Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:33:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525262.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_SRR10525262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:33:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,210,974
Mapped reads	1,102,528 / 91.04%
Unmapped reads	108,446 / 8.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,253 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	34,277 / 2.83%
Duplication rate	2.28%
Clipped reads	1,104,405 / 91.2%

2.2. ACGT Content

Number/percentage of A's	16,059,110 / 25.35%
Number/percentage of C's	11,411,558 / 18.01%
Number/percentage of T's	20,890,956 / 32.98%
Number/percentage of G's	14,984,097 / 23.65%
Number/percentage of N's	1,200 / 0%
GC Percentage	41.67%

2.3. Coverage

Mean	0.0205

Standard Deviation	0.2191

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

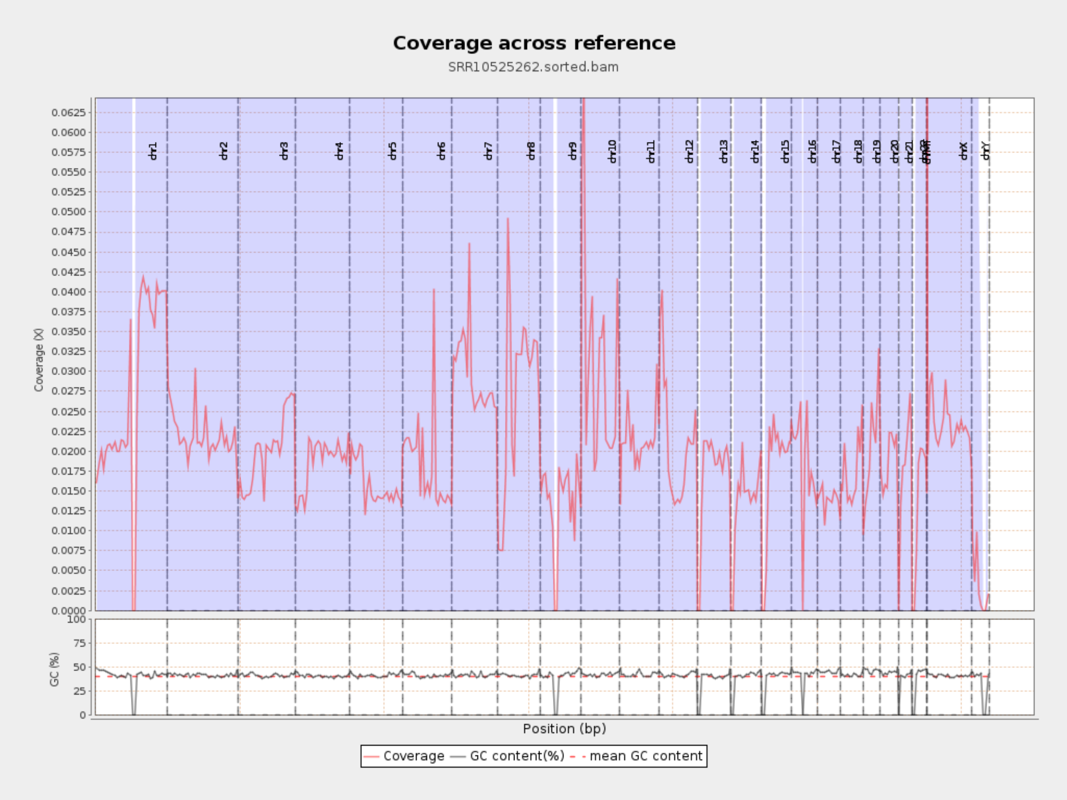
General error rate	0.52%
Mismatches	321,675
Insertions	4,156
Mapped reads with at least one insertion	0.38%
Deletions	13,103
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.5%

2.6. Chromosome stats

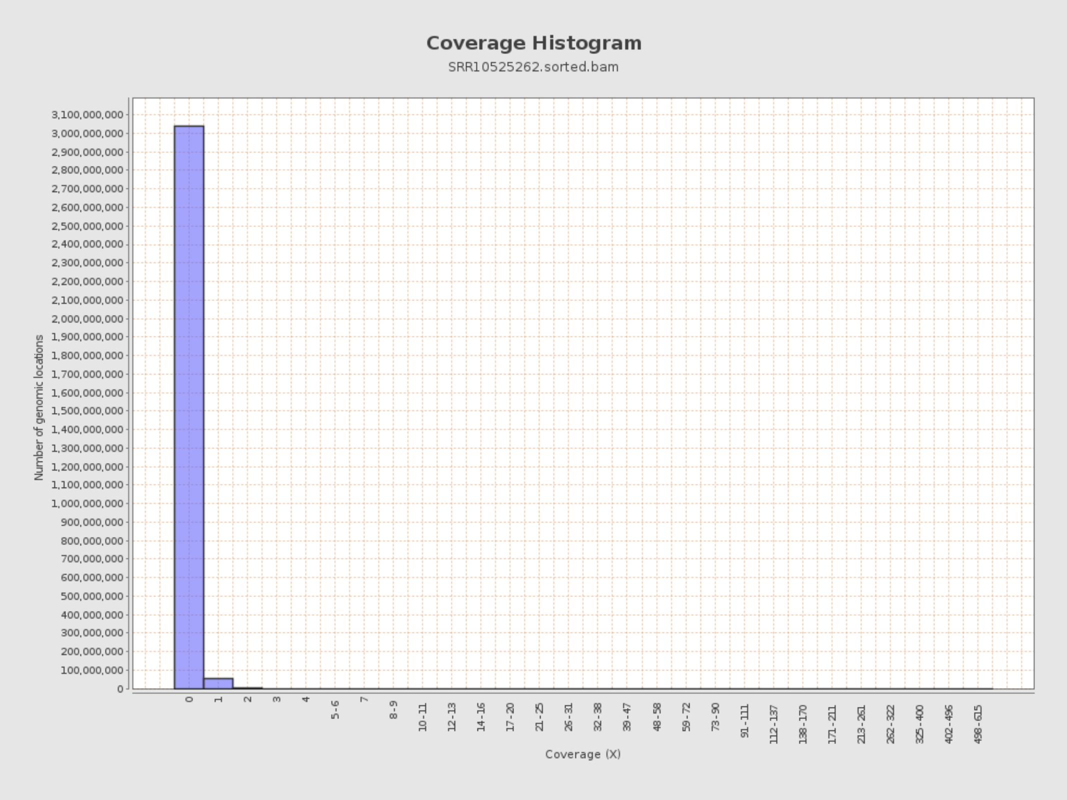
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6800680	0.0273	0.3797
chr2	243199373	5349768	0.022	0.2919
chr3	198022430	3944435	0.0199	0.1505
chr4	191154276	3565384	0.0187	0.1489
chr5	180915260	2855776	0.0158	0.134
chr6	171115067	3156286	0.0184	0.1629
chr7	159138663	4709975	0.0296	0.361

chr8	146364022	4022207	0.0275	0.2262
chr9	141213431	1905726	0.0135	0.1508
chr10	135534747	4230303	0.0312	0.2337
chr11	135006516	2885602	0.0214	0.1855
chr12	133851895	2832454	0.0212	0.1552
chr13	115169878	1969873	0.0171	0.1405
chr14	107349540	1446759	0.0135	0.1278
chr15	102531392	1750119	0.0171	0.1428
chr16	90354753	1665880	0.0184	0.1564
chr17	81195210	1134394	0.014	0.1283
chr18	78077248	1344083	0.0172	0.2901
chr19	59128983	1229187	0.0208	0.2625
chr20	63025520	1171975	0.0186	0.1474
chr21	48129895	876494	0.0182	0.148
chr22	51304566	689547	0.0134	0.1227
chrMT	16571	2243	0.1354	0.3885
chrX	155270560	3640795	0.0234	0.1726
chrY	59373566	187565	0.0032	0.0902

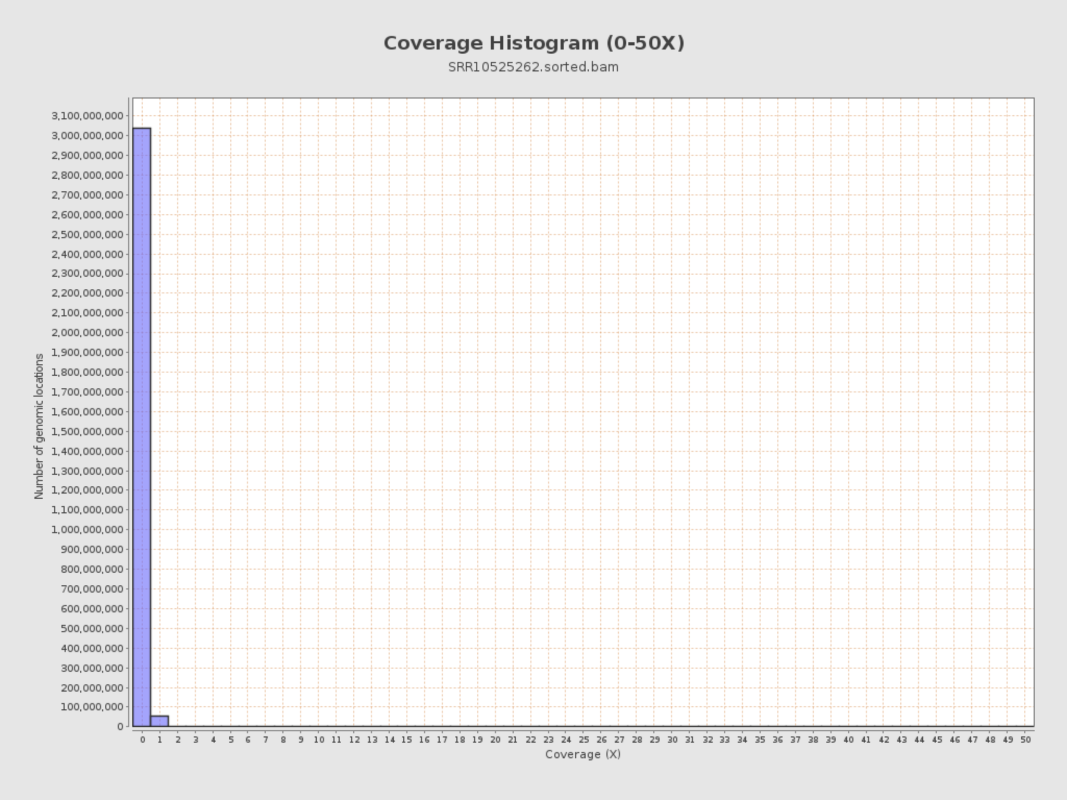
3. Results : Coverage across reference



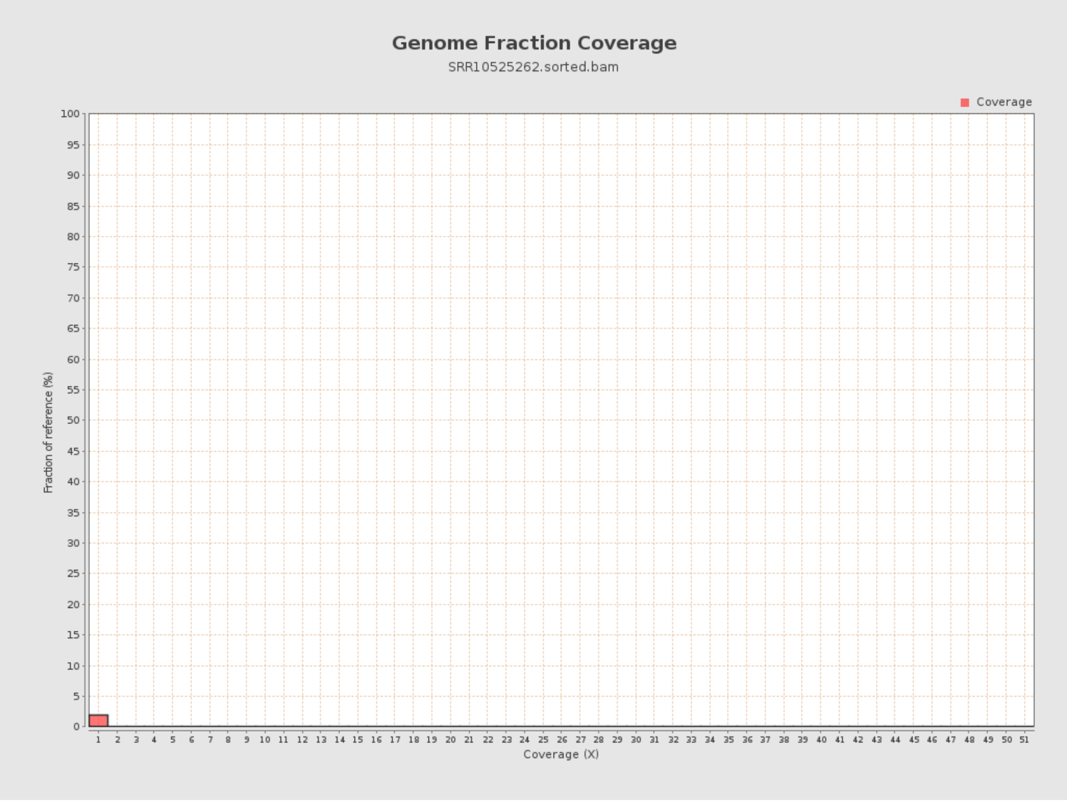
4. Results : Coverage Histogram



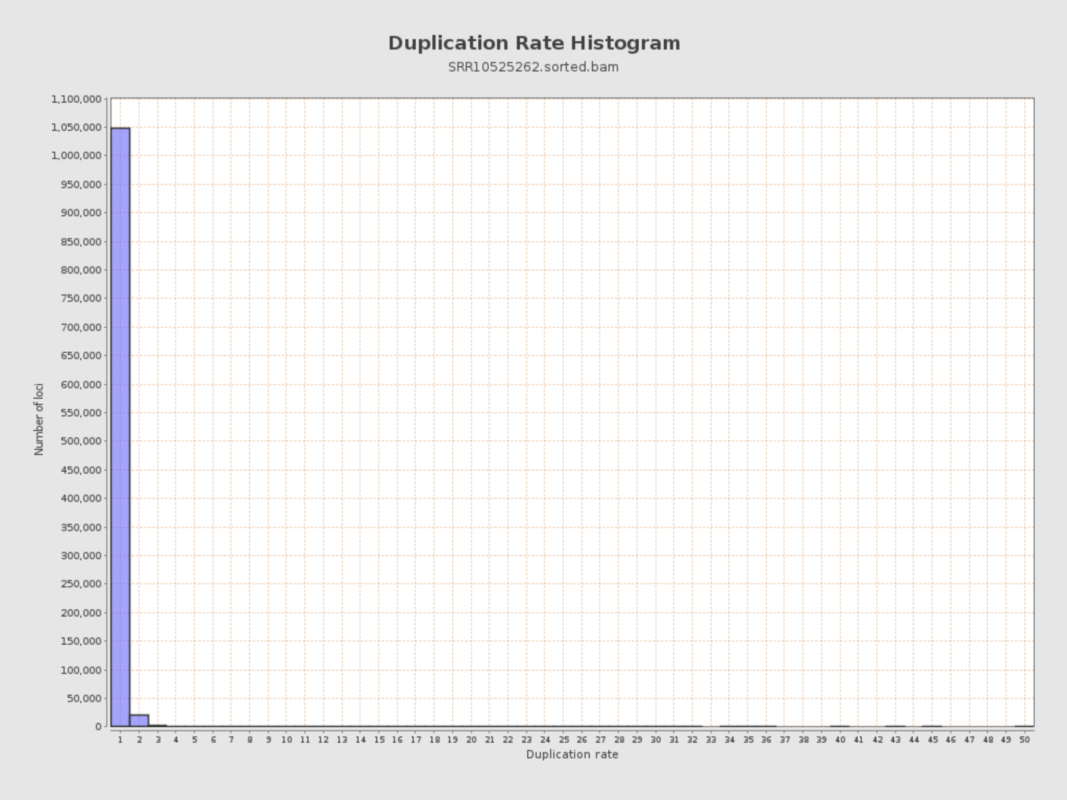
5. Results : Coverage Histogram (0-50X)



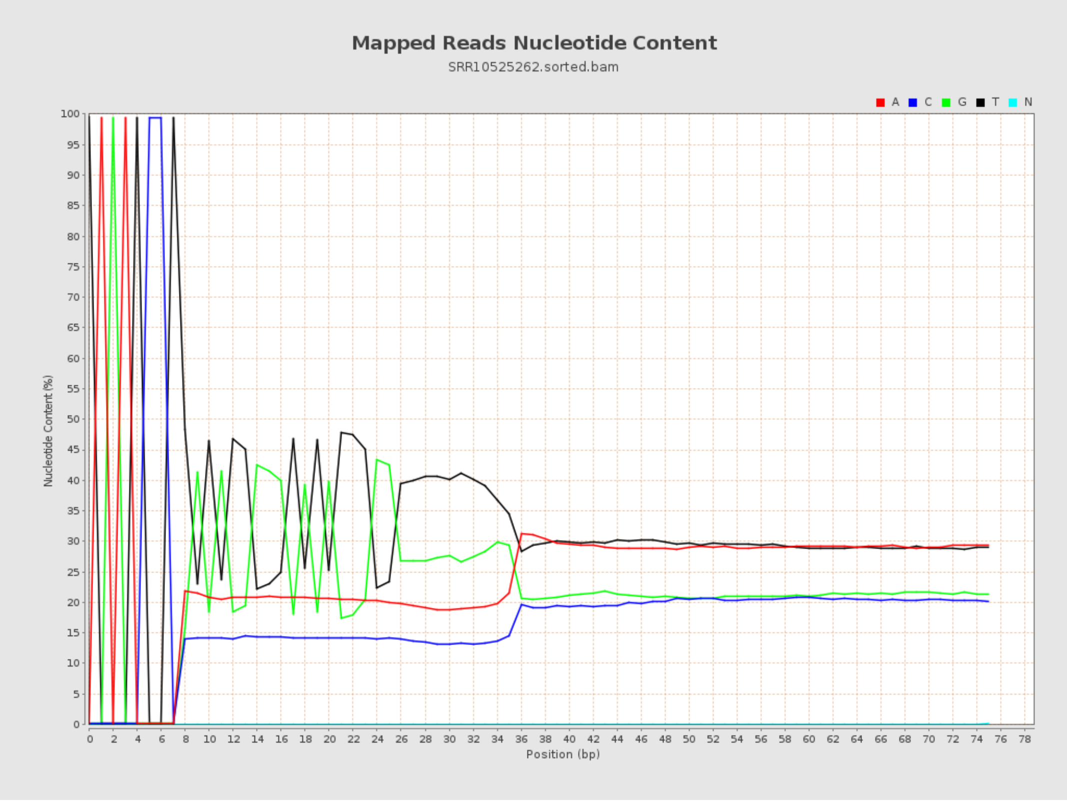
6. Results : Genome Fraction Coverage



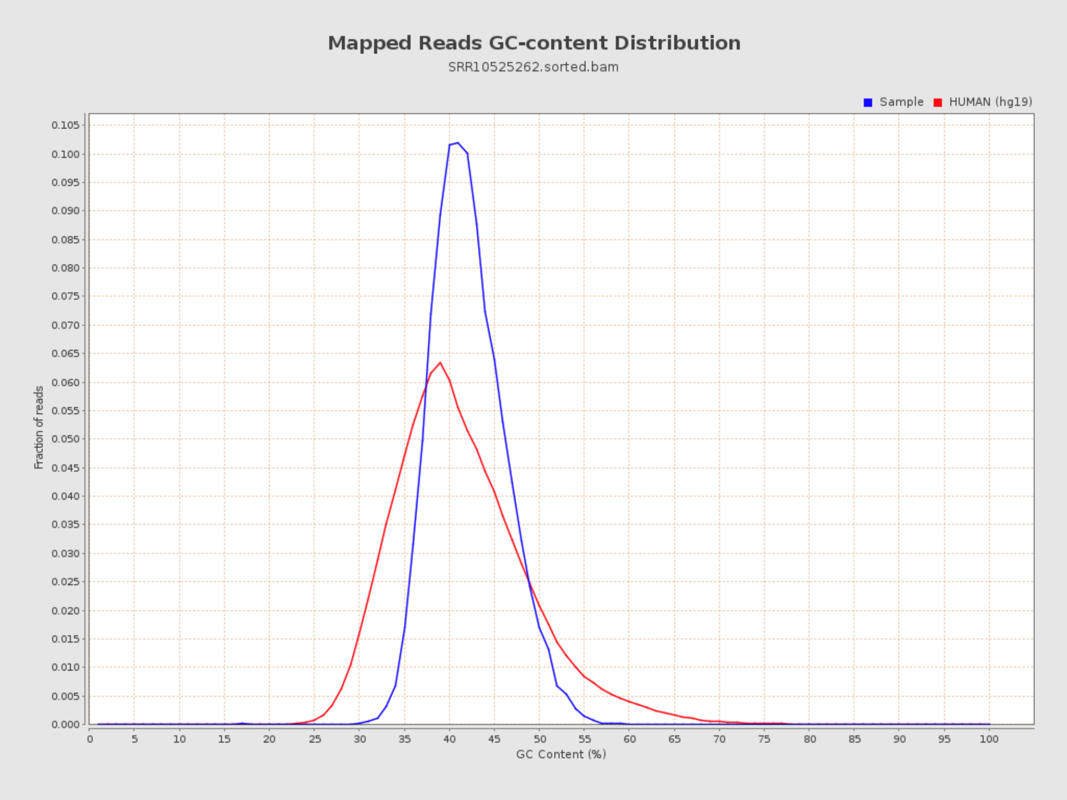
7. Results : Duplication Rate Histogram



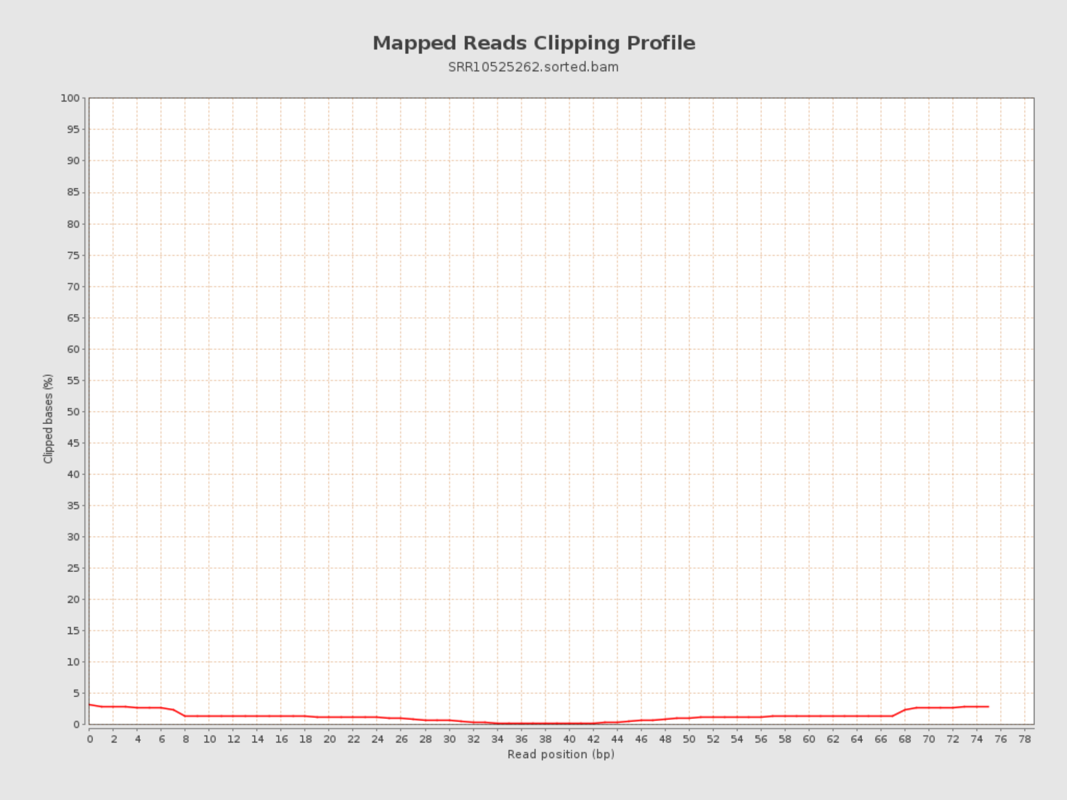
8. Results : Mapped Reads Nucleotide Content



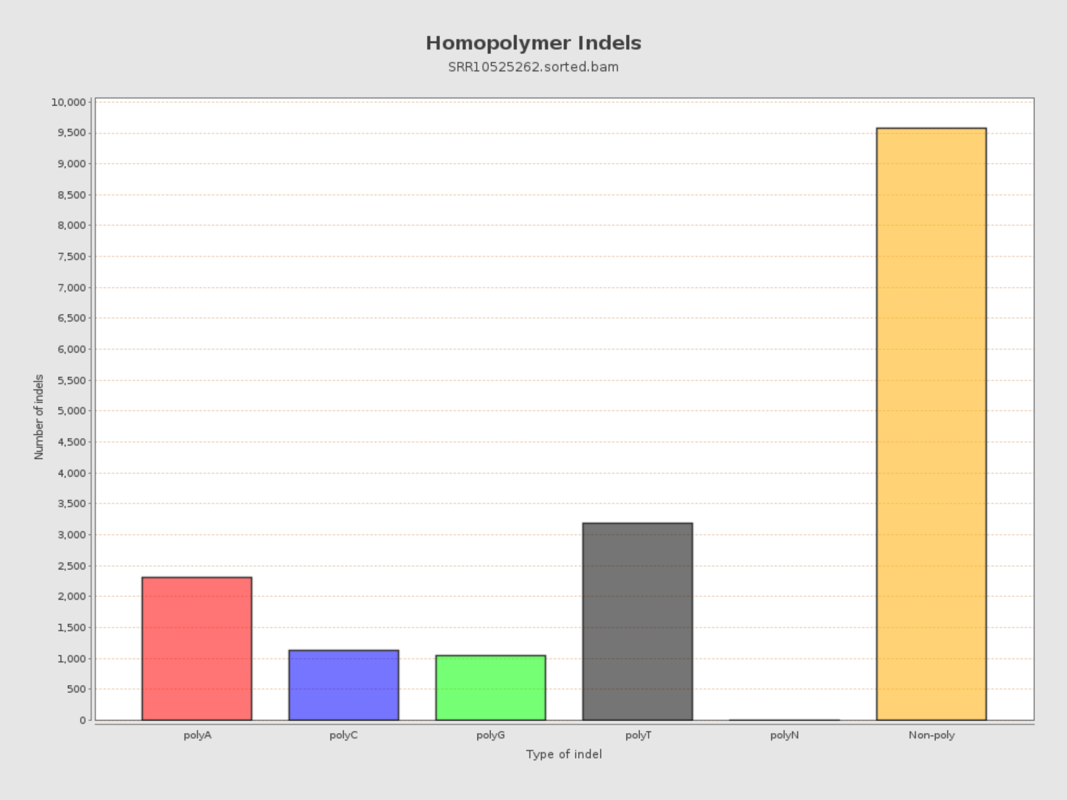
9. Results : Mapped Reads GC-content Distribution



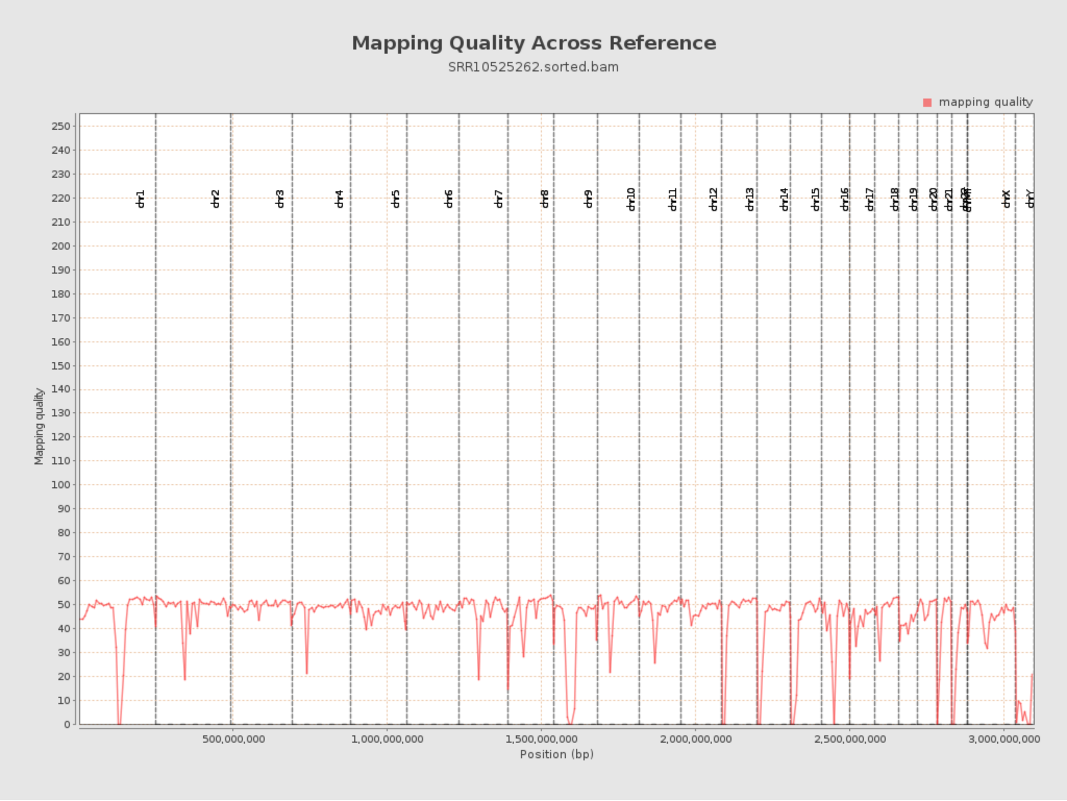
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram