Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 18:40:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779224.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_SRR1779224 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779224_1.fastq.gz SRR1779224_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 18:40:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779224.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,195,158
Mapped reads	8,966,537 / 97.51%
Unmapped reads	228,621 / 2.49%
Mapped paired reads	8,966,537 / 97.51%
Mapped reads, first in pair	4,521,177 / 49.17%
Mapped reads, second in pair	4,445,360 / 48.34%
Mapped reads, both in pair	8,877,826 / 96.55%
Mapped reads, singletons	88,711 / 0.96%
Secondary alignments	0
Supplementary alignments	20,358 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	122,194 / 1.33%
Duplication rate	1.18%
Clipped reads	295,927 / 3.22%

2.2. ACGT Content

Number/percentage of A's	217,440,590 / 30.48%
Number/percentage of C's	138,413,472 / 19.4%
Number/percentage of T's	216,553,254 / 30.35%
Number/percentage of G's	140,950,459 / 19.75%
Number/percentage of N's	135,664 / 0.02%

GC Percentage	39.15%

2.3. Coverage

Mean	0.2305
Standard Deviation	0.8251

2.4. Mapping Quality

Mean Mapping Quality	53.1

2.5. Insert size

Mean	41,327.82
Standard Deviation	1,897,955.88
P25/Median/P75	150 / 201 / 274

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	2,796,544
Insertions	50,626
Mapped reads with at least one insertion	0.56%
Deletions	64,449
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.63%

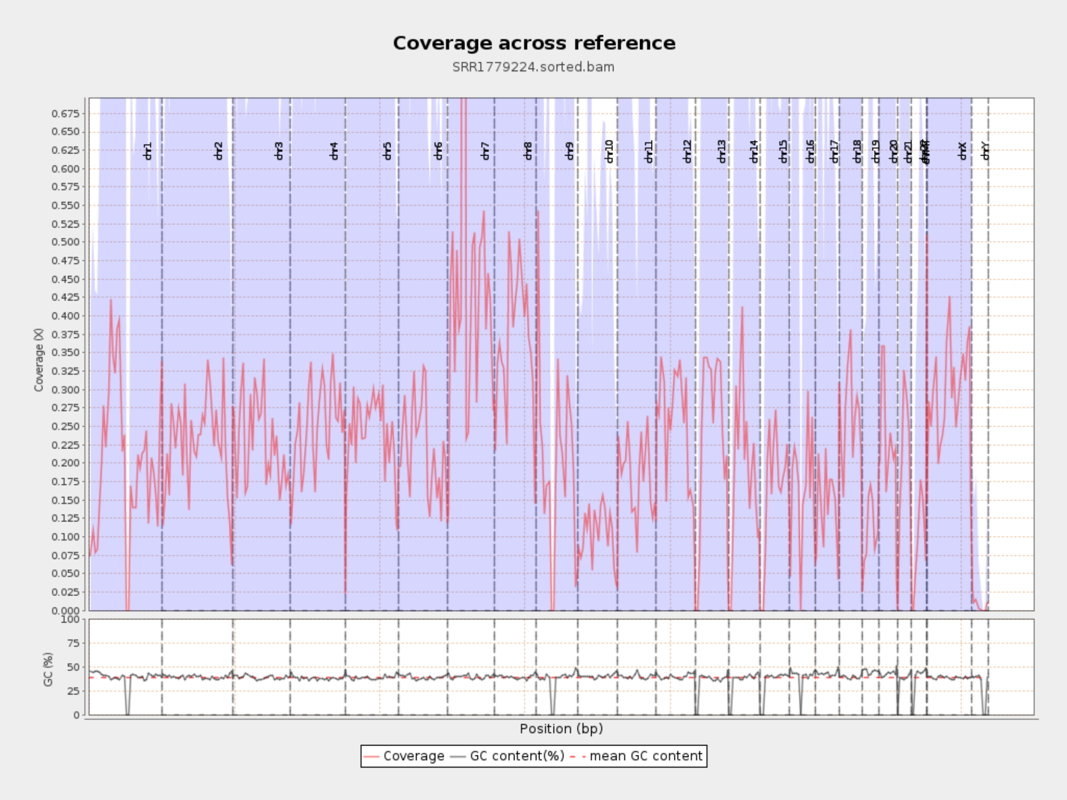
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

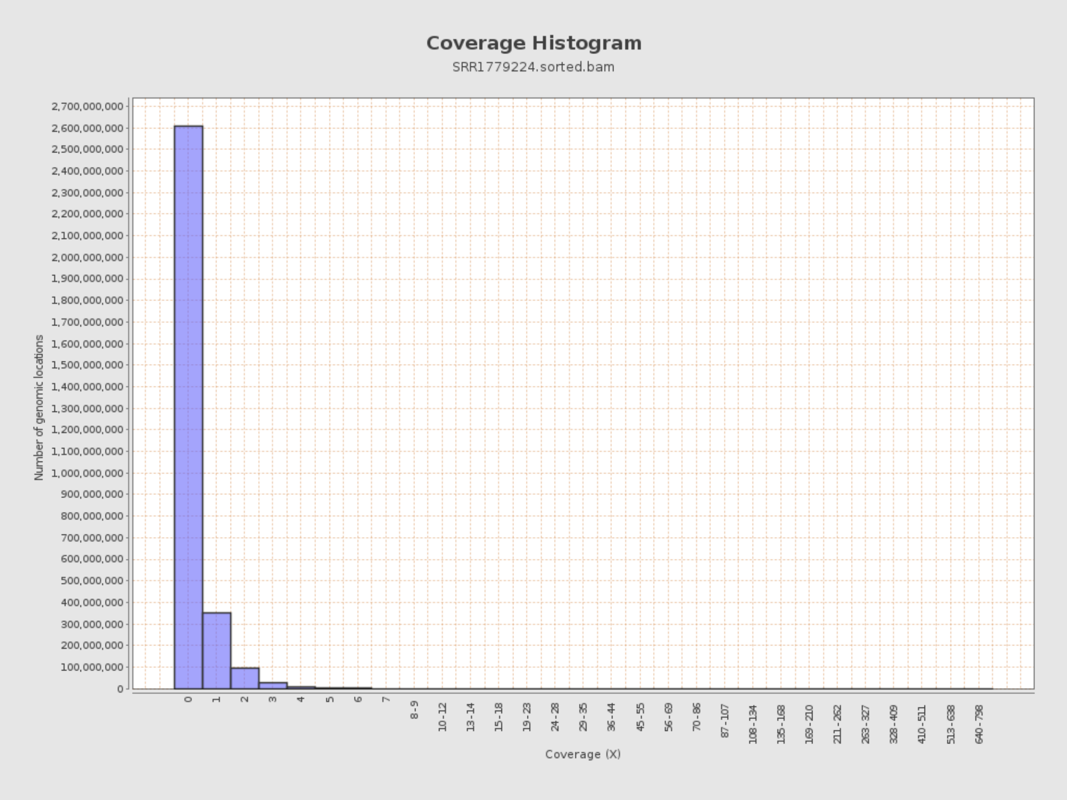
		bases	coverage	deviation
chr1	249250621	49889549	0.2002	0.9745
chr2	243199373	55352670	0.2276	0.6077
chr3	198022430	45820891	0.2314	0.6069
chr4	191154276	48005828	0.2511	0.6363
chr5	180915260	43959701	0.243	0.6251
chr6	171115067	37664212	0.2201	0.6178
chr7	159138663	81718338	0.5135	2.2033
chr8	146364022	54198227	0.3703	0.7929
chr9	141213431	29092078	0.206	0.6257
chr10	135534747	14504901	0.107	0.903
chr11	135006516	24567760	0.182	0.5403
chr12	133851895	34590224	0.2584	0.65
chr13	115169878	27625107	0.2399	0.6302
chr14	107349540	20523449	0.1912	0.5614
chr15	102531392	16877820	0.1646	0.5205
chr16	90354753	15152691	0.1677	0.5154
chr17	81195210	11335902	0.1396	0.5061
chr18	78077248	20702473	0.2652	0.6775
chr19	59128983	6731764	0.1138	0.6258
chr20	63025520	14800982	0.2348	0.6294
chr21	48129895	9644838	0.2004	0.5827
chr22	51304566	4583752	0.0893	0.3695
chrMT	16571	8469	0.5111	0.7278
chrX	155270560	45834108	0.2952	0.7274

chrY	59373566	442364	0.0075	0.1144

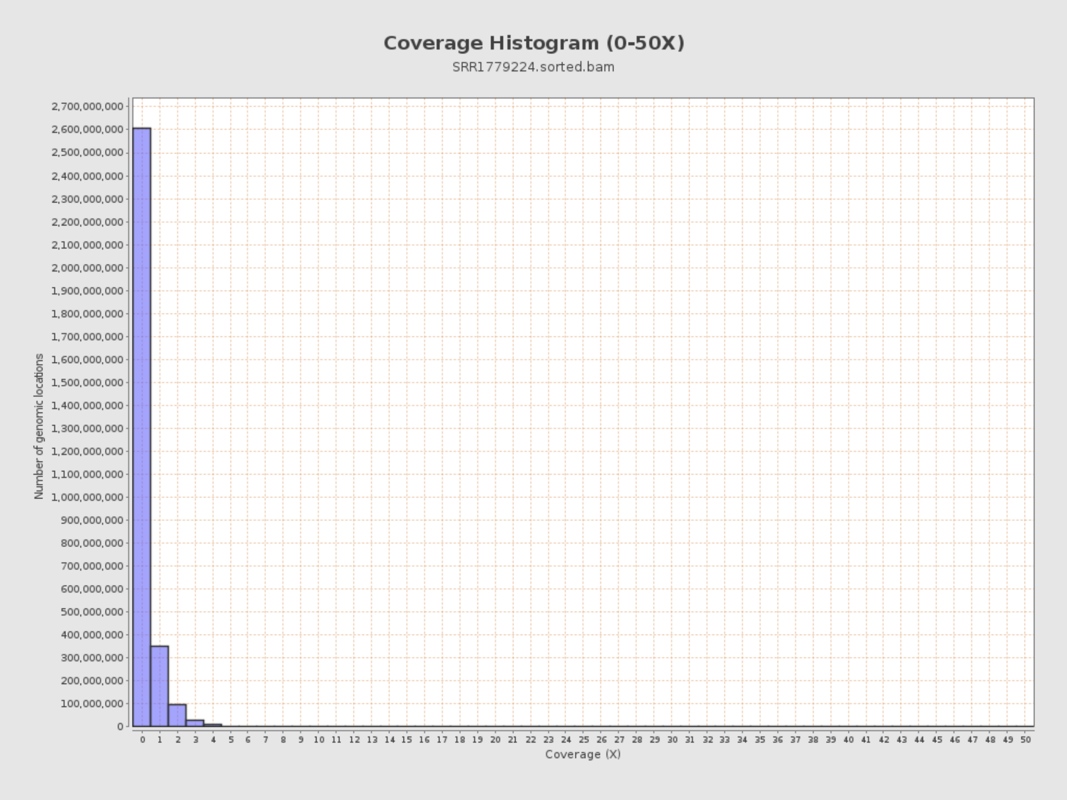
3. Results : Coverage across reference



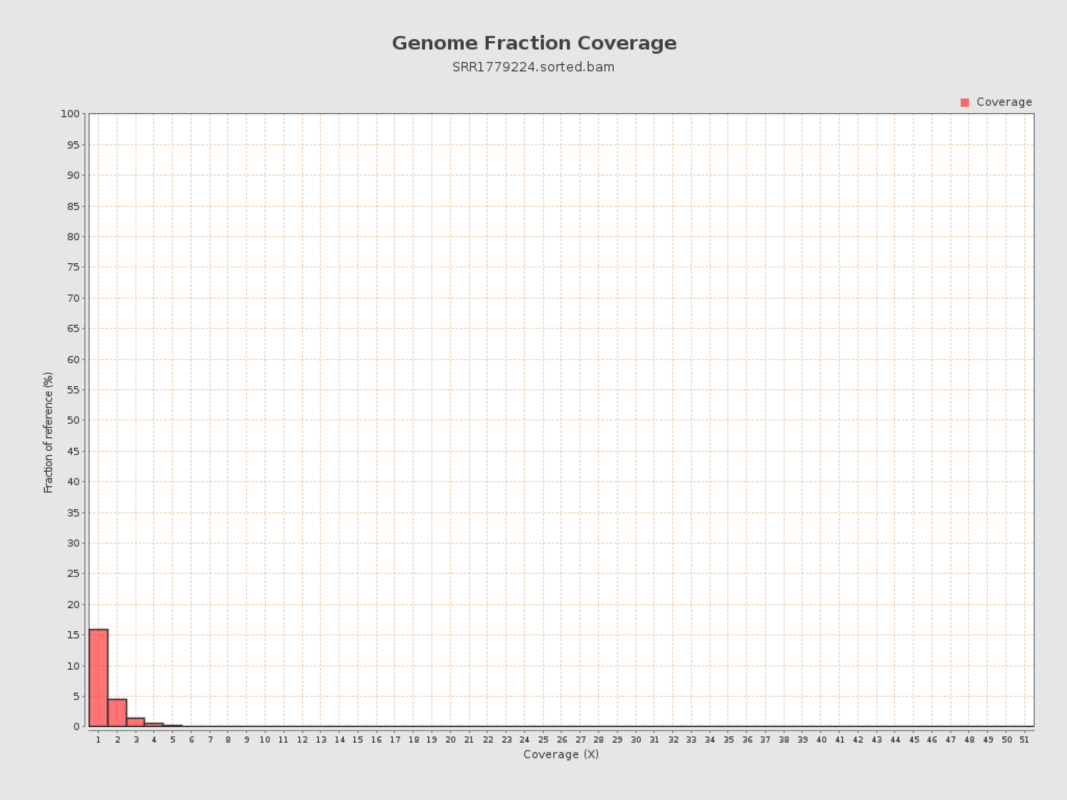
4. Results : Coverage Histogram



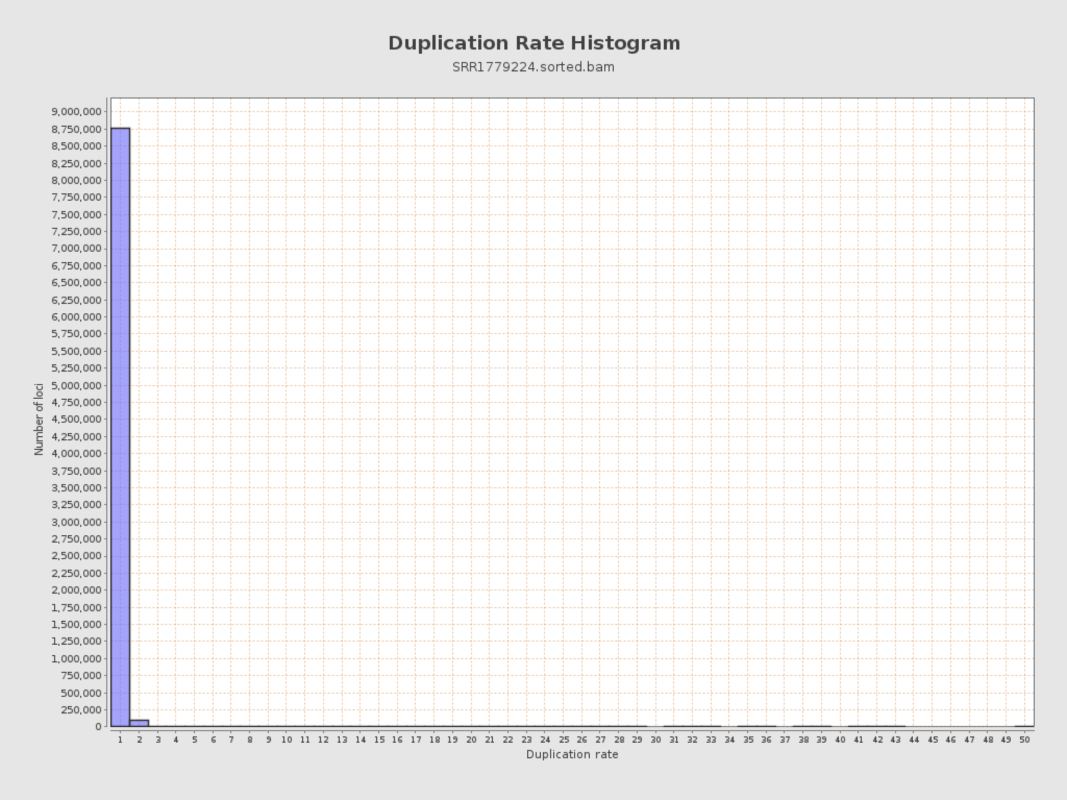
5. Results : Coverage Histogram (0-50X)



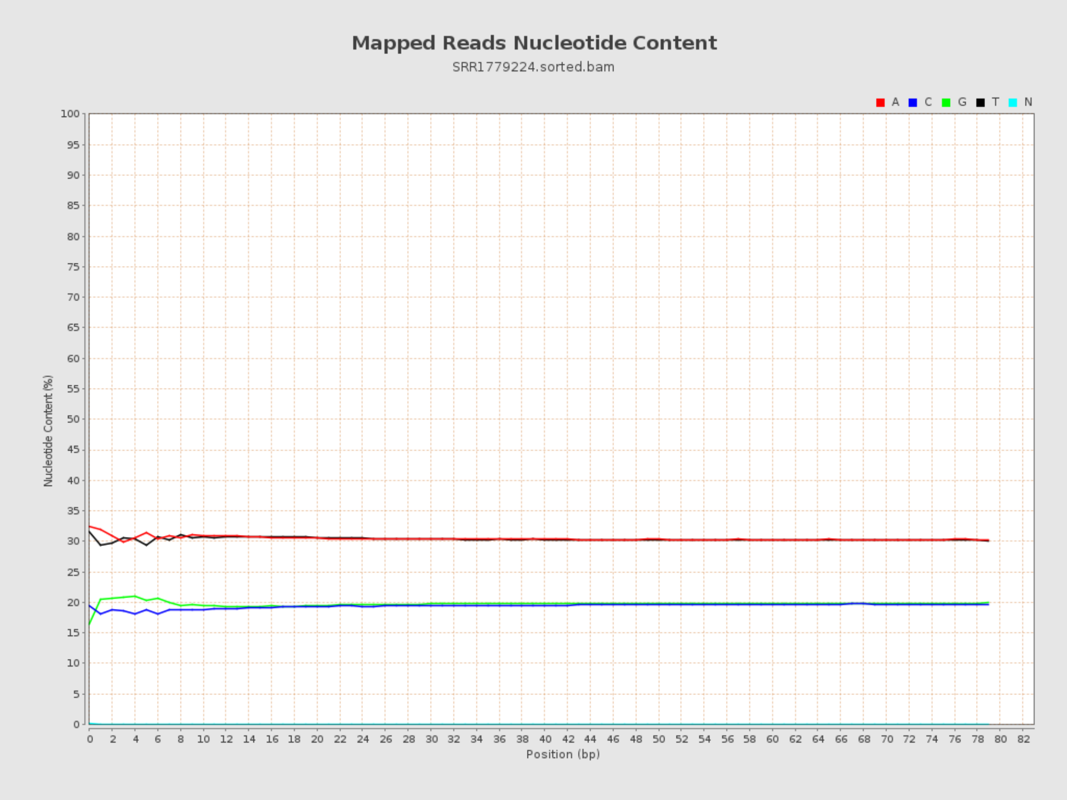
6. Results : Genome Fraction Coverage



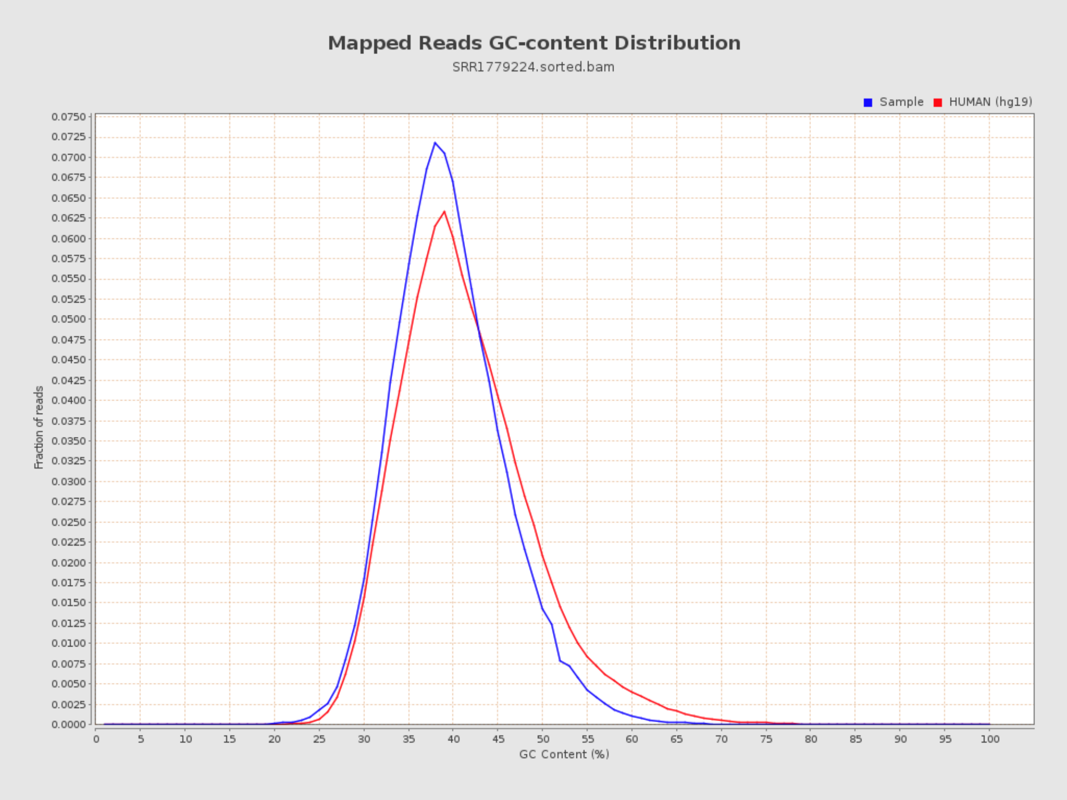
7. Results : Duplication Rate Histogram



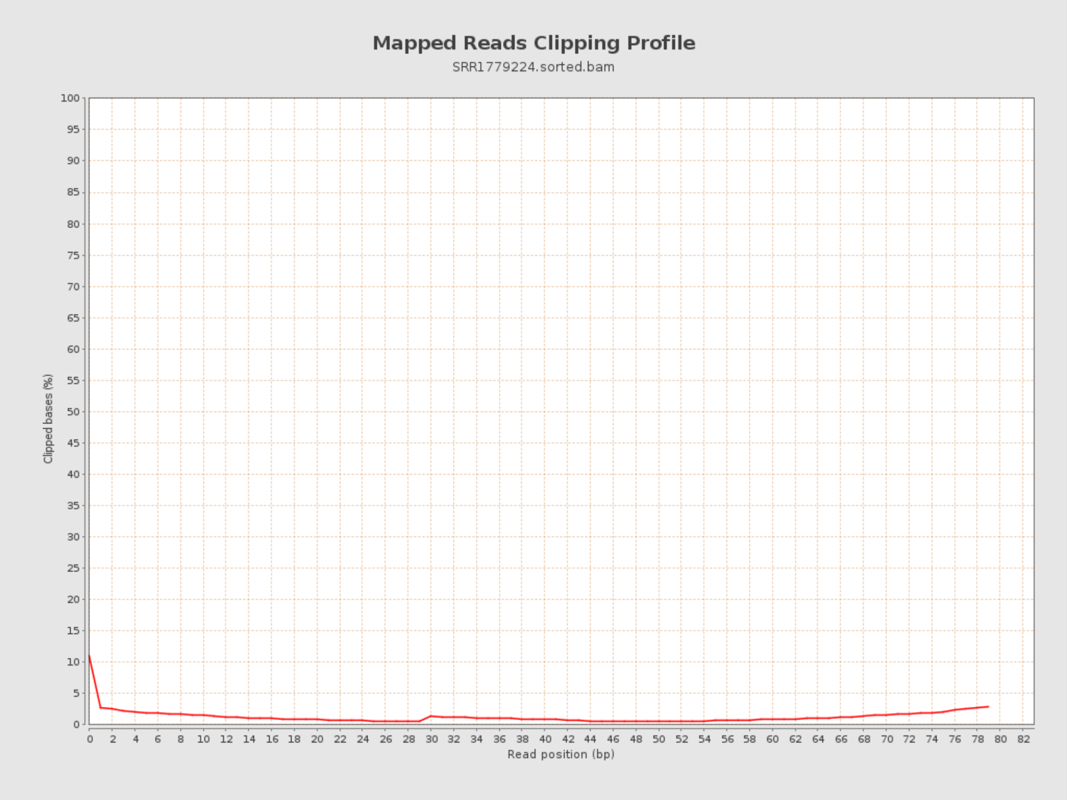
8. Results : Mapped Reads Nucleotide Content



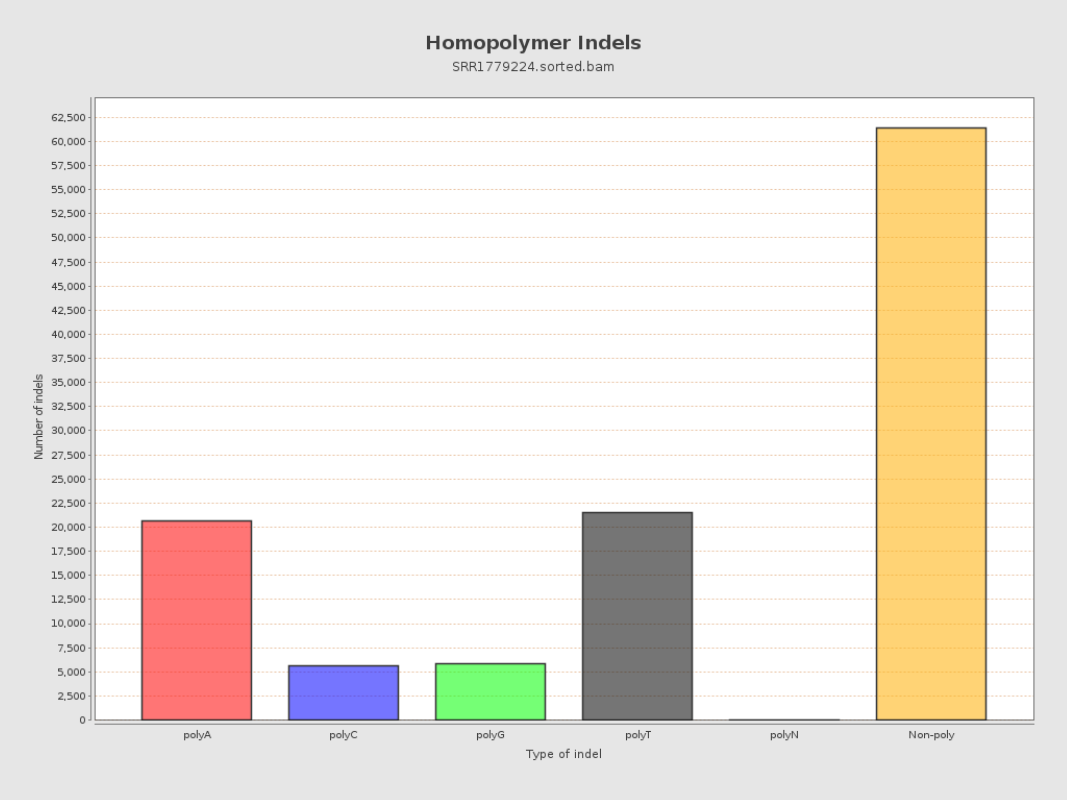
9. Results : Mapped Reads GC-content Distribution



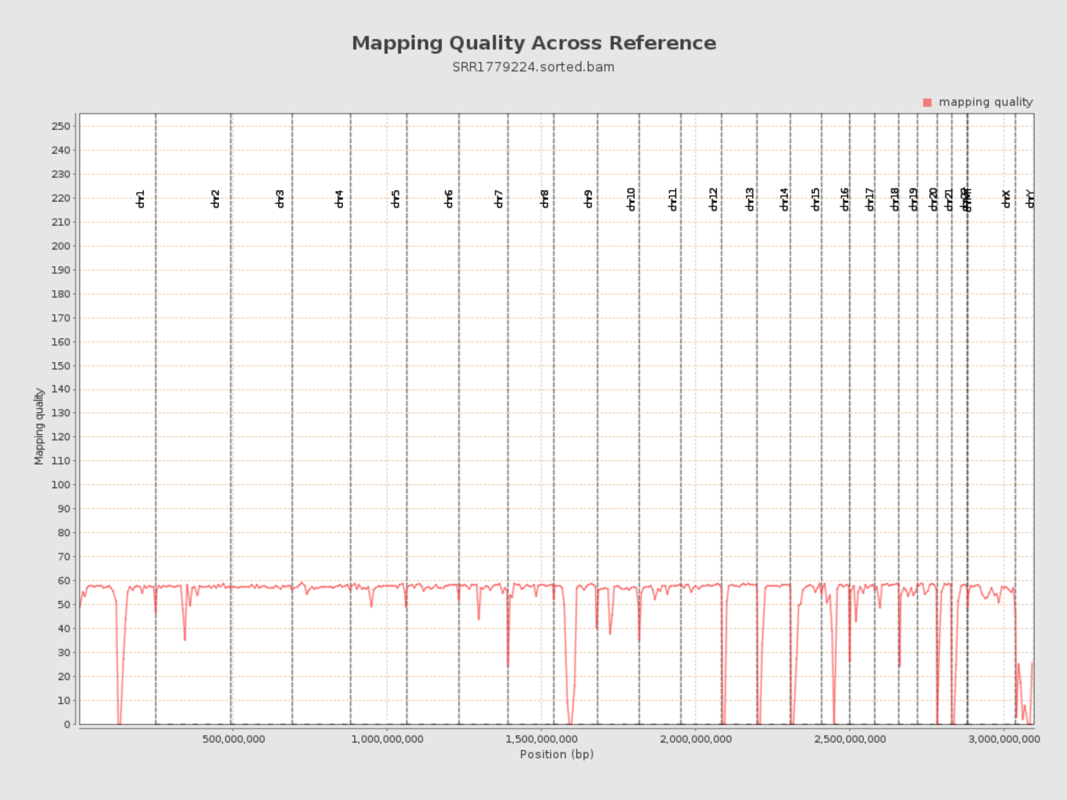
10. Results : Mapped Reads Clipping Profile



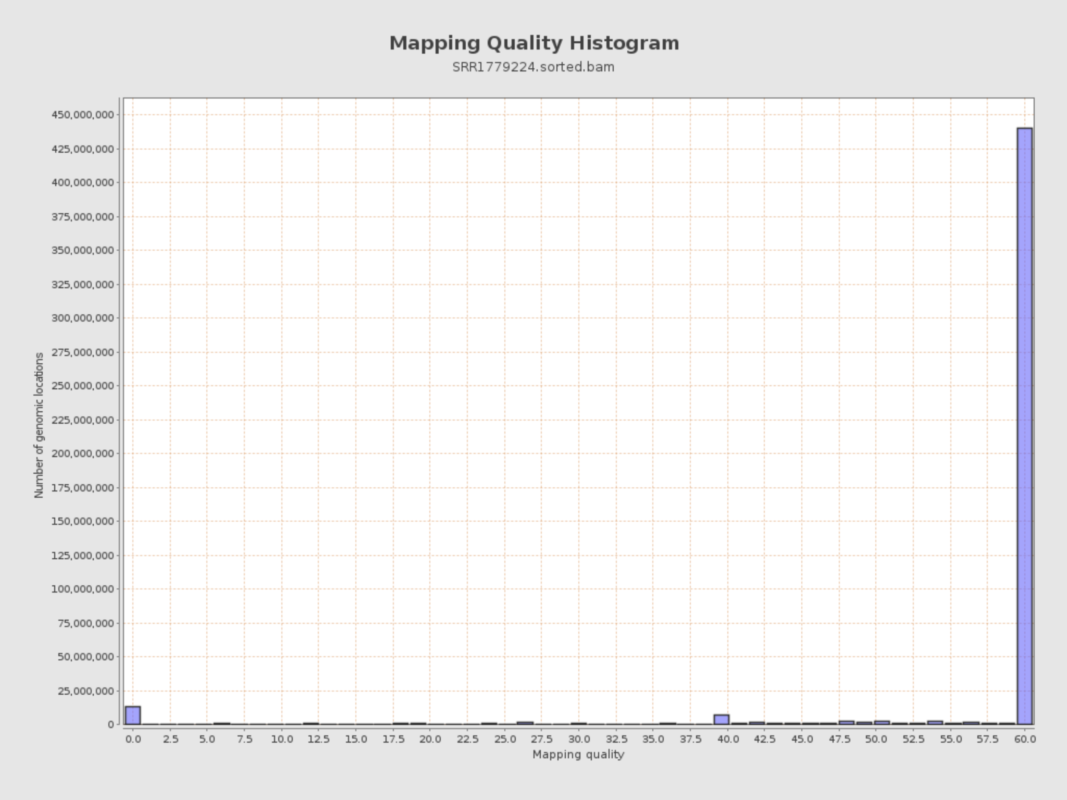
11. Results : Homopolymer Indels



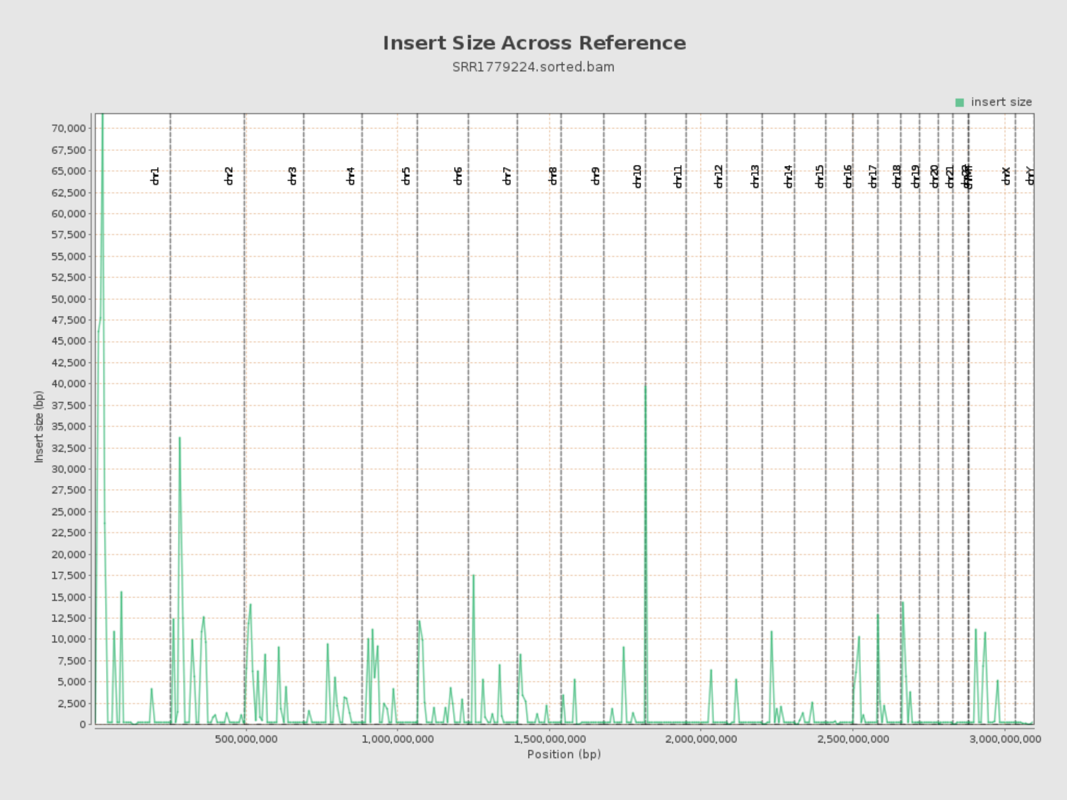
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram