

Supplemental Data to:

STAT3 signaling stimulates miR-21 expression in bovine cumulus cells during *in vitro* oocyte maturation

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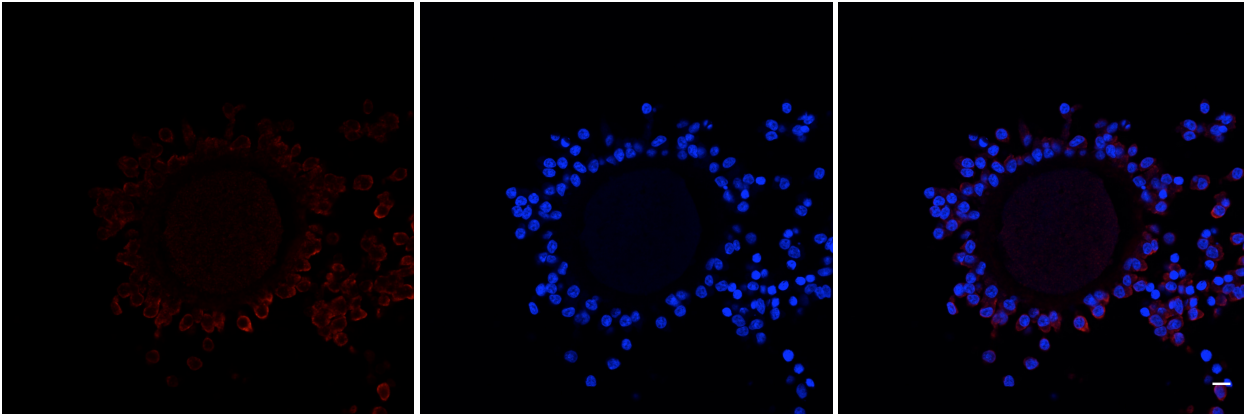
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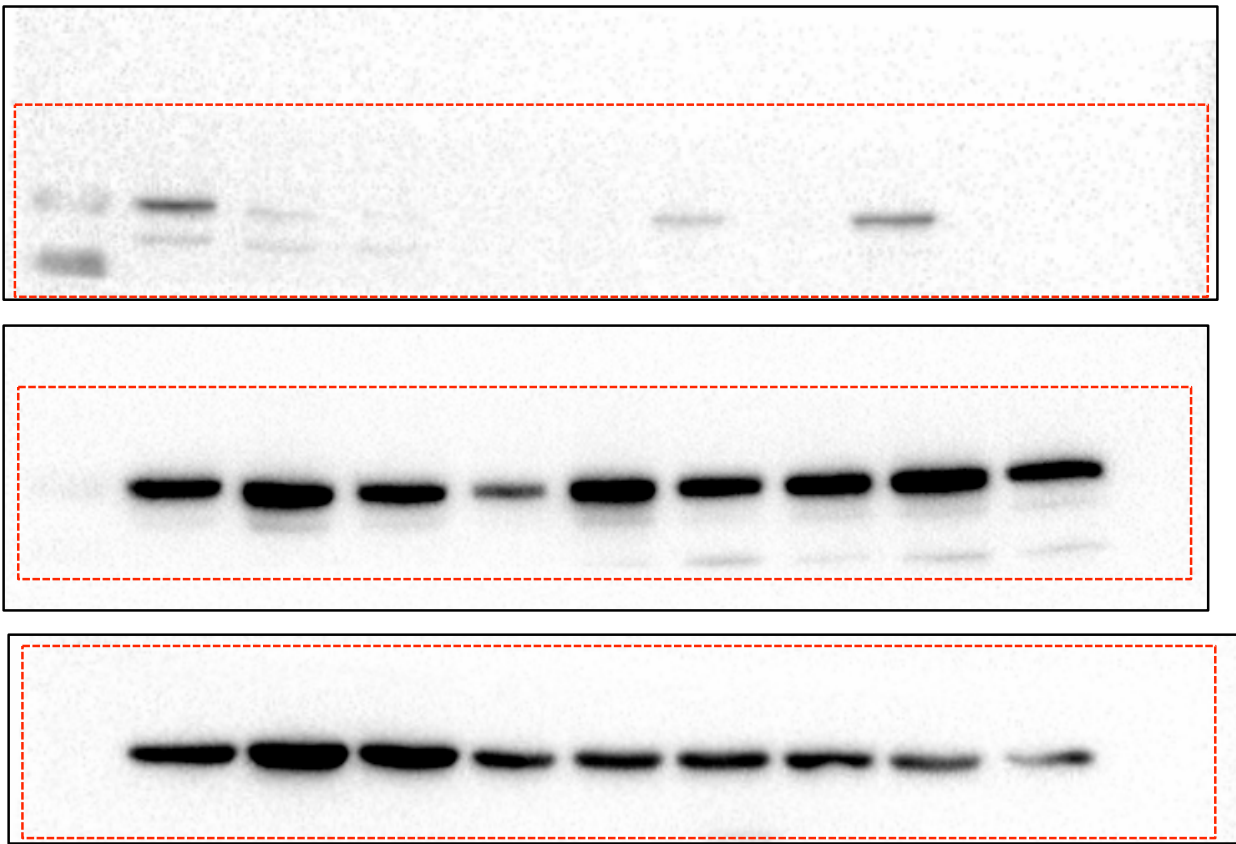
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Supplemental Figure 1



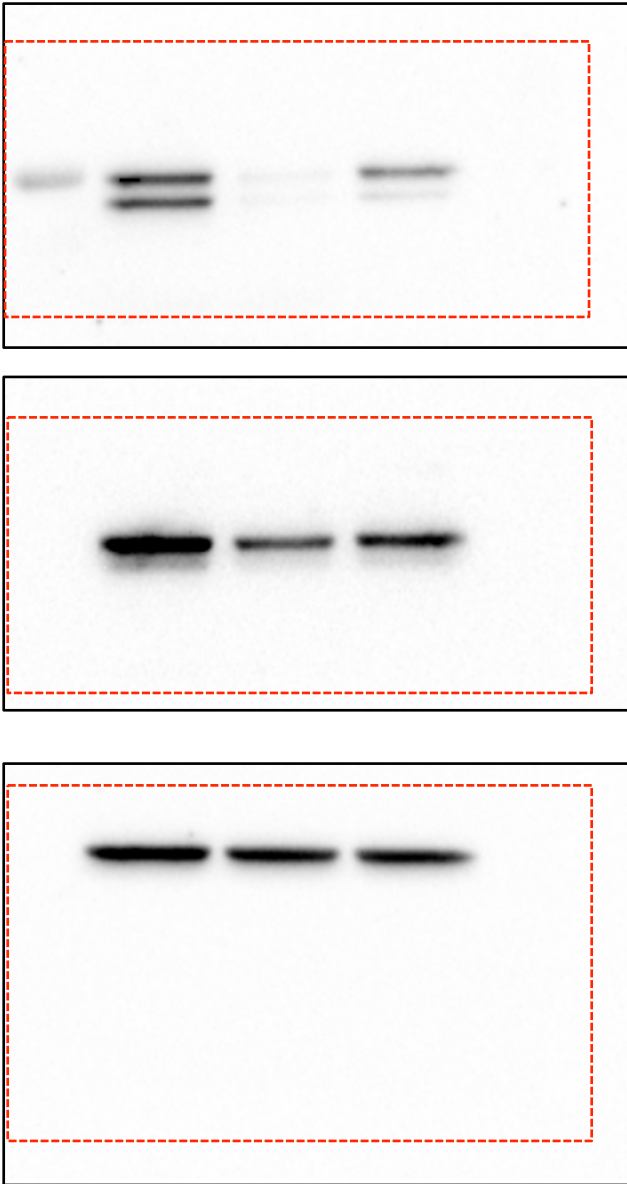
Supplemental Figure 1: RNA in situ hybridization of mature COC. Left panel: scrambled RNA probe, center panel: nuclei stained with DAPI, right panel: merged image. Scale bar represents 10 μ m.

Supplemental Figure 2



Supplemental Figure 2: Representative Western blot of STAT3 phosphorylation (Y705) and inhibition by Stattic in cumulus cells from 0-8hr IVM. Full-length blots corresponding to the cropped images presented in the main text, Figure 4. Red hatched lines delineate the approximate boundaries of the original membrane.

Supplemental Figure 3



Supplemental Figure 3: Representative Western blot of STAT3 phosphorylation (Y705) in cumulus cells at 7hr IVM, in serum free, non-supplemented media containing vehicle (ethanol), cycloheximide (CHX) or CHX+LIF. Full-length blots corresponding to the cropped images presented in the main text, Figure 5. Red hatched lines delineate the approximate boundaries of the original membrane.

Supplemental Table 1: Transcription factors predicted to bind miPPR-21 on plus strand

TF	<i>Bos taurus</i>					Seq1	<i>Homo sapiens</i>					Seq2
	Position (TSS=+1)	Start1	End1	Strand1	Score1		%Score1	Position (TSS=+1)	Start2	End2	Strand2	
HNF4A	-306	-294	+	8.096	80.7	GATTC AAGGTCA	-305	-293	+	10.627	86.8	GATTC AAGGTCA
ARID3A	-305	-300	+	5.399	82.7	ATTC A A	-304	-299	+	5.399	82.7	ATTC A A
HNF4A	-299	-287	+	8.42	81.5	GGTTC ATAGTCC	-298	-286	+	8.468	81.6	AGTTC ATAGTCC
ELF5	-293	-285	+	9.888	94.4	TAGTTCCTT	-292	-284	+	9.888	94.4	TAGTTCCTT
Sox17	-286	-278	+	6.176	82.3	TTCTTTGTT	-285	-277	+	6.176	82.3	TTCTTTGTT
ELF5	-282	-274	+	7.685	87.2	TTGTTCCTT	-281	-273	+	7.685	87.2	TTGTTCCTT
NFATC2	-281	-275	+	6.724	82.9	TGTTCCCT	-280	-274	+	6.724	82.9	TGTTCCCT
Sox17	-278	-270	+	5.776	81	TCCTTTGTT	-277	-269	+	5.776	81	TCCTTTGTT
Sox2	-277	-263	+	10.246	81.6	CCTTTGTAATCACT	-276	-262	+	10.246	81.6	CCTTTGTAATCACT
HNF1A	-273	-260	+	9.304	80.2	TGTTAATCACTGAC	-272	-259	+	9.304	80.2	TGTTAATCACTGAC
AP1	-271	-265	+	7.573	88.7	TTAATCA	-270	-264	+	7.573	88.7	TTAATCA
Gfi	-271	-262	+	9.241	90	TTAATCACTG	-270	-261	+	9.241	90	TTAATCACTG
Nkx2-5	-271	-265	+	5.339	84	TTAATCA	-270	-264	+	5.339	84	TTAATCA
Pdx1	-271	-266	+	5.014	81.3	TTAATC	-270	-265	+	5.014	81.3	TTAATC
Nobox	-270	-263	+	5.881	81.9	TAATCACT	-269	-262	+	5.881	81.9	TAATCACT
CREB1	-263	-256	+	6.22	80.4	TGACTTCT	-262	-255	+	6.22	80.4	TGACTTCT
HIF1A::ARNT	-247	-240	+	5.827	84	GGAGGTGC	-246	-239	+	5.827	84	GGAGGTGC
HOXA5	-229	-222	+	5.112	83.3	TGCTAATG	-228	-221	+	5.112	83.3	TGCTAATG
Pdx1	-227	-222	+	8.73	96.5	CTAATG	-226	-221	+	8.73	96.5	CTAATG
Gata1	-213	-203	+	4.964	82.4	TTGGATAAGGA	-212	-202	+	4.964	82.4	TTGGATAAGGA
AP1	-202	-196	+	7.794	89.5	TGACGCA	-201	-195	+	7.794	89.5	TGACGCA
NR3C1	-200	-183	+	8.953	80.9	ACGCACAGATTGCCTAA	-199	-182	+	8.953	80.9	ACGCACAGATTGCCTAA
HOXA5	-197	-190	+	5.427	84.4	CACAGATT	-196	-189	+	5.427	84.4	CACAGATT
Sox17	-195	-187	+	8.241	89	CAGATTGTC	-194	-186	+	8.241	89	CAGATTGTC
SRF	-189	-178	+	11.428	84	GTCCTAATAAGG	-188	-177	+	11.428	84	GTCCTAATAAGG
Gata1	-187	-177	+	3.954	80.6	CCTAATAAGGA	-186	-176	+	3.954	80.6	CCTAATAAGGA
Pdx1	-186	-181	+	6.478	87.3	CTAATA	-185	-180	+	6.478	87.3	CTAATA
Nobox	-185	-178	+	6.312	83.3	TAATAAGG	-184	-177	+	6.312	83.3	TAATAAGG
Gata1	-171	-161	+	4.475	81.5	ATTGAGAAAGG	-170	-160	+	4.906	82.3	ATTGAGAAAGG
SPIB	-169	-163	+	5.592	83.3	TGAGAAA	-168	-162	+	5.592	83.3	TGAGAAA
Gata1	-151	-141	+	6.204	84.7	TCTGAGAAAGAT	-151	-141	+	7.096	86.3	TCTGAGAAAGAG
Nkx2-5	-137	-131	+	4.492	80.6	ACAAGTC	-137	-131	+	4.492	80.6	ACAAGTC
Gfi	-136	-127	+	6.451	81.6	CAAGTCAGTG	-136	-127	+	6.318	81.2	CAAGTCAGAG
Gata1	-130	-120	+	3.927	80.5	AGTGAGAGGGCA	-130	-120	+	5.157	82.8	AGAGAGAGGGCA
Klf4	-124	-115	+	6.983	85.5	AGGGCGGGCA	-124	-115	+	6.983	85.5	AGGGCGGGCA
Myb	-118	-111	+	7.335	87.2	GGCAGTTT	-118	-111	+	7.335	87.2	GGCAGTTT
HLF	-96	-85	+	7.924	83.2	GATGACACAAGC	-96	-85	+	7.924	83.2	GATGACACAAGC
AP1	-94	-88	+	8.773	93.1	TGACACA	-94	-88	+	8.773	93.1	TGACACA
CEBPA	-94	-86	+	6.201	81.9	TGACACAAG	-94	-86	+	6.201	81.9	TGACACAAG
CREB1	-94	-87	+	6.329	80.8	TGACACAA	-94	-87	+	6.329	80.8	TGACACAA
Nr2e3	-89	-83	+	7.33	84.5	CAAGCAT	-89	-83	+	7.33	84.5	CAAGCAT
Nkx2-5	-84	-78	+	5.972	86.5	ATAAGTC	-84	-78	+	5.972	86.5	ATAAGTC
ELF5	-78	-70	+	10.352	96	CATTTCCTT	-78	-70	+	10.352	96	CATTTCCTT
NFATC2	-77	-71	+	7.175	84.6	ATTTCTT	-77	-71	+	7.175	84.6	ATTTCTT
Pdx1	-72	-67	+	5.029	81.3	CTTATT	-72	-67	+	5.029	81.3	CTTATT
Nobox	-71	-64	+	5.629	81.1	TTATTAAT	-71	-64	+	5.629	81.1	TTATTAAT
Prrx2	-70	-66	+	4.918	82.6	TATTA	-70	-66	+	4.918	82.6	TATTA
ARID3A	-69	-64	+	8.299	94	ATTAAT	-69	-64	+	8.299	94	ATTAAT
Nkx2-5	-68	-62	+	7.328	92	TTAATCG	-68	-62	+	9.317	100	TTAATTG
Pdx1	-68	-63	+	5.014	81.3	TTAATC	-68	-63	+	8.106	94	TTAATT
Nobox	-67	-60	+	6.919	85.3	TAATCGGT	-67	-60	+	11.363	100	TAATTGGT
Tcfcp2l1	-64	-51	+	11.265	89.6	TCGGTTC A AACCAG	-64	-51	+	8.52	85.6	TTGGTTC A AACCAG
Tcfcp2l1	-54	-41	+	9.483	87	CCAGTCTTACAGG	-54	-41	+	10.401	88.3	CCAGTCTTACAGG
STAT1	-50	-36	+	9.154	82.9	TCCTTACAGGAAGTCTG	-50	-36	+	8.978	82.7	TTCTTACAGGAAGTCTG
Stat3	-47	-38	+	9.082	85.5	TTACAGGAAC	-47	-38	+	9.082	85.5	TTACAGGAAC
SPIB	-45	-39	+	9.504	96.7	ACAGGAA	-45	-39	+	9.504	96.7	ACAGGAA
FEV	-44	-37	+	8.915	89	CAGGAACCT	-44	-37	+	8.915	89	CAGGAACCT
GABPA	-44	-34	+	7.913	84.5	CAGGAACCTGGT	-44	-34	+	5.997	81.2	CAGGAACCTAGT
Myf	-44	-33	+	12.077	91	CAGGAACCTGGTG	-44	-33	+	7.989	81.6	CAGGAACCTAGTG
SPI1	-43	-37	+	8.637	90.3	AGGAACT	-43	-37	+	8.637	90.3	AGGAACT
MZF1_1-4	-34	-29	+	5.838	85.2	TGGTGA	-34	-29	+	5.838	85.2	TGGTGA
Gata1	-33	-23	+	8.662	89.2	GGTGATAAATG	-33	-23	+	8.662	89.2	GGTGATAAATG
HOXA5	-30	-23	+	4.334	80.6	GATAAATG	-30	-23	+	4.334	80.6	GATAAATG
ARID3A	-29	-24	+	5.307	82.3	ATAAAT	-29	-24	+	5.307	82.3	ATAAAT
Nkx2-5	-29	-23	+	5.577	84.9	ATAAATG	-29	-23	+	5.577	84.9	ATAAATG