Cowpea - MNPs Analysis

Original Data Extracted from VCF File

In [1]:
```
from VCFtoTable import *
from GTtable import *
from GTplots import *
from GTplot import *
from BarPlots import *
from CTbarPlots import *
from variant_hist import*
from stats import *
from FilterVCF import *
from GTfilter import*
```

In [2]:
```
vcf_cowpea = '/home/anibal/genome_files/freebayes~bwa~GCF_004118075.1_ASM411807v
```

In [3]:
```
samples_all, vcf_df, chrom_len = VCFtoTable(vcf_cowpea)
```

In [4]:
```
samples_all
```

Out[4]:
```
array(['CBC1_P1', 'CBC5_A1'], dtype=object)
```

In [5]:
```
progenitor = 'CBC1_P1'
mutant = 'CBC5_A1'
samples = [progenitor, mutant]
samples
```

Out[5]:
```
['CBC1_P1', 'CBC5_A1']
```

In [6]:
```
vcf_df
```

Out[6]:

	CHROM	POS	REF	
0	NC_018051.1	11786	T	
1	NC_018051.1	11801	TCTTCCT	
2	NC_018051.1	11813	AGCC	
3	NC_018051.1	11825	GGTAGGTAAT	A(
4	NC_018051.1	18327	G	
...	...	...	...	
1968687	NC_040289.1	41659114	T	
1968688	NC_040289.1	41659137	G	
1968689	NC_040289.1	41667130	GTTTCA	
1968690	NC_040289.1	41667148	T	

	CHROM	POS	REF
1968691	NC_040289.1	41668013	CAGGGTTTAGGGTTTAGGGTTCAGGGTTTAGGGTTTAGGGTTCAGG...

1968692 rows × 14 columns

In [7]:
```
chrom_len
```

Out[7]:

	LEN
CHROM	
NC_040279.1	42129361
NC_040280.1	33908088
NC_040281.1	65292630
NC_040282.1	42731077
NC_040283.1	48746289
NC_040284.1	34463471
NC_040285.1	40876636
NC_040286.1	38363498
NC_040287.1	43933251
NC_040288.1	41327797
NC_040289.1	41684185
NC_018051.1	152415

PART 0: Raw

Contingency Table - RAW - All Chromosomes - (No 0/0, 0/1, 1/1 Filtered)

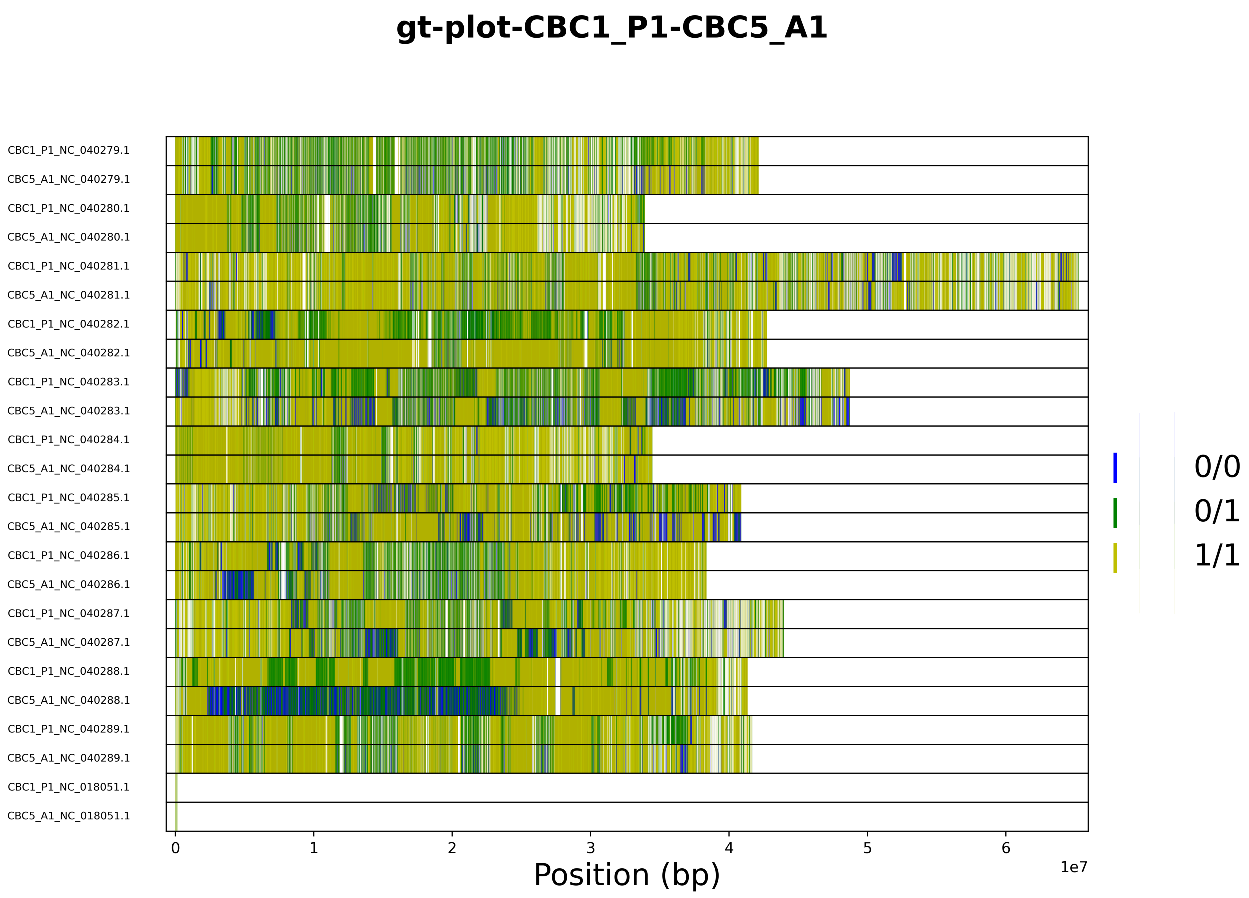
In [8]:
```
contingency_table_0 = contingency_table(samples, vcf_df, 'all')
```

```
Contingency Table - Chromosome all

                 CBC5_A1_GT
                        0/0     0/1     1/1  other
CBC1_P1_GT 0/0            0   52496  132507  45048
           0/1       287090  273476  178974  45048
           1/1       211458   19728  767915  45048
           other      45048   45048   45048  45048
```

