Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:17:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525273.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_SRR10525273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525273.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:17:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,323,758
Mapped reads	1,208,749 / 91.31%
Unmapped reads	115,009 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,112 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	38,128 / 2.88%
Duplication rate	2.28%
Clipped reads	1,210,762 / 91.46%

2.2. ACGT Content

Number/percentage of A's	18,041,075 / 25.74%
Number/percentage of C's	13,301,727 / 18.98%
Number/percentage of T's	22,452,010 / 32.03%
Number/percentage of G's	16,293,831 / 23.25%
Number/percentage of N's	1,524 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2412

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

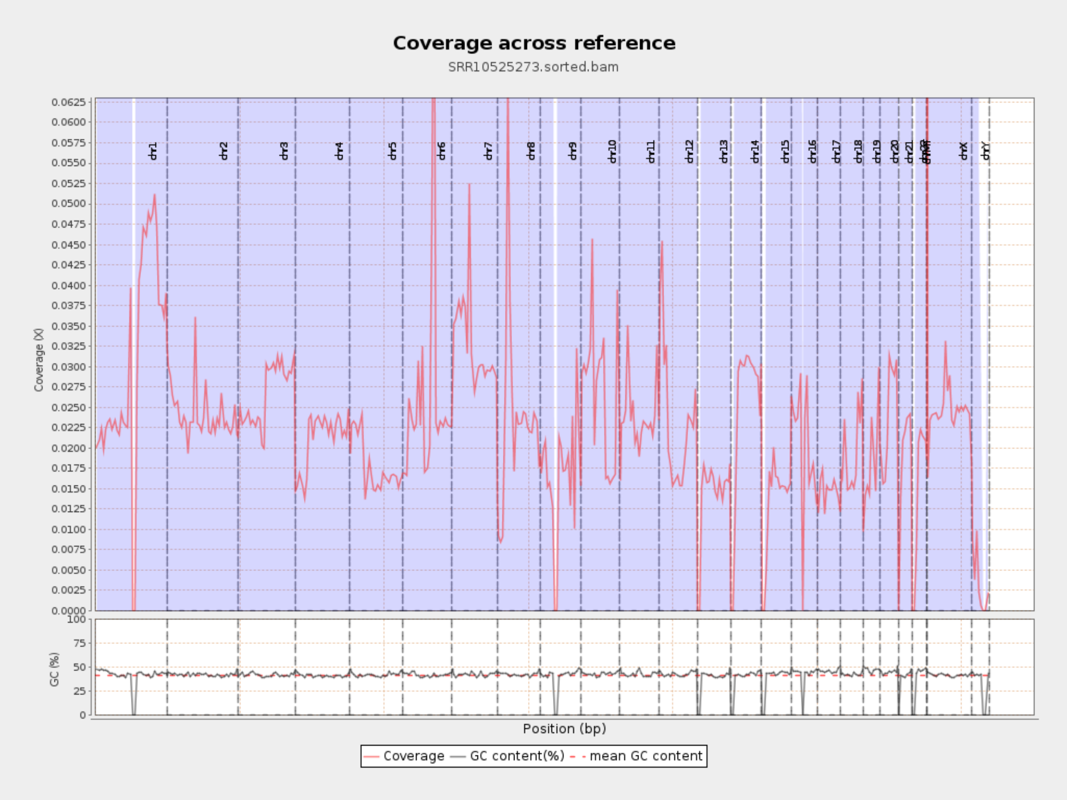
General error rate	0.52%
Mismatches	355,472
Insertions	4,588
Mapped reads with at least one insertion	0.38%
Deletions	14,806
Mapped reads with at least one deletion	1.22%
Homopolymer indels	44.27%

2.6. Chromosome stats

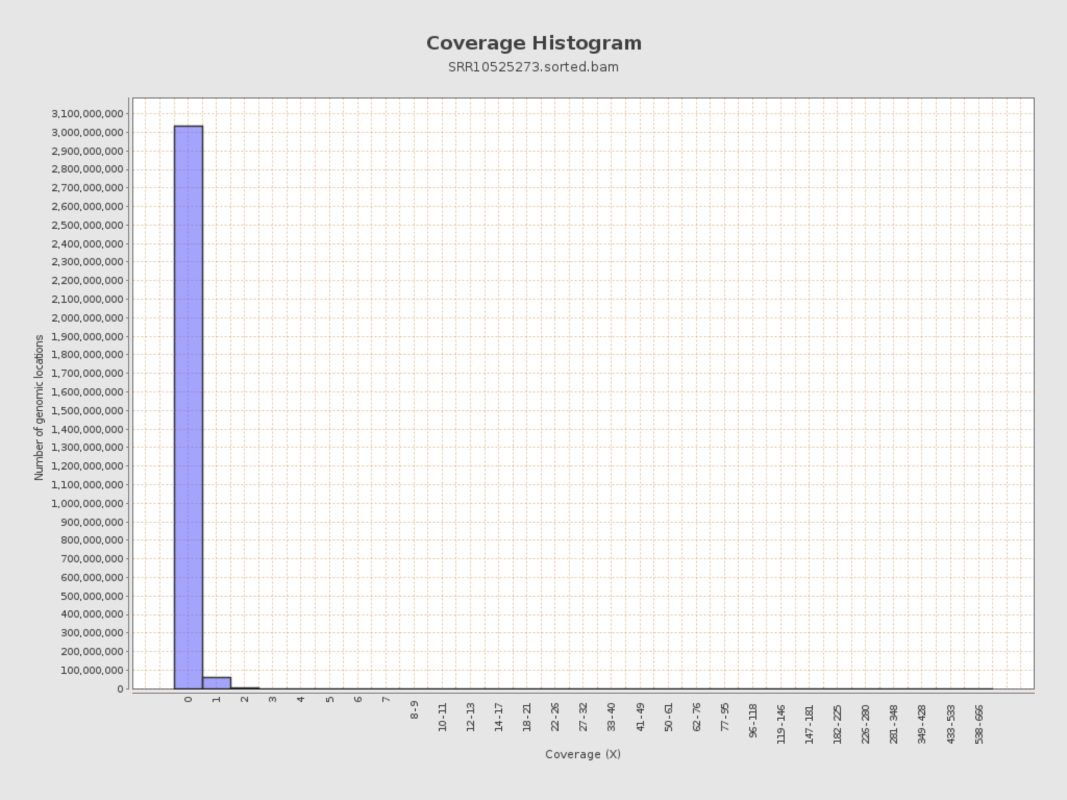
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7578536	0.0304	0.4196
chr2	243199373	5865834	0.0241	0.3171
chr3	198022430	5259667	0.0266	0.1751
chr4	191154276	4036156	0.0211	0.1596
chr5	180915260	3215180	0.0178	0.1419
chr6	171115067	4555356	0.0266	0.1897
chr7	159138663	5218290	0.0328	0.4034

chr8	146364022	3505894	0.024	0.226
chr9	141213431	2337165	0.0166	0.1738
chr10	135534747	3664690	0.027	0.2471
chr11	135006516	3212096	0.0238	0.2021
chr12	133851895	3130296	0.0234	0.1643
chr13	115169878	1618223	0.0141	0.13
chr14	107349540	2634322	0.0245	0.1689
chr15	102531392	1330232	0.013	0.1247
chr16	90354753	1813752	0.0201	0.1638
chr17	81195210	1186632	0.0146	0.1327
chr18	78077248	1494153	0.0191	0.3388
chr19	59128983	1092703	0.0185	0.2922
chr20	63025520	1506085	0.0239	0.1654
chr21	48129895	909213	0.0189	0.1519
chr22	51304566	756204	0.0147	0.1282
chrMT	16571	168239	10.1526	6.0437
chrX	155270560	3835552	0.0247	0.1782
chrY	59373566	189075	0.0032	0.0906

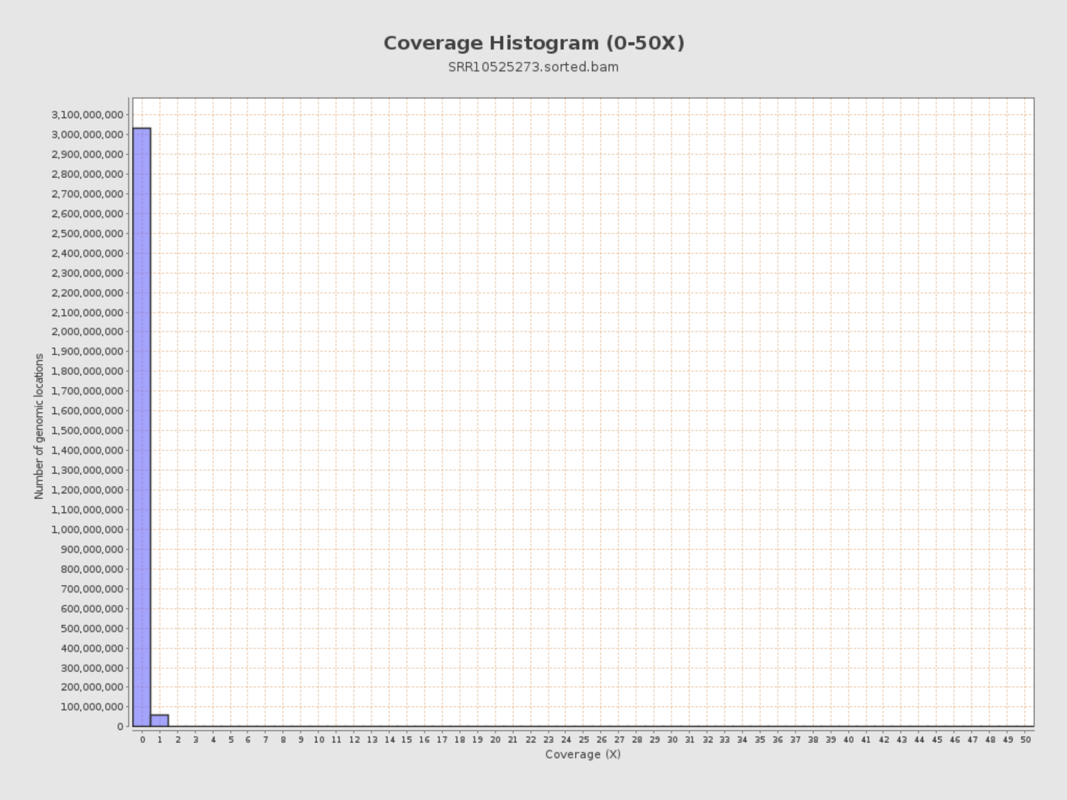
3. Results : Coverage across reference



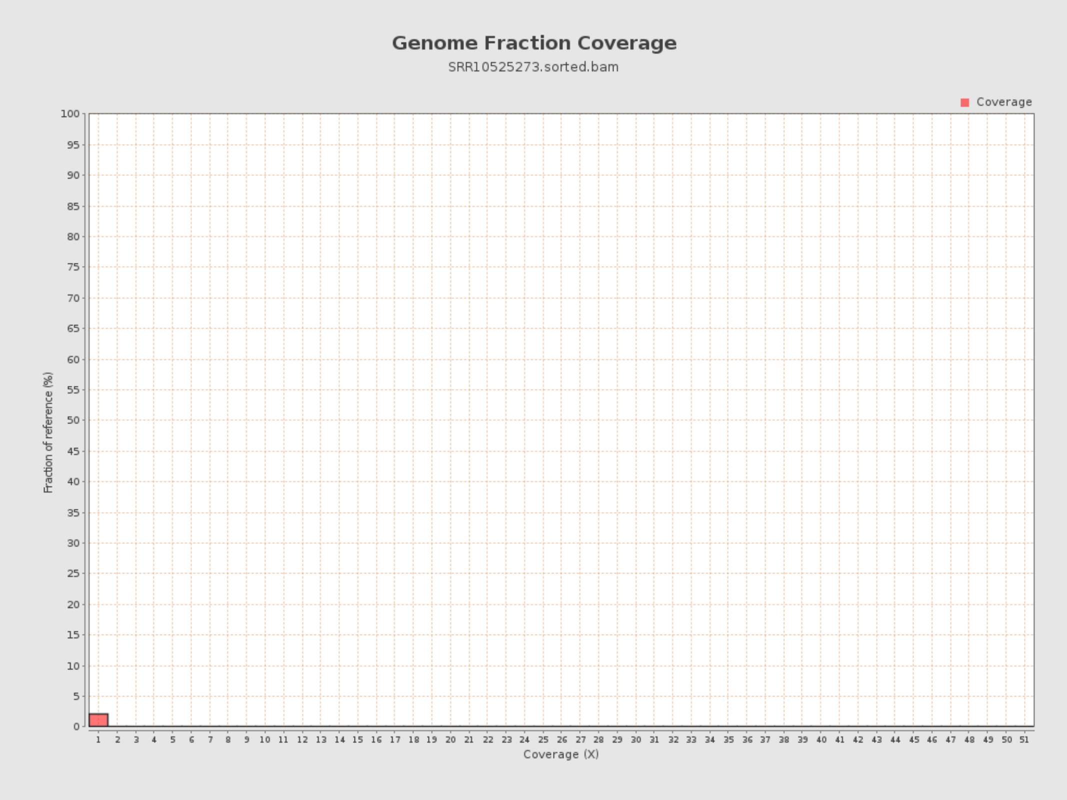
4. Results : Coverage Histogram



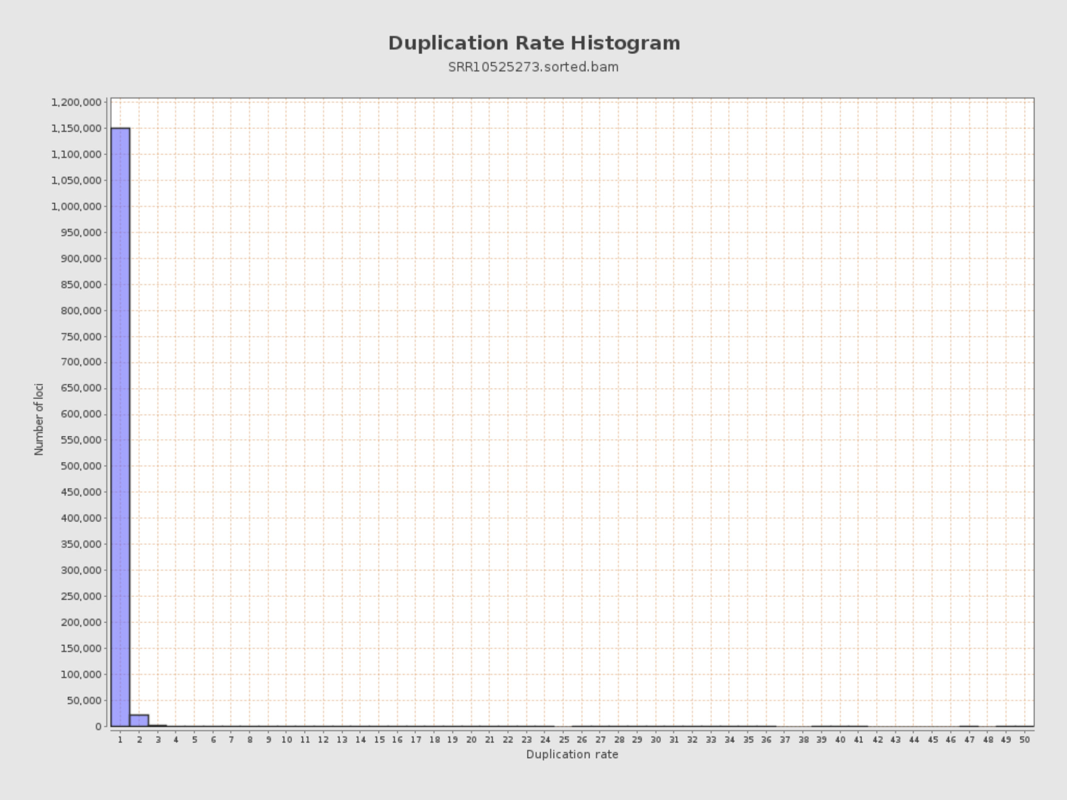
5. Results : Coverage Histogram (0-50X)



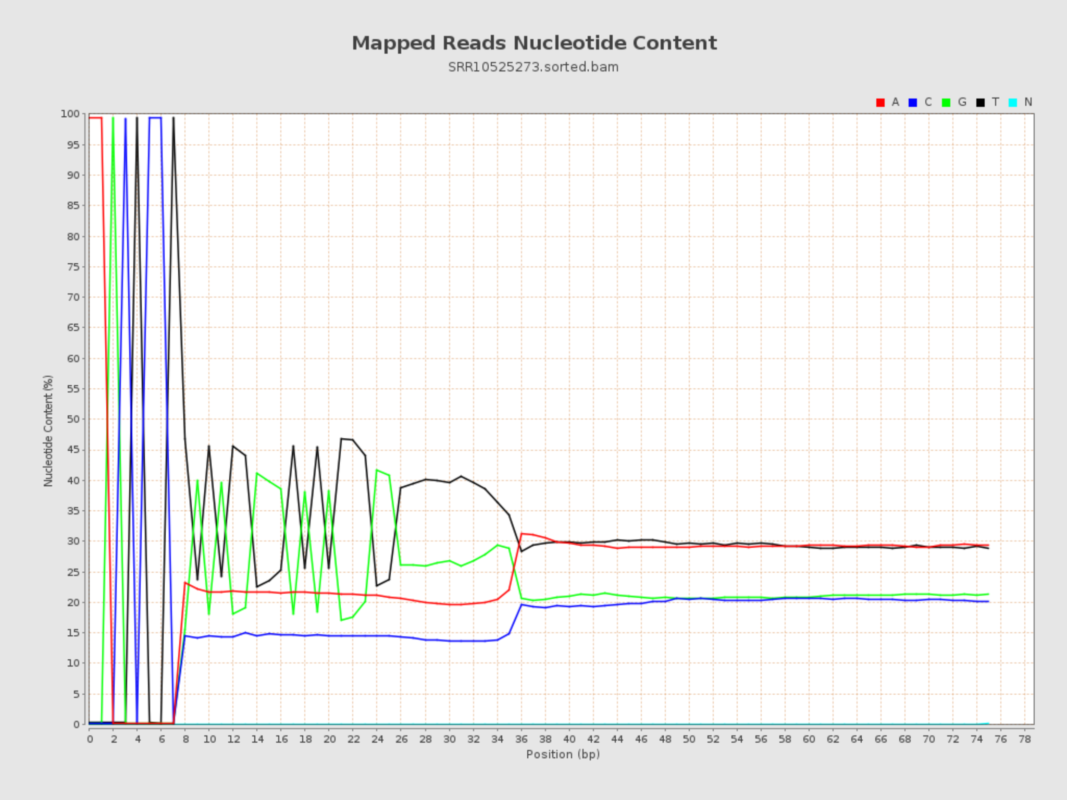
6. Results : Genome Fraction Coverage



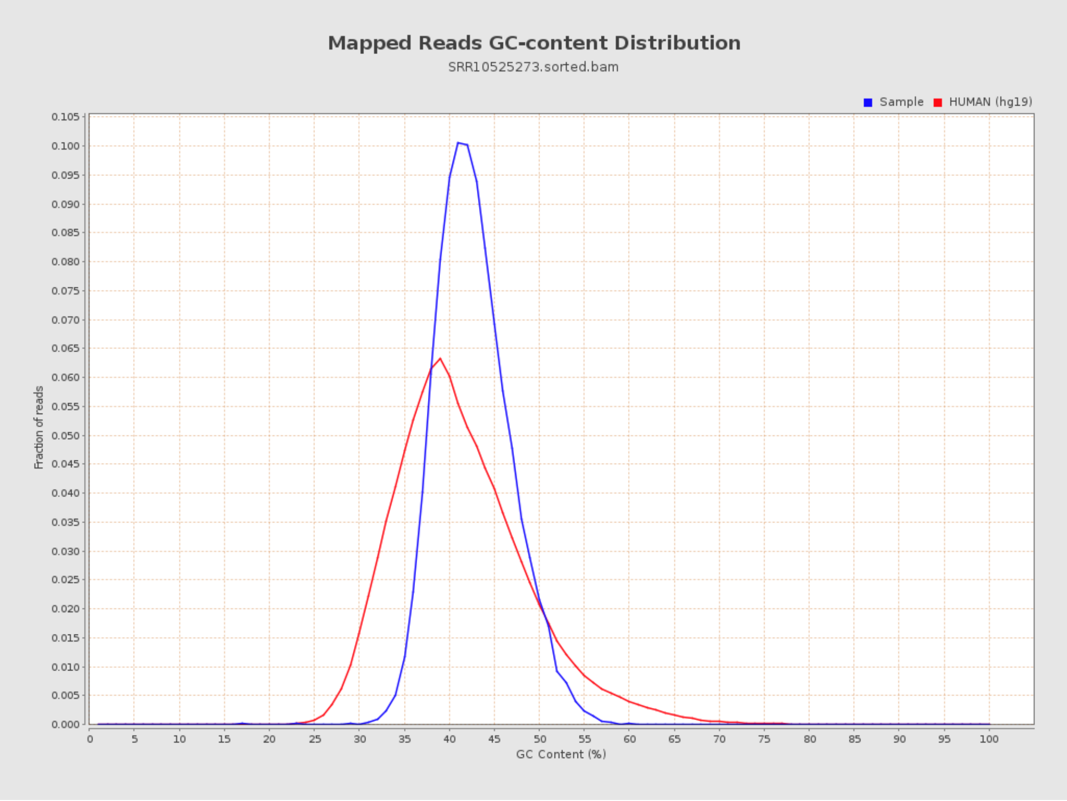
7. Results : Duplication Rate Histogram



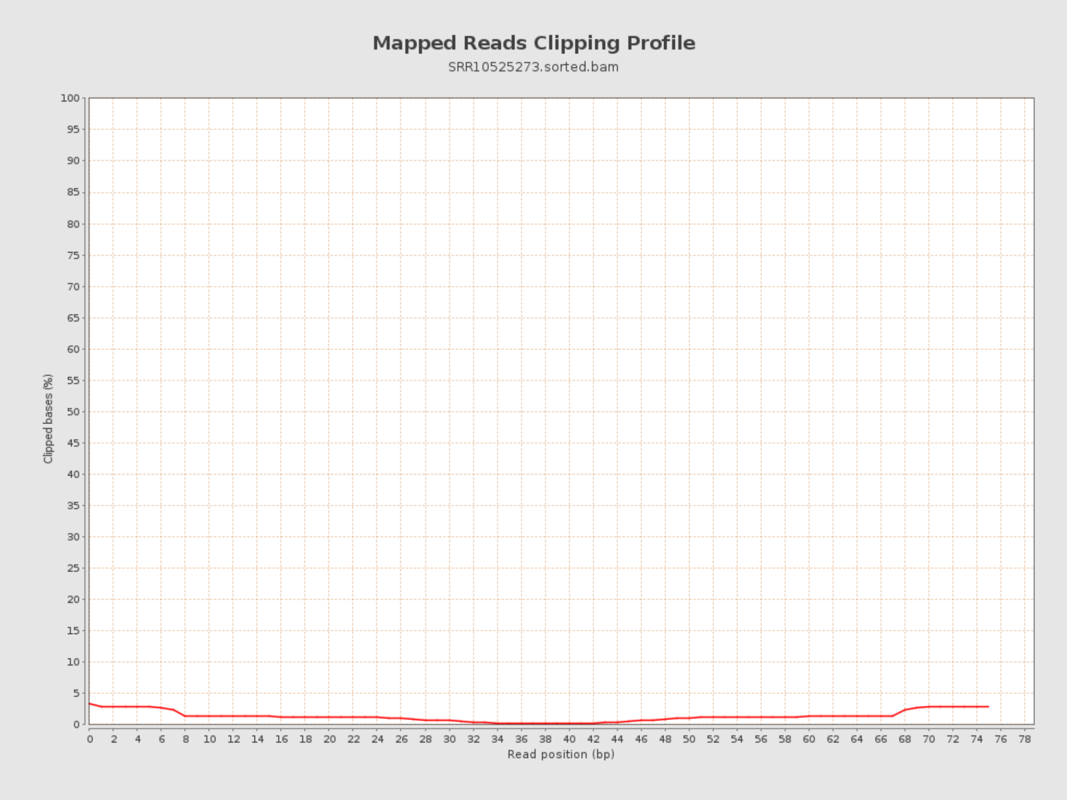
8. Results : Mapped Reads Nucleotide Content



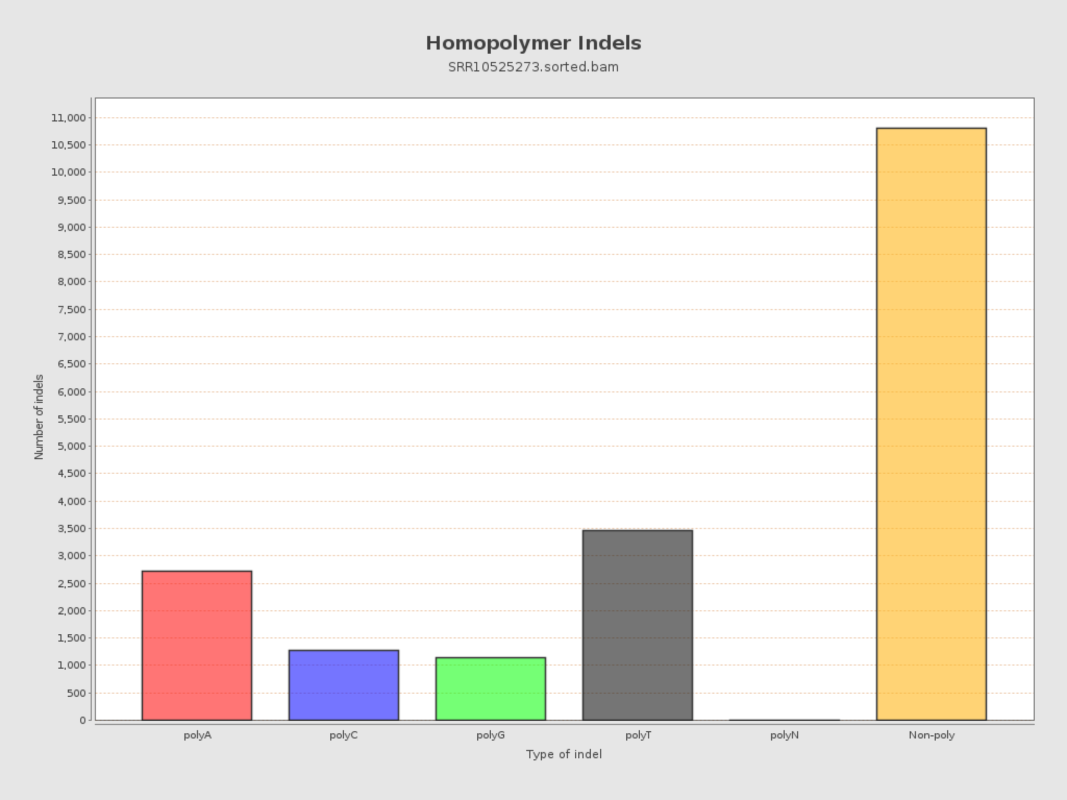
9. Results : Mapped Reads GC-content Distribution



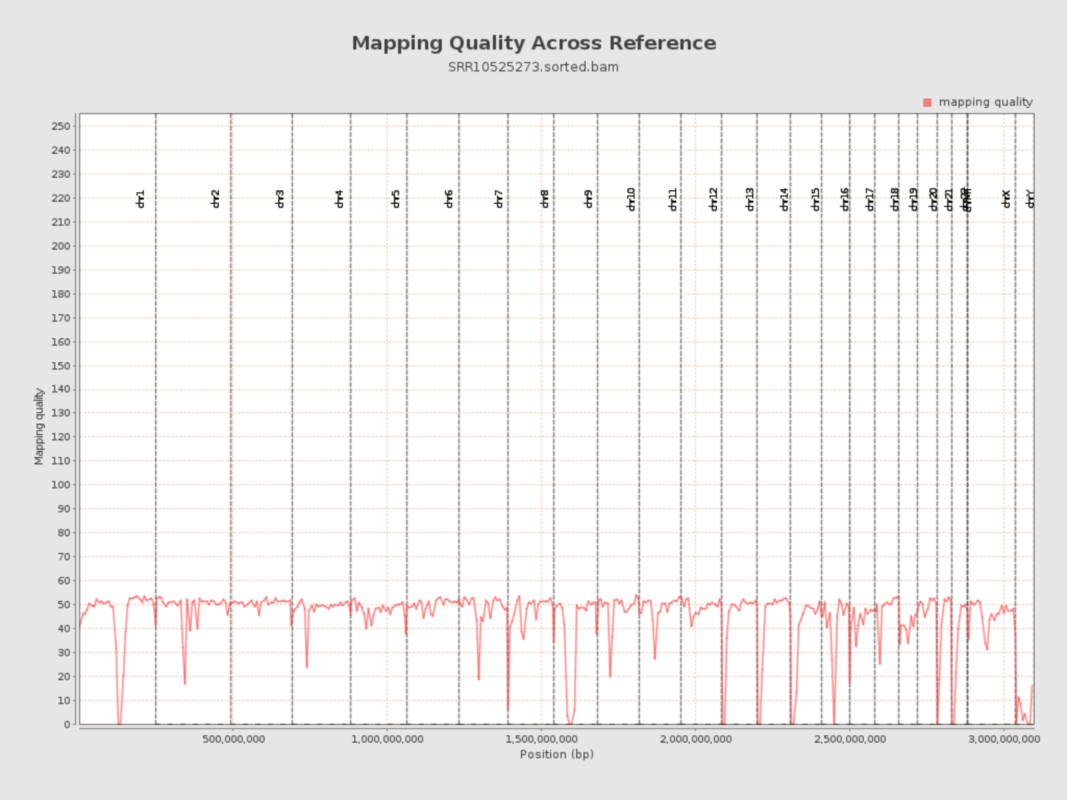
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram