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# THE LANCET

## **Supplementary webappendix**

This webappendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Holmes MV, Newcombe P, Hubacek JA, et al. Effect modification by population dietary folate on the association between MTHFR genotype, homocysteine, and stroke risk: a meta-analysis of genetic studies and randomised trials. *Lancet* 2011; published online Aug 1. DOI:10.1016/S0140-6736(11)60872-6.

**Effect modification by population dietary folate on the association between *MTHFR* genotype, homocysteine, and stroke risk: a meta-analysis of genetic studies and randomised trials**

## **Supplementary materials**

### **Methods**

#### ***Search Strategy***

##### *Randomised clinical trials*

For MEDLINE, the Mesh terms “cardiovascular disease”, “coronary heart disease”, “coronary stenosis”, “myocardial infarction”, “cerebrovascular accident”, “stroke”, and “randomised controlled trial”, “clinical trial”, and “folic acid” were utilised. We also searched for trials published only as an abstract in conferences or meetings<sup>1</sup> as well as in previously published meta-analyses addressing this question<sup>2,3</sup>.

For inclusion in the analysis, studies had to: (i) be randomised and parallel in design; (ii) be conducted in adults; (iii) examine the effects of folic acid supplementation (with or without additional vitamin B supplementation); (iv) record stroke as an outcome, and; (v) have 12 months minimum follow-up. Studies using folic acid combined with a multivitamin/mineral tablet versus placebo/standard care were excluded<sup>4</sup>.

##### *Genetic studies*

We used the text words, which were also MeSH terms, “polymorphism”, “mutation”, “genotype”, “genetic”, “gene(s)”, “allele(s)” in combination with “stroke”, “cerebrovascular disorder/disease”, “cerebral ischemia”, “hemorrhagic stroke”, “(silent) brain infarction”. Literature searches were limited to “human”. All languages were included. Additional studies in the references of all identified publications, including previous relevant meta-analyses were identified.

In the analysis of the *MTHFR/C677T* variant on Hcy levels, studies were included if the design was case-control, cohort or cross-sectional. For inclusion in the analysis of *MTHFR/C677T* variant and stroke, case-control, cohort, or cross-sectional studies evaluating ischaemic, haemorrhagic or undifferentiated stroke were included. In all searches, when relevant information was not reported or there was doubt about duplicate publications, we contacted authors for clarification.

We supplemented information from published studies with unpublished genetic data obtained through direct contact with investigators of any study that had previously reported at least one genetic finding in stroke (for case-control studies) or in cardiovascular disease (for cohorts) in a peer reviewed journal. This allowed us to minimise the scope for reporting and publication bias. A total of 52 investigators of newly identified studies were asked to provide the most up-to-date information on the *MTHFR/C677T* variant and stroke risk in the form of genotype counts by disease status (cases [ischaemic, hemorrhagic or undifferentiated stroke] and controls) and the average values of Hcy and

folic acid by *MTHFR*/C677T genotypes in subjects without cardiovascular disease. Authors of 44 studies replied and provided information.

### **Data extraction**

#### *Randomised trials*

For randomised trials, the following variables were extracted (by MVH and JPC, **see eTable 5**): study design, patient characteristics, calendar years in which trial conducted; geographical region; type of stroke outcome(s) recorded; mean follow-up period, and; type of intervention(s) used as comparator (usual care, placebo, lower-dose folic acid, B vitamin alone). In addition, in each arm we recorded: (a) number of participants; (b) number of stroke events; (c) baseline and post-intervention levels of Hcy (where applicable), and; (d) doses of intervention(s) used. To determine the risk of bias, we evaluated: (i) sequence generation; (ii) allocation concealment; (iii) incomplete outcome data, and; (iv) selective outcome reporting, as suggested by the Cochrane Handbook for Systematic Reviews of Interventions<sup>5</sup>. Disagreements were resolved by consensus.

For each trial, point estimates of relative risk with 95% confidence intervals were derived using values of outcome events in each study arm. For all studies, we used intention to treat analysis. In cases of discrepancy or doubt about the number of events (stroke/TIA), we contacted authors to clarify details. Outcomes were recorded separately for (i) stroke, excluding TIA, and, (ii) stroke including TIA with comparator arms classified as (i) placebo, B-vitamins and/or folic acid [where folic acid in the comparator arm was low-dose compared to the intervention arm], and (ii) placebo only, excluding studies in which no placebo or usual care was used (i.e. Wrone<sup>6</sup> and Toole<sup>7</sup>), or events in participants randomised to vitamin B6 as one of three arms (i.e. Ebbing<sup>8</sup> and Bonaa<sup>9</sup>). To increase comparability of RCTs with genetic studies, we selected only stroke events excluding TIA as the main outcome and compared intervention with any of placebo, vitamin B and/or (low-dose) folic acid.

#### *Genetic studies*

For genetic studies the following variables were extracted (by PN and MVH, **see eTable 1 and 2**): study design, participant characteristics, country and calendar year in which the study was conducted, study design, proportion of males, mean age of participants, frequency of genotypes and alleles by case control status, average value (mean, median) and measure of dispersion (standard deviation, standard error, confidence interval, inter-quartile range or range) of Hcy and folic acid concentrations, stroke sub-type(s), language of publication, and ethnic background. We also calculated Hardy-Weinberg equilibriums (HWE) and disequilibrium coefficients for all genetic studies: in studies of *MTHFR*-stroke, only allele frequencies in controls were used; in *MTHFR*-homocysteine studies, allele frequencies of all participants were used. Where the number of subjects per genotype was selected/restricted *a priori* by the study investigators, HWE values were not estimated. For plots of allele frequency, we categorized studies into (i) probable folate status category, and (ii) ethnicity.

Ethnicity was classified according to the subjects investigated: studies or study subsets were categorized as follows: (i) Caucasian: including Israel and Turkey; (ii) African; (iii) East Asia including individuals from Japan, China, Korea, Hong Kong and Mongolia; (iv) South Asia including India, Pakistan and Bangladesh; (v) Latin America, and; (vii) mixed ethnicity. Plots were restricted to those studies that had values for all 3 genotypes and/or had not selected the number of subjects per genotype status.

### ***Categorization of genetic studies by probable folate status***

These categories (developed and validated by Dr Robert Clarke, Clinical Trial Service Unit (CTSU) and Epidemiological Studies Unit, University of Oxford, UK) used information on geographical location and dates during which the genetic study was conducted. and considered: (i) whether policies for folic acid fortification had been initiated and the date of implementation, and; (ii) whether there had been a change in folic acid levels at population levels through time. This information was derived from population based studies with information on folic acid. Geographical regions served as proxies of folate supplementation status. Categories were sorted according to the level of folic supplementation from the lowest to the highest as follows. (1) **Asia**: in addition to Asian countries (e.g. China, India, Hong Kong, Korea, Thailand, Mongolia) this category also included countries from North and sub-Saharan Africa conducted at any time. (2) **Europe-low** (pre-fortification): including studies from Ireland, Scandinavia (Denmark, Norway, Sweden, Finland), Netherlands, Russia and Turkey conducted at any time, and European countries conducted prior to folic acid fortification of cereal and flour, initiated in 1996. (3) **Europe mid** (post-fortification): including all European countries in 1996 or thereafter (except Ireland, Scandinavia, Netherlands, Russia or Turkey). (4) **America & Australia & New Zealand mid** (pre-fortification): which included studies from North-America, Australia and New Zealand prior to 1996, and studies from Central and South America conducted at any time, except for Chile, in which only studies conducted prior to 2000 were classified in this category. (5) **America & Australia & New Zealand high** (post-fortification): which included studies from North-America, Australia and New Zealand conducted in 1996 and thereafter, and studies conducted in Chile in 2000 and thereafter. For 67 studies (of 137) on which information was unavailable (from the publication, or previous publications from the same study, or after contacting study authors) on the timing of the study, 2-years prior to the publication date was used as the year the study was conducted. This value (median) was derived from the 70 studies that provided information on time of study conducted and year of publication. Information on the categories allocated to each genetic dataset included in the analysis is described in **eTables 1 and 2**.

### ***Data Analysis***

All meta analyses were performed using the 'metan' command<sup>10</sup> in Stata (StataCorp, Texas, USA) version 11.1. For meta-analysis of genetic association studies, we followed guidance from the Human Genome Epidemiology Network (HuGENet) HuGE Review Handbook<sup>11</sup>.

### *MTHFR and homocysteine level*

The estimate of the mean difference was restricted to individuals without clinical evidence of cardiovascular disease (ischaemic heart disease, stroke, or venous thrombosis). In order to explore the modifying effect of folic acid levels on the *MTHFR/C677T*-Hcy association, two strategies were utilized. First, we conducted a stratified meta analysis of the effect of the *MTHFR/C677T* variant on Hcy levels according to the 'probable folate categories'. Second, we performed a meta-regression analysis of the difference in Hcy levels by genotype against the average concentration of folic acid in each study. Analyses were then repeated only in studies with sample size  $\geq 500$  individuals in order to explore the influence of small-study bias in addition to funnel plot and Egger regression tests<sup>12</sup>.

### *MTHFR and Stroke*

The outcome 'main stroke comparison' was used to make comparisons with results from RCTs of Hcy lowering therapies. The 'main stroke comparison' included studies reporting: (i) only-ischaemic stroke, (ii) only-haemorrhagic stroke, (iii) both (ischaemic and haemorrhagic separately) stroke, or (iv) only unclassified stroke (studies in which neuroimaging tools were not available to classify the event as haemorrhagic or ischaemic). For studies reporting ischaemic and/or haemorrhagic stroke, diagnosis was by neuroimaging (MRI or CT). For this meta-analysis, we assumed equivalence between risk ratio and OR. We used the probable folate status categories to explore whether the *MTHFR/C677T* effect on stroke was modified by folic acid levels in a meta-regression. For studies with information on Hcy levels and stroke, the effect of the *MTHFR/C677T* variant on stroke was stratified according to the difference in Hcy levels (in tertiles) determined by the genetic variant.

### *Evaluation of small study bias*

To evaluate the potential influence of small-study bias on risk of stroke (*MTHFR* TT vs CC) in Asia, we first restricted the analysis to large studies with  $\geq 400$  stroke events. Second, we performed Egger regression tests<sup>12</sup>, which tests the null hypothesis that the funnel plot is symmetrical. Third, we implemented Duval and Tweedie's 'trim and fill' method<sup>13</sup> using the 'metatrim' command in Stata<sup>14</sup>. This method uses the observed asymmetry in the funnel plot to estimate the number and outcomes of missing studies, and adjusts the meta-analysis to incorporate missing data. Fourth, we generated a hypothetical study with 400 cases distributed evenly to CC and TT genotype groups according to a TT frequency of 15% (derived from HapMap values obtained at dbSNP; [www.ncbi.nlm.nih.gov/projects/SNP](http://www.ncbi.nlm.nih.gov/projects/SNP)) for genotype frequencies in Asian populations). We sequentially added the hypothetical studies and the used cumulative meta-analysis to estimate the number of such studies that would have to exist to:

- (a) reduce the point estimate to 1.15; the threshold at which evidence for a genetic association is downgraded based on the Venice criteria<sup>15</sup>;
- (b) reduce the point estimate to 1.10 (comparable to an expected relative risk reduction of 10% in an RCT of a Hcy lowering intervention), a threshold below which the sample size of a trial of a Hcy-lowering intervention on stroke risk might become too large to be considered practical;
- (c) reduce the lower bound of the 95%CI to 1.00.

Finally, we compared the number of large studies ( $\geq 400$  stroke cases) from Asia (low-folate region) category with other geographical regions.

Although Mendelian randomisation studies minimise confounding by environmental factors that may confound the blood marker-disease association, they can still suffer from confounding by linkage disequilibrium (LD). This is particularly relevant since in recent years, genome wide association studies have identified hits for established cardiovascular risk factors such as blood pressure, among those a variant (rs17367504) within the *MTHFR* gene<sup>16</sup>. In addition, since we included studies from different genetic ancestries, it might be possible that a different set of correlations (LD) of the rs1801133 variant occurs amongst different ethnic groups (e.g. Asians vs. Europeans), which therefore could confound our analyses. To explore this, we used the GLIDERS software<sup>17</sup> to evaluate long range LD for the rs1801133 variant among the main ethnic groups and cross-checked this information with genome wide association studies repositories (see Bioinformatics Tools below).

#### *Randomised clinical trials*

The trial arm containing Hcy-lowering treatment was assigned as the experimental group and compared against placebo, usual care, vitamin-B6 and/or low-dose folic acid. For the stroke outcome, we estimated log relative risk and log upper and log lower 95%CI and pooled estimates across studies using random (DerSimonian & Laird) and fixed (Mantel and Haenszel) effects modelling. The mean difference in change of Hcy between randomised groups ( $\Delta$ -experimental arm minus  $\Delta$ -comparator) was calculated. In a similar fashion to the genetic studies, we evaluated the potential effect of folate status intake on the results of the randomised trials. We conducted meta-regression analysis of the log of the relative risk of the trials against: (i) the probable folate status categories (using the same criteria as for genetic studies) and separately (ii) the mean difference in Hcy achieved by the intervention. Sensitivity analyses were conducted according to: (i) sample size (using 1000 randomised participants as a cut-point to dichotomise studies); (ii) risk of bias (low vs. any/high, according to Cochrane guidance<sup>5</sup>; see **eTable 5**); (iii) the outcome recorded (stroke only vs. stroke plus transient ischaemic attack - we re-estimated the relative risk of stroke for stroke plus TIA in studies where TIA was reported separately as a clinical event (HOPE-2<sup>18</sup>, Righetti<sup>19</sup> and Wrona<sup>6</sup> and; (iv) according to the reference arm used (placebo only vs. [placebo or vitamin-B6 alone]). In addition, the meta-analysis estimate computed by omitting one study at a time was conducted to check that no individual trial had a major influence on the summary estimate (**eFigure 7**). We used the DerSimonian and Laird Q test in all meta-analyses to evaluate the degree of heterogeneity between studies, and the  $I^2$  measure<sup>20</sup> to describe the proportion of total variation in study estimates due to heterogeneity. Funnel plot and Egger regression tests were conducted to evaluate the presence of small-study bias.

#### *Bioinformatics tools*

We used GLIDERS<sup>17</sup> (<http://mather.well.ox.ac.uk/GLIDERS>) to check for potential confounding by long-range linkage disequilibrium (LD). GLIDERS is a web-based tool that allows users to check long-range LD ( $>200$ kb) between SNPs. Using HapMap phase 3, the following criteria were used: Build 36,

MAF $\geq$ 0.05, cis- and trans-chromosome,  $r^2\geq$ 0.3, no lower/upper range (i.e. associations between any pair-wise HapMap SNPs over any distance would be retrieved), and searching all ancestries (Asian, European, African) separately. We searched for SNPs in long-range LD with rs1801133 retrieved from GLIDERS using 2 genome wide association studies repositories for associations with CVD traits and/or outcomes: (1) NHGRI GWAS Catalog<sup>21</sup> and (2) SNPnexus <http://www.snp-nexus.org>. Both were accessed on 30th April 2009.

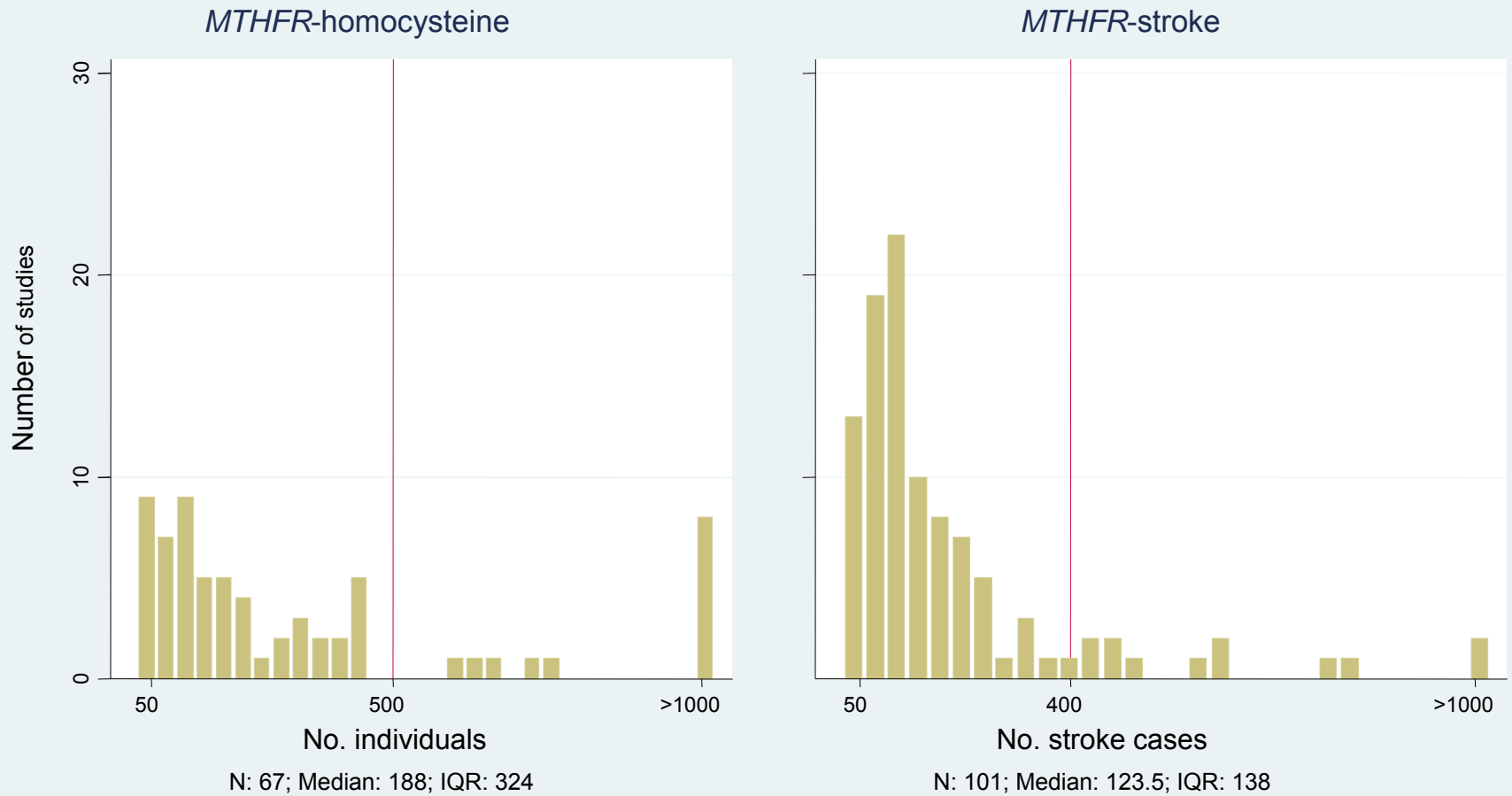
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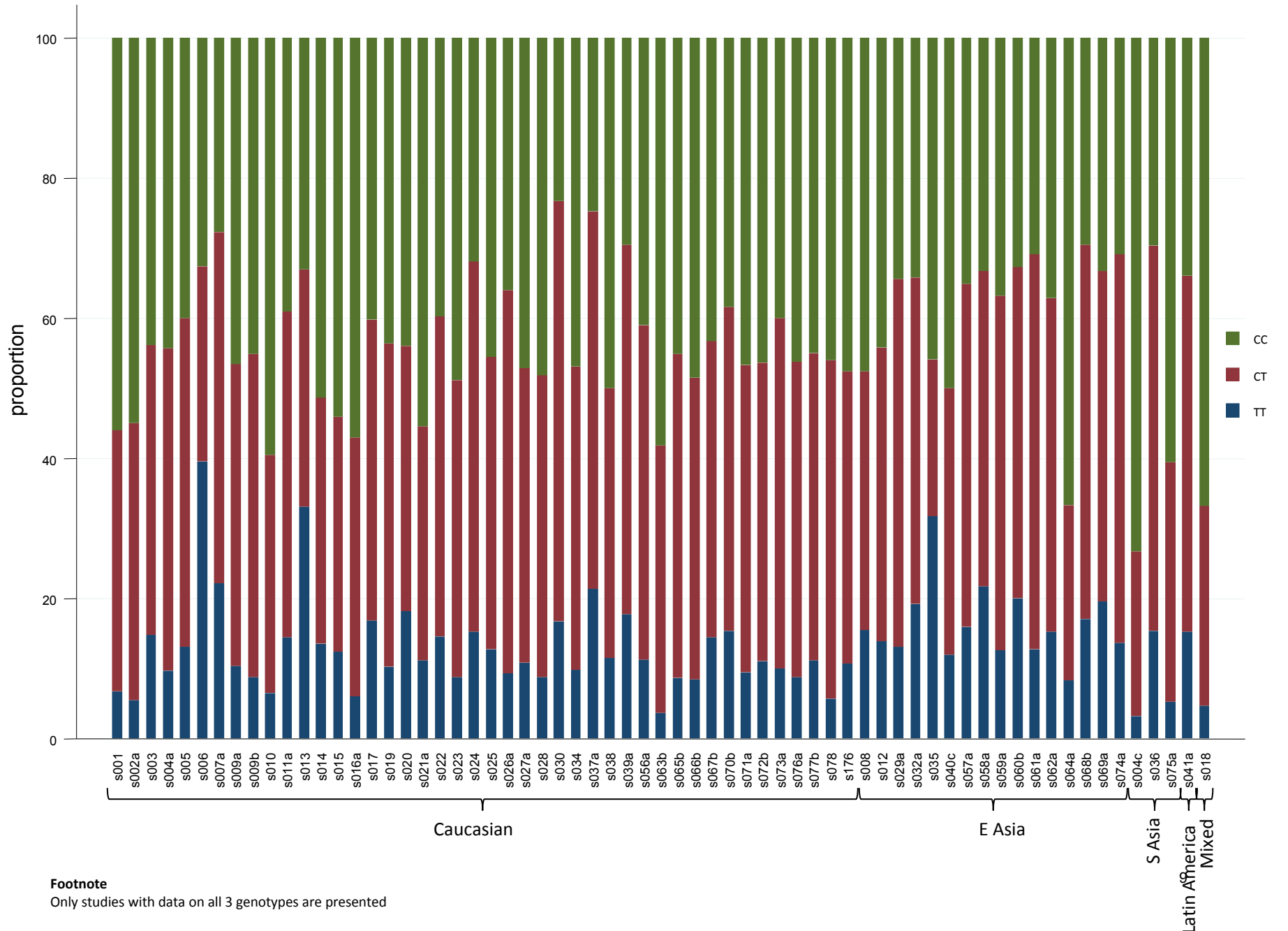


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**eFigure 1.** Frequency histogram of sample size and number of stroke cases for *MTHFR*-homocysteine (left panel) and *MTHFR*-stroke (right panel) datasets.



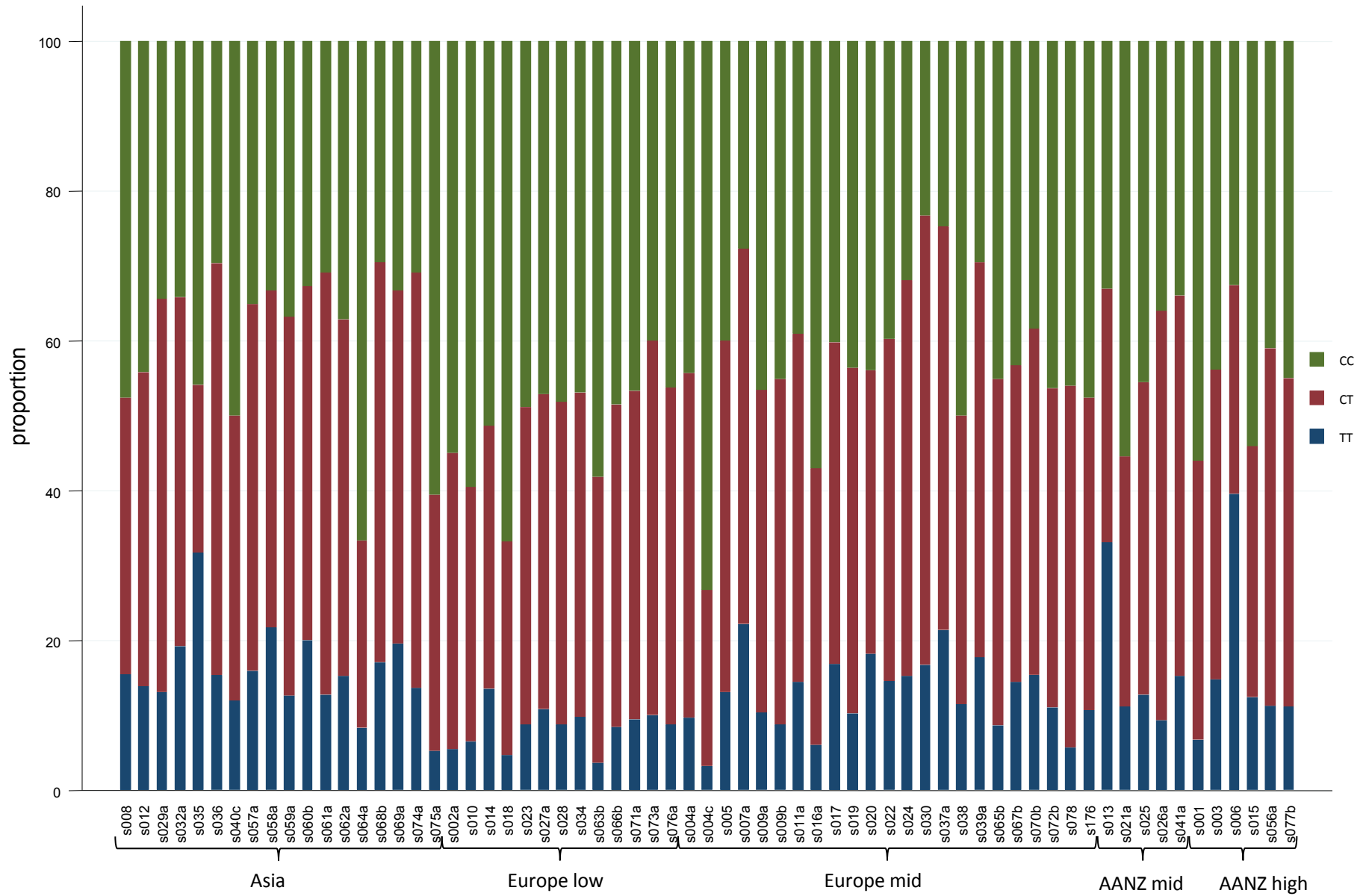
**eFigure 2(a) and (b)** Genotype frequency of *MTHFR*/C677T variant in studies used to determine the effect on homocysteine levels, classified by (a) ethnicity, and (b) probable folate status categories.



**Footnote**

Only studies with data on all 3 genotypes are presented

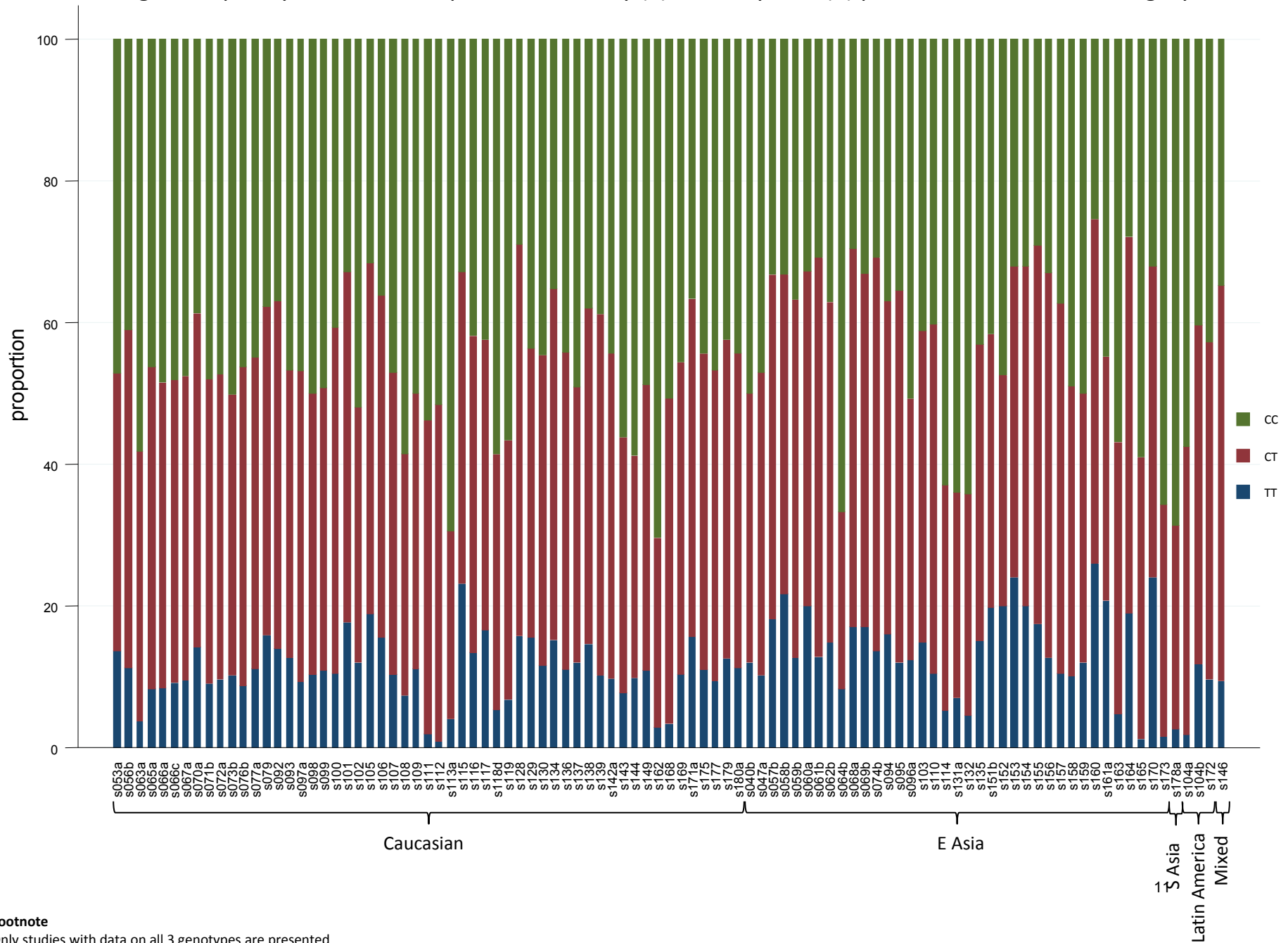
eFigure 2(b)



**Footnote**

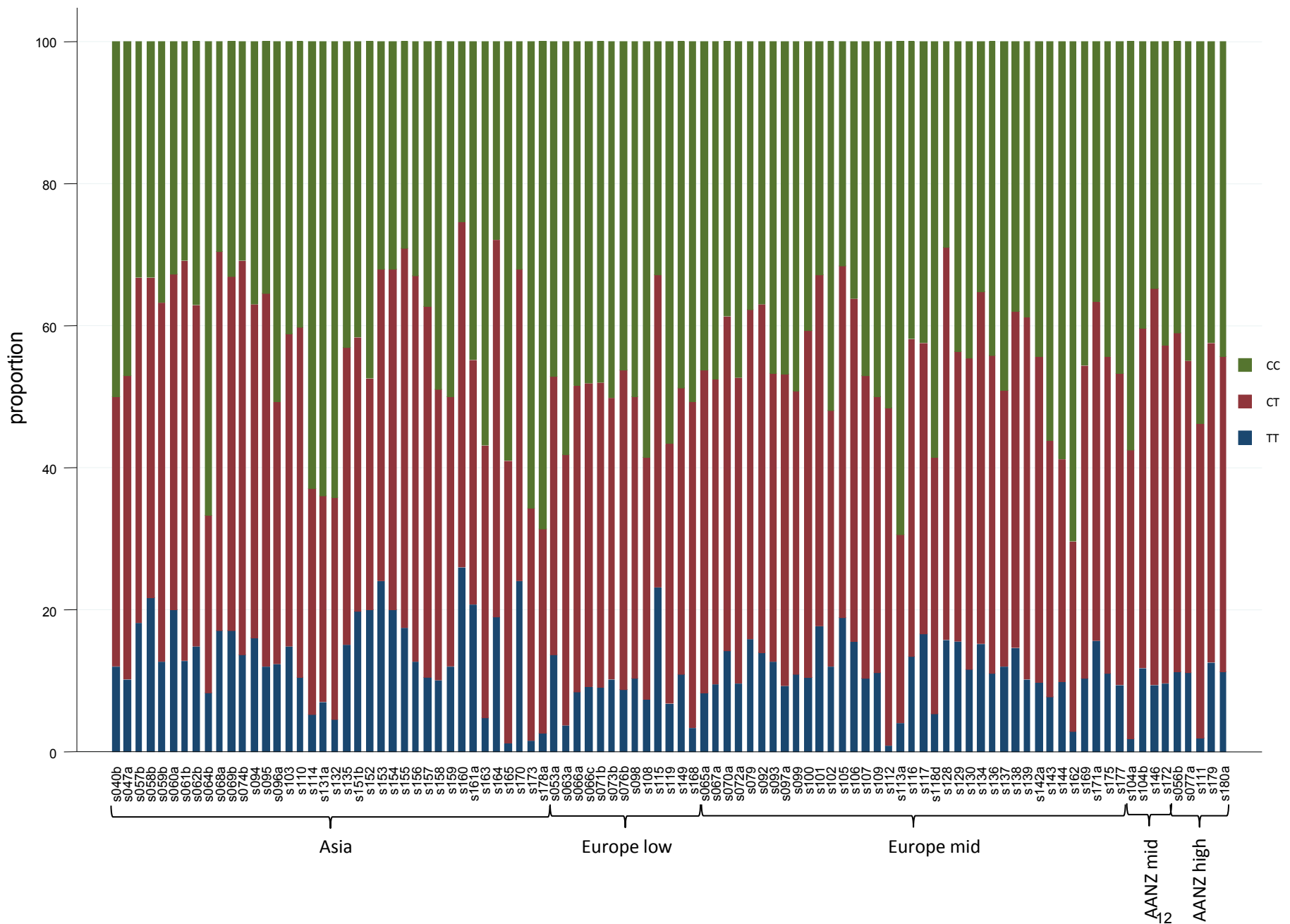
Only studies with data on all 3 genotypes are presented

**eFigure 3(a) and (b)** Genotype frequency of *MTHFR*/C677T variant in studies utilised to estimate the effect on stroke, according to frequency in control samples, classified by (a) ethnicity, and (b) probable folate status category.



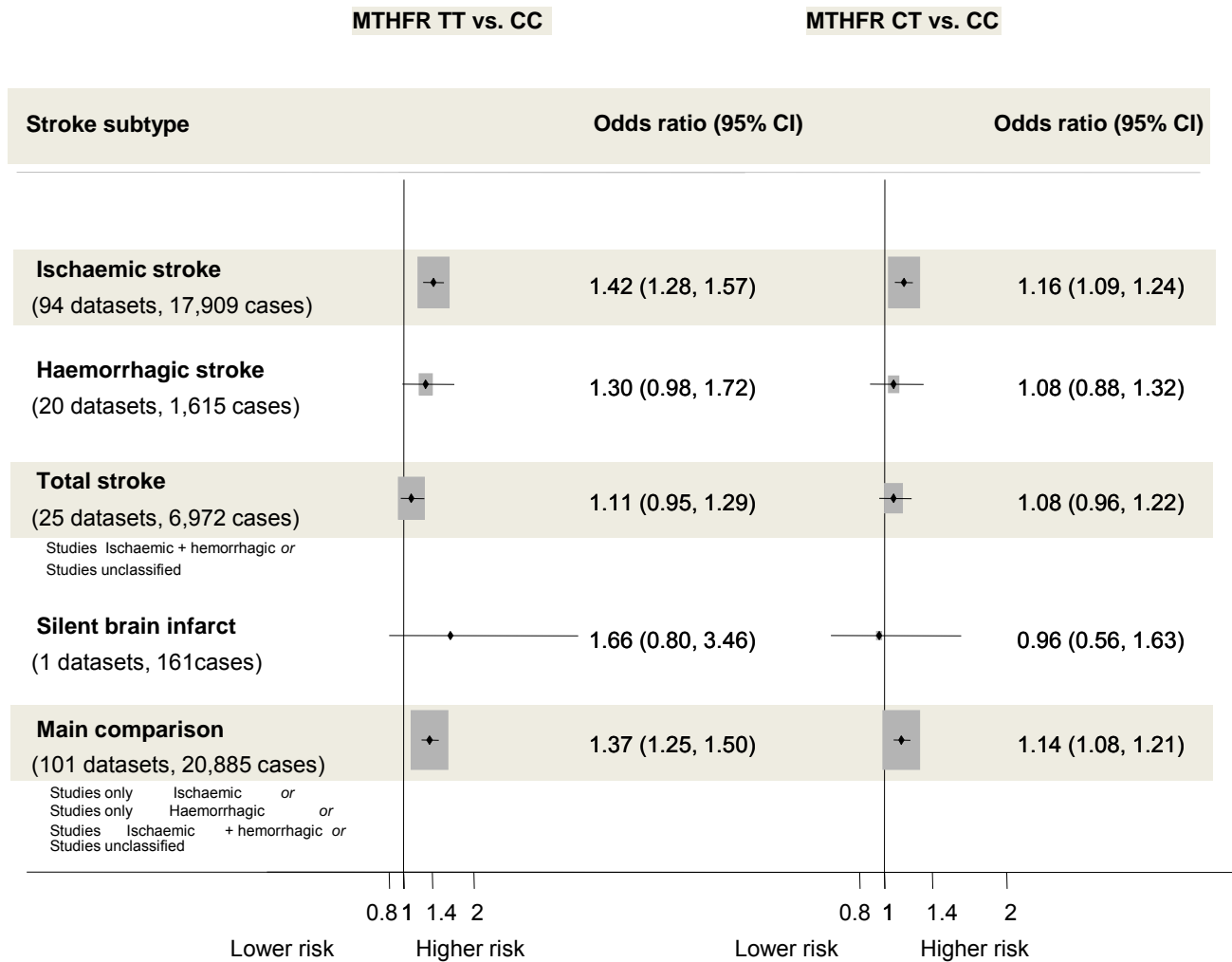
**Footnote**  
Only studies with data on all 3 genotypes are presented

**eFigure 3(b)**

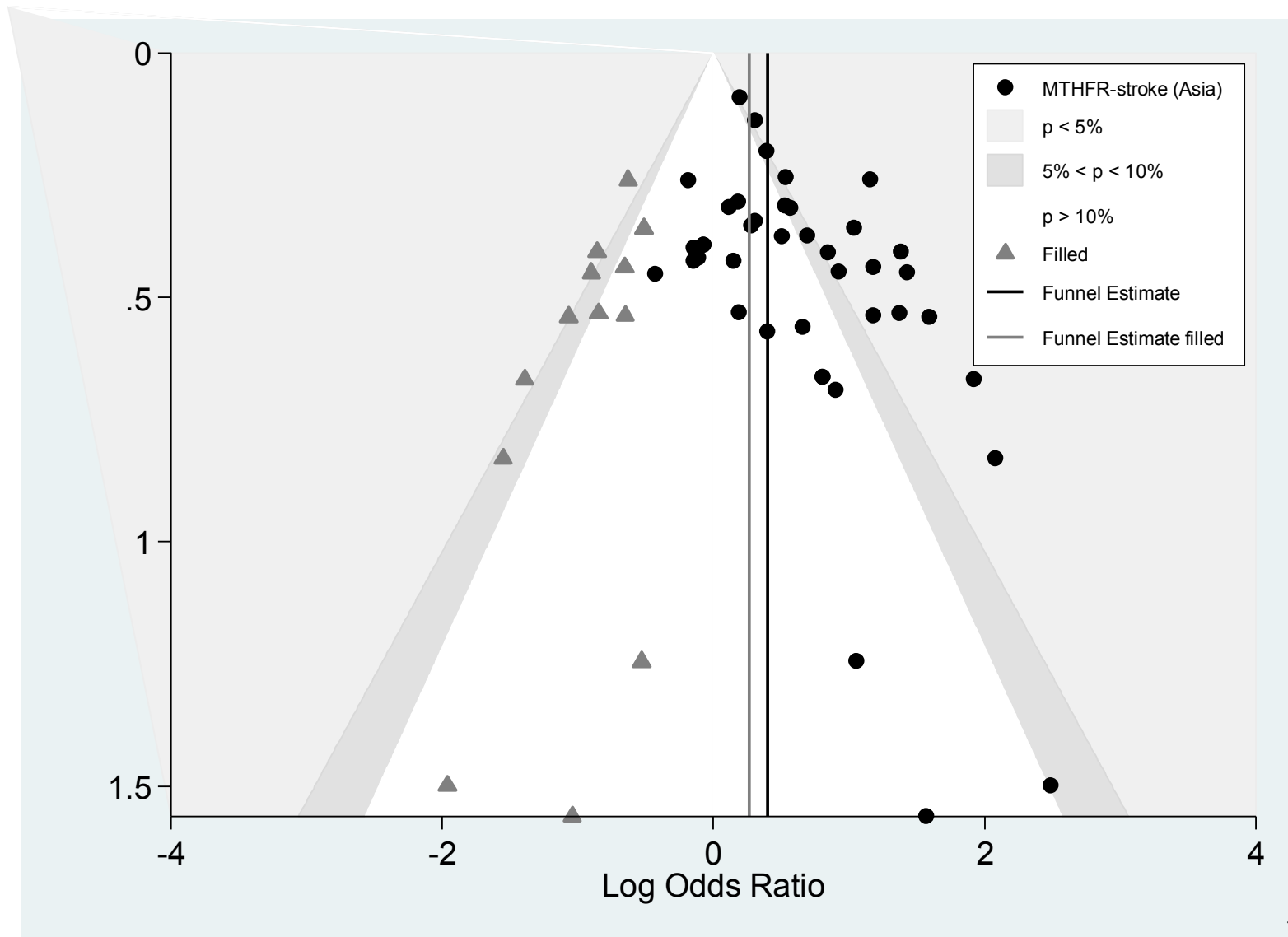


**Footnote**  
Only studies with data on all 3 genotypes are presented

**eFigure 4** Odds ratio of the *MTHFR*/C677T variant on different stroke sub-types. Left panel compares individuals homozygous for T allele with CC subjects. Right panel compares heterozygous with CC subjects.

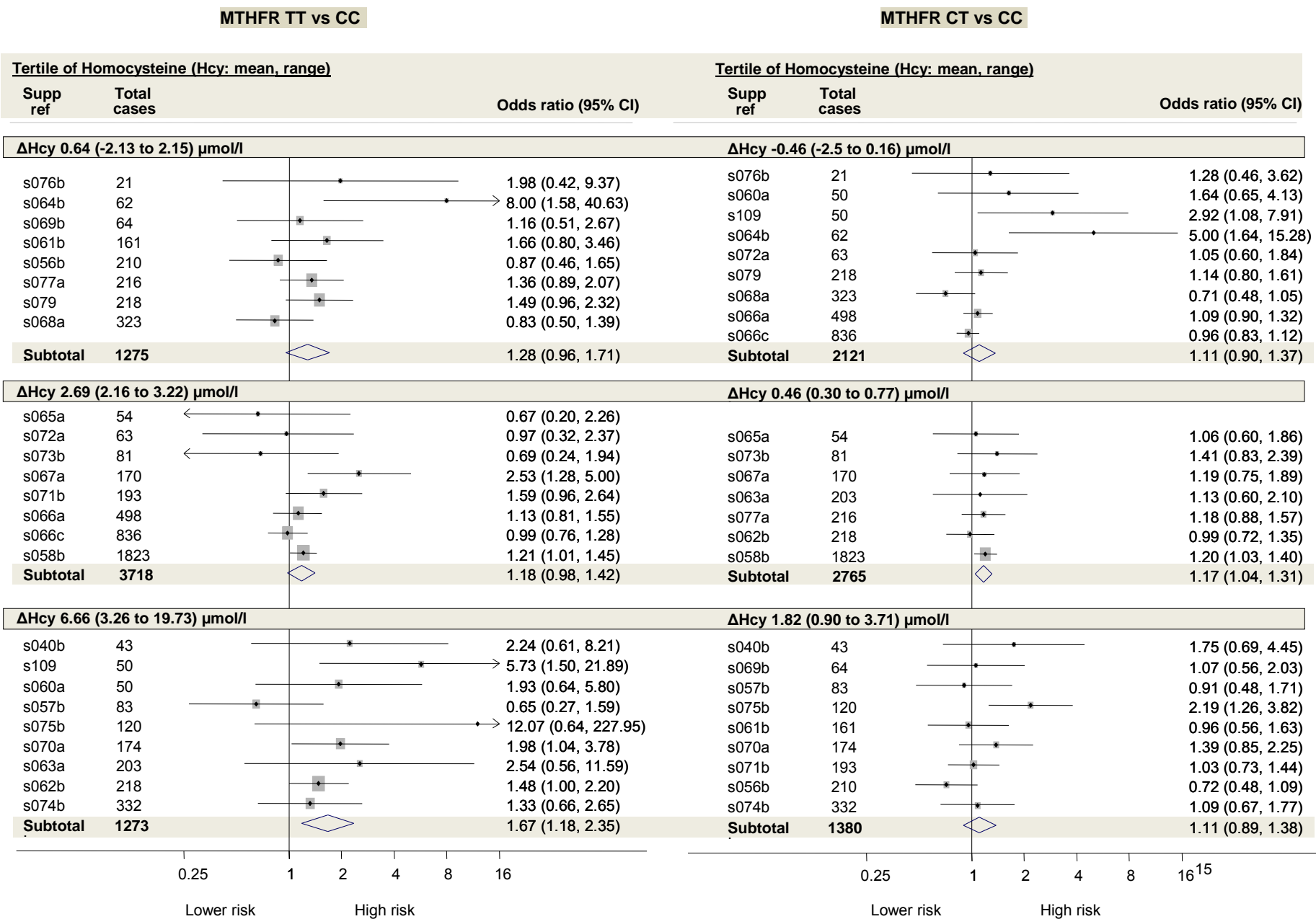


**eFigure 5** Contour-enhanced funnel plot of *MTHFR*-stroke studies in Asia using the trim and fill analysis. The black dots represent the observed studies and the grey triangles represent hypothetical missing studies.

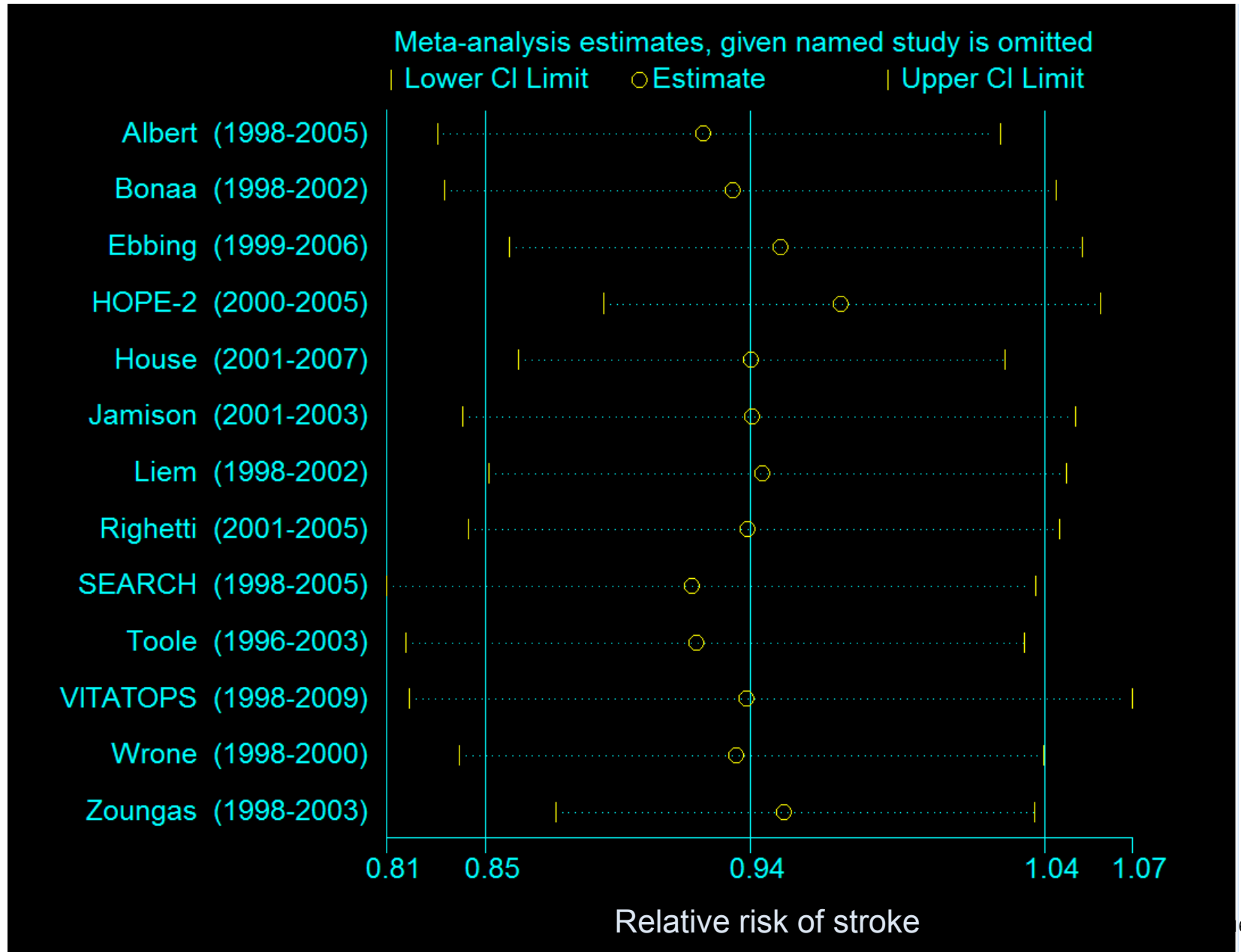




**eFigure 6.** Odds ratio of the *MTHFR*/C677T variant on stroke stratified according to the tertile of difference in homocysteine determined by the genetic variant. Left panel compares individuals homozygous for T-allele with CC subjects. Right panel compares heterozygous with CC subjects.



**eFigure 7** Influence analysis to evaluate the effect of individual trials, omitted one at a time, on the summary estimate of randomised clinical trials of homocysteine-lowering interventions in stroke risk.



## Supplementary Tables

**eTable 1.** Characteristics of genetic studies included in the analysis of *MTHFR/C677T* and homocysteine levels.

**eTable 2.** Characteristics of genetic studies included in the analysis of *MTHFR/C677T* and stroke risk.

**eTable 3.** Sensitivity analysis to illustrate the number of hypothetical large null studies that are needed to shift the point estimate observed in the *MTHFR/C677T*-stroke meta-analysis to several thresholds.

**eTable 4.** Linkage disequilibrium of the *MTHFR/C677T* variant by ethnic group.

**eTable 5.** Characteristics of randomised clinical trials of homocysteine-lowering interventions in stroke.



Zee RY_WHS	s077b	1992-2000	NA	USA	America-ANZ high	Caucasian	0	NR	2773	10966	11229	2729.96	11052.09	11185.96	0.2189	0.0017
Eikelboom JW	s056a	1996-1998	NA	Australia	America-ANZ high	Caucasian	60	NR	23	98	84	25.29	93.42	86.29	0.5419	-0.0112
Bailey LB	s015	NR	2000	USA	America-ANZ high	Caucasian	0	NR	23	62	100	15.76	76.48	92.76	0.0123	0.0391

**Footnotes**

Arranged by folate regional supplementation.

† year of conduct calculated for unknown studies by subtracting the median time between study conclusion and publication date (2 years)

For HWE calculations, allele frequencies from all individuals included

References with suffix a,b,c denotes different datasets used from same study

ANZ: Australia & New Zealand; NR: Not reported; NA: Not applicable





**Table 3.** Sensitivity analysis to illustrate the number of hypothetical large null studies that are needed to shift the point estimate observed in the *MTHFR* /C677T-stroke meta-analysis to several thresholds.

Analysis	<i>MTHFR</i> TT vs. CC – Asia (low folate region)			
	All studies		Large-studies (≥400 cases)	
	No. of hypothetical studies	OR (95%CI)	No. of hypothetical studies	OR (95%CI)
<b>Observed result meta-analysis</b>	0	1.68 (1.44, 1.97)	0	1.28 (1.11, 1.48)
<b>Reduce point estimate to 1.15</b>	41	1.15 (1.07, 1.23)	6	1.14 (1.03, 1.27)
<b>Reduce point estimate to 1.10</b>	60	1.10 (1.04, 1.16)	12	1.10 (1.00, 1.20)
<b>Lower 95%CI to cross line of 1.00</b>	260	1.02 (1.00, 1.05)	14	1.09 (1.00, 1.18)

**Footnotes**

The sample size of the hypothetical studies was 400 cases and 400 controls with equal distribution to TT and CC alleles – i.e. generating an OR of 1.0 (95%CI: 0.76, 1.32).

Each hypothetical study was added to the dataset of studies on *MTHFR* -stroke using cumulative meta-analysis techniques.



**eTable 4.** Linkage disequilibrium of the *MTHFR* /C677T variant by ethnic group.

Ancestry	SNP rs number	Chromosome number	Position (base pair)	r2 with rs1801133	Complex disease association	
					SNPnexus†	GWAS catalog‡
Asian	9651118	1	11784801	0.38	none	none
	7554327	1	11784801	0.31	none	none
	2336377	1	11872557	0.3	none	none
	2639453	1	11905131	0.33	none	none
European	6540999	1	11755953	0.32	none	none
	11121828	1	11757041	0.32	none	none
	7538516	1	11759269	0.32	none	none
	6697244	1	11761435	0.32	none	none
	4845882	1	11765754	0.34	none	none
	1994798	1	11777342	0.35	none	none
	6541003	1	11778454	0.36	none	none
	4846052	1	11780538	0.37	none	none
	4846054	1	11791817	0.34	none	none
	12404124	1	11796456	0.37	none	none
	198391	1	11799004	0.37	none	none
	198393	1	11802272	0.37	none	none
	198401	1	11810971	0.38	none	none
	535107	1	11812055	0.37	none	none
198406	1	11820179	0.37	none	none	
Africa	4846052	1	11780538	0.56	none	none
	198401	1	11810971	0.62	none	none
	2639453	1	11905131	0.35	none	none

**Footnotes**

SNPs in long-range LD with rs1801133 identified through Genome-wide Linkage Disequilibrium Repository and Search (GLIDERS) from HapMap phase 3 Build 36, MAF $\geq$ 0.05, cis- and trans-chromosome, r $2\geq$ 0.3, no lower/upper range - i.e. associations between any pair-wise HapMap SNPs over any distance would be retrieved (<http://mather.well.ox.ac.uk/GLIDERS>). Accessed 30th April 2010

† SNPnexus (<http://www.snp-nexus.org>); all SNPs uploaded using population data from HapMap (not limited to any ancestry) and outcome listed for Complex Diseases and Disorders. Accessed 30th April 2010

‡ from Hindorff LA, Junkins HA, Mehta JP, and Manolio TA. A Catalog of Published Genome-Wide Association Studies. Available at: [www.genome.gov/gwastudies](http://www.genome.gov/gwastudies). Accessed 30th April 2010.

SNP-trait associated traits are limited to those with P $<$ 1.0 x 10 $^{-5}$ ; studies reported in the catalog have genotyped at least 100,000 SNPs in the initial stage.

eTable 5. Characteristics of randomised clinical trials of homocysteine-lowering interventions in stroke

Trial (reference)	Years conducted	Characteristics of participants at study entry	Outcome reported	Geographical Location	Folic acid			Comparator arm (B vitamins and/or placebo or usual care)			Follow-up (months)	Mean Age (years)	Participants with homocysteine measured (%)	Folic acid dose (mg/day)	Vit-B12 dose (mg/day)	Vit-B6 dose (mg/day)	Reference arm	Risk of Bias evaluation (using Cochrane collaboration nomenclature)				
					Number randomised	Stroke only (fatal and non-fatal)	TIA only	Number randomised	Stroke only (fatal and non-fatal)	TIA only								Sequence generation	Allocation concealment	Blinding	Incomplete outcome data	Selective outcome reporting
Righetti (45)	2001-2005	Chronic kidney disease	Fatal and nonfatal stroke and TIA	Italy	37	1	3	51	2	8	29	64	†	5	0.25	125	Placebo	low-risk	low-risk	unclear	low-risk	low-risk
House (49)	2001-2007	Type 1 or 2 diabetes and diabetic nephropathy	Stroke (fatal and non-fatal) ‡	Canada	128	6	NA	124	1	NA	32	60.4		2.5	1	25	Placebo	low-risk	low-risk	low-risk	low-risk	low-risk
Liem (42)	1998-2002	Stable CHD	Fatal stroke, non-fatal stroke and TIA	Netherlands	300	8*	NA	293	12*	NA	42	65	‡	0.5	0	0	Usual care	low-risk	unclear	high-risk	low-risk	low-risk
Zoungas (50)	1998-2003	Chronic kidney disease	Fatal and nonfatal stroke	Australia, New Zealand	156	8	NA	159	18	NA	43	56	†	15	0	0	Placebo	unclear	unclear	low-risk	low-risk	low-risk
Wrone (51)	1998-2000	Chronic kidney disease	Stroke (unspecified) and TIA	USA	351.8	19	6	177	8	1	24	60	†	5 or 15	0.006	12.5	1 mg/d folic acid	low-risk	low-risk	low-risk	low-risk	low-risk
Jamison (52)	2001-2003	Chronic kidney disease	Fatal and nonfatal thromboembolic stroke	USA	1032	37	NA	1024	41	NA	38	66	113 (5.5)	40	2	100	Placebo	low-risk	unclear	low-risk	low-risk	low-risk
Ebbing (43)	1999-2006	Stable angina, ACS or aortic valve stenosis	Nonfatal thromboembolic stroke and fatal stroke	Norway	1544	28	NA	1552	39	NA	38	61	2557 (82.6)	0.8	0.4	40	Placebo / B6	low-risk	low-risk	low-risk	low-risk	high-risk
Bonaa (44)	1998-2002	Myocardial infarction	Any fatal and nonfatal stroke (including SAH)	Norway	1872	49	NA	1877	49	NA	36	63	3027 (80.7)	0.8	0.4	40	Placebo / B6	low-risk	low-risk	low-risk	low-risk	low-risk
Albert (53)	1998-2005	CVD or 3 risk factors for CVD	Fatal and nonfatal stroke (ischaemic, haemorrhagic)	USA	2721	79	NA	2721	69	NA	87	64	600 (11)	2.5	1	50	Placebo	unclear	unclear	low-risk	low-risk	low-risk
HOPE-2 (48)	2000-2005	CVD or diabetes	Fatal and nonfatal stroke (ischaemic, haemorrhagic) and TIA	Canada, USA (72.1 %); Brazil, Western Europe, Slovakia (27.9 %)	2758	111	131	2764	147	120	60	69	1064 (19.3)	2.5	1	50	Placebo	low-risk	low-risk	low-risk	low-risk	low-risk
Toole (54)	1996-2003	Ischaemic Stroke	Recurrent ischaemic stroke (fatal & non-fatal)	USA, Canada, Scotland	1827	152	NA	1853	148	NA	24	66	†	2.5	0.4	25	20 micro g/d folic acid †	low-risk	low-risk	low-risk	low-risk	low-risk
SEARCH (46)	1998-2005	Myocardial infarction	Any fatal and nonfatal stroke (including SAH)	United Kingdom	6033	269	NA	6031	265	NA	80	64	§ (10)	2	1	0	Placebo	low-risk	low-risk	low-risk	low-risk	low-risk
VITATOPS (47)	1998-2009	Stroke or TIA	Fatal and nonfatal stroke	20 Countries †	4089	360	NA	4075	388	NA	41	62.6	1164 (14.3)	2	0.5	25	Placebo	low-risk	low-risk	low-risk	low-risk	low-risk

**Footnotes**

Studies were independently reviewed for risk of bias (MVH and JPC)  
 ACS, acute coronary syndrome; CHD, coronary heart disease; CVD, cardiovascular disease; SAH, subarachnoid haemorrhage; TIA, transient ischaemic attack  
 \* TIA reported together with stroke values  
 † No specific value reported in manuscript for the number of participants tested for Hcy  
 ‡ Only the group randomised to intervention was tested for Hcy at follow-up  
 § No absolute value of the number of participants tested for Hcy recorded in manuscript (percentage reported)  
 † reference arm also contained 200 µg B6 and 5µg of B12  
 ‡ For Wrone (51), we combined doses of 15mg/day and 5mg/day folic acid together as the intervention arm against the comparator group of 1mg/day folic acid  
 § House (49) used the same diagnostic criteria as Toole (54)  
 † 20 countries: Australia, Austria, Belgium, Brazil, Hong Kong, India, Italy, Malaysia, Moldova, Netherlands, New Zealand, Pakistan, Philippines, Portugal, Republic of Georgia, Serbia & Monte Negro, Singapore, Sri Lanka, United Kingdom and United States of America

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