main_noMHC

August 31, 2021

1 Venn diagram and summary

[1]:
```
import numpy as np
import pandas as pd
from venn import venn
from matplotlib import pyplot as plt
```

1.1 Prepare data

[2]:
```
def limiting_features(set_dict, f1, f2):
    xx = len(set_dict[f1] & set_dict[f2]) / len(set_dict[f2]) * 100
    print("Comparing %s with %s: %0.2f%%" % (f1, f2, xx))
    print("Features in common: %d" % len(set_dict[f1] & set_dict[f2]))
```

1.1.1 Load PGC2+CLOZUK GWAS

[3]:
```
pgc2_file = '/ceph/projects/v4_phase3_paper/inputs/sz_gwas/'+\
            'pgc2_clozuk/map_phase3/_m/libd_hg38_pgc2sz_snps.tsv'
pgc2_df = pd.read_csv(pgc2_file, sep='\t', low_memory=False, index_col=0)
```

```
/home/jbenja13/.local/lib/python3.9/site-packages/numpy/lib/arraysetops.py:583:
FutureWarning: elementwise comparison failed; returning scalar instead, but in
the future will perform elementwise comparison
  mask |= (ar1 == a)
```

1.1.2 With no MHC

Genes

[4]:
```
genes = pd.read_csv('/ceph/projects/v4_phase3_paper/analysis/twas/'+\
                    'gene_weights/fusion_pgc2/summary_stats/_m/
 ↪fusion_associations_noMHC.txt', sep='\t')
annot = pd.read_csv('../../../differential_expression/_m/genes/
 ↪diffExpr_szVctl_full.txt', sep='\t')
genes = annot[['ensemblID']].merge(genes, left_on='ensemblID', right_on='FILE')
genes = genes[['FILE', 'ensemblID', 'ID', 'HSQ', 'BEST.GWAS.ID', 'EQTL.ID',
               'TWAS.Z', 'TWAS.P', 'FDR', 'Bonferroni']]
genes['Type'] = 'Gene'
genes.rename(columns={'FILE': 'Feature'}, inplace=True)
```

```
genes.sort_values('TWAS.P').head(2)
```

[4]:

	Feature	ensemblID	ID	HSQ	BEST.GWAS.ID	EQTL.ID	TWAS.Z	TWAS.P	FDR	Bonferroni	Type
3154	ENSG00000100138	ENSG00000100138	SNU13	0.071722	chr22:41944840:T:C	chr22:42069256:T:C	-8.100041	5.494072e-16	4.437562e-12	4.437562e-12	Gene
4190	ENSG00000088808	ENSG00000088808	PPP1R13B	0.269173	chr14:103847845:G:A	chr14:103756555:C:T	7.012638	2.338656e-12	8.058985e-09	1.888933e-08	Gene

Transcripts

```
trans = pd.read_csv('/ceph/projects/v4_phase3_paper/analysis/twas/'+\
                    'transcript_weights/fusion_pgc2/summary_stats/_m/
 ↪fusion_associations_noMHC.txt', sep='\t')
annot = pd.read_csv('../../../differential_expression/_m/transcripts/
 ↪diffExpr_szVctl_full.txt', sep='\t')
annot['ensemblID'] = annot.gene_id.str.replace('\\..*', '', regex=True)
annot['FILE'] = annot.transcript_id.str.replace('\\..*', '', regex=True)
trans = annot[['ensemblID', 'FILE']].merge(trans, on='FILE')
trans = trans[['FILE', 'ensemblID', 'ID', 'HSQ', 'BEST.GWAS.ID', 'EQTL.ID',
               'TWAS.Z', 'TWAS.P', 'FDR', 'Bonferroni']]
trans['Type'] = 'Transcript'
trans.rename(columns={'FILE': 'Feature'}, inplace=True)
trans.sort_values('TWAS.P').head(2)
```

[5]:

	Feature	ensemblID	ID	HSQ	BEST.GWAS.ID	EQTL.ID	TWAS.Z	TWAS.P	FDR	Bonferroni	Type
2276	ENST00000433628	ENSG00000148842	CNNM2	0.077605	chr10:103092132:T:C	chr10:103085115:T:C	7.652389	1.972789e-14	2.180951e-10	2.856796e-10	Transcript
13474	ENST00000553286	ENSG00000126214	KLC1	0.430065	chr14:103847845:G:A	chr14:103673689:C:T	-7.597796	3.012155e-14	2.180951e-10	4.361902e-10	Transcript

Exons

```
exons = pd.read_csv('/ceph/projects/v4_phase3_paper/analysis/twas/'+\
                    'exon_weights/fusion_pgc2/summary_stats/_m/
 ↪fusion_associations_noMHC.txt', sep='\t')
annot = pd.read_csv('../../../differential_expression/_m/exons/
 ↪diffExpr_szVctl_full.txt', sep='\t', index_col=0)
```

```
exons = annot[['ensemblID']].merge(exons, left_index=True, right_on='FILE')
exons = exons[['FILE', 'ensemblID', 'ID', 'HSQ', 'BEST.GWAS.ID', 'EQTL.ID',
               'TWAS.Z', 'TWAS.P', 'FDR', 'Bonferroni']]
exons['Type'] = 'Exon'
exons.rename(columns={'FILE': 'Feature'}, inplace=True)
exons.sort_values('TWAS.P').head(2)
```

[6]:

	Feature	ensemblID	ID	HSQ	BEST.GWAS.ID	EQTL.ID	TWAS.Z	TWAS.P	FDR	Bonferroni	Type
65506	e177288	ENSG00000162971	TYW5	0.042222	chr2:199850665:T:G	chr2:200108846:G:A	-7.961678	1.697215e-15	4.032619e-11	1.132908e-10	Exon
65508	e177302	ENSG00000162971	TYW5	0.042222	chr2:199850665:T:G	chr2:200108846:G:A	-7.961678	1.697215e-15	4.032619e-11	1.132908e-10	Exon

1.1.3 Junctions

[7]:
```
dj_file = '../../../differential_expression/_m/junctions/diffExpr_szVctl_full.
 ↪txt'
dj = pd.read_csv(dj_file, sep='\t', index_col=0)
dj = dj[['Symbol', 'ensemblID']]

jannot_file = '/ceph/projects/v4_phase3_paper/analysis/twas/'+\
              '_m/junctions/jxn_annotation.tsv'
jannot = pd.read_csv(jannot_file, sep='\t', index_col=1)

jannot = jannot[['JxnID']]
annot = pd.merge(jannot, dj, left_index=True, right_index=True)

juncs = pd.read_csv('/ceph/projects/v4_phase3_paper/analysis/twas/'+\
                    'junction_weights/fusion_pgc2/summary_stats/_m/
 ↪fusion_associations_noMHC.txt', sep='\t')
juncs = pd.merge(annot, juncs, left_on='JxnID', right_on='FILE')
juncs = juncs[['FILE', 'ensemblID', 'Symbol', 'HSQ', 'BEST.GWAS.ID', 'EQTL.ID',
               'TWAS.Z', 'TWAS.P', 'FDR', 'Bonferroni']]
juncs['Type'] = 'Junction'
juncs.rename(columns={'Symbol': 'ID', 'FILE': 'Feature'}, inplace=True)
juncs.sort_values('TWAS.P').head(2)
```

```
/usr/lib/python3.9/site-packages/IPython/core/interactiveshell.py:3146:
DtypeWarning: Columns (2) have mixed types.Specify dtype option on import or set
low_memory=False.
  has_raised = await self.run_ast_nodes(code_ast.body, cell_name,
```

[7]:
```
      Feature        ensemblID           ID       HSQ         BEST.GWAS.ID  \
2595  j17393  ENSG00000270316  BORCS7-ASMT  0.150648  chr10:103092132:T:C
2593  j17391              NaN          NaN  0.226750  chr10:103092132:T:C

                   EQTL.ID    TWAS.Z        TWAS.P           FDR    Bonferroni  \
2595  chr10:102911075:C:A -9.579719  9.730918e-22  2.237430e-17  2.237430e-17
2593  chr10:102911075:C:A -8.094280  5.760397e-16  5.242528e-12  1.324488e-11

          Type
2595  Junction
2593  Junction
```

1.2 Heritable features

1.2.1 Feature summary

[8]:
```
gg = len(set(genes['Feature']))
tt = len(set(trans['Feature']))
ee = len(set(exons['Feature']))
jj = len(set(juncs['Feature']))

print("===Unique Features===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes['ensemblID']))
tt = len(set(trans['ensemblID']))
ee = len(set(exons['ensemblID']))
jj = len(set(juncs['ensemblID']))

print("===Unique Ensembl Gene===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes['ID']))
tt = len(set(trans['ID']))
ee = len(set(exons['ID']))
jj = len(set(juncs['ID']))

print("===Unique Gene Name===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

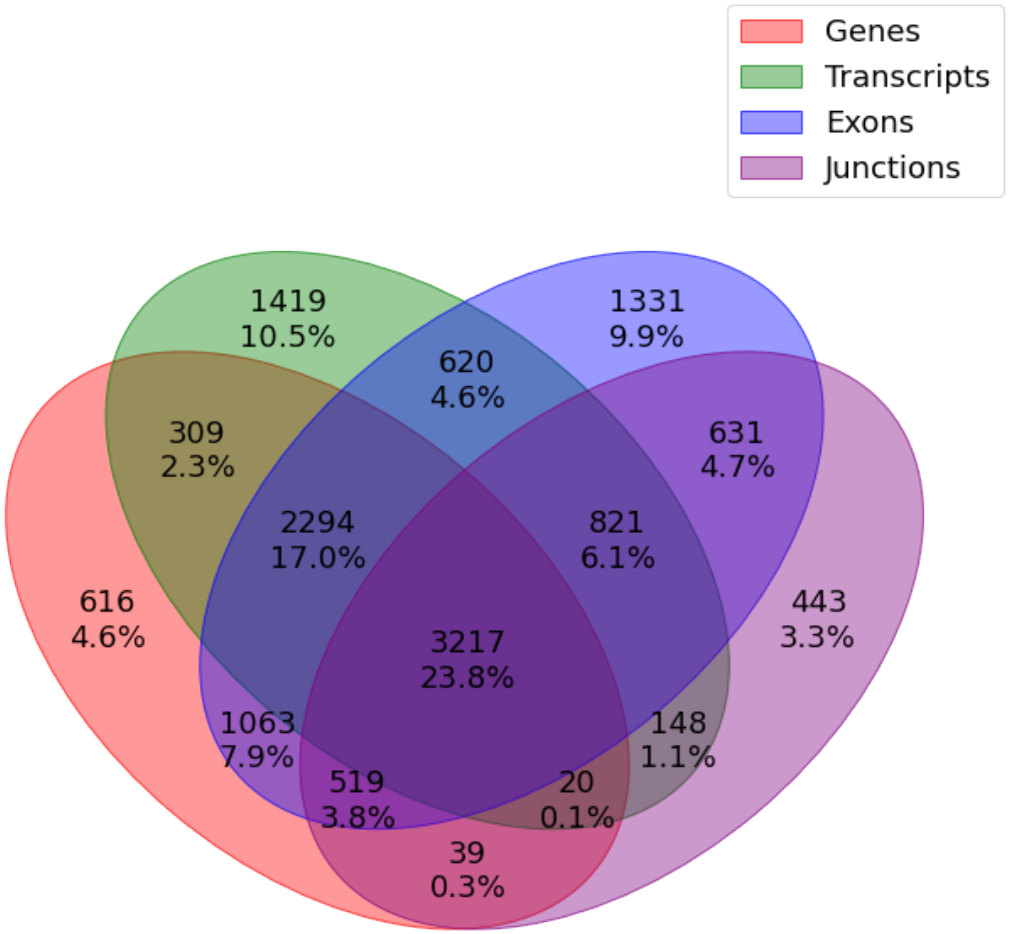
```
===Unique Features===
Gene:           8077
Transcript:     14481
Exon:           66751
Junction:       22993

===Unique Ensembl Gene===
Gene:           8077
```

```
Transcript:     8848
Exon:           10496
Junction:       5838

===Unique Gene Name===
Gene:           8076
Transcript:     8842
Exon:           12375
Junction:       5836
```

1.2.2 Plot venn

[9]:
```
features = {
    'Genes': set(genes['ensemblID']),
    'Transcripts': set(trans['ensemblID']),
    'Exons': set(exons['ensemblID']),
    'Junctions': set(juncs['ensemblID']),
}
```

[10]:
```
venn(features, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('heritable_allFeatures_venn_diagram_percentage.png')
plt.savefig('heritable_allFeatures_venn_diagram_percentage.pdf')
plt.savefig('heritable_allFeatures_venn_diagram_percentage.svg')
plt.show()
```



[11]:
```
limiting_features(features, 'Genes', 'Transcripts')
limiting_features(features, 'Genes', 'Junctions')
limiting_features(features, 'Exons', 'Genes')
```

```
Comparing Genes with Transcripts: 66.00%
Features in common: 5840
Comparing Genes with Junctions: 65.01%
Features in common: 3795
Comparing Exons with Genes: 87.82%
Features in common: 7093
```

[12]:
```
limiting_features(features, 'Transcripts', 'Junctions')
limiting_features(features, 'Exons', 'Transcripts')
```

```
limiting_features(features, 'Exons', 'Junctions')
```

```
Comparing Transcripts with Junctions: 72.05%
Features in common: 4206
Comparing Exons with Transcripts: 78.57%
Features in common: 6952
Comparing Exons with Junctions: 88.87%
Features in common: 5188
```

[13]:
```
len(features['Genes'] & features['Transcripts'] & features['Exons'] &␣
↪features['Junctions'])
```

[13]:
```
3217
```

[14]:
```
len(features['Genes'] | features['Transcripts'] | features['Exons'] |␣
↪features['Junctions'])
```

[14]:
```
13490
```

1.2.3 SNPs not in significant PGC2+CLOZUK GWAS

[15]:
```
new_genes = pd.merge(genes, pgc2_df, left_on='BEST.GWAS.ID',␣
↪right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_trans = pd.merge(trans, pgc2_df, left_on='BEST.GWAS.ID',␣
↪right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_exons = pd.merge(exons, pgc2_df, left_on='BEST.GWAS.ID',␣
↪right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_juncs = pd.merge(juncs, pgc2_df, left_on='BEST.GWAS.ID',␣
↪right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])

new_genes = new_genes[(new_genes['P'] > 5e-8)].copy()
new_trans = new_trans[(new_trans['P'] > 5e-8)].copy()
new_exons = new_exons[(new_exons['P'] > 5e-8)].copy()
new_juncs = new_juncs[(new_juncs['P'] > 5e-8)].copy()
```

[16]:
```
gg = len(set(new_genes['BEST.GWAS.ID']))
tt = len(set(new_trans['BEST.GWAS.ID']))
ee = len(set(new_exons['BEST.GWAS.ID']))
jj = len(set(new_juncs['BEST.GWAS.ID']))

print("===Unique novel SNPs===\nGene:\t\t%d\nTranscript:\t%d\nExon:
↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

```
===Unique novel SNPs===
Gene:           2800
Transcript:     3005
Exon:           3727
```

```
Junction:       2994
```

[17]:
```
len(set(new_genes['BEST.GWAS.ID']) | set(new_trans['BEST.GWAS.ID']) |
    set(new_exons['BEST.GWAS.ID']) | set(new_juncs['BEST.GWAS.ID']))
```

[17]: 4345

1.3 TWAS P-value < 0.05

1.3.1 Feature summary

[18]:
```
gg = len(set(genes[(genes['TWAS.P'] <= 0.05)].loc[:, 'Feature']))
tt = len(set(trans[(trans['TWAS.P'] <= 0.05)].loc[:, 'Feature']))
ee = len(set(exons[(exons['TWAS.P'] <= 0.05)].loc[:, 'Feature']))
jj = len(set(juncs[(juncs['TWAS.P'] <= 0.05)].loc[:, 'Feature']))

print("===Unique Features===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes[(genes['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']))
tt = len(set(trans[(trans['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']))
ee = len(set(exons[(exons['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']))
jj = len(set(juncs[(juncs['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']))

print("===Unique Ensembl Gene===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes[(genes['TWAS.P'] <= 0.05)].loc[:, 'ID']))
tt = len(set(trans[(trans['TWAS.P'] <= 0.05)].loc[:, 'ID']))
ee = len(set(exons[(exons['TWAS.P'] <= 0.05)].loc[:, 'ID']))
jj = len(set(juncs[(juncs['TWAS.P'] <= 0.05)].loc[:, 'ID']))

print("===Unique Gene Names===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

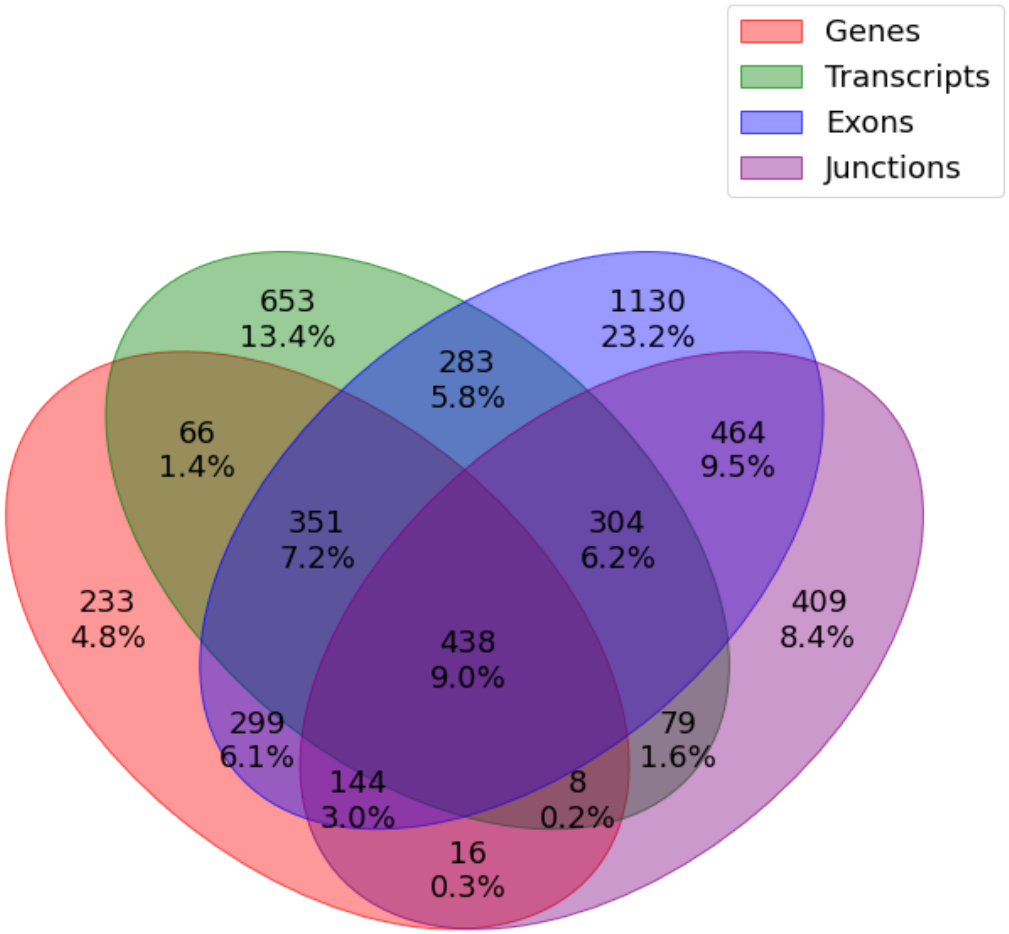
```
===Unique Features===
Gene:           1555
Transcript:     2934
Exon:           13617
Junction:       4593

===Unique Ensembl Gene===
Gene:           1555
Transcript:     2182
Exon:           3413
Junction:       1862
```

```
===Unique Gene Names===
Gene:           1555
Transcript:     2180
Exon:           3688
Junction:       1862
```

1.3.2 Plot venn

[19]:
```
features = {
    'Genes': set(genes[(genes['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']),
    'Transcripts': set(trans[(trans['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']),
    'Exons': set(exons[(exons['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']),
    'Junctions': set(juncs[(juncs['TWAS.P'] <= 0.05)].loc[:, 'ensemblID']),
}
```

[20]:
```
venn(features, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('sigPval_allFeatures_venn_diagram_percentage.png')
plt.savefig('sigPval_allFeatures_venn_diagram_percentage.pdf')
plt.savefig('sigPval_allFeatures_venn_diagram_percentage.svg')
plt.show()
```



[21]:
```
limiting_features(features, 'Genes', 'Transcripts')
limiting_features(features, 'Genes', 'Junctions')
limiting_features(features, 'Exons', 'Genes')
```

```
Comparing Genes with Transcripts: 39.55%
Features in common: 863
Comparing Genes with Junctions: 32.55%
Features in common: 606
Comparing Exons with Genes: 79.23%
Features in common: 1232
```

[22]:
```
limiting_features(features, 'Transcripts', 'Junctions')
limiting_features(features, 'Exons', 'Transcripts')
```

```
limiting_features(features, 'Exons', 'Junctions')
```

```
Comparing Transcripts with Junctions: 44.52%
Features in common: 829
Comparing Exons with Transcripts: 63.06%
Features in common: 1376
Comparing Exons with Junctions: 72.50%
Features in common: 1350
```

[23]:
```
len(features['Genes'] & features['Transcripts'] & features['Exons'] &␣
↪features['Junctions'])
```

[23]:
```
438
```

[24]:
```
len(features['Genes'] | features['Transcripts'] | features['Exons'] |␣
↪features['Junctions'])
```

[24]:
```
4877
```

1.3.3 SNPs not in significant PGC2+CLOZUK GWAS

[25]:
```
new_genes = pd.merge(genes[(genes['TWAS.P'] <= 0.05)], pgc2_df, left_on='BEST.
↪GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_trans = pd.merge(trans[(trans['TWAS.P'] <= 0.05)], pgc2_df, left_on='BEST.
↪GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_exons = pd.merge(exons[(exons['TWAS.P'] <= 0.05)], pgc2_df, left_on='BEST.
↪GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_juncs = pd.merge(juncs[(juncs['TWAS.P'] <= 0.05)], pgc2_df, left_on='BEST.
↪GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])

new_genes = new_genes[(new_genes['P'] > 5e-8)].copy()
new_trans = new_trans[(new_trans['P'] > 5e-8)].copy()
new_exons = new_exons[(new_exons['P'] > 5e-8)].copy()
new_juncs = new_juncs[(new_juncs['P'] > 5e-8)].copy()
```

[26]:
```
gg = len(set(new_genes['BEST.GWAS.ID']))
tt = len(set(new_trans['BEST.GWAS.ID']))
ee = len(set(new_exons['BEST.GWAS.ID']))
jj = len(set(new_juncs['BEST.GWAS.ID']))

print("===Unique novel SNPs===\nGene:\t\t%d\nTranscript:\t%d\nExon:
↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

```
===Unique novel SNPs===
```

```
Gene:           811
Transcript:     1059
Exon:           1600
Junction:       1127
```

[27]:
```
len(set(new_genes['BEST.GWAS.ID']) | set(new_trans['BEST.GWAS.ID']) |
    set(new_exons['BEST.GWAS.ID']) | set(new_juncs['BEST.GWAS.ID']))
```

[27]: 2045

1.4 TWAS FDR < 0.05

1.4.1 Feature summary

[28]:
```
gg = len(set(genes[(genes['FDR'] <= 0.05)].loc[:, 'Feature']))
tt = len(set(trans[(trans['FDR'] <= 0.05)].loc[:, 'Feature']))
ee = len(set(exons[(exons['FDR'] <= 0.05)].loc[:, 'Feature']))
jj = len(set(juncs[(juncs['FDR'] <= 0.05)].loc[:, 'Feature']))

print("===Unique Features===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes[(genes['FDR'] <= 0.05)].loc[:, 'ensemblID']))
tt = len(set(trans[(trans['FDR'] <= 0.05)].loc[:, 'ensemblID']))
ee = len(set(exons[(exons['FDR'] <= 0.05)].loc[:, 'ensemblID']))
jj = len(set(juncs[(juncs['FDR'] <= 0.05)].loc[:, 'ensemblID']))

print("===Unique Ensembl Gene===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes[(genes['FDR'] <= 0.05)].loc[:, 'ID']))
tt = len(set(trans[(trans['FDR'] <= 0.05)].loc[:, 'ID']))
ee = len(set(exons[(exons['FDR'] <= 0.05)].loc[:, 'ID']))
jj = len(set(juncs[(juncs['FDR'] <= 0.05)].loc[:, 'ID']))

print("===Unique Gene Name===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

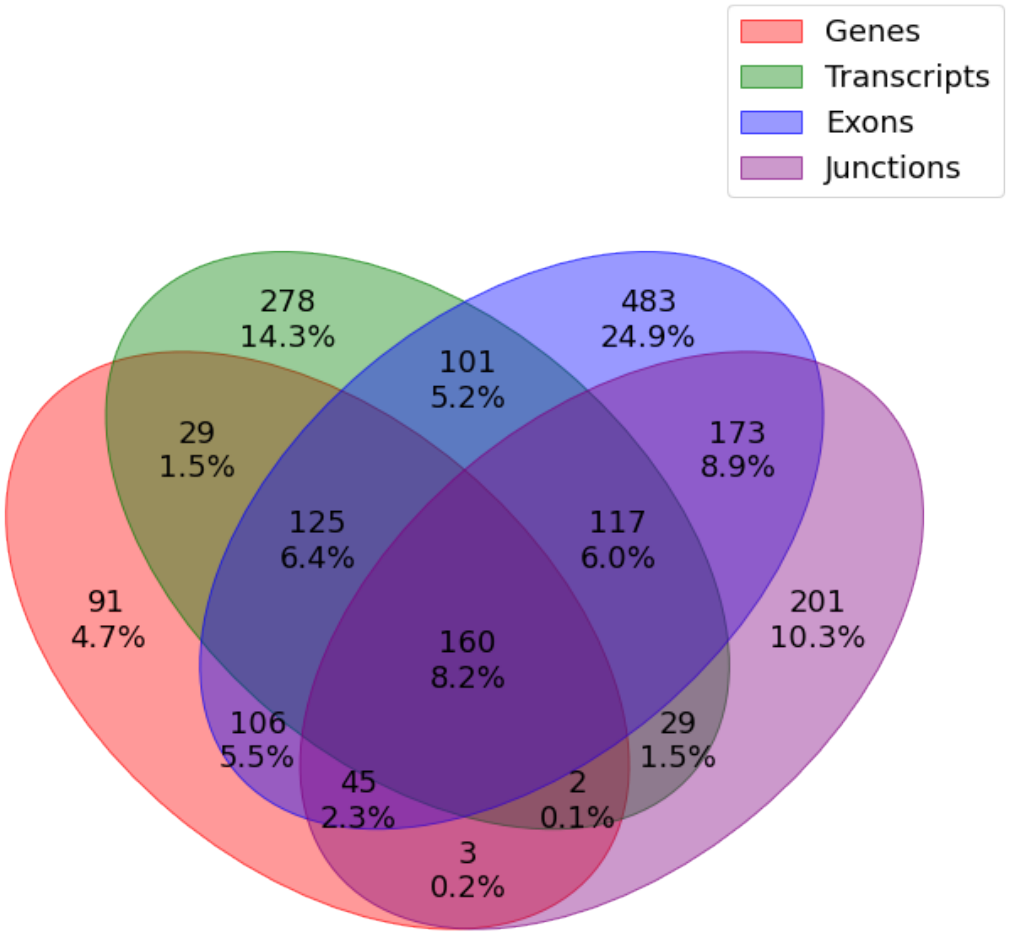
```
===Unique Features===
Gene:           561
Transcript:     1116
Exon:           4865
Junction:       1657

===Unique Ensembl Gene===
Gene:           561
Transcript:     841
```

```
Exon:           1310
Junction:       730

===Unique Gene Name===
Gene:           561
Transcript:     841
Exon:           1398
Junction:       730
```

1.4.2 Plot venn

[29]:
```
features = {
    'Genes': set(genes[(genes['FDR'] <= 0.05)].loc[:, 'ensemblID']),
    'Transcripts': set(trans[(trans['FDR'] <= 0.05)].loc[:, 'ensemblID']),
    'Exons': set(exons[(exons['FDR'] <= 0.05)].loc[:, 'ensemblID']),
    'Junctions': set(juncs[(juncs['FDR'] <= 0.05)].loc[:, 'ensemblID']),
}
```

[30]:
```
venn(features, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('fdr_allFeatures_venn_diagram_percentage.png')
plt.savefig('fdr_allFeatures_venn_diagram_percentage.pdf')
plt.savefig('fdr_allFeatures_venn_diagram_percentage.svg')
plt.show()
```



[31]:
```
limiting_features(features, 'Genes', 'Transcripts')
limiting_features(features, 'Genes', 'Junctions')
limiting_features(features, 'Exons', 'Genes')
```

```
Comparing Genes with Transcripts: 37.57%
Features in common: 316
Comparing Genes with Junctions: 28.77%
Features in common: 210
Comparing Exons with Genes: 77.72%
Features in common: 436
```

[32]:
```
limiting_features(features, 'Transcripts', 'Junctions')
limiting_features(features, 'Exons', 'Transcripts')
```

```
limiting_features(features, 'Exons', 'Junctions')
```

```
Comparing Transcripts with Junctions: 42.19%
Features in common: 308
Comparing Exons with Transcripts: 59.81%
Features in common: 503
Comparing Exons with Junctions: 67.81%
Features in common: 495
```

[33]:
```
len(features['Genes'] & features['Transcripts'] & features['Exons'] &␣
↪features['Junctions'])
```

[33]:
```
160
```

[34]:
```
len(features['Genes'] | features['Transcripts'] | features['Exons'] |␣
↪features['Junctions'])
```

[34]:
```
1943
```

1.4.3 SNPs not in significant PGC2+CLOZUK GWAS

[35]:
```
new_genes = pd.merge(genes[(genes['FDR'] <= 0.05)], pgc2_df, left_on='BEST.GWAS.
↪ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_trans = pd.merge(trans[(trans['FDR'] <= 0.05)], pgc2_df, left_on='BEST.GWAS.
↪ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_exons = pd.merge(exons[(exons['FDR'] <= 0.05)], pgc2_df, left_on='BEST.GWAS.
↪ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_juncs = pd.merge(juncs[(juncs['FDR'] <= 0.05)], pgc2_df, left_on='BEST.GWAS.
↪ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])

new_genes = new_genes[(new_genes['P'] > 5e-8)].copy()
new_trans = new_trans[(new_trans['P'] > 5e-8)].copy()
new_exons = new_exons[(new_exons['P'] > 5e-8)].copy()
new_juncs = new_juncs[(new_juncs['P'] > 5e-8)].copy()
```

[36]:
```
gg = len(set(new_genes['BEST.GWAS.ID']))
tt = len(set(new_trans['BEST.GWAS.ID']))
ee = len(set(new_exons['BEST.GWAS.ID']))
jj = len(set(new_juncs['BEST.GWAS.ID']))

print("===Unique novel SNPs===\nGene:\t\t%d\nTranscript:\t%d\nExon:
↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

```
===Unique novel SNPs===
```

```
Gene:           254
Transcript:     375
Exon:           586
Junction:       407
```

[37]:
```
len(set(new_genes['BEST.GWAS.ID']) | set(new_trans['BEST.GWAS.ID']) |
    set(new_exons['BEST.GWAS.ID']) | set(new_juncs['BEST.GWAS.ID']))
```

[37]: 783

1.5 TWAS Bonferroni < 0.05

1.5.1 Feature summary

[38]:
```
gg = len(set(genes[(genes['Bonferroni'] <= 0.05)].loc[:, 'Feature']))
tt = len(set(trans[(trans['Bonferroni'] <= 0.05)].loc[:, 'Feature']))
ee = len(set(exons[(exons['Bonferroni'] <= 0.05)].loc[:, 'Feature']))
jj = len(set(juncs[(juncs['Bonferroni'] <= 0.05)].loc[:, 'Feature']))

print("===Unique Features===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes[(genes['Bonferroni'] <= 0.05)].loc[:, 'ensemblID']))
tt = len(set(trans[(trans['Bonferroni'] <= 0.05)].loc[:, 'ensemblID']))
ee = len(set(exons[(exons['Bonferroni'] <= 0.05)].loc[:, 'ensemblID']))
jj = len(set(juncs[(juncs['Bonferroni'] <= 0.05)].loc[:, 'ensemblID']))

print("===Unique Ensembl Gene===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))

gg = len(set(genes[(genes['Bonferroni'] <= 0.05)].loc[:, 'ID']))
tt = len(set(trans[(trans['Bonferroni'] <= 0.05)].loc[:, 'ID']))
ee = len(set(exons[(exons['Bonferroni'] <= 0.05)].loc[:, 'ID']))
jj = len(set(juncs[(juncs['Bonferroni'] <= 0.05)].loc[:, 'ID']))

print("===Unique Gene Name===\nGene:\t\t%d\nTranscript:\t%d\nExon:
 ↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

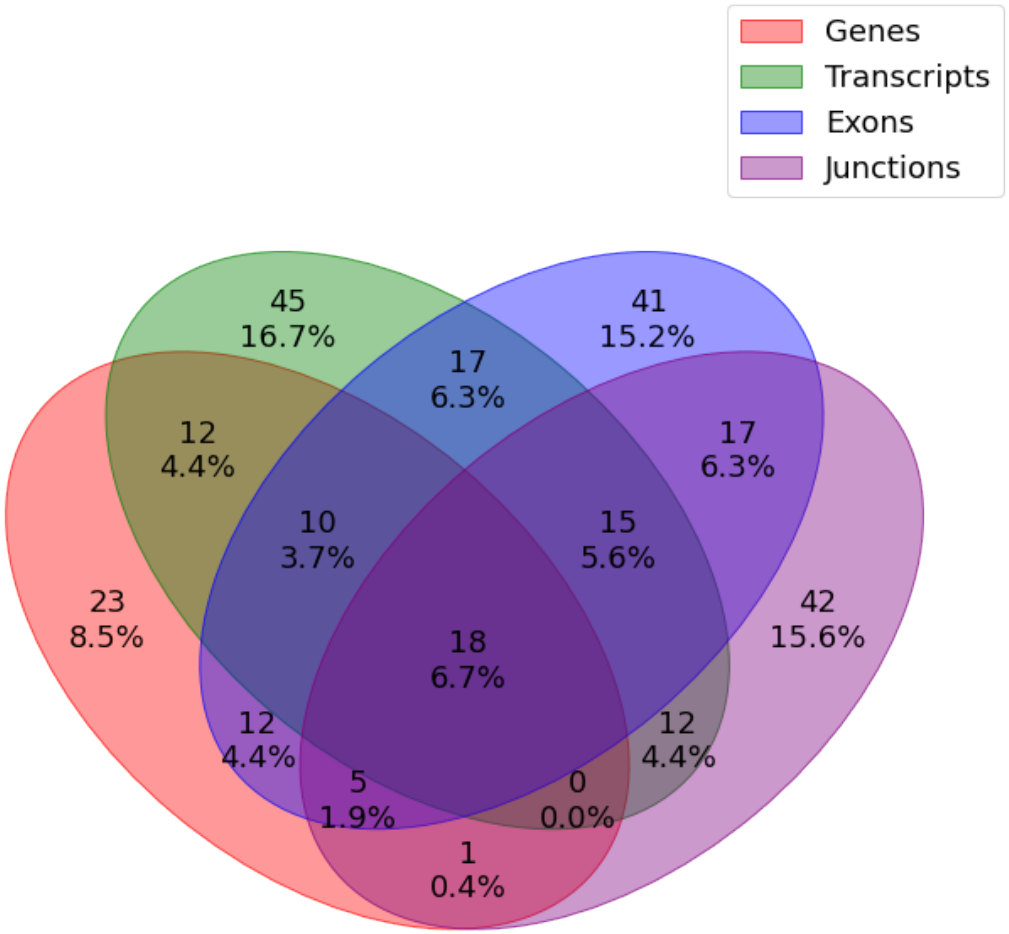
```
===Unique Features===
Gene:           81
Transcript:     158
Exon:           448
Junction:       211

===Unique Ensembl Gene===
Gene:           81
Transcript:     129
```

```
Exon:           135
Junction:       110

===Unique Gene Name===
Gene:           81
Transcript:     129
Exon:           143
Junction:       110
```

1.5.2 Plot venn

[39]:
```
features = {
    'Genes': set(genes[(genes['Bonferroni'] <= 0.05)].loc[:, 'ensemblID']),
    'Transcripts': set(trans[(trans['Bonferroni'] <= 0.05)].loc[:,␣
 ↪'ensemblID']),
    'Exons': set(exons[(exons['Bonferroni'] <= 0.05)].loc[:, 'ensemblID']),
    'Junctions': set(juncs[(juncs['Bonferroni'] <= 0.05)].loc[:, 'ensemblID']),
}
```

[40]:
```
venn(features, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('bonferroni_allFeatures_venn_diagram_percentage.png')
plt.savefig('bonferroni_allFeatures_venn_diagram_percentage.pdf')
plt.savefig('bonferroni_allFeatures_venn_diagram_percentage.svg')
plt.show()
```



[41]:
```
limiting_features(features, 'Genes', 'Transcripts')
limiting_features(features, 'Genes', 'Junctions')
limiting_features(features, 'Exons', 'Genes')
```

```
Comparing Genes with Transcripts: 31.01%
Features in common: 40
Comparing Genes with Junctions: 21.82%
Features in common: 24
Comparing Exons with Genes: 55.56%
Features in common: 45
```

[42]:
```
limiting_features(features, 'Transcripts', 'Junctions')
limiting_features(features, 'Exons', 'Transcripts')
```

```
limiting_features(features, 'Exons', 'Junctions')
```

```
Comparing Transcripts with Junctions: 40.91%
Features in common: 45
Comparing Exons with Transcripts: 46.51%
Features in common: 60
Comparing Exons with Junctions: 50.00%
Features in common: 55
```

[43]:
```
len(features['Genes'] & features['Transcripts'] & features['Exons'] &␣
↪features['Junctions'])
```

[43]: 18

[44]:
```
len(features['Genes'] | features['Transcripts'] | features['Exons'] |␣
↪features['Junctions'])
```

[44]: 270

1.5.3 SNPs not in significant PGC2+CLOZUK GWAS

[45]:
```
new_genes = pd.merge(genes[(genes['Bonferroni'] <= 0.05)], pgc2_df,␣
↪left_on='BEST.GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_trans = pd.merge(trans[(trans['Bonferroni'] <= 0.05)], pgc2_df,␣
↪left_on='BEST.GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_exons = pd.merge(exons[(exons['Bonferroni'] <= 0.05)], pgc2_df,␣
↪left_on='BEST.GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])
new_juncs = pd.merge(juncs[(juncs['Bonferroni'] <= 0.05)], pgc2_df,␣
↪left_on='BEST.GWAS.ID',
                     right_on='our_snp_id', suffixes=['_TWAS', '_PGC2'])

new_genes = new_genes[(new_genes['P'] > 5e-8)].copy()
new_trans = new_trans[(new_trans['P'] > 5e-8)].copy()
new_exons = new_exons[(new_exons['P'] > 5e-8)].copy()
new_juncs = new_juncs[(new_juncs['P'] > 5e-8)].copy()
```

[46]:
```
gg = len(set(new_genes['BEST.GWAS.ID']))
tt = len(set(new_trans['BEST.GWAS.ID']))
ee = len(set(new_exons['BEST.GWAS.ID']))
jj = len(set(new_juncs['BEST.GWAS.ID']))

print("===Unique novel SNPs===\nGene:\t\t%d\nTranscript:\t%d\nExon:
↪\t\t%d\nJunction:\t%d\n" % (gg, tt, ee, jj))
```

```
===Unique novel SNPs===
```

```
Gene:           15
Transcript:     26
Exon:           19
Junction:       23
```

[47]:
```
len(set(new_genes['BEST.GWAS.ID']) | set(new_trans['BEST.GWAS.ID']) |
    set(new_exons['BEST.GWAS.ID']) | set(new_juncs['BEST.GWAS.ID']))
```

[47]: 53

1.6 Session Information

[48]:
```
import types
from IPython import sys_info

def imports():
    for name, val in globals().items():
        if isinstance(val, types.ModuleType):
            yield val.__name__

#exclude all modules not listed by `!pip freeze`
excludes = ['__builtin__', 'types', 'IPython.core.shadowns', 'sys', 'os']
function_modules = []
imported_modules = [module for module in imports() if module not in excludes] +␣
 ↪function_modules
pip_modules = !pip freeze #you could also use `!conda list` with anaconda
```

[49]:
```
print(sys_info())
#print the names and versions of the imported modules
print("\nImported Modules:")
for module in pip_modules[2:]:
    name, version = module.split('==')
    if name in imported_modules:
        print(name + ':\t' + version)
```

```
{'commit_hash': '<not found>',
 'commit_source': '(none found)',
 'default_encoding': 'utf-8',
 'ipython_path': '/usr/lib/python3.9/site-packages/IPython',
 'ipython_version': '7.19.0',
 'os_name': 'posix',
 'platform': 'Linux-5.10.14-arch1-1-x86_64-with-glibc2.33',
 'sys_executable': '/usr/bin/python',
 'sys_platform': 'linux',
 'sys_version': '3.9.1 (default, Feb  6 2021, 06:49:13) \n[GCC 10.2.0]'}

Imported Modules:
```

```
numpy:  1.19.5
pandas: 1.1.5
```