Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:13:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525232.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_SRR10525232 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525232.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:13:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,178,407
Mapped reads	638,007 / 54.14%
Unmapped reads	540,400 / 45.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,173 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	13,105 / 1.11%
Duplication rate	1.49%
Clipped reads	638,188 / 54.16%

2.2. ACGT Content

Number/percentage of A's	10,025,801 / 26%
Number/percentage of C's	7,229,347 / 18.75%
Number/percentage of T's	12,221,559 / 31.7%
Number/percentage of G's	9,081,016 / 23.55%
Number/percentage of N's	794 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0125

Standard Deviation	0.1486

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

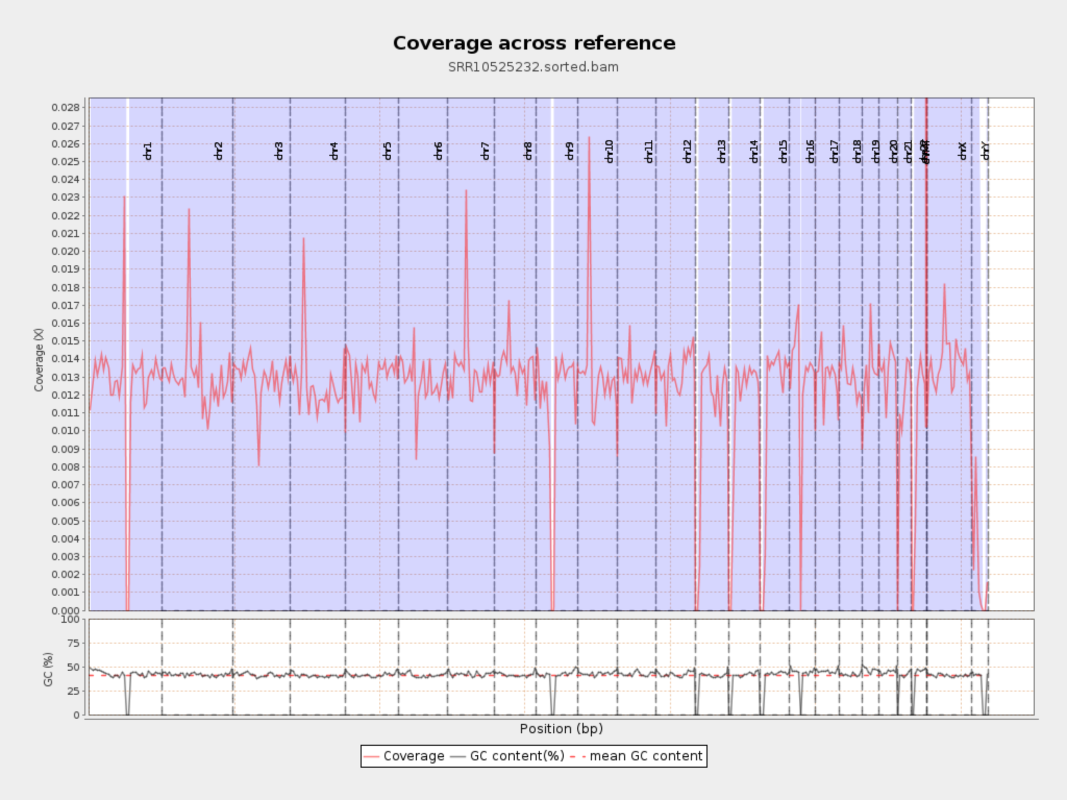
General error rate	0.51%
Mismatches	192,867
Insertions	2,717
Mapped reads with at least one insertion	0.42%
Deletions	8,154
Mapped reads with at least one deletion	1.27%
Homopolymer indels	43.6%

2.6. Chromosome stats

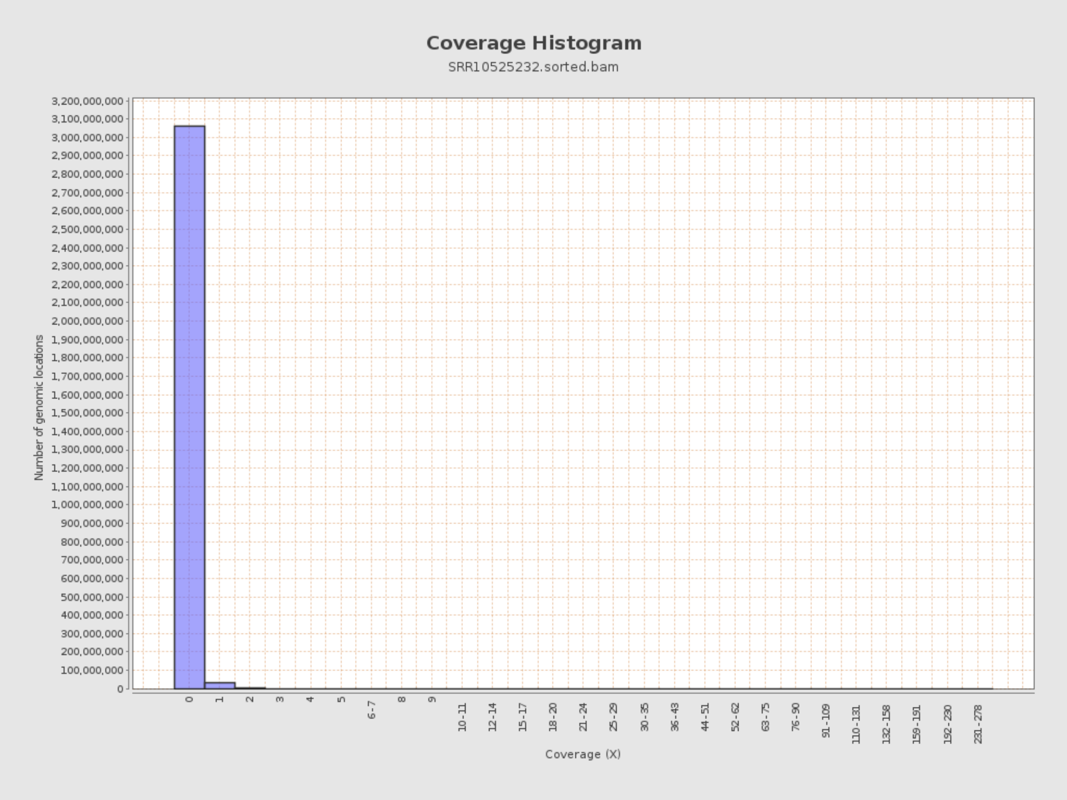
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3118426	0.0125	0.2462
chr2	243199373	3180131	0.0131	0.1686
chr3	198022430	2560203	0.0129	0.1178
chr4	191154276	2399793	0.0126	0.1218
chr5	180915260	2370218	0.0131	0.1184
chr6	171115067	2197392	0.0128	0.1254
chr7	159138663	2158787	0.0136	0.1943

chr8	146364022	1979360	0.0135	0.1402
chr9	141213431	1604489	0.0114	0.1276
chr10	135534747	1811347	0.0134	0.1534
chr11	135006516	1793573	0.0133	0.132
chr12	133851895	1781858	0.0133	0.1201
chr13	115169878	1214167	0.0105	0.1059
chr14	107349540	1162313	0.0108	0.1105
chr15	102531392	1121385	0.0109	0.108
chr16	90354753	1162356	0.0129	0.1243
chr17	81195210	1056287	0.013	0.1228
chr18	78077248	1022166	0.0131	0.2062
chr19	59128983	784626	0.0133	0.1903
chr20	63025520	840418	0.0133	0.1207
chr21	48129895	529289	0.011	0.1155
chr22	51304566	461304	0.009	0.0983
chrMT	16571	4918	0.2968	0.5586
chrX	155270560	2125628	0.0137	0.1268
chrY	59373566	131197	0.0022	0.0845

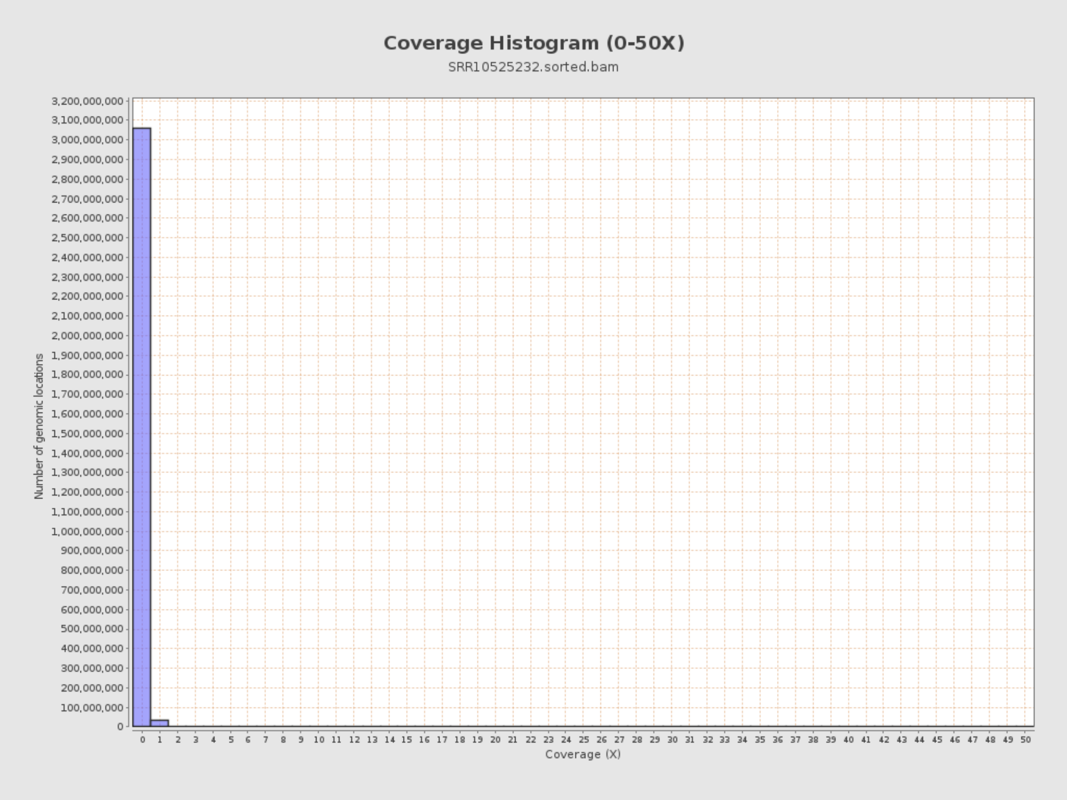
3. Results : Coverage across reference



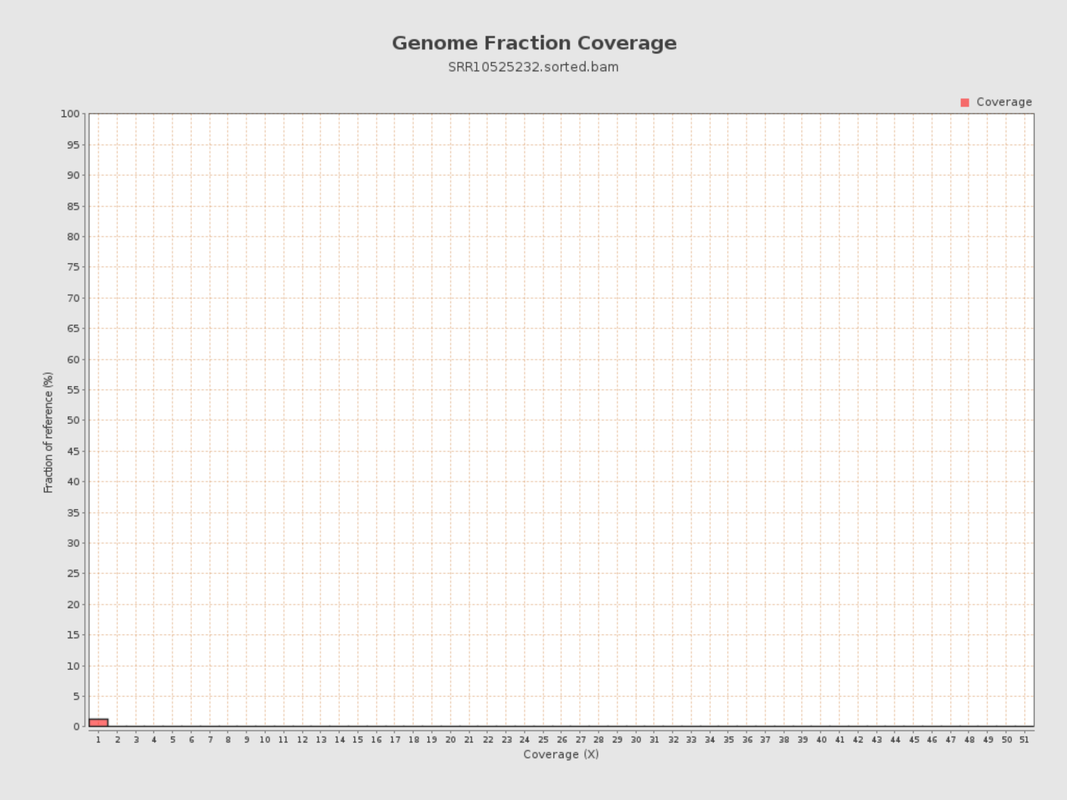
4. Results : Coverage Histogram



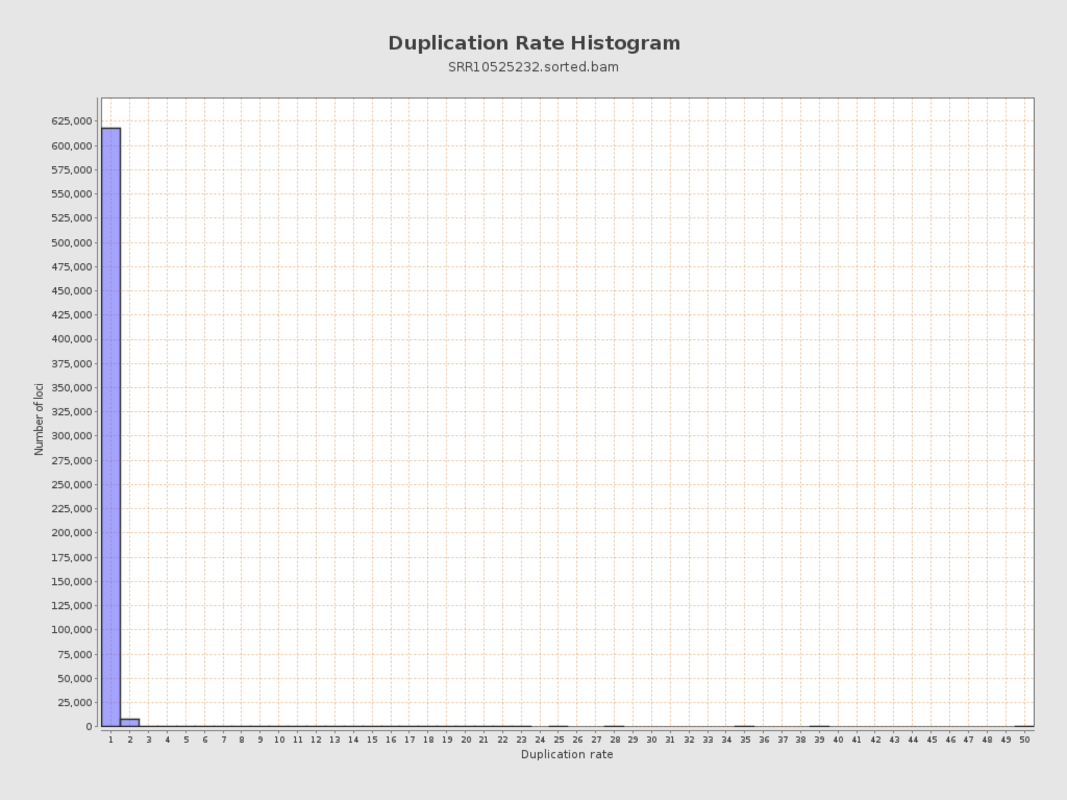
5. Results : Coverage Histogram (0-50X)



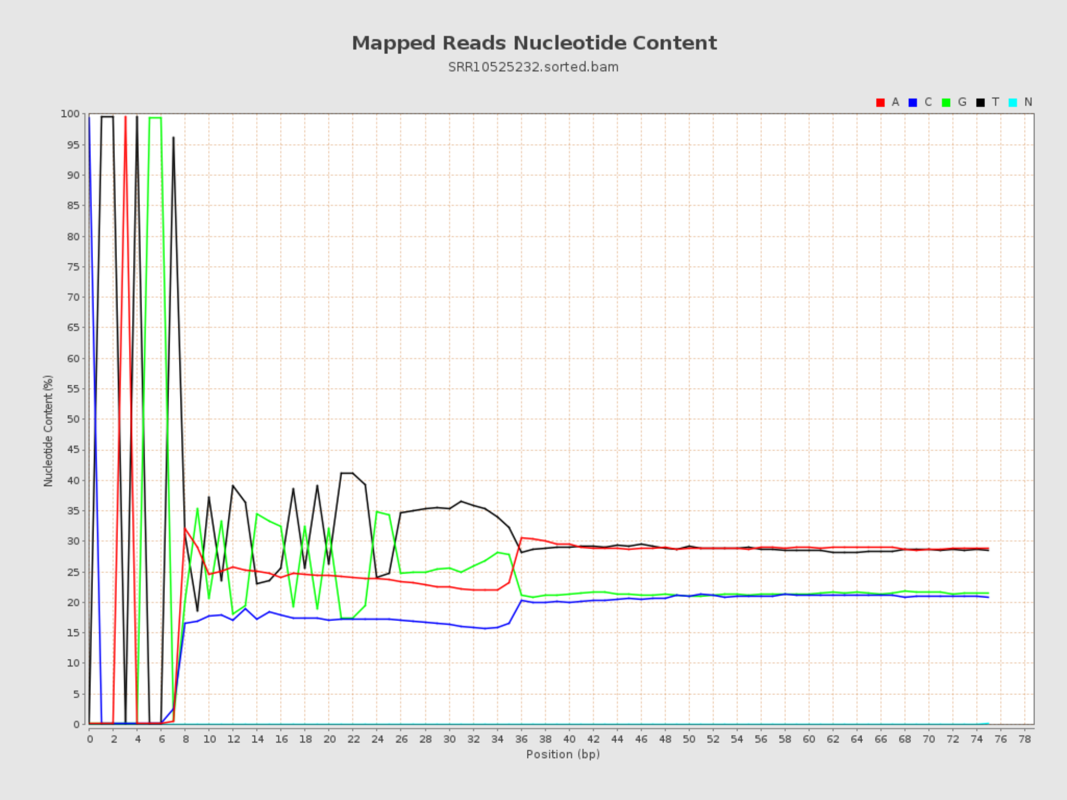
6. Results : Genome Fraction Coverage



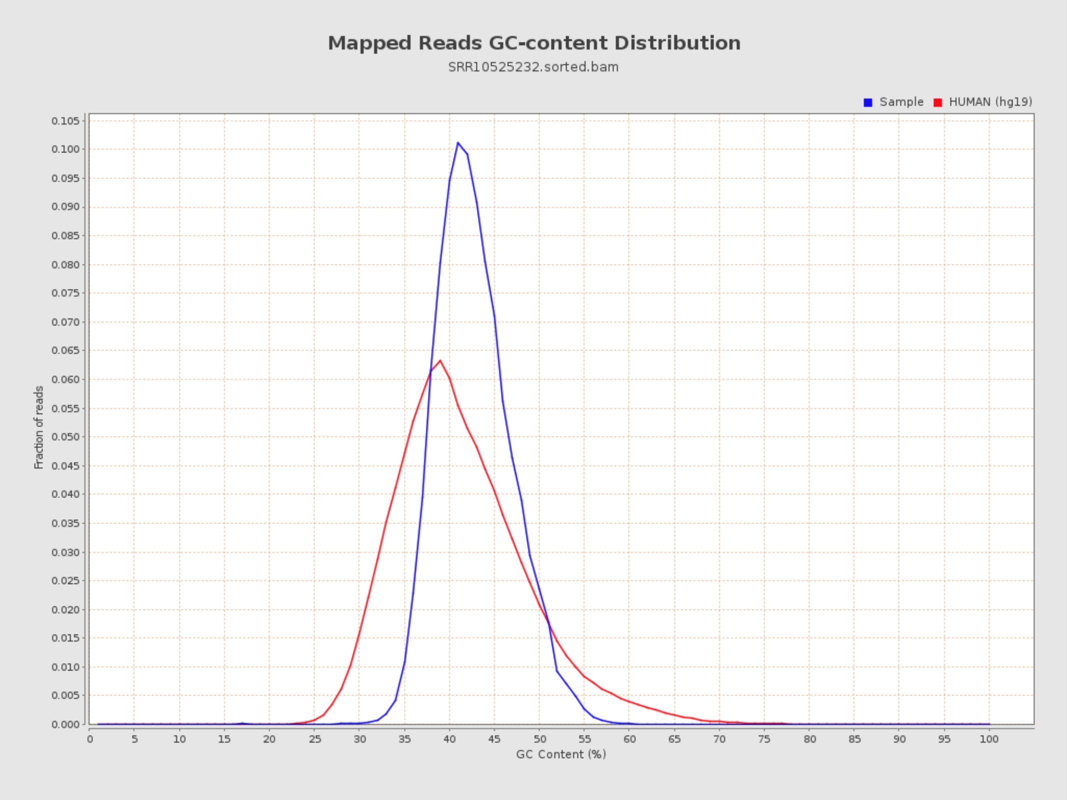
7. Results : Duplication Rate Histogram



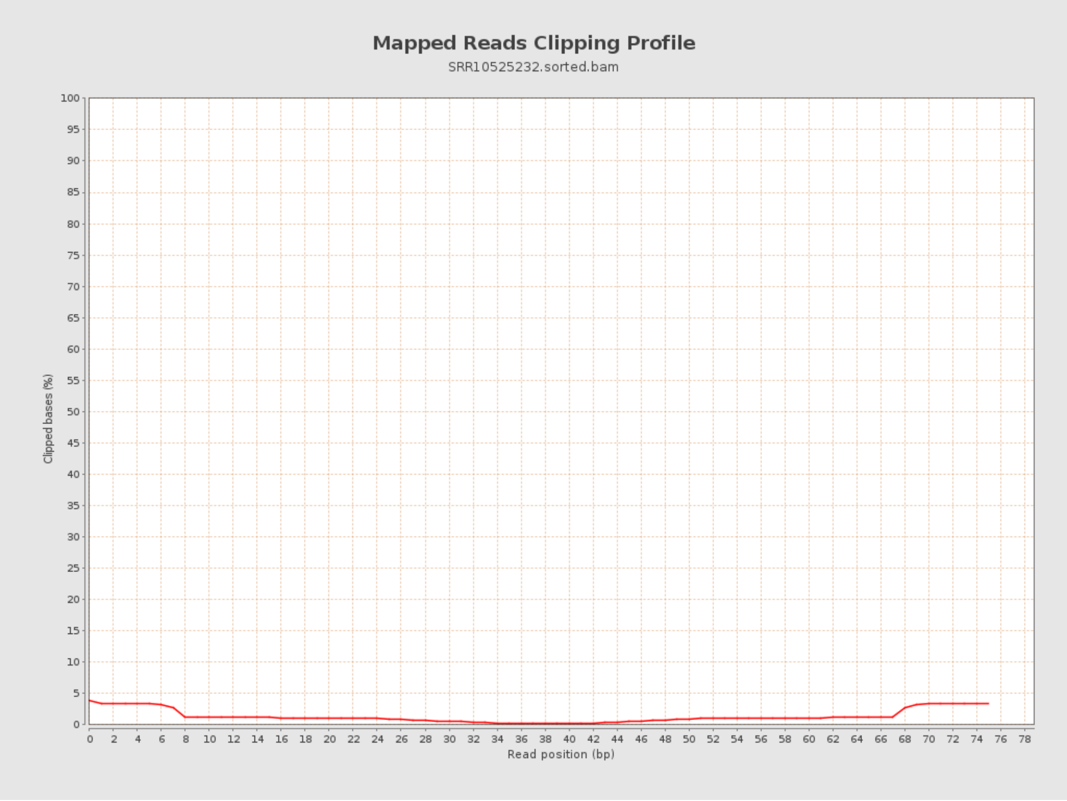
8. Results : Mapped Reads Nucleotide Content



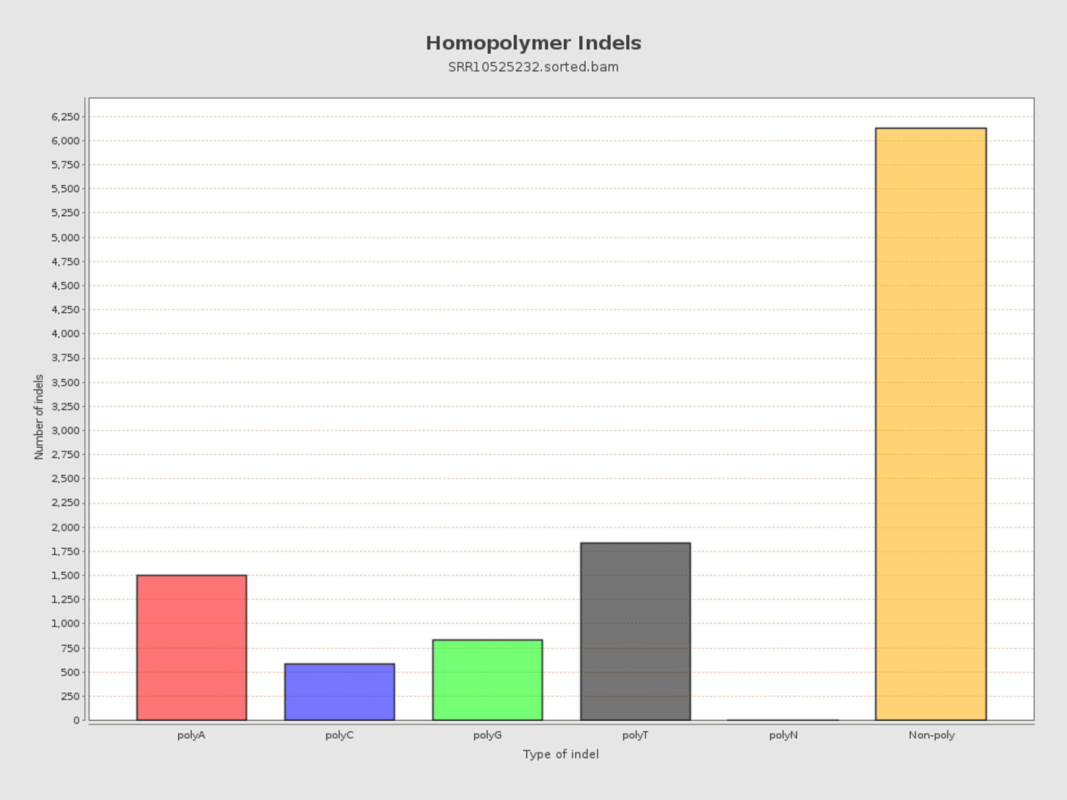
9. Results : Mapped Reads GC-content Distribution



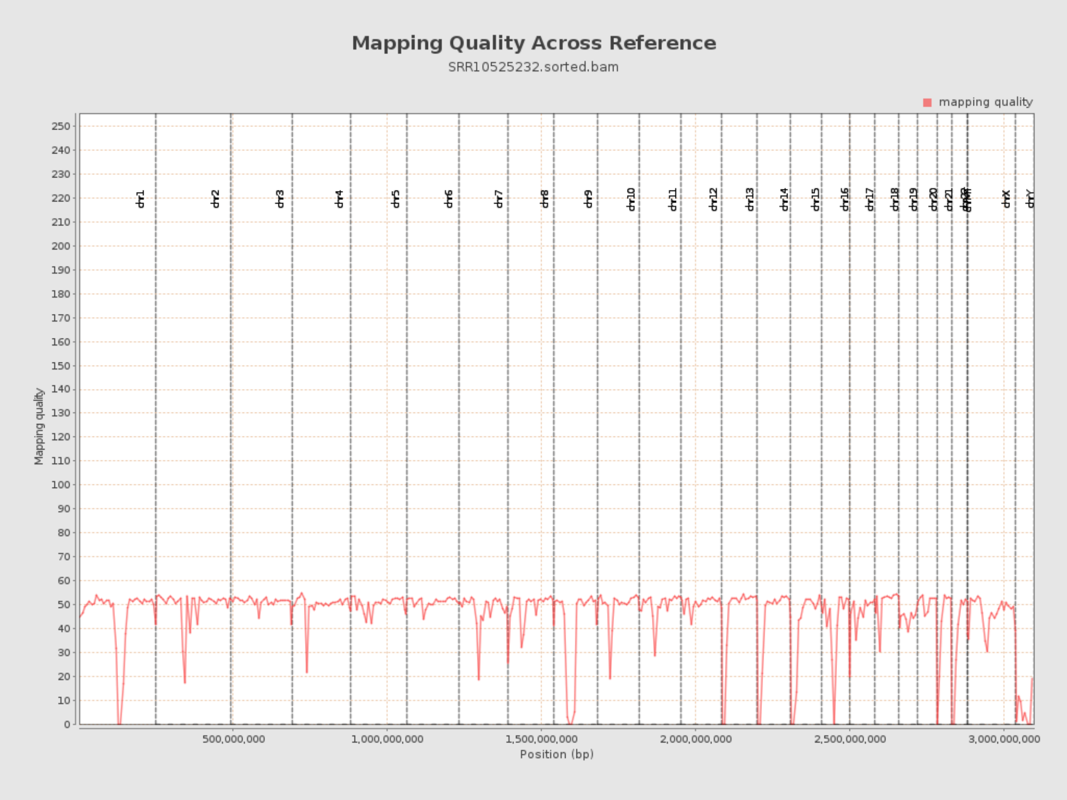
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram