

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 18:52:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620538.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR620538.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 18:52:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620538.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,501,626
Mapped reads	6,847,362 / 44.17%
Unmapped reads	8,654,264 / 55.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	219 / 0%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	688,925 / 4.44%
Duplication rate	4.99%
Clipped reads	1,588,325 / 10.25%

2.2. ACGT Content

Number/percentage of A's	78,736,184 / 25.13%
Number/percentage of C's	65,665,907 / 20.96%
Number/percentage of T's	92,084,175 / 29.39%
Number/percentage of G's	76,765,967 / 24.5%
Number/percentage of N's	36,035 / 0.01%
GC Percentage	45.46%

2.3. Coverage

Mean	0.1012

Standard Deviation	1.1474
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2.4. Mapping Quality

Mean Mapping Quality	39.02
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2.5. Mismatches and indels

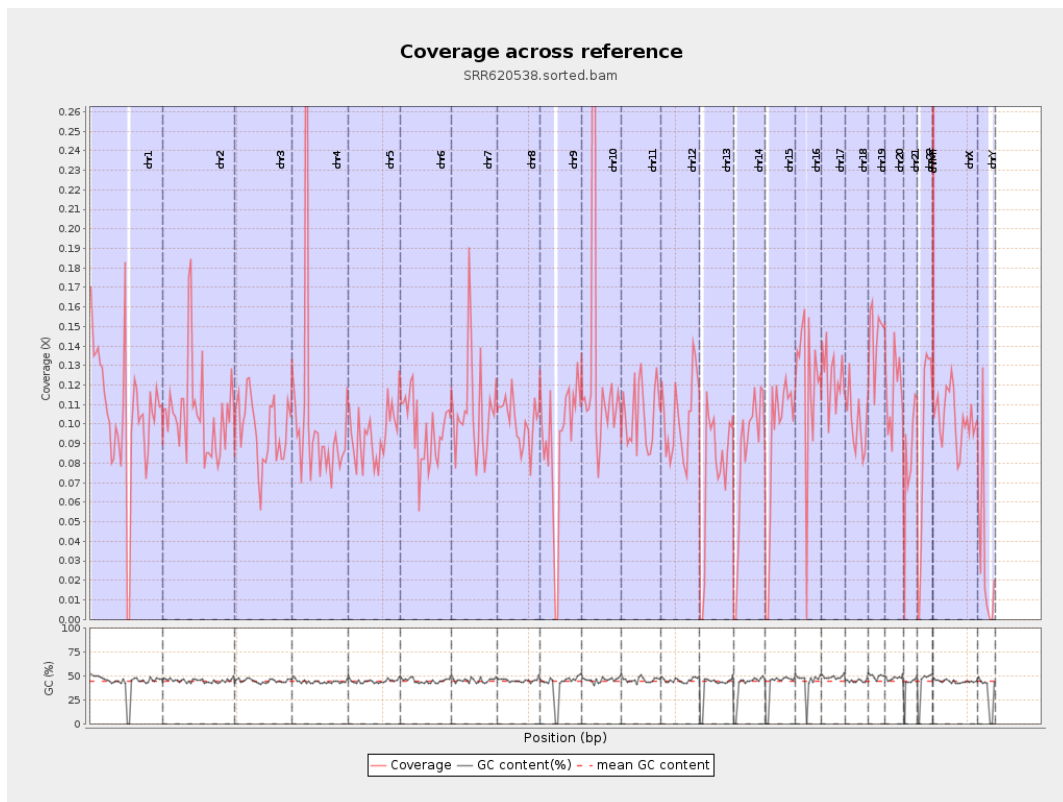
General error rate	0.73%
Mismatches	2,243,916
Insertions	19,213
Mapped reads with at least one insertion	0.28%
Deletions	45,131
Mapped reads with at least one deletion	0.65%
Homopolymer indels	40.68%

2.6. Chromosome stats

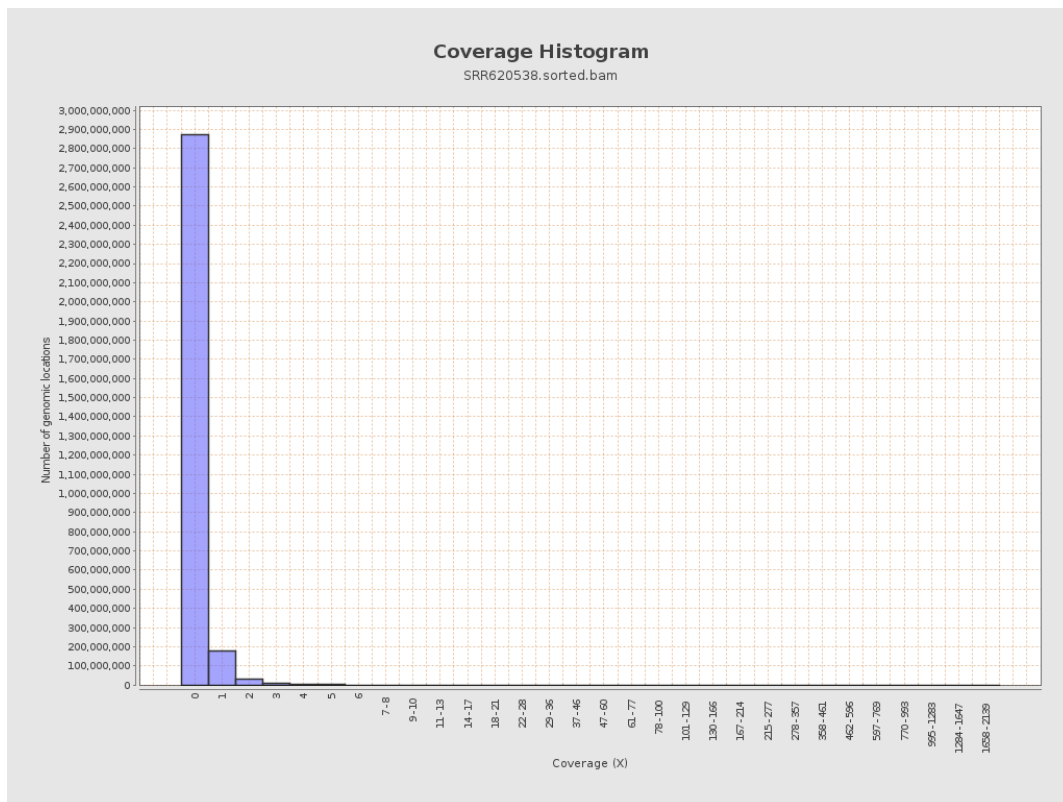
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26096020	0.1047	1.8043
chr2	243199373	25722947	0.1058	1.4034
chr3	198022430	19194691	0.0969	0.5589
chr4	191154276	19919846	0.1042	1.3123
chr5	180915260	17244415	0.0953	0.5043
chr6	171115067	16557620	0.0968	0.6708
chr7	159138663	17132157	0.1077	1.2165

chr8	146364022	14816765	0.1012	0.7825
chr9	141213431	12787974	0.0906	0.7094
chr10	135534747	17468422	0.1289	2.7046
chr11	135006516	14074238	0.1042	0.9765
chr12	133851895	13890229	0.1038	0.5757
chr13	115169878	8757490	0.076	0.5553
chr14	107349540	9096409	0.0847	0.5876
chr15	102531392	9308529	0.0908	0.5718
chr16	90354753	10850204	0.1201	0.8309
chr17	81195210	10136039	0.1248	0.7381
chr18	78077248	7826235	0.1002	1.4662
chr19	59128983	8591344	0.1453	1.3871
chr20	63025520	7289731	0.1157	0.7134
chr21	48129895	4094572	0.0851	0.8304
chr22	51304566	4642999	0.0905	0.5676
chrMT	16571	60906	3.6755	3.535
chrX	155270560	15987638	0.103	0.69
chrY	59373566	1811359	0.0305	0.9986

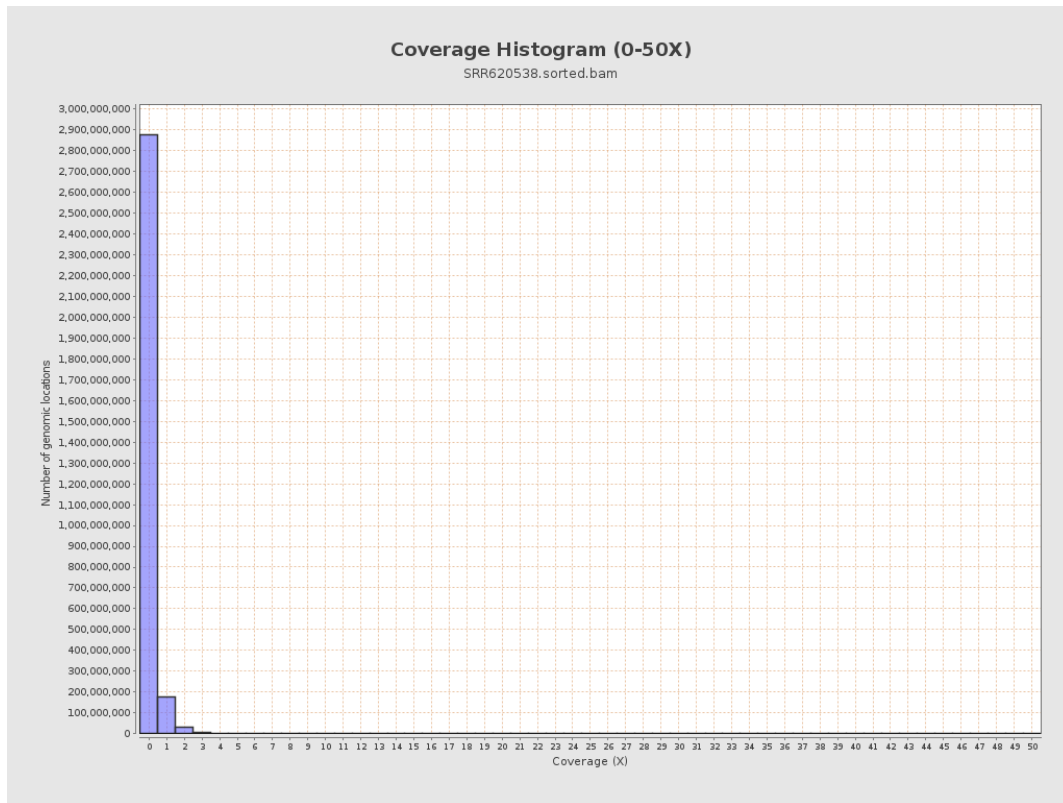
3. Results : Coverage across reference



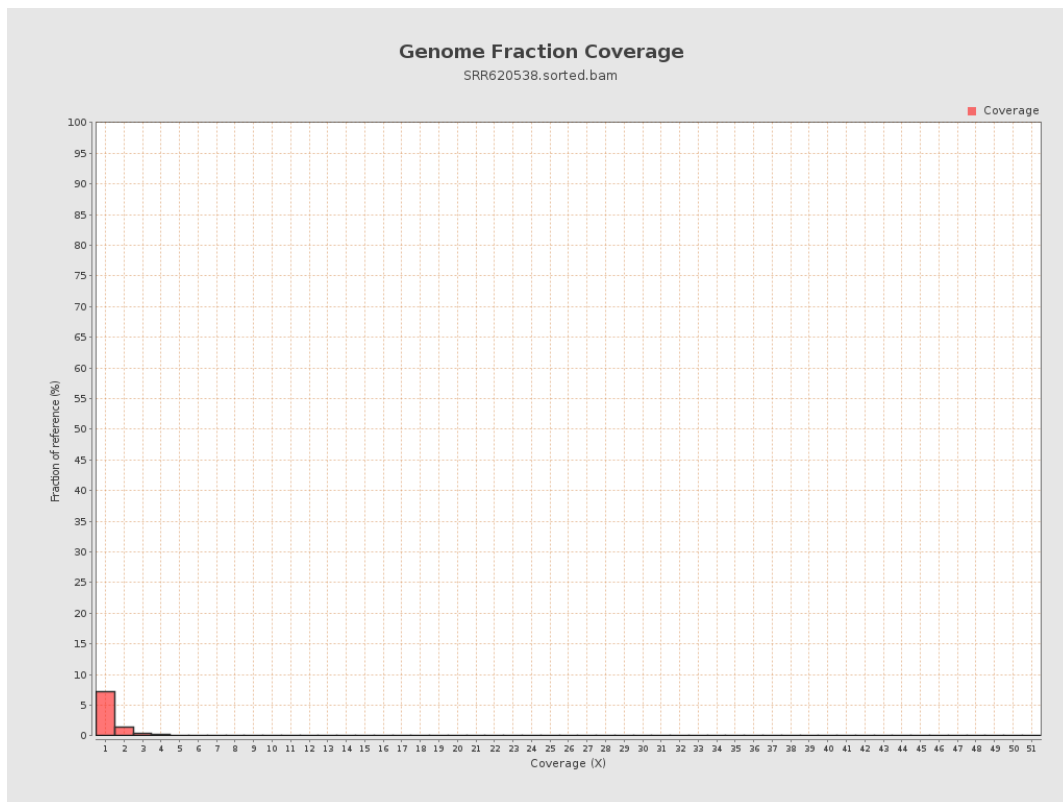
4. Results : Coverage Histogram



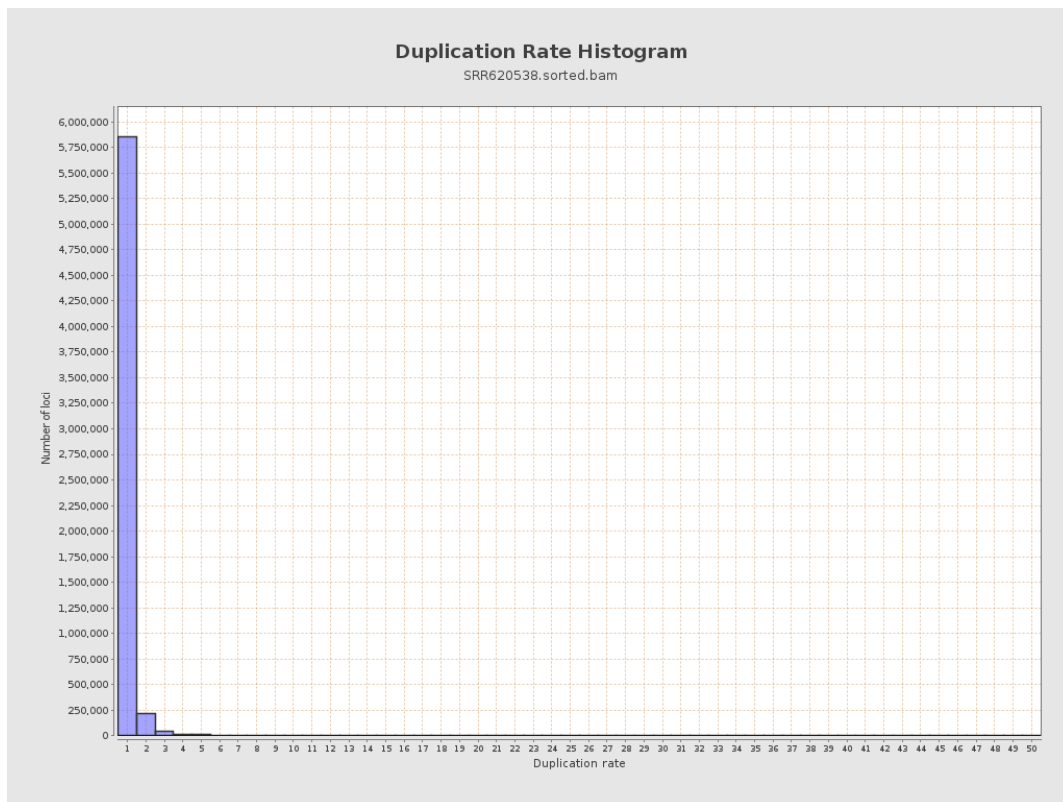
5. Results : Coverage Histogram (0-50X)



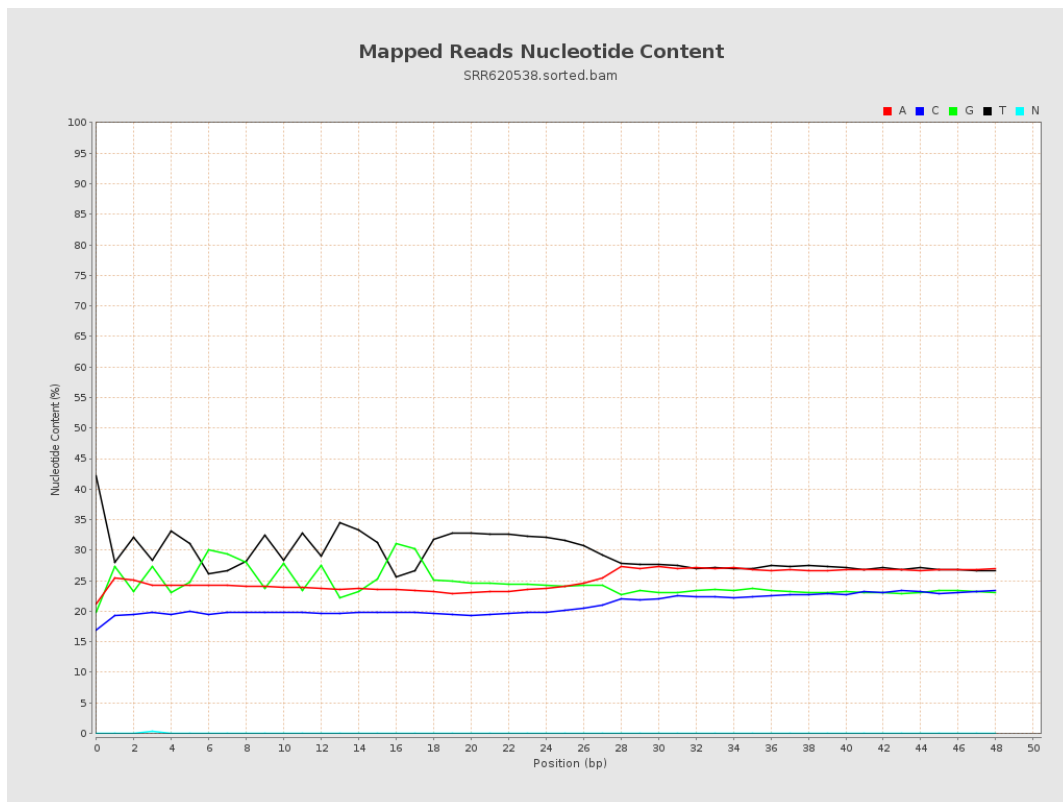
6. Results : Genome Fraction Coverage



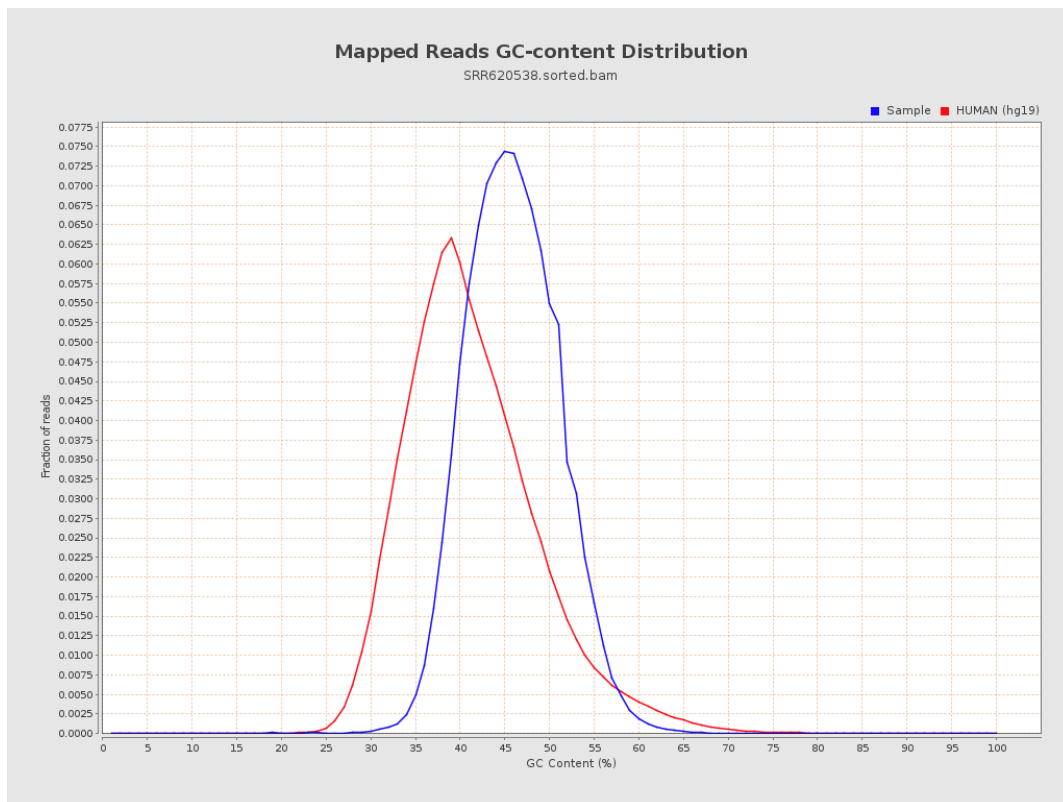
7. Results : Duplication Rate Histogram



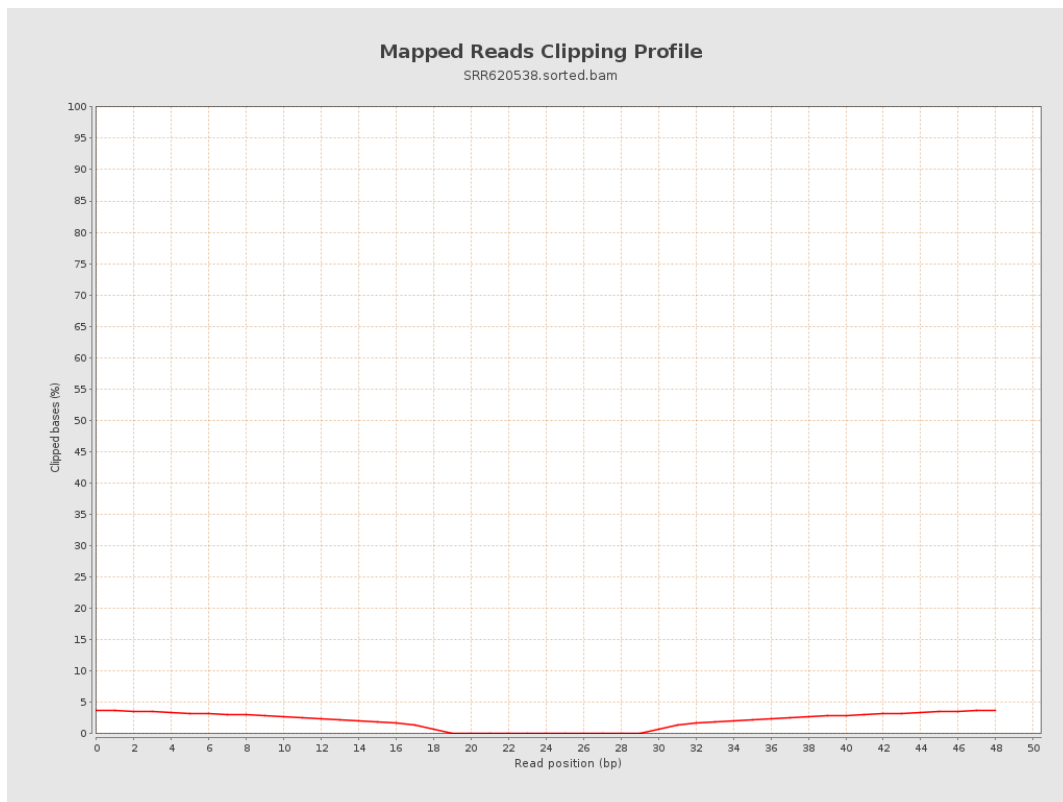
8. Results : Mapped Reads Nucleotide Content



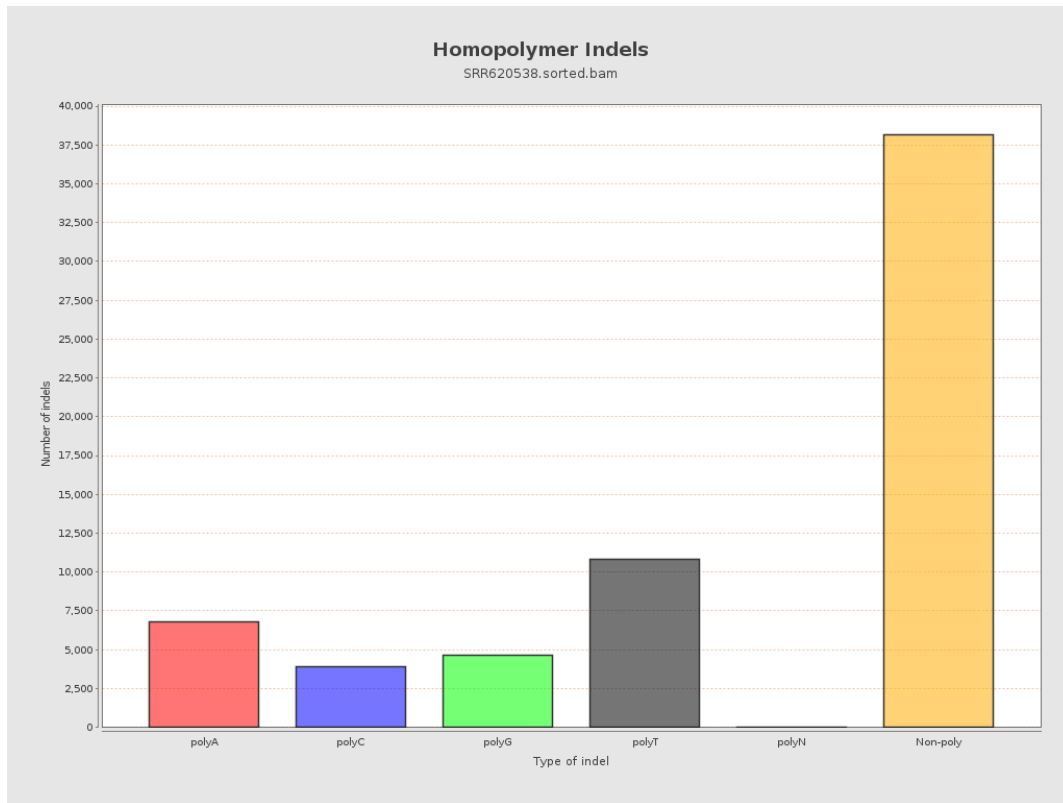
9. Results : Mapped Reads GC-content Distribution



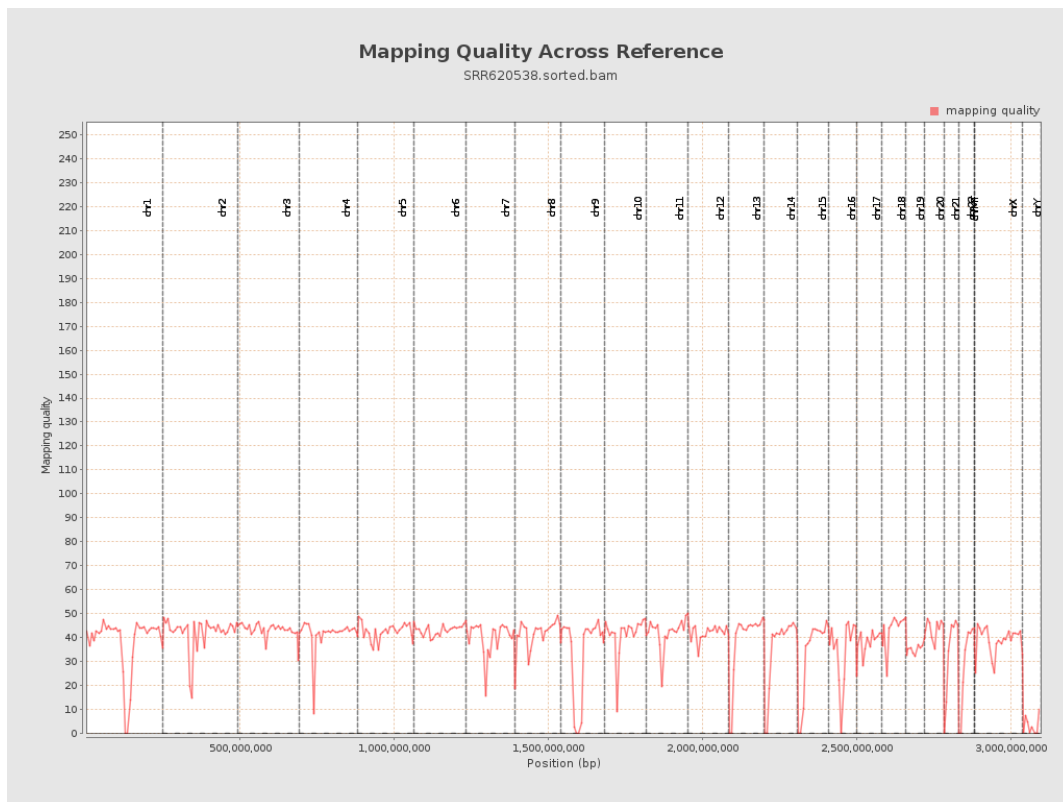
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

