In [ ]:
```
import sys
!{sys.executable} -m pip install --user scikit-allel
```

In [1]:
```
import numpy as np
import scipy
import pandas
import matplotlib as mpl
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns
sns.set_style('white')
sns.set_style('ticks')
sns.set_context('notebook')
import h5py
import allel; print('scikit-allel', allel.__version__)
```

```
scikit-allel 1.3.8
```

VCF to HDF5

In [4]:
```
allel.vcf_to_hdf5('/users/mcevoysu/scratch/output/Qpubescens/vcf_filterin
```

Get data

In [5]:
```
callset_var_fn = '/users/mcevoysu/scratch/output/Qpubescens/scikit-allel/
callset_var = h5py.File(callset_var_fn, mode='r')
```

In [6]:
```
calldata_var = callset_var['calldata']
list(calldata_var)
```

Out[6]:
```
['AD', 'DP', 'GQ', 'GT', 'MIN_DP', 'PGT', 'PID', 'PL', 'PS', 'RGQ', 'S
B']
```

In [7]:
```
list(callset_var['variants'])
```

Out[7]:
```
['AC',
 'AF',
 'ALT',
 'AN',
 'BaseQRankSum',
 'CHROM',
 'DP',
 'END',
 'ExcessHet',
 'FILTER_LowQual',
 'FILTER_PASS',
 'FS',
 'ID',
 'InbreedingCoeff',
 'MLEAC',
 'MLEAF',
 'MQ',
 'MQRankSum',
 'POS',
 'QD',
 'QUAL',
 'RAW_MQandDP',
 'REF',
 'ReadPosRankSum',
 'SOR',
 'altlen',
 'is_snp',
 'numalt']
```

Make datasets

In [8]:
```
variants = allel.VariantChunkedTable(callset_var['variants'])
variants
```

Out[8]: <VariantChunkedTable shape=(670805,) dtype=[('AC', '<i4', (3,)), ('AF', '<f4', (3,)), ('ALT', 'O', (3,)), ('AN', '<i4'), ('BaseQRankSum', '<f4'), ('CHROM', 'O'), ('DP', '<i4'), ('END', '<i4'), ('ExcessHet', '<f4'), ('FILTER_LowQual', '?'), ('FILTER_PASS', '?'), ('FS', '<f4'), ('ID', 'O'), ('InbreedingCoeff', '<f4'), ('MLEAC', '<i4', (3,)), ('MLEAF', '<f4', (3,)), ('MQ', '<f4'), ('MQRankSum', '<f4'), ('POS', '<i4'), ('QD', '<f4'), ('QUAL', '<f4'), ('RAW_MQandDP', '<i4', (2,)), ('REF', 'O'), ('ReadPosRankSum', '<f4'), ('SOR', '<f4'), ('altlen', '<i4', (3,)), ('is_snp', '?'), ('numalt', '<i4')] nbytes=114.5M cbytes=24.3M cratio=4.7 values=h5py._hl.group.Group>

	AC	AF	ALT	AN	BaseQRankSum	CHROM	DP
0	[4 -1 -1]	[0.016 nan nan]	[b'G' b'' b'']	250	nan	b'Qrob_Chr01'	17
1	[2 -1 -1]	[0.007874 nan nan]	[b'C' b'' b'']	250	nan	b'Qrob_Chr01'	18
2	[1 -1 -1]	[0.003937 nan nan]	[b'A' b'' b'']	250	0.0	b'Qrob_Chr01'	44
...							
670802	[15 -1 -1]	[0.059 nan nan]	[b'G' b'' b'']	250	3.27	b'Qrob_H2.3_Sc0001194'	182
670803	[15 -1 -1]	[0.059 nan nan]	[b'G' b'' b'']	250	3.27	b'Qrob_H2.3_Sc0001194'	180
670804	[18 -1 -1]	[0.071 nan nan]	[b'T' b'' b'']	250	1.81	b'Qrob_H2.3_Sc0001194'	168

In [9]:
```
variants_np = variants[:]
rawsnps = variants_np.query('(is_snp == True)')
rawsnps
```

Out[9]: <VariantTable shape=(452557,) dtype=(numpy.record, [('AC', '<i4', (3,)), ('AF', '<f4', (3,)), ('ALT', 'O', (3,)), ('AN', '<i4'), ('BaseQRankSum', '<f4'), ('CHROM', 'O'), ('DP', '<i4'), ('END', '<i4'), ('ExcessHet', '<f4'), ('FILTER_LowQual', '?'), ('FILTER_PASS', '?'), ('FS', '<f4'), ('ID', 'O'), ('InbreedingCoeff', '<f4'), ('MLEAC', '<i4', (3,)), ('MLEAF', '<f4', (3,)), ('MQ', '<f4'), ('MQRankSum', '<f4'), ('POS', '<i4'), ('QD', '<f4'), ('QUAL', '<f4'), ('RAW_MQandDP', '<i4', (2,)), ('REF', 'O'), ('ReadPosRankSum', '<f4'), ('SOR', '<f4'), ('altlen', '<i4', (3,)), ('is_snp', '?'), ('numalt', '<i4')])>

	AC	AF	ALT	AN	BaseQRankSum	CHROM	DP
0	[4 -1 -1]	[0.016 nan nan]	[b'G' b'' b'']	250	nan	b'Qrob_Chr01'	17
1	[2 -1 -1]	[0.007874 nan nan]	[b'C' b'' b'']	250	nan	b'Qrob_Chr01'	18
2	[1 -1 -1]	[0.003937 nan nan]	[b'A' b'' b'']	250	0.0	b'Qrob_Chr01'	44
...							
452554	[15 -1 -1]	[0.059 nan nan]	[b'G' b'' b'']	250	3.27	b'Qrob_H2.3_Sc0001194'	182
452555	[15 -1 -1]	[0.059 nan nan]	[b'G' b'' b'']	250	3.27	b'Qrob_H2.3_Sc0001194'	180
452556	[18 -1 -1]	[0.071 nan nan]	[b'T' b'' b'']	250	1.81	b'Qrob_H2.3_Sc0001194'	168

In [10]:
```
notsnp = variants_np.query('(is_snp != True)')
notsnp
```

Out[10]: <VariantTable shape=(218248,) dtype=(numpy.record, [('AC', '<i4', (3,)), ('AF', '<f4', (3,)), ('ALT', 'O', (3,)), ('AN', '<i4'), ('BaseQRankSum', '<f4'), ('CHROM', 'O'), ('DP', '<i4'), ('END', '<i4'), ('ExcessHet', '<f4'), ('FILTER_LowQual', '?'), ('FILTER_PASS', '?'), ('FS', '<f4'), ('ID', 'O'), ('InbreedingCoeff', '<f4'), ('MLEAC', '<i4', (3,)), ('MLEAF', '<f4', (3,)), ('MQ', '<f4'), ('MQRankSum', '<f4'), ('POS', '<i4'), ('QD', '<f4'), ('QUAL', '<f4'), ('RAW_MQandDP', '<i4', (2,)), ('REF', 'O'), ('ReadPosRankSum', '<f4'), ('SOR', '<f4'), ('altlen', '<i4', (3,)), ('is_snp', '?'), ('numalt', '<i4')])>

	AC	AF	ALT	AN	BaseQRankSum	CHROM	DP
0	[2 -1 -1]	[0.007874 nan nan]	[b'*' b'' b'']	250	-1.169	b'Qrob_Chr01'	189
1	[16 -1 -1]	[0.064 nan nan]	[b'*' b'' b'']	246	nan	b'Qrob_Chr01'	82
2	[16 -1 -1]	[0.065 nan nan]	[b'*' b'' b'']	244	nan	b'Qrob_Chr01'	80
...							
218245	[2 -1 -1]	[0.007874 nan nan]	[b'*' b'' b'']	250	nan	b'Qrob_H2.3_Sc0001163'	91
218246	[1 -1 -1]	[0.003937 nan nan]	[b'*' b'' b'']	250	nan	b'Qrob_H2.3_Sc0001163'	275
218247	[1 -1 -1]	[0.003937 nan nan]	[b'*' b'' b'']	250	nan	b'Qrob_H2.3_Sc0001163'	275

Plot function

In [11]:
```
def plot_hist(f, dsubset='', bins=30, ):
    if dsubset == 'var':
        x = variants[f][:]
        l = 'Variant'
    elif dsubset == 'snp':
        x = rawsnps[f][:]
        l = 'Raw SNP'
    elif dsubset == 'notsnp':
        x = notsnp[f][:]
        l = 'Raw Not SNP'
    elif dsubset == 'biallelic':
        x = biallelic_np[f][:]
        l = 'Biallelic SNP'
    elif dsubset == 'varsel':
        x = var_selection[f][:]
        l = 'Filtered Variants'
    elif dsubset == 'snpsel':
        x = snp_selection[f][:]
        l = 'Filtered SNP'
    else:
```

```
        x = bi_selection[f][:]
        l = 'Biallelic SNP'
    fig, ax = plt.subplots(figsize=(10, 5))
    sns.despine(ax=ax, offset=10)
    ax.hist(x, bins=bins)
    ax.set_xlabel(f)
    ax.set_ylabel('No. variants')
    ax.set_title('%s %s distribution' % (l, f))
```

Find Biallelic SNPS

In [12]:
```
numalt = rawsnps['numalt']
np.max(numalt)
```

Out[12]:
```
3
```

In [13]:
```
count_numalt = np.bincount(numalt)
count_numalt
```

Out[13]:
```
array([     0, 433684,  18479,    394])
```

In [14]:
```
n_multiallelic = np.sum(count_numalt[2:])
n_multiallelic
```

Out[14]:
```
18873
```

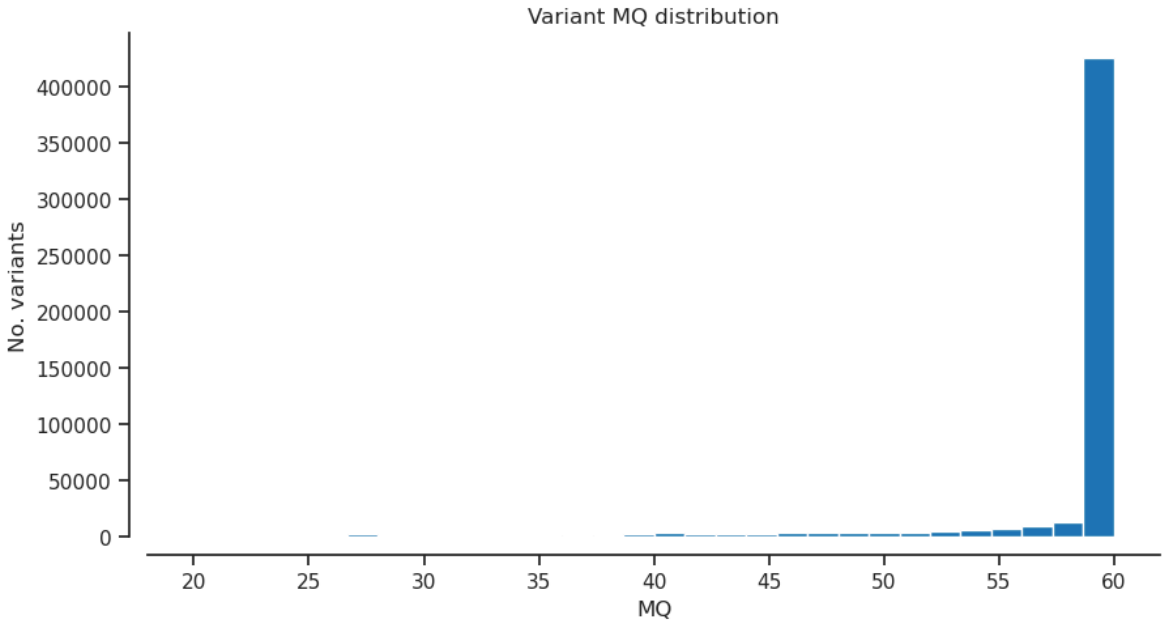
In [15]:
```
filter_expression = '(numalt == 1)'
biallelic_np = rawsnps.query(filter_expression)[:]
biallelic_np
```

Out[15]: <VariantTable shape=(433684,) dtype=(numpy.record, [('AC', '<i4', (3,)), ('AF', '<f4', (3,)), ('ALT', 'O', (3,)), ('AN', '<i4'), ('BaseQRankSum', '<f4'), ('CHROM', 'O'), ('DP', '<i4'), ('END', '<i4'), ('ExcessHet', '<f4'), ('FILTER_LowQual', '?'), ('FILTER_PASS', '?'), ('FS', '<f4'), ('ID', 'O'), ('InbreedingCoeff', '<f4'), ('MLEAC', '<i4', (3,)), ('MLEAF', '<f4', (3,)), ('MQ', '<f4'), ('MQRankSum', '<f4'), ('POS', '<i4'), ('QD', '<f4'), ('QUAL', '<f4'), ('RAW_MQandDP', '<i4', (2,)), ('REF', 'O'), ('ReadPosRankSum', '<f4'), ('SOR', '<f4'), ('altlen', '<i4', (3,)), ('is_snp', '?'), ('numalt', '<i4')])>

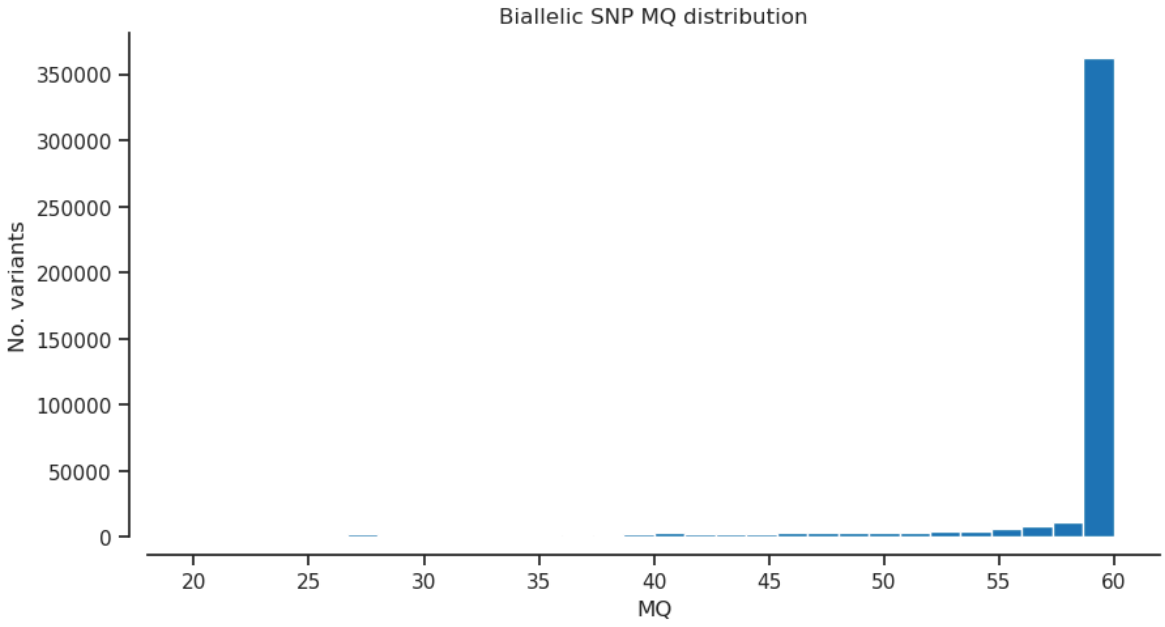
	AC	AF	ALT	AN	BaseQRankSum	CHROM	DP
0	[4 -1 -1]	[0.016 nan nan]	[b'G' b'' b'']	250	nan	b'Qrob_Chr01'	17
1	[2 -1 -1]	[0.007874 nan nan]	[b'C' b'' b'']	250	nan	b'Qrob_Chr01'	18
2	[1 -1 -1]	[0.003937 nan nan]	[b'A' b'' b'']	250	0.0	b'Qrob_Chr01'	44
...							
433681	[15 -1 -1]	[0.059 nan nan]	[b'G' b'' b'']	250	3.27	b'Qrob_H2.3_Sc0001194'	182
433682	[15 -1 -1]	[0.059 nan nan]	[b'G' b'' b'']	250	3.27	b'Qrob_H2.3_Sc0001194'	180
433683	[18 -1 -1]	[0.071 nan nan]	[b'T' b'' b'']	250	1.81	b'Qrob_H2.3_Sc0001194'	168

MQ - RMS mapping quality

In [16]:
```
plot_hist('MQ','var') # RMS mapping quality
```

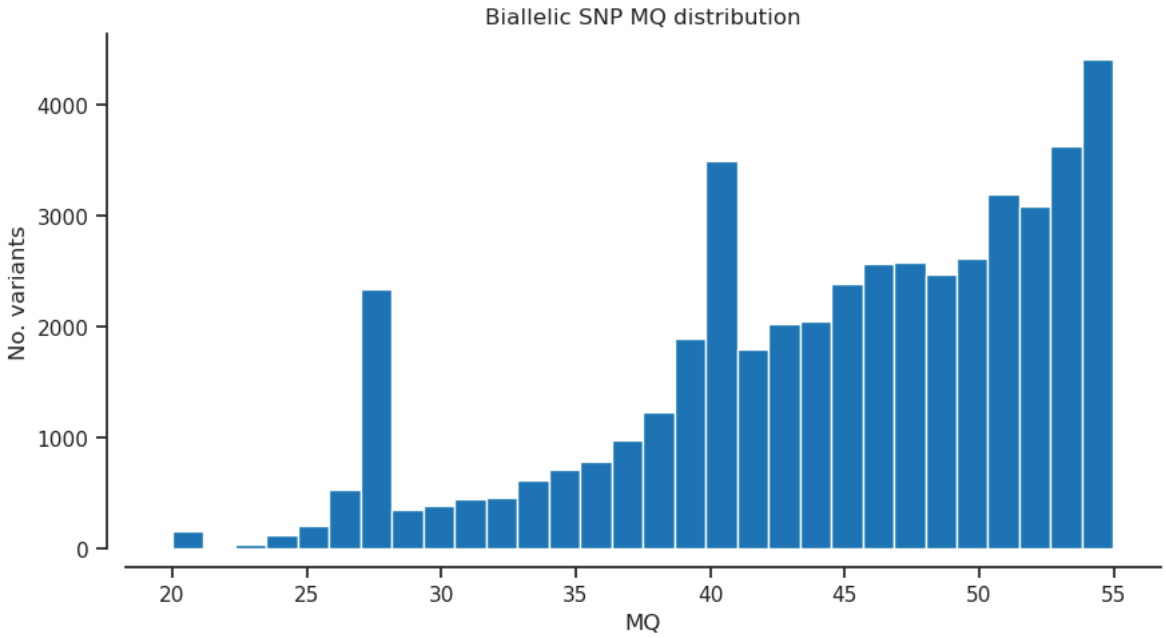


In [17]:
```
plot_hist('MQ','biallelic') # RMS mapping quality
```



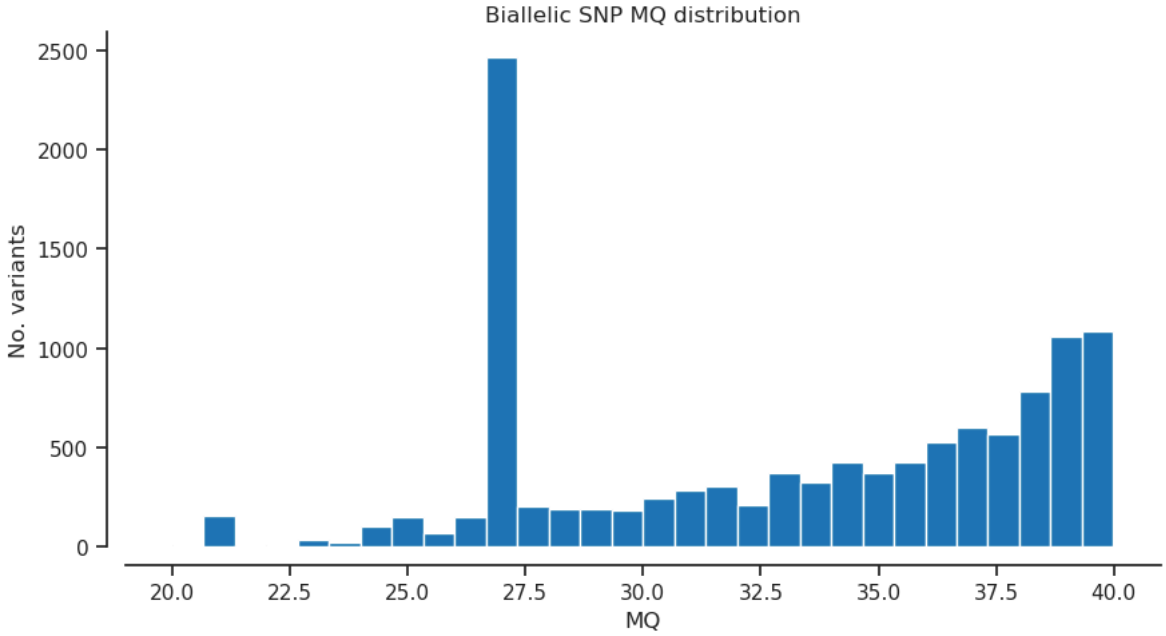
In [18]:
```
filter_expression = '(MQ < 55)'
bi_selection = biallelic_np.query(filter_expression)[:]
#np.count_nonzero(var_selection)
```

In [19]:
```
plot_hist('MQ')
```

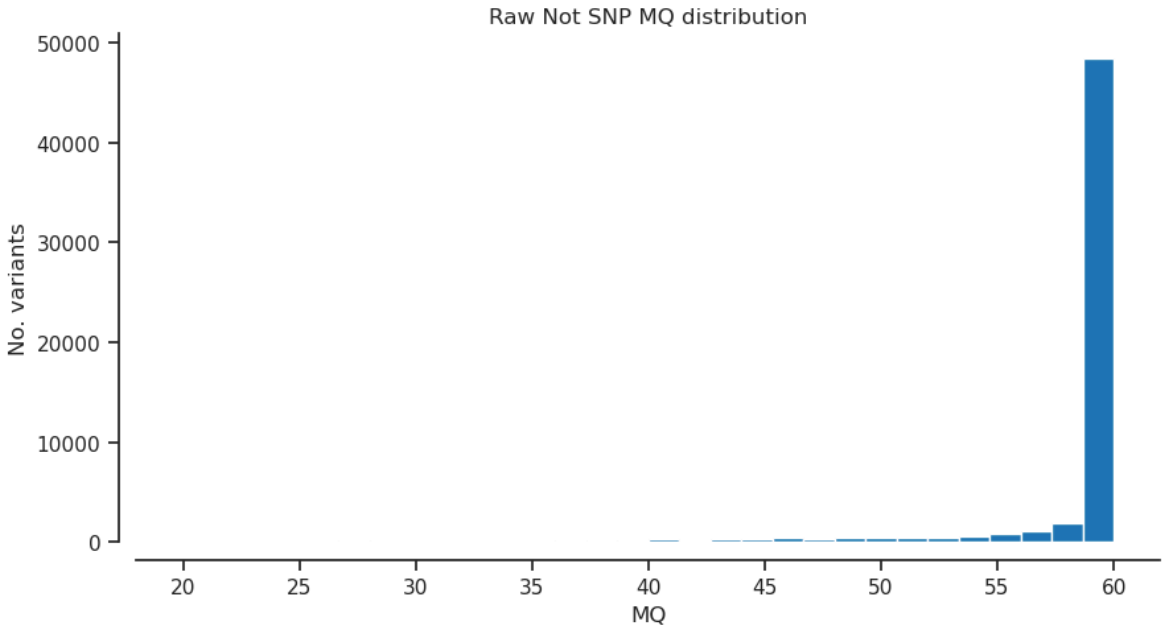


In [20]:
```
filter_expression = '(MQ < 40)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [21]:
```
plot_hist('MQ')
```

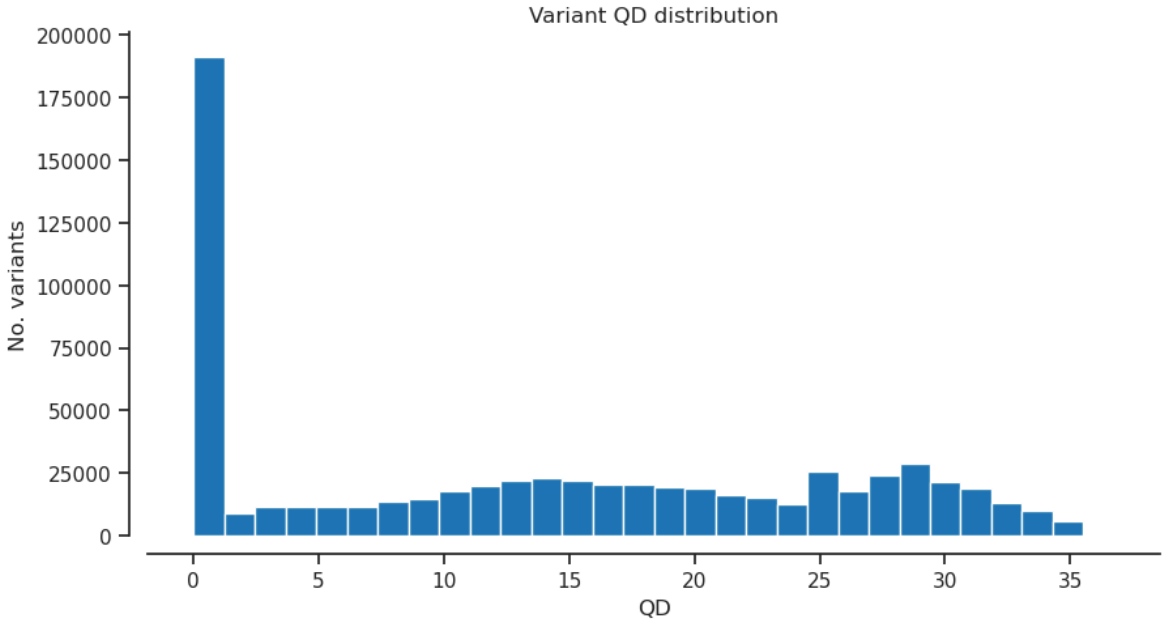


In [22]:
```
plot_hist('MQ','notsnp')
```

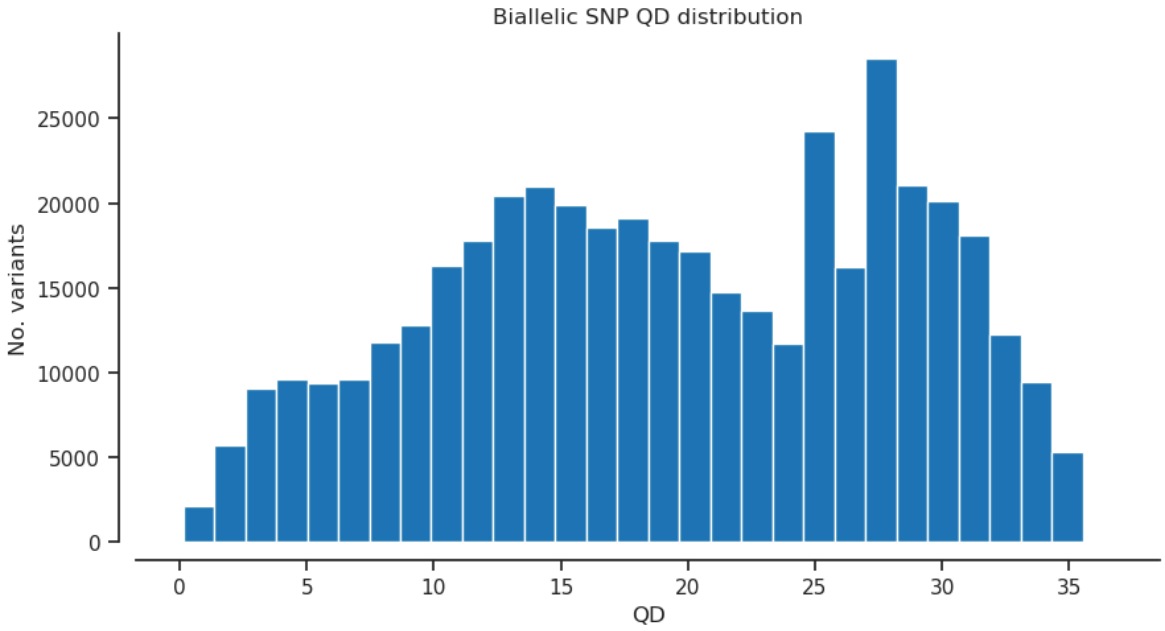


QD - Variant Confidence/Quality by Depth

In [23]:
```
plot_hist('QD','var') # Variant Confidence/Quality by Depth
```

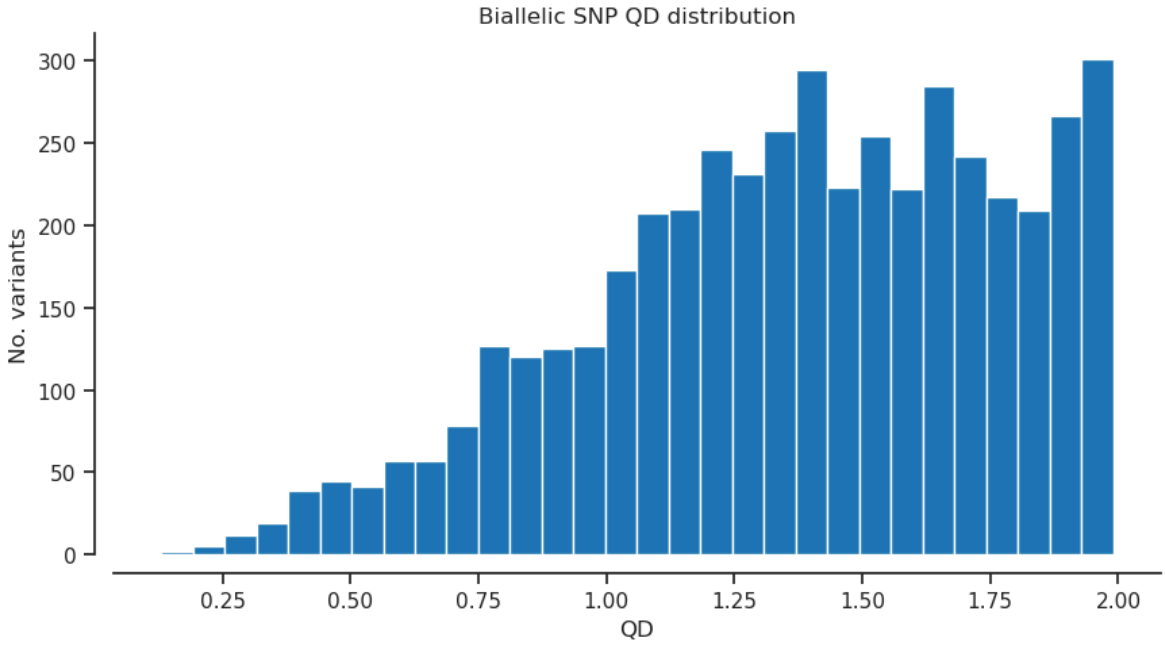


In [24]:
```
plot_hist('QD','biallelic') # Variant Confidence/Quality by Depth
```

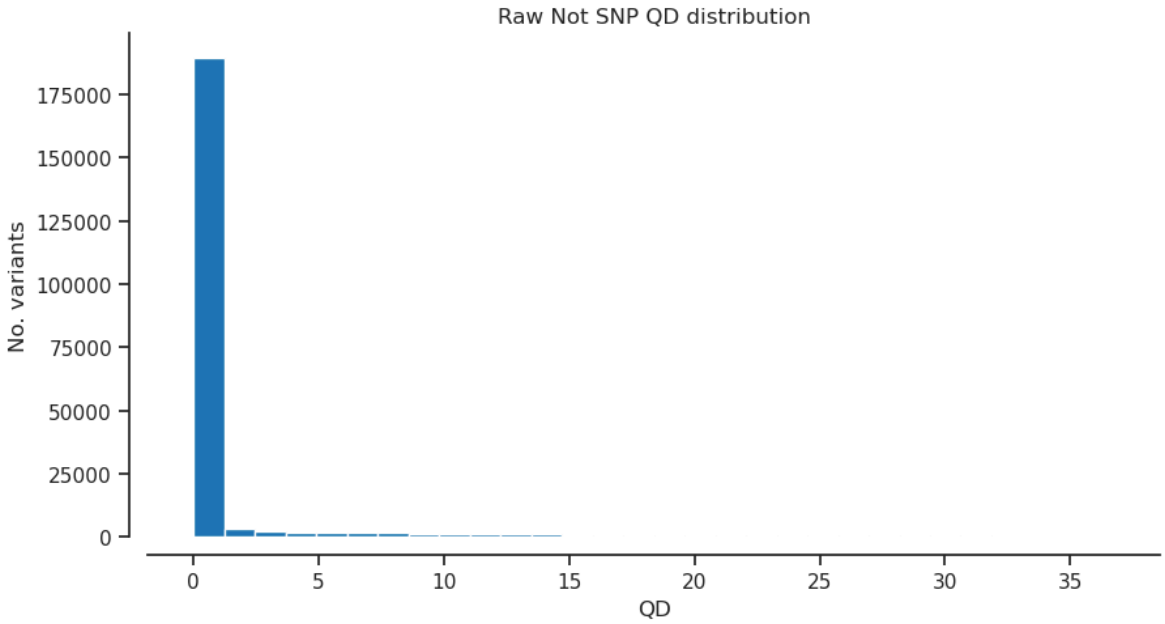


In [25]:
```
filter_expression = '(QD < 2)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [26]:
```
plot_hist('QD')
```

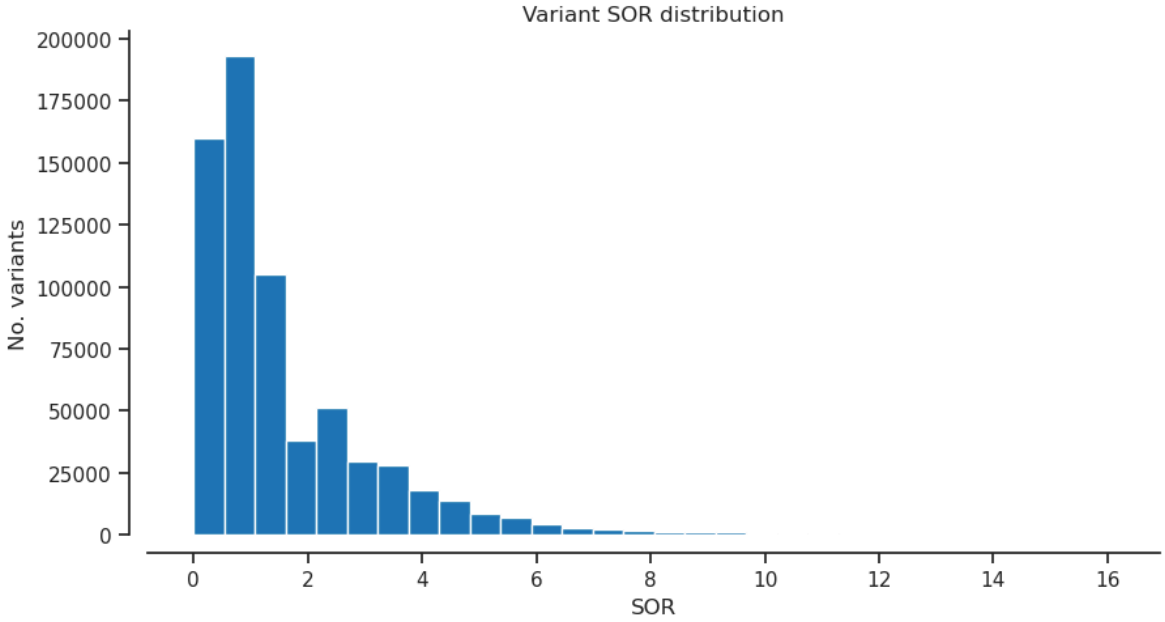


In [27]:
```
plot_hist('QD','notsnp') # Variant Confidence/Quality by Depth
```

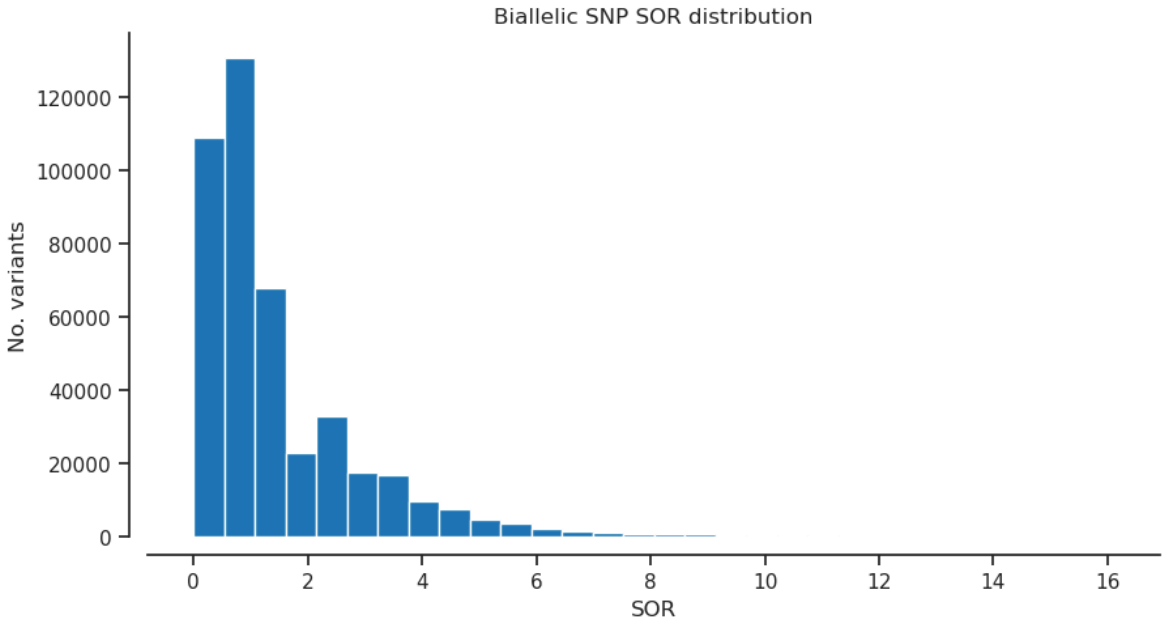


SOR - Symmetric Odds Ratio of 2x2 contingency table to detect strand bias

In [28]:
```
plot_hist('SOR', 'var') # Symmetric Odds Ratio of 2x2 contingency table t
```

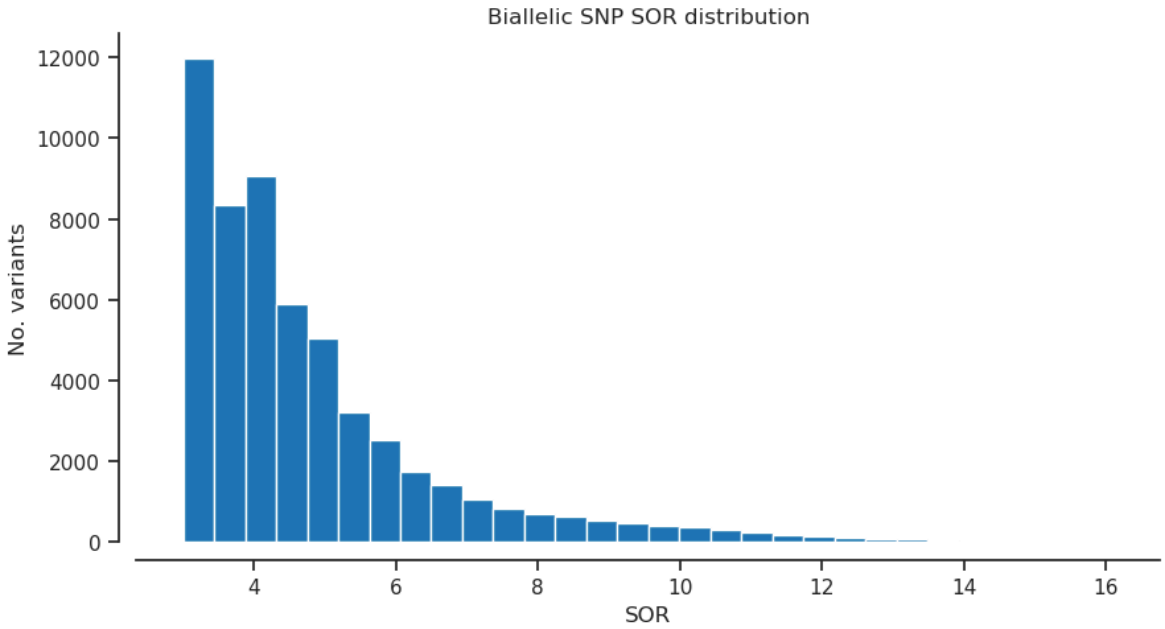


In [29]:
```
plot_hist('SOR','biallelic') # Symmetric Odds Ratio of 2x2 contingency ta
```

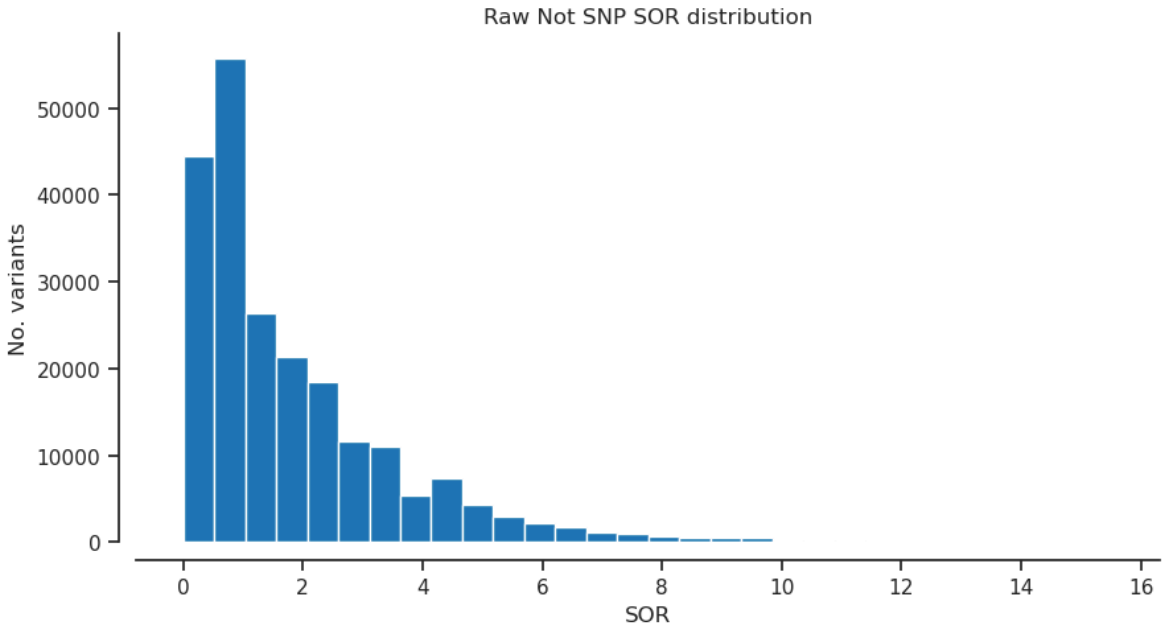


In [30]:
```
filter_expression = '(SOR > 3)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [31]:
```
plot_hist('SOR') # Symmetric Odds Ratio of 2x2 contingency table to detec
```

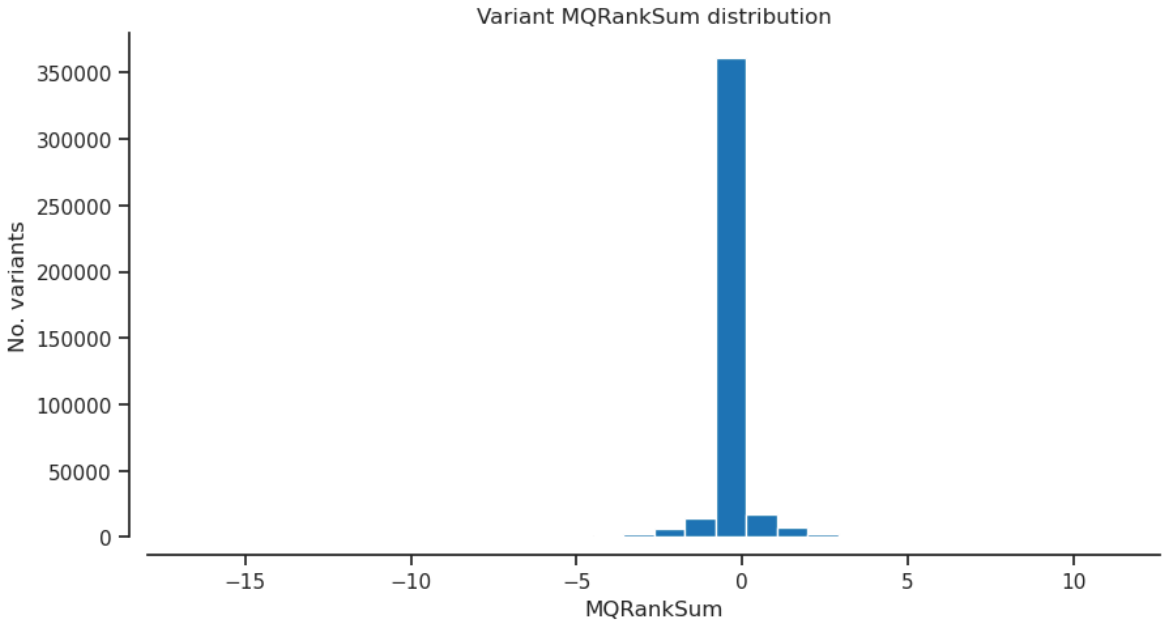


In [32]:
```
plot_hist('SOR','notsnp') # Symmetric Odds Ratio of 2x2 contingency table
```

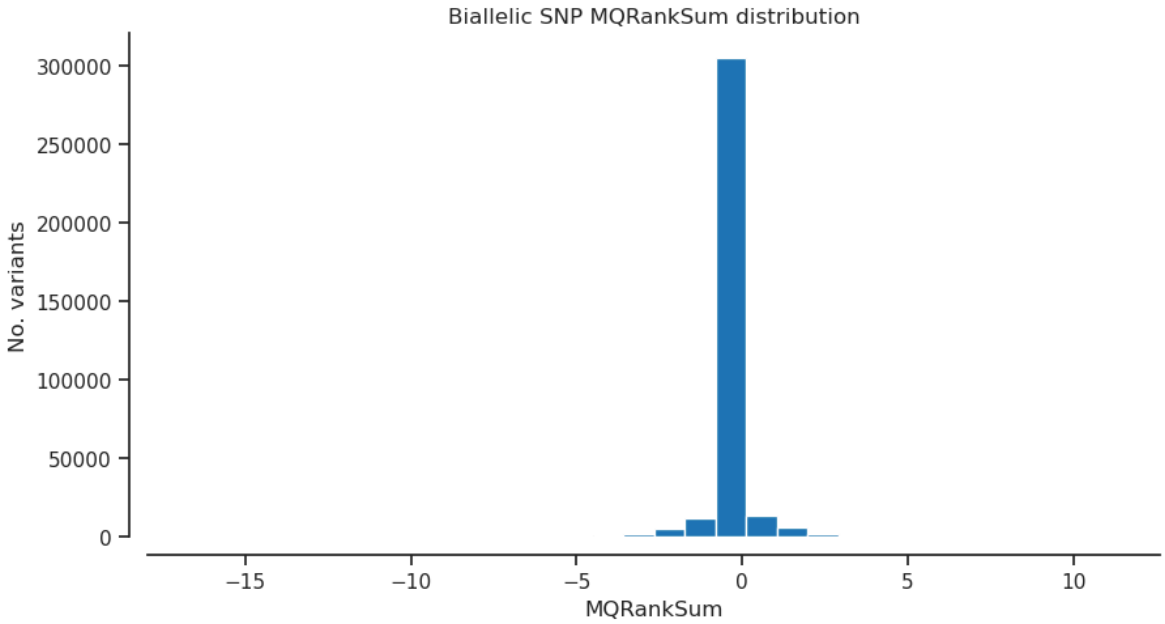


MQRankSum - Z-score From Wilcoxon rank sum test of Alt vs. Ref read mapping qualities

In [33]:
```
plot_hist('MQRankSum','var') # Z-score From Wilcoxon rank sum test of Alt
```

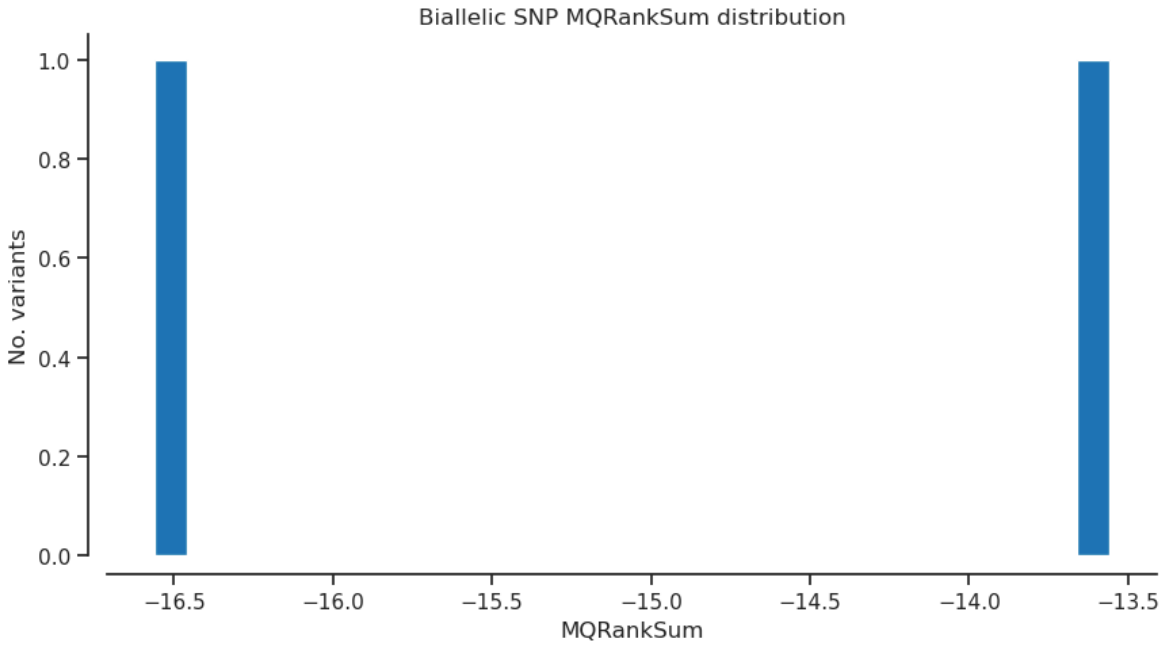


In [34]:
```
plot_hist('MQRankSum','biallelic') # Z-score From Wilcoxon rank sum test
```

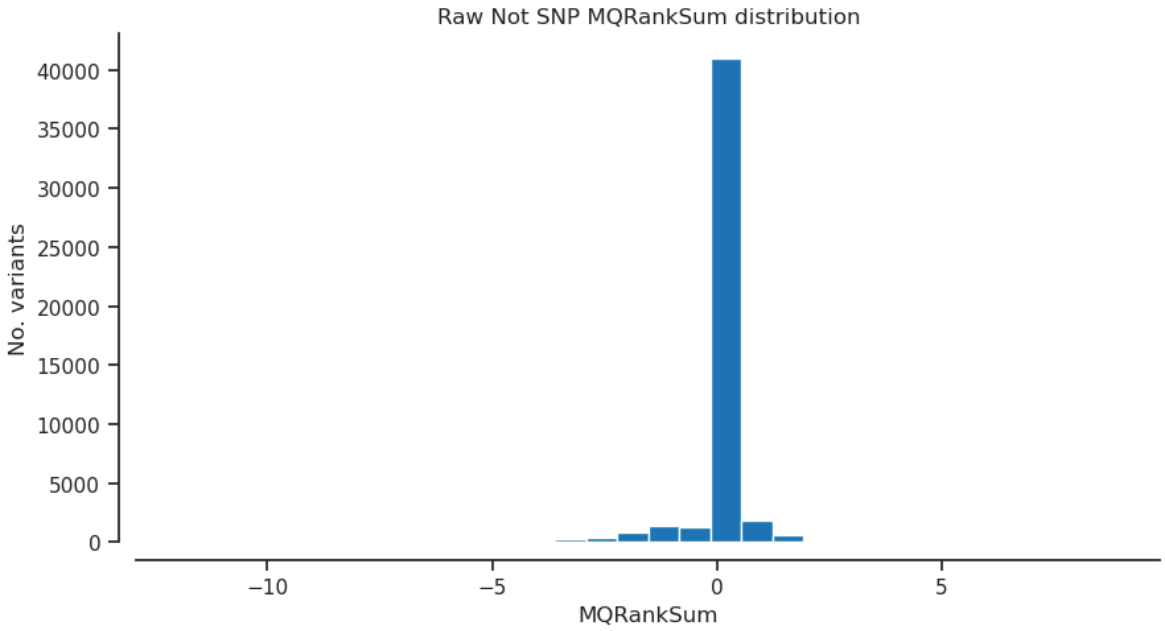


In [35]:
```
filter_expression = '(MQRankSum < -12.5)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [36]:
```
plot_hist('MQRankSum') # Z-score From Wilcoxon rank sum test of Alt vs. R
```

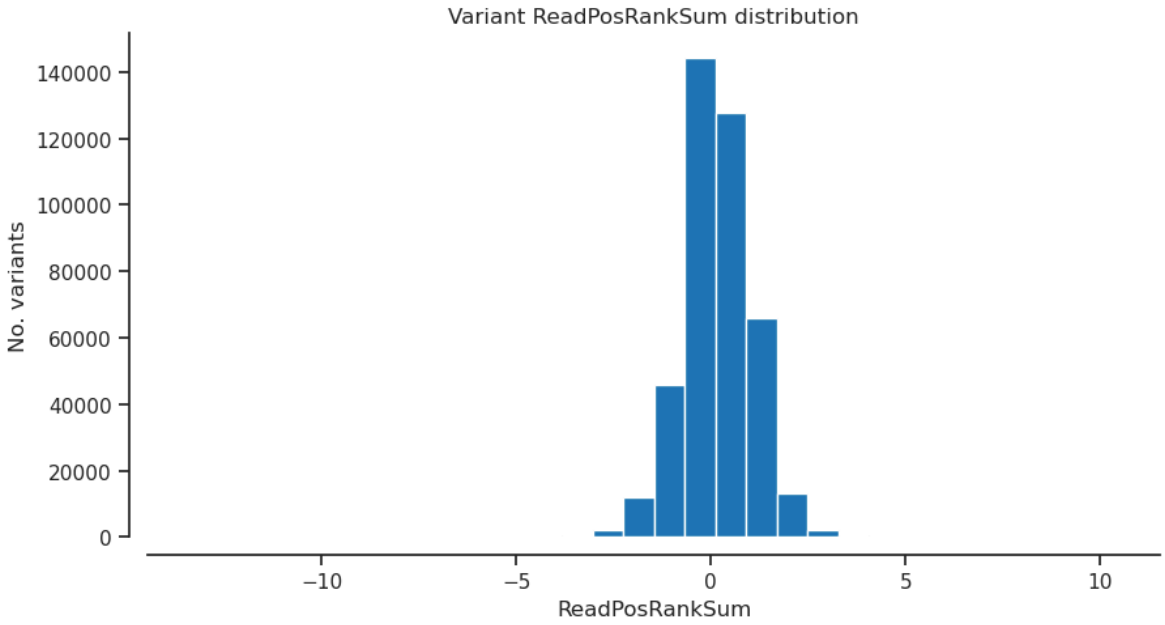


In [37]:
```
plot_hist('MQRankSum','notsnp') # Z-score From Wilcoxon rank sum test of
```

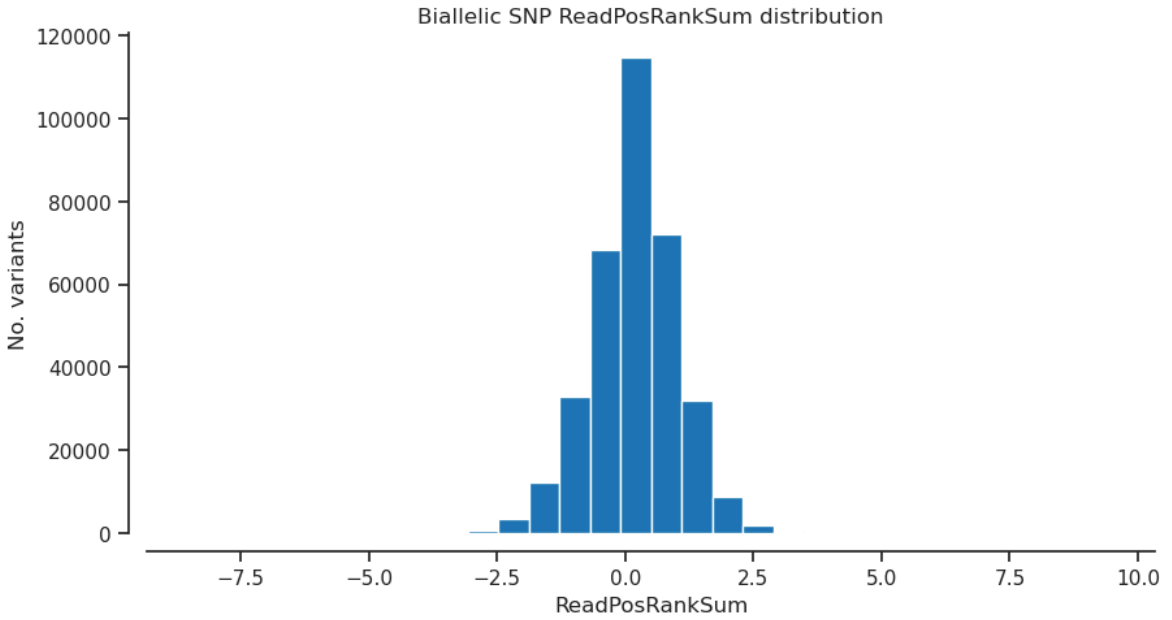


ReadPosRankSum - Z-score from Wilcoxon rank sum test of Alt vs. Ref read position bias

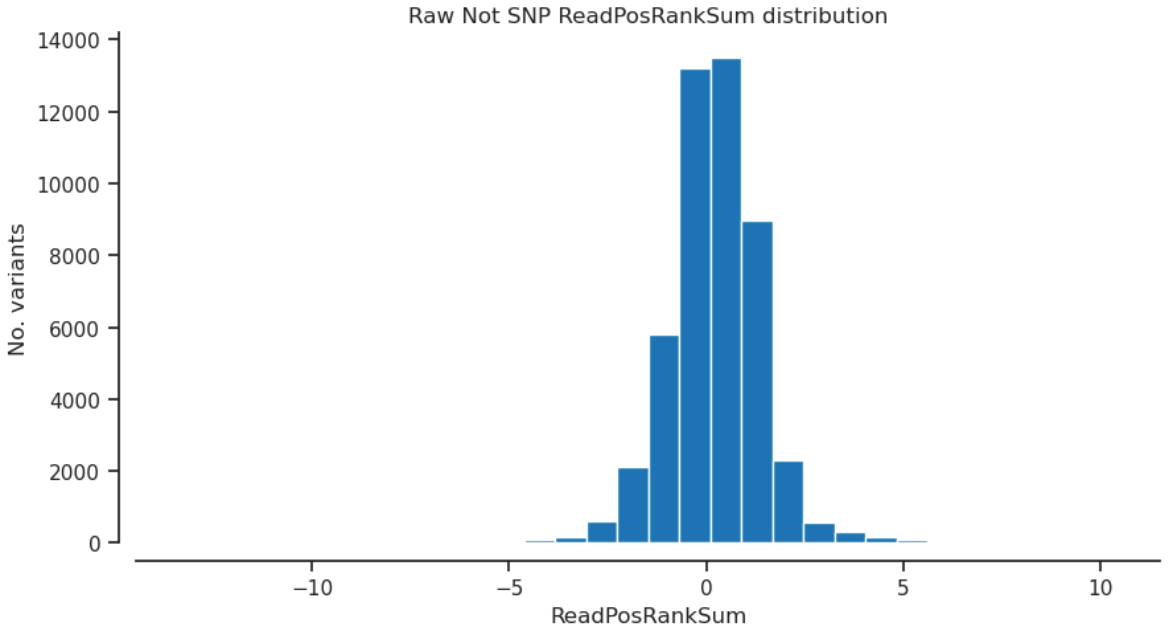
In [38]:
```
plot_hist('ReadPosRankSum','var') # Z-score from Wilcoxon rank sum test o
```



In [39]:
```
plot_hist('ReadPosRankSum','biallelic') # Z-score from Wilcoxon rank sum
```

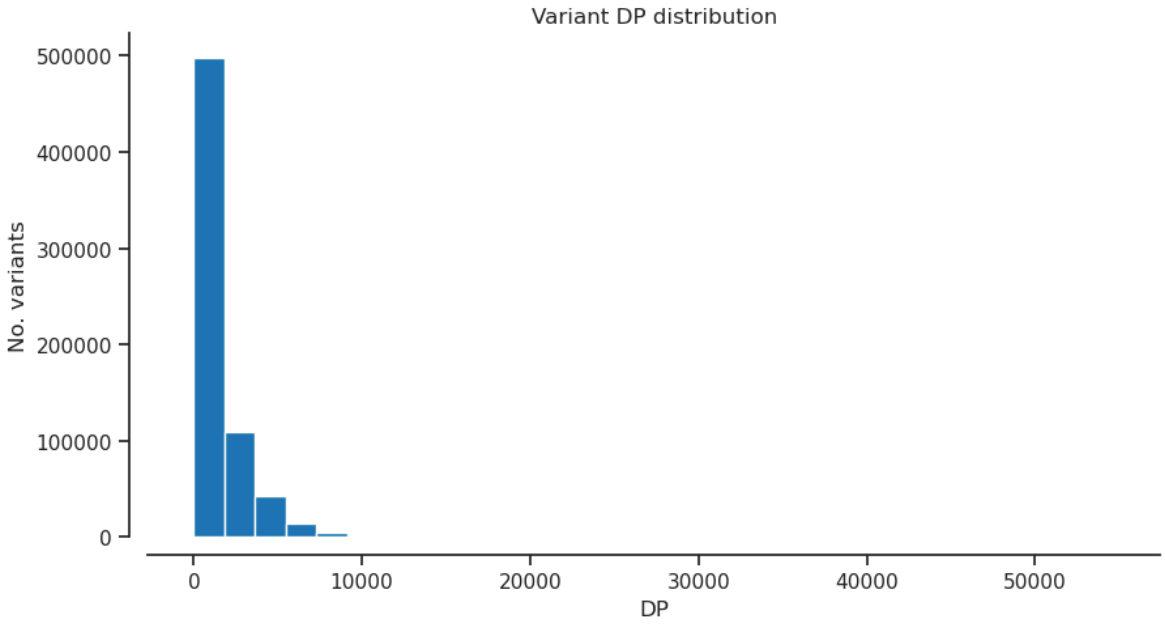


In [40]:
```
plot_hist('ReadPosRankSum','notsnp') # Z-score from Wilcoxon rank sum tes
```

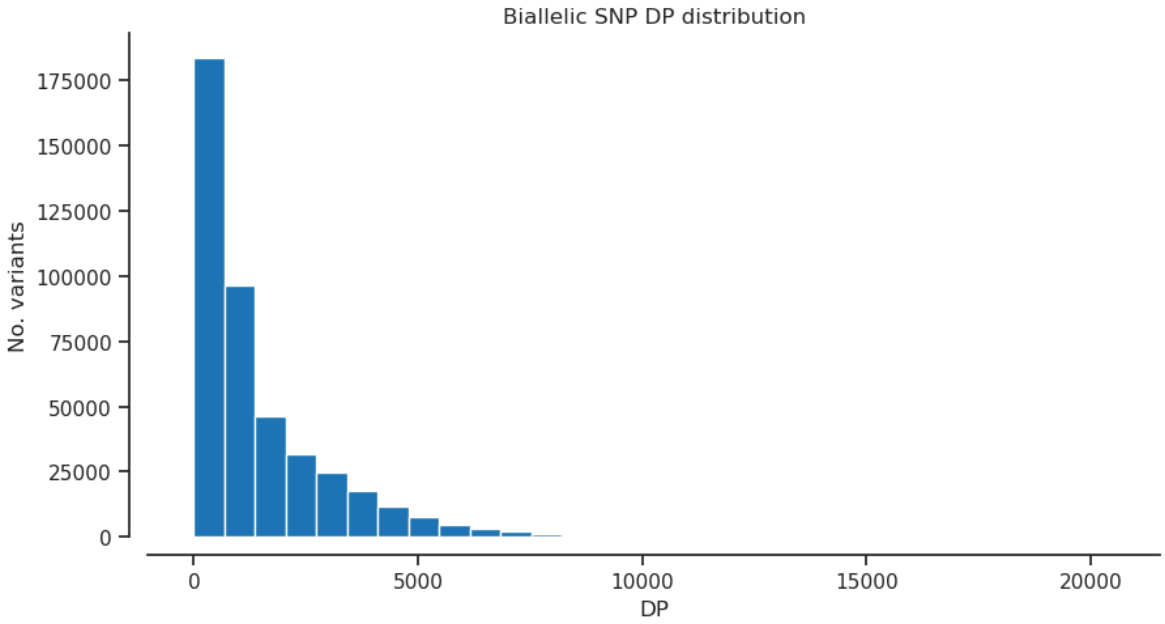


DP - Approximate read depth

In [41]:
```
plot_hist('DP','var')
```

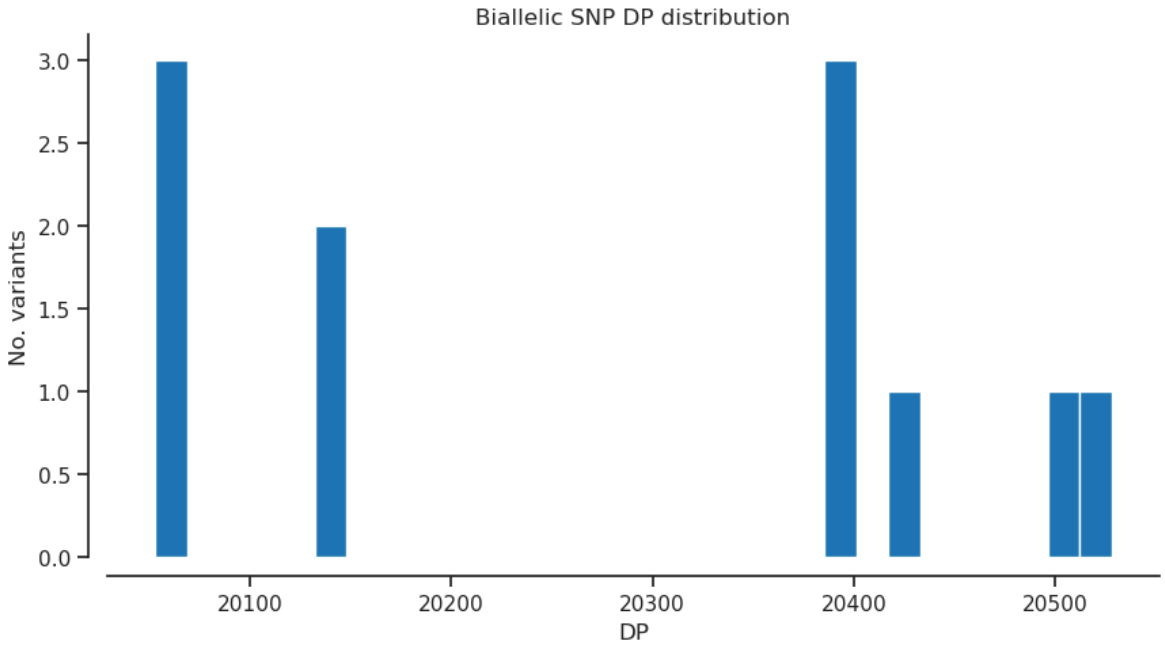


In [42]:
```
plot_hist('DP','biallelic')
```

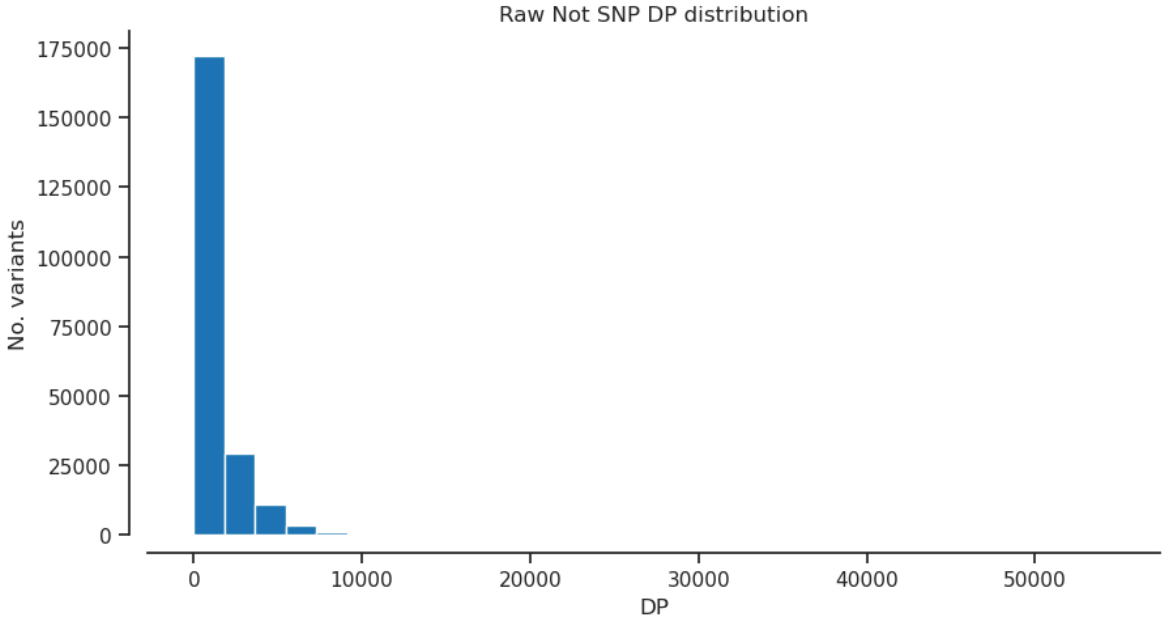


In [43]:
```
filter_expression = '(DP > 20000) & (DP < 40000)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [44]:
```
plot_hist('DP')
```

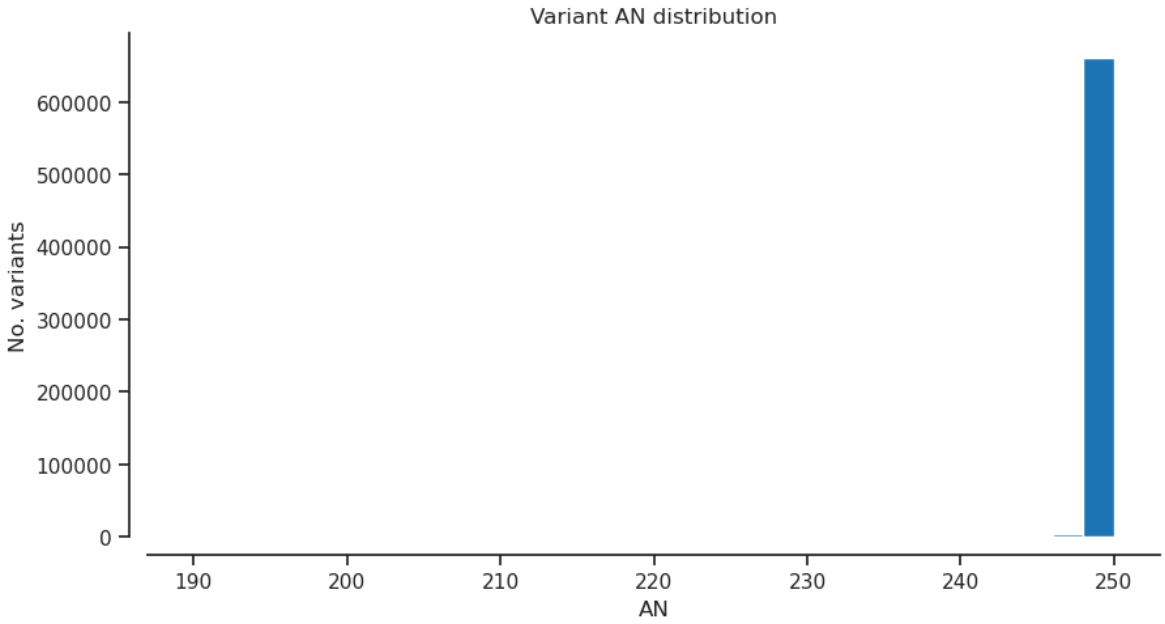


In [45]:
```
plot_hist('DP','notsnp')
```

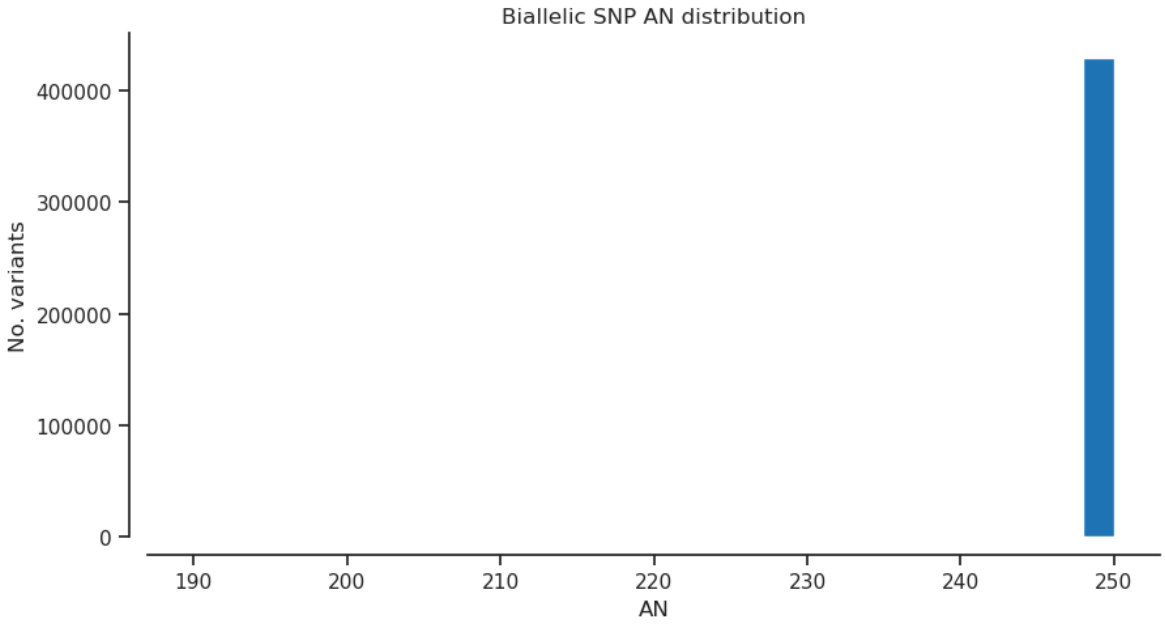


AN - Total number of alleles in called genotypes

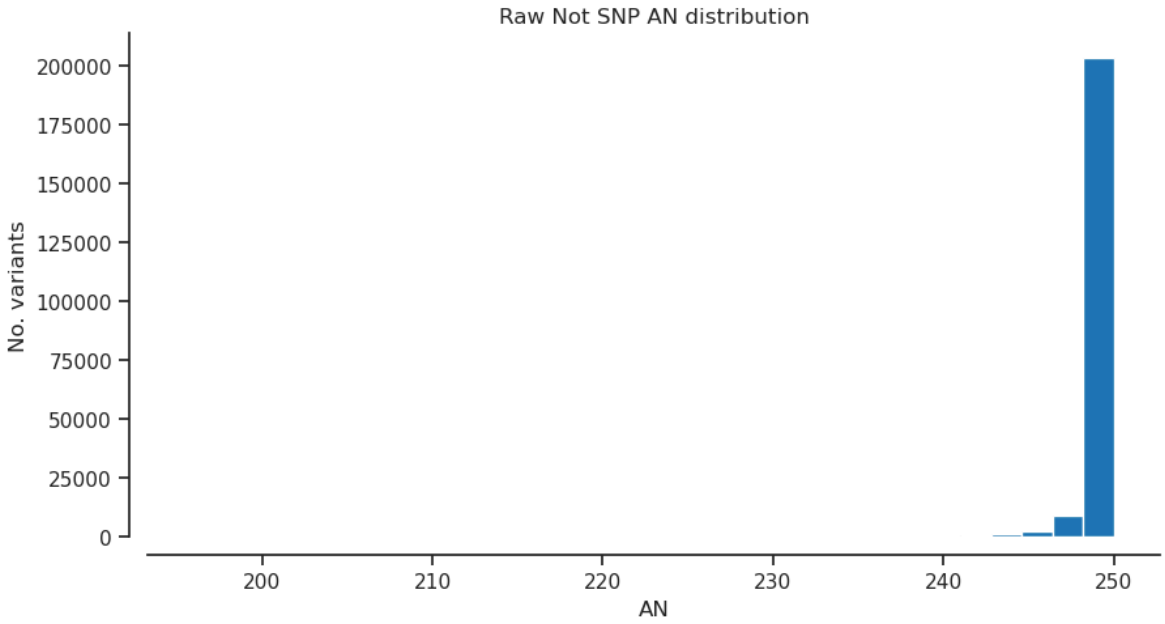
In [46]:
```
plot_hist('AN','var') # Total number of alleles in called genotypes
```



In [47]:
```
plot_hist('AN','biallelic') # Total number of alleles in called genotypes
```



In [48]:
```
plot_hist('AN','notsnp') # Total number of alleles in called genotypes
```



Selected filter

In [49]:
```
# QD: Variant Confidence/Quality by Depth
# AN: Total number of alleles in called genotypes
filter_expression = '(QD >= 2) & (MQ >= 40) & (MQRankSum >= -12.5) & (is_
variant_selection = variants_np.eval(filter_expression)[:]
np.count_nonzero(variant_selection)
```

Out[49]:
```
354570
```

Genotype

In [50]:
```
calldata_var = callset_var['calldata']
list(calldata_var)
```

Out[50]:
```
['AD', 'DP', 'GQ', 'GT', 'MIN_DP', 'PGT', 'PID', 'PL', 'PS', 'RGQ', 'S
B']
```

In [51]:
```
genotypes_var = allel.GenotypeChunkedArray(calldata_var['GT'])
genotypes_var
```

Out[51]: <GenotypeChunkedArray shape=(670805, 125, 2) dtype=int8 chunks=(65536, 64, 2) nbytes=159.9M cbytes=8.7M cratio=18.3 compression=gzip compression_opts=1 values=h5py._hl.dataset.Dataset>

	0	1	2	3	4	...	120	121	122	123	124
0	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
1	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
2	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
...						...					
670802	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
670803	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
670804	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0

In [52]:
```
# using the selected filters set above
gt_filtered_snps = genotypes_var.subset(variant_selection)
gt_filtered_snps
```

Out[52]: <GenotypeChunkedArray shape=(354570, 125, 2) dtype=int8 chunks=(5541, 125, 2) nbytes=84.5M cbytes=8.9M cratio=9.5 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1	2	3	4	...	120	121	122	123	124
0	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
1	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	1/1	0/0	0/0
2	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
...						...					
354567	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
354568	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
354569	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0

In [53]:
```
# grab the allele counts for the populations
ac = gt_filtered_snps.count_alleles()
ac
```

Out[53]: <AlleleCountsChunkedArray shape=(354570, 4) dtype=int32 chunks=(22161, 4) nbytes=5.4M cbytes=651.4K cratio=8.5 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1	2	3
0	249	1	0	0
1	238	12	0	0
2	249	1	0	0
...		...		
354567	247	3	0	0
354568	240	2	8	0
354569	241	9	0	0

In [54]:
```
ac[:]
```

Out[54]: <AlleleCountsArray shape=(354570, 4) dtype=int32>

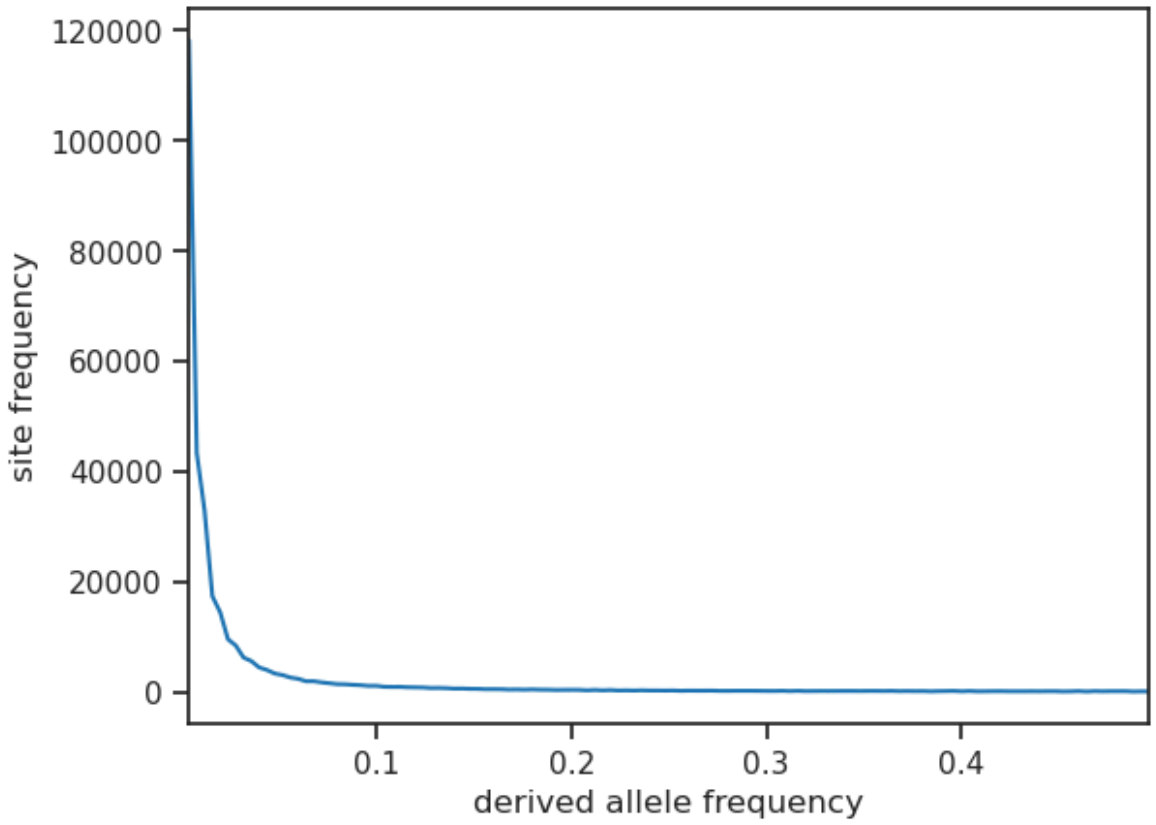
	0	1	2	3
0	249	1	0	0
1	238	12	0	0
2	249	1	0	0
...		...		
354567	247	3	0	0
354568	240	2	8	0
354569	241	9	0	0

In [55]:
```
# Which ones are biallelic?
is_biallelic_01 = ac.is_biallelic_01()[:]
ac1 = ac.compress(is_biallelic_01, axis=0)[:, :2]
ac1
##this part of the code is only for graphing the SFS, is not useful for f
```

Out[55]:
```
array([[249,   1],
       [238,  12],
       [249,   1],
       ...,
       [247,   3],
       [247,   3],
       [241,   9]], dtype=int32)
```

In [56]:
```
# plot the sfs of the derived allele
s = allel.sfs_folded(ac1)
allel.plot_sfs(s, yscale="linear", n=ac1.sum(axis=1).max())
```

Out[56]:
```
<Axes: xlabel='derived allele frequency', ylabel='site frequency'>
```



In [57]:
```
biallelic = (ac.max_allele() == 1)
###This is the filter expression for biallelic sites
biallelic
```

Out[57]:
```
<ChunkedArrayWrapper shape=(354570,) dtype=bool chunks=(177285,)
   nbytes=346.3K cbytes=66.9K cratio=5.2
   compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shu
ffle': 1, 'blocksize': 0}
   values=zarr.core.Array>
```

In [58]:
```
# select only the biallelic variants
gt_biallelic = gt_filtered_snps.compress(biallelic)
gt_biallelic
```

Out[58]: <GenotypeChunkedArray shape=(336497, 125, 2) dtype=int8 chunks=(5258, 125, 2) nbytes=80.2M cbytes=8.2M cratio=9.8 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1	2	3	4	...	120	121	122	123	124
0	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
1	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	1/1	0/0	0/0
2	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
...						...					
336494	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
336495	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
336496	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0

In [59]:
```
n_variants = len(gt_biallelic)
n_variants
```

Out[59]: 336497

In [60]:
```
pc_missing = gt_biallelic.count_missing(axis=0)[:] * 100 / n_variants
pc_het = gt_biallelic.count_het(axis=0)[:] * 100 / n_variants
```

Samples

In [61]:
```
samples_var = callset_var['samples']
samples_var = list(samples_var)
samples_var
```

Out[61]:
```
[b'BIH00040-001',
 b'BIH00040-002',
 b'BIH00040-003',
 b'BIH00040-004',
 b'BIH00040-005',
 b'BIH00040-006',
 b'BIH00040-007',
 b'BIH00040-008',
 b'BIH00040-009',
 b'BIH00040-010',
 b'BIH00040-011',
 b'BIH00040-012',
 b'BIH00040-013',
 b'BIH00040-014',
 b'BIH00040-015',
 b'BIH00040-016',
 b'BIH00040-017',
 b'BIH00040-018',
 b'BIH00040-019',
 b'BIH00040-020',
 b'BIH00040-021',
 b'BIH00040-022',
 b'BIH00040-023',
 b'BIH00040-024',
 b'BIH00040-025',
 b'HUN00008-001',
 b'HUN00008-002',
 b'HUN00008-003',
 b'HUN00008-004',
 b'HUN00008-005',
 b'HUN00008-006',
 b'HUN00008-007',
 b'HUN00008-008',
 b'HUN00008-009',
 b'HUN00008-010',
 b'HUN00008-011',
 b'HUN00008-012',
 b'HUN00008-013',
 b'HUN00008-014',
 b'HUN00008-015',
 b'HUN00008-016',
 b'HUN00008-017',
 b'HUN00008-018',
 b'HUN00008-019',
 b'HUN00008-020',
 b'HUN00008-021',
 b'HUN00008-022',
 b'HUN00008-023',
 b'HUN00008-024',
 b'HUN00008-025',
 b'HUN00010-001',
 b'HUN00010-002',
 b'HUN00010-003',
 b'HUN00010-004',
 b'HUN00010-005',
 b'HUN00010-006',
 b'HUN00010-007',
 b'HUN00010-008',
 b'HUN00010-009',
 b'HUN00010-010',
```

```
b'HUN00010-011',
b'HUN00010-012',
b'HUN00010-013',
b'HUN00010-015',
b'HUN00010-016',
b'HUN00010-017',
b'HUN00010-018',
b'HUN00010-019',
b'HUN00010-020',
b'HUN00010-021',
b'HUN00010-022',
b'HUN00010-023',
b'HUN00010-024',
b'HUN00010-025',
b'HUN00010-026',
b'ROU00385-001',
b'ROU00385-002',
b'ROU00385-003',
b'ROU00385-004',
b'ROU00385-005',
b'ROU00385-006',
b'ROU00385-007',
b'ROU00385-008',
b'ROU00385-009',
b'ROU00385-010',
b'ROU00385-011',
b'ROU00385-012',
b'ROU00385-013',
b'ROU00385-014',
b'ROU00385-015',
b'ROU00385-016',
b'ROU00385-017',
b'ROU00385-018',
b'ROU00385-019',
b'ROU00385-020',
b'ROU00385-021',
b'ROU00385-022',
b'ROU00385-023',
b'ROU00385-024',
b'ROU00385-025',
b'SVN00040-001',
b'SVN00040-002',
b'SVN00040-003',
b'SVN00040-004',
b'SVN00040-005',
b'SVN00040-006',
b'SVN00040-007',
b'SVN00040-008',
b'SVN00040-009',
b'SVN00040-010',
b'SVN00040-011',
b'SVN00040-012',
b'SVN00040-013',
b'SVN00040-014',
b'SVN00040-015',
b'SVN00040-016',
b'SVN00040-017',
b'SVN00040-018',
b'SVN00040-019',
b'SVN00040-020',
```

```
 b'SVN00040-021',
 b'SVN00040-022',
 b'SVN00040-023',
 b'SVN00040-024',
 b'SVN00040-025']
```

In [62]:
```
samples_fn = '~/scratch/data/Qpubescens/Quercus_pubescens_sample_list_sci
samples = pandas.read_csv(samples_fn, sep='\t')
samples
```

Out[62]:

	ID	Population
0	BIH00040-001	BIH00040
1	BIH00040-002	BIH00040
2	BIH00040-003	BIH00040
3	BIH00040-004	BIH00040
4	BIH00040-005	BIH00040
...	...	...
120	SVN00040-021	SVN00040
121	SVN00040-022	SVN00040
122	SVN00040-023	SVN00040
123	SVN00040-024	SVN00040
124	SVN00040-025	SVN00040

125 rows × 2 columns

In [63]:
```
samples.Population.value_counts()
```

Out[63]:
```
Population
BIH00040    25
HUN00008    25
HUN00010    25
ROU00385    25
SVN00040    25
Name: count, dtype: int64
```

In [64]:
```
populations = samples.Population.unique()
populations
###This identifiers come from the metadata file
```

Out[64]:
```
array(['BIH00040', 'HUN00008', 'HUN00010', 'ROU00385', 'SVN00040'],
      dtype=object)
```

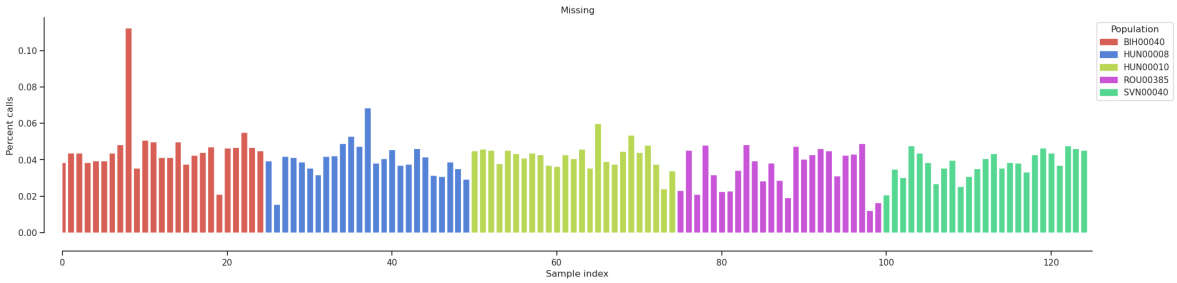
Gt frequency function

In [65]:
```
def plot_genotype_frequency(pc, title):
    fig, ax = plt.subplots(figsize=(24, 5))
    sns.despine(ax=ax, offset=24)
    left = np.arange(len(pc))
    palette = sns.color_palette("hls", 5)
    pop2color = {'BIH00040': palette[0],
```

```
                'HUN00008': palette[3],
                'HUN00010': palette[1],
                'ROU00385': palette[4],
                'SVN00040': palette[2]}
    colors = [pop2color[p] for p in samples.Population]
    ax.bar(left, pc, color=colors)
    ax.set_xlim(0, len(pc))
    ax.set_xlabel('Sample index')
    ax.set_ylabel('Percent calls')
    ax.set_title(title)
    handles = [mpl.patches.Patch(color=palette[0]),
               mpl.patches.Patch(color=palette[3]),
               mpl.patches.Patch(color=palette[1]),
               mpl.patches.Patch(color=palette[4]),
               mpl.patches.Patch(color=palette[2])]
    ax.legend(handles=handles, labels=['BIH00040', 'HUN00008', 'HUN00010'
              bbox_to_anchor=(1, 1), loc='upper left')
```

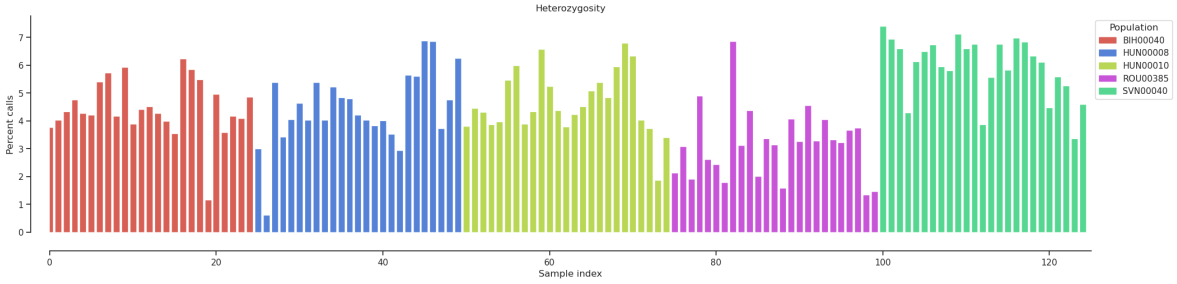
Plot missing

In [66]:
```
plot_genotype_frequency(pc_missing, 'Missing')
```



Plot heterozygosity

In [67]:
```
plot_genotype_frequency(pc_het, 'Heterozygosity')
```



PCA

In [68]:
```
palette = sns.color_palette("hls",5)
pop_colours = {
                'BIH00040': palette[0],
                'HUN00008': palette[3],
                'HUN00010': palette[1],
                'ROU00385': palette[4],
                'SVN00040': palette[2]
}
```

In [69]:
```
def plot_pca_coords(coords, model, pc1, pc2, ax, sample_population):
    sns.despine(ax=ax, offset=5)
    x = coords[:, pc1]
    y = coords[:, pc2]
    for pop in populations:
        flt = (sample_population == pop)
        ax.plot(x[flt], y[flt], marker='o', linestyle=' ', color=pop_colo
                label=pop, markersize=6, mec='k', mew=.5)
    ax.set_xlabel('PC%s (%.1f%%)' % (pc1+1, model.explained_variance_rati
    ax.set_ylabel('PC%s (%.1f%%)' % (pc2+1, model.explained_variance_rati


def fig_pca(coords, model, title, sample_population=None):
    if sample_population is None:
        sample_population = samples.Population
    # plot coords for PCs 1 vs 2, 3 vs 4
    fig = plt.figure(figsize=(10, 5))
    ax = fig.add_subplot(1, 2, 1)
    plot_pca_coords(coords, model, 0, 1, ax, sample_population)
    ax = fig.add_subplot(1, 2, 2)
    plot_pca_coords(coords, model, 2, 3, ax, sample_population)
    ax.legend(bbox_to_anchor=(1, 1), loc='upper left')
    fig.suptitle(title, y=1.02)
    fig.tight_layout()
```

In [70]:
```
ac2 = gt_biallelic.count_alleles()
ac2
```

Out[70]: <AlleleCountsChunkedArray shape=(336497, 2) dtype=int32 chunks=(42063, 2) nbytes=2.6M cbytes=488.5K cratio=5.4 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1
0	249	1
1	238	12
2	249	1
...	...	
336494	247	3
336495	247	3
336496	241	9

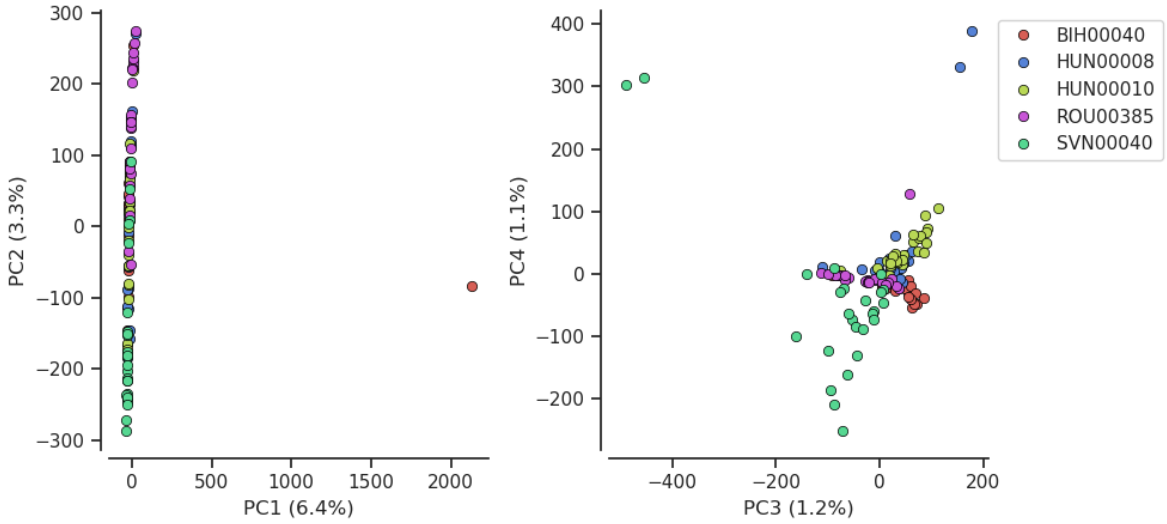
In [71]:
```
flt = (ac2[:, :2].min(axis=1) > 1)
gf = gt_biallelic.compress(flt, axis=0)
gn = gf.to_n_alt()
gn
```

Out[71]:
```
<ChunkedArrayWrapper shape=(218252, 125) dtype=int8 chunks=(6821, 125)
   nbytes=26.0M cbytes=5.4M cratio=4.8
   compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shu
ffle': 1, 'blocksize': 0}
   values=zarr.core.Array>
```

In [72]:
```
coords1, model1 = allel.pca(gn, n_components=10, scaler='patterson')
```

In [73]:
```
fig_pca(coords1, model1, 'Figure 1. Conventional PCA.')
```

Figure 1. Conventional PCA.



In [74]:
```
outliers = coords1[:,0]>1000
samples[outliers]
```

Out[74]:

	ID	Population
8	BIH00040-009	BIH00040

In [75]:
```
pc_het[outliers]
```

Out[75]:
```
array([4.17121104])
```

In [76]:
```
pc_missing[outliers]
```

Out[76]:
```
array([0.11233384])
```