Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:03:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525168.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_SRR10525168 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525168.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:03:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525168.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	628,623
Mapped reads	590,302 / 93.9%
Unmapped reads	38,321 / 6.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,007 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	9,769 / 1.55%
Duplication rate	1.21%
Clipped reads	589,909 / 93.84%

2.2. ACGT Content

Number/percentage of A's	9,471,713 / 25.77%
Number/percentage of C's	7,324,292 / 19.93%
Number/percentage of T's	11,130,821 / 30.29%
Number/percentage of G's	8,820,453 / 24%
Number/percentage of N's	982 / 0%
GC Percentage	43.93%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.1421

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

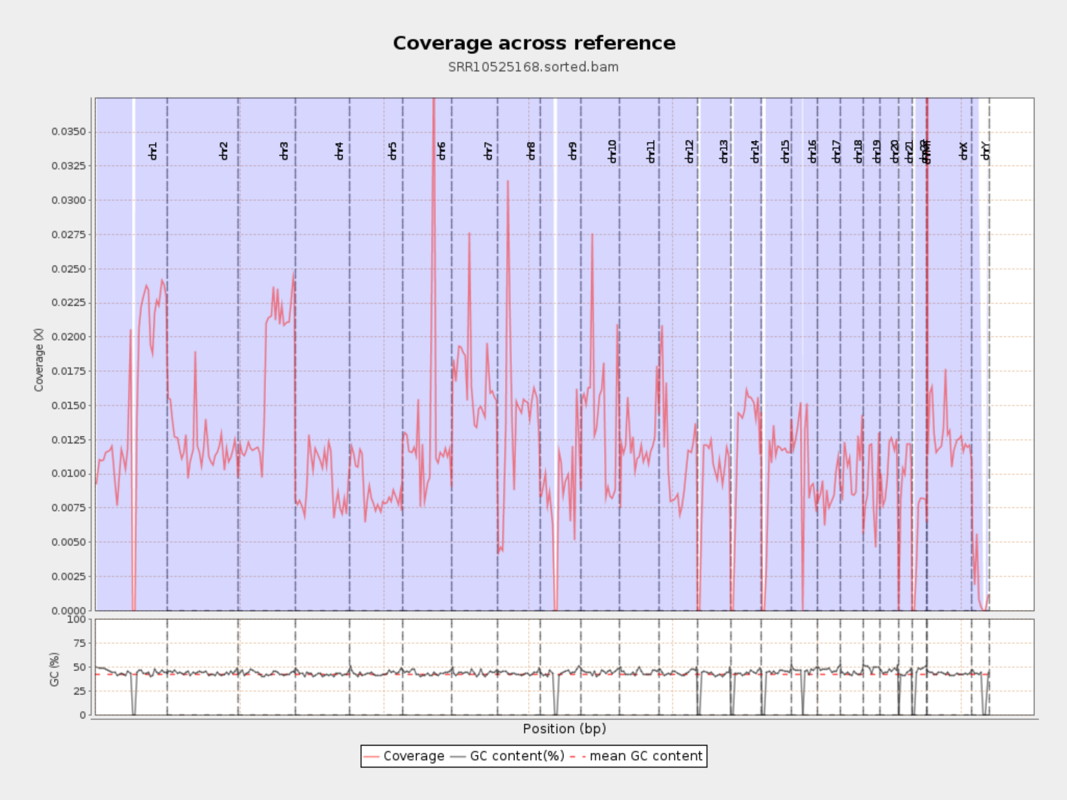
General error rate	0.5%
Mismatches	177,962
Insertions	2,623
Mapped reads with at least one insertion	0.44%
Deletions	7,809
Mapped reads with at least one deletion	1.31%
Homopolymer indels	43.34%

2.6. Chromosome stats

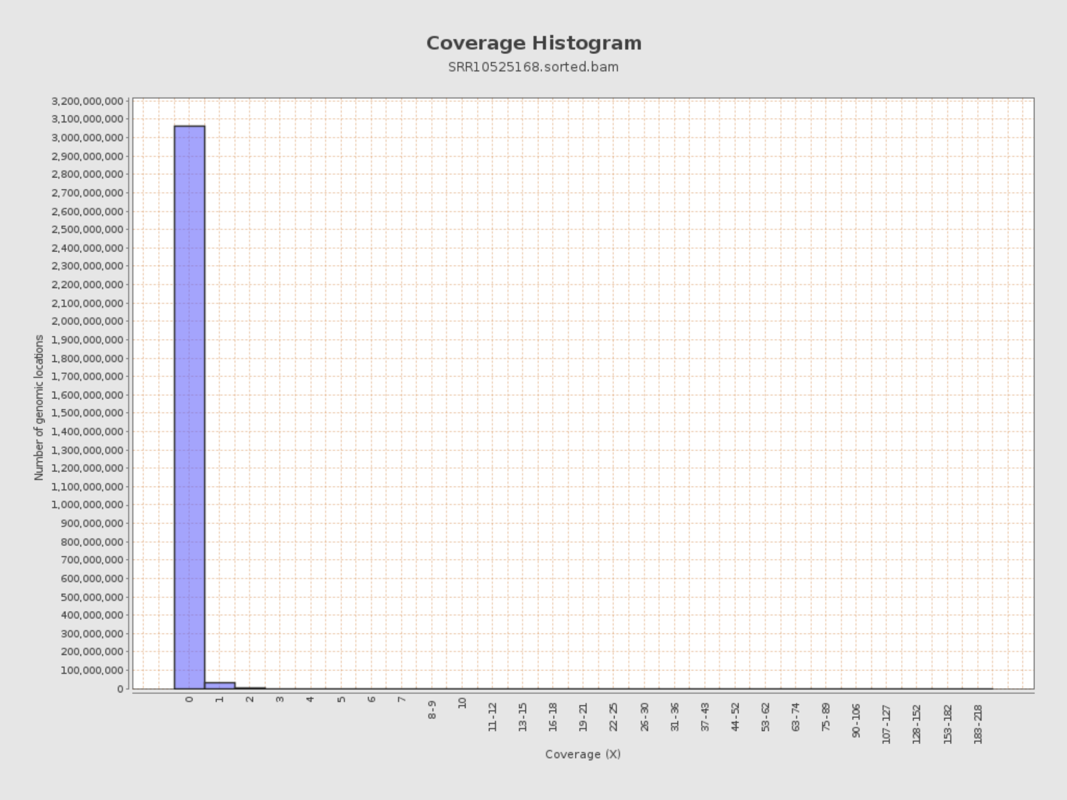
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3782879	0.0152	0.2244
chr2	243199373	2954017	0.0121	0.1418
chr3	198022430	3372100	0.017	0.1363
chr4	191154276	1805540	0.0094	0.1021
chr5	180915260	1597879	0.0088	0.0969
chr6	171115067	2263927	0.0132	0.1251
chr7	159138663	2693261	0.0169	0.241

chr8	146364022	2050136	0.014	0.1366
chr9	141213431	1201888	0.0085	0.1118
chr10	135534747	1958918	0.0145	0.1641
chr11	135006516	1637490	0.0121	0.1247
chr12	133851895	1522139	0.0114	0.1105
chr13	115169878	1097885	0.0095	0.1003
chr14	107349540	1304564	0.0122	0.1168
chr15	102531392	976340	0.0095	0.1013
chr16	90354753	960975	0.0106	0.1133
chr17	81195210	705933	0.0087	0.0989
chr18	78077248	810044	0.0104	0.18
chr19	59128983	537294	0.0091	0.1643
chr20	63025520	661282	0.0105	0.1067
chr21	48129895	461782	0.0096	0.1047
chr22	51304566	288639	0.0056	0.077
chrMT	16571	21428	1.2931	1.3669
chrX	155270560	1991617	0.0128	0.1206
chrY	59373566	102872	0.0017	0.0615

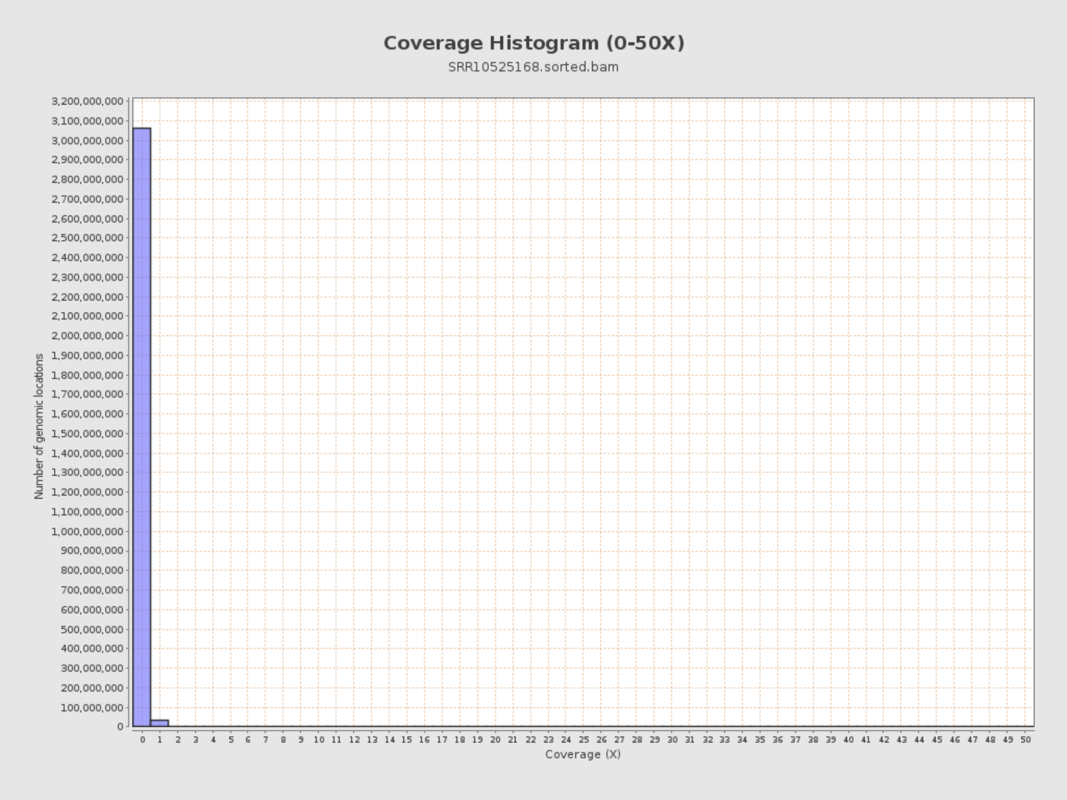
3. Results : Coverage across reference



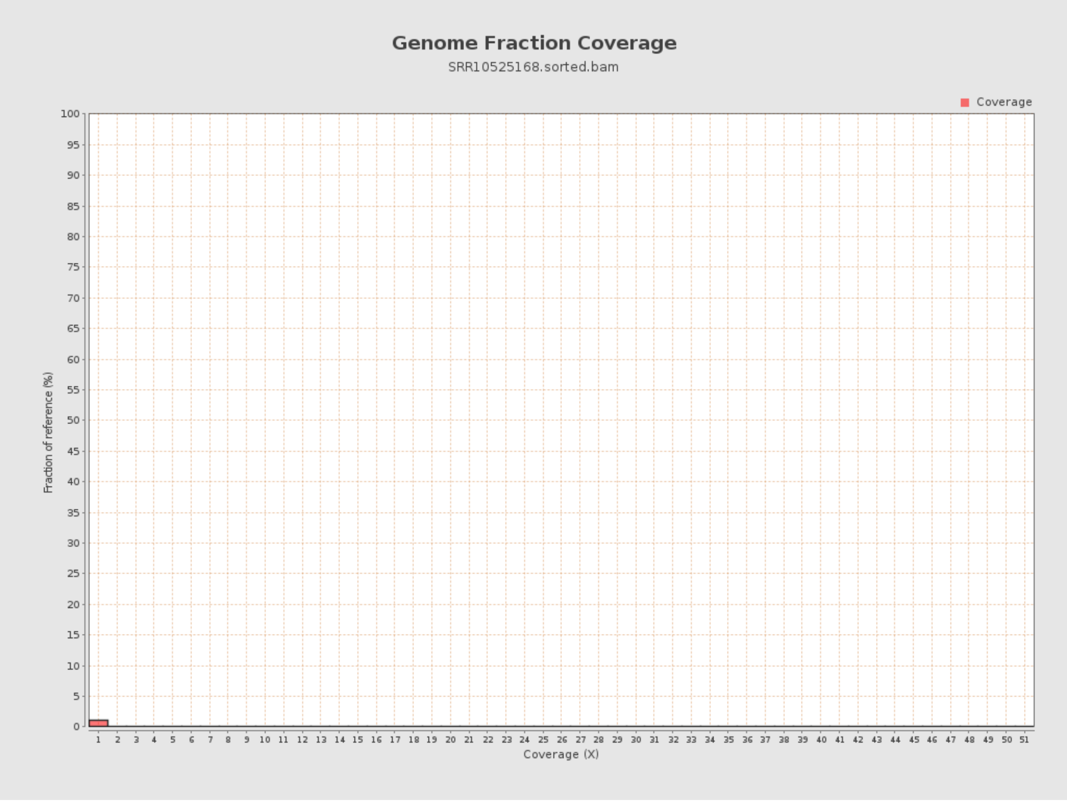
4. Results : Coverage Histogram



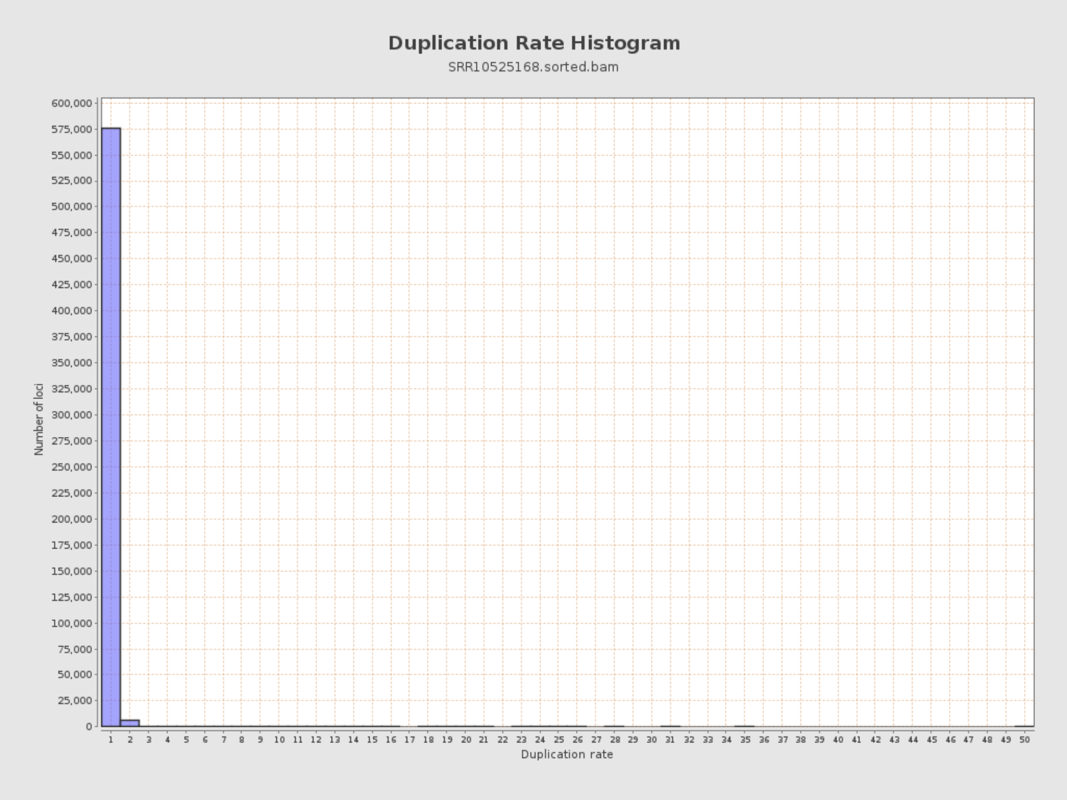
5. Results : Coverage Histogram (0-50X)



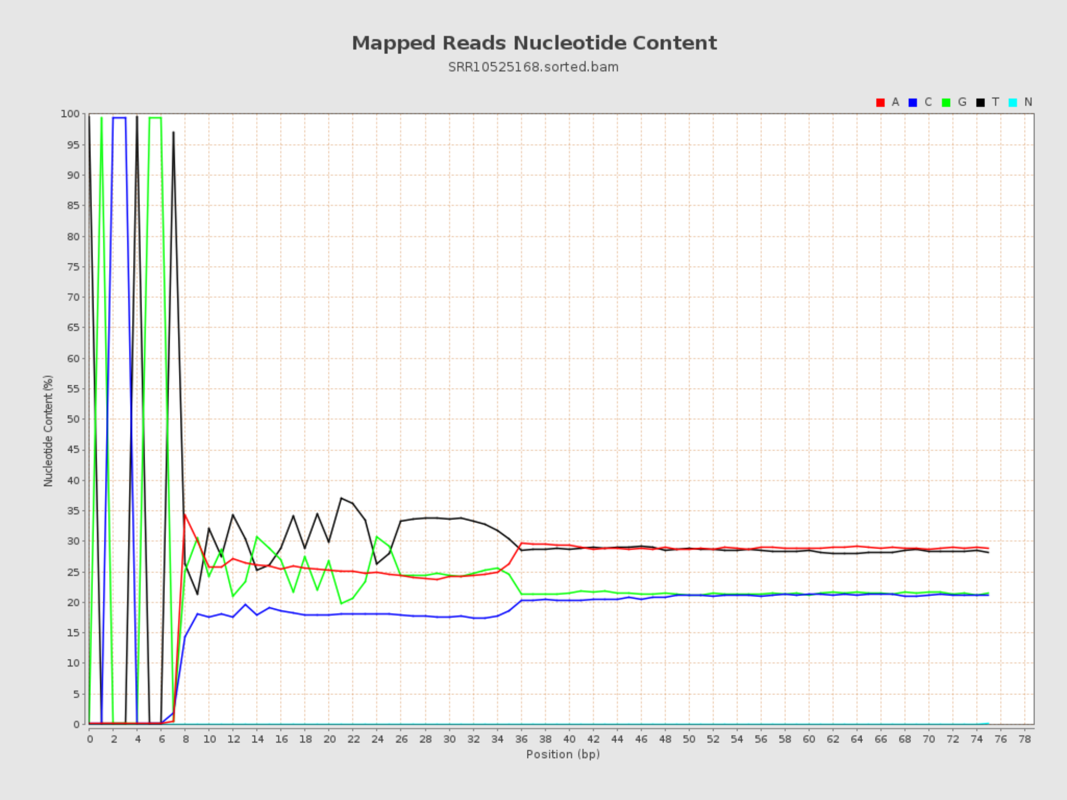
6. Results : Genome Fraction Coverage



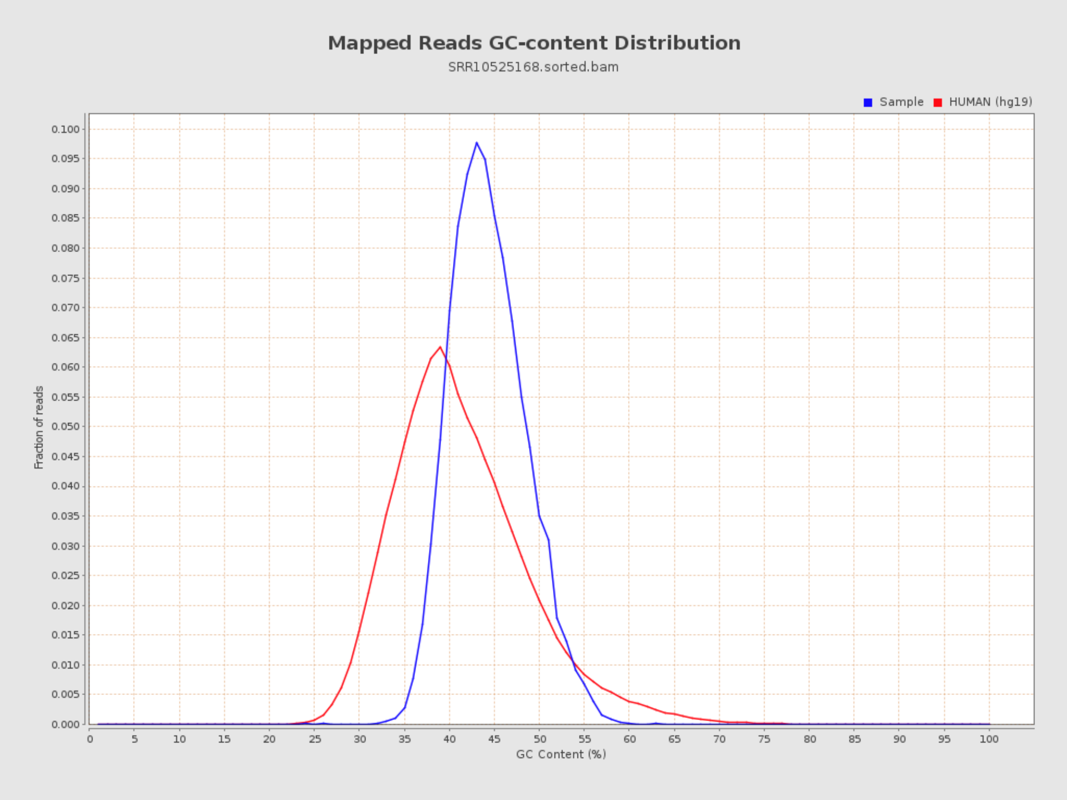
7. Results : Duplication Rate Histogram



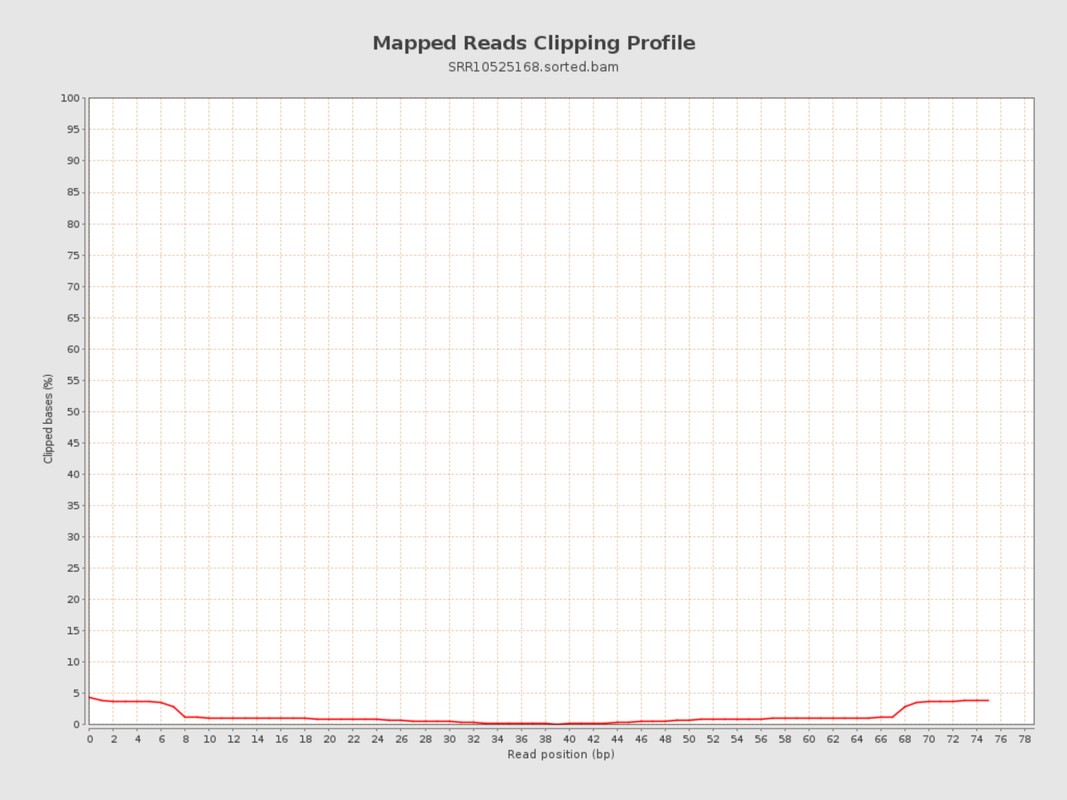
8. Results : Mapped Reads Nucleotide Content



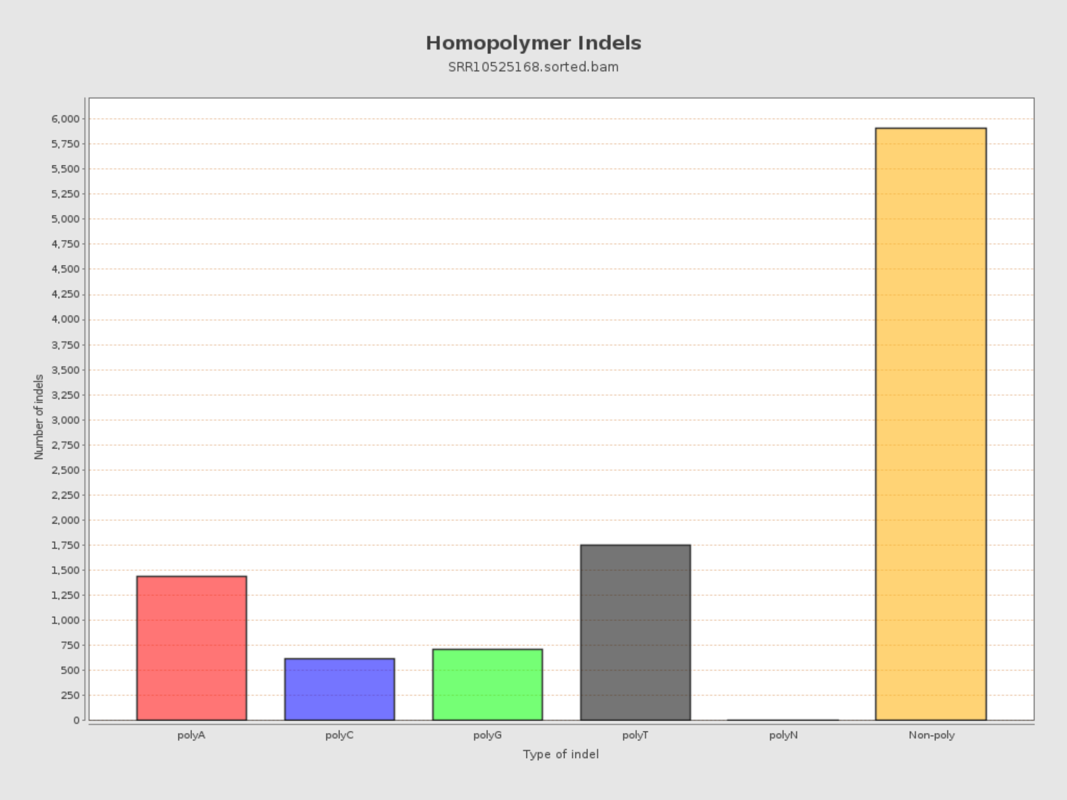
9. Results : Mapped Reads GC-content Distribution



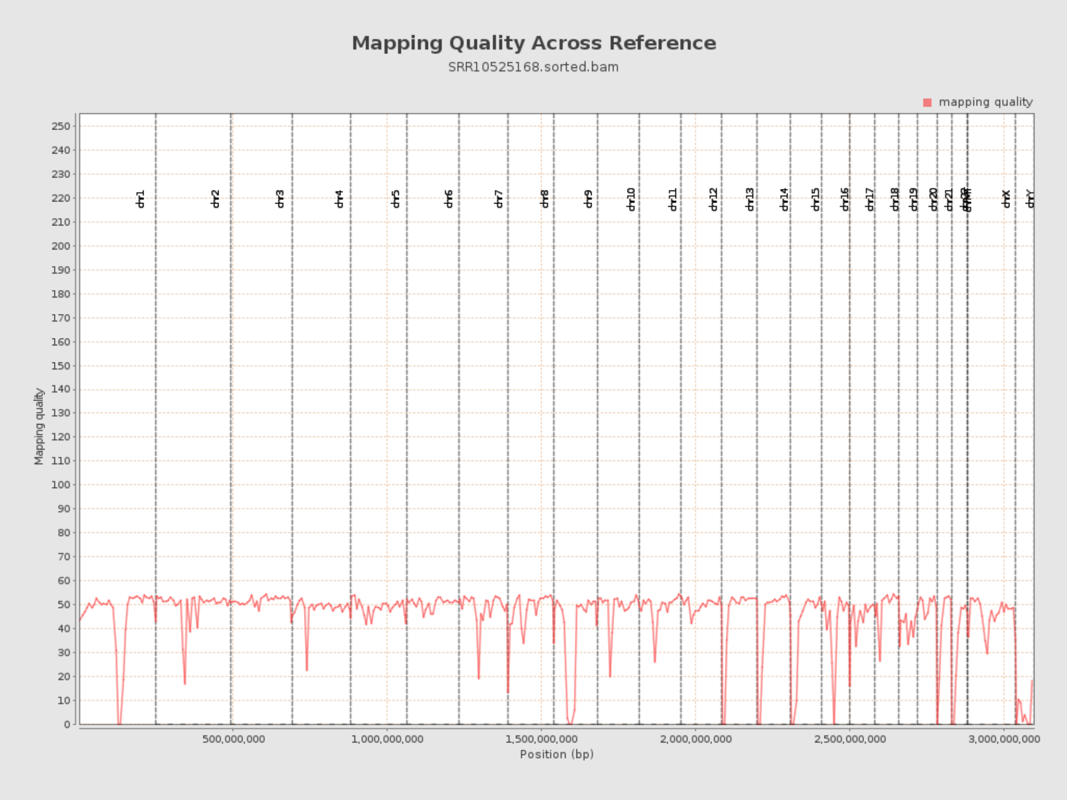
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram