Region [a]	SNP [b]	RefSNP [c]	TFBS name [d]	Source [e]	Motif [f] Position(chr:start-end:strand)	Ref allele score [g]	Non-ref allele score [h]	Tool [i]	MCS [j]
upstream	**novel-1** (+YY1)	[G/A]	YY1 (Yin and Yang 1)	Transfac:v7.0:M00059	taatCCCAGc[G/A]ctttgg 19:47049005-47049021:+1	-	0.996/0.976	pMATCH (minSUM)	(N | N)
			Pax-2 (Paired box 2)	Transfac:v7.0:M00098	aatcCCAGC[g/a]ctttgggag 19:47049006-47049024:+1	0.992/0.943	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	atccCAGC[G/A]ctttgggagg 19:47049007-47049025:+1	0.918/0.940	0.910/0.936		(N | N)
			HOXA3 (Homeobox cluster protein)	Transfac:v7.0:M00395	AGC[G/A]Ctttg 19:47049012-47049020:+1	1.000/0.963	-		(N | N)
			HOXA3	Transfac:v7.0:M00395	C[G/A]CTTTggg 19:47049014-47049022:+1	0.940/0.941	0.956/0.953		(N | N)
			CdxA (CdxA homeobox gene)	Transfac:v7.0:M00100	[g/a]CTTTGgg 19:47049016-47049022:+1	1.000/0.992	1.000/0.992		(N | N)
upstream	**rs4803512** (+HOXA3) (- 2 x Pax-2, YY1, 2 x HOXA3)	[A/C]	YY1	Transfac:v7.0:M00069	ttgaACCATtc[a/c]gtaca 19:47049284-47049300:+1	0.996/0.982	-	pMATCH (minSUM)	(N | N)
			Pax-2	Transfac:v7.0:M00098	tgaaCCATTc[a/c]gtacatag 19:47049285-47049303:+1	0.982/0.922	0.982/0.919		(N | N)
			Evi-1 (Ectopic viral integration site 1)	Transfac:v7.0:M00081	aaccattc[a/c]GTACAt 19:47049287-47049301:+1	0.794/0.863	0.794/0.863		(N | N)
			HOXA3	Transfac:v7.0:M00395	ACCATtc[a/c]g 19:47049288-47049296:+1	0.954/0.948	0.954/0.948		(N | N)
			Pax-2	Transfac:v7.0:M00098	accaTTC[A/C]Gtacataggaa 19:47049288-47049306:+1	0.947/0.891	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	ccatTC[A/C]GTacataggaaa 19:47049289-47049307:+1	0.975/0.903	-		(N | N)
			CdxA	Transfac:v7.0:M00100	CATTC[a/c]g 19:47049290-47049296:+1	1.000/0.975	1.000/0.971		(N | N)
			HOXA3	Transfac:v7.0:M00395	CATTC[a/c]gta 19:47049290-47049298:+1	0.970/0.946	-		(N | N)
			HOXA3	Transfac:v7.0:M00395	TTC[A/C]Gtaca 19:47049292-47049300:+1	1.000/0.975	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	ttc[a/c]GTACAtaggaaaacc 19:47049292-47049310:+1	0.981/0.946	0.981/0.945		(N | N)
			HOXA3	Transfac:v7.0:M00395	[A/C]GTACatag 19:47049295-47049303:+1	-	0.957/0.961		(N | N)
			Msx-1 (Msh-like homeobox protein 1)	Transfac:v7.0:M00394	c[a/c]gTACATa 19:47049294-47049302:+1	1.000/1.000	1.000/1.000	pMATCH (minSUM, minFP)	(N | N)
upstream	**rs3214574** (+Pax-6, C/EBPalpha, C/EBPbeta, 2 x Evi-1, C/EBP) (- HOXA3, 2 x Evi-1) (+ Pax-2, novel-6;) (- Spz1, novel-15;)	[-/CT]	Pax-2	Transfac:v7.0:M00098	cttcCCTCCccttag[-/ct]at 19:47049605-47049623:+1	0.924/0.893	0.924/0.894 (cttcCCTCCccttagataa)	pMATCH (minSUM)	(N | N)
			HOXA3	Transfac:v7.0:M00395	CCCCTtag[-/ct] 19:47049612-47049620:+1	0.926/0.942	-		(N | N)
			C/EBPalpha (CCAAT/enhancer binding protein)	Transfac:v7.0:M00116	ccCTTAGataactt 19:47049613-47049626:+1	-	1.000/0.997		(N | N)
			C/EBPbeta	Transfac:v7.0:M00117	cccTTAGAtaactt 19:47049613-47049626:+1	-	1.000/0.977		(N | N)
			HOXA3	Transfac:v7.0:M00395	CCTTAg[-/ct]a 19:47049614-47049622:+1	0.987/0.942	0.987/0.959 (CCTTAgata)		(N | N)
			Evi-1	Transfac:v7.0:M00081	ccttagataACTTAg 19:47049614-47049628:+1	-	0.805/0.874		(N | N)
			C/EBP	Transfac:v7.0:M00159	ccTTAGAtaactt 19:47049614-47049626:+1	-	0.980/0.973		(N | N)
			Msx-1	Transfac:v7.0:M00394	cctTAG[-/CT]a 19:47049614-47049622:+1	0.955/0.933	0.962/0.938 (cctTAGATa)		(N | N)
			Evi-1	Transfac:v7.0:M00081	ccttagataACTTAg 19:47049614-47049628:+1	-	0.805/0.874		(N | N)
			HOXA3	Transfac:v7.0:M00395	CTTAG[-/ct]at 19:47049615-47049623:+1	0.957/0.943	-		(N | N)
			Evi-1	Transfac:v7.0:M00081	ag[-/ct]ataacTTAGAt 19:47049618-47049632:+1	0.898/0.844	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	ag[-/ct]ATAACttagatatat 19:47049618-47049636:+1	0.972/0.897	0.972/0.896 (ttagATAACttagatatat, 19:47049616-47049634:+1)		(N | N)
			Oct-1 (octamer-binding factor 1)	Transfac:v7.0:M00137	g[-/ct]ATAACttaga 19:47049619-47049631:+1	0.996/0.992	0.996/0.992 (tagATAACttaga, 19:47049617-47049629:+1)		(N | N)
			Evi-1	Transfac:v7.0:M00081	[-/ct]ataacttAGATAt 19:47049620-47049634:+1	0.931/0.828	-		(N | N)
			Oct-1	Transfac:v7.0:M00162	[-/ct]ataacttaGATATa 19:47049622-47049635:+1	0.982/0.960	0.982/0.960 (19:47049620-47049633:+1)		(N | N)
			Pax-6	Transfac:v7.0:M00097	cctccCCTTAgataacttaga 19:47049609-47049629:+1	-	0.987/0.976	pMATCH (minSUM, minFP)	(N | N)
			HOXA3	Transfac:v7.0:M00395	[-/ct]ATAACttag 19:47049622-47049630:+1	1.000/0.995	1.000/0.995		(N | N)
			GATA-1 (GATA-binding factor 1)	Transfac:v7.0:M00346	ttaGATAAct 19:47049616-47049625:+1	-/0.9	1629.46/0.9	MotifScanner	(N | N)
			GATA-2 (GATA-binding factor 2)	Transfac:v7.0:M00082	ttaGATAAct 19:47049616-47049625:+1	-/0.9	3124.5/0.9		(N | N)
			Evi-1	Transfac:v7.0:M00082	AGATAACTTAG 19:47049618-47049628:+1	-/0.9	670.903/0.9		(N | N)
			Cdc5 (Cdc5 cell division control protein 5)	Transfac:v7.0:M00478	G[-/ct]aTAacttag 19:47049619-47049630:+1	3343.59/0.9	-/0.9		(N | N)
upstream	**rs6509002** (- Evi-1, RORalpha1, Pax-2, PPARalpha, PPARgamma)	[C/T]	Pax-2	Transfac:v7.0:M00098	aggaGTAGActagagg[c/t]ca 19:47049893-47049911:+1	0.915/0.916	0.915/0.916	pMATCH (minSUM)	(y+ | N)
			Evi-1	Transfac:v7.0:M00081	gagtagactAGAGG[c/t] 19:47049895-47049909:+1	0.773/0.866	0.773/0.866		(y+ | N)
			Pax-2	Transfac:v7.0:M00098	agtaGACTAgagg[c/t]cacct 19:47049896-47049914:+1	0.840/0.906	0.840/0.906		(y | N)
			Evi-1	Transfac:v7.0:M00081	gactagagg[c/T]CACCt 19:47049900-47049914:+1	0.796/0.885	-		(y+ | N)
			RORalpha1 (RAR-related orphan receptor alpha1)	Transfac:v7.0:M00156	gactagaGG[c/T]CAc 19:47049900-47049912:+1	1.000/0.994	-		(y+ | N)
			Pax-2	Transfac:v7.0:M00098	agagG[c/T]CACctctccttca 19:47049904-47049922:+1	0.992/0.914	-		(y- | N)
			Evi-1	Transfac:v7.0:M00082	gactAGAGG[c/t]c 19:47049900-47049910:+1	0.975/0.987	0.975/0.981	pMATCH (minSUM, minFP)	(y+ | N)
			PPARalpha (PPAR:RXR heterodimers)	Transfac:v12.1:M00242	aAggAgTAGactAgAGG[c/T]CA 19:47049892-47049911:+1	0.784/0.784	-	MATCH (minFP)	(y+ | N)
			PPARgamma	Transfac:v7.0:M00528	gagtaGactAgaGg[C/T]ca 19:47049895-47049911:+1	3331.06/0.9	-/0.9	MotifScanner	(y | N)
upstream	**novel-3** (+ Pax-2, COMP-1)	[C/T]	Pax-2	Transfac:v7.0:M00098	cagaGTTCCcta[c/t]gttccc 19:47050781-47050799:+1	-	0.915/0.916	pMATCH (minSUM)	(Y | N)
			Pax-2	Transfac:v7.0:M00098	agagTTCCCta[c/t]gttccca 19:47050782-47050800:+1	0.982/0.911	0.982/0.899		(Y | N)
			C/EBPalpha	Transfac:v7.0:M00116	gaGTTCCcta[c/t]gtt 19:47050783-47050796:+1	0.999/0.995	0.999/0.996		(y | N)
			COMP1	Transfac:v7.0:M00057	agttccCTA[C/t]Gttcccaaggggcc 19:47050784-47050807:+1	-	0.878/0.833		(y- | N)
			Msx-1	Transfac:v7.0:M00394	cccTA[C/T]GTt 19:47050788-47050796:+1	0.955/0.940	0.992/0.965		(Y | N)
			HOXA3	Transfac:v7.0:M00395	CCTA[C/T]gttc 19:47050789-47050797:+1	0.987/0.943	1.000/0.945		(Y | N)
			Pax-2	Transfac:v7.0:M00098	cta[c/t]GTTCCcaaggggcca 19:47050790-47050808:+1	0.963/0.928	0.963/0.928		(y+ | N)
			PPARgamma2 (peroxisome proliferator-activated receptor gamma)	Transfac:v12.1:M00515	ctcTcaGgCAgaGTtcCCtA[C/t]gT 19:47050773-47050795:+1	0.604/0.675	0.604/0.682	MATCH (minFP)	(y+ | N)
			box_1_2_CTATGT	Model:EPD Human 3*	CTA[c/T]GT 19:47050790-47050795:+1	6336.9	N.A.	MotifSampler	(Y | N)
upstream	**rs7258162** (- Msx-1, HOXA3)	[C/G]	Pax-2	Transfac:v7.0:M00098	gcgcCCACCacct[c/g]cccca 19:47052562-47052580:+1	0.992/0.947	0.992/0.921	pMATCH (minSUM)	(N | N)
			Msx-1	Transfac:v7.0:M00394	cacCACCT[c/g] 19:47052567-47052575:+1	0.906/0.936	-		(N | N)
			HOXA3	Transfac:v7.0:M00395	ACCACct[c/g]c 19:47052568-47052576:+1	1.000/0.941	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	t[c/g]ccCCAGCtaatgttttg 19:47052574-47052592:+1	0.992/0.930	0.992/0.929		(N | N)
			MyoD (myoblast determining factor)	Transfac:v7.0:M00184	acCAccT[C/G]cc 19:47052568-47052577:+1	3593.57/0.9	-/0.9	MotifScanner	(N | N)
			Ebox (E-box)	Transfac:v12.1:M01034	cCACCT[c/G]cCc 19:47052569-47052578:+1	0.998/0.996	-	MATCH (minFP)	(N | N)
upstream	**novel-4** (+Pax-2, Msx-1) (- 3 x Evi-1)	[G/T]	Pax-2	Transfac:v7.0:M00098	tatcCCACTgttt[g/t]taggt 19:47052881-47052899:+1	-	1.000/0.900	pMATCH (minSUM)	(N | N)
			Evi-1	Transfac:v7.0:M00081	tcccactgtTT[g/T]TAg 19:47052883-47052897:+1	0.898/0.838	-		(N | N)
			Msx-1	Transfac:v7.0:M00394	cacTGTTT[g/t] 19:47052886-47052894:+1	-	0.951/0.959		(N | N)
			Pax-2	Transfac:v7.0:M00098	cactGTTT[G/T]taggtactac 19:47052886-47052904:+1	0.971/0.951	0.974/0.952		(N | N)
			En-1	Transfac:v7.0:M00396	GTTT[g/T]ta 19:47052890-47052896:+1	1.000/0.990	-		(N | N)
			Evi-1	Transfac:v7.0:M00081	tt[g/t]taggtaCTACAg 19:47052892-47052906:+1	0.794/0.823	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	[g/t]tagGTACTacagcctcaa 19:47052894-47052912:+1	0.903/0.899	0.903/0.898		(N | N)
upstream	**novel-5** (+ Oct-1, HOXA3, CREB_Q2; Broad-complex_3, 671.634/0.9;)	[A/G]	Pax-2	Transfac:v7.0:M00098	gtatGATTCcaactat[a/g]tg 19:47053105-47053123:+1	0.992/0.935	0.992/0.923	pMATCH (minSUM)	(N | N)
			Evi-1	Transfac:v7.0:M00081	tatgattccAACTAt[a/g] 19:47053106-47053120:+1	0.782/0.842	0.782/0.842		(N | N)
			Evi-1	Transfac:v7.0:M00081	ttccaactaT[A/G]TGAc 19:47053111-47053125:+1	0.842/0.875	0.772/0.850		(N | N)
			v-Myb	Transfac:v7.0:M00003	tccAACTAt[a/g] 19:47053112-47053121:+1	1.000/0.982	1.000/0.968		(N | N)
			Msx-1	Transfac:v7.0:M00394	aacTAT[A/G]Tg 19:47053115-47053123:+1	0.909/0.931	0.917/0.936		(N | N)
			Pbx-1	Transfac:v7.0:M00096	actAT[A/G]TGa 19:47053116-47053124:+1	0.964/0.944	1.000/0.971		(N | N)
			Oct-1	Transfac:v7.0:M00162	ctat[a/g]tgaCATTCt 19:47053117-47053130:+1	-	0.964/0.971		(N | N)
			Pax-2	Transfac:v7.0:M00098	tat[a/g]TGACAttctggaaaa 19:47053118-47053136:+1	0.929/0.902	0.929/0.903		(N | N)
			Pax-2	Transfac:v7.0:M00098	at[a/g]tGACATtctggaaaaa 19:47053119-47053137:+1	0.992/0.899	0.992/0.912		(N | N)
			HOXA3	Transfac:v7.0:M00395	[A/g]TGACattc 19:47053121-47053129:+1	-	0.967/0.962		(N | N)
			Broad-complex_2	Jaspar:v3.0:MA0011	aaCTAt[a/g]t 19:47053115-47053122:+1	953.749/0.9	1187.41/0.9	MotifScanner	(N | N)
			Broad-complex_3	Jaspar:v3.0:MA0012	ccAACTAt[a/g]tg 19:47053113-47053123:+1	-/0.9	671.634/0.9 542.52/0.9		(N | N)
			CREB_Q2 (cyclic AMP response element-binding protein) (CCAAT-enhancer binding protein)	Transfac:v7.0:M00177	t[a/g]TGACaTtctg 19:47053120-47053131:+1	-/0.9	67.5249/0.9		(N | N)
upstream	**novel-6** (+ Pax-2, YY!) (- HOXA3)	[T/G]	p300	Transfac:v7.0:M00033	aactGTAGTacca[t/g] 19:47053609-47053622:+1	0.994/0.980	1.000/0.979	pMATCH (minSUM)	(N | N)
			YY1	Transfac:v7.0:M00059	tagtACCA[T/g]ctactcga 19:47053614-47053630:+1	-	0.998/0.990		(N | N)
			Pax-2	Transfac:v7.0:M00098	agtaCCA[T/G]Ctactcgacag 19:47053615-47053633:+1	0.992/0.909	0.974/0.899		(N | N)
			HOXA3	Transfac:v7.0:M00395	[t/G]CTACtcga 19:47053622-47053630:+1	0.987/0.964	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	[t/g]actcGACAGgctgaggtag 19:47053623-47053641:+1	-	0.972/0.983	pMATCH (minFP)	(N | N)
upstream	**novel-7** (+ HOXA3; Broad-complex_3, novel-5, 542.52/0.9;) (- Evi-1, 2 x HOXA3, SRY)	[G/A]	Oct-1	Transfac:v7.0:M00137	cctGTAAAa[g/a]cta 19:47053892-47053904:+1	1.000/0.996	1.000/0.994	pMATCH (minSUM)	(N | N)
			Evi-1	Transfac:v7.0:M00081	tgtaaaa[g/a]cTAACAt 19:47053894-47053908:+1	0.851/0.821	0.851/0.850		(N | N)
			En-1	Transfac:v7.0:M00396	GTAAAa[g/a] 19:47053895-47053901:+1	0.996/0.990	-		(N | N)
			Evi-1	Transfac:v7.0:M00081	taaaa[g/a]ctaACATGt 19:47053896-47053910:+1	0.805/0.834	0.805/0.839		(N | N)
			HOXA3	Transfac:v7.0:M00395	AAA[g/A]Ctaac 19:47053898-47053906:+1	0.984/0.975	-		(N | N)
			SRY (sex-determining region Y)	Transfac:v7.0:M00148	AA[g/A]CTaa 19:47053899-47053905:+1	1.000/1.000	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	a[g/a]ctAACATgtacaaaaat 19:47053900-47053918:+1	0.899/0.922	0.899/0.923		(N | N)
			Msx-1	Transfac:v7.0:M00394	a[g/a]cTAACAt 19:47053900-47053908:+1	0.949/0.940	0.949/0.940		(N | N)
			YY1	Transfac:v7.0:M00059	a[g/a]ctAACATgtacaaaa 19:47053900-47053916:+1	0.985/0.978	0.985/0.981		(N | N)
			HOXA3	Transfac:v7.0:M00395	[g/A]CTAAcatg 19:47053901-47053909:+1	0.951/0.944	-		(N | N)
			Msx-1	Transfac:v7.0:M00394	[g/a]ctAACATg 19:47053901-47053909:+1	0.962/0.967	0.962/0.957		(N | N)
			HOXA3	Transfac:v7.0:M00395	[G/a]CTAAcatg 19:47053901-47053909:+1	-	1.000/0.982		(N | N)
			Broad-complex_3	Jaspar:v3.0:MA0012	aAA[G/A]CTAacat 19:47053898-47053908:+1	953.749/0.9	-/0.9	MotifScanner	(N | N)
upstream	**novel-8** (+ FOXJ2, Msx-1, Evi-1Pax-2, CdxA, YY1) (- Pbx-1, 2 x Msx-1, v-Myb)	[G/A]	Pax-2	Transfac:v7.0:M00098	acatGTACAaaaatt[g/a]aca 19:47053905-47053923:+1	0.915/0.904	0.915/0.907	pMATCH (minSUM)	(N | N)
			FOXJ2 (fork head box J 2)	Transfac:v7.0:M00423	tgtaCAAAAatt[g/a]a 19:47053908-47053921:+1	-	0.968/0.891		(N | N)
			Evi-1	Transfac:v7.0:M00081	tacaaaaatT[G/A]ACAc 19:47053910-47053924:+1	0.851/0.867	0.921/0.892		(N | N)
			HOXA3	Transfac:v7.0:M00395	[G/A]ACAAAatt 19:47053911-47053919:+1	0.973/0.974	0.973/0.974		(N | N)
			Msx-1	Transfac:v7.0:M00394	caaAAATT[g/a] 19:47053912-47053920:+1	-	0.989/0.978		(N | N)
			Pbx-1a (homeo domain factor Pbx-1)	Transfac:v7.0:M00096	aaaAATT[G/A]a 19:47053913-47053921:+1	0.983/0.955	-		(N | N)
			HOXA3	Transfac:v7.0:M00395	AAAAT[g/a]ac 19:47053914-47053922:+1	0.970/0.964	0.970/0.964		(N | N)
			En-1	Transfac:v7.0:M00396	AAAATt[g/a] 19:47053914-47053920:+1	-	1.000/0.996		(N | N)
			Msx-1	Transfac:v7.0:M00394	aaaTT[G/A]ACa 19:47053915-47053923:+1	0.913/0.931	-		(N | N)
			Msx-1	Transfac:v7.0:M00394	aatT[g/A]ACAc 19:47053916-47053924:+1	0.949/0.948	-		(N | N)
			v-Myb	Transfac:v7.0:M00003	aatT[g/A]ACAcc 19:47053916-47053925:+1	1.000/0.977	-		(N | N)
			Pax-2	Transfac:v7.0:M00098	aatt[G/a]ACACcagggacaca 19:47053916-47053934:+1	-	1.000/0.920		(N | N)
			CdxA	Transfac:v7.0:M00100	ATT[G/a]Aca 19:47053917-47053923:+1	-	1.000/0.982		(N | N)
			YY1	Transfac:v7.0:M00059	t[g/a]acACCAGggacacag 19:47053919-47053935:+1	-	1.000/0.978		(N | N)
upstream	**novel-9** (+ HOXA3, HLF, AP-2alpha, bZIP910, CREB, CREB1, CREBP1) (- Msx-1, CdxA, POU3F2)	[C/T]	Msx-1	Transfac:v7.0:M00394	tgcCTTA[c/T]g 19:47054208-47054216:+1	0.917/0.943	-	pMATCH (minSUM)	(N | N)
			CdxA	Transfac:v7.0:M00100	CCTTA[c/t]g 19:47054210-47054216:+1	0.971/0.973	-		(N | N)
			HOXA3	Transfac:v7.0:M00395	CCTTA[c/t]gtc 19:47054210-47054218:+1	-	0.987/0.953		(N | N)
			Msx-1	Transfac:v7.0:M00394	cctTA[C/T]GTc 19:47054210-47054218:+1	0.955/0.933	0.992/0.958		(N | N)
			HOXA3	Transfac:v7.0:M00395	CTTA[C/T]gtcc 19:47054211-47054219:+1	0.970/0.959	0.957/0.948		(N | N)
			HLF	Transfac:v7.0:M00260	CTTA[C/t]gtcca 19:47054211-47054220:+1	-	0.939/0.953		(N | N)
			YY1	Transfac:v7.0:M00059	ta[c/t]gTCCATcaaaactc 19:47054213-47054229:+1	1.000/0.983	1.000/0.981		(N | N)
			Msx-1	Transfac:v7.0:M00394	a[c/t]gTCCATc 19:47054214-47054222:+1	0.902/0.933	0.902/0.933		(N | N)
			Pbx-1b (homeo domain factor Pbx-1)	Transfac:v7.0:M00124	ta[c/t]gTCcATCAAaac 19:47054213-47054227:+1	2253.81/0.9	10900.5/0.9	MotifScanner	(N | N)
			Oct-1 (octamer-binding factor 1, POU2F1)	Transfac:v7.0:M00161	ctgcTTgGcTta[c/t] 19:47054202-47054215:+1	180.893/0.9	101.817/0.9		(N | N)
			CREB (deltaCREB)	Transfac:v7.0:M00113	tgccTtA[C/t]GTcc 19:47054208-47054219:+1	-/0.9	259.949/0.9		(N | N)
			AP-2alpha (Activator Protein-2)	Transfac:v7.0:M00469	GCCtta[c/t]Gt 19:47054209-47054217:+1	-/0.9	384.776/0.9		(N | N)
			CREB	Transfac:v7.0:M00039	TTA[C/T]GTCC 19:47054212-47054219:+1	-/0.9	149.021/0.9		(N | N)
			CREBP1	Transfac:v7.0:M00040	TTA[C/T]GTCC 19:47054212-47054219:+1	-/0.9	1153.47/0.9		(N | N)
			POU3F2 (N-Oct-5a, N-Oct-5b)	Transfac:v7.0:M00464	TTA[C/T]GtccAT 19:47054212-47054221:+1	137.922/0.9	-/0.9		(N | N)
			CREB1 (cyclic AMP response element-binding protein)	Jaspar:v3.0:MA0018	ttgccTtA[C/t]Gtc 19:47054207-47054218:+1	-/0.9	358.13/0.9		(N | N)
			AP-2alpha	Jaspar:v3.0:MA0003	GCCtta[c/t]Gt 19:47054209-47054217:+1	-/0.9	383.363/0.9		(N | N)
			bZIP910	Jaspar:v3.0:MA0096	cTtA[C/t]GT 19:47054211-47054217:+1	-/0.9	202.172/0.9		(N | N)
			Pbx1	Jaspar:v3.0:MA0070	a[c/t]gTCcATCAaa 19:47054214-47054225:+1	2378.14/0.9	8330.43/0.9		(N | N)
upstream	**novel-10** (- C/EBPalpha)	[T/C]	Pax-6	Transfac:v7.0:M00097	ctctgCTTTAtataaatttta[t/c] 19:47054227-47054247:+1	0.948/0.968	0.948/0.968	pMATCH (minSUM)	(N | N)
			Oct-1	Transfac:v7.0:M00137	tatATAAAtttta[t/c] 19:47054235-47054247:+1	1.000/0.995	1.000/0.995		(N | N)
			Evi-1	Transfac:v7.0:M00081	atataaattTTA[T/C]Ct 19:47054236-47054250:+1	0.819/0.832	0.898/0.861		(N | N)
			Pax-2	Transfac:v7.0:M00098	ataaATTTTa[t/c]ctaagctt 19:47054238-47054256:+1	0.982/0.932	0.982/0.941		(N | N)
			C/EBPalpha	Transfac:v7.0:M00116	atTTTA[T/c]ctaagct 19:47054242-47054255:+1	1.000/0.998	-		(N | N)
			CdxA	Transfac:v7.0:M00100	ATTTTa[t/c] 19:47054242-47054248:+1	0.979/0.981	0.979/0.972		(N | N)
			CdxA	Transfac:v7.0:M00100	TTTTa[t/c]c 19:47054243-47054249:+1	0.982/0.983	1.000/0.972		(N | N)
			Pax-2	Transfac:v7.0:M00098	ttta[T/C]CTAAgcttcactct 19:47054244-47054262:+1	0.924/0.907	0.949/0.922		(N | N)
			Msx-1	Transfac:v7.0:M00394	a[t/c]cTAAGCt 19:47054247-47054255:+1	0.989/0.968	0.989/0.967		(N | N)
			HOXA3	Transfac:v7.0:M00395	[T/C]CTAAgctt 19:47054248-47054256:+1	1.000/0.955	0.951/0.946		(N | N)
			box_2_2_TTACCTA	Model:EPD Vertebrate 3*	TTA[t/C]CTA 19:47054245-47054251:+1	17423.7	N.A.	MotifSampler	(N | N)
			box_2_2_mTGTTACCTA	Model:EPD Vertebrate 3*	ATTTTA[t/C]CTA 19:47054242-47054251:+1	61169.9	N.A.		(N | N)
upstream	**novel-11** (+ Oct-1, Pax-2, SRY) (- YY1)	[T/C]	Oct-1	Transfac:v7.0:M00137	cctGTAATc[t/c]cag 19:47054440-47054452:+1	-	1.000/0.996	pMATCH (minSUM)	(N | N)
			HOXA3	Transfac:v7.0:M00395	CCTGTaatc[t/c] 19:47054440-47054448:+1	0.970/0.958	0.970/0.958		(N | N)
			Pax-2	Transfac:v7.0:M00098	gtaaTC[T/c]CAgcattttggg 19:47054443-47054461:+1	-	0.989/0.931		(N | N)
			En-1	Transfac:v7.0:M00396	GTAATc[t/c] 19:47054443-47054449:+1	0.992/0.992	0.992/0.992		(N | N)
			YY1	Transfac:v7.0:M00059	taatC[t/C]CAGcattttgg 19:47054444-47054460:+1	0.996/0.973	-		(N | N)
			SRY	Transfac:v7.0:M00148	AATC[T/c]ca 19:47054445-47054451:+1	-	1.000/0.976		(N | N)
			Pax-2	Transfac:v7.0:M00098	aatc[T/C]CAGCattttgggag 19:47054445-47054463:+1	0.992/0.952	0.966/0.937		(N | N)
			Pax-2	Transfac:v7.0:M00098	atc[t/c]CAGCAttttgggagg 19:47054446-47054464:+1	0.918/0.927	0.918/0.927		(N | N)
			YY1	Transfac:v7.0:M00059	tc[t/c]cAGCATtttgggag 19:47054447-47054463:+1	0.998/0.990	0.998/0.988		(N | N)
upstream	**rs930102** (- Pax-2, HOXA2, Evi-1)	[C/T]	Pax-2	Transfac:v7.0:M00098	cgagG[c/T]GGCagggccggac 19:47056230-47056248:+1	0.914/0.926	-	pMATCH (minSUM)	(Y | N)
			HOXA3	Transfac:v7.0:M00395	CGAGG[c/t]ggc 19:47056230-47056238:+1	0.973/0.979	-		(Y | N)
			COMP1	Transfac:v7.0:M00057	cgagg[c/t]GGCAGggccggacgccga 19:47056230-47056253:+1	0.929/0.834	0.929/0.834		(Y | N)
			En-1	Transfac:v7.0:M00396	GAGG[c/T]gg 19:47056231-47056237:+1	0.992/0.988	-		(Y | N)
			Pax-2	Transfac:v7.0:M00098	agg[c/t]GGCAGggccggacgc 19:47056232-47056250:+1	0.887/0.901	0.887/0.902		(Y | N)
			Sp1 (stimulating protein 1)	Transfac:v7.0:M00008	g[c/t]GGCAGggc 19:47056234-47056243:+1	1.000/0.976	1.000/0.976		(Y | N)
			Pax-5 (B-cell-specific activating protein)	Transfac:v7.0:M00143	accgggcgCgagG[c/t] gGcagggccggacg 19:47056222-47056249:+1	2609.34/0.9	1057.56/0.9	MotifScanner	(y+ | N)
upstream	**novel-12** (+ 2 x Sp1, Pax-5, AP-2alpha) (- Sp1, Pax-2)	[G/C]	Sp1	Transfac:v7.0:M00008	ccGG[g/C]GCggg 19:47056289-47056298:+1	1.000/0.949	-	pMATCH (minSUM)	(y | N)
			Sp1	Transfac:v7.0:M00008	cgG[G/c]GCGggc 19:47056290-47056299:+1	-	0.957/0.956		(y | N)
			Sp1	Transfac:v7.0:M00008	gg[G/c]GCGGgcc 19:47056291-47056300:+1	-	1.000/0.985		(y+ | N)
			Pax-2	Transfac:v7.0:M00098	gg[g/c]gCGGGCccgtcccgcc 19:47056291-47056309:+1	0.938/0.891	-		(y+ | N)
			AP-2alpha	Jaspar:v3.0:MA0003	GCCcgg[g/c]gc 19:47056287-47056295:+1	53.929/0.9	170.435/0.9	MotifLocator	(y- | N)
			Pax-5	Transfac:v7.0:M00144	cccgaGgcgcccgg[g/c] GCGggcCcgtccc 19:47056279-47056306:+1	84.2745/0.9	379.43/0.9	MotifScanner	(y- | N)
			Pax-5	Transfac:v12.1:M00144	cccgaggcgcccgG[G/C] GCGggcccgtccc 19:47056279-47056306:+1	0.839/0.753	0.873/0.767	MATCH (minFP)	(y| N)
			AP-2alpha	Transfac:v11.2:M00469	GCCCGg[g/c]gc 19:47056287-47056295:+1	-	1.000/1.000		(y- | N)
upstream	**novel-13** (+AP-2alpha; Eip74EF; PU.1/Spi-1; Pax-2; c-Ets-1/p54; v-Myb) (- AP-2alpha)	[A/G]	AP-2alpha	Jaspar:v7.0:MA0003	GCCgga[a/g]cc 19:47056536-47056544:+1	-/0.9	31.5705/0.9	MotifLocator	(Y | N)
			Eip74EF	Jaspar:v7.0:MA0026	ccGGA[A/g]c 19:47056537-47056543:+1	-/0.9	394.501/0.9		(Y | N)
			PU.1 (Spi-1)	Jaspar:v7.0:MA0080	cGGA[A/g]c 19:47056538-47056543:+1	-/0.9	311.828/0.9		(Y | N)
			AP-2alpha	Jaspar:v3.0:MA0003	[A/G]CCcggcgt 19:47056542-47056550:+1	41.181/0.9	-/0.9		(y- | N)
			Pax-2	Transfac:v7.0:M00098	ggagCCGGA[a/g]cccggcgtt 19:47056533-47056551:+1	-	0.969/0.893	pMATCH (minSUM)	(y | N)
			c-Ets-1 (p54)	Transfac:v7.0:M00032	gCCGGA[a/g]ccc 19:47056536-47056545:+1	-	1.000/0.982		(Y | N)
			COMP1	Transfac:v7.0:M00057	ccgga[a/g]CCCGGcgttgaaggggcc 19:47056537-47056560:+1	0.807/0.852	0.807/0.844		(y- | N)
			v-Myb	Transfac:v7.0:M00003	cggA[A/g]CCCgg 19:47056538-47056547:+1	-	0.972/0.971		(y | N)
			p300	Transfac:v7.0:M00033	[a/g]cccGGCGTtgaag 19:47056542-47056555:+1	1.000/0.979	1.000/0.979		(y- | N)
upstream	**novel-14** (+ HOXA3, SRY) (- Sp1)	[A/G]	COMP1	Transfac:v7.0:M00057	ccggagCCCGGcgttgaagg[a/g]gcc 19:47056537-47056560:+1	0.807/0.852	0.807/0.844	pMATCH (minSUM)	(y | N)
			Pax-2	Transfac:v7.0:M00098	cggcGTTGAagg[a/g]gccgtg 19:47056545-47056563:+1	0.982/0.935	0.982/0.939		(y | N)
			Pax-2	Transfac:v7.0:M00098	ggcgTTGAAgg[a/g]gccgtgg 19:47056546-47056564:+1	0.955/0.930	0.955/0.941		(y- | N)
			Msx-1	Transfac:v7.0:M00394	cgtTGAAGg[a/g] 19:47056548-47056556:+1	0.963/0.938	0.963/0.938		(y- | N)
			HOXA3	Transfac:v7.0:M00395	CGTTGaagg[a/g] 19:47056548-47056556:+1	1.000/0.976	1.000/0.976		(y- | N)
			HOXA3	Transfac:v7.0:M00395	TTGAAgg[a/g]g 19:47056550-47056558:+1	-	0.973/0.943		(y- | N)
			HOXA3	Transfac:v7.0:M00395	TGAAGg[a/g]gc 19:47056551-47056559:+1	1.000/0.954	1.000/0.954		(y- | N)
			SRY	Transfac:v7.0:M00148	AAGG[A/G]gc 19:47056553-47056559:+1	-	1.000/0.975		(y- | N)
			Sp1	Transfac:v7.0:M00008	gg[a/G]GCCGtgg 19:47056555-47056564:+1	0.981/0.942	-		(y | N)
			AP-2alpha	Jaspar:v3.0:MA0003	[a/g]GCCgtgga 19:47056558-47056566:+1	51.4922/0.9	40.4248/0.9	MotifLocator	(y | N)
upstream	**novel-15** (+ YY1, Evi-1, Pbx-1) (- 2 x Pax-2, Kid3, v-Myb, Tst-1, GR-a)	[A/G]	COMP1	Transfac:v7.0:M00057	aagtaaCGGGGggtaccac[a/g]gttt 19:47056566-47056589:+1	0.807/0.842	0.807/0.842	pMATCH (minSUM)	(y- | N)
			COMP1	Transfac:v7.0:M00057	agtaacGGGGGgtaccac[a/g]gttta 19:47056567-47056590:+1	0.893/0.832	0.893/0.832		(y- | N)
			p300	Transfac:v7.0:M00033	acggGGGGTaccac[a/g] 19:47056571-47056584:+1	1.000/0.997	1.000/0.997		(y- | N)
			Pax-2	Transfac:v7.0:M00098	ggggGTACCac[a/g]gtttagg 19:47056574-47056592:+1	0.895/0.891	-		(y- | N)
			YY1	Transfac:v7.0:M00059	gtacCAC[A/G]Gtttaggat 19:47056578-47056594:+1	-	0.996/0.980		(y- | N)
			Evi-1	Transfac:v7.0:M00081	taccac[a/g]gtTTAGGa 19:47056579-47056593:+1	-	0.819/0.822		(y- | N)
			Pbx-1	Transfac:v7.0:M00096	accAC[A/G]GTt 19:47056580-47056588:+1	-	0.930/0.937		(y- | N)
			HOXA3	Transfac:v7.0:M00395	C[A/G]GTTtagg 19:47056584-47056592:+1	0.956/0.953	0.940/0.941		(y- | N)
			Msx-1	Transfac:v7.0:M00394	c[a/g]gTTTAGg 19:47056584-47056592:+1	0.940/0.959	0.940/0.959		(y- | N)
			HOXA3	Transfac:v7.0:M00395	ACCAC[a/g]gtt 19:47056580-47056588:+1	1.000/0.995	1.000/0.995	pMATCH (minSUM, minFP)	(y+ | N)
			Pax-2	Jaspar:v3.0:MA0067	tacCAc[a/g]g 19:47056579-47056586:+1	112.092/0.9	-/0.9	MotifLocator	(Y | N)
			v-Myb	Transfac:v7.0:M00227	taccAC[A/G]Gt 19:47056579-47056587:+1	96.1399/0.9	-/0.9	MotifScanner	(y+ | N)
			Tst-1 (POU-factor Tst-1/Oct-6)	Transfac:v7.0:M00133	cac[a/g]gtTtaggatgc 19:47056582-47056596:+1	181.713/0.9	-/0.9		(y- | N)
			GR-a (Glucocorticoid response el.)	Transfac:v7.0:M00205	[a/g]gtttaggatGcgCTg 19:47056585-47056600:+1	1248.57/0.9	-/0.9		(y- | N)
			Spz1 (spermatogenic Zip)	Transfac:v7.0:M00446	aacGGgGGgtaccac[A/G] 19:47056570-47056584:+1	705.638/0.9	705.638/0.9		(y | N)
			Ik-2 (Ikaros 2)	Transfac:v7.0:M00087	[A/G]gttTaGGAtgcgctg 19:47056586-47056597:+1	591.664/0.9	359.408/0.9		(y- | N)
			Spz1	Transfac:v7.0:M00446	aacGGGGGgtaccac[a/g] 19:47056570-47056584:+1	705.638/0.9	705.638/0.9		(y- | N)
			GR-alpha (Glucocorticoid response element)	Transfac:v7.0:M00205	[a/g]gtttAggaTGcgCTg 19:47056585-47056600:+1	170.47/0.9	-/0.9		(y- | N)
			Spz1	Transfac:v12.1:M00446	aacGGGGGgtaccac[a/g] 19:47056570-47056584:+1	0.998/0.962	0.998/0.962	MATCH (minFP)	(y- | N)
			Kid3 (ZNF354C)	Transfac:v12.1:M01160	CCAC[a/g] 19:47056581-47056585:+1	1.000/1.000	-		(Y | N)
2nd intron	**novel-16**	[CC/C]	box_2_1_GGTyCTAG	Model:EPD Human 3*	GGTC[CC/C]TGG 19:47056832-47056839:+1	4788.67	N.A.	MotifSampler	(N | N)
			box_2_1_GGGCCTnCs	Model:EPD Vertebrate 3*	GGTC[CC/C]TGGC 19:47056832-47056840:+1	2321.43	N.A.		(N | N)
	rs2075749	[C/G]	Sp1	Transfac:v7.0:M00008	[c/g]GAGGCTTGTT 19:47056845-47056854:+1	111.864/0.3	188.282/0.3	MotifScanner	(Y | N)
	novel-17	[-/T]	box_1_2_CTGnmTTG	Model:EPD Vertebrate 3*	CTGTTT[-/T]G 19:47057006-47057013:+1	1441.2	N.A.	MotifSampler	(y- | N)
			box_1_1_TGTnTTsnGG	Model:EPD Human 3*	TGTTT[-/T]GGTC 19:47057007-47057016:+1	1385.25	N.A.		(y | N)
			box_1_1_TTGGnCnTA	Model:EPD Vertebrate 3*	T[-/T]GGTCTTA 19:47057011-47057019:+1	37103.9	N.A.		(Y | N)
			box_1_2_GGnCTkAG	Model:EPD Human 3*	[-/t]GGTCTTAG 19:47057013-47057020:+1	10389.1	N.A.		(Y | N)
			box_2_1_GGTyCTAG	Model:EPD Human 3*	[-/t]GGTCTTAG 19:47057013-47057020:+1	12925.1	N.A.		(Y | N)
4th intron	**rs1366610** (- Sp1, MZF1_5-13, Mzf1;) (+ Spz1; Zic1; Zic2; Olf-1, novel-42, 2012.2/0.9; E47, 5494.35/0.9; HSF1, novel-41, 613.405/0.9; HSF2, novel-42, 630.919/0.9;)	[A/G]	Szf1-1	Transfac:v11.2:M01109	gCAGGGtag[a/g]ggggg 19:47065129-47065143:+1	1.000/0.815	1.000/0.818	MATCH (minFP)	(y | N)
			Spz1 (spermatogenic Zip)	Transfac:v7.0:M00446	taaGcaGGgtag[a/g]gg 19:47065126-47065140:+1	-/0.5	201.793/0.5	MotifScanners	(y- | N)
			Mzf1	Transfac:v7.0:M00084	agggtAG[a/G]GGggg 19:47065131-47065143:+1	201.027/0.5	-/0.5		(y | N)
			MZF1_5-13	Jaspar:v3.0:MA0057	gtAg[a/G]GGggg 19:47065134-47065143:+1	1253.7/0.5	-/0.5		(y- | N)
			Sp1	Jaspar:v3.0:MA0079	ag[a/G]Gggggct 19:47065136-47065145:+1	104.692/0.5	-/0.5		(y- | N)
			Zic3 (zinc finger protein of the cerebellum 3)	Transfac:v7.0:M00450	aG[a/G]GgGGgc 19:47065136-47065144:+1	-/0.4	48.1223/0.4		(y- | N)
	novel-41 (- MZF1_5-13, Mzf1, Sp1;) (+ Zic1; Zic2; Olf-1, novel-42, 2012.2/0.9; Spz1. rs1366610, 526.149/0.9; E47, novel-42, 5494.35/0.9; HSF1, novel-42, 613.405/0.9; HSF2, novel-42, 630.919/0.9;)	[C/G]	Szf1-1	Transfac:v11.2:M01109	gCAGGGtaggggg[c/g]g 19:47065129-47065143:+1	1.000/0.815	1.000/0.823	MATCH (minFP)	(y | N)
			Mzf1	Transfac:v7.0:M00084	agggtAGGGGg[c/g]g 19:47065131-47065143:+1	201.027/0.5	-/0.5	MotifScanner	(y | N)
			MZF1_5-13	Jaspar:v3.0:MA0057	gtAgGGGg[c/g]g 19:47065134,47065143:+1	1253.7/0.5	-/0.5		(y- | N)
			Sp1	Jaspar:v3.0:MA0079	agGGgg[c/g]gct 19:47065136-47065145:+1	104.692/0.5	-/0.5		(y- | N)
			Zic3	Transfac:v7.0:M00450	aGGGgG[c/G]gC 19:47065136-47065144:+1	-/0.4	48.1223/0.4		(y- | N)
	novel-42 (+ HOXA3; E47, rs2075750, 5494.35/0.1; Spz1, rs1366610,; Zic3, novel-41) (-Olf-1, HSF1, HSF2)	[T/G]	Olf-1 (olfactory neuron-specific factor)	Transfac:v7.0:M00261	atCaAtTCCCcAac[t/G]Aatggtc [illegible]	7791.08/0.1	-/0.1	MotifScanner	(y | N)
			HOXA3	Transfac:v7.0: M00395	ac[T/g]Aatggt [illegible]	-/0.4	121.962/0.4		(y- | N)
			HSF1 (heat shock factor 1)	Transfac:v7.0:M00146	c[t/G]AAtggTCc 19:47065189-47065198:+1	644.977/0.4	-/0.4		(y- | N)
			HSF2 (heat shock factor 2)	Transfac:v7.0:M00147	c[t/G]AAtggTCc 19:47065189-47065198:+1	654.993/0.4	-/0.4		(y- | N)
			Zic1 (zinc finger protein of the cerebellum 1)	Transfac:v7.0:M00448	c[t/G]aaTGGTC 19:47065189-47065197:+1	-/0.5	121.655/0.5		(y- | N)
			Zic2 (zinc finger protein of the cerebellum 2)	Transfac:v7.0:M00449	c[t/G]aaTGGTC 19:47065189-47065197:+1	-/0.5	49.014/0.5		(y- | N)
			box_2_2_yCCCAAsG	Model:EPD Vertebrate 3*	CCCCAAC[T/G] 19:47065183-47065190:+1	18227.9	N.A.	MotifSampler	(Y | N)
			box_1_1_CnAACGA	Model:EPD Human 3*	CCAAC[T/G]A 19:47065185-47065191:+1	2477.93	N.A.		(Y | N)
			box_1_2_AACGA	Model:EPD Vertebrate 3*	AAC[T/G]A 19:47065187-47065191:+1	2035.61	N.A.		(Y | N)
			box_2_2_CCAAGGGTm	Model:EPD Vertebrate 3*	C[T/G]AATGGTC 19:47065189-47065197:+1	31751.6	N.A.		(y- | N)
	rs2075750 (-Olf-1, novel-42)	[C/T]	E47	Transfac:v7.0:M00002	gcgGCAGGTGgctt[c/t] 19:47065505-47065519:+1	4874.7/0.1	5494.35/0.1 7751.3/0.1	MotifScanner	(Y | N)
			NF-1 (myogenin / NF-1 myogenin / nuclear factor 1 or related factors)	Transfac:v11.2:M00056	tt[c/t] ttgagaagcCTGGCtcacagccagga 19:47065517,47065545:+1	-	0.900/0.713	MATCH (minFP)	(Y | N)