Supplementary material for Y. Gao et al. 2015. Effects of microgravity on DNA damage response in *Caenorhabditis elegans* during Shenzhou-8 spaceflight. International Journal of Radiation Biology 91;531–539.

Supplemental Table I. Real time quantitative PCR primer sequences.

Gene symbol	Relative expression		Primer sequences	Product size (bp)
	Microarray	qRT-PCR		
<i>gpd-2</i>	1.00	1.00	F:5'- ATGTTTCGTCGTCGGAGTCAA -3' R:5'- CAAGTGGAGCAAGGCAGTTAG -3'	97
H21P03.2	1.23	0.62	F:5'- AAGTAACTGGTGCGATGAATGG -3' R:5'- CGGGCGTCTTTGTACATATCG -3'	84
<i>exo-3</i>	1.49	0.32	F:5'- AAACCCTCGTCGTCTCCACA -3' R:5'- TCGGTCAGCAGCTTCTCCC -3'	245
<i>him-6</i>	1.24	1.25	F:5'- CTCAGAAGCCCAGGCACTAA -3' R:5'- TAAGGACCGGATAATCCAGAAC -3'	126
<i>air-2</i>	1.21 1.19	1.09 2.26	F:5'- ATGGGCAATCGGCGTTCT -3' R:5'- TTCCTTCACCTGTTCAAGCGTA -3'	202
<i>cdh-3</i>	1.48	2.80	F:5'- CGTCACTTTCAGCGACCTCC -3' R:5'- TTTCCCAGCAACCGTAATCC -3'	251
<i>dyf-2</i>	-1.06	-1.05	F:5'- GAGAAATCCGAGAATTACCAGA -3' R:5'- CCAGAATAATCGCACAATCCCT -3'	160
<i>sir-2.2</i>	-1.31	-0.96	F:5'- GTTCCAAATTCCCAGAGTGC -3' R:5'- CAGATAACACCGCCAACGAC -3'	162
<i>hda-4</i>	-1.13	-0.18	F:5'- AGATGTGATGCGAGACCCA -3' R:5'- ATTTCCGGTGTGACTTCATATC -3'	159
Y56A3A.33	-1.90	0.133	F:5'- TGCTCCAAACGATTCTACCG -3' R:5'- GGACTAACCACAACTCCCACA -3'	249

The list of genes and their forward and reverse primer sequences used for validating microarray data by qRT-PCR. F, Forward. R, Reverse. *gpd-2* was the endogenous control gene. Relative expression of microarray and qRT-PCR were transformed as log2.

Supplementary Table II. Genes involving in DNA repair pathways.

Cat. System	Repair pathway	Genes
Single-strand DNA lesions		
KEGG:cel03410 GO:0006284	Base excision repair (BER)	<i>ung-1</i> <i>exo-3</i> <i>pme-1</i> <i>pme-2</i> <i>pole-2</i> <i>crn-1</i> <i>lig-1</i> <i>nth-1</i> <i>apn-1</i> Y53F4B.3 R04F11.3 F33H2.5 F10C2.4 F12F6.7
KEGG:cel03420 GO:0006289	Nucleotide excision repair (NER)	<i>lig-4</i> <i>rbx-1</i> <i>csb-1</i> <i>xpa-1</i> <i>cul-4</i> <i>ddb-1</i> <i>xpc-1</i> <i>rad-23</i> <i>csb-1</i> <i>cdk-7</i> <i>mnat-1</i> <i>cyh-1</i> <i>rpa-1</i> <i>rpa-2</i> <i>rpa-4</i> <i>ercc-1</i> <i>rfc-1</i> <i>rfc-2</i> <i>rfc-3</i> <i>rfc-4</i> <i>pole-2</i> <i>lig-1</i> <i>rpb-9</i> <i>xpf-1</i> <i>brc-1</i> <i>fed-2</i> <i>mrt-2</i> <i>ubql-1</i> <i>hus-1</i> <i>xpg-1</i> <i>dog-1</i> <i>mrt-1</i> Y66D12A.15 Y50D7A.2 Y55B1A.2 R02D3.3 T16H12.4 Y73F8A.24 Y47D3A.29 Y37B11A.2 C47D12.8 F10C2.4 F12F6.7 R04F11.3 F33H2.5 Y53F4B.3 ZK1128.4 K07C5.3 F44B9.8
KEGG:cel03430 GO:0000710	Mismatch repair	<i>msh-2</i> <i>msh-6</i> <i>pms-2</i> <i>mlh-1</i> <i>msh-6</i> <i>msh-2</i> <i>rfc-1</i> <i>rfc-4</i> <i>rfc-2</i> <i>rfc-3</i> <i>exo-1</i> <i>rpa-1</i> <i>rpa-2</i> <i>rpa-4</i> <i>lig-1</i> <i>xpf-1</i> <i>msh-5</i> <i>him-14</i> F10C2.4 F12F6.7 R04F11.3 F44B9.8
Double-strands DNA breaks		
KEGG:cel03450 GO:0006303	Non-homologous end-joining (NHEJ)	<i>lig-4</i> <i>cku-70</i> <i>cku-80</i> <i>rad-50</i> <i>mre-11</i> <i>crn-1</i>
KEGG:cel03440 GO:0000724	Homologous recombination (HR)	<i>him-6</i> <i>atm-1</i> <i>atl-1</i> <i>rad-54</i> <i>rad-50</i> <i>mre-11</i> <i>rad-51</i> <i>top-3</i> <i>dna-2</i> <i>brc-2</i> <i>brc-1</i> <i>mre-11</i> <i>xpf-1</i> <i>rpa-1</i> <i>smc-6</i> <i>rpa-2</i> <i>smc-5</i> <i>rpa-4</i> <i>gen-1</i> <i>top-3</i> <i>mus-81</i> <i>dss-1</i> <i>rtel-1</i> Y116A8C.13 F10C2.4 F12F6.7 R04F11.3 C23H4.6 ZK1248.11
KEGG:cel03460	Fanconi anemia pathway (FA)	<i>polk-1</i> <i>him-6</i> <i>clk-2</i> <i>fnci-1</i> <i>rad-51</i> <i>dog-1</i> <i>fan-1</i> <i>mlh-1</i> <i>pms-2</i> <i>rev-1</i> <i>polh-1</i> <i>top-3</i> <i>rpa-1</i> <i>rpa-2</i> <i>rpa-4</i> <i>mus-81</i> <i>ercc-1</i> <i>slx-1</i> C47D12.8 F35H10.5 F35G12.4 Y37B11A.2
Others involving DNA repair GO:0006281	DNA repair	<i>gei-17</i> C11G6.2 <i>dpy-27</i> <i>pif-1</i> <i>lig-1</i> <i>rec-8</i> <i>ekl-4</i> <i>hpr-17</i> <i>hmg-3</i> <i>him-1</i> <i>his-12</i> <i>rfs-1</i> <i>hmg-4</i> <i>rps-3</i> <i>ubc-1</i> <i>gyd-1</i> <i>prp-19</i> <i>wrn-1</i> <i>smc-4</i> <i>brd-1</i> <i>snfc-5</i> <i>duc-1</i> <i>hpr-9</i> <i>spt-16</i> <i>pme-5</i> <i>chk-2</i> <i>xnp-1</i> H21P03.2 Y63D3A.4 C25F9.2 C27H6.9 T19C9.10 Y16E11A.2 M03C11.8 Y116F11A.1 Y46B2A.2 F59H6.5 Y73B6BL.14 F52G3.3 ZK973.1 C44C10.10 T27A3.7 C08H9.3 F23F1.5 F42A6.5 F33H12.6

Combined chart of GeneOntology (GO) and KEGG Payhways giving the genes of GO identifiers and pathways involving in DNA repair.

Supplementary Figure 1. Supplementary Sample images of experiment hardware in SIMBOX Project. SIMBOX Project of Shenzhou-8 space mission was Sino-German cooperated and culture hardware were developed by Germany. (A) Passive Experiment Unique Equipment. It is approximately $80 \times 40 \times 30$ mm and divided into four culture chambers (volume ratio, 2:2:1:1). Worms were cultured in the chambers during spaceflight. (B) Type I passive Experiment Container. It was vented and had no power and signal input/output demands. (C) Internal view of Biobox. Biobox was equipped with a centrifuge that could hold up to containers enduring 1 g centrifugal force, with additional maintained experiment containers around enduring microgravity during spaceflight. (D) The appearance of Biobox.

Supplementary Figure 2. Supplementary Hierarchical clusters of miRNA expression profiling. 23 miRNAs differentially expressed in response to different spaceflight conditions. Fold change values ($\log_2$) determined by microarray analysis are shown for SF environment and SR environment.