Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:16:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008780.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_SRR6008780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008780.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:16:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,059,593
Mapped reads	1,857,816 / 90.2%
Unmapped reads	201,777 / 9.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,326 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	85,982 / 4.17%
Duplication rate	3.68%
Clipped reads	804,110 / 39.04%

2.2. ACGT Content

Number/percentage of A's	32,964,942 / 26.64%
Number/percentage of C's	24,077,622 / 19.46%
Number/percentage of T's	37,968,418 / 30.69%
Number/percentage of G's	28,546,509 / 23.07%
Number/percentage of N's	174,067 / 0.14%
GC Percentage	42.53%

2.3. Coverage

Mean	0.04

Standard Deviation	0.3524

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

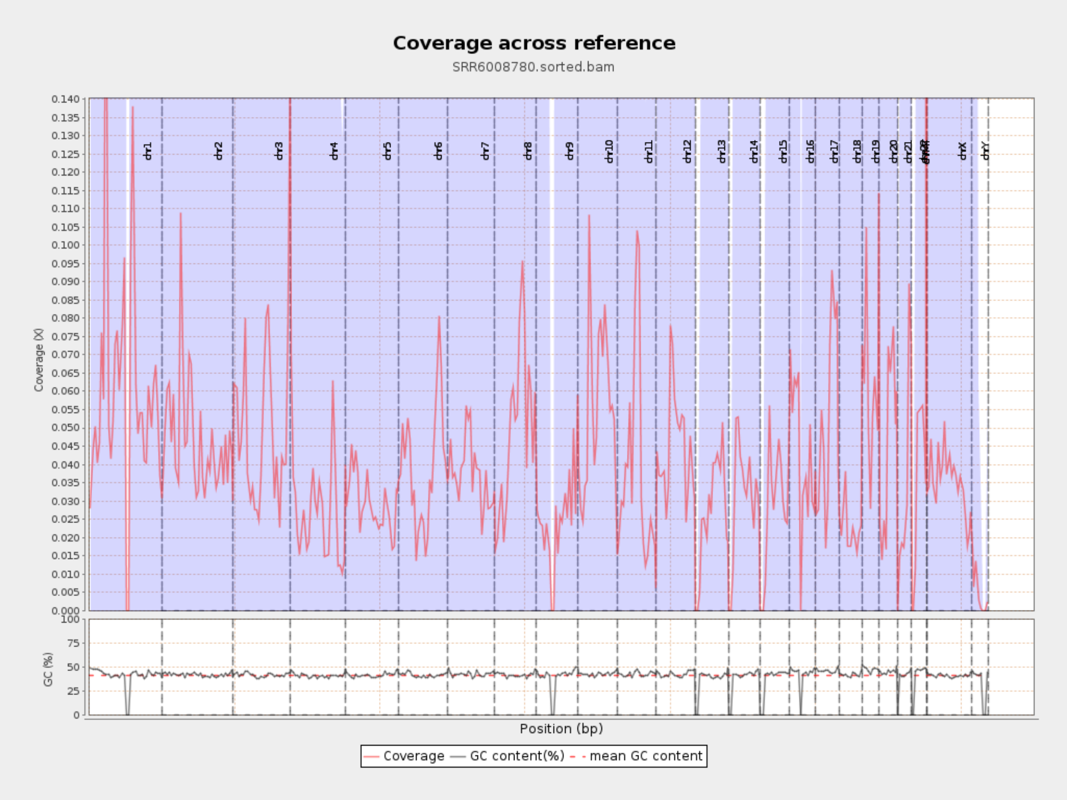
General error rate	0.83%
Mismatches	1,013,665
Insertions	8,756
Mapped reads with at least one insertion	0.46%
Deletions	35,521
Mapped reads with at least one deletion	1.89%
Homopolymer indels	45.74%

2.6. Chromosome stats

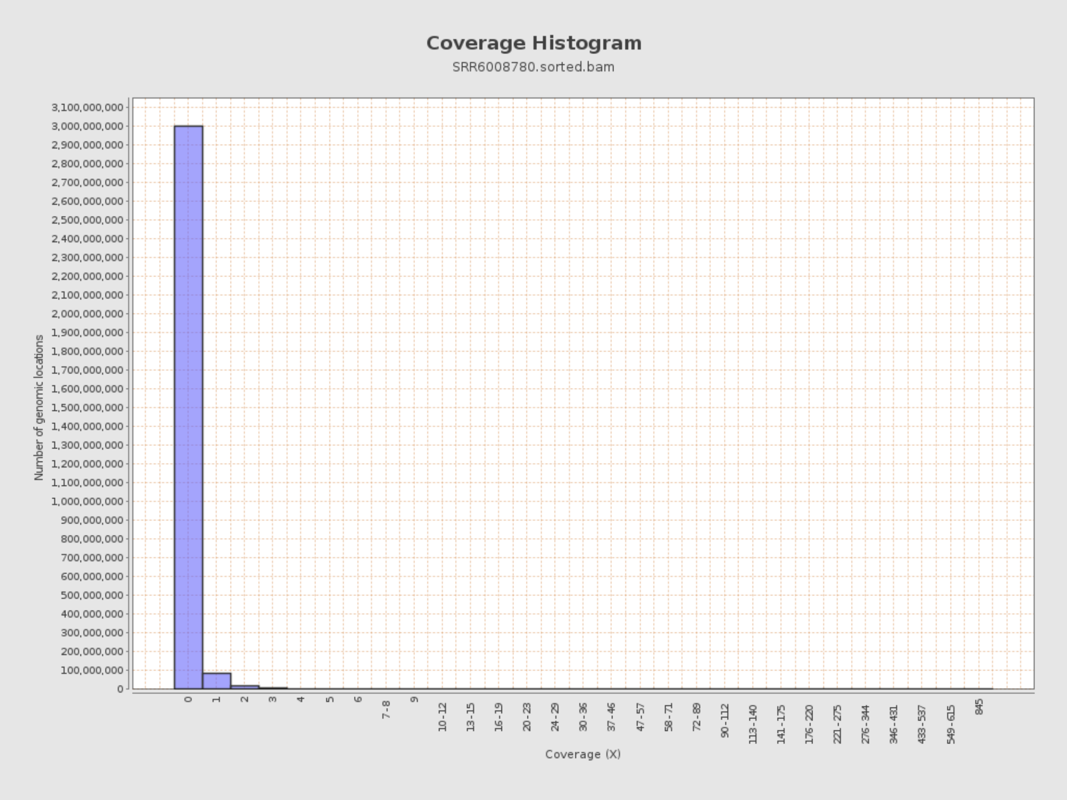
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15039077	0.0603	0.5894
chr2	243199373	11581162	0.0476	0.4721
chr3	198022430	9704581	0.049	0.2984
chr4	191154276	5102266	0.0267	0.2018
chr5	180915260	5362537	0.0296	0.2056
chr6	171115067	6683120	0.0391	0.2728
chr7	159138663	6009094	0.0378	0.3709

chr8	146364022	7236499	0.0494	0.3813
chr9	141213431	3337119	0.0236	0.219
chr10	135534747	7486657	0.0552	0.6405
chr11	135006516	5240258	0.0388	0.2826
chr12	133851895	6027947	0.045	0.2565
chr13	115169878	3139849	0.0273	0.1997
chr14	107349540	3321819	0.0309	0.2152
chr15	102531392	2880715	0.0281	0.2015
chr16	90354753	3818060	0.0423	0.3285
chr17	81195210	4262580	0.0525	0.3185
chr18	78077248	1772606	0.0227	0.3191
chr19	59128983	3630147	0.0614	0.4538
chr20	63025520	2819827	0.0447	0.262
chr21	48129895	1672173	0.0347	0.2339
chr22	51304566	1784396	0.0348	0.2262
chrMT	16571	87595	5.286	3.9441
chrX	155270560	5506348	0.0355	0.239
chrY	59373566	288183	0.0049	0.1431

