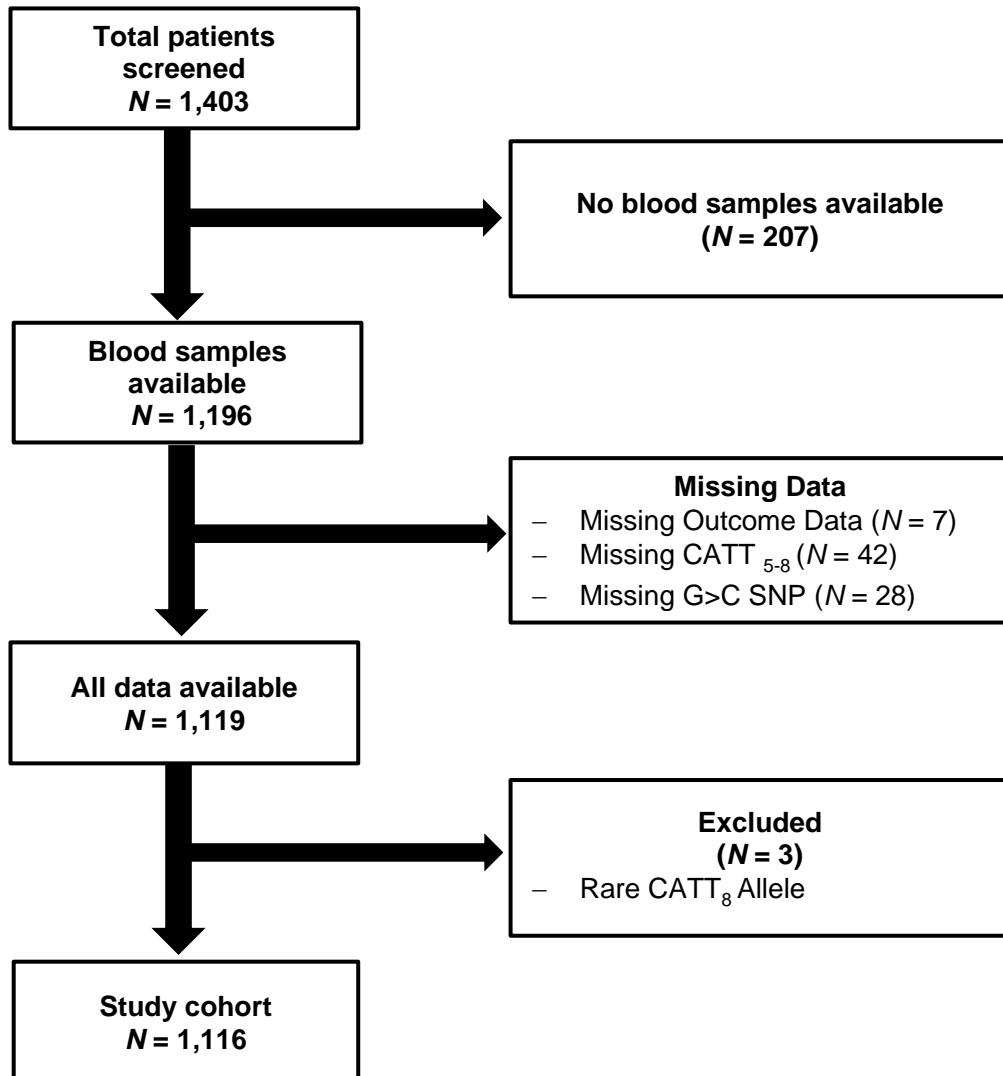


## SUPPLEMENTAL MATERIAL

Supplemental Figure 1. Flowchart of the patients screened and included in the study.

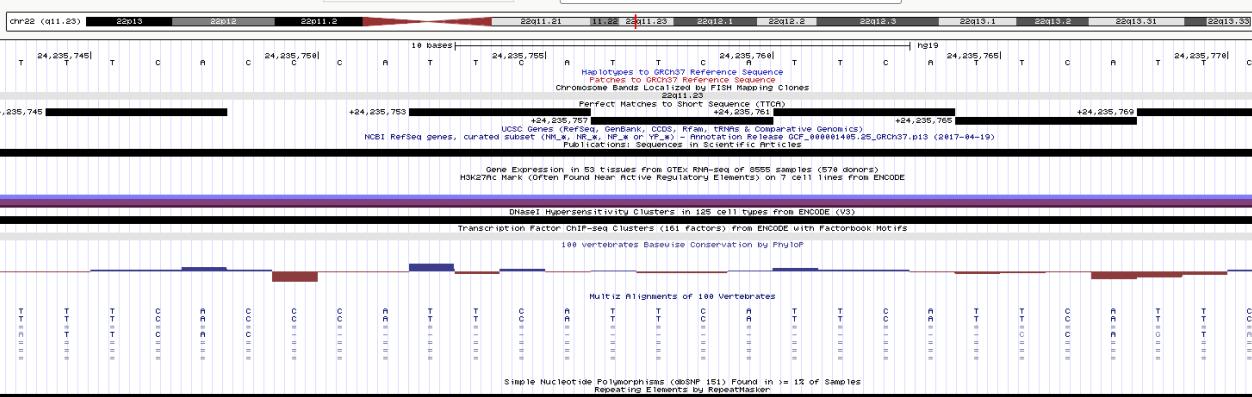


**Supplemental Figure 2. SNP rs5844572 region (CATT<sub>n</sub> tetranucleotide repeat) and rs755622 (G>C) with UCSC genome browser (Geb. 2009; GRCh37/hg19 Assembly)**

**UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly**

move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

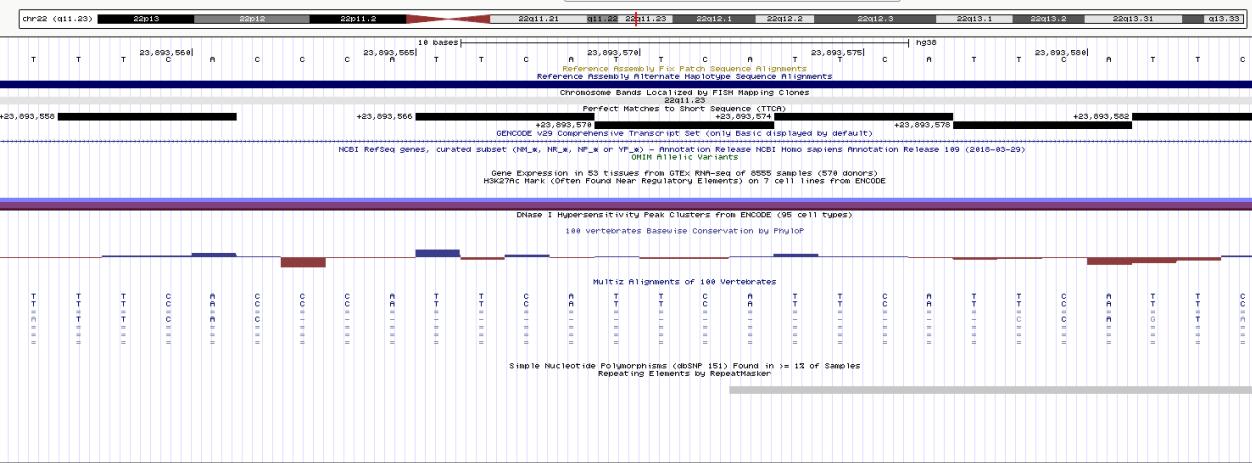
chr22:24,235,743-24,235,774 32 bp enter position, gene symbol, HGVS or search terms go



**UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly**

move <<< << < > >> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr22:23,893,556-23,893,587 32 bp chr22:23,893,550-23,893,588 go



**Supplemental Table 1.** Primer sequences used for genotyping of the tetranucleotide repeat polymorphismCATT<sub>n</sub> (rs3063368)

	Forward primer	Backward primer	Annealing temperature
<b>Set 1</b>	ggtcgctatgaacgcacag	cttaaccgcgttccagt	69 °C
<b>Set 2</b>	ggtacccttaggcaggccaatc	cacggaaagtcaagagcttgg	70 °C
<b>Set 3</b>	gtatcggtatccctgccc	tgcgcacttgaagatgg	69 °C
<b>Set 4</b>	gctacacctccacacctgag	tctccagccccagatct	65 °C

MIF Polymorphism	Myocardial infarction (N = 93)						P-value	
	Patients carrying this allele/genotype		Patients NOT carrying this allele/genotype		OR	(95% CI)		
	N	Prevalence, %	N	Prevalence, %				
<b>CATT repeat allele carriers (rs3063368)</b>								
CATT <sub>5</sub>	40	8.20	53	8.44	0.97	(0.61-1.52)	0.9134	
CATT <sub>6</sub>	80	8.36	13	8.18	1.02	(0.55-2.06)	1.000	
CATT <sub>7</sub>	27	9.75	66	7.87	1.26	(0.76-2.06)	0.3184	
<b>Genotypes</b>								
G>C (rs755622)								
GG	61	8.01	32	9.04	0.88	(0.55-1.42)	0.562	
GC	30	9.15	63	7.99	1.16	(0.71-1.86)	0.553	
CC	2	7.69	91	8.35	0.91	(0.10-3.78)	1.000	
CATT repeat (rs3063368)								
CATT <sub>5,5</sub>	5	7.04	88	8.42	0.82	(0.25-2.10)	0.827	
CATT <sub>5,6</sub>	27	7.83	66	8.56	0.91	(0.55-1.47)	0.726	
CATT <sub>5,7</sub>	8	11.1	85	8.14	1.41	(0.56-3.08)	0.376	
CATT <sub>6,6</sub>	34	8.04	59	8.51	0.94	(0.59-1.49)	0.824	
CATT <sub>6,7</sub>	19	10.05	74	7.98	1.29	(0.71-2.22)	0.385	
CATT <sub>7,7</sub>	0	0.00	93	8.45	0.00	(0.00-2.27)	0.388	
<b>Individual genotype combinations</b>								
#								
CATT <sub>5,5-</sub> GG (6.1%)	5	7.35	88	8.40	0.87	(0.26-2.21)	1.000	
CATT <sub>5,6-</sub> GG (29.5%)	25	7.60	68	8.64	0.87	(0.52-1.43)	0.635	
CATT <sub>6,6-</sub> GG (32.3%)	31	8.61	62	8.20	1.05	(0.65-1.69)	0.817	
CATT <sub>6,6-</sub> CG (5.6%)	3	4.76	90	8.55	0.54	(0.11-1.69)	0.477	
CATT <sub>5,7-</sub> CG (6.2%)	8	11.59	85	8.12	1.48	(0.59-3.25)	0.3637	
CATT <sub>6,7-</sub> CG (15.8%)	17	9.66	76	8.09	1.22	(0.66-2.14)	0.460	

**Supplemental Table 2. Association of MIF promoter polymorphisms with Myocardial Infarction.** Association between two of the polymorphisms in the *MIF* gene and risk of postoperative myocardial infarction. CI, confidence interval; OR, odds ratio; SNP, Single nucleotide polymorphism; CATT<sub>7x</sub>, patients carrying at least one CATT<sub>7</sub> allele.

<sup>#</sup> genotypes with a frequency of > 5%. Data presented as absolute numbers and percentage. *P* value calculated by Fisher exact test; bold fonts indicate *P*-values < 0.05.

MIF Polymorphism	Stroke (N = 24)						P-value	
	Patients carrying this allele/genotype		Patients NOT carrying this allele/genotype		OR			
	N	Prevalence, %	N	Prevalence, %	(95% CI)			
<b>CATT repeat allele carriers (rs3063368)</b>								
CATT <sub>5</sub>	7	1.43	17	2.71	0.52	(0.18-1.34)	0.211	
CATT <sub>6</sub>	22	2.30	2	1.26	1.85	(0.45-16.35)	0.561	
CATT <sub>7</sub>	6	2.17	18	2.15	1.01	(0.32-2.69)	1.000	
<b>Genotypes</b>								
G>C (rs755622)								
GG	16	2.10	8	2.26	0.93	(0.37-2.53)	0.828	
GC	8	2.44	16	2.03	1.21	(0.44-3.02)	0.655	
CC	0	0.00	24	2.20	0.00	(0.00-5.76)	1.000	
CATT repeat (rs3063368)								
CATT <sub>5,5</sub>	1	1.41	23	2.20	0.63	(0.02-4.03)	1.000	
CATT <sub>5,6</sub>	5	1.45	19	2.46	0.58	(0.17-1.63)	0.373	
CATT <sub>5,7</sub>	1	1.39	23	2.20	0.63	(0.01-3.97)	1.000	
CATT <sub>6,6</sub>	12	2.84	12	1.73	1.66	(0.67-4.07)	0.287	
CATT <sub>6,7</sub>	5	2.65	19	2.05	1.30	(0.37-3.66)	0.583	
CATT <sub>7,7</sub>	0	0.00	24	2.18	0.00	(0.00-9.77)	1.000	
<b>Individual genotype combinations</b>								
#								
CATT <sub>5,5-</sub> GG (6.1%)	1	1.47	23	2.19	0.67	(0.02-4.23)	1.000	
CATT <sub>5,6-</sub> GG (29.5%)	5	1.52	19	2.41	0.62	(0.18-1.75)	0.497	
CATT <sub>6,6-</sub> GG (32.3%)	10	2.78	14	1.85	1.51	(0.60-3.71)	0.377	
CATT <sub>6,6-</sub> CG (5.6%)	2	3.17	22	2.09	1.54	(0.17-6.49)	0.642	
CATT <sub>5,7-</sub> CG (6.2%)	1	1.45	23	2.20	0.65	(0.02-4.16)	1.000	
CATT <sub>6,7-</sub> CG (15.8%)	5	2.84	19	2.02	1.42	(0.41-3.99)	0.568	

**Supplemental Table 3. Association of MIF promoter polymorphisms with Stroke**

Association between two of the polymorphisms in the *MIF* gene and risk of postoperative stroke. CI, confidence interval; OR, odds ratio; SNP, Single nucleotide polymorphism; CATT<sub>7x</sub>, patients carrying at least one CATT<sub>7</sub> allele.

\* genotypes with a frequency of > 5%. Data presented as absolute numbers and percentage. P value calculated by Fisher exact test; bold fonts indicate P-values < 0.05.

MIF Polymorphism	Delir (N = 144)						P-value	
	Patients carrying this allele/genotype		Patients NOT carrying this allele/genotype		OR	(95% CI)		
	N	Prevalence, %	N	Prevalence, %				
<b>CATT repeat allele carriers (rs3063368)</b>								
CATT <sub>5</sub>	61	12.50	83	13.22	0.94	(0.65-1.36)	0.787	
CATT <sub>6</sub>	119	12.43	25	15.72	0.76	(0.47-1.27)	0.251	
CATT <sub>7</sub>	44	15.88	100	11.92	1.40	(0.93-2.08)	0.098	
<b>Genotypes</b>								
G>C (rs755622)								
GG	92	12.07	52	14.69	0.80	(0.55-1.18)	0.250	
GC	47	14.33	97	12.31	1.19	(0.80-1.76)	0.378	
CC	5	19.23	139	12.75	1.63	(0.47-4.53)	0.367	
CATT repeat (rs3063368)								
CATT <sub>5,5</sub>	12	16.90	132	12.63	1.41	(0.67-2.73)	0.277	
CATT <sub>5,6</sub>	38	11.01	106	13.75	0.78	(0.51-1.17)	0.246	
CATT <sub>5,7</sub>	11	15.28	133	12.74	1.24	(0.57-2.45)	0.584	
CATT <sub>6,6</sub>	50	11.82	94	13.56	0.85	(0.58-1.25)	0.409	
CATT <sub>6,7</sub>	31	16.40	113	12.19	1.41	(0.89-2.21)	0.122	
CATT <sub>7,7</sub>	2	12.5	142	12.91	0.96	(0.11-4.27)	1.00	
<b>Individual genotype combinations</b>								
#								
CATT <sub>5,5-</sub> GG (6.1%)	12	17.65	132	12.60	1.49	(0.71-2.90)	0.260	
CATT <sub>5,6-</sub> GG (29.5%)	36	10.94	108	13.72	0.77	(0.50-1.17)	0.240	
CATT <sub>6,6-</sub> GG (32.3%)	43	11.94	101	13.36	0.88	(0.59-1.30)	0.567	
CATT <sub>6,6-</sub> CG (5.6%)	7	11.11	137	13.01	0.84	(0.31-1.89)	0.847	
CATT <sub>5,7-</sub> CG (6.2%)	11	15.94	133	12.70	1.30	(0.60-2.59)	0.457	
CATT <sub>6,7-</sub> CG (15.8%)	27	15.34	117	12.45	1.27	(0.78-2.03)	0.323	

**Supplemental Table 4. Association of MIF promoter polymorphisms with delir** Association between two of the polymorphisms in the *MIF* gene and risk of postoperative delir. CI, confidence interval; OR, odds ratio; SNP, Single nucleotide polymorphism; CATT<sub>7\*</sub>, patients carrying at least one CATT<sub>7</sub> allele. \* genotypes with a frequency of > 5%. Data presented as absolute numbers and percentage. P value calculated by Fisher exact test; bold fonts indicate P-values < 0.05.

<i>MIF</i> Polymorphism	Atrial Fibrillation (N = 245)						<i>P</i> -value
	Patients carrying this allele/genotype		Patients NOT carrying this allele/genotype		OR	(95% CI)	
	N	Prevalence, %	N	Prevalence, %			
<b>CATT repeat allele carriers (rs3063368)</b>							
CATT <sub>5</sub>	104	21.31	139	22.13	0.95	(0.71-1.28)	0.770
CATT <sub>6</sub>	209	21.84	34	21.38	1.03	(0.67-1.60)	1.000
CATT <sub>7</sub>	56	20.22	187	22.29	0.88	(0.62-1.25)	0.502
<b>Genotypes</b>	<b>Genotypes</b>						
G>C (rs755622)	G>C (rs755622)						
GG	170	22.31	73	20.62	1.11	(0.80-1.53)	0.586
GC	69	21.04	174	22.08	0.94	(0.68-1.30)	0.750
CC	4	15.38	239	21.93	0.65	(0.16-1.93)	0.630
CATT repeat (rs3063368)	CATT repeat (rs3063368)						
CATT <sub>5,5</sub>	14	19.72	229	21.91	0.88	(0.44-1.63)	0.767
CATT <sub>5,6</sub>	73	21.16	170	22.05	0.95	(0.69-1.30)	0.754
CATT <sub>5,7</sub>	17	23.61	226	21.65	1.12	(0.60-2.00)	0.660
CATT <sub>6,6</sub>	100	23.64	143	20.63	1.19	(0.88-1.61)	0.122
CATT <sub>6,7</sub>	36	19.05	207	22.33	0.82	(0.54-1.23)	0.335
CATT <sub>7,7</sub>	3	18.75	240	21.82	0.83	(0.15-3.04)	1.000
<b>Individual genotype combinations</b>	<b>Individual genotype combinations</b>						
#	#						
CATT <sub>5,5-</sub> GG (6.1%)	13	19.12	230	21.95	0.84	(0.41-1.59)	0.652
CATT <sub>5,6-</sub> GG (29.5%)	72	21.88	171	21.73	1.01	(0.73-1.39)	1.000
CATT <sub>6,6-</sub> GG (32.3%)	84	23.33	159	21.03	1.14	(0.83-1.56)	0.394
CATT <sub>6,6-</sub> CG (5.6%)	16	25.40	227	21.56	1.24	(0.64-2.27)	0.529
CATT <sub>5,7-</sub> CG (6.2%)	16	23.19	227	21.68	1.09	(0.57-1.98)	0.764
CATT <sub>6,7-</sub> CG (15.8%)	35	19.89	208	22.13	0.87	(0.57-1.32)	0.551

**Supplemental Table 5. Association of MIF regulatory polymorphisms with atrial fibrillation.** Association

between two of the polymorphisms in the *MIF* gene and risk of postoperative atrial fibrillation. CI, confidence interval; OR, odds ratio; SNP, Single nucleotide polymorphism; CATT<sub>7</sub>, patients carrying at least one CATT<sub>7</sub> allele.

<sup>#</sup> genotypes with a frequency of > 5%. Data presented as absolute numbers and percentage. *P* value calculated by Fisher exact test; bold fonts indicate *P*-values < 0.05.



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