

1a) Stage 1 discovery study

- Genome-wide linkage analysis
- 847 multiplex families from AGRE
- SNP genotypes from Illumina 550K & Omni-1

1b) Linkage signals in samples including AGRE

Source	Subgrp	Locus	Peak LOD
Liu et al. (2001)	ALL	5p13.1	2.55
	ALL	Xq26.1	2.56
Yonan et al. (2003)	ALL	5p13.1	2.54
	ALL	11p13-11.2	2.24
	ALL	17q11.2	2.83
Stone et al. (2004)	MO	17q11	4.3*
	FC	4q32.3-35.1	2.7
Cantor et al. (2005)	MO	17q21	3.6*
McCauley et al. (2005)	ALL	3p25.3	2.22
Szatmari et al. (2007)	MO	5q12	2.31
	MO	9q33.3	2.36
	ALL	11p12	2.77
	FC	11p12	2.86
Weiss et al. (2009)	ALL	6q27	2.94
	ALL	20p13	3.81*

* Genome-wide significant linkage

2) Combined stage extension study

- Regional linkage analysis in loci with suggestive LOD scores
- 1008 multiplex families from AGRE
- SNP genotypes from Illumina Omni-1 & Omni-2.5

3) Replication study

- Regional linkage analysis in loci with genome-wide significant LOD scores (LOD>3.6)
- Multiplex families from AGRE not tested in the corresponding discovery sample