Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 08:54:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090158.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_SRR090158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 08:54:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,227,727
Mapped reads	14,910,147 / 91.88%
Unmapped reads	1,317,580 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	99,483 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	3,102,248 / 19.12%
Duplication rate	13.78%
Clipped reads	7,763,490 / 47.84%

2.2. ACGT Content

Number/percentage of A's	251,902,448 / 26.11%
Number/percentage of C's	175,836,123 / 18.22%
Number/percentage of T's	305,133,824 / 31.62%
Number/percentage of G's	231,460,343 / 23.99%
Number/percentage of N's	573,806 / 0.06%
GC Percentage	42.21%

2.3. Coverage

Mean	0.3118

Standard Deviation	2.5131

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

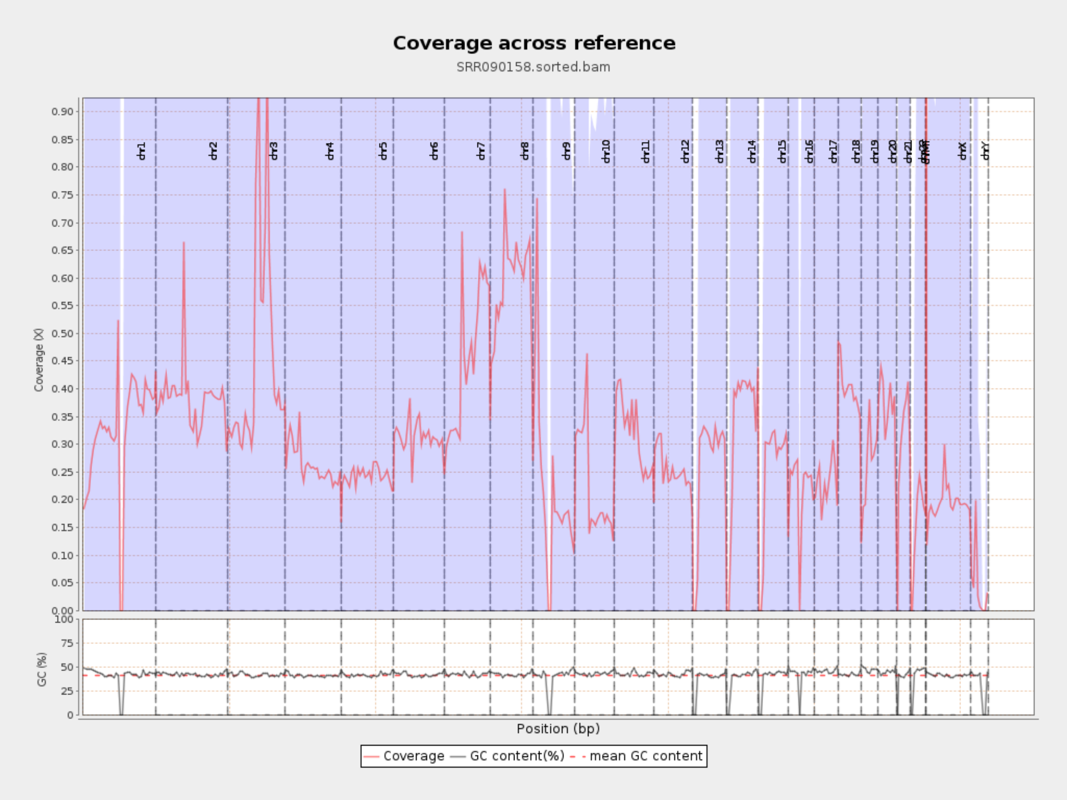
General error rate	0.66%
Mismatches	6,297,433
Insertions	61,357
Mapped reads with at least one insertion	0.41%
Deletions	192,418
Mapped reads with at least one deletion	1.28%
Homopolymer indels	47.43%

2.6. Chromosome stats

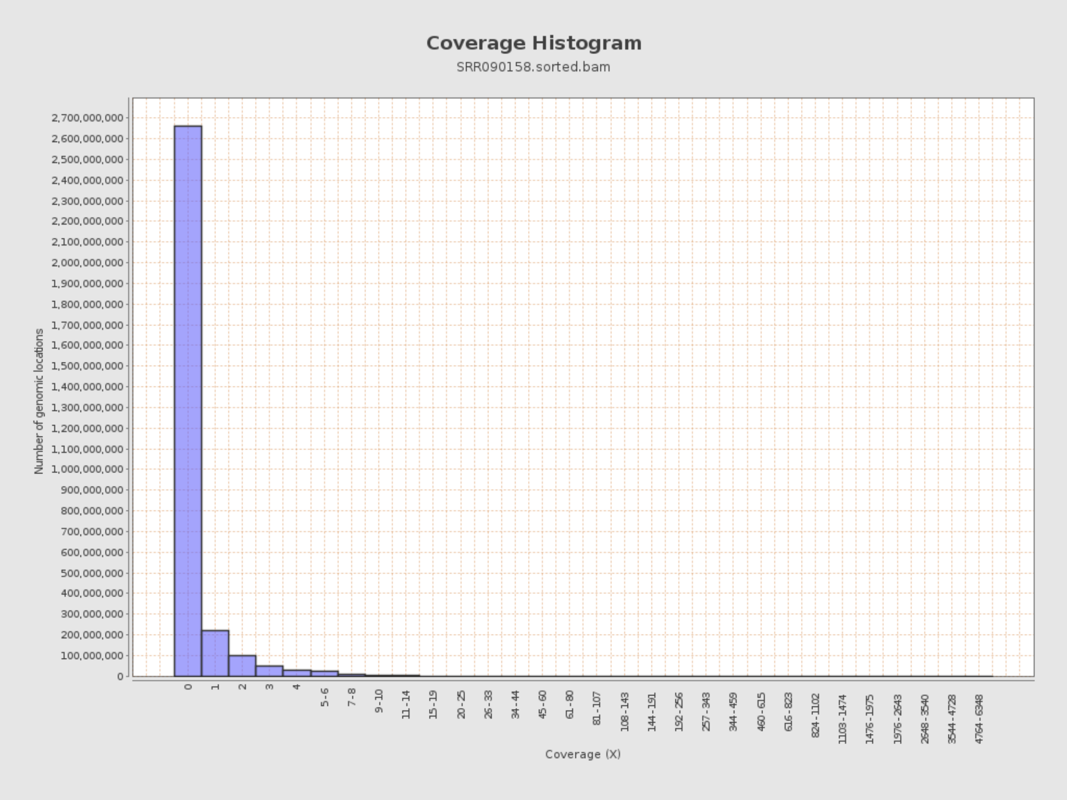
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	80446908	0.3228	5.0214
chr2	243199373	93670662	0.3852	2.9201
chr3	198022430	90043565	0.4547	1.3449
chr4	191154276	50326369	0.2633	1.1831
chr5	180915260	43896795	0.2426	0.9452
chr6	171115067	53844380	0.3147	1.3546
chr7	159138663	72131542	0.4533	4.5071

chr8	146364022	87148521	0.5954	4.0034
chr9	141213431	30804900	0.2181	1.8435
chr10	135534747	30280810	0.2234	2.1996
chr11	135006516	43042112	0.3188	1.7807
chr12	133851895	34206778	0.2556	1.0355
chr13	115169878	29921123	0.2598	0.9433
chr14	107349540	35670306	0.3323	1.1822
chr15	102531392	24845570	0.2423	0.9539
chr16	90354753	19225542	0.2128	1.0158
chr17	81195210	18987479	0.2338	1.2219
chr18	78077248	31399713	0.4022	3.5277
chr19	59128983	15829137	0.2677	2.6815
chr20	63025520	23496426	0.3728	1.2751
chr21	48129895	14341258	0.298	1.2445
chr22	51304566	7708077	0.1502	0.7217
chrMT	16571	1192773	71.9795	36.5399
chrX	155270560	30101497	0.1939	1.067
chrY	59373566	2685939	0.0452	2.34

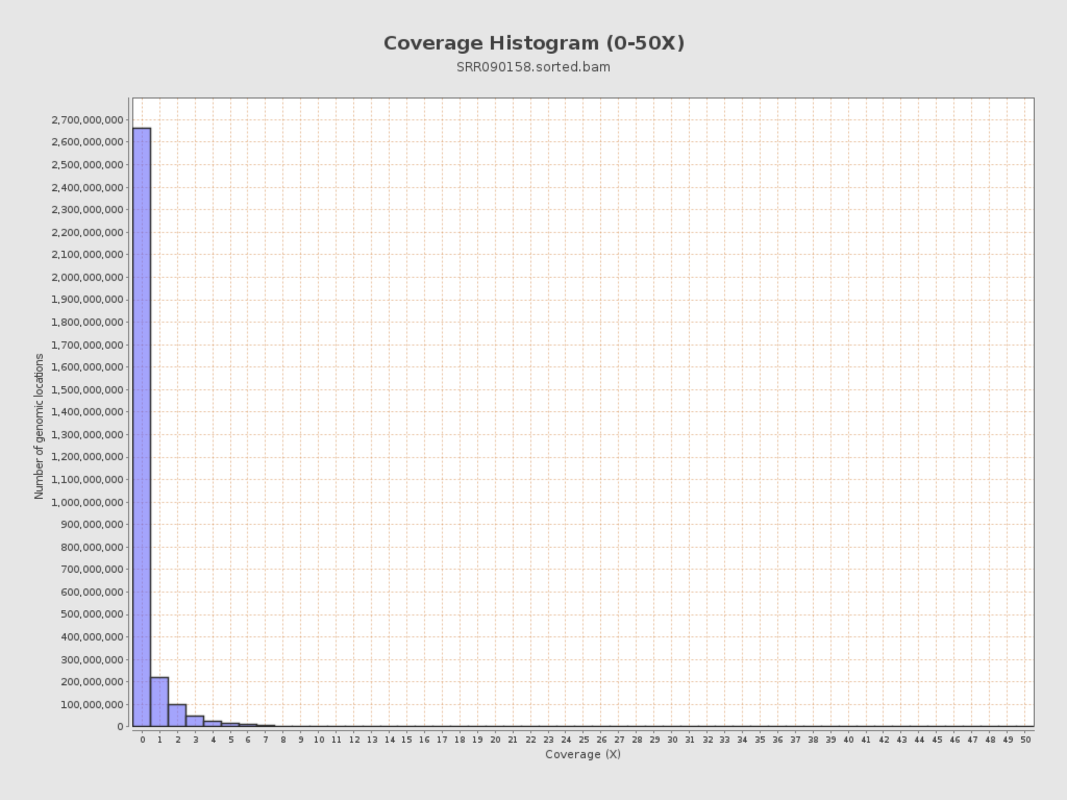
3. Results : Coverage across reference



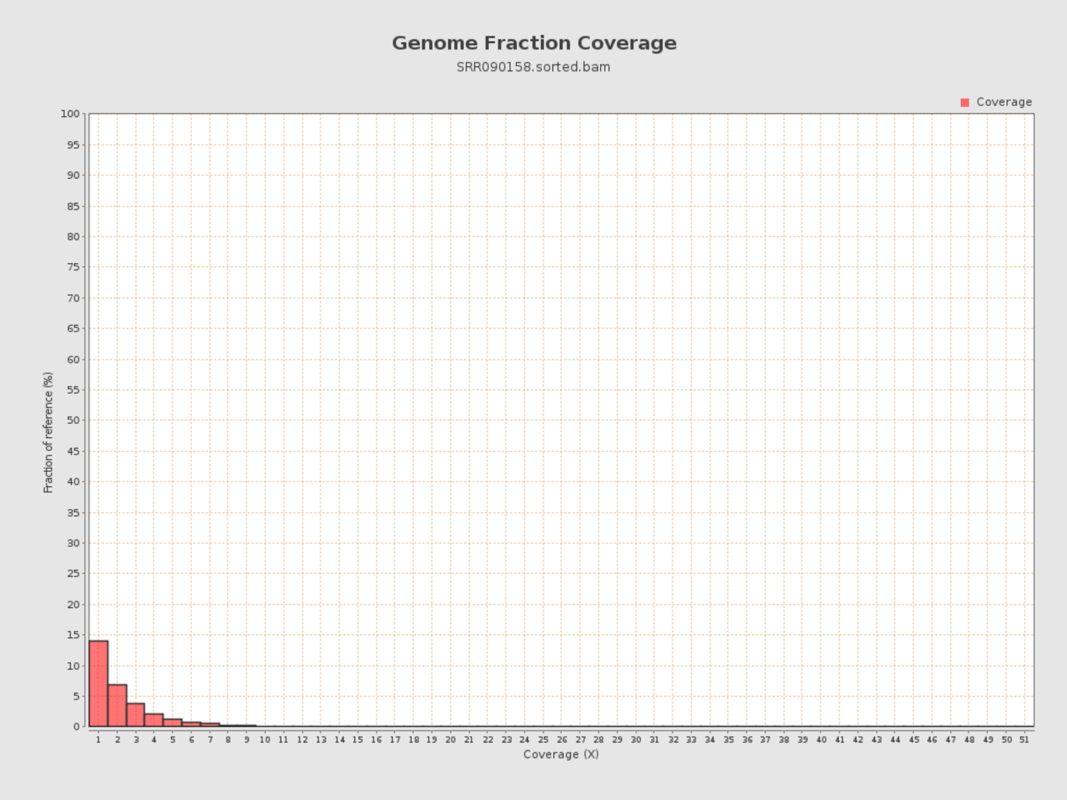
4. Results : Coverage Histogram



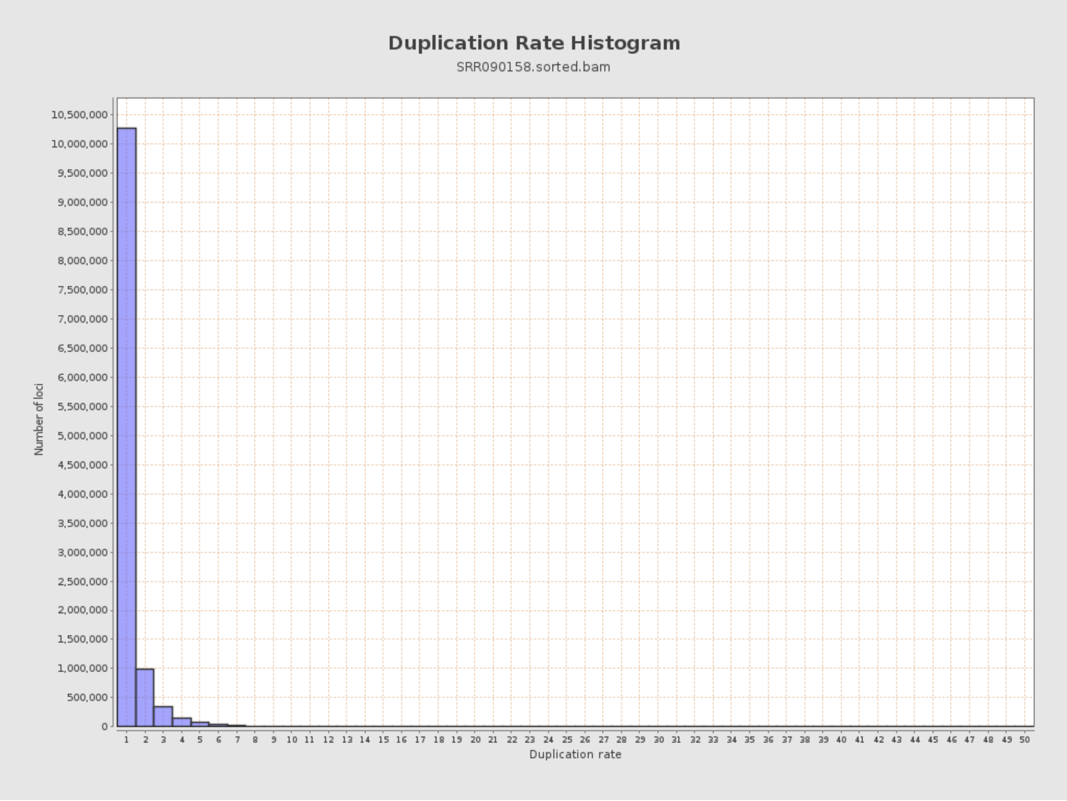
5. Results : Coverage Histogram (0-50X)



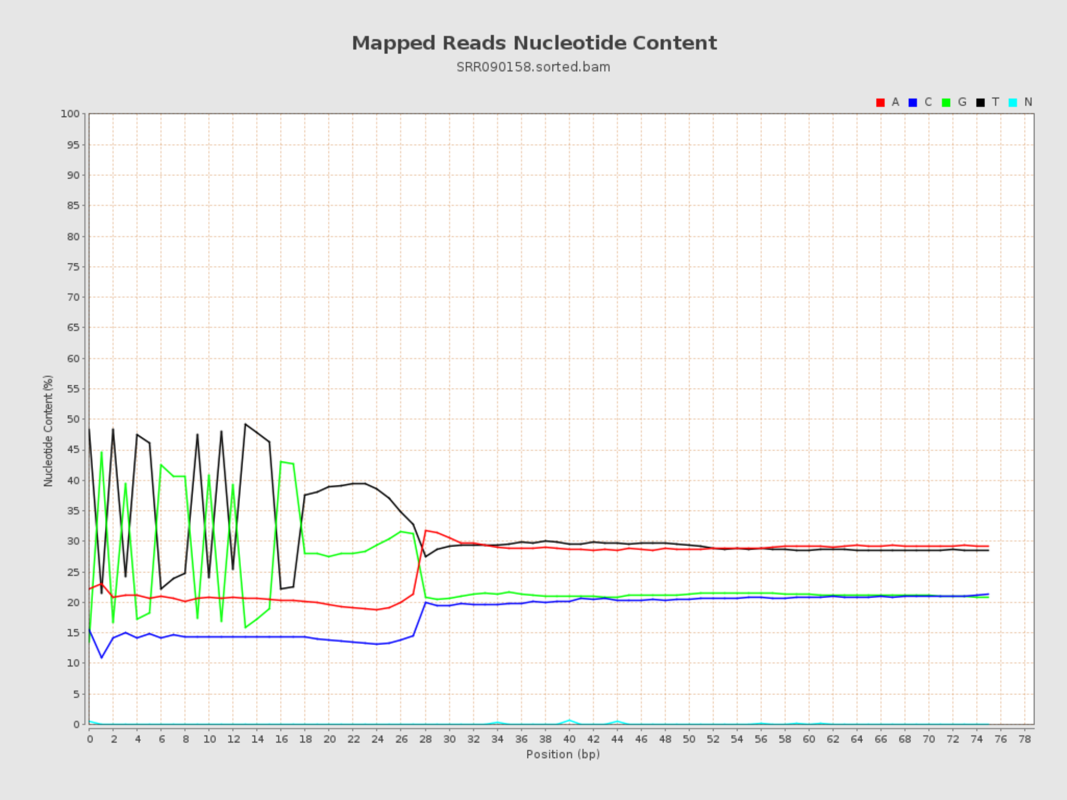
6. Results : Genome Fraction Coverage



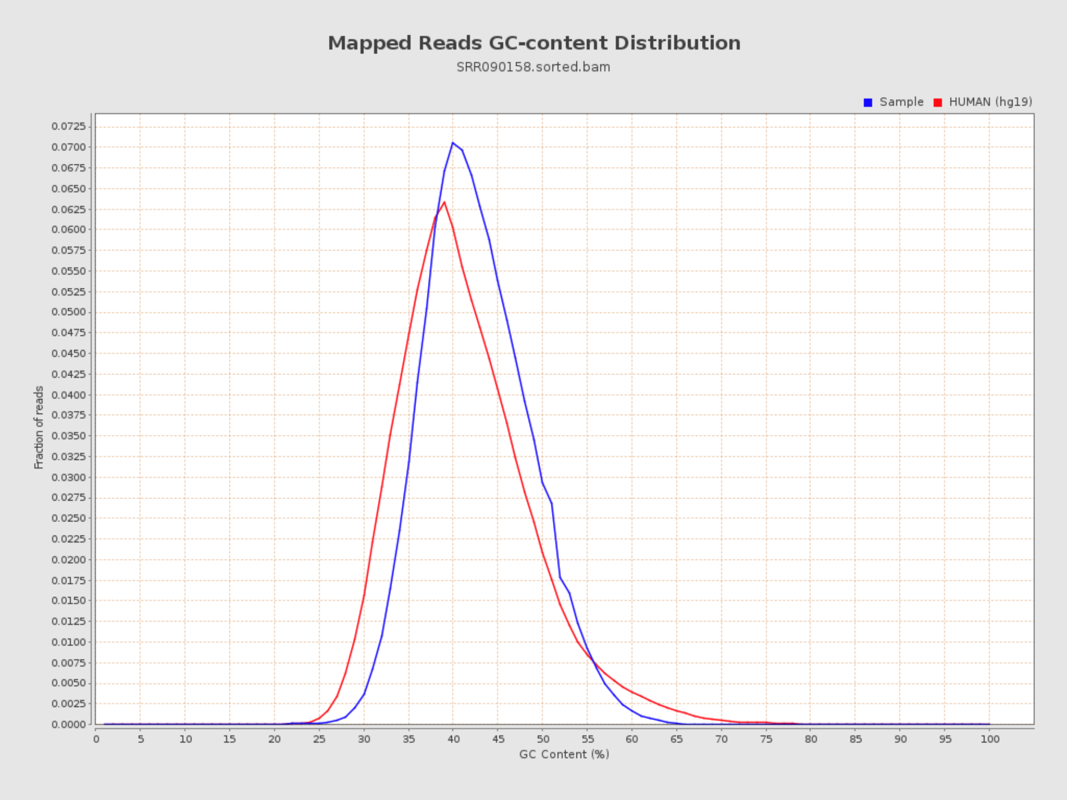
7. Results : Duplication Rate Histogram



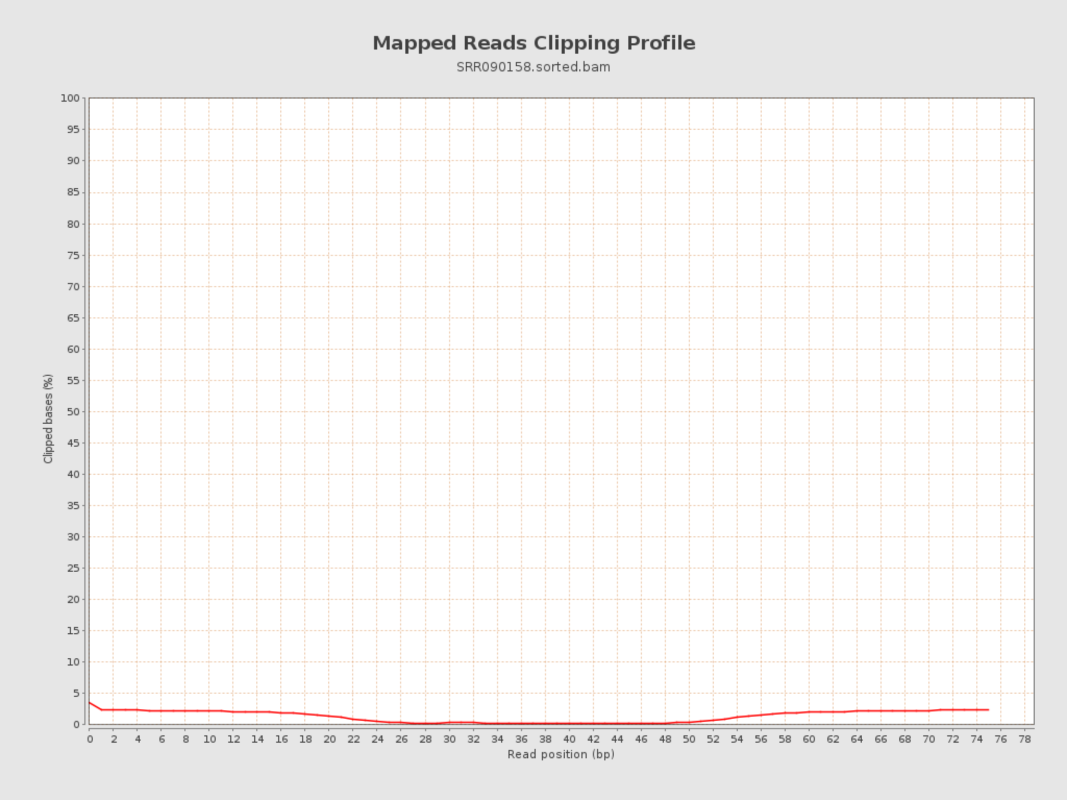
8. Results : Mapped Reads Nucleotide Content



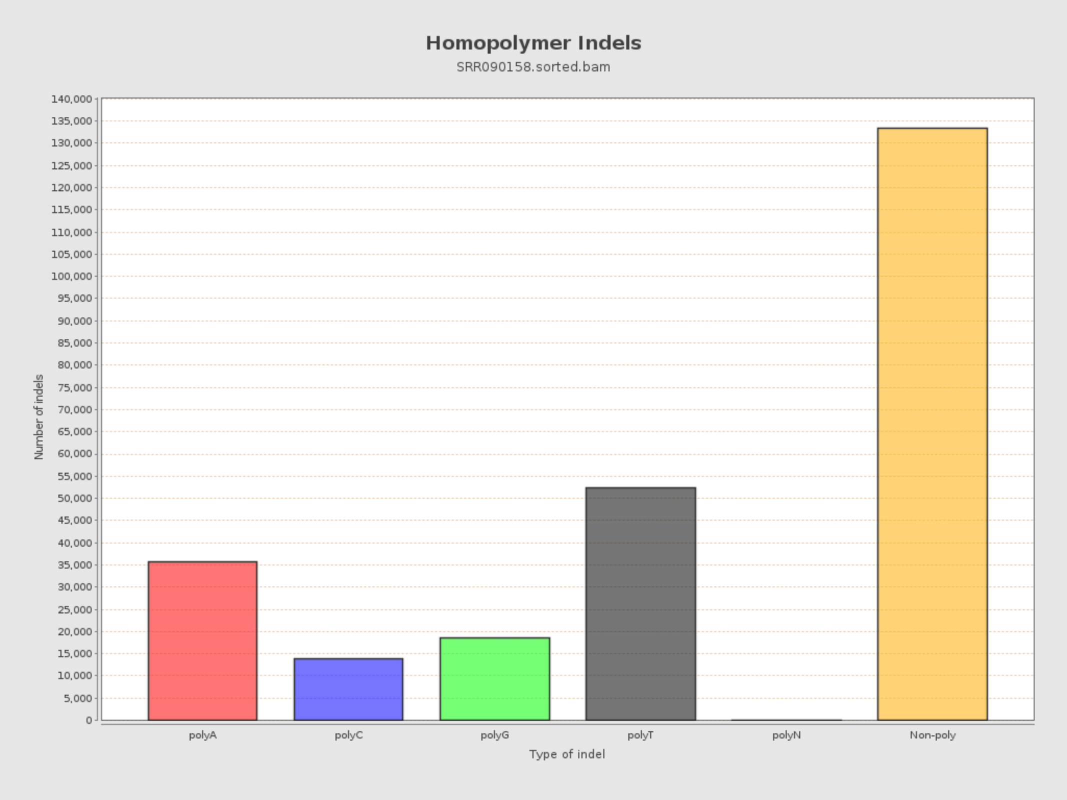
9. Results : Mapped Reads GC-content Distribution



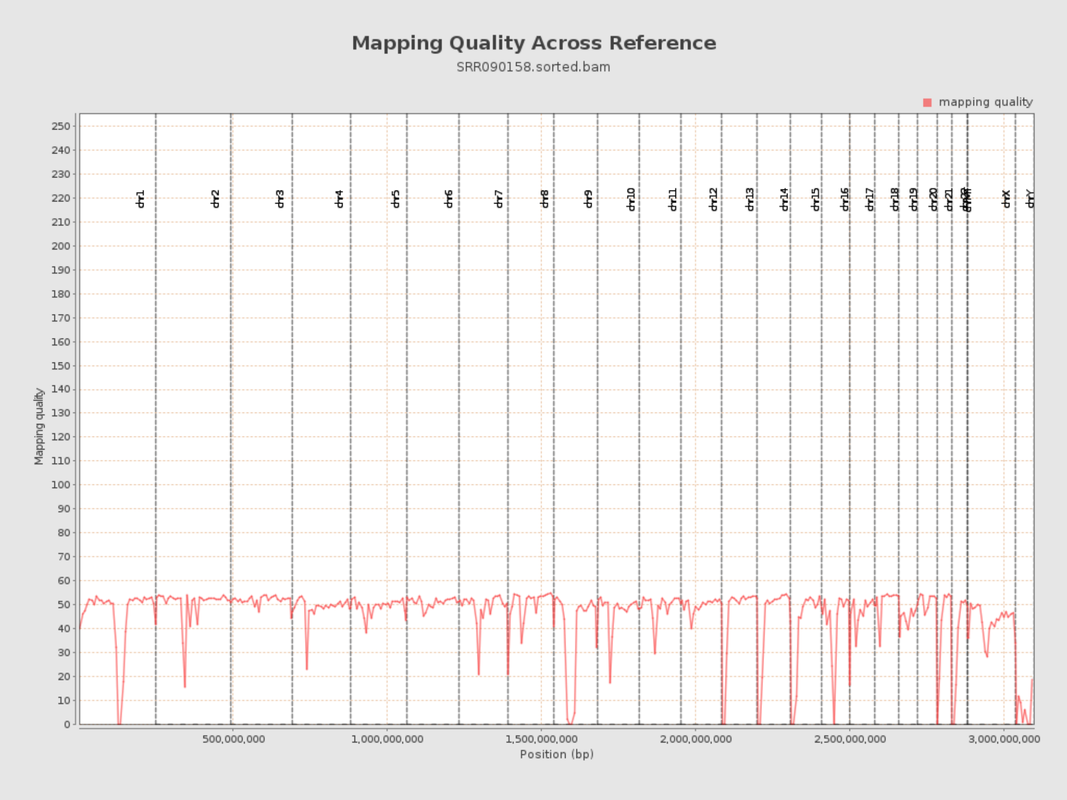
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram