

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:07:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008689.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_SRR6008689 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008689.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:07:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008689.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,548,308
Mapped reads	1,312,207 / 84.75%
Unmapped reads	236,101 / 15.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,237 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	43,279 / 2.8%
Duplication rate	1.97%
Clipped reads	770,423 / 49.76%

2.2. ACGT Content

Number/percentage of A's	21,624,098 / 26.12%
Number/percentage of C's	15,593,663 / 18.84%
Number/percentage of T's	25,273,402 / 30.53%
Number/percentage of G's	20,257,995 / 24.47%
Number/percentage of N's	24,669 / 0.03%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.3537
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	41.39
----------------------	-------

2.5. Mismatches and indels

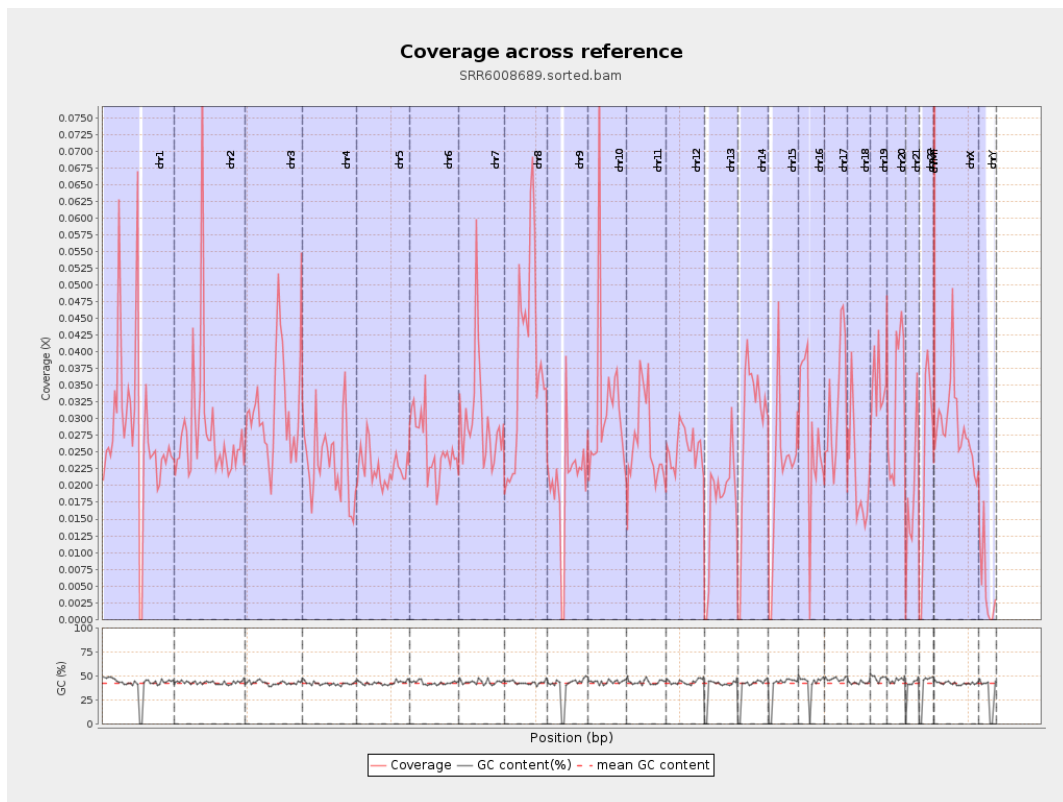
General error rate	0.95%
Mismatches	772,154
Insertions	6,366
Mapped reads with at least one insertion	0.48%
Deletions	37,343
Mapped reads with at least one deletion	2.8%
Homopolymer indels	41.63%

2.6. Chromosome stats

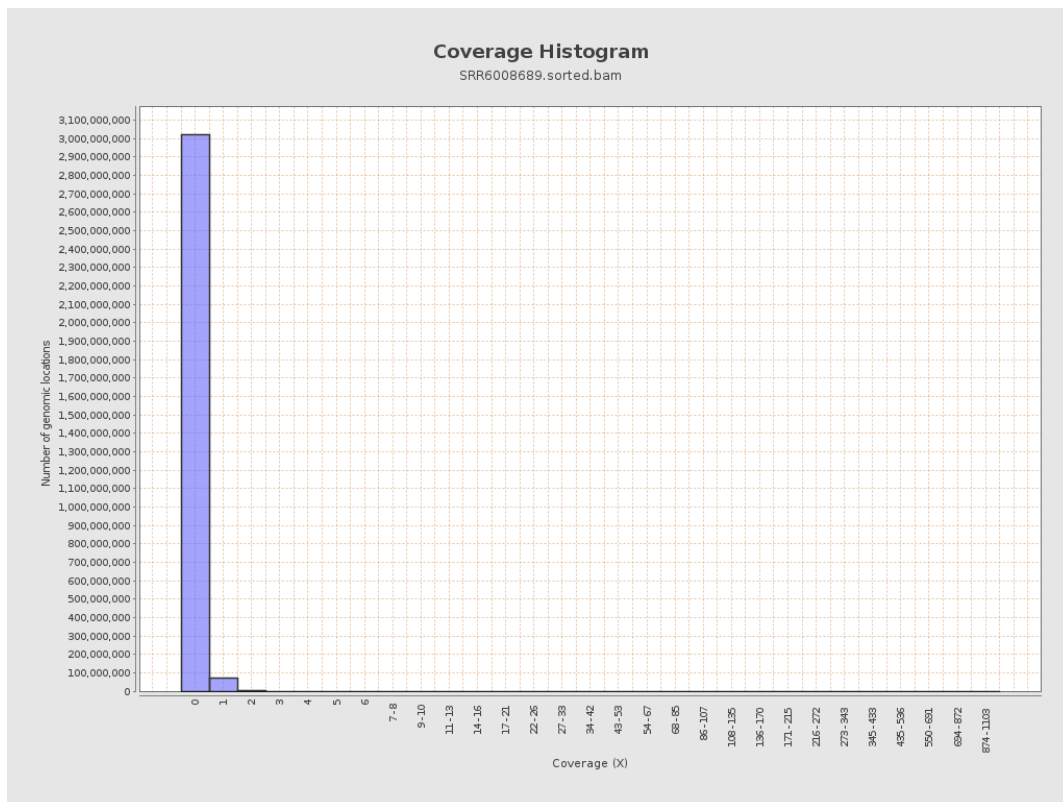
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6832970	0.0274	0.7975
chr2	243199373	6850765	0.0282	0.4194
chr3	198022430	6180792	0.0312	0.1985
chr4	191154276	4533785	0.0237	0.177
chr5	180915260	4099649	0.0227	0.1617
chr6	171115067	4399332	0.0257	0.2074
chr7	159138663	4789199	0.0301	0.3742

chr8	146364022	5646716	0.0386	0.2834
chr9	141213431	2850826	0.0202	0.305
chr10	135534747	4308790	0.0318	0.4461
chr11	135006516	3619063	0.0268	0.282
chr12	133851895	3427926	0.0256	0.1742
chr13	115169878	2004620	0.0174	0.1374
chr14	107349540	3125162	0.0291	0.1965
chr15	102531392	2255624	0.022	0.162
chr16	90354753	2489481	0.0276	0.2268
chr17	81195210	2613875	0.0322	0.229
chr18	78077248	1632940	0.0209	0.537
chr19	59128983	2095041	0.0354	0.5132
chr20	63025520	2049540	0.0325	0.197
chr21	48129895	904123	0.0188	0.166
chr22	51304566	1245764	0.0243	0.1631
chrMT	16571	97715	5.8967	4.2195
chrX	155270560	4490699	0.0289	0.2207
chrY	59373566	294993	0.005	0.1575

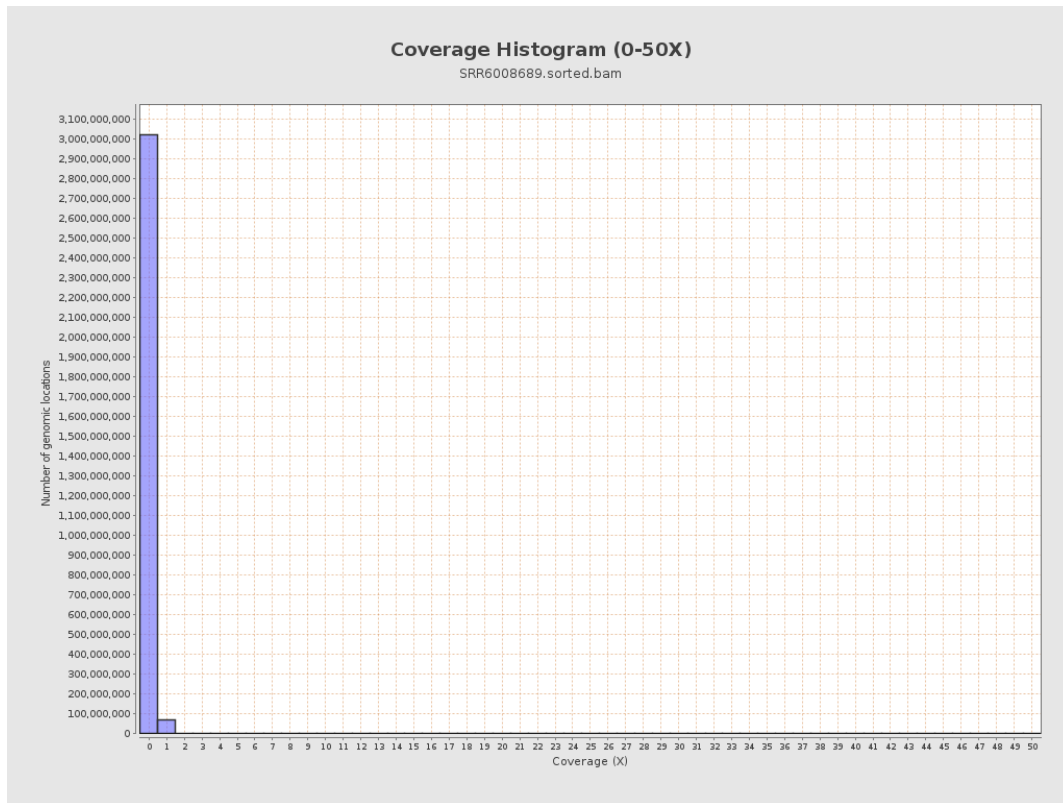
3. Results : Coverage across reference



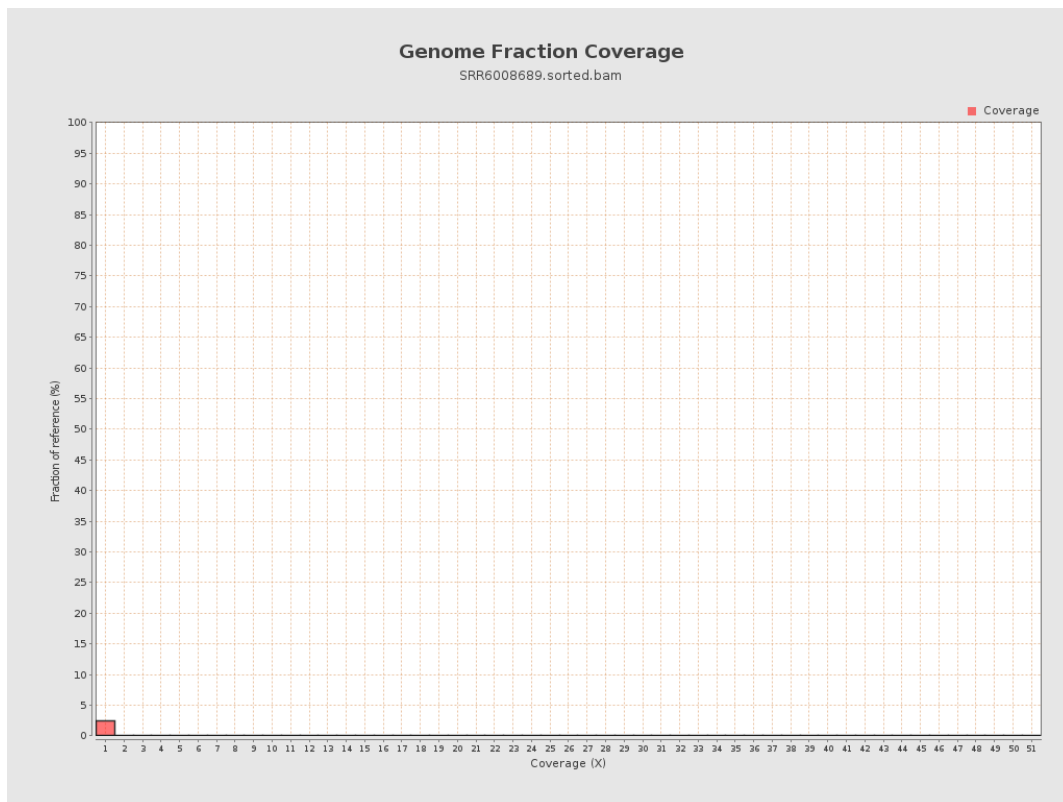
4. Results : Coverage Histogram



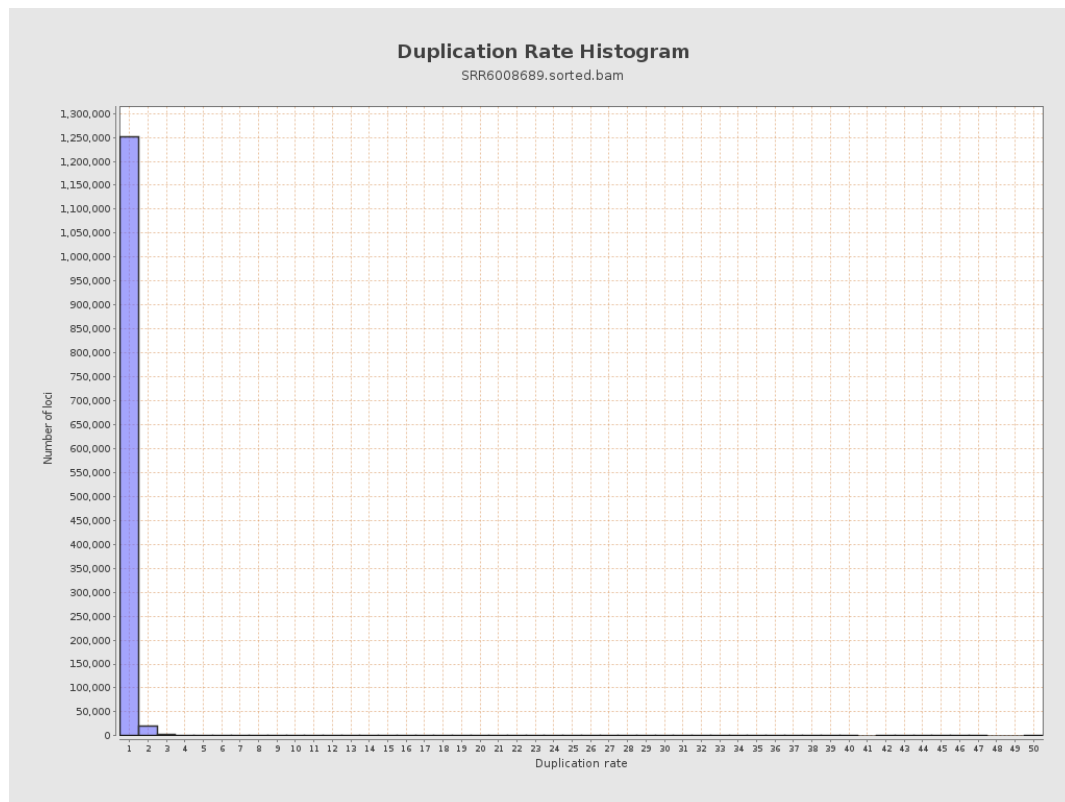
5. Results : Coverage Histogram (0-50X)



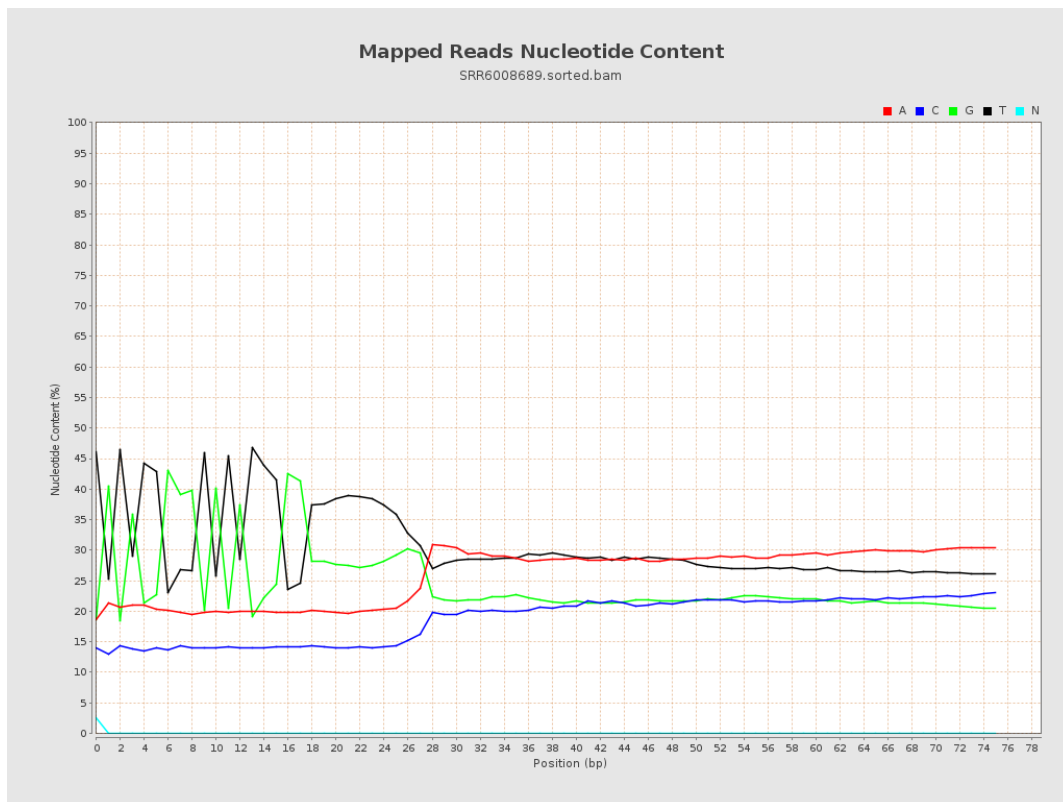
6. Results : Genome Fraction Coverage



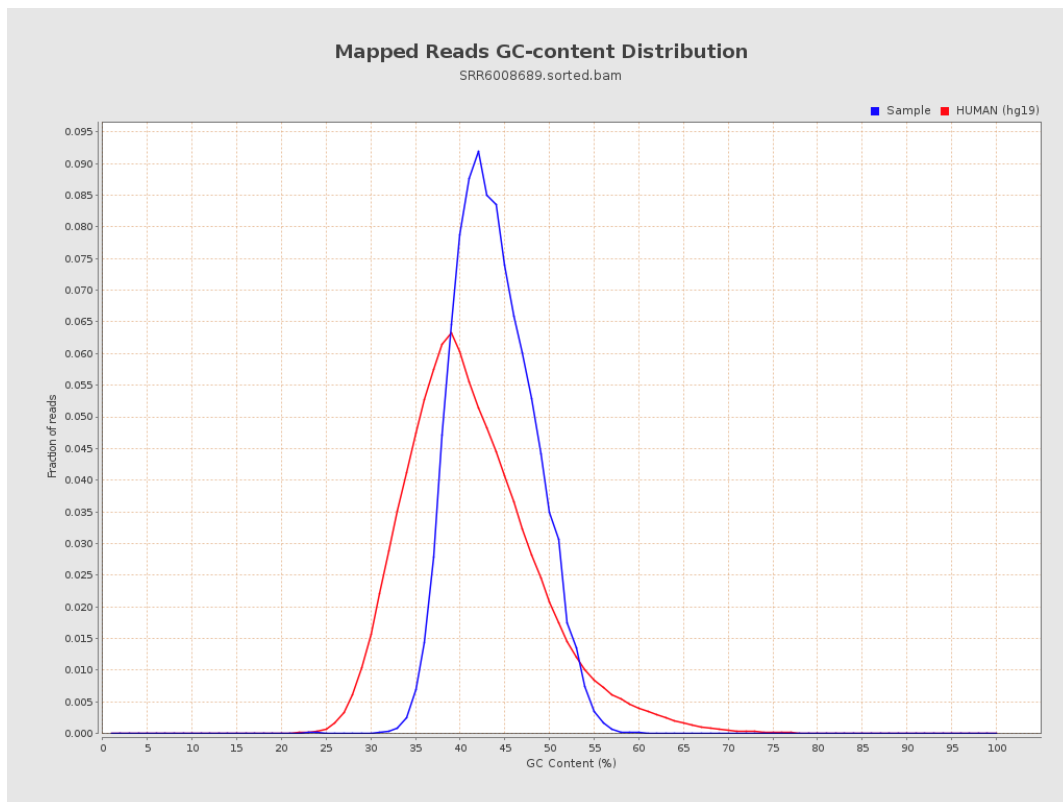
7. Results : Duplication Rate Histogram



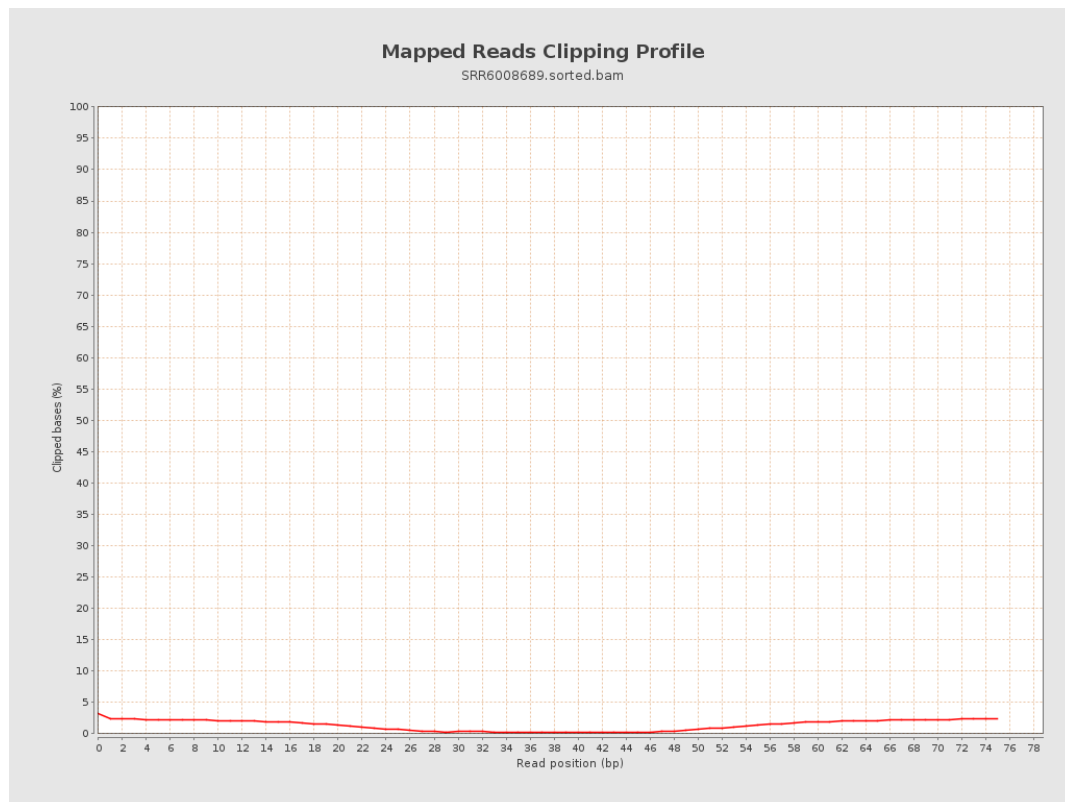
8. Results : Mapped Reads Nucleotide Content



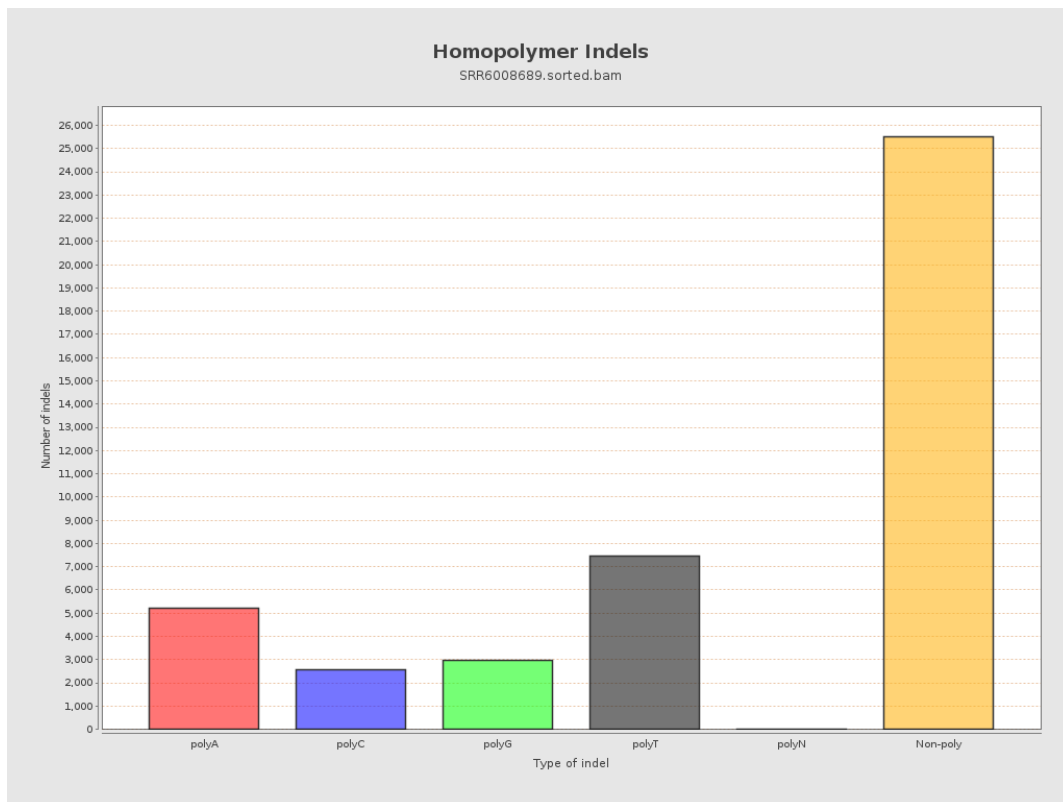
9. Results : Mapped Reads GC-content Distribution



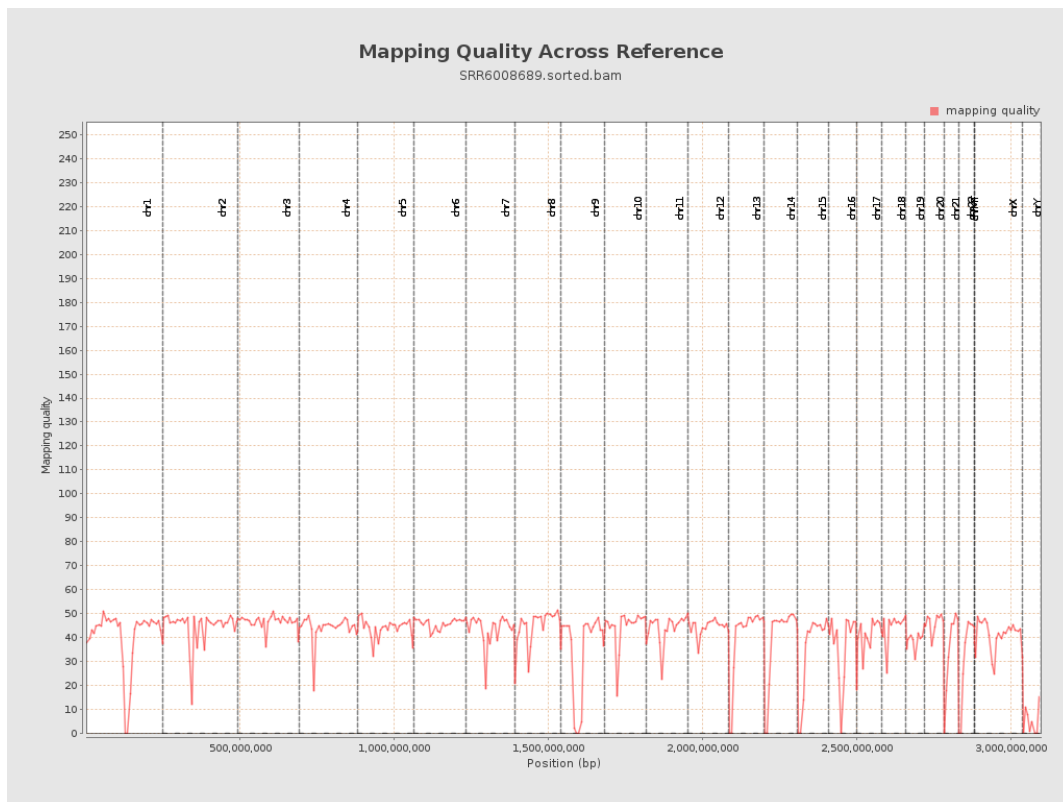
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

