

1 **Small Glutamine-Rich Tetratricopeptide Repeat-Containing Protein Alpha (SGTA) Ablation**  
2 **Limits Offspring Viability and Growth in Mice**

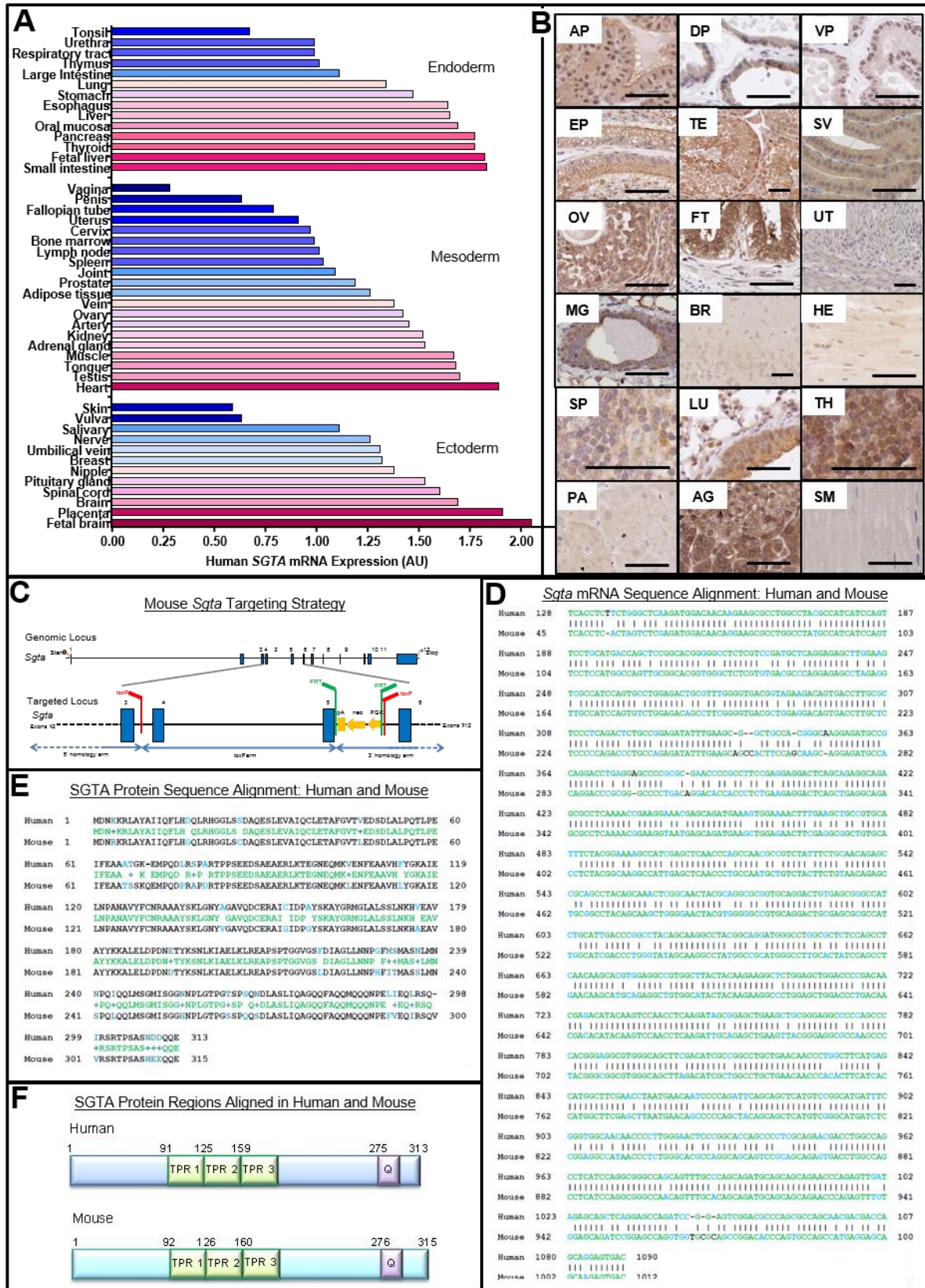
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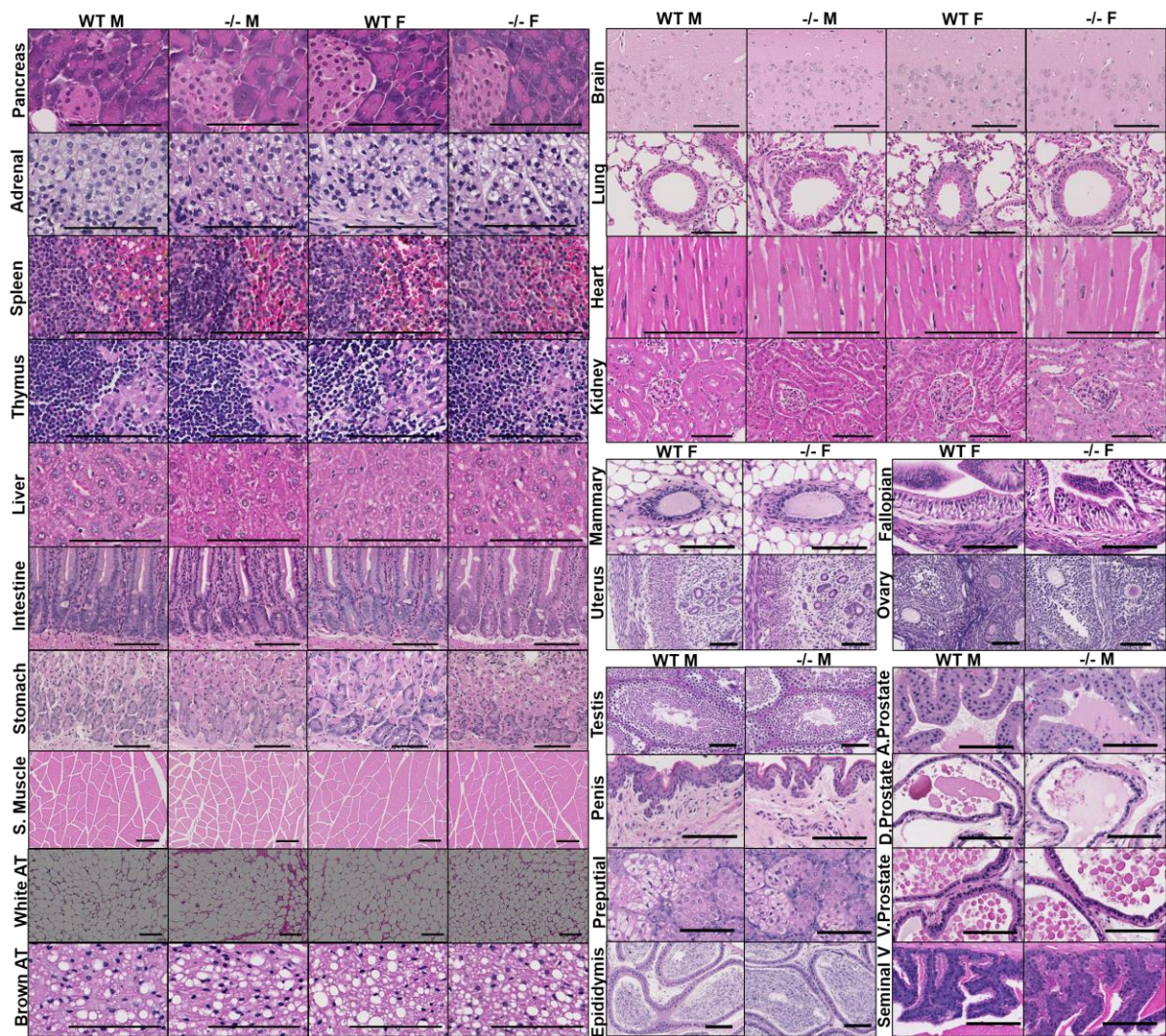
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 21 **Suppl Figure 1[A-F]. Generation of *Sgta*-null Mice and Comparison of SGTA mRNA and**  
 22 **Protein Sequence between *Homo sapiens* and *Mus musculus*. [A] SGTA mRNA expression in**  
 23 **normal human tissues grouped by developmental origin (endo-, meso- and ecto-derm). [B] SGTA**

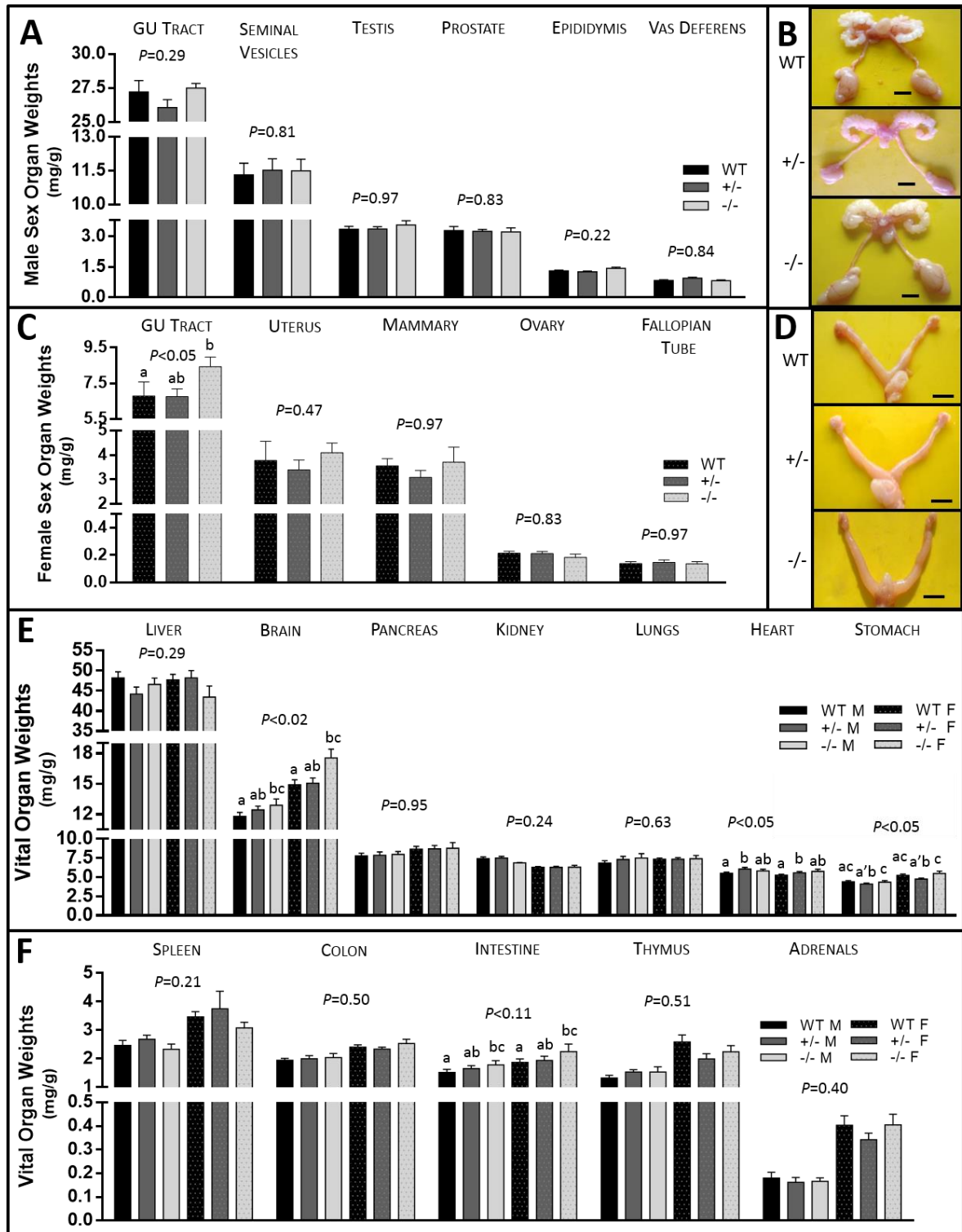
24 immunostaining depicting broad protein expression in normal C57BL/6 mouse tissues [antibody  
25 dilution]: AP, anterior prostate [1:500]; DP, dorsolateral prostate [1:500]; VP, ventral prostate  
26 [1:500]; EP, epididymis [1:500]; TE, testis [1:500]; SV, seminal vesicles [1:1000]; OV, ovary [1:500];  
27 FT, fallopian tubes [1:500]; UT, uterus [1:1000]; MG, mammary gland [1:1000]; BR, brain [1:2000];  
28 HE, heart [1:500]; SP, spleen [1:500]; LU, lungs [1:500]; TH, thymus [1:500]; PA, pancreas [1:2000];  
29 AG, adrenal gland [1:500]; SM, skeletal muscle [1:1000]. Scale bars represent 50 $\mu$ m. **[C]** Schematic  
30 representation of the targeting strategy employed to ablate mouse *Sgta*. **[D]** Sequence alignment of  
31 human and mouse *Sgta* mRNA. Green letters represent 83% identity (identical residues at the same  
32 positions in an alignment), black letters (1%) represent a gap, introduced to improve alignment,  
33 compensating for insertions and deletions and blue letters (16%) represent positive residues have  
34 preserved physicochemical properties. **[E]** Sequence alignment of human and mouse SGTA protein,  
35 green letters represent 88% identity, teal letters represent 94% positives, blue letters and a gap in the  
36 central sequence represents dissimilar residues and black letters and a gap in the central sequence  
37 represents an inserted gap (0%). **[F]** Alignment of functional SGTA protein regions in human and  
38 mouse: TPR, tetratricopeptide repeat; Q, glutamine-rich domain.  
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41 **Suppl Figure 2. Cell Morphology and Pathology of Adult Male and Female Wild-type (WT) and**  
 42 ***Sgta*-null (-/-) Organs.** Haematoxylin and Eosin stained tissue sections of the pancreas, adrenal  
 43 gland, spleen, thymus, liver, intestine, stomach, skeletal muscle (S. muscle, gastrocnemius muscle),  
 44 white adipose tissue (White AT, perirenal-retroperitoneal fat pad), brown adipose tissue (Brown AT,  
 45 interscapular brown fat pad), brain, lung, heart, kidney, in male (M) and female (F) mice;  
 46 Haematoxylin and Eosin stained female tissues, including the mammary, uterus, fallopian tube and  
 47 ovary; and male tissues, including the testis, penis, preputial gland, prostate (A, anterior lobe; D,  
 48 dorsolateral lobe; V, ventral lobe) and seminal vesicles (Seminal V). All scale bars represent 100µm.

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51 **Suppl Figure 3. Weights of Reproductive and Vital Organs in Adult *Sgta*-deficient Mice.**

52 [A]. In male (M) mice, relative weight (mg/g body weight) of the whole genitourinary (GU) tract,  
 53 seminal vesicles, testis, prostate, epididymis and vas deferens (n= 7-10/group, except prostate n=12-  
 54 15/group). WT, wild-type, +/-, *Sgta*<sup>+/-</sup> and -/-, *Sgta*<sup>-/-</sup>. [B] Representative male genitourinary tract  
 55 relative to genotype. Scale bar = 5 mm. [C] In female (F) mice, relative weight (mg/g body weight) of

56 the whole genitourinary (GU) tract, uterus, mammary, ovary and fallopian tube (n = 8-9/group GU,  
57 uterus; n=8-14/group ovary, mammary, fallopian tube). Means with different letters are significantly  
58 different,  $P<0.05$ . **[D]** Representative female genitourinary tract relative to genotype. Scale bar = 5  
59 mm. **[E]** Relative weight (mg/g body weight) of vital organs, the liver, brain, pancreas, kidney, lungs,  
60 heart and stomach (n=7-9/group). Means with different letters are significantly different,  $P<0.05$ ; a'  
61 trend,  $P<0.06$ , +/- vs WT. **[F]** Relative weight (mg/g body weight) of more vital organs, the spleen,  
62 colon, intestine, thymus and adrenals (n=7-10/group). Means with different letters are significantly  
63 different,  $P<0.05$ .

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<b>Suppl Table 1. Target and Reference* Gene Primer Sequences (Forward, FWD; Reverse, REV) utilised for mRNA Expression Analyses by qRT-PCR and their Optimised Annealing Temperature.</b>			
<b>Gene Symbol &amp; Accession #</b>	<b>FWD Sequence (5'-3')</b>	<b>REV Sequence (5'-3')</b>	<b>Annealing Temp (°C)</b>
<b>Ar</b> (NM_013476)	TCCCAGTCCCAATTGTGTCAA	TCGATGGGTAAAACATGGTCC	58.0
<b>Dnajc7</b> (NM_019795)	AATGGCGGCATGTCGTAGTT	CATGACGGCATTGGCGTT	58.0
<b>Fkbp4</b> (NM_010219)	GAGTGGACATCAGCCCCAAA	CAAAGACTCGGTCCCCGAT	62.5
<b>Fkbp5</b> (NM_010220)	CACGACATTCCGATTGGGAT	CCAAACTTAGGCTTCCCGG	61.5
<b>Ghr</b> (NM_010284)	CTGCAAAGAATCAATCCAAGCC	CAGTTCAGGGGAACGACTT	60
<b>Hp-1</b> (NM_017370)	GCTATGTGGAGCACTTGGTTC	CACCCATTGCTTCTCGTCGTT	67
<b>Igf-1</b> (NM_184052)	CACTCATCCACAATGCCTGT	TGGATGCTCTTCAGTTCGTG	60.5
<b>Igf-1r</b> (NM_010513)	CATGTGCTGGCAGTATAACCC	TCGGGAGGCTTGTTCCT	60.5
<b>Odc1</b> (NM_013614)	GACGAGTTTGACTGCCACATC	CGCAACATAGAACGCATCCTT	61.1
<b>Ppid</b> (NM_026352)	ACCGGGAAGCCTCTCCATT	TTCGCCACCTGTCCCATT	59.0
<b>Ppp5c</b> (NM_011155)	TCAAGACACAGGCCAACGACTA	ATTGCCGGGGTTCAACTCGAT	63.0
<b>Rhox5</b> (NM_008818)	CATTTTGCAGCGCACTAATTCC	AGCCCTCCTGATCTTAAACCA	61.5
<b>Sgta Exon1-3</b> (NM_024499)	GTCTTCGGTTCGACTGAGAGAT	GCCATGGAGGAAGTGGATGA	60.0
<b>Sgta Exon 4-5</b> (NM_024499)	GACAGGACACCACCTCTGAA	TTGCCGTAGAGGTGCACAGC	60.0
<b>Sgtb</b> (NM_144838)	GGCTGAGGTTTGAGATGGCTA	CATCATCCCTGACATTAGCTGC	61.5
<b>Stub1</b> (NM_019719)	TACACTGCCACAAGTGGGTT	GCGCAAGAGCTCAAGGAG	57.4
<b>Actb*</b> (NM_007393)	GGCTGTATTCCCCTCCATCG	CCAGTTGGTAACAATGCCATGT	64.5
<b>Gapdh*</b> (NM_017008)	TGCCGCCTGGAGAAACCTG	CTGTTGAAGTCACAGGAGAC	58.0
<b>Tbp*</b> (NM_013684)	CCTTGTACCCTTCACCAATGAC	ACAGCCAAGATTCACGGTAGA	60.0
<b>Tfrc*</b> (NM_011638)	GGACTGTAGAGGCGCTTCCTA	GGGTGTATGACAATGGTTCCC	60.0
<b>Hprt1*</b> (NM_012583)	CCTTGACTATAATGAGCACTTC	GCCACATCAACAGGACTC	56.4