

**ANNEX 09** - Transcription factors identified from differentially expressed protein genes for number of teats (group 10), through an input file in Fasta format  
TFM Explorer

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;Date      : Mon Nov  8 19:08:19 2021
;Scanned location  : -3000:300
;Scanned sequences : None (8 sequences)
;Scanned matrices  : (130 matrices)
;Parameters      : minsize= 30, maxsize= 1500, ratio=3.0, top=25
;
; headers
;  1  rank      window rank
;  2  matrix     matrix name
;  3  tf         transcription factor name
;  4  info       information of content of the matrix
;  5  gc         gc content of the matrix (G+C)%
;  6  location   location of the window (relatively to TSS)
;  7  pvalue     pvalue of the window
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1  MA0156.1      FEV    12.1208832256  0.442307695746 -105:93 2.90279458821e-08
    list of hits
    ASTE1 -0092  -84   -    5.90   ACATCCGG
    ASTE1 -0023  -15   +    7.28   CGGGAAGT
    ASTE1 +0015  23    +    6.19   GCGGAAGT
    ASTE1 +0073  81    -    5.79   ACTTCCCT
    ATP2C1      -0105 -97   -    6.19   ACTTCCGC
    ATP2C1      -0050 -42   +    6.19   GCGGAAGT
    COL6A6      -0031 -23   -    5.26   ATTTCCCC
    COL6A6      +0084 92    -    5.11   ACTTCCCC
    COLQ +0093  101   +    7.43   TAGGAAAT
    METTL6      -0043 -35   -    8.36   ACTTCCGG
    METTL6      -0023 -15   -    8.36   ACTTCCGG
    METTL6      -0008 0     +    6.19   GCGGAAGT
    _PIK3R4      +0006 14    -    6.19   ACTTCCGC
    _PIK3R4      +0021 29    +    9.45   CAGGAAGT

2  MA0080.2      SPI1   9.64024729829  0.435374151649 -105:223 6.0179808516e-07
    list of hits
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ANKRD28	+0096	103	+	6.31	AGGAAGA
ASTE1 -0022	-15	+	6.96	GGGAAGT	
ASTE1 +0016	23	+	6.28	CGGAAGT	
ASTE1 +0073	80	-	6.96	ACTTCCC	
ASTE1 +0223	230	-	6.28	ACTTCCG	
ATP2C1	-0105	-98	-	6.28	ACTTCCG
ATP2C1	-0049	-42	+	6.28	CGGAAGT
COL6A6	+0029	36	+	6.81	AGGAAGC
COL6A6	+0084	91	-	6.96	ACTTCCC
COL6A6	+0190	197	+	6.31	AGGAAGA
COLQ +0094	101	+	6.78	AGGAAAT	
METTL6	-0061	-54	+	6.81	AGGAAGC
METTL6	-0043	-36	-	6.28	ACTTCCG
METTL6	-0023	-16	-	6.28	ACTTCCG
METTL6	-0007	0	+	6.28	CGGAAGT
METTL6	+0172	179	+	6.28	AGGAACT
_PIK3R4	-0088	-81	-	6.31	TCTTCCT
_PIK3R4	+0006	13	-	6.28	ACTTCCG
_PIK3R4	+0022	29	+	8.65	AGGAAGT
_PIK3R4	+0112	119	-	5.92	CCTTCCT
_PIK3R4	+0197	204	+	5.92	AGGAAGG

3 MA0062.2 GABPA 13.3349243401 0.647453861192 -108:28 1.85620420697e-06

list of hits

ASTE1 -0095	-84	-	5.57	CTCACATCCGG	
ASTE1 -0023	-12	+	4.99	CGGGAAGTCGG	
ASTE1 +0015	26	+	10.02	GCGGAAGTGCG	
ATP2C1	-0108	-97	-	10.06	TCCACTTCCGC
ATP2C1	-0050	-39	+	10.48	GCGGAAGTGCG
COL6A6	+0028	39	+	4.78	GAGGAAGCTCC
METTL6	-0062	-51	+	6.59	GAGGAAGCGGG
METTL6	-0048	-37	+	4.98	GCGGAACTTCC
METTL6	-0026	-15	-	9.95	GGGACTTCCGG
METTL6	-0008	3	+	10.48	GCGGAAGTGCG
_PIK3R4	+0003	14	-	10.03	GTCACTTCCGC
_PIK3R4	+0021	32	+	8.43	CAGGAAGTGAG

4 MA0152.1 NFATC2 9.85861508532 0.346153842592 -2185:-1901 2.81850167085e-06

list of hits

ASTE1	-2148	-2141	-	6.92	GGGAAAA
ASTE1	-2082	-2075	-	6.92	GGGAAAA
ATP2C1		-2185	-2178	-	6.92 GGGAAAA
ATP2C1		-2037	-2030	-	6.81 TGGAAAT
ATP2C1		-1980	-1973	-	6.37 TGGAAGA
COL6A6		-2152	-2145	+	6.81 ATTTCCA
COL6A6		-2109	-2102	-	6.37 TGGAAGA
COL6A6		-1986	-1979	+	6.92 TTTTCCC
COLQ	-2001	-1994	-	8.69	TGGAAAA
FRMPD4		-2030	-2023	+	6.81 ATTTCCA
FRMPD4		-1905	-1898	+	6.42 GTTTCCA
METTL6		-2163	-2156	-	6.92 GGGAAAA
METTL6		-2067	-2060	-	8.69 TGGAAAA
METTL6		-2021	-2014	-	8.69 TGGAAAA
METTL6		-1901	-1894	+	7.20 TTTTCCT
_PIK3R4		-1969	-1962	-	7.20 AGGAAAA
_PIK3R4		-1915	-1908	-	7.20 AGGAAAA

5 MA0046.1 HNF1A 15.5481691653 0.25850340857 -2654:-2513 1.39664249298e-05

list of hits

ASTE1	-2642	-2628	-	4.40	TGTATAGAGTAATC
ASTE1	-2571	-2557	-	4.14	GCTAAATTTTTATC
ASTE1	-2546	-2532	-	4.28	GTTATTGATAATCT
ATP2C1		-2654	-2640	+	11.85 AGTTAATTTTTAAA
COL6A6		-2653	-2639	+	5.56 AGATTATCATTACA
COL6A6		-2605	-2591	+	5.39 GGTAAGTATTCAAT
COL6A6		-2578	-2564	+	4.44 AATTAATGAATCAA
COLQ	-2634	-2620	-	4.65	GGAAAAAAACAACC
COLQ	-2534	-2520	-	5.76	TTAAATTATAAATT
METTL6		-2536	-2522	+	5.45 GGTTAAACAACATC
METTL6		-2513	-2499	+	4.42 GGTTAGTTGTCCGC

6 MA0131.1 MIZF 13.1966528521 0.610000000149 -107:15 1.40787426186e-05

list of hits					
ASTE1	+0015	25	-	5.84	GCGGAAGTGG
ATP2C1		-0107	-97	+	5.84 CCACTTCCGC
ATP2C1		-0050	-40	-	5.84 GCGGAAGTGG
METTTL6		-0048	-38	-	5.39 GCGGAACTTC
METTTL6		-0008	2	-	5.84 GCGGAAGTGG
_PIK3R4		+0004	14	+	5.99 TCACTTCCGC

7	MA0025.1	NFIL3	14.13850704	0.264822136611	-1303:-1130	2.6652261317e-05
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list of hits					
ATP2C1		-1303	-1292	-	4.98 TGATTACAACA
ATP2C1		-1268	-1257	+	5.63 TGTTGTAACAA
COL6A6		-1151	-1140	+	5.34 TGATATAAGGA
COL6A6		-1130	-1119	+	4.28 TTACTTAATTT
METTTL6		-1273	-1262	+	5.09 TTATCTAACAC
_PIK3R4		-1273	-1262	-	4.69 TTATTATGAAA
_PIK3R4		-1239	-1228	-	9.04 ATATTACATCA
_PIK3R4		-1157	-1146	+	5.41 TTATGTATTGT

8	MA0077.1	SOX9	9.07881468797	0.358187139655	-2848:-2682	3.94879605582e-05
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list of hits					
ASTE1	-2762	-2753	+	7.52	AAACAATGA
ATP2C1		-2701	-2692	+	6.46 AAACAATGT
COL6A6		-2799	-2790	+	6.57 AAACCATGG
COL6A6		-2682	-2673	-	6.00 ATATTGTTT
COLQ	-2737	-2728	-	6.12	CTATAGTTA
FRMPD4		-2848	-2839	-	5.81 CCATTATTT
FRMPD4		-2817	-2808	-	5.74 TCATTGTAT
FRMPD4		-2742	-2733	-	6.55 CTATTGTAA
_PIK3R4		-2844	-2835	-	6.57 CCATAGTTA

9	MA0124.1	NKX3-111.1268615571	0.178571427507	-2924:-2511	4.94686860648e-05
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list of hits					
ANKRD28		-2528	-2521	+	8.97 ATACTTA
ASTE1	-2924	-2917	-	6.07	TAAATAT
ATP2C1		-2824	-2817	+	6.07 ATACTTG

ATP2C1	-2708	-2701	+	7.51	GTACTTA
COL6A6	-2919	-2912	-	6.07	CAAGTAT
COL6A6	-2844	-2837	+	6.45	CTACTTA
COL6A6	-2808	-2801	-	6.07	TAAGTGT
COL6A6	-2746	-2739	+	7.51	TTACTTA
COL6A6	-2687	-2680	-	8.97	TAAGTAT
COL6A6	-2603	-2596	-	8.97	TAAGTAT
COLQ -2716	-2709	+	6.07	ATACTTG	
COLQ -2677	-2670	+	6.07	ATACTTG	
COLQ -2649	-2642	-	6.07	TAAGTGT	
FRMPD4	-2807	-2800	-	6.07	TATGTAT
FRMPD4	-2511	-2504	-	6.07	TATGTAT

10	MA0007.1	Ar	15.7033954759	0.498106069863	-1519:-1487	4.94795580397e-05
	list of hits					
	COL6A6	-1487	-1465	-	5.61	TTGTTGTTTCAGGCAGTACTATC
	FRMPD4	-1502	-1480	-	5.88	TTTCTTGACTGTCTGTTCTAAG
	METTL6	-1515	-1493	+	11.26	TAAAGCACAACTGAACAGCAC
	_PIK3R4	-1519	-1497	-	3.68	GATTAAAACATTTTGTGCTTCA

11	MA0136.1	ELF5	8.69309550562	0.429292928841	-107:95	5.42555602463e-05
	list of hits					
	ANKRD28	+0095	104	-	6.03	GAGGAAGAA
	ASTE1 +0015	24	-	6.12	GCGGAAGTG	
	ATP2C1	-0106	-97	+	6.12	CACTTCCGC
	ATP2C1	-0050	-41	-	6.12	GCGGAAGTG
	COL6A6	+0074	83	+	6.08	CACTTCCAT
	METTL6	-0107	-98	-	6.07	CTGGAAATA
	METTL6	-0044	-35	+	6.72	AACTTCCGG
	METTL6	-0008	1	-	6.12	GCGGAAGTG
	_PIK3R4	-0089	-80	+	6.03	TTCTTCCTC
	_PIK3R4	+0005	14	+	6.12	CACTTCCGC
	_PIK3R4	+0021	30	-	7.29	CAGGAAGTG

12	MA0136.1	ELF5	8.69309550562	0.429292928841	-1387:-1333	5.79706609027e-05
	list of hits					

ASTE1	-1351	-1342	-	6.49	AAGGAAGGA
COL6A6		-1340	-1331	+	6.93 TATTTCCCTA
COLQ	-1333	-1324	-	7.36	CAGGATGTA
METTL6		-1387	-1378	-	7.13 CAGGAAATG
METTL6		-1369	-1360	+	6.25 CACATCCTC
METTL6		-1360	-1351	+	6.37 AATATCCTC

13	MA0083.1	SRF	17.9647717767	0.465579714133	-2668:-2624	6.56289173689e-05
		list of hits				
		ANKRD28	-2631	-2619	-	2.59 CCATATGTTGCA
		ATP2C1	-2633	-2621	+	3.60 GGCCATATTTTG
		COLQ	-2624	-2612	+	4.10 AACCATATGAGG
		METTL6	-2668	-2656	+	3.59 TGCCATATACAG