

**ANNEX 02** - Transcription factors identified from differentially expressed protein genes for number of teats (group 2), through an input file in Fasta format;

TFM Explorer

```
;Date      : Mon Nov  8 17:37:09 2021
;Scanned location : -3000:300
;Scanned sequences : None (16 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
```

```
1  MA0037.1      GATA3 6.62989112102  0.349206356021 -2337:-2228      8.51095511447e-09
```

list of hits

```
AP3B2 -2228  -2222  -      6.21  CTATCT
FAM219B -2318  -2312  +      6.21  AGATAG
GNMT -2337  -2331  +      6.21  AGATAG
GNMT -2329  -2323  +      6.21  AGATAG
GNMT -2317  -2311  +      6.21  AGATAG
GNMT -2309  -2303  +      6.21  AGATAG
GNMT -2301  -2295  +      6.21  AGATAG
GNMT -2293  -2287  +      6.21  AGATAG
GNMT -2285  -2279  +      6.21  AGATAG
GNMT -2268  -2262  +      6.21  AGATAG
```

```
2  MA0029.1      Evf1 17.9085404291  0.280423281291 -627:-555      5.91374941757e-06
```

list of hits

```
ANPEP -0599  -585  +      2.84  ACTGCAAGATAATA
ARNT2 -0572  -558  +      2.28  GATTTAAGACAAAC
CEMIP -0579  -565  -      6.64  GGTATCCTGTATA
```

FAM219B	-0615	-601	-	3.05	TTTTCTCCTATCCC
KLHDC3	-0627	-613	+	5.01	GAGACAGGAGAACA
KLHDC3	-0613	-599	+	6.34	GAGATCAGACAAAA
KLHDC3	-0589	-575	-	2.39	CTTTAGCCTGTCAT
PPP2R5D	-0583	-569	-	9.66	ACTGATCTTATCTA
SCAPER	-0602	-588	-	4.81	GTCTATCTTTTATG
SCAPER	-0555	-541	-	4.15	CCTTATCCTATGCA

3 MA0061.1 NF-kappaB 13.3447617922 0.621052631736 -2396:-1373 1.18879440609e-05

list of hits

ANPEP -1930	-1920	-	5.18	AGGAGTTCCC	
ANPEP -1727	-1717	+	5.38	GGGAACCTCC	
ANPEP -1373	-1363	-	7.36	AGGAAGCCCC	
AP3B2 -1583	-1573	+	5.12	GGGAATGTTC	
ARNT2 -2095	-2085	+	8.14	GGGAACTTCC	
CEMIP -1420	-1410	+	5.64	GGGAGTTTCT	
FAM219B	-2061	-2051	+	5.38	GGGAACCTCC
FAM219B	-1829	-1819	+	4.91	GGGAGTTCTC
FAM219B	-1633	-1623	+	8.14	GGGAACTTCC
GNMT -2381	-2371	+	11.35	GGGAATTTCC	
GNMT -1919	-1909	+	8.14	GGGAACTTCC	
GNMT -1794	-1784	-	5.18	AGGAGTTCCC	
GNMT -1592	-1582	+	5.38	GGGAACCTCC	
GNMT -1382	-1372	-	5.67	GTAAACTCCC	
KLHDC3	-1442	-1432	-	5.60	GTGACTCCCC
LOC102167410	-2202	-2192	+	8.38	GGGAGTTCCC
LOC102167410	-1524	-1514	+	8.03	GGGAACTCCC
MAN2A2	-2386	-2376	+	4.96	GGAAGTTTCC
MAN2A2	-2190	-2180	+	5.18	GGGAACTCCT
MAN2A2	-2039	-2029	-	6.43	GAGATTTCCC
MAN2A2	-1842	-1832	+	4.96	GGAAGTTTCC
PEX11A	-1765	-1755	+	8.59	GGGAATCTCC
PEX11A	-1451	-1441	+	5.53	GGGAGTTCCT
PPP2R5D	-2029	-2019	+	5.18	GGGAACTCCT
PPP2R5D	-1391	-1381	-	6.80	GGAAAGCTCC
RCCD1 -2198	-2188	+	4.62	GGGGACGCCC	

RCCD1 -2077	-2067	+	5.38	GGGAACCTCC
RCCD1 -1436	-1426	-	4.88	AGGAACCCCC
RCCD1 -1405	-1395	-	8.10	GGGCAGTCCC
SCAPER	-2147	-2137	+	5.38 GGGAACCTCC
SPTB -2381	-2371	+	6.11	GGGGCAGCCC
SPTB -2311	-2301	-	8.01	AGGAAGTCCC
UNC45A	-2396	-2386	+	8.14 GGGAACCTCC
UNC45A	-2299	-2289	+	4.52 GGAACTTCAC
UNC45A	-2234	-2224	-	4.91 GAGAACTCCC
UNC45A	-1967	-1957	-	6.45 GAGAAATCCC

4 MA0083.1 SRF 17.9647717767 0.465579714133 -2097:-821 1.50799972671e-05

list of hits

ANPEP -2024	-2012	-	6.53	TCAAATATGGCC
ANPEP -1701	-1689	+	3.38	GCCCTAAAAAGC
AP3B2 -1288	-1276	+	3.32	GACAATATGAGG
AP3B2 -1059	-1047	+	4.02	GCCCTAAAAAGA
ARNT2 -2069	-2057	+	4.02	GCCCTAAAAAGA
ARNT2 -1835	-1823	-	4.09	CCTTTTATTGCC
CEMIP -1882	-1870	-	2.36	CGTGATATGGGC
CEMIP -1708	-1696	-	2.29	TCATATAAGTCC
CEMIP -1212	-1200	+	4.02	GCCCTAAAAAGA
CEMIP -0839	-827	-	2.59	CCATATGTTGCA
CEMIP -0821	-809	+	4.00	GCCCTAAAAAAG
FAM219B	-2036	-2024	+	5.09 GGCCCTATAAAG
FAM219B	-1384	-1372	-	5.64 TCAAATAAGGAC
KLHDC3	-1144	-1132	+	4.02 GCCCTAAAAAGA
LOC102167410	-0856	-844	-	4.02 TCTTTTTAGGGC
MAN2A2	-1340	-1328	+	3.31 TGCCATATAAGT
MAN2A2	-1034	-1022	-	2.31 TCATTTAAGGAA
PEX11A	-2097	-2085	-	2.51 TCAAATGAGGGA
PEX11A	-1739	-1727	+	4.02 GCCCTAAAAAGA
PPP2R5D	-1989	-1977	-	4.02 TCTTTTTAGGGC
PPP2R5D	-1050	-1038	-	5.94 CCTTTTAATGGC
SCAPER	-1901	-1889	+	5.56 GTCCATATCAGG
SCAPER	-1076	-1064	-	5.04 CTATTTAAGGGA

SPTB	-1438	-1426	+	3.08	TTCCTTATATTG
SPTB	-1403	-1391	-	4.76	CTTAATAAGGGT
SPTB	-0940	-928	+	3.71	GACCTTGTATAG
UNC45A		-1612	-1600	+	4.75 AAACATATATGG
ZNF804A		-2014	-2002	-	2.43 TCACATATGGGG
ZNF804A		-1778	-1766	+	3.75 CACAATATTTGG
ZNF804A		-1301	-1289	-	3.71 ATATATATGGGA

5 MA0162.1 Egr1 14.4555832005 0.739393945445 -111:107 1.7561234316e-05

list of hits

ANPEP	-0111	-100	+	5.72	AGTGGAGGTGG
AP3B2	+0021	32	+	5.14	TGAGGGGGCGG
ARNT2	+0045	56	-	9.07	CCGCCCCCGCC
CEMIP	-0092	-81	+	5.75	AGCGCGGGCGT
GNMT	+0072	83	+	4.93	CCTGGGGGTGG
KLHDC3		-0016	-5	-	5.84 CCGCCTCCACC
LOC102167410	+0028	39	-	8.84	CCTCCCCCGCG
LOC102167410	+0100	111	+	5.39	GCCGTGAGCGG
MAN2A2	-0048	-37	+	4.46	TGCCTGGGCGA
MAN2A2	-0018	-7	+	10.43	CGCGGGGGCGG
MAN2A2	+0096	107	+	5.63	AGCGGGAGCGA
MAN2A2	+0107	118	+	5.96	CGGGTGGGCGG
PEX11A	+0038	49	-	4.44	CCGCCCCTGCG
PPP2R5D	-0065	-54	-	9.93	CCTCCCACGCT
SPTB	-0078	-67	+	7.19	TGCGGGAGTGG
SPTB	-0013	-2	-	9.07	CCGCCCCCGCC
UNC45A	-0025	-14	-	9.07	CCGCCCCCGCC
UNC45A	+0039	50	+	7.30	GACGGGGGCGG
UNC45A	+0101	112	+	4.69	CGCGTGCGTGT
ZNF804A	-0101	-90	-	5.69	ACGCTCCCACT
ZNF804A	-0057	-46	+	4.38	AGCGGCGGCGG
ZNF804A	-0045	-34	+	4.38	AGCGGCGGCGG
ZNF804A	-0021	-10	+	7.48	GGCGGGGGAGG

6 MA0041.1 Foxd3 12.944828444 0.223404252126 -2003:-1872 2.5011322442e-05

list of hits

CEMIP	-1993	-1981	-	6.37	AAAAAAAAAAAAA
CEMIP	-1981	-1969	-	6.37	AAAAAAAAAAAAA
FAM219B		-2003	-1991	-	6.37 AAAAAAAAAAAAA
FAM219B		-1935	-1923	-	5.96 AAATCAATGTAT
FAM219B		-1919	-1907	+	8.10 ATATGTTGTTTC
FAM219B		-1880	-1868	-	6.48 ATTAAAACAATC
GNMT	-1888	-1876	-	6.37	AAAAAAAAAAAAA
GNMT	-1872	-1860	-	6.44	GAAAAAAAAAATT
LOC102167410		-1953	-1941	-	6.36 ACAACAACAAAA
LOC102167410		-1928	-1916	-	8.75 AAAAAAATAAAAA
LOC102167410		-1915	-1903	-	9.35 AAATAAATAAAT
MAN2A2		-1954	-1942	+	7.82 TCTTGTTTTTTT
MAN2A2		-1940	-1928	+	11.64 GTTTGTTTGTTT
MAN2A2		-1894	-1882	+	5.54 CTTTTTTTTTTT
MAN2A2		-1879	-1867	+	5.36 TTTTTTTTGCTT
PEX11A		-2003	-1991	-	7.29 AGAAAAACAAAT
PPP2R5D		-2002	-1990	+	5.90 TAAATTTTTTTT
SPTB	-1927	-1915	+	5.57	ATTAATTTTTTTT
SPTB	-1903	-1891	-	5.72	AATTATACATTT
ZNF804A		-1955	-1943	+	5.72 GAACATTTTATC
ZNF804A		-1911	-1899	-	9.87 AAAAAAACATAA

7 MA0136.1 ELF5 8.69309550562 0.429292928841 -2428:-2378 3.06590513423e-05

list of hits

ANPEP	-2421	-2412	-	6.21	ATGGAAATT
GNMT	-2378	-2369	+	6.21	AATTTCCAT
MAN2A2		-2428	-2419	+	6.82 TTTTCCTT
MAN2A2		-2388	-2379	-	6.37 ATGGAAGTT
PEX11A		-2382	-2373	-	6.81 GAGGAAATG
PPP2R5D		-2393	-2384	+	6.23 TACTTCCAG
UNC45A		-2393	-2384	+	6.37 AACTTCCAT
ZNF804A		-2422	-2413	-	6.20 TAGGATATA

8 MA0149.1 EWSR1-FLI1 32.8714828257 0.554497355492 -948:-904 3.34582756477e-05

list of hits

ARNT2	-0948	-930	-	-7.49	CCTGCTTTGCATTTTCCC
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ARNT2 -0924	-906	-	-8.66	TCTACCCCTCTCTCCGCCC
GNMT -0942	-924	-	-9.02	ACTTCCACCCCTCACTCT
KLHDC3	-0925	-907	-	-6.19 CATACTGGATTTCGATCC
LOC102167410	-0948	-930	-	-4.67 ACCACCTTCTCTTCTCCC
PPP2R5D	-0907	-889	-	-8.00 TCATCCTCAATGCCTCCC
RCCD1 -0908	-890	-	-6.45	CCTGCCAGCACTGCCTCC
SCAPER	-0936	-918	+	-7.85 GAGAGAAATTAAGTTAGG
SPTB -0929	-911	+	-3.47	GTAAGAAAGTCAAGAAAG
ZNF804A	-0904	-886	+	-9.13 TGAGGGAACGCAGCAGAC

9 MA0141.1 Esrrb 12.8061908542 0.523864734014 -2366:-2161 4.31449673016e-05

list of hits

AP3B2 -2348	-2336	-	4.90	TGAACTTGGTAT
ARNT2 -2308	-2296	-	10.49	TGACCTTGAAAA
ARNT2 -2174	-2162	+	5.31	TGGTATAGGTCA
CEMIP -2295	-2283	+	6.30	TTGTCATGGTCA
FAM219B	-2161	-2149	-	5.06 TGGCCTTGCTCG
LOC102167410	-2366	-2354	-	6.00 TGACCTACACCA
LOC102167410	-2322	-2310	+	6.55 TGAGCGAGGTCA
MAN2A2	-2305	-2293	-	6.00 TGACCTACACCA
MAN2A2	-2182	-2170	+	5.00 CTCACAAGGCCA
PPP2R5D	-2183	-2171	-	5.01 TGACCTATGCCA
RCCD1 -2331	-2319	+	5.41	TTTCCAAGGTCC
RCCD1 -2252	-2240	-	6.82	TGACCCTGACTA
SCAPER	-2280	-2268	-	5.05 TGGCCTTGCTCA
UNC45A	-2293	-2281	-	5.82 TCACCTTTGGGC
UNC45A	-2264	-2252	-	7.69 TGACCTTCTGGA

10 MA0154.1 EBF1 11.5644748683 0.648000004888 -331:-233 8.28278386106e-05

list of hits

ANPEP -0316	-306	+	8.35	TCTCCAGGGA
CEMIP -0278	-268	+	7.22	CCCTCGGGGA
GNMT -0233	-223	+	7.51	TCCCCTGGGA
KLHDC3	-0286	-276	+	6.60 CTCTAAGGGA
KLHDC3	-0241	-231	+	6.89 CCCCAGGAGA
PEX11A	-0331	-321	-	6.10 TCCCAGAAGT

PEX11A	-0310	-300	+	8.15	GCTCAAGGGA
PEX11A	-0248	-238	+	8.68	ACTCAGGGGA
PPP2R5D	-0304	-294	+	7.98	ACTCCTGGGA
SPTB	-0248	-238	+	6.83	CCTCAGGGGG
UNC45A	-0291	-281	+	6.34	CCCACAGGGG