Results

Three regions survived the stringent Bonferroni multiple comparison cutoff of , 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.

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| **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 |

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| **Discovery** |  |  | |  | |  | |  | | **Validation** | |  | |
| Number of permutations | 100000 | |  | |  | |  | |  | | Number of permutations | | 1000 | |
| Number of comparisons | 1282 | |  | |  | |  | |  | | Number of comparisons | | 3 | |
| Bonferroni p-value | 0.000039 | |  | |  | |  | |  | | 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.