

Table S3. Binding Sites in *MITF-A* promoter

Transcript Accession # NM_198159

Genome Assembly: hg18

Location	+/-	BBLs	BLS	NLOD	Z-Score	FDR	Motif ID	TF Name	Gene	Distance (bp)	Region
chr3:69870544..69870561	-	0.242	1.57	0.857	4.316	0.193	0.017745	RXR::RAR_DR5	MITF	-714	Upstream
chr3:69870735..69870762	-	0.554	1.898	0.817	4.578	0.276	0.17229	GR	MITF	-513	Upstream
chr3:69870735..69870762	-	0.341	1.665	0.793	4.538	0.404	0.239734	PR	MITF	-513	Upstream
chr3:69870944..69870955	+	1.024	1.805	0.935	4.552	0.474	0.368917	AhR	MITF	-331	Upstream
chr3:69870946..69870955	+	1.117	1.805	0.949	4.353	0.41	0.269831	AhR, Arnt, HIF-1	MITF	-329	Upstream
chr3:69871055..69871062	+	1.868	2.591	1	4.241	0.365	0.176799	MZF1	MITF	-220	Upstream
chr3:69871080..69871086	+	2.591	2.591	1	3.817	0.026	0	MAFB	MITF	-195	Upstream
chr3:69871078..69871085	-	2.516	2.591	1	4.054	0.058	0	MAFA	MITF	-190	Upstream
chr3:69871127..69871138	-	1.241	2.794	0.878	4.39	0.116	0.070463	MYC::MAX	MITF	-137	Upstream
chr3:69871149..69871156	+	2.459	2.794	1	3.933	0.484	0.182584	NURR1	MITF	-126	Upstream
chr3:69871150..69871172	+	2.34	2.794	0.952	6.758	0	0	LM4_M2	MITF	-125	Upstream
chr3:69871144..69871165	-	0.601	2.154	0.89	4.818	0.038	0.007155	Staf	MITF	-110	Upstream
chr3:69871184..69871191	-	1.986	2.794	1	4.241	0.358	0.172302	MZF1	MITF	-84	Upstream
chr3:69871199..69871209	+	0.551	1.028	0.924	4.319	0.059	0	NF-kappaB	MITF	-76	Upstream
chr3:69871199..69871210	+	0.477	1.159	0.896	4.37	0.216	0.031858	NFKB1	MITF	-76	Upstream
chr3:69871199..69871209	-	0.45	1.159	0.897	4.416	0.074	0	NF-kappaB (p50)	MITF	-66	Upstream
chr3:69871200..69871210	-	0.555	1.028	0.936	4.412	0.052	0	NF-kappaB	MITF	-65	Upstream
chr3:69871200..69871210	-	0.759	1.296	0.975	4.72	0.052	0	REL	MITF	-65	Upstream
chr3:69871199..69871210	-	0.477	1.159	0.888	4.303	0.23	0.018875	NFKB1	MITF	-65	Upstream
chr3:69871200..69871210	-	0.763	1.296	0.975	4.714	0.338	0.057601	c-Rel	MITF	-65	Upstream
chr3:69871198..69871214	-	0.362	1.028	0.884	4.454	0.165	0.07197	NF-kappaB	MITF	-61	Upstream
chr3:69871219..69871241	-	1.417	2.794	0.843	5.562	0	0	LM4_M2	MITF	-34	Upstream
chr3:69871553..69871559	+	2.612	2.695	1	3.989	0.007	0	Neuro D	MITF	278	Downstream
chr3:69871547..69871558	-	1.716	2.391	0.957	4.454	0.08	0.008152	TGIF	MITF	283	Downstream
chr3:69871553..69871559	-	2.612	2.695	1	3.989	0.007	0	Neuro D	MITF	284	Downstream
chr3:69871546..69871562	-	0.054	2.019	0.871	4.321	0.161	0.048591	PKNOX2	MITF	287	Downstream
chr3:69871546..69871562	-	0.439	2.182	0.84	4.405	0.257	0.174713	TGIF2	MITF	287	Downstream
chr3:69871640..69871658	-	1.024	2.337	0.836	4.387	0.071	0.032818	ESR2	MITF	383	Downstream
chr3:69871641..69871661	-	0.869	2.486	0.792	4.39	0.064	0.010943	ESR1	MITF	386	Downstream
chr3:69871646..69871664	-	0.341	1.456	0.818	4.353	0.434	0.275125	MIF-1	MITF	389	Downstream
chr3:69871668..69871686	-	1.026	2.337	0.842	4.439	0.067	0.026511	ESR2	MITF	411	Downstream
chr3:69871813..69871823	+	1.128	2.106	0.989	4.563	0.009	0	TAL1	MITF	538	Downstream
chr3:69871813..69871822	+	1.335	1.485	1	4.335	0.014	0	AP-4	MITF	538	Downstream
chr3:69871813..69871821	+	1.455	1.688	1	4.607	0.016	0	HEB	MITF	538	Downstream
chr3:69871815..69871821	+	1.912	2.103	1	3.989	0.013	0	Neuro D	MITF	540	Downstream
chr3:69871815..69871821	-	1.912	2.103	1	3.989	0.013	0	Neuro D	MITF	546	Downstream
chr3:69871818..69871825	-	1.771	2.103	1	4.054	0.07	0	MAFA	MITF	550	Downstream
chr3:69871839..69871846	+	1.509	1.632	1	4.241	0.423	0.208925	MZF1	MITF	564	Downstream
chr3:69872140..69872149	+	1.524	1.844	1	4.003	0.074	0.019945	PUR1	MITF	865	Downstream