

main

September 7, 2021

1 Examine integration results for TWAS associations

```
[1]: import pandas as pd
```

```
[2]: df = pd.read_csv("../manuscript_supp_data/_m/
↳BrainSeq_Phase3_Caudate_GWAS_DE_eQTL_Integration.txt.gz", sep='\t')
df = df[(df["Feature_Type"] == "Gene")].copy()
df["ensemblID"] = df.gene_id.str.replace("\\.*", "", regex=True)
df = df.groupby("gene_id").first().reset_index()
df.head()
```

```
[2]:
```

	gene_id	Symbol	variant_id	rsid	A1	A2	OR	\
0	ENSG00000028116.16	VRK2	chr2:57944085:A:C	rs1518393	A	C	0.94149	
1	ENSG00000066248.14	NGEF	chr2:232925939:G:T	rs1878287	G	T	0.92380	
2	ENSG00000100403.11	ZC3H7B	chr22:41357599:G:A	rs11090045	G	A	0.94102	
3	ENSG00000104765.15	BNIP3L	chr8:26411675:C:T	rs1042992	C	T	0.92930	
4	ENSG00000105708.8	ZNF14	chr19:19629920:C:G	rs880090	C	G	1.06150	

	P	pval_nominal	adj.P.Val	logFC	t	eqtl_slope	\
0	7.780000e-10	4.532180e-04	0.010761	-0.127117	-3.431328	1	
1	1.230000e-13	2.215200e-04	0.009144	0.104229	3.493550	-1	
2	1.760000e-08	1.177050e-07	0.012553	-0.055238	-3.367649	1	
3	3.670000e-09	1.163410e-04	0.010653	-0.063722	-3.435641	-1	
4	2.440000e-08	6.133540e-04	0.016532	0.074769	3.254277	1	

	de_dir	eqtl_gwas_dir	agree_direction	pgc2_a1_same_as_our_counted	\
0	-1	1	No	False	
1	1	-1	No	False	
2	-1	1	No	False	
3	-1	-1	Yes	False	
4	1	1	Yes	False	

	Feature_Type	ensemblID
0	Gene	ENSG00000028116
1	Gene	ENSG00000066248
2	Gene	ENSG00000100403
3	Gene	ENSG00000104765

```
[3]: twas_df = pd.read_csv("../.../twas/feature_comparison/manuscript_supp_data/_m/
↳BrainSeq_Phase3_Caudate_TWAS_associations_allFeatures.txt.gz", sep='\t')
twas_df = twas_df[(twas_df["Type"] == "Gene") & (twas_df["FDR"] < 0.05)].copy()
twas_df.head()
```

```
[3]:
```

	Feature	ensemblID	ID	HSQ	BEST.GWAS.ID	\
15	ENSG00000132563	ENSG00000132563	REEP2	0.077983	chr5:138519616:T:C	
34	ENSG00000171246	ENSG00000171246	NPTX1	0.199819	chr17:80587803:G:A	
52	ENSG00000165434	ENSG00000165434	PGM2L1	0.160964	chr11:74445493:G:A	
63	ENSG00000065833	ENSG00000065833	ME1	0.090729	chr6:83697747:C:T	
70	ENSG00000146828	ENSG00000146828	SLC12A9	0.082561	chr7:100717894:A:G	

	EQTL.ID	TWAS.Z	TWAS.P	FDR	Bonferroni	Type
15	chr5:138453285:C:A	3.355851	7.912109e-04	0.014566	1.000000	Gene
34	chr17:80546983:C:T	3.547619	3.887305e-04	0.008697	1.000000	Gene
52	chr11:74393463:T:C	-3.322061	8.935515e-04	0.015812	1.000000	Gene
63	chr6:83457558:A:G	-5.406853	6.414180e-08	0.000006	0.000527	Gene
70	chr7:100846338:G:A	3.167074	1.539812e-03	0.023946	1.000000	Gene

```
[4]: len(set(df.ensemblID) & set(twas_df.ensemblID))
```

```
[4]: 16
```

```
[5]: df[(df["ensemblID"].isin(list(set(df.ensemblID) & set(twas_df.ensemblID))))]
```

```
[5]:
```

	gene_id	Symbol	variant_id	rsid	\
6	ENSG00000112511.17	PHF1	chr6:33427422:G:A	rs9461856	
7	ENSG00000114054.13	PCCB	chr3:136569563:G:A	rs7432375	
8	ENSG00000120733.13	KDM3B	chr5:138439892:C:G	rs982085	
9	ENSG00000124613.8	ZNF391	chr6:27424023:C:T	rs34071253	
10	ENSG00000132563.15	REEP2	chr5:138439892:C:G	rs982085	
14	ENSG00000148842.17	CNNM2	chr10:102852578:T:A	rs11191419	
17	ENSG00000161896.11	IP6K3	chr6:33773939:A:G	rs4711350	
19	ENSG00000166166.12	TRMT61A	chr14:103809712:C:T	rs12880821	
23	ENSG00000198911.11	SREBF2	chr22:41938949:C:G	rs1047997	
24	ENSG00000204256.12	BRD2	chr6:32669525:G:A	rs2395231	
26	ENSG00000204463.12	BAG6	chr6:31358852:C:T	rs2523594	
30	ENSG00000228223.2	HCG11	chr6:26466161:G:A	rs1977199	
31	ENSG00000228944.1	ENSG00000228944.1	chr7:24695385:G:C	rs112509803	
32	ENSG00000244731.7	C4A	chr6:31793436:G:A	rs2607014	
33	ENSG00000249484.8	LINC01470	chr5:152797561:A:G	rs111294930	
34	ENSG00000253553.5	ENSG00000253553.5	chr8:88310775:A:C	rs3844198	

A1	A2	OR	P	pval_nominal	adj.P.Val	logFC	\
6	G	A	0.93180	1.680000e-13	2.090630e-04	2.281934e-02	-0.046170

7	G	A	1.07020	4.070000e-12	3.669320e-14	3.397384e-02	-0.058710
8	C	G	1.05710	1.030000e-08	8.821430e-05	1.518040e-02	-0.031591
9	C	T	1.26640	6.220000e-41	4.376050e-04	2.054017e-02	0.082216
10	C	G	1.05710	1.030000e-08	3.553170e-06	6.655155e-09	0.137644
14	T	A	1.08750	2.090000e-16	2.573560e-10	3.899296e-03	0.053701
17	A	G	0.92386	2.300000e-10	3.005850e-10	2.435252e-03	-0.233018
19	C	T	0.93470	4.690000e-12	3.767620e-04	4.958693e-02	-0.058611
23	C	G	1.08230	8.080000e-11	6.029740e-04	9.947151e-04	-0.075761
24	G	A	1.21970	6.820000e-30	1.131810e-05	1.718619e-02	-0.051562
26	C	T	0.91831	2.410000e-16	7.590350e-04	1.241493e-02	-0.044002
30	G	A	0.91432	1.020000e-14	1.374100e-05	1.181958e-03	0.114043
31	G	C	0.91974	2.310000e-08	1.514450e-04	2.256942e-02	0.278474
32	G	A	1.20320	1.200000e-31	1.732000e-33	7.880375e-03	0.358141
33	A	G	1.08580	9.040000e-12	6.338820e-14	1.143030e-02	0.406227
34	A	C	1.06450	1.210000e-08	7.121140e-04	2.909648e-02	0.202146

	t	eqtl_slope	de_dir	eqtl_gwas_dir	agree_direction	\
6	-3.123441	-1	-1	-1	Yes	
7	-2.946922	-1	-1	-1	Yes	
8	-3.287837	-1	-1	-1	Yes	
9	3.166580	-1	1	-1	No	
10	6.993625	1	1	1	Yes	
14	3.799656	-1	1	-1	No	
17	-3.959823	1	-1	1	No	
19	-2.775075	-1	-1	-1	Yes	
23	-4.243388	-1	-1	-1	Yes	
24	-3.239197	-1	-1	-1	Yes	
26	-3.373864	1	-1	1	No	
30	4.193600	1	1	1	Yes	
31	3.127826	1	1	1	Yes	
32	3.550690	1	1	1	Yes	
33	3.407085	1	1	1	Yes	
34	3.016220	-1	1	-1	No	

	pgc2_a1_same_as_our_counted	Feature_Type	ensemblID
6	False	Gene	ENSG00000112511
7	False	Gene	ENSG00000114054
8	False	Gene	ENSG00000120733
9	False	Gene	ENSG00000124613
10	False	Gene	ENSG00000132563
14	False	Gene	ENSG00000148842
17	False	Gene	ENSG00000161896
19	False	Gene	ENSG00000166166
23	False	Gene	ENSG00000198911
24	False	Gene	ENSG00000204256
26	False	Gene	ENSG00000204463
30	False	Gene	ENSG00000228223

31	False	Gene	ENSG00000228944
32	False	Gene	ENSG00000244731
33	False	Gene	ENSG00000249484
34	False	Gene	ENSG00000253553

[]: