Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 02:25:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089731.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_SRR089731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089731.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 02:25:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,993,432
Mapped reads	14,636,337 / 86.13%
Unmapped reads	2,357,095 / 13.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	80,052 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	4,490,827 / 26.43%
Duplication rate	16.22%
Clipped reads	7,505,471 / 44.17%

2.2. ACGT Content

Number/percentage of A's	245,061,744 / 25.92%
Number/percentage of C's	176,079,495 / 18.62%
Number/percentage of T's	296,191,386 / 31.32%
Number/percentage of G's	227,827,085 / 24.09%
Number/percentage of N's	392,367 / 0.04%
GC Percentage	42.72%

2.3. Coverage

Mean	0.3055

Standard Deviation	2.4515

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

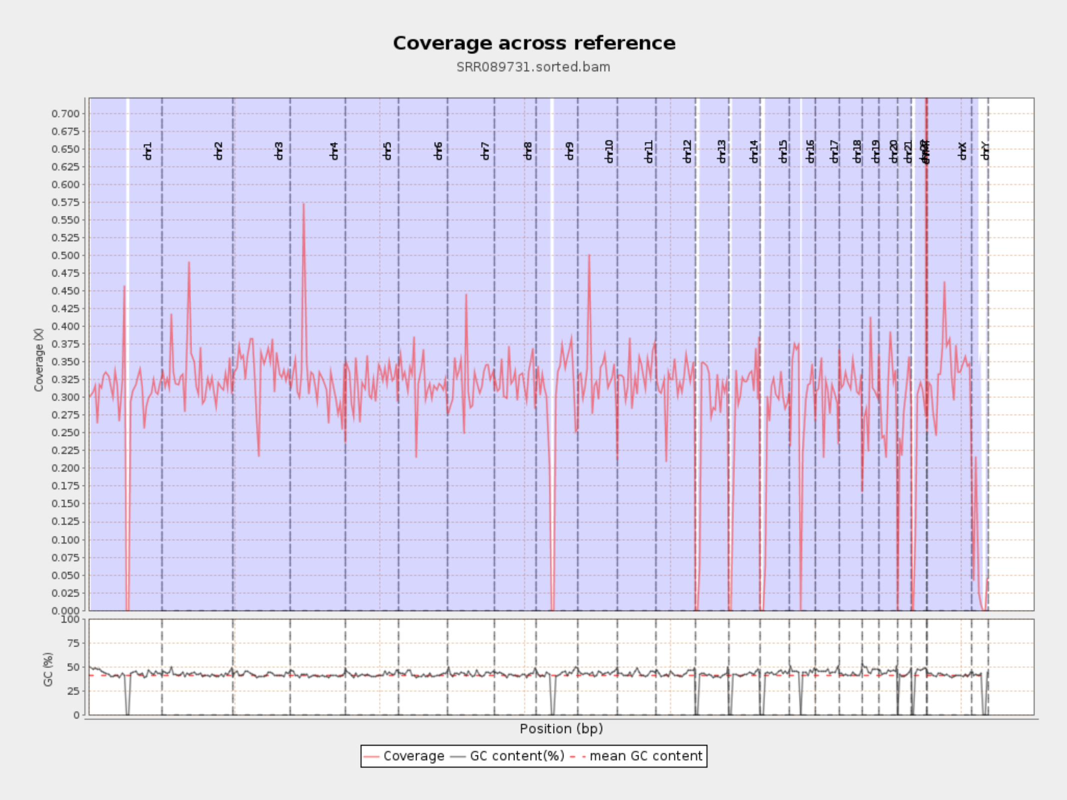
General error rate	0.68%
Mismatches	6,293,440
Insertions	62,640
Mapped reads with at least one insertion	0.42%
Deletions	176,395
Mapped reads with at least one deletion	1.19%
Homopolymer indels	45.65%

2.6. Chromosome stats

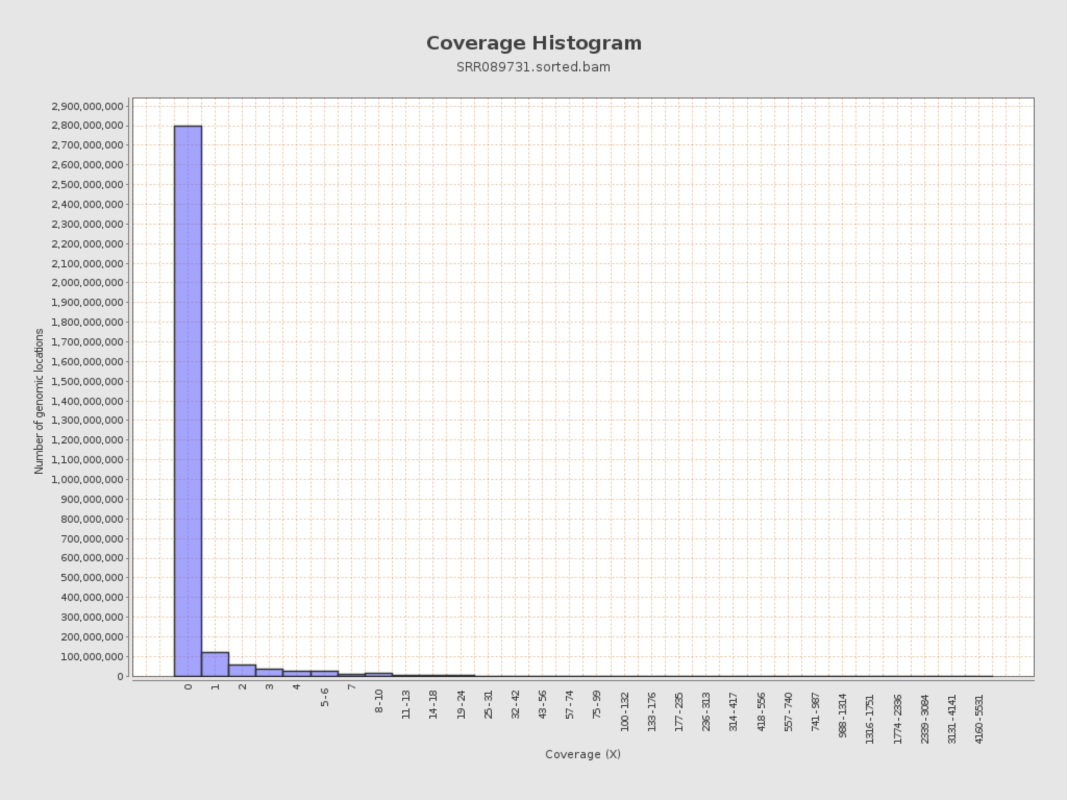
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	73634487	0.2954	4.5415
chr2	243199373	80621735	0.3315	3.7694
chr3	198022430	67467376	0.3407	1.4543
chr4	191154276	62176487	0.3253	1.8271
chr5	180915260	58266280	0.3221	1.4346
chr6	171115067	55076322	0.3219	1.6726
chr7	159138663	51581207	0.3241	2.9004

chr8	146364022	47531980	0.3248	2.7139
chr9	141213431	40660916	0.2879	2.1882
chr10	135534747	45140960	0.3331	2.3758
chr11	135006516	44758863	0.3315	1.8735
chr12	133851895	42851272	0.3201	1.549
chr13	115169878	30209619	0.2623	1.2845
chr14	107349540	29010624	0.2702	1.3943
chr15	102531392	24844902	0.2423	1.356
chr16	90354753	26570015	0.2941	1.4762
chr17	81195210	24205574	0.2981	1.6764
chr18	78077248	25364280	0.3249	3.2793
chr19	59128983	17610594	0.2978	2.9992
chr20	63025520	18720142	0.297	1.5472
chr21	48129895	12436042	0.2584	1.6129
chr22	51304566	10807453	0.2107	1.2195
chrMT	16571	754451	45.5284	30.7913
chrX	155270560	52364790	0.3372	1.6876
chrY	59373566	3195217	0.0538	1.8963

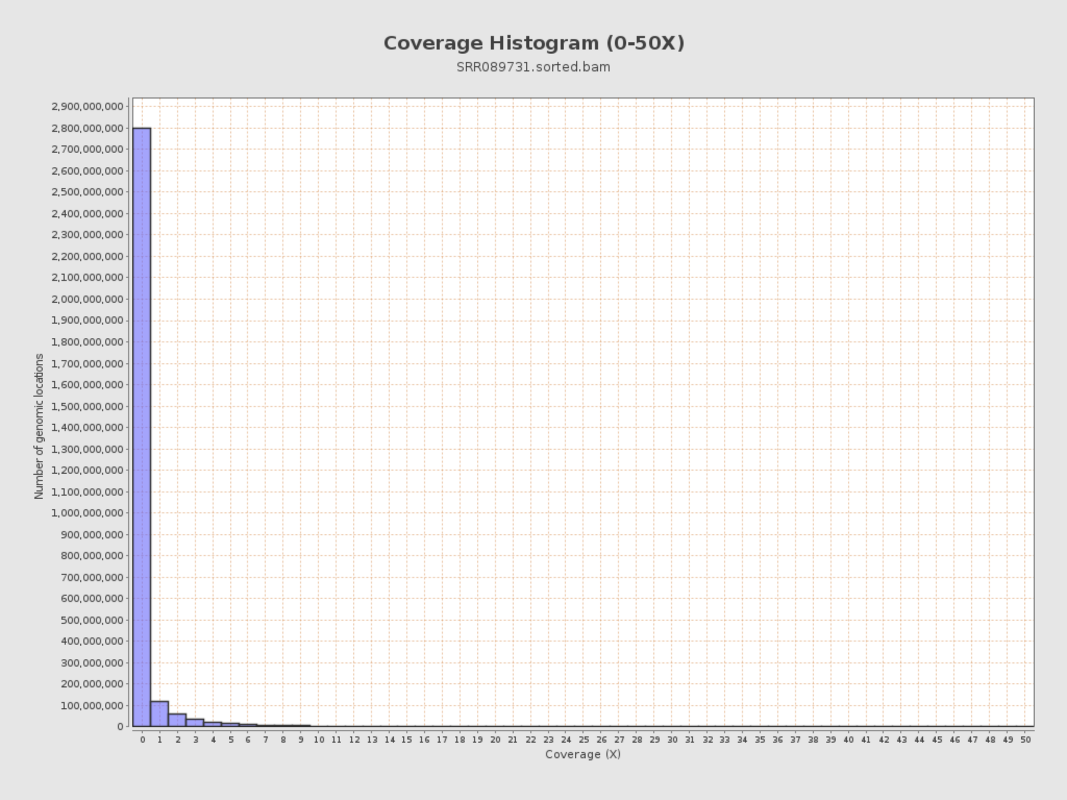
3. Results : Coverage across reference



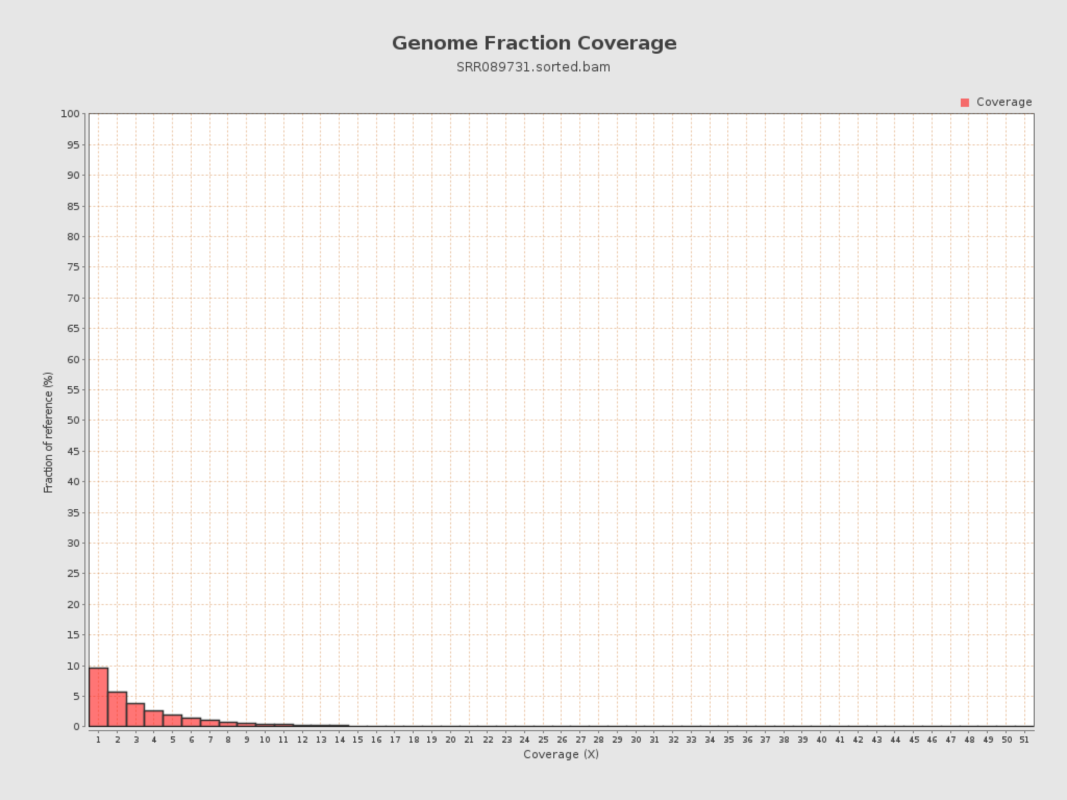
4. Results : Coverage Histogram



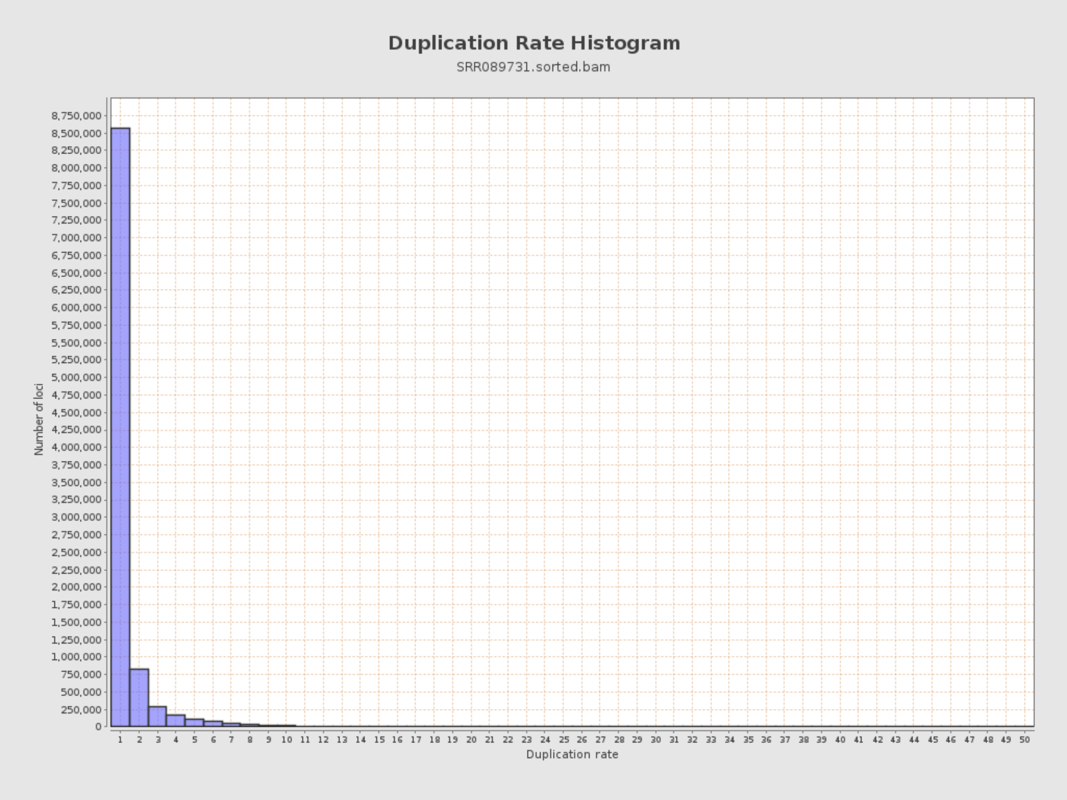
5. Results : Coverage Histogram (0-50X)



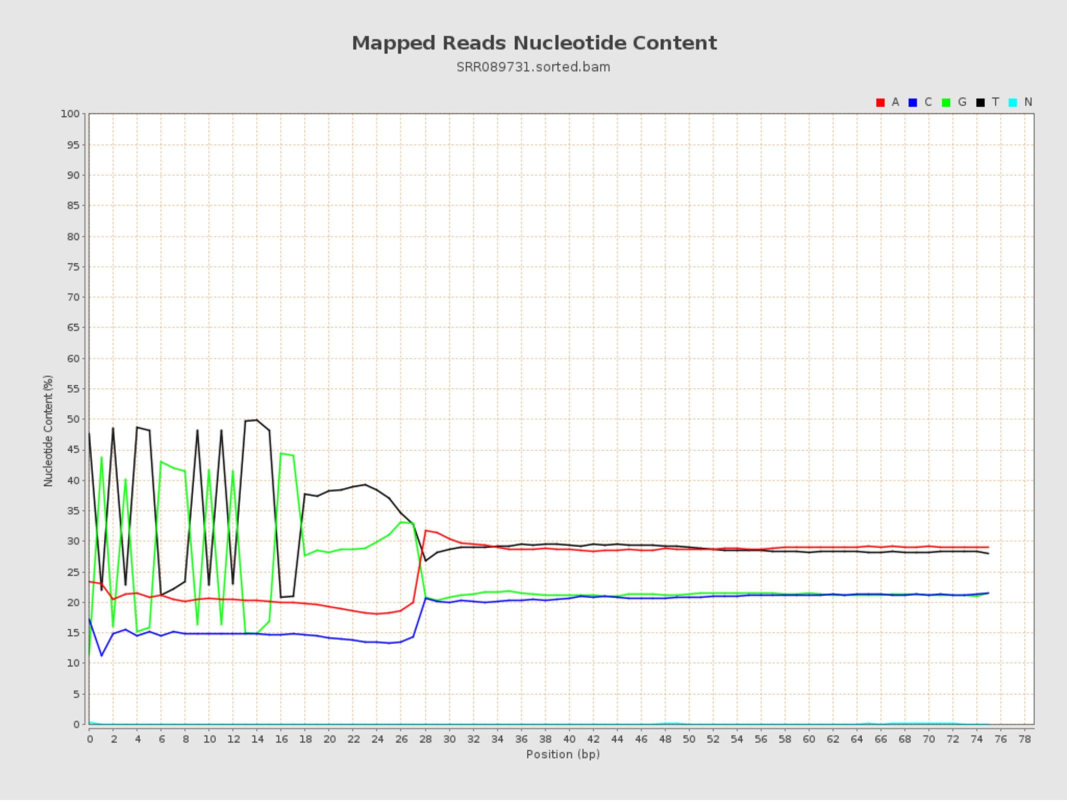
6. Results : Genome Fraction Coverage



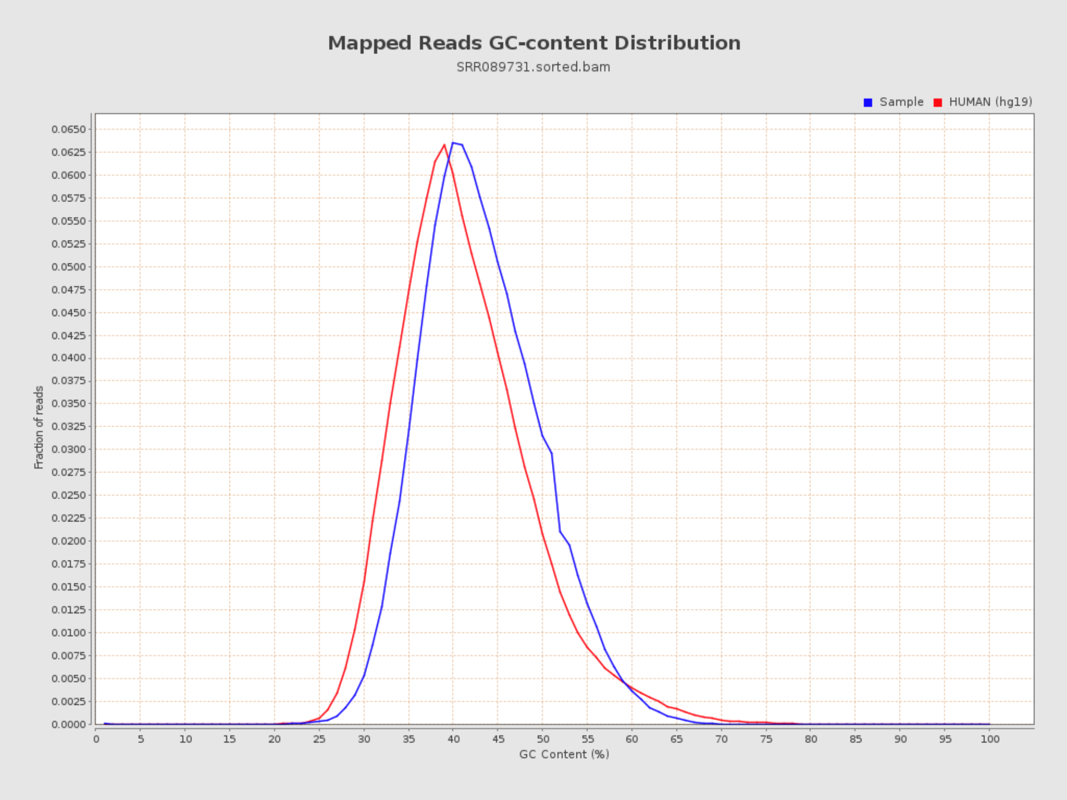
7. Results : Duplication Rate Histogram



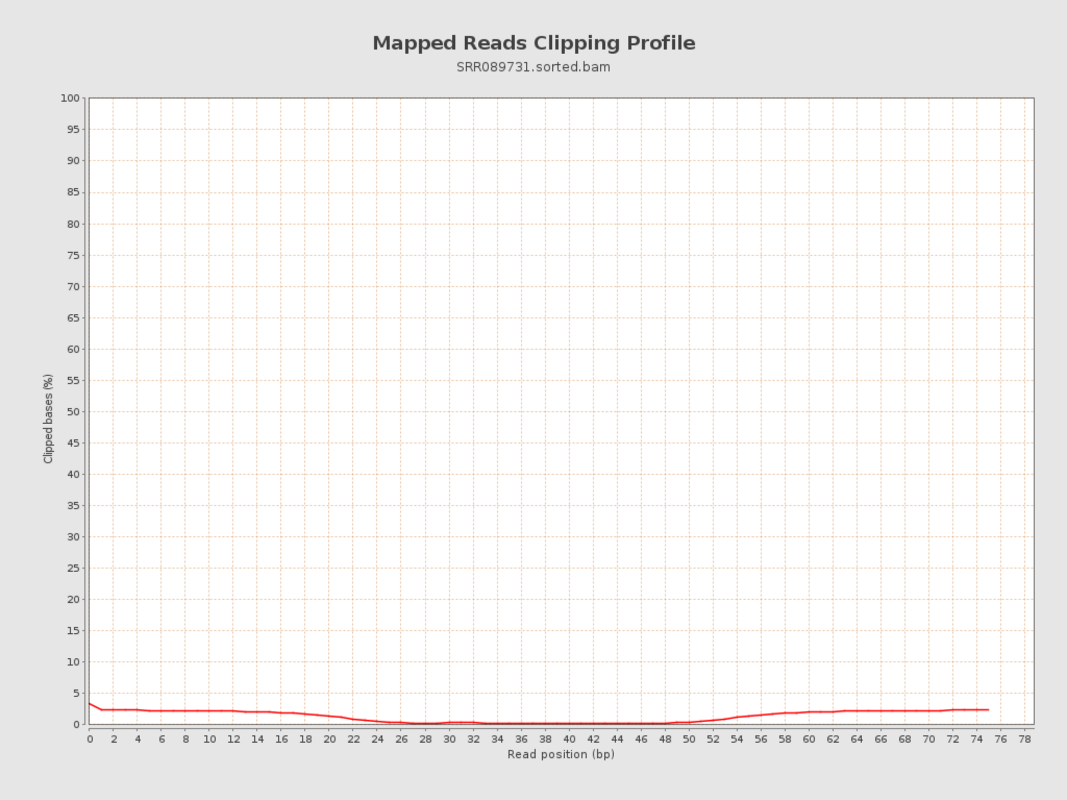
8. Results : Mapped Reads Nucleotide Content



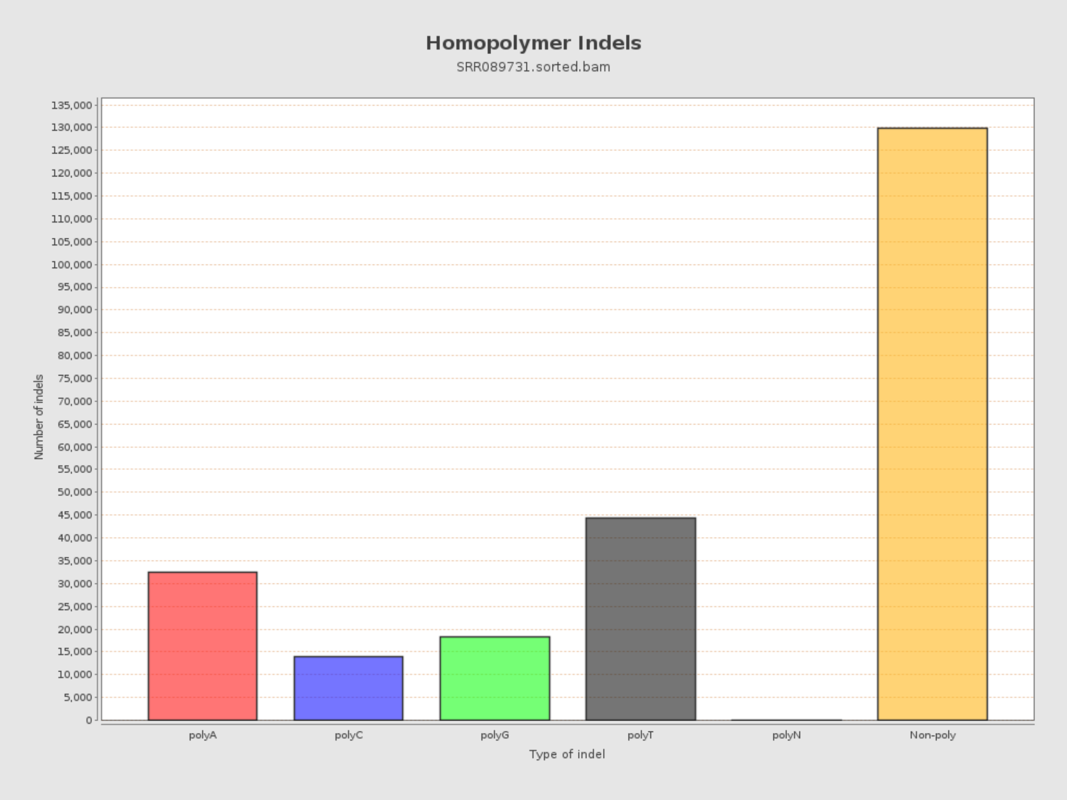
9. Results : Mapped Reads GC-content Distribution



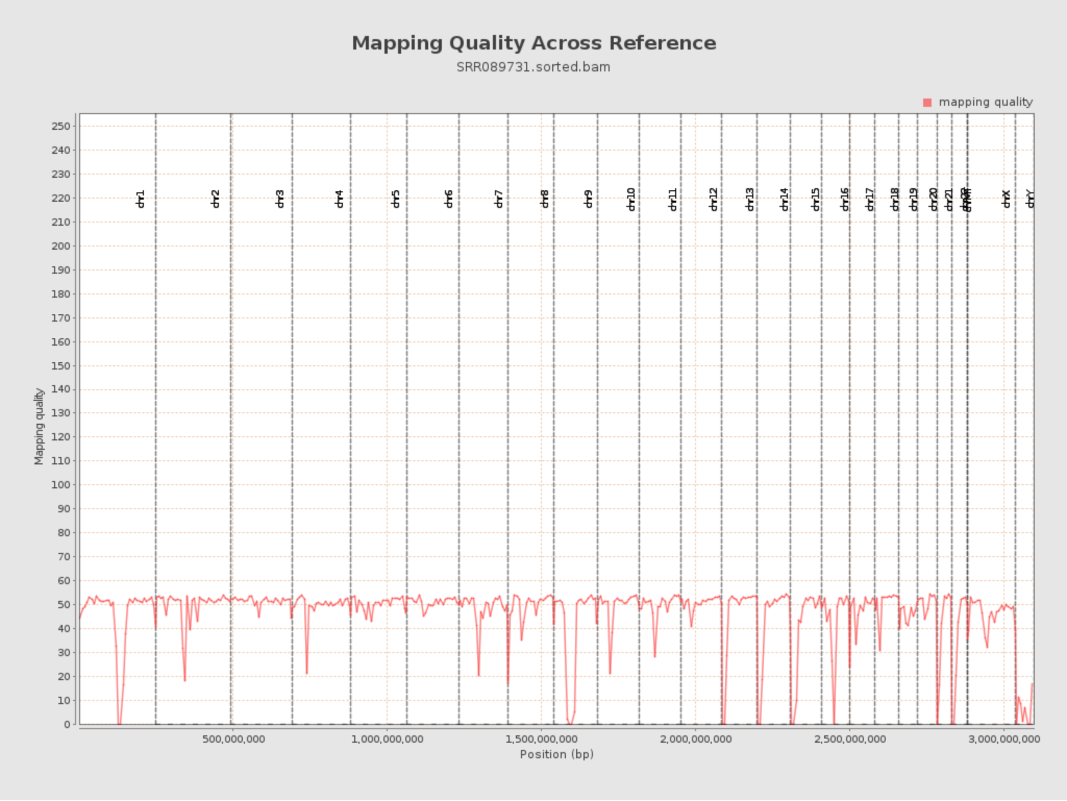
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram