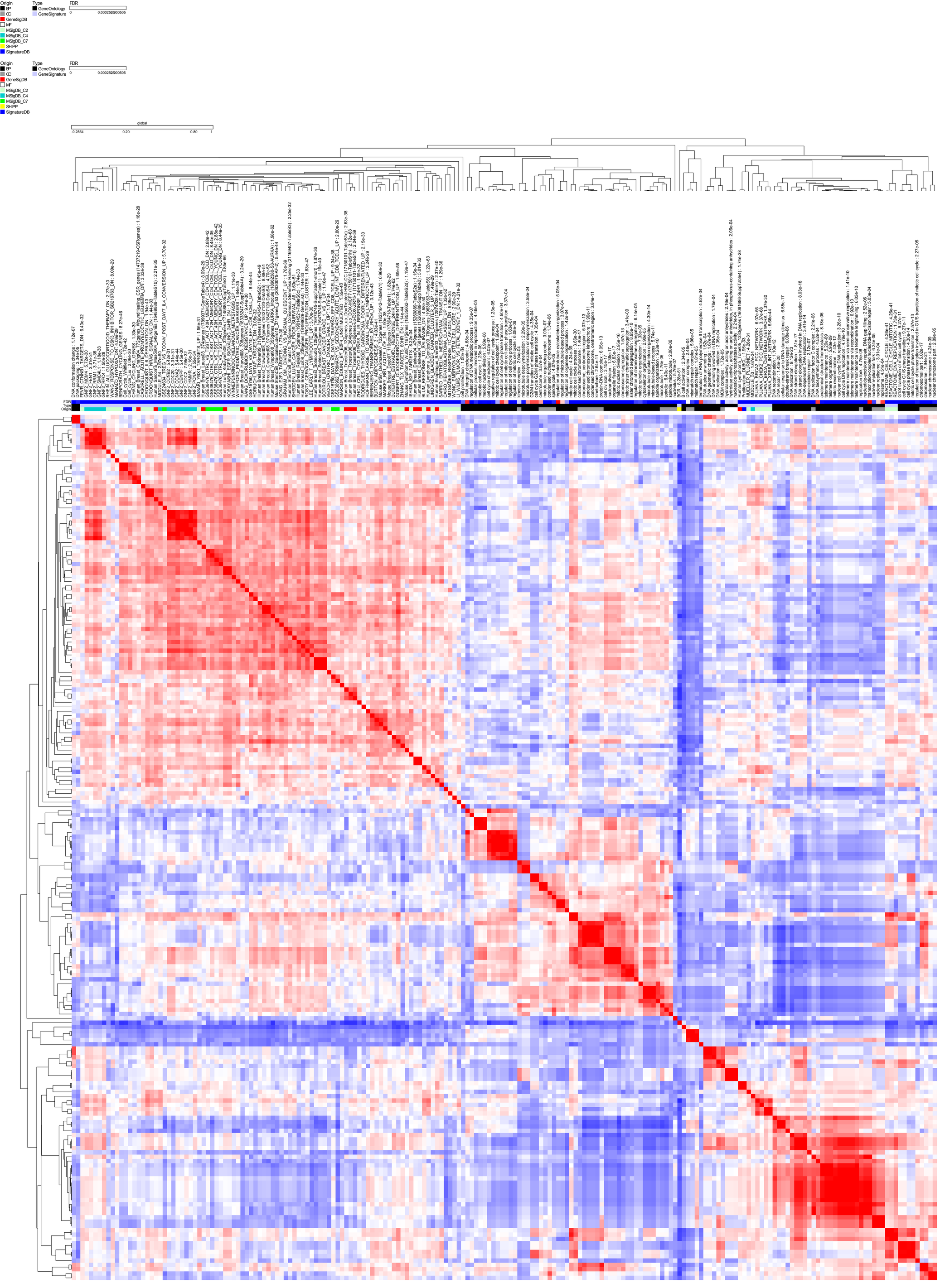
Origin
BP
CC
GeneSigDB
MF
MSigDB_C2
MSigDB_C4
MSigDB_C7
SHIPP
SignatureDB
Type
GeneOntology
GeneSignature
FDR
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0.000252
0.000505
global
-0.2564
0.20
0.80
1
Name
DNA conformation change : 1.12e-07
DNA packaging : 3.34e-05
FEVR_CTNNB1_TARGETS_DN : 6.43e-32
GNF2_MCM4 : 5.72e-30
GNF2_FEN1 : 3.31e-31
GNF2_RRM1 : 3.71e-36
GNF2_SMC4L1 : 1.18e-38
GNF2_RFC4 : 1.50e-28
RHEIN_ALL_GLUCOCORTICOID_THERAPY_DN : 2.27e-30
WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN : 8.09e-29
MANALO_HYPOXIA_DN : 4.09e-29
BENPORATH_CYCLING_GENES : 8.27e-46
Cell_cycle_Whitfield : 1.72e-42
Cell_cycle_Liu : 2.09e-30
CHANG_CYCLING_GENES : 1.33e-30
Human Breast_Chang04_772genes_WoundHealing_CSR_genes (14737219-CSRgenes) : 1.16e-28
CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_DN : 3.33e-38
CROONQUIST_IL6_DEPRIVATION_DN : 1.94e-43
CROONQUIST_NRAS_SIGNALING_DN : 1.44e-33
Human Sarcoma_Mason04_549genes (15489886-TableS1b) : 2.21e-35
MODULE_54 : 2.97e-50
GSE24634_TREG_VS_TCONV_POST_DAY7_IL4_CONVERSION_UP : 5.70e-32
GNF2_CCNB2 : 5.42e-31
GNF2_CDC20 : 3.31e-31
GNF2_CCNA2 : 5.44e-44
GNF2_CENPF : 5.45e-30
GNF2_CDC2 : 7.98e-32
GNF2_HMMR : 2.16e-31
GNF2_PCNA : 2.55e-34
BASAKI_YBX1_TARGETS_UP : 1.56e-31
Human Breast_Lauss08_374genes (17899371-GeneTable4) : 8.09e-29
GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_TCELL_OLD_DN : 2.88e-42
GSE36476_CTRL_VS_TSST_ACT_72H_MEMORY_CD4_TCELL_OLD_DN : 8.44e-35
GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_TCELL_YOUNG_DN : 2.88e-42
GSE36476_CTRL_VS_TSST_ACT_72H_MEMORY_CD4_TCELL_YOUNG_DN : 8.44e-35
Human Lung_Kobayashi06_320genes (17145885-SuppTable2) : 4.85e-66
KOBAYASHI_EGFR_SIGNALING_24HR_DN : 1.73e-67
WINNEPENNINCKX_MELANOMA_METASTASIS_UP : 1.11e-33
WHITEFORD_PEDIATRIC_CANCER_MARKERS : 1.64e-35
Human Breast_Harvell08_308genes (18338247-SuppTable4A) : 3.24e-29
KANG_DOXORUBICIN_RESISTANCE_UP : 9.44e-30
GSE15750_DAY6_VS_DAY10_EFF_CD8_TCELL_UP : 8.44e-44
HORIUCHI_WTAP_TARGETS_DN : 9.08e-32
Human Breast_Thorner09_217genes (19043454-TableS2) : 1.45e-49
Human Breast_Crawford08_187genes (18427120-DataS5) : 8.88e-51
Human Breast_Crawford08_971genes (18427120-DataS4) : 4.70e-52
Human Breast_Wirapati08_355genes_AURKA_Module (18662380-S3-AURKA) : 1.98e-62
Mouse StemCell_GarciaEscudero10_371genes_p53 (20630075-AF-2) : 5.44e-44
KONG_E2F3_TARGETS : 1.77e-36
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP : 1.76e-39
Human StemCell_Shats10_100genes_Consensus Stemness Ranking (21169407-TableS3) : 2.25e-32
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 : 3.63e-51
Human Breast_Reyal08_72genes (19014521-TableS6c) : 1.74e-33
Human Breast_Loi08_239genes (18498629-GeneList) : 1.44e-33
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER : 1.83e-47
LEE_EARLY_T_LYMPHOCYTE_UP : 3.70e-30
Human Breast_Sotiriou06_128genes (16478745-SuppTable1-short) : 1.87e-36
Human Breast_Sotiriou06_242genes (16478745-SuppTable1) : 1.19e-40
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP : 1.16e-47
VECCHI_GASTRIC_CANCER_EARLY_UP : 1.17e-34
GSE15750_DAY6_VS_DAY10_TRAF6KO_EFF_CD8_TCELL_UP : 9.34e-38
GSE30962_PRIMARY_VS_SECONDARY_ACUTE_LCMV_INF_CD8_TCELL_UP : 2.80e-29
MARSON_BOUND_BY_E2F4_UNSTIMULATED : 1.55e-40
Human Breast_Troester06_134genes_up_DoxTreated-HME-CC (17150101-TableS1c) : 2.63e-38
Human Breast_Troester06_364genes_up_DOX-MCF7 (17150101-TableS1h) : 2.12e-63
Human Breast_Troester06_436genes-up-DOX-ZR75-1 (17150101-TableS1l) : 2.04e-59
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR : 1.69e-32
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_UP : 2.15e-30
HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP : 3.24e-29
BERENJENO_TRANSFORMED_BY_RHOA_UP : 3.12e-43
BURTON_ADIPOGENESIS_3 : 4.03e-41
Mouse Brain_DeSmaele07_122genes (18231642-TableW1) : 6.96e-32
MARKEY_RB1_ACUTE_LOF_DN : 1.90e-38
Mouse Breast_Deeb07_119genes (17804718-Table1) : 1.82e-29
DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP : 5.74e-62
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP : 1.69e-58
ZHANG_TLX_TARGETS_60HR_DN : 1.14e-44
Mouse Lymphoma_Wu08_1167genes (18535662-TableS2d) : 1.19e-47
ISHIDA_E2F_TARGETS : 8.22e-34
Human Breast_Daikee04_479genes (15260889-TableS2a) : 1.15e-34
Human Breast_Daikee04_681genes (15260889-SuppTable2) : 5.01e-32
BLUM_RESPONSE_TO_SALIRASIB_DN : 4.58e-50
Human Lymphoma_Gentles09_780genes (19636063-TableS6) : 1.22e-63
LINDGREN_BLADDER_CANCER_CLUSTER_3_UP : 1.49e-29
Human Esophagus_Barrett03_104genes (12874028-Table1) : 2.37e-40
SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_UP : 1.29e-36
CAIRO_HEPATOBLASTOMA_CLASSES_UP : 1.32e-52
MITSIADES_RESPONSE_TO_APLIDIN_DN : 5.05e-34
WONG_EMBRYONIC_STEM_CELL_CORE : 2.90e-29
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN : 4.21e-32
cell proliferation : 1.00e-04
DNA integrity checkpoint : 4.68e-04
regulation of DNA metabolic process : 9.33e-07
cellular process involved in reproduction : 4.46e-05
meiotic cell cycle : 1.25e-06
meiotic nuclear division : 5.93e-06
cell cycle checkpoint : 6.02e-07
negative regulation of cell cycle process : 1.23e-05
mitotic cell cycle checkpoint : 1.66e-04
regulation of cell cycle phase transition : 4.50e-04
regulation of mitotic cell cycle phase transition : 3.37e-04
regulation of cell cycle process : 1.63e-07
regulation of mitotic cell cycle : 6.08e-06
kinesin complex : 2.04e-04
microtubule depolymerization : 2.29e-05
microtubule polymerization or depolymerization : 3.58e-04
G2/M transition of mitotic cell cycle : 4.35e-04
cell cycle G2/M phase transition : 4.35e-04
centrosome : 3.57e-04
microtubule organizing center : 3.09e-07
condensed nuclear chromosome : 1.34e-06
spindle pole : 4.07e-05
regulation of microtubule cytoskeleton organization : 5.05e-04
regulation of microtubule-based process : 3.07e-04
regulation of organelle organization : 1.42e-04
mitotic cell cycle : 4.24e-39
mitotic cell cycle process : 3.66e-30
condensed chromosome : 1.46e-17
chromosome, centromeric region : 5.07e-13
condensed chromosome kinetochore : 1.90e-11
condensed chromosome, centromeric region : 3.84e-11
kinetochore : 2.64e-11
protein-DNA complex : 6.05e-13
cell division : 3.15e-17
nuclear division : 1.38e-17
organelle fission : 6.83e-17
mitotic nuclear division : 2.95e-16
chromosome segregation : 1.57e-13
mitotic sister chromatid segregation : 3.41e-09
sister chromatid segregation : 8.95e-10
regulation of chromosome segregation : 6.14e-05
mitotic spindle organization : 7.33e-05
cytoskeleton organization : 2.90e-05
microtubule cytoskeleton organization : 4.30e-14
microtubule-based process : 5.74e-11
spindle organization : 9.28e-10
microtubule : 1.76e-06
spindle : 6.40e-11
spindle microtubule : 2.08e-06
nucleolus : 5.76e-07
BCR : 8.28e-61
B cell activation : 2.34e-05
DNA repair complex : 2.46e-04
mismatch repair complex : 5.96e-05
mismatch repair : 1.81e-05
termination of RNA polymerase II transcription : 4.52e-04
DNA duplex unwinding : 1.52e-04
DNA geometric change : 1.67e-04
DNA unwinding involved in DNA replication : 1.76e-04
DNA replication initiation : 2.35e-04
MCM complex : 1.72e-05
hydrolase activity, acting on acid anhydrides : 2.16e-04
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides : 2.06e-04
nucleoside-triphosphatase activity : 2.21e-04
Human Lymphoma_Tome05_1333genes (16081686-SuppTable4) : 1.74e-28
Proliferation_DLBCL : 1.96e-33
MUELLER_PLURINET : 4.26e-31
MODULE_53 : 1.67e-34
PUJANA_BRCA2_PCC_NETWORK : 6.07e-56
PUJANA_CHEK2_PCC_NETWORK : 3.37e-68
PUJANA_BRCA_CENTERED_NETWORK : 1.37e-30
PUJANA_XPRSS_INT_NETWORK : 5.66e-44
DNA recombination : 1.10e-12
DNA repair : 1.43e-20
cellular response to DNA damage stimulus : 6.55e-17
double-strand break repair : 6.08e-06
DNA replication : 9.12e-23
DNA strand elongation : 1.81e-17
DNA strand elongation involved in DNA replication : 8.03e-18
DNA-dependent DNA replication : 3.41e-14
base-excision repair : 2.12e-07
DNA replication factor C complex : 2.21e-06
DNA biosynthetic process : 4.52e-04
anatomical structure homeostasis : 8.18e-06
telomere maintenance : 5.20e-09
telomere organization : 5.98e-09
mitotic recombination : 7.43e-12
nuclear cell cycle DNA replication : 3.26e-10
cell cycle DNA replication : 4.79e-10
telomere maintenance via semi-conservative replication : 1.41e-10
telomere maintenance via recombination : 6.92e-10
telomere maintenance via telomere lengthening : 6.03e-10
replication fork : 4.75e-08
nucleotide-excision repair, DNA gap filling : 2.52e-06
transcription-coupled nucleotide-excision repair : 5.03e-04
nuclear replication fork : 6.34e-05
nuclear replisome : 3.01e-04
replisome : 4.51e-04
REACTOME_CELL_CYCLE : 4.26e-41
REACTOME_CELL_CYCLE_MITOTIC : 4.26e-41
REACTOME_DNA_REPLICATION : 1.73e-31
G1/S transition of mitotic cell cycle : 9.27e-11
cell cycle G1/S phase transition : 9.27e-11
cell cycle phase transition : 4.30e-14
mitotic cell cycle phase transition : 2.57e-13
regulation of transcription involved in G1/S transition of mitotic cell cycle : 2.27e-05
chromosomal part : 5.02e-17
chromosome : 7.94e-21
nuclear chromosome : 4.24e-09
nuclear chromosome part : 2.89e-05