GHP-2-2 and PAHAT_1 - InDels 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*
from CTguide import *
```

In [2]:
```
vcf_sorghum = '/home/anibal/genome_files/freebayes~bwa~GCF_000003195.3_Sorghum_b
```

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

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

Out[4]:
```
array(['GHP-2-2', 'PAHAT_1', 'PAHAT_2'], dtype=object)
```

In [5]:
```
progenitor = 'PAHAT_1'
mutant = 'GHP-2-2'
samples = [progenitor, mutant]
samples
```

Out[5]:
```
['PAHAT_1', 'GHP-2-2']
```

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

Out[6]:

	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP
0	NC_008360.1	3598	GAAAAAACT	GAAAAAAAACT	2072.229980	1771	187
1	NC_008360.1	3788	AT	AG	41349.500000	1477	189
2	NC_008360.1	4068	T	A	38302.101562	1387	177
3	NC_008360.1	7055	G	A	7958.569824	351	70
4	NC_008360.1	9183	G	A	246.141006	26	11
...	...	...	...	...	...	...	...
2276907	NC_012879.2	61191248	GCCA	ACCG	27.908600	71	16
	NC_012879.2	61191286	C	T	13.749700	70	19

	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP
2276909	NC_012879.2	61191293	G	C	23.474300	65	17
2276910	NC_012879.2	61233448	GTTTAGGGTTAAGGGT	GTTTTAGGGTT	432.449005	139	15
2276911	NC_012879.2	61233618	GTTTTAG	GTTTAG	304.154999	117	24

2276912 rows × 17 columns

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

Out[7]:

CHROM	LEN
NC_012870.2	80884392
NC_012871.2	77742459
NC_012872.2	74386277
NC_012873.2	68658214
NC_012874.2	71854669
NC_012875.2	61277060
NC_012876.2	65505356
NC_012877.2	62686529
NC_012878.2	59416394
NC_012879.2	61233695
NC_008360.1	468628
NC_008602.1	140754

PART 0: Raw

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

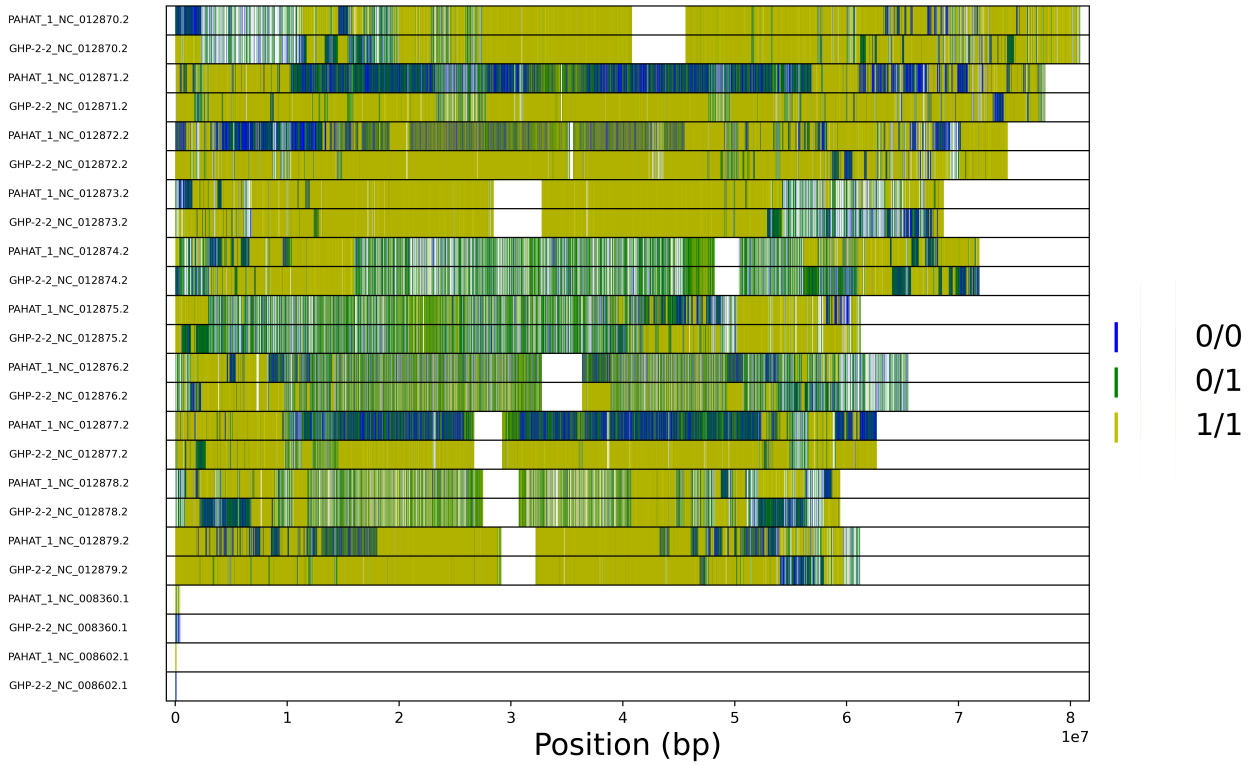
In [8]:
```
contingency_table_0 = contingency_table(samples, vcf_df, 'all')
```

```
Contingency Table - Chromosome all

                GHP-2-2_GT
                       0/0     0/1     1/1  other
PAHAT_1_GT 0/0        7586  212925  620457  68933
           0/1      119419  225957   42168  68933
           1/1      307284   54103  618080  68933
           other     68933   68933   68933  68933
```

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

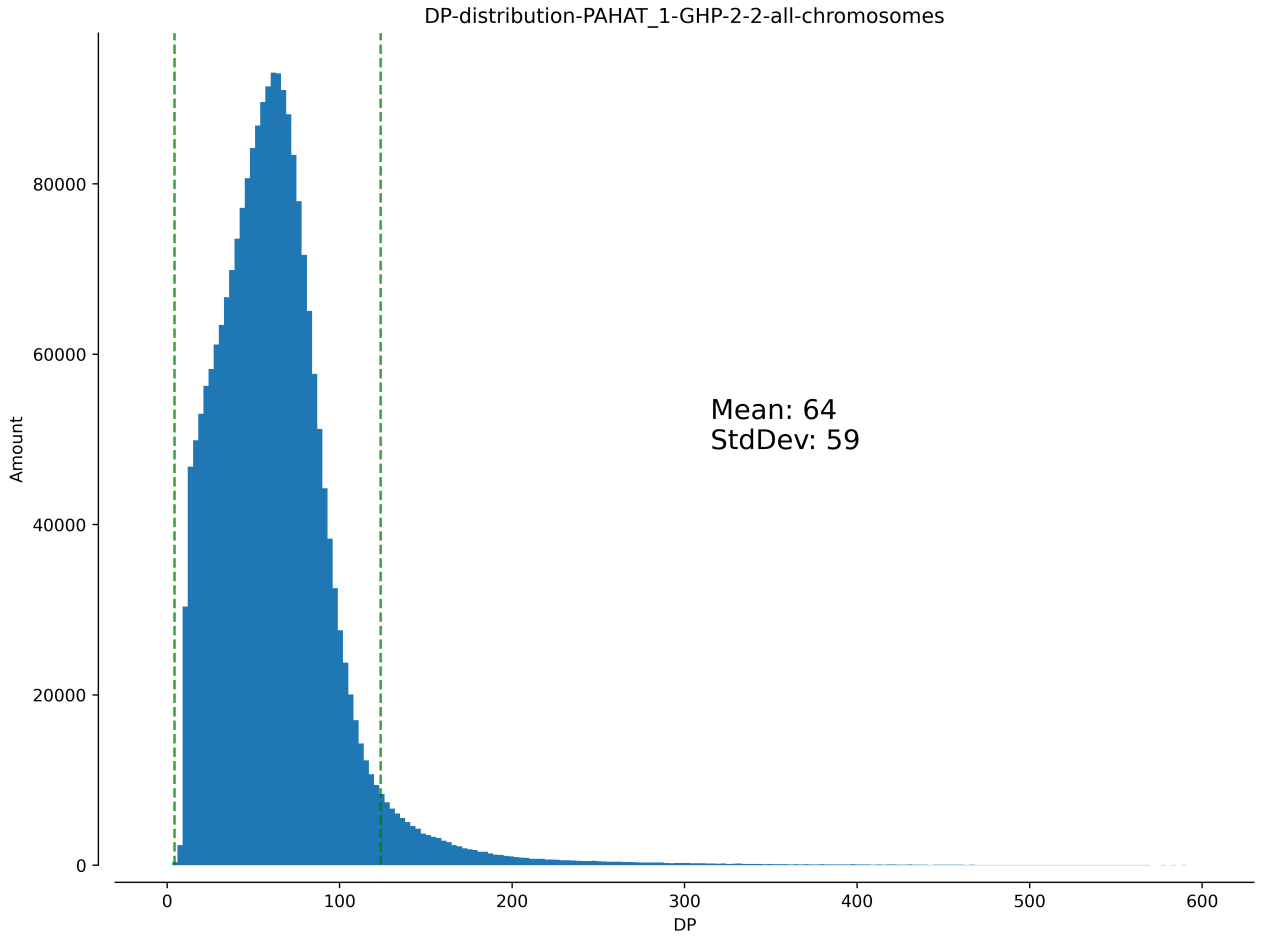

```
ose('all')
```

```
GTplot(samples, vcf_df, chrom_len)
```

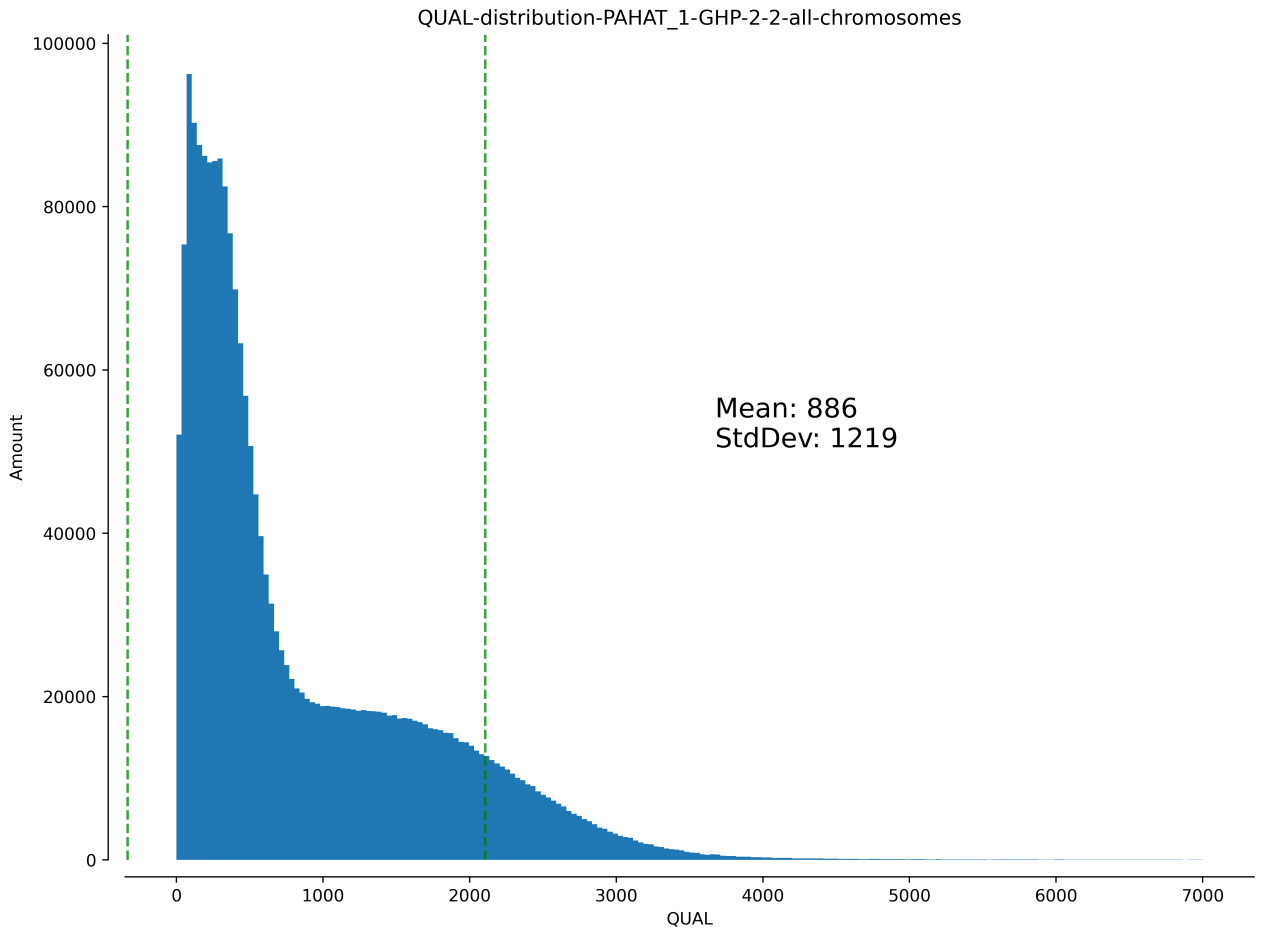


Histograms - DP , QUAL , TYPE and GT Attributes - All Chromosomes - Unfiltered

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

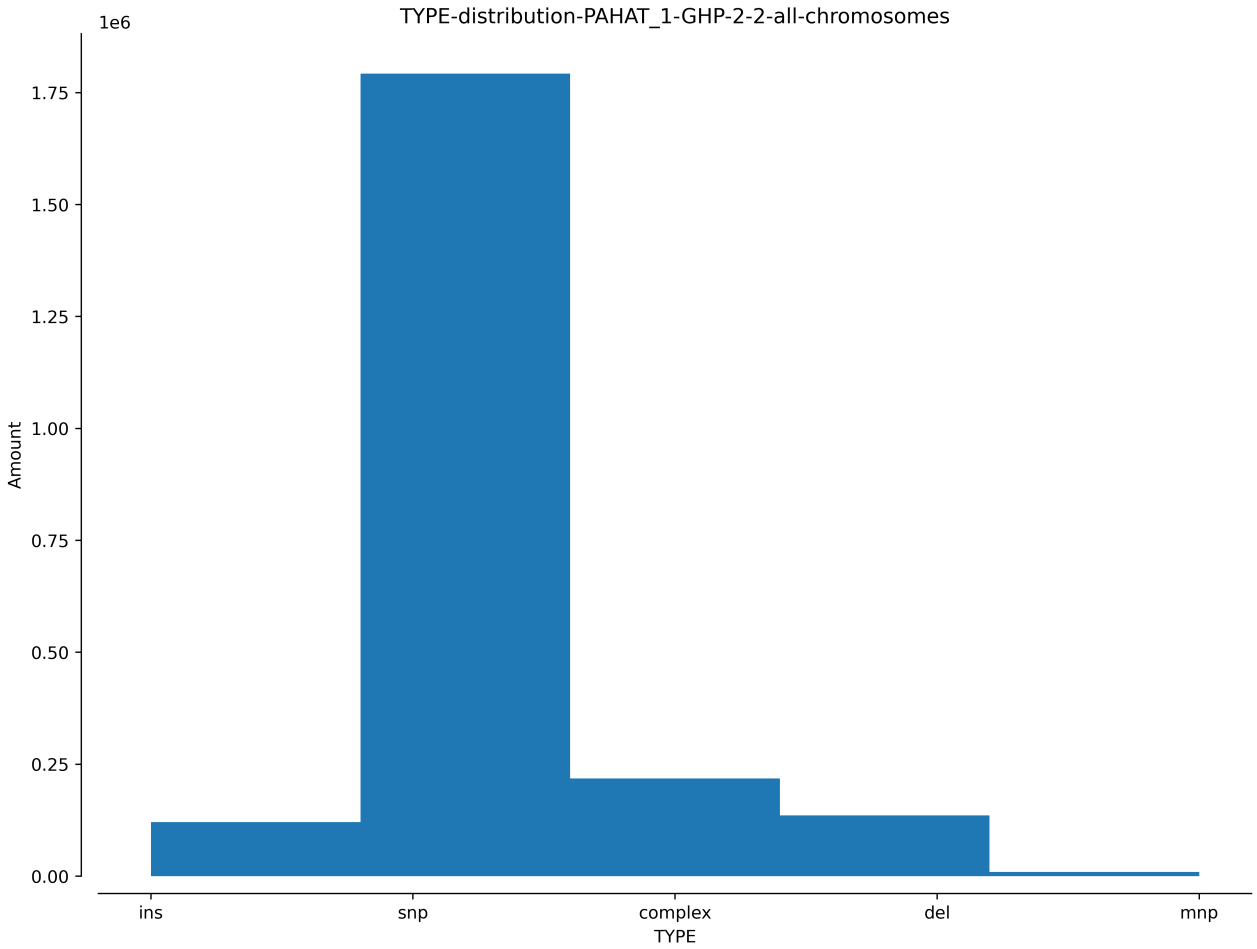


In [11]:
```
plot_variant_hist(samples, vcf_df, 'all', 'QUAL', bins=200,  MSTD=True, xmax=700
```



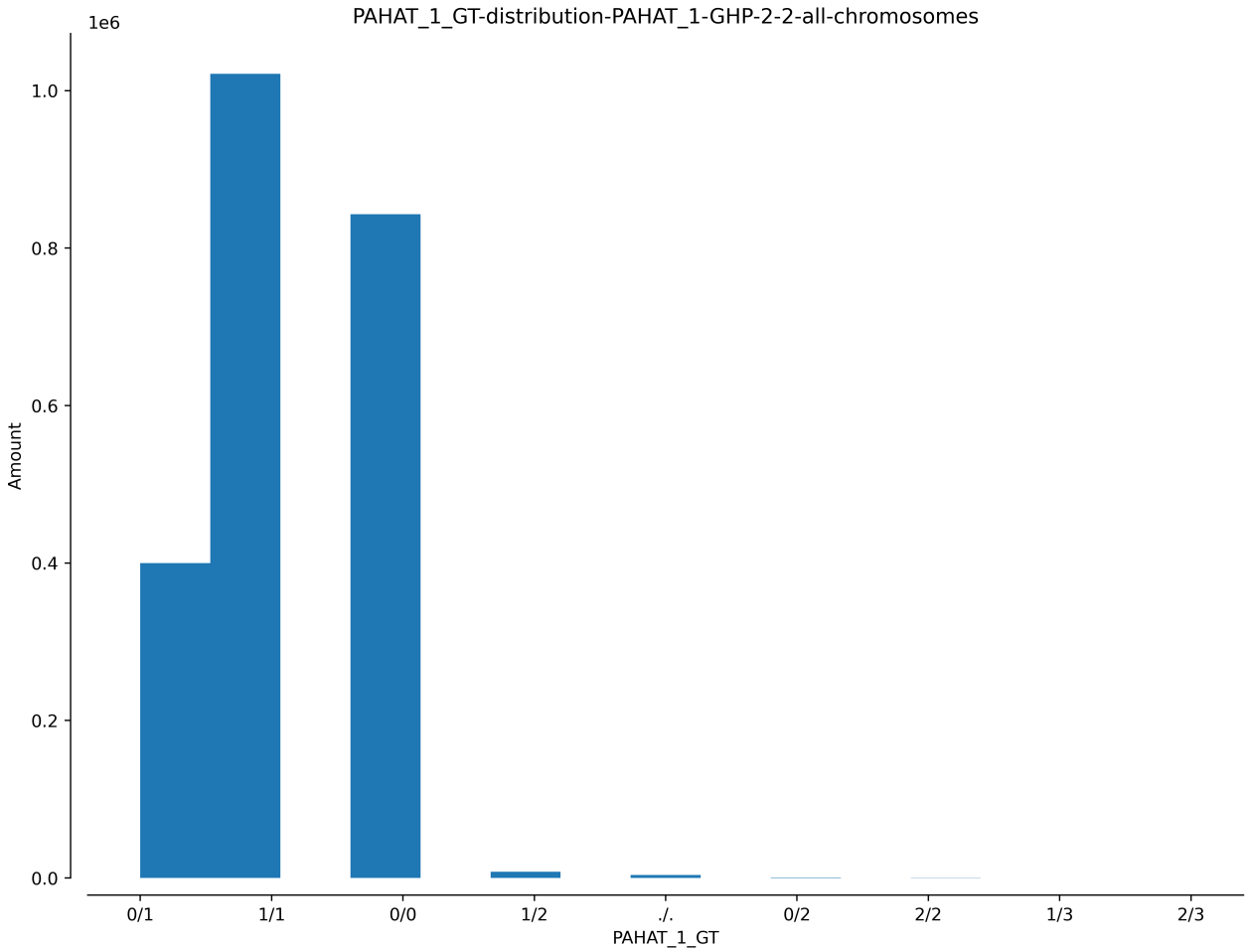
In [12]:

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

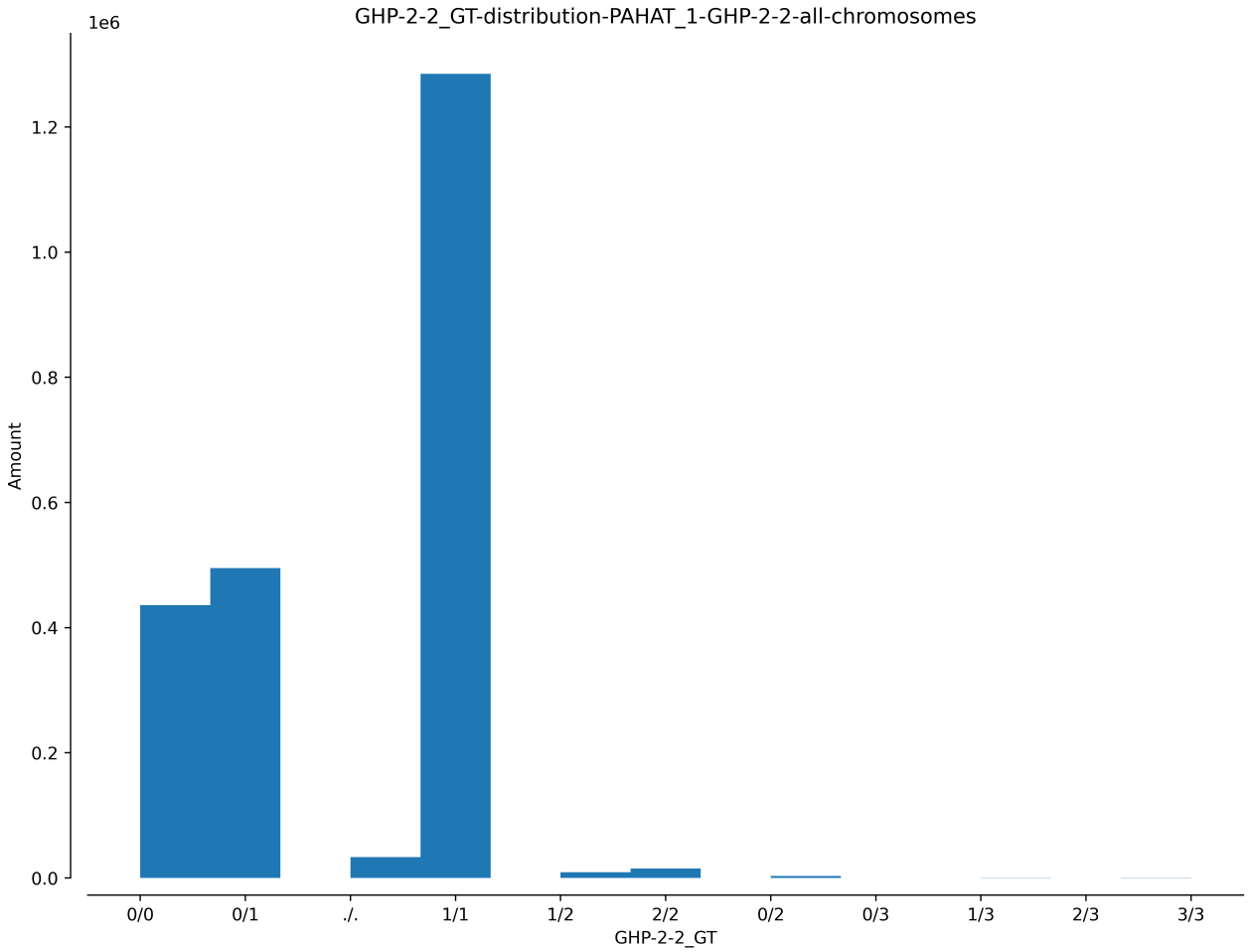


In [13]:

```
plot_variant_hist(samples, vcf_df, 'all', 'PAHAT_1_GT', bins=15)
```



In [14]:
```
plot_variant_hist(samples, vcf_df, 'all', 'GHP-2-2_GT', bins=15)
```



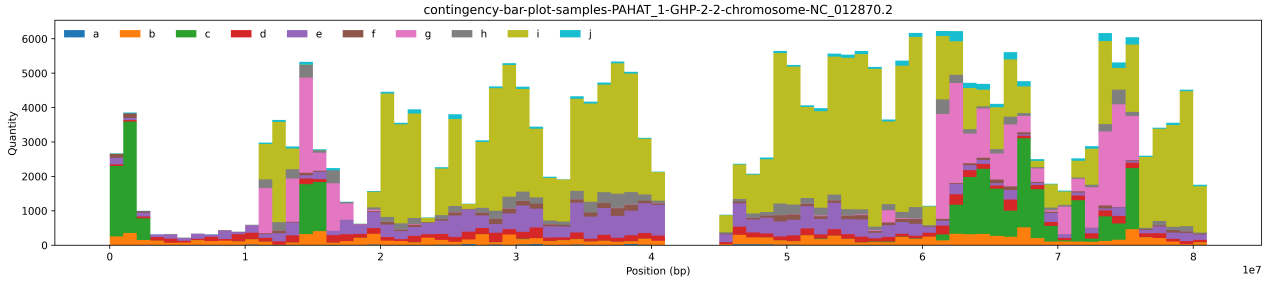
Stacked Bar Plots - RAW

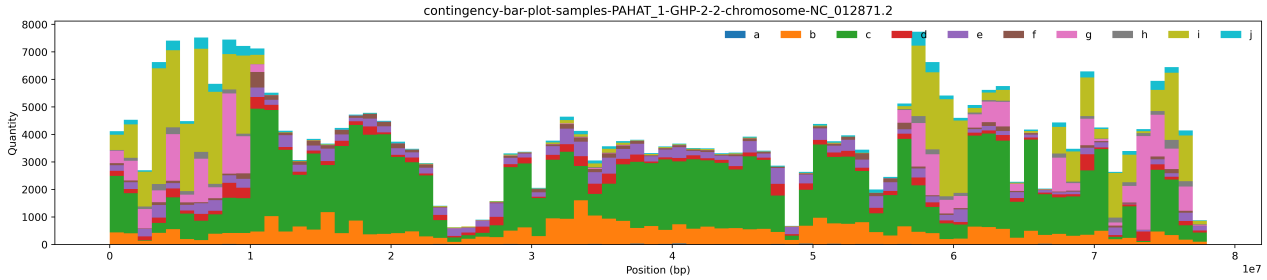
In [15]:
```
ct_guide()
```

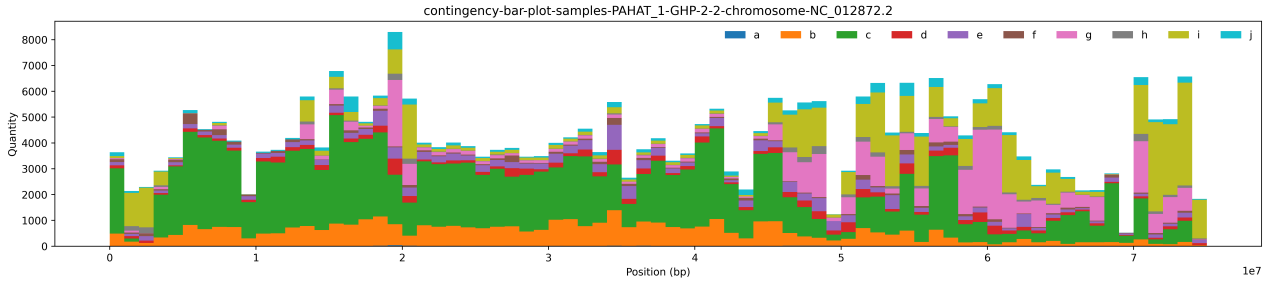
Out[15]:

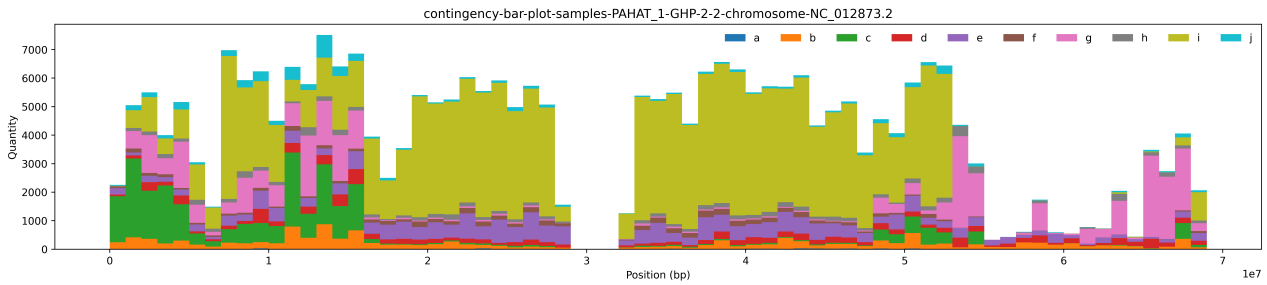
		Mutant			
		0/0	**0/1**	**1/1**	**other**
Progenitor	**0/0**	a	b	c	
	0/1	d	e	f	
	1/1	g	h	i	
	other				j

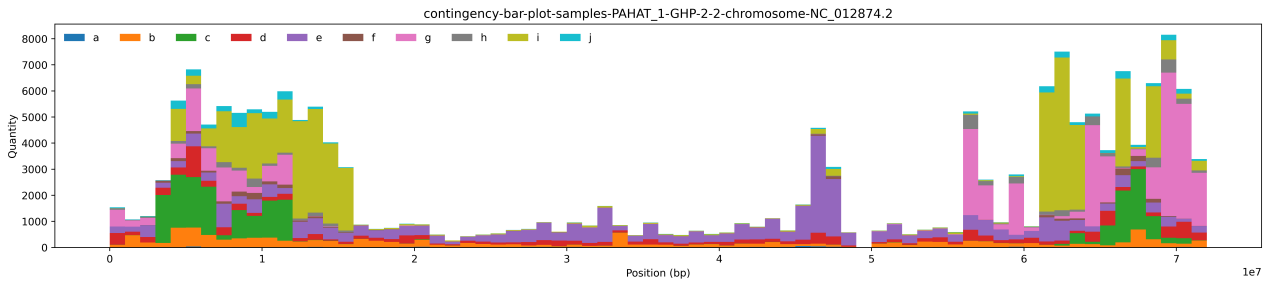
In [16]:
```
plt.close('all')
window_size = 1000000
CTbarPlots(samples, vcf_df, chrom_len, window_size)
```

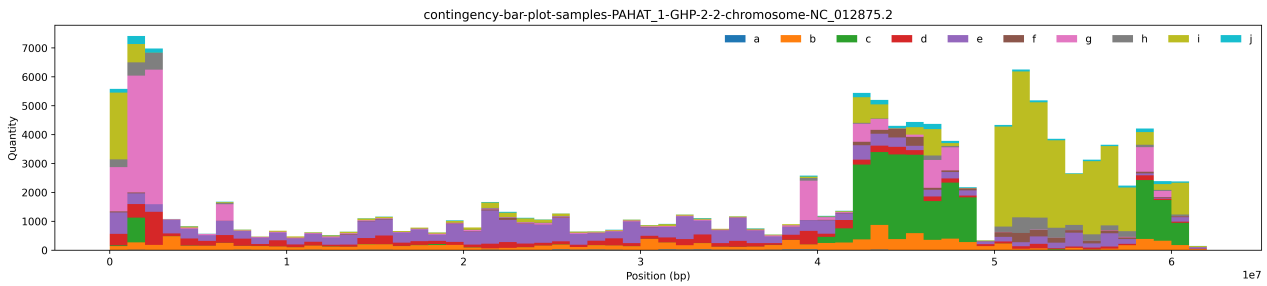


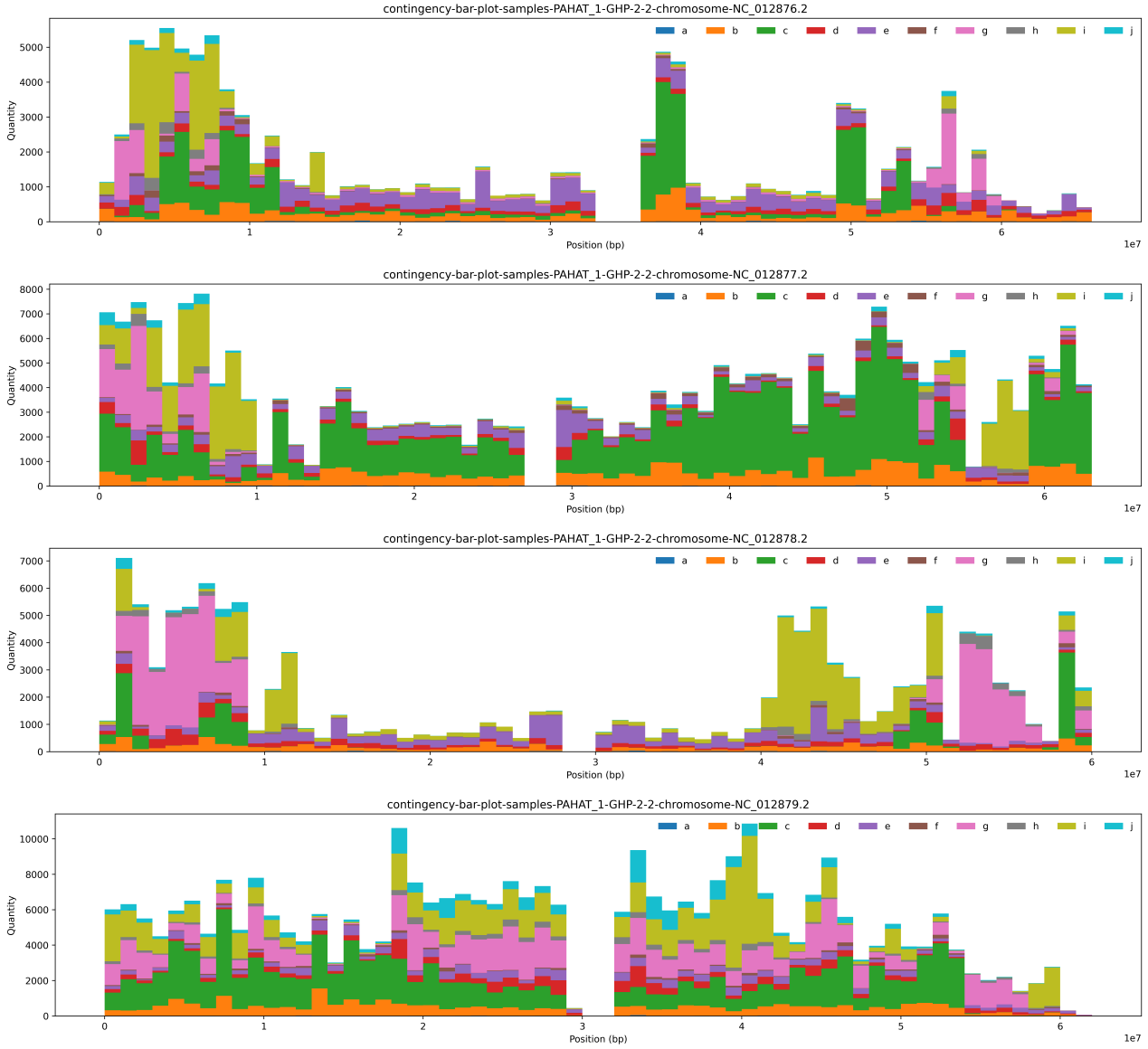












PART 1: Filter Out Mitochondria and Chloroplast Chromosomes

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

In [17]:
```
drop_mito_chloro = "CHROM != NC_008360.1, CHROM != NC_008602.1"
vcf_df_00 = filter_vcf(vcf_df, drop_mito_chloro)
vcf_df_00
```

Out[17]:

	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP	PAI
0	NC_012870.2	91	C	A	113.435997	13	-1	
1	NC_012870.2	111	C	A	226.643997	16	-1	
2	NC_012870.2	744	C	A	178.729996	43	8	
	NC_012870.2	871	C	T	499.332001	61	18	

	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP	PAI
4	NC_012870.2	1143	T	G	176.011002	16	9	
...	...	...	...	...	...	...	...	
2276576	NC_012879.2	61191248	GCCA	ACCG	27.908600	71	16	
2276577	NC_012879.2	61191286	C	T	13.749700	70	19	
2276578	NC_012879.2	61191293	G	C	23.474300	65	17	
2276579	NC_012879.2	61233448	GTTTAGGGTTAAGGGT	GTTTTAGGGTT	432.449005	139	15	
2276580	NC_012879.2	61233618	GTTTTAG	GTTTAG	304.154999	117	24	

2276581 rows × 17 columns

In [18]:
```
mito_chloro = ['NC_008360.1','NC_008602.1']
chrom_len_00 = chrom_len.drop(mito_chloro)
chrom_len_00
```

Out[18]:

CHROM	LEN
NC_012870.2	80884392
NC_012871.2	77742459
NC_012872.2	74386277
NC_012873.2	68658214
NC_012874.2	71854669
NC_012875.2	61277060
NC_012876.2	65505356
NC_012877.2	62686529
NC_012878.2	59416394
NC_012879.2	61233695

Create Mitochrondria and Chloroplast Variants and Chomosome Length Dataframes

In [19]:
```
drop_chrom = "CHROM!=NC_012870.2, CHROM!=NC_012871.2, CHROM!=NC_012872.2, CHROM!
vcf_df_mito_chloro = filter_vcf(vcf_df, drop_chrom)
vcf_df_mito_chloro
```

Out[19]:

	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP	PAHAT_1_DI
0	NC_008360.1	3598	GAAAAAACT	GAAAAAAAACT	2072.229980	1771	187	85
	_008360.1	3788	AT	AG	41349.500000	1477	189	69

	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP	PAHAT_1_DI
2	NC_008360.1	4068	T	A	38302.101562	1387	177	63
3	NC_008360.1	7055	G	A	7958.569824	351	70	16
4	NC_008360.1	9183	G	A	246.141006	26	11	
...	...	...	...	...	...	...	...	.
326	NC_008602.1	111981	CACCCGCAG	CACCTGCAG	294407.000000	13776	4663	461
327	NC_008602.1	115489	AAG	AAA	74523.203125	3835	1330	111
328	NC_008602.1	115682	CA	CC	178725.000000	8256	2511	281
329	NC_008602.1	118002	GGCTGCTACC	GGCAGCTACC	263337.000000	12914	4653	417
330	NC_008602.1	130073	AGAGGAT	ACGAGAT	113.835999	12	-1	

331 rows × 17 columns

In [20]:
```
mito_chloro_len = chrom_len.loc[mito_chloro]
mito_chloro_len
```

Out[20]:

CHROM	LEN
NC_008360.1	468628
NC_008602.1	140754

Contingency Table - No Mitochondria/Chloroplast

In [21]:
```
contingency_table_1 = contingency_table(samples, vcf_df_00, 'all')
```

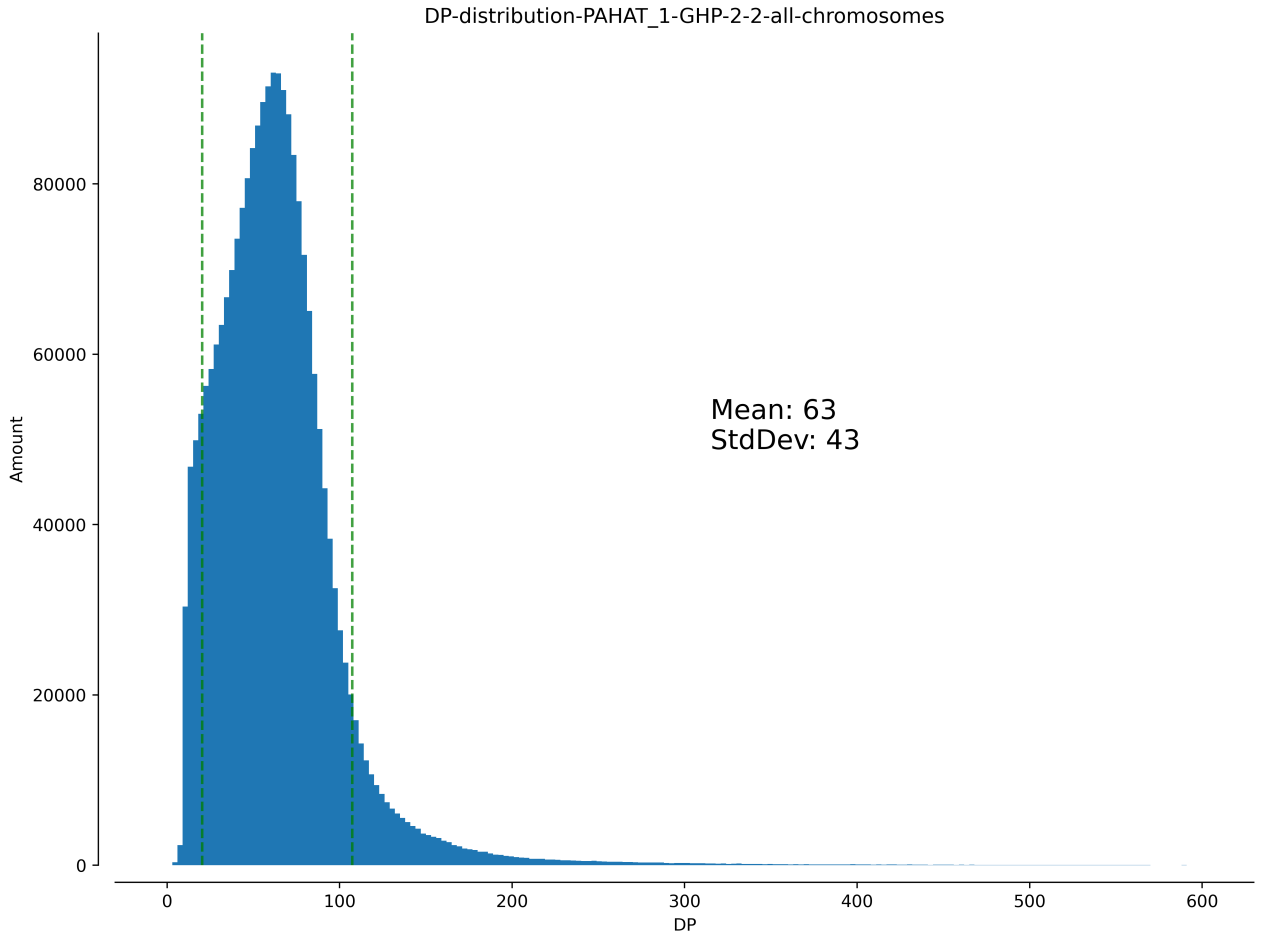
```
Contingency Table - Chromosome all

                GHP-2-2_GT
                       0/0     0/1     1/1  other
PAHAT_1_GT 0/0        7585  212887  620457  68924
           0/1      119369  225903   42168  68924
           1/1      307108   54103  618077  68924
           other     68924   68924   68924  68924
```

GT Plot - No Mitochondria/Chloroplast

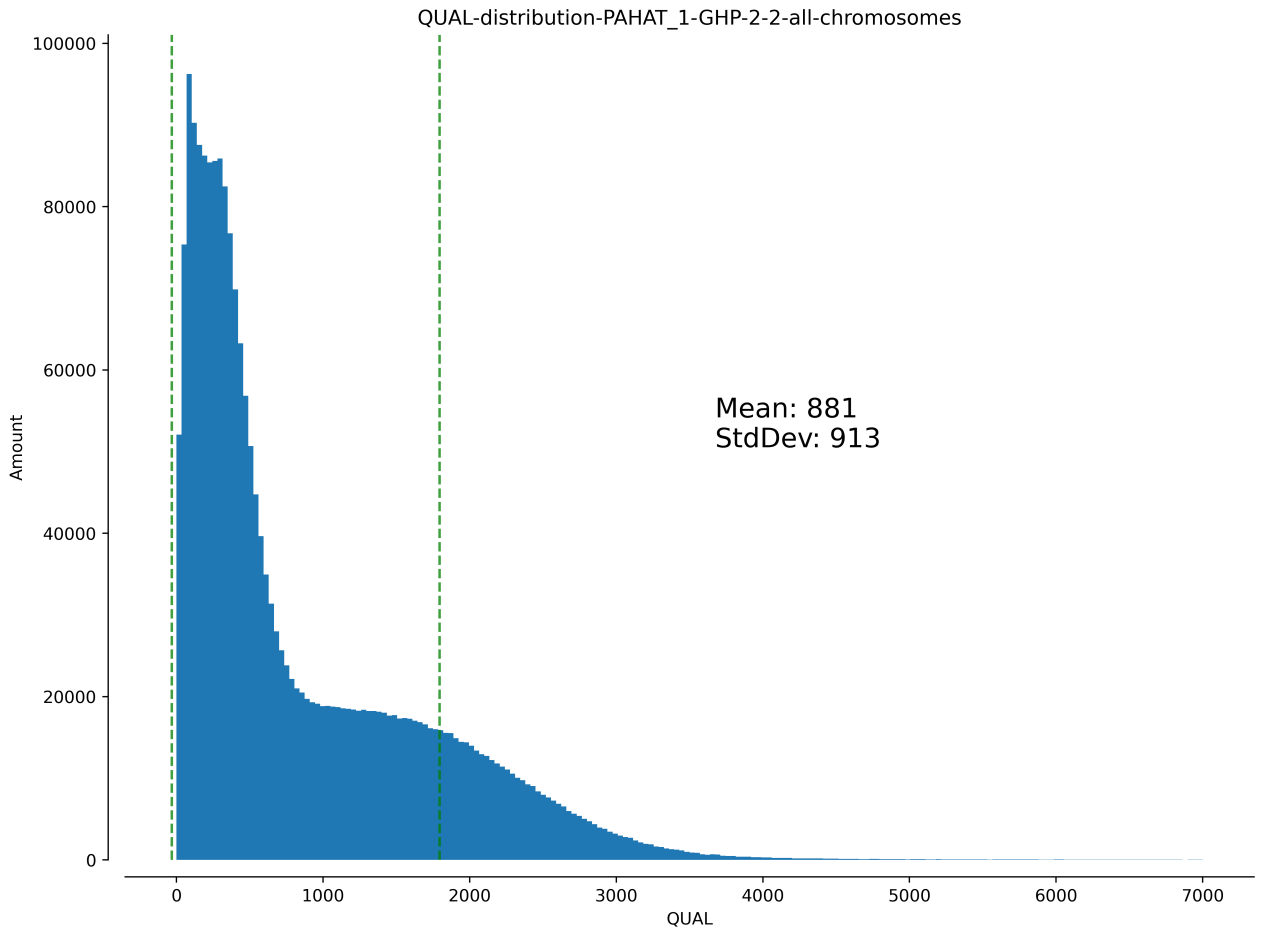
In [22]:
```
# plt.close('all')
# GTplot(samples, vcf_df_00, chrom_len_00)
```

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

In [23]:
```
plot_variant_hist(samples, vcf_df_00, 'all', 'DP', bins=200, MSTD=True, xmax=600
```

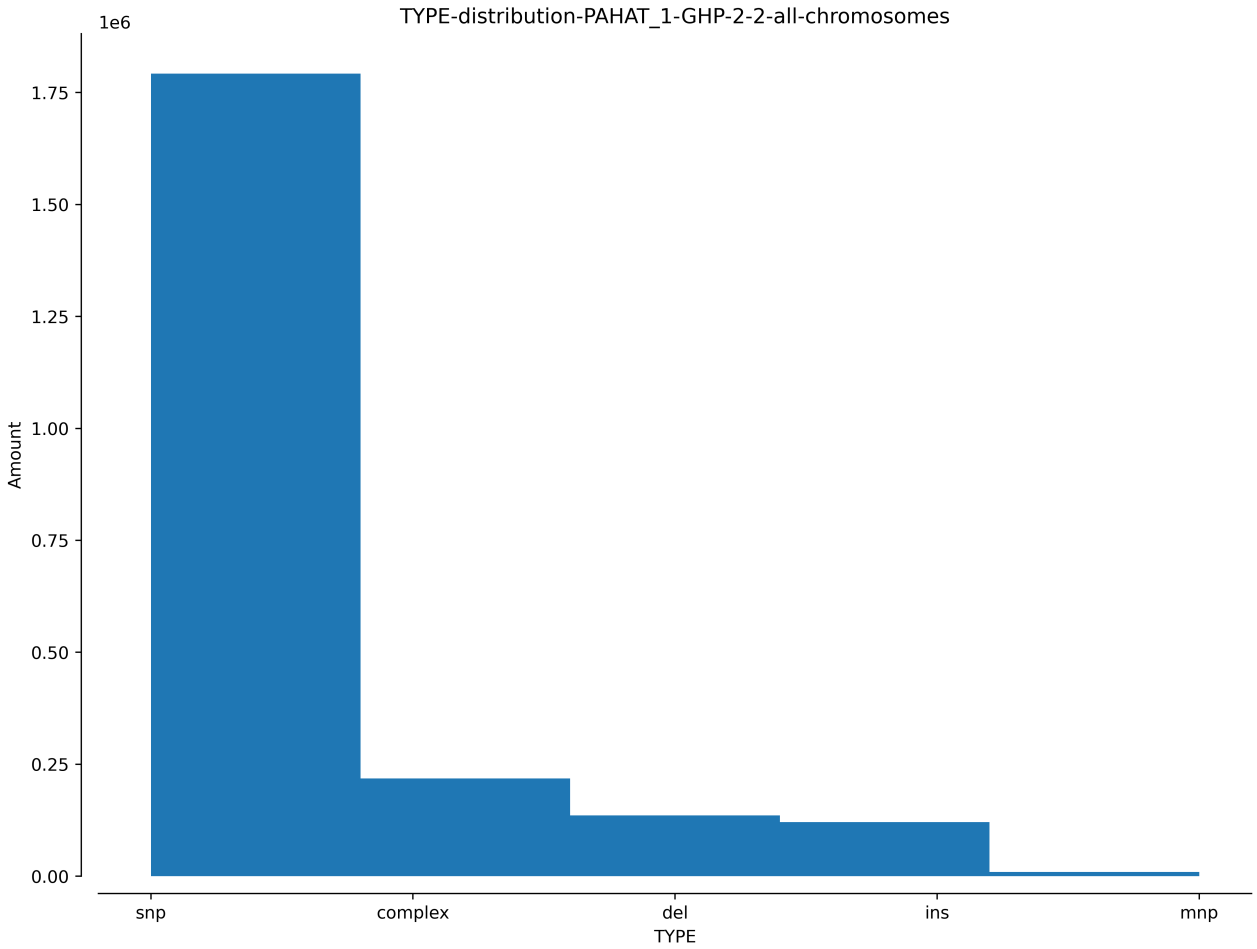


In [24]:
```
plot_variant_hist(samples, vcf_df_00, 'all', 'QUAL', bins=200,  MSTD=True, xmax=
```



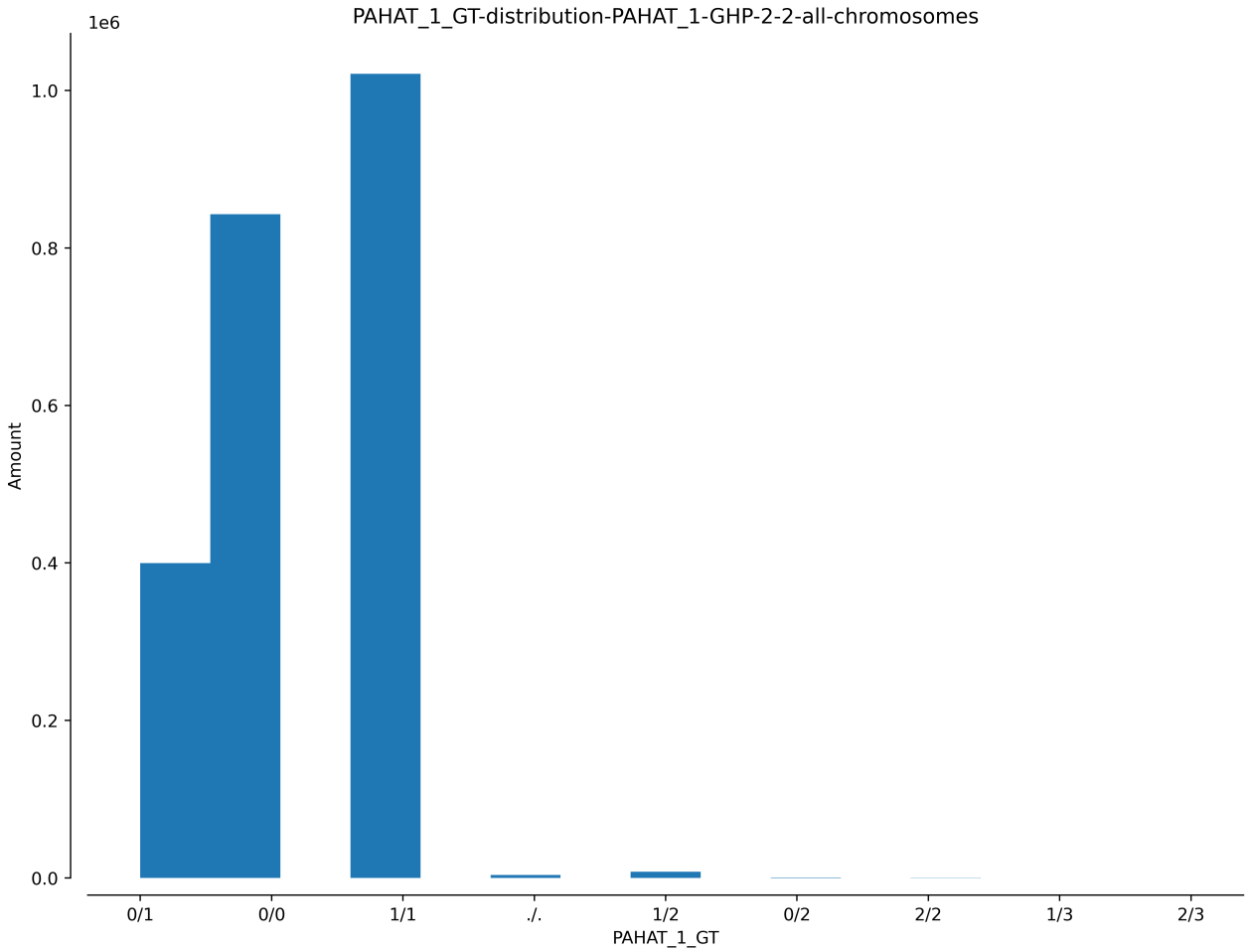
In [25]:

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



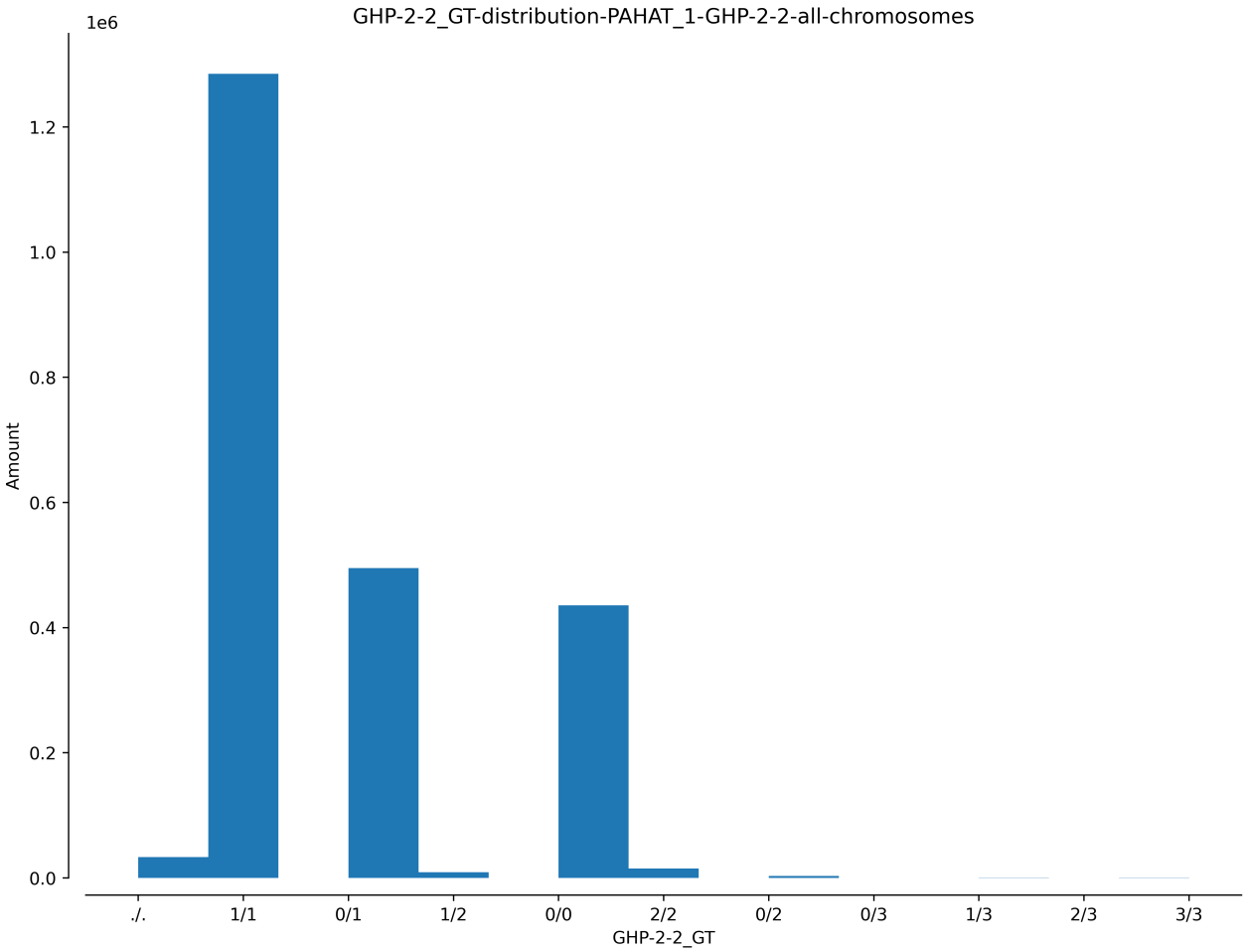
In [26]:

```
plot_variant_hist(samples, vcf_df_00, 'all', 'PAHAT_1_GT', bins=15)
```



In [27]:

```
plot_variant_hist(samples, vcf_df_00, 'all', 'GHP-2-2_GT', bins=15)
```



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

In [28]:

```
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
```

```
DP >= -23, DP <= 150
```

Out[28]:

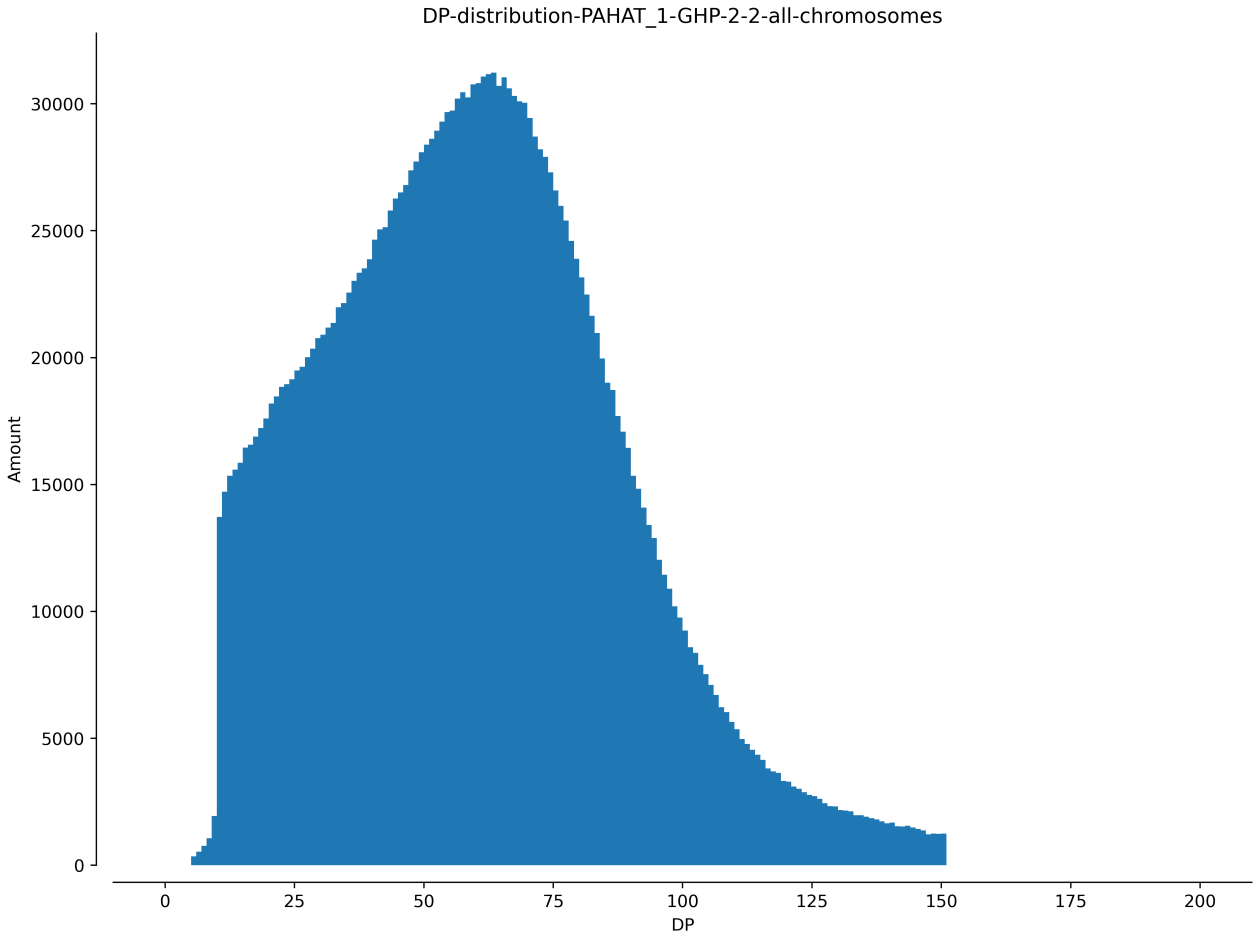
	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP	PAI
0	NC_012870.2	91	C	A	113.435997	13	-1	
1	NC_012870.2	111	C	A	226.643997	16	-1	
2	NC_012870.2	744	C	A	178.729996	43	8	
3	NC_012870.2	871	C	T	499.332001	61	18	
4	NC_012870.2	1143	T	G	176.011002	16	9	
	...	...	...	...	...	...	...	

	CHROM	POS	REF	ALT	QUAL	DP	GHP-2-2_DP	PAI
2217645	NC_012879.2	61191248	GCCA	ACCG	27.908600	71	16	
2217646	NC_012879.2	61191286	C	T	13.749700	70	19	
2217647	NC_012879.2	61191293	G	C	23.474300	65	17	
2217648	NC_012879.2	61233448	GTTTAGGGTTAAGGGT	GTTTTAGGGTT	432.449005	139	15	
2217649	NC_012879.2	61233618	GTTTTAG	GTTTAG	304.154999	117	24	

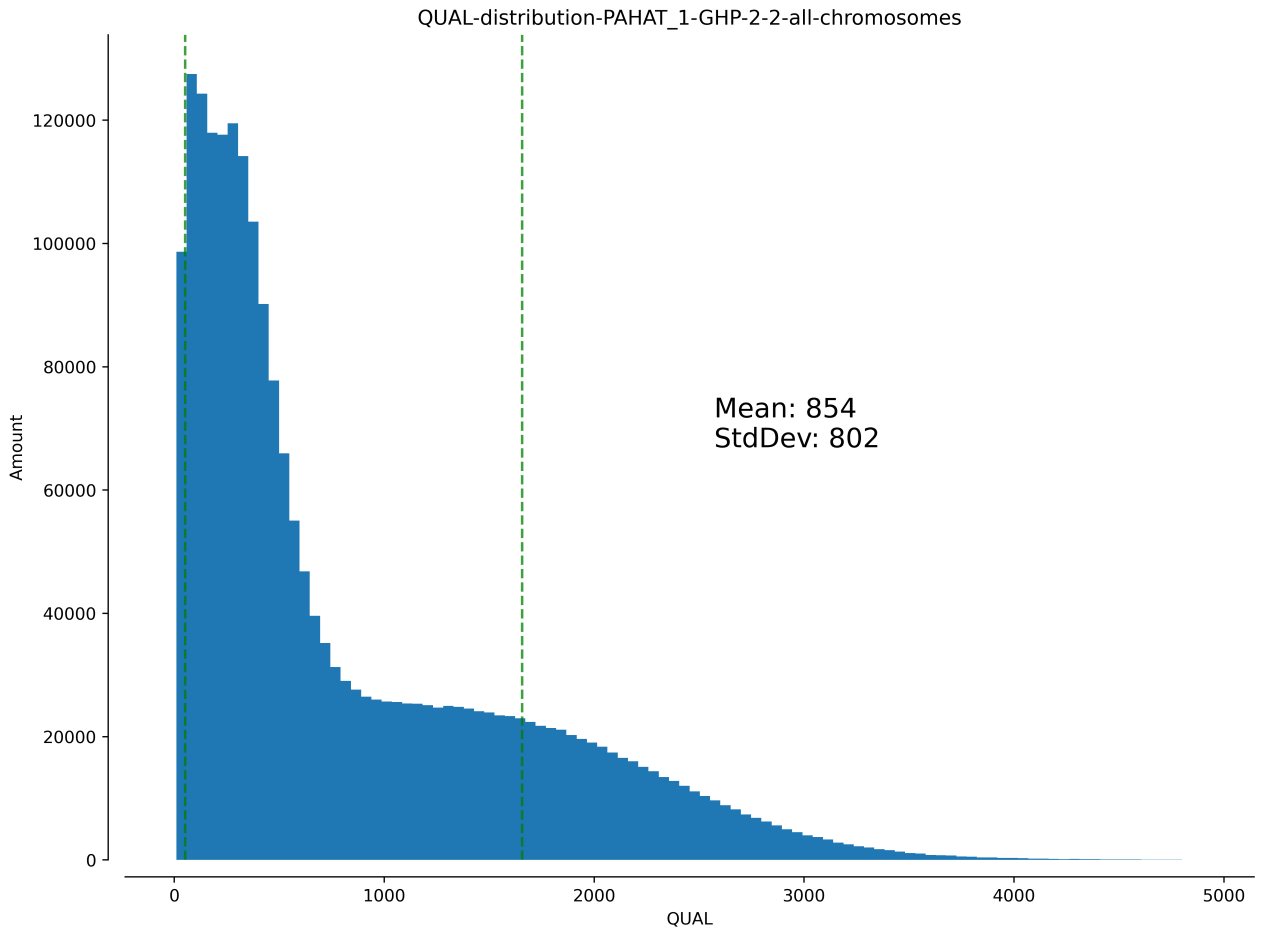
2217650 rows × 17 columns

Verify DP Histogram Cutoff Off by Mean±StdDev

In [29]:
```
plot_variant_hist(samples, vcf_df_01, 'all', 'DP', bins=200, xmax=200)
```



In [30]:
```
plot_variant_hist(samples, vcf_df_01, 'all', 'QUAL', bins=100, MSTD=True)
```



Contingency Table After DP Cutoff by Mean±StdDev

In [31]:
```
contingency_table_2 = contingency_table(samples, vcf_df_01, 'all')
```

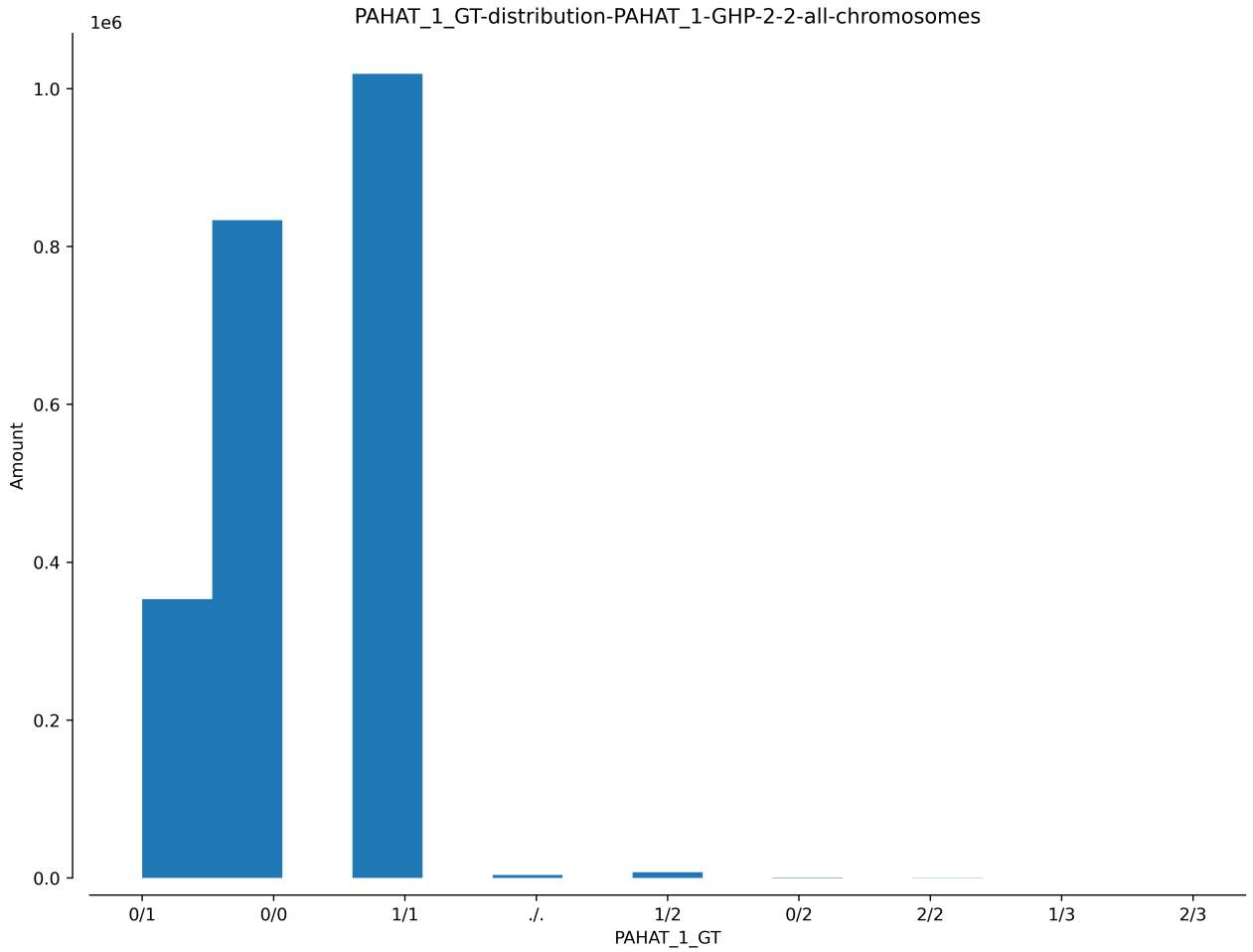
```
Contingency Table - Chromosome all

                GHP-2-2_GT
                       0/0     0/1     1/1  other
PAHAT_1_GT 0/0        7349  206016  618142  67287
           0/1      110174  191367   40272  67287
           1/1      306772   53835  616436  67287
           other     67287   67287   67287  67287
```

GT Plot After DP Cutoff by Mean±StdDev

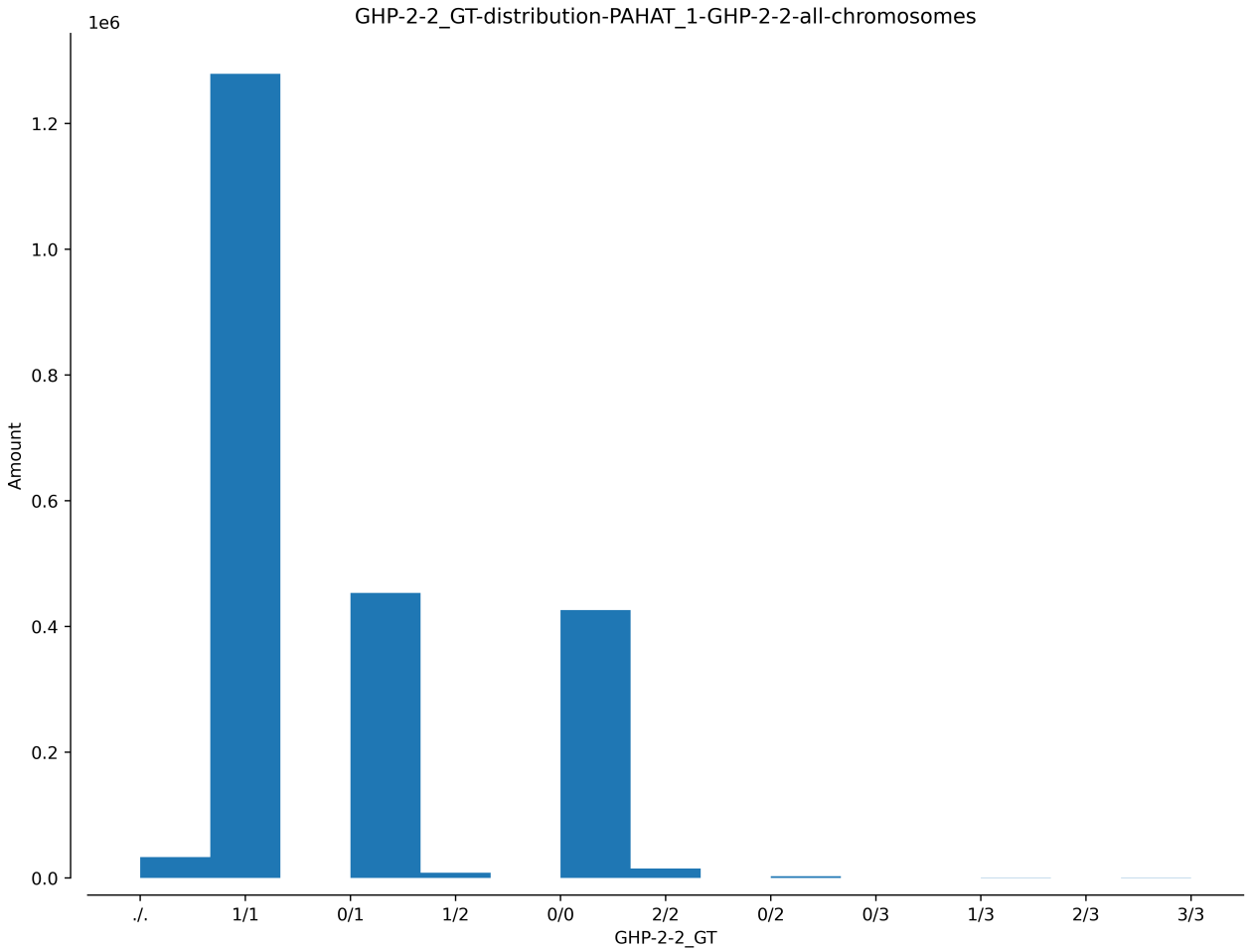
In [32]:
```
# plt.close('all')
# GTplot(samples, vcf_df_01, chrom_len_00)
```

Histogram 'GT' Attribute after DP Cutoff

In [33]:
```
plot_variant_hist(samples, vcf_df_01, 'all', 'PAHAT_1_GT', bins=15)
```



In [34]:
```
plot_variant_hist(samples, vcf_df_01, 'all', 'GHP-2-2_GT', bins=15)
```



PART 3: Extract $\in s$ and ∂ from $TYPE$ Attribute

Extract `ins` and `del` TYPE Attribute

In [35]:
```
extract_type = "TYPE != snp, TYPE != complex, TYPE != mnp"
vcf_df_02 = filter_vcf(vcf_df_01, extract_type)
vcf_df_02
```

Out[35]:

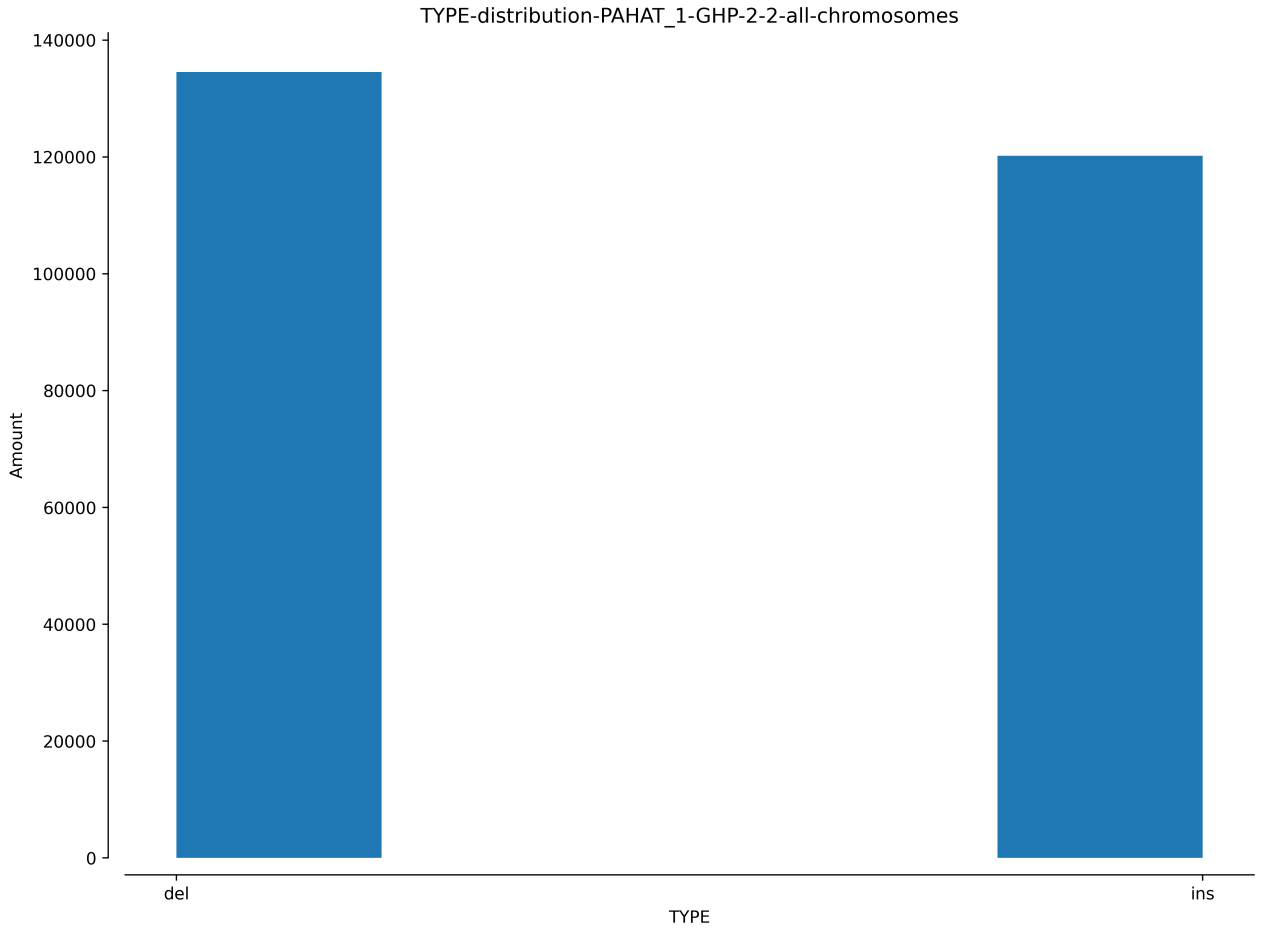
	CHROM	POS	REF	
0	NC_012870.2	1639	ACCCCCCCAGCA	
1	NC_012870.2	2881	GTTTTTTTGTCG	
2	NC_012870.2	3806	ATTTTTTTTACA	
3	NC_012870.2	4512	TATTTCCCACACAAACCACACTCACCCGCTAAAGTGAGCTACAGAT...	
4	NC_012870.2	10162	TGGGGGCA	
...	...	...	...	
254720	NC_012879.2	60955570	TAAAAAAAAAAAAGAAAAGAAAGGGGGAGT	TAA
254721	NC_012879.2	60989473	GATACCCAAA	
	NC_012879.2	61137974	ATTTTTTTAGA	

	CHROM	POS	REF
254723	NC_012879.2	61160465	GCG
254724	NC_012879.2	61233618	GTTTTAG

254725 rows × 17 columns

TYPE `ins` and `del` Histogram Verification

In [36]:
```
plot_variant_hist(samples, vcf_df_02, 'all', 'TYPE', bins=5)
```



Contingency Table - `ins` and `del` TYPE only

In [37]:
```
contingency_table_3 = contingency_table(samples, vcf_df_02, 'all')
```

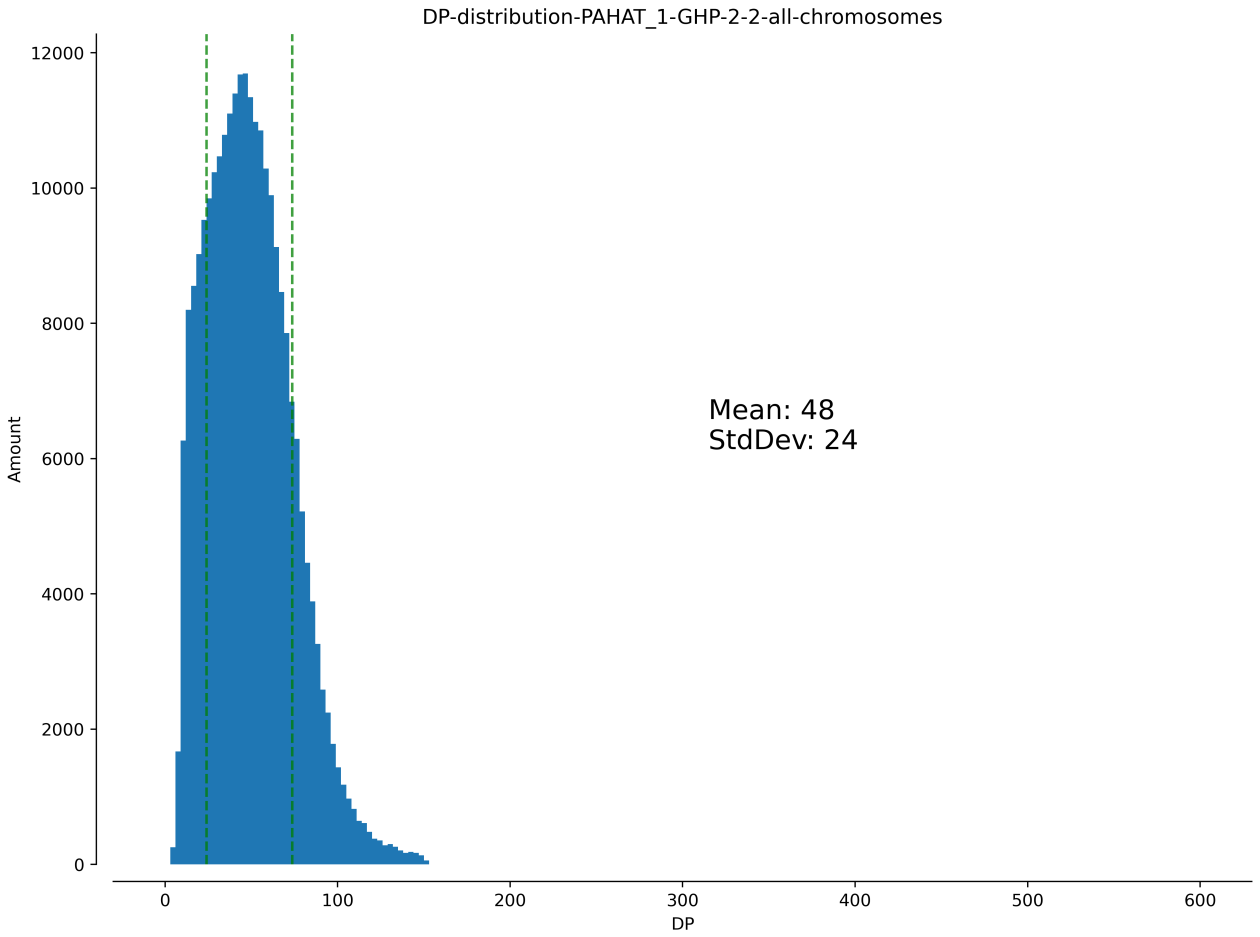
```
Contingency Table - Chromosome all

                GHP-2-2_GT
                       0/0    0/1    1/1  other
PAHAT_1_GT 0/0         305  15850  69051  13418
           0/1        8133   9738   4646  13418
           1/1       48313   7313  77958  13418
           other     13418  13418  13418  13418
```

GT Plot - `ins` and `del` TYPE only

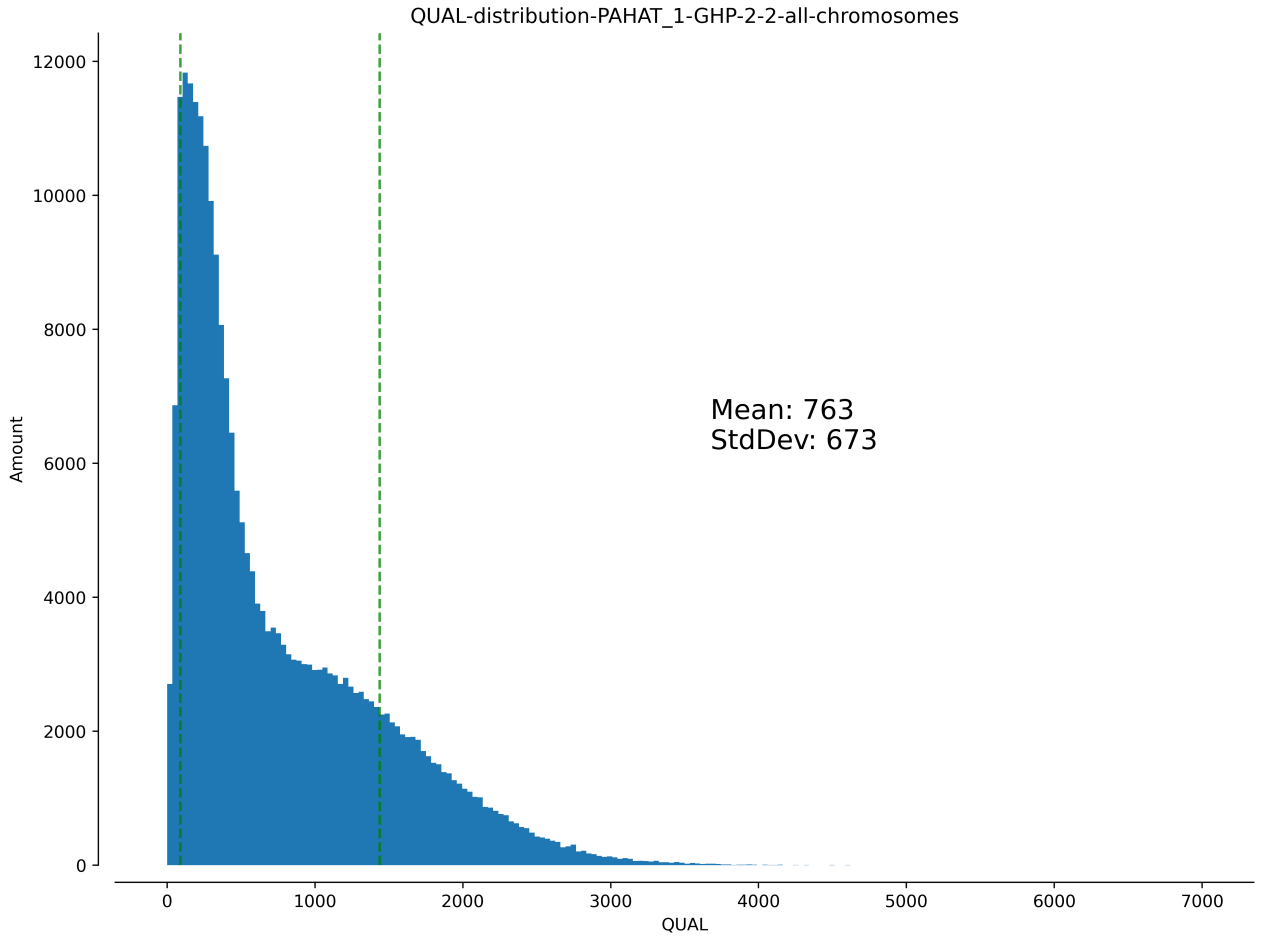
In [38]:
```
# plt.close('all')
# GTplot(samples, vcf_df_02, chrom_len_00)
```

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

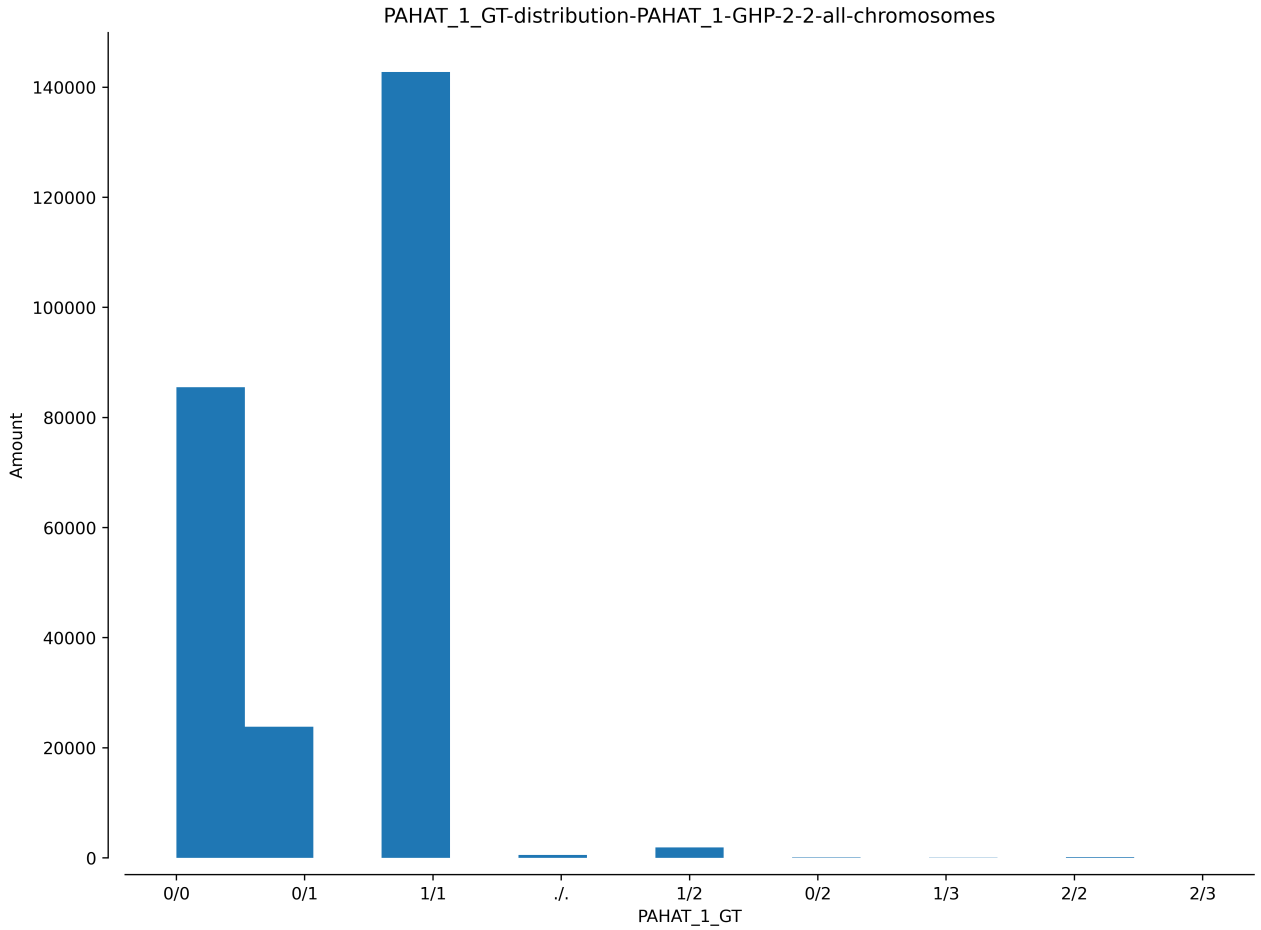
In [39]:
```
plot_variant_hist(samples, vcf_df_02, 'all', 'DP', bins=200, MSTD=True, xmax=600
```



In [40]:
```
plot_variant_hist(samples, vcf_df_02, 'all', 'QUAL', bins=200,  MSTD=True, xmax=
```

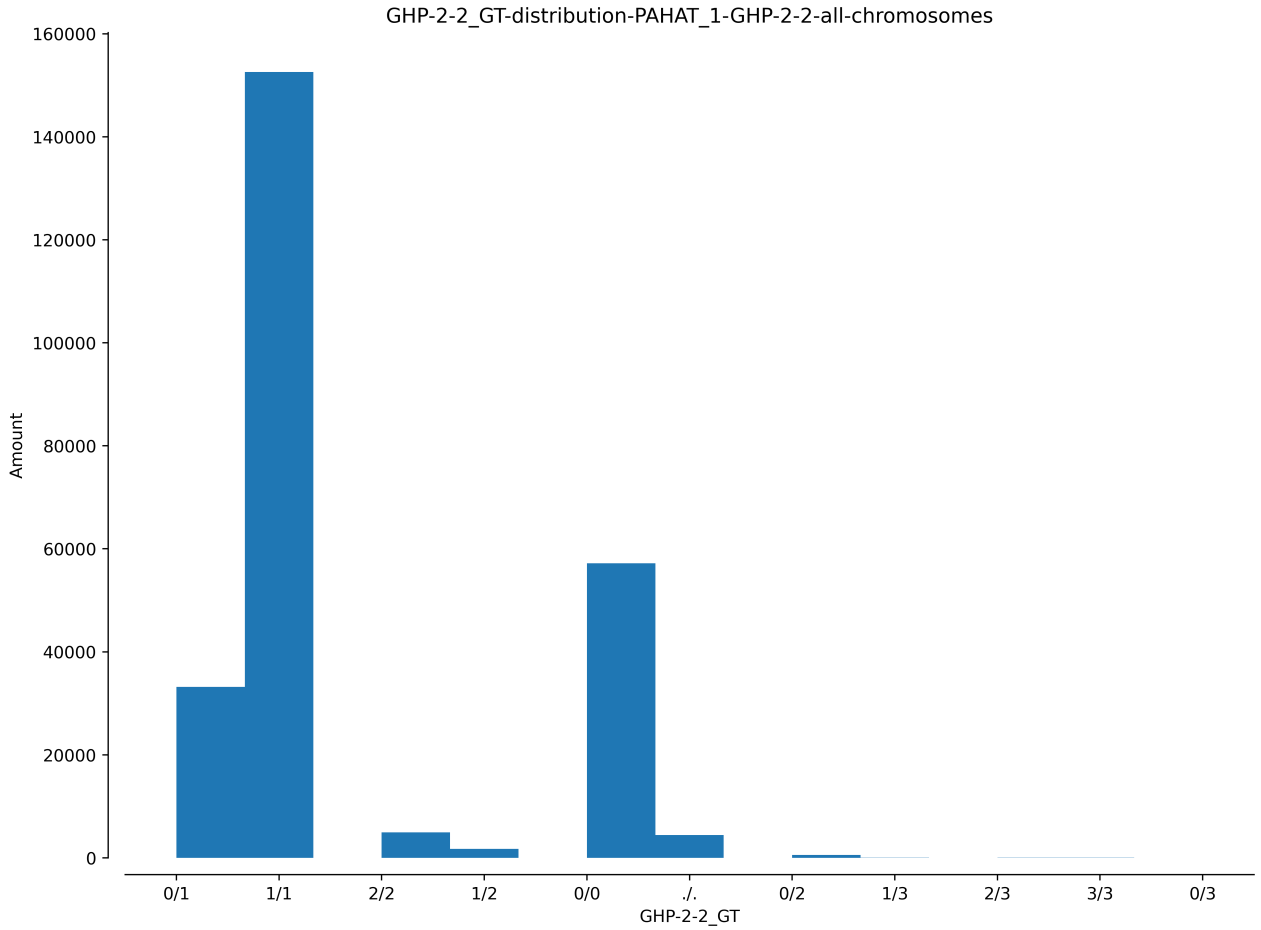


In [41]:
```
plot_variant_hist(samples, vcf_df_02, 'all', 'PAHAT_1_GT', bins=15)
```



In [42]:

```
plot_variant_hist(samples, vcf_df_02, 'all', 'GHP-2-2_GT', bins=15)
```



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

In [43]:
```
# 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 [44]:
```
# plot_variant_hist(samples, vcf_df_03, 'all', 'DP', bins=200, xmax=200)
```

In [45]:
```
# plot_variant_hist(samples, vcf_df_03, 'all', 'QUAL', bins=100, xmax=3500)
```

Contingency Table After QUAL Cutoff by Mean±StdDev

In [46]:
```
# contingency_table_4 = contingency_table(samples, vcf_df_03, 'all')
# contingency_table_4
```

GT Plot After QUAL Cutoff by Mean±StdDev

In [47]:
```
# plt.close('all')
# GTplot(samples, vcf_df_03, chrom_len_00)
```

Histograms after QUAL Cutoff by Mean±StdDev

In [48]:
```
# plot_variant_hist(samples, vcf_df_03, 'all', 'PAHAT_1_GT', bins=9)
```

In [49]:
```
# 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 [50]:
```
PAHAT_gts_filter = "PAHAT_1_GT != ./., PAHAT_1_GT != 0/2, PAHAT_1_GT != 1/2, PAH
vcf_df_04 = filter_vcf(vcf_df_02, PAHAT_gts_filter)

GHP_gts_filter = "GHP-2-2_GT != ./., GHP-2-2_GT != 0/2, GHP-2-2_GT != 1/2, GHP-2
vcf_df_04 = filter_vcf(vcf_df_04, GHP_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
```

Out[50]:

	CHROM	POS	REF	
0	NC_012870.2	1639	ACCCCCCCAGCA	
1	NC_012870.2	2881	GTTTTTTTGTCG	
2	NC_012870.2	3806	ATTTTTTTTACA	
3	NC_012870.2	4512	TATTTCCCACACAAACCACACTCACCCGCTAAAGTGAGCTACAGAT...	
4	NC_012870.2	10162	TGGGGGCA	
...	...	...	...	
163039	NC_012879.2	60955570	TAAAAAAAAAAAAGAAAAGAAAGGGGGAGT	TAA
163040	NC_012879.2	60989473	GATACCCAAA	
163041	NC_012879.2	61137974	ATTTTTTTAGA	
163042	NC_012879.2	61160465	GCG	
163043	NC_012879.2	61233618	GTTTTAG	

163044 rows × 17 columns

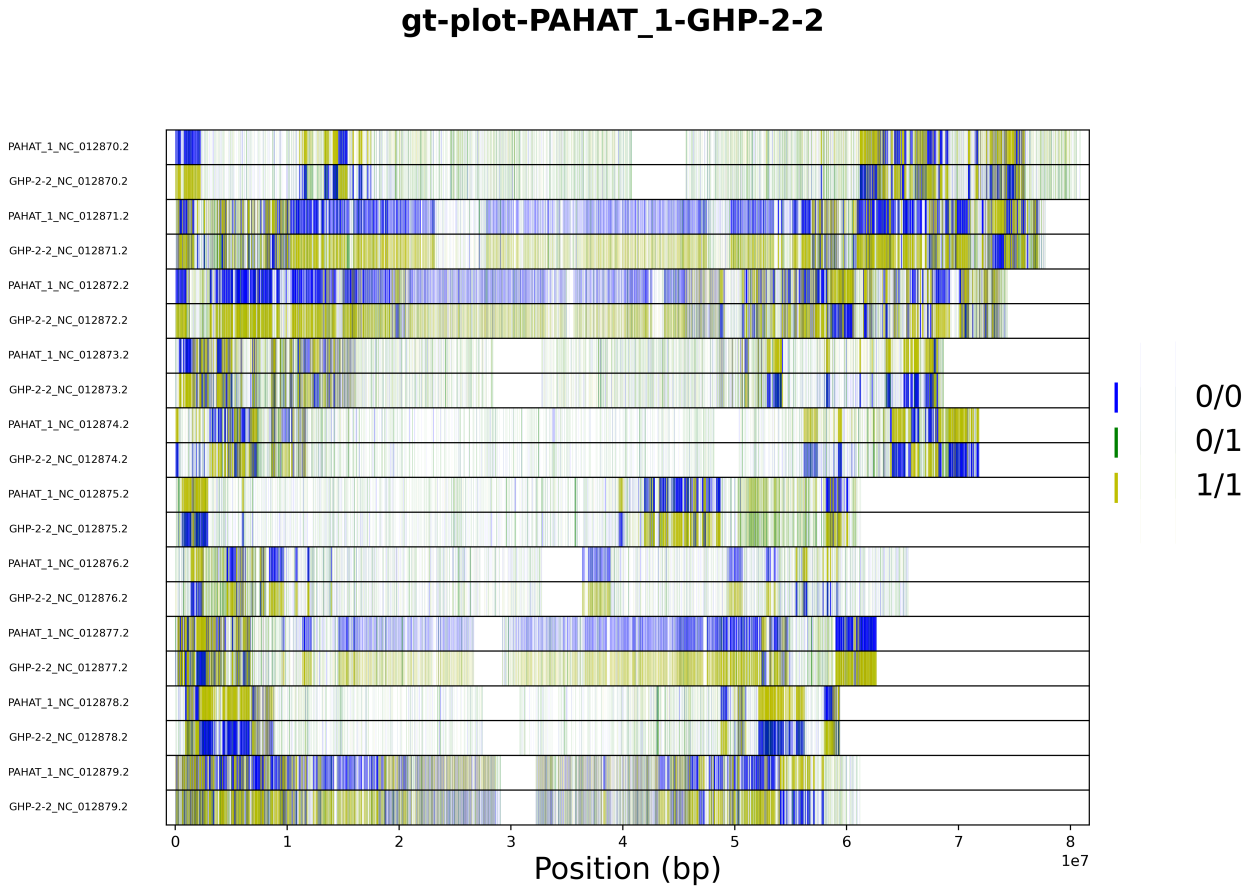
gency Table after GT Filtering

In [51]:
```
contingency_table_5 = contingency_table(samples, vcf_df_04, 'all')
```

```
Contingency Table - Chromosome all

                    GHP-2-2_GT
                           0/0    0/1    1/1 other
PAHAT_1_GT 0/0               0  15850  69051     0
           0/1            8133   9738   4646     0
           1/1           48313   7313      0     0
           other             0      0      0     0
```

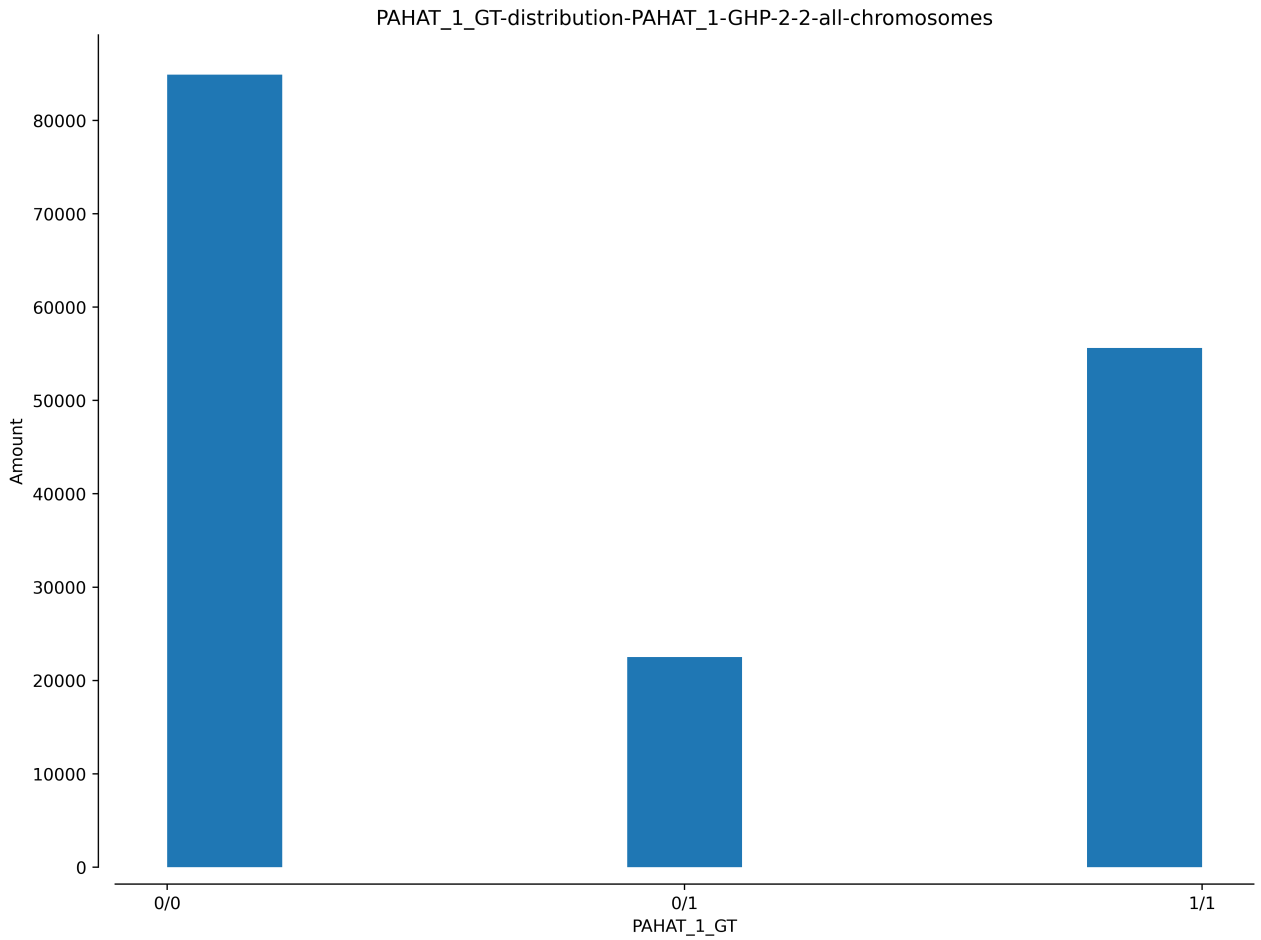
GT Plot after GT Filtering

In [52]:
```
plt.close('all')
GTplot(samples, vcf_df_04, chrom_len_00)
```

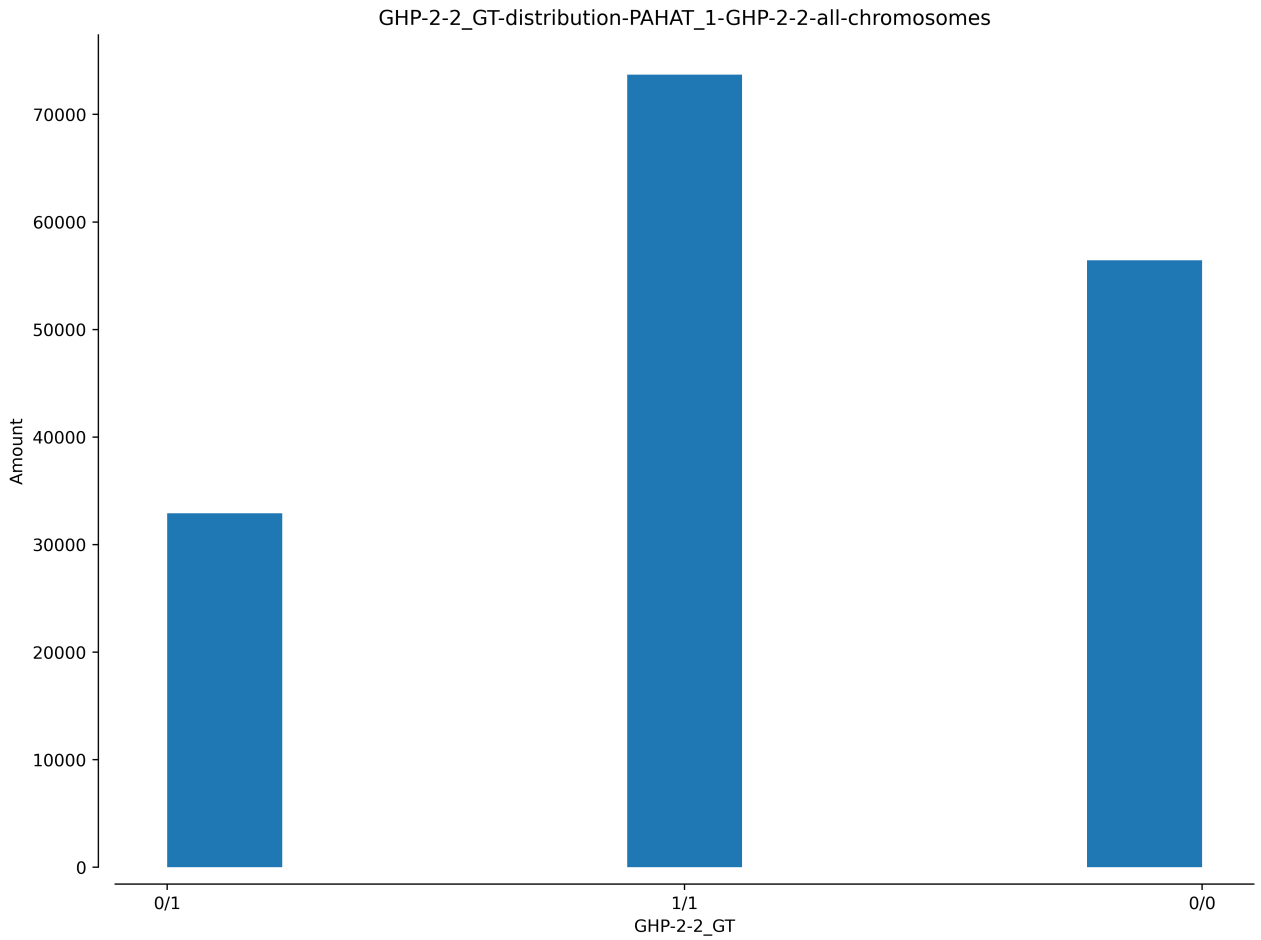


Histograms GT after GT Filtering

In [53]:
```
plot_variant_hist(samples, vcf_df_04, 'all', 'PAHAT_1_GT', bins=9)
```



In [54]:
```
plot_variant_hist(samples, vcf_df_04, 'all', 'GHP-2-2_GT', bins=9)
```



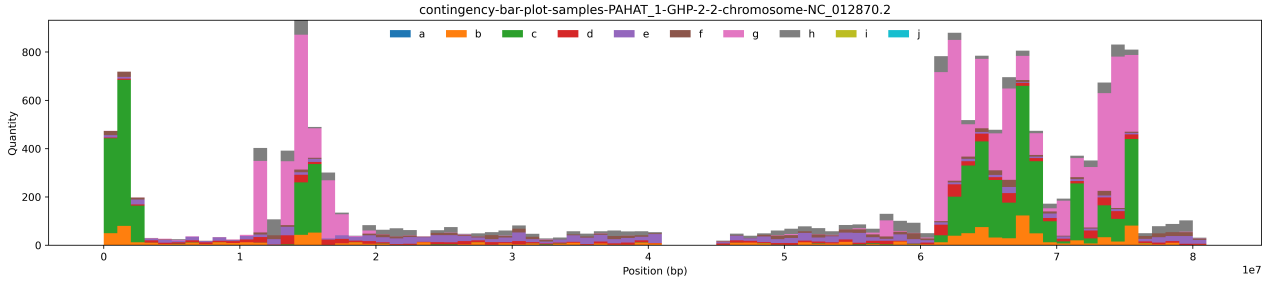
PART 6: Stacked Bar Plots

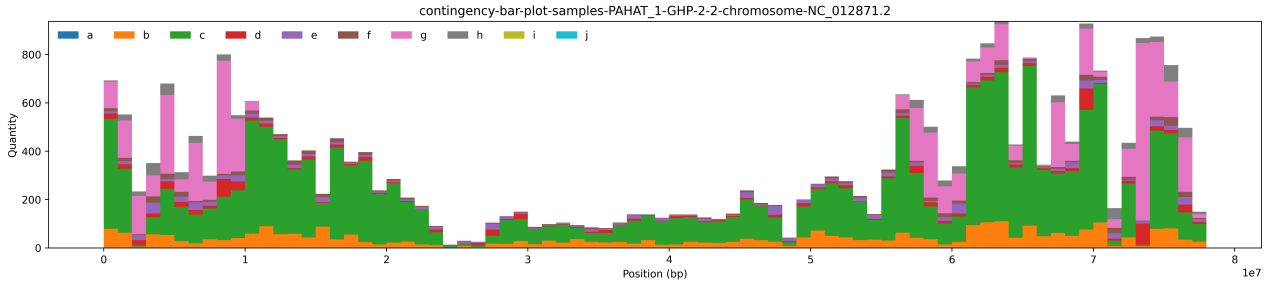
In [59]:
```
ct_guide()
```

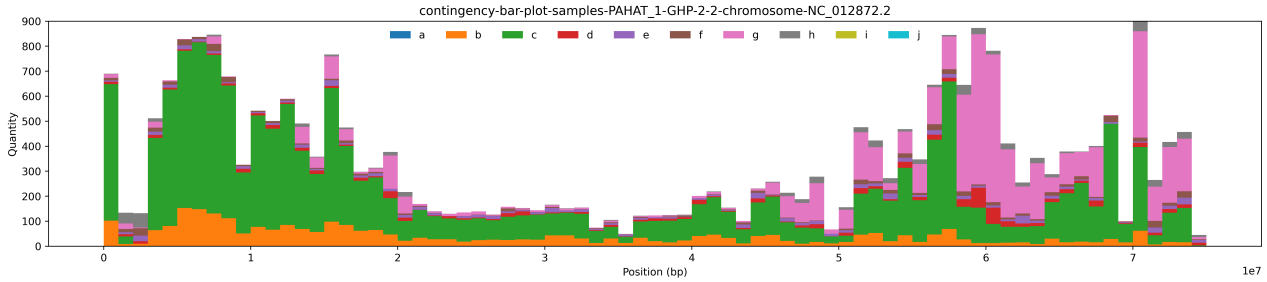
Out[59]:

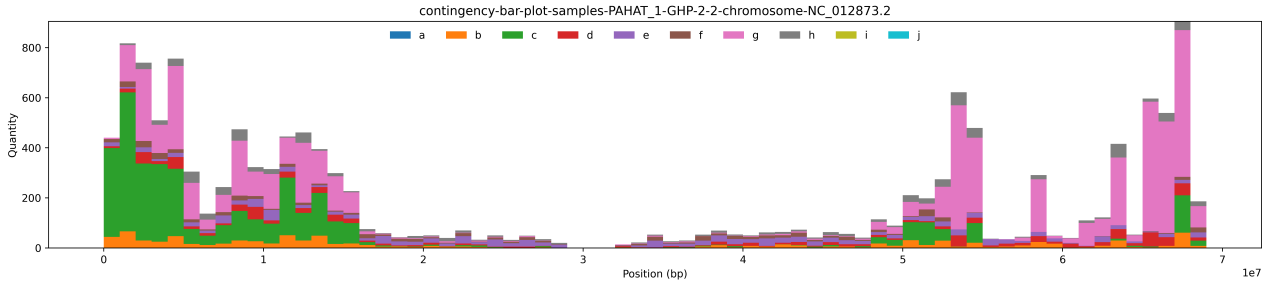
		Mutant			
		0/0	**0/1**	**1/1**	**other**
Progenitor	**0/0**	a	b	c	
	0/1	d	e	f	
	1/1	g	h	i	
	other				j

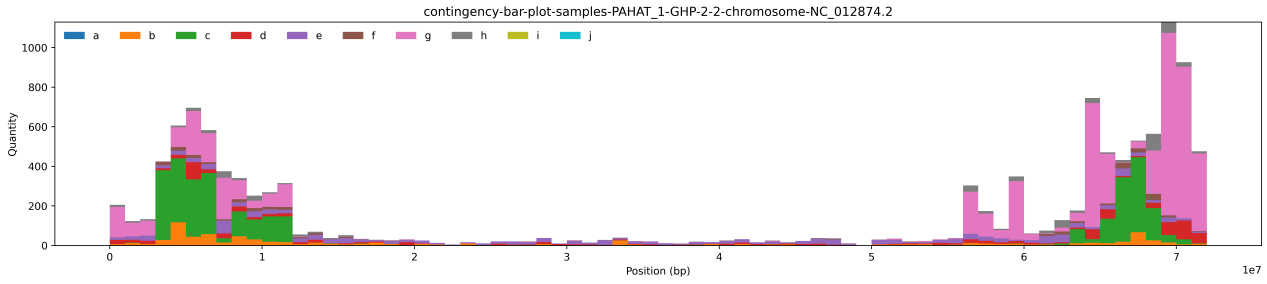
In [55]:
```
plt.close('all')
window_size = 1000000
CTbarPlots(samples, vcf_df_04, chrom_len_00, window_size)
```

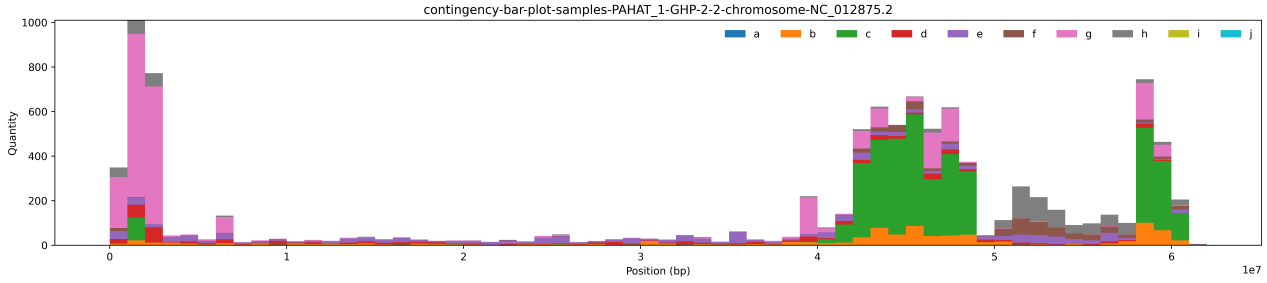




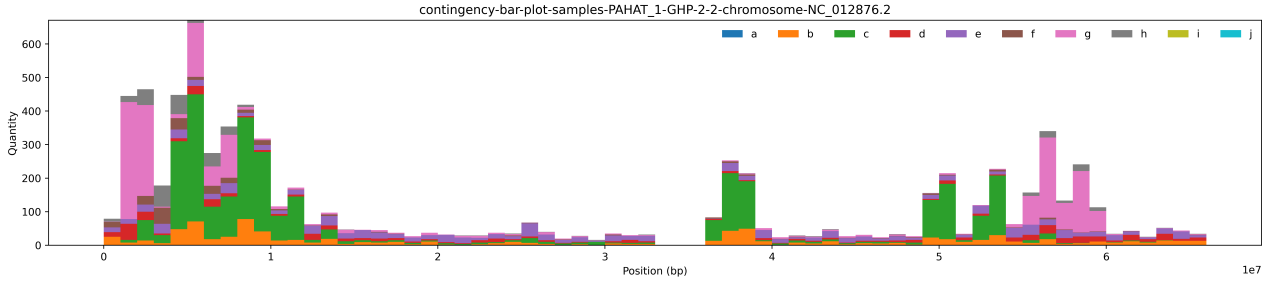


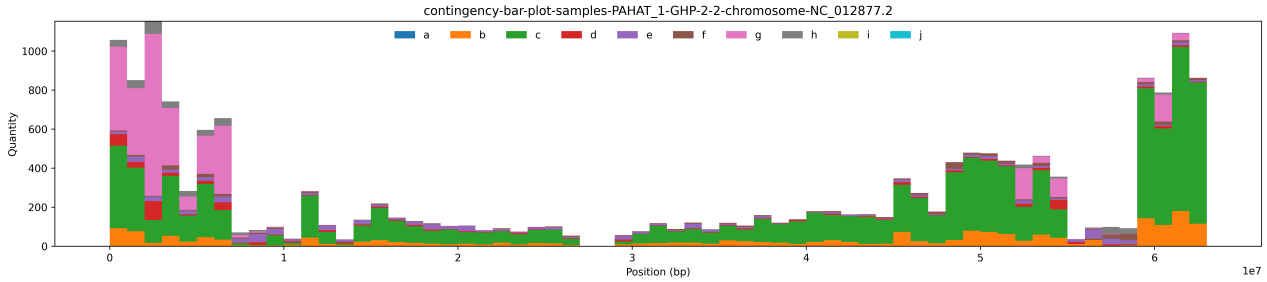


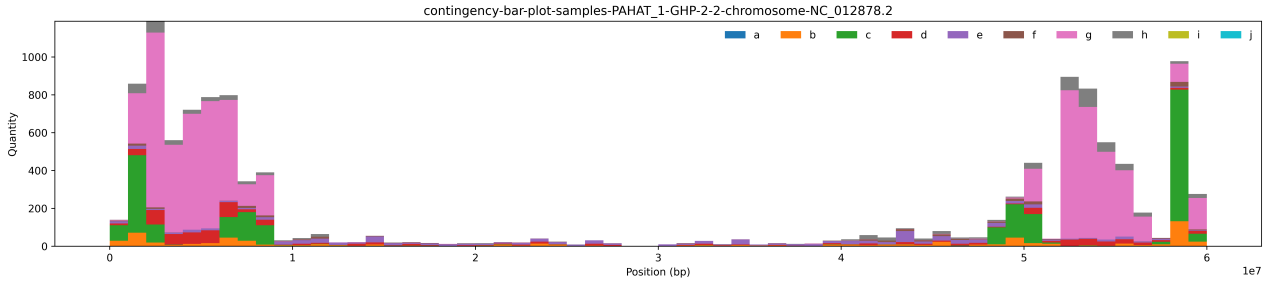


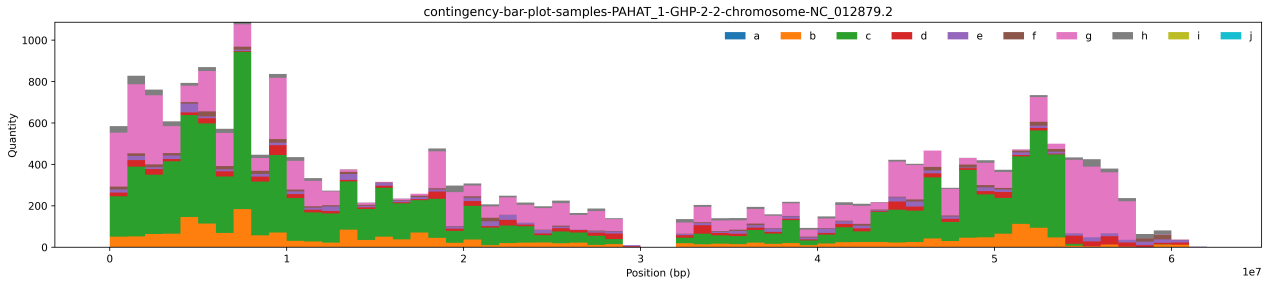


Processing math: 100%





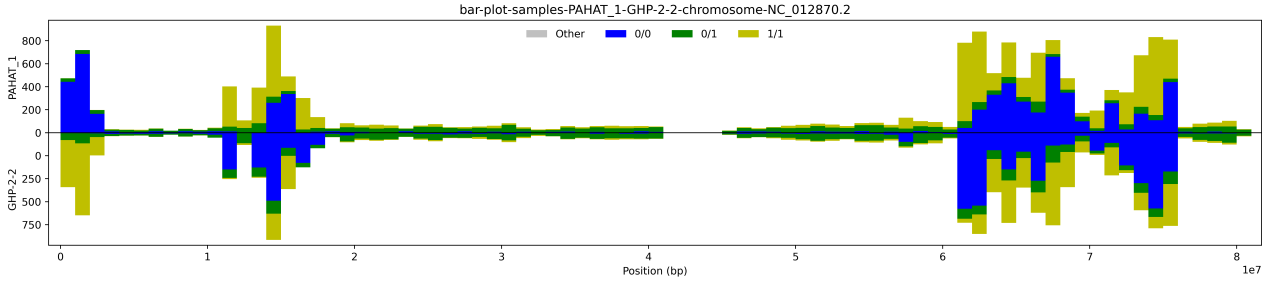




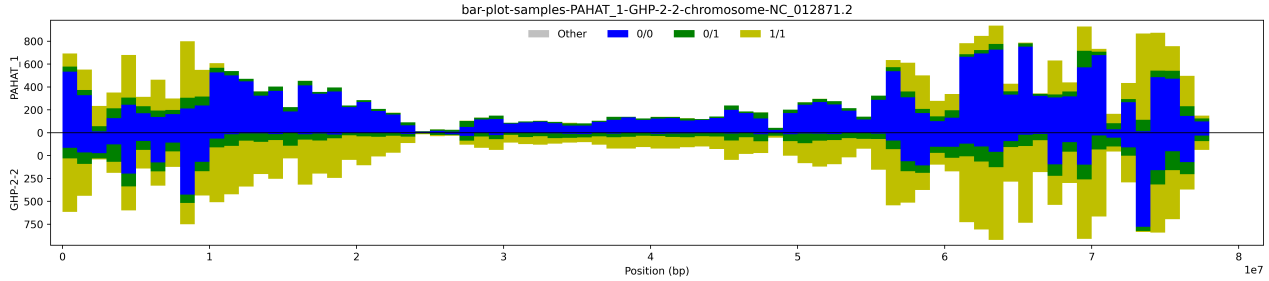
PART 7: Bar Plots per Chromosome

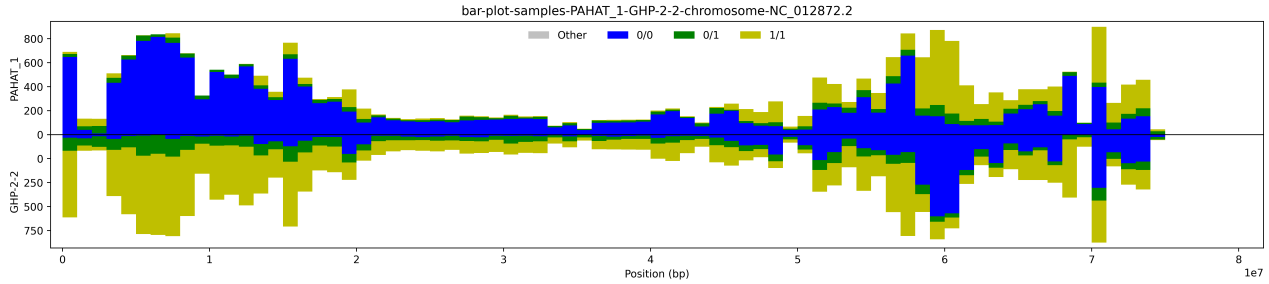
In [56]:

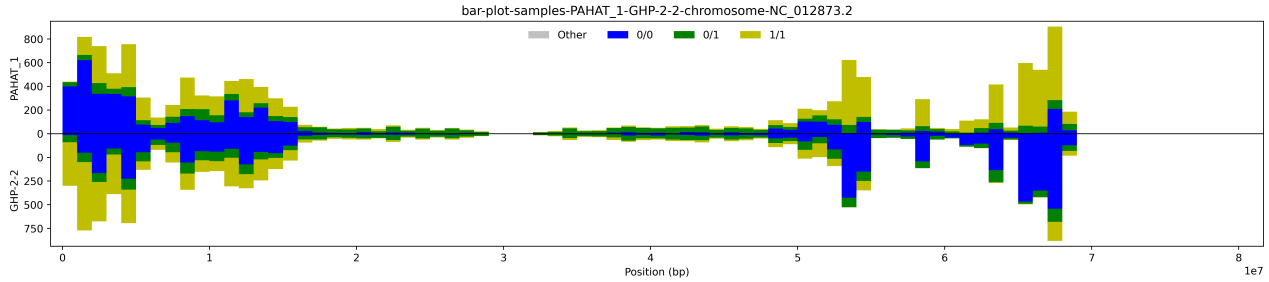
```
# suppress all the warnings from the inverted tickes of bar plots
import warnings
warnings.filterwarnings('ignore')

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

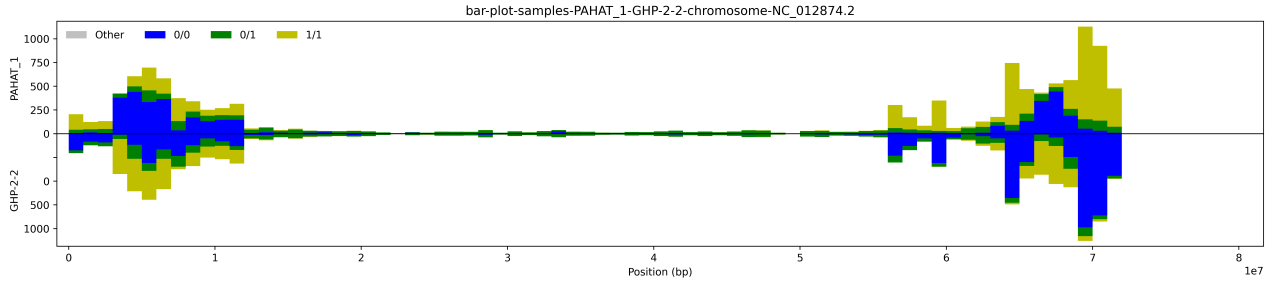


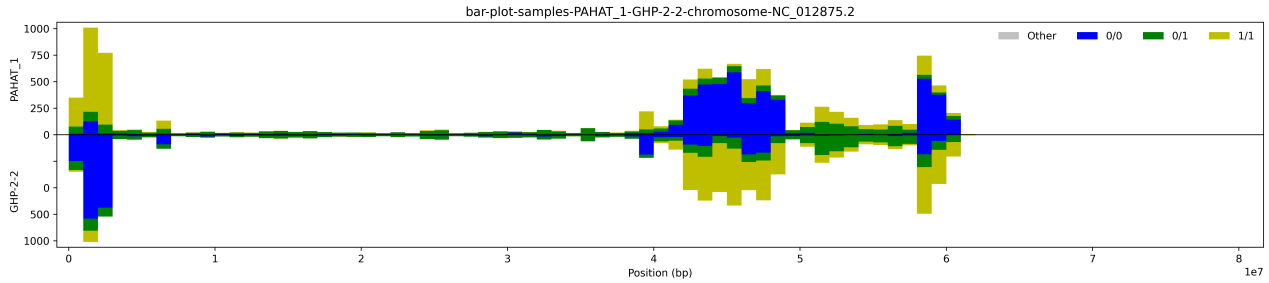
Processing math: 100%

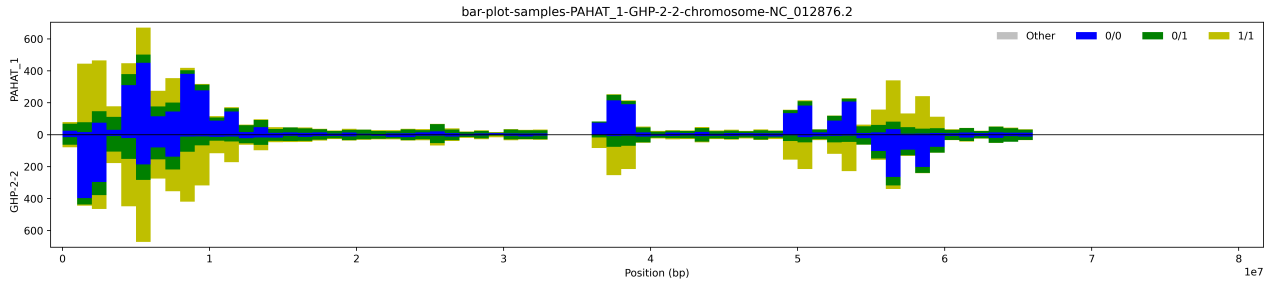


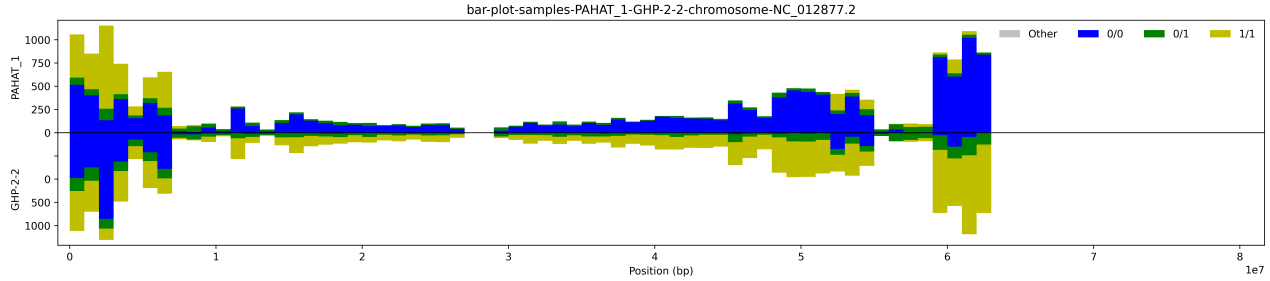


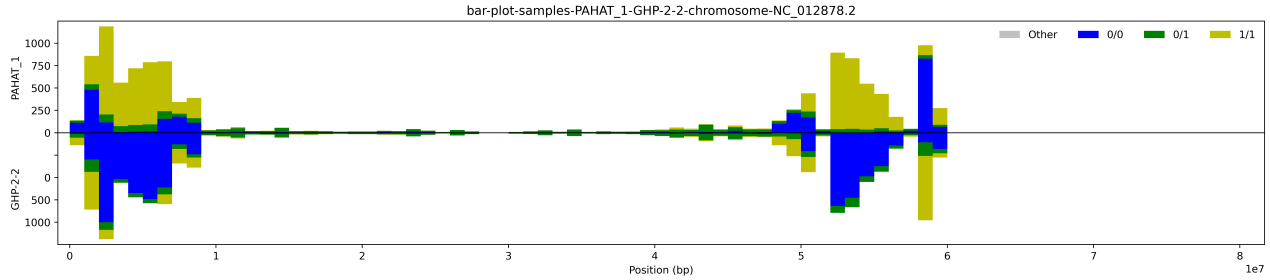


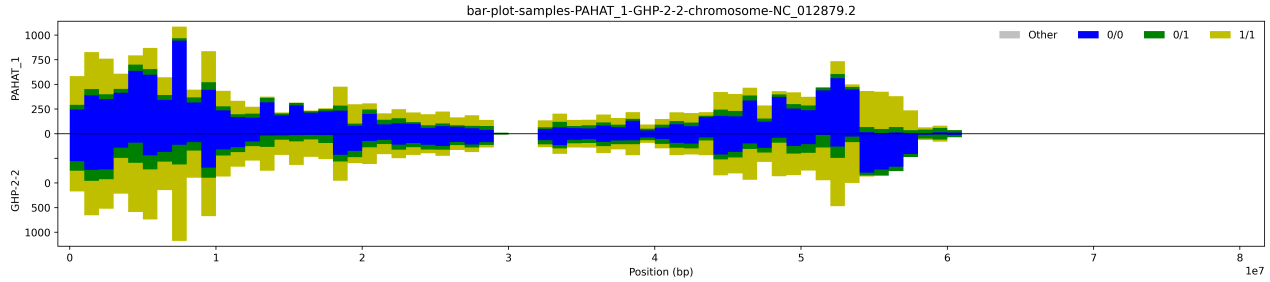








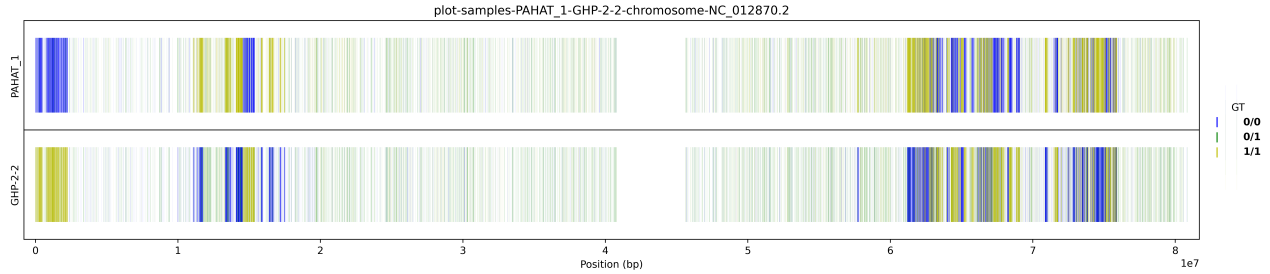


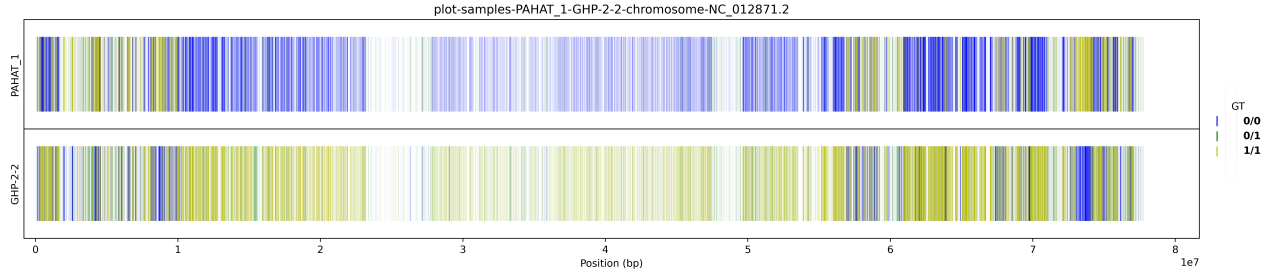


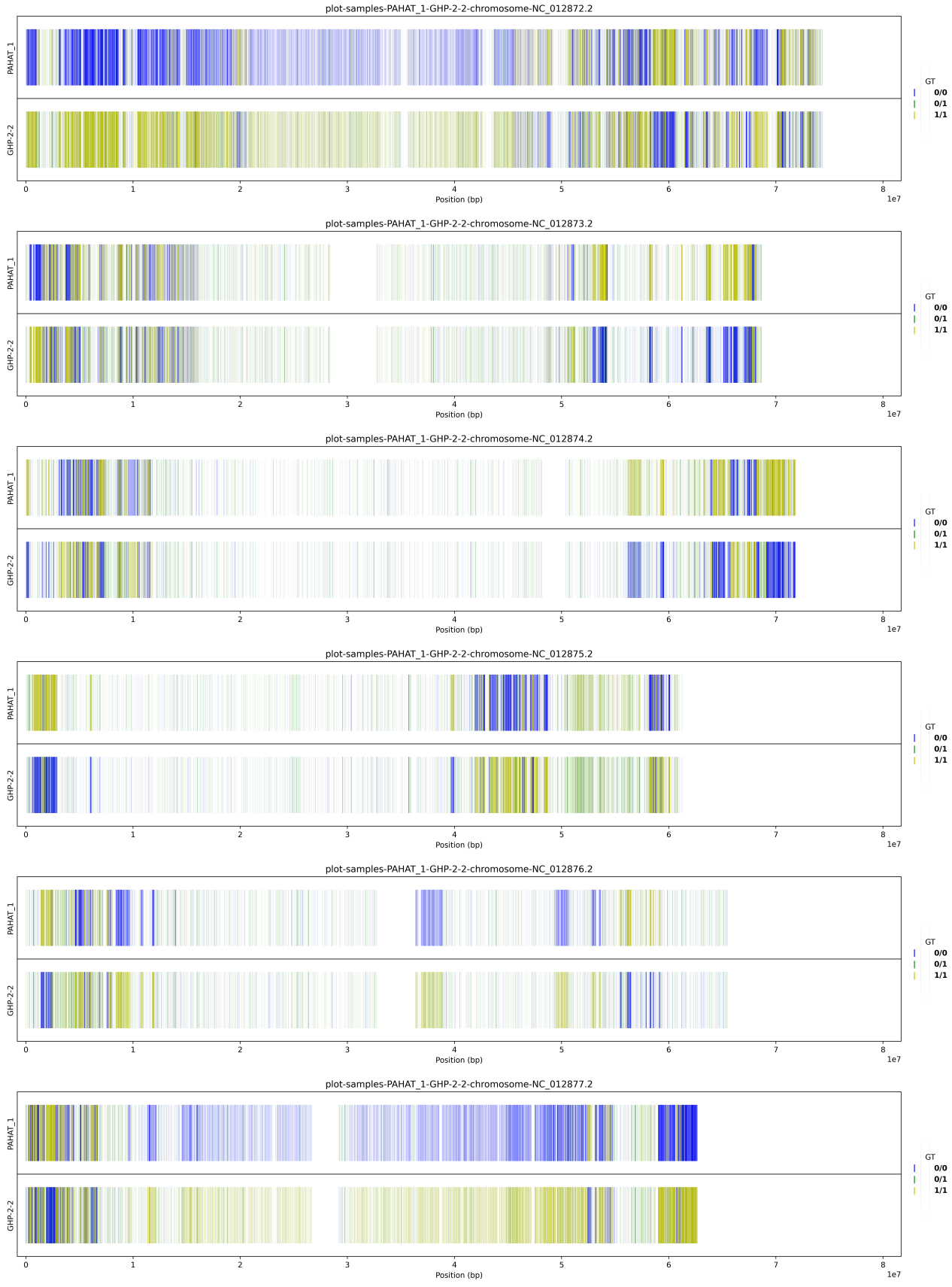
PART 8: GT Plots per Chromosome

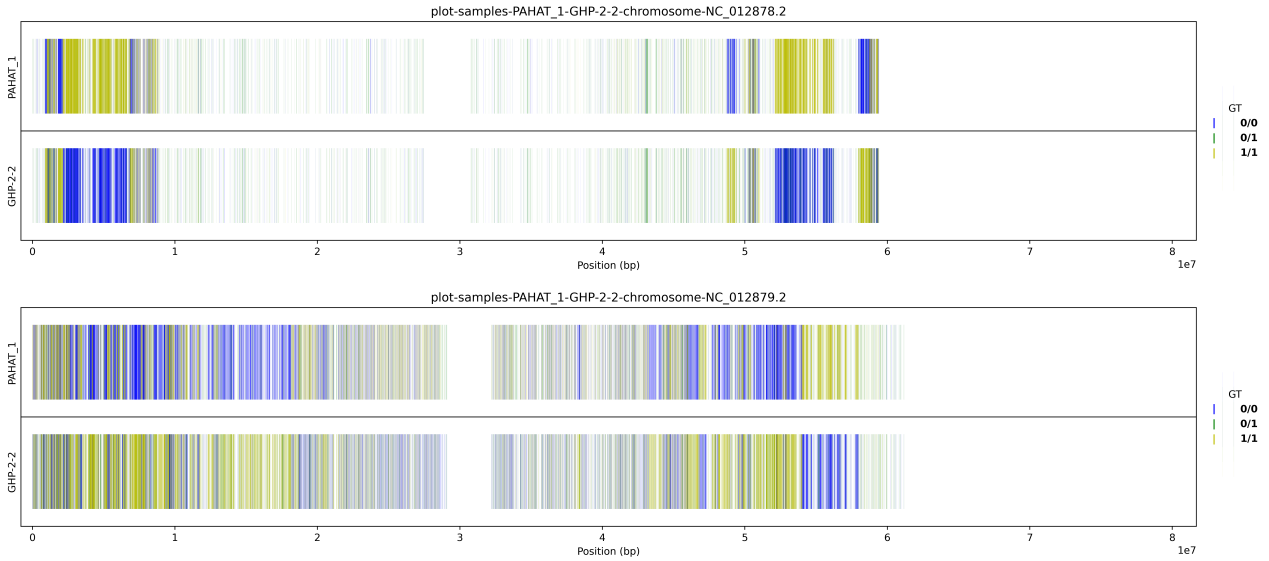
In [57]:

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









PART 9: Contingency Table per Chromosome

In [58]:

```
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)
```

```
Contingency Table - Chromosome NC_012870.2

                GHP-2-2_GT
                       0/0   0/1   1/1 other
PAHAT_1_GT 0/0           0  1179  4670     0
           0/1         871  1278   635     0
           1/1        5900  1419     0     0
           other         0     0     0     0

Contingency Table - Chromosome NC_012871.2

                GHP-2-2_GT
                       0/0   0/1    1/1 other
PAHAT_1_GT 0/0           0  3090  15467     0
           0/1        1039  1010    656     0
           1/1        5268   733      0     0
           other         0     0      0     0

Contingency Table - Chromosome NC_012872.2

                GHP-2-2_GT
                       0/0   0/1    1/1 other
PAHAT_1_GT 0/0           0  3002  14417     0
           0/1         888   777    638     0
           1/1        5683   685      0     0
           other         0     0      0     0

Contingency Table - Chromosome NC_012873.2

                GHP-2-2_GT
                       0/0   0/1   1/1 other
```

```
PAHAT_1_GT 0/0            0   946  3526     0
           0/1          901  1090   551     0
           1/1         5780   882     0     0
           other          0     0     0     0

Contingency Table - Chromosome NC_012874.2

                 GHP-2-2_GT
                        0/0   0/1   1/1 other
PAHAT_1_GT 0/0            0   850  2945     0
           0/1          894  1206   302     0
           1/1         5307   564     0     0
           other          0     0     0     0

Contingency Table - Chromosome NC_012875.2

                 GHP-2-2_GT
                        0/0   0/1   1/1 other
PAHAT_1_GT 0/0            0   905  3644     0
           0/1          599  1049   509     0
           1/1         2659   855     0     0
           other          0     0     0     0

Contingency Table - Chromosome NC_012876.2

                 GHP-2-2_GT
                        0/0  0/1   1/1 other
PAHAT_1_GT 0/0            0  873  2815     0
           0/1          553  988   261     0
           1/1         1819  365     0     0
           other          0    0     0     0

Contingency Table - Chromosome NC_012877.2

                 GHP-2-2_GT
                        0/0   0/1   1/1 other
PAHAT_1_GT 0/0            0  2006  9975     0
           0/1          603   856   449     0
           1/1         3038   414     0     0
           other          0     0     0     0

Contingency Table - Chromosome NC_012878.2

                 GHP-2-2_GT
                        0/0  0/1   1/1 other
PAHAT_1_GT 0/0            0  708  2152     0
           0/1          811  711   208     0
           1/1         6689  714     0     0
           other          0    0     0     0

Contingency Table - Chromosome NC_012879.2

                 GHP-2-2_GT
                        0/0   0/1   1/1 other
PAHAT_1_GT 0/0            0  2291  9440     0
           0/1          974   773   437     0
           1/1         6170   682     0     0
           other          0     0     0     0
```