Table S1. Frequency of *CHD8* Mutations by Cohort, Related to Figure 1 and Table 1

Cohort	Cohort Type[a]	QC Passing	Putative LoF[b]	Unknown Severity Hits	Focal CNVs[c]
Gecz	DD/ID	808	0	1 ms-near-splice	0
Nijmegen	DD/ID	1249	1 ms-near-splice, 1 fs	1 coding	0
Sage	DD/ID	108	0	0	0
Troina	DD/ID	689	2 fs	0	0
Leuven	ASD	720	0	1 ms-near-splice	3 (dup)
APP	ASD	156	1 ns	0	0
Simons	ASD	2446	3 ns, 4 fs, 1 sp	1 coding	0
Siblings (Simons)	Control	1688	0	0	0
Signature Genomics	DD/ID	29,206	0	0	4 (dup)

[a]DD = developmental delay; ID = intellectual disability; ASD = autism spectrum disorder.
[b]LoF = loss-of-function; ms = missense; fs = frameshift; ns = nonsense; sp = splice variant.
[c]dup = duplication.

Table S2. Splice Variant Scores, Related to Figure 1 and Table 1

Sample	Variant	Splice Type[a]	SSF [0-100]	MaxEnt [0-12]
11654.p1	Chr14(GRCh37):g.21871373T>C	A	84.05 ⇒ —	9.78 ⇒ —
Gecz4801	Chr14(GRCh37):g.21876472C>T	D	86.68 ⇒ 95.64 (+10.3%)	9.89 ⇒ 10.67 (+7.9%)
Nij07-06646	Chr14(GRCh37):g.21863071C>T	D	73.30 ⇒ —	6.53 ⇒ —
Leuven445853	Chr14(GRCh37):g.21863510C>A	A	= 84.48	7.60 ⇒ 8.19 (+7.7%)

[a]A = acceptor; D = donor.

Table S3. Proband Evidence for Coexpressed Genes, Related to Figure 3

Gene	Proband evidence[a]
SETD2	1 frameshift
MLL5	1 frameshift
ADNP	1 frameshift
POGZ	2 frameshift
ARID1B	1 frameshift
PHF2	1 frameshift
DYRK1A	1 splice, 1 frameshift
SUV420H1	1 splice (2 missense)
MBD5	1 frameshift
NAV1	(1 missense)
MLL	(1 missense)

[a]Evidence listed in parentheses are not predicted to be putative loss-of-function mutations.

Table S4. *CHD8* Coexpression of Neocortical Top Genes, Related to Figure 3

Gene	r	CI (95%)
NAV1	0.934	0.922-0.945
MLL	0.902	0.883-0.918
ARID1A	0.967	0.961-0.973
RPRD2	0.968	0.962-0.974
ZNF462	0.900	0.881-0.917