Results

Three regions survived the stringent Bonferroni multiple comparison cutoff of $3.9 \cdot 10^{-5}$, accounting for 1282 multiple comparisons. Those are 9_24, 15_29 and 19_5. The results are based on 30,000 permutations so far.

Now to validate those results we found all the SNPs belonging to the same interval and cut it into a region, that can have more or less than 1000 SNPs. Based on those 3 regions true phenotype result as well as 1000 permutation test has been performed. Mean posterior inclusion probability was chosen to be the metric of comparison. All three regions were found to be significant.

Discovery MGS winners:						**Validation SWD p-values**		
chromosome	chunk	start	end	MGS p-value	verdict	# of SNPs in validation	validation p-value	verdict
9	**24**	34,905,605	70,379,322	0.00003	significant	955	0.002	significant
15	**29**	83,907,801	86,887,657	0	significant	645	0.001	significant
19	**5**	15,724,023	22,638,628	0	significant	1513	0	significant

Discovery

Number of permutations	100000
Number of comparisons	1282
Bonferroni p-value	0.000039

Validation

Number of permutations	1000
Number of comparisons	3
Bonferroni p-value	0.01667

For chromosome 19 chunk 5 markers: rs2965189, rs2916074, rs4808200, rs4808203, rs10419912, rs2965189, rs2916074, rs4808200, rs4808203, rs10419912 were found to be in LD with previously found marker rs2905426 (rank 51) (Consortium et al., 2014).

For chromosomes 9 and 15 no LD with 2014 study markers was found.