Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/22 07:56:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504600.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_SRR504600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504600_1.fastq.gz SRR504600_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 22 07:56:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	430,651,964
Mapped reads	370,698,643 / 86.08%
Unmapped reads	59,953,321 / 13.92%
Mapped paired reads	370,698,643 / 86.08%
Mapped reads, first in pair	185,640,754 / 43.11%
Mapped reads, second in pair	185,057,889 / 42.97%
Mapped reads, both in pair	368,508,258 / 85.57%
Mapped reads, singletons	2,190,385 / 0.51%
Secondary alignments	0
Supplementary alignments	2,055,010 / 0.48%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	91,190,360 / 21.17%
Duplication rate	21.96%
Clipped reads	18,533,321 / 4.3%

2.2. ACGT Content

Number/percentage of A's	9,712,011,763 / 26.4%
Number/percentage of C's	8,604,747,013 / 23.39%
Number/percentage of T's	9,740,247,808 / 26.48%
Number/percentage of G's	8,720,620,262 / 23.71%
Number/percentage of N's	7,318,192 / 0.02%

GC Percentage	47.1%

2.3. Coverage

Mean	11.8857
Standard Deviation	24.526

2.4. Mapping Quality

Mean Mapping Quality	53.97

2.5. Insert size

Mean	29,909.26
Standard Deviation	1,680,108.67
P25/Median/P75	180 / 212 / 265

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	180,592,219
Insertions	2,793,346
Mapped reads with at least one insertion	0.73%
Deletions	3,708,903
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.45%

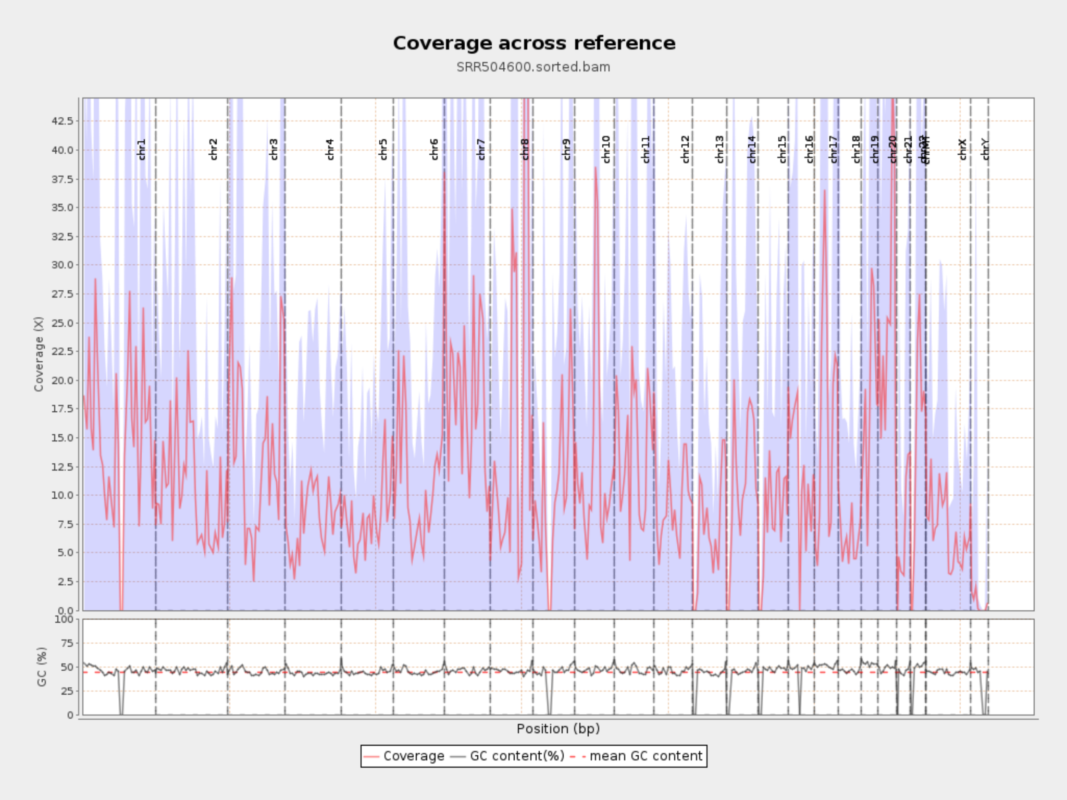
2.7. Chromosome stats

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

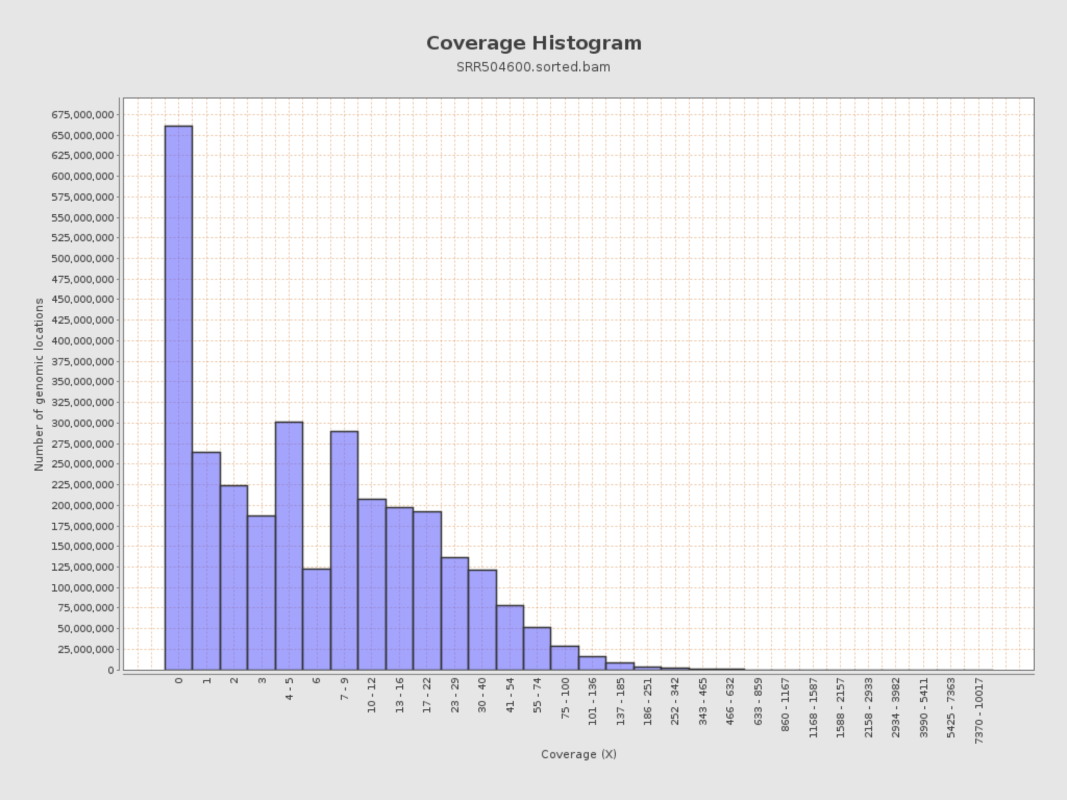
		bases	coverage	deviation
chr1	249250621	3776324307	15.1507	25.4908
chr2	243199373	2524194417	10.3791	18.5224
chr3	198022430	2726871816	13.7705	22.6771
chr4	191154276	1544285428	8.0787	12.768
chr5	180915260	1499302227	8.2873	13.8901
chr6	171115067	1882200739	10.9996	17.8821
chr7	159138663	2995863134	18.8255	27.8433
chr8	146364022	2813392090	19.2219	47.154
chr9	141213431	1446004754	10.2399	19.9339
chr10	135534747	1730690532	12.7693	24.0978
chr11	135006516	1873757850	13.879	23.4121
chr12	133851895	1255004628	9.3761	15.8122
chr13	115169878	837306999	7.2702	13.6103
chr14	107349540	1229547240	11.4537	19.8572
chr15	102531392	819326362	7.991	14.8871
chr16	90354753	1072252253	11.8671	20.3319
chr17	81195210	1329552756	16.3748	50.2931
chr18	78077248	481906336	6.1722	28.9009
chr19	59128983	1079467224	18.2561	31.5964
chr20	63025520	1652535006	26.2201	39.0298
chr21	48129895	348721508	7.2454	18.2997
chr22	51304566	753545657	14.6877	27.2347
chrMT	16571	245789	14.8325	11.2966
chrX	155270560	1085144700	6.9887	12.3063

chrY	59373566	37029380	0.6237	14.8931

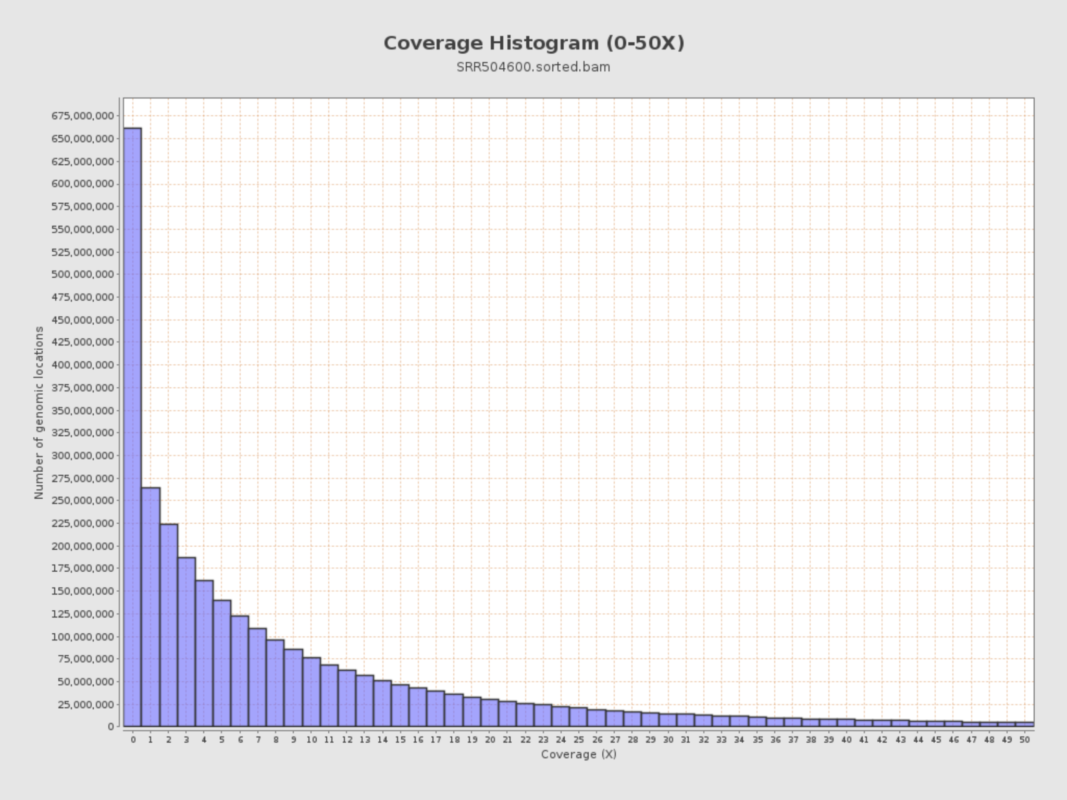
3. Results : Coverage across reference



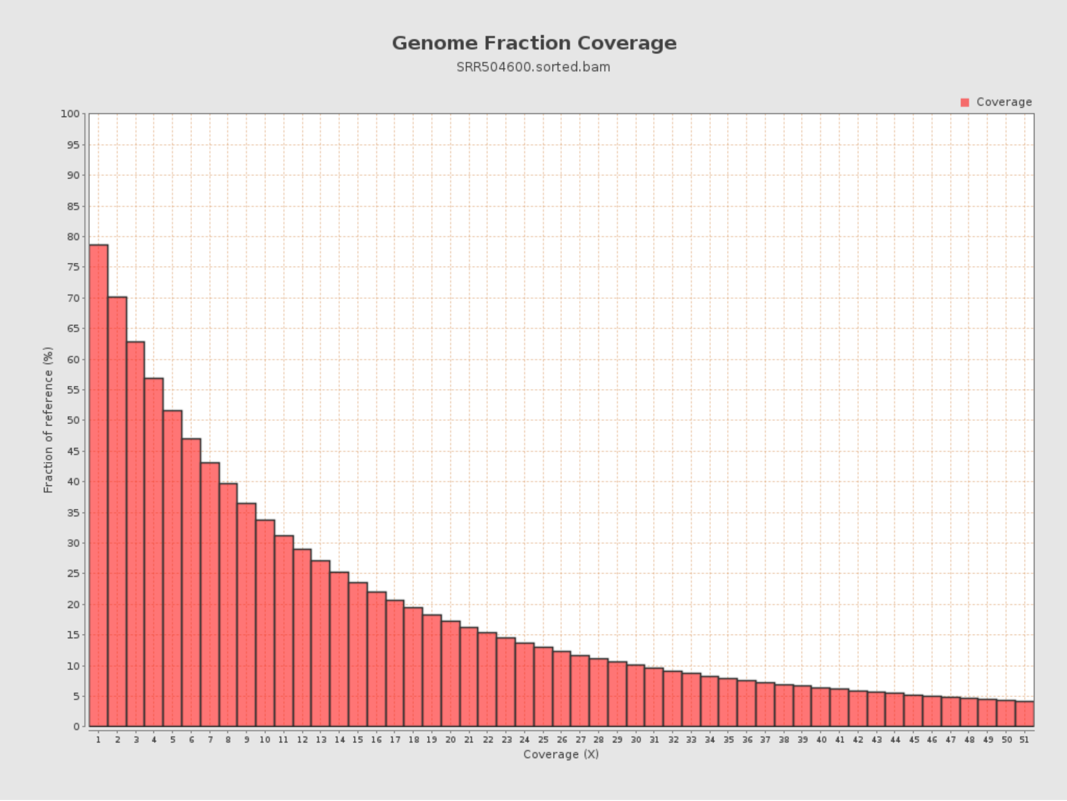
4. Results : Coverage Histogram



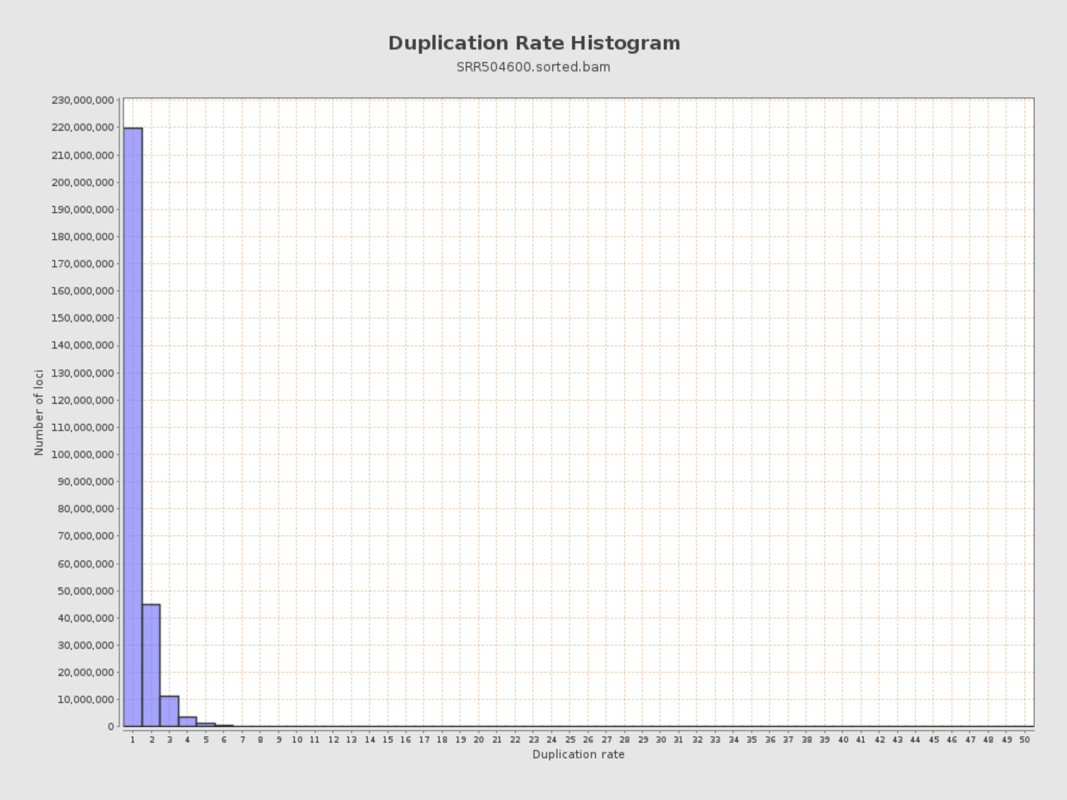
5. Results : Coverage Histogram (0-50X)



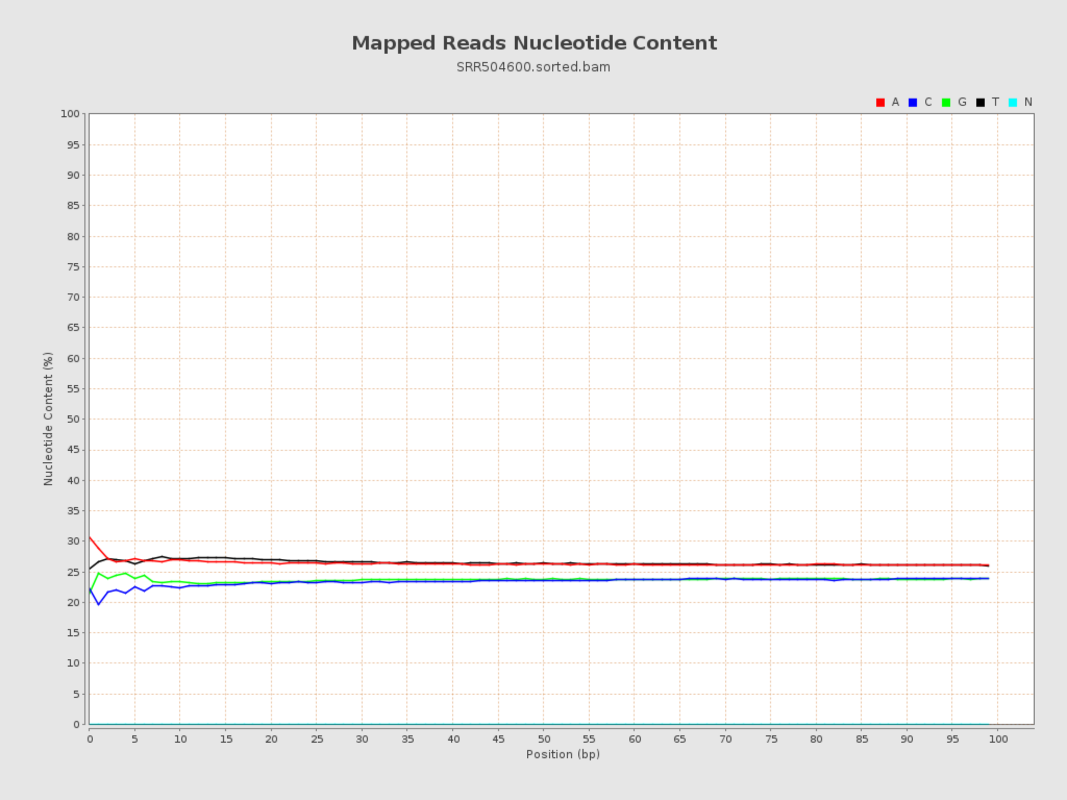
6. Results : Genome Fraction Coverage



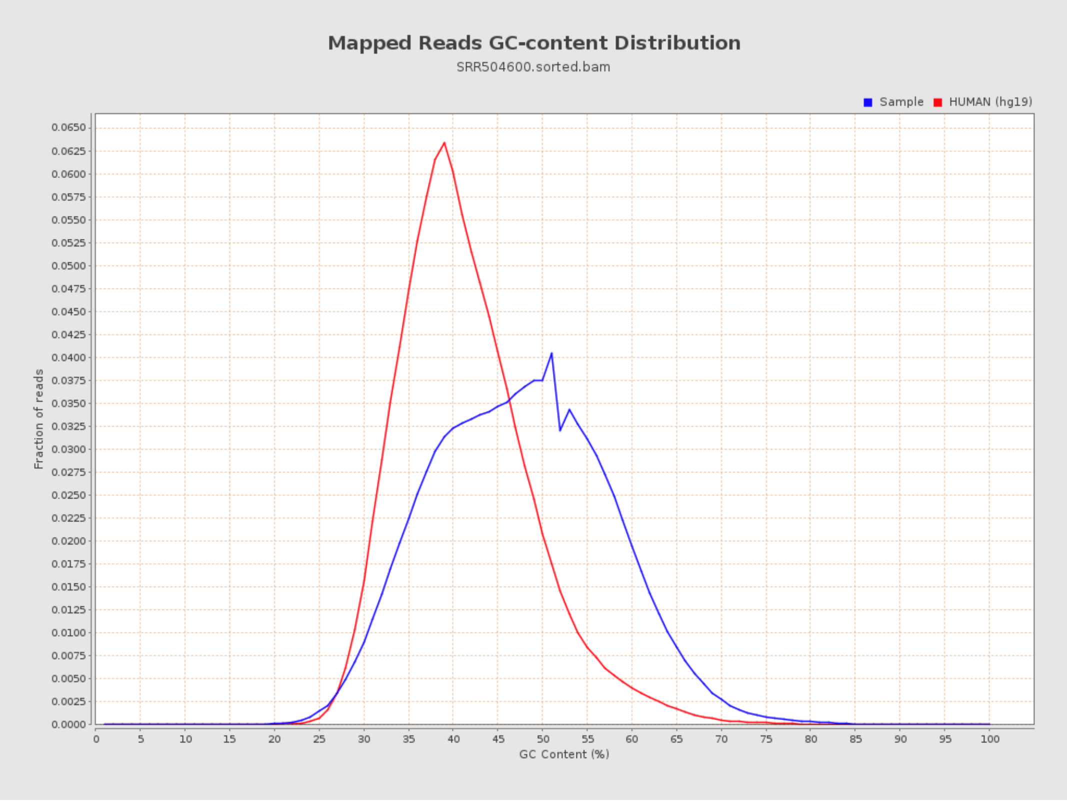
7. Results : Duplication Rate Histogram



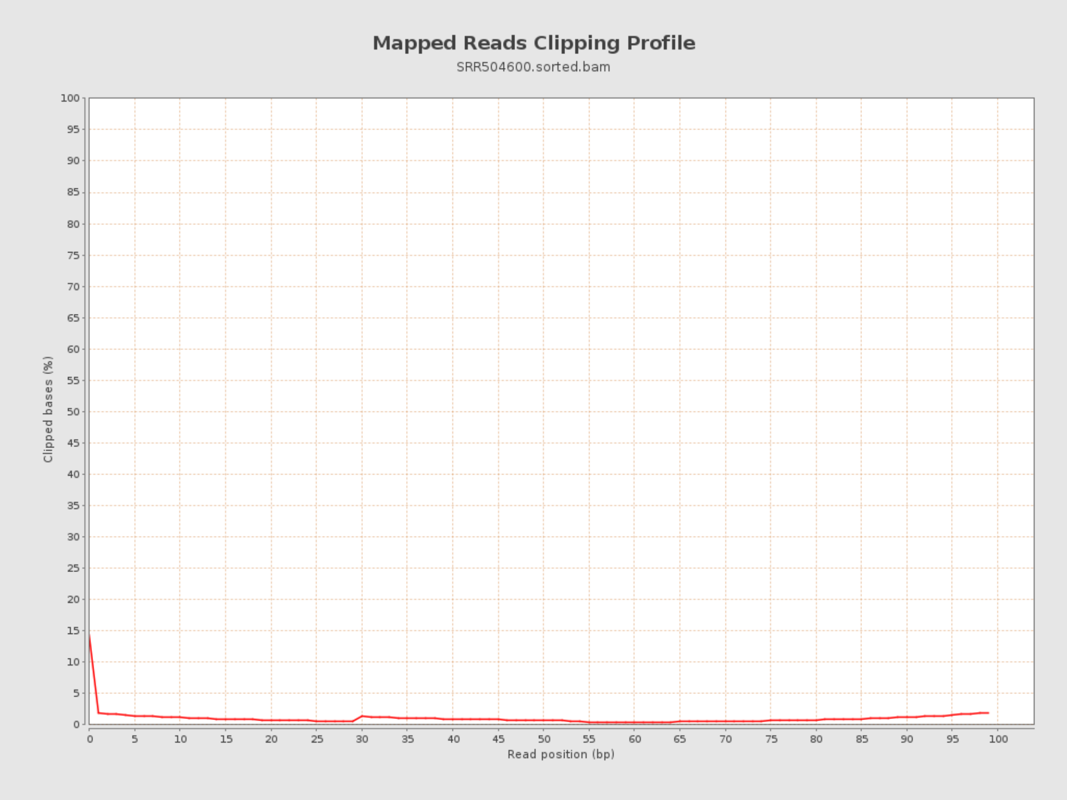
8. Results : Mapped Reads Nucleotide Content



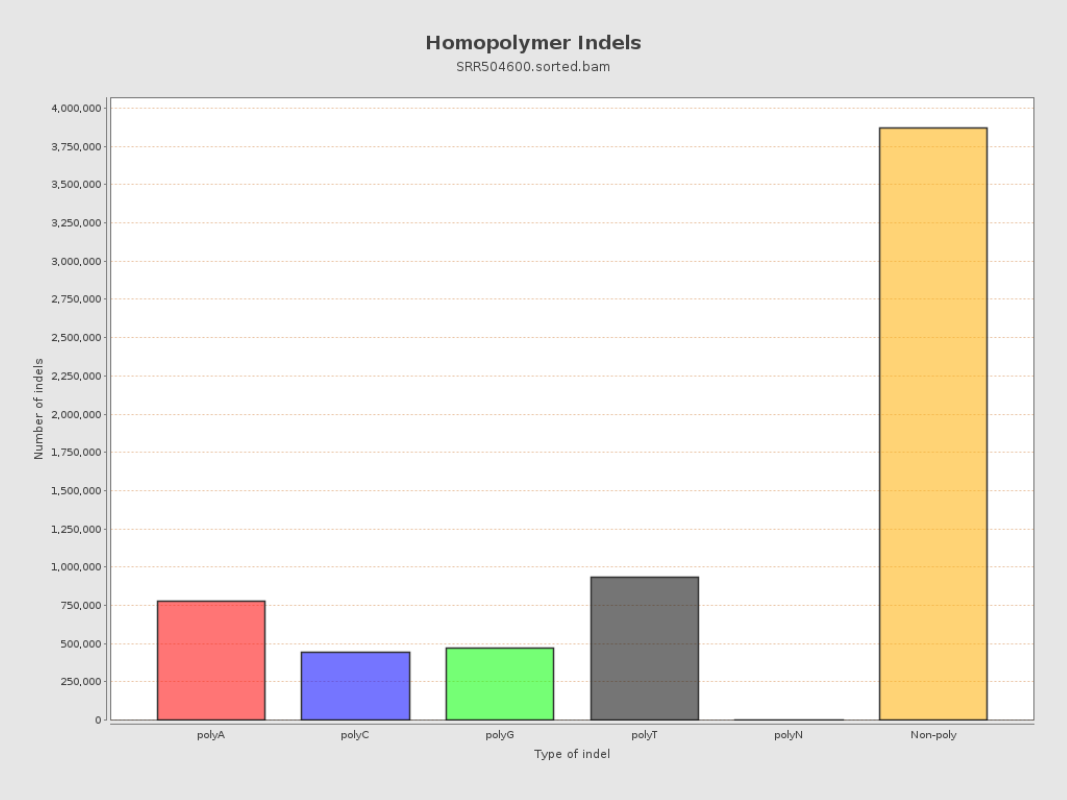
9. Results : Mapped Reads GC-content Distribution



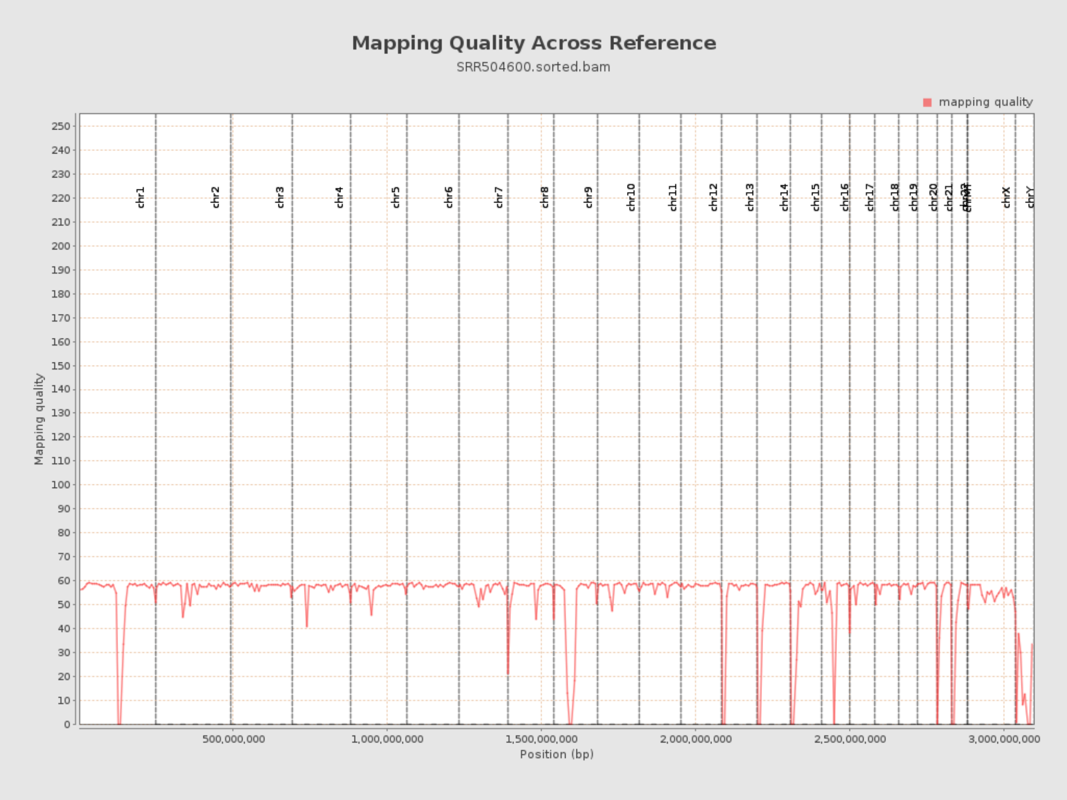
10. Results : Mapped Reads Clipping Profile



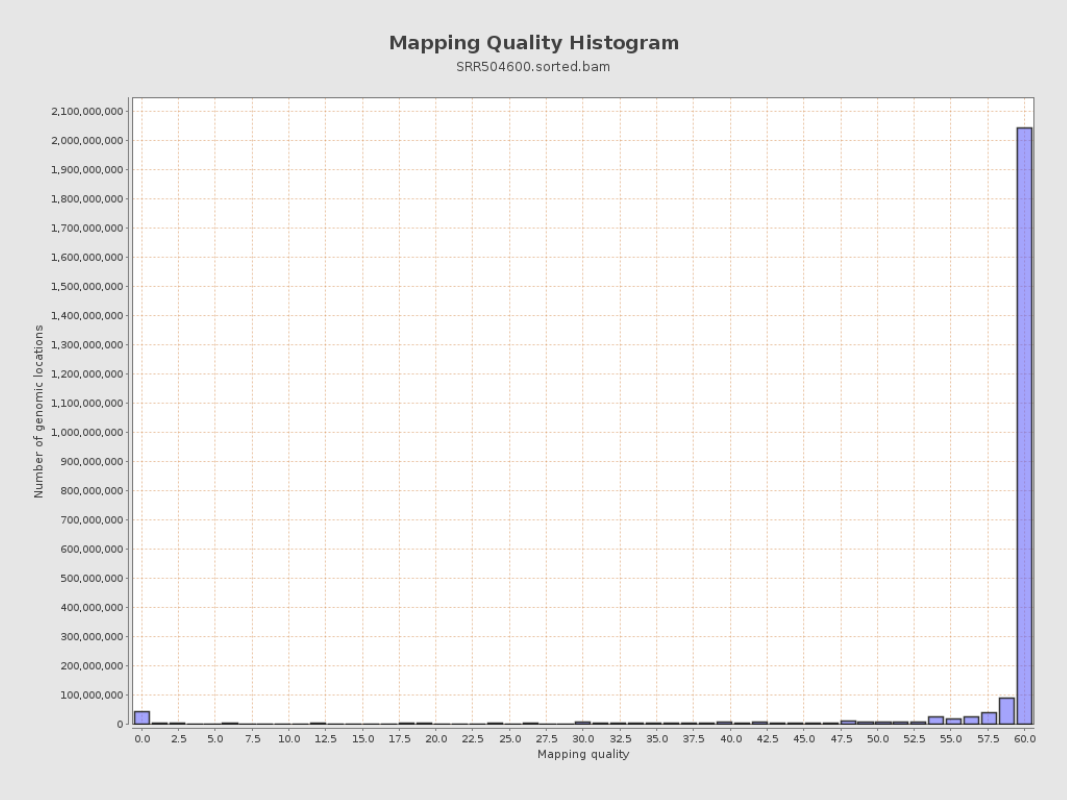
11. Results : Homopolymer Indels



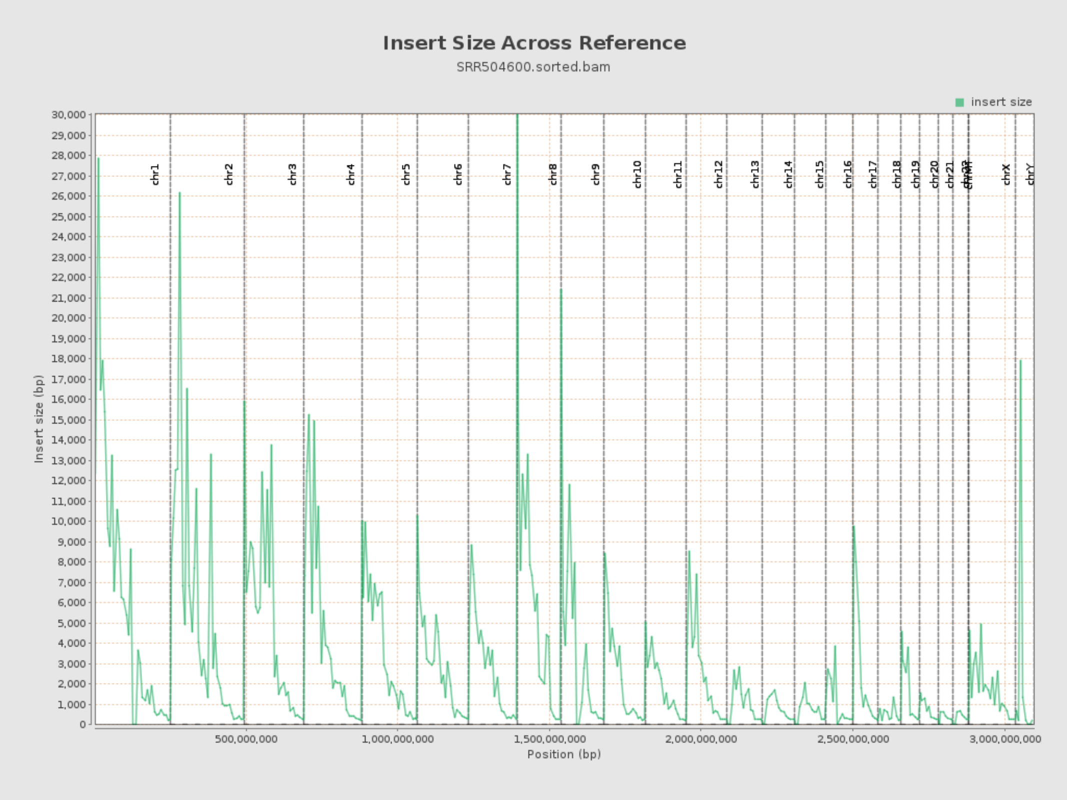
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram