In [3]:
```python
import pandas as pd
import numpy as np

# Example SNP dataset (Replace this with actual data)
df_snp = pd.DataFrame({
    'SNP1': ['A/A', 'A/G', 'G/G', 'A/G'],
    'SNP2': ['C/C', 'C/T', 'T/T', 'C/T'],
    'SNP3': ['G/G', 'A/G', 'A/A', 'A/G']
})

# Function to encode SNPs numerically
def encode_snp(genotype):
    mapping = {'A/A': 0, 'A/G': 1, 'G/G': 2,
               'C/C': 0, 'C/T': 1, 'T/T': 2}
    return mapping.get(genotype, np.nan)

# Apply encoding
snp_encoded = df_snp.applymap(encode_snp)

print(snp_encoded.head())  # Check encoded SNP data
```

```
   SNP1  SNP2  SNP3
0     0     0     2
1     1     1     1
2     2     2     0
3     1     1     1
```

In [4]:
```python
# Compute correlation
snp_corr = snp_encoded.corr()

print(snp_corr)  # Check correlation values
```
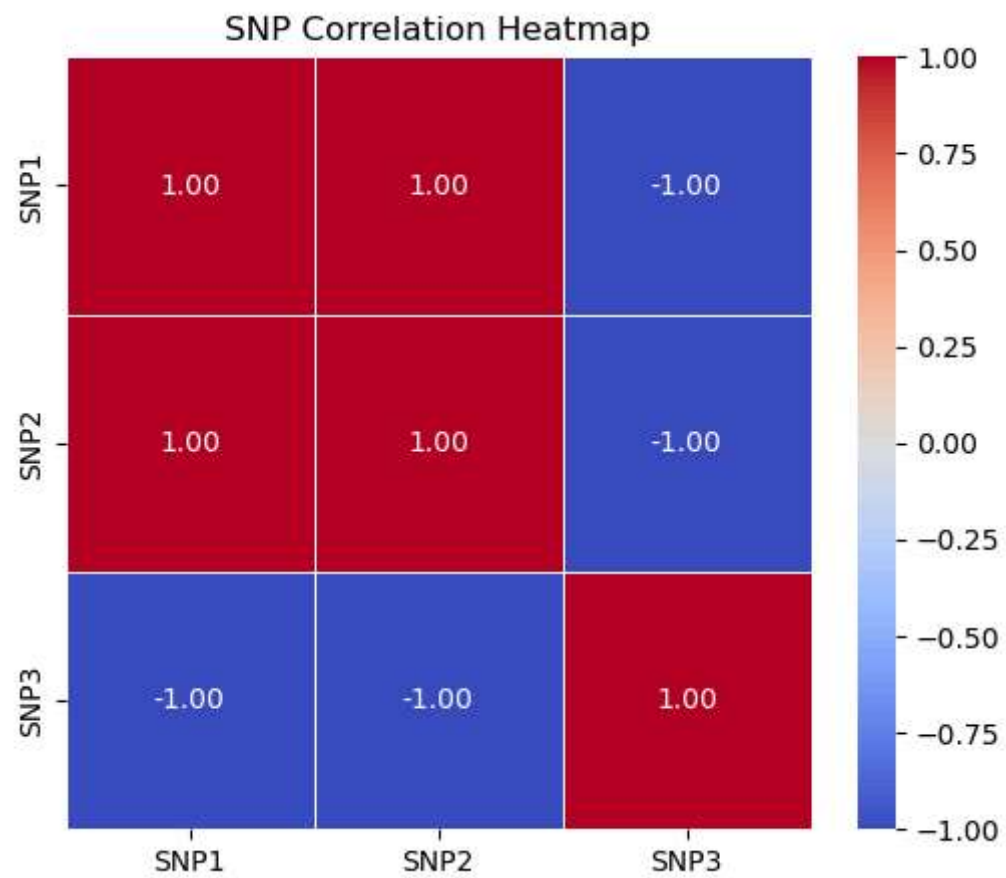
```
      SNP1  SNP2  SNP3
SNP1   1.0   1.0  -1.0
SNP2   1.0   1.0  -1.0
SNP3  -1.0  -1.0   1.0
```

In [5]:
```python
import seaborn as sns
import matplotlib.pyplot as plt

# Plot heatmap
plt.figure(figsize=(6, 5))
sns.heatmap(snp_corr, annot=True, cmap="coolwarm", fmt=".2f", linewidths=0.5)
```

```
plt.title("SNP Correlation Heatmap")
plt.show()
```


In [ ]: