Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:50:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525025.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_SRR10525025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525025.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:50:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,617,744
Mapped reads	1,489,469 / 92.07%
Unmapped reads	128,275 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,861 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	51,620 / 3.19%
Duplication rate	2.54%
Clipped reads	1,491,470 / 92.19%

2.2. ACGT Content

Number/percentage of A's	22,846,502 / 26%
Number/percentage of C's	17,398,637 / 19.8%
Number/percentage of T's	27,191,892 / 30.94%
Number/percentage of G's	20,441,235 / 23.26%
Number/percentage of N's	907 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.257

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

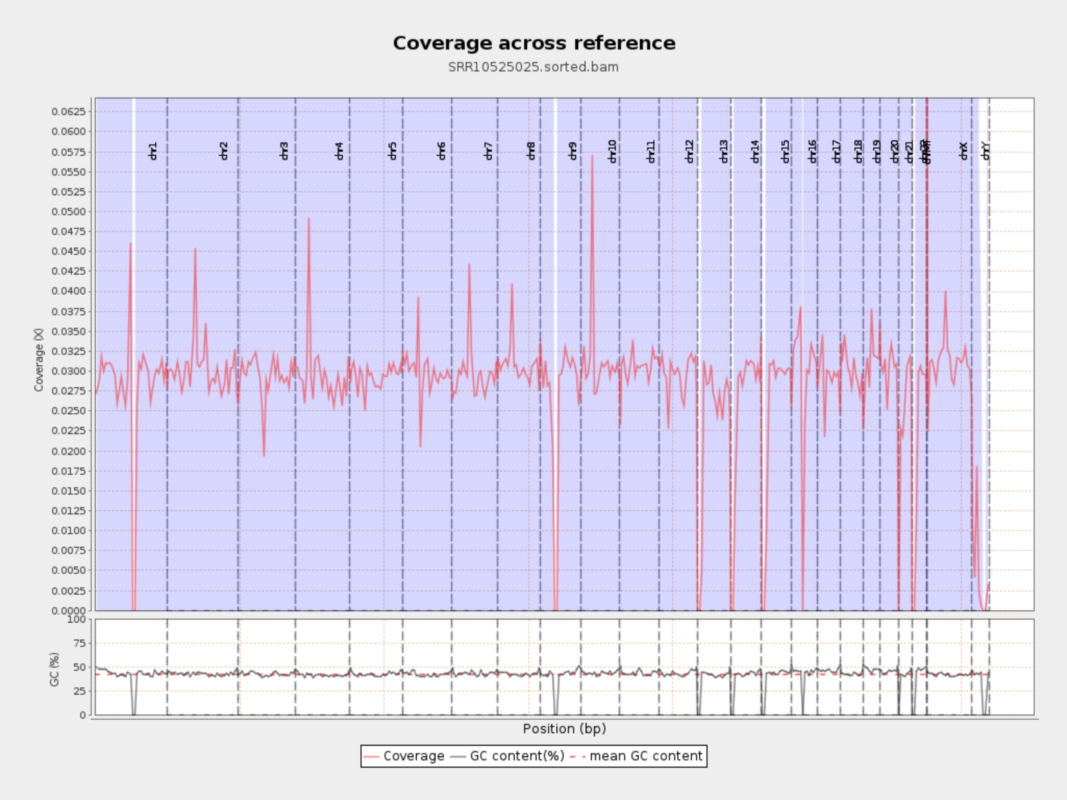
General error rate	0.5%
Mismatches	429,314
Insertions	6,319
Mapped reads with at least one insertion	0.42%
Deletions	17,802
Mapped reads with at least one deletion	1.18%
Homopolymer indels	41.99%

2.6. Chromosome stats

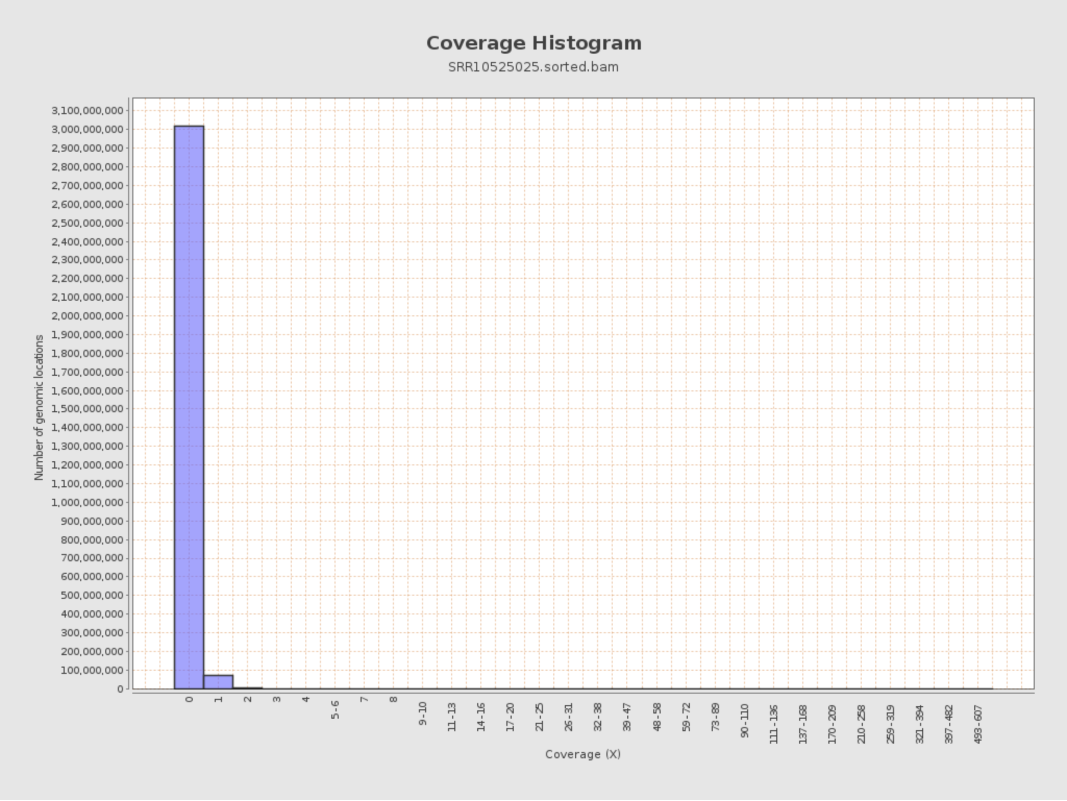
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6981747	0.028	0.4632
chr2	243199373	7407056	0.0305	0.2798
chr3	198022430	5814795	0.0294	0.1848
chr4	191154276	5650183	0.0296	0.2127
chr5	180915260	5310472	0.0294	0.1854
chr6	171115067	5104733	0.0298	0.2301
chr7	159138663	4730121	0.0297	0.289

chr8	146364022	4520634	0.0309	0.277
chr9	141213431	3702874	0.0262	0.2109
chr10	135534747	4289744	0.0317	0.286
chr11	135006516	4139293	0.0307	0.245
chr12	133851895	3958456	0.0296	0.1884
chr13	115169878	2656195	0.0231	0.1648
chr14	107349540	2696116	0.0251	0.1766
chr15	102531392	2504068	0.0244	0.1722
chr16	90354753	2606393	0.0288	0.1956
chr17	81195210	2375649	0.0293	0.2055
chr18	78077248	2357565	0.0302	0.3714
chr19	59128983	1855368	0.0314	0.3153
chr20	63025520	1893867	0.03	0.1925
chr21	48129895	1174092	0.0244	0.1957
chr22	51304566	1062113	0.0207	0.1552
chrMT	16571	1714	0.1034	0.3431
chrX	155270560	4840357	0.0312	0.2072
chrY	59373566	275374	0.0046	0.1537

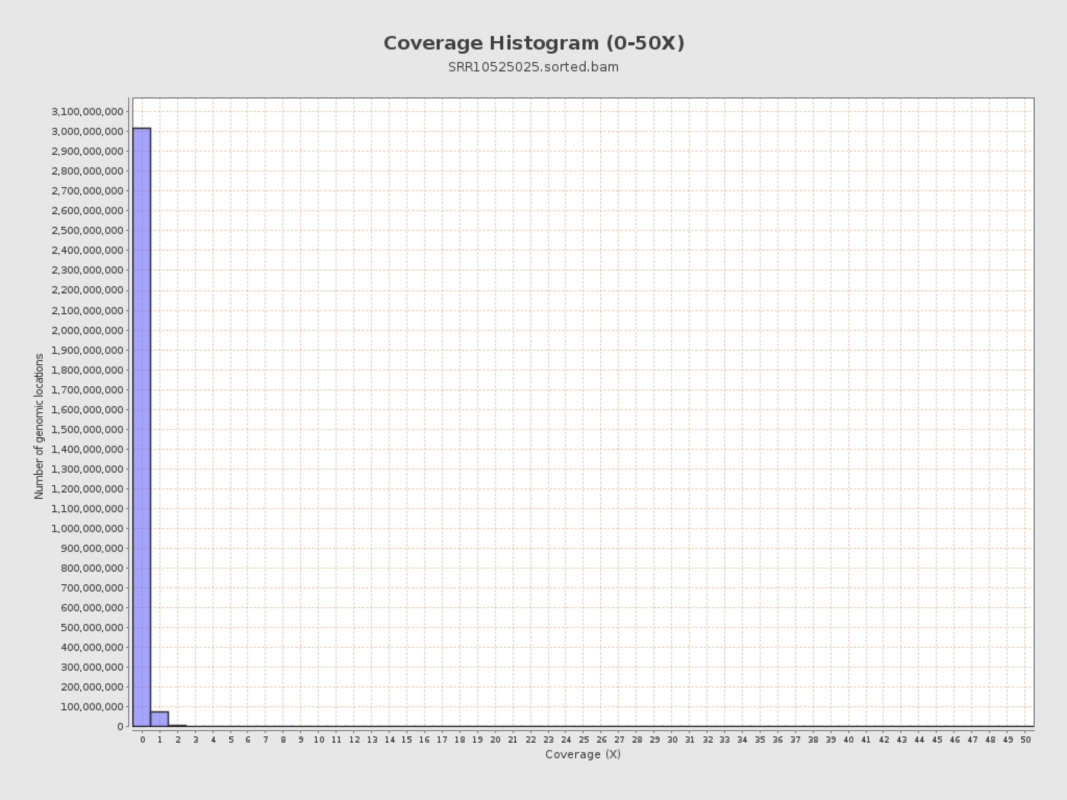
3. Results : Coverage across reference



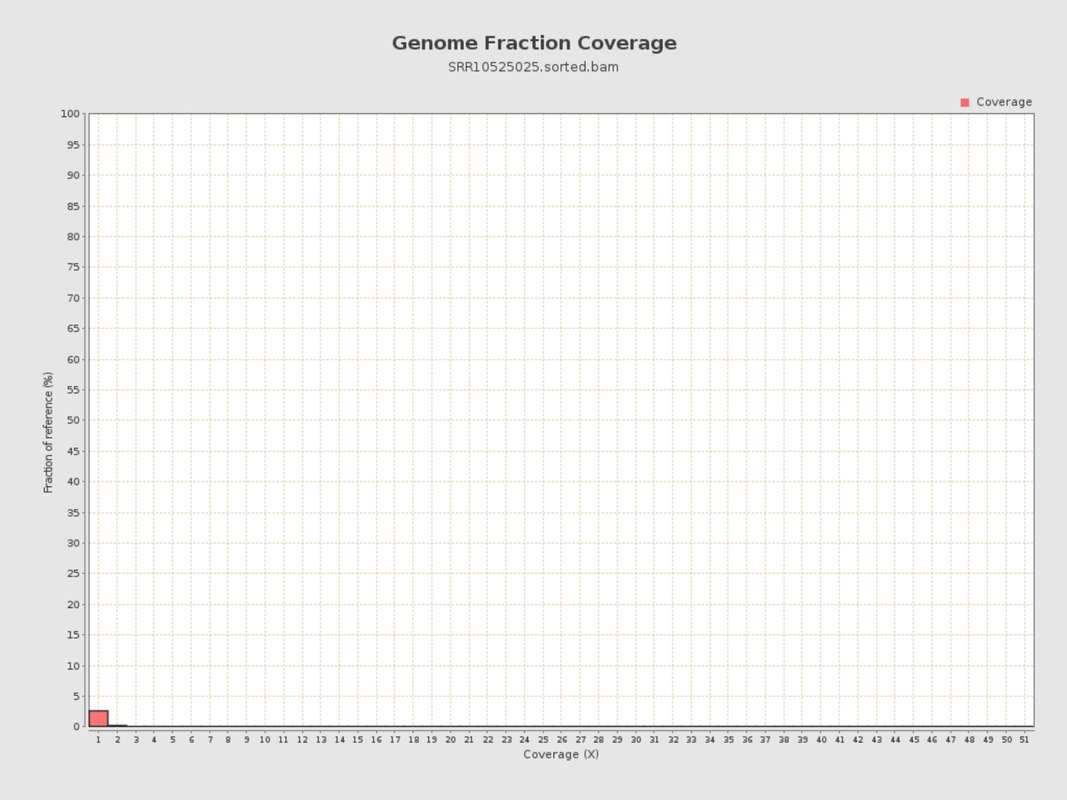
4. Results : Coverage Histogram



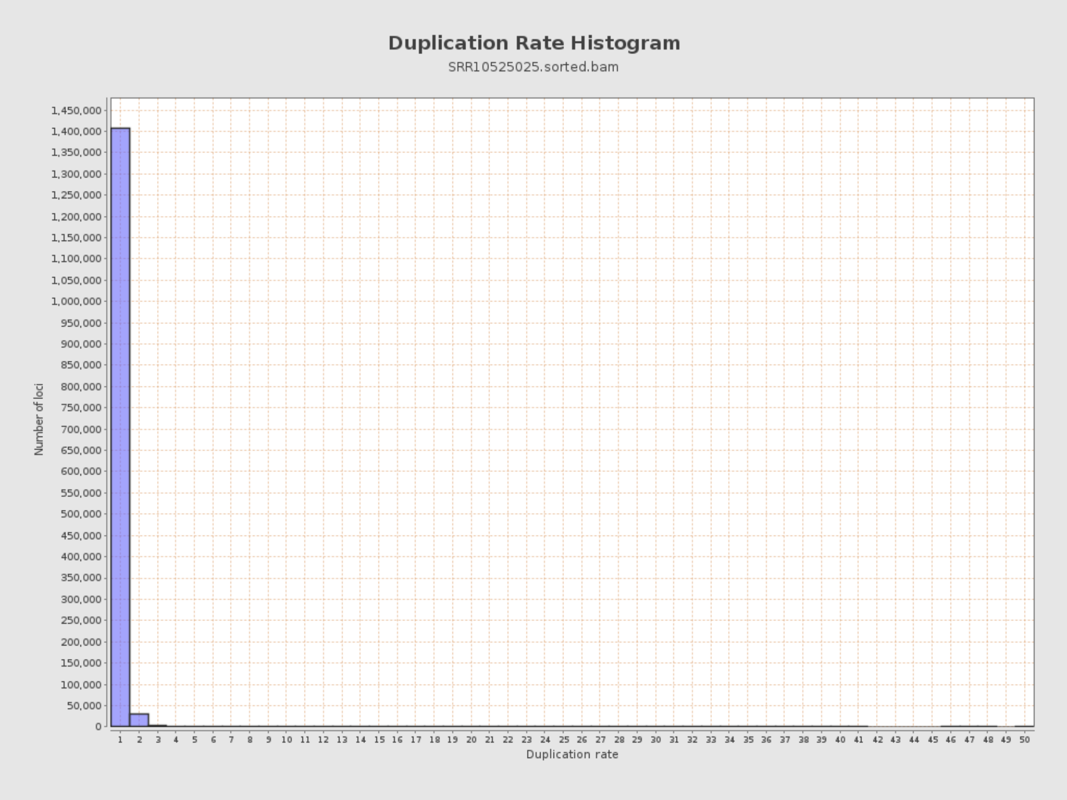
5. Results : Coverage Histogram (0-50X)



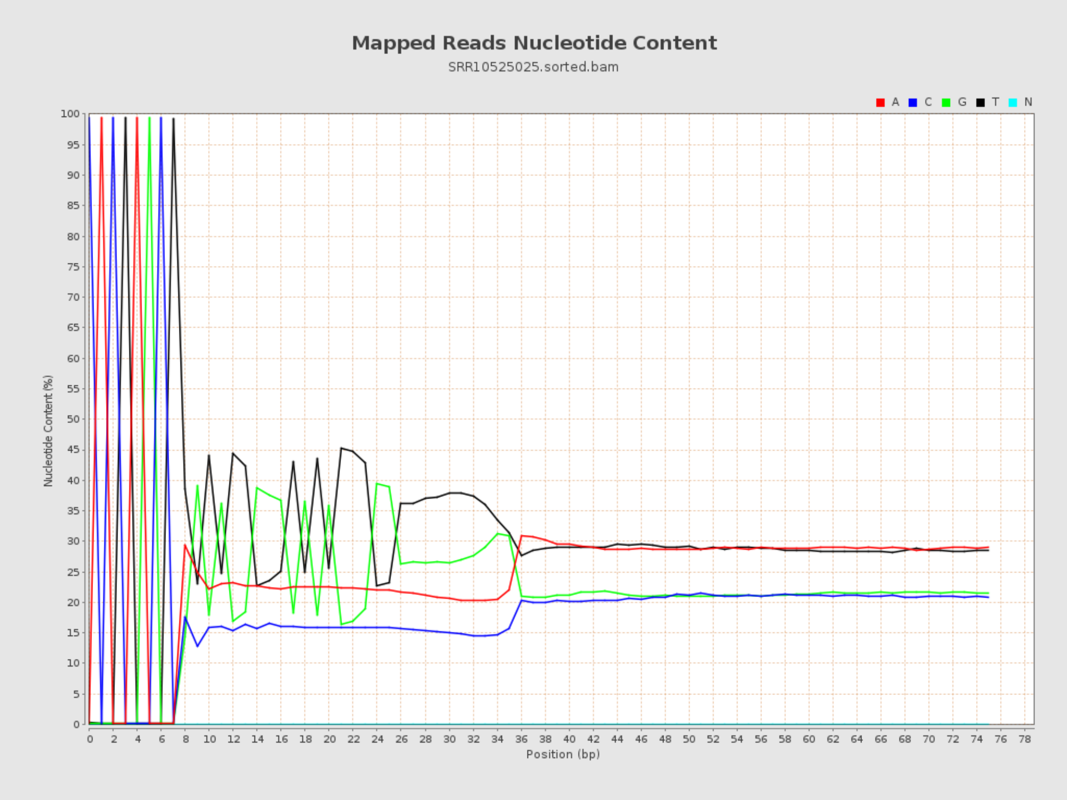
6. Results : Genome Fraction Coverage



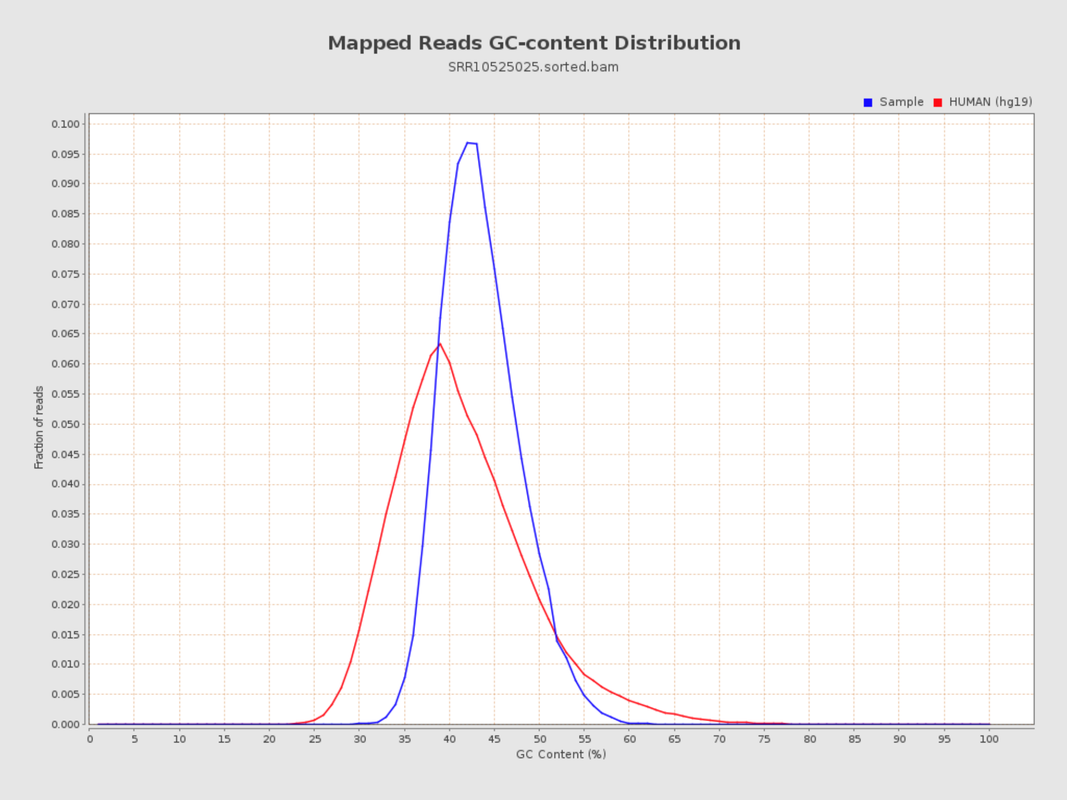
7. Results : Duplication Rate Histogram



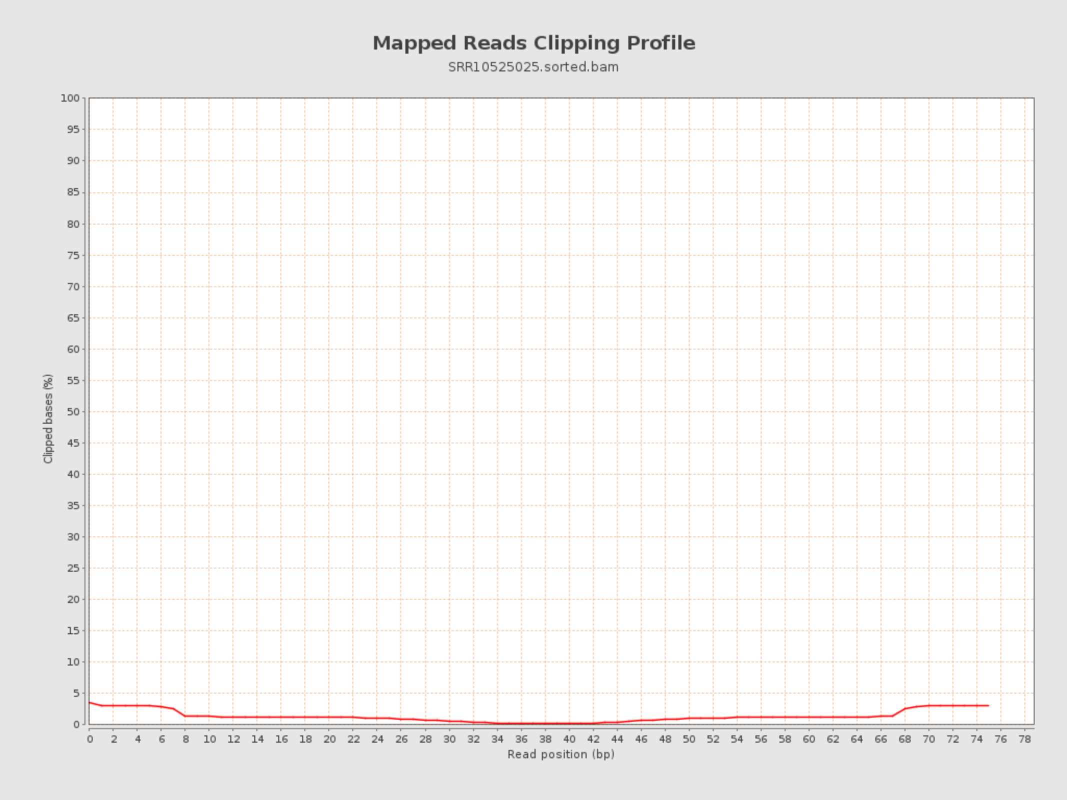
8. Results : Mapped Reads Nucleotide Content



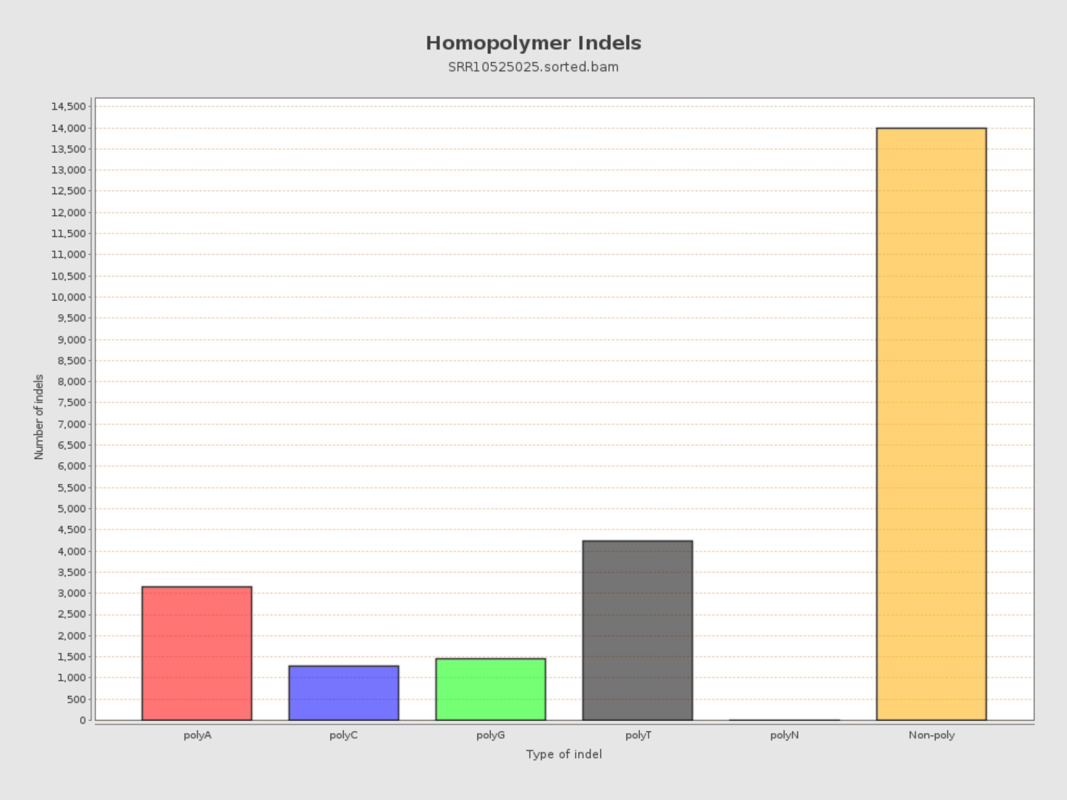
9. Results : Mapped Reads GC-content Distribution



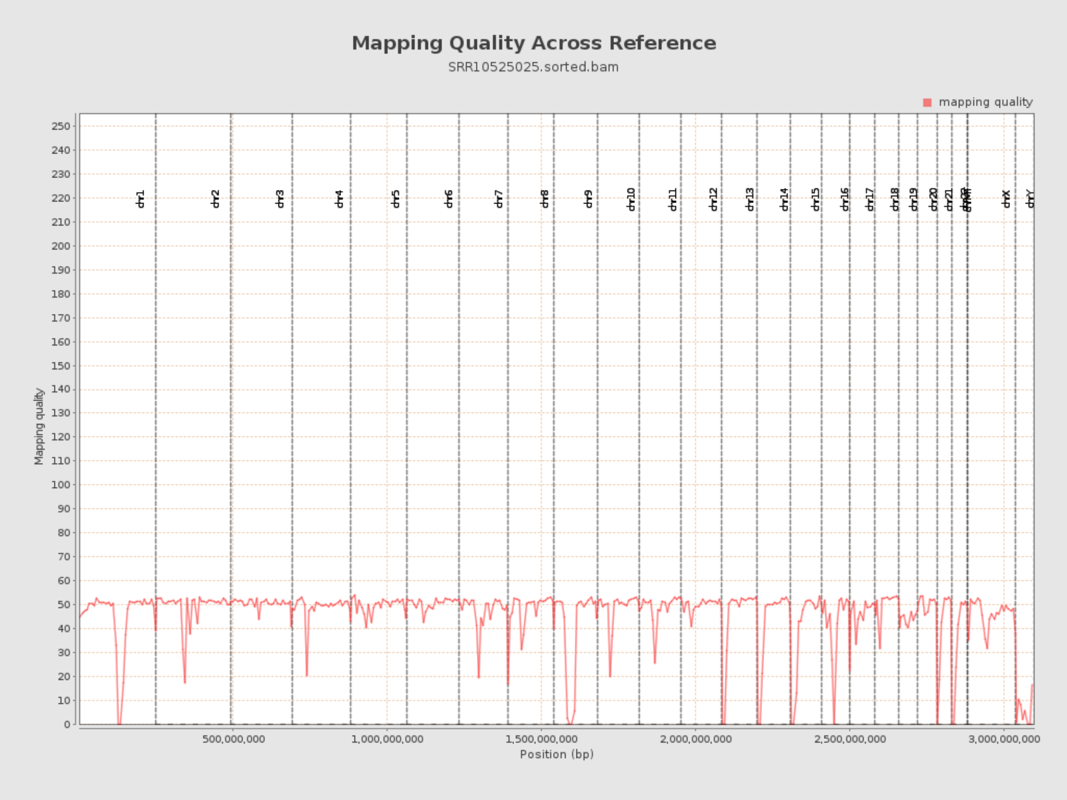
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram