Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 17:35:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926988.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_SRR926988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926988_1.fastq.gz SRR926988_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 17:35:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,386,082
Mapped reads	20,003,908 / 98.13%
Unmapped reads	382,174 / 1.87%
Mapped paired reads	20,003,908 / 98.13%
Mapped reads, first in pair	10,042,967 / 49.26%
Mapped reads, second in pair	9,960,941 / 48.86%
Mapped reads, both in pair	19,781,132 / 97.03%
Mapped reads, singletons	222,776 / 1.09%
Secondary alignments	0
Supplementary alignments	483,987 / 2.37%
Read min/max/mean length	30 / 101 / 101.99
Duplicated reads (estimated)	1,376,787 / 6.75%
Duplication rate	5.41%
Clipped reads	6,873,701 / 33.72%

2.2. ACGT Content

Number/percentage of A's	532,995,967 / 28.64%
Number/percentage of C's	368,853,294 / 19.82%
Number/percentage of T's	542,098,847 / 29.13%
Number/percentage of G's	417,151,860 / 22.41%
Number/percentage of N's	149,919 / 0.01%

GC Percentage	42.23%

2.3. Coverage

Mean	0.6017
Standard Deviation	2.4111

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	254,067.28
Standard Deviation	4,957,222.51
P25/Median/P75	136 / 173 / 228

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	17,588,036
Insertions	320,395
Mapped reads with at least one insertion	1.57%
Deletions	966,241
Mapped reads with at least one deletion	4.71%
Homopolymer indels	52.13%

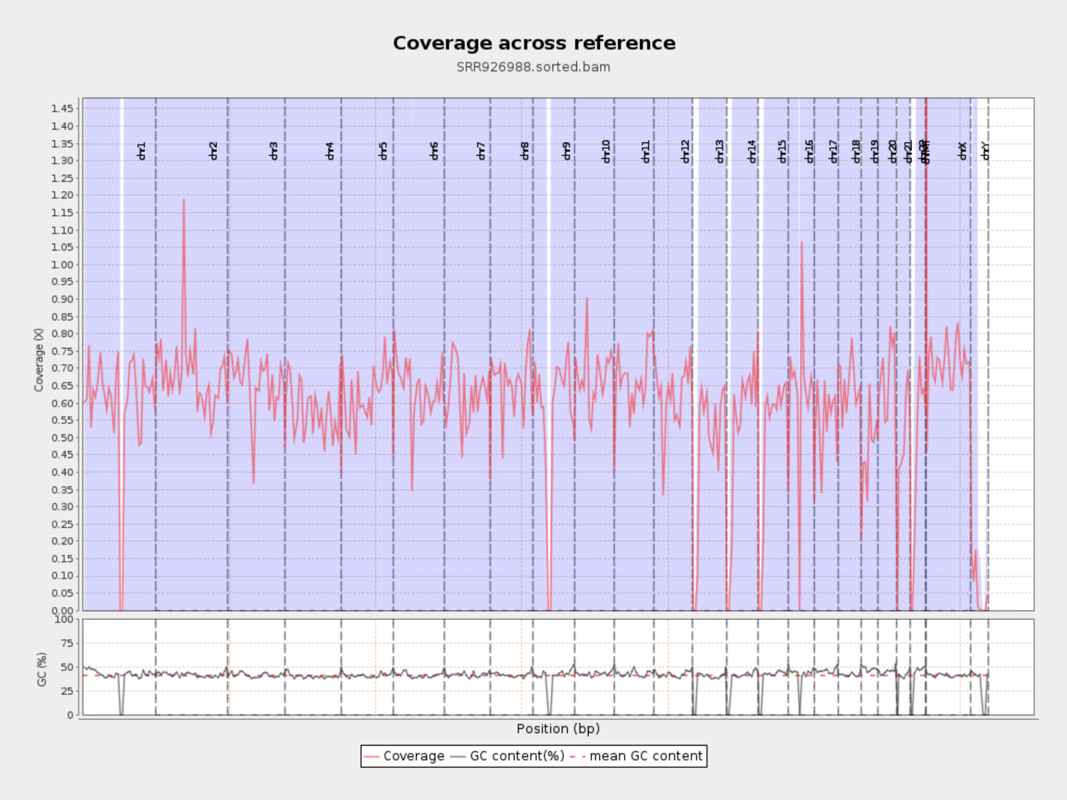
2.7. Chromosome stats

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

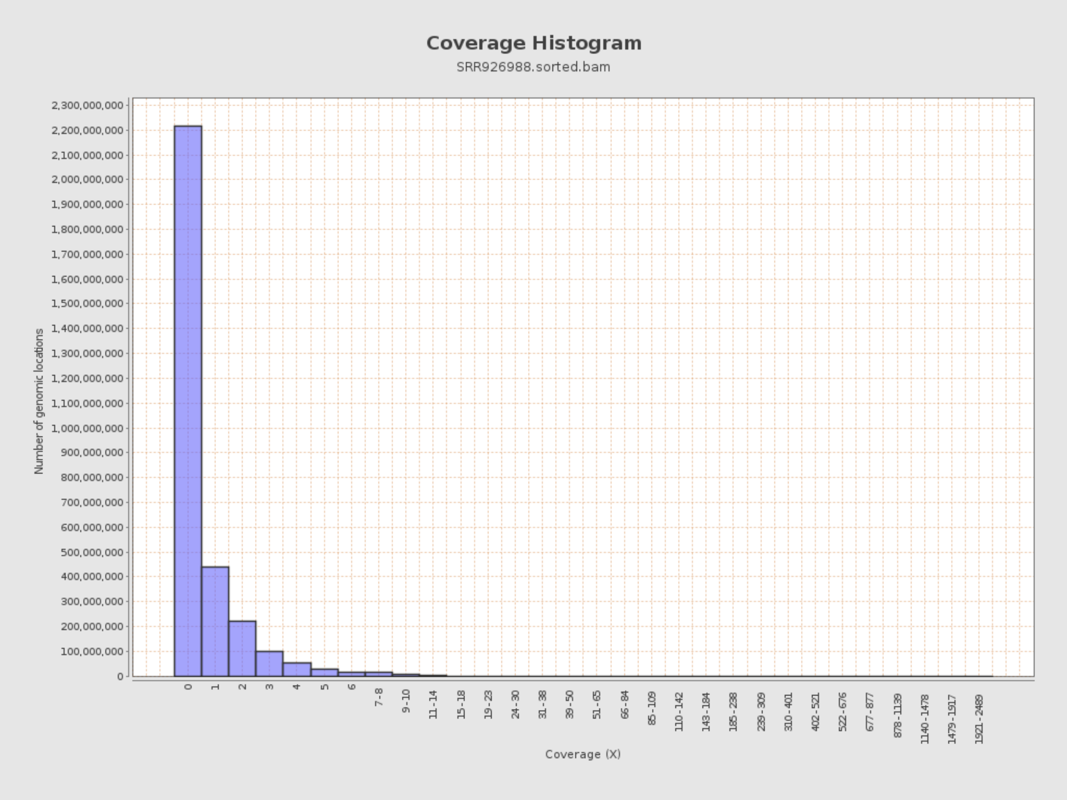
		bases	coverage	deviation
chr1	249250621	148919106	0.5975	2.8737
chr2	243199373	166688196	0.6854	4.0735
chr3	198022430	130177845	0.6574	1.367
chr4	191154276	111284071	0.5822	1.9677
chr5	180915260	112757796	0.6233	1.3189
chr6	171115067	109013703	0.6371	1.6935
chr7	159138663	99979749	0.6283	1.9762
chr8	146364022	96824897	0.6615	1.626
chr9	141213431	80043046	0.5668	3.021
chr10	135534747	91652281	0.6762	3.4497
chr11	135006516	90520128	0.6705	3.184
chr12	133851895	84011394	0.6276	1.6343
chr13	115169878	53830883	0.4674	1.2174
chr14	107349540	54876146	0.5112	1.2427
chr15	102531392	50294523	0.4905	1.2594
chr16	90354753	55970168	0.6194	4.1617
chr17	81195210	45306737	0.558	1.6983
chr18	78077248	50701561	0.6494	3.1459
chr19	59128983	27655107	0.4677	1.8852
chr20	63025520	43031747	0.6828	1.4962
chr21	48129895	22827946	0.4743	1.773
chr22	51304566	22403265	0.4367	1.1939
chrMT	16571	193282	11.6639	10.702
chrX	155270560	110421545	0.7112	1.7649

chrY	59373566	3272236	0.0551	1.7569

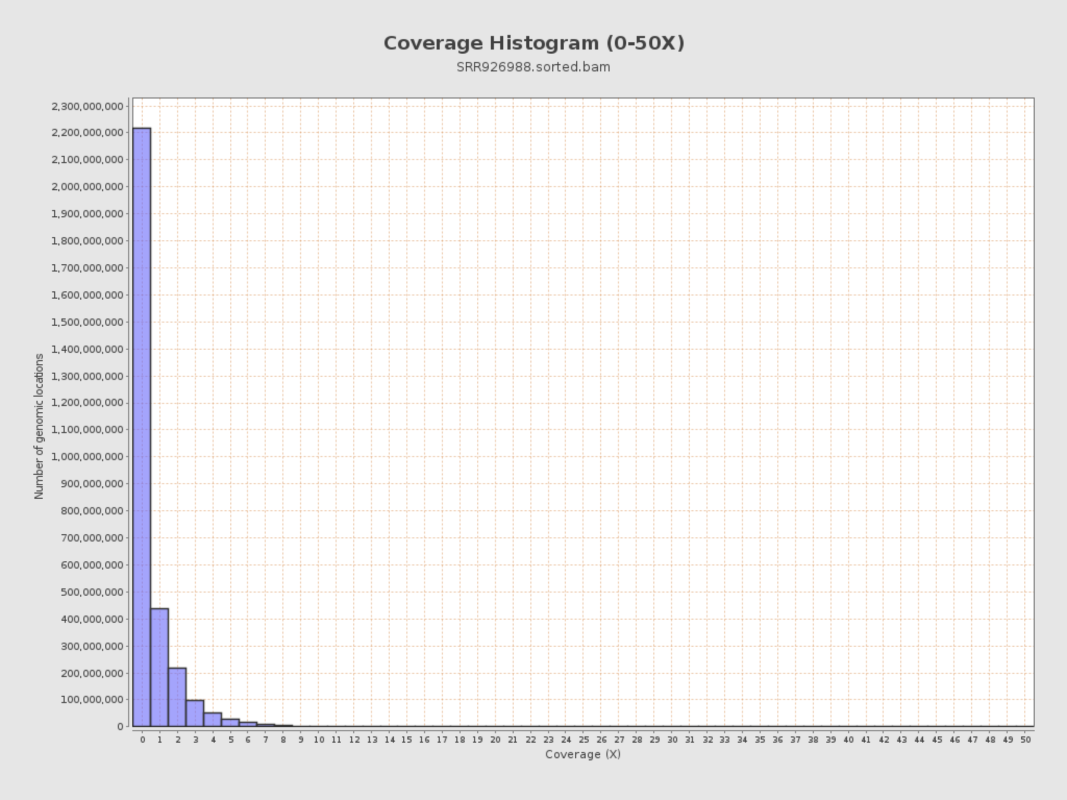
3. Results : Coverage across reference



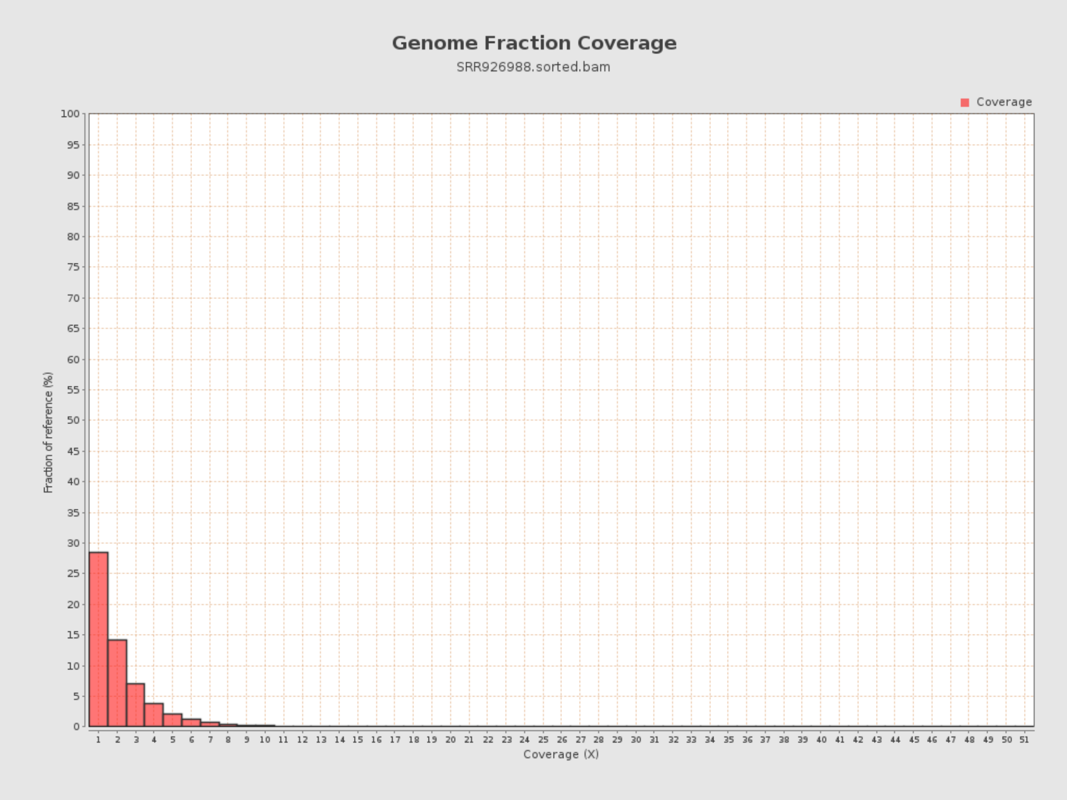
4. Results : Coverage Histogram



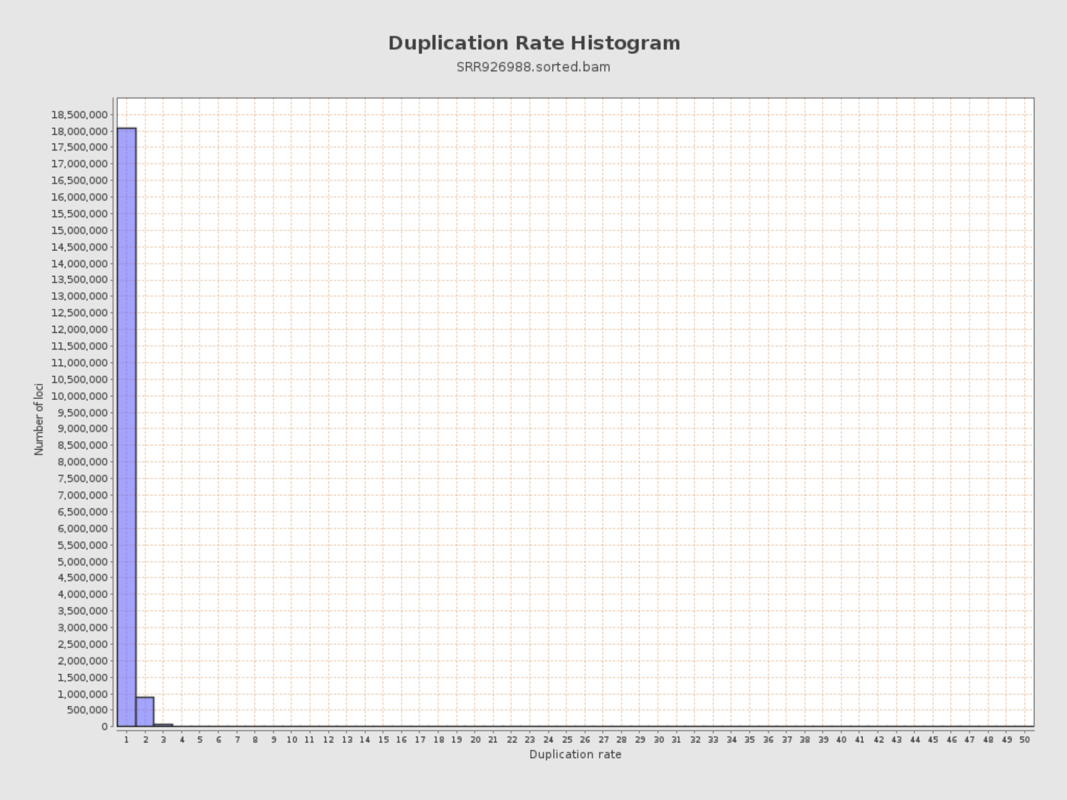
5. Results : Coverage Histogram (0-50X)



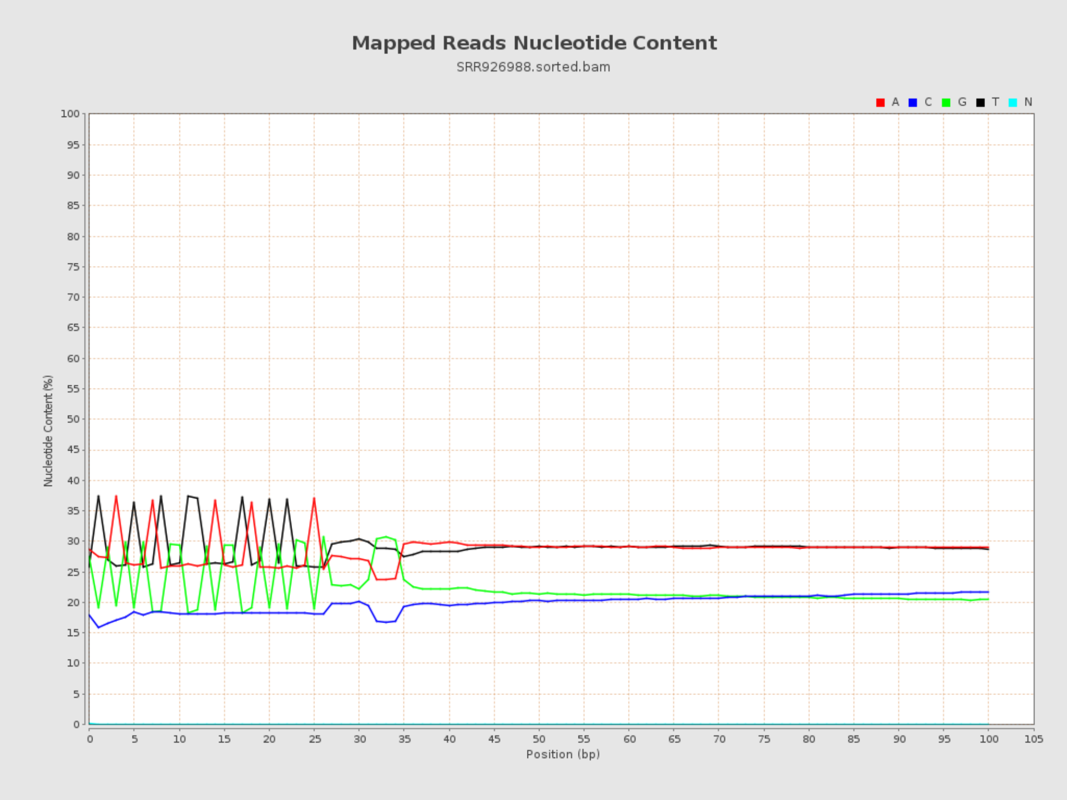
6. Results : Genome Fraction Coverage



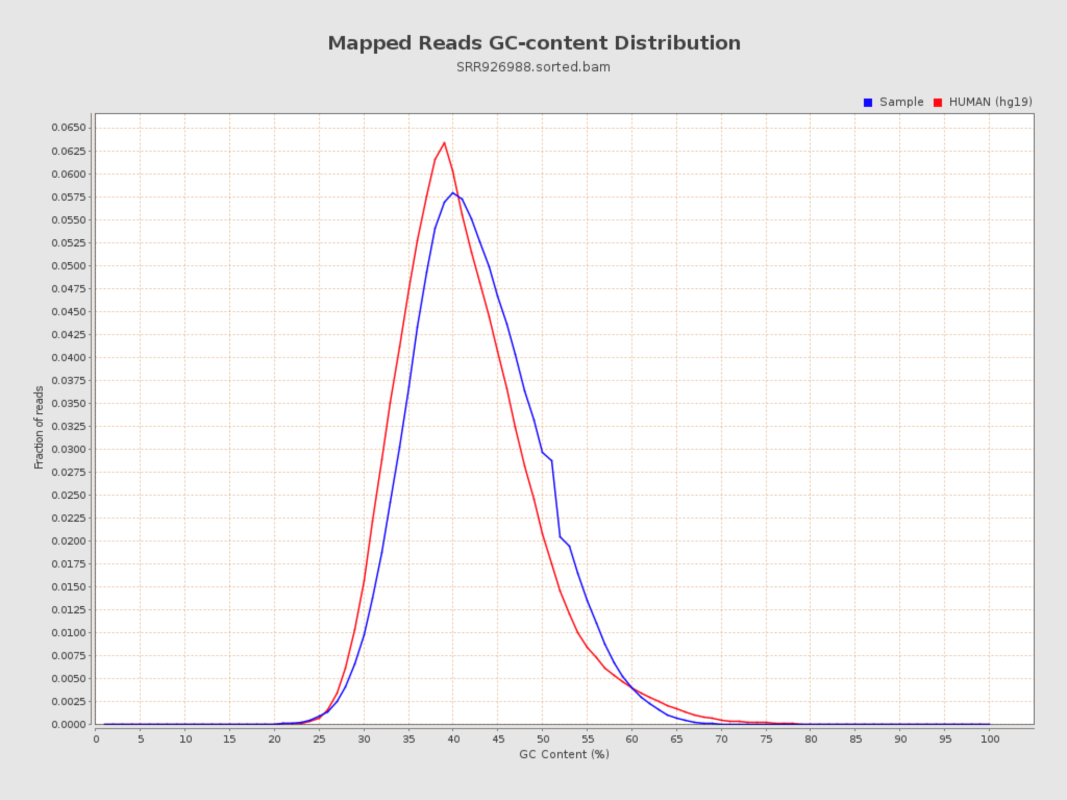
7. Results : Duplication Rate Histogram



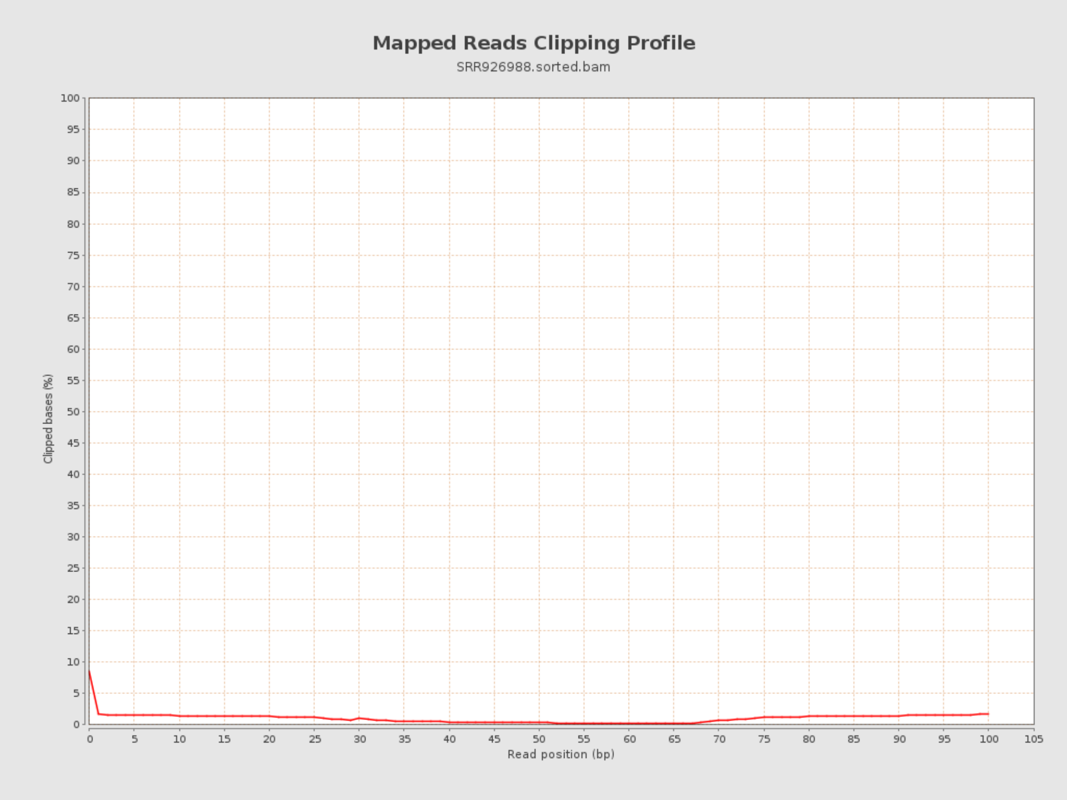
8. Results : Mapped Reads Nucleotide Content



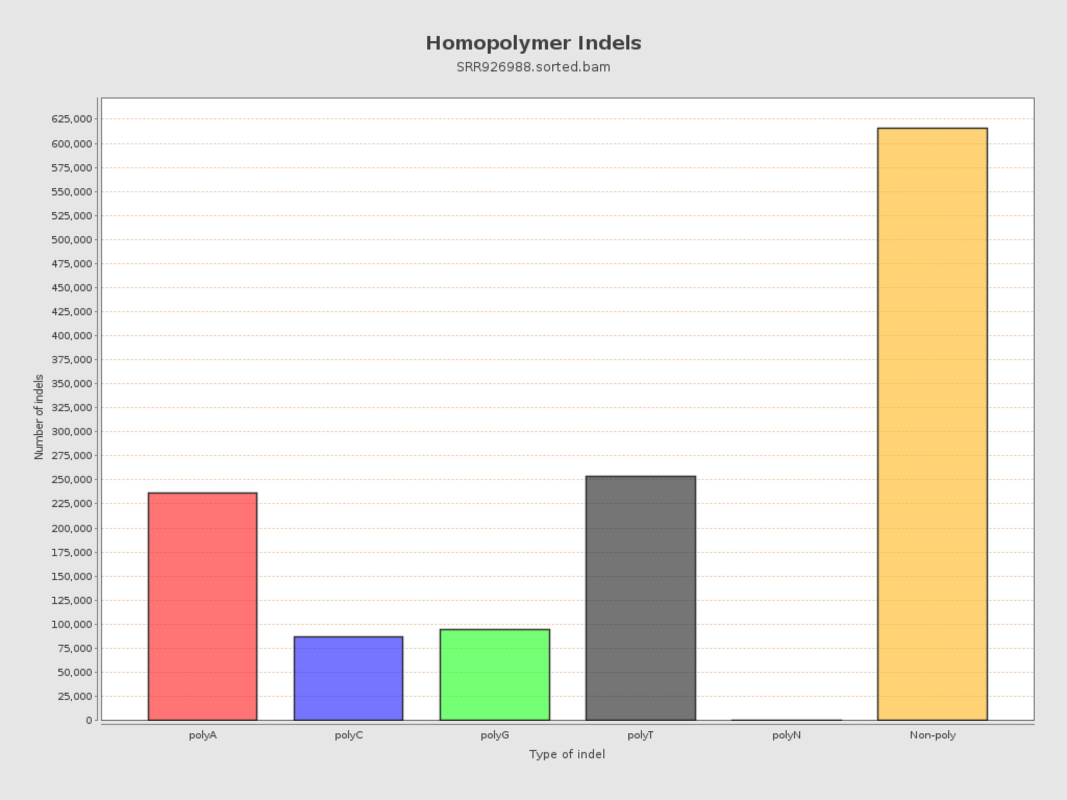
9. Results : Mapped Reads GC-content Distribution



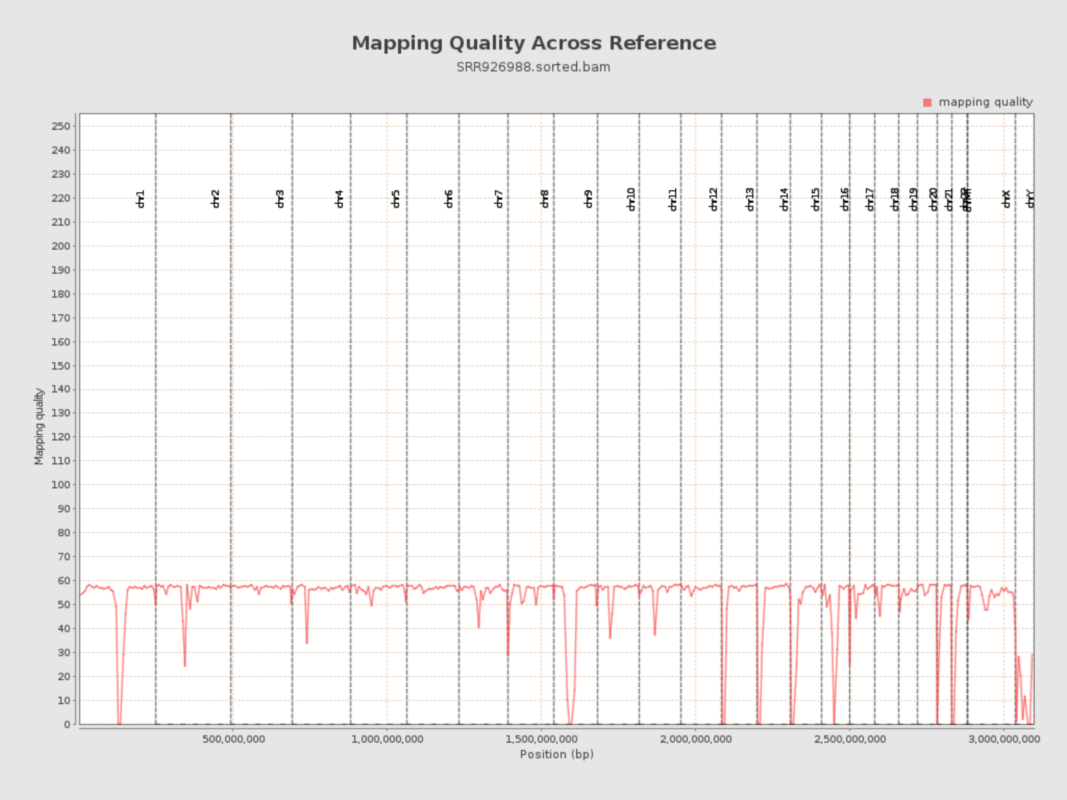
10. Results : Mapped Reads Clipping Profile



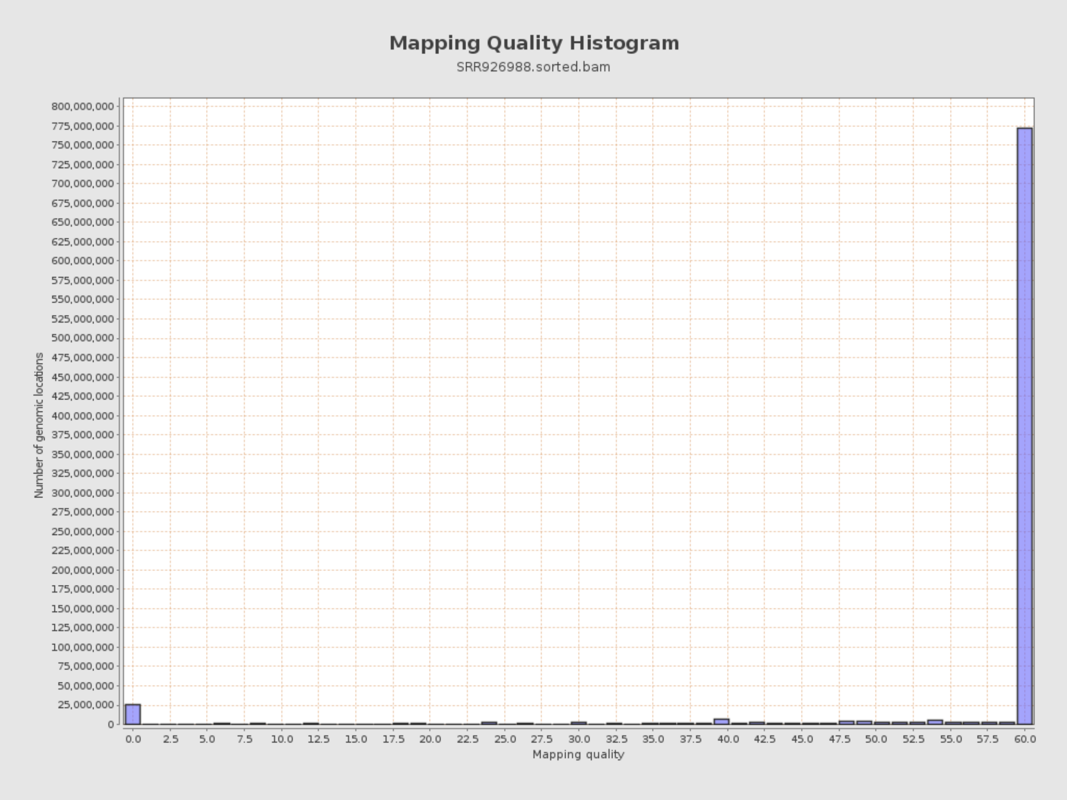
11. Results : Homopolymer Indels



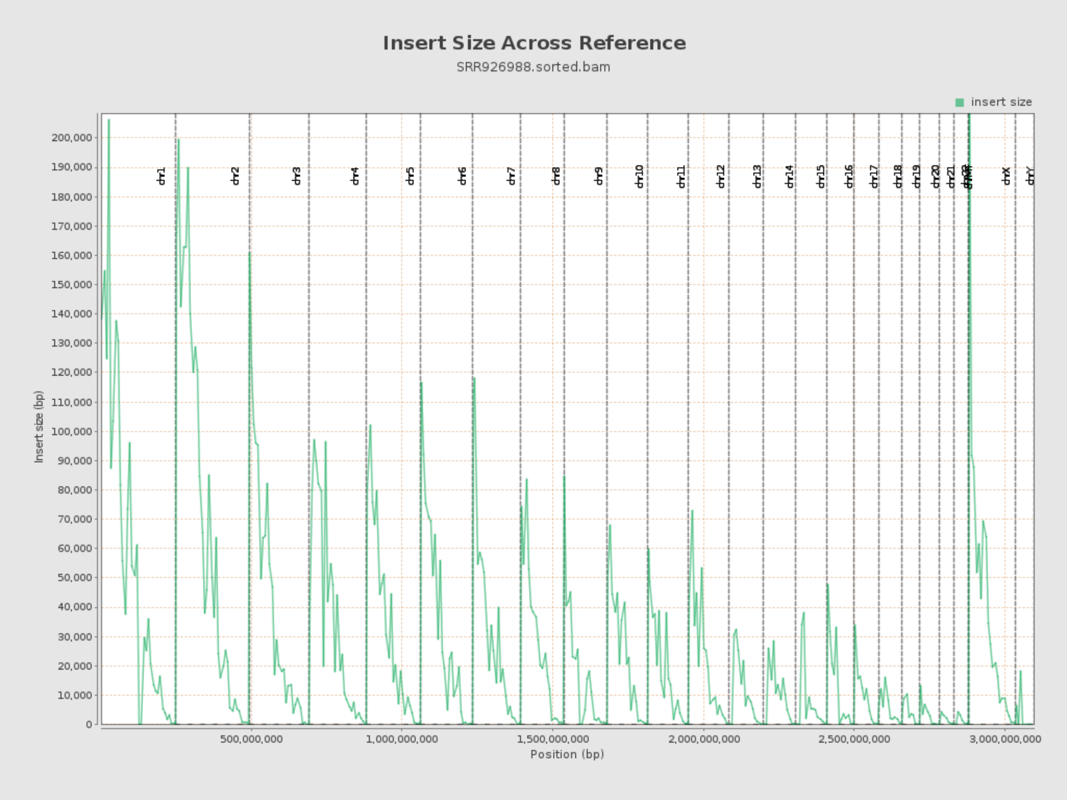
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram