

Table S1: 101 Amino Acid Metabolism-related Genes
AMINO_ACID_AND_DERIVATIVE_METABOLIC_PROCESS

AARS1
ADI1
AIMP1
ALDH18A1
ALDH4A1
ALDH5A1
ALDH6A1
AMT
ARG1
ASL
ASMTL
ASPA
ASRGL1
ATF4
BAAT
BBOX1
BCAT1
BCKDHA
BCKDHB
BCKDK
BPHL
CDO1
COLQ
DARS1
DCT
DDAH1
DDAH2
DDO
DHPS
DIO1
DIO2
ETNK1
FAH
FARS2
FPGS
GAD1
GAD2
GAMT
GATM
GCLC
GCLM

GCSH
GGT1
GGT5
GLDC
GLS2
GLUD1
GLUD2
GOT1
GOT2
GSS
GSTZ1
HDC
HGD
HPD
HPRT1
IDO1
KARS1
KYAT1
MARS2
MAT1A
MAT2B
MCCC2
MSRA
MTHFR
NFS1
OAZ1
OAZ2
OTUB2
P4HB
PAH
PEPD
PLOD1
PRG3
PTS
PYCR1
QDPR
RARS1
SARS2
SCLY
SDS
SLC25A15
SLC3A1
SLC5A7
SLC6A14

SLC6A6
 SLC7A2
 SLC7A4
 SLC7A5
 SLC7A6
 SLC7A7
 SLC7A8
 SLC7A9
 SMS
 SNCAIP
 SULT1B1
 TGFB2
 TYR
 WARS1
 YARS1
 YOD1

Table S2: Clinical information of 871 gastric cancer patients.

| Id | Age | Gender | T | N | futime | fustat | Dataset |
|------------|-----|--------|----|----|--------|--------|----------|
| GSM2235556 | 61 | MALE | T3 | N1 | 2100 | 1 | GSE84337 |
| GSM2235557 | 47 | FEMALE | T4 | N3 | 690 | 1 | GSE84337 |
| GSM2235558 | 72 | MALE | T4 | N1 | 720 | 1 | GSE84337 |
| GSM2235559 | 78 | MALE | T3 | N2 | 1770 | 1 | GSE84337 |
| GSM2235560 | 58 | MALE | T4 | N0 | 360 | 1 | GSE84337 |
| GSM2235561 | 33 | FEMALE | T4 | N2 | 2550 | 0 | GSE84337 |
| GSM2235562 | 81 | FEMALE | T4 | N2 | 540 | 1 | GSE84337 |
| GSM2235563 | 60 | FEMALE | T3 | N2 | 420 | 1 | GSE84337 |
| GSM2235564 | 61 | MALE | T3 | N1 | 2520 | 0 | GSE84337 |
| GSM2235565 | 49 | FEMALE | T4 | N0 | 1950 | 1 | GSE84337 |
| GSM2235566 | 44 | MALE | T4 | N2 | 330 | 1 | GSE84337 |
| GSM2235567 | 51 | MALE | T4 | N2 | 1290 | 1 | GSE84337 |
| GSM2235568 | 58 | FEMALE | T3 | N1 | 2460 | 0 | GSE84337 |
| GSM2235569 | 79 | MALE | T4 | N1 | 2460 | 0 | GSE84337 |
| GSM2235570 | 77 | MALE | T4 | N0 | 2430 | 0 | GSE84337 |
| GSM2235571 | 85 | FEMALE | T3 | N1 | 2400 | 0 | GSE84337 |
| GSM2235572 | 68 | FEMALE | T4 | N1 | 2580 | 0 | GSE84337 |
| GSM2235573 | 52 | MALE | T4 | N2 | 2460 | 0 | GSE84337 |
| GSM2235574 | 72 | MALE | T4 | N2 | 330 | 1 | GSE84337 |
| GSM2235575 | 59 | MALE | T3 | N1 | 2580 | 0 | GSE84337 |
| GSM2235576 | 78 | FEMALE | T3 | N2 | 120 | 1 | GSE84337 |
| GSM2235577 | 32 | FEMALE | T4 | N0 | 570 | 1 | GSE84337 |
| GSM2235578 | 68 | MALE | T4 | N2 | 630 | 1 | GSE84337 |
| GSM2235579 | 74 | MALE | T3 | N1 | 510 | 1 | GSE84337 |
| GSM2235580 | 61 | MALE | T4 | N2 | 750 | 1 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235582 | 65 | MALE | T4 | N0 | 390 | 1 | GSE84337 |
| GSM2235584 | 71 | MALE | T4 | N2 | 1710 | 1 | GSE84337 |
| GSM2235585 | 71 | MALE | T3 | N1 | 690 | 1 | GSE84337 |
| GSM2235586 | 71 | MALE | T4 | N1 | 2310 | 0 | GSE84337 |
| GSM2235587 | 72 | MALE | T4 | N1 | 1920 | 1 | GSE84337 |
| GSM2235588 | 56 | MALE | T4 | N1 | 1530 | 1 | GSE84337 |
| GSM2235589 | 66 | MALE | T4 | N2 | 2310 | 0 | GSE84337 |
| GSM2235593 | 56 | MALE | T4 | N0 | 2310 | 0 | GSE84337 |
| GSM2235595 | 74 | MALE | T4 | N1 | 450 | 1 | GSE84337 |
| GSM2235596 | 63 | MALE | T3 | N1 | 2250 | 0 | GSE84337 |
| GSM2235597 | 68 | MALE | T2 | N1 | 2520 | 0 | GSE84337 |
| GSM2235598 | 74 | MALE | T3 | N1 | 630 | 1 | GSE84337 |
| GSM2235599 | 62 | MALE | T3 | N2 | 2400 | 0 | GSE84337 |
| GSM2235600 | 53 | MALE | T4 | N2 | 2220 | 0 | GSE84337 |
| GSM2235601 | 79 | MALE | T4 | N2 | 2220 | 0 | GSE84337 |
| GSM2235602 | 61 | FEMALE | T3 | N1 | 2460 | 0 | GSE84337 |
| GSM2235603 | 60 | FEMALE | T4 | N1 | 2400 | 0 | GSE84337 |
| GSM2235604 | 75 | MALE | T3 | N1 | 2220 | 0 | GSE84337 |
| GSM2235605 | 54 | FEMALE | T4 | N1 | 2010 | 1 | GSE84337 |
| GSM2235606 | 38 | MALE | T4 | N2 | 2190 | 0 | GSE84337 |
| GSM2235607 | 65 | MALE | T3 | N2 | 180 | 1 | GSE84337 |
| GSM2235608 | 55 | MALE | T3 | N1 | 2400 | 0 | GSE84337 |
| GSM2235609 | 73 | FEMALE | T4 | N2 | 240 | 1 | GSE84337 |
| GSM2235610 | 76 | MALE | T4 | N2 | 690 | 1 | GSE84337 |
| GSM2235611 | 78 | FEMALE | T4 | N2 | 240 | 1 | GSE84337 |
| GSM2235612 | 69 | MALE | T4 | N2 | 870 | 1 | GSE84337 |
| GSM2235613 | 68 | MALE | T2 | N1 | 2490 | 0 | GSE84337 |
| GSM2235614 | 27 | MALE | T4 | N2 | 2310 | 0 | GSE84337 |
| GSM2235615 | 68 | MALE | T3 | N2 | 2310 | 0 | GSE84337 |
| GSM2235616 | 73 | MALE | T4 | N1 | 30 | 1 | GSE84337 |
| GSM2235617 | 54 | MALE | T4 | N2 | 2130 | 0 | GSE84337 |
| GSM2235618 | 73 | FEMALE | T4 | N2 | 2130 | 0 | GSE84337 |
| GSM2235619 | 55 | FEMALE | T4 | N1 | 2100 | 0 | GSE84337 |
| GSM2235620 | 65 | MALE | T3 | N2 | 2130 | 0 | GSE84337 |
| GSM2235621 | 63 | MALE | T4 | N2 | 990 | 1 | GSE84337 |
| GSM2235622 | 50 | MALE | T3 | N2 | 690 | 1 | GSE84337 |
| GSM2235623 | 56 | MALE | T3 | N1 | 630 | 1 | GSE84337 |
| GSM2235624 | 59 | MALE | T3 | N1 | 2310 | 0 | GSE84337 |
| GSM2235625 | 53 | FEMALE | T4 | N0 | 2100 | 0 | GSE84337 |
| GSM2235626 | 46 | MALE | T4 | N2 | 2310 | 0 | GSE84337 |
| GSM2235627 | 68 | MALE | T3 | N1 | 2100 | 0 | GSE84337 |
| GSM2235628 | 43 | MALE | T3 | N1 | 2220 | 0 | GSE84337 |
| GSM2235629 | 78 | MALE | T4 | N1 | 1080 | 1 | GSE84337 |
| GSM2235630 | 65 | MALE | T4 | N1 | 2100 | 0 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235631 | 66 | FEMALE | T4 | N0 | 2070 | 0 | GSE84337 |
| GSM2235632 | 60 | MALE | T3 | N1 | 2280 | 0 | GSE84337 |
| GSM2235633 | 63 | MALE | T4 | N2 | 510 | 1 | GSE84337 |
| GSM2235634 | 64 | FEMALE | T4 | N1 | 2220 | 0 | GSE84337 |
| GSM2235635 | 73 | MALE | T2 | N2 | 2160 | 0 | GSE84337 |
| GSM2235636 | 32 | FEMALE | T4 | N2 | 2070 | 0 | GSE84337 |
| GSM2235637 | 75 | FEMALE | T4 | N0 | 2040 | 0 | GSE84337 |
| GSM2235695 | 42 | FEMALE | T4 | N1 | 3630 | 0 | GSE84337 |
| GSM2235696 | 60 | MALE | T4 | N1 | 3240 | 0 | GSE84337 |
| GSM2235697 | 49 | MALE | T3 | N0 | 1170 | 1 | GSE84337 |
| GSM2235698 | 34 | MALE | T3 | N3 | 690 | 1 | GSE84337 |
| GSM2235699 | 68 | MALE | T4 | N3 | 690 | 1 | GSE84337 |
| GSM2235700 | 59 | MALE | T4 | N2 | 3510 | 0 | GSE84337 |
| GSM2235701 | 61 | MALE | T3 | N0 | 3240 | 0 | GSE84337 |
| GSM2235702 | 74 | FEMALE | T4 | N1 | 540 | 1 | GSE84337 |
| GSM2235703 | 35 | MALE | T4 | N2 | 1290 | 1 | GSE84337 |
| GSM2235704 | 53 | FEMALE | T4 | N1 | 3270 | 0 | GSE84337 |
| GSM2235705 | 67 | MALE | T4 | N1 | 3420 | 0 | GSE84337 |
| GSM2235706 | 71 | MALE | T4 | N2 | 60 | 1 | GSE84337 |
| GSM2235707 | 63 | FEMALE | T2 | N1 | 3480 | 0 | GSE84337 |
| GSM2235708 | 66 | MALE | T4 | N1 | 3270 | 0 | GSE84337 |
| GSM2235709 | 54 | FEMALE | T2 | N0 | 3240 | 0 | GSE84337 |
| GSM2235710 | 54 | MALE | T4 | N0 | 390 | 1 | GSE84337 |
| GSM2235711 | 65 | MALE | T4 | N1 | 570 | 1 | GSE84337 |
| GSM2235712 | 70 | FEMALE | T2 | N0 | 3240 | 0 | GSE84337 |
| GSM2235713 | 59 | MALE | T4 | N0 | 3480 | 1 | GSE84337 |
| GSM2235714 | 61 | MALE | T2 | N1 | 1380 | 1 | GSE84337 |
| GSM2235715 | 58 | MALE | T4 | N1 | 3540 | 0 | GSE84337 |
| GSM2235716 | 46 | MALE | T3 | N1 | 3120 | 1 | GSE84337 |
| GSM2235717 | 43 | FEMALE | T4 | N3 | 90 | 1 | GSE84337 |
| GSM2235718 | 46 | MALE | T4 | N1 | 3570 | 0 | GSE84337 |
| GSM2235719 | 68 | MALE | T4 | N2 | 30 | 1 | GSE84337 |
| GSM2235720 | 56 | MALE | T1 | N0 | 3570 | 0 | GSE84337 |
| GSM2235721 | 41 | MALE | T2 | N1 | 3570 | 0 | GSE84337 |
| GSM2235722 | 63 | FEMALE | T4 | N2 | 1080 | 1 | GSE84337 |
| GSM2235723 | 52 | MALE | T3 | N2 | 3540 | 0 | GSE84337 |
| GSM2235724 | 74 | MALE | T3 | N3 | 300 | 1 | GSE84337 |
| GSM2235725 | 65 | FEMALE | T4 | N0 | 3660 | 0 | GSE84337 |
| GSM2235726 | 68 | MALE | T4 | N2 | 30 | 1 | GSE84337 |
| GSM2235727 | 71 | MALE | T4 | N3 | 3540 | 0 | GSE84337 |
| GSM2235728 | 40 | FEMALE | T4 | N1 | 1050 | 1 | GSE84337 |
| GSM2235729 | 67 | MALE | T4 | N2 | 150 | 1 | GSE84337 |
| GSM2235730 | 68 | FEMALE | T1 | N1 | 1470 | 1 | GSE84337 |
| GSM2235731 | 63 | FEMALE | T2 | N1 | 3540 | 0 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235732 | 74 | MALE | T2 | N1 | 3540 | 0 | GSE84337 |
| GSM2235733 | 72 | MALE | T3 | N1 | 4320 | 0 | GSE84337 |
| GSM2235734 | 45 | FEMALE | T4 | N1 | 4320 | 0 | GSE84337 |
| GSM2235735 | 53 | MALE | T3 | N2 | 4350 | 0 | GSE84337 |
| GSM2235736 | 61 | MALE | T4 | N2 | 270 | 1 | GSE84337 |
| GSM2235737 | 51 | MALE | T4 | N2 | 1350 | 1 | GSE84337 |
| GSM2235738 | 59 | FEMALE | T4 | N2 | 4590 | 0 | GSE84337 |
| GSM2235739 | 66 | MALE | T3 | N2 | 420 | 1 | GSE84337 |
| GSM2235740 | 69 | MALE | T3 | N1 | 120 | 1 | GSE84337 |
| GSM2235741 | 49 | MALE | T4 | N2 | 3810 | 0 | GSE84337 |
| GSM2235742 | 62 | MALE | T4 | N2 | 90 | 1 | GSE84337 |
| GSM2235743 | 64 | FEMALE | T4 | N1 | 120 | 1 | GSE84337 |
| GSM2235744 | 38 | FEMALE | T4 | N1 | 1470 | 1 | GSE84337 |
| GSM2235745 | 53 | MALE | T4 | N2 | 3180 | 0 | GSE84337 |
| GSM2235746 | 53 | MALE | T3 | N1 | 3330 | 0 | GSE84337 |
| GSM2235747 | 53 | FEMALE | T4 | N2 | 360 | 1 | GSE84337 |
| GSM2235748 | 80 | MALE | T4 | N2 | 60 | 1 | GSE84337 |
| GSM2235749 | 65 | MALE | T4 | N3 | 1170 | 1 | GSE84337 |
| GSM2235750 | 70 | MALE | T4 | N1 | 210 | 1 | GSE84337 |
| GSM2235751 | 40 | MALE | T3 | N1 | 3030 | 0 | GSE84337 |
| GSM2235752 | 42 | MALE | T4 | N1 | 4470 | 0 | GSE84337 |
| GSM2235753 | 72 | MALE | T4 | N1 | 930 | 1 | GSE84337 |
| GSM2235754 | 37 | FEMALE | T4 | N1 | 4140 | 0 | GSE84337 |
| GSM2235755 | 62 | FEMALE | T4 | N1 | 2610 | 1 | GSE84337 |
| GSM2235756 | 48 | FEMALE | T4 | N2 | 4200 | 0 | GSE84337 |
| GSM2235757 | 44 | MALE | T4 | N2 | 1200 | 1 | GSE84337 |
| GSM2235758 | 42 | MALE | T4 | N2 | 390 | 1 | GSE84337 |
| GSM2235759 | 54 | MALE | T4 | N2 | 360 | 1 | GSE84337 |
| GSM2235760 | 64 | MALE | T4 | N2 | 600 | 1 | GSE84337 |
| GSM2235761 | 63 | FEMALE | T4 | N1 | 4020 | 0 | GSE84337 |
| GSM2235762 | 65 | MALE | T4 | N2 | 1170 | 1 | GSE84337 |
| GSM2235763 | 74 | FEMALE | T4 | N1 | 3270 | 1 | GSE84337 |
| GSM2235764 | 58 | MALE | T4 | N2 | 270 | 1 | GSE84337 |
| GSM2235765 | 68 | MALE | T4 | N1 | 4140 | 0 | GSE84337 |
| GSM2235766 | 61 | MALE | T4 | N2 | 450 | 1 | GSE84337 |
| GSM2235767 | 53 | MALE | T4 | N2 | 540 | 1 | GSE84337 |
| GSM2235768 | 46 | MALE | T4 | N1 | 4320 | 0 | GSE84337 |
| GSM2235769 | 64 | MALE | T3 | N2 | 660 | 1 | GSE84337 |
| GSM2235770 | 85 | MALE | T3 | N1 | 210 | 1 | GSE84337 |
| GSM2235771 | 53 | MALE | T4 | N1 | 4290 | 0 | GSE84337 |
| GSM2235772 | 60 | MALE | T4 | N2 | 1800 | 1 | GSE84337 |
| GSM2235773 | 30 | MALE | T4 | N2 | 510 | 1 | GSE84337 |
| GSM2235774 | 47 | MALE | T4 | N1 | 360 | 1 | GSE84337 |
| GSM2235775 | 60 | MALE | T4 | N1 | 3600 | 0 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235776 | 80 | MALE | T4 | N0 | 600 | 1 | GSE84337 |
| GSM2235777 | 49 | FEMALE | T4 | N1 | 3450 | 1 | GSE84337 |
| GSM2235778 | 61 | MALE | T4 | N3 | 690 | 1 | GSE84337 |
| GSM2235779 | 63 | MALE | T4 | N0 | 1470 | 1 | GSE84337 |
| GSM2235780 | 75 | MALE | T4 | N3 | 0 | 1 | GSE84337 |
| GSM2235781 | 56 | MALE | T1 | N0 | 3450 | 0 | GSE84337 |
| GSM2235782 | 62 | MALE | T4 | N2 | 120 | 1 | GSE84337 |
| GSM2235783 | 71 | MALE | T3 | N1 | 2250 | 1 | GSE84337 |
| GSM2235784 | 80 | MALE | T2 | N0 | 3090 | 1 | GSE84337 |
| GSM2235785 | 64 | FEMALE | T3 | N0 | 3420 | 0 | GSE84337 |
| GSM2235786 | 50 | FEMALE | T4 | N1 | 3240 | 0 | GSE84337 |
| GSM2235787 | 58 | FEMALE | T4 | N2 | 750 | 1 | GSE84337 |
| GSM2235788 | 56 | MALE | T2 | N0 | 3510 | 0 | GSE84337 |
| GSM2235789 | 64 | MALE | T4 | N2 | 1110 | 1 | GSE84337 |
| GSM2235790 | 67 | FEMALE | T4 | N0 | 3570 | 0 | GSE84337 |
| GSM2235791 | 36 | FEMALE | T4 | N1 | 750 | 1 | GSE84337 |
| GSM2235792 | 60 | FEMALE | T4 | N1 | 2760 | 1 | GSE84337 |
| GSM2235793 | 83 | MALE | T3 | N2 | 2610 | 1 | GSE84337 |
| GSM2235794 | 55 | MALE | T1 | N1 | 3630 | 0 | GSE84337 |
| GSM2235795 | 73 | FEMALE | T4 | N0 | 3630 | 0 | GSE84337 |
| GSM2235796 | 62 | MALE | T4 | N3 | 1320 | 1 | GSE84337 |
| GSM2235797 | 79 | FEMALE | T3 | N0 | 3450 | 0 | GSE84337 |
| GSM2235798 | 76 | MALE | T4 | N2 | 750 | 1 | GSE84337 |
| GSM2235799 | 62 | MALE | T4 | N3 | 360 | 1 | GSE84337 |
| GSM2235800 | 62 | MALE | T3 | N1 | 3420 | 0 | GSE84337 |
| GSM2235801 | 50 | MALE | T2 | N1 | 3390 | 0 | GSE84337 |
| GSM2235802 | 60 | MALE | T1 | N0 | 3180 | 0 | GSE84337 |
| GSM2235803 | 46 | MALE | T3 | N0 | 3210 | 0 | GSE84337 |
| GSM2235804 | 64 | MALE | T4 | N0 | 3420 | 0 | GSE84337 |
| GSM2235805 | 61 | FEMALE | T4 | N1 | 150 | 1 | GSE84337 |
| GSM2235806 | 55 | MALE | T4 | N0 | 3030 | 1 | GSE84337 |
| GSM2235807 | 70 | MALE | T4 | N3 | 990 | 1 | GSE84337 |
| GSM2235808 | 59 | MALE | T4 | N1 | 690 | 1 | GSE84337 |
| GSM2235809 | 58 | MALE | T4 | N1 | 4380 | 0 | GSE84337 |
| GSM2235810 | 54 | MALE | T4 | N1 | 210 | 1 | GSE84337 |
| GSM2235811 | 55 | MALE | T4 | N2 | 360 | 1 | GSE84337 |
| GSM2235812 | 68 | MALE | T4 | N3 | 1020 | 1 | GSE84337 |
| GSM2235813 | 64 | MALE | T3 | N0 | 780 | 1 | GSE84337 |
| GSM2235814 | 66 | MALE | T4 | N3 | 3390 | 0 | GSE84337 |
| GSM2235815 | 71 | FEMALE | T4 | N2 | 3390 | 0 | GSE84337 |
| GSM2235816 | 48 | MALE | T4 | N3 | 120 | 1 | GSE84337 |
| GSM2235817 | 68 | FEMALE | T4 | N1 | 1650 | 1 | GSE84337 |
| GSM2235818 | 74 | FEMALE | T4 | N3 | 300 | 1 | GSE84337 |
| GSM2235819 | 68 | MALE | T4 | N1 | 630 | 1 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235820 | 75 | MALE | T4 | N1 | 720 | 1 | GSE84337 |
| GSM2235821 | 67 | MALE | T4 | N1 | 3360 | 0 | GSE84337 |
| GSM2235822 | 55 | MALE | T3 | N1 | 3360 | 0 | GSE84337 |
| GSM2235823 | 32 | FEMALE | T4 | N1 | 270 | 1 | GSE84337 |
| GSM2235824 | 49 | FEMALE | T4 | N2 | 2370 | 1 | GSE84337 |
| GSM2235825 | 69 | MALE | T4 | N0 | 690 | 1 | GSE84337 |
| GSM2235826 | 79 | MALE | T3 | N2 | 330 | 1 | GSE84337 |
| GSM2235827 | 47 | MALE | T4 | N2 | 1290 | 1 | GSE84337 |
| GSM2235828 | 55 | MALE | T4 | N1 | 3210 | 0 | GSE84337 |
| GSM2235829 | 52 | MALE | T4 | N0 | 3270 | 0 | GSE84337 |
| GSM2235830 | 75 | MALE | T4 | N2 | 2940 | 0 | GSE84337 |
| GSM2235831 | 81 | MALE | T4 | N3 | 1170 | 1 | GSE84337 |
| GSM2235837 | 56 | FEMALE | T2 | N0 | 3390 | 0 | GSE84337 |
| GSM2235838 | 65 | MALE | T4 | N3 | 120 | 1 | GSE84337 |
| GSM2235839 | 63 | MALE | T3 | N1 | 3030 | 1 | GSE84337 |
| GSM2235840 | 71 | MALE | T2 | N0 | 2760 | 1 | GSE84337 |
| GSM2235841 | 84 | FEMALE | T4 | N1 | 480 | 1 | GSE84337 |
| GSM2235842 | 72 | MALE | T4 | N3 | 420 | 1 | GSE84337 |
| GSM2235843 | 60 | MALE | T2 | N1 | 390 | 1 | GSE84337 |
| GSM2235844 | 54 | FEMALE | T4 | N2 | 3060 | 0 | GSE84337 |
| GSM2235845 | 51 | MALE | T4 | N2 | 930 | 1 | GSE84337 |
| GSM2235846 | 67 | MALE | T4 | N2 | 2760 | 1 | GSE84337 |
| GSM2235847 | 53 | FEMALE | T4 | N1 | 3330 | 0 | GSE84337 |
| GSM2235848 | 52 | MALE | T4 | N2 | 1200 | 1 | GSE84337 |
| GSM2235849 | 61 | FEMALE | T4 | N2 | 30 | 1 | GSE84337 |
| GSM2235850 | 51 | MALE | T2 | N1 | 3480 | 0 | GSE84337 |
| GSM2235851 | 81 | MALE | T1 | N0 | 2790 | 1 | GSE84337 |
| GSM2235852 | 69 | MALE | T4 | N3 | 1440 | 1 | GSE84337 |
| GSM2235853 | 58 | FEMALE | T2 | N1 | 3330 | 0 | GSE84337 |
| GSM2235854 | 66 | FEMALE | T4 | N3 | 3330 | 0 | GSE84337 |
| GSM2235855 | 68 | MALE | T2 | N1 | 3300 | 0 | GSE84337 |
| GSM2235862 | 66 | MALE | T4 | N0 | 2550 | 1 | GSE84337 |
| GSM2235863 | 67 | MALE | T4 | N0 | 3990 | 0 | GSE84337 |
| GSM2235864 | 54 | MALE | T4 | N1 | 360 | 1 | GSE84337 |
| GSM2235865 | 44 | MALE | T4 | N1 | 990 | 1 | GSE84337 |
| GSM2235866 | 79 | FEMALE | T4 | N2 | 3870 | 0 | GSE84337 |
| GSM2235867 | 69 | FEMALE | T4 | N2 | 3750 | 0 | GSE84337 |
| GSM2235878 | 51 | FEMALE | T4 | N3 | 3750 | 0 | GSE84337 |
| GSM2235879 | 68 | FEMALE | T3 | N1 | 180 | 1 | GSE84337 |
| GSM2235880 | 67 | FEMALE | T4 | N2 | 510 | 1 | GSE84337 |
| GSM2235881 | 72 | MALE | T4 | N0 | 3750 | 0 | GSE84337 |
| GSM2235882 | 55 | MALE | T4 | N1 | 390 | 1 | GSE84337 |
| GSM2235883 | 66 | FEMALE | T4 | N2 | 570 | 1 | GSE84337 |
| GSM2235884 | 44 | MALE | T4 | N0 | 3780 | 0 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235885 | 73 | FEMALE | T4 | N1 | 3720 | 0 | GSE84337 |
| GSM2235886 | 76 | FEMALE | T2 | N1 | 1530 | 1 | GSE84337 |
| GSM2235887 | 81 | MALE | T3 | N2 | 2370 | 1 | GSE84337 |
| GSM2235888 | 36 | FEMALE | T4 | N1 | 2040 | 1 | GSE84337 |
| GSM2235889 | 66 | MALE | T4 | N1 | 2790 | 1 | GSE84337 |
| GSM2235899 | 48 | MALE | T4 | N1 | 1020 | 1 | GSE84337 |
| GSM2235900 | 46 | MALE | T4 | N1 | 3810 | 0 | GSE84337 |
| GSM2235901 | 66 | FEMALE | T3 | N1 | 1740 | 1 | GSE84337 |
| GSM2235902 | 34 | MALE | T4 | N1 | 1020 | 1 | GSE84337 |
| GSM2235903 | 50 | MALE | T4 | N1 | 3930 | 0 | GSE84337 |
| GSM2235904 | 62 | MALE | T4 | N1 | 630 | 1 | GSE84337 |
| GSM2235905 | 63 | MALE | T4 | N1 | 60 | 1 | GSE84337 |
| GSM2235906 | 70 | FEMALE | T4 | N1 | 3600 | 1 | GSE84337 |
| GSM2235907 | 77 | FEMALE | T4 | N0 | 3690 | 0 | GSE84337 |
| GSM2235908 | 32 | FEMALE | T3 | N0 | 3690 | 0 | GSE84337 |
| GSM2235909 | 63 | MALE | T4 | N2 | 540 | 1 | GSE84337 |
| GSM2235910 | 56 | MALE | T4 | N1 | 4170 | 0 | GSE84337 |
| GSM2235921 | 57 | MALE | T2 | N2 | 4170 | 0 | GSE84337 |
| GSM2235922 | 68 | MALE | T4 | N1 | 4140 | 0 | GSE84337 |
| GSM2235923 | 77 | FEMALE | T4 | N1 | 420 | 1 | GSE84337 |
| GSM2235924 | 54 | MALE | T4 | N2 | 4050 | 0 | GSE84337 |
| GSM2235925 | 64 | MALE | T4 | N1 | 4020 | 0 | GSE84337 |
| GSM2235926 | 47 | MALE | T4 | N2 | 4200 | 0 | GSE84337 |
| GSM2235927 | 65 | MALE | T4 | N1 | 0 | 1 | GSE84337 |
| GSM2235928 | 56 | FEMALE | T4 | N1 | 3960 | 0 | GSE84337 |
| GSM2235929 | 74 | MALE | T4 | N2 | 1800 | 1 | GSE84337 |
| GSM2235930 | 63 | MALE | T4 | N2 | 2220 | 1 | GSE84337 |
| GSM2235931 | 34 | MALE | T4 | N1 | 3960 | 0 | GSE84337 |
| GSM2235932 | 71 | FEMALE | T4 | N2 | 1770 | 0 | GSE84337 |
| GSM2235933 | 57 | FEMALE | T4 | N0 | 1230 | 0 | GSE84337 |
| GSM2235934 | 63 | MALE | T4 | N2 | 1410 | 0 | GSE84337 |
| GSM2235935 | 65 | MALE | T4 | N2 | 570 | 1 | GSE84337 |
| GSM2235936 | 63 | FEMALE | T1 | N0 | 1260 | 0 | GSE84337 |
| GSM2235937 | 54 | FEMALE | T4 | N2 | 1110 | 0 | GSE84337 |
| GSM2235938 | 62 | FEMALE | T1 | N0 | 2760 | 0 | GSE84337 |
| GSM2235939 | 42 | FEMALE | T2 | N0 | 1350 | 0 | GSE84337 |
| GSM2235940 | 63 | MALE | T4 | N2 | 990 | 1 | GSE84337 |
| GSM2235941 | 36 | FEMALE | T2 | N1 | 1230 | 0 | GSE84337 |
| GSM2235942 | 67 | MALE | T1 | N0 | 1260 | 0 | GSE84337 |
| GSM2235943 | 65 | MALE | T4 | N1 | 3810 | 0 | GSE84337 |
| GSM2235944 | 47 | MALE | T3 | N0 | 3780 | 0 | GSE84337 |
| GSM2235945 | 59 | FEMALE | T4 | N1 | 1110 | 1 | GSE84337 |
| GSM2235946 | 55 | MALE | T4 | N2 | 3930 | 0 | GSE84337 |
| GSM2235947 | 62 | MALE | T4 | N1 | 3870 | 0 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235948 | 36 | MALE | T4 | N1 | 3960 | 0 | GSE84337 |
| GSM2235949 | 43 | MALE | T4 | N1 | 3960 | 0 | GSE84337 |
| GSM2235950 | 45 | MALE | T4 | N1 | 3840 | 0 | GSE84337 |
| GSM2235951 | 61 | FEMALE | T4 | N1 | 150 | 1 | GSE84337 |
| GSM2235952 | 56 | FEMALE | T4 | N1 | 30 | 1 | GSE84337 |
| GSM2235953 | 58 | FEMALE | T4 | N1 | 300 | 1 | GSE84337 |
| GSM2235954 | 39 | FEMALE | T3 | N1 | 4470 | 0 | GSE84337 |
| GSM2235955 | 48 | MALE | T4 | N2 | 4470 | 0 | GSE84337 |
| GSM2235956 | 68 | FEMALE | T4 | N2 | 4050 | 1 | GSE84337 |
| GSM2235957 | 69 | FEMALE | T3 | N2 | 4440 | 0 | GSE84337 |
| GSM2235958 | 55 | MALE | T4 | N2 | 4560 | 0 | GSE84337 |
| GSM2235959 | 61 | MALE | T3 | N2 | 4320 | 0 | GSE84337 |
| GSM2235960 | 66 | MALE | T4 | N1 | 4260 | 0 | GSE84337 |
| GSM2235961 | 55 | MALE | T4 | N1 | 4230 | 0 | GSE84337 |
| GSM2235962 | 64 | MALE | T4 | N1 | 810 | 1 | GSE84337 |
| GSM2235963 | 58 | FEMALE | T4 | N2 | 810 | 1 | GSE84337 |
| GSM2235964 | 64 | MALE | T4 | N2 | 660 | 1 | GSE84337 |
| GSM2235965 | 58 | MALE | T3 | N1 | 1890 | 1 | GSE84337 |
| GSM2235966 | 40 | MALE | T4 | N3 | 990 | 0 | GSE84337 |
| GSM2235967 | 61 | MALE | T4 | N2 | 300 | 1 | GSE84337 |
| GSM2235968 | 52 | MALE | T2 | N0 | 1770 | 0 | GSE84337 |
| GSM2235969 | 72 | FEMALE | T2 | N1 | 1920 | 0 | GSE84337 |
| GSM2235970 | 66 | FEMALE | T4 | N2 | 540 | 1 | GSE84337 |
| GSM2235971 | 45 | MALE | T3 | N2 | 1890 | 0 | GSE84337 |
| GSM2235972 | 67 | MALE | T4 | N3 | 1710 | 0 | GSE84337 |
| GSM2235973 | 59 | FEMALE | T3 | N0 | 1860 | 0 | GSE84337 |
| GSM2235974 | 63 | MALE | T4 | N2 | 360 | 1 | GSE84337 |
| GSM2235975 | 59 | MALE | T3 | N3 | 1830 | 0 | GSE84337 |
| GSM2235976 | 67 | FEMALE | T3 | N1 | 1650 | 0 | GSE84337 |
| GSM2235977 | 72 | MALE | T4 | N2 | 210 | 1 | GSE84337 |
| GSM2235978 | 65 | MALE | T4 | N2 | 1020 | 0 | GSE84337 |
| GSM2235979 | 54 | FEMALE | T2 | N1 | 1260 | 0 | GSE84337 |
| GSM2235980 | 66 | MALE | T4 | N1 | 180 | 1 | GSE84337 |
| GSM2235981 | 69 | MALE | T4 | N1 | 1080 | 0 | GSE84337 |
| GSM2235982 | 51 | MALE | T3 | N2 | 1110 | 0 | GSE84337 |
| GSM2235983 | 46 | MALE | T3 | N1 | 1140 | 0 | GSE84337 |
| GSM2235984 | 69 | MALE | T4 | N3 | 240 | 1 | GSE84337 |
| GSM2235985 | 69 | FEMALE | T4 | N3 | 1050 | 0 | GSE84337 |
| GSM2235986 | 53 | FEMALE | T3 | N3 | 1050 | 0 | GSE84337 |
| GSM2235987 | 69 | MALE | T4 | N1 | 1050 | 0 | GSE84337 |
| GSM2235988 | 54 | FEMALE | T1 | N0 | 2100 | 0 | GSE84337 |
| GSM2235991 | 77 | MALE | T3 | N2 | 960 | 1 | GSE84337 |
| GSM2235992 | 59 | MALE | T4 | N1 | 3840 | 0 | GSE84337 |
| GSM2235993 | 27 | MALE | T3 | N1 | 3780 | 0 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2235994 | 42 | FEMALE | T3 | N1 | 3690 | 0 | GSE84337 |
| GSM2235995 | 57 | FEMALE | T3 | N2 | 300 | 1 | GSE84337 |
| GSM2235996 | 53 | FEMALE | T4 | N1 | 180 | 1 | GSE84337 |
| GSM2235997 | 74 | MALE | T4 | N1 | 3840 | 0 | GSE84337 |
| GSM2235998 | 68 | MALE | T4 | N1 | 3660 | 0 | GSE84337 |
| GSM2235999 | 60 | MALE | T4 | N1 | 2850 | 1 | GSE84337 |
| GSM2236000 | 64 | FEMALE | T3 | N1 | 3660 | 0 | GSE84337 |
| GSM2236001 | 48 | FEMALE | T4 | N2 | 3720 | 0 | GSE84337 |
| GSM2236002 | 68 | FEMALE | T4 | N1 | 3870 | 0 | GSE84337 |
| GSM2236003 | 55 | MALE | T4 | N1 | 3780 | 0 | GSE84337 |
| GSM2236004 | 66 | MALE | T4 | N1 | 1380 | 1 | GSE84337 |
| GSM2236005 | 72 | FEMALE | T4 | N2 | 270 | 1 | GSE84337 |
| GSM2236006 | 42 | MALE | T4 | N1 | 720 | 1 | GSE84337 |
| GSM2236007 | 76 | FEMALE | T4 | N1 | 630 | 1 | GSE84337 |
| GSM2236008 | 64 | FEMALE | T3 | N1 | 900 | 1 | GSE84337 |
| GSM2236009 | 66 | MALE | T4 | N1 | 810 | 1 | GSE84337 |
| GSM2236010 | 61 | MALE | T4 | N1 | 1140 | 1 | GSE84337 |
| GSM2236011 | 64 | MALE | T3 | N2 | 780 | 1 | GSE84337 |
| GSM2236012 | 33 | MALE | T4 | N3 | 90 | 1 | GSE84337 |
| GSM2236013 | 67 | FEMALE | T2 | N1 | 1590 | 1 | GSE84337 |
| GSM2236014 | 68 | MALE | T3 | N0 | 3150 | 1 | GSE84337 |
| GSM2236015 | 66 | MALE | T4 | N2 | 3300 | 0 | GSE84337 |
| GSM2236016 | 53 | MALE | T4 | N2 | 600 | 1 | GSE84337 |
| GSM2236017 | 61 | MALE | T4 | N2 | 510 | 1 | GSE84337 |
| GSM2236018 | 36 | MALE | T4 | N2 | 3480 | 0 | GSE84337 |
| GSM2236019 | 77 | MALE | T3 | N2 | 2760 | 1 | GSE84337 |
| GSM2236020 | 70 | FEMALE | T4 | N0 | 3270 | 0 | GSE84337 |
| GSM2236021 | 32 | MALE | T4 | N3 | 1530 | 1 | GSE84337 |
| GSM2236022 | 53 | MALE | T4 | N3 | 3120 | 0 | GSE84337 |
| GSM2236023 | 61 | FEMALE | T2 | N0 | 3240 | 0 | GSE84337 |
| GSM2236024 | 54 | MALE | T3 | N1 | 3090 | 0 | GSE84337 |
| GSM2236025 | 68 | FEMALE | T3 | N1 | 1170 | 1 | GSE84337 |
| GSM2236026 | 65 | MALE | T3 | N1 | 1920 | 1 | GSE84337 |
| GSM2236027 | 80 | FEMALE | T4 | N1 | 3720 | 0 | GSE84337 |
| GSM2236028 | 68 | MALE | T3 | N0 | 2850 | 1 | GSE84337 |
| GSM2236029 | 44 | MALE | T2 | N1 | 4140 | 0 | GSE84337 |
| GSM2236030 | 63 | MALE | T4 | N0 | 4140 | 0 | GSE84337 |
| GSM2236031 | 52 | FEMALE | T4 | N0 | 4020 | 0 | GSE84337 |
| GSM2236032 | 44 | MALE | T4 | N0 | 4020 | 0 | GSE84337 |
| GSM2236033 | 69 | MALE | T3 | N0 | 3600 | 0 | GSE84337 |
| GSM2236034 | 55 | MALE | T4 | N0 | 3660 | 0 | GSE84337 |
| GSM2236036 | 62 | MALE | T1 | N1 | 1230 | 0 | GSE84337 |
| GSM2236037 | 64 | FEMALE | T4 | N1 | 1230 | 0 | GSE84337 |
| GSM2236038 | 65 | MALE | T4 | N2 | 1200 | 0 | GSE84337 |

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|------------|----|--------|----|----|------|---|----------|
| GSM2236039 | 56 | MALE | T2 | N0 | 1260 | 0 | GSE84337 |
| GSM2236040 | 71 | FEMALE | T3 | N1 | 1110 | 0 | GSE84337 |
| GSM2236041 | 50 | MALE | T4 | N1 | 1230 | 0 | GSE84337 |
| GSM2236042 | 69 | FEMALE | T4 | N2 | 1110 | 0 | GSE84337 |
| GSM2236043 | 48 | MALE | T3 | N1 | 1200 | 0 | GSE84337 |
| GSM2236044 | 48 | MALE | T2 | N2 | 4230 | 0 | GSE84337 |
| GSM2236045 | 63 | MALE | T4 | N1 | 4830 | 0 | GSE84337 |
| GSM2236046 | 64 | MALE | T4 | N1 | 1050 | 1 | GSE84337 |
| GSM2236047 | 49 | FEMALE | T4 | N2 | 1470 | 1 | GSE84337 |
| GSM2236048 | 64 | MALE | T3 | N0 | 3060 | 0 | GSE84337 |
| GSM2236049 | 44 | FEMALE | T4 | N1 | 990 | 1 | GSE84337 |
| GSM2236050 | 65 | MALE | T3 | N1 | 3030 | 0 | GSE84337 |
| GSM2236051 | 34 | MALE | T4 | N2 | 1140 | 1 | GSE84337 |
| GSM2236052 | 61 | MALE | T4 | N1 | 3480 | 0 | GSE84337 |
| GSM2236053 | 41 | FEMALE | T4 | N2 | 660 | 1 | GSE84337 |
| GSM2236054 | 49 | FEMALE | T4 | N0 | 2370 | 1 | GSE84337 |
| GSM2236055 | 55 | MALE | T4 | N0 | 3990 | 0 | GSE84337 |
| GSM2236056 | 54 | MALE | T4 | N0 | 3840 | 0 | GSE84337 |
| GSM2236057 | 62 | MALE | T2 | N1 | 1110 | 1 | GSE84337 |
| GSM2236058 | 62 | MALE | T2 | N1 | 4080 | 0 | GSE84337 |
| GSM2236059 | 75 | FEMALE | T2 | N1 | 4110 | 0 | GSE84337 |
| GSM2236060 | 47 | MALE | T4 | N3 | 1110 | 1 | GSE84337 |
| GSM2236061 | 68 | FEMALE | T2 | N1 | 3870 | 0 | GSE84337 |
| GSM2236062 | 69 | MALE | T3 | N1 | 3870 | 0 | GSE84337 |
| GSM2236063 | 48 | FEMALE | T2 | N1 | 3930 | 0 | GSE84337 |
| GSM2236064 | 70 | MALE | T4 | N0 | 2310 | 1 | GSE84337 |
| GSM2236065 | 58 | MALE | T4 | N2 | 3570 | 0 | GSE84337 |
| GSM2236066 | 63 | FEMALE | T4 | N1 | 3810 | 0 | GSE84337 |
| GSM2236067 | 47 | MALE | T4 | N2 | 510 | 1 | GSE84337 |
| GSM2236068 | 44 | MALE | T4 | N0 | 1260 | 1 | GSE84337 |
| GSM2236069 | 69 | MALE | T3 | N1 | 3450 | 0 | GSE84337 |
| GSM2236070 | 71 | MALE | T3 | N1 | 3720 | 0 | GSE84337 |
| GSM2236071 | 54 | FEMALE | T4 | N1 | 3420 | 0 | GSE84337 |
| GSM2236072 | 49 | MALE | T3 | N3 | 990 | 1 | GSE84337 |
| GSM2236073 | 60 | MALE | T4 | N2 | 660 | 1 | GSE84337 |
| GSM2236074 | 62 | MALE | T2 | N1 | 4290 | 0 | GSE84337 |
| GSM2236075 | 44 | MALE | T4 | N1 | 1170 | 1 | GSE84337 |
| GSM2236076 | 63 | MALE | T3 | N1 | 1050 | 0 | GSE84337 |
| GSM2236077 | 68 | MALE | T4 | N2 | 1140 | 0 | GSE84337 |
| GSM2236078 | 60 | MALE | T4 | N0 | 4260 | 0 | GSE84337 |
| GSM2236079 | 67 | MALE | T2 | N1 | 4230 | 0 | GSE84337 |
| GSM2236080 | 62 | MALE | T4 | N0 | 420 | 1 | GSE84337 |
| GSM2236082 | 53 | FEMALE | T4 | N0 | 3930 | 0 | GSE84337 |
| GSM2236083 | 64 | FEMALE | T4 | N2 | 210 | 1 | GSE84337 |

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|--------------|----|--------|--------|--------|------|---|----------|
| GSM2236084 | 59 | FEMALE | T3 | N2 | 3840 | 0 | GSE84337 |
| GSM2236085 | 55 | MALE | T4 | N0 | 4560 | 0 | GSE84337 |
| GSM2236086 | 36 | FEMALE | T4 | N0 | 4470 | 0 | GSE84337 |
| GSM2236087 | 68 | MALE | T3 | N1 | 4650 | 0 | GSE84337 |
| GSM2236088 | 61 | FEMALE | T4 | N0 | 1020 | 1 | GSE84337 |
| GSM2236089 | 69 | FEMALE | T4 | N0 | 4320 | 0 | GSE84337 |
| GSM2236090 | 86 | MALE | T4 | N0 | 930 | 1 | GSE84337 |
| GSM2236091 | 77 | MALE | T3 | N0 | 3690 | 1 | GSE84337 |
| GSM2236092 | 58 | MALE | T4 | N0 | 4470 | 0 | GSE84337 |
| GSM2236093 | 59 | MALE | T3 | N0 | 4530 | 0 | GSE84337 |
| GSM2236094 | 64 | MALE | T4 | N0 | 1110 | 1 | GSE84337 |
| GSM2236095 | 51 | MALE | T4 | N0 | 4500 | 0 | GSE84337 |
| TCGA-3M-AB46 | 70 | MALE | T2 | N0 | 1765 | 0 | TCGA |
| TCGA-B7-5816 | 51 | FEMALE | T4 | N0 | 812 | 0 | TCGA |
| TCGA-B7-5818 | 62 | MALE | T2 | N0 | 356 | 0 | TCGA |
| TCGA-B7-A5TI | 52 | MALE | T4 | N3 | 595 | 0 | TCGA |
| TCGA-B7-A5TJ | 74 | MALE | T4 | unknow | 335 | 0 | TCGA |
| TCGA-B7-A5TK | 51 | MALE | T4 | unknow | 288 | 0 | TCGA |
| TCGA-B7-A5TN | 60 | MALE | T4 | unknow | 287 | 0 | TCGA |
| TCGA-BR-4183 | 55 | FEMALE | T3 | N1 | 201 | 1 | TCGA |
| TCGA-BR-4184 | 70 | MALE | T3 | N1 | 212 | 1 | TCGA |
| TCGA-BR-4187 | 56 | MALE | unknow | unknow | 141 | 1 | TCGA |
| TCGA-BR-4188 | 53 | FEMALE | unknow | N1 | 226 | 1 | TCGA |
| TCGA-BR-4191 | 72 | MALE | unknow | N1 | 558 | 1 | TCGA |
| TCGA-BR-4201 | 66 | FEMALE | T2 | unknow | 940 | 1 | TCGA |
| TCGA-BR-4253 | 80 | FEMALE | T3 | N1 | 124 | 1 | TCGA |
| TCGA-BR-4255 | 76 | FEMALE | T3 | N1 | 124 | 1 | TCGA |
| TCGA-BR-4256 | 80 | MALE | unknow | N1 | 284 | 1 | TCGA |
| TCGA-BR-4257 | 79 | FEMALE | unknow | unknow | 294 | 1 | TCGA |
| TCGA-BR-4267 | 51 | MALE | T2 | N0 | 188 | 1 | TCGA |
| TCGA-BR-4279 | 43 | MALE | T2 | N1 | 291 | 1 | TCGA |
| TCGA-BR-4280 | 78 | FEMALE | T2 | N1 | 201 | 1 | TCGA |
| TCGA-BR-4292 | 73 | FEMALE | T1 | unknow | 0 | 0 | TCGA |
| TCGA-BR-4294 | 65 | MALE | T2 | unknow | 0 | 0 | TCGA |
| TCGA-BR-4357 | 58 | MALE | T3 | unknow | 0 | 0 | TCGA |
| TCGA-BR-4361 | 66 | FEMALE | T4 | N0 | 0 | 0 | TCGA |
| TCGA-BR-4362 | 74 | FEMALE | unknow | N1 | 0 | 0 | TCGA |
| TCGA-BR-4363 | 60 | FEMALE | T3 | unknow | 0 | 0 | TCGA |
| TCGA-BR-4366 | 87 | MALE | unknow | unknow | 0 | 0 | TCGA |
| TCGA-BR-4367 | 78 | MALE | unknow | N1 | 0 | 0 | TCGA |
| TCGA-BR-4368 | 78 | FEMALE | T4 | N2 | 0 | 0 | TCGA |
| TCGA-BR-4369 | 75 | MALE | unknow | unknow | 0 | 0 | TCGA |
| TCGA-BR-4370 | 74 | FEMALE | unknow | unknow | 0 | 0 | TCGA |
| TCGA-BR-4371 | 71 | FEMALE | T2 | unknow | 0 | 0 | TCGA |

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|--------------|----|--------|----|----|------|---|------|
| TCGA-BR-6452 | 78 | FEMALE | T3 | N0 | 1055 | 0 | TCGA |
| TCGA-BR-6453 | 54 | MALE | T2 | N1 | 485 | 0 | TCGA |
| TCGA-BR-6454 | 58 | MALE | T3 | N0 | 0 | 0 | TCGA |
| TCGA-BR-6455 | 59 | MALE | T3 | N1 | 422 | 1 | TCGA |
| TCGA-BR-6456 | 74 | FEMALE | T3 | N1 | 526 | 1 | TCGA |
| TCGA-BR-6457 | 69 | MALE | T3 | N0 | 416 | 0 | TCGA |
| TCGA-BR-6458 | 57 | FEMALE | T3 | N1 | 588 | 1 | TCGA |
| TCGA-BR-6563 | 60 | MALE | T3 | N1 | 1190 | 0 | TCGA |
| TCGA-BR-6564 | 46 | FEMALE | T3 | N2 | 794 | 1 | TCGA |
| TCGA-BR-6565 | 67 | MALE | T4 | N0 | 279 | 1 | TCGA |
| TCGA-BR-6566 | 64 | FEMALE | T3 | N0 | 997 | 0 | TCGA |
| TCGA-BR-6705 | 68 | FEMALE | T3 | N3 | 779 | 1 | TCGA |
| TCGA-BR-6706 | 63 | MALE | T3 | N1 | 549 | 1 | TCGA |
| TCGA-BR-6707 | 75 | MALE | T3 | N0 | 605 | 1 | TCGA |
| TCGA-BR-6709 | 57 | FEMALE | T3 | N3 | 370 | 1 | TCGA |
| TCGA-BR-6710 | 41 | MALE | T2 | N0 | 273 | 0 | TCGA |
| TCGA-BR-6801 | 70 | MALE | T3 | N0 | 1223 | 0 | TCGA |
| TCGA-BR-6802 | 65 | MALE | T3 | N2 | 940 | 0 | TCGA |
| TCGA-BR-6803 | 54 | FEMALE | T3 | N0 | 949 | 0 | TCGA |
| TCGA-BR-6852 | 64 | FEMALE | T3 | N0 | 1367 | 0 | TCGA |
| TCGA-BR-7196 | 64 | MALE | T3 | N3 | 666 | 0 | TCGA |
| TCGA-BR-7197 | 69 | MALE | T3 | N0 | 280 | 0 | TCGA |
| TCGA-BR-7703 | 81 | MALE | T1 | N0 | 1100 | 0 | TCGA |
| TCGA-BR-7704 | 69 | FEMALE | T3 | N0 | 1072 | 0 | TCGA |
| TCGA-BR-7707 | 69 | FEMALE | T2 | N0 | 1090 | 0 | TCGA |
| TCGA-BR-7715 | 65 | MALE | T3 | N0 | 1023 | 0 | TCGA |
| TCGA-BR-7716 | 62 | FEMALE | T3 | N1 | 1210 | 0 | TCGA |
| TCGA-BR-7717 | 63 | MALE | T4 | N1 | 552 | 1 | TCGA |
| TCGA-BR-7722 | 62 | MALE | T3 | N1 | 466 | 1 | TCGA |
| TCGA-BR-7723 | 59 | MALE | T3 | N3 | 874 | 1 | TCGA |
| TCGA-BR-7851 | 74 | MALE | T4 | N0 | 378 | 0 | TCGA |
| TCGA-BR-7901 | 74 | MALE | T3 | N1 | 105 | 1 | TCGA |
| TCGA-BR-7957 | 50 | FEMALE | T3 | N3 | 276 | 1 | TCGA |
| TCGA-BR-7958 | 60 | MALE | T4 | N0 | 899 | 0 | TCGA |
| TCGA-BR-7959 | 59 | MALE | T4 | N1 | 1010 | 0 | TCGA |
| TCGA-BR-8058 | 53 | FEMALE | T4 | N2 | 1133 | 0 | TCGA |
| TCGA-BR-8059 | 72 | MALE | T4 | N1 | 439 | 1 | TCGA |
| TCGA-BR-8060 | 75 | FEMALE | T2 | N2 | 348 | 1 | TCGA |
| TCGA-BR-8077 | 58 | FEMALE | T4 | N1 | 21 | 0 | TCGA |
| TCGA-BR-8078 | 70 | FEMALE | T4 | N0 | 900 | 0 | TCGA |
| TCGA-BR-8080 | 72 | FEMALE | T4 | N3 | 292 | 1 | TCGA |
| TCGA-BR-8081 | 71 | FEMALE | T4 | N0 | 981 | 0 | TCGA |
| TCGA-BR-8284 | 72 | FEMALE | T4 | N3 | 245 | 1 | TCGA |
| TCGA-BR-8285 | 57 | FEMALE | T4 | N3 | 17 | 1 | TCGA |

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|--------------|----|--------|----|----|-----|---|------|
| TCGA-BR-8286 | 49 | MALE | T3 | N0 | 895 | 0 | TCGA |
| TCGA-BR-8289 | 57 | MALE | T4 | N3 | 81 | 1 | TCGA |
| TCGA-BR-8291 | 61 | MALE | T3 | N1 | 607 | 1 | TCGA |
| TCGA-BR-8295 | 60 | FEMALE | T4 | N0 | 67 | 1 | TCGA |
| TCGA-BR-8296 | 58 | FEMALE | T4 | N2 | 474 | 1 | TCGA |
| TCGA-BR-8297 | 58 | MALE | T4 | N3 | 225 | 0 | TCGA |
| TCGA-BR-8360 | 66 | MALE | T3 | N0 | 188 | 0 | TCGA |
| TCGA-BR-8361 | 71 | FEMALE | T4 | N2 | 946 | 0 | TCGA |
| TCGA-BR-8362 | 65 | MALE | T4 | N3 | 398 | 1 | TCGA |
| TCGA-BR-8363 | 73 | FEMALE | T2 | N0 | 8 | 1 | TCGA |
| TCGA-BR-8364 | 42 | FEMALE | T4 | N2 | 675 | 0 | TCGA |
| TCGA-BR-8365 | 70 | FEMALE | T3 | N0 | 533 | 1 | TCGA |
| TCGA-BR-8366 | 80 | FEMALE | T3 | N0 | 29 | 0 | TCGA |
| TCGA-BR-8367 | 55 | MALE | T3 | N3 | 801 | 1 | TCGA |
| TCGA-BR-8368 | 84 | FEMALE | T2 | N0 | 131 | 0 | TCGA |
| TCGA-BR-8369 | 76 | FEMALE | T3 | N3 | 427 | 0 | TCGA |
| TCGA-BR-8370 | 64 | MALE | T3 | N3 | 101 | 0 | TCGA |
| TCGA-BR-8371 | 62 | MALE | T3 | N3 | 359 | 1 | TCGA |
| TCGA-BR-8372 | 63 | MALE | T4 | N3 | 951 | 0 | TCGA |
| TCGA-BR-8373 | 65 | FEMALE | T4 | N1 | 450 | 0 | TCGA |
| TCGA-BR-8380 | 55 | MALE | T4 | N3 | 21 | 0 | TCGA |
| TCGA-BR-8381 | 51 | MALE | T3 | N1 | 224 | 0 | TCGA |
| TCGA-BR-8382 | 67 | FEMALE | T4 | N3 | 762 | 1 | TCGA |
| TCGA-BR-8384 | 69 | MALE | T4 | N2 | 113 | 0 | TCGA |
| TCGA-BR-8483 | 59 | MALE | T3 | N2 | 164 | 0 | TCGA |
| TCGA-BR-8484 | 61 | MALE | T4 | N1 | 766 | 1 | TCGA |
| TCGA-BR-8485 | 68 | FEMALE | T4 | N3 | 280 | 0 | TCGA |
| TCGA-BR-8486 | 90 | FEMALE | T1 | N0 | 0 | 0 | TCGA |
| TCGA-BR-8487 | 64 | FEMALE | T3 | N0 | 34 | 0 | TCGA |
| TCGA-BR-8588 | 55 | FEMALE | T4 | N0 | 389 | 0 | TCGA |
| TCGA-BR-8589 | 56 | MALE | T4 | N1 | 825 | 0 | TCGA |
| TCGA-BR-8590 | 62 | MALE | T4 | N2 | 284 | 1 | TCGA |
| TCGA-BR-8591 | 79 | MALE | T4 | N3 | 856 | 0 | TCGA |
| TCGA-BR-8592 | 63 | FEMALE | T4 | N1 | 191 | 1 | TCGA |
| TCGA-BR-8676 | 59 | MALE | T3 | N3 | 229 | 0 | TCGA |
| TCGA-BR-8677 | 74 | FEMALE | T3 | N3 | 813 | 0 | TCGA |
| TCGA-BR-8678 | 76 | MALE | T2 | N0 | 754 | 0 | TCGA |
| TCGA-BR-8679 | 63 | FEMALE | T2 | N0 | 0 | 0 | TCGA |
| TCGA-BR-8680 | 45 | MALE | T4 | N2 | 972 | 0 | TCGA |
| TCGA-BR-8682 | 52 | MALE | T4 | N0 | 991 | 0 | TCGA |
| TCGA-BR-8683 | 75 | MALE | T4 | N2 | 300 | 1 | TCGA |
| TCGA-BR-8686 | 69 | MALE | T4 | N1 | 635 | 1 | TCGA |
| TCGA-BR-8687 | 67 | FEMALE | T4 | N2 | 250 | 1 | TCGA |
| TCGA-BR-8690 | 54 | FEMALE | T3 | N3 | 325 | 0 | TCGA |

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|--------------|----|--------|----|--------|------|---|------|
| TCGA-BR-A44T | 53 | FEMALE | T3 | N0 | 1038 | 0 | TCGA |
| TCGA-BR-A44U | 70 | MALE | T3 | N3 | 422 | 1 | TCGA |
| TCGA-BR-A452 | 57 | MALE | T4 | N1 | 229 | 1 | TCGA |
| TCGA-BR-A453 | 51 | MALE | T4 | N3 | 185 | 1 | TCGA |
| TCGA-BR-A4CQ | 58 | MALE | T4 | N1 | 1064 | 0 | TCGA |
| TCGA-BR-A4CR | 70 | FEMALE | T4 | N3 | 0 | 0 | TCGA |
| TCGA-BR-A4CS | 77 | MALE | T4 | N3 | 45 | 1 | TCGA |
| TCGA-BR-A4IU | 34 | FEMALE | T4 | N1 | 838 | 0 | TCGA |
| TCGA-BR-A4IV | 47 | MALE | T4 | N2 | 869 | 1 | TCGA |
| TCGA-BR-A4IY | 58 | MALE | T4 | N0 | 392 | 0 | TCGA |
| TCGA-BR-A4IZ | 45 | FEMALE | T4 | N2 | 273 | 1 | TCGA |
| TCGA-BR-A4J1 | 63 | MALE | T4 | N1 | 22 | 1 | TCGA |
| TCGA-BR-A4J2 | 70 | MALE | T4 | N0 | 431 | 0 | TCGA |
| TCGA-BR-A4J4 | 39 | MALE | T4 | N2 | 16 | 0 | TCGA |
| TCGA-BR-A4J5 | 56 | MALE | T4 | N1 | 862 | 0 | TCGA |
| TCGA-BR-A4J6 | 69 | FEMALE | T3 | N0 | 20 | 0 | TCGA |
| TCGA-BR-A4J7 | 49 | MALE | T4 | unknow | 989 | 0 | TCGA |
| TCGA-BR-A4J8 | 71 | FEMALE | T3 | N3 | 411 | 0 | TCGA |
| TCGA-BR-A4J9 | 55 | MALE | T3 | N0 | 14 | 0 | TCGA |
| TCGA-BR-A4PD | 72 | FEMALE | T4 | N0 | 628 | 0 | TCGA |
| TCGA-BR-A4PE | 68 | FEMALE | T2 | N0 | 621 | 0 | TCGA |
| TCGA-BR-A4PF | 72 | MALE | T4 | N2 | 35 | 0 | TCGA |
| TCGA-BR-A4QI | 70 | FEMALE | T3 | N0 | 652 | 1 | TCGA |
| TCGA-BR-A4QL | 75 | FEMALE | T3 | N3 | 491 | 1 | TCGA |
| TCGA-BR-A4QM | 65 | MALE | T3 | N2 | 156 | 0 | TCGA |
| TCGA-CD-5798 | 82 | MALE | T3 | N0 | 408 | 0 | TCGA |
| TCGA-CD-5799 | 45 | MALE | T2 | N1 | 396 | 0 | TCGA |
| TCGA-CD-5800 | 51 | FEMALE | T3 | N0 | 400 | 0 | TCGA |
| TCGA-CD-5801 | 69 | MALE | T3 | N1 | 401 | 1 | TCGA |
| TCGA-CD-5802 | 58 | MALE | T3 | N0 | 406 | 0 | TCGA |
| TCGA-CD-5803 | 78 | FEMALE | T3 | N0 | 341 | 1 | TCGA |
| TCGA-CD-5804 | 90 | MALE | T3 | N1 | 0 | 0 | TCGA |
| TCGA-CD-5813 | 60 | MALE | T3 | N0 | 377 | 1 | TCGA |
| TCGA-CD-8524 | 61 | FEMALE | T3 | N0 | 388 | 0 | TCGA |
| TCGA-CD-8525 | 82 | FEMALE | T3 | N1 | 383 | 0 | TCGA |
| TCGA-CD-8526 | 73 | FEMALE | T3 | N1 | 381 | 0 | TCGA |
| TCGA-CD-8527 | 72 | FEMALE | T2 | N1 | 218 | 1 | TCGA |
| TCGA-CD-8528 | 43 | FEMALE | T4 | N0 | 375 | 0 | TCGA |
| TCGA-CD-8529 | 65 | MALE | T4 | N0 | 374 | 0 | TCGA |
| TCGA-CD-8530 | 51 | MALE | T3 | N0 | 377 | 0 | TCGA |
| TCGA-CD-8531 | 66 | FEMALE | T3 | N1 | 383 | 0 | TCGA |
| TCGA-CD-8532 | 52 | MALE | T3 | N0 | 354 | 1 | TCGA |
| TCGA-CD-8533 | 48 | MALE | T3 | N0 | 468 | 0 | TCGA |
| TCGA-CD-8534 | 41 | MALE | T3 | N0 | 367 | 0 | TCGA |

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|--------------|----|--------|----|----|------|---|------|
| TCGA-CD-8535 | 59 | MALE | T3 | N1 | 390 | 0 | TCGA |
| TCGA-CD-8536 | 74 | MALE | T3 | N0 | 378 | 0 | TCGA |
| TCGA-CD-A486 | 68 | MALE | T3 | N0 | 192 | 1 | TCGA |
| TCGA-CD-A487 | 51 | MALE | T3 | N1 | 374 | 0 | TCGA |
| TCGA-CD-A489 | 58 | MALE | T3 | N0 | 344 | 1 | TCGA |
| TCGA-CD-A48A | 57 | MALE | T3 | N0 | 378 | 0 | TCGA |
| TCGA-CD-A48C | 79 | FEMALE | T3 | N1 | 353 | 1 | TCGA |
| TCGA-CD-A4MG | 76 | MALE | T3 | N0 | 200 | 1 | TCGA |
| TCGA-CD-A4MH | 86 | FEMALE | T3 | N0 | 371 | 0 | TCGA |
| TCGA-CD-A4MI | 62 | MALE | T3 | N1 | 358 | 1 | TCGA |
| TCGA-CD-A4MJ | 60 | MALE | T2 | N0 | 384 | 0 | TCGA |
| TCGA-CG-4300 | 79 | MALE | T3 | N2 | 609 | 1 | TCGA |
| TCGA-CG-4301 | 75 | FEMALE | T4 | N1 | 92 | 0 | TCGA |
| TCGA-CG-4305 | 69 | MALE | T2 | N1 | 485 | 0 | TCGA |
| TCGA-CG-4306 | 90 | MALE | T3 | N2 | 1 | 1 | TCGA |
| TCGA-CG-4436 | 57 | MALE | T2 | N0 | 243 | 0 | TCGA |
| TCGA-CG-4437 | 83 | MALE | T2 | N1 | 245 | 0 | TCGA |
| TCGA-CG-4438 | 56 | MALE | T4 | N2 | 1645 | 0 | TCGA |
| TCGA-CG-4440 | 68 | FEMALE | T3 | N3 | 122 | 1 | TCGA |
| TCGA-CG-4441 | 83 | MALE | T2 | N2 | 426 | 1 | TCGA |
| TCGA-CG-4442 | 85 | MALE | T2 | N0 | 0 | 0 | TCGA |
| TCGA-CG-4443 | 68 | MALE | T1 | N0 | 912 | 0 | TCGA |
| TCGA-CG-4444 | 76 | MALE | T2 | N2 | 1431 | 0 | TCGA |
| TCGA-CG-4449 | 81 | MALE | T2 | N1 | 580 | 0 | TCGA |
| TCGA-CG-4455 | 72 | MALE | T2 | N1 | 366 | 0 | TCGA |
| TCGA-CG-4460 | 66 | FEMALE | T4 | N1 | 669 | 1 | TCGA |
| TCGA-CG-4462 | 72 | FEMALE | T3 | N3 | 0 | 1 | TCGA |
| TCGA-CG-4465 | 69 | FEMALE | T4 | N3 | 274 | 1 | TCGA |
| TCGA-CG-4466 | 81 | FEMALE | T2 | N0 | 577 | 0 | TCGA |
| TCGA-CG-4469 | 70 | MALE | T3 | N3 | 215 | 1 | TCGA |
| TCGA-CG-4472 | 49 | MALE | T4 | N1 | 365 | 0 | TCGA |
| TCGA-CG-4474 | 67 | FEMALE | T4 | N2 | 0 | 0 | TCGA |
| TCGA-CG-4475 | 76 | MALE | T3 | N1 | 699 | 0 | TCGA |
| TCGA-CG-4476 | 69 | MALE | T4 | N3 | 0 | 0 | TCGA |
| TCGA-CG-4477 | 58 | FEMALE | T2 | N0 | 942 | 0 | TCGA |
| TCGA-CG-5716 | 86 | MALE | T4 | N2 | 0 | 0 | TCGA |
| TCGA-CG-5717 | 58 | MALE | T2 | N1 | 212 | 1 | TCGA |
| TCGA-CG-5718 | 78 | FEMALE | T2 | N1 | 1095 | 1 | TCGA |
| TCGA-CG-5719 | 54 | FEMALE | T4 | N0 | 31 | 0 | TCGA |
| TCGA-CG-5720 | 71 | MALE | T2 | N0 | 30 | 1 | TCGA |
| TCGA-CG-5721 | 58 | MALE | T4 | N1 | 183 | 0 | TCGA |
| TCGA-CG-5722 | 67 | FEMALE | T3 | N2 | 30 | 0 | TCGA |
| TCGA-CG-5723 | 83 | MALE | T2 | N1 | 2496 | 0 | TCGA |
| TCGA-CG-5724 | 59 | MALE | T3 | N3 | 366 | 1 | TCGA |

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|--------------|----|--------|----|----|------|---|------|
| TCGA-CG-5725 | 72 | MALE | T2 | N0 | 457 | 1 | TCGA |
| TCGA-CG-5726 | 73 | MALE | T1 | N0 | 881 | 1 | TCGA |
| TCGA-CG-5727 | 66 | MALE | T3 | N0 | 2405 | 0 | TCGA |
| TCGA-CG-5728 | 88 | FEMALE | T2 | N0 | 579 | 0 | TCGA |
| TCGA-CG-5730 | 80 | FEMALE | T2 | N1 | 122 | 0 | TCGA |
| TCGA-CG-5732 | 66 | MALE | T2 | N3 | 2100 | 1 | TCGA |
| TCGA-CG-5733 | 83 | FEMALE | T2 | N2 | 641 | 1 | TCGA |
| TCGA-CG-5734 | 68 | MALE | T3 | N1 | 243 | 1 | TCGA |
| TCGA-D7-5577 | 53 | FEMALE | T2 | N3 | 782 | 1 | TCGA |
| TCGA-D7-5578 | 80 | MALE | T3 | N2 | 385 | 0 | TCGA |
| TCGA-D7-5579 | 74 | MALE | T3 | N2 | 636 | 0 | TCGA |
| TCGA-D7-6518 | 75 | MALE | T2 | N3 | 582 | 0 | TCGA |
| TCGA-D7-6519 | 64 | FEMALE | T2 | N1 | 625 | 0 | TCGA |
| TCGA-D7-6520 | 53 | MALE | T2 | N2 | 573 | 0 | TCGA |
| TCGA-D7-6521 | 65 | MALE | T2 | N2 | 564 | 0 | TCGA |
| TCGA-D7-6522 | 58 | MALE | T2 | N0 | 566 | 0 | TCGA |
| TCGA-D7-6524 | 53 | MALE | T2 | N1 | 543 | 0 | TCGA |
| TCGA-D7-6525 | 58 | MALE | T2 | N2 | 406 | 1 | TCGA |
| TCGA-D7-6526 | 67 | FEMALE | T3 | N2 | 523 | 0 | TCGA |
| TCGA-D7-6527 | 62 | MALE | T2 | N1 | 312 | 1 | TCGA |
| TCGA-D7-6528 | 70 | FEMALE | T2 | N0 | 463 | 0 | TCGA |
| TCGA-D7-6815 | 70 | FEMALE | T2 | N2 | 486 | 0 | TCGA |
| TCGA-D7-6817 | 63 | MALE | T2 | N3 | 389 | 0 | TCGA |
| TCGA-D7-6818 | 53 | MALE | T2 | N3 | 376 | 1 | TCGA |
| TCGA-D7-6820 | 64 | MALE | T2 | N1 | 344 | 0 | TCGA |
| TCGA-D7-6822 | 77 | MALE | T2 | N0 | 375 | 0 | TCGA |
| TCGA-D7-8570 | 44 | MALE | T3 | N3 | 752 | 0 | TCGA |
| TCGA-D7-8572 | 57 | MALE | T2 | N2 | 511 | 0 | TCGA |
| TCGA-D7-8573 | 57 | MALE | T3 | N0 | 593 | 0 | TCGA |
| TCGA-D7-8574 | 72 | MALE | T2 | N3 | 523 | 0 | TCGA |
| TCGA-D7-8575 | 75 | MALE | T3 | N2 | 554 | 1 | TCGA |
| TCGA-D7-8576 | 54 | FEMALE | T3 | N3 | 446 | 1 | TCGA |
| TCGA-D7-8578 | 72 | MALE | T2 | N0 | 643 | 0 | TCGA |
| TCGA-D7-8579 | 66 | FEMALE | T2 | N2 | 636 | 0 | TCGA |
| TCGA-D7-A4YT | 56 | MALE | T2 | N3 | 434 | 0 | TCGA |
| TCGA-D7-A4YU | 73 | MALE | T3 | N3 | 500 | 0 | TCGA |
| TCGA-D7-A4YV | 69 | FEMALE | T3 | N1 | 180 | 0 | TCGA |
| TCGA-D7-A4YX | 63 | MALE | T3 | N1 | 1108 | 0 | TCGA |
| TCGA-D7-A4YY | 61 | MALE | T3 | N3 | 419 | 0 | TCGA |
| TCGA-D7-A4Z0 | 60 | FEMALE | T2 | N2 | 449 | 0 | TCGA |
| TCGA-D7-A6ET | 76 | MALE | T3 | N3 | 804 | 0 | TCGA |
| TCGA-D7-A6EV | 71 | FEMALE | T2 | N2 | 342 | 0 | TCGA |
| TCGA-D7-A6EX | 72 | FEMALE | T3 | N2 | 344 | 0 | TCGA |
| TCGA-D7-A6EY | 72 | FEMALE | T3 | N3 | 348 | 1 | TCGA |

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|--------------|--------|--------|----|--------|------|---|------|
| TCGA-D7-A6EZ | 66 | MALE | T3 | N2 | 618 | 1 | TCGA |
| TCGA-D7-A6F0 | 79 | FEMALE | T2 | N0 | 678 | 0 | TCGA |
| TCGA-D7-A6F2 | 62 | MALE | T2 | N0 | 476 | 0 | TCGA |
| TCGA-D7-A747 | 57 | MALE | T3 | N1 | 255 | 1 | TCGA |
| TCGA-D7-A748 | 41 | FEMALE | T4 | N3 | 132 | 1 | TCGA |
| TCGA-D7-A74A | 61 | FEMALE | T3 | N2 | 607 | 0 | TCGA |
| TCGA-D7-A74B | 52 | FEMALE | T3 | N3 | 217 | 1 | TCGA |
| TCGA-EQ-5647 | 86 | FEMALE | T4 | N3 | 19 | 1 | TCGA |
| TCGA-EQ-8122 | 71 | FEMALE | T3 | N1 | 243 | 1 | TCGA |
| TCGA-EQ-A4SO | 70 | MALE | T4 | N1 | 494 | 0 | TCGA |
| TCGA-F1-6177 | 90 | MALE | T1 | N1 | 0 | 0 | TCGA |
| TCGA-F1-6874 | 79 | MALE | T2 | N0 | 440 | 0 | TCGA |
| TCGA-F1-6875 | 79 | MALE | T2 | N0 | 2197 | 1 | TCGA |
| TCGA-F1-A448 | 70 | MALE | T3 | N3 | 647 | 0 | TCGA |
| TCGA-F1-A72C | 68 | MALE | T3 | N0 | 346 | 0 | TCGA |
| TCGA-FP-7735 | 77 | MALE | T2 | N0 | 106 | 1 | TCGA |
| TCGA-FP-7829 | 69 | MALE | T3 | N1 | 594 | 0 | TCGA |
| TCGA-FP-7916 | 77 | MALE | T4 | N3 | 428 | 1 | TCGA |
| TCGA-FP-7998 | 77 | MALE | T4 | N3 | 678 | 0 | TCGA |
| TCGA-FP-8099 | 79 | MALE | T3 | N0 | 519 | 0 | TCGA |
| TCGA-FP-8209 | 49 | MALE | T2 | N0 | 1811 | 1 | TCGA |
| TCGA-FP-8210 | 48 | MALE | T3 | N1 | 153 | 1 | TCGA |
| TCGA-FP-8211 | 62 | MALE | T3 | N1 | 413 | 0 | TCGA |
| TCGA-FP-8631 | 68 | MALE | T3 | N2 | 17 | 0 | TCGA |
| TCGA-FP-A4BE | 55 | MALE | T3 | N0 | 337 | 0 | TCGA |
| TCGA-FP-A4BF | 68 | MALE | T3 | N2 | 168 | 1 | TCGA |
| TCGA-FP-A8CX | 60 | MALE | T4 | N3 | 7 | 0 | TCGA |
| TCGA-FP-A9TM | 77 | MALE | T1 | N1 | 189 | 0 | TCGA |
| TCGA-HF-7132 | unknow | MALE | T2 | N1 | 2351 | 0 | TCGA |
| TCGA-HF-7133 | unknow | FEMALE | T2 | N3 | 1918 | 0 | TCGA |
| TCGA-HF-7134 | unknow | MALE | T1 | N0 | 1588 | 0 | TCGA |
| TCGA-HF-A5NB | 75 | FEMALE | T4 | N3 | 928 | 0 | TCGA |
| TCGA-HJ-7597 | 71 | FEMALE | T2 | N0 | 805 | 1 | TCGA |
| TCGA-HU-8238 | 56 | MALE | T3 | unknow | 46 | 0 | TCGA |
| TCGA-HU-8243 | 66 | MALE | T4 | N3 | 180 | 1 | TCGA |
| TCGA-HU-8244 | 77 | FEMALE | T1 | N0 | 742 | 0 | TCGA |
| TCGA-HU-8245 | 72 | MALE | T3 | N0 | 552 | 0 | TCGA |
| TCGA-HU-8249 | 76 | MALE | T3 | N2 | 881 | 0 | TCGA |
| TCGA-HU-8602 | 58 | FEMALE | T4 | N0 | 679 | 0 | TCGA |
| TCGA-HU-8604 | 82 | FEMALE | T3 | N0 | 694 | 0 | TCGA |
| TCGA-HU-8608 | 70 | MALE | T4 | N2 | 641 | 0 | TCGA |
| TCGA-HU-8610 | 75 | MALE | T1 | N0 | 23 | 0 | TCGA |
| TCGA-HU-A4G2 | 45 | MALE | T3 | N1 | 739 | 0 | TCGA |
| TCGA-HU-A4G3 | 54 | MALE | T2 | N2 | 170 | 0 | TCGA |

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|--------------|----|--------|----|----|------|---|------|
| TCGA-HU-A4G6 | 74 | MALE | T1 | N0 | 738 | 0 | TCGA |
| TCGA-HU-A4G8 | 71 | FEMALE | T3 | N1 | 690 | 0 | TCGA |
| TCGA-HU-A4G9 | 67 | FEMALE | T1 | N0 | 736 | 0 | TCGA |
| TCGA-HU-A4GC | 74 | MALE | T4 | N2 | 99 | 0 | TCGA |
| TCGA-HU-A4GD | 56 | MALE | T3 | N1 | 692 | 0 | TCGA |
| TCGA-HU-A4GF | 69 | MALE | T3 | N0 | 785 | 0 | TCGA |
| TCGA-HU-A4GH | 75 | MALE | T1 | N0 | 358 | 0 | TCGA |
| TCGA-HU-A4GJ | 60 | FEMALE | T4 | N3 | 650 | 0 | TCGA |
| TCGA-HU-A4GN | 61 | MALE | T2 | N1 | 912 | 0 | TCGA |
| TCGA-HU-A4GP | 62 | FEMALE | T2 | N1 | 273 | 0 | TCGA |
| TCGA-HU-A4GQ | 71 | MALE | T4 | N2 | 3 | 1 | TCGA |
| TCGA-HU-A4GT | 71 | FEMALE | T3 | N0 | 198 | 0 | TCGA |
| TCGA-HU-A4GU | 73 | MALE | T3 | N1 | 200 | 0 | TCGA |
| TCGA-HU-A4GX | 70 | FEMALE | T4 | N2 | 616 | 0 | TCGA |
| TCGA-HU-A4GY | 76 | FEMALE | T4 | N1 | 8 | 0 | TCGA |
| TCGA-HU-A4H0 | 72 | MALE | T4 | N3 | 64 | 0 | TCGA |
| TCGA-HU-A4H2 | 58 | FEMALE | T3 | N3 | 394 | 0 | TCGA |
| TCGA-HU-A4H3 | 56 | FEMALE | T4 | N3 | 882 | 0 | TCGA |
| TCGA-HU-A4H4 | 53 | FEMALE | T2 | N2 | 725 | 0 | TCGA |
| TCGA-HU-A4H5 | 71 | MALE | T2 | N0 | 724 | 0 | TCGA |
| TCGA-HU-A4H6 | 72 | FEMALE | T3 | N2 | 644 | 0 | TCGA |
| TCGA-HU-A4H8 | 77 | MALE | T1 | N1 | 270 | 0 | TCGA |
| TCGA-HU-A4HB | 68 | MALE | T2 | N2 | 477 | 1 | TCGA |
| TCGA-HU-A4HD | 73 | MALE | T3 | N2 | 1016 | 0 | TCGA |
| TCGA-IN-7806 | 50 | MALE | T3 | N1 | 1106 | 0 | TCGA |
| TCGA-IN-7808 | 59 | MALE | T3 | N3 | 105 | 1 | TCGA |
| TCGA-IN-8462 | 80 | MALE | T2 | N1 | 572 | 0 | TCGA |
| TCGA-IN-8663 | 68 | MALE | T2 | N2 | 103 | 1 | TCGA |
| TCGA-IN-A6RI | 45 | MALE | T1 | N0 | 559 | 0 | TCGA |
| TCGA-IN-A6RJ | 64 | MALE | T1 | N0 | 379 | 0 | TCGA |
| TCGA-IN-A6RL | 84 | MALE | T2 | N1 | 406 | 1 | TCGA |
| TCGA-IN-A6RN | 72 | FEMALE | T1 | N2 | 594 | 0 | TCGA |
| TCGA-IN-A6RP | 63 | MALE | T1 | N3 | 196 | 0 | TCGA |
| TCGA-IN-A6RR | 84 | MALE | T3 | N1 | 205 | 1 | TCGA |
| TCGA-IN-A6RS | 76 | MALE | T1 | N0 | 383 | 0 | TCGA |
| TCGA-IN-A7NR | 64 | FEMALE | T3 | N3 | 198 | 0 | TCGA |
| TCGA-IN-A7NT | 73 | FEMALE | T3 | N1 | 323 | 0 | TCGA |
| TCGA-IN-A7NU | 69 | MALE | T3 | N3 | 356 | 0 | TCGA |
| TCGA-IN-AB1V | 63 | MALE | T1 | N0 | 479 | 0 | TCGA |
| TCGA-IN-AB1X | 78 | FEMALE | T3 | N0 | 411 | 0 | TCGA |
| TCGA-IP-7968 | 74 | MALE | T3 | N2 | 77 | 0 | TCGA |
| TCGA-KB-A6F5 | 73 | MALE | T3 | N2 | 169 | 0 | TCGA |
| TCGA-KB-A6F7 | 54 | FEMALE | T1 | N1 | 1935 | 0 | TCGA |
| TCGA-KB-A93G | 68 | MALE | T2 | N0 | 613 | 0 | TCGA |

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|--------------|----|--------|----|--------|------|---|------|
| TCGA-KB-A93H | 79 | FEMALE | T3 | N1 | 1145 | 0 | TCGA |
| TCGA-KB-A93J | 78 | MALE | T2 | N1 | 1124 | 0 | TCGA |
| TCGA-MX-A5UG | 78 | MALE | T3 | N1 | 113 | 1 | TCGA |
| TCGA-MX-A5UJ | 86 | FEMALE | T3 | N2 | 600 | 0 | TCGA |
| TCGA-MX-A663 | 66 | MALE | T3 | N0 | 300 | 1 | TCGA |
| TCGA-MX-A666 | 61 | MALE | T2 | unknow | 427 | 0 | TCGA |
| TCGA-R5-A7O7 | 51 | MALE | T3 | N1 | 1389 | 0 | TCGA |
| TCGA-R5-A7ZE | 66 | FEMALE | T3 | N2 | 554 | 1 | TCGA |
| TCGA-R5-A7ZF | 65 | FEMALE | T4 | N1 | 259 | 1 | TCGA |
| TCGA-R5-A7ZI | 44 | FEMALE | T4 | N1 | 2267 | 0 | TCGA |
| TCGA-R5-A7ZR | 70 | FEMALE | T3 | unknow | 185 | 1 | TCGA |
| TCGA-R5-A804 | 54 | MALE | T3 | N2 | 140 | 1 | TCGA |
| TCGA-R5-A805 | 71 | MALE | T3 | N2 | 281 | 1 | TCGA |
| TCGA-RD-A7BS | 46 | MALE | T3 | N1 | 336 | 1 | TCGA |
| TCGA-RD-A7BT | 66 | MALE | T3 | N3 | 262 | 1 | TCGA |
| TCGA-RD-A7BW | 68 | FEMALE | T2 | N0 | 156 | 1 | TCGA |
| TCGA-RD-A7C1 | 82 | MALE | T2 | N0 | 507 | 1 | TCGA |
| TCGA-RD-A8MV | 56 | MALE | T3 | N2 | 3720 | 0 | TCGA |
| TCGA-RD-A8MW | 72 | MALE | T3 | N2 | 1153 | 1 | TCGA |
| TCGA-RD-A8N0 | 53 | FEMALE | T3 | N2 | 1236 | 0 | TCGA |
| TCGA-RD-A8N1 | 70 | MALE | T3 | N2 | 3519 | 0 | TCGA |
| TCGA-RD-A8N2 | 59 | FEMALE | T2 | N0 | 3540 | 0 | TCGA |
| TCGA-RD-A8N4 | 58 | FEMALE | T3 | N1 | 2171 | 0 | TCGA |
| TCGA-RD-A8N5 | 78 | MALE | T3 | N1 | 1747 | 1 | TCGA |
| TCGA-RD-A8N6 | 78 | FEMALE | T2 | N2 | 272 | 1 | TCGA |
| TCGA-RD-A8N9 | 63 | FEMALE | T2 | N1 | 1083 | 0 | TCGA |
| TCGA-RD-A8NB | 80 | FEMALE | T3 | N1 | 513 | 1 | TCGA |
| TCGA-SW-A7EA | 61 | FEMALE | T2 | N0 | 579 | 0 | TCGA |
| TCGA-SW-A7EB | 45 | MALE | T3 | N2 | 176 | 0 | TCGA |
| TCGA-VQ-A8DL | 69 | FEMALE | T3 | N0 | 28 | 1 | TCGA |
| TCGA-VQ-A8DT | 43 | MALE | T3 | N3 | 1484 | 0 | TCGA |
| TCGA-VQ-A8DU | 63 | MALE | T3 | N2 | 166 | 1 | TCGA |
| TCGA-VQ-A8DV | 48 | MALE | T2 | N0 | 403 | 1 | TCGA |
| TCGA-VQ-A8DZ | 70 | MALE | T4 | N3 | 396 | 1 | TCGA |
| TCGA-VQ-A8E0 | 68 | MALE | T3 | N2 | 562 | 1 | TCGA |
| TCGA-VQ-A8E2 | 57 | MALE | T3 | N2 | 1319 | 0 | TCGA |
| TCGA-VQ-A8E3 | 79 | MALE | T3 | N0 | 661 | 1 | TCGA |
| TCGA-VQ-A8E7 | 59 | MALE | T3 | N1 | 1138 | 0 | TCGA |
| TCGA-VQ-A8P2 | 68 | MALE | T4 | N1 | 1160 | 0 | TCGA |
| TCGA-VQ-A8P3 | 72 | MALE | T4 | N1 | 1132 | 0 | TCGA |
| TCGA-VQ-A8P5 | 67 | MALE | T3 | N0 | 235 | 1 | TCGA |
| TCGA-VQ-A8P8 | 72 | FEMALE | T4 | N0 | 942 | 0 | TCGA |
| TCGA-VQ-A8PB | 65 | FEMALE | T3 | N0 | 1043 | 1 | TCGA |
| TCGA-VQ-A8PC | 65 | MALE | T3 | N1 | 1407 | 1 | TCGA |

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|--------------|----|--------|----|--------|------|---|------|
| TCGA-VQ-A8PD | 69 | MALE | T4 | N3 | 496 | 1 | TCGA |
| TCGA-VQ-A8PE | 78 | MALE | T3 | N3 | 675 | 1 | TCGA |
| TCGA-VQ-A8PF | 76 | MALE | T3 | N3 | 76 | 1 | TCGA |
| TCGA-VQ-A8PH | 62 | MALE | T3 | N3 | 389 | 1 | TCGA |
| TCGA-VQ-A8PJ | 53 | MALE | T4 | N2 | 82 | 1 | TCGA |
| TCGA-VQ-A8PK | 58 | MALE | T3 | N3 | 543 | 1 | TCGA |
| TCGA-VQ-A8PM | 56 | MALE | T4 | N3 | 57 | 1 | TCGA |
| TCGA-VQ-A8PO | 74 | MALE | T4 | N0 | 282 | 1 | TCGA |
| TCGA-VQ-A8PP | 76 | MALE | T4 | N1 | 712 | 1 | TCGA |
| TCGA-VQ-A8PQ | 50 | FEMALE | T4 | N1 | 476 | 1 | TCGA |
| TCGA-VQ-A8PS | 76 | MALE | T3 | N1 | 406 | 1 | TCGA |
| TCGA-VQ-A8PT | 65 | MALE | T4 | N0 | 900 | 0 | TCGA |
| TCGA-VQ-A8PU | 72 | FEMALE | T4 | N1 | 832 | 1 | TCGA |
| TCGA-VQ-A8PX | 51 | MALE | T1 | N0 | 1964 | 0 | TCGA |
| TCGA-VQ-A8PY | 47 | FEMALE | T3 | N2 | 436 | 1 | TCGA |
| TCGA-VQ-A8PZ | 56 | FEMALE | T3 | N0 | 2233 | 0 | TCGA |
| TCGA-VQ-A91A | 67 | MALE | T3 | N3 | 1200 | 0 | TCGA |
| TCGA-VQ-A91D | 70 | MALE | T4 | N2 | 356 | 1 | TCGA |
| TCGA-VQ-A91E | 67 | FEMALE | T4 | N0 | 664 | 0 | TCGA |
| TCGA-VQ-A91K | 69 | MALE | T3 | N1 | 1862 | 0 | TCGA |
| TCGA-VQ-A91N | 59 | FEMALE | T4 | N3 | 570 | 1 | TCGA |
| TCGA-VQ-A91Q | 61 | MALE | T3 | N3 | 633 | 1 | TCGA |
| TCGA-VQ-A91S | 63 | MALE | T4 | N1 | 1000 | 0 | TCGA |
| TCGA-VQ-A91U | 78 | MALE | T3 | N1 | 52 | 1 | TCGA |
| TCGA-VQ-A91V | 58 | MALE | T3 | N2 | 1297 | 0 | TCGA |
| TCGA-VQ-A91W | 30 | MALE | T3 | N1 | 1851 | 0 | TCGA |
| TCGA-VQ-A91X | 74 | MALE | T3 | N2 | 289 | 1 | TCGA |
| TCGA-VQ-A91Y | 67 | MALE | T4 | N3 | 296 | 1 | TCGA |
| TCGA-VQ-A91Z | 67 | FEMALE | T3 | N1 | 1690 | 0 | TCGA |
| TCGA-VQ-A922 | 70 | MALE | T4 | N1 | 275 | 1 | TCGA |
| TCGA-VQ-A923 | 90 | MALE | T3 | N1 | 0 | 1 | TCGA |
| TCGA-VQ-A924 | 69 | MALE | T3 | N0 | 1686 | 1 | TCGA |
| TCGA-VQ-A925 | 66 | MALE | T3 | N2 | 138 | 1 | TCGA |
| TCGA-VQ-A927 | 81 | MALE | T3 | N3 | 200 | 1 | TCGA |
| TCGA-VQ-A928 | 49 | MALE | T3 | N3 | 174 | 1 | TCGA |
| TCGA-VQ-A92D | 67 | MALE | T2 | N0 | 2032 | 0 | TCGA |
| TCGA-VQ-A94O | 74 | MALE | T4 | N3 | 640 | 1 | TCGA |
| TCGA-VQ-A94P | 57 | MALE | T4 | unknow | 81 | 1 | TCGA |
| TCGA-VQ-A94R | 63 | MALE | T4 | N2 | 1294 | 1 | TCGA |
| TCGA-VQ-A94T | 73 | MALE | T3 | N2 | 342 | 1 | TCGA |
| TCGA-VQ-A94U | 70 | MALE | T4 | N0 | 819 | 0 | TCGA |
| TCGA-VQ-AA64 | 68 | MALE | T3 | N2 | 560 | 1 | TCGA |
| TCGA-VQ-AA68 | 52 | FEMALE | T4 | N3 | 1328 | 0 | TCGA |
| TCGA-VQ-AA69 | 35 | MALE | T3 | N2 | 864 | 0 | TCGA |

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|--------------|----|--------|----|----|------|---|------|
| TCGA-VQ-AA6A | 56 | MALE | T4 | N3 | 1184 | 0 | TCGA |
| TCGA-VQ-AA6B | 48 | MALE | T3 | N2 | 1002 | 0 | TCGA |
| TCGA-VQ-AA6D | 52 | FEMALE | T4 | N1 | 521 | 0 | TCGA |
| TCGA-VQ-AA6F | 57 | MALE | T3 | N1 | 1646 | 0 | TCGA |
| TCGA-VQ-AA6G | 68 | MALE | T3 | N0 | 792 | 1 | TCGA |
| TCGA-VQ-AA6I | 68 | MALE | T3 | N3 | 491 | 1 | TCGA |
| TCGA-VQ-AA6J | 75 | MALE | T4 | N2 | 838 | 0 | TCGA |
| TCGA-VQ-AA6K | 59 | MALE | T4 | N3 | 378 | 1 | TCGA |
| TCGA-ZA-A8F6 | 71 | MALE | T2 | N0 | 525 | 0 | TCGA |
| TCGA-ZQ-A9CR | 79 | FEMALE | T4 | N3 | 24 | 1 | TCGA |

Table S3: Univariate Cox regression analysis and Kaplan–Meier analysis of 91 AAM genes associated with OS in GC patients

| Gene | HR | HR.95L | HR.95H | pvalue | km |
|----------|-------------------|---------------------|----------------------|-------------------|-------------------|
| ADI1 | 1.00174646397098 | 0.982368851655377 | 0.327261274863479 | 0.858118587898907 | 1.1694141022343 |
| ALDH18A1 | 0.799712349528558 | 0.00995767210312522 | 0.0028404816083667 | 0.674710662806953 | 0.947872736037478 |
| ALDH4A1 | 0.9719597370333 | 0.715625061699372 | 0.100446981316063 | 0.834059744240584 | 1.13265954499938 |
| ALDH5A1 | 0.836274426383648 | 0.00188651702777313 | 0.000416559574462738 | 0.747090555188134 | 0.936104614583418 |
| ALDH6A1 | 0.991062396651671 | 0.917708368238673 | 0.0631509025289497 | 0.835868823165565 | 1.17507035414623 |
| AMT | 0.944557720924208 | 0.351166158653554 | 0.0258622698042629 | 0.837825001720617 | 1.06488740050162 |
| ARG1 | 1.42983696883856 | 0.032964163291279 | 0.0202950589517812 | 1.02935506403356 | 1.98613076176676 |
| ASL | 1.00082365612439 | 0.991295879436772 | 0.096904617856806 | 0.863212020737436 | 1.16037307937682 |
| ASMTL | 1.11985135472322 | 0.188820328169196 | 0.00665898919465457 | 0.945882061001551 | 1.32581757111194 |
| ASPA | 1.12868168760335 | 0.221200690666622 | 0.0136266557409527 | 0.929703860312815 | 1.37024530747081 |
| ASRGL1 | 0.964332265440422 | 0.592914729544902 | 0.0409067796289762 | 0.844111970629395 | 1.10167460067658 |
| ATF4 | 0.898894273141465 | 0.37079405912389 | 0.103273453290716 | 0.711759789330325 | 1.13522978735109 |
| BAAT | 1.03341637629638 | 0.409865079176275 | 0.166309429265701 | 0.95570852463128 | 1.11744258764414 |
| BBOX1 | 1.06273930288991 | 0.537879211440503 | 0.181748769256794 | 0.875681882353449 | 1.28975470278266 |
| BCAT1 | 1.05284443491271 | 0.308017808268028 | 0.0100512736549896 | 0.953597113351494 | 1.16242109860298 |

BCKDHA 0.903658613966065 0.744884372003528 1.09627604133867
0.304148079876206 0.036665976937089
BCKDHB 0.876415332096402 0.731271007705279 1.05036823043751
0.153290168409827 0.0129485811877016
BCKDK 1.10859381307574 0.88847167535153 1.38325202309184
0.361315104038893 0.0223563855177843
BPHL 0.988564561357313 0.834644088745518 1.17087020102234
0.894043263438464 0.068935225436323
CDO1 1.25749393806685 1.12329660047948 1.40772348425153
6.91380819554865e-05 5.50210532157536e-05
COLQ 1.13849597747286 0.890515906617442 1.45553053133583
0.300740050290794 0.0694668183649071
DCT 1.36630300284808 0.63250048809065 2.95143471150039
0.427047030892985 0.0316487568495282
DDAH1 0.864266858280976 0.764766791227345 0.976712392445944
0.0194106309681599 0.00520172855819467
DDAH2 1.14327401370393 0.998065289170769 1.30960918548392
0.0533569740932295 9.41054522721751e-05
DDO 1.06246262139361 0.882944510672644 1.27847991375882
0.521117919984694 0.049553230046522
DHPS 0.923561022545136 0.71434604126805 1.19405010049542
0.544022744878366 0.0188708212736672
DIO1 1.20641085628642 1.01756474724529 1.43030422202205
0.0307391248526856 0.0443657947961452
DIO2 1.11992317618927 1.01929994537434 1.23047972901171
0.0183768040427819 0.00377396722434864
ETNK1 0.90983385480201 0.795845213344879 1.040149050925
0.166484493221839 0.0129708999219375
FAH 1.252048809374 1.0711959121544 1.46343558938909 0.00474250906988168
0.000660120646866491
FARS2 1.14875821134392 0.905303685610694 1.4576825976798
0.253759860268709 0.00481266737780217
FPGS 0.92060035262286 0.728540781736865 1.16329110256375
0.488318753964278 0.00025197574203073
GAD1 0.81982051860333 0.736465329923223 0.912610078729845
0.00028173374820204 0.000958238277350754
GAD2 1.451922503893 0.920207755413119 2.29087284356185
0.109027145811798 0.0805120219676523
GAMT 1.05321958510304 0.960628975762248 1.15473457748287
0.269410135753702 0.0356167154234883
GATM 1.02478091632845 0.953931819942761 1.10089201818846
0.503057374081466 0.0735196558226684
GCLC 0.953667616874221 0.800296257925679 1.13643155827303
0.595897468115777 0.173803326893341

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|-------|----------------------|----------------------|-------------------|
| GCLM | 1.15181962433143 | 0.973180407147603 | 1.36325026403227 |
| | 0.100218087004504 | 0.0428118361484553 | |
| GCSH | 0.977667177621329 | 0.804518896388809 | 1.18808037261578 |
| | 0.82034492083209 | 0.0460430815137004 | |
| GGT1 | 0.96336395171671 | 0.86745409490799 | 1.06987805915617 |
| | 0.485443429746908 | 0.00778135333840169 | |
| GGT5 | 1.22058746150676 | 1.0850364790562 | 1.37307250027523 |
| | 0.000904068720004667 | 4.98633577727947e-06 | |
| GLDC | 0.971985116251252 | 0.898251654033474 | 1.05177102872193 |
| | 0.480223918784569 | 0.0676942117183205 | |
| GLS2 | 0.571256507883707 | 0.442996654196104 | 0.736651156861848 |
| | 1.58991431827653e-05 | 9.22527976232601e-09 | |
| GLUD1 | 0.92360768917798 | 0.76226863320075 | 1.11909519341855 |
| | 0.417211325467283 | 0.0495523610545477 | |
| GLUD2 | 1.0638826489952 | 0.858433006683366 | 1.31850276261631 |
| | 0.571636635352258 | 0.211829504059333 | |
| GOT1 | 0.736858847460897 | 0.617131728922253 | 0.87981371826339 |
| | 0.000737276152581613 | 6.3079321200199e-05 | |
| GOT2 | 0.825919893942639 | 0.681684837652132 | 1.00067308752189 |
| | 0.0508085966776446 | 0.00555708806906674 | |
| GSS | 0.888858515100246 | 0.746624324857068 | 1.05818874842775 |
| | 0.18541972031342 | 0.0136893855710744 | |
| GSTZ1 | 0.792834194076367 | 0.647317507880444 | 0.971062966232669 |
| | 0.0248462744999556 | 0.0129265844741671 | |
| HDC | 1.0813914674453 | 0.979785039635591 | 1.19353476380741 |
| | 0.120111411515459 | 0.0150463709539435 | |
| HGD | 1.04374351918494 | 0.957486623790451 | 1.13777102130984 |
| | 0.330639080158697 | 0.0574359354993736 | |
| HPD1 | 1.16184700494843 | 0.971661232639785 | 1.38925833156923 |
| | 0.100018853987814 | 0.000135467488746155 | |
| HPRT1 | 0.928503141017326 | 0.77985218748765 | 1.10548908717742 |
| | 0.404650425788632 | 0.0262600771276817 | |
| MARS2 | 0.751839315988572 | 0.626449090455626 | 0.902327684209806 |
| | 0.00218385881882696 | 0.000161471513919098 | |
| MAT1A | 1.01946234650283 | 0.889628525532191 | 1.16824432457956 |
| | 0.78153065363508 | 0.160692058280003 | |
| MAT2B | 0.883348583793041 | 0.725291346645473 | 1.07585003474554 |
| | 0.217531679841845 | 0.0279656657884771 | |
| MCCC2 | 0.888283051986453 | 0.756174930502154 | 1.04347122420785 |
| | 0.149303638836523 | 0.00833293866524931 | |
| MSRA | 0.966251609375152 | 0.844127314613349 | 1.10604426187503 |
| | 0.618498000676938 | 0.0810515303577689 | |
| MTHFR | 0.774206042260862 | 0.647090535273415 | 0.926292324179899 |
| | 0.00516316234074466 | 0.000941858441157239 | |

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|----------|----------------------|----------------------|-------------------|
| NFS1 | 0.756247001058717 | 0.638144530973139 | 0.896206891780721 |
| | 0.00126041506877505 | 0.000103304450621233 | |
| OAZ1 | 0.847231128548354 | 0.628373665924973 | 1.14231487426308 |
| | 0.276905575045745 | 0.0174622047105574 | |
| OTUB2 | 0.956804999301164 | 0.809056388100743 | 1.13153523061202 |
| | 0.605878009843561 | 0.0242287569942863 | |
| P4HB | 1.09450293763531 | 0.919530139203443 | 1.30277043613825 |
| | 0.309614310840122 | 0.0659715246773801 | |
| PAH1 | 1.01895530362876 | 0.862340710242213 | 1.20401356269213 |
| | 0.825452147803527 | 0.00379635747601759 | |
| PEPD | 1.20055968371531 | 1.00704849097877 | 1.43125536364365 |
| | 0.0415212641056748 | 0.0159555848018774 | |
| PLOD1 | 1.16208859617085 | 0.980314578004041 | 1.3775679110066 |
| | 0.0834733771652625 | 0.0252859868291549 | |
| PRG3 | 1.11384197201441 | 0.644012608751838 | 1.92642802603733 |
| | 0.699708799241656 | 0.0211082062719685 | |
| PTS | 1.01356930406881 | 0.813775914163853 | 1.26241477078624 |
| | 0.904227962965163 | 0.0771674166000599 | |
| PYCR1 | 0.99111948397238 | 0.87164683189233 | 1.12696770706673 |
| | 0.891735530690999 | 0.153156643414112 | |
| QDPR | 0.823011217104925 | 0.680181448362126 | 0.995833486949077 |
| | 0.0451884560068993 | 0.00765673361105756 | |
| SARS2 | 0.903810704938695 | 0.74900672650851 | 1.09060941838217 |
| | 0.291384712520831 | 0.0103293012786352 | |
| SCLY | 0.609496333366849 | 0.473027149042266 | 0.785337123122379 |
| | 0.000128981983105709 | 0.000715864600808858 | |
| SDS | 1.0104080667276 | 0.908799231630868 | 1.12337733767241 |
| | 0.125812833533185 | | 0.848150049064186 |
| SLC25A15 | 0.761596041797367 | 0.655975033278384 | 0.884223486346107 |
| | 0.000349778489485684 | 0.00102849904335112 | |
| SLC3A1 | 1.01137484719326 | 0.941911355901881 | 1.08596108872239 |
| | 0.755380567296961 | 0.115560582353611 | |
| SLC5A7 | 1.21823651443969 | 0.926891865377868 | 1.60115787024318 |
| | 0.156903622325038 | 0.00182061284675883 | |
| SLC6A14 | 0.970913931617269 | 0.908099851745129 | 1.03807291763888 |
| | 0.387047551812105 | 0.0709696221494099 | |
| SLC6A6 | 1.06036556310239 | 0.899292950984454 | 1.25028793585293 |
| | 0.485639661757652 | 0.0499452720331957 | |
| SLC7A2 | 1.15279911317564 | 1.06688611154273 | 1.24563042011754 |
| | 0.000320156932551117 | 2.60307587429676e-06 | |
| SLC7A4 | 1.02316782616606 | 0.93041887588225 | 1.12516246997753 |
| | 0.636635380231267 | 0.135735265454388 | |
| SLC7A5 | 0.986085933061717 | 0.904153584406813 | 1.07544280546113 |
| | 0.751552906431935 | 0.0673805410979365 | |

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|---------|----------------------|----------------------|-------------------|
| SLC7A6 | 0.819373091435239 | 0.689246332764805 | 0.974067225392457 |
| | 0.0239617476645511 | 0.00032347241040831 | |
| SLC7A7 | 1.00418993187887 | 0.886642606077796 | 1.13732118485452 |
| | 0.947516447631222 | 0.0102821166883966 | |
| SLC7A8 | 0.926776722584183 | 0.820516785709604 | 1.0467977114948 |
| | 0.221001444290149 | 0.0168755160267675 | |
| SLC7A9 | 0.998669874130724 | 0.929352205571036 | 1.07315774527426 |
| | 0.971071525253462 | 0.00991778616183858 | |
| SMSO | 0.953779868817382 | 0.800235873884654 | 1.13678487537092 |
| | 0.597213734442098 | 0.0202726898671511 | |
| SNCAIP | 1.06528440042038 | 0.985255087672938 | 1.15181425397087 |
| | 0.112476373523116 | 0.000942817151252662 | |
| SULT1B1 | 0.969501081987901 | 0.894766297936978 | 1.05047804118558 |
| | 0.449187959818148 | 0.033811632046732 | |
| TGFB2 | 1.27789496188588 | 1.1423749258349 | 1.42949175151043 |
| | 1.80974008142564e-05 | 1.86341887198349e-06 | |
| TYR | 2.50909620519858 | 1.32737835151791 | 4.74285553907269 |
| | 0.0046295745132407 | 1.07303122397484e-05 | |
| YOD1 | 0.944245460977272 | 0.815421954980489 | 1.09342100139739 |
| | 0.443334811615382 | 0.18595490964165 | |

Table S4: Univariate Cox regression analysis of 51 AAM genes associated with OS in GC patients

| Gene | HR | HR.95L | HR.95H | pvalue |
|-----------|----------------------|--------|------------------|------------------|
| ABCA8 | 1.17882522730858 | | 1.08485972039834 | 1.28092958970666 |
| | 0.000103696663481678 | | | |
| C14orf132 | 1.18011942485332 | | 1.08772988686242 | 1.28035634005916 |
| | 6.84191570938418e-05 | | | |
| MFAP4 | 1.10462498705652 | | 1.03768800093171 | 1.17587980292152 |
| | 0.00180905263181363 | | | |
| SETBP1 | 1.1339809558188 | | 1.03389065011499 | 1.24376094127237 |
| | 0.00765569863961746 | | | |
| OGN | 1.0954012441409 | | 1.03826834731432 | 1.15567799863034 |
| | 0.000855906380018473 | | | |
| RGMA | 1.12116570143558 | | 1.05528916213135 | 1.19115459078227 |
| | 0.000214079043842086 | | | |
| FHL1 | 1.12422718905317 | | 1.06074747771842 | 1.1915058005369 |
| | 7.85925376397373e-05 | | | |
| SFRP1 | 1.09279669071199 | | 1.03527359267519 | 1.15351595528019 |
| | 0.00129788834513371 | | | |
| PODN | 1.14685302297636 | | 1.06995568561618 | 1.22927694482278 |
| | 0.000109077928077847 | | | |
| RERG | 1.18100922176595 | | 1.09038421840114 | 1.27916633270923 |
| | 4.42322813697123e-05 | | | |

| | | | |
|----------|--|-------------------|-------------------|
| MGP | 1.14864117160047 1.30097383906572e-05 | 1.07926762182168 | 1.22247393919662 |
| SPARCL1 | 1.16019620377598 2.47950526517536e-05 | 1.08277016799795 | 1.24315877093757 |
| C7 | 1.10080906898222 0.000111165726996023 | 1.04847645355646 | 1.15575376275081 |
| SVEP1 | 1.16151444826887 0.000262138799070512 | 1.07178797730792 | 1.25875251645013 |
| FBLN1 | 1.11222089269384 0.00135556233203594 | 1.04216006329529 | 1.18699167019815 |
| CYBRD1 | 1.16456351410663 0.000201724259591929 | 1.0746674177551 | 1.26197943287551 |
| PGM5 | 1.09875052922391 0.000995671546506279 | 1.03883615476985 | 1.1621204363428 |
| FRZB | 1.12495353719087 0.00159496220523995 | 1.04565133546742 | 1.21027001822988 |
| RCAN2 | 1.12779767057667 0.00425754130409298 | 1.03852578423986 | 1.22474338630805 |
| HSPB8 | 1.14173414764464 2.83115752151946e-05 | 1.07304044418054 | 1.21482547183328 |
| PBK | 0.871959358025581 0.0035126628711943 | 0.795318489219901 | 0.955985724403499 |
| CHRD12 | 1.12001747270527 0.000121005182346884 | 1.05712604659836 | 1.18665048808669 |
| CH25H | 1.14766062518601 0.00192246135881624 | 1.05201146787862 | 1.25200622884685 |
| SPON1 | 1.12541000760327 0.000237022814455758 | 1.0567010680212 | 1.19858654783547 |
| PPP1R14A | 1.18878804676826 2.15008296869133e-06 | 1.10672868890217 | 1.27693176684609 |
| PTGIS | 1.07753002789566 0.0259753876693945 | 1.00898141274845 | 1.150735728475 |
| THBS4 | 1.0895934476232 0.000167267765135649 | 1.04198145061962 | 1.13938101335434 |
| RAI21 | 1.17182827487594 0.00213693875083002 | 1.05902644144892 | 1.29664515639478 |
| APOD | 1.12070233178318 2.7804716676723e-06 | 1.06854368592275 | 1.17540698898019 |
| CPE | 1.15229796341795 0.000214933427918499 | 1.06895546114065 | 1.24213837223893 |
| RBPMS2 | 1.1446063745883 8.44829838258775e-06 | 1.07855388310704 | 1.21470403404793 |
| EFEMP1 | 1.1382095521346 0.000535666836759358 | 1.05777947825036 | 1.22475526440853 |

| | | | |
|---------|--|-------------------|-------------------|
| PALM | 1.14623424705007 0.00372030261126714 | 1.04526555765193 | 1.25695612898781 |
| PPP1R3C | 1.13992238949547 0.000164461556107565 | 1.06485923325882 | 1.22027683424072 |
| PSAT1 | 0.893872858172021 0.00793140964814335 | 0.822822943092409 | 0.971057860362655 |
| ZSCAN18 | 1.13285479536731 0.00649546340482605 | 1.03552710354082 | 1.23933017590604 |
| MYH11 | 1.09662699007269 4.1010364840195e-05 | 1.04934223868804 | 1.1460424549949 |
| PTGER1 | 1.11907203302804 0.00906681658809494 | 1.02839912802108 | 1.21773947583495 |
| CGNL1 | 1.10194085880887 0.0291326630661333 | 1.00991426359558 | 1.2023532096569 |
| PDK4 | 1.15629396836594 1.74392222652968e-05 | 1.08215755102125 | 1.23550932118682 |
| RGS5 | 1.18522148598597 0.000226311803251064 | 1.08286866540931 | 1.29724870218847 |
| CBX6 | 1.11422287163255 0.0202897388698102 | 1.01696423330989 | 1.22078296070298 |
| KIT | 1.13846378038783 0.00229888135923155 | 1.04739762864079 | 1.23744769303793 |
| SGCE | 1.27323445506077 2.51008385594641e-07 | 1.16154651453583 | 1.39566169521994 |
| DES | 1.07860741124751 1.97275466534454e-05 | 1.04176940944061 | 1.11674804141422 |
| ACTG2 | 1.10373951592336 2.72389341986843e-05 | 1.05400002415152 | 1.15582627238688 |
| MATN2 | 1.10558262391399 0.00870478069594842 | 1.02570931378293 | 1.19167577195192 |
| REEP1 | 1.11769653632824 0.00523426307044846 | 1.03372240054092 | 1.20849228638796 |
| MYOM1 | 1.15152032928628 0.000969827147252959 | 1.05893945904317 | 1.25219535209096 |
| CPA3 | 1.10192043228343 0.00526132107831538 | 1.02930965756953 | 1.17965340182547 |
| AGMAT | 0.877865576026485 0.00635477904324659 | 0.799459508606213 | 0.963961227899922 |