

Appendix. Significant and Downstream Results Tables

Source files: *sig_summary (45).txt* and *downstream_summary.txt*. Source folder: /content/088CvBpI_results. Generated on 2026-06-27. Diseases: schizophrenia (*scz*) and clozapine-proxied treatment-resistant schizophrenia (*trs*). Gene sets: 10 KEGG pathways.

Display note: Pipeline p values reported as 0 are displayed as <.001 for APA-style readability. No scroll containers are used; tables are intended to copy cleanly into Microsoft Word.

Appendix Table A1. Input status and analytic thresholds

Category	Item	Status or threshold
Input file	enrichment_summary	OK; 140 rows
Input file	pairwise_disease_stats	OK; 10 rows
Input file	gene_influence	OK; 2,697 rows
Input file	all_genes_all_genesets	OK; 1,788 rows
Input file	proximity	OK; 10 rows
Input file	differential_pairwise	OK; 10 rows
Input file	family_wise_fdr	OK; 190 rows
Threshold	Raw p value	< .05
Threshold	FDR / global FDR	< .05; FDR gate applied when available
Threshold	Stouffer Z	> 1.96
Threshold	Cohen's d	> 0.50
Threshold	Lin's CCC	> 0.50
Threshold	Sign-concordance rate	> 0.70
Threshold	Kendall tau	> 0.30
Threshold	Pearson r and rank-biserial r	> 0.30

Note. In pairwise tables, mean difference was defined as Disease 1 minus Disease 2. No borderline findings were included in the supplied significant-results summary.

Appendix Table A2. Meta-across-tissue gene-set enrichment rankings

KEGG pathway	scz Stouffer r Z	scz Z	scz coverage	scz perm p	scz Wilcoxon p	trs Stouffer r Z	trs Z	trs coverage	trs perm p	trs Wilcoxon p
Fatty acid degradation	+4.600	2.162	81%	.1158	.03414	+4.706	2.288	84%	.09779	.1011
Synaptic vesicle cycle	+3.565	1.685	73%	.2109	.0637	+2.620	1.686	77%	.3570	.2671
Citrate cycle / TCA cycle	+3.142	2.013	87%	.2738	.1227	+1.573	1.901	87%	.5707	.4374
Regulation of actin cytoskeleton	+2.133	1.946	76%	.4649	.3189	+2.311	2.015	76%	.4077	.5373
Endocytosis	+2.101	2.115	84%	.4732	.1924	+2.353	2.132	84%	.4011	.3352
Autophagy, animal	+2.077	2.083	82%	.4779	.5890	+0.627	2.090	81%	.8274	.8569
Neuroactive ligand-receptor interaction	+1.987	1.843	66%	.4949	.3433	+3.260	1.587	67%	.2466	.02775
PPAR signaling pathway	+1.545	1.655	79%	.5870	.2478	+1.855	1.752	79%	.5162	.2002
MAPK signaling pathway	+1.260	2.049	74%	.6649	.9263	+1.967	2.039	77%	.4846	.9321
Ras signaling pathway	+0.595	1.865	71%	.8371	.8132	−0.835	1.830	73%	.7741	.7042

Note. The |Z| column is reproduced as reported in the downstream summary. Coverage indicates gene-set coverage in the meta-across-tissue analysis.

Appendix Table A3. Significant per-disease enrichment findings reported by the pipeline

N o.	KEGG pathway	Disease	Tissue/model	n	Stouffer r Z	95% CI	perm p	Wilcoxon p
1	Neuroactive ligand-receptor interaction	trs	Brain hippocampus, S-PrediXcan	142	4.558	NA	NA	2.70E−05

2	Neuroactive ligand-receptor interaction	scz	Brain hippocampus, S-PrediXcan	1 3 8	3.805	NA	NA	.00196 5
3	Autophagy, animal	scz	Brain amygdala, S-PrediXcan	9 0	2.951	NA	NA	.02514
4	Fatty acid degradation	scz	Brain frontal cortex BA9, S-PrediXcan	3 0	2.892	NA	NA	.03098
5	Fatty acid degradation	scz	Brain nucleus accumbens basal ganglia, S-PrediXcan	2 9	3.416	NA	NA	.03453
6	Fatty acid degradation	trs	Brain frontal cortex BA9, S-PrediXcan	2 9	3.049	NA	NA	.04803
7	Fatty acid degradation	trs	Brain nucleus accumbens basal ganglia, S-PrediXcan	2 9	3.423	NA	NA	.05623
8	Fatty acid degradation	trs	Meta across tissues	3 6	4.706	[-1.06, 10.51]	.097 79	.1011
9	Regulation of actin cytoskeleton	trs	Brain hippocampus, S-PrediXcan	1 2 6	2.274	NA	NA	.09804
1 0	Autophagy, animal	scz	Brain caudate basal ganglia, S-PrediXcan	1 1 0	2.822	NA	NA	.1044
1 1	Fatty acid degradation	scz	Meta across tissues	3 5	4.600	[-0.62, 9.47]	.115 8	.03414
1 2	Citrate cycle / TCA cycle	scz	Brain anterior cingulate cortex BA24, S-PrediXcan	2 1	2.787	NA	NA	.1373
1 3	Fatty acid degradation	trs	Brain hippocampus, S-PrediXcan	2 8	2.514	NA	NA	.1502
1 4	MAPK signaling pathway	scz	Brain anterior cingulate cortex BA24, S-PrediXcan	1 5 4	2.907	NA	NA	.1616
1 5	Synaptic vesicle cycle	scz	Brain amygdala, S-PrediXcan	3 2	2.034	NA	NA	.1716

1 6	MAPK signaling pathway	trs	Brain anterior cingulate cortex BA24, S-PrediXcan	1 5 5	2.695	NA	NA	.1928
1 7	Synaptic vesicle cycle	scz	Meta across tissues	5 8	3.565	[-1.01, 8.04]	.210 9	.0637
1 8	Citrate cycle / TCA cycle	scz	Brain caudate basal ganglia, S-PrediXcan	2 4	2.036	NA	NA	.2292
1 9	Neuroactive ligand-receptor interaction	trs	Meta across tissues	2 4 8	3.260	[-0.82, 7.48]	.246 6	.02775
2 0	Fatty acid degradation	trs	Brain caudate basal ganglia, S-PrediXcan	3 2	2.046	NA	NA	.2618
2 1	Citrate cycle / TCA cycle	scz	Meta across tissues	2 6	3.142	[-1.94, 8.79]	.273 8	.1227
2 2	MAPK signaling pathway	scz	Brain frontal cortex BA9, S-PrediXcan	1 4 1	2.371	NA	NA	.3171
2 3	Endocytosis	trs	Brain caudate basal ganglia, S-PrediXcan	1 5 7	2.473	NA	NA	.3191
2 4	Synaptic vesicle cycle	trs	Meta across tissues	6 1	2.620	[-1.30, 6.74]	.357 0	.2671
2 5	Endocytosis	trs	Meta across tissues	2 0 9	2.353	[-3.65, 9.22]	.401 1	.3352
2 6	Regulation of actin cytoskeleton	trs	Meta across tissues	1 7 6	2.311	[-3.05, 7.75]	.407 7	.5373
2 7	Regulation of actin cytoskeleton	scz	Meta across tissues	1 7 6	2.133	[-2.85, 7.09]	.464 9	.3189
2 8	Endocytosis	scz	Meta across tissues	2 1 1	2.101	[-3.70, 8.18]	.473 2	.1924

29	Autophagy, animal	scz	Meta across tissues	139	2.077	[−3.37, 7.42]	.4779	.5890
30	MAPK signaling pathway	trs	Meta across tissues	230	1.967	[−3.38, 7.77]	.4846	.9321
31	Neuroactive ligand-receptor interaction	scz	Meta across tissues	243	1.987	[−2.88, 6.56]	.4949	.3433

Note. The table reproduces all 31 enrichment findings listed in the significant-results summary. Some rows were flagged by the |Stouffer Z| criterion rather than by a nominal p-value criterion.

Appendix Table A4. Disease divergence by Stouffer Z difference

Ran k	KEGG pathway	scz Stouffer Z	trs Stouffer Z	Delta, trs – scz	Interpretive direction
1	Citrate cycle / TCA cycle	+3.14	+1.57	−1.569	Higher aggregate signal in scz
2	Autophagy, animal	+2.08	+0.63	−1.450	Higher aggregate signal in scz
3	Ras signaling pathway	+0.59	−0.83	−1.429	Directionally lower in trs
4	Neuroactive ligand-receptor interaction	+1.99	+3.26	+1.274	Higher aggregate signal in trs
5	Synaptic vesicle cycle	+3.56	+2.62	−0.945	Higher aggregate signal in scz
6	MAPK signaling pathway	+1.26	+1.97	+0.707	Higher aggregate signal in trs
7	PPAR signaling pathway	+1.55	+1.85	+0.309	Higher aggregate signal in trs
8	Endocytosis	+2.10	+2.35	+0.252	Higher aggregate signal in trs
9	Regulation of actin cytoskeleton	+2.13	+2.31	+0.179	Higher aggregate signal in trs
10	Fatty acid degradation	+4.60	+4.71	+0.106	Highly similar signal

Note. No pairwise disease statistical test was significant at the supplied thresholds.

Appendix Table A5. Concordance and proximity between scz and trs gene-level profiles

KEGG pathway	n paired	Pearson r	Spearman rho	Cosine	Sign rate	Lin's CCC	Kendall tau
Fatty acid degradation	35	.876	.808	.884	.857	.866	.650
MAPK signaling pathway	221	.863	.801	.863	.786	.863	.625
Citrate cycle / TCA cycle	26	.850	.770	.851	.846	.834	.625
Ras signaling pathway	168	.829	.812	.828	.820	.827	.635
Neuroactive ligand-receptor interaction	240	.812	.774	.813	.800	.808	.588
Autophagy, animal	134	.810	.714	.809	.759	.809	.542
Endocytosis	204	.806	.672	.806	.756	.806	.527
PPAR signaling pathway	60	.801	.794	.802	.867	.782	.615
Synaptic vesicle cycle	58	.761	.697	.768	.724	.756	.527
Regulation of actin cytoskeleton	172	.753	.698	.754	.789	.753	.538

Note. All 10 pathways met the supplied high-agreement criteria. Pipeline p values for Pearson, Spearman, sign-concordance, and Kendall tests were significant; p values reported as 0 by the pipeline are treated as <.001 for display.

Appendix Table A6. Top leave-one-out driver entries by disease

Disease	Gene	KEGG pathway	Gene Z	Delta Stouffer	Delta %	Sign flip
scz	MAPK3	Ras signaling pathway	+13.63	+1.05	118.5%	Yes
scz	CALML6	Ras signaling pathway	+10.12	+0.78	87.9%	No
scz	GNG3	Ras signaling pathway	+9.34	+0.72	81.2%	No
scz	BAD	Ras signaling pathway	+7.03	+0.54	61.0%	No
scz	ABL2	Ras signaling pathway	-6.81	-0.53	59.6%	No
scz	TAOK2	MAPK signaling pathway	+15.72	+1.05	58.2%	No
scz	EGF	Ras signaling pathway	-6.58	-0.51	57.6%	No

scz	LAT	Ras signaling pathway	+6.24	+0.48	54.1%	No
scz	PAK5	Ras signaling pathway	−6.14	−0.48	53.8%	No
scz	OGDH	Citrate cycle / TCA cycle	+8.79	+1.69	53.0%	No
scz	ANGPT1	Ras signaling pathway	−6.02	−0.47	52.8%	No
scz	MAPK3	Autophagy, animal	+13.63	+1.15	52.7%	No
scz	RHOA	Ras signaling pathway	−5.87	−0.45	51.5%	No
scz	ARFGAP2	Endocytosis	+14.78	+1.02	50.9%	No
scz	MAPK3	MAPK signaling pathway	+13.63	+0.91	50.5%	No
scz	PLA2G12A	Ras signaling pathway	+5.73	+0.44	49.7%	No
scz	VPS29	Endocytosis	−14.17	−0.98	49.3%	No
scz	ATG13	Autophagy, animal	−12.50	−1.07	49.1%	No
scz	CPT2	PPAR signaling pathway	+5.74	+0.73	45.4%	No
scz	VPS45	Endocytosis	−12.98	−0.90	45.1%	No
scz	MAPK3	Regulation of actin cytoskeleton	+13.63	+1.02	44.3%	No
scz	FABP3	PPAR signaling pathway	−5.37	−0.71	44.1%	No
scz	ACOX1	PPAR signaling pathway	−5.36	−0.71	44.0%	No
scz	RASA3	Ras signaling pathway	+4.98	+0.38	43.1%	No
scz	RRAS	Ras signaling pathway	−4.87	−0.38	42.7%	No
scz	SLC27A4	PPAR signaling pathway	−4.95	−0.66	40.7%	No
scz	PLA2G6	Ras signaling pathway	−4.63	−0.36	40.7%	No
scz	ATP6V1E2	Synaptic vesicle cycle	+11.13	+1.44	39.7%	No
scz	IDH3B	Citrate cycle / TCA cycle	−6.00	−1.26	39.5%	No
scz	EFNA5	Ras signaling pathway	+4.44	+0.34	38.4%	No

trs	ATG13	Autophagy, animal	−12.08	−1.04	306.5%	No
trs	MAPK3	Autophagy, animal	+10.36	+0.89	262.2%	Yes
trs	VPS39	Autophagy, animal	+8.90	+0.76	225.1%	Yes
trs	RPTOR	Autophagy, animal	−8.78	−0.75	222.7%	No
trs	TAX1BP1	Autophagy, animal	+8.22	+0.70	207.8%	Yes
trs	PIK3R4	Autophagy, animal	+8.02	+0.69	202.7%	Yes
trs	MAP1LC3A	Autophagy, animal	+6.46	+0.55	163.3%	Yes
trs	AKT3	Autophagy, animal	−5.96	−0.51	151.3%	No
trs	RRAS2	Autophagy, animal	+5.48	+0.47	138.4%	Yes
trs	RPS6KB2	Autophagy, animal	−5.26	−0.45	133.6%	No
trs	SNAP29	Autophagy, animal	−5.20	−0.45	132.1%	No
trs	RRAS	Autophagy, animal	−5.14	−0.44	130.6%	No
trs	DAPK3	Autophagy, animal	+5.04	+0.43	127.4%	Yes
trs	MTMR3	Autophagy, animal	−5.01	−0.43	127.2%	No
trs	PRKCQ	Autophagy, animal	−5.00	−0.43	127.1%	No
trs	MAPK3	Ras signaling pathway	+10.36	+0.79	121.0%	No
trs	YKT6	Autophagy, animal	−4.74	−0.41	120.4%	No
trs	NBR1	Autophagy, animal	−4.63	−0.40	117.7%	No
trs	RHEB	Autophagy, animal	−4.60	−0.40	116.8%	No
trs	GABARAP	Autophagy, animal	+4.38	+0.37	110.6%	Yes
trs	VPS11	Autophagy, animal	+4.30	+0.37	108.7%	Yes
trs	AMBRA1	Autophagy, animal	+4.19	+0.36	105.7%	Yes
trs	CALCOCO2	Autophagy, animal	+4.07	+0.35	102.9%	Yes

trs	PIK3R1	Autophagy, animal	−3.87	−0.33	98.4%	No
trs	ATG7	Autophagy, animal	+3.74	+0.32	94.5%	No
trs	BAD	Autophagy, animal	+3.68	+0.31	92.9%	No
trs	NRBF2	Autophagy, animal	−3.62	−0.31	92.0%	No
trs	LAT	Ras signaling pathway	+7.86	+0.60	91.8%	No
trs	RAB8A	Autophagy, animal	+3.58	+0.31	90.3%	No
trs	WIPI1	Autophagy, animal	−3.46	−0.30	88.1%	No

Note. The source summary reported 131 influential gene-set entries for scz and 232 for trs. This table contains the top 30 entries printed in the downstream summary for each disease.

Appendix Table A7. Recurrent driver genes across gene sets and diseases

Gene	Entries	Gene sets	Diseases	Sign flips	Maximum Delta %
MAPK3	8	4	2	2	262.2
EGF	6	3	2	0	83.1
BAD	4	2	2	0	92.9
CPT2	4	2	2	0	53.1
AKT3	3	3	1	0	151.3
RRAS2	3	2	2	1	138.4
RRAS	3	2	2	0	130.6
PIK3R1	3	2	2	0	98.4
ANGPT1	3	2	2	0	73.0
MAPK1	3	2	2	0	72.2
CPT1C	3	2	2	0	67.8
RHOA	3	2	2	0	55.3
PAK5	3	2	2	0	53.8

PCK2	3	2	2	0	31.6
LPAR2	3	2	2	0	26.5
CACNA1B	3	2	2	0	22.5
ATG13	2	1	2	0	306.5
RPTOR	2	1	2	0	222.7
TAX1BP1	2	1	2	1	207.8
PIK3R4	2	1	2	1	202.7
MAP1LC3A	2	1	2	1	163.3
RPS6KB2	2	1	2	0	133.6
PRKCQ	2	1	2	0	127.1
LAT	2	1	2	0	91.8
CALML6	2	1	2	0	87.9
GNG3	2	1	2	0	81.2
OGDH	2	1	2	0	77.7
RASA3	2	1	2	0	75.5
FABP3	2	1	2	0	74.7
GNB2	2	1	2	0	71.8

Appendix Table A8. Discordant genes with opposite sign between diseases

Gene	KEGG pathway	scz Z	trs Z	Absolute separation
ARPC3	Endocytosis	-4.23	+10.26	14.49
ARPC3	Regulation of actin cytoskeleton	-4.23	+10.26	14.49
EHD4	Endocytosis	-3.72	+4.66	8.38
VTA1	Endocytosis	+3.49	-2.50	5.99

C8G	Regulation of actin cytoskeleton	+2.01	−3.53	5.54
RAB8A	Endocytosis	−1.75	+3.58	5.33
RAB8A	Autophagy, animal	−1.75	+3.58	5.33
RAB11FIP2	Endocytosis	−3.70	+1.60	5.29
FGF18	MAPK signaling pathway	+3.43	−1.67	5.10
FGF18	Regulation of actin cytoskeleton	+3.43	−1.67	5.10
FGF18	Ras signaling pathway	+3.43	−1.67	5.10
DLD	Citrate cycle / TCA cycle	+2.30	−2.68	4.99
IRAK4	MAPK signaling pathway	+2.69	−2.28	4.97
CHMP6	Endocytosis	+2.46	−2.27	4.72
PPP2CA	Autophagy, animal	+2.13	−2.54	4.67
NFKB2	MAPK signaling pathway	+3.01	−1.26	4.27
ATP6V0B	Synaptic vesicle cycle	+1.37	−2.87	4.24
MDM2	Endocytosis	+2.46	−1.73	4.20
ITGA2	Regulation of actin cytoskeleton	+2.03	−2.17	4.19
MAPKAPK3	MAPK signaling pathway	−1.12	+2.91	4.03
FABP1	PPAR signaling pathway	−1.84	+2.12	3.96
PIP5K1B	Regulation of actin cytoskeleton	−2.48	+1.40	3.89
PIP5K1B	Endocytosis	−2.48	+1.40	3.89
CHMP7	Endocytosis	+1.31	−2.55	3.86
P2RX1	Neuroactive ligand-receptor interaction	−2.39	+1.31	3.71
MYH14	Regulation of actin cytoskeleton	−1.03	+2.60	3.63
PTH2R	Neuroactive ligand-receptor interaction	−2.07	+1.43	3.51

PPP1R12C	Regulation of actin cytoskeleton	+2.07	−1.16	3.23
ADCYAP1	Neuroactive ligand-receptor interaction	+1.65	−1.51	3.16
ADH1C	Fatty acid degradation	−1.68	+1.44	3.11

Note. The downstream summary reported 41 discordant gene entries and printed the 30 entries shown here.

Appendix Table A9. Genes recurrent across many gene sets

Gene	No. of gene sets	scz Z	trs Z
HRAS	5	+1.52	+0.29
FGFR3	4	+1.53	+2.27
FGFR2	4	NA	−1.08
AKT1	4	−4.33	−1.53
MRAS	4	NA	NA
AKT2	4	NA	NA
AKT3	4	+0.45	−5.96
MAP2K1	4	−1.21	−0.71
MAP2K2	4	+2.15	+2.09
KRAS	4	NA	−0.26
EGFR	4	−1.18	−1.14
RAF1	4	−1.64	−0.17
INS	4	NA	NA
IGF1R	4	NA	NA
NRAS	4	+0.09	−1.02
MAPK3	4	+13.63	+10.36
FGFR4	4	+2.00	+3.73

RRAS	4	−4.87	−5.14
MAPK1	4	+2.69	+2.86
RRAS2	4	+3.90	+5.48
PDGFRA	4	NA	NA
CDC42	4	+1.08	+1.32
PIK3CA	3	+2.20	+2.28
PRKACA	3	−0.92	+0.23
PIK3CB	3	−0.35	−2.03
PIK3CD	3	−2.59	−1.11
TRAF6	3	−0.24	+0.64
PIK3R2	3	−1.89	−0.54
PIK3R3	3	+1.40	+2.23
PRKACB	3	−0.66	−0.57

Appendix Table A10. Family-wise FDR survivors pooled across in-run p values

KEGG pathway	Metric family	Contrast	p value	FDR
Autophagy, animal	Proximity / Pearson p	scz vs trs	<.001	<.001
Autophagy, animal	Proximity / Spearman p	scz vs trs	<.001	<.001
Autophagy, animal	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
Autophagy, animal	Pairwise stats / sign-concordance p	scz vs trs	<.001	<.001
Citrate cycle / TCA cycle	Proximity / Pearson p	scz vs trs	<.001	<.001
Endocytosis	Proximity / Pearson p	scz vs trs	<.001	<.001
Endocytosis	Proximity / Spearman p	scz vs trs	<.001	<.001

Endocytosis	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
Endocytosis	Pairwise stats / sign-concordance p	scz vs trs	<.001	<.001
Fatty acid degradation	Proximity / Pearson p	scz vs trs	<.001	<.001
Fatty acid degradation	Proximity / Spearman p	scz vs trs	<.001	<.001
Fatty acid degradation	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
MAPK signaling pathway	Proximity / Pearson p	scz vs trs	<.001	<.001
MAPK signaling pathway	Proximity / Spearman p	scz vs trs	<.001	<.001
MAPK signaling pathway	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
MAPK signaling pathway	Pairwise stats / sign-concordance p	scz vs trs	<.001	<.001
Neuroactive ligand-receptor interaction	Proximity / Pearson p	scz vs trs	<.001	<.001
Neuroactive ligand-receptor interaction	Proximity / Spearman p	scz vs trs	<.001	<.001
Neuroactive ligand-receptor interaction	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
Neuroactive ligand-receptor interaction	Pairwise stats / sign-concordance p	scz vs trs	<.001	<.001
PPAR signaling pathway	Proximity / Pearson p	scz vs trs	<.001	<.001
PPAR signaling pathway	Proximity / Spearman p	scz vs trs	<.001	<.001
PPAR signaling pathway	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
PPAR signaling pathway	Pairwise stats / sign-concordance p	scz vs trs	<.001	<.001
Ras signaling pathway	Proximity / Pearson p	scz vs trs	<.001	<.001
Ras signaling pathway	Proximity / Spearman p	scz vs trs	<.001	<.001
Ras signaling pathway	Pairwise stats / Kendall p	scz vs trs	<.001	<.001

Ras signaling pathway	Pairwise stats / sign-concordance p	scz vs trs	<.001	<.001
Regulation of actin cytoskeleton	Proximity / Pearson p	scz vs trs	<.001	<.001
Regulation of actin cytoskeleton	Proximity / Spearman p	scz vs trs	<.001	<.001
Regulation of actin cytoskeleton	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
Regulation of actin cytoskeleton	Pairwise stats / sign-concordance p	scz vs trs	<.001	<.001
Synaptic vesicle cycle	Proximity / Pearson p	scz vs trs	<.001	<.001
Synaptic vesicle cycle	Proximity / Spearman p	scz vs trs	<.001	<.001
Synaptic vesicle cycle	Pairwise stats / Kendall p	scz vs trs	<.001	<.001
Citrate cycle / TCA cycle	Pairwise stats / Kendall p	scz vs trs	2.00E-06	1.90E-05
Citrate cycle / TCA cycle	Proximity / Spearman p	scz vs trs	4.00E-06	2.533E-05
Fatty acid degradation	Pairwise stats / sign-concordance p	scz vs trs	2.20E-05	1.045E-04
Citrate cycle / TCA cycle	Pairwise stats / sign-concordance p	scz vs trs	.000534	.002536
Synaptic vesicle cycle	Pairwise stats / sign-concordance p	scz vs trs	.000862	.004095

Appendix Table A11. Section-level totals from supplied summaries

Source summary	Section	Count
sig_summary (45).txt	Per-disease enrichment	31
sig_summary (45).txt	Differential tests	0
sig_summary (45).txt	Profile proximity	10
sig_summary (45).txt	Pairwise disease statistical tests	0
sig_summary (45).txt	Concordance metrics	10

sig_summary (45).txt	Gene-level LOO influential entries	363
sig_summary (45).txt	Family-wise FDR survivors	40
sig_summary (45).txt	Grand total	454
downstream_summary.txt	Significant enrichments	13
downstream_summary.txt	Pairwise differential	0
downstream_summary.txt	High-concordance sets	10
downstream_summary.txt	Influential gene entries	363
downstream_summary.txt	Discordant genes	41
downstream_summary.txt	Significant proximity	10
downstream_summary.txt	Family-wise FDR survivors	40
downstream_summary.txt	Grand total	477

Note. The two summaries count overlapping result classes differently. The significant-results summary includes 31 enrichment findings, including tissue-specific rows, whereas the downstream summary reports 13 significant meta-across-tissue enrichment findings and separately reports 41 discordant gene entries.