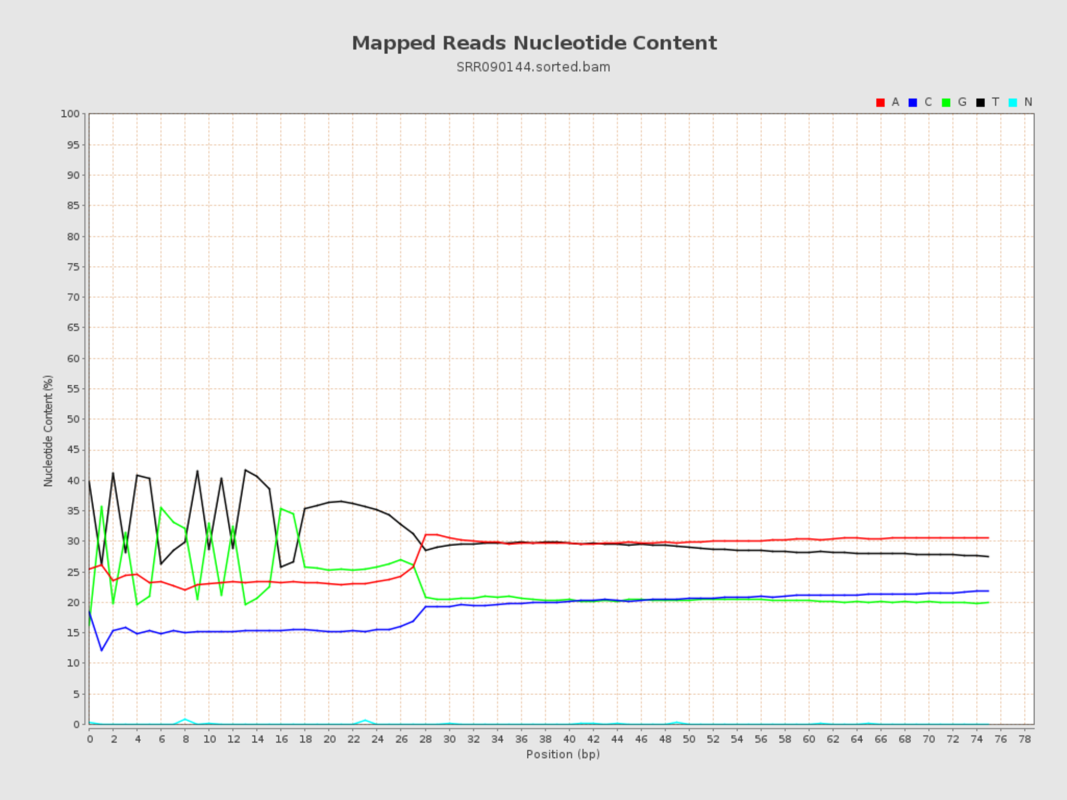
6. Results : Genome Fraction Coverage



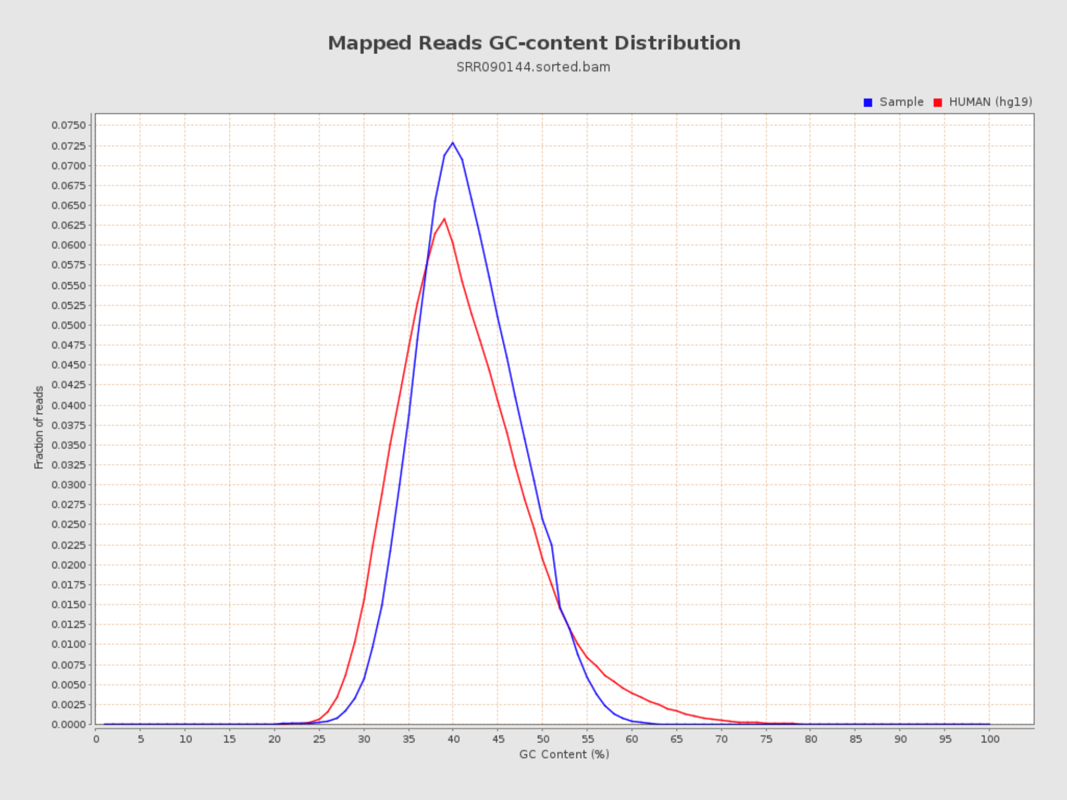
7. Results : Duplication Rate Histogram



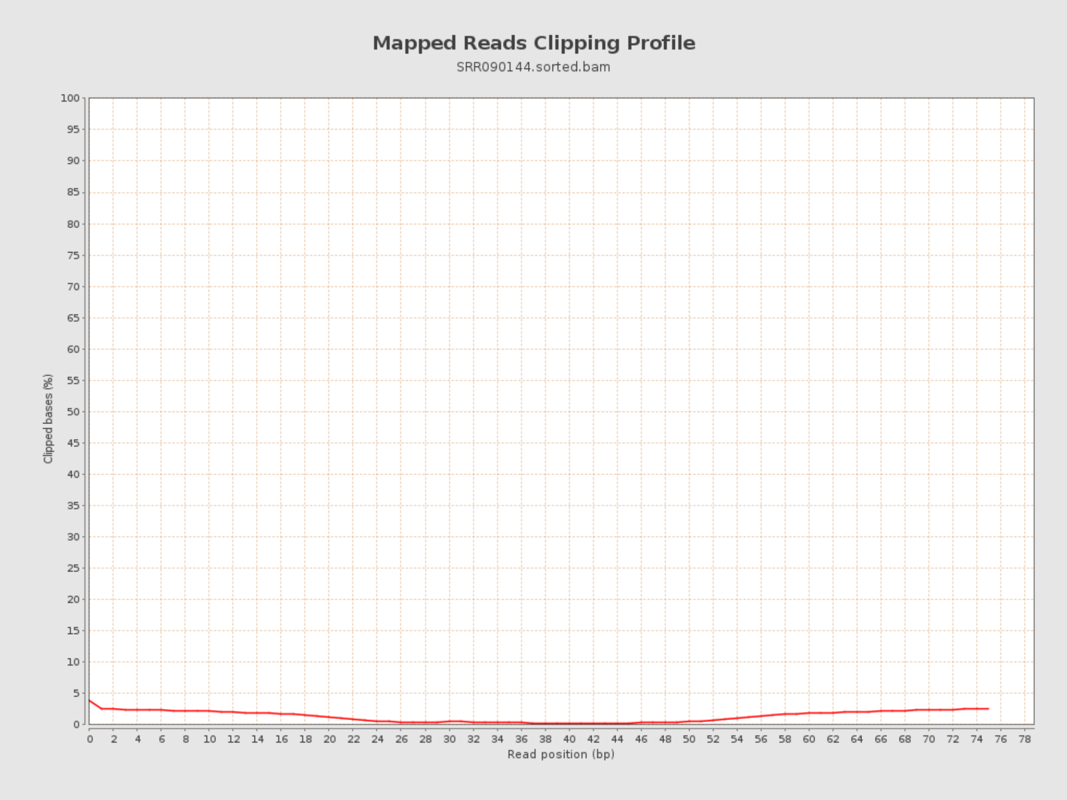
8. Results : Mapped Reads Nucleotide Content



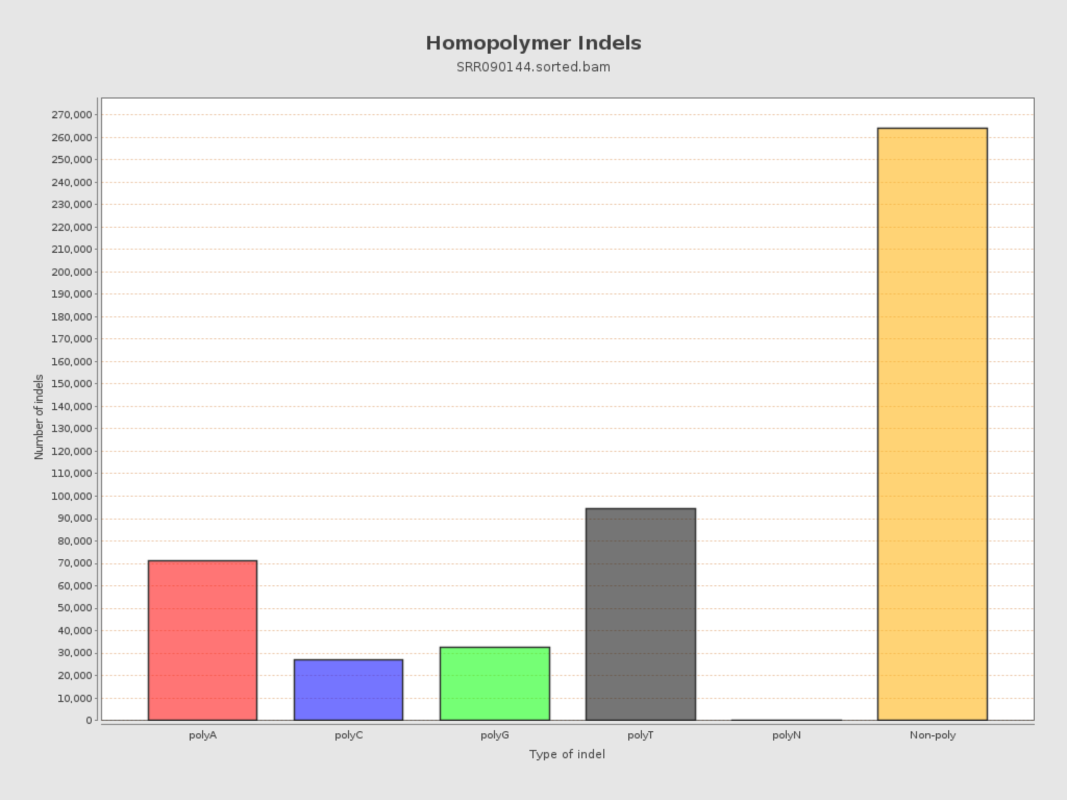
9. Results : Mapped Reads GC-content Distribution



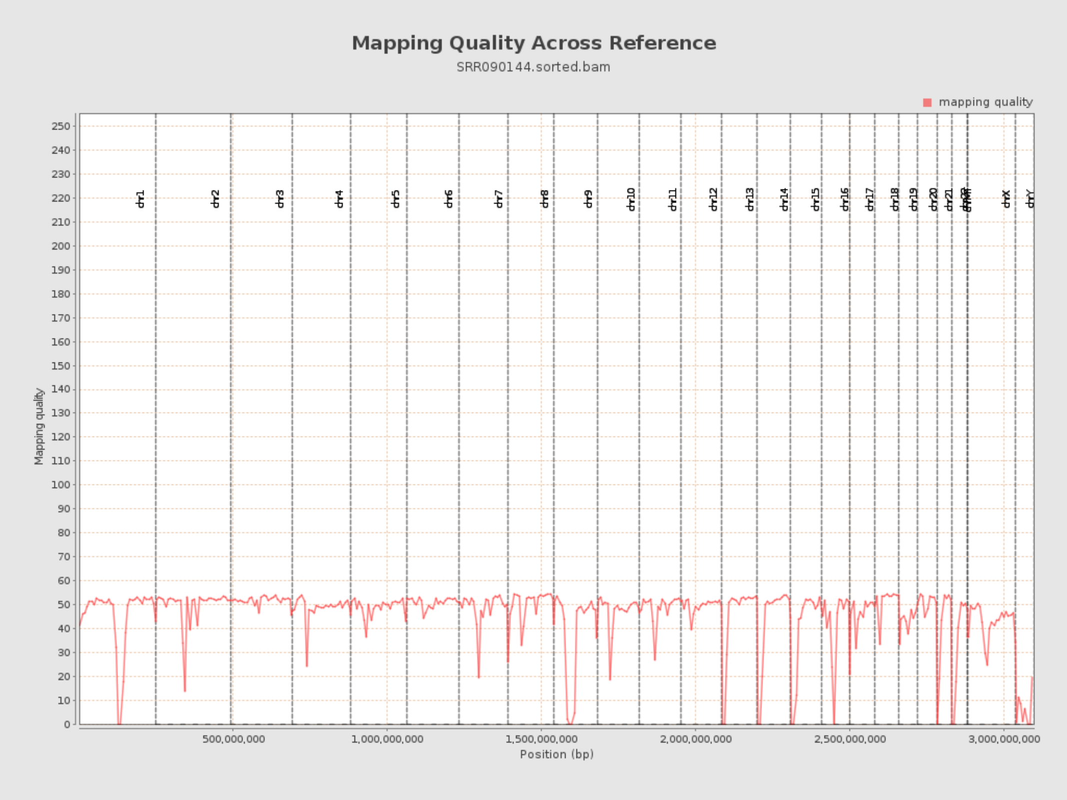
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram