Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 11:48:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089523.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_SRR089523 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089523.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 11:48:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089523.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,553,878
Mapped reads	7,384,790 / 77.3%
Unmapped reads	2,169,088 / 22.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	332 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,349,242 / 24.59%
Duplication rate	24.17%
Clipped reads	865,501 / 9.06%

2.2. ACGT Content

Number/percentage of A's	110,027,280 / 31.74%
Number/percentage of C's	67,412,647 / 19.45%
Number/percentage of T's	92,259,300 / 26.62%
Number/percentage of G's	76,851,601 / 22.17%
Number/percentage of N's	61,613 / 0.02%
GC Percentage	41.62%

2.3. Coverage

Mean	0.112

Standard Deviation	0.9678

2.4. Mapping Quality

Mean Mapping Quality	43.34

2.5. Mismatches and indels

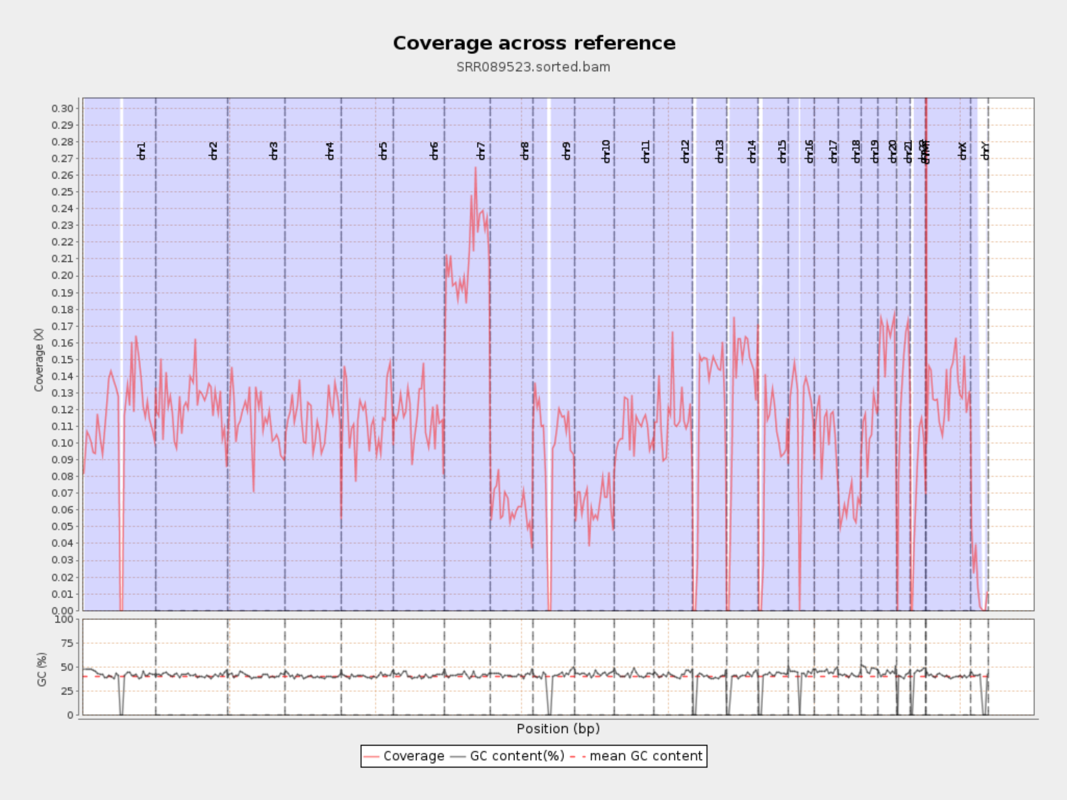
General error rate	0.58%
Mismatches	1,974,872
Insertions	15,365
Mapped reads with at least one insertion	0.21%
Deletions	45,996
Mapped reads with at least one deletion	0.62%
Homopolymer indels	44.27%

2.6. Chromosome stats

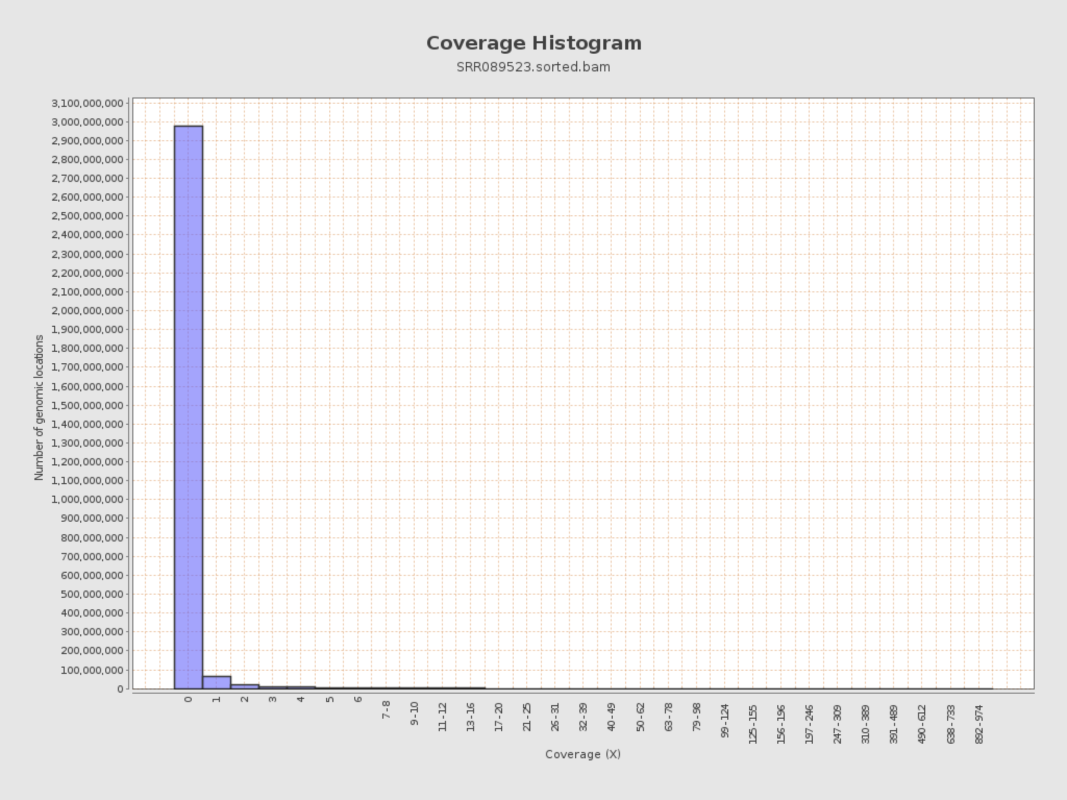
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28060771	0.1126	1.0187
chr2	243199373	30040189	0.1235	1.0754
chr3	198022430	22209743	0.1122	0.9115
chr4	191154276	21975351	0.115	0.9344
chr5	180915260	20534994	0.1135	0.9025
chr6	171115067	19849156	0.116	0.9547
chr7	159138663	33748228	0.2121	1.5013

chr8	146364022	8947214	0.0611	0.8072
chr9	141213431	13799141	0.0977	0.8693
chr10	135534747	8571655	0.0632	0.6723
chr11	135006516	14608109	0.1082	0.9778
chr12	133851895	15538235	0.1161	0.9341
chr13	115169878	14029633	0.1218	0.9791
chr14	107349540	13908288	0.1296	1.0676
chr15	102531392	9183674	0.0896	0.7915
chr16	90354753	10300534	0.114	0.9187
chr17	81195210	8911935	0.1098	0.8826
chr18	78077248	4774032	0.0611	0.7335
chr19	59128983	6449583	0.1091	0.9132
chr20	63025520	10226493	0.1623	1.1285
chr21	48129895	6020315	0.1251	1.012
chr22	51304566	3701130	0.0721	0.6912
chrMT	16571	70699	4.2664	14.9678
chrX	155270560	20278988	0.1306	1.02
chrY	59373566	944271	0.0159	0.3196

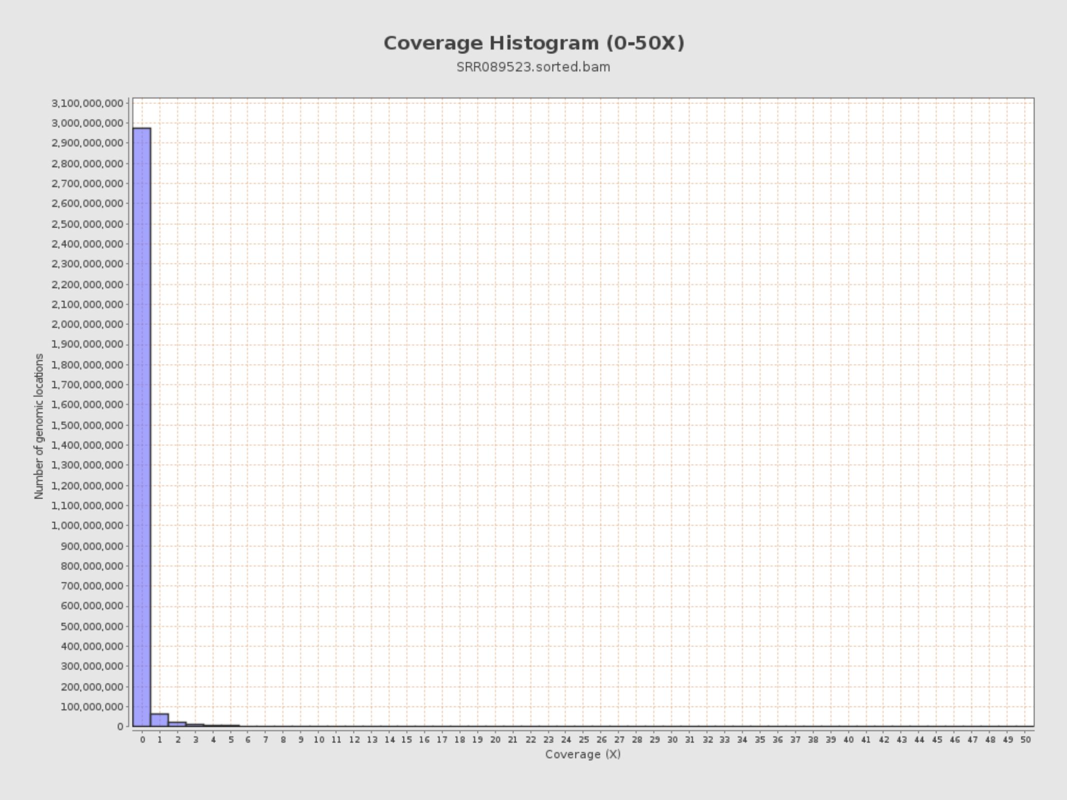
3. Results : Coverage across reference



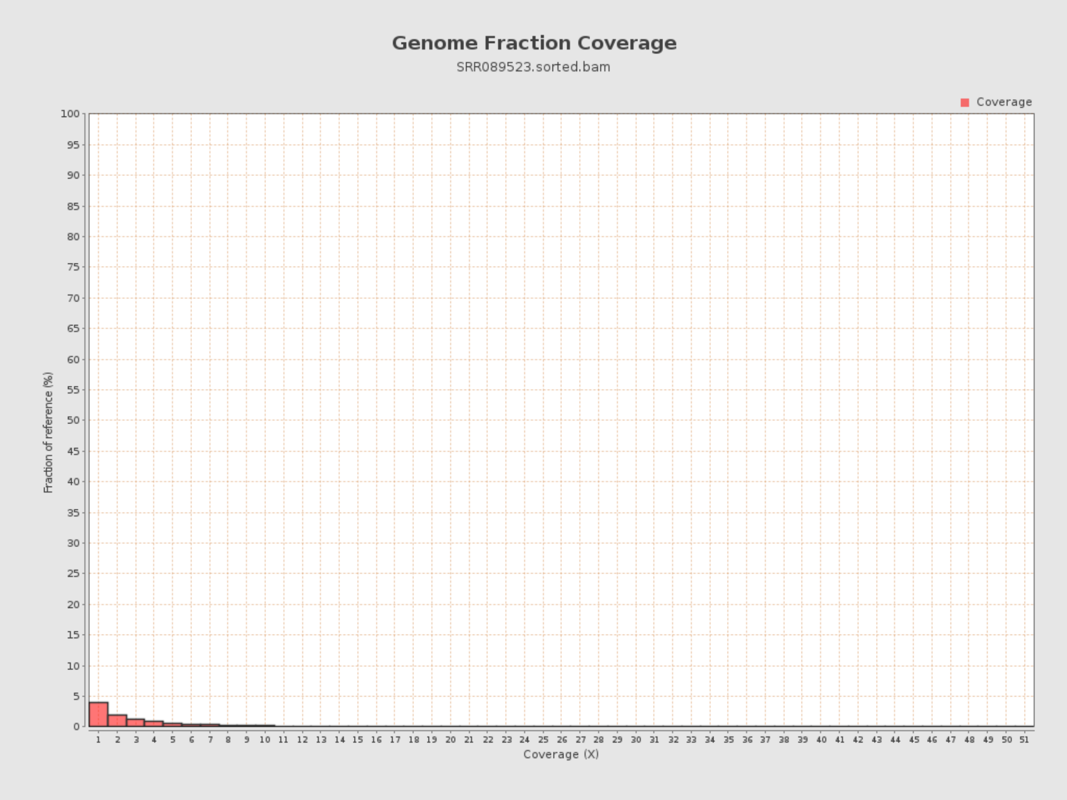
4. Results : Coverage Histogram



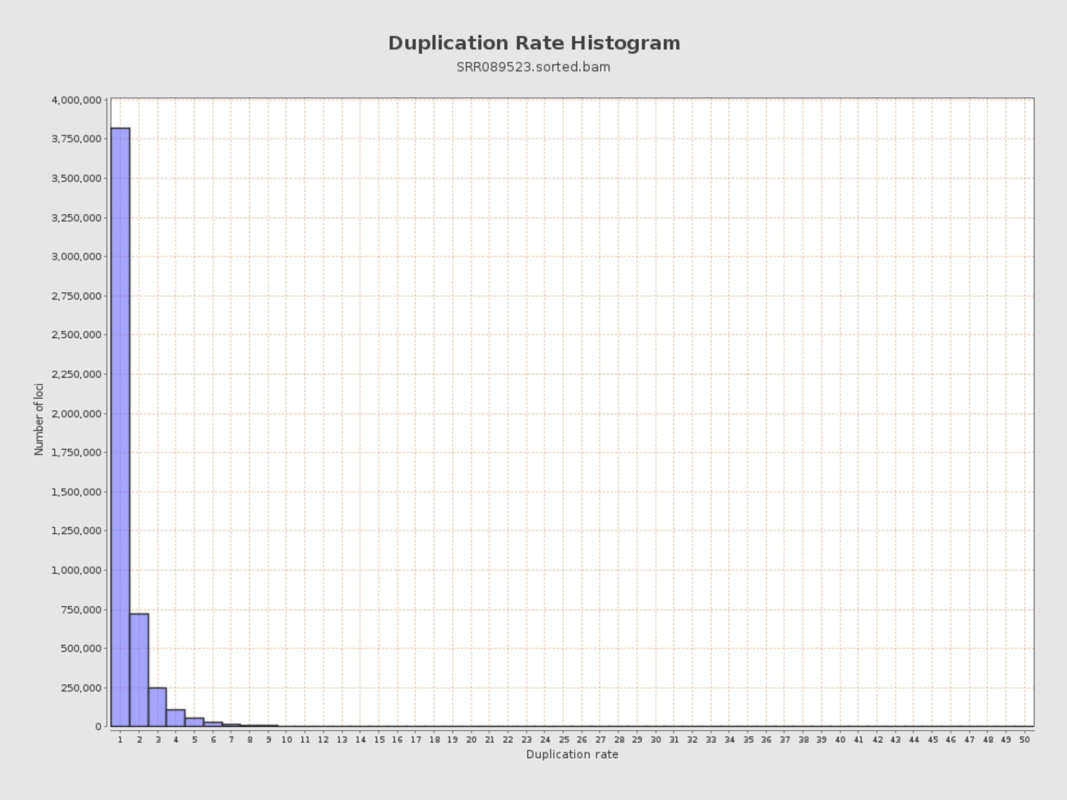
5. Results : Coverage Histogram (0-50X)



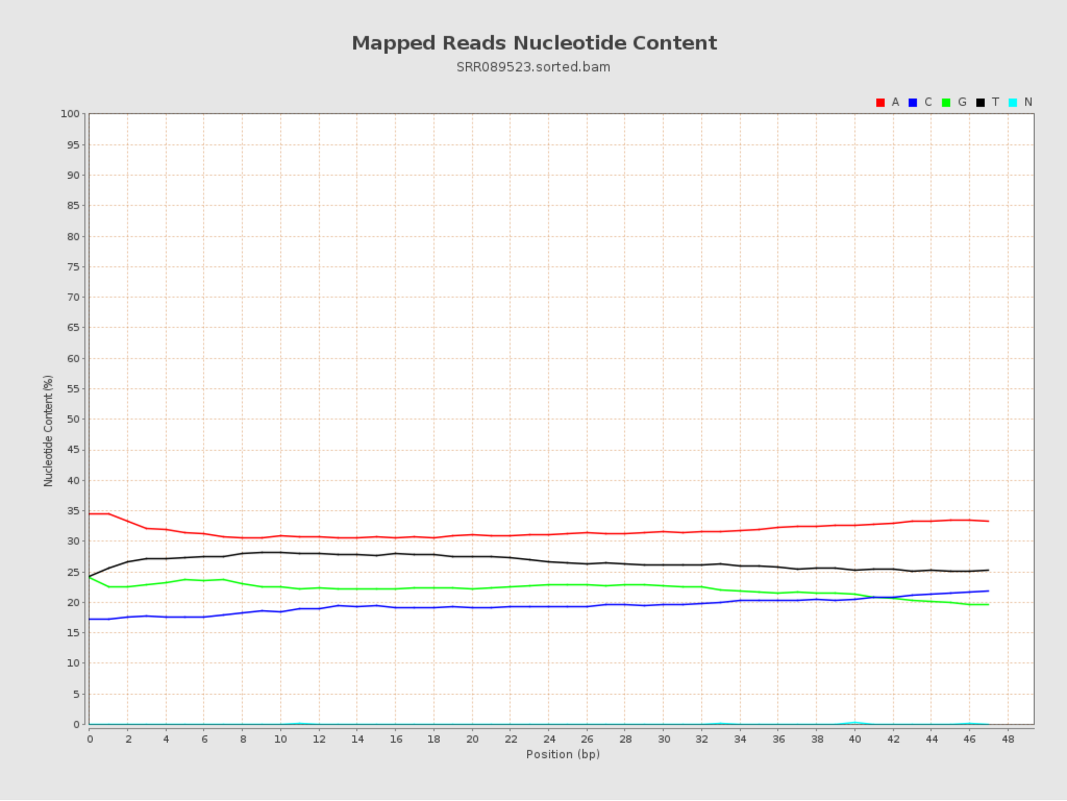
6. Results : Genome Fraction Coverage



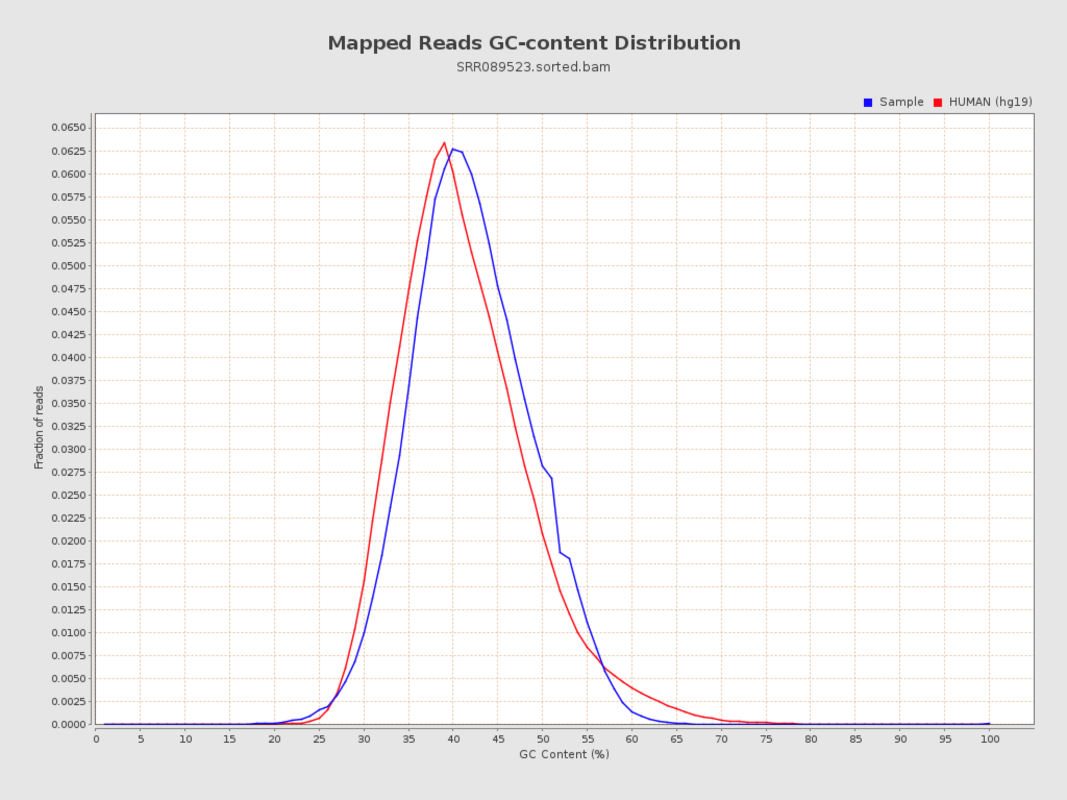
7. Results : Duplication Rate Histogram



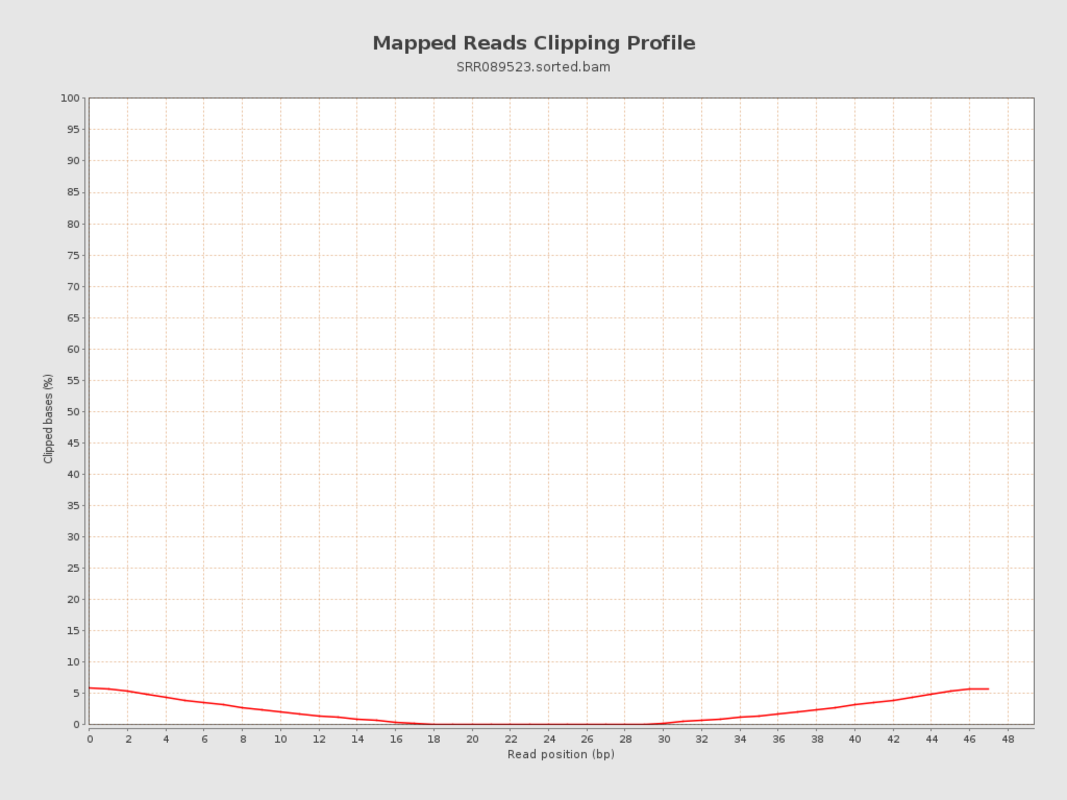
8. Results : Mapped Reads Nucleotide Content



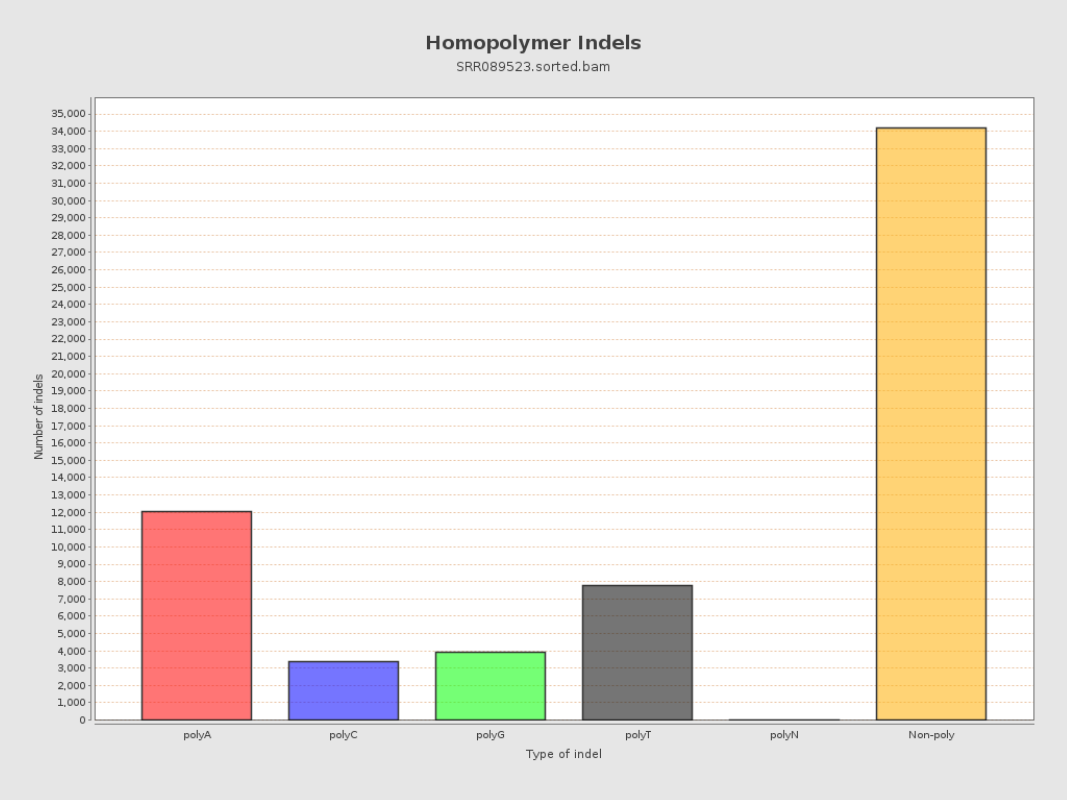
9. Results : Mapped Reads GC-content Distribution



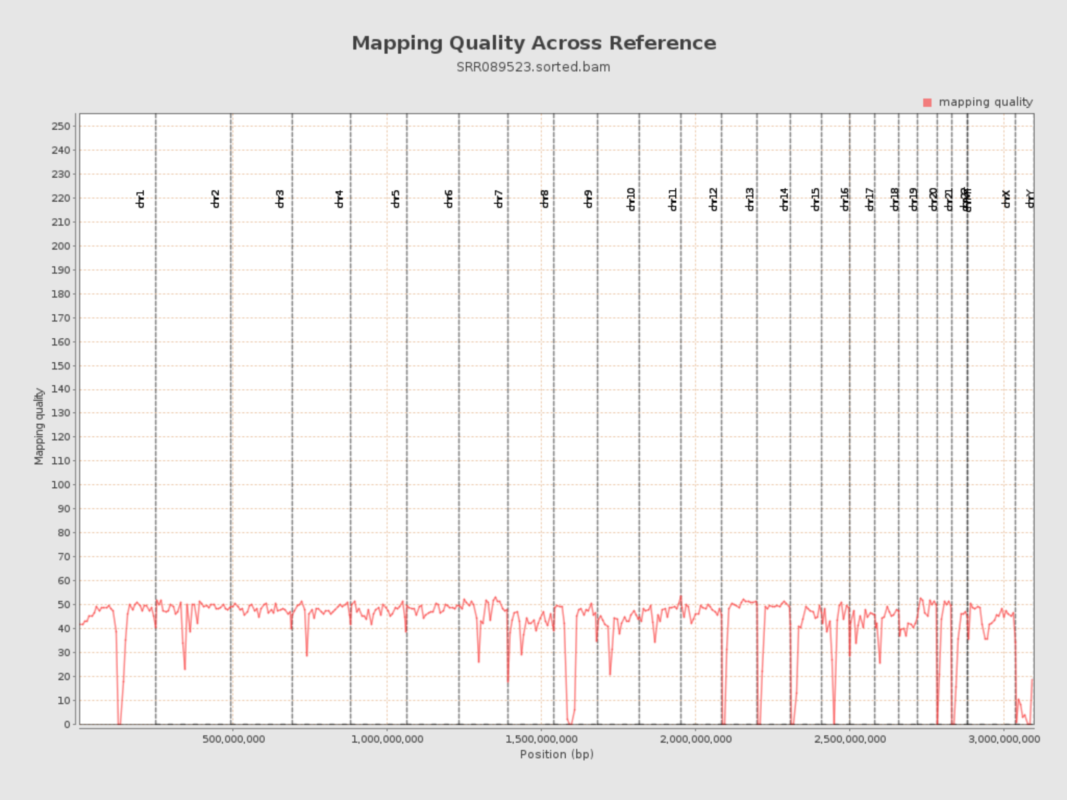
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram