

Supplemental Tables:

Table S1. The quality control criteria based on CNV metrics applied to each cohort.

Disease Cohort	genotyping rate	LRR SD	 GCWF 	CNV count
Janssen SCZ & BD	>98%	<0.3	<0.05	<100
CHOP SCZ	>96%	<0.35	<0.02	<80
CHOP ASD	>98%	<0.3	<0.05	<100
CHOP ADHD	>98%	<0.3	<0.05	<100
Depression	>98%	<0.25	<0.02	<100

LRR SD= the SD of log R ratio; |GCWF|= the absolute value of GC base pair wave factor; CNV count= CNV count per sample.

Table S2. The number of histone marks, DNase and eQTLs in each *DOCK8* CNVs.

Disease Cohort	CNVR (hg18)	H3K4me1 Enh	H3K4me3 Pro	H3K27ac Enh	H3K9ac Pro	Dnase	GTE_x	GRASP
JANSSEN SCZ & BD	chr9:396118-474850	269	102	204	110	57	1	1
CHOP SCZ	chr9:372245-389052	303	120	204	110	59	1	1
CHOP ASD	chr9:407918-474786	151	32	158	161	17	0	0
CHOP ADHD	chr9: 293639-352917	276	71	167	221	45	2	1
Depression	chr9: 283360-294957	92	39	63	0	12	1	0