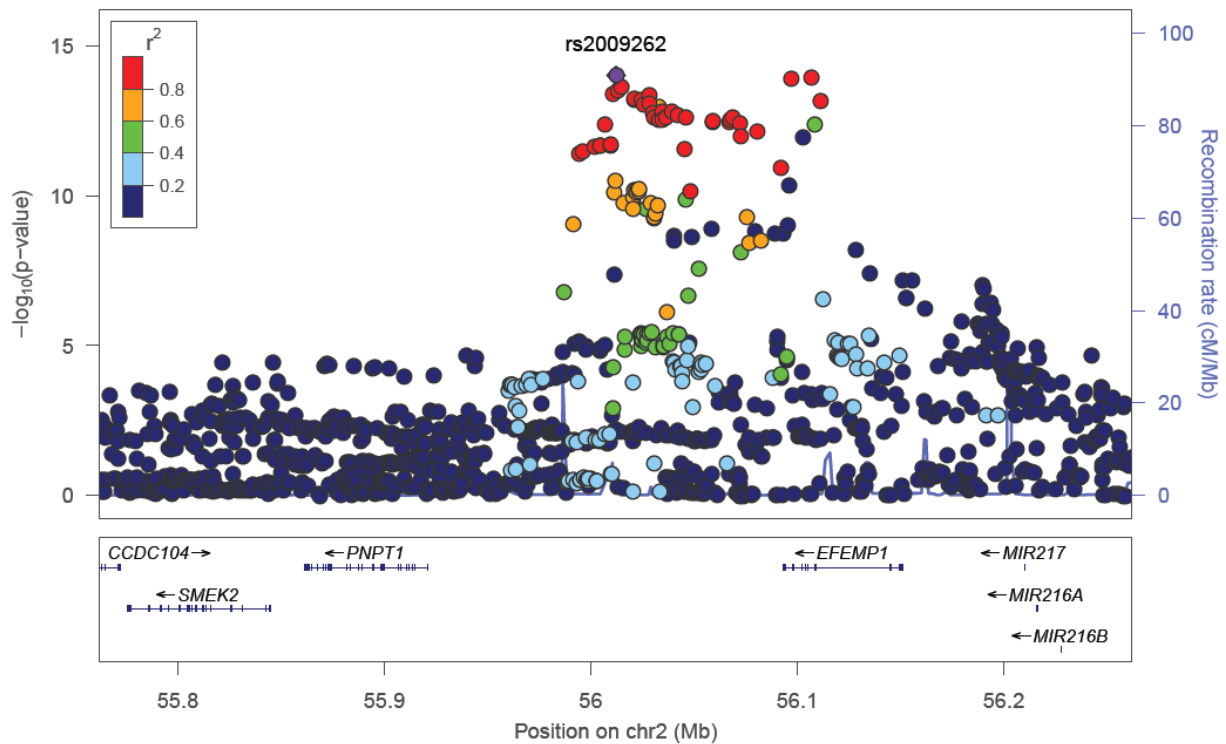
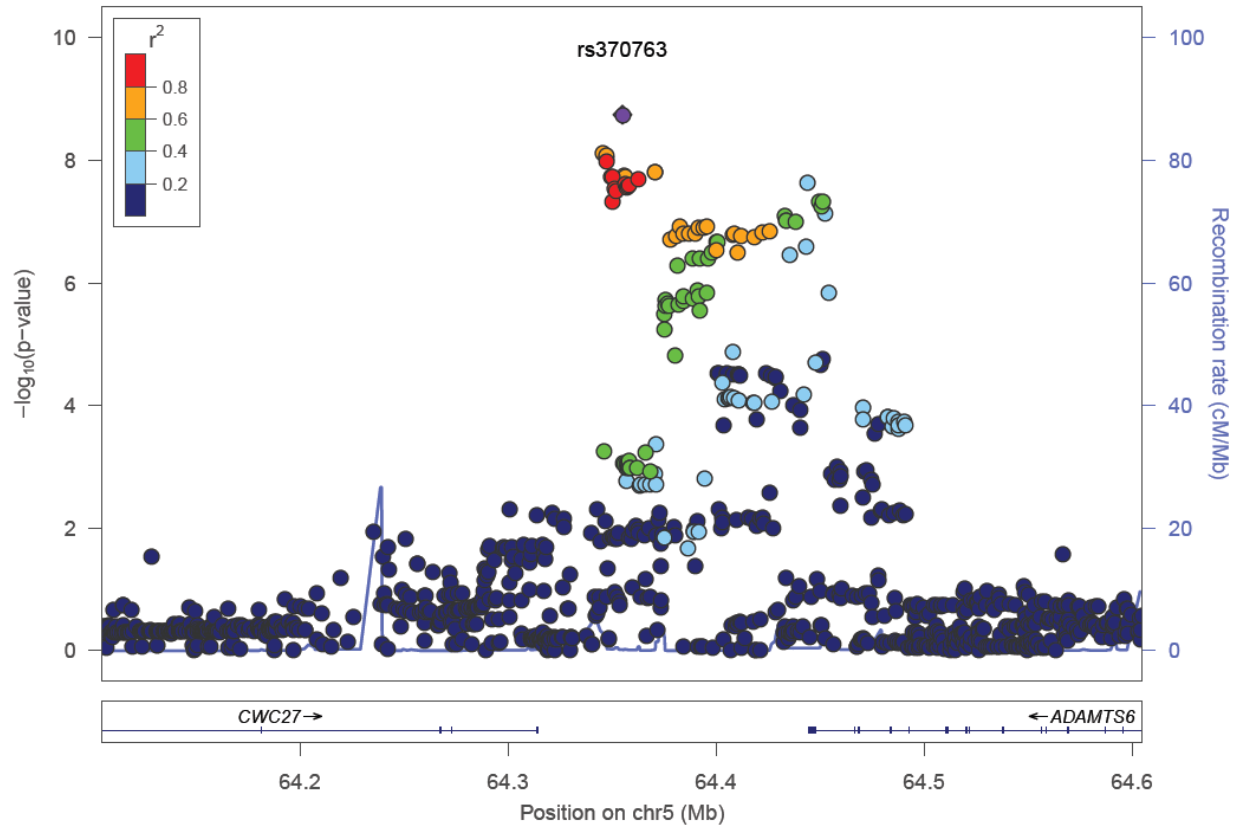


Supplementary Figures

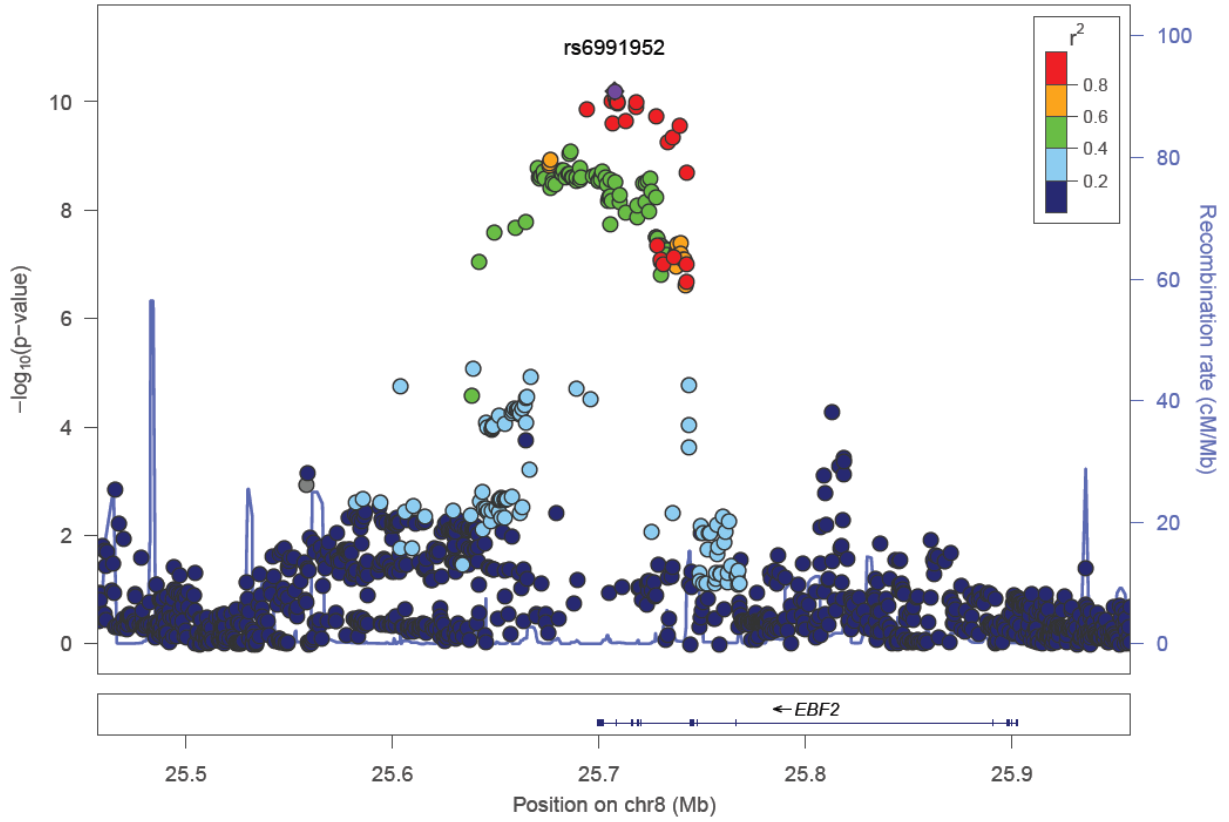
Supplementary Figure 1: (A-D) Locus Zoom plots of the top four loci associated with inguinal hernia in the GERA discovery cohort. Plots show association results of SNPs in the GWAS of the GERA cohort samples and recombination rates. Each circle represents the $-\log_{10} P$ value (y axes) and chromosomal position (x axes) of SNPs tested for association. The top associated SNP in each region is identified by its rsID. The color of each circle reflects the extent of LD with the top SNP. Physical positions are based on NCBI build 37 of the human genome. The relative position of genes and transcripts are displayed below the association plot.



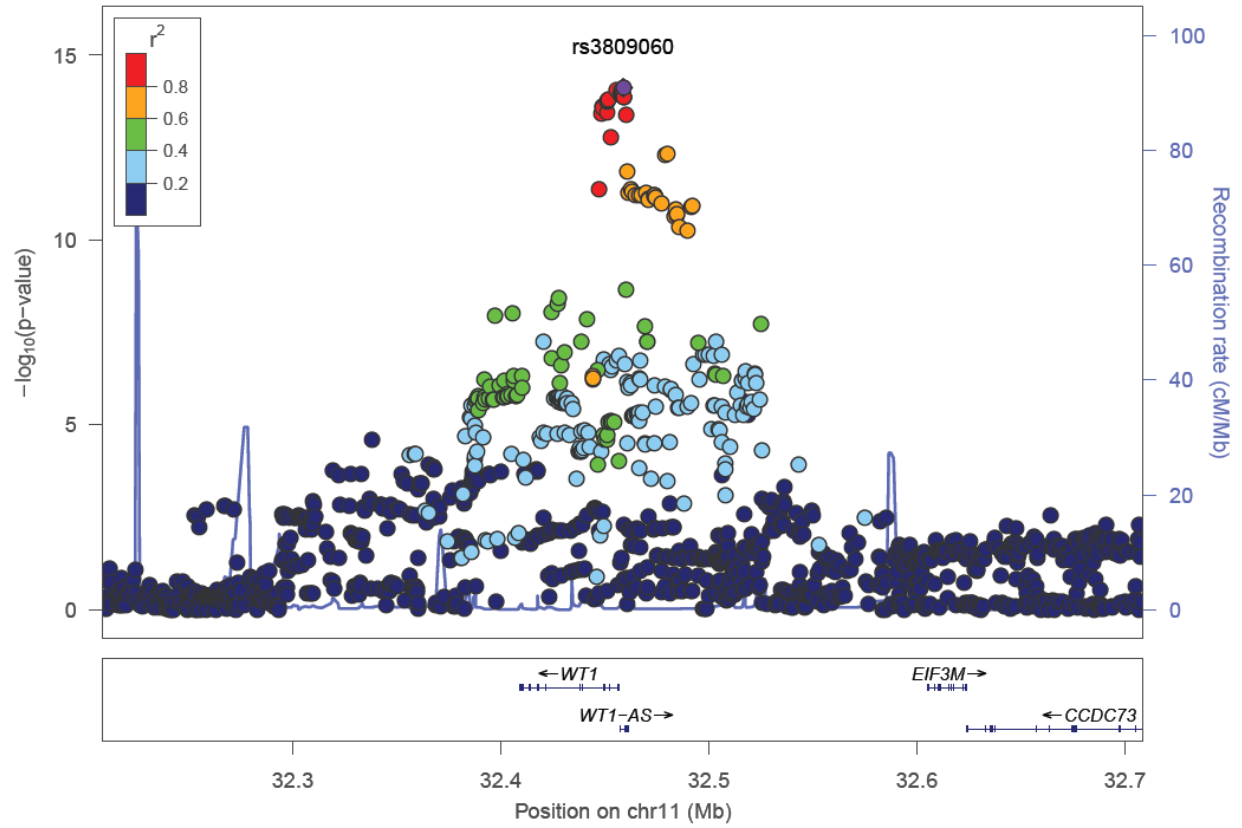
A. Chromosome 2



B. Chromosome 5

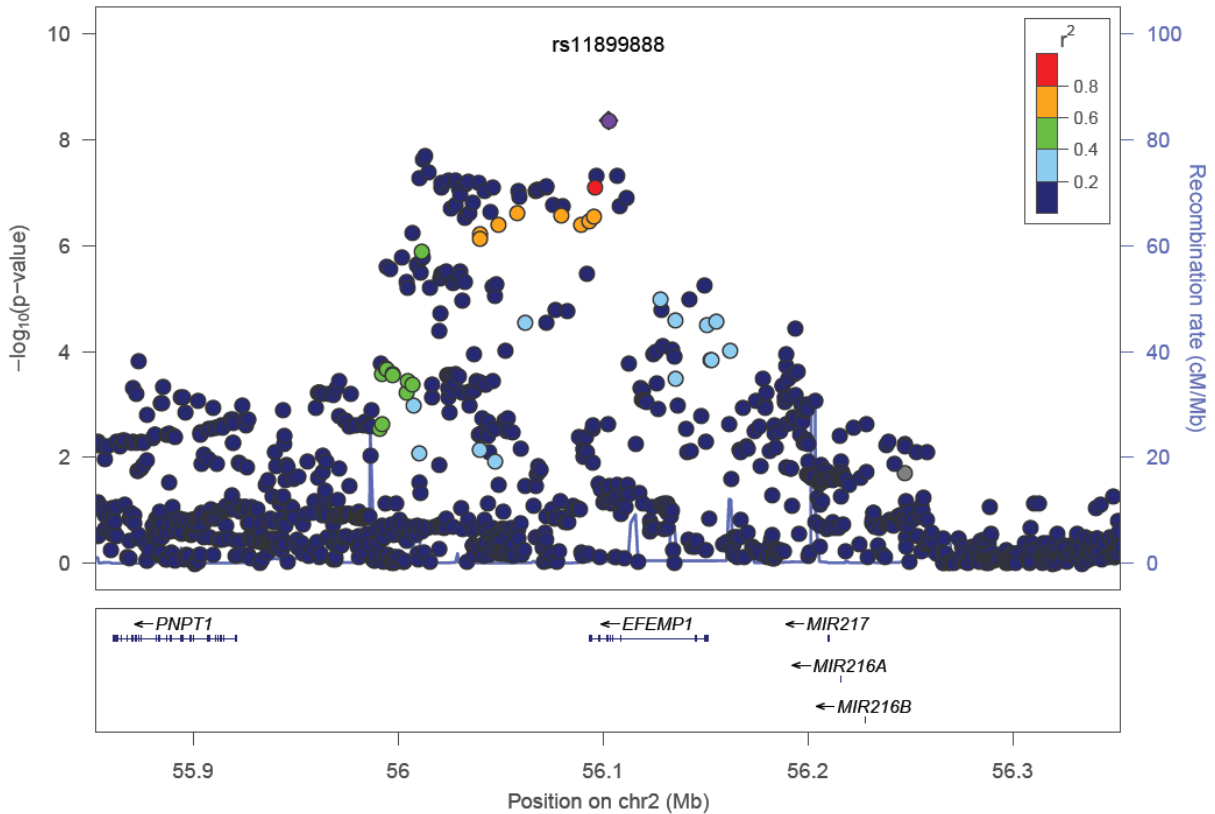


C. Chromosome 8

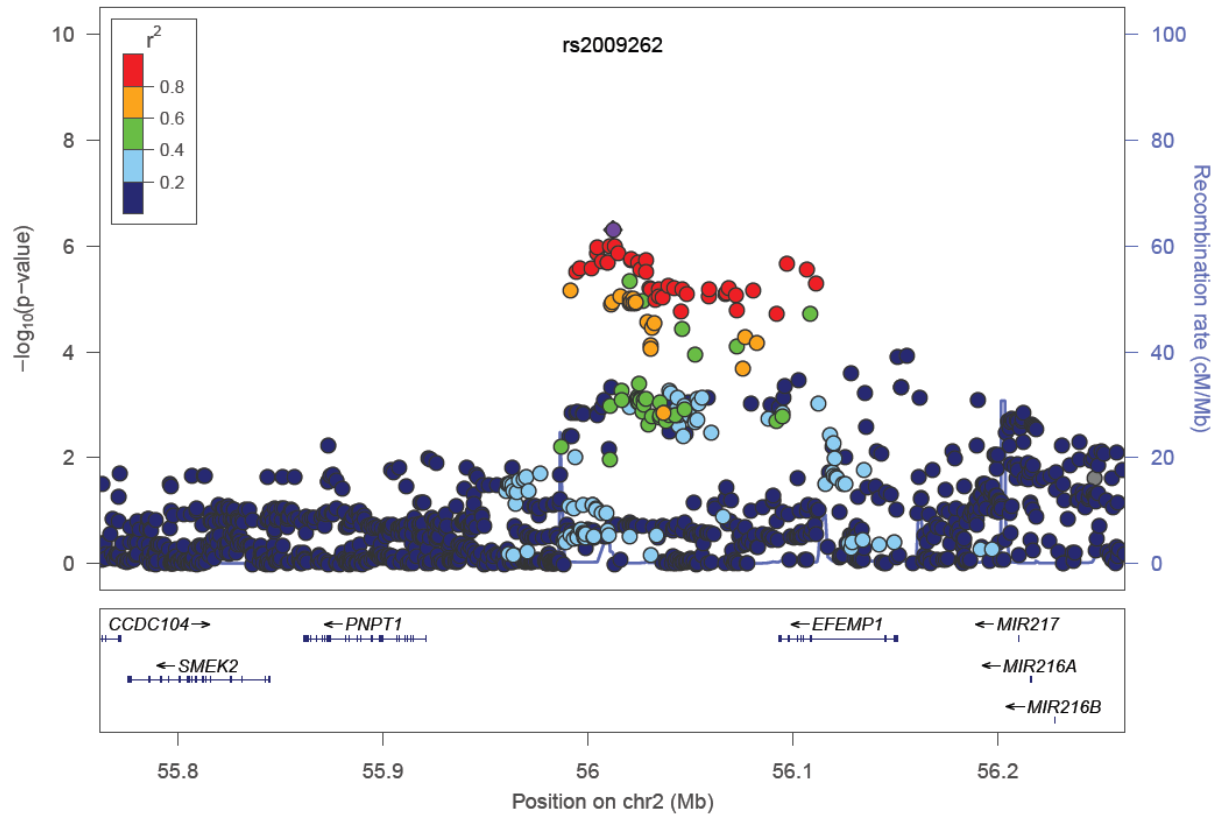


D. Chromosome 11

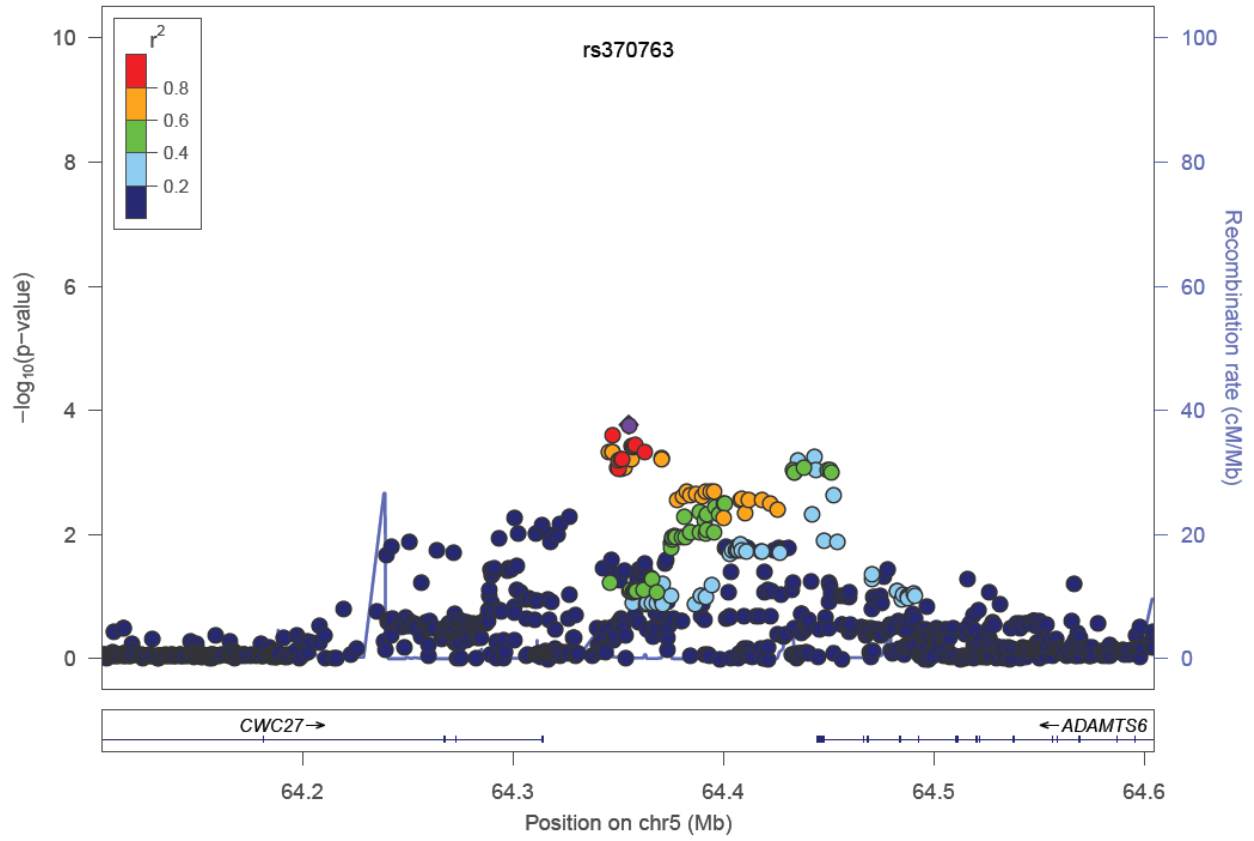
Supplementary Figure 2: (A-H) Locus Zoom plots of the top four loci associated with inguinal hernia in GERA cohort men, for direct and indirect inguinal hernia. Plots show association results of SNPs in the GWAS of the GERA cohort samples and recombination rates. Each circle represents the $-\log_{10} P$ value (y axes) and chromosomal position (x axes) of SNPs tested for association. The top associated SNP in each region is identified by its rsID. The color of each circle reflects the extent of LD with the top SNP. Physical positions are based on NCBI build 37 of the human genome. The relative position of genes and transcripts are displayed below the association plot.



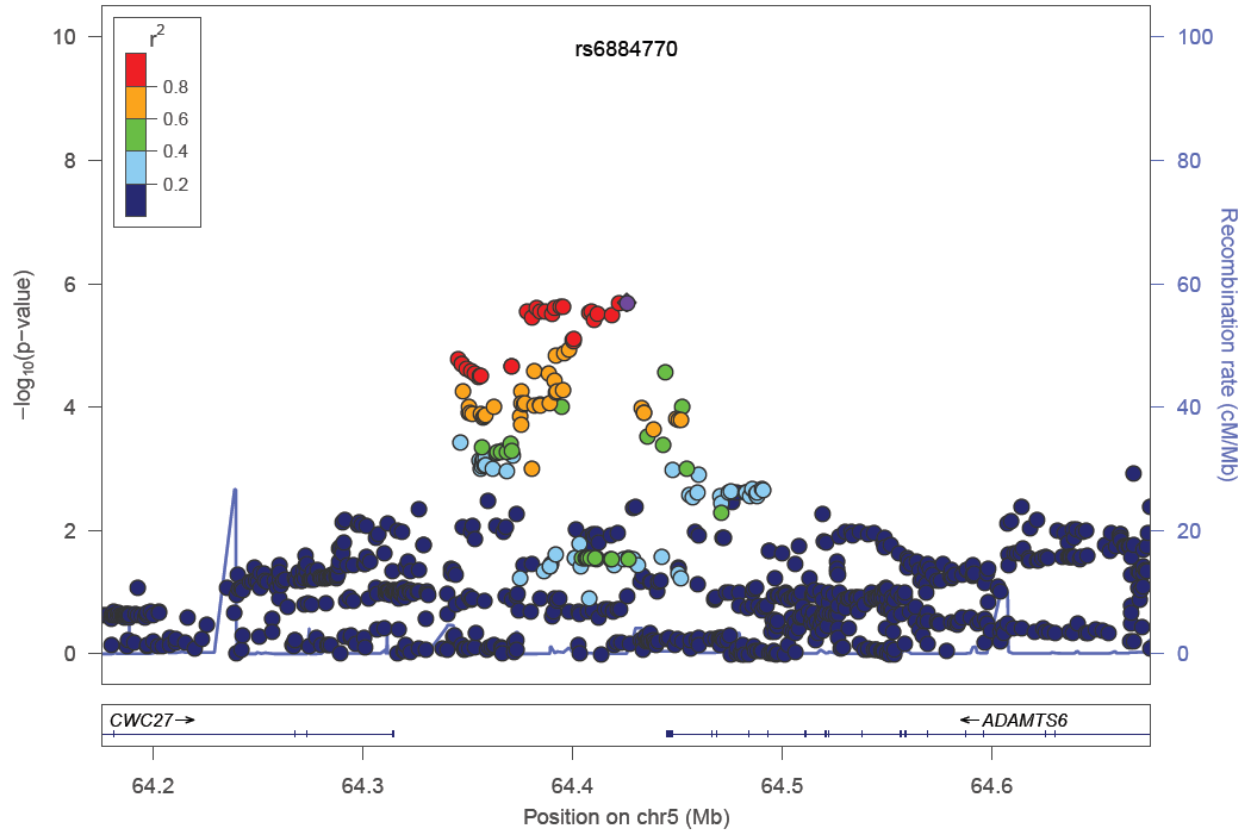
A. Chromosome 2 Direct Inguinal Hernia in GERA Men



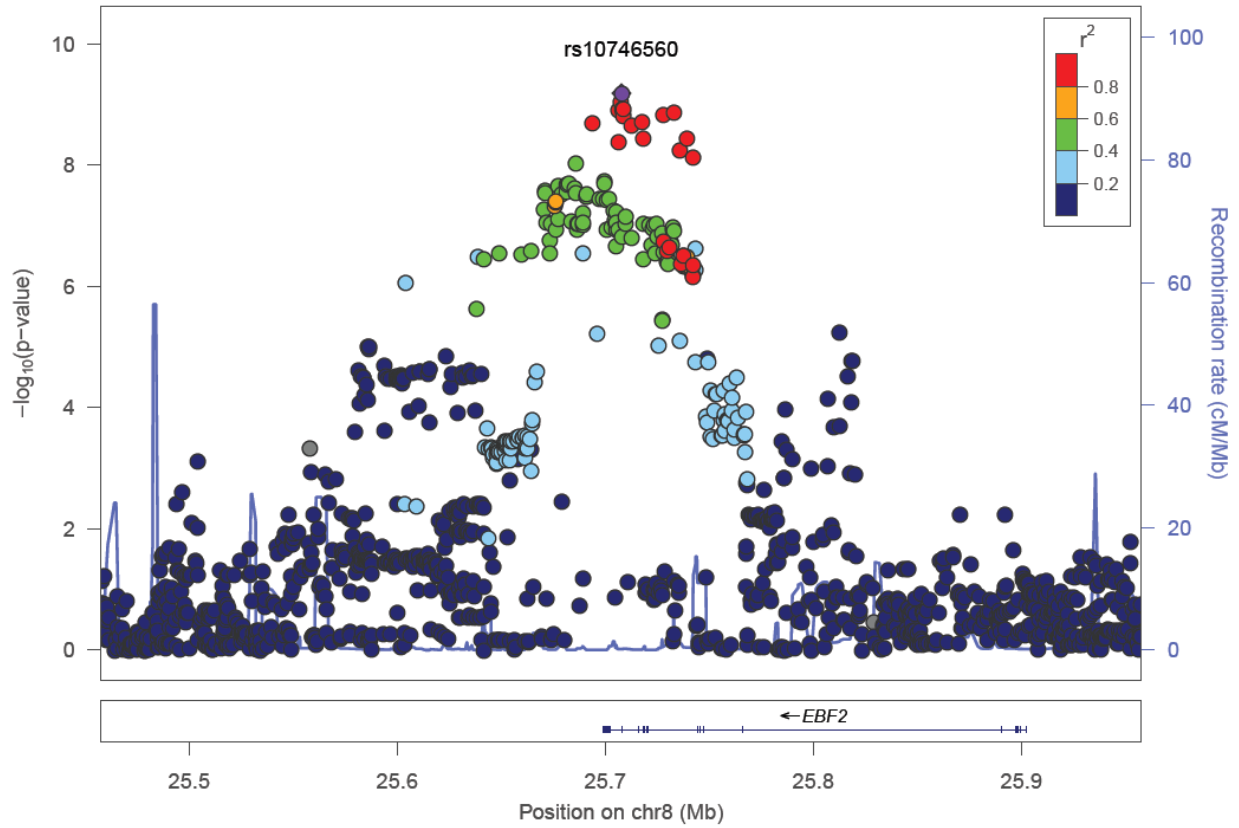
B. Chromosome 2 Indirect Inguinal Hernia in GERA Men



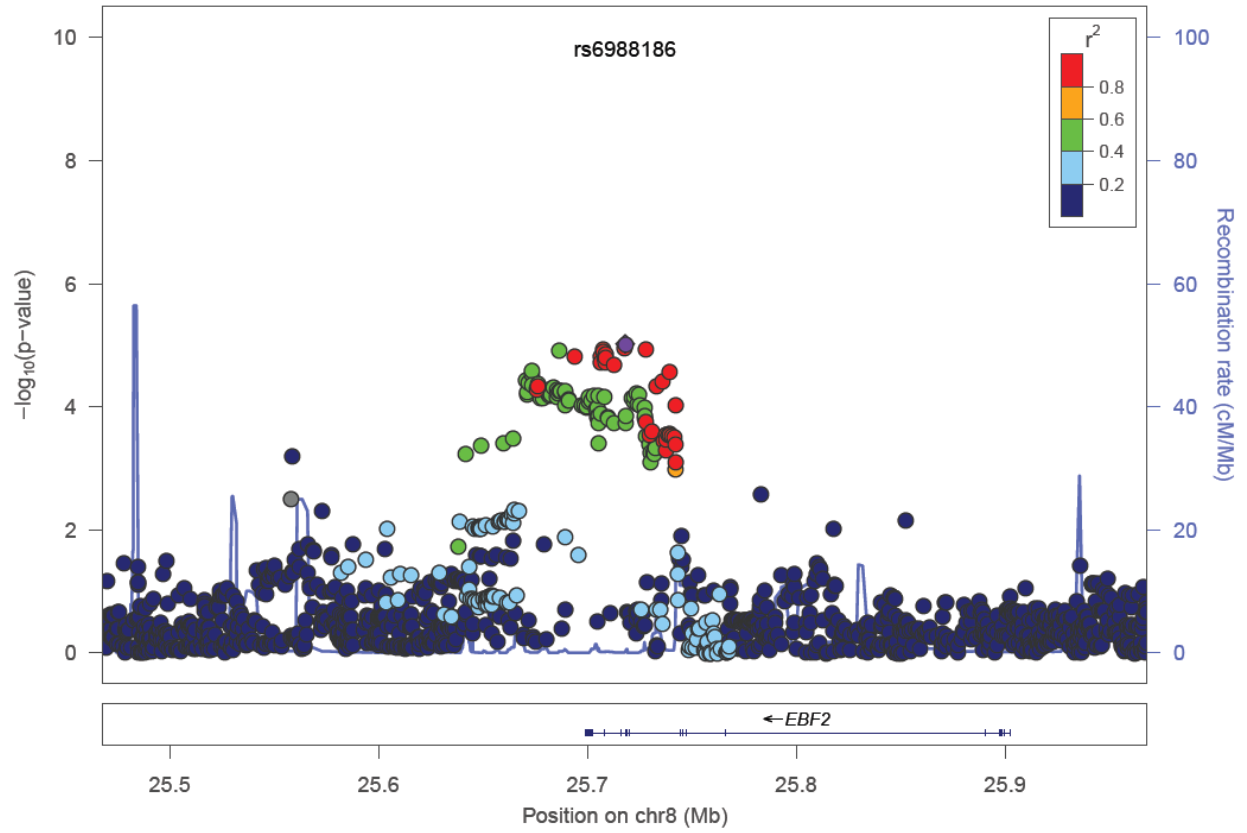
C. Chromosome 5 Direct Inguinal Hernia in GERA Men



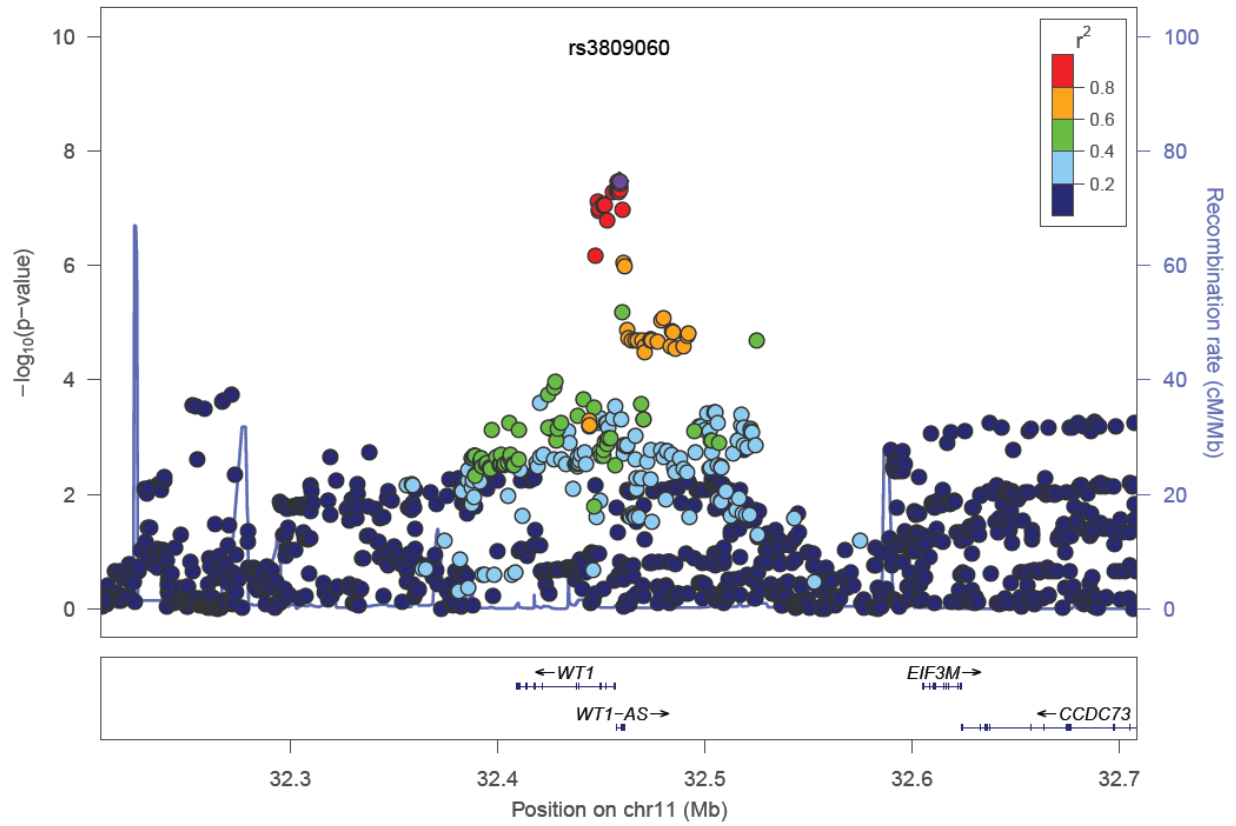
D. Chromosome 5 Indirect Inguinal Hernia in GERA Men



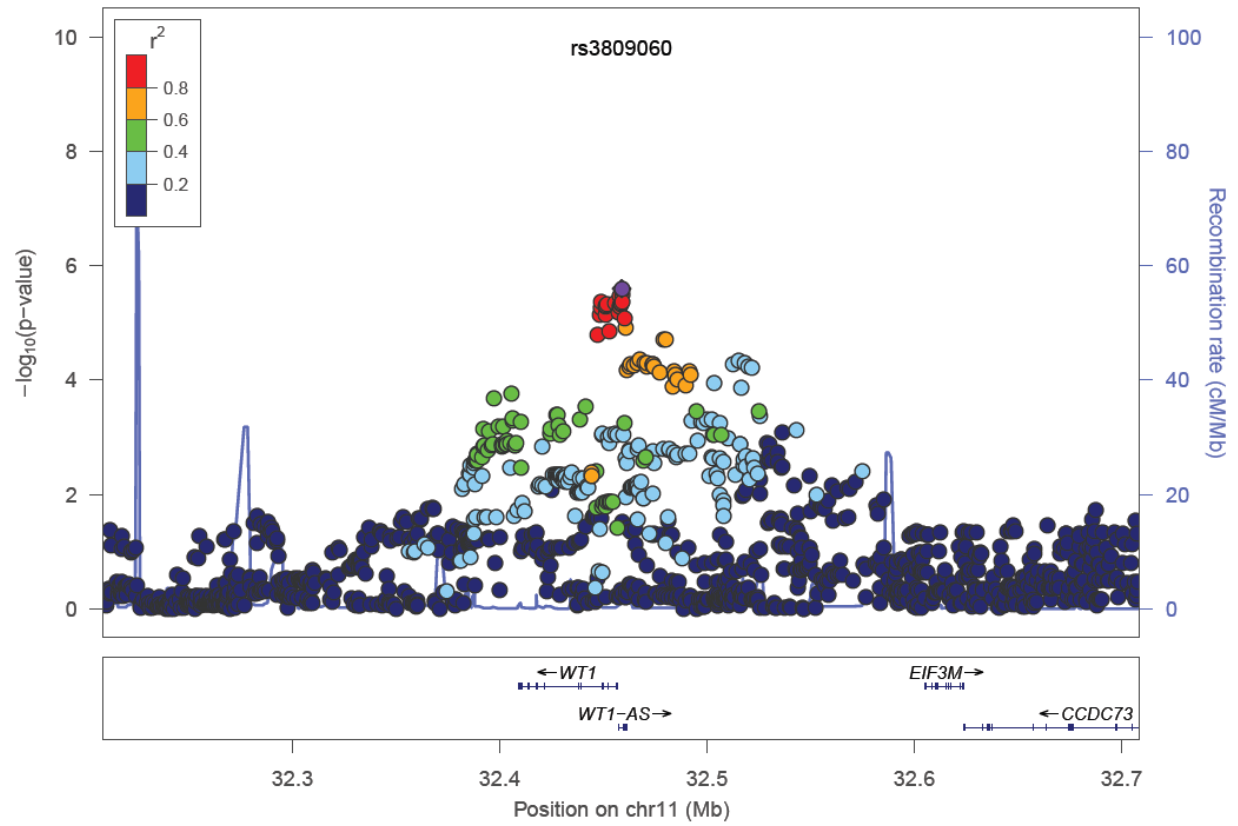
E. Chromosome 8 Direct Inguinal Hernia in GERA Men



F. Chromosome 8 Indirect Inguinal Hernia in GERA Men



G. Chromosome 11 Direct Inguinal Hernia in GERA Men



H. Chromosome 11 Indirect Inguinal Hernia in GERA Men

Supplementary Tables

Supplementary Table 1: Characteristics of GERA discovery cohort subjects

| | Inguinal Hernia (n=5,295) | | | | | | Controls (n=67,510) | |
|----------------------------|---------------------------|-------|------------------|-------|--------------------|-------|---------------------|-------|
| | All (n=5,295) | | Direct (n=2,335) | | Indirect (n=2,647) | | N | % |
| | N | % | N | % | N | % | | |
| Men | 4,746 | 89.6% | 2,193 | 93.9% | 2,408 | 91.0% | 25,011 | 37.1% |
| Women | 549 | 10.4% | 142 | 6.1% | 239 | 9.0% | 42,499 | 63.0% |
| | Mean | SD | Mean | SD | Mean | SD | Mean | SD |
| Age At Specimen Collection | 70.1 | 10.6 | 69.7 | 10.3 | 69.8 | 10.5 | 62.6 | 13.4 |

Supplementary Table 2: Characteristics of the 23andMe replication cohort subjects

| | Hernia repair cases (n=9,701) | | Controls (n=82,743) | |
|-------|-------------------------------|-------|---------------------|-------|
| Men | 6,812 | 70.2% | 41,611 | 50.2% |
| Age | | | | |
| <30 | 246 | 3.6% | 5,147 | 12.4% |
| 31-45 | 1,087 | 16.0% | 14,109 | 33.9% |
| 46-60 | 1,605 | 23.6% | 10,259 | 24.7% |
| >60 | 3,874 | 56.9% | 12,096 | 29.1% |
| Women | 1,889 | 29.8% | 41,132 | 49.8% |
| Age | | | | |
| <30 | 63 | 3.3% | 4,252 | 10.3% |
| 31-45 | 317 | 16.8% | 11,099 | 27.0% |
| 46-60 | 603 | 31.9% | 11,431 | 27.8% |
| >60 | 906 | 48.0% | 14,350 | 34.9% |

Supplementary Table 3: Gene sets enriched for association signals in the GSEA (FDR < 0.05)

| Gene Set | Database | Gene Set Size | Median Gene Size | p | FDR |
|--|-----------|---------------|------------------|--------|--------|
| JAK Stat Signaling | Ingenuity | 10 | 53 | 0.0011 | 0.0125 |
| Leukocyte Extravasation Signaling | Ingenuity | 47 | 39 | 0.0002 | 0.0149 |
| Actin Cytoskeleton Signaling | Ingenuity | 28 | 80 | 0.0018 | 0.0273 |
| Glycosaminoglycan Biosynthesis Chondroitin Sulfate | KEGG | 22 | 40 | 0.0006 | 0.0276 |

Supplementary Table 4: SNPs classified as likely to affect binding according to RegulomeDB in the four inguinal hernia risk loci

| SNP | Chromosome | Start Position | End Position | RegulomeDB Score |
|------------|------------|----------------|--------------|------------------|
| rs11888023 | 2 | 56,006,984 | 56,006985 | 2b |
| rs6739641 | 2 | 56,020,961 | 56,020962 | 2b |
| rs3791679 | 2 | 56,096,891 | 56,096892 | 2b |
| rs447583 | 5 | 64,357,582 | 64,357583 | 2b |
| rs264735 | 5 | 64,362,410 | 64,362411 | 2b |
| rs6449773 | 5 | 64,438,515 | 64,438516 | 2b |
| rs4568629 | 8 | 25,729,751 | 25,729752 | 2b |
| rs7925851 | 11 | 32,396,171 | 32,396172 | 2b |
| rs10835894 | 11 | 32,401,413 | 32,401414 | 2b |
| rs11031762 | 11 | 32,407,853 | 32,407854 | 2b |
| rs5030178 | 11 | 32,448,568 | 32,448569 | 2b |
| rs11031779 | 11 | 32,452,887 | 32,452888 | 2b |
| rs1799925 | 11 | 32,456,561 | 32,456562 | 2b |
| rs2301251 | 11 | 32,457,984 | 32,457985 | 2b |

Supplementary Table 5: Diagnosis and procedure codes

| Hernia Type | ICD9 | ICD9 Procedure Codes | CPT4 Codes |
|-------------------|-----------|---|---|
| | Diagnosis | | |
| | Codes | | |
| Inguinal Hernia | 550.x | 17.x, 53.0x, 53.1x | 49491, 49492, 49495, 49496, 49500, 49501, 49505, 49507, 49520, 49521, 49525, 49650, 49651, 49659 |
| Direct Inguinal | | 17.11, 17.21, 17.23, 53.01, 53.03, 53.11, 53.14, 53.13, 53.16, 53.17 | |
| Indirect Inguinal | | 17.12, 17.22, 17.23, 53.02, 53.04, 53.12, 53.15, 53.13, 53.16, 53.17 | |

Supplementary Table 6: Primer sequences for qRT-PCR

| Gene | Primer Sequence |
|-----------|-------------------------|
| Efemp1_F | GCGCTGGTCAAGTCACAGTA |
| Efemp1_R | AAGCATCTGGGACAATGTCAC |
| Wt1_F | GAGAGCCAGCCTACCATCC |
| Wt1_R | GGGTCCTCGTGTTGAAGGAA |
| Ebf2_F | GGGATTCAAGATACGCTAGGAAG |
| Ebf2_R | GGAGGTTGCTTTCAAATGGG |
| Adamts6_F | TGGTGGCTGAATAAGACATCATC |
| Adamts6_R | GGAGTCACGATAAAGTTTGGCAA |
| Col12a1_F | TTGCAGCTAGTACCACTGAAAC |
| Col12a1_R | CCCTGGCTTTGTAGGACCAC |
| Oct4_F | AGCGATCAAGCAGCGACTAT |
| Oct4_R | TAGCCTGGGGTACCAAATG |