1 Lactic acid is a sperm motility inactivation factor in the sperm storage tubules

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Supplementary Table S1

Enrichment of gene ontology terms in differentially expressed sequences between SSTs and non-SST cells detected by PAGE

GO_id	GO_name	Number of sequences	Z score	P-value	False discovery rate
GO:0005515	MF protein binding	2354	-7.794049752	6.43929E-15	1.71E-12
GO:0005840	CC ribosome	98	6.548828012	5.79903E-11	5.93E-09
GO:0003735	MF structural constituent of ribosome	99	6.527433457	6.69063E-11	5.93E-09
GO:0006412	BP translation	99	6.373236731	1.8508E-10	1.23E-08
GO:0005576	CC extracellular region	110	6.049948334	1.44892E-09	7.71E-08
GO:0006820	BP anion transport	20	-5.426567452	5.74481E-08	2.55E-06
GO:0005524	MF ATP binding	929	-5.361703161	8.24409E-08	3.13E-06
GO:0008289	MF lipid binding	21	5.334001178	9.60719E-08	3.19E-06
GO:0003777	MF microtubule motor activity	38	-4.870426596	1.11358E-06	3.29E-05
GO:0007018	BP microtubule-based movement	39	-4.827499659	1.38258E-06	3.44E-05
GO:0003774	MF motor activity	58	-4.804414293	1.55205E-06	3.44E-05
GO:0016459	CC myosin complex	58	-4.804414293	1.55205E-06	3.44E-05
GO:0006468	BP protein phosphorylation	423	-4.718625472	2.37444E-06	4.86E-05
GO:0017048	MF Rho GTPase binding	12	-4.468511328	7.87658E-06	0.000149655
GO:0005622	CC intracellular	367	4.357143873	1.31771E-05	0.000233674
GO:0004672	MF protein kinase activity	415	-4.332896983	1.4716E-05	0.000244654
GO:0005262	MF calcium channel activity	10	-4.269214999	1.96162E-05	0.000306936

GO:0007156	BP homophilic cell adhesion via plasma membrane adhesion	53	-4.232014107	2.31608E-05	0.000342265
GO:0005882	CC intermediate filament	31	4.116758099	3.84239E-05	0.000537935
GO:0070588	BP calcium ion transmembrane transport	10	-4.036394977	5.42788E-05	0.000721908
GO:0005856	CC cytoskeleton	42	-3.603256105	0.000314256	0.003980576
GO:0016311	BP dephosphorylation	20	-3.210644436	0.001324377	0.016012922
GO:0004198	MF calcium-dependent cysteine-type endopeptidase activity	13	-3.162832965	0.00156242	0.017429501
GO:0030036	BP actin cytoskeleton organization	18	-3.152004905	0.001621535	0.017429501
GO:0005737	CC cytoplasm	221	3.149034063	0.001638111	0.017429501
GO:0008017	MF microtubule binding	36	-3.130481343	0.001745201	0.017854749
GO:0015074	BP DNA integration	13	-3.091820668	0.00198933	0.019598584
GO:0004867	MF serine-type endopeptidase inhibitor activity	18	3.072754654	0.002120928	0.019921593
GO:0004871	MF signal transducer activity	46	-3.065659791	0.002171903	0.019921593
GO:0005179	MF hormone activity	13	3.000344938	0.00269674	0.023911095
GO:0008236	MF serine-type peptidase activity	21	2.976241845	0.002918046	0.025038717
GO:0008146	MF sulfotransferase activity	34	2.892907378	0.003816938	0.031728297
GO:0005509	MF calcium ion binding	269	-2.864577588	0.004175658	0.032881818
GO:0019001	MF guanyl nucleotide binding	15	-2.853316217	0.004326555	0.032881818
GO:0031683	MF G-protein beta/gamma-subunit complex binding	15	-2.853316217	0.004326555	0.032881818
GO:0016791	MF phosphatase activity	25	-2.831161577	0.004637929	0.034269142
GO:0005198	MF structural molecule activity	60	2.801202112	0.005091262	0.035857906

GO:0006810	BP transport	127	-2.799224055	0.005122558	0.035857906
GO:0008237	MF metallopeptidase activity	18	-2.79045819	0.00526335	0.035898746
GO:0008168	MF methyltransferase activity	63	2.775133315	0.005517908	0.036694088
GO:0030286	CC dynein complex	12	-2.752165169	0.005920265	0.038409524
GO:0005215	MF transporter activity	54	-2.736886144	0.006202376	0.039281715
GO:0008233	MF peptidase activity	17	2.727139113	0.00638861	0.039520239
GO:0016491	MF oxidoreductase activity	200	2.706477648	0.006800116	0.041109792
GO:0016020	CC membrane	689	-2.668275556	0.00762417	0.045067316
GO:0036459	MF ubiquitinyl hydrolase activity	51	-2.616318016	0.008888373	0.051397983
GO:0006457	BP protein folding	51	2.565771027	0.010294676	0.058263485
GO:0004129	MF cytochrome-c oxidase activity	15	2.515646606	0.011881425	0.065842897
GO:0004553	MF hydrolase activity, hydrolyzing O-glycosyl compounds	39	-2.383112906	0.017166928	0.093191895
GO:0006629	BP lipid metabolic process	37	2.279286886	0.022650017	0.12049809
GO:0045454	BP cell redox homeostasis	43	2.243244467	0.024881054	0.129771772
GO:0004866	MF endopeptidase inhibitor activity	10	-2.23035619	0.025723806	0.131587161
GO:0006814	BP sodium ion transport	25	2.215630772	0.0267168	0.134088091
GO:0006281	BP DNA repair	65	2.142772777	0.032131348	0.15827664
GO:0005085	MF guanyl-nucleotide exchange factor activity	25	-2.106623274	0.035150248	0.167675308
GO:0005507	MF copper ion binding	18	2.097576928	0.035942535	0.167675308
GO:0030001	BP metal ion transport	19	-2.079932185	0.037531753	0.167675308

GO:0003723	MF RNA binding	128	2.079504008	0.03757105	0.167675308
GO:0005525	MF GTP binding	280	2.078047394	0.037704994	0.167675308
GO:0016887	MF ATPase activity	87	-2.076784014	0.037821498	0.167675308
GO:0042626	MF ATPase activity, coupled to transmembrane movement of substances	28	-2.039379711	0.041412146	0.176095407
GO:0008083	MF growth factor activity	31	2.037561024	0.041593853	0.176095407
GO:0003779	MF actin binding	63	-2.036433876	0.041706807	0.176095407
GO:0006418	BP tRNA aminoacylation for protein translation	37	1.999249884	0.045581324	0.189447378
GO:0006470	BP protein dephosphorylation	85	-1.988998362	0.046701384	0.190822657
GO:0009058	BP biosynthetic process	52	1.98318315	0.047346975	0.190822657
GO:0006955	BP immune response	31	1.967460774	0.049130114	0.193423393

Notes: GO, gene ontology; PAGE, parametric analysis of gene set enrichment; BP, biological process; MF, molecular function; and CC, cellular component. We used log2 Fold Change values between SSTs and non-SST cells to calculate Z scores and corresponding P-values for each GO term.



Supplementary Figure S1: Expression of *monocarboxylate transporter 4 (MCT4)* 55 mRNA in the utero-vaginal junction (UVJ). a-b, Autoradiograms of the UVJ sections 56 after hybridization with 33 P-labeled antisense probe specific for *MCT4* (a) or sense 57 58 probe (b) are shown. The autoradiogram was observed under a stereomicroscope (c) and 59 the corresponding area of the glass slide was photographed (d). Arrows in panel d 60 indicate SSTs. Note that the corresponding areas of the autoradiogram in panel c are 61 positively labeled. Representative results of two experiments are shown (n= 2). Scale 62 bar = 200 μ m.



Supplementary Figure S2: Effects of treatment with various acids on sperm **motility.** Ejaculated sperm were incubated with various organic acids including lactic acid (Lac), acetic acid (Ac), malic acid (Mal), oxaloacetic acid (Ox) and citric acid (Cit) at a final concentration of 10 mM. In controls, the effects of medium alone (none) and non-organic acid (HCl) were also examined. a, Sperm motility was scored (n=3) after 10 min incubation of sperm with these media. ** denotes a significant difference from medium alone (P < 0.01). **b**, The relationship between medium pH (x-axis) and motility score (y-axis) was indicated (n=3).





76 Supplementary Figure S3: Effects of oligomycin and sodium vanadate on ATPase

activity of sperm. De-membraned sperm were incubated with 1 mM ATP in the

78 presence or absence of 10 μM oligomicin (OLG) or 20 μM sodium vanadate (VND),

and the free phosphoric acid in the incubation mixture was measured using a microplate

80 reader. Values are mean \pm SEM of three independent experiments. * denotes a

81 significant difference from respective control (P < 0.05).



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Supplementary Figure S4: Effects of in vitro storage on the morphology of spermatozoa. Ejaculated sperm were suspended in either a medium alone (*a*) or a medium containing 10 mM L-lactic acid with nitrogen gas bubbled through it for 5 min (*b*). After being stored for 5 days at 41.5°C, sperm were fixed with 3.7% formalin and smeared on a glass slide. Sperm morphology was observed under a microscope. The images shown are representative of images obtained from three independent experiments. Scale bar = 50 μ m.

93 Supplementary Movie 1. Effects of a flow-through fraction of utero vaginal junction 94 (UVJ) extracts on sperm motility. UVJ extracts were passed through an ultrafiltration 95 membrane (MW cutoff 10 kDa) and the flow-through fraction was examined using a 96 sperm motility assay. Sperm movement was recorded using a high-speed camera (200 97 frames per second), which showed that sperm motility was strongly suppressed by the 98 addition of the fraction.

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100 Supplementary Movie 2. Sperm motility in Hank's balanced salt solution (HBSS).

Ejaculated sperm were suspended in HBSS and sperm movement was recorded using ahigh-speed camera (200 frames per second).

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104 Supplementary Movie 3. Effects of L-lactic acid and D-lactic acid on sperm motility.

105 Ejaculated sperm were suspended in Hank's balanced salt solution and 10 mM L-lactic

106 acid or D-lactic acid was injected into sperm suspensions using a glass capillary. Sperm

107 movement was recorded under a stereomicroscope.

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109 Supplementary Movie 4. Axonemal sliding of de-membraned sperm in a buffer at pH

110 7.4. Vigorous axonemal sliding was observed subsequent to perfusion of the ATP111 solution.

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113 Supplementary Movie 5. Axonemal sliding of de-membraned sperm in a buffer at pH

114 5.4. Little axonemal sliding was observed subsequent to perfusion of the ATP solution.