



Supplementary Material

10.1302/2046-3758.121.BJR-2022-0225.R1

Table i. Common significant genes in two different tissues identified by transcriptome-wide association study analysis.

Gene	CHR	TWAS.P _{WB}	TWAS.P _{SM}
DCBLD1	6	0.000347	0.000799
SCFD1	14	0.00833	0.00133
TOR1A	9	0.00308	0.0014
RP11-797A18.4	15	0.0422	0.00298
RP3-525N10.2	6	0.014006	0.005269
SPCS1	3	0.045468	0.00569
FRA10AC1	10	0.0157	0.00609
FUT10	8	0.00783	0.00859
ALDH16A1	19	0.0109	0.008632
RP11-722E23.2	8	0.00919	0.01002
VNN2	6	0.01487	0.011442
RP11-611E13.2	12	0.01457	0.01457
COG4	16	0.0347	0.014647
RP11-666A8.9	17	0.00606	0.01541
ST6GALNAC2	17	0.02948	0.0186
SIGLEC14	19	0.0138	0.019017
RP11-797A18.6	15	0.0148	0.01965
GOLGA6L4	15	0.0124	0.02
ADH5	4	0.0258	0.02013
LRRFIP2	3	0.030587	0.0216
PPM1F	22	0.00869	0.02545
BRK1	3	0.032121	0.02795
RP11-449P15.2	7	0.0044	0.02884
LL22NC03-86G7.1	22	0.00142	0.0315
AC091729.9	7	0.02846	0.03214
SLC22A18	11	0.03645	0.032242
ACTR1B	2	0.0327	0.03900
STARD10	11	0.03582	0.039324
EPHB4	7	0.00531	0.04092
RP13-582O9.5	8	0.02667	0.04095
DBF4B	17	0.03174	0.04723
MGMT	10	0.0232	0.04757
NT5C3B	17	0.02841	0.0481

CHR, chromosome localization; TWAS, transcriptome-wide association study.