

main

August 7, 2021

1 Examining the overlap between antipsychotics analysis with main DE analysis

```
[1]: import pandas as pd
import matplotlib.pyplot as plt
from matplotlib_venn import venn2,venn3
```

1.1 Load DE genes results

```
[2]: ap = pd.read_csv("../_m/genes/diffExpr_sz_APVctl_full.txt", sep='\t',
    ↪index_col=0)
noap = pd.read_csv("../_m/genes/diffExpr_sz_noAPVctl_full.txt", sep='\t',
    ↪index_col=0)
degs = pd.read_csv("../_m/genes/diffExpr_szVctl_full.txt", sep='\t',
    ↪index_col=0)
```

1.1.1 FDR 5% comparison

```
[3]: def get_degs(df, fdr):
    return df[(df["adj.P.Val"] < fdr)]
```

```
[4]: len(set(get_degs(ap, 0.05).index) & set(get_degs(noap, 0.05).index))
```

```
[4]: 331
```

```
[5]: len(set(get_degs(ap, 0.05).index) & set(get_degs(noap, 0.05).index)) /
    ↪len(set(get_degs(noap, 0.05).index))
```

```
[5]: 0.4962518740629685
```

```
[6]: len(set(get_degs(ap, 0.05).index) & set(get_degs(degs, 0.05).index))
```

```
[6]: 1929
```

```
[7]: len(set(get_degs(ap, 0.05).index) & set(get_degs(degs, 0.05).index)) /
    ↪len(set(get_degs(ap, 0.05).index))
```

```
[7]: 0.7165676077265973
```

```
[8]: len(set(get_degs(noap, 0.05).index) & set(get_degs(degs, 0.05).index))
```

```
[8]: 520
```

```
[9]: len(set(get_degs(noap, 0.05).index) & set(get_degs(degs, 0.05).index)) /   
      ↪ len(set(get_degs(noap, 0.05).index))
```

```
[9]: 0.7796101949025487
```

1.2 Plot venn diagrams

```
[10]: plt.rcParams.update({'font.size': 22, 'font.weight': 'bold'})
```

```
[11]: def get_deg_df(feature):  
    ap = pd.read_csv("../_m/%s/diffExpr_sz_APVctl_full.txt" % feature,  
                     sep='\t', index_col=0)  
    noap = pd.read_csv("../_m/%s/diffExpr_sz_noAPVctl_full.txt" % feature,  
                       sep='\t', index_col=0)  
    degs = pd.read_csv("../_m/%s/diffExpr_szVctl_full.txt" % feature,  
                       sep='\t', index_col=0)  
    return ap[(ap['adj.P.Val'] <= 0.05)], noap[(noap['adj.P.Val'] <= 0.05)],   
           ↪ degs[(degs['adj.P.Val'] <= 0.05)]  
  
def plot_pairwise_venn(feature, ANTI="Yes"):  
    aa, nn, df2 = get_deg_df(feature)  
    label2 = "SZ"  
    if ANTI == "Yes":  
        label = "AP"  
        fn = "venn_SZ_vs_AP_%s" % feature  
        df1 = aa  
    elif ANTI == "No":  
        label = "No AP"  
        fn = "venn_SZ_vs_noAP_%s" % feature  
        df1 = nn  
    else:  
        label = "AP"  
        label2 = "No AP"  
        df1 = aa; df2 = nn  
        fn = "venn_AP_vs_noAP_%s" % feature  
    plt.figure(figsize=(8,8))  
    v = venn2([set(df1.index), set(df2.index)],  
              set_labels = (label, label2))  
    v.get_patch_by_id('10').set_color('red')  
    v.get_patch_by_id('10').set_alpha(0.75)
```

```

v.get_patch_by_id('01').set_color('blue')
v.get_patch_by_id('01').set_alpha(0.75)
try:
    v.get_patch_by_id('11').set_color('purple')
    v.get_patch_by_id('11').set_alpha(0.75)
except AttributeError:
    print("There is no overlap!")
plt.savefig('%s.png' % fn)
plt.savefig('%s.pdf' % fn)

def plot_venn3(feature):
    aa, nn, dd = get_deg_df(feature)
    plt.figure(figsize=(10,10))
    v = venn3([set(aa.index), set(nn.index), set(dd.index)],
               set_labels = ('AP', "No AP", 'SZ'))
    plt.savefig('venn_antipsychotics_%s.png' % (feature))
    plt.savefig('venn_antipsychotics_%s.pdf' % (feature))

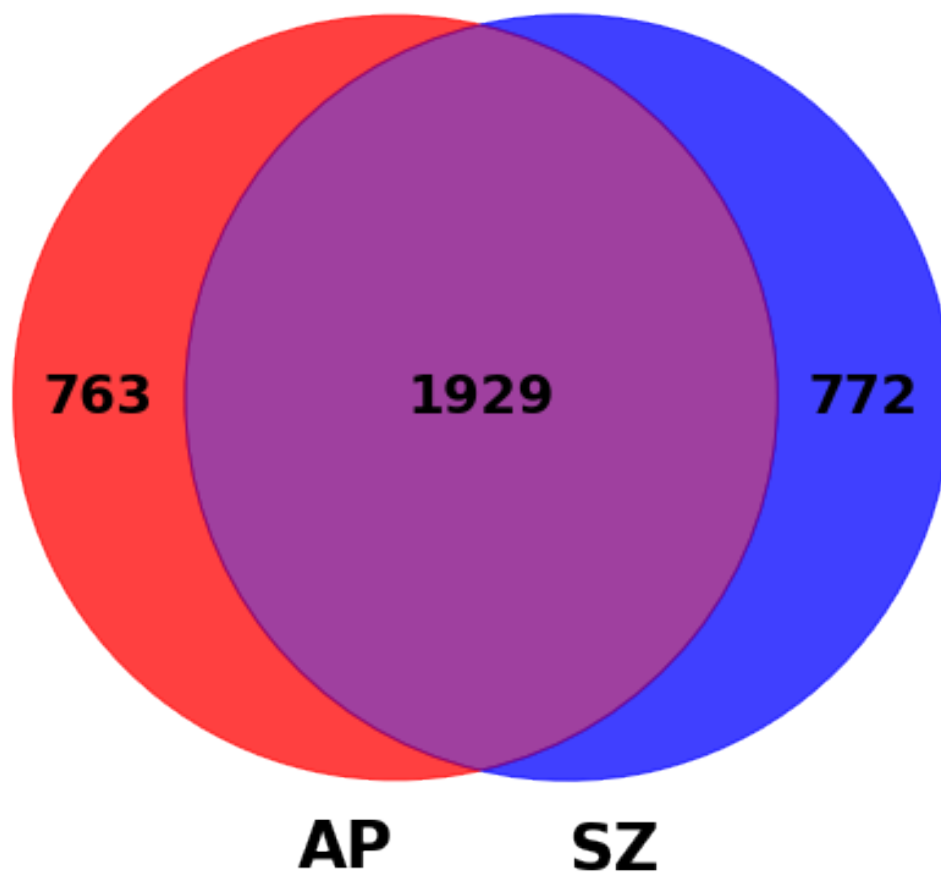
```

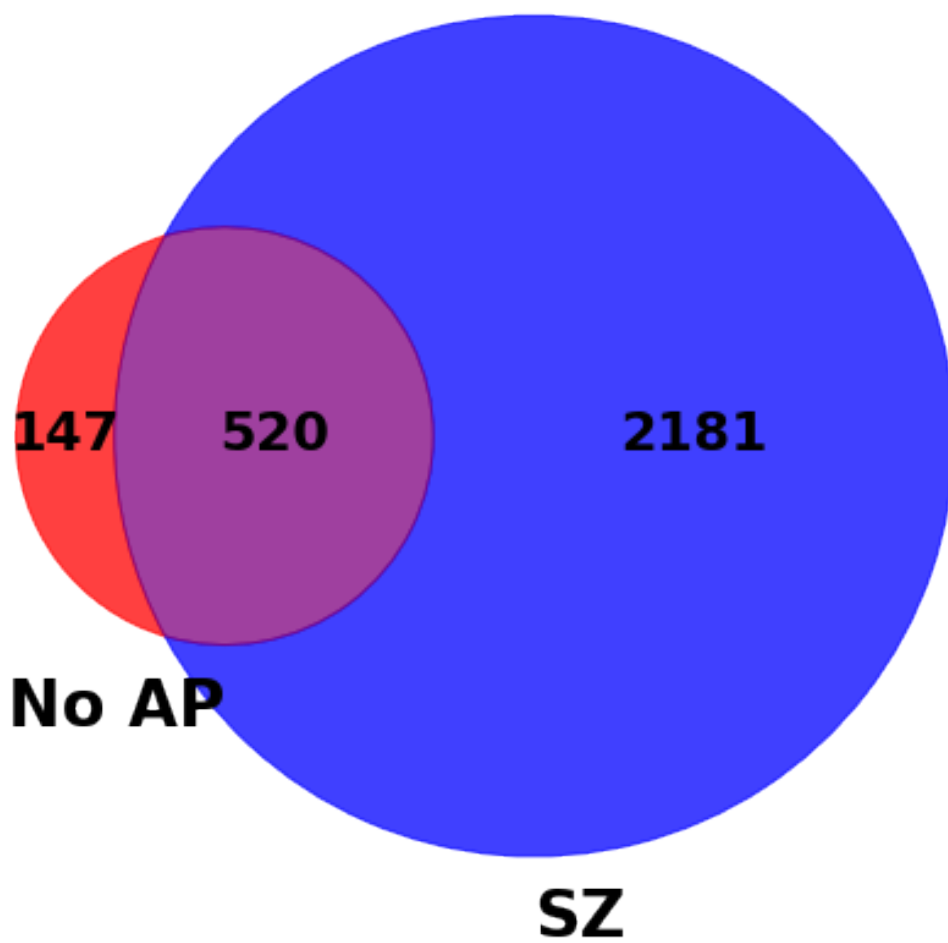
1.2.1 Plot overlaps

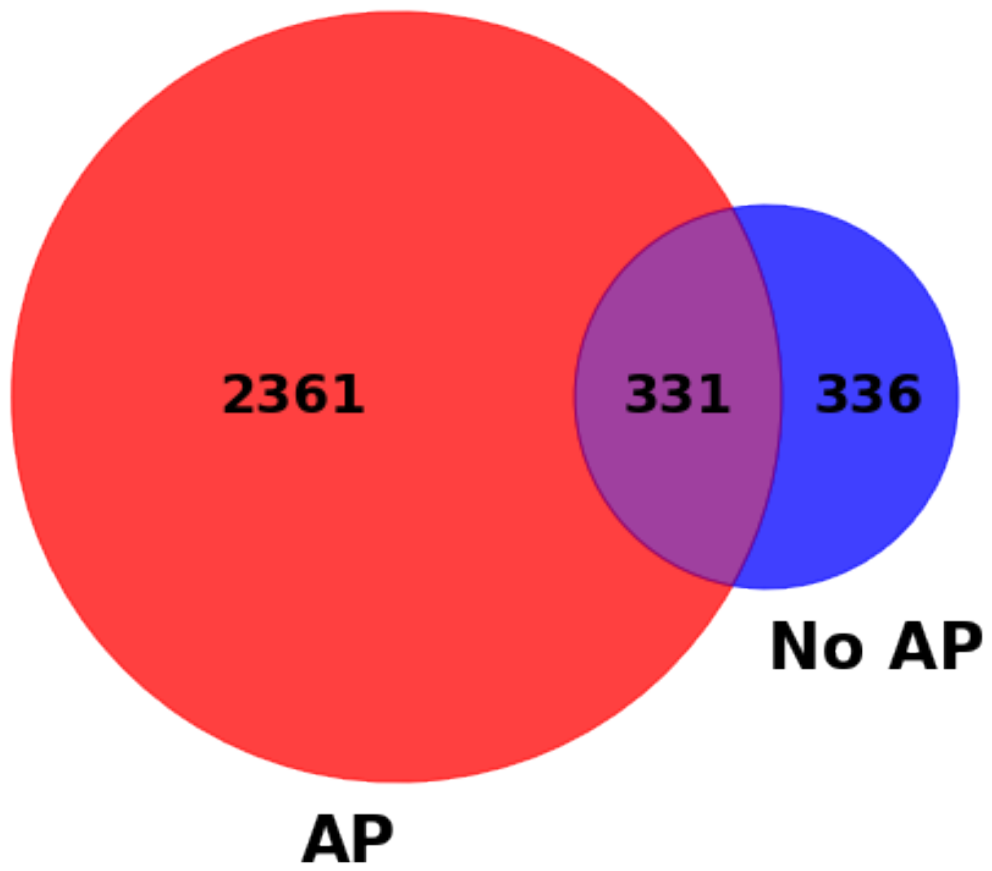
```

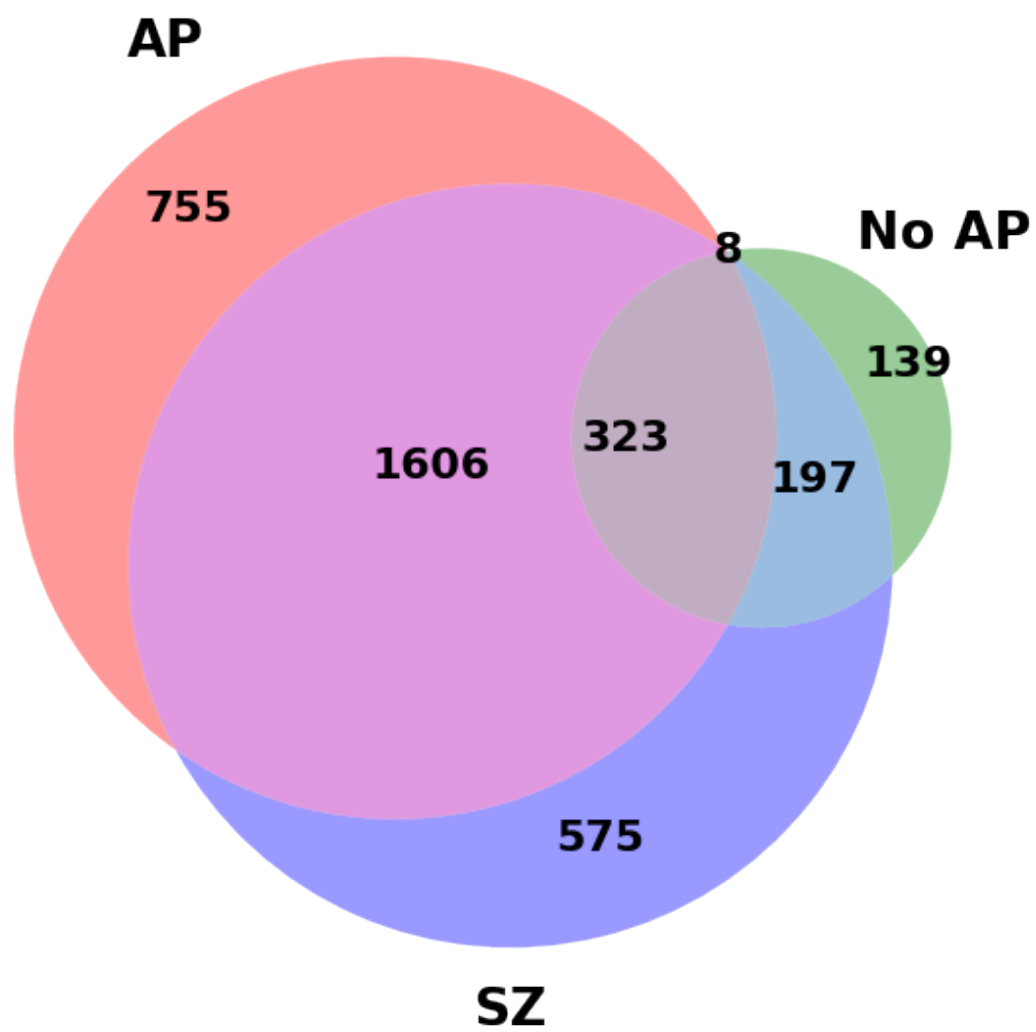
[12]: for feature in ["genes", "transcripts", "exons", "junctions"]:
    plot_pairwise_venn(feature, "Yes")
    plot_pairwise_venn(feature, "No")
    plot_pairwise_venn(feature, "Both")
    plot_venn3(feature)

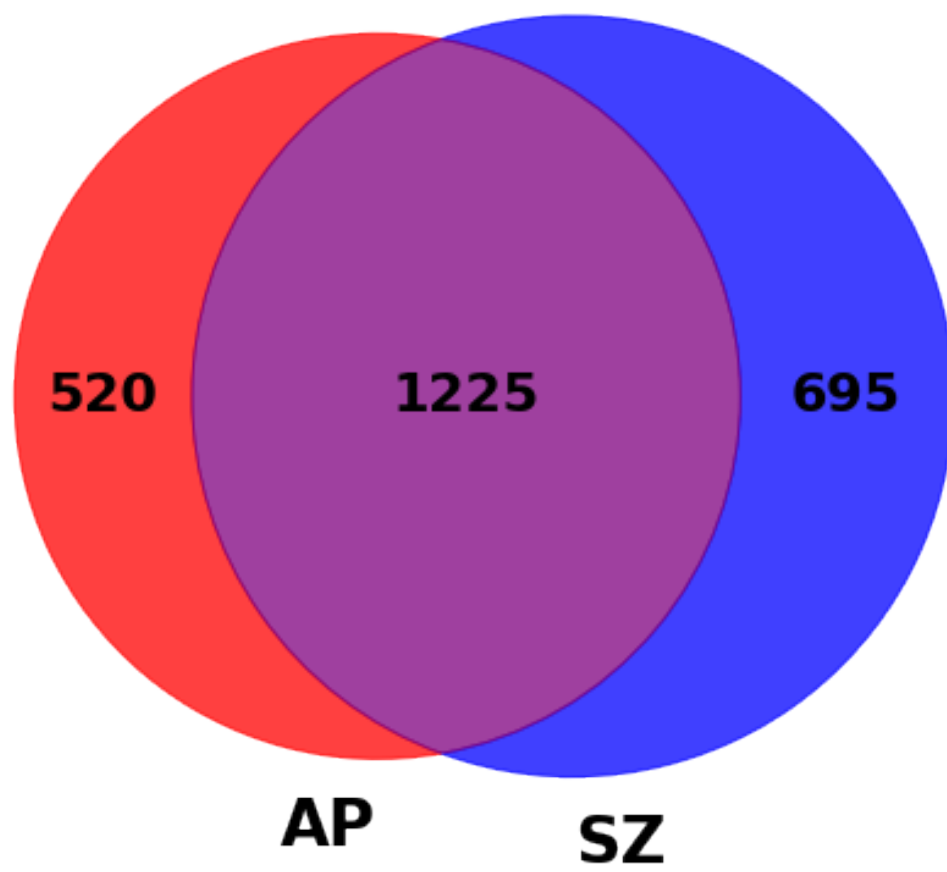
```

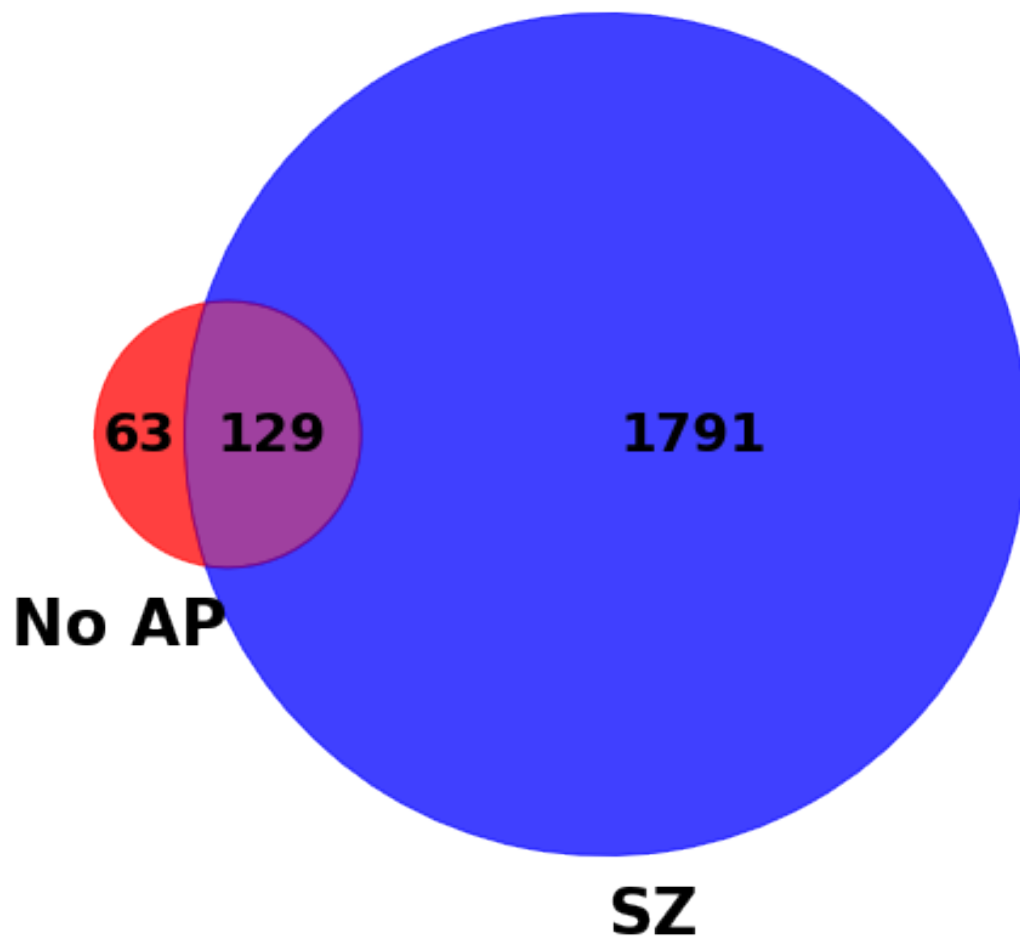


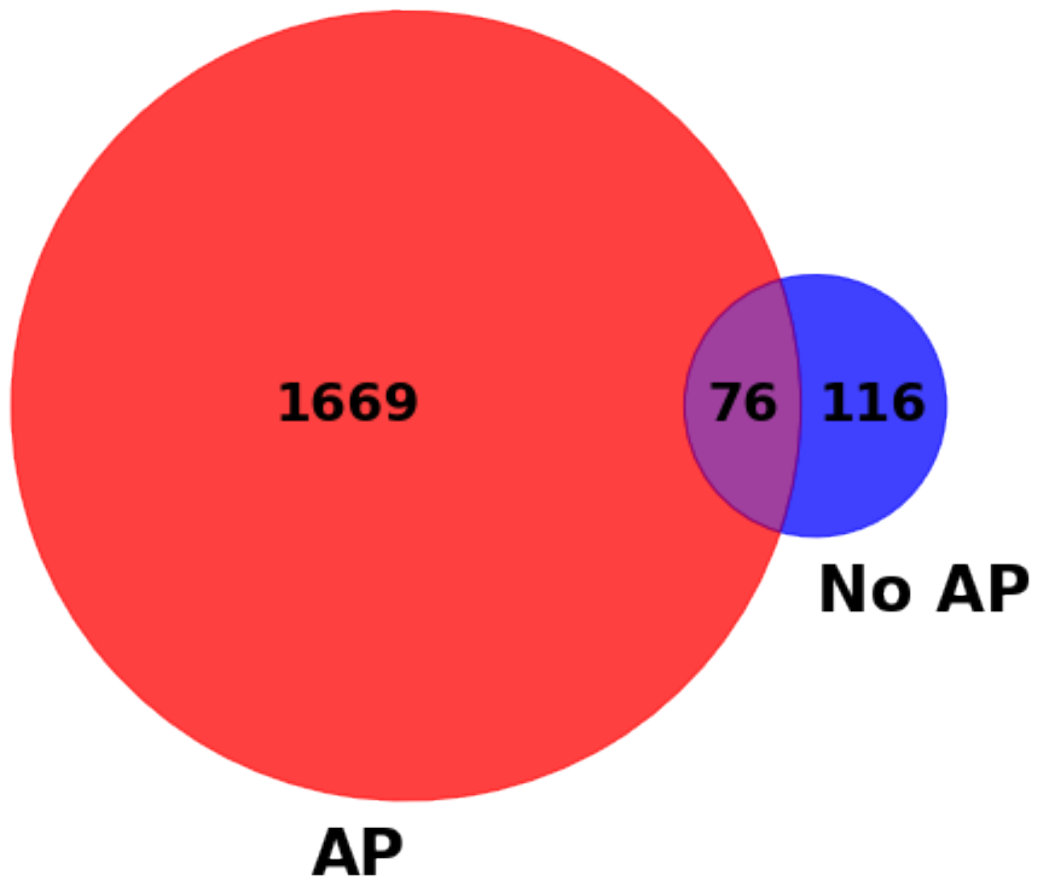


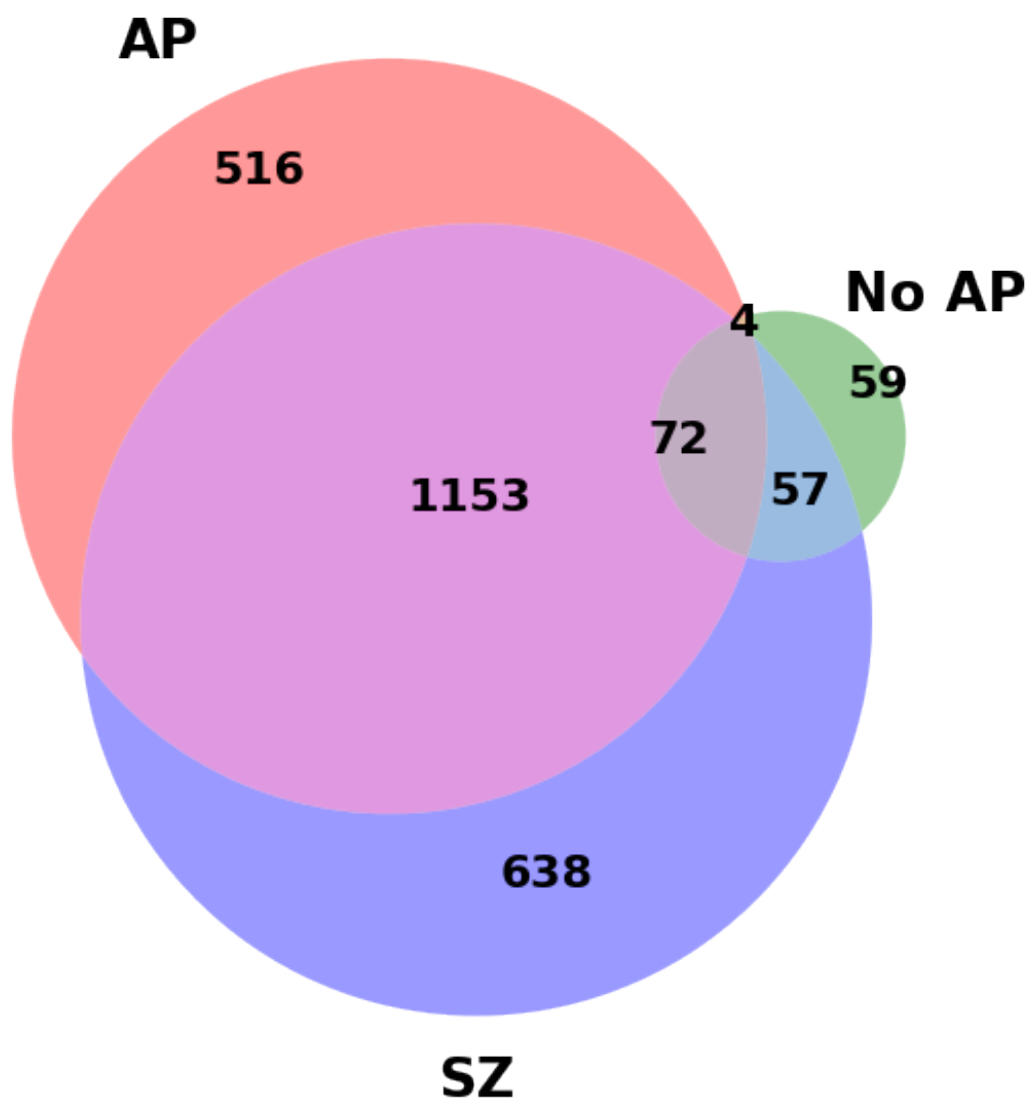


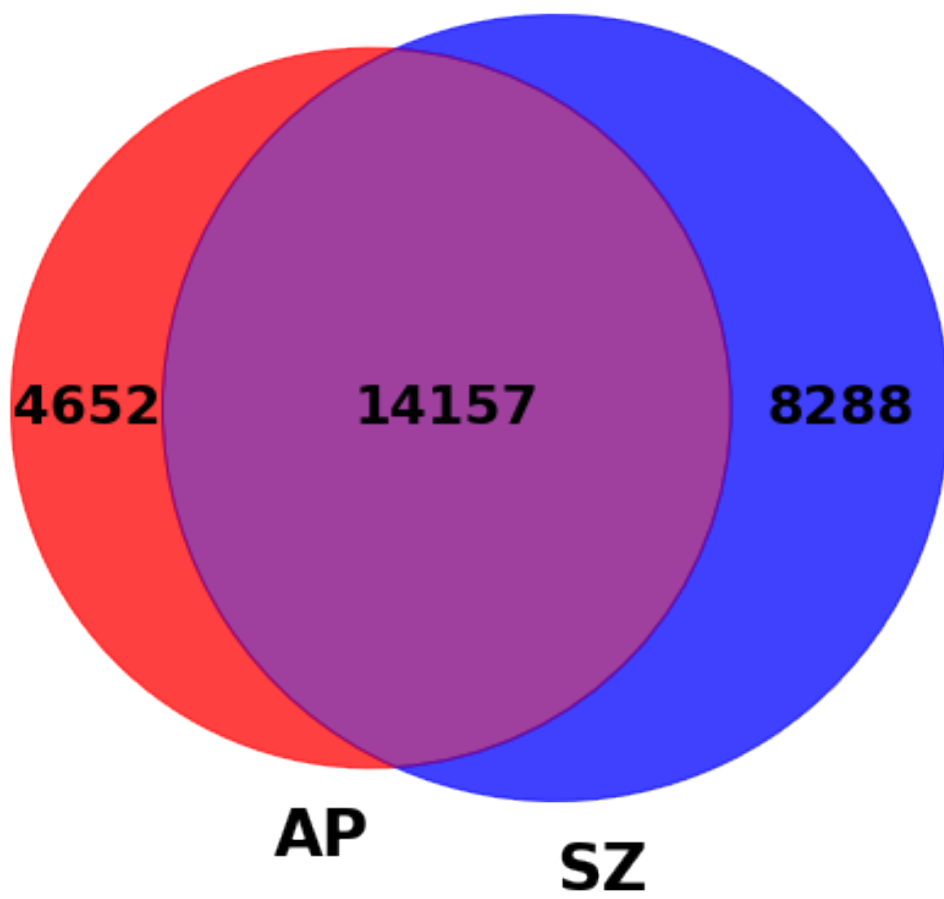


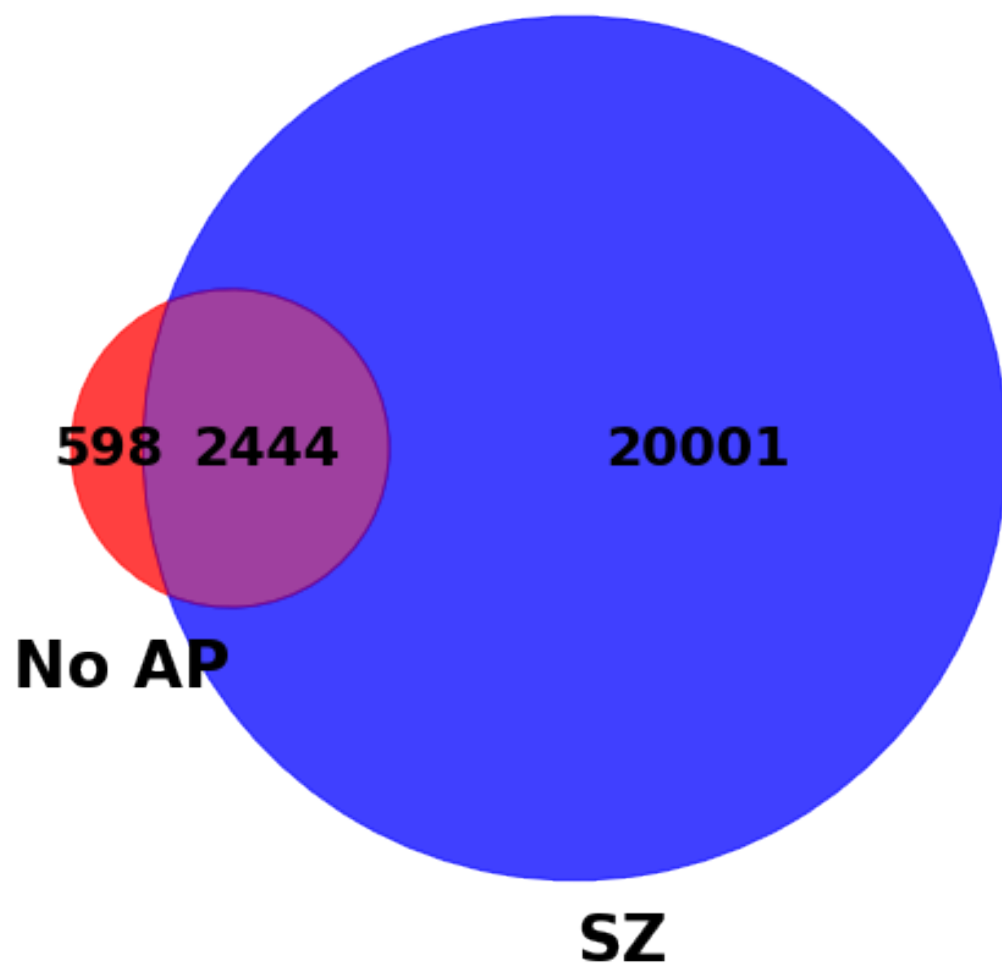


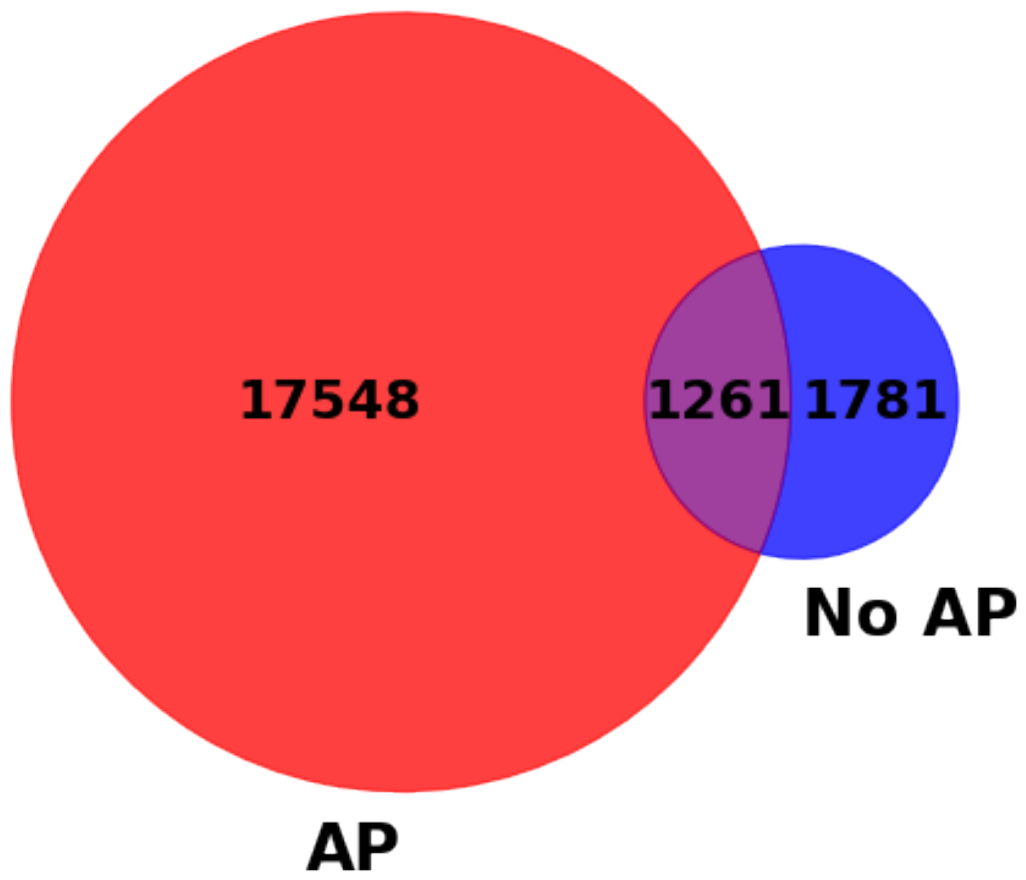


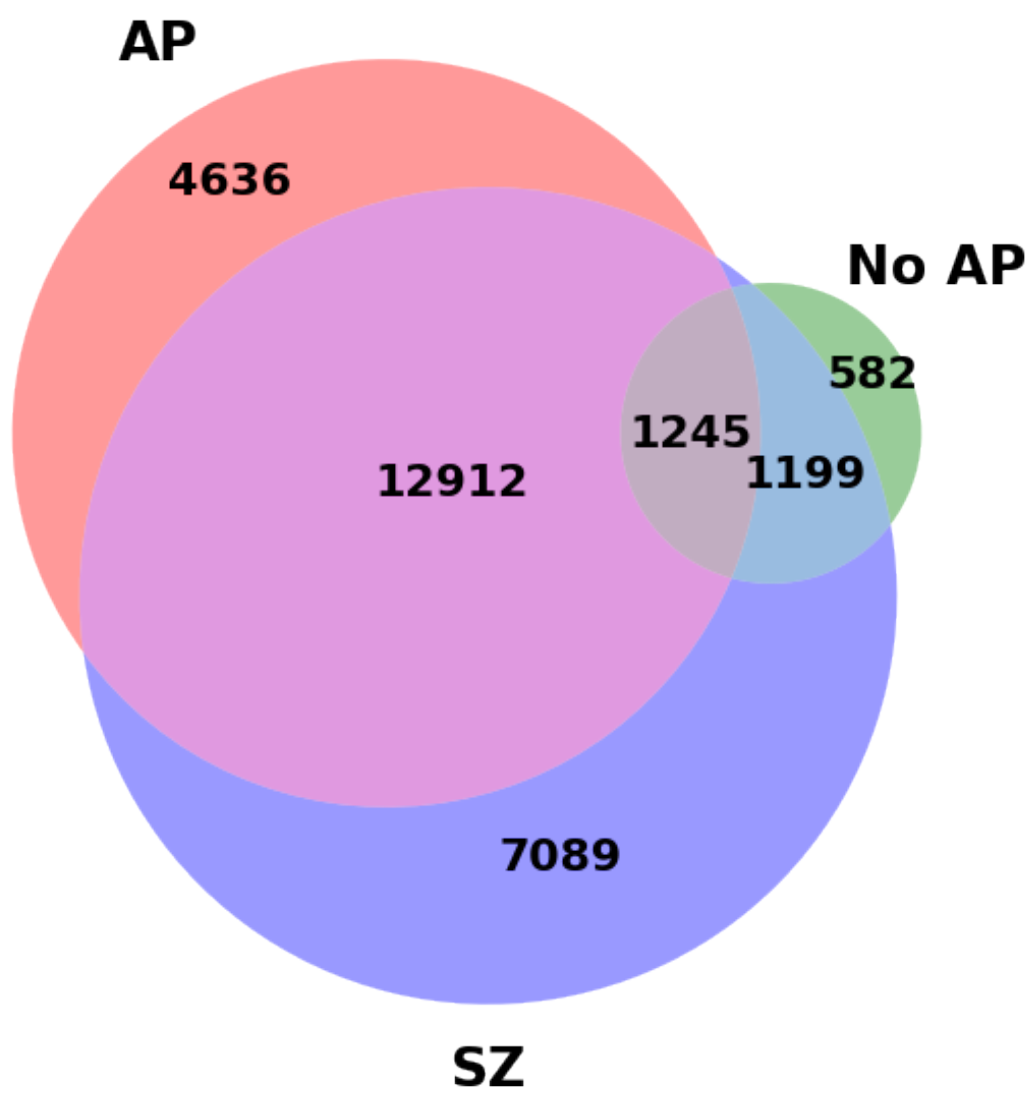


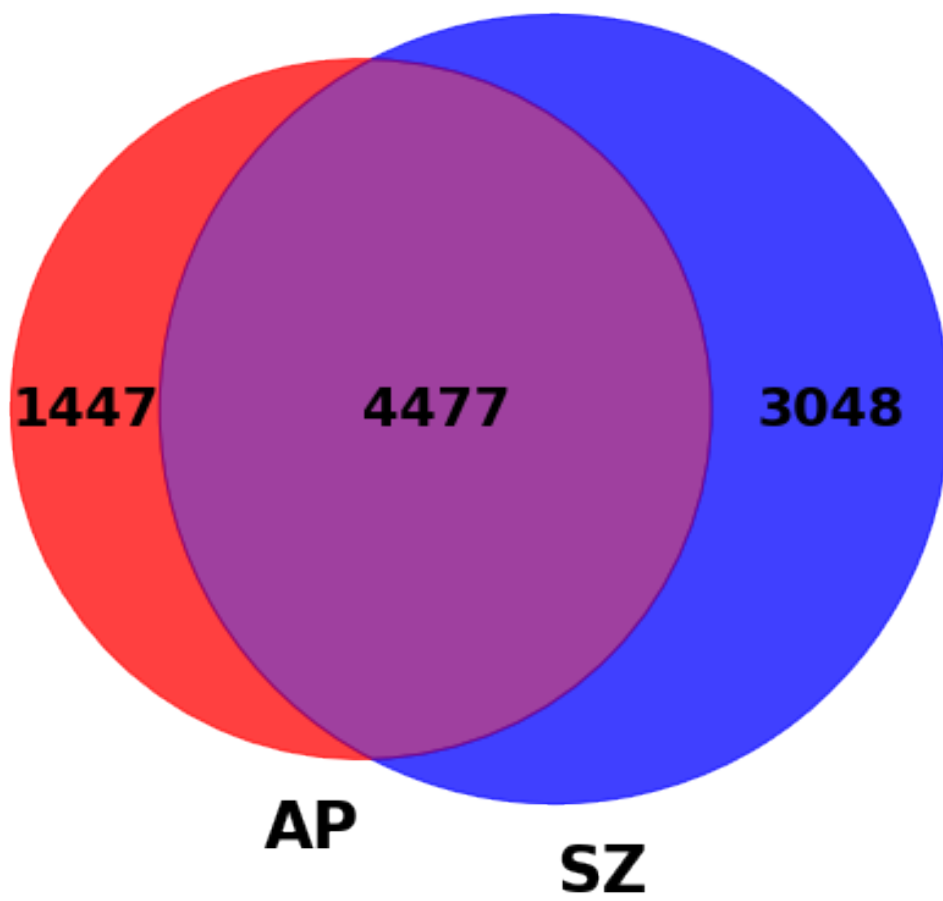


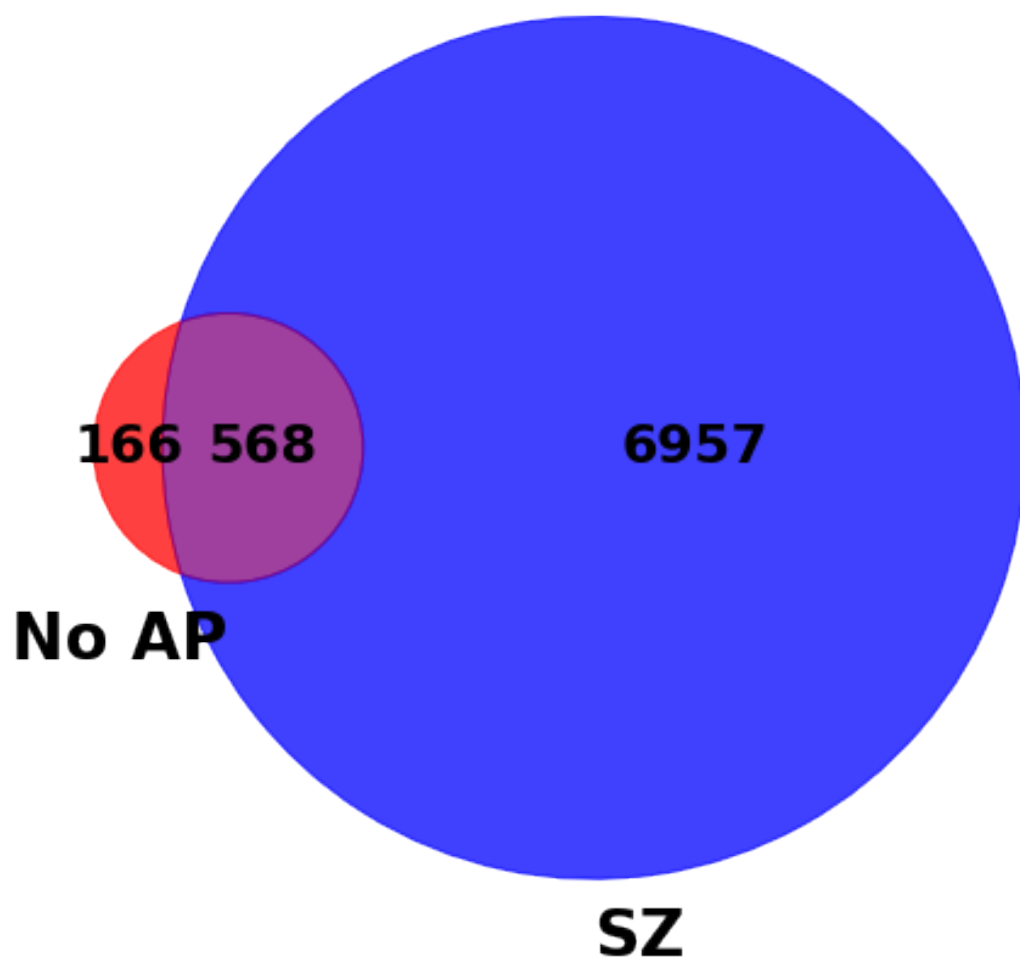


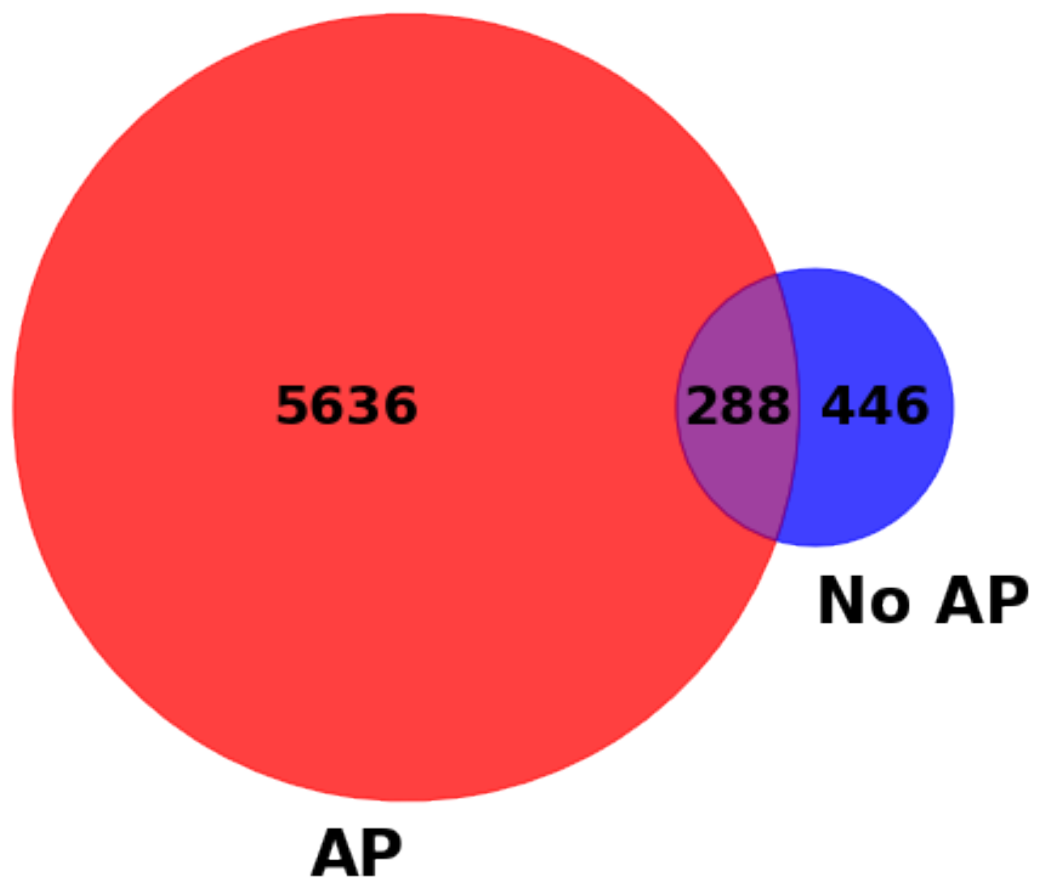


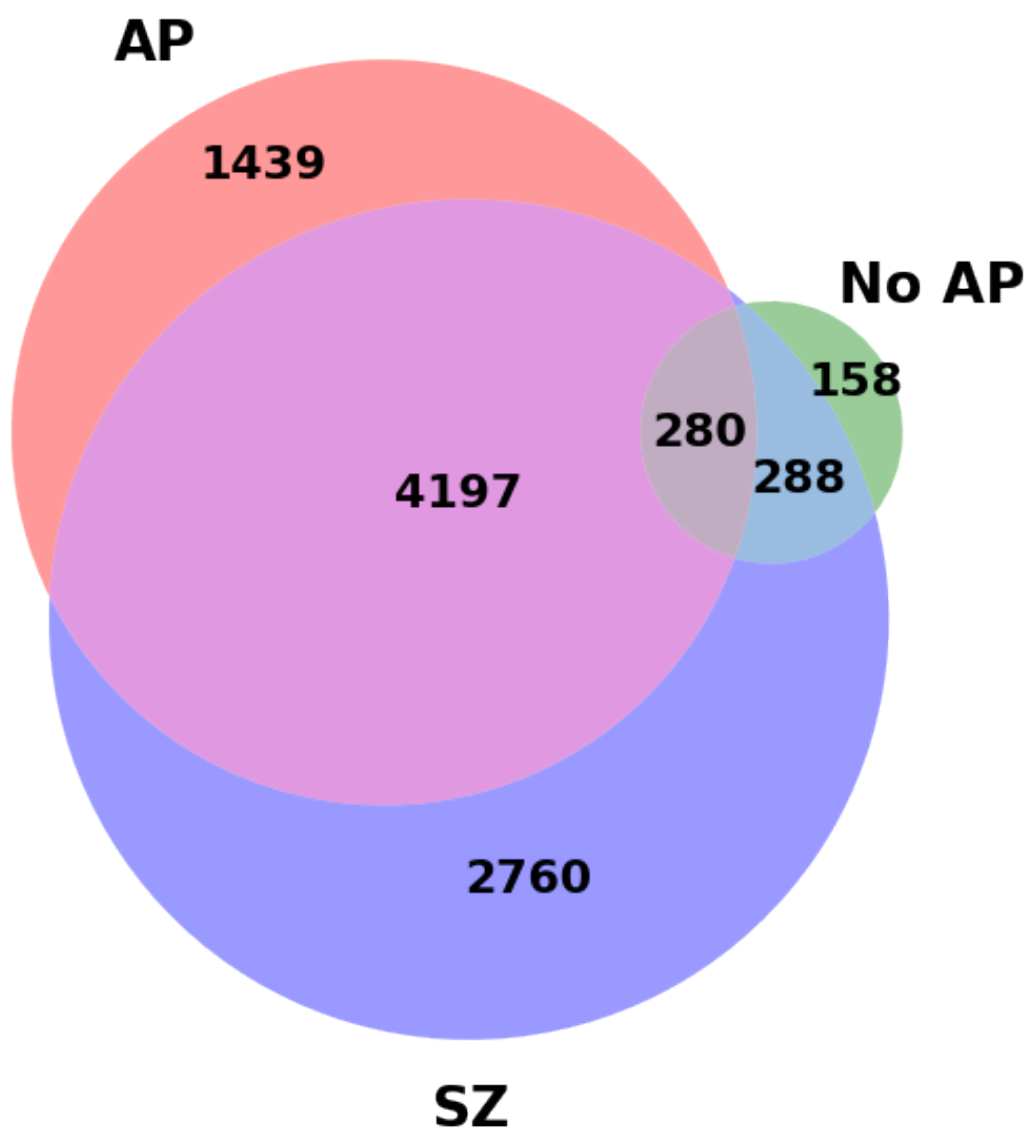












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