

1 **Supplementary Data**

2 **Table 1. Bioinformatic Analysis of SOX9 up 7 MatInspector**

Matrix	Detailed Matrix Information	Anchor	Strand	Matrix Similarity	Sequence
SF1.01	SF1 steroidogenic factor 1	1498	(-)	1	ccctCAAGgtcacct
SF1.01	SF1 steroidogenic factor 1	1521	(+)	0.996	ggtgCAAGgtcagag
SF1.01	SF1 steroidogenic factor 1	1096	(-)	0.993	actcCAAGgccatca
SOX3.01	SRY-box containing gene 3	2436	(-)	0.99	atctcaCAAagggaacatgtat
SOX5.01	Sox-5	2202	(-)	0.986	tccaaaCAATttaaagtggcatc
SOX5.01	Sox-5	737	(+)	0.984	ataaaaCAATcagggttctgttt
SOX6.01	SRY (sex determining region Y)-box 6	1452	(+)	0.98	tctgtACAAagacctaattatag
SF1.01	SF1 steroidogenic factor 1	1403	(-)	0.958	tcacCAAGgcaatat

3

4 **Table 2: Bioinformatic Analysis of SOX9 up 7 JASPAR**

Matrix	Score	Relative score	Start	End	Strand	Predicted site sequence
Sox17	10.360	0.9580037	306	314	1	CATATTGTC
SOX10	8.910	1.00000919	400	405	1	CTTTGT
SOX10	8.625	0.98735660	676	681	1	CATTGT

SRY	8.994	0.91067981	677	685	-1	TTTTACAAT
Sox17	9.669	0.93568096	712	720	1	TCTATTGTG
SOX9	9.595	0.90244614	713	721	1	CTATTGTGC
SRY	10.762	0.969871586	727	735	1	TAAAACAAT
Sox5	10.898	0.999999093	729	735	-1	ATTGTTT
SOX10	7.097	0.91952100	773	778	1	CTGTGT
SOX10	8.910	1.00000919	1446	1451	-1	CTTTGT
Sox3	9.114	0.9005362	2073	2082	-1	CTTTTGTTGT
Sox3	11.463	0.93530231	2080	2089	-1	GTTTTGTCTT
Sox6	9.753	0.90040453	2080	2089	-1	GTTTTGTCTT
SRY	9.093	0.9139942	2204	2212	-1	CCAAACAAT
Sox5	10.898	0.9999990	2204	2210	1	ATTGTTT
SOX10	7.097	0.9195210	2411	2416	-1	CTGTGT
Sox2	12.638	0.9764408	2436	2443	1	CCTTTGTG
SOX10	8.910	1.000009	2437	2442	1	CTTTGT

5

6

7

8 **Table 3: Bioinformatic Analysis of SOX9 up 1 MatInspector**

Matrix	Detailed Matrix Information	Anchor	Strand	Matrix Similarity	Sequence
SOX5.01	Sox-5	361	(+)	0.997	ttcaaaCAATacagtctttacaa
SOX6.01	SRY (sex determining region Y)-box 6	626	(+)	0.994	acaaaACAAagaacaaacaaaa
SOX6.01	SRY (sex determining region Y)-box 6	31	(+)	0.978	ctgtgACAAagagcatcctttgc
SRY.01	Sex-determining region Y gene product	616	(+)	0.933	ggaaaACAAaacaacaaagaa
SOX4.01	SRY-related HMG-box gene 4	638	(+)	0.91	aacaaACAAaaaaaccacaaaa
SOX15.01	SRY-related HMG-box gene 15	165	(+)	0.884	tatagACAAttacaagtctcaa

9

10 **Table 4: Bioinformatic Analysis of SOX9 up 1 JASPAR**

Model name	Score	Relative score	Start	End	Strand	Predicted site sequence
SOX10	8.910	1.00000	25	30	-1	CTTTGT
Sox17	9.118	0.91788	158	166	-1	TAAATTGTC
SRY	9.653	0.93274	351	359	1	TCAAACAAT
SOX9	9.679	0.90485	353	361	-1	GTATTGTTT
Sox5	10.898	0.99999	353	359	-1	ATTGTTT

SOX10	8.625	0.98735	369	374	-1	CATTGT
SRY	9.754	0.93612	606	614	1	GAAAACAAA
Sox3	12.130	0.94517	607	616	-1	GTTTTGTTTT
Sox6	9.914	0.90347	607	616	-1	GTTTTGTTTT
SRY	8.914	0.90800	611	619	1	CAAAACAAA
Sox3	12.130	0.94517	612	621	-1	GTTTTGTTTT
Sox6	9.914	0.90347	612	621	-1	GTTTTGTTTT
SRY	8.914	0.90800	616	624	1	CAAAACAAA
Sox3	13.315	0.96271	617	626	-1	TCTTTGTTTT
Sox6	12.882	0.96003	617	626	-1	TCTTTGTTTT
SOX10	8.910	1.00000	620	625	-1	CTTTGT
Sox3	10.398	0.91953	629	638	-1	TTTTTGTTTG

- 11
- 12 **Table 5: Bioinformatic Analysis of SOX9 up 2 MatInspector**

Matrix	Detailed Matrix Information	Anchor	Strand	Matrix Similarity	Sequence
SOX5.01	Sox-5	810	(+)	0.99	ccacaaCAATaagaactgtgata
SOX5.01	Sox-5	1752	(-)	0.989	ctctaaCAATgccgctgctctt

SOX5.01	Sox-5	156	(+)	0.989	gggtaaCAATgaacaagtaatat
SOX3.01	SRY-box containing gene 3	1616	(-)	0.988	gagccaCAAAGgggaaattcatct
SOX30.01	SRY-related HMG-box gene 30	318	(+)	0.988	gatgaACAAtgaaactattttca
SOX5.01	Sox-5	17	(-)	0.988	caaaaaCAATtctgagtggtaa
SOX5.01	Sox-5	1001	(+)	0.987	ggaaaaCAATgtgaacagctgta
SOX6.01	SRY (sex determining region Y)-box 6	723	(+)	0.972	aattcACAAagaccaatagcaaa
SOX3.01	SRY-box containing gene 3	1181	(+)	0.971	tttcaaCAAAGatgaagggaag
HBP1.01	HMG box-containing protein 1	1538	(+)	0.967	gttgattgAATGaacaaatggat
SOX3.01	SRY-box containing gene 3	1546	(+)	0.954	aatgaaCAAAtggattaattaat

13

14 **Table 6: Bioinformatic Analysis of SOX9 up 2 JASPAR**

Model name	Score	Relative score	Start	End	Strand	Predicted site sequence
SRY	10.202	0.95112	19	27	-1	AAAAACAAT
Sox5	10.898	0.99999	19	25	1	ATTGTTT
SRY	9.706	0.93451	146	154	1	GGTAACAAT
SOX9	9.602	0.90264	148	156	-1	TCATTGTTA

Sox5	10.898	0.99999	148	154	-1	ATTGTTA
Sox17	9.890	0.94282	149	157	-1	TTCATTGTT
SOX10	8.625	0.98735	150	155	-1	CATTGT
SRY	8.904	0.90766	308	316	1	ATGAACAAT
Sox6	10.607	0.91668	309	318	-1	TCATTGTTCA
SOX9	10.639	0.93241	310	318	-1	TCATTGTTC
Sox5	9.767	0.95785	310	316	-1	ATTGTTC
Sox17	9.890	0.94282	311	319	-1	TTCATTGTT
SOX10	8.625	0.98735	312	317	-1	CATTGT
SOX10	7.094	0.91938	337	342	-1	CCTTGT
SOX10	7.097	0.91952	636	641	1	CTGTGT
SOX10	8.910	1.00000	717	722	-1	CTTTGT
Sox5	10.075	0.96933	802	808	-1	ATTGTTG
Sox17	8.990	0.91374	803	811	-1	CTTATTGTT
SRY	11.042	0.97924	991	999	1	GAAAACAAT

Sox6	10.809	0.92053	992	1001	-1	ACATTGTTTT
Sox5	10.898	0.99999	993	999	-1	ATTGTTT
Sox17	9.490	0.92989	994	1002	-1	CACATTGTT
SOX10	8.625	0.98735	995	1000	-1	CATTGT
SOX10	7.097	0.91952	1119	1124	1	CTGTGT
SOX10	7.097	0.91952	1270	1275	1	CTGTGT
Sox2	12.638	0.97644	1616	1623	1	CCTTTGTG
SOX10	8.910	1.00000	1617	1622	1	CTTTGT
SOX9	9.976	0.91338	1752	1760	1	CAATTGTTA
SRY	9.126	0.91509	1754	1762	-1	TCTAACAAT
Sox5	10.898	0.99999	1754	1760	1	ATTGTTA

15

16 **Table 7: Bioinformatic Analysis of NEIL2 I MatInspector**

Matrix	Detailed Matrix Information	Anchor	Strand	Matrix Similarity	Sequence
SOX12.01	SRY-related HMG-box gene 12	2424	(+)	1	tcagaACAAttacattagcctac

SOX5.01	Sox-5	849	(-)	0.995	ttgaaaCAATactggcaacacat
SOX6.01	SRY (sex determining region Y)-box 6	1598	(-)	0.993	aagagACAAagcaaagtaaact
SOX6.01	SRY (sex determining region Y)-box 6	2463	(+)	0.98	ctaacACAAagcttgttctataa
SOX6.01	SRY (sex determining region Y)-box 6	1641	(-)	0.98	gaccaACAAagtagataaactca
SOX3.01	SRY-box containing gene 3	446	(-)	0.959	aaaataCAAagttagccggtgt
SOX9.01	SOX (SRY-related HMG box)	2605	(-)	0.918	gacttaCAATgggtcacttttaa

17

18 **Table 8: Bioinformatic Analysis of NEIL2 | JASPAR**

Model name	Score	Relative score	Start	End	Strand	Predicted site sequence
Sox17	8.590	0.90082	199	207	1	TATATTGTT
SRY	9.093	0.91399	202	210	-1	ACAAACAAT
Sox5	10.898	0.99999	202	208	1	ATTGTTT
Sox3	13.700	0.96841	288	297	1	GCTTTGTTTT
Sox6	12.730	0.95714	288	297	1	GCTTTGTTTT
SOX10	8.910	1.00000	289	294	1	CTTTGT
SRY	8.914	0.90800	290	298	-1	CAAAACAAA
SOX10	6.812	0.90686	657	662	1	CAGTGT

SRY	8.914	0.90800	824	832	-1	AAAAACAAA
SOX9	9.679	0.90485	849	857	1	GTATTGTTT
Sox6	10.034	0.90576	849	858	1	GTATTGTTTC
SRY	9.953	0.94278	851	859	-1	TGAAACAAT
Sox5	10.898	0.99999	851	857	1	ATTGTTT
Sox3	12.445	0.94983	1598	1607	1	GCTTTGTCTC
Sox6	11.846	0.94029	1598	1607	1	GCTTTGTCTC
SOX10	8.910	1.00000	1599	1604	1	CTTTGT
SOX10	8.910	1.00000	1642	1647	1	CTTTGT
Sox5	9.767	0.95785	2416	2422	-1	ATTGTTC
Sox3	11.615	0.93755	2454	2463	-1	GCTTTGTGTT
SOX10	8.910	1.00000	2457	2462	-1	CTTTGT
SOX9	9.628	0.90339	2605	2613	1	CCATTGTAA
SOX10	8.625	0.98735	2606	2611	1	CATTGT

19

20