Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:07:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549057.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_SRR1549057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:07:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,159,665
Mapped reads	2,749,864 / 87.03%
Unmapped reads	409,801 / 12.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	93,165 / 2.95%
Duplication rate	2.39%
Clipped reads	173,920 / 5.5%

2.2. ACGT Content

Number/percentage of A's	31,833,051 / 29.22%
Number/percentage of C's	22,217,882 / 20.4%
Number/percentage of T's	32,610,144 / 29.94%
Number/percentage of G's	22,274,229 / 20.45%
Number/percentage of N's	911 / 0%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0352
Standard Deviation	0.358

2.4. Mapping Quality

Mean Mapping Quality	42.19

2.5. Mismatches and indels

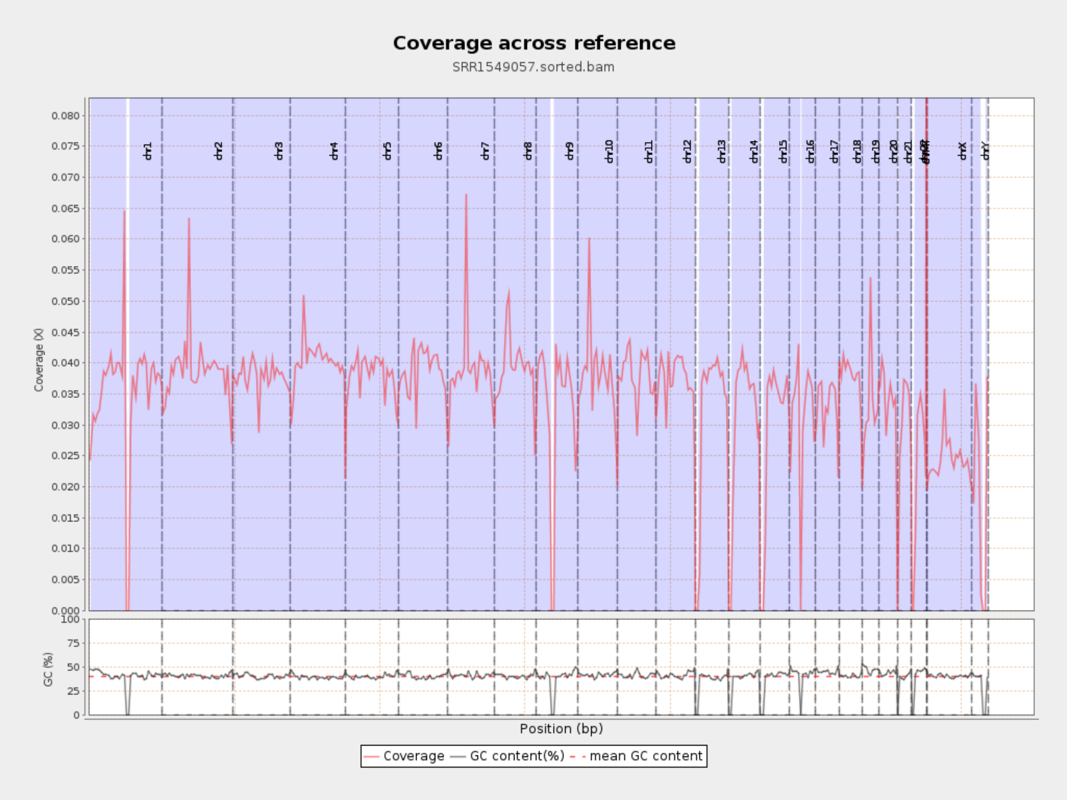
General error rate	0.25%
Mismatches	268,017
Insertions	2,800
Mapped reads with at least one insertion	0.1%
Deletions	8,036
Mapped reads with at least one deletion	0.29%
Homopolymer indels	42.5%

2.6. Chromosome stats

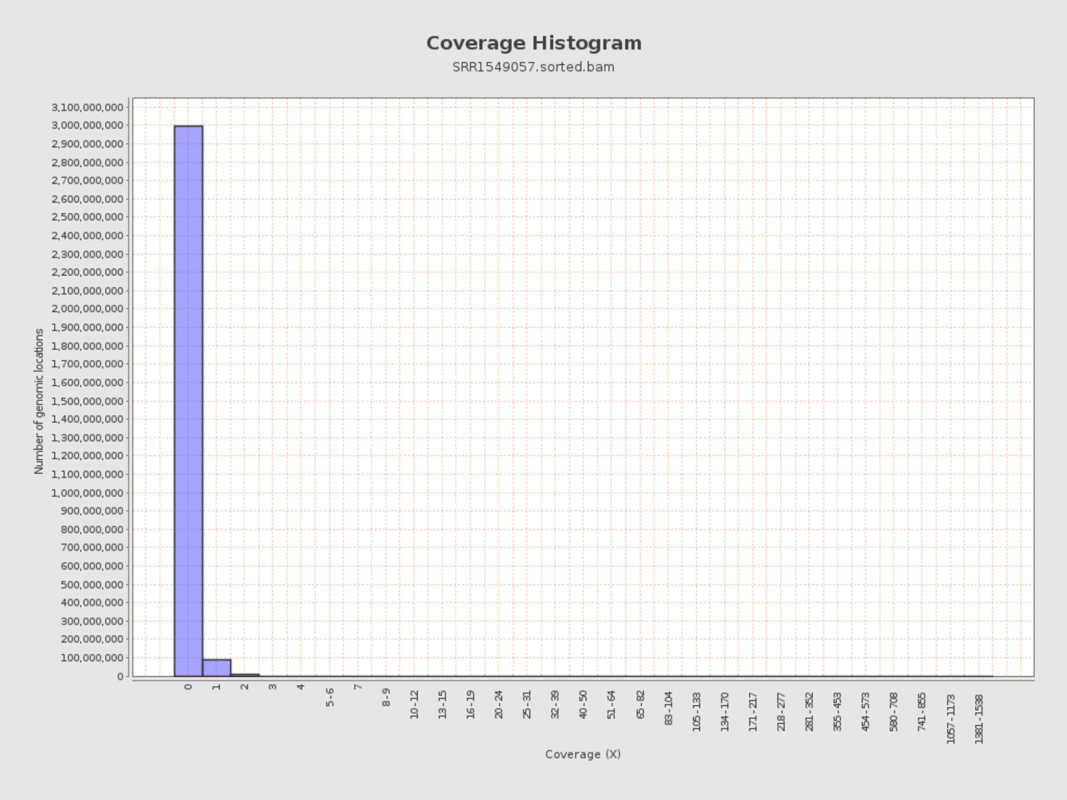
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8826920	0.0354	0.6436
chr2	243199373	9469416	0.0389	0.3062
chr3	198022430	7500514	0.0379	0.2118
chr4	191154276	7708521	0.0403	0.2258
chr5	180915260	6894449	0.0381	0.2141
chr6	171115067	6640340	0.0388	0.2274
chr7	159138663	6263603	0.0394	0.4161
chr8	146364022	5732929	0.0392	0.7865

chr9	141213431	4634840	0.0328	0.2922
chr10	135534747	5222837	0.0385	0.2917
chr11	135006516	5124659	0.038	0.2625
chr12	133851895	5023573	0.0375	0.217
chr13	115169878	3625376	0.0315	0.1898
chr14	107349540	3309591	0.0308	0.216
chr15	102531392	2973179	0.029	0.183
chr16	90354753	2853673	0.0316	0.2092
chr17	81195210	2655051	0.0327	0.2032
chr18	78077248	2991752	0.0383	0.5347
chr19	59128983	1989046	0.0336	0.5653
chr20	63025520	2160612	0.0343	0.2062
chr21	48129895	1392113	0.0289	0.219
chr22	51304566	1110532	0.0216	0.1851
chrMT	16571	3981	0.2402	0.5189
chrX	155270560	3797908	0.0245	0.212
chrY	59373566	1041521	0.0175	0.2149

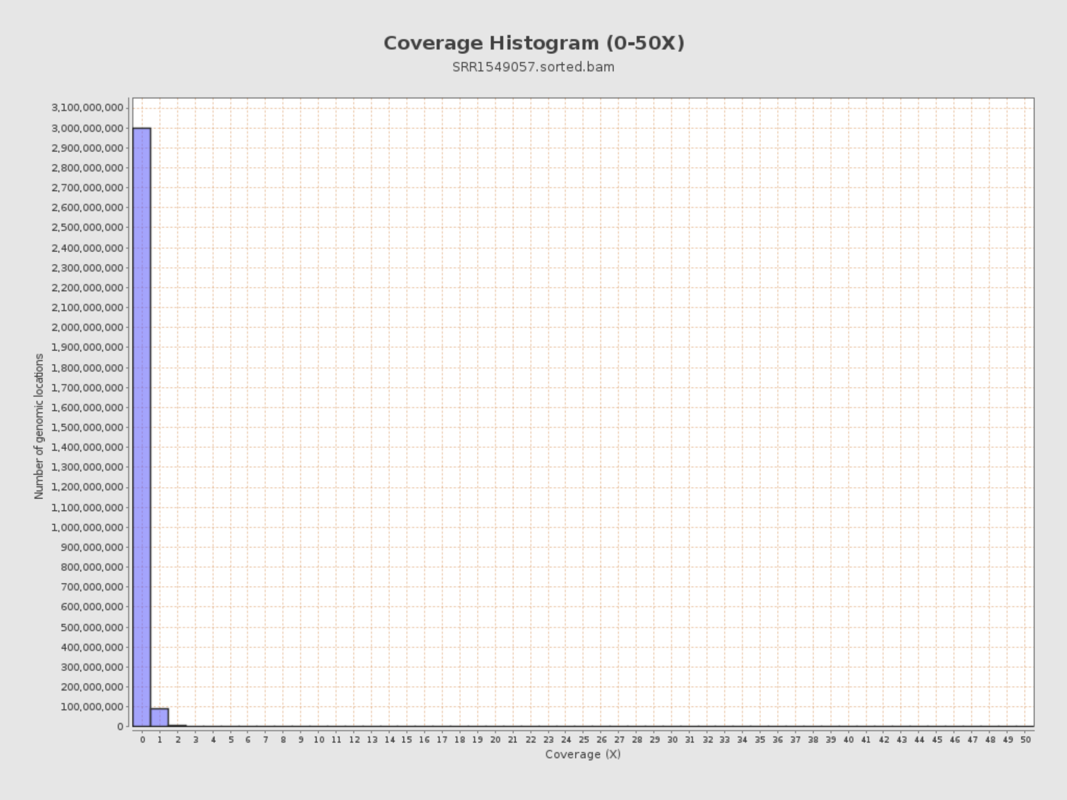
3. Results : Coverage across reference



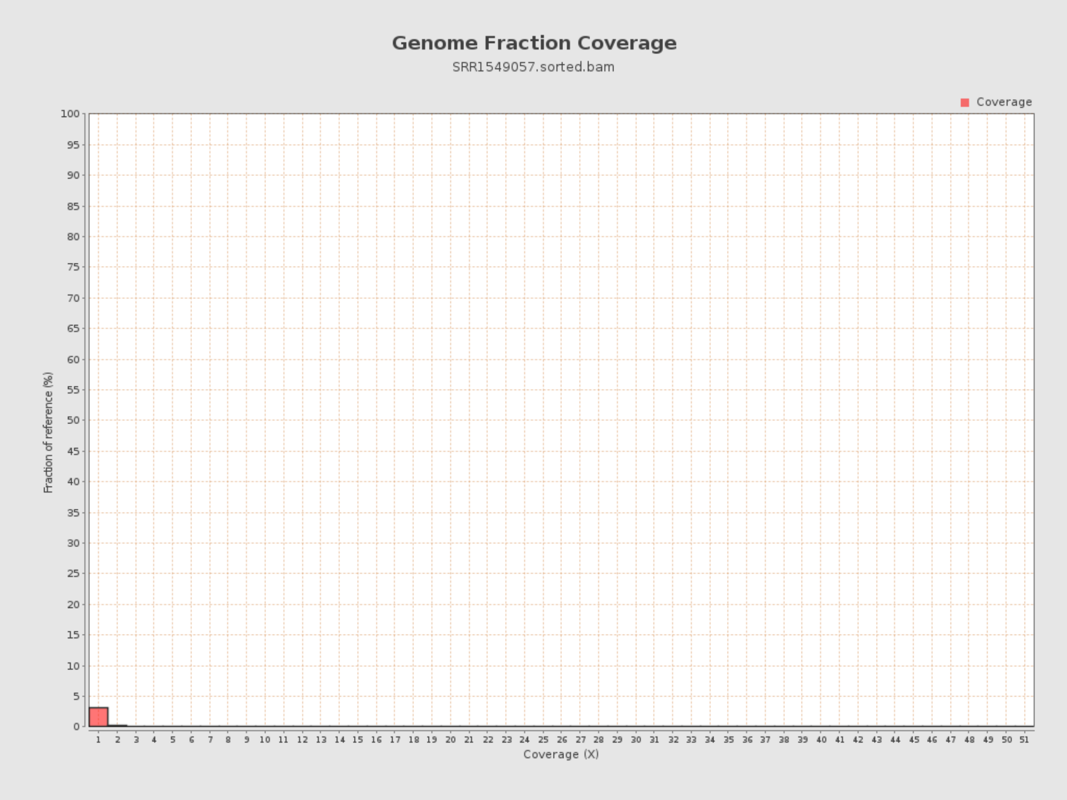
4. Results : Coverage Histogram



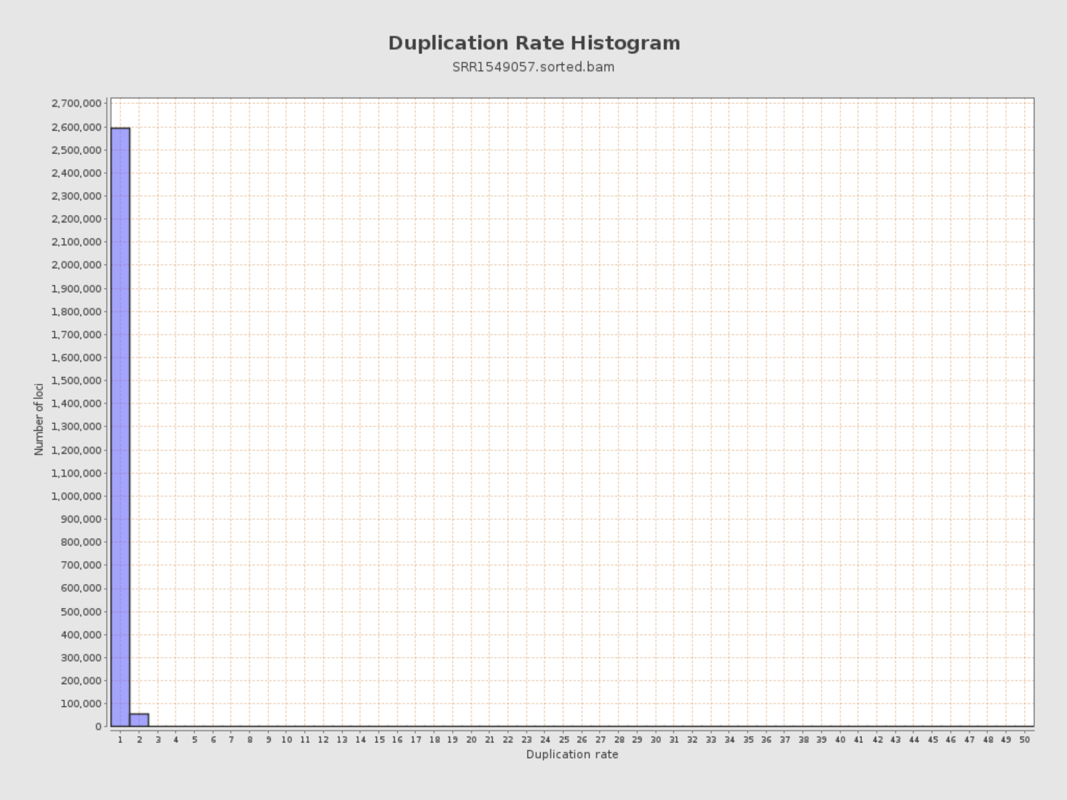
5. Results : Coverage Histogram (0-50X)



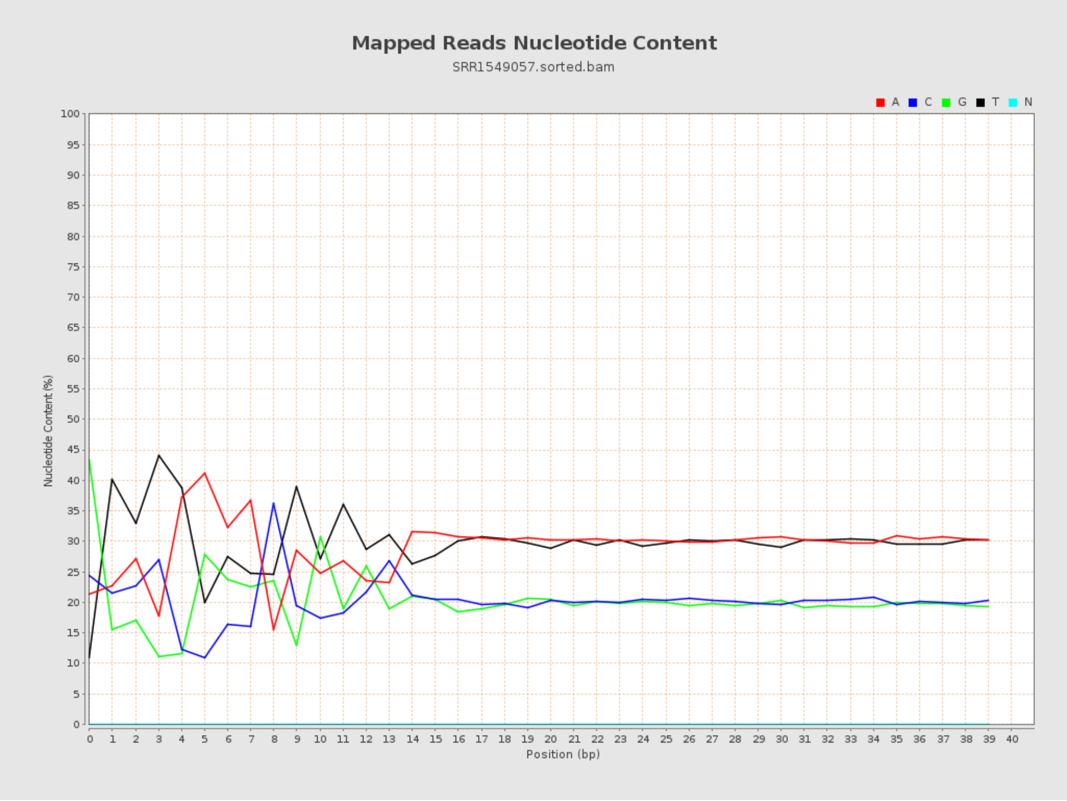
6. Results : Genome Fraction Coverage



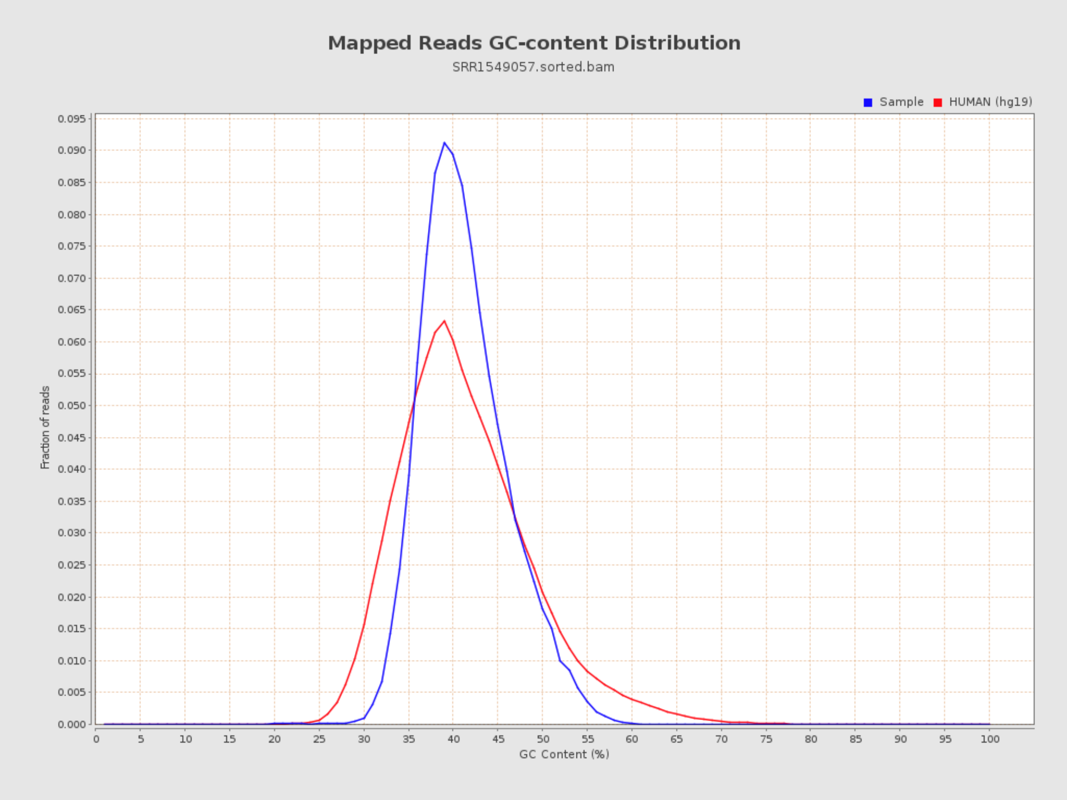
7. Results : Duplication Rate Histogram



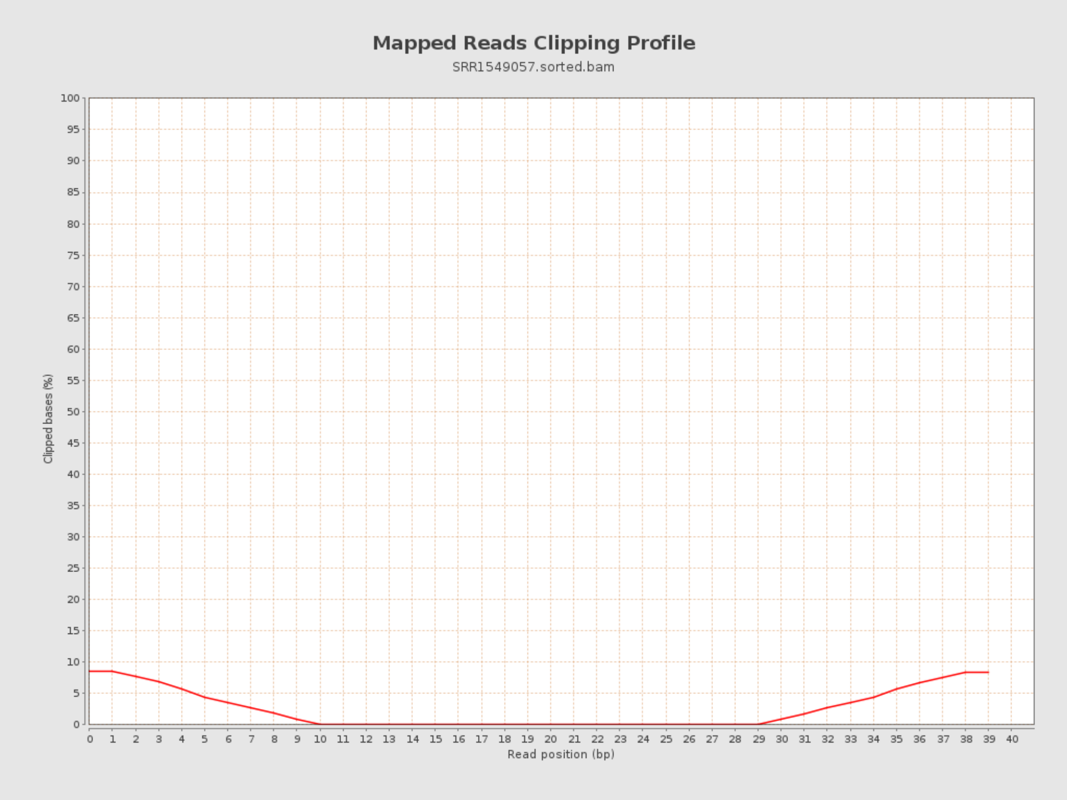
8. Results : Mapped Reads Nucleotide Content



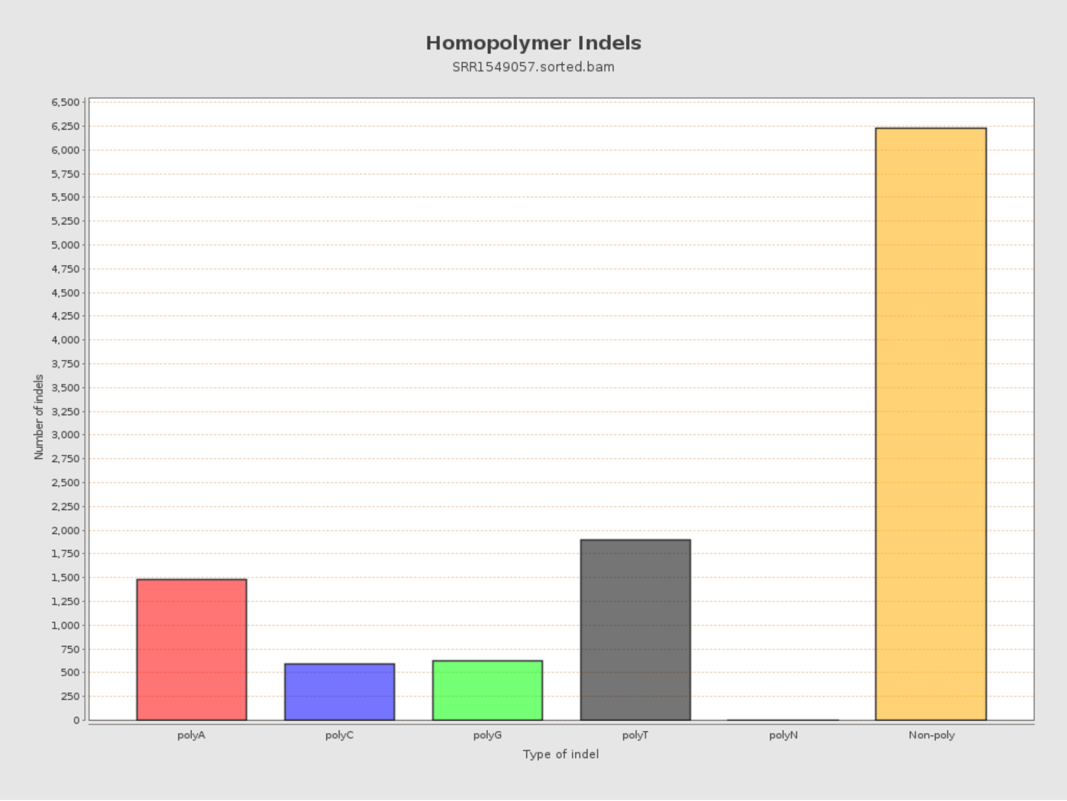
9. Results : Mapped Reads GC-content Distribution



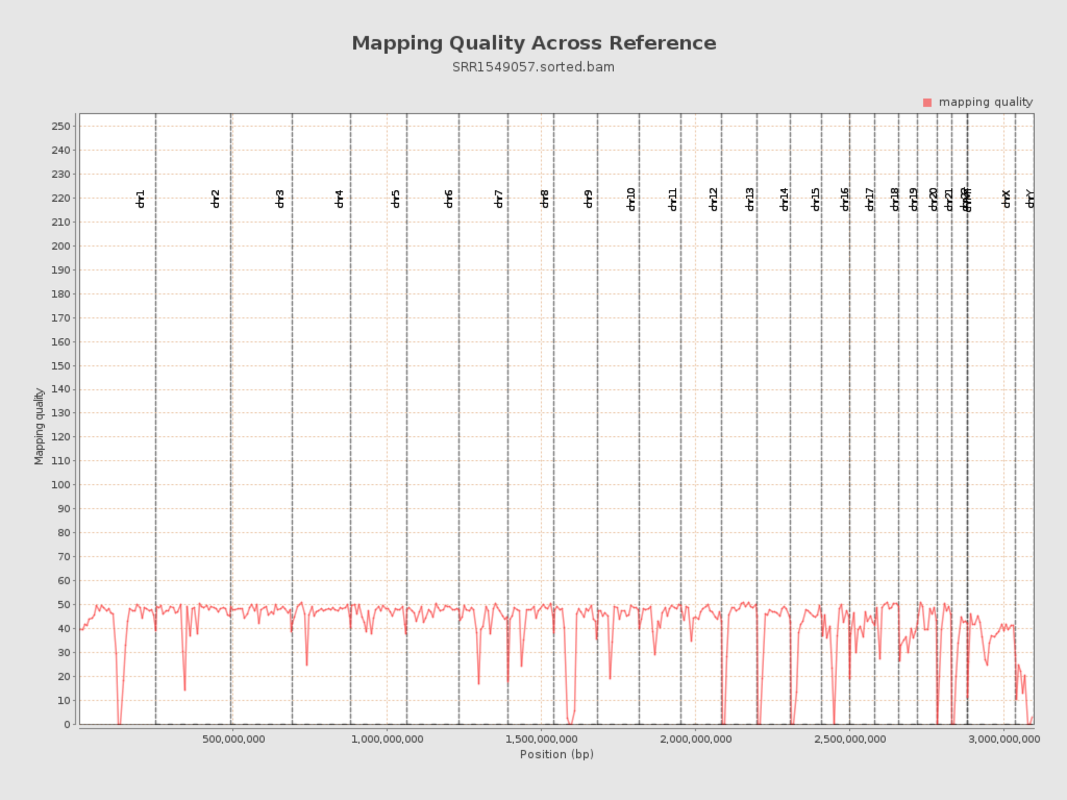
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram