**Supplementary Table 3. Meta-analysis model and specification in BUGS language**

Let k (=1, …, K) and nkj be the number of patients in the j*th* study of version k. Each study's success probability pkj is considered to have been selected from a population specific to the IMD version. This three-level hierarchical model can be expressed as follows:

ykj ~ *Binomial* (pkj , nkj)

logit(pkj) = θk + σ zkj zkj ~ *N*(0,1) (1)

θk = μ + ν εk  εk ~ *N*(0,1)

σ ~ *logN*(0,1) ν ~ *logN*(0,1) μ ~ *N* (0,106)

where the underlying success probabilities *pkj*, on the logit scale, of version *k* of the IMD from the *jth* study are distributed about an overall effect, *θk*, for the *kth* version of IMD, with σ representing the inter-study variability, which is assumed to be the same for all of the IMD versions. The version effects, *θk*, are distributed about an overall population effect *μ*, with *ν* representing the inter-version variability. Random effects were denoted with *zkj* and *εk* and wereassumed to be drawn from a standard normal distribution.

**BUGS Specification**

{

for( k in 1 : K ) {

for( j in 1 : J[k] ) {

y[k , j] ~ dbin(p[k , j],n[k , j])

logit(p[k , j]) <- b[k , j]

b[k , j] <- theta[k] + v\*z[k, j]

z[k, j] ~ dnorm( 0,1)

}

theta[k] <- mu + (sigma\*epsilon[k])

epsilon[k] ~ dnorm( 0,1)

P[k]<-exp(theta[k])/(1+exp(theta[k]))

}

for( k in 2 : K ) {

d[k-1]<-P[k]-P[k-1]

proba[k-1]<-step(d[k-1])

}

mu ~ dnorm( 0,1.0E-6)

sigma ~ dlnorm( 0,1)

PI<-exp(mu)/(1+exp(mu))

v ~ dlnorm( 0,1)

}