Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 15:20:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927036.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_SRR927036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927036_1.fastq.gz SRR927036_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 15:20:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,891,440
Mapped reads	44,165,811 / 98.38%
Unmapped reads	725,629 / 1.62%
Mapped paired reads	44,165,811 / 98.38%
Mapped reads, first in pair	22,211,093 / 49.48%
Mapped reads, second in pair	21,954,718 / 48.91%
Mapped reads, both in pair	43,738,550 / 97.43%
Mapped reads, singletons	427,261 / 0.95%
Secondary alignments	0
Supplementary alignments	254,624 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	3,746,397 / 8.35%
Duplication rate	6.5%
Clipped reads	10,314,649 / 22.98%

2.2. ACGT Content

Number/percentage of A's	1,224,726,006 / 29.24%
Number/percentage of C's	818,925,359 / 19.55%
Number/percentage of T's	1,238,376,628 / 29.57%
Number/percentage of G's	905,509,034 / 21.62%
Number/percentage of N's	678,162 / 0.02%

GC Percentage	41.17%

2.3. Coverage

Mean	1.3539
Standard Deviation	5.6014

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	69,575.66
Standard Deviation	2,587,299.2
P25/Median/P75	149 / 189 / 251

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	45,823,885
Insertions	678,976
Mapped reads with at least one insertion	1.51%
Deletions	2,251,636
Mapped reads with at least one deletion	4.96%
Homopolymer indels	53.21%

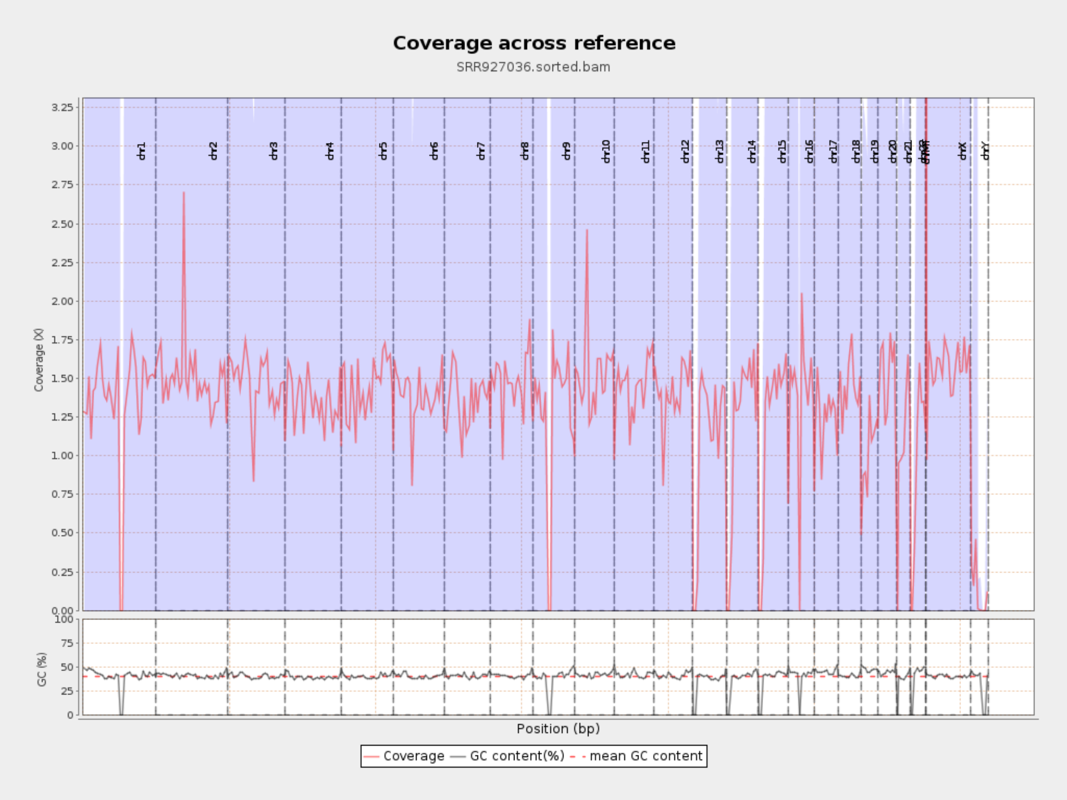
2.7. Chromosome stats

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

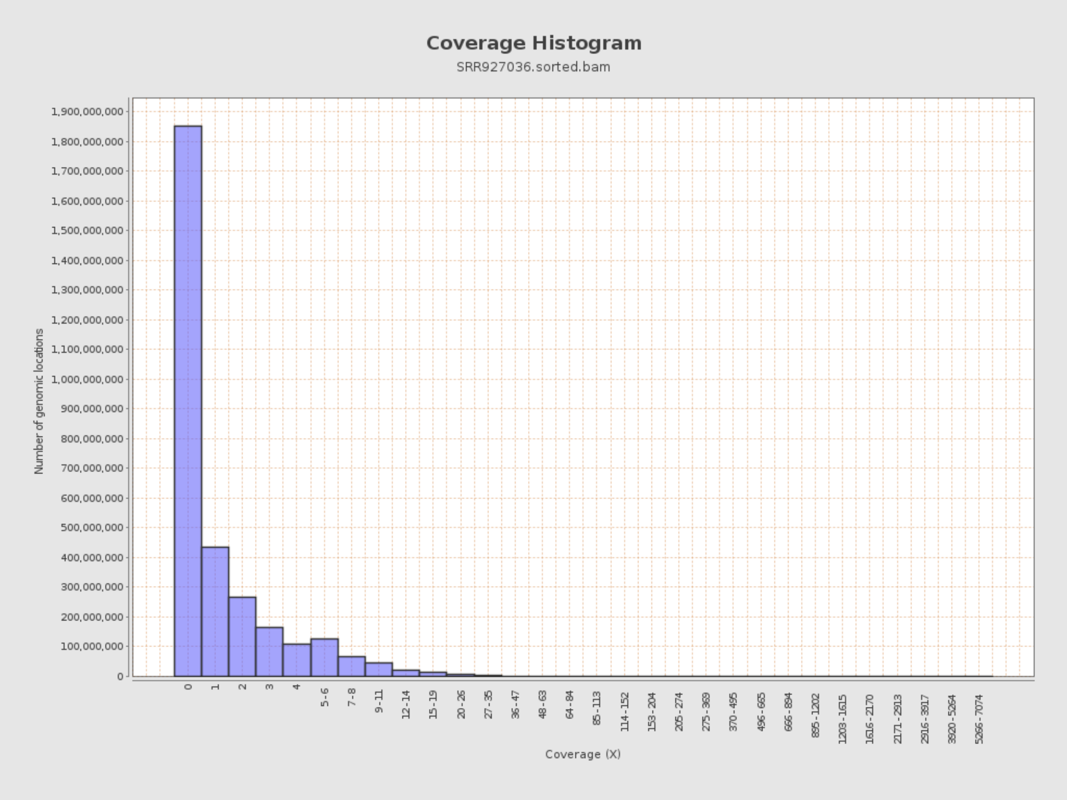
		bases	coverage	deviation
chr1	249250621	341256059	1.3691	7.934
chr2	243199373	367977582	1.5131	8.7791
chr3	198022430	289817390	1.4636	2.7653
chr4	191154276	260597491	1.3633	4.2001
chr5	180915260	261724036	1.4467	2.6992
chr6	171115067	238044598	1.3911	2.7124
chr7	159138663	215658904	1.3552	3.8059
chr8	146364022	216725332	1.4807	3.4248
chr9	141213431	181240347	1.2834	7.5913
chr10	135534747	206988549	1.5272	12.054
chr11	135006516	195674591	1.4494	4.8698
chr12	133851895	189749955	1.4176	2.7276
chr13	115169878	126589971	1.0992	2.3581
chr14	107349540	129187710	1.2034	2.6424
chr15	102531392	121241247	1.1825	2.5597
chr16	90354753	123324647	1.3649	6.7066
chr17	81195210	103040457	1.269	4.4083
chr18	78077248	112737525	1.4439	7.8377
chr19	59128983	60724363	1.027	4.3103
chr20	63025520	96752033	1.5351	3.1497
chr21	48129895	52525144	1.0913	3.5886
chr22	51304566	47881982	0.9333	2.3835
chrMT	16571	334192	20.1673	16.061
chrX	155270560	244165815	1.5725	3.6237

