Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:25:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524572.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_SRR10524572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524572.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:25:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,498,411
Mapped reads	2,239,058 / 89.62%
Unmapped reads	259,353 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,255 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	101,063 / 4.05%
Duplication rate	3.31%
Clipped reads	2,242,839 / 89.77%

2.2. ACGT Content

Number/percentage of A's	32,590,133 / 25.24%
Number/percentage of C's	24,064,970 / 18.64%
Number/percentage of T's	41,499,127 / 32.14%
Number/percentage of G's	30,949,027 / 23.97%
Number/percentage of N's	1,757 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.3612

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Mismatches and indels

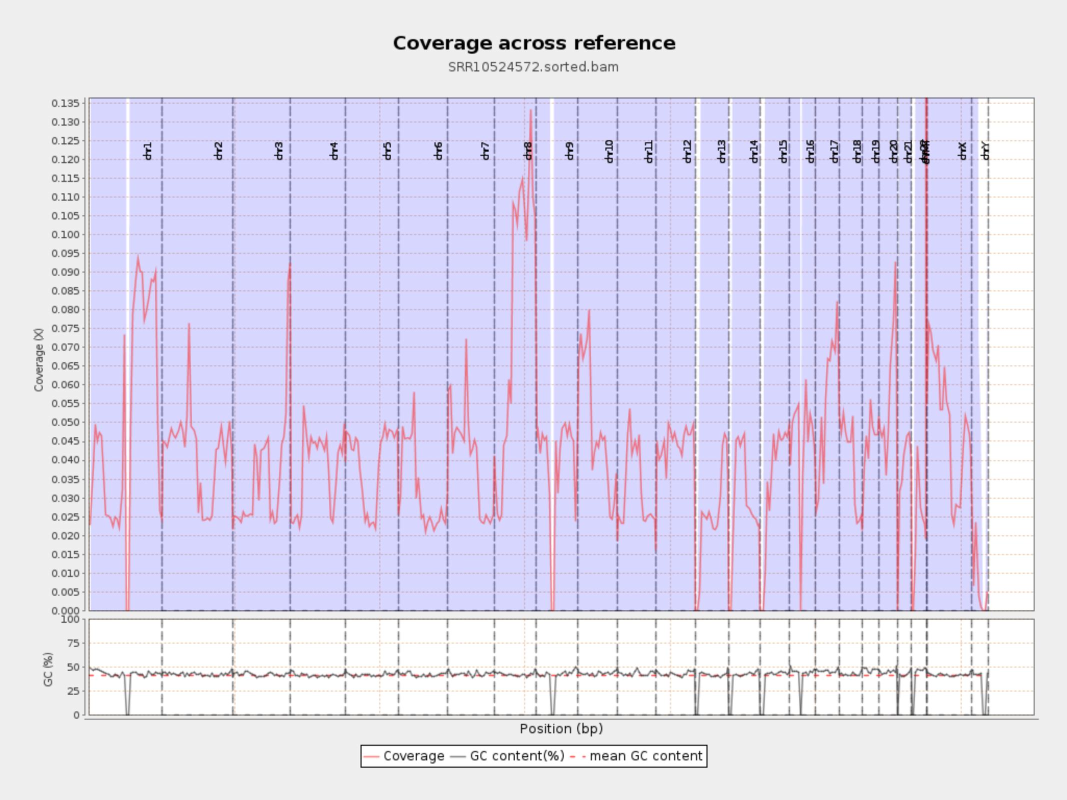
General error rate	0.53%
Mismatches	669,781
Insertions	8,164
Mapped reads with at least one insertion	0.36%
Deletions	23,398
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.13%

2.6. Chromosome stats

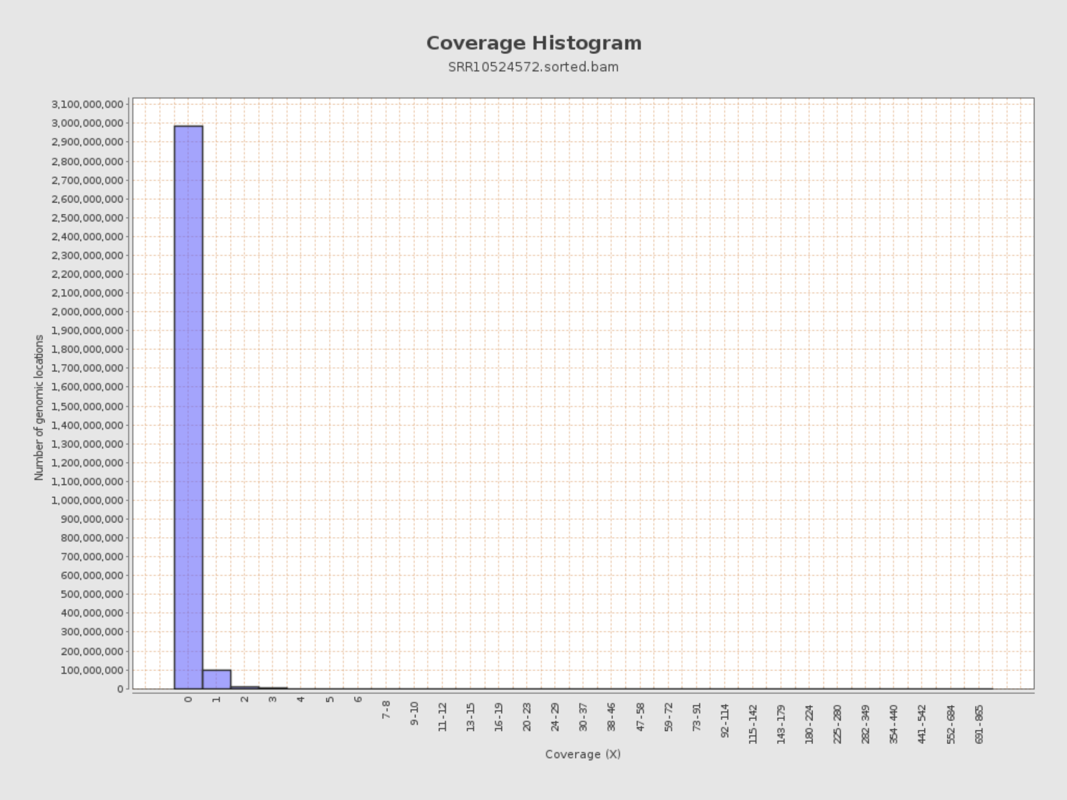
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12667962	0.0508	0.6675
chr2	243199373	10277381	0.0423	0.4378
chr3	198022430	7026058	0.0355	0.2158
chr4	191154276	7214498	0.0377	0.2486
chr5	180915260	7068359	0.0391	0.2233
chr6	171115067	5446008	0.0318	0.271
chr7	159138663	6481273	0.0407	0.4834

chr8	146364022	11743228	0.0802	0.3833
chr9	141213431	5417487	0.0384	0.3073
chr10	135534747	6687788	0.0493	0.372
chr11	135006516	4412552	0.0327	0.3171
chr12	133851895	5997716	0.0448	0.2412
chr13	115169878	2892186	0.0251	0.1791
chr14	107349540	3114065	0.029	0.1991
chr15	102531392	3446694	0.0336	0.2153
chr16	90354753	4064117	0.045	0.2617
chr17	81195210	4578119	0.0564	0.2843
chr18	78077248	3127138	0.0401	0.5956
chr19	59128983	2678337	0.0453	0.4674
chr20	63025520	3675136	0.0583	0.2762
chr21	48129895	1760570	0.0366	0.238
chr22	51304566	1071086	0.0209	0.1614
chrMT	16571	30360	1.8321	1.6572
chrX	155270560	7850798	0.0506	0.298
chrY	59373566	414959	0.007	0.1861

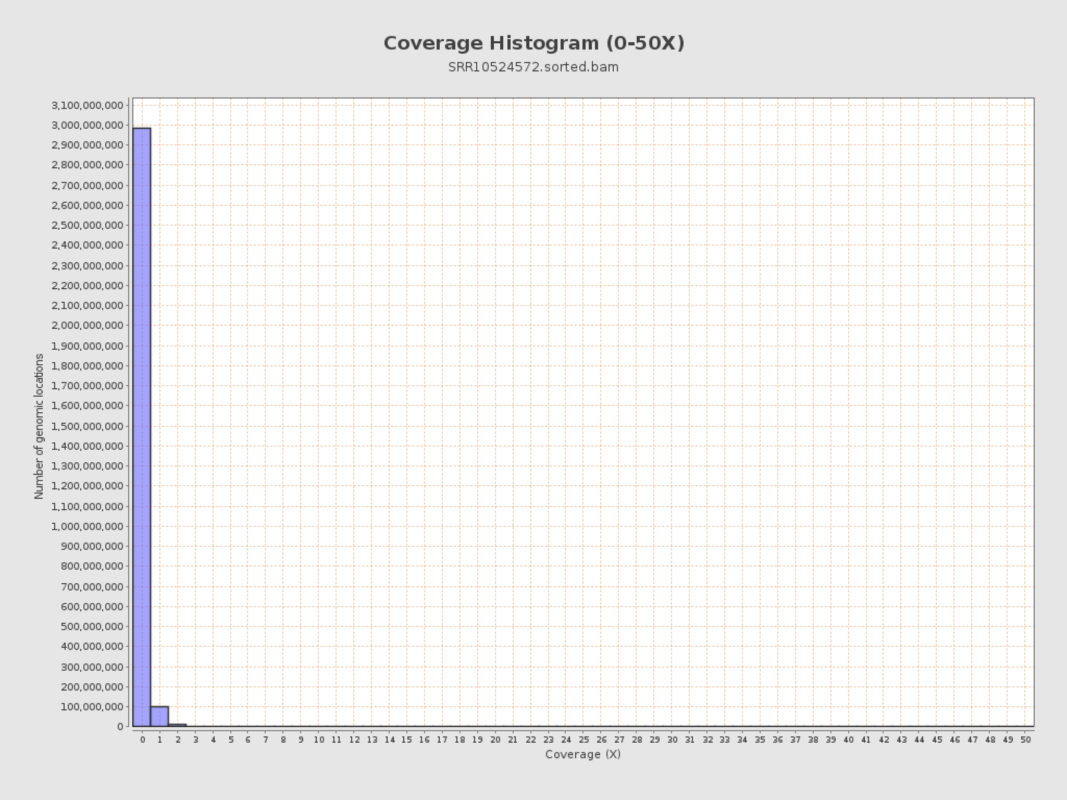
3. Results : Coverage across reference



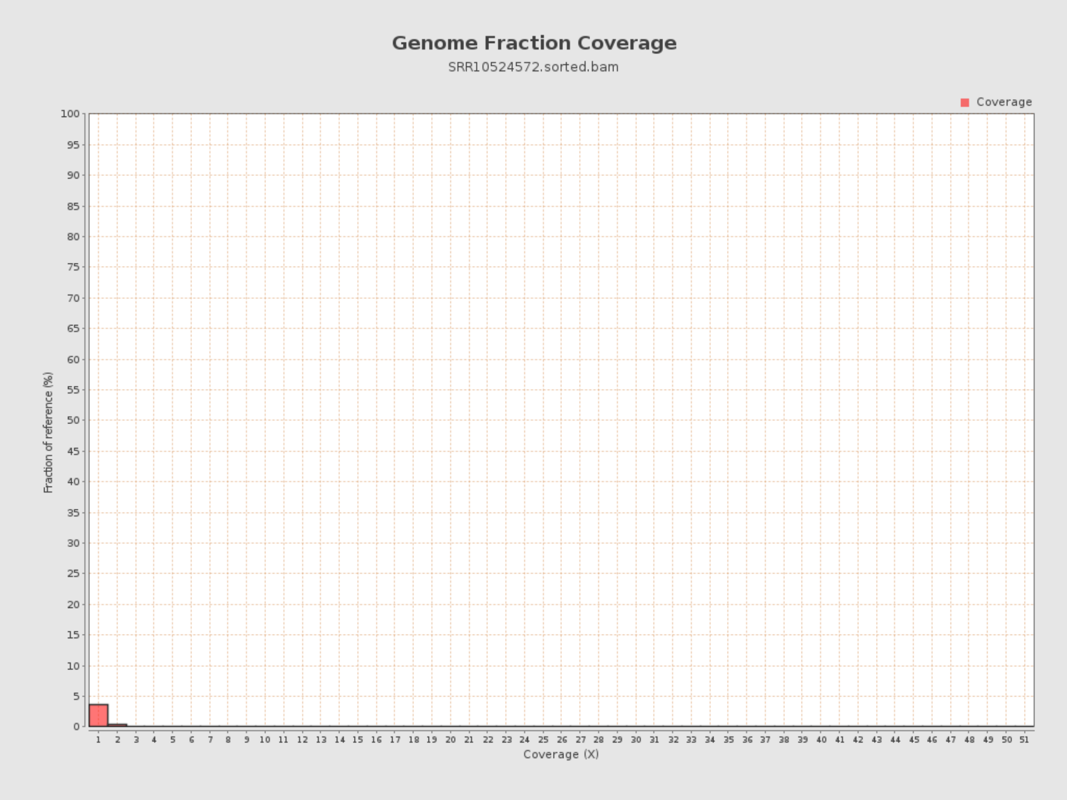
4. Results : Coverage Histogram



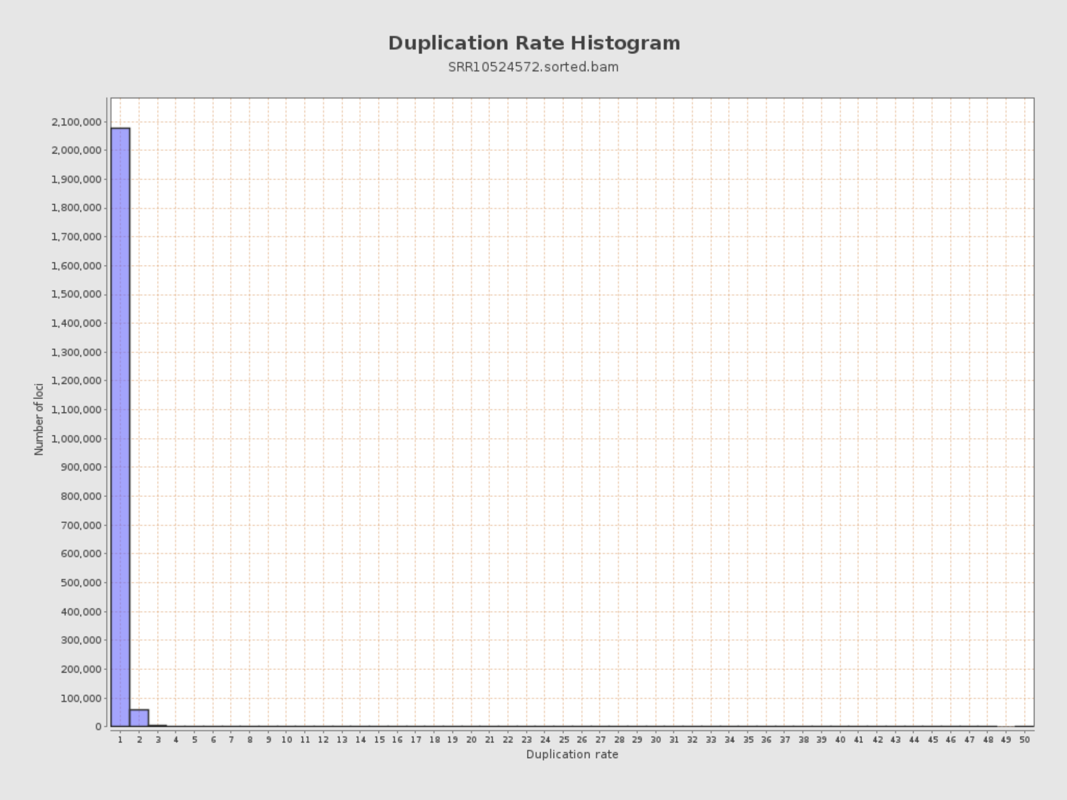
5. Results : Coverage Histogram (0-50X)



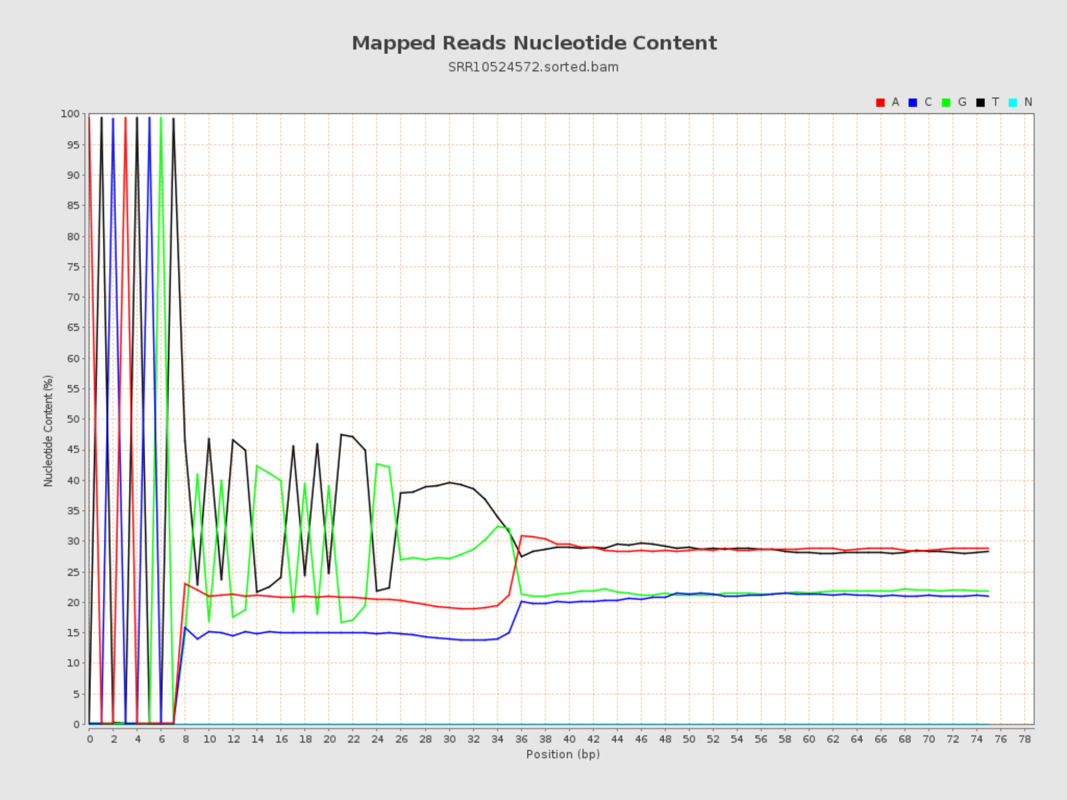
6. Results : Genome Fraction Coverage



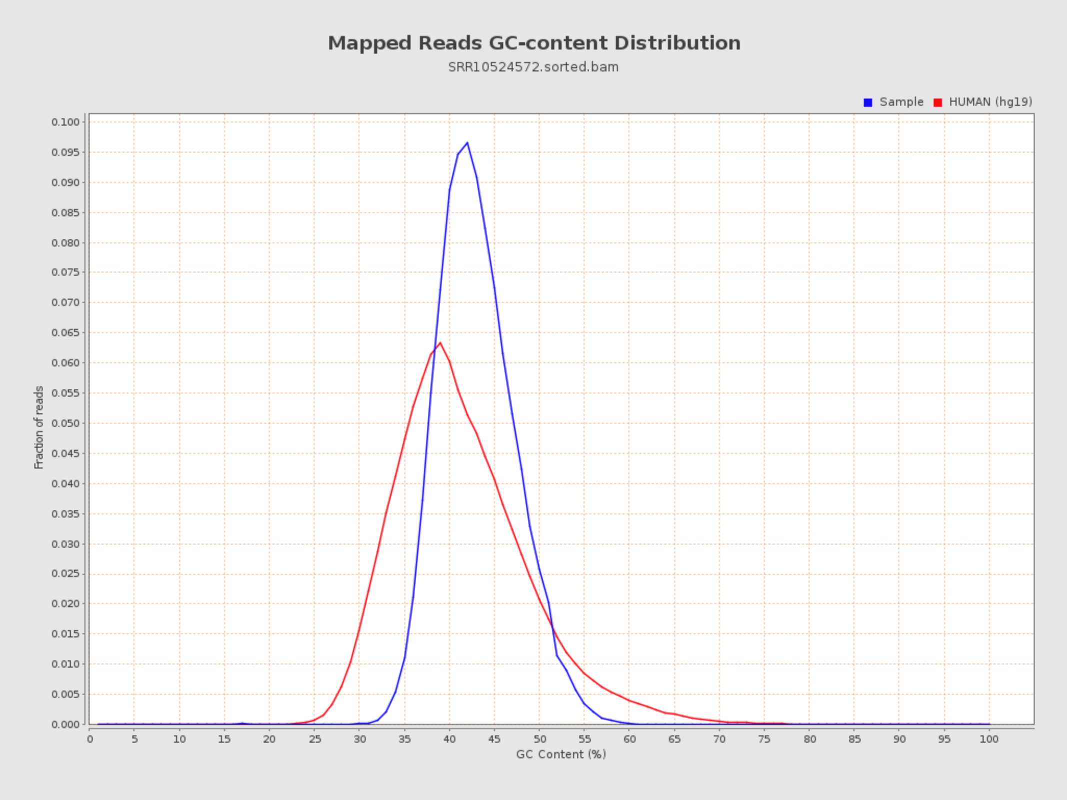
7. Results : Duplication Rate Histogram



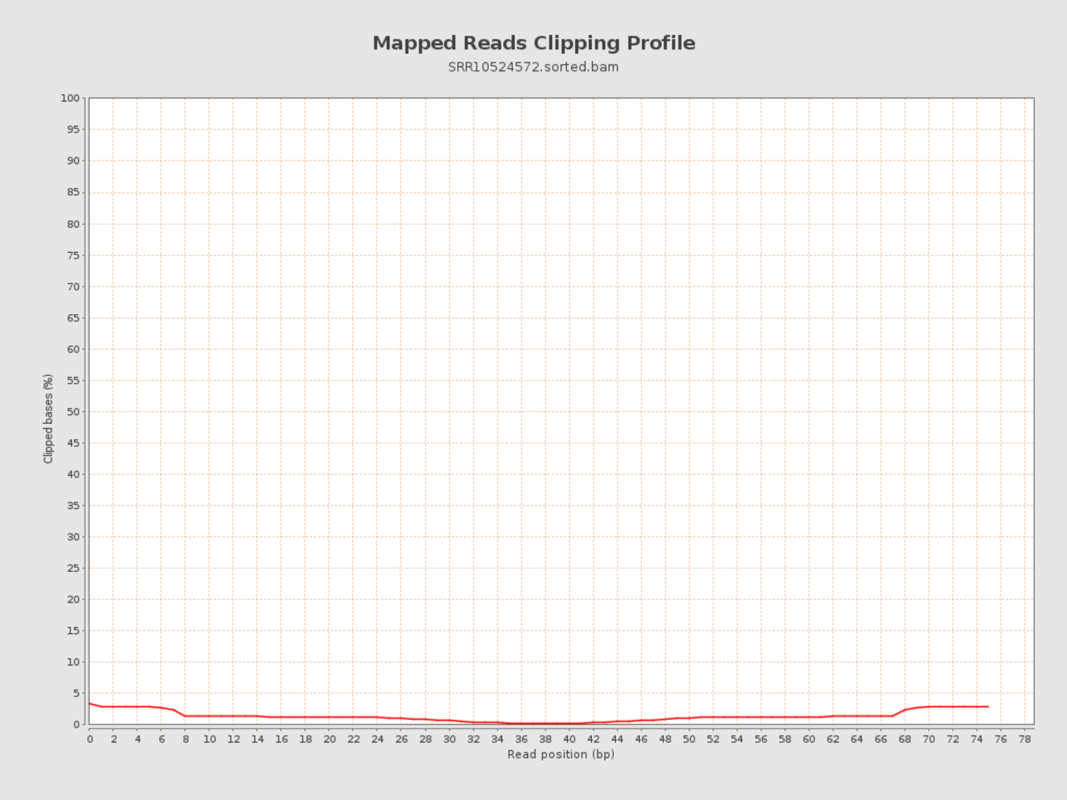
8. Results : Mapped Reads Nucleotide Content



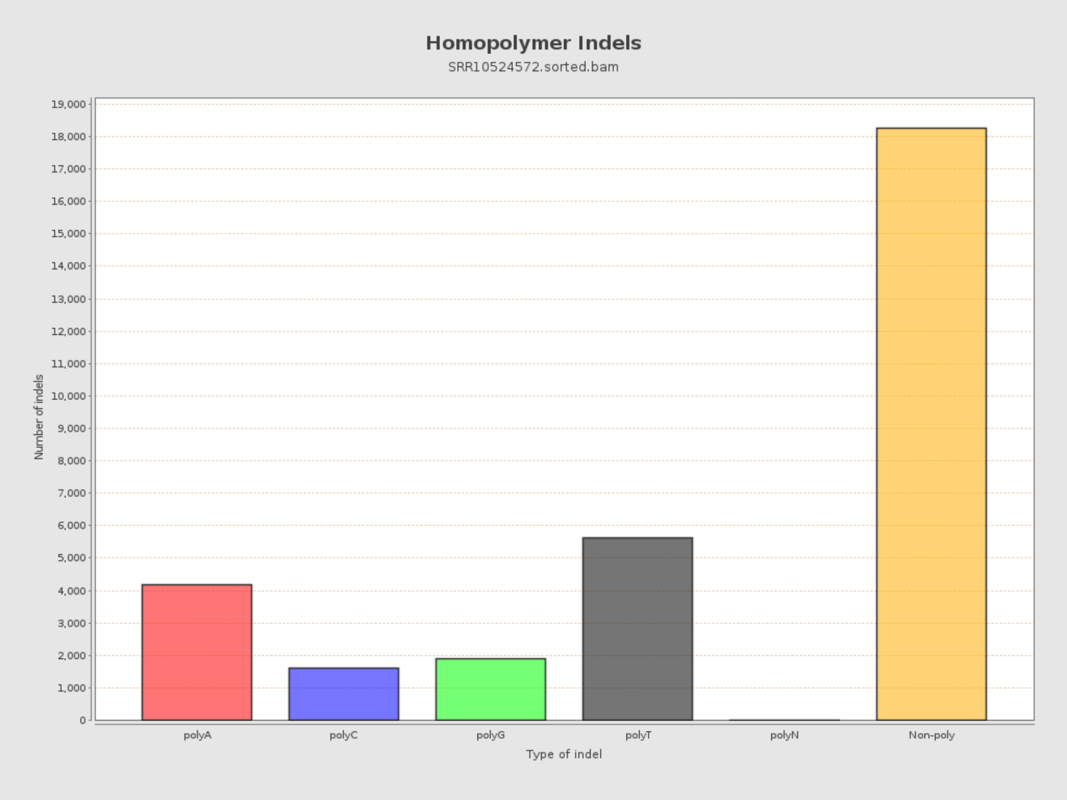
9. Results : Mapped Reads GC-content Distribution



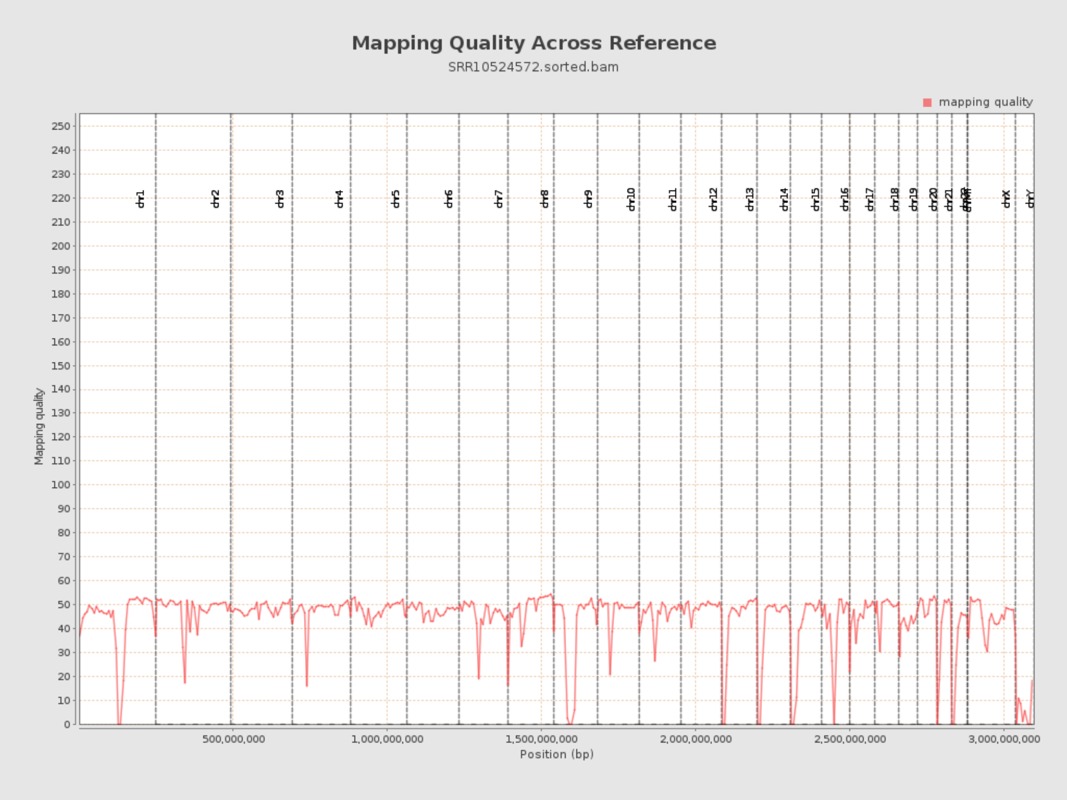
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram