


Association between SNPs in microRNA machinery genes and gastric cancer susceptibility, invasion, and metastasis in Chinese Han population

SUPPLEMENTARY MATERIALS



Supplementary Figure 1: *In-silico* analysis of microRNA-binding. rs3742330 was located at the fourth nucleotides from 5' end of the has-miR-632. The arrows indicated the position of rs3742330.



PolyPhen-2 prediction of functional effects of human nsSNPs

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PolyPhen-2 report for P57678 R1033C (rs7813)

Query

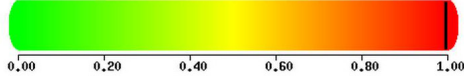
Protein Acc	Position	AA ₁	AA ₂	Description
P57678	1033	R	C	Canonical; RecName: Full=Gem-associated protein 4; Short=Gemin-4; AltName: Full=Component of gems 4; AltName: Full=p97; Length: 1058

Results

Prediction/Confidence PolyPhen-2 v2.2.2r398

HumDiv

This mutation is predicted to be **PROBABLY DAMAGING** with a score of 0.995 (sensitivity: 0.68; specificity: 0.97)



0.00 0.20 0.40 0.60 0.80 1.00

HumVar

Details

Multiple sequence alignment UniProtKB/UniRef100 Release 2011_12 (14-Dec-2011)

3D Visualization PDB/DSSP Snapshot 03-Jan-2012 (78304 Structures)

Software & web support: [ivan adzhubey](#) Web design & development: [biobite solutions](#)

Supplementary Figure 2: The predicted analysis for rs7813.

Supplementary Table 1: MiRNA-related genes and polymorphisms evaluated in this study

Gene	SNP ID	Position	Major/minor allele	MAF%
<i>DROSHA</i>	rs642321	3'UTR	C/T	0.467
	rs6877568	5'UTR	A/C	0.216
	rs10719	3'UTR	C/T	0.233
<i>DGCR8</i>	rs3757	3'UTR	A/G	0.178
	rs720012	3'UTR	A/G	0.444
	rs417309	3'UTR	A/G	0.100
	rs1640299	3'UTR	G/T	0.222
<i>RAN</i>	rs14035	3'UTR	C/T	0.178
<i>DICER</i>	rs3742330	3'UTR	A/G	0.267
<i>AGO1</i>	rs595961	intron	A/G	0.128
	rs636832	intron	A/G	0.198
<i>AGO2</i>	rs4961280	promotor	A/C	0.111
<i>GEMIN4</i>	rs104591	3'UTR	A/G	0.148
	rs104581	Coding exon	C/T	0.133
	rs7813	Coding exon	C/T	0.289
	rs2740349	Coding exon	A/G	0.211
	rs3744741	Coding exon	C/T	0.267
<i>GEMIN3</i>	rs197412	Coding exon	C/T	0.333
<i>HIWI</i>	rs1106042	Coding exon	A/G	0.122
	rs10773771	3'UTR	G/T	0.409