Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 10:44:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090211.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_SRR090211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090211.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 10:44:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,391,670
Mapped reads	23,685,850 / 86.47%
Unmapped reads	3,705,820 / 13.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,243 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,601,712 / 16.8%
Duplication rate	12.5%
Clipped reads	2,154,818 / 7.87%

2.2. ACGT Content

Number/percentage of A's	325,669,721 / 29.18%
Number/percentage of C's	229,986,676 / 20.6%
Number/percentage of T's	319,824,888 / 28.65%
Number/percentage of G's	240,709,374 / 21.57%
Number/percentage of N's	2,541 / 0%
GC Percentage	42.17%

2.3. Coverage

Mean	0.3606

Standard Deviation	1.7531

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

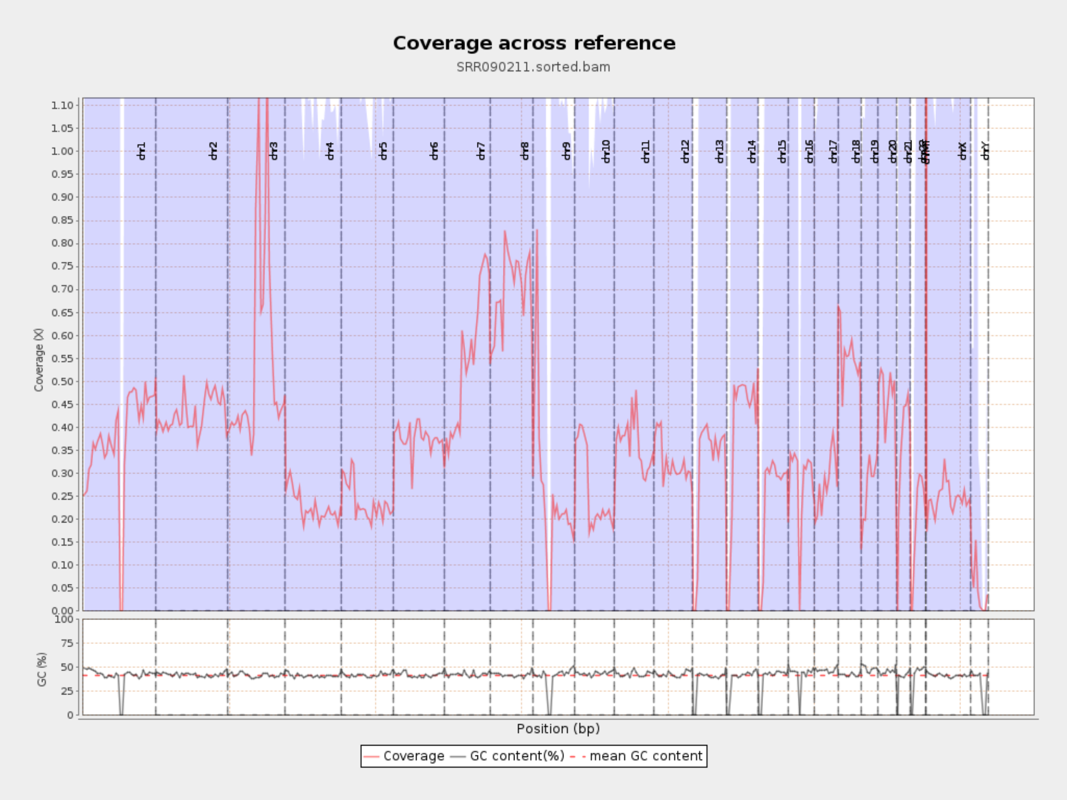
General error rate	0.37%
Mismatches	4,097,834
Insertions	39,162
Mapped reads with at least one insertion	0.17%
Deletions	131,609
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.46%

2.6. Chromosome stats

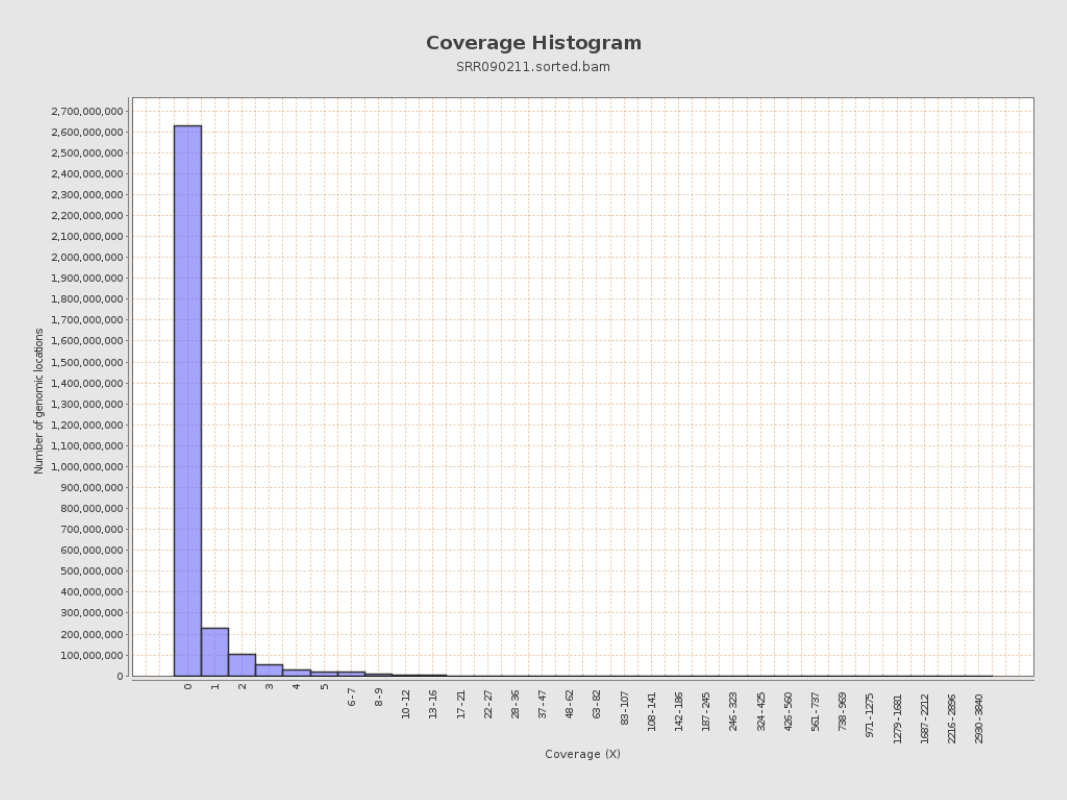
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	93045370	0.3733	2.66
chr2	243199373	104541166	0.4299	1.9776
chr3	198022430	108038517	0.5456	1.5612
chr4	191154276	43306476	0.2266	0.9582
chr5	180915260	42901269	0.2371	0.9598
chr6	171115067	64232961	0.3754	1.3549
chr7	159138663	86824845	0.5456	2.8436

chr8	146364022	102540191	0.7006	2.8239
chr9	141213431	35816086	0.2536	1.5649
chr10	135534747	35432669	0.2614	1.4311
chr11	135006516	48571183	0.3598	1.6868
chr12	133851895	43522543	0.3252	1.1765
chr13	115169878	35732833	0.3103	1.1173
chr14	107349540	42241199	0.3935	1.3113
chr15	102531392	24778390	0.2417	0.9782
chr16	90354753	24814853	0.2746	1.111
chr17	81195210	22722555	0.2799	1.2084
chr18	78077248	43362569	0.5554	2.5885
chr19	59128983	16253967	0.2749	1.8735
chr20	63025520	29644543	0.4704	1.4656
chr21	48129895	16698308	0.3469	1.3098
chr22	51304566	9989735	0.1947	0.8947
chrMT	16571	762073	45.9884	27.2205
chrX	155270560	37909004	0.2441	1.1048
chrY	59373566	2711590	0.0457	1.1276

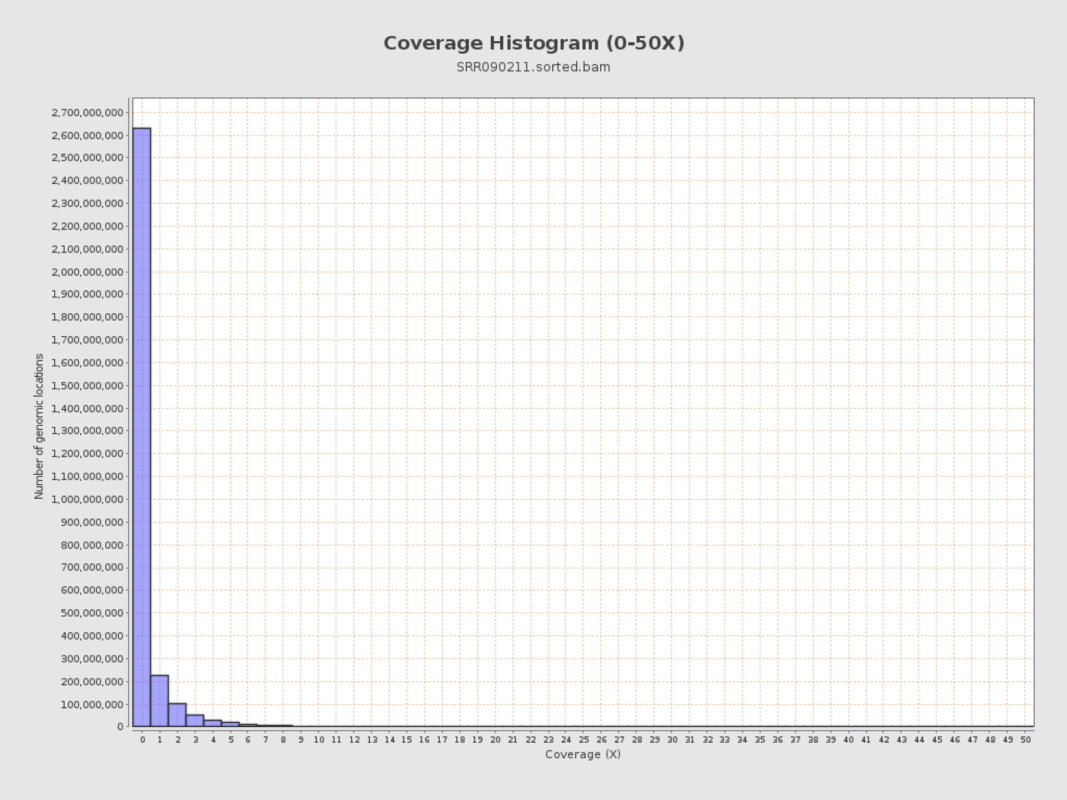
3. Results : Coverage across reference



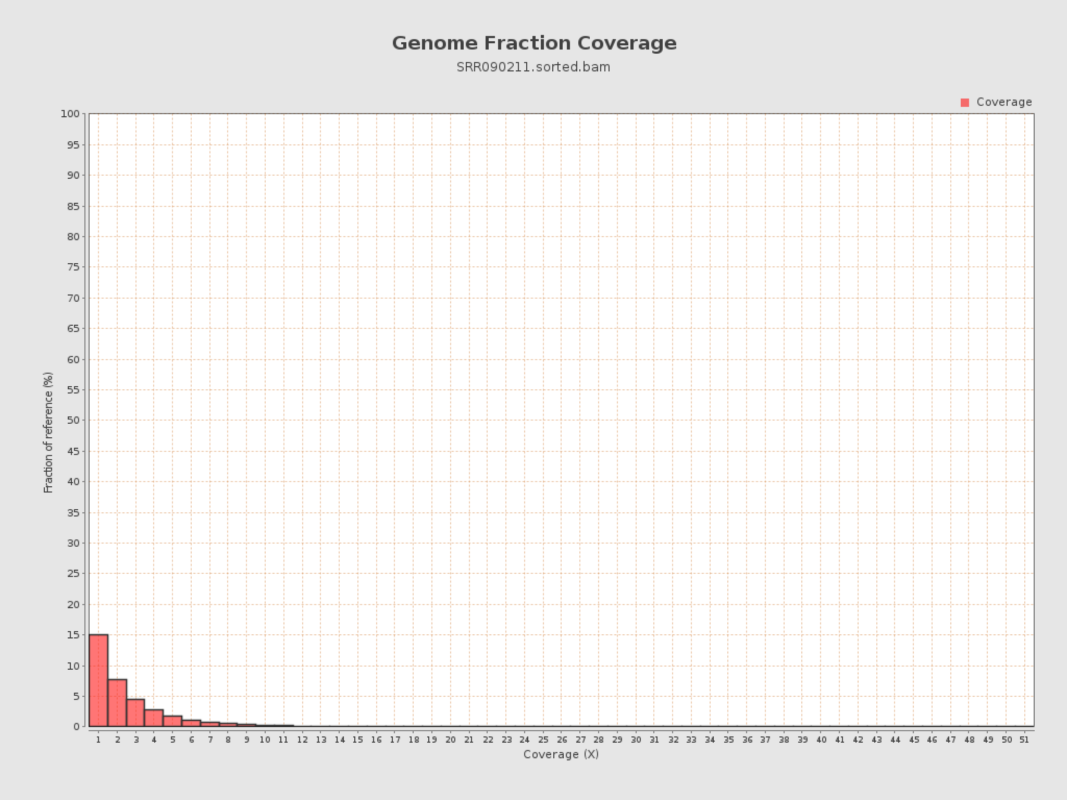
4. Results : Coverage Histogram



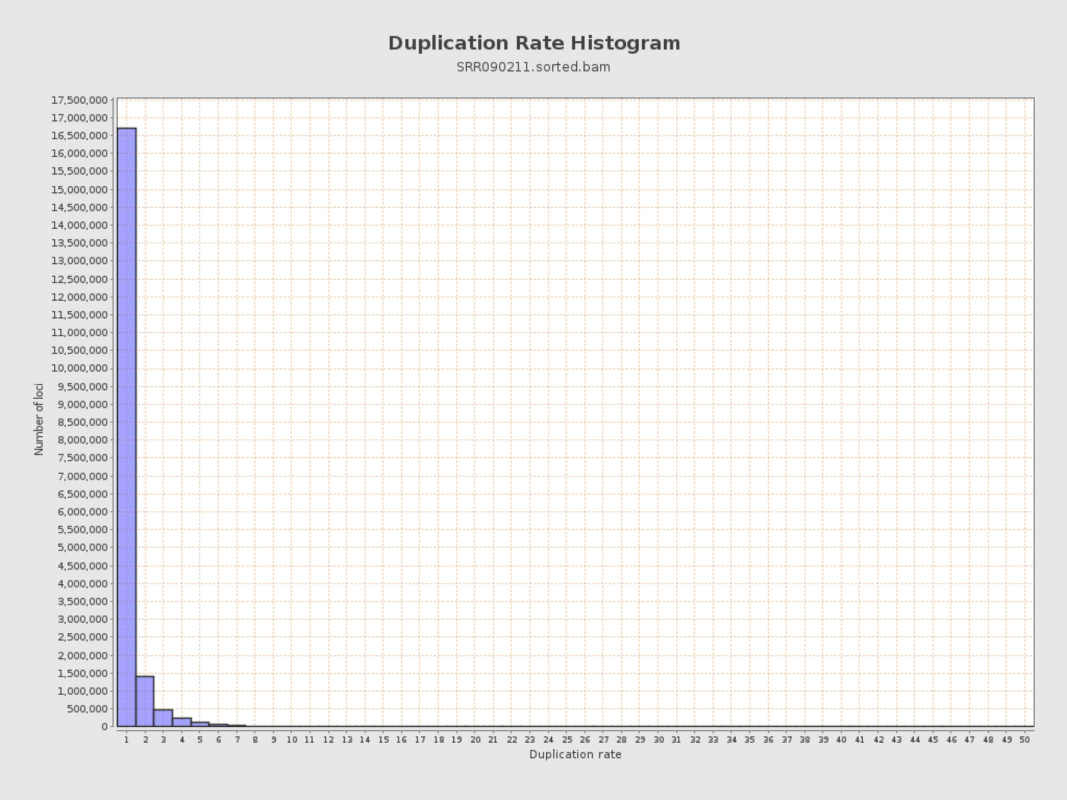
5. Results : Coverage Histogram (0-50X)



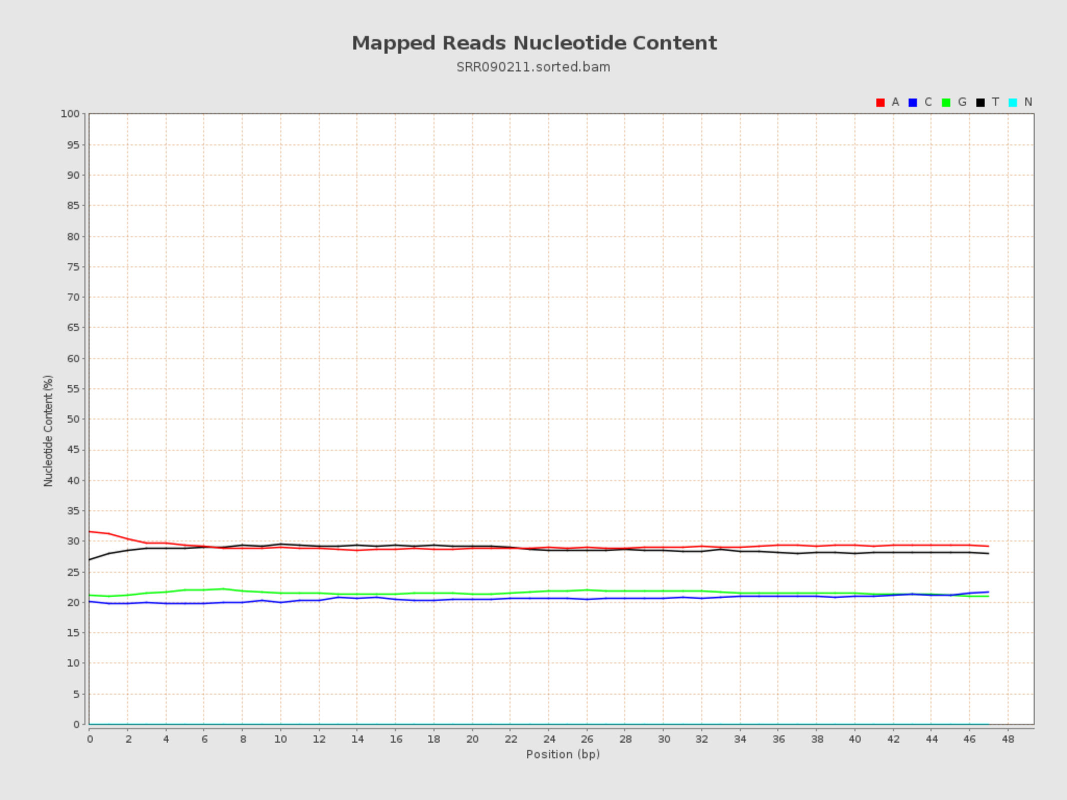
6. Results : Genome Fraction Coverage



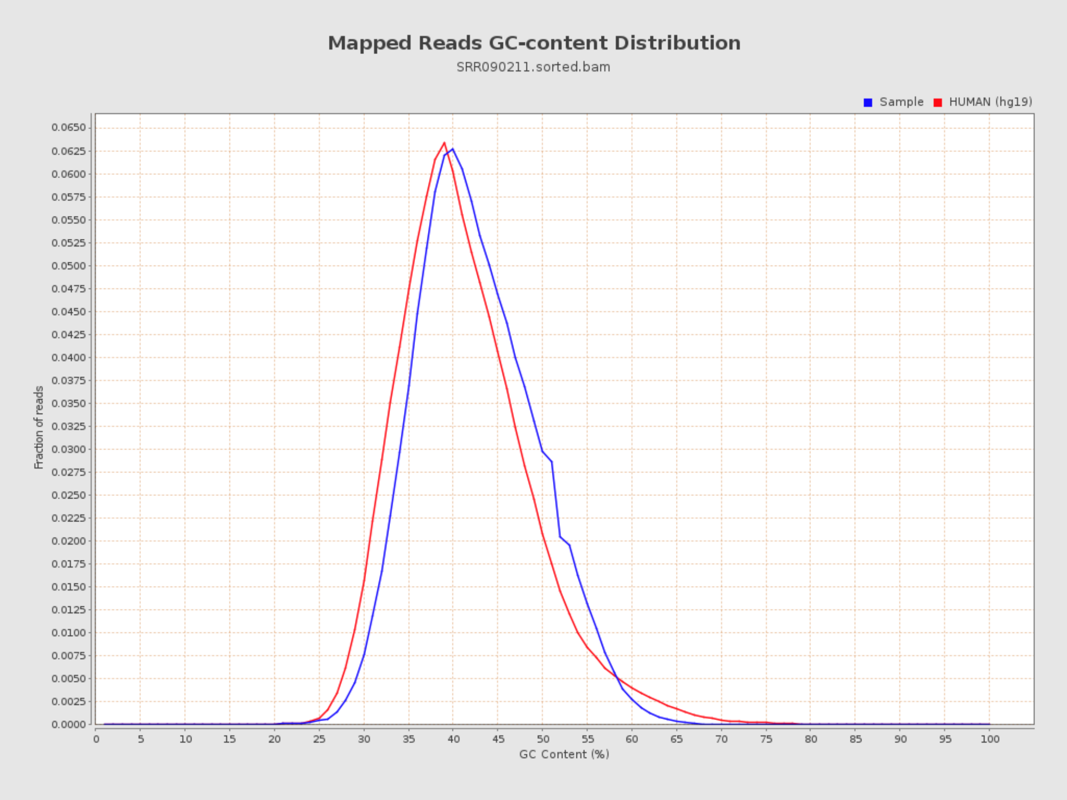
7. Results : Duplication Rate Histogram



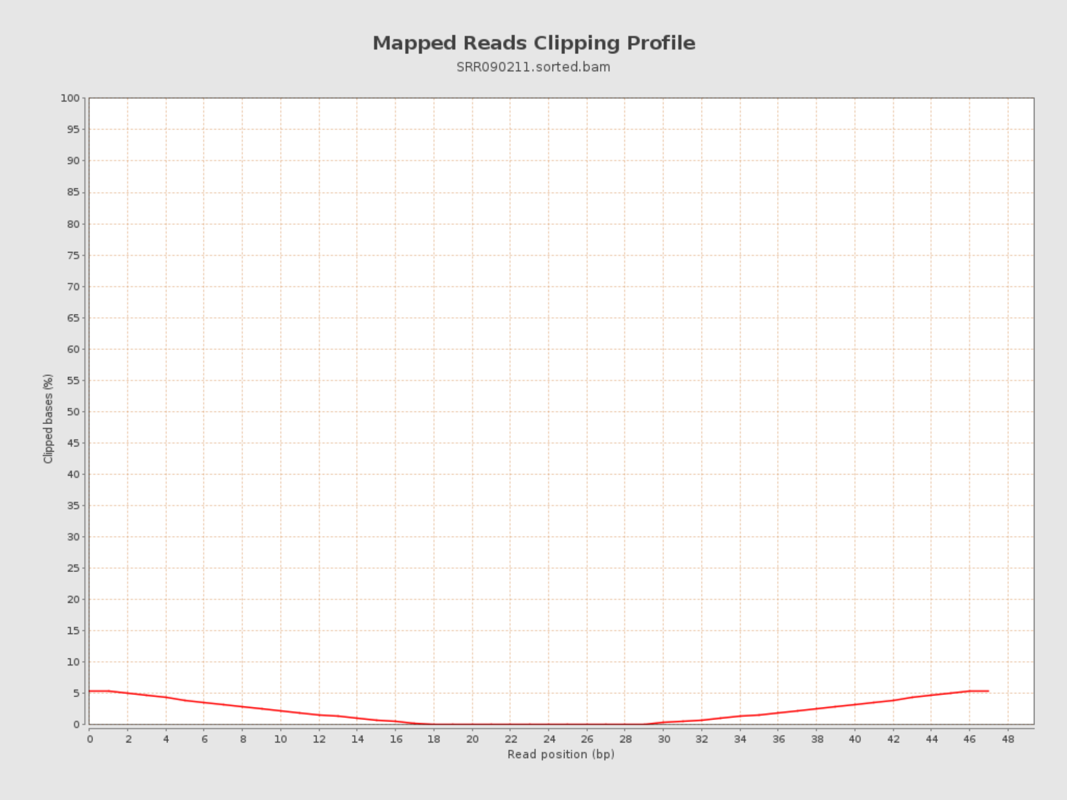
8. Results : Mapped Reads Nucleotide Content



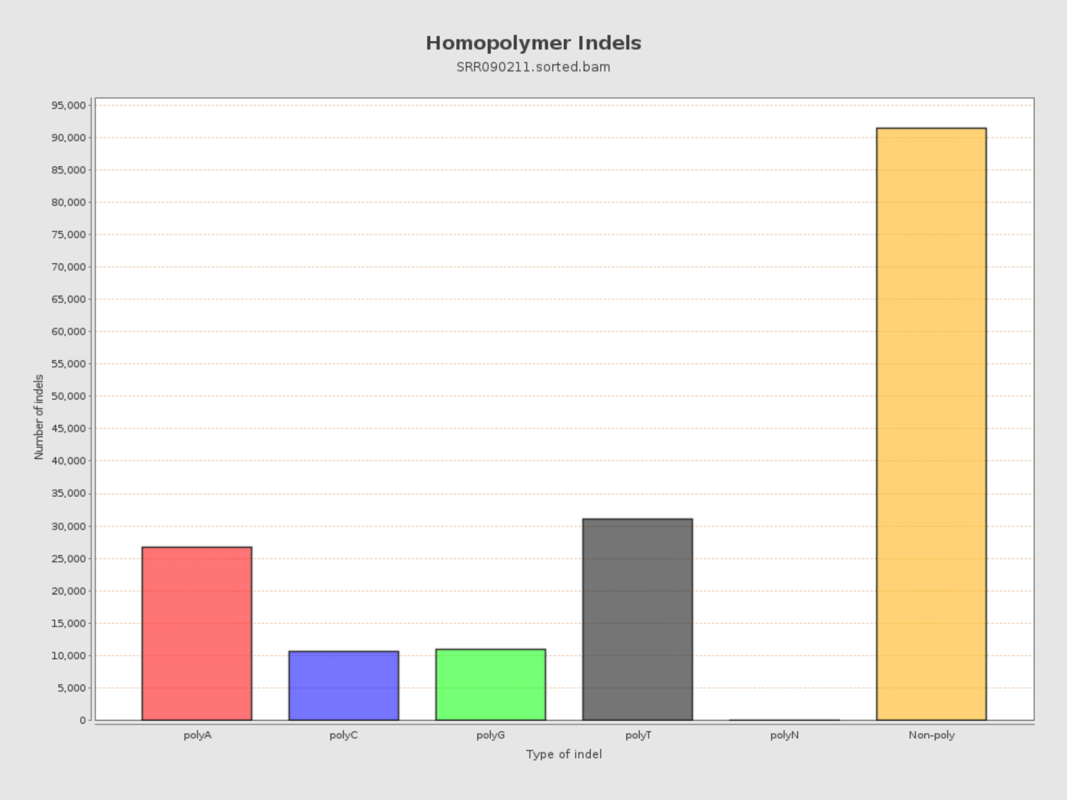
9. Results : Mapped Reads GC-content Distribution



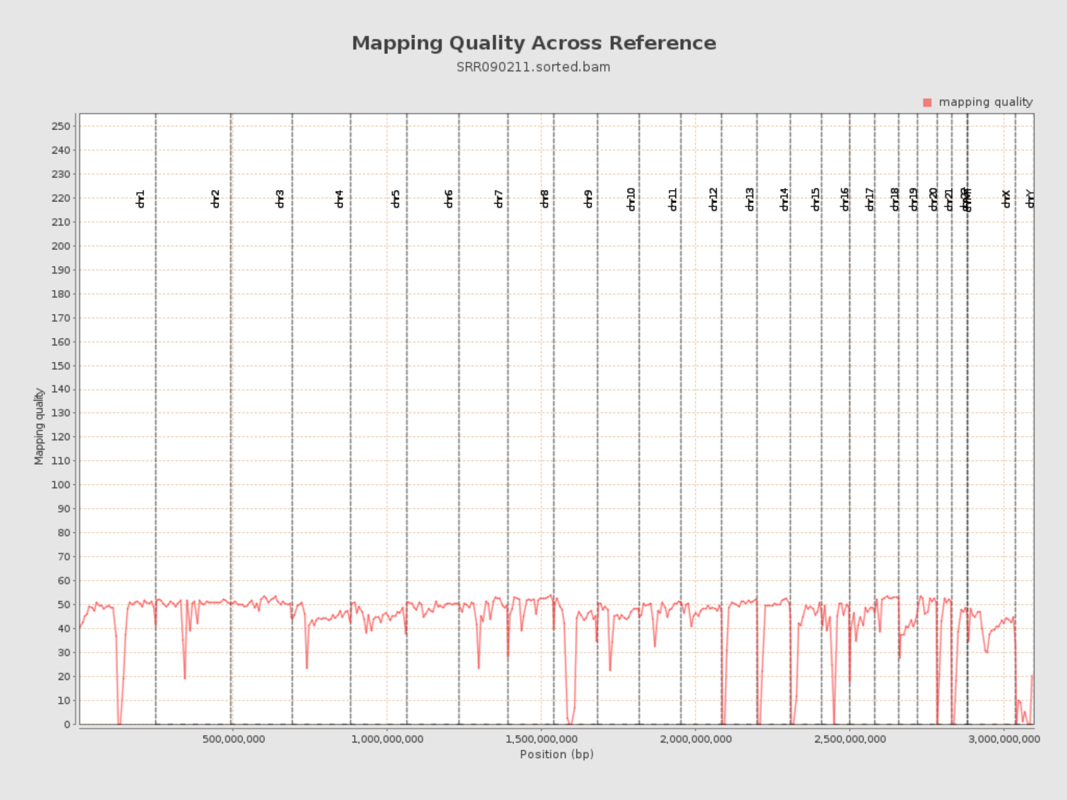
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram