Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:25:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524685.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_SRR10524685 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524685.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:25:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524685.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	746,109
Mapped reads	692,423 / 92.8%
Unmapped reads	53,686 / 7.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,733 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	14,245 / 1.91%
Duplication rate	1.47%
Clipped reads	692,312 / 92.79%

2.2. ACGT Content

Number/percentage of A's	10,195,507 / 24.73%
Number/percentage of C's	8,093,128 / 19.63%
Number/percentage of T's	13,469,235 / 32.67%
Number/percentage of G's	9,459,124 / 22.95%
Number/percentage of N's	6,257 / 0.02%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1515

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

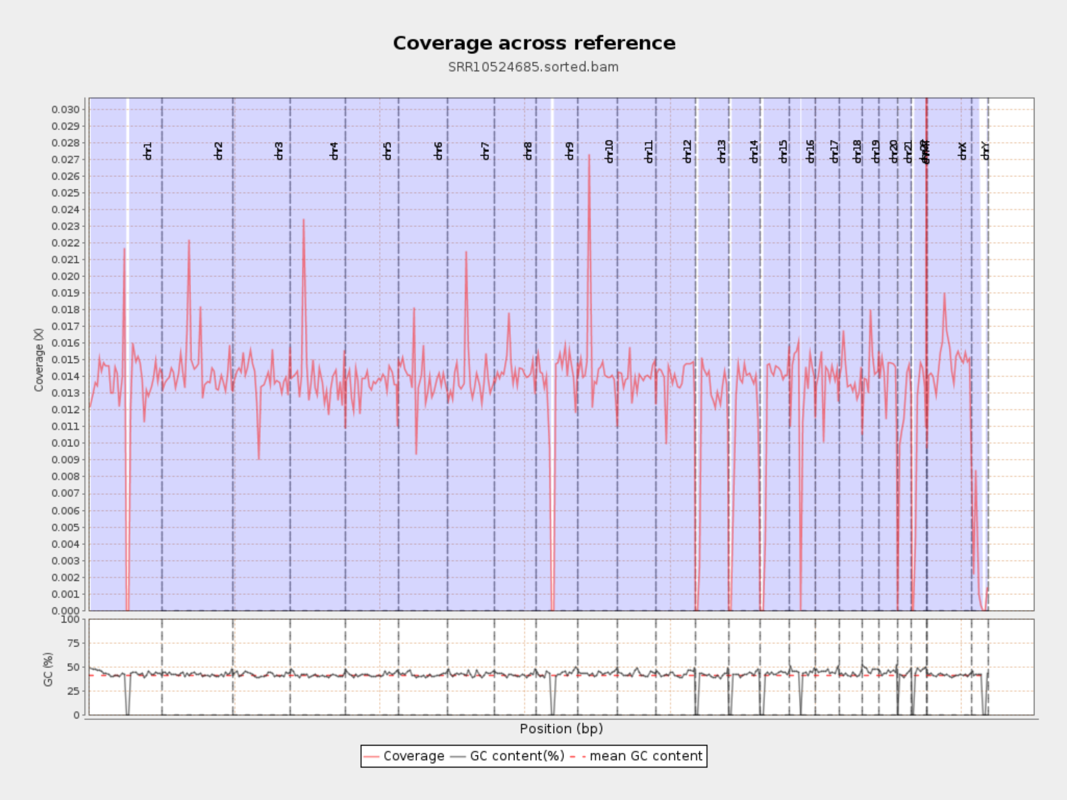
General error rate	0.51%
Mismatches	204,869
Insertions	3,355
Mapped reads with at least one insertion	0.48%
Deletions	7,968
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.93%

2.6. Chromosome stats

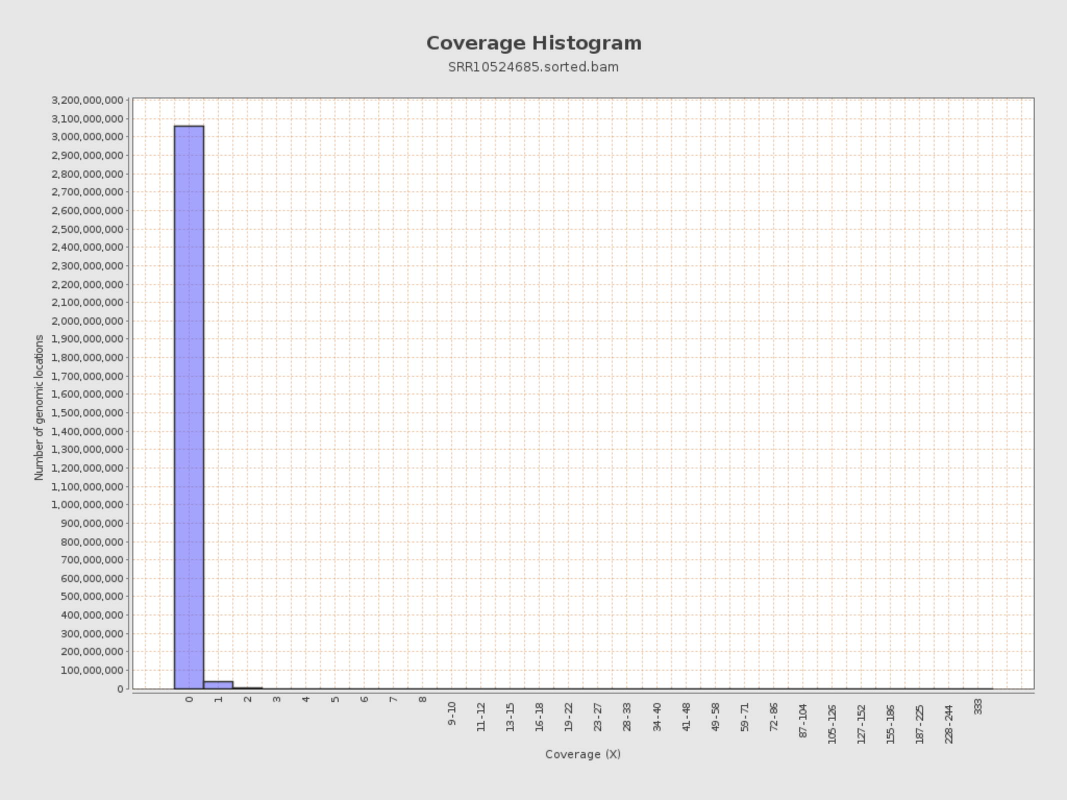
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3299627	0.0132	0.2272
chr2	243199373	3523963	0.0145	0.193
chr3	198022430	2741524	0.0138	0.1225
chr4	191154276	2676484	0.014	0.1316
chr5	180915260	2459131	0.0136	0.1214
chr6	171115067	2375508	0.0139	0.1317
chr7	159138663	2232040	0.014	0.1706

chr8	146364022	2101706	0.0144	0.1622
chr9	141213431	1781571	0.0126	0.137
chr10	135534747	2003115	0.0148	0.1605
chr11	135006516	1881917	0.0139	0.1412
chr12	133851895	1867653	0.014	0.123
chr13	115169878	1299101	0.0113	0.1106
chr14	107349540	1220117	0.0114	0.1136
chr15	102531392	1186896	0.0116	0.1118
chr16	90354753	1178692	0.013	0.1247
chr17	81195210	1120843	0.0138	0.1266
chr18	78077248	1090634	0.014	0.2182
chr19	59128983	856300	0.0145	0.1869
chr20	63025520	886376	0.0141	0.1244
chr21	48129895	536437	0.0111	0.1164
chr22	51304566	483332	0.0094	0.1006
chrMT	16571	1040	0.0628	0.2542
chrX	155270560	2302372	0.0148	0.1329
chrY	59373566	129571	0.0022	0.0841

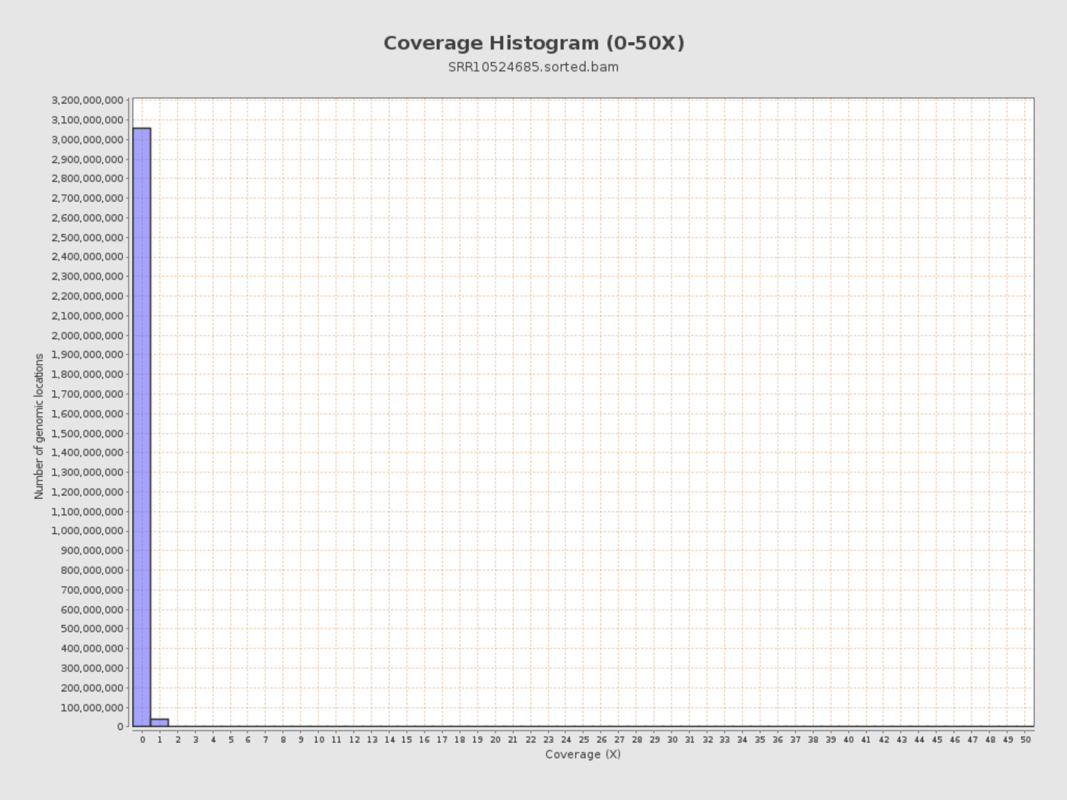
3. Results : Coverage across reference



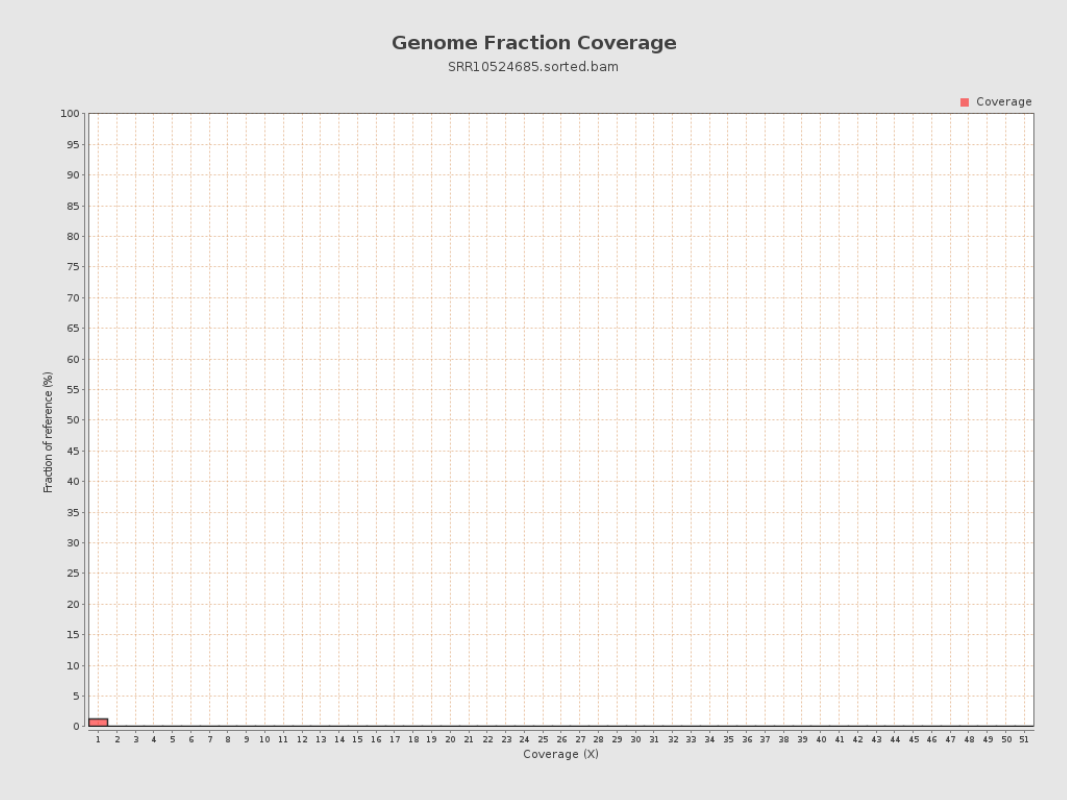
4. Results : Coverage Histogram



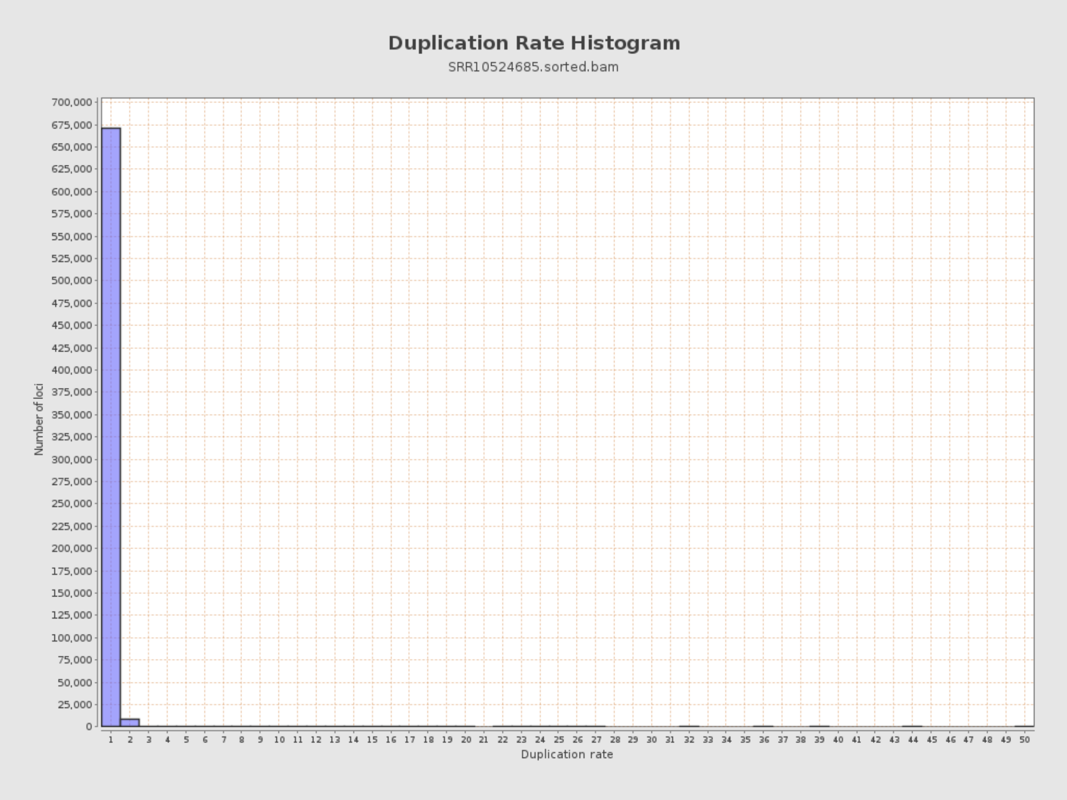
5. Results : Coverage Histogram (0-50X)



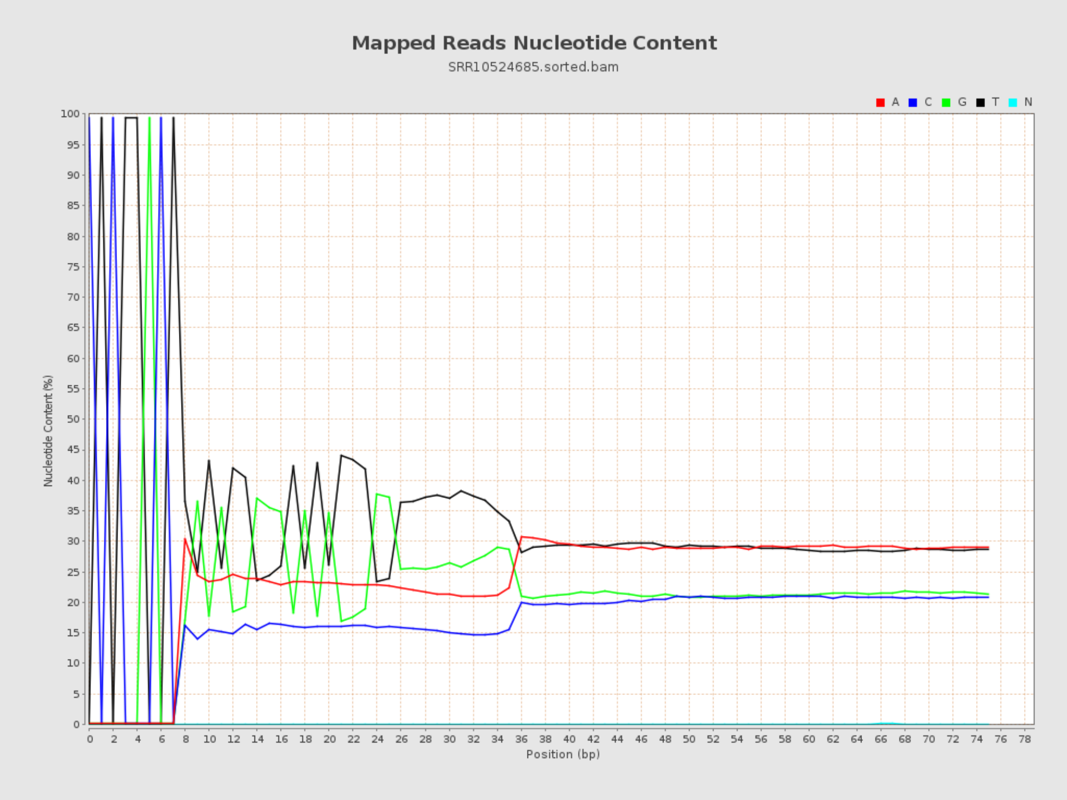
6. Results : Genome Fraction Coverage



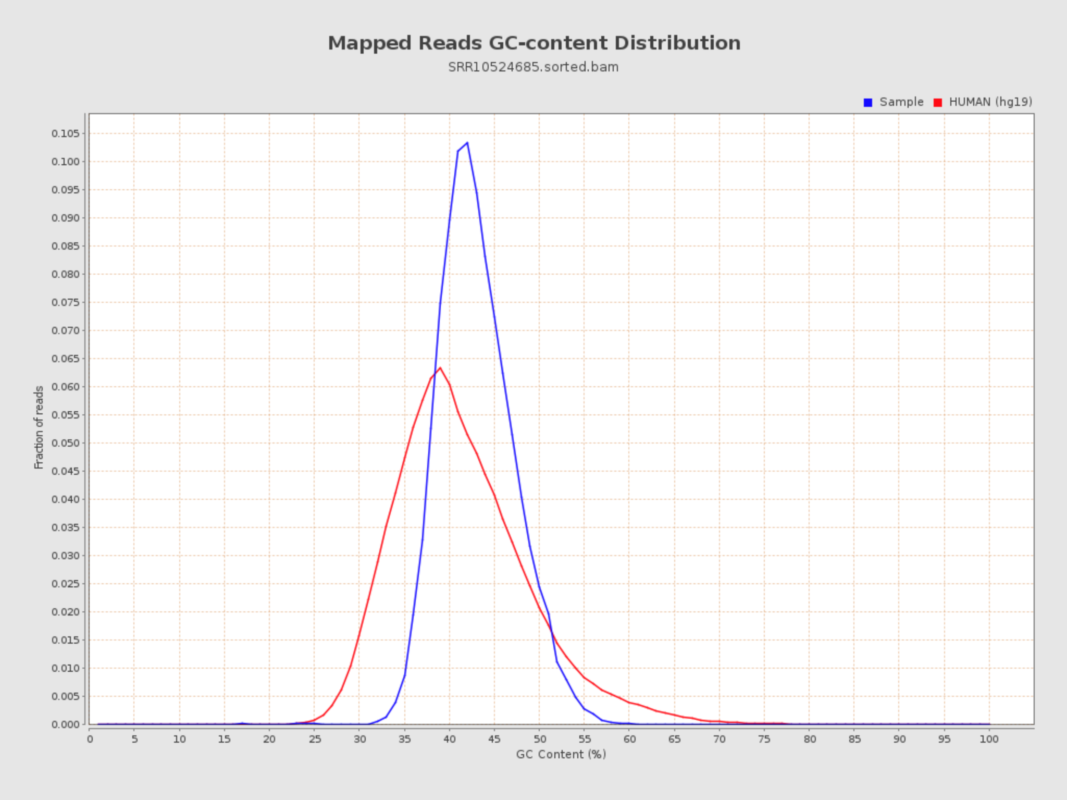
7. Results : Duplication Rate Histogram



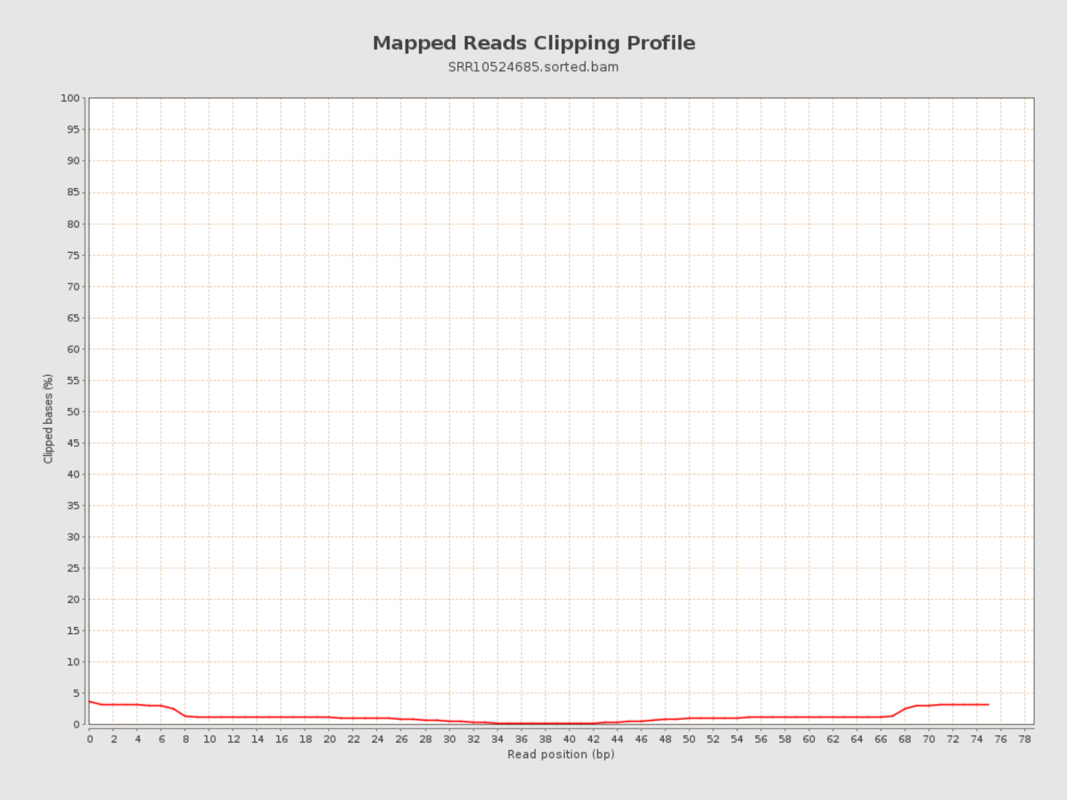
8. Results : Mapped Reads Nucleotide Content



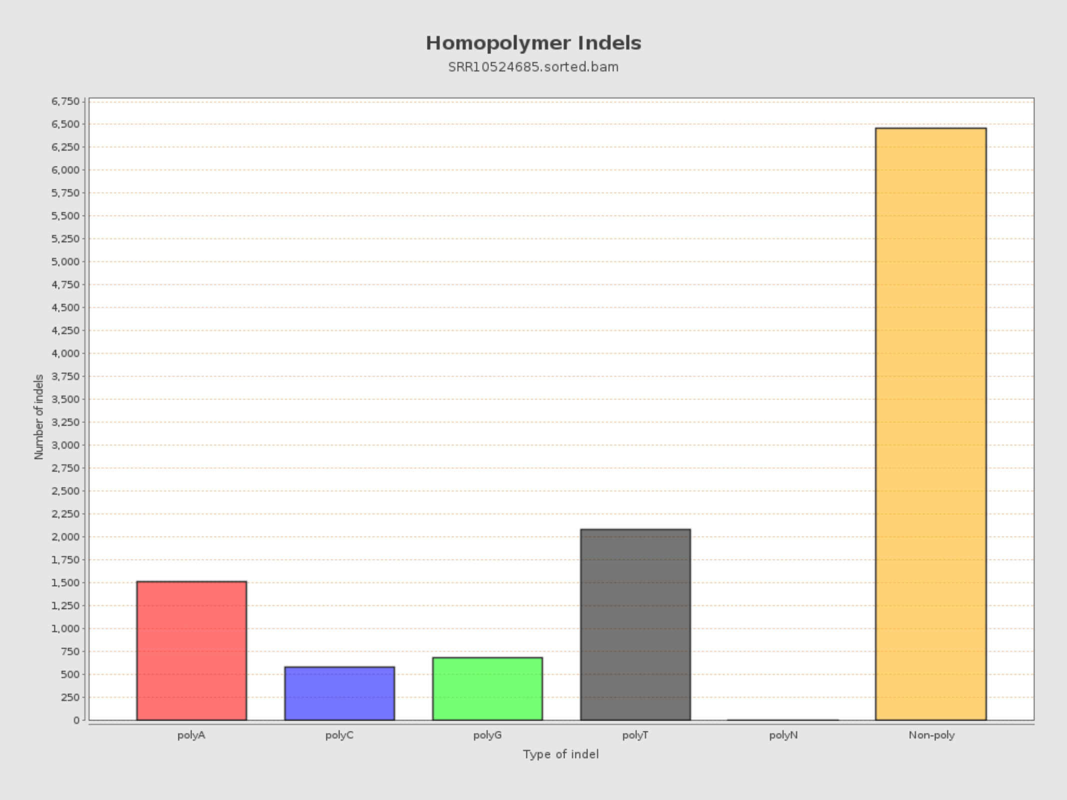
9. Results : Mapped Reads GC-content Distribution



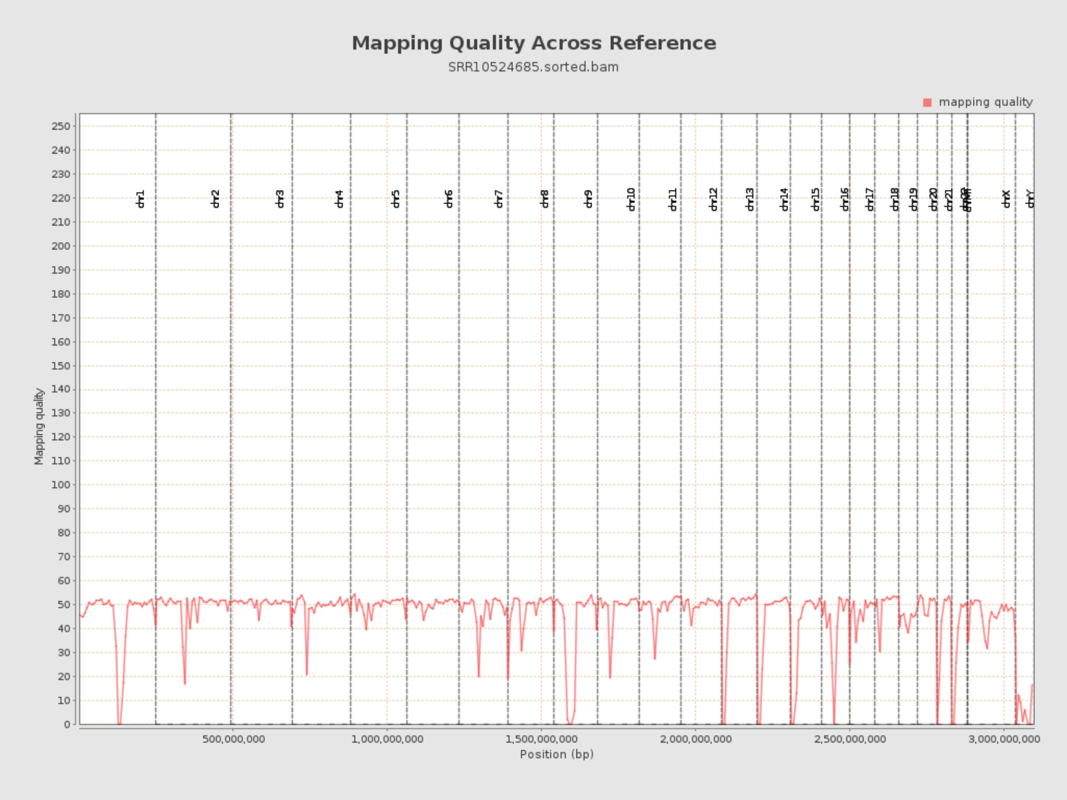
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram