

Supplementary Table S8. The prediction of the transcription factors of MAGI2-AS3.

seqname	source	feature	start	end	score	strand	frame	attributes
MAGI2-AS3 NR_038345	TFBS	TFBS	1067	1072		1	+	. TF=ZNF354C; class=C 2H2 zinc finger factors; sequence=A TCCAC
MAGI2-AS3 NR_038345	TFBS	TFBS	479	486		1	-	. TF=GATA3; class=0th er C4 zinc finger-type factors; sequence=A GATAAGA
MAGI2-AS3 NR_038345	TFBS	TFBS	1396	1403		1	+	. TF=TFE3; class=Basi c helix-loop-helix factors (bHLH) ; sequence=CA CGTGAC
MAGI2-AS3 NR_038345	TFBS	TFBS	358	365		1	+	. TF=HOXA4; class=Hom eo domain factors; sequence=G TCATTAG
MAGI2-AS3 NR_038346	TFBS	TFBS	1067	1072		1	+	. TF=ZNF354C; class=C 2H2 zinc finger factors; sequence=A TCCAC
MAGI2-AS3 NR_038346	TFBS	TFBS	479	486		1	-	. TF=GATA3; class=0th er C4 zinc finger-type factors; sequence=A GATAAGA
MAGI2-AS3 NR_038346	TFBS	TFBS	1396	1403		1	+	. TF=TFE3; class=Basi c helix-loop-helix factors (bHLH) ; sequence=CA CGTGAC
MAGI2-AS3 NR_038346	TFBS	TFBS	358	365		1	+	. TF=HOXA4; class=Hom eo domain factors; sequence=G TCATTAG
MAGI2-AS3 NR_038344	TFBS	TFBS	64	69		1	+	. TF=ZNF354C; class=C 2H2 zinc finger factors; sequence=A TCCAC

MAGI2-AS3 NR _038344	TFB S	TFBS	111 5	11 22		1	-	.	TF=ARNT::HIF1A;cla ss=Basic helix-loop-helix factors (bHLH) ; sequence=GG ACGTGC
MAGI2-AS3 NR _038344	TFB S	TFBS	393	40 0		1	+	.	TF=TFE3;class=Basi c helix-loop-helix factors (bHLH) ; sequence=CA CGTGAC
MAGI2-AS3 NR _038344	TFB S	TFBS	144 3	14 52		1	-	.	TF=PLAGL2;class=C2 H2 zinc finger factors;sequence=T GGGCCCTT
MAGI2-AS3 NR _038343	TFB S	TFBS	64	69		1	+	.	TF=ZNF354C;class=C 2H2 zinc finger factors;sequence=A TCCAC
MAGI2-AS3 NR _038343	TFB S	TFBS	111 5	11 22		1	-	.	TF=ARNT::HIF1A;cla ss=Basic helix-loop-helix factors (bHLH) ; sequence=GG ACGTGC
MAGI2-AS3 NR _038343	TFB S	TFBS	393	40 0		1	+	.	TF=TFE3;class=Basi c helix-loop-helix factors (bHLH) ; sequence=CA CGTGAC
MAGI2-AS3 NR _038343	TFB S	TFBS	144 3	14 52		1	-	.	TF=PLAGL2;class=C2 H2 zinc finger factors;sequence=T GGGCCCTT
MAGI2-AS3 NR _038345	TFB S	TFBS	358	36 5	0.99964	62	+	.	TF=HOXC4;class=Hom eo domain factors;sequence=G TCATTAG
MAGI2-AS3 NR _038346	TFB S	TFBS	358	36 5	0.99964	62	+	.	TF=HOXC4;class=Hom eo domain factors;sequence=G TCATTAG
MAGI2-AS3 NR _038345	TFB S	TFBS	46	53	0.99956	5985	-	.	TF=HOXC4;class=Hom eo domain

MAGI2-AS3 NR _038346	TFB S	TFBS	46	53	0.99956	-	.	factors;sequence=A TCATTA TF=HOXC4;class=Hom eo domain
MAGI2-AS3 NR _038345	TFB S	TFBS	358	36 5	0.99955 7369	+	.	factors;sequence=G TCATTAG TF=HOXD4;class=Hom eo domain
MAGI2-AS3 NR _038346	TFB S	TFBS	358	36 5	0.99955 7369	+	.	factors;sequence=G TCATTAG TF=ARNT2;class=Bas ic helix-loop-helix
MAGI2-AS3 NR _038345	TFB S	TFBS	139 4	14 03	0.99949 5867	-	.	factors (bHLH) ;sequence=GT CACGTGCG
MAGI2-AS3 NR _038346	TFB S	TFBS	139 4	14 03	0.99949 5867	-	.	TF=ARNT2;class=Bas ic helix-loop-helix factors (bHLH) ;sequence=GT CACGTGCG
MAGI2-AS3 NR _038344	TFB S	TFBS	391	40 0	0.99949 5867	-	.	TF=ARNT2;class=Bas ic helix-loop-helix factors (bHLH) ;sequence=GT CACGTGCG
MAGI2-AS3 NR _038343	TFB S	TFBS	391	40 0	0.99949 5867	-	.	TF=ARNT2;class=Bas ic helix-loop-helix factors (bHLH) ;sequence=GT CACGTGCG
MAGI2-AS3 NR _038345	TFB S	TFBS	46	53	0.99933 1142	-	.	TF=HOXD4;class=Hom eo domain factors;sequence=A TCATTA TF=HOXD4;class=Hom
MAGI2-AS3 NR _038346	TFB S	TFBS	46	53	0.99933 1142	-	.	eo domain factors;sequence=A TCATTA
MAGI2-AS3 NR _038345	TFB S	TFBS	225 9	22 69	0.99925 1668	+	.	TF=FOS;class=Basic leucine zipper

MAGI2-AS3 NR _038346	TFB S	TFBS	225 9	22 69	0.99925 1668	+	.	factors (bZIP) ; sequence=TC TGACTCATT TF=FOS; class=Basic leucine zipper			
MAGI2-AS3 NR _038344	TFB S	TFBS	225 9	22 69	0.99925 1668	+	.	factors (bZIP) ; sequence=TC TGACTCATT TF=FOS; class=Basic leucine zipper			
MAGI2-AS3 NR _038345	TFB S	TFBS	358	36 5	0.99905 3421	+	.	factors (bZIP) ; sequence=TC TGACTCATT TF=HOXB4; class=Hom eo domain			
MAGI2-AS3 NR _038345	TFB S	TFBS	46	53	0.99905 3421	-	.	factors; sequence=G TCATTAG TF=HOXB4; class=Hom eo domain			
MAGI2-AS3 NR _038346	TFB S	TFBS	358	36 5	0.99905 3421	+	.	factors; sequence=A TCATTA TF=HOXB4; class=Hom eo domain			
MAGI2-AS3 NR _038346	TFB S	TFBS	46	53	0.99905 3421	-	.	factors; sequence=A TCATTA TF=FOXL1; class=For k head / winged			
MAGI2-AS3 NR _038345	TFB S	TFBS	683	68 9	0.99630 5873	-	.	helix factors; sequence=A TAAACA TF=FOXL1; class=For k head / winged			
MAGI2-AS3 NR _038346	TFB S	TFBS	683	68 9	0.99630 5873	-	.	helix factors; sequence=A TAAACA TF=GSX2; class=Home			
MAGI2-AS3 NR _038345	TFB S	TFBS	358	36 5	0.99621 3057	+	.	o domain factors; sequence=G TCATTAG			
MAGI2-AS3 NR	TFB	TFBS	358	36	0.99621	+	.	TF=GSX2; class=Home			

_038346	S		5	3057		o domain
MAGI2-AS3 NR	TFB	TFBS	187	18	0.99569	factors;sequence=G
_038345	S		5	84	1748	TCATTAG
MAGI2-AS3 NR	TFB	TFBS	187	18	0.99569	TF=KLF5;class=C2H2
_038346	S		5	84	1748	zinc finger
MAGI2-AS3 NR	TFB	TFBS	872	88	0.99569	factors;sequence=G
_038344	S		1		1748	CCCCTCCCC
MAGI2-AS3 NR	TFB	TFBS	872	88	0.99569	TF=KLF5;class=C2H2
_038343	S		1		1748	zinc finger
MAGI2-AS3 NR	TFB	TFBS	179	18	0.99523	factors;sequence=G
_038345	S		7	04	7296	CCCCTCCCC
MAGI2-AS3 NR	TFB	TFBS	179	18	0.99523	TF=NR2C2(var. 2);class=Nuclear
_038346	S		7	04	7296	receptors with C4
MAGI2-AS3 NR	TFB	TFBS	794	80	0.99523	zinc
_038344	S		1		7296	fingers;sequence=G
MAGI2-AS3 NR	TFB	TFBS	794	80	0.99523	AGGTAG
_038343	S		1		7296	TF=NR2C2(var. 2);class=Nuclear
MAGI2-AS3 NR	TFB	TFBS	236	23	0.99498	receptors with C4
					-	zinc
					.	fingers;sequence=G
					.	AGGTAG
					.	TF=MEIS1;class=Hom

_038345	S		4	70	9704		eo domain factors;sequence=C
MAGI2-AS3 NR	TFB	TFBS	236	23	0.99498	-	TGACAG
_038346	S		4	70	9704	.	TF=MEIS1;class=Hom
MAGI2-AS3 NR	TFB	TFBS	236	23	0.99498	-	eo domain factors;sequence=C
_038344	S		4	70	9704	.	TGACAG
MAGI2-AS3 NR	TFB	TFBS	786	79	0.99414	-	TF=HOXA4;class=Hom
_038345	S		786	3	8567	.	eo domain factors;sequence=G
MAGI2-AS3 NR	TFB	TFBS	786	79	0.99414	-	TCATTAC
_038346	S		786	3	8567	.	TF=HOXA4;class=Hom
MAGI2-AS3 NR	TFB	TFBS	243	24	0.99406	+	eo domain factors;sequence=G
_038343	S		6	43	9584	.	h-mobility group (HMG) domain
MAGI2-AS3 NR	TFB	TFBS	73	78	0.99404	+	factors;sequence=G
_038345	S				8003	.	ACAATGC
MAGI2-AS3 NR	TFB	TFBS	73	78	0.99404	+	TF=ZNF354C;class=C
_038346	S				8003	.	2H2 zinc finger
MAGI2-AS3 NR	TFB	TFBS	216	21	0.99353	+	factors;sequence=C
_038345	S		8	76	6806	.	TCCAC
MAGI2-AS3 NR	TFB	TFBS	216	21	0.99353	+	TF=ZNF354C;class=C
_038346	S		8	76	6806	.	2H2 zinc finger
MAGI2-AS3 NR	TFB	TFBS	216	21	0.99353	+	factors;sequence=C
_038344	S		8	76	6806	.	CCATTAAA
MAGI2-AS3 NR	TFB	TFBS	216	21	0.99353	+	TF=NKX6-3;class=Ho
_038346	S		8	76	6806	.	meo domain
MAGI2-AS3 NR	TFB	TFBS	216	21	0.99353	+	factors;sequence=C
_038344	S		8	76	6806	.	CCATTAAA
MAGI2-AS3 NR	TFB	TFBS	216	21	0.99353	+	TF=NKX6-3;class=Ho
_038344	S		8	76	6806	.	meo domain
MAGI2-AS3 NR	TFB	TFBS	216	21	0.99353	+	factors;sequence=C
_038344	S		8	76	6806	.	CCATTAAA

MAGI2-AS3 NR _038345	TFB S	TFBS	855	86 3	0.99310 2439	+	.	TF=POU3F4; class=Ho meo domain factors; sequence=T ATGCTAAT
MAGI2-AS3 NR _038346	TFB S	TFBS	855	86 3	0.99310 2439	+	.	TF=POU3F4; class=Ho meo domain factors; sequence=T ATGCTAAT
MAGI2-AS3 NR _038344	TFB S	TFBS	181	18 3	0.99303 22	-	.	TF=BHLHE22 (var. 2) ; class=Basic helix-loop-helix factors (bHLH) ; sequence=TG CAGCTGCC
MAGI2-AS3 NR _038343	TFB S	TFBS	181	18 3	0.99303 22	-	.	TF=BHLHE22 (var. 2) ; class=Basic helix-loop-helix factors (bHLH) ; sequence=TG CAGCTGCC
MAGI2-AS3 NR _038344	TFB S	TFBS	181	18 3	0.99302 22	+	.	TF=BHLHE22 (var. 2) ; class=Basic helix-loop-helix factors (bHLH) ; sequence=GG CAGCTGCA
MAGI2-AS3 NR _038343	TFB S	TFBS	181	18 3	0.99302 22	+	.	TF=BHLHE22 (var. 2) ; class=Basic helix-loop-helix factors (bHLH) ; sequence=GG CAGCTGCA
MAGI2-AS3 NR _038345	TFB S	TFBS	187	18 4	0.99274 84	+	.	TF=MAZ; class=C2H2 zinc finger factors; sequence=T GCCCTCCCC
MAGI2-AS3 NR _038346	TFB S	TFBS	187	18 4	0.99274 84	+	.	TF=MAZ; class=C2H2 zinc finger factors; sequence=T GCCCTCCCC
MAGI2-AS3 NR _038344	TFB S	TFBS	871	88 1	0.99274 6735	+	.	TF=MAZ; class=C2H2 zinc finger factors; sequence=T GCCCTCCCC

MAGI2-AS3 NR _038343	TFB S	TFBS	871	88 1	0.99274 6735	+	.	TF=MAZ;class=C2H2 zinc finger factors;sequence=T CCCCCTCCCC
MAGI2-AS3 NR _038345	TFB S	TFBS	143 5	14 45	0.99248 4811	-	.	TF=MAZ;class=C2H2 zinc finger factors;sequence=T CCCCCTCCCC
MAGI2-AS3 NR _038346	TFB S	TFBS	143 5	14 45	0.99248 4811	-	.	TF=MAZ;class=C2H2 zinc finger factors;sequence=T CCCCCTCCCC
MAGI2-AS3 NR _038344	TFB S	TFBS	432	44 2	0.99248 4811	-	.	TF=MAZ;class=C2H2 zinc finger factors;sequence=T CCCCCTCCCC
MAGI2-AS3 NR _038343	TFB S	TFBS	432	44 2	0.99248 4811	-	.	TF=MAZ;class=C2H2 zinc finger factors;sequence=T CCCCCTCCCC
MAGI2-AS3 NR _038345	TFB S	TFBS	786	79 3	0.99225 0779	-	.	TF=HOXC4;class=Hom eo domain factors;sequence=G TCATTAC
MAGI2-AS3 NR _038346	TFB S	TFBS	786	79 3	0.99225 0779	-	.	TF=HOXC4;class=Hom eo domain factors;sequence=G TCATTAC
MAGI2-AS3 NR _038345	TFB S	TFBS	139 4	14 03	0.99203 9415	+	.	TF=BHLHE40;class=B asic helix-loop-helix factors (bHLH) ;sequence=CG CACGTGAC
MAGI2-AS3 NR _038346	TFB S	TFBS	139 4	14 03	0.99203 9415	+	.	TF=BHLHE40;class=B asic helix-loop-helix factors (bHLH) ;sequence=CG CACGTGAC
MAGI2-AS3 NR _038344	TFB S	TFBS	391	40 0	0.99203 9415	+	.	TF=BHLHE40;class=B asic helix-loop-helix factors

MAGI2-AS3 NR _038343	TFB S	TFBS	391	40 0	0.99203 9415	+	.	(bHLH) ; sequence=CG CACGTGAC TF=BHLHE40; class=Basic helix-loop-helix factors
MAGI2-AS3 NR _038343	TFB S	TFBS	247 3	24 82	0.99190 4082	+	.	(bHLH) ; sequence=CG CACGTGAC TF=HAND2; class=Basic helix-loop-helix factors
MAGI2-AS3 NR _038345	TFB S	TFBS	238 9	23 96	0.99181 4605	+	.	(bHLH) ; sequence=AA CAGATGCC TF=BARX1; class=Homeo domain factors; sequence=A CAATTAA
MAGI2-AS3 NR _038346	TFB S	TFBS	238 9	23 96	0.99181 4605	+	.	TF=BARX1; class=Homeo domain factors; sequence=A CAATTAA
MAGI2-AS3 NR _038344	TFB S	TFBS	238 9	23 96	0.99181 4605	+	.	TF=BARX1; class=Homeo domain factors; sequence=A CAATTAA
MAGI2-AS3 NR _038345	TFB S	TFBS	46	53	0.99152 8411	-	.	TF=HOXA4; class=Homeo domain factors; sequence=A TCATTAA
MAGI2-AS3 NR _038346	TFB S	TFBS	46	53	0.99152 8411	-	.	TF=HOXA4; class=Homeo domain factors; sequence=A TCATTAA
MAGI2-AS3 NR _038345	TFB S	TFBS	786	79 3	0.99131 454	-	.	TF=HOXA7; class=Homeo domain factors; sequence=G TCATTAC
MAGI2-AS3 NR _038346	TFB S	TFBS	786	79 3	0.99131 454	-	.	TF=HOXA7; class=Homeo domain factors; sequence=G TCATTAC
MAGI2-AS3 NR _038345	TFB S	TFBS	786	79 3	0.99084 7565	-	.	TF=HOXD8; class=Homeo domain factors; sequence=G

MAGI2-AS3 NR _038346	TFB S	TFBS	786	79 3	0.99084 7565	-	.	TCATTAC TF=HOXD8; class=Hom eo domain factors; sequence=G
MAGI2-AS3 NR _038345	TFB S	TFBS	786	79 3	0.99075 971	-	.	TCATTAC TF=HOXB8; class=Hom eo domain factors; sequence=G
MAGI2-AS3 NR _038346	TFB S	TFBS	786	79 3	0.99075 971	-	.	TCATTAC TF=HOXB8; class=Hom eo domain factors; sequence=G
MAGI2-AS3 NR _038345	TFB S	TFBS	139 4	14 04	0.99052 1718	+	.	TCATTAC TF=TFEC; class=Basi c helix-loop-helix factors (bHLH) ; sequence=CG
MAGI2-AS3 NR _038346	TFB S	TFBS	139 4	14 04	0.99052 1718	+	.	CACGTGACG TF=TFEC; class=Basi c helix-loop-helix factors (bHLH) ; sequence=CG
MAGI2-AS3 NR _038344	TFB S	TFBS	391	40 1	0.99052 1718	+	.	CACGTGACG TF=TFEC; class=Basi c helix-loop-helix factors (bHLH) ; sequence=CG
MAGI2-AS3 NR _038343	TFB S	TFBS	391	40 1	0.99052 1718	+	.	CACGTGACG TF=TFEC; class=Basi c helix-loop-helix factors (bHLH) ; sequence=CG
MAGI2-AS3 NR _038345	TFB S	TFBS	682	68 9	0.99019 2875	-	.	TAAACAA TF=FOXG1; class=For k head / winged helix factors; sequence=A
MAGI2-AS3 NR _038346	TFB S	TFBS	682	68 9	0.99019 2875	-	.	TAAACAA TF=FOXG1; class=For k head / winged helix factors; sequence=A