S1 Table 9. Summary-based Mendelian Randomisation (SMR) for inguinal hernia using eQTL data from GTEx v7. The three probes (genes) that met the Bonferroni-corrected significance threshold $P_{SMR} < 1.12 \times 10^{-4}$ (0.05/4,455) and passed the HEIDI test ($P_{HEIDI} \geq 8.33 \times 10^{-3}$) (0.05/6)) are shown. eQTL tissues tested were for both GTEx v7 Skeletal muscle and Cells Transformed Fibroblast, however only three probes from skeletal muscle tissue met the HEIDI enrichment threshold. All three were mapped to within the realms of the FUMA-defined susceptibility loci.

<table>
<thead>
<tr>
<th>Probe ID</th>
<th>Chr</th>
<th>Gene</th>
<th>Top SNP</th>
<th>A1</th>
<th>A2</th>
<th>A1Freq</th>
<th>BETA</th>
<th>SE</th>
<th>$P_{GWAS}$</th>
<th>$P_{eQTL}$</th>
<th>$P_{SMR}$</th>
<th>$P_{HEIDI}$</th>
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</thead>
<tbody>
<tr>
<td>ENSG00000197279.3</td>
<td>6</td>
<td>ZNF165</td>
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<td>0.00167788</td>
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<td>G</td>
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<td>0.00226295</td>
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<td>0.00251022</td>
<td>3.90×10^{-8}</td>
<td>1.17×10^{-32}</td>
<td>6.05×10^{-7}</td>
<td>8.23×10^{-2}</td>
</tr>
</tbody>
</table>

aProbe ID.
bProbe chromosome.
cGene name.
dSNP name.
eAllele 1.
fAllele 2.
gFrequency of Allele 1 in the study population.
hEffect size of the allele.
iStandard error of the effect size.
jGWAS P-value.
k$P_{eQTL}$ P-value.
l$P_{SMR}$ P-value.
m$P_{HEIDI}$ P-value. Probes mapped to within the realms of the FUMA-defined susceptibility loci are highlighted in red.