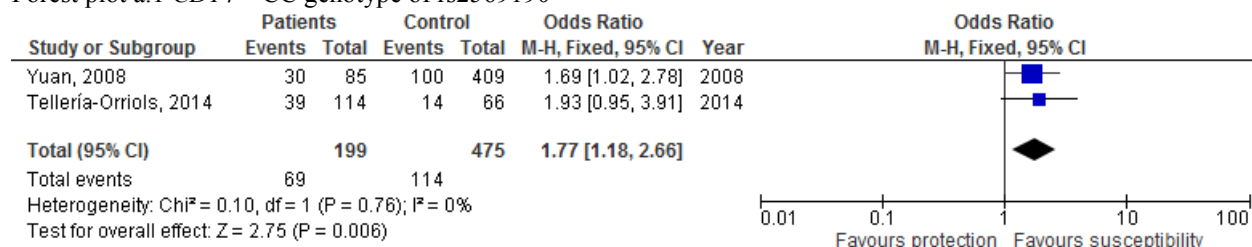


Additional file 2 - Meta-analyses of genetic association studies on susceptibility and outcome of pneumococcal disease

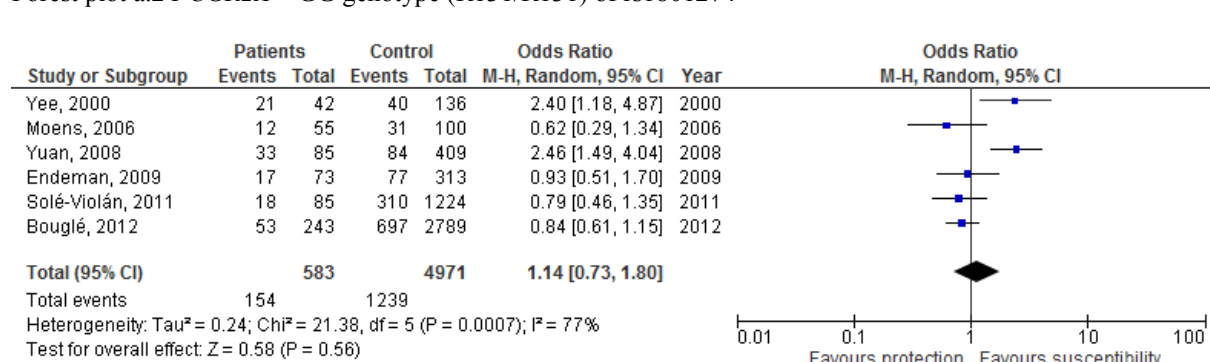
a. Susceptibility studies †

Forest plot a.1 *CD14* – CC genotype of rs2569190*



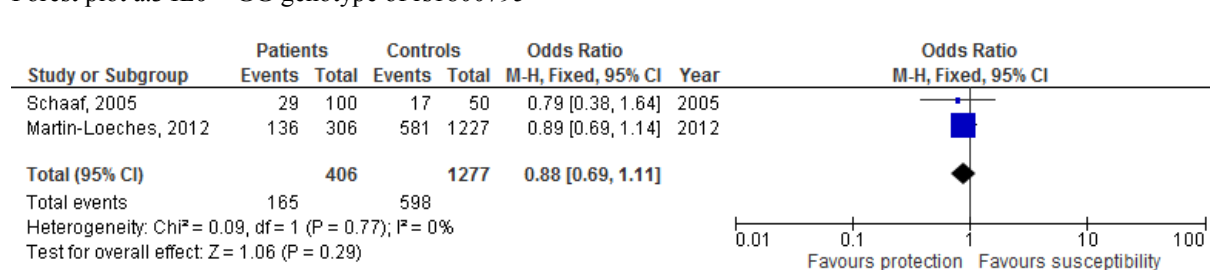
* Human Genome Variation Society (HGVS) representation: NM_000591.3(CD14):c.-260T>C

Forest plot a.2 *FCGR2A* – GG genotype (R131/R131) of rs1801274*



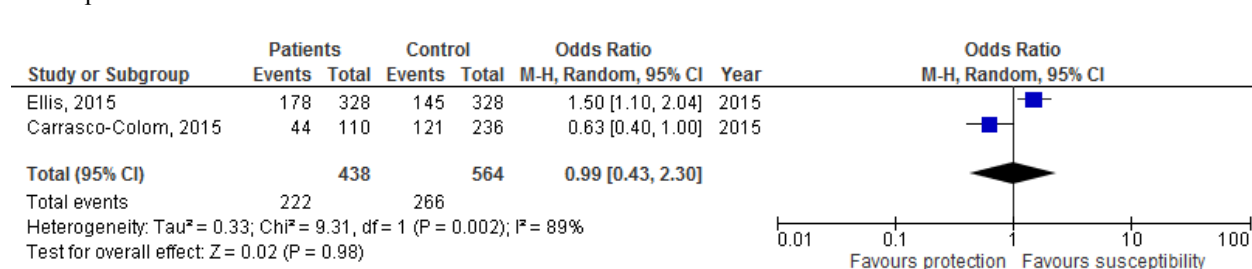
* HGVS representation: NM_021642.3(FCGR2A):c.497A>G (p.His166Arg)

Forest plot a.3 *IL6* – GG genotype of rs1800795*



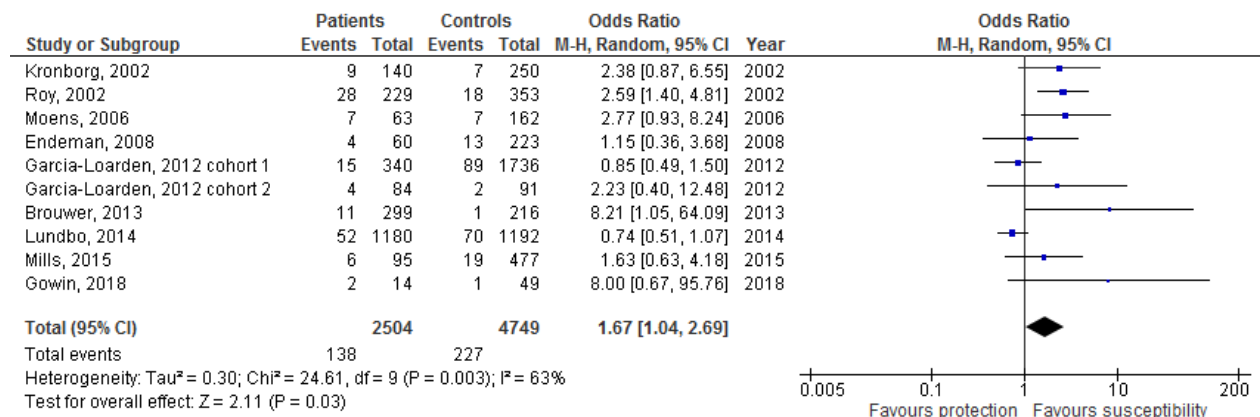
* HGVS representation: NC_000007.14(IL6):g.22727026C>G

Forest plot a.4 *IRAK4* – G allele of rs4251513*



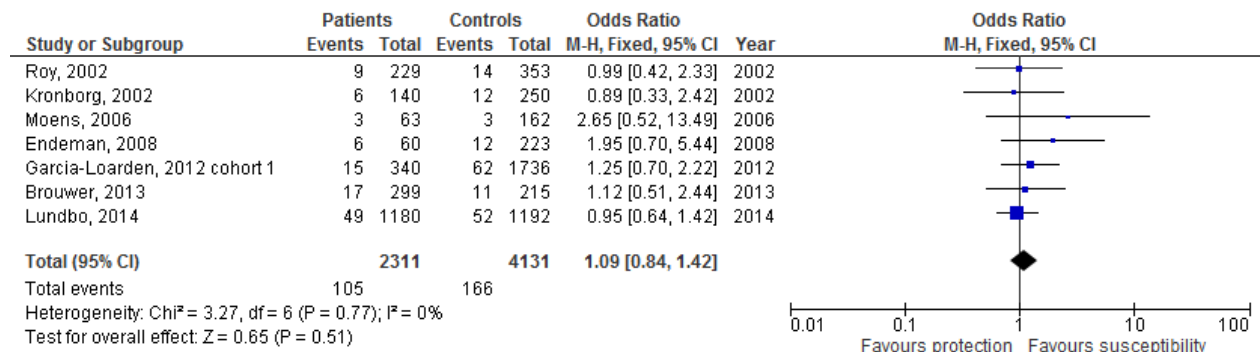
* HGVS representation: NC_000012.12(IRAK4):g.43780401G>C

Forest plot a.5 *MBL2* – variant alleles (O/O genotype) of rs1800450, rs1800451 or rs5030737 *



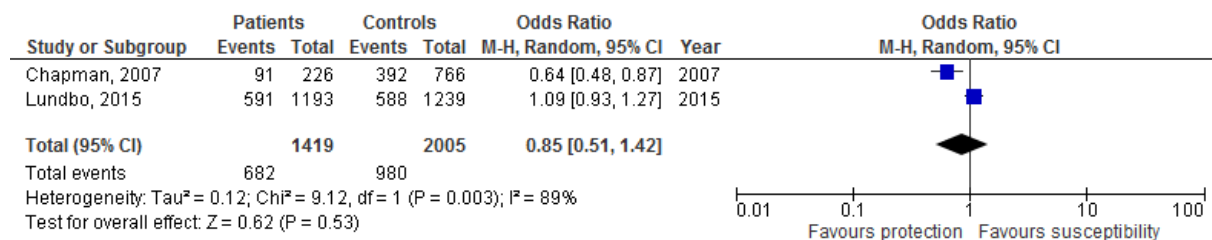
* HGVS representations: rs1800450; (NM_000242.2(MBL2):c.161G>A (p.Gly54Asp). rs1800451; NM_000242.2(MBL2):c.170G>A (p.Gly57Glu); rs5030737; NM_000242.2(MBL2):c.154C>T (p.Arg52Cys)

Forest plot a.6 *MBL2* – variant allele (X/X genotype) of rs7096206*



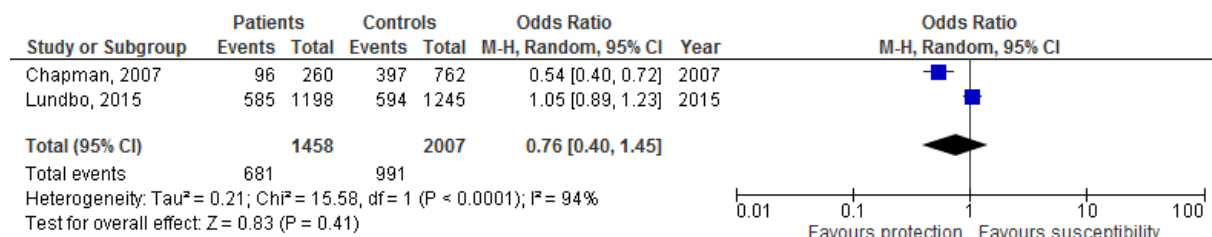
* HGVS representation: NC_000010.11(MBL2):g.52771925G>A,

Forest plot a.7 *NFKB1A* - BB+AB genotype (carriers variant allele) of rs3138053*



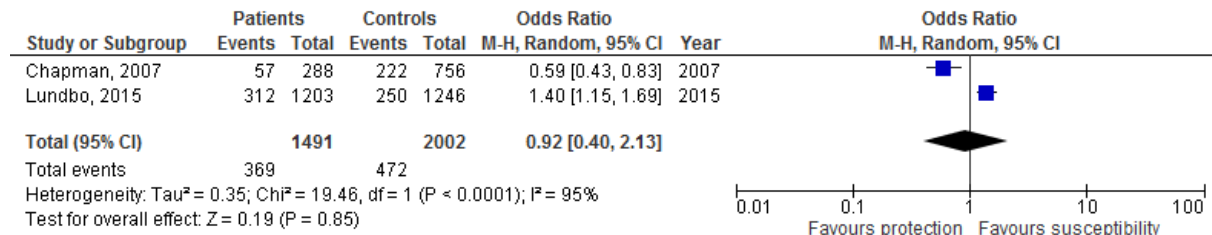
* HGVS representation: NC_000014.9(NFKB1A):g.35405648T>C

Forest plot a.8 *NFKB1A* - BB+AB genotype (carriers variant allele) of rs2233406*



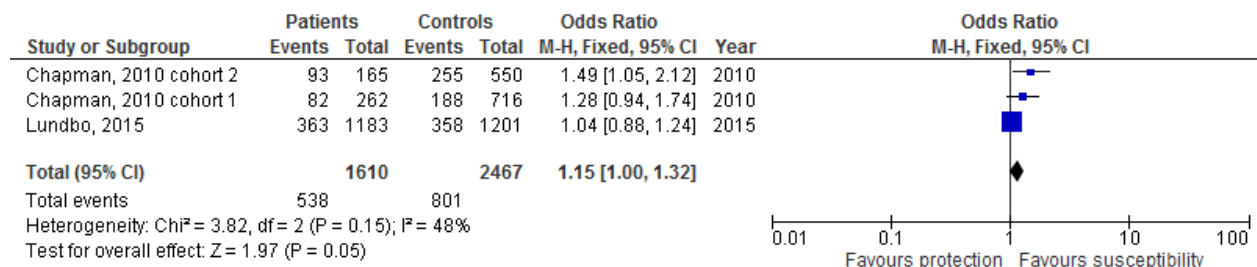
* HGVS representation: NC_000014.9(NFKBIA):g.35405593G>A

Forest plot a.9 *NFKBIE* - BB+AB genotypes (carriers variant allele) of rs529948*



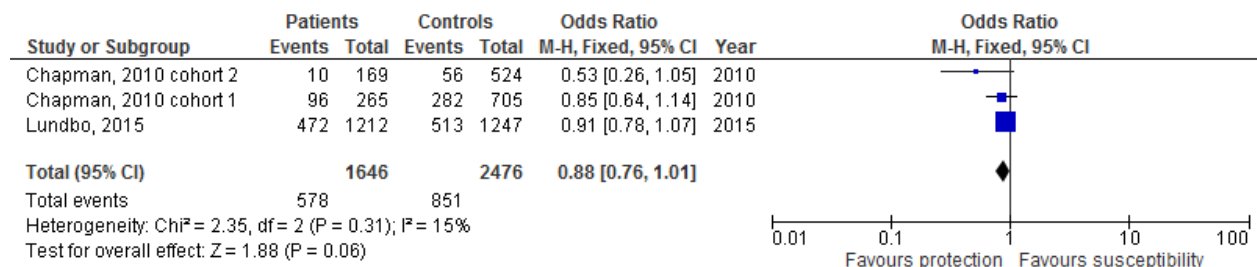
* HGVS representation: NC_000006.12(NFKBIE):g.44268632A>G

Forest plot a.10 *NFKBIL2* - AA genotype (wildtype) of rs760477*



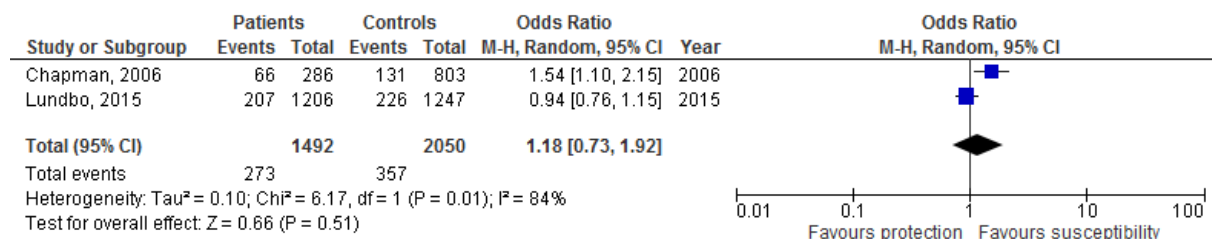
* HGVS representation: NC_000008.11(NFKBIL2):g.144443060G>A,

Forest plot a.11 *NFKBIZ* - BB+AB genotypes (carriers variant allele) of rs616597*



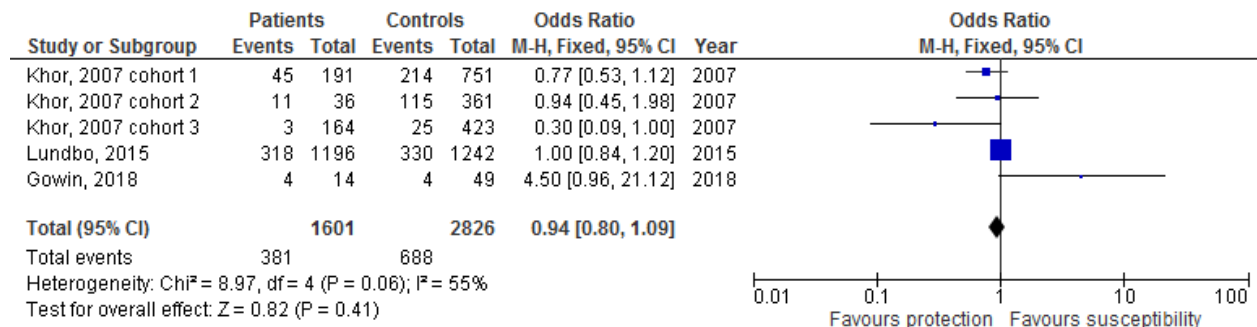
* HGVS representation: NC_000003.12(NFKBIZ):g.101850882A>C

Forest plot a.12 *PTPN22* - CT+TT genotypes of rs2476601*



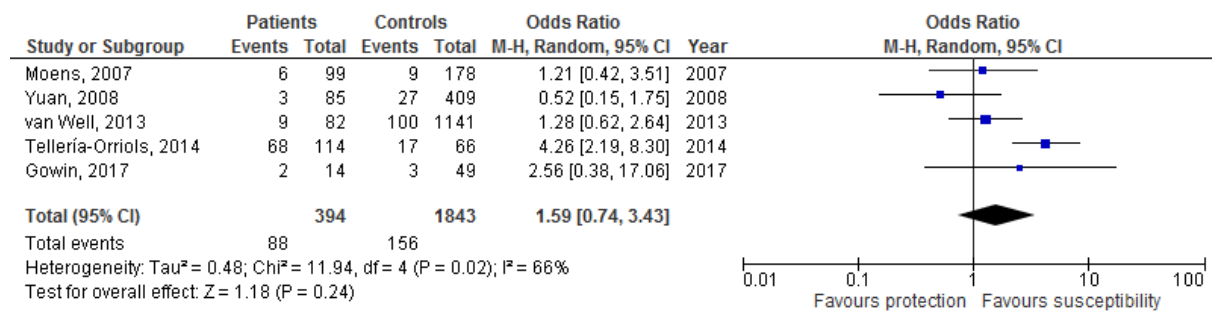
* HGVS representation: NM_015967.6(PTPN22):c.1858C>T (p.Arg620Trp)

Forest plot a.13 *TIRAP* - CT+TT genotypes (carriers variant allele) of rs8177374*



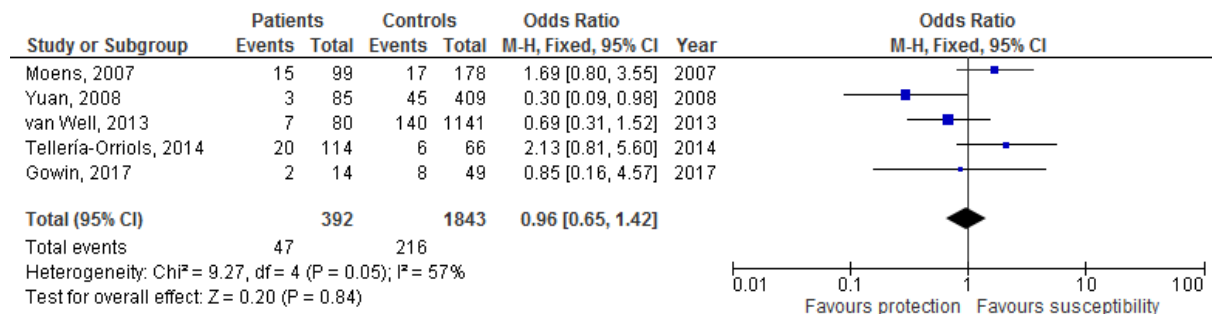
* HGVS representation: NM_001039661.1(*TIRAP*):c.539C>T (p.Ser180Leu)

Forest plot a.14 *TLR2* - GA+AA genotypes (RQ+QQ) of rs5743708*



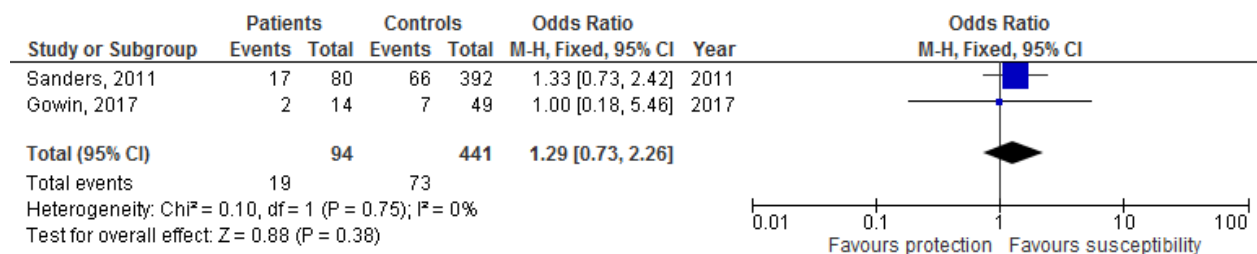
* HGVS representation: NM_003264.4(*TLR2*):c.2258G>A (p.Arg753Gln)

Forest plot a.15 *TLR4* - AG+GG genotypes (D299G+G299G) of rs4986790*



* HGVS representation: NM_138554.4(*TLR4*):c.896A>G (p.Asp299Gly)

Forest plot a.16 *TLR9* – CC genotype (wildtype) of rs352140*

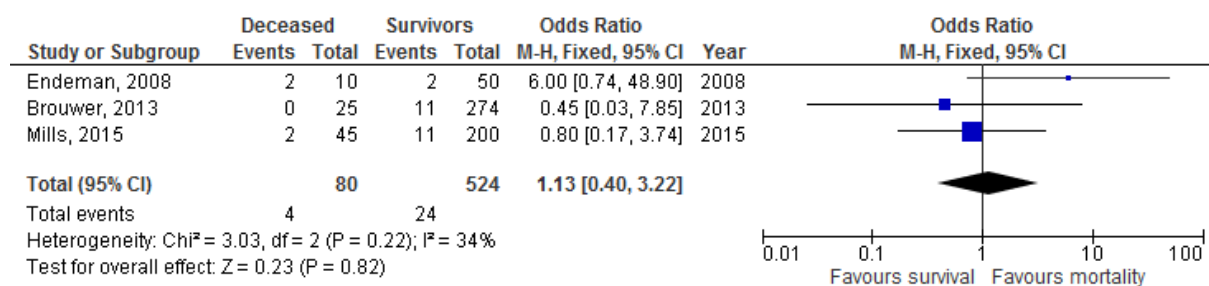


* HGVS representation: NC_000003.12(TLR9):g.52222681C>A

† Events are amount of patients or controls with reference genotype (in plot title)

b. Outcome studies †

Forest plot b.1 on mortality and *MBL2* – variant alleles of rs1800450, rs1800451 or rs5030737 (O/O genotype)*



* HGVS representations: rs1800450; (NM_000242.2(MBL2):c.161G>A (p.Gly54Asp). rs1800451; NM_000242.2(MBL2):c.170G>A (p.Gly57Glu); rs5030737; NM_000242.2(MBL2):c.154C>T (p.Arg52Cys)

† Events are amount of patients with reference genotype (in plot title)