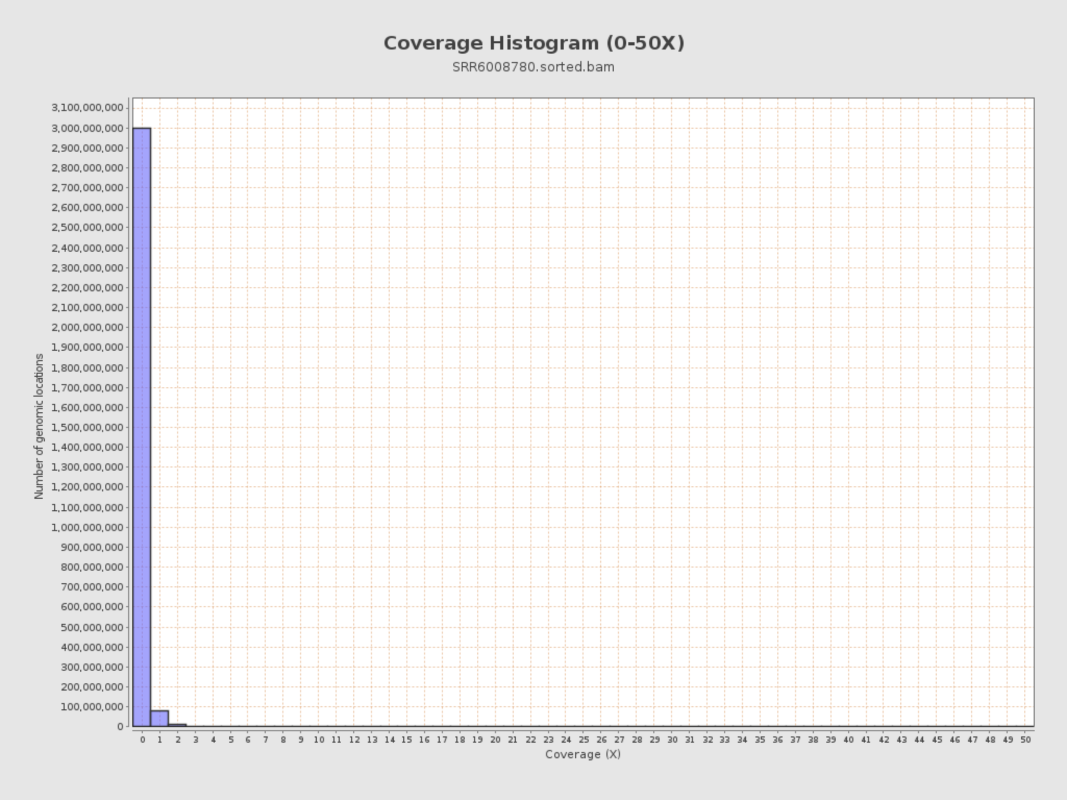
3. Results : Coverage across reference



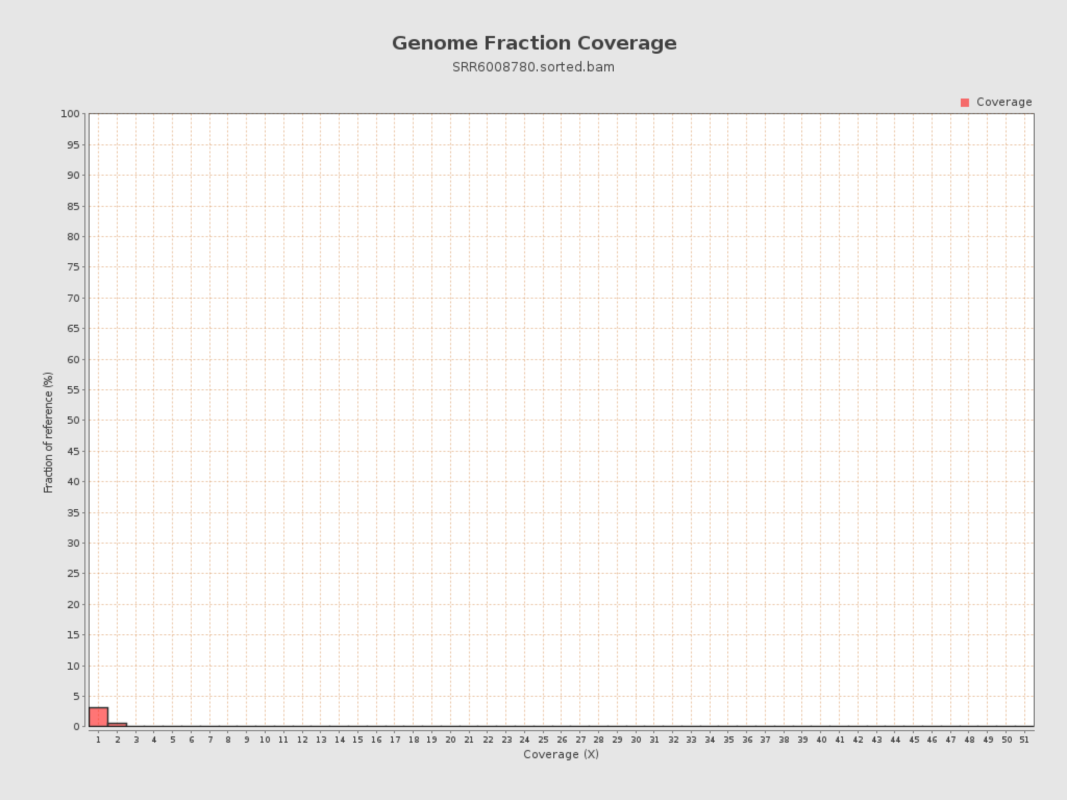
4. Results : Coverage Histogram



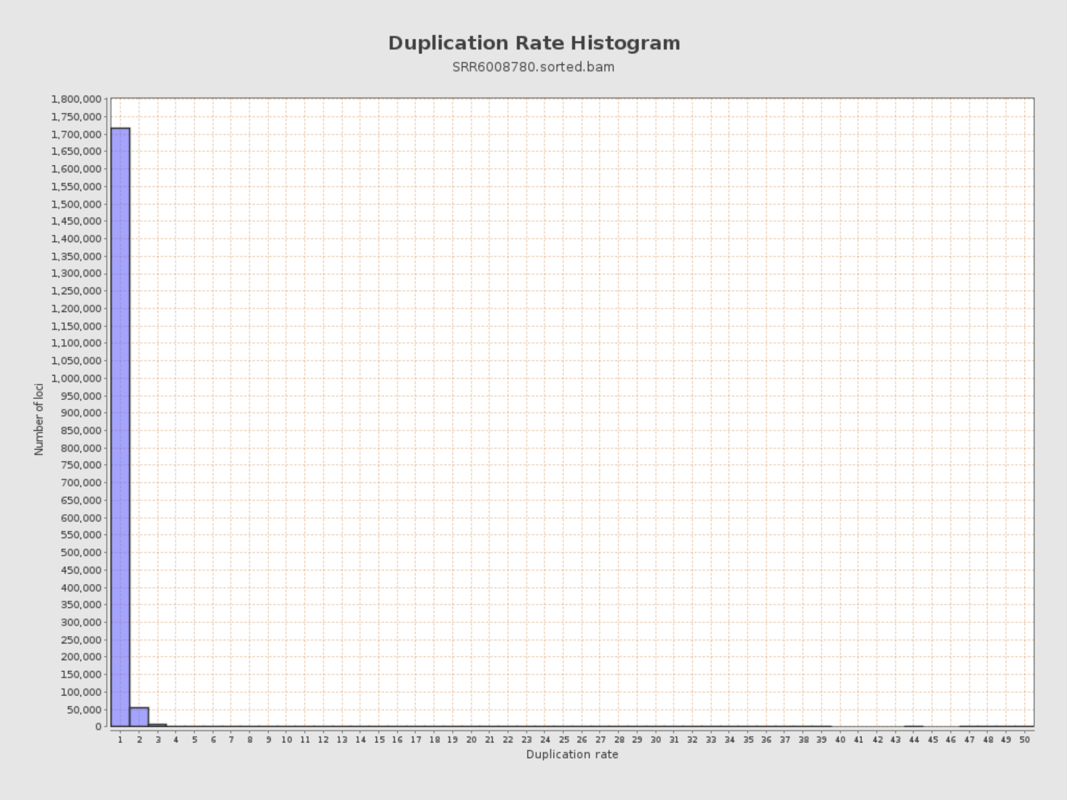
5. Results : Coverage Histogram (0-50X)



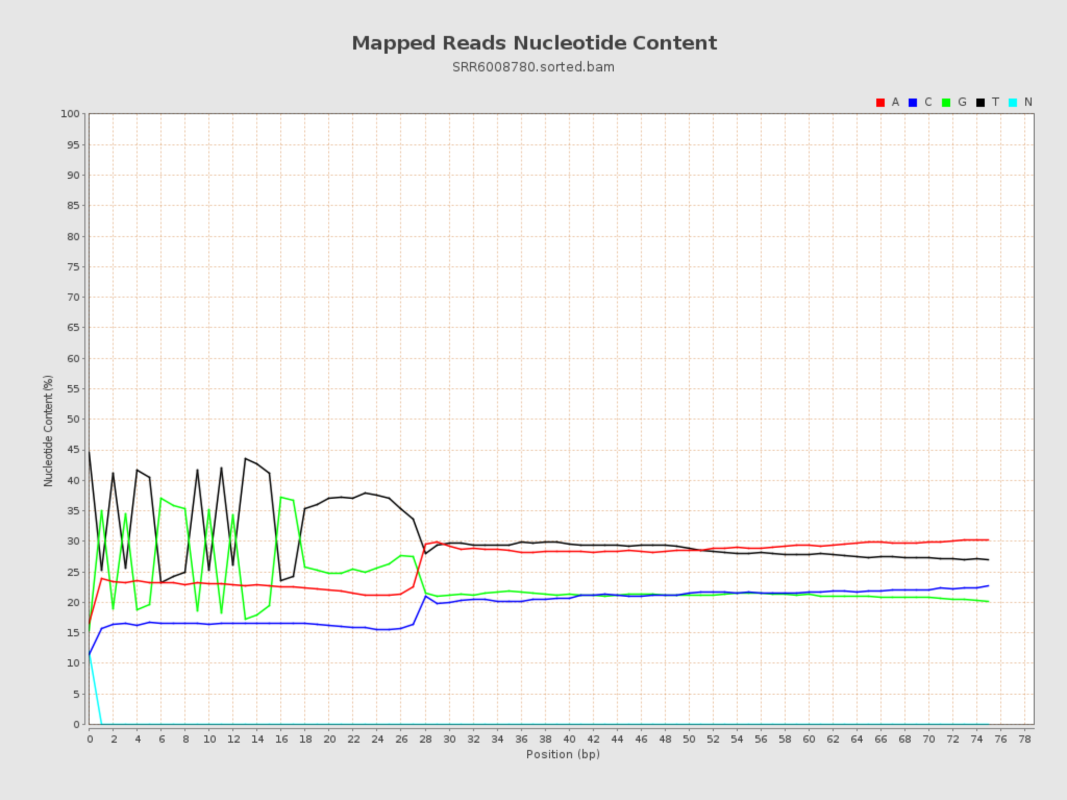
6. Results : Genome Fraction Coverage



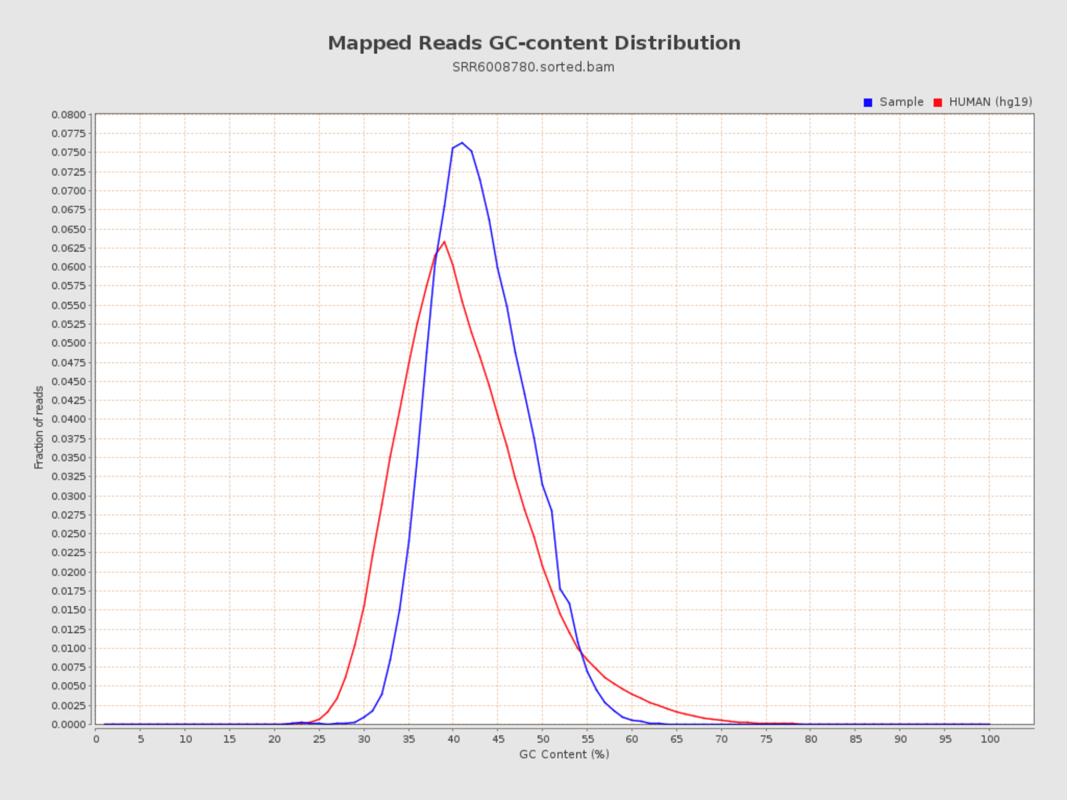
7. Results : Duplication Rate Histogram



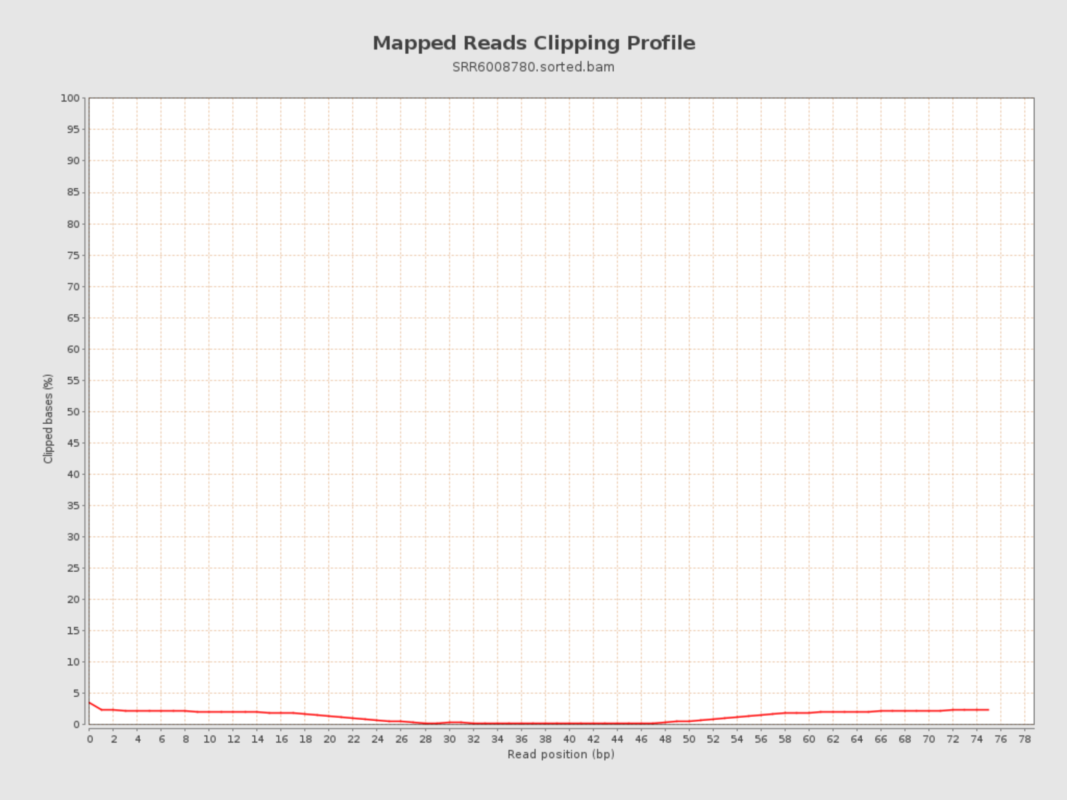
8. Results : Mapped Reads Nucleotide Content



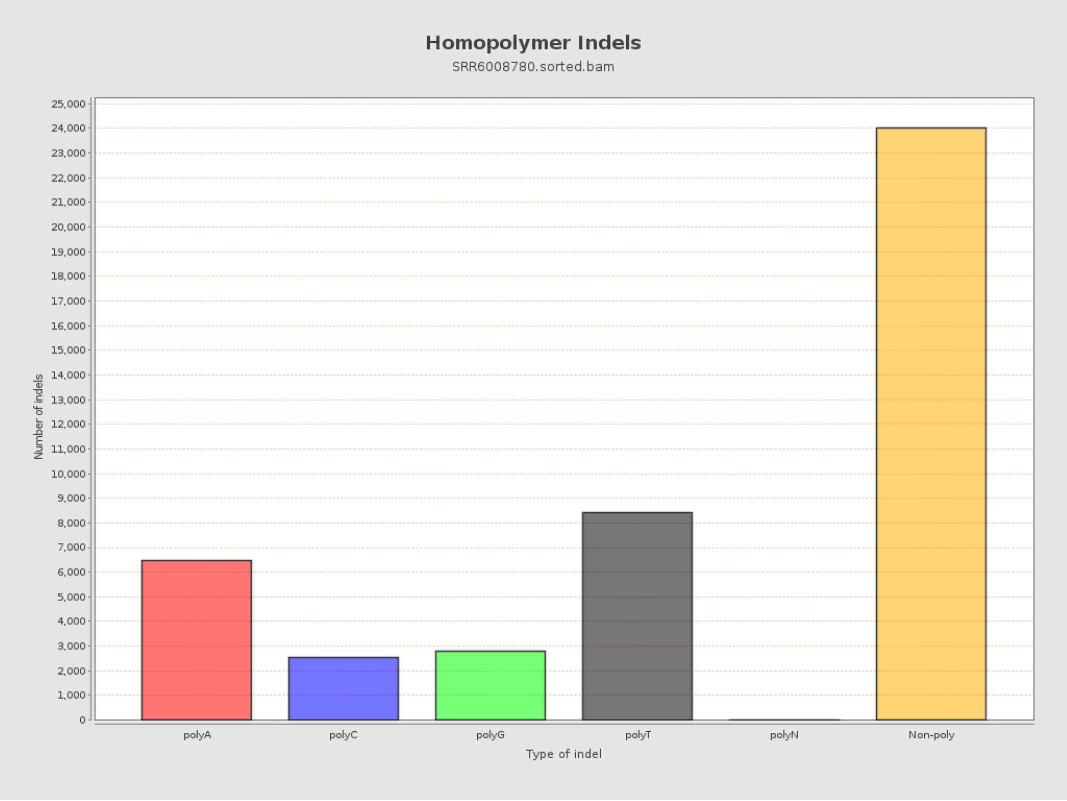
9. Results : Mapped Reads GC-content Distribution



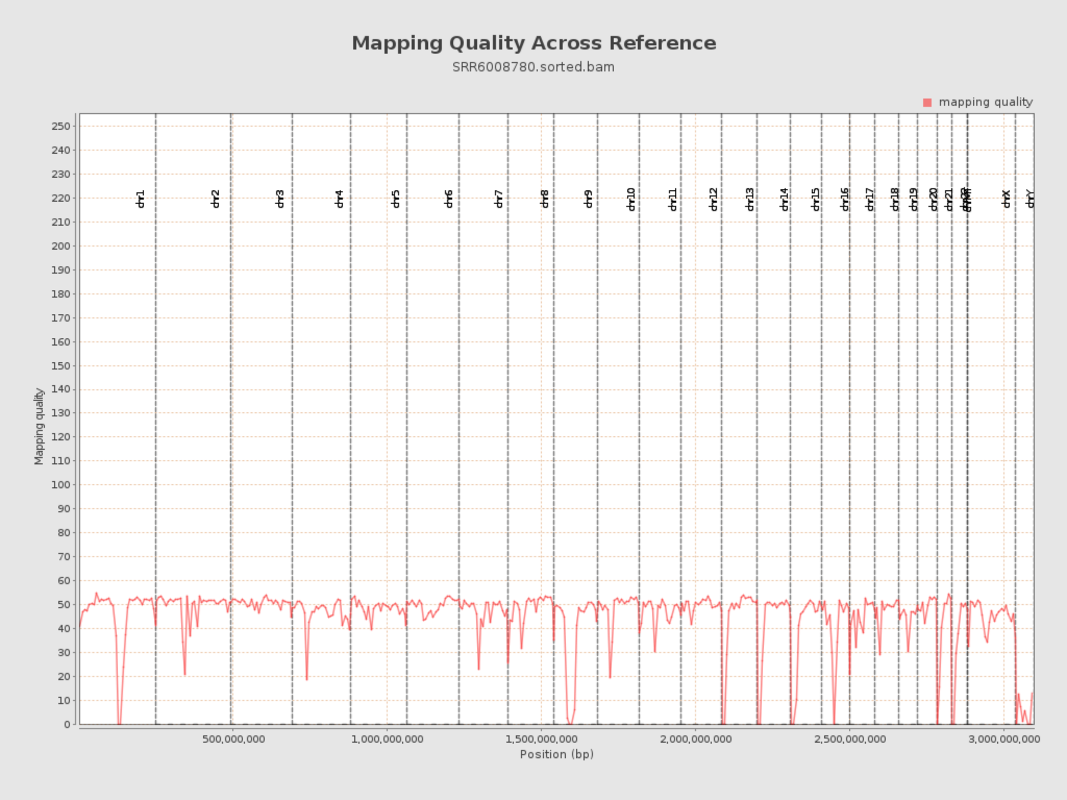
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram