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 [22]:
```
#allel.vcf_to_hdf5('/users/mcevoysu/scratch/output/Phalepensis/vcf_filter
```

Get data

In [2]:
```
callset_var_fn = '/users/mcevoysu/scratch/output/Phalepensis/scikit-allel
callset_var = h5py.File(callset_var_fn, mode='r')
```

In [3]:
```
calldata_var = callset_var['calldata']
list(calldata_var)
```

Out[3]:
```
['AD', 'DP', 'GQ', 'GT', 'MIN_DP', 'PGT', 'PID', 'PL', 'PS', 'RGQ', 'S
B']
```

In [4]:
```
list(callset_var['variants'])
```

Out[4]:
```
['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 [5]:
```
variants = allel.VariantChunkedTable(callset_var['variants'])
variants
```

Out[5]: <VariantChunkedTable shape=(212695,) 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=36.3M cbytes=7.9M cratio=4.6 values=h5py._hl.group.Group>

	AC	AF	ALT	AN	BaseQRankSum	CHROM	DP	END
0	[2 -1 -1]	[0.002674 nan nan]	[b'T' b'' b'']	742	-1.242	b'chr1.c1000'	2855	-1
1	[2 -1 -1]	[0.002674 nan nan]	[b'A' b'' b'']	742	1.27	b'chr1.c1000'	2858	-1
2	[3 -1 -1]	[0.004011 nan nan]	[b'C' b'' b'']	742	-1.128	b'chr1.c1000'	2842	-1
...								
212692	[2 -1 -1]	[0.002674 nan nan]	[b'T' b'' b'']	742	-0.524	b'tig10501301_1_2'	8484	-1
212693	[1 -1 -1]	[0.001337 nan nan]	[b'T' b'' b'']	742	-0.674	b'tig10501301_1_2'	8555	-1
212694	[1 -1 -1]	[0.001337 nan nan]	[b'G' b'' b'']	742	0.0	b'tig10501301_1_2'	8525	-1

In [6]:
```
variants_np = variants[:]
rawsnps = variants_np.query('(is_snp == True)')
rawsnps
```

Out[6]: <VariantTable shape=(162334,) 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	END
0	[2 -1 -1]	[0.002674 nan nan]	[b'T' b'' b'']	742	-1.242	b'chr1.c1000'	2855	-1
1	[2 -1 -1]	[0.002674 nan nan]	[b'A' b'' b'']	742	1.27	b'chr1.c1000'	2858	-1
2	[3 -1 -1]	[0.004011 nan nan]	[b'C' b'' b'']	742	-1.128	b'chr1.c1000'	2842	-1
...								
162331	[2 -1 -1]	[0.002674 nan nan]	[b'T' b'' b'']	742	-0.524	b'tig10501301_1_2'	8484	-1
162332	[1 -1 -1]	[0.001337 nan nan]	[b'T' b'' b'']	742	-0.674	b'tig10501301_1_2'	8555	-1
162333	[1 -1 -1]	[0.001337 nan nan]	[b'G' b'' b'']	742	0.0	b'tig10501301_1_2'	8525	-1

In [7]:
```
notsnp = variants_np.query('(is_snp != True)')
notsnp
```

Out[7]: <VariantTable shape=(50361,) 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	END
0	[2 -1 -1]	[0.002674 nan nan]	[b'*' b'' b'']	742	nan	b'chr1.c1000'	2855	-1
1	[1 -1 -1]	[0.001337 nan nan]	[b'*' b'' b'']	742	0.0	b'chr1.c1000'	2732	-1
2	[1 -1 -1]	[0.001337 nan nan]	[b'*' b'' b'']	742	nan	b'chr1.c1007'	1139	-1
...								
50358	[140 -1 -1]	[0.191 nan nan]	[b'*' b'' b'']	738	nan	b'tig00294850'	268	-1
50359	[21 -1 -1]	[0.028 nan nan]	[b'*' b'' b'']	740	nan	b'tig10501301_1_2'	600	-1
50360	[11 -1 -1]	[0.015 nan nan]	[b'*' b'' b'']	742	nan	b'tig10501301_1_2'	2254	-1

Plot function

In [8]:
```
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 [9]:
```
numalt = rawsnps['numalt']
np.max(numalt)
```

Out[9]:
```
3
```

In [10]:
```
count_numalt = np.bincount(numalt)
count_numalt
```

Out[10]:
```
array([     0, 158136,   4102,     96])
```

In [11]:
```
n_multiallelic = np.sum(count_numalt[2:])
n_multiallelic
```

Out[11]:
```
4198
```

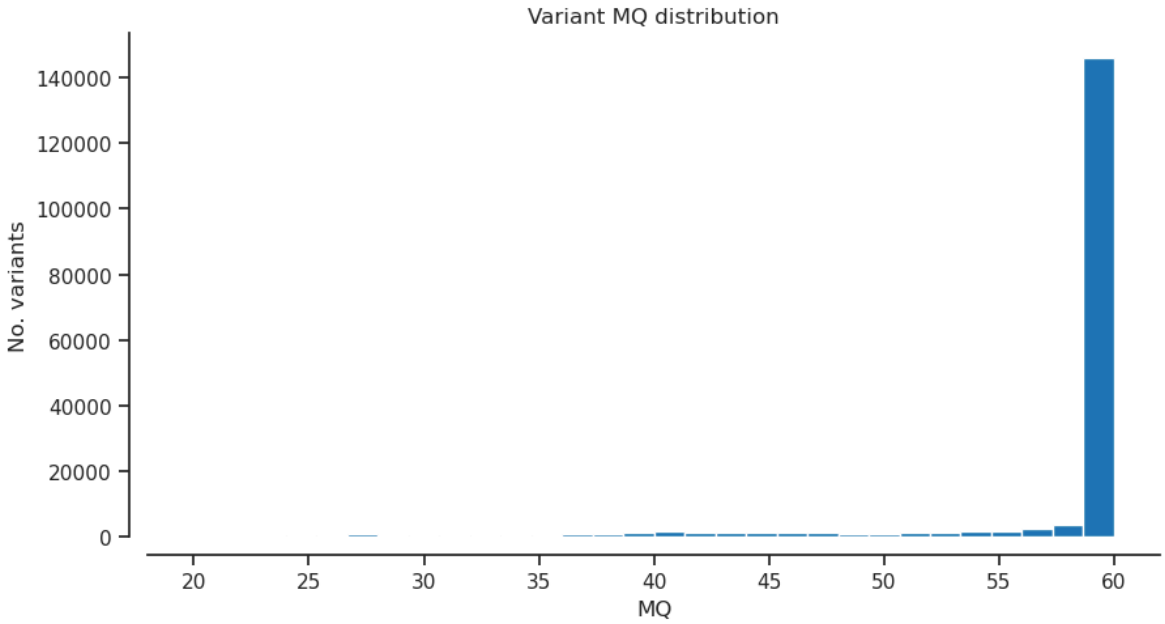
In [12]:
```
filter_expression = '(numalt == 1)'
biallelic_np = rawsnps.query(filter_expression)[:]
biallelic_np
```

Out[12]: <VariantTable shape=(158136,) 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')])>

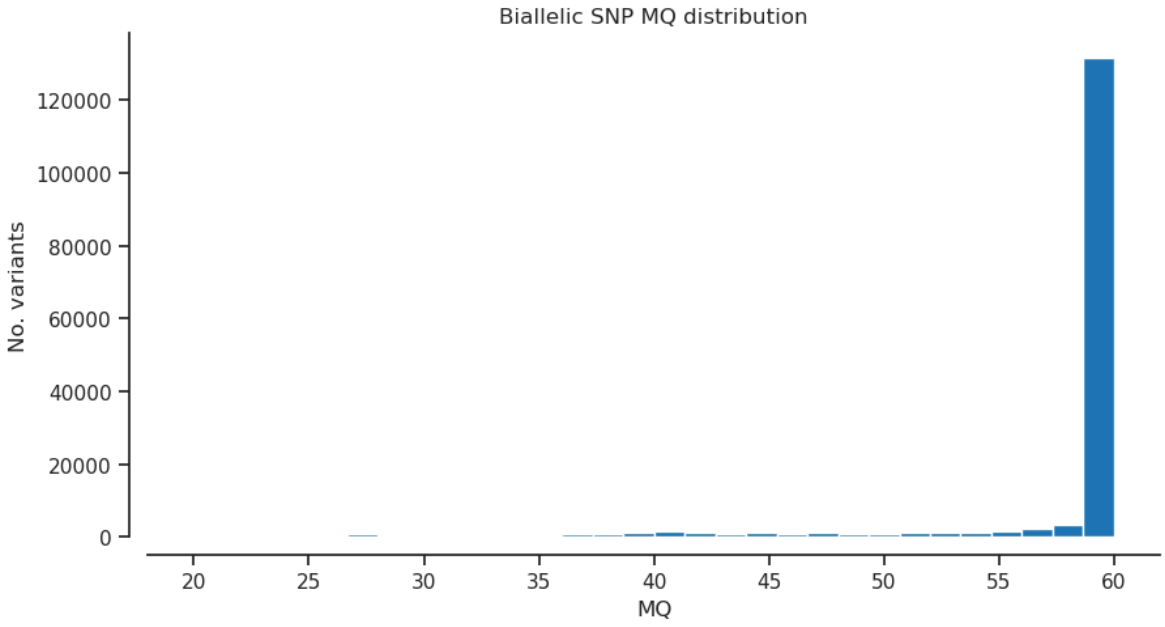
	AC	AF	ALT	AN	BaseQRankSum	CHROM	DP	END
0	[2 -1 -1]	[0.002674 nan nan]	[b'T' b'' b'']	742	-1.242	b'chr1.c1000'	2855	-1
1	[2 -1 -1]	[0.002674 nan nan]	[b'A' b'' b'']	742	1.27	b'chr1.c1000'	2858	-1
2	[3 -1 -1]	[0.004011 nan nan]	[b'C' b'' b'']	742	-1.128	b'chr1.c1000'	2842	-1
...								
158133	[2 -1 -1]	[0.002674 nan nan]	[b'T' b'' b'']	742	-0.524	b'tig10501301_1_2'	8484	-1
158134	[1 -1 -1]	[0.001337 nan nan]	[b'T' b'' b'']	742	-0.674	b'tig10501301_1_2'	8555	-1
158135	[1 -1 -1]	[0.001337 nan nan]	[b'G' b'' b'']	742	0.0	b'tig10501301_1_2'	8525	-1

MQ - RMS mapping quality

In [13]:
```
plot_hist('MQ','var') # RMS mapping quality
```

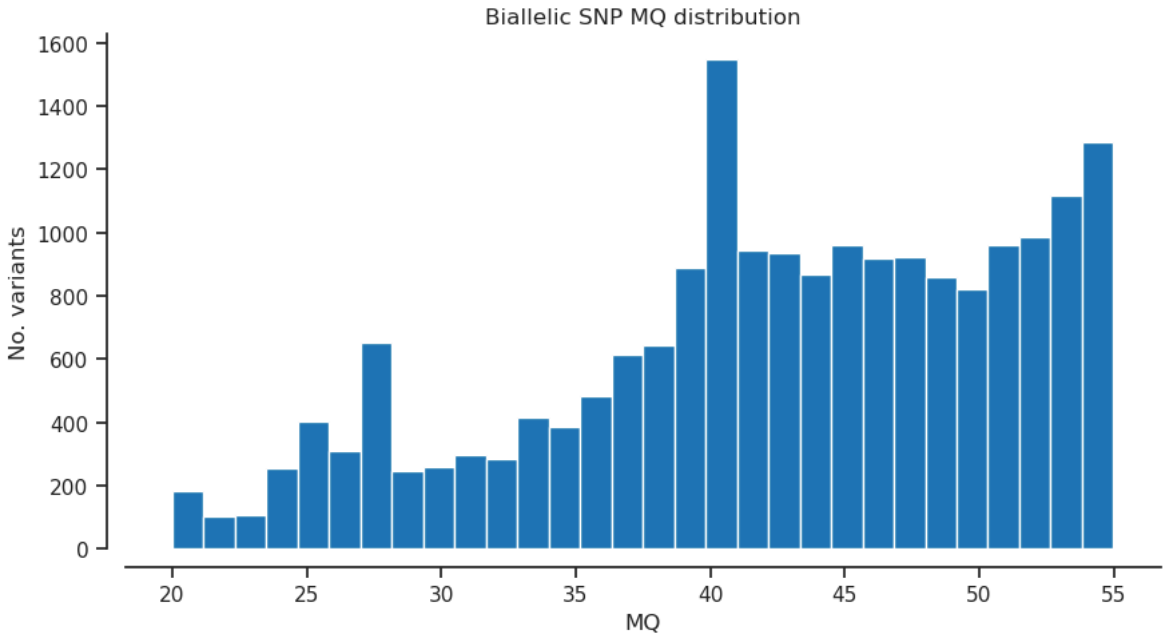


In [14]:
```
plot_hist('MQ','biallelic') # RMS mapping quality
```



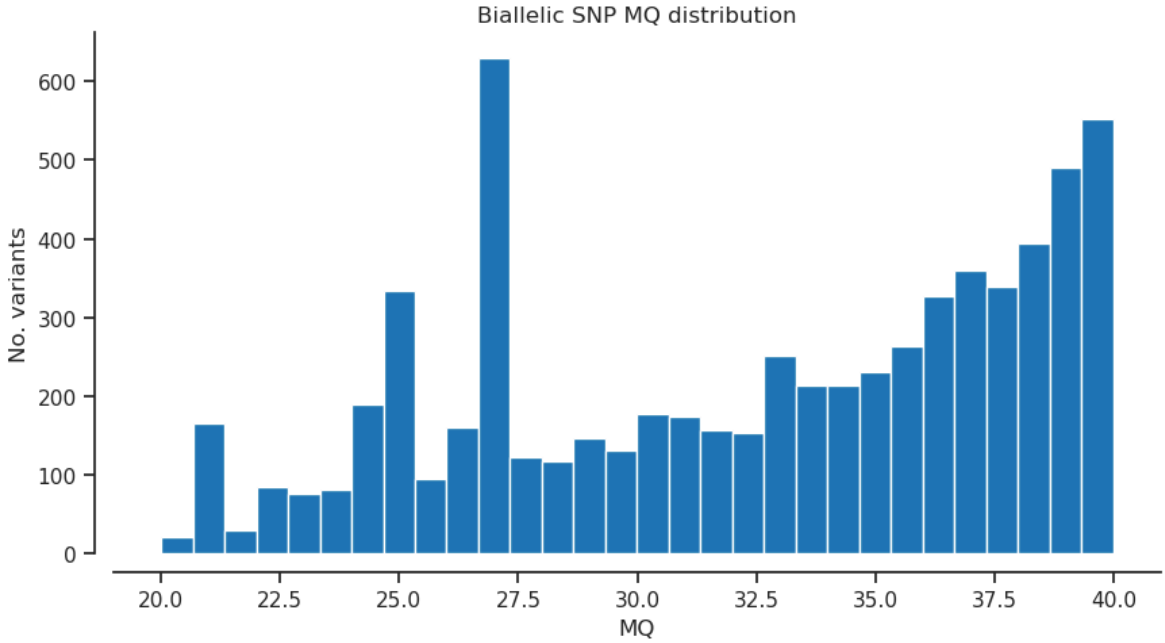
In [15]:
```
filter_expression = '(MQ < 55)'
bi_selection = biallelic_np.query(filter_expression)[:]
#np.count_nonzero(var_selection)
```

In [16]:
```
plot_hist('MQ')
```

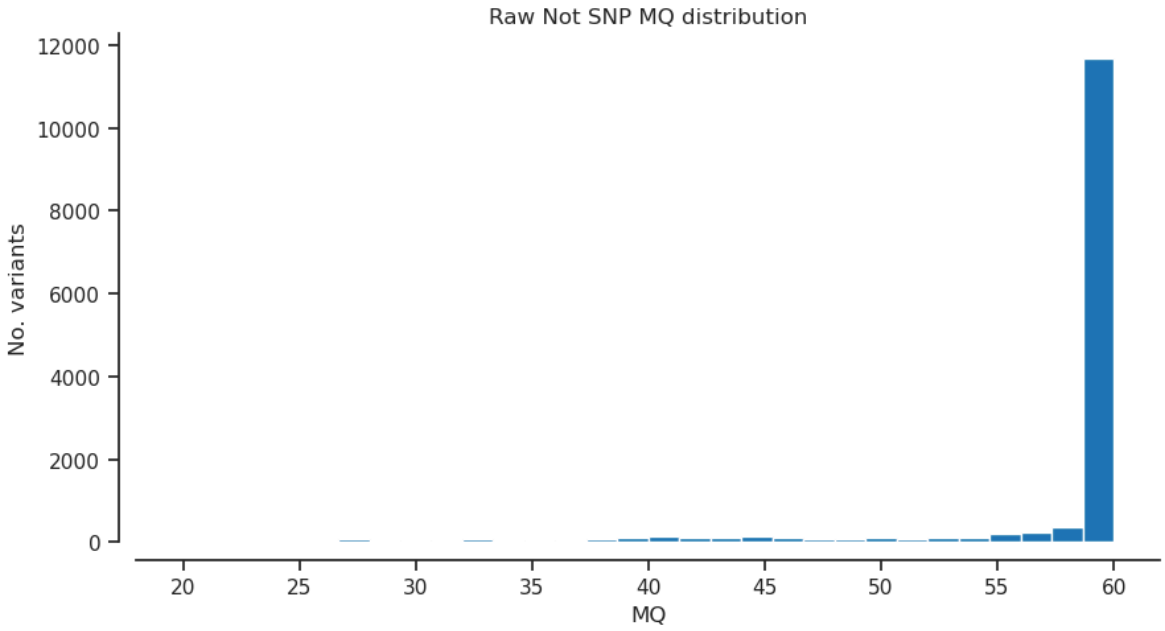


In [17]:
```
filter_expression = '(MQ < 40)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [18]:
```
plot_hist('MQ')
```

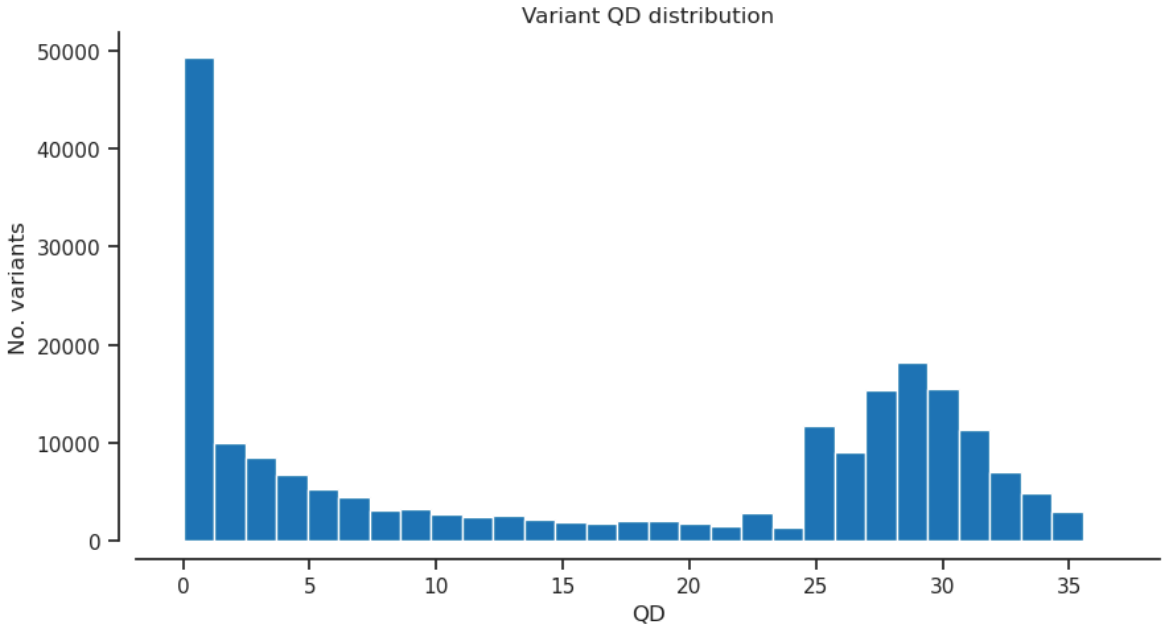


In [19]:
```
plot_hist('MQ','notsnp')
```

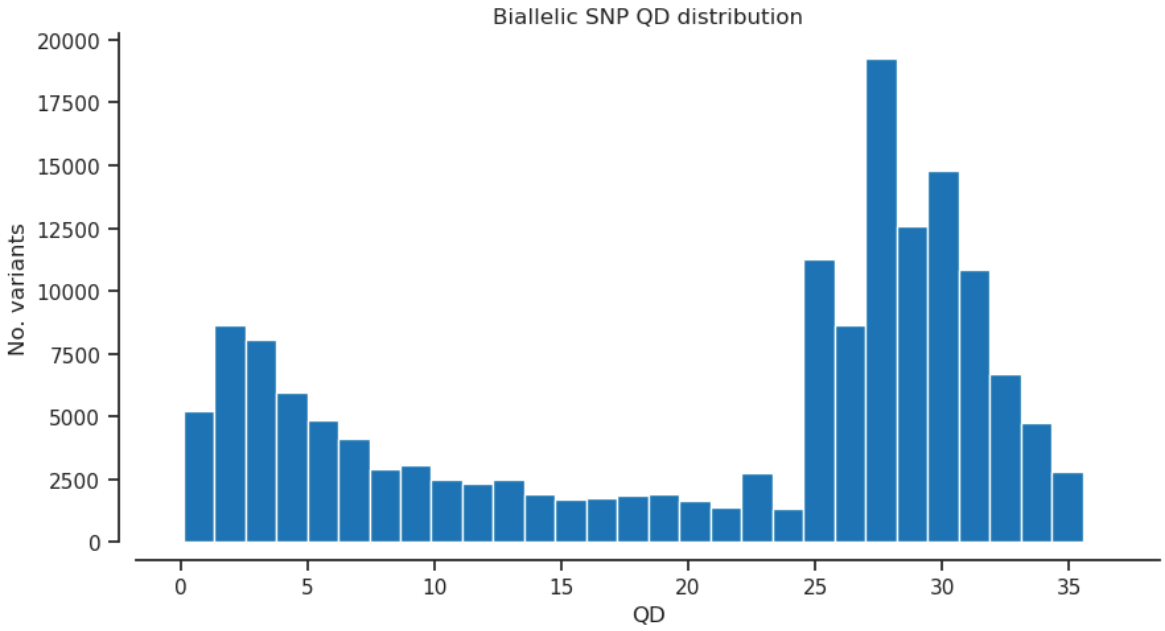


QD - Variant Confidence/Quality by Depth

In [20]:
```
plot_hist('QD','var') # Variant Confidence/Quality by Depth
```

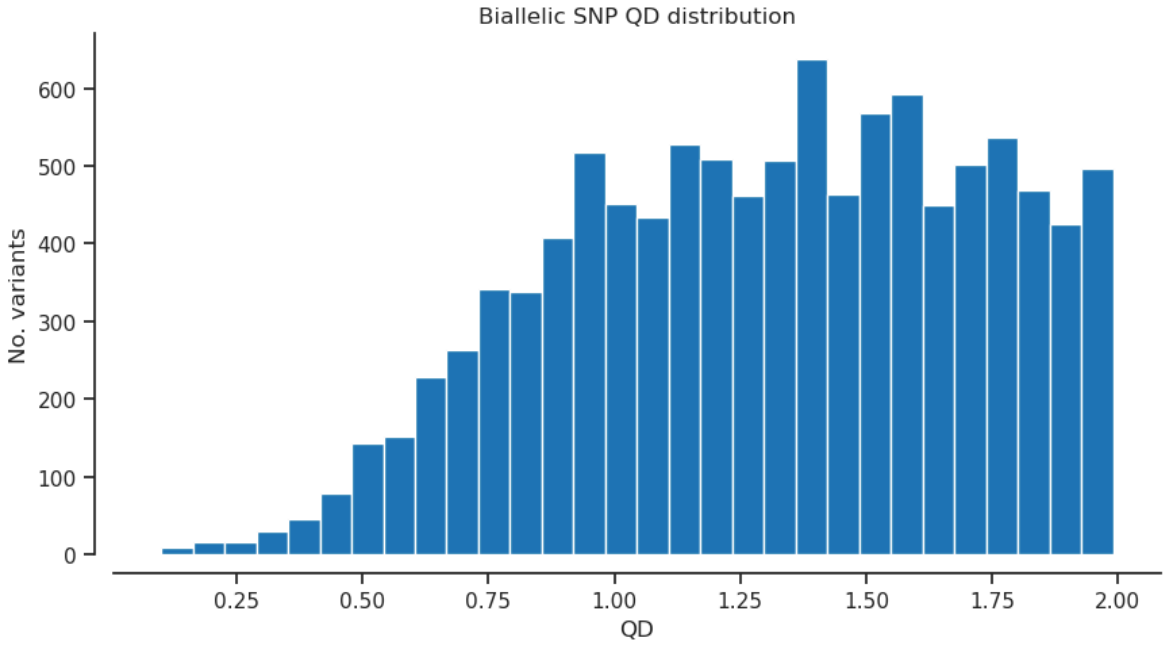


In [21]:
```
plot_hist('QD','biallelic') # Variant Confidence/Quality by Depth
```

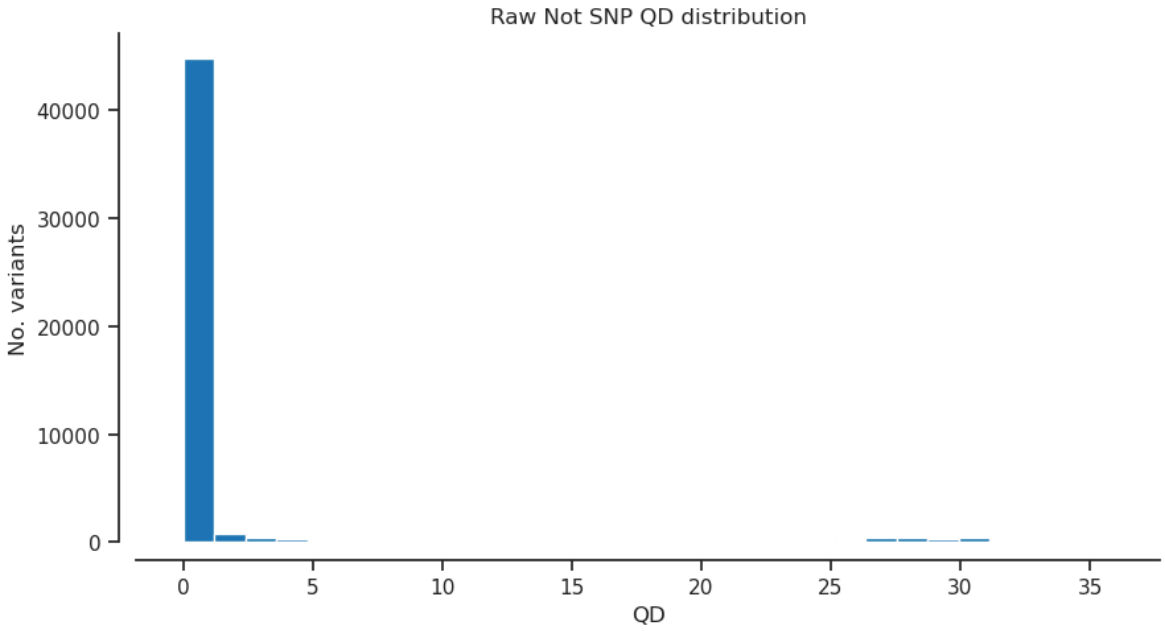


In [22]:
```
filter_expression = '(QD < 2)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [23]:
```
plot_hist('QD')
```

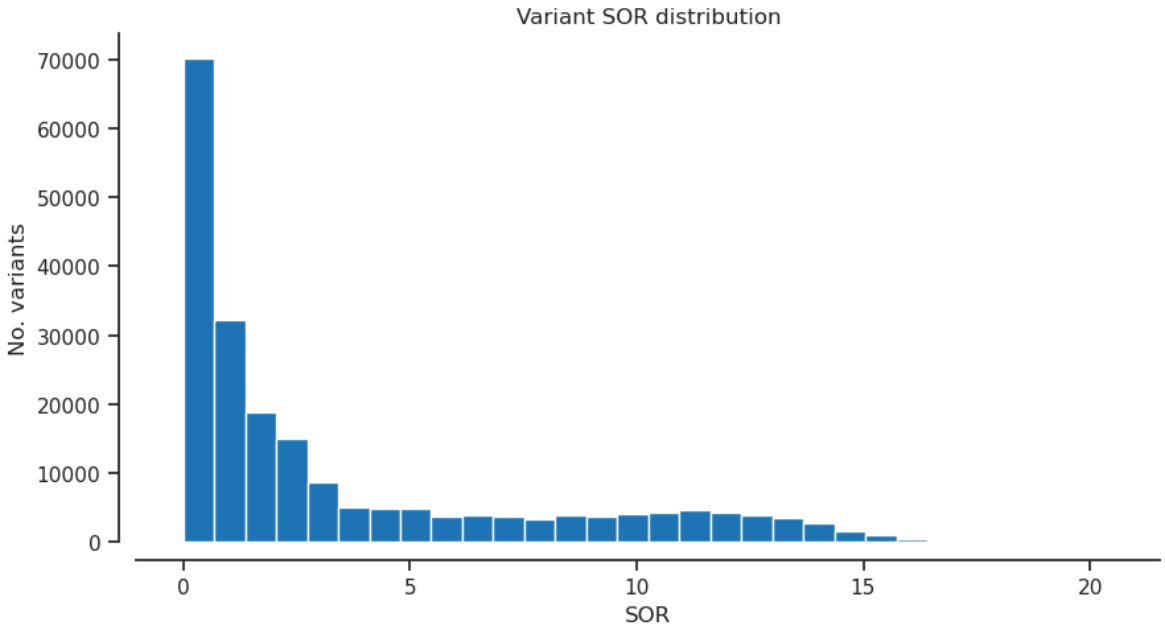


In [24]:
```
plot_hist('QD','notsnp') # Variant Confidence/Quality by Depth
```

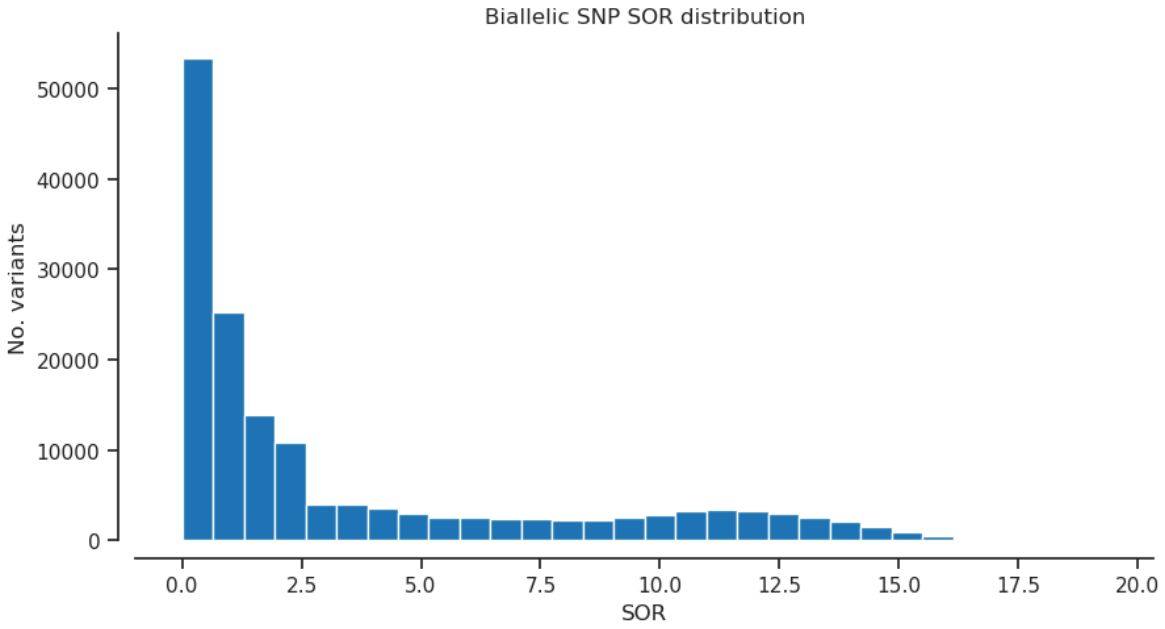


SOR - Symmetric Odds Ratio of 2x2 contingency table to detect strand bias

In [25]:
```
plot_hist('SOR', 'var') # Symmetric Odds Ratio of 2x2 contingency table t
```

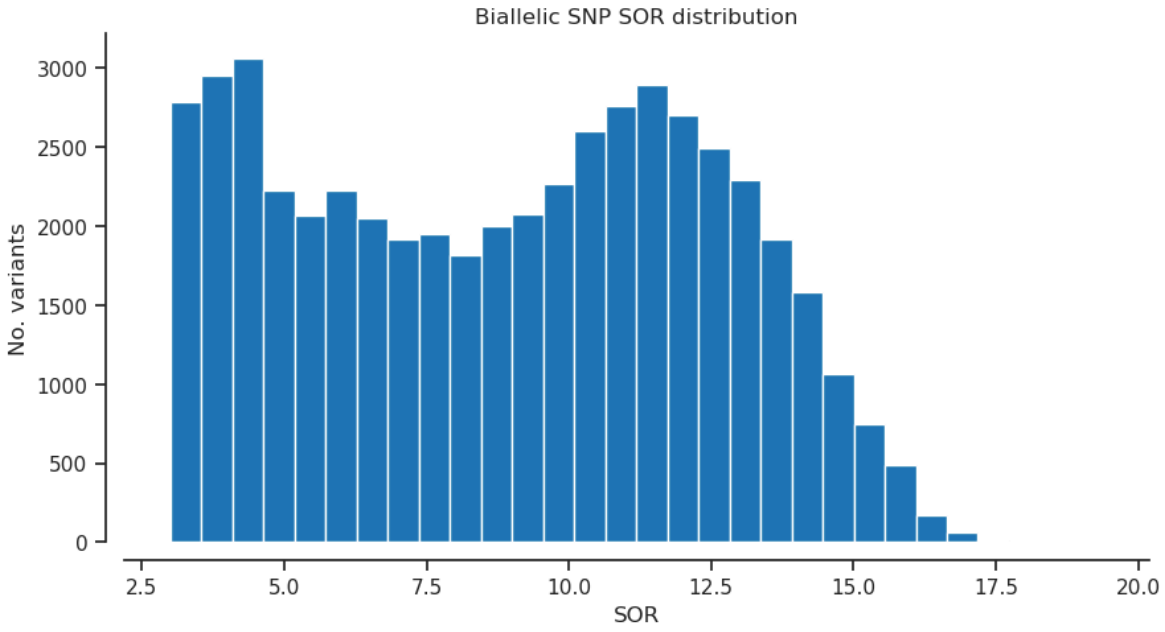


In [26]:
```
plot_hist('SOR','biallelic') # Symmetric Odds Ratio of 2x2 contingency ta
```

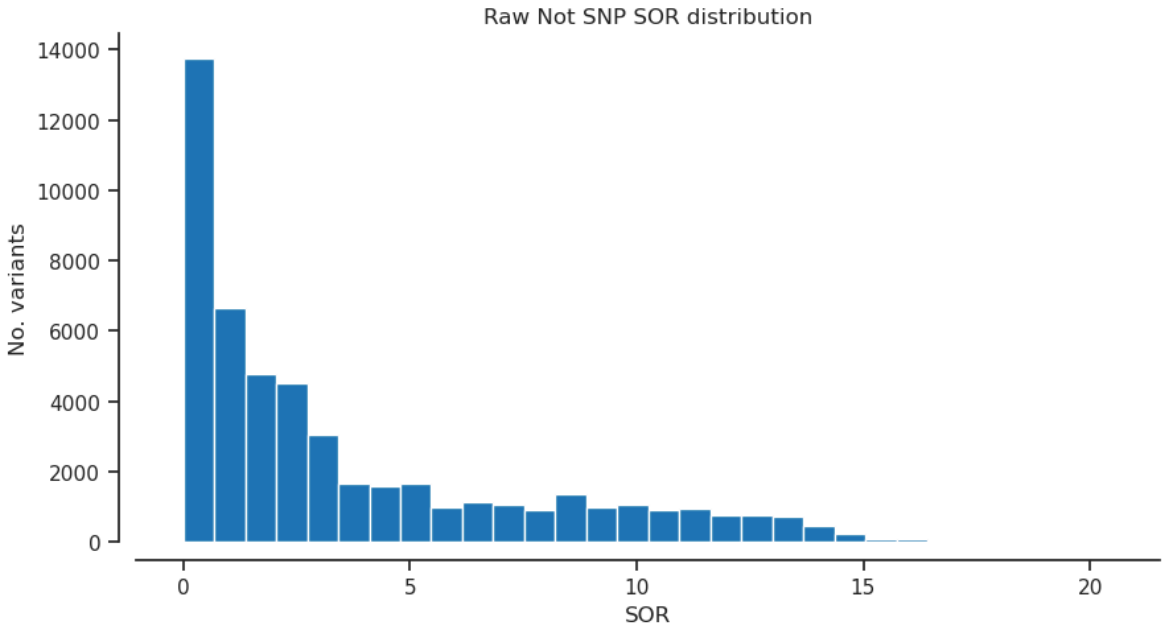


In [27]:
```
filter_expression = '(SOR > 3)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

In [28]:
```
plot_hist('SOR') # Symmetric Odds Ratio of 2x2 contingency table to detec
```

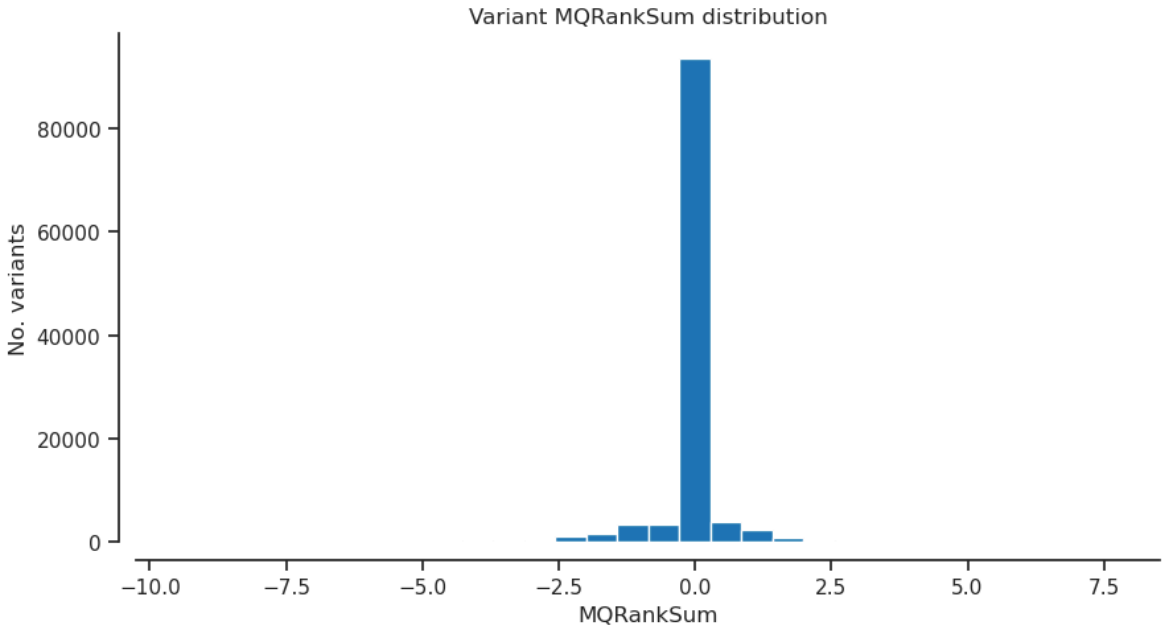


In [29]:
```
plot_hist('SOR','notsnp') # Symmetric Odds Ratio of 2x2 contingency table
```

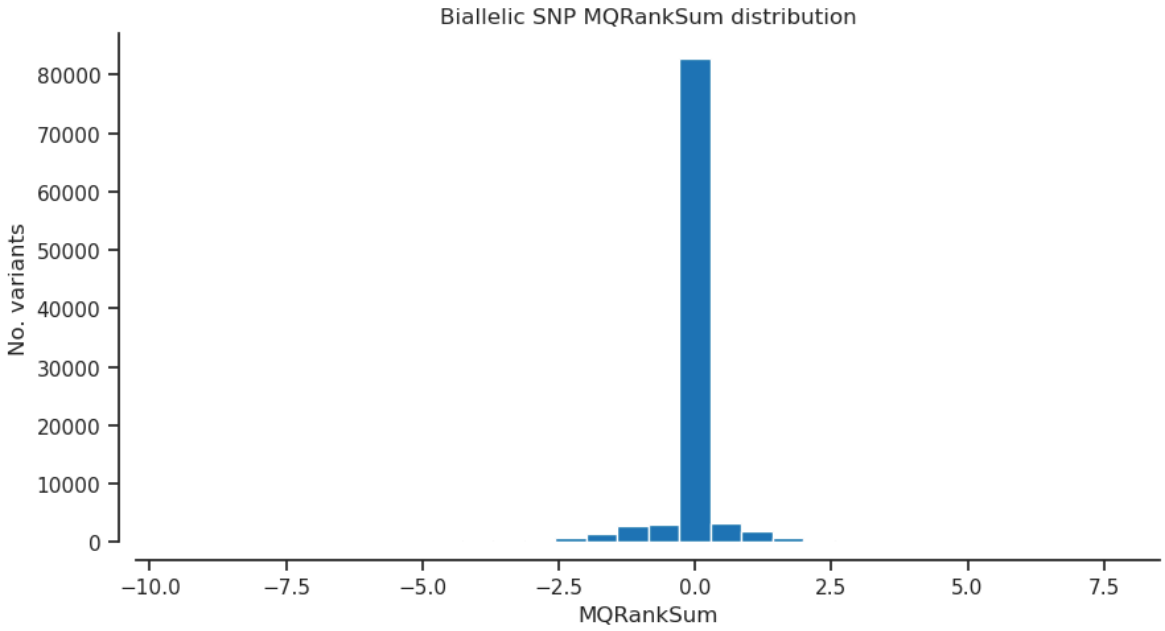


MQRankSum - Z-score From Wilcoxon rank sum test of Alt vs. Ref read mapping qualities

In [30]:
```
plot_hist('MQRankSum','var') # Z-score From Wilcoxon rank sum test of Alt
```

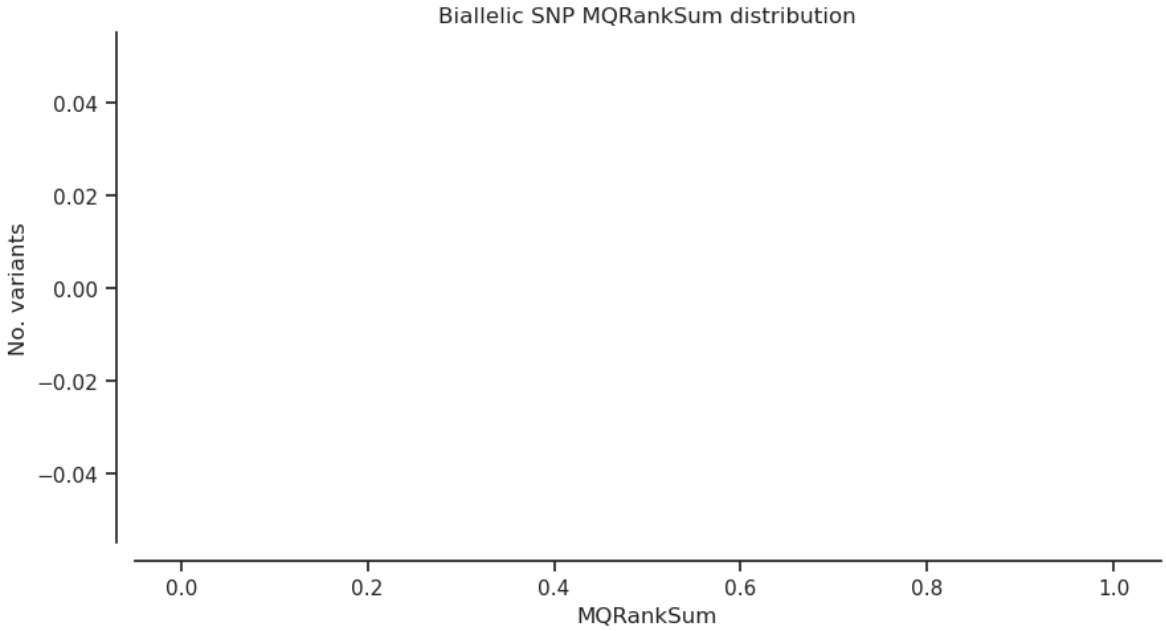


In [31]:
```
plot_hist('MQRankSum','biallelic') # Z-score From Wilcoxon rank sum test
```

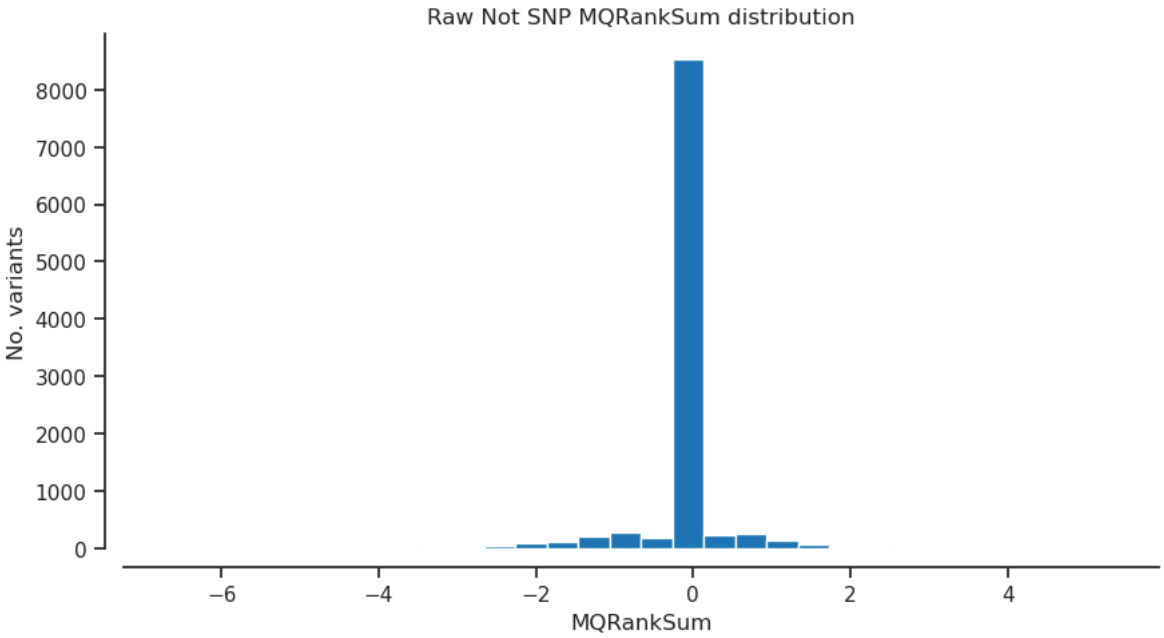


In [32]:
```
filter_expression = '(MQRankSum < -12.5)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

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

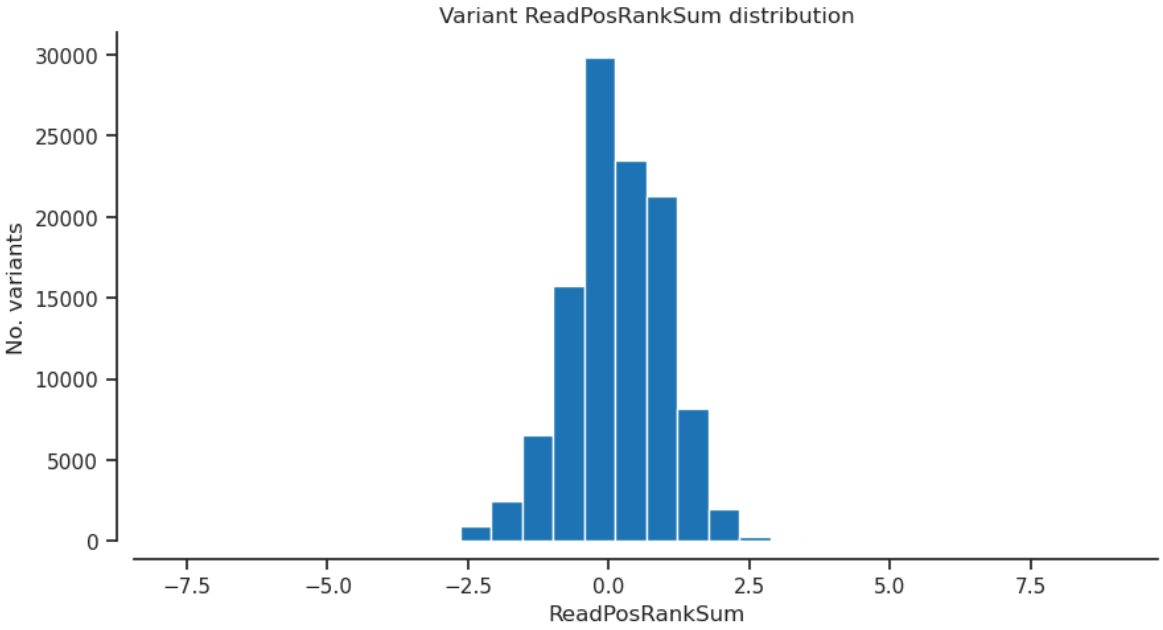


In [34]:
```
plot_hist('MQRankSum','notsnp') # Z-score From Wilcoxon rank sum test of
```

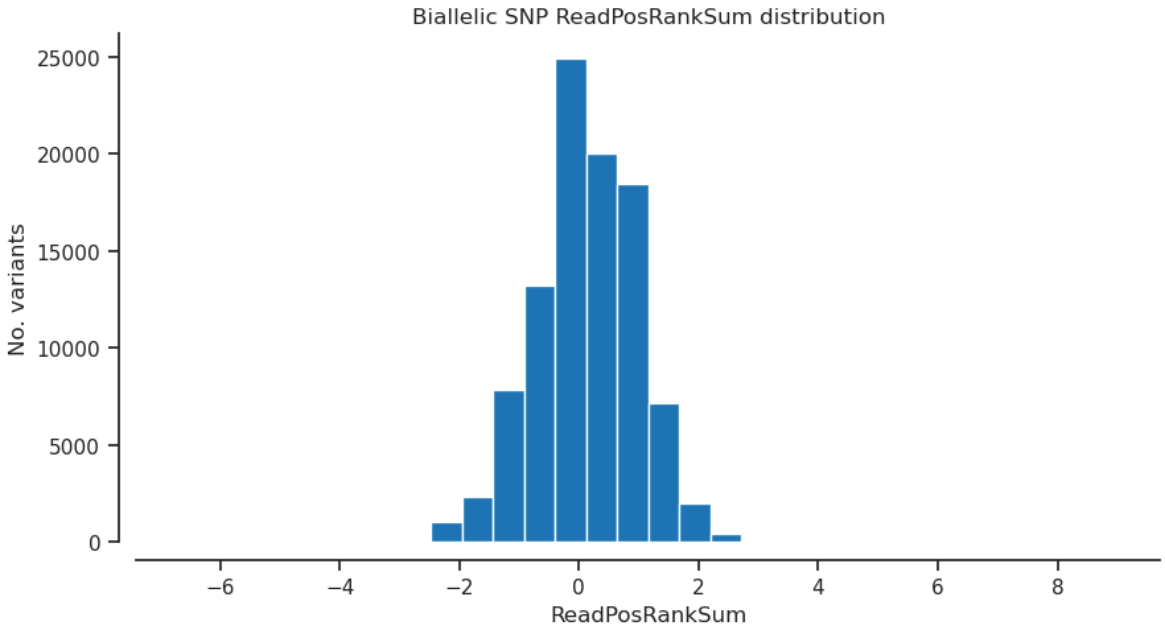


ReadPosRankSum - Z-score from Wilcoxon rank sum test of Alt vs. Ref read position bias

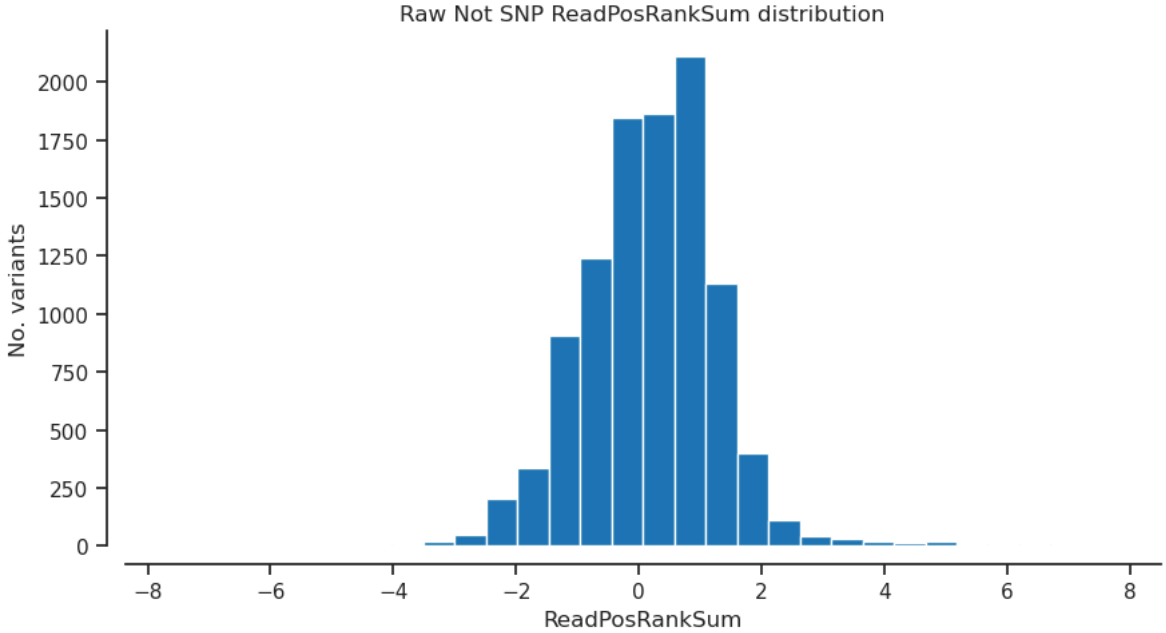
In [35]:
```
plot_hist('ReadPosRankSum','var') # Z-score from Wilcoxon rank sum test o
```



In [36]:
```
plot_hist('ReadPosRankSum','biallelic') # Z-score from Wilcoxon rank sum
```

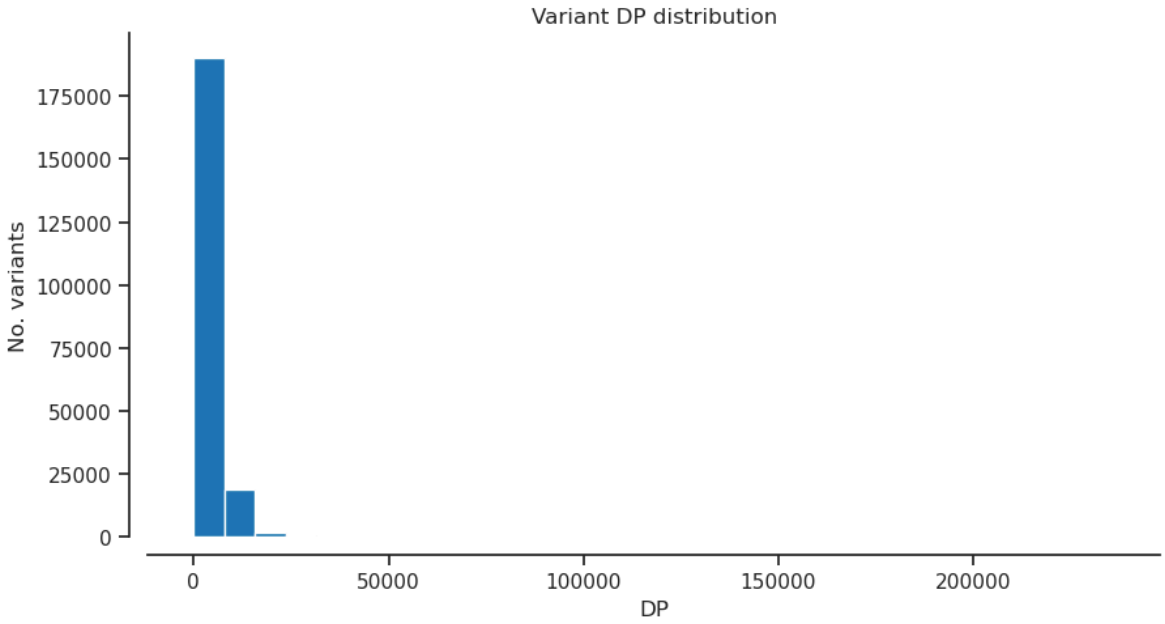


In [37]:
```
plot_hist('ReadPosRankSum','notsnp') # Z-score from Wilcoxon rank sum tes
```

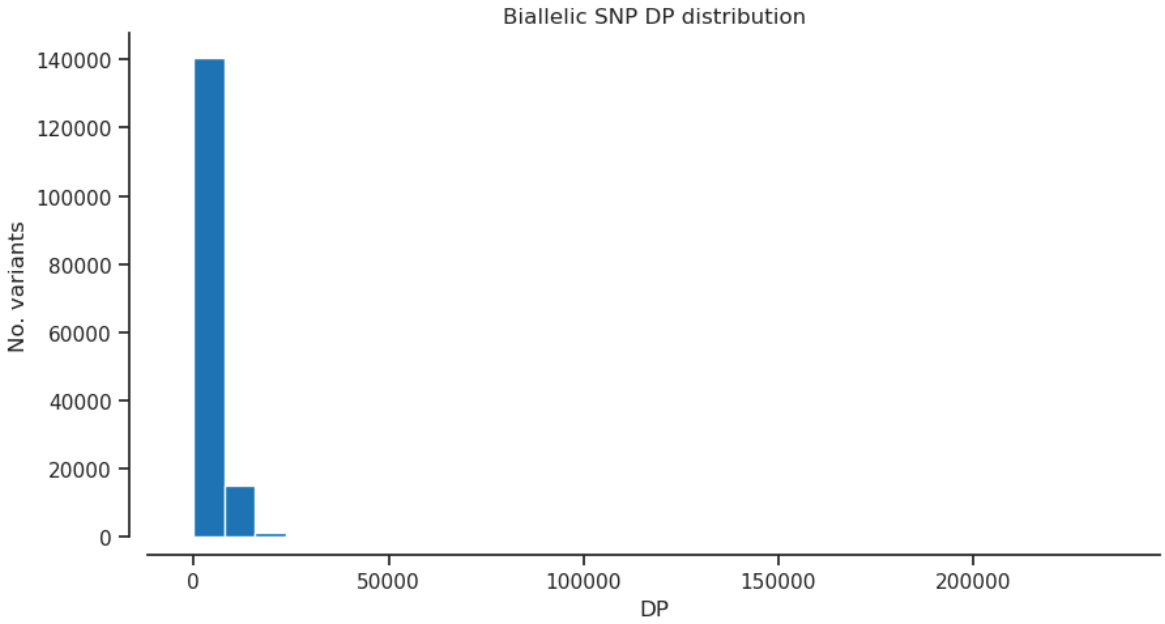


DP - Approximate read depth

In [38]:
```
plot_hist('DP','var')
```

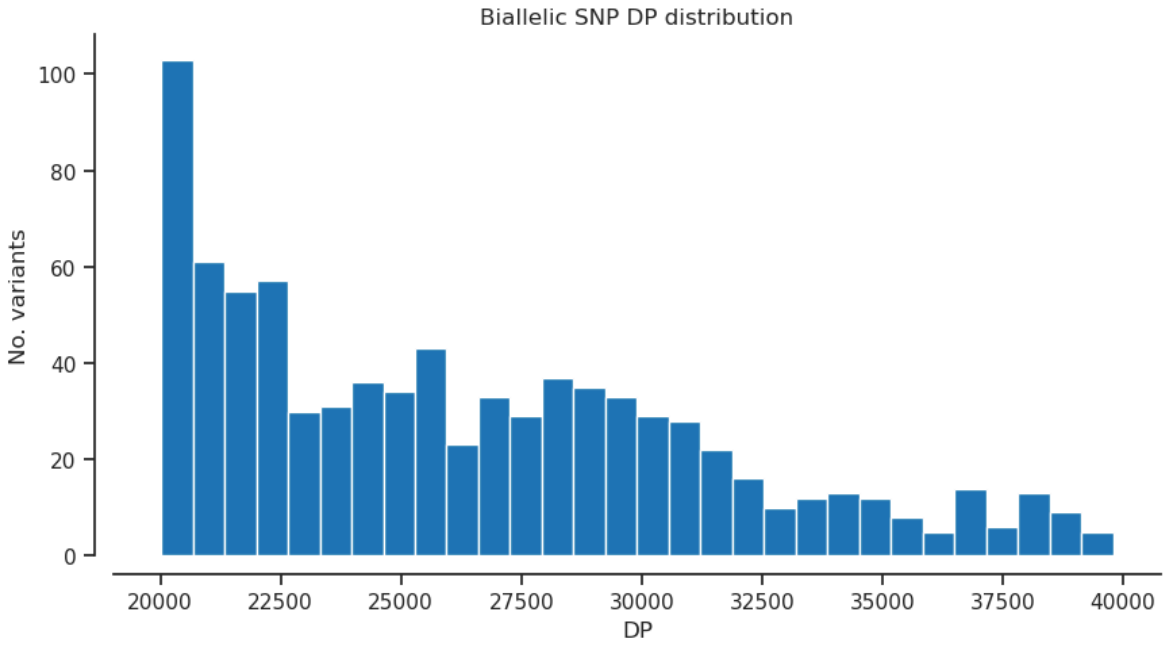


In [39]:
```
plot_hist('DP','biallelic')
```

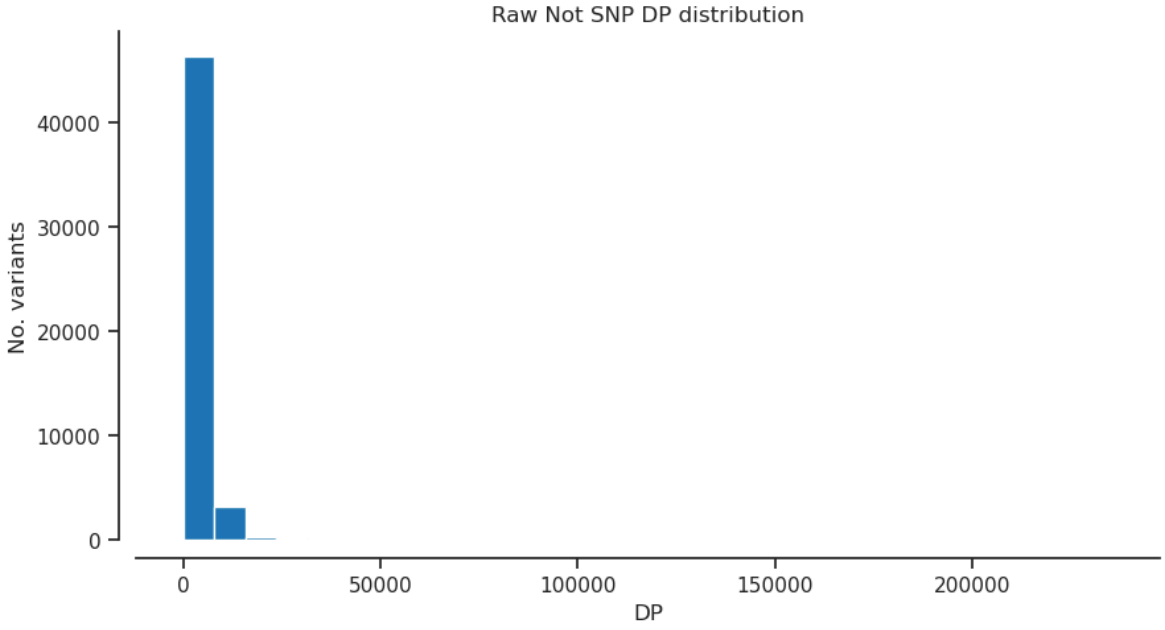


In [40]:
```
filter_expression = '(DP > 20000) & (DP < 40000)'
bi_selection = biallelic_np.query(filter_expression)[:]
```

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

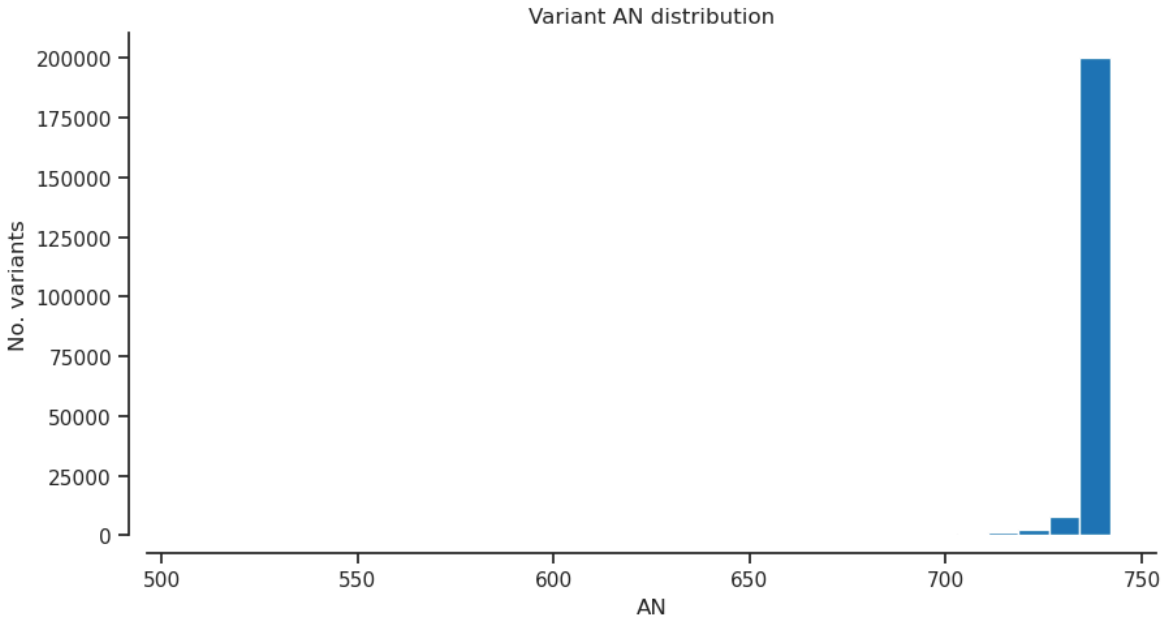


In [42]:
```
plot_hist('DP','notsnp')
```

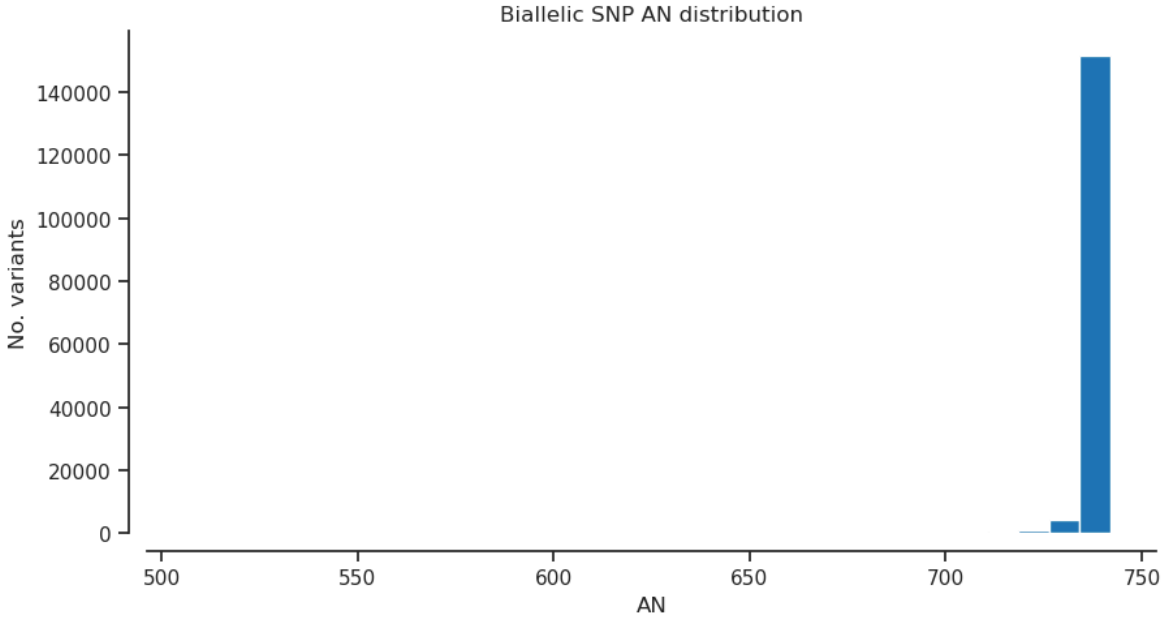


AN - Total number of alleles in called genotypes

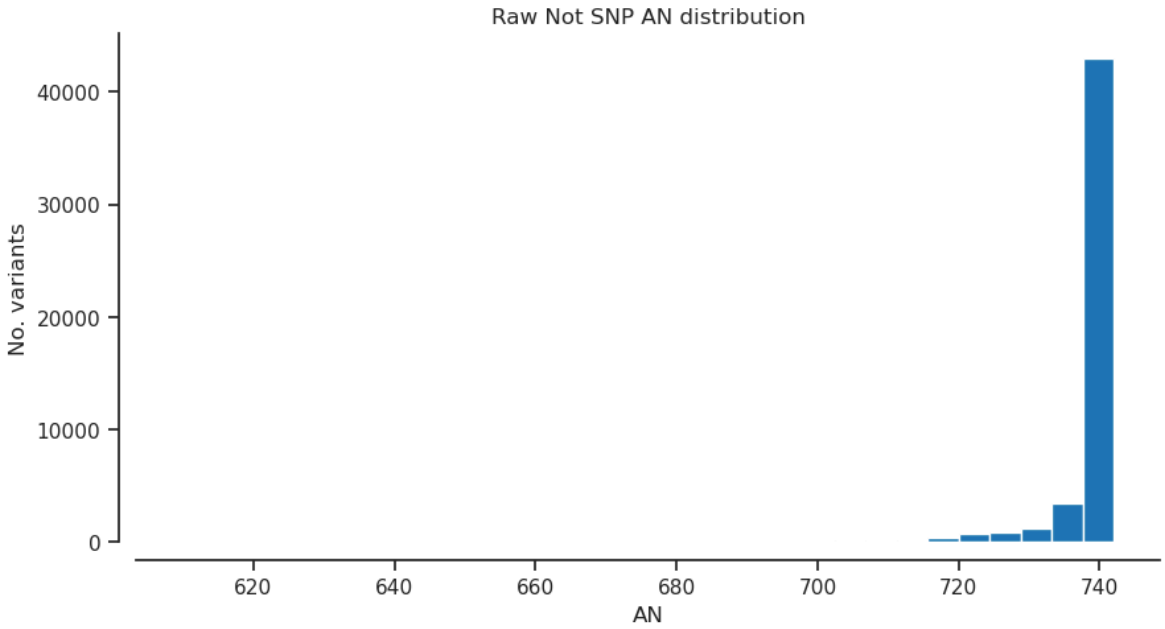
In [43]:
```
plot_hist('AN','var') # Total number of alleles in called genotypes
```



In [44]:
```
plot_hist('AN','biallelic') # Total number of alleles in called genotypes
```



In [45]:
```
plot_hist('AN','notsnp') # Total number of alleles in called genotypes
```



Selected filter

In [46]:
```
# 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[46]: 87121

Genotype

In [47]:
```
calldata_var = callset_var['calldata']
list(calldata_var)
```

Out[47]: ['AD', 'DP', 'GQ', 'GT', 'MIN_DP', 'PGT', 'PID', 'PL', 'PS', 'RGQ', 'S
B']

In [48]:
```
genotypes_var = allel.GenotypeChunkedArray(calldata_var['GT'])
genotypes_var
```

Out[48]: <GenotypeChunkedArray shape=(212695, 371, 2) dtype=int8 chunks=(65536, 64, 2) nbytes=150.5M cbytes=8.3M cratio=18.2 compression=gzip compression_opts=1 values=h5py._hl.dataset.Dataset>

	0	1	2	3	4	...	366	367	368	369	370
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
...						...					
212692	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
212693	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
212694	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0

In [49]:
```
# using the selected filters set above
gt_filtered_snps = genotypes_var.subset(variant_selection)
gt_filtered_snps
```

Out[49]: <GenotypeChunkedArray shape=(87121, 371, 2) dtype=int8 chunks=(1362, 371, 2) nbytes=61.6M cbytes=6.1M cratio=10.1 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1	2	3	4	...	366	367	368	369	370
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
...						...					
87118	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
87119	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
87120	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0

In [50]:
```
# grab the allele counts for the populations
ac = gt_filtered_snps.count_alleles()
ac
```

Out[50]: <AlleleCountsChunkedArray shape=(87121, 4) dtype=int32 chunks=(21781, 4) nbytes=1.3M cbytes=268.7K cratio=5.1 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1	2	3
0	740	2	0	0
1	740	2	0	0
2	739	3	0	0
...		...		
87118	740	2	0	0
87119	741	1	0	0
87120	741	1	0	0

In [51]:
```
ac[:]
```

Out[51]: <AlleleCountsArray shape=(87121, 4) dtype=int32>

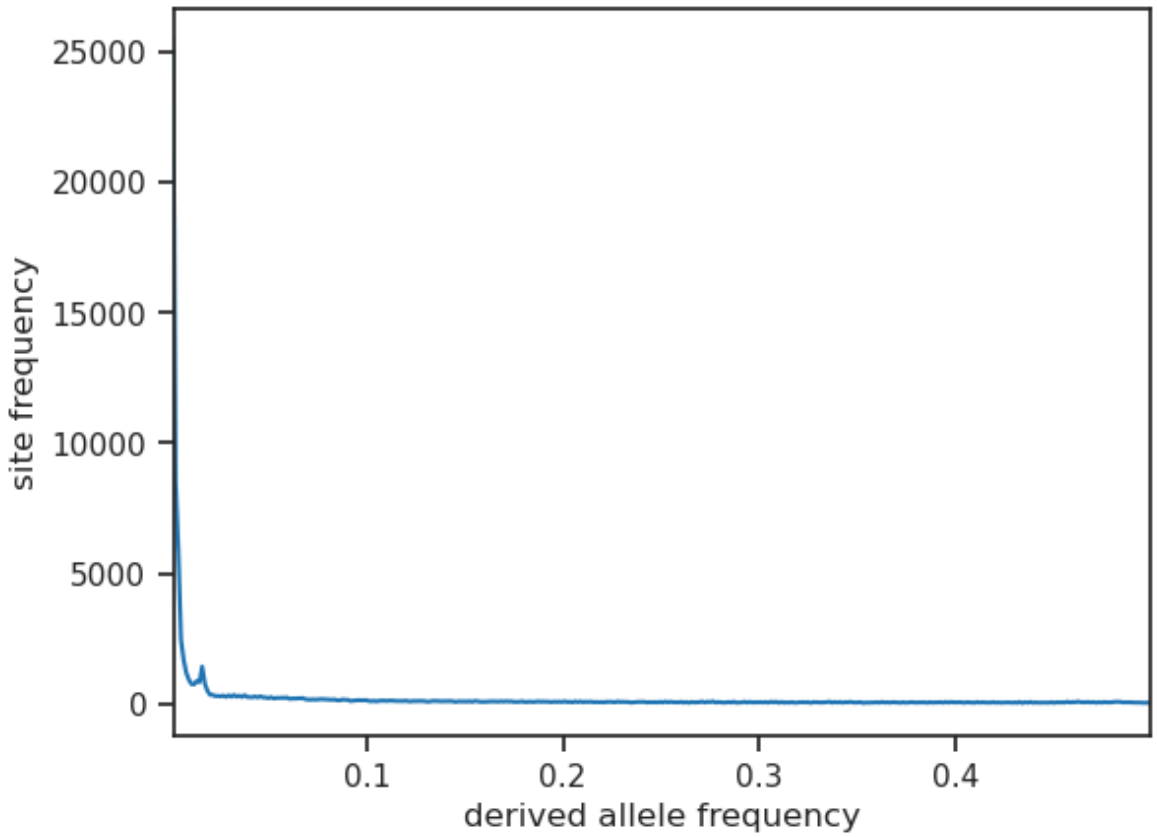
	0	1	2	3
0	740	2	0	0
1	740	2	0	0
2	739	3	0	0
...		...		
87118	740	2	0	0
87119	741	1	0	0
87120	741	1	0	0

In [52]:
```
# 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[52]:
```
array([[740,   2],
       [740,   2],
       [739,   3],
       ...,
       [740,   2],
       [741,   1],
       [741,   1]], dtype=int32)
```

In [53]:
```
# 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[53]:
```
<Axes: xlabel='derived allele frequency', ylabel='site frequency'>
```



In [54]:
```
biallelic = (ac.max_allele() == 1)
###This is the filter expression for biallelic sites
biallelic
```

Out[54]:
```
<ChunkedArrayWrapper shape=(87121,) dtype=bool chunks=(87121,)
   nbytes=85.1K cbytes=11.3K cratio=7.5
   compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shu
ffle': 1, 'blocksize': 0}
   values=zarr.core.Array>
```

In [55]:
```
# select only the biallelic variants
gt_biallelic = gt_filtered_snps.compress(biallelic)
gt_biallelic
```

Out[55]: <GenotypeChunkedArray shape=(84345, 371, 2) dtype=int8 chunks=(1318, 371, 2) nbytes=59.7M cbytes=5.8M cratio=10.3 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1	2	3	4	...	366	367	368	369	370
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
...						...					
84342	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
84343	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0
84344	0/0	0/0	0/0	0/0	0/0	...	0/0	0/0	0/0	0/0	0/0

In [56]:
```
n_variants = len(gt_biallelic)
n_variants
```

Out[56]: 84345

In [57]:
```
pc_missing = gt_biallelic.count_missing(axis=0)[:] * 100 / n_variants
pc_het = gt_biallelic.count_het(axis=0)[:] * 100 / n_variants
```

Samples

In [58]:
```
samples_var = callset_var['samples']
samples_var = list(samples_var)
samples_var
```

Out[58]:
```
[b'ESP00057-001',
 b'ESP00057-002',
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 b'ITA00270-021',
 b'ITA00270-022',
 b'ITA00270-023',
 b'ITA00270-024',
 b'ITA00270-025']
```

In [59]:
```
samples_fn = '~/scratch/data/Phalepensis/Pinus_halepensis_sample_list_sci
samples = pandas.read_csv(samples_fn, sep='\t')
samples
```

Out[59]:

	ID	Population
0	ESP00057-001	ESP00057
1	ESP00057-002	ESP00057
2	ESP00057-003	ESP00057
3	ESP00057-004	ESP00057
4	ESP00057-005	ESP00057
...	...	...
366	ITA00270-021	ITA00270
367	ITA00270-022	ITA00270
368	ITA00270-023	ITA00270
369	ITA00270-024	ITA00270
370	ITA00270-025	ITA00270

371 rows × 2 columns

In [60]:
```
samples.Population.value_counts()
```

Out[60]:
```
Population
ITA00025    25
ESP00166    25
ESP00106    25
ITA00076    25
ITA00075    25
ITA00046    25
ITA00027    25
ITA00133    25
ITA00165    25
ITA00261    25
ITA00270    25
ESP00377    24
ESP00057    24
ESP00091    24
ESP00094    24
Name: count, dtype: int64
```

In [61]:
```
populations = samples.Population.unique()
populations
###This identifiers come from the metadata file
```

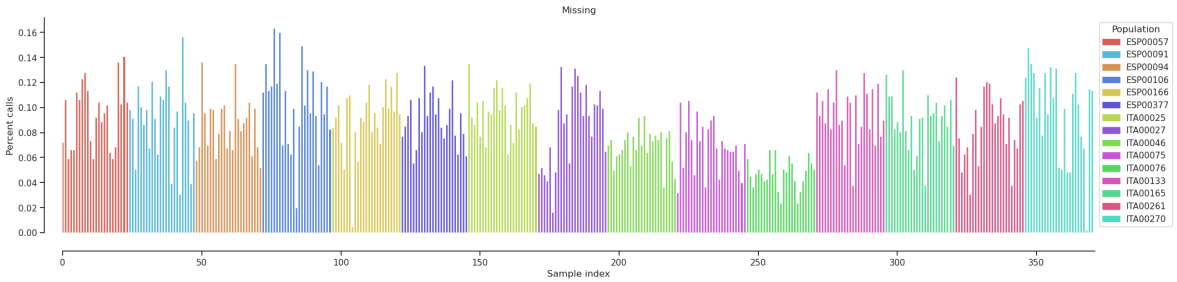
Out[61]:
```
array(['ESP00057', 'ESP00091', 'ESP00094', 'ESP00106', 'ESP00166',
       'ESP00377', 'ITA00025', 'ITA00027', 'ITA00046', 'ITA00075',
       'ITA00076', 'ITA00133', 'ITA00165', 'ITA00261', 'ITA00270'],
      dtype=object)
```

Gt frequency function

In [64]:
```
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", 15)
    pop2color = {'ESP00057': palette[0],
                 'ESP00091': palette[8],
                 'ESP00094': palette[1],
                 'ESP00106': palette[9],
                 'ESP00166': palette[2],
                 'ESP00377': palette[10],
                 'ITA00025': palette[3],
                 'ITA00027': palette[11],
                 'ITA00046': palette[4],
                 'ITA00075': palette[12],
                 'ITA00076': palette[5],
                 'ITA00133': palette[13],
                 'ITA00165': palette[6],
                 'ITA00261': palette[14],
                 'ITA00270': palette[7]}
    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[8]),
               mpl.patches.Patch(color=palette[1]),
               mpl.patches.Patch(color=palette[9]),
               mpl.patches.Patch(color=palette[2]),
               mpl.patches.Patch(color=palette[10]),
               mpl.patches.Patch(color=palette[3]),
               mpl.patches.Patch(color=palette[11]),
               mpl.patches.Patch(color=palette[4]),
               mpl.patches.Patch(color=palette[12]),
               mpl.patches.Patch(color=palette[5]),
               mpl.patches.Patch(color=palette[13]),
               mpl.patches.Patch(color=palette[6]),
               mpl.patches.Patch(color=palette[14]),
               mpl.patches.Patch(color=palette[7]),
               mpl.patches.Patch(color="#DFFF00")]
    ax.legend(handles=handles, labels=['ESP00057', 'ESP00091', 'ESP00094'
       'ESP00377', 'ITA00025', 'ITA00027', 'ITA00046', 'ITA00075',
       'ITA00076', 'ITA00133', 'ITA00165', 'ITA00261', 'ITA00270'], title
              bbox_to_anchor=(1, 1), loc='upper left')
```

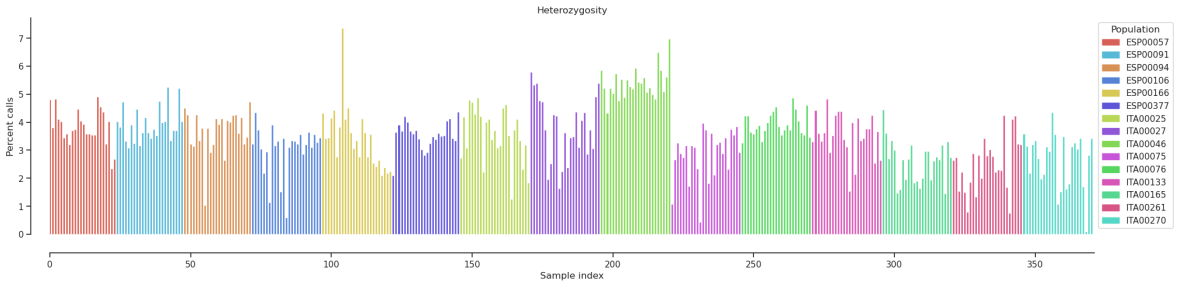
Plot missing

In [65]:
```
plot_genotype_frequency(pc_missing, 'Missing')
```



Plot heterozygosity

In [66]:
```
plot_genotype_frequency(pc_het, 'Heterozygosity')
```



PCA

In [68]:
```
palette = sns.color_palette("hls",15)
pop_colours = {
                'ESP00057': palette[0],
                 'ESP00091': palette[8],
                 'ESP00094': palette[1],
                 'ESP00106': palette[9],
                 'ESP00166': palette[2],
                 'ESP00377': palette[10],
                 'ITA00025': palette[3],
                 'ITA00027': palette[11],
                 'ITA00046': palette[4],
                 'ITA00075': palette[12],
                 'ITA00076': palette[5],
                 'ITA00133': palette[13],
                 'ITA00165': palette[6],
                 'ITA00261': palette[14],
                 'ITA00270': palette[7]
}
```

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=(84345, 2) dtype=int32 chunks=(42173, 2) nbytes=658.9K cbytes=197.4K cratio=3.3 compression=blosc compression_opts={'cname': 'lz4', 'clevel': 5, 'shuffle': 1, 'blocksize': 0} values=zarr.core.Array>

	0	1
0	740	2
1	740	2
2	739	3
...	...	
84342	740	2
84343	741	1
84344	741	1

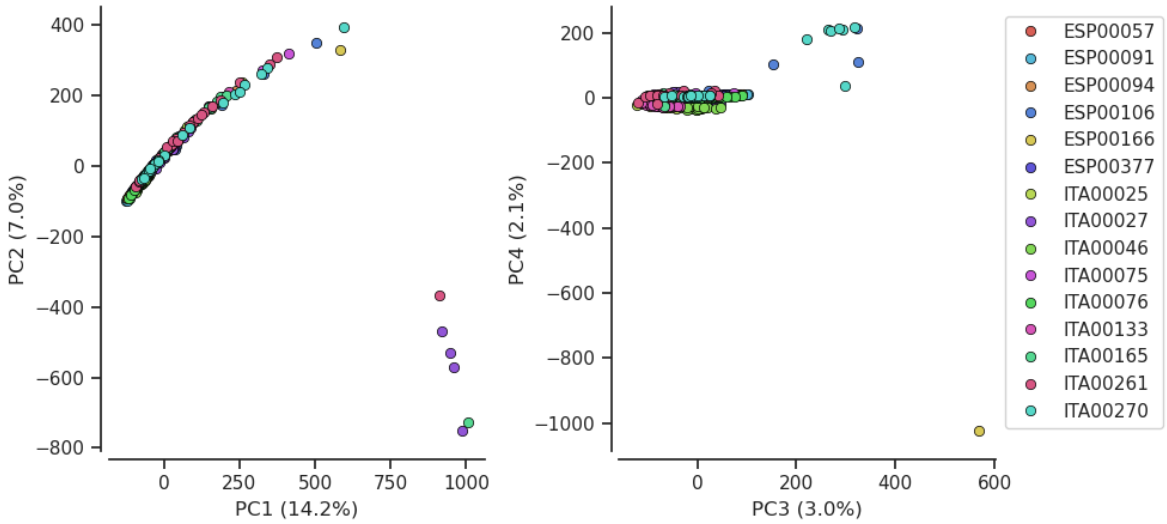
In [71]:
```
flt = (ac2[:, :2].min(axis=1) > 1)
gf = gt_biallelic.compress(flt, axis=0)
gn = gf.to_n_alt()
gn
```

Out[71]:
```
<ChunkedArrayWrapper shape=(58928, 371) dtype=int8 chunks=(1842, 371)
   nbytes=20.8M cbytes=3.9M cratio=5.3
   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]:
```
weirdos = coords1[:,2]>500
samples[weirdos]
```

Out[74]:

	ID	Population
104	ESP00166-008	ESP00166

In [75]:
```
pc_het[weirdos]
```

Out[75]:
```
array([7.36024661])
```

In [76]:
```
pc_missing[weirdos]
```

Out[76]:
```
array([0.00474243])
```

In [77]:
```
weirdos2 = coords1[:,1]<-300
samples[weirdos2]
```

Out[77]:

	ID	Population
176	ITA00027-006	ITA00027
177	ITA00027-007	ITA00027
181	ITA00027-011	ITA00027
182	ITA00027-012	ITA00027
320	ITA00165-025	ITA00165
323	ITA00261-003	ITA00261

In [78]:
```
weirdos3 = coords1[:,1]<-700
samples[weirdos3]
```

Out[78]:

	ID	Population
176	ITA00027-006	ITA00027
320	ITA00165-025	ITA00165

In [79]:
```
pc_het[weirdos2]
```

Out[79]:
```
array([3.73347561, 1.96217915, 1.65155018, 2.25620962, 2.75416444,
       1.55314482])
```

In [80]:
```
pc_missing[weirdos2]
```

Out[80]:
```
array([0.01659849, 0.04860988, 0.09484854, 0.05572352, 0.0699508 ,
       0.04860988])
```

In [81]:
```
pc_het[weirdos3]
```

Out[81]:
```
array([3.73347561, 2.75416444])
```

In [82]:
```
pc_missing[weirdos3]
```

Out[82]:
```
array([0.01659849, 0.0699508 ])
```

In [83]:
```
coords1[323]
```

Out[83]:
```
array([ 9.1116418e+02, -3.6735449e+02, -2.7487478e+01,  2.3352139e+01,
        3.2546886e+01,  1.3368362e+02,  4.4097351e+01,  5.9502289e+02,
       -2.2757989e-01,  3.3078189e+02], dtype=float32)
```

In [84]:
```
coords1[320]
```

Out[84]:
```
array([ 1.0059885e+03, -7.2601581e+02, -5.9366253e+01,  9.1340218e+00,
       -1.0663336e+01, -9.4203011e+01, -8.9557725e-01, -2.6242108e+02,
        6.1044697e+01,  2.8970868e+02], dtype=float32)
```

In [85]:
```
coords1[182]
```

Out[85]:
```
array([ 957.2276   , -571.38837  ,  -49.857384 ,   17.57669  ,
          1.9413402,  -18.343372 ,  -11.991859 ,  -30.981314 ,
        -35.495697 , -221.56584  ], dtype=float32)
```