

Supplementary Information

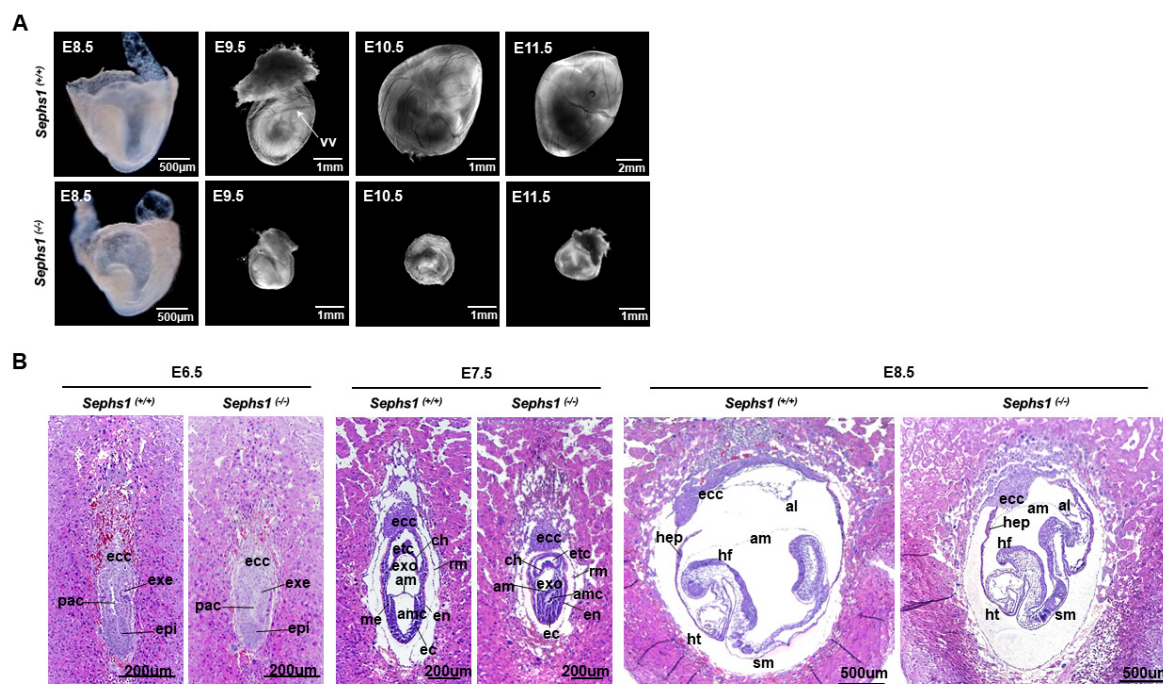


Figure S1. Morphology of *Sephs1*^{-/-} embryos. (A) Embryos were photographed in the yolk sac immediately after dissection. (B) Paraffin-embedded section of *Sephs1*^{-/-} embryo stained with Hematoxylin & eosin stain. exe, extraembryonic region; epi, epiblast; pac, pro-amniotic cavity; ecc, ectoplacental cone; am, amnion; etc, ectoplacental cavity; exo, exocoelomic cavity; amc, amniotic cavity; ec, ectoderm; en, endoderm; me, mesoderm; ch, chorion; hep, hemato-endothelial progenitor; hf, head fold; ht, heart; sm, somite; and al, allantois.

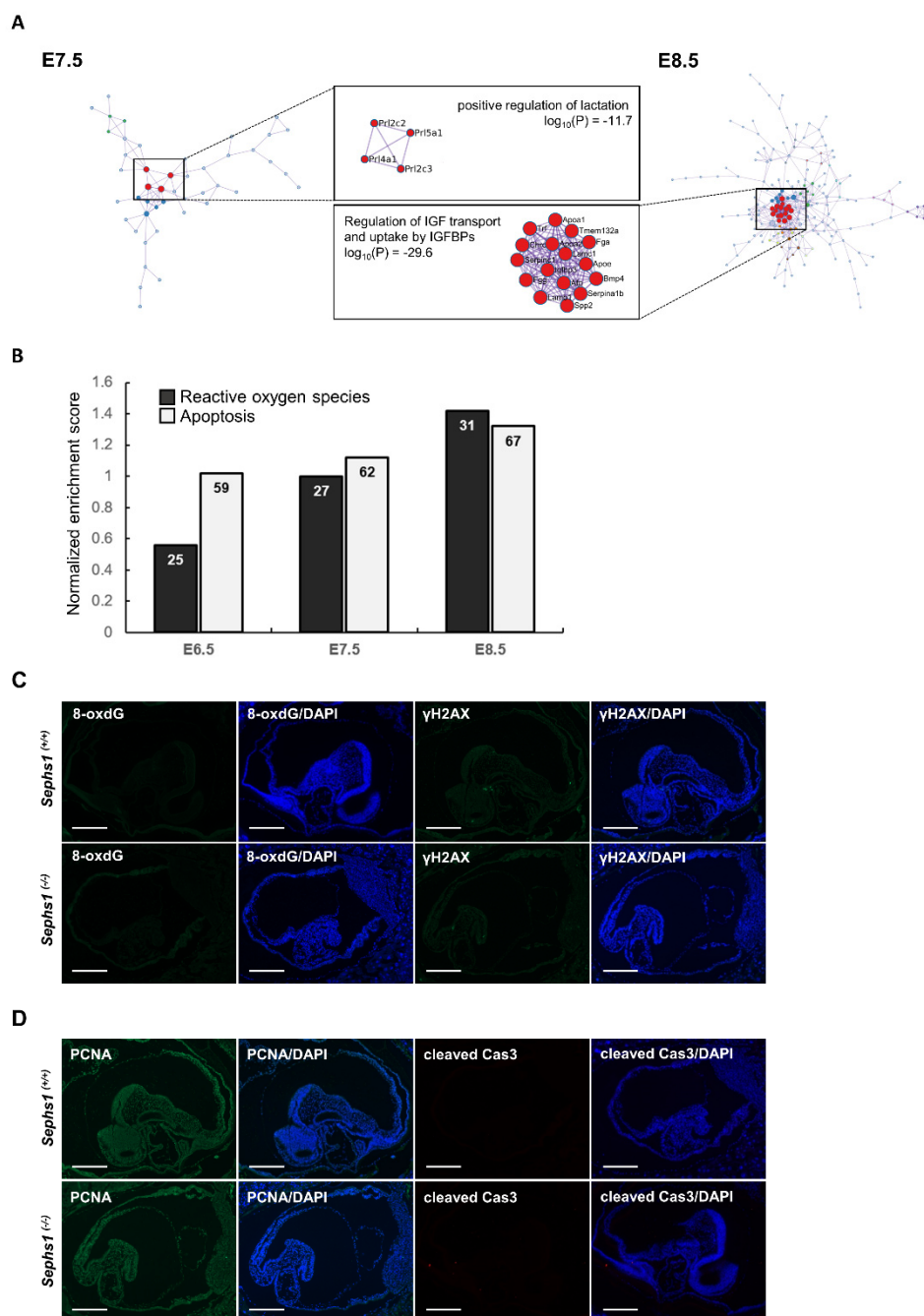


Figure S2. PPI analysis and GSEA on ‘Reactive Oxygen Species’ and ‘Apoptosis’ gene sets. **(A)** PPI analysis at E7.5 and E8.5. **(B)** Normalized enrichment score of GSEA with gene sets of ‘Reactive Oxygen Species’ and ‘Apoptosis’. Each number in the bar graph indicates the number of genes in the LES. **(C)** Level of DNA damage induced by oxidative stress markers at E8.5. Scale bars represent 500 μ m. **(D)** Level of proliferation marker and apoptosis marker at E8.5. Scale bars represent 500 μ m.

Table S1. Top 25 up-regulated and top 25 down-regulated DEGs lists at E6.5, E7.5 and E8.5.

Top 25 downregulated at E6.5				Top 25 upregulated at E6.5			
Gene_symbol	Description	p-val	log2FC	Gene_symbol	Description	p-val	log2FC
Hba-a2	hemoglobin alpha, adult chain 2	9.81E-03	-8.78	Pr14a1	prolactin family 4, subfamily a, member 1	4.61E+00	6.18
Foxc2	forkhead box C2	6.35E-05	-4.41	Pr3d2	prolactin family 3, subfamily d, member 1	4.34E+00	4.43
Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	8.33E-04	-3.94	Pr15a1	prolactin family 5, subfamily a, member 1	3.67E+00	4.32
Cntnap2	contactin associated protein-like 2	9.56E-03	-3.71	Pr17a1	prolactin family 7, subfamily a, member 1	3.73E+00	4.10
Vat1l	vesicle amine transport protein 1 like	2.50E-04	-3.45	Nppb	natriuretic peptide type B	3.01E+00	3.87
Amica1	adhesion molecule, interacts with CXADR antigen 1	3.47E-03	-3.23	Cts8	cathepsin 8	2.88E+00	3.61
Atp6v0d2	ATPase, H ⁺ transporting, lysosomal V0 subunit D2	5.72E-03	-3.12	Cts7	cathepsin 7	3.36E+00	3.53
Rab39b	RAB39B, member RAS oncogene family	3.63E-04	-3.07	Pip1	pore forming protein-like	2.92E+00	3.18
Ldhd	lactate dehydrogenase D	6.78E-05	-3.04	Bmp8b	bone morphogenetic protein 8b	2.23E+00	3.09
Ampd3	adenosine monophosphate deaminase 3	2.10E-03	-3.00	AU018091	expressed sequence AU018091	2.45E+00	3.03
Mlph	melanophilin	6.84E-03	-2.95	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	2.08E+00	3.02
Galnt16	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl	3.37E-05	-2.84	Ap2c2	ATPase, Ca ⁺⁺ transporting, type 2C, member 2	1.65E+00	2.95
Fan1	FANCD2/FANCI-associated nuclease 1	9.44E-03	-2.83	Mmp9	matrix metalloproteinase 9	2.69E+00	2.90
Htra3	HtrA serine peptidase 3	6.39E-04	-2.83	Adm	adrenomedullin	2.66E+00	2.84
Nlgn3	neuroligin 3	4.02E-03	-2.77	Duoax2	dual oxidase maturation factor 2	1.92E+00	2.80
Gpmnb	glycoprotein (transmembrane) nmb	1.14E-03	-2.76	Rhox1	reproductive homeobox 1	1.48E+00	2.68
Spr2g	small proline-rich protein 2G	4.11E-03	-2.75	Scin	scinderin	2.19E+00	2.56
Erv3	endogenous retroviral sequence 3	6.81E-03	-2.70	Igfb3	integrin beta 3	1.82E+00	2.55
Acss1	acyl-CoA synthetase short-chain family member 1	5.04E-03	-2.65	Gjb5	gap junction protein, beta 5	2.20E+00	2.54
Wnt3a	wingless-type MMTV integration site family, member 3A	8.36E-04	-2.65	Gjb3	gap junction protein, beta 3	2.18E+00	2.54
Prp1	proline-rich acidic protein 1	6.91E-04	-2.54	Gpx1	glutathione peroxidase 1	4.88E-01	2.49
Rbm24	RNA binding motif protein 24	2.54E-03	-2.50	Gm1673	predicted gene 1673	1.97E+00	2.47
Nolo	nolochord homeobox	8.77E-04	-2.43	Elf5	E74-like factor 5	2.25E+00	2.39
Tmem213	transmembrane protein 213	1.99E-03	-2.42	Tacs1d2	tumor-associated calcium signal transducer 2	1.83E+00	2.36
Heph1l	hephaestin-like 1	4.89E-03	-2.36	Plau	plasminogen activator, urokinase	1.41E+00	2.32

Top 25 downregulated at E7.5				Top 25 upregulated at E7.5			
Gene_symbol	Description	p-val	log2FC	Gene_symbol	Description	p-val	log2FC
Slmn2	stathmin-like 2	2.18E-03	-6.76	Pr12c3	prolactin family 2, subfamily c, member 3	2.69E+00	5.92
Tmem176a	transmembrane protein 176A	2.67E-03	-5.50	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradn	2.12E+00	5.07
Vat1l	vesicle amine transport protein 1 like	1.29E-04	-5.33	Pr14a1	prolactin family 4, subfamily a, member 1	3.36E+00	4.95
Tmem100	transmembrane protein 100	3.45E-03	-4.92	Ceacam9	carcinoembryonic antigen-related cell adhesion molecule 9	1.81E+00	4.65
Tmem35	transmembrane protein 35	1.14E-04	-4.78	Cts8	cathepsin 8	2.44E+00	4.65
Them6	thioesterase superfamily member 6	2.72E-03	-4.63	Grem2	gremlin 2, DAN family BMP antagonist	1.75E+00	4.54
Rtn4r2	reticulon 4 receptor-like 2	4.59E-03	-4.41	Igf1bp1	insulin-like growth factor binding protein 1	3.13E+00	4.32
Cntnap2	contactin associated protein-like 2	3.65E-03	-4.35	Thbd	thrombospondin	2.61E+00	4.30
Rab39b	RAB39B, member RAS oncogene family	7.88E-04	-4.11	Mmp1a	matrix metalloproteinase 1a (interstitial collagenase)	2.52E+00	4.30
Maneal	mannosidase, endo-alpha-like	7.26E-04	-3.95	Pr17a1	prolactin family 7, subfamily a, member 1	3.52E+00	4.00
Tmem132a	transmembrane protein 132A	2.06E-03	-3.70	Psg22	pregnancy-specific glycoprotein 22	2.59E+00	3.95
Mlbp2	microfibrillar-associated protein 2	3.24E-03	-3.64	Pip1	pore forming protein-like	2.80E+00	3.91
Adck2	aarF domain containing kinase 2	1.06E-03	-3.60	Lama1	laminin, alpha 1	3.65E+00	3.86
Gsta4	glutathione S-transferase, alpha 4	1.51E-03	-3.05	Cts7	cathepsin 7	3.27E+00	3.82
Mlbp1	mitochondrial fission process 1	8.83E-03	-3.02	Pr15a1	prolactin family 5, subfamily a, member 1	2.63E+00	3.72
Vash1	vasohibin 1	3.61E-03	-2.78	Mmp9	matrix metalloproteinase 9	2.88E+00	3.70
Ghdc	GH3 domain containing	7.18E-04	-2.74	Serpina1b	serine (or cysteine) peptidase inhibitor, clade A, member 1	1.98E+00	3.57
Lrn3	leucine rich repeat and fibronectin type III domain containi	6.81E-03	-2.71	Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2.69E+00	3.47
Fkbp10	FK506 binding protein 10	8.86E-03	-2.68	Ceacam15	carcinoembryonic antigen-related cell adhesion molecule 1	2.70E+00	3.42
Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	5.72E-03	-2.62	Nid1	nidogen 1	3.15E+00	3.34
Vwa5a	von Willebrand factor A domain containing 5A	5.18E-03	-2.57	Pr12c2	prolactin family 2, subfamily c, member 2	2.69E+00	3.24
Sh3gl2	SH3-domain GRB2-like 2	1.51E-03	-2.55	Srgn	serglycin	2.99E+00	3.20
Gng3	guanine nucleotide binding protein (G protein), gamma 3	1.55E-03	-2.52	Adm	adrenomedullin	2.93E+00	3.14
Fut10	fucosyltransferase 10	9.09E-04	-2.45	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	2.61E+00	2.95
Nlgn3	neuroligin 3	8.56E-03	-2.39	Cdh5	cadherin 5	2.83E+00	2.85

Top 25 downregulated at E8.5				Top 25 upregulated at E8.5			
Gene_symbol	Description	p-val	log2FC	Gene_symbol	Description	p-val	log2FC
Tmem176b	transmembrane protein 176B	7.39E-03	-5.41	Pr12c4	prolactin family 2, subfamily c, member 4	4.70E-03	10.02
Vat1l	vesicle amine transport protein 1 like	3.16E-03	-5.29	Orm2	orosomucoid 2	5.20E-03	5.49
Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	3.05E-03	-5.13	Heph1l	hephaestin-like 1	1.46E-04	5.40
Cntnap2	contactin associated protein-like 2	5.18E-03	-5.00	Erv3	endogenous retroviral sequence 3	2.03E-03	4.91
Fxyd3	FXD domain-containing ion transport regulator 3	7.04E-03	-4.69	Klk7	kallikrein related-peptidase 7 (chymotryptic, stratum corneu	5.08E-03	4.76
Ghdc	GH3 domain containing	5.08E-03	-4.31	PscA	prostate stem cell antigen	4.86E-04	4.49
Tmem176a	transmembrane protein 176A	6.16E-03	-4.14	Pr18a2	prolactin family 8, subfamily a, member 2	1.55E-04	4.21
Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradn	1.76E-06	-3.92	Htra3	HtrA serine peptidase 3	5.11E-04	3.90
Galnt16	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl	4.50E-03	-3.87	Gpmnb	glycoprotein (transmembrane) nmb	2.33E-03	3.87
Chrd1l	chordin-like 1	6.77E-04	-3.46	Htra1	HtrA serine peptidase 1	6.06E-04	3.74
Pr14a1	prolactin family 4, subfamily a, member 1	2.93E-03	-3.38	Gp1hbp1	GPI-anchored HDL-binding protein 1	8.00E-04	3.72
Rtn4r2	reticulon 4 receptor-like 2	9.25E-03	-3.23	Adamts5	a disintegrin-like and metalloproteinase (reprolys in type) wit	3.66E-04	3.37
Hsd3b6	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid	2.09E-03	-3.17	Mlbp5	microfibrillar associated protein 5	3.62E-03	3.25
Mlbp1	mitochondrial fission process 1	1.12E-03	-3.09	Il1r2	interleukin 1 receptor, type II	3.86E-03	3.22
Them6	thioesterase superfamily member 6	4.68E-03	-3.09	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	6.35E-03	2.86
Lox1	lysyl oxidase-like 1	1.02E-03	-2.99	A2m	alpha-2-macroglobulin	3.28E-04	2.76
Dnase113	deoxyribonuclease 1-like 3	8.09E-03	-2.97	Lipg	lipase, endothelial	6.87E-03	2.67
Adck2	aarF domain containing kinase 2	2.04E-03	-2.95	Psap	prosaposin	5.88E-04	2.64
Tmem132a	transmembrane protein 132A	1.41E-03	-2.84	Spr2g	small proline-rich protein 2G	1.47E-03	2.55
Thbd	thrombospondin	8.01E-04	-2.52	Krt20	keratin 20	4.62E-03	2.32
Lama1	laminin, alpha 1	9.63E-04	-2.47	Fabp4	fatty acid binding protein 4, adipocyte	6.20E-03	2.21
Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	9.33E-03	-2.45	Rbp2	retinol binding protein 2, cellular	7.18E-03	2.03
Msh3	msh homeobox 3	2.75E-04	-2.44	S100a8	S100 calcium binding protein A8 (calgranulin A)	4.10E-03	2.01
Grem2	gremlin 2, DAN family BMP antagonist	8.25E-04	-2.43	Accl12	amine oxidase copper containing 1-like 2	8.27E-03	1.96
Arifp5	ADP-ribosylation factor-like 6 interacting protein 5	1.80E-03	-2.43	Ambp	alpha 1 microglobulin/bikunin	4.94E-03	1.96

Table S2. Canonical pathways obtained from IPA

Embryonic Day	Name	$\log_{10}(p)^*$	Z score	LXR/RXR/FXR Gene list
E6.5	LXR/RXR Activation	-8.93	2.27	APOA1, APOA2, APOA4, APOC2, APOM, C3, FGA, IL1R1, KNG1, LPL, LY96, MMP9, NFKB1, NOS2, PLTP, RBP4, S100A8, SERPINF1, SERPINF2, TF, TTR
	Coagulation System	-6.75	1.90	A2M, FGA, FGB, FGG, KNG1, PLAU, PLAUR, SERPINE1, SERPINF2, THBD
	Regulation Of The Epithelial Mesenchymal Transition In Development Pathway	-6.62	-2.84	APH1B, FZD3, GLI1, JAG1, NFKB1, S100A4, SNAI2, TWIST1, WNT2, WNT2B, WNT3A, WNT5A, WNT6, WNT7B, WNT8A
E7.5	Coagulation System	-11.90	1.29	F2, F3, FGA, FGB, FGG, PLAT, PLAU, PLAUR, PLG, PROS1, SERPINA1, SERPINC1, SERPINF2, TFPI, THBD
	LXR/RXR Activation	-7.86	2.63	ABCA1, AMBP, APOA1, APOA2, APOA4, APOB, APOC2, FGA, GC, IL1R2, LCAT, LPL, LYZ, MMP9, NGFR, PLTP, RBP4, SERPINA1, SERPINF2, TF, TTR
	LPS/IL-1 Mediated Inhibition of RXR Function	-5.59	-1.16	ABCA1, ABCC2, ABCC4, ACOX1, APOC2, CHST11, CHST3, Cyp2d26, FABP1, FABP2, FABP3, FMO1, FMO4, GSTM2, Gstm3, GSTM4, GSTM5, HS3ST1, IL1R2, LIPC, MAOB, MAP2K7, MYD88, NGFR, PLTP, PPARGC1B, SULT1E1
E8.5	Coagulation System	-7.20	-1.00	A2M, F3, F5, FGA, FGG, KNG1, SERPINA1, SERPINF2, THBD
	LXR/RXR Activation	-6.87	1.29	AMBP, APOA2, APOA4, FGA, IL1R2, IL33, KNG1, LBP, RXRG, S100A8, SERPINA1, SERPINF1, SERPINF2, TF, TNFRSF1A
	Acute Phase Response Signaling	-5.72	1.60	ADAMTS5, CEBPB, CTNNA2, DCN, DDIT4, DDR2, FGF18, FZD9, GLI1, GREM1, HTRA1, IL1R2, ITGA2B, PTH1R, S100A8, SPHK1, Tcf7, TNFRSF1A, WNT8A

* Pathways with $\log_{10}(p) < -5$ were selected.

Table S3. List of genes in LES obtained from GSEA on 'Reactive Oxygen Species'.

Total		E6.5		E7.5		E8.5	
Gene symbol	RM score	Gene symbol	RM score	Gene symbol	RM score	Gene symbol	RM score
GLRX	1.221	PRDX6	1.044	PRDX6	1.727	GLRX	1.515
PRDX6	0.665	GLRX	0.97	PRDX2	1.264	NDUFB4	0.595
PRDX2	0.598	PRDX2	0.835	MGST1	1.251	HMOX2	0.518
NDUFS2	0.294	GPX3	0.684	GLRX	1.241	PTPA	0.307
NDUFB4	0.278	HHEX	0.543	NDUFB4	0.822	SOD2	0.266
HHEX	-0.154	NDUFB4	0.314	FES	0.81	GPX4	-0.261
MSRA	-0.16	SCAF4	0.283	MBP	0.627	GCLC	-0.275
SELENOS	-0.168	EGLN2	-0.363	NDUFS2	0.52	STK25	-0.277
LAMTOR5	-0.178	ATOX1	-0.363	ERCC2	0.4	LAMTOR5	-0.28
ATOX1	-0.196	PRDX1	-0.399	ABCC1	0.384	GCLM	-0.315
SCAF4	-0.224	GSR	-0.426	GSR	-0.3	MBP	-0.319
PRDX1	-0.231	PTPA	-0.457	SOD1	-0.39	MSRA	-0.329
SRXN1	-0.248	GPX4	-0.46	SCAF4	-0.489	FTL	-0.341
GPX4	-0.289	LAMTOR5	-0.478	TXN	-0.544	NDUFA6	-0.411
PRNP	-0.32	CAT	-0.492	CDKN2D	-0.592	SBNO2	-0.422
TXN	-0.34	PDLIM1	-0.61	PFKP	-0.619	GSR	-0.427
GSR	-0.365	CDKN2D	-0.707	LSP1	-0.684	CAT	-0.435
CAT	-0.478	SOD1	-0.72	TXNRD1	-0.726	ATOX1	-0.464
GCLM	-0.498	FTL	-0.843	GCLM	-0.777	SCAF4	-0.478
PFKP	-0.542	PFKP	-0.895	TXNRD2	-0.896	FES	-0.578
PDLIM1	-0.577	TXNRD1	-0.916	FTL	-0.904	CDKN2D	-0.592
TXNRD1	-0.597	GCLM	-0.949	CAT	-0.986	PRDX1	-0.633
SOD1	-0.602	TXNRD2	-1.28	PDLIM1	-1.179	SOD1	-0.696
CDKN2D	-0.635	JUNB	-1.657	NQO1	-1.216	TXN	-0.727
FTL	-0.707	NQO1	-2.043	GPX3	-1.416	HHEX	-0.891
JUNB	-0.744			JUNB	-2.065	TXNRD2	-0.905
TXNRD2	-0.914			SRXN1	-2.342	JUNB	-1.008
NQO1	-1.303					SRXN1	-1.281
						GPX3	-1.3
						PRNP	-2.155
						NQO1	-2.641

* RM score; rank metric score.

Table S4. List of genes in LES obtained from GSEA on ‘Apoptosis’.

Total		E6.5		E7.5		E8.5	
Gene symbol	RM score	Gene symbol	RM score	Gene symbol	RM score	Gene symbol	RM score
MADD	1.425	MADD	2.905	MADD	3.048	LMNA	2.225
CCND1	1.117	CCND2	2.735	CD44	2.032	FEZ1	2.091
CASP8	1.057	CD44	2.344	BMF	1.587	EMP1	2.08
PPP2R5B	0.786	ATF3	1.744	CASP8	1.307	CD44	1.921
CD44	0.732	CASP8	1.468	CCND1	1.154	SATB1	1.883
CASP3	0.669	LEF1	1.353	PPP2R5B	1.126	CAV1	1.581
BMF	0.669	BMF	1.316	CDKN1B	1.028	MADD	1.537
CDKN1B	0.589	CDKN1B	1.257	CASP3	1.017	BMF	1.129
LEF1	0.549	F2R	1.245	BIK	0.969	CCND1	1.089
PAK1	0.459	SAT1	1.203	DIABLO	0.789	NEDD9	1.063
CASP2	0.41	LGALS3	1.195	IGFBP6	0.781	BGN	0.999
DIABLO	0.34	DAP	1.185	LEF1	0.765	PLAT	0.862
TIMP3	0.301	CASP3	1.129	PAK1	0.714	TIMP2	0.838
TIMP2	0.298	CCND1	1.116	RARA	0.711	PPP2R5B	0.785
CASP7	0.291	JUN	1.084	GADD45A	0.644	CASP8	0.782
FEZ1	0.278	PMAIP1	1.007	SATB1	0.628	CCND2	0.753
BCL2L1	0.265	NEDD9	0.938	CASP2	0.586	PDGFRB	0.737
NEDD9	0.256	TIMP2	0.937	PSEN2	0.468	TIMP3	0.716
CTNNA1	0.218	ISG20	0.926	TSPO	0.451	CDKN1B	0.542
BAX	-0.168	DCN	0.912	HMGB2	0.448	SLC20A1	0.531
IRF1	-0.172	ROCK1	0.861	LMNA	-0.436	DIABLO	0.506
BCAP31	-0.173	CASP2	0.844	IRF1	-0.442	CASP7	0.491
IGF2R	-0.18	GSR	-0.426	DFFA	-0.459	ERBB3	0.472
IFNGR1	-0.191	GCH1	-0.431	RHOB	-0.509	RHOB	0.463
GSN	-0.219	BGN	-0.446	IFITM3	-0.536	FDXR	0.384
ROCK1	-0.219	BAX	-0.45	SC5D	-0.609	RARA	0.376
CD38	-0.224	IFITM3	-0.453	BGN	-0.612	GPX1	-0.417
DNM1L	-0.228	GPX4	-0.46	DNM1L	-0.625	GSR	-0.427
PPT1	-0.276	RARA	-0.461	CASP6	-0.632	BNIP3L	-0.427
SPTAN1	-0.277	CDKN1A	-0.463	DNAJC3	-0.647	BMP2	-0.49
SC5D	-0.278	SLC20A1	-0.472	KRT18	-0.666	IGF2R	-0.494
CFLAR	-0.285	FDXR	-0.488	ISG20	-0.67	HMGB2	-0.503
GPX4	-0.289	IGF2R	-0.545	CFLAR	-0.671	IFNGR1	-0.514
TNFRSF12A	-0.293	PLAT	-0.55	BMP2	-0.684	SMAD7	-0.543
ERBB3	-0.305	IGFBP6	-0.592	SQSTM1	-0.761	SQSTM1	-0.552
IFITM3	-0.332	SATB1	-0.611	RETSAT	-0.831	ROCK1	-0.56
HSPB1	-0.351	CDC25B	-0.663	TIMP1	-0.877	CYLD	-0.645
IER3	-0.352	IRF1	-0.688	ROCK1	-0.893	SOD1	-0.696
CDK2	-0.363	MGMT	-0.709	CD38	-0.94	KRT18	-0.707
GSR	-0.365	SOD1	-0.72	TGFB3	-0.94	CFLAR	-0.719
RETSAT	-0.375	RETSAT	-0.764	BTG2	-1.001	CLU	-0.729
BCL2L2	-0.393	BIK	-0.891	DAP	-1.059	CASP6	-0.735
CASP6	-0.409	HSPB1	-0.921	PDCD4	-1.066	BAX	-0.749
ANKH	-0.427	SQSTM1	-0.923	IGF2R	-1.207	AIFM3	-0.762
TIMP1	-0.444	EMP1	-0.947	CLU	-1.22	BCL2L2	-0.793
GNA15	-0.444	TIMP1	-0.988	SAT1	-1.281	GADD45A	-0.834
BTG2	-0.521	PLCB2	-1.183	SMAD7	-1.284	GADD45B	-0.845
GADD45B	-0.548	GSTM1	-1.214	GPX3	-1.416	TSPO	-0.966
CLU	-0.554	CLU	-1.22	NEDD9	-1.448	PDCD4	-1.077
PLCB2	-0.595	ERBB3	-1.263	GADD45B	-1.538	IRF1	-1.114
SOD1	-0.602	TNFRSF12A	-1.302	EMP1	-1.546	TGFB2	-1.158
HMOX1	-0.608	KRT18	-1.386	ATF3	-1.607	SAT1	-1.183
H1-O	-0.613	F2	-1.447	HMOX1	-1.646	LGALS3	-1.294
CDKN1A	-0.614	GADD45B	-1.643	HSPB1	-1.74	GPX3	-1.3
SQSTM1	-0.757	TAP1	-1.656	IER3	-1.798	MGMT	-1.31
SMAD7	-0.766	SMAD7	-1.773	GSN	-1.906	IFITM3	-1.375
MGMT	-0.77	HMOX1	-2.45	PLAT	-1.921	F2	-1.403
PDCD4	-0.798	GNA15	-2.72	ANXA1	-2.257	BTG2	-1.432
KRT18	-0.867	GPX1	-3.487	LGALS3	-2.371	IER3	-1.472
GPX1	-1.054			F2	-2.447	CDKN1A	-1.545
GSTM1	-1.09			GSTM1	-2.531	GSN	-1.557
F2	-1.102			GPX1	-3.228	CDK2	-1.599
TAP1	-1.153					GSTM1	-1.677
						ANXA1	-1.799
						PMAIP1	-2.077
						ISG20	-2.499
						DCN	-3.063

* RM score; rank metric score.

Video S1: 3D reconstruction of wild-type embryo at E8.5

Video S2: 3D reconstruction of *Sephs1*^{-/-} embryo at E8.5

Video S3: 3D reconstruction of wild-type embryo at E9.5

Video S4: 3D reconstruction of *Sephs1*^{-/-} embryo at E9.5