chrY	59373566	7392328	0.1245	5.5767

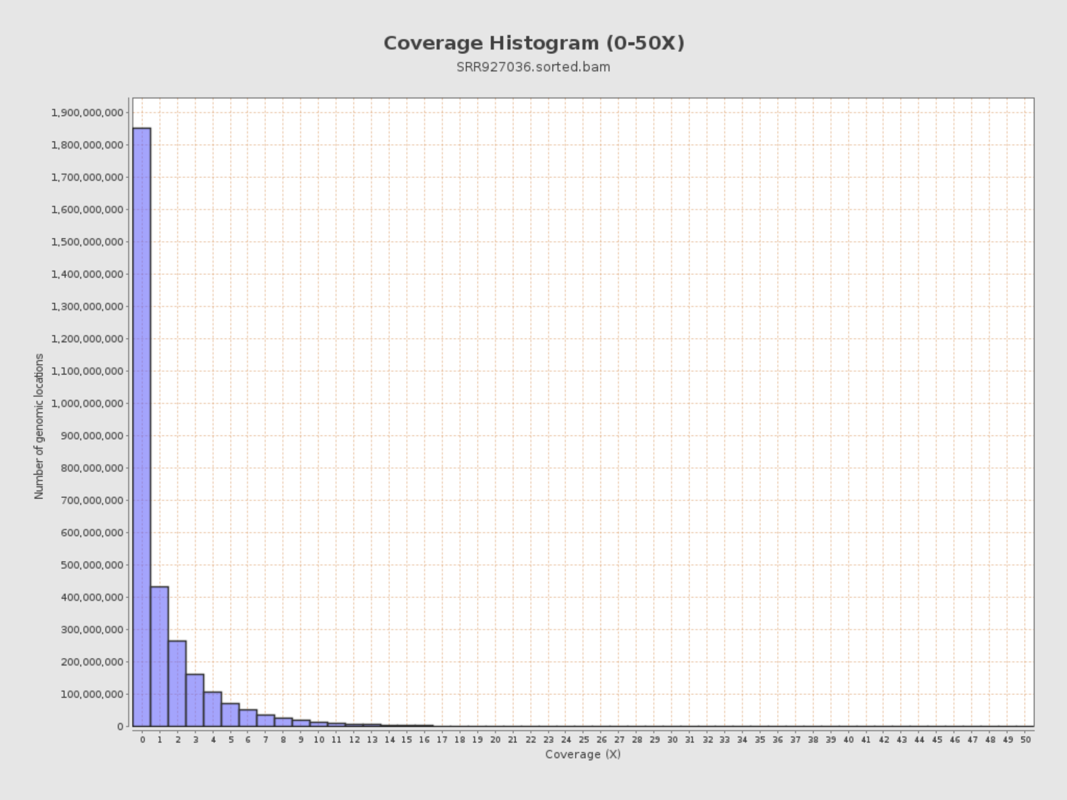
3. Results : Coverage across reference



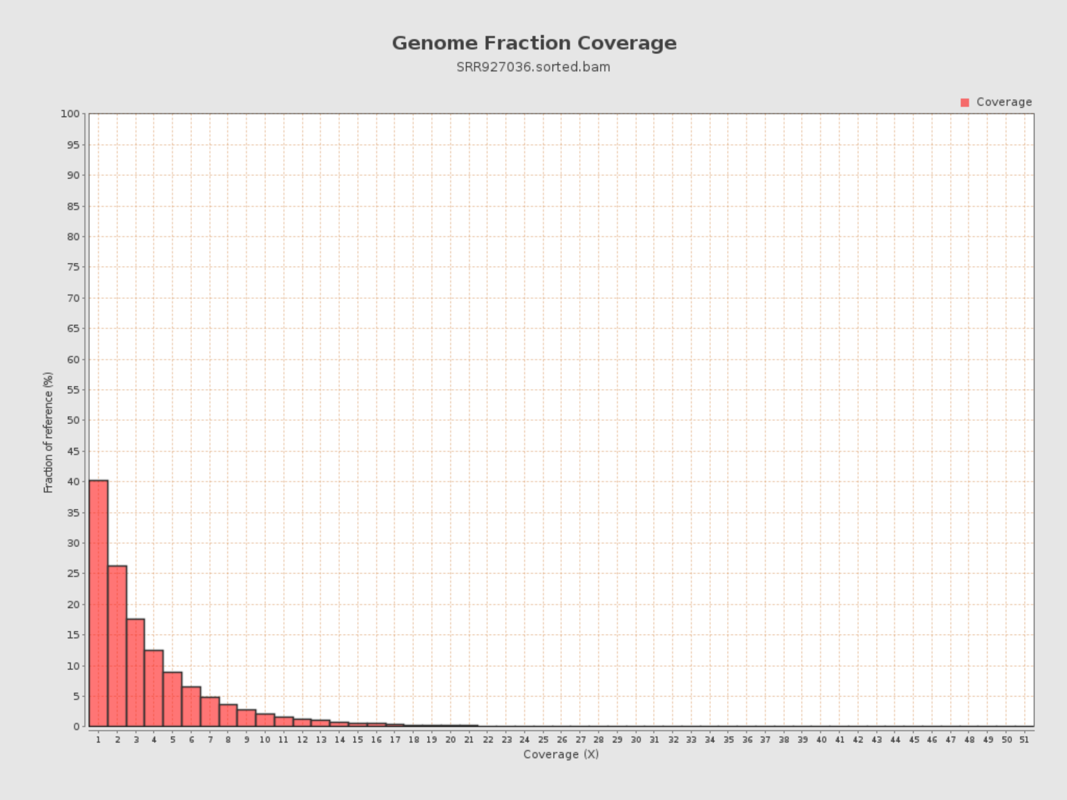
4. Results : Coverage Histogram



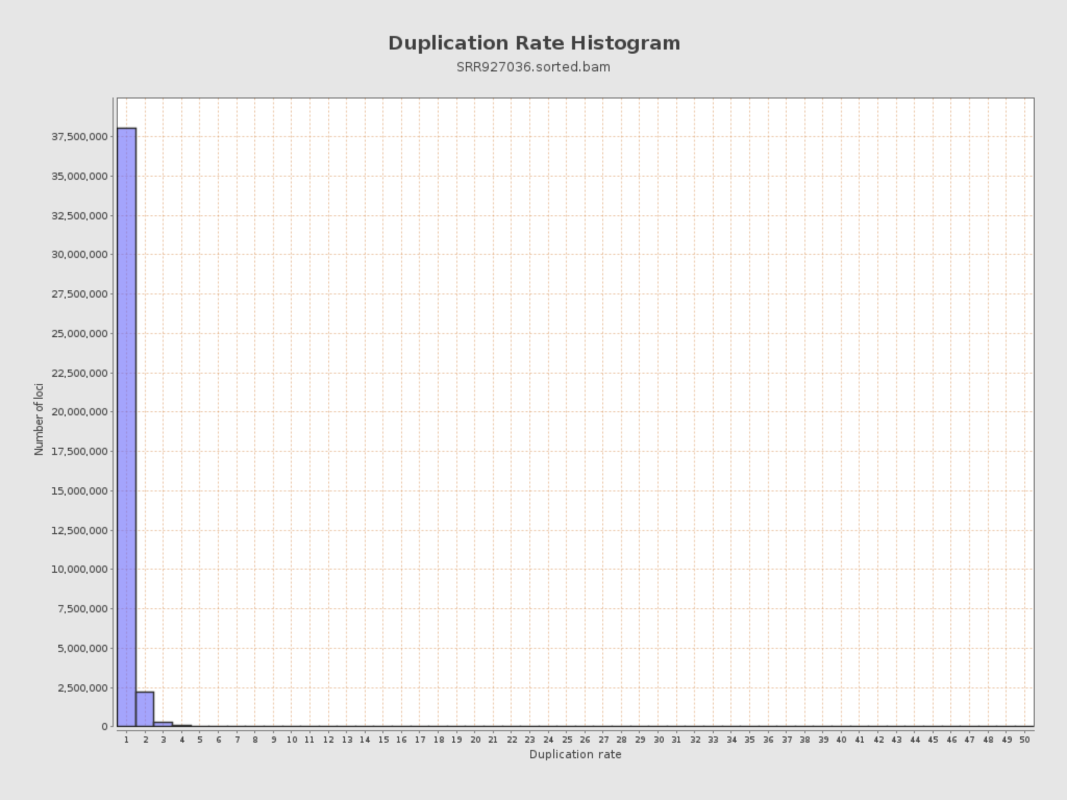
5. Results : Coverage Histogram (0-50X)



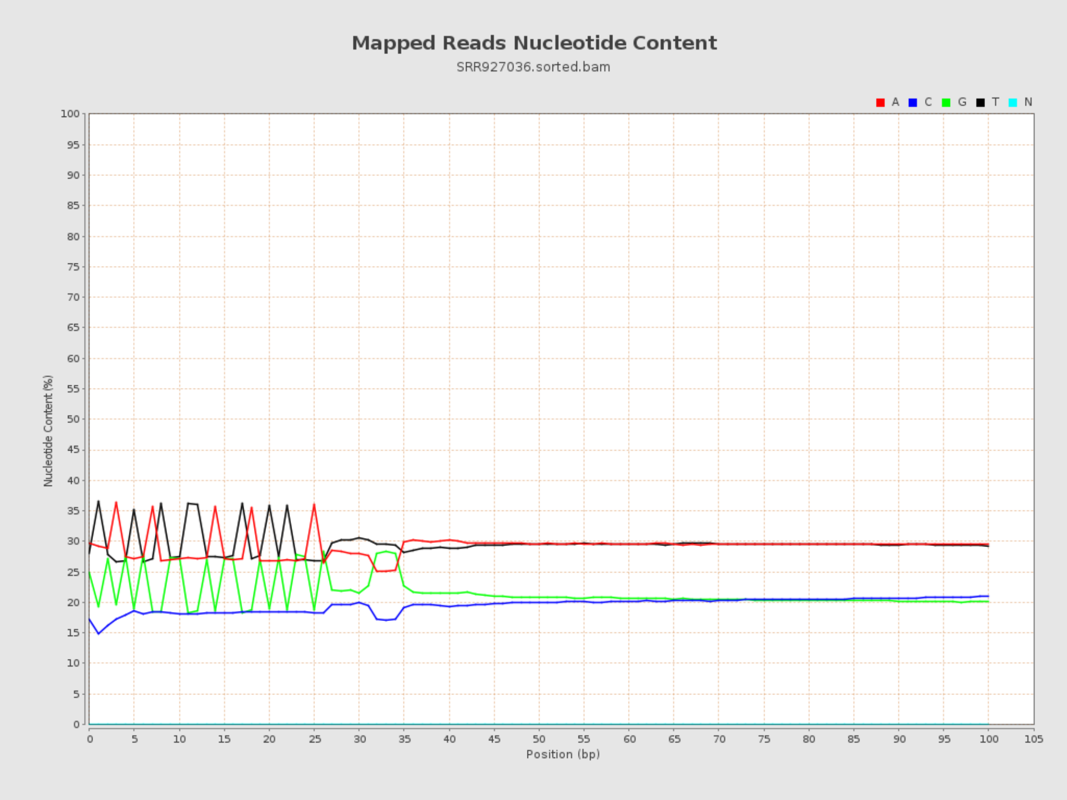
6. Results : Genome Fraction Coverage



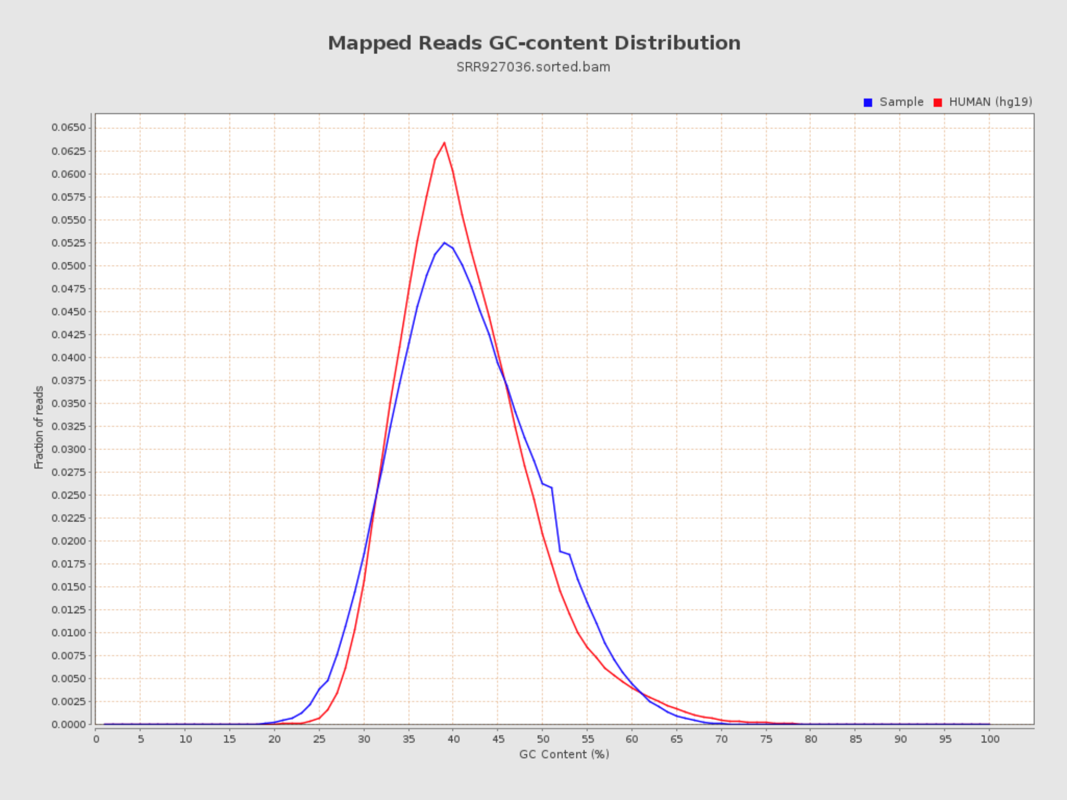
7. Results : Duplication Rate Histogram



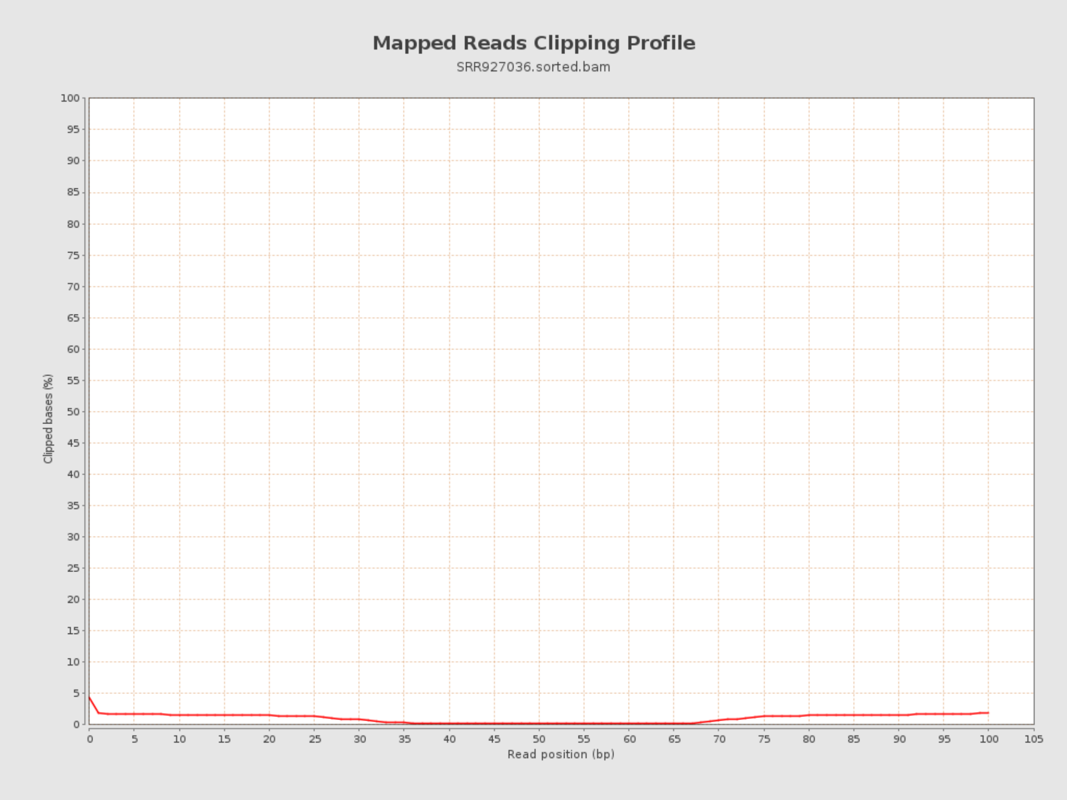
8. Results : Mapped Reads Nucleotide Content



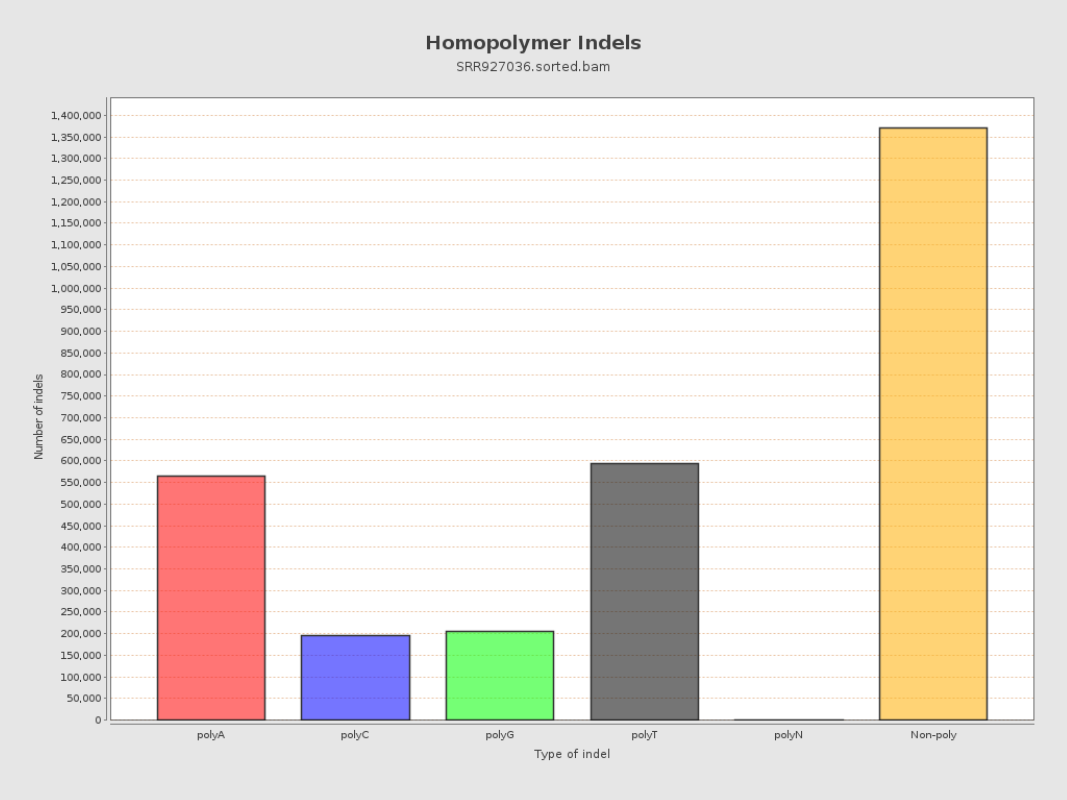
9. Results : Mapped Reads GC-content Distribution



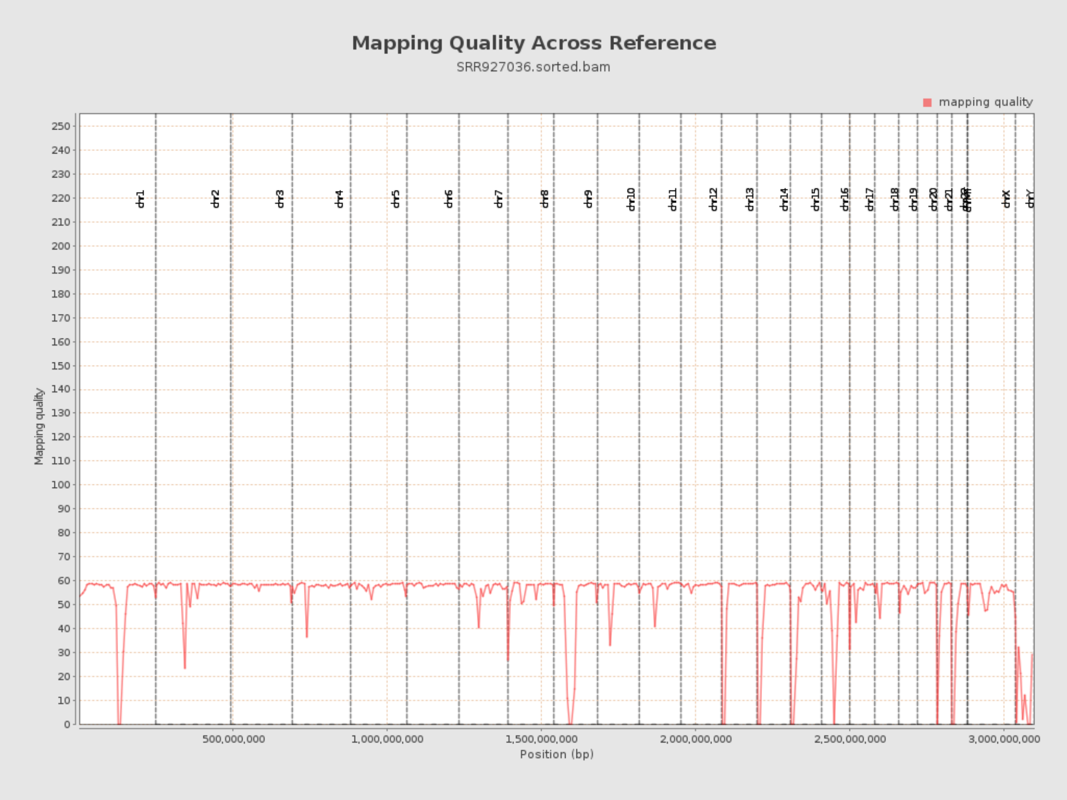
10. Results : Mapped Reads Clipping Profile



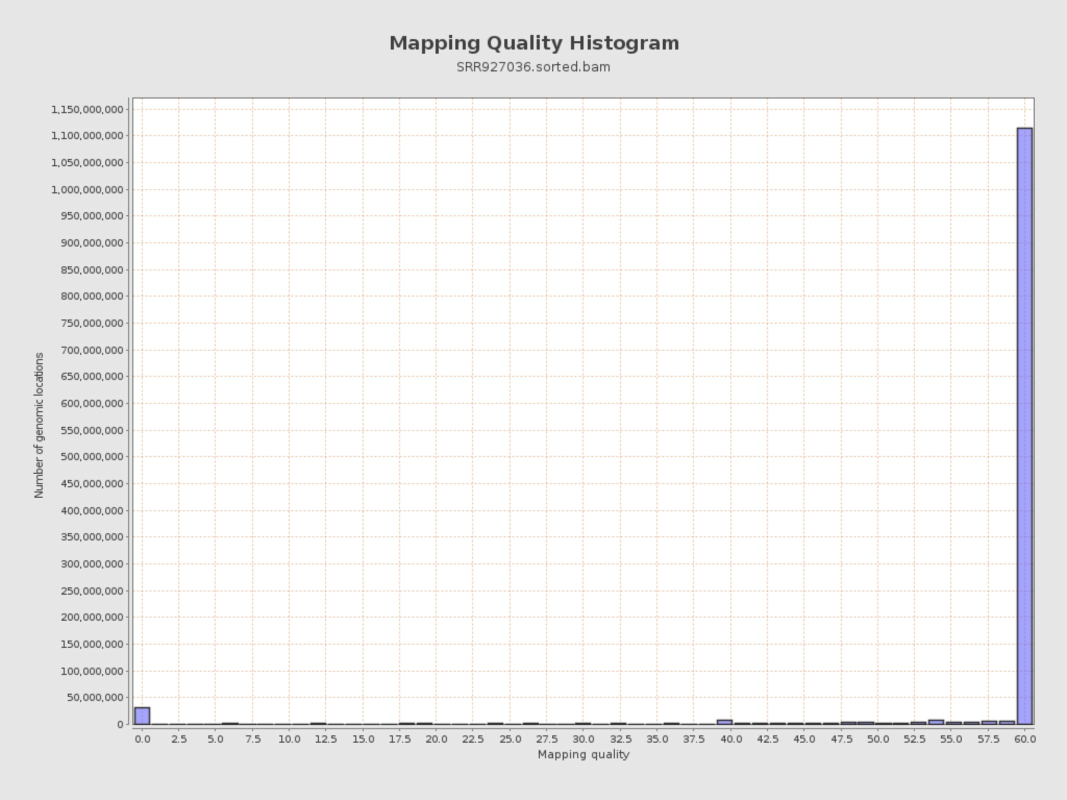
11. Results : Homopolymer Indels



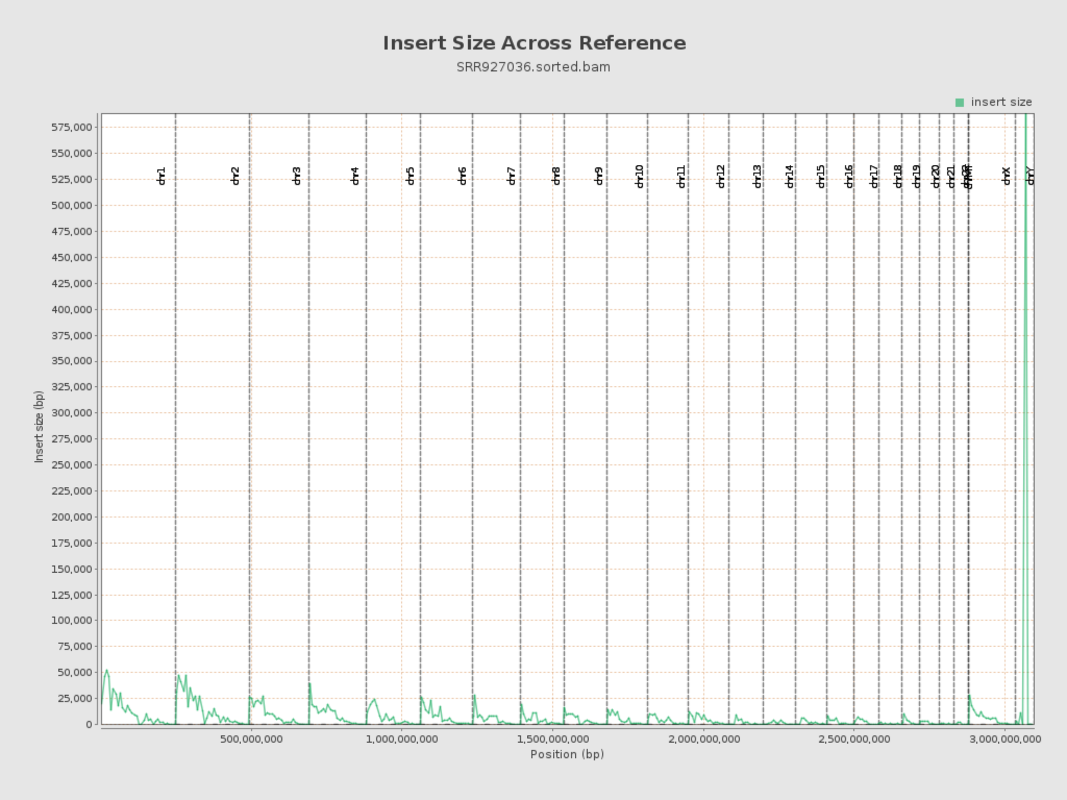
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram