Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:26:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525212.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_SRR10525212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:26:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	569,746
Mapped reads	472,101 / 82.86%
Unmapped reads	97,645 / 17.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,514 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	7,383 / 1.3%
Duplication rate	1.13%
Clipped reads	471,888 / 82.82%

2.2. ACGT Content

Number/percentage of A's	7,864,245 / 27.07%
Number/percentage of C's	5,542,996 / 19.08%
Number/percentage of T's	8,656,125 / 29.8%
Number/percentage of G's	6,987,664 / 24.05%
Number/percentage of N's	730 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.0094

Standard Deviation	0.1254

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

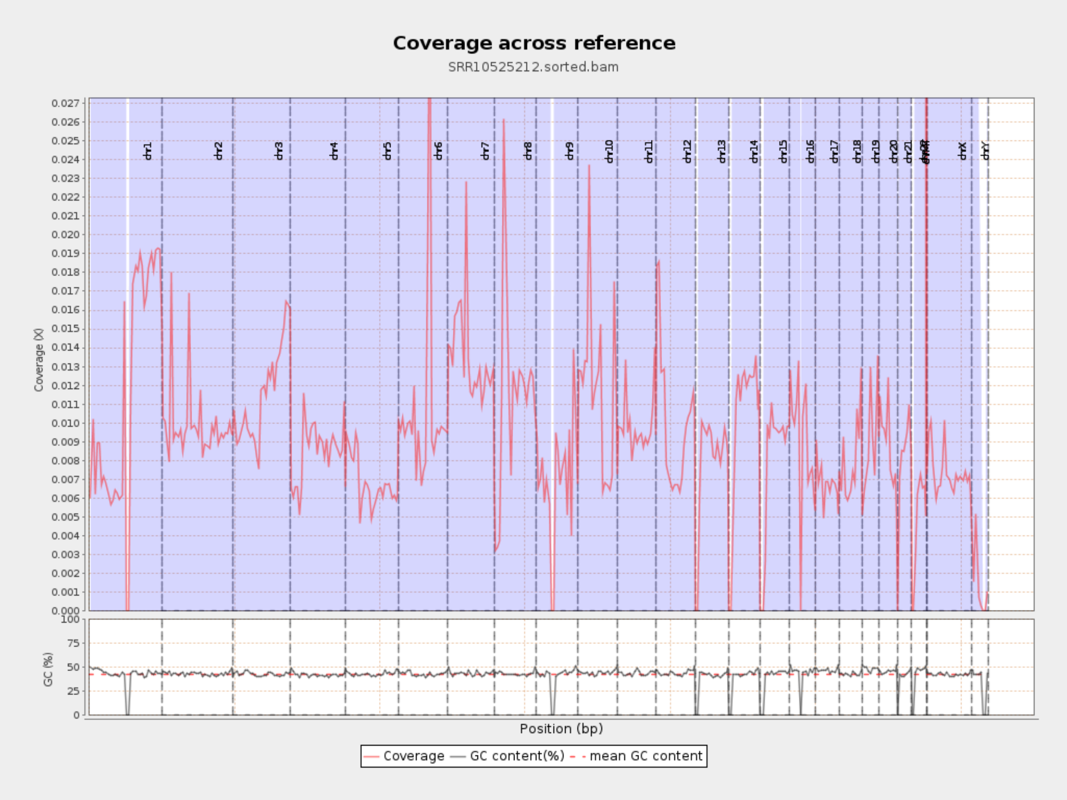
General error rate	0.51%
Mismatches	144,305
Insertions	1,991
Mapped reads with at least one insertion	0.42%
Deletions	6,285
Mapped reads with at least one deletion	1.32%
Homopolymer indels	42.82%

2.6. Chromosome stats

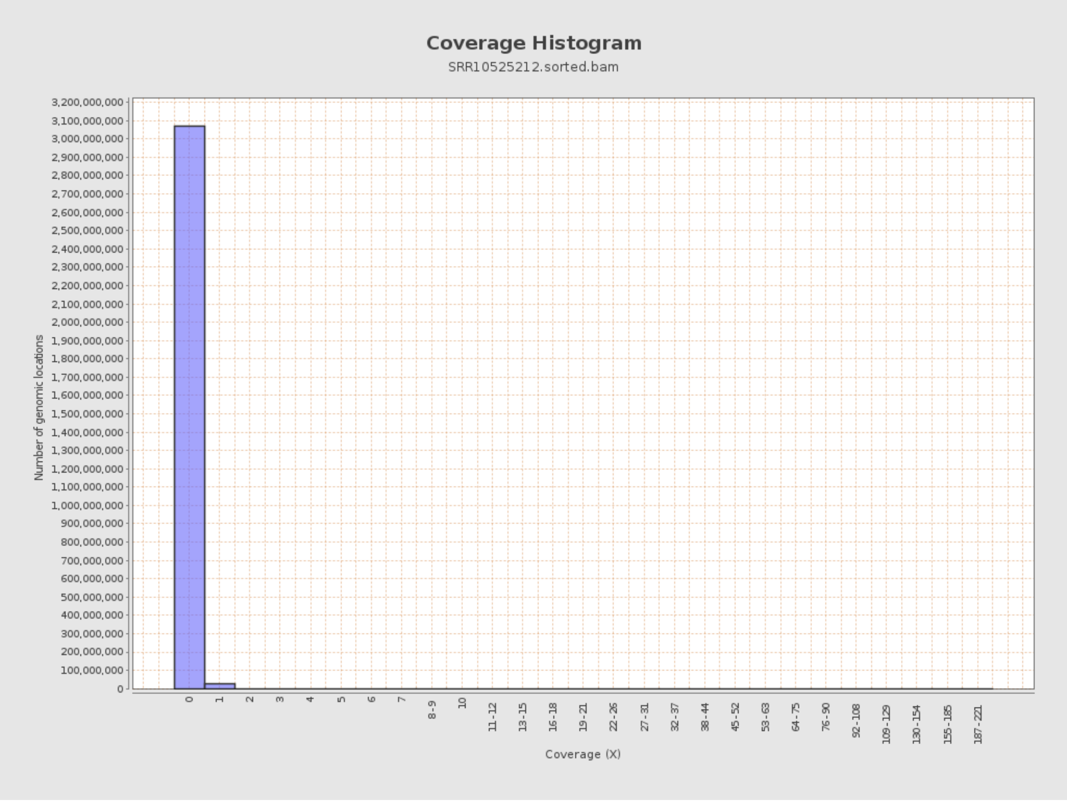
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2872828	0.0115	0.2083
chr2	243199373	2414195	0.0099	0.1269
chr3	198022430	2269931	0.0115	0.1104
chr4	191154276	1619693	0.0085	0.0964
chr5	180915260	1229495	0.0068	0.0846
chr6	171115067	1862051	0.0109	0.1114
chr7	159138663	2175899	0.0137	0.2014

chr8	146364022	1664138	0.0114	0.12
chr9	141213431	975235	0.0069	0.0983
chr10	135534747	1601601	0.0118	0.1465
chr11	135006516	1327394	0.0098	0.1101
chr12	133851895	1324602	0.0099	0.1028
chr13	115169878	908553	0.0079	0.091
chr14	107349540	1081579	0.0101	0.1041
chr15	102531392	801838	0.0078	0.0907
chr16	90354753	795781	0.0088	0.1023
chr17	81195210	547674	0.0067	0.0855
chr18	78077248	616086	0.0079	0.1484
chr19	59128983	534069	0.009	0.1535
chr20	63025520	564089	0.009	0.0976
chr21	48129895	387291	0.008	0.0945
chr22	51304566	236990	0.0046	0.0697
chrMT	16571	19901	1.201	1.3257
chrX	155270560	1148051	0.0074	0.0912
chrY	59373566	83025	0.0014	0.0591

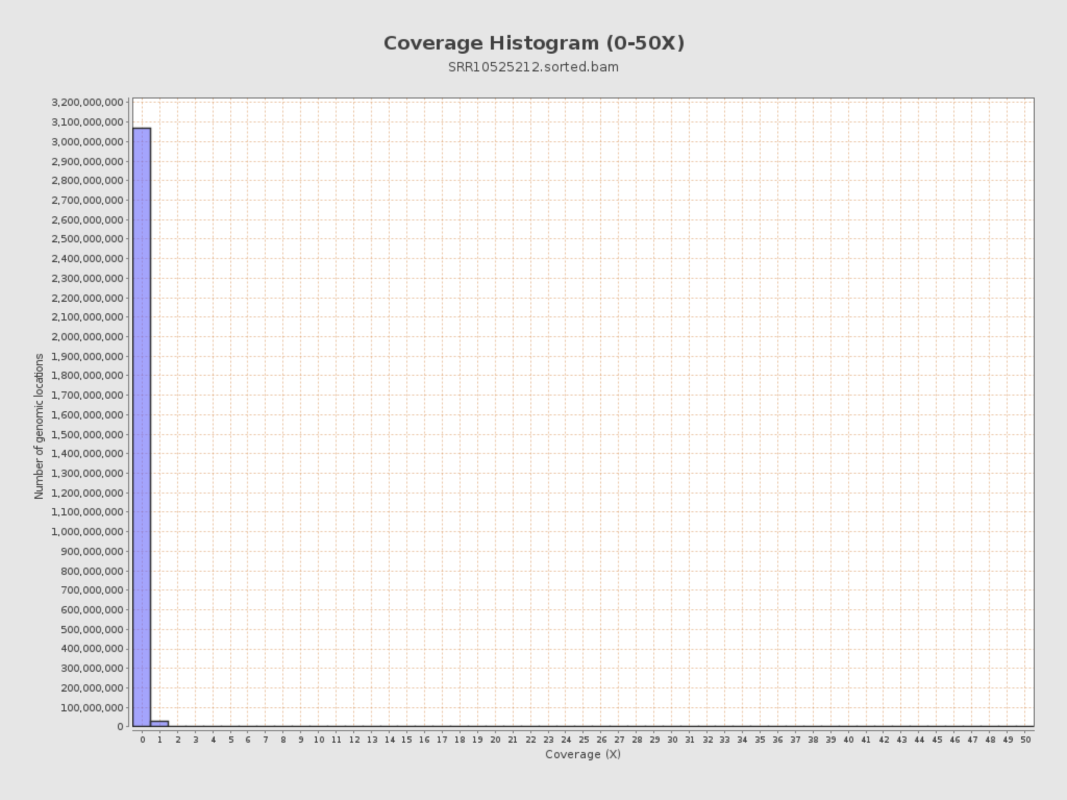
3. Results : Coverage across reference



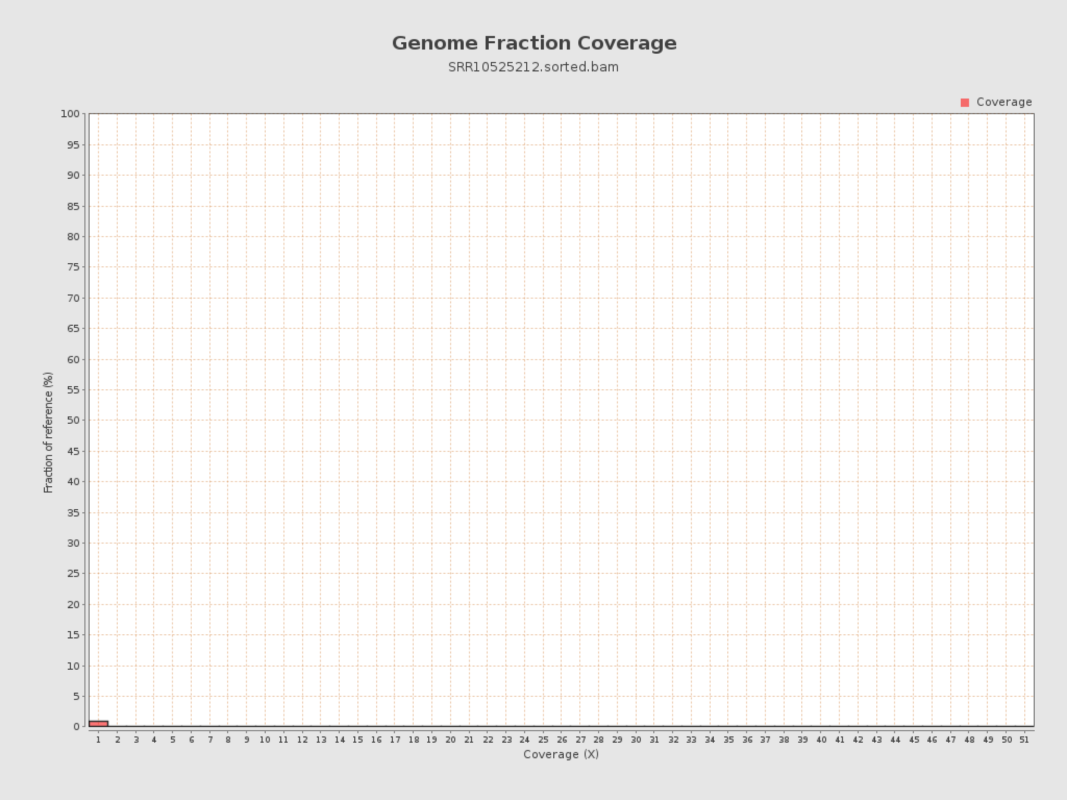
4. Results : Coverage Histogram



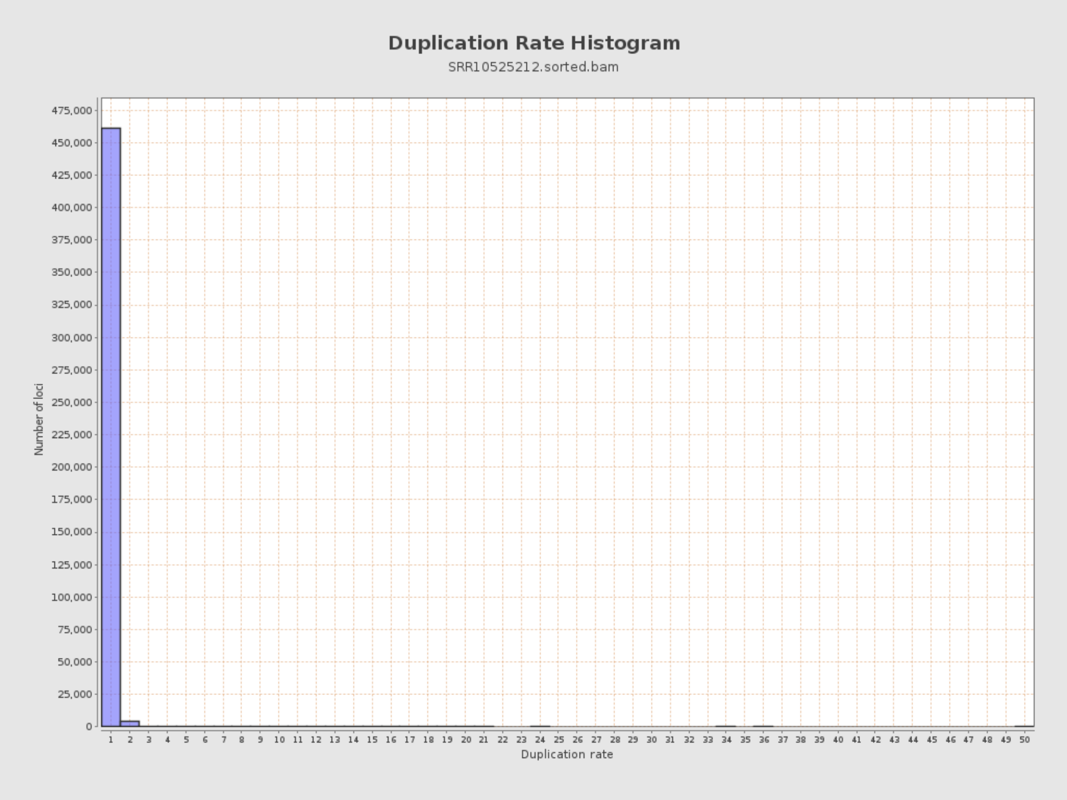
5. Results : Coverage Histogram (0-50X)



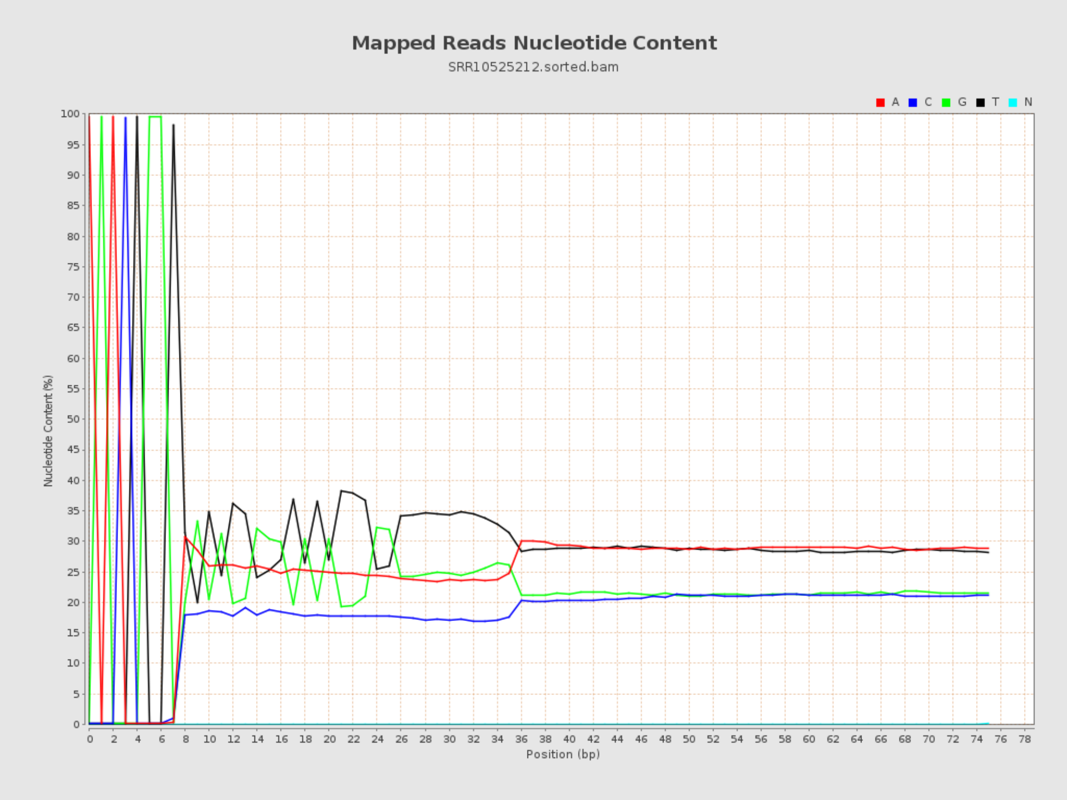
6. Results : Genome Fraction Coverage



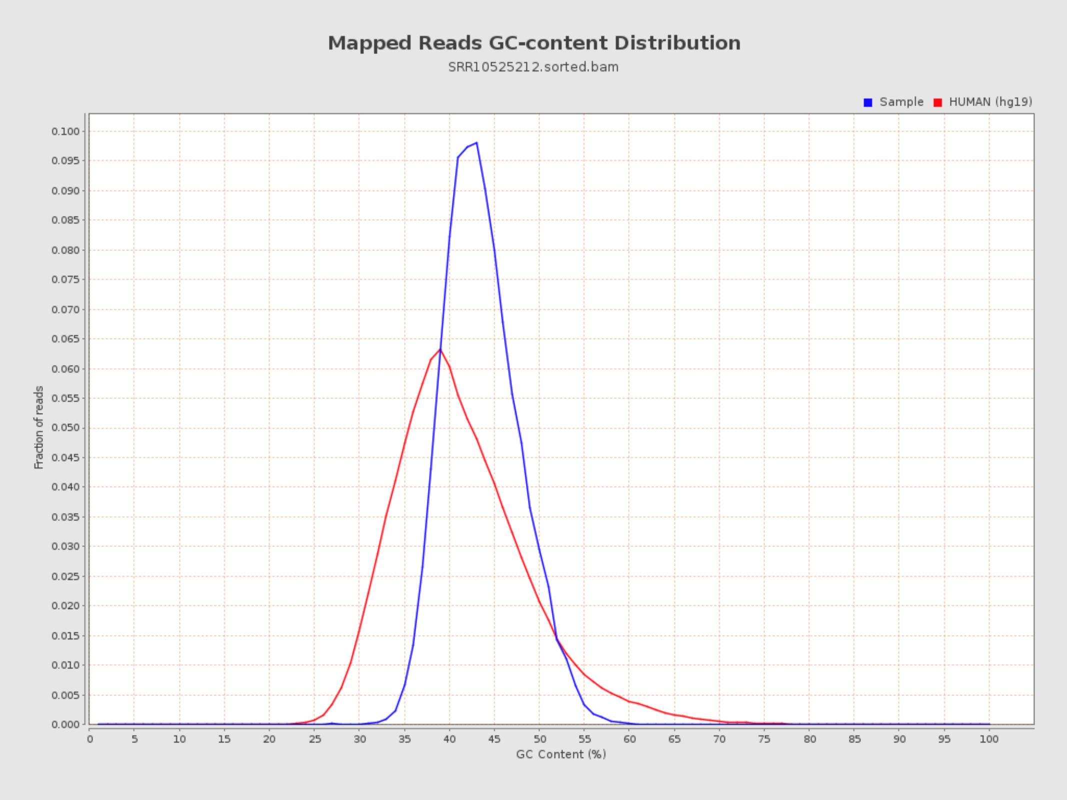
7. Results : Duplication Rate Histogram



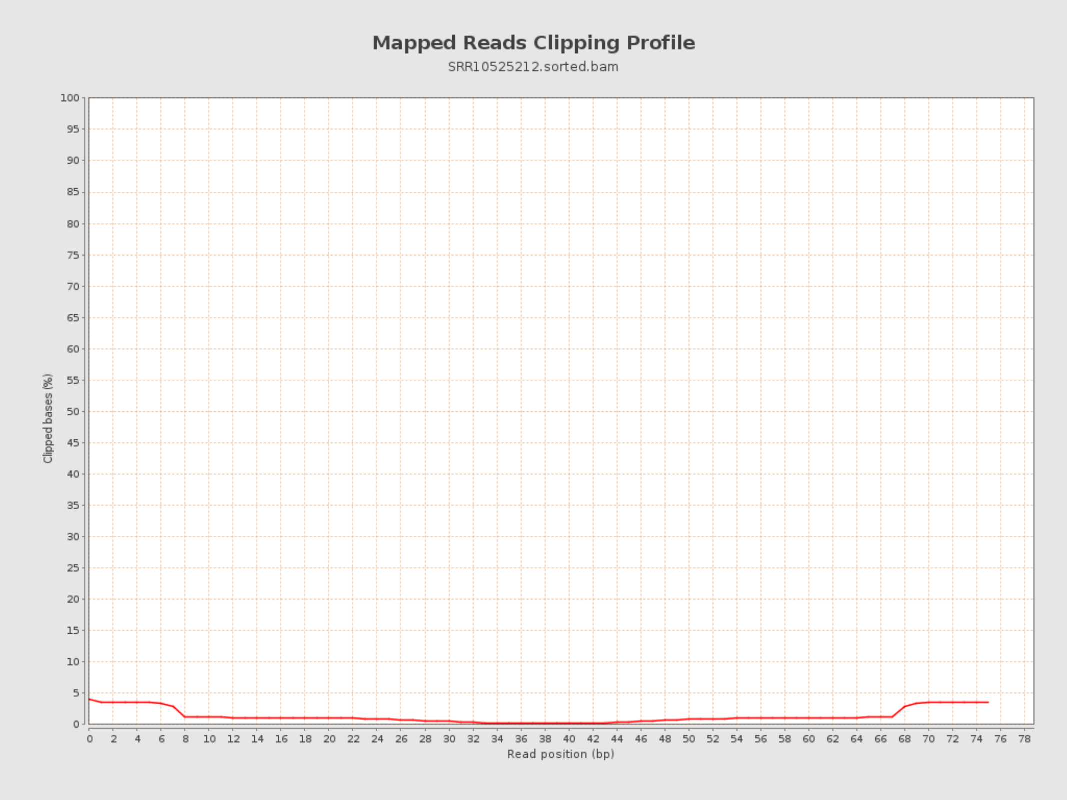
8. Results : Mapped Reads Nucleotide Content



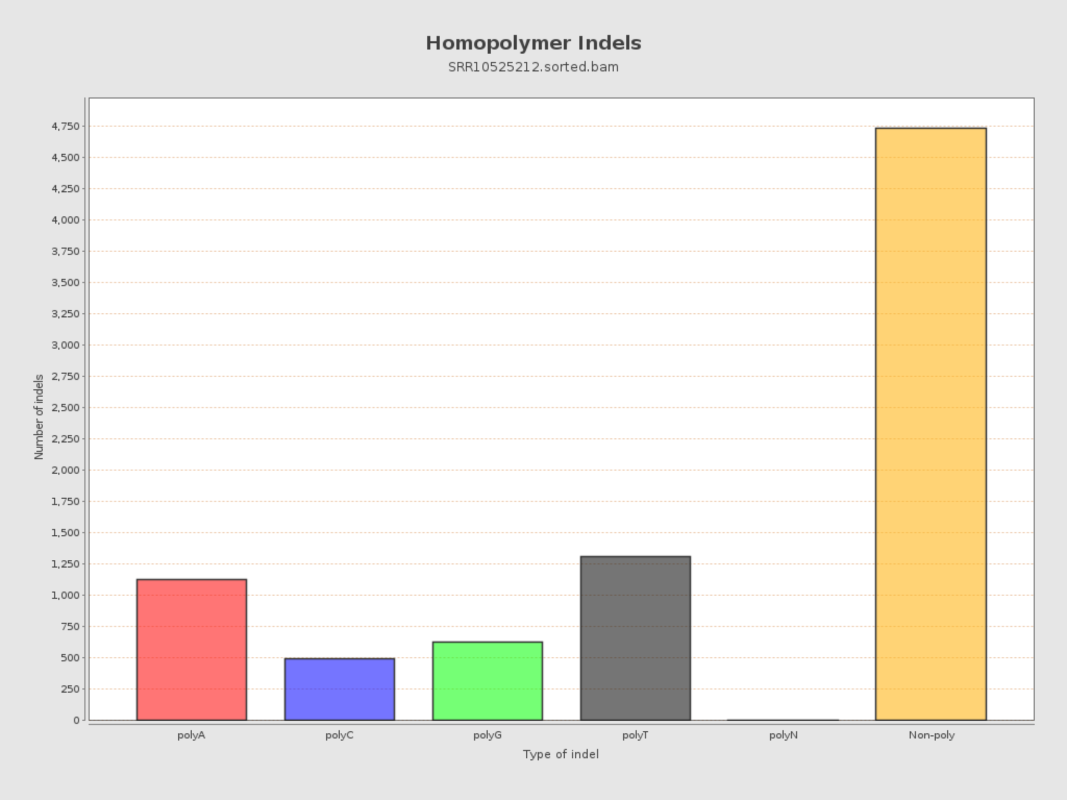
9. Results : Mapped Reads GC-content Distribution



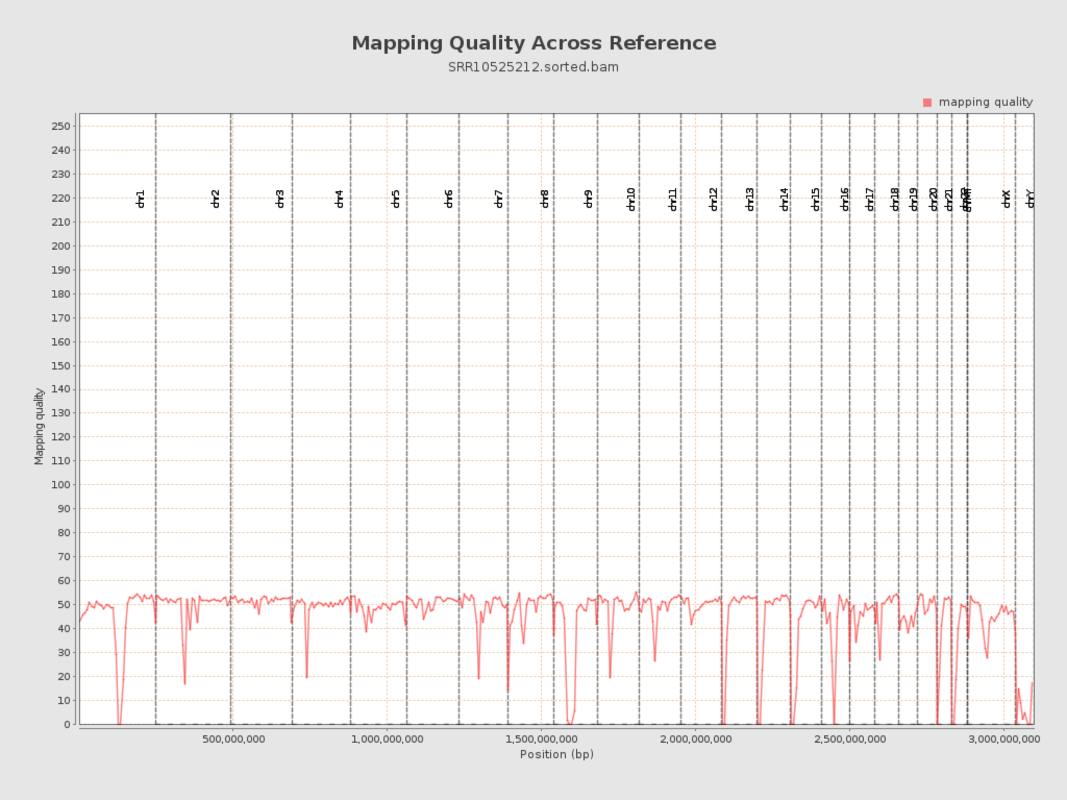
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram