Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:05:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525268.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_SRR10525268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:05:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	983,269
Mapped reads	899,722 / 91.5%
Unmapped reads	83,547 / 8.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,479 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	24,440 / 2.49%
Duplication rate	1.93%
Clipped reads	901,667 / 91.7%

2.2. ACGT Content

Number/percentage of A's	12,481,407 / 24.02%
Number/percentage of C's	9,388,048 / 18.07%
Number/percentage of T's	17,080,000 / 32.87%
Number/percentage of G's	13,014,671 / 25.04%
Number/percentage of N's	1,059 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.1905

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

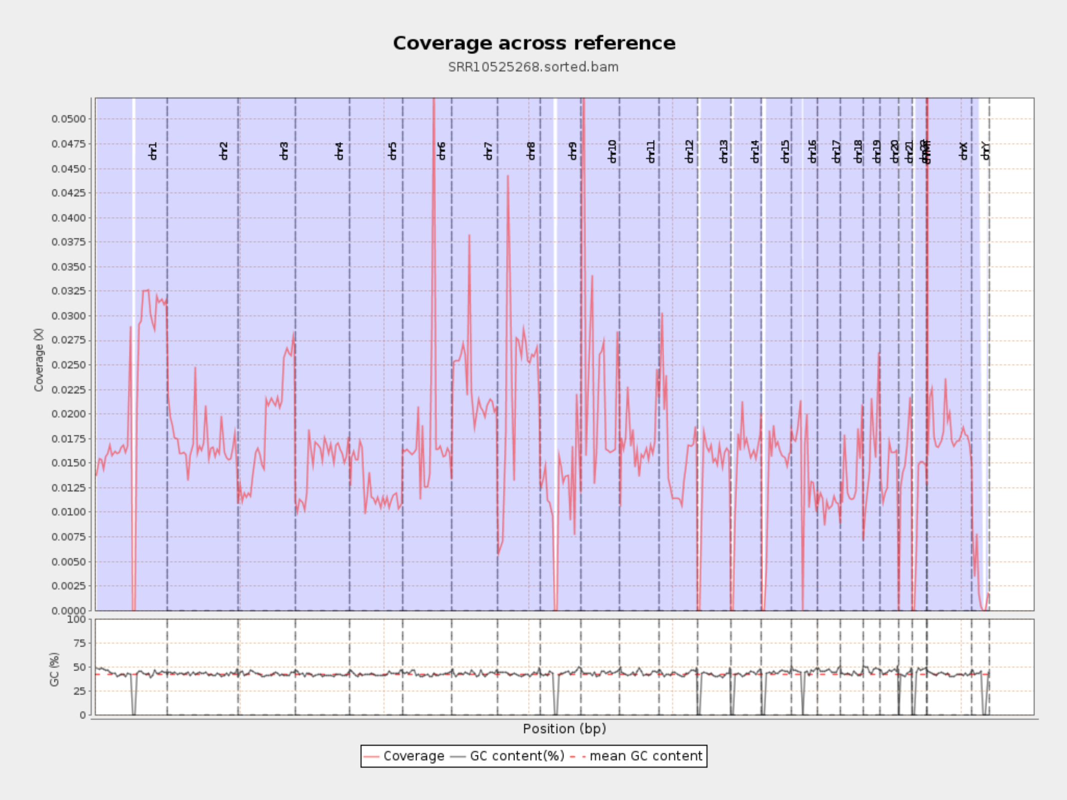
General error rate	0.52%
Mismatches	261,879
Insertions	3,354
Mapped reads with at least one insertion	0.37%
Deletions	10,704
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.55%

2.6. Chromosome stats

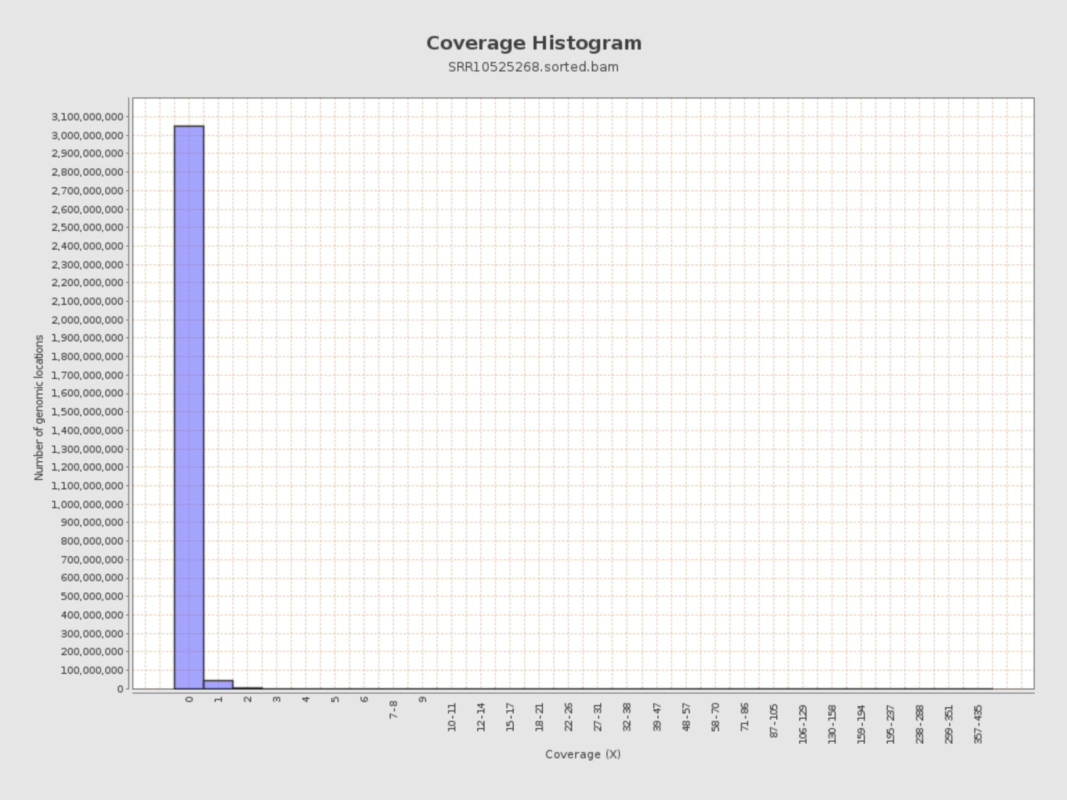
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5382709	0.0216	0.3251
chr2	243199373	4139747	0.017	0.2267
chr3	198022430	3672575	0.0185	0.1453
chr4	191154276	2899200	0.0152	0.133
chr5	180915260	2263070	0.0125	0.1174
chr6	171115067	3118239	0.0182	0.1544
chr7	159138663	3685126	0.0232	0.3084

chr8	146364022	3379634	0.0231	0.2022
chr9	141213431	1697587	0.012	0.1432
chr10	135534747	3298895	0.0243	0.2117
chr11	135006516	2301047	0.017	0.1671
chr12	133851895	2184039	0.0163	0.1349
chr13	115169878	1597599	0.0139	0.125
chr14	107349540	1552429	0.0145	0.129
chr15	102531392	1355680	0.0132	0.1224
chr16	90354753	1318808	0.0146	0.1372
chr17	81195210	873738	0.0108	0.1115
chr18	78077248	1086018	0.0139	0.2651
chr19	59128983	972274	0.0164	0.2281
chr20	63025520	890800	0.0141	0.1266
chr21	48129895	709759	0.0147	0.1307
chr22	51304566	536169	0.0105	0.1066
chrMT	16571	58969	3.5586	2.517
chrX	155270560	2849031	0.0183	0.1504
chrY	59373566	159126	0.0027	0.0741

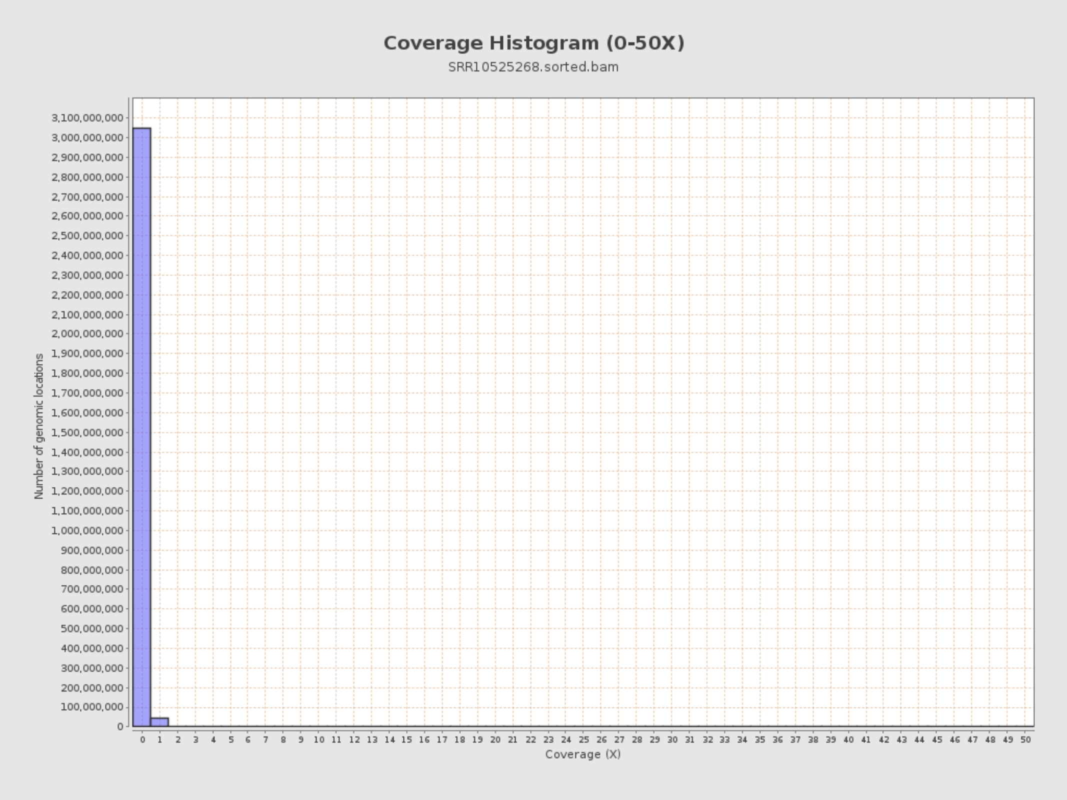
3. Results : Coverage across reference



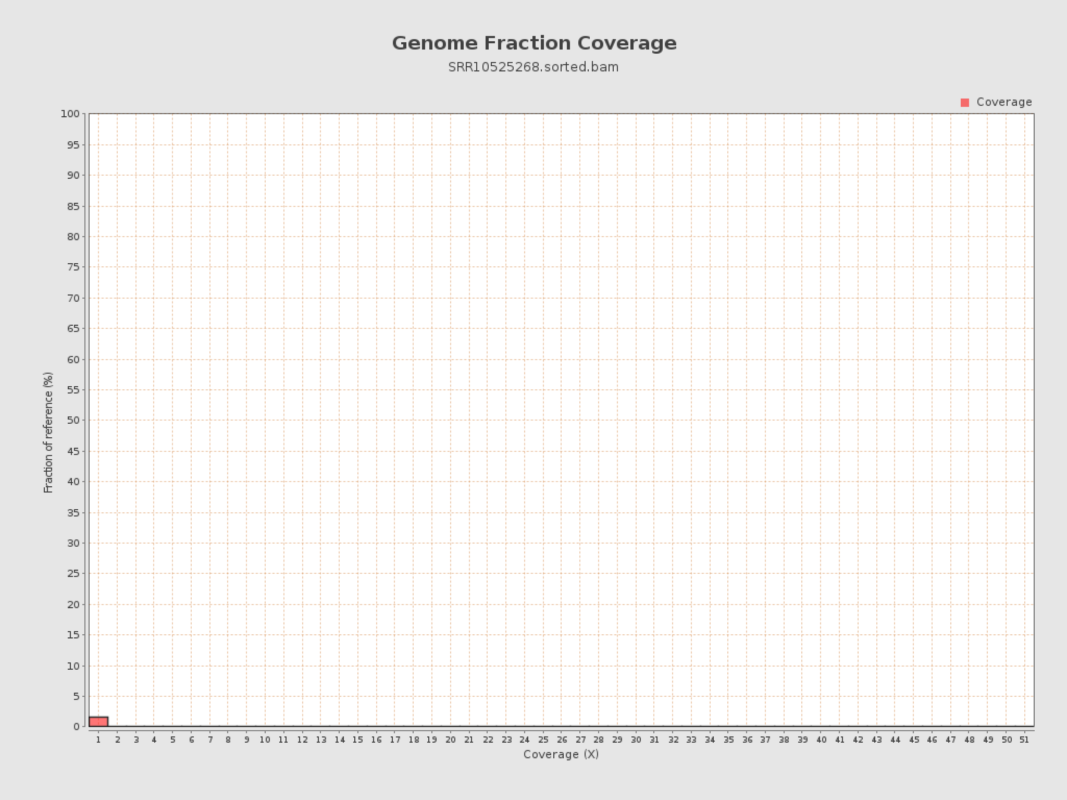
4. Results : Coverage Histogram



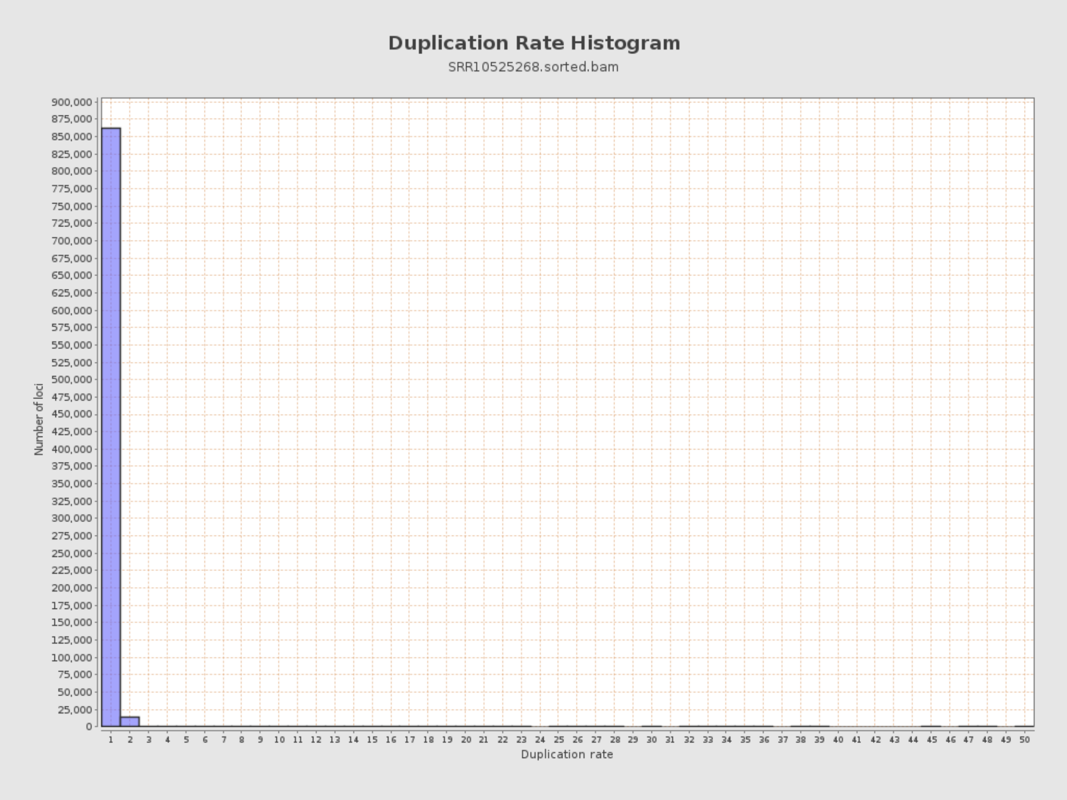
5. Results : Coverage Histogram (0-50X)



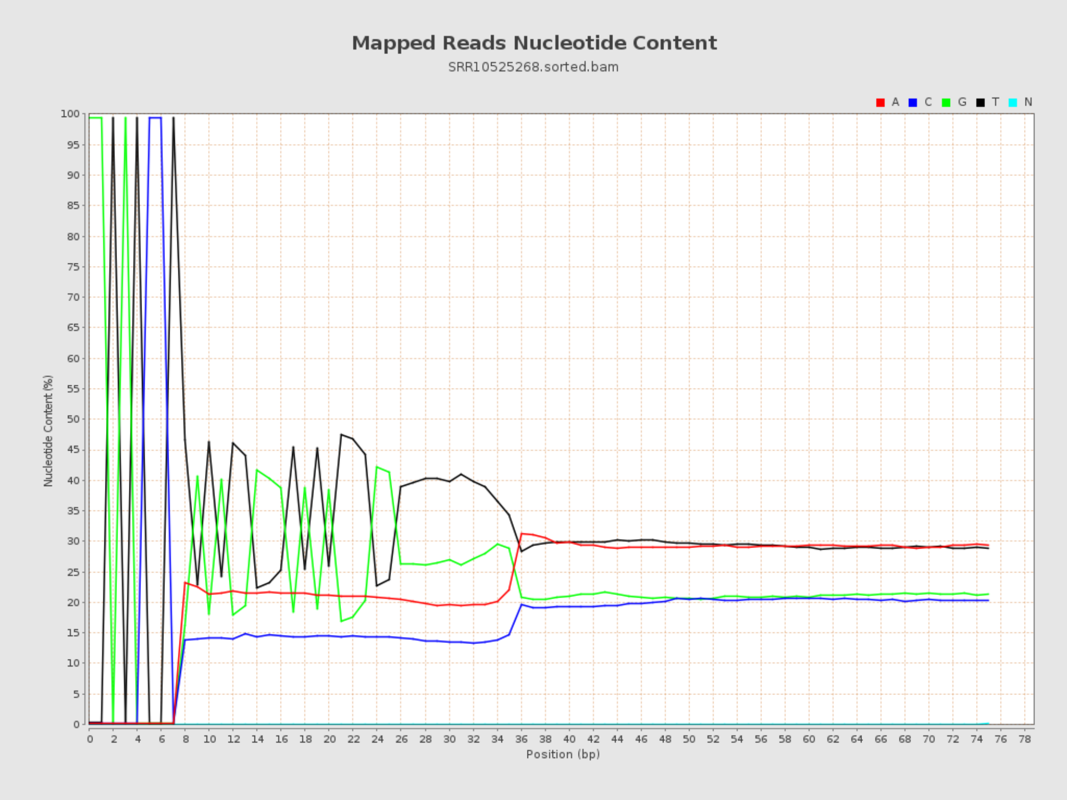
6. Results : Genome Fraction Coverage



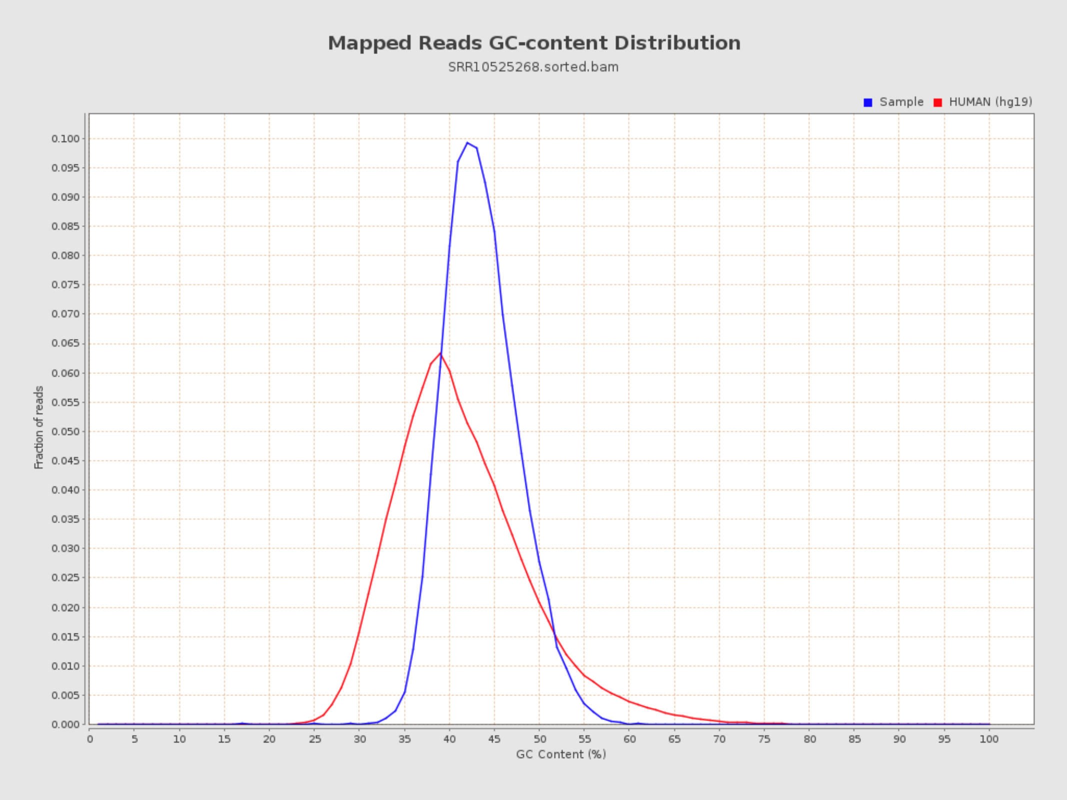
7. Results : Duplication Rate Histogram



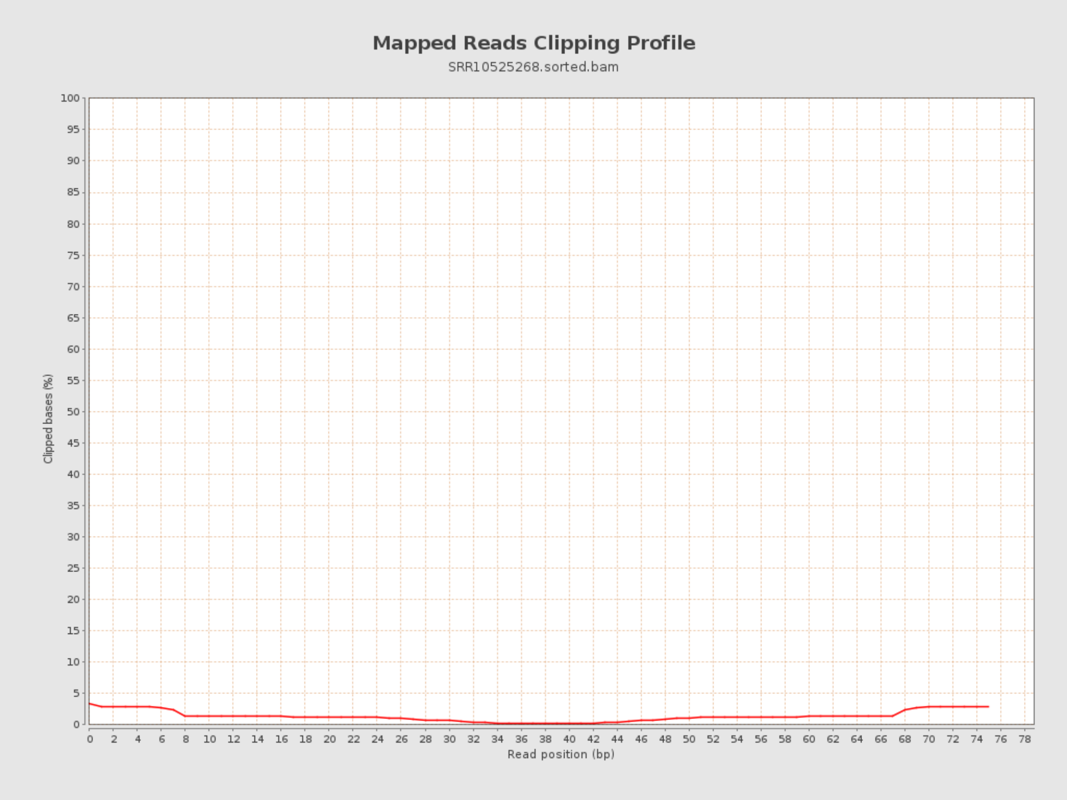
8. Results : Mapped Reads Nucleotide Content



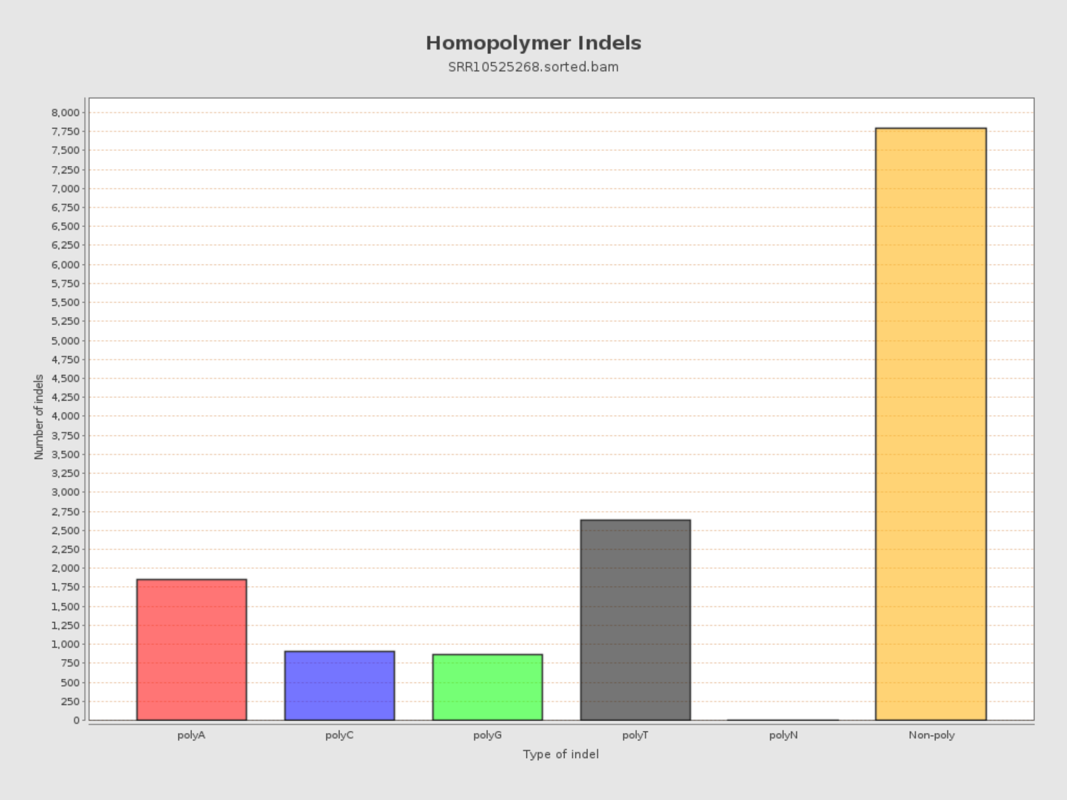
9. Results : Mapped Reads GC-content Distribution



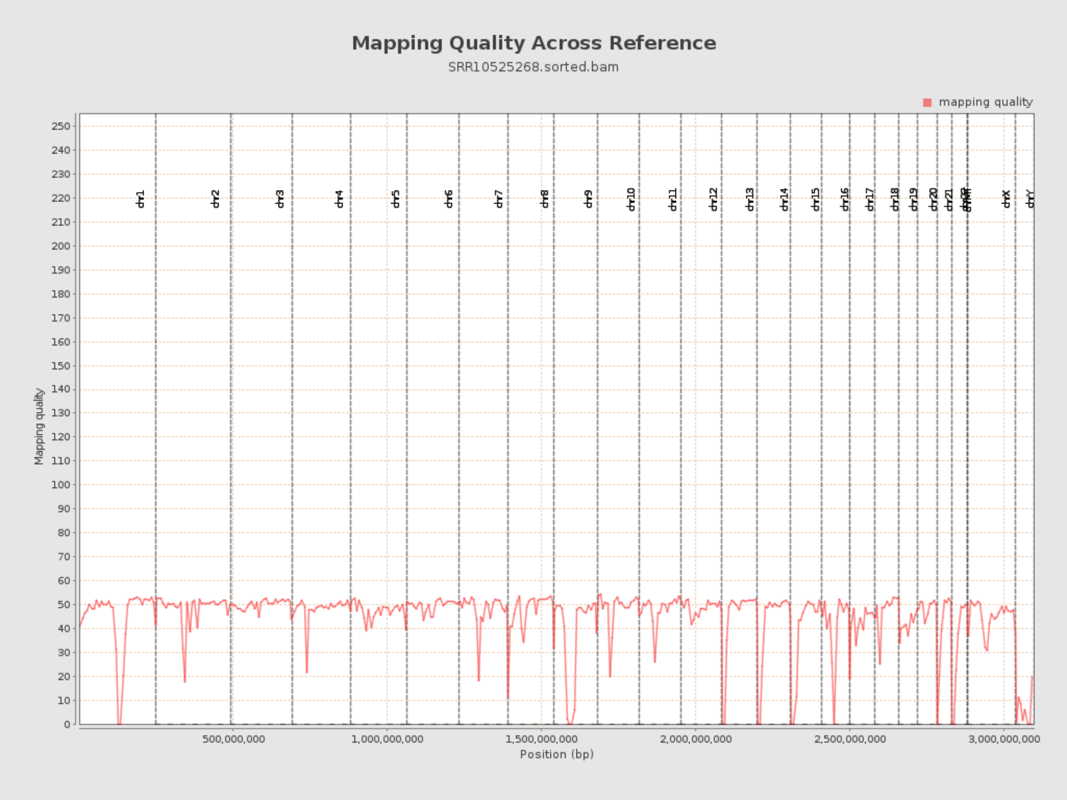
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram