### S3 Table. GG-NER Incision Complex genes

<table>
<thead>
<tr>
<th>Gene</th>
<th>Position</th>
<th>Burden (p-value)</th>
<th>SGS</th>
<th>SNV</th>
<th>Intolerance to MS (Z)</th>
<th>Intolerance to LoF (pLI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>USP45</td>
<td>6:99880182-99963565</td>
<td>0.711</td>
<td>significant</td>
<td>Y</td>
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<tr>
<td>CHD1L</td>
<td>1:146714291-146767447</td>
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<td>PARP1</td>
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<td>RPA2</td>
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<td>ERCC3</td>
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<td>GTF2H2</td>
<td>5:70330951-70363497</td>
<td>0.005*</td>
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<td>GTF2H5</td>
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<td>GTF2H4</td>
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<td>GTF2H1</td>
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</table>

**Legend:** Position – build HG19; Burden – p-values based on the c-alpha test of high-impact variants with AAF < 0.001 (see Methods section), "*" indicates gene not tested (no variants observed), †significant after multiple testing correction p < 0.002 (=0.05/23), ‡nominally significant p < 0.05; SGS – gene captured by a genome-wide significant or suggestive shared genomic segment, "-" indicates not tested (SGS only looks at autosomal chromosomes); SNV – "Y" indicates a single nucleotide variant with AAF < 0.001, high or moderate deleteriousness, and observed segregating in a high-risk MM pedigree or pathogenic in ClinVar; Intolerance to MS – gene’s intolerance to missense variants based on analysis of ExAC data, signed Z score based on deviation of observed counts from expected, positive Z indicates intolerance to variation; LoF – based on analysis of ExAC data, Loss of Function (LoF) variants include splice donor or acceptor or non-sense SNVs, genes with a probability of LoF Intolerance (pLI) >= 0.9 are considered extremely intolerant to LoF SNVs.