Supplemental file 1

Ferroptosis-associated molecular classification characterized by distinct tumor microenvironment profiles in colorectal cancer

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Figure S1. The entire analytical process of the study.
Figure S2. Ferroptosis-associated molecular classification in colorectal cancer, related to Figure 1

(A) Heatmap representation of NMF clustering for ferroptosis-associated genes in TCGA cohort with cluster numbers from 2 to 6. (B) Kaplan-Meier curves for overall survival of three NMF clusters in TCGA and for relapse-free survival of three clusters in meta-GEO cohort. The P value was calculated by the log-rank test. (C) Heatmap shows expression
of ferroptosis-associated genes in tumor and normal samples.

Figure S3. Clinical characteristics and biological molecular changes underlying three clusters in CRC, related to Figure 2

(A) Heatmap shows molecular characteristics of three clusters in meta-GEO cohort. (B) Quantification of gene signatures related to CMS
subtypes among three clusters of TCGA and meta-GEO cohort. The statistical difference of three clusters was compared through the Kruskal-Wallis H test. *P < 0.05; **P < 0.01; ***P < 0.001. (C) Heatmap shows correlation between ferroptosis score and gene signatures.

Figure S4. Single-cell transcriptome profiling of CRC cells based on
**ferroptosis-associated molecular classification, related to Figure 3**

(A) t-SNE visualization of 2,212 tumor epithelial cells from KUL single-cell cohort (top panel). Cells are colored according to clusters. Dot plot for the score of gene signatures associated with CRC cellular phenotype and responses to therapy in each cell type. Color represents the mean score in each cell cluster, and size indicates the fraction of cells expressing gene score (bottom panel). (B) Barplot shows the proportion of different molecular characteristics in CRC tumor cells. Bars are colored according to clusters. (C) t-SNE visualization of MHC-I (HLA-A, HLA-B), MHC-II (HLA-DRA) molecular expression and the score of ferroptosis-associated genes. (D) GO analysis of differential expressed genes between FAC1-like and FAC2-like CRC tumor cells. (E) Tumor purity and stromal score of three ferroptosis-associated clusters in TCGA and meta-GEO cohort. The statistical difference of three clusters was compared through the Kruskal-Wallis H test. *P < 0.05; **P < 0.01; ***P < 0.001. The difference of two clusters was compared through the wilcox test. *P < 0.05; **P < 0.01; ***P < 0.001.
Figure S5. Distinct tumor microenvironment infiltration in three tumor clusters, related to Figure 4
(A) Heatmap shows the ssGSEA score of 31 cell subtypes in three ferroptosis-associated clusters in meta-GEO cohort. (B-D) ssGSEA score of corresponding signatures among three clusters in TCGA and meta-GEO cohort. The statistical difference of three clusters was compared through the Kruskal-Wallis H test. *P < 0.05; **P < 0.01; ***P < 0.001.
Figure S6. Identifying specific ferroptosis-associated genes correlated with immune activation, related to Figure 5

(A) CNV frequency of immune-activated Fersig in CRC tumors. (B) Univariate analysis of immune-activated Fersig in CRC patients. (C) Expression of immune-activated Fersig among three clusters. The statistical difference of three clusters was compared through the Kruskal-Wallis H test. *P < 0.05; **P < 0.01; ***P < 0.001. (D) Correlation between immune-activated Fersig and different gene signatures, including stromal cells, T cells, cytotoxic CD8+ T, myofibroblasts, EMT, TGF-β, MHC-I and MHC-II.
Figure S7. Identifying specific ferroptosis-associated genes correlated with stromal activation, related to Figure 6

(A) CNV frequency of stromal-activated Fersig in CRC tumors. (B) Univariate analysis of stromal-activated Fersig in CRC patients. (C) Expression of stromal-activated Fersig among three clusters. The statistical difference of three clusters was compared through the Kruskal-Wallis H test. *P < 0.05; **P < 0.01; ***P < 0.001. (D) Correlation between stromal-activated Fersig and different gene
signatures, including stromal cells, T cells, cytotoxic CD8+ T, myofibroblasts, EMT, TGF-β, MHC-I and MHC-II.

**Figure S8.** Examining expression of immune-activated and stromal-activated Fersig at single-cell level, related to Figure 7

(A) t-SNE visualization of 6,470 single cells of CRC in KUL cohort. Cells are colored according to cell types. (B) t-SNE visualization of score of immune-activated Fersig and stromal-activated Fersig. (C) Violin plots shows the score of immune-activated Fersig and stromal-activated Fersig
among different cell subtypes.

Figure S9. Ferroptosis phenotype-related DEGs in colorectal cancer, related to Figure 8
(A) Venn diagram shows shared genes between DEGs among three ferroptosis-associated clusters. (B) NMF rank survey was shown. The optimal number of clusters: k=3. (C) GO analyses of genes A-B. (D-E) ssGSEA score of corresponding signatures among three gene clusters.

**Figure S10. Ferroptosis phenotype-related DEGs in colorectal cancer, related to Figure 8**

(A) Kaplan-Meier curves for overall survival of three gene clusters in meta-GEO cohort. The P value was calculated by the log-rank test. (B) ssGSEA score of signatures of TME cell types, EMT and TGF-β among three gene clusters in TCGA. The statistical difference of three clusters was compared through the Kruskal-Wallis H test. *P < 0.05; **P < 0.01; ***P < 0.001. The difference of two clusters was compared through the
wilcox test. *P < 0.05; **P < 0.01; ***P < 0.001. (C-D) ssGSEA score of signatures of cytotoxic CD8+ T cells, immune-activated and stromal-activated ferroptosis-associated genes among three gene clusters. The statistical difference of three clusters was compared through the Kruskal-Wallis H test. *P < 0.05; **P < 0.01; ***P < 0.001. The difference of two clusters was compared through the wilcox test. *P < 0.05; **P < 0.01; ***P < 0.001.
**Figure S11. Further construction of Fersig score, related to Figure 9**

(A) Kaplan-Meier curves for relapse-free survival of meta-GEO. The high and low groups were divided by the median value of the PCA score of Fersig. The P value was calculated by the log-rank test. (B) Barplots show the proportion of molecular characteristics between high and low groups of Fersig. (C) ssGSEA score of signatures of TME cell types, EMT, TGF-β and other stromal-related signatures between high and low groups in meta-GEO cohort. The difference of two clusters was compared through the wilcox test. *P < 0.05; **P < 0.01; ***P < 0.001. (D) ssGSEA score of immune-activated and stromal-activated Fersig between high and low groups in meta-GEO cohort. The difference of two clusters was compared through the wilcox test. *P < 0.05; **P < 0.01; ***P < 0.001. (E) ssGSEA score of 31 cell subtypes between high and low groups in meta-GEO cohort. The difference of two clusters was compared through the wilcox test. *P < 0.05; **P < 0.01; ***P < 0.001.
Figure S12. Expression of immune-activated and stromal-activated Fersig with significant prognosis in the Liu et al. cohort.

(A-B) Barplots show the expression of immune-activated and stromal-activated Fersig with significant prognosis in the Liu et al. cohort. The difference of two clusters was compared through the wilcoxon test. *P < 0.05; **P < 0.01; ***P < 0.001.
B. Supplementary Tables

**Supplementary Table S1.** The description of patients with bulk RNA expression data, including clinical characteristics and NMF clusters.

*Please see separated Excel spreadsheet file.*

**Supplementary Table S2.** The basic information for single-cell datasets.

*Please see separated Excel spreadsheet file.*

**Supplementary Table S3.** The biological information of ferroptosis-associated genes.

*Please see separated Excel spreadsheet file.*

**Supplementary Table S4.** The cell type annotation of single cells.

*Please see separated Excel spreadsheet file.*

**Supplementary Table S5.** Gene clusters in TCGA and meta-GEO cohorts, and genes A-C.

*Please see separated Excel spreadsheet file.*

**Supplementary Table S6.** The Fersig score of each database.

*Please see separated Excel spreadsheet file.*
| samples          | MSI status | Metastasis status | Stage   |
|------------------|------------|-------------------|---------|
| TCGA.3L.AA1B.01  | MSS        | M0                | Stage I |
| TCGA.4N.A93T.01  | MSS        | M0                | Stage III|
| TCGA.4T.AA8H.01  | Indeterminate | MX              | Stage II|
| TCGA.5M.AA1E.01  | MSS        | M0                | Stage II|
| TCGA.A6.5656.01  | NA         | M0                | Stage I |
| TCGA.A6.5659.01  | NA         | M0                | Stage I |
| TCGA.A6.5660.01  | MSS        | M0                | Stage III|
| TCGA.A6.5662.01  | MSS        | M1                | Stage IV|
| TCGA.A6.5666.01  | MSI-L      | M0                | Stage II|
| TCGA.A6.5667.01  | MSS        | MX                | Stage III|
| TCGA.A6.6140.01  | MSS        | M0                | Stage II|
| TCGA.A6.6648.01  | MSS        | M1a               | Stage IV|
| TCGA.A6.6652.01  | MSS        | M1                | Stage IV|
| TCGA.A6.A56B.01  | MSS        | M0                | Stage III|
| TCGA.AA.3496.01  | MSI-L      | M0                | Stage II|
| TCGA.AA.3509.01  | MSS        | M0                | Stage II|
| TCGA.AA.3511.01  | MSS        | M0                | Stage II|
| TCGA.AA.3660.01  | MSS        | M0                | Stage II|
| TCGA.AA.3662.01  | MSS        | M1                | Stage IV|
| TCGA.AA.3675.01  | MSS        | M0                | Stage II|
| TCGA.AA.A01X.01  | MSS        | M0                | Stage III|
| TCGA.AD.6888.01  | MSS        | M0                | Stage III|
| TCGA.AD.6890.01  | MSS        | MX                | NA      |
| TCGA.AD.6965.01  | MSS        | M0                | Stage III|
| TCGA.AD.A5EK.01  | MSS        | MX                | Stage I |
| TCGA.AF.3911.01  | MSI-L      | MX                | Stage III|
| TCGA.AF.4110.01  | MSS        | MX                | Stage IV|
| TCGA.AF.6136.01  | MSS        | MX                | Stage III|
| TCGA.AF.6672.01  | MSS        | MX                | Stage IV|
| TCGA.AF.A56L.01  | MSS        | M0                | Stage III|
| TCGA.AF.A56N.01  | MSS        | M0                | Stage II|
| TCGA.AG.3732.01  | MSS        | M0                | Stage I |
| TCGA.AH.6544.01  | MSS        | M1                | NA      |
| TCGA.AH.6549.01  | MSI-L      | MX                | NA      |
| TCGA.AH.6643.01  | MSS        | M0                | Stage III|
| TCGA.AH.6897.01  | MSI-L      | M0                | Stage I |
| TCGA.AH.6903.01  | MSS        | M0                | Stage III|
| TCGA.AM.5820.01  | MSS        | M1                | Stage IV|
| TCGA.AY.A54L.01  | MSI-L      | M0                | Stage I |
| TCGA.AY.A69D.01  | MSI-L      | M0                | Stage II|
| TCGA.AY.A71X.01  | MSS        | M0                | Stage I |
| TCGA.AY.A8YK.01  | MSS        | M1                | Stage IV|
| TCGA.AZ.4684.01  | MSI-L      | M1                | Stage IV|
| TCGA.CA.5255.01  | MSS        | M0                | Stage II|
| TCGA.CA.5256.01  | MSS        | M0                | Stage II|
| TCGA.CA.5797.01  | MSS        | M0                | Stage II|
| TCGA.CA.6715.01  | MSS        | M0                | Stage III|
| TCGA.CA.6716.01  | MSS        | M0                | Stage II|
| TCGA.CI.6619.01  | MSS        | M1                | Stage IV|
| TCGA.CI.6620.01  | MSS        | M1                | Stage IV|
| TCGA.CI.6622.01  | MSS        | M0                | Stage II|
| TCGA.CK.5912.01  | MSS        | MX                | Stage I |
| TCGA.CK.5915.01  | MSS        | MX                | Stage I |
| TCGA.CL.4957.01  | MSS        | M0                | NA      |
| TCGA.CL.5917.01  | MSS        | MX                | Stage III|
| TCGA.CL.5918.01  | MSS        | MX                | Stage II|
TCGA.EI.6513.01  MSS  M0  Stage III
TCGA.EI.6514.01  MSS  M0  Stage II
TCGA.EI.6814.01  MSS  M0  Stage III
TCGA.EI.6833.01  MSS  M0  Stage II
TCGA.EI.7002.01  MSI-L  M1  Stage IV
TCGA.F4.6463.01  MSS  M0  Stage II
TCGA.F4.6806.01  MSS  M0  Stage I
TCGA.F4.6808.01  MSS  M0  Stage I
TCGA.F4.6854.01  MSS  M0  Stage II
TCGA.F5.6571.01  MSI-L  M0  Stage II
TCGA.F5.6814.01  MSS  M0  Stage II
TCGA.F5.6861.01  MSS  M0  Stage II
TCGA.F5.6863.01  MSI-L  M0  Stage III
TCGA.F5.6864.01  MSI-L  M0  Stage III
TCGA.F5.6865.01  MSI-L  M1  Stage III
TCGA.F5.6866.01  MSI-L  M1  Stage IV
TCGA.G4.6303.01  MSI-L  M1  Stage IV
TCGA.G4.6304.01  MSI-H  M0  Stage II
TCGA.G4.6307.01  MSS  M0  Stage III
TCGA.G4.6310.01  MSS  M0  Stage III
TCGA.G4.6315.01  MSS  M1  Stage IV
TCGA.G4.6317.01  MSI-L  MX  Stage III
TCGA.G5.6235.01  MSS  MX  Stage III
TCGA.G5.6641.01  MSS  MX  Stage III
TCGA.NH.A6GC.01  MSS  MX  Stage III
TCGA.NH.A8F7.01  Indeterminate  MX  Stage II
TCGA.NH.A8F8.01  MSS  M1  Stage IV
TCGA.QG.A5YV.01  MSS  MX  Stage III
TCGA.QG.A5YX.01  MSI-L  MX  Stage II
TCGA.QG.A5Z1.01  MSI-L  MX  Stage III
TCGA.QL.A97D.01  MSS  MX  Stage I
TCGA.RU.A8FL.01  MSS  MX  Stage III
TCGA.SS.A7HO.01  MSS  M0  Stage II
TCGA.T9.A92H.01  MSS  M0  Stage II
| OS (days) | Dead | Sample type | NMF clusters | CMS subtypes |
|-----------|------|-------------|--------------|--------------|
| 475       | 0    | Tumor       | CC1          | CMS2         |
| 146       | 0    | Tumor       | CC1          | NA           |
| 385       | 0    | Tumor       | CC1          | CMS3         |
| 1200      | 0    | Tumor       | CC1          | CMS2         |
| 1001      | 0    | Tumor       | CC1          | CMS2         |
| 926       | 0    | Tumor       | CC1          | CMS2         |
| 888       | 0    | Tumor       | CC1          | CMS2         |
| 718       | 0    | Tumor       | CC1          | CMS2         |
| 995       | 0    | Tumor       | CC1          | CMS2         |
| 887       | 0    | Tumor       | CC1          | CMS4         |
| 734       | 0    | Tumor       | CC1          | CMS2         |
| 766       | 0    | Tumor       | CC1          | CMS2         |
| 751       | 0    | Tumor       | CC1          | CMS2         |
| 1595      | 1    | Tumor       | CC1          | CMS4         |
| 31        | 0    | Tumor       | CC1          | CMS4         |
| 1915      | 0    | Tumor       | CC1          | CMS2         |
| 212       | 0    | Tumor       | CC1          | CMS4         |
| 2375      | 0    | Tumor       | CC1          | CMS2         |
| 184       | 0    | Tumor       | CC1          | CMS2         |
| 1431      | 0    | Tumor       | CC1          | CMS3         |
| 791       | 0    | Tumor       | CC1          | CMS2         |
| 155       | 1    | Tumor       | CC1          | CMS2         |
| 746       | 0    | Tumor       | CC1          | CMS2         |
| 805       | 0    | Tumor       | CC1          | CMS2         |
| 500       | 0    | Tumor       | CC1          | NA           |
| 1148      | 0    | Tumor       | CC1          | CMS2         |
| 912       | 0    | Tumor       | CC1          | CMS4         |
| 741       | 0    | Tumor       | CC1          | CMS3         |
| 748       | 0    | Tumor       | CC1          | CMS3         |
| 2007      | 0    | Tumor       | CC1          | CMS2         |
| 360       | 0    | Tumor       | CC1          | CMS2         |
| 1003      | 0    | Tumor       | CC1          | CMS3         |
| 1173      | 0    | Tumor       | CC1          | CMS3         |
| 532       | 0    | Tumor       | CC1          | CMS4         |
| 21        | 1    | Tumor       | CC1          | CMS4         |
| 804       | 0    | Tumor       | CC1          | NA           |
| 592       | 0    | Tumor       | CC1          | CMS3         |
| 14        | 0    | Tumor       | CC1          | NA           |
| 525       | 0    | Tumor       | CC1          | CMS3         |
| 543       | 0    | Tumor       | CC1          | CMS3         |
| 588       | 0    | Tumor       | CC1          | CMS3         |
| 573       | 0    | Tumor       | CC1          | CMS2         |
| 1977      | 0    | Tumor       | CC1          | CMS4         |
| 376       | 0    | Tumor       | CC1          | CMS1         |
| 379       | 0    | Tumor       | CC1          | CMS2         |
| 383       | 0    | Tumor       | CC1          | CMS2         |
| 383       | 0    | Tumor       | CC1          | CMS2         |
| 371       | 0    | Tumor       | CC1          | CMS2         |
| 184       | 0    | Tumor       | CC1          | CMS4         |
| 1009      | 0    | Tumor       | CC1          | NA           |
| 1362      | 0    | Tumor       | CC1          | CMS2         |
| 1466      | 1    | Tumor       | CC1          | NA           |
| 0         | 0    | Tumor       | CC1          | CMS2         |
| 425       | 1    | Tumor       | CC1          | CMS2         |
| 2376      | 0    | Tumor       | CC1          | CMS4         |
| 218       | 0    | Tumor       | CC1          | CMS2         |
|     | Tumor | CC   |     |
|-----|--------|------|-----|
| 761 | 0      | CC1  | NA  |
| 670 | 0      | CC1  | CMS4|
| 457 | 0      | CC1  | CMS2|
| 518 | 0      | CC1  | CMS4|
| 457 | 0      | CC1  | CMS2|
| 427 | 0      | CC1  | NA  |
| 883 | 0      | CC1  | CMS2|
| 488 | 0      | CC1  | CMS4|
| 669 | 0      | CC1  | CMS2|
| 457 | 0      | CC1  | CMS2|
| 335 | 0      | CC1  | CMS3|
| 337 | 0      | CC1  | CMS2|
| 335 | 0      | CC1  | CMS3|
| 456 | 1      | CC1  | CMS2|
| 1706| 0      | CC1  | NA  |
| 1701| 0      | CC1  | CMS2|
| 555 | 0      | CC1  | CMS2|
| 775 | 0      | CC1  | CMS2|
| 521 | 0      | CC1  | CMS2|
| 308 | 0      | CC1  | CMS4|
| 378 | 0      | CC1  | CMS4|
| 435 | 0      | CC1  | CMS4|
| 275 | 0      | CC1  | CMS4|
| 408 | 0      | CC1  | CMS4|
| 346 | 0      | CC1  | CMS4|
| 639 | 0      | CC1  | NA  |
| 762 | 0      | CC1  | CMS2|
| 943 | 0      | CC1  | CMS2|
| 365 | 0      | CC1  | CMS2|
| 425 | 0      | CC1  | NA  |
| 1581| 0      | CC1  | CMS2|
| 790 | 0      | CC1  | CMS4|
| 762 | 0      | CC1  | NA  |
| 762 | 0      | CC1  | CMS2|
| 3974| 0      | CC1  | CMS2|
| 2821| 1      | CC1  | NA  |
| 1518| 1      | CC1  | CMS3|
| 405 | 1      | CC1  | NA  |
| 383 | 1      | CC1  | NA  |
| 4270| 0      | CC1  | NA  |
| 4000| 0      | CC1  | NA  |
| 4233| 0      | CC1  | CMS2|
| 427 | 1      | CC1  | NA  |
| 805 | 1      | CC1  | CMS2|
| 2475| 1      | CC1  | NA  |
| 3648| 0      | CC1  | NA  |
| 1094| 1      | CC1  | CMS2|
| 1849| 1      | CC1  | CMS3|
| 3561| 0      | CC1  | NA  |
| 3846| 0      | CC1  | CMS2|
| 1741| 1      | CC1  | CMS2|
| 734 | 1      | CC1  | CMS4|
| 992 | 1      | CC1  | NA  |
| 106 | 0      | CC1  | CMS2|
| 127 | 0      | CC1  | CMS4|
| 636 | 0      | CC1  | CMS3|
| 517 | 0      | CC1  | CMS4|
| 538 | 0      | CC1  | CMS1|
|   | Tumor | CC | CMS |   |
|---|-------|----|-----|---|
| 497 | 0 Tumor | CC1 | CMS2 |   |
| 496 | 0 Tumor | CC1 | CMS4 |   |
| 499 | 0 Tumor | CC1 | CMS2 |   |
| 350 | 0 Tumor | CC1 | CMS2 |   |
| 364 | 0 Tumor | CC1 | CMS2 |   |
| 1087 | 0 Tumor | CC1 | CMS4 |   |
| 1260 | 0 Tumor | CC1 | CMS3 |   |
| 1024 | 0 Tumor | CC1 | CMS2 |   |
| 16 | 0 Tumor | CC1 | CMS2 |   |
| 1288 | 0 Tumor | CC1 | CMS4 |   |
| 1131 | 0 Tumor | CC1 | CMS1 |   |
| 1160 | 0 Tumor | CC1 | CMS2 |   |
| 23 | 1 Tumor | CC1 | CMS4 |   |
| 14 | 0 Tumor | CC1 | CMS4 |   |
| 1882 | 1 Tumor | CC1 | CMS4 |   |
| 1631 | 0 Tumor | CC1 | NA |   |
| 1674 | 0 Tumor | CC1 | CMS2 |   |
| 1935 | 0 Tumor | CC1 | CMS4 |   |
| 1883 | 0 Tumor | CC1 | CMS2 |   |
| 1095 | 0 Tumor | CC1 | CMS2 |   |
| 1696 | 0 Tumor | CC1 | CMS2 |   |
| 804 | 0 Tumor | CC1 | CMS3 |   |
| 553 | 0 Tumor | CC1 | CMS2 |   |
| 182 | 1 Tumor | CC1 | CMS1 |   |
| 389 | 0 Tumor | CC1 | CMS3 |   |
| 543 | 0 Tumor | CC1 | CMS2 |   |
| 167 | 1 Tumor | CC1 | CMS4 |   |
| 1301 | 0 Tumor | CC1 | CMS2 |   |
| 1003 | 0 Tumor | CC1 | CMS3 |   |
| 202 | 1 Tumor | CC1 | CMS4 |   |
| 666 | 0 Tumor | CC1 | NA |   |
| 1177 | 0 Tumor | CC1 | NA |   |
| 1829 | 0 Tumor | CC1 | NA |   |
| 362 | 0 Tumor | CC1 | CMS2 |   |
| samples     | Stage | RFS (days) | RFS, event | Sample type |
|-------------|-------|------------|------------|-------------|
| GSM358341   | stage I | 109.2      | 0          | Tumor       |
| GSM358342   | stage I | 435.9      | 1          | Tumor       |
| GSM358343   | stage I | 494.1      | 0          | Tumor       |
| GSM358344   | stage I | 592.5      | 0          | Tumor       |
| GSM358345   | stage I | 600.6      | 0          | Tumor       |
| GSM358346   | stage I | 718.8      | 0          | Tumor       |
| GSM358347   | stage I | 810.6      | 1          | Tumor       |
| GSM358348   | stage I | 868.8      | 0          | Tumor       |
| GSM358349   | stage I | 1313.7     | 0          | Tumor       |
| GSM358350   | stage I | 1567.2     | 0          | Tumor       |
| GSM358351   | stage I | 1653.9     | 0          | Tumor       |
| GSM358352   | stage I | 1733.7     | 0          | Tumor       |
| GSM358353   | stage I | 1785.9     | 0          | Tumor       |
| GSM358354   | stage I | 1923       | 0          | Tumor       |
| GSM358355   | stage I | 1931.1     | 0          | Tumor       |
| GSM358356   | stage I | 1976.4     | 0          | Tumor       |
| GSM358357   | stage I | 2015.7     | 0          | Tumor       |
| GSM358358   | stage I | 2034.6     | 0          | Tumor       |
| GSM358359   | stage I | 2055.3     | 0          | Tumor       |
| GSM358360   | stage I | 2282.1     | 0          | Tumor       |
| GSM358361   | stage I | 2468.7     | 0          | Tumor       |
| GSM358362   | stage I | 2508       | 0          | Tumor       |
| GSM358363   | stage I | 2511.9     | 0          | Tumor       |
| GSM358364   | stage I | 2523.9     | 0          | Tumor       |
| GSM358365   | stage I | 3276.3     | 0          | Tumor       |
| GSM358366   | stage I | 3576.3     | 0          | Tumor       |
| GSM358367   | stage I | 3681.6     | 0          | Tumor       |
| GSM358368   | stage I | 4276.5     | 0          | Tumor       |
| GSM358370   | stage I | 684        | 0          | Tumor       |
| GSM358371   | stage I | 432        | 0          | Tumor       |
| GSM358373   | stage I | 1632       | 0          | Tumor       |
| GSM358374   | stage I | 1935       | 0          | Tumor       |
| GSM358375   | stage I | 54         | 0          | Tumor       |
| GSM358376   | stage I | 1260       | 0          | Tumor       |
| GSM358377   | stage I | 1695       | 0          | Tumor       |
| GSM358378   | stage I | 1089       | 0          | Tumor       |
| GSM358380   | stage I | 1326       | 0          | Tumor       |
| GSM358381   | stage I | 1563       | 0          | Tumor       |
| GSM358382   | stage I | 900        | 0          | Tumor       |
| GSM358383   | stage I | 1317       | 0          | Tumor       |
| GSM358384   | stage I | 2424       | 0          | Tumor       |
| GSM358385   | stage II| 67.8       | 0          | Tumor       |
| GSM358386   | stage II| 180.3      | 1          | Tumor       |
| GSM358387   | stage II| 298.8      | 1          | Tumor       |
| GSM358388   | stage II| 423.9      | 1          | Tumor       |
| GSM358389   | stage II| 427.8      | 1          | Tumor       |
| GSM358390   | stage II| 451.5      | 0          | Tumor       |
| GSM358391   | stage II| 471.3      | 0          | Tumor       |
| GSM358392   | stage II| 538.5      | 0          | Tumor       |
| GSM358393   | stage II| 545.4      | 0          | Tumor       |
| GSM358394   | stage II| 580.8      | 1          | Tumor       |
| GSM358395   | stage II| 660.6      | 0          | Tumor       |
| GSM358396   | stage II| 671.4      | 1          | Tumor       |
| GSM358397   | stage II| 671.4      | 1          | Tumor       |
| GSM358398   | stage II| 725.7      | 0          | Tumor       |
| GSM358399   | stage II| 756.3      | 1          | Tumor       |
| Sample ID   | Stage   | Value  | Tumor | Notes |
|------------|---------|--------|-------|-------|
| GSM358400  | stage II | 757.2  | 0     | Tumor |
| GSM358401  | stage II | 768.3  | 0     | Tumor |
| GSM358402  | stage II | 795.9  | 0     | Tumor |
| GSM358403  | stage II | 799.8  | 0     | Tumor |
| GSM358404  | stage II | 804.6  | 0     | Tumor |
| GSM358405  | stage II | 814.5  | 0     | Tumor |
| GSM358406  | stage II | 829.2  | 1     | Tumor |
| GSM358407  | stage II | 858.9  | 0     | Tumor |
| GSM358408  | stage II | 865.8  | 0     | Tumor |
| GSM358409  | stage II | 876.6  | 0     | Tumor |
| GSM358410  | stage II | 931.8  | 0     | Tumor |
| GSM358411  | stage II | 996    | 0     | Tumor |
| GSM358412  | stage II | 1010.7 | 0     | Tumor |
| GSM358413  | stage II | 1077   | 0     | Tumor |
| GSM358414  | stage II | 1102.5 | 0     | Tumor |
| GSM358415  | stage II | 1119.3 | 1     | Tumor |
| GSM358416  | stage II | 1119.3 | 0     | Tumor |
| GSM358417  | stage II | 1177.5 | 0     | Tumor |
| GSM358418  | stage II | 1349.1 | 0     | Tumor |
| GSM358419  | stage II | 1401.3 | 0     | Tumor |
| GSM358420  | stage II | 1435.8 | 0     | Tumor |
| GSM358421  | stage II | 1495.2 | 0     | Tumor |
| GSM358422  | stage II | 1564.2 | 0     | Tumor |
| GSM358423  | stage II | 1575   | 0     | Tumor |
| GSM358424  | stage II | 1659.9 | 0     | Tumor |
| GSM358425  | stage II | 1677.6 | 0     | Tumor |
| GSM358426  | stage II | 1740.6 | 0     | Tumor |
| GSM358427  | stage II | 1788   | 0     | Tumor |
| GSM358428  | stage II | 1798.8 | 0     | Tumor |
| GSM358429  | stage II | 1897.5 | 0     | Tumor |
| GSM358430  | stage II | 1945.8 | 0     | Tumor |
| GSM358431  | stage II | 2119.5 | 0     | Tumor |
| GSM358432  | stage II | 2281.2 | 0     | Tumor |
| GSM358433  | stage II | 2373.9 | 0     | Tumor |
| GSM358434  | stage II | 2407.5 | 0     | Tumor |
| GSM358435  | stage II | 2558.4 | 0     | Tumor |
| GSM358436  | stage II | 2592.9 | 0     | Tumor |
| GSM358437  | stage II | 2669.7 | 0     | Tumor |
| GSM358438  | stage II | 2809.8 | 1     | Tumor |
| GSM358439  | stage II | 3208.2 | 0     | Tumor |
| GSM358440  | stage II | 3323.7 | 0     | Tumor |
| GSM358441  | stage II | 3557.4 | 0     | Tumor |
| GSM358442  | stage II | 363    | 0     | Tumor |
| GSM358443  | stage II | 888    | 0     | Tumor |
| GSM358444  | stage II | 1110   | 0     | Tumor |
| GSM358445  | stage II | 855    | 0     | Tumor |
| GSM358446  | stage II | 1689   | 0     | Tumor |
| GSM358447  | stage II | 1422   | 0     | Tumor |
| GSM358448  | stage II | 405    | 0     | Tumor |
| GSM358449  | stage II | 1704   | 0     | Tumor |
| GSM358450  | stage II | 1584   | 0     | Tumor |
| GSM358451  | stage II | 1359   | 0     | Tumor |
| GSM358452  | stage II | 1671   | 0     | Tumor |
| GSM358453  | stage II | 1200   | 0     | Tumor |
| GSM358454  | stage II | 426    | 1     | Tumor |
| GSM358455  | stage II | 123    | 0     | Tumor |
| GSM358456  | stage II | 1785   | 0     | Tumor |
| GSM358457  | stage II | 1287   | 0     | Tumor |
| GSM358458 | stage II | 978 | 1 Tumor |
| GSM358459 | stage II | 939 | 0 Tumor |
| GSM358460 | stage II | 1017 | 0 Tumor |
| GSM358461 | stage II | 1431 | 0 Tumor |
| GSM358462 | stage II | 1146 | 0 Tumor |
| GSM358463 | stage II | 1332 | 0 Tumor |
| GSM358464 | stage II | 1344 | 0 Tumor |
| GSM358465 | stage II | 1710 | 0 Tumor |
| GSM358466 | stage II | 1212 | 0 Tumor |
| GSM358467 | stage II | 156 | 0 Tumor |
| GSM358468 | stage II | 348 | 0 Tumor |
| GSM358469 | stage II | 1752 | 0 Tumor |
| GSM358470 | stage II | 1086 | 0 Tumor |
| GSM358471 | stage II | 1362 | 0 Tumor |
| GSM358472 | stage II | 1527 | 0 Tumor |
| GSM358473 | stage II | 1677 | 0 Tumor |
| GSM358474 | stage II | 429 | 1 Tumor |
| GSM358475 | stage II | 1014 | 0 Tumor |
| GSM358476 | stage II | 1140 | 0 Tumor |
| GSM358477 | stage II | 2226 | 0 Tumor |
| GSM358478 | stage II | 2547 | 0 Tumor |
| GSM358479 | stage III | 27.6 | 0 Tumor |
| GSM358480 | stage III | 47.1 | 1 Tumor |
| GSM358481 | stage III | 99.6 | 1 Tumor |
| GSM358482 | stage III | 127.2 | 0 Tumor |
| GSM358483 | stage III | 156.6 | 0 Tumor |
| GSM358484 | stage III | 160.5 | 1 Tumor |
| GSM358485 | stage III | 246.3 | 1 Tumor |
| GSM358486 | stage III | 249.3 | 1 Tumor |
| GSM358487 | stage III | 257.4 | 1 Tumor |
| GSM358488 | stage III | 286.8 | 1 Tumor |
| GSM358489 | stage III | 357 | 1 Tumor |
| GSM358490 | stage III | 441.6 | 1 Tumor |
| GSM358491 | stage III | 482.1 | 1 Tumor |
| GSM358492 | stage III | 567.9 | 1 Tumor |
| GSM358493 | stage III | 568.8 | 0 Tumor |
| GSM358494 | stage III | 599.4 | 0 Tumor |
| GSM358495 | stage III | 613.2 | 0 Tumor |
| GSM358496 | stage III | 631.2 | 1 Tumor |
| GSM358497 | stage III | 638.1 | 1 Tumor |
| GSM358498 | stage III | 667.5 | 0 Tumor |
| GSM358499 | stage III | 700.2 | 1 Tumor |
| GSM358500 | stage III | 723.9 | 1 Tumor |
| GSM358501 | stage III | 745.5 | 1 Tumor |
| GSM358502 | stage III | 787.8 | 0 Tumor |
| GSM358503 | stage III | 807.6 | 0 Tumor |
| GSM358504 | stage III | 827.4 | 1 Tumor |
| GSM358505 | stage III | 832.2 | 1 Tumor |
| GSM358506 | stage III | 881.7 | 1 Tumor |
| GSM358507 | stage III | 940.8 | 0 Tumor |
| GSM358508 | stage III | 957.6 | 0 Tumor |
| GSM358509 | stage III | 1025.7 | 1 Tumor |
| GSM358510 | stage III | 1107.6 | 1 Tumor |
| GSM358511 | stage III | 1107.6 | 0 Tumor |
| GSM358512 | stage III | 1142.1 | 0 Tumor |
| GSM358513 | stage III | 1161.6 | 0 Tumor |
| GSM358514 | stage III | 1231.8 | 1 Tumor |
| GSM358515 | stage III | 1340.1 | 0 Tumor |
| GSM358516 | stage III | 1342.2 | 0 | Tumor |
| GSM358517 | stage III | 1434   | 0 | Tumor |
| GSM358518 | stage III | 1473.3 | 0 | Tumor |
| GSM358519 | stage III | 1512.9 | 0 | Tumor |
| GSM358520 | stage III | 1517.7 | 0 | Tumor |
| GSM358521 | stage III | 1585.8 | 0 | Tumor |
| GSM358522 | stage III | 1647   | 0 | Tumor |
| GSM358523 | stage III | 1753.5 | 0 | Tumor |
| GSM358524 | stage III | 1772.1 | 0 | Tumor |
| GSM358525 | stage III | 1780.2 | 0 | Tumor |
| GSM358526 | stage III | 1929.9 | 0 | Tumor |
| GSM358527 | stage III | 1947.9 | 0 | Tumor |
| GSM358528 | stage III | 1966.5 | 0 | Tumor |
| GSM358529 | stage III | 2162.7 | 0 | Tumor |
| GSM358530 | stage III | 2230.8 | 0 | Tumor |
| GSM358531 | stage III | 2235.9 | 0 | Tumor |
| GSM358532 | stage III | 2383.8 | 1 | Tumor |
| GSM358533 | stage III | 2568.3 | 0 | Tumor |
| GSM358534 | stage III | 2575.2 | 1 | Tumor |
| GSM358535 | stage III | 2688.6 | 0 | Tumor |
| GSM358536 | stage III | 2852.1 | 0 | Tumor |
| GSM358537 | stage III | 2985.3 | 0 | Tumor |
| GSM358538 | stage III | 3155.1 | 0 | Tumor |
| GSM358539 | stage III | 3369.9 | 0 | Tumor |
| GSM358540 | stage III | 927    | 0 | Tumor |
| GSM358541 | stage III | 720    | 0 | Tumor |
| GSM358542 | stage III | 948    | 0 | Tumor |
| GSM358543 | stage III | 1488   | 0 | Tumor |
| GSM358544 | stage III | 456    | 1 | Tumor |
| GSM358545 | stage III | 726    | 0 | Tumor |
| GSM358546 | stage III | 2073   | 0 | Tumor |
| GSM358547 | stage III | 2043   | 0 | Tumor |
| GSM358548 | stage III | 309    | 1 | Tumor |
| GSM358549 | stage III | 1776   | 0 | Tumor |
| GSM358550 | stage III | 1842   | 0 | Tumor |
| GSM358551 | stage III | 450    | 0 | Tumor |
| GSM358552 | stage III | 1734   | 0 | Tumor |
| GSM358553 | stage III | 564    | 0 | Tumor |
| GSM358554 | stage III | 135    | 1 | Tumor |
| GSM358555 | stage III | 1143   | 1 | Tumor |
| GSM358556 | stage III | 1212   | 0 | Tumor |
| GSM358557 | stage III | 171    | 1 | Tumor |
| GSM358558 | stage III | 306    | 0 | Tumor |
| GSM358559 | stage III | 2541   | 0 | Tumor |
| GSM358560 | stage III | 507    | 0 | Tumor |
| GSM358561 | stage III | 285    | 1 | Tumor |
| GSM358562 | stage III | 2061   | 0 | Tumor |
| GSM358563 | stage III | 1785   | 0 | Tumor |
| GSM358564 | stage III | 561    | 0 | Tumor |
| GSM358565 | stage III | 2124   | 0 | Tumor |
| GSM358566 | stage III | 133.2  | 1 | Tumor |
| GSM358567 | stage III | 1200   | 1 | Tumor |
| GSM358568 | stage III | 2187   | 1 | Tumor |
| GSM358569 | stage III | 540    | 1 | Tumor |
| NMF clusters | CC2 | CC3 | CC1 | CC3 | CC1 | CC3 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 | CC1 |
|--------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| samples   | Stage   | RFS (days) | RFS.event | Sample type |
|-----------|---------|------------|-----------|-------------|
| GSM971957 | stage IV| 0          | 1         | Tumor       |
| GSM971958 | stage IV| 0          | 1         | Tumor       |
| GSM971959 | stage II| 120        | 1         | Tumor       |
| GSM971960 | stage I | 2220       | 0         | Tumor       |
| GSM971961 | stage IV| 30         | 1         | Tumor       |
| GSM971962 | stage III| 2190      | 0        | Tumor       |
| GSM971963 | stage II| 510        | 1         | Tumor       |
| GSM971964 | stage III| 1050      | 0        | Tumor       |
| GSM971965 | stage II| 990        | 0         | Tumor       |
| GSM971966 | stage III| 1890      | 0        | Tumor       |
| GSM971968 | stage II| 2790       | 1         | Tumor       |
| GSM971969 | stage I | 1890       | 0         | Tumor       |
| GSM971970 | stage I | 2580       | 0         | Tumor       |
| GSM971971 | stage IV| 1950       | 0         | Tumor       |
| GSM971972 | stage I | 2250       | 0         | Tumor       |
| GSM971973 | stage II| 1380       | 0         | Tumor       |
| GSM971974 | stage IV| 1680       | 0         | Tumor       |
| GSM971975 | stage II| 1380       | 0         | Tumor       |
| GSM971976 | stage II| 1080       | 0         | Tumor       |
| GSM971977 | stage III| 1470      | 0        | Tumor       |
| GSM971978 | stage I | 3270       | 0         | Tumor       |
| GSM971979 | stage II| 1590       | 0         | Tumor       |
| GSM971980 | stage III| 1770      | 0        | Tumor       |
| GSM971981 | stage II| 1440       | 0         | Tumor       |
| GSM971982 | stage III| 1260      | 0        | Tumor       |
| GSM971983 | stage III| 2610      | 0        | Tumor       |
| GSM971984 | stage II| 150        | 1         | Tumor       |
| GSM971985 | stage 0 | 210        | 0         | Tumor       |
| GSM971986 | stage II| 2040       | 0         | Tumor       |
| GSM971987 | stage II| 2040       | 0         | Tumor       |
| GSM971988 | stage IV| 450        | 1         | Tumor       |
| GSM971989 | stage I | 480        | 1         | Tumor       |
| GSM971990 | stage I | 360        | 0         | Tumor       |
| GSM971991 | stage II| 1650       | 0         | Tumor       |
| GSM971992 | stage II| 600        | 0         | Tumor       |
| GSM971993 | stage II| 1680       | 0         | Tumor       |
| GSM971994 | stage II| 1290       | 0         | Tumor       |
| GSM971995 | stage II| 750        | 0         | Tumor       |
| GSM971996 | stage III| 2280     | 0        | Tumor       |
| GSM971997 | stage III| 2670      | 0        | Tumor       |
| GSM971998 | stage III| 540       | 1         | Tumor       |
| GSM971999 | stage III| 30        | 0         | Tumor       |
| GSM972000 | stage III| 270       | 1         | Tumor       |
| GSM972001 | stage III| 2190      | 0        | Tumor       |
| GSM972002 | stage III| 750       | 1         | Tumor       |
| GSM972003 | stage IV| 0          | 1         | Tumor       |
| GSM972004 | stage IV| 2670       | 0         | Tumor       |
| GSM972005 | stage IV| 0          | 1         | Tumor       |
| GSM972006 | stage IV| 0          | 1         | Tumor       |
| GSM972007 | stage IV| 60         | 0         | Tumor       |
| GSM972008 | stage IV| 60         | 1         | Tumor       |
| GSM972009 | stage IV| 0          | 1         | Tumor       |
| GSM972010 | stage IV| 300        | 1         | Tumor       |
| GSM972011 | stage IV| 540        | 1         | Tumor       |
| GSM972012 | stage IV| 3030       | 0         | Tumor       |
| GSM972013 | stage IV| 1290       | 0         | Tumor       |
| GSM972014 | stage IV | 0 | 1 Tumor |
| GSM972015 | stage II | 2730 | 0 Tumor |
| GSM972016 | stage II | 420 | 1 Tumor |
| GSM972017 | stage III | 1290 | 0 Tumor |
| GSM972018 | stage III | 3510 | 0 Tumor |
| GSM972019 | stage III | 630 | 1 Tumor |
| GSM972020 | stage III | 270 | 1 Tumor |
| GSM972021 | stage III | 150 | 1 Tumor |
| GSM972022 | stage III | 2460 | 0 Tumor |
| GSM972023 | stage III | 180 | 1 Tumor |
| GSM972024 | stage III | 1110 | 1 Tumor |
| GSM972025 | stage III | 1590 | 0 Tumor |
| GSM972026 | stage III | 960 | 1 Tumor |
| GSM972027 | stage III | 2820 | 0 Tumor |
| GSM972028 | stage III | 2340 | 0 Tumor |
| GSM972029 | stage III | 1080 | 0 Tumor |
| GSM972030 | stage III | 1560 | 0 Tumor |
| GSM972031 | stage II | 1650 | 0 Tumor |
| GSM972032 | stage II | 1800 | 0 Tumor |
| GSM972033 | stage II | 1500 | 0 Tumor |
| GSM972034 | stage II | 1500 | 0 Tumor |
| GSM972035 | stage II | 1170 | 0 Tumor |
| GSM972036 | stage II | 1500 | 0 Tumor |
| GSM972037 | stage II | 990 | 0 Tumor |
| GSM972038 | stage II | 30 | 0 Tumor |
| GSM972039 | stage IV | 0 | 1 Tumor |
| GSM972040 | stage II | 1890 | 0 Tumor |
| GSM972041 | stage II | 1650 | 0 Tumor |
| GSM972042 | stage II | 1530 | 0 Tumor |
| GSM972043 | stage IV | 0 | 1 Tumor |
| GSM972044 | stage II | 1260 | 0 Tumor |
| GSM972045 | stage IV | 0 | 1 Tumor |
| GSM972046 | stage II | 630 | 1 Tumor |
| GSM972047 | stage II | 990 | 0 Tumor |
| GSM972048 | stage IV | 0 | 1 Tumor |
| GSM972049 | stage II | 780 | 0 Tumor |
| GSM972050 | stage II | 570 | 0 Tumor |
| GSM972051 | stage IV | 0 | 1 Tumor |
| GSM972052 | stage II | 450 | 0 Tumor |
| GSM972053 | stage II | 870 | 0 Tumor |
| GSM972054 | stage II | 780 | 0 Tumor |
| GSM972055 | stage II | 2790 | 0 Tumor |
| GSM972056 | stage II | 2760 | 0 Tumor |
| GSM972057 | stage II | 780 | 0 Tumor |
| GSM972058 | stage II | 1800 | 0 Tumor |
| GSM972059 | stage II | 1770 | 0 Tumor |
| GSM972060 | stage II | 2460 | 0 Tumor |
| GSM972061 | stage II | 1290 | 0 Tumor |
| GSM972062 | stage II | 0 | 1 Tumor |
| GSM972063 | stage II | 2100 | 0 Tumor |
| GSM972064 | stage IV | 0 | 1 Tumor |
| GSM972065 | stage II | 1380 | 0 Tumor |
| GSM972066 | stage IV | 0 | 1 Tumor |
| GSM972067 | stage II | 5490 | 0 Tumor |
| GSM972068 | stage II | 90 | 1 Tumor |
| GSM972069 | stage II | 6030 | 0 Tumor |
| GSM972070 | stage II | 2040 | 0 Tumor |
| GSM972071 | stage II | 5490 | 0 Tumor |
| Sample ID   | Stage   | Value | Tumor |
|-------------|---------|-------|-------|
| GSM972072   | stage II | 5160  | 0 Tumor |
| GSM972073   | stage II | 4890  | 0 Tumor |
| GSM972074   | stage II | 30    | 1 Tumor |
| GSM972075   | stage II | 1320  | 0 Tumor |
| GSM972076   | stage II | 4590  | 0 Tumor |
| GSM972077   | stage II | 780   | 1 Tumor |
| GSM972078   | stage II | 1620  | 1 Tumor |
| GSM972079   | stage II | 5040  | 0 Tumor |
| GSM972080   | stage II | 1590  | 1 Tumor |
| GSM972081   | stage II | 780   | 0 Tumor |
| GSM972082   | stage II | 3570  | 1 Tumor |
| GSM972083   | stage II | 3810  | 0 Tumor |
| GSM972084   | stage II | 3870  | 0 Tumor |
| GSM972085   | stage II | 2910  | 0 Tumor |
| GSM972086   | stage II | 1290  | 0 Tumor |
| GSM972087   | stage II | 240   | 1 Tumor |
| GSM972088   | stage II | 2370  | 0 Tumor |
| GSM972089   | stage II | 2610  | 0 Tumor |
| GSM972090   | stage II | 2070  | 0 Tumor |
| GSM972091   | stage II | 1350  | 1 Tumor |
| GSM972092   | stage II | 1410  | 0 Tumor |
| GSM972093   | stage II | 2220  | 0 Tumor |
| GSM972094   | stage II | 1830  | 0 Tumor |
| GSM972095   | stage II | 2010  | 0 Tumor |
| GSM972096   | stage III| 90    | 1 Tumor |
| GSM972097   | stage III| 360   | 1 Tumor |
| GSM972098   | stage III| 450   | 0 Tumor |
| GSM972099   | stage III| 450   | 0 Tumor |
| GSM972100   | stage III| 750   | 0 Tumor |
| GSM972101   | stage III| 630   | 1 Tumor |
| GSM972102   | stage III| 1380  | 0 Tumor |
| GSM972103   | stage III| 840   | 1 Tumor |
| GSM972104   | stage III| 1230  | 0 Tumor |
| GSM972105   | stage III| 960   | 0 Tumor |
| GSM972106   | stage III| 270   | 1 Tumor |
| GSM972107   | stage III| 1800  | 0 Tumor |
| GSM972108   | stage III| 3090  | 0 Tumor |
| GSM972109   | stage III| 1080  | 0 Tumor |
| GSM972110   | stage III| 120   | 1 Tumor |
| GSM972111   | stage III| 390   | 1 Tumor |
| GSM972112   | stage III| 960   | 0 Tumor |
| GSM972113   | stage III| 540   | 1 Tumor |
| GSM972114   | stage III| 1380  | 0 Tumor |
| GSM972115   | stage III| 330   | 1 Tumor |
| GSM972116   | stage III| 60    | 1 Tumor |
| GSM972117   | stage III| 330   | 1 Tumor |
| GSM972118   | stage III| 570   | 1 Tumor |
| GSM972119   | stage III| 750   | 1 Tumor |
| GSM972120   | stage III| 1080  | 0 Tumor |
| GSM972121   | stage III| 1050  | 0 Tumor |
| GSM972122   | stage III| 570   | 1 Tumor |
| GSM972123   | stage II | 2130  | 0 Tumor |
| GSM972124   | stage II | 2250  | 0 Tumor |
| GSM972125   | stage II | 420   | 1 Tumor |
| GSM972126   | stage II | 1890  | 0 Tumor |
| GSM972127   | stage II | 2550  | 0 Tumor |
| GSM972128   | stage II | 2790  | 0 Tumor |
| GSM972129   | stage II | 330   | 0 Tumor |
| Sample ID   | Stage  | Value  | Tumor Type |
|-------------|--------|--------|------------|
| GSM972130   | stage II | 1650   | 0 Tumor    |
| GSM972131   | stage II | 2580   | 0 Tumor    |
| GSM972132   | stage II | 1830   | 0 Tumor    |
| GSM972133   | stage III| 810    | 1 Tumor    |
| GSM972134   | stage III| 210    | 1 Tumor    |
| GSM972135   | stage II | 120    | 1 Tumor    |
| GSM972136   | stage III| 1830   | 1 Tumor    |
| GSM972137   | stage II | 270    | 1 Tumor    |
| GSM972138   | stage II | 1350   | 1 Tumor    |
| GSM972139   | stage III| 1140   | 1 Tumor    |
| GSM972140   | stage II | 1680   | 1 Tumor    |
| GSM972141   | stage III| 450    | 1 Tumor    |
| GSM972142   | stage III| 60     | 1 Tumor    |
| GSM972143   | stage II | 4620   | 0 Tumor    |
| GSM972144   | stage II | 3630   | 0 Tumor    |
| GSM972145   | stage III| 4050   | 0 Tumor    |
| GSM972146   | stage III| 1980   | 0 Tumor    |
| GSM972147   | stage II | 4200   | 0 Tumor    |
| GSM972148   | stage III| 3810   | 0 Tumor    |
| GSM972149   | stage II | 3960   | 0 Tumor    |
| GSM972150   | stage III| 3270   | 0 Tumor    |
| GSM972151   | stage III| 2310   | 0 Tumor    |
| GSM972152   | stage II | 1680   | 0 Tumor    |
| GSM972153   | stage II | 1980   | 0 Tumor    |
| GSM972154   | stage III| 90     | 1 Tumor    |
| GSM972155   | stage III| 180    | 1 Tumor    |
| GSM972156   | stage III| 3360   | 0 Tumor    |
| GSM972157   | stage III| 3540   | 0 Tumor    |
| GSM972158   | stage III| 3600   | 0 Tumor    |
| GSM972159   | stage III| 2790   | 0 Tumor    |
| GSM972160   | stage II | 1170   | 1 Tumor    |
| GSM972161   | stage II | 270    | 1 Tumor    |
| GSM972162   | stage III| 2310   | 0 Tumor    |
| GSM972163   | stage II | 1230   | 0 Tumor    |
| GSM972164   | stage III| 90     | 1 Tumor    |
| GSM972165   | stage II | 1080   | 1 Tumor    |
| GSM972166   | stage III| 90     | 1 Tumor    |
| GSM972167   | stage II | 1080   | 1 Tumor    |
| GSM972168   | stage III| 120    | 1 Tumor    |
| GSM972169   | stage II | 4920   | 0 Tumor    |
| GSM972170   | stage III| 2190   | 0 Tumor    |
| GSM972171   | stage III| 3900   | 0 Tumor    |
| GSM972172   | stage II | 120    | 1 Tumor    |
| GSM972173   | stage II | 450    | 1 Tumor    |
| GSM972174   | stage III| 2910   | 0 Tumor    |
| GSM972175   | stage III| 840    | 1 Tumor    |
| GSM972176   | stage III| 1050   | 1 Tumor    |
| GSM972177   | stage II | 600    | 1 Tumor    |
| GSM972178   | stage III| 630    | 1 Tumor    |
| GSM972179   | stage II | 510    | 1 Tumor    |
| GSM972180   | stage II | 570    | 1 Tumor    |
| GSM972181   | stage III| 390    | 1 Tumor    |
| GSM972182   | stage II | 690    | 1 Tumor    |
| GSM972183   | stage III| 330    | 1 Tumor    |
| GSM972184   | stage II | 120    | 1 Tumor    |
| GSM972185   | stage III| 660    | 1 Tumor    |
| GSM972186   | stage III| 420    | 1 Tumor    |
| GSM972187   | stage II | 270    | 1 Tumor    |
| GSM972188 | stage III | 330 | 1 Tumor |
| GSM972189 | stage III | 5760 | 0 Tumor |
| GSM972190 | stage II  | 3240 | 0 Tumor |
| GSM972191 | stage III | 3660 | 0 Tumor |
| GSM972192 | stage II  | 4740 | 0 Tumor |
| GSM972193 | stage III | 2190 | 0 Tumor |
| GSM972194 | stage III | 2490 | 0 Tumor |
| GSM972195 | stage II  | 3600 | 0 Tumor |
| GSM972196 | stage II  | 2190 | 0 Tumor |
| GSM972197 | stage II  | 1500 | 0 Tumor |
| GSM972198 | stage III | 1710 | 0 Tumor |
| GSM972199 | stage III | 1980 | 0 Tumor |
| GSM972200 | stage II  | 1620 | 0 Tumor |
| GSM972201 | stage III | 2010 | 0 Tumor |
| GSM972202 | stage III | 1590 | 0 Tumor |
| GSM972203 | stage III | 1620 | 0 Tumor |
| GSM972204 | stage II  | 120  | 1 Tumor |
| GSM972205 | stage II  | 210  | 1 Tumor |
| GSM972206 | stage II  | 0    | 1 Tumor |
| GSM972207 | stage III | 1020 | 1 Tumor |
| GSM972208 | stage IV  | 0    | 1 Tumor |
| GSM972209 | stage IV  | 0    | 1 Tumor |
| GSM972210 | stage IV  | 0    | 1 Tumor |
| GSM972211 | stage III | 1710 | 0 Tumor |
| GSM972212 | stage IV  | 0    | 1 Tumor |
| GSM972213 | stage IV  | 0    | 1 Tumor |
| GSM972214 | stage IV  | 0    | 1 Tumor |
| GSM972215 | stage III | 1410 | 0 Tumor |
| GSM972216 | stage IV  | 0    | 1 Tumor |
| GSM972217 | stage IV  | 0    | 1 Tumor |
| GSM972218 | stage IV  | 0    | 1 Tumor |
| GSM972219 | stage IV  | 0    | 1 Tumor |
| GSM972220 | stage III | 30   | 0 Tumor |
| GSM972221 | stage II  | 1950 | 0 Tumor |
| GSM972222 | stage II  | 1710 | 0 Tumor |
| GSM972223 | stage II  | 990  | 0 Tumor |
| GSM972224 | stage III | 600  | 1 Tumor |
| GSM972225 | stage II  | 1110 | 0 Tumor |
| GSM972226 | stage II  | 600  | 0 Tumor |
| GSM972227 | stage IV  | 600  | 0 Tumor |
| GSM972228 | stage II  | 30   | 0 Tumor |
| GSM972229 | stage II  | 0    | 0 Tumor |
| GSM972230 | stage III | 810  | 0 Tumor |
| GSM972231 | stage IV  | 420  | 0 Tumor |
| GSM972232 | stage IV  | 630  | 0 Tumor |
| GSM972233 | stage II  | 450  | 0 Tumor |
| GSM972234 | stage IV  | 300  | 0 Tumor |
| GSM972235 | stage III | 210  | 0 Tumor |
| GSM972236 | stage IV  | 360  | 0 Tumor |
| GSM972237 | stage I   | 750  | 0 Tumor |
| GSM972238 | stage III | 570  | 0 Tumor |
| GSM972239 | stage II  | 420  | 0 Tumor |
| GSM972240 | stage IV  | 420  | 0 Tumor |
| GSM972241 | stage II  | 510  | 0 Tumor |
| GSM972242 | stage I   | 510  | 0 Tumor |
| GSM972243 | stage II  | 60   | 0 Tumor |
| GSM972244 | stage I   | 420  | 0 Tumor |
| GSM972245 | stage IV  | 0    | 0 Tumor |
| GSM972246 | stage III | 0 | 0 | Tumor |
| GSM972247 | stage II | 180 | 0 | Tumor |
| GSM972248 | stage II | 420 | 0 | Tumor |
| GSM972249 | stage I | 420 | 0 | Tumor |
| GSM972250 | stage III | 360 | 0 | Tumor |
| GSM972251 | stage IV | 210 | 0 | Tumor |
| GSM972252 | stage IV | 480 | 0 | Tumor |
| GSM972253 | stage IV | 480 | 0 | Tumor |
| GSM972254 | stage IV | 270 | 1 | Tumor |
| GSM972255 | stage II | 150 | 0 | Tumor |
| GSM972256 | stage IV | 390 | 1 | Tumor |
| GSM972257 | stage II | 270 | 1 | Tumor |
| GSM972258 | stage II | 0 | 0 | Tumor |
| GSM972259 | stage II | 870 | 0 | Tumor |
| GSM972260 | stage IV | 390 | 0 | Tumor |
| GSM972261 | stage III | 210 | 0 | Tumor |
| GSM972262 | stage II | 150 | 0 | Tumor |
| GSM972263 | stage III | 2280 | 0 | Tumor |
| GSM972264 | stage II | 2190 | 0 | Tumor |
| GSM972265 | stage III | 1800 | 0 | Tumor |
| GSM972266 | stage IV | 600 | 0 | Tumor |
| GSM972267 | stage II | 2010 | 0 | Tumor |
| GSM972268 | stage III | 1440 | 0 | Tumor |
| GSM972269 | stage I | 2370 | 0 | Tumor |
| GSM972270 | stage II | 1950 | 0 | Tumor |
| GSM972271 | stage III | 390 | 1 | Tumor |
| GSM972272 | stage IV | 450 | 0 | Tumor |
| GSM972273 | stage 0 | 480 | 0 | Tumor |
| GSM972274 | stage III | 1710 | 0 | Tumor |
| GSM972275 | stage II | 90 | 1 | Tumor |
| GSM972276 | stage III | 1290 | 0 | Tumor |
| GSM972277 | stage II | 1530 | 0 | Tumor |
| GSM972278 | stage I | 1350 | 0 | Tumor |
| GSM972279 | stage III | 1560 | 0 | Tumor |
| GSM972280 | stage II | 1380 | 0 | Tumor |
| GSM972281 | stage I | 1680 | 0 | Tumor |
| GSM972282 | stage I | 1530 | 0 | Tumor |
| GSM972283 | stage II | 1530 | 0 | Tumor |
| GSM972284 | stage IV | 810 | 0 | Tumor |
| GSM972285 | stage II | 60 | 0 | Tumor |
| GSM972286 | stage II | 1110 | 0 | Tumor |
| GSM972287 | stage II | 1290 | 0 | Tumor |
| GSM972288 | stage IV | 1050 | 0 | Tumor |
| GSM972289 | stage IV | 510 | 0 | Tumor |
| GSM972290 | stage I | 1170 | 0 | Tumor |
| GSM972291 | stage III | 300 | 1 | Tumor |
| GSM972292 | stage II | 750 | 0 | Tumor |
| GSM972293 | stage I | 1500 | 0 | Tumor |
| GSM972294 | stage II | 750 | 0 | Tumor |
| GSM972295 | stage III | 1830 | 0 | Tumor |
| GSM972296 | stage 0 | 660 | 0 | Tumor |
| GSM972297 | stage I | 1380 | 0 | Tumor |
| GSM972298 | stage II | 270 | 0 | Tumor |
| GSM972299 | stage IV | 1230 | 0 | Tumor |
| GSM972300 | stage 0 | 1230 | 0 | Tumor |
| GSM972301 | stage III | 3150 | 0 | Tumor |
| GSM972302 | stage III | 810 | 0 | Tumor |
| GSM972303 | stage I | 570 | 0 | Tumor |
| GSM972304 | stage II | 900  | 0 Tumor |
| GSM972305 | stage III | 930  | 0 Tumor |
| GSM972306 | stage II | 1680 | 0 Tumor |
| GSM972307 | stage II | 2460 | 0 Tumor |
| GSM972308 | stage III | 2760 | 0 Tumor |
| GSM972309 | stage II | 2850 | 0 Tumor |
| GSM972310 | stage III | 750  | 0 Tumor |
| GSM972311 | stage II | 3180 | 0 Tumor |
| GSM972312 | stage II | 2910 | 0 Tumor |
| GSM972313 | stage I | 2730 | 0 Tumor |
| GSM972314 | stage III | 1380 | 0 Tumor |
| GSM972315 | stage I | 2520 | 0 Tumor |
| GSM972316 | stage II | 2490 | 0 Tumor |
| GSM972317 | stage II | 150  | 1 Tumor |
| GSM972318 | stage II | 1080 | 0 Tumor |
| GSM972319 | stage II | 2340 | 0 Tumor |
| GSM972320 | stage III | 300  | 1 Tumor |
| GSM972321 | stage III | 270  | 0 Tumor |
| GSM972322 | stage II | 1980 | 1 Tumor |
| GSM972323 | stage III | 2400 | 0 Tumor |
| GSM972324 | stage II | 2460 | 0 Tumor |
| GSM972325 | stage III | 1590 | 1 Tumor |
| GSM972326 | stage II | 2550 | 0 Tumor |
| GSM972327 | stage II | 2490 | 0 Tumor |
| GSM972328 | stage III | 2340 | 1 Tumor |
| GSM972329 | stage II | 2340 | 0 Tumor |
| GSM972330 | stage II | 2580 | 0 Tumor |
| GSM972331 | stage II | 2250 | 0 Tumor |
| GSM972332 | stage II | 2610 | 0 Tumor |
| GSM972333 | stage II | 2400 | 0 Tumor |
| GSM972334 | stage III | 2310 | 0 Tumor |
| GSM972335 | stage I | 1380 | 0 Tumor |
| GSM972336 | stage III | 1500 | 0 Tumor |
| GSM972337 | stage III | 1230 | 0 Tumor |
| GSM972338 | stage II | 2220 | 0 Tumor |
| GSM972339 | stage III | 2280 | 0 Tumor |
| GSM972340 | stage II | 1440 | 1 Tumor |
| GSM972341 | stage III | 2070 | 0 Tumor |
| GSM972342 | stage I | 840  | 0 Tumor |
| GSM972343 | stage II | 1560 | 0 Tumor |
| GSM972344 | stage II | 2250 | 0 Tumor |
| GSM972345 | stage III | 1230 | 1 Tumor |
| GSM972346 | stage III | 2160 | 0 Tumor |
| GSM972347 | stage II | 210  | 0 Tumor |
| GSM972348 | stage II | 1860 | 0 Tumor |
| GSM972349 | stage III | 150  | 0 Tumor |
| GSM972350 | stage II | 720  | 0 Tumor |
| GSM972351 | stage III | 2220 | 1 Tumor |
| GSM972352 | stage III | 3990 | 0 Tumor |
| GSM972353 | stage I | 690  | 1 Tumor |
| GSM972354 | stage II | 510  | 1 Tumor |
| GSM972355 | stage II | 1260 | 0 Tumor |
| GSM972356 | stage II | 2430 | 0 Tumor |
| GSM972357 | stage II | 360  | 1 Tumor |
| GSM972358 | stage III | 4230 | 0 Tumor |
| GSM972359 | stage III | 540  | 1 Tumor |
| GSM972360 | stage III | 2940 | 0 Tumor |
| GSM972361 | stage III | 4200 | 0 Tumor |
| Sample ID   | Stage  | Count | Tumor |
|------------|--------|-------|-------|
| GSM972364  | III    | 3090  | 0     |
| GSM972365  | III    | 1410  | 0     |
| GSM972366  | III    | 420   | 1     |
| GSM972367  | III    | 2850  | 0     |
| GSM972368  | III    | 2760  | 0     |
| GSM972369  | III    | 540   | 1     |
| GSM972370  | III    | 960   | 1     |
| GSM972371  | III    | 2430  | 0     |
| GSM972372  | III    | 990   | 1     |
| GSM972373  | III    | 1110  | 1     |
| GSM972374  | III    | 2700  | 0     |
| GSM972375  | III    | 3510  | 0     |
| GSM972376  | III    | 2610  | 0     |
| GSM972377  | III    | 2460  | 0     |
| GSM972378  | III    | 2580  | 0     |
| GSM972379  | III    | 2850  | 0     |
| GSM972380  | III    | 180   | 1     |
| GSM972381  | II     | 810   | 1     |
| GSM972382  | II     | 1110  | 1     |
| GSM972383  | II     | 2760  | 0     |
| GSM972384  | II     | 3180  | 0     |
| GSM972385  | II     | 1890  | 0     |
| GSM972386  | II     | 2700  | 0     |
| GSM972387  | II     | 720   | 1     |
| GSM972388  | II     | 2490  | 0     |
| GSM972389  | II     | 2790  | 0     |
| GSM972390  | III    | 180   | 1     |
| GSM972391  | II     | 1290  | 1     |
| GSM972392  | II     | 630   | 1     |
| GSM972393  | II     | 150   | 1     |
| GSM972394  | III    | 180   | 1     |
| GSM972395  | III    | 4410  | 0     |
| GSM972396  | II     | 3210  | 0     |
| GSM972397  | II     | 3150  | 0     |
| GSM972398  | II     | 1920  | 0     |
| GSM972399  | III    | 2700  | 0     |
| GSM972400  | IV     | 240   | 1     |
| GSM972401  | II     | 0     | 0     |
| GSM972402  | II     | 0     | 1     |
| GSM972403  | II     | 1680  | 0     |
| GSM972404  | II     | 1440  | 0     |
| GSM972405  | II     | 2370  | 0     |
| GSM972406  | II     | 3180  | 0     |
| GSM972407  | II     | 3960  | 0     |
| GSM972408  | II     | 960   | 0     |
| GSM972409  | II     | 3120  | 0     |
| GSM972410  | II     | 2730  | 0     |
| GSM972411  | III    | 3750  | 0     |
| GSM972412  | III    | 150   | 1     |
| GSM972413  | III    | 480   | 1     |
| GSM972414  | II     | 1590  | 0     |
| GSM972415  | III    | 240   | 1     |
| GSM972416  | II     | 150   | 1     |
| GSM972417  | II     | 4380  | 0     |
| GSM972418  | II     | 2100  | 0     |
| GSM972419  | III    | 900   | 1     |
| GSM972420  | III    | 180   | 1     |
| GSM972421  | III    | 660   | 1     |
| Sample ID       | Stage | Tumor | Notes |
|-----------------|-------|-------|-------|
| GSM972422       | stage II | 390   | 1 Tumor |
| GSM972423       | stage II | 390   | 1 Tumor |
| GSM972424       | stage II | 3120  | 0 Tumor |
| GSM972425       | stage III| 1770  | 0 Tumor |
| GSM972426       | stage II | 2430  | 0 Tumor |
| GSM972427       | stage II | 1590  | 0 Tumor |
| GSM972428       | stage III| 1650  | 0 Tumor |
| GSM972429       | stage III| 1860  | 0 Tumor |
| GSM972430       | stage II | 1590  | 0 Tumor |
| GSM972431       | stage III| 1620  | 0 Tumor |
| GSM972432       | stage III| 570   | 1 Tumor |
| GSM972433       | stage III| 90    | 1 Tumor |
| GSM972434       | stage II | 570   | 1 Tumor |
| GSM972435       | stage III| 420   | 1 Tumor |
| GSM972436       | stage II | 60    | 1 Tumor |
| GSM972437       | stage IV | 0     | 1 Tumor |
| GSM972438       | stage IV | 0     | 1 Tumor |
| GSM972439       | stage IV | 0     | 1 Tumor |
| GSM972440       | stage II | 1560  | 0 Tumor |
| GSM972441       | stage IV | 0     | 1 Tumor |
| GSM972442       | stage IV | 0     | 1 Tumor |
| GSM972443       | stage II | 1440  | 0 Tumor |
| GSM972444       | stage III| 150   | 1 Tumor |
| GSM972445       | stage II | 1050  | 0 Tumor |
| GSM972447       | stage II | 930   | 0 Tumor |
| GSM972449       | stage III| 570   | 1 Tumor |
| GSM972450       | stage II | 570   | 1 Tumor |
| GSM972451       | stage II | 2910  | 0 Tumor |
| GSM972452       | stage III| 2970  | 0 Tumor |
| GSM972453       | stage III| 3000  | 0 Tumor |
| GSM972454       | stage I  | 2250  | 0 Tumor |
| GSM972455       | stage III| 2220  | 0 Tumor |
| GSM972456       | stage II | 0     | 0 Tumor |
| GSM972457       | stage III| 1020  | 1 Tumor |
| GSM972458       | stage II | 510   | 0 Tumor |
| GSM972459       | stage II | 360   | 0 Tumor |
| GSM972460       | stage II | 2880  | 0 Tumor |
| GSM972461       | stage II | 2880  | 0 Tumor |
| GSM972462       | stage I  | 2640  | 0 Tumor |
| GSM972464       | stage I  | 2580  | 0 Tumor |
| GSM972465       | stage II | 2520  | 0 Tumor |
| GSM972466       | stage III| 2250  | 0 Tumor |
| GSM972467       | stage III| 2160  | 0 Tumor |
| GSM972468       | stage II | 720   | 0 Tumor |
| GSM972469       | stage I  | 2580  | 0 Tumor |
| GSM972470       | stage II | 2550  | 0 Tumor |
| GSM972472       | stage II | 2400  | 0 Tumor |
| GSM972473       | stage II | 1350  | 1 Tumor |
| GSM972474       | stage III| 270   | 1 Tumor |
| GSM972475       | stage II | 2610  | 0 Tumor |
| GSM972476       | stage III| 1920  | 0 Tumor |
| GSM972477       | stage II | 2430  | 0 Tumor |
| GSM972478       | stage II | 2070  | 0 Tumor |
| GSM972479       | stage III| 90    | 0 Tumor |
| GSM972480       | stage II | 2070  | 0 Tumor |
| GSM972481       | stage III| 1950  | 0 Tumor |
| GSM972482       | stage II | 1260  | 0 Tumor |
| GSM972483       | stage II | 690   | 1 Tumor |
| GSM   | Stage | Value | Tumor |
|-------|-------|-------|-------|
| GSM972484 | stage II | 2280 | 0 Tumor |
| GSM972485 | stage II | 2250 | 0 Tumor |
| GSM972486 | stage II | 990 | 0 Tumor |
| GSM972487 | stage II | 2010 | 0 Tumor |
| GSM972488 | stage II | 1470 | 0 Tumor |
| GSM972489 | stage II | 2220 | 0 Tumor |
| GSM972490 | stage II | 2220 | 0 Tumor |
| GSM972491 | stage II | 2100 | 0 Tumor |
| GSM972492 | stage I | 2040 | 0 Tumor |
| GSM972493 | stage II | 1770 | 0 Tumor |
| GSM972494 | stage I | 1710 | 0 Tumor |
| GSM972495 | stage III | 540 | 1 Tumor |
| GSM972496 | stage I | 4260 | 0 Tumor |
| GSM972497 | stage III | 30 | 0 Tumor |
| GSM972498 | stage III | 570 | 1 Tumor |
| GSM972499 | stage III | 2160 | 0 Tumor |
| GSM972501 | stage III | 3180 | 0 Tumor |
| GSM972502 | stage II | 3930 | 0 Tumor |
| GSM972503 | stage II | 4380 | 0 Tumor |
| GSM972504 | stage III | 720 | 1 Tumor |
| GSM972505 | stage II | 4320 | 0 Tumor |
| GSM972506 | stage II | 4230 | 0 Tumor |
| GSM972507 | stage III | 1260 | 0 Tumor |
| GSM972508 | stage I | 4020 | 0 Tumor |
| GSM972509 | stage I | 420 | 0 Tumor |
| GSM972510 | stage II | 2580 | 0 Tumor |
| GSM972511 | stage III | 1410 | 0 Tumor |
| GSM972512 | stage III | 120 | 1 Tumor |
| GSM972513 | stage III | 390 | 1 Tumor |
| GSM972515 | stage II | 3540 | 0 Tumor |
| GSM972516 | stage II | 1980 | 0 Tumor |
| GSM972517 | stage II | 960 | 1 Tumor |
| GSM972518 | stage III | 450 | 1 Tumor |
| GSM972519 | stage II | 330 | 1 Tumor |
| GSM972520 | stage III | 1860 | 0 Tumor |
| GSM972521 | stage II | 2280 | 0 Tumor |
| GSM972522 | stage II | 2970 | 0 Tumor |
| Subtype                        | NMF clusters |
|-------------------------------|--------------|
| CINWntUp                      | CC2          |
| CSC                           | CC3          |
| KRASm                         | CC2          |
| CINImmuneDown                 | CC1          |
| CSC                           | CC3          |
| CSC                           | CC3          |
| dMMR                          | CC2          |
| CINImmuneDown                 | CC2          |
| CINImmuneDown                 | CC3          |
| CINWntUp                      | CC1          |
| CSC                           | CC3          |
| dMMR                          | CC2          |
| KRASm                         | CC2          |
| dMMR                          | CC2          |
| CINImmuneDown                 | CC2          |
| CINWntUp                      | CC2          |
| KRASm                         | CC2          |
| CINImmuneDown                 | CC1          |
| CINWntUp                      | CC1          |
| dMMR                          | CC2          |
| dMMR                          | CC2          |
| dMMR                          | CC2          |
| dMMR                          | CC2          |
| dMMR                          | CC2          |
| dMMR                          | CC2          |
| KRASm                         | CC2          |
| CINWntUp                      | CC3          |
| CINnormL                      | CC3          |
| dMMR                          | CC2          |
| KRASm                         | CC2          |
| KRASm                         | CC2          |
| CINWntUp                      | CC1          |
| CINImmuneDown                 | CC1          |
| KRASm                         | CC2          |
| CINWntUp                      | CC1          |
| CINnormL                      | CC2          |
| CSC                           | CC3          |
| dMMR                          | CC2          |
| CINnormL                      | CC2          |
| CINnormL                      | CC2          |
| CINWntUp                      | CC1          |
| CINImmuneDown                 | CC1          |
| KRASm                         | CC2          |
| CINImmuneDown                 | CC2          |
| CINImmuneDown                 | CC1          |
| KRASm                         | CC1          |
| CINWntUp                      | CC3          |
| CSC                           | CC3          |
| CSC                           | CC3          |
| CINnormL                      | CC3          |
| CINWntUp                      | CC3          |
| CSC                           | CC3          |
| KRASm                         | CC2          |
| CINWntUp                      | CC1          |
CSC  CC2
CSC  CC3
CINImmuneDown  CC1
dMMR  CC2
dMMR  CC2
CINnormL  CC3
CINWntUp  CC3
dMMR  CC3
dMMR  CC3
CINImmuneDown  CC2
dMMR  CC3
CINWntUp  CC3
CINnormL  CC3
CINImmuneDown  CC2
CINImmuneDown  CC1
CINImmuneDown  CC1
CINnormL  CC3
CSC  CC3
CINImmuneDown  CC1
KRASm  CC2
CINWntUp  CC3
CINWntUp  CC1
CINWntUp  CC3
CINWntUp  CC1
CINImmuneDown  CC1
CSC  CC3
KRASm  CC2
CINWntUp  CC1
KRASm  CC2
CINnormL  CC3
CINnormL  CC3
dMMR  CC2
CSC  CC3
CINWntUp  CC3
CINWntUp  CC1
CINnormL  CC3
CINWntUp  CC1
dMMR  CC2
KRASm  CC2
KRASm  CC2
CSC  CC3
CSC  CC3
KRASm  CC2
CINnormL  CC3
CINnormL  CC3
dMMR  CC2
CINImmuneDown  CC2
CINWntUp  CC1
CINWntUp  CC2
KRASm  CC2
CINWntUp  CC1
CINImmuneDown  CC1
CINnormL  CC1
CINnormL  CC3
CINWntUp  CC3
CINWntUp  CC3
dMMR  CC2
CINWntUp CC1
CINImmuneDown CC1
CINImmuneDown CC1
CINImmuneDown CC1
CINWntUp CC1
CINWntUp CC1
CINWntUp CC1
CINImmuneDown CC1
CINWntUp CC3
CINWntUp CC3
CINImmuneDown CC1
CINImmuneDown CC1
CINImmuneDown CC1
KRASm CC3
CINImmuneDown CC3
dMMR CC2
CSC CC3
dMMR CC2
dMMR CC2
dMMR CC2
dMMR CC1
CINImmuneDown CC1
KRASm CC2
KRASm CC3
dMMR CC2
CINWntUp CC1
CINImmuneDown CC1
KRASm CC1
dMMR CC2
CSC CC3
dMMR CC2
dMMR CC2
dMMR CC2
CSC CC2
dMMR CC2
CINWntUp CC2
dMMR CC1
dMMR CC1
CINWntUp CC2
dMMR CC2
dMMR CC2
CINWntUp CC2
dMMR CC2
CINWntUp CC2
CINWntUp CC1
CINWntUp CC1
CINImmuneDown CC1
CINWntUp CC1
CSC CC1
dMMR CC2
dMMR CC2
dMMR CC2
dMMR CC2
KRASm CC1
KRASm CC2
dMMR CC3
KRASm CC2
dMMR CC1
CINWntUp CC1
CINImmuneDown CC1
CINWntUp CC1
CSC CC1
dMMR CC2
dMMR CC2
dMMR CC2
KRASm CC2
KRASm CC1
dMMR CC2
CINWntUp CC1
KRASm CC1
CINnormL CC2
CINImmuneDown CC1
CINImmuneDown CC1
| Condition          | Category |
|-------------------|----------|
| KRASm             | CC2      |
| dMMR              | CC2      |
| CINImmuneDown     | CC1      |
| CINImmuneDown     | CC1      |
| dMMR              | CC2      |
| CINImmuneDown     | CC1      |
| CINImmuneDown     | CC2      |
| CINWntUp          | CC3      |
| CINWntUp          | CC1      |
| CINWntUp          | CC1      |
| dMMR              | CC2      |
| KRASm             | CC2      |
| dMMR              | CC2      |
| dMMR              | CC2      |
| CINImmuneDown     | CC1      |
| CINImmuneDown     | CC1      |
| CINnormL          | CC1      |
| CINnormL          | CC1      |
| CINImmuneDown     | CC1      |
| CINWntUp          | CC1      |
| KRASm             | CC2      |
| dMMR              | CC2      |
| CINWntUp          | CC1      |
| CINnormL          | CC1      |
| dMMR              | CC2      |
| CINWntUp          | CC1      |
| dMMR              | CC2      |
| CINImmuneDown     | CC1      |
| dMMR              | CC2      |
| CINnormL          | CC1      |
| dMMR              | CC2      |
| CINWntUp          | CC1      |
| CINImmuneDown     | CC1      |
| CINWntUp          | CC1      |
| CSC               | CC1      |
| dMMR              | CC2      |
| CINWntUp          | CC1      |
| CINImmuneDown     | CC1      |
| CSC               | CC3      |
| CINnormL          | CC1      |
| CINWntUp          | CC3      |
| dMMR              | CC2      |
| dMMR              | CC1      |
| CINWntUp          | CC3      |
| CINnormL          | CC3      |
| CINWntUp          | CC1      |
| CINnormL          | CC3      |
| CINWntUp          | CC1      |
| CSC               | CC3      |
| CINImmuneDown     | CC1      |
| CINWntUp          | CC1      |
CINWntUp  CC1
CINWntUp  CC1
CINWntUp  CC1
KRASm  CC2
KRASm  CC2
KRASm  CC2
CINImmuneDown  CC1
CINWntUp  CC1
CINWntUp  CC1
CINWntUp  CC1
dMMR  CC2
CINWntUp  CC1
KRASm  CC1
CINWntUp  CC1
CINImmuneDown  CC1
dMMR  CC2
CINWntUp  CC1
KRASm  CC2
CInnormL  CC3
CINImmuneDown  CC3
CINImmuneDown  CC2
CInnormL  CC3
dMMR  CC2
CINImmuneDown  CC1
CINImmuneDown  CC1
KRASm  CC1
CINWntUp  CC1
KRASm  CC2
CINWntUp  CC1
CINImmuneDown  CC1
CINImmuneDown  CC1
CINWntUp  CC1
CInnormL  CC3
CInnormL  CC3
dMMR  CC2
CSC  CC3
dMMR  CC3
| samples    | Stage   | RFS (days) | RFS.event |
|------------|---------|------------|-----------|
| GSM929508  | stage II| 438.9999999| 1         |
| GSM929511  | stage III| 858        | 1         |
| GSM929622  | stage III| 78         | 1         |
| GSM929546  | stage II | 263        | 1         |
| GSM929623  | stage III| 350.0000001| 1         |
| GSM929539  | stage II | 383.0000001| 1         |
| GSM929614  | stage III| 561        | 1         |
| GSM929496  | stage III| 165        | 1         |
| GSM929574  | stage III| 645        | 1         |
| GSM929590  | stage III| 551.0000001| 1         |
| GSM929586  | stage II | 750.9999999| 1         |
| GSM929585  | stage II | 840.9999999| 1         |
| GSM929612  | stage III| 993        | 1         |
| GSM929609  | stage III| 204        | 1         |
| GSM929497  | stage III| 209        | 1         |
| GSM929593  | stage III| 438        | 1         |
| GSM929591  | stage II | 519        | 1         |
| GSM929551  | stage II | 1387       | 1         |
| GSM929587  | stage II | 1150       | 1         |
| GSM929523  | stage III| 300.9999999| 1         |
| GSM929519  | stage III| 779.0000001| 1         |
| GSM929524  | stage III| 591        | 1         |
| GSM929525  | stage III| 111        | 1         |
| GSM929599  | stage III| 1015       | 1         |
| GSM929617  | stage III| 336.9999999| 1         |
| GSM929576  | stage III| 137        | 1         |
| GSM929572  | stage III| 366        | 1         |
| GSM929499  | stage III| 965.0000001| 1         |
| GSM929504  | stage III| 965.0000001| 1         |
| GSM929610  | stage III| 1156       | 1         |
| GSM929498  | stage III| 1140       | 1         |
| GSM929618  | stage III| 608.0000001| 1         |
| GSM929575  | stage III| 549.9999999| 1         |
| GSM929577  | stage III| 426        | 1         |
| GSM929502  | stage III| 199        | 1         |
| GSM929503  | stage III| 200        | 1         |
| GSM929500  | stage III| 1721       | 1         |
| GSM929494  | stage II | 1705       | 0         |
| GSM929495  | stage II | 1211       | 0         |
| GSM929501  | stage III| 1757       | 0         |
| GSM929505  | stage II | 2773       | 0         |
| GSM929506  | stage II | 1259       | 0         |
| GSM929507  | stage II | 2600       | 0         |
| GSM929509  | stage II | 2308       | 0         |
| GSM929510  | stage II | 357.9999999| 0         |
| GSM929512  | stage III| 981.9999999| 0         |
| GSM929513  | stage III| 1259       | 0         |
| GSM929514  | stage II | 2168       | 0         |
| GSM929515  | stage II | 1941       | 0         |
| GSM929516  | stage II | 1695       | 0         |
| GSM929517  | stage II | 1399       | 0         |
| GSM929518  | stage III| 461.0000001| 0         |
| GSM929520  | stage III| 1107       | 0         |
| GSM929521  | stage III| 1100       | 0         |
| GSM929522  | stage III| 1083       | 0         |
| GSM929526  | stage III| 459        | 0         |
| Sample ID   | Stage   | Value     | Count |
|------------|---------|-----------|-------|
| GSM929527  | III     | 774.9999999 | 0     |
| GSM929528  | II      | 1621      | 0     |
| GSM929529  | II      | 1096      | 0     |
| GSM929530  | II      | 1240      | 0     |
| GSM929531  | II      | 1355      | 0     |
| GSM929532  | II      | 1348      | 0     |
| GSM929533  | II      | 1369      | 0     |
| GSM929534  | II      | 1390      | 0     |
| GSM929535  | II      | 1326      | 0     |
| GSM929536  | II      | 1736      | 0     |
| GSM929537  | II      | 1349      | 0     |
| GSM929538  | II      | 1285      | 0     |
| GSM929540  | II      | 1948      | 0     |
| GSM929541  | II      | 1700      | 0     |
| GSM929542  | II      | 1553      | 0     |
| GSM929543  | II      | 1282      | 0     |
| GSM929544  | II      | 1006      | 0     |
| GSM929545  | II      | 1323      | 0     |
| GSM929547  | II      | 1456      | 0     |
| GSM929548  | II      | 2429      | 0     |
| GSM929549  | II      | 2654      | 0     |
| GSM929550  | II      | 2124      | 0     |
| GSM929552  | II      | 1444      | 0     |
| GSM929553  | II      | 2274      | 0     |
| GSM929554  | II      | 1878      | 0     |
| GSM929555  | II      | 2059      | 0     |
| GSM929556  | II      | 468.9999999 | 0     |
| GSM929557  | II      | 899.0000001 | 0    |
| GSM929558  | II      | 1788      | 0     |
| GSM929559  | II      | 17.00000001 | 0   |
| GSM929560  | II      | 1032      | 0     |
| GSM929561  | II      | 39        | 0     |
| GSM929562  | II      | 804       | 0     |
| GSM929563  | II      | 816       | 0     |
| GSM929564  | II      | 590.0000001 | 0     |
| GSM929565  | II      | 1693      | 0     |
| GSM929566  | II      | 1834      | 0     |
| GSM929567  | II      | 1522      | 0     |
| GSM929568  | II      | 1545      | 0     |
| GSM929569  | II      | 2101      | 0     |
| GSM929570  | II      | 1210      | 0     |
| GSM929571  | II      | 1534      | 0     |
| GSM929573  | III     | 1430      | 0     |
| GSM929578  | III     | 999       | 0     |
| GSM929579  | II      | 1685      | 0     |
| GSM929580  | II      | 1663      | 0     |
| GSM929581  | II      | 1680      | 0     |
| GSM929582  | II      | 1939      | 0     |
| GSM929583  | II      | 1771      | 0     |
| GSM929584  | II      | 1779      | 0     |
| GSM929588  | II      | 2155      | 0     |
| GSM929589  | III     | 1904      | 0     |
| GSM929592  | III     | 1432      | 0     |
| GSM929594  | III     | 1820      | 0     |
| GSM929595  | III     | 1804      | 0     |
| GSM929596  | III     | 3137.0000001 | 0 |
| GSM929597  | III     | 1787      | 0     |
| GSM929598  | III     | 1668      | 0     |
| Sample Code | Stage  | Count  | MI  |
|-------------|--------|--------|-----|
| GSM929600   | III    | 2163   | 0   |
| GSM929601   | III    | 1853   | 0   |
| GSM929602   | II     | 1096   | 0   |
| GSM929603   | III    | 1496   | 0   |
| GSM929604   | III    | 2818   | 0   |
| GSM929605   | III    | 1407   | 0   |
| GSM929606   | III    | 1099   | 0   |
| GSM929607   | III    | 2864   | 0   |
| GSM929608   | III    | 1149   | 0   |
| GSM929611   | III    | 1327   | 0   |
| GSM929613   | II     | 1416   | 0   |
| GSM929615   | III    | 2135   | 0   |
| GSM929616   | II     | 160    | 0   |
| GSM929619   | II     | 1887   | 0   |
| GSM929620   | II     | 2624   | 0   |
| GSM929621   | II     | 2860   | 0   |
| Sample type | NMF clusters |
|-------------|--------------|
| Tumor       | CC3          |
| Tumor       | CC2          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC3          |
| Tumor       | CC3          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC1          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC1          |
| Tumor       | CC3          |
| Tumor       | CC2          |
| Tumor       | CC1          |
| Tumor       | CC3          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC1          |
| Tumor       | CC3          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC1          |
| Tumor       | CC2          |
| Tumor       | CC2          |
| Tumor       | CC3          |
| Tumor       | CC1          |
| Tumor       | CC1          |
Tumor CC3
Tumor CC3
Tumor CC1
Tumor CC1
Tumor CC2
Tumor CC2
Tumor CC3
Tumor CC1
Tumor CC1
Tumor CC1
Tumor CC1
Tumor CC1
Tumor CC3
Tumor CC1
Tumor CC3
Tumor CC3
| Tumor  | Sample type | Gender | Age | TNM stage  | Stage |
|-------|-------------|--------|-----|------------|-------|
| SMC01-T | Colorectal cancer | F | 64 | T3 N0 M0 | IIA |
| SMC02-T | Colorectal cancer | M | 66 | T3 N1b M0 | IIIB |
| SMC03-T | Colorectal cancer | F | 83 | T4b N2a M0 | IIIC |
| SMC04-T | Colorectal cancer | M | 69 | T3 N1b M0 | IIIB |
| SMC05-T | Colorectal cancer | F | 58 | T3 N0 M0 | IIA |
| SMC06-T | Colorectal cancer | M | 46 | T3 N1b M0 | IIIB |
| SMC07-T | Colorectal cancer | F | 67 | T2 N0 M0 | I |
| SMC08-T | Colorectal cancer | M | 68 | T3 N1b M0 | IIIB |
| SMC09-T | Colorectal cancer | M | 75 | T3 N0 M0 | IIA |
| SMC10-T | Colorectal cancer | F | 77 | T3 N0 M0 | IIA |
| SMC11-T | Colorectal cancer | F | 38 | T2 N1a M0 | IIIA |
| SMC12-T | Colorectal cancer | M | 77 | T4a N1b M0 | IIIB |
| SMC13-T | Colorectal cancer | M | 56 | T3 N0 M0 | IIA |
| SMC14-T | Colorectal cancer | M | 59 | T4a N1b M0 | IIIB |
| SMC15-T | Colorectal cancer | M | 47 | T4a N1b M0 | IIIB |
| SMC16-T | Colorectal cancer | F | 63 | T3 N0 M0 | IIA |
| SMC17-T | Colorectal cancer | F | 80 | T3 N1 M0 | IIIB |
| SMC18-T | Colorectal cancer | F | 65 | T4a N1c M0 | IIIB |
| SMC19-T | Colorectal cancer | M | 51 | T3 N1 M1a | IVA |
| SMC20-T | Colorectal cancer | M | 76 | T3 N1b M0 | IIIB |
| SMC21-T | Colorectal cancer | M | 67 | T3 N1b M0 | IIIB |
| SMC22-T | Colorectal cancer | F | 48 | T1 N0 M0 | I |
| SMC23-T | Colorectal cancer | F | 57 | T3 N2b M1a | IVA |
| Anatomic region Left/Right-sided | MSI   | MSS   | MSI-H | MSS   | MSS   | MSI-H | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
|---------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| rectum left                     | MSI   | MSS   | MSI-H | MSS   | MSS   | MSI-H | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| hepatic flexure right           | MSI-H | MSS   | MSI-H | MSS   | MSS   | MSI-H | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| ascending right                 | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| sigmoid left                    | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| rectosigmoid left               | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| sigmoid left                    | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| hepatic flexure right           | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| sigmoid left                    | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| ascending right                 | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| ascending right                 | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| rectum left                     | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| sigmoid left                    | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| ascending right                 | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| ascending right                 | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| sigmoid left                    | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   | MSS   |
| Pathological subtype                                                                 | Bulk CMS subtypes |
|--------------------------------------------------------------------------------------|-------------------|
| Adenocarcinoma, well differentiated                                                  | CMS3              |
| Adenocarcinoma, well differentiated                                                  | CMS4              |
| Adenocarcinoma, poorly differentiated                                               | CMS1              |
| Adenocarcinoma, moderately differentiated                                            | CMS4              |
| Adenocarcinoma, well differentiated with mucin production (<10%)                     | CMS3              |
| Adenocarcinoma, well differentiated                                                  | CMS1              |
| Adenocarcinoma, well differentiated                                                  | CMS2              |
| Adenocarcinoma, moderately differentiated                                            | CMS1              |
| Adenocarcinoma, well differentiated                                                  | CMS2              |
| Adenocarcinoma, moderately differentiated                                            | CMS1              |
| Adenocarcinoma, well differentiated                                                  | CMS2              |
| Adenocarcinoma, moderately differentiated                                            | CMS2              |
| Adenocarcinoma, moderately differentiated                                            | CMS4              |
| Adenocarcinoma, moderately differentiated                                            | CMS1              |
| Adenocarcinoma, moderately differentiated                                            | CMS3              |
| Mucinous adenocarcinoma                                                             | CMS4              |
| Adenocarcinoma, moderately differentiated                                            | CMS2              |
| Adenocarcinoma, moderately differentiated                                            | CMS3              |
| Mucinous adenocarcinoma                                                             | CMS4              |
| Adenocarcinoma, moderately differentiated                                            | CMS2              |
| Adenocarcinoma, moderately differentiated                                            | CMS2              |
| Adenocarcinoma, moderately differentiated                                            | CMS2              |
| Adenocarcinoma, well differentiated with mucin production (10%)                      | CMS4              |
| Adenocarcinoma, moderately differentiated                                            | CMS2              |
| KRAS | BRAF  | TP53 | APC   | SMAD4 |
|------|-------|------|-------|-------|
| Mutant | Wildtype | Mutant | Mutant | Wildtype |
| Wildtype | Wildtype | Mutant | Mutant | Mutant |
| Wildtype | Mutant | Wildtype | Mutant | Wildtype |
| Mutant | Wildtype | Mutant | Mutant | Wildtype |
| Mutant | Wildtype | Wildtype | Mutant | Wildtype |
| Mutant | Wildtype | Mutant | Mutant | Wildtype |
| Wildtype | Wildtype | Mutant | Mutant | Wildtype |
| Wildtype | Mutant | Wildtype | Mutant | Wildtype |
| Wildtype | Wildtype | Mutant | Mutant | Wildtype |
| Mutant | Wildtype | Wildtype | Wildtype | Wildtype |
| Wildtype | Wildtype | Wildtype | Wildtype | Wildtype |
| Wildtype | Wildtype | Wildtype | Wildtype | Wildtype |
| Wildtype | Wildtype | Wildtype | Wildtype | Mutant |
| Mutant | Wildtype | Mutant | Mutant | Wildtype |
| Wildtype | Mutant | Wildtype | Mutant | Wildtype |
| Wildtype | Mutant | Mutant | Mutant | Wildtype |
| Mutant | Mutant | Mutant | Mutant | Wildtype |
| Mutant | Mutant | Wildtype | Mutant | Wildtype |
| Wildtype | Mutant | Mutant | Mutant | Wildtype |
| Wildtype | Wildtype | Mutant | Mutant | Wildtype |
| Wildtype | Wildtype | Mutant | Mutant | Wildtype |
| Mutant | Mutant | Mutant | Mutant | Wildtype |
| Wildtype | Wildtype | Mutant | Mutant | Wildtype |
| Wildtype | Mutant | Mutant | Mutant | Wildtype |
| Mutant | Mutant | Wildtype | Mutant | Wildtype |
| Wildtype | Wildtype | Mutant | Mutant | Wildtype |
| Patient | Core     | Sample type          | Gender | Age |
|---------|----------|----------------------|--------|-----|
| KUL01   | KUL01-T  | Colorectal cancer    | F      | 81  |
| KUL19   | KUL19-T  | Colorectal cancer    | F      | 86  |
| KUL21   | KUL21-T  | Colorectal cancer    | F      | 50  |
| KUL28   | KUL28-T  | Colorectal cancer    | M      | 52  |
| KUL30   | KUL30-T  | Colorectal cancer    | M      | 84  |
| KUL31   | KUL31-T  | Colorectal cancer    | M      | 85  |
and KUL cohorts

| TNM stage   | Stage | Anatomic region | Left/Right-sided | MSI  |
|-------------|-------|-----------------|------------------|------|
| pT4aN0      | IIB   | caecum          | right            | MSI-H|
| pT3N1b      | IIIB  | rectosigmoid    | left             | MSS  |
| pT4aN1aM1a  | IVA   | sigmoid         | left             | MSS  |
| pT3N0L1     | IIA   | sigmoid         | left             | MSS  |
| pT3N0L1     | IIA   | ascending       | right            | MSS  |
| pT1N0       | I     | sigmoid         | left             | MSS  |
Pathological subtype
Global moderately differentiated adenocarcinoma with mixed glandular, mucinous growth pattern, mod-
Moderately differentiated adenocarcinoma NST
Moderately differentiated adenocarcinoma
Moderately differentiated adenocarcinoma
Moderately differentiated adenocarcinoma
Well differentiated adenocarcinoma NST
| Bulk CMS subtypes | TP53 | APC   | KRAS  | BRAF  | SMAD4 |
|-------------------|------|-------|-------|-------|-------|
| Unknown           | Mutant | Wildtype | Wildtype | Mutant  | Wildtype |
| CMS4              | Mutant | Mutant | Wildtype | Wildtype | Wildtype |
| CMS1              | Mutant | Mutant | Mutant | Wildtype | Wildtype |
| CMS2              | Mutant | Mutant | Wildtype | Wildtype | Wildtype |
| CMS2              | Wildtype | Mutant | Mutant | Wildtype | Mutant |
| CMS3              | Wildtype | Mutant | Mutant | Wildtype | Wildtype |
Table S3. Biological information of ferroptosis-associated genes (human genes)

| Symbol | Biological Information |
|--------|------------------------|
| RPL8   |                        |
| IREB2  |                        |
| ATP5MC3|                        |
| CS     |                        |
| EMC2   |                        |
| ACFS2  |                        |
| NOX1   |                        |
| CYBB   |                        |
| NOX3   |                        |
| NOX4   |                        |
| NOX5   |                        |
| DUOX1  |                        |
| DUOX2  |                        |
| G6PD   |                        |
| PGD    |                        |
| VDAC2  |                        |
| TP53   |                        |
| ACSL4  |                        |
| LPCAT3 |                        |
| NRAS   |                        |
| KRAS   |                        |
| HRAS   |                        |
| CARS1  |                        |
| KEAP1  |                        |
| HMOX1  |                        |
| ATG5   |                        |
| ATG7   |                        |
| NCOA4  |                        |
| ALOX12 |                        |
| ALOX12B|                        |
| ALOX15 |                        |
| ALOX15B|                        |
| ALOXE3 |                        |
| PHKG2  |                        |
| SAT1   |                        |
| EGFR   |                        |
| MAPK3  |                        |
| MAPK1  |                        |
| ZEB1   |                        |
| DPP4   |                        |
| CDKN2A |                        |
| PEBP1  |                        |
| SOCS1  |                        |
| CDO1   |                        |
| MYB    |                        |
| CHAC1  |                        |
| LINC00472|                    |
| PRKAA2 |                        |
| PRKAA1 |                        |
| ELAVL1 |                        |
| BAP1   |                        |
| ABCC1  |                        |
| MIR6852|                        |
| ACVR1B |                        |
| TGFR1  |                        |
IFNG
ANO6
HMGB1
TNFAIP3
ATF3
ATM
YY1AP1
EGLN2
MIOX
TAZ
MTDH
IDH1
FBXW7
PANX1
DNAJB6
LONP1
PTGS2
DUSP1
NOS2
NCF2
MT3
UBC
ALB
TXNRD1
SRXN1
GPX2
BNIP3
OXSR1
SELENOS
ANGPTL7
CHAC1
SLC7A11
DDIT4
LOC284561
ASNS
TSC22D3
DDIT3
JDP2
SESN2
SLC1A4
PCK2
TXNIP
VLDLR
GPT2
PSAT1
LURAP1L
SLC7A5
HERPUD1
XBP1
ATF3
SLC3A2
CBS
ATF4
ZNF419
KLHL24
TRIB3
ZFP69B
ATP6V1G2
AKR1C3
RB1
HSPB1
HSF1
NFE2L2
SQSTM1
NQO1
HMOX1
FTH1
MUC1
MT1G
SLC40A1
CISD1
HSPA5
ATF4
TP53
HELS5
SCD
FADS2
SRC
STAT3
PML
NFS1
TP63
CDKN1A
MIR137
VDAC2
FH
CISD2
MIR9-1
MIR9-2
MIR9-3
CBS
ISCU
ACSL3
OTUB1
CD44
LINC00336
BRD4
PRDX6
MIR17
SESN2
NF2
ARNTL
HIF1A
JUN
CA9
TMBIM4
PLIN2
AIFM2
LAMP2
ZFP36
PROM2
CHMP5
CHMP6
CAV1
GCH1
Biological information of ferroptosis-associated genes (human genes)

**Name**
- Ribosomal protein L8
- Iron response element binding protein 2
- ATP synthase membrane subunit c locus 3
- Citrate synthase
- ER membrane protein complex subunit 2
- Acyl-CoA synthetase family member 2
- Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 1
- Cytochrome b-245 beta chain
- Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 3
- Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 4
- Nicotinamide adenine dinucleotide phosphate (NADPH) oxidase (NOX) 5
- Dual oxidase 1
- Dual oxidase 2
- Glucose-6-phosphate dehydrogenase
- Phosphoglycerate dehydrogenase
- Voltage-dependent anion channels 2
- Tumor protein p53
- Acyl-CoA synthetase long chain family member 4
- Lysophosphatidylcholine acyltransferase 3
- NRAS proto-oncogene, GTPase
- KRAS proto-oncogene, GTPase
- HRas proto-oncogene, GTPase
- Cysteinyl-tRNA synthetase 1
- Kelch like ECH associated protein 1
- Heme oxygenase 1
- Autophagy related 5
- Autophagy related 7
- Nuclear receptor coactivator 4
- Arachidonate 12-lipoxygenase, 12S type
- Arachidonate 12-lipoxygenase, 12R type
- Arachidonate 15-lipoxygenase
- Arachidonate 15-lipoxygenase type B
- Arachidonate lipoxygenase 3
- Phosphorylase kinase catalytic subunit gamma 2
- Spermidine/spermine N1-acetyltransferase 1
- Epidermal growth factor receptor
- Mitogen-activated protein kinase 3
- Mitogen-activated protein kinase 1
- Zinc finger E-box binding homeobox 1
- Dipeptidyl peptidase 4
- Cyclin dependent kinase inhibitor 2A
- Phosphatidylethanolamine binding protein 1
- Suppressor of cytokine signaling 1
- Cysteine dioxygenase type 1
- MYB proto-oncogene, transcription factor
- ChaC glutathione specific gamma-glutamylcyclotransferase 1
- Long intergenic non-protein coding RNA 472
- Protein kinase AMP-activated catalytic subunit alpha 2
- Protein kinase AMP-activated catalytic subunit alpha 1
- ELAV like RNA binding protein 1
- BRCA1 associated protein 1
- ATP binding cassette subfamily C member 1
- microRNA 6852
- Activin A receptor type 1B
- Transforming growth factor beta receptor 1
Interferon gamma
Anoctamin 6
High mobility group box 1
TNF alpha induced protein 3
Activating transcription factor 3
ATM serine/threonine kinase
YY1 associated protein 1
Egl-9 family hypoxia inducible factor 2
Myo-inositol oxygenase
Tafazzin
Metadherin
Isocitrate dehydrogenase (NADP(+)) 1
F-box and WD repeat domain containing 7
Pannexin 1
DnaJ heat shock protein family (Hsp40) member B6
Lon peptidase 1, mitochondrial
Prostaglandin-endoperoxide synthase 2
Dual specificity phosphatase 1
Nitric oxide synthase 2
Neutrophil cytosolic factor 2
Metallothionein 3
Ubiquitin C
Albumin
Thioredoxin reductase 1
Sulfiredoxin 1
Glutathione peroxidase 2
BCL2 interacting protein 3
Oxidative stress responsive kinase 1
Selenoprotein S
Angiopoietin like 7
ChaC glutathione specific gamma-glutamylcyclotransferase 1
Solute carrier family 7 member 11
DNA damage inducible transcript 4
Asparagine synthetase (glutamine-hydrolyzing)
TSC22 domain family member 3
DNA damage inducible transcript 3
Jun dimerization protein 2
Sestrin 2
Solute carrier family 1 member 4
Phosphoenolpyruvate carboxykinase 2, mitochondrial
Thioredoxin interacting protein
Very low density lipoprotein receptor
Glutamic--pyruvic transaminase 2
Phosphoserine aminotransferase 1
Leucine rich adaptor protein 1 like
Solute carrier family 7 member 5
Homocysteine inducible ER protein with ubiquitin like domain 1
X-box binding protein 1
Activating transcription factor 3
Solute carrier family 3 member 2
Cystathionine beta-synthase
Activating transcription factor 4
Zinc finger protein 419
Kelch like family member 24
Tribbles pseudokinase 3
ZFP69 zinc finger protein B
ATPase H+ transporting V1 subunit G2
| Gene Name |
|-----------|
| Vascular endothelial growth factor A |
| Growth differentiation factor 15 |
| Tubulin epsilon 1 |
| Arrestin domain containing 3 |
| CCAAT enhancer binding protein gamma |
| Small nucleolar RNA, H/ACA box 16A |
| Regulator of G protein signaling 4 |
| BLOC1S5-TXNDC5 readthrough (NMD candidate) |
| _NA_ |
| Eukaryotic translation initiation factor 2 subunit 1 |
| Hydroxysteroid 17-beta dehydrogenase 11 |
| 1-acylglycerol-3-phosphate O-acyltransferase 3 |
| SET domain containing 1B, histone lysine methyltransferase |
| Heme oxygenase 1 |
| Transferrin |
| Ferritin light chain |
| Ribosomal protein L8 |
| ATP synthase membrane subunit c locus 3 |
| Transferrin receptor |
| MAF bZIP transcription factor G |
| Ferritin heavy chain 1 |
| Dopamine receptor D5 |
| Dopamine receptor D4 |
| Mitogen-activated protein kinase kinase kinase 5 |
| Mitogen-activated protein kinase 14 |
| Solute carrier family 2 member 1 |
| Solute carrier family 2 member 3 |
| Solute carrier family 2 member 6 |
| Solute carrier family 2 member 8 |
| Solute carrier family 2 member 12 |
| _NA_ |
| Solute carrier family 2 member 14 |
| Eukaryotic translation initiation factor 2 alpha kinase 4 |
| Arachidonate 5-lipoxygenase |
| Arachidonate 12-lipoxygenase, 12S type |
| Arachidonate 15-lipoxygenase |
| High mobility group box 1 |
| ELAV like RNA binding protein 1 |
| Hemoglobin subunit alpha 1 |
| Nicotinamide N-methyltransferase |
| Perilipin 4 |
| HIC ZBTB transcriptional repressor 1 |
| Stathmin 1 |
| Ribonucleotide reductase regulatory subunit M2 |
| Capping actin protein, gelsolin like |
| Hepatocyte nuclear factor 4 alpha |
| Neuroglobin |
| Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon |
| GA binding protein transcription factor subunit beta 1 |
| Aurora kinase A |
| microRNA 4715 |
| Receptor interacting serine/threonine kinase 1 |
| Peroxiredoxin 1 |
| microRNA 30b |
| Solute carrier family 7 member 11 |
| Glutathione peroxidase 4 |
| Aldo-keto reductase family 1 member C1 |
| Aldo-keto reductase family 1 member C2 |
Aldo-keto reductase family 1 member C3
RB transcriptional corepressor 1
Heat shock protein family B (small) member 1
Heat shock transcription factor 1
Nuclear factor, erythroid 2 like 2
Sequestosome 1
NAD(P)H quinone dehydrogenase 1
Heme oxygenase 1
Ferritins heavy chain 1
Mucin 1, cell surface associated
Metallothionein 1G
Solute carrier family 40 member 1
CDGSH iron sulfur domain 1
Heat shock protein family A (Hsp70) member 5
Activating transcription factor 4
Tumor protein p53
Helicase, lymphoid specific
Stearoyl-CoA desaturase
Fatty acid desaturase 2
SRC proto-oncogene, non-receptor tyrosine kinase
Signal transducer and activator of transcription 3
Promyelocytic leukemia
NFS1 cysteine desulfurase
Tumor protein p63
Cyclin dependent kinase inhibitor 1A
microRNA 137
Voltage dependent anion channel 2
Fumarate hydratase
CDGSH iron sulfur domain 2
microRNA 9-1
c microRNA 9-2
microRNA 9-3
Cystathionine beta-synthase
Iron-sulfur cluster assembly enzyme
Acyl-CoA synthetase long chain family member 3
OTU deubiquitinase, ubiquitin aldehyde binding 1
CD44 molecule (Indian blood group)
Long intergenic non-protein coding RNA 336
Bromodomain containing 4
Peroxisiredoxin 6
c microRNA 17
Sestrin 2
Neurofibromin 2
Aryl hydrocarbon receptor nuclear translocator like
Hypoxia inducible factor 1 subunit alpha
Jun proto-oncogene, AP-1 transcription factor subunit
Carbonic anhydrase 9
Transmembrane BAX inhibitor motif containing 4
Perilipin 2
Apoptosis inducing factor mitochondria associated 2
Lysosomal associated membrane protein 2
ZFP36 ring finger protein
Prominin 2
Charged multivesicular body protein 5
Charged multivesicular body protein 6
Caveolin 1
GTP cyclohydrolase 1
| HGNC_ID   |
|-----------|
| HGNC:10368|
| HGNC:6115 |
| HGNC:843  |
| HGNC:2422 |
| HGNC:28963|
| HGNC:26101|
| HGNC:7889 |
| HGNC:2578 |
| HGNC:7890 |
| HGNC:7891 |
| HGNC:14874|
| HGNC:3062 |
| HGNC:13273|
| HGNC:4057 |
| HGNC:8891 |
| HGNC:12672|
| HGNC:11998|
| HGNC:3571 |
| HGNC:30244|
| HGNC:7989 |
| HGNC:6407 |
| HGNC:5173 |
| HGNC:1493 |
| HGNC:23177|
| HGNC:5013 |
| HGNC:589  |
| HGNC:16935|
| HGNC:7671 |
| HGNC:429  |
| HGNC:430  |
| HGNC:433  |
| HGNC:434  |
| HGNC:13743|
| HGNC:8931 |
| HGNC:10540|
| HGNC:3236 |
| HGNC:6877 |
| HGNC:6871 |
| HGNC:11642|
| HGNC:3009 |
| HGNC:1787 |
| HGNC:8630 |
| HGNC:19383|
| HGNC:1795 |
| HGNC:7545 |
| HGNC:28680|
| HGNC:21380|
| HGNC:9377 |
| HGNC:9376 |
| HGNC:3312 |
| HGNC:950  |
| HGNC:51   |
| HGNC:49993|
| HGNC:172  |
| HGNC:11772|
| HGNC:5438  | HGNC:25240  | HGNC:4983  | HGNC:11896  | HGNC:785  | HGNC:795  | HGNC:30935  | HGNC:14660  | HGNC:14522  | HGNC:11577  | HGNC:29608  | HGNC:5382  | HGNC:16712  | HGNC:8599  | HGNC:14888  | HGNC:9479  | HGNC:9605  | HGNC:3064  | HGNC:7873  | HGNC:7661  | HGNC:7408  | HGNC:12468  | HGNC:399  | HGNC:12437  | HGNC:16132  | HGNC:4554  | HGNC:1084  | HGNC:8508  | HGNC:30396  | HGNC:24078  | HGNC:28680  | HGNC:11059  | HGNC:24944  | HGNC:753  | HGNC:3051  | HGNC:2726  | HGNC:17546  | HGNC:20746  | HGNC:10942  | HGNC:8725  | HGNC:16952  | HGNC:12698  | HGNC:18062  | HGNC:19129  | HGNC:31452  | HGNC:11063  | HGNC:13744  | HGNC:12801  | HGNC:785  | HGNC:11026  | HGNC:1550  | HGNC:786  | HGNC:20648  | HGNC:25947  | HGNC:16228  | HGNC:28053  | HGNC:862  |
Table S3. Biological information of ferroptosis-associated genes (human genes)

Inhibition attenuated erastin-induced ferroptosis.

Promotes ferroptosis. Binds to LINC0033 and serves as a negative upstream regulator of CBS-mediated ferroptosis inhibition.

Accelerates ferroptosis. Disruption of MRP1 inhibited ferroptosis potently.

Suppresses SLC7A11-mediated cystine uptake and promotes ferroptosis. BAP1 mutants lose their abilities to repress SLC7A11 and to promote ferroptosis.

ELAVL1 siRNA led to ferroptosis resistance, whereas ELAVL1 plasmid contributed to classical ferroptotic events.

Inhibition of PRKAA/AMPKalpha diminishes ferroptosis.

Increases erastin-induced growth inhibition, whereas depletion of P53RRA decreased erastin-induced growth inhibition.

Inhibits cystine uptake and sensitizes cells to ferroptosis. Erastin induced high levels of cell death in p53+ cells.

Deletion of this gene likely suppress ferroptosis by limiting the membrane-resident pool of oxidation-sensitive fatty acids.

NRAS12V mutant protects RMS13 cells from ferroptotic cell death.

KRAS12V mutant protects RMS13 cells from ferroptotic cell death.

HRAS12V mutant protects RMS13 cells from ferroptotic cell death.

Required in erastin-induced ferroptosis.

Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.

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Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.

Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.

Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.

Knockdown of Keap1 reversed loss of p62-mediated degradation of Nrf2 in ferroptosis. Keap1 knockdc zinc protoporphyrin IX, a HO-1 inhibitor, prevented Erastin-triggered ferroptotic cancer cell death. Overexpression or deletion limited Erastin-induced ferroptosis.

Inhibition suppressed ferroptosis, and overexpression promoted ferroptosis.

Silencing ALOX genes made cells resistant to ferroptosis.

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Silencing ALOX genes made cells resistant to ferroptosis.

Erastin-induced cell death was rescued by silencing ALOX genes. Erastin-induced cell death was rescued by silencing U-2-OS cells became resistant to erastin upon PHKG2 silencing. Erastin-treated HT-1080 cells were less sensitive to cystine starvation. Erastin-induced activation of SAT1 contributes to ferroptotic cell death in the presence of ROS stress. Knockdown of SAT1 reversed loss of p62-mediated degradation of Nrf2 in ferroptosis. Inhibiting EGFR and MAPK signaling rescues cells from cystine withdrawal. Knockdown of ZEB1 prevents cell death induced by GPX4 inhibition. Required in erastin-induced ferroptosis.

Combination of ARF induction and ROS treatment induced ferroptotic cell death. Knockdown of endogenous ARF resulted in increased sensitivity of HK2 cells to ROS. Expression of SOCS1 sensitized cells to ferroptosis inducer. This effect of SOCS1 was efficiently blocked by ferroptosis inhibitor.

Erasin-induced ferroptosis was restrained when c-Myb was suppressed.

CHAC1 degradation of GSH might enhance cystine-starvation-induced cell death.

Increases erastin-induced growth inhibition, whereas depletion of P53RRA decreased erastin-induced growth inhibition.

Expression of SOCS1 sensitized cells to ferroptosis inducer. This effect of SOCS1 was efficiently blocked by ferroptosis inhibitor.

Required in erastin-induced ferroptosis. Silencing of it conferred against erastin-induced ferroptosis.

Inhibition of PRKAA/AMPKalpha diminishes ferroptosis.

Inhibition of PRKAA/AMPKalpha diminishes ferroptosis.

ELAVL1 siRNA led to ferroptosis resistance, whereas ELAVL1 plasmid contributed to classical ferroptotic cell death. Suppression of SLC7A11-mediated cystine uptake promotes ferroptosis. BAP1 mutants lose their ability to promote ferroptosis. Disruption of MRP1 inhibited ferroptosis potently.

Promotes ferroptosis. Binds to LINC0033 and serves as a negative upstream regulator of CBS-mediated ferroptosis. Inhibition attenuated erastin-induced ferroptosis.

Inhibition attenuated erastin-induced ferroptosis.
Interferon gamma released from CD8+ T cells downregulates the expression of SLC3A2 and SLC7A11, and as a consequence, promotes tumour cell lipid peroxidation and ferroptosis.

Essential for ferroptosis. Inhibition blocked ferroptotic cell death induced by RSL3/erastin.

Required for erastin-induced ferroptosis. Knockdown of HMGB1 decreased erastin-induced cell death. Overexpression increased ROS generation and enhanced erastin-induced ferroptosis, whereas knockdov Promotes ferroptosis induced by erastin.

Essential for ferroptosis. Genetic knockdown and chemical inhibition of ATM both suppress ferroptotic cell death. Inhibiting EGLN2 activation diminished ferroptotic tumor cell death.

Overexpression exacerbates cell death, knockdown inhibits ferroptosis.

TAZ removal confers ferroptosis resistance, whereas overexpression of TAZS89A sensitizes cells to ferropenia. Can enhance sensitivity to inducers of ferroptosis. Enhances the vulnerability of cancer cells to ferroptosis.

Deletion of the mutant IDH1 allele or pharmacological inhibition of mutant IDH1 confers resistance to erastin-induced ferroptosis. FBXW7 plasmid induces ferroptosis.

Deletion protects against ferroptotic cell death. Silenced Panx1 expression significantly attenuated ferroptosis in esophageal squamous cell carcinoma.

Inhibition of LONP1 negatively regulates erastin-induced cell death. Simply a downstream marker of ferroptosis. The most upregulated gene in BJeLR cells upon treatment with erastin.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was upregulated during ferroptosis induced by erastin or RSL3.

Expression was downregulated during ferroptosis induced by erastin or RSL3.

Up-regulated in erastin-treated samples. A useful pharmacodynamic marker of system Xc- inhibition. Similar to erastin treatment, silencing of this gene inhibits glutamate release. Erastin specifically inhibits system Xc-.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.

Up-regulated (>= 2 fold) in erastin-treated samples.
Up-regulated (>= 2 fold) in erastin-treated samples.

Down-regulated (>= 2 fold) in erastin-treated samples.

Phosphorylated in erastin-treated sample.

Enriched in RSL3-resistant cells.

Down-regulated (>= 2 fold) in erastin-treated samples.

Expression of this gene is increased in response to artesunate-induced ferroptosis, indicating activation of ROS-mediated signaling pathways.

Increased at LSH overexpression. Decreased at LSH knockdown. LSH can inhibit ferroptosis.

Overexpression sensitizes cells to ferroptosis.

Associated with ferroptotic cell death. Ferroptosis activators induce HMGB1 release.

Binds to and increases the expression of the negative ferroptosis regulator LINC00336.

Upregulated in cells treated with ferroptosis inducer erastin. Stimulates ferroptosis possibly in a GSH-dependent manner.

Increased at LSH overexpression. Decreased at LSH knockdown. LSH can inhibit ferroptosis.

Overexpression sensitizes cells to ferroptosis.

 Associated with ferroptotic cell death. Ferroptosis activators induce HMGB1 release.

Binds to and increases the expression of the negative ferroptosis regulator LINC00336.

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Overexpression sensitizes cells to ferroptosis.

Associated with ferroptotic cell death. Ferroptosis activators induce HMGB1 release.

Binds to and increases the expression of the negative ferroptosis regulator LINC00336.
Up-regulated in DU-145 erastin-resistant clones. Participate in the detoxification of toxic lipid metabolites. Rb knock-down cells exposed to sorafenib encounter ferroptosis. Lack of Rb sensitized HCC cells to the induction of ferroptosis, whereas heat shock pretreatment abrogated the sensitization.

Knockdown of NDRG1 enhances erastin-induced ferroptosis, whereas heat shock pretreatment blocks erastin-induced ferroptosis.

Rb is a negative regulator of ferroptosis and is required for exogenous monounsaturated fatty acids to protect cells against ferroptosis. Overexpression of Rb could partially protect cells from ferroptosis. Inhibition of Rb blocks resistance to ferroptotic cell death.

Overexpression of miR-9 suppressed GOT1, which subsequently reduced ferroptosis. Suppression of miR-9 increased the sensitivity of melanoma cells to ferroptosis inducers.

Overexpression of miR-9 conferred resistance to ferroptosis. Inhibition blocked resistance to ferroptotic cell death.

FH inactivation (FH-/-) proves synthetic lethal with inducers of ferroptosis. FH-/- sensitizes cells to multiple ferroptosis inducers.

Depletion of the SCD1 and FADS2 metabolic genes induces ferroptosis. Depletion of the SCD1 and FADS2 metabolic genes induces ferroptosis.

Src-STAT3 activation renders the cell unable to undergo ferroptosis. Src inhibition decreased cell viability.

Suppression of NFS1 cooperates with inhibition of cysteine transport to trigger ferroptosis in vitro and in vivo. Delta Np63 alpha can inhibit ferroptosis independent of p53. Overexpression protects cells from ferroptosis.

Required to suppress ferroptosis.

MUC1-C (C-terminal subunit) blocks erastin-induced ferroptosis and induces increases in GSH.

NRF2 plays a central role in protecting hepatocellular carcinoma (HCC) cells against ferroptosis. Overexpression of NRF2 inhibits ferroptosis by decreasing the intracellular levels of iron and lipid ROS.

Inhibits ferroptosis in human colorectal cancer (CRC) cells. Loss of TP53 restored erastin sensitivity. Inhibiting LSH inhibits ferroptosis.

Rb knock-down cells exposed to sorafenib encounter ferroptosis. Lack of Rb sensitized HCC cells to the induction of ferroptosis, whereas heat shock pretreatment abrogated the sensitization.
Test method
- shRNA screening, qPCR, gene silencing
- Inhibition test by diphenylene iodonium (DPI) and GKT137831.
- Retroviral-mediated insertional mutagenesis and sequencing
- Cell viability assessed by MTT assay, western blot
- siRNA screen, shRNA, western blot, cell viability
- Western blot, shRNA knockdown, cell viability
- Cell viability assay, qRT-PCR, western blot
- shRNA
- shRNA, gene transfection
- qPCR
- qPCR, siRNA
- shRNA suppressor screen, qPCR, cellular iron staining, cell viability
- qRT-PCR, siRNA, CRISPR-cas9, western blot

Table S3. Biological information of ferroptosis-associated genes (human genes)
BODIPY-C11, liperfluo staining, cell death measurement, FACS, cell proliferation and viability estimation.

Immunocytochemistry, RT-PCR, TUNEL Assay, flow Cytometry, LDH assay, gene knockout, siRNA.

Gene transfection, RNAi, cell viability assay, ELISA, LDH assay, flow cytometry, qPCR, western blot.

Lentivirus transduction, CCK-8 assay, DYE670 staining assay, ROS staining assay, RT-qPCR, western blot.

Cell viability assay, transfection, lentiviral infection, qRT-PCR, western blot.

siRNA, western blot, nuclear/cytosol fraction, cell viability, cell death, GSH assay, kinome screen.

Cell death, cell viability, lipid peroxidation, immunoblotting, CRISPR/Cas9, ChIP assay, qRT-PCR.

Cytotoxicity assays, western blot, immunoprecipitation, RNA interference, gene transfection, qRT-PCR.

MTT assay, measurement of GPX4 activity, labile iron pool assay, evaluation of cell death and cell viability.

Cell death, western blot, siRNA, qRT-PCR, microarray, immunofluorescence staining.

Cell viability, qRT-PCR, western blotting, GSH assay, GPx4 activity assay, tumor xenograft model.

Cell transfection, cell viability, GSH assay, lipid ROS assay.

Cell viability, lipid peroxidation, iron, GSH and ROS assays, western blot, RT-PCR, RNA-seq.

Cell viability, cell death, qRT-PCR, western blot, lipid peroxidation detection, shRNA.

Western blot, immunohistochemistry, lentivirus infection, colony-forming, RT-qPCR, CCK-8, transwell.

Cell viability, western blot, qRT-PCR, lipid peroxidation assay, glutathione assay.

RT-qPCR, cell viability.

RT-qPCR, cell viability.

RT-qPCR, cell viability.

RT-qPCR, cell viability.

RT-qPCR, cell viability.

RT-qPCR, cell viability.

RT-qPCR, cell viability.

RNA-seq, RT-qPCR.

RNA silencing, RT-qPCR.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.

RNA-seq.
RNA-seq
Western blot
Gene trap insertion
Gene trap insertion
Gene trap insertion
Western blotting
Gene expression analysis
Gene expression analysis
Gene expression analysis
Gene expression analysis
Gene expression analysis
Western blot
Immunoblotting, q-PCR
Western blot, Q-PCR
Western blot, Q-PCR
LDH assay, immunoblot, RNAi, CCK-8
LDH assay, immunoblot, RNAi, CCK-8
ChIP analysis, RT-qPCR
RT-qPCR
RT-qPCR
RT-qPCR
RT-qPCR
RT-qPCR
Western blot, real-time PCR, cell viability assay, siRNA, GSH assay kit
Western blot, mass spectrometry, cell viability assay, gene overexpression
Western blot, mass spectrometry, cell viability assay, gene overexpression
Western blot, mass spectrometry, cell viability assay, gene overexpression
ELISA, western blot, RNAi
RNA pulldown, mass spectrometry, qRT-PCR, gene overexpression, gene knockdown, western
Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC
Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC
Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC
Immunohistochemistry, immunofluorescence, western blot, qPCR, metabolites examination, Cl
Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC
Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC
Tandem mass tags, RNA-seq, DNase-seq, qPCR, Western blot, IHC
Immunohistochemistry, immunofluorescence, western blot, qPCR, metabolites examination, Cl
Cell death, cell viability, lipid peroxidation assay, RT-qPCR
Mass spectrometry, siRNA, western blot
RT-qPCR, western blot, siRNA, cell viability, lipid peroxidation assay
qRT-PCR, western blot, lentiviral infection, CellTiter-Glo luminescence assay
qRT-PCR, western blot, lentiviral infection, CellTiter-Glo luminescence assay
Cell viability, western blot, RNA-seq, GSH assay, qRT-PCR, immunofluorescence imaging
Western blot, siRNA, flow cytometry, cell viability, RT-PCR
GSH assay, MDA measurement, western blot, immunohistochemistry, microarray, RT-qPCR, Ial
RT-qPCR, siRNA, gene transfection, cell viability
Affinity-based chemoproteomics, western blotting, and RNAi
RNA-seq, glutamate release assay, cell growth, flow cytometry
RNA-seq, glutamate release assay, cell growth, flow cytometry
RNA-seq, glutamate release assay, cell growth, flow cytometry
RNA interference, cell viability assay, oxidative stress measurement
RNAi, RT-qPCR, western blot, cell viability
RNAi, RT-qPCR, western blot, cell viability
Cell Viability Analysis, western blot, RNAi, qRT-PCR
Immunoprecipitation assay, shRNA knockdown, iron assay, lipid peroxidation assay, glutathione
qRT-PCR, RNA interference
qRT-PCR, RNA interaction
qRT-PCR, RNA interference
shRNA, GSH level measurement, cell death test
RNA interference, cell viability assay, colony formation assay, western blot, qRT-PCR, glutathiono Western blot, densitometry quantification, siRNA, gene transfection, cell death test
Cytotoxicity assays, western blot, p-PCR, RNAi
Cell viability assay, western blot, shRNA, gene transfection
CCK8 cell viability assay, clonogenic cell survival assay, western blot, q-PCR, RNAi
RNAi, live-cell imaging, cell viability, qPCR, western blot
Plate-colony formation assay; measurement of total ROS, Lipid ROS, and intracellular iron shRNA, RT-qPCR, MTT assay, total iron detection, lipid ROS detection
shRNA, RT-qPCR, MTT assay, total iron detection, lipid ROS detection
Immunoblotting, RNAi, qPCR, western blot, cell viability
Immunoblotting, RNAi, qPCR, western blot, cell viability
Cell death assessment
RNAi, cell viability assay, flow cytometry
siRNA, cell death quantification
CRISPR, shRNA, immunoblotting, cell-cycle profile, cell death quantification
Immunoblotting, luciferase reporter assay, qRT-PCR, cell viability assay, colony formation assay Western blot, cell viability assay
CRISPR/Cas9, sgRNA, cell viability assay, immunoblotting, qPCR,
Cell viability and death assay, GSH and ROS levels and lipid peroxidation assays, RNAi, gene transfection
Immunoblotting, luciferase reporter assay, qPCR, cell viability assay, MDA assay, iron assay, glutathione
Immunoblotting, luciferase reporter assay, qPCR, cell viability assay, MDA assay, iron assay, glutathione
Cell viability, western blotting, LC/ESI-MS/MS, flow cytometry, xenograft mice
Cell viability, cell cycle, ROS determination, western blot, immunofluorescence, ectopic expression
Dead cell count, gene knockout, confocal imaging, thin-layer chromatography, BODIPY 493/5
CRISPR/Cas9, RNAi, cell death, western blot, qRT-PCR
Western blot, siRNA, cell death
qRT-PCR, MTT assay, colony-formation assay, lipid ROS assays, iron assay, immunoblotting
Cell proliferation assay, migration and invasion assays, RT-PCR, western blot, immunohistochemistry
Western blot, flow cytometry, SRB assay, gene transfection, shRNA, LOOH quantification
Lentivirus transduction, CCK-8 assay, DYE670 staining assay, ROS staining assay, RT-qPCR, we MTT assay, RT-PCR, luciferase assay, immunoblot, siRNA, Lipid peroxidation assay, GSH measurement
Cell death, cell viability, lipid peroxidation, immunoblotting, CRISPR/Cas9, ChIP assay, qRT-PCR Cytotoxicity assays, western blot, immunoprecipitation, RNA interference, gene transfection, q DNA microarray, western blot, immunoprecipitation, RNA interference, gene transfection, q
Immunofluorescence, western blotting, immunohistochemistry, cell viability, colony formation, qRT-PCR, western blot, cell viability assay, siRNA, ROS detection
Cell viability and clonogenic survival assay, immunofluorescence, western blot, RNAi, gene transfection
Cell proliferation and clonogenic assay, cell survival analysis, xenografts tumor, RNA-seq, RT-qPCR
Expression cloning, cell death, cell viability, LDH assay, western blot, LC-MS, NADH consumption
Cell viability, western blot, ROS induction, glutathione assay, lipid peroxidation assay
Cell viability, lipid peroxidation, iron, GSH and ROS assays, western blot, RT-PCR, RNA-seq
RNA-seq, western blot, qPCR, siRNA, cell count, cell death, iron assay
RNAi, western blot, iron, malondialdehyde and cytotoxicity assays
RNAi, western blot, iron, malondialdehyde and cytotoxicity assays
Immunofluorescence, western blot, ROS detection
CRISPR activation screening, qRT-PCR, cell viability, cell counts, western blot
Table S3. Biological information of ferroptosis-associated genes (human genes)
Test setting
NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell
NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell
NRAS mutant HT-1080 fibrosarcoma cells; KRAS mutant Calu-1 non small cell lung cancer cell
KRAS mutant Calu-1 non small cell lung cancer cell
KRAS mutant Calu-1 non small cell lung cancer cell
KRAS mutant Calu-1 non small cell lung cancer cell
KRAS mutant Calu-1 non small cell lung cancer cell
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KRAS mutant Calu-1 non small cell lung cancer cell
KRAS mutant Calu-1 non small cell lung cancer cell
KRAS mutant Calu-1 non small cell lung cancer cell
KRAS mutant Calu-1 non small cell lung cancer cell
H1299, U2OS and MCF7 cells, mouse embryonic fibroblasts
Chronic myeloid leukemia cell line KBM7
Chronic myeloid leukemia cell line KBM7
RMS13 cells
RMS13 cells
RMS13 cells
HT-1080 fibrosarcoma cells, BJeLR fibroblast cells, Panc1 cells, A673 (Ewing’s sarcoma) and 143B (osteosarcoma)
HepG2, Hepa1-6, Hep3B, and SNU-182 cells
HT-1080 fibrosarcoma cells, mice lung fibroblastic cells
Mouse embryonic fibroblasts, human pancreatic cancer cell lines (PANC1 and PANC2.03), and the human pancreatic carcinoma cells
Human mammary epithelial cells
Human mammary epithelial cells
Human mammary epithelial cells
KP4 pancreatic cancer cells
TP53-/- HCT116 cells, athymic nude mice
H1299, SaoS2, U2OS cells, mouse embryonic fibroblasts
HK2, HAEC and HT22 cells
U2OS or IMR90 cells
Gastric cancer cells AGS, BGC823, athymic nude mice
Gastric cancer cells AGS, BGC823, MKN45, SGC7901, and MGC803
MDA-MB-231, Hs 578T, and HCC 1937 cells
Lung cancer A549, SPCA1, and H522 cells
HCT116 and CX-1 cells
HCT116 and CX-1 cells
Human liver specimens and hepatic stellate cell; C57BL/6 mice; mouse hepatocyte and hepatic stellate cell
HEK-293T, Caki1, 786-O, 769-P, ACHN and NCI-H226 cell lines; RCC4, UMRC2, SLR20, and UMRC6 cell
HAP1, H1299, U-2 OS cells
A549 and SPC-A-1 cells
HK-2 cells
HK-2 cells
HT-1080, A375, B16-F0, ID8 cells, female NSG and C57BL/6 mice
A549, Cal27, HT29 and MG-63 cells, Cx3cr1-Cre mice
HL-60 cell, male NOD/SCID mice
HUVEC cells
HT1080 cells, retinal pigment epithelial cells
MDA-MB-231, RCC4, 293T, and HT-1080 cell lines
Mouse embryonic fibroblasts, NF639 cells, human epithelial tumour cells, human mesothelioma cells, xer
Calu-1, THP1, HT1080, and HL-60 cells, athymic nude mice
HK-2 cells, C57BL/6J mice
RCC4, 786O cells, JAX NOD.CB17-PrkdcSCID-J mice
Cell lines A549, H1975, DMS53, DMS273, KLE, AN3CA, RL95, Hec1A, Ishikawa, MDA-MB-231, MCF-7, Hc
HEK293T, HT-1080 and KYSE-170 cells
Hepatic stellate cells, C57BL/6 mice
HK-2 cells, C57BL/6 mice
Cell lines TE-1, Eca9706, Eca109, KYSE150, and KYSE450, BALB/c athymic nude mice
PANC1, BxPC3 cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
BJeLR cells
HT-1080 and Calu-1 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
HT-1080 cells
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HT-1080 cells
Chronic myeloid leukemia cell line KBM7
Chronic myeloid leukemia cell line KBM7
Chronic myeloid leukemia cell line KBM7
Pancreatic adenocarcinoma cell line Panc-1 cells
Patient PDAC tissues
Patient PDAC tissues
Patient PDAC tissues
Patient PDAC tissues
Patient PDAC tissues
HepG2, Hepa1-6, Hep3B, and SNU-182 cells
HT1080 cells
PANC1 cells
PANC1 cells
A549 cells
A549 cells
H358, A549 cells
H358, A549 cells
H358, A549 cells
H358, A549 cells
H358, A549 cells
H358, A549 cells
H358, A549 cells
H358, A549 cells
H358, A549 cells
MDA-MB-231, Hs 578T, and HCC 1937 cells
HEK293 cells
HEK293 cells
HEK293 cells
HT1080 and PANC1 cells, mouse embryonic fibroblasts
H358, PC9, SPC-A-1, and A549 cells
HepG2, Bel-7402 cells
HepG2, Bel-7402 cells
HepG2, Bel-7402 cells
HepG2, Bel-7402 cells
HepG2, Bel-7402 cells
HepG2, Bel-7402 cells
HepG2, Bel-7402 cells
HepG2, Bel-7402 cells
SH-SY5Y cells
HEK293T cells
HepG2, Huh7, and Hep3B cells
OE33, STKM2, MKN45 cells
OE33, STKM2, MKN45 cells
Patient-derived fibroblasts
Primary corneal endothelial cells, B4G12 and HT1080 cells
Trophoblasts, preeclampsia model, HTR-8/SVneo and TEV-1 cells
HT-1080 cells
HRAS mutant BJelR-engineered tumor cells, HT-1080 cells, xenograft mouse model (athymic nude mice
DU-145 prostate cancer cells
DU-145 prostate cancer cells
DU-145 prostate cancer cells
HCC cell lines Huh7 and PLC/PRF5; Balb/c nude mice received tumour xenografts derived from HCC cell:
HeLa and U2OS cells, human xenograft mouse tumor derived from HeLa (#CCL-2) cells.
HeLa and U2OS cells, human xenograft mouse tumor derived from HeLa (#CCL-2) cells.
HepG2, Hepa1-6, Hep3B, and SNU-182 cells, C57BL/6 mice
HepG2, Hepa1-6, Hep3B, and SNU-182 cells
HepG2, Hepa1-6, Hep3B, and SNU-182 cells
HepG2, Hepa1-6, Hep3B, and SNU-182 cells
MDA-MB-468, BT-20 cells
HCC cells (HepaG2, Hep3B, and Huh7 cells), nude mice.
MDA MB 231 and SKBr3 cells
HepG2 and Hep3B cells
Pancreatic ductal adenocarcinoma cell lines (PANC1, CFPAC1, MiaPaCa2), nude mice, B6 mice
Pancreatic ductal adenocarcinoma cells (e.g., PANC1, CFPAC1, MiaPaCa2, and Panc2.03)
HCT116, athymic nude mice
Lung cancer H358 and PC9 cells, SCID Mice
A549 cancer cells
A549 cancer cells
MCF-10A and SUM-159 cells
MCF-10A and SUM-159 cells
IMR90 cells
MDA-MB-231 cells, NOD.CB17 Scid/J mice
ME-180 cells
HT-1080 cells
Melanoma cell lines A375 and G-361, C57BL/6 mice
HT1080 cells
UOK262, HT1080, HK2, A498 cells
Head and neck cancer cells
A375 and G-361 cells
A375 and G-361 cells
A375 and G-361 cells
HepG2 cells, female ICR mice
HL60, KG1, THP-1 cells
HEK293, HT-1080 cells
H1299, SK-N-BE(2)C, T24, UM-UC-.3, SW780 cells, nude mice
H1299 cells
A549 and SPC-A-1 cells
MDA-MB-231, Hs578T, H1299, A549 and MCF-10A cells, female athymic BALB/c nude mice
H1299 cells
HUVEC cells
HepG2 and AML-12 cell lines, mouse embryonic fibroblasts cells, ICR mice
Mouse embryonic fibroblasts, NF639 cells, human epithelial tumour cells, human mesothelioma cells, xer
Calu-1, THP1, HT1080, and HL-60 cells, athymic nude mice
Calu-1, THP1, HT1080, and HL-60 cells, athymic nude mice
Bel-7402, SMMC-7721 cells, athymic nude mice
Mesothelioma cell lines ACC-Meso-1, NCI-H2373 and NCI-H2052, mesothelial cell line MeT-5A
Hep G2, Huh-7, SMMC-7721 and PLC/PRF/5 cells, nude mice
SGC7901 and MGC803 cells, nude mice
MCF-7, HT1080, Pfa1 cells
ARPE-19, hfrPE cells
Hepatic stellate cells, C57BL/6 mice
MCF10A, Hs578t and MDA-MB-231 cells
PANC1 and HepG2 cells, athymic nude or B6 mice
PANC1 and HepG2 cells, athymic nude or B6 mice
LO2 cells, mice model
HT-1080,786-O, A-498, Caki-1, AU565, DU4475, MCF-7 cells
| Pathway       | Confidence   |
|--------------|--------------|
| RPL8         | +: Ferroptosis Validated |
| IREB2        | +: Ferroptosis Validated |
| ATP5MC3      | +: Ferroptosis Validated |
| CS           | +: Ferroptosis Validated |
| EMC2         | +: Ferroptosis Validated |
| ACSF2        | +: Ferroptosis Validated |
| NOX1         | +: Ferroptosis Deduced  |
| CYBB         | +: Ferroptosis Deduced  |
| NOX3         | +: Ferroptosis Deduced  |
| NOX4         | +: Ferroptosis Deduced  |
| NOX5         | +: Ferroptosis Deduced  |
| DUOX1        | +: Ferroptosis Deduced  |
| DUOX2        | +: Ferroptosis Deduced  |
| G6PD         | +: Ferroptosis Validated |
| PGD          | +: Ferroptosis Validated |
| VDAC2        | +: Ferroptosis Validated |
| TP53         | -:: SLC7A11, SLC7A11 ::+ Cystine, Validated |
| ACSL4        | +: Ferroptosis Predicted |
| LPCAT3       | +: Ferroptosis Predicted |
| NRAS         | +: Ferroptosis Deduced  |
| KRAS         | +: Ferroptosis Deduced  |
| HRAS         | +: Ferroptosis Deduced  |
| CARPS        | -:: Transsulfuration pathway, Tr:: Validated |
| KEAP1        | -:: NFE2L2, NFE2L2 ::+ Ferroptosis Validated |
| HMOX1        | +: Lipid ROS, Lipid ROS ::+ Fe Validated |
| ATG5         | +: Ferroptosis Validated |
| ATG7         | +: Ferroptosis Validated |
| NCOA4        | -:: FTH1, FTH1 -:: Ferroptosis Validated |
| ALOX12       | +: PUFAs peroxidation, PUFAs Validated |
| ALOX12B      | +: PUFAs peroxidation, PUFAs Validated |
| ALOX15       | +: PUFAs peroxidation, PUFAs Validated |
| ALOX15B      | +: PUFAs peroxidation, PUFAs Validated |
| ALOX3        | +: PUFAs peroxidation, PUFAs Validated |
| PHKG2        | +: PUFAs peroxidation, PUFAs Validated |
| SAT1         | +: ALOX15, ALOX15 ::+ Lipid RO:: Validated |
| EGFR         | -:: MAPK, MAPK -:: Ferroptosis Validated |
| MAPK         | -:: GPX4, GPX4 ::- Lipid ROS, MA Validated |
| ZEB1         | +: Lipid ROS, Lipid ROS ::+ Ferro:: Validated |
| DPP4         | +: Lipid ROS, Lipid ROS ::+ Ferro:: Validated |
| CDKN2A       | -:: NFE2L2, NFE2L2 ::+ SLC7A:: Validated |
| (PEBP1/15LO) | +: Ferroptosis Validated |
| SOCS1        | +: p53, p53 ::- SLC7A11, SLC7A Validated |
| CDO1         | -:: GPX4, GPX4 ::- Ferroptosis Validated |
| MYB          | +: CDO1, CDO1 -:: GPX4, GPX4 ::- Validated |
| CHAC1        | -:: GSH, GSH -:: Ferroptosis Validated |
| LINC00472    | +: p53, p53 ::- Ferroptosis Validated |
| PRKAA2       | +: (BECN1/SLC7A11), (BECN1/Validated |
| PRKAA1       | +: (BECN1/SLC7A11), (BECN1/ Validated |
| ELAVL1       | +: Ferroptosis Validated |
| BAP1         | -:: SLC7A11, SLC7A11 -:: Lipid RC Validated |
| ABCCC1       | -:: GSH, GSH -:: Ferroptosis Validated |
| MIR6852      | -:: CBS, CBS -:: Ferroptosis Validated |
| ACVR1B       | -:: NFE2L2, NFE2L2 -:: Ferropt:: Validated |
| TGFBR1       | -:: NFE2L2, NFE2L2 -:: Ferropt:: Validated |
| Gene          | Function and Validation Details                           |
|--------------|-----------------------------------------------------------|
| IFNG         | SLC3A2, SLC7A11, SLC | Ferroptosis | Validated |
| ANO6         | +: Ferroptosis                                            |             |            |
| HMGB1        | +: Ferroptosis                                            |             |            |
| TNFAIP3      | +: ACSL4, ACSL4, Lipid ROS, | Ferroptosis, | Validated |
| ATF3         | -: SLC7A11, SLC7A11 | System | Validated |
| ATM          | -: MTF1, MTF1, FTL, MTF1, FTH1, FTL, FTH1 | Ferroptosis | Validated |
| YAP          | +: ACSL4, ACSL4 | Ferroptosis, Y | Validated |
| EGLN2        | +: HIF1A, HIF1A, Lipid ROS, | Ferroptosis, | Validated |
| MIOX         | +: GPX4, GPX4 | Ferroptosis, M | Validated |
| TAZ          | +: EMP1, EMP1 | NOX4, NOX4 | Validated |
| MTDH         | +: Cysteine, Cystein, Ferroptosis, | Validated |
| IDH1         | +: GPX4, GPX4 | Lipid ROS, Lipid | Validated |
| YAP          | +: ACSL4 | Ferroptosis, Y | Validated |
| EGLN2        | +: HIF1A, HIF1A | Lipid ROS, | Validated |
| MIOX         | +: GPX4, GPX4 | Ferroptosis, M | Validated |
| TAZ          | +: EMP1, EMP1 | NOX4, NOX4 | Validated |
| MTDH         | +: Cysteine, Cystein, Ferroptosis, | Validated |
| IDH1         | +: GPX4, GPX4 | Lipid ROS, Lipid | Validated |
| FBXW7        | +: Ferroptosis                                            |             |            |
| PANX1        | +: HMOX1, HMOX1, Ferropt | Validated |
| DNAJB6       | +: GPX4, GPX4 | Ferroptosis, Predicted |
| LONP1        | +: Nrf2/Keap1 pathway, Nrf2/K | Validated |

Inferred as ferroptotic marker because of change (|delta ct| > 2) in gene expression.
Further study needed to confirm connection to ferroptosis.

Validated

An error may exist in the original article, where the authors wrote "ferritin light chain 1 (FTH1)". According to HGNC, FTH1 is the official symbol for "ferritin heavy chain 1".

Not essential but may play a role in ferroptosis initiation.

SLC7A11 :+ Cystine, Cystine :-: Ferroptosis Validated
GPX4 :: Lipid ROS, Lipid ROS :+: Ferroptosis Validated
AKR1C1 ::: Ferroptosis Validated
AKR1C2 ::: Ferroptosis Validated
AKR1C3 :: Ferroptosis Validated
RB1 :: Ferroptosis Validated
HSPB1 :: Ferroptosis Validated
HSF1 :: Ferroptosis Validated
NFE2L2 :: (NQO1/HMOX1/FTH1), (NQO1/HMOX1/FTH1) :: Ferroptosis Validated
SQSTM1 :: KEAP1, KEAP1 :: NFE2L2, NFE2L2 :: Ferroptosis Validated
NQO1 :: Ferroptosis Validated
HMOX1 :: Ferroptosis Validated
FTH1 :: Ferroptosis Validated
MUC1 :: System Xc-, System Xc- :: G Validated
MT1G :: Ferroptosis Validated
SLC40A1 :: Lipid ROS, Lipid ROS :: Fe Validated
CISD1 :: Mitochondrial lipid ROS, Mito Validated
HSPA5 :: GPX4, GPX4 :: Lipid ROS, Liq Validated
ATF4 :: HSPA5, HSPA5 :: GPX4, GPX4 Validated
TP53 :: Nucleus DPP4, Nucleus DPP4 :: Ferroptosis Validated
HELS :: GLUT1, HELLS :: SCD, HELLS Validated
SCD :: Ferroptosis Validated
FADS2 :: Ferroptosis Validated
SRC :: STAT3, STAT3 :: ACSL4, ACSL4 Validated
STAT3 :: ACSL4, ACSL4 :: Ferroptosis Validated
PML :: Ferroptosis Validated
NFS1 :: TFRC, TFRC :: Ferroptosis Validated
TP63 :: Ferroptosis Validated
CDKN1A :: GSH, GSH :: Lipid ROS, Liq Validated
MIR137 :: SLC1A5, SLC1A5 :: Glutami Validated
VDAC2 :: Ferroptosis Validated
FH :: GPX4, GPX4 :: Ferroptosis Validated
CISD2 :: Lipid ROS, Lipid ROS :: Ferro Validated
MIR9 :: GOT1, GOT1 :: alpha KG, alp Validated
MIR9 :: GOT1, GOT1 :: alpha KG, alp Validated
MIR9 :: GOT1, GOT1 :: alpha KG, alp Validated
CBS :: Ferroptosis Validated
ISCU :: GSH, GSH :: Ferroptosis Validated
ACSL3 :: Ferroptosis Validated
OTUB1 :: SLC7A11, SLC7A11 :: Ferroq Validated
CD44 :: SLC7A11, SLC7A11 :: Ferropt Validated
(LINCO0336/ELAVL1) :: Ferroptosis Validated
BRD4 :: Ferritinophagy, Ferritinophagy Validated
PRDX6 :: Lipid ROS, Lipid ROS :: Ferro Validated
MIR17 :: A20, A20 :: ACSL4, ACSL4 :: Ferro Validated
SES2N2 :: Lipid ROS, Lipid ROS :: Ferro Validated
NF2 :: YAP, YAP :: Ferroptosis Validated
ARNTL :: EGLN2, EGLN2 :: HIF1A, HIF Validated
HIF1A :: Lipid ROS, Lipid ROS :: Ferro Validated
JUN :: GSH, GSH :: Ferroptosis, JUN :: Deduced
CA9 :: Ferroptosis Validated
S1R :: Ferroptosis Validated
PLIN2 :: Ferroptosis Screened
FPS1 :: CoQ10, CoQ10 :: Lipid ROS, L Validated
LAMP2 :: Cysteine, Cysteine :: GSH, C Validated
ZFP36 :: ATG16L1, ATG16L1 :: Ferropt Validated
Prominin2 :: Ferritin-containing MVB, Validated
CHMP5 :: Ferroptosis Validated
CHMP6 :: Ferroptosis Validated
CAV-1 :: xCT, xCT :: GPX4, GPX4 :: F Validated
GCH1 :: Phospholipid, Phospholipid :: Validated
The presented inhibition study is not sufficient to confirm its role in ferroptosis.

The presented inhibition study is not sufficient to confirm its role in ferroptosis.

The presented inhibition study is not sufficient to confirm its role in ferroptosis.

The presented inhibition study is not sufficient to confirm its role in ferroptosis.

The acetylation-defective mutant (p53[3KR]) also retains the ability to induce ferroptosis upon reactive oxygen species (ROS)-induced stress.

Author prediction based on gene function.

Inferred as a promoter because RAS mutant is resistant to ferroptosis.

Inferred as a promoter because RAS mutant is resistant to ferroptosis.

Inferred as a promoter because RAS mutant is resistant to ferroptosis.

Other articles (PMID 26403645, 28515173) suggest it a suppressor.

Activated by p53.

Also triggers apoptosis.
Prostaglandin G/H synthase 2
Dual specificity protein phosphatase 1
Nitric oxide synthase
Neutrophil cytosol factor 2
Metallothionein-3
Polyubiquitin-C
Serum albumin
Thioredoxin reductase 1
Sulfiredoxin-1
Glutathione peroxidase 2
BCL2/adenovirus E1B 19 kDa protein-interacting protein 3
Serine/threonine-protein kinase OSR1
Selenoprotein S
Angiopoietin-related protein 7
Glutathione-specific gamma-glutamylcyclotransferase 1
Cystine/glutamate transporter
DNA damage-inducible transcript 4 protein
Asparagine synthetase [glutamine-hydrolyzing]
TSC22 domain family protein 3
DDIT3 upstream open reading frame protein
Jun dimerization protein 2
Sestrin-2
Neutral amino acid transporter A
Phosphoenolpyruvate carboxykinase [GTP]
Thioredoxin-interacting protein
Very low-density lipoprotein receptor
Alanine aminotransferase 2
Phosphoserine aminotransferase
Leucine rich adaptor protein 1-like
Large neutral amino acids transporter small subunit 1
Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein
X-box-binding protein 1
Cyclic AMP-dependent transcription factor ATF-3
4F2 cell-surface antigen heavy chain
Cystathionine beta-synthase
Cyclic AMP-dependent transcription factor ATF-4
Zinc finger protein 419
Kelch-like protein 24
Tribbles homolog 3
Zinc finger protein 69 homolog B
V-type proton ATPase subunit G 2
Vascular endothelial growth factor A
Growth/differentiation factor 15
Tubulin epsilon chain
Arrestin domain-containing protein 3
CCAAT/enhancer-binding protein gamma
NA
Regulator of G-protein signaling 4
NA
NA
Eukaryotic translation initiation factor 2 subunit 1
Estradiol 17-beta-dehydrogenase 11
1-acyl-sn-glycerol-3-phosphate acyltransferase gamma
Histone-lysine N-methyltransferase SETD1B
Heme oxygenase 1
Serotransferrin
Ferritin light chain
60S ribosomal protein L8
ATP synthase F(0) complex subunit C3
Transferrin receptor protein 1
Transcription factor MafG
Ferritin heavy chain
D(1B) dopamine receptor
D(4) dopamine receptor
Mitogen-activated protein kinase kinase kinase 5
Mitogen-activated protein kinase 14
Solute carrier family 2
Solute carrier family 2
Solute carrier family 2
Solute carrier family 2
Solute carrier family 2
NA
Solute carrier family 2
eIF-2-alpha kinase GCN2
Arachidonate 5-lipoxygenase
Arachidonate 12-lipoxygenase
Arachidonate 15-lipoxygenase
High mobility group protein B1
ELAV-like protein 1
Hemoglobin subunit alpha
Nicotinamide N-methyltransferase
Perilipin-4
Hypermethylated in cancer 1 protein
Stathmin
Ribonucleoside-diphosphate reductase subunit M2
Macrophage-capping protein
Hepatocyte nuclear factor 4-alpha
Neuroglobin
14-3-3 protein epsilon
GA-binding protein subunit beta-1
Aurora kinase A
NA
Receptor-interacting serine/threonine-protein kinase 1
Peroxisidoxin-1
NA
NA
NA
NA
NA
Article (PMID 26405158) suggests it a driver.

Promotes ferroptosis via a transcription-dependent mechanism in non-CRC cells.
| Protein encoded                                      |
|-----------------------------------------------------|
| 60S ribosomal protein L8                            |
| Iron-responsive element-binding protein 2           |
| ATP synthase F(0) complex subunit C3                |
| Citrate synthase                                    |
| ER membrane protein complex subunit 2               |
| Medium-chain acyl-CoA ligase ACSF2                  |
| NADPH oxidase 1                                     |
| Cytochrome b-245 heavy chain                        |
| NADPH oxidase 3                                     |
| NADPH oxidase 4                                     |
| NADPH oxidase 5                                     |
| Dual oxidase 1                                      |
| Dual oxidase 2                                      |
| Glucose-6-phosphate 1-dehydrogenase                 |
| 6-phosphogluconate dehydrogenase                    |
| Voltage-dependent anion-selective channel protein 2 |
| Cellular tumor antigen p53                          |
| Long-chain-fatty-acid--CoA ligase 4                 |
| Lysophospholipid acyltransferase 5                  |
| GTPase NRas                                         |
| GTPase KRas                                         |
| GTPase HRas                                         |
| Kelch-like ECH-associated protein 1                 |
| Heme oxygenase 1                                    |
| Autophagy protein 5                                 |
| Ubiquitin-like modifier-activating enzyme ATG7      |
| Nuclear receptor coactivator 4                      |
| Arachidonate 12-lipoxygenase                        |
| Arachidonate 12-lipoxygenase                        |
| Arachidonate 15-lipoxygenase                        |
| Arachidonate 15-lipoxygenase B                      |
| Hydroperoxide isomerase ALOXE3                      |
| Phosphorylase b kinase gamma catalytic chain        |
| Diamine acetyltransferase 1                         |
| Epidermal growth factor receptor                    |
| Mitogen-activated protein kinase 3                  |
| Mitogen-activated protein kinase 1                  |
| Zinc finger E-box-binding homeobox 1                |
| Dipeptidyl peptidase 4                              |
| Cyclin-dependent kinase inhibitor 2A                |
| Phosphatidylethanolamine-binding protein 1          |
| Suppressor of cytokine signaling 1                  |
| Cysteine dioxygenase type 1                         |
| Transcriptional activator Myb                       |
| Glutathione-specific gamma-glutamylcycotransferase 1|
| Putative uncharacterized protein encoded by LINC00472|
| 5’-AMP-activated protein kinase catalytic subunit alpha-2|
| 5’-AMP-activated protein kinase catalytic subunit alpha-1|
| ELAV-like protein 1                                 |
| Ubiquitin carboxyl-terminal hydrolase BAP1          |
| Multidrug resistance-associated protein 1           |
| _NA_                                                |
| Activin receptor type-1B                            |
| TGF-beta receptor type-1                            |
Interferon gamma
Anoctamin-6
High mobility group protein B1
Tumor necrosis factor alpha-induced protein 3
Cyclic AMP-dependent transcription factor ATF-3
Serine-protein kinase ATM
YY1-associated protein 1
Egl nine homolog 2
Inositol oxygenase
Tafazzin
Protein LYRIC
Isocitrate dehydrogenase [NADP] cytoplasmic
F-box/WD repeat-containing protein 7
Pannexin-1
DnaJ homolog subfamily B member 6
Lon protease homolog, mitochondrial
P35354 (PGH2_HUMAN)
P28562 (DUS1_HUMAN)
P35228 (NOS2_HUMAN)
P19878 (NCF2_HUMAN)
P25713 (MT3_HUMAN)
P0CG48 (UBC_HUMAN)
P02768 (ALBU_HUMAN)
Q16881 (TRXR1_HUMAN)
Q9BYN0 (SRXN1_HUMAN)
P18283 (GPX2_HUMAN)
Q12983 (BNIP3_HUMAN)
Q95747 (OXSR1_HUMAN)
Q9BQE4 (SELS_HUMAN)
Q43827 (ANGL7_HUMAN)
Q98UX1 (CHAC1_HUMAN)
Q9UPY5 (XCT_HUMAN)
Q9NX09 (DDIT4_HUMAN)
NA
P08243 (ASNS_HUMAN)
Q99576 (T22D3_HUMAN)
P0DPQ6 (DT3UO_HUMAN)
Q8WYK2 (JDP2_HUMAN)
P58004 (SESN2_HUMAN)
P43007 (SATT_HUMAN)
Q16822 (PCKGM_HUMAN)
Q9H3M7 (TXNIP_HUMAN)
P98155 (VLDLR_HUMAN)
Q8TD30 (ALAT2_HUMAN)
Q9Y617 (SERC_HUMAN)
Q8IV03 (LUR1L_HUMAN)
Q01650 (LAT1_HUMAN)
Q15011 (HERP1_HUMAN)
P17861 (XBP1_HUMAN)
P18847 (ATF3_HUMAN)
P08195 (4F2_HUMAN)
P35520 (CBS_HUMAN)
P18848 (ATF4_HUMAN)
Q96HQ0 (ZN419_HUMAN)
Q6TFL4 (KLH24_HUMAN)
Q96RU7 (TRIB3_HUMAN)
Q9UIJ9 (ZF69B_HUMAN)
O95670 (VATG2_HUMAN)
| Gene ID   | Description                                      |
|----------|--------------------------------------------------|
| P15692   | VEGFA_HUMAN                                      |
| Q99988   | GDF15_HUMAN                                      |
| Q9UTJ0   | TBE_HUMAN                                        |
| Q96867   | ARRD3_HUMAN                                      |
| P53567   | CEBPG_HUMAN                                      |
| _NA_     |                                                 |
| P49798   | RGS4_HUMAN                                       |
| _NA_     |                                                 |
| _NA_     |                                                 |
| P05198   | IF2A_HUMAN                                       |
| Q8NBQ5   | DHB11_HUMAN                                      |
| Q9NRZ7   | PLCC_HUMAN                                       |
| Q9UP56   | SET1B_HUMAN                                      |
| P09601   | HMOX1_HUMAN                                      |
| P02787   | TRFE_HUMAN                                       |
| P02792   | FRIL_HUMAN                                       |
| P62917   | RL8_HUMAN                                        |
| P48201   | AT5G3_HUMAN                                      |
| P02786   | TFR1_HUMAN                                       |
| O15525   | MAFG_HUMAN                                       |
| P02794   | FRIH_HUMAN                                       |
| P21918   | DRD5_HUMAN                                       |
| P21917   | DRD4_HUMAN                                       |
| Q99683   | M3K5_HUMAN                                       |
| Q16539   | MK14_HUMAN                                       |
| P11166   | GTR1_HUMAN                                       |
| P11169   | GTR3_HUMAN                                       |
| Q9UGQ3   | GTR6_HUMAN                                       |
| Q9NY64   | GTR8_HUMAN                                       |
| Q8TD20   | GTR12_HUMAN                                      |
| _NA_     |                                                 |
| Q8TDB8   | GTR14_HUMAN                                      |
| Q9P2K8   | E2AK4_HUMAN                                      |
| P09917   | LOX5_HUMAN                                       |
| P18054   | LOX12_HUMAN                                      |
| P16050   | LOX15_HUMAN                                      |
| P09429   | HMGB1_HUMAN                                      |
| Q15717   | ELAV1_HUMAN                                      |
| P69905   | HBA_HUMAN                                        |
| P40261   | NNMT_HUMAN                                       |
| Q96Q06   | PLIN4_HUMAN                                      |
| Q14526   | HIC1_HUMAN                                       |
| P16949   | STMN1_HUMAN                                      |
| P31350   | RIR2_HUMAN                                       |
| P40121   | CAPG_HUMAN                                       |
| P41235   | HNF4A_HUMAN                                      |
| Q9NPG2   | NGB_HUMAN                                        |
| P62258   | 1433E_HUMAN                                      |
| Q06547   | GABP1_HUMAN                                      |
| Q14965   | AURKA_HUMAN                                      |
| _NA_     |                                                 |
| Q13546   | RIPK1_HUMAN                                      |
| Q06830   | PRDX1_HUMAN                                      |
| _NA_     |                                                 |

Cystine/glutamate transporter
Phospholipid hydroperoxide glutathione peroxidase
Aldo-keto reductase family 1 member C1
Aldo-keto reductase family 1 member C2
Aldo-keto reductase family 1 member C3
Retinoblastoma-associated protein
Heat shock protein beta-1
Heat shock factor protein 1
Nuclear factor erythroid 2-related factor 2
Sequestosome-1
NAD(P)H dehydrogenase [quinone] 1
Heme oxygenase 1
Ferritin heavy chain
Mucin-1
Metallothionein-1G
Solute carrier family 40 member 1
CDGSH iron-sulfur domain-containing protein 1
Endoplasmic reticulum chaperone BiP
Cyclic AMP-dependent transcription factor ATF-4
Cellular tumor antigen p53
Lymphoid-specific helicase
Acyl-CoA desaturase
Acyl-CoA 6-desaturase
Proto-oncogene tyrosine-protein kinase Src
Signal transducer and activator of transcription 3
Protein PML
Cysteine desulfurase
Tumor protein 63
Cyclin-dependent kinase inhibitor 1
Voltage-dependent anion-selective channel protein 2
Fumarate hydratase
CDGSH iron-sulfur domain-containing protein 2
Iron-sulfur cluster assembly enzyme ISCU
Long-chain-fatty-acid--CoA ligase 3
Ubiquitin thioesterase OTUB1
CD44 antigen
Putative uncharacterized protein encoded by LINC00336
Peroxisiredoxin-6
Sestrin-2
Merlin
Aryl hydrocarbon receptor nuclear translocator-like protein 1
Hypoxia-inducible factor 1-alpha
Transcription factor AP-1
Carbonic anhydrase 9
Protein lifeguard 4
Perilipin-2
Apoptosis-inducing factor 2
Lysosome-associated membrane glycoprotein 2
mRNA decay activator protein ZFP36
Prominin-2
Charged multivesicular body protein 5
Charged multivesicular body protein 6
Caveolin-1
GTP cyclohydrolase 1
| UniProtKB       | PMID     | Remark                                       |
|-----------------|----------|----------------------------------------------|
| P62917 (RL8_HUMAN) | 22632970  | _NA_                                         |
| P48200 (IREB2_HUMAN) | 22632970  | _NA_                                         |
| P48201 (AT5G3_HUMAN) | 22632970  | ATP5G3 in article                            |
| O75390 (CISY_HUMAN) | 22632970  | _NA_                                         |
| Q15006 (EMG2_HUMAN) | 22632970  | TTC35 in article                             |
| Q96CM8 (ACSF2_HUMAN) | 22632970  | _NA_                                         |
| Q9Y558 (NOX1_HUMAN) | 22632970  | _NA_                                         |
| P04839 (CY24B_HUMAN) | 22632970  | NOX2 in article                              |
| Q9HBY0 (NOX3_HUMAN) | 22632970  | _NA_                                         |
| Q9NP5H5 (NOX4_HUMAN) | 22632970  | _NA_                                         |
| Q96PH1 (NOX5_HUMAN) | 22632970  | _NA_                                         |
| P01111 (RASN_HUMAN) | 26157704  | _NA_                                         |
| P01116 (RASK_HUMAN)  | 26157704  | _NA_                                         |
| P01112 (RASH_HUMAN)   | 26157704  | _NA_                                         |
| P49589 (SYCC_HUMAN)  | 26184909  | CARS in article                              |
| Q14145 (KEAP1_HUMAN) | 26403645  | _NA_                                         |
| P09601 (HMOX1_HUMAN) | 26405158  | HO-1 in article                              |
| Q9H1Y0 (ATG5_HUMAN)  | 27245739  | _NA_                                         |
| Q95352 (ATG7_HUMAN)  | 27245739  | _NA_                                         |
| Q13772 (NCOA4_HUMAN) | 27245739  | _NA_                                         |
| P18054 (LOX12_HUMAN) | 27506793  | _NA_                                         |
| O75342 (LX12B_HUMAN) | 27506793  | _NA_                                         |
| P16050 (LOX15_HUMAN) | 27506793  | _NA_                                         |
| O15296 (LX15B_HUMAN) | 27506793  | _NA_                                         |
| Q9BYJ1 (LOXE3_HUMAN) | 27506793  | _NA_                                         |
| P15735 (PHKG2_HUMAN) | 27506793  | _NA_                                         |
| P21673 (SAT1_HUMAN)  | 27698118  | _NA_                                         |
| P00533 (EGFR_HUMAN)  | 28297659  | _NA_                                         |
| P27361 (MK03_HUMAN)  | 28297659  | ERK1 in article                              |
| P28482 (MK01_HUMAN)  | 28297659  | ERK2 in article                              |
| P37275 (ZEB1_HUMAN)  | 28678785  | _NA_                                         |
| P27487 (DPP4_HUMAN)  | 28813679  | _NA_                                         |
| P42771 (CDN2A_HUMAN) | 28985506  | ARF in article                               |
| P30086 (PEBP1_HUMAN) | 29053969  | _NA_                                         |
| Q15524 (SOC51_HUMAN) | 29081404  | _NA_                                         |
| Q16878 (CDO1_HUMAN)  | 29144989  | _NA_                                         |
| P10242 (MYB_HUMAN)   | 29144989  | _NA_                                         |
| Q98UX1 (CHAC1_HUMAN) | 29383104  | _NA_                                         |
| Q9H8W2 (CF155_HUMAN) | 2958351  | P53RRA in article                            |
| P54646 (AAPK2_HUMAN) | 30057310  | PRKAA in article                             |
| Q13131 (AAPK1_HUMAN) | 30057310  | AMPK alpha in article                        |
| Q15717 (ELAV1_HUMAN) | 30081711  | _NA_                                         |
| Q92560 (BAP1_HUMAN)  | 30202049  | _NA_                                         |
| P33527 (MRP1_HUMAN)  | 30726737  | MRP1 in article                              |
| P36896 (ACV1B_HUMAN) | 30804470  | ALK4 in article                              |
| P36897 (TGFR1_HUMAN) | 30804470  | ALK5 in article                              |
| Gene ID      | HGNC ID | Description                                    |
|-------------|---------|------------------------------------------------|
| P01579      | 31043744| IFNgamma in article                            |
| Q4KMQ2      | 31060306| _NA_                                           |
| P09429      | 31105999| _NA_                                           |
| P21580      | 31160087| Zinc lipoprotein A20 in article                |
| P18847      | 31273299| _NA_                                           |
| Q13315      | 31320750| _NA_                                           |
| Q9H869      | 31341276| YAP in article                                  |
| Q96KS0      | 31355331| _NA_                                           |
| Q9UGB7      | 31437128| _NA_                                           |
| Q16635      | 31484063| _NA_                                           |
| Q86UE4      | 31527591| _NA_                                           |
| O75874      | 31591388| _NA_                                           |
| Q969H0      | 31679460| _NA_                                           |
| Q96RD7      | 31694915| _NA_                                           |
| O75190      | 31701262| _NA_                                           |
| P36776      | 31822343| _NA_                                           |

24439385 May promote ferroptosis.  marker
24439385 May promote ferroptosis.  marker
24439385 May promote ferroptosis.  marker
24439385 May promote ferroptosis.  marker
24439385 May promote ferroptosis.  marker
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24439385 May promote ferroptosis.  marker
24439385 May promote ferroptosis.  marker
24439385 May promote ferroptosis.  marker
24439385 SELS in article. May promote marker
24439385 May promote ferroptosis.  marker
24844246 _NA_ marker
24844246 May inhibit ferroptosis.  marker
24844246 May promote ferroptosis.  marker
24844246 Not found in HGNC. May prc marker
24844246 May promote ferroptosis.  marker
24844246 May promote ferroptosis.  marker
24844246 May promote ferroptosis.  marker
24844246 May promote ferroptosis.  marker
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24844246 May promote ferroptosis.  marker
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24844246 C9ORF150 in article. May prom marker
24844246 May promote ferroptosis.  marker
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24844246 May promote ferroptosis.  marker
24844246 May promote ferroptosis.  marker
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24844246 May promote ferroptosis.  marker
24844246 May promote ferroptosis.  marker
24844246 May promote ferroptosis.  marker
24844246 ZNF643 in article. May prom marker
24844246 May promote ferroptosis.  marker
May promote ferroptosis.
May inhibit ferroptosis.
MUTED-TXNDC5 in article. May inhibit ferroptosis.
Not found in HGNC. May inhibit ferroptosis.
eIF2alpha in article. May promote ferroptosis.
HO-1 in article. May promote ferroptosis.
ATP5G3 in article. May promote ferroptosis.
GLUT1 in article. May inhibit ferroptosis.
GLUT3 in article. May inhibit ferroptosis.
GLUT6 in article. May inhibit ferroptosis.
GLUT8 in article. May inhibit ferroptosis.
GLUT12 in article. May inhibit ferroptosis.
Not found in HGNC. May inhibit ferroptosis.
GLUT14 in article. May inhibit ferroptosis.
GCN2 in article. May promote ferroptosis.
5-LOX in article
p12-LOX in article
15-LOX-1 in article
Q9UPY5 (XCT_HUMAN)
P36969 (GPX4_HUMAN)
Q04828 (AK1C1_HUMAN)
P52895 (AK1C2_HUMAN)
| Protein ID  | Accession   | Description                          |
|------------|-------------|--------------------------------------|
| P42330     | (AK1C3_HUMAN) | 24844246  
| P06400     | (RB_HUMAN)  | 25444922   
| P04792     | (HSPB1_HUMAN) | 25728673   
| Q00613     | (HSF1_HUMAN) | 25728673   
| Q16236     | (NF2L2_HUMAN) | 26043645 NRF2 in article   
| Q13501     | (SQSTM_HUMAN) | 26043645 p62 in article.  
| P15559     | (NQO1_HUMAN) | 26043645  
| P09601     | (HMOX1_HUMAN) | 26043645  
| P02794     | (FRIH_HUMAN) | 26930718   
| P15941     | (MUC1_HUMAN) | 26930718   
| P13640     | (MT1G_HUMAN) | 27015352 MT-1G in article   
| Q9NP59     | (S40A1_HUMAN) | 27441659 Ferroportin-1 (FPN) in article   
| Q9NZ45     | (CISD1_HUMAN) | 27510639  
| P11021     | (BIP_HUMAN) | 28130223   
| P18848     | (ATF4_HUMAN) | 28130223   
| P04637     | (P53_HUMAN) | 28813679   
| Q9NRZ9     | (HELLS_HUMAN) | 28900510 LSH in article   
| O00767     | (ACOD_HUMAN) | 28900510 SCD1 in article   
| O95864     | (FADS2_HUMAN) | 28900510  
| P12931     | (SRC_HUMAN) | 28972104   
| P40763     | (STAT3_HUMAN) | 28972104   
| P29590     | (PML_HUMAN) | 29081404   
| Q9Y697     | (NFS1_HUMAN) | 29168506   
| Q9H3D4     | (P63_HUMAN) | 29212036 Delta Np63 alpha in article   
| P38936     | (CDN1A_HUMAN) | 29346757 Encoding p21   
| _NA_       |             | 29348676   
| P45880     | (VDAC2_HUMAN) | 29569437   
| P07954     | (FUMH_HUMAN) | 29917289   
| Q8N5K1     | (CISD2_HUMAN) | 29928961   
| _NA_       |             | _NA_       
| P35520     | (CBS_HUMAN) | 30035324 miR-9 in article   
| Q9H1K1     | (ISCU_HUMAN) | 30035324 miR-9 in article   
| O95573     | (ACSL3_HUMAN) | 30035324 miR-9 in article   
| Q96FW1     | (OTUB1_HUMAN) | 30035324 miR-9 in article   
| P16070     | (CD44_HUMAN) | 30308739   
| Q6ZUF6     | (NC336_HUMAN) | 30988278   
| O60885     | (BRD4_HUMAN) | 31038677   
| P30041     | (PRDX6_HUMAN) | 31160087 miR-17-92 in article   
| _NA_       |             | 31323261 Sesn2 in article   
| P58004     | (SESN2_HUMAN) | 31341276 Also known as merlin   
| P35240     | (MERL_HUMAN) | 31355331   
| O00327     | (BMAL1_HUMAN) | 31355331   
| Q16665     | (HIF1A_HUMAN) | 31394193 c-Jun in article   
| P05412     | (JUN_HUMAN) | 31442913   
| Q16790     | (CAV1_HUMAN) | 31507082 S1R in article   
| Q9HC24     | (LFG4_HUMAN) | 31520166 Also known as ADRP   
| Q99541     | (PLIN2_HUMAN) | 31634899 FSP1 in article   
| Q9BRQ8     | (AIFM2_HUMAN) | 31672277   
| P13473     | (LAMP2_HUMAN) | 31679460   
| P26651     | (TPP_HUMAN) | 31735663 Promin1 in article   
| Q8N271     | (PRM2_HUMAN) | 31761326   
| Q9NZZ3     | (CHMP5_HUMAN) | 31761326   
| Q96FZ7     | (CHMP6_HUMAN) | 31877357 Cav-1 in article   
| Q03135     | (CAV1_HUMAN) | 31989025   
| P30793     | (GCH1_HUMAN) | 31989025   

| Gene Reference | Accession | Description |
|----------------|-----------|-------------|
| 24844246       | _NA_      |            |
| 25444922       | _NA_      |            |
| 25728673       | _NA_      |            |
| 25728673       | _NA_      |            |
| 26043645       | NRF2 in article |  
| 26043645       | p62 in article.  |  
| 26043645       | _NA_      |            |
| 26043645       | _NA_      |            |
| 26930718       | _NA_      |            |
| 27015352       | MT-1G in article |  
| 27441659       | Ferroportin-1 (FPN) in article |  
| 27510639       | _NA_      |            |
| 28130223       | _NA_      |            |
| 28130223       | _NA_      |            |
| 28813679       | _NA_      |            |
| 28900510       | LSH in article |  
| 28900510       | SCD1 in article |  
| 28900510       | _NA_      |            |
| 28972104       | _NA_      |            |
| 28972104       | _NA_      |            |
| 29081404       | _NA_      |            |
| 29168506       | _NA_      |            |
| 29212036       | Delta Np63 alpha in article |  
| 29346757       | Encoding p21 |  
| 29348676       | _NA_      |            |
| 29569437       | _NA_      |            |
| 29917289       | _NA_      |            |
| 29928961       | _NA_      |            |
| 30035324       | miR-9 in article |  
| 30035324       | miR-9 in article |  
| 30308739       | _NA_      |            |
| 30988278       | _NA_      |            |
| 31038677       | _NA_      |            |
| 31160087       | miR-17-92 in article |  
| 31323261       | Sesn2 in article |  
| 31341276       | Also known as merlin |  
| 31355331       | _NA_      |            |
| 31355331       | _NA_      |            |
| 31394193       | c-Jun in article |  
| 31442913       | _NA_      |            |
| 31507082       | S1R in article |  
| 31520166       | Also known as ADRP |  
| 31634899       | FSP1 in article |  
| 31672277       | _NA_      |            |
| 31679460       | _NA_      |            |
| 31735663       | Promin1 in article |  
| 31761326       | _NA_      |            |
| 31761326       | _NA_      |            |
| 31877357       | Cav-1 in article |  
| 31989025       | _NA_      |            |
Table S3. Biological information of ferroptosis-associated genes (human genes)

| Subtypes | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver | driver |
| cell name                                      | annotation |
|-----------------------------------------------|------------|
| SMC01.T.AAACCTGCATACGCCG                      | CC1        |
| SMC01.T.AAACCTGTCGATAT                        | CC1        |
| SMC01.T.AAACCTGTCCCTTGCA                      | CC1        |
| SMC01.T.AAACCGGAGGGAAAACA                     | CC1        |
| SMC01.T.AAACCGGATATGGAAATCC                  | CC2        |
| SMC01.T.AAACATGTCAGGGGTA                     | CC1        |
| SMC01.T.AAACAGGTCGAGGCTGA                    | CC1        |
| SMC01.T.AAACATGTCGAGGCTGA                    | CC1        |
| SMC01.T.AAACATGTCGAGGCTGA                    | CC1        |
| SMC01.T.AAACATGTCGAGGCTGA                    | CC1        |
| SMC01.T.AAACATGTCGAGGCTGA                    | CC1        |
| Table S4. The annotation of single cells      |            |
SMC03.T.CATGACACATCGATGT  CC2
SMC03.T.CATGCCTAGTGCTGCC  CC2
SMC03.T.CATGCCTTCCCTGTG  CC2
SMC03.T.CATGCCTTCTGCTTG  CC2
SMC03.T.CATGGCGCATCACGTA  CC2
SMC03.T.CATGGCGGTAGGAGTC  CC2
SMC03.T.CATGGCGGTTATCACG  CC2
SMC03.T.CATGGCGTCAAGCCTA  CC2
SMC03.T.CATTATCAGTGGTAGC  CC2
SMC03.T.CATTATCCATAGACTC  CC2
SMC03.T.CATTTCGCAGAATTCCC  CC2
SMC03.T.CATTTCGCGTCCGACGT  CC2
SMC03.T.CCACCTATCGCCTGAG  CC2
SMC03.T.CCACGGACATCTATGG  CC2
SMC03.T.CCACTACAGTTGGCGC  CC2
SMC03.T.CCACTACGTTTGGCGC  CC2
SMC03.T.CCCAGCGAAGTTGTCGT  CC2
SMC03.T.CCATTCGCAGGTCTCG  CC2
SMC03.T.CCCAATCAGTACATGA  CC1
SMC03.T.CCCAATCTCACCATAG  CC2
SMC03.T.CCCAGTTTCATCTACGA  CC2
SMC03.T.CCCAGTTGTCTCTCGT  CC2
SMC03.T.CCCATACCATCCTTGC  CC2
SMC03.T.CCCTCCTAGAGGGCTT  CC2
SMC03.T.CCCTCCTTCCGGCACA  CC2
SMC03.T.CCATCGAAGGGAACGG  CC2
SMC03.T.CCGGTAGGTACTTAGC  CC1
SMC03.T.CCGTACTAGCACAGGT  CC2
SMC03.T.CCGTGGAAGCCACTAT  CC1
SMC03.T.CCGTGGAAGTTACTGAC  CC2
SMC03.T.CCGTTCAAGAAATGG  CC1
SMC03.T.CCGTTCAAGATGAGAG  CC2
SMC03.T.CCGTTCAAGTATGACA  CC2
SMC03.T.CCTAAAGAGTACGACG  CC2
SMC03.T.CCTAAAGCACAGCGTC  CC2
SMC03.T.CCTAAAGTCCGCATCT  CC2
SMC03.T.CCTACACCATACTACG  CC1
SMC03.T.CCTACCACATGCCTTC  CC1
SMC03.T.CCTAGCTGTGGAAAGA  CC2
SMC03.T.CCTATTACAGGCTGAA  CC2
SMC03.T.CCTCAGTAGTCGATAA  CC2
SMC03.T.CCTCTGAAGCTGATAA  CC2
SMC03.T.CCTCTGAGTGTTGGGA  CC2
SMC03.T.CCTCTGATCTAGAGTC  CC2
SMC03.T.CCTTCCCCAGTAGAGC  CC2
SMC03.T.CCTTCGATCTCGTATT  CC2
SMC03.T.CCTTTCTAGAAACCGC  CC2
SMC03.T.CCTTTCTAGAAGAAGC  CC2
SMC03.T.CGGAATGTAGCTAGTCT  CC1
SMC03.T.CGGAATGTCAGCCAGTC  CC2
SMC03.T.CGACCTCAGCCAGAA  CC2
SMC03.T.CGACCTCAGTCCTTC  CC2
SMC03.T.CGACTTCAGACAATAC  CC2
SMC03.T.CGACTTCAGATCCGAG  CC2
SMC03.T.CGACTTCGTTCCATGA  CC2
SMC03.T.CGACTTCTCTCCCTGA  CC2
SMC03.T.CGAGAAGCAATGGTCT  CC2
SMC03.T.CGAGAAGCACATGACT  CC2
SMC03.T.CGAGAAGTCTTTACGT  CC2
SMC03.T.CGAGCACAGGAGGCT  CC2
SMC03.T.CGAGCACTCAAGGTTCA  CC2
SMC03.T.CGATCGGTCACTGATC  CC2
SMC03.T.CGATGTACATAGTAAG  CC2
SMC03.T.CGATGTACATCGGACC  CC2
SMC03.T.CGATGTATCTTTAGGG  CC2
SMC03.T.CGATTGAGTCTTGATG  CC2
SMC03.T.CGATTGATCCTCATTA  CC2
SMC03.T.CGCGAAGATGATCGATA  CC2
SMC03.T.CGCCAAGAGATCGATA  CC2
SMC03.T.CGCGGTAAGATTACCC  CC2
SMC03.T.CGCGGTAAGTGTTTGC  CC2
SMC03.T.CGCGTTTAGGCTAGCA  CC2
SMC03.T.CGCTATCTCACCAGGC  CC2
SMC03.T.CGCTATCTCTGGTTCC  CC2
SMC03.T.CGCTTCAGTAGCGTAG  CC2
SMC03.T.CGCTTCAGTGGCGAAT  CC2
SMC03.T.CGCTTCATCCAAGTAC  CC2
SMC03.T.CGAGACACGTAAGAGAG  CC2
SMC03.T.CGAGACGTGTATTCGTG  CC2
SMC03.T.CGAGACGTGTTCGTCTC  CC2
SMC03.T.CGAGACGTTCCGTAGGC  CC2
SMC03.T.CGAGACTGCATTCTCAT  CC2
SMC03.T.CGAGACTGGTACTCGCG  CC2
SMC03.T.CGAGAGCTTCGTACCGG  CC2
SMC03.T.CGAGAGTCGTGACGGTA  CC2
SMC03.T.CGAGAGTCTCACTTACT  CC2
SMC03.T.CGAGGTACGTAAGGTTCA  CC2
SMC03.T.CGAGTACGTAACACAC  CC2
SMC03.T.CGAGAATCCCAACGG  CC1
SMC03.T.CGTCAGGCAGTAGAGC  CC2
SMC03.T.CGTCCATCACATTTCT  CC2
SMC03.T.CGTGAGCAAGACTAAGT  CC2
SMC03.T.CGTGAGCCACTGTCGG  CC2
SMC03.T.CGGAATGACAGGGT  CC2
SMC03.T.CGTTAATCACAACAC  CC2
SMC03.T.CGTAACGTTAGCTGTA  CC1
SMC03.T.GTCGTAAGTTCGTGAT  CC1
SMC03.T.GTCGTAATCCATGACTG  CC2
SMC03.T.GTCTCGTAGCTTTTG  CC2
SMC03.T.GTCTCGTGTTAAGATG  CC2
SMC03.T.GTCTCGTTCAAGGCTT  CC2
SMC03.T.GTCTCGTTCCGGGTGT  CC2
SMC03.T.GTCTTCGCACGGTAGA  CC2
SMC03.T.GTGAAGGTCACAACGT  CC2
SMC03.T.GTGCAGCAGGGATCTG  CC2
SMC03.T.GTGCAGCCAGACGTAG  CC2
SMC03.T.GTGCAGCCATTAGGCT  CC2
SMC03.T.GTGCATACAGTTCCCT  CC2
SMC03.T.GTGCGGTAGCACACAG  CC2
SMC03.T.GTGCGGTCAGTAGAGC  CC1
SMC03.T.GTGCTTCCAGAGCCAA  CC2
SMC03.T.GTGCTTCCAGCTGTAT  CC2
SMC03.T.GTTAAGCGTAGGCATG  CC2
SMC03.T.GTTCATTAGAAACGAG  CC2
SMC03.T.GTTCGGGAGATATACG  CC2
SMC03.T.GTTCTCGCAGCTCGAC  CC1
SMC03.T.GTTCTCGGTAGCTGCC  CC2
SMC03.T.GTTTCTAAGAAACGCC  CC2
SMC03.T.TAACCCGCAAAGAGC  CC2
SMC03.T.TAACCCGTCGGTGTTA  CC2
SMC03.T.TAAGAGACACTACAGT  CC2
SMC03.T.TAAGCGTAGCTAGTGG  CC2
SMC03.T.TAAGTGCCAATCTACG  CC2
SMC03.T.TAAGTGCTCACTATTC  CC2
SMC03.T.TACACGACAACAGATT  CC2
SMC03.T.TACAGTAGAAACAATC  CC2
SMC03.T.TACAGTAGCAACAGCC  CC2
SMC03.T.TACTTATAGAGTAATC  CC2
SMC03.T.TACGGATAGTGCCATC  CC2
SMC03.T.TACGGGGCATCCTGACT  CC2
SMC03.T.TACGGGTATCCCTGACT  CC2
SMC03.T.TAGACCATCATATCGG  CC2
SMC03.T.TAGAGCTCAATGGAAT  CC2
SMC03.T.TAGCCGGAGGAATCGC  CC2
SMC03.T.TAGTTGGAGCGACGTA  CC2
SMC03.T.TAGTTGGCATGCTAGT  CC2
SMC03.T.TAGTTGGTCAAAGTAG  CC1
SMC03.T.TAGTTGGTCACCGTAA  CC2
SMC03.T.TATCAGGGTGTAATGA  CC2
SMC04.T.TCAGCTCCAGTATCTGC
SMC04.T.TCGAGGCTCATCGATGC
SMC04.T.TGCGAGGCGCTTGGTGC
SMC04.T.TCGCGAGTCGCCCTTG
SMC04.T.TCGCGAGGTTTGGCGTC
SMC04.T.TCGGTGTACCAGC
SMC04.T.TCGTACCAGGACGAAA
SMC04.T.TCGTACCCATCACGTA
SMC04.T.TCGTAGATCCACGAAT
SMC04.T.TCTCATACAGAGCCAA
SMC04.T.TCTCATAGTGGTCCGT
SMC04.T.TCTTCGGAGAGCTATA
SMC04.T.TCTTCGGCATCCGCGA
SMC04.T.TGAGCATAGACCACGA
SMC04.T.TGATTTCTCCTC
SMC04.T.TGCCAAAAGGCGATAC
SMC04.T.TGCCAAATCCGAACGC
SMC04.T.TGCCCATTCGTCGTTC
SMC04.T.TGCGCAGTCGCTTGTC
SMC04.T.TGCGGGTCATCGATTG
SMC04.T.TGCTACCGTGTGACGA
SMC04.T.TGCTGCTCATCATCCC
SMC04.T.TGGCCAGTCCTTTACA
SMC04.T.TGGCTGGCAGCTGTTA
SMC04.T.TGGGAAGAGGACAGCT
SMC04.T.TGTTCCGAGCTAGTTC
SMC04.T.TGTTCCGAGTAAGTAC
SMC05.T.CCACTACCATTGTGCA
SMC05.T.CCGTACTAGTATGACA
SMC07.T.TAGCCGGTCTGGGCCA  CC1
SMC07.T.TATCTCAGTGAGGCTA  CC1
SMC07.T.TATCTCATCATCTGT  CC1
SMC07.T.TCAACAGTTGGCCTCT  CC1
SMC07.T.TCAACAGAACCAGCCA  CC1
SMC07.T.TCACAGAAGAACACAGA  CC1
SMC07.T.TCAAGCTCCAGGGATTG  CC1
SMC07.T.TCAAGCTCGTTCCAAATG  CC1
SMC07.T.TCAAGCTCTCATGCATG  CC1
SMC07.T.TCAAGGATAGAATTGTG  CC1
SMC07.T.TCAAGGATGTTCAGACT  CC1
SMC07.T.TCAAGGTAAGCACAGGT  CC1
SMC07.T.TCAAGGTAGTGTCGCTG  CC1
SMC07.T.TCCACACAGAATCTCC  CC1
SMC07.T.TCCACACGTATGGTTCC  CC1
SMC07.T.TCCCGAGTATGCTAGGCT  CC1
SMC07.T.TCCCGATCAACGCACC  CC1
SMC07.T.TCCCGATCGACGAGC  CC1
SMC07.T.TCCCGGTCCGAGATG  CC1
SMC07.T.TCCCGGTGCGGGTAA  CC1
SMC07.T.TCCCGGTCTGGCCAA  CC1
SMC07.T.TCCCTAAGCTAGCCC  CC2
SMC07.T.TCCCTAGTAAATACG  CC1
SMC07.T.TCCCTAGTCGTTGTA  CC1
SMC07.T.TCCCTAGTCTCTTTA  CC1
SMC07.T.TCCCTAGTCTTGATG  CC1
SMC07.T.TGCGCAGCAGGCAGTA  CC1
SMC07.T.TGCGCCGTCACAAGG  CC1
SMC07.T.TGCGGGTGTCGCATAT  CC1
SMC07.T.TGCGTGGCACTCTGTC  CC1
SMC07.T.TGCGTGGTCTCATTCA  CC1
SMC07.T.TGAGCCGGTCACAAGG  CC1
SMC07.T.TGCCCATCATGGGACA  CC1
SMC07.T.TGCCCTAAGCTAGCCC  CC1
SMC07.T.TGCCCTAGTAAATACG  CC2
SMC07.T.TGCCCTAGTCGTTGTA  CC1
SMC07.T.TGCCCTAGTCTCTTTA  CC1
SMC07.T.TGCCCTAGTCTTGATG  CC1
SMC07.T.TGACCGCAAGGGGTAA  CC1
SMC07.T.TGACGGCAGATATGGT  CC1
SMC07.T.TGACGGCCAACGCCCAC  CC1
SMC07.T.TGACTACGTCAAGGAG  CC1
SMC07.T.TGACTTTAGGGTATCG  CC2
SMC07.T.TGACTTTGATTAGTG  CC1
SMC07.T.TGAGCCGGTCTGGCCCA  CC1
SMC07.T.TGACGTGGCTCACCACAG  CC1
SMC07.T.TGACGTGGGCTCCTCAG  CC1
SMC07.T.TGACGTGGTCTCTCAG  CC1
SMC07.T.TGACGTGGTCTCTGTC  CC2
SMC08.T.GTTCTCGCAGCCTATA  CC1
SMC08.T.GTTCTCGCAGTCAGCC  CC1
SMC08.T.GTTTCTAAGACCTTTG  CC1
SMC08.T.TAAGAGATCGGTGTCG  CC1
SMC08.T.TACCGGACAGAGGCTT  CC1
SMC08.T.TAACGGCCACCCAGTG  CC1
SMC08.T.TACTCATTCTCTGCTG  CC1
SMC08.T.TACTTACTCCAAGTAC  CC1
SMC08.T.TAGAGCTGTTGATTGC  CC1
SMC08.T.TAGGCATAGATGCGAC  CC1
SMC08.T.TAGGCATGTTTGTG  CC1
SMC08.T.TAGTGGTCTCATGCT  CC1
SMC08.T.TATTACCTCAACACCA  CC1
SMC08.T.TCAGGAGCACCCAGTG  CC1
SMC08.T.TTACGTCACTGGCTCA  CC1
SMC08.T.TTATTCCGATCCAGGAG  CC1
SMC08.T.TACTCATTCTCTGCTG  CC1
SMC08.T.TCAGGACAGAGGCTT  CC1
SMC08.T.TCGCGAGCACCTCGTT  CC1
SMC08.T.TCTATTGCAATCCGAT  CC1
SMC08.T.TCAGGACAGAGGCTT  CC1
SMC08.T.TCTTTCCGTACCGCTG  CC1
SMC08.T.TGGACGCCAAGTTCTG  CC1
SMC08.T.TTACGTCACTGGCTCA  CC1
SMC08.T.TTTCGGTTTACTCCCA  CC1
SMC08.T.TGAGCCACAGGGCATGT  CC1
SMC08.T.TGGCGCAAGGGCATGT  CC1
SMC08.T.TGACTTTAGACTGTAA  CC1
SMC08.T.TTCTTCCGCTTCCCATC  CC1
SMC08.T.TCTTATTGCTAGTGACT  CC1
SMC08.T.TGCAGGAACTTGCTCA  CC1
SMC08.T.TTATTCAGCTCCAG  CC1
SMC08.T.TGAGGAATCACCTCGC  CC1
SMC08.T.TGACGGCTGCTGCTG  CC1
SMC08.T.TTGCGCAAGGGCATGT  CC1
SMC08.T.TGGCCAGAGGCACCAC  CC1
SMC08.T.TGGCGTGGTCTGGTATG  CC1
SMC08.T.TGCTACCCACTCTGTC  CC1
SMC08.T.TGCGTGGTCCTGCAGG  CC1
SMC08.T.TGCTACCTCGCTAGCG  CC1
SMC08.T.TGGACGCCAAGTTCTG  CC1
SMC08.T.TGGGAAGGACGCCGT  CC1
SMC08.T.TGGGAAGTCTCAACTT  CC1
SMC08.T.TGGTTAGCATGCTCCT  CC1
SMC09.T.ATAAGAGGTCCGAACC  CC1
SMC09.T.ATAGACCTCCGAACGC  CC1
SMC09.T.ATAGACCTCTTGTTTG  CC1
SMC09.T.ATCACGAAGTACGCCC  CC1
SMC09.T.ATCACGACAGGAATGC  CC1
SMC09.T.ATCACGAGTCGGGTCT  CC2
SMC09.T.ATCATCTAGAAGAAGC  CC1
SMC09.T.ATCATCTCAAACTGTC  CC1
SMC09.T.ATCATCTCATATGGTC  CC1
SMC09.T.ATCATCTCATCTCCCA  CC1
SMC09.T.ATCATCTCATGTCCTC  CC1
SMC09.T.ATCATCTGTTTGGGCC  CC1
SMC09.T.ATCATCTTCCACTGGG  CC1
SMC09.T.ATCATGGAAGGCTCC  CC2
SMC09.T.ATCCACCCAAGACGTG  CC2
SMC09.T.ATCCACCCAGCTGTAT  CC1
SMC09.T.ATCCACCGTCAACATC  CC1
SMC09.T.ATCCACCGTGGTCCGT  CC2
SMC09.T.ATCCACCTCCACGCAG  CC1
SMC09.T.ATCCACCTCGATGAGG  CC1
SMC09.T.ATCCGAACACTCGACG  CC2
SMC09.T.ATCCGAATCACCCTCA  CC1
SMC09.T.ATCCGAATCCAGGGCT  CC1
SMC09.T.ATCGAGTCAGTACACT  CC1
SMC09.T.ATCGAGTGTGAGGGAG  CC1
SMC09.T.ATCGAGTGTGTGAATA  CC1
SMC09.T.ATCTACTCAAGAGGCT  CC1
SMC09.T.ATCTACTGTGGTCTCG  CC1
SMC09.T.ATCTGCCAGAGTACCG  CC1
SMC09.T.ATCTGCCGTACATGTC  CC2
SMC09.T.ATGAGGGAGAGTAAGG  CC1
SMC09.T.ATGAGGGAGTACGTAA  CC1
SMC09.T.ATGAGGGAGTGCGATG  CC1
SMC09.T.ATGAGGGCAGCAGTTT  CC1
SMC09.T.ATGAGGGTCCAAGCCG  CC1
SMC09.T.ATGGGAGAGACTTGAA  CC1
SMC09.T.ATGGGAGGTCTCTCGT  CC1
SMC09.T.ATGGGAGGTGGCGAAT  CC1
SMC09.T.ATGGGAGTCATATCGG  CC1
SMC09.T.ATGTGTGAGCAATATG  CC1
SMC09.T.ATGTGTGTCCACGAAT  CC1
SMC09.T.ATTACTCCAGTGAGTG  CC1
SMC09.T.ATTACTCCATTTCACT  CC1
SMC09.T.ATTATCCAGAGCTGCA  CC1
SMC09.T.ATTATCCAGAGCTTCT  CC2
SMC09.T.ATTATCCAGGCAGGTT  CC2
SMC09.T.ATTATCCAGTGCGATG  CC1
SMC09.T.ATTATCCCAGGACCCT  CC1
SMC09.T.ATTATCCTCTGCCCTA  CC1
| SMC09.T.GATTCAGCAATGGAAT | CC1  |
| SMC09.T.GATTCAGGCTCTCAACA | CC1  |
| SMC09.T.GATTCAGTTAAGGGCC | CC1  |
| SMC09.T.GCAACTGTATTAGCC | CC1  |
| SMC09.T.GAATCAAGGGCTTCCA | CC1  |
| SMC09.T.GAATCAATACAGCT | CC2  |
| SMC09.T.GAATCACATTGCTT | CC1  |
| SMC09.T.GATCAGGTCTCAACA | CC1  |
| SMC09.T.GATTCAGGTTAAGGGC | CC1  |
| SMC09.T.GCAAACTGTATTAGCC | CC1  |
| SMC09.T.GCAATCAAGCGCTCCA | CC1  |
| SMC09.T.GCAATCACAATACGCT | CC1  |
| SMC09.T.GCAATCACATTTGCTT | CC1  |
| SMC09.T.GCACATAGTCTTTCAT | CC1  |
| SMC09.T.GCACATAGTGCTGCA | CC1  |
| SMC09.T.GCACATAGTCTTTCAT | CC1  |
| SMC09.T.GCACATAGTGCCTGCA | CC1  |
| SMC09.T.GCACTCTAGATGCCTT | CC1  |
| SMC09.T.GCATACACAACTGCT | CC2  |
| SMC09.T.GCATACACACTTTCCTT | CC1  |
| SMC09.T.GCATACCATCTGACTCTTT | CC1  |
| SMC09.T.GCATACCATCAGCTTCCA | CC1  |
| SMC09.T.GCATACCATCCAACGA | CC1  |
| SMC09.T.GCATGTAAGAGTAATC | CC1  |
| SMC09.T.GCATGTAAGGCACATG | CC1  |
| SMC09.T.GCATGTAAGAGGTATG | CC1  |
| SMC09.T.GCATGTAAGGAGTAGA | CC1  |
| SMC09.T.GCATGTAAGAGGAAGT | CC1  |
| SMC09.T.GCATGTAAGGCAGTACG | CC1  |
| SMC09.T.GCATGTAAGGTCATGC | CC1  |
| SMC09.T.GCCAAATGTGAAAGAG | CC1  |
| SMC09.T.GCCAAATGCTCTATG | CC1  |
| SMC09.T.GCCAAATGCTATGATC | CC1  |
| SMC09.T.GCCAAATGCTGCTTCC | CC1  |
| SMC09.T.GCCAAATGCTGCTGCA | CC1  |
| SMC09.T.GCCAAATGTGACTCAG | CC1  |
| SMC09.T.GCCAAATGTGCAAGTC | CC1  |
| SMC09.T.GCCAAATGTGCGGCG | CC1  |
| SMC09.T.GCCAAATGTGCTGTCC | CC1  |
| SMC09.T.GCCAAATGTGCTACAG | CC1  |
| SMC09.T.GCCAAATGTGCTTCGC | CC1  |
| SMC09.T.GCCAAATGTGCTTGTC | CC1  |
| SMC09.T.GCCAAATGTGCTGTA | CC1  |
| SMC09.T.GCCAAATGTGCTTTG | CC1  |
| SMC09.T.GCCAAATGTGCTGGA | CC1  |
| SMC09.T.GCCAAATGTGCTGCG | CC1  |
| SMC09.T.GCCAAATGTGCTGTC | CC1  |
| SMC09.T.GCCAAATGTGCTGCT | CC1  |
| SMC09.T.GCCAAATGTGCTGGA | CC1  |
| SMC09.T.GCCAAATGTGCTGCG | CC1  |
| SMC09.T.GCCAAATGTGCTGTC | CC1  |
| SMC09.T.GCCAAATGTGCTGCT | CC1  |
| SMC09.T.GCCAAATGTGCTGGA | CC1  |
| SMC09.T.GCCAAATGTGCTGCG | CC1  |
| SMC09.T.GCCAAATGTGCTGTC | CC1  |
| SMC09.T.GCCAAATGTGCTGCT | CC1  |
| SMC09.T.GCCAAATGTGCTGGA | CC1  |
| SMC09.T.GCCAAATGTGCTGCG | CC1  |
| SMC09.T.GCCAAATGTGCTGTC | CC1  |
| SMC09.T.GCCAAATGTGCTGCT | CC1  |
| SMC09.T.GCCAAATGTGCTGGA | CC1  |
| SMC09.T.GCCAAATGTGCTGCG | CC1  |
| SMC09.T.GCCAAATGTGCTGTC | CC1  |
| SMC09.T.GCCAAATGTGCTGCT | CC1  |
SMC10.T.AGACGTTGTCTCATCC  CC2
SMC10.T.AGAGCGACACATTCGA  CC2
SMC10.T.AGAGCGACAGTGACAG  CC2
SMC10.T.AGAGGATGCTAGAAG  CC2
SMC10.T.AGAGTGGCACACATGT  CC2
SMC10.T.AGAGTGGGTATGAAAC  CC2
SMC10.T.AGAGTGGGTCTAACGT  CC2
SMC10.T.AGAGTGGTCTCGGACG  CC2
SMC10.T.AGATTGCAGCTCAACT  CC2
SMC10.T.AGCAGCCGTAATCGTC  CC2
SMC10.T.AGCATACTCAAGGCTT  CC2
SMC10.T.AGCGTCGAGCTCCTTC  CC1
SMC10.T.AGCTCCTGTTGCGTTA  CC2
SMC10.T.AGCTCTGCTACGCTA  CC2
SMC10.T.AGCTTGAAGATGTTAG  CC2
SMC10.T.AGCTTGAGTGGTTTCA  CC2
SMC10.T.AGGGATGCATCATCCC  CC2
SMC10.T.AGGGATGGTCCAGTAT  CC2
SMC10.T.AGGTCATGTAAGTGGC  CC2
SMC10.T.AGTAGTCTCACAGGCC  CC2
SMC10.T.AGTAGTCTCGTAGATC  CC2
SMC10.T.AGTCTTTAGATATGCA  CC2
SMC10.T.AGTCTTTCATGTTCCC  CC1
SMC10.T.AGTGAGGTCTCAACTT  CC2
SMC10.T.AGTGGGATCACAGGCC  CC1
SMC10.T.AGTGTCAAGTCCATAC  CC2
SMC10.T.ATAACGCGTATCGCAT  CC2
SMC10.T.ATAAGAGCAGAGCCAA  CC1
SMC10.T.ATAAGGAGTGCAGGACA  CC1
SMC10.T.ATCCACCGTAGCGTCC  CC1
SMC10.T.ATCCGAAAGTTCCACA  CC2
SMC10.T.ATCCGAATCCCTTGTG  CC2
SMC10.T.ATCTACTAGGACACCA  CC2
SMC10.T.ATCTACTCATCATGACT  CC2
SMC10.T.ATCTGCCAGGGATCTG  CC1
SMC10.T.ATGAGGGGTGTCCTCT  CC1
SMC10.T.ATGCGATCAGGATTGG  CC2
SMC10.T.ATGGGAGCATGTAAGA  CC1
SMC10.T.ATGTGTGCAAGGCTCC  CC2
SMC10.T.ATTACTCAGGGTTCCC  CC2
SMC10.T.ATTAGGACAGTTACCA  CC2
SMC10.T.ATTGGACTCTCTGTCG  CC2
SMC10.T.ATTCTGGTCGGCACT  CC2
SMC10.T.CAACCTCCATCGATGT  CC1
SMC10.T.CAAGAAAAGTTTCCTT  CC2
SMC10.T.CAAGATCTCATGTGGT  CC2
SMC10.T.CACAAACTCCGTTGCC  CC2
SMC10.T.CACACTCCAAGCGATG  CC2
SMC10.T.CACAGGCGTCGCTTTC  CC2
SMC10.T.CACAAGCTCCGCTTTC  CC2
SMC10.T.CACACTCAAGCGATG  CC2
SMC10.T.CACACTCCAAGCGATG  CC2
SMC10.T.CACAGGCGTCGCTTTC  CC2
SMC10.T.CACCAGAGAGTGAGA  CC2
SMC11.T.TACACGAAGCTCCTCT  CC1
SMC11.T.TACAGTCATAAGACAC  CC1
SMC11.T.TACCTATACGTCAACGC  CC1
SMC11.T.TACCTATGTCGCTTCT  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TAGAGCTAGTAGATGT  CC1
SMC11.T.TAGAGCTAGTGGTAAT  CC1
SMC11.T.TAGCC GGAGTCAAGCG  CC1
SMC11.T.TAGCCGGTCTCCCTGA  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TACACGAAGCAAGACC  CC1
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SMC11.T.TACGGCCAAATCCGT  CC1
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SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
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SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
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SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
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SMC11.T.TACACGAAGCAAGACC  CC1
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SMC11.T.TACGGCCAAATCCGT  CC1
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SMC11.T.TACACGAAGCAAGACC  CC1
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SMC11.T.TACGGCCAAATCCGT  CC1
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SMC11.T.TACACGAAGCAAGACC  CC1
SMC11.T.TACGGGCAGCCTATGT  CC1
SMC11.T.TACGGCCAAATCCGT  CC1
SMC11.T.TACTTACCATCGATTG  CC1
SMC16.T.AAAGCAACACATTTCT  CC1
SMC16.T.AAAGCAAGTCTTGCAGG  CC2
SMC16.T.AAAGCAAGTGCTCCA  CC2
SMC16.T.AAAGCAAGTTTACTCT  CC2
SMC16.T.AAAGCAATCCACGTTCC  CC1
SMC16.T.AAAGCAATCCGCGGTT  CC2
SMC16.T.AAAGTACCAAGCCCC  CC2
SMC16.T.AAAGTAGTACCTACGAG  CC2
SMC16.T.AAAGTAGGGTACCTACA  CC2
SMC16.T.AAAGTAGTCTCGTAA  CC2
SMC16.T.AAATGCCACCAACTCT  CC2
SMC16.T.AAATGCCCTCGCTGATA  CC2
SMC16.T.AAATGCCCTTTAACCT  CC1
SMC16.T.AAACAGGAGATGCGATAC  CC2
SMC16.T.AAACAGGAGGTGCTTT  CC2
SMC16.T.AAACAGGAGTACGCCC  CC2
SMC16.T.AAACATGCAGGCGGTT  CC1
SMC16.T.AAACATGCAGCTTCGG  CC2
SMC16.T.AAACATGCTCTTCATGTT  CC2
SMC16.T.AAACCATGCACGGTTTA  CC2
SMC16.T.AAACCATGCAGCTTCGG  CC2
SMC16.T.AAACCATGGTCTCGTTC  CC1
SMC16.T.AAACCATGGTCTTCTCG  CC2
SMC16.T.AAACCATGGTTGTGGAG  CC1
SMC16.T.AAACCATGTCGCTGATA  CC2
SMC16.T.AAACCATGTCTGCTGCT  CC1
SMC16.T.AACCGCGAGAAACGAG  CC2
SMC16.T.AACCGCGAGACTCGGA  CC2
SMC16.T.AACCGCGGTACAGTGG  CC2
SMC16.T.AACGTTGAGCATCATC  CC2
SMC16.T.AACGTTGAGCCGTCGT  CC2
SMC16.T.AACGTTGCAAGGTTCT  CC1
SMC16.T.AACGTTGCACTATCTT  CC2
SMC16.T.AACGTTGGTCTCGTCC  CC2
SMC16.T.AACTCCAGAGAGACGAA  CC1
SMC16.T.AACTCCAGAGCATCATC  CC2
SMC16.T.AACTCCAGCACCGCTAG  CC1
SMC16.T.AACTCCAGCATTCGACA  CC1
SMC16.T.AACTCCAGCATACACAC  CC2
SMC16.T.AACTCCAGTACCGGCC  CC2
SMC16.T.AACTCCAGTTCTGTCGTA  CC2
SMC16.T.AACTCCAGTTGCAAGGTTCT  CC1
SMC16.T.AACTCCAGTTGCAGCTAT  CC2
SMC16.T.AACTCCAGTTGCATTCC  CC2
| Gene     | Sequence                          |
|----------|----------------------------------|
| SMC16.T  | ACCAGTAAAGTGCAGTAA               |
|          | ACCAGTAAATCTGCA                  |
|          | ACCAGTACAGACTGCG                 |
|          | ACCAGTAGTAGAATCGTG               |
|          | ACCAGTACAGACGAGATCC              |
|          | ACCAGTAGCTTGACGACC               |
|          | ACCAGTAGTTCATTTCCCT              |
|          | ACCAGTAGAACATGGAT                |
|          | ACCAGTAGTCATGAGT                 |
|          | ACCAGTGGGATAGGCTG                |
|          | ACCAGTGAAGATGCTAAG               |
|          | ACCAGTAGATCCAAAGCTG              |
|          | ACCAGTAAAGTGCAGTAA               |
|          | ACCAGTAAATCTGCA                  |
|          | ACCAGTACAGACTGCG                 |
|          | ACCAGTAGTAGAATCGTG               |
|          | ACCAGTACAGACGAGATCC              |
|          | ACCAGTAGCTTGACGACC               |
|          | ACCAGTAGTTCATTTCCCT              |
|          | ACCAGTAGAACATGGAT                |
|          | ACCAGTAGTCATGAGT                 |
|          | ACCAGTGGGATAGGCTG                |
|          | ACCAGTGAAGATGCTAAG               |
|          | ACCAGTAGATCCAAAGCTG              |
|          | ACCAGTAAAGTGCAGTAA               |
|          | ACCAGTAAATCTGCA                  |
|          | ACCAGTACAGACTGCG                 |
|          | ACCAGTAGTAGAATCGTG               |
|          | ACCAGTACAGACGAGATCC              |
|          | ACCAGTAGCTTGACGACC               |
|          | ACCAGTAGTTCATTTCCCT              |
|          | ACCAGTAGAACATGGAT                |
|          | ACCAGTAGTCATGAGT                 |
|          | ACCAGTGGGATAGGCTG                |
|          | ACCAGTGAAGATGCTAAG               |
|          | ACCAGTAGATCCAAAGCTG              |
|          | ACCAGTAAAGTGCAGTAA               |
|          | ACCAGTAAATCTGCA                  |
|          | ACCAGTACAGACTGCG                 |
|          | ACCAGTAGTAGAATCGTG               |
|          | ACCAGTACAGACGAGATCC              |
|          | ACCAGTAGCTTGACGACC               |
|          | ACCAGTAGTTCATTTCCCT              |
|          | ACCAGTAGAACATGGAT                |
|          | ACCAGTAGTCATGAGT                 |
|          | ACCAGTGGGATAGGCTG                |
|          | ACCAGTGAAGATGCTAAG               |
|          | ACCAGTAGATCCAAAGCTG              |
|          | ACCAGTAAAGTGCAGTAA               |
|          | ACCAGTAAATCTGCA                  |
|          | ACCAGTACAGACTGCG                 |
|          | ACCAGTAGTAGAATCGTG               |
|          | ACCAGTACAGACGAGATCC              |
|          | ACCAGTAGCTTGACGACC               |
SMC16.T.ACGCCAGCACTACAGT CC2
SMC16.T.ACGCCAGCATACTCCGAT CC1
SMC16.T.ACGCCAGTTCTTGCTCC CC2
SMC16.T.ACGCCAGTTCTGCTTT CC2
SMC16.T.ACGCCAGTCCATGCTC CC2
SMC16.T.ACGCCGAGAGACTAAGT CC2
SMC16.T.ACGCCGAGAGATGTAAC CC1
SMC16.T.ACGCCGAGAGCCTCGTG CC1
SMC16.T.ACGCCGAGAGTCTCCTC CC1
SMC16.T.ACGCCGACATGAACCT CC1
SMC16.T.ACGCCGAGTCGAGTTT CC1
SMC16.T.ACGCCGATCCACTCCA CC2
SMC16.T.ACGCCGATCTGAGTGT CC2
SMC16.T.ACGGAGACACACATGT CC1
SMC16.T.ACGGAGACAGCTGGCT CC2
SMC16.T.ACGGAGACATGGGAAC CC2
SMC16.T.ACGGAGAGTAAAGGAG CC2
SMC16.T.ACGGAGAGTTGCGTTA CC1
SMC16.T.ACGGAGATCACTTACT CC1
SMC16.T.ACGGAGATCTACTTAC CC1
SMC16.T.ACGGCCAAGGCGACAT CC1
SMC16.T.ACGGCCAAGTGCTGCC CC1
SMC16.T.ACGGCCACACTCTGTC CC1
SMC16.T.ACGGCCACAGACGCCT CC2
SMC16.T.ACGGCCAGTAAACACA CC1
SMC16.T.ACGGCCATCAACGAAA CC1
SMC16.T.ACGGCTAGAGCTGGTT CC2
SMC16.T.ACGGCTAGTGAACGC CC1
SMC16.T.ACGGCTCACATCCAA CC2
SMC16.T.ACGGCTCAGCCTTTC CC1
SMC16.T.ACGGCTCAGCGTCCA CC2
SMC16.T.ACGGCTCAGGTCCAC CC1
SMC16.T.ACGGCTCATGAGCGA CC2
SMC16.T.ACGGCTGTTCGTGAT CC2
SMC16.T.ACGGCTTCACCTTAT CC1
SMC16.T.ACGGCTTCGCGCCAA CC2
SMC16.T.ACGGCTTCGTCTAT CC1
SMC16.T.ACGGGCTCTTATTGCTCC CC2
SMC16.T.ACGGGCTCTTCTTGCAGGT CC2
SMC16.T.ACGGGCTCAAGAAGGTTT CC2
SMC16.T.ACGGGCTCAATGAGGT CC1
SMC16.T.ACGGGCTCAATGAGGT CC1
SMC16.T.ACGGGCTCAATGAGGT CC1
SMC16.T.ACGGGCTCAATGAGGT CC1
SMC16.T.ACGGGCTCAATGAGGT CC1
SMC16.T.ACGGGTCAAGAAGGTTT CC2
SMC16.T.ACGGGTCAAGAAGGTTT CC2
SMC16.T.ACGGGTCAGATATGGT CC1
SMC16.T.ACGGTGAAGAAGGTTT CC2
SMC16.T.CGGAGTCAGAGGTTAT  CC2
SMC16.T.CGGAGTCAGTAGGTGC  CC2
SMC16.T.CGGAGTCAGGAAGGC  CC1
SMC16.T.CGGAGTCCTCGCAGGA  CC2
SMC16.T.CGGAGTCGTGCCTTGG  CC2
SMC16.T.CGGAGTCGTTGAGTC  CC2
SMC16.T.CGGAGTCCTCAACTCT  CC2
SMC16.T.CGGAGTCGGATTTGCT  CC1
SMC16.T.CGGAGTCTCCGCGGTA  CC2
SMC16.T.CGGAGTCTCGATGAGG  CC2
SMC16.T.CGGAGTCTCTGCTAAG  CC2
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SMC16.T.CGGCTAGCAAGCGATG  CC1
SMC16.T.CGGCTAGCAATCTGCA  CC1
SMC16.T.CGGCTAGGTCATACTG  CC1
SMC16.T.CGGCTAGGTCATCTGGG  CC1
SMC16.T.CGGCTAGTCCTCCTAG  CC2
SMC16.T.CGGGTCAAGTGCTGCC  CC2
SMC16.T.CGGGTCAAGTGGGCTA  CC1
SMC16.T.CGGGTCAAGTGTACGG  CC2
SMC16.T.CGGGTCAGTCTAAAGA  CC2
SMC16.T.CGGGTCATCTAGAGTC  CC1
SMC16.T.CGGGTCATCTTATCTG  CC2
SMC16.T.CGGTTAAAGAGACTTA  CC1
SMC16.T.CGGTTAAAGCTGCAAG  CC2
SMC16.T.CGGTTAAAGGTAAACT  CC2
SMC16.T.CGGTTAACAGTATAAG  CC1
SMC16.T.CGGTTAACATAAAGGT  CC2
SMC16.T.CGGTTAAGTCGACTGC  CC2
SMC16.T.CGGTTAAGTTGTGGAG  CC1
SMC16.T.CGTAGCGAGAGGTTGC  CC1
SMC16.T.CGTAGCGCAGGAATCG  CC1
SMC16.T.CGTAGCGGTAACGCGA  CC2
SMC16.T.CGTAGCGGTACTTAGC  CC1
SMC16.T.CGTAGCGGTCACCTAA  CC2
SMC16.T.CGTAGGCAGCAGATCG  CC1
SMC16.T.CGTAGGCAGGCTATCT  CC1
SMC16.T.CGTAGGCCATGCAATC  CC1
SMC16.T.CGTAGGCCATCGCTTC  CC1
SMC16.T.CGTAGGCCGTACCGTTA  CC2
SMC16.T.CGTAGGCCGTCTGCTCG  CC2
SMC16.T.CGTAGGCCGTACGGCTA  CC2
SMC16.T.CGTAGGCTCAAGCCTA  CC2
SMC16.T.CGTAGGCTCACTGCTC  CC2
SMC16.T.CGTCACTCAGCGAACA  CC1
SMC16.T.CGTCACTTCATGTCCC  CC1
SMC16.T.CGTCACTTCTATCGCC  CC2
SMC16.T.CGTCAGGAGACTTGAA  CC2
SMC16.T.CGTCAGGAGCGATTCT  CC2
SMC16.T.CGTCAGGTCAAGCCTA  CC1
SMC16.T.CGTCAGTCCTGCCAT  CC1
SMC16.T.CGTCCATAGCTACCGC  CC1
SMC16.T.CGTCCATAGGAGCGAG  CC1
SMC16.T.CGTCCATAGTCCATAC  CC2
SMC16.T.CGTCCATACAGCGCTG  CC2
SMC16.T.CGTCCATACCTATCAC  CC2
SMC16.T.CGTCCATTCAACACTG  CC2
SMC16.T.CGTCCATTCCACGACG  CC2
SMC16.T.CGTCTACAGAGGTGCA  CC1
SMC16.T.CGTCTACAGCTGCTG  CC2
SMC16.T.CGTGAGCCAATGGATA  CC2
SMC16.T.GCTTCCAAGGCATGTG CC1
SMC16.T.GCTTCCACACGCTGAGA CC2
SMC16.T.GCTTCCAGCTCGAC CC2
SMC16.T.GCTTCACTATCGG CC1
SMC16.T.GCTTGAAGAAACGCC CC1
SMC16.T.GCTTGAACATCGACGC CC2
SMC16.T.GCTTGAAGTAGCAAAT CC1
SMC16.T.GCTTGAAGTGACGCCT CC2
SMC16.T.GGAAAGCGTGCGCTTG CC1
SMC16.T.GGAAAGCGTTTACTCT CC2
SMC16.T.GGAAAGCTCTGCAAGT CC1
SMC16.T.GGAACTTAGTTCGCGC CC2
SMC16.T.GGAACTTCAAAGCAAT CC1
SMC16.T.GGACAAGAGCGATAGC CC1
SMC16.T.GGACAAGCATGCCTAA CC2
SMC16.T.GGACAGAAGTGTTGAA CC1
SMC16.T.GGACAGACAAGGTGTG CC2
SMC16.T.GGACAGAGTCTCTCTG CC2
SMC16.T.GGACATTAGGGTCTCC CC2
SMC16.T.GGACATTAGTCCGGTC CC2
SMC16.T.GGACATTAGTGAAGTT CC1
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SMC16.T.GGACATTGCAGGACCT CC2
SMC16.T.GGACAGACAAAGTGTG CC2
SMC16.T.GGACAGATCTCTCTG CC2
SMC16.T.GGACAGTGGCCCTTG CC2
SMC16.T.GGACGTCTCATCGCTC CC1
SMC16.T.GGACGTCTCTGGGCA CC2
SMC16.T.GGAGCAACAGGACCCT CC2
SMC16.T.GGAGCAAGTCTGGTA CC2
SMC16.T.GGAGCAATCAACACCA CC2
SMC16.T.GGAGCAATCCAGCCG CC1
SMC16.T.GGAGCAATCCCGACTT CC1
SMC16.T.GGAGCAATCTTTAGTC CC1
SMC16.T.GGATGTTAGAGTCTGG CC2
SMC16.T.GGATGTTAGCTCCTCC CC2
SMC16.T.GGATGTTCAATGAATG CC2
SMC16.T.GGATGTTCACAACTGT CC2
SMC16.T.GGATGTTCATGTTCC CC1
SMC16.T.GGATGTTGTCTGGAGA CC2
SMC16.T.GGATGTTGTGGTTCC CC2
SMC16.T.GGTGCGTGTCCGACT  CC2
SMC16.T.GGTGCGTGTCCGCTCT  CC1
SMC16.T.GGTGTTAAGACTACAA  CC1
SMC16.T.GGTGTTAAGCAGCCCC  CC2
SMC16.T.GGTGTTACAAGGCTCTC  CC2
SMC16.T.GGTGTTACACCACGAG  CC2
SMC16.T.GGTGTTACACCACACG  CC2
SMC16.T.GGTGTTACACCACCTG  CC2
SMC16.T.GTAAACTGCAGATCCAT  CC2
SMC16.T.GTAACTGCAGATCCACT  CC2
SMC16.T.GTAACTGCAGATCCACTG  CC2
SMC16.T.GTAACTGCAGATCAGAG  CC2
SMC16.T.GTAACTGCAGATCCGCG  CC2
SMC16.T.GTAACTGCAGATCCGCA  CC2
SMC16.T.GTAACTGCAGATCCGCGG  CC2
SMC16.T.GTAACTGCAGATCCGCGT  CC2
SMC16.T.GTAACTGCAGATCCTGCT  CC2
SMC16.T.GTAACTGCAGATCCTTAT  CC2
SMC16.T.GTAACTGCAGATCCTTATG  CC2
SMC16.T.GTAACTGCAGATCCTTATG  CC2
| Sequence | Type |
|----------|------|
| SMC16.T.TACCTATTTCATGTCTT | CC1 |
| SMC16.T.TACCTATTCGTCACGG | CC1 |
| SMC16.T.TACCTACACAACGT | CC1 |
| SMC16.T.TACCTTACTTCCGCTC | CC1 |
| SMC16.T.TACCTTAGTAGAGCTG | CC2 |
| SMC16.T.TACCTTAGTAGAGTGC | CC2 |
| SMC16.T.TACGGATAGGATGCGT | CC2 |
| SMC16.T.TACGGATAGTCCCACG | CC1 |
| SMC16.T.TACGGATTCAGCTCGG | CC2 |
| SMC16.T.TACGGATTCAGTTGAC | CC1 |
| SMC16.T.TACGGATTCGAGCCCA | CC2 |
| SMC16.T.TACGGATTCGGTGTCG | CC2 |
| SMC16.T.TACGGGCAGACCGGAT | CC2 |
| SMC16.T.TACGGGCAGTGTTTGC | CC2 |
| SMC16.T.TACGGGCCAAGCGCTC | CC2 |
| SMC16.T.TACGGGCCACATCTTT | CC2 |
| SMC16.T.TACGGGCCAGGAACGT | CC2 |
| SMC16.T.TACGGGCTCATGCATG | CC2 |
| SMC16.T.TACGGGCTCTAACCGA | CC2 |
| SMC16.T.TACGGGCTCTATGTT | CC1 |
| SMC16.T.TACGGGCTCTCTTTC | CC1 |
| SMC16.T.TACGGGCAGACCGGAT | CC2 |
| SMC16.T.TACGGGCTCACATTTC | CC1 |
| SMC16.T.TACGGTACACATTCGA | CC2 |
| SMC16.T.TACGGTAGTAGAAAGG | CC1 |
| SMC16.T.TACGGTATCACTGGGC | CC2 |
| SMC16.T.TACGGTATCTATCT | CC2 |
| SMC16.T.TACGGTATCTCGTTC | CC2 |
| SMC16.T.TACTCATAGAAACGAG | CC2 |
| SMC16.T.TACTCATCAATCTACG | CC2 |
| SMC16.T.TACTCATCACGGCTAC | CC2 |
| SMC16.T.TACTCATGTGAGGGAG | CC2 |
| SMC16.T.TACTCATGTGATAAAC | CC1 |
| SMC16.T.TACTCATGTTGCTCCT | CC2 |
| SMC16.T.TACTCGCAGTGGGATC | CC2 |
| SMC16.T.TACTCGCCAATGAACC | CC2 |
| SMC16.T.TACTCGGTTGGCTTA | CC2 |
| SMC16.T.TACTTACAGGCCTCT | CC1 |
| SMC16.T.TACTTACAGGCTCTTA | CC1 |
| SMC16.T.TACTTACAGGAGGTAA | CC2 |
| SMC16.T.TACTTACAGGAGGAGG | CC2 |
| SMC16.T.TACTTACAGGAGGAGG | CC2 |
| SMC16.T.TACTTACTACCTAT | CC1 |
| SMC16.T.TACTTACTACTAACC | CC1 |
| SMC16.T.TACTTGCAAGTTAAG | CC2 |
| SMC16.T.TACTTGTCACATCTT | CC2 |
| SMC16.T.TACTTGTCAGATCTGT | CC1 |
| SMC16.T.TACTTGTCAGTGAGCC | CC2 |
| SMC16.T.TACTTGTCGGTACA | CC1 |
| SMC16.T.TACTTTCCGTTATCTC | CC1 |
| SMC16.T.TAGACCAACACTGCCC | CC2 |
| SMC16.T.TAGACCATGCCCCGA | CC2 |
| SMC16.T.TAGACCAGTACCTGGA | CC1 |
| SMC16.T.TAGAGCTAGACATAAC | CC2 |
| SMC16.T.TAGAGCTAGGTGGTGA | CC1 |
| SMC16.T.TAGAGCTTTGTTATC | CC1 |
SMC16.T.TCGAGGCCTTGGAGGTCC1
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SMC16.T.TCGCGAGGTCACCCAGCC1
SMC16.T.TCGCGAGGTCCATCCTCC1
SMC16.T.TCGCGAGGTCTAACGTCC1
SMC16.T.TCGCGAGGTGGAAAGACC1
SMC16.T.TCGCGTTCAATAACGACC1
SMC16.T.TCGGGACAGGAATGGACC1
SMC16.T.TCGGGACCAAACTGTCCC2
SMC16.T.TCGGGACCATAGAAACC1
SMC16.T.TCGGGACGTTGCGCACCC1
SMC16.T.TCGGGACTCAGAGCTTCC1
SMC16.T.TCGGGACTCAGAGGTGCC1
SMC16.T.TCGGGACTCTGTACGC2
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SMC16.T.TCGGTAAAGTTAGC GCC1
SMC16.T.TCGTAACATAGACTCC2
SMC16.T.TCGTACCAGACTAAGTCC1
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SMC16.T.TCGTAGATCTTGAGGCTC2
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SMC16.T.TCTATTGCACTGTCGGCC2
SMC16.T.TCTATTGGTAAGGGACC2
SMC16.T.TCTATTGTCTTAACCTCC1
SMC16.T.TCTCATAAGTCATCCACCC1
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SMC22.T.TCCCGATTCACCACCT CC1
SMC22.T.TCCCGATTCCAGTAGT CC1
SMC22.T.TCCCGATTCTGCAAGT CC1
SMC22.T.TCGAGGCAGGCTATCT CC1
SMC22.T.TCGAGGCAGTCAAGCG CC1
SMC22.T.TCGAGGCTCAGCAACT CC2
SMC22.T.TCGCGAGAGAAGGCCT CC1
SMC22.T.TCGCGAGAGTCCCACG CC2
SMC22.T.TCGCGAGCAATAGCGG CC1
SMC22.T.TCGCGAGCATAGACTC CC2
SMC22.T.TCGCGAGTCATCATTC CC1
SMC22.T.TCGCGAGTCCGTACAA CC1
SMC22.T.TCGCGTTAGGAACTGC CC1
SMC22.T.TCGCGTTGTTCGAATC CC1
SMC22.T.TCGCGTTTCCCAAGAT CC1
SMC22.T.TCGCGTTTCCGCATAA CC1
SMC22.T.TCGCGTTTCCCTAAATCC1
SMC22.T.TCGGGACAGACTCGGA CC1
SMC22.T.TCGGGACAGCAGACTG CC1
SMC23.T.GGGACCTCAATCGGTT      CC1
SMC23.T.GGGACCTCATACGCTA      CC1
SMC23.T.GGGAGATCAATGGAAT      CC1
SMC23.T.GGGTCTGTCTGGGCCA      CC1
SMC23.T.GGGTTGCGTTGGTAAA      CC1
SMC23.T.GGTATTGAGTACGACG      CC1
SMC23.T.GGTGAAGCATATCTCTT     CC1
SMC23.T.GGTGAAGCATCACCCT     CC1
SMC23.T.GGTGAAGGACGAAA       CC1
SMC23.T.GGTGAAGGATTGGGA      CC1
SMC23.T.GGTGCGTTCCCAACCG     CC1
SMC23.T.GGTGTTAGTGGCAAAC     CC1
SMC23.T.GTAACGTAGGGTGTTG     CC2
SMC23.T.GTAACGTCAAGCGAGT     CC1
SMC23.T.GTAACGTCACAGGCT      CC1
SMC23.T.GTAACGTCAGGGTGAT     CC1
SMC23.T.GTACTCCCATCCCATC     CC1
SMC23.T.GTACTCCCATTAGGCT     CC1
SMC23.T.GTACTTCTCACAAGCTG    CC1
SMC23.T.GTACTTCTCAGC        CC1
SMC23.T.GTCACAAGTCACCTATCC    CC1
SMC23.T.GTCACAAGTCTCGGTTAAA   CC1
SMC23.T.GTCACAACAGACACTTT    CC1
SMC23.T.GTCACCGGAGCTCTAG     CC2
SMC23.T.GTCACGGTACGAGAAGG    CC1
SMC23.T.GTCCTCAAGGGCATTGG    CC1
SMC23.T.GTCCTCAGTGAGACGCT    CC1
SMC23.T.GTCGGGTCATTACCTT     CC1
SMC23.T.GTCGTTACGC        CC1
SMC23.T.GTCCTACTCCCTGAC      CC1
SMC23.T.GTCCTCAGGCT        CC1
SMC23.T.GTCCAAGTGCTGGCT      CC1
SMC23.T.GTGCCAGGAGGATTGA     CC1
SMC23.T.GTGCCACAGATGTAAC     CC2
SMC23.T.GTGCAAGCCACCTCGTT    CC1
SMC23.T.GTGCAATAACAGAAGCTC    CC1
SMC23.T.GTGCACTACCATCCGG     CC1
SMC23.T.GTGCGTAGAGATGAGG     CC1
SMC23.T.GTGCTTCCAGTAACGG     CC1
SMC23.T.GTGCTTCCATTGCAGA     CC1
SMC23.T.GTGCTTCTCACAAGCG     CC1
SMC23.T.GTGCTTCTCCAAACAC     CC2
SMC23.T.GTGCTGAGTACCTC       CC1
SMC23.T.GTTAAAGGCACCGAAGGATA  CC1
SMC23.T.GTTACAGTCCGTCATC     CC1
SMC23.T.GTTACATTGCCAGAGTC     CC1
SMC23.T.GTTCTCAGGACACATG     CC1
SMC23.T.GTTCTATCGAGGTTG     CC1
SMC23.T.TAAACCGGTACCTAAA     CC1
SMC23.T.TAAGAGAAGCCCAAC     CC1
SMC23.T.TAAGAGACAGATGAGC     CC1
SMC23.T.TAAGAGACATTCTGC     CC1
SMC23.T.TAAGTGCAGAGGACA     CC1
SMC23.T.TAAGTGCAGCTCAACT     CC2
SMC23.T.TACACGAGTACACCT     CC1
SMC23.T.TACACGAGTTAGGGTG  CC1
SMC23.T.TACACGATCTTGACGA  CC1
SMC23.T.TACAGTAGCGTGAGT  CC1
SMC23.T.TACAGTCATCCAAC  CC1
SMC23.T.TACCTATCATCACAAC  CC1
SMC23.T.TACGGGCGTGTTGGGA  CC1
SMC23.T.TACGGTAAGGGTATCG  CC1
SMC23.T.TACGGTAGTCCCGACA  CC1
SMC23.T.TACGGTAGTGCGATAG  CC1
SMC23.T.TACTCATCAGTCACTA  CC1
SMC23.T.TACTCATGTACTTCTT  CC1
SMC23.T.TACTTACTCATCAACC  CC1
SMC23.T.TAGAGTCAGTTAACC  CC1
SMC23.T.TAGCCGAGACTCGGA  CC1
SMC23.T.TAGGCATAGATGCAGA  CC1
SMC23.T.TAGGCATAGATGTGTA  CC1
SMC23.T.TAGTGGTCAATGTAAG  CC1
SMC23.T.TAGTGGTGCCTCTTTG  CC1
SMC23.T.TAGTTGCGAGATGGAGC  CC1
SMC23.T.TAGTTGCTCTCTACG  CC1
SMC23.T.TATCAGGAGAAGGTTT  CC1
SMC23.T.TATCAGGCAGGGTACA  CC1
SMC23.T.TATCTCATCCAGTATG  CC1
SMC23.T.TATCTCATCCCATTAT  CC1
SMC23.T.TATGCCCGTCGTTGTA  CC1
SMC23.T.TATGCCCTCCTCAATT  CC1
SMC23.T.TATTACCATATCTCG  CC1
SMC23.T.TCAACGAAGACGACTG  CC1
SMC23.T.TCAACGATCGGTTCGG  CC1
SMC23.T.TCAATCTCAGATCGGA  CC1
SMC23.T.TCACAGTAGATTTCGGA  CC1
SMC23.T.TCAGATGGTGTGACGA  CC1
SMC23.T.TCAGGATTCGAACTGT  CC1
SMC23.T.TCATTACACGGTTTA  CC1
SMC23.T.TCATTTGGTCCGAACC  CC1
SMC23.T.TCATTTGTCAAGGCTT  CC1
SMC23.T.TCCACACGTCTCCACT  CC1
SMC23.T.TCCCGATGTTTGACAC  CC1
SMC23.T.TCAGCTCAGCTGCCCA  CC1
SMC23.T.TCAGGATGTCGAACAG  CC1
SMC23.T.TCAAGTAGCAGACTGT  CC1
SMC23.T.TCTATTGGTGGTCCGT  CC2
SMC23.T.TCTATTGGTTCACGGC  CC1
SMC23.T.TCTATTGTCATCATTC  CC1
SMC23.T.TCTCATAAGATATGGT  CC1
SMC24.T.CGGACTGTCTTTAGTC  CC2
SMC24.T.CGTTAACACCCAGTG  CC2
SMC24.T.CGTTAATCCGAACGC  CC2
SMC24.T.CGTCAGTCCGCTGTGT  CC2
SMC24.T.CGTCAGGCCATCCAG  CC2
SMC24.T.CGTGAAAGCCGCTTTAT  CC2
SMC24.T.CTAGTGAACACCCAGC  CC2
SMC24.T.CTAGTGAAGCGCTTAT  CC2
SMC24.T.CCTAACTCAATAGCAGG  CC2
SMC24.T.CCTCAACAGTCCAGAAGC  CC2
SMC24.T.CCTCGGAGTCAGCTGCC  CC2
SMC24.T.CCTACAGTTGGTAC  CC2
SMC24.T.CCTAGCTCAGTGTGTT  CC2
SMC24.T.CCTTAGCTGCTGCTGTT  CC2
SMC24.T.CCTTAACTCAATAGCAGG  CC2
SMC24.T.CCTTAACTCAATAGCAGG  CC2
SMC24.T.CCTTAACTCAATAGCAGG  CC2
SMC24.T.CCTTAACTCAATAGCAGG  CC2
SMC24.T.CCTTAACTCAATAGCAGG  CC2
SMC24.T.CCTTAACTCAATAGCAGG  CC2
| Sequence | CC1 |
|----------|-----|
| SMC25.T.GACTGCGAGACGCTTT | |
| SMC25.T.GACTGCGCAGGGATAG | |
| SMC25.T.GACTGCGACGCTCCA | |
| SMC25.T.GAGCAGAGTCTTCGTCC | |
| SMC25.T.GAGGTGATCTGGCGTG | |
| SMC25.T.GATCAGTCATGGTCAT | |
| SMC25.T.GATCAGTGTTACGACT | |
| SMC25.T.GATCTAGCAGTATGCT | |
| SMC25.T.GATGAAACATGTCCTC | |
| SMC25.T.GATGAAATCTGTCTCG | |
| SMC25.T.GATGAGGAGCCGGTAA | |
| SMC25.T.GATGAGGTCTGGTTCC | |
| SMC25.T.GATTCAGGTCGGCACT | |
| SMC25.T.GATTCAGTTCCATGA | |
| SMC25.T.GCAAACTCAGGGTGTC | |
| SMC25.T.GCAATCAAGAGTACCG | |
| SMC25.T.GCACTCTCAGGGTGTC | |
| SMC25.T.GCATACATCAATACCG | |
| SMC25.T.GCATGATAGGAATTAC | |
| SMC25.T.GCATGATGTCTGGAGA | |
| SMC25.T.GCATGATGTGTCGCTG | |
| SMC25.T.GCATGTAGTAGCTTGT | |
| SMC25.T.GCATGTATCACTTCAT | |
| SMC25.T.GCATGTATCTTCGAGA | |
| SMC25.T.GCCAAATCATTTGCCC | |
| SMC25.T.GCGAGAATCTGGAGGCC | |
| SMC25.T.GCGCAACAGCTCCCGG | |
| SMC25.T.GCGCAACAGTTCCACA | |
| SMC25.T.GGAGCAAAGGCTAGCA | |
| SMC25.T.GGAGCAAGTTAAGGGC | |
| SMC25.T.GGATGTTAGCAATATG | |
| SMC25.T.GGATTACAGTGTACTC | |
| SMC25.T.GGCAATTCACGCATCG | |
| SMC25.T.GGCGACTGTGAGCGAT | |
| SMC25.T.GGCGACTGTTGTGGAG | |
| SMC25.T.GGCGTGTTCTGAGTGT | |
| SMC25.T.GGAGCAAGTTAAGGGC | |
| SMC25.T.GGACAAGTCTCAGGCA | |
| SMC25.T.GGCAGTTACATGCATG | |
| SMC25.T.GGATGTTAGCAATATG | |
| SMC25.T.GGATTACAGTGTACTC | |
| SMC25.T.GGCCAATTCACGCATCG | |
| SMC25.T.GGCAGCTGTTGGAG | |
| SMC25.T.GGCGTGTCTGAGCTG | |
|          |                  |     |
|----------|------------------|-----|
| SMC25.T  | TTCTACATCTTAGAGC | CC1 |
| SMC25.T  | TTCTCAAAGGTTCTTA | CC1 |
| SMC25.T  | TTCTCAACATAGACTC | CC1 |
| SMC25.T  | TTCTCTGTGTAGATGA | CC1 |
| SMC25.T  | TTGAACGAGGCGACAT | CC1 |
| SMC25.T  | TTGAACGGTATGCTTG | CC1 |
| SMC25.T  | TTGGACGTCAACTGT  | CC1 |
| SMC25.T  | TTGGAGGTCATATGC  | CC1 |
| SMC25.T  | TTTGCGCAGACACGAC | CC1 |
| SMC25.T  | TTTGCGCCATGGAATA | CC1 |
| SMC25.T  | TTTGGTGTAGGTAC   | CC2 |
| SMC25.T  | TTTGTCAAGAGGGATA | CC2 |
| cell name                     | annotation |
|------------------------------|------------|
| KUL01.T_AAACCTGGGTCTTTCAT    | CC2        |
| KUL01.T_AAACGGGTCGGTTAAC     | CC2        |
| KUL01.T_AAGAAGTGAGTTAGGAGG  | CC1        |
| KUL01.T_AAAGATGCTGGCCCTA     | CC2        |
| KUL01.T_AAAGCAAGTAAACACCA    | CC2        |
| KUL01.T_AAAGCAATCATCCATCA    | CC2        |
| KUL01.T_AAAGTAGTCGTCATC      | CC2        |
| KUL01.T_AAATGCAAGTCCGTGTTT   | CC2        |
| KUL01.T_AAATGCACTGACTCT      | CC2        |
| KUL01.T_AAATGCCCACTCACCAC    | CC2        |
| KUL01.T_AAATGGTCAACACCAG     | CC2        |
| KUL01.T_AAATGCCCTCCCTCAGT    | CC2        |
| KUL01.T_AAACACGTACGTCTCT     | CC2        |
| KUL01.T_AAACACGTCACGTCTCT    | CC2        |
| KUL01.T_AAACCGGTGTCAGTAGT    | CC2        |
| KUL01.T_AACCCGTCAGAGAGCT    | CC2        |
| KUL01.T_AACCATGGTCATGCTCAT   | CC1        |
| KUL01.T_AACCATCAGTTAAATACG   | CC2        |
| KUL01.T_AACCGCGCAATGAATG     | CC2        |
| KUL01.T_AACGTTGGTCAAAGAT     | CC2        |
| KUL01.T_AACTCAGAGCTACTGC     | CC2        |
| KUL01.T_AACTCTTCCCCAATAAC    | CC2        |
| KUL01.T_AACTGTCTAGTGAGCAG    | CC2        |
| KUL01.T_AACCTTTCCAACGTCCA    | CC2        |
| KUL01.T_AACTCGCTTCCATACAT    | CC2        |
| KUL01.T_AACTTGCTTCGTTGAAAT   | CC2        |
| KUL01.T_AAGACCTAGAGGAGATA    | CC2        |
| KUL01.T_AAGACCTAGGGAGTGTT    | CC2        |
| KUL01.T_AAGACCTAGTCCATCCA    | CC1        |
| KUL01.T_AAGACCTATCCAGGAT    | CC2        |
| KUL01.T_AAGGCAGAGCTATCC      | CC2        |
| KUL01.T_AAGGCAGTCATCACCAC    | CC2        |
| KUL01.T_AAGGCATCTGAGGAGA     | CC2        |
| KUL01.T_AAGGTCTAGGGAGTAAGT   | CC1        |
| KUL01.T_AAGTCTGCAGCTTTGAGGAT| CC2        |
| KUL01.T_AATCCAGATGCGTGTCC    | CC2        |
| KUL01.T_AATCCAGGTGTTTCTCATT  | CC2        |
| KUL01.T_AATCCGTTCACCACTC     | CC1        |
| KUL01.T_AACACAAAGAAGAAGA     | CC2        |
| KUL01.T_AACACGCTACATCATTAT   | CC2        |
| KUL01.T_AACACTGAGTAACTCACC   | CC2        |
| KUL01.T_AACAGGCCGACCAACCAG   | CC2        |
| KUL01.T_AACAGCCGACTCCCGA     | CC1        |
| KUL01.T_AACAGCCGCTACCTGC     | CC1        |
| KUL01.T_AACAGCTAAAGGAGTGA    | CC2        |
| KUL01.T_AACAGCTAGTTGTTTCTTT  | CC2        |
| KUL01.T_ACATACGAAGAGCCCT     | CC2        |
| KUL01.T_ACATACGAGTCCACCAG    | CC2        |
| KUL01.T_ACATACGACTGTTTA      | CC2        |
| KUL01.T_ACATACGCTCAGTTC      | CC1        |
| KUL01.T_ACATACGTCCTATTCA     | CC2        |
| KUL01.T_ACATGCGTCCGGATC      | CC1        |
| KUL01.T_ACCTCTGAGATATCCAG    | CC2        |
| KUL01.T_ACGTTGGCTCGGATC      | CC2        |
| KUL01.T | ACCGTAAGTTACTGAC | CC2 |
|----------|------------------|-----|
| KUL01.T | ACCCTTACACTACAGT | CC1 |
| KUL01.T | ACGAGGACACGGATAG | CC2 |
| KUL01.T | ACAGATGTAGTCCAGGA | CC2 |
| KUL01.T | ACAGATGTGTCTAGTGT | CC2 |
| KUL01.T | AGCGACAGGTGTATTA | CC2 |
| KUL01.T | ACCTTACAGGTTTCCA | CC2 |
| KUL01.T | ACCTTTACACTACAGT | CC2 |
| KUL01.T | ACGAGGACACGGATAG | CC2 |
| KUL01.T | ACGATGTAGTCCAGGA | CC2 |
| KUL01.T | ACGGCTCGTATAGAAA | CC2 |
| KUL01.T | AGCCTAAAGCGAGAAA | CC2 |
| KUL01.T | ACTATCTCATACACAAC | CC2 |
| KUL01.T | ACTATCTTCTTTCTGAC | CC2 |
| KUL01.T | ACTGAACAGGCTACGA | CC2 |
| KUL01.T | ACTGAACGTGACTACT | CC2 |
| KUL01.T | ACTGAGTAAAGTGACG | CC2 |
| KUL01.T | ACTGGGCAGTACCCAG | CC2 |
| KUL01.T | ACTGAGGCTGACAAA | CC2 |
| KUL01.T | ACTGACTGACTGACTG | CC2 |
| KUL01.T | AGACTTACCTACCCAG | CC2 |
| KUL01.T | AGAGCGACAGGAGAG | CC2 |
| KUL01.T | AGATCTGCAATGGAGC | CC2 |
| KUL01.T | AGATTGCCACGAAACG | CC2 |
| KUL01.T | AGATTGCTGAGAAAACG | CC2 |
| KUL01.T | ACGAGCAGGATCGA | CC2 |
| KUL01.T | ACGGCTGACTCCTG | CC2 |
KUL01.T_AGCGTCGAGAAGCTGTA   CC2
KUL01.T_AGCTCTCAGACTGGGT   CC2
KUL01.T_AGCTCTCCACACGCTG   CC1
KUL01.T_AGCTCTGTCCGATCC   CC1
KUL01.T_AGCTCTCTGCGTTTC   CC2
KUL01.T_AGCTTGACATTTCAT   CC2
KUL01.T_AGCTTTGATCTCACATT   CC2
KUL01.T_AGGCCACTCAGAGGTG   CC2
KUL01.T_AGGCCACTCCACCCA   CC2
KUL01.T_AGGGAGTCTGGGCTGCA   CC2
KUL01.T_AGGGATGGTGGCTCCA   CC2
KUL01.T_AGGGATGTCTACCAT   CC2
KUL01.T_AGGGTGATCTCACATT   CC2
KUL01.T_AGGTCCGAGACTTTCG   CC1
KUL01.T_AGGTCCGAGTACTTCG   CC1
KUL01.T_AGGTCCGTCGGAGCAA   CC2
KUL01.T_AGGCCACTCAGAGGTG   CC2
KUL01.T_AGGCCACTCCACCCA   CC2
KUL01.T_AGGGAGTCTGGGCTGCA   CC2
KUL01.T_AGGGATGGTGGCTCCA   CC2
KUL01.T_AGGGATGTCTACCAT   CC2
KUL01.T_AGGGTGATCTCACATT   CC2
KUL01.T_AGGTCCGAGACTTTCG   CC2
KUL01.T_AGGTCCGAGTACTTCG   CC2
KUL01.T_AGGTCGAGACTTCGA   CC1
KUL01.T_AGGTCGGAGGCTACA   CC2
KUL01.T_AGTTGGTCAGGGATTG   CC2
KUL01.T_AGTTGGTGTTACGTCA   CC2
KUL01.T_ATAACGCCAGAGTGTG   CC2
KUL01.T_ATAAGAGGTACGCTGC   CC2
KUL01.T_ATAAGAGGTTATCCGA   CC1
KUL01.T_ATAAGAGGTTTGTTGG   CC2
KUL01.T_ATAAGAGTCAAACCGT   CC2
KUL01.T_ATAAGAGTCTCCAACC   CC2
KUL01.T_ATCACGACATTTGCTT   CC2
KUL01.T_ATCACGATCAGTTCGA   CC1
KUL01.T_ATCATCTTCGTGGACAT   CC2
KUL01.T_ATCATGGCACGTGCAC   CC2
KUL01.T_ATCATGGGTACAGTGC   CC2
KUL01.T_ATCATGTCCTCTAGTGA   CC1
KUL01.T_ATCATGGTCCTGCCTT   CC2
KUL01.T_ATCCACCCTATCTCCT   CC1
KUL01.T_ATCCCGATACATACC   CC2
KUL01.T_ATCCGAATCACACTAC   CC2
KUL01.T_ATCCGATTCAAAGACA   CC2
KUL01.T_ATCTACTAGCTCCCAG   CC2
KUL01.T_ATCTACTCAAAACCTAC   CC2
KUL01.T_ATGCGATAGGTACTC   CC1
KUL01.T_ATGCGATTCTCCGATG   CC2
KUL01.T_ATGGGAGTACCTCGGT   CC1
KUL01.T_ATGGGAGTCTACTTAC   CC2
KUL01.T_ATGTGAGGACAGAAG   CC2
KUL01.T_ATTACTCAGTGGATAA   CC2
KUL01.T_ATTATCCACCACCTAG   CC2
KUL01.T_ATTATCCCGGGCCCTA   CC2
KUL01.T_ATTCTACAGCAGCGAA   CC2
KUL01.T_ATTCTACCACCTTGTC   CC2
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KUL19.T_ACTTGTTTCATATGAGA  CC1
KUL19.T_ACTTTTCATCCTACAGA  CC1
KUL19.T_AGAATACAGAGTCTGTC  CC1
KUL19.T_AGACGTTAGCCACTAT  CC1
KUL19.T_AGAGCGAAGGCTATCT  CC1
KUL19.T_AGAGTGCGCAGCTATA  CC1
KUL19.T_AGACTACGTCATGCAT  CC1
KUL19.T_AGCACCGTACTCGGAG  CC1
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KUL19.T_AGCGGTCGTACTGAC  CC1
KUL19.T_AGCGGTCGTCACTTCC  CC1
KUL19.T_AGCGGTCGTTAAAGTG  CC1
KUL19.T_AGCGGTCTCCTTTCTC  CC1
KUL19.T_AGCGTATAGGCTAGCA  CC1
KUL19.T_AGCGTATTCCGTTGCT  CC1
KUL19.T_AGCGTCGTCGAGGTAG  CC1
KUL19.T_AGCGTCGTCTGATACG  CC1
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KUL19.T_AGGCCACAGGAGTTTA  CC1
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KUL19.T_AGGTCATAGAGCTGCA  CC1
KUL19.T_AGGTCATCAAGTAGTA  CC1
KUL19.T_AGGTCATTCATCTGCC  CC1
KUL19.T_AGGTCCGGTTGTCGCG  CC1
KUL19.T_AGTAGTCCATCGGTTA  CC1
KUL19.T_AGTCTTTAGTCCGTAT  CC1
KUL19.T_AGTGGGACACCATCCT  CC1
KUL19.T_AGTGTACAGTAAGTCC  CC1
KUL19.T_AGTTGGTAGAATCTCC  CC1
KUL19.T_AGTTGGTCTCCTATGTT  CC1
KUL19.T_ATAACGCAGGCTTGA  CC1
KUL19.T_ATAACGCTCAAGCCTA  CC1
KUL19.T_ATAACGCTCGACCAGC  CC1
KUL19.T_ATAACGGTCACATTAGC  CC1
KUL19.T_ATAGACGAGGAATGGA  CC1
KUL19.T_ATAGACCAGAACCATC  CC1
KUL19.T_ATAGACCACCATCCT  CC1
KUL19.T_ATACAGAGTCTTGTC  CC1
KUL19.T_ATCACGATCACCATAG  CC1
KUL19.T_ATCATCTCATGGGAAC  CC1
KUL19.T_ATCATCTGTACCGGCT  CC1
KUL19.T_ATCCGAACACGGTAAG  CC1
KUL19.T_ATCAGAAGAGTTACGT  CC1
KUL19.T_ATAGACCAAAACCAG  CC1
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KUL19.T_ATCATCTGTACCGGCT  CC1
KUL19.T_ATCCGAACACGGTAAG  CC1
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KUL19.T_ATCTGGCAACTGGGCC  CC1
KUL19.T_ATCTGCTCTGAGGCC  CC1
KUL19.T_ATGAGGAGCACTTCTT  CC1
KUL19.T_ATGAGGAGGAATGGA  CC1
KUL19.T_ATGTGCTGTTAAAGTG  CC1
KUL19.T_ATGTGCTGTTAAAGTG  CC1
| KUL31.T_TATCAGGCACGAAAGC | CC1          |
|--------------------------|-------------|
| KUL31.T_TCGAGCTCTTTACA   | CC1          |
| KUL31.T_TCTTTCCCCAGGCTCG| CC1          |
| KUL31.T_TGACAAGTCCTTTTA  | CC1          |
| KUL31.T_TGCTGCTATCCAAA   | CC2          |
| KUL31.T_TGTTCCGATGCTAGT  | CC1          |
| KUL31.T_TTCTTAGCATTTTAC  | CC1          |
| KUL31.T_TGGAACGTCGGGAGTA | CC1          |
| KUL31.T_TGACTTGAAACACA   | CC1          |
| KUL31.T_TGACTTGATTACAG   | CC1          |
| samples              | NMF clusters | Gene clusters |
|----------------------|--------------|---------------|
| TCGA.A6.5656.01      | CC1          | Gene cluster A |
| TCGA.A6.5659.01      | CC1          | Gene cluster A |
| TCGA.A6.5662.01      | CC1          | Gene cluster A |
| TCGA.A6.5667.01      | CC1          | Gene cluster A |
| TCGA.A6.A56B.01      | CC1          | Gene cluster A |
| TCGA.AA.A01X.01      | CC1          | Gene cluster A |
| TCGA.AF.3911.01      | CC1          | Gene cluster A |
| TCGA.AF.4110.01      | CC1          | Gene cluster A |
| TCGA.AH.6643.01      | CC1          | Gene cluster A |
| TCGA.AM.5820.01      | CC1          | Gene cluster A |
| TCGA.CA.5797.01      | CC1          | Gene cluster A |
| TCGA.CA.6716.01      | CC1          | Gene cluster A |
| TCGA.CM.4747.01      | CC1          | Gene cluster A |
| TCGA.CM.5344.01      | CC1          | Gene cluster A |
| TCGA.CM.6164.01      | CC1          | Gene cluster A |
| TCGA.CM.6165.01      | CC1          | Gene cluster A |
| TCGA.CM.6678.01      | CC1          | Gene cluster A |
| TCGA.D5.6922.01      | CC1          | Gene cluster A |
| TCGA.D5.6924.01      | CC1          | Gene cluster A |
| TCGA.D5.6926.01      | CC1          | Gene cluster A |
| TCGA.DC.6681.01      | CC1          | Gene cluster A |
| TCGA.DC.6683.01      | CC1          | Gene cluster A |
| TCGA.DY.A1DD.01      | CC1          | Gene cluster A |
| TCGA.DY.A1DF.01      | CC1          | Gene cluster A |
| TCGA.El.6514.01      | CC1          | Gene cluster A |
| TCGA.El.6883.01      | CC1          | Gene cluster A |
| TCGA.El.7002.01      | CC1          | Gene cluster A |
| TCGA.F4.6463.01      | CC1          | Gene cluster A |
| TCGA.F4.6854.01      | CC1          | Gene cluster A |
| TCGA.F5.6571.01      | CC1          | Gene cluster A |
| TCGA.F5.6814.01      | CC1          | Gene cluster A |
| TCGA.F5.6861.01      | CC1          | Gene cluster A |
| TCGA.F5.6863.01      | CC1          | Gene cluster A |
| TCGA.F5.6864.01      | CC1          | Gene cluster A |
| TCGA.G4.6303.01      | CC1          | Gene cluster A |
| TCGA.G4.6310.01      | CC1          | Gene cluster A |
| TCGA.NH.A8F8.01      | CC1          | Gene cluster A |
| TCGA.QG.A5Z1.01      | CC1          | Gene cluster A |
| TCGA.A6.6649.01      | CC2          | Gene cluster A |
| TCGA.AD.5900.01      | CC2          | Gene cluster A |
| TCGA.A6.2684.01      | CC3          | Gene cluster A |
| TCGA.A6.2685.01      | CC3          | Gene cluster A |
| TCGA.A6.5657.01      | CC3          | Gene cluster A |
| TCGA.A6.5664.01      | CC3          | Gene cluster A |
| TCGA.A6.6651.01      | CC3          | Gene cluster A |
| TCGA.AF.2687.01      | CC3          | Gene cluster A |
| TCGA.AF.2690.01      | CC3          | Gene cluster A |
| TCGA.AG.4022.01      | CC3          | Gene cluster A |
| TCGA.AH.6644.01      | CC3          | Gene cluster A |
| TCGA.CA.6717.01      | CC3          | Gene cluster A |
| TCGA.CA.6719.01      | CC3          | Gene cluster A |
| TCGA.CK.6748.01      | CC3          | Gene cluster A |
| TCGA.CM.5348.01      | CC3          | Gene cluster A |
| TCGA.CM.5349.01      | CC3          | Gene cluster A |
| TCGA.CM.6167.01      | CC3          | Gene cluster A |
| TCGA.Identification  | Group | Description     |
|----------------------|-------|-----------------|
| TCGA.AZ.4315.01      | CC2   | Gene cluster B  |
| TCGA.AZ.4615.01      | CC2   | Gene cluster B  |
| TCGA.BM.6198.01      | CC2   | Gene cluster B  |
| TCGA.CA.5254.01      | CC2   | Gene cluster B  |
| TCGA.CA.6718.01      | CC2   | Gene cluster B  |
| TCGA.CK.4948.01      | CC2   | Gene cluster B  |
| TCGA.CK.4951.01      | CC2   | Gene cluster B  |
| TCGA.CK.4953.01      | CC2   | Gene cluster B  |
| TCGA.CK.4954.01      | CC2   | Gene cluster B  |
| TCGA.CK.4957.01      | CC2   | Gene cluster B  |
| TCGA.CK.5913.01      | CC2   | Gene cluster B  |
| TCGA.CK.6751.01      | CC2   | Gene cluster B  |
| TCGA.CM.4743.01      | CC2   | Gene cluster B  |
| TCGA.CM.4751.01      | CC2   | Gene cluster B  |
| TCGA.CM.5860.01      | CC2   | Gene cluster B  |
| TCGA.CM.5861.01      | CC2   | Gene cluster B  |
| TCGA.CM.5863.01      | CC2   | Gene cluster B  |
| TCGA.CM.6162.01      | CC2   | Gene cluster B  |
| TCGA.CM.6169.01      | CC2   | Gene cluster B  |
| TCGA.CM.6171.01      | CC2   | Gene cluster B  |
| TCGA.CM.6674.01      | CC2   | Gene cluster B  |
| TCGA.CM.6675.01      | CC2   | Gene cluster B  |
| TCGA.CM.6680.01      | CC2   | Gene cluster B  |
| TCGA.D5.5538.01      | CC2   | Gene cluster B  |
| TCGA.D5.5539.01      | CC2   | Gene cluster B  |
| TCGA.D5.6529.01      | CC2   | Gene cluster B  |
| TCGA.D5.6530.01      | CC2   | Gene cluster B  |
| TCGA.D5.6531.01      | CC2   | Gene cluster B  |
| TCGA.D5.6532.01      | CC2   | Gene cluster B  |
| TCGA.D5.6536.01      | CC2   | Gene cluster B  |
| TCGA.D5.6540.01      | CC2   | Gene cluster B  |
| TCGA.D5.6541.01      | CC2   | Gene cluster B  |
| TCGA.D5.6928.01      | CC2   | Gene cluster B  |
| TCGA.D5.6930.01      | CC2   | Gene cluster B  |
| TCGA.D5.6931.01      | CC2   | Gene cluster B  |
| TCGA.D5.7000.01      | CC2   | Gene cluster B  |
| TCGA.DC.6158.01      | CC2   | Gene cluster B  |
| TCGA.DM.A1HB.01      | CC2   | Gene cluster B  |
| TCGA.DM.A280.01      | CC2   | Gene cluster B  |
| TCGA.DM.A28K.01      | CC2   | Gene cluster B  |
| TCGA.El.6511.01      | CC2   | Gene cluster B  |
| TCGA.El.6917.01      | CC2   | Gene cluster B  |
| TCGA.F4.6570.01      | CC2   | Gene cluster B  |
| TCGA.F5.6811.01      | CC2   | Gene cluster B  |
| TCGA.G4.6297.01      | CC2   | Gene cluster B  |
| TCGA.G4.6299.01      | CC2   | Gene cluster B  |
| TCGA.G4.6311.01      | CC2   | Gene cluster B  |
| TCGA.G4.6585.01      | CC2   | Gene cluster B  |
| TCGA.G4.6588.01      | CC2   | Gene cluster B  |
| TCGA.G4.6628.01      | CC2   | Gene cluster B  |
| TCGA.NH.A50V.01      | CC2   | Gene cluster B  |
| TCGA.NH.A5IV.01      | CC2   | Gene cluster B  |
| TCGA.A6.2675.01      | CC3   | Gene cluster B  |
| TCGA.A6.6142.01      | CC3   | Gene cluster B  |
| TCGA.A6.6654.01      | CC3   | Gene cluster B  |
| TCGA.A6.6781.01      | CC3   | Gene cluster B  |
| TCGA.A6.6782.01      | CC3   | Gene cluster B  |
| TCGA.A6.A5ZU.01      | CC3   | Gene cluster B  |
| TCGA.AA.3489.01      | CC3   | Gene cluster B  |
| TCGA.AD.6899.01      | CC3   | Gene cluster B  |
| Sample ID          | Cluster | Description |
|-------------------|---------|-------------|
| TCGA.CM.6676.01   | CC1     | Gene cluster C |
| TCGA.D5.5537.01   | CC1     | Gene cluster C |
| TCGA.D5.5540.01   | CC1     | Gene cluster C |
| TCGA.D5.6532.01   | CC1     | Gene cluster C |
| TCGA.D5.6533.01   | CC1     | Gene cluster C |
| TCGA.D5.6538.01   | CC1     | Gene cluster C |
| TCGA.D5.6923.01   | CC1     | Gene cluster C |
| TCGA.DC.4745.01   | CC1     | Gene cluster C |
| TCGA.DC.4749.01   | CC1     | Gene cluster C |
| TCGA.DC.5869.01   | CC1     | Gene cluster C |
| TCGA.DC.6155.01   | CC1     | Gene cluster C |
| TCGA.DC.6157.01   | CC1     | Gene cluster C |
| TCGA.DC.6682.01   | CC1     | Gene cluster C |
| TCGA.DM.A1D0.01   | CC1     | Gene cluster C |
| TCGA.DM.A1D4.01   | CC1     | Gene cluster C |
| TCGA.DM.A1D6.01   | CC1     | Gene cluster C |
| TCGA.DM.A1D7.01   | CC1     | Gene cluster C |
| TCGA.DM.A1D8.01   | CC1     | Gene cluster C |
| TCGA.DM.A1D9.01   | CC1     | Gene cluster C |
| TCGA.DM.A282.01   | CC1     | Gene cluster C |
| TCGA.DM.A288.01   | CC1     | Gene cluster C |
| TCGA.DM.A28C.01   | CC1     | Gene cluster C |
| TCGA.DM.A28E.01   | CC1     | Gene cluster C |
| TCGA.DM.A28F.01   | CC1     | Gene cluster C |
| TCGA.DM.A28G.01   | CC1     | Gene cluster C |
| TCGA.DM.A28H.01   | CC1     | Gene cluster C |
| TCGA.DY.A0XA.01   | CC1     | Gene cluster C |
| TCGA.DY.A1H8.01   | CC1     | Gene cluster C |
| TCGA.EF.5830.01   | CC1     | Gene cluster C |
| TCGA.EF.5831.01   | CC1     | Gene cluster C |
| TCGA.EI.6508.01   | CC1     | Gene cluster C |
| TCGA.EI.6512.01   | CC1     | Gene cluster C |
| TCGA.EI.6513.01   | CC1     | Gene cluster C |
| TCGA.EI.6881.01   | CC1     | Gene cluster C |
| TCGA.F4.6806.01   | CC1     | Gene cluster C |
| TCGA.F4.6808.01   | CC1     | Gene cluster C |
| TCGA.G4.6307.01   | CC1     | Gene cluster C |
| TCGA.G4.6315.01   | CC1     | Gene cluster C |
| TCGA.G4.6317.01   | CC1     | Gene cluster C |
| TCGA.G5.6235.01   | CC1     | Gene cluster C |
| TCGA.G5.6641.01   | CC1     | Gene cluster C |
| TCGA.NH.A50T.01   | CC1     | Gene cluster C |
| TCGA.NH.A8F7.01   | CC1     | Gene cluster C |
| TCGA.QG.A5YV.01   | CC1     | Gene cluster C |
| TCGA.QG.A5YX.01   | CC1     | Gene cluster C |
| TCGA.QL.A97D.01   | CC1     | Gene cluster C |
| TCGA.RU.A8FL.01   | CC1     | Gene cluster C |
| TCGA.SS.A7HO.01   | CC1     | Gene cluster C |
| TCGA.T9.A92H.01   | CC1     | Gene cluster C |
| TCGA.A6.6137.01   | CC2     | Gene cluster C |
| TCGA.A6.6141.01   | CC2     | Gene cluster C |
| TCGA.A6.6650.01   | CC2     | Gene cluster C |
| TCGA.AA.3495.01   | CC2     | Gene cluster C |
| TCGA.AA.3502.01   | CC2     | Gene cluster C |
| TCGA.AA.3526.01   | CC2     | Gene cluster C |
| TCGA.AA.3655.01   | CC2     | Gene cluster C |
| TCGA.AA.3685.01   | CC2     | Gene cluster C |
| TCGA.AA.3697.01   | CC2     | Gene cluster C |
**Table S5. meta-GEO gene clusters**

| meta-GEO samples | Gene clusters |
|------------------|---------------|
| GSM358341        | C             |
| GSM358342        | C             |
| GSM358343        | B             |
| GSM358344        | C             |
| GSM358345        | C             |
| GSM358346        | A             |
| GSM358347        | C             |
| GSM358348        | C             |
| GSM358349        | C             |
| GSM358350        | C             |
| GSM358351        | C             |
| GSM358352        | C             |
| GSM358353        | B             |
| GSM358354        | B             |
| GSM358355        | B             |
| GSM358356        | C             |
| GSM358357        | C             |
| GSM358358        | B             |
| GSM358359        | A             |
| GSM358360        | B             |
| GSM358361        | B             |
| GSM358362        | B             |
| GSM358363        | C             |
| GSM358364        | B             |
| GSM358365        | C             |
| GSM358366        | B             |
| GSM358367        | B             |
| GSM358368        | C             |
| GSM358370        | C             |
| GSM358371        | C             |
| GSM358373        | B             |
| GSM358374        | B             |
| GSM358375        | B             |
| GSM358376        | C             |
| GSM358377        | B             |
| GSM358378        | C             |
| GSM358380        | C             |
| GSM358381        | C             |
| GSM358382        | A             |
| GSM358383        | C             |
| GSM358384        | A             |
| GSM358385        | A             |
| GSM358386        | A             |
| GSM358387        | B             |
| GSM358388        | B             |
| GSM358389        | A             |
| GSM358390        | A             |
| GSM358391        | B             |
| GSM358392        | A             |
| GSM358393        | A             |
| GSM358394        | B             |
| GSM358395        | B             |
| GSM358396        | C             |
| GSM358397        | A             |
| GSM358398        | B             |
| GSM929532 | C |
| GSM929533 | C |
| GSM929534 | C |
| GSM929535 | C |
| GSM929536 | C |
| GSM929537 | C |
| GSM929538 | B |
| GSM929540 | A |
| GSM929541 | B |
| GSM929542 | B |
| GSM929543 | B |
| GSM929544 | B |
| GSM929545 | A |
| GSM929547 | C |
| GSM929548 | A |
| GSM929549 | A |
| GSM929550 | C |
| GSM929552 | A |
| GSM929553 | A |
| GSM929554 | C |
| GSM929555 | A |
| GSM929556 | A |
| GSM929557 | C |
| GSM929558 | B |
| GSM929559 | B |
| GSM929560 | B |
| GSM929561 | B |
| GSM929562 | A |
| GSM929563 | B |
| GSM929564 | C |
| GSM929565 | C |
| GSM929566 | B |
| GSM929567 | B |
| GSM929568 | B |
| GSM929569 | B |
| GSM929570 | C |
| GSM929571 | C |
| GSM929573 | C |
| GSM929578 | B |
| GSM929579 | C |
| GSM929580 | B |
| GSM929581 | C |
| GSM929582 | A |
| GSM929583 | C |
| GSM929584 | C |
| GSM929588 | A |
| GSM929589 | C |
| GSM929592 | B |
| GSM929594 | A |
| GSM929595 | C |
| GSM929596 | C |
| GSM929597 | C |
| GSM929598 | C |
| GSM929600 | A |
| GSM929601 | C |
| GSM929602 | B |
| GSM929603 | B |
| GSM929604 | B |
| GSM929605 | B |
| GSM929606 | A |
| GSM929607 | C |
| GSM929608 | A |
| GSM929611 | A |
| GSM929613 | C |
| GSM929615 | B |
| GSM929616 | C |
| GSM929619 | A |
| GSM929620 | A |
| GSM929621 | B |
| GSM971957 | A |
| GSM971958 | A |
| GSM971959 | B |
| GSM971960 | C |
| GSM971961 | C |
| GSM971962 | A |
| GSM971963 | A |
| GSM971964 | B |
| GSM971965 | A |
| GSM971966 | C |
| GSM971968 | A |
| GSM971969 | B |
| GSM971970 | B |
| GSM971971 | B |
| GSM971972 | C |
| GSM971973 | B |
| GSM971974 | B |
| GSM971975 | B |
| GSM971976 | C |
| GSM971977 | A |
| GSM971978 | B |
| GSM971979 | B |
| GSM971980 | B |
| GSM971981 | B |
| GSM971982 | B |
| GSM971983 | B |
| GSM971984 | B |
| GSM971985 | C |
| GSM971986 | B |
| GSM971987 | A |
| GSM971988 | B |
| GSM971989 | B |
| GSM971990 | B |
| GSM971991 | C |
| GSM971992 | B |
| GSM971993 | B |
| GSM971994 | A |
| GSM971995 | B |
| GSM971996 | A |
| GSM971997 | B |
| GSM971998 | C |
| GSM971999 | A |
| GSM972000 | A |
| GSM972001 | C |
| GSM972002 | B |
| GSM972003 | B |
| GSM972004 | C |
GSM972005   B
GSM972006   C
GSM972007   A
GSM972008   A
GSM972009   B
GSM972010   A
GSM972011   A
GSM972012   B
GSM972013   A
GSM972014   C
GSM972015   B
GSM972016   B
GSM972017   A
GSM972018   A
GSM972019   A
GSM972020   C
GSM972021   C
GSM972022   A
GSM972023   A
GSM972024   A
GSM972025   C
GSM972026   A
GSM972027   A
GSM972028   C
GSM972029   A
GSM972030   A
GSM972031   C
GSM972032   A
GSM972033   C
GSM972034   C
GSM972035   C
GSM972036   C
GSM972037   B
GSM972038   B
GSM972039   A
GSM972040   A
GSM972041   A
GSM972042   B
GSM972043   C
GSM972044   B
GSM972045   B
GSM972046   B
GSM972047   B
GSM972048   B
GSM972049   B
GSM972050   C
GSM972051   A
GSM972052   A
GSM972053   C
GSM972054   A
GSM972055   B
GSM972056   B
GSM972057   A
GSM972058   B
GSM972059   A
GSM972060   A
GSM972061   B
GSM972062   A
GSM972063  A
GSM972064  B
GSM972065  C
GSM972066  B
GSM972067  A
GSM972068  B
GSM972069  A
GSM972070  C
GSM972071  C
GSM972072  B
GSM972073  A
GSM972074  C
GSM972075  C
GSM972076  A
GSM972077  B
GSM972078  B
GSM972079  B
GSM972080  B
GSM972081  B
GSM972082  A
GSM972083  C
GSM972084  A
GSM972085  C
GSM972086  A
GSM972087  C
GSM972088  A
GSM972089  A
GSM972090  C
GSM972091  C
GSM972092  A
GSM972093  A
GSM972094  C
GSM972095  A
GSM972096  B
GSM972097  B
GSM972098  C
GSM972099  C
GSM972100  B
GSM972101  C
GSM972102  C
GSM972103  B
GSM972104  A
GSM972105  A
GSM972106  C
GSM972107  C
GSM972108  C
GSM972109  B
GSM972110  C
GSM972111  C
GSM972112  B
GSM972113  A
GSM972114  B
GSM972115  C
GSM972116  A
GSM972117  B
GSM972118  B
GSM972119  A
GSM972120  C
| GSM972121 | B |
| GSM972122 | C |
| GSM972123 | C |
| GSM972124 | C |
| GSM972125 | A |
| GSM972126 | C |
| GSM972127 | A |
| GSM972128 | B |
| GSM972129 | C |
| GSM972130 | C |
| GSM972131 | A |
| GSM972132 | A |
| GSM972133 | A |
| GSM972134 | A |
| GSM972135 | C |
| GSM972136 | C |
| GSM972137 | C |
| GSM972138 | C |
| GSM972139 | C |
| GSM972140 | A |
| GSM972141 | C |
| GSM972142 | C |
| GSM972143 | A |
| GSM972144 | C |
| GSM972145 | C |
| GSM972146 | A |
| GSM972147 | A |
| GSM972148 | A |
| GSM972149 | C |
| GSM972150 | C |
| GSM972151 | C |
| GSM972152 | C |
| GSM972153 | C |
| GSM972154 | B |
| GSM972155 | B |
| GSM972156 | C |
| GSM972157 | A |
| GSM972158 | C |
| GSM972159 | B |
| GSM972160 | C |
| GSM972161 | C |
| GSM972162 | A |
| GSM972163 | C |
| GSM972164 | C |
| GSM972165 | B |
| GSM972166 | A |
| GSM972167 | C |
| GSM972168 | B |
| GSM972169 | C |
| GSM972170 | A |
| GSM972171 | A |
| GSM972172 | B |
| GSM972173 | C |
| GSM972174 | C |
| GSM972175 | B |
| GSM972176 | A |
| GSM972177 | C |
| GSM972178 | C |
| GSM972354 | A    |
| GSM972355 | C    |
| GSM972357 | A    |
| GSM972358 | C    |
| GSM972359 | A    |
| GSM972360 | C    |
| GSM972361 | B    |
| GSM972362 | C    |
| GSM972363 | C    |
| GSM972364 | C    |
| GSM972365 | B    |
| GSM972366 | C    |
| GSM972367 | A    |
| GSM972368 | B    |
| GSM972369 | C    |
| GSM972370 | C    |
| GSM972371 | A    |
| GSM972372 | A    |
| GSM972373 | A    |
| GSM972374 | C    |
| GSM972375 | A    |
| GSM972376 | A    |
| GSM972377 | A    |
| GSM972378 | B    |
| GSM972379 | C    |
| GSM972380 | A    |
| GSM972381 | C    |
| GSM972382 | A    |
| GSM972383 | C    |
| GSM972384 | A    |
| GSM972385 | A    |
| GSM972386 | C    |
| GSM972387 | C    |
| GSM972388 | C    |
| GSM972389 | B    |
| GSM972390 | B    |
| GSM972391 | B    |
| GSM972392 | C    |
| GSM972393 | B    |
| GSM972394 | A    |
| GSM972395 | C    |
| GSM972396 | B    |
| GSM972397 | B    |
| GSM972398 | C    |
| GSM972399 | A    |
| GSM972400 | C    |
| GSM972401 | B    |
| GSM972402 | B    |
| GSM972403 | B    |
| GSM972404 | A    |
| GSM972405 | C    |
| GSM972406 | A    |
| GSM972407 | A    |
| GSM972408 | B    |
| GSM972409 | C    |
| GSM972410 | A    |
| GSM972411 | C    |
| GSM972412 | B    |
### Table S5. TCGA gene clusters and genes /

| DEGs overlapped | Genes A-C |
|-----------------|-----------|
| TET1            | genes A   |
| VLDLR           | genes A   |
| DIRAS2          | genes A   |
| MUM1L1          | genes A   |
| RASL1B          | genes A   |
| TRAM1L1         | genes A   |
| DTNA            | genes A   |
| CC2D2A          | genes A   |
| TNFAIP8L3       | genes A   |
| GHR             | genes A   |
| ST6GAL2         | genes A   |
| CLSTN2          | genes A   |
| SNORD116-28     | genes A   |
| IPW             | genes A   |
| PAR-SN          | genes A   |
| ZNF415          | genes A   |
| ZNF134          | genes A   |
| ZNF471          | genes A   |
| ZSCAN18         | genes A   |
| FGF13           | genes A   |
| KL              | genes A   |
| TXLNB           | genes A   |
| DAB2            | genes A   |
| TGFBR2          | genes A   |
| KLF7            | genes A   |
| KIAA0355        | genes A   |
| MBD5            | genes A   |
| KIDINS220       | genes A   |
| BMPR2           | genes A   |
| RNF146          | genes A   |
| TSPYL4          | genes A   |
| NIPSNAP3B       | genes A   |
| RCBTB2          | genes A   |
| ODZ2            | genes A   |
| CGNL1           | genes A   |
| GPRASP2         | genes A   |
| NFASC           | genes A   |
| RAI2            | genes A   |
| ZNF167          | genes A   |
| ZNF569          | genes A   |
| ZNF287          | genes A   |
| GBGT1           | genes A   |
| MAGEE1          | genes A   |
| ZNF853          | genes A   |
| SMO             | genes A   |
| ZNF423          | genes A   |
| HDGFRP3         | genes A   |
| LOC285548       | genes A   |
| RAB9B           | genes A   |
| C11orf63        | genes A   |
| SEMA4C          | genes A   |
| CRY2            | genes A   |
| ZFHX3           | genes A   |
| SMTN            | genes A   |
| ZNF362          | genes A   |
| Genes A | Genes A | Genes A |
|---------|---------|---------|
| AKAP6   |         | 5-Sep   |
| RBM20   |         |         |
| BRSK1   |         |         |
| PCDHGC3 |         |         |
| CILP2   |         |         |
| KIF7    |         |         |
| TSPYL2  |         |         |
| MECP2   |         |         |
| PCP4L1  |         |         |
| HRNBP3  |         |         |
| C6orf168|         |         |
| CCDC136 |         |         |
| LOC100128239|   |         |
| NCRNA00085|       |         |
| TF      |         |         |
| SLC7A10 |         |         |
| FNDC5   |         |         |
| TERF2IP |         |         |
| CDH8    |         | 7-Sep   |
| TMEM43  |         |         |
| NXPH3   |         |         |
| NPTXR   |         |         |
| SPEG    |         |         |
| AGTR1   |         |         |
| GPRASP1 |         |         |
| LIMS2   |         |         |
| TCF7L1  |         |         |
| MAP6    |         |         |
| PDZD4   |         |         |
| MPPED2  |         |         |
| HSPB6   |         |         |
| OGN     |         |         |
| CDON    |         |         |
| PCYT1B  |         |         |
| DCHS2   |         |         |
| C1orf95 |         |         |
| ADCY5   |         |         |
| ATP1A2  |         |         |
| CASQ2   |         |         |
| SYNM    |         |         |
| MYH11   |         |         |
| LMO3    |         |         |
| HSPB7   |         |         |
| CARTPT  |         |         |
| ASB5    |         |         |
| HAND1   |         |         |
| CHRM2   |         |         |
| NRSN1   |         |         |
| KIF1A   |         |         |
| FMN2    |         |         |
| PGM5P2  |         |         |
| PGM5    |         |         |
| DDIT4L  |         |         |
| DYNC1I1 |         |         |
| WASF3   |         |         |
| SORBS3  |         |         |
|         |         |         |

**7-Sep Genes A**

| Genes A | Genes A |
|---------|---------|
| TMEM43  |         |
| NXPH3   |         |
| NPTXR   |         |
| SPEG    |         |
| AGTR1   |         |
| GPRASP1 |         |
| LIMS2   |         |
| TCF7L1  |         |
| MAP6    |         |
| PDZD4   |         |
| MPPED2  |         |
| HSPB6   |         |
| OGN     |         |
| CDON    |         |
| PCYT1B  |         |
| DCHS2   |         |
| C1orf95 |         |
| ADCY5   |         |
| ATP1A2  |         |
| CASQ2   |         |
| SYNM    |         |
| MYH11   |         |
| LMO3    |         |
| HSPB7   |         |
| CARTPT  |         |
| ASB5    |         |
| HAND1   |         |
| CHRM2   |         |
| NRSN1   |         |
| KIF1A   |         |
| FMN2    |         |
| PGM5P2  |         |
| PGM5    |         |
| DDIT4L  |         |
| DYNC1I1 |         |
| WASF3   |         |
| SORBS3  |         |

**WASF3 Genes A**

| Genes A |
|---------|
|         |

**SORBS3 Genes A**

| Genes A |
|---------|
|         |
RBMS1  genes A
NRXN2  genes A
LG4  genes A
PPP1R14A  genes A
HRC  genes A
SLC35F1  genes A
RGS5  genes A
FLJ22536  genes A
RPRM  genes A
TMEM35  genes A
ISLR2  genes A
ABCB4  genes A
ORAI2  genes A
MAPK8IP1  genes A
BCAM  genes A
RND2  genes A
WFIKKN2  genes A
LEFTY2  genes A
PTPRT  genes A
HLF  genes A
LOC643763  genes A
ABL2  genes A
STAT5B  genes A
NNAT  genes A
NRIP2  genes A
AASS  genes A
KCTD7  genes A
ZNF333  genes B
IGFL2  genes B
KLF2  genes B
ACTB  genes B
PLOD1  genes B
TREML3  genes B
DCBLD1  genes B
ANXA5  genes B
GUCA1A  genes B
IKBIP  genes B
TMEM45A  genes B
COL6A6  genes B
ALOX15B  genes B
ADAM8  genes B
VMO1  genes B
NFATC1  genes B
TGFBI  genes B
HAPLN3  genes B
SPHK1  genes B
AMZ1  genes B
CLEC4E  genes B
CCL18  genes B
C19orf59  genes B
KCNJ15  genes B
BCL2A1  genes B
TREM1  genes B
AQP9  genes B
CAMK1G  genes B
CHST11  genes B
FCGR2B  genes B
FCGR2C  genes B
| Gene   | Type |
|--------|------|
| CD14   | B    |
| FCGR2A | B    |
| PILRA  | B    |
| C5AR1  | B    |
| LILRA6 | B    |
| LILRB3 | B    |
| HK3    | B    |
| NCF2   | B    |
| ITGAM  | B    |
| FGR    | B    |
| ITGAX  | B    |
| ALOX5AP| B    |
| SIGLEC5| B    |
| LILRA2 | B    |
| FPR1   | B    |
| CSF3R  | B    |
| MCHR1  | B    |
| MMP9   | B    |
| SPP1   | B    |
| MARCO  | B    |
| SLC11A1| B    |
| CLEC5A | B    |
| RGS16  | B    |
| SOCS3  | B    |
| OSM    | B    |
| CHSY1  | B    |
| STC1   | B    |
| SLC2A3 | B    |
| EMP3   | B    |
| LGALS1 | B    |
| NNMT   | B    |
| TSPAN4 | B    |
| PLEKHO1| B    |
| GYPC   | B    |
| A4GALT | B    |
| PTGIR  | B    |
| ALPK2  | B    |
| BCAT1  | B    |
| ADAM12 | B    |
| TNFAIP6| B    |
| LOX    | B    |
| PRRX1  | B    |
| KCND2  | B    |
| MDGA1  | B    |
| HS3ST3A1| B   |
| PDPN   | B    |
| PRR16  | B    |
| WISP1  | B    |
| GPR176 | B    |
| XIRP1  | B    |
| PLAU   | B    |
| NID2   | B    |
| ADAMTS2| B    |
| ZNF469 | B    |
| COL5A3 | B    |
| ADAMTS4| B    |
| SLC2A6 | B    |
| ZNF467 | B    |
| Gene Name   | Annotation |
|------------|------------|
| FAM167B    | genes B    |
| ESAM       | genes B    |
| SH2D3C     | genes B    |
| STARID8    | genes B    |
| CD93       | genes B    |
| CLEC1A     | genes B    |
| PECAM1     | genes B    |
| SCARF1     | genes B    |
| SEMA6B     | genes B    |
| ENG        | genes B    |
| DEGS1      | genes B    |
| TFPI       | genes B    |
| AIF1L      | genes B    |
| HOXC4      | genes B    |
| HOXC9      | genes B    |
| ANXA8L2    | genes B    |
| UNC5A      | genes B    |
| IRF1       | genes B    |
| NFIL3      | genes B    |
| FGFBP2     | genes B    |
| HRASLS5    | genes B    |
| VIT        | genes B    |
| PDE4DIP    | genes B    |
| FGF11      | genes B    |
| VAMP2      | genes B    |
| SMG6       | genes B    |
| WDR81      | genes B    |
| ABHD4      | genes B    |
| KLHL22     | genes B    |
| ADRB2      | genes B    |
| ARHGDIB    | genes B    |
| RNASE6     | genes B    |
| PDE6B      | genes B    |
| MAL        | genes B    |
| LTA        | genes B    |
| LTB        | genes B    |
| NAPSB      | genes B    |
| AMICA1     | genes B    |
| CLEC10A    | genes B    |
| RAB33A     | genes B    |
| ITM2A      | genes B    |
| CIC2       | genes B    |
| GIMAP1     | genes B    |
| GIMAP5     | genes B    |
| GIMAP7     | genes B    |
| ARHGAP15   | genes B    |
| GGT1A      | genes B    |
| SLC9A9     | genes B    |
| BIN2       | genes B    |
| SIGLEC8    | genes B    |
| GZMK       | genes B    |
| PLA2G2D    | genes B    |
| TNFSF14    | genes B    |
| SPOCK2     | genes B    |
| ZNF831     | genes B    |
| GVIN1      | genes B    |
| KIAA0748   | genes B    |
| PPP1R16B   | genes B    |
| Gene       | Location |
|------------|----------|
| PRKCB      | genes B  |
| IL16       | genes B  |
| LY9        | genes B  |
| P2RY8      | genes B  |
| ABCD2      | genes B  |
| LOC100233209 | genes B |
| TRAF3IP3   | genes B  |
| ARHGAP9    | genes B  |
| RASAL3     | genes B  |
| IL21R      | genes B  |
| CCR5       | genes B  |
| WDFY4      | genes B  |
| SELL       | genes B  |
| CR1        | genes B  |
| HLA-DQA1   | genes B  |
| FGD2       | genes B  |
| EVI2B      | genes B  |
| CD180      | genes B  |
| FYB        | genes B  |
| APBB1IP    | genes B  |
| DOCK10     | genes B  |
| ARHGAP25   | genes B  |
| KLHL6      | genes B  |
| RCSD1      | genes B  |
| C17orf87   | genes B  |
| STX11      | genes B  |
| IL10RA     | genes B  |
| NCKAP1L    | genes B  |
| SLA        | genes B  |
| PIK3R5     | genes B  |
| CD53       | genes B  |
| BTK        | genes B  |
| LILRB1     | genes B  |
| SIGLEC10   | genes B  |
| FAM78A     | genes B  |
| MYO1G      | genes B  |
| CYTH4      | genes B  |
| FMNL1      | genes B  |
| MYO1F      | genes B  |
| LCP1       | genes B  |
| WAS        | genes B  |
| HCLS1      | genes B  |
| ARHGAP30   | genes B  |
| DOCK2      | genes B  |
| ITGAL      | genes B  |
| SASH3      | genes B  |
| PTPRC      | genes B  |
| IKZF1      | genes B  |
| NCF1       | genes B  |
| LSP1       | genes B  |
| CD37       | genes B  |
| RHOH       | genes B  |
| TAGAP      | genes B  |
| TNFSF8     | genes B  |
| NCF1C      | genes B  |
| NCF1B      | genes B  |
| KLRG1      | genes B  |
| LOC254559  | genes B  |
| Gene          | Type |
|--------------|------|
| PTCRA        | B    |
| C17orf60     | B    |
| LILRA4       | B    |
| HLA-DQA2     | B    |
| HLA-DQB2     | B    |
| HLA-DPB2     | B    |
| CD52         | B    |
| CD48         | B    |
| GNGT2        | B    |
| HCST         | B    |
| GMFG         | B    |
| TNFAIP8L2    | B    |
| LST1         | B    |
| AIF1         | B    |
| PSTPIP1      | B    |
| LIMD2        | B    |
| FCRL6        | B    |
| LOC400759    | B    |
| IL18BP       | B    |
| ATP6V0D2     | B    |
| LIPA         | B    |
| SLC2A5       | B    |
| GM2A         | B    |
| HS3ST2       | B    |
| TREM2        | B    |
| APOE         | B    |
| APOC1        | B    |
| OSCAR        | B    |
| SLC1A3       | B    |
| OLR1         | B    |
| MSR1         | B    |
| GPNMB        | B    |
| CTS1L        | B    |
| C1orf162     | B    |
| FCGR1C       | B    |
| FCGR3A       | B    |
| FCGR1B       | B    |
| FCGR1A       | B    |
| PLD3         | B    |
| PSAP         | B    |
| KCNE1        | B    |
| CD68         | B    |
| CTSB         | B    |
| MRO          | B    |
| CPVL         | B    |
| TNNI2        | B    |
| BAI2         | B    |
| PLEKHF1      | B    |
| FLT3LG       | B    |
| NAGK         | B    |
| PPM1M        | B    |
| CACNA1A      | B    |
| MX2          | B    |
| RSAD2        | B    |
| DDX58        | B    |
| DRAM1        | B    |
| PPM1K        | B    |
| HOXB2        | B    |
ERMN genes B
RNFI22 genes B
PDE10A genes B
CD109 genes B
FBLN7 genes B
CALHM2 genes B
LOC400043 genes B
PDGFRL genes B
DZIP1L genes B
ARHGAP24 genes B
ARHGAP20 genes B
PLXDC2 genes B
PALLD genes B
FYN genes B
PLXND1 genes B
CHST15 genes B
PEAR1 genes B
C6orf204 genes B
DOCK8 genes B
TLR6 genes B
FZD2 genes B
ARHGAP22 genes B
MOBKL2A genes B
S1PR2 genes B
RIMBP3 genes B
MAMLD1 genes B
EID3 genes B
NCRNA00181 genes B
NTRK1 genes B
CCDC88A genes B
OPRL1 genes B
HSD17B14 genes B
HVCN1 genes B
LYL1 genes B
SPATC1 genes B
PLCB2 genes B
STAT2 genes B
NLRP1 genes B
C9orf139 genes B
HSPA7 genes B
CORO1A genes B
SYTL3 genes B
CD72 genes B
GPSM3 genes B
MFNG genes B
DOK3 genes B
PIK3CD genes B
POU2F2 genes B
FERMT3 genes B
GPR132 genes B
SUCNR1 genes B
PLA2G7 genes B
CLEC4A genes B
EVII2A genes B
SRGN genes B
SAMSN1 genes B
PDCD1LG2 genes B
MNDA genes B
LCP2
genes B
PLEK
genes B
GPR65
genes B
C1orf128
genes B
KCNK13
genes B
GPR34
genes B
MS4A6A
genes B
MS4A4A
genes B
MS4A7
genes B
TLR8
genes B
CYBB
genes B
CD84
genes B
TFEC
genes B
CLEC7A
genes B
IGSF6
genes B
TLR1
genes B
PLXNC1
genes B
TLR7
genes B
MPEG1
genes B
CMKLR1
genes B
CD4
genes B
CSF1R
genes B
GPR141
genes B

1-Mar genes B
EMILIN2
genes B
PTAFR
genes B
CD300C
genes B
NLRP3
genes B
CASS4
genes B
FCN1
genes B
RASGRP4
genes B
HRH2
genes B
C1orf38
genes B
EMR2
genes B
MS4A14
genes B
SDS
genes B
CD300LB
genes B
DPEP2
genes B
LY86
genes B
PIK3R6
genes B
PRAM1
genes B
PARVG
genes B
EVL
genes B
ESR1
genes B
CECR1
genes B
SLC37A2
genes B
ZNF804A
genes B
SLC31A2
genes B
PDE6G
genes B
CLEC12A
genes B
KMO
genes B
RAB42
genes B
ADORA3
genes B
P2RX7
genes B
FAM20A
genes B
PLEKHO2
genes B
MRC1
genes B
VSIG4
genes B
| Gene    | Type  |
|---------|-------|
| CD33    | genes B |
| CCR1    | genes B |
| SIRPB2  | genes B |
| LILRB2  | genes B |
| SIGLEC9 | genes B |
| LRR2C25 | genes B |
| SIGLEC7 | genes B |
| CD163   | genes B |
| C3AR1   | genes B |
| FPR3    | genes B |
| SIGLEC1 | genes B |
| NLRC4   | genes B |
| TNFSF13B | genes B |
| HLA-DPB1 | genes B |
| HLA-DOA | genes B |
| SLC15A3 | genes B |
| NFAM1   | genes B |
| ADAP2   | genes B |
| CD300A  | genes B |
| CD300LF | genes B |
| HCK     | genes B |
| SLAMF8  | genes B |
| LAPT5M5 | genes B |
| ITGB2   | genes B |
| SPI1    | genes B |
| LAIR1   | genes B |
| TYRO8B  | genes B |
| FCER1G  | genes B |
| LILRB4  | genes B |
| CD86    | genes B |
| HAVCR2  | genes B |
| TRPV2   | genes B |
| ABI3    | genes B |
| DOK2    | genes B |
| C1QA    | genes B |
| C1QB    | genes B |
| C1QC    | genes B |
| MATK    | genes B |
| ACP5    | genes B |
| DNAJC5B | genes B |
| STEAP4  | genes B |
| LOC339524 | genes B |
| CD36    | genes B |
| SSTR2   | genes B |
| CYTL1   | genes B |
| NLRP12  | genes B |
| STAC    | genes B |
| CCL8    | genes B |
| CCL7    | genes B |
| DSE     | genes B |
| RNASE2  | genes B |
| GLIPR2  | genes B |
| VAMP5   | genes B |
| C1orf54 | genes B |
| CLEC2B  | genes B |
| LY96    | genes B |
| NCRNA00189 | genes B |
| IL4I1   | genes B |
ICAM1 genes B
JAK3 genes B
TNFRSF4 genes B
ADORA2A genes B
TNFRSF8 genes B
SIRPB1 genes B
P2RY6 genes B
LILRA5 genes B
GPR84 genes B
ZNF385A genes B
RGS19 genes B
MCTP1 genes B
LAT2 genes B
KIAA1949 genes B
ARL4C genes B
RASGRF2 genes B
SPON1 genes B
ANXA1 genes B
RGS2 genes B
PNMA1 genes B
ATP8B3 genes B
ADCY7 genes B
PMP22 genes B
C10orf10 genes B
LOXL1 genes B
PRKCDBP genes B
ABLIIM3 genes B
MAPK11 genes B
KIFC3 genes B
GNAI2 genes B
MAP7D1 genes B
ANKRD34A genes B
BCL6 genes B
SLC43A3 genes B
ITPR1PL2 genes B
TOX2 genes B
NFIC genes B
C14orf49 genes B
CCL23 genes B
MFSD7 genes B
MCOLN1 genes B
ACP2 genes B
C10orf54 genes B
MGAT1 genes B
KLF9 genes B
AGPAT4 genes B
GLIS3 genes B
MFSD1 genes B
RNFI44B genes B
GPR137B genes B
TCL1A genes B
CLEC17A genes B
FAIM3 genes B
TNFRSF13B genes B
FCRL3 genes B
CD22 genes B
FCRLA genes B
BLK genes B
| Gene   | Type | Description |
|--------|------|-------------|
| CXCR5  | genes B | |
| MS4A1  | genes B | |
| CD79B  | genes B | |
| TLR10  | genes B | |
| AFF2   | genes B | |
| TREML1 | genes B | |
| PER1   | genes B | |
| NR4A3  | genes B | |
| ITPRIP | genes B | |
| SERPINE1 | genes B | |
| EGR3   | genes B | |
| SGK1   | genes B | |
| TNFAIP3 | genes B | |
| DUSP1  | genes B | |
| GPR183 | genes B | |
| RGS1   | genes B | |
| B4GALT1 | genes B | |
| KCTD11 | genes B | |
| EMP1   | genes B | |
| SEMA7A | genes B | |
| PLEKHG1 | genes B | |
| KCTD12 | genes B | |
| PDE5A  | genes B | |
| ARSB   | genes B | |
| SLC16A7 | genes B | |
| TRAM2  | genes B | |
| ST5    | genes B | |
| AHNAK  | genes B | |
| AHDC1  | genes B | |
| GSN    | genes B | |
| C17orf107 | genes B | |
| SIDT2  | genes B | |
| ASAP3  | genes B | |
| RNF24  | genes B | |
| PPFIBP1 | genes B | |
| HTR1B  | genes B | |
| IFNAR2 | genes B | |
| TCN2   | genes B | |
| SLCO2B1 | genes B | |
| IL1RL1 | genes B | |
| CTSG   | genes B | |
| SIGLEC6 | genes B | |
| SIGLEC3P | genes B | |
| HDC    | genes B | |
| TPSAB1 | genes B | |
| TPSB2  | genes B | |
| CPA3   | genes B | |
| MS4A2  | genes B | |
| C1orf150 | genes B | |
| C1orf186 | genes B | |
| BEND4  | genes B | |
| CAMK4  | genes B | |
| CLEC9A | genes B | |
| FLT3   | genes B | |
| KCND3  | genes B | |
| CCDC69 | genes B | |
| FAM65B | genes B | |
| FAM55C | genes B | |
| Genes B                  |
|-------------------------|
| PIP4K2A                 |
| CCR7                    |
| CCL22                   |
| TNFRSF9                 |
| FOXP3                   |
| CCR8                    |
| SPN                     |
| CD28                    |
| CCR4                    |
| PRKAR2B                 |
| S100B                   |
| CCDC141                 |
| EPB41L3                 |
| SASH1                   |
| TIAM1                   |
| ROR1                    |
| STK10                   |
| TMEM140                 |
| RUNDC2A                 |
| LYST                    |
| KIAA0247                |
| CYLD                    |
| GIT2                    |
| LOC257358               |
| EMR4P                   |
| EMR1                    |
| CEBPE                   |
| CEACAM4                 |
| CFP                     |
| CLEC4G                  |
| CCL13                   |
| LILRB5                  |
| FOLR2                   |
| PDE4B                   |
| IL10                    |
| SLC24A4                 |
| CXCR4                   |
| SELPLG                  |
| RASSF5                  |
| CHI3L2                  |
| PLCG2                   |
| C16orf54                |
| LRMP                    |
| STOM                    |
| ITGA1                   |
| AVPR1A                  |
| TRPC6                   |
| CAV1                    |
| STK32B                  |
| COL6A1                  |
| ITGA5                   |
| IRAK3                   |
| HHEX                    |
| CITED2                  |
| LHFPFL2                 |
| TCP11L1                 |
| SWAP70                  |
| RAB88B                  |
| Gene   | Expression |
|--------|------------|
| SNRK   | genes B    |
| CHST2  | genes B    |
| KCNN3  | genes B    |
| ZNF366 | genes B    |
| SFMBT2 | genes B    |
| STAB1  | genes B    |
| P2RY13 | genes B    |
| RGS18  | genes B    |
| ST8SIA4| genes B    |
| ITGA4  | genes B    |
| CYSLTR1| genes B    |
| CSF2RB | genes B    |
| PIK3CG | genes B    |
| ATP8B4 | genes B    |
| GAB3   | genes B    |
| Cxorf21| genes B    |
| CCR2   | genes B    |
| FGL2   | genes B    |
| CYSLTR2| genes B    |
| GJD3   | genes B    |
| TMEM26 | genes B    |
| DOCK4  | genes B    |
| RASGRP3| genes B    |
| NR3C1  | genes B    |
| GNG2   | genes B    |
| VCAM1  | genes B    |
| FAM49A | genes B    |
| GIMAP4 | genes B    |
| GIMAP6 | genes B    |
| FLI1   | genes B    |
| GIMAP8 | genes B    |
| RASSF2 | genes B    |
| ARHGEF6| genes B    |
| MYO5A  | genes B    |
| WIPF1  | genes B    |
| GPR77  | genes B    |
| CLEC4D | genes B    |
| FCAR   | genes B    |
| CD300E | genes B    |
| GPR97  | genes B    |
| GLT1D1 | genes B    |
| EMR3   | genes B    |
| LILRA1 | genes B    |
| FAM196B| genes B    |
| PAPPA  | genes B    |
| APBA2  | genes B    |
| C3     | genes B    |
| BASP1  | genes B    |
| GPR68  | genes B    |
| MSC    | genes B    |
| SDK1   | genes B    |
| ETS1   | genes B    |
| ARHGAP31| genes B   |
| SLFN11 | genes B    |
| HSD11B1| genes B    |
| CCL2   | genes B    |
| CSF1   | genes B    |
| NRP1   | genes B    |
DPYD  genes B
LRRC8C  genes B
MSN  genes B
IL1R1  genes B
ATP8B2  genes B
ASAM  genes B
OSMR  genes B
COLEC12  genes B
VIM  genes B
RAB31  genes B
CFH  genes B
GNB4  genes B
ZEB2  genes B
MAFB  genes B
MAF  genes B
FUT11  genes B
LIMS1  genes B
SH2B3  genes B
PLBD2  genes B
MTIF2  genes C
OLA1  genes C
HSPE1  genes C
CCDC58  genes C
GPR35  genes C
DUS1L  genes C
TBRG4  genes C
LY6G6D  genes C
EBPL  genes C
KIF11  genes C
HNRNPF  genes C
P8K  genes C
RRM2  genes C
H2AFZ  genes C
CENPM  genes C
ORC1L  genes C
CDC20  genes C
PPA2  genes C
NDUFA9  genes C
PSMA5  genes C
PGAM5  genes C
SORD  genes C
CCNO  genes C
TMC5  genes C
CASP5  genes C
F2RL1  genes C
| samples               | TCGA PC1 of genes A | TCGA PC1 of genes B |
|-----------------------|---------------------|---------------------|
| TCGA.3L.AA1B.01       | 6.106741023         | 0.533374706         |
| TCGA.4N.A93T.01       | -4.003593467        | -5.882265235        |
| TCGA.4T.AA8H.01       | -5.088839373        | -11.04406171        |
| TCGA.5M.AATE.01       | -0.88023619         | -6.21739114         |
| TCGA.6/56.01          | 2.252418895         | -4.092000021        |
| TCGA.6/56.01          | 4.681027345         | -3.63126201         |
| TCGA.6/56.01          | -0.921547602        | -1.05371654         |
| TCGA.6/56.01          | 5.032663199         | 0.021882242         |
| TCGA.6/56.01          | -4.445944747        | -7.24440768         |
| TCGA.6/56.01          | 7.104003138         | -1.80036602         |
| TCGA.6/61.01          | -2.860856999        | -6.459034155        |
| TCGA.6/66.01          | -3.39725703         | -7.94652783         |
| TCGA.6/66.01          | 0.0194015           | -3.948648302        |
| TCGA.6/66.01          | 3.554120817         | 0.09027404          |
| TCGA.6/34.01          | 0.213615277         | 4.261033879         |
| TCGA.6/35.01          | -0.973032235        | -1.452295053        |
| TCGA.6/35.01          | 0.114176832         | -0.977031466        |
| TCGA.6/36.01          | -0.443400259        | -0.598829175        |
| TCGA.6/36.01          | 0.666778463         | 3.491179044         |
| TCGA.6/36.01          | -3.948033571        | -2.768542773        |
| TCGA.6/36.01          | 7.271196211         | 0.046633991         |
| TCGA.6/68.01          | -3.763744025        | -6.71520917         |
| TCGA.6/68.01          | -1.792776229        | -0.928164178        |
| TCGA.6/69.01          | -1.069447019        | -1.858086372        |
| TCGA.6/56.01          | 0.611075789         | -4.633043265        |
| TCGA.6/39.01          | 2.906885555         | -0.369744072        |
| TCGA.6/41.01          | 4.758278296         | 3.568795123         |
| TCGA.6/61.01          | -2.00597497         | -6.31284676         |
| TCGA.6/66.01          | -0.166197322        | -3.61045943         |
| TCGA.6/56.01          | 1.318026665         | -0.239484987        |
| TCGA.6/34.01          | 0.589778126         | -1.36476293         |
| TCGA.6/37.01          | 2.683045617         | -0.683470644        |
| TCGA.6/65.01          | -4.574266663        | -9.11945896         |
| TCGA.6/65.01          | 0.40364921          | -0.80859357         |
| TCGA.6/66.01          | 2.276623768         | 1.35370853          |
| TCGA.6/68.01          | -6.719275678        | -10.45582888        |
| TCGA.6/69.01          | -0.251306905        | -8.59831181         |
| TCGA.6/58.01          | 4.247883091         | -1.539574333        |
| TCGA.6/67.01          | -4.877384839        | -10.03260249        |
| TCGA.6/56.01          | -2.370839207        | -4.597192035        |
| TCGA.6/71.01          | -4.74452655         | -5.89066046         |
| TCGA.6/68.01          | -1.002426935        | -5.06904886         |
| TCGA.2/46.01          | -2.39119509         | 1.413205018         |
| TCGA.6/52.01          | -3.62841184         | -2.596260521        |
| TCGA.6/52.01          | -5.06904353         | -4.925853831        |
| TCGA.6/57.01          | 3.161237437         | -1.618276822        |
| TCGA.6/67.01          | -0.301610154        | -6.578457066        |
| TCGA.6/67.01          | 5.73933306          | -3.732349026        |
| TCGA.6/61.01          | 0.859732824         | 1.841168667         |
| TCGA.6/62.01          | 0.171798414         | -2.367265541        |
| TCGA.6/62.01          | -3.3873679451       | -6.12340271         |
| TCGA.6/59.01          | -0.463601179        | -6.311815034        |
| TCGA.6/59.01          | -4.436511113        | -10.87521785        |
| TCGA.6/49.01          | -2.035585154        | -4.590217721        |
| TCGA.6/59.01          | 2.796565609         | -3.022237556        |
| TCGA.CL.5918.01 | -4.081078176 | -6.377236846 |
| TCGA.CM.4747.01 | 2.954262705 | -0.487979847 |
| TCGA.CM.5344.01 | 3.04988584 | 1.636199627 |
| TCGA.CM.5864.01 | -2.722207575 | -4.824768607 |
| TCGA.CM.5868.01 | 0.892339004 | 0.727116234 |
| TCGA.CM.6161.01 | 0.214456657 | -0.761702501 |
| TCGA.CM.6163.01 | 0.067228065 | 0.128579629 |
| TCGA.CM.6164.01 | 5.276615509 | -0.875323542 |
| TCGA.CM.6165.01 | 3.684613692 | -0.237323149 |
| TCGA.CM.6166.01 | 2.980372817 | -5.609978774 |
| TCGA.CM.6170.01 | -0.248324353 | -0.034327402 |
| TCGA.CM.6172.01 | 0.032855894 | -2.719250779 |
| TCGA.CM.6676.01 | 4.663828882 | -2.149020374 |
| TCGA.CM.6678.01 | 2.911152199 | -2.545613689 |
| TCGA.D5.5537.01 | -0.362006647 | -0.657571902 |
| TCGA.D5.5540.01 | -5.826025153 | -4.790648002 |
| TCGA.D5.5541.01 | -2.362055155 | -2.94190328 |
| TCGA.D5.6532.01 | -2.08129148 | 1.065629384 |
| TCGA.D5.6533.01 | 0.363412518 | 2.090976781 |
| TCGA.D5.6538.01 | 5.235267931 | 4.105890878 |
| TCGA.D5.6539.01 | 5.042093148 | 4.451609014 |
| TCGA.D5.6540.01 | 0.48752229 | 3.355905052 |
| TCGA.D5.6541.01 | 1.535238798 | 2.035321213 |
| TCGA.DC.4745.01 | -0.606299397 | -3.864471382 |
| TCGA.DC.4749.01 | -3.69424284 | -6.964755107 |
| TCGA.DC.5869.01 | -2.834777495 | -3.725632938 |
| TCGA.DC.6154.01 | 0.798217709 | 0.067032734 |
| TCGA.DC.6155.01 | -4.440453025 | 0.496270604 |
| TCGA.DC.6157.01 | 0.431743062 | -4.359996769 |
| TCGA.DC.6681.01 | 9.099296742 | -1.033910713 |
| TCGA.DC.6682.01 | 0.188388727 | -5.855982917 |
| TCGA.DC.6683.01 | -5.865095382 | -6.81404498 |
| TCGA.DM.A1D0.01 | 1.969410331 | 2.97140644 |
| TCGA.DM.A1D4.01 | -6.458430046 | -7.312130059 |
| TCGA.DM.A1D6.01 | -5.485881254 | -9.13036791 |
| TCGA.DM.A1D7.01 | -2.432946468 | -4.60018109 |
| TCGA.DM.A1D8.01 | -1.757671388 | -5.946725555 |
| TCGA.DM.A1D9.01 | -2.89365544 | -5.20652875 |
| TCGA.DM.A1HA.01 | -2.972324905 | -0.73343662 |
| TCGA.DM.A282.01 | 0.2206868 | -5.57492534 |
| TCGA.DM.A288.01 | -6.322859464 | -3.887999736 |
| TCGA.DM.A28A.01 | -0.38901767 | 0.724523418 |
| TCGA.DM.A28C.01 | -2.352105986 | -8.878141 |
| TCGA.DM.A28E.01 | -6.043655429 | -11.94813216 |
| TCGA.DM.A28F.01 | -4.391994742 | -5.628105274 |
| TCGA.DM.A28G.01 | 0.220658788 | -5.50978773 |
| TCGA.DM.A28H.01 | -4.61375594 | -5.39614161 |
| TCGA.DY.A0XA.01 | -1.00008412 | -4.637225877 |
| TCGA.DY.A1DD.01 | 10.56051893 | -0.360316804 |
| TCGA.DY.A1DF.01 | 8.627181408 | 1.700845055 |
| TCGA.DY.A1H8.01 | -2.06709282 | -5.190427466 |
| TCGA.EF.5830.01 | -2.155012108 | -4.779546277 |
| TCGA.EF.5831.01 | -1.212166209 | -1.044365571 |
| TCGA.EI.6508.01 | -0.320985231 | -4.85197741 |
| TCGA.EI.6509.01 | 1.737121259 | 1.331630087 |
| TCGA.A6.6654.01 | 7.274137046 | 11.48416726 |
|----------------|-------------|-------------|
| TCGA.A6.6781.01 | 4.232819474 | 12.07492863 |
| TCGA.A6.6782.01 | 4.859953505 | 5.960906391 |
| TCGA.AA.3489.01 | 0.989490391 | 4.645079177 |
| TCGA.AD.6899.01 | 4.39500818  | 6.387497351 |
| TCGA.AD.6901.01 | 5.990541715 | 8.787979223 |
| TCGA.AD.6964.01 | 2.113843236 | 9.663704245 |
| TCGA.AF.2687.01 | 10.93908263 | 8.979900343 |
| TCGA.AF.2690.01 | 10.79885501 | 11.16273241 |
| TCGA.AG.3731.01 | 3.259988309 | 5.205676931 |
| TCGA.AG.4021.01 | 2.754047275 | 5.262928808 |
| TCGA.AG.4022.01 | 5.211213917 | 2.121218383 |
| TCGA.AH.6547.01 | 2.471349543 | 5.987590666 |
| TCGA.AH.6644.01 | 4.748890978 | 1.819736616 |
| TCGA.CA.6717.01 | 8.807642289 | 6.823871783 |
| TCGA.CA.6719.01 | 8.27359786  | 4.185092669 |
| TCGA.CA.6722.01 | 6.03298263  | 4.11338817  |
| TCGA.CA.6723.01 | 9.250311696 | 10.30417511 |
| TCGA.CM.5348.01 | 6.425604149 | 4.83985192  |
| TCGA.CM.5349.01 | 15.98868497 | 10.00454205 |
| TCGA.CM.5350.01 | 7.573552903 | 6.937548229 |
| TCGA.CM.5351.01 | 6.447407071 | 3.607256673 |
| TCGA.CM.5352.01 | 7.401545214 | 14.08175841 |
| TCGA.CM.5353.01 | 6.231590763 | 2.050573968 |
| TCGA.CM.5354.01 | 3.811238228 | 9.410915627 |
| TCGA.CM.5355.01 | 10.75346714 | 9.937244547 |
| TCGA.DC.6156.01 | 3.87184254  | 1.975300279 |
| TCGA.EI.6507.01 | -0.848757043 | 8.592787685 |
| TCGA.EI.6885.01 | 6.747309155 | 4.451038751 |
| TCGA.EI.7004.01 | 8.577877432 | 10.45317886 |
| TCGA.F4.6459.01 | 11.67105574 | 4.451128356 |
| TCGA.F4.6460.01 | 12.36288397 | 2.834763785 |
| TCGA.F4.6461.01 | 5.318422465 | 5.57593087  |
| TCGA.F4.6462.01 | 5.846503035 | 9.156126485 |
| TCGA.F4.6703.01 | 5.305187627 | 14.99402296 |
| TCGA.F4.6704.01 | 10.36056256 | 6.642276603 |
| TCGA.F4.6805.01 | 7.688367011 | 6.203013471 |
| TCGA.F4.6807.01 | 8.538313206 | 5.728614435 |
| TCGA.F4.6809.01 | 11.57035791 | 6.925163496 |
| TCGA.F4.6855.01 | 2.301461094 | 5.556455031 |
| TCGA.F5.6464.01 | 11.83021194 | 10.38806979 |
| TCGA.F5.6465.01 | 5.256024367 | 3.947375001 |
| TCGA.F5.6702.01 | 8.740060788 | 7.56354364 |
| TCGA.F5.6812.01 | 12.58596618 | 5.23910996 |
| TCGA.F5.6813.01 | 6.506760519 | 2.845762577 |
| TCGA.G4.6302.01 | 18.51110043 | 11.06526433 |
| TCGA.G4.6314.01 | 10.25675486 | 3.782415273 |
| TCGA.G4.6625.01 | 2.736153601 | 4.45538478 |
| TCGA.G4.6627.01 | 8.535697381 | 5.152899908 |
| TCGA.WS.AB45.01 | 5.183020692 | 13.12808786 |
| TCGA Fersig score |
|------------------|
| 6.640115729      |
| -9.885858702     |
| -16.13290109     |
| -7.09762733      |
| -1.839581126     |
| 1.049765335      |
| -1.975264142     |
| 5.054545441      |
| -11.69034551     |
| 5.303636536      |
| -9.319891155     |
| -11.34378486     |
| -3.929246802     |
| 3.644394857      |
| 4.474649156      |
| -2.425327288     |
| -0.862854633     |
| -1.042229434     |
| 4.157957507      |
| -6.716576345     |
| 7.317830202      |
| -10.47895319     |
| -2.720940407     |
| -2.927533391     |
| -4.021967479     |
| 2.536944482      |
| 8.327073488      |
| -8.317259646     |
| -3.776656752     |
| 1.078541678      |
| -0.774898167     |
| 1.999574973      |
| -13.69408562     |
| -0.404940147     |
| 3.630332308      |
| -17.17510456     |
| -8.849618715     |
| 2.708308757      |
| -14.90998733     |
| -6.968031241     |
| -10.63520312     |
| -6.071475795     |
| -0.977914491     |
| -6.223101705     |
| -9.992762734     |
| 1.542960615      |
| -6.880067219     |
| 2.006984034      |
| 2.700901951      |
| -2.195467128     |
| -10.00001972     |
| -6.775206823     |
| -15.31172898     |
| -6.625802875     |
| -0.225681047     |
-10.45831502
  2.466282858
  4.686085467
  -7.546976181
  1.619455238
  -0.547245843
  0.195807694
  4.401291967
  3.447290543
  -2.629605957
  -0.282651755
  -2.686394885
  2.514808508
  0.36553851
  -1.019578549
  -11.43880526
  5.362500384
  -11.3748548
  -5.480245482
  -5.413301341
  9.773831213
  2.454389299
  9.341158809
  9.493648432
  3.40465728
  3.570560011
  -4.470770779
  -10.65899795
  -6.560410433
  0.865250443
  -3.943982422
  -3.928253707
  8.06538603
  -5.66759419
  -1.001996109
  -10.40010481
  -13.77056011
  -14.61624916
  -7.033127558
  -7.704396942
  -8.099668419
  -3.705761525
  -5.35423854
  -10.2018592
  0.340621651
  -11.13951999
  -17.99178758
  -10.02010002
  -5.289019985
  -10.01251705
  -5.637309996
  10.20020212
  10.32802646
  -7.257520286
  -6.934558384
  -2.25653178
  -5.17262641
  3.068751346
| Value 1  | Value 2  | Value 3  |
|---------|---------|---------|
| -5.379184062 | -16.81110489 | 7.029261533 |
| 3.410191113   | -7.010922439  | 4.097542977  |
| -7.953644303  | -5.890546521   | -2.969285175  |
| -11.356999665 | 0.860521608    | 5.306274235   |
| -8.396962647  | -5.604922952   | -11.36236921  |
| -3.205509014  | 2.264237671    | -3.040182482  |
| 3.588508762   | -12.2370278    | -9.543388126  |
| -9.513491172  | -15.53952825   | -9.827810812  |
| 0.979682345   | -12.4077511    | 5.022513399   |
| -3.311457923  | -13.05315329   | 9.416145899   |
| 0.30358994    | -9.953743947   | 2.656209531   |
| -4.024930657  | 1.568765171    | -2.521342194  |
| 3.058908808   | -11.58788763   | -5.477035169  |
| -11.02238919  | -6.833449962   | -5.632249883  |
| 5.793244224   | -11.1836519    | 2.140317796   |
| 0.335168052   | -3.842157334   | 5.864730062   |
| 13.17615653   | 8.761342504    | -4.796300191  |
| 4.135168483   | -5.683439194   | -1.573316207  |
| 5.291934103   | 6.090412518    | 3.102099038   |
| 6.084130039   |                    |                |
18.75830431
16.30774811
10.8208599
5.634569568
16.59183501
10.78250553
14.77852094
11.77754748
19.91898297
21.96158742
8.46566524
8.016976084
7.3324323
8.45894861
6.568627594
15.63151407
12.45865245
10.14637049
19.5544868
11.26458934
25.99322702
14.51110113
10.05466368
21.48330363
8.282164731
13.22215385
20.69071169
6.751484534
7.744030641
11.19834791
19.03105629
16.1221841
15.19764775
10.89435555
15.00262952
20.29921059
17.00283917
13.89138048
14.26692764
18.49552141
7.857916125
22.21828172
9.203399369
16.30341515
17.82507614
9.352523096
29.57636476
14.03917013
7.191512078
13.68859729
18.31110855
Table S6. Fersig score of different databases

| samples     | GEO PC1 of genes A | GEO PC1 of genes B |
|-------------|--------------------|--------------------|
| GSM929508   | 8.85130345         | -7.295086787       |
| GSM929511   | -0.957958463       | -6.285103184       |
| GSM929622   | 10.79007285        | -1.560711018       |
| GSM929546   | -1.634714291       | 3.770913664        |
| GSM929623   | -0.308297316       | 1.974421849        |
| GSM929539   | 15.07758073        | -10.21946797       |
| GSM929614   | 0.13553872         | -20.61409952       |
| GSM929496   | 10.79007285        | -1.560711018       |
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### GEO Fersig score

| Score 1 | Score 2 | Score 3 | Score 4 | Score 5 | Score 6 | Score 7 | Score 8 | Score 9 | Score 10 |
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| Patient96     | 0.933685419        | 0.667551842        | 0.246133577     |
| Patient83     | 0.41275053         | -2.641835437       | 3.054585966     |
| Patient121    | 2.792776258        | 2.81556443         | -0.022789185    |
| Patient48     | -2.645320039       | 2.653624975        | 0.008304935     |
| Patient94     | 1.60283282         | 1.136807624        | 0.466025196     |
| Patient117    | 3.074452009        | 3.835144862        | -0.760692854    |
| Patient146    | 1.053291252        | 1.406463501        | -0.353172249    |
| Patient99     | 0.303442657        | 3.587045674        | -3.283603017    |
| Patient185    | 1.382480485        | 1.755067352        | -0.372586867    |
| Patient78     | 1.789925535        | 3.474724229        | -1.684798694    |
| Patient201    | 1.943360436        | -0.442985813       | 2.386346249     |
| Patient112    | 1.783808945        | 2.267832144        | -0.484023199    |
| Patient24     | 1.61770294         | 1.247336656        | 0.370366284     |
| Patient187    | 1.071112201        | 0.894927489        | 0.176184712     |
| Patient79     | 3.041668211        | 3.066675126        | -0.025006915    |
| Patient181    | 2.196966207        | 1.849659937        | 0.34730627      |
| Patient8      | 0.444599999        | -0.256362493       | 0.700964933     |
| Patient40     | -0.971389054       | -1.580215117       | 0.608826063     |
| Patient11     | -0.2528136         | 0.531041628        | -0.783855228    |
| Patient34     | 5.062675306        | -0.261274943       | 5.323950249     |
| Patient72     | 1.913935463        | 0.732770315        | 1.181165148     |
| Patient27     | 0.406591344        | 0.100316383        | 0.306274961     |
| Patient38     | -0.038110319       | -0.426205025       | 0.388094706     |
| Patient167    | 2.758938477        | 2.851642142        | -0.092730365    |
| Patient67     | -1.450615964       | -3.245409576       | 1.749739612     |
| Patient193    | 2.553249606        | 2.247023189        | 0.306226427     |
| Patient170    | 0.829382499        | 0.964034115        | -0.134651616    |
| Patient140    | -0.98296165        | -0.696718896       | -0.286242753    |
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| Patient98     | 1.794997348        | 1.93847633         | -0.143478982    |
| Patient42     | -0.603488467       | 0.1744312          | -0.777919667    |
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| Patient45     | 0.071840621        | 3.097589103        | -3.025748481    |
| Patient116    | 3.655870399        | 0.925544728        | 2.730325671     |
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| Patient7      | 1.216125365        | 0.566764125        | 0.64936124      |
| Patient144    | -1.65378019        | -3.528023601       | 1.87424341      |
| Patient100    | 1.19096903         | 4.351230409        | -3.160261379    |
| Patient141    | -2.418873163       | -1.805382651       | -0.613490512    |
| Patient47     | 1.845747249        | -1.054179787       | 2.899927037     |
| Patient105    | -3.977244541       | -3.614320486       | -0.362924056    |
| Patient162    | -1.140134543       | -0.298694532       | -0.84140011     |
| Patient33     | 1.806144436        | 2.685720564        | -0.879576128    |
| Patient62     | 1.454475477        | 3.238365037        | -1.78388956     |
| Patient155    | 0.266507263         | 0.646653726        | -0.380146464    |
| Patient165    | -0.163396392       | 0.591365087        | -0.754761479    |
| Patient56     | 3.15697418         | 2.538536897        | 0.618438021     |
| Patient126    | 1.032414905        | 1.928625853        | -0.896210949    |
| Patient37     | 0.885131038        | 2.06995457         | -1.184823532    |
| Patient63     | 0.074084714        | -1.782649768       | 1.856734481     |
Patient142 -1.996396708 -0.285794148 -1.71060256
Patient169 0.116358406 0.573725974 -0.457367568
Patient18 0.809596044 -0.463951832 1.273547876
Patient61 0.989425751 -6.157680499 7.14710625
Patient58 -2.373672222 -1.769546122 -0.604126101
Patient4 0.244497144 0.423024919 0.098664995
Patient189 2.303382586 1.249142973 1.054239613
Patient196 1.062229884 0.424820022 0.637409862
Patient31 1.315893821 0.412302491 0.903591329
Patient10 1.341338084 -0.155986767 1.497324851
Patient197 0.751217163 0.123655566 1.685922322
Patient20 -1.366353705 2.659680346 -4.026034051
Patient166 -0.705025849 -0.603426611 -0.101599238
Patient149 0.535824092 4.064162713 -3.52833862
Patient200 4.26668939 2.580767068 1.685922322
Patient23 1.87754961 0.542128147 1.335421463
Patient87 0.016382122 0.607271898 -0.590845067
Patient44 -3.84433739 -1.036468702 -2.808365036
Patient145 0.9245577 1.69285488 -0.58629711
Patient135 -1.847963631 0.104534324 -1.952500684
Patient132 0.764876713 2.667547886 -1.902591274
Patient204 2.772685234 1.61381357 1.158903877
Patient134 0.877819315 0.94226027 -0.071406713
Patient77 0.314650879 2.010746607 -1.696095728
Patient184 -0.774963192 0.522513402 -1.29746594
Patient32 -0.34642393 -0.616998341 0.27054411
Patient108 -13.8330556 -14.28659754 0.90329588
Patient137 -2.162367978 2.298234442 -4.45520242
Patient51 -6.820141305 -2.217801681 -4.60339624
Patient133 -1.939638529 0.509636183 -2.449274712
Patient143 -3.273298265 -32.64521923 -0.087763423
Patient159 1.721914672 1.682767075 0.039147597
Patient195 1.296482828 1.30847624 -0.012364797
Patient25 3.20899635 1.82323897 1.38567538
Patient131 -4.473734865 -2.282169814 -2.191565051
Patient15 1.339210945 -0.397970588 1.737181532
Patient154 4.644832971 0.51381743 4.131015541
Patient106 0.061858344 0.047281109 -0.985422766
Patient17 0.065701761 1.958406443 -1.30130468
Patient130 1.591998421 1.47439849 0.117999343
Patient156 2.239646316 1.957140312 0.282506005
Patient172 2.542570493 2.519602529 0.022987969
Patient150 0.530360057 0.285899604 0.244466453
Patient173 1.835108623 1.937728116 -0.102619493
Patient203 2.652659229 1.99624396 0.656415269
Patient21 -0.45584902 0.190779717 -0.646687373
Patient125 -2.2709535 0.972462635 -3.243416135
Patient6 0.449403283 0.770109375 -0.275706093
Patient158 1.748657638 1.10975492 0.638682146
Patient188 1.563543324 -0.620622648 2.184165792
Patient147 -1.358950435 -1.159199734 -0.199750701
Patient36 0.869128135 -0.93591417 1.805042552
Patient1 -0.307812025 -1.991628532 1.68381328
Patient102 1.751691564 1.893929239 -0.142237676
Patient75 -2.681846211 2.572965989 -5.254812199
Patient168 -0.183834071 0.54772504 -0.731591111
Patient30 -1.190000963 0.015312335 -1.205321938
Patient148 0.732437992 0.435434977 0.297003014
| Patient  | Value1   | Value2   | Value3   |
|----------|----------|----------|----------|
| Patient14| 2.179404815 | 1.953417323 | 0.225987492 |
| Patient9 | 1.762107117 | -0.15093356  | 1.913040677 |
| Patient73| 1.551758102 | 0.21521774  | 1.336540362 |
| Patient86| 0.059454268 | 0.968457244 | -0.909002977 |
| Patient127| 3.005069489 | 1.434361698 | 1.570707791 |
| Patient13 | 2.629219031 | 0.808248371 | 1.820970659 |
| Patient179| -6.80245096 | -7.997613106 | 1.195162146 |
| Patient22 | 0.601541363 | -0.422716544 | 1.024257906 |
| OS   | Dead | BRgroup |
|------|------|---------|
| 47   | 0 CR/PR |
| 173  | 1 PD/SD |
| 913  | 0 CR/PR |
| 71   | 1 PD/SD |
| 1306 | 0 CR/PR |
| 53   | 1 PD/SD |
| 40   | 1 PD/SD |
| 295  | 1 PD/SD |
| 612  | 0 CR/PR |
| 921  | 0 CR/PR |
| 203  | 0 PD/SD |
| 356  | 1 PD/SD |
| 167  | 1 PD/SD |
| 521  | 1 PD/SD |
| 137  | 1 PD/SD |
| 617  | 0 CR/PR |
| 849  | 0 PD/SD |
| 476  | 0 CR/PR |
| 1005 | 1 PD/SD |
| 468  | 1 PD/SD |
| 160  | 1 PD/SD |
| 1691 | 0 CR/PR |
| 395  | 0 PD/SD |
| 431  | 0 PD/SD |
| 343  | 1 PD/SD |
| 282  | 1 PD/SD |
| 136  | 1 PD/SD |
| 659  | 0 PD/SD |
| 347  | 0 PD/SD |
| 351  | 1 PD/SD |
| 658  | 0 CR/PR |
| 683  | 1 PD/SD |
| 1027 | 0 CR/PR |
| 572  | 1 PD/SD |
| 392  | 1 PD/SD |
| 131  | 1 PD/SD |
| 1666 | 0 CR/PR |
| 118  | 1 PD/SD |
| 90   | 1 PD/SD |
| 968  | 1 PD/SD |
| 269  | 1 PD/SD |
| 662  | 0 CR/PR |
| 938  | 1 CR/PR |
| 875  | 0 CR/PR |
| 937  | 0 PD/SD |
| 521  | 1 CR/PR |
| 201  | 1 PD/SD |
| 1679 | 0 CR/PR |
| 1001 | 0 CR/PR |
| 475  | 0 PD/SD |
| 75   | 0 PD/SD |
| 122  | 1 PD/SD |
| 992  | 0 CR/PR |
| 275  | 1 PD/SD |
| 178  | 1 PD/SD |
|   | PD/SD | CR/PR |
|---|-------|-------|
| 996 | 0     | 1     |
| 543 | 0     | 1     |
| 130 | 1     | 0     |
| 987 | 0     | 1     |
| 303 | 1     | 0     |
| 600 | 1     | 0     |
| 718 | 0     | 1     |
| 81  | 1     | 0     |
| 426 | 1     | 0     |
| 1139| 1     | 0     |
| 960 | 0     | 0     |
| 242 | 1     | 0     |
| 205 | 1     | 0     |
| 497 | 1     | 0     |
| 512 | 1     | 0     |
| 975 | 0     | 0     |
| 1263| 0     | 0     |
| 922 | 0     | 0     |
| 833 | 0     | 0     |
| 628 | 0     | 0     |
| 739 | 0     | 0     |
| 819 | 0     | 0     |
| 590 | 1     | 0     |
| 444 | 1     | 0     |
| 513 | 0     | 0     |
| 53  | 1     | 0     |
| 165 | 1     | 0     |
| 772 | 0     | 0     |
| 1547| 0     | 0     |
| 370 | 1     | 0     |
| 630 | 0     | 0     |
| 288 | 0     | 0     |
| 895 | 0     | 0     |
| 1096| 0     | 0     |
| 833 | 0     | 0     |
| 149 | 1     | 0     |
| 635 | 0     | 0     |
| 780 | 0     | 0     |
| 686 | 1     | 0     |
| 192 | 1     | 0     |
| 87  | 1     | 0     |
| 272 | 0     | 0     |
| 685 | 0     | 0     |
| 42  | 1     | 0     |
| 626 | 1     | 0     |
| 906 | 0     | 0     |
| 978 | 0     | 0     |
| 687 | 1     | 0     |
| 194 | 0     | 0     |
| 74  | 1     | 0     |
| 960 | 0     | 0     |
| 451 | 1     | 0     |
| 283 | 1     | 0     |
| 785 | 0     | 0     |
| 891 | 0     | 0     |
| 623 | 0     | 0     |
| 213 | 1     | 0     |
| 792 | 0     | 0     |
| Number | Description  |
|--------|--------------|
| 186    | 1 PD/SD      |
| 963    | 0 PD/SD      |
| 846    | 1 PD/SD      |
| 1327   | 0 PD/SD      |
| 866    | 0 CR/PR      |
| 58     | 1 PD/SD      |
| 653    | 0 CR/PR      |
| 253    | 1 PD/SD      |
Table S6. Fersig score of different databases

| samples     | Vanallen PC1 of genes A | Vanallen PC1 of genes B |
|-------------|-------------------------|-------------------------|
| Pt1.baseline| -0.361057658            | -0.99009198             |
| Pt2.baseline| -0.070806538            | -0.703963262            |
| Pt4.baseline| 0.941912746             | 1.025178075             |
| Pt5.baseline| 2.832124426             | -4.772701248            |
| Pt6.baseline| -1.043321579            | 0.62301097              |
| Pt7.baseline| -1.333143924            | 2.390269156             |
| Pt8.baseline| -1.416292151            | 1.088585952             |
| Pt9.baseline| 0.635362935             | -0.290027741            |
| Pt10.baseline| 0.468505343             | 2.149579516             |
| Pt12.baseline| -1.921825859            | 1.979360996             |
| Pt13.baseline| 0.612200365             | 0.286403325             |
| Pt14.baseline| -0.35186344             | 1.67918879              |
| Pt15.baseline| -1.869728786            | 0.632739384             |
| Pt19.baseline| -1.334422477            | -0.053248537            |
| Pt20.baseline| -3.756047795            | 2.026191197             |
| Pt22.baseline| 0.915378015             | -0.654642908            |
| Pt23.baseline| -3.136455353            | 2.979018214             |
| Pt25.baseline| -3.591950585            | 3.947589642             |
| Pt28.baseline| -2.571244128            | 4.599635325             |
| Pt29.baseline| -1.754614963            | 2.899474904             |
| Pt31.baseline| 1.653638057             | -3.608233836            |
| Pt32.baseline| 3.293402175             | -0.264777681            |
| Pt35.baseline| 3.45491312              | -4.540842878            |
| Pt37.baseline| 2.299128939             | -3.606734371            |
| Pt38.baseline| 2.483781707             | -3.876667891            |
| Vanallen Fersig score | Overall.Survival | Dead | BRgroup |
|-----------------------|------------------|------|---------|
| -0.629034323          | 607              | 1 PD |         |
| -0.633156723          | 927              | 0 CR/PR |     |
| 0.083265329           | 948              | 0 CR/PR |     |
| -7.604825674          | 439              | 0 CR/PR |     |
| 1.666332548           | 882              | 0 CR/PR |     |
| 3.72341308            | 662              | 1 PD |         |
| 2.504878103 NA        | 1054             | 0 CR/PR |     |
| -0.925390676          | 387              | 0 PD |         |
| 1.681074173           | 327              | 1 PD |         |
| -0.32579704           | 917              | 0 CR/PR |   |
| 2.03105223            | 54               | 0 PD |         |
| 2.50246817            | 980              | 1 CR/PR | | |
| 1.28117394            | 1060             | 0 CR/PR |     |
| 5.782238992           | 337              | 1 PD |         |
| -1.570020923          | 182              | 1 PD |         |
| 6.115473567           | 103              | 1 PD |         |
| 7.53940227            | 262              | 1 PD |         |
| 7.170879452           | 439              | 1 CR/PR |     |
| 4.654069867           | 269              | 1 PD |         |
| -5.261871893          | 704              | 0 PD |         |
| -5.558179856          | 171              | 1 PD |         |
| -7.995755998          | 427              | 0 CR/PR |     |
| -5.90586331           | 364              | 0 CR/PR |     |
| -6.360449598          | 448              | 0 CR/PR |     |