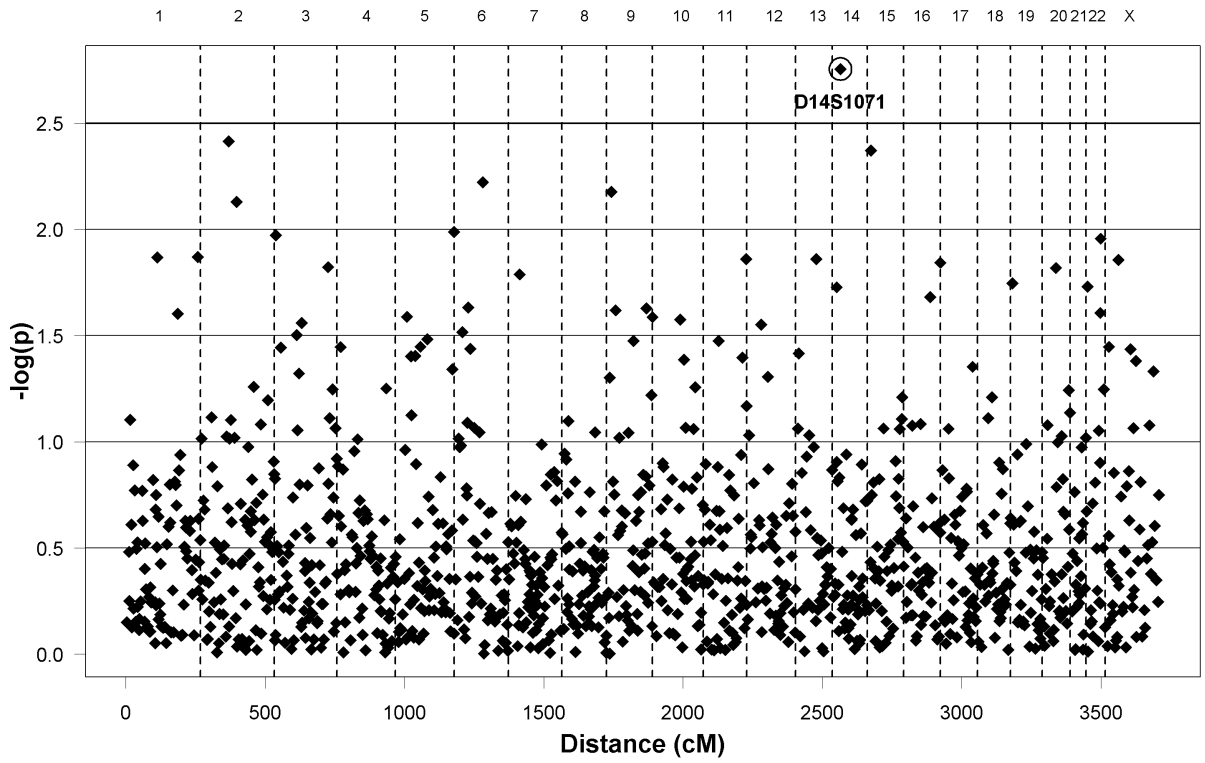


Figure S1 Distribution of microsatellite marker LD+Linkage values of the initial genome-wide scan. Results produced by dominant Pseudomarker analysis in the extended pedigree (Set 1). The y-axis presents –log(p) values as a function of genetic distance (x-axis, in cM). The single marker with –log(p)>2.5 is displayed. Detailed results for D14S1071 (chromosome 14q12; genetic distance 28.2 cM, deCODE Genetic map) are: LD+Linkage –log(p)=2.76, LD|Linkage –log(p)=2.93.

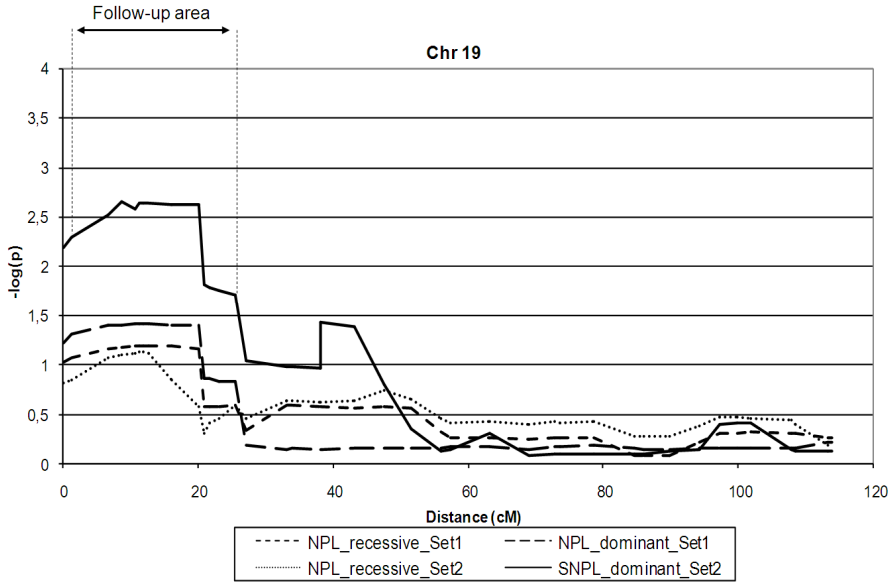
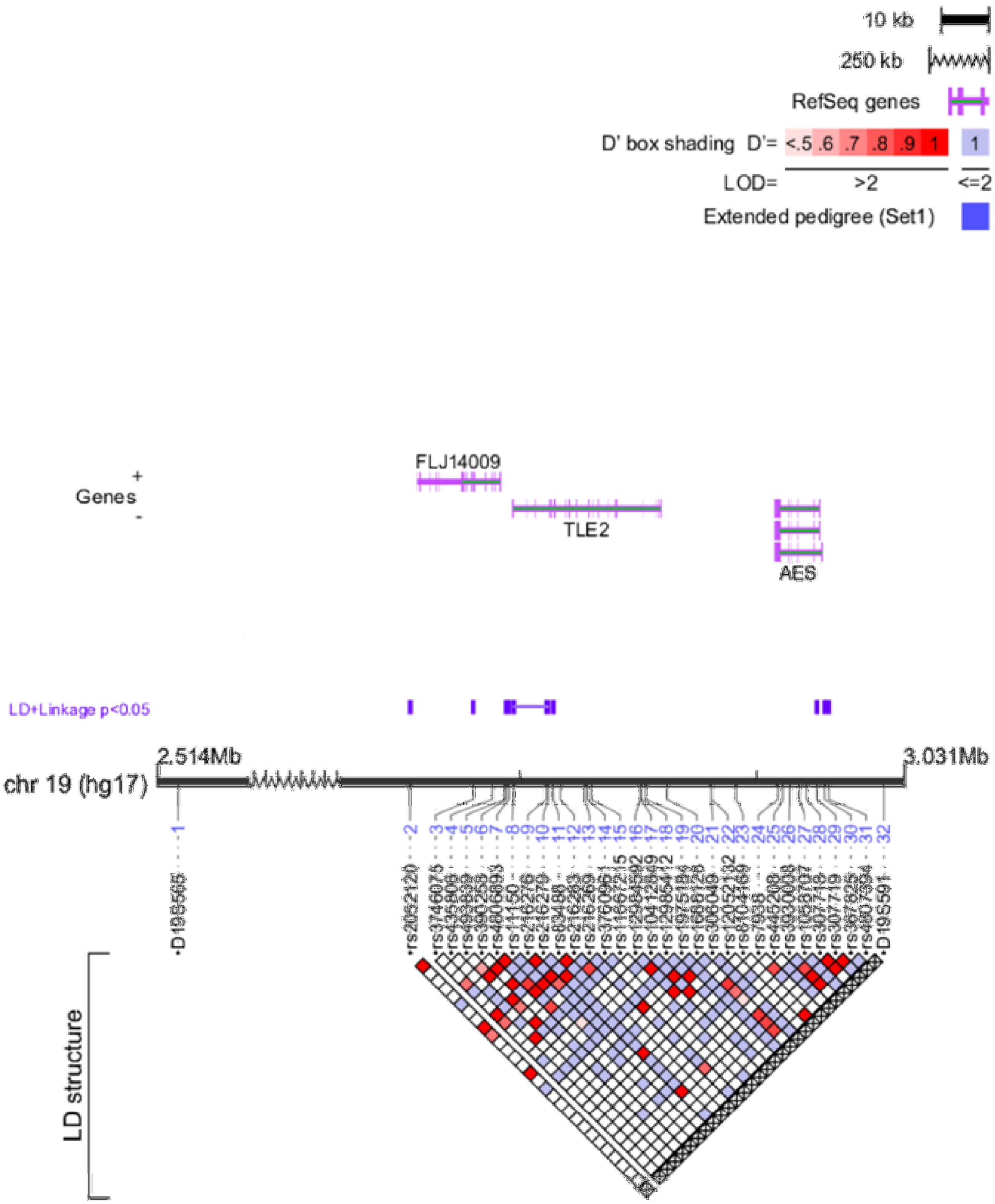
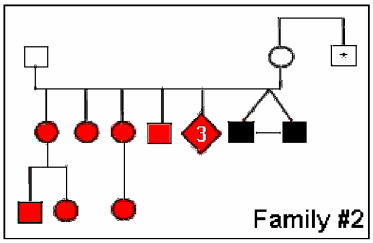


Figure S2 Multipoint linkage results at chromosome 19p after the inclusion of seven follow-up microsatellites. Original number of markers in the initial scan was 34. Results produced by non-parametric Simwalk2 analysis in the extended pedigree. "NPL_dominant" equals to the Simwalk2 "MAX-TREE" statistic, while "NPL_recessive" equals to the "BLOCKS" statistics.



10 kb
250 kb
RefSeq genes
D' box shading D'= <.5 .6 .7 .8 .9 1 1
LOD= >2 <=2
Extended pedigree (Set1)
Genes
+
-
FLJ14009
TLE2
AES
LD+Linkage p<0.05
2.514Mb
3.031Mb
chr 19 (hg17)
LD structure

Figure S3 The TLE gene cluster at 19p13.3. Figure illustrating the organization of the TLE-locus, including pairwise marker LD structure and markers giving significant association in the extended pedigree (Set1 results). Eight consecutive SNPs with $p<0.04$ in the same analysis are connected with a line. FLJ14009 stands for TLE6. Figure generated with LocusView 2.0 program (T. Petryshen, A. Kirby, M. Ainscow, unpublished software; http://www.broad.mit.edu/mpg/locusview/).



Chr19 p13.3 p12 q12 q13.2

AUT	2	4	1	3	6	2	2	1	8	2	4	2	3	2	3	1	1	4	1	2	4	7	5	5	2	5	4	6	6	7	6	3	1	2
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	5	4	3	1	6	7	5	6	1	3	3	6	1	4	3	3	1	3
AS	1	4	8	3	6	2	2	1	8	2	4	2	3	2	3	1	1	4	1	2	4	7	5	5	2	5	4	6	6	7	5	3	3	2
	1	8	1	4	5	2	3	1	4	2	3	7	6	2	3	4	1	3	3	1	6	7	5	6	1	3	3	6	1	7	5	3	1	4
AS	2	4	1	3	6	10	2	1	3	2	5	7	3	3	3	4	1	1	1	7	6	2	6	5	8	11	3	6	6	7	6	3	1	2
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	5	4	3	1	6	7	5	6	1	3	3	6	1	7	3	3	1	3
AS	2	4	1	3	6	10	2	1	8	2	4	2	3	2	3	1	1	4	1	2	4	7	5	5	2	5	4	6	6	7	6	3	1	2
	1	8	1	4	5	2	3	1	4	2	3	7	3	1	3	4	5	4	3	1	6	7	5	6	1	3	3	6	1	7	5	3	1	4
AS	2	4	1	3	6	10	2	1	3	2	5	7	3	3	3	4	1	1	1	7	6	2	6	5	8	11	3	1	6	3	5	3	3	2
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	1	3	3	1	6	7	5	6	1	3	3	6	1	7	5	3	1	4
AS	2	4	1	3	6	10	2	1	3	2	5	7	3	3	3	4	1	1	1	7	6	2	6	5	8	11	3	1	6	3	5	3	3	2
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	1	3	2	5	6	7	1	6	1	3	3	6	1	7	5	3	1	4
AS	2	4	1	3	6	10	2	1	3	2	5	7	3	3	3	4	1	4	1	2	4	7	5	5	2	5	4	6	6	7	6	3	3	2
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	1	3	2	5	6	7	1	6	1	3	3	6	1	4	3	3	1	3
AS	2	4	1	3	6	10	2	1	3	2	5	7	3	3	3	4	1	1	1	2	4	7	5	5	2	5	4	6	6	7	6	3	1	2
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	1	3	2	5	6	7	1	6	1	3	3	6	1	4	3	3	1	3
AS	2	3	9	4	4	3	4	1	8	1	4	2	7	2	3	4	5	5	3	7	7	5	6	2	1	11	1	7	8	3	3	3	1	5
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	1	3	3	7	6	2	6	5	8	3	3	6	1	7	5	3	1	4
AS	2	4	3	3	5	2	3	1	2	3	3	12	3	1	7	3	1	2	3	1	6	3	1	5	1	9	3	8	3	7	1	3	1	4
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	5	4	3	7	6	2	6	5	8	11	3	6	6	7	6	3	1	2
AS	1	3	8	3	6	7	3	1	2	3	3	12	3	1	7	3	1	2	3	1	6	3	1	5	1	9	3	8	3	7	1	3	3	2
	3	4	7	4	2	2	4	2	4	2	4	8	3	1	3	4	1	1	1	7	6	2	6	5	8	11	3	6	6	7	6	3	1	2

Figure S4 Chromosome 19 microsatellite haplotypes of affected individuals in family #2 indicating shared regions. In the pedigree picture, autism is indicated with black and AS in red. Only microsatellites from the initial scan are included. The follow-up area from markers two to eight is delimited with borders. The family contains one additional individual with AS-diagnosis (*), but the sample was not available for the initial scan.