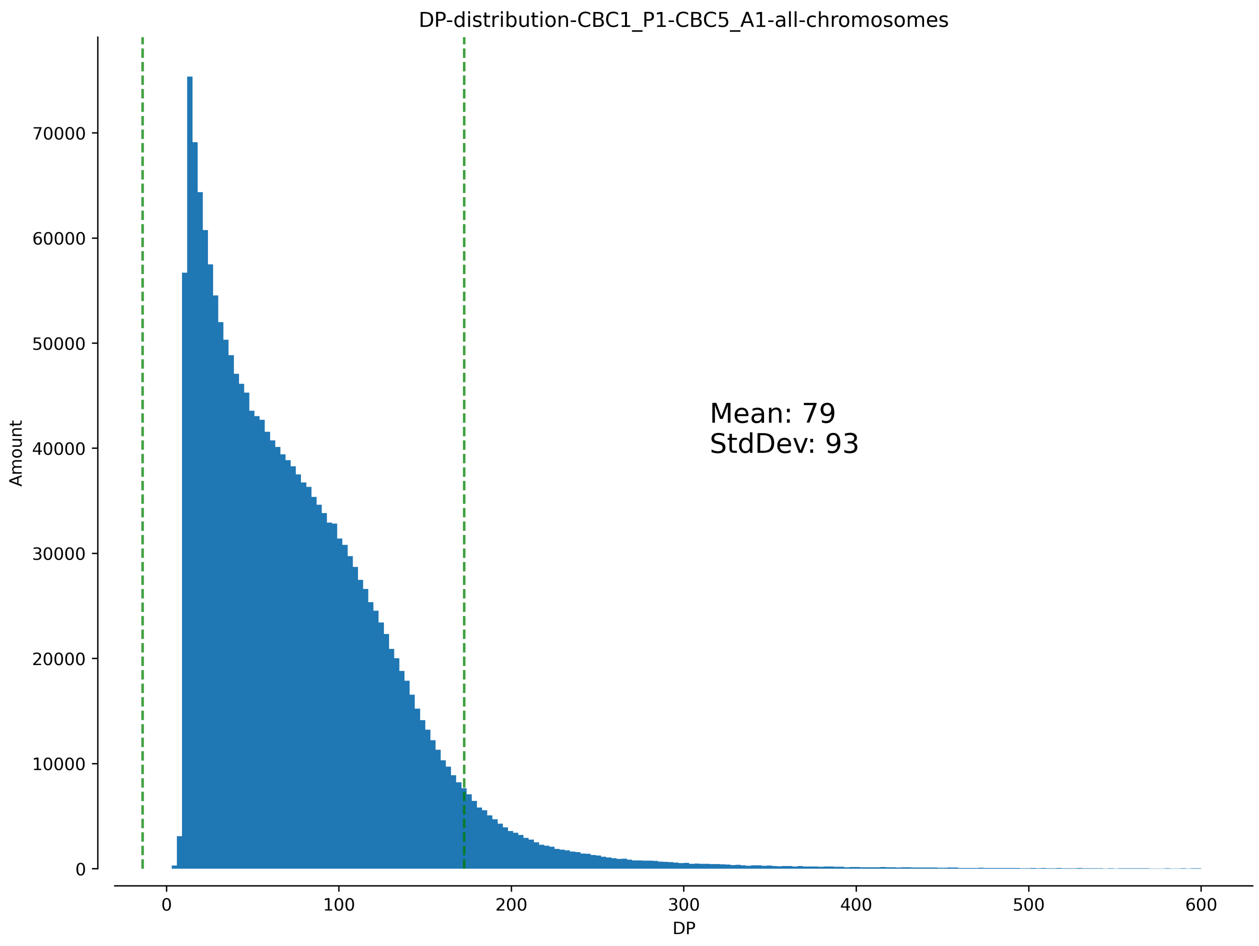
GT Plot - RAW - All Chromosomes - (No 0/0, 1/1, 'Other' GTs Filtered)

In [9]:
```
plt.close('all')
GTplot(samples, vcf_df, chrom_len)
```

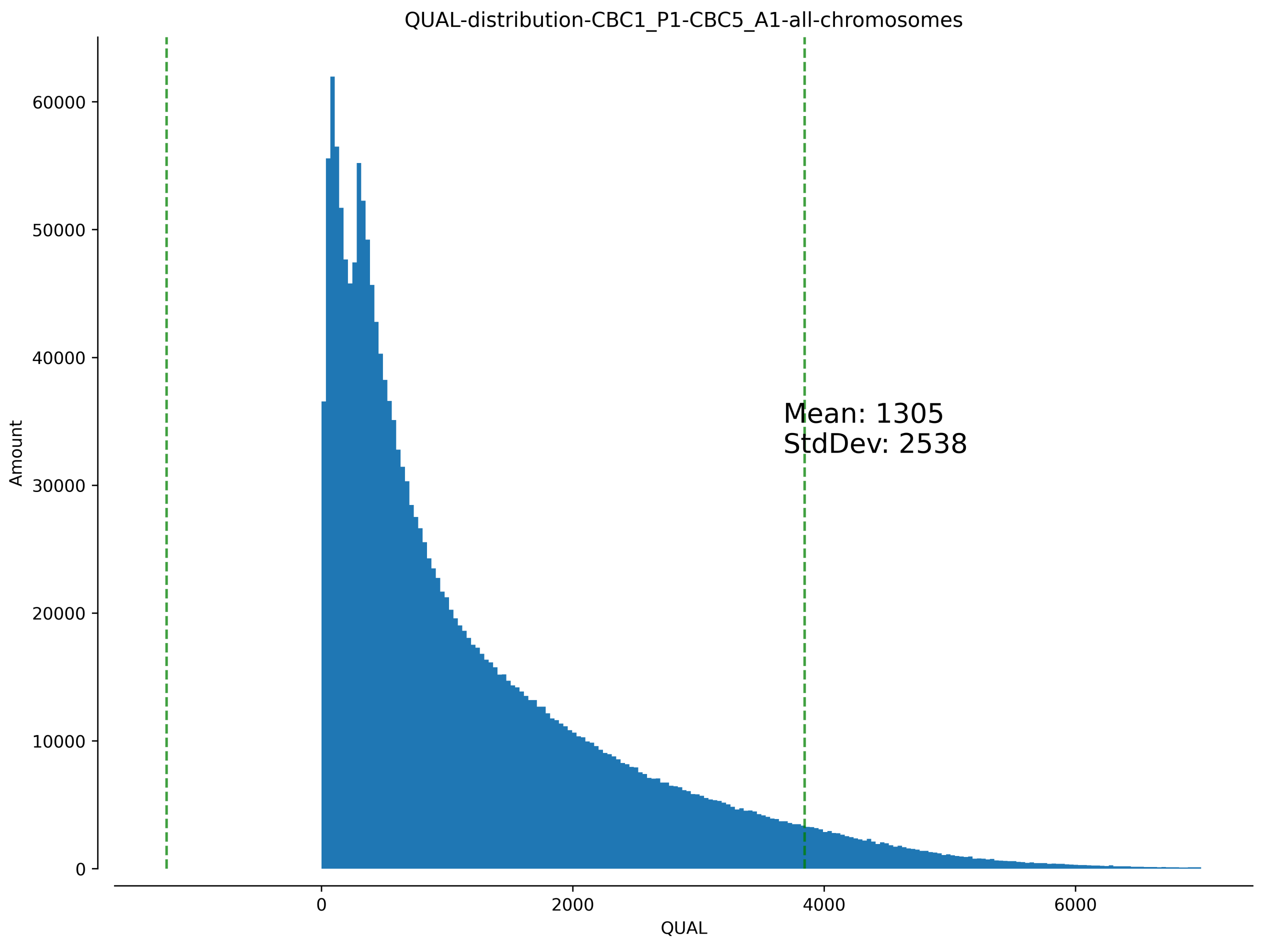


Histograms - `DP` , `QUAL` , `TYPE` and `GT` Attributes - All Chromosomes - Unfiltered

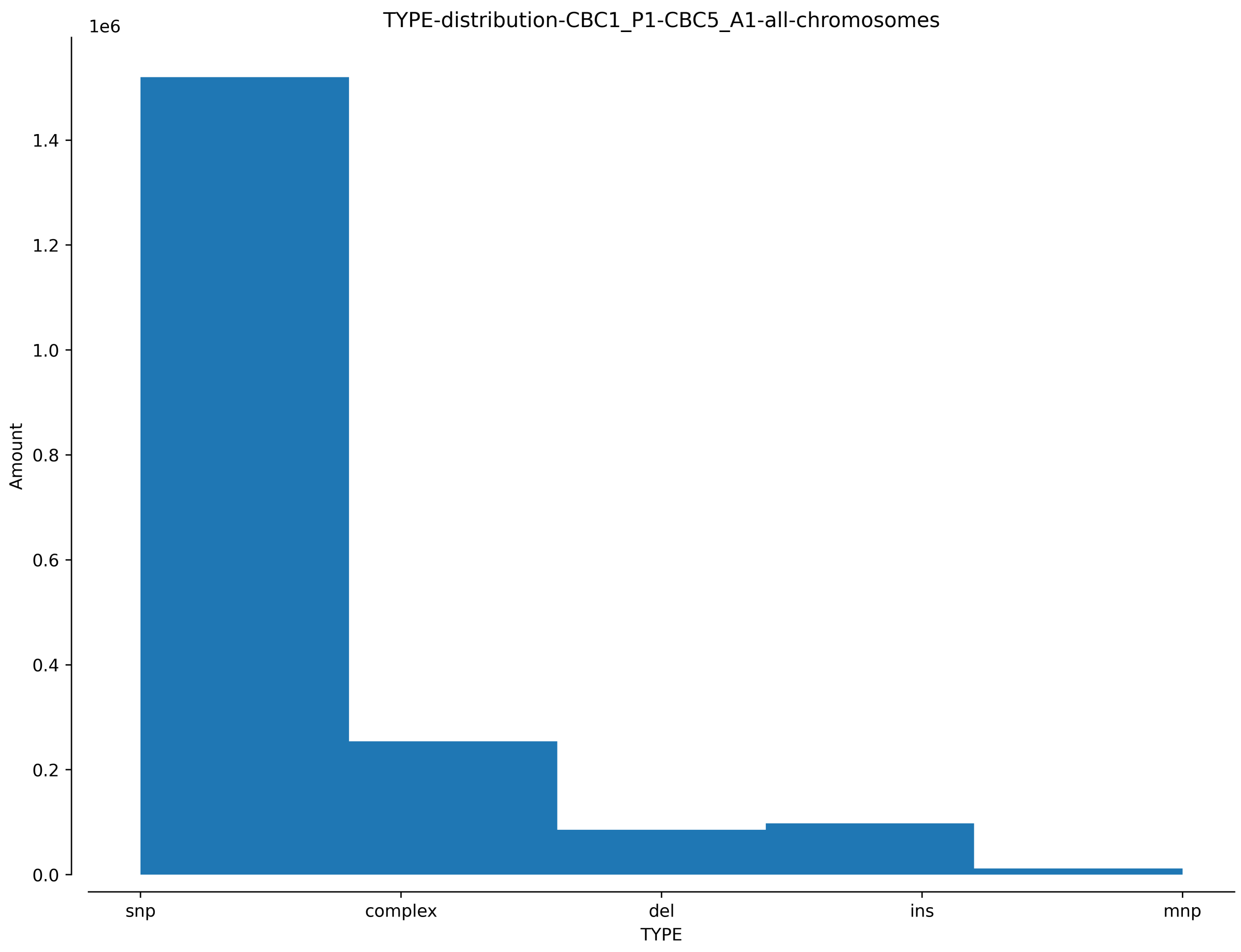
In [10]:
```
plot_variant_hist(samples, vcf_df, 'all', 'DP', bins=200, MSTD=True, xmax=600)
```



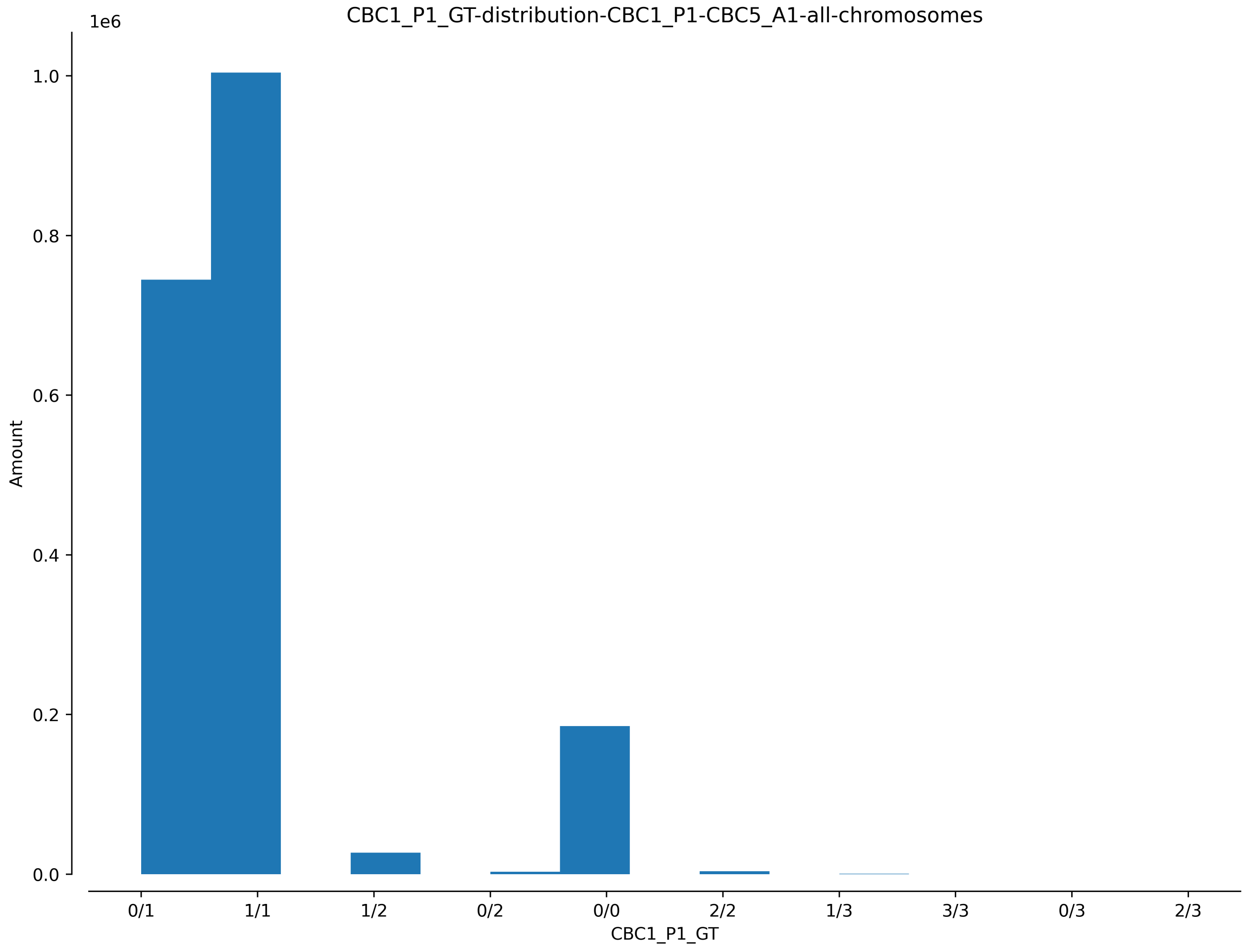
```
In [11]: plot_variant_hist(samples, vcf_df, 'all', 'QUAL', bins=200,  MSTD=True, xmax=700
```



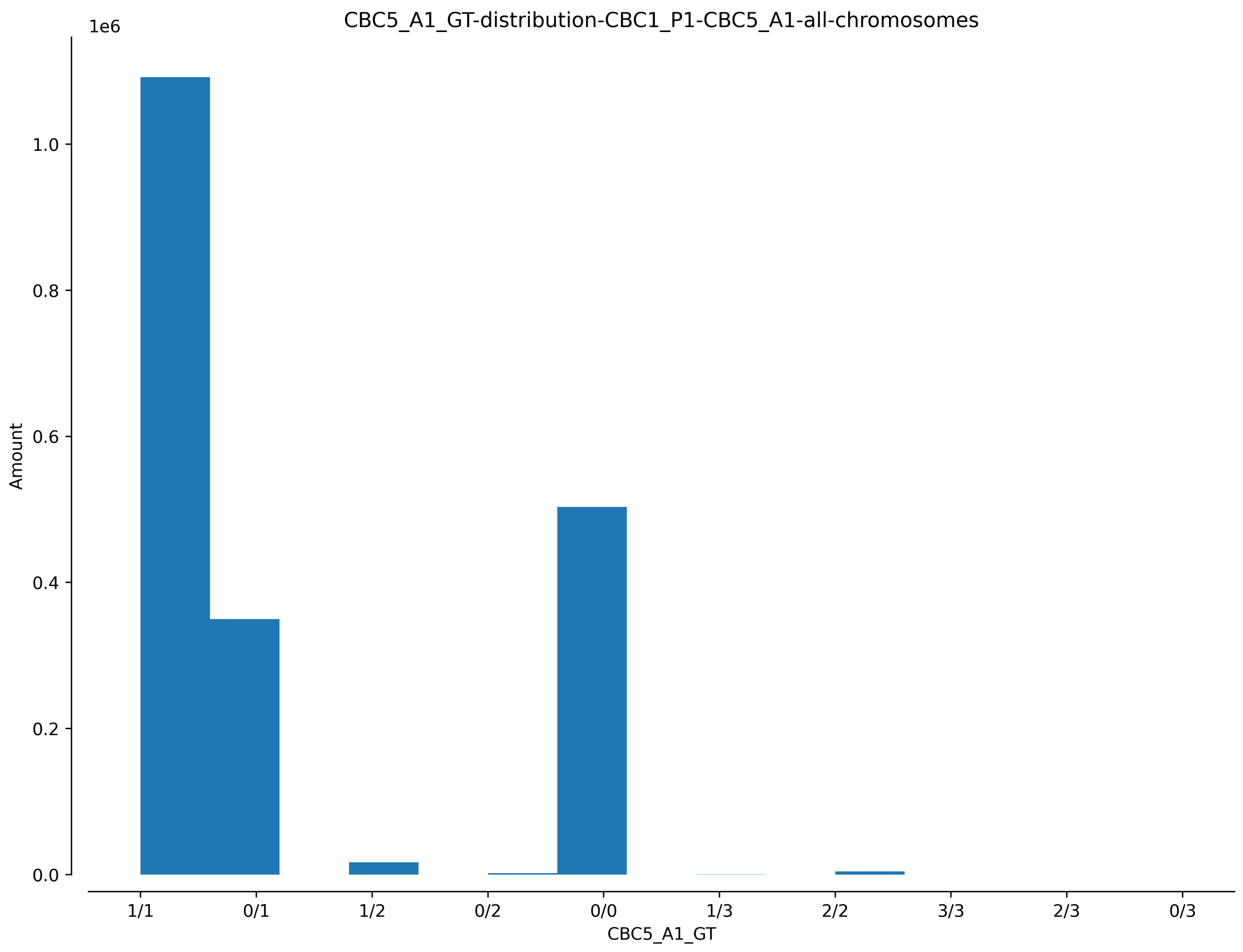
In [12]:
```
plot_variant_hist(samples, vcf_df, 'all', 'TYPE', bins=5)
```



In [14]:
```
plot_variant_hist(samples, vcf_df, 'all', 'CBC1_P1_GT', bins=15)
```



```
In [15]: plot_variant_hist(samples, vcf_df, 'all', 'CBC5_A1_GT', bins=15)
```



Stacked Bar Plots - RAW

```
In [16]: ct_guide()
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
<ipython-input-16-913d2e3ed022> in <module>()
----> 1 ct_guide()

NameError: name 'ct_guide' is not defined
```

```
In [ ]: plt.close('all')
        window_size = 1000000
        CTbarPlots(samples, vcf_df, chrom_len, window_size)
```

PART 1: Filter Out Mitochondria and Chloroplast Chromosomes

Drop Mitochrondria and Chloroplast Chromosomes from `vcf_df` and `chrom_len`

```
In [ ]: drop_mito_chloro = "CHROM != NC_018051.1"
        vcf_df_00 = filter_vcf(vcf_df, drop_mito_chloro)
        vcf_df_00
```

In [ ]:

```
mito_chloro = ['NC_018051.1']
chrom_len_00 = chrom_len.drop(mito_chloro)
chrom_len_00
```

Create Mitochrondria and Chloroplast Variants and Chomosome Length Dataframes

In [ ]:

```
drop_chrom = "CHROM!=NC_040279.1, CHROM!=NC_040280.1, CHROM!=NC_040281.1, CHROM!
vcf_df_mito_chloro = filter_vcf(vcf_df, drop_chrom)
vcf_df_mito_chloro
```

In [ ]:

```
mito_chloro_len = chrom_len.loc[mito_chloro]
mito_chloro_len
```

Contingency Table - No Mitochondria/Chloroplast

In [ ]:

```
contingency_table_1 = contingency_table(samples, vcf_df_00, 'all')
```

GT Plot - No Mitochondria/Chloroplast

In [ ]:

```
# plt.close('all')
# GTplot(samples, vcf_df_00, chrom_len_00)
```

Histograms - `DP` , `QUAL` , `TYPE` and `GT` Attributes - No Mitochondria/Chloroplast

In [ ]:

```
plot_variant_hist(samples, vcf_df_00, 'all', 'DP', bins=200, MSTD=True, xmax=60(
```

In [ ]:

```
plot_variant_hist(samples, vcf_df_00, 'all', 'QUAL', bins=200,  MSTD=True, xmax=
```

In [ ]:

```
plot_variant_hist(samples, vcf_df_00, 'all', 'TYPE', bins=5)
```

In [ ]:

```
plot_variant_hist(samples, vcf_df_00, 'all', '%s_GT' % progenitor, bins=15)
```

In [ ]:

```
plot_variant_hist(samples, vcf_df_00, 'all', '%s_GT' % mutant, bins=15)
```

PART 2: Cutting Off by Mean±2StdDev Histograms of DP Attribute

In [ ]:

```
cutoff_left = vcf_df_00.DP.mean() - (2 * vcf_df_00.DP.std())
cutoff_right = vcf_df_00.DP.mean() + (2 * vcf_df_00.DP.std())

filter_dp = "DP >= %i, DP <= %i" % (cutoff_left, cutoff_right)
```

```
print(filter_dp)

vcf_df_01 = filter_vcf(vcf_df_00, filter_dp)
vcf_df_01
```

Verify DP Histogram Cutoff Off by Mean±StdDev

In [ ]:
```
plot_variant_hist(samples, vcf_df_01, 'all', 'DP', bins=200, xmax=200)
```

In [ ]:
```
plot_variant_hist(samples, vcf_df_01, 'all', 'QUAL', bins=100, MSTD=True)
```

Contingency Table After DP Cutoff by Mean±StdDev

In [ ]:
```
contingency_table_2 = contingency_table(samples, vcf_df_01, 'all')
```

GT Plot After DP Cutoff by Mean±StdDev

In [ ]:
```
# plt.close('all')
# GTplot(samples, vcf_df_01, chrom_len_00)
```

Histogram 'GT' Attribute after DP Cutoff

In [ ]:
```
plot_variant_hist(samples, vcf_df_01, 'all', '%s_GT' % progenitor, bins=15)
```

In [ ]:
```
plot_variant_hist(samples, vcf_df_01, 'all', '%s_GT' % mutant, bins=15)
```

PART 3: Extract mnp from $TYPE$ Attribute

Extract `mnp` `TYPE` Attribute

In [ ]:
```
extract_type = "TYPE != snp, TYPE != complex, TYPE != ins, TYPE != del"
vcf_df_02 = filter_vcf(vcf_df_01, extract_type)
vcf_df_02
```

Examples of `mnp` mutation type

In [ ]:
```
vcf_df_02[ ['REF', 'ALT'] ].head()
```

In [ ]:
```
vcf_df_02[ ['REF', 'ALT'] ].tail()
```

TYPE `mnp` Histogram Verification

In [ ]:
```
plot_variant_hist(samples, vcf_df_02, 'all', 'TYPE', bins=5)
```

Contingency Table - `mnp` TYPE only

In [ ]:
```
contingency_table_3 = contingency_table(samples, vcf_df_02, 'all')
```

GT Plot - `mnp` TYPE only

In [ ]:
```
# plt.close('all')
# GTplot(samples, vcf_df_02, chrom_len_00)
```

Histograms - DP, QUAL, and GT Attributes after TYPE Filtering

In [ ]:
```
plot_variant_hist(samples, vcf_df_02, 'all', 'DP', bins=200, MSTD=True, xmax=60
```

In [ ]:
```
plot_variant_hist(samples, vcf_df_02, 'all', 'QUAL', bins=200,  MSTD=True, xmax=
```

In [ ]:
```
plot_variant_hist(samples, vcf_df_02, 'all', '%s_GT' % progenitor, bins=15)
```

In [ ]:
```
plot_variant_hist(samples, vcf_df_02, 'all', '%s_GT' % mutant, bins=15)
```

PART 4: Cutting Off by Mean±StdDev Histograms of $QUAL$ Attribute

In [ ]:
```
# cutoff_left = vcf_df_02.QUAL.mean() - vcf_df_02.QUAL.std()
# cutoff_right = vcf_df_02.QUAL.mean() + vcf_df_02.QUAL.std()

# filter_qual = "QUAL >= %i, QUAL <= %i" % (cutoff_left, cutoff_right)
# print(filter_qual)

# vcf_df_03 = filter_vcf(vcf_df_02, filter_qual)
# vcf_df_03
```

Verify `DP` and `QUAL` Histograms after `QUAL` Cutoff Off by Mean±StdDev

In [ ]:
```
# plot_variant_hist(samples, vcf_df_03, 'all', 'DP', bins=200, xmax=200)
```

In [ ]:
```
# plot_variant_hist(samples, vcf_df_03, 'all', 'QUAL', bins=100, xmax=3500)
```

Contingency Table After QUAL Cutoff by Mean±StdDev

In [ ]:
```
# contingency_table_4 = contingency_table(samples, vcf_df_03, 'all')
# contingency_table_4
```

GT Plot After QUAL Cutoff by Mean±StdDev

In [ ]:
```
# plt.close('all')
# GTplot(samples, vcf_df_03, chrom_len_00)
```

Histograms after QUAL Cutoff by Mean±StdDev

In [ ]:
```
# plot_variant_hist(samples, vcf_df_03, 'all', 'PAHAT_1_GT', bins=9)
```

In [ ]:
```
# plot_variant_hist(samples, vcf_df_03, 'all', 'GHP-2-2_GT', bins=9)
```

PART 5: Filtering GTs 0/0, 1/1, 'Other'

Filter out where samples GTs are the same (0/0, 1/1) and have 'Other'

In [ ]:
```
progenitor_gts_filter = "CBC1_P1_GT != ./., CBC1_P1_GT != 0/2, CBC1_P1_GT != 1/2
vcf_df_04 = filter_vcf(vcf_df_02, progenitor_gts_filter)

mutant_gts_filter = "CBC5_A1_GT != ./., CBC5_A1_GT != 0/2, CBC5_A1_GT != 1/2, CE
vcf_df_04 = filter_vcf(vcf_df_04, mutant_gts_filter)

genotypes = ['0/0', '1/1']
for genotype in genotypes:
    vcf_df_04 = filter_similar_gt(samples, vcf_df_04, genotype)

vcf_df_04
```

Contingency Table after GT Filtering

In [ ]:
```
contingency_table_5 = contingency_table(samples, vcf_df_04, 'all')
```

GT Plot after GT Filtering

In [ ]:
```
plt.close('all')
GTplot(samples, vcf_df_04, chrom_len_00)
```

Histograms GT after GT Filtering

In [ ]:
```
plot_variant_hist(samples, vcf_df_04, 'all', '%s_GT' % progenitor, bins=9)
```

In [ ]:
```
plot_variant_hist(samples, vcf_df_04, 'all', '%s_GT' % mutant, bins=9)
```

PART 6: Stacked Bar Plots

In [ ]:
```
ct_guide()
```

In [ ]:
```
plt.close('all')
window_size = 1000000
```

```
CTbarPlots(samples, vcf_df_04, chrom_len_00, window_size)
```

PART 7: Bar Plots per Chromosome

In [ ]:

```
# suppress all the warnings from the inverted tickes of bar plots
import warnings
warnings.filterwarnings('ignore')

plt.close('all')
GTbarPlots(samples, vcf_df_04, chrom_len_00, window_size)
```

PART 8: GT Plots per Chromosome

In [ ]:

```
plt.close('all')
GTplots(samples, vcf_df_04, chrom_len_00)
```

PART 9: Contingency Table per Chromosome

In [ ]:

```
import dataframe_image as dfi

for chromosome in chrom_len_00.index:
    chromosome_df = vcf_df_04[ vcf_df_04.CHROM == chromosome ]

    # reset chromosome_df indexes for contingency table
    chromosome_df.reset_index(inplace=True, drop=True)
    chromosome_ct = contingency_table(samples, chromosome_df, chromosome)
```