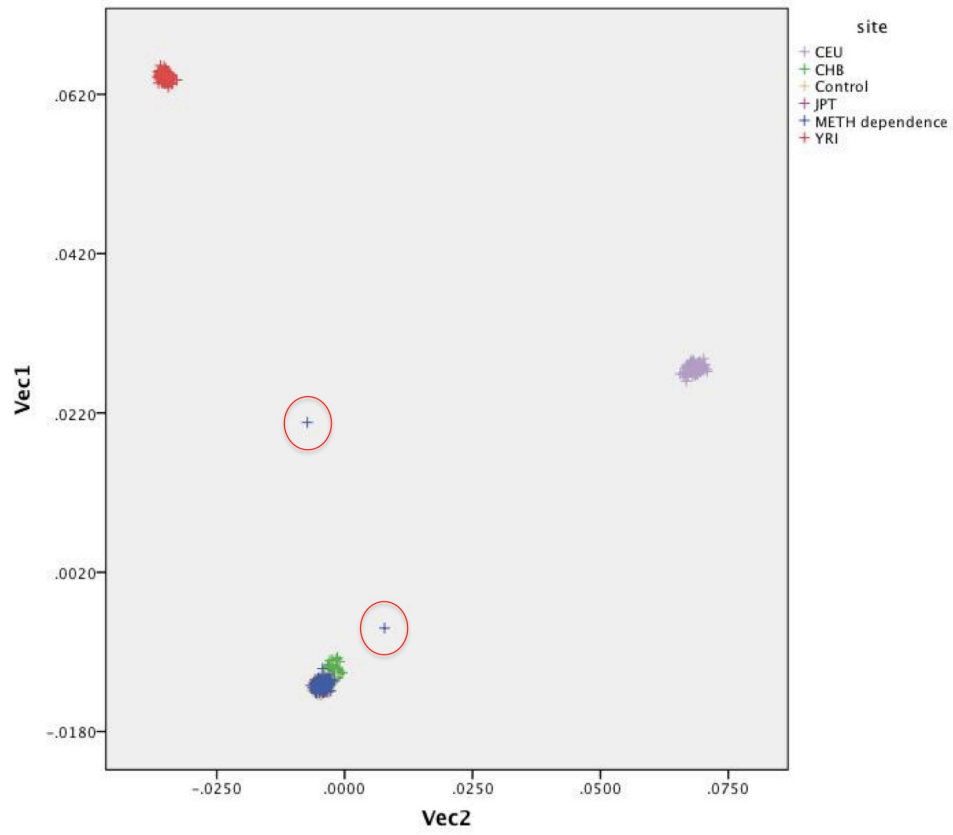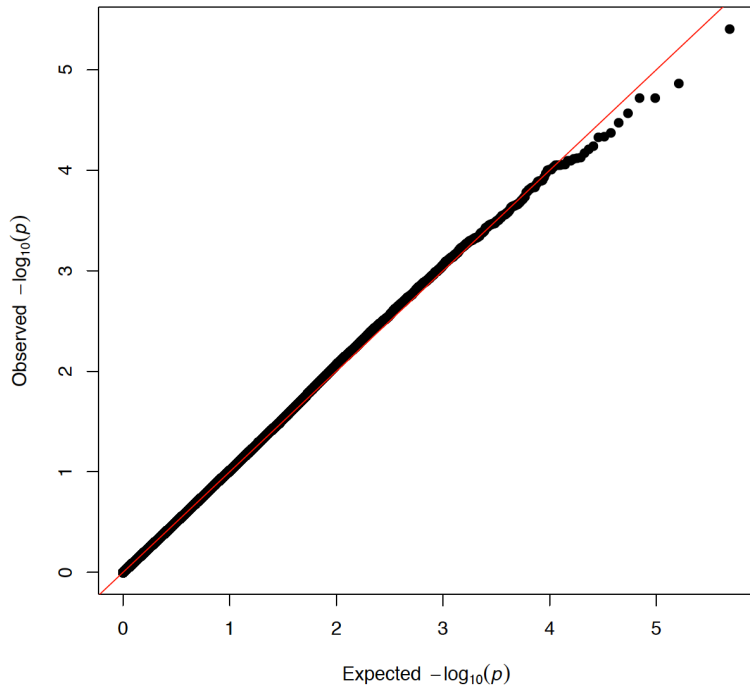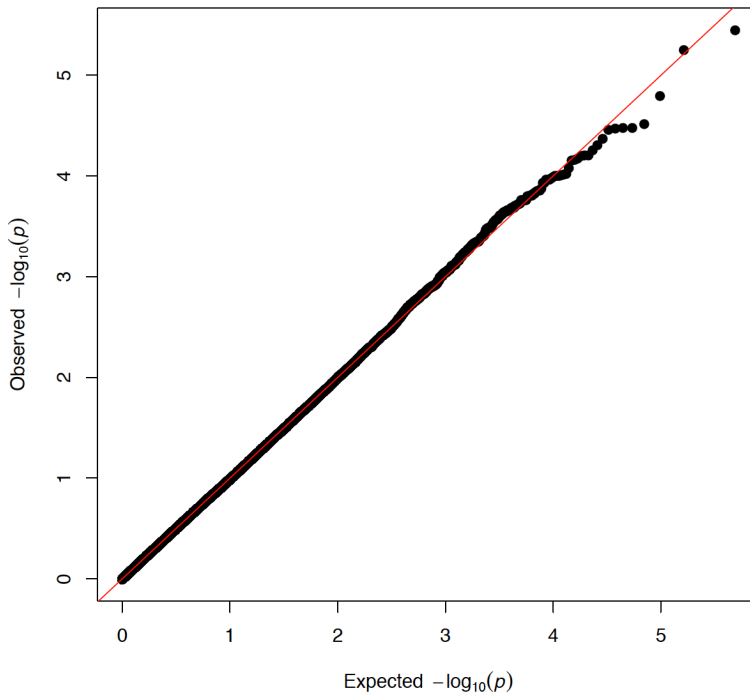Supplementary material

Evidence for shared genetic risk between

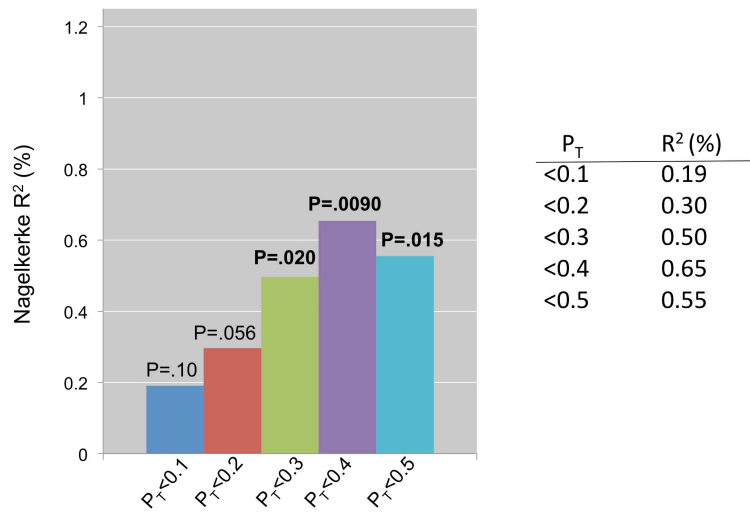methamphetamine-induced psychosis and schizophrenia

FigureS1. Principal Component analysis: Scatter plot of Eigenvectors 1&2

Red circles represents outliers

Supplementary FigureS2: QQ plot of METH-dependence GWAS (λ=1.024)

Supplementary FigureS3: QQ plot of METH-induced psychosis GWAS (λ=1.016)

P_T	R^2 (%)
<0.1	0.19
<0.2	0.30
<0.3	0.50
<0.4	0.65
<0.5	0.55

Supplementary FigureS4: Polygenic component analysis for the pairs of METH-induced psychosis/schizophrenia

Discovery: METH-induced psychosis vs METH non-psychosis

Target: Schizophrenia vs healthy controls

P_T	R^2 (%)
<0.1	0.0024
<0.2	0.24
<0.3	0.73
<0.4	0.93
<0.5	1.2
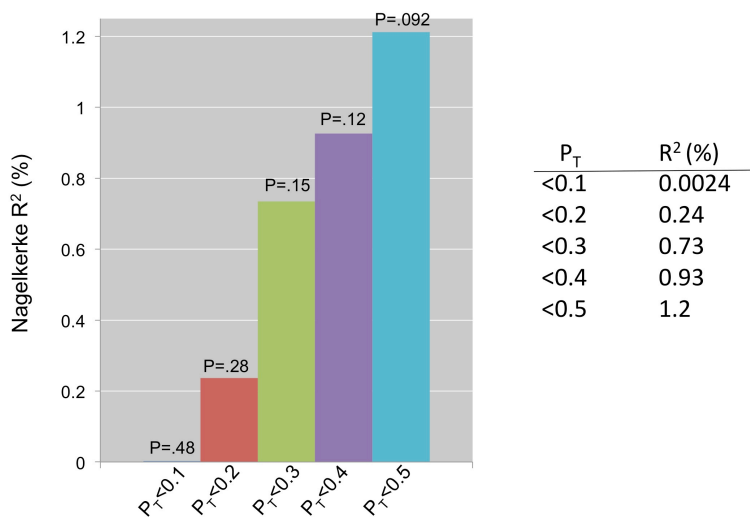
Supplementary FigureS5: Polygenic component analysis for the pairs of schizophrenia/ METH-induced psychosis

Discovery: Schizophrenia vs healthy controls

Target: METH-induced psychosis vs METH non-psychosis

P_T	R^2 (%)
<0.1	1.1
<0.2	1.8
<0.3	1.3
<0.4	1.5
<0.5	1.5

Supplementary FigureS6: Polygenic component analysis for the pairs of METH-dependence/METH-induced psychosis

Discovery: METH dependence vs healthy control

Target: METH-induced psychosis vs METH non-psychosis

(NOTE: Scale of Y axis is different from other figures)

P_T	R^2 (%)
<0.1	0.0064
<0.2	0.14
<0.3	0.029
<0.4	0.051
<0.5	0.038
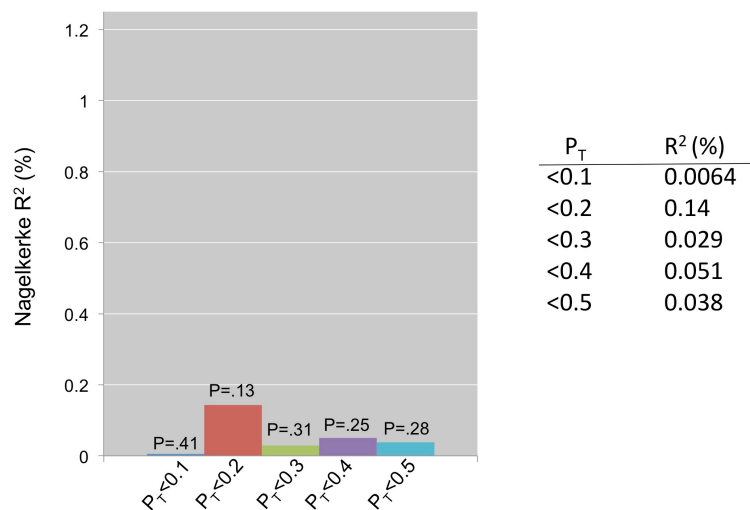
Supplementary FigureS7: Polygenic component analysis for the pairs of METH-dependence/schizophrenia

Discovery: METH dependence vs healthy control

Target: Schizophrenia vs healthy controls

P_T	R^2 (%)
<0.1	0.0015
<0.2	0.0059
<0.3	0.00081
<0.4	0.00013
<0.5	0.00041
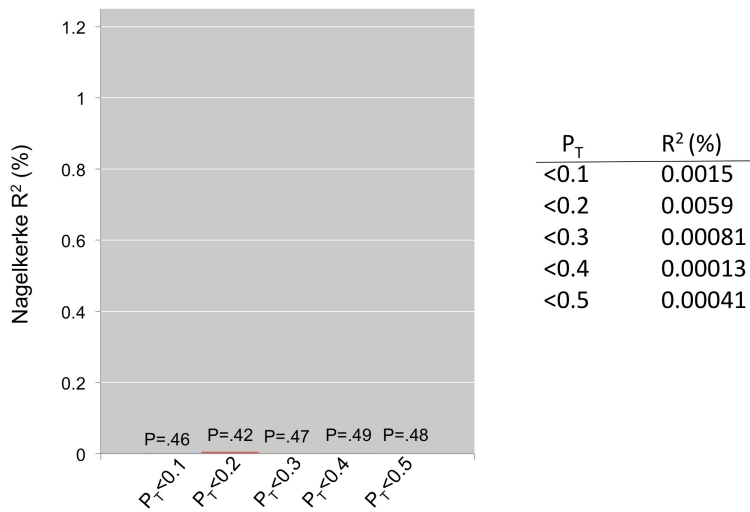
Supplementary FigureS8: Polygenic component analysis for the pairs of METH-induced psychosis/METH-dependence

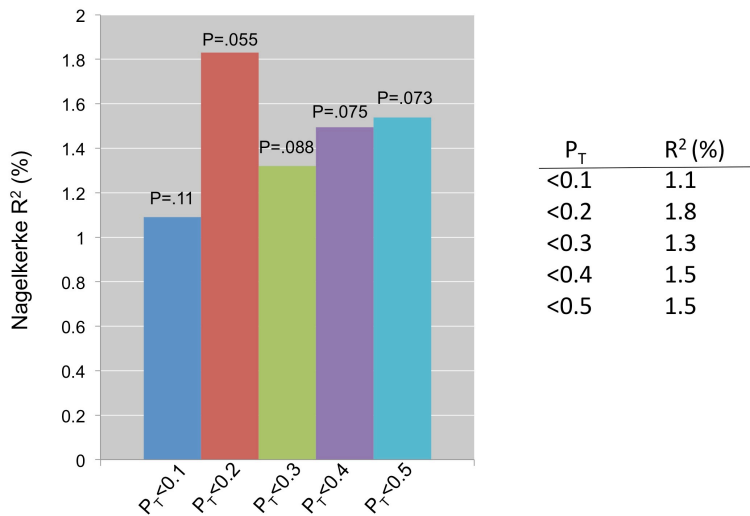Discovery: METH-induced psychosis vs METH non-psychosis

Target: METH dependence vs healthy control

P_T	R^2 (%)
<0.1	0.066
<0.2	0.016
<0.3	0.042
<0.4	0.011
<0.5	0.015
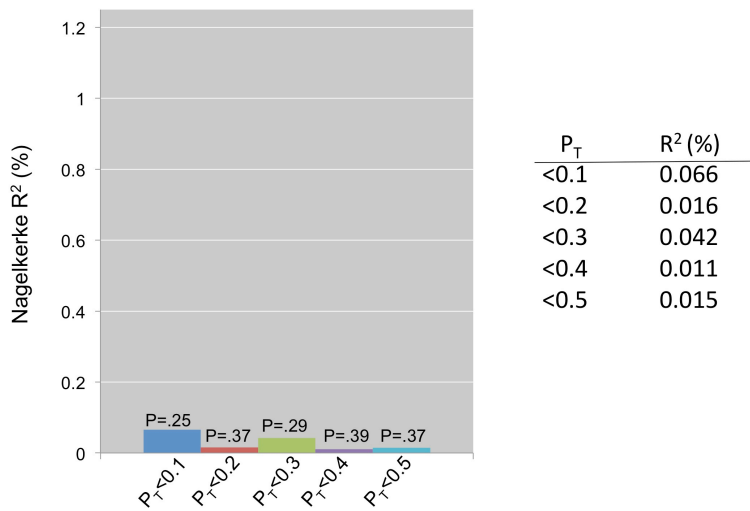
Supplementary FigureS9: Polygenic component analysis for the pairs of schizophrenia/ METH-dependence

Discovery: Schizophrenia vs healthy controls

Target: METH dependence vs healthy control

P_T	R^2 (%)
<0.1	0.19
<0.2	0.27
<0.3	0.38
<0.4	0.62
<0.5	0.54
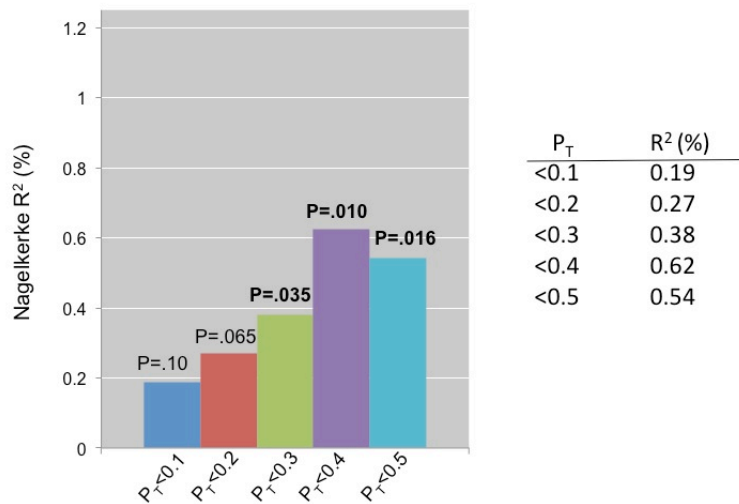
Supplementary FigureS10: Polygenic component analysis for the pairs of METH-induced psychosis/schizophrenia with adjustment of principle component (first 4 components) in the discovery statistics

Discovery: METH-induced psychosis vs METH non-psychosis

Target: Schizophrenia vs healthy controls

P_T	R^2 (%)
<0.1	0.40
<0.2	0.29
<0.3	0.46
<0.4	0.56
<0.5	0.62
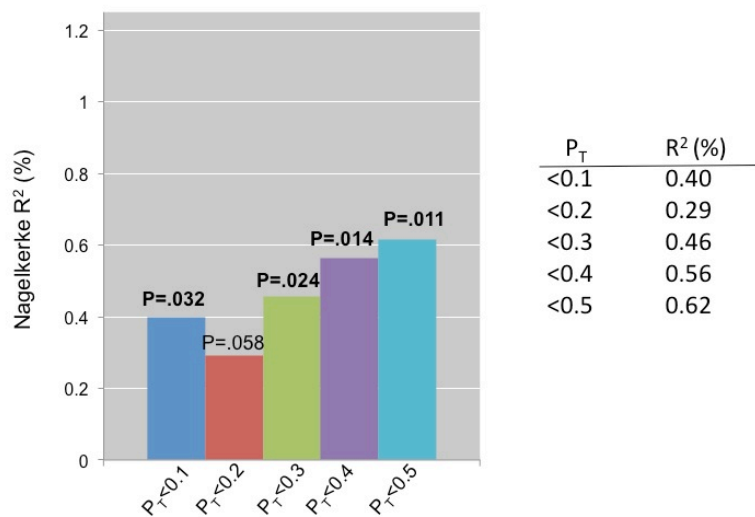
Supplementary FigureS11: Polygenic component analysis for the pairs of METH-induced psychosis/schizophrenia with covariating gender in the discovery statistics

Discovery: METH-induced psychosis vs METH non-psychosis

Target: Schizophrenia vs healthy controls

SNP	rank	CHR[a]	BP[b]	A1[c]	F[d] of A1 in case	F[d] of A1 in 'control'	A2[e]	OR[f]	P_GC[g]	Gene[h]	SNP type	Closest Gene[i]	left_gene	right_gene
rs4427170	1	8	14853781	T	0.515	0.3947	A	1.629	3.9E-06	SGCZ	intron		MIR383	TUSC3
rs7826857	2	8	99436341	A	0.08079	0.1624	G	0.4533	1.4E-05	NA	NA	KCNS2	LOC100131849	KCNS2
rs12894058	3	14	33532016	A	0.2222	0.14	G	1.754	1.9E-05	NPAS3	intron		AKAP6	EGLN3
rs2326193	4	8	120029709	A	0.3376	0.2386	C	1.627	1.9E-05	NA	NA	NA	LOC100286746	COLEC10
rs4915748	5	1	61954169	T	0.1496	0.2416	C	0.5521	2.7E-05	NA	NA	NA	NFIA	MGC34796
rs617231	6	11	84837898	C	0.1309	0.07035	T	1.99	3.4E-05	DLG2	intron		LOC100421794	LOC100419092
rs6022102	7	20	51425077	C	0.2094	0.1325	T	1.734	4.2E-05	NA	NA	NA	TRNAI30P	RPL36P1
rs6940190	8	6	148644731	A	0.2799	0.3831	T	0.626	4.6E-05	NA	NA	SASH1	SAMD5	SASH1
rs2416305	9	5	112483604	G	0.197	0.2933	A	0.591	4.7E-05	MCC	intron		DCP2	YTHDC2
rs17111695	10	5	150432446	C	0.1859	0.1145	T	1.765	5.7E-05	TNIP1	intron		GPX3	ANXA6
rs10070761	11	5	148774984	T	0.1731	0.2639	C	0.5838	6.2E-05	NA	NA	IL17B	IL17B	MIR147
rs11225508	12	11	97097033	T	0.1816	0.1117	C	1.765	6.7E-05	NA	NA	NA	LOC100131233	LOC100289416
rs12202025	13	6	79945057	G	0.1453	0.08353	T	1.865	7.4E-05	LOC100288198	NA		HMGN3	LOC100131959
rs6060163	14	20	33611738	T	0.2521	0.1705	C	1.64	7.5E-05	TRPC4AP	intron		MYH7B	EDEM2
rs6076036	15	20	23173497	G	0.1738	0.2636	T	0.5877	7.7E-05	NA	NA	LOC100505664	LOC100505664	NXT1
rs12811063	16	12	81440720	C	0.3462	0.2535	G	1.559	8E-05	NA	NA	NA	LIN7A	ACSS3
rs10506839	17	12	81445603	G	0.3462	0.2535	A	1.559	8E-05	NA	NA	NA	LIN7A	ACSS3
rs6432978	18	2	167989231	T	0.1385	0.07855	A	1.886	8.8E-05	XIRP2	intron		SCN7A	LOC100996260
rs254230	19	5	115885858	T	0.4145	0.518	C	0.6589	8.8E-05	SEMA6A	intron		COMMD10	RPS14P8
rs11856426	20	15	99175000	G	0.5662	0.4629	A	1.515	8.9E-05	NA	NA	IGF1R	FAM169B	IGF1R
rs16955219	21	18	45108497	G	0.3476	0.2552	A	1.555	8.9E-05	NA	NA	NA	MIR4527	TPMTP1
rs6088677	22	20	33607464	C	0.2521	0.1713	T	1.631	8.9E-05	TRPC4AP	intron		MYH7B	EDEM2
rs382004	23	21	20304155	G	0.08547	0.04051	A	2.214	9.3E-05	NA	NA	NA	PPIAP22	SLC6A6P
rs7844579	24	8	19748603	C	0.3312	0.4323	T	0.6503	9.8E-05	NA	NA	NA	INTS10	LPL
rs10989456	25	9	104011196	C	0.2771	0.376	T	0.6359	9.9E-05	LPPR1	intron		LOC100422500	BAATP1
rs12327437	26	18	45117529	C	0.3526	0.2604	A	1.547	1E-04	NA	NA	NA	MIR4527	TPMTP1
rs10501586	27	11	84756077	C	0.1218	0.06678	T	1.938	0.00011	DLG2	intron		LOC100421794	LOC100419092
rs7822518	28	8	19748856	C	0.3355	0.4356	T	0.6541	0.00012	NA	NA	NA	INTS10	LPL
rs6764198	29	3	62117185	G	0.3333	0.2442	T	1.547	0.00012	PTPRG	intron		ID2B	LOC100506994
rs7677817	30	4	96763977	C	0.1645	0.1002	T	1.768	0.00013	NA	NA	PDHA2	PDHA2	LOC100418701
rs7236339	31	18	77579773	A	0.1923	0.1227	G	1.703	0.00013	NA	NA	NA	CTDP1	KCNG2
rs1816366	32	9	103989475	T	0.3312	0.4305	C	0.6552	0.00013	LPPR1	intron		LOC100422500	BAATP1
rs2009141	33	4	173756533	C	0.03205	0.08449	G	0.3588	0.00014	GALNT6	intron		LOC100506133	GALNT7
rs2416306	34	5	112483932	A	0.2073	0.297	G	0.6189	0.00015	MCC	intron		DCP2	YTHDC2
rs34984260	35	7	114947770	G	0.513	0.4132	A	1.496	0.00015	NA	NA	NA	RAC1P6	TFEC
rs3825490	36	13	111117984	T	0.221	0.3124	C	0.6247	0.00015	COL4A2	intron		COL4A1	RAB20
rs16852911	37	4	41205654	T	0.07692	0.1443	A	0.4942	0.00015	APBB2	intron		NSUN7	UCHL1
rs17310782	38	20	33565665	T	0.25	0.1719	C	1.606	0.00015	MYH7B	intron		GSS	TRPC4AP
rs41443246	39	4	137943051	T	0.1073	0.05699	C	1.989	0.00016	NA	intron		TRRF1P3	SERF1AP1
rs6083037	40	20	23182559	T	0.1752	0.2605	A	0.6032	0.00016	NA	NA	NA	CD93	NXT1
rs4649307	41	1	233513117	T	0.3043	0.4016	A	0.6518	0.00016	KIAA1804	intron		PCNXL2	KCNK1
rs11158089	42	14	56783688	G	0.4979	0.4005	T	1.484	0.00018	NA	NA	PELI2	PELI2	C14orf101
rs17469669	43	2	140955729	T	0.4295	0.3351	C	1.494	0.00018	NA	NA	NA	RPL9P13	MTND2P19
rs1485283	44	8	120001663	T	0.1278	0.2059	C	0.5648	0.00019	NA	NA	LOC100286746	LOC100286746	COLEC10
rs17054037	45	8	25481787	C	0.2372	0.162	G	1.608	0.0002	NA	NA	NA	CDCA2	EBF2
rs1327126	46	1	115973920	T	0.4573	0.3619	C	1.485	0.0002	NA	NA	NA	NGF	TCEB1P20
rs11668252	47	19	16072153	T	0.4893	0.3929	G	1.48	0.00021	NA	NA	OR10H4	OR10H4	LOC100996403
rs2295701	48	20	33596117	G	0.2511	0.1741	C	1.59	0.00021	TRPC4AP	intron		MYH7B	EDEM2
rs3734369	49	6	71569129	T	0.4849	0.3886	C	1.481	0.00022	SMAP1	intron		LOC100419975	B3GAT2
rs4944507	50	11	84783389	T	0.1047	0.05613	G	1.966	0.00022	DLG2	intron		LOC100421794	LOC100419092
rs2828970	51	21	25671052	T	0.3269	0.4225	C	0.664	0.00022	NA	NA	NA	VN2R20P	LOC100419737
rs1598570	52	4	96789975	A	0.1609	0.0993	G	1.74	0.00022	NA	NA	NA	PDHA2	LOC100418701
rs891140	53	16	57055714	C	0.3391	0.252	A	1.523	0.00023	NLRC5	intron		LOC100130044	CPNE2
rs641655	54	11	84775335	C	0.1379	0.08121	T	1.81	0.00023	DLG2	intron		LOC100421794	LOC100419092
rs964038	55	2	140950689	T	0.1695	0.252	G	0.6058	0.00023	NA	NA	NA	RPL9P13	MTND2P19
rs1025445	56	2	222169464	G	0.3761	0.4728	C	0.6721	0.00023	NA	NA	NA	MIR4268	EPHA4
rs902891	57	12	129978517	C	0.3376	0.2514	T	1.517	0.00023	TMEM132D	intron		TRNAI29P	FZD10
rs16920100	58	9	104024328	C	0.2778	0.3701	T	0.6547	0.00025	LPPR1	intron		LOC100422500	BAATP1
rs4584622	59	12	72672823	C	0.04274	0.09664	T	0.4173	0.00025	TRHDE	intron	TRHDE-AS1	TRHDE-AS1	LOC100422354
rs555259	60	11	84761929	T	0.1261	0.07259	A	1.843	0.00026	DLG2	intron		LOC100421794	LOC100419092
rs542892	61	11	84791038	G	0.1111	0.06134	A	1.913	0.00026	DLG2	NA		LOC100421794	LOC100419092
rs16958320	62	17	9376028	G	0.2382	0.1641	T	1.592	0.00027	STX8	intron		NTN1	WDR16
rs17049438	63	3	8710790	G	0.08547	0.04282	C	2.089	0.00027	NA	NA	C3orf32	C3orf32	OR7E122P
rs17067210	64	13	77686033	C	0.1731	0.11	T	1.694	0.00027	MYCBP2	intron		FBXL3	SCEL
rs4941375	65	18	55944135	C	0.2115	0.2977	A	0.633	0.00027	NEDD4L	intron		HMGN1P30	MIR122
rs16972470	66	15	42312142	T	0.04405	0.09894	C	0.4197	0.00028	PLA2G4E	intron		EHD4	PLA2G4D
rs7237852	67	18	7171101	A	0.188	0.2714	G	0.6217	0.00028	NA	NA	NA	SLC25A51P2	LRRC30
rs2196515	68	4	96685664	C	0.4722	0.3785	A	1.469	0.00028	NA	NA	NA	RPL30P6	PDHA2
rs2643338	69	8	97247469	G	0.3889	0.2997	A	1.487	0.00028	UQCRB	intron		GDF6	MTERFD1
rs515867	70	11	63214549	T	0.2393	0.1657	C	1.584	0.00029	NA	NA	HRASLS5	SLC22A9	HRASLS5
rs1894209	71	11	97100891	G	0.1987	0.1314	C	1.64	0.0003	NA	NA	NA	LOC100131233	LOC100289416
rs11028374	72	11	3618417	T	0.1545	0.09524	A	1.736	0.0003	NA	NA	OR7E117P	LOC100132021	OR7E117P
rs11623641	73	14	56750158	G	0.4145	0.3241	C	1.477	0.0003	PELI2	intron		LINC00520	C14orf101
rs2136665	74	16	84122206	A	0.1303	0.07648	T	1.81	0.00031	MBTPS1	intron		SLC38A8	RMST
rs10777875	75	12	97916146	A	0.2927	0.3843	G	0.6632	0.00031	RMST	NA		MIR1251	MIR135A2
rs17155006	76	7	107757843	C	0.5022	0.4079	T	1.464	0.00032	LAMB4	intron		LAMB1	NRCAM
rs34855831	77	4	62728124	T	0.4274	0.3364	C	1.472	0.00032	LPHN3	intron		RPS12P9	RPS15AP17
rs6022097	78	20	51415335	G	0.2137	0.1443	A	1.612	0.00032	NA	NA	NA	TRNAI30P	RPL36P1
rs7141728	79	14	34239296	A	0.3333	0.2494	C	1.505	0.00032	NPAS3	intron		AKAP6	EGLN3
rs11152064	80	18	55954081	C	0.2103	0.2951	T	0.636	0.00033	NEDD4L	intron		HMGN1P30	MIR122
rs6088660	81	20	33542896	T	0.2457	0.1719	C	1.57	0.00033	GSS	intron		ACSS2	MYH7B
rs9916292	82	17	9336658	G	0.1368	0.08169	A	1.781	0.00034	STX8	intron		NTN1	WDR16
rs12040431	83	1	61935306	T	0.3133	0.4056	C	0.6686	0.00034	NA	NA	NFIA	NFIA	MGC34796
rs4741904	84	9	4176178	C	0.2179	0.3032	T	0.6403	0.00034	GLIS3	intron		RFX3	SLC1A1
rs9891309	85	17	18814976	T	0.08547	0.04333	C	2.064	0.00034	PRPSAP2	intron		LOC100419620	SLC5A10
rs17091651	86	8	19749883	T	0.2661	0.3556	A	0.6569	0.00034	NA	NA	NA	INTS10	LPL
rs1908786	87	15	86866875	A	0.3846	0.2969	G	1.48	0.00034	AGBL1	intron		LOC727915	LINC00052
rs7814519	88	8	14862125	C	0.3355	0.2517	G	1.501	0.00035	SGCZ	intron		MIR383	TUSC3
rs17140021	89	5	115855201	T	0.1453	0.08854	A	1.75	0.00035	SEMA6A	intron		COMMD10	RPS14P8
rs7263251	90	20	33554320	C	0.2468	0.1729	T	1.568	0.00035	MYH7B	intron		GSS	TRPC4AP
rs10094191	91	8	15411367	T	0.3226	0.2401	C	1.508	0.00035	TUSC3	intron		SGCZ	LOC100431174
rs17808941	92	17	9331007	A	0.1068	0.05903	C	1.907	0.00036	STX8	intron		NTN1	WDR16
rs7460113	93	8	17297693	G	0.5726	0.4786	C	1.46	0.00036	NA	NA	NA	MTMR7	SLC7A2
rs10888095	94	8	14862414	A	0.3355	0.252	C	1.498	0.00037	SGCZ	intron		MIR383	TUSC3
rs906319	95	6	79520689	A	0.07479	0.1366	G	0.511	0.00037	NA	NA	NA	RPS6P7	IRAK1BP1
rs6698922	96	1	23073167	G	0.1624	0.1024	A	1.699	0.00037	EPHB2	intron		MIR4684	MIR4253
rs4646344	97	17	17492060	G	0.05342	0.109	A	0.4611	0.00037	PEMT	intron		RASD1	RAI1
rs1832413	98	6	101873533	A	0.109	0.06076	G	1.89	0.00037	GRIK2	intron		LOC728098	LOC100418924
rs1572203	99	10	45010936	G	0.5043	0.4115	A	1.455	0.00038	NA	NA	NA	RPL9P21	EIF2AP4
rs12138574	100	1	56790773	T	0.06838	0.128	C	0.4998	0.0004	NA	NA	NA	RPSAP20	PPAP2B

Table S1: Top 100 in METH dependence GWAS
a: CHR: Chromosome
b: BP: base position based upon hg19
c: A1: minor allele name based upon whole sample
d: F: Frequency
e: A2: major allele name
f: OR: odds ratio (for A1: A2 is reference)
g: P_{GC}: P-value adjusted Genomic control (two-sided)
h: Gene name
i: gene (+/-20kb)

SNP	rank	CHR[a]	BP[b]	A1[c]	F[d] of A1 in case	F[d] of A1 in control	A2[e]	OR[f]	P_GC[g]	Gene[h]	SNP type	Closest Gene[i]	left_gene	right_gene
rs12591257	1	15	87064089	C	0.04145	0.1829	A	0.1932	3.6E-06	AGBL1	intron		KLHL25	LINC00052
rs2346713	2	15	87078337	C	0.06736	0.2317	A	0.2395	5.6E-06	AGBL1	intron		KLHL25	LINC00052
rs16977267	3	15	86993464	T	0.07254	0.2317	G	0.2593	1.6E-05	AGBL1	intron		KLHL25	LINC00052
rs13414154	4	2	129012073	A	0.1451	0.3415	G	0.3273	3.1E-05	NA	NA	HS6ST1	UGCGL1	HS6ST1
rs6767236	5	3	143758399	G	0.1891	0.4024	T	0.3463	3.3E-05	NA	NA	NA	C3orf58	LOC100421509
rs6091985	6	20	53445939	C	0.04404	0.1707	G	0.2238	3.3E-05	NA	NA	NA	DOK5	RPL12P4
rs7333069	7	13	82458858	A	0.3938	0.6463	C	0.3554	3.4E-05	NA	NA	NA	HIGD1AP2	GYG1P2
rs8026683	8	15	86825255	A	0.09845	0.2683	C	0.2978	3.5E-05	AGBL1	intron		KLHL25	LINC00052
rs6064117	9	20	53458592	G	0.04663	0.175	A	0.2306	4.2E-05	NA	NA	NA	DOK5	CBLN4
rs2768428	10	10	12523129	T	0.05181	0.1829	C	0.2441	4.9E-05	CAMK1D	intron		CDC123	CCDC3
rs12605879	11	18	67365926	A	0.4237	0.1829	G	3.284	5.5E-05	DOK6	intron		CCDC102B	CD226
rs6023649	12	20	53470583	A	0.04663	0.1707	G	0.2376	6.2E-05	NA	NA	NA	DOK5	CBLN4
rs17314203	13	4	162158922	T	0.2824	0.5122	C	0.3748	6.2E-05	NA	NA	NA	RPS14P7	FSTL5
rs11245346	14	10	126425537	C	0.1736	0.375	G	0.3501	6.3E-05	FAM53B	intron		LHPP	METTL10
rs7239623	15	18	8484922	A	0.2581	0.4872	G	0.3661	6.7E-05	NA	NA	NA	PTPRM	LOC100420484
rs4965381	16	15	101932462	A	0.4508	0.6951	G	0.36	6.8E-05	PCSK6	intron		LOC100507472	LOC100289564
rs4426448	17	18	67365668	A	0.4197	0.1829	G	3.23	7E-05	DOK6	intron		CCDC102B	CD226
rs7185087	18	16	6055190	T	0.2073	0.4146	C	0.3691	8.3E-05	NA	NA	RBFOX1	LOC100287538	RBFOX1
rs3780260	19	9	134522471	A	0.1458	0.3293	G	0.3478	9.4E-05	RAPGEF1	intron		UCK1	EIF4A1P3
rs9668269	20	12	65680026	T	0.1684	0.3625	C	0.3561	9.6E-05	MSRB3	intron		LEMD3	LOC100507065
rs9542732	21	13	72247171	C	0.228	0.439	G	0.3773	9.8E-05	DACH1	intron		RABEPKP1	RPS10P21
rs940281	22	8	111278308	A	0.1295	0.3049	T	0.3393	9.8E-05	NA	NA	NA	RPSAP48	LOC100132280
rs10505143	23	8	111280576	C	0.1295	0.3049	T	0.3393	9.8E-05	NA	NA	NA	RPSAP48	LOC100132280
rs17314252	24	4	162159122	T	0.2775	0.5	G	0.3841	9.9E-05	NA	NA	NA	RPS14P7	FSTL5
rs3923952	25	8	135398062	A	0.3523	0.5854	C	0.3853	0.0001	NA	NA	NA	LOC100419617	ZFAT
rs12477752	26	2	215928091	C	0.2682	0.4878	T	0.3849	0.00011	ABCA12	intron		BARD1	ATIC
rs1879873	27	7	68738072	C	0.09845	0.2561	T	0.3172	0.00011	NA	NA	NA	MTND4P3	AUTS2
rs17107371	28	14	38426837	T	0.09845	0.2561	A	0.3172	0.00011	NA	NA	NA	LOC100652860	SSTR1
rs17107373	29	14	38426891	A	0.09845	0.2561	C	0.3172	0.00011	NA	NA	NA	LOC100652860	SSTR1
rs1898265	30	3	143776096	A	0.2202	0.4268	G	0.3792	0.00012	NA	NA	NA	C3orf58	LOC100421509
rs4673939	31	2	215936259	A	0.2694	0.4878	C	0.3872	0.00012	ABCA12	intron		BARD1	ATIC
rs17314364	32	4	162159479	A	0.2812	0.5	G	0.3913	0.00013	NA	NA	NA	RPS14P7	FSTL5
rs12683131	33	9	134538406	A	0.1451	0.325	G	0.3524	0.00014	RAPGEF1	intron		UCK1	EIF4A1P3
rs17117757	34	14	83438398	T	0.1667	0.3537	C	0.3655	0.00014	NA	NA	NA	ENSAP2	RNU7-51P
rs10800476	35	1	169751853	T	0.07772	0.2195	C	0.2996	0.00014	NA	NA	METTL18	SELE	METTL18
rs7073663	36	10	126358094	A	0.1943	0.3902	G	0.3768	0.00014	FAM53B	intron		LHPP	METTL10
rs11138359	37	9	82415788	C	0.4145	0.6463	T	0.3874	0.00015	NA	NA	NA	TLE4	LOC100533675
rs16977283	38	15	86996860	C	0.2682	0.4872	T	0.3858	0.00015	AGBL1	intron		KLHL25	LINC00052
rs17115667	39	14	45333584	C	0.1088	0.2683	T	0.333	0.00016	DOCK11P1	NA		FSCB	LOC401770
rs8011828	40	14	45337702	G	0.1088	0.2683	A	0.333	0.00016	NA	NA	DOCK11P1	DOCK11P1	LOC401770
rs17115674	41	14	45339443	C	0.1088	0.2683	T	0.333	0.00016	NA	NA	DOCK11P1	DOCK11P1	LOC401770
rs10064443	42	5	180136233	C	0.101	0.2561	T	0.3265	0.00016	NA	NA	OR2AI1P	OR2AI1P	OR2Y1
rs17107386	43	14	38441430	C	0.101	0.2561	T	0.3265	0.00016	NA	NA	NA	LOC100652860	SSTR1
rs747808	44	1	216157829	G	0.03886	0.1463	A	0.2358	0.00017	USH2A	intron		KCTD3	MRPS18BP1
rs707741	45	9	79240450	G	0.03886	0.1463	A	0.2358	0.00017	PRUNE2	intron		LOC392352	LOC100421411
rs11034368	46	11	4880892	C	0.03886	0.1463	T	0.2358	0.00017	NA	NA	OR51H1P	OR51S1	OR51H1P
rs17250577	47	11	4883396	G	0.03886	0.1463	C	0.2358	0.00017	NA	NA	OR51H1P	OR51H1P	OR51H2P
rs12923113	48	16	49614518	G	0.3161	0.5366	A	0.3991	0.00017	ZNF423	intron		ADAM3B	MRPS21P7
rs12445187	49	16	49615387	C	0.3161	0.5366	T	0.3991	0.00017	ZNF423	intron		ADAM3B	MRPS21P7
rs12439060	50	15	87050430	G	0.2448	0.4512	A	0.3942	0.00018	AGBL1	intron		KLHL25	LINC00052
rs2988677	51	6	86962565	G	0.06736	0.2	A	0.2889	0.00019	NA	NA	NA	LOC100289579	LOC100652960
rs17472290	52	7	33131424	A	0.3717	0.5976	G	0.3985	0.00019	NA	NA	RP9	NT5C3	RP9
rs4917818	53	10	100092168	G	0.2552	0.4634	A	0.3968	0.00019	NA	NA	NA	LOXL4	PYROXD2
rs4527375	54	3	143735515	T	0.2161	0.4146	A	0.3893	0.00019	NA	NA	NA	C3orf58	LOC100421509
rs17032625	55	3	35077009	T	0.2358	0.439	C	0.3942	0.0002	NA	NA	NA	FECHP	KRT8P18
rs13154022	56	5	57415978	A	0.1269	0.2927	C	0.3514	0.0002	NA	NA	NA	LOC100996645	PGAM1P1
rs4785326	57	16	49615587	C	0.329	0.5488	T	0.4032	0.0002	ZNF423	intron		ADAM3B	MRPS21P7
rs12686345	58	9	134538386	T	0.1484	0.325	A	0.362	0.0002	RAPGEF1	intron		UCK1	EIF4A1P3
rs12443065	59	15	87050351	T	0.2461	0.4512	C	0.397	0.0002	AGBL1	intron		KLHL25	LINC00052
rs4493016	60	15	87050994	T	0.2461	0.4512	C	0.397	0.0002	AGBL1	intron		KLHL25	LINC00052
rs41356944	61	14	38468593	T	0.1192	0.2805	C	0.3471	0.00021	NA	NA	NA	LOC100652860	SSTR1
rs82648	62	18	34256668	A	0.4688	0.2439	G	2.735	0.00022	FHOD3	intron		LOC791126	TPGS2
rs4616638	63	3	143735423	A	0.2176	0.4146	T	0.3927	0.00022	NA	NA	NA	C3orf58	LOC100421509
rs7611326	64	3	143736374	A	0.2176	0.4146	G	0.3927	0.00022	NA	NA	NA	C3orf58	LOC100421509
rs1025984	65	3	143756187	G	0.2176	0.4146	C	0.3927	0.00022	NA	NA	NA	C3orf58	LOC100421509
rs9365334	66	6	162302398	G	0.2176	0.4146	C	0.3927	0.00022	PARK2	intron		AGPAT4	KRT8P44
rs10968301	67	9	28043906	C	0.0544	0.175	T	0.2712	0.00022	LINGO2	intron		CTAGE12P	LOC100421194
rs1564935	68	2	134847518	T	0.1036	0.2561	C	0.3358	0.00022	NA	NA	NA	NCKAP5	MIR3679
rs11836915	69	12	46912752	A	0.09585	0.2439	G	0.3287	0.00023	LOC100288798	intron		SLC38A2	OR7A19P
rs10956757	70	8	135385238	G	0.3523	0.5732	T	0.4051	0.00023	NA	NA	NA	LOC100419617	ZFAT
rs7836091	71	8	135388625	G	0.3523	0.5732	T	0.4051	0.00023	NA	NA	NA	LOC100129104	ZFAT
rs9459684	72	21	17100275	T	0.1702	0.0122	C	16.61	0.00023	NA	NA	USP25	RAD23BLP	USP25
rs41341253	73	13	108019412	T	0.3756	0.6	A	0.4011	0.00024	FAM155A	intron		PPIAP24	LIG4
rs10245553	74	7	33133742	C	0.3756	0.5976	T	0.4052	0.00024	NA	intron	RP9	NT5C3	RP9
rs7112865	75	11	45326538	G	0.1632	0.3415	A	0.3762	0.00024	NA	NA	SYT13	SYT13	FLJ41423
rs4887475	76	15	87053559	A	0.2383	0.439	T	0.3998	0.00024	AGBL1	intron		KLHL25	LINC00052
rs289572	77	8	13255926	C	0.1813	0.3659	G	0.384	0.00024	DLC1	intron		KIAA1456	C8orf48
rs4708688	78	6	168595919	C	0.4585	0.6829	A	0.3932	0.00026	NA	NA	NA	FRMD1	CTAGE13P
rs11000445	79	10	74672399	C	0.2098	0.4024	T	0.3943	0.00026	OIT3	intron		MCU	LOC100422312
rs2288975	80	7	132114617	G	0.2005	0.3902	A	0.3919	0.00026	PLXNA4	intron		LOC100533635	LOC100506937
rs11000413	81	10	74541864	G	0.1295	0.2927	A	0.3596	0.00027	MCU	intron		MICU	OIT3
rs9932030	82	16	74089082	G	0.2435	0.06098	A	4.958	0.00027	NA	NA	NA	RPSAP56	LOC100996503
rs3097778	83	5	150938507	A	0.1554	0.3293	G	0.3749	0.00027	FAT2	intron		SLC36A1	SPARC
rs2072134	84	12	113409176	A	0.1554	0.3293	G	0.3749	0.00027	OAS3	intron		OAS1	OAS2
rs4613453	85	3	143735600	G	0.2202	0.4146	C	0.3987	0.00027	NA	NA	NA	C3orf58	LOC100421509
rs1489123	86	7	118941365	C	0.1036	0.2564	T	0.3353	0.00028	NA	NA	NA	LOC648442	KCND2
rs9599058	87	13	66612121	C	0.5026	0.2805	A	2.592	0.00028	NA	NA	NA	MIR548X2	MIR4704
rs11771864	88	7	33138875	A	0.3782	0.5976	T	0.4097	0.00029	RP9	intron		NT5C3	BBS9
rs10163015	89	15	94781904	T	0.07513	0.2073	C	0.3106	0.0003	NA	NA	NA	LOC100996270	RPL26P5
rs7776898	90	7	132124470	C	0.2021	0.3902	T	0.3957	0.0003	PLXNA4	intron		LOC100533635	LOC100506937
rs3808518	91	8	11143272	G	0.3238	0.5366	T	0.4136	0.00031	MTMR9	intron		XKR6	SLC35G5
rs1701644	92	18	61447835	T	0.3237	0.5366	C	0.4133	0.00031	SERPINB7	intron		SERPINB11	SERPINB2
rs7742202	93	6	139074280	A	0.01862	0.09756	G	0.1755	0.00031	LOC100507462	intron		FLJ46906	CCDC28A
rs2326689	94	6	6021878	A	0.09067	0.2317	G	0.3306	0.00032	NA	NA	NRN1	NRN1	F13A1
rs4758423	95	11	6532519	T	0.09067	0.2317	A	0.3306	0.00032	DNHD1L	missence		LOC644169	RRP8
rs424872	96	2	147849192	C	0.2927	0.5	T	0.4139	0.00033	NA	NA	NA	PABPCP2	LOC100133235
rs3793602	97	9	23813023	C	0.2927	0.5	T	0.4139	0.00033	ELAVL2	intron		LOC402360	LOC100419692
rs6485602	98	11	45247238	T	0.3684	0.5854	A	0.4132	0.00033	PRDM11	intron		LOC100507338	SYT13
rs7512836	99	1	109052161	T	0.2824	0.4878	C	0.4132	0.00033	NA	NA	NA	LOC100420430	RPL26P14
rs1519320	100	4	186940136	A	0.3212	0.122	G	3.408	0.00033	NA	NA	NA	SORBS2	TLR3

Table S2: Top 100 in METH-induced psychosis GWAS
a: CHR: Chromosome
b: BP: base position based upon hg19
c: A1: minor allele name based upon whole sample
d: F: Frequency
e: A2: major allele name
f: OR: odds ratio (for A1: A2 is reference)
g: P_GC: P-value adjusted Genomic control (two-sided)
h: Gene name
i: gene (+/-20kb)

TableS3 Genes overlapping among METH-dependence, METH-induced psychosis and schizophrenia (SCZ)

1)

		METH-dependence		
		P<0.05	P≥0.05	total
METH-induced	P<0.05	55	804	859
Psychosis	P≥0.05	866	15,324	16,190
	total	921	16,128	17,049

(Hypergeometric P_{gene}=0.11)

2)

		SCZ		
		P<0.05	P≥0.05	total
METH-induced	P<0.05	67	792	859
Psychosis	P≥0.05	919	15,271	16,190
	total	986	16,063	17,049

(Hypergeometric P_{gene}=**0.0075**)

3)

		METH-dependence		
		P<0.05	P≥0.05	total
SCZ	P<0.05	58	928	986
	P≥0.05	863	15,200	16,063
	total	921	16,128	17,049

(Hypergeometric P_{gene}=0.27)

Gene-based analysis between
1) METH-dependence and METH-induced psychosis
2) METH-induced psychosis and SCZ
3) METH-dependence and SCZ

		METH-induced Psychosis				Schizophrenia			
Chr	Gene	N of SNPs	P value	Best SNP	SNP Pvalue	N of SNPs	P value	Best SNP	SNP Pvalue
1	C1orf156	11	0.00462	rs10800476	0.0001401	17	0.04248	rs12135656	0.0069
1	KIF26B	63	0.0461	rs2941280	0.004024	78	0.02109	rs6677662	0.003868
1	SAMD13	24	0.02728	rs172735	0.02473	29	0.0129	rs7528615	0.003198
2	ABCB6	6	0.03782	rs3731885	0.02143	7	0.00747	rs2385394	0.008777
2	ANKZF1	7	0.04723	rs3731885	0.02143	8	0.00876	rs2891733	0.003445
2	ATG9A	8	0.04496	rs3731885	0.02143	9	0.0058	rs2891733	0.003445
2	DNAJB2	4	0.03845	rs6723299	0.02425	6	0.03967	rs2891733	0.003445
2	GLB1L	7	0.0477	rs3731885	0.02143	8	0.01786	rs2891733	0.003445
2	PTPRN	5	0.04865	rs6723299	0.02425	9	0.03875	rs2891733	0.003445
2	STK16	7	0.04793	rs3731885	0.02143	8	0.0182	rs2891733	0.003445
2	TUBA4A	7	0.0479	rs3731885	0.02143	8	0.01842	rs2891733	0.003445
3	ARMET	5	0.00276	rs7633708	0.001194	8	0.01624	rs17712228	0.003692
3	C3orf18	5	0.01051	rs762889	0.004041	7	0.00629	rs12487817	0.003087
3	CISH	12	0.006	rs813243	0.002789	13	0.00758	rs616689	0.003018
3	DOCK3	41	0.00574	rs7633708	0.001194	60	0.01791	rs4346580	0.002578
3	GRM2	1	0.03126	rs4687773	0.03164	2	0.003627	rs4687773	0.003902
3	HEMK1	9	0.00545	rs813243	0.002789	10	0.00651	rs616689	0.003018
3	MAPKAPK3	14	0.00465	rs7615703	0.00264	15	0.01033	rs616689	0.003018
3	OSTalpha	4	0.04985	rs4916519	0.0259	5	0.00386	rs2342309	0.001115
3	PCYT1A	4	0.0471	rs4916519	0.0259	5	0.00481	rs2342309	0.001115
3	RAD54L2	3	0.00311	rs4494918	0.001146	6	0.01934	rs4687592	0.008201
3	RBM15B	5	0.0025	rs7633708	0.001194	7	0.02162	rs17712228	0.003692
3	TEX264	3	0.00342	rs4494918	0.001146	5	0.0109	rs4687773	0.003902
3	VPRBP	4	0.00722	rs17661242	0.00578	6	0.01031	rs17712228	0.003692
4	DKK2	22	0.03072	rs405252	0.001657	23	0.01295	rs10489127	0.007531
4	HSPA4L	5	0.03014	rs1824331	0.01623	7	0.0363	rs1380156	0.005484
4	RAP1GDS1	4	0.03791	rs12650841	0.008755	4	0.001114	rs3775537	0.000791
5	ANXA6	27	0.00741	rs7724316	0.0009782	38	0.01576	rs7707871	0.002366
5	CSF1R	24	0.02591	rs4705408	0.01619	26	0.02065	rs1433010	0.005289
5	ERBB2IP	23	0.0248	rs251300	0.007621	28	0.01442	rs251614	0.0004325
5	FAM114A2	24	0.04393	rs4958354	0.01887	27	0.02408	rs7709154	0.005123
5	MFAP3	14	0.03698	rs4958354	0.01887	17	0.01779	rs2882468	0.004059
5	SFRS12	6	0.01898	rs27077	0.01195	7	0.02685	rs27085	0.005252
5	TNIP1	26	0.01086	rs7724316	0.0009782	30	0.01618	rs7707871	0.002366
6	FKBPL	3	0.02584	rs17421624	0.006961	4	0.01037	rs17421624	0.008884
6	NOTCH4	17	0.03128	rs3130311	0.003584	24	0.01787	rs2071286	0.0004878
7	GALNTL5	11	0.03254	rs4726118	0.002041	11	0.00606	rs4298423	0.00391
8	CHCHD7	1	0.04935	rs7830138	0.05044	1	0.02899	rs7830138	0.02754
8	PLAG1	1	0.04973	rs7830138	0.05044	1	0.02693	rs7830138	0.02754
10	ANXA8-2	1	0.04546	rs4342964	0.04549	1	0.03654	rs4342964	0.03651
10	ANXA8L1-2	1	0.04685	rs4342964	0.04549	1	0.03731	rs4342964	0.03651
10	SYNPO2L	3	0.04906	rs10824026	0.0404	4	0.04709	rs1004059	0.04153
13	DLEU7	22	0.03088	rs2796843	0.007729	27	0.00124	rs7320457	0.0002884
13	RFXAP	11	0.04384	rs4943419	0.02264	15	0.02304	rs6563500	0.02494
14	TNFAIP2	13	0.0222	rs944007	0.002186	17	0.04048	rs8008371	0.008582
15	AGBL1	169	3.9E-05	rs12591257	3.57E-06	201	0.02772	rs4393536	0.0005199
15	FURIN	3	0.0309	rs8041787	0.04697	3	0.03806	rs7171099	0.003971
16	DHODH	5	0.01224	rs7204798	0.009094	8	0.03758	rs7205297	0.01713
16	GNPTG	1	0.04633	rs3759937	0.04669	1	0.01498	rs3759937	0.01469
16	NDUFB10	4	0.02183	rs1742402	0.01629	5	0.00603	rs17602	0.0007807
16	RNF151	4	0.02271	rs1742402	0.01629	6	0.0059	rs17602	0.0007807
16	RPS2	4	0.02238	rs1742402	0.01629	6	0.00615	rs17602	0.0007807
16	TBL3	3	0.01287	rs1742402	0.01629	5	0.00394	rs17602	0.0007807
16	UNKL-1	1	0.04629	rs3759937	0.04669	1	0.01491	rs3759937	0.01469
17	ABCA9	9	0.04642	rs11077858	0.02678	13	0.03241	rs7215642	0.01887
17	CYB5D2	9	0.02413	rs7219437	0.00947	10	0.03717	rs1377806	0.005633
17	CYGB	9	0.01356	rs3809700	0.01202	12	0.04553	rs752049	0.02379
17	RHBDF2	5	0.03903	rs752049	0.02727	7	0.04113	rs752049	0.02379
17	ZZEF1	16	0.03514	rs7219437	0.00947	18	0.01557	rs781850	0.003054
19	TLE6	2	0.0258	rs4806893	0.05288	4	0.03351	rs390258	0.0269
19	ZNF536	29	0.00577	rs10402889	0.009126	37	0.02308	rs16964244	0.002864
21	KCNJ6	68	0.03621	rs858009	0.0004127	83	0.00964	rs858009	0.002051
22	KREMEN1	29	0.00226	rs16987014	0.0005741	35	0.03639	rs5762996	0.004994
22	LZTR1	4	0.04258	rs2541953	0.002118	7	0.04729	rs2239961	0.009702
22	PATZ1	5	0.03675	rs2073860	0.02441	10	0.00262	rs5753559	0.0007666
22	PIK3IP1	7	0.03867	rs2073860	0.02441	15	0.00277	rs5753559	0.0007666
22	THAP7	4	0.04333	rs2541953	0.002118	7	0.04774	rs2239961	0.009702

Table S4: Overlap genes between METH-induced psychosis and SCZ based upon gene-based analysis

Members of JGIDA

Hiroshi Ujike (Department of Neuropsychiatry, Okayama University Graduate School of Medicine, Dentistry and Pharmaceutical Sciences), Ichiro Sora (Department of Biological Psychiatry, Tohoku University Graduate School of Medicine), Masaomi Iyo (Department of Psychiatry, Chiba University Graduate School of Medicine), Mujun Won (Kojin Hospital), Naoki Kondo (Seimei Hospital), Nobuya Naruse (Saitama Prefectural Psychiatric Hospital), Kumi Aoyama-Uehara (Serigaya Hospital), Norio Ozaki (Department of Psychiatry, Nagoya University Graduate School of Medicine)and Nakao Iwata (Department of Psychiatry, Fujita Health University School of Medicine)