Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 11:03:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090212.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_SRR090212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 11:02:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,854,184
Mapped reads	22,376,715 / 86.55%
Unmapped reads	3,477,469 / 13.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,023 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,187,738 / 16.2%
Duplication rate	12.74%
Clipped reads	1,916,594 / 7.41%

2.2. ACGT Content

Number/percentage of A's	309,918,762 / 29.35%
Number/percentage of C's	214,749,911 / 20.34%
Number/percentage of T's	304,722,130 / 28.86%
Number/percentage of G's	226,440,623 / 21.45%
Number/percentage of N's	3,152 / 0%
GC Percentage	41.79%

2.3. Coverage

Mean	0.3411

Standard Deviation	2.1046

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Mismatches and indels

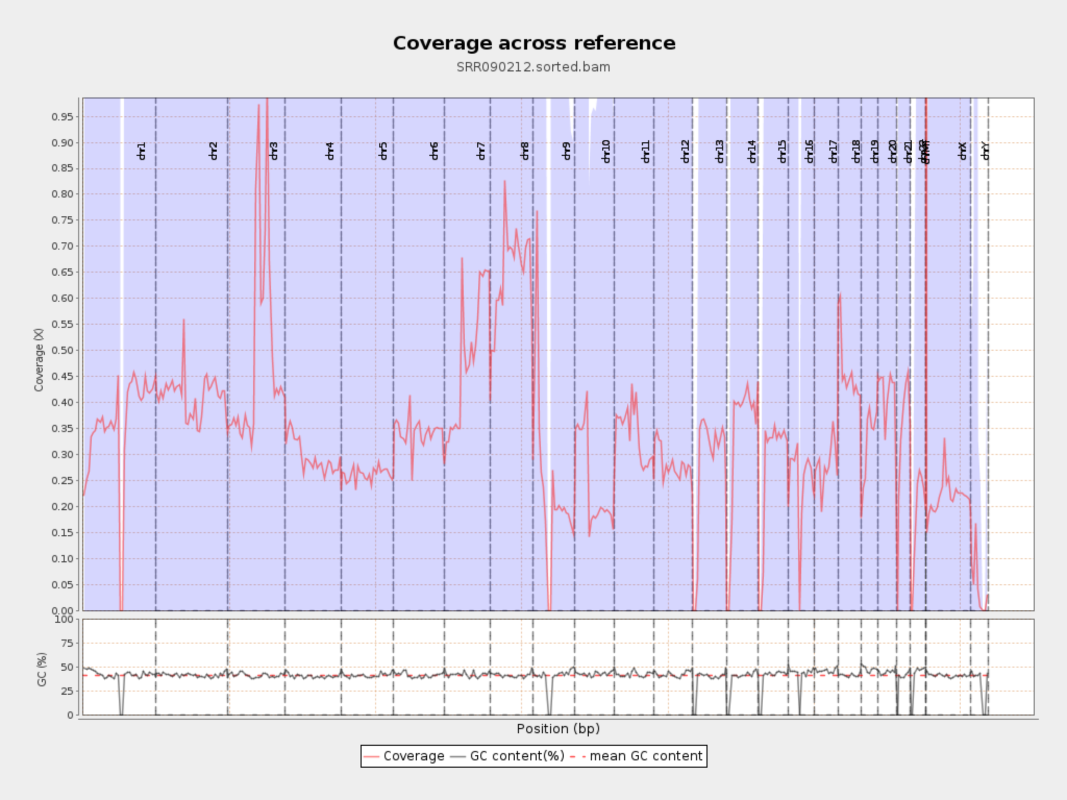
General error rate	0.39%
Mismatches	4,019,841
Insertions	39,465
Mapped reads with at least one insertion	0.18%
Deletions	130,430
Mapped reads with at least one deletion	0.58%
Homopolymer indels	47.13%

2.6. Chromosome stats

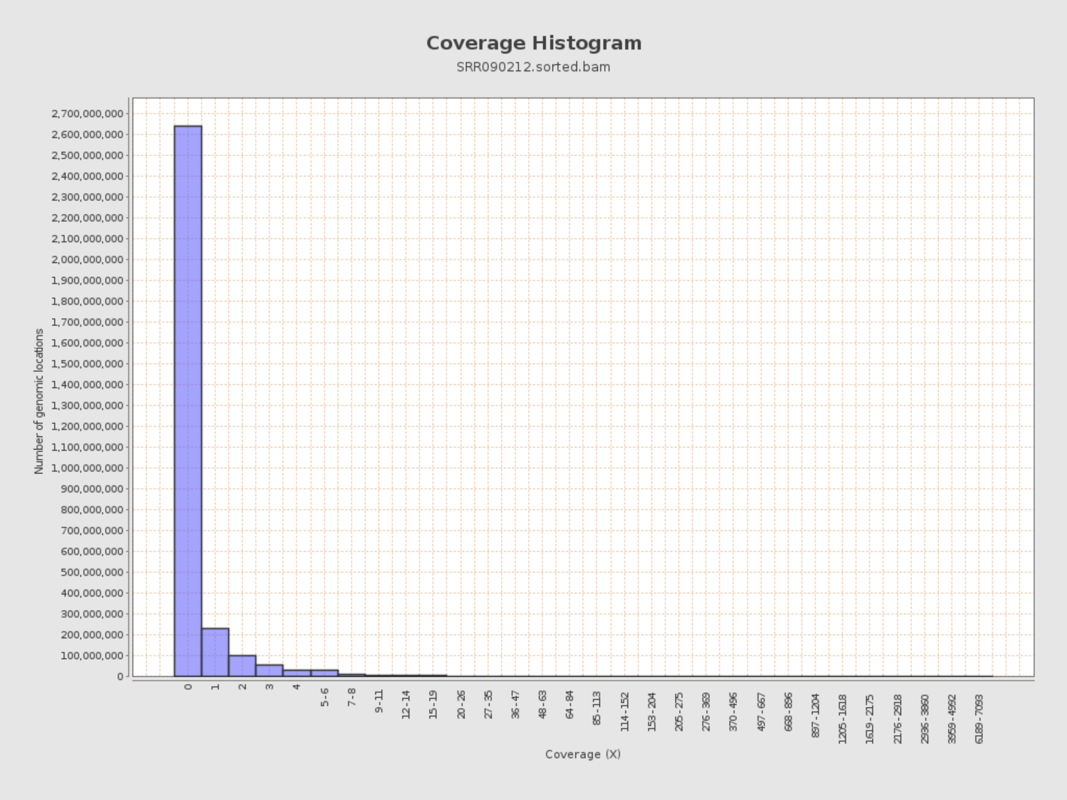
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	88528943	0.3552	3.1511
chr2	243199373	100892466	0.4149	2.3624
chr3	198022430	96196045	0.4858	1.4395
chr4	191154276	56539061	0.2958	1.1118
chr5	180915260	47399847	0.262	1.0172
chr6	171115067	58724571	0.3432	1.4022
chr7	159138663	77294201	0.4857	3.8783

chr8	146364022	95601907	0.6532	4.2197
chr9	141213431	33280948	0.2357	1.7706
chr10	135534747	32884466	0.2426	1.7281
chr11	135006516	45704454	0.3385	1.8033
chr12	133851895	38014566	0.284	1.1134
chr13	115169878	32214550	0.2797	1.033
chr14	107349540	35759504	0.3331	1.1976
chr15	102531392	27588441	0.2691	1.0202
chr16	90354753	22116566	0.2448	1.1364
chr17	81195210	23030521	0.2836	1.2382
chr18	78077248	35815396	0.4587	2.8152
chr19	59128983	19518546	0.3301	2.2832
chr20	63025520	26364476	0.4183	1.3822
chr21	48129895	16022830	0.3329	1.3533
chr22	51304566	8983598	0.1751	0.8008
chrMT	16571	579068	34.9447	22.0789
chrX	155270560	34209623	0.2203	1.2339
chrY	59373566	2768469	0.0466	1.6364

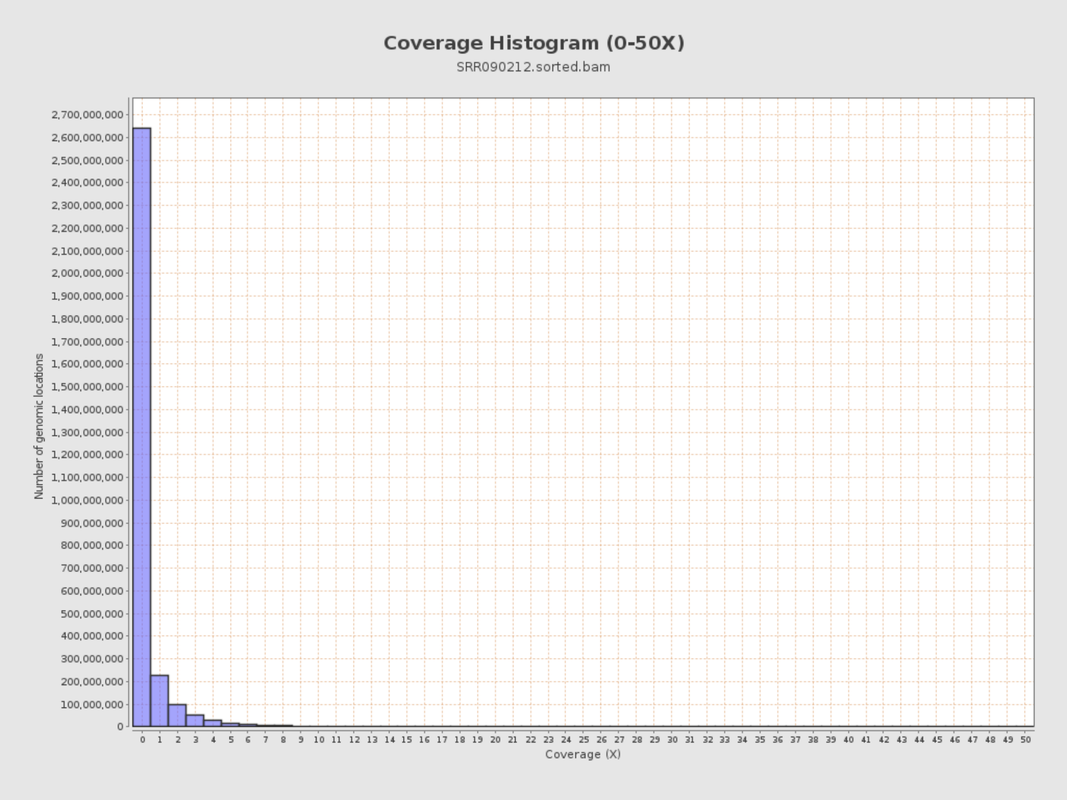
3. Results : Coverage across reference



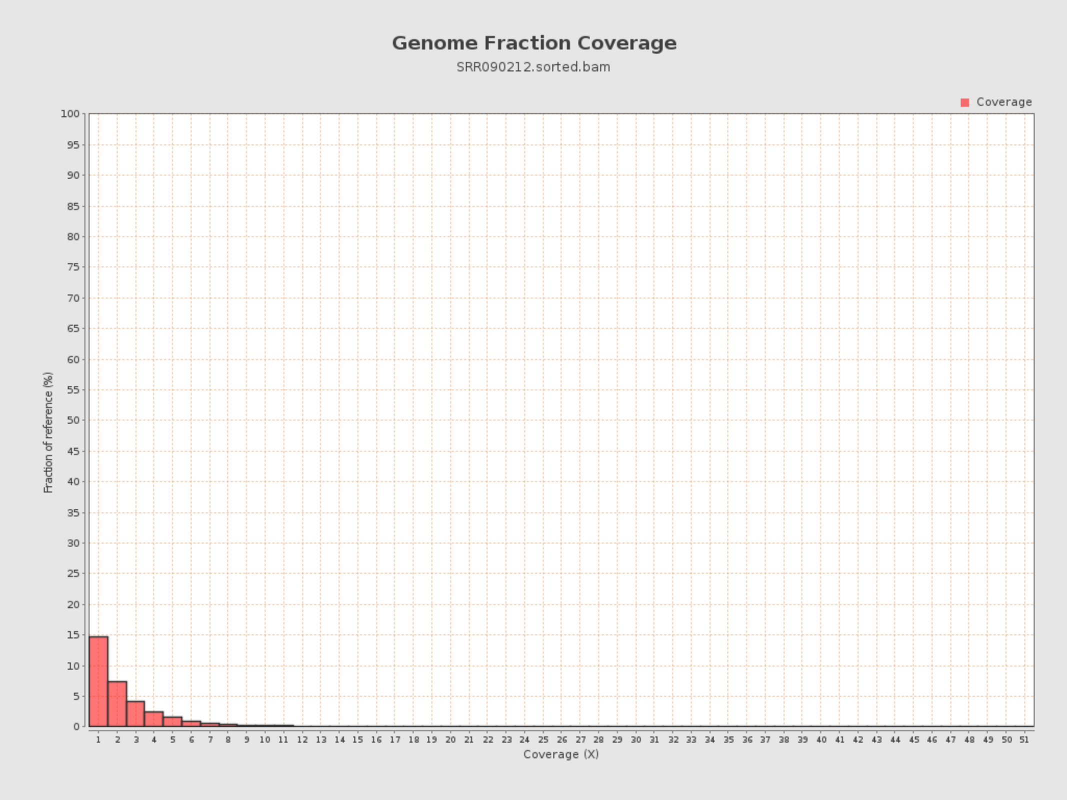
4. Results : Coverage Histogram



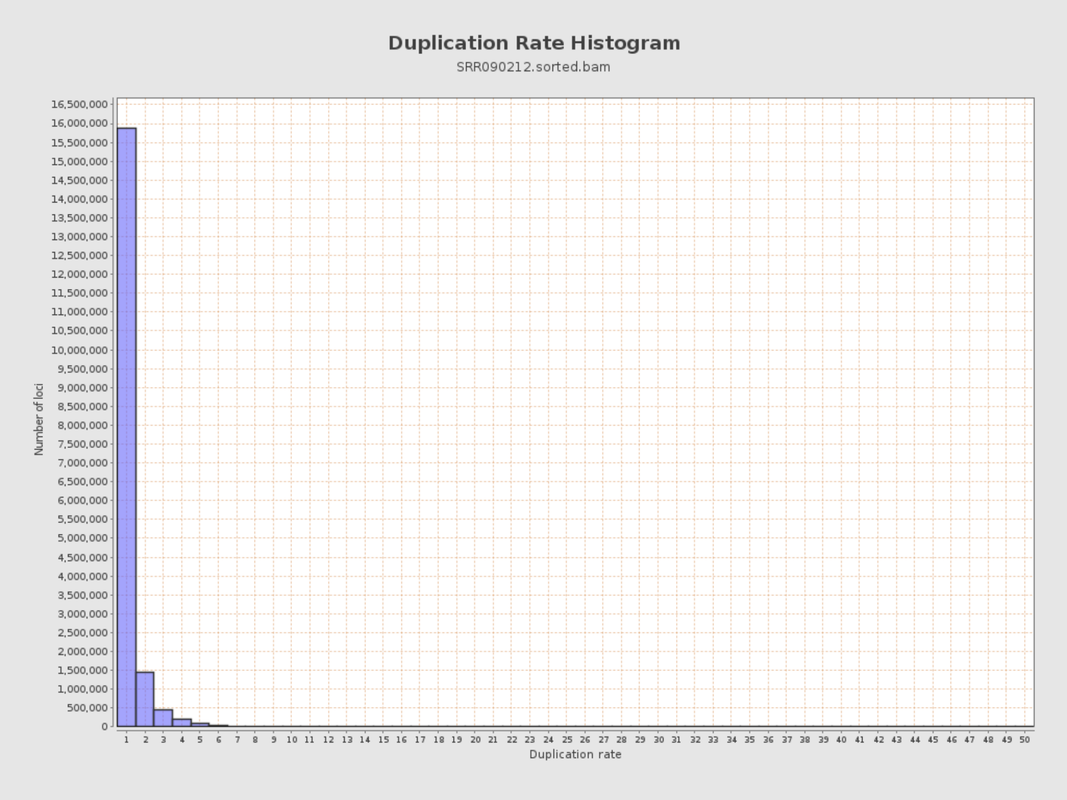
5. Results : Coverage Histogram (0-50X)



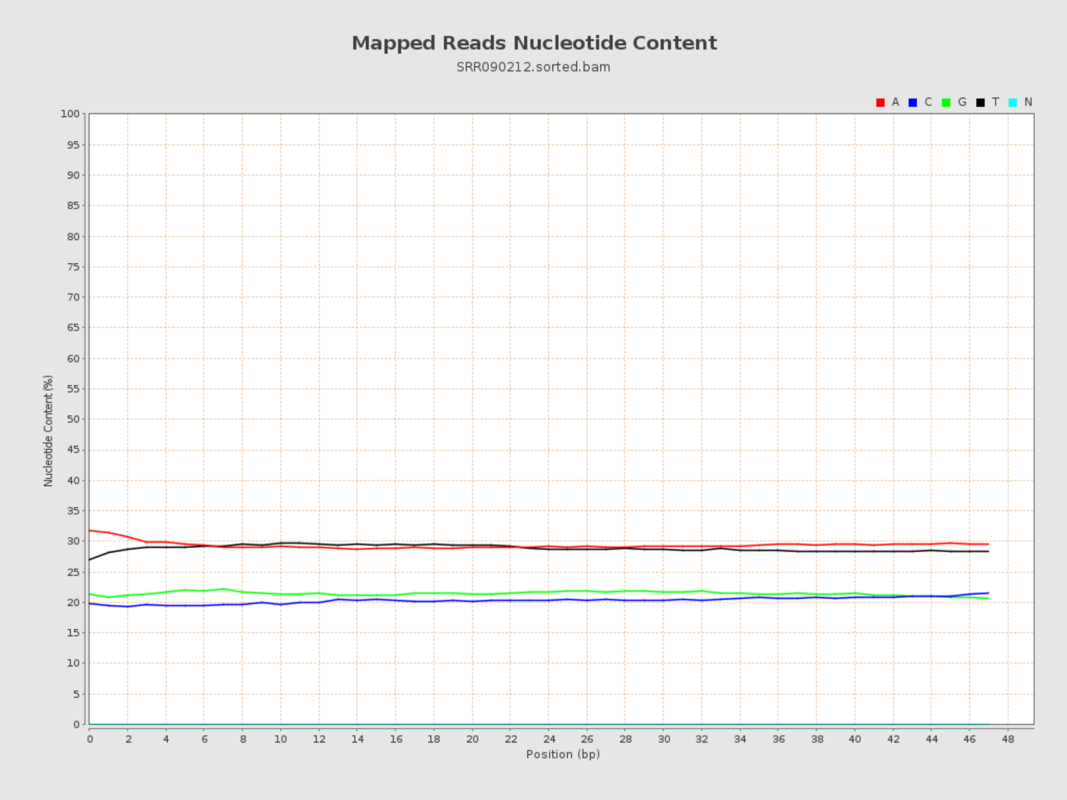
6. Results : Genome Fraction Coverage



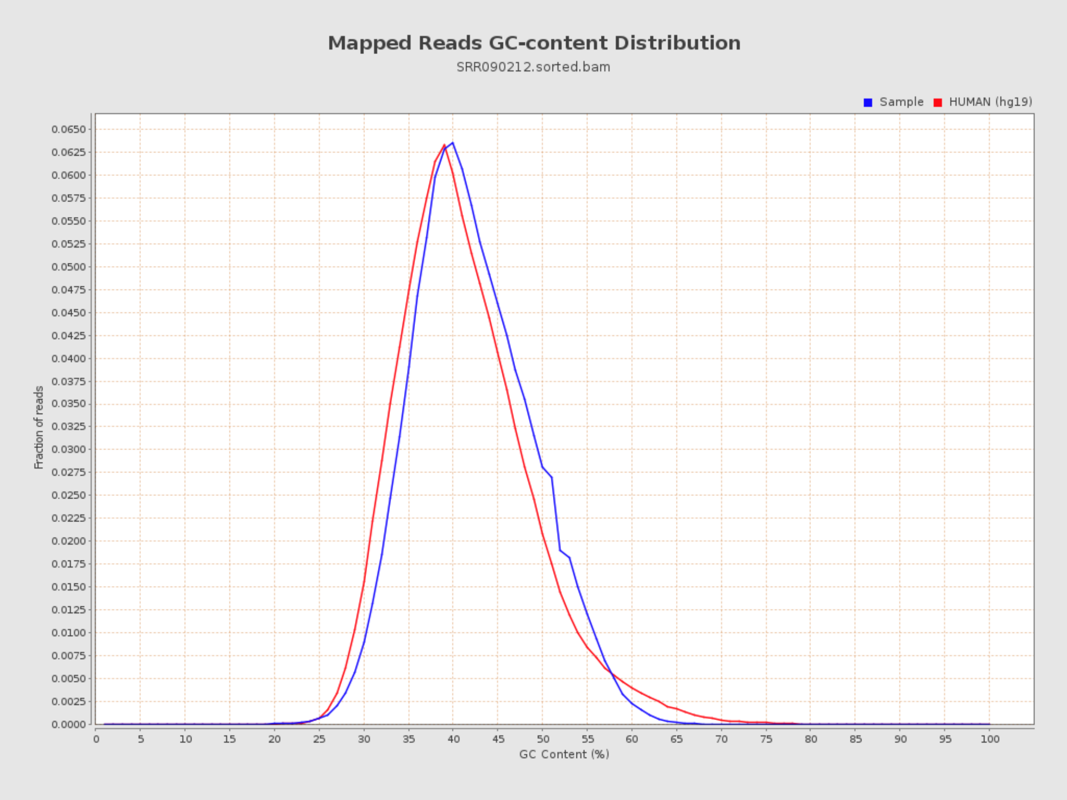
7. Results : Duplication Rate Histogram



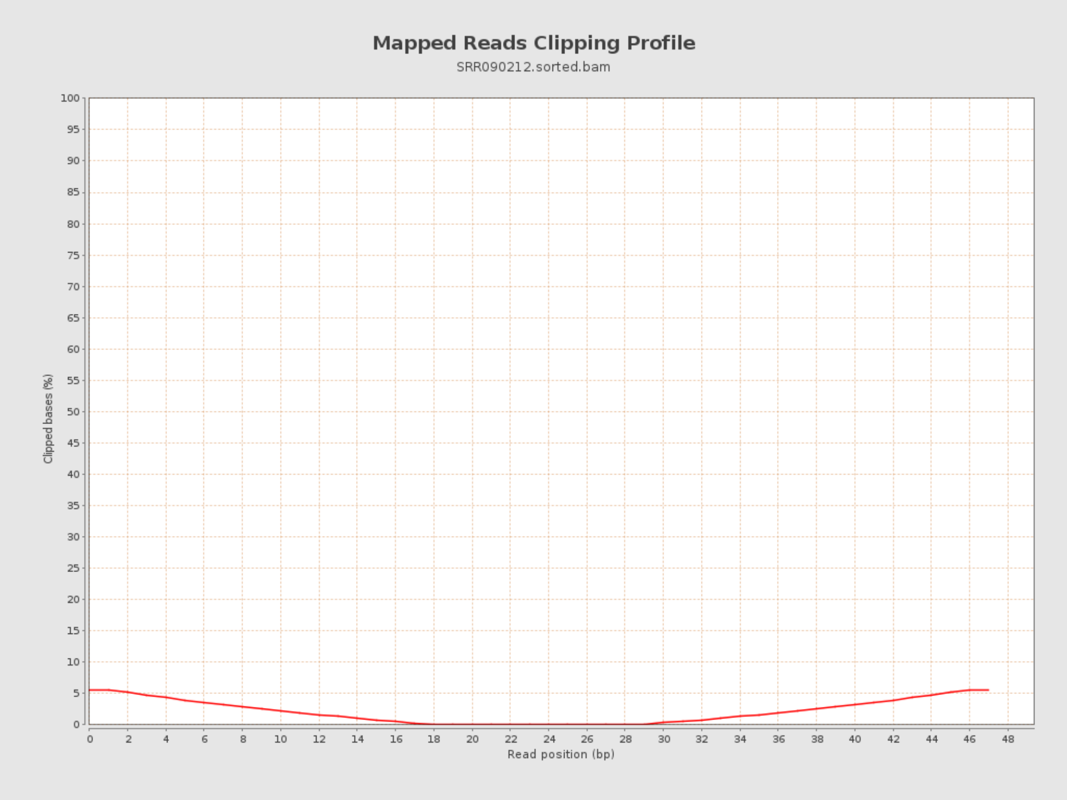
8. Results : Mapped Reads Nucleotide Content



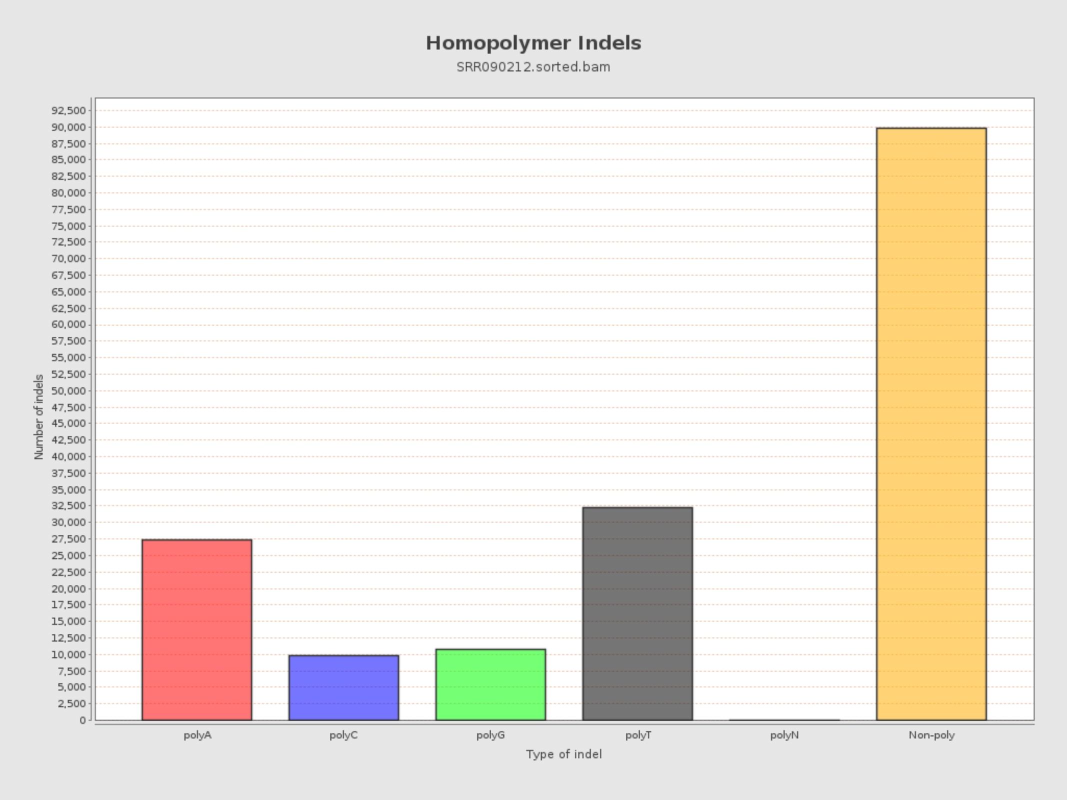
9. Results : Mapped Reads GC-content Distribution



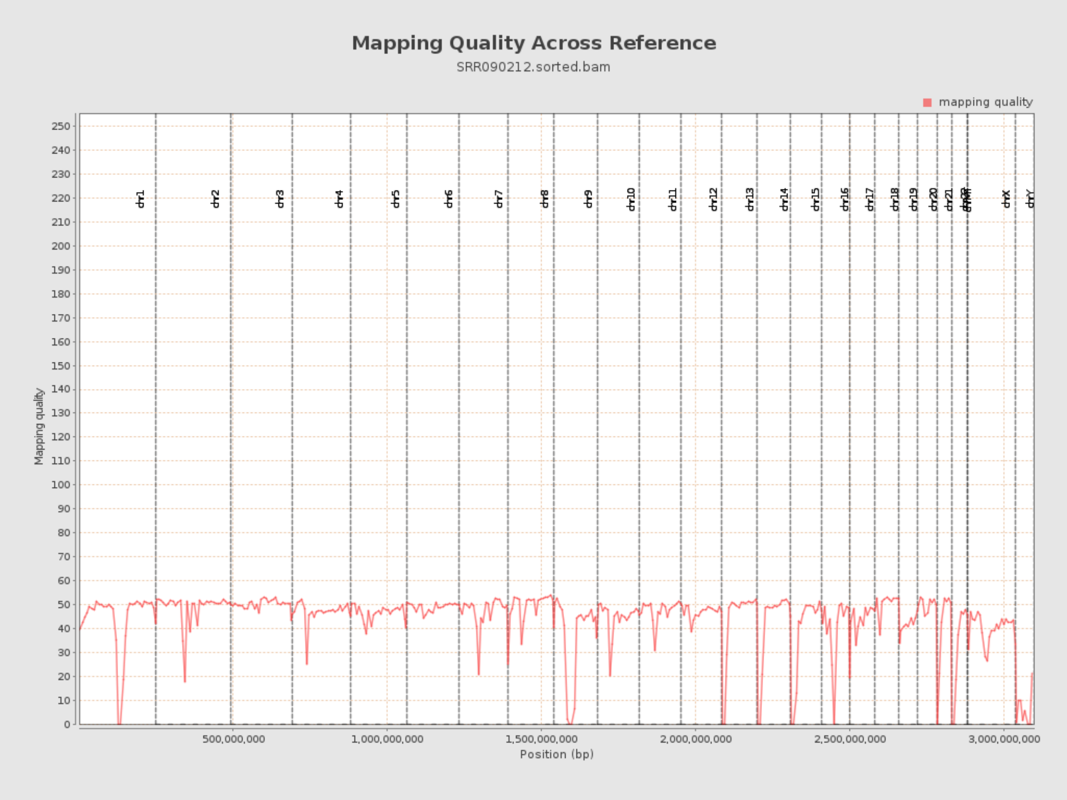
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram