

Supplementary Information:

Supplementary Form 1: Data extraction form

Supplementary Form 2: Risk of bias assessment form based on Newcastle Ottawa Scale

Supplementary Figure 1 to Supplementary Figure 28: Results of random effect model analysis showing strength of association between various genetic factors and risk of development of oral squamous cell carcinoma.

Supplementary Figure 29: Results of random effect model analysis showing strength of association between positive family history and risk of development of oral squamous cell carcinoma.

Supplementary Figure 30: Results of random effect model analysis showing strength of association between positive family history and risk of development of oral squamous cell carcinoma.

Supplementary Data Extraction Form 1

Title:

Comments by review authors: *(Please fill this section after the completion of data extraction)*

Study ID:		Date form completed:
First author:	Year of study:	Data extractor:
Reference:		Language:
Citation:		

Corresponding Author details:

1. General Information

Publication type		Journal Article ☐	Abstract ☐	Other (specify e.g. book chapter) _____
Country of study:				
Funding source of study:			Potential conflict of interest from funding?	

Eligibility	Confirm eligibility for Review (Highlight the appropriate choice):	
	Yes	No
	If No , reason for exclusion:	
Type of study	☐ Case control study ☐ Observational Study– cross sectional	
Participants (Review authors insert inclusion criteria as defined in Protocol)	Population:	Gender:
	Sample size calculation:	
	Do the participants meet the criteria for inclusion?	Yes ☐ No ☐ Unclear ☐
	Are healthy controls included in this study for comparison?	Yes ☐ No ☐ Unclear ☐
	Study focusing tobacco associated OSCC	Yes ☐ No ☐ Details:
	Histological type of OSCC (Grading of OSCC)	
	Studies focusing on Genetic susceptibility/risk of development of OSCC	Yes ☐ No ☐ Details:

	Habit of tobacco consumption	Yes ☐ No ☐ Details:
	Habit of alcohol drinking	Yes ☐ No ☐ Details:
	Does the factor of family history of disease is considered in the study?	Yes ☐ No ☐ Details:
	What is the sample type used in study	Saliva ☐ Tissue ☐ Blood/serum/plasma ☐ Cell lines ☐
	Method of assessment of genetic abnormality	qPCR ☐ western blot ☐ Details:
	Does the study measure the odd's ratio or fold change as an outcome?	Yes ☐ No ☐ Details:
	Any genetic pathway explored in the study?	Yes ☐ No ☐ Details:
	Does the study is Homogenous (if all the study samples are depicting uniform features except biological variations)	Yes ☐ No ☒ Details:
Notes	Key conclusions	
Missing Data if any		

Continuous Data (please add groups if necessary)

Outcome

1. Correlation of genetic abnormality with susceptibility/risk of development of OSCC:
Yes ☐ No ☐
2. Which particular gene or group of gene shows high risk for development of OSCC:
3. How other confounding factors like habit of tobacco consumption, alcohol drinking and family history influences the susceptibility/risk of development of OSCC.
4. Genetic mechanism if any explored in the study.

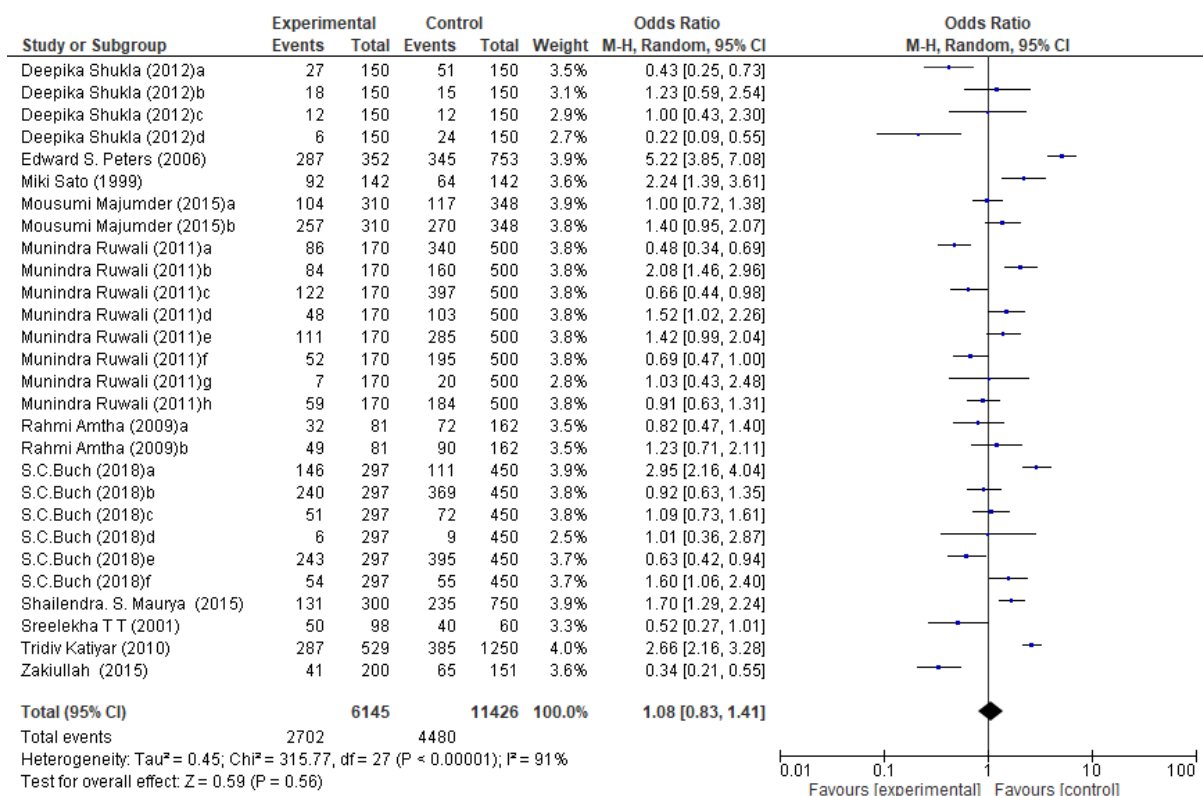
Supplementary Form 2: Risk of bias: New castle Ottawa scale

A study can be awarded a maximum of one star for each numbered item within the Selection Category. A maximum of two stars can be given for Comparability. A maximum of three stars given for outcome and Exposure categories			
Study Title:			*
Selection	1) Is the case definition as OSCC or Oral cavity cancer is adequate?	a) Yes, with Histological confirmation	
		b) Yes, with linkage to records from archival or reports	
		c)No description	

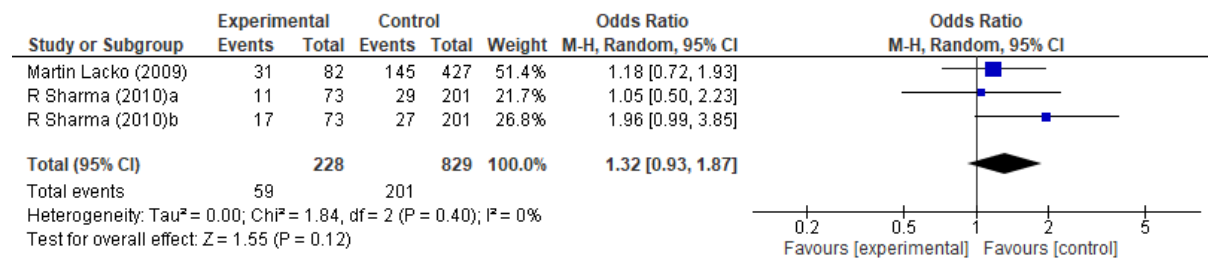
	2) Representativeness of the cases	a) Consecutive or obviously representative series of cases	
		b) Potential for selection biases or not stated	
	3) Selection of Controls	a) Healthy controls	
		b) Adjacent/contralateral healthy area	
		c) No description	
	4) Definition of Controls	a) No history of disease	
		b) No risky habits	
	Comparability	1) Comparability of cases and controls on the basis of the design or analysis	
		a) study controls for segregation of diseases	
Exposure/Intervention	1) Ascertainment of exposure -- Genetic assessment	b) study controls for any additional factor	
		a) Single gene or group of gene assessment	
		b) Odds ratio of association or fold change mentioned	
	2) Same method of gene assessment for cases and controls	c) no description	
		Yes	
		No	
Outcome -- Susceptibility /risk of OSCC	a) Independent blind assessment		
	b) Linked to family history		
	c) Linked to risky habits		

Results in Random effects

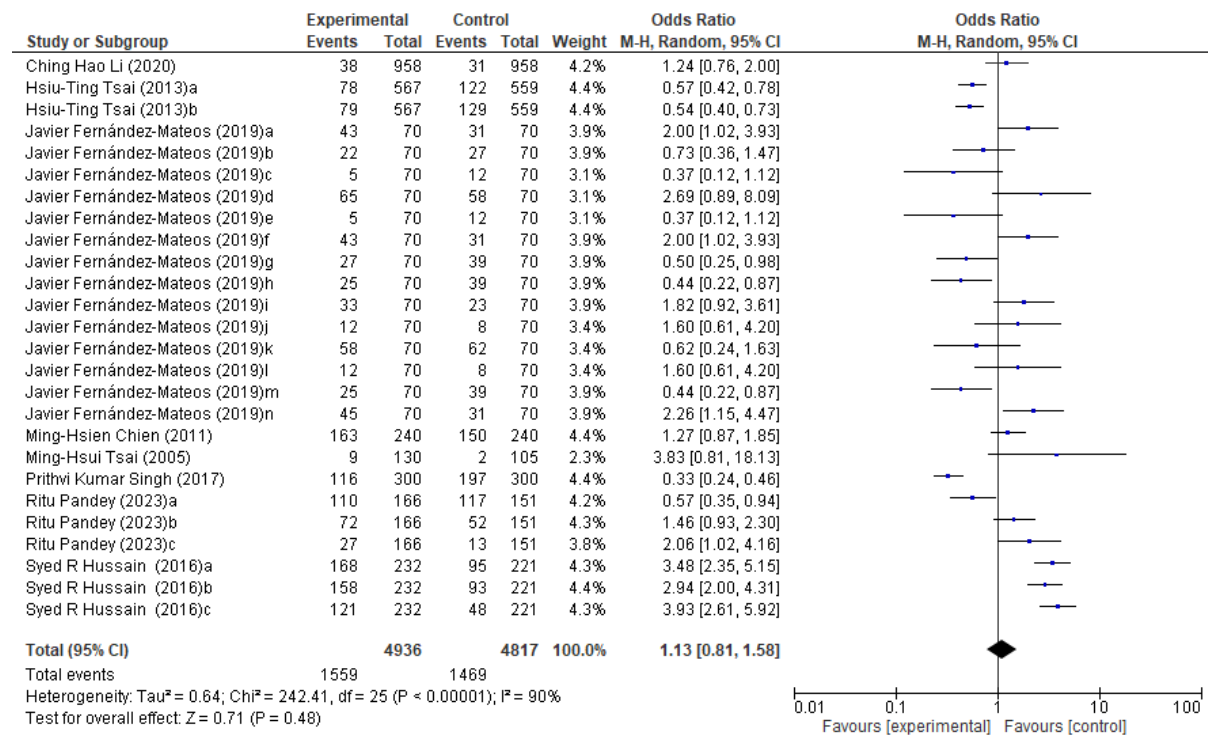
Supplementary Figure 1: GSTM



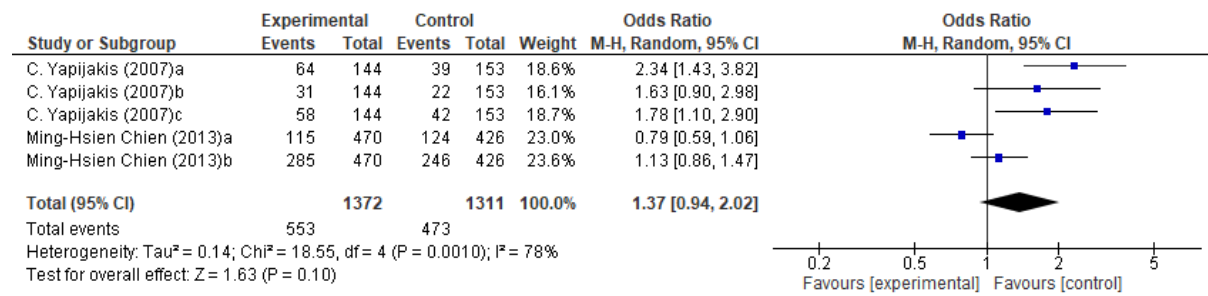
Supplementary Figure 2: UGT



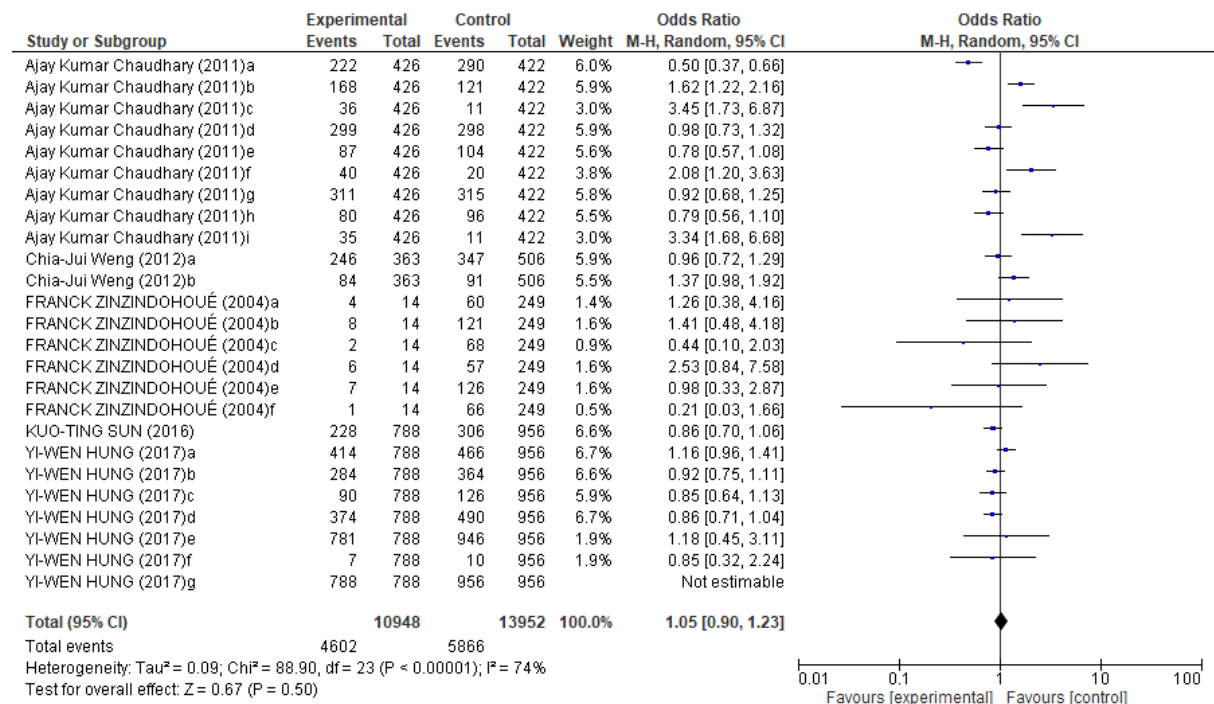
Supplementary Figure 3: Interleukin



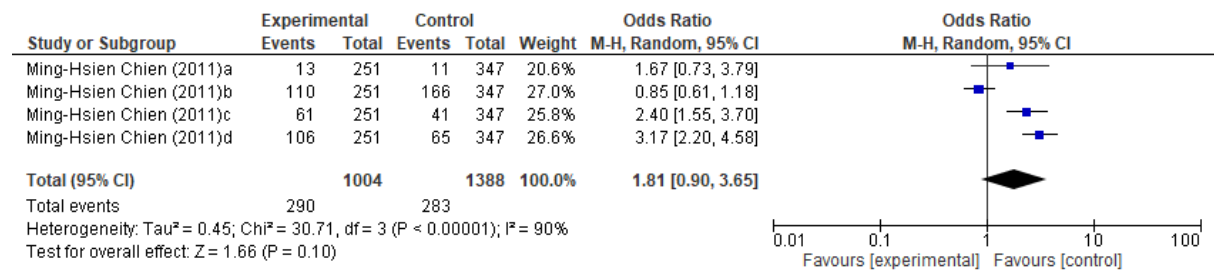
Supplementary Figure 4: VEGF



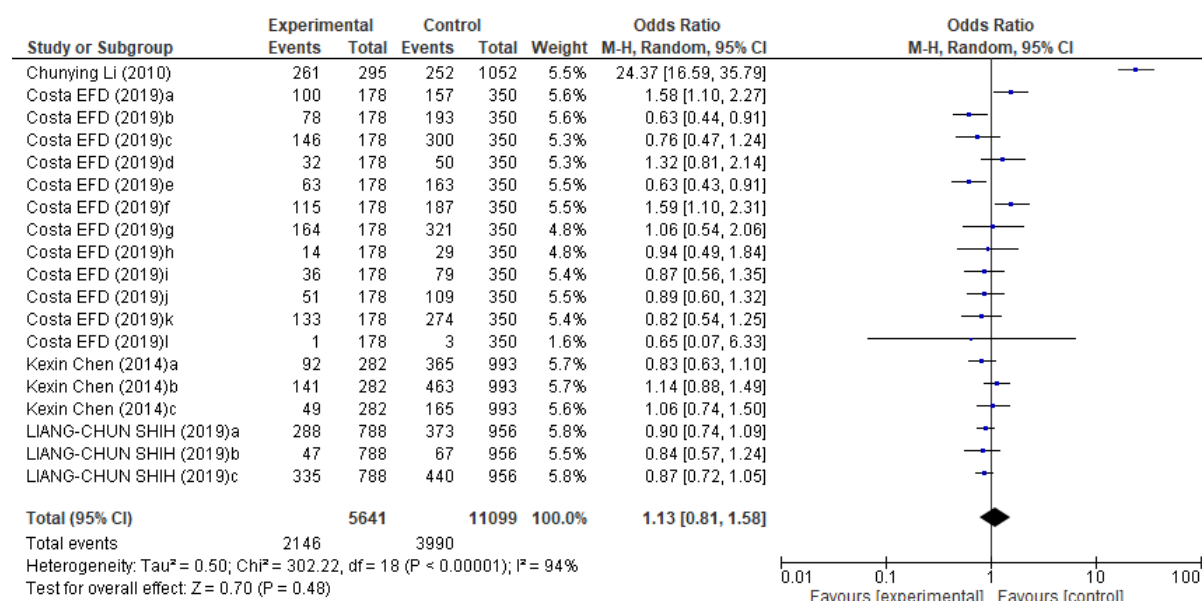
Supplementary Figure 5: MMP



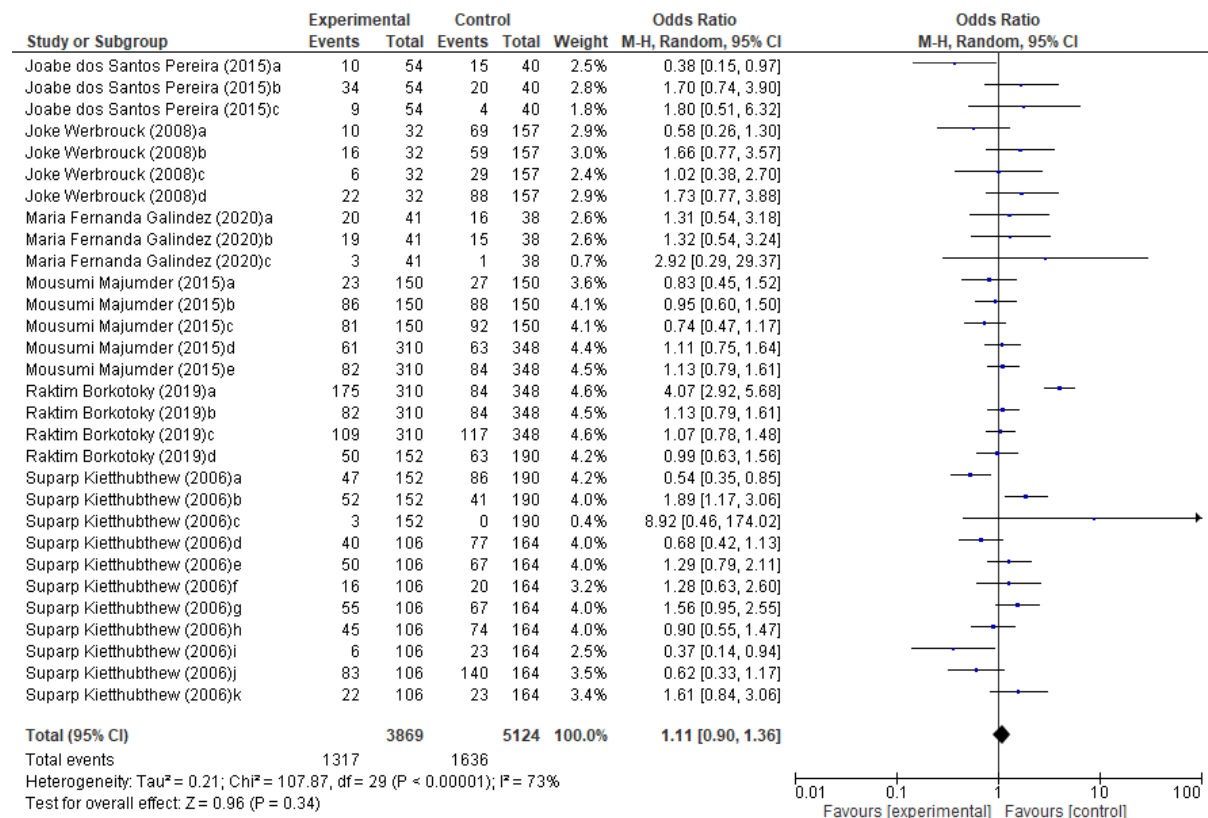
Supplementary Figure 6: Ecadherin



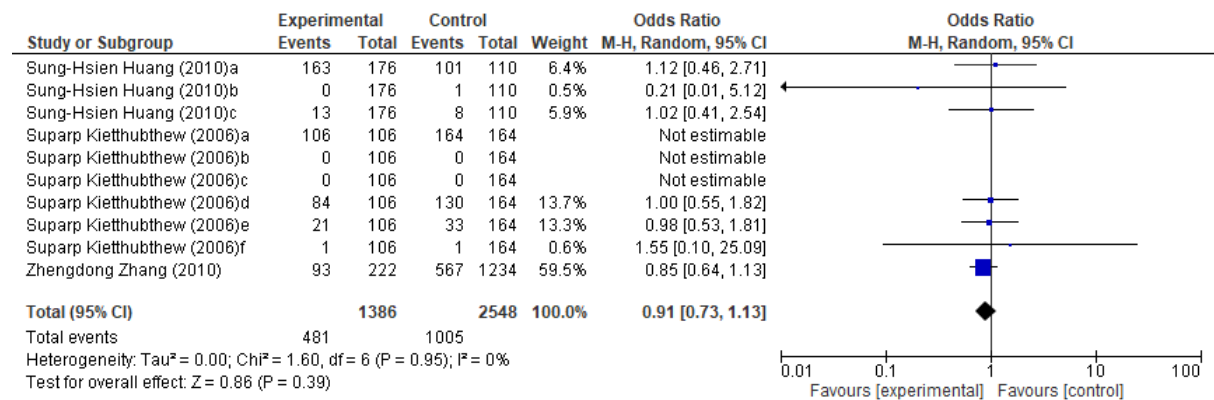
Supplementary Figure 7:CASP 8



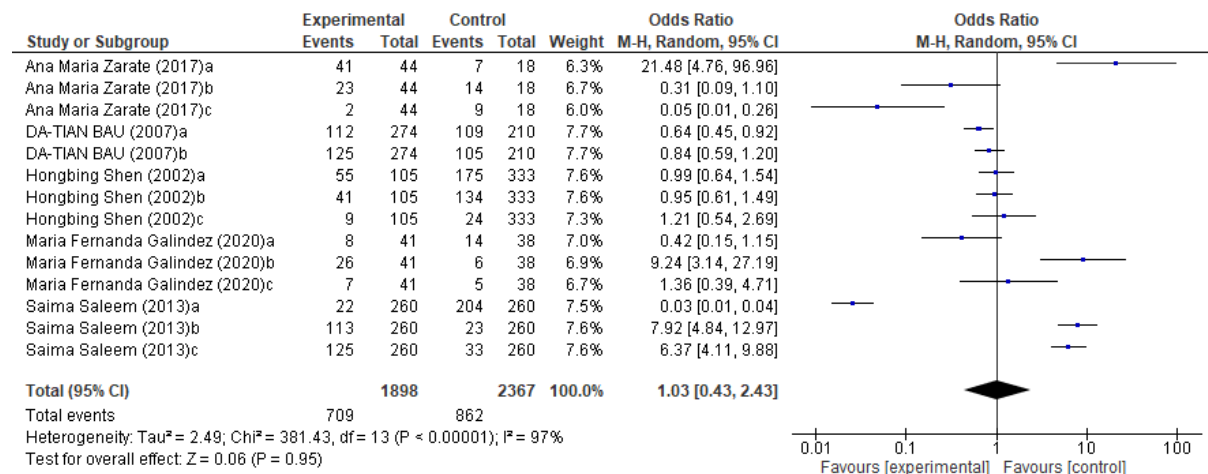
Supplementary Figure 8: XrCC 1



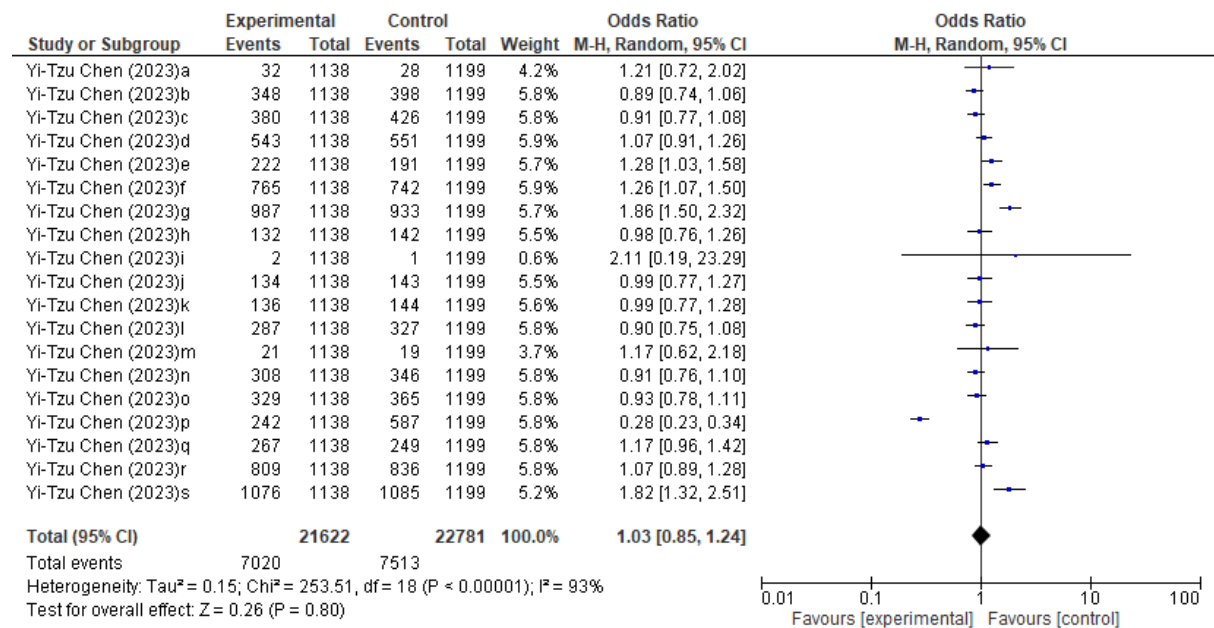
Supplementary Figure 9: MGMT



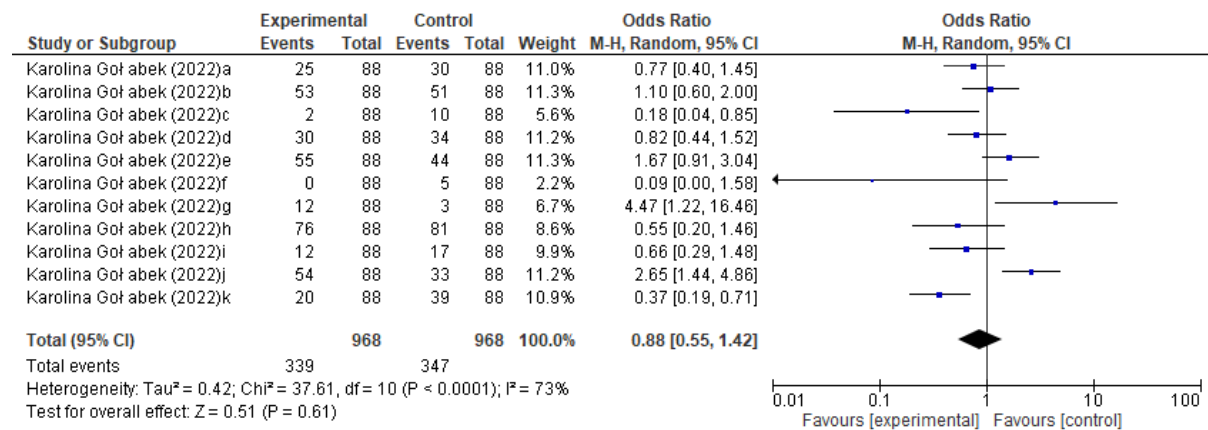
Supplementary Figure 10: P53



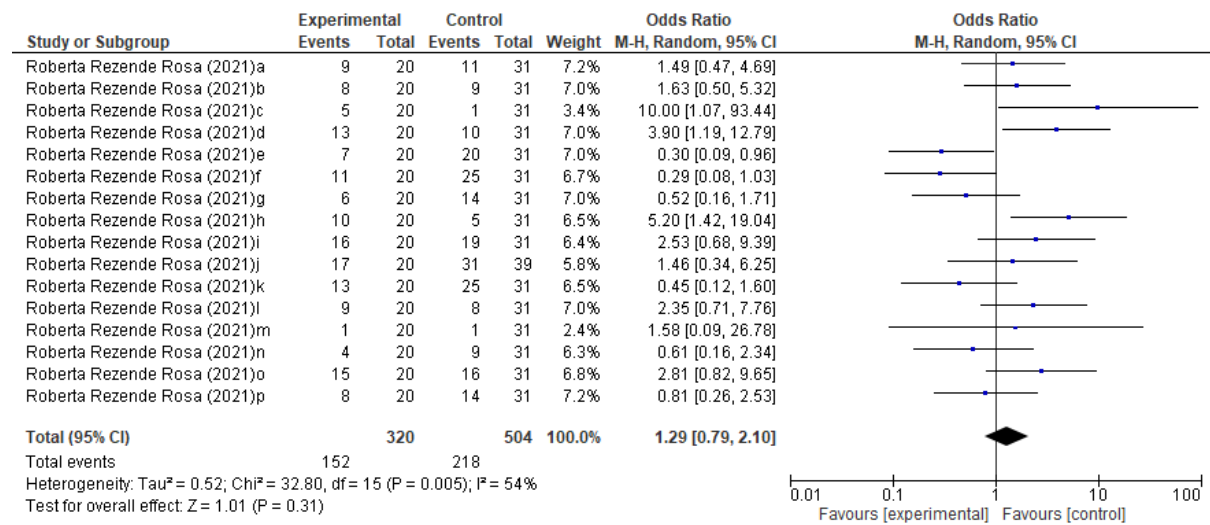
Supplementary Figure 11: Adam 1



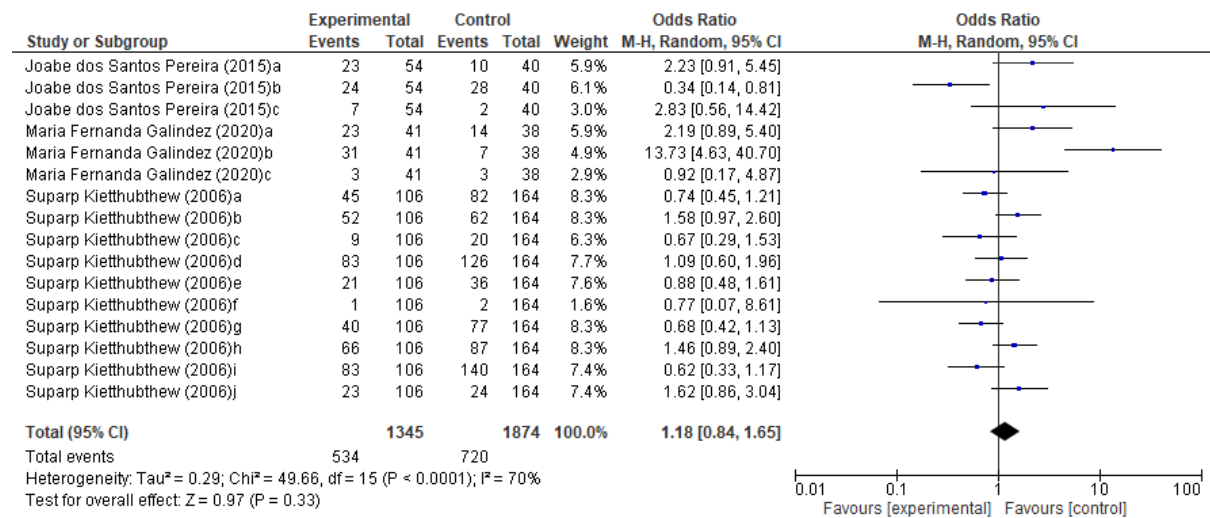
Supplementary Figure 12: LTF



Supplementary Figure 13: MT genes



Supplementary Figure 14: XPD genes



Supplementary Figure 15: NFKappa beta

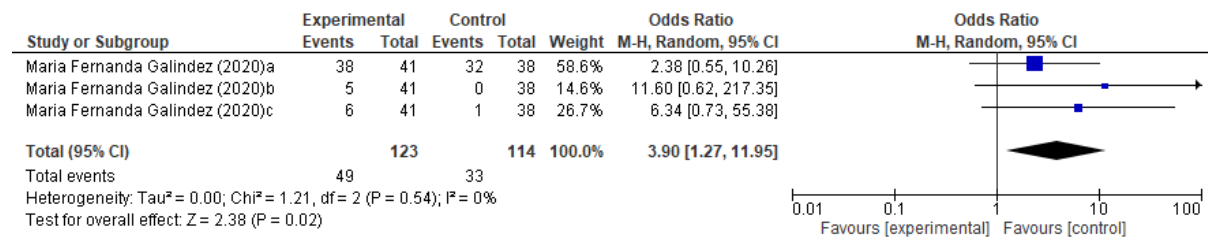
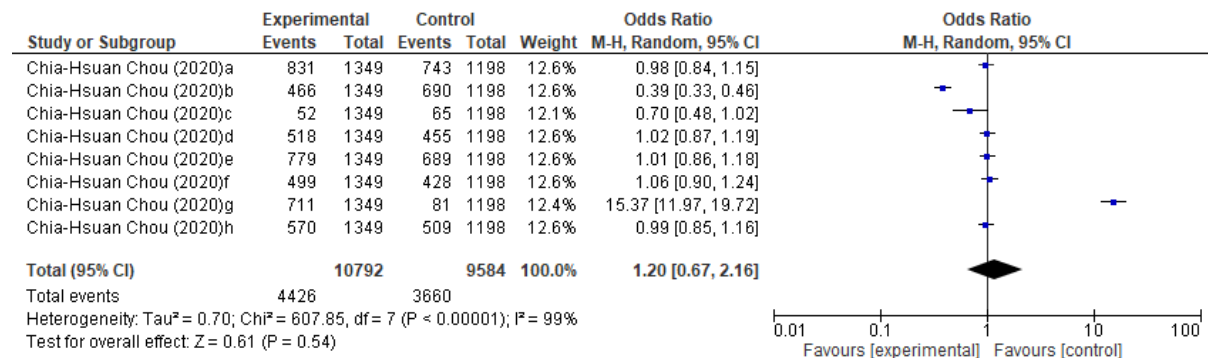
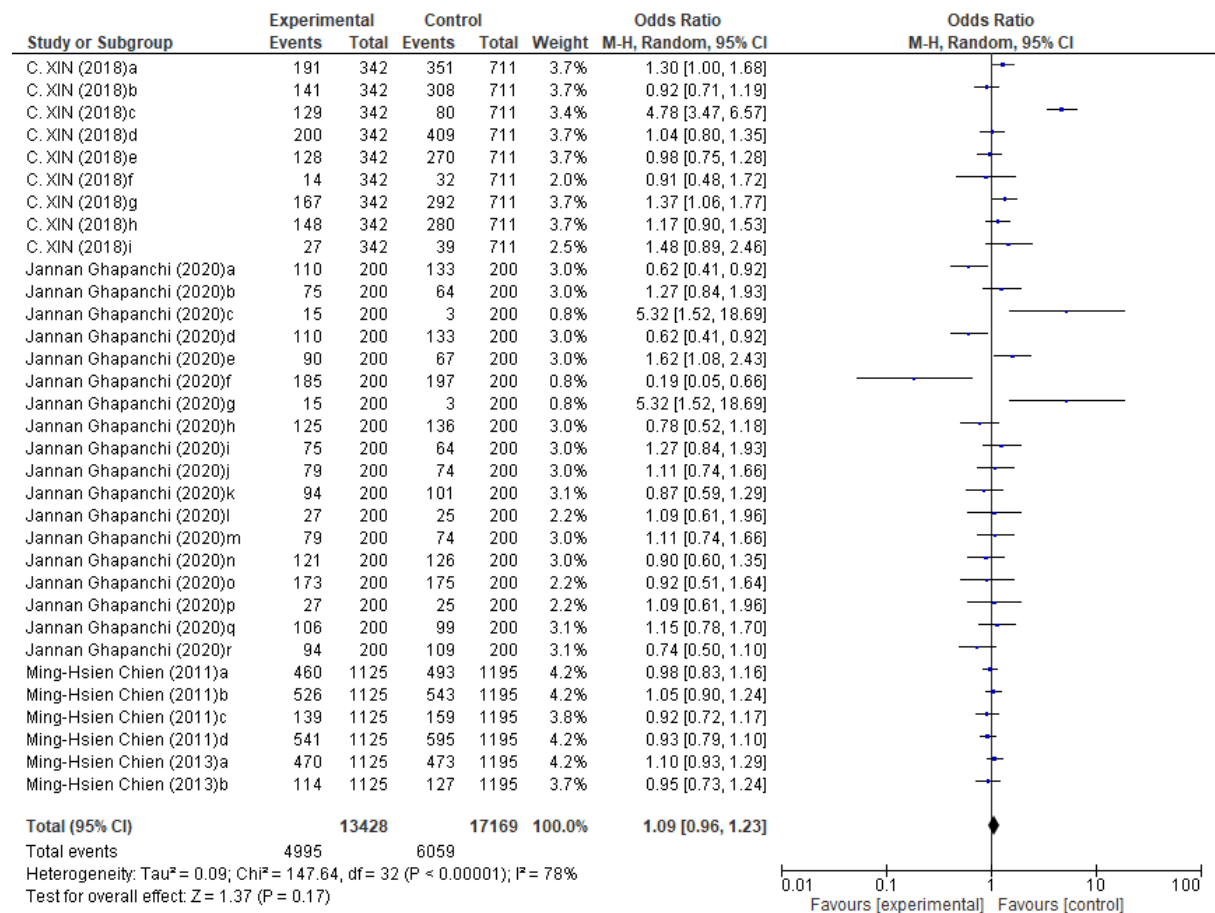


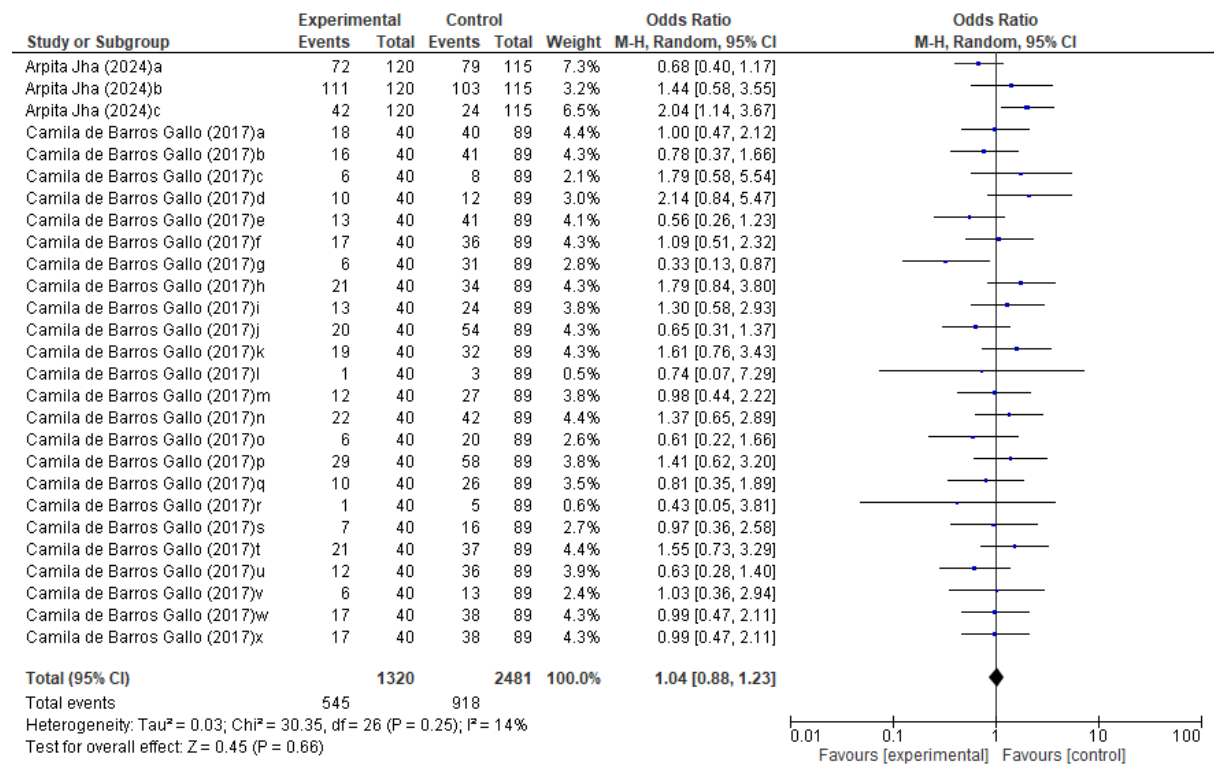
Figure 16: IGF 2



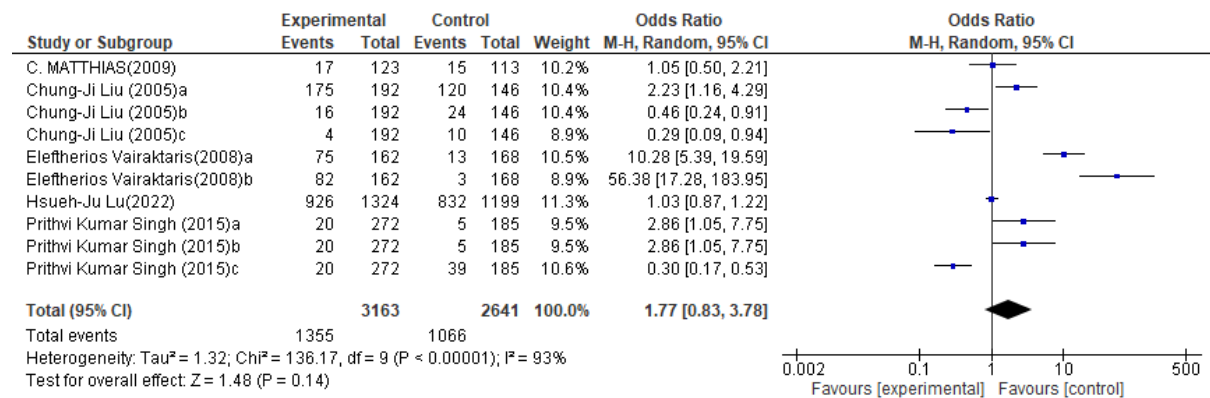
Supplementary Figure 17: LNCRNA



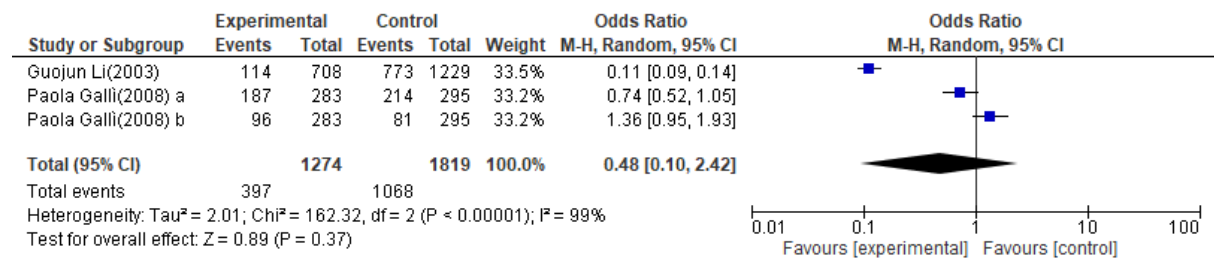
Supplementary Figure 18: TLR



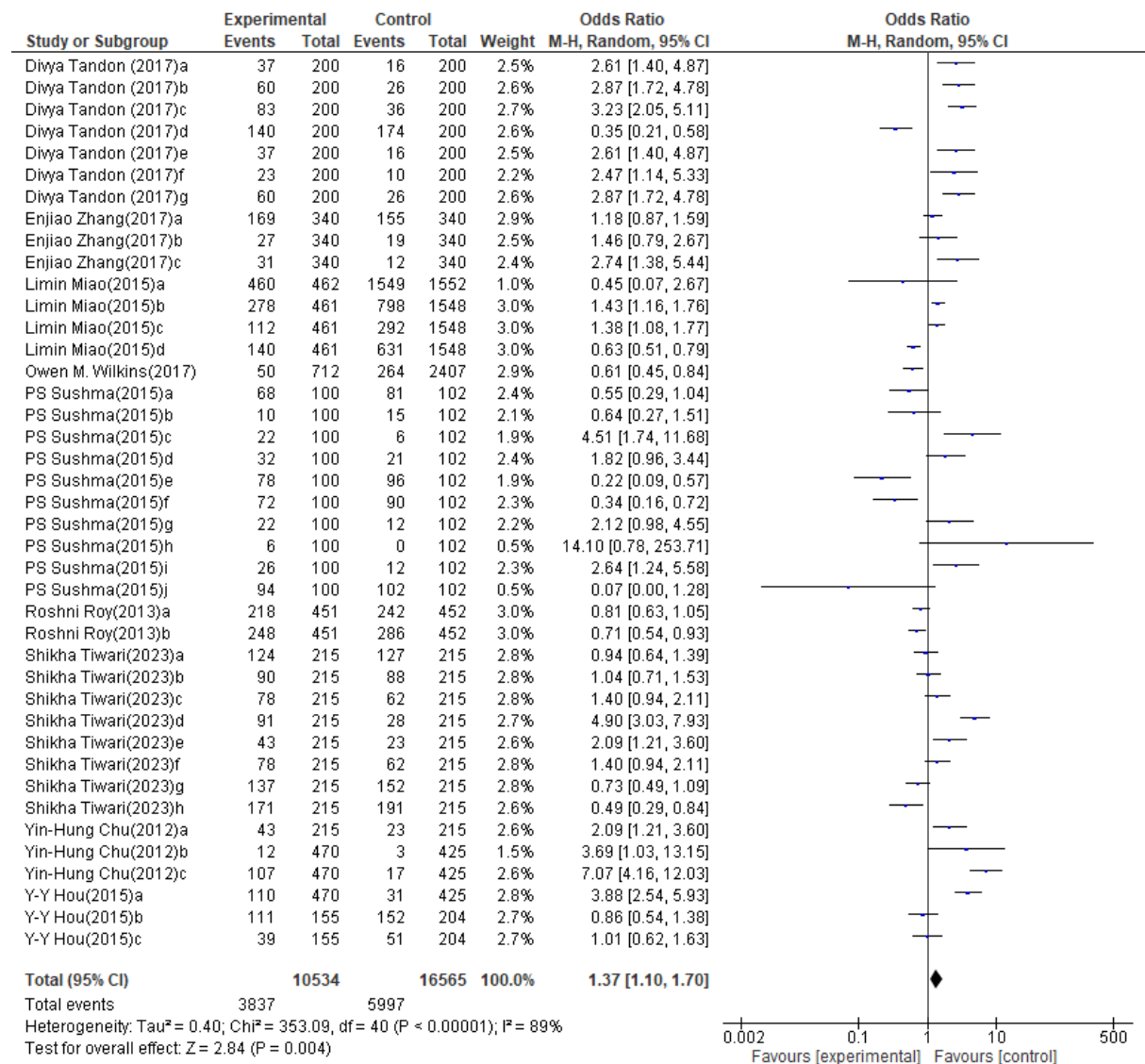
Supplementary Figure 19 :TNF



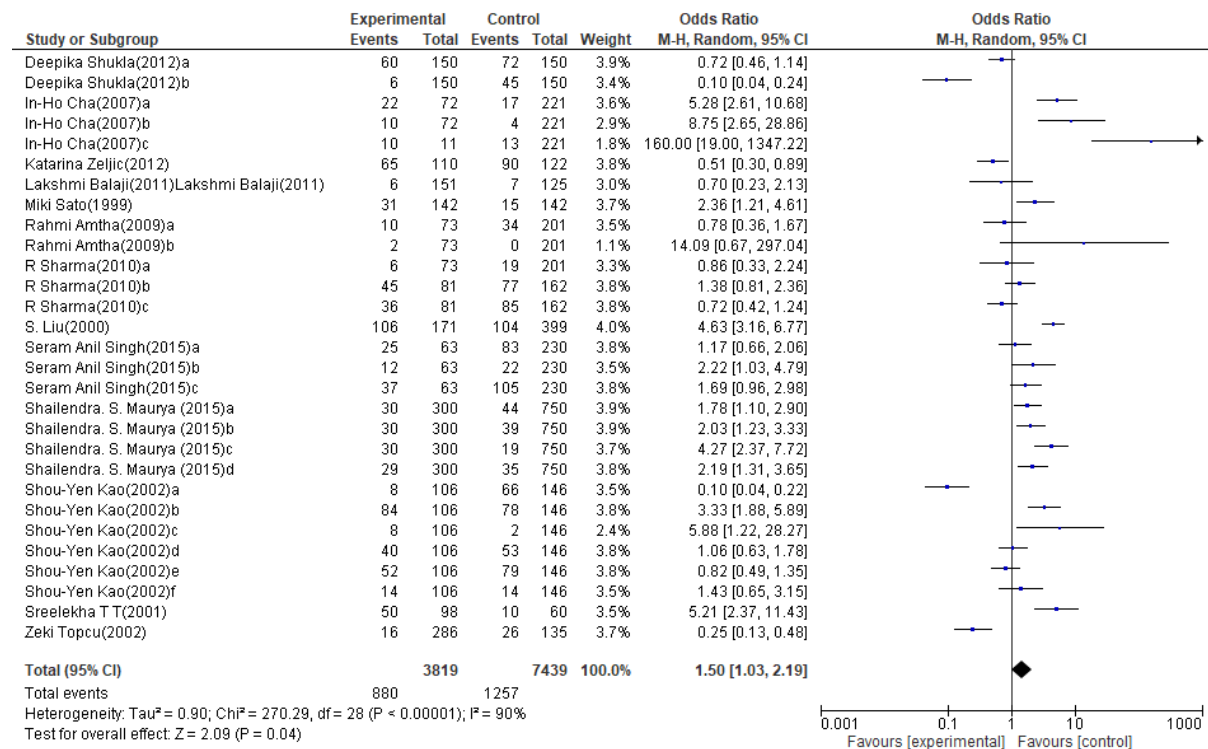
Supplementary Figure 20: P73



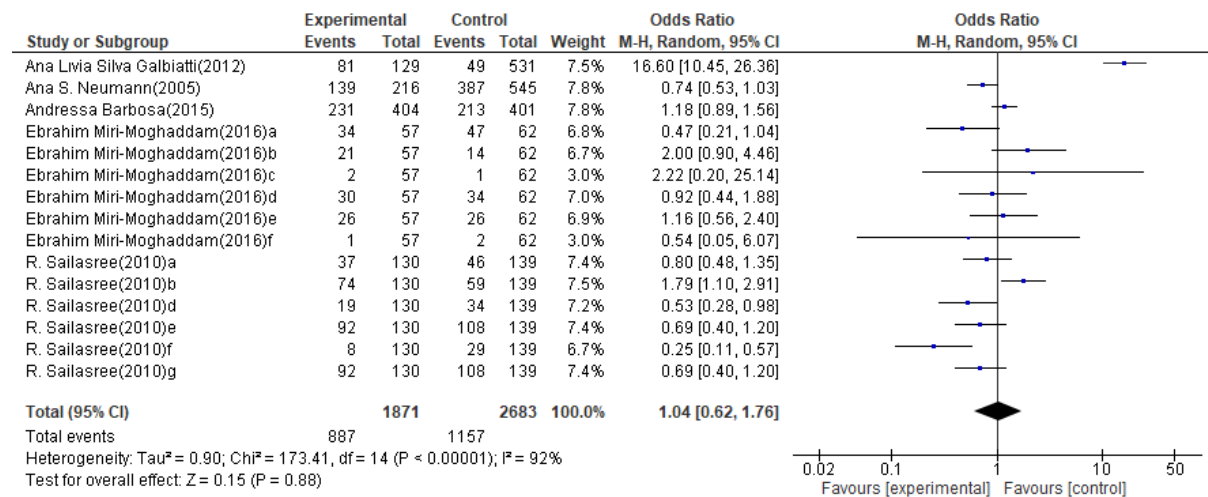
Supplementary Figure 21: MiRNA



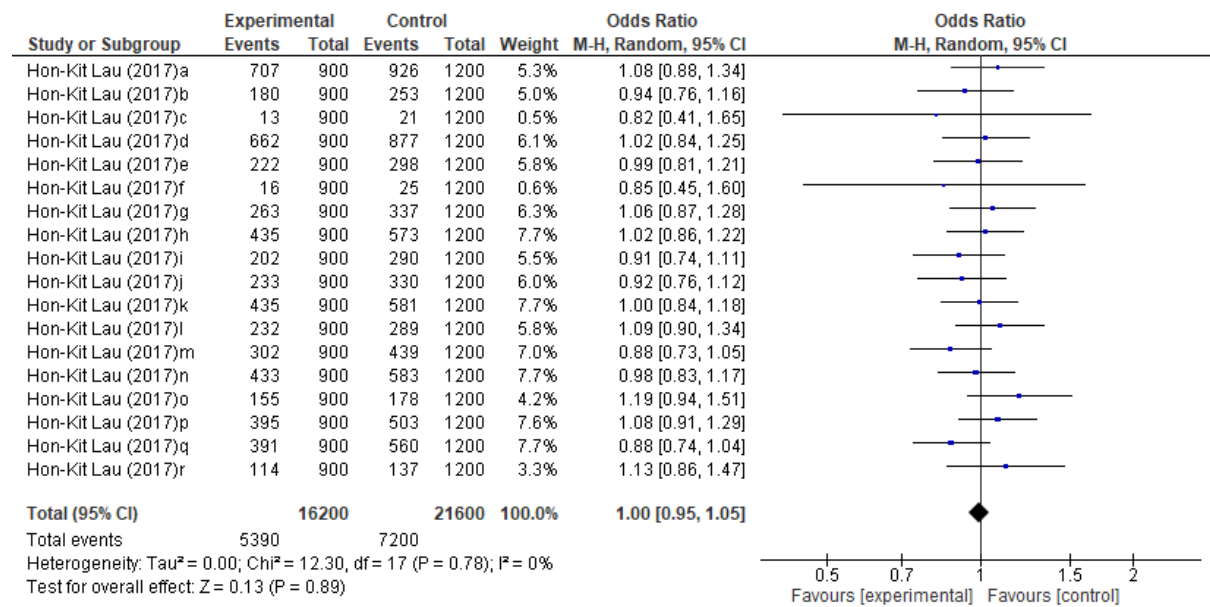
Supplementary Figure 22 : CYP



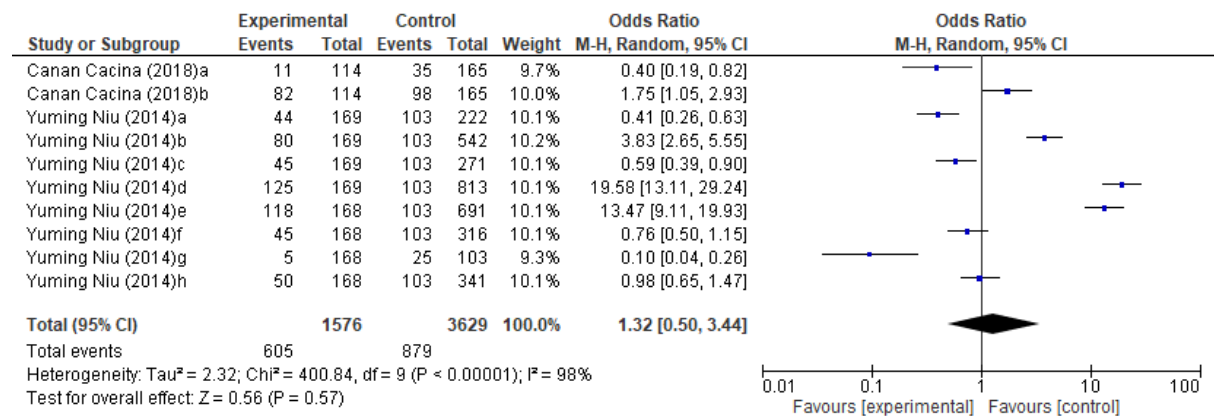
Supplementary Figure 23: MTHFR



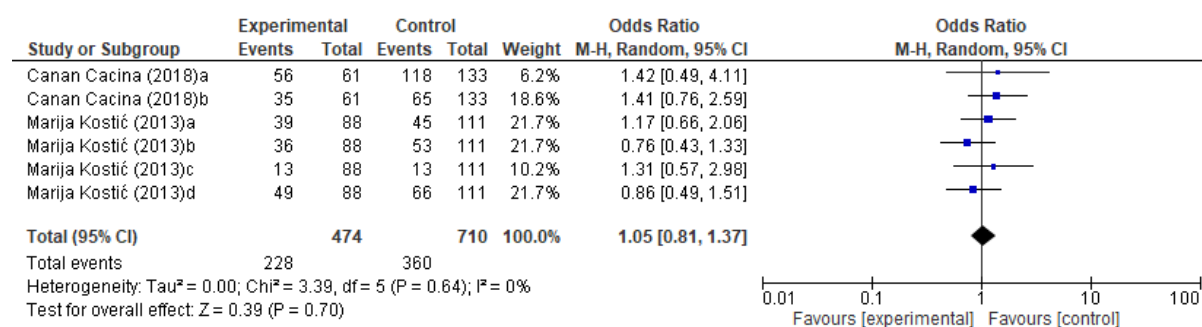
Supplementary Figure 24: Wisp



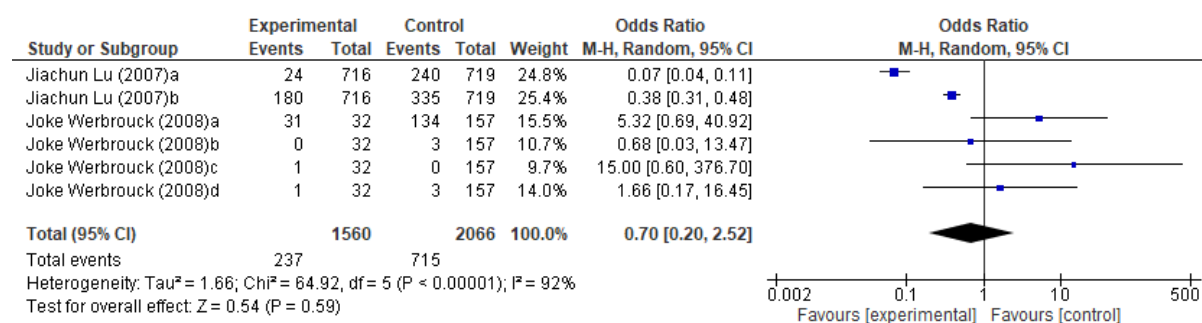
Supplementary Figure 25: COX 2



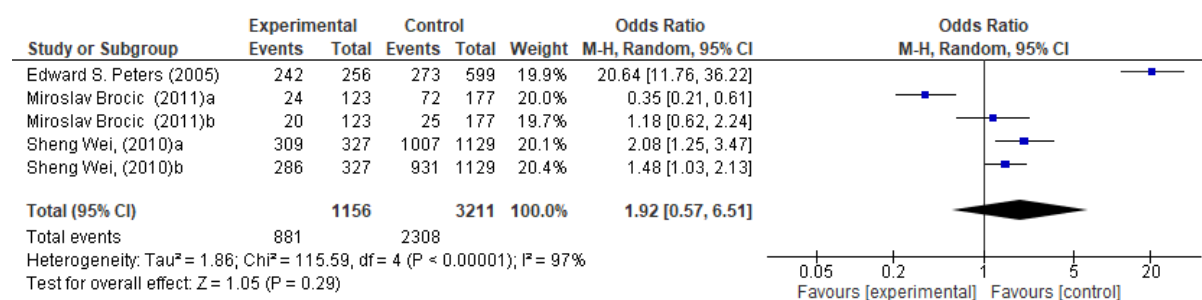
Supplementary Figure 26: Survivin



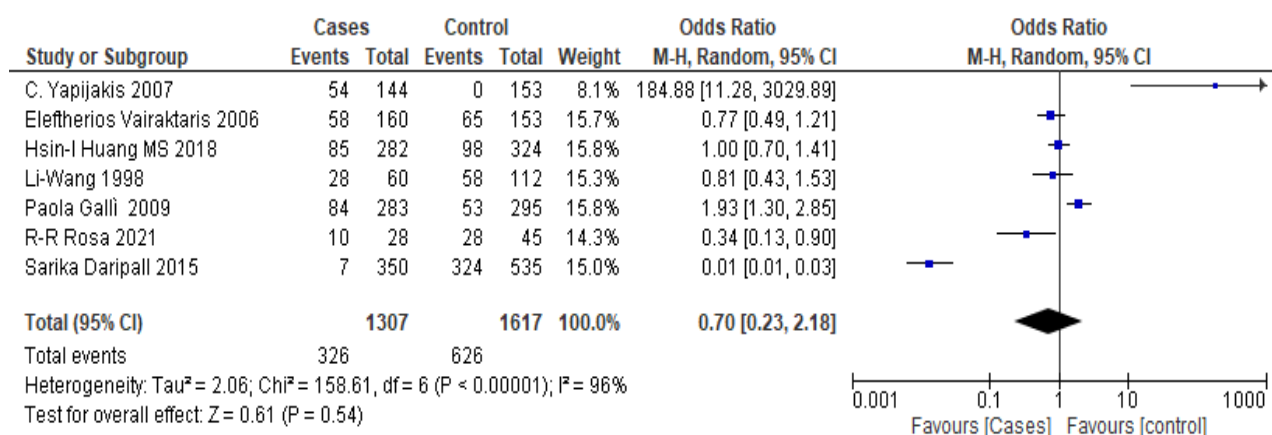
Supplementary Figure 27: RAD 5



Supplementary Figure 28: ADH1C



Supplementary Figure 29: Assessment of strength of association between family history and gene affected



Supplementary Figure 30: Assessment of strength of association between chronic mucosal trauma and gene